



**Institute
of Animal Reproduction and Food Research
Polish Academy of Sciences
in Olsztyn**

mgr inż. Anna Wójtowicz

**The effect of Th1 and Th2 cell subsets and their
mediators on the processes associated with the
development of fibrosis in the progression of
endometriosis in the mare**

A doctoral thesis was completed in the Reproductive Immunology and Pathology Group
at the Institute of Animal Reproduction and Food Research,
Polish Academy of Sciences in Olsztyn,
under the supervision of dr hab. Anna Szóstek-Mioduchowska

Doctoral thesis carried out under the project Sonata 2019/35/D/NZ9/02989 funded by
the National Science Centre, Poland

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ABSTRACT

THE EFFECT OF Th1 AND Th2 CELL SUBSETS AND THEIR MEDIATORS ON THE PROCESSES ASSOCIATED WITH THE DEVELOPMENT OF FIBROSIS IN THE PROGRESSION OF ENDOMETROSIS IN THE MARE

mgr inż. Anna Wójtowicz

A doctoral thesis was completed under the supervision of dr hab. Anna Szóstek-Mioduchowska at the Institute of Animal Reproduction and Food Research, Polish Academy of Sciences in Olsztyn.

Mare endometriosis is a chronic, degenerative condition of the endometrium, characterized by the progressive accumulation of extracellular matrix (ECM) components within the endometrial stroma accompanied by disruption of glandular structures. This condition compromises the functional capacity of the endometrium, thereby contributing to infertility in mares. The results of the recent study suggest the involvement of T helper (Th) cells in the progression of endometriosis in mares. T helper 1 cell-secreted cytokines, such as interferon (IFN)- γ , modulate inflammation and processes associated with the development of tissue fibrosis. In turn, Th2 cell-secreted cytokines, including interleukin (IL)-4 and IL-13, modulate tissue repair by affecting fibroblast activity, collagen (COL) production, and tissue remodeling. However, to date, there has been no study about the effect of Th cells on the processes associated with the development of fibrosis in the progression of endometriosis in the mare. Thus, the main aim of the study was to determine the impact of two distinct subsets of Th cells: Th1 and Th2 cells, as well as their mediators: IFN- γ , IL-4, and IL-13 on cellular and molecular processes in mare endometrial fibroblasts. The primary hypothesis of the study postulated that Th1 cells and IFN- γ exert anti-fibrotic effects, whereas Th2 cells as well as IL-4 and IL-13 exert pro-fibrotic effects in the development of endometrial fibrosis in the progression of endometriosis in the mare.

The first research task included the determination of changes in the amount of Th1 and Th2 cells as well as the expression of IFN- γ , IL-4, and IL-13 and their receptors in the endometrium of mares in the mid-luteal and follicular phases of the oestrous cycle at each stage of endometriosis, according to Kenney and Doig (1986). In the second research task, the effect of the Th1 and Th2 cell secretome on the functional characteristics, expression of selected ECM-associated markers, and the transcriptomic profile of endometrial fibroblasts derived from non-fibrotic (category I) endometria was determined. In the third research task, the influence of IFN- γ , IL-4, and IL-13 on the

functional characteristics, expression of selected ECM-associated markers, and transcriptome in fibroblasts derived from the non-fibrotic (category I) and fibrotic (category IIB) endometrium was investigated.

The obtained results demonstrated that Th1 cells affected the expression of genes involved in the cell cycle, metabolism, and those crucial for ECM deposition, such as ECM-receptor interaction, protein digestion and absorption, focal adhesion, NF- κ B, and JAK-STAT signaling pathways as well as collagen binding. Interferon γ affected mare endometrial fibroblast proliferation but did not affect transcriptomic profile and the gene expression of ECM-associated markers in mare endometrial fibroblasts. T helper 2 cells regulated the expression of genes annotated to tissue remodeling and cell cycle as well as NF- κ B, TGF- β , and AGE-RAGE signaling pathways, which suggest their role as pro-fibrotic mediators. Moreover, IL-4 stimulated fibroblast proliferation and affected the turnover of ECM by increasing fibronectin and COL3 protein abundance, while simultaneously decreasing the metalloproteinase expression and activity and enhancing tissue metalloproteinase inhibitor level as well as the expression of genes involved in canonical glycolysis, cell cycle, cholesterol and fatty acid biosynthetic processes, cell-matrix, and focal adhesion, ECM organization, HIF-1, PI3K-Akt, and IGFR signaling pathways which suggest the role of IL-4 as a pro-fibrotic factor. Interleukin-13 increased fibroblast proliferation, affected the turnover of ECM and the expression of genes annotated to biological processes including cell-matrix adhesion, ECM organization, and ECM-receptor interactions which indicate the pro-fibrotic properties of IL-13. Furthermore, the different responses of fibroblasts derived from categories I and IIB endometria to the examined cytokines may result from variations in intracellular signaling or cellular microenvironment, as well as adaptive changes in fibroblasts due to excessive ECM production during fibrosis.

STRESZCZENIE

WPLYW SUBPOPULACJI LIMFOCYTÓW POMOCNICZYCH Th1 i Th2 ORAZ ICH MEDIATORÓW NA PROCESY ZWIĄZANE Z ROZWOJEM WŁÓKNIENIA W PRZEBIEGU ENDOMETROSIS U KLACZY

mgr inż. Anna Wójtowicz

Praca doktorska została wykonana pod kierunkiem dr hab. Anny Szóstek-Mioduchowskiej w Instytucie Rozrodu Zwierząt i Badań Żywności Polskiej Akademii Nauk w Olsztynie.

Endometrosis to chroniczne, degenerujące zapalenie błony śluzowej macicy u klaczy, charakteryzujące się postępującym nagromadzeniem składników macierzy pozakomórkowej (ECM) w zrębie łącznotkankowym błony śluzowej macicy, czemu towarzyszą zmiany w obrębie nabłonka gruczołowego. Zmiany histologiczne zaburzają funkcje błony śluzowej macicy, co w konsekwencji przyczynia się do niepłodności u klaczy. Wyniki badań wskazują na potencjalny udział limfocytów pomocniczych T (Th) w przebiegu endometrosis u klaczy. Cytokiny uwalniane przez limfocyty Th1, takie jak interferon (IFN)- γ , regulują stan zapalny oraz procesy związane z rozwojem włóknienia tkanek. Z kolei cytokiny wydzielane przez limfocyty Th2, w tym interleukina (IL)-4 i IL-13, wpływają na procesy naprawcze tkanek poprzez zmianę aktywności fibroblastów, produkcję kolagenu oraz przebudowę tkanek. Dotychczas jednak nie przeprowadzono badań dotyczących wpływu limfocytów pomocniczych Th na procesy związane z włóknieniem błony śluzowej macicy w przebiegu endometrosis u klaczy. Dlatego głównym celem pracy było określenie wpływu dwóch subpopulacji limfocytów pomocniczych Th: Th1 i Th2 oraz ich mediatorów: IFN- γ , IL-4 i IL-13 na procesy komórkowe i molekularne zachodzące w fibroblastach błony śluzowej macicy klaczy. Hipoteza pracy zakładała, że limfocyty pomocnicze Th1 i IFN- γ wykazują działanie hamujące włóknienie, natomiast limfocyty pomocnicze Th2 oraz IL-4 i IL-13 sprzyjają procesom włóknienia błony śluzowej macicy w przebiegu endometrosis u klaczy.

Pierwsze zadanie badawcze obejmowało określenie zmian w ilości limfocytów Th1 i Th2, a także ekspresji IFN- γ , IL-4 i IL-13 oraz ich receptorów w błonie śluzowej macicy klaczy w środkowej fazie lutealnej i pęcherzykowej cyklu rujowego na każdym etapie endometrosis zgodnie z klasyfikacją Kenney'a i Doig'a (1986). W drugim zadaniu badawczym określono wpływ czynników uwalnianych przez limfocyty pomocnicze Th1 i Th2 na cechy funkcjonalne fibroblastów, ekspresję genów wybranych markerów związanych z ECM oraz profil transkryptomyczny fibroblastów pochodzących z błony

śluzowej macicy bez cech włóknienia (kategoria I). W trzecim zadaniu badawczym określono wpływ IFN- γ , IL-4 i IL-13 na cechy funkcjonalne fibroblastów, ekspresję wybranych markerów związanych z ECM oraz transkryptom fibroblastów pochodzących z błony śluzowej macicy bez cech włóknienia (kategoria I) i z zaawansowanym włóknieniem (kategoria IIB) zrębu łącznotkankowego błony śluzowej macicy.

Uzyskane wyniki wskazują, że limfocyty pomocnicze Th1 wpływały na ekspresję genów zaangażowanych w cykl komórkowy, metabolizm oraz procesy kluczowe dla odkładania ECM, takie jak interakcja ECM-receptor, trawienie i wchłanianie białek, adhezja ogniskowa, szlaki sygnałowe NF- κ B i JAK-STAT, a także wiązanie kolagenu. Interferon γ wpływał na proliferację fibroblastów, ale nie miał wpływu na profil transkryptomowy i ekspresję genów markerów związanych z ECM w fibroblastach endometrium klaczy. Konieczne są dalsze badania w celu wyjaśnienia roli limfocytów pomocniczych Th1 i IFN- γ w procesach związanych z rozwojem włóknienia w przebiegu endometrosis. Limfocyty pomocnicze Th2 wpływały na ekspresję genów związanych z przebudową tkanek, cyklem komórkowym, szlakami sygnałowymi NF- κ B, TGF- β i AGE-RAGE, co sugeruje ich profibrotyczną rolę. Ponadto IL-4 zwiększała proliferację fibroblastów i wpływała na przemiany ECM poprzez zwiększenie ekspresji fibronektyny i kolagenu typu III, jednocześnie zmniejszając ekspresję i aktywność metaloproteinaz oraz zwiększając poziom ich tkankowych inhibitorów, a także wpływając na ekspresję genów zaangażowanych w glikolizę, cykl komórkowy, procesy biosyntezy cholesterolu i kwasów tłuszczowych, macierz komórkową, adhezję ogniskową, organizację ECM, a także szlaki sygnałowe HIF-1, PI3K-Akt i IGFR, co sugeruje profibrotyczną rolę IL-4. Interleukina 13 zwiększała proliferację fibroblastów, wpływała na przemiany ECM i ekspresję genów przypisanych do takich procesów jak adhezja komórka-macierz, organizacja ECM, interakcja ECM-receptor, co wskazuje na właściwości profibrotyczne IL-13. Różnice w odpowiedzi fibroblastów pochodzących z błony śluzowej macicy kategorii I i IIB na badane cytokiny mogą wynikać z odmiennej sygnalizacji wewnątrzkomórkowej lub mikrośrodowiska tkanki, a także zmian adaptacyjnych w fibroblastach spowodowanych nadmierną produkcją ECM podczas procesu włóknienia.

List of abbreviations

ACTA2 or α -SMA – α -smooth muscle actin

AGE-RAGE – advanced glycosylation end product-receptor for advanced glycation endproducts

Akt – protein kinase B

ALOX15 – 15-lipoxygenase

APC – antigen presenting cell

BCA – bicinchoninic acid

BLM – bleomycin

BP – biological processes

BrdU – bromodeoxyuridine

BSA – bovine serum albumin

CC – cellular components

CCL – chemokine (C-C motif) ligand

CD – cluster of differentiation

cDNA – complementary DNA

CL – corpus luteum

CM – conditioned medium

COL – collagen

Ct – cycle threshold

CTGF – connective tissue growth factor

CX3CL1 – C-X3-C motif chemokine ligand 1

CXCL – chemokine (C-X-C motif) ligand

DEGs – differentially expressed genes

DMEM/F12 – Dulbecco's Modified Eagle's Medium/Nutrient Mixture F-12 Ham medium

DMSO – dimethyl sulfoxide

DPBS – Dulbecco's Phosphate Buffered Saline

ECM – extracellular matrix

EDTA – ethylenediaminetetraacetic acid

ELISA – enzyme-linked immunosorbent assay

EMT – epithelial-to-mesenchymal transition

EndMT – endothelial-to-mesenchymal transition

FBS – fetal bovine serum

FC – flow cytometry
FN – fibronectin
GA – gentamycin-amphotericin
GATA3 – GATA-binding protein 3
GM-CSF – granulocyte-macrophage colony stimulating factor
GO – Gene Ontology
H₂O₂ – hydrogen peroxide
HAS – hyaluronan synthase
HBSS – Hank’s balanced salt solution
hFGF – human fibroblastic growth factor
HIF – hypoxia-inducible factor
HK – hexokinase
HPRT1 – hypoxanthine phosphoribosyltransferase 1
HRP – horseradish peroxidase
IAA – ionomycin
IF – immunofluorescent staining
IFN – interferon
IFNGR1 – interferon-gamma receptor 1
IFNGR2 – interferon-gamma receptor 2
Ig – immunoglobulin
IGF – insulin-like growth factor
IL – interleukin
ILC1 – innate lymphoid cell group 1
JAK – Janus kinase
KEGG – Kyoto Encyclopedia of Genes and Genomes
MAPK – mitogen-activated protein kinases
MCP-1 – C-C Motif Chemokine Ligand 2
MF – molecular functions
MHC – major histocompatibility complex
miRNA – microRNA
MMP – matrix metalloproteinase
MON – monensin
MTT – 3-[4,5- dimethylthiazol-2-yl]-2,5-diphenyl tetrazolium bromide
NEAA – non-essential amino acids

NF-κB – nuclear factor kappa B
NGS – Next Generation Sequencing
NK – natural killer cells
P4 – progesterone
PBMCs – peripheral blood mononuclear cells
PBS – phosphate-buffered saline
PDGF – platelet-derived growth factor
PG – prostaglandin
PI3K – phosphoinositide 3-kinase
PMA – phorbol 12-myristate 13-acetate
qPCR – quantitative Real-Time PCR
Rap1 – Ras-proximate-1
RelA – RELA proto-oncogene, NF-kB subunit
RIN – RNA integrity number
RNA – ribonucleic acid
ROS – reactive oxygen species
RPMI – Roswell Park Memorial Institute
RT – reverse-transcription
SD – standard deviation
SDHA – succinate dehydrogenase complex flavoprotein subunit A
SDS-PAGE – sodium dodecyl sulfate polyacrylamide gel electrophoresis
SRA – Sequence Read Archive
STAT – signal transducers and activators of transcription
Tbet – T-box expressed in T cells
TCR – T-cell receptor
TGF – transforming growth factor
Th – T helper cell
TIMP – tissue inhibitor of matrix metalloproteinase
TMB – 3,3',5,5'-Tetramethylbenzidine
TNF – tumour necrosis factor
Wnt – wingless-related integration site

1. Introduction

Mare endometrosis is a chronic, degenerative condition of the endometrium, characterized by the progressive accumulation of extracellular matrix (ECM) components within the endometrial stroma accompanied by disruption of glandular structures (Kenney 1978, Kenney & Doig 1986). These alterations compromise the functional capacity of the endometrium, thereby contributing to infertility in mares, particularly as they age. Despite years of research on endometrosis, the pathogenesis of this condition remains incompletely understood, which has resulted in a lack of satisfactory treatment options (Schoniger & Schoon, 2020; Katila & Ferreira-Dias, 2022).

Immune cells, including neutrophils, macrophages and T cells seem to play a crucial role in the development of mare endometrosis by perpetuating chronic inflammation and contributing to fibrotic tissue remodeling (Skarzynski et al., 2020). The results of the recent study indicated an alteration in the expression of genes associated with inflammation, cellular infiltration of macrophages, neutrophil extracellular trap signaling pathway and T helper (Th)1 and Th2 activation pathways in the mare endometrium at the different stages of endometrosis (Szóstek-Mioduchowska et al., 2023). Nevertheless, the potential involvement of Th1 and Th2 cell subsets in the pathogenesis of fibrosis in the progression of endometrosis remains to be elucidated. Traditionally Th1 and Th2 cells are considered to be critical components of the immune response. However, a growing body of evidence from studies on animal models of fibrotic disorders suggests the role of Th cells in the development of tissue fibrosis. It has been demonstrated that cytokines secreted by Th cells exert an influence on fibroblast activity, which encompasses the production and remodeling of the ECM (Sun et al., 2023). Cytokines secreted by Th1 cells, such as interferon (IFN)- γ , can modulate inflammation and processes associated with the development of fibrosis (Kanai et al., 2021). In turn, Th2 cells secrete cytokines, including interleukin (IL)-4 and IL-13, arrange type 2 innate responses and modulate tissue repair by affecting fibroblast activity, collagen (COL) production and tissue remodeling (Allen, 2023). The equilibrium between distinct T cell subsets has been demonstrated to influence the degree of fibrosis (Deng et al., 2023). Results of recent research suggest that targeting the interactions between immune cells and fibroblasts may represent a potential therapeutic strategy for fibrotic diseases (Levick & Goldspink, 2014; Vu et al., 2019; Gasparini et al., 2020). Thus, a comprehensive understanding of the role of Th1 and Th2 cells in the development of fibrosis-related to

the progression of mare endometrosis could facilitate the identification of potential therapeutic targets for future treatment strategies.

1.1. Endometrosis

Endometrosis, previously known as chronic degenerative *endometritis*, is a chronic degenerative condition affecting mare endometrium (Kenney, 1978; Kenney & Doig, 1986; Bracher et al., 1996). This term refers to a range of specific alterations in the endometrium, with fibrosis being the most common and significant (Kenney, 1978; Kenney & Doig, 1986; Ricketts & Alonso, 1991; Bracher et al., 1996). The other histopathological alterations within the endometrium include the formation of glandular nests, glandular atrophy or hyperplasia, ectasias, lymphatic lacunae, glandular and lymphatic cysts, pleomorphism, and inflammation (Kenney, 1978; Kenney & Doig, 1986; Flores et al., 1995). Endometrosis results in the impairment of the histological structure and function of the endometrium. Additionally, changes in the structure and function of the myometrium are also observed (Hanada et al., 2014). In the endometrium of mares with progressive fibrosis, the disruption of the secretory function can subsequently alter the uterine environment, potentially affecting sperm motility, embryo migration and implantation as well as the development of the placenta (Bracher et al., 1996; Lehmann et al., 2011). The impaired uterine contractility, immune function, and clearance of uterine fluids that are often associated with endometrosis may affect the ability to conceive and maintain a pregnancy (Schoniger & Schoon, 2020). Consequently, endometrosis results in a reduction of fertility in mares, as the physiological processes required for successful reproduction are disrupted (Schoniger & Schoon, 2020). Since endometrosis correlates with reduced conception rates, heightened pregnancy loss, and less-than-optimal foaling rates, it presents obstacles to breeding initiatives and reproductive oversight (Ebert et al., 2014). The results of the retrospective study conducted by Ebert et al. (2014) demonstrated the age-dependent prevalence of endometrosis in horses. The findings indicated that the prevalence of endometrosis was 32% for mares aged ≤ 5 years and 93% for mares aged >20 years (Ebert et al., 2014).

The gold standard for assessing the occurrence and severity of endometrosis is a histopathological examination of equine endometrial biopsy according to the classification proposed by Kenney and Doig (1986) and modified by Schoon (1992). The classification provides a standardized framework for the histopathological assessment of endometrial biopsies, thereby facilitating the diagnosis and grading of endometrial pathology in mares. The classification system considers a number of histopathological

features observed in the endometrium to categorize the degree of inflammation and fibrosis. These features include the presence of an inflammatory infiltration, changes in glandular appearance, excessive deposition of ECM around glands and in the stroma, and accumulation of fluid and haemorrhage (Kenney, 1978; Kenney & Doig, 1986; Flores et al., 1995). This categorization divides mares' endometria into the following categories: I, IIA, IIB, and III (Kenney & Doig, 1986). Mare endometrium category I is characterised by the absence of significant fibrotic alterations and the absence of sign of inflammation. The expected foaling rate, defined as a term pregnancy and delivery of a live foal, is above 80% (Table 1). Endometrium category IIA is defined by mild fibrotic changes, inflammation and lymphatic lacunae, with an anticipated foaling rate within the range of 50 to 80%. Endometrial tissue category IIB is characterised by moderate inflammation and fibrotic changes, lymphatic lacunae and is associated with a two-year or longer period of infertility. The foaling rate in mare with category IIB endometrium decreases to a range of 10-50%. The most severe category of endometrosis, category III endometrium, is characterized by marked inflammation, fibrotic changes, lymphatic lacunae, deep endometrial atrophy during the breeding, and a foaling rate of less than 10% (Schoniger & Schoon, 2020). This classification system, considering multiple histological features, enables a more accurate characterisation of the severity and nature of endometrial lesions.

Table 1. Percentage of altered endometrial glands and expected foaling rate of mares according Kenney and Doig (1986) categorization of mare's endometrium.

Category	Degree of endometrial changes	Percentage of altered glands	Expected foaling rate
I	absent	0%	80-90%
IIA	mild	10-35%	50-80%
IIB	moderate	35-60%	10-50%
III	severe	>60%	<10%

Endometritis, defined as chronic and persistent inflammation of the endometrium, is widely regarded as the underlying cause of endometrosis (Kenney, 1978; Schoniger & Schoon, 2020). The most common cause of *endometritis* in mares is bacterial infection. Bacteria such as *Streptococcus equi subsp. zooepidemicus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae* can invade the uterus, leading to inflammation. Less commonly, fungal organisms e.g. *Candida* species can cause *endometritis* (Morris et al., 2020). Moreover, *endometritis* can be caused by the difficulty of clearing the uterus of fluid, debris, and pathogens after breeding (Canisso et al., 2020). This can lead to the accumulation of irritants in the uterus. Furthermore, mares with

conformational defects, such as a tipped vulva or poor perineal conformation, are more prone to *endometritis* because these conditions can allow fecal matter or urine to enter the reproductive tract. Older mares are more susceptible to *endometritis* due to reduced immune response and changes in uterine tone and elasticity (Scoggin, 2015). Imbalances in the progesterone (P4) and oestrogen levels, can also contribute to the development and persistence of *endometritis* in mares (Evans et al., 1986).

There is currently no fully effective treatment for endometrosis. Over the past three decades, several of therapeutic approaches have been proposed. The efficacy of currently available therapeutic modalities is limited to a transient period, with only a partial reduction in inflammation. Furthermore, they do not have the capacity to stop or reverse the progression of endometrosis. One of the first treatment strategies was based on mechanical curettage, which is seldom employed in present clinical practice. Although curettage was observed to improve the degree of endometrosis in 80% of the treated mares and 60% of the mares increased pregnancy rates, the prognosis was found to be less favorable in older mares, where curettage had no discernible effect (Ricketts, 1985). The chemical curettage is becoming increasingly popular over mechanical curettage, due to concerns about its potential invasiveness on the endometrium and doubts about its effectiveness. The chemical agents that have been employed for chemical curettage include hydrogen peroxide (H₂O₂), kerosene, and diluted disinfectants such as povidone-iodine 0.2% solutions (Liu & Troedsson, 2008). Dimethyl sulfoxide (DMSO) was used to treat endometrosis for its anti-inflammatory properties, reducing chronic inflammatory cell infiltrates and periglandular fibrosis in 30% of mares without causing harmful histological changes. Nevertheless, it did not improve pregnancy rates compared to a control group (Ley et al., 1989). Kerosene was previously used to treat endometrosis by irrigating the uterus causing short-term uterine oedema and expulsion of retained excretions, which temporarily improved fertility rates (Bracher et al., 1996). However, this treatment often led to miscarriages in half of the pregnant mares (Allen, 1993) and did not affect the endometrial histopathological grade (Podico et al., 2020). Additionally, stem cells have been also proposed as a potential approach to treating endometrosis (Mambelli et al., 2013; Mambelli et al., 2014; Falomo et al., 2015) but further studies are required. Nonetheless, the aforementioned treatment methods remain insufficient. Therefore, a comprehensive understanding of the underlying processes involved in the development of endometrosis is essential for the future development of effective therapeutic interventions.

1.2. The cellular and molecular mechanisms underlying the development of fibrosis

The pathogenesis of fibrotic disorders involves an interplay of both cellular and molecular mechanisms that lead to excessive ECM deposition. One of the most characteristic cellular mechanisms underlying all fibrotic diseases is the activation of fibroblasts by factors such as cytokines, growth factors and oxidative stress (Wynn, 2008; Ung et al., 2021;). Activated fibroblasts differentiate into myofibroblasts, which are responsible for excessive ECM deposition (Brouty-Boye et al., 2000; Lindner et al., 2012). Fibroblasts are therefore key cells in the process of fibrosis development.

The development of mare endometrial fibrosis, as well as other fibrotic diseases, involves several stages, including fibroblast activation and ECM production, tissue remodeling, and fibrosis progression (Distler et al., 2019). Fibrotic diseases may arise from different initial triggers, but they ultimately follow common pathways as tissue remodeling progresses. Despite the varied causes, whether they arise from chronic inflammation, persistent infections, or autoimmune responses, the underlying pathways driving fibrosis tend to follow a similar trajectory (Figure 1).

Fibroblasts are central players in fibrotic diseases, responsible for synthesizing and remodeling of the ECM which provides structural support to tissues. They synthesize various ECM components, including COL, elastin, and glycoproteins, which are essential for tissue integrity and repair. In a fibrotic environment, fibroblasts can be differentiated into myofibroblasts, which produce excessive amounts of COL and other ECM proteins, leading to tissue stiffening and organ dysfunction (Gomes et al., 2021). Beyond their role in ECM production, fibroblasts also act as sentinel cells within the tissue microenvironment (Di et al., 2024). As sentinel cells, fibroblasts are capable of detecting and responding to changes in their surrounding environment, such as injury or infection, by secreting signaling molecules that recruit and activate immune cells. This sentinel role is crucial for initiating appropriate immune responses and ensuring effective tissue repair (LeBleu & Neilson, 2020). As sentinel cells, fibroblasts are also involved in mediating inflammatory responses by producing cytokines, including IL-6 and IL-8, and chemokines, including chemokine (C-C motif) ligand 2 (CCL2), CCL3, CCL5, CCL7, CCL8 and chemokine (C-X-C motif) ligand 1 (CXCL1), CXCL2, CXCL8, CXCL9, and C-X3-C motif chemokine ligand 1 (CX3CL1) that attract and influence immune cell behaviour (Di et al., 2024). Fibroblasts are essential for maintaining structural integrity through the production of ECM, as well as for their role in tissue defence and repair. This highlights the importance of fibroblasts in both physiology and pathological conditions.

Their dual function in ECM production and immune surveillance positions fibroblasts as key regulators of tissue homeostasis and repair (Di et al., 2024). When tissues are damaged, fibroblasts are promptly activated to initiate the wound healing processes, including ECM remodeling and the formation of granulation tissue. However, in chronic injury or persistent inflammation, their prolonged activation can lead to excessive ECM deposition, contributing to fibrosis and organ dysfunction (Darby & Hewitson, 2007).

The differentiation of fibroblasts into myofibroblasts is a pivotal event in the development of fibrosis. Myofibroblasts are cells with unique characteristics that allow them to effectively contribute to tissue repair and remodeling through the production of ECM components: including COLs type I, III, IV, V, VI, glycoproteins, such as fibronectin (FN), laminin, tenascin and proteoglycans (Klingberg et al., 2013). Myofibroblasts can be derived from many sources, including fibroblasts, epithelial cells via epithelial-to-mesenchymal transition (EMT), endothelial cells via endothelial-to-mesenchymal transition (EndMT), and pericytes. Myofibroblast differentiation is mostly induced by transforming growth factor (TGF)- β 1 (Frangogiannis, 2020; Meng et al., 2016). The characteristic feature of myofibroblasts is the presence of α -smooth muscle actin (ACTA2, or α -SMA), which is a hallmark protein of their contractile function. During the normal process of tissue repair, myofibroblasts undergo apoptosis as soon as their role in tissue repair ends. Nevertheless, failure to undergo apoptosis may lead to persistent myofibroblast activity and fibrosis (Younesi et al., 2024). In tissue repair under normal physiological conditions, resolution restores the normal function of the organ, whereas, in fibrotic diseases, the resolution is absent, leading to ongoing fibrosis progression. Multiple stimuli are responsible for the resolution, which if not triggered will result in the development of fibrosis.

As this remodeling continues, feedback loops develop, fuelled by factors such as increased tissue stiffness and low oxygen levels – hypoxia. These loops keep myofibroblasts in an active state, contributing to the chronic nature of fibrotic diseases. Immune cells also play a key role in either resolving or perpetuating fibrosis. When disease-specific and site-specific factors trigger the initial infiltration of neutrophils into the tissue, a sustained influx of immune cells including macrophages, T cells, and mast cells – ensues. This continued infiltration perpetuates inflammation and fibrosis, contributing to the chronicity and persistence of the condition (Wynn, 2008). This convergence leads to the excessive deposition of ECM components, resulting in tissue stiffening and scarring that characterize fibrotic disorders (Ung et al., 2021). In addition,

these immune responses lead to the secretion of numerous cytokines to activate the defence against bacteria or pathogens, which also have profibrotic properties.

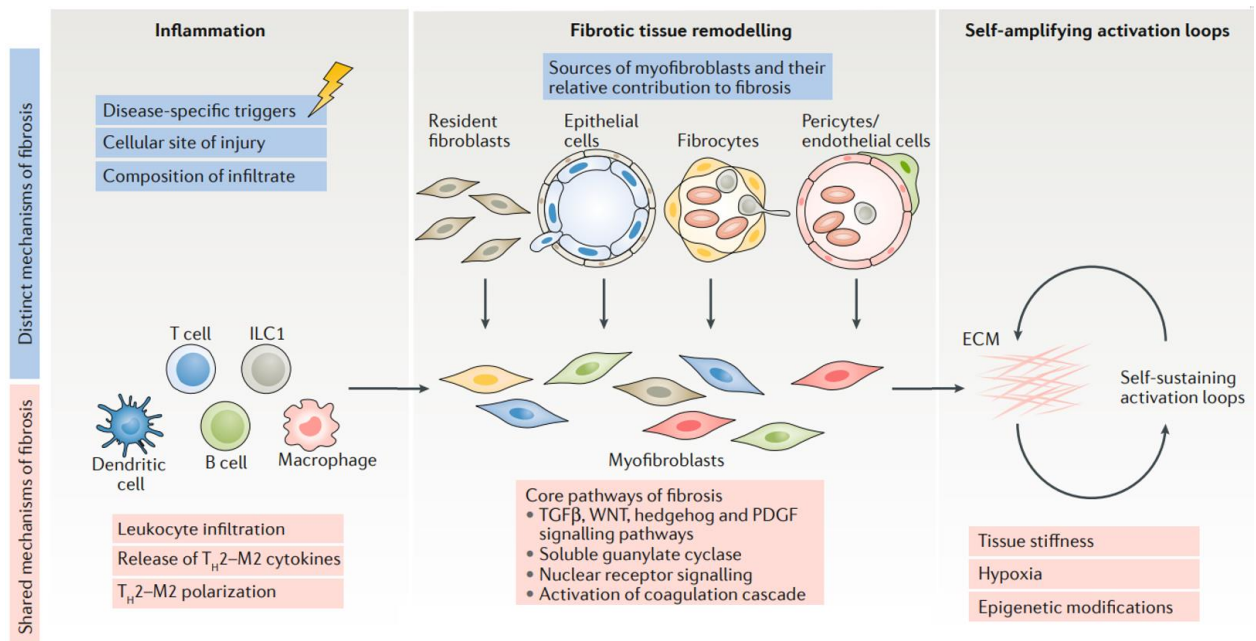


Figure 1. Shared and distinct mechanisms of organ fibrosis. ECM – extracellular matrix; ILC1 – innate lymphoid cell group 1; PDGF – platelet-derived growth factor; TGF β – transforming growth factor- β . Modified from Distler et al. (2019).

Many factors, including a number of cytokines, contribute to the development of fibrosis. Transforming growth factor β 1 is considered to be the most potent profibrotic cytokine that stimulates fibroblast activation, myofibroblast differentiation and excessive ECM deposition (Meng et al., 2016). Moreover, platelet-derived growth factor (PDGF) play an important role at the site of fibrosis by promoting fibroblast proliferation and migration (Xiang et al., 2019). Connective tissue growth factor (CTGF) was also found to play a profibrotic role by enhancing fibrotic responses (Tsai et al., 2018). Importantly, cytokines, such as IL-1 and IL-6 contribute to fibrosis by modulating inflammation and affecting both immune cells and fibroblasts (She et al., 2021). Signaling pathways known to be dysregulated at the site of fibrosis include TGF- β /Smad, mitogen-activated protein kinases (MAPK), phosphoinositide 3-kinase (PI3K)/protein kinase B (Akt), and Wingless-related integration site (Wnt)- β -catenin pathway (Zhao et al., 2022).

1.2.1. Matrix metalloproteinases and their role in fibrotic diseases

Matrix metalloproteinases (MMPs) are a diverse family of calcium-dependent zinc-containing endopeptidases that play a central role in orchestrating tissue remodeling and ECM degradation. Their substrates include a wide range of ECM components,

including COLs, elastin, gelatin, matrix glycoproteins, and proteoglycans. Their activity is regulated by a spectrum of factors including hormones, growth factors, and cytokines. Matrix metalloproteinases play an essential role in several physiological processes, such as angiogenesis, wound healing, inflammation, endometrial cycling, and in many pathological processes, such as carcinogenesis, metastasis, cardiovascular disease, and fibrosis (Verma & Hansch, 2007).

Matrix metalloproteinases are produced by a variety of connective tissue and immune cells, including fibroblasts, osteoblasts, endothelial cells, macrophages, neutrophils, and T cells. Initially synthesized as inactive precursors, known as zymogens, MMPs are subsequently activated through the actions of other proteolytic enzymes, such as serine proteases, and plasmin, to generate their active forms (Kontogiorgis et al., 2005; Verma & Hansch, 2007). Under physiological conditions, the proteolytic activity of MMPs is rigorously regulated by the activation of their zymogen forms, transcriptional control of their expression, and inhibition of their active forms by tissue inhibitors of MMPs – TIMPs. The primary role of TIMPs is to inhibit the activity of MMP thereby preventing excessive tissue remodeling. However, in pathological conditions, the balance between MMPs and TIMPs is disrupted as presented in Figure 2. The shift towards elevated MMP activity contributes significantly to the progression of various diseases and pathological conditions characterized by tissue degradation and remodeling, such as cancer metastasis (Gonzalez-Avila et al., 2019). On the other hand, under the conditions of reduced MMP activity and increased TIMP level, ECM remodeling is inhibited and ECM deposition is increased. This, in turn, leads to the development of fibrotic diseases (Craig et al., 2015).

The growing body of evidence indicates that MMPs not only regulate ECM remodeling but also play an important role in many biological processes. These enzymes can selectively cleave various non-matrix components within the extracellular environment, including cell surface receptors, latent forms of cytokines (IL-1 β , tumour necrosis factor (TNF)- α) and chemokines, cell-cell adhesion molecules (eg. cluster of differentiation (CD)44, clotting factors (plasminogen), and other proteinases like binding proteins (Overall, 2002).

This cleavage allows MMPs to play a significant role in processes such as inflammation and immune responses (Bian et al., 2023). Moreover, it was found that MMPs can activate latent forms of growth factors and cytokines considered to be pro-fibrotic factors, such as pro-TGF- β 1, pro-TNF- α , and pro-IL-1 β (Overall, 2002;

Kobayashi et al., 2014). Additionally, MMPs were found to influence cell proliferation (Quintero-Fabian et al., 2019). For instance, MMP-1 increased the proliferation of human umbilical venous endothelial cells (Mazor et al., 2013). Moreover, MMP-3 and MMP-7 were shown to promote epithelial-to-mesenchymal transition in the lungs of mice and humans (Zuo et al., 2002) and rats (Yamashita et al., 2011).

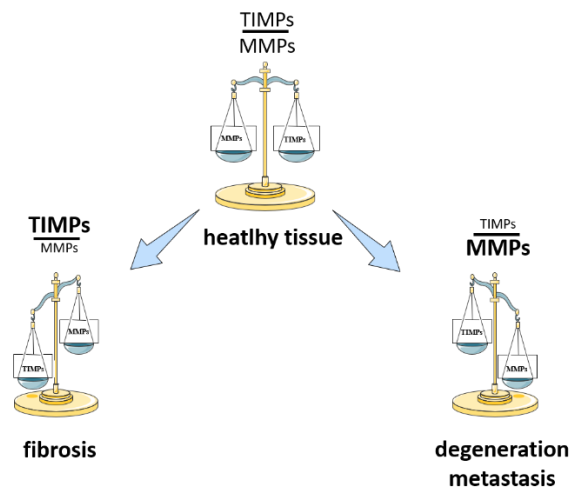


Figure 2. A diagram showing disturbances in the expression profile of matrix metalloproteinases (MMPs) and tissue inhibitors of matrix metalloproteinases (TIMPs) and the consequences in the development of a pathological state based on (Roeb, 2018). The figure was drawn by using pictures from Servier Medical Art by Servier, licensed under a Creative Commons Attribution 3.0 Unported License.

1.2.2. Pathogenesis of mare endometriosis

The pathogenesis of mare endometriosis involves several processes, including tissue damage caused by inflammation, abnormal tissue repair, and excessive deposition of ECM components, leading to the formation of fibrotic lesions around endometrial glands and in the stroma. Endometriosis is linked to persistent inflammation, disrupted immune response, and compromised immune tolerance within the endometrium, all of which can further contribute to the advancement of this condition. The initial indication of endometriosis often manifests through distinctive morphological and functional variances observed in the periglandular endometrial stromal cells. This atypical differentiation, characterized by aberrant cellular morphology and altered functional behaviour, serves as a hallmark of endometriosis (Walter et al., 2001). In the initial phase of endometriosis, a distinct profile emerges within the tissue, featuring notably enlarged periglandular stromal cells with polygonal shapes. These cells play a pivotal role in the synthesis of COL fibres, laying the groundwork for the fibrotic process (Hoffmann et al., 2009a, 2009b). As fibrosis progresses into its advanced stages, a shift occurs in the cellular

landscape. Metabolically active or inactive fibroblasts and myofibroblasts become more abundant (Walter et al., 2001, Hoffmann et al., 2009a).

Throughout the progression of endometriosis, the fibroblasts exhibit a remarkable capacity to deposit excessive amounts of ECM components, such as COLs. This accumulation of COLs typically manifests near the glands or in conjunction with the basement membrane (Kenney & Doig, 1986). The expression of the marker of myofibroblasts – ACTA2 - was found to be elevated in the endometrium of the mare at the final stage of endometriosis (Szóstek-Mioduchowska et al., 2019b). The expression profile of MMP-1, MMP-2, MMP-3, and MMP-9 was also found to be disturbed in the endometrial tissue at different stages of endometriosis (Szóstek-Mioduchowska et al., 2020a). Moreover, the transcriptomic study indicated changes in the expression of genes associated with immune response, steroid hormone biosynthesis, as well as the metabolism of sulfur in the endometrium with endometriosis compared to non-fibrotic endometrial tissue in non-cyclic mares (Witkowski et al., 2022). Results of the recent study of Szóstek-Mioduchowska et al. (2023) reported that the most pronounced transcriptomic alterations occurred in category IIB endometrium. A transcriptomic analysis revealed significant changes in 230 transcripts in category IIA endometrium and 1101 transcripts in category IIB endometrium, both compared to category I endometrium. Additionally, a marked difference in the expression of 2111 transcripts was observed between categories IIB and IIA. The functional enrichment analysis of these data indicates that inflammation and metabolic alterations are characteristic of both mild (category IIA) and moderate (category IIB) stages of endometriosis. The differentially expressed genes (DEGs) were linked to various processes, including organ inflammation, leukocyte, macrophage, and phagocyte infiltration, as well as the movement of phagocytes and leukocytes, and cytokine levels in the endometrium of categories IIA and IIB compared to category I. These findings, together with previous results corroborate studies on fibrosis development in various organs across different species, suggesting that pro-inflammatory cytokines, growth factors, and other inflammatory agents regulate fibrosis indirectly by recruiting inflammatory cells to the inflammation site, as well as directly impacting various tissues (Szóstek et al., 2013; Szóstek-Mioduchowska et al., 2019a, 2019b; Szóstek-Mioduchowska et al., 2020a, 2020b). Furthermore, the changes in the expression of genes involved in processes such as apoptosis, ferroptosis, wound healing, oxidative stress, as well as cellular metabolism were found in the endometrium of mares with endometriosis, opening up a new direction of research.

The signaling pathways that are activated in endometriosis remain poorly understood. In mare endometriosis, the transcriptomic analysis showed the changes in the expression genes associated with the Wnt/ β -catenin signaling in category IIB compared to category I endometria (Szóstek-Mioduchowska et al. 2023). Results of other studies pointed to activation of the nuclear factor kappa B (NF- κ B)-dependent pathway in the endometrium of mares with endometriosis in the follicular phase of the oestrous cycle (Jasinski et al., 2021, 2022). The canonical NF- κ B signaling pathway was found to be activated during the follicular phase of the oestrous cycle when compared to mid-luteal phase of the oestrous cycle in cases of active, destructive endometriosis (Domino et al., 2020).

In addition, results of the recent study pointed out changes in the expression profile of microRNA (miRNA), which may regulate the expression of genes associated with multiple signaling pathways, including focal adhesion and ECM-receptor interaction, in fibrotic endometria (Wójtowicz et al., 2023). Thus, epigenetic mechanisms seem to play an important role in processes underlying endometriosis. Furthermore, in aged mares, along with the severity of endometriosis, DNA methyltransferase expression in the endometrium becomes disturbed (Alpoim-Moreira et al., 2019).

The results of recent studies suggest that pro-inflammatory cytokines, growth factors and other factors with inflammatory properties indirectly regulate fibrosis by attracting inflammatory cells to the site of inflammation and directly affecting surrounding cells such as fibroblasts or epithelial cells. In a transcriptomic study, a huge number of inflammatory mediators such as TGF- β 1, IL-6, TNF α , PDGF, IL-4, IL-13, IL-17 and IFN- γ were determined as potential regulator of DEGs identified in mare's endometrium with endometriosis (Szóstek-Mioduchowska et al, 2023). Szóstek-Mioduchowska et al. (2019b, 2020a) demonstrated that TGF- β 1, the most profibrotic factor, affected the expression of ECM-associated genes and proteins in mare endometrial fibroblasts as well as fibroblast proliferation and fibroblast to myofibroblast differentiation. Furthermore, the expression profile of profibrotic cytokines IL-1 β and IL-6 exhibited increased expression with the progression of endometriosis (Szóstek et al., 2013). These cytokines have been demonstrated to regulate the expression of ECM-related factors such as COL1, COL3, FN, MMPs and TIMPs in endometrial explants (Szóstek-Mioduchowska et al., 2019a). Cytokine signaling not only modulates the expression of ECM-associated factors but also plays a crucial role in the recruitment and infiltration of immune cells, which further impact endometrial function and immune homeostasis. The results presented by Klose and Schoon (2016) showed that in the

endometrial tissue with fibrotic changes, the glandular nests are infiltrated by immune cells, including T cells (Klose & Schoon, 2016). However, the role of Th cells, especially Th1 and Th2 and their cytokines including IFN- γ , IL-4 and IL-13 in the processes associated with the development of endometriosis remains unknown. Understanding these immunological changes is crucial to understanding the mechanisms underlying endometrial fibrosis in the progression of mare endometriosis.

1.3. T helper cells

T helper cells are immune system cells that serve as key mediators of immune function as they are responsible for the production of factors that activate virtually all other immune system cells (Sun et al., 2023). These include B cells, which are responsible for antibody production, and cytotoxic T cells, whose pivotal role is to eliminate cells harbouring pathogens, macrophages, and other effector cells, engaged in the assault against invading pathogens. T helper cells are identified by the expression of the CD3 marker on their surface, which is a major surface marker of T cells. Additionally, they express a surface protein known as CD4, which plays a pivotal role in activating Th cells. This protein interacts with class II major histocompatibility complex (MHC) molecules, which aid the immune system in identifying foreign substances (Alberts, 2002).

T helper cells are a heterogeneous group of cells, distinguished by their unique function and secreted factors (Swain, 1991; Williams et al., 1991). These cells develop from lymphoid progenitors in the bone marrow. After leaving the bone marrow and migrating to the thymus, T-cell precursors undergo differentiation and enter a phase of intense proliferation to become thymocytes. Thymocytes, in turn, undergo positive and negative selections within the thymus that aim at selection of thymocytes that appropriately recognize self-MHC molecules and do not react excessively to self-antigens. Thymocytes that have undergone both of these selections then differentiate into naïve T cells (Th0) that exert a CD4 marker on their surface. Depending on the activation factor, Th0 can differentiate into mature Th cell subsets. For a T cell to be activated, two signals must be transmitted inside the immunological synapse. One of the signals is the recognition of a specific antigen on the antigen-presenting cell (APC) in the context of MHC by the T-cell receptor (TCR) on the T cells. The second signal is the interaction of co-stimulatory molecules on both cells, e.g. CD28. After completing the two-signal activation process, Th cells proceed to initiate their proliferation. It accomplishes this by secreting a powerful

T cell cytokine – IL-2, which then acts on the Th cell itself in an autocrine manner (Alberts, 2002).

1.3.1. Th1 cells and IFN- γ : role in physiology and fibrosis

T helper 1 cells represent a mature form of differentiated Th0 (Th naïve) cells, occurring under conditions of IL-2 and IL-12 (Sekiya & Yoshimura, 2016). Interleukin 12 is responsible for initiating the differentiation of Th0 into Th1 effector cells by activating the signal transducers and activators of transcription (STAT) 4 transcription factor. In turn, STAT4 triggers IFN- γ production, further promoting Th1 differentiation through the activation of transcription factors STAT1 and T-box expressed in T cells (Tbet), which is recognized as the master regulator of Th1 differentiation, enhances IFN- γ expression, establishing a positive feedback loop that strengthens the Th1 response. In addition to IFN- γ , Th1 cells secrete TNF- α , granulocyte-macrophage colony-stimulating factor (GM-CSF), IL-2, IL-3, and IL-10. T helper 1 cells provide helper functions to other immune system cells, particularly macrophages and dendritic cells which are APCs (Romagnani, 1999). The primary functions of Th1 cells are in cell-mediated immunity and inflammation, including the activation of other immune cells' effector functions. Effector Th1 cells secrete significant quantities of IFN- γ , which not only contributes to the amplification of Th1 responses but also plays a crucial role in activating the cytolytic functions of macrophages.

In general, IFNs are cytokines that play a key role in host defence against pathogens. Interferon γ is the sole type II interferon. It is a 25 kDa cytokine that is produced and secreted not only by Th1 cells but also by the adaptive immune system cells including natural killer (NK) cells, and CD8⁺ cytotoxic T cells. The secretion of IFN- γ is precisely modulated by the level of cytokines (Castro et al., 2018). As a pleiotropic cytokine IFN- γ exhibits a multitude of functions, encompassing antiviral, antitumor, and immunomodulatory roles. Consequently, it serves as a crucial coordinator of both innate and adaptive immune responses (Mendoza et al., 2019). The cellular responses to IFN- γ are triggered by its binding to a heterodimeric receptor composed of IFN- γ receptor 1 (IFNGR1) and IFN- γ receptor 2 (IFNGR2). This binding initiates the activation of the Janus kinase (JAK)-STAT pathway. Subsequently, activation of the JAK-STAT pathway leads to the upregulation of IFN-stimulated genes, including MHCII (Hu & Ivashkiv, 2009). The cellular signaling of IFN- γ through IFNGR1 and IFNGR2 is presented in Figure 3.

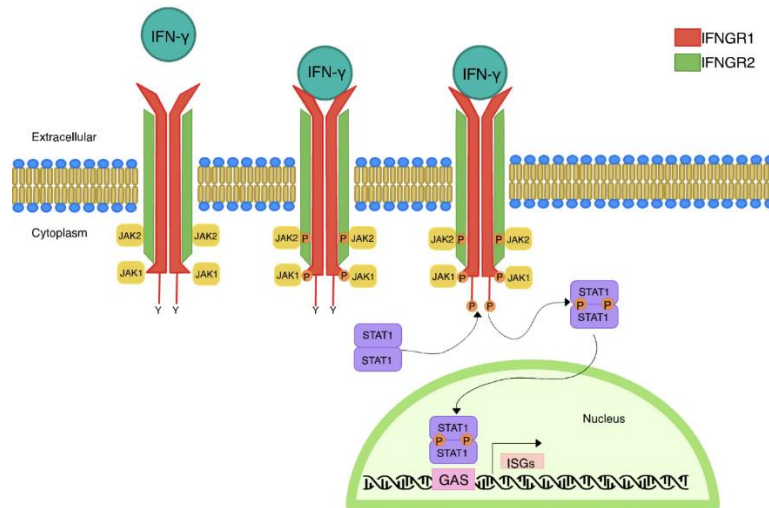


Figure 3. The heterotetrameric receptor complex responsible for binding interferon (IFN)- γ consists of IFN- γ receptor (IFNGR)1 and IFNGR2. Intracellularly, JAK1 and JAK2 proteins associate with the domains of IFNGR1 and IFNGR2, respectively. Upon IFN- γ binding to its receptor complex, JAK1/2 undergo transphosphorylation, leading to the phosphorylation of IFNGR1 and subsequent recruitment of STAT1. STAT1 is then phosphorylated by JAK proteins. Phosphorylated STAT1 translocates into the nucleus, where it modulates the transcription of genes containing gamma-activated sequence motifs in their promoter regions (Tecalco-Cruz et al., 2024).

As previously stated, Th1 cells play a significant role in the immune response, particularly in the host defence against intracellular pathogens. Nevertheless, their effect is considerably more far-reaching. Interferon γ plays an important role in both physiological and pathological processes within the endometrium. This cytokine has the capacity to influence the properties of connective tissue cells, thereby modulating a range of multiple processes, including the maintenance of a physiological endometrial environment (Murphy et al., 2009). It exerts its role in maintaining immune homeostasis during physiological post-breeding *endometritis* by enhancing the endometrial ability to resist bacterial infections by upregulating antimicrobial peptides and enzymes (Park & Han, 2022). Increased *IFN- γ* gene expression in the endometrium in day 25 of equine pregnancy indicates its crucial role in the modulation of immune response in the mare endometrium during early pregnancy (Tachibana et al., 2013).

Moreover, Th1 cells and IFN- γ have been demonstrated to regulate processes associated with the development of fibrosis, exhibiting both pro- and anti-fibrotic effects in disparate experimental models (Zhang & Zhang, 2020). On the one hand, Th1 cells were shown to induce MMPs expression, thus decreasing ECM deposition in murine models of hepatic fibrosis (Roderfeld et al., 2012). Conversely, Th1 cells have been demonstrated to stimulate the differentiation of fibroblasts into myofibroblasts and to

induce the expression of the most profibrotic cytokine, TGF- β 1, thus exacerbating fibrosis in the murine model of cardiac fibrosis (Nevers et al., 2017). Nevertheless, both, the effect of Th1 cells and IFN- γ on the processes related to the development of equine endometrial fibrosis remain unknown. However, elevated levels of IFN- γ in the uterine fluid were also found in mare endometrium with acute *endometritis* and with chronic endometrial fibrotic, suggesting an important role in both regulation of immune response and the processes related to the development of endometriosis (Lecton et al., 2024).

1.3.2. Th2 cells, IL-4 and IL-13: role in physiology and fibrosis

T helper 2 cells, a subset of CD3⁺ CD4⁺ T cells, play a pivotal role in host defence mechanisms against pathogens and allergens. This role of Th2 cells results from the action of secreted cytokines, such as IL-4, IL-5, and IL-13 (Walker & McKenzie, 2018). T helper 2 cells differentiate from Th0 cells when triggered with IL-4 and IL-2. Stimulation by IL-4 triggers the phosphorylation of STAT6 and the subsequent increase in GATA-binding protein 3 (GATA3) levels, a critical transcription factor for Th2 cell maturation. Then, GATA3 collaborates with IL-2-induced STAT5 signaling to enhance the expression of IL-4, a hallmark of Th2 cytokine. This cascade initiates a positive feedback loop driven by IL-4, where continued IL-4-STAT6-GATA3 and IL-5-STAT5 signaling further amplifies the Th2 gene expression profile (Maier et al., 2012).

In addition to triggering type 2 inflammatory responses the type 2 cytokines released by Th2 cells also facilitate the repair of damaged tissue (Walker & McKenzie, 2018). They achieve this by directly or indirectly influencing a diverse range of immune and non-immune cell types, including fibroblasts, epithelial cells, macrophages, and endothelial cells. Research utilising various cytokine-deficient mouse models has revealed a significant correlation between liver fibrosis development and the activation of the Th2 cell response, which encompasses IL-4, IL-5, IL-13, and IL-21 (Wynn, 2008).

Interleukin 4 is an around 15 kDa protein cytokine that is produced and secreted by activated Th2 cells, mast cells, eosinophils and basophils (Gadani et al., 2012). This cytokine plays an important role in the immune system. Its capacity to stimulate the proliferation of B and T cells is essential for the mounting of an effective immune response against pathogens. Furthermore, IL-4 contributes to the production of antibodies, which are essential for neutralizing pathogens and providing immunity by promoting the differentiation of B cells into plasma cells. The induction of the B cell class switching to immunoglobulin (Ig)E by IL-4 is important in the context of allergic

response and defence against parasites (Gadani et al., 2012). Furthermore, IL-4 up-regulates MHCII production, which, in turn, enhances the antigen presentation capacity of APCs, such as macrophages and dendritic cells. This facilitates the activation of Th cells, which, in turn, orchestrate various aspects of the immune response, including the activation of B cells and cytotoxic T cells. Overall, the multifaceted functions of IL-4 highlight its importance in orchestrating both humoral and cellular immune responses, making it a key regulator in adaptive immunity. The overexpression of IL-4 has been associated with the development of allergies and fibrotic disorders (Hershey et al., 1997; Huaux et al., 2003).

Interleukin 13 is a small, around 13 kDa protein cytokine, secreted by Th2 cells, NK cells, mast cells, basophils, and eosinophils (Rael & Lockey, 2011). This cytokine plays a pivotal role as a regulator in various physiological processes such as IgE synthesis, goblet cell hyperplasia, mucus hypersecretion, airway hyperresponsiveness, fibrosis, and up-regulation of chitinase. It serves as a key mediator in allergic inflammation and is implicated in a range of conditions, notably asthma (Rael & Lockey, 2011).

Interleukin 13 exerts a similar effect to IL-4 on monocytes and macrophage function (Zurawski & de Vries, 1994). Homology of protein sequences between IL-13 and IL-4 is around 30 %. Interleukin 4 and IL-13 share similarities in receptor usage but exhibit distinct signaling pathways (Figure 4). Both IL-4 and IL-13 can bind to IL-4R α , but IL-13 uniquely interacts with IL-13R α 1. The formation of the heterodimeric complex between IL-4R α and IL-13R α 1 is crucial for IL-13 signaling, hence termed type II IL-4R. This complex allows IL-13 to initiate downstream signaling. On the other hand, IL-4 primarily signals through the type I IL-4R, composed of IL-4R α and γ c chains. This receptor complex mediates the biological effects of IL-4, such as B cell proliferation and antibody class switching. Interestingly, IL-13R α 2, despite its high affinity for IL-13, does not induce the activation of IL-13-responsive genes. Instead, it acts as a decoy receptor, essentially sequestering IL-13 and preventing it from binding to functional signaling receptors (Roeb, 2023). This regulatory role helps modulate the intensity and duration of IL-13-mediated responses.

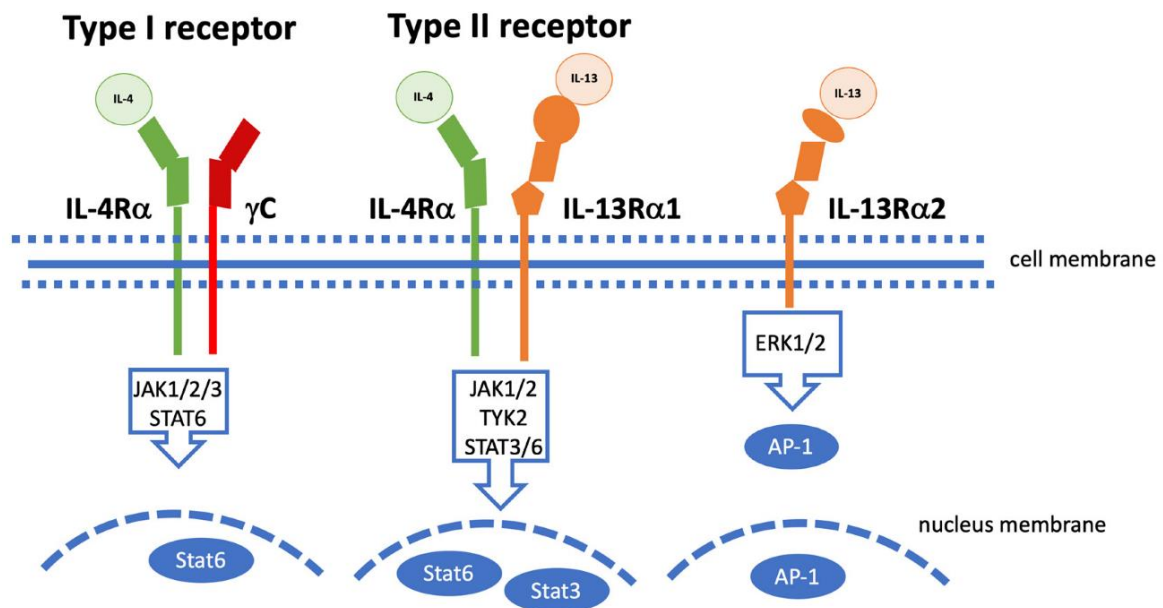


Figure 4. Interleukin (IL)-4 and IL-13 signaling. Interleukin 4 binds to two types of receptors: type I, with IL-4Rα and γC, and type II, with IL-4Rα and IL-13Rα1 (Roeb, 2023).

T helper 2 cells have been demonstrated to exert a pro-fibrotic influence in both human and animal models of lung fibrosis (Kreindler et al., 2010; Morimoto et al., 2018). Moreover, both IL-4 and IL-13 have been shown to have profibrotic effects in animal models of fibrotic diseases. As a result, targeting IL-4/IL-13 signaling has been proposed as a potential avenue for future treatment strategies (Lee et al., 2001; Melo-Cardenas et al., 2022; Arndt et al., 2023). Therefore, an understanding of the role of Th2 cells, IL-4 and IL-13 is essential to indicate a potential direction of research on treatment strategies for fibrosis. Nevertheless, a comprehensive understanding of the actions of Th2, IL-4 and IL-13 action on mare endometrial fibroblasts remains unknown.

2. Research hypotheses

The primary hypothesis state that Th1 cells and IFN- γ exert an anti-fibrotic effect, whereas Th2 cells and IL-4 and IL-13 exert a pro-fibrotic effect on the cellular and molecular processes related with the development of equine endometrial fibrosis in the progression of endometrosis in the mare.

Specific hypotheses assume that:

1. The number of Th2 cells, the ratio of Th2 to Th1 cells as well as the expression of IFN- γ , IL-4, and IL-13 and their receptors, increase in the endometrium in the progression of endometrosis.
2. T helper 1 and Th2 cells, through their secretome, exert a distinct effect on the processes involved in the development of endometrial fibrosis in the progression of mare endometrosis, primarily by affecting the gene expression profile and functional characteristics of endometrial fibroblasts.
3. Interferon γ exerts an anti-fibrotic effect on mare endometrial fibroblasts by decreasing the expression of ECM components, affecting fibroblast functional characteristics, and the expression of genes associated with processes related with the development of equine endometrial fibrosis in the progression of endometrosis.
4. Interleukin 4 and IL-13 exert a pro-fibrotic effect on mare endometrial fibroblasts by increasing the expression of ECM components, affecting fibroblast functional characteristics and the expression of genes associated with processes related with the development of equine endometrial fibrosis in the progression of endometrosis.
5. The response of mare endometrial fibroblasts to IFN- γ , IL-4, and IL-13 varies depending on the stage of endometrosis.

3. Research objectives

The main aim of the study was to determine the impact of two distinct subsets of Th cells: Th1 and Th2 cells, and their mediators: IFN- γ , IL-4, and IL-13 on cellular and molecular processes related to the development of fibrosis in the progression of endometriosis in the mare.

Specific objectives were as follows:

1. The analysis of the endometrial ratio of Th1 and Th2 cells as well as the expression of IFN- γ , IL-4 and IL-13, and their respective receptors (IFN γ R1, IL-4RA, and IL-13RA) in endometria assigned to categories I, IIA, IIB and III according to Kenney and Doig (1986) in the mid-luteal and follicular phases of the oestrous cycle.
2. The investigation of the influence of Th1 and Th2 cell secretome on functional characteristics and gene expression of ECM-associated markers in *in vitro* cultured mare endometrial fibroblasts derived from category I endometria.
3. The investigation of the impact of Th1 and Th2 cell secretome on prospective signaling pathways as well as biological and molecular processes through transcriptomic and bioinformatic analysis in *in vitro* cultured mare endometrial fibroblasts derived from category I endometria.
4. The investigation of the effect of IFN- γ , IL-4, and IL-13 on potential signaling pathways as well as biological and molecular processes via transcriptomic and bioinformatic analysis in *in vitro* cultured mare endometrial fibroblasts derived from categories I and IIB endometria.
5. The investigation of the effect of IFN- γ , IL-4, and IL-13 on the functional characteristics and expression of ECM-associated markers in *in vitro* cultured mare endometrial fibroblasts derived from categories I and IIB endometria.

4. Materials and methods

4.1. Research material

4.1.1. Mare's endometrial tissue collection

The study was conducted between April and July 2021-2023. Cycling mares (n=67; weighing 500±100 kg) at age 2-20 years were used in this study. The animals were euthanised in accordance with European legislation (European Food Safety Authority, AHAW/04-027). The collection of material did not require ethical approval as the animals were slaughtered as part of routine meat production. All mares were clinically healthy, as confirmed by the veterinarian and the breeder. Endometrial tissue samples were collected from mares in the mid-luteal and follicular phases of the oestrous cycle. The phases of the oestrous cycle were identified based on macroscopic observations of ovaries. The mid-luteal phase of oestrous cycle was identified when well-developed corpus luteum (CL) was observed associated with 15-20 mm ovarian follicles. The follicular phase was characterized by the absence of an active CL and the presence of follicles of various sizes, but always >35 mm in diameter. Endometrial tissue, from the uteri tubal horn, located on the side of the active ovary was excised, rinsed with cold sterile RNase-free saline solution, divided, and put in liquid nitrogen for RNA and protein extraction or in 4% formaldehyde for haematoxylin-eosin staining and histological examination. Additionally, uterine horns were transported on ice in sterile saline or Roswell Park Memorial Institute (RPMI) 1640 Medium (RPMI 1640 medium; R6504, Sigma) to the laboratory for further isolation of fibroblasts and T cells, respectively.

Following haematoxylin-eosin staining, endometrial samples were retrospectively classified according to the Kenney and Doig (1986) classification system. This classification is based on the presence of fibrosis and inflammation as well as endometrial atrophy and the dilatation of lymphatic vessels. Endometrium without pathological changes was classified as category I, as presented in Figure 5. Category IIA includes endometrium with mild to moderate inflammation, with few dilated lymphatic vessels. A small degree of fibrosis affects individual branches of the endometrial glands, and there are no fibrotic nests around glands in 4 adjacent visual fields. Category IIB includes moderately inflamed endometrium with numerous dilated lymphatic vessels. Fibrosis is more severe than category IIA, with 2-4 fibrotic glandular nests in 4 adjacent visual fields. Changes affect up to 60% of the uterine glands. Category III includes an endometrium with massive inflammation and greatly dilated lymphatic vessels. The fibrosis is massive,

5 or more fibrotic glands are found in 4 adjacent visual fields. Changes affect over 60% of the uterine glands in the most severe endometriosis stage (Snider et al., 2011).

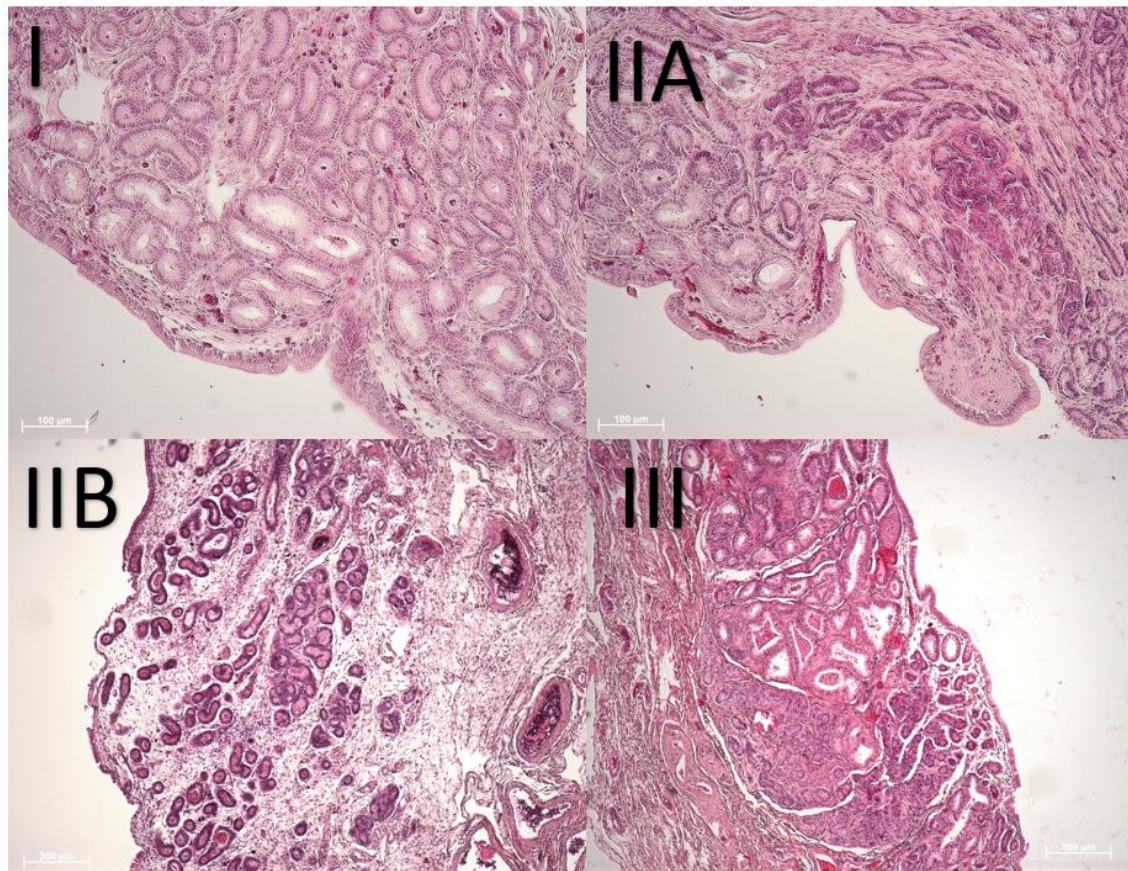


Figure 5. Histological pictures of mare endometrium. Categories of mare endometrium: I – no changes, IIA – mild condition, IIB – moderate condition, and III – severe condition, according to Kenney and Doig (1986). Magnification 10X, scale bar = 100 µm (I, IIA) 200 µm (IIB, III).

4.1.2. Mare's peripheral blood collection

The study was conducted in December 2022 and January 2023. Mares (n=5; weighing 500±100 kg) at age 2-8 years were used in this study. All mares were clinically healthy, as confirmed by veterinary inspection and individual mare health records. The experimental protocol was approved by the Local Ethics Committee for Experiments on Animals in Olsztyn, Poland (Approval No. 27/2022). All methods were carried out in accordance with relevant guidelines and regulations. All methods are reported in accordance with ARRIVE guidelines for the reporting of animal experiment. To exclude the possible influence of fluctuations in ovarian steroid characteristics oestrous cycle, T cells were isolated from non-cycling mares during the winter months. Mare's genital tract was examined by ultrasonography to confirm anoestrous by veterinarian. Moreover, a clinical exam including physical examination, heart rate, and rectal temperature was performed to ensure that the horses were healthy. Peripheral blood

(15 ml) was collected from mare (n=5) by a veterinarian. Then, the blood was transferred to 50 ml tube, mixed with an anticoagulant, containing ethylenediaminetetraacetic acid (EDTA, 0.38 M; 879810112, POCH) and acetylsalicylic acid (55 mM; 2091299, Polpharma) and transported to the laboratory.

4.2. Cell isolation and culture

4.2.1. Fibroblast isolation and culture

The fibroblasts were isolated from the endometrium of mare in the follicular phase of the oestrous cycle. The follicular phase of the oestrous cycle was selected based on a previous study (Szóstek-Mioduchowska et al., 2023), which described transcriptomic changes in the mare endometrium at different stages of endometrosis. A comparative analysis of category IIB and category I endometria in the follicular phase of the oestrous cycle, revealed the differential expression of genes involved in a number of pathways, including: fibrosis, inflammatory response, IL-13 signaling pathway, and Th1 and Th2 activation pathway (Szóstek-Mioduchowska et al. 2023).

Fibroblasts were cultured, and passaged, as previously described with modifications (Szóstek et al. 2012; Szóstek-Mioduchowska et al. 2023). Prior to the fibroblast isolation, the uterine horns were washed with sterile phosphate-buffered saline (PBS, P4417; Sigma), and the epithelial cell layer was scrapped off with a scalpel blade. Further, the endometrial layer was dissected from underlying myometrium using scissors and submerged in digestion solution: Hank's balances salt solution (HBSS; H1387, Sigma) containing 0.1% bovine serum albumin (BSA; A2153, Sigma), collagenase I (0.05%; C2674, Sigma), DNase I (0.05%; 11284932001, Roche), and cut into small pieces. The digestion was performed in 37°C with constant stirring. After 45 minutes, cells were filtered through a series of 100, 70, and 40 µm cell strainers, and centrifuged at $100 \times g$ for 10 minutes at 4°C. Then, supernatant was discarded and cell pellet was suspended in 2 ml of red blood lysis buffer (R7757, Sigma) and mixed for 1 minute, and then washed with HBSS containing 0.1% BSA. After centrifugation, cells were suspended in Dulbecco's Modified Eagle's Medium/Nutrient Mixture F-12 Ham (DMEM/Ham's F-12 medium; D8900, Sigma) containing 10% fetal bovine serum (FBS; F9665, Sigma) and counted using a haemocytometer. The viability of endometrial cells was higher than 95% as assessed by the trypan blue exclusion test, using Trypan Blue Solution (0.4%, 1520061, Gibco). The cells were counted using Countess 3FL (Thermofisher) and seeded at a density of 5×10^5 viable cells/ml and cultured at 38.0°C

in a humidified atmosphere of 5% CO₂ in the air. To purify the fibroblast population, 18 hours after plating, by which time selective attachment of fibroblasts had occurred, the medium was changed to fresh fibroblast culture medium – BMTM Basal Medium (CC-3131, Lonza) and FGMTM-2 SingleQuotsTM supplements (CC-4126, Lonza) including 2% FBS, insulin, human fibroblastic growth factor (hFGF)-B, gentamycin-amphotericin (GA), and 100 ng/ml ascorbic acid (A4403, Sigma).

The fibroblast homogeneity was confirmed using immunofluorescent (IF) staining for vimentin based on the protocol described recently (Szóstek-Mioduchowska et al., 2021). The fibroblast population exhibited a purity of approximately 96% following the isolation process. The IF staining of vimentin in mare endometrial fibroblasts is presented in Figure 6. Once the cells had reached 90% of confluency, they were cryopreserved as described previously (Szóstek et al., 2012). For this purpose, the cells were washed with sterile PBS and detached from cell culture dish using 0.025% trypsin-EDTA solution (T4049, Sigma). To inhibit trypsin activity, medium containing 10% FBS was added after detachment. Then, cells were centrifuged at $200 \times g$ for 10 minutes and counted using haemocytometer. Subsequently, 1×10^6 cells were suspended in 1 ml of cell freezing medium, comprising 84% of inactivated FBS and 16% DMSO (D2650, Sigma) and frozen. The samples were stored at -80°C until further experiments.

For cell-based analyses, mare endometrial fibroblasts derived from the selected category, as defined by Kenney and Doig (1986), were thawed by placing them at 37°C for 2 minutes. Subsequently, the cells were transferred into 50 ml tubes, containing fibroblast culture medium, supplemented with 2% FBS, hFGF- β , insulin, GA, and 100 ng/ml ascorbic acid and centrifuged at $100 \times g$ for 10 minutes. After centrifugation, cell pellet was suspended in 2 ml of fibroblast culture medium, followed by counting using Trypan blue exclusion test. The viability of thawed cells was over 90%. Then, the cells were suspended in an appropriate volume of medium, resulting in a concentration 5×10^5 viable cells/ml, and seeded in 15 ml onto T75 cell culture flasks. Fibroblasts were cultured under normal growth conditions at 38.0°C in a humidified atmosphere of 5% CO₂ in the air, until reaching 90% of confluence. The culture medium was changed every 2 days to maintain optimal nutrient levels. After reaching 90% of confluence, fibroblasts were trypsinized and passaged at desired concentrations for further assays. The seeding density of the fibroblasts and the culture dishes used were dependent on the experimental design, as detailed in the section devoted to the experimental design.

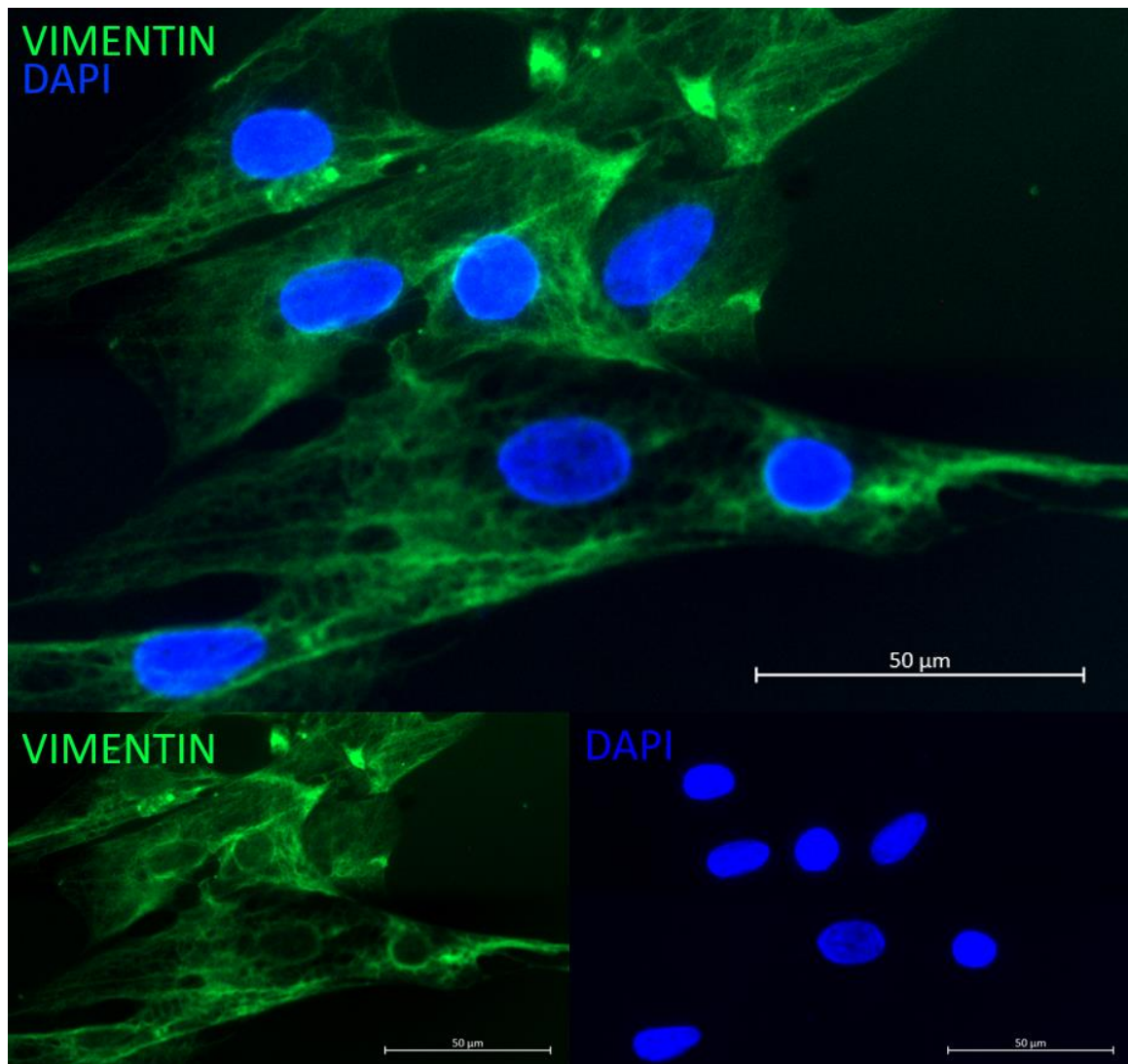


Figure 6. Representative image of vimentin – marker of fibroblasts immunostaining in *in vitro* cultured mare endometrial fibroblasts. Magnification 40X, scale bar = 50 μ m.

4.2.2. Isolation of T cells from mare's endometrium

The T cells were isolated from endometrium of mares in the mid-luteal and follicular phases of the oestrous cycle ($n=6$ per category in each phase, $\sum n=48$). Prior to T cell isolation, the uterine horns were washed with sterile PBS and the endometrial layer was dissected from underlying myometrium using scissors and submerged in digestion solution: HBSS containing 0.1% BSA collagenase IV (0.05%, C5138, Sigma), DNase I (0.05%), and cut into small pieces. The digestion was performed in 37°C with constant stirring. After 45 minutes, cells were filtered using successively 100, 70, and 40 μ m cell strainers, and centrifuged at $100 \times g$ for 10 minutes at 4°C. Then, supernatant was discarded and cell pellet was suspended in 20 ml of HBSS containing 0.1% BSA. Then, 20 ml of cell suspension was gently placed onto 20 ml of Ficoll-Paque Plus (GE17-1440,

Cytiva) in 50 ml centrifuge tubes, followed by centrifugation at $400 \times g$ for 40 minutes at 18°C , with the acceleration and deceleration value at the minimum. Subsequently, the upper layer of cells was transferred to a new, sterile tube, and washed twice with HBSS containing 0.1% BSA at $500 \times g$ for 10 minutes at 18°C . After centrifugation, cells were counted using a haemocytometer and suspended in a cell freezing medium, containing 90% of FBS and 10% of DMSO (Worsham et al., 2017). The concentration of cells in the cell freezing medium was 1×10^7 cells/ml (Worsham et al., 2017). Isolated cells were stored at -80°C until subsequent analysis was conducted using a flow cytometer.

4.2.3. Isolation of mare's peripheral blood mononuclear cells

For T cells differentiation, T cells were isolated from mare peripheral blood mononuclear cells (PBMCs; $n=5$). For T cells isolation, 15 ml of blood with anticoagulant and 15 ml of sterile-filtered HBSS containing BSA (0.1%) were mixed using a pipette. Then, HBSS-diluted blood was gently placed onto 20 ml of Ficoll-Paque Plus in 50 ml centrifuge tubes, followed by centrifugation at $400 \times g$ for 40 minutes at 18°C , with the acceleration and deceleration value at the minimum. Subsequently, the upper layer of cells was transferred to a new, sterile tube, and washed twice with HBSS containing 0.1% BSA at $500 \times g$ for 10 minutes at 18°C . Then, cells were counted using haemocytometer and suspended in cell freezing medium, containing 90% of FBS and 10% of DMSO. The concentration of cells in the cell freezing medium was 1×10^7 cells/ml (Worsham et al., 2017). Isolated peripheral blood mononuclear cells (PBMCs) were stored at -80°C until subsequent Th1 and Th2 differentiation.

4.2.4. Th1 and Th2 cell differentiation

T helper naïve cells (Th0) were separated from PBMCs, using negative selection kit. For this purpose, PBMCs ($n=5$; 2×10^7 cells) were thawed by placing them at 37°C for 2 minutes. Subsequently, the cells were transferred into 50 ml tubes, containing T cell culture medium: RPMI 1640 medium containing 10% FBS, 1% antibiotic-antimycotics solution (AA; A5955; Sigma), 1% of Non-Essential Amino Acids Solution (NEAA; 11140050, Gibco), 50 nM of 2-mercaptoethanol (31350010, Gibco), and 10 ng/ml ascorbic acid. Then, cells were centrifuged at $500 \times g$ for 10 minutes at 18°C . After centrifugation, the supernatant was removed, and the cell pellet was suspended in RPMI 1640 medium containing 10% FBS, 1% antibiotic-antimycotic solution, 50 nM of 2-

mercaptoethanol and 100 ng/ml ascorbic acid. Then, cell quantity and viability were assessed using Trypan blue exclusion test. The viability of thawed cells was over 95%.

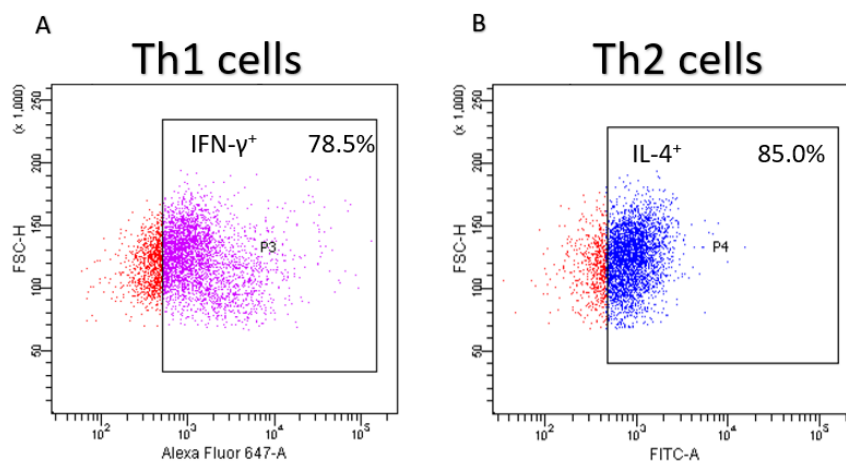
Undifferentiated Th (Th0) cells were isolated using EasySep™ Human Naïve CD4⁺ T Cell Isolation Kit (19555, STEMCELL technologies), according to manufacturer's instructions. For the selection of Th0 cells, 18×10^6 of thawed PBMCs were placed in a new 15 ml tube and centrifuged at $500 \times g$ for 10 minutes at 18°C. Then, cell pellet was suspended in 800 µl of Easy Sep buffer (20144, STEMCELL technologies). Next, 40 µl of EasySep™ Biotinylated AntiCD45RO Antibody and 40 µl of EasySep™ Human Naïve CD4⁺ T Cell Isolation Cocktail were added and mixed by pipetting. After 5 minutes of incubation, 40 µl of EasySep™ Dextran RapidSpheres™ were added, and the mixture was incubated for additional 5 minutes at room temperature. Following incubation, Easy Sep buffer was added to top up the sample to 2.5 ml and mixed by gently pipetting up and down 3 times. Then, the 15 ml tube was placed twice onto the magnet and incubated for 5 minutes, followed by collection of supernatants containing Th0 cells. Subsequently cells were washed, counted, and 6×10^6 Th0 cells derived from each mare were transferred into new 15 ml tubes, suspended in 12 ml of T cell culture medium to obtain cell concentration at 0.5×10^6 cells/ml.

Then, Th0 cells were differentiated *in vitro* to Th1 or Th2 cells. For Th1 and Th2 differentiation, to each tube, containing 5×10^5 Th0 cells/ml, appropriate treatment was added, as depicted in Table 2 (Sekiya & Yoshimura, 2016; Yang et al., 2020). The medium for Th1 cells differentiation contained anti-CD28, anti-IL-4, IL-12 and IL-2, whilst Th2 cells differentiating medium contained of anti-CD28, anti-IFN- γ , IL-4 and IL-2 (Table 2). Then, cells were transferred to 48-well plate, previously coated with anti-CD3 ϵ antibodies (145-2C11, Invitrogen). The coating of plates was performed the day before differentiation protocol. Coating of a culture dish was done by adding 500 µl of anti-CD3 ϵ antibodies at the concentration of 1 µg/ml (Sekiya & Yoshimura, 2016) in Dulbecco's Phosphate Buffered Saline (DPBS; D5652, Sigma) per a well of 48-well cell culture dish. The plates were then sealed with parafilm and incubated at 4°C overnight, and then coating solution was aspirated.

Table 2. The concentration of stimulators used for Th1 and Th2 cells differentiation.

	anti-CD28	anti-IL-4	anti-IFN-γ	IL-12	IL-2	IL-4
	eBioscience; cat. no 16-0281	eBioscience cat. No 14-7041	eBioscience cat. No 14-7311	Bon- Opus cat. No CM39	Kingfisher Biotech cat.no RP0006E	Kingfisher Biotech cat. No RP0003E
	concentration (ng/ml)					
Th1	1000	1000	-	10	10	20
Th2	1000	-	5000	-	10	-

Undifferentiated Th0 cells were cultured in RPMI 1640 medium containing 10% FBS, 1% antibiotic-antimycotics solution, 1% NEAA, 50 nM of 2-mercaptoethanol, and 100 ng/ml ascorbic acid in the presence of stimulators, as indicated in the Table 2. T helper cells were cultured for a period of six days at 38°C, 5% CO₂ and humidity. Every two days, half the volume of the medium was replaced with medium containing the indicated concentrations of treatments. The efficiency of Th1 and Th2 cell differentiation assessed using flow cytometry (FC) was around 78% and 85% for Th1 and Th2 cells, respectively, as presented in Figure 7. The IF staining indicated the presence of Th1 and Th2 secreted cytokines: IFN- γ and IL-13 as well as CD4 – surface marker of T helper cells in the differentiated cells is presented in Figure 8.

**Figure 7.** The representative image of the flow cytometry staining of IFN- γ ⁺ cells (A, P3) in Th1 *in vitro* differentiated and IL-4⁺ cells (B, P4) in Th2 *in vitro* differentiated cells. The values 78.5% and 85.0% stands for percentage of IFN- γ -positive and IL-4-positive cells after Th1 and Th2 differentiation, respectively.

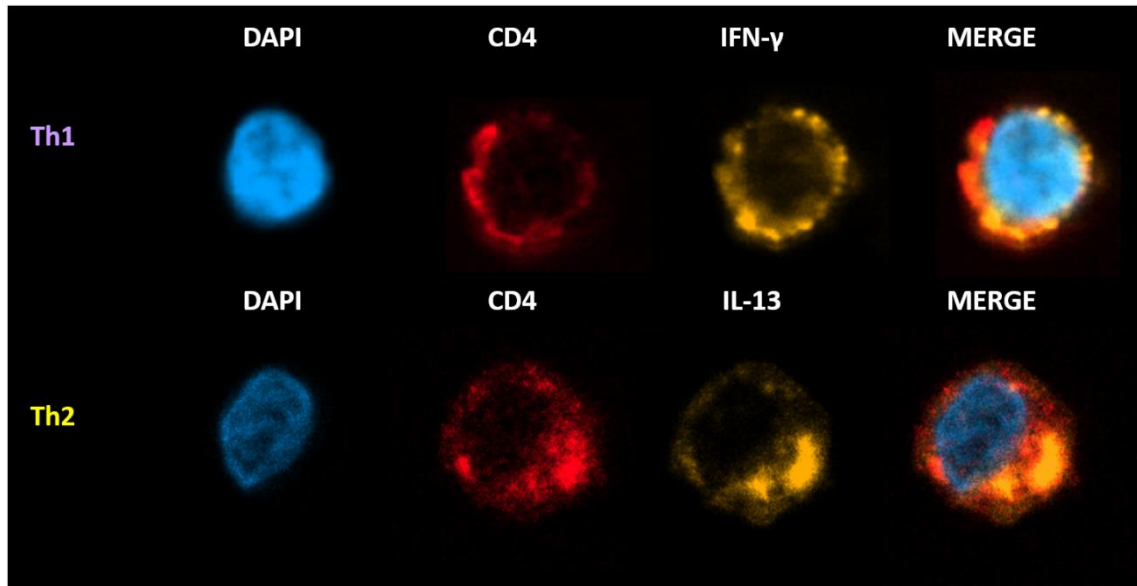


Figure 8. The representative image of CD4 (T helper cells marker), IFN- γ (Th1-secreted cytokine) and IL-13 (Th2-secreted cytokine) immunostaining in *in vitro* differentiated Th1 and Th2 cells.

4.2.5. Obtaining of Th1 and Th2 conditioned media

Following a six-day of T cell differentiation, Th1 and Th2 cells were collected, washed with sterile-filtered PBS and suspended in RPMI 1640 medium containing 5% FBS, NEAA, 2-mercaptoethanol and ascorbic acid) at a concentration 0.5×10^6 cells/ml for the purpose of obtaining Th1 and Th2 conditioned media (CM), respectively. Then, Th1 and Th2 cells were transferred into fresh 48-well plates, previously coated with anti-CD3 ϵ (5 μ g/ml in DPBS) and anti-CD28 (5 μ g/ml in DPBS) antibodies (Rao et al., 2005). Subsequently, the Th1 and Th2 cells were incubated for 24 hours to allow conditioning of the media. Th1-CM and Th2-CM were then collected and centrifuged at $1000 \times g$ for 10 minutes. In order to obtain medium from different biological replicates, obtained media were pulled in equal ratios between biological replicates (n=5), and stored at -80°C until fibroblast treatment. Moreover, to obtain appropriate control of Th-CM, equal amount of RPMI 1640 medium containing 5% FBS, NEAA, 2-mercaptoethanol and ascorbic acid (100 ng/ml) was placed at -80°C for further experiments.

4.3. Experimental design

The research presented in the dissertation is comprised of three research tasks (Figure 9):

Research task 1: Analysis of Th1/Th2 cell ratios and their cytokine expression in the endometrium of mares with endometrosis.

Research task 2: The effect of the Th1 and Th2 cell secretome on the processes associated with the development of fibrosis in the mare endometrial fibroblasts in the progression of endometrosis

Research task 3: The effect of IFN- γ , IL-4, and IL-13 on endometrial fibroblasts: transcriptomic analysis, ECM-associated marker expression, and functional characteristics.

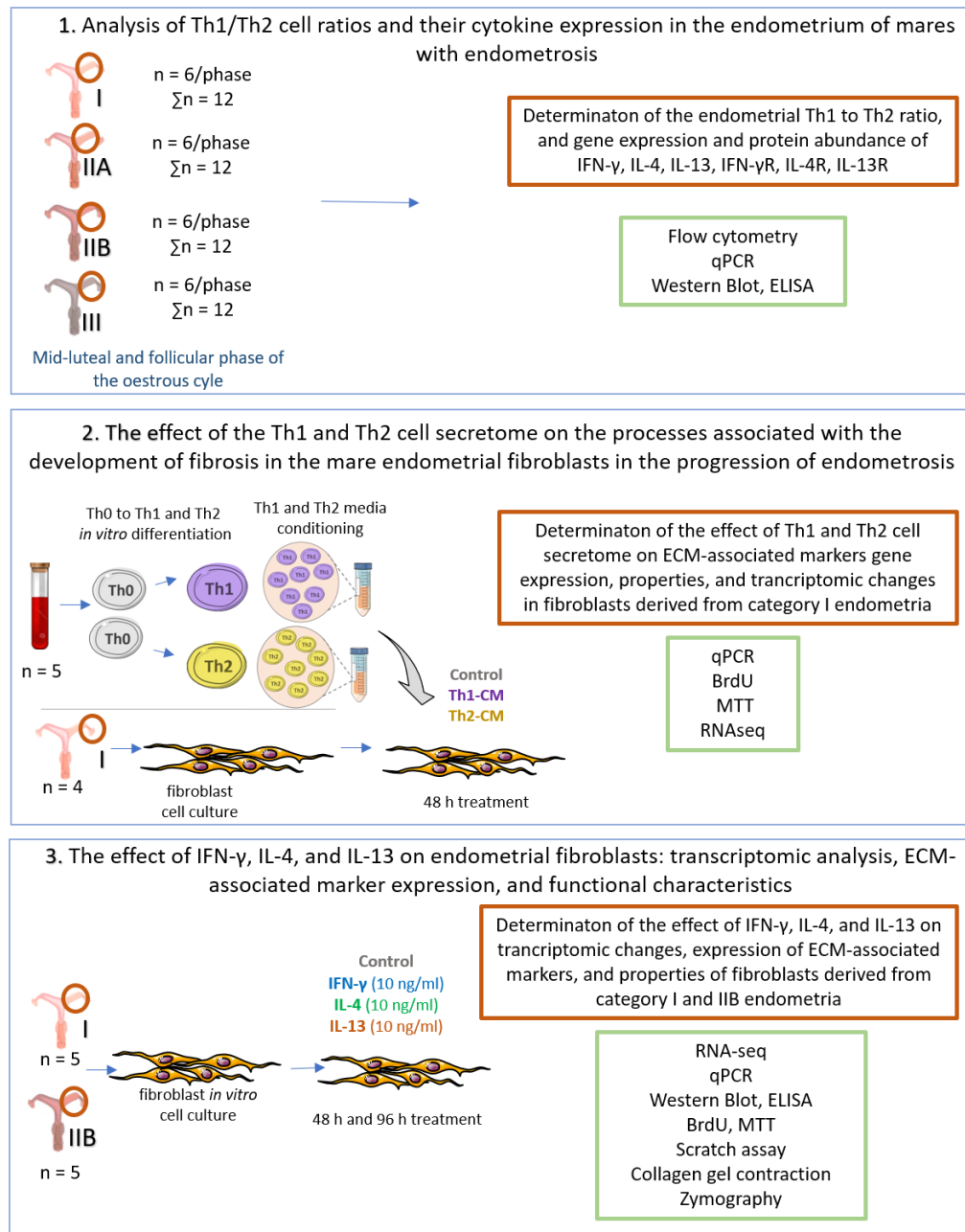


Figure 9. Experimental design.

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4.3.1. Research task 1: Analysis of Th1/Th2 cell ratios and their cytokine expression in the endometrium of mares with endometrosis

4.3.1.1 Experiment 1. The endometrial Th1/Th2 cell ratios in the endometrium of mares with endometrosis

The aim of the experiment was to analyse the endometrial percentage and ratio of Th1 cells ($CD3^+ CD4^+ IFN-\gamma^+$) and Th2 cells ($CD3^+ CD4^+ IL-4^+$) at different stages of endometrosis. The ratio of Th1 and Th2 cells in category I, IIA, IIB, and III endometria ($n=6$ per category, $\sum n=48$) of mares in the mid-luteal and follicular phases of the oestrous cycle was determined using FC as described in section 4.4.2.10.

4.3.1.2. Experiment 2. The endometrial expression of IFN- γ , IL-4 and IL-13 and their respective receptors in the endometrium of mares with endometrosis

The aim of the experiment was to determine the expression of selected cytokines secreted by Th1 cells (IFN- γ) and Th2 (IL-4 and IL-13) and their respective receptors (IFN- γ R, IL-4R, and IL-13R) in category I, IIA, IIB and III endometria in the mid-luteal and follicular phases of the oestrous cycle.

Gene expression and protein abundance of IFN- γ , IL-4, IL-13, IFN- γ R, IL-4R, and IL-13R as well as the concentration of IFN- γ , IL-4, IL-13 in mare endometrium in each category of endometrosis (I, IIA, IIB, and III; $n=6$ per category, $\sum n=48$) in the mid-luteal and follicular phases of the oestrous cycle were determined using qPCR, Western Blot, and enzyme-linked immunosorbent assay (ELISA), respectively as described in chapter 4.4.2. The concentration of all cytokines was determined per 1 μ g of protein.

4.3.2. Research task 2: The effect of the Th1 and Th2 cell secretome on the processes associated with the development of fibrosis in the mare endometrial fibroblasts in the progression of endometrosis

4.3.2.1. Experiment 1. The effect of the Th1 and Th2 cell secretome on functional characteristic of endometrial fibroblasts

The aim of the experiment was to describe the influence of Th1 and Th2 cell secretome on mare endometrial fibroblast proliferation and viability.

The research material was endometrial fibroblasts derived from category I endometria (n=4) and Th1-CM and Th2-CM pulled from five biological replicates, as described in 4.2.2-4.2.3 subchapters. At 90% confluence, the fibroblasts were trypsinized and passaged into 96-well plates at a concentration of 1×10^5 cells/ml, 100 μ l of medium per well, in fibroblast culture medium, supplemented with 2% FBS, hFGF- β , insulin, GA, and ascorbic acid (100 ng/ml), under normal growth conditions (38°C, 5% CO₂, humidity). At 80% confluence, the cell culture medium was removed, cells were washed with sterile-filtered PBS and next treated with 100 μ l of with vehicle (control group, RPMI 1640 medium containing 5% FBS, 2-mercaptoethanol, NEAA, and ascorbic acid), Th1-CM or Th2-CM for 48 hours. The treatments were performed in four biological replicates and three technical replicates. For the BrdU (proliferation) and MTT (viability) analyses, cells were proceeded further, as described in subchapters 4.4.1.1-2.

4.3.2.2. Experiment 2. The effect of the Th1 and Th2 cell secretome on ECM-associated markers gene expression in endometrial fibroblasts

The aim of the experiment was to determine the influence of Th1 and Th2 cell secretome on gene expression of ECM-associated markers (*Col1a1*, *Col3a1*, *ACTA2*, *FN1*, *MMP-2*, -3, -9, *TIMP-1*, and -2) in endometrial fibroblasts.

The research material was endometrial fibroblasts derived from category I endometria (n=4) and Th1-CM and Th2-CM pulled from five biological replicates, as described in 4.2.2-4.2.3 subchapters. At 90% confluence, the fibroblasts were trypsinized and passaged into a 6-well cell culture plate at a concentration of 5×10^4 cells/ml, 3 ml of medium per well, in fibroblast culture medium, supplemented with 2% FBS, hFGF- β , insulin, GA, and 100 ng/ml ascorbic acid, under normal growth conditions (38°C, 5% CO₂, humidity). At 80% confluence, cell culture medium was removed, cells were washed with sterile-filtered PBS and cells were treated with either medium alone (RPMI 1640 medium containing 5% FBS, 2-mercaptoethanol, NEAA and ascorbic acid), Th1-CM or Th2-CM. After 48 hours of treatment, the medium was collected, the cells were washed with sterile-filtered PBS, and suspended in 1 ml of TRI reagent (T9424, Sigma) for subsequent RNA isolation, as described in section 4.4.2.2.

4.3.2.3. Experiment 3. The effect of the Th1 and Th2 cell secretome on the transcriptome of endometrial fibroblasts

The aim of the experiment was to determine the impact of Th1 and Th2 cell secretome on prospective signaling pathways, biological and molecular processes through transcriptomic and bioinformatic analysis in endometrial fibroblasts.

The research material was endometrial fibroblasts derived from category I endometria (n=4) and Th1-CM and Th2-CM pulled from five biological replicates, as described in 4.2.2-4.2.3 subchapters. At 90% confluence, the fibroblasts were trypsinized and passaged into a 6-well cell culture plate at a concentration of 5×10^4 cells/ml in a volume of 3 ml of fibroblast culture medium, supplemented with 2% FBS, hFGF- β , insulin, GA, and 100 ng/ml ascorbic acid per well. The cells were cultured under normal growth conditions (38°C, 5% CO₂, humidity). At 80% confluence, fibroblast culture medium was removed, cells were washed with sterile-filtered PBS and treated with vehicle (control group, RPMI 1640 medium containing 5% FBS, 2-mercaptoethanol, NEAA, and ascorbic acid), Th1-CM or Th2-CM. After 48 hours of treatment, the medium was collected, the cells were washed with sterile-filtered PBS and were suspended in 1 ml of TRI reagent for subsequent RNA isolation as described in section 4.4.2.2.

4.3.3. Research task 3: The effect of IFN- γ , IL-4, and IL-13 on endometrial fibroblasts: functional characteristics, ECM-associated marker expression, and transcriptomic analysis

4.3.3.1. Experiment 1. The effect of IFN- γ , IL-4 and IL-13 on the transcriptome of endometrial fibroblasts

The aim of the experiment was to determine and compare the effect of IFN- γ , IL-4, and IL-13 on potential signaling pathways, and biological and molecular processes using transcriptomic and bioinformatic analysis in *in vitro* cultured fibroblasts derived at different stages of endometriosis.

Endometrial fibroblasts derived from category I (n=5) and category IIB (n=5) endometria were used. At 90% confluence, the fibroblasts were trypsinized and passaged in fibroblast culture medium containing supplements indicated in 4.2.1. into 6-well cell culture plates at a concentration of 5×10^4 cells/ml. The seeding volume was 3 ml and the cells were cultured under normal growth conditions (38°C, humidity, 5% CO₂). After reaching 80% confluence, cells were washed with sterile-filtered PBS, the culture

medium was replaced with fresh Dulbecco's Modified Eagle's Medium/Nutrient Mixture F-12 Ham without phenol red (D2906, Sigma), and the cells were incubated at 38.0°C in 5% CO₂. After serum starvation, fibroblasts were treated with vehicle (control group), IFN-γ (10 ng/ml; RP0012E, Kingfisher Biotech), IL-4 (10 ng/ml; RP0003E, Kingfisher Biotech), and IL-13 (10 ng/ml; RP0102E, Kingfisher Biotech) in DMEM/Ham's F-12 without phenol red, supplemented with 1% of AA solution, ascorbic acid (100 ng/ml) and 0.1% (w/v) BSA. Based on previous studies, the doses of cytokines were selected (Eickelberg et al., 2001; Huaux et al., 2003; Leonardi et al., 2003; Sato et al., 2011; Vu et al., 2019). After 48 hours, the cells were washed with sterile-filtered PBS, and lysed with TRI Reagent. The samples were stored at -80°C for subsequent RNA extraction, NGS, followed by bioinformatical analysis, as described in analytical methods subchapters 4.4.2.2, 4.2.2.5-6.

4.3.3.2. Experiment 2. The effect of IFN-γ, IL-4 and IL-13 on expression of ECM-associated markers in fibroblasts derived at different stages of endometriosis

The aim of the experiment was to determine and compare the effect of IFN-γ, IL-4, and IL-13 on the gene expression and protein abundance of ECM-associated markers (COL1, COL3, ACTA2, FN1, MMP-2, -3, -9, TIMP-1, and -2) in fibroblasts derived at different stages of endometriosis.

Endometrial fibroblasts derived from category I (n=5) and category IIB (n=5) endometria were used. At 90% confluence, the fibroblasts were trypsinized and passaged in fibroblast culture medium supplemented with 2% FBS, insulin, hFGF-B, GA and 100 ng/ml ascorbic acid. At 90% confluence, the fibroblasts were trypsinized and seeded into 6-well cell culture plates at a concentration of 5×10^4 cells/ml for gene expression analysis and into T25 cell culture flasks at a concentration of 5×10^4 cells/ml for protein abundance analysis. After reaching 80% confluence for 48 hours of treatment and 60% for 96-hour treatment, the culture medium was replaced with fresh DMEM/Ham's F-12 supplemented with 1% of AA solution, ascorbic acid (100 ng/ml) and 0.1% (w/v) BSA (A1470, Sigma), and the cells were incubated at 38.0°C in 5% CO₂. After serum starvation, cells were treated with vehicle (control group), IFN-γ (10 ng/ml) for gene expression analysis, IL-4 (10 ng/ml) for gene expression and protein abundance analyses, and IL-13 (10 ng/ml) for gene expression and protein abundance analyses. The treatment periods were 48 and 96 hours. After treatment, the cells were washed with sterile PBS, and lysed with either TRI Reagent or RIPA buffer (Cayman 10010262) for RNA and protein analyses, respectively.

The samples were stored at -80°C for subsequent RNA and protein extraction and analyses, as described in analytical methods subchapter (4.4.2.). Moreover, the culture media were collected and stored at -20°C for determination of MMP-2 and MMP-9 activity using zymography, as described in 4.4.2.9.

Given the absence of an effect of IFN- γ on the gene expression of ECM-associated markers and transcriptomic alteration, the further experiments were performed with the omission of IFN- γ treatment when determining the effect of cytokines on the protein abundance of ECM-associated markers in mare endometrial fibroblasts.

4.3.3.3. Experiment 3. The effect of IFN- γ , IL-4 and IL-13 on the functional characteristic of endometrial fibroblasts

The aim of the experiment was to determine and compare the effect of IFN- γ , IL-4, and IL-13 on the functional characteristics of mare endometrial fibroblasts derived at different stages of endometrosis.

To assess cell proliferation and viability, fibroblasts derived from category I (n=5) and category IIB (n=5) endometria were seeded at a concentration of 1×10^5 cells/ml in a volume of 100 μ l of fibroblast culture medium supplemented with 2% FBS, insulin, hFGF- β , GA, and 100 ng/ml ascorbic acid into a 96-well plate. At 80% and 60% of confluence following 48 and 96 hours of treatment, respectively, fibroblasts were treated with vehicle (control group), IFN- γ (10 ng/ml), IL-4 (10 ng/ml), and IL-13 (10 ng/ml) in DMEM/Ham's F-12 supplemented with 1% of AA solution, ascorbic acid (100 ng/ml) and 0.1% (w/v) BSA. The cells were incubated at 38.0°C in 5% CO₂. After treatment, the proliferation and viability of fibroblasts were determined using BrdU and MTT assay, respectively, as described in 4.4.1.1 and 4.4.1.2 subchapters.

Given the absence of an effect of IFN- γ on the gene expression of ECM-associated markers and transcriptomic changes, the experiment was conducted without the inclusion of IFN- γ treatment when determining the effect on fibroblast migration and the capacity to the contraction of the collagen gel.

To determine the effect of IL-4 and IL-13 on the migration and ability to contract of the collagen gels, endometrial fibroblasts derived from category I (n=5) and category IIB (n=5) endometria were used. At 90% confluence, the fibroblasts were trypsinized and seeded into 2-wells inserts in fibroblast culture medium supplemented with 2% FBS, insulin, hFGF- β , GA, and ascorbic acid (100 ng/ml). A total of 70 μ l of cell suspension at a concentration of 1.4×10^5 cells/ml were added per each insert well for migration

assay, as described in chapter 4.4.1.3. In turn, 2×10^4 cells in 250 μ l of medium were embedded in collagen disc in a 48-well plate as described in 4.4.1.4. Then, cells were treated with vehicle (control group), IL-4 (10 ng/ml) or IL-13 (10 ng/ml) for 96 hours DMEM/Ham's F-12 supplemented with 1% of AA solution, ascorbic acid (100 ng/ml) and 0.1% (w/v) BSA, and the cells were cultured at 38.0°C in 5% CO₂. The analysis of cell migration and contraction of collagen gel was performed as described in 4.4.1.3. and 4.4.1.4. subchapters.

4.4. Methods

4.4.1. Methods used for cell functional characteristic assessment

4.4.1.1. Cell proliferation assay – BrdU assay

The proliferation of mare endometrial fibroblasts was assessed using an ELISA bromodeoxyuridine (BrdU) incorporation assay (11647229001, Roche), which is based on BrdU incorporation, as a thymidine analogue, into nuclear DNA of proliferating cells (Adan et al., 2016). This can be further tracked using anti-BrdU antibodies.

To perform the BrdU assay, mare endometrial fibroblasts were seeded into 96-well plates, at a concentration of 1×10^4 cells per 100 μ l of medium per well. After reaching desired confluence, cells were treated for indicated periods of time, and then labelled with BrdU (final concentration 10 μ M) for two hours. The labelling medium was then removed by tapping off. To fix the cells, 200 μ l of FixDenat solution was added and incubated for 30 minutes at 25°C. Subsequently, the FixDenat solution was removed thoroughly by flicking and tapping. Thereafter, 100 μ l of antibody-conjugate (anti-BrdU-POD working solution) was added per each well, followed by incubation for 90 minutes at 25°C. The antibody-conjugate was then removed by flicking off and rinsed three times with 200 μ l per well of washing solution (PBS 1X). After third washing, the plates were tapped to remove any residuals of washing solution and 100 μ l of substrate solution was added per well, followed by 30 minutes of incubation at 25°C. After incubation period, the colour development was observed, and the absorbance of the samples was measured in an ELISA reader (BioTek Microplate Reader, Epoch) at the wavelength 370 nm. The absorbance value of the control group (untreated cells) was established as 100%, while that of the treated cells was calculated as a ratio to the control cells $\times 100\%$.

4.4.1.2. Cell viability and metabolic activity assay – MTT assay

The viability (metabolic activity) of cells was determined using the MTT assay (Mosmann, 1983). The MTT kit (TOX1, Sigma), which was employed to ascertain the viability and metabolic activity of cells. This assay is based on the reduction of MTT (3-[4,5- dimethylthiazol-2-yl]-2,5-diphenyl tetrazolium bromide), a yellow tetrazolium salt, by metabolically active cells into purple, water-insoluble formazan crystals (Vistica et al., 1991). Viable cells contain NADH-dependent oxidoreductase enzymes which reduce the MTT to water-insoluble formazan, which is further solubilized in acidic isopropanol (solvent), and its concentration can then be detected spectrophotometrically, at a wavelength of 570 nm.

To perform the MTT assay, mare endometrial fibroblasts were seeded at a concentration 1×10^4 cells per 100 μ l of medium per well into 96-well plates. Once the cells had reached desired confluence, cells were treated. After treatment, the MTT solution was added to the wells reaching a concentration of 0.5 mg of MTT per 1 ml of medium. The cells were then incubated for a further three hours under normal growth conditions (38°C, 5% CO₂). Following the incubation, which resulted in the transformation of yellow MTT into purple formazan crystals, 100 μ l of MTT solubilization solution was added to each well, followed by thorough mixing by pipetting. The concentration of formazan was then measured using a BioTek Microplate Reader (Epoch) at a wavelength of 570 nm. The absorbance value of the control group (untreated cells) was established as 100%, while that of the treated cells was calculated as a ratio to the control cells $\times 100\%$.

4.4.1.3. Cell migration assay

The cell migration assay, known also as the scratch assay was conducted in accordance with the previously described methodology (Bukowska et al., 2018) with modifications. The cell migration assay enables the determination of the impact of selected treatments on the capacity of cells to migrate across a gap between cells created by a scratch. To ensure the accurate detection of cell migration, rather than cell proliferation, the protocol involves the pre-treatment of cells with mitomycin C, a DNA synthesis inhibitor.

To perform a cell migration assay, fibroblasts from mare endometrium were diluted in cell culture medium at a concentration of 1.4×10^5 cells/ml and then placed into wells, with 70 μ l of cell suspension per well within 2-well inserts (80209, Ibidi).

Once the cells had reached 100% confluence, they were treated with mitomycin C (10 µg/ml; M0503, Sigma) in DMEM/F12 medium supplemented with 0.1% BSA for two hours. Then, inserts were removed and cells were washed with PBS. Subsequently, cells were treated and the free area between cells was observed by capturing images for four days every 24 hours with an Olympus microscope (IX51) equipped with an Olympus digital camera. The areas between cells were calculated using Zen 3.2 (Carl Zeiss Microscopy GmbH). The free area between cells seeded onto each well of a 2-well insert at time 0 was considered as 100%.

4.4.1.4. Collagen gel contraction assay

The collagen contraction assay also known as collagen gel contraction is a three-dimensional *in vitro* method used to identify the factors influencing the contractile behaviour of activated cells, such as fibroblasts, whether in both physiological and pathological conditions. The assay permits the observation of alteration in the surface area of collagen gels over a specific time period. The collagen gel contraction assay was performed in accordance with the methodology previously described by (Bukowska et al., 2018). For this purpose, fibroblasts (2×10^4 cells suspended in 250 µl of fibroblast culture medium) were mixed with 250 µl of a cold rat tail collagen solution (3440-100-01, R&D Systems), followed by neutralization with 4 µl of 1 M NaOH (810981118, POCH). Subsequently, 250 µl of the aforementioned mixture was poured into each well of a 48-well plate where it was allowed to polymerize at room temperature for 20 minutes. Following solidification, the gel matrices were overlaid with 500 µl of DMEM/F12 medium containing 0.1% BSA. The edge of the gel was carefully outlined with a pipette tip to detach it from the plate walls, and then cells were treated. The collagen gels were photographed every 24 hours using the ChemiDoc Touch Imaging System (BioRad). The areas of the gels were quantified using the ImageJ software (SciJava software; National Institutes of Health; NIH). The extent of gel contraction was calculated as the percentage of the initial gel area at time 0, which was considered to be 100%.

4.4.2. Molecular biology methods

4.4.2.1. RNA extraction from tissue

Total ribonucleic acid (RNA) was extracted from tissues using miRVANA kit (AM1560, Invitrogen) in research task 1. For this purpose, 50 mg of frozen mare's

endometrium was pulverised with liquid nitrogen in a pre-chilled mortar and pestle. Using small amounts of liquid nitrogen, the powdered tissue was poured into prechilled 1.5 ml tubes. Then, 500 µl of Lysis/Binding buffer was added to each tube and was mixed thoroughly, until homogeneity. Before organic extraction, 50 µl of miRNA Homogenate Additive was added into each tube, mixed by vortexing, and the tubes were left on ice for 10 minutes. The organic extraction was performed by adding 500 µl of Acid-Phenol:Chloroform provided with the kit, mixing the tubes by vortexing for 60 seconds, and centrifuging for 5 minutes at maximum speed ($10.000 \times g$) at room temperature to separate the aqueous and organic phases. After centrifugation, the aqueous (upper) phase was collected into new 1.5 ml tube, and the volume of the collected phase was noted. Further, 1.25 volume (usually around 500 µl) of 100% ethanol (1.08543, Sigma) was added to each tube. The lysate/ethanol mixture was then transferred onto the filter cartridges, placed into a collection tubes, and centrifuged for 15 seconds to pass the mixture through the filter cartridges at $10.000 \times g$ at room temperature. Then, the flow-through was discarded, and the filter was washed with 700 µl of Wash Solution 1, followed by 10 seconds of centrifugation at $10.000 \times g$. The flow-through was discarded and the Filter Cartridges was placed in the same collection tube. Then, the Filter was washed twice with 500 µl of Wash Solution 2/3, the flow-through was discarded, the filters were placed in the same collection tubes and centrifuged for 1 minute to remove residual fluid from the filter. Next, the Filter Cartridges were transferred into new collection tubes. The elution of RNA was performed using 100 µl of preheated to 95°C nuclease-free water to the centre of the filter cartridges. To recover RNA, the tubes with filters were centrifuged for 30 seconds at a maximum speed. The concentration and quality of total RNA was determined spectrophotometrically using DeNovix Spectrofotometer. The ratio of absorbance at 260 and 280 nm ($A_{260/280}$) was approximately 2. RNA sample were stored at -80°C for further analysis.

4.4.2.2. RNA extraction from cells

Total RNA was extracted from *in vitro* cultured fibroblasts (Research task 2 and 3) using TRI Reagent according to the manufacturer's instruction. After desired treatments, cells were washed with sterile PBS, and 333 µl of TRI reagent was poured into each well of 6-well cell culture plates. Since each experiment was performed in three technical replicates, the total volume for each biological replicates was 1 ml of TRI Reagent. Then, cells were scrapped using a 1 ml pipette tip. Subsequently, cells

suspension in TRI reagent was transferred into 1.5 ml tubes and stored at -80°C until RNA extraction. At the day of isolation, TRI reagent mixtures were incubated 5 minutes at room temperature. Then, the mixture was pipetted several times, and 200 µl of chloroform was added to each tube. Next, the tubes were inverted several times to mix the contents, incubated for 5 minutes at room temperature and centrifuged at $12.000 \times g$ for 15 minutes at 4°C. After centrifugation, the upper (aqueous) phase, containing RNA, was transferred into new collection tube, and mixed with 500 µl of isopropanol (751500111, POCH), and incubated for 15 minutes on ice. Then, tubes were centrifuged at $12.000 \times g$ for 10 minutes at 4°C. After centrifugation, the supernatant was discarded and the pellet was washed twice with 1 ml of 75% ethanol and centrifuged at $8.000 \times g$ for 6 minutes at 4°C. After second centrifugation, the supernatant was discarded and the pellet was dried in inverted tubes placed on paper towels for 15-30 minutes. Then, the pellet was suspended in 50 µl of nuclease-free water. The concentration and quality of total RNA was determined spectrophotometrically using DeNovix Spectrophotometer. The ratio of absorbance at 260 and 280 nm (A_{260}/A_{280}) was approximately 2. Moreover, RNA integrity number (RIN), which is a measure of the integrity and level of degradation of an RNA sample was assessed for each RNA isolate using Agilent 2100 system and Expert software (Agilent Technologies, Inc., Santa Clara, CA, USA). All samples had RIN approximately 10 and were processed further. The isolated RNA was stored at -80°C for further analysis.

4.4.2.3. Reverse transcription

Total RNA (2 µg) extracted from tissues and cells was used to obtain complementary DNA (cDNA). At first 2 µg of RNA diluted in 10 µl of nuclease-free water was treated with DNase (AMPD1, Sigma). For this purpose, 2 µl of 1:1 mixture of DNase I and Reaction Buffer was added to each RNA sample, and the DNase treatment was performed at room temperature for 15 minutes. After incubation, 1 µl of Stop solution was added to each tube followed by incubation for 10 minutes at 70°C. Then, tubes were placed on ice and proceed to reverse-transcription (RT). The RT was performed with the use of High-Capacity cDNA Reverse Transcription Kit (4368813, Applied Biosystems). To obtain cDNA, to tubes with DNase-treated RNA, 7 µl of 2X RT master mix was added. The 2X RT master mix contained of 2 µl of 10X RT buffer, 0.8 µl of 25X dNTP mix, 2 µl of 10X RT random primers, 1 µl of Multiscribe Reverse Transcriptase, 0.2 µl of nuclease-free water, and 1 µl of RNase Inhibitor for each reaction. Then, tubes were placed in a thermal cycler. The cycling conditions were as follows: 10 minutes at 25°C,

120 minutes at 37°C, followed by 5 minutes at 85°C. After RT, cDNA was stored at -20°C until qPCR analysis.

4.4.2.4. qPCR

The qPCR reaction was performed in a final volume of 10 µl, using 3 µl of cDNA (in total 10 ng), 0.5 µl of specific TaqMan primers with probes, 5 µl TaqMan Universal PCR Master Mix II (4440049; Applied Biosystems), and 1.5 µl nuclease-free water, on 384-well plates. The complete list of used TaqMan Probes (Applied Biosystems) is presented in the Table 3. All samples were run in duplicates. Amplification was performed with initial denaturation for 10 minutes at 95°C, followed by 45 cycles of 15 seconds at 95°C and 60 seconds at 60°C with 7900HT QPCR System (Agilent Technologies, Waltham, MA, USA). As a negative control, nuclease-free water instead of template cDNA was used.

Table 3. The list of TaqMan probes used for qPCR.

gene name	gene symbol	TaqMan probe
actin alpha 2 smooth muscle	ACTA2	Ec07040967_m1
collagen type I alpha 1 chain	COL1A1	Ec03469676_m1
collagen type III alpha 1 chain	COL3A1	Ec03469743_m1
fibronectin 1	FN1	Ec03470760_m1
hypoxanthine phosphoribosyl transferase 1	HPRT1	Ec03470217_m1
interferon gamma	IFNG	Ec03468606_m1
interferon gamma receptor 1	IFNGR1	Ec07052884_m1
interleukin 13	IL-13	Ec03470543_m1
interleukin 13 receptor subunit alpha 1	IL13RA1	Ec07012041_m1
interleukin 4	IL-4	Ec03468790_m1
interleukin 4 receptor	IL4R	Ec03467555_m1
matrix metalloproteinase 2	MMP2	Ec03469995_m1
matrix metalloproteinase 3	MMP3	Ec03468676_m1
matrix metalloproteinase 9	MMP9	Ec03469193_m1
succinate dehydrogenase complex flavoprotein subunit A	SDHA	Ec03470487_m1
tissue metalloproteinase inhibitor 1	TIMP1	Ec03468772_m1
tissue metalloproteinase inhibitor 2	TIMP2	Ec03470558_m1

The qPCR data were analysed by the method described previously (Zhao & Fernald, 2005) (<http://miner.ewindup.cn/miner/>). It is a method for quantifying qPCR results using calculations based on the kinetics of individual PCR reaction without the need for the standard curve, independent of any assumptions or subjective judgments, which allows direct calculation of efficiency and the cycle of threshold (Ct). Two

housekeeping genes: *succinate dehydrogenase complex flavoprotein subunit A (SDHA)* and *hypoxanthine phosphoribosyltransferase 1 (HPRT1)* were used to normalize mRNA levels between samples, as described previously (Szóstek-Mioduchowska et al., 2023). The relative concentration of mRNA (R0) for each target and reference RNAs – *SDHA* and *HPRT* was calculated using the equation $R0 = 1 / (1 + E)^{Ct}$, where, E is the average gene efficiency and Ct is the cycle number at the threshold. The relative gene expression was calculated as $R0_{\text{target gene}} / R0_{\text{reference gene}}$ and was expressed in arbitrary units. NormFinder was used to confirm the selection of the most stable reference genes for the normalization of the results (Andersen et al., 2004).

4.4.2.5. Library preparation and Next Generation Sequencing (NGS)

The library preparation and NGS analysis was performed by MacroGen Europe, Netherlands. Standard library preparation steps including mRNA selection, fragmentation, cDNA synthesis, end repair, adenylation, indexed adapters ligation, and amplification were followed by a qualitative evaluation (Agilent TapeStation 2200) and quantitation (Qubit, Thermo Fisher Scientific). In total, 1000 ng of RNA was used for library construction with the TruSeq RNA Sample Prep v2 kit (Illumina, San Diego, CA). The libraries were sequenced in a single 50 bp run (1×50 bp) on the HiScanSQ system using the TruSeq SBSv3 Sequencing kit, to obtain 15-20 million reads/sample. The NGS analysis was performed with the use of NovaSeq6000 sequencing platform.

4.4.2.6. The bioinformatic analysis of NGS data

RNA-seq data generated as part of this study are openly available without restrictions. The data have been deposited in the Sequence Read Archive (SRA) under accession number PRJNA115274 (Research task 2) and PRJNA1154451 (Research task 3).

The raw reads underwent initial quality assessment and clean-up procedures using FastQC (Andrews, 2015) and Trimmomatic (Bolger et al., 2014). Subsequently, the reads were aligned to the horse reference genome (EquCab3.0) employing STAR (Dobin et al., 2013), followed by read counting using feature Counts 2.0.3 (Liao et al., 2014). To compare transcriptomic profiles across samples, Principal Component Analysis (PCA) was conducted on rlog-transformed count values (Love, 2014), revealing distinct major clusters corresponding to each category and treatment.

Differential gene expression analysis was performed using DESeq2 (Love, 2014), with a predefined criterion of an absolute value of log2fold change ($\log_2FC \geq 1.0$) and a false discovery rate (FDR) adjusted p-value < 0.05 to identify significantly differentially expressed genes (DEGs).

To identify the biological functions associated with these genes, gene ontology (GO) enrichment analysis was carried out using the R package topGO (Alexa, 2022) with Fisher's exact test. Gene names were mapped to GO terms utilizing the org.Hs.eg.db package (Carlson, 2019), and only GO terms with an adjusted p-value < 0.05 were considered significantly enriched.

To obtain more comprehensive view of gene functions and interactions gene enrichment was also performed based on the Kyoto Encyclopedia of Genes and Genomes (KEGG) database using clusterProfiler (Wu et al., 2012). Kyoto Encyclopedia of Genes and Genomes categories exhibiting an adjusted p-value < 0.05 were considered significantly enriched. The results of the analysis were visualized using R (R Core Team, 2021).

4.4.2.7. Protein extraction

The protein extraction was performed using RIPA buffer (Cayman 1001026 containing 10 ml of 250 mM Tris-HCl, pH 7.6, containing 750 mM sodium chloride, 5% NP-40, 2.5% sodium deoxycholate, and 0.5% SDS) in the presence of a protease inhibitors (S8820, SIGMAFAST™, Sigma) and phosphatase inhibitor (4906845001, PhosSTOP™, Roche).

For protein extraction, 100 mg of mare's frozen endometria were grinded with liquid nitrogen in a prechilled mortar and pestle sitting in a bed of dry ice. Using small amounts of liquid nitrogen, the powdered tissue was poured into prechilled 1.5 ml tubes, and proceed for protein extraction. Whilst cultured fibroblasts were washed with sterile PBS, RIPA buffer was added to the culture flasks and cells were scraped on ice using cell scrapers. Subsequently, both tissue homogenates and cell lysates were sonicated 5 times with settings: cycle at 0.5, amplitude 20, being constantly placed on ice. Then, tubes were incubated on ice for 1 hour. After incubation, tubes were centrifuged at $12.000 \times g$ for 15 minutes at 4°C. Subsequently, the supernatant was collected and aliquoted and stored at -80°C until further analysis.

The protein concentration was determined using the bicinchoninic acid (BCA) protein assay kit (BCA1; Sigma). For BCA protein assay, 10 µl protein samples were

placed in duplicated into 96-well plate. Then, 200 µl of 49:1 ratio of BCA solution and 4% (w/v) CuSO₄ · 5H₂O Solution was added into each well. The plates were covered with adherent foil and incubated at 37°C for 30 minutes. The absorbance was measured using BioTek Microplate reader at a wavelength 562 nm. The protein concentration was determined by comparison to a standard curve which ranged from 125 to 1000 µg/ml of BSA. The protein samples then were stored at -80°C for further analysis.

4.4.2.8. Western Blot

Equal amounts of protein were dissolved in SDS gel-loading buffer, containing 0.25 M Tris-HCl (T3253, Sigma), 10% SDS (L3771, Sigma), 50% glycerol (44320113, POCH), 0.25% bromophenol blue (B-8026, Sigma), 2% 2-mercaptoethanol (M3148, Sigma), and heated to 95 °C for 5 minutes. Then, the tubes were spinned to remove any precipitates placed into wells of gels, and separated according to protein molecular weight using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). For visualization of protein separation, as indicator of selected molecular weight of proteins within the range of 10 to 250 kDa, Prestained Plus Protein Ladder was loaded on gels along with protein lysates (26619, Thermo Fisher Scientific). Separated proteins were then electroblotted using a semi-dry transfer method using Trans-Blot Turbo Transfer System (Bio-Rad) onto PVDF membranes (Immobilon-P Transfer Membrane; IPVH00010; Millipore, Billerica, MA, USA) under following parameters: 90 minutes, 200 mA, 17V. Then, non-specific binding sites in the membranes were blocked in 5% non-fat dry milk in TBS-T buffer (Tris-buffered saline, containing 0.1% Tween-20) for 1 hour at room temperature. Subsequently, the membranes were incubated overnight with primary antibodies at 4°C. The full list of used primary antibodies as well as concentration is depicted in the Table 4. After primary antibody incubation, membranes were washed three times for 10 minutes with TBS-T. Then, the proteins were detected by incubating membranes for 1 hour at room temperature with secondary antibodies. After three 10 minutes washing with TBS-T, signals were detected by chemiluminescence using Westar Eta C Ultra 2.0 HRP Substrate (XLS075; Cyanagen, Bologna, Italy) using ChemiDoc Touch Imaging System (Bio-Rad). GAPDH protein expression was used as an internal control. The intensity of the chemiluminescence reaction was estimated by measuring the optical density in the defined area by computerized densitometry using Image Lab Software version 6.0 (Bio-Rad Laboratories).

Table 4. The list of antibodies used for western blot (WB) analysis.

primary antibodies				
antigen		catalogue number and company	host species	concentration
α-smooth muscle actin	ACTA2	Ab5694, Abcam	rabbit	1:2000
collagen type I	COL1	20121, Novotec	rabbit	1:1000
collagen type III	COL3	Ab7778, Abcam	rabbit	1:1000
glyceraldehyde 3-phosphate dehydrogenase	GAPDH	Ab8245, Abcam	mouse	1:10000
fibronectin 1	FN1	Ab2413, Abcam	rabbit	1:2000
metalloproteinase 2	MMP-2	Ab97779, Abcam	rabbit	1:1000
metalloproteinase 3	MMP-3	Ab223666, Abcam	goat	1:1000
metalloproteinase 9	MMP-9	Ab73734, Abcam	rabbit	1:1000
interferon gamma receptor	IFN- γ R1	AF7734, Affinity	rabbit	1:1000
interleukin 4 receptor subunit alpha	IL-4RA	Ab203398, Abcam	rabbit	1:1000
interleukin 13 receptor alpha 1	IL-13RA	Ab233528, Abcam	rabbit	1:1000
secondary antibodies				
species reactivity	conjugate	catalogue number	host	concentration
mouse	HRP	A90-116P, Bethyl	goat	1:7500
rabbit	HRP	Ab205718, Abcam	goat	1:25000
goat	HRP	A50-100P, Bethyl	rabbit	1:7500

4.4.2.9. Zymography

The gelatinolytic activity of MMP-2 and MMP-9 was detected using zymography, as described previously (Kotłowska et al., 2005). The samples (cell culture media: 5 μ g of protein per well for MMP-2 and 25 μ g of protein for MMP-9 gelatinolytic activity) were loaded with nonreducing loading buffer into SDS polyacrylamide (10% v:v) gel polymerized with 0.1% gelatin. After electrophoresis, electrophoretograms were washed twice with 2.5% Triton X-100 for 40 minutes, incubated in development solution (50 mM Tris-HCl buffer, pH 7.5, containing 200 mM NaCl, 0.02% Triton X-100 with or without 5 mM CaCl₂) at 37 °C for 24 h. Electrophoretograms were then stained with Coomassie brilliant blue (0.025%) for 24 h and stored in 2% acetic acid. Matrix metalloproteinase 2 and MMP-9 degrade gelatin present in the acrylamide electrophoretograms. Thus, a clear lysis band indicates the presence of gelatinases and absence of gelatin band. In these samples, two major bands indicating potential gelatinolytic activity were obtained at

approximately 92 kDa for the pro-MMP-9 form and at approximately 72 kDa for the pro-MMP-2 form. The gelatinolytic activity was inhibited when electrophoretograms were incubated with development solution containing 5 mM EDTA, which inhibits MMP activity by chelating Ca^{2+} . Stimulation by Ca^{2+} and inhibition by EDTA strongly indicated the presence of MMP-9. The electrophoretograms were photographed, and digitized images were stored for further densitometric analysis using ImageJ software (National Institutes of Health, Bethesda, MD).

4.2.2.10. Flow cytometry

For FC analysis, cells (Th cells isolated from endometrium in research task 1 and differentiated Th1 and Th2 cells in Research Task 2) were washed in PBS and suspended in RPMI 1640 medium containing 10% FBS, containing Phorbol 12-myristate 13-acetate (PMA, P1585, SIGMA) at a concentration 50 ng/ml and calcium ionophore – ionomycin (IAA, I9657, Sigma) at a concentration 1 $\mu\text{g/ml}$ for 2 hours and monensin solution (00-4505-51, eBioscience) at a final concentration 2 μM , for additional 3 hours. Both PMA and IAA are commonly used for inducing cytokine production in assays requiring the intracellular detection of cytokines in immune cells. Monensin is an inhibitor of intracellular protein transport. The incubation of cells with monensin results in the accumulation of proteins within the endoplasmic reticulum. The addition of monensin to differentiated T cells results in enhanced detection of intracellular cytokines by FC. Subsequently, the presence of Th cells markers: CD3 and CD4 as well as cytokines secreted by Th1 ($\text{IFN-}\gamma$) and Th2 (IL-4) was confirmed by FC based on the protocols described recently (Espinosa et al., 2020; Yang et al., 2020). The staining of CD3+, CD4+ and $\text{IFN-}\gamma$ or IL-4 positive cells was performed using Leucoperm (BUF09B, Bio-Rad) according to manufacturer's instructions. Briefly, 1×10^6 cells were suspended in 90 μl of PBS containing 1% BSA and 10 μl of CD4 antibodies conjugated with PE (MA5-28356, Thermo Fisher Scientific) was added. The suspension was incubated at room temperature for 1 hour. After incubation, cells were washed with PBS containing 1% BSA. Then, supernatant was removed and cells were suspended in 100 μl of fixation buffer (Reagent A), and incubated for 15 minutes at room temperature, followed by washing with PBS containing 1% BSA. Subsequently, the supernatant was removed and cells were suspended in permeabilization medium (Reagent B), 10 μl of anti-CD3 antibodies conjugated with PB fluorochrome (MCA1477, BioRad), 10 μl of anti- $\text{IFN-}\gamma$ antibodies conjugated with Alexa Fluor 647 fluorochrome (MCA1783A647, Bio-Rad),

20 µl of anti-IL-4 antibodies conjugated with Alexa Fluor 488 fluorochrome (53-7049-42, eBioscience) were added. Then, cells were incubated for 1 hour, at room temperature in darkness. After incubation, cells were washed with PBS containing 1% BSA (5 minutes, 500 × g, room temperature) and suspended in 1 ml of PBS containing 1% BSA and subjected to FC analysis, using BD FACSAria II Cell Sorter, Beckton Dickinson and analysed using BD FCSDiva Software v6.1.3.

4.4.2.11. Immunofluorescence staining

To perform immunofluorescence staining of ECM-associated markers in mare endometrial fibroblasts, the cells were seeded onto 8-well chamber slides (Nunc™ Lab-Tek™ Chamber Slide System, 177429). Following the desired treatments, the cells were washed with sterile-filtered PBS, fixed using 4% paraformaldehyde (715400427, POCH) at room temperature for 10 minutes, washed three times with PBS containing 0.1% Tween-20 (P1379, Sigma), and permeabilized with PBS containing 0.5% TritonX-100 (T8787, Sigma), followed by blocking of non-specific binding sites for one hour in room temperature with 3% BSA in PBS in a humid chamber. Then, the blocking solution was removed and the primary antibodies at the concentration specified in the Table 5 were added and incubated for one hour at room temperature in a humid chamber. This was followed by overnight incubation at 4°C. A negative control was conducted by omitting the primary antibodies.

On the following day, the cells were washed with three times for 5 minutes with PBS containing 0.1% Tween-20. Then, they were incubated with secondary antibodies for one hour in room temperature in a humid chamber with the absence of light. Subsequently, the cells were washed three times for five minutes with PBS containing 0.1% Tween-20. The upper chambers were detached from a microscopic slide, mounted in Fluoroshield with DAPI (F6057, Sigma), and covered with cover slips.

Table 5. The antibodies used for immunofluorescence staining (IF).

primary antibodies				
Antigen		catalogue number and company	host species	concentration
α -smooth muscle actin	ACTA2	Ab5694, Abcam	rabbit	1:100
collagen type I	COL1	20121, Novotec	rabbit	1:50
collagen alpha-1(III) chain	COL3A1	Ab7778, Abcam	rabbit	1:100
fibronectin 1	FN1	Ab2413, Abcam	rabbit	1:100
metalloproteinase 2	MMP2	Ab97779, Abcam	rabbit	1:100
metalloproteinase 3	MMP3	Ab223666, Abcam	goat	1:75
metalloproteinase 9	MMP9	Ab73734, Abcam	rabbit	1:200
vimentin	VIM	V6630, Sigma	mouse	1:40
interleukin 13	IL-13	KP1557E, KingFisher	rabbit	1:50
interferon γ	IFN- γ	PB028E, KingFisher	rabbit	1:50
cluster of differentiation 4	CD4	MA5-28356, Creative Biolabs	mouse	1:10
secondary antibodies				
species reactivity	fluorochrome	catalogue number and company	host species	concentration
mouse	Alexa Fluor 488	A11029 Thermo Fisher	goat	1:200
rabbit	Alexa Fluor 594	A210207, Thermo Fisher	donkey	1:200
goat	Alexa Fluor 488	A11055, Thermo Fisher	donkey	1:200

4.4.2.12. Enzyme-linked immunosorbent assay (ELISA)

The enzyme-linked immunosorbent assay (ELISA) was employed to determine the protein concentration of IFN- γ , IL-4 and IL-13 in the lysates of mare endometrial tissue as well as TIMP1 and TIMP2 concentration in lysates of mare endometrial fibroblasts treated with IL-4 and IL-13. The amount of protein used for each assay along with the inter- and intra-assay precision of used kits is provided in the Table 6. The analyses were performed following manufacturer's instructions. Briefly, 100 μ l of standards solutions as well as samples were loaded into wells of precoated plates. Subsequently, the plates were sealed with adhesive foil and incubated at 37°C. After the incubation, the cover was removed, the liquid was discarded, and wells were washed three times with 1X wash buffer. Then, 100 μ l of biotin-labelled antibodies working solution was poured into each well, followed by sealing the plates and incubation for 30 minutes at 37°C. Then, wells were washed three times with washing buffer and 100 μ l of streptavidin-horseradish peroxidase (HRP) working solution was added into each well, followed by 50 minutes of incubation at 37°C. After the incubation, wells were washed five times and then 90 μ l of 3,3',5,5'-Tetramethylbenzidine (TMB) was added to each well, and plates were incubated

at 37°C for 20 minutes. After incubation, 10 µl of stop solution was added into each well, followed by immediate measurement of absorbance at 450 nm.

Table 6. The ELISA kits used for the determination of IFN- γ , IL-4 and IL-13 concentration in the tissue lysates and TIMP1 and TIMP2 concentration in the cell lysates.

	catalogue number and company	amount of protein loaded into each well	range pf the standard curve	intra- assay CV	inter- assay CV
equine interferon γ	EHS0005, Fine Test	400 µg	500-7.812 pg/ml	<6%	<6%
equine interleukin 4	EHS0032, Fine test	100 µg	500-7.813 pg/ml	<7%	<10%
animal interleukin 13	orb779722, biorbyt	200 µg	500-7.82 pg/ml	<8%	<10%
equine tissue inhibitor of metalloproteinase 1	orb780284, biorbyt	15 µg	40-0.63 ng/ml	<8%	<10%
equine tissue inhibitor of metalloproteinase 2	orb779686, biorbyt	15 µg	500-7.82 ng/ml	<8%	<10%

4.5. Statistical analysis

All data were subjected to a test for normality using the Shapiro-Wilk test (GraphPad Prism version 10.2.0 for Windows, GraphPad Software, San Diego, California USA). A number of statistical tests were employed, dependent on the nature of the experiments conducted. In the event that the assumptions of normal distribution were not met, non-parametric statistical analyses were conducted. The results were considered to be significantly different when the p value was less than 0.05. The results are presented as the mean $\pm$ standard deviation (SD).

In the research task 1, statistical differences in the endometrial ratio of Th1 to Th2 cells, the gene expression of *IFN- γ* , *IFN- γ R*, *IL-4*, *IL-4R*, *IL-13*, and *IL-13R*, protein abundance of IFN- γ R, IL-4R, and IL-13R as well as concentration of IFN- γ , IL-4, IL-13, in mare endometria in the mid-luteal and follicular phases of the oestrous cycle at each category according to Kenney and Doig (1986) were determined using two-way ANOVA followed by post-hoc Tukey test.

In the research task 2, statistical differences in the proliferation, viability, and gene expression of ECM-associated markers (*Col1a1*, *Col3a1*, *FN1*, *ACTA2*, *MMP-2*, *-3*, *-9*, *TIMP1*, and *-2*) after Th1-CM and Th2-CM treatment were determined using Student t-test. If the data did not show a normal distribution, the nonparametric Mann Whitney U test was performed.

In the research task 3, statistical differences in the proliferation, viability, gene expression of ECM-associated markers (*Col1a1*, *Col3a1*, *FN1*, *ACTA2*, *MMP-2*, *-3*, *-9*, *TIMP1*, and *TIMP2*), protein abundance of ECM-associated markers (COL1, COL2, FN1, ACTA2, MMP2, MMP3, MMP9), level of TIMP-1 and TIMP-2, gelatinolytic activity of MMP2 and MMP9, and cell migration after cytokine treatment were determined using Student t-test. Whenever the normal distribution of data was not reached, the nonparametric Mann Whitney U test was performed.

5. Results

5.1 Research task 1: Analysis of Th1/Th2 cell ratios and cytokine expression in the endometrium of mares with endometrosis

5.1.1. Experiment 1. The endometrial Th1/Th2 cell ratios in the endometrium of mares with endometrosis

The percentage of Th1 cells (CD3⁺ CD4⁺ IFN- γ ⁺), Th2 cells (CD3⁺ CD4⁺ IL-4⁺), and the ratio of Th1 cells (CD3⁺ CD4⁺ IFN- γ ⁺) to Th2 cells (CD3⁺ CD4⁺ IL-4⁺) in the categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrous cycle are presented in Figure 10. There were no differences in the presence of Th1 cells (CD3⁺ CD4⁺ IFN- γ ⁺) ($p>0.05$; Fig. 10A), Th2 (CD3⁺ CD4⁺ IL-4⁺) ($p>0.05$; Fig. 10B), or Th1 cells (CD3⁺ CD4⁺ IFN- γ ⁺) to Th2 ratio (CD3⁺ CD4⁺ IL-4⁺) ($p>0.05$; Fig. 10B) categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrous cycle.

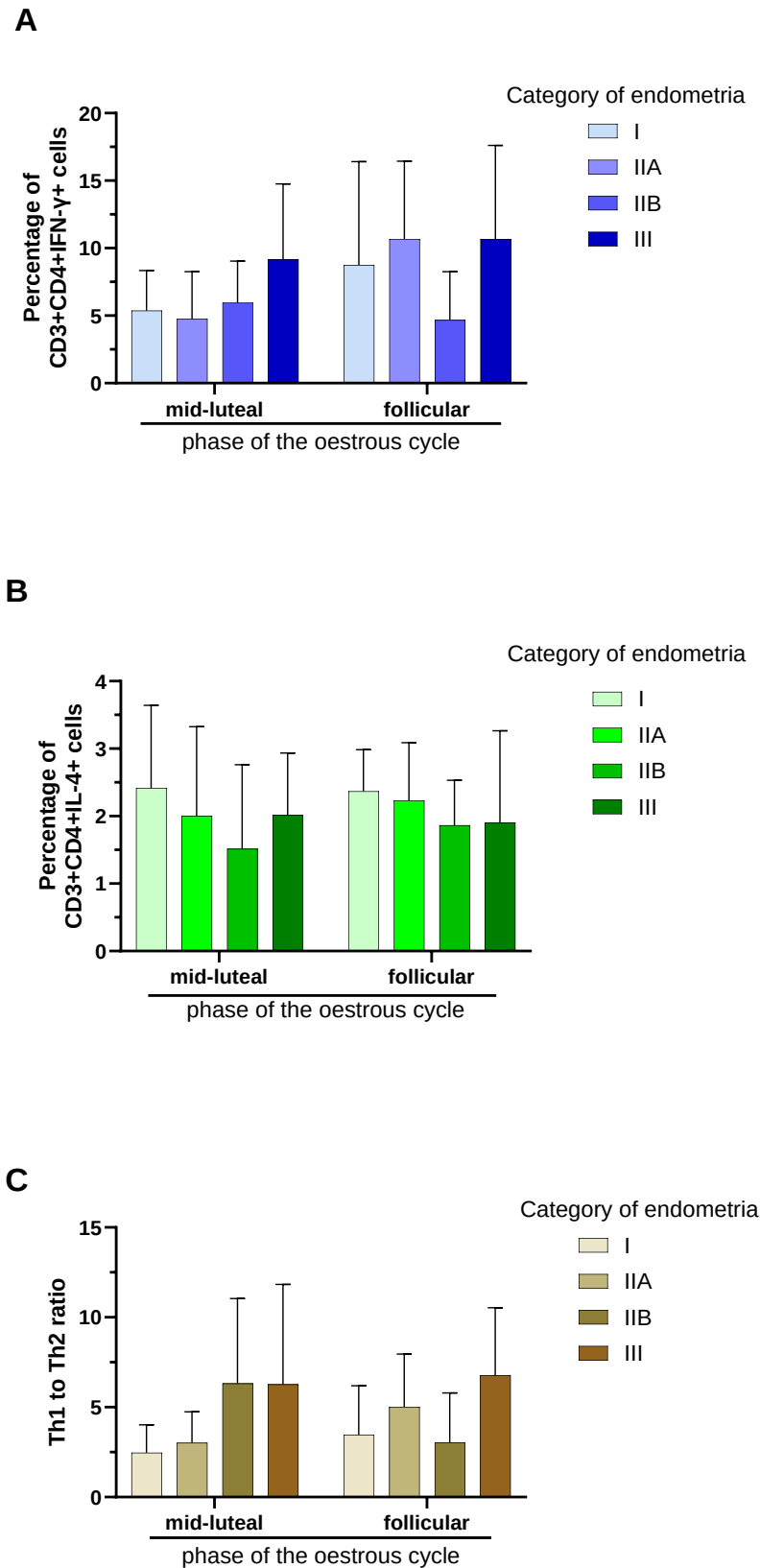


Figure 10. The percentage of Th1 cells (CD3⁺CD4⁺IFN⁺) (A) and Th 2 cells (CD3⁺CD4⁺IL-4⁺) (B) as well as the ratio of Th1 cells (CD3⁺CD4⁺IFN⁺) and Th 2 cells (CD3⁺CD4⁺IL-4⁺; C) in categories I, IIA, IIB, and III endometria of mare in the mid-luteal and follicular phases of the oestrus cycle. Results are presented as a mean $\pm$ standard deviation (SD). Data were analysed using a two-way ANOVA test ($p > 0.05$).

5.1.2. Experiment 2. The endometrial expression of IFN- γ , IL-4 and IL-13 and their respective receptors in the endometrium of mares with endometrosis

The gene expression and concentration of IFN- γ , IL-4, and IL-13, as well as the gene expression and protein abundance of their receptors: IFN- γ R1, IL-4RA, IL-13RA in categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrous cycle is shown in Figures 11-13.

No significant differences were observed in the endometrial gene expression of IFN- γ as well as in the gene expression and protein abundance of IFN- γ R1 within categories of endometria and phases of the oestrous cycle ($p>0.05$; Fig. 11A, C, D). The endometrial concentration of IFN- γ was down-regulated in categories I, IIA, IIB, and III endometria in the follicular phase of the oestrous cycle compared to the respective categories in the mid-luteal phase of the oestrous cycle ($p<0.05$, Fig. 11B).

No significant differences were observed in the endometrial gene expression and concentration of IL-4 as well as in the gene expression and protein abundance of IL-4RA within categories of endometria and phases of the oestrous cycle ($p>0.05$; Fig. 12A, B, C, D).

No significant differences were observed in the endometrial gene expression and concentration of IL-13 within categories of endometria and phases of the oestrous cycle ($p>0.05$; Fig. 13A, B). The gene expression of *IL-13RA* was down-regulated in category IIB and III endometria of mares in the follicular phase of the oestrous cycle, in comparison to the respective categories in the mid-luteal phase ($p<0.05$; Fig. 13C). The endometrial protein abundance of IL-13RA was down-regulated in categories I, IIA, IIB and III endometria in the follicular phase compared to the respective categories in the mid-luteal phase of the oestrous cycle ($p<0.05$; Fig. 13D).

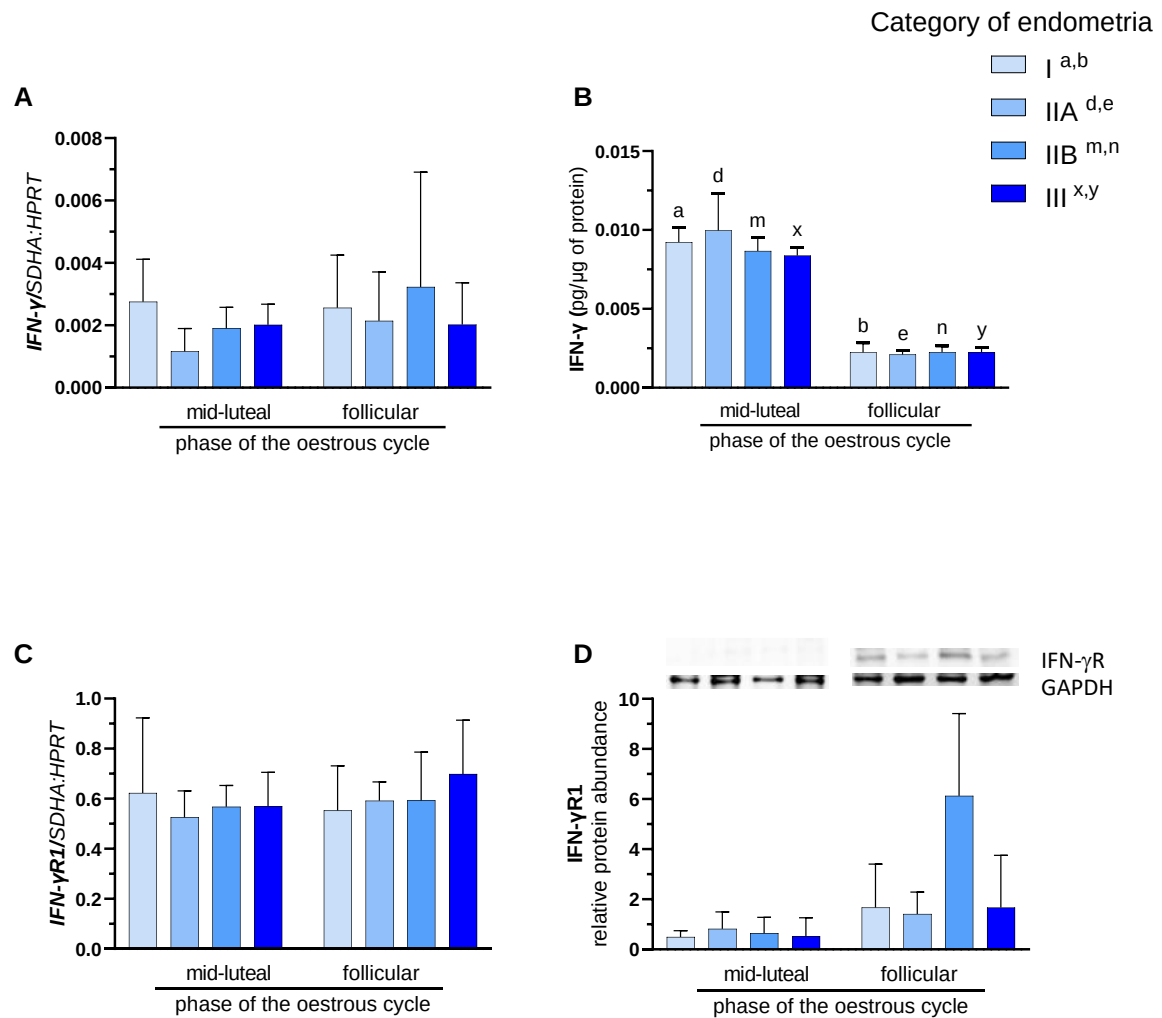


Figure 11. The gene expression and concentration of interferon (IFN)- γ (A, B) and the gene expression and protein abundance of IFN- γ receptor (IFN- γ R1; C, D) in categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrous cycle. Results are presented as a mean $\pm$ standard deviation (SD). The data were analysed using Kruskal-Wallis non-parametric test. Different letters above bars denote statistical differences between mid-luteal and follicular phases of the oestrous cycle within the respective endometrial categories ($p < 0.05$).

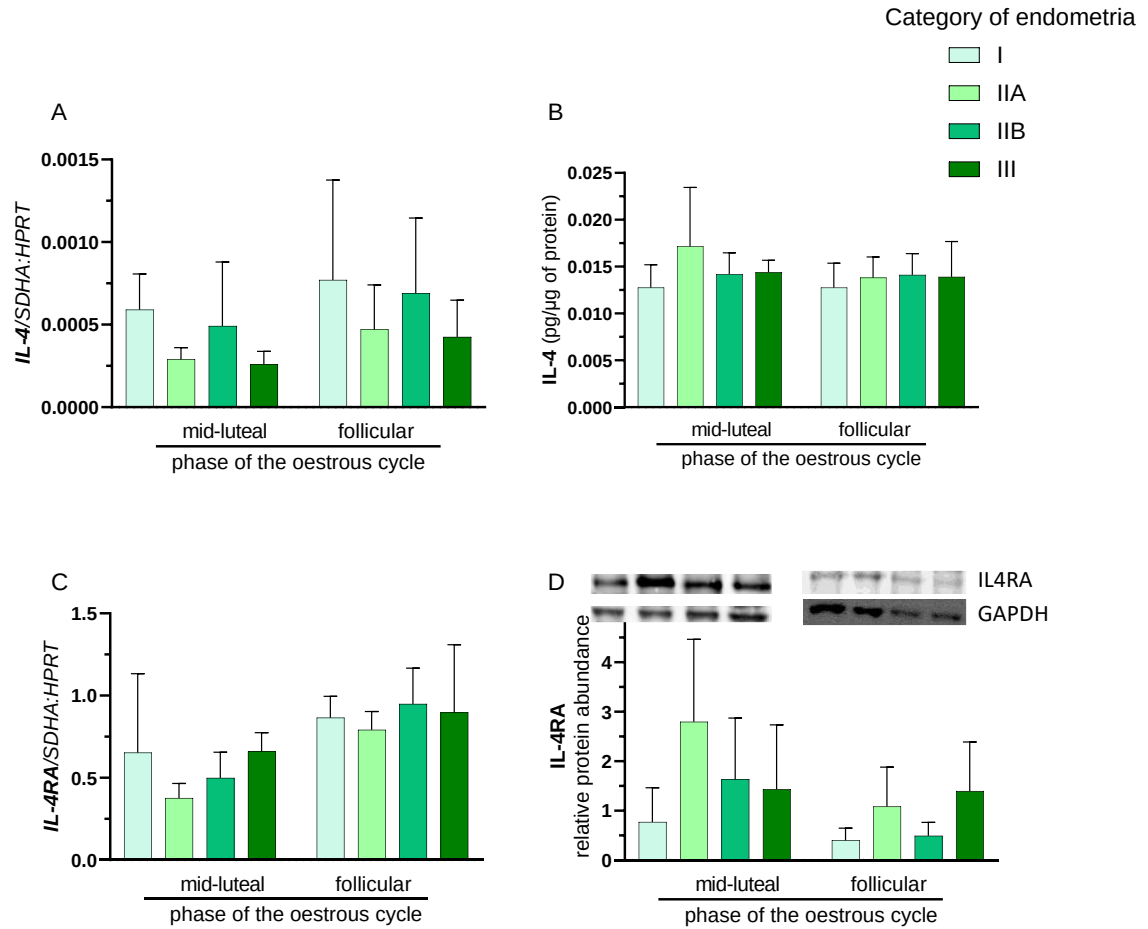


Figure 12. The gene expression and concentration of interleukin (IL)-4 (A, B) and the gene expression and protein abundance of IL-4 receptor (IL-4R1; C, D) in categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrus cycle. Results are presented as a mean $\pm$ standard deviation (SD). Data were analysed using a two-way ANOVA test ($p > 0.05$).

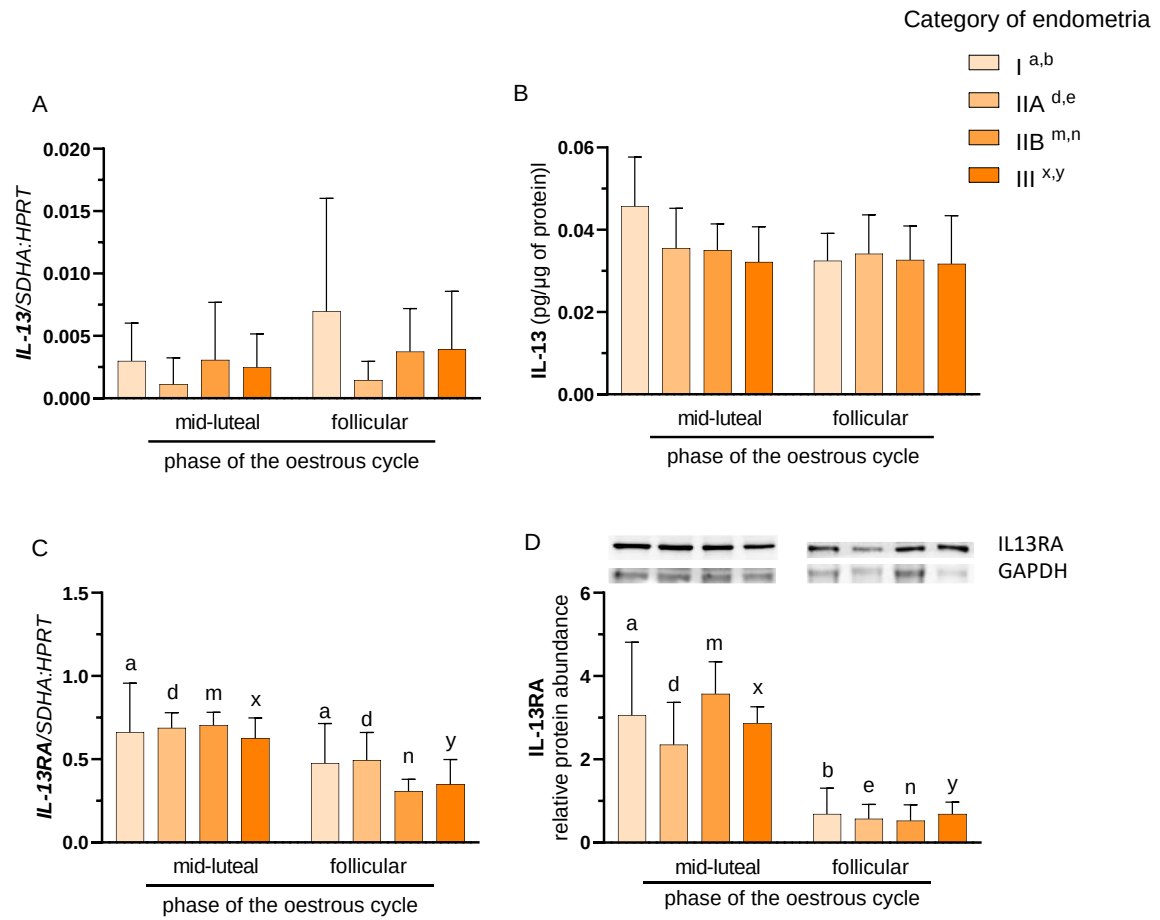


Figure 13. The gene expression and concentration of interleukin (IL)-13 (A, B) and the gene expression and protein abundance of IL-13 receptor (IL-13R1; C, D) in categories I, IIA, IIB, and III endometria of mares in the mid-luteal and follicular phases of the oestrus cycle. Results are presented as a mean $\pm$ standard deviation (SD). The data were analysed using Kruskal-Wallis non-parametric test. Different letters above bars denote statistical differences between mid-luteal and follicular phases of the oestrous cycle within the respective endometrial categories ($p < 0.05$).

5.2. Research task 2: The effect of the Th1 and Th2 cell secretome on the processes associated with the development of fibrosis in the mare endometrial fibroblasts in the progression of endometriosis

5.2.1. Experiment 1. The effect of the Th1 and Th2 secretome on the functional characteristic of mare endometrial fibroblasts

The effects of Th1-CM and Th2-CM treatment on the proliferation and viability of fibroblasts derived from category I endometria after 48 hours are shown in Figure 14. Both Th1-CM and Th2-CM increased proliferation ($p<0.05$; Fig. 14 A, C) and viability ($p<0.01$; Fig. 14 B, D) of endometrial fibroblasts.

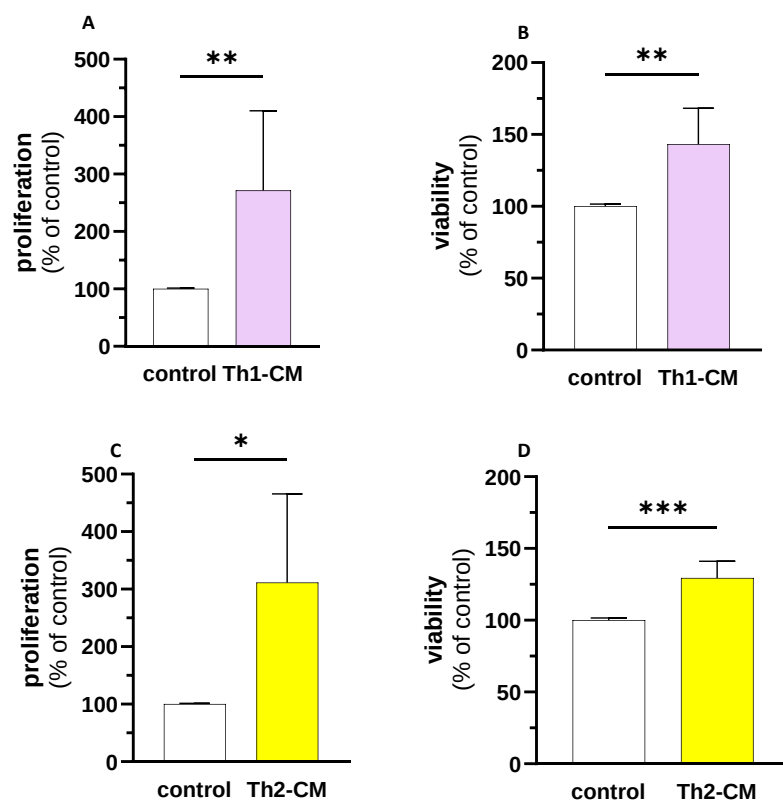


Figure 14. The effect of Th1 conditioned medium (Th1-CM; A, B) and Th2-CM (C, D) treatment on proliferation and viability of mare endometrial fibroblasts after 48 hours. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a percentage of the respective control group. Asterisks denote statistical differences (* $p<0.05$, ** $p<0.01$, *** $p<0.001$). The differences in proliferation and viability of fibroblasts between the control group and the Th1-CM treated group were determined using the unpaired Student-t test, while between the control group and the Th2-CM treated group were determined U-Mann Whitney non-parametric test.

5.2.2. Experiment 2. The effect of the Th1 and Th2 cell secretome on ECM-associated marker gene expression in endometrial fibroblasts

The effect of Th1-CM treatment on the gene expression of ECM-associated markers in fibroblasts derived from category I endometria after 48 hours is shown in Figure 15. Treatment with Th1-CM decreased *FN1* ($p<0.0001$; Fig. 15C), *ACTA2* ($p<0.001$; Fig. 15D), *MMP2* ($p<0.0001$; Fig. 15E), *TIMP2* ($p<0.0001$; Fig. 15I) and increased *TIMP1* ($P<0.0001$; Fig. 15H) gene expression in fibroblasts derived from category I endometria after 48 hours.

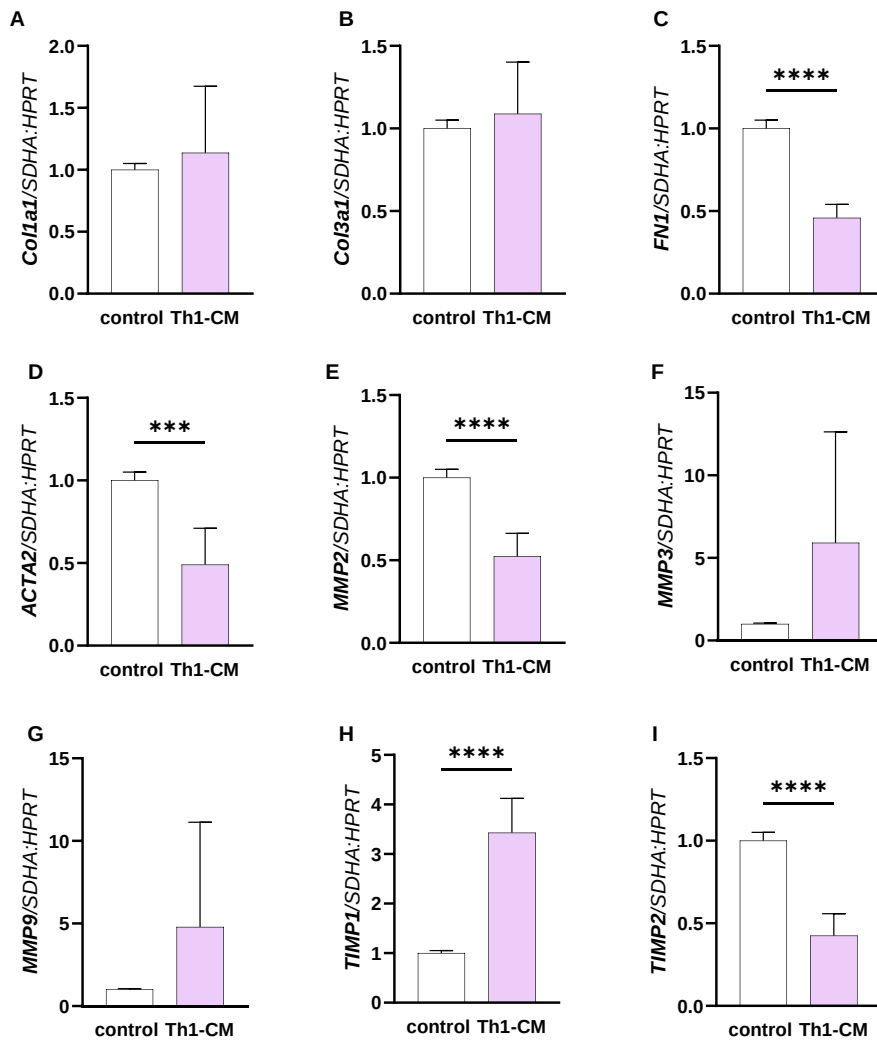


Figure 15. The effect of Th1 conditioned medium (Th1-CM) on gene expression of collagen (*Col*)1a1 (A), *Col3a1* (B), fibronectin 1 (*FN1*; C), α -smooth muscle actin (*ACTA2*; D), matrix metalloproteinase (*MMP*) 2 (E), *MMP3* (F), *MMP9* (G), tissue inhibitor of matrix metalloproteinase (*TIMP*)1 (H), and *TIMP2* (I) in fibroblasts derived from category I endometria after 48 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the control group. Asterisks denote statistical differences (*** $p<0.001$, **** $p<0.0001$), as determined by unpaired Student t-test.

The effect of Th2-CM treatment on the gene expression of ECM-associated markers in fibroblasts derived from category I endometria after 48 hours is shown in Figure 16. Treatment with Th2-CM decreased *FN1* ($p<0.0001$; Fig. 16C), *ACTA2* ($p<0.01$; Fig. 16D), *MMP2* ($p<0.001$; Fig. 16E), and *TIMP2* ($p<0.01$; Fig. 16I) and increased *TIMP1* ($p<0.0001$; Fig. 16H) gene expression in mare endometrial fibroblasts.

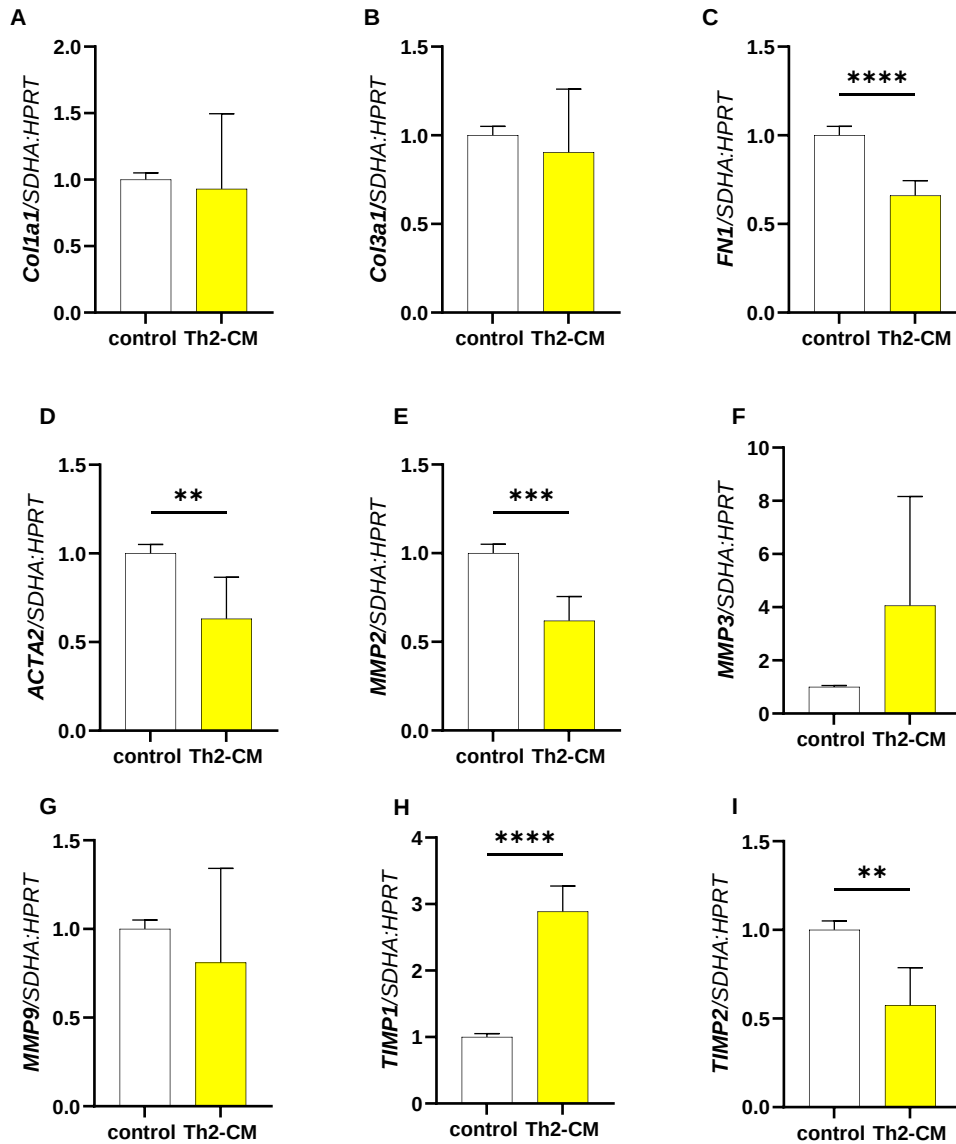


Figure 16. The effect of Th2 conditioned medium (Th2-CM) on gene expression of collagen (*Col*)1a1 (A), *Col3a1* (B), fibronectin 1 (*FN1*; C), α -smooth muscle actin (*ACTA2*; D), matrix metalloproteinase (*MMP*) 2 (E), *MMP3* (F), *MMP9* (G), tissue inhibitor of matrix metalloproteinase (*TIMP*)1 (H), and *TIMP2* (I) in fibroblasts derived category I endometria after 48 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the control group. Asterisks denote statistical differences (** $p<0.01$, *** $p<0.001$, **** $p<0.0001$), as determined by unpaired Student t-test.

5.2.3. Experiment 3. The effect of the Th1 and Th2 cell secretome on the transcriptome of endometrial fibroblasts

Between 20.977.026 and 25.774.507 reads were obtained in individual samples. Subsequent filtering resulted in an average of 19.794.574 reads, which were further mapped to the *Equus caballus* genome (EquCab3.0; Supplementary Table 1). The PCA results of mRNA expression patterns in fibroblasts derived from category I endometria in response to Th1-CM and Th2-CM treatment are presented in Figure 17 A and B, respectively. A summary of the datasets used in this experiment is presented in Supplementary Table 1.

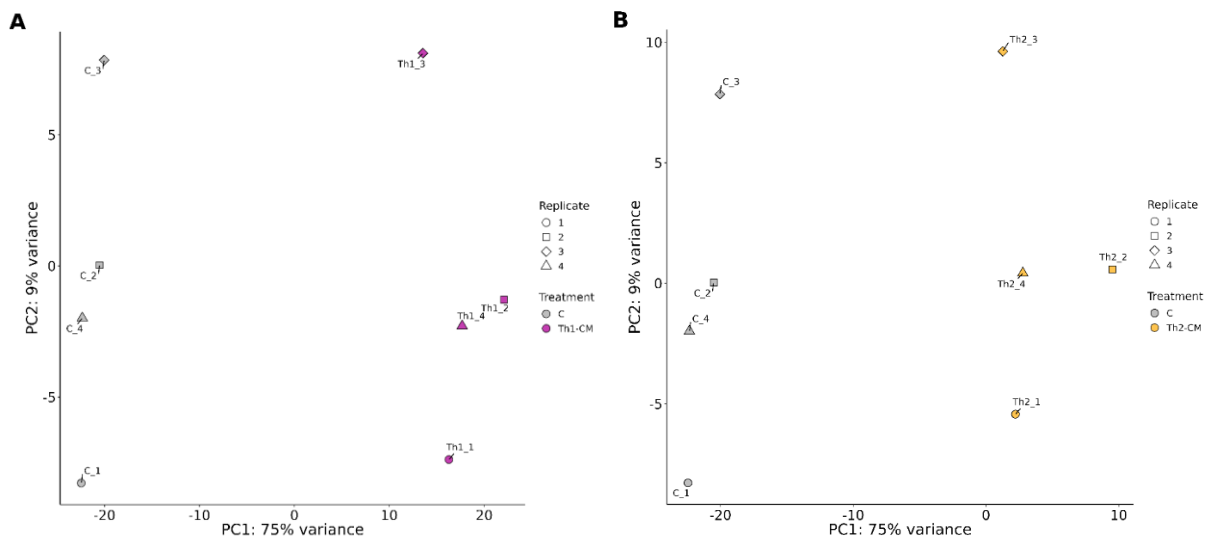


Figure 17. Graphical presentation of the first (PC1) and second (PC2) principal components (PCA) of the mRNA expression pattern in mare endometrial fibroblasts treated with Th1 conditioned medium (CM; A) and Th2-CM (B) for 48 hours. C – control group.

The treatment of fibroblasts derived from category I endometria with Th1-CM for 48 hours resulted in identification of 2140 DEGs. Out of these, expression of 1057 was downregulated, while expression of 1083 was upregulated as presented in Figure 18B. The five most upregulated DEGs were *COL6A5*, *CSF3R*, *ALOX15*, *NTRK1*, and *PDCD1LG2*. The five most significantly downregulated genes after Th1-CM treatment were *PRLR*, *CCDC3*, *DYSF*, *LMCD1*, and *ADAMTS8*. The full list of DEGs identified in this research task is provided in Supplementary Table 2.

Differentially expressed genes identified in fibroblasts treated with Th1-CM, derived from category I endometria, were subjected to functional analyses. The analysis involving Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes database (KEGG) indicated 902 biological processes (BP), 70 cellular components (CC), and 93 molecular function (MF) terms, as well as 19 KEGG pathways in which identified DEGs may be involved. Selected most enriched GO terms and KEGG pathways are presented in Figure 19.

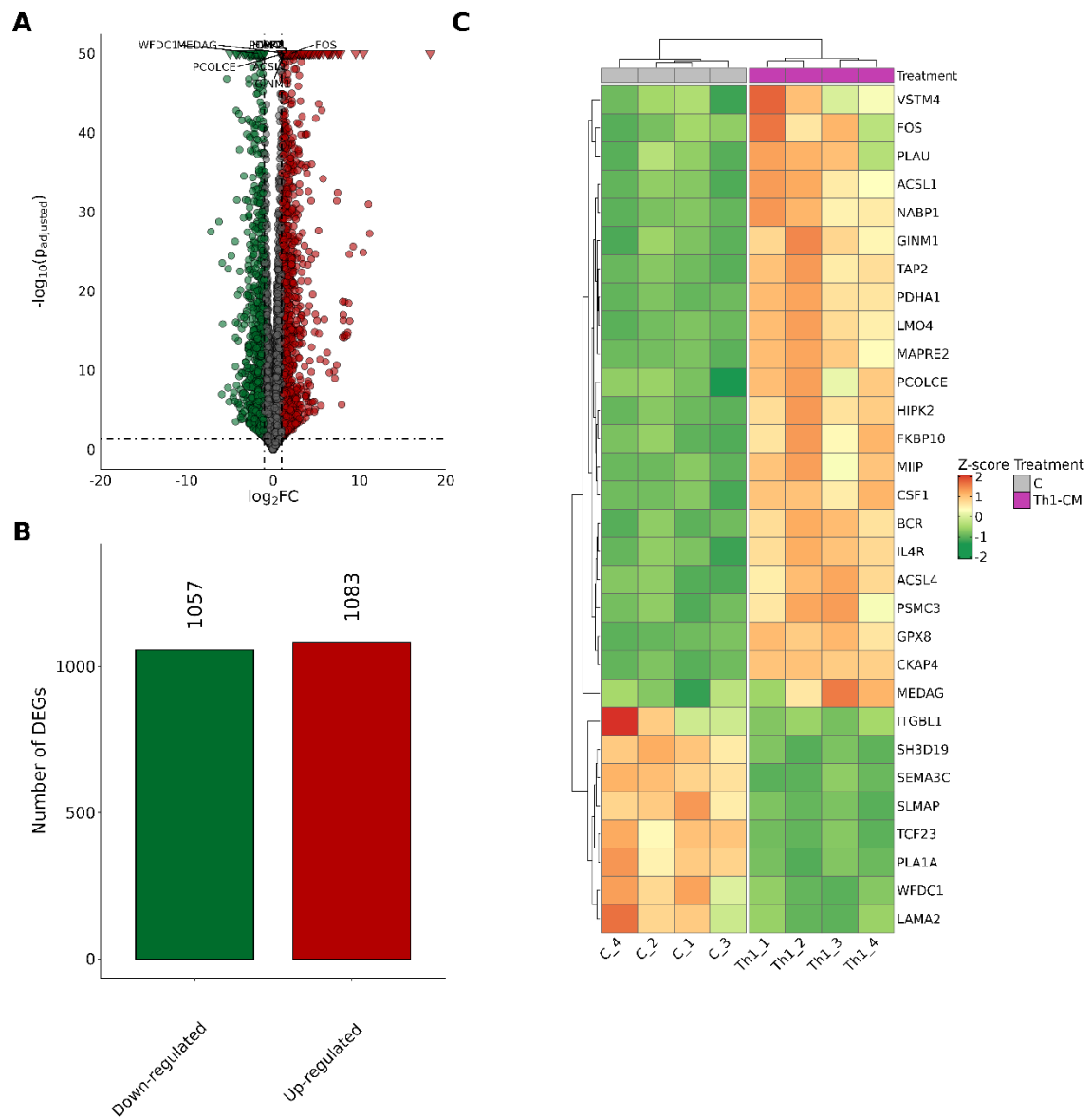


Figure 18. The effect of Th1 conditioned medium (Th1-CM) on the transcriptome of mare fibroblasts derived from category I endometria (n=4) after 48 hours of treatment. The volcano plot (A) presents differentially expressed genes (DEGs; $P_{\text{adjusted}} \leq 0.05$ and $\log_2FC \geq 1.0$ or $\log_2FC \leq -1.0$) which are represented by multi-coloured circles, where red colour is up-regulated genes and green down-regulated genes. (B) The number of identified up- and down-regulated DEGs. Heatmap (C) illustrating the expression profile of DEGs. The colour scale of the heatmap shows the normalized (Z-score) expression level where red blocks represent up-regulated DEGs, and green blocks represent down-regulated DEGs. C – control group (untreated cells).

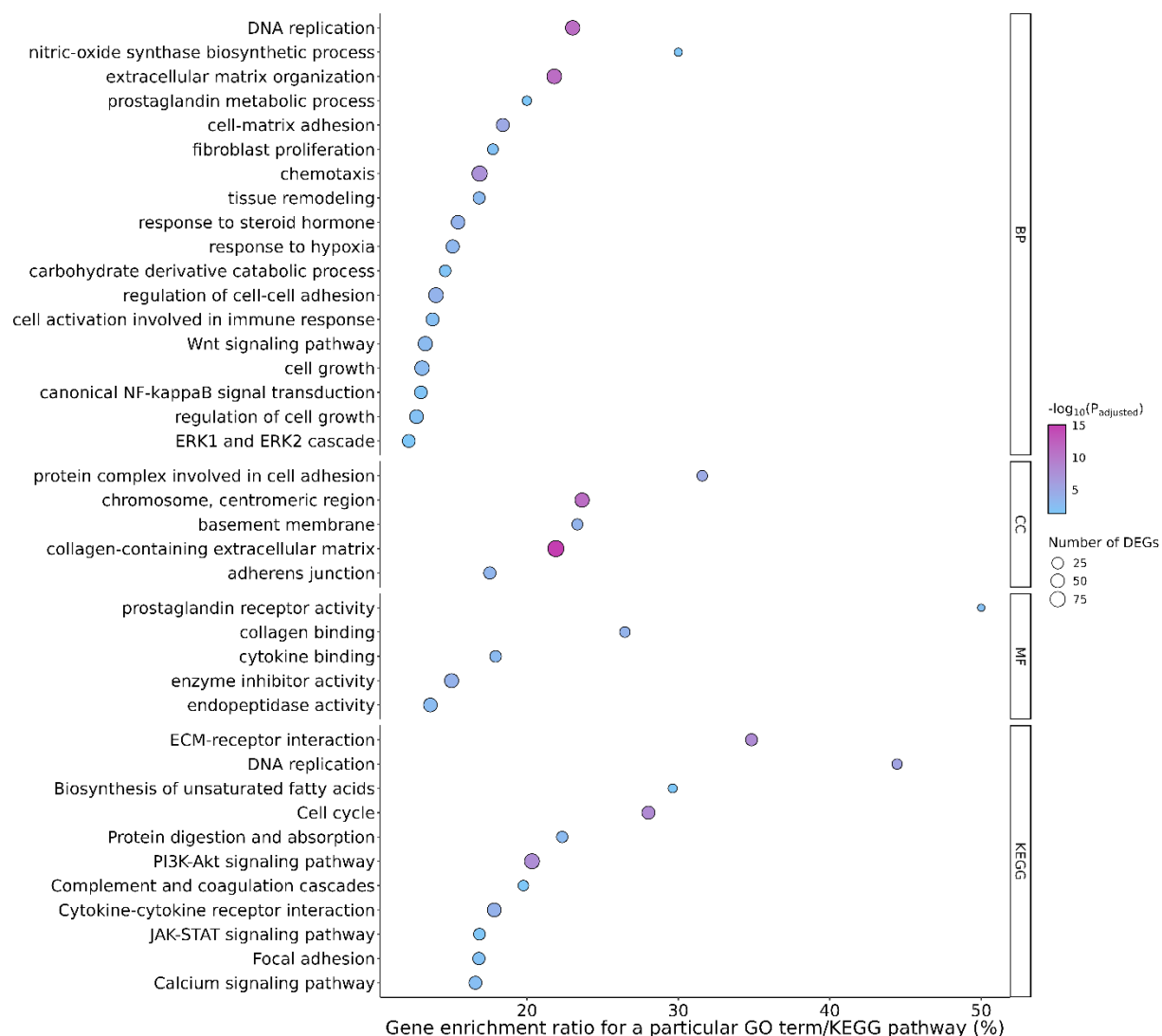


Figure 19. Selected Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms enriched by identified differentially expressed genes (DEGs, $p_{\text{adjusted}} \leq 0.05$ and $\log_2\text{FC} \geq 1.0$ or $\log_2\text{FC} \leq -1.0$) in fibroblasts derived from category I endometria (n=4) treated with Th1-CM for 48 hours. The y-axis is GO/KEGG categories. The x-axis refers to GO/KEGG enrichment. BP– Biological Processes, CC – cellular components, MF – molecular functions.

The treatment of fibroblasts derived from category I endometria with Th2-CM for 48 hours resulted in identification of 1033 DEGs, 411 of them were downregulated, while 622 were upregulated as presented in Figure 20B. The full list of DEGs identified in this study is presented in Supplementary Table 3. The top five upregulated DEGs were *COL6A5*, *ALOX15*, *NTRK1*, *CCL26*, and *CXCL9*. The most five downregulated DEGs after Th2-CM treatment were *PTGER3*, *GPX3*, *ADAMTS8*, *IGSF10*, and *PRLR*.

Differentially expressed genes identified in fibroblasts treated with Th2-CM were then subjected to functional analyses involving the GO and KEGG database. It revealed 919 BP, 59 CC, 83 MF terms, and 21 KEGG pathways in which identified DEGs may be involved. Selected most enriched GO terms and KEGG pathways are presented in Figure 21.

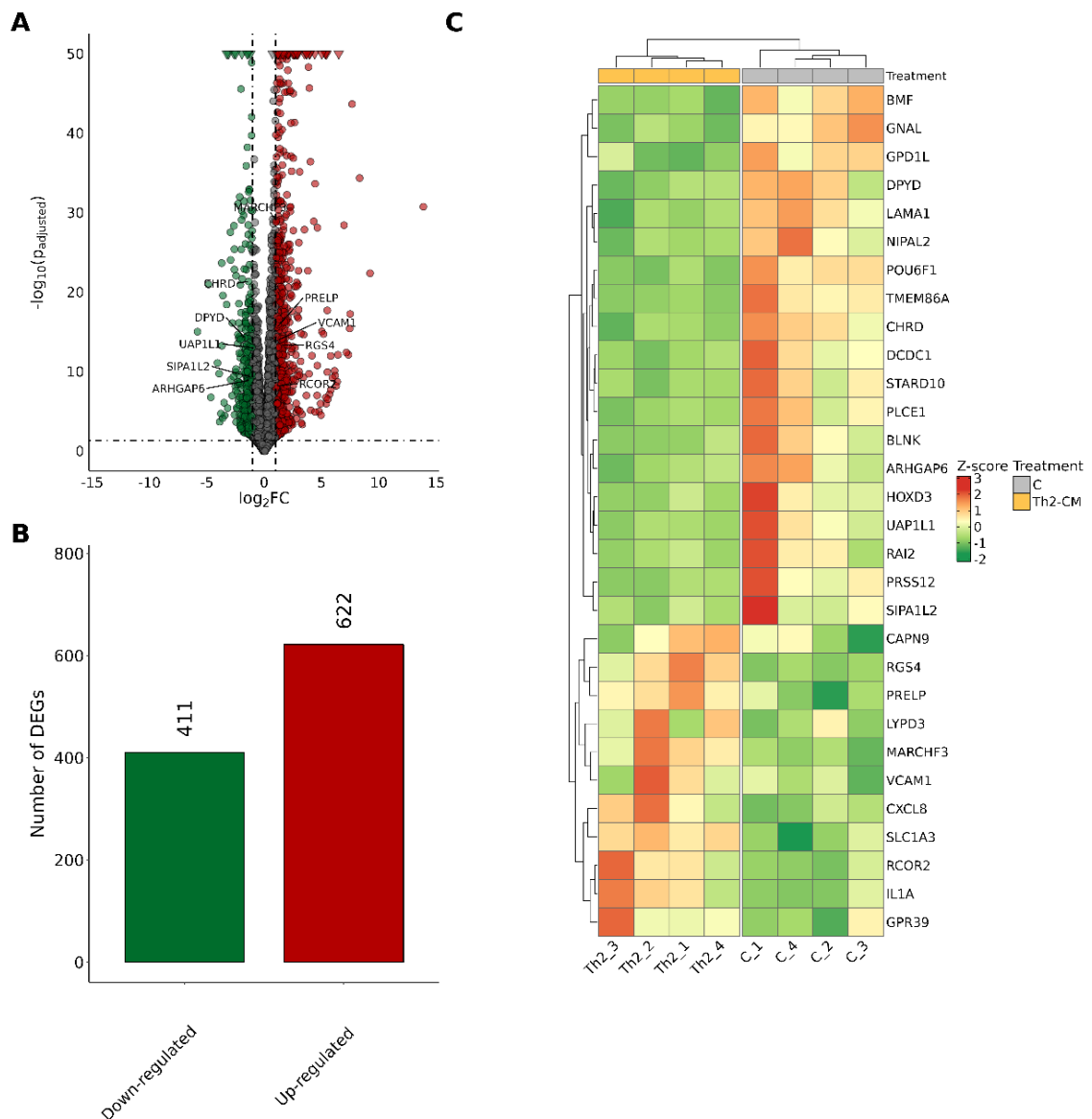


Figure 20. The effect of Th2 conditioned medium (Th2-CM) on the transcriptome of mare fibroblasts derived from category I endometria (n=4) after 48 hours of treatment. The volcano plot (A) presents differentially expressed genes (DEGs; $p_{\text{adjusted}} \leq 0.05$ and $\log_2FC \geq 1.0$ or $\log_2FC \leq -1.0$) which are represented by multi-coloured circles, where red colour is up-regulated genes and green down-regulated genes. (B) The number of identified up- and down-regulated. Heatmap (C) illustrating the expression profile of DEGs. The colour scale of the heatmap shows the normalized (Z-score) expression level where red blocks represent up-regulated DEGs, and green blocks represent down-regulated DEGs. C – control group (untreated cells).

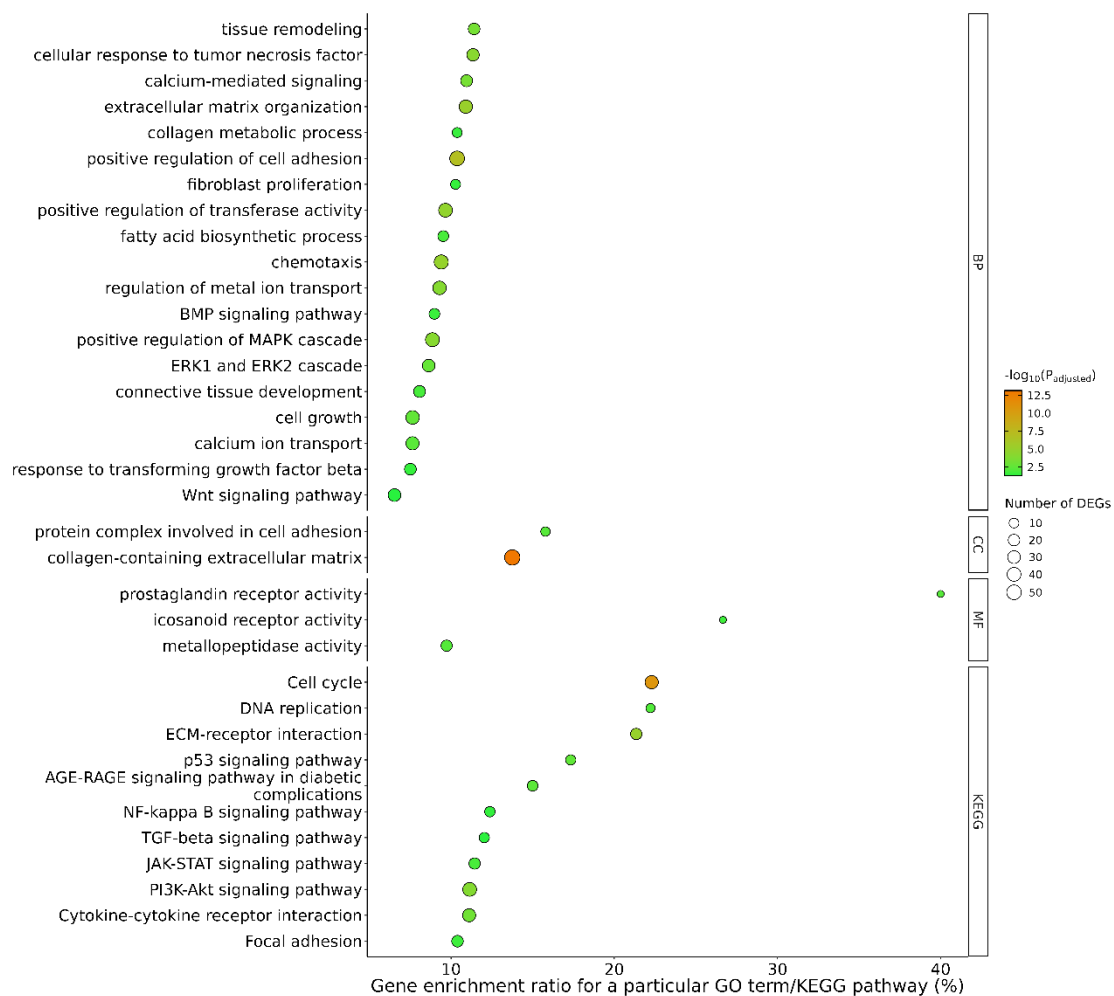


Figure 21. Selected Gene Ontology (GO) and KEGG (Kyoto Encyclopedia of Genes and Genomes) terms enriched by identified differentially expressed genes (DEGs, $p_{\text{adjusted}} \leq 0.05$ and $\log_2\text{FC} \geq 1.0$ or $\log_2\text{FC} \leq -1.0$) in fibroblasts derived from category I endometria (n=4) treated with Th2-CM for 48 hours. The y-axis is GO/KEGG categories. The x-axis refers to GO/KEGG enrichment. BP– Biological Processes, CC – cellular components, MF – molecular functions.

5.3. Research task 3: The effect of IFN- γ , IL-4, and IL-13 on endometrial fibroblasts: functional characteristics, ECM marker expression, and transcriptomic changes

5.3.1. Experiment 1. The effect of IFN- γ , IL-4 and IL-13 on the transcriptome of endometrial fibroblasts

The number of reads obtained for each sample ranged from 20.670.315 to 26.673.751. Following the application of filtering, an average of 19.787.006 reads were obtained, which were subsequently mapped to the *Equus caballus* genome (EquCab3.0). The summary of the datasets used in this experiment is presented in Supplementary Table 4. The comparison of selected DEGs expression using NGS and validation using qPCR is presented in Supplementary Table 5.

The PCA of mRNA expression pattern in fibroblasts derived from category I and IIB endometria, treated with IFN- γ , IL-4, and IL-13 for 48 hours is presented in Figure 22. These findings suggest that IFN- γ does not influence the transcriptome of fibroblasts derived from either category I or category IIB endometria. Conversely, both IL-4 and IL-13 have been demonstrated to impact the transcriptomic profile of mare fibroblasts derived from category I or category IIB endometria.

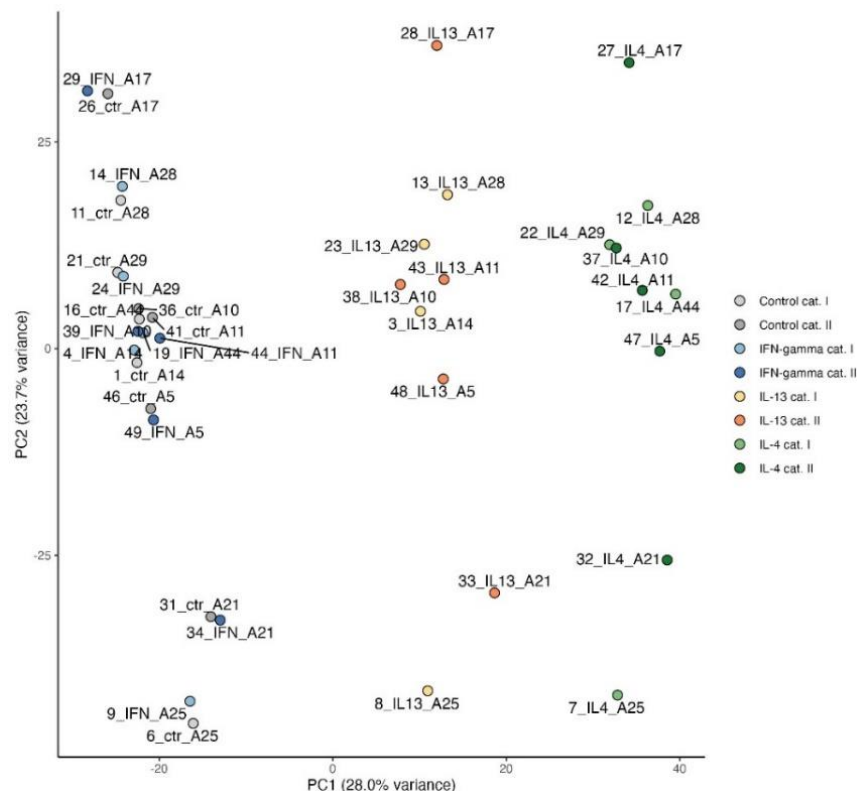


Figure 22. Graphical presentation of the first (PC1) and second (PC2) principal components (PCA) of the mRNA expression pattern in fibroblasts derived from category I and category IIB endometria treated with interferon γ (IFN- γ), interleukin-4 (IL-4) or IL-13 for 48 hours. Control – untreated cells.

5.3.1.1. The effect of IL-4 on the transcriptome of endometrial fibroblasts

Interleukin 4 treatment resulted in identification of 1288 DEGs in fibroblasts derived from category I endometria (Fig. 23A). Of these, 611 were upregulated and 617 were downregulated. The top 5 upregulated DEGs were *COL6A5*, *CISH*, *NTRK1*, *CSF3R*, and *CCL8*, whilst most downregulated were *ASPA*, *GDPD4*, *RBFOX1*, *SLC6A6*, and *ADAMTS8*. The full list of DEGs identified in this experiment is enclosed in Supplementary Table 6. Further functional analysis of DEGs identified after IL-4 treatment in fibroblasts derived from category I endometria using the GO database indicated 410 BP, 101 MF, and 92 CC GO categories and 102 KEGG pathways. Among most enriched GO terms were: canonical glycolysis (GO:0061621), cell adhesion (GO:0007155), cell-matrix adhesion (GO:0007160), insulin-like growth factor receptor signaling pathway (GO:0048009), focal adhesion (KEGG ID: hsa04510), cell cycle (KEGG ID: hsa04110), HIF-1 signaling pathway (KEGG ID: hsa04066), PI3K-Akt signaling pathway (KEGG ID: hsa04151), and ECM-receptor interaction (KEGG ID: hsa04512). The top 15 BP, 5 MF, 5 CC, and 12 KEGG results are presented in Figure 24A.

Interleukin 4 treatment resulted in 1187 DEGs in fibroblasts derived from category IIB endometria (Fig. 23B). Of these, 603 were upregulated and 584 were downregulated. The top five upregulated DEGs were *COL6A5*, *SERPINA3*, *CMKLR2*, *PDCD1LG2*, and *CSF3R*, and most five downregulated were *CHST7*, *RBFOX1*, *SLC6A6*, *MLANA*, and *ADAMTS8*. The full list of DEGs identified in this experiment is enclosed in Supplementary Table 7. The functional analysis of DEGs identified in fibroblasts derived from category IIB endometria after IL-4 treatment revealed 537 BP, 131 MF, 108 CC among GO categories, and 88 KEGG pathways. Among the most enriched GO and KEGG terms were cellular response to glucose stimulus (GO:0071333), extracellular matrix structural constituent (GO:0005201), collagen-containing extracellular matrix (GO:0062023), Rap1 signaling pathway (KEGG ID: hsa04015), focal adhesion (KEGG ID: hsa04510), cell cycle (KEGG ID: hsa04110), PI3K-Akt signaling pathway (KEGG ID: hsa04151), and biosynthesis of nucleotide sugars (KEGG ID: hsa01250). The top 15 BP, 5 MF, 5 CC, and 12 KEGG results are presented in Figure 24B.

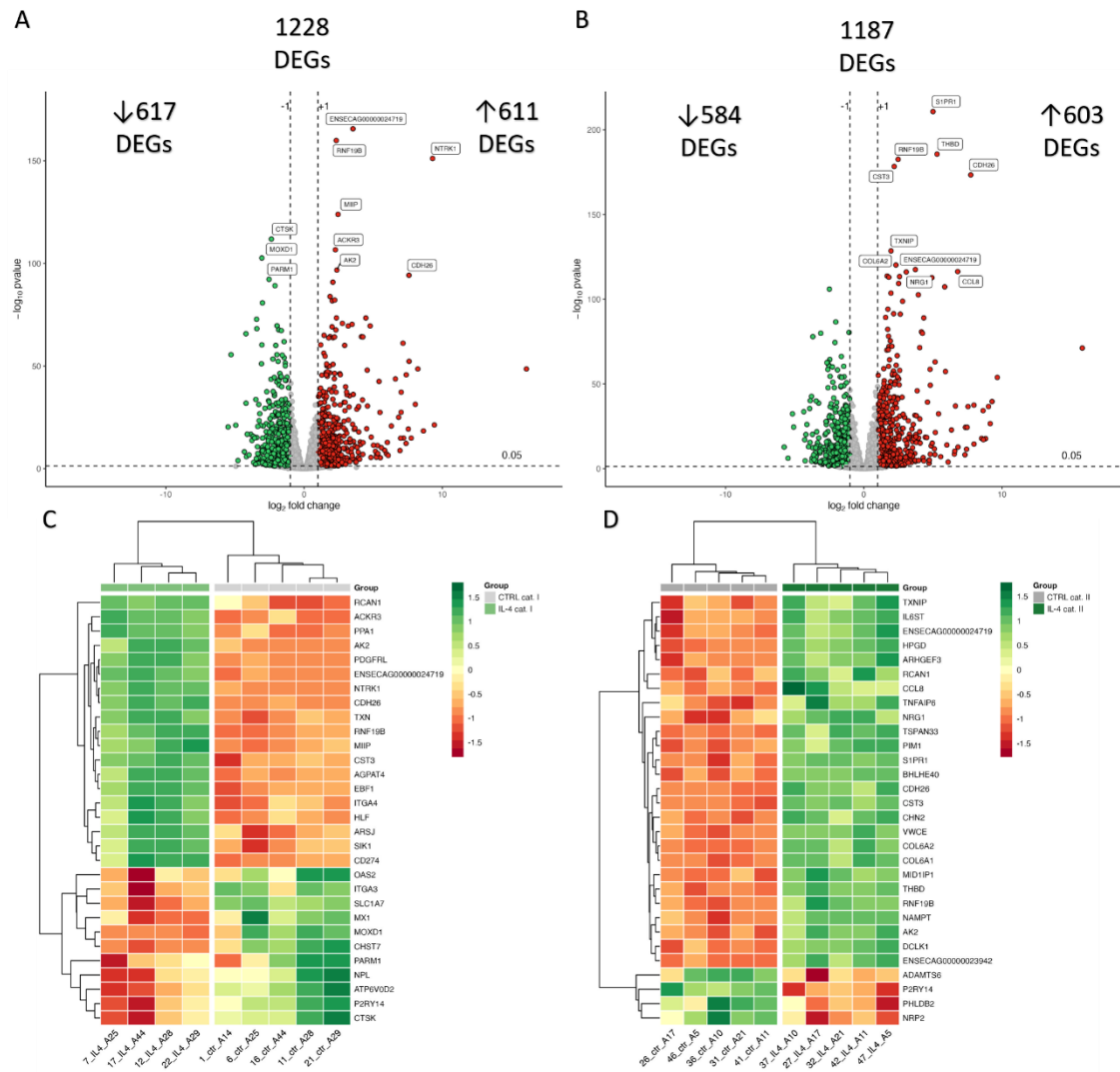


Figure 23. The effect of interleukin 4 (IL-4) on the transcriptome of fibroblasts derived from category I (n=5; A and C) and category IIB endometria (n=5; B and D) after 48 hours of treatment. The volcano plots (A, B) presents differentially expressed genes (DEGs; P-adjusted ≤ 0.05 and $\log_2FC \geq 1.0$ or $\log_2FC \leq -1.0$) which are represented by multi-coloured circles, where red colour is upregulated DEGs and green downregulated DEGs. The heatmaps (B, C) present the expression profile of the DEGs. CTRL – control group (untreated cells).

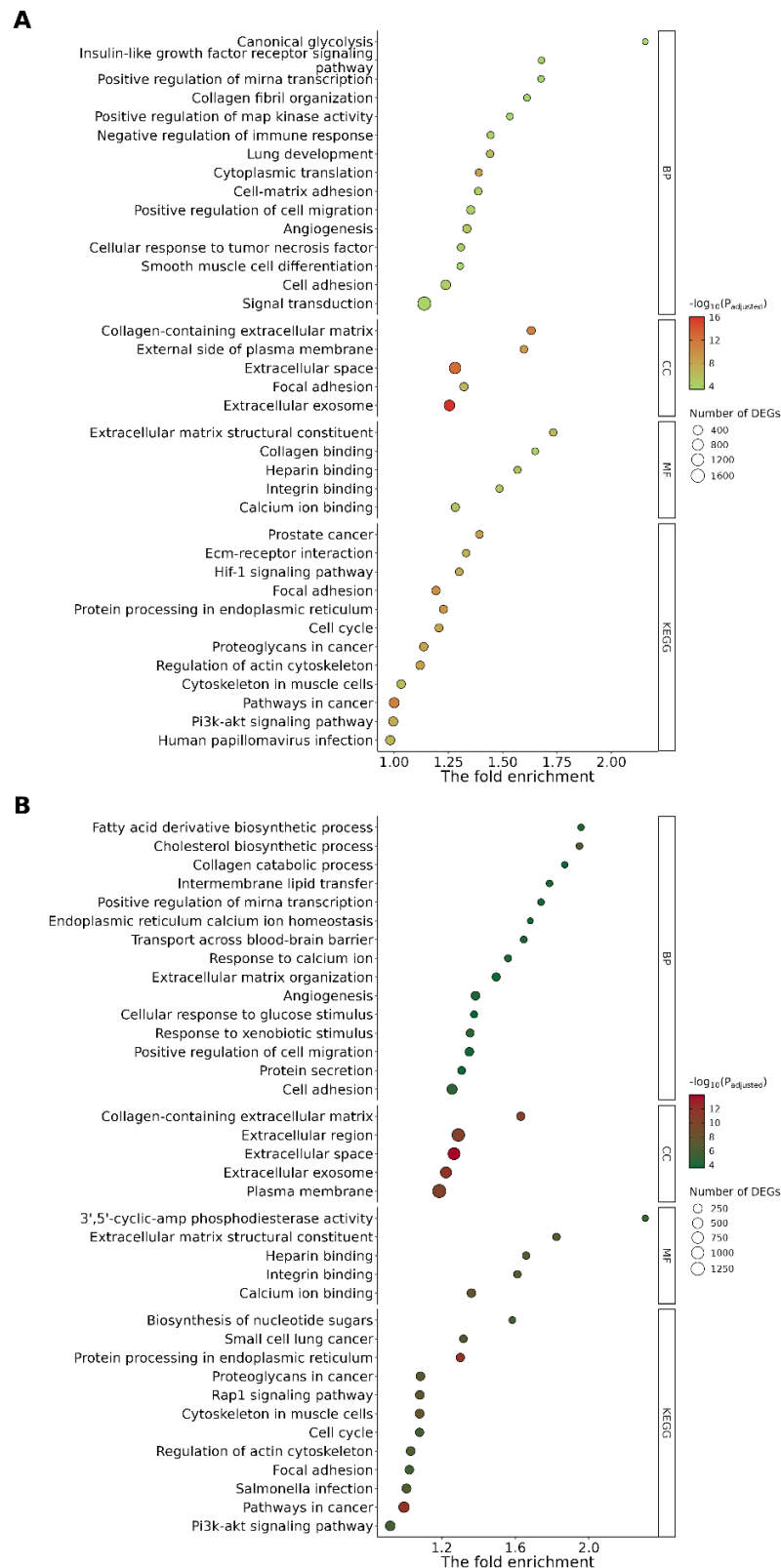


Figure 24. Selected Gene Ontology categories and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms enriched by identified differentially expressed genes (DEGs, $p_{\text{adjusted}} \leq 0.05$ and $\log_2\text{FC} \geq 1.0$ or $\log_2\text{FC} \leq -1.0$) after interleukin 4 (IL-4) treatment for 48 hours in fibroblasts derived from category I (n=5; A) and IIB (n=5; B) endometria. The y-axis is pathway categories. The x-axis refers to pathway enrichment. BP – Biological Processes, CC – cellular components, MF – molecular functions.

In response to IL-4 treatment, 331 DEGs (Fig. 25A) were identified exclusively in fibroblasts derived from category I endometria, 290 DEGs (Fig. 27A) were identified exclusively in fibroblasts derived from category IIB endometria, while 897 DEGs (Fig. 26A) were identified in fibroblasts derived both from category I and IIB endometria.

Functional enrichment analysis for DEGs identified in response to IL-4 treatment in fibroblasts derived from category I exclusively, both category I and IIB, and category IIB endometria exclusively were performed. Analyses revealed 269 GO and 33 KEGG, as well as 345 GO and 105 KEGG terms enriched by DEGs expressed exclusively in response to IL-4 treatment in fibroblasts derived from category I and exclusively in fibroblasts derived from category IIB endometria, respectively. Moreover, 199 GO and 70 KEGG terms enriched by DEGs expressed in response in fibroblasts derived both from category I and IIB endometria were identified.

The selected most enriched GO BP processes and KEGG pathways in fibroblasts derived from category I endometria exclusively (331 DEGs; Fig. 25B and C), in fibroblasts derived both from category I and IIB endometria (897 shared DEGs; Fig. 26 B and C), in fibroblasts derived from category IIB endometria exclusively (290 DEGs; Figure 27 B and C) in response to IL-4 treatment are presented in Figures 25-27.

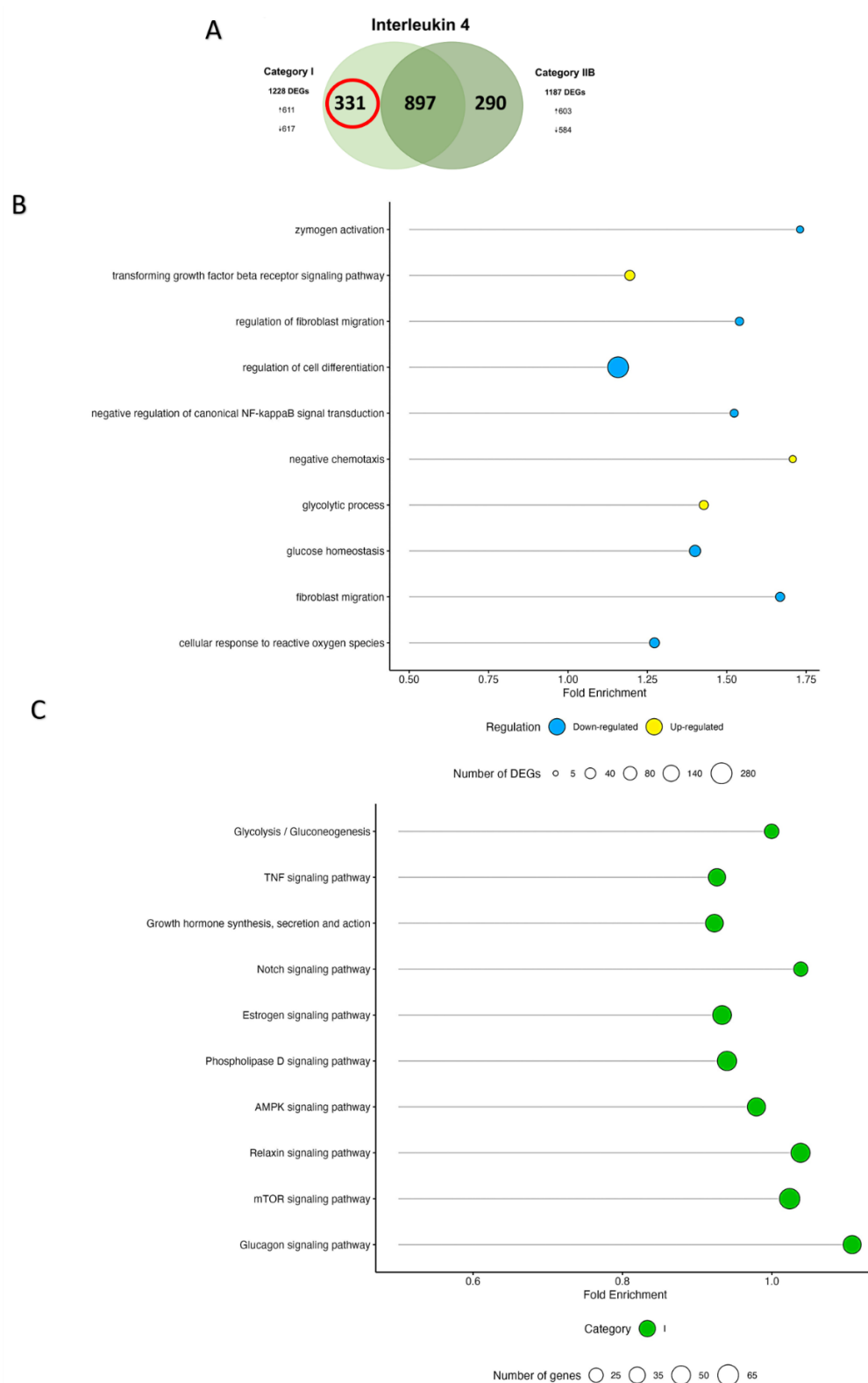


Figure 25. The effect of interleukin 4 (IL-4) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, log2FC ≥ 1.0/log2FC ≤ - 1.0). The red-coloured circle indicates 331 DEGs identified exclusively in response to IL-4 treatment in fibroblasts derived from category I endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by exclusively identified 331 DEGs in fibroblasts derived from category I endometria in response to IL-4. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

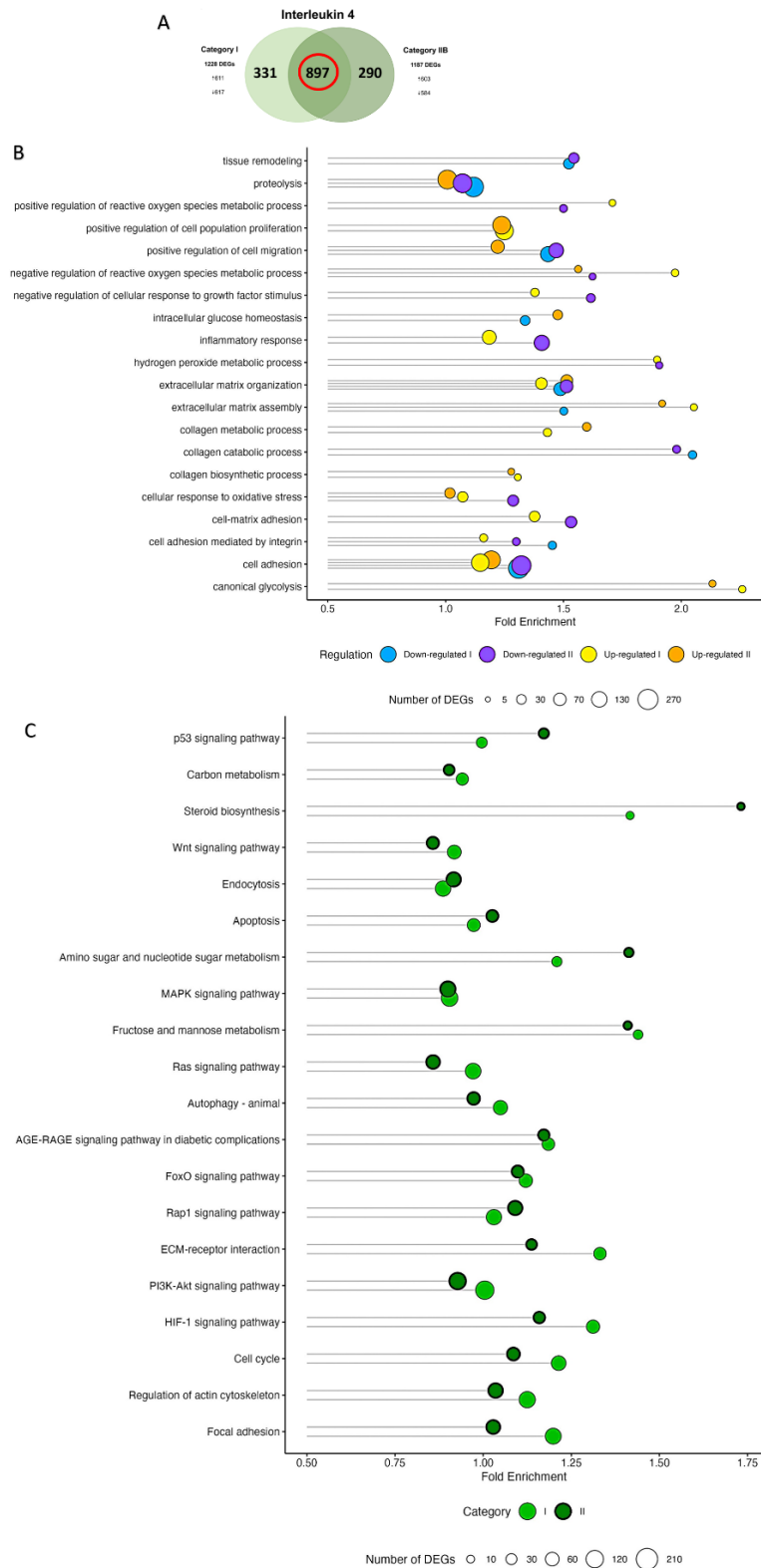


Figure 26. The effect of interleukin 4 (IL-4) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, log2FC ≥ 1.0/log2FC ≤ - 1.0). The red-coloured circle indicates 897 DEGs identified both in response to IL-4 treatment in fibroblasts derived from category I and category IIB endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by identified shared 897 DEGs in fibroblasts derived from category I and category IIB endometria in response to IL-4. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

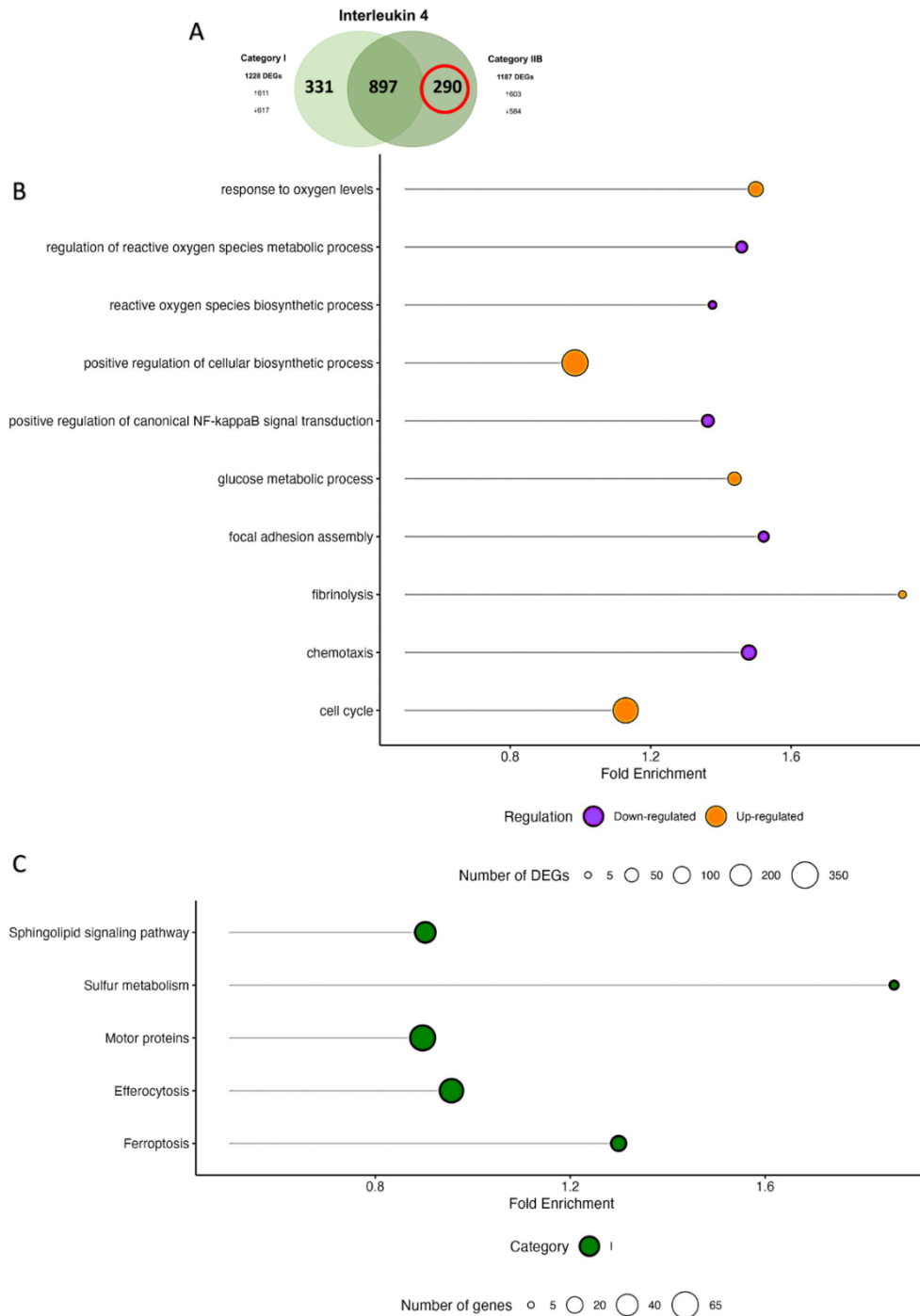


Figure 27. The effect of interleukin 4 (IL-4) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, log2FC ≥ 1.0/log2FC ≤ - 1.0). The red-coloured circle indicates 290 DEGs identified exclusively in response to IL-4 treatment in fibroblasts derived from category IIB endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by exclusively identified 290 DEGs in fibroblasts derived from category IIB endometria in response to IL-4. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

5.3.1.2. The effect of IL-13 on the transcriptome of endometrial fibroblasts

As presented in Figure 28A, IL-13 treatment of fibroblasts derived from category I endometria resulted in 471 DEGs, 265 of which were up-regulated while 206 were down-regulated. The full list of DEGs identified in this study is provided in Supplementary Table 8. The top five up-regulated DEGs were *COL6A5*, *CISH*, *NTRK1*, *CCL8*, and *ALOX15*, whilst most down-regulated were *ADAMTS8*, *SLC6A6*, *TRIM22*, *NOTUM*, and *ADAD1*. Further functional analysis of DEGs identified after IL-13 treatment in fibroblasts derived from category I endometria using GO database indicated 520 BP, 120 MF, and 81 CC GO categories and 34 KEGG pathways. Among most enriched GO and KEGG terms were extracellular matrix organization (GO:0030198), cellular response to tumor necrosis factor (GO:0071356), cell-matrix adhesion (GO:0007160), extracellular matrix structural constituent (GO:0005201), HIF-1 signaling pathway (KEGG ID: hsa04066), ECM-receptor interaction (KEGG ID: hsa04512), FoxO signaling pathway (KEGG ID: hsa04068), PI3K-Akt signaling pathway (KEGG ID: hsa04151), and focal adhesion (KEGG ID: hsa04510). The top 15 BP, 5 MF, 5 CC, and 12 KEGG results are presented in Figure 29A.

As presented in Figure 28B, IL-13 treatment of fibroblasts derived from category IIB endometria resulted in 465 DEGs, 257 of which were up-regulated and 208 were down-regulated. The most five up-regulated DEGs were *COL6A5*, *PDCD1LG2*, *SERPINA3*, *ALOX15*, and *FETUB*, whilst most down-regulated were *CHST7*, *SEMA4D*, *ADAMTS8*, *U2*, and *SLC6A6*. The full list of DEGs identified in this study is provided in Supplementary Table 9. The functional analysis of DEGs identified in fibroblasts derived from category IIB endometria after IL-13 treatment revealed 545 BP, 120 MF, 84 CC among GO categories, and 23 KEGG pathways. Among most enriched GO and KEGG terms were response to hypoxia (GO:0001666), inflammatory response (GO:0006954), extracellular matrix organization (GO:0030198), cell adhesion (GO:0007155), collagen-containing extracellular matrix (GO:0062023), amino sugar and nucleotide sugar metabolism (KEGG ID: hsa00520), HIF-1 signaling pathway (KEGG ID: hsa04066), protein processing in endoplasmic reticulum (KEGG ID: hsa04141), AGE-RAGE signaling pathway in diabetic complications (KEGG ID: hsa04933), Rap1 signaling pathway (KEGG ID: hsa04015), ECM-receptor interaction (KEGG ID: hsa04512), focal adhesion (KEGG ID: hsa04510), and carbon metabolism (KEGG ID: hsa01200). The top 15 BP, 5 MF, 5 CC, and 12 KEGG results are presented in Figure 29B.

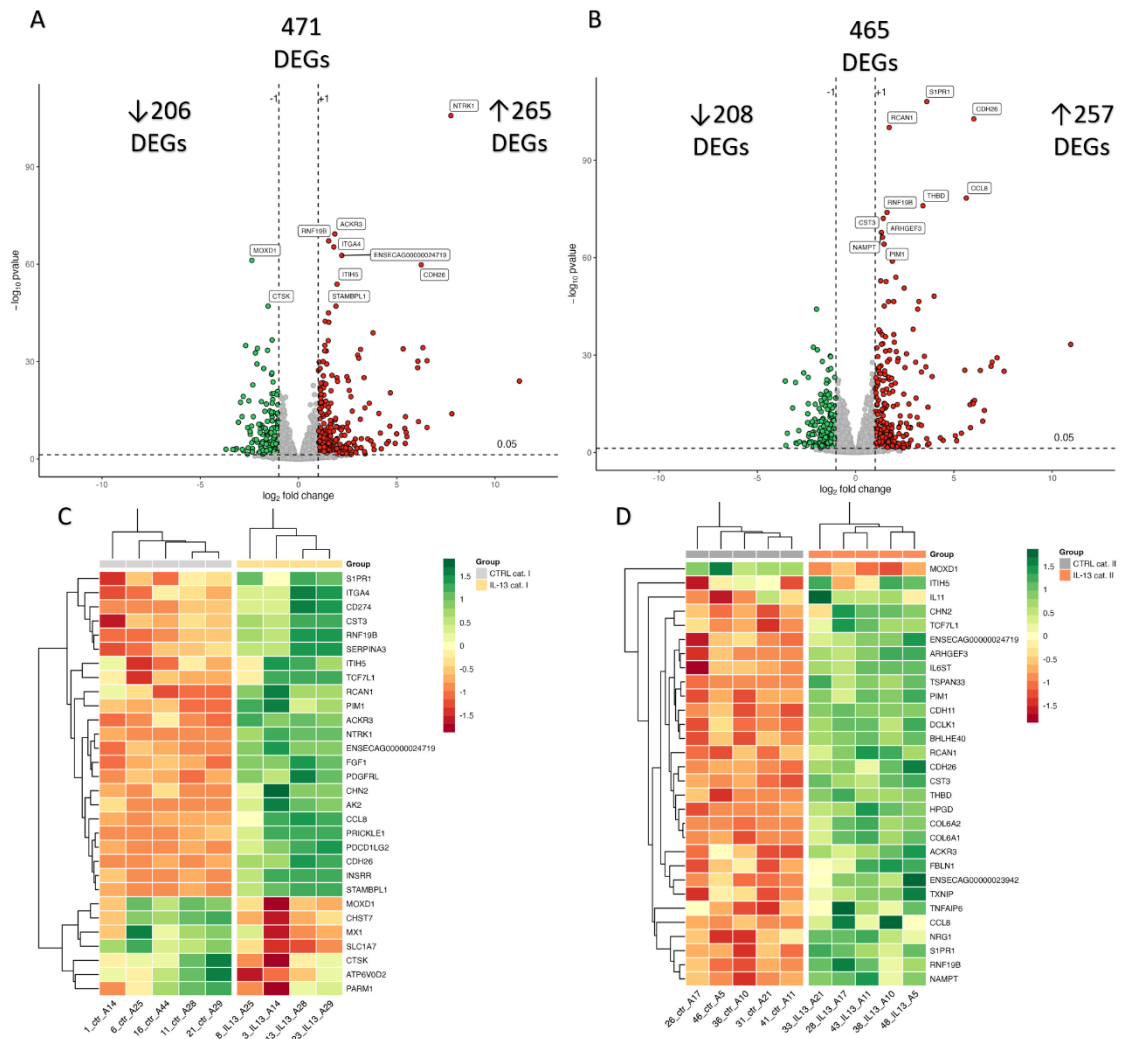


Figure 28. The effect of interleukin 13 (IL-13) on the transcriptome of fibroblasts derived from category I (n=5; A and C) and category IIB endometria (n=5; B and D) after 48 hours of treatment. The volcano plots (A, B) presents differentially expressed genes (DEGs; $P\text{-adjusted} \leq 0.05$ and $\log_2FC \geq 1.0$ or $\log_2FC \leq -1.0$) which are represented by multi-coloured circles, where red colour is upregulated DEGs and green downregulated DEGs. The heatmaps (B, C) present the expression profile of the DEGs. CTRL – control group (untreated cells).

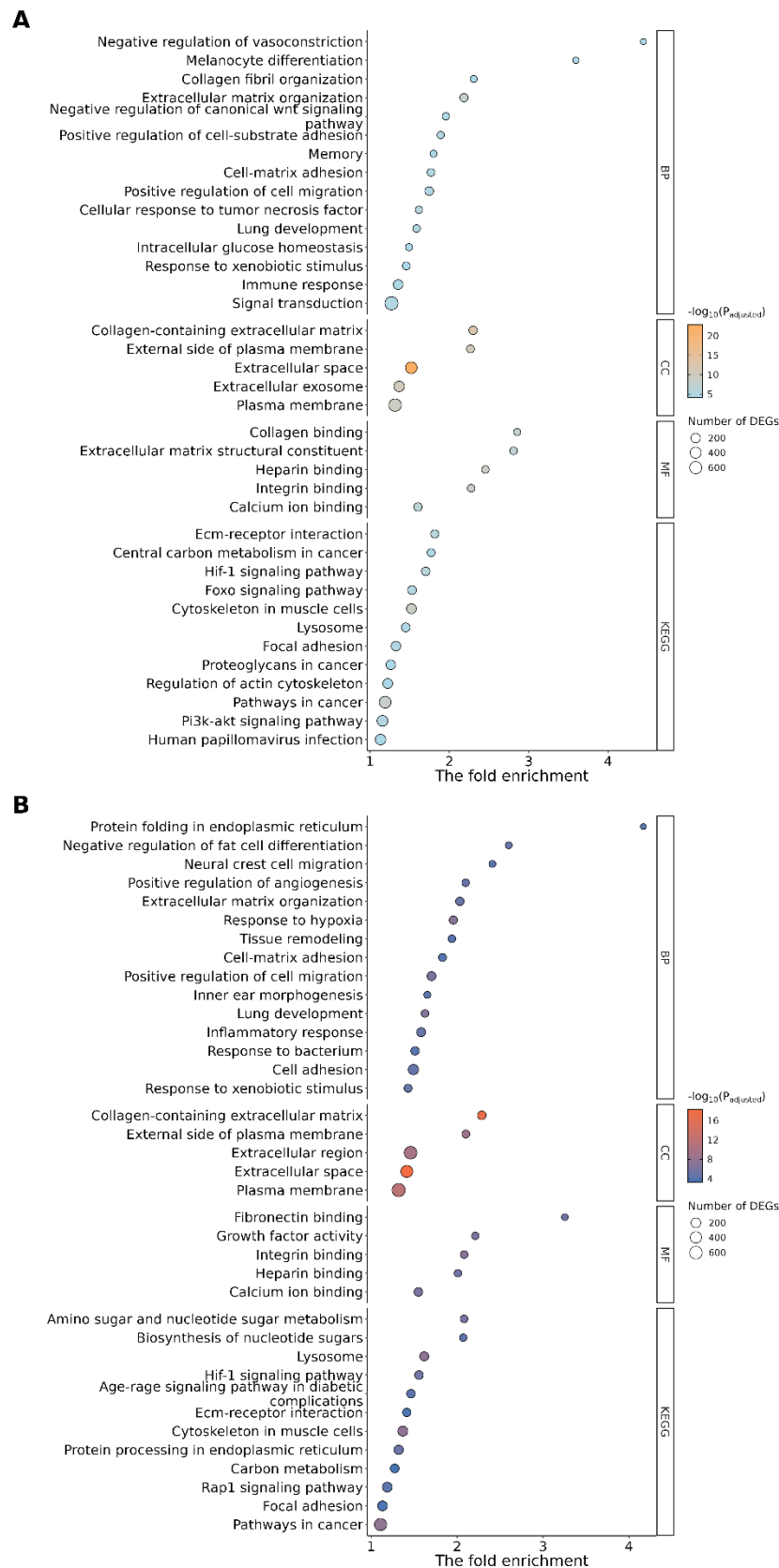


Figure 29. Selected Gene Ontology categories and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms enriched by identified differentially expressed genes (DEGs, $p_{\text{adjusted}} \leq 0.05$ and $\log_2\text{FC} \geq 1.0$ or $\log_2\text{FC} \leq -1.0$) after interleukin 13 (IL-13) treatment for 48 hours in fibroblasts derived from category I (n=5; A) and IIB (n=5; B) endometria. The y-axis is pathway categories. The x-axis refers to pathway enrichment. BP – Biological Processes, CC – cellular components, MF – molecular functions.

In response to IL-13 treatment, 166 DEGs (Fig. 30A) were identified exclusively in fibroblasts derived from category I endometria, 160 DEGs (Fig. 32A) were identified exclusively in fibroblasts derived from category IIB endometria, while 305 DEGs (Fig. 31A) were identified in fibroblasts derived both from category I and IIB endometria.

Functional enrichment analysis for DEGs identified in response to IL-13 treatment in fibroblasts derived from category I exclusively, both category I and IIB, and category IIB endometria exclusively were performed.

Analyses revealed 305 BP and 18 KEGG, as well as 315 GO and 7 KEGG terms enriched by DEGs expressed exclusively in response to IL-13 treatment in fibroblasts derived from category I and exclusively in fibroblasts derived from category IIB endometria, respectively. Moreover, 222 GO and 16 KEGG terms enriched by DEGs expressed in response to IL-13 in fibroblasts derived both from category I and IIB endometria were identified.

The selected most enriched GO BP processes and KEGG pathways in fibroblasts derived from category I endometria exclusively (166 DEGs; Fig. 30B and C), in fibroblasts derived from both category I and IIB endometria (305 shared DEGs; Fig. 31B and C), and in fibroblasts derived from category IIB endometria exclusively (160 DEGs; Fig. 32 B and C) in response to IL-13 treatment are presented in Figures 30-32.

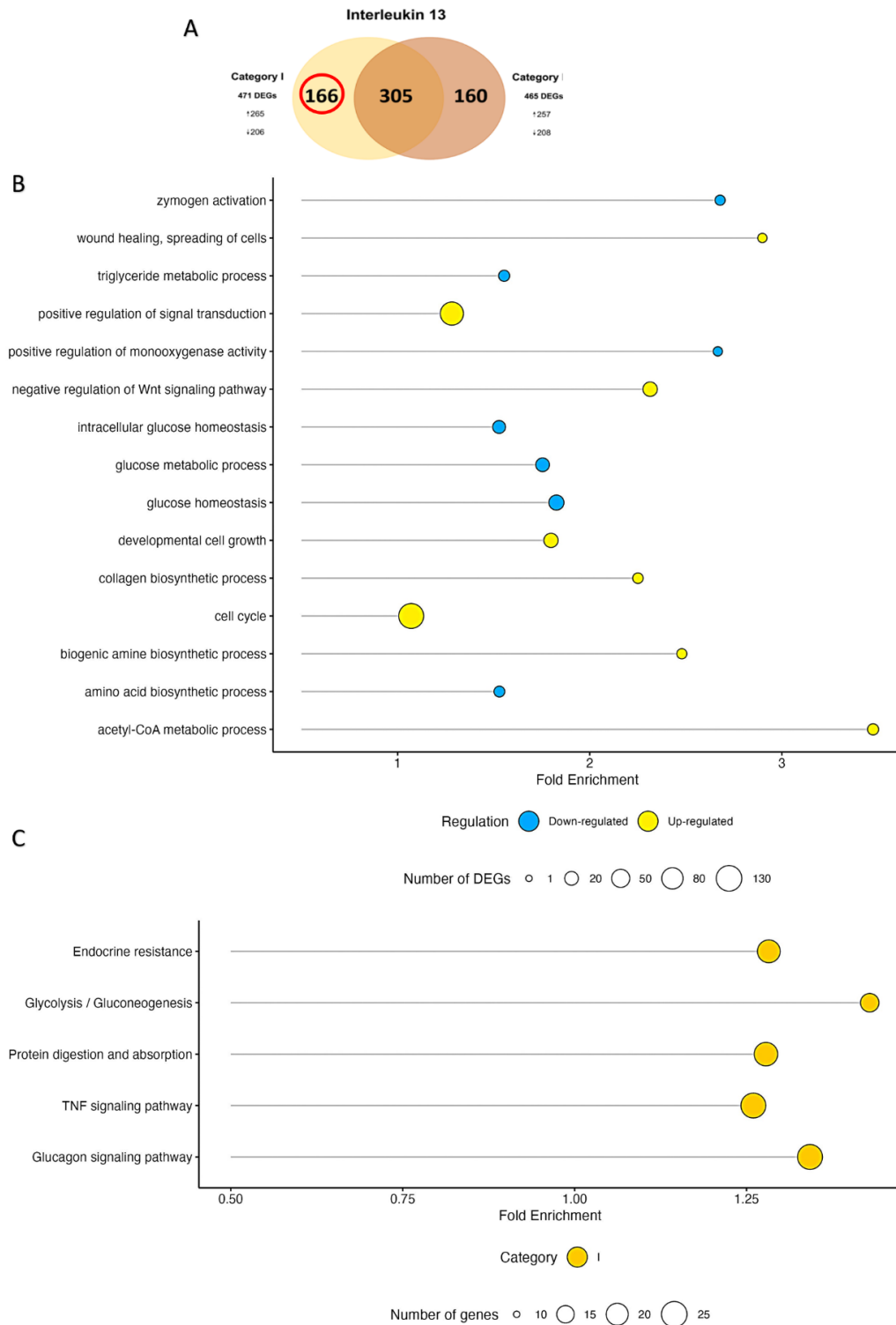


Figure 30. The effect of interleukin IL-13 (IL-13) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, $\log_2FC \geq 1.0/\log_2FC \leq -1.0$). The red-coloured circle indicates 166 DEGs identified exclusively in response to IL-13 treatment in fibroblasts derived from category I endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by exclusively identified 166 DEGs in fibroblasts derived from category I endometria in response to IL-13. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

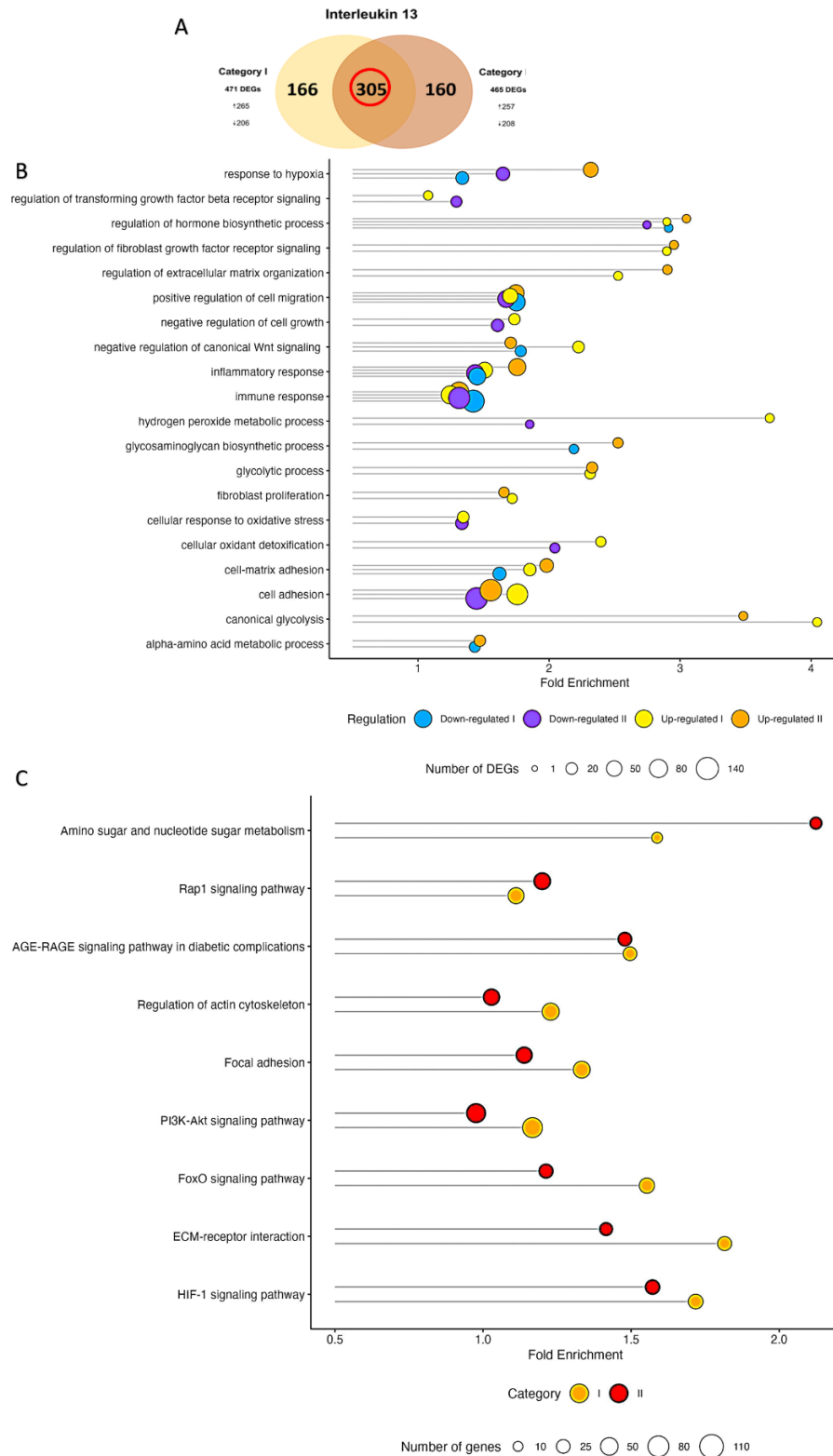


Figure 31. The effect of interleukin 13 (IL-13) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, log2FC $\geq$ 1.0/log2FC $\leq$ -1.0). The red-coloured circle indicates 305 DEGs identified both in response to IL-13 treatment in fibroblasts derived from category I and category IIB endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by identified shared 305 DEGs in fibroblasts derived from category I and category IIB endometria in response to IL-13. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

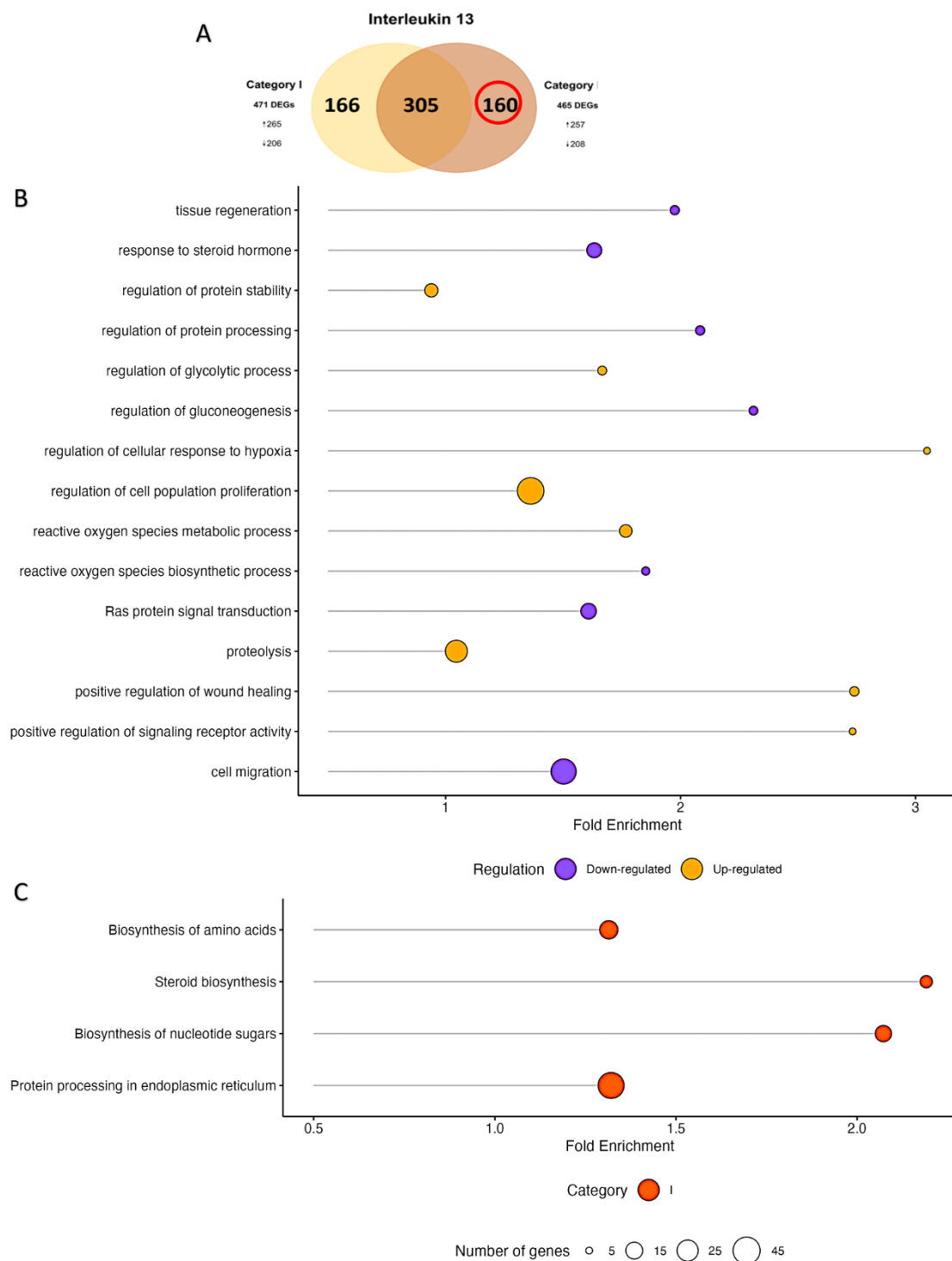


Figure 32. The effect of interleukin 13 (IL-13) on the transcriptome of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 hours of treatment. The Venn diagram (A) presents identified differentially expressed genes (DEGs; padjusted < 0.05, $\log_2FC \geq 1.0/\log_2FC \leq -1.0$). The red-coloured circle indicates 160 DEGs identified exclusively in response to IL-13 treatment in fibroblasts derived from category IIB endometria. Gene Ontology (GO) categories (B) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (C) enriched by exclusively identified 160 DEGs in fibroblasts derived from category IIB endometria in response to IL-13. The y-axis is pathway categories. The x-axis refers to pathway enrichment.

5.3.2. Experiment 2. The effect of IFN- γ , IL-4 and IL-13 on expression of ECM-associated markers in fibroblasts derived at different stages of endometriosis

5.3.2.1. The effect of IFN- γ on expression of ECM-associated markers in fibroblasts derived at different stages of endometriosis

The effect of IFN- γ treatment on the gene expression of ECM-associated markers in fibroblasts derived from category I and IIB endometria after 48 and 98 hours of treatment is presented in Figures 33-34.

The treatment with IFN- γ had no effect on the gene expression of *Col1a1* ($p>0.05$; Fig. 33A), *Col3a1* ($p>0.05$; Fig. 33B), *FN1* ($p>0.05$; Fig. 33C) and *ACTA2* ($p>0.05$; Fig. 33D), *MMP-2* ($p>0.05$; Fig. 34A), *MMP-3* ($p>0.05$; Fig. 34B), *MMP-9* ($p>0.05$; Fig. 34C), *TIMP-1* ($p>0.05$; Fig. 34D), *TIMP-2* ($p>0.05$; Fig. 34E) in fibroblasts derived from category I and IIB endometria after 48 and 98 hours of treatment in comparison to the respective control groups.

Due to the lack of the effect of IFN- γ treatment on the transcriptome and gene expression of ECM-associated markers, protein-based analyses were not performed.

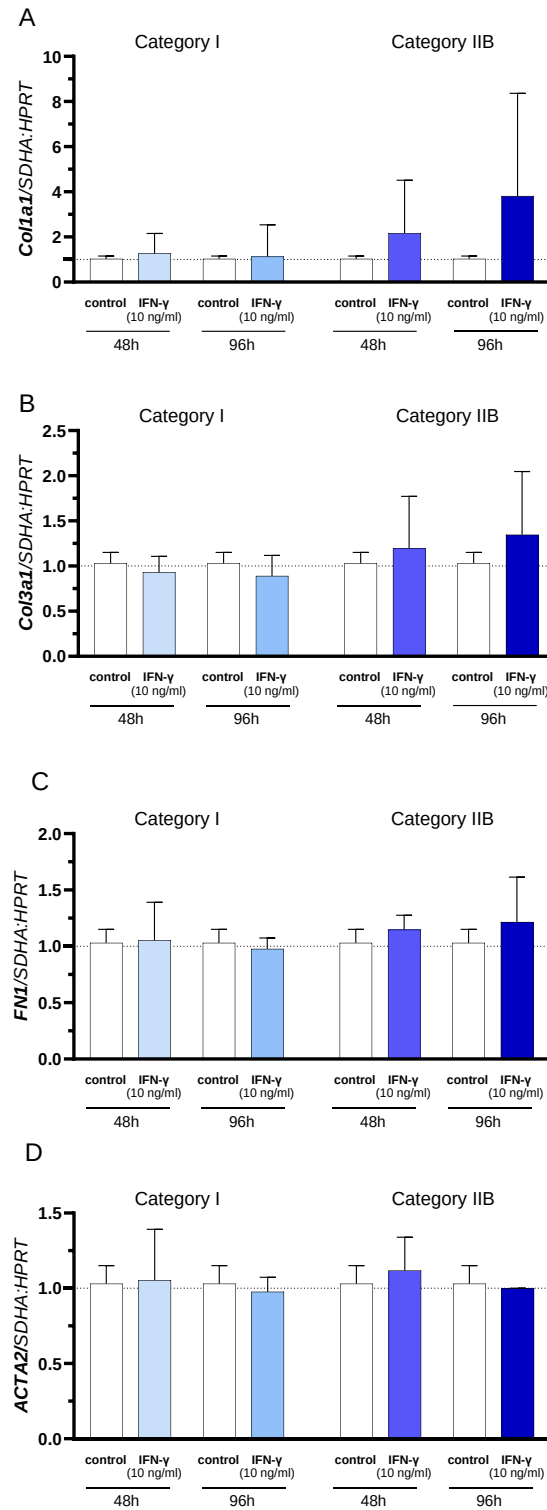


Figure 33. The effect of interferon (IFN)- γ treatment on the gene expression of collagen type I (*Col1a1*; A), collagen type III (*Col3a1*; B), fibronectin I (*FN1*; C), and α -smooth muscle actin (*ACTA2*; D) in fibroblasts derived from category I (n=5) and IIB endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. The results were analyzed using Student-t test.

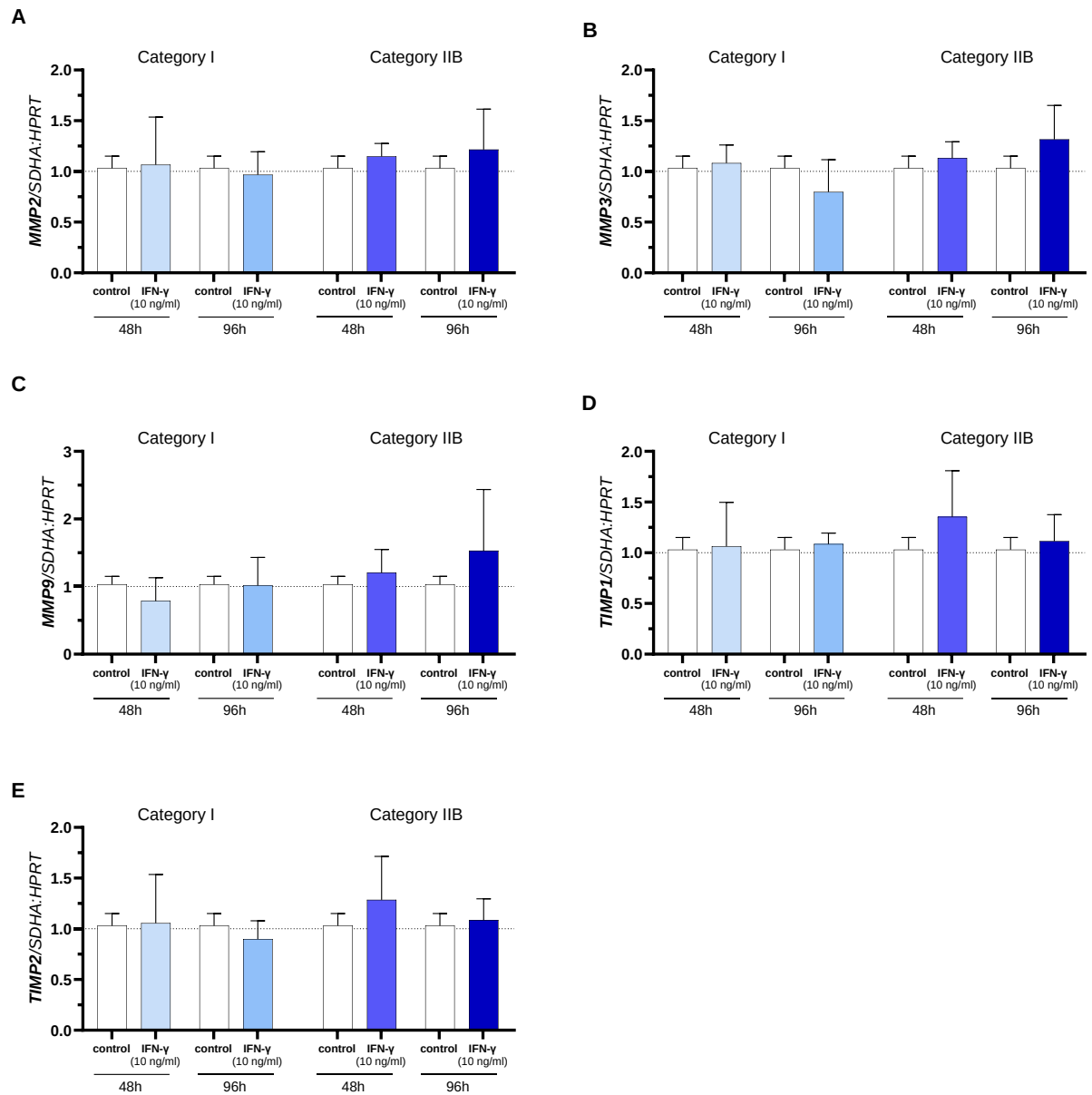


Figure 34. The effect of interferon (IFN) γ on the gene expression *matrix metalloproteinase* (MMP)-2 (A) *MMP3* (B), *MMP9* (C), *tissue inhibitor of matrix metalloproteinase* (TIMP)1 (D) and *TIMP2* (E) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as a mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. The results were analyzed using Student-t test.

5.3.2.2. The effect of IL-4 on the expression of ECM-associated markers in fibroblasts derived at different stages of endometriosis

Interleukin 4 treatment increased the gene expression of *Col1a1* in fibroblasts derived from category IIB endometria after 96 hours compared to the respective control group ($p < 0.05$; Fig. 35A). Additionally, IL-4 treatment decreased protein abundance of COL1 in fibroblasts derived from category I endometria after 48 hours ($p < 0.01$; Fig. 35B) and in fibroblasts derived from category IIB endometria after 48 and 96 hours ($p < 0.01$; $p < 0.001$; Fig. 35B) in comparison to the respective control groups. In endometrial fibroblasts treated with IL-4 for 48 hours, COL1 was localized in the cytoplasm (Fig. 35C).

Interleukin 4 treatment decreased the gene expression of *Col3a1* and protein abundance of COL3 in fibroblasts derived from category I endometria after 48 and 96 hours ($p < 0.01$; Fig. 36 A and B), while increased both gene expression and protein abundance of COL3 in fibroblasts derived from category IIB endometria in comparison to the respective control groups ($p < 0.05$; Fig. 36A and B). In endometrial fibroblasts treated with IL-4 for 48 hours, COL3 was localized in the cytoplasm (Fig. 36C).

Interleukin 4 treatment decreased the gene expression of *FN1* in fibroblasts derived from category I endometria after 96 hours ($p < 0.001$; Fig. 37A), but increased its expression in fibroblasts derived from category IIB endometria after 96 hours in comparison to the respective control groups ($p < 0.01$; Fig. 37A). Moreover, IL-4 treatment increased the protein abundance of FN1 in fibroblasts derived from category I after 48 and 96 hours and from category IIB endometria after 96 hours in comparison to the respective control group ($p < 0.01$; Fig. 37B). In endometrial fibroblasts treated with IL-4 for 48 hours, FN1 was localized in the cytoplasm (Fig. 37C).

Interleukin 4 treatment decreased gene expression of *ACTA2* in fibroblasts derived from endometria category I after 48 ($p < 0.01$) and 96 hours ($p < 0.0001$) of treatment (Fig. 38A) and decreased protein abundance of ACTA2 in fibroblasts derived from category I after 48 ($p < 0.01$) and 96 hours ($p < 0.001$) and IIB endometria after 48 ($p < 0.05$) and 96 hours ($p < 0.01$) in comparison to the respective control group (Fig. 38B). In endometrial fibroblasts treated with IL-4 for 48 hours, ACTA2 was localized in the cytoplasm (Fig. 38C).

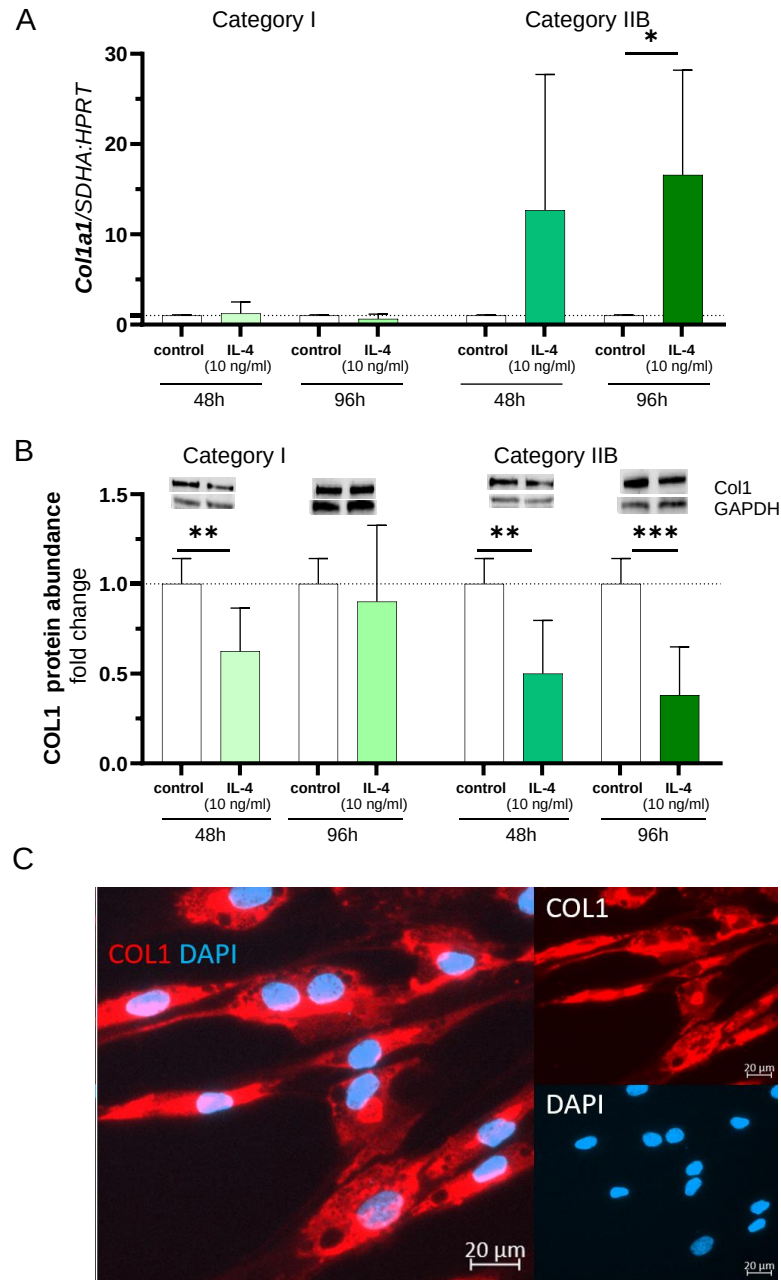


Figure 35. The effect of interleukin 4 (IL-4) on gene expression (A) and protein abundance (B) of collagen type I (COL1) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of COL1 after 48 hours of IL-4 treatment in fibroblasts derived from category I endometria (C). Results were presented as a mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterix denote statistically differences (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$) within each category and time of treatment in the comparison to the respective control group, as determined by the Student t-test.

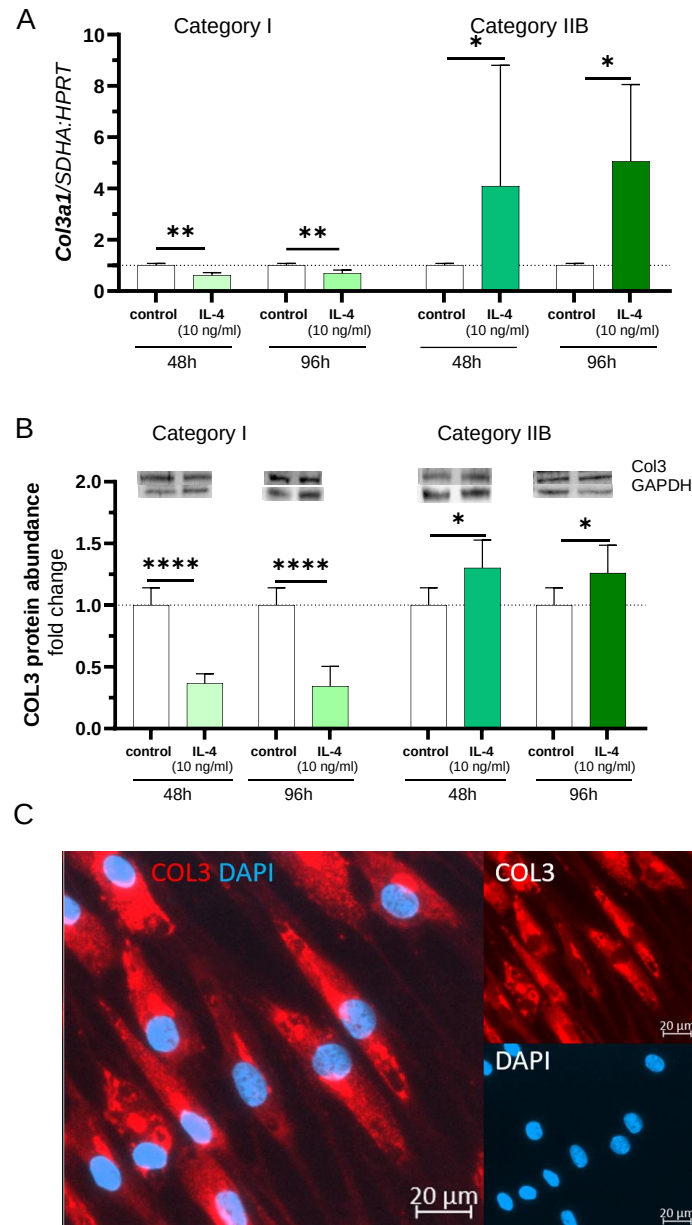


Figure 36. The effect of interleukin 4 (IL-4) on gene expression (A) and protein abundance (B) of collagen type III (COL3) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of COL3 after 48 hours of IL-4 treatment in fibroblasts derived from category I endometria C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterix denote statistical differences (* $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$) within each category and time of treatment, as determined by the Student t-test.

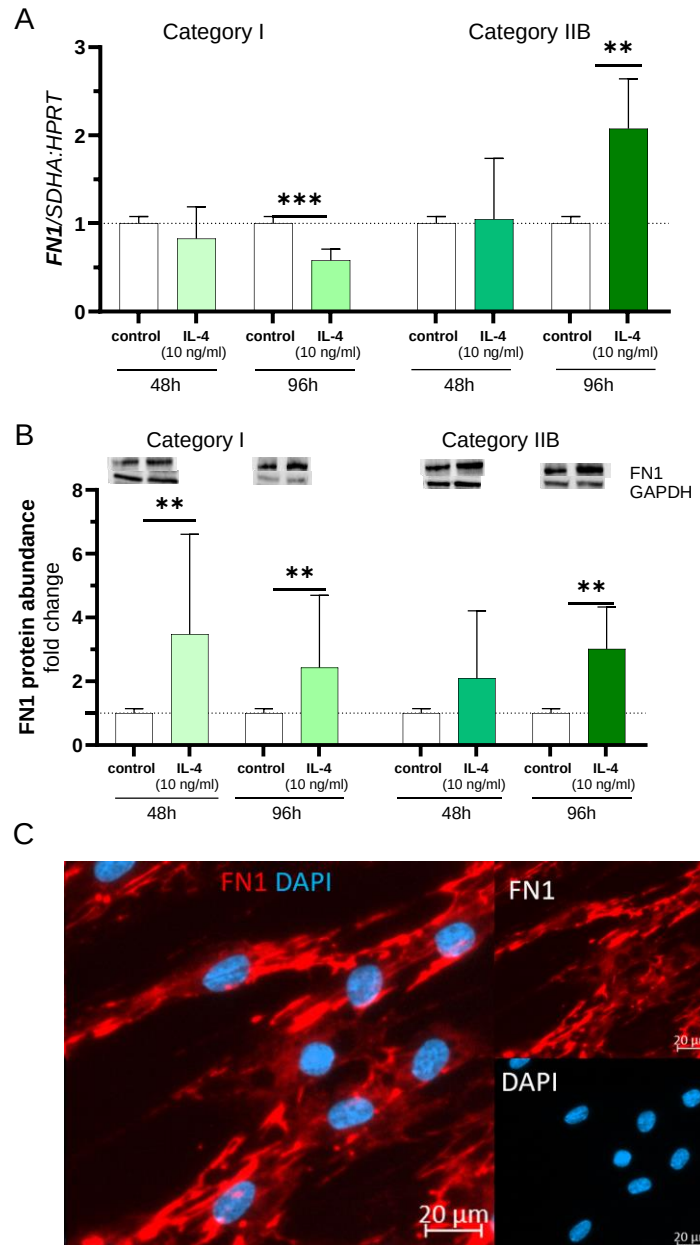


Figure 37. The effect of interleukin 4 (IL-4) on gene expression (A) and protein abundance (B) of fibronectin 1 (FN1) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of FN1 after 48 hours of IL-4 treatment in fibroblasts derived from category I endometria (C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (** $p < 0.01$, *** $p < 0.001$) within each category and time of treatment, as determined by the Student t-test.

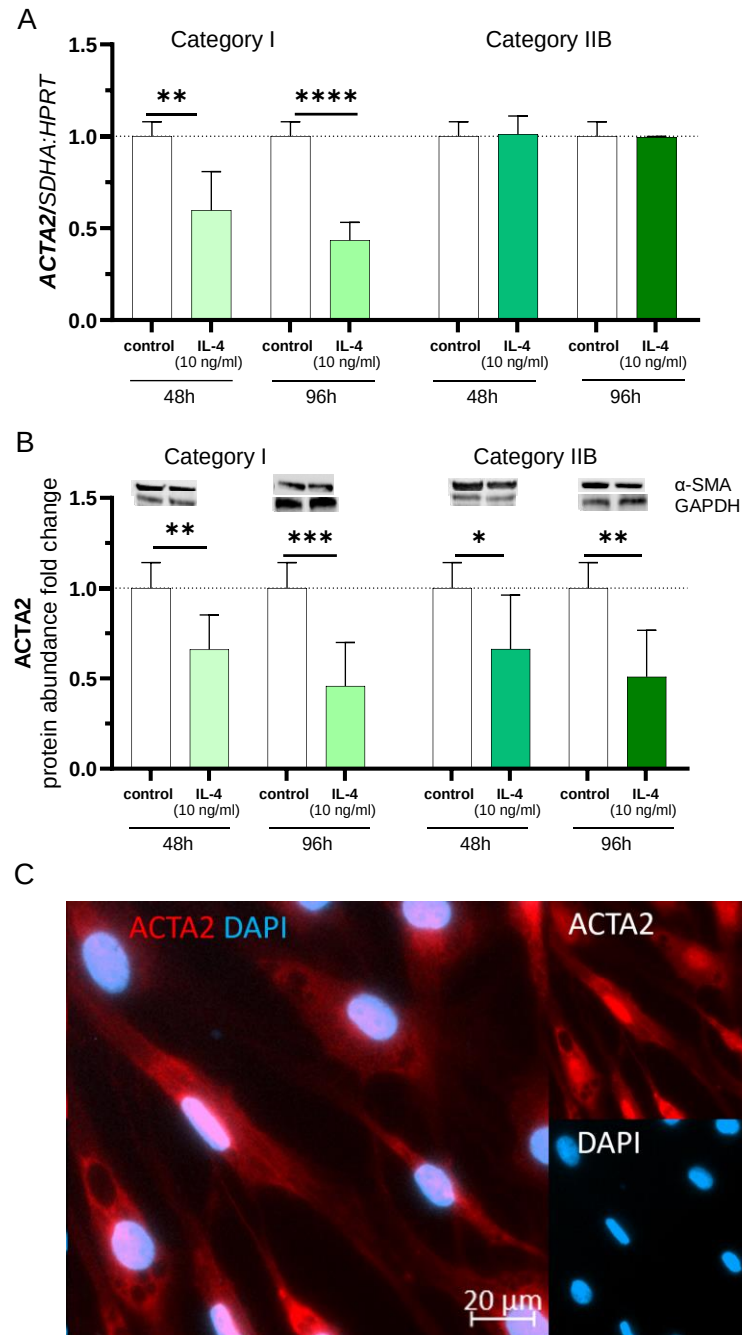


Figure 38. The effect of interleukin 4 (IL-4) on gene expression (A) and protein abundance (B) of α -smooth muscle actin (ACTA2) in fibroblasts derived from category I (n=5) and IIB (n= 5) endometria after 48 and 96 hours of treatment. The cellular localization of ACTA2 (C) after 48 hours of IL-4 treatment in endometrial fibroblasts derived from category I endometrium. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$) within each category and time of treatment, as determined by the Student t-test.

Interleukin 4 treatment decreased the gene expression and protein abundance of MMP-2 in fibroblasts derived from category I endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 39 A and B). Moreover, IL-4 decreased the gelatinolytic activity of pro-MMP-2 in fibroblasts derived from category IIB endometria after 96 hours in comparison to the respective control group ($p < 0.05$; Fig. 39C).

Interleukin 4 treatment decreased the gene expression and protein abundance of MMP-3 in fibroblasts derived from categories I and IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 40 A and B).

Interleukin 4 treatment decreased the gene expression of *MMP-9* in fibroblasts derived from category I endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 41A). Moreover, IL-4 treatment decreased the protein abundance of MMP-9 in fibroblasts derived from category IIB endometria after 48 hours in comparison to the respective control groups ($p < 0.01$; Fig. 41B). Interleukin 4 treatment decreased the gelatinolytic activity of pro-MMP-9 in fibroblasts derived from category I and IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.01$; Fig. 41C).

Interleukin 4 treatment increased the gene expression of *TIMP-1* in fibroblasts derived from category IIB endometria after 48 and 96 hours ($p < 0.05$, Fig. 42A), and increased TIMP1 level in fibroblasts derived from category I and IIB endometria in comparison to the respective control groups ($p < 0.05$; Fig. 42B).

Interleukin 4 treatment decreased the gene expression of *TIMP-2* in fibroblasts derived from category I endometria after 48 and 96 hours ($p < 0.001$, Fig. 42C), and increased TIMP-2 level in fibroblasts derived from category I and IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 42D).

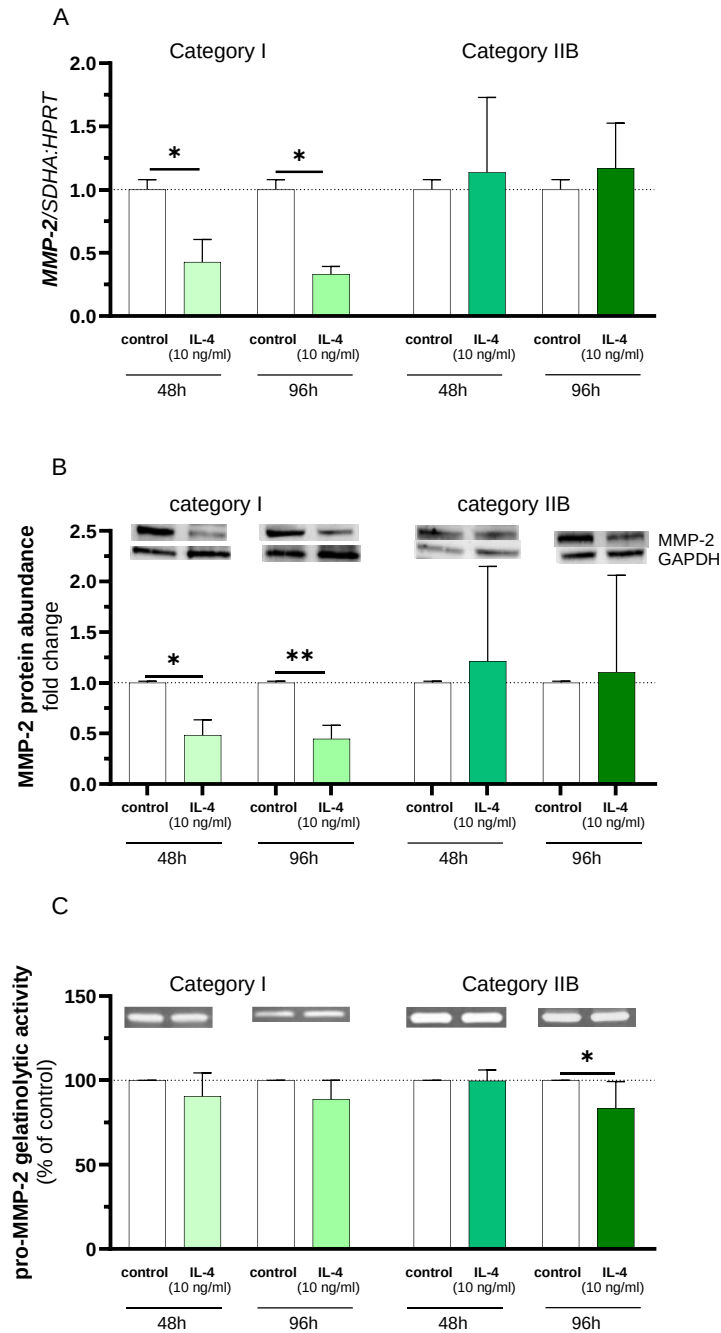


Figure 39. The effect of interleukin 4 (IL-4) on gene expression (A), protein abundance (B), and gelatinolytic activity (C) of matrix metalloproteinase 2 (MMP-2) in fibroblasts derived from category I (n=5) and IIB (n= 5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

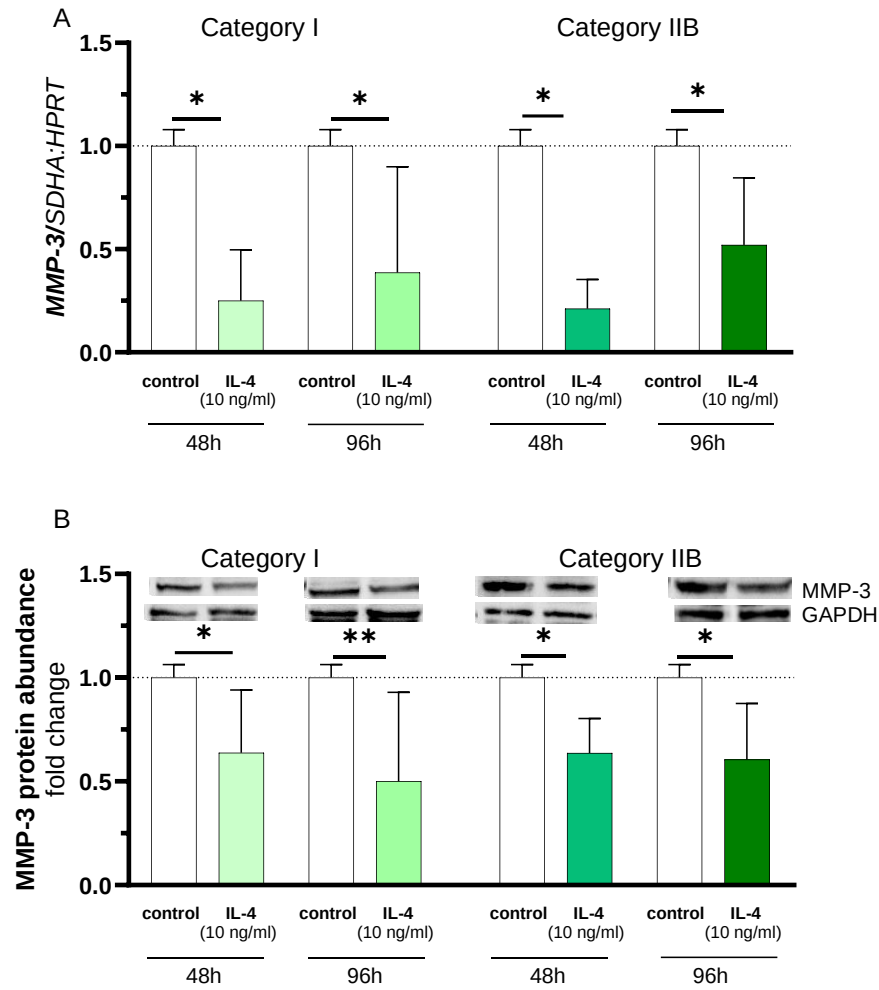


Figure 40. The effect of interleukin 4 (IL-4) on gene expression (A) and protein abundance (B) of matrix metalloproteinase 3 (MMP-3) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

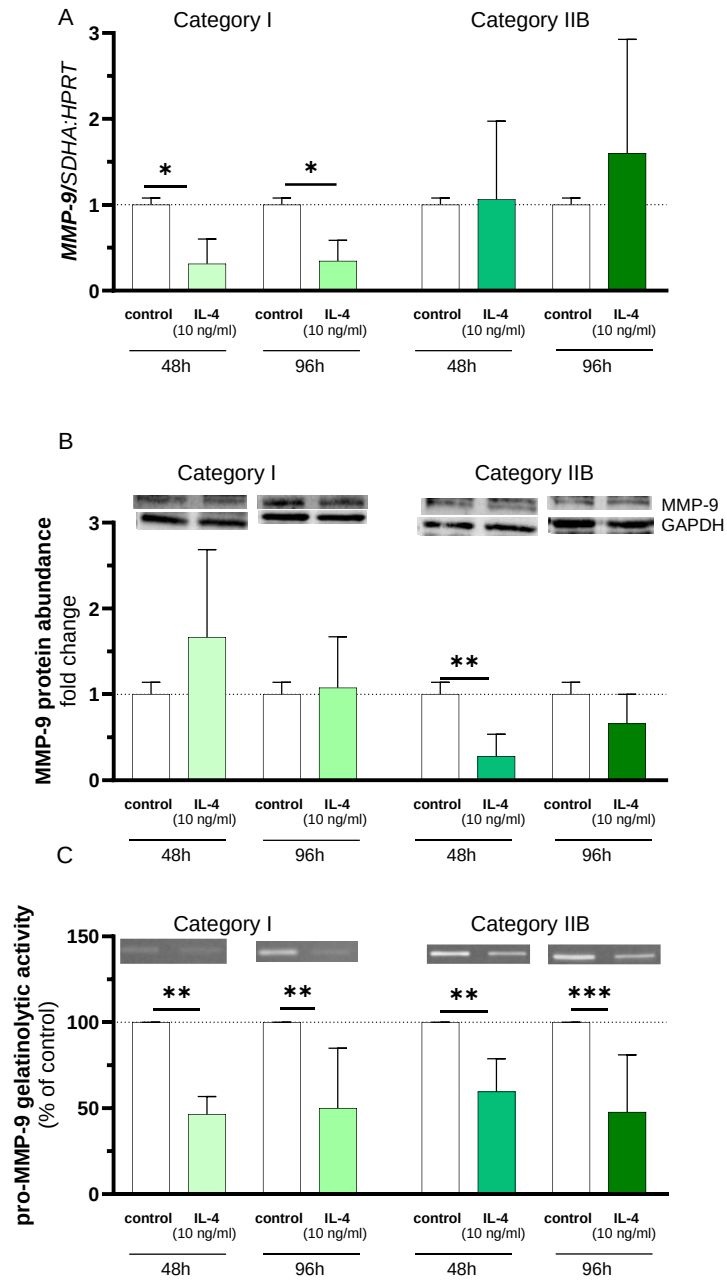


Figure 41. The effect of interleukin 4 (IL-4) on gene expression (A), protein abundance (B), and gelatinolytic activity (C) of matrix metalloproteinase 9 (MMP-9) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean ± standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* p<0.05, ** p<0.01, *** p<0.001), within each category and time of treatment, as determined by the Student t-test.

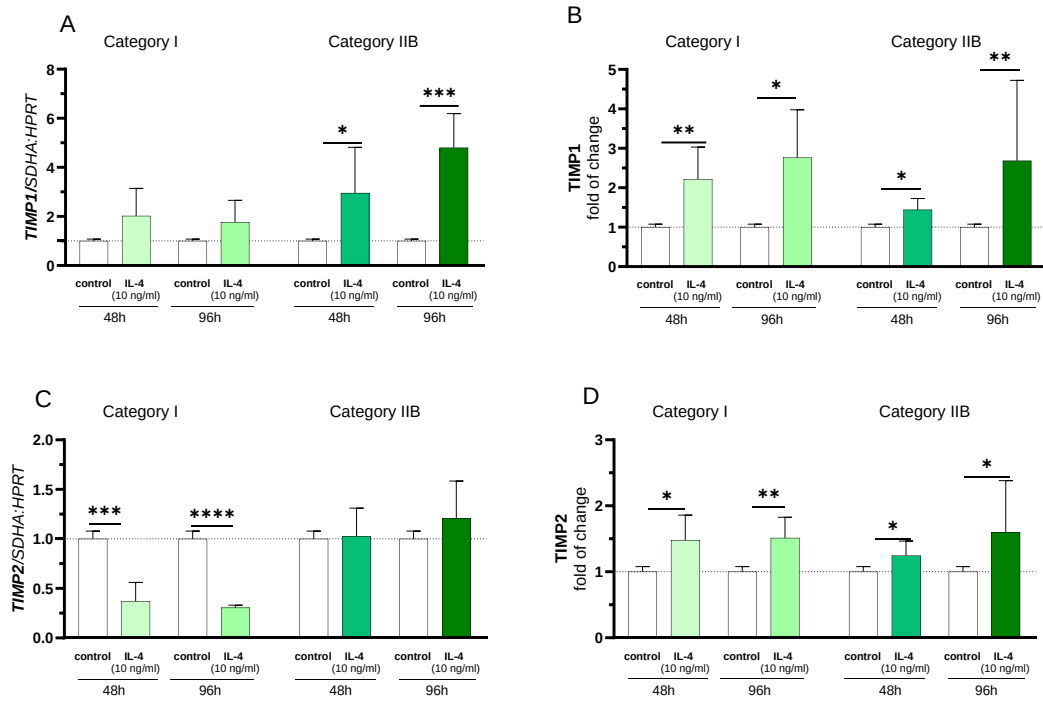


Figure 42. The effect of interleukin 4 (IL-4) on gene expression (A, C) and level (B, D) of the tissue inhibitor of matrix metalloproteinase (TIMP)-1 (A, B) and TIMP2 (C, D) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* p<0.05, ** p<0.01, **** p<0.0001) within each category and time of treatment, as determined by the Student t-test.

5.3.2.3. The effect of IL-13 on the expression of ECM-associated markers in fibroblasts derived at different stages of endometriosis

Interleukin 13 treatment decreased gene expression of *Col1a1* in fibroblasts derived from category I endometria after 48 hours ($p < 0.05$; Fig. 43A), and increased *Col1a1* expression in fibroblasts derived from category IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 43A). Moreover, IL-13 treatment decreased the protein abundance of COL1 in fibroblasts derived from category I and IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 43B). In endometrial fibroblasts treated with IL-13 for 48 hours, COL1 was localized in the cytoplasm (Fig. 43C).

Interleukin 13 increased the gene expression of *Col3a1* in fibroblasts derived from category IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 44A). Moreover, IL-13 treatment decreased the protein abundance of COL3 in fibroblasts derived from category I endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; Fig. 44B). In endometrial fibroblasts treated with IL-13 for 48 hours, COL1 was localized in the cytoplasm (Fig. 44C).

Interleukin 13 treatment decreased the gene expression of *FN1* in fibroblasts derived from category I endometria after 48 and 96 hours in comparison to the respective control groups ($p < 0.05$; $p < 0.01$; Fig. 45A). However, IL-13 treatment increased the protein abundance of FN1 in fibroblasts derived from category I endometria after 48 hours in comparison to the respective control group ($p < 0.05$; Fig. 45A). In endometrial fibroblasts treated with IL-13 for 48 hours, FN1 was localized in the cytoplasm (Fig. 45C).

Interleukin 13 treatment decreased the gene expression of *ACTA2* in fibroblasts derived from category I endometria after 96 hours in comparison to the respective control group ($p < 0.01$; Fig. 46A). Moreover, IL-13 treatment decreased the protein abundance of ACTA2 in fibroblasts derived from category I endometria after 48 and 96 hours ($p < 0.05$; Fig. 46B) and after 96 hours in fibroblasts derived from category IIB endometria ($p < 0.05$; Fig. 46B) in comparison to the respective control groups. In endometrial fibroblasts treated with IL-13 for 48 hours, ACTA2 was localized in the cytoplasm (Fig. 46C).

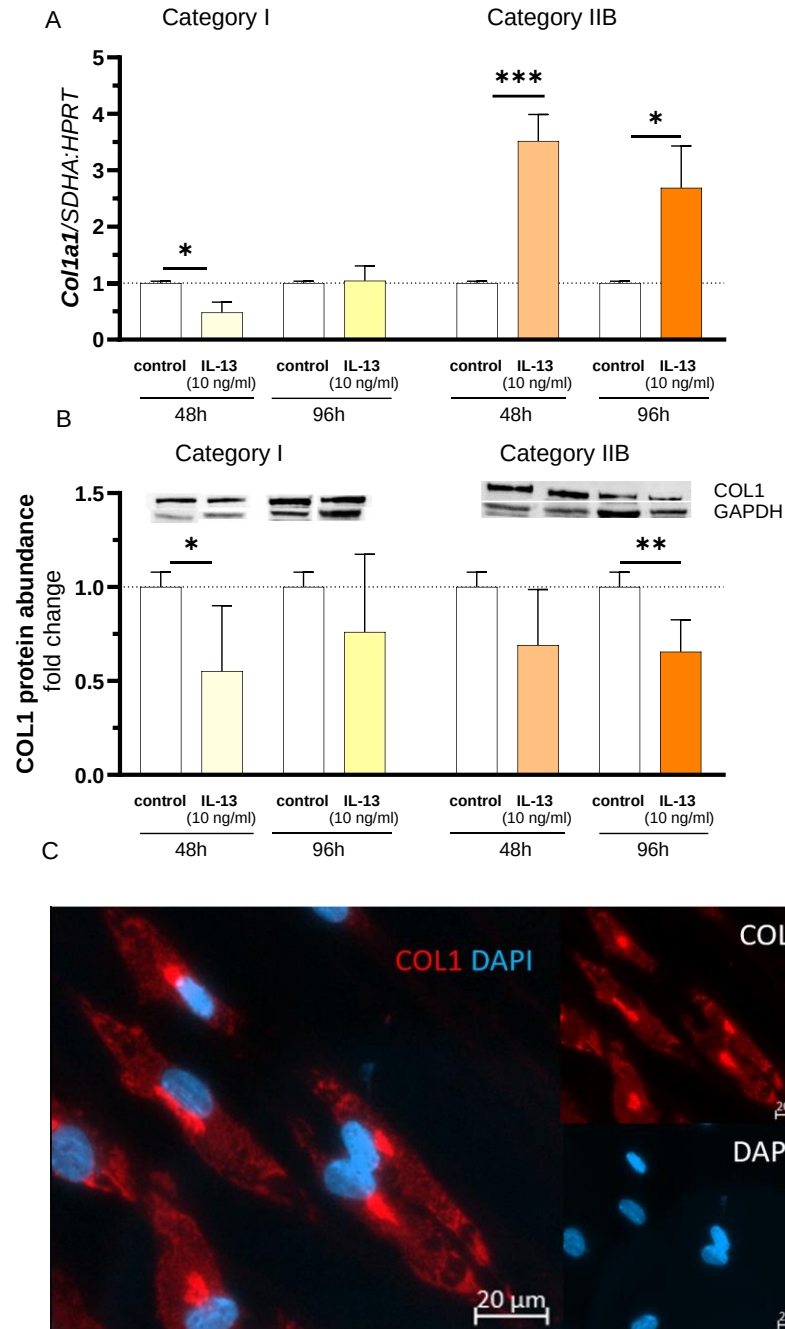


Figure 43. The effect of interleukin 13 (IL-13) on gene expression (A) and protein abundance (B) of collagen type I (COL1) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of COL1 after 48 hours of IL-13 treatment (C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

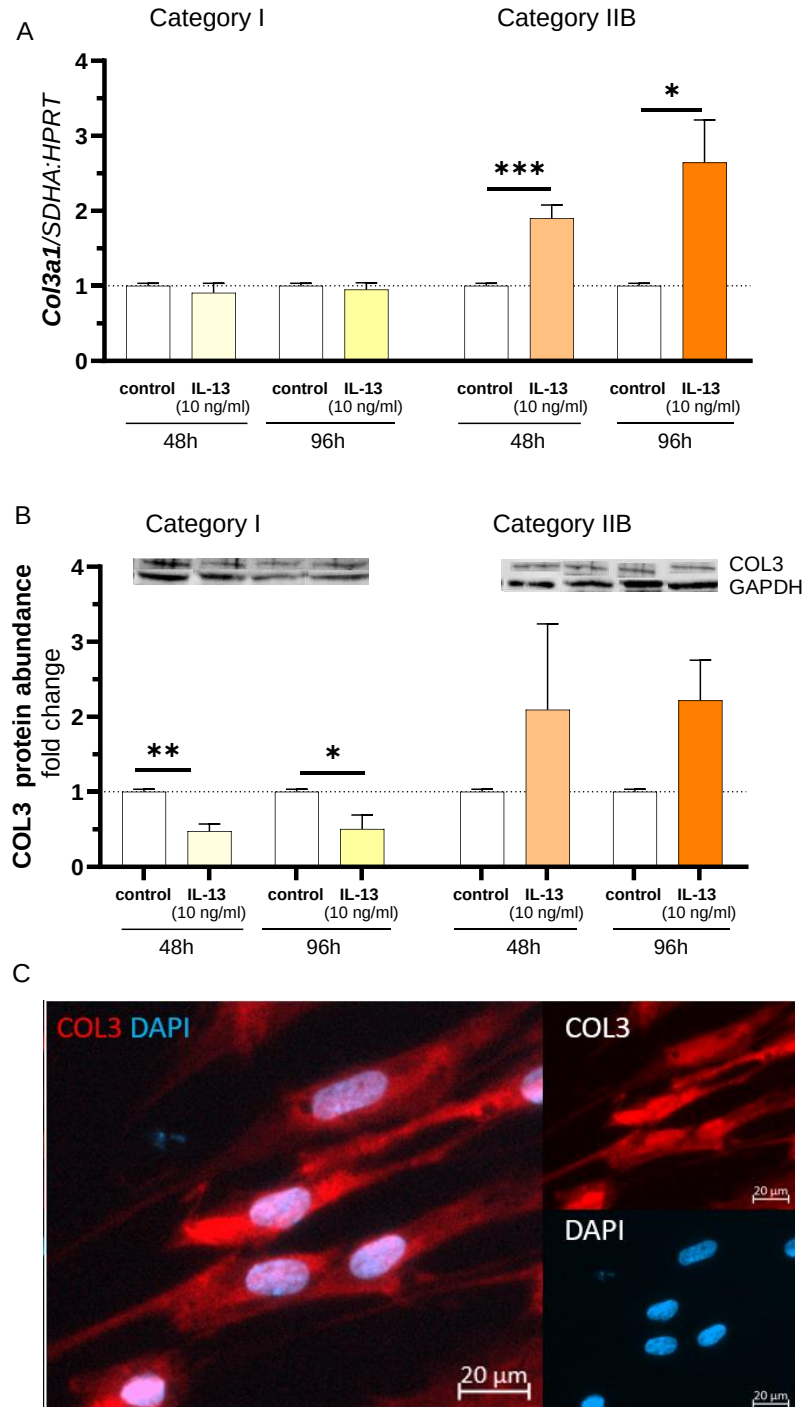


Figure 44. The effect of interleukin 13 (IL-13) on gene expression (A) and protein abundance (B) of collagen type III (COL3) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of COL3 after 48 hours of IL-4 treatment (C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$) within each category and time of treatment, as determined by the Student t-test.

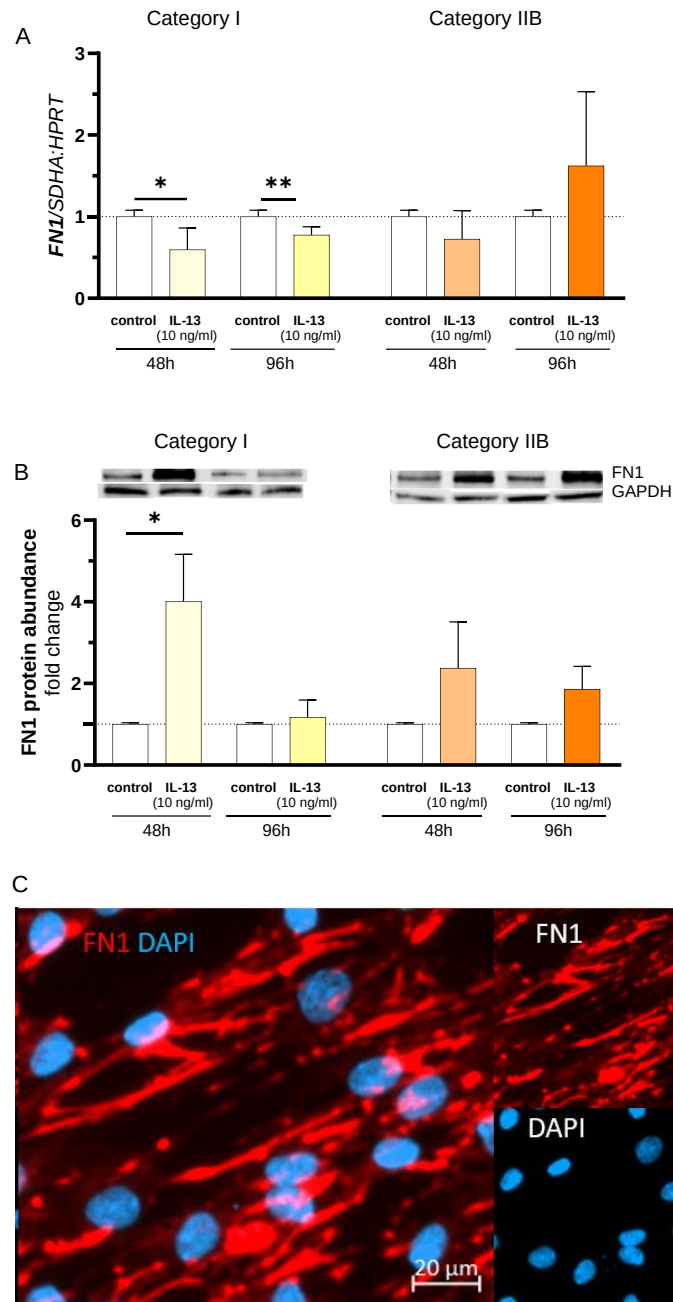


Figure 45. The effect of interleukin 13 (IL-13) on gene expression (A) and protein abundance (B) of fibronectin 1 (FN1) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of FN1 after 48 hours of IL-13 treatment (C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

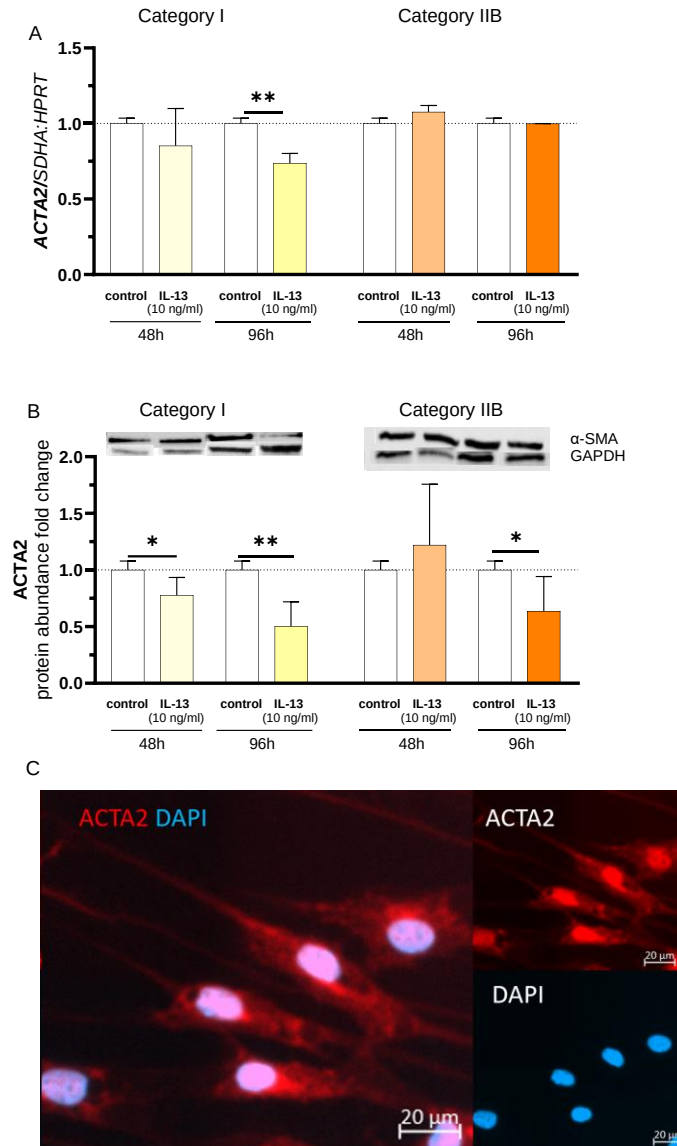


Figure 46. The effect of interleukin 13 (IL-13) on gene expression (A) and protein abundance (B) of α -smooth muscle actin (ACTA2) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. The cellular localization of ACTA2 after 48 hours of IL-13 treatment (C). Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

Interleukin 13 treatment decreased the gene expression of *MMP-2* in fibroblasts derived from category I endometria after 48 and 96 hours in comparison to the respective control group ($p<0.05$; Fig. 47A). IL-13 treatment decreased MMP-2 protein abundance in fibroblasts derived from category IIB endometria after 96 hours in comparison to the respective control group ($p<0.05$; Fig. 47B). The gelatinolytic activity of MMP-2 was not affected by IL-13 treatment in fibroblasts derived from both category I and IIB endometria in comparison to the respective control group ($p>0.05$; Fig. 47C).

Interleukin 13 treatment decreased the gene expression of *MMP-3* in fibroblasts derived from categories I and IIB endometria after 48 hours in comparison to the respective control group ($p<0.001$; Fig. 48A). The protein abundance of MMP-3 was not affected by IL-13 treatment in fibroblasts derived from both category I and IIB endometria in comparison to the respective control group ($p>0.05$; Fig. 48B).

Interleukin 13 treatment decreased the gene expression of *MMP-9* in fibroblasts derived from category I endometria after 48 hours in comparison to the respective control group ($p<0.05$; Fig. 49A). The protein abundance of MMP-9 decreased after 96 hours of IL-13 treatment in fibroblasts derived from category I endometria in comparison to the respective control group ($p<0.01$; Fig. 49B). The gelatinolytic activity of MMP-9 was found to be decreased after 48 and 96 hours of IL-13 treatment in fibroblasts derived from only category I endometria in comparison to the respective control group ($p<0.001$; Fig. 49C).

The gene expression of *TIMP-1* increased after IL-13 treatment in fibroblasts derived from category I endometria after 48 hours ($p<0.05$, Fig. 50A) and category IIB endometria after 48 and 96 hours in comparison to the respective control group ($p<0.05$; $P<0.0001$ Fig. 50A). Interleukin 13 treatment increased TIMP1 level in fibroblasts derived from both category I and IIB endometria after 48 and 96 hours in comparison to the respective control group ($p<0.05$; Fig. 50B).

The gene expression of *TIMP-2* decreased after IL-13 treatment in fibroblasts derived from category I endometria ($p<0.05$, Fig. 50C), while TIMP-2 level increased after IL-13 treatment in fibroblasts derived from both category I and IIB endometria after 48 and 96 hours in comparison to the respective control group ($p<0.05$; Fig. 50D).

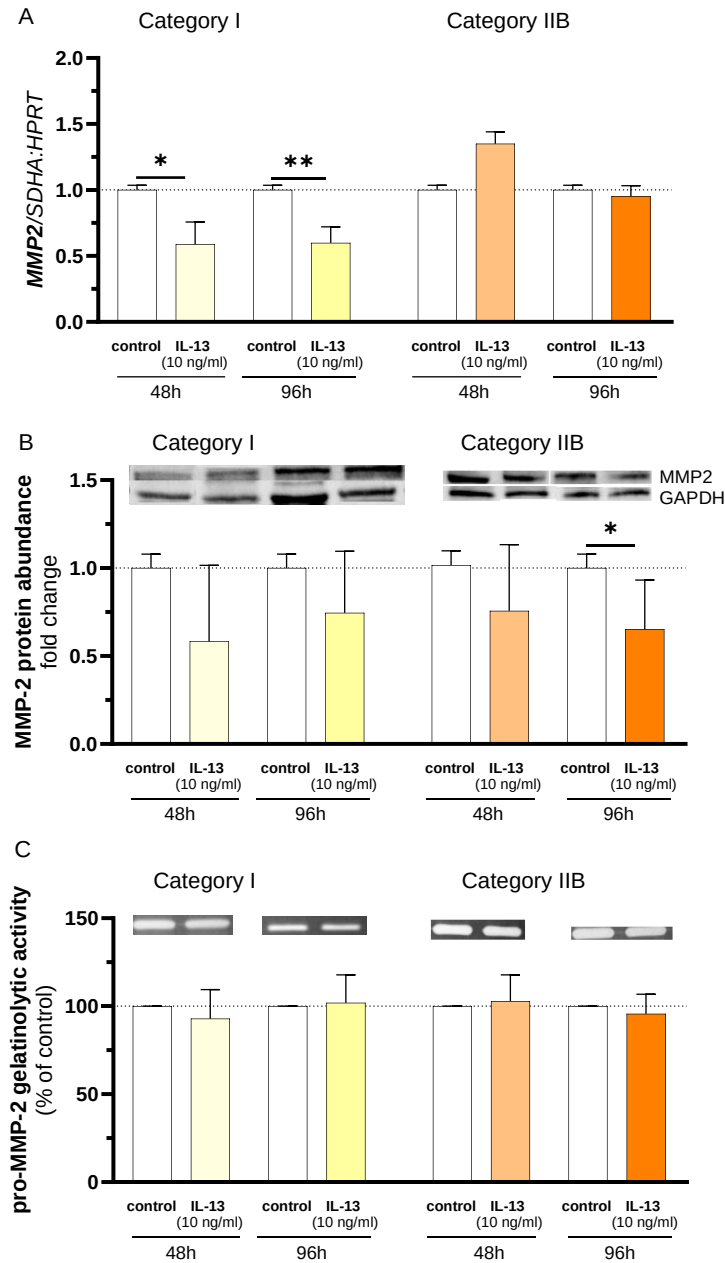


Figure 47. The effect of interleukin 13 (IL-13) on gene expression (A), protein abundance (B), and gelatinolytic activity (C) of matrix metalloproteinase 2 (MMP2) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results are calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold (A, B) and percentage (C) to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$) within each category and time of treatment, as determined by the Student t-test.

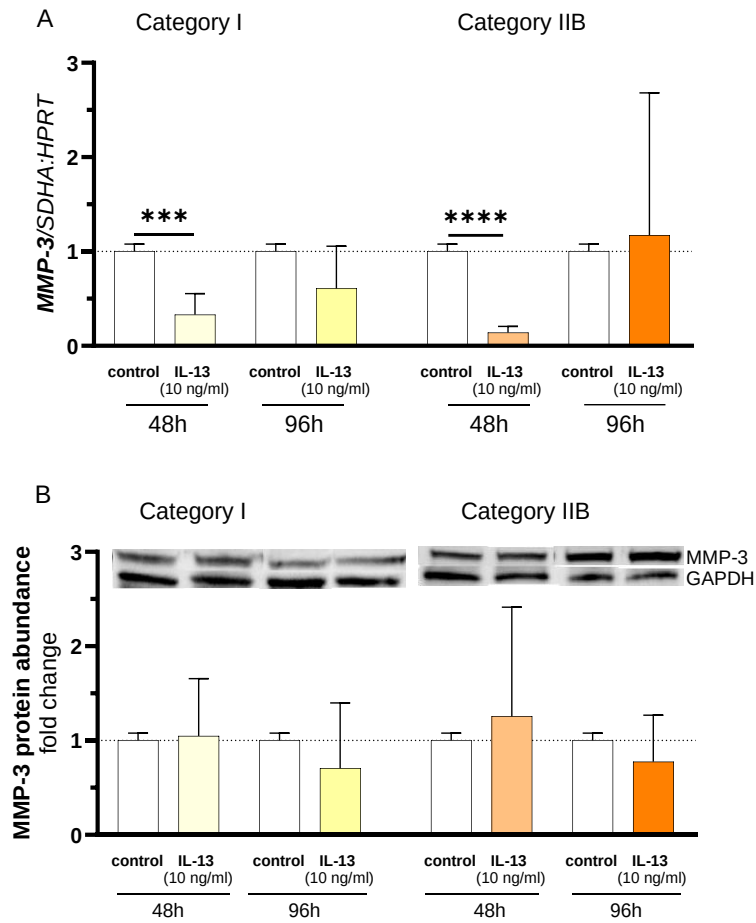


Figure 48. The effect of interleukin 13 (IL-13) on gene expression (A) and protein abundance (B) of matrix metalloproteinase 3 (MMP3) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (***) $p < 0.001$, **** $p < 0.0001$) within each category and time of treatment in comparison to the respective control group, as determined by the Student t-test.

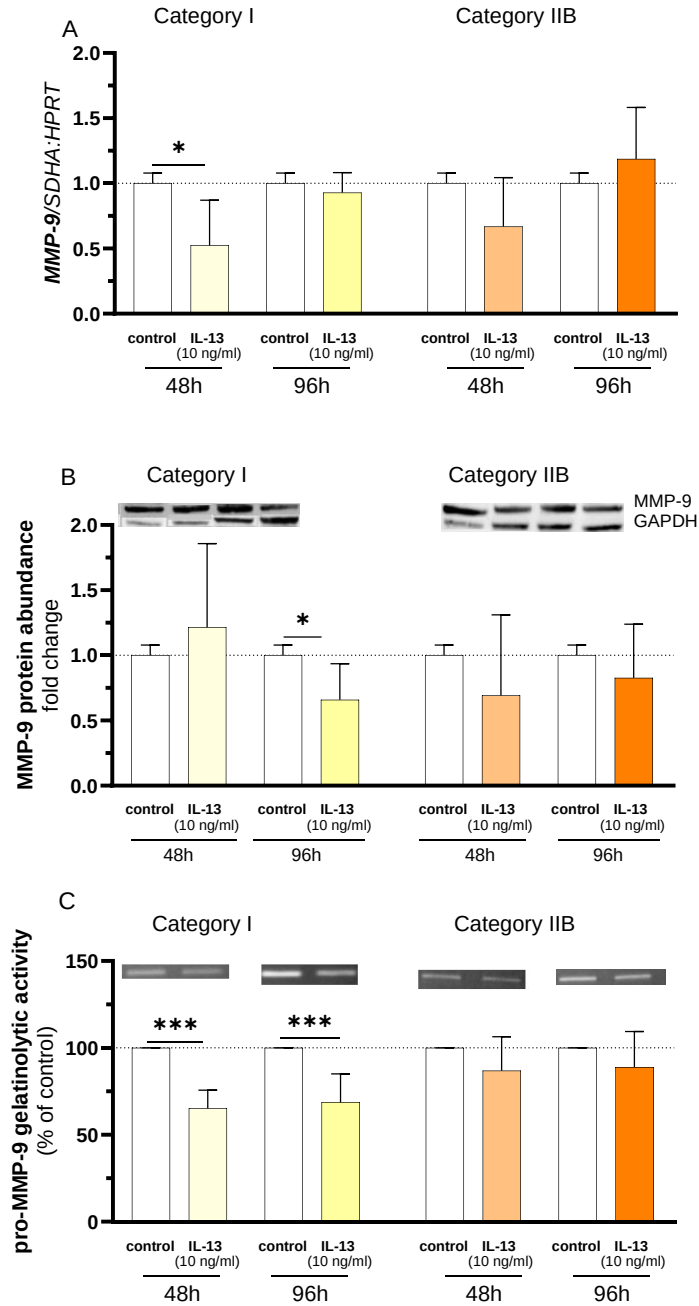


Figure 49. The effect of interleukin IL-13 (IL-13) on gene expression (A), protein abundance (B), and gelatinolytic activity (C) of matrix metalloproteinase 9 (MMP-9) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change (A, B) and a percentage (C) to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, *** $p < 0.001$) within each category and time of treatment, as determined by the Student t-test.

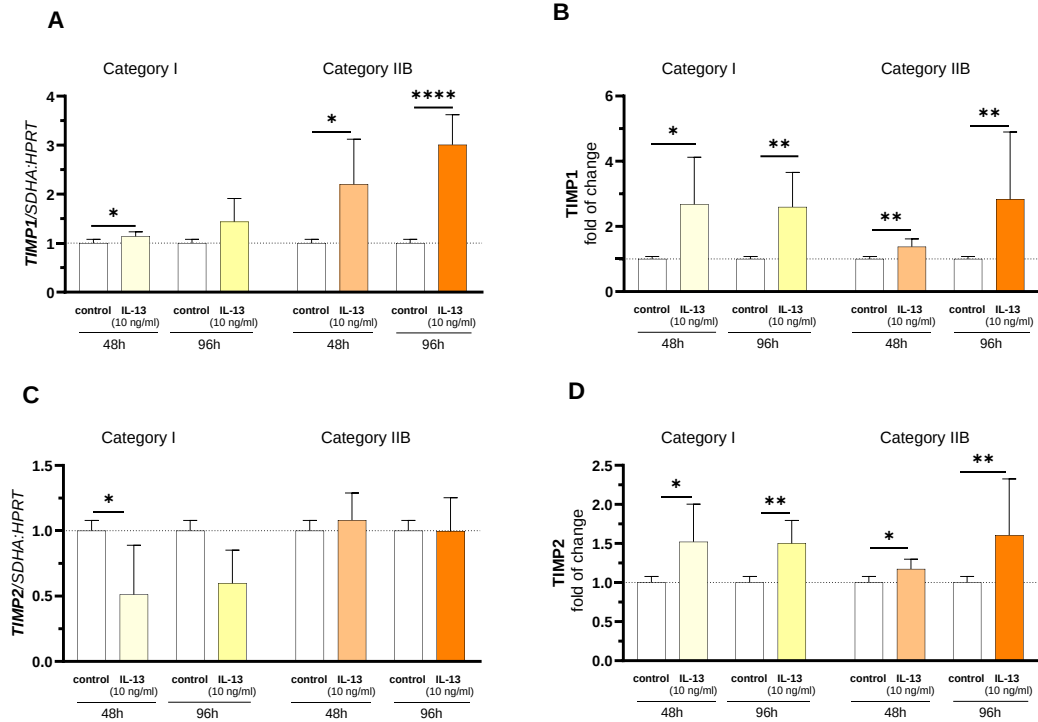


Figure 50. The effect of interleukin 13 (IL-13) on gene expression (A, C) and level (B, D) of the tissue inhibitor of matrix metalloproteinase (TIMP)-1 (A, B) and TIMP2 (C, D) in fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results were calculated as the mean $\pm$ standard deviation (SD) and expressed as a fold change to the respective control group within each category and time of treatment. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$) within each category and time of treatment in comparison to the respective group, as determined by the Student t-test.

5.3.3. Experiment 3. The effect of IFN- γ , IL-4, and IL-13 on functional characteristic of endometrial fibroblasts

5.3.3.1. The effect of IFN- γ on functional characteristic of endometrial fibroblasts

The treatment with IFN- γ resulted in a decrease in proliferation of fibroblasts derived from category I endometria after 48 hours in comparison to the control group ($p < 0.05$; Fig. 51A). The proliferation of fibroblasts derived from category IIB endometria increased after 96 hours of IFN- γ treatment in comparison to the control group ($p < 0.05$; Fig. 51A). The viability of fibroblasts derived from either category I or IIB endometria was not affected by IFN- γ treatment at either 48 or 96 hour in comparison to the control group ($p > 0.05$; Fig. 51B).

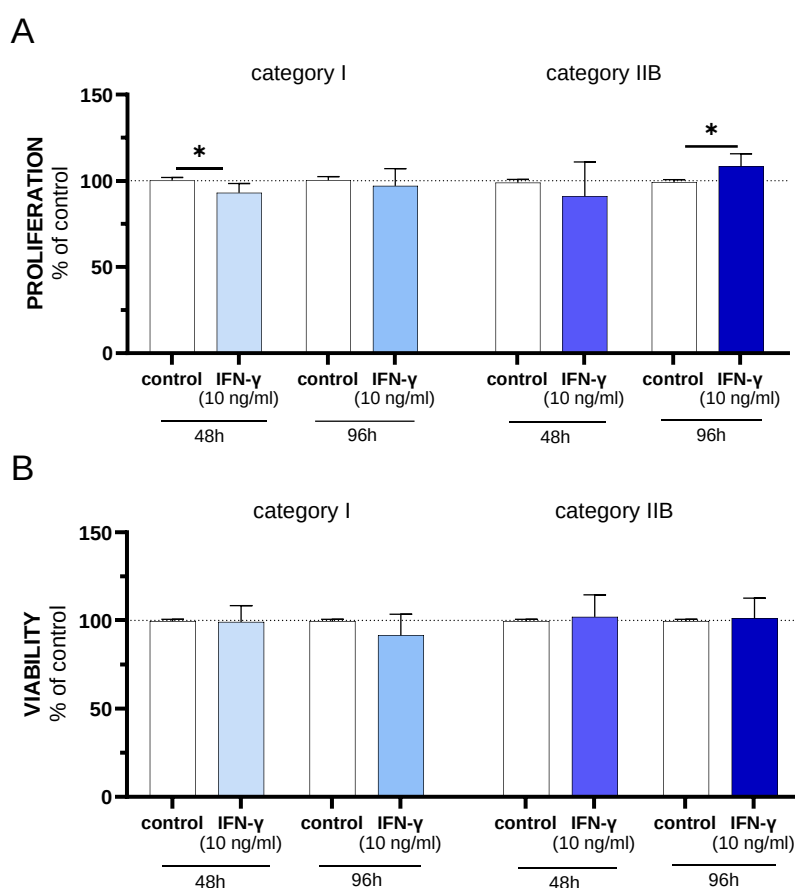


Figure 51. The effect of interferon γ (IFN- γ) on the proliferation (A) and viability (B) of fibroblasts derived from category I ($n=5$) and IIB ($n=5$) endometria after 48 and 96 hours of treatment. Results are calculated as the mean $\pm$ standard deviation (SD) and expressed as a percentage to the respective control group. Asterisks denote statistical differences (* $p < 0.05$) within each category and time of treatment, as determined by the Student t-test.

5.3.3.2. The effect of IL-4 on functional characteristic of endometrial fibroblasts

The treatment with IL-4 increased the proliferation ($p < 0.05$; Fig. 52A) and viability ($p < 0.0001$; Fig. 52B) of fibroblasts derived from categories I and IIB endometria after 48 and 96 hours in comparison to the respective control groups.

The effect of IL-4 on the migration of fibroblasts and contraction of collagen gel discs by fibroblasts derived from category I and IIB endometria is presented in Figure 53. Interleukin 4 decreased the migration of fibroblasts derived from category I endometria after 96 hours in comparison to the respective control groups. ($p < 0.05$; Fig. 53A). The capacity of fibroblasts to contract the collagen discs was unaltered after IL-4 treatment in cells derived from both category I and IIB endometria in comparison to the respective control groups ($p > 0.05$, Fig. 53 C and D).

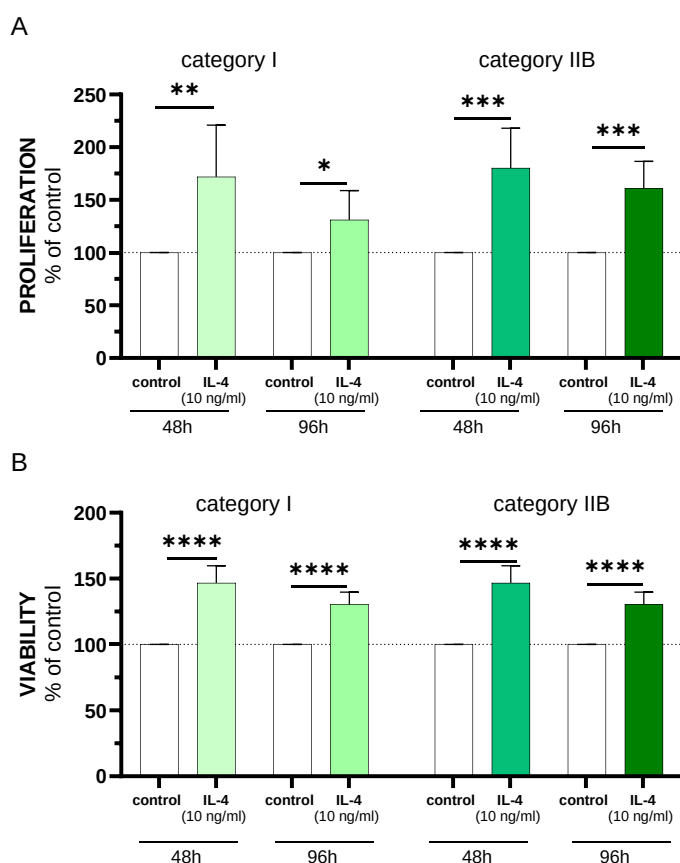


Figure 52. The effect of interleukin 4 (IL-4) on the proliferation (A) and viability (B) of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results are calculated as the mean $\pm$ standard deviation (SD) and expressed as a percentage to the respective control group. Asterisks denote statistical differences (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$) within each category and time of treatment, as determined by the Student t-test.

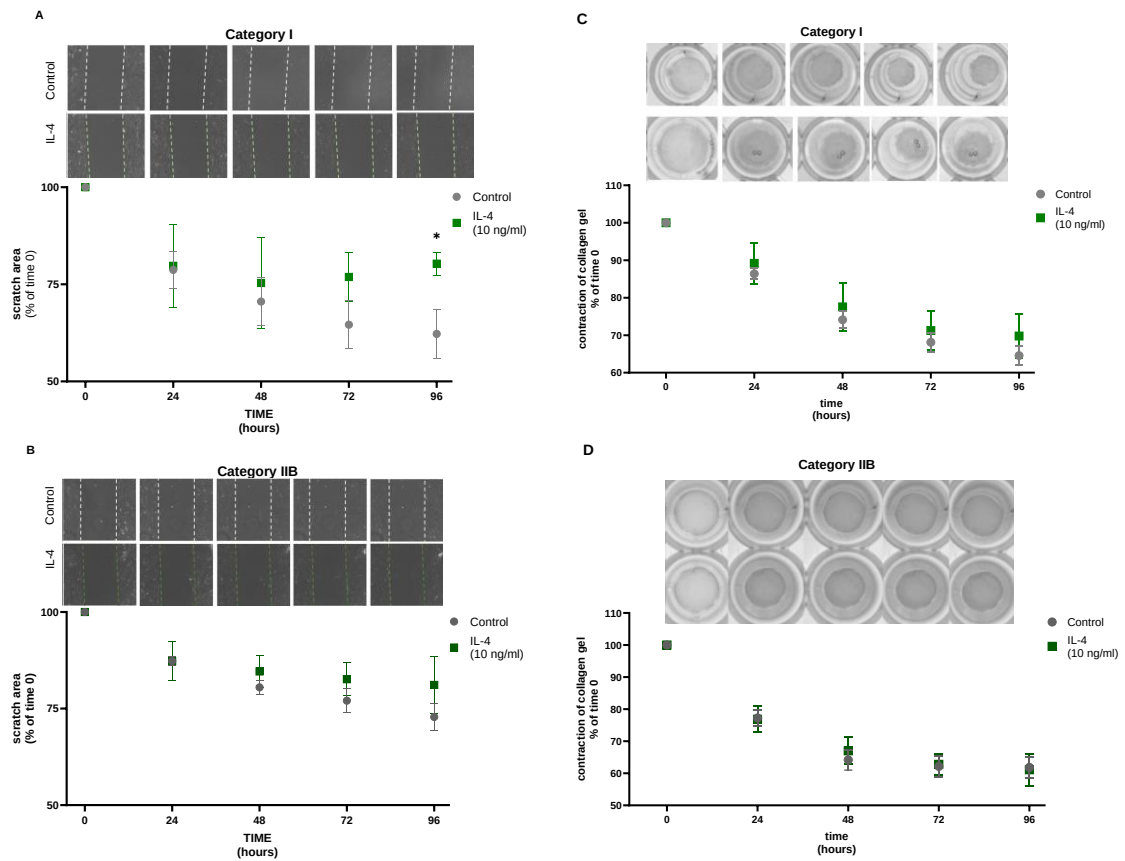


Figure 53. The effect of interleukin 4 (IL-4) on the migration (A, B) and on the capacity to contract collagen gel discs (C, D) by fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 0, 24, 48, 72 and 96 hours of treatment. The results are presented as the mean $\pm$ standard deviation (SD) and expressed as a percentage of the scratch area (A, B) and collagen disc area (C, D) at time 0. Asterisk denotes statistical difference (* $p < 0.05$), as determined by the Student t-test.

5.3.3.3. The effect of IL-13 on functional characteristic of endometrial fibroblasts

The treatment with IL-13 increased the proliferation of fibroblasts derived from categories I and IIB endometria after 48 and 96 hours in comparison to the respective control groups ($p<0.05$; Fig. 54A). The viability of fibroblasts derived from category I endometria increased after 48 and 96 hours of IL-13 treatment ($p<0.01$; Fig. 54B), while in fibroblasts derived from category IIB endometria, the viability was observed to be increased only after 48 hours of treatment in comparison to the respective control groups ($p<0.01$; Fig. 54B).

The effect of IL-13 on migration of fibroblasts and contraction of collagen gel discs by fibroblasts derived from category I and IIB endometria at different time points: 0, 24, 48, 72, and 96 hours of treatment is presented in Figure 55. Interleukin 13 treatment did not affect the migration and contractility of fibroblasts derived from both categories of endometria in comparison to the respective control groups ($p>0.05$; Fig. 55 A-D).

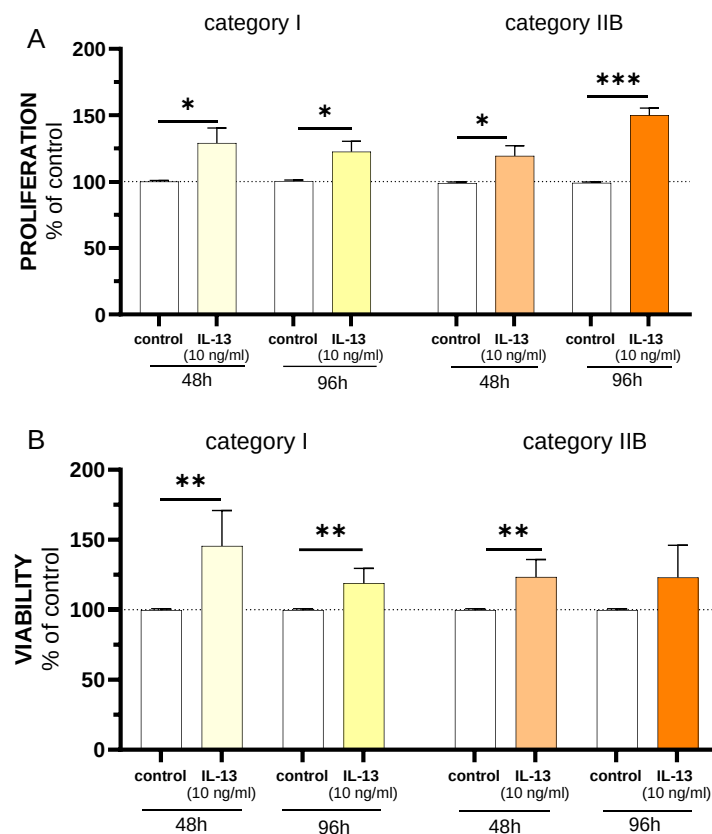


Figure 37. The effect of interleukin 13 (IL-13) on the proliferation (A) and viability (B) of fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 48 and 96 hours of treatment. Results are calculated as the mean $\pm$ standard deviation (SD) and expressed as a percentage to the respective control groups. Asterisks denote statistical differences (* $p<0.05$, ** $p<0.01$, *** $p<0.001$) within each category and time of treatment, as determined by the Student t-test.

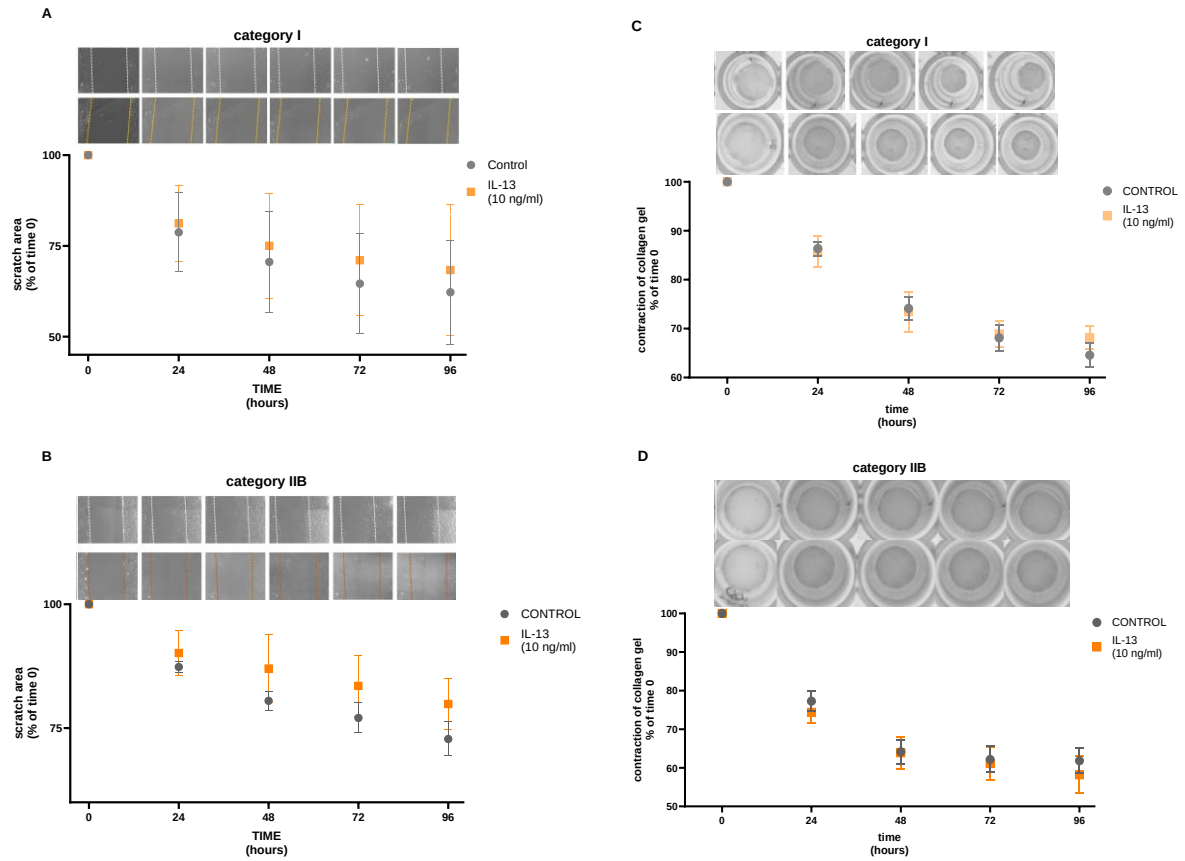


Figure 55. The effect of interleukin 13 (IL-13) on the migration (A, B) and the capacity to contract collagen gel discs (C, D) by fibroblasts derived from category I (n=5) and IIB (n=5) endometria after 0, 24, 48, 72 and 96 hours of treatment. Results are calculated as the mean $\pm$ standard deviation (SD) and expressed as a percentage of the scratch area (A, B) and collagen disc area (C, D) at time 0.

6. Discussion

Fibrosis is a complex and multifaceted process that involves the coordinated activity of multiple cell types, including fibroblasts, immune and epithelial cells. It is tightly regulated by a myriad of factors and molecules, including cytokines, growth factors, and MMPs. This intricate interplay can result in excessive tissue remodeling and fibrosis when dysregulated, contributing to various chronic diseases. The role of Th1 and Th2 cell subsets in the development of fibrosis was demonstrated by targeting fibroblasts in human liver as well as human and murine hearts and lungs (Zhang & Zhang, 2020). The traditional view categorizes Th1 cells as anti-fibrotic and Th2 cells as profibrotic. The results of different studies suggest that this view is an oversimplification and should be interpreted within a broader biological context. A comprehensive understanding of the role of Th1 and Th2 cells requires considering tissue-specific contexts, alternative signaling pathways, and the intricate cross-talk between these immune cell populations. Moreover, their functions are complex, as they influence inflammatory processes, which, through cytokine release, can affect fibroblasts, contributing to the activation of macrophages. Despite years of research on mare endometrosis, the role of Th1 and Th2 cell subsets in the processes associated with the development of endometrial fibrosis in the progression of endometrosis remains unknown. Thus, this dissertation aimed to present a comprehensive analysis of the potential involvement of Th1 and Th2 cells in the development of mare endometrial fibrosis in the progression of endometrosis. Firstly, the ratio of Th1 to Th2 cell subsets along with the gene expression and concentration of IFN- γ , IL-4, and IL-13 as well as the gene expression and protein abundance of their respective receptors in the endometrium during the progression of endometrosis in both the mid-luteal and follicular phases of the oestrous cycle was determined. Subsequently, the effect of the Th1 and Th2 cell secretome on the transcriptomic changes, the expression of ECM-associated genes, and functional characteristics of mare endometrial fibroblasts were investigated. Eventually, the effect of IFN- γ , IL-4, and IL-13 on the transcriptomic changes, the expression of ECM-associated genes, and the protein abundance, in addition, to the functional characteristic of endometrial fibroblasts obtained at varying stages of endometrosis were determined.

6.1. Th1 to Th2 cell ratios and cytokine expression in the endometrium of mares with endometrosis

The presence of Th1 and Th2 cells in the endometrium of mares with endometrosis was confirmed using flow cytometry in research task 1. However, no alterations were observed in the distribution of Th1 or Th2 and Th1 to Th2 ratio in the endometrium between categories of mare endometrosis in both the mid-luteal and follicular phases of the oestrous cycle. Furthermore, there were no alterations in IFN- γ , IL-4, and IL-13 gene expression and concentration as well as IFN- γ R1, IL-4RA, and IL-13RA gene expression and protein abundance between endometrial categories in the mid-luteal and follicular phases of the oestrus cycle.

The infiltration of T cells (CD3⁺) has been observed in the endometria of mare with endometrosis. More precisely, the T cells were highly prevalent within the fibrotic glands of the equine endometrium (Klose & Schoon, 2016). T cells appear to play an important role in the endometrium of mares, influencing both the inflammatory response, which is a critical factor in the development of endometrosis, and the remodeling of the endometrium during the oestrous cycle (Klose & Schoon, 2016). Nevertheless, to the best of my knowledge, there is no study concerning the endometrial presence of Th1 (CD3+CD4+IFN- γ +) or Th2 (CD3+CD4+IL-4+) cell subsets in the mare endometrium with endometrosis. The role of Th1 and Th2 cell subsets in the development of fibrosis in various organs and tissues is a topic of ongoing research, as previously reviewed (Wynn, 2004). In a murine model of radiation-induced lung fibrosis, the infiltration of Th cells was observed, indicating their importance in the development of fibrosis (Westermann et al., 1999). Results of the study on patients with progressive fibrosing interstitial lung diseases demonstrated increased numbers of Th2 cells in both peripheral blood and bronchoalveolar lavage fluid (Tsukuda et al., 2022). In patients with renal fibrosis and in mice with experimentally induced renal fibrosis, elevated numbers of Th2 cells have been observed. Moreover, the Th2 to Th1 ratio has been shown to increase in parallel with the development of experimentally induced renal fibrosis in mice (Liu et al., 2012). The results of studies analyzing the role of Th1 and Th2 cells in the development of fibrosis indicate that Th1 cells may play an anti-fibrotic role, while Th2 cells may have a profibrotic effect (Wynn, 2004, 2008). However, the interpretation of the results requires careful consideration, as the presence of a subpopulation of Th cells observed in fibrotic diseases and experimentally induced models of organ fibrosis in animals may be

driven by two distinct mechanisms: the progression of fibrosis and the associated inflammatory response (Yanguas et al., 2016; Padmanabhan et al., 2019).

Interferon γ plays a pivotal role in modulating a vast array of immunological and inflammatory pathways within the human body. Significant variations in its levels have been observed between healthy and fibrotic tissues (Tau & Rothman, 1999). It has been demonstrated that the level of IFN- γ varies in different organs undergoing fibrosis in different species (Sakkas et al., 1999; Hu et al., 2020; Attallah et al., 2016). A positive correlation was observed between the level of IFN- γ and the development of liver fibrosis in humans (Attallah et al., 2016). On the other hand, lower serum levels of IFN- γ were associated with an increased degree of pulmonary fibrosis in COVID-19 patients (Hu et al., 2020). However, not all research results clearly indicate a correlation between IFN- γ levels and the development of fibrosis. For instance, no alteration in IFN- γ serum levels was observed in patients with systemic sclerosis (Sakkas et al., 1999). In the current study, no differences were found in the concentration of IFN- γ and its receptor at both gene and protein levels between various endometrial categories of mare endometriosis. To the best of my knowledge, no study focusing on IFN- γ and its receptor gene expression and protein abundance in the mare endometrium with endometriosis is available. However, the results of the present dissertation are consistent with those previously published, which found no differences in the gene expression of *IFN- γ* and its receptor in mare endometria in the mid-luteal and follicular phase of the oestrous cycle (Galvao et al., 2013). Moreover, despite no alteration in the gene expression, Galvao et al (2013) reported a decrease in protein abundance of both IFN- γ as well as its receptor in the follicular phase of the oestrous cycle, which is consistent with results presented in this dissertation.

In the current study, no changes in the gene expression and protein abundance of both IL-4 and its receptor were found in the mare endometrium at different stages of endometriosis. In the development of fibrotic disorders, IL-4 levels are often elevated which, in turn, favours fibrosis development (Gieseck et al., 2018). An increase in IL-4 gene expression was specifically observed in CD4⁺ T cells isolated from irradiated lungs, suggesting a Th2-dominated T cell response (Westermann et al., 1999). Furthermore, elevated tissue levels of IL-4 were observed in a rodent model of experimentally induced lung fibrosis (Buttner et al., 1997; Gharaee-Kermani et al., 2001) as well as in the IPF patients (Ando et al., 1999; Wallace & Howie, 1999). In systemic sclerosis patients, IL-4 blood levels were found to be higher when compared to healthy individuals (Sakkas

et al., 1999). Additionally, elevated levels of IL-4 in blood serum were observed in liver fibrosis, particularly in advanced fibrosis accompanying chronic hepatitis C (Batsaikhan et al., 2019).

The present study did not reveal any alterations in the endometrial level of IL-13 observed in either the mid-luteal or follicular phases of the oestrous cycle. Interestingly, we found a reduction of IL-13R protein abundance in all categories of endometria in the follicular phase of the oestrous cycle compared to the mid-luteal phase of the oestrous cycle, similar to IFN- γ protein concentration. However, no alterations were observed within endometrial categories. In fibrotic conditions, IL-13 levels are typically elevated and contribute significantly to the pathological processes that lead to tissue and fibrosis. More precisely, the level of IL-13 in blood plasma was significantly elevated in patients diagnosed with IPF (Wijsenbeek et al., 2018) and asthma-related lung fibrosis (Doran et al., 2017). Moreover, the level of IL-13 in blood plasma was significantly higher in patients with systemic sclerosis and localized scleroderma compared to healthy controls. These elevated levels were positively correlated with the severity of skin fibrosis and the presence of inflammatory biomarkers (Hasegawa et al., 1997; Hasegawa et al., 2003; Fuschiotti et al., 2009). Elevated IL-13 serum levels were also associated with increased cirrhosis-associated liver fibrosis in patients (Hasegawa et al., 2003) and in non-alcoholic steatohepatitis in rat models (Shimamura et al., 2008).

The results of research task 1 demonstrated the lack of differences in the presence of the Th cell subsets, the levels of IFN- γ , IL-4, and IL-13, and their receptors expression within endometrial categories. However, it is possible that these results do not fully reflect the presence of Th cell subsets and their cytokines in mare endometrium in the progression of endometriosis. Endometriosis is a complex condition with multiple characteristics, including the formation of glandular nests and cysts, atrophy, ectasias, lymphatic lacunae, inflammation, and most predominant: fibrotic changes. Nevertheless, it should be noted that the fibrotic changes are dispersed within the stroma and around the endometrial glands. For example, it was previously demonstrated that the expression of steroid receptors in the mare endometrium with endometriosis is distributed unevenly (Lehmann et al., 2011). More precisely, Lehmann et al. (2011) have shown that the steroid hormone receptors distribution in the glandular nests of the mare endometrium with endometriosis, outside the nests, and in the stroma are distributed with different intensities. It would be advantageous to differentiate between endometrial sections that are affected by fibrotic changes and those that are not and to analyse this distinction. The endometrium

consists of multiple cell types, including luminal and glandular epithelial cells, fibroblasts, immune cells, and endothelial cells. Klose & Schoon (2016) demonstrated that T cells were abundant inside fibrotic glands of the endometria of mares with endometrosis. However, the analysis of protein, RNA, or T cells isolated from whole endometrial tissue appears to present a significant challenge in capturing changes that are limited to a specific area of the endometrium. To detect changes and overcome the limitations resulting from the dispersed distribution of fibrotic changes in the endometrium of mares with endometrosis, it seems that a different research approach is required. This should involve methods such as laser microdissection, spatial proteomics, single-cell RNA sequencing, and immunohistochemistry. A spatial proteomic analysis of autopsy-derived lung samples from patients with COVID-19 enabled to describe the changes in lungs and indicated changes between fibrotic and non-fibrotic lung regions (Mao et al., 2024). Recent studies with the use of single-cell RNA sequencing identified all cell types that infiltrate the liver with cirrhosis, which is characterized by progressive fibrosis (Ramachandran et al., 2019) and sclerosing cholangitis, which is characterized by inflammation and scarring in the bile ducts (Poch et al., 2021).

The presence of the Th1 and Th2 cells in the endometrium at different stages of endometrosis, along with the expression of cytokines and their respective receptors was confirmed. Furthermore, in light of the findings from our preceding studies, which suggested the activation of Th1 and Th2 cells in the endometrium of category IIB mares in comparison to category I, the subsequent objective was to ascertain the impact of Th1 and Th2 cell subsets and the cytokines secreted by them on the fibroblasts of the mare endometrium. A comprehensive understanding of these interactions is essential for elucidating the role of Th1 and Th2 cell subsets in the pathogenesis of fibrosis.

6.2. The effect of the Th1 secretome on the functional characteristics, ECM-associated gene expression and the transcriptome of mare endometrial fibroblasts

It is established that Th1 cells contribute to the development of fibrosis by promoting inflammation through the release of pro-inflammatory cytokines, including IFN- γ , TNF- α , and IL-2. These cytokines can activate macrophages and modulate fibroblast activity (Wynn, 2004), which may ultimately lead to the onset of tissue inflammation and heart fibrosis in mice (Nevers et al., 2017). Interferon- γ -/- mice, deficient in Th1 cells have been observed to develop significantly greater lung fibrosis compared to mice without IFN- γ deficiency (Paun et al., 2017). Nevertheless, Th1 cells

have also been identified as a pro-fibrotic contributor in cardiac fibrosis by utilizing integrin $\alpha 4$ to adhere to cardiac fibroblasts and promote TGF- β production which is mediated by IFN- γ (Nevers et al., 2017). Nevertheless, the precise influence of Th1 cells on the development of endometrial fibrosis in the progression of mare endometriosis remains unknown, as no studies have directly addressed this issue. Briefly, the results of the present study indicated that treatment with Th1-CM increased the proliferation and metabolic activity of mare endometrial fibroblasts. Th1 cell secretome affected gene expression of selected ECM-associated factors in endometrial fibroblasts. Moreover, a total of 2140 genes were identified as being affected by the Th1 cell secretome, which may be involved in multiple biological processes and signaling pathways.

The results of the present study indicated that Th1-CM treatment increased both the proliferation and viability of the mare endometrial fibroblasts. To the best of my knowledge, there are no studies regarding the effect of Th1 cells and Th1 cell secretome on the proliferation and metabolic activity of fibroblasts. The literature indicates, however, that Th1-secreted cytokines, including IFN- γ and TNF- α , have been shown to modulate the behaviour and proliferation of fibroblasts (Miao et al., 2021). Fibroblast proliferation and metabolic activity play a crucial role in the development and progression of fibrotic disorders. In fibrotic disorders, fibroblasts are often abnormally activated and proliferate in response to various stimuli, including cytokines, growth factors, and mechanical stress (Wynn, 2008). This proliferation leads to an increased number of fibroblasts within the affected tissue, which then produce excessive amounts of ECM components (Younesi et al., 2024). The accumulation of ECM components consequently disrupts the normal tissue architecture and function, contributing to the stiffening and scarring that are characteristic of fibrosis.

Fibrosis develops when the balance of ECM turnover is disturbed, leading to excessive ECM deposition without proper resolution. This imbalance leads to the disruption of tissue architecture, thereby contributing to the progression of fibrotic diseases. The next step was to investigate the effect of Th1 cell secretome on the gene expression of selected ECM-associated markers in endometrial fibroblasts, focusing on ECM components like COLs and FN, the myofibroblast marker ACTA2, and enzymes involved in ECM turnover, such as MMPs and their tissue inhibitors. The treatment of fibroblasts with Th1 cell secretome decreased *FN1*, *ACTA2*, *MMP2* and *TIMP2* gene expression, and increased *TIMP1* gene expression. The decrease in the gene expression of ECM-associated factors (*FN1*, *ACTA2*) may suggest the anti-fibrotic action of the Th1

cell secretome. The expression of *ACTA2* was found to be increased in the mare endometrium category IIB compared to category I endometrium (Szóstek-Mioduchowska et al., 2019b). Thus, Th1 cells may exert anti-fibrotic action by inhibiting myofibroblast differentiation. Moreover, the decrease in *FN1* expression also suggests that Th1 cells may attenuate processes contributing to fibrosis, as targeting of FN1 expression has been proposed as a treatment option for cardiac fibrosis (Valiente-Alandi et al., 2018). The increase in *TIMP1* gene expression, on the other hand, may indicate the pro-fibrotic effect of Th1 cells. Increased levels of TIMP 1 may result in the inhibition of MMP-9 activity, whose main role is to degrade ECM, and this, in turn, leads to excessive ECM deposition. However, a study on liver fibrosis showed that the presence of TIMP1 may contribute to the progression of fibrosis but is not necessary (Thiele et al., 2017). Moreover, Th1 cell secretome decreased *MMP-2* gene expression. Although MMP-2 activity was previously shown to be crucial in the TGF- β 2-induced matrix contraction in human lens epithelial cell-line (Eldred et al., 2012), the reduced MMP-2 activity was shown to promote cardiac fibrosis, as shown in the experimental model of diabetic cardiomyopathy (Van Linthout et al., 2008). What is more, Th1-CM reduced *TIMP-2* gene expression, whose pivotal role is to inhibit MMP-2 activity (Brew et al., 2000) thus suggesting that Th1 may play an anti-fibrotic role in mare endometrial fibroblasts. However, further studies on the effect of Th1 on the protein abundance of selected ECM-associated markers are essential to determine if Th1 cells play pro- or anti-fibrotic role on mare endometrial fibroblasts.

To accurately analyse how Th1 cells may affect endometrial fibroblasts, and to gain a comprehensive and high-resolution understanding of their potential contribution to the development of fibrosis, NGS was used. This allowed to discover possible processes and signaling pathways in which the DEGs identified after Th1 cell secretome treatment may be involved. To the best of my knowledge, this is the first study aimed at the determining of Th1-CM on the transcriptome of fibroblasts. T helper 1 cell secretome induced changes in mare endometrial fibroblasts resulting in 2140 DEGs (1047 down- and 1083 up-regulated), which enriched 902 BP, 70 CC and 93 MF GO terms and 19 KEGG pathways. The bioinformatic analysis assigned DEGs to the most enriched KEGG pathways and GO terms from the BP, CC, and MF categories including DNA replication, cell cycle, metabolism of collagens and unsaturated fatty acids, and ECM-receptor interaction. Moreover, DEGs were assigned to enriched GO terms from the BP, CC, and MF such as extracellular matrix organization, fibroblast proliferation, Wnt signaling pathway and canonical NF- κ B signal transduction. In the development of human fibrosis

in many organs but also equine endometriosis, the importance of these pathways and processes have already been demonstrated (Burgy & Konigshoff, 2018; Piersma et al., 2015; Vellaichamy et al., 2005).

The Th1-CM treatment changed the expression profile of genes associated with the metabolism of collagens in endometrial fibroblasts. Disturbances in collagen metabolism processes are key factors contributing to the development of fibrosis (Bhogal et al., 2005). Results of the recent transcriptomic study on mare endometrium with endometriosis revealed alteration in the expression of genes involved in the catabolism of collagens (e.g. *MMP7*) (Witkowski et al., 2022). In this dissertation, seven other MMPs were found to be dysregulated after Th1-CM treatment: two were upregulated (*MMP23* and *MMP25*), while five were downregulated (*MMP11*, *MMP12*, *MMP13*, *MMP19*, and *MMMP24*). The down-regulation of these MMP expression may indicate the disturbances of the ECM turnover and thus excessive ECM deposition. It was previously reviewed that MMPs, especially MMP12 and MMP13, may play both pro- or anti-fibrotic roles in experimentally induced fibrosis in rodents, depending on the cause of the fibrosis and the affected organ (Giannandrea & Parks, 2014). These findings implicate the importance of Th1 cells in endometrial remodeling. For example, MMP-13, known also as collagenase 3, activity allows to activation and release of active forms of TNF- α and insulin-like growth factor (IGF). The ability to activate and release TNF- α is also a characteristic of MMP-12 and MMP-7 (Overall, 2002). Tumor necrosis factor- α , in turn, can modulate immune cells, including T cells and macrophages as well as other cells (e.g. endothelial, epithelial, smooth muscle cells, and fibroblasts), thus affecting fibrosis outcome (Steele et al., 2023). Moreover, the importance of TNF- α in fibrotic disorders is reflected by the use of TNF- α antagonists in the treatment of inflammatory diseases with terminal fibrosis, such as rheumatoid arthritis, spondyloarthropathies, Crohn's disease, and ulcerative colitis in humans (Steele et al., 2023). The dysregulation of MMP expression in endometrial fibroblasts after Th1 cell secretome treatment indicates that Th1 cells may play an important role in the development of fibrosis in endometriosis progression.

Differentially expressed genes identified in fibroblasts treated with Th1-CM were also associated with such processes as ECM-receptor interaction (e.g. *ITGA1*, *THBS1*, *LAMA2*, *LAMA3*, *COL4A5*, *FRAS1*, *COL4A3*), protein digestion and absorption (e.g. *COL6A5*, *COL6A6*, *COL6A1*, *COL6A2*, *COL6A3*, *ELN*), and focal adhesion (e.g. *ITGA4*, *TNC*, *COL6A2*, *COL6A3*, *VEGFA*, *PDGFC*, *BCL2*). Extracellular matrix-receptor interactions are fundamental to cell signaling processes that regulate cell functions,

including proliferation, migration, and differentiation. These altered ECM-receptor interactions promote the differentiation of fibroblasts into myofibroblasts (Zhang et al., 2023). Focal adhesions are specialized structures that connect cells to the ECM via integrin receptors (Wehrle-Haller, 2012). Beyond their role as physical attachment points, they function as signaling hubs that regulate essential cellular processes such as survival, proliferation, and migration (Wehrle-Haller, 2012). In fibrotic tissues, focal adhesions are crucial in mechanotransduction, the process by which mechanical signals from the ECM are transformed into biochemical signals within the cell. These signals sustain the activation of fibrogenic pathways, thereby advancing the progression of fibrosis (Ando et al., 1999). Results of our recent study indicated that target genes of the microRNAs, which were found to be dysregulated in endometria with endometriosis (categories IIA, IIB, and III, compared to endometria category I) can be involved in ECM-receptor interaction according to KEGG pathway database (Wójtowicz et al., 2023). These findings suggest that these processes play an important role in the development of fibrosis in the progression of endometriosis.

The findings of this dissertation indicate that the Th1 cell secretome may modulate processes associated with the development of fibrosis in the endometriosis progression which are not directly connected with ECM deposition. The treatment of fibroblasts with the Th1 cell secretome resulted in alterations in the expression of genes, which are involved in the metabolic processes of fatty acid (including *ALOX15*, *SCD*, *HPGD*, *GPAM*, and *FADS2*). It is of great importance since excessive lipid accumulation or impaired fatty acid oxidation is linked to heightened lipotoxicity, which plays a direct role in the development of fibrosis (Hwang & Chung, 2021). Metabolic disruptions play a critical role in fibrotic disorders by altering cellular energy balance and promoting the activation of fibroblasts, which leads to excessive ECM deposition. These metabolic changes can exacerbate inflammation and tissue remodeling, contributing to the progression of fibrosis (Bos & Laukens, 2020; Ung et al., 2021; Wang et al., 2022). Results of our recent study revealed that DEGs identified in the endometria with endometriosis may be involved in the metabolism of carbohydrates, amino acids, proteins, and synthesis of lipids, as well as in lipid metabolism (Szóstek-Mioduchowska et al., 2023). Furthermore, results of the study conducted by Witkowski et al. (2022) also demonstrated alterations in the expression of genes involved in the lipid metabolic process (e.g. *EPP6*) in endometria with endometriosis. Taken together, these results indicate that changes in the cellular metabolism are present in endometria with

endometriosis, but also in other tissues undergoing fibrosis. One of the top up-regulated DEGs in fibroblast after Th1-CM treatment is *15-lipoxygenase (ALOX15)*. 15-lipoxygenase, is an enzyme that can oxidize polyunsaturated fatty acids, and is involved in the production of specialized pro-resolving lipid mediators, which, in turn, were shown to be crucial for resolving inflammation and modulating inflammatory responses (Montford et al., 2022). The data suggests that Th1 cells, through the secretion of specific factors, may exert a significant influence on fibroblast metabolism. Furthermore, it suggests that metabolic reprogramming in the mare's endometrial fibroblasts may be influenced by the Th1 secretome.

Moreover, DEGs identified in endometrial fibroblasts after Th1-CM treatment were found to enrich the process of prostaglandin (PG) receptor activity (*PTGDR2*, *PTGDR*, *HPGD*, *PTGFR*, *PTGIR*). Prostaglandins play a role in the regulation of various physiological processes in the endometrium. These molecules are involved in managing inflammation, vascular function, and cellular responses within the endometrial tissue (Jabbour & Sales, 2004). Thus, it seems that Th1 cells may play an important, modulative effect in mare endometrium also by affecting PG action. It has been demonstrated that during the progression of endometriosis alterations in the PG concentration as well as the expression of the PG receptors occur (Szóstek et al., 2013). Prostaglandins were shown to play an important role in processes related to the development of fibrosis (Li et al., 2021). However, it seems that PGs may be involved in the progression of mare endometriosis by regulating ECM-associated marker expression in endometrial fibroblasts (Szóstek-Mioduchowska et al., 2020b). The treatment of mare endometrial fibroblasts with PGE₂ resulted in increased *TIMP1* gene expression as well as MMP-2 and MMP-9 concentration, whereas MMP-13 gene expression and concentration were decreased after PGE₂ treatment. In turn, the treatment of mare endometrial fibroblasts with PGF_{2α} resulted in a decrease in MMP-1 concentration and an increase in MMP-2 and MMP-13 protein concentration. Moreover, PGF_{2α} affected *TIMP-1* and *TIMP-2* gene expression, as well as *COL1A1* gene expression and COL1 protein concentration. Thus, PGE₂ seems to be mostly anti-fibrotic, while PGF_{2α} exhibits a pro-fibrotic action in the mare endometrial fibroblasts (Szóstek-Mioduchowska et al., 2020b). All these results suggest that Th1 cells regulate the expression of PG receptors and Th1 may indirectly affect prostaglandin action, while PGs have been shown to influence the expression of ECM-related factors.

T helper 1 cell secretome affected the expression of genes, which are involved in DNA replication (e.g. *PCNA*, *MCM5*, *FBXO5*, *ESCO2*, and *TTK*), and cell cycle (e.g. *MCM2*, *LIG1*, *PRIM1*, *POLA2*) in endometrial fibroblasts. The changes in the expression of Ki-67, a marker of cell proliferation, have been demonstrated in the mare endometria with inactive endometrosis (Hoffmann et al., 2009a). The findings indicate alterations in the proliferation and, consequently, in the cellular cycle of the endometrial cells in mares with endometrosis. The dysregulation of the gene expression associated with the cell cycle has been demonstrated to contribute to the development of renal fibrosis (Wu et al., 2021). Moreover, changes in the expression of genes related to the cell cycle were shown in the lungs of IPF patients (Korthagen et al., 2012). Furthermore, the alterations in DEGs associated with cell viability and cell cycle were identified previously in category IIB endometria compared to category I endometria in mare with endometrosis (Szóstek-Mioduchowska et al., 2023). The data suggests that Th1 cells, via their secretome, may be involved in the regulation of processes that are important in the development of endometrosis. However, further studies are necessary to elucidate the effect of Th1 cells on the cellular cycle in the mare endometrium.

T helper 1 cells are generally considered to be cells with predominantly anti-fibrotic properties (Zhang & Zhang, 2020). The findings presented in this dissertation indicate that Th1 cells may be involved in the regulation of processes associated with the development of fibrosis in the progression of equine endometrosis. These cells exert a direct effect on equine endometrial fibroblasts, increasing their proliferation. Furthermore, they modulate the expression of genes involved in a multitude of biological processes and signaling pathways including cell cycle, metabolism, and those crucial for ECM deposition, such as ECM-receptor interaction, protein digestion and absorption, focal adhesion, and collagen binding. However, further studies are required to ascertain whether the action of Th1 cells is pro- or anti-fibrotic. A potential approach to elucidating the impact of Th1 cells on equine endometrial fibroblasts would be to conduct a proteomic and metabolomic analysis.

6.3. The effect of the Th2 secretome on the functional characteristic of mare endometrial fibroblasts

Th2 cells are primarily considered pro-fibrotic due to production of cytokines like IL-4, IL-5, and IL-13, which promote the activation of fibroblasts and enhance collagen production (Cheever et al., 1994; Bailey et al., 2012; D'Arcy et al., 2022; Allen, 2023;

Arndt et al., 2023). These cytokines drive the deposition of ECM, contributing to tissue scarring and fibrosis. T helper 2 cell-mediated responses are associated with chronic inflammation and impaired tissue repair, which are key processes in the development and progression of fibrotic diseases. However, there are no studies concerning the effect of Th2 cells on the development of fibrosis in the progression of mare endometriosis. The results of this study indicate that Th2-CM treatment increased both mare endometrial fibroblast proliferation and metabolic activity. The secretome of Th2 cells was observed to influence the gene expression of the studied ECM-associated markers in endometrial fibroblasts. Furthermore, the transcriptomic study demonstrated that the Th2 cell secretome affected the expression of 1033 genes including 411 down- and 622 up-regulated in endometrial fibroblasts.

The mechanisms by which Th2 cells may contribute to the development of fibrosis involve the deposition of ECM by fibroblasts in response to various cytokines and growth factors produced by fibroblasts (Nowarski et al., 2017). Despite the absence of studies examining the effect of Th2-CM on fibroblast proliferation and metabolic activity, there is a body of evidence on Th2-specific cytokines that corroborates the findings of this study. The treatment with IL-4 and IL-13 (10 ng/ml) increased the metabolic activity of normal human lung fibroblasts (Saito et al., 2003). Furthermore, IL-4 and IL-13 have been demonstrated to stimulate the proliferation and production of ECM components by hepatic fibroblasts in mice (Cheever et al., 1994). Similarly, another Th2-secreted cytokine – IL-5 have been shown to increase the proliferation of asthmatic fibroblasts (Bajbouj et al., 2023).

The study on the effect of Th2 cell secretome on the expression of ECM-associated genes in endometrial fibroblasts revealed changes similar to Th1-CM treatment on the fibroblasts. T helper cell secretome decreased *FN1*, *ACTA2*, *MMP2* and *TIMP2* gene expression, and increased *TIMP1* gene expression in endometrial fibroblasts. The reduction of *FN1* and *ACTA2* suggests that Th2-CM may also exhibit anti-fibrotic action in mare endometrial fibroblasts. The reduction in the expression of these ECM components could be associated with a dampened fibrotic response to Th2-CM treatment. Fibronectin was suggested as a target in the treatment strategy for liver and heart fibrosis (Altrock et al., 2015; Valiente-Alandi et al., 2018), indicating its importance in the development of fibrotic diseases. However, on the other hand, the study on hepatic stellate cells – key cells in liver fibrosis indicated that FN may regulate the expression of growth factors, including TGF- β . The study on FN-depleted mice shows that lack of FN increases

TGF- β levels and signaling, enhances hepatic stellate cell proliferation and activation, (Kawelke et al., 2011). These results indicate that FN may also exhibit anti-fibrotic action by ameliorating processes associated with the excessive ECM components deposition. However, the action of FN may be both species and tissue-dependent, thus to establish the role of FN in mare endometrial fibroblasts further studies are needed. A reduction in *MMP2* gene expression implies a decrease in ECM degradation activity. However, in the context of fibrosis, this could be complex because while reduced MMP activity might slow ECM remodeling, it could also lead to a decrease in the resolution of fibrosis if not balanced properly (Giannandrea & Parks, 2014). The shift in *TIMP* gene expression suggests a change in the regulation of ECM turnover. Increased *TIMP1* gene expression alongside decreased *TIMP2* gene expression might indicate a more complex regulation of MMP expression, possibly leading to altered ECM dynamics that could affect the progression or resolution of fibrosis (Giannandrea & Parks, 2014).

The results of the transcriptomic study on the effect of Th2-CM treatment on mare endometrial fibroblasts indicate that Th2 cells can affect multiple processes associated with the development of fibrosis. Identified DEGs may be involved in a number of biological processes, including cell growth, ECM-receptor interaction, focal adhesion, tissue remodeling, inflammatory response to wounding, cellular response to TNF, NF- κ B signaling pathway, TGF- β signaling pathway, and advanced glycosylation end product-receptor for advanced glycation endproducts (AGE-RAGE) signaling pathway.

T helper 2 cell secretome affected the expression of genes involved in tissue remodeling (e.g. *TIMP1*, *IL1A*, *RUNX1*, *CST3*, *EPAS1*, *IL15*, *TFRC*) and inflammatory response to wounding (e.g. *IL33*, *IL6*, *TIMP1*, *IL1A*, *NFKBIZ*, *TLR3*). Furthermore, identified DEGs may participate in collagen-containing extracellular matrix (e.g. *COL6A5*, *ICAM1*, *TNN*, *COL6A1*, *OGN*, *ASPN*) and adherens junction (e.g. *CDH26*, *CDH11*, *MPP3*, *CDH17*, *CDHR3*, *SYNM*). Proper tissue remodeling is essential for maintaining tissue structure and function during the healing processes. In pathological states, the mechanism responsible for tissue remodeling is disturbed. The inflammatory response is a critical element of tissue remodeling, initiating the repair process by removing damaged cells and promoting the recruitment of immune cells (Van Linthout et al., 2014). However, if the inflammatory response is prolonged or dysregulated, it can disrupt normal remodeling and thus contribute to excessive ECM deposition. T helper 2 cells may not only induce and modulate a type 2 immune response, which is crucial for fibrosis outcome (Bleriot et al., 2015) but also affect the expression of genes directly

constituting ECM, including collagens and proteins involved in cell-to-cell adhesion, e.g. cadherins.

T helper 2 cell secretome treatment resulted in altered expression of genes involved in e.g. NF- κ B signaling pathway (e.g. *CXCL12*, *ICAM1*, *PTGS2*, *CXCL8*, *TNFSF13B*, *TNFSF14*, *MALT1*, *VCAM1*, *RIGI*, *EDA*, *BLNK*, *CARD10*, *BCL2*). The nuclear factor NF- κ B pathway has traditionally been recognized as a key proinflammatory signaling pathway, predominantly due to its function in regulating the expression of proinflammatory genes including cytokines, chemokines, and adhesion molecules (Lawrence, 2009). The NF- κ B signaling pathway has previously been identified as an important signaling pathway in numerous fibrotic disorders (Wu & Zern, 1999; Vellaichamy et al., 2005; Tabary et al., 2006). A recent study by Domino et al. (2020) reported changes in the expression of selected genes of NK- κ B1 signaling pathway. Interestingly, all changes in the expression of selected genes of NK- κ B1 signaling pathway were observed only in endometria collected in the follicular phase, while no changes were observed in the mid-luteal phase of the oestrous cycle. Specifically, there was an increased gene expression of *RelA* (*RELA* proto-oncogene, NF- κ B subunit) in category III, *NK- κ B1* in category IIA and *NK- κ B2* in both category IIA and IIB compared to category I endometria. Additionally, an increase in *hyaluronan synthase* (*HAS*)-1 gene expression was observed in category IIA endometria, while *HAS3* gene expression was elevated in categories IIA, IIB, and III compared to category I endometria. These findings suggest that the NF- κ B signaling pathway may play a role in the progression of endometriosis, through both canonical and noncanonical pathways (Domino et al., 2020). The findings of this dissertation along with available literature data suggest that Th2 cells may modulate processes related to the development of endometriosis by regulating the expression of components of NF- κ B signaling pathway.

Differentially expressed genes identified in endometrial fibroblasts after Th2-CM treatment were annotated to the TGF- β signaling pathway (e.g. *TFRC*, *RGMA*, *DCN*, *EMP3*, *ACVR2A*, *THBS1*, *FMOD*, *ID2*, *ID4*, *CHRD*, *BAMBI*, *GREM1*, *INHBB*). Transforming growth factor- β 1 is widely recognized as the most potent profibrotic cytokine, playing a central role in the development and progression of fibrosis across various tissues. It has been demonstrated that there is a positive correlation between the levels of TGF- β 1 in mare endometria and the progression of endometriosis (Ganjam & Evans, 2006). Furthermore, TGF- β 1 was observed to enhance the gene expression of *Col1a1*, *Col3a1*, *FN1*, and *ACTA2*, as well as their protein abundance, in a manner that

was dependent on both time and dose in endometrial fibroblast (Szóstek-Mioduchowska et al., 2019b). Additionally, TGF- β 1 was demonstrated to stimulate the proliferation of mare endometrial fibroblasts *in vitro* (Szóstek-Mioduchowska et al., 2019b).

All these results indicate that Th2 cells can directly affect fibroblast properties and expression of ECM-associated markers. Moreover, the Th2 cell secretome may regulate the expression of genes involved in multiple signaling pathways and cellular processes, which were described as important in the development of mare endometrosis, but also in the development of other fibrotic disorders. However, further studies are needed to precisely answer the question, whether Th2 cells play an anti- or pro-fibrotic role in mare endometrosis. It could be achieved by using other available multi-throughput analysis methods, such as proteomics, metabolomics, and lipidomics, and then by integrating the acquired data.

6.4. The effect of IFN- γ on mare endometrial fibroblasts transcriptome, characteristics and ECM-associated gene expression

Interferon γ has been implicated as a factor in the regulation of fibrotic processes (Yang et al., 2016). This cytokine has been shown to have anti-fibrotic effects, inhibiting fibroblast proliferation and COL synthesis (Yang et al., 2016). The role of IFN- γ in the development of fibrosis is complex, and its effects may vary depending on the specific disease context and the timing of its expression. The administration of murine recombinant IFN- γ ameliorated the accumulation of COL in the lungs of mice treated with bleomycin (BLM) (Giri et al., 1986). However, another study on IFN- γ knockout mice revealed that IFN- γ deficient mice had slightly lower content of COL in the lungs, indicating that IFN- γ partially mediates BLM-induced pulmonary fibrosis and inflammation (Chen et al., 2001). The study on mice with tetrachloride-induced liver fibrosis indicated that targeted-IFN- γ constructs bind specifically to fibroblasts and hepatic stellate cells and inhibit liver fibrogenesis by targeting the liver key pathogenic cells (Bansal et al., 2011). However, in a study on experimental nephropathy in rats, a protracted high-dose treatment with IFN- γ was found to be ineffective in preventing the development of chronic experimental nephropathy with interstitial fibrosis (Ginevri et al., 1994). In the BLM-induced mouse pulmonary fibrosis model, IFN- γ was observed to reduce both *procollagen I* and *III*, as well as *TGF- β* gene expression. Moreover, in the study on human fibroblasts, IFN- γ was shown to inhibit COL production (Jimenez et al., 1984). Similarly, IFN- γ treatment of the human fibroblast cell line blocked the

differentiation into myofibroblasts induced by TGF- β 1 (Tanaka et al., 2003). This suggests that IFN- γ exerts an anti-fibrotic effect.

The role of IFN- γ in the processes associated with the development of fibrosis in the progression of endometriosis remained unknown. However, in this study, IFN- γ did not affect the transcriptome profile of mare endometrial fibroblasts derived from neither category I nor category IIB endometria. Moreover, no changes in the expression of ECM-associated markers gene expression were observed. The lack of a direct effect of IFN- γ treatment on the transcriptome and expression of ECM-related markers in equine endometrial fibroblasts suggests that the cellular response to the same factor differs between cells derived from different species and tissues. The distinct biophysical needs of different types of tissue are reflected in the proliferation, COL and MMP production, contractility, and immunomodulatory functions of the fibroblasts derived from them (Brouty-Boye et al., 2000; Lindner et al., 2012). These characteristic phenotypic variations among fibroblasts from different tissues persist even after extended *in vitro* culture, indicating that fibroblasts retain positional identity. Fibrotic disorders share common mechanisms like fibroblast activation and ECM deposition, but tissue-specific characteristics influence their development (Distler et al., 2019).

The absence of the direct effect of IFN- γ treatment on endometrial fibroblasts may suggest its indirect effect, through other immune cells modulating processes associated to the development of fibrosis. Through the production of IFN- γ , Th1 cells can affect the differentiation, migration, and activation of macrophages, as well as regulate their C-C Motif Chemokine Ligand 2 (MCP-1) expression, thus modulating inflammation and fibrosis (Wynn, 2004; Van Linthout et al., 2014). Moreover, IFN- γ may exert its action at the site of fibrosis by promoting the polarization of macrophages towards the macrophage type 1 phenotype, which is characterized by a pro-inflammatory and anti-fibrotic properties. Macrophage type 1 produce high levels of pro-inflammatory cytokines such as TNF- α and IL-12, which can inhibit the activation of myofibroblasts and reduce the production of ECM components, thereby preventing excessive tissue scarring (Chen et al., 2023). On the other hand, IFN- γ can ameliorate the polarization of macrophages into type 2 phenotype, which is associated with tissue repair and fibrosis. Macrophages type 2 produce anti-inflammatory cytokines, including TGF- β 1, the latter being a potent promoter of fibrosis by stimulating fibroblast proliferation and COL deposition (Chen et al., 2023). The study on human bronchial epithelial cells indicated that IFN- γ attenuates IL-4 and IL-13 stimulated TGF- β 2 production (Wen et al., 2002) thus preventing the

development of subepithelial fibrosis in asthma. Furthermore, IFN- γ has been demonstrated to prevent the differentiation of fibroblast-like cells, namely fibrocytes, into myofibroblasts in response to IL-4 and IL-13 (Shao et al., 2008). In this manner, IFN- γ can regulate fibrosis progression, with the omission of the direct action on the fibroblasts.

The subsequent stage of the research should be to ascertain whether IFN- γ exerts an influence on the activity of TGF- β 1 and other pro-fibrotic factors, as research findings indicate that it may regulate these pathways (Weng et al., 2007; Chang et al., 2021). Given the established anti-fibrotic properties of IFN- γ in certain contexts, an investigation into its potential impact on TGF- β signaling may offer insights into its involvement in the pathogenesis of fibrosis in endometriosis. Additionally, examining its effect on the expression of both pro-inflammatory and pro-fibrotic cytokines in fibroblasts would help clarify its broader impact on fibroblast activation and ECM turnover, shedding light on its regulatory functions in fibrotic processes.

Interestingly, despite no effect observed after IFN- γ treatment on the transcriptome of fibroblasts, IFN- γ affected mare endometrial fibroblast proliferation. More precisely, treatment with IFN- γ resulted in a decrease of the proliferation of fibroblasts derived from category I endometria after 48 hours. Conversely, the proliferation of fibroblasts derived from category IIB endometria slightly increased after 96 hours. The obtained results demonstrate that cells exhibit disparate responses to IFN- γ treatment, depending on the extent of fibrotic alterations present in the tissue from which they were derived. The results obtained for fibroblasts derived from category I endometria are consistent with those reported in the existing literature. In other study, IFN- γ has been demonstrated to reduce proliferation in human stellate cells (Mallat et al., 1995), human Peyronie's disease fibroblasts (Duncan et al., 1991), and inhibit TGF- β induced proliferation in normal lung fibroblast cell line (Vu et al., 2019).

There are indications that IFN- γ could be an important player in the development of fibrosis, despite no direct effect on the transcriptome and ECM-associated genes having been demonstrated in this dissertation. This does not exclude its potential role in the complex processes underlying fibrosis. Future research should focus on investigating: whether IFN- γ modulates the profibrotic effects of TGF- β 1 in mare endometrial fibroblasts and whether IFN- γ affects the expression of key profibrotic and anti-fibrotic cytokines, including TGF- β 1, amphiregulin (AREG), IL-6, CTGF, IL-10.

6.5. The effect of IL-4 on mare endometrial fibroblast transcriptome, functional characteristics and ECM-associated marker expression

In general, IL-4 has been demonstrated as a pro-fibrotic factor in *in vitro* studies showing that it can regulate fibroblast function including chemotaxis, proliferation, COL synthesis, and myofibroblast differentiation (Postlethwaite et al., 1992; Sempowski et al., 1994; Borthwick et al., 2013). Results of the studies conducted on mice with IL-4 and IL-13 deficiency suggest that both cytokines play an important role in promoting fibrosis across different organ systems. The study on experimentally induced liver fibrosis in mice showed that IL-4 and IL-13 deficiency ameliorates the expression of Col1a1, compared to wild-type mice, indicating the pro-fibrotic direction of their action (Weng et al., 2018). Similar findings have been observed in models of cardiac fibrosis, where IL-4 deficiency leads to less severe fibrotic changes in the heart. This is partly due to the reduced activation of cardiac fibroblasts and lower production of ECM components (Peng et al., 2015). However, another study on IL-4 deficient and overexpressed mice with experimentally induced lung fibrosis showed that the degree of fibrotic changes was decreased in mice with IL-4 overexpression compared to IL-4 deficient mice. These data challenge the notion that IL-4 plays a critical pro-fibrotic role in BLM-induced lung fibrosis (Izbicki et al., 2002).

To date, there was no study about the effect of IL-4 on the transcriptome and functional characteristics in mare endometrial fibroblasts. The current study results indicate that this cytokine profoundly affects gene expression profile in fibroblasts derived from category I and IIB endometria. Moreover, IL-4 induces changes in gene expression and protein abundance of ECM-associated markers, activity of ECM-remodeling enzymes as well as cellular properties including proliferation, viability, and migration of mare endometrial fibroblasts.

The results of a transcriptomic study on the effect of IL-4 treatment of mare fibroblasts derived from categories I and IIB endometria revealed 1288 and 1187 DEGs, respectively. Importantly, DEGs identified in fibroblasts derived from categories I and IIB endometria were subjected to multiple different pathways, indicating that cells obtained from tissue at different stages of endometriosis respond differently to IL-4 treatment. The bioinformatic analysis assigned DEGs to KEGG and GO terms from the BP, CC, and MF categories, including ECM organization, collagen metabolic processes, ECM-receptor interaction, collagen-containing ECM, inflammatory response, metalloproteinase activity which seems to play a pivotal role in the development of tissue

fibrosis. However, the obtained results suggest the existence of novel pathways and factors, which have not been previously identified in the context of the development of endometrial fibrosis in the progression of mare endometriosis but were investigated in the pathogenesis of the other types of tissue fibrosis. These processes encompass the following: canonical glycolysis, hypoxia-inducible factor HIF-1 signaling pathway, fatty acid, and cholesteric biosynthetic process, and PI3K-Akt signaling pathway.

In fibroblasts derived from category I endometria after IL-4 treatment, one of the most significantly enriched GO terms among BP category was canonical glycolysis (e.g. *ENO1*, *ENO2*, *ENO3*, *HK1*, *HK2*, *PFKL*, *PGK1*, *PKM*). Glycolysis plays a critical role in the metabolism of cells, providing energy and biosynthetic intermediates necessary for various cellular functions. In fibrotic disorders, the role of glycolysis and its deregulation has become increasingly recognized (Henderson & O'Reilly, 2021). Fibroblasts are key effector cells in fibrosis. Under normal conditions, these cells have low metabolic demands. However, in fibrotic states, fibroblasts undergo metabolic reprogramming, which includes a shift towards increased glycolysis, even under aerobic conditions. This shift to glycolysis supports the energy and biosynthetic needs of activated fibroblasts, which proliferate and synthesize large amounts of ECM components like COL (Henderson & O'Reilly, 2021). Glycolytic enzymes, such as hexokinase-2 (HK2), and lactate dehydrogenase (LDH), are often upregulated in fibrotic tissues. Increased glycolysis not only provides adenosine triphosphate (ATP) but also generates metabolic intermediates that contribute to the activation of fibroblasts (Yin et al., 2019). Moreover, increased glycolysis in fibrosis is associated with elevated production of reactive oxygen species (ROS). Reactive oxygen species can cause oxidative damage and further activate pro-fibrotic signaling pathways, leading to a vicious cycle of fibrosis progression (Rabbani & Thornalley, 2019; Cui et al., 2022). Szóstek-Mioduchowska et al. (2023) indicated transcriptomic changes related to oxidative stress in category IIA compared to category I endometria, suggesting the importance of response to ROS in endometriosis progression. What is more, that study indicated that TGF- β 1 induced *HK2* gene expression in fibroblasts derived from category I and IIA endometria, but decreased *HK2* gene expression in fibroblasts derived from category IIB endometria (Szóstek-Mioduchowska et al., 2023). In this study, IL-4 treatment increased *HK2* gene expression in fibroblasts derived from category I and IIB endometria. Glycolysis is crucial for the metabolic and biosynthetic needs of cells. However, its deregulation in fibrotic disorders contributes significantly to disease progression. Understanding how IL-4 affects the

metabolic state of the cells may point out possible therapeutic targets aimed at restoring normal cellular metabolism and preventing or reversing fibrotic tissue damage.

Hypoxia-inducible factor-1 signaling pathway was among KEGG pathways that were enriched by DEGs identified after IL-4 treatment in fibroblasts derived from both endometrial categories (e.g. *HIF1A*, *EGLN3*, *ENO1*, *PRKCA*, *HK1*). Hypoxia-inducible factor-1 is a key transcription factor that responds to low oxygen levels, known as hypoxia, by regulating the expression of various genes involved in metabolism, angiogenesis, and cell survival. The role of HIF-1 activation plays a significant role in the pathogenesis of fibrotic disorders. Hypoxia-inducible factor-1 promotes the activation of fibroblasts and their differentiation into myofibroblasts (Higgins et al., 2008). Our recent study results indicate changes in the expression of genes related to HIF-1 α signaling pathway in category IIA compared to category I endometria (Szóstek-Mioduchowska et al., 2023). It suggests that HIF-1 signaling pathway plays an important role in the development of mare endometrosis, and its expression may be regulated by IL-4. Moreover, HIF-1 induces a shift towards glycolysis, even in the presence of oxygen which is known as aerobic glycolysis or the Warburg effect, which provides the energy and biosynthetic intermediates needed for the fibrotic process (Bos & Laukens, 2020). Additionally, HIF-1 regulates cell proliferation as well as apoptosis (Higgins et al., 2008), which are crucial in the progression of fibrosis.

Differentially expressed genes identified in fibroblasts derived from category I and IIB endometria after IL-4 treatment were found to be involved in the cell cycle KEGG pathway (e.g. *MTBP*, *PLK1*, *BUB1*, *KNL1*, *TTK*, *MCM2*, *MDM2*, *ATR*). Dysregulation of the cell cycle in fibrotic disorders can have profound implications for the development and progression of fibrosis. The cell cycle plays an important role in the regulation of cell proliferation, growth, and survival. Its disruption can lead to pathological states, including excessive tissue scarring and fibrosis (Wu et al., 2021). Dysregulation of cell cycle checkpoints, particularly those controlling the transition from the G1 to the S phase, can lead to uncontrolled fibroblast proliferation (Wu et al., 2021). Moreover, under physiological conditions, myofibroblasts undergo apoptosis once tissue repair is complete. However, in fibrosis, dysregulation of the cell cycle can prevent these cells from exiting the cycle and undergoing apoptosis. It may then cause continuous ECM production and progression of fibrosis (Hinz, 2006; Younesi et al., 2024).

Among metabolic processes, in which identified DEGs after IL-4 treatment of fibroblasts derived from category IIB endometria may be involved are fatty acid

derivative and cholesterol biosynthesis processes (e.g. *ACAA2*, *ACLY*, *CYP51A1*, *CYP7A1*, *DHCR24*). Dysregulation of lipid metabolism and biosynthesis plays a significant role in the development and progression of fibrosis. Lipids are not only structural components of cell membranes but also serve as signaling molecules that influence cellular processes, including inflammation, cell proliferation, and fibrosis (Tian et al., 2023). Enhanced fatty acid synthesis is often observed in fibrotic cells, providing the necessary lipids for membrane expansion and signaling (Ung et al., 2021). Cholesterol and its derivatives can influence fibrotic processes. Dysregulation in cholesterol biosynthesis and homeostasis may promote fibroblast activation and ECM deposition (Hwang & Chung, 2021). Targeting these lipid-related pathways presents a promising strategy for the treatment of fibrotic disorders (Hwang & Chung, 2021).

To discover whether the response of fibroblasts to IL-4 treatment differs between cells derived from non-fibrotic and fibrotic endometria, further functional analyses were performed. The DEGs which were identified in fibroblasts derived from categories I and IIB (897 common DEGs) or in either category I (331 DEGs) or IIB (290 DEGs) endometria revealed changes in the biological processes and signaling pathways in which the identified DEGs may be involved.

In fibroblasts derived from category I endometria, down-regulated genes were assigned to zymogen activation, regulation of cell migration, and differentiation and cellular response to ROS. Up-regulated DEGs identified only in fibroblasts derived from category I endometria were assigned to TGF- β receptor signaling, negative chemotaxis, and glycolytic process. Moreover, DEGs identified exclusively in fibroblasts derived from category IIB endometria were also assigned to, among others, glycolysis/gluconeogenesis, TNF, Notch, estrogen, relaxin, mTOR, and glucagon signaling pathways. The analysis of DEGs identified in fibroblasts derived from category I and IIB endometria treated with IL-4 revealed multiple processes among BP category including tissue remodeling, proteolysis, collagen metabolism, cellular response to oxidative stress, intracellular glucose homeostasis, and inflammatory response.

It is noteworthy that IL-4 had various effects on DEGs, with some common DEGs between fibroblasts derived from category I and IIB endometria displaying disparate expression patterns in response to treatment. For example, DEGs enriching inflammatory response term were found to be up-regulated (*CCL26*, *CCL8*, *CD200*, *CD40*, *CD47*, *CD81*) in fibroblasts derived from category I endometria, while in fibroblasts derived from category IIB endometria, DEGs enriching this term were found to be down-

regulated (*CCN3*, *CCN4*, *CD44*, *CD68*) after IL-4 treatment. Similarly, in fibroblasts derived from category I endometria up-regulated and in fibroblasts derived from category IIB endometria down-regulated DEGs were found to be involved in such processes as positive regulation of ROS metabolic process (up-regulated *PTK2B*, *SNCA*, *SOD2*, *SYK* and down-regulated: *DCXR*, *DUOX1*, *GNAI2*), hydrogen peroxide metabolic process (up-regulated *DUOX1*, *DUOX2*, *DUOX1* and down-regulated *HBQ1*, *HDAC6*, *PINK1*) and cell-matrix adhesion (up-regulated *ITGA1*, *ITGA10*, *ITGA4*, *ITGA5* and down-regulated: *CD44*, *CDH13*, *CDK5*, *CDKN2A*). On the contrary, down-regulated DEGs in fibroblasts derived from category I endometria and up-regulated DEGs in fibroblasts derived from category IIB endometria in response to IL-4 treatment were found to be involved in intracellular glucose homeostasis (up-regulated *HK1*, *HK2*, *ICAM1*, down-regulated: *FOXO1*, *GAS6*, *GCLC*). In both fibroblasts derived from category I and IIB endometria in response to IL-4 treatment, down-regulated DEGs were found to be involved in tissue remodeling (*LIF*, *LIPA*, *MMP2*) and collagen catabolic process (eg. *MMP11*, *MMP12*, *MMP14*). Conversely, up-regulated DEGs in both categories were found to enrich collagen metabolic (*COL1A1*, *COL1A2*, *CREB3L1*, *CST3*) and biosynthetic processes (*CYP7A1*, *P3H3*, *P3H4*).

The treatment of fibroblasts with IL-4 resulted in changes in the expression profile of selected ECM-associated markers. The treatment with IL-4 decreased the protein abundance of COL1 in fibroblasts derived from category I (48 hours) and IIB (48 and 96 hours) endometria. The protein abundance of COL3 decreased after IL-4 treatment in fibroblasts derived from category I endometria while in fibroblasts derived from category IIB endometria, COL3 protein abundance increased. This is in contrary to previous results, where IL-4 treatment resulted in an increase in both COL1 and COL3 abundance in immortalized human prostate fibroblasts (D'Arcy et al., 2022). The distinct response of fibroblasts obtained from either category I or IIB endometria suggests that the mechanisms involved in ECM remodeling, which are regulated by IL-4, may become dysregulated in the fibroblasts obtained from endometria at different stages of endometriosis. Interestingly, and notably, the concentration of IL-4 and the protein abundance of its receptor were unchanged, yet a distinct effect is observed in fibroblasts derived from category I and IIB endometria. Additionally, the protein abundance of FN1 increased after IL-4 treatment in fibroblasts derived from both endometrial categories. It may suggest a pro-fibrotic mechanism of IL-4 action on mare endometrial fibroblasts. In the study on human fibrogenic fibroblast-like cells, IL-4 also increased FN1 production

(Sato et al., 2011). In this dissertation, the ACTA2 protein abundance decreased in fibroblasts derived from both category I and IIB endometria after IL-4 treatment. The study on immortalized human prostate fibroblasts indicated that IL-4 treatment had no effect on ACTA2 expression (D'Arcy et al., 2022). Interestingly, IL-4 affected also the expression profile of MMPs and TIMPs, which are responsible for ECM homeostasis and turnover. The protein abundance of MMP-2 decreased in fibroblasts which were derived from category I endometria, with no effect on fibroblasts derived from category IIB endometria. The protein abundance of MMP-3 decreased in fibroblasts derived from both category I and IIB endometria, while MMP-9 protein abundance after IL-4 treatment was found to be only decreased in fibroblasts derived from category IIB endometria. The pivotal role of MMPs is to degrade ECM (Brew et al., 2000; Giannandrea & Parks, 2014; Quintero-Fabian et al., 2019). Additionally, MMPs may regulate the activity of multiple pro-fibrotic and pro-inflammatory factors activity, including TGF- β and TNF- α (Overall, 2002). Thus, the decrease in MMP abundance in the fibroblasts suggests that IL-4 regulate ECM turnover mostly by inhibition of ECM degradation. Moreover, IL-4 was shown to increase TIMP-1 and TIMP-2 level in fibroblasts derived from category I and IIB fibroblasts. It is consistent with previous studies which showed that IL-4 induces the expression of TIMPs in human adult skin fibroblasts (Ihn et al., 2002) and conjunctival fibroblasts (Leonardi et al., 2003). While TIMPs main role is to inhibit MMPs action, IL-4 may contribute to excessive ECM deposition by mare endometrial fibroblasts by inhibiting the processes of ECM turnover.

The results demonstrated that the transcriptomic profile and ECM-associated marker expression in fibroblasts is altered in response to IL-4 during the development of fibrosis, which consequently could affect cell function. Findings from the literature support these results. A series of studies have demonstrated that fibroblasts from patients with systemic sclerosis and interstitial lung disease exhibit accelerated migration, increased expression of COL1, and enhanced contraction compared to healthy fibroblasts (Denton et al., 2018; Dufour et al., 2018; Krempaska et al., 2020; Molina-Molina et al., 2018; Shi-wen et al., 2010). Additionally, fibroblasts isolated from patients with IPF exhibit specific characteristics, including impaired autophagy (Araya et al., 2013; Sosulski et al., 2015). It has been shown that impaired autophagy in IPF lungs may contribute to fibrogenesis and promote fibroblast activation and extracellular matrix production (Patel et al., 2012). Moreover, the differential response of equine endometrial cultured explants and cells to cytokines has been observed to depend on the severity of

endometriosis (Szóstek et al., 2013; Szóstek-Mioduchowska et al., 2020a, 2020b; Szóstek-Mioduchowska et al., 2023; Wójtowicz et al., 2023). These findings may indicate differences in intercellular signaling or suggest that the cellular microenvironment varies between different categories of endometria. It may be the result of adaptive changes in fibroblasts that alter their behaviour in response to a changing microenvironment. In this context, excessive ECM production and subsequent fibrosis may cause fibroblasts to become less or more responsive to the factors. However, this issue needs to be investigated.

The results of the current study demonstrated that IL-4 treatment increased the proliferation and viability of fibroblasts derived from category I and IIB endometria after 48 and 96 hours. The results on the effect of IL-4 on fibroblast proliferation and viability has been observed to vary according to species, tissue origin and the experimental design. It has been demonstrated that IL-4 treatment increased the viability (Saito et al., 2003) and proliferation (Izbicki et al., 2002) of human pulmonary fibroblasts as well as the proliferation of skin fibroblasts (Monroe et al., 1988). Conversely, IL-4 treatment did not affect the proliferation of pulmonary fibroblasts derived from wild type-mice (Huaux et al., 2003) and human intrahepatic fibroblasts (Aoudjehane et al., 2008). The observed increase in endometrial fibroblast proliferation following IL-4 treatment highlights its potential fibrotic effects. The elevated fibroblast activity may result in an imbalance between ECM production and degradation, which could lead to excessive ECM deposition. Such dysregulation may contribute to the development of fibrosis. Moreover, the ability of IL-4 to activate fibroblasts suggests a role in perpetuating chronic inflammatory conditions, where persistent fibroblast activation can exacerbate tissue remodeling and fibrosis.

In addition to alterations in the gene expression level, the origin of fibroblasts can influence their functional characteristics. In this study, IL-4 treatment decreased the migration of fibroblasts derived from category I endometria after 96 hours but did not affect the migration of fibroblasts derived from category IIB endometria. These results contradict those of other studies where IL-4 was shown to induce the migration of fibroblasts derived from human skin (Postlethwaite & Seyer, 1991) and of human embryonic stem cells differentiated into fibrogenic fibroblast-like cells (Sato et al., 2011). Moreover, no changes in the contraction of collagen gel discs were observed in fibroblasts derived from category I and IIB endometria after IL-4 treatment. A previous study on human embryonic stem cells indicated that IL-4 treatment of fibroblast-like cells induces

the contraction of collagen gel discs (Sato et al., 2011). Another study on contractile myofibroblasts derived from human joints indicated that IL-4 increased collagen gel contraction (Mattyasovszky et al., 2017). These results suggest that the effect of IL-4 on fibroblast migration can vary according to species and tissue origin. The presented findings emphasise the significance of IL-4 as a pro-fibrotic mediator, thereby justifying further investigation into its role in fibrotic processes.

6.6. The effect of IL-13 on mare endometrial fibroblast transcriptome, functional characteristics and ECM-associated marker expression

Interleukin 13 is a key cytokine involved in the regulation of immune responses and has been identified as an important player in the development of fibrosis. Acting primarily through the activation of fibroblasts and the promotion of ECM deposition, IL-13 contributes to tissue remodeling and scarring of the lung, liver, adipose tissue, and in systemic sclerosis (Lee et al., 2001). Its effects are mediated by signaling pathways that enhance COL synthesis and inhibit ECM degradation in intestinal fibrosis in Crohn's patients (Bailey et al., 2012). However, to date there are no studies concerning the effect of IL-13 on the mare endometrial fibroblast transcriptome, the ECM-associated marker expression as well as the functional characteristics. The results of this dissertation indicate that IL-13 affects the transcriptome of fibroblasts and the response of fibroblasts differs depending on the category of endometria from which cells were isolated.

The results of the transcriptomic study revealed that IL-13 induced changes in the expression of 471 (206 down- and 265 up-regulated) and 305 (208 down- and 257 up-regulated) DEGs in fibroblasts derived from category I and IIB endometria, respectively. The functional analysis revealed that DEGs identified in fibroblasts derived from category I endometria may be involved in 520 BP, 120 MF, and 81 CC among GO terms and 34 KEGG pathways. These pathways included intracellular glucose homeostasis, ECM organization, collagen-containing ECM, and negative regulation of the Wnt signaling pathway. Identified DEGs in fibroblasts derived from category IIB endometria in response to IL-13 treatment were annotated to 545 BP, 120 MF, and 84 CC among GO terms and 23 KEGG pathways. Among these processes were carbon metabolism, biosynthesis of nucleotide sugars, ECM organization, and AGE-RAGE signaling pathway.

The IL-13 treatment resulted in changed expression of genes involved in such processes as collagen fibril organization, ECM organization, cell-matrix adhesion,

collagen and integrin binding, and ECM-receptor interaction (e.g. *COL6A5*, *COL6A1*, *SV2C*, *ITGB8*, *ITGA4*, *COL6A2*, *COL4A2*, *COL4A1*, *COL4A3*). All these processes are directly associated with ECM components. Dysregulation and modulation of the expression of genes involved in ECM homeostasis may be a direct effect of IL-13 contributing to the development of endometrial fibrosis in the progression of endometriosis. Disruption in ECM homeostasis is a central feature of fibrosis. Interleukin 13 seems to play a critical role in the disruption of ECM homeostasis during fibrosis (Roeb, 2023). What is more, in rat model, IL-13-induced TGF- β 1 production in hepatic stellate cells – key cells in liver fibrosis development may accelerate progression of fibrosis (Shimamura et al., 2008). Interleukin 13 exerts its pro-fibrotic effects through several mechanisms including stimulation of ECM deposition and induction of TGF- β 1 creating a positive feedback loop that drives fibrosis. The most up-regulated DEG following treatment with either IL-13 or IL-4 in fibroblasts derived from category I and IIB endometria was *collagen type VI alpha 5 chain (COL6A5)*. The collagen type VI alpha 5 chain is part of the collagen VI family, which plays a key role in maintaining the structure of the ECM. While research on COL6A5 specifically in fibrotic disorders is limited, the COLVI family in general is known to contribute to tissue integrity and ECM organization. It is now recognized that COLVI family contributes to human fibrosis of the liver, lungs, heart, and kidneys. Notably, COLVI has been identified as a potential biomarker for liver fibrosis, offering a non-invasive diagnostic method (Williams et al., 2022).

Interestingly, IL-13 induced changes in the expression of genes involved in the AGE-RAGE signaling pathway (eg. *PIK3R3*, *TGFB1*, *NOX4*, *CCND1*, *VEGFC*, *F3*, *PLCE1*) in fibroblasts derived from category IIB endometria. The AGE-RAGE signaling pathway plays a significant role in the development and progression of fibrosis. Advanced glycation end products are a group of modified proteins and lipids that form through non-enzymatic glycation, typically as a result of chronic hyperglycemia, oxidative stress, or aging. The receptor for AGEs – is a multi-ligand receptor of the immunoglobulin superfamily, which, when activated by binding to AGEs, triggers a cascade of intracellular signaling events that contribute to fibrotic processes (Zhao et al., 2014). The binding of AGEs to RAGE activates several pro-inflammatory signaling pathways, including NF- κ B and MAPKs. These pathways lead to the upregulation of pro-inflammatory cytokines, such as TNF- α and IL-6 which perpetuate chronic inflammation, a principal factor in the development of fibrosis (Solini et al., 2006; Ramasamy et al.,

2011). The AGE-RAGE interaction enhanced the production of ROS within cells, and ROS, in turn, enhances inflammation and activates pro-fibrotic signaling pathways (Tan et al., 2007). Through these mechanisms, IL-13 may contribute to the disruption of ECM homeostasis in fibrosis, making it a key target for therapeutic intervention in fibrotic diseases.

To discover whether the response of fibroblasts to IL-13 treatment differs between cells derived from category I and IIB endometria, further functional analyses were performed. The common 305 DEGs in fibroblasts derived from both endometrial categories were assigned to KEGG pathways including amino sugar and nucleotide sugar metabolism, focal adhesion, PI3K-Akt, and HIF-1 signaling pathways. Up-regulated DEGs identified in fibroblasts derived from both categories I and IIB endometria in response to IL-13 were found to be enriched in processes of regulation of ECM organization, glycolytic process, fibroblast proliferation as well as canonical glycolysis. The processes in which DEGs identified in fibroblasts derived from only category I endometria were up-regulated while DEGs identified in fibroblasts derived from category IIB endometria were down-regulated were assigned to regulation of TGF- β signaling, negative regulation of cell growth, hydrogen peroxide metabolic process, cellular response to oxidative stress as well as cellular oxidant detoxification. Conversely, processes such as glycosaminoglycan biosynthesis and alpha-amino acid metabolic process were found to be enriched by down-regulated DEGs in fibroblasts derived from category I endometria and up-regulated DEGs identified in fibroblasts derived from category IIB endometria in response to IL-13. These results indicate that despite the same processes were enriched in fibroblasts derived from category I and IIB endometria, the manner of IL-13 action differed depending on the physiological state of the tissue from which the fibroblasts were isolated.

In the present study, 160 DEGs were identified exclusively in response to IL-13 treatment in fibroblasts derived from category IIB endometria. Among them, 31 genes involved in Ras-proximate-1 (Rap1) signaling pathway, including *CCNB3*, *FOXM1*, *MAPK13*, *CCNB1*, *CCNB2*, *MYBL2*, *CDK1*, and *CCND2* were identified. The Ras-proximate-1 signaling pathway plays an important role in the regulation of cellular processes that may contribute to fibrosis, including the formation of connective tissue. Ras-proximate-1, a small GTPase from the Ras family, is involved in multiple cellular functions, including cell adhesion, migration, and proliferation (Boettner & Van Aelst, 2009; Moon et al., 2013; Li et al., 2018; Rothenberg et al., 2023). The Ras-proximate-1

signaling was shown to control and modulate the migration of hepatic stellate cells treated with TGF- β 1 (Moon et al., 2019). Additionally, the Rap1 signaling pathway regulates integrin-mediated cell adhesion to the ECM and the dysregulation of Rap1 signaling pathway can lead to aberrant interactions between cells and the ECM, promoting excessive deposition of ECM components (Luo et al., 2020; Wu et al., 2021; Rothenberg et al., 2023). Furthermore, the Rap1 signaling pathway can modulate inflammatory signaling, influencing immune cell infiltration and the production of pro-fibrotic cytokines. For instance, the Rap1 signaling pathway can impact the migration of immune cells to sites of tissue injury (Lorenowicz et al., 2006; Moon et al., 2013; Lin et al., 2016), affecting the immune response at the site of fibrotic lesions. However, to date, no studies have shown the effect of IL-13 on the activation of the Rap1 signaling pathway. Thus, further studies are needed to determine if regulation of the Rap1 signaling pathway could provide a potential therapeutic target in the future.

Interleukin 13 treatment decreased the protein abundance of COL1 after 48 hours in fibroblasts derived from category I endometria and after 96 hours of treatment in fibroblasts derived from category IIB endometria. Moreover, the protein abundance of COL3 decreased in response to IL-13 only in fibroblasts derived from category I endometria. These results are in contrast to the study on human dermal fibroblasts, where IL-13 at a dose of 100 ng/ml, increased *Col1a1* gene expression and COL1 protein abundance (O'Reilly et al., 2016), and increased *Col1a1* gene expression in mouse airway fibroblasts (Lu et al., 2014). Moreover, *Col3a1* gene expression was increased in response to IL-13 in fibrocytes derived from asthmatic patients (Bellini et al., 2012). Additionally, the protein abundance of ACTA2 decreased in fibroblasts derived from both category I and IIB endometria. However, IL-13 increased the protein abundance of FN1 after 48 hours in fibroblasts derived from category I endometria, consistent with other studies. The study on primary retinal microvascular endothelial cells indicated that IL-13 induce *FN* expression (Kubo et al., 2020). This effect of IL-13 is similar to the effect of IL-4 shown in this dissertation. Interleukin 13 has previously been shown to promote prostatic fibrosis by inducing ECM expression (D'Arcy et al., 2022). The discrepancy in these results may be due to differences in the response to IL-13 between different organs and may also be due to interspecies differences (Shi-wen et al., 2010; Patel et al., 2012; Araya et al., 2013; Dufour et al., 2018; Krempaska et al., 2020; Plikus et al., 2021;). Furthermore, the effect of IL-13 on the processes related to the development of fibrosis in the course of endometriosis, similar to the effect of IL-4, may depend on the regulation

of MMP and TIMP expression. As indicated in the results section, IL-13 decreased MMP-2 protein abundance in fibroblasts derived from category IIB endometria. In addition, IL-13 reduced the protein abundance of MMP-9 and the gelatinolytic activity of pro-MMP-9 in fibroblasts derived from category I endometria. The results concerning IL-13 downregulating MMPs may suggest the pro-fibrotic action of IL-13 in fibroblasts derived from category I endometria. What is more, in the present study IL-13 increased TIMP-1 and TIMP-2 level in fibroblasts derived from categories I and IIB endometria. The study on human conjunctival fibroblasts indicated that IL-13 increased *TIMP-1* gene expression (Leonardi et al., 2003), which is consistent with our results. The expression profile of TIMPs is known to be increased in tissues with ongoing fibrosis (Thiele et al., 2017). Moreover, it was previously reported, that along with the development of endometriosis the expression profile of MMPs and TIMPs becomes disturbed. For instance, the protein level of TIMP1 is higher in mare endometria category IIB compared to category I endometria in the follicular phase of the oestrous cycle. Moreover, TIMP2 protein level increase in endometria category IIA compared to category I in both mid-luteal and follicular phase of the oestrous cycle (Szóstek-Mioduchowska et al., 2020). It suggests that IL-13 modulates processes associated with the development of fibrosis in the mare endometrium by affecting the expression profile of MMPs and TIMPs.

As presented in this dissertation, IL-13 increased the proliferation of mare endometrial fibroblasts derived from category I and IIB endometria after 48 and 96 hours of IL-13 treatment. The viability of fibroblasts derived from category I endometria increased after 48 and 96 hours of IL-13 treatment. The viability of fibroblasts derived from category IIB endometria increased only after 48 hours in response to IL-13. Another study results showed that IL-13 treatment (10 ng/ml, 3 days) induced the viability of lung fibroblasts (Saito et al., 2003). Moreover, IL-13 (50 ng/ml, 48 hours) has been demonstrated to induce the proliferation of human lung fibroblasts (Izbicki et al., 2002). The study on human lung mesenchymal cells revealed that IL-13 enhanced the contraction of collagen discs (Liu et al., 2002). However, in this study, IL-13 did not affect the contraction of collagen discs in fibroblasts derived from either category I or category IIB endometria. Nevertheless, IL-13 may exert its pro-fibrotic effects by inducing the proliferation of fibroblasts, leading to an increased number of cells that produce and deposit ECM. The obtained results suggest that IL-13 may contribute to the processes associated with the development of fibrosis in the progression of endometriosis.

6.7. Future implications

Despite years of research on the mechanisms underlying the development of endometriosis in mares, no effective treatment has yet been found. The research results presented in this thesis contribute to a deeper understanding of the mechanisms involved in the development of endometrial fibrosis. Further investigation is necessary to elucidate the role of Th1 cells and IFN- γ in the processes associated with the development of fibrosis in the progression of endometriosis. Our results suggest that Th2-cell secreted cytokines: IL-4 and IL-13 modulate processes already known to be important in the development of fibrotic disorders as well as the expression profile of MMPs and TIMPs in mare endometrial fibroblasts. Given the complexity of the mechanisms of action of IL-4 and IL-13 on mare endometrial fibroblasts, these cytokines may be the future therapeutic targets. To date, the anti-IL-4 and anti-IL-13 antibodies, known as Dupilumab, Lebrikizumab, and Tralokinumab, are used in treating atopic dermatitis. All show great potential in inhibiting IL-4 (Dupilumab) and IL-13 (Dupilumab, Lebrikizumab, and Tralokinumab), which induce a proinflammatory response in patients with atopic dermatitis (Ratnarajah et al., 2021; Silverberg et al., 2023). However, although the results in atopic dermatitis patients are promising, further studies are needed to fully assess the efficacy of these therapies and whether they could be used to treat endometrial fibrosis in mare. The evolving nature of fibrosis research requires ongoing investigation, and it is only through further research to understand the mechanisms underlying the development of endometriosis that it may be possible to find an effective therapy in the future.

7. Summary of results

1. The number of Th2 cells, the ratio of Th2 to Th1 cells as well as the expression of IFN- γ , IL-4, and IL-13 and their receptors IFN- γ R1, IL-4RA, and IL-13RA was not altered in the mare endometrium in the progression of endometriosis.
2. The secretome of Th1 and Th2 cells increased the proliferation of mare fibroblasts derived from category I endometrium cultured in *in vitro* conditions.
3. The secretome of Th1 cells induced changes in the gene expression of ECM-associated markers (*FN1*, *ACTA2*, *MMP2*, *TIMP1* and *TIMP2*), and transcriptome of mare fibroblasts derived from category I endometrium cultured in *in vitro* conditions, resulting in the identification of 2140 DEGs annotated to 902 BP (e.g. ECM organization, tissue remodeling), 70 CC (e.g. protein complex involved in cell adhesion and basement membrane), and 93 MF (e.g. collagen binding, and cytokine binding), GO terms as well as 19 KEGG pathways (e.g. ECM-receptor interaction and cell cycle).
4. The secretome of Th2 cells induced changes in the gene expression of ECM-associated markers (*FN1*, *ACTA2*, *MMP2*, *TIMP1* and *TIMP2*) and transcriptome of mare fibroblasts derived from category I endometrium cultured in *in vitro* conditions, resulting in the identification of 1033 DEGs annotated to 919 BP (e.g. tissue remodeling and cellular response to TNF), 59 CC (e.g. protein complex involved in cell adhesion and collagen containing ECM), 83 MF (e.g. PR receptor activity and metalloproteinase activity), GO terms as well as 21 KEGG pathways (e.g. TGF- β and NF- κ B signaling pathways).
5. Interferon γ affected mare fibroblast proliferation, but did not affect transcriptomic profile and the gene expression of ECM-associated markers in fibroblasts derived from category I and IIB endometria cultured in *in vitro* conditions.
6. Interleukin 4 and IL-13 increased the proliferation of mare fibroblasts and affected the expression of ECM-associated markers (e.g. COL1, COL3, FN1, and ACTA2) in fibroblasts derived from category I and IIB endometria cultured in *in vitro* conditions. The response of fibroblasts to the examined cytokines differed depending on the category of the endometrium from which fibroblasts were derived.

7. Interleukin 4 induced alteration in the expression of 1288 and 1187 DEGs in mare fibroblasts derived from category I and IIB endometria cultured in *in vitro* conditions, respectively. The functional analysis revealed that DEGs identified in fibroblasts derived from category I endometria were involved in 410 BP (e.g. canonical glycolysis and cell adhesion), 101 MF (e.g. collagen binding and ECM structural constituent), and 92 CC (e.g. collagen-containing ECM and focal adhesion), among GO terms and 102 KEGG pathways (e.g. ECM-receptor interaction and HIF-1 signaling pathway). Differentially expressed genes identified in fibroblasts derived from category IIB endometria were annotated to 537 BP (e.g. cholesterol biosynthesis process and cell adhesion), 131 MF (e.g. ECM structural constituent and integrin binding), and 108 CC (e.g. extracellular space and plasma membrane), among GO terms and to 88 KEGG pathways (e.g. biosynthesis of nucleotide sugars and cell cycle).
8. Interleukin 13 induced alteration in the expression of 471 and 465 DEGs in mare fibroblasts derived from category I and IIB endometria cultured in *in vitro* conditions, respectively. The functional analysis revealed that DEGs identified in fibroblasts derived from category I endometria were involved in 520 BP (e.g. collagen fibril organization and ECM organization), 120 MF (e.g. collagen binding and integrin binding), and 81 CC (e.g. extracellular space and plasma membrane), among GO terms and 34 KEGG pathways (e.g. ECM-receptor interaction and regulation of actin cytoskeleton). Differentially expressed genes identified in fibroblasts derived from category IIB endometria were annotated to 545 BP (e.g. tissue remodeling and cell adhesion), 120 MF (e.g. fibronectin binding and growth factor activity), and 84 CC (e.g. collagen-containing ECM and plasma membrane), among GO terms and to 23 KEGG pathways (e.g. carbon metabolism and biosynthesis of nucleotide sugars).

8. Conclusion

1. In mare fibroblasts derived from category I endometria, Th1 cells regulated the expression of genes involved in the cell cycle, metabolism, and those crucial for ECM deposition, such as ECM-receptor interaction, protein digestion and absorption, focal adhesion, NF- κ B, and JAK-STAT signaling pathways as well as collagen binding. However, in light of the inconclusive results, it is challenging to ascertain unequivocally whether Th1 cells exert pro-fibrotic or anti-fibrotic effects. Further investigation is necessary to elucidate this issue.
2. In mare fibroblasts derived from category I endometria, Th2 cells regulated the expression of genes annotated to tissue remodeling, cellular response to TNF, cell cycle as well as NF- κ B, TGF- β , and AGE-RAGE signaling pathways, which suggest the role of Th2 cells as pro-fibrotic mediators.
3. In mare fibroblasts derived from category I and IIB endometria, IL-4 increased cell proliferation and affected the turnover of ECM by increasing FN1 and COL3 protein abundance, while simultaneously decreasing the MMP expression and activity and enhancing TIMP level. Moreover, IL-4 regulated the expression of genes involved in canonical glycolysis, cell cycle, cholesterol and fatty acid biosynthetic processes, cell-matrix, and focal adhesion, ECM organization as well as HIF-1, PI3-K-Akt, and IGF1R signaling pathways which suggest the role of IL-4 as a pro-fibrotic mediator.
4. In mare fibroblasts derived from category I and IIB endometria, IL-13 increased cell proliferation and affected the turnover of ECM by increasing FN1 protein abundance, while simultaneously decreasing the MMP expression and activity and enhancing TIMP levels. Moreover, IL-13 regulated the expression of genes annotated to various processes including carbon metabolism, ECM organization, ECM-receptor interactions as well as the Wnt, HIF-1, FoxO, and AGE-RAGE signaling pathways which suggest the role of IL-13 as a pro-fibrotic mediator.
5. The different responses of fibroblasts derived from categories I and IIB endometria to examined cytokines may result from variations in intracellular signaling or cellular microenvironments, as well as adaptive changes in fibroblasts due to excessive ECM production during fibrosis.

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10. Supplementary data

Supplementary Table 1. Summary of datasets used in Research task 2, Experiment 3.

Replicate	Treatment	Reads before QC	Reads after QC	Uniquely mapped genes (%)	Number of expressed genes
rep_1	Control	24811533	20974279	95,33	17632
	Th1-CM	24610023	20717247	95,37	16990
	Th2-CM	20977026	17551851	95,36	17150
rep_2	Control	25774507	21393536	95,41	18038
	Th1-CM	24861509	19921644	94,81	17544
	Th2-CM	24539826	20389125	95,18	17587
rep_3	Control	23174385	18924264	95,13	17514
	Th1-CM	24794981	20728290	94,89	17279
	Th2-CM	21744567	17820369	94,8	17172
rep_4	Control	25742738	21226590	95,11	18182
	Th1-CM	23015552	18986635	95,24	17339
	Th2-CM	23111155	18901059	95,22	17611

Supplementary Table 2. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category I endometria treated with T-helper 1 cells -conditioned medium (Th1-CM) for 48 hours in comparison to the control group (Research task 2, Experiment 3).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	Padj
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	18,192	8,86E-53
2.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	11,167	5,35E-28
3.	ENSECAG00000038698	ALOX15	arachidonate 15-lipoxygenase	11,037	1,08E-31
4.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	10,446	9,69E-55
5.	ENSECAG00000020578	PDCD1LG2	programmed cell death 1 ligand 2	10,422	1,33E-25
6.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	9,5561	3,09E-68
7.	ENSECAG00000051569	ENSECAG00000051569		9,2528	2,3E-26
8.	ENSECAG00000020422	PCSK1	proprotein convertase subtilisin/kexin type 1	8,8536	5,74E-17
9.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	8,8286	2,18E-25
10.	ENSECAG00000047988	ENSECAG00000047988		8,758	3,26E-19
11.	ENSECAG00000057530	ENSECAG00000057530		8,648	1,77E-15
12.	ENSECAG00000022118	IDO1	indoleamine 2,3-dioxygenase 1	8,5539	4,01E-15
13.	ENSECAG00000046132	CXCL9	C-X-C motif chemokine ligand 9	8,2677	2,19E-19
14.	ENSECAG00000012253	CXCL11	C-X-C motif chemokine ligand 11	8,2419	3,8E-15
15.	ENSECAG00000019282	HDC	histidine decarboxylase	8,2378	6,92E-15
16.	ENSECAG00000014650	INSRR	insulin receptor related receptor	8,112	1E-17
17.	ENSECAG00000010928	MMP25	matrix metalloproteinase 25	8,1008	4,75E-17
18.	ENSECAG00000001714	PTGDR2	prostaglandin D2 receptor 2	8,0623	2,02E-19
19.	ENSECAG00000050680	ENSECAG00000050680		8,0438	6,29E-15
20.	ENSECAG00000056261	ENSECAG00000056261		7,9372	2,27E-06
21.	ENSECAG00000020738	CDH26	cadherin 26	7,7984	8,31E-81
22.	ENSECAG00000016312	CD274	CD274 molecule	7,5015	0
23.	ENSECAG00000055535	ENSECAG00000055535		7,5011	2,4E-231
24.	ENSECAG00000023841	POSTN	periostin	7,4496	3,62E-33
25.	ENSECAG00000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	7,3632	4,21E-32
26.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	7,3467	2,21E-11
27.	ENSECAG00000043919	ENSECAG00000043919		7,1402	1,04E-09
28.	ENSECAG00000007247	ALPK1	alpha kinase 1	7,0515	1,26E-10
29.	ENSECAG00000013482	SERPINA3	serpin family A member 3	6,8973	2,84E-82
30.	ENSECAG00000046493	GBP5	guanylate binding protein 5	6,6423	1,83E-58
31.	ENSECAG00000000152	KITLG	KIT ligand	6,5241	2,7E-204
32.	ENSECAG00000049130	ENSECAG00000049130		6,5147	2,08E-10
33.	ENSECAG00000049658	ENSECAG00000049658		6,3578	3,4E-121
34.	ENSECAG00000026965	SOCS1	suppressor of cytokine signaling 1	6,3162	1,17E-62
35.	ENSECAG00000047919	ENSECAG00000047919		6,2529	5,87E-13
36.	ENSECAG00000015449	IRF8	interferon regulatory factor 8	6,08	8,7E-12
37.	ENSECAG00000016867	CISH	cytokine inducible SH2 containing protein	5,9131	3,6E-17
38.	ENSECAG00000006205	CD7	CD7 molecule	5,7721	6,55E-35
39.	ENSECAG00000017217	CA12	carbonic anhydrase 12	5,769	0
40.	ENSECAG00000036638	SLC6A12	solute carrier family 6 member 12	5,6169	1,48E-43
41.	ENSECAG00000023032	AZIN2	antizyme inhibitor 2	5,5016	3,02E-06
42.	ENSECAG00000024259	Eqca-DQA1		5,4163	4,21E-12
43.	ENSECAG00000012791	GBP6	guanylate binding protein family member 6	5,3547	1,04E-85
44.	ENSECAG00000040532	ENSECAG00000040532		5,2979	1,69E-92
45.	ENSECAG00000002249	PLEKHG4B	pleckstrin homology and RhoGEF domain containing G4B	5,2965	2,4E-15
46.	ENSECAG00000021343	NRG1	neuregulin 1	5,2653	2,24E-44
47.	ENSECAG00000013703	PPP1R3C	protein phosphatase 1 regulatory subunit 3C	5,2466	2,26E-28
48.	ENSECAG00000019551	CXCL12	C-X-C motif chemokine ligand 12	5,2074	1E-152
49.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	5,142	4,83E-88
50.	ENSECAG00000055019	ENSECAG00000055019		5,0752	5,25E-17
51.	ENSECAG00000016482	IL6	interleukin 6	4,9264	1,5E-42
52.	ENSECAG00000010475	IL33	interleukin 33	4,8938	2,11E-25
53.	ENSECAG00000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	4,8898	8,8E-18
54.	ENSECAG00000043493	ENSECAG00000043493		4,8348	8,72E-06
55.	ENSECAG00000012826	CDO1	cysteine dioxygenase type 1	4,8287	9,56E-92

56.	ENSECAG00000012660	HLA-DRA	major histocompatibility complex, class II, DR alpha	4,8156	1,56E-15
57.	ENSECAG00000044483	ENSECAG00000044483		4,7778	8,13E-07
58.	ENSECAG00000044850	ENSECAG00000044850		4,7715	1,77E-05
59.	ENSECAG00000036649	ENSECAG00000036649		4,6382	4,46E-55
60.	ENSECAG00000010750	VWCE	von Willebrand factor C and EGF domains	4,5766	2,75E-20
61.	ENSECAG00000017948	BTN1A1	butyrophilin subfamily 1 member A1	4,5647	9,81E-07
62.	ENSECAG00000034282	CCL8	chemokine (C-C motif) ligand 8	4,4949	7,2E-275
63.	ENSECAG00000011897	CHRD12	chordin like 2	4,4466	1,22E-13
64.	ENSECAG00000032992	TIAM1	TIAM Rac1 associated GEF 1	4,4412	9,66E-37
65.	ENSECAG00000055416	ENSECAG00000055416		4,4089	8,74E-25
66.	ENSECAG00000050432	ENSECAG00000050432		4,4084	1,6E-10
67.	ENSECAG00000012104	TNFAIP6	TNF alpha induced protein 6	4,3943	4,11E-32
68.	ENSECAG00000022734	SGPP2	sphingosine-1-phosphate phosphatase 2	4,3724	1,16E-06
69.	ENSECAG00000019215	ITGB8	integrin subunit beta 8	4,3115	3,61E-68
70.	ENSECAG00000009767	P2RX1	purinergic receptor P2X 1	4,3115	9,6E-09
71.	ENSECAG00000030750	ENSECAG00000030750		4,2484	1,79E-54
72.	ENSECAG00000009142	ENSECAG00000009142		4,2408	6,61E-12
73.	ENSECAG00000008503	CD74	CD74 molecule	4,2307	1,74E-05
74.	ENSECAG00000055770	KCNE4	potassium voltage-gated channel subfamily E regulatory subunit 4	4,203	2,5E-110
75.	ENSECAG00000046182	ENSECAG00000046182		4,185	7,13E-19
76.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	4,1723	9,49E-26
77.	ENSECAG00000005126	TRIM22	tripartite motif containing 22	4,1187	4,29E-06
78.	ENSECAG00000010963	SERPING1	serpin family G member 1	4,0894	3,4E-278
79.	ENSECAG00000006763	GPBAR1	G protein-coupled bile acid receptor 1	4,0859	2,2E-09
80.	ENSECAG00000007432	PTGDR	prostaglandin D2 receptor	4,0813	2,45E-33
81.	ENSECAG00000022686	MRAP2	melanocortin 2 receptor accessory protein 2	4,0673	4,53E-09
82.	ENSECAG00000020365	CELF3	CUGBP Elav-like family member 3	4,0663	8,9E-07
83.	ENSECAG00000005307	RNF183	ring finger protein 183	4,0576	3,87E-56
84.	ENSECAG00000001189	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	4,05	5,37E-22
85.	ENSECAG00000023534	CIITA	class II major histocompatibility complex transactivator	4,0217	4,49E-24
86.	ENSECAG00000057579	ENSECAG00000057579		3,9845	1,92E-05
87.	ENSECAG00000021796	HLA-DMB	major histocompatibility complex, class II, DM beta	3,9472	6,32E-08
88.	ENSECAG00000021775	KRT8	keratin 8	3,9286	1,32E-36
89.	ENSECAG00000060335	ENSECAG00000060335		3,9283	4,95E-18
90.	ENSECAG00000018057	IL2RA	interleukin 2 receptor subunit alpha	3,9158	1,45E-40
91.	ENSECAG00000015333	ADAP2	ArfGAP with dual PH domains 2	3,9154	1,39E-35
92.	ENSECAG00000021604	PDGFRL	platelet derived growth factor receptor like	3,915	2,39E-66
93.	ENSECAG00000018409	NOX5	NADPH oxidase 5	3,9079	1,14E-07
94.	ENSECAG00000024611	NTF3	neurotrophin 3	3,8494	1,71E-07
95.	ENSECAG00000047572	ENSECAG00000047572		3,8052	4,03E-07
96.	ENSECAG00000052882	ENSECAG00000052882		3,7878	0,000104
97.	ENSECAG00000009700	ANK3	ankyrin 3	3,7744	1,18E-08
98.	ENSECAG00000014645	OASL	2'-5'-oligoadenylate synthetase-like	3,7681	1,71E-07
99.	ENSECAG00000014812	KRT23	keratin 23	3,7296	1,53E-40
100.	ENSECAG00000013883	ICAM1	intercellular adhesion molecule 1	3,7186	0
101.	ENSECAG00000019800	TSPAN33	tetraspanin 33	3,7147	1,66E-40
102.	ENSECAG00000013362	CRYM	crystallin mu	3,7135	1,69E-07
103.	ENSECAG00000004709	C2	complement C2	3,6827	2,47E-36
104.	ENSECAG00000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	3,6473	5,1E-219
105.	ENSECAG00000015651	ARSF	arylsulfatase F	3,6459	3,4E-11
106.	ENSECAG00000056002	ENSECAG00000056002		3,6388	2,63E-05
107.	ENSECAG00000045914	ENSECAG00000045914		3,6224	7,87E-17
108.	ENSECAG00000017826	TMEM26	transmembrane protein 26	3,6199	1,77E-26
109.	ENSECAG00000035459	BATF2	basic leucine zipper ATF-like transcription factor 2	3,5735	7,6E-113
110.	ENSECAG00000003563	BST2	bone marrow stromal cell antigen 2	3,5598	1,36E-72
111.	ENSECAG00000020767	IL7	interleukin 7	3,5583	1E-118

112.	ENSECAG00000035561	ENSECAG00000035561		3,54	2,06E-15
113.	ENSECAG00000021220	GBP1	guanylate binding protein 1	3,5375	1,89E-54
114.	ENSECAG00000000235	MTBP	MDM2 binding protein	3,4846	1,47E-73
115.	ENSECAG00000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	3,4839	1,1E-129
116.	ENSECAG00000011042	BATF3	basic leucine zipper ATF-like transcription factor 3	3,4557	0,000211
117.	ENSECAG00000015842	ANKRD55	ankyrin repeat domain 55	3,4527	3,5E-24
118.	ENSECAG00000016131	FRMD4B	FERM domain containing 4B	3,4406	8,04E-81
119.	ENSECAG00000024719	ENSECAG00000024719		3,4349	8,15E-70
120.	ENSECAG00000011006	TGFA	transforming growth factor alpha	3,4011	1,88E-96
121.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	3,3869	4,32E-28
122.	ENSECAG00000039617	SNCB	synuclein beta	3,3852	3,87E-14
123.	ENSECAG00000017181	PTGS2	prostaglandin-endoperoxide synthase 2	3,3616	8,94E-43
124.	ENSECAG00000008739	ENSECAG00000008739		3,3579	7,72E-16
125.	ENSECAG00000010445	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	3,3419	3,03E-86
126.	ENSECAG00000014480	AIM2	absent in melanoma 2	3,3116	1,23E-17
127.	ENSECAG00000004805	B3GALT5	beta-1,3-galactosyltransferase 5	3,3074	6,26E-06
128.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	3,296	4,05E-23
129.	ENSECAG00000059829	ENSECAG00000059829		3,2928	1,15E-36
130.	ENSECAG00000028459	ENSECAG00000028459		3,2901	2,3E-136
131.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	3,2646	1,21E-49
132.	ENSECAG00000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	3,2533	9,4E-102
133.	ENSECAG00000046588	ENSECAG00000046588		3,2369	2,67E-08
134.	ENSECAG00000015034	PLAC8B	placenta associated 8 B	3,2366	5,02E-22
135.	ENSECAG00000020053	SLC4A4	solute carrier family 4 member 4	3,2333	1,1E-17
136.	ENSECAG00000020167	RGMA	repulsive guidance molecule BMP co-receptor a	3,2307	1,79E-54
137.	ENSECAG00000013324	TXN	thioredoxin	3,2214	1,64E-40
138.	ENSECAG00000029679	ENSECAG00000029679		3,214	7,76E-25
139.	ENSECAG00000008615	ENSECAG00000008615		3,2112	3,51E-78
140.	ENSECAG00000019573	PCDH15	protocadherin related 15	3,2041	1,08E-07
141.	ENSECAG00000050162	ENSECAG00000050162		3,1695	2,19E-06
142.	ENSECAG00000058677	ENSECAG00000058677		3,161	7,76E-19
143.	ENSECAG00000024959	FBXO39	F-box protein 39	3,1559	2,57E-17
144.	ENSECAG00000023918	DUOX1	dual oxidase 1	3,1525	1,49E-09
145.	ENSECAG00000008876	PTPRE	protein tyrosine phosphatase receptor type E	3,1498	1,01E-44
146.	ENSECAG00000016560	CRABP2	cellular retinoic acid binding protein 2	3,1338	1,01E-08
147.	ENSECAG00000018324	SLC43A2	solute carrier family 43 member 2	3,1227	4,77E-15
148.	ENSECAG00000024172	ADAMTS4	ADAM metalloproteinase with thrombospondin type 1 motif 4	3,1008	5,12E-15
149.	ENSECAG00000016934	IL31RA	interleukin 31 receptor A	3,0916	3,89E-31
150.	ENSECAG00000017896	PDLIM3	PDZ and LIM domain 3	3,0839	5,26E-16
151.	ENSECAG00000020238	GRAMD1B	GRAM domain containing 1B	3,0643	9,61E-37
152.	ENSECAG00000017185	ZBP1	Z-DNA binding protein 1	3,0494	3,23E-34
153.	ENSECAG00000007706	PHACTR3	phosphatase and actin regulator 3	3,044	1,17E-05
154.	ENSECAG00000014259	TIMP1	TIMP metalloproteinase inhibitor 1	3,0391	2,52E-57
155.	ENSECAG00000015644	SLC1A2	solute carrier family 1 member 2	3,0306	9,37E-16
156.	ENSECAG00000033385	LGALS3BP	galectin 3 binding protein	3,0306	0
157.	ENSECAG00000050023	ENSECAG00000050023		3,0253	0,000347
158.	ENSECAG00000035471	ENSECAG00000035471		3,0201	0,000127
159.	ENSECAG00000007972	SUSD5	sushi domain containing 5	3,0188	2,95E-33
160.	ENSECAG00000024746	PDGFD	platelet derived growth factor D	3,0128	5,08E-10
161.	ENSECAG00000015695	PTPRO	protein tyrosine phosphatase receptor type O	3,0114	4,14E-14
162.	ENSECAG00000014519	ETV7	ETS variant transcription factor 7	3,0069	5,69E-48
163.	ENSECAG00000018961	ACTN3	actinin alpha 3	2,9989	7,9E-21
164.	ENSECAG00000046504	ENSECAG00000046504		2,9933	2,71E-12
165.	ENSECAG00000014732	ATP10A	ATPase phospholipid transporting 10A (putative)	2,9932	8,38E-42
166.	ENSECAG00000009303	GFPT2	glutamine-fructose-6-phosphate transaminase 2	2,986	4,54E-38

167.	ENSECAG00000024961	XAF1	XIAP associated factor 1	2,9855	1,01E-52
168.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	2,9853	2,97E-62
169.	ENSECAG00000021206	HAS2	hyaluronan synthase 2	2,9839	2,46E-12
170.	ENSECAG00000053465	ENSECAG00000053465		2,9809	1,51E-27
171.	ENSECAG00000009299	ICAM5	intercellular adhesion molecule 5	2,9809	1,94E-06
172.	ENSECAG00000009020	IFI44	interferon induced protein 44	2,9311	6,43E-14
173.	ENSECAG00000059698	H3C11	H3 clustered histone 11	2,9269	3,93E-06
174.	ENSECAG00000019438	OSMR	oncostatin M receptor	2,9143	1,6E-109
175.	ENSECAG00000011669	TNN	tenascin N	2,9112	7,6E-140
176.	ENSECAG00000014126	CFAP161	cilia and flagella associated protein 161	2,9099	2,29E-08
177.	ENSECAG00000005241	THBD	thrombomodulin	2,908	1,37E-38
178.	ENSECAG00000032271	ENSECAG00000032271		2,9075	2,14E-38
179.	ENSECAG00000012742	CXCL6	C-X-C motif chemokine ligand 6	2,9036	1,32E-46
180.	ENSECAG00000009618	IFI44L	interferon induced protein 44 like	2,8966	1,47E-18
181.	ENSECAG00000016169	COL6A6	collagen type VI alpha 6 chain	2,8892	0,000237
182.	ENSECAG00000016056	BICDL2	BICD family like cargo adaptor 2	2,8856	6,88E-20
183.	ENSECAG00000057566	ENSECAG00000057566		2,8854	6,58E-05
184.	ENSECAG00000008493	SERPINB10	serpin family B member 10	2,8677	2,14E-08
185.	ENSECAG00000022093	SLC2A5	solute carrier family 2 member 5	2,8671	0,000244
186.	ENSECAG00000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	2,8589	2,42E-30
187.	ENSECAG00000053421	ENSECAG00000053421		2,8427	2,51E-05
188.	ENSECAG00000033890	CIDEA	cell death inducing DFFA like effector c	2,8242	5,05E-27
189.	ENSECAG00000029465	CHI3L1	chitinase 3 like 1	2,8108	5,57E-36
190.	ENSECAG00000030025	ENSECAG00000030025		2,804	2,24E-06
191.	ENSECAG00000051467	SLC6A13	solute carrier family 6 member 13	2,8013	1,46E-25
192.	ENSECAG00000011893	CNTNAP4	contactin associated protein family member 4	2,7885	6,04E-05
193.	ENSECAG00000001481	SAMD9L	sterile alpha motif domain containing 9 like	2,7879	5,52E-42
194.	ENSECAG00000009420	NT5E	5'-nucleotidase ecto	2,7599	1,8E-112
195.	ENSECAG00000009752	APOA1	apolipoprotein A1	2,7593	2,22E-07
196.	ENSECAG00000035391	ENSECAG00000035391		2,7494	7,17E-25
197.	ENSECAG000000049724	PTAFR	platelet activating factor receptor	2,7409	2,19E-15
198.	ENSECAG00000008059	PDE4C	phosphodiesterase 4C	2,739	1,26E-08
199.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	2,734	4,6E-17
200.	ENSECAG00000011704	TNFAIP2	TNF alpha induced protein 2	2,7234	5,1E-197
201.	ENSECAG00000048408	ENSECAG00000048408		2,7193	0,000574
202.	ENSECAG00000022739	CA4	carbonic anhydrase 4	2,7188	8,5E-74
203.	ENSECAG00000003289	RAPSN	receptor associated protein of the synapse	2,7104	0,000564
204.	ENSECAG00000047192	ENSECAG00000047192		2,7053	4,21E-05
205.	ENSECAG00000032055	PROKR2	prokineticin receptor 2	2,6968	3,34E-08
206.	ENSECAG00000045402	ENSECAG00000045402		2,6882	2,45E-19
207.	ENSECAG00000030620	ENSECAG00000030620		2,6882	4,41E-07
208.	ENSECAG00000050999	ENSECAG00000050999		2,6875	7,5E-24
209.	ENSECAG00000009913	CDC6	cell division cycle 6	2,6848	7,41E-59
210.	ENSECAG00000024322	ARSJ	arylsulfatase family member J	2,6769	7,93E-82
211.	ENSECAG00000009121	NEIL3	nei like DNA glycosylase 3	2,6664	1,59E-16
212.	ENSECAG00000055388	ENSECAG00000055388		2,6579	3,48E-18
213.	ENSECAG00000047563	ENSECAG00000047563		2,6562	6,41E-20
214.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	2,6539	5,1E-37
215.	ENSECAG00000018752	APOL6	apolipoprotein L6	2,6534	9,18E-49
216.	ENSECAG00000017172	IFI27	interferon, alpha-inducible protein 27	2,643	1,31E-87
217.	ENSECAG00000059506	ENSECAG00000059506		2,6415	3,35E-05
218.	ENSECAG00000039680	ENSECAG00000039680		2,641	8,78E-30
219.	ENSECAG00000001399	SAMD9	sterile alpha motif domain containing 9	2,6368	1,12E-79
220.	ENSECAG00000011037	WARS1	tryptophanyl-tRNA synthetase 1	2,6344	3,7E-148
221.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	2,6293	1,4E-92
222.	ENSECAG00000033029	ENSECAG00000033029		2,6256	7,25E-13
223.	ENSECAG00000038893	CST3	cystatin C	2,6229	5,9E-171
224.	ENSECAG00000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	2,6206	1,02E-31
225.	ENSECAG00000000532	EPS8L1	EPS8 like 1	2,6097	1,3E-30
226.	ENSECAG00000008823	CDH11	cadherin 11	2,6031	1,7E-172

227.	ENSECAG00000035846	ENSECAG00000035846		2,595	0,000377
228.	ENSECAG00000059594	ENSECAG00000059594		2,5922	0,000587
229.	ENSECAG00000015198	CPM	carboxypeptidase M	2,5855	0,000145
230.	ENSECAG00000018996	PLEK	pleckstrin	2,5843	3,06E-07
231.	ENSECAG00000022850	CERKL	ceramide kinase like	2,5776	1,29E-07
232.	ENSECAG00000032875	SULT4A1	sulfotransferase family 4A member 1	2,5697	3,5E-07
233.	ENSECAG00000057675	ENSECAG00000057675		2,5678	8,81E-06
234.	ENSECAG00000007464	RRM2	ribonucleotide reductase regulatory subunit M2	2,5634	3,35E-27
235.	ENSECAG00000046105	ENSECAG00000046105		2,5621	4,69E-07
236.	ENSECAG00000014305	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	2,5439	8,76E-07
237.	ENSECAG00000017917	CYBB	cytochrome b-245 beta chain	2,5381	7,62E-05
238.	ENSECAG00000009039	STAT1	signal transducer and activator of transcription 1	2,5333	3,6E-185
239.	ENSECAG00000009054	CKB	creatine kinase B	2,5323	4,76E-14
240.	ENSECAG00000014511	IL11	interleukin 11	2,5287	2,24E-07
241.	ENSECAG00000019779	KCNS3	potassium voltage-gated channel modifier subfamily S member 3	2,5226	0,00056
242.	ENSECAG00000014406	IL15	interleukin 15	2,5216	7,97E-21
243.	ENSECAG00000011708	GAREM1	GRB2 associated regulator of MAPK1 subtype 1	2,5213	1,02E-15
244.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	2,5209	1,06E-63
245.	ENSECAG00000018322	EXO1	exonuclease 1	2,5176	5,46E-20
246.	ENSECAG00000004372	SLC22A3	solute carrier family 22 member 3	2,5086	5,51E-27
247.	ENSECAG00000013575	CNTN3	contactin 3	2,5047	1,31E-06
248.	ENSECAG00000011788	CDC45	cell division cycle 45	2,4998	9,07E-39
249.	ENSECAG00000056994	ENSECAG00000056994		2,4855	0,000919
250.	ENSECAG00000009370	ORC1	origin recognition complex subunit 1	2,4819	5,47E-38
251.	ENSECAG00000025128	PIWIL2	piwi like RNA-mediated silencing 2	2,4816	6,94E-08
252.	ENSECAG00000048661	ENSECAG00000048661		2,4785	1,32E-15
253.	ENSECAG00000022722	ESPL1	extra spindle pole bodies like 1, separase	2,4765	1,76E-21
254.	ENSECAG00000019758	TNFSF13B	TNF superfamily member 13b	2,4698	4,65E-30
255.	ENSECAG00000022866	SPNS3	SPNS lysolipid transporter 3, sphingosine-1-phosphate (putative)	2,4613	0,000506
256.	ENSECAG00000029514	SLC2A6	solute carrier family 2 member 6	2,4603	9,82E-49
257.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	2,4484	1,62E-05
258.	ENSECAG00000018665	RECQL4	RecQ like helicase 4	2,4255	3,2E-23
259.	ENSECAG00000012629	MASTL	microtubule associated serine/threonine kinase like	2,4221	8,05E-36
260.	ENSECAG00000018828	STEAP4	STEAP4 metalloredutase	2,4111	1,81E-05
261.	ENSECAG00000059003	ISG15	ISG15 ubiquitin like modifier	2,4084	2,74E-11
262.	ENSECAG00000047309	ENSECAG00000047309		2,4082	1,12E-15
263.	ENSECAG00000008461	DEPDC1	DEP domain containing 1	2,4021	9,19E-26
264.	ENSECAG00000002570	HS3ST1	heparan sulfate-glucosamine 3-sulfotransferase 1	2,3988	9,42E-07
265.	ENSECAG00000010500	ITGA4	integrin subunit alpha 4	2,393	5,53E-82
266.	ENSECAG00000011776	MX1	MX dynamin like GTPase 1	2,3903	4,08E-12
267.	ENSECAG00000057855	ENSECAG00000057855		2,3887	0,001002
268.	ENSECAG00000031322	ENSECAG00000031322		2,3814	8,91E-22
269.	ENSECAG00000006288	SIK1	salt inducible kinase 1	2,3809	5,85E-50
270.	ENSECAG00000015657	TNNT1	tropoin T1, slow skeletal type	2,3752	2,19E-11
271.	ENSECAG00000018699	CHTF18	chromosome transmission fidelity factor 18	2,3732	1,19E-05
272.	ENSECAG00000033821	ANKRD33B	ankyrin repeat domain 33B	2,3716	6,11E-29
273.	ENSECAG00000000373	LOXL3	lysyl oxidase like 3	2,3669	3,8E-120
274.	ENSECAG00000022731	COL6A1	collagen type VI alpha 1 chain	2,3563	4E-109
275.	ENSECAG00000014368	MCM5	minichromosome maintenance complex component 5	2,3534	1,08E-36
276.	ENSECAG00000019411	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	2,3522	2,26E-50
277.	ENSECAG00000018510	RGS20	regulator of G protein signaling 20	2,3521	1,22E-15
278.	ENSECAG00000052745	ENSECAG00000052745		2,3486	0,000993
279.	ENSECAG00000020769	FGF1	fibroblast growth factor 1	2,3486	5,6E-99

280.	ENSECAG00000009787	SNAI1	snail family transcriptional repressor 1	2,3413	9,99E-93
281.	ENSECAG00000009716	CDK1	cyclin dependent kinase 1	2,3354	8,04E-33
282.	ENSECAG00000019038	KIF2C	kinesin family member 2C	2,323	7E-34
283.	ENSECAG00000009400	ARRDC4	arrestin domain containing 4	2,32	1,22E-67
284.	ENSECAG00000033034	RAB20	RAB20, member RAS oncogene family	2,3196	7,78E-16
285.	ENSECAG00000014867	PLBD1	phospholipase B domain containing 1	2,3192	1,56E-36
286.	ENSECAG00000014794	MIIP	migration and invasion inhibitory protein	2,319	2,33E-59
287.	ENSECAG00000014658	SCD	stearoyl-CoA desaturase	2,3139	7,98E-88
288.	ENSECAG00000032074	ENSECAG00000032074		2,3121	3,27E-06
289.	ENSECAG00000009034	DUOXA1	dual oxidase maturation factor 1	2,3079	0,002672
290.	ENSECAG00000009472	CLSPN	claspin	2,3028	1,52E-23
291.	ENSECAG00000010053	HJURP	Holliday junction recognition protein	2,2993	1,93E-11
292.	ENSECAG00000009173	ZNF367	zinc finger protein 367	2,2988	3,99E-40
293.	ENSECAG00000000426	CENPL	centromere protein L	2,2898	2E-14
294.	ENSECAG00000020881	CTSC	cathepsin C	2,2897	3,11E-07
295.	ENSECAG00000036105	ENSECAG00000036105		2,2867	1,12E-15
296.	ENSECAG00000024269	UGT8	UDP glycosyltransferase 8	2,2867	1,83E-05
297.	ENSECAG00000024851	EDNRB	endothelin receptor type B	2,2845	3,48E-31
298.	ENSECAG00000021776	ENSECAG00000021776		2,2787	0,000114
299.	ENSECAG00000026891	ENSECAG00000026891		2,2781	2,74E-23
300.	ENSECAG00000015871	CDCA8	cell division cycle associated 8	2,2777	8,61E-27
301.	ENSECAG00000010326	MIS18A	MIS18 kinetochore protein A	2,2777	1,08E-21
302.	ENSECAG00000023019	KIF18B	kinesin family member 18B	2,2725	1,08E-27
303.	ENSECAG00000005379	HPGD	15-hydroxyprostaglandin dehydrogenase	2,2723	1,01E-08
304.	ENSECAG00000053139	ENSECAG00000053139		2,2716	1,13E-13
305.	ENSECAG00000023874	SPINT1	serine peptidase inhibitor, Kunitz type 1	2,269	2,09E-07
306.	ENSECAG00000026928	ASCL4	achaete-scute family bHLH transcription factor 4	2,2664	4,25E-06
307.	ENSECAG00000024473	MCM10	minichromosome maintenance 10 replication initiation factor	2,2663	6,03E-23
308.	ENSECAG00000004587	ANKRD34B	ankyrin repeat domain 34B	2,2663	5,65E-06
309.	ENSECAG00000025092	CDC25B	cell division cycle 25B	2,2589	7,2E-107
310.	ENSECAG00000025143	CYP27B1	cytochrome P450 family 27 subfamily B member 1	2,2481	6,88E-11
311.	ENSECAG00000011878	DTL	denticleless E3 ubiquitin	2,2472	5,74E-51
312.	ENSECAG00000050918	ENSECAG00000050918		2,2454	1,01E-10
313.	ENSECAG00000003943	SYT5	synaptotagmin 5	2,2437	8,46E-34
314.	ENSECAG00000005086	EGLN3	egl-9 family hypoxia inducible factor 3	2,2368	2,09E-50
315.	ENSECAG00000021452	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	2,2367	2,3E-11
316.	ENSECAG00000008193	UPP1	uridine phosphorylase 1	2,236	4,46E-36
317.	ENSECAG00000017433	TNC	tenascin C	2,2333	2,32E-76
318.	ENSECAG00000013053	TOP2A	DNA topoisomerase II alpha	2,2333	6,7E-22
319.	ENSECAG00000030406	CYP2C114	cytochrome P450 family 2 subfamily C member 114	2,2328	0,000368
320.	ENSECAG00000011003	PDE4B	phosphodiesterase 4B	2,2318	9,94E-72
321.	ENSECAG00000023525	NDUFA4L2	NDUFA4 mitochondrial complex associated like 2	2,2314	6,14E-25
322.	ENSECAG00000015060	PRR11	proline rich 11	2,2288	1,06E-14
323.	ENSECAG00000020270	CCNE2	cyclin E2	2,2284	6,7E-25
324.	ENSECAG00000008809	OAS3	2'-5'-oligoadenylate synthetase 3	2,2278	5,72E-14
325.	ENSECAG00000056831	ENSECAG00000056831		2,2224	7,9E-31
326.	ENSECAG00000057869	ENSECAG00000057869		2,2222	4,33E-13
327.	ENSECAG00000019322	IL21R	interleukin 21 receptor	2,2203	8,5E-58
328.	ENSECAG00000005925	MYBL2	MYB proto-onco like 2	2,2201	1,35E-26
329.	ENSECAG00000015369	NID2	nidogen 2	2,213	2,2E-128
330.	ENSECAG00000015641	DSCC1	DNA replication and sister chromatid cohesion 1	2,213	1,78E-30
331.	ENSECAG00000020111	IQGAP3	IQ motif containing GTPase activating protein 3	2,2032	3,9E-28
332.	ENSECAG00000019578	CDCA5	cell division cycle associated 5	2,2028	9,71E-25
333.	ENSECAG00000032131	UBE2L6	ubiquitin conjugating enzyme E2 L6	2,2004	2,5E-130
334.	ENSECAG00000017864	FMOD	fibromodulin	2,1983	2,64E-06
335.	ENSECAG00000008655	DLGAP5	DLG associated protein 5	2,1965	4,64E-24
336.	ENSECAG00000029594	ENSECAG00000029594		2,195	1,69E-09

337.	ENSECAG00000019369	CCNF	cyclin F	2,193	4,88E-31
338.	ENSECAG00000023355	GTSE1	G2 and S-phase expressed 1	2,1914	3,5E-24
339.	ENSECAG00000054624	ENSECAG00000054624		2,1875	0,000538
340.	ENSECAG00000000633	ZWINT	ZW10 interacting kinetochore protein	2,1864	4,62E-15
341.	ENSECAG00000007974	GALNT3	polypeptide N-acetylglucosaminyltransferase 3	2,1845	0,000683
342.	ENSECAG00000057145	C3	complement C3	2,1834	2,3E-125
343.	ENSECAG00000049355	ENSECAG00000049355		2,1796	2,14E-39
344.	ENSECAG00000003462	RUNX1	RUNX family transcription factor 1	2,1682	6,8E-22
345.	ENSECAG00000023961	AURKA	aurora kinase A	2,1676	2,2E-44
346.	ENSECAG00000053648	DDX60	DExD/H-box helicase 60	2,1645	5,13E-15
347.	ENSECAG00000052587	ENSECAG00000052587		2,1617	3,41E-05
348.	ENSECAG00000020506	MCM3	minichromosome maintenance complex component 3	2,1586	1,07E-45
349.	ENSECAG00000007872	TCF19	transcription factor 19	2,1573	3,99E-36
350.	ENSECAG00000007881	IFIH1	interferon induced with helicase C domain 1	2,1567	8,67E-45
351.	ENSECAG00000011492	CDCA7	cell division cycle associated 7	2,1566	2,53E-87
352.	ENSECAG00000019705	CDC20	cell division cycle 20	2,152	6,14E-12
353.	ENSECAG00000014384	AURKB	aurora kinase B	2,1422	4,52E-16
354.	ENSECAG00000015835	NT5DC2	5'-nucleotidase domain containing 2	2,1406	6,69E-16
355.	ENSECAG00000021453	TICRR	TOPBP1 interacting checkpoint and replication regulator	2,1398	3,32E-21
356.	ENSECAG00000020919	HROB	homologous recombination factor with OB-fold	2,1386	7,94E-08
357.	ENSECAG00000010859	KIF4A	kinesin family member 4A	2,1377	2,73E-27
358.	ENSECAG00000012818	TUBB3	tubulin beta 3 class III	2,1326	8,04E-38
359.	ENSECAG00000020601	ZYG11A	zyg-11 family member A, cell cycle regulator	2,1315	3,19E-09
360.	ENSECAG00000018373	FAM234B	family with sequence similarity 234 member B	2,131	1,18E-36
361.	ENSECAG00000017671	ROBO1	roundabout guidance receptor 1	2,1305	1,22E-65
362.	ENSECAG00000049174	ENSECAG00000049174		2,1298	1,18E-17
363.	ENSECAG00000017742	ERN2	endoplasmic reticulum to nucleus signaling 2	2,1287	0,00102
364.	ENSECAG00000045049	ENSECAG00000045049		2,1195	0,001139
365.	ENSECAG00000004795	ENSECAG00000004795		2,1186	7,89E-16
366.	ENSECAG00000023922	E2F2	E2F transcription factor 2	2,1182	2,2E-05
367.	ENSECAG00000010525	KEL	Kell metallo-endorpeptidase	2,1171	1,74E-15
368.	ENSECAG00000018918	TRIP13	thyroid hormone receptor interactor 13	2,1161	2,14E-24
369.	ENSECAG00000024694	KIF14	kinesin family member 14	2,1153	4,04E-24
370.	ENSECAG00000008634	NCAPH	non-SMC condensin I complex subunit H	2,1132	1,69E-21
371.	ENSECAG00000017628	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	2,1109	2,18E-08
372.	ENSECAG00000017396	STING1	stimulator of interferon response cGAMP interactor 1	2,1099	2,93E-18
373.	ENSECAG00000017926	TROAP	trophinin associated protein	2,1076	3,31E-16
374.	ENSECAG00000014501	TMEM54	transmembrane protein 54	2,1039	3,65E-39
375.	ENSECAG00000002513	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	2,1007	1,14E-35
376.	ENSECAG00000002675	ZGRF1	zinc finger GRF-type containing 1	2,0977	3,81E-25
377.	ENSECAG00000014742	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	2,0938	3,98E-22
378.	ENSECAG00000014422	OAS2	2'-5'-oligoadenylate synthetase 2	2,0929	8,39E-22
379.	ENSECAG00000014813	CCNB2	cyclin B2	2,092	8,31E-19
380.	ENSECAG00000016860	KIF20A	kinesin family member 20A	2,0904	1,02E-14
381.	ENSECAG00000020456	ZBTB7C	zinc finger and BTB domain containing 7C	2,0899	1,55E-06
382.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	2,0897	6,55E-16
383.	ENSECAG00000024293	AMDHD1	amidohydrolase domain containing 1	2,0876	0,000694
384.	ENSECAG00000010499	TRABD2A	TraB domain containing 2A	2,0875	5,84E-08
385.	ENSECAG00000034739	ADORA2A	adenosine A2a receptor	2,0868	2,79E-61
386.	ENSECAG00000014260	FOS	Fos proto-onco, AP-1 transcription factor subunit	2,081	6,85E-97
387.	ENSECAG00000009501	DAAM2	dishevelled associated activator of morphosis 2	2,0781	1,4E-143
388.	ENSECAG00000009568	CENPI	centromere protein I	2,0764	7,94E-40

389.	ENSECAG00000018134	STMN2	stathmin 2	2,0728	0,003325
390.	ENSECAG00000015848	HHIP.L2	HHIP like 2	2,0656	1,38E-05
391.	ENSECAG00000017777	PLK1	polo like kinase 1	2,0632	6,05E-25
392.	ENSECAG00000014536	KIF23	kinesin family member 23	2,0572	1,54E-16
393.	ENSECAG00000024583	SYT16	synaptotagmin 16	2,0552	0,000284
394.	ENSECAG00000017522	TNFSF14	TNF superfamily member 14	2,0538	3,13E-05
395.	ENSECAG00000024519	SPC25	SPC25 component of NDC80 kinetochore complex	2,0487	2,7E-15
396.	ENSECAG00000014787	RCAN1	regulator of calcineurin 1	2,0426	7,03E-85
397.	ENSECAG00000012475	SGO1	shugoshin 1	2,0357	4,79E-26
398.	ENSECAG00000000284	USP18	ubiquitin specific peptidase 18	2,0349	8,29E-20
399.	ENSECAG00000009801	EXOC3L4	exocyst complex component 3 like 4	2,032	5,44E-08
400.	ENSECAG00000011979	FTCD	formimidoyltransferase cyclodeaminase	2,0275	1,69E-37
401.	ENSECAG00000017103	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	2,026	1,41E-21
402.	ENSECAG00000014916	TNFRSF11B	TNF receptor superfamily member 11b	2,0236	0,002066
403.	ENSECAG00000057464	ENSECAG00000057464		2,015	2,39E-15
404.	ENSECAG00000001653	POLE	DNA polymerase epsilon, catalytic subunit	2,0147	2,82E-44
405.	ENSECAG00000030653	GAP43	growth associated protein 43	2,0135	8,12E-05
406.	ENSECAG00000014452	KIF22	kinesin family member 22	2,0133	5,78E-37
407.	ENSECAG00000007620	DEPDC1B	DEP domain containing 1B	2,0116	1,94E-13
408.	ENSECAG00000005316	PIF1	PIF1 5'-to-3' DNA helicase	2,0076	2,17E-07
409.	ENSECAG00000012022	PSMB10	proteasome 20S subunit beta 10	2,0059	4,6E-106
410.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	1,9935	1,49E-75
411.	ENSECAG00000046384	SMIM4		1,9932	3,61E-37
412.	ENSECAG00000024650	FADS2	fatty acid desaturase 2	1,9829	2,1E-104
413.	ENSECAG00000021155	MXD3	MAX dimerization protein 3	1,9821	2,63E-09
414.	ENSECAG00000013009	KIF26B	kinesin family member 26B	1,9802	8,76E-06
415.	ENSECAG00000056440	ENSECAG00000056440		1,9797	1,37E-05
416.	ENSECAG00000017104	ERRFI1	ERBB receptor feedback inhibitor 1	1,9727	4,6E-198
417.	ENSECAG00000048862	ENSECAG00000048862		1,9722	0,001397
418.	ENSECAG00000013188	CDCA2	cell division cycle associated 2	1,9573	1,37E-22
419.	ENSECAG00000015461	CACNA1G	calcium voltage-gated channel subunit alpha1 G	1,9572	1,75E-11
420.	ENSECAG00000059825	ENSECAG00000059825		1,9559	0,000654
421.	ENSECAG00000033470	ENSECAG00000033470		1,9548	1,28E-30
422.	ENSECAG00000021429	C1R	complement C1r	1,9547	9,5E-123
423.	ENSECAG00000000281	SHCBP1	SHC binding and spindle associated 1	1,951	4,68E-14
424.	ENSECAG00000020277	SLC4A11	solute carrier family 4 member 11	1,9439	0,001804
425.	ENSECAG00000020362	MND1	meiotic nuclear divisions 1	1,9421	2,68E-06
426.	ENSECAG00000024196	KIFC1	kinesin family member C1	1,9419	5E-20
427.	ENSECAG00000055873	ABCA6	ATP binding cassette subfamily A member 6	1,9389	2,11E-06
428.	ENSECAG00000008096	FAM111B	FAM111 trypsin like peptidase B	1,9367	3,86E-82
429.	ENSECAG00000005547	CDT1	chromatin licensing and DNA replication factor 1	1,9365	1,82E-20
430.	ENSECAG00000008827	NDC80	NDC80 kinetochore complex component	1,9361	5,12E-19
431.	ENSECAG00000024267	TFRC	transferrin receptor	1,9357	1,58E-53
432.	ENSECAG00000016029	TRAF1	TRAF interacting protein	1,9355	4,36E-12
433.	ENSECAG00000032009	ENSECAG00000032009		1,9339	4,32E-19
434.	ENSECAG00000024558	ENSECAG00000024558		1,9337	1,64E-16
435.	ENSECAG00000054990	CCNA2	cyclin A2	1,9302	3,13E-34
436.	ENSECAG00000016646	PARPBP	PARP1 binding protein	1,9297	4,42E-17
437.	ENSECAG00000023599	HPSE	heparanase	1,9296	9,8E-05
438.	ENSECAG00000023071	DDIAS	DNA damage induced apoptosis suppressor	1,928	7,02E-55
439.	ENSECAG0000002992	MID1IP1	MID1 interacting protein 1	1,9272	6,1E-101
440.	ENSECAG00000018649	UCP2	uncoupling protein 2	1,9254	8,9E-50
441.	ENSECAG00000022901	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	1,9252	1,06E-10
442.	ENSECAG00000013691	MALT1	MALT1 paracaspase	1,9236	1,69E-37
443.	ENSECAG00000056818	TMEM71	transmembrane protein 71	1,9223	0,000295
444.	ENSECAG00000016578	ENSECAG00000016578		1,9203	2,33E-10
445.	ENSECAG00000015806	CCNB1	cyclin B1	1,9132	6,58E-27
446.	ENSECAG00000014377	CHAF1A	chromatin assembly factor 1 subunit A	1,9039	8,65E-37

447.	ENSECAG00000019631	MCM2	minichromosome maintenance complex component 2	1,9032	1,49E-56
448.	ENSECAG00000016953	HLF	HLF transcription factor, PAR bZIP family member	1,9028	7,74E-41
449.	ENSECAG00000011380	TACC3	transforming acidic coiled-coil containing protein 3	1,9009	3,9E-23
450.	ENSECAG00000004845	CHEK2	checkpoint kinase 2	1,9006	1,77E-23
451.	ENSECAG00000017794	IRF1	interferon regulatory factor 1	1,9001	2,32E-52
452.	ENSECAG00000008506	HMMR	hyaluronan mediated motility receptor	1,8989	2,95E-22
453.	ENSECAG00000058229	ENSECAG00000058229		1,8962	6E-12
454.	ENSECAG00000015966	SERPINB6	serpin family B member 6	1,8954	3,59E-53
455.	ENSECAG00000059928	ENSECAG00000059928		1,8914	9,12E-35
456.	ENSECAG00000010821	RACGAP1	Rac GTPase activating protein 1	1,891	1,89E-24
457.	ENSECAG00000011496	NFKBIZ	NFKB inhibitor zeta	1,8908	4,66E-60
458.	ENSECAG00000019129	FOXN1	forkhead box M1	1,8867	1,81E-22
459.	ENSECAG00000017388	CENPT	centromere protein T	1,8814	9,75E-18
460.	ENSECAG00000039393	ENSECAG00000039393		1,8786	3,48E-10
461.	ENSECAG00000018810	HELLS	helicase, lymphoid specific	1,8718	8,54E-18
462.	ENSECAG00000036440	RGS16	regulator of G protein signaling 16	1,8716	0,001716
463.	ENSECAG00000000132	MAOB	monoamine oxidase B	1,8616	0,001998
464.	ENSECAG00000015822	VDR	vitamin D receptor	1,8606	6,15E-80
465.	ENSECAG00000023992	S100P	S100 calcium binding protein P	1,859	0,001349
466.	ENSECAG00000014314	POLQ	DNA polymerase theta	1,8582	3,33E-17
467.	ENSECAG00000000179	SCN1B	sodium voltage-gated channel beta subunit 1	1,8565	4,02E-19
468.	ENSECAG00000000910	ENSECAG00000000910		1,8537	5,5E-184
469.	ENSECAG00000014517	CDCA3	cell division cycle associated 3	1,8534	4,17E-09
470.	ENSECAG00000021525	IL4R	interleukin 4 receptor	1,8496	2,05E-59
471.	ENSECAG00000012773	CMPK2	cytidine/uridine monophosphate kinase 2	1,8471	8,72E-16
472.	ENSECAG00000019329	MPP3	MAGUK p55 scaffold protein 3	1,8453	6,14E-15
473.	ENSECAG00000024428	PROCR	protein C receptor	1,8414	2,44E-58
474.	ENSECAG000000046407	ENSECAG000000046407		1,8349	1,25E-09
475.	ENSECAG00000016271	CENPA	centromere protein A	1,8303	5,43E-09
476.	ENSECAG00000011630	FBXO5	F-box protein 5	1,8301	1,37E-34
477.	ENSECAG00000018476	TPX2	TPX2 microtubule nucleation factor	1,8262	4,27E-11
478.	ENSECAG00000007942	LMNB1	lamin B1	1,8208	3,92E-39
479.	ENSECAG00000016773	NABP1	nucleic acid binding protein 1	1,8195	7,8E-60
480.	ENSECAG00000008760	RAD54L	RAD54 like	1,8156	5,17E-20
481.	ENSECAG00000038102	ENSECAG00000038102		1,8125	7,07E-05
482.	ENSECAG00000046266	ENSECAG00000046266		1,8123	0,003219
483.	ENSECAG00000038834	MTFR2	mitochondrial fission regulator 2	1,809	1,42E-17
484.	ENSECAG00000012899	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	1,8074	5,37E-30
485.	ENSECAG00000014232	NR4A2	nuclear receptor subfamily 4 group A member 2	1,8001	1,08E-27
486.	ENSECAG00000014404	WDR62	WD repeat domain 62	1,7998	5,4E-29
487.	ENSECAG000000053819	ENSECAG000000053819		1,7989	9,65E-08
488.	ENSECAG000000006607	KIF11	kinesin family member 11	1,797	3,12E-32
489.	ENSECAG00000032959	ENSECAG00000032959		1,7942	5,06E-36
490.	ENSECAG00000017839	ENSECAG00000017839		1,7901	3,46E-59
491.	ENSECAG00000047112	ENSECAG00000047112		1,7888	0,003873
492.	ENSECAG00000012331	PARP9	poly(ADP-ribose) polymerase family member 9	1,7843	6,83E-66
493.	ENSECAG00000009519	C1S	complement C1s	1,7836	4,45E-85
494.	ENSECAG00000020645	ASPM	assembly factor for spindle microtubules	1,7803	4,11E-12
495.	ENSECAG00000003049	ENSECAG00000003049		1,78	1,87E-33
496.	ENSECAG00000020698	MELK	maternal embryonic leucine zipper kinase	1,7772	5,29E-33
497.	ENSECAG00000006917	P4HA3	prolyl 4-hydroxylase subunit alpha 3	1,7762	2,2E-39
498.	ENSECAG00000000303	SLC2A1	solute carrier family 2 member 1	1,7742	7,78E-71
499.	ENSECAG00000018253	FGFRL1	fibroblast growth factor receptor like 1	1,7713	6,54E-45
500.	ENSECAG00000023149	SCIN	scinderin	1,7699	2,41E-05
501.	ENSECAG00000008787	CCNB3	cyclin B3	1,7677	2,21E-08
502.	ENSECAG00000001041	CENPN	centromere protein N	1,7673	9,07E-22
503.	ENSECAG00000043057	ENSECAG00000043057		1,7617	2,27E-05

504.	ENSECAG00000020413	DCN	decorin	1,7616	8,9E-147
505.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	1,7602	1,5E-20
506.	ENSECAG00000003278	TRIM9	tripartite motif containing 9	1,7594	5,45E-10
507.	ENSECAG000000057591	MATK	megakaryocyte-associated tyrosine kinase	1,7567	1,07E-06
508.	ENSECAG00000005344	FEN1	flap structure-specific endonuclease 1	1,7558	2,55E-41
509.	ENSECAG00000003235	FANCI	FA complementation group I	1,7558	3,16E-25
510.	ENSECAG000000042596	ENSECAG000000042596		1,7534	1,48E-30
511.	ENSECAG000000002402	ENSECAG000000002402		1,7502	2,29E-16
512.	ENSECAG000000056672	ENSECAG000000056672		1,7486	1,45E-16
513.	ENSECAG000000012514	ENSECAG000000012514		1,7471	1,36E-07
514.	ENSECAG000000034734	EBF3	EBF transcription factor 3	1,7469	0,002419
515.	ENSECAG000000015967	ASF1B	anti-silencing function 1B histone chaperone	1,7461	8,68E-09
516.	ENSECAG000000038379	ENSECAG000000038379		1,7451	0,001858
517.	ENSECAG000000015069	BHLHE40	basic helix-loop-helix family member e40	1,7446	1,28E-17
518.	ENSECAG000000014594	EPAS1	endothelial PAS domain protein 1	1,7426	9,57E-63
519.	ENSECAG000000046674	ENSECAG000000046674		1,7418	2,94E-23
520.	ENSECAG000000016248	JPH1	junctophilin 1	1,7394	5,2E-07
521.	ENSECAG000000006788	PCSK5	proprotein convertase subtilisin/kexin type 5	1,736	7,54E-66
522.	ENSECAG000000000292	THSD7A	thrombospondin type 1 domain containing 7A	1,7357	9,12E-05
523.	ENSECAG000000013223	PBK	PDZ binding kinase	1,7337	1,11E-13
524.	ENSECAG000000016495	NUSAP1	nucleolar and spindle associated protein 1	1,7291	4,41E-31
525.	ENSECAG000000009163	NUF2	NUF2 component of NDC80 kinetochore complex	1,7264	2,81E-30
526.	ENSECAG000000045451	ENSECAG000000045451		1,7203	1,08E-27
527.	ENSECAG000000008270	FABP5	fatty acid binding protein 5	1,7183	2,07E-09
528.	ENSECAG000000023776	TTK	TTK protein kinase	1,7159	5,22E-25
529.	ENSECAG000000024194	POLA2	DNA polymerase alpha 2, accessory subunit	1,7158	1,38E-22
530.	ENSECAG000000014254	LCTL	lactase like	1,7134	4,15E-05
531.	ENSECAG0000000035500	ENSECAG0000000035500		1,7132	1,69E-12
532.	ENSECAG000000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,7114	8,7E-112
533.	ENSECAG000000013728	MFSD2A	MFSD2 lysolipid transporter A, lysophospholipid	1,7113	1,11E-36
534.	ENSECAG000000008432	HASPIN	histone H3 associated protein kinase	1,7093	3,86E-13
535.	ENSECAG000000029510	ENSECAG000000029510		1,7025	5,27E-09
536.	ENSECAG000000003201	PRSS35	serine protease 35	1,701	2,61E-19
537.	ENSECAG000000001964	PDHA1	pyruvate dehydrogenase E1 subunit alpha 1	1,699	3,3E-70
538.	ENSECAG000000020438	RASGEF1B	RasGEF domain family member 1B	1,6987	3,9E-09
539.	ENSECAG000000022278	KNL1	kinetochore scaffold 1	1,6979	2,26E-10
540.	ENSECAG000000010233	WDR25	WD repeat domain 25	1,696	1,03E-27
541.	ENSECAG000000023331	KIF20B	kinesin family member 20B	1,6939	3,96E-21
542.	ENSECAG000000008363	SLC4A9	solute carrier family 4 member 9	1,6935	0,004035
543.	ENSECAG000000012263	RNF19B	ring finger protein 19B	1,6926	2,23E-47
544.	ENSECAG000000000968	ENSECAG000000000968		1,6897	3,44E-79
545.	ENSECAG000000038504	ENSECAG000000038504		1,6867	0,005883
546.	ENSECAG000000044027	ENSECAG000000044027		1,6865	3,65E-48
547.	ENSECAG000000002308	RSPO4	R-spondin 4	1,6855	0,003749
548.	ENSECAG000000008441	ADORA2B	adenosine A2b receptor	1,6854	4,15E-23
549.	ENSECAG000000020887	COL6A3	collagen type VI alpha 3 chain	1,6842	3,44E-08
550.	ENSECAG000000022842	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1,6814	2,97E-91
551.	ENSECAG000000000685	B2M	beta-2-microglobulin	1,6767	3,9E-111
552.	ENSECAG000000021989	RIGI	RNA sensor RIG-I	1,6766	3,91E-53
553.	ENSECAG000000010805	PGM5	phosphoglucomutase 5	1,6723	3,12E-05
554.	ENSECAG000000038313	ENSECAG000000038313		1,6701	1,66E-22
555.	ENSECAG000000023808	ATAD2	ATPase family AAA domain containing 2	1,6696	2,95E-38
556.	ENSECAG000000024127	CENPF	centromere protein F	1,6663	9,32E-08
557.	ENSECAG000000034339	ENSECAG000000034339		1,6656	3,16E-66
558.	ENSECAG000000041545	GJD3	gap junction protein delta 3	1,6648	0,001836
559.	ENSECAG000000016742	TJP2	tight junction protein 2	1,6643	2,9E-33

560.	ENSECAG00000015510	FGF7	fibroblast growth factor 7	1,6638	7,07E-47
561.	ENSECAG00000006776	IL15RA	interleukin 15 receptor subunit alpha	1,6637	2,64E-36
562.	ENSECAG00000052358	ENSECAG00000052358		1,6632	0,001556
563.	ENSECAG00000036591	APLN	apelin	1,6604	6,94E-07
564.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,6603	1,26E-30
565.	ENSECAG00000048767	ENSECAG00000048767		1,656	9,46E-05
566.	ENSECAG00000014890	BRCA2	BRCA2 DNA repair associated	1,6529	9,24E-21
567.	ENSECAG00000009746	UBXN11	UBX domain protein 11	1,6526	7,67E-13
568.	ENSECAG00000014953	KIF15	kinesin family member 15	1,6475	5,52E-22
569.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,6421	4,94E-06
570.	ENSECAG00000024810	PLA2G4A	phospholipase A2 group IVA	1,6404	3,59E-55
571.	ENSECAG00000011854	CFB	complement factor B	1,6404	1,85E-12
572.	ENSECAG00000017843	ENSECAG00000017843		1,64	0,004994
573.	ENSECAG00000009462	COL14A1	collagen type XIV alpha 1 chain	1,6354	6,65E-10
574.	ENSECAG00000024671	IL12A	interleukin 12A	1,6338	1,19E-09
575.	ENSECAG00000058364	ENSECAG00000058364		1,6318	0,001134
576.	ENSECAG00000030455	ENSECAG00000030455		1,6274	1,64E-11
577.	ENSECAG00000013488	TMEM38B	transmembrane protein 38B	1,6257	2,15E-18
578.	ENSECAG00000025066	PLA2G3	phospholipase A2 group III	1,6244	8,18E-07
579.	ENSECAG00000017971	DDX43	DEAD-box helicase 43	1,6204	0,000529
580.	ENSECAG00000019061	ADAMTS3	ADAM metalloproteinase with thrombospondin type 1 motif 3	1,6199	2,24E-26
581.	ENSECAG00000003310	LY6E	lymphocyte antigen 6 family member E	1,6169	2,96E-87
582.	ENSECAG00000018151	OPTC	opticin	1,6158	0,000428
583.	ENSECAG00000047718	ENSECAG00000047718		1,6112	9,17E-09
584.	ENSECAG00000008906	PARP15	poly(ADP-ribose) polymerase family member 15	1,6089	1,6E-15
585.	ENSECAG00000015456	SPAG5	sperm associated antigen 5	1,6071	1,52E-31
586.	ENSECAG00000024297	COL27A1	collagen type XXVII alpha 1 chain	1,607	1,41E-31
587.	ENSECAG00000023264	RTP4	receptor transporter protein 4	1,6058	1,54E-11
588.	ENSECAG00000007964	EBF1	EBF transcription factor 1	1,605	1,77E-27
589.	ENSECAG00000042977	ENSECAG00000042977		1,6026	4,19E-23
590.	ENSECAG00000017715	CSF1	colony stimulating factor 1	1,6024	7E-104
591.	ENSECAG00000007571	PLAT	plasminogen activator, tissue type	1,6023	8,29E-13
592.	ENSECAG00000014145	TLL2	tolloid like 2	1,5989	4,87E-07
593.	ENSECAG00000014948	CIP2A	cellular inhibitor of PP2A	1,5978	5,29E-29
594.	ENSECAG00000007165	TRAF5	TNF receptor associated factor 5	1,596	7,02E-34
595.	ENSECAG00000009707	PTGS1	prostaglandin-endoperoxide synthase 1	1,5946	8,51E-08
596.	ENSECAG00000000197	TLR3	toll like receptor 3	1,5945	1,54E-28
597.	ENSECAG00000019932	ENSECAG00000019932		1,5944	6,47E-14
598.	ENSECAG00000010977	ARHGAP45	Rho GTPase activating protein 45	1,592	1,64E-10
599.	ENSECAG00000050101	EMP3	epithelial membrane protein 3	1,5914	7,58E-32
600.	ENSECAG00000003460	CKS1B	CDC28 protein kinase regulatory subunit 1B	1,5868	2,43E-15
601.	ENSECAG00000007152	TAP2	transporter 2, ATP binding cassette subfamily B member	1,5844	1,4E-85
602.	ENSECAG00000000574	NIPAL4	NIPA like domain containing 4	1,5806	4,48E-23
603.	ENSECAG000000037422	ENSECAG000000037422		1,5783	6,85E-07
604.	ENSECAG00000026830	ENSECAG00000026830		1,5758	1,5E-14
605.	ENSECAG00000009073	ARHGEF39	Rho guanine nucleotide exchange factor 39	1,5751	1,45E-19
606.	ENSECAG00000009189	XRCC3	X-ray repair cross complementing 3	1,5747	1,32E-33
607.	ENSECAG00000016898	PSMB9	proteasome 20S subunit beta 9	1,5719	1,83E-57
608.	ENSECAG00000002238	MIS12	MIS12 kinetochore complex component	1,571	1,57E-19
609.	ENSECAG00000024906	SPOCK3	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 3	1,5661	4,4E-07
610.	ENSECAG00000020920	NEK2	NIMA related kinase 2	1,5658	4,86E-13
611.	ENSECAG00000008187	PLK4	polo like kinase 4	1,5635	6,97E-23
612.	ENSECAG00000014969	TP53I3	tumor protein p53 inducible protein 3	1,5619	1,1E-38
613.	ENSECAG00000019780	ENSECAG00000019780		1,5606	4,29E-42
614.	ENSECAG00000039655	RARRES1	retinoic acid receptor responder 1	1,5603	3,41E-51
615.	ENSECAG00000024392	BRIP1	BRCA1 interacting helicase 1	1,5602	2,01E-21
616.	ENSECAG00000050552	ENSECAG00000050552		1,5585	1,82E-35
617.	ENSECAG00000018406	CXCL16	C-X-C motif chemokine ligand 16	1,5578	2,95E-47

618.	ENSECAG00000009402	VEGFA	vascular endothelial growth factor A	1,5557	8,59E-84
619.	ENSECAG00000008927	HIPK2	homeodomain interacting protein kinase 2	1,5552	5,95E-71
620.	ENSECAG00000007300	DCLK1	doublecortin like kinase 1	1,5544	3,16E-53
621.	ENSECAG00000005559	GABRA5	gamma-aminobutyric acid type A receptor subunit alpha5	1,5543	2,99E-05
622.	ENSECAG00000036575	MACIR	macrophage immunometabolism regulator	1,5541	2,28E-05
623.	ENSECAG00000009119	JAK2	Janus kinase 2	1,5533	9,24E-39
624.	ENSECAG00000002892	TIMELESS	timeless circadian regulator	1,551	1,34E-33
625.	ENSECAG00000008287	SLC39A14	solute carrier family 39 member 14	1,5508	4,79E-31
626.	ENSECAG00000017458	BNIP3	BCL2 interacting protein 3	1,5501	2E-12
627.	ENSECAG00000022533	GPRC5B	G protein-coupled receptor class C group 5 member B	1,5497	3,44E-41
628.	ENSECAG00000003636	ERAP1	endoplasmic reticulum aminopeptidase 1	1,5457	1E-126
629.	ENSECAG00000014702	MEDAG	mesenteric estrogen dependent adiposis	1,5448	7,39E-86
630.	ENSECAG00000019880	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif 9	1,5447	2,6E-32
631.	ENSECAG00000024817	P4HA2	prolyl 4-hydroxylase subunit alpha 2	1,5439	2E-154
632.	ENSECAG00000046970	ENSECAG00000046970		1,5429	0,00444
633.	ENSECAG00000013435	OAS1	2'-5'-oligoadenylate synthetase 1	1,5425	1,2E-40
634.	ENSECAG00000021634	SLC29A4	solute carrier family 29 member 4	1,5412	7,71E-11
635.	ENSECAG00000007918	TNS4	tensin 4	1,5406	5,88E-10
636.	ENSECAG00000016546	GALNT12	polypeptide N-acetylgalactosaminyltransferase 12	1,5395	1,62E-14
637.	ENSECAG00000021707	RTEL1	regulator of telomere elongation helicase 1	1,5391	1,81E-15
638.	ENSECAG00000009686	DTX3L	deltex E3 ubiquitin ligase 3L	1,5368	6,69E-41
639.	ENSECAG00000045200	ENSECAG00000045200		1,5323	6,19E-05
640.	ENSECAG00000015621	ARHGEF16	Rho guanine nucleotide exchange factor 16	1,5283	0,002029
641.	ENSECAG00000016121	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif 12	1,5273	4,42E-35
642.	ENSECAG00000021019	CPXM1	carboxypeptidase X, M14 family member 1	1,5271	1,71E-31
643.	ENSECAG00000045438	ENSECAG00000045438		1,5237	0,004729
644.	ENSECAG00000060045	ENSECAG00000060045		1,5235	3,75E-24
645.	ENSECAG00000046324	TEX2	testis expressed 2	1,5214	5,01E-59
646.	ENSECAG00000053054	ENSECAG00000053054		1,5213	0,004964
647.	ENSECAG00000016998	CD40	CD40 molecule	1,5211	5,18E-26
648.	ENSECAG00000017906	PRC1	protein regulator of cytokinesis 1	1,521	2,17E-28
649.	ENSECAG00000040575	ENSECAG00000040575		1,5203	2,52E-39
650.	ENSECAG00000001633	FZD10	frizzled class receptor 10	1,5194	1,13E-05
651.	ENSECAG00000009621	INCENP	inner centromere protein	1,5165	6,96E-22
652.	ENSECAG00000023026	PAPPA	pappalysin 1	1,513	4,25E-33
653.	ENSECAG00000004523	TIFA	TRAF interacting protein with forkhead associated domain	1,5127	6,03E-31
654.	ENSECAG00000026863	EFS	embryonal Fyn-associated substrate	1,5094	4,7E-21
655.	ENSECAG00000003634	RHNO1	RAD9-HUS1-RAD1 interacting nuclear orphan 1	1,5082	7,15E-25
656.	ENSECAG00000019161	DIAPH3	diaphanous related formin 3	1,5079	1,22E-19
657.	ENSECAG00000001290	CABP1	calcium binding protein 1	1,5079	7,33E-06
658.	ENSECAG00000011152	STIL	STIL centriolar assembly protein	1,5066	1E-10
659.	ENSECAG00000024121	TCF7L2	transcription factor 7 like 2	1,5049	3,01E-30
660.	ENSECAG00000016241	SEMA5A	semaphorin 5A	1,5007	6,47E-12
661.	ENSECAG00000025993	eca-mir-221	eca-mir-221	1,499	8,15E-05
662.	ENSECAG00000006038	SGO2	shugoshin 2	1,4978	4,81E-16
663.	ENSECAG00000018966	FBXO48	F-box protein 48	1,4974	0,000385
664.	ENSECAG00000000480	ABI3BP	ABI family member 3 binding protein	1,4959	5,44E-41
665.	ENSECAG00000023420	NFKBIA	NF-kB inhibitor alpha	1,4948	4,64E-57
666.	ENSECAG00000025150	LMO4	LIM domain only 4	1,493	7,09E-65
667.	ENSECAG00000006686	NCAPG2	non-SMC condensin II complex subunit G2	1,4925	1,72E-25
668.	ENSECAG00000024215	GINS2	GINS complex subunit 2	1,4887	4,11E-17
669.	ENSECAG00000013935	MTUS2	microtubule associated scaffold protein 2	1,488	0,000202
670.	ENSECAG00000023279	GATA6	GATA binding protein 6	1,4871	1,19E-22

671.	ENSECAG00000003836	LRRC75A	leucine rich repeat containing 75A	1,4867	2,02E-09
672.	ENSECAG00000010914	CHSY1	chondroitin sulfate synthase 1	1,4864	4,46E-55
673.	ENSECAG00000030219	ENSECAG00000030219		1,4862	1,57E-16
674.	ENSECAG00000011929	NR4A3	nuclear receptor subfamily 4 group A member 3	1,4852	3,54E-13
675.	ENSECAG00000016705	UGP2	UDP-glucose pyrophosphorylase 2	1,4843	9,33E-83
676.	ENSECAG00000017203	BTG2	BTG anti-proliferation factor 2	1,482	1,92E-35
677.	ENSECAG00000011641	TVP23A	trans-golgi network vesicle A	1,4808	7,7E-08
678.	ENSECAG00000055331	SPNS2	SPNS lysolipid transporter 2, sphingosine-1-phosphate	1,4789	3,04E-26
679.	ENSECAG00000029766	H2AX	H2A.X histone	1,4762	6,99E-10
680.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,4758	1,63E-11
681.	ENSECAG00000006554	PRRG4	proline rich and Gla domain 4	1,4752	4,42E-20
682.	ENSECAG00000007536	HELB	DNA helicase B	1,4752	3,15E-55
683.	ENSECAG00000017451	FAM110A	family with sequence similarity 110 member A	1,4724	2,01E-07
684.	ENSECAG00000017804	UPB1	beta-ureidopropionase 1	1,4716	0,001094
685.	ENSECAG00000009067	SLC16A6	solute carrier family 16 member 6	1,4693	2,16E-10
686.	ENSECAG00000011226	CENPQ	centromere protein Q	1,4687	2,46E-12
687.	ENSECAG00000011673	ENSECAG00000011673		1,4687	3,52E-20
688.	ENSECAG00000020431	SGK1	serum/glucocorticoid regulated kinase 1	1,4686	6,51E-26
689.	ENSECAG00000022610	TAP1	transporter 1, ATP binding cassette subfamily B member	1,4654	3,46E-33
690.	ENSECAG00000021812	STARD5	StAR related lipid transfer domain containing 5	1,4647	2,51E-20
691.	ENSECAG00000023800	AK2	adenylate kinase 2	1,4634	2,29E-37
692.	ENSECAG00000034840	TNFSF13	TNF superfamily member 13	1,4606	6,44E-23
693.	ENSECAG00000012845	MAPRE2	microtubule associated protein RP/EB family member 2	1,46	1,05E-62
694.	ENSECAG00000006229	PIMREG	PICALM interacting mitotic regulator	1,4598	4,26E-08
695.	ENSECAG00000017783	FST	folliculin	1,4596	6,22E-18
696.	ENSECAG00000010371	GAS2L3	growth arrest specific 2 like 3	1,4564	1,75E-11
697.	ENSECAG00000002745	MARCHF8	membrane associated ring-CH-type finger 8	1,4536	2,39E-54
698.	ENSECAG00000011206	MVD	mevalonate diphosphate decarboxylase	1,4505	1,77E-24
699.	ENSECAG00000024852	FABP3	fatty acid binding protein 3	1,4501	2,35E-11
700.	ENSECAG00000022051	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1,4493	3,74E-59
701.	ENSECAG00000016217	RNF213	ring finger protein 213	1,4489	2,75E-33
702.	ENSECAG00000009562	ZC3H12A	zinc finger CCCH-type containing 12A	1,4468	1,11E-31
703.	ENSECAG00000002113	BARD1	BRCA1 associated RING domain 1	1,4452	6,2E-12
704.	ENSECAG00000059404	ENSECAG00000059404		1,4436	5,52E-49
705.	ENSECAG00000052689	ENSECAG00000052689		1,4408	2,19E-07
706.	ENSECAG00000039158	FDPS	farnesyl diphosphate synthase	1,4401	1,88E-60
707.	ENSECAG00000016974	BRCA1	BRCA1 DNA repair associated	1,4396	5,04E-18
708.	ENSECAG0000001598	IFI35	interferon induced protein 35	1,439	5,82E-33
709.	ENSECAG00000051452	ENSECAG00000051452		1,4388	0,006148
710.	ENSECAG00000013035	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	1,4386	6,03E-18
711.	ENSECAG00000006133	NXPH4	neurexophilin 4	1,4382	0,000747
712.	ENSECAG00000019276	MCM4	minichromosome maintenance complex component 4	1,4368	1,51E-41
713.	ENSECAG00000016382	ANLN	anillin, actin binding protein	1,4333	2,92E-26
714.	ENSECAG00000020563	PIM1	Pim-1 proto-onc, serine/threonine kinase	1,4333	9,27E-80
715.	ENSECAG00000005865	HAUS8	HAUS augmin like complex subunit 8	1,4322	2,1E-31
716.	ENSECAG00000017194	FANCB	FA complementation group B	1,4291	4,3E-09
717.	ENSECAG00000009797	PRTFDC1	phosphoribosyl transferase domain containing 1	1,4281	2,08E-10
718.	ENSECAG00000010188	ABHD3	abhydrolase domain containing 3, phospholipase	1,4261	2,49E-31
719.	ENSECAG00000013037	ALDOC	aldolase, fructose-bisphosphate C	1,4249	7,8E-33
720.	ENSECAG00000000138	ACVR2A	activin A receptor type 2A	1,4237	4,72E-56
721.	ENSECAG00000019750	IL6ST	interleukin 6 cytokine family signal transducer	1,4211	4,82E-40
722.	ENSECAG00000020295	GEN1	GEN1 Holliday junction 5' flap endonuclease	1,4186	9,99E-17
723.	ENSECAG00000057046	ENSECAG00000057046		1,4149	0,012702

724.	ENSECAG00000034395	ENSECAG00000034395		1,4144	3,38E-39
725.	ENSECAG00000055030	ENSECAG00000055030		1,4133	1,49E-08
726.	ENSECAG00000008759	DRAM1	DNA damage regulated autophagy modulator 1	1,4118	1,61E-23
727.	ENSECAG00000010858	ANKRD37	ankyrin repeat domain 37	1,4108	7,93E-12
728.	ENSECAG00000014059	ECT2	epithelial cell transforming 2	1,4069	1,94E-27
729.	ENSECAG00000005447	GUCY1A1	guanylate cyclase 1 soluble subunit alpha 1	1,4039	0,000933
730.	ENSECAG00000039673	ENSECAG00000039673		1,4033	2,77E-51
731.	ENSECAG00000030805	ENSECAG00000030805		1,4025	7,3E-13
732.	ENSECAG00000015412	WDHD1	WD repeat and HMG-box DNA binding protein 1	1,402	3,29E-53
733.	ENSECAG00000045231	CHEK1	checkpoint kinase 1	1,4019	4,1E-11
734.	ENSECAG00000019382	S100A10	S100 calcium binding protein A10	1,4002	3,07E-10
735.	ENSECAG00000050186	ENSECAG00000050186		1,4002	1,39E-06
736.	ENSECAG00000015115	RHBDL1	rhomboid like 1	1,3994	3,7E-06
737.	ENSECAG00000015140	LIPG	lipase G, endothelial type	1,3988	2,82E-16
738.	ENSECAG00000013162	PCNA	proliferating cell nuclear antigen	1,3948	5,66E-43
739.	ENSECAG00000012132	ENSECAG00000012132		1,392	7,23E-28
740.	ENSECAG00000018634	UBASH3B	ubiquitin associated and SH3 domain containing B	1,3912	0,005073
741.	ENSECAG00000033714	ENSECAG00000033714		1,3896	0,002769
742.	ENSECAG00000020766	NHS	NHS actin remodeling regulator	1,3895	4,09E-12
743.	ENSECAG00000015102	MYOZ3	myozenin 3	1,3889	1,53E-05
744.	ENSECAG00000015249	REEP4	receptor accessory protein 4	1,3884	1,91E-22
745.	ENSECAG00000059103	IL36G	interleukin 36 gamma	1,3881	8,97E-05
746.	ENSECAG00000008517	PNMA2	PNMA family member 2	1,3874	1,13E-07
747.	ENSECAG00000010619	F12	coagulation factor XII	1,3868	2,05E-06
748.	ENSECAG00000017796	NCAPD2	non-SMC condensin I complex subunit D2	1,3846	9,63E-42
749.	ENSECAG00000010666	KNSTRN	kinetochore localized astrin (SPAG5) binding protein	1,3846	3,36E-14
750.	ENSECAG00000018503	PARP3	poly(ADP-ribose) polymerase family member 3	1,3841	1,14E-49
751.	ENSECAG00000030260	OR5D132P	olfactory receptor family 5 subfamily D member 132, pseudo	1,3838	0,004257
752.	ENSECAG00000017386	ITGA1	integrin subunit alpha 1	1,3828	1,81E-45
753.	ENSECAG00000015119	PHACTR1	phosphatase and actin regulator 1	1,3785	0,006889
754.	ENSECAG00000024138	CREG1	cellular repressor of E1A stimulateds 1	1,3783	5,25E-31
755.	ENSECAG00000044187	ENSECAG00000044187		1,3782	1,92E-28
756.	ENSECAG00000008358	ADA	adenosine deaminase	1,3778	6,98E-39
757.	ENSECAG00000017483	PSD3	pleckstrin and Sec7 domain containing 3	1,3776	1,06E-17
758.	ENSECAG00000006077	POLD1	DNA polymerase delta 1, catalytic subunit	1,3772	1,18E-18
759.	ENSECAG00000018544	SPDL1	spindle apparatus coiled-coil protein 1	1,3757	5,4E-28
760.	ENSECAG00000060206	ENSECAG00000060206		1,3756	2,88E-38
761.	ENSECAG00000044515	ENSECAG00000044515		1,3744	3,02E-21
762.	ENSECAG00000003029	CDC25C	cell division cycle 25C	1,3726	4,3E-14
763.	ENSECAG00000006801	NMI	N-myc and STAT interactor	1,3722	1,89E-43
764.	ENSECAG00000024182	VSTM4	V-set and transmembrane domain containing 4	1,3722	3,83E-68
765.	ENSECAG00000017127	CENPO	centromere protein O	1,3709	9,19E-12
766.	ENSECAG00000016173	TK1	thymidine kinase 1	1,3698	2,73E-15
767.	ENSECAG00000017482	RNF24	ring finger protein 24	1,3683	5,13E-79
768.	ENSECAG00000018887	PSMB8	proteasome 20S subunit beta 8	1,3647	8,66E-45
769.	ENSECAG00000018935	SRPX	sushi repeat containing protein X-linked	1,364	3,81E-27
770.	ENSECAG00000029763	5_8S_rRNA	5.8S ribosomal RNA	1,3636	0,000618
771.	ENSECAG00000000398	PITRM1	pitrilysin metalloproteinase 1	1,3604	3,55E-40
772.	ENSECAG00000013924	SERPIND1	serpin family D member 1	1,3604	0,010591
773.	ENSECAG00000041174	ENSECAG00000041174		1,3603	0,001036
774.	ENSECAG00000018012	SELENBP1	selenium binding protein 1	1,3567	0,000197
775.	ENSECAG00000000288	IL1R2	interleukin 1 receptor type 2	1,3555	0,009278
776.	ENSECAG00000007808	DCBLD1	discoidin, CUB and LCCL domain containing 1	1,3555	3,94E-24
777.	ENSECAG00000023113	SASS6	SAS-6 centriolar assembly protein	1,355	5,28E-22
778.	ENSECAG00000003944	ENSECAG00000003944		1,3527	9,66E-14
779.	ENSECAG00000057059	ENSECAG00000057059		1,3511	0,000235

780.	ENSECAG00000016383	USP53	ubiquitin specific peptidase 53	1,3508	4,12E-25
781.	ENSECAG00000035182	ENSECAG00000035182		1,3504	8,48E-22
782.	ENSECAG00000018444	NEFH	neurofilament heavy chain	1,3496	0,008046
783.	ENSECAG00000047032	ENSECAG00000047032		1,3492	0,009316
784.	ENSECAG00000015746	SMC1B	structural maintenance of chromosomes 1B	1,3475	5,75E-06
785.	ENSECAG00000035238	IFITM5	interferon induced transmembrane protein 5	1,3434	2,23E-17
786.	ENSECAG00000015438	SUV39H1	SUV39H1 histone lysine methyltransferase	1,3409	5,05E-13
787.	ENSECAG00000007470	NCAPG	non-SMC condensin I complex subunit G	1,3385	1,27E-28
788.	ENSECAG00000021857	ENSECAG00000021857		1,3351	0,00031
789.	ENSECAG00000020326	CLSTN3	calsyntenin 3	1,3333	1,61E-19
790.	ENSECAG00000013291	PER1	period circadian regulator 1	1,333	5,04E-24
791.	ENSECAG00000011558	RITA1	RBPJ interacting and tubulin associated 1	1,332	2,17E-22
792.	ENSECAG00000047831	ENSECAG00000047831		1,3312	4,23E-26
793.	ENSECAG00000047048	GARIN1A	golgi associated RAB2 interactor 1A	1,3284	1,01E-10
794.	ENSECAG00000008596	THEMIS2	thymocyte selection associated family member 2	1,3279	0,001382
795.	ENSECAG00000020448	UBE2T	ubiquitin conjugating enzyme E2 T	1,327	3,99E-10
796.	ENSECAG00000024214	FANCA	FA complementation group A	1,3233	2,18E-20
797.	ENSECAG00000031808	SAPCD2	suppressor APC domain containing 2	1,3227	3,98E-05
798.	ENSECAG00000023496	IRX3	iroquois homeobox 3	1,3221	4,59E-05
799.	ENSECAG00000021462	SFMBT2	Scm like with four mbt domains 2	1,3216	1,68E-17
800.	ENSECAG00000008466	BIRC5	baculoviral IAP repeat containing 5	1,3171	1,2E-13
801.	ENSECAG00000009553	CADM3	cell adhesion molecule 3	1,3156	4,01E-27
802.	ENSECAG00000023566	DHRS9	dehydrogenase/reductase 9	1,3154	1,93E-45
803.	ENSECAG00000011728	PYGL	glycogen phosphorylase L	1,3151	1,15E-41
804.	ENSECAG00000003345	ENO1	enolase 1	1,3121	7,63E-41
805.	ENSECAG00000031911	ENSECAG00000031911		1,3117	0,000427
806.	ENSECAG00000004590	TIPIN	TIMELESS interacting protein	1,3106	4,64E-33
807.	ENSECAG00000017894	CKAP2	cytoskeleton associated protein 2	1,307	4,51E-17
808.	ENSECAG00000013825	NOD1	nucleotide binding oligomerization domain containing 1	1,3062	1,05E-21
809.	ENSECAG00000016394	IL1R1	interleukin 1 receptor type 1	1,3057	4,57E-31
810.	ENSECAG00000021072	KNTC1	kinetochore associated 1	1,3053	1,66E-25
811.	ENSECAG00000010035	SCUBE2	signal peptide, CUB domain and EGF like domain containing 2	1,3046	3,59E-22
812.	ENSECAG00000024465	ERAP2	endoplasmic reticulum aminopeptidase 2	1,3041	2,8E-56
813.	ENSECAG00000001935	LRRC14B	leucine rich repeat containing 14B	1,3026	0,005121
814.	ENSECAG00000002958	LRRC4	leucine rich repeat containing 4	1,302	0,006249
815.	ENSECAG00000055909	ENSECAG00000055909		1,301	0,003219
816.	ENSECAG00000000122	GDA	guanine deaminase	1,3001	3,43E-32
817.	ENSECAG00000008281	SPATA20	spermatosis associated 20	1,299	0,000629
818.	ENSECAG00000047787	ENSECAG00000047787		1,2977	7E-14
819.	ENSECAG00000052890	ENSECAG00000052890		1,2977	1,93E-06
820.	ENSECAG00000019391	TNFSF10	TNF superfamily member 10	1,2948	2,7E-09
821.	ENSECAG00000017120	GINM1	glycosylated integral membrane protein 1	1,2943	7,16E-74
822.	ENSECAG00000020174	CENPW	centromere protein W	1,2941	3,8E-11
823.	ENSECAG00000010558	PTGFR	prostaglandin F receptor	1,2931	5,92E-23
824.	ENSECAG00000020125	BCR	BCR activator of RhoGEF and GTPase	1,293	5,55E-62
825.	ENSECAG00000000171	NPAS2	neuronal PAS domain protein 2	1,293	1,13E-19
826.	ENSECAG00000023134	KCNK5	potassium two pore domain channel subfamily K member 5	1,2923	4,27E-20
827.	ENSECAG00000004433	ENSECAG00000004433		1,2906	2,5E-10
828.	ENSECAG00000016971	TRERF1	transcriptional regulating factor 1	1,2882	1,51E-16
829.	ENSECAG00000011017	LMNB2	lamin B2	1,2865	1,14E-30
830.	ENSECAG00000007848	ITGA9	integrin subunit alpha 9	1,2862	2,09E-22
831.	ENSECAG00000034330	ENSECAG00000034330		1,2843	4,15E-08
832.	ENSECAG00000024522	POLH	DNA polymerase eta	1,284	2,06E-36
833.	ENSECAG00000016576	C1QTNF12	C1q and TNF related 12	1,2833	5,85E-06
834.	ENSECAG00000013659	TUBB4B	tubulin beta 4B class IVb	1,2812	7,71E-22
835.	ENSECAG00000008679	ACSL1	acyl-CoA synthetase long chain family member 1	1,281	1,45E-82

836.	ENSECAG00000022251	MAP3K15	mitogen-activated protein kinase kinase kinase 15	1,2802	0,001371
837.	ENSECAG00000015424	LIG1	DNA ligase 1	1,2799	1,63E-23
838.	ENSECAG00000033152	ENSECAG00000033152		1,279	7,13E-19
839.	ENSECAG00000025038	LOXL2	lysyl oxidase like 2	1,2784	1,55E-25
840.	ENSECAG00000052431	ENSECAG00000052431		1,2784	6,71E-08
841.	ENSECAG00000048720	ENSECAG00000048720		1,2751	4,16E-08
842.	ENSECAG00000023527	PHF19	PHD finger protein 19	1,275	4,3E-17
843.	ENSECAG00000011355	TRAF3IP3	TRAF3 interacting protein 3	1,2747	0,012881
844.	ENSECAG00000035538	ENSECAG00000035538		1,2746	0,010348
845.	ENSECAG00000004572	CH25H	cholesterol 25-hydroxylase	1,2742	8,42E-39
846.	ENSECAG00000017218	EPB41L1	erythrocyte membrane protein band 4.1 like 1	1,2721	1,8E-12
847.	ENSECAG00000004544	HRH1	histamine receptor H1	1,2705	7,63E-14
848.	ENSECAG00000021538	CKAP2L	cytoskeleton associated protein 2 like	1,2673	1,81E-15
849.	ENSECAG00000024862	HDX	highly divergent homeobox	1,2665	7,55E-05
850.	ENSECAG00000010069	XRCC2	X-ray repair cross complementing 2	1,2628	2,83E-08
851.	ENSECAG00000044966	ENSECAG00000044966		1,2623	3,76E-05
852.	ENSECAG00000046910	ENSECAG00000046910		1,26	0,000782
853.	ENSECAG00000037361	TMEM190	transmembrane protein 190	1,2593	0,015786
854.	ENSECAG00000003367	RAD51C	RAD51 paralog C	1,2561	2,08E-14
855.	ENSECAG00000014323	SKA3	spindle and kinetochore associated complex subunit 3	1,2541	7,23E-15
856.	ENSECAG00000015448	TAPBP	TAP binding protein	1,2527	1,89E-51
857.	ENSECAG00000014491	NLRC5	NLR family CARD domain containing 5	1,2509	6,76E-41
858.	ENSECAG00000012086	NECAB3	N-terminal EF-hand calcium binding protein 3	1,2477	2,46E-22
859.	ENSECAG00000000721	MYCBPAP	MYCBP associated protein	1,2476	7,46E-05
860.	ENSECAG00000059078	ENSECAG00000059078		1,2461	3,52E-28
861.	ENSECAG00000014774	MMP23	matrix metalloproteinase 23	1,2454	9,85E-14
862.	ENSECAG00000000684	KDM8	lysine demethylase 8	1,2432	3,44E-27
863.	ENSECAG00000016661	NR4A1	nuclear receptor subfamily 4 group A member 1	1,242	1,06E-13
864.	ENSECAG00000011993	THBS3	thrombospondin 3	1,2406	4,01E-21
865.	ENSECAG00000021211	COL15A1	collagen type XV alpha 1 chain	1,2406	7,72E-30
866.	ENSECAG00000009192	SRGN	serglycin	1,2405	0,000107
867.	ENSECAG00000016902	PRR16	proline rich 16	1,239	0,002675
868.	ENSECAG00000052464	APOLD1	apolipoprotein L domain containing 1	1,2381	0,013914
869.	ENSECAG00000006359	PDP2	pyruvate dehydrogenase phosphatase catalytic subunit 2	1,2379	1,82E-12
870.	ENSECAG00000008840	MCM6	minichromosome maintenance complex component 6	1,2377	1,37E-37
871.	ENSECAG00000018531	GEM	GTP binding protein overexpressed in skeletal muscle	1,236	1,6E-29
872.	ENSECAG00000025636	SNORD7	small nucleolar RNA, C/D box 7	1,2335	0,00611
873.	ENSECAG00000012830	CHN2	chimerin 2	1,2299	5,03E-09
874.	ENSECAG00000022705	IL16	interleukin 16	1,2265	3,38E-22
875.	ENSECAG00000011823	ARHGAP19	Rho GTPase activating protein 19	1,226	9,29E-08
876.	ENSECAG00000013771	PDE4D	phosphodiesterase 4D	1,2254	5,03E-32
877.	ENSECAG00000010059	CA9	carbonic anhydrase 9	1,2253	1,3E-07
878.	ENSECAG00000021301	MAN1A1	mannosidase alpha class 1A member 1	1,225	9,1E-55
879.	ENSECAG00000016722	CENPU	centromere protein U	1,2238	1,05E-28
880.	ENSECAG00000018864	CPNE2	copine 2	1,2232	5,13E-29
881.	ENSECAG00000019398	TFPI2	tissue factor pathway inhibitor 2	1,221	3,17E-22
882.	ENSECAG00000011475	ZNF703	zinc finger protein 703	1,2209	2,43E-14
883.	ENSECAG00000000949	GPR84	G protein-coupled receptor 84	1,2191	0,014785
884.	ENSECAG00000017143	ENSECAG00000017143		1,2186	0,000385
885.	ENSECAG00000021766	PCOLCE	procollagen C-endopeptidase enhancer	1,2186	4,9E-146
886.	ENSECAG00000012252	SLC17A9	solute carrier family 17 member 9	1,2185	3,23E-40
887.	ENSECAG00000010132	HMGB2	high mobility group box 2	1,2153	3,71E-28
888.	ENSECAG00000002250	SPRY2	sprouty RTK signaling antagonist 2	1,2132	7,28E-19
889.	ENSECAG00000038539	UBALD2	UBA like domain containing 2	1,2093	8,59E-27
890.	ENSECAG00000015739	TOPBP1	DNA topoisomerase II binding protein 1	1,2088	1,03E-44
891.	ENSECAG00000047970	ENSECAG00000047970		1,2063	0,000188
892.	ENSECAG00000001064	RET	ret proto-onco	1,2044	0,004179

893.	ENSECAG00000035532	ENSECAG00000035532		1,2041	1,94E-49
894.	ENSECAG00000002184	ENSECAG00000002184		1,204	0,004591
895.	ENSECAG00000000843	FOXC2	forkhead box C2	1,2025	0,009668
896.	ENSECAG00000047800	ENSECAG00000047800		1,202	6,53E-25
897.	ENSECAG00000007476	RELT	RELT TNF receptor	1,2011	2,91E-09
898.	ENSECAG00000023301	GPX8	glutathione peroxidase 8 (putative)	1,1997	1,23E-65
899.	ENSECAG00000011797	SOD2	superoxide dismutase 2	1,1988	9,18E-08
900.	ENSECAG00000054832	ENSECAG00000054832		1,1981	1,08E-09
901.	ENSECAG00000056325	SERPINB2	serpin family B member 2	1,1929	1,5E-10
902.	ENSECAG00000009634	IL17RC	interleukin 17 receptor C	1,1925	4,3E-17
903.	ENSECAG00000045453	ENSECAG00000045453		1,1922	0,00254
904.	ENSECAG00000018438	CEP55	centrosomal protein 55	1,191	4,42E-09
905.	ENSECAG00000001372	SYN1	synapsin I	1,1904	2,4E-05
906.	ENSECAG00000020789	SPON1	spondin 1	1,1881	3,69E-19
907.	ENSECAG00000017558	MLKL	mixed lineage kinase domain like pseudokinase	1,1879	3,67E-12
908.	ENSECAG00000023146	RDH13	retinol dehydrogenase 13	1,1869	2,6E-34
909.	ENSECAG00000018306	CREB3L1	cAMP responsive element binding protein 3 like 1	1,1853	5,71E-43
910.	ENSECAG00000012179	RGS2	regulator of G protein signaling 2	1,1848	1,61E-26
911.	ENSECAG00000001249	SOCS3	suppressor of cytokine signaling 3	1,1841	2,7E-15
912.	ENSECAG00000010055	RSAD2	radical S-adenosyl methionine domain containing 2	1,184	0,016694
913.	ENSECAG00000013870	CERCAM	cerebral endothelial cell adhesion molecule	1,1835	5,71E-38
914.	ENSECAG00000031050	ENSECAG00000031050		1,1832	0,000774
915.	ENSECAG00000019433	CDKN3	cyclin dependent kinase inhibitor 3	1,1781	4,69E-07
916.	ENSECAG00000014691	DENND3	DENN domain containing 3	1,1763	8,26E-21
917.	ENSECAG00000020669	LDHA	lactate dehydrogenase A	1,1727	4,07E-28
918.	ENSECAG00000021905	HK2	hexokinase 2	1,1726	2,94E-26
919.	ENSECAG00000002911	KCTD11	potassium channel tetramerization domain containing 11	1,1713	1,58E-17
920.	ENSECAG00000021909	TEDC1	tubulin epsilon and delta complex 1	1,1686	3,67E-11
921.	ENSECAG00000021598	ZFAND2A	zinc finger AN1-type containing 2A	1,1675	1,63E-15
922.	ENSECAG00000002377	SPESP1	sperm equatorial segment protein 1	1,1662	7,15E-33
923.	ENSECAG00000005082	LRRC3	leucine rich repeat containing 3	1,166	0,001336
924.	ENSECAG00000008923	THBS1	thrombospondin 1	1,1654	8,55E-27
925.	ENSECAG00000000781	ANKLE1	ankyrin repeat and LEM domain containing 1	1,1647	1,48E-09
926.	ENSECAG00000010916	TRAM2	translocation associated membrane protein 2	1,1646	2,45E-43
927.	ENSECAG00000016676	SEMA6D	semaphorin 6D	1,1621	2,86E-11
928.	ENSECAG00000017910	PSME2	proteasome activator subunit 2	1,1615	4,45E-42
929.	ENSECAG00000054242	ENSECAG00000054242		1,1614	9,23E-28
930.	ENSECAG00000011656	DPH5	diphthamide biosynthesis 5	1,1599	8,71E-23
931.	ENSECAG00000035160	MLNR	motilin receptor	1,1592	0,013681
932.	ENSECAG00000017598	IMPA2	inositol monophosphatase 2	1,1582	8,36E-10
933.	ENSECAG00000000874	ACKR1	atypical chemokine receptor 1	1,1566	4,85E-07
934.	ENSECAG00000019767	ENSECAG00000019767		1,1565	5,41E-25
935.	ENSECAG00000015547	MBOAT7	membrane bound O-acyltransferase domain containing 7	1,1555	5,87E-41
936.	ENSECAG00000014207	TENT5A	terminal nucleotidyltransferase 5A	1,1549	7,94E-14
937.	ENSECAG00000009576	MMS22L	MMS22 like, DNA repair protein	1,1544	6,55E-15
938.	ENSECAG00000021015	ATP8B1	ATPase phospholipid transporting 8B1	1,1533	1,05E-51
939.	ENSECAG00000051789	ENSECAG00000051789		1,151	9,23E-23
940.	ENSECAG00000010078	CIT	citron rho-interacting serine/threonine kinase	1,1501	1,87E-20
941.	ENSECAG00000022137	DNA2	DNA replication helicase/nuclease 2	1,1495	3,56E-08
942.	ENSECAG00000008049	EPOR	erythropoietin receptor	1,1492	6,18E-07
943.	ENSECAG00000023484	SKA1	spindle and kinetochore associated complex subunit 1	1,149	0,000133
944.	ENSECAG00000015297	PRIM1	DNA primase subunit 1	1,148	2,88E-22
945.	ENSECAG00000016854	ACSL4	acyl-CoA synthetase long chain family member 4	1,1474	1,94E-69
946.	ENSECAG00000021209	CRELD2	cysteine rich with EGF like domains 2	1,1465	1,04E-24
947.	ENSECAG00000010241	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	1,1442	1,55E-07
948.	ENSECAG00000032390	TNFRSF6B	TNF receptor superfamily member 6b	1,144	0,012875

949.	ENSECAG00000047793	ENSECAG00000047793		1,1416	0,01414
950.	ENSECAG00000000263	SLC35A2	solute carrier family 35 member A2	1,14	1,33E-25
951.	ENSECAG00000024590	SLC39A13	solute carrier family 39 member 13	1,1392	1,74E-49
952.	ENSECAG00000013089	FKBP10	FKBP prolyl isomerase 10	1,1382	1,31E-58
953.	ENSECAG00000010043	SATB2	SATB homeobox 2	1,1349	1,1E-05
954.	ENSECAG00000018874	PRICKLE1	prickle planar cell polarity protein 1	1,1349	2,97E-26
955.	ENSECAG00000024429	IRF9	interferon regulatory factor 9	1,1336	2,35E-16
956.	ENSECAG00000013731	STC1	stanniocalcin 1	1,1325	2,19E-05
957.	ENSECAG00000050881	ENSECAG00000050881		1,132	0,008237
958.	ENSECAG00000012414	ASPHD1	aspartate beta-hydroxylase domain containing 1	1,1302	4,43E-20
959.	ENSECAG00000024050	SCLT1	sodium channel and clathrin linker 1	1,13	7,82E-10
960.	ENSECAG00000006881	CKAP4	cytoskeleton associated protein 4	1,1288	1,34E-67
961.	ENSECAG00000002569	FLRT3	fibronectin leucine rich transmembrane protein 3	1,125	1,48E-11
962.	ENSECAG00000021764	WDR90	WD repeat domain 90	1,1248	2,65E-16
963.	ENSECAG00000022178	EBP	EBP cholesterol delta-isomerase	1,1187	1,81E-21
964.	ENSECAG00000012634	CEP78	centrosomal protein 78	1,118	1,26E-12
965.	ENSECAG00000007439	GRIN2C	glutamate ionotropic receptor NMDA type subunit 2C	1,1176	0,01502
966.	ENSECAG00000037807	ENSECAG00000037807		1,1154	0,000116
967.	ENSECAG00000022164	SMC4	structural maintenance of chromosomes 4	1,1152	4,01E-32
968.	ENSECAG00000009783	NRIP3	nuclear receptor interacting protein 3	1,1141	6,63E-07
969.	ENSECAG00000001407	CHSY3	chondroitin sulfate synthase 3	1,1133	6,73E-26
970.	ENSECAG00000009992	PGP	phosphoglycolate phosphatase	1,1114	1,17E-27
971.	ENSECAG00000031932	TMEM63C	transmembrane protein 63C	1,1112	0,001981
972.	ENSECAG00000017765	MYO1B	myosin IB	1,1101	1,82E-42
973.	ENSECAG00000024988	PARP14	poly(ADP-ribose) polymerase family member 14	1,1075	2,45E-39
974.	ENSECAG00000056686	ENSECAG00000056686		1,1068	0,015329
975.	ENSECAG00000023118	MCC	MCC regulator of WNT signaling pathway	1,1065	4,63E-27
976.	ENSECAG00000023280	FADS1	fatty acid desaturase 1	1,1055	1,22E-54
977.	ENSECAG00000059651	ENSECAG00000059651		1,1055	0,001382
978.	ENSECAG00000024406	KCP	kielin cysteine rich BMP regulator	1,1035	0,0023
979.	ENSECAG00000006418	H3C12	H3 clustered histone 12	1,1022	0,013605
980.	ENSECAG00000016855	PSME1	proteasome activator subunit 1	1,1021	1,74E-47
981.	ENSECAG00000017197	RANBP1	RAN binding protein 1	1,1006	1,05E-51
982.	ENSECAG00000018367	ZWILCH	zwilch kinetochore protein	1,1003	3,17E-27
983.	ENSECAG00000008700	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	1,0992	0,00801
984.	ENSECAG00000017922	ADAM19	ADAM metalloproteinase domain 19	1,0983	1,3E-50
985.	ENSECAG00000016606	LPAR1	lysophosphatidic acid receptor 1	1,0977	3,87E-39
986.	ENSECAG00000013124	BCL3	BCL3 transcription coactivator	1,0958	5,35E-22
987.	ENSECAG00000015218	DBF4B	DBF4 zinc finger B	1,0938	6,6E-05
988.	ENSECAG00000026827	ENSECAG00000026827		1,0936	5,83E-15
989.	ENSECAG00000006445	CDCA4	cell division cycle associated 4	1,0935	1,95E-28
990.	ENSECAG00000009864	PTPRD	protein tyrosine phosphatase receptor type D	1,0926	5,95E-09
991.	ENSECAG00000006204	CCDC73	coiled-coil domain containing 73	1,0923	0,00047
992.	ENSECAG00000022780	TTYH2	tweety family member 2	1,0912	0,000462
993.	ENSECAG00000015780	ADRB3	adrenoceptor beta 3	1,0896	0,017141
994.	ENSECAG00000013636	HELZ2	helicase with zinc finger 2	1,0889	1,66E-25
995.	ENSECAG00000017845	GGCT	gamma-glutamylcyclotransferase	1,0881	1,55E-06
996.	ENSECAG00000011711	SUSD6	sushi domain containing 6	1,086	3,77E-31
997.	ENSECAG00000022933	ELL2	elongation factor for RNA polymerase II 2	1,0847	7,36E-30
998.	ENSECAG00000021529	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit	1,0815	1E-13
999.	ENSECAG00000014563	POLR1F	RNA polymerase I subunit F	1,0802	1,52E-22
1000.	ENSECAG00000008609	TACR2	tachykinin receptor 2	1,0796	0,002626
1001.	ENSECAG00000048969	ENSECAG00000048969		1,0792	9,61E-07
1002.	ENSECAG00000019125	FASN	fatty acid synthase	1,0771	9,32E-21
1003.	ENSECAG00000024654	CD81	CD81 molecule	1,0769	4,82E-40
1004.	ENSECAG00000011978	LRR1	leucine rich repeat protein 1	1,0766	2,99E-07
1005.	ENSECAG00000039860	EXOSC6	exosome component 6	1,0747	1,43E-09

1006.	ENSECAG00000021289	CCNE1	cyclin E1	1,0736	1,12E-10
1007.	ENSECAG00000007588	EREGB	epiregulin	1,0734	2,68E-07
1008.	ENSECAG00000059075	FAM180A	family with sequence similarity 180 member A	1,0714	5,11E-11
1009.	ENSECAG00000056346	ENSECAG00000056346		1,0714	0,001759
1010.	ENSECAG00000045610	ENSECAG00000045610		1,071	8,15E-05
1011.	ENSECAG00000021358	SFRP1	secreted frizzled related protein 1	1,0709	6,58E-32
1012.	ENSECAG00000009676	SAP30	Sin3A associated protein 30	1,0689	1,89E-19
1013.	ENSECAG00000021799	MYRF	myelin regulatory factor	1,0677	1,09E-06
1014.	ENSECAG00000051098	ENSECAG00000051098		1,0673	0,026585
1015.	ENSECAG00000015149	MCM7	minichromosome maintenance complex component 7	1,0655	4,49E-48
1016.	ENSECAG00000037706	GMFG	glia maturation factor gamma	1,0655	0,007771
1017.	ENSECAG00000035032	NXT1	nuclear transport factor 2 like export factor 1	1,0653	3,43E-27
1018.	ENSECAG00000031941	ENSECAG00000031941		1,0632	0,000889
1019.	ENSECAG00000000579	ADAMTS17	ADAM metalloproteinase with thrombospondin type 1 motif 17	1,0629	1,68E-10
1020.	ENSECAG00000030024	MAPK13	mitogen-activated protein kinase 13	1,0623	0,000249
1021.	ENSECAG00000025101	NELL2	neural EGFL like 2	1,0608	0,000103
1022.	ENSECAG00000019253	CBX8	chromobox 8	1,06	4,56E-07
1023.	ENSECAG00000011882	THOP1	thimet oligopeptidase 1	1,0597	8,32E-38
1024.	ENSECAG00000010720	ELOVL6	ELOVL fatty acid elongase 6	1,0591	3,73E-18
1025.	ENSECAG00000005228	PHGDH	phosphoglycerate dehydrogenase	1,0588	2,6E-19
1026.	ENSECAG00000019410	FXVD5	FXVD domain containing ion transport regulator 5	1,0587	4,75E-28
1027.	ENSECAG00000012035	HAUS5	HAUS augmin like complex subunit 5	1,0585	1,19E-11
1028.	ENSECAG00000019890	VRK1	VRK serine/threonine kinase 1	1,058	7,31E-11
1029.	ENSECAG00000024967	CTSZ	cathepsin Z	1,0578	7,8E-27
1030.	ENSECAG00000032492	ENSECAG00000032492		1,0577	0,002191
1031.	ENSECAG00000015446	PLP1	proteolipid protein 1	1,0571	0,010292
1032.	ENSECAG00000021614	RFC3	replication factor C subunit 3	1,0546	7E-08
1033.	ENSECAG00000010356	FAM78A	family with sequence similarity 78 member A	1,0542	0,018987
1034.	ENSECAG00000032606	ENSECAG00000032606		1,0535	0,000294
1035.	ENSECAG00000020036	KRT10A	keratin 10A	1,0534	9,71E-11
1036.	ENSECAG00000004444	C26H21orf91	chromosome 26 C21orf91 homolog	1,0533	3,7E-14
1037.	ENSECAG00000021815	P3H3	prolyl 3-hydroxylase 3	1,0528	1,05E-51
1038.	ENSECAG00000004339	MIS18BP1	MIS18 binding protein 1	1,0525	3,43E-20
1039.	ENSECAG00000015009	UGDH	UDP-glucose 6-dehydrogenase	1,0467	4,7E-34
1040.	ENSECAG00000019989	SNRPG	small nuclear ribonucleoprotein polypeptide G	1,046	5,53E-27
1041.	ENSECAG00000016545	SDK1	sidekick cell adhesion molecule 1	1,0458	2,52E-25
1042.	ENSECAG00000014231	TONSL	tonsoku like, DNA repair protein	1,0431	7,78E-30
1043.	ENSECAG00000010786	PGAM1	phosphoglycerate mutase 1	1,043	5,43E-27
1044.	ENSECAG00000022964	CDC7	cell division cycle 7	1,0422	1,02E-20
1045.	ENSECAG00000010512	RCN3	reticulocalbin 3	1,0413	1,05E-51
1046.	ENSECAG00000059551	TUBA1B	tubulin alpha 1b	1,0412	1,3E-45
1047.	ENSECAG00000017630	MOCOS	molybdenum cofactor sulfurase	1,0388	2,69E-19
1048.	ENSECAG00000026912	CENPH	centromere protein H	1,0388	2,96E-14
1049.	ENSECAG00000017109	QSOX1	quiescin sulphydryl oxidase 1	1,0372	1,42E-45
1050.	ENSECAG00000021428	GYS1	glycogen synthase 1	1,037	1,03E-30
1051.	ENSECAG00000011530	MOV10	Mov10 RISC complex RNA helicase	1,0365	1,24E-45
1052.	ENSECAG00000019266	SLC35F2	solute carrier family 35 member F2	1,0357	8,25E-27
1053.	ENSECAG00000023847	RRM1	ribonucleotide reductase catalytic subunit M1	1,0347	4,83E-35
1054.	ENSECAG00000023266	OSBPL10	oxysterol binding protein like 10	1,0335	1,44E-29
1055.	ENSECAG00000036729	C1QL1	complement C1q like 1	1,0331	0,015955
1056.	ENSECAG00000016522	SCG3	secretogranin III	1,0326	7,4E-09
1057.	ENSECAG00000000367	RFC2	replication factor C subunit 2	1,032	1,08E-24
1058.	ENSECAG00000012954	ORAI1	ORAI calcium release-activated calcium modulator 1	1,0311	5,11E-12
1059.	ENSECAG00000007133	TPPP3	tubulin polymerization promoting protein family member 3	1,0309	0,010856
1060.	ENSECAG00000017324	ENSECAG00000017324		1,028	1,29E-12
1061.	ENSECAG00000018995	CD47	CD47 molecule	1,0273	1,41E-33
1062.	ENSECAG00000017487	MXRA5	matrix remodeling associated 5	1,0258	7,54E-08

1063.	ENSECAG00000018024	TMEM150C	transmembrane protein 150C	1,0244	9,64E-05
1064.	ENSECAG00000003669	HLA-DMA	major histocompatibility complex, class II, DM alpha	1,0221	8,71E-07
1065.	ENSECAG00000055995	ENSECAG00000055995		1,0199	0,01797
1066.	ENSECAG00000020093	NPR3	natriuretic peptide receptor 3	1,0187	4,17E-05
1067.	ENSECAG00000013693	COL1A1	collagen type I alpha 1 chain	1,0174	3,8E-08
1068.	ENSECAG00000010468	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	1,0167	7,83E-28
1069.	ENSECAG00000020252	PDIA3	protein disulfide isomerase family A member 3	1,0165	5,99E-34
1070.	ENSECAG00000042118	XNDC1	XRCC1 N-terminal domain containing 1	1,0157	3,17E-09
1071.	ENSECAG00000023472	KCNK2	potassium two pore domain channel subfamily K member 2	1,0146	0,001044
1072.	ENSECAG00000015396	KIF17	kinesin family member 17	1,0142	0,021619
1073.	ENSECAG00000000015	KIAA1217	KIAA1217	1,0136	1,98E-05
1074.	ENSECAG00000046292	ENSECAG00000046292		1,0123	0,013189
1075.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,0092	2,64E-24
1076.	ENSECAG00000007351	PLAU	plasminogen activator, urokinase	1,0084	7,05E-60
1077.	ENSECAG00000023693	ECI1	enoyl-CoA delta isomerase 1	1,0069	1,19E-35
1078.	ENSECAG00000024786	PSMC3	proteasome 26S subunit, ATPase 3	1,0062	1,66E-68
1079.	ENSECAG00000012945	TPST2	tyrosylprotein sulfotransferase 2	1,005	1,78E-07
1080.	ENSECAG00000023588	EHHADH	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase	1,0047	5,23E-14
1081.	ENSECAG00000022323	PSMC3IP	PSMC3 interacting protein	1,0034	7,63E-10
1082.	ENSECAG00000047393	ENSECAG00000047393		1,0031	0,005851
1083.	ENSECAG00000007444	MOB3A	MOB kinase activator 3A	1,0001	3,63E-26
1084.	ENSECAG00000011007	ACAD8	acyl-CoA dehydrogenase family member 8	-1	4,45E-16
1085.	ENSECAG00000052116	EPB41L5	erythrocyte membrane protein band 4.1 like 5	-1,001	1,29E-09
1086.	ENSECAG00000008808	NTNG2	netrin G2	-1,001	1,55E-05
1087.	ENSECAG00000045190	ENSECAG00000045190		-1,001	4,97E-05
1088.	ENSECAG00000007498	AP1AR	adaptor related protein complex 1 associated regulatory protein	-1,002	7,55E-19
1089.	ENSECAG00000022741	CDC42EP3	CDC42 effector protein 3	-1,002	2,11E-11
1090.	ENSECAG00000006696	TMTC4	transmembrane O-mannosyltransferase targeting cadherins 4	-1,003	3,33E-19
1091.	ENSECAG00000013382	SLC25A34	solute carrier family 25 member 34	-1,003	3,9E-06
1092.	ENSECAG00000019793	SETBP1	SET binding protein 1	-1,005	4,52E-13
1093.	ENSECAG00000030788	DIO2	iodothyronine deiodinase 2	-1,005	1,9E-07
1094.	ENSECAG00000031389	CDKN1C	cyclin dependent kinase inhibitor 1C	-1,007	5,48E-08
1095.	ENSECAG00000048330	ENSECAG00000048330		-1,008	0,002898
1096.	ENSECAG00000009954	OTOGL	otogelin like	-1,009	0,00944
1097.	ENSECAG00000019505	PAWR	pro-apoptotic WT1 regulator	-1,01	6,92E-14
1098.	ENSECAG00000002021	ENSECAG00000002021		-1,012	3,6E-05
1099.	ENSECAG00000058540	ENSECAG00000058540		-1,013	0,018321
1100.	ENSECAG00000000203	TRPA1	transient receptor potential cation channel subfamily A member 1	-1,013	0,002183
1101.	ENSECAG00000015764	ARHGAP36	Rho GTPase activating protein 36	-1,014	0,000654
1102.	ENSECAG00000029829	RGS9	regulator of G protein signaling 9	-1,016	4,44E-05
1103.	ENSECAG00000008538	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	-1,016	1,53E-18
1104.	ENSECAG00000050821	ENSECAG00000050821		-1,016	0,031937
1105.	ENSECAG00000045759	ENSECAG00000045759		-1,017	1,78E-11
1106.	ENSECAG00000003209	ZNF772	zinc finger protein 772	-1,017	9,61E-05
1107.	ENSECAG00000020085	RELL2	RELT like 2	-1,017	0,001666
1108.	ENSECAG00000013789	EPN2	epsin 2	-1,017	6,27E-17
1109.	ENSECAG00000014440	DISP1	dispatched RND transporter family member 1	-1,019	1,13E-14
1110.	ENSECAG00000041701	ENSECAG00000041701		-1,019	0,009878
1111.	ENSECAG00000020599	HOXD10	homeobox D10	-1,02	3,93E-13
1112.	ENSECAG00000019226	CASTOR2	cytosolic arginine sensor for mTORC1 subunit 2	-1,02	2,87E-12
1113.	ENSECAG00000054634	ENSECAG00000054634		-1,021	0,000101
1114.	ENSECAG00000015389	SV2B	synaptic vesicle glycoprotein 2B	-1,021	0,018989
1115.	ENSECAG00000000343	HACD4	3-hydroxyacyl-CoA dehydratase 4	-1,023	0,011487

1116.	ENSECAG00000019509	IGF2R	insulin like growth factor 2 receptor	-1,023	7,62E-58
1117.	ENSECAG00000056693	ENSECAG00000056693		-1,024	7,95E-36
1118.	ENSECAG00000017297	GRIA3	glutamate ionotropic receptor AMPA type subunit 3	-1,025	5,93E-12
1119.	ENSECAG00000023791	SLC16A11	solute carrier family 16 member 11	-1,025	3,81E-11
1120.	ENSECAG00000052201	ENSECAG00000052201		-1,026	0,008671
1121.	ENSECAG00000023626	PTGIR	prostaglandin I2 receptor	-1,028	0,016496
1122.	ENSECAG00000017059	OTULINL	OTU deubiquitinase with linear linkage specificity like	-1,028	1,77E-23
1123.	ENSECAG00000056511	ENSECAG00000056511		-1,028	0,015139
1124.	ENSECAG00000018928	PER3	period circadian regulator 3	-1,028	7,84E-15
1125.	ENSECAG00000000927	ENSECAG00000000927		-1,029	9,27E-05
1126.	ENSECAG00000020278	RAP1GAP2	RAP1 GTPase activating protein 2	-1,029	0,001175
1127.	ENSECAG00000000014	GAS6	growth arrest specific 6	-1,029	1,48E-14
1128.	ENSECAG00000013284	PTGR2	prostaglandin reductase 2	-1,03	2,72E-15
1129.	ENSECAG00000020932	SVIL	supervillin	-1,03	1,24E-07
1130.	ENSECAG00000032483	GPR85	G protein-coupled receptor 85	-1,031	0,000837
1131.	ENSECAG00000006777	CFAP46	cilia and flagella associated protein 46	-1,031	2,09E-05
1132.	ENSECAG00000010574	KLHL7	kelch like family member 7	-1,032	4,05E-31
1133.	ENSECAG00000008298	WNT10B	Wnt family member 10B	-1,032	0,000119
1134.	ENSECAG00000046287	ENSECAG00000046287		-1,032	0,007036
1135.	ENSECAG00000000420	BANP	BTG3 associated nuclear protein	-1,032	6,06E-10
1136.	ENSECAG00000003045	HOXD11	homeobox D11	-1,032	1,91E-25
1137.	ENSECAG00000008425	LURAP1L	leucine rich adaptor protein 1 like	-1,033	0,000504
1138.	ENSECAG00000019025	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	-1,035	0,00106
1139.	ENSECAG00000033399	TSC22D3	TSC22 domain family member 3	-1,036	2,27E-16
1140.	ENSECAG00000004437	SH3GLB2	SH3 domain containing GRB2 like, endophilin B2	-1,037	1,35E-15
1141.	ENSECAG00000014142	PRKCI	protein kinase C iota	-1,037	8,14E-21
1142.	ENSECAG00000018131	CTNNAL1	catenin alpha like 1	-1,038	2,15E-21
1143.	ENSECAG00000046273	GVQW3	GVQW motif containing 3	-1,04	4,26E-08
1144.	ENSECAG00000001230	CCDC153	coiled-coil domain containing 153	-1,04	0,025466
1145.	ENSECAG00000000331	KDM1B	lysine demethylase 1B	-1,041	3,11E-24
1146.	ENSECAG00000020944	SLC25A4	solute carrier family 25 member 4	-1,042	9,65E-12
1147.	ENSECAG00000012963	TBCEL	tubulin folding cofactor E like	-1,042	2,71E-31
1148.	ENSECAG00000024399	FGF12	fibroblast growth factor 12	-1,042	0,00241
1149.	ENSECAG00000059658	ENSECAG00000059658		-1,043	7,29E-09
1150.	ENSECAG00000040891	ENSECAG00000040891		-1,043	9,07E-06
1151.	ENSECAG00000006162	GRINA	glutamate ionotropic receptor NMDA type subunit associated protein 1	-1,044	1,9E-07
1152.	ENSECAG00000018739	GRIK5	glutamate ionotropic receptor kainate type subunit 5	-1,044	1,74E-08
1153.	ENSECAG00000012109	SOSTDC1	sclerostin domain containing 1	-1,044	0,017607
1154.	ENSECAG00000045464	ENSECAG00000045464		-1,045	1,09E-29
1155.	ENSECAG00000004450	ZBTB5	zinc finger and BTB domain containing 5	-1,045	1,25E-12
1156.	ENSECAG00000010245	ZNF365	zinc finger protein 365	-1,046	8,82E-09
1157.	ENSECAG00000010869	CAPN6	calpain 6	-1,046	0,022577
1158.	ENSECAG00000017641	PTPN21	protein tyrosine phosphatase non-receptor type 21	-1,046	2,41E-27
1159.	ENSECAG00000002986	GHR	growth hormone receptor	-1,047	3,2E-22
1160.	ENSECAG00000024278	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	-1,047	5,86E-25
1161.	ENSECAG00000012771	ALOXE3	arachidonate lipooxygenase 3	-1,047	5,62E-08
1162.	ENSECAG00000002522	RAB15	RAB15, member RAS onco family	-1,048	3,93E-22
1163.	ENSECAG00000018808	TG	thyroglobulin	-1,048	0,016095
1164.	ENSECAG00000014636	WDR27	WD repeat domain 27	-1,048	0,000573
1165.	ENSECAG00000004270	MED7	mediator complex subunit 7	-1,048	3,8E-14
1166.	ENSECAG00000059570	PLEKHO1	pleckstrin homology domain containing O1	-1,052	1,29E-30
1167.	ENSECAG00000038257	PKN1	protein kinase N1	-1,052	7,8E-25
1168.	ENSECAG00000036444	ENSECAG00000036444		-1,053	0,015642
1169.	ENSECAG00000006153	C5AR1	complement C5a receptor 1	-1,054	0,02043
1170.	ENSECAG00000010120	SNAI2	snail family transcriptional repressor 2	-1,054	2,52E-14
1171.	ENSECAG00000020666	ZNF311	zinc finger protein 311	-1,055	0,000433
1172.	ENSECAG00000021969	ITGB6	integrin subunit beta 6	-1,055	0,007095

1173.	ENSECAG00000012801	KBTBD3	kelch repeat and BTB domain containing 3	-1,055	0,000323
1174.	ENSECAG00000013487	URAH	urate (hydroxyiso-) hydrolase	-1,056	4,54E-05
1175.	ENSECAG00000042479	ENSECAG00000042479		-1,057	4,32E-07
1176.	ENSECAG00000012260	FAM118A	family with sequence similarity 118 member A	-1,057	1,45E-20
1177.	ENSECAG00000015083	EAF2	ELL associated factor 2	-1,057	3,77E-20
1178.	ENSECAG00000016225	TMEM144	transmembrane protein 144	-1,058	0,017274
1179.	ENSECAG00000010414	PON2	paraoxonase 2	-1,058	2,76E-06
1180.	ENSECAG00000026972	DACT3	dishevelled binding antagonist of beta catenin 3	-1,058	1,83E-13
1181.	ENSECAG00000009893	CDK19	cyclin dependent kinase 19	-1,058	3,22E-52
1182.	ENSECAG00000023477	STN1	STN1 subunit of CST complex	-1,059	1,19E-10
1183.	ENSECAG00000013024	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	-1,062	7,09E-06
1184.	ENSECAG00000013156	LAD1	ladinin 1	-1,063	9,43E-05
1185.	ENSECAG00000016361	COL18A1	collagen type XVIII alpha 1 chain	-1,063	3,07E-25
1186.	ENSECAG00000044465	ENSECAG00000044465		-1,064	0,015665
1187.	ENSECAG00000014993	SCNN1B	sodium channel epithelial 1 subunit beta	-1,064	0,025225
1188.	ENSECAG00000020875	RUNX2	RUNX family transcription factor 2	-1,064	9,96E-25
1189.	ENSECAG00000000650	NPL	N-acetylneuraminate pyruvate lyase	-1,067	7,03E-14
1190.	ENSECAG00000014410	CASZ1	castor zinc finger 1	-1,068	0,028335
1191.	ENSECAG00000003007	ZNF391	zinc finger protein 391	-1,068	1,32E-15
1192.	ENSECAG00000001634	INSYN1	inhibitory synaptic factor 1	-1,069	2,4E-23
1193.	ENSECAG000000021239	CCDC92	coiled-coil domain containing 92	-1,069	2,7E-09
1194.	ENSECAG000000011229	SLC1A4	solute carrier family 1 member 4	-1,07	3,96E-47
1195.	ENSECAG00000011829	PID1	phosphotyrosine interaction domain containing 1	-1,071	8,1E-35
1196.	ENSECAG00000020590	ALDH5A1	aldehyde dehydrogenase 5 family member A1	-1,071	1,58E-07
1197.	ENSECAG00000048239	ENSECAG00000048239		-1,073	0,002442
1198.	ENSECAG00000019616	ACVR2B	activin A receptor type 2B	-1,074	8,15E-06
1199.	ENSECAG00000026917	FOXN3	forkhead box N3	-1,075	8,26E-21
1200.	ENSECAG00000003353	RPP25	ribonuclease P and MRP subunit p25	-1,075	0,010689
1201.	ENSECAG00000013135	PLS3	plastin 3	-1,075	7,71E-38
1202.	ENSECAG00000020957	LCN2	lipocalin 2	-1,078	8,8E-16
1203.	ENSECAG00000012987	DIXDC1	DIX domain containing 1	-1,078	1,7E-31
1204.	ENSECAG00000054917	PRCD		-1,079	0,014748
1205.	ENSECAG00000019338	DRC3	dynein regulatory complex subunit 3	-1,079	0,000343
1206.	ENSECAG00000059626	ENSECAG00000059626		-1,08	0,000877
1207.	ENSECAG00000007646	NR1D2	nuclear receptor subfamily 1 group D member 2	-1,081	3,07E-38
1208.	ENSECAG00000054635	ENSECAG00000054635		-1,082	1,06E-06
1209.	ENSECAG00000013579	COPG2	COPI coat complex subunit gamma 2	-1,082	1,45E-21
1210.	ENSECAG00000008465	STRBP	spermatid perinuclear RNA binding protein	-1,083	2,36E-13
1211.	ENSECAG00000008098	TCF7	transcription factor 7	-1,083	0,008819
1212.	ENSECAG00000009911	SLC12A7	solute carrier family 12 member 7	-1,084	3,25E-08
1213.	ENSECAG00000015950	CCDC68	coiled-coil domain containing 68	-1,084	3,41E-11
1214.	ENSECAG00000047356	ENSECAG00000047356		-1,084	6,75E-06
1215.	ENSECAG00000044157	ENSECAG00000044157		-1,084	6,91E-07
1216.	ENSECAG00000028267	CYP2C11	cytochrome P450 family 2 subfamily C member 11	-1,085	1,24E-11
1217.	ENSECAG00000020749	SCN2A	sodium voltage-gated channel alpha subunit 2	-1,087	3,4E-05
1218.	ENSECAG00000037214	TUBB4A	tubulin beta 4A class IVa	-1,087	0,001555
1219.	ENSECAG00000056232	ENSECAG00000056232		-1,088	3,4E-05
1220.	ENSECAG00000033234	CBLN2	cerebellin 2 precursor	-1,088	0,000857
1221.	ENSECAG00000043452	ENSECAG00000043452		-1,089	0,005969
1222.	ENSECAG00000022166	AKAP12	A-kinase anchoring protein 12	-1,089	1,56E-43
1223.	ENSECAG00000008975	PPM1H	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1H	-1,089	1,16E-15
1224.	ENSECAG00000022258	SDSL	serine dehydratase like	-1,089	0,001486
1225.	ENSECAG00000019807	CASQ1	calsequestrin 1	-1,089	0,017487
1226.	ENSECAG00000044680	ENSECAG00000044680		-1,09	0,020408
1227.	ENSECAG00000010856	TSHZ2	teashirt zinc finger homeobox 2	-1,09	2,06E-17
1228.	ENSECAG00000044441	ENSECAG00000044441		-1,09	0,00054
1229.	ENSECAG00000022594	SCEL	sciellin	-1,091	0,012524

1230.	ENSECAG00000054770	ENSECAG00000054770		-1,091	1,23E-06
1231.	ENSECAG00000014952	CYRIA	CYFIP related Rac1 interactor A	-1,092	2,62E-20
1232.	ENSECAG00000059097	ENSECAG00000059097		-1,093	9,36E-13
1233.	ENSECAG00000017264	FAM171A2	family with sequence similarity 171 member A2	-1,094	0,002121
1234.	ENSECAG00000016720	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	-1,094	0,000329
1235.	ENSECAG00000008487	ATL1	atlastin GTPase 1	-1,094	2,58E-06
1236.	ENSECAG00000022432	PLEKHH1	pleckstrin homology, MyTH4 and FERM domain containing H1	-1,094	5,02E-08
1237.	ENSECAG00000007309	FZD5	frizzled class receptor 5	-1,097	8,01E-16
1238.	ENSECAG00000000026	XG	Xg glycoprotein	-1,098	1,71E-20
1239.	ENSECAG00000012083	ATP2A3	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 3	-1,098	2,52E-09
1240.	ENSECAG00000020702	NPHP1	nephrocystin 1	-1,099	6,22E-11
1241.	ENSECAG00000052406	ENSECAG00000052406		-1,1	1,19E-06
1242.	ENSECAG00000024842	SH3BP5	SH3 domain binding protein 5	-1,101	2,84E-41
1243.	ENSECAG00000047193	ENSECAG00000047193		-1,104	0,000214
1244.	ENSECAG00000049707	ENSECAG00000049707		-1,107	3,19E-05
1245.	ENSECAG00000024216	SLC25A27	solute carrier family 25 member 27	-1,108	6,94E-09
1246.	ENSECAG00000015026	C9orf50	chromosome 9 open reading frame 50	-1,109	3,39E-05
1247.	ENSECAG00000012235	BAZ2B	bromodomain adjacent to zinc finger domain 2B	-1,109	5,88E-26
1248.	ENSECAG00000040835	ENSECAG00000040835		-1,109	0,009187
1249.	ENSECAG00000009099	TCP11L2	t-complex 11 like 2	-1,11	1,09E-24
1250.	ENSECAG00000012368	ZNF385D	zinc finger protein 385D	-1,11	6,47E-06
1251.	ENSECAG00000015444	SLC37A1	solute carrier family 37 member 1	-1,111	2,86E-10
1252.	ENSECAG00000018677	SCTR	secretin receptor	-1,111	0,010183
1253.	ENSECAG00000015608	CRIM1	cysteine rich transmembrane BMP regulator 1	-1,111	5,45E-07
1254.	ENSECAG00000053838	SOCS5	suppressor of cytokine signaling 5	-1,113	1,95E-29
1255.	ENSECAG00000008799	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-1,113	3,41E-06
1256.	ENSECAG00000058607	FAM171B	family with sequence similarity 171 member B	-1,113	5,11E-21
1257.	ENSECAG00000018924	PTK2B	protein tyrosine kinase 2 beta	-1,114	4,52E-09
1258.	ENSECAG00000043020	ENSECAG00000043020		-1,115	2,04E-05
1259.	ENSECAG00000028052	ZNF575	zinc finger protein 575	-1,118	5,71E-07
1260.	ENSECAG00000050008	ENSECAG00000050008		-1,118	9,86E-05
1261.	ENSECAG00000014003	TMEM192	transmembrane protein 192	-1,118	6,06E-23
1262.	ENSECAG00000000586	KIFC2	kinesin family member C2	-1,12	5,24E-05
1263.	ENSECAG00000013243	ANKRD45	ankyrin repeat domain 45	-1,12	0,000257
1264.	ENSECAG00000010966	TSPAN2	tetraspanin 2	-1,12	0,020872
1265.	ENSECAG00000032694	HMGN3	high mobility group nucleosomal binding domain 3	-1,121	1,03E-16
1266.	ENSECAG00000023978	ENSECAG00000023978		-1,122	1,06E-09
1267.	ENSECAG00000059096	ENSECAG00000059096		-1,123	0,018646
1268.	ENSECAG00000011659	KIAA1549	KIAA1549	-1,123	5,81E-10
1269.	ENSECAG00000032923	ENSECAG00000032923		-1,125	3,55E-15
1270.	ENSECAG00000033101	ZSWIM9	zinc finger SWIM-type containing 9	-1,126	0,002406
1271.	ENSECAG00000017943	ZNF608	zinc finger protein 608	-1,127	1,52E-05
1272.	ENSECAG00000034367	ENSECAG00000034367		-1,131	0,003818
1273.	ENSECAG00000012680	N4BP2L1	NEDD4 binding protein 2 like 1	-1,133	1,27E-17
1274.	ENSECAG00000021865	UST	uronyl 2-sulfotransferase	-1,135	3,59E-33
1275.	ENSECAG00000022703	LY5	lymphocyte antigen 75	-1,135	7,1E-09
1276.	ENSECAG00000053590	ENSECAG00000053590		-1,135	0,000825
1277.	ENSECAG00000013597	DAB2	DAB adaptor protein 2	-1,135	6,48E-40
1278.	ENSECAG00000016826	SGPL1	sphingosine-1-phosphate lyase 1	-1,136	2,6E-29
1279.	ENSECAG00000014275	DBP	D-box binding PAR bZIP transcription factor	-1,136	2,97E-10
1280.	ENSECAG00000049339	ENSECAG00000049339		-1,137	3,7E-05
1281.	ENSECAG00000011871	DNER	delta/notch like EGF repeat containing	-1,137	1,57E-08
1282.	ENSECAG00000034308	TRIM6	tripartite motif containing 6	-1,138	0,004562
1283.	ENSECAG00000058755	ENSECAG00000058755		-1,138	0,01389
1284.	ENSECAG00000058674	ENSECAG00000058674		-1,139	8,36E-05
1285.	ENSECAG00000040848	ENSECAG00000040848		-1,14	0,009295
1286.	ENSECAG00000013832	DES	desmin	-1,14	6,05E-08

1287.	ENSECAG00000024315	TARS3	threonyl-tRNA synthetase 3	-1,141	2,61E-05
1288.	ENSECAG00000020400	ENO3	enolase 3	-1,141	7,92E-08
1289.	ENSECAG00000000897	ITGAE	integrin subunit alpha E	-1,142	5,51E-11
1290.	ENSECAG00000046716	ENSECAG00000046716		-1,144	0,022269
1291.	ENSECAG00000010160	AR	androgen receptor	-1,145	1,32E-19
1292.	ENSECAG00000015163	SHC4	SHC adaptor protein 4	-1,145	0,00579
1293.	ENSECAG00000013582	DHRS3	dehydrogenase/reductase 3	-1,146	1,02E-46
1294.	ENSECAG00000018340	USP43	ubiquitin specific peptidase 43	-1,146	0,004309
1295.	ENSECAG00000013242	ABCA3	ATP binding cassette subfamily A member 3	-1,147	1,22E-18
1296.	ENSECAG00000021165	STAC	SH3 and cysteine rich domain	-1,15	1,27E-06
1297.	ENSECAG00000030367	ENSECAG00000030367		-1,151	0,000163
1298.	ENSECAG00000014470	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	-1,152	8,36E-21
1299.	ENSECAG00000014750	ALDH1A2	aldehyde dehydrogenase 1 family member A2	-1,152	3,54E-42
1300.	ENSECAG00000006866	KIF5A	kinesin family member 5A	-1,152	3,47E-20
1301.	ENSECAG00000008401	S100A6	S100 calcium binding protein A6	-1,154	1,38E-08
1302.	ENSECAG00000044664	ENSECAG00000044664		-1,156	6,35E-07
1303.	ENSECAG00000002083	KCTD12	potassium channel tetramerization domain containing 12	-1,156	1,71E-08
1304.	ENSECAG00000022851	ENSECAG00000022851		-1,156	1,3E-55
1305.	ENSECAG00000010971	COL9A2	collagen type IX alpha 2 chain	-1,157	0,012943
1306.	ENSECAG00000015080	SLC2A11	solute carrier family 2 member 11	-1,158	2,46E-10
1307.	ENSECAG00000006717	ASS1	argininosuccinate synthase 1	-1,16	0,003069
1308.	ENSECAG00000024047	IL6R	interleukin 6 receptor	-1,162	0,000421
1309.	ENSECAG00000021888	NPAS3	neuronal PAS domain protein 3	-1,164	0,0138
1310.	ENSECAG00000024038	YPEL3	yippee like 3	-1,169	4,97E-16
1311.	ENSECAG00000009401	NUDT7	nudix hydrolase 7	-1,169	5,61E-15
1312.	ENSECAG00000010312	RHPN2	rhophilin Rho GTPase binding protein 2	-1,17	0,001629
1313.	ENSECAG00000018049	PAMR1	peptidase domain containing associated with muscle retraction 1	-1,171	1,08E-16
1314.	ENSECAG00000009288	ICA1L	islet cell autoantigen 1 like	-1,172	8,3E-13
1315.	ENSECAG00000057318	ENSECAG00000057318		-1,172	8,25E-05
1316.	ENSECAG00000001100	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	-1,173	7,46E-08
1317.	ENSECAG00000018663	PLB1	phospholipase B1	-1,173	4,84E-05
1318.	ENSECAG00000020421	TOMM34	translocase of outer mitochondrial membrane 34	-1,174	2,89E-09
1319.	ENSECAG00000017090	CLEC2L	C-type lectin domain family 2 member L	-1,174	5,37E-05
1320.	ENSECAG00000002538	TAC1	tachykinin 1	-1,174	0,020665
1321.	ENSECAG00000002496	ZFP3	ZFP3 zinc finger protein	-1,175	4,51E-11
1322.	ENSECAG00000017800	GRAMD2B	GRAM domain containing 2B	-1,178	2,55E-19
1323.	ENSECAG00000008973	TMEM25	transmembrane protein 25	-1,178	0,002705
1324.	ENSECAG00000002716	KDM7A	lysine demethylase 7A	-1,178	1,16E-17
1325.	ENSECAG00000033567	ENSECAG00000033567		-1,179	2,46E-41
1326.	ENSECAG00000000077	CPEB3	cytoplasmic polyadenylation element binding protein 3	-1,179	0,000147
1327.	ENSECAG00000014247	TINAGL1	tubulointerstitial nephritis antigen like 1	-1,18	1,4E-07
1328.	ENSECAG00000012152	CHRD1	chordin like 1	-1,181	3,9E-48
1329.	ENSECAG00000020489	SLITRK2	SLIT and NTRK like family member 2	-1,182	1,65E-17
1330.	ENSECAG00000015680	LRRC9	leucine rich repeat containing 9	-1,183	1,6E-05
1331.	ENSECAG00000012002	LRRC8B	leucine rich repeat containing 8 VRAC subunit B	-1,186	0,000321
1332.	ENSECAG00000048547	ENSECAG00000048547		-1,186	0,004265
1333.	ENSECAG00000045040	ENSECAG00000045040		-1,186	7,32E-13
1334.	ENSECAG00000000136	FERMT1	FERM domain containing kindlin 1	-1,186	2,14E-05
1335.	ENSECAG00000041756	ENSECAG00000041756		-1,187	3,75E-07
1336.	ENSECAG00000018784	NIM1K	NIM1 serine/threonine protein kinase	-1,187	2,09E-14
1337.	ENSECAG00000039277	ENSECAG00000039277		-1,188	0,001781
1338.	ENSECAG00000014448	ZNF660	zinc finger protein 660	-1,191	1,57E-06
1339.	ENSECAG00000020013	ZKSCAN4	zinc finger with KRAB and SCAN domains 4	-1,193	5,32E-05
1340.	ENSECAG00000014954	DNAH5	dynein axonemal heavy chain 5	-1,193	0,013282
1341.	ENSECAG00000019600	GRP	gastrin releasing peptide	-1,193	0,000109
1342.	ENSECAG00000006846	GFRA1	GDNF family receptor alpha 1	-1,194	0,005843

1343.	ENSECAG00000016733	PDLIM5	PDZ and LIM domain 5	-1,195	5,32E-31
1344.	ENSECAG00000058350	ENSECAG00000058350		-1,195	4,76E-23
1345.	ENSECAG00000016879	ZSCAN23	zinc finger and SCAN domain containing 23	-1,195	0,000411
1346.	ENSECAG00000014633	CTC1	CST telomere replication complex component 1	-1,197	8,45E-10
1347.	ENSECAG00000023797	KCNH2	potassium voltage-gated channel subfamily H member 2	-1,198	0,002615
1348.	ENSECAG00000007153	HUNK	hormonally up-regulated Neu-associated kinase	-1,199	9,55E-05
1349.	ENSECAG00000008983	LRRTM1	leucine rich repeat transmembrane neuronal 1	-1,201	3,98E-05
1350.	ENSECAG00000049917	CHML	CHM like Rab escort protein	-1,202	7,78E-26
1351.	ENSECAG00000035441	ENSECAG00000035441		-1,202	0,009398
1352.	ENSECAG00000017390	KIF1C	kinesin family member 1C	-1,202	4,27E-20
1353.	ENSECAG00000021651	NPC1	NPC intracellular cholesterol transporter 1	-1,202	1,49E-19
1354.	ENSECAG00000010814	ENSECAG00000010814		-1,205	0,008511
1355.	ENSECAG00000017927	DOK7	docking protein 7	-1,205	0,013311
1356.	ENSECAG00000015878	AMOT	angiomin	-1,205	1,51E-22
1357.	ENSECAG00000010713	KCNMA1	potassium calcium-activated channel subfamily M alpha 1	-1,206	9,73E-05
1358.	ENSECAG00000022204	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1,206	6,46E-46
1359.	ENSECAG00000013608	KAZALD1	Kazal type serine peptidase inhibitor domain 1	-1,207	1,54E-05
1360.	ENSECAG00000024940	RNF207	ring finger protein 207	-1,207	2,08E-06
1361.	ENSECAG00000014947	OPN3	opsin 3	-1,208	0,002017
1362.	ENSECAG00000015093	NUDT12	nudix hydrolase 12	-1,209	3,87E-05
1363.	ENSECAG00000020251	ETV1	ETS variant transcription factor 1	-1,21	1,04E-10
1364.	ENSECAG00000042557	ENSECAG00000042557		-1,211	4,96E-18
1365.	ENSECAG00000021238	IGF1R	insulin like growth factor 1 receptor	-1,212	4,8E-34
1366.	ENSECAG00000032051	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1,214	0,010529
1367.	ENSECAG00000046946	ENSECAG00000046946		-1,214	0,00349
1368.	ENSECAG00000011432	SLC46A3	solute carrier family 46 member 3	-1,214	6,92E-07
1369.	ENSECAG00000021304	ZNF362	zinc finger protein 362	-1,215	2,88E-16
1370.	ENSECAG00000049532	ENSECAG00000049532		-1,216	0,006747
1371.	ENSECAG00000010708	ZNF662	zinc finger protein 662	-1,217	8,69E-06
1372.	ENSECAG00000041010	SPINK8	serine peptidase inhibitor Kazal type 8 (putative)	-1,217	0,007904
1373.	ENSECAG00000012990	CALCRL	calcitonin receptor like receptor	-1,218	4,44E-08
1374.	ENSECAG0000001988	FAT3	FAT atypical cadherin 3	-1,218	0,000117
1375.	ENSECAG00000045176	ENSECAG00000045176		-1,219	6,6E-05
1376.	ENSECAG00000033602	GPRIN3	GPRIN family member 3	-1,22	0,00728
1377.	ENSECAG00000014486	CADPS	calcium dependent secretion activator	-1,221	2,69E-07
1378.	ENSECAG00000020808	TRIL	TLR4 interactor with leucine rich repeats	-1,221	1,91E-09
1379.	ENSECAG00000058353	ENSECAG00000058353		-1,223	0,001632
1380.	ENSECAG00000045936	ENSECAG00000045936		-1,225	1,38E-06
1381.	ENSECAG00000012196	LRRC1	leucine rich repeat containing 1	-1,225	9,53E-11
1382.	ENSECAG00000016917	TES	testin LIM domain protein	-1,225	3,64E-34
1383.	ENSECAG00000013228	GLT1D1	glycosyltransferase 1 domain containing 1	-1,226	0,000587
1384.	ENSECAG00000034866	GATA5	GATA binding protein 5	-1,227	0,000789
1385.	ENSECAG00000018573	SLC3A1	solute carrier family 3 member 1	-1,229	3,1E-08
1386.	ENSECAG00000009616	LMO7	LIM domain 7	-1,23	3,08E-08
1387.	ENSECAG00000010573	CELSR1	cadherin EGF LAG seven-pass G-type receptor 1	-1,232	0,00033
1388.	ENSECAG00000053486	ENSECAG00000053486		-1,233	0,008888
1389.	ENSECAG00000014382	ZDHHC23	zinc finger DHHC-type palmitoyltransferase 23	-1,233	8,31E-10
1390.	ENSECAG00000021368	FGGY	FGGY carbohydrate kinase domain containing	-1,234	3,75E-05
1391.	ENSECAG00000044393	ENSECAG00000044393		-1,234	8,84E-06
1392.	ENSECAG0000001652	ITGA6	integrin subunit alpha 6	-1,234	2,1E-06
1393.	ENSECAG00000017132	FRZB	frizzled related protein	-1,234	1,56E-21
1394.	ENSECAG00000058069	ENSECAG00000058069		-1,235	2,16E-43

1395.	ENSECAG00000009311	SH3TC2	SH3 domain and tetratricopeptide repeats 2	-1,235	2,57E-05
1396.	ENSECAG00000005649	PAQR7	progesterone and adipoQ receptor family member 7	-1,236	6,4E-19
1397.	ENSECAG00000017668	KERA	keratocan	-1,238	0,009532
1398.	ENSECAG00000038375	NEBL	nebulin	-1,238	1,2E-05
1399.	ENSECAG00000018112	FAM241B	family with sequence similarity 241 member B	-1,238	0,001228
1400.	ENSECAG00000048219	ENSECAG00000048219		-1,238	0,0031
1401.	ENSECAG00000024264	ARMH1	armadillo like helical domain containing 1	-1,238	0,010918
1402.	ENSECAG00000019716	CCDC88C	coiled-coil domain containing 88C	-1,239	5,22E-08
1403.	ENSECAG00000013957	PDE5A	phosphodiesterase 5A	-1,241	5,53E-36
1404.	ENSECAG00000047198	ENSECAG00000047198		-1,242	0,006693
1405.	ENSECAG00000024593	SLC35G1	solute carrier family 35 member G1	-1,242	0,002469
1406.	ENSECAG00000013384	STX3	syntaxin 3	-1,242	9,37E-31
1407.	ENSECAG00000058761	ENSECAG00000058761		-1,243	0,003753
1408.	ENSECAG00000016984	RANBP3L	RAN binding protein 3 like	-1,243	0,000494
1409.	ENSECAG00000013468	MYOM1	myomesin 1	-1,244	2,12E-14
1410.	ENSECAG00000019602	DLEC1	DLEC1 cilia and flagella associated protein	-1,244	0,000106
1411.	ENSECAG00000031250	KLRG2	killer cell lectin like receptor G2	-1,245	4,15E-18
1412.	ENSECAG00000024049	S100A13	S100 calcium binding protein A13	-1,246	3,49E-38
1413.	ENSECAG00000017321	PCDH17	protocadherin 17	-1,248	4,31E-11
1414.	ENSECAG00000031607	ENSECAG00000031607		-1,248	7,72E-05
1415.	ENSECAG00000056235	ENSECAG00000056235		-1,248	6,98E-19
1416.	ENSECAG00000035522	PALM	paralemmin	-1,249	1,33E-28
1417.	ENSECAG00000010054	NOX4	NADPH oxidase 4	-1,25	1,17E-25
1418.	ENSECAG00000013641	HOOK1	hook microtubule tethering protein 1	-1,25	0,008542
1419.	ENSECAG00000024778	MMP24	matrix metalloproteinase 24	-1,251	0,017115
1420.	ENSECAG00000039591	ZNF469	zinc finger protein 469	-1,252	1,3E-24
1421.	ENSECAG00000013939	ZFH2	zinc finger homeobox 2	-1,254	0,000496
1422.	ENSECAG00000005704	CARD11	caspase recruitment domain family member 11	-1,254	0,000603
1423.	ENSECAG00000010739	ITGA2	integrin subunit alpha 2	-1,255	1,21E-06
1424.	ENSECAG00000043319	ENSECAG00000043319		-1,255	9,6E-05
1425.	ENSECAG00000000784	ESRP1	epithelial splicing regulatory protein 1	-1,257	0,006889
1426.	ENSECAG00000019132	SLMAP	sarcolemma associated protein	-1,257	2,48E-63
1427.	ENSECAG00000053213	ENSECAG00000053213		-1,259	0,000224
1428.	ENSECAG00000011632	SNX30	sorting nexin family member 30	-1,26	4,54E-44
1429.	ENSECAG00000013233	FAT4	FAT atypical cadherin 4	-1,261	2,66E-19
1430.	ENSECAG00000015846	VASH2	vasohibin 2	-1,262	2,86E-07
1431.	ENSECAG00000015620	ENSECAG00000015620		-1,262	6,94E-06
1432.	ENSECAG00000020970	SLC25A23	solute carrier family 25 member 23	-1,262	6,72E-11
1433.	ENSECAG00000008471	GPR155	G protein-coupled receptor 155	-1,266	4,9E-22
1434.	ENSECAG00000007355	PIK3IP1	phosphoinositide-3-kinase interacting protein 1	-1,267	9,09E-07
1435.	ENSECAG00000016973	FILIP1L	filamin A interacting protein 1 like	-1,268	4,64E-33
1436.	ENSECAG00000024870	CWH43	cell wall biogenesis 43 C-terminal homolog	-1,268	5,16E-06
1437.	ENSECAG00000008946	ENSECAG00000008946		-1,27	1,21E-10
1438.	ENSECAG00000006195	ENSECAG00000006195		-1,27	0,002494
1439.	ENSECAG00000016958	CXXC5	CXXC finger protein 5	-1,272	2,59E-35
1440.	ENSECAG00000016734	INPP5K	inositol polyphosphate-5-phosphatase K	-1,273	5,62E-29
1441.	ENSECAG00000019512	PDGFC	platelet derived growth factor C	-1,274	9,94E-20
1442.	ENSECAG00000019562	RGN	regucalcin	-1,274	0,002677
1443.	ENSECAG00000037336	ENSECAG00000037336		-1,276	0,000656
1444.	ENSECAG00000018559	GLP2R	glucagon like peptide 2 receptor	-1,277	0,009024
1445.	ENSECAG00000003546	ENSECAG00000003546		-1,277	0,00179
1446.	ENSECAG00000014888	NEK5	NIMA related kinase 5	-1,278	0,000143
1447.	ENSECAG00000014730	PELI3	pellino E3 ubiquitin protein ligase family member 3	-1,281	0,001426
1448.	ENSECAG00000047859	ENSECAG00000047859		-1,282	0,011762
1449.	ENSECAG00000025138	MARCHF9	membrane associated ring-CH-type finger 9	-1,282	6,45E-10
1450.	ENSECAG00000015566	NSG1	neuronal vesicle trafficking associated 1	-1,283	3,87E-34
1451.	ENSECAG00000014558	DUSP22	dual specificity phosphatase 22	-1,284	5,35E-12
1452.	ENSECAG00000022969	ELOVL4	ELOVL fatty acid elongase 4	-1,284	0,000169

1453.	ENSECAG00000043859	ENSECAG00000043859		-1,284	0,00115
1454.	ENSECAG00000013252	SNCG	synuclein gamma	-1,284	0,000496
1455.	ENSECAG00000030282	ENSECAG00000030282		-1,284	9,09E-05
1456.	ENSECAG00000012652	CHDH	choline dehydrogenase	-1,285	1,66E-07
1457.	ENSECAG00000020159	FAM131B	family with sequence similarity 131 member B	-1,285	0,001526
1458.	ENSECAG00000000121	NAV3	neuron navigator 3	-1,286	7,52E-21
1459.	ENSECAG00000025107	COBL1	cordon-bleu WH2 repeat protein like 1	-1,286	5E-56
1460.	ENSECAG00000047929	ENSECAG00000047929		-1,287	0,001203
1461.	ENSECAG00000047010	ENSECAG00000047010		-1,288	2,67E-07
1462.	ENSECAG00000011301	SPINT2	serine peptidase inhibitor, Kunitz type 2	-1,289	8,6E-10
1463.	ENSECAG00000022720	ZNF641	zinc finger protein 641	-1,289	2,89E-25
1464.	ENSECAG00000008087	ENSECAG00000008087		-1,29	0,000167
1465.	ENSECAG00000033155	C17orf113	chromosome 17 open reading frame 113	-1,291	0,009406
1466.	ENSECAG00000017829	KLHL8	kelch like family member 8	-1,291	4,79E-10
1467.	ENSECAG00000023844	LAMA2	laminin subunit alpha 2	-1,292	1,08E-59
1468.	ENSECAG00000016987	NES	nestin	-1,293	6,57E-18
1469.	ENSECAG00000011401	CATSPERD	cation channel sperm associated auxiliary subunit delta	-1,295	1,06E-33
1470.	ENSECAG00000009025	CDHR3	cadherin related family member 3	-1,295	6,87E-06
1471.	ENSECAG00000043975	ENSECAG00000043975		-1,295	2,21E-08
1472.	ENSECAG00000004241	ASIP	agouti signaling protein	-1,295	0,013201
1473.	ENSECAG00000009648	CLIP1	CAP-Gly domain containing linker protein 1	-1,296	4,38E-53
1474.	ENSECAG00000015492	VWA5A	von Willebrand factor A domain containing 5A	-1,298	7,87E-60
1475.	ENSECAG00000029898	MPND	MPN domain containing	-1,299	3,35E-14
1476.	ENSECAG00000018792	ZNF782	zinc finger protein 782	-1,3	2,98E-18
1477.	ENSECAG00000020419	RAB3D	RAB3D, member RAS onco family	-1,301	1,03E-22
1478.	ENSECAG00000024566	PITPNM2	phosphatidylinositol transfer protein membrane associated 2	-1,301	8,21E-09
1479.	ENSECAG00000023651	SLC18B1	solute carrier family 18 member B1	-1,301	0,002838
1480.	ENSECAG00000025982	eca-mir-421	eca-mir-421	-1,302	4,5E-06
1481.	ENSECAG00000007211	KIAA1671	KIAA1671	-1,302	6,92E-15
1482.	ENSECAG00000018292	FZD3	frizzled class receptor 3	-1,302	7,25E-06
1483.	ENSECAG00000021296	RFTN2	raftlin family member 2	-1,303	1,57E-29
1484.	ENSECAG00000008173	HSD17B11	hydroxysteroid 17-beta dehydrogenase 11	-1,304	1,91E-28
1485.	ENSECAG00000020112	LZTS1	leucine zipper tumor suppressor 1	-1,306	8,35E-14
1486.	ENSECAG00000026969	RIMKLB	ribosomal modification protein rimK like family member B	-1,316	1,54E-21
1487.	ENSECAG00000019482	ZNF554	zinc finger protein 554	-1,317	1,1E-07
1488.	ENSECAG00000012244	ENSECAG00000012244		-1,318	5,22E-07
1489.	ENSECAG00000015808	DNAI7	dynein axonemal intermediate chain 7	-1,318	0,001421
1490.	ENSECAG00000015220	PKP1	plakophilin 1	-1,32	1,37E-07
1491.	ENSECAG00000053473	ENSECAG00000053473		-1,322	0,004011
1492.	ENSECAG00000020778	FBLN7	fibulin 7	-1,323	0,000353
1493.	ENSECAG00000016147	MYH10	myosin heavy chain 10	-1,324	2,21E-41
1494.	ENSECAG000000031178	ENSECAG000000031178		-1,327	0,003605
1495.	ENSECAG00000060322	ENSECAG00000060322		-1,329	6,29E-05
1496.	ENSECAG00000059781	ENSECAG00000059781		-1,329	0,005727
1497.	ENSECAG00000011349	SDR42E1	short chain dehydrogenase/reductase family 42E, member 1	-1,331	2,16E-06
1498.	ENSECAG00000009384	NECAB1	N-terminal EF-hand calcium binding protein 1	-1,331	0,004287
1499.	ENSECAG00000054585	ENSECAG00000054585		-1,332	4,08E-11
1500.	ENSECAG00000017974	LRRC43	leucine rich repeat containing 43	-1,332	0,008988
1501.	ENSECAG00000013154	SERAC1	serine active site containing 1	-1,336	8,85E-13
1502.	ENSECAG00000008985	NBEA	neurobeachin	-1,338	5,29E-49
1503.	ENSECAG00000013892	PPEF1	protein phosphatase with EF-hand domain 1	-1,338	0,000963
1504.	ENSECAG00000010142	ZNF185	zinc finger protein 185 with LIM domain	-1,338	5,43E-05
1505.	ENSECAG00000045529	ENSECAG00000045529		-1,338	1,18E-09
1506.	ENSECAG00000019877	DENND11	DENN domain containing 11	-1,341	6,19E-09
1507.	ENSECAG00000021609	SLC40A1	solute carrier family 40 member 1	-1,342	1,53E-36
1508.	ENSECAG00000050953	ENSECAG00000050953		-1,342	0,001151

1509.	ENSECAG00000021174	ACKR4	atypical chemokine receptor 4	-1,342	9,9E-08
1510.	ENSECAG00000052301	ENSECAG00000052301		-1,345	2,07E-05
1511.	ENSECAG00000016820	KANK2	KN motif and ankyrin repeat domains 2	-1,345	1,18E-26
1512.	ENSECAG00000044939	ENSECAG00000044939		-1,346	0,002207
1513.	ENSECAG00000016983	ANKRD1	ankyrin repeat domain 1	-1,348	5,5E-08
1514.	ENSECAG00000013130	CCDC170	coiled-coil domain containing 170	-1,35	3,59E-17
1515.	ENSECAG00000040039	FGFBP1	fibroblast growth factor binding protein 1	-1,351	0,006704
1516.	ENSECAG00000012241	SLC51B	solute carrier family 51 subunit beta	-1,353	1,25E-09
1517.	ENSECAG00000013723	SLC7A8	solute carrier family 7 member 8	-1,354	0,012867
1518.	ENSECAG00000056418	ENSECAG00000056418		-1,356	8,91E-07
1519.	ENSECAG00000013079	USP54	ubiquitin specific peptidase 54	-1,356	5,68E-36
1520.	ENSECAG00000048355	ENSECAG00000048355		-1,357	0,001056
1521.	ENSECAG00000004050	SLC8A1	solute carrier family 8 member A1	-1,357	3,78E-14
1522.	ENSECAG00000050116	ENSECAG00000050116		-1,359	0,000358
1523.	ENSECAG00000007088	KBTBD8	kelch repeat and BTB domain containing 8	-1,36	2,59E-08
1524.	ENSECAG00000016835	STXBP6	syntaxin binding protein 6	-1,361	2,36E-13
1525.	ENSECAG00000011511	PGR	progesterone receptor	-1,362	2,41E-30
1526.	ENSECAG00000020473	CTIF	cap binding complex dependent translation initiation factor	-1,364	6,24E-30
1527.	ENSECAG00000018579	F11R	F11 receptor	-1,367	5,99E-09
1528.	ENSECAG00000016824	NRP2	neuropilin 2	-1,368	5,08E-29
1529.	ENSECAG00000011729	ST6GAL2	ST6 beta-galactoside alpha-2,6-sialyltransferase 2	-1,369	8,91E-25
1530.	ENSECAG00000053646	ENSECAG00000053646		-1,373	0,000203
1531.	ENSECAG00000016526	NUBPL	NUBP iron-sulfur cluster assembly factor, mitochondrial	-1,374	4,44E-17
1532.	ENSECAG00000019290	CAMK1D	calcium/calmodulin dependent protein kinase ID	-1,376	3,03E-26
1533.	ENSECAG00000016038	ZNF892	zinc finger protein 892	-1,377	1,71E-07
1534.	ENSECAG00000016431	MAG11	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1,378	2,35E-11
1535.	ENSECAG00000007565	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor 2	-1,379	1,4E-13
1536.	ENSECAG00000017147	CCDC9B	coiled-coil domain containing 9B	-1,38	6,75E-36
1537.	ENSECAG00000000512	LBH	LBH regulator of WNT signaling pathway	-1,381	2,53E-27
1538.	ENSECAG00000049782	ENSECAG00000049782		-1,381	1,16E-06
1539.	ENSECAG00000007499	SLC28A1	solute carrier family 28 member 1	-1,383	0,013446
1540.	ENSECAG00000058617	ENSECAG00000058617		-1,385	0,002419
1541.	ENSECAG00000015048	CGN	cingulin	-1,386	2,45E-05
1542.	ENSECAG00000019717	ECM2	extracellular matrix protein 2	-1,388	2,95E-23
1543.	ENSECAG00000021712	EYA2	EYA transcriptional coactivator and phosphatase 2	-1,389	0,00254
1544.	ENSECAG00000049618	ENSECAG00000049618		-1,393	0,011589
1545.	ENSECAG00000022826	NIPAL3	NIPA like domain containing 3	-1,398	1,57E-24
1546.	ENSECAG00000020812	MPPED1	metallophosphoesterase domain containing 1	-1,398	7,58E-17
1547.	ENSECAG00000016600	PPFIA4	PTPRF interacting protein alpha 4	-1,399	1,49E-12
1548.	ENSECAG00000012940	NLG1	neuroligin 1	-1,4	0,000979
1549.	ENSECAG00000018307	TNIK	TRAF2 and NCK interacting kinase	-1,401	4,5E-18
1550.	ENSECAG00000018533	SALL4	spalt like transcription factor 4	-1,402	2,73E-11
1551.	ENSECAG00000056115	ENSECAG00000056115		-1,405	0,000117
1552.	ENSECAG00000048094	ENSECAG00000048094		-1,405	5,42E-07
1553.	ENSECAG00000020113	SEMA3C	semaphorin 3C	-1,406	2,17E-59
1554.	ENSECAG00000010437	TCEA3	transcription elongation factor A3	-1,407	2,21E-17
1555.	ENSECAG00000060384	ENSECAG00000060384		-1,409	3,43E-11
1556.	ENSECAG00000053137	ENSECAG00000053137		-1,413	6,53E-06
1557.	ENSECAG00000035486	ZNF48	zinc finger protein 48	-1,416	8,05E-13
1558.	ENSECAG00000048941	ENSECAG00000048941		-1,42	0,009424
1559.	ENSECAG00000058574	ENSECAG00000058574		-1,421	1,44E-15
1560.	ENSECAG00000022595	TLCD5	TLC domain containing 5	-1,421	7,84E-10
1561.	ENSECAG00000028572	ENSECAG00000028572		-1,423	3,29E-22
1562.	ENSECAG00000003259	FLYWCH1	FLYWCH-type zinc finger 1	-1,426	9,75E-06
1563.	ENSECAG00000054202	ENSECAG00000054202		-1,427	5,43E-08
1564.	ENSECAG00000049448	ENSECAG00000049448		-1,428	0,00103

1565.	ENSECAG00000006860	F5	coagulation factor V	-1,429	0,000857
1566.	ENSECAG00000010189	TAF9B	TATA-box binding protein associated factor 9b	-1,43	1,24E-11
1567.	ENSECAG00000006249	AFF3	ALF transcription elongation factor 3	-1,431	3,74E-20
1568.	ENSECAG00000019434	PLEK2	pleckstrin 2	-1,431	0,001448
1569.	ENSECAG00000011096	ENSECAG00000011096		-1,431	1,33E-12
1570.	ENSECAG00000000487	SYNM	synemin	-1,434	2,38E-22
1571.	ENSECAG00000009515	ATRNL1	attractin like 1	-1,435	4,01E-26
1572.	ENSECAG00000055735	ENSECAG00000055735		-1,437	4,86E-06
1573.	ENSECAG00000022638	PLD1	phospholipase D1	-1,44	2,37E-18
1574.	ENSECAG00000009418	RASSF7	Ras association domain family member 7	-1,44	5,1E-05
1575.	ENSECAG00000017486	CCDC159	coiled-coil domain containing 159	-1,44	4,48E-09
1576.	ENSECAG00000011593	MEF2A	myocyte enhancer factor 2A	-1,44	1,15E-86
1577.	ENSECAG00000031302	ENSECAG00000031302		-1,443	3,78E-16
1578.	ENSECAG00000021162	CDH13	cadherin 13	-1,444	2,85E-27
1579.	ENSECAG00000024459	MARK1	microtubule affinity regulating kinase 1	-1,447	8,76E-69
1580.	ENSECAG00000001716	PLXNA2	plexin A2	-1,447	3,12E-38
1581.	ENSECAG00000049085	ENSECAG00000049085		-1,449	0,000688
1582.	ENSECAG00000016928	DCHS2	dachsous cadherin-related 2	-1,449	0,000168
1583.	ENSECAG00000024132	FAM169A	family with sequence similarity 169 member A	-1,452	4,15E-05
1584.	ENSECAG00000020311	BCO2	beta-carotene oxygenase 2	-1,454	7,46E-06
1585.	ENSECAG00000000751	NEDD4L	NEDD4 like E3 ubiquitin protein ligase	-1,454	3,14E-32
1586.	ENSECAG00000012905	FNBP1	formin binding protein 1	-1,455	4,3E-33
1587.	ENSECAG00000008335	PDK4	pyruvate dehydrogenase kinase 4	-1,458	1,29E-07
1588.	ENSECAG00000014398	ENSECAG00000014398		-1,46	7,69E-05
1589.	ENSECAG00000004274	IQGAP2	IQ motif containing GTPase activating protein 2	-1,461	0,000101
1590.	ENSECAG00000019060	ESYT3	extended synaptotagmin 3	-1,461	2,01E-07
1591.	ENSECAG00000019087	CTSK	cathepsin K	-1,468	7,68E-08
1592.	ENSECAG00000050788	ENSECAG00000050788		-1,468	3,55E-08
1593.	ENSECAG00000028005	FRAT1	FRAT regulator of WNT signaling pathway 1	-1,473	0,002796
1594.	ENSECAG00000013290	C25H9orf152	chromosome 25 C9orf152 homolog	-1,475	7,85E-05
1595.	ENSECAG00000015450	TET1	tet methylcytosine dioxygenase 1	-1,482	1,15E-17
1596.	ENSECAG00000021544	FAIM2	Fas apoptotic inhibitory molecule 2	-1,483	1,14E-11
1597.	ENSECAG00000015379	FGD4	FYVE, RhoGEF and PH domain containing 4	-1,483	1,65E-10
1598.	ENSECAG00000017905	LTBP4	latent transforming growth factor beta binding protein 4	-1,487	1,43E-55
1599.	ENSECAG00000009971	AJUBA	ajuba LIM protein	-1,488	8,27E-32
1600.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-1,488	8,32E-06
1601.	ENSECAG00000024742	PFN2	profilin 2	-1,489	9,95E-56
1602.	ENSECAG00000011463	CCSER1	coiled-coil serine rich protein 1	-1,489	0,003365
1603.	ENSECAG00000044963	ENSECAG00000044963		-1,49	3,92E-10
1604.	ENSECAG00000011718	ENSECAG00000011718		-1,492	0,000615
1605.	ENSECAG00000002797	ENSECAG00000002797		-1,498	6,09E-11
1606.	ENSECAG00000040873	ENSECAG00000040873		-1,498	0,002
1607.	ENSECAG00000046815	ENSECAG00000046815		-1,5	0,002882
1608.	ENSECAG00000022950	NDRG2	NDRG family member 2	-1,501	5,9E-17
1609.	ENSECAG00000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-1,502	1,27E-11
1610.	ENSECAG00000027851	ENSECAG00000027851		-1,503	2,12E-10
1611.	ENSECAG00000019789	STOML1	stomatin like 1	-1,504	9,59E-19
1612.	ENSECAG00000014945	CER1	cerberus 1, DAN family BMP antagonist	-1,507	0,009565
1613.	ENSECAG00000012700	JADE3	jade family PHD finger 3	-1,508	1,26E-09
1614.	ENSECAG00000023101	TP53I11	tumor protein p53 inducible protein 11	-1,509	1,31E-44
1615.	ENSECAG00000011912	RAB36	RAB36, member RAS onco family	-1,513	1,3E-07
1616.	ENSECAG00000000207	ACTA1	actin alpha 1, skeletal muscle	-1,515	0,000194
1617.	ENSECAG00000024900	HOXC11	homeobox C11	-1,516	0,001105
1618.	ENSECAG00000056397	ENSECAG00000056397		-1,518	0,001248
1619.	ENSECAG00000019508	COL8A1	collagen type VIII alpha 1 chain	-1,523	4,12E-09
1620.	ENSECAG00000040881	ENSECAG00000040881		-1,523	2,99E-48
1621.	ENSECAG00000009424	CCDC171	coiled-coil domain containing 171	-1,528	5,27E-16

1622.	ENSECAG00000000813	SCN5A	sodium voltage-gated channel alpha subunit 5	-1,528	0,005498
1623.	ENSECAG000000003193	BAMBI	BMP and activin membrane bound inhibitor	-1,53	1,38E-11
1624.	ENSECAG000000002490	RNF144B	ring finger protein 144B	-1,531	1,93E-14
1625.	ENSECAG000000005360	MITF	melanocyte inducing transcription factor	-1,531	1,84E-42
1626.	ENSECAG000000045840	ENSECAG000000045840		-1,532	0,004278
1627.	ENSECAG000000013016	TMEM82	transmembrane protein 82	-1,536	0,005188
1628.	ENSECAG000000003569	ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1	-1,54	3,81E-13
1629.	ENSECAG000000016806	CLCN4	chloride voltage-gated channel 4	-1,541	2,56E-12
1630.	ENSECAG000000000954	NPR1	natriuretic peptide receptor 1	-1,542	2,83E-06
1631.	ENSECAG000000047763	ENSECAG000000047763		-1,542	0,000795
1632.	ENSECAG000000015144	CADM1	cell adhesion molecule 1	-1,546	4,37E-15
1633.	ENSECAG000000023963	NMNAT2	nicotinamide nucleotide adenyltransferase 2	-1,547	1,27E-24
1634.	ENSECAG000000023765	IGSF9	immunoglobulin superfamily member 9	-1,547	0,000343
1635.	ENSECAG000000020337	DOCK11	dedicator of cytokinesis 11	-1,548	6,49E-51
1636.	ENSECAG000000017566	MVB12B	multivesicular body subunit 12B	-1,551	7,47E-32
1637.	ENSECAG000000024358	ZBTB16	zinc finger and BTB domain containing 16	-1,556	0,004541
1638.	ENSECAG000000019233	ELMO1	engulfment and cell motility 1	-1,556	8,67E-21
1639.	ENSECAG000000059686	ENSECAG000000059686		-1,557	0,002712
1640.	ENSECAG000000017938	BLK	BLK proto-onco, Src family tyrosine kinase	-1,558	0,000438
1641.	ENSECAG000000008738	ID2	inhibitor of DNA binding 2	-1,558	2,05E-35
1642.	ENSECAG000000006567	SLITRK4	SLIT and NTRK like family member 4	-1,56	0,00021
1643.	ENSECAG000000012012	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5	-1,562	7,57E-57
1644.	ENSECAG000000039301	FAM110C	family with sequence similarity 110 member C	-1,563	1,2E-19
1645.	ENSECAG000000016598	HINT3	histidine triad nucleotide binding protein 3	-1,563	1,31E-11
1646.	ENSECAG000000018191	GUCY1A2	guanylate cyclase 1 soluble subunit alpha 2	-1,564	1,61E-21
1647.	ENSECAG000000009930	PCNX2	pecanex 2	-1,564	3,01E-15
1648.	ENSECAG000000027518	ENSECAG000000027518		-1,567	0,000175
1649.	ENSECAG000000013956	ROBO3	roundabout guidance receptor 3	-1,568	0,000261
1650.	ENSECAG000000044368	ENSECAG000000044368		-1,568	5,78E-09
1651.	ENSECAG000000019504	SYN3	synapsin III	-1,571	2,6E-09
1652.	ENSECAG000000054666	ENSECAG000000054666		-1,571	5,66E-07
1653.	ENSECAG000000017907	RNFT2	ring finger protein, transmembrane 2	-1,573	1,43E-05
1654.	ENSECAG000000016667	ENSECAG000000016667		-1,575	2,14E-15
1655.	ENSECAG000000008824	EFCAB3	EF-hand calcium binding domain 3	-1,575	0,003275
1656.	ENSECAG000000014418	GABRP	gamma-aminobutyric acid type A receptor subunit pi	-1,579	3,74E-05
1657.	ENSECAG000000051604	ENSECAG000000051604		-1,58	3,21E-05
1658.	ENSECAG000000014962	FAXDC2	fatty acid hydroxylase domain containing 2	-1,582	4,51E-09
1659.	ENSECAG000000015952	BDNF	brain derived neurotrophic factor	-1,585	2,44E-10
1660.	ENSECAG000000013480	ANO4	anoctamin 4	-1,59	1,02E-06
1661.	ENSECAG000000006796	ZSCAN26	zinc finger and SCAN domain containing 26	-1,594	2,07E-06
1662.	ENSECAG000000015180	NEXN	nexilin F-actin binding protein	-1,595	1,48E-32
1663.	ENSECAG000000005506	MMP13	matrix metalloproteinase 13	-1,597	1,09E-07
1664.	ENSECAG000000031200	ENSECAG000000031200		-1,597	2,08E-46
1665.	ENSECAG000000014358	RERG	RAS like estrogen regulated growth inhibitor	-1,597	0,007522
1666.	ENSECAG000000035205	ZNF853	zinc finger protein 853	-1,6	1,19E-17
1667.	ENSECAG000000015845	PLD5	phospholipase D family member 5	-1,604	0,002249
1668.	ENSECAG000000015189	FAM216B	family with sequence similarity 216 member B	-1,604	0,005034
1669.	ENSECAG000000008259	MASP1	MBL associated serine protease 1	-1,605	3,35E-20
1670.	ENSECAG000000024757	ENSECAG000000024757		-1,605	3,83E-13
1671.	ENSECAG000000017478	B4GALT6	beta-1,4-galactosyltransferase 6	-1,606	4,05E-50
1672.	ENSECAG000000007087	FBXL13	F-box and leucine rich repeat protein 13	-1,606	6,93E-13

1673.	ENSECAG00000009660	PLEKHA6	pleckstrin homology domain containing A6	-1,609	1,24E-14
1674.	ENSECAG00000002620	ENSECAG00000002620		-1,609	0,000952
1675.	ENSECAG00000017454	KIAA1755	KIAA1755	-1,61	8,35E-05
1676.	ENSECAG00000055038	ENSECAG00000055038		-1,617	1,77E-09
1677.	ENSECAG00000047002	ENSECAG00000047002		-1,618	5,39E-10
1678.	ENSECAG00000006591	ATG9B	autophagy related 9B	-1,622	3,63E-12
1679.	ENSECAG00000049316	ENSECAG00000049316		-1,626	1,15E-05
1680.	ENSECAG00000006848	SLC27A6	solute carrier family 27 member 6	-1,627	1E-11
1681.	ENSECAG00000011887	ADAMTSL2	ADAMTS like 2	-1,629	0,001282
1682.	ENSECAG00000019137	MAML3	mastermind like transcriptional coactivator 3	-1,631	3,07E-14
1683.	ENSECAG00000006338	ANKH	ANKH inorganic pyrophosphate transport regulator	-1,634	4,66E-28
1684.	ENSECAG00000024847	DGAT2	diacylglycerol O-acyltransferase 2	-1,635	9,7E-19
1685.	ENSECAG00000013108	C1H1orf198	chromosome 1 C1orf198 homolog	-1,636	2,83E-12
1686.	ENSECAG00000019364	GALNT18	polypeptide N-acetylgalactosaminyltransferase 18	-1,637	0,002018
1687.	ENSECAG00000013428	ID4	inhibitor of DNA binding 4	-1,637	6,48E-21
1688.	ENSECAG00000009422	RGS7	regulator of G protein signaling 7	-1,638	0,000392
1689.	ENSECAG00000004502	WFDC1	WAP four-disulfide core domain 1	-1,64	3,84E-88
1690.	ENSECAG00000000734	HMG1A	high mobility group AT-hook 1	-1,64	7,83E-18
1691.	ENSECAG00000049298	ENSECAG00000049298		-1,641	1,45E-17
1692.	ENSECAG00000017135	ZC3H12D	zinc finger CCCH-type containing 12D	-1,643	0,004565
1693.	ENSECAG00000007373	SHTN1	shootin 1	-1,647	1,84E-49
1694.	ENSECAG00000008830	WNT5A	Wnt family member 5A	-1,65	4,5E-138
1695.	ENSECAG00000008221	S100A4	S100 calcium binding protein A4	-1,65	1,47E-12
1696.	ENSECAG00000019648	MID1	midline 1	-1,653	1,73E-14
1697.	ENSECAG00000053294	ENSECAG00000053294		-1,654	0,00254
1698.	ENSECAG00000020399	CTHRC1	collagen triple helix repeat containing 1	-1,657	2,66E-30
1699.	ENSECAG00000024806	GPR176	G protein-coupled receptor 176	-1,658	3,47E-05
1700.	ENSECAG00000016231	HSPA12A	heat shock protein family A (Hsp70) member 12A	-1,658	2,65E-11
1701.	ENSECAG00000002251	TLL1	tolloid like 1	-1,659	1,57E-06
1702.	ENSECAG00000015023	FAM184A	family with sequence similarity 184 member A	-1,66	1,09E-12
1703.	ENSECAG00000016047	CPA6	carboxypeptidase A6	-1,661	8,61E-14
1704.	ENSECAG00000001734	SPATA25	spermatosis associated 25	-1,662	0,000172
1705.	ENSECAG00000032331	ZNF594	zinc finger protein 594	-1,663	1,4E-07
1706.	ENSECAG00000018004	CA8	carbonic anhydrase 8	-1,663	2,56E-08
1707.	ENSECAG00000005563	PRSS23	serine protease 23	-1,666	8,07E-54
1708.	ENSECAG00000000178	RUNX1T1	RUNX1 partner transcriptional co-repressor 1	-1,668	1,88E-54
1709.	ENSECAG00000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,67	8,66E-36
1710.	ENSECAG00000041218	LPAR4	lysophosphatidic acid receptor 4	-1,671	0,001641
1711.	ENSECAG00000010143	CRB3	crumbs cell polarity complex component 3	-1,671	0,001257
1712.	ENSECAG00000017986	AXIN2	axin 2	-1,674	1,41E-07
1713.	ENSECAG00000054486	ENSECAG00000054486		-1,678	0,001576
1714.	ENSECAG00000010989	SH3YL1	SH3 and SYLF domain containing 1	-1,679	1,45E-22
1715.	ENSECAG00000021374	TCF23	transcription factor 23	-1,683	6,78E-64
1716.	ENSECAG00000007718	TMOD1	tropomodulin 1	-1,686	4,72E-36
1717.	ENSECAG00000002548	RNF182	ring finger protein 182	-1,687	0,001039
1718.	ENSECAG00000013176	MEGF6	multiple EGF like domains 6	-1,688	3,16E-20
1719.	ENSECAG00000023120	ZFP69B	ZFP69 zinc finger protein B	-1,692	3,18E-05
1720.	ENSECAG00000019664	HID1	HID1 domain containing	-1,697	2,25E-06
1721.	ENSECAG00000028562	ENSECAG00000028562		-1,703	0,000318
1722.	ENSECAG00000017689	ARHGEF28	Rho guanine nucleotide exchange factor 28	-1,705	9,94E-40
1723.	ENSECAG00000000274	SPAG16	sperm associated antigen 16	-1,708	7,31E-08
1724.	ENSECAG00000016906	ZNF184	zinc finger protein 184	-1,708	1,2E-28
1725.	ENSECAG00000019677	EPHX1	epoxide hydrolase 1	-1,709	8,02E-07
1726.	ENSECAG00000017897	FAM167A	family with sequence similarity 167 member A	-1,713	9,07E-10
1727.	ENSECAG00000005880	RIMKLA	ribosomal modification protein rimK like family member A	-1,714	0,001472

1728.	ENSECAG00000000257	CNNM1	cyclin and CBS domain divalent metal cation transport mediator 1	-1,715	1,1E-05
1729.	ENSECAG00000032497	ENSECAG00000032497		-1,715	9,91E-06
1730.	ENSECAG00000021938	SYNC	syncoilin, intermediate filament protein	-1,717	1,55E-16
1731.	ENSECAG00000015772	GALNT17	polypeptide N-acetylgalactosaminyltransferase 17	-1,717	4,58E-08
1732.	ENSECAG00000014416	BTBD8	BTB domain containing 8	-1,719	4,25E-05
1733.	ENSECAG00000007542	SH3D19	SH3 domain containing 19	-1,721	1,32E-60
1734.	ENSECAG00000048134	ENSECAG00000048134		-1,721	0,001525
1735.	ENSECAG00000018888	RENNP	renin binding protein	-1,722	1,16E-15
1736.	ENSECAG00000024367	CASP1	caspase 1	-1,722	0,000217
1737.	ENSECAG00000010522	BACH2	BTB domain and CNC homolog 2	-1,722	3,51E-10
1738.	ENSECAG00000004135	AMPH	amphiphysin	-1,727	4,56E-05
1739.	ENSECAG00000039710	ZNF543	zinc finger protein 543	-1,732	1,38E-13
1740.	ENSECAG0000003602	SLC26A7	solute carrier family 26 member 7	-1,739	1,53E-06
1741.	ENSECAG00000055848	ENSECAG00000055848		-1,742	2,08E-10
1742.	ENSECAG00000010830	MMP11	matrix metalloproteinase 11	-1,744	7,5E-32
1743.	ENSECAG00000046304	ENSECAG00000046304		-1,745	1,63E-06
1744.	ENSECAG00000009138	MME	membrane metalloproteinase	-1,747	1,18E-08
1745.	ENSECAG00000012910	ACE	angiotensin I converting enzyme	-1,755	0,001
1746.	ENSECAG00000019993	KALRN	kalirin RhoGEF kinase	-1,756	1,07E-11
1747.	ENSECAG00000026898	SIRT5	sirtuin 5	-1,758	1,3E-33
1748.	ENSECAG00000021979	CARD10	caspase recruitment domain family member 10	-1,76	3,11E-08
1749.	ENSECAG00000011898	SPEF2	sperm flagellar 2	-1,762	1,68E-07
1750.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-1,765	3,23E-19
1751.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-1,767	1,62E-09
1752.	ENSECAG00000060330	PLSCR4	phospholipid scramblase 4	-1,767	3,82E-24
1753.	ENSECAG00000047497	ENSECAG00000047497		-1,768	2,88E-09
1754.	ENSECAG00000033026	ENSECAG00000033026		-1,769	1,41E-07
1755.	ENSECAG00000045941	ENSECAG00000045941		-1,77	1,36E-10
1756.	ENSECAG00000021277	LAMA3	laminin subunit alpha 3	-1,771	1,29E-08
1757.	ENSECAG00000022448	INHBA	inhibin subunit beta A	-1,771	7,94E-33
1758.	ENSECAG00000019790	CAMK2A	calcium/calmodulin dependent protein kinase II alpha	-1,773	4,34E-06
1759.	ENSECAG00000059950	ENSECAG00000059950		-1,773	3,71E-14
1760.	ENSECAG00000022899	ARSG	arylsulfatase G	-1,776	2,42E-10
1761.	ENSECAG00000059237	ENSECAG00000059237		-1,779	5,55E-08
1762.	ENSECAG00000015195	EHD3	EH domain containing 3	-1,78	1,07E-45
1763.	ENSECAG00000017015	MYH11	myosin heavy chain 11	-1,781	4,62E-15
1764.	ENSECAG00000008324	LECT2	leukocyte cell derived chemotaxin 2	-1,786	0,001298
1765.	ENSECAG00000027719	ENSECAG00000027719		-1,787	1,82E-08
1766.	ENSECAG00000016080	KCNB1	potassium voltage-gated channel subfamily B member 1	-1,787	5,15E-08
1767.	ENSECAG00000015388	EDIL3	EGF like repeats and discoidin domains 3	-1,789	5,1E-06
1768.	ENSECAG00000015840	PODN	podocan	-1,79	5,02E-13
1769.	ENSECAG00000021850	CLDN16	claudin 16	-1,79	0,000477
1770.	ENSECAG00000013566	PKP2	plakophilin 2	-1,793	0,00013
1771.	ENSECAG00000013515	SEMA3B	semaphorin 3B	-1,793	1,73E-18
1772.	ENSECAG00000003137	P4HTM	prolyl 4-hydroxylase, transmembrane	-1,793	5,38E-14
1773.	ENSECAG00000020239	SLC2A12	solute carrier family 2 member 12	-1,797	0,001357
1774.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-1,801	9,11E-15
1775.	ENSECAG00000007176	ELOVL7	ELOVL fatty acid elongase 7	-1,803	2,14E-18
1776.	ENSECAG00000046600	ENSECAG00000046600		-1,804	3,47E-05
1777.	ENSECAG00000010195	LRRC38	leucine rich repeat containing 38	-1,806	7,64E-05
1778.	ENSECAG00000053885	ENSECAG00000053885		-1,807	8,77E-21
1779.	ENSECAG00000000354	PLK2	polo like kinase 2	-1,812	1,43E-75
1780.	ENSECAG00000011901	UNC5D	unc-5 netrin receptor D	-1,814	1,42E-07
1781.	ENSECAG00000046450	ENSECAG00000046450		-1,816	2,69E-07
1782.	ENSECAG00000022407	SLIT2	slit guidance ligand 2	-1,817	1,35E-22
1783.	ENSECAG00000000217	MTSS2	MTSS I-BAR domain containing 2	-1,817	1,02E-26
1784.	ENSECAG00000018005	PMEPA1	prostate transmembrane protein, androgen induced 1	-1,819	5,01E-38
1785.	ENSECAG00000024798	TBC1D30	TBC1 domain family member 30	-1,824	0,000136
1786.	ENSECAG00000057783	ENSECAG00000057783		-1,828	1,2E-14

1787.	ENSECAG00000043642	NREP	neuronal reration related protein	-1,831	1,39E-46
1788.	ENSECAG00000009699	DNAH7	dynein axonemal heavy chain 7	-1,832	5,56E-07
1789.	ENSECAG00000048455	ENSECAG00000048455		-1,832	5,21E-13
1790.	ENSECAG00000059312	ENSECAG00000059312		-1,834	6,86E-40
1791.	ENSECAG00000010184	ADAMTSL3	ADAMTS like 3	-1,834	5,74E-10
1792.	ENSECAG00000006829	KAZN	kazrin, periplakin interacting protein	-1,835	1,17E-30
1793.	ENSECAG00000009280	SPARCL1	SPARC like 1	-1,835	5,21E-32
1794.	ENSECAG00000041924	COL23A1	collagen type XXIII alpha 1 chain	-1,836	1,82E-07
1795.	ENSECAG00000017743	SESN3	sestrin 3	-1,837	2,13E-42
1796.	ENSECAG00000018159	CNNM2	cyclin and CBS domain divalent metal cation transport mediator 2	-1,843	1,78E-29
1797.	ENSECAG00000028788	HES4	hes family bHLH transcription factor 4	-1,844	0,000318
1798.	ENSECAG00000016721	RUBCNL	rubicon like autophagy enhancer	-1,846	4,26E-10
1799.	ENSECAG00000000046	FAM13C	family with sequence similarity 13 member C	-1,851	1,66E-05
1800.	ENSECAG00000021066	KLHL24	kelch like family member 24	-1,855	1,36E-75
1801.	ENSECAG00000019090	MAB21L3	mab-21 like 3	-1,856	7,87E-09
1802.	ENSECAG00000006980	FEZ1	fasciculation and elongation protein zeta 1	-1,86	2,19E-12
1803.	ENSECAG00000008564	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1,861	0,00082
1804.	ENSECAG00000045790	ENSECAG00000045790		-1,861	3,28E-29
1805.	ENSECAG00000015853	SORT1	sortilin 1	-1,861	1,31E-08
1806.	ENSECAG00000053849	ENSECAG00000053849		-1,863	3,6E-06
1807.	ENSECAG00000057105	ENSECAG00000057105		-1,863	0,001146
1808.	ENSECAG00000017812	AHRR	aryl hydrocarbon receptor repressor	-1,874	1,37E-06
1809.	ENSECAG00000002579	MATN2	matrilin 2	-1,875	2,39E-19
1810.	ENSECAG000000023607	DOCK5	dedicator of cytokinesis 5	-1,875	7,54E-21
1811.	ENSECAG00000053674	MORN4	MORN repeat containing 4	-1,875	1,11E-28
1812.	ENSECAG00000017844	OXTR	oxytocin receptor	-1,877	1,07E-41
1813.	ENSECAG00000034239	ZNF467	zinc finger protein 467	-1,879	0,003794
1814.	ENSECAG00000032719	ENSECAG00000032719		-1,883	8,46E-05
1815.	ENSECAG00000012282	MPP7	MAGUK p55 scaffold protein 7	-1,888	3,92E-09
1816.	ENSECAG00000048830	ENSECAG00000048830		-1,891	0,000157
1817.	ENSECAG00000044193	ENSECAG00000044193		-1,893	0,00199
1818.	ENSECAG00000011193	KBTBD12	kelch repeat and BTB domain containing 12	-1,894	2,23E-08
1819.	ENSECAG00000024701	AOX4	aldehyde oxidase 4	-1,9	4,33E-09
1820.	ENSECAG00000010695	FGF21	fibroblast growth factor 21	-1,904	1,27E-10
1821.	ENSECAG00000045708	ENSECAG00000045708		-1,905	1,29E-06
1822.	ENSECAG00000024637	P2RX5	purinergic receptor P2X 5	-1,911	4,54E-06
1823.	ENSECAG00000020437	BCL2	BCL2 apoptosis regulator	-1,912	2,57E-17
1824.	ENSECAG00000020395	ISM2	isthmin 2	-1,913	0,003575
1825.	ENSECAG00000021042	VASH1	vasohibin 1	-1,914	1,26E-45
1826.	ENSECAG00000038056	ENSECAG00000038056		-1,914	1,69E-13
1827.	ENSECAG00000019083	SORL1	sortilin related receptor 1	-1,92	1,03E-32
1828.	ENSECAG00000019343	ALDH1A1	aldehyde dehydrogenase 1 family member A1	-1,921	1,45E-33
1829.	ENSECAG00000049223	ENSECAG00000049223		-1,927	4,04E-05
1830.	ENSECAG00000020901	CLCA2	chloride channel accessory 2	-1,929	0,000382
1831.	ENSECAG00000021643	LIX1	limb and CNS expressed 1	-1,93	8,3E-12
1832.	ENSECAG00000051305	ENSECAG00000051305		-1,932	0,002198
1833.	ENSECAG00000012960	IRAK2	interleukin 1 receptor associated kinase 2	-1,936	5,53E-47
1834.	ENSECAG00000004707	MFSD6	major facilitator superfamily domain containing 6	-1,937	2,05E-09
1835.	ENSECAG00000001488	GPR171	G protein-coupled receptor 171	-1,938	5,72E-07
1836.	ENSECAG00000016430	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	-1,939	1,91E-05
1837.	ENSECAG00000021653	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	-1,951	4,3E-185
1838.	ENSECAG00000011187	TSPAN11	tetraspanin 11	-1,952	4,97E-09
1839.	ENSECAG00000022513	NPAS1	neuronal PAS domain protein 1	-1,954	0,000505
1840.	ENSECAG00000009086	BEND7	BEN domain containing 7	-1,962	7,83E-23
1841.	ENSECAG00000053823	ENSECAG00000053823		-1,963	1E-06
1842.	ENSECAG00000001279	AGTR1	angiotensin II receptor type 1	-1,966	1,21E-06
1843.	ENSECAG00000019176	KRT80	keratin 80	-1,969	0,000195

1844.	ENSECAG00000020731	MXRA8	matrix remodeling associated 8	-1,969	6,78E-19
1845.	ENSECAG00000029419	ENSECAG00000029419		-1,972	1,58E-05
1846.	ENSECAG00000043884	ENSECAG00000043884		-1,972	1,37E-05
1847.	ENSECAG00000037540	ENSECAG00000037540		-1,974	0,001004
1848.	ENSECAG00000015951	PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	-1,976	5,49E-16
1849.	ENSECAG00000013574	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	-1,98	3,46E-15
1850.	ENSECAG00000036138	ENSECAG00000036138		-1,99	1,3E-06
1851.	ENSECAG00000012955	CD163L1	CD163 molecule like 1	-1,992	0,000921
1852.	ENSECAG00000037655	GDNF	glial cell derived neurotrophic factor	-1,993	1,33E-05
1853.	ENSECAG00000023578	ELOVL3	ELOVL fatty acid elongase 3	-1,994	2,13E-13
1854.	ENSECAG00000019701	ANKFN1	ankyrin repeat and fibronectin type III domain containing 1	-1,995	1,93E-08
1855.	ENSECAG00000034852	COL4A5	collagen type IV alpha 5 chain	-1,998	2,42E-14
1856.	ENSECAG00000050004	BTC	betacellulin	-2,001	1,52E-06
1857.	ENSECAG00000017301	C3H4orf19	chromosome 3 C4orf19 homolog	-2,006	0,000733
1858.	ENSECAG00000008038	TENM4	teneurin transmembrane protein 4	-2,009	1,21E-41
1859.	ENSECAG00000041546	ENSECAG00000041546		-2,012	0,001692
1860.	ENSECAG00000012115	SEMA3D	semaphorin 3D	-2,012	5,79E-16
1861.	ENSECAG00000017816	ADORA1	adenosine A1 receptor	-2,023	1,34E-23
1862.	ENSECAG00000032702	ENSECAG00000032702		-2,029	4,57E-12
1863.	ENSECAG00000011747	BCL7A	BAF chromatin remodeling complex subunit BCL7A	-2,037	5,7E-15
1864.	ENSECAG00000011618	EDN1	endothelin 1	-2,041	2,69E-10
1865.	ENSECAG00000014710	FZD6	frizzled class receptor 6	-2,041	3,49E-07
1866.	ENSECAG00000022107	SLC16A4	solute carrier family 16 member 4	-2,043	8,09E-05
1867.	ENSECAG00000009250	RAMP1	receptor activity modifying protein 1	-2,045	0,000297
1868.	ENSECAG00000015892	CACNA1D	calcium voltage-gated channel subunit alpha1 D	-2,045	1,14E-38
1869.	ENSECAG00000019042	UPK1B	uroplakin 1B	-2,047	3,51E-26
1870.	ENSECAG00000035101	ANOS1	anosmin 1	-2,048	0,000124
1871.	ENSECAG00000010004	PRUNE2	prune homolog 2 with BCH domain	-2,049	1,66E-28
1872.	ENSECAG00000016907	NKD2	NKD inhibitor of WNT signaling pathway 2	-2,053	1,14E-20
1873.	ENSECAG00000018067	ITGBL1	integrin subunit beta like 1	-2,056	3,8E-63
1874.	ENSECAG00000018419	ANXA3	annexin A3	-2,073	5,37E-09
1875.	ENSECAG00000023825	EXOC6	exocyst complex component 6	-2,077	1,43E-16
1876.	ENSECAG00000008768	PARD3B	par-3 family cell polarity regulator beta	-2,077	2,97E-85
1877.	ENSECAG00000013393	AHR	aryl hydrocarbon receptor	-2,087	8,78E-48
1878.	ENSECAG00000022054	CLSTN2	calsyntenin 2	-2,094	1,48E-40
1879.	ENSECAG00000022683	RSPO1	R-spondin 1	-2,095	1,48E-13
1880.	ENSECAG00000017502	PCDH9	protocadherin 9	-2,101	8,24E-16
1881.	ENSECAG00000021387	MYOM3	myomesin 3	-2,108	2,39E-09
1882.	ENSECAG00000053581	ENSECAG00000053581		-2,123	3,65E-06
1883.	ENSECAG00000051853	ENSECAG00000051853		-2,126	0,000377
1884.	ENSECAG00000012754	HSPB2	heat shock protein family B (small) member 2	-2,126	3,49E-05
1885.	ENSECAG00000012967	PRKAA2	protein kinase AMP-activated catalytic subunit alpha 2	-2,126	4,25E-10
1886.	ENSECAG00000003570	PICK1	protein interacting with PRKCA 1	-2,128	3,06E-24
1887.	ENSECAG00000010700	CREG2	cellular repressor of E1A stimulated genes 2	-2,13	6,55E-10
1888.	ENSECAG00000010967	MMP19	matrix metalloproteinase 19	-2,132	2,46E-41
1889.	ENSECAG00000012767	C7H11orf52	chromosome 7 C11orf52 homolog	-2,142	9,94E-07
1890.	ENSECAG00000025076	CTTNBP2	cortactin binding protein 2	-2,152	8,12E-27
1891.	ENSECAG00000011749	MSX2	msh homeobox 2	-2,153	4,77E-26
1892.	ENSECAG00000018803	PGM2L1	phosphoglucomutase 2 like 1	-2,158	3,22E-39
1893.	ENSECAG00000049093	ENSECAG00000049093		-2,164	9,4E-06
1894.	ENSECAG00000018692	SEPTIN12	septin 12	-2,167	4,81E-15
1895.	ENSECAG00000030526	ENSECAG00000030526		-2,168	0,000133
1896.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-2,177	5,23E-34
1897.	ENSECAG00000014646	KNG1	kininogen 1	-2,182	2,11E-21
1898.	ENSECAG00000002390	ENSECAG00000002390		-2,185	3,99E-19
1899.	ENSECAG00000044544	ENSECAG00000044544		-2,188	1,06E-07
1900.	ENSECAG00000008762	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	-2,188	6,26E-11

1901.	ENSECAG00000015715	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif 15	-2,193	6,74E-29
1902.	ENSECAG00000004854	PLPPR4	phospholipid phosphatase related 4	-2,194	2,39E-07
1903.	ENSECAG00000007274	PLCL1	phospholipase C like 1 (inactive)	-2,194	6,48E-07
1904.	ENSECAG000000044332	ENSECAG000000044332		-2,201	0,002221
1905.	ENSECAG000000054519	ENSECAG000000054519		-2,204	9,68E-05
1906.	ENSECAG000000057732	ENSECAG000000057732		-2,208	0,001246
1907.	ENSECAG000000016277	SGCD	sarcoglycan delta	-2,218	2,42E-25
1908.	ENSECAG000000019055	TSGA10	testis specific 10	-2,219	5,28E-05
1909.	ENSECAG000000013390	ZMAT1	zinc finger matrin-type 1	-2,221	8,99E-08
1910.	ENSECAG000000057723	ENSECAG000000057723		-2,222	3,84E-23
1911.	ENSECAG000000002935	KCNF1	potassium voltage-gated channel modifier subfamily F member 1	-2,222	4,09E-14
1912.	ENSECAG000000024137	ENDOU	endonuclease, poly(U) specific	-2,222	3,67E-13
1913.	ENSECAG000000009375	GASK1A	golgi associated kinase 1A	-2,238	2,79E-07
1914.	ENSECAG000000010553	NGF	nerve growth factor	-2,239	4,02E-21
1915.	ENSECAG000000011594	KCND3	potassium voltage-gated channel subfamily D member 3	-2,242	5,16E-32
1916.	ENSECAG000000007044	FRAS1	Fraser extracellular matrix complex subunit 1	-2,249	0,000758
1917.	ENSECAG000000015134	PELI2	pellino E3 ubiquitin protein ligase family member 2	-2,249	5,36E-18
1918.	ENSECAG000000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-2,254	9,4E-16
1919.	ENSECAG000000024448	TRIM63	tripartite motif containing 63	-2,255	1,37E-40
1920.	ENSECAG000000019940	AKAP6	A-kinase anchoring protein 6	-2,266	5,08E-27
1921.	ENSECAG000000022387	RUNDC3B	RUN domain containing 3B	-2,273	0,000342
1922.	ENSECAG000000008237	KLHL13	kelch like family member 13	-2,275	7,03E-85
1923.	ENSECAG000000010262	PERP	p53 apoptosis effector related to PMP22	-2,275	8,36E-13
1924.	ENSECAG000000025633	MIR27B	microRNA 27b	-2,278	0,000148
1925.	ENSECAG000000010242	MCTP1	multiple C2 and transmembrane domain containing 1	-2,286	2,19E-75
1926.	ENSECAG000000015552	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-2,297	5,38E-05
1927.	ENSECAG000000017459	ARRB1	arrestin beta 1	-2,298	2,92E-25
1928.	ENSECAG000000000794	EMB	embigin	-2,301	2,08E-05
1929.	ENSECAG000000022370	NEFM	neurofilament medium chain	-2,302	7,33E-10
1930.	ENSECAG000000046102	ENSECAG000000046102		-2,304	1,63E-05
1931.	ENSECAG000000007220	HEYL	hes related family bHLH transcription factor with YRPW motif like	-2,305	3,65E-10
1932.	ENSECAG000000010926	ELMOD1	ELMO domain containing 1	-2,311	0,000976
1933.	ENSECAG000000018472	PDGFB	platelet derived growth factor subunit B	-2,312	3,13E-07
1934.	ENSECAG000000011467	ALPL	alkaline phosphatase, biomineralization associated	-2,314	3,05E-18
1935.	ENSECAG000000027835	LRATD1	LRAT domain containing 1	-2,318	3,33E-05
1936.	ENSECAG000000021576	SGCG	sarcoglycan gamma	-2,331	6,96E-14
1937.	ENSECAG000000021132	AFF2	ALF transcription elongation factor 2	-2,333	2,02E-50
1938.	ENSECAG000000007183	SEMA3E	semaphorin 3E	-2,333	5,04E-05
1939.	ENSECAG000000006137	FAM227A	family with sequence similarity 227 member A	-2,345	0,000329
1940.	ENSECAG000000059741	ENSECAG000000059741		-2,345	6,47E-09
1941.	ENSECAG000000023080	PPP1R12B	protein phosphatase 1 regulatory subunit 12B	-2,345	1,36E-18
1942.	ENSECAG000000006020	RRAGB	Ras related GTP binding B	-2,356	6,04E-49
1943.	ENSECAG000000011138	COL4A4	collagen type IV alpha 4 chain	-2,358	1,17E-09
1944.	ENSECAG000000028399	DTX1	deltex E3 ubiquitin ligase 1	-2,362	0,001227
1945.	ENSECAG000000054414	PLA1A	phospholipase A1 member A	-2,362	3,87E-58
1946.	ENSECAG000000002430	PRKAG3	protein kinase AMP-activated non-catalytic subunit gamma 3	-2,371	1,27E-15
1947.	ENSECAG000000021856	PADI2	peptidyl arginine deiminase 2	-2,373	3,72E-21
1948.	ENSECAG000000012507	CRYAB	crystallin alpha B	-2,375	4,61E-35
1949.	ENSECAG000000023039	CCN3	cellular communication network factor 3	-2,388	5,41E-11
1950.	ENSECAG000000007878	FRMD3	FERM domain containing 3	-2,389	1,31E-08
1951.	ENSECAG000000008094	BCL11A	BCL11 transcription factor A	-2,391	0,000377
1952.	ENSECAG000000019193	NCAM1	neural cell adhesion molecule 1	-2,394	1,8E-159
1953.	ENSECAG000000022629	SLC1A7	solute carrier family 1 member 7	-2,397	2,3E-38

1954.	ENSECAG00000018314	TIMP3	TIMP metallopeptidase inhibitor 3	-2,399	2,22E-33
1955.	ENSECAG00000007798	ME3	malic enzyme 3	-2,402	2,14E-14
1956.	ENSECAG00000042387	ENSECAG00000042387		-2,404	0,000539
1957.	ENSECAG00000022853	CD28	CD28 molecule	-2,415	0,001598
1958.	ENSECAG00000025179	TEKT3	tektin 3	-2,417	0,000114
1959.	ENSECAG00000039231	ATOH8	atonal bHLH transcription factor 8	-2,418	0,000205
1960.	ENSECAG00000021360	KCNMB1	potassium calcium-activated channel subfamily M regulatory beta subunit 1	-2,419	5,69E-29
1961.	ENSECAG00000013400	AADAT	aminoadipate aminotransferase	-2,42	7,5E-11
1962.	ENSECAG00000008053	TMEM170B	transmembrane protein 170B	-2,426	6,04E-42
1963.	ENSECAG00000015826	RRAGD	Ras related GTP binding D	-2,427	7,02E-05
1964.	ENSECAG00000018927	ANGPTL4	angiopoietin like 4	-2,429	2,91E-17
1965.	ENSECAG00000048469	ENSECAG00000048469		-2,43	2,05E-05
1966.	ENSECAG00000021621	MOB3B	MOB kinase activator 3B	-2,432	2,71E-07
1967.	ENSECAG00000040382	ENSECAG00000040382		-2,435	1,23E-27
1968.	ENSECAG00000010939	ANGPTL1	angiopoietin like 1	-2,44	4,7E-15
1969.	ENSECAG00000009813	CD83	CD83 molecule	-2,444	1,06E-08
1970.	ENSECAG00000007281	SAMD11	sterile alpha motif domain containing 11	-2,447	5,17E-25
1971.	ENSECAG00000018863	ADGRL3	adhesion G protein-coupled receptor L3	-2,455	4,27E-20
1972.	ENSECAG00000019335	TLCD4	TLC domain containing 4	-2,458	1,93E-23
1973.	ENSECAG00000010901	CTNND2	catenin delta 2	-2,46	2,83E-05
1974.	ENSECAG00000026884	NRG4	neuregulin 4	-2,469	3,6E-06
1975.	ENSECAG00000007792	EFCAB6	EF-hand calcium binding domain 6	-2,483	2,14E-05
1976.	ENSECAG00000021663	SMOC1	SPARC related modular calcium binding 1	-2,483	8,36E-06
1977.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-2,488	6,15E-06
1978.	ENSECAG00000023274	LAMA5	laminin subunit alpha 5	-2,49	1,89E-16
1979.	ENSECAG00000053524	BEX4	brain expressed X-linked 4	-2,501	3,04E-06
1980.	ENSECAG00000050236	ENSECAG00000050236		-2,506	4,21E-06
1981.	ENSECAG00000033590	ENSECAG00000033590		-2,509	0,000389
1982.	ENSECAG00000013884	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	-2,509	2,49E-07
1983.	ENSECAG00000020677	LHCGR	luteinizing hormone/choriogonadotropin receptor	-2,523	2,78E-05
1984.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-2,526	5,08E-19
1985.	ENSECAG00000014200	TMEM178B	transmembrane protein 178B	-2,532	2,42E-05
1986.	ENSECAG00000019851	DMGDH	dimethylglycine dehydrogenase	-2,545	9,11E-05
1987.	ENSECAG00000016786	JPH2	junctophilin 2	-2,557	8,12E-06
1988.	ENSECAG00000013986	TMEM178A	transmembrane protein 178A	-2,561	8,69E-05
1989.	ENSECAG00000021092	KLF15	KLF transcription factor 15	-2,566	8,15E-23
1990.	ENSECAG00000032860	ENSECAG00000032860		-2,571	4,93E-26
1991.	ENSECAG00000000709	ENSECAG00000000709		-2,591	9,54E-06
1992.	ENSECAG00000006879	PLA2G5	phospholipase A2 group V	-2,591	4,82E-40
1993.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-2,596	3,52E-09
1994.	ENSECAG00000047402	ENSECAG00000047402		-2,607	0,00014
1995.	ENSECAG00000040326	ENSECAG00000040326		-2,608	6,92E-10
1996.	ENSECAG00000000787	ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif 16	-2,609	0,000126
1997.	ENSECAG00000015834	DMD	dystrophin	-2,619	7,73E-20
1998.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-2,621	1,41E-08
1999.	ENSECAG00000000658	GPNMB	glycoprotein nmb	-2,631	9,2E-222
2000.	ENSECAG00000018631	LTBP2	latent transforming growth factor beta binding protein 2	-2,638	1,75E-38
2001.	ENSECAG00000011774	APCDD1	APC down-regulated 1	-2,652	1,27E-13
2002.	ENSECAG00000013625	FN3KRP	fructosamine 3 kinase related protein	-2,655	0,000582
2003.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-2,659	2,55E-06
2004.	ENSECAG00000013036	MCAM	melanoma cell adhesion molecule	-2,662	1,16E-13
2005.	ENSECAG00000016234	ANGPTL2	angiopoietin like 2	-2,668	3,57E-57
2006.	ENSECAG00000024039	HFM1	helicase for meiosis 1	-2,69	4,95E-15
2007.	ENSECAG00000012962	SAMD12	sterile alpha motif domain containing 12	-2,691	2,88E-50
2008.	ENSECAG00000012105	IGSF9B	immunoglobulin superfamily member 9B	-2,691	1,92E-06

2009.	ENSECAG00000010747	SH3BGR	SH3 domain binding glutamate rich protein	-2,698	9,95E-56
2010.	ENSECAG00000054922	ENSECAG00000054922		-2,706	0,000153
2011.	ENSECAG00000024045	EFHD1	EF-hand domain family member D1	-2,709	1,33E-26
2012.	ENSECAG00000018280	TACC2	transforming acidic coiled-coil containing protein 2	-2,71	3,96E-42
2013.	ENSECAG00000026951	ARVCF	ARVCF delta catenin family member	-2,717	5,94E-11
2014.	ENSECAG00000018543	RCAN2	regulator of calcineurin 2	-2,72	1,79E-23
2015.	ENSECAG00000006902	GDF6	growth differentiation factor 6	-2,723	7,05E-13
2016.	ENSECAG00000024612	SNED1	sushi, nidogen and EGF like domains 1	-2,723	5,94E-06
2017.	ENSECAG00000015961	PPP1R9A	protein phosphatase 1 regulatory subunit 9A	-2,725	3,5E-40
2018.	ENSECAG00000013217	ECHDC2	enoyl-CoA hydratase domain containing 2	-2,743	2,71E-31
2019.	ENSECAG00000045707	ENSECAG00000045707		-2,746	0,000597
2020.	ENSECAG00000014320	PPL	periplakin	-2,761	7,02E-13
2021.	ENSECAG00000047272	ENSECAG00000047272		-2,764	4,45E-14
2022.	ENSECAG00000000417	VWA2	von Willebrand factor A domain containing 2	-2,772	0,000206
2023.	ENSECAG00000035477	ENSECAG00000035477		-2,775	0,000307
2024.	ENSECAG00000020101	SLC24A2	solute carrier family 24 member 2	-2,78	3,04E-21
2025.	ENSECAG00000015365	GCSAML	germinal center associated signaling and motility like	-2,78	0,000269
2026.	ENSECAG00000060299	ENSECAG00000060299		-2,79	4,72E-10
2027.	ENSECAG00000059852	ENSECAG00000059852		-2,79	0,000468
2028.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-2,791	5,28E-05
2029.	ENSECAG00000019008	SHROOM3	shroom family member 3	-2,794	4,68E-30
2030.	ENSECAG00000013677	FRY	FRY microtubule binding protein	-2,794	6,68E-47
2031.	ENSECAG00000013893	SCARA5	scavenger receptor class A member 5	-2,797	0,000585
2032.	ENSECAG00000013301	MFAP4	microfibril associated protein 4	-2,808	2,51E-30
2033.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-2,822	1,68E-47
2034.	ENSECAG00000015569	MATCAP2	microtubule associated tyrosine carboxypeptidase 2	-2,823	7,17E-20
2035.	ENSECAG00000020869	FGFR4	fibroblast growth factor receptor 4	-2,828	4,44E-20
2036.	ENSECAG00000012212	LRP1B	LDL receptor related protein 1B	-2,829	1,65E-09
2037.	ENSECAG00000010880	SOX6	SRY-box transcription factor 6	-2,834	2,28E-12
2038.	ENSECAG00000007385	NIBAN1	niban apoptosis regulator 1	-2,835	1,2E-111
2039.	ENSECAG00000060247	ENSECAG00000060247		-2,84	7,84E-77
2040.	ENSECAG00000010667	ERG	ETS transcription factor ERG	-2,842	9,66E-14
2041.	ENSECAG00000023960	KLHL30	kelch like family member 30	-2,843	7,04E-09
2042.	ENSECAG00000022874	SCG5	secretogranin V	-2,847	9,5E-19
2043.	ENSECAG00000000149	CNKSR2	connector enhancer of kinase suppressor of Ras 2	-2,849	0,000232
2044.	ENSECAG00000021292	ENSECAG00000021292		-2,85	1,15E-24
2045.	ENSECAG00000014313	DCLK2	doublecortin like kinase 2	-2,852	2,36E-13
2046.	ENSECAG00000015760	ITGA3	integrin subunit alpha 3	-2,852	3,36E-30
2047.	ENSECAG00000026945	HES1	hes family bHLH transcription factor 1	-2,887	7,7E-14
2048.	ENSECAG00000016015	PCDH19	protocadherin 19	-2,899	2,92E-20
2049.	ENSECAG00000048282	ENSECAG00000048282		-2,907	5,67E-24
2050.	ENSECAG00000046252	ENSECAG00000046252		-2,91	5,73E-14
2051.	ENSECAG00000048971	RNF152	ring finger protein 152	-2,915	2,24E-13
2052.	ENSECAG00000000166	SPHKAP	SPHK1 interactor, AKAP domain containing	-2,916	2,22E-23
2053.	ENSECAG00000012667	RBFOX1	RNA binding fox-1 homolog 1	-2,916	4,02E-22
2054.	ENSECAG00000029885	CHST7	carbohydrate sulfotransferase 7	-2,919	2,21E-20
2055.	ENSECAG00000022890	NEFL	neurofilament light chain	-2,935	2,09E-13
2056.	ENSECAG00000010327	INPP4B	inositol polyphosphate-4-phosphatase type II B	-2,938	2,41E-06
2057.	ENSECAG00000014287	OMD	osteomodulin	-2,942	1,97E-42
2058.	ENSECAG00000039359	CYS1	cystin 1	-2,943	3,9E-32
2059.	ENSECAG00000000435	LRP2	LDL receptor related protein 2	-2,946	5,73E-11
2060.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-2,985	1,51E-08
2061.	ENSECAG00000013450	CORO6	coronin 6	-2,996	2,63E-11
2062.	ENSECAG00000034955	BHLHE41	basic helix-loop-helix family member e41	-2,999	3,51E-28
2063.	ENSECAG00000013960	FGFR2	fibroblast growth factor receptor 2	-3	2,67E-07

2064.	ENSECAG00000018933	WNT4	Wnt family member 4	-3,041	2,91E-06
2065.	ENSECAG00000031034	ENSECAG00000031034		-3,051	3,2E-09
2066.	ENSECAG00000057017	ABCA8	ATP binding cassette subfamily A member 8	-3,051	1,17E-08
2067.	ENSECAG00000059760	ADRA2A	adrenoceptor alpha 2A	-3,064	1,47E-40
2068.	ENSECAG00000044796	GREM1	gremlin 1, DAN family BMP antagonist	-3,082	4,03E-17
2069.	ENSECAG00000003230	AKAP5	A-kinase anchoring protein 5	-3,089	3,27E-20
2070.	ENSECAG00000036870	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-3,093	3,54E-18
2071.	ENSECAG00000009528	CDH3	cadherin 3	-3,125	8,94E-07
2072.	ENSECAG00000004258	IL17RB	interleukin 17 receptor B	-3,143	1,08E-10
2073.	ENSECAG00000018771	PKNOX2	PBX/knotted 1 homeobox 2	-3,17	9,43E-18
2074.	ENSECAG00000054759	ENSECAG00000054759		-3,194	8,19E-09
2075.	ENSECAG00000008518	NPNT	nephronectin	-3,204	3,09E-32
2076.	ENSECAG00000022441	ESR1	estrogen receptor 1	-3,207	1,3E-171
2077.	ENSECAG00000056462	MMP12	matrix metalloproteinase 12	-3,213	1,28E-07
2078.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-3,224	8,88E-12
2079.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-3,225	9,7E-12
2080.	ENSECAG00000033624	ENSECAG00000033624		-3,236	1,03E-07
2081.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-3,242	3,84E-58
2082.	ENSECAG00000044498	CA3	carbonic anhydrase 3	-3,247	4,66E-09
2083.	ENSECAG00000030850	FGF18	fibroblast growth factor 18	-3,265	2,43E-10
2084.	ENSECAG00000000501	UNC5CL	unc-5 family C-terminal like	-3,351	1,54E-05
2085.	ENSECAG00000016129	ABLIM3	actin binding LIM protein family member 3	-3,355	1,91E-17
2086.	ENSECAG00000023387	FRRS1	ferric chelate reductase 1	-3,376	1,76E-16
2087.	ENSECAG00000017802	OGN	osteoglycin	-3,396	2,97E-35
2088.	ENSECAG00000031859	ENSECAG00000031859		-3,433	5,45E-30
2089.	ENSECAG00000004445	PDE11A	phosphodiesterase 11A	-3,435	7,7E-113
2090.	ENSECAG00000042911	ENSECAG00000042911		-3,446	2,61E-07
2091.	ENSECAG00000009125	UPK3A	uroplakin 3A	-3,455	8E-08
2092.	ENSECAG000000039579	GDF15	growth differentiation factor 15	-3,537	0,000149
2093.	ENSECAG00000019495	C5H1orf141	chromosome 5 C1orf141 homolog	-3,591	2,93E-05
2094.	ENSECAG00000053078	ENSECAG00000053078		-3,597	8,65E-08
2095.	ENSECAG00000011653	ADRA1B	adrenoceptor alpha 1B	-3,603	2,77E-05
2096.	ENSECAG00000049817	ENSECAG00000049817		-3,611	2,4E-10
2097.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-3,616	2,69E-42
2098.	ENSECAG00000017701	CELSR2	cadherin EGF LAG seven-pass G-type receptor 2	-3,642	5,89E-16
2099.	ENSECAG00000042952	GPX3	glutathione peroxidase 3	-3,67	1,86E-10
2100.	ENSECAG00000057296	ENSECAG00000057296		-3,712	0,000162
2101.	ENSECAG00000015927	CABLES1	Cdk5 and Abl enzyme substrate 1	-3,733	1,67E-17
2102.	ENSECAG00000013221	PTPRQ	protein tyrosine phosphatase receptor type Q	-3,788	8,12E-05
2103.	ENSECAG00000014504	KIF1A	kinesin family member 1A	-3,802	7,18E-21
2104.	ENSECAG00000002874	LRRN1	leucine rich repeat neuronal 1	-3,807	2,67E-08
2105.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-3,817	5,94E-06
2106.	ENSECAG00000015484	ATP6V0D2	ATPase H+ transporting V0 subunit d2	-3,847	3,12E-23
2107.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-3,889	1,4E-113
2108.	ENSECAG00000041748	COL4A3	collagen type IV alpha 3 chain	-3,9	1,42E-38
2109.	ENSECAG00000023089	SLAIN1	SLAIN motif family member 1	-3,932	1,93E-06
2110.	ENSECAG00000018716	FGF9	fibroblast growth factor 9	-3,947	5,51E-10
2111.	ENSECAG00000007047	ASPN	asporin	-3,982	4,01E-43
2112.	ENSECAG00000001197	TNFRSF19	TNF receptor superfamily member 19	-4,033	1,81E-14
2113.	ENSECAG00000007989	C1QTNF7	C1q and TNF related 7	-4,052	1,05E-06
2114.	ENSECAG00000016251	ENSECAG00000016251		-4,086	1,36E-16
2115.	ENSECAG00000015000	FAM83G	family with sequence similarity 83 member G	-4,101	3,13E-20
2116.	ENSECAG00000013817	CYP1A1	cytochrome P450 family 1 subfamily A member 1	-4,11	1,78E-06
2117.	ENSECAG00000038712	TNXB	tenascin XB	-4,197	5,2E-230
2118.	ENSECAG00000014285	INHBB	inhibin subunit beta B	-4,198	3,2E-32
2119.	ENSECAG00000047821	ENSECAG00000047821		-4,226	8,19E-09
2120.	ENSECAG00000040154	ELN	elastin	-4,283	1,36E-53
2121.	ENSECAG00000015934	MAMDC2	MAM domain containing 2	-4,284	1,6E-43

2122.	ENSECAG00000000278	FCAMR	Fc alpha and mu receptor	-4,34	0,000317
2123.	ENSECAG000000021078	GRB14	growth factor receptor bound protein 14	-4,34	8,46E-17
2124.	ENSECAG000000015460	HCLS1	hematopoietic cell-specific Lyn substrate 1	-4,373	7,17E-15
2125.	ENSECAG000000048070	ENSECAG000000048070		-4,376	3,42E-11
2126.	ENSECAG000000012993	JAG1	jagged canonical Notch ligand 1	-4,403	5,49E-27
2127.	ENSECAG000000008618	LCA5L	lebercilin LCA5 like	-4,435	7,95E-07
2128.	ENSECAG000000028632	ENSECAG000000028632		-4,565	6,8E-08
2129.	ENSECAG000000003067	PWWP3B	PWWP domain containing 3B	-4,66	2,69E-07
2130.	ENSECAG000000014513	TNFSF15	TNF superfamily member 15	-4,849	3,61E-25
2131.	ENSECAG000000010721	MGP	matrix Gla protein	-5,011	5,7E-260
2132.	ENSECAG000000056537	ENSECAG000000056537		-5,097	9,34E-07
2133.	ENSECAG000000023161	IGSF10	immunoglobulin superfamily member 10	-5,209	1,59E-23
2134.	ENSECAG000000017460	ATP12A	ATPase H+/K+ transporting non-gastric alpha2 subunit	-5,257	1,61E-08
2135.	ENSECAG000000018308	GREB1	growth regulating estrogen receptor binding 1	-5,377	1,55E-47
2136.	ENSECAG000000009483	PRLR	prolactin receptor	-5,848	1,43E-16
2137.	ENSECAG000000036634	CCDC3	coiled-coil domain containing 3	-5,91	2,82E-24
2138.	ENSECAG000000006772	DYSF	dysferlin	-5,947	1,09E-07
2139.	ENSECAG000000010791	LMCD1	LIM and cysteine rich domains 1	-6,278	1,78E-29
2140.	ENSECAG000000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-7,205	3,11E-28

Supplementary Table 3. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category I endometria treated with T-helper 2 cells -conditioned medium (Th2-CM) for 48 hours in comparison to the control group (Research task 2, Experiment 3).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	P _{adj}
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	13,8807	1,773E-31
2.	ENSECAG00000038698	ALOX15	arachidonate 15-lipoxygenase	9,23554	4,189E-23
3.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	8,32228	4,418E-35
4.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	7,66649	2,089E-44
5.	ENSECAG00000051569	ENSECAG00000051569		7,49684	5,6E-18
6.	ENSECAG00000046132	CXCL9	C-X-C motif chemokine ligand 9	7,45967	3,794E-16
7.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	7,3542	7,657E-13
8.	ENSECAG00000020578	PDCD1LG2	programmed cell death 1 ligand 2	7,17534	3,983E-13
9.	ENSECAG00000023841	POSTN	periostin	6,96295	3,79E-29
10.	ENSECAG00000020738	CDH26	cadherin 26	6,49783	3,451E-56
11.	ENSECAG00000001714	PTGDR2	prostaglandin D2 receptor 2	6,43646	7,797E-13
12.	ENSECAG00000020422	PCSK1	proprotein convertase subtilisin/kexin type 1	6,36263	1,849E-09
13.	ENSECAG00000057530	ENSECAG00000057530		6,27818	6,423E-09
14.	ENSECAG00000047988	ENSECAG00000047988		6,18475	3,145E-10
15.	ENSECAG00000014650	INSRR	insulin receptor related receptor	6,14264	7,998E-11
16.	ENSECAG00000010928	MMP25	matrix metalloproteinase 25	5,96475	6,333E-10
17.	ENSECAG00000050680	ENSECAG00000050680		5,80597	1,979E-08
18.	ENSECAG00000024259	Eqca-DQA1		5,80188	1,073E-12
19.	ENSECAG00000019282	HDC	histidine decarboxylase	5,69323	7,385E-08
20.	ENSECAG00000022118	IDO1	indoleamine 2,3-dioxygenase 1	5,54029	3,041E-07
21.	ENSECAG00000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	5,50777	1,99E-18
22.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	5,50324	1,154E-10
23.	ENSECAG00000016312	CD274	CD274 molecule	5,45438	9,6E-250
24.	ENSECAG00000007247	ALPK1	alpha kinase 1	5,41887	1,106E-06
25.	ENSECAG00000012253	CXCL11	C-X-C motif chemokine ligand 11	5,37946	1,831E-07
26.	ENSECAG00000055535	ENSECAG00000055535		5,34844	3,8E-117
27.	ENSECAG00000000152	KITLG	KIT ligand	5,3481	4,16E-136
28.	ENSECAG00000009142	ENSECAG00000009142		5,17362	1,849E-15
29.	ENSECAG00000049658	ENSECAG00000049658		5,02652	1,358E-75
30.	ENSECAG00000012660	HLA-DRA	major histocompatibility complex, class II, DR alpha	5,02428	8,616E-16
31.	ENSECAG00000018134	STMN2	stathmin 2	4,96346	3,004E-05
32.	ENSECAG00000049130	ENSECAG00000049130		4,91454	1,09E-06
33.	ENSECAG000000008503	CD74	CD74 molecule	4,78025	1,019E-05
34.	ENSECAG00000046493	GBP5	guanylate binding protein 5	4,6475	7,833E-29
35.	ENSECAG00000002249	PLEKHG4B	pleckstrin homology and RhoGEF domain containing G4B	4,63047	1,736E-11
36.	ENSECAG00000047919	ENSECAG00000047919		4,61349	1,009E-07
37.	ENSECAG00000013482	SERPINA3	serpin family A member 3	4,43913	2,322E-34
38.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	4,43697	1,181E-05
39.	ENSECAG00000017217	CA12	carbonic anhydrase 12	4,39915	0
40.	ENSECAG00000026965	SOC1	suppressor of cytokine signaling 1	4,31786	1,222E-29
41.	ENSECAG00000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	4,1608	9,974E-13
42.	ENSECAG00000020365	CELF3	CUGBP Elav-like family member 3	4,0601	7,449E-06
43.	ENSECAG00000021775	KRT8	keratin 8	4,03554	3,88E-37
44.	ENSECAG00000019551	CXCL12	C-X-C motif chemokine ligand 12	3,98423	7,645E-89
45.	ENSECAG00000012791	GBP6	guanylate binding protein family member 6	3,94525	2,049E-46
46.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	3,94314	1,222E-51
47.	ENSECAG00000055019	ENSECAG00000055019		3,90993	1,945E-10
48.	ENSECAG00000040532	ENSECAG00000040532		3,87117	4,834E-49
49.	ENSECAG00000021343	NRG1	neuregulin 1	3,81064	2,064E-23
50.	ENSECAG00000034282	CCL8	chemokine (C-C motif) ligand 8	3,71522	6,29E-187
51.	ENSECAG00000016867	CISH	cytokine inducible SH2 containing protein	3,68186	1,016E-07
52.	ENSECAG00000012826	CDO1	cysteine dioxygenase type 1	3,67739	4,711E-52
53.	ENSECAG00000029679	ENSECAG00000029679		3,51209	1,343E-28
54.	ENSECAG00000012742	CXCL6	C-X-C motif chemokine ligand 6	3,50644	3,187E-66
55.	ENSECAG00000055416	ENSECAG00000055416		3,44968	2,295E-15

56.	ENSECAG00000009752	APOA1	apolipoprotein A1	3,41783	5,449E-10
57.	ENSECAG00000043493	ENSECAG00000043493		3,32448	0,0004597
58.	ENSECAG00000015449	IRF8	interferon regulatory factor 8	3,30449	2,483E-05
59.	ENSECAG00000052882	ENSECAG00000052882		3,23762	0,0002887
60.	ENSECAG00000023534	CIITA	class II major histocompatibility complex transactivator	3,20623	1,581E-15
61.	ENSECAG00000006205	CD7	CD7 molecule	3,17663	5,146E-12
62.	ENSECAG00000021796	HLA-DMB	major histocompatibility complex, class II, DM beta	3,1202	9,945E-06
63.	ENSECAG00000019215	ITGB8	integrin subunit beta 8	3,10249	7,191E-36
64.	ENSECAG00000010750	VWCE	von Willebrand factor C and EGF domains	3,07449	2,805E-10
65.	ENSECAG00000046182	ENSECAG00000046182		3,04106	9,497E-11
66.	ENSECAG00000019800	TSPAN33	tetraspanin 33	3,03093	5,952E-27
67.	ENSECAG00000017826	TMEM26	transmembrane protein 26	3,00963	1,647E-18
68.	ENSECAG00000036649	ENSECAG00000036649		2,99811	1,996E-23
69.	ENSECAG00000032992	TIAM1	TIAM Rac1 associated GEF 1	2,96981	1,81E-17
70.	ENSECAG00000055770	KCNE4	potassium voltage-gated channel subfamily E regulatory subunit 4	2,95835	5,058E-54
71.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	2,95511	1,141E-21
72.	ENSECAG00000015119	PHACTR1	phosphatase and actin regulator 1	2,95154	7,181E-06
73.	ENSECAG00000010475	IL33	interleukin 33	2,90098	3,461E-10
74.	ENSECAG00000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	2,89093	2,649E-80
75.	ENSECAG00000009299	ICAM5	intercellular adhesion molecule 5	2,88919	5,551E-06
76.	ENSECAG00000007432	PTGDR	prostaglandin D2 receptor	2,88831	1,121E-17
77.	ENSECAG00000004709	C2	complement C2	2,84426	5,865E-22
78.	ENSECAG00000020767	IL7	interleukin 7	2,83205	7,133E-74
79.	ENSECAG00000018057	IL2RA	interleukin 2 receptor subunit alpha	2,8217	1,897E-21
80.	ENSECAG00000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	2,81586	1,18E-128
81.	ENSECAG00000047572	ENSECAG00000047572		2,81426	8,821E-05
82.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	2,8	1,023E-06
83.	ENSECAG00000050432	ENSECAG00000050432		2,79402	1,171E-05
84.	ENSECAG00000014480	AIM2	absent in melanoma 2	2,76848	8,168E-13
85.	ENSECAG00000013703	PPP1R3C	protein phosphatase 1 regulatory subunit 3C	2,7564	1,154E-09
86.	ENSECAG00000013883	ICAM1	intercellular adhesion molecule 1	2,72185	1,64E-173
87.	ENSECAG00000016482	IL6	interleukin 6	2,69189	9,542E-14
88.	ENSECAG00000014812	KRT23	keratin 23	2,65199	1,992E-21
89.	ENSECAG00000024719	ENSECAG00000024719		2,65113	4,595E-42
90.	ENSECAG00000011669	TNN	tenascin N	2,64263	7,01E-115
91.	ENSECAG00000036638	SLC6A12	solute carrier family 6 member 12	2,63503	4,19E-11
92.	ENSECAG00000022739	CA4	carbonic anhydrase 4	2,63468	3,028E-69
93.	ENSECAG00000028459	ENSECAG00000028459		2,59553	6,063E-84
94.	ENSECAG00000010963	SERPING1	serpin family G member 1	2,59309	4,56E-112
95.	ENSECAG00000021206	HAS2	hyaluronan synthase 2	2,56733	8,986E-10
96.	ENSECAG00000039617	SNCB	synuclein beta	2,5583	5,068E-09
97.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	2,54554	1,012E-45
98.	ENSECAG00000003563	BST2	bone marrow stromal cell antigen 2	2,54418	1,352E-37
99.	ENSECAG00000021604	PDGFRL	platelet derived growth factor receptor like	2,53864	1,771E-28
100.	ENSECAG00000015644	SLC1A2	solute carrier family 1 member 2	2,51602	1,578E-11
101.	ENSECAG00000005126	TRIM22	tripartite motif containing 22	2,49623	0,0004498
102.	ENSECAG00000015034	PLAC8B	placenta associated 8 B	2,49331	7,257E-14
103.	ENSECAG00000033385	LGALS3BP	galectin 3 binding protein	2,48773	1,78E-209
104.	ENSECAG00000060335	ENSECAG00000060335		2,45917	2,916E-08
105.	ENSECAG00000030750	ENSECAG00000030750		2,41008	2,623E-18
106.	ENSECAG00000059829	ENSECAG00000059829		2,40703	3,026E-20
107.	ENSECAG00000024959	FBXO39	F-box protein 39	2,39905	8,175E-11
108.	ENSECAG00000055388	ENSECAG00000055388		2,39661	3,516E-15
109.	ENSECAG00000014259	TIMP1	TIMP metalloproteinase inhibitor 1	2,39204	6,158E-36
110.	ENSECAG00000013362	CRYM	crystallin mu	2,39197	0,0002191

111.	ENSECAG00000018409	NOX5	NADPH oxidase 5	2,38528	0,0002974
112.	ENSECAG00000009618	IFI44L	interferon induced protein 44 like	2,36546	3,54E-13
113.	ENSECAG00000018961	ACTN3	actinin alpha 3	2,36249	1,341E-13
114.	ENSECAG00000056002	ENSECAG00000056002		2,35911	0,0005898
115.	ENSECAG00000008615	ENSECAG00000008615		2,33847	5,231E-42
116.	ENSECAG00000016131	FRMD4B	FERM domain containing 4B	2,33749	7,475E-38
117.	ENSECAG00000045914	ENSECAG00000045914		2,33433	4,005E-08
118.	ENSECAG00000009020	IFI44	interferon induced protein 44	2,33104	1,095E-09
119.	ENSECAG00000017185	ZBP1	Z-DNA binding protein 1	2,32411	1,81E-20
120.	ENSECAG00000032271	ENSECAG00000032271		2,3195	1,119E-24
121.	ENSECAG00000024851	EDNRB	endothelin receptor type B	2,29915	1,773E-31
122.	ENSECAG00000021220	GBP1	guanylate binding protein 1	2,29609	9,277E-24
123.	ENSECAG00000006763	GPBAR1	G protein-coupled bile acid receptor 1	2,2938	0,0001168
124.	ENSECAG00000019573	PCDH15	protocadherin related 15	2,28885	4,417E-05
125.	ENSECAG00000035459	BATF2	basic leucine zipper ATF-like transcription factor 2	2,27885	4,031E-46
126.	ENSECAG00000024961	XAF1	XIAP associated factor 1	2,27354	7,106E-31
127.	ENSECAG00000000235	MTBP	MDM2 binding protein	2,25831	2,2E-31
128.	ENSECAG00000000574	NIPAL4	NIPA like domain containing 4	2,25359	5,992E-46
129.	ENSECAG00000017181	PTGS2	prostaglandin-endoperoxide synthase 2	2,24492	5,456E-20
130.	ENSECAG00000023727	IL1A	interleukin 1 alpha	2,24125	7,807E-05
131.	ENSECAG00000014519	ETV7	ETS variant transcription factor 7	2,22649	9,611E-27
132.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	2,21768	1,18E-11
133.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	2,20944	4,763E-26
134.	ENSECAG00000005307	RNF183	ring finger protein 183	2,19872	6,39E-17
135.	ENSECAG00000053465	ENSECAG00000053465		2,19292	2,251E-15
136.	ENSECAG00000008763	LYPD3	LY6/PLAUR domain containing 3	2,19216	2,808E-06
137.	ENSECAG00000014645	OASL	2'-5'-oligoadenylate synthetase-like	2,19059	0,0002645
138.	ENSECAG00000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	2,16855	2,9E-22
139.	ENSECAG00000015842	ANKRD55	ankyrin repeat domain 55	2,16824	1,196E-10
140.	ENSECAG00000001481	SAMD9L	sterile alpha motif domain containing 9 like	2,16702	7,46E-26
141.	ENSECAG00000047192	ENSECAG00000047192		2,15245	0,0002588
142.	ENSECAG00000009039	STAT1	signal transducer and activator of transcription 1	2,14598	7,29E-133
143.	ENSECAG00000010500	ITGA4	integrin subunit alpha 4	2,14036	1,031E-65
144.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	2,13662	3,652E-08
145.	ENSECAG00000058677	ENSECAG00000058677		2,12718	1,23E-09
146.	ENSECAG00000005241	THBD	thrombomodulin	2,12464	2,484E-21
147.	ENSECAG00000011704	TNFAIP2	TNF alpha induced protein 2	2,1228	3,64E-119
148.	ENSECAG00000033890	CIDEA	cell death inducing DFFA like effector c	2,12214	9,831E-16
149.	ENSECAG00000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	2,1088	5,149E-47
150.	ENSECAG00000057579	ENSECAG00000057579		2,10163	0,0018536
151.	ENSECAG00000057145	C3	complement C3	2,09527	2,61E-115
152.	ENSECAG00000009370	ORC1	origin recognition complex subunit 1	2,08595	9,612E-27
153.	ENSECAG00000020238	GRAMD1B	GRAM domain containing 1B	2,0822	1,722E-17
154.	ENSECAG00000018322	EXO1	exonuclease 1	2,0649	4,811E-14
155.	ENSECAG00000024322	ARSJ	arylsulfatase family member J	2,05871	1,204E-48
156.	ENSECAG00000017172	IFI27	interferon, alpha-inducible protein 27	2,05649	3,551E-53
157.	ENSECAG00000008739	ENSECAG00000008739		2,05007	4,321E-07
158.	ENSECAG00000016560	CRABP2	cellular retinoic acid binding protein 2	2,03753	4,2E-05
159.	ENSECAG00000026928	ASCL4	achaete-scute family bHLH transcription factor 4	2,02254	1,984E-05
160.	ENSECAG00000020769	FGF1	fibroblast growth factor 1	2,0218	1,582E-73
161.	ENSECAG00000050918	ENSECAG00000050918		2,00008	5,387E-09
162.	ENSECAG00000001399	SAMD9	sterile alpha motif domain containing 9	1,99672	6,122E-46
163.	ENSECAG00000015657	TNNT1	troponin T1, slow skeletal type	1,98927	1,433E-08
164.	ENSECAG00000009121	NEIL3	nei like DNA glycosylase 3	1,98767	5,5E-10
165.	ENSECAG00000022850	CERKL	ceramide kinase like	1,98442	1,979E-05

166.	ENSECAG00000011006	TGFA	transforming growth factor alpha	1,98284	5,608E-33
167.	ENSECAG00000014732	ATP10A	ATPase phospholipid transporting 10A (putative)	1,9715	9,798E-19
168.	ENSECAG00000012104	TNFAIP6	TNF alpha induced protein 6	1,96292	3,999E-08
169.	ENSECAG00000019438	OSMR	oncostatin M receptor	1,96246	5,156E-50
170.	ENSECAG00000009303	GFPT2	glutamine-fructose-6-phosphate transaminase 2	1,96233	2,855E-17
171.	ENSECAG00000012629	MASTL	microtubule associated serine/threonine kinase like	1,95964	8,125E-24
172.	ENSECAG00000014867	PLBD1	phospholipase B domain containing 1	1,95954	2,226E-26
173.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	1,95886	6,569E-38
174.	ENSECAG00000048661	ENSECAG00000048661		1,95334	2,085E-10
175.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	1,93744	1,401E-09
176.	ENSECAG00000015342	CXCL8	C-X-C motif chemokine ligand 8	1,93113	5,552E-07
177.	ENSECAG00000008059	PDE4C	phosphodiesterase 4C	1,93045	1,83E-05
178.	ENSECAG00000016934	IL31RA	interleukin 31 receptor A	1,92794	1,058E-12
179.	ENSECAG00000009913	CDC6	cell division cycle 6	1,9259	1,727E-30
180.	ENSECAG00000024473	MCM10	minichromosome maintenance 10 replication initiation factor	1,91895	3,695E-17
181.	ENSECAG00000014511	IL11	interleukin 11	1,91115	5,534E-05
182.	ENSECAG00000009472	CLSPN	claspin	1,90971	1,26E-16
183.	ENSECAG00000016056	BICDL2	BICD family like cargo adaptor 2	1,89767	1,901E-09
184.	ENSECAG00000015641	DSCC1	DNA replication and sister chromatid cohesion 1	1,89113	2,073E-22
185.	ENSECAG00000036105	ENSECAG00000036105		1,88066	2,668E-11
186.	ENSECAG00000030025	ENSECAG00000030025		1,85986	0,0003235
187.	ENSECAG00000007464	RRM2	ribonucleotide reductase regulatory subunit M2	1,85946	5,771E-15
188.	ENSECAG00000056325	SERPINB2	serpin family B member 2	1,8552	3,425E-24
189.	ENSECAG00000008823	CDH11	cadherin 11	1,84909	3,582E-87
190.	ENSECAG00000025066	PLA2G3	phospholipase A2 group III	1,84667	1,465E-08
191.	ENSECAG00000019758	TNFSF13B	TNF superfamily member 13b	1,83808	5,127E-17
192.	ENSECAG00000000633	ZWINT	ZW10 interacting kinetochore protein	1,82559	4,81E-11
193.	ENSECAG00000009054	CKB	creatine kinase B	1,82557	3,585E-08
194.	ENSECAG00000059594	ENSECAG00000059594		1,81718	0,0025683
195.	ENSECAG00000018841	CGA	glycoprotein hormones, alpha polypeptide	1,81655	0,0017899
196.	ENSECAG00000023019	KIF18B	kinesin family member 18B	1,81461	8,716E-18
197.	ENSECAG00000019411	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	1,81294	3,657E-30
198.	ENSECAG00000034739	ADORA2A	adenosine A2a receptor	1,80999	6,958E-46
199.	ENSECAG00000010525	KEL	Kell metallo-endopeptidase	1,79426	1,357E-11
200.	ENSECAG00000011776	MX1	MX dynamin like GTPase 1	1,79262	1,675E-07
201.	ENSECAG00000025092	CDC25B	cell division cycle 25B	1,78997	6,021E-67
202.	ENSECAG00000009707	PTGS1	prostaglandin-endoperoxide synthase 1	1,78797	1,626E-09
203.	ENSECAG00000013053	TOP2A	DNA topoisomerase II alpha	1,77957	3,366E-14
204.	ENSECAG00000053819	ENSECAG00000053819		1,77845	1,108E-07
205.	ENSECAG00000023525	NDUFA4L2	NDUFA4 mitochondrial complex associated like 2	1,7748	4,202E-16
206.	ENSECAG00000002513	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	1,77198	1,193E-25
207.	ENSECAG00000015060	PRR11	proline rich 11	1,77077	5,801E-10
208.	ENSECAG00000014305	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3	1,76382	0,0003458
209.	ENSECAG00000024694	KIF14	kinesin family member 14	1,75687	5,45E-17
210.	ENSECAG00000009173	ZNF367	zinc finger protein 367	1,75224	2,947E-23
211.	ENSECAG00000014368	MCM5	minichromosome maintenance complex component 5	1,75165	9,802E-21
212.	ENSECAG00000020111	IQGAP3	IQ motif containing GTPase activating protein 3	1,75132	2,882E-18
213.	ENSECAG00000015651	ARSF	arylsulfatase F	1,75073	0,0002974
214.	ENSECAG00000010859	KIF4A	kinesin family member 4A	1,74892	1,099E-18
215.	ENSECAG00000011788	CDC45	cell division cycle 45	1,74875	4,119E-19
216.	ENSECAG00000035391	ENSECAG00000035391		1,73866	1,634E-10

217.	ENSECAG00000011037	WARS1	tryptophanyl-tRNA synthetase 1	1,73858	1,096E-64
218.	ENSECAG00000017522	TNFSF14	TNF superfamily member 14	1,72614	0,0001743
219.	ENSECAG00000000532	EPS8L1	EPS8 like 1	1,72497	4,915E-14
220.	ENSECAG00000000426	CENPL	centromere protein L	1,72258	6,585E-09
221.	ENSECAG000000022686	MRAP2	melanocortin 2 receptor accessory protein 2	1,72094	0,0011671
222.	ENSECAG00000006288	SIK1	salt inducible kinase 1	1,72014	1,459E-26
223.	ENSECAG000000026891	ENSECAG000000026891		1,7189	6,44E-14
224.	ENSECAG000000024611	NTF3	neurotrophin 3	1,7164	0,0025122
225.	ENSECAG000000014314	POLQ	DNA polymerase theta	1,71335	1,53E-14
226.	ENSECAG000000005316	PIF1	PIF1 5'-to-3' DNA helicase	1,71263	6,45E-06
227.	ENSECAG000000008461	DEPDC1	DEP domain containing 1	1,71087	1,13E-13
228.	ENSECAG000000022901	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	1,70655	8,626E-09
229.	ENSECAG000000010053	HJURP	Holliday junction recognition protein	1,70235	2,77E-07
230.	ENSECAG000000045402	ENSECAG000000045402		1,6986	1,4E-08
231.	ENSECAG000000011878	DTL	denticleless E3 ubiquitin	1,69608	4,901E-29
232.	ENSECAG000000018649	UCP2	uncoupling protein 2	1,69591	1,92E-38
233.	ENSECAG000000039680	ENSECAG000000039680		1,69545	8,766E-13
234.	ENSECAG000000000284	USP18	ubiquitin specific peptidase 18	1,69423	5,46E-14
235.	ENSECAG000000014658	SCD	stearoyl-CoA desaturase	1,69188	4,85E-47
236.	ENSECAG000000032055	PROKR2	prokineticin receptor 2	1,69036	0,0001682
237.	ENSECAG000000008655	DLGAP5	DLG associated protein 5	1,68886	6,298E-15
238.	ENSECAG000000053139	ENSECAG000000053139		1,68871	3,037E-08
239.	ENSECAG000000016860	KIF20A	kinesin family member 20A	1,68505	3,195E-10
240.	ENSECAG000000009716	CDK1	cyclin dependent kinase 1	1,68497	1,088E-17
241.	ENSECAG000000019038	KIF2C	kinesin family member 2C	1,68467	2,35E-18
242.	ENSECAG000000014384	AURKB	aurora kinase B	1,68166	2,221E-10
243.	ENSECAG000000015369	NID2	nidogen 2	1,68015	7,58E-74
244.	ENSECAG000000011492	CDCA7	cell division cycle associated 7	1,67717	3,888E-52
245.	ENSECAG0000000018752	APOL6	apolipoprotein L6	1,67608	4,214E-20
246.	ENSECAG000000020270	CCNE2	cyclin E2	1,67566	1,847E-14
247.	ENSECAG000000000480	ABI3BP	ABI family member 3 binding protein	1,67461	1,256E-50
248.	ENSECAG000000013691	MALT1	MALT1 paracaspase	1,67387	1,571E-28
249.	ENSECAG000000018665	RECQL4	RecQ like helicase 4	1,67304	1,349E-11
250.	ENSECAG000000024558	ENSECAG000000024558		1,67201	8,685E-13
251.	ENSECAG000000024406	KCP	kielin cysteine rich BMP regulator	1,66592	2,42E-05
252.	ENSECAG000000033029	ENSECAG000000033029		1,66494	5,665E-06
253.	ENSECAG000000059003	ISG15	ISG15 ubiquitin like modifier	1,65811	2,79E-06
254.	ENSECAG0000000038379	ENSECAG0000000038379		1,65339	0,001308
255.	ENSECAG000000019322	IL21R	interleukin 21 receptor	1,64344	7,907E-32
256.	ENSECAG000000022722	ESPL1	extra spindle pole bodies like 1, separase	1,64226	2,997E-10
257.	ENSECAG000000009568	CENPI	centromere protein I	1,64093	4,992E-25
258.	ENSECAG000000018918	TRIP13	thyroid hormone receptor interactor 13	1,64091	3,693E-15
259.	ENSECAG000000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	1,63838	1,534E-10
260.	ENSECAG000000003462	RUNX1	RUNX family transcription factor 1	1,63088	7,034E-13
261.	ENSECAG0000000038102	ENSECAG0000000038102		1,6299	0,0001947
262.	ENSECAG000000017896	PDLIM3	PDZ and LIM domain 3	1,62963	1,028E-05
263.	ENSECAG000000007881	IFIH1	interferon induced with helicase C domain 1	1,62541	1,228E-25
264.	ENSECAG000000021452	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	1,62408	7,292E-07
265.	ENSECAG000000006229	PIMREG	PICALM interacting mitotic regulator	1,6225	1,185E-09
266.	ENSECAG000000014787	RCAN1	regulator of calcineurin 1	1,61892	3,728E-53
267.	ENSECAG000000018810	HELLS	helicase, lymphoid specific	1,61157	1,913E-13
268.	ENSECAG000000017926	TROAP	trophinin associated protein	1,61088	5,026E-10
269.	ENSECAG000000020506	MCM3	minichromosome maintenance complex component 3	1,60972	8,067E-26
270.	ENSECAG000000023355	GTSE1	G2 and S-phase expressed 1	1,60105	2,007E-13
271.	ENSECAG000000022731	COL6A1	collagen type VI alpha 1 chain	1,59547	4,26E-50
272.	ENSECAG000000017671	ROBO1	roundabout guidance receptor 1	1,59079	1E-36
273.	ENSECAG000000008493	SERPINB10	serpin family B member 10	1,5899	0,0004986
274.	ENSECAG000000018510	RGS20	regulator of G protein signaling 20	1,58857	8,94E-08

275.	ENSECAG00000014742	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	1,58516	4,485E-13
276.	ENSECAG00000029514	SLC2A6	solute carrier family 2 member 6	1,58423	1,44E-20
277.	ENSECAG00000024519	SPC25	SPC25 component of NDC80 kinetochore complex	1,58134	2,143E-09
278.	ENSECAG00000012475	SGO1	shugoshin 1	1,58079	9,274E-16
279.	ENSECAG00000015871	CDCA8	cell division cycle associated 8	1,5796	1,755E-13
280.	ENSECAG00000008193	UPP1	uridine phosphorylase 1	1,57886	1,798E-18
281.	ENSECAG00000019161	DIAPH3	diaphanous related formin 3	1,57774	3,819E-21
282.	ENSECAG00000014232	NR4A2	nuclear receptor subfamily 4 group A member 2	1,57699	3,11E-21
283.	ENSECAG00000005925	MYBL2	MYB proto-onco like 2	1,57698	5,537E-14
284.	ENSECAG00000053648	DDX60	DEx/D/H-box helicase 60	1,57522	9,789E-09
285.	ENSECAG00000000949	GPR84	G protein-coupled receptor 84	1,57213	0,0043969
286.	ENSECAG00000017777	PLK1	polo like kinase 1	1,56849	6,682E-15
287.	ENSECAG00000011003	PDE4B	phosphodiesterase 4B	1,56848	1,733E-35
288.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	1,56808	1,821E-16
289.	ENSECAG00000004795	ENSECAG00000004795		1,56804	4,259E-09
290.	ENSECAG00000006607	KIF11	kinesin family member 11	1,5674	1,749E-24
291.	ENSECAG00000009787	SNAI1	snail family transcriptional repressor 1	1,5625	3,664E-41
292.	ENSECAG00000012899	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	1,5594	3,12E-22
293.	ENSECAG00000008827	NDC80	NDC80 kinetochore complex component	1,55622	9,974E-13
294.	ENSECAG00000050999	ENSECAG00000050999		1,5553	1,275E-08
295.	ENSECAG00000014536	KIF23	kinesin family member 23	1,55428	4,121E-10
296.	ENSECAG00000008809	OAS3	2'-5'-oligoadenylate synthetase 3	1,55362	1,156E-07
297.	ENSECAG00000019329	MPP3	MAGUK p55 scaffold protein 3	1,55328	7,277E-11
298.	ENSECAG00000054990	CCNA2	cyclin A2	1,55283	2,214E-22
299.	ENSECAG00000009801	EXOC3L4	exocyst complex component 3 like 4	1,55045	2,37E-05
300.	ENSECAG00000059928	ENSECAG00000059928		1,5503	5,138E-23
301.	ENSECAG00000004805	B3GALT5	beta-1,3-galactosyltransferase 5	1,5498	0,0026235
302.	ENSECAG00000010821	RACGAP1	Rac GTPase activating protein 1	1,54824	1,052E-16
303.	ENSECAG00000049724	PTAFR	platelet activating factor receptor	1,54132	7,304E-06
304.	ENSECAG00000000281	SHCBP1	SHC binding and spindle associated 1	1,53863	3,688E-09
305.	ENSECAG000000023776	TTK	TTK protein kinase	1,53517	5,035E-20
306.	ENSECAG00000020919	HROB	homologous recombination factor with OB-fold	1,53453	5,75E-05
307.	ENSECAG00000007942	LMNB1	lamin B1	1,53278	7,546E-28
308.	ENSECAG00000019705	CDC20	cell division cycle 20	1,52617	8,912E-07
309.	ENSECAG00000011854	CFB	complement factor B	1,52513	7,445E-11
310.	ENSECAG00000008506	HMMR	hyaluronan mediated motility receptor	1,52229	1,082E-14
311.	ENSECAG000000023331	KIF20B	kinesin family member 20B	1,52109	3,6E-17
312.	ENSECAG00000030620	ENSECAG00000030620		1,52082	0,0008733
313.	ENSECAG00000008876	PTPRE	protein tyrosine phosphatase receptor type E	1,51927	8,368E-11
314.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	1,51757	4,127E-09
315.	ENSECAG00000017103	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	1,51723	8,455E-13
316.	ENSECAG00000010326	MIS18A	MIS18 kinetochore protein A	1,51634	5,36E-10
317.	ENSECAG00000020645	ASPM	assembly factor for spindle microtubules	1,51571	3,356E-09
318.	ENSECAG00000014890	BRCA2	BRCA2 DNA repair associated	1,51468	1,937E-17
319.	ENSECAG00000002675	ZGRF1	zinc finger GRF-type containing 1	1,5141	1,883E-13
320.	ENSECAG00000024196	KIFC1	kinesin family member C1	1,50829	1,607E-12
321.	ENSECAG00000005086	EGLN3	egl-9 family hypoxia inducible factor 3	1,50733	2,16E-23
322.	ENSECAG00000019578	CDCA5	cell division cycle associated 5	1,50522	4,131E-12
323.	ENSECAG00000015806	CCNB1	cyclin B1	1,50506	7,074E-17
324.	ENSECAG00000057566	ENSECAG00000057566		1,50119	0,0051158
325.	ENSECAG00000018261	RGS4	regulator of G protein signaling 4	1,50101	4,062E-14
326.	ENSECAG00000001653	POLE	DNA polymerase epsilon, catalytic subunit	1,50098	9,577E-25
327.	ENSECAG00000045451	ENSECAG00000045451		1,49871	9,049E-21
328.	ENSECAG00000010445	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1,49715	1,046E-17
329.	ENSECAG00000023961	AURKA	aurora kinase A	1,49494	2,276E-21

330.	ENSECAG00000019369	CCNF	cyclin F	1,49046	9,678E-15
331.	ENSECAG00000019129	FOXM1	forkhead box M1	1,48584	2,721E-14
332.	ENSECAG00000016646	PARBP	PARP1 binding protein	1,48564	1,722E-10
333.	ENSECAG00000000373	LOXL3	lysyl oxidase like 3	1,48031	6,427E-47
334.	ENSECAG00000009163	NUF2	NUF2 component of NDC80 kinetochore complex	1,47592	3,638E-22
335.	ENSECAG00000009400	ARRDC4	arrestin domain containing 4	1,47297	1,657E-27
336.	ENSECAG00000017104	ERRFI1	ERBB receptor feedback inhibitor 1	1,47202	9,67E-110
337.	ENSECAG00000021429	C1R	complement C1r	1,47155	2,15E-69
338.	ENSECAG00000044738	ENSECAG00000044738		1,46589	0,0073048
339.	ENSECAG00000023264	RTP4	receptor transporter protein 4	1,46355	1,213E-09
340.	ENSECAG00000008634	NCAPH	non-SMC condensin I complex subunit H	1,45929	7,298E-11
341.	ENSECAG00000014452	KIF22	kinesin family member 22	1,45706	1,725E-19
342.	ENSECAG00000010977	ARHGAP45	Rho GTPase activating protein 45	1,44931	7,383E-09
343.	ENSECAG00000013188	CDC42	cell division cycle associated 2	1,44702	8,803E-13
344.	ENSECAG00000039393	ENSECAG00000039393		1,44585	1,333E-06
345.	ENSECAG00000022278	KNL1	kinetochore scaffold 1	1,44534	6,856E-08
346.	ENSECAG00000017433	TNC	tenascin C	1,44516	3,498E-32
347.	ENSECAG00000007588	EREG	epiregulin	1,44474	8,858E-12
348.	ENSECAG00000019631	MCM2	minichromosome maintenance complex component 2	1,43693	3,477E-32
349.	ENSECAG00000046407	ENSECAG00000046407		1,43502	2,107E-06
350.	ENSECAG00000032009	ENSECAG00000032009		1,42909	8,24E-11
351.	ENSECAG00000023032	AZIN2	antizyme inhibitor 2	1,42865	0,004661
352.	ENSECAG00000010941	CCDC150	coiled-coil domain containing 150	1,42816	0,0010631
353.	ENSECAG00000009067	SLC16A6	solute carrier family 16 member 6	1,42192	1,052E-09
354.	ENSECAG00000012773	CMPK2	cytidine/uridine monophosphate kinase 2	1,42112	1,052E-09
355.	ENSECAG00000015966	SERPINF6	serpin family B member 6	1,4202	6,973E-30
356.	ENSECAG00000005559	GABRA5	gamma-aminobutyric acid type A receptor subunit alpha5	1,41955	0,0001199
357.	ENSECAG00000020601	ZYG11A	zyg-11 family member A, cell cycle regulator	1,41922	5,774E-05
358.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	1,41915	2,692E-27
359.	ENSECAG00000009420	NT5E	5'-nucleotidase ecto	1,41759	1,322E-29
360.	ENSECAG00000017615	CDH17	cadherin 17	1,41619	9,39E-05
361.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,41247	2,9E-22
362.	ENSECAG00000014813	CCNB2	cyclin B2	1,41068	3,489E-09
363.	ENSECAG00000015140	LIPG	lipase G, endothelial type	1,40963	2,784E-16
364.	ENSECAG00000006788	PCSK5	proprotein convertase subtilisin/kexin type 5	1,40951	3,161E-43
365.	ENSECAG00000011355	TRAF3IP3	TRAF3 interacting protein 3	1,40887	0,0067934
366.	ENSECAG00000014422	OAS2	2'-5'-oligoadenylate synthetase 2	1,40515	2,902E-10
367.	ENSECAG00000014377	CHAF1A	chromatin assembly factor 1 subunit A	1,40473	3,634E-20
368.	ENSECAG00000013009	KIF26B	kinesin family member 26B	1,39595	0,0005765
369.	ENSECAG00000014953	KIF15	kinesin family member 15	1,39359	8,781E-16
370.	ENSECAG00000021155	MXD3	MAX dimerization protein 3	1,3917	2,199E-05
371.	ENSECAG00000038834	MTFR2	mitochondrial fission regulator 2	1,39108	1,544E-10
372.	ENSECAG00000023279	GATA6	GATA binding protein 6	1,3895	8,857E-20
373.	ENSECAG00000023808	ATAD2	ATPase family AAA domain containing 2	1,38555	1,935E-26
374.	ENSECAG00000058229	ENSECAG00000058229		1,38127	7,069E-07
375.	ENSECAG00000034339	ENSECAG00000034339		1,38113	4,166E-45
376.	ENSECAG00000038893	CST3	cystatin C	1,37813	4,85E-47
377.	ENSECAG00000001041	CENPN	centromere protein N	1,37692	1,461E-13
378.	ENSECAG00000009501	DAAM2	dishevelled associated activator of morphosis 2	1,37512	1,514E-62
379.	ENSECAG00000018253	FGFR1	fibroblast growth factor receptor like 1	1,37437	3,994E-27
380.	ENSECAG00000018476	TPX2	TPX2 microtubule nucleation factor	1,37437	9,274E-07
381.	ENSECAG00000017742	ERN2	endoplasmic reticulum to nucleus signaling 2	1,3743	0,0077679
382.	ENSECAG00000012331	PARP9	poly(ADP-ribose) polymerase family member 9	1,37402	8,949E-39

383.	ENSECAG00000023071	DDIAS	DNA damage induced apoptosis suppressor	1,37353	9,346E-28
384.	ENSECAG00000007872	TCF19	transcription factor 19	1,37071	5,284E-15
385.	ENSECAG00000024650	FADS2	fatty acid desaturase 2	1,36667	3,254E-49
386.	ENSECAG00000046504	ENSECAG00000046504		1,36486	0,0005171
387.	ENSECAG00000014594	EPAS1	endothelial PAS domain protein 1	1,36367	3,182E-38
388.	ENSECAG00000007300	DCLK1	doublecortin like kinase 1	1,36363	8,22E-41
389.	ENSECAG00000020698	MELK	maternal embryonic leucine zipper kinase	1,35368	2,651E-19
390.	ENSECAG00000008787	CCNB3	cyclin B3	1,35071	1,559E-05
391.	ENSECAG00000024127	CENPF	centromere protein F	1,35022	1,113E-05
392.	ENSECAG00000014059	ECT2	epithelial cell transforming 2	1,34857	5,032E-25
393.	ENSECAG00000014406	IL15	interleukin 15	1,34648	7,617E-07
394.	ENSECAG00000016495	NUSAP1	nucleolar and spindle associated protein 1	1,34504	4,353E-19
395.	ENSECAG00000015102	MYOZ3	myozenin 3	1,34042	2,916E-05
396.	ENSECAG00000024267	TFRC	transferrin receptor	1,33933	1,015E-25
397.	ENSECAG00000016382	ANLN	anillin, actin binding protein	1,33865	1,67E-22
398.	ENSECAG00000009519	C1S	complement C1s	1,33769	1,479E-47
399.	ENSECAG00000021453	TICRR	TOPBP1 interacting checkpoint and replication regulator	1,33649	6,561E-09
400.	ENSECAG00000024862	HDX	highly divergent homeobox	1,33593	4,406E-05
401.	ENSECAG00000013728	MFSD2A	MFSD2 lysolipid transporter A, lysophospholipid	1,33565	1,674E-22
402.	ENSECAG00000018544	SPDL1	spindle apparatus coiled-coil protein 1	1,33406	4,701E-26
403.	ENSECAG00000003201	PRSS35	serine protease 35	1,33299	5,795E-12
404.	ENSECAG00000015967	ASF1B	anti-silencing function 1B histone chaperone	1,33202	1,003E-05
405.	ENSECAG00000011673	ENSECAG00000011673		1,33038	1,86E-16
406.	ENSECAG00000020167	RGMA	repulsive guidance molecule BMP co-receptor a	1,32994	5,435E-10
407.	ENSECAG00000007620	DEPDC1B	DEP domain containing 1B	1,32852	1,475E-06
408.	ENSECAG00000016271	CENPA	centromere protein A	1,32847	1,798E-05
409.	ENSECAG00000014948	CIP2A	cellular inhibitor of PP2A	1,32018	8,321E-20
410.	ENSECAG00000000685	B2M	beta-2-microglobulin	1,31895	1,867E-68
411.	ENSECAG00000003235	FANCI	FA complementation group I	1,31688	1,53E-14
412.	ENSECAG00000017922	ADAM19	ADAM metalloproteinase domain 19	1,31198	4,329E-71
413.	ENSECAG00000023566	DHRS9	dehydrogenase/reductase 9	1,3115	1,307E-44
414.	ENSECAG00000024810	PLA2G4A	phospholipase A2 group IVA	1,31146	3,363E-35
415.	ENSECAG00000011380	TACC3	transforming acidic coiled-coil containing protein 3	1,3081	2,322E-11
416.	ENSECAG00000030455	ENSECAG00000030455		1,30511	8,711E-08
417.	ENSECAG00000014969	TP53I3	tumor protein p53 inducible protein 3	1,30443	7,278E-27
418.	ENSECAG00000001290	CABP1	calcium binding protein 1	1,30163	8,188E-05
419.	ENSECAG00000055909	ENSECAG00000055909		1,30106	0,0029821
420.	ENSECAG00000014501	TMEM54	transmembrane protein 54	1,29996	8,357E-15
421.	ENSECAG00000004845	CHEK2	checkpoint kinase 2	1,29899	4,014E-11
422.	ENSECAG00000011630	FBXO5	F-box protein 5	1,29741	2,407E-17
423.	ENSECAG00000013223	PBK	PDZ binding kinase	1,29593	3,453E-08
424.	ENSECAG00000006917	P4HA3	prolyl 4-hydroxylase subunit alpha 3	1,29245	4,031E-21
425.	ENSECAG00000024817	P4HA2	prolyl 4-hydroxylase subunit alpha 2	1,29075	1,65E-107
426.	ENSECAG00000019780	ENSECAG00000019780		1,28516	2,292E-28
427.	ENSECAG00000011496	NFKBIZ	NFKB inhibitor zeta	1,28268	1,836E-27
428.	ENSECAG00000033470	ENSECAG00000033470		1,28255	1,065E-13
429.	ENSECAG00000018373	FAM234B	family with sequence similarity 234 member B	1,28195	2,992E-13
430.	ENSECAG00000044966	ENSECAG00000044966		1,27947	4,294E-05
431.	ENSECAG00000025128	PIWIL2	piwi like RNA-mediated silencing 2	1,27846	0,0015953
432.	ENSECAG00000023026	PAPPA	pappalysin 1	1,27577	2,124E-23
433.	ENSECAG00000033034	RAB20	RAB20, member RAS oncogene family	1,27438	8,424E-06
434.	ENSECAG00000016735	VCAM1	vascular cell adhesion molecule 1	1,27404	9,875E-15
435.	ENSECAG00000017143	ENSECAG00000017143		1,27391	0,0002463
436.	ENSECAG00000046674	ENSECAG00000046674		1,27275	9,658E-13
437.	ENSECAG00000002250	SPRY2	sprouty RTK signaling antagonist 2	1,27179	3,124E-20
438.	ENSECAG00000033821	ANKRD33B	ankyrin repeat domain 33B	1,26976	6,623E-09

439.	ENSECAG00000009073	ARHGEF39	Rho guanine nucleotide exchange factor 39	1,26752	7,386E-13
440.	ENSECAG00000017906	PRC1	protein regulator of cytokinesis 1	1,26564	8,566E-20
441.	ENSECAG00000002402	ENSECAG00000002402		1,26495	6,012E-09
442.	ENSECAG00000042596	ENSECAG00000042596		1,26224	6,224E-16
443.	ENSECAG00000005547	CDT1	chromatin licensing and DNA replication factor 1	1,25965	3,422E-09
444.	ENSECAG00000016974	BRCA1	BRCA1 DNA repair associated	1,25706	8,406E-14
445.	ENSECAG00000054624	ENSECAG00000054624		1,2559	0,0092413
446.	ENSECAG00000048720	ENSECAG00000048720		1,25569	1,119E-07
447.	ENSECAG00000032074	ENSECAG00000032074		1,2523	0,0043793
448.	ENSECAG00000023922	E2F2	E2F transcription factor 2	1,25157	0,0025689
449.	ENSECAG00000032131	UBE2L6	ubiquitin conjugating enzyme E2 L6	1,25103	1,466E-41
450.	ENSECAG00000060206	ENSECAG00000060206		1,24914	4,439E-31
451.	ENSECAG00000011708	GAREM1	GRB2 associated regulator of MAPK1 subtype 1	1,24907	5,488E-05
452.	ENSECAG00000008187	PLK4	polo like kinase 4	1,24879	9,662E-15
453.	ENSECAG00000059506	ENSECAG00000059506		1,24842	0,0090784
454.	ENSECAG00000014517	CDC43	cell division cycle associated 3	1,24448	5,79E-05
455.	ENSECAG00000013771	PDE4D	phosphodiesterase 4D	1,24098	4,948E-32
456.	ENSECAG00000056818	TMEM71	transmembrane protein 71	1,24052	0,0054156
457.	ENSECAG00000045231	CHEK1	checkpoint kinase 1	1,23762	9,564E-09
458.	ENSECAG00000052587	ENSECAG00000052587		1,23545	0,0033844
459.	ENSECAG00000050552	ENSECAG00000050552		1,23353	3,294E-22
460.	ENSECAG00000020053	SLC4A4	solute carrier family 4 member 4	1,23066	0,0005164
461.	ENSECAG00000017948	BTN1A1	butyrophilin subfamily 1 member A1	1,23012	0,0095735
462.	ENSECAG00000017388	CENPT	centromere protein T	1,2288	3,593E-08
463.	ENSECAG00000019276	MCM4	minichromosome maintenance complex component 4	1,22862	2,567E-30
464.	ENSECAG00000017458	BNIP3	BCL2 interacting protein 3	1,22858	6,067E-08
465.	ENSECAG00000053421	ENSECAG00000053421		1,22564	0,010051
466.	ENSECAG00000023472	KCNK2	potassium two pore domain channel subfamily K member 2	1,22502	0,0001813
467.	ENSECAG00000047831	ENSECAG00000047831		1,22488	7,05E-22
468.	ENSECAG00000014404	WDR62	WD repeat domain 62	1,22481	1,026E-13
469.	ENSECAG00000035548	ENSECAG00000035548		1,22406	3,053E-25
470.	ENSECAG00000013324	TXN	thioredoxin	1,21962	7,243E-07
471.	ENSECAG00000002992	MID1IP1	MID1 interacting protein 1	1,21926	3,338E-40
472.	ENSECAG00000059404	ENSECAG00000059404		1,21905	1,05E-34
473.	ENSECAG00000031808	SAPCD2	suppressor APC domain containing 2	1,21847	0,0001594
474.	ENSECAG00000000197	TLR3	toll like receptor 3	1,2144	1,205E-16
475.	ENSECAG00000020413	DCN	decorin	1,21343	2,41E-69
476.	ENSECAG00000015456	SPAG5	sperm associated antigen 5	1,21323	3,497E-18
477.	ENSECAG00000011979	FTCD	formimidoyltransferase cyclodeaminase	1,21301	8,452E-14
478.	ENSECAG00000006686	NCAPG2	non-SMC condensin II complex subunit G2	1,21194	5,967E-17
479.	ENSECAG00000000910	ENSECAG00000000910		1,20861	3,853E-77
480.	ENSECAG00000003943	SYT5	synaptotagmin 5	1,2058	3,619E-10
481.	ENSECAG00000016241	SEMA5A	semaphorin 5A	1,2045	6,374E-08
482.	ENSECAG00000009402	VEGFA	vascular endothelial growth factor A	1,20281	1,009E-49
483.	ENSECAG00000000171	NPAS2	neuronal PAS domain protein 2	1,20176	7,631E-17
484.	ENSECAG00000008760	RAD54L	RAD54 like	1,20161	3,328E-09
485.	ENSECAG00000054832	ENSECAG00000054832		1,19981	1,849E-09
486.	ENSECAG00000006038	SGO2	shugoshin 2	1,19955	1,314E-10
487.	ENSECAG00000000303	SLC2A1	solute carrier family 2 member 1	1,1979	3,105E-32
488.	ENSECAG00000050101	EMP3	epithelial membrane protein 3	1,19708	2,393E-18
489.	ENSECAG00000013435	OAS1	2'-5'-oligoadenylate synthetase 1	1,1964	2,066E-24
490.	ENSECAG000000011823	ARHGAP19	Rho GTPase activating protein 19	1,19613	2,986E-07
491.	ENSECAG00000021211	COL15A1	collagen type XV alpha 1 chain	1,19569	2,994E-27
492.	ENSECAG00000009864	PTPRD	protein tyrosine phosphatase receptor type D	1,18932	5,496E-10
493.	ENSECAG00000020295	GEN1	GEN1 Holliday junction 5' flap endonuclease	1,18778	8,935E-12
494.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	1,1873	5,636E-27
495.	ENSECAG00000002892	TIMELESS	timeless circadian regulator	1,18697	7,605E-20

496.	ENSECAG00000018531	GEM	GTP binding protein overexpressed in skeletal muscle	1,18604	6,713E-27
497.	ENSECAG00000017194	FANCB	FA complementation group B	1,18303	1,472E-06
498.	ENSECAG00000007470	NCAPG	non-SMC condensin I complex subunit G	1,17964	3,342E-22
499.	ENSECAG00000017482	RNF24	ring finger protein 24	1,17798	4,178E-58
500.	ENSECAG00000024215	GINS2	GINS complex subunit 2	1,17758	8,24E-11
501.	ENSECAG00000052431	ENSECAG00000052431		1,1762	1,096E-06
502.	ENSECAG00000017794	IRF1	interferon regulatory factor 1	1,17522	3,258E-20
503.	ENSECAG00000016898	PSMB9	proteasome 20S subunit beta 9	1,17374	8,538E-32
504.	ENSECAG00000012132	ENSECAG00000012132		1,17254	1,34E-19
505.	ENSECAG00000015510	FGF7	fibroblast growth factor 7	1,17199	1,728E-23
506.	ENSECAG00000007686	RP1	RP1 axonemal microtubule associated	1,1718	0,0010637
507.	ENSECAG00000008358	ADA	adenosine deaminase	1,16838	1,073E-27
508.	ENSECAG00000022866	SPNS3	SPNS lysolipid transporter 3, sphingosine-1-phosphate (putative)	1,16633	0,0132607
509.	ENSECAG00000004590	TIPIN	TIMELESS interacting protein	1,16291	1,004E-25
510.	ENSECAG00000022842	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1,16203	2,22E-43
511.	ENSECAG00000008432	HASPIN	histone H3 associated protein kinase	1,162	1,606E-06
512.	ENSECAG00000016578	ENSECAG00000016578		1,15779	8,856E-05
513.	ENSECAG00000048408	ENSECAG00000048408		1,15679	0,0140931
514.	ENSECAG00000008287	SLC39A14	solute carrier family 39 member 14	1,1546	2,885E-17
515.	ENSECAG00000023033	RCOR2	REST corepressor 2	1,15238	6,228E-09
516.	ENSECAG00000021707	RTEL1	regulator of telomere elongation helicase 1	1,15157	4,294E-09
517.	ENSECAG00000017127	CENPO	centromere protein O	1,15018	1,945E-08
518.	ENSECAG00000005577	GPR39	G protein-coupled receptor 39	1,14985	4,513E-07
519.	ENSECAG00000050186	ENSECAG00000050186		1,1496	7,682E-05
520.	ENSECAG00000004372	SLC22A3	solute carrier family 22 member 3	1,14909	1,141E-06
521.	ENSECAG00000047393	ENSECAG00000047393		1,14857	0,0021379
522.	ENSECAG00000021776	ENSECAG00000021776		1,14823	0,0114419
523.	ENSECAG00000016217	RNF213	ring finger protein 213	1,14804	9,312E-21
524.	ENSECAG00000029465	CHI3L1	chitinase 3 like 1	1,14645	9,52E-07
525.	ENSECAG00000049355	ENSECAG00000049355		1,14555	1,101E-11
526.	ENSECAG00000005344	FEN1	flap structure-specific endonuclease 1	1,14373	1,189E-17
527.	ENSECAG000000030805	ENSECAG000000030805		1,14266	9,451E-09
528.	ENSECAG00000012022	PSMB10	proteasome 20S subunit beta 10	1,14212	3,413E-34
529.	ENSECAG00000000968	ENSECAG00000000968		1,13554	3,146E-35
530.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	1,1355	4,114E-07
531.	ENSECAG00000009686	DTX3L	deltex E3 ubiquitin ligase 3L	1,13461	2,617E-22
532.	ENSECAG00000011152	STIL	STIL centriolar assembly protein	1,1335	1,351E-06
533.	ENSECAG00000016029	TRAIIP	TRAF interacting protein	1,13147	4,957E-05
534.	ENSECAG00000007972	SUSD5	sushi domain containing 5	1,13062	1,74E-05
535.	ENSECAG00000059781	ENSECAG00000059781		1,12947	0,004447
536.	ENSECAG00000018126	PRELP	proline and arginine rich end leucine rich repeat protein	1,12857	2,617E-16
537.	ENSECAG00000019371	SLC1A3	solute carrier family 1 member 3	1,1271	7,333E-05
538.	ENSECAG00000003460	CKS1B	CDC28 protein kinase regulatory subunit 1B	1,12641	2,953E-08
539.	ENSECAG00000011226	CENPQ	centromere protein Q	1,12592	1,285E-07
540.	ENSECAG00000006776	IL15RA	interleukin 15 receptor subunit alpha	1,12571	6,294E-17
541.	ENSECAG00000021989	RIGI	RNA sensor RIG-I	1,12556	6,361E-24
542.	ENSECAG00000012818	TUBB3	tubulin beta 3 class III	1,12509	3,43E-11
543.	ENSECAG00000016705	UGP2	UDP-glucose pyrophosphorylase 2	1,1239	4,656E-47
544.	ENSECAG00000009700	ANK3	ankyrin 3	1,11983	0,0075411
545.	ENSECAG00000017894	CKAP2	cytoskeleton associated protein 2	1,11913	1,111E-12
546.	ENSECAG00000039158	FDPS	farnesyl diphosphate synthase	1,1171	2,696E-36
547.	ENSECAG00000046105	ENSECAG00000046105		1,11626	0,0053121
548.	ENSECAG00000010371	GAS2L3	growth arrest specific 2 like 3	1,11398	3,761E-07
549.	ENSECAG00000013037	ALDOC	aldolase, fructose-bisphosphate C	1,1077	5,003E-20
550.	ENSECAG00000024172	ADAMTS4	ADAM metalloproteinase with thrombospondin type 1 motif 4	1,1076	0,0014367
551.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,10754	0,0009585
552.	ENSECAG00000017843	ENSECAG00000017843		1,10319	0,0154172

553.	ENSECAG00000038313	ENSECAG00000038313		1,10046	2,981E-10
554.	ENSECAG00000019932	ENSECAG00000019932		1,09851	2,827E-07
555.	ENSECAG00000035561	ENSECAG00000035561		1,09767	0,0034396
556.	ENSECAG00000009562	ZC3H12A	zinc finger CCCH-type containing 12A	1,09699	2,469E-18
557.	ENSECAG00000020563	PIM1	Pim-1 proto-onco, serine/threonine kinase	1,09576	3,419E-46
558.	ENSECAG00000003636	ERAP1	endoplasmic reticulum aminopeptidase 1	1,09488	5,751E-63
559.	ENSECAG00000024297	COL27A1	collagen type XXVII alpha 1 chain	1,09394	4,504E-15
560.	ENSECAG00000024392	BRIP1	BRCA1 interacting helicase 1	1,09329	8,721E-11
561.	ENSECAG00000008906	PARP15	poly(ADP-ribose) polymerase family member 15	1,09252	8,335E-08
562.	ENSECAG00000026863	EFS	embryonal Fyn-associated substrate	1,08855	3,872E-11
563.	ENSECAG00000021072	KNTC1	kinetochore associated 1	1,08599	9,848E-18
564.	ENSECAG00000036591	APLN	apelin	1,08519	0,0006454
565.	ENSECAG00000022051	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1,08429	6,079E-33
566.	ENSECAG00000046324	TEX2	testis expressed 2	1,08393	8,858E-30
567.	ENSECAG00000019382	S100A10	S100 calcium binding protein A10	1,08283	2,302E-06
568.	ENSECAG00000018699	CHTF18	chromosome transmission fidelity factor 18	1,08269	0,0065171
569.	ENSECAG00000055030	ENSECAG00000055030		1,08079	1,628E-05
570.	ENSECAG00000015438	SUV39H1	SUV39H1 histone lysine methyltransferase	1,08058	9,457E-09
571.	ENSECAG00000022533	GPRC5B	G protein-coupled receptor class C group 5 member B	1,07788	2,719E-20
572.	ENSECAG00000003634	RHNO1	RAD9-HUS1-RAD1 interacting nuclear orphan 1	1,07678	5,702E-13
573.	ENSECAG00000014323	SKA3	spindle and kinetochore associated complex subunit 3	1,07571	5,041E-11
574.	ENSECAG00000052890	ENSECAG00000052890		1,07379	8,673E-05
575.	ENSECAG00000015069	BHLHE40	basic helix-loop-helix family member e40	1,0732	3,017E-07
576.	ENSECAG00000017796	NCAPD2	non-SMC condensin I complex subunit D2	1,07297	3,651E-25
577.	ENSECAG00000015822	VDR	vitamin D receptor	1,07104	1,576E-26
578.	ENSECAG00000021538	CKAP2L	cytoskeleton associated protein 2 like	1,0688	3,275E-11
579.	ENSECAG00000008096	FAM111B	FAM111 trypsin like peptidase B	1,0678	4,671E-25
580.	ENSECAG00000003310	LY6E	lymphocyte antigen 6 family member E	1,06621	1,001E-37
581.	ENSECAG00000021857	ENSECAG00000021857		1,06575	0,002163
582.	ENSECAG00000020221	KNDC1	kinase non-catalytic C-lobe domain containing 1	1,06427	0,0022892
583.	ENSECAG00000020920	NEK2	NIMA related kinase 2	1,0639	1,798E-06
584.	ENSECAG00000017324	ENSECAG00000017324		1,06152	5,803E-13
585.	ENSECAG00000005447	GUCY1A1	guanylate cyclase 1 soluble subunit alpha 1	1,06102	0,0043277
586.	ENSECAG00000034395	ENSECAG00000034395		1,05892	3,892E-22
587.	ENSECAG00000040575	ENSECAG00000040575		1,05555	2,713E-19
588.	ENSECAG00000016576	C1QTNF12	C1q and TNF related 12	1,04794	0,0001878
589.	ENSECAG00000057464	ENSECAG00000057464		1,04684	4,132E-05
590.	ENSECAG00000024428	PROCR	protein C receptor	1,04607	4,283E-19
591.	ENSECAG00000021358	SFRP1	secreted frizzled related protein 1	1,04287	1,499E-29
592.	ENSECAG00000022137	DNA2	DNA replication helicase/nuclease 2	1,04274	8,191E-07
593.	ENSECAG00000016971	TRERF1	transcriptional regulating factor 1	1,03991	5,198E-11
594.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,03627	3,819E-06
595.	ENSECAG00000007518	MARCHF3	membrane associated ring-CH-type finger 3	1,03569	8,858E-30
596.	ENSECAG00000017451	FAM110A	family with sequence similarity 110 member A	1,03453	0,00017
597.	ENSECAG00000000138	ACVR2A	activin A receptor type 2A	1,03349	1,307E-29
598.	ENSECAG00000016121	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif 12	1,03331	2,784E-16
599.	ENSECAG00000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,03296	1,647E-40
600.	ENSECAG00000023113	SASS6	SAS-6 centriolar assembly protein	1,0328	4,961E-13
601.	ENSECAG00000014703	CAPN9	calpain 9	1,03225	2,173E-05
602.	ENSECAG00000018966	FBXO48	F-box protein 48	1,03177	0,0077901

603.	ENSECAG00000057855	ENSECAG00000057855		1,03102	0,0185223
604.	ENSECAG00000008923	THBS1	thrombospondin 1	1,03047	1,366E-20
605.	ENSECAG00000003049	ENSECAG00000003049		1,02996	7,655E-12
606.	ENSECAG00000024465	ERAP2	endoplasmic reticulum aminopeptidase 2	1,02627	1,391E-34
607.	ENSECAG00000015249	REEP4	receptor accessory protein 4	1,02459	1,376E-12
608.	ENSECAG00000017864	FMOD	fibromodulin	1,02343	0,0077903
609.	ENSECAG00000033714	ENSECAG00000033714		1,02237	0,0135336
610.	ENSECAG00000011206	MVD	mevalonate diphosphate decarboxylase	1,02196	1,107E-12
611.	ENSECAG00000024194	POLA2	DNA polymerase alpha 2, accessory subunit	1,02171	1,136E-08
612.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,02149	3,59E-24
613.	ENSECAG00000018438	CEP55	centrosomal protein 55	1,02136	5,528E-07
614.	ENSECAG00000015835	NT5DC2	5'-nucleotidase domain containing 2	1,0207	7,086E-05
615.	ENSECAG00000024671	IL12A	interleukin 12A	1,01492	0,0001108
616.	ENSECAG00000007964	EBF1	EBF transcription factor 1	1,01152	1,454E-11
617.	ENSECAG00000035532	ENSECAG00000035532		1,00993	1,902E-34
618.	ENSECAG00000015412	WDHD1	WD repeat and HMG-box DNA binding protein 1	1,00726	3,855E-27
619.	ENSECAG00000011641	TVP23A	trans-golgi network vesicle A	1,00513	0,0001659
620.	ENSECAG00000026830	ENSECAG00000026830		1,00461	1,502E-06
621.	ENSECAG00000019398	TFPI2	tissue factor pathway inhibitor 2	1,00353	2,954E-15
622.	ENSECAG00000015115	RHBDL1	rhomboid like 1	1,00102	0,0005029
623.	ENSECAG00000013130	CCDC170	coiled-coil domain containing 170	-1,0037	3,132E-10
624.	ENSECAG00000000787	ADAMTS16	ADAM metalloproteinase with thrombospondin type 1 motif 16	-1,0042	0,0162387
625.	ENSECAG00000017459	ARRB1	arrestin beta 1	-1,0048	2,266E-06
626.	ENSECAG00000005958	EFNA4	ephrin A4	-1,0086	0,0040721
627.	ENSECAG00000020812	MPPED1	metallophosphoesterase domain containing 1	-1,0125	1,22E-09
628.	ENSECAG00000019877	DENND11	DENN domain containing 11	-1,0127	8,085E-06
629.	ENSECAG00000035300	ENSECAG00000035300		-1,0137	0,0080191
630.	ENSECAG00000044441	ENSECAG00000044441		-1,0149	0,0010419
631.	ENSECAG00000022432	PLEKHH1	pleckstrin homology, MyTH4 and FERM domain containing H1	-1,0155	6,667E-07
632.	ENSECAG00000012539	RASGRP3	RAS guanyl releasing protein 3	-1,017	0,019856
633.	ENSECAG00000010312	RHPN2	rophilin Rho GTPase binding protein 2	-1,0202	0,0036455
634.	ENSECAG00000019193	NCAM1	neural cell adhesion molecule 1	-1,0278	5,986E-31
635.	ENSECAG00000047272	ENSECAG00000047272		-1,0284	0,0010049
636.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-1,0303	0,0001518
637.	ENSECAG00000009250	RAMP1	receptor activity modifying protein 1	-1,0311	0,0147671
638.	ENSECAG00000014626	WNT8A	Wnt family member 8A	-1,0319	0,0195288
639.	ENSECAG00000016721	RUBCNL	rubicon like autophagy enhancer	-1,0331	0,0001871
640.	ENSECAG00000018061	LAMA1	laminin subunit alpha 1	-1,0337	3,172E-05
641.	ENSECAG000000006829	KAZN	kazrin, periplakin interacting protein	-1,0352	3,965E-11
642.	ENSECAG00000007798	ME3	malic enzyme 3	-1,0368	0,0002924
643.	ENSECAG00000026865	EDA	ectodysplasin A	-1,0397	0,0021679
644.	ENSECAG00000013243	ANKRD45	ankyrin repeat domain 45	-1,0424	0,0006364
645.	ENSECAG00000003230	AKAP5	A-kinase anchoring protein 5	-1,0429	0,0008319
646.	ENSECAG00000015358	STARD10	StAR related lipid transfer domain containing 10	-1,0459	1,717E-06
647.	ENSECAG00000000217	MTSS2	MTSS I-BAR domain containing 2	-1,0459	7,94E-10
648.	ENSECAG00000035101	ANOS1	anosmin 1	-1,046	0,0119965
649.	ENSECAG00000021953	RUNDC3A	RUN domain containing 3A	-1,0462	0,0002758
650.	ENSECAG00000015745	BLNK	B cell linker	-1,0483	5,394E-07
651.	ENSECAG00000024742	PFN2	profilin 2	-1,0493	1,97E-28
652.	ENSECAG00000005343	GNAL	G protein subunit alpha L	-1,0515	8,582E-06
653.	ENSECAG00000019482	ZNF554	zinc finger protein 554	-1,0524	1,795E-05
654.	ENSECAG00000012283	AGR3	anterior gradient 3, protein disulphide isomerase family member	-1,0536	0,001519
655.	ENSECAG00000031034	ENSECAG00000031034		-1,0558	0,0054261
656.	ENSECAG00000000512	LBH	LBH regulator of WNT signaling pathway	-1,0576	1,98E-16

657.	ENSECAG00000021360	KCNMB1	potassium calcium-activated channel subfamily M regulatory beta subunit 1	-1,0577	6,753E-07
658.	ENSECAG00000008799	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-1,0594	1,373E-05
659.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-1,0602	0,0104481
660.	ENSECAG00000006338	ANKH	ANKH inorganic pyrophosphate transport regulator	-1,061	1,34E-12
661.	ENSECAG00000024630	EPCAM	epithelial cell adhesion molecule	-1,0614	0,0005858
662.	ENSECAG00000008237	KLHL13	kelch like family member 13	-1,0639	1,99E-21
663.	ENSECAG00000016234	ANGPTL2	angiopoietin like 2	-1,0654	1,886E-10
664.	ENSECAG00000018150	GPD1L	glycerol-3-phosphate dehydrogenase 1 like	-1,0672	2,341E-05
665.	ENSECAG00000023080	PPP1R12B	protein phosphatase 1 regulatory subunit 12B	-1,0675	3,833E-05
666.	ENSECAG00000012012	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5	-1,0687	1,628E-27
667.	ENSECAG00000011045	SLC29A2	solute carrier family 29 member 2	-1,0702	0,0056932
668.	ENSECAG00000021012	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	-1,0705	9,444E-14
669.	ENSECAG00000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,0727	3,375E-15
670.	ENSECAG00000049782	ENSECAG00000049782		-1,0733	9,358E-05
671.	ENSECAG00000013468	MYOM1	myomesin 1	-1,08	8,368E-11
672.	ENSECAG00000010269	NIPAL2	NIPA like domain containing 2	-1,0809	8,105E-07
673.	ENSECAG00000021651	NPC1	NPC intracellular cholesterol transporter 1	-1,081	8,565E-16
674.	ENSECAG00000016907	NKD2	NKD inhibitor of WNT signaling pathway 2	-1,0813	4,018E-07
675.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-1,0867	0,0150328
676.	ENSECAG00000011593	MEF2A	myocyte enhancer factor 2A	-1,0878	1,334E-49
677.	ENSECAG00000011747	BCL7A	BAF chromatin remodeling complex subunit BCL7A	-1,0897	1,107E-05
678.	ENSECAG00000022823	PLCE1	phospholipase C epsilon 1	-1,0903	9,137E-07
679.	ENSECAG00000020490	TNFRSF17	TNF receptor superfamily member 17	-1,0914	0,0104184
680.	ENSECAG00000011145	PTGER4	prostaglandin E receptor 4	-1,0943	0,0012067
681.	ENSECAG00000017743	SESN3	sestrin 3	-1,0947	4,269E-16
682.	ENSECAG00000015492	VWA5A	von Willebrand factor A domain containing 5A	-1,0977	8,966E-43
683.	ENSECAG00000017175	REM1	RRAD and GEM like GTPase 1	-1,0988	0,0009589
684.	ENSECAG00000012990	CALCRL	calcitonin receptor like receptor	-1,1013	9,547E-07
685.	ENSECAG00000000420	BANP	BTG3 associated nuclear protein	-1,1022	1,943E-10
686.	ENSECAG00000024459	MARK1	microtubule affinity regulating kinase 1	-1,1026	1,959E-40
687.	ENSECAG00000053065	ENSECAG00000053065		-1,1026	0,0003932
688.	ENSECAG00000000077	CPEB3	cytoplasmic polyadenylation element binding protein 3	-1,1037	0,0003903
689.	ENSECAG00000021979	CARD10	caspase recruitment domain family member 10	-1,1046	0,0001861
690.	ENSECAG00000048330	ENSECAG00000048330		-1,1051	0,0014982
691.	ENSECAG00000022683	RSP01	R-spondin 1	-1,1053	5,349E-05
692.	ENSECAG00000008768	PARD3B	par-3 family cell polarity regulator beta	-1,1064	3,845E-26
693.	ENSECAG00000018159	CNNM2	cyclin and CBS domain divalent metal cation transport mediator 2	-1,1092	1,194E-11
694.	ENSECAG00000019087	CTSK	cathepsin K	-1,1101	6,048E-05
695.	ENSECAG00000047308	ENSECAG00000047308		-1,1106	0,0133397
696.	ENSECAG00000022348	PRSS12	serine protease 12	-1,1112	3,693E-06
697.	ENSECAG00000024200	POU6F1	POU class 6 homeobox 1	-1,1132	1,023E-08
698.	ENSECAG00000018631	LTBP2	latent transforming growth factor beta binding protein 2	-1,1136	9,81E-08
699.	ENSECAG00000020957	LCN2	lipocalin 2	-1,1137	4,726E-16
700.	ENSECAG00000059312	ENSECAG00000059312		-1,1158	4,103E-16
701.	ENSECAG00000013884	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	-1,1167	0,0030189
702.	ENSECAG00000023578	ELOVL3	ELOVL fatty acid elongase 3	-1,1184	1,972E-05
703.	ENSECAG00000051604	ENSECAG00000051604		-1,1187	0,0021522

704.	ENSECAG00000048239	ENSECAG00000048239		-1,1199	0,0019684
705.	ENSECAG00000009025	CDHR3	cadherin related family member 3	-1,1206	9,318E-05
706.	ENSECAG00000035205	ZNF853	zinc finger protein 853	-1,1257	1,731E-09
707.	ENSECAG00000029419	ENSECAG00000029419		-1,1268	0,0025731
708.	ENSECAG00000024315	TARS3	threonyl-tRNA synthetase 3	-1,1283	4,942E-05
709.	ENSECAG00000000487	SYNM	synemin	-1,129	2,935E-14
710.	ENSECAG00000010120	SNAI2	snail family transcriptional repressor 2	-1,132	1,185E-15
711.	ENSECAG00000011774	APCDD1	APC down-regulated 1	-1,1322	0,000562
712.	ENSECAG00000015023	FAM184A	family with sequence similarity 184 member A	-1,1357	7,465E-07
713.	ENSECAG00000032702	ENSECAG00000032702		-1,1365	6,236E-05
714.	ENSECAG00000028572	ENSECAG00000028572		-1,1372	1,947E-14
715.	ENSECAG00000010939	ANGPTL1	angiopoietin like 1	-1,1417	8,188E-05
716.	ENSECAG00000009424	CCDC171	coiled-coil domain containing 171	-1,1435	9,682E-10
717.	ENSECAG00000011912	RAB36	RAB36, member RAS onco family	-1,1445	4,156E-05
718.	ENSECAG00000017689	ARHGEF28	Rho guanine nucleotide exchange factor 28	-1,1453	7,874E-19
719.	ENSECAG00000000354	PLK2	polo like kinase 2	-1,1461	4,744E-31
720.	ENSECAG00000019233	ELMO1	engulfment and cell motility 1	-1,1462	8,684E-12
721.	ENSECAG00000034308	TRIM6	tripartite motif containing 6	-1,1525	0,0031984
722.	ENSECAG00000004050	SLC8A1	solute carrier family 8 member A1	-1,1528	2,694E-10
723.	ENSECAG00000052116	EPB41L5	erythrocyte membrane protein band 4.1 like 5	-1,1531	2,192E-11
724.	ENSECAG00000020002	DCDC1	doublecortin domain containing 1	-1,1535	2,161E-05
725.	ENSECAG00000009422	RG57	regulator of G protein signaling 7	-1,1535	0,0033575
726.	ENSECAG00000059686	ENSECAG00000059686		-1,1547	0,0121546
727.	ENSECAG00000010830	MMP11	matrix metalloproteinase 11	-1,1586	4,071E-15
728.	ENSECAG00000011618	EDN1	endothelin 1	-1,1604	0,0001539
729.	ENSECAG00000004085	FAM78B	family with sequence similarity 78 member B	-1,163	0,0051336
730.	ENSECAG00000015195	EHD3	EH domain containing 3	-1,169	1,488E-20
731.	ENSECAG00000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-1,1737	6,286E-06
732.	ENSECAG00000008162	SIPA1L2	signal induced proliferation associated 1 like 2	-1,1745	4,83E-10
733.	ENSECAG00000016667	ENSECAG00000016667		-1,1775	5,241E-09
734.	ENSECAG00000022387	RUNDC3B	RUN domain containing 3B	-1,1778	0,0112223
735.	ENSECAG00000010414	PON2	paraoxonase 2	-1,181	4,4E-07
736.	ENSECAG00000023538	ENOX1	ecto-NOX disulfide-thiol exchanger 1	-1,1818	0,0009179
737.	ENSECAG00000007718	TMOD1	tropomodulin 1	-1,1833	1,769E-18
738.	ENSECAG000000008830	WNT5A	Wnt family member 5A	-1,1886	5,171E-72
739.	ENSECAG00000021042	VASH1	vasohibin 1	-1,1902	1,632E-18
740.	ENSECAG00000021066	KLHL24	kelch like family member 24	-1,1905	2,749E-32
741.	ENSECAG00000016431	MAG11	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1,1972	7,063E-09
742.	ENSECAG00000007087	FBXL13	F-box and leucine rich repeat protein 13	-1,1981	6,067E-08
743.	ENSECAG00000013242	ABCA3	ATP binding cassette subfamily A member 3	-1,1993	1,167E-19
744.	ENSECAG00000015824	APOM	apolipoprotein M	-1,202	0,0051595
745.	ENSECAG00000008335	PKD4	pyruvate dehydrogenase kinase 4	-1,2023	1,068E-05
746.	ENSECAG00000012652	CHDH	choline dehydrogenase	-1,2038	1,27E-06
747.	ENSECAG00000059950	ENSECAG00000059950		-1,2044	1,638E-07
748.	ENSECAG00000015760	ITGA3	integrin subunit alpha 3	-1,2093	1,606E-06
749.	ENSECAG00000021132	AFF2	ALF transcription elongation factor 2	-1,2104	3,542E-16
750.	ENSECAG00000012071	TCP11	t-complex 11	-1,2114	0,009892
751.	ENSECAG00000009138	MME	membrane metalloendopeptidase	-1,2132	3,923E-05
752.	ENSECAG00000057783	ENSECAG00000057783		-1,2138	1,336E-07
753.	ENSECAG00000016277	SGCD	sarcoglycan delta	-1,2154	5,371E-09
754.	ENSECAG00000029898	MPND	MPN domain containing	-1,216	2,262E-12
755.	ENSECAG00000020468	RELN	reelin	-1,2195	0,0016394
756.	ENSECAG00000015772	GALNT17	polypeptide N-acetylgalactosaminyltransferase 17	-1,2218	5,332E-05
757.	ENSECAG00000007088	KBTD8	kelch repeat and BTB domain containing 8	-1,2254	6,475E-07
758.	ENSECAG00000014312	PRKCZ	protein kinase C zeta	-1,2256	0,0061895

759.	ENSECAG00000033624	ENSECAG00000033624		-1,2306	0,0049002
760.	ENSECAG00000003137	P4HTM	prolyl 4-hydroxylase, transmembrane	-1,2313	1,705E-07
761.	ENSECAG00000018803	PGM2L1	phosphoglucomutase 2 like 1	-1,2314	7,848E-14
762.	ENSECAG00000013723	SLC7A8	solute carrier family 7 member 8	-1,2386	0,0093489
763.	ENSECAG00000010747	SH3BGR	SH3 domain binding glutamate rich protein	-1,2396	7,546E-14
764.	ENSECAG00000031607	ENSECAG00000031607		-1,244	9,847E-05
765.	ENSECAG00000011432	SLC46A3	solute carrier family 46 member 3	-1,2536	6,294E-07
766.	ENSECAG00000060330	PLSCR4	phospholipid scramblase 4	-1,2543	1,075E-12
767.	ENSECAG00000015853	SORT1	sortilin 1	-1,2571	5,018E-05
768.	ENSECAG00000000166	SPHKAP	SPHK1 interactor, AKAP domain containing	-1,2572	4,348E-06
769.	ENSECAG00000024039	HFM1	helicase for meiosis 1	-1,265	3,495E-05
770.	ENSECAG00000012700	JADE3	jade family PHD finger 3	-1,2707	3,017E-07
771.	ENSECAG00000001988	FAT3	FAT atypical cadherin 3	-1,2766	8,007E-05
772.	ENSECAG00000008738	ID2	inhibitor of DNA binding 2	-1,2779	3,59E-24
773.	ENSECAG00000010242	MCTP1	multiple C2 and transmembrane domain containing 1	-1,2801	1,204E-26
774.	ENSECAG00000011187	TSPAN11	tetraspanin 11	-1,2805	5,421E-05
775.	ENSECAG00000015566	NSG1	neuronal vesicle trafficking associated 1	-1,2807	1,423E-33
776.	ENSECAG00000011749	MSX2	msh homeobox 2	-1,2834	2,075E-10
777.	ENSECAG00000023088	BMF	Bcl2 modifying factor	-1,2847	1,03E-08
778.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-1,2848	0,0026232
779.	ENSECAG00000012812	SYBU	syntabulin	-1,2878	0,0057344
780.	ENSECAG00000024399	FGF12	fibroblast growth factor 12	-1,2882	0,0004228
781.	ENSECAG00000022556	ABCA9	ATP binding cassette subfamily A member 9	-1,2899	0,0004036
782.	ENSECAG00000015144	CADM1	cell adhesion molecule 1	-1,2903	6,206E-11
783.	ENSECAG00000013633	ARHGAP6	Rho GTPase activating protein 6	-1,292	1,252E-09
784.	ENSECAG00000021609	SLC40A1	solute carrier family 40 member 1	-1,2949	1,119E-33
785.	ENSECAG00000010901	CTNND2	catenin delta 2	-1,2977	0,0033918
786.	ENSECAG00000008564	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1,3019	0,0052771
787.	ENSECAG00000013428	ID4	inhibitor of DNA binding 4	-1,3021	7,825E-14
788.	ENSECAG00000013393	AHR	aryl hydrocarbon receptor	-1,3116	4,452E-20
789.	ENSECAG00000000149	CNKSR2	connector enhancer of kinase suppressor of Ras 2	-1,3192	0,0072501
790.	ENSECAG00000017897	FAM167A	family with sequence similarity 167 member A	-1,3202	1,663E-06
791.	ENSECAG00000017502	PCDH9	protocadherin 9	-1,321	1,655E-07
792.	ENSECAG00000023089	SLAIN1	SLAIN motif family member 1	-1,322	0,0074511
793.	ENSECAG000000056462	MMP12	matrix metalloproteinase 12	-1,3273	0,0021111
794.	ENSECAG00000048282	ENSECAG00000048282		-1,3294	1,776E-07
795.	ENSECAG00000019701	ANKFN1	ankyrin repeat and fibronectin type III domain containing 1	-1,3306	6,521E-05
796.	ENSECAG00000059690	ENSECAG00000059690		-1,3317	0,0083155
797.	ENSECAG00000044952	ENSECAG00000044952		-1,3321	0,0077011
798.	ENSECAG00000019664	HID1	HID1 domain containing	-1,3325	0,0001069
799.	ENSECAG00000046252	ENSECAG00000046252		-1,3326	5,596E-05
800.	ENSECAG00000003570	PICK1	protein interacting with PRKCA 1	-1,3387	4,226E-11
801.	ENSECAG000000020437	BCL2	BCL2 apoptosis regulator	-1,344	1,397E-09
802.	ENSECAG00000031200	ENSECAG00000031200		-1,3454	2,474E-33
803.	ENSECAG00000021277	LAMA3	laminin subunit alpha 3	-1,3487	1,185E-05
804.	ENSECAG00000016430	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	-1,3497	0,0008645
805.	ENSECAG00000024701	AOX4	aldehyde oxidase 4	-1,3509	1,369E-05
806.	ENSECAG00000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-1,3513	1,407E-09
807.	ENSECAG00000008762	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	-1,3516	1,792E-05
808.	ENSECAG00000034367	ENSECAG00000034367		-1,3543	0,0011637
809.	ENSECAG00000011154	CHRD	chordin	-1,3578	4,589E-22
810.	ENSECAG00000000207	ACTA1	actin alpha 1, skeletal muscle	-1,3607	0,0004675
811.	ENSECAG00000057169	ENSECAG00000057169		-1,3701	0,0066878

812.	ENSECAG00000014962	FAXDC2	fatty acid hydroxylase domain containing 2	-1,3716	3,235E-07
813.	ENSECAG00000015569	MATCAP2	microtubule associated tyrosine carboxypeptidase 2	-1,3741	5,628E-07
814.	ENSECAG00000025633	MIR27B	microRNA 27b	-1,3742	0,004636
815.	ENSECAG00000000794	EMB	embigin	-1,376	0,001779
816.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-1,3776	3,585E-12
817.	ENSECAG00000018419	ANXA3	annexin A3	-1,3778	5,671E-05
818.	ENSECAG00000013582	DHRS3	dehydrogenase/reductase 3	-1,3781	3,825E-66
819.	ENSECAG000000021969	ITGB6	integrin subunit beta 6	-1,3838	0,001071
820.	ENSECAG00000000751	NEDD4L	NEDD4 like E3 ubiquitin protein ligase	-1,3845	3,558E-29
821.	ENSECAG00000023607	DOCK5	dedicator of cytokinesis 5	-1,3851	4,502E-12
822.	ENSECAG00000021663	SMOC1	SPARC related modular calcium binding 1	-1,3889	0,0029152
823.	ENSECAG00000043884	ENSECAG00000043884		-1,3907	0,0005755
824.	ENSECAG00000021576	SGCG	sarcoglycan gamma	-1,394	1,675E-06
825.	ENSECAG00000012212	LRP1B	LDL receptor related protein 1B	-1,3941	0,00038
826.	ENSECAG00000043642	NREP	neuronal reraction related protein	-1,395	5,675E-28
827.	ENSECAG00000022407	SLIT2	slit guidance ligand 2	-1,3986	4,963E-14
828.	ENSECAG00000022054	CLSTN2	calsyntenin 2	-1,399	1,826E-19
829.	ENSECAG00000010989	SH3YL1	SH3 and SYLF domain containing 1	-1,3995	2,625E-16
830.	ENSECAG00000022129	HOXD3	homeobox D3	-1,4027	2,017E-06
831.	ENSECAG00000046600	ENSECAG00000046600		-1,4052	0,0004409
832.	ENSECAG00000002579	MATN2	matrilin 2	-1,4072	9,403E-12
833.	ENSECAG00000057732	ENSECAG00000057732		-1,4073	0,0070527
834.	ENSECAG00000006020	RRAGB	Ras related GTP binding B	-1,4084	2,684E-19
835.	ENSECAG00000032860	ENSECAG00000032860		-1,4167	2,786E-09
836.	ENSECAG00000014646	KNG1	kininogen 1	-1,427	5,28E-10
837.	ENSECAG00000021850	CLDN16	claudin 16	-1,4283	0,0016656
838.	ENSECAG00000021856	PADI2	peptidyl arginine deiminase 2	-1,4307	2,365E-09
839.	ENSECAG00000024637	P2RX5	purinergic receptor P2X 5	-1,4379	0,000193
840.	ENSECAG000000022629	SLC1A7	solute carrier family 1 member 7	-1,4438	3,148E-15
841.	ENSECAG00000022890	NEFL	neurofilament light chain	-1,4444	2,895E-05
842.	ENSECAG00000030788	DIO2	iodothyronine deiodinase 2	-1,4459	2,532E-13
843.	ENSECAG00000053674	MORN4	MORN repeat containing 4	-1,4562	5,401E-18
844.	ENSECAG00000033026	ENSECAG00000033026		-1,4579	8,338E-06
845.	ENSECAG00000000709	ENSECAG00000000709		-1,4581	0,0015327
846.	ENSECAG00000045190	ENSECAG00000045190		-1,4583	4,671E-08
847.	ENSECAG00000016786	JPH2	junctophilin 2	-1,4617	0,0017706
848.	ENSECAG00000003193	BAMBI	BMP and activin membrane bound inhibitor	-1,4655	1,021E-10
849.	ENSECAG00000010262	PERP	p53 apoptosis effector related to PMP22	-1,4659	1,165E-06
850.	ENSECAG00000005360	MITF	melanocyte inducing transcription factor	-1,4699	5,979E-39
851.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-1,472	0,0013201
852.	ENSECAG00000013301	MFAP4	microfibril associated protein 4	-1,4722	1,518E-09
853.	ENSECAG00000012507	CRYAB	crystallin alpha B	-1,4748	6,669E-15
854.	ENSECAG00000016015	PCDH19	protocadherin 19	-1,4767	6,712E-08
855.	ENSECAG00000016573	TSPAN7	tetraspanin 7	-1,4779	0,000198
856.	ENSECAG00000012115	SEMA3D	semaphorin 3D	-1,4846	1,146E-09
857.	ENSECAG00000013425	IGFBP5	insulin like growth factor binding protein 5	-1,4883	0,0004673
858.	ENSECAG00000004258	IL17RB	interleukin 17 receptor B	-1,4884	0,0002332
859.	ENSECAG00000021653	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	-1,489	2,24E-109
860.	ENSECAG00000032285	EMCN	endomucin	-1,4897	0,0007777
861.	ENSECAG00000037540	ENSECAG00000037540		-1,4915	0,0041115
862.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-1,4941	8,741E-11
863.	ENSECAG00000046102	ENSECAG00000046102		-1,5031	0,0009307
864.	ENSECAG00000015134	PELI2	pellino E3 ubiquitin protein ligase family member 2	-1,5041	4,491E-09
865.	ENSECAG00000007183	SEMA3E	semaphorin 3E	-1,5112	0,0014068

866.	ENSECAG00000047495	ENSECAG00000047495		-1,5158	0,000294
867.	ENSECAG00000000274	SPAG16	sperm associated antigen 16	-1,5167	1,379E-06
868.	ENSECAG00000038375	NEBL	nebulette	-1,5182	2,168E-07
869.	ENSECAG00000026951	ARVCF	ARVCF delta catenin family member	-1,5238	5,75E-05
870.	ENSECAG00000017802	OGN	osteoglycin	-1,5279	2,458E-08
871.	ENSECAG00000018314	TIMP3	TIMP metalloproteinase inhibitor 3	-1,5283	4,517E-14
872.	ENSECAG00000040382	ENSECAG00000040382		-1,5288	3,905E-13
873.	ENSECAG00000017938	BLK	BLK proto-onco, Src family tyrosine kinase	-1,5296	0,0004229
874.	ENSECAG00000013217	ECHDC2	enoyl-CoA hydratase domain containing 2	-1,5319	3,378E-11
875.	ENSECAG00000019008	SHROOM3	shroom family member 3	-1,5336	3,007E-10
876.	ENSECAG00000013450	CORO6	coronin 6	-1,5366	7,288E-05
877.	ENSECAG00000014200	TMEM178B	transmembrane protein 178B	-1,5367	0,0014068
878.	ENSECAG00000018888	RENBP	renin binding protein	-1,5378	8,708E-13
879.	ENSECAG00000010184	ADAMTSL3	ADAMTS like 3	-1,5425	1,336E-07
880.	ENSECAG00000009813	CD83	CD83 molecule	-1,5437	8,7E-05
881.	ENSECAG00000017812	AHRR	aryl hydrocarbon receptor repressor	-1,5474	4,245E-05
882.	ENSECAG00000024137	ENDOU	endonuclease, poly(U) specific	-1,5541	1,391E-07
883.	ENSECAG00000022370	NEFM	neurofilament medium chain	-1,5544	7,408E-06
884.	ENSECAG00000021544	FAIM2	Fas apoptotic inhibitory molecule 2	-1,5552	2,217E-12
885.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-1,5569	0,0007759
886.	ENSECAG00000015892	CACNA1D	calcium voltage-gated channel subunit alpha1 D	-1,5587	1,489E-23
887.	ENSECAG00000012667	RBFOX1	RNA binding fox-1 homolog 1	-1,5615	1,44E-08
888.	ENSECAG00000020677	LHCGR	luteinizing hormone/choriogonadotropin receptor	-1,5631	0,001208
889.	ENSECAG00000007385	NIBAN1	niban apoptosis regulator 1	-1,5661	1,283E-36
890.	ENSECAG00000049817	ENSECAG00000049817		-1,5704	0,0003363
891.	ENSECAG00000019600	GRP	gastrin releasing peptide	-1,5791	1,446E-06
892.	ENSECAG00000053524	BEX4	brain expressed X-linked 4	-1,5806	0,0005326
893.	ENSECAG00000032497	ENSECAG00000032497		-1,5852	2,862E-05
894.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-1,5901	2,953E-18
895.	ENSECAG00000022537	MAL2	mal, T cell differentiation protein 2	-1,5947	0,0019041
896.	ENSECAG00000019042	UPK1B	uroplakin 1B	-1,5991	8,118E-17
897.	ENSECAG00000018863	ADGRL3	adhesion G protein-coupled receptor L3	-1,6043	3,461E-10
898.	ENSECAG00000000435	LRP2	LDL receptor related protein 2	-1,607	2,588E-05
899.	ENSECAG00000022874	SCG5	secretogranin V	-1,6087	9,05E-08
900.	ENSECAG00000057723	ENSECAG00000057723		-1,6152	1,315E-13
901.	ENSECAG00000017816	ADORA1	adenosine A1 receptor	-1,6183	5,796E-16
902.	ENSECAG00000048455	ENSECAG00000048455		-1,6226	1,398E-10
903.	ENSECAG00000015715	ADAMTS15	ADAM metalloproteinase with thrombospondin type 1 motif 15	-1,6271	4,414E-17
904.	ENSECAG00000019940	AKAP6	A-kinase anchoring protein 6	-1,6302	5,071E-15
905.	ENSECAG00000015927	CABLES1	Cdk5 and Abl enzyme substrate 1	-1,6303	2,045E-05
906.	ENSECAG00000060247	ENSECAG00000060247		-1,6349	8,597E-27
907.	ENSECAG00000013677	FRY	FRY microtubule binding protein	-1,6351	8,176E-18
908.	ENSECAG00000018280	TACC2	transforming acidic coiled-coil containing protein 2	-1,637	5,565E-17
909.	ENSECAG00000004707	MFSD6	major facilitator superfamily domain containing 6	-1,6395	2,429E-07
910.	ENSECAG00000006060	RAI2	retinoic acid induced 2	-1,6427	3,382E-07
911.	ENSECAG00000026945	HES1	hes family bHLH transcription factor 1	-1,6436	3,299E-06
912.	ENSECAG00000025076	CTTNBP2	cortactin binding protein 2	-1,6485	7,787E-17
913.	ENSECAG00000059741	ENSECAG00000059741		-1,6657	1,03E-05
914.	ENSECAG00000019495	C5H1orf141	chromosome 5 C1orf141 homolog	-1,6748	0,0034614
915.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-1,6762	7,636E-07
916.	ENSECAG00000018472	PDGFB	platelet derived growth factor subunit B	-1,6818	4,533E-05
917.	ENSECAG00000015834	DMD	dystrophin	-1,6881	2,718E-09
918.	ENSECAG00000010880	SOX6	SRY-box transcription factor 6	-1,6931	2,243E-06
919.	ENSECAG00000010881	DPYD	dihydropyrimidine dehydrogenase	-1,6947	5,635E-15
920.	ENSECAG00000017398	CD180	CD180 molecule	-1,7038	0,0050276

921.	ENSECAG00000044796	GREM1	gremlin 1, DAN family BMP antagonist	-1,7072	2,471E-06
922.	ENSECAG00000040326	ENSECAG00000040326		-1,7136	7,804E-06
923.	ENSECAG00000036634	CCDC3	coiled-coil domain containing 3	-1,7166	1,615E-06
924.	ENSECAG00000024612	SNED1	sushi, nidogen and EGF like domains 1	-1,7294	0,000774
925.	ENSECAG00000008053	TMEM170B	transmembrane protein 170B	-1,732	1,244E-23
926.	ENSECAG00000001488	GPR171	G protein-coupled receptor 171	-1,7344	4,006E-06
927.	ENSECAG00000023960	KLHL30	kelch like family member 30	-1,7345	7,413E-05
928.	ENSECAG00000024045	EFHD1	EF-hand domain family member D1	-1,7366	3,339E-12
929.	ENSECAG00000016129	ABLIM3	actin binding LIM protein family member 3	-1,7369	1,132E-06
930.	ENSECAG00000053411	ENSECAG00000053411		-1,7403	0,0017908
931.	ENSECAG00000016251	ENSECAG00000016251		-1,7407	6,056E-05
932.	ENSECAG00000018692	SEPTIN12	septin 12	-1,7414	1,06E-10
933.	ENSECAG00000008038	TENM4	teneurin transmembrane protein 4	-1,7562	3,512E-32
934.	ENSECAG00000053581	ENSECAG00000053581		-1,7574	4,486E-05
935.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1,7802	1,064E-05
936.	ENSECAG00000051305	ENSECAG00000051305		-1,7817	0,0027281
937.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-1,7857	7,987E-05
938.	ENSECAG00000011467	ALPL	alkaline phosphatase, biomineralization associated	-1,789	4,34E-12
939.	ENSECAG00000054759	ENSECAG00000054759		-1,7957	0,0002133
940.	ENSECAG00000033602	GPRIN3	GPRIN family member 3	-1,7987	0,0008381
941.	ENSECAG00000010967	MMP19	matrix metalloproteinase 19	-1,801	2,144E-30
942.	ENSECAG00000022853	CD28	CD28 molecule	-1,8039	0,0041366
943.	ENSECAG00000006848	SLC27A6	solute carrier family 27 member 6	-1,8152	7,048E-14
944.	ENSECAG00000030850	FGF18	fibroblast growth factor 18	-1,8269	4,13E-05
945.	ENSECAG00000021078	GRB14	growth factor receptor bound protein 14	-1,8329	4,984E-06
946.	ENSECAG00000023039	CCN3	cellular communication network factor 3	-1,8585	1,567E-07
947.	ENSECAG00000012993	JAG1	jagged canonical Notch ligand 1	-1,8646	1,033E-06
948.	ENSECAG00000018927	ANGPTL4	angiopoietin like 4	-1,8781	1,873E-11
949.	ENSECAG00000014504	KIF1A	kinesin family member 1A	-1,8924	6,17E-07
950.	ENSECAG00000015961	PPP1R9A	protein phosphatase 1 regulatory subunit 9A	-1,9109	2,187E-22
951.	ENSECAG00000011358	TMEM86A	transmembrane protein 86A	-1,9125	3,311E-07
952.	ENSECAG00000014313	DCLK2	doublecortin like kinase 2	-1,917	1,326E-07
953.	ENSECAG00000024448	TRIM63	tripartite motif containing 63	-1,929	6,291E-31
954.	ENSECAG00000000658	GNPMB	glycoprotein nmb	-1,9411	5,21E-124
955.	ENSECAG00000018771	PKNOX2	PBX/knotted 1 homeobox 2	-1,9477	4,448E-09
956.	ENSECAG00000002874	LRRN1	leucine rich repeat neuronal 1	-1,9497	0,0002025
957.	ENSECAG00000021092	KLF15	KLF transcription factor 15	-1,952	7,622E-15
958.	ENSECAG00000019335	TLCD4	TLC domain containing 4	-1,9672	3,134E-16
959.	ENSECAG00000013426	DLG2	discs large MAGUK scaffold protein 2	-1,9754	0,0006371
960.	ENSECAG00000012962	SAMD12	sterile alpha motif domain containing 12	-1,9755	8,016E-30
961.	ENSECAG00000032719	ENSECAG00000032719		-1,978	3,049E-05
962.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-1,9943	5,18E-13
963.	ENSECAG00000039579	GDF15	growth differentiation factor 15	-1,9957	0,0017982
964.	ENSECAG00000011594	KCND3	potassium voltage-gated channel subfamily D member 3	-2	4,114E-26
965.	ENSECAG00000009586	C13H16orf89	chromosome 13 C16orf89 homolog	-2,0074	0,0014468
966.	ENSECAG00000007281	SAMD11	sterile alpha motif domain containing 11	-2,0219	3,82E-18
967.	ENSECAG00000004445	PDE11A	phosphodiesterase 11A	-2,0253	2,702E-46
968.	ENSECAG00000007220	HEYL	hes related family bHLH transcription factor with YRPW motif like	-2,0313	1,296E-08
969.	ENSECAG00000000501	UNC5CL	unc-5 family C-terminal like	-2,0617	0,0009274
970.	ENSECAG00000017460	ATP12A	ATPase H ⁺ /K ⁺ transporting non-gastric alpha2 subunit	-2,0755	0,0007015
971.	ENSECAG00000031859	ENSECAG00000031859		-2,0784	8,935E-15
972.	ENSECAG00000059760	ADRA2A	adrenoceptor alpha 2A	-2,0817	1,184E-21

973.	ENSECAG00000027835	LRATD1	LRAT domain containing 1	-2,0832	0,0001789
974.	ENSECAG00000003067	PWWP3B	PWWP domain containing 3B	-2,0834	0,0004963
975.	ENSECAG00000009528	CDH3	cadherin 3	-2,0882	9,601E-05
976.	ENSECAG00000020869	FGFR4	fibroblast growth factor receptor 4	-2,103	1,719E-12
977.	ENSECAG00000006137	FAM227A	family with sequence similarity 227 member A	-2,1054	0,0007022
978.	ENSECAG00000007878	FRMD3	FERM domain containing 3	-2,1236	1,698E-07
979.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-2,1297	1,017E-32
980.	ENSECAG00000050236	ENSECAG00000050236		-2,1334	2,588E-05
981.	ENSECAG00000006980	FEZ1	fasciculation and elongation protein zeta 1	-2,1369	3,707E-15
982.	ENSECAG00000023387	FRRS1	ferric chelate reductase 1	-2,1423	2,968E-09
983.	ENSECAG00000023274	LAMA5	laminin subunit alpha 5	-2,1727	4,649E-13
984.	ENSECAG00000021621	MOB3B	MOB kinase activator 3B	-2,1826	1,489E-06
985.	ENSECAG00000002390	ENSECAG00000002390		-2,1987	2,884E-19
986.	ENSECAG00000018543	RCAN2	regulator of calcineurin 2	-2,2039	7,503E-17
987.	ENSECAG00000011898	SPEF2	sperm flagellar 2	-2,2062	2,578E-10
988.	ENSECAG00000007047	ASPN	asporin	-2,2074	6,076E-15
989.	ENSECAG00000048971	RNF152	ring finger protein 152	-2,2158	2,063E-09
990.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-2,2383	3,936E-07
991.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-2,2792	7,68E-32
992.	ENSECAG00000020101	SLC24A2	solute carrier family 24 member 2	-2,2794	2,163E-15
993.	ENSECAG00000029885	CHST7	carbohydrate sulfotransferase 7	-2,2887	2,935E-14
994.	ENSECAG00000011138	COL4A4	collagen type IV alpha 4 chain	-2,2949	1,845E-09
995.	ENSECAG00000017701	CELSR2	cadherin EGF LAG seven-pass G-type receptor 2	-2,3071	3,784E-09
996.	ENSECAG00000060299	ENSECAG00000060299		-2,3304	5,044E-08
997.	ENSECAG00000048070	ENSECAG00000048070		-2,336	4,457E-06
998.	ENSECAG00000044498	CA3	carbonic anhydrase 3	-2,3924	3,671E-06
999.	ENSECAG00000024302	MAP7	microtubule associated protein 7	-2,4419	0,0002263
1000.	ENSECAG00000046304	ENSECAG00000046304		-2,4515	1,187E-10
1001.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-2,4534	8,511E-23
1002.	ENSECAG00000015460	HCLS1	hematopoietic cell-specific Lyn substrate 1	-2,4541	2,524E-08
1003.	ENSECAG00000015000	FAM83G	family with sequence similarity 83 member G	-2,4572	4,839E-11
1004.	ENSECAG00000022441	ESR1	estrogen receptor 1	-2,4811	1,23E-111
1005.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-2,5055	7,078E-09
1006.	ENSECAG00000028788	HES4	hes family bHLH transcription factor 4	-2,5787	2,754E-05
1007.	ENSECAG00000015934	MAMDC2	MAM domain containing 2	-2,5922	1,418E-23
1008.	ENSECAG00000039359	CYS1	cystin 1	-2,5951	3,913E-26
1009.	ENSECAG00000038712	TNXB	tenascin XB	-2,625	4,77E-94
1010.	ENSECAG00000040154	ELN	elastin	-2,6279	4,432E-29
1011.	ENSECAG000000014513	TNFSF15	TNF superfamily member 15	-2,6581	4,282E-10
1012.	ENSECAG00000014285	INHBB	inhibin subunit beta B	-2,7693	7,631E-17
1013.	ENSECAG00000057017	ABCA8	ATP binding cassette subfamily A member 8	-2,7835	1,083E-07
1014.	ENSECAG00000001197	TNFRSF19	TNF receptor superfamily member 19	-2,9113	1,042E-09
1015.	ENSECAG00000041748	COL4A3	collagen type IV alpha 3 chain	-2,9198	8,846E-25
1016.	ENSECAG00000008518	NPNT	nephronectin	-2,9404	2,954E-28
1017.	ENSECAG000000010721	MGP	matrix Gla protein	-3,111	7,44E-108
1018.	ENSECAG00000015826	RRAGD	Ras related GTP binding D	-3,183	3,975E-06
1019.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-3,2507	1,305E-84
1020.	ENSECAG00000036870	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-3,2708	3,679E-19
1021.	ENSECAG00000013817	CYP1A1	cytochrome P450 family 1 subfamily A member 1	-3,4394	3,29E-05
1022.	ENSECAG00000042911	ENSECAG00000042911		-3,4954	8,248E-07
1023.	ENSECAG00000015484	ATP6V0D2	ATPase H+ transporting V0 subunit d2	-3,5973	2,616E-20
1024.	ENSECAG00000006772	DYSF	dysferlin	-3,624	7,59E-05
1025.	ENSECAG00000010791	LMCD1	LIM and cysteine rich domains 1	-3,6824	5,566E-14
1026.	ENSECAG00000018308	GREB1	growth regulating estrogen receptor binding 1	-3,6993	2,191E-24
1027.	ENSECAG00000056537	ENSECAG00000056537		-3,7679	1,887E-05

1028.	ENSECAG00000014239	PTGER3	prostaglandin E receptor 3	-3,8755	0,0002075
1029.	ENSECAG00000042952	GPX3	glutathione peroxidase 3	-3,9241	1,782E-10
1030.	ENSECAG00000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-4,0699	8,133E-12
1031.	ENSECAG00000028632	ENSECAG00000028632		-4,6422	1,734E-07
1032.	ENSECAG00000023161	IGSF10	immunoglobulin superfamily member 10	-4,8469	1,098E-21
1033.	ENSECAG00000009483	PRLR	prolactin receptor	-5,8094	9,613E-16

Supplementary Table 4. The summary of datasets used in Research task 3, Experiment 1.

Category of endometria	Replicate	Treatment	Reads before QC	Reads after QC	Uniquely mapped genes (%)	Number of expressed genes
I	rep_1	Control	24811533	20974279	95,33	17632
		IFN-γ	24433102	20309561	95,2	17199
		IL-4	24610023	20717247	95,37	16990
		IL-13	20977026	17551851	95,36	17150
	rep_2	Control	25774507	21393536	95,41	18038
		IFN-γ	20670315	17096698	94,77	17359
		IL-4	24861509	19921644	94,81	17544
		IL-13	24539826	20389125	95,18	17587
	rep_3	Control	23174385	18924264	95,13	17514
		IFN-γ	21790572	17946701	95	17255
		IL-4	24794981	20728290	94,89	17279
		IL-13	21744567	17820369	94,8	17172
	rep_4	Control	25742738	21226590	95,11	18182
		IFN-γ	26673715	21868994	94,73	17945
		IL-4	23015552	18986635	95,24	17339
		IL-13	23111155	18901059	95,22	17611
	rep_5	Control	25742738	21226590	95,11	18182
		IFN-γ	26673715	21868994	94,73	17945
		IL-4	23015552	18986635	95,24	17339
		IL-13	23111155	18901059	95,22	17611
IIB	rep_1	Control	24811533	20974279	95,33	17632
		IFN-γ	24433102	20309561	95,2	17199
		IL-4	24610023	20717247	95,37	16990
		IL-13	20977026	17551851	95,36	17150
	rep_2	Control	25774507	21393536	95,41	18038
		IFN-γ	20670315	17096698	94,77	17359
		IL-4	24861509	19921644	94,81	17544
		IL-13	24539826	20389125	95,18	17587
	rep_3	Control	23174385	18924264	95,13	17514
		IFN-γ	21790572	17946701	95	17255
		IL-4	24794981	20728290	94,89	17279
		IL-13	21744567	17820369	94,8	17172
	rep_4	Control	25742738	21226590	95,11	18182
		IFN-γ	26673715	21868994	94,73	17945
		IL-4	23015552	18986635	95,24	17339
		IL-13	23111155	18901059	95,22	17611
	rep_5	Control	25742738	21226590	95,11	18182
		IFN-γ	26673715	21868994	94,73	17945
		IL-4	23015552	18986635	95,24	17339
		IL-13	23111155	18901059	95,22	17611

Supplementary Table 5. The comparison of selected extracellular matrix (ECM)-associated marker gene expression in the endometrial fibroblasts derived from category I and IIB endometria in response to interleukin 4 (IL-4) and IL-13 using RNA sequencing (RNA-seq) and quantitative polymerase chain reaction (qPCR) (Research task 3, Experiment 1).

	RNA-Seq		qPCR	
	log2FC	padj	fold change	p value
IL-4 vs. Control cat. I				
<i>COL4A3</i>	-1,81533	9,90896E-07	-4,399	<0,0001
<i>TIMP1</i>	1,272731	2,69E-23	2,023	0,076
<i>MMP9</i>	-1,66732	2,33E-19	-2,93	0,0006
IL-4 vs. Control cat IIB				
<i>COL4A3</i>	-2,1901	4,78E-25	-2,63	<0,0001
<i>TIMP1</i>	1,435416	1,46E-20	2,96	0,046
<i>MMP9</i>	-1,40023	4,96E-05	-3,18	0,0009
IL-13 vs. Control cat I				
<i>COL4A3</i>	-1,46726	0,000222	-2,82	0,0016
<i>TIMP1</i>	1,069489	4,11E-16	1,14	0,0436
IL-13 vs. Control cat IIB				
<i>COL4A3</i>	-1,70209	1,04E-15	-2,36	<0,0001
<i>TIMP1</i>	1,130875	1,7E-12	2,02	0,0196

Supplementary Table 6. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category I endometria treated with interleukin IL-4 for 48 hours (Research task 3, Experiment 1).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	p _{adj}
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	16,0893	2,7E-49
2.	ENSECAG00000016867	CISH	Cytokine Inducible SH2 Containing Protein	9,42692	5,1E-22
3.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	9,29826	7E-152
4.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	8,63549	4,2E-19
5.	ENSECAG00000034282	CCL8	C-C motif chemokine 7	8,23078	2,6E-49
6.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	8,0499	4,6E-32
7.	ENSECAG00000038698	ALOX15	Arachidonate 15-Lipoxygenase	7,75096	1,3E-15
8.	ENSECAG00000013482	SERPINA3	Serpin Family A Member 3	7,59804	5,2E-53
9.	ENSECAG00000020738	CDH26	cadherin 26	7,58854	6E-95
10.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	7,54288	5E-20
11.	ENSECAG00000020578	PDCD1LG2	Programmed Cell Death 1 Ligand 2	7,38961	1,9E-46
12.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	7,37724	5E-13
13.	ENSECAG00000008739	ENSECAG00000008739		7,19818	1,3E-15
14.	ENSECAG00000014650	INSRR	insulin receptor related receptor	7,15743	7,3E-62
15.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	7,02681	5,5E-38
16.	ENSECAG00000011581	ENSECAG00000011581		7,01929	3,3E-28
17.	ENSECAG00000018409	NOX5	NADPH oxidase 5	6,98425	1,5E-15
18.	ENSECAG00000019282	HDC	histidine decarboxylase	6,9392	1,6E-09
19.	ENSECAG00000023918	DUOX1	dual oxidase 1	6,84027	9,4E-26
20.	ENSECAG00000023032	AZIN2	Antizyme Inhibitor 2	6,60841	1,8E-44
21.	ENSECAG00000000706	MEGF11	multiple EGF like domains 11	6,31309	1,6E-21
22.	ENSECAG00000016169	COL6A6	collagen type VI alpha 6 chain	6,0885	3,7E-07
23.	ENSECAG00000002249	PLEKHG4B	Pleckstrin Homology And RhoGEF Domain Containing G4B	6,02184	1,6E-13
24.	ENSECAG00000017948	BTN1A1	butyrophilin subfamily 1 member A1	5,96238	6,2E-08
25.	ENSECAG00000009034	DUOXA1	dual oxidase maturation factor 1	5,83035	1,2E-09
26.	ENSECAG00000004201	FETUB	fetuin B	5,59449	6,2E-11
27.	ENSECAG00000017764	DUOX2	dual oxidase 2	5,51499	4,9E-06
28.	ENSECAG00000023942	ENSECAG00000023942	ras GTPase-activating protein 4	5,49166	3,8E-28
29.	ENSECAG00000005241	THBD	thrombomodulin	5,42235	3,2E-43
30.	ENSECAG00000021182	TNFSF4	TNF superfamily member 4	5,33704	4E-08
31.	ENSECAG00000009916	GRIA4	glutamate ionotropic receptor AMPA type subunit 4	5,31065	5E-12
32.	ENSECAG00000010048	IGSF11	immunoglobulin superfamily member 11	5,24063	2E-07
33.	ENSECAG00000008034	PLPPR5	phospholipid phosphatase related 5	5,22774	2,9E-06
34.	ENSECAG00000014916	TNFRSF11B	TNF receptor superfamily member 11b	5,15984	3,4E-09
35.	ENSECAG00000026965	SOCS1	suppressor of cytokine signaling 1	5,02118	4E-12
36.	ENSECAG00000023841	POSTN	periostin	4,85483	4,4E-16
37.	ENSECAG00000017896	PDLIM3	PDZ and LIM domain 3	4,8347	3,5E-06
38.	ENSECAG00000016312	CD274	CD274 molecule	4,78035	2,9E-70
39.	ENSECAG00000013703	PPP1R3C	Protein Phosphatase 1 Regulatory Subunit 3C	4,58543	3E-31
40.	ENSECAG00000019800	TSPAN33	Tetraspanin 33	4,56665	1E-48
41.	ENSECAG00000007825	CALCA	calcitonin-related polypeptide alpha	4,526	3,6E-20
42.	ENSECAG00000021604	PDGFRL	platelet derived growth factor receptor like	4,4684	3,9E-74
43.	ENSECAG00000009767	P2RX1	purinergic receptor P2X 1	4,26286	2,2E-13
44.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	4,25174	6,3E-65

45.	ENSECAG00000032667	INA	Internexin Neuronal Intermediate Filament Protein Alpha	4,24959	1E-07
46.	ENSECAG00000010750	VWCE	von Willebrand factor C and EGF domains	4,2247	3,3E-34
47.	ENSECAG00000012830	CHN2	Chimerin 2	4,14906	5E-65
48.	ENSECAG00000035561	ENSECAG00000035561	ubiquitin conjugating enzyme E2 Q family like 1	4,09664	1,6E-12
49.	ENSECAG00000004587	ANKRD34B	ankyrin repeat domain 34B	4,0565	1E-13
50.	ENSECAG00000022686	MRAP2	melanocortin 2 receptor accessory protein 2	4,02052	2,3E-05
51.	ENSECAG00000009769	CNTN4	contactin 4	3,95573	1,3E-18
52.	ENSECAG00000005307	RNF183	ring finger protein 183	3,94478	4,7E-31
53.	ENSECAG00000005379	HPGD	15-Hydroxyprostaglandin Dehydrogenase	3,93088	3,2E-06
54.	ENSECAG00000015333	ADAP2	ArfGAP With Dual PH Domains 2	3,92288	1,3E-30
55.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	3,91497	8,6E-09
56.	ENSECAG00000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	3,83821	4,3E-11
57.	ENSECAG00000021057	ADGRV1	adhesion G protein-coupled receptor V1	3,81459	1,1E-29
58.	ENSECAG00000013584	PSAPL1	prosaposin like 1	3,7612	0,00057
59.	ENSECAG00000006763	GPBAR1	G protein-coupled bile acid receptor 1	3,75828	9E-05
60.	ENSECAG00000015449	IRF8	interferon regulatory factor 8	3,74217	0,00077
61.	ENSECAG00000023173	EDN2	Endothelin 2	3,7182	0,00011
62.	ENSECAG00000015842	ANKRD55	ankyrin repeat domain 55	3,69798	1,2E-11
63.	ENSECAG00000021914	PDE1C	phosphodiesterase 1C	3,69545	9,9E-05
64.	ENSECAG00000015657	TNNT1	troponin T1, slow skeletal type	3,67612	1,8E-20
65.	ENSECAG00000016048	ANKRD24	ankyrin repeat domain 24	3,62883	2,9E-05
66.	ENSECAG00000000152	KITLG	KIT ligand	3,62445	7,1E-20
67.	ENSECAG00000015651	ARSF	arylsulfatase F	3,57737	5,6E-14
68.	ENSECAG00000004372	SLC22A3	Solute Carrier Family 22 Member 3	3,55499	7E-37
69.	ENSECAG00000024719	ENSECAG00000024719	solute carrier family 22 member 3	3,5352	3E-166
70.	ENSECAG00000014817	RND2	Rho Family GTPase 2	3,5101	2,4E-22
71.	ENSECAG00000001603	PEG10	Paternally Expressed 10	3,49622	8,6E-06
72.	ENSECAG00000001064	RET	ret proto-oncogene	3,48007	4,2E-07
73.	ENSECAG00000016953	HLF	HLF transcription factor, PAR bZIP family member	3,47092	4,8E-71
74.	ENSECAG00000024845	PII6	peptidase inhibitor 16	3,44087	1,7E-10
75.	ENSECAG00000003201	PRSS35	serine protease 35	3,41423	1,7E-08
76.	ENSECAG00000020238	GRAMD1B	GRAM domain containing 1B	3,34403	7,3E-14
77.	ENSECAG00000010805	PGM5	phosphoglucomutase 5	3,31607	3,1E-15
78.	ENSECAG00000020258	SSC4D	scavenger receptor cysteine rich family member with 4 domains	3,31045	0,00037
79.	ENSECAG00000014126	CFAP161	Cilia And Flagella Associated Protein 161	3,30654	2,1E-13
80.	ENSECAG00000017217	CA12	carbonic anhydrase 12	3,28964	3,1E-36
81.	ENSECAG00000019438	OSMR	oncostatin M receptor	3,25386	8,5E-31
82.	ENSECAG00000012826	CDO1	Cysteine Dioxygenase Type 1	3,2355	5,2E-14
83.	ENSECAG00000023895	EXOC3L2	exocyst complex component 3 like 2	3,20564	1,9E-24
84.	ENSECAG00000001189	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	3,19286	3E-70
85.	ENSECAG00000024694	KIF14	kinesin family member 14	3,18953	4,1E-09
86.	ENSECAG00000008880	SLC22A16	solute carrier family 22 member 16	3,15106	0,00011
87.	ENSECAG00000023685	GJA4	gap junction protein alpha 4	3,11867	9,6E-06
88.	ENSECAG00000008787	CCNB3	cyclin B3	3,11122	0,0003
89.	ENSECAG00000010445	ST3GAL6	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 6	3,0939	8,6E-37
90.	ENSECAG00000008059	PDE4C	phosphodiesterase 4C	3,09204	5E-06
91.	ENSECAG00000017598	IMPA2	inositol monophosphatase 2	3,08644	5,1E-18
92.	ENSECAG00000011669	TNN	tenascin N	3,07282	4,8E-38
93.	ENSECAG00000000681	ENSECAG00000000681		3,05067	0,00081

94.	ENSECAG00000009535	FCER1G	Fc Epsilon Receptor Ig	3,04356	1,2E-10
95.	ENSECAG00000029510	ENSECAG00000029510		3,0272	2E-13
96.	ENSECAG00000022014	RAVER2	Ribonucleoprotein, PTB Binding 2	3,01588	0,00105
97.	ENSECAG00000001649	WDFY4	WDFY family member 4	3,00559	0,00803
98.	ENSECAG00000016576	C1QTNF12	C1q And TNF Related 12	3,00165	1,4E-40
99.	ENSECAG00000009046	BIN2	Bridging Integrator 2	2,99792	1,6E-19
100.	ENSECAG00000011893	CNTNAP4	Contactin Associated Protein Family Member 4	2,98298	4,7E-06
101.	ENSECAG00000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	2,96592	4,9E-33
102.	ENSECAG00000019600	GRP	gastrin releasing peptide	2,95162	5,5E-29
103.	ENSECAG00000013009	KIF26B	kinesin family member 26B	2,93449	8,9E-61
104.	ENSECAG00000021654	SLC10A4	solute carrier family 10 member 4	2,91078	2,3E-10
105.	ENSECAG00000016560	CRABP2	Cellular Retinoic Acid Binding Protein 2	2,89413	4,6E-33
106.	ENSECAG00000000574	NIPAL4	NIPA Like Domain Containing 4	2,88654	8,5E-24
107.	ENSECAG00000010053	HJURP	Holliday junction recognition protein	2,88471	1,3E-16
108.	ENSECAG00000019170	MN1	MN1 Proto-Oncogene, Transcriptional Regulator	2,86247	4,7E-05
109.	ENSECAG00000019551	CXCL12	C-X-C motif chemokine ligand 12	2,86233	1,4E-20
110.	ENSECAG00000019578	CDCA5	cell division cycle associated 5	2,849	3E-05
111.	ENSECAG00000017570	SYT4	synaptotagmin 4	2,84775	1,1E-10
112.	ENSECAG00000013207	SHISA2	shisa family member 2	2,84457	0,00011
113.	ENSECAG00000024779	SERPINA5	serpin family A member 5	2,78096	2,4E-06
114.	ENSECAG00000024322	ARSJ	arylsulfatase family member J	2,76847	1,6E-71
115.	ENSECAG00000011113	ADGRF1	Adhesion G Protein-Coupled Receptor F1	2,75386	0,00862
116.	ENSECAG00000014145	TLL2	tolloid like 2	2,73898	0,00094
117.	ENSECAG00000022093	SLC2A5	solute carrier family 2 member 5	2,69638	2,1E-07
118.	ENSECAG00000018996	PLEK	pleckstrin	2,68536	0,00146
119.	ENSECAG00000033890	CIDEA	cell death inducing DFFA like effector c	2,66063	6,1E-14
120.	ENSECAG00000001372	SYN1	synapsin I	2,64745	6,1E-05
121.	ENSECAG00000003943	SYT5	synaptotagmin 5	2,61638	1,7E-46
122.	ENSECAG00000019705	CDC20	Cell Division Cycle 20	2,61601	5E-22
123.	ENSECAG00000023149	SCIN	scinderin	2,60772	9,2E-32
124.	ENSECAG00000010188	ABHD3	abhydrolase domain containing 3, phospholipase	2,58319	5,3E-47
125.	ENSECAG00000010525	KEL	Kell metallo-endopeptidase	2,56759	0,00444
126.	ENSECAG00000014536	KIF23	kinesin family member 23	2,56492	3,4E-21
127.	ENSECAG00000024127	CENPF	centromere protein F	2,56405	1,1E-16
128.	ENSECAG00000024750	NCALD	neurocalcin delta	2,54738	8,8E-10
129.	ENSECAG00000021155	MXD3	MAX dimerization protein 3	2,52077	6,8E-05
130.	ENSECAG00000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	2,51402	4,8E-10
131.	ENSECAG00000019129	FOXN1	forkhead box M1	2,51366	2,1E-08
132.	ENSECAG00000020111	IQGAP3	IQ Motif Containing GTPase Activating Protein 3	2,51128	8,2E-11
133.	ENSECAG00000016742	TJP2	tight junction protein 2	2,49965	7,5E-15
134.	ENSECAG00000000651	SPINK5	serine peptidase inhibitor Kazal type 5	2,4923	0,02364
135.	ENSECAG00000017035	SHF	Src homology 2 domain containing F	2,48661	6,1E-16
136.	ENSECAG00000024340	TTYH1	tweety family member 1	2,48496	3,6E-05
137.	ENSECAG00000039680	ENSECAG00000039680	RecQ mediated genome instability 2	2,48003	0,00052
138.	ENSECAG00000017388	CENPT	centromere protein T	2,47784	3,8E-05
139.	ENSECAG00000019038	KIF2C	kinesin family member 2C	2,47666	4,3E-13
140.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	2,47508	4,2E-22
141.	ENSECAG00000023496	IRX3	iroquois homeobox 3	2,46838	0,04132
142.	ENSECAG00000013731	STC1	Stanniocalcin 1	2,46012	1,6E-20

143.	ENSECAG00000013035	ENPP1	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1	2,45817	4,8E-16
144.	ENSECAG00000036105	ENSECAG00000036105		2,45789	2,5E-07
145.	ENSECAG00000014794	MIIP	Migration And Invasion Inhibitory Protein	2,45455	1E-124
146.	ENSECAG00000022731	COL6A1	collagen type VI alpha 1 chain	2,43588	4,7E-25
147.	ENSECAG00000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	2,4211	2E-05
148.	ENSECAG00000026891	ENSECAG00000026891	PCNA clamp associated factor	2,39826	7,9E-06
149.	ENSECAG00000019779	KCNS3	potassium voltage-gated channel modifier subfamily S member 3	2,37701	0,03137
150.	ENSECAG00000024172	ADAMTS4	ADAM Metalloproteinase With Thrombospondin Type 1 Motif 4	2,37466	9,8E-13
151.	ENSECAG00000015069	BHLHE40	basic helix-loop-helix family member e40	2,37262	4,6E-21
152.	ENSECAG00000023800	AK2	adenylate kinase 2	2,36997	1,7E-97
153.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	2,35868	1,6E-25
154.	ENSECAG00000009700	ANK3	ankyrin 3	2,35847	1,7E-09
155.	ENSECAG00000023199	COL24A1	Collagen Type XXIV Alpha 1 Chain	2,34137	2,7E-05
156.	ENSECAG00000007964	EBF1	EBF transcription factor 1	2,33859	3,7E-74
157.	ENSECAG00000020881	CTSC	cathepsin C	2,33811	1,1E-07
158.	ENSECAG00000012263	RNF19B	Ring Finger Protein 19B	2,325	1E-160
159.	ENSECAG00000024110	PENK	proenkephalin	2,32109	7,6E-14
160.	ENSECAG00000009081	KIAA1210	KIAA1210	2,31522	9,3E-23
161.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	2,3108	5,4E-38
162.	ENSECAG00000006288	SIK1	salt inducible kinase 1	2,29948	2,6E-68
163.	ENSECAG00000018322	EXO1	exonuclease 1	2,29653	2,6E-09
164.	ENSECAG00000014813	CCNB2	Cyclin B2	2,29435	2,9E-08
165.	ENSECAG00000005925	MYBL2	MYB Proto-Oncogene Like 2	2,29371	2,4E-12
166.	ENSECAG00000009121	NEIL3	nei like DNA glycosylase 3	2,29138	0,00073
167.	ENSECAG00000038775	KCNK3	potassium two pore domain channel subfamily K member 3	2,29084	0,0053
168.	ENSECAG00000016934	IL31RA	Interleukin 31 Receptor A	2,2896	1,5E-05
169.	ENSECAG00000004795	ENSECAG00000004795		2,28328	0,00559
170.	ENSECAG00000016860	KIF20A	kinesin family member 20A	2,28	3,1E-20
171.	ENSECAG00000014379	BMP3	bone morphogenetic protein 3	2,26562	2,8E-12
172.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	2,26391	2E-107
173.	ENSECAG00000031941	ENSECAG00000031941		2,26032	0,00544
174.	ENSECAG00000017826	TMEM26	transmembrane protein 26	2,25281	1,5E-15
175.	ENSECAG00000033164	ENSECAG00000033164	NAC alpha domain containing	2,24968	7E-10
176.	ENSECAG00000008506	HMMR	Hyaluronan Mediated Motility Receptor	2,24133	9,5E-09
177.	ENSECAG00000010326	MIS18A	MIS18 kinetochore protein A	2,2394	4,2E-05
178.	ENSECAG00000019398	TFPI2	Tissue Factor Pathway Inhibitor 2	2,22529	2,2E-23
179.	ENSECAG00000011994	CYFIP2	cytoplasmic FMR1 interacting protein 2	2,22507	1,3E-09
180.	ENSECAG0000001988	FAT3	FAT atypical cadherin 3	2,22035	5,2E-05
181.	ENSECAG00000034739	ADORA2A	adenosine A2a receptor	2,21655	1,2E-16
182.	ENSECAG00000018118	BMERB1	bMERB domain containing 1	2,21654	1,1E-08
183.	ENSECAG00000013324	TXN	Thioredoxin	2,2157	7,2E-83
184.	ENSECAG00000007562	AUNIP	Aurora Kinase A And Ninein Interacting Protein	2,21341	0,03907
185.	ENSECAG00000024558	ENSECAG00000024558	centromere protein E	2,21303	0,00202
186.	ENSECAG00000021343	NRG1	neuregulin 1	2,21175	2,2E-11
187.	ENSECAG00000000235	MTBP	MDM2 binding protein	2,20603	5,5E-32
188.	ENSECAG00000003789	RASL11B	RAS like family 11 member B	2,20409	3,6E-47
189.	ENSECAG00000019229	STAMBPL1	STAM binding protein like 1	2,20053	7E-65
190.	ENSECAG00000014254	LCCTL	Lactase Like	2,19353	0,02273
191.	ENSECAG00000015966	SERPINF6	Serpin Family B Member 6	2,18496	1,5E-44
192.	ENSECAG00000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	2,18192	1,5E-40

193.	ENSECAG00000007706	PHACTR3	phosphatase and actin regulator 3	2,17224	0,00665
194.	ENSECAG00000006060	RAI2	retinoic acid induced 2	2,17215	6,7E-16
195.	ENSECAG00000023019	KIF18B	kinesin family member 18B	2,16227	8,3E-07
196.	ENSECAG00000015593	EGFL7	EGF like domain multiple 7	2,1616	0,00237
197.	ENSECAG00000015695	PTPRO	protein tyrosine phosphatase receptor type O	2,16073	8,8E-26
198.	ENSECAG00000036261	eca-mir-8996	microRNA mir-8996	2,16031	0,02998
199.	ENSECAG00000018151	OPTC	opticin	2,14809	0,03772
200.	ENSECAG00000022404	TRPV6	transient receptor potential cation channel subfamily V member 6	2,13738	2,6E-24
201.	ENSECAG00000020808	TRIL	TLR4 interactor with leucine rich repeats	2,11233	8,1E-08
202.	ENSECAG00000018476	TPX2	TPX2 microtubule nucleation factor	2,1109	9,9E-16
203.	ENSECAG0000003278	TRIM9	tripartite motif containing 9	2,10272	8,6E-12
204.	ENSECAG00000030455	ENSECAG00000030455		2,09927	6,1E-06
205.	ENSECAG00000012104	TNFAIP6	TNF Alpha Induced Protein 6	2,09107	1,5E-51
206.	ENSECAG00000014511	IL11	Interleukin 11	2,08703	1,7E-64
207.	ENSECAG00000017777	PLK1	polo like kinase 1	2,08483	1,6E-16
208.	ENSECAG00000010500	ITGA4	integrin subunit alpha 4	2,08201	1,4E-91
209.	ENSECAG00000007918	TNS4	tensin 4	2,07889	1,5E-34
210.	ENSECAG00000024113	ABLIM1	actin binding LIM protein 1	2,07366	0,00194
211.	ENSECAG00000010858	ANKRD37	ankyrin repeat domain 37	2,0671	8,2E-07
212.	ENSECAG00000007300	DCLK1	doublecortin like kinase 1	2,06296	5,5E-19
213.	ENSECAG00000024712	CASR	calcium sensing receptor	2,05981	0,01198
214.	ENSECAG00000009580	LVRN	laeverin	2,05082	5E-05
215.	ENSECAG00000021452	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	2,04528	1,2E-13
216.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	2,04354	1,5E-21
217.	ENSECAG00000015806	CCNB1	cyclin B1	2,04259	1,2E-21
218.	ENSECAG00000008655	DLGAP5	DLG Associated Protein 5	2,04188	9,9E-08
219.	ENSECAG00000038834	MTFR2	Mitochondrial Fission Regulator 2	2,04106	3,9E-09
220.	ENSECAG00000023525	NDUFA4L2	NDUFA4 Mitochondrial Complex Associated Like 2	2,04058	0,00037
221.	ENSECAG00000002513	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	2,03768	9,6E-13
222.	ENSECAG00000014787	RCAN1	regulator of calcineurin 1	2,03537	1,7E-82
223.	ENSECAG00000017864	FMOD	fibromodulin	2,02775	9,9E-08
224.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	2,02026	7,7E-70
225.	ENSECAG00000018841	CGA	Glycoprotein Hormones, Alpha Polypeptide	2,01855	0,00177
226.	ENSECAG00000007018	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	2,01216	4,6E-09
227.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	2,01162	3,2E-08
228.	ENSECAG00000020270	CCNE2	cyclin E2	1,9974	0,00045
229.	ENSECAG00000032416	APC2	APC regulator of WNT signaling pathway 2	1,99461	5,6E-05
230.	ENSECAG00000007165	TRAF5	TNF receptor associated factor 5	1,99409	3,6E-38
231.	ENSECAG00000009568	CENPI	centromere protein I	1,99338	5,5E-11
232.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	1,99293	2,2E-05
233.	ENSECAG00000009716	CDK1	cyclin dependent kinase 1	1,98633	8,6E-17
234.	ENSECAG00000036591	APLN	apelin	1,98574	3E-12
235.	ENSECAG00000007133	TPPP3	tubulin polymerization promoting protein family member 3	1,97431	0,02611
236.	ENSECAG00000010859	KIF4A	kinesin family member 4A	1,96601	3,7E-06
237.	ENSECAG00000008461	DEPDC1	DEP domain containing 1	1,9653	0,0006
238.	ENSECAG00000015871	CDCA8	cell division cycle associated 8	1,96384	1,6E-07
239.	ENSECAG00000024519	SPC25	SPC25 component of NDC80 kinetochore complex	1,95887	4,4E-06
240.	ENSECAG00000032004	FOXA2	forkhead box A2	1,94793	0,0156

241.	ENSECAG00000001407	CHSY3	chondroitin sulfate synthase 3	1,94348	6,3E-12
242.	ENSECAG00000009403	IL1RAPL2	interleukin 1 receptor accessory protein like 2	1,94278	1,4E-05
243.	ENSECAG000000016976	RARB	retinoic acid receptor beta	1,94151	7,3E-05
244.	ENSECAG000000023076	GPCPD1	glycerophosphocholine phosphodiesterase 1	1,94048	1,2E-14
245.	ENSECAG000000015770	DYDC2	DPY30 Domain Containing 2	1,93964	0,04996
246.	ENSECAG000000014305	CACNA2D3	Calcium Voltage-Gated Channel Auxiliary Subunit Alpha2delta 3	1,93649	0,02992
247.	ENSECAG000000010821	RACGAP1	Rac GTPase activating protein 1	1,93365	8,3E-10
248.	ENSECAG000000011788	CDC45	cell division cycle 45	1,92629	1,2E-06
249.	ENSECAG000000012179	RGS2	regulator of G protein signaling 2	1,91421	1,5E-19
250.	ENSECAG000000020767	IL7	interleukin 7	1,90968	2,1E-11
251.	ENSECAG000000021775	KRT8	keratin 8	1,9072	6,5E-08
252.	ENSECAG000000021746	SHROOM1	Shroom Family Member 1	1,90227	4,4E-26
253.	ENSECAG000000037361	TMEM190	Transmembrane Protein 190	1,89717	0,02099
254.	ENSECAG000000008827	NDC80	NDC80 kinetochore complex component	1,89265	8,3E-06
255.	ENSECAG000000024406	KCP	kielin cysteine rich BMP regulator	1,88784	0,00012
256.	ENSECAG000000020769	FGF1	fibroblast growth factor 1	1,88084	4,5E-65
257.	ENSECAG000000038893	CST3	cystatin C	1,87628	1,4E-84
258.	ENSECAG000000001041	CENPN	centromere protein N	1,86246	4,9E-08
259.	ENSECAG000000015127	SLC13A4	solute carrier family 13 member 4	1,86159	8,2E-08
260.	ENSECAG000000008517	PNMA2	PNMA family member 2	1,86136	0,00042
261.	ENSECAG000000014384	AURKB	aurora kinase B	1,85542	9E-06
262.	ENSECAG000000016248	JPH1	junctophilin 1	1,85509	0,00589
263.	ENSECAG000000019880	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif 9	1,85484	3,1E-39
264.	ENSECAG000000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	1,85412	1,8E-47
265.	ENSECAG000000016495	NUSAP1	nucleolar and spindle associated protein 1	1,84641	1,1E-11
266.	ENSECAG000000010725	STXBPL	syntactin binding protein 5L	1,84248	1,6E-05
267.	ENSECAG000000002992	MID1IP1	MID1 interacting protein 1	1,83506	1,1E-50
268.	ENSECAG000000007464	RRM2	ribonucleotide reductase regulatory subunit M2	1,83032	1,2E-13
269.	ENSECAG000000018519	FANCD2	FA complementation group D2	1,83031	4,8E-09
270.	ENSECAG000000023922	E2F2	E2F transcription factor 2	1,82911	0,03273
271.	ENSECAG000000021976	LRATD2	LRAT domain containing 2	1,82743	0,00037
272.	ENSECAG000000024574	GATA3	GATA binding protein 3	1,82253	0,00045
273.	ENSECAG000000002377	SPESP1	Sperm Equatorial Segment Protein 1	1,82005	1,4E-22
274.	ENSECAG000000000532	EPS8L1	EPS8 like 1	1,81797	1,4E-12
275.	ENSECAG000000008493	SERPINB10	serpin family B member 10	1,81304	3,7E-09
276.	ENSECAG000000007974	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	1,80955	0,00239
277.	ENSECAG000000011099	VAV3	Vav Guanine Nucleotide Exchange Factor 3	1,80577	3,6E-12
278.	ENSECAG000000012921	ALPK2	alpha kinase 2	1,80384	0,03907
279.	ENSECAG000000031911	ENSECAG000000031911		1,80267	0,04225
280.	ENSECAG000000013691	MALT1	MALT1 paracaspase	1,78154	2,2E-27
281.	ENSECAG000000020563	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1,77892	1,9E-64
282.	ENSECAG000000000122	GDA	Guanine Deaminase	1,77318	7,3E-08
283.	ENSECAG000000013053	TOP2A	DNA topoisomerase II alpha	1,77246	1,4E-18
284.	ENSECAG000000024186	KIF21A	kinesin family member 21A	1,76879	2,1E-07
285.	ENSECAG000000018373	FAM234B	family with sequence similarity 234 member B	1,7627	2,7E-10
286.	ENSECAG000000020920	NEK2	NIMA related kinase 2	1,76015	5,5E-06
287.	ENSECAG000000007172	PSD	pleckstrin and Sec7 domain containing	1,75748	1,2E-14
288.	ENSECAG000000005547	CDT1	Chromatin Licensing And DNA Replication Factor 1	1,75559	2,5E-06
289.	ENSECAG000000007432	PTGDR	Prostaglandin D2 Receptor	1,75371	4,9E-07

290.	ENSECAG00000011407	STON2	Stonin 2	1,75234	0,03767
291.	ENSECAG00000010447	EFEMP1	EGF Containing Fibulin Extracellular Matrix Protein 1	1,75036	0,0001
292.	ENSECAG00000022595	TLCD5	TLC domain containing 5	1,74946	0,00034
293.	ENSECAG00000009913	CDC6	cell division cycle 6	1,74671	4,9E-08
294.	ENSECAG00000011656	DPH5	diphthamide biosynthesis 5	1,73769	8,8E-31
295.	ENSECAG00000019433	CDKN3	cyclin dependent kinase inhibitor 3	1,7344	0,00313
296.	ENSECAG00000009472	CLSPN	claspin	1,73288	1,1E-05
297.	ENSECAG00000009299	ICAM5	intercellular adhesion molecule 5	1,73125	0,00054
298.	ENSECAG00000017015	MYH11	myosin heavy chain 11	1,72266	8,9E-14
299.	ENSECAG00000023134	KCNK5	potassium two pore domain channel subfamily K member 5	1,72148	1,3E-50
300.	ENSECAG00000022794	ENSECAG00000022794	cystathionine beta-synthase	1,72018	0,01009
301.	ENSECAG00000002570	HS3ST1	heparan sulfate-glucosamine 3-sulfotransferase 1	1,71477	6,6E-07
302.	ENSECAG00000030024	MAPK13	mitogen-activated protein kinase 13	1,71461	1,4E-22
303.	ENSECAG00000013298	POLE2	dynein axonemal assembly factor 2	1,71411	0,00029
304.	ENSECAG00000000015	KIAA1217	KIAA1217	1,71199	1,2E-11
305.	ENSECAG00000023908	OLFML2A	olfactomedin like 2A	1,70767	0,00013
306.	ENSECAG00000002675	ZGRF1	zinc finger GRF-type containing 1	1,70314	0,0008
307.	ENSECAG00000015746	SMC1B	structural maintenance of chromosomes 1B	1,70275	0,04537
308.	ENSECAG00000014368	MCM5	minichromosome maintenance complex component 5	1,70226	9,4E-17
309.	ENSECAG00000022931	TCF7L1	transcription factor 7 like 1	1,69828	6,1E-48
310.	ENSECAG00000016121	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif 12	1,69242	2E-07
311.	ENSECAG00000023355	GTSE1	G2 and S-phase expressed 1	1,68721	1,1E-06
312.	ENSECAG00000024473	MCM10	minichromosome maintenance 10 replication initiation factor	1,68632	1,7E-07
313.	ENSECAG00000041708	ENSECAG00000041708		1,67934	1,5E-06
314.	ENSECAG00000000633	ZWINT	ZW10 interacting kinetochore protein	1,67863	0,00369
315.	ENSECAG00000024428	PROCR	protein C receptor	1,67692	1,1E-45
316.	ENSECAG00000008765	MYCL	MYCL Proto-Oncogene, BHLH Transcription Factor	1,67069	0,00058
317.	ENSECAG00000016056	BICDL2	BICD family like cargo adaptor 2	1,66918	0,00148
318.	ENSECAG00000014517	CDCA3	cell division cycle associated 3	1,66362	1E-07
319.	ENSECAG00000033207	TWIST1	twist family bHLH transcription factor 1	1,65894	3,8E-12
320.	ENSECAG00000010587	ISM1	Isthmin 1	1,65654	1,3E-08
321.	ENSECAG00000018665	RECQL4	RecQ like helicase 4	1,6559	2,6E-06
322.	ENSECAG00000015060	PRR11	proline rich 11	1,65463	0,00084
323.	ENSECAG00000021550	ZMAT4	zinc finger matrin-type 4	1,64388	0,00084
324.	ENSECAG00000024008	SCAI	suppressor of cancer cell invasion	1,63746	5,8E-06
325.	ENSECAG00000021015	ATP8B1	ATPase phospholipid transporting 8B1	1,63586	2,9E-08
326.	ENSECAG00000008823	CDH11	cadherin 11	1,63566	7,5E-51
327.	ENSECAG00000043057	ENSECAG00000043057		1,63423	0,01317
328.	ENSECAG00000019624	OSTF1	Osteoclast Stimulating Factor 1	1,63161	3,6E-26
329.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,62787	0,00089
330.	ENSECAG00000010963	SERPING1	Serpin Family G Member 1	1,62761	5,5E-36
331.	ENSECAG00000022294	PITX3	Paired Like Homeodomain 3	1,62713	0,01097
332.	ENSECAG00000018874	PRICKLE1	Prickle Planar Cell Polarity Protein 1	1,62525	1E-51
333.	ENSECAG00000016271	CENPA	Centromere Protein A	1,62317	0,00172
334.	ENSECAG00000017671	ROBO1	roundabout guidance receptor 1	1,6231	2,5E-10
335.	ENSECAG00000016974	BRCA1	BRCA1 DNA Repair Associated	1,61658	9,3E-12
336.	ENSECAG00000016029	TRAIIP	TRAF interacting protein	1,61422	0,04417

337.	ENSECAG00000009501	DAAM2	dishevelled associated activator of morphogenesis 2	1,61253	2,3E-30
338.	ENSECAG00000021262	MMP7	matrix metalloproteinase 7	1,60802	0,03337
339.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,60677	2,2E-46
340.	ENSECAG00000017103	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	1,60641	1,2E-07
341.	ENSECAG00000016902	PRR16	proline rich 16	1,60578	2,3E-22
342.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	1,60301	9,7E-12
343.	ENSECAG00000019369	CCNF	Cyclin F	1,60248	1,8E-06
344.	ENSECAG00000021088	GDF9	Growth Differentiation Factor 9	1,60029	0,00027
345.	ENSECAG00000019215	ITGB8	Integrin Subunit Beta 8	1,59818	3,4E-21
346.	ENSECAG00000005814	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	1,5966	0,00179
347.	ENSECAG00000006607	KIF11	kinesin family member 11	1,59591	3,3E-13
348.	ENSECAG00000015641	DSCC1	DNA Replication And Sister Chromatid Cohesion 1	1,59478	5,7E-07
349.	ENSECAG00000010643	TPD52L1	TPD52 like 1	1,59278	0,00392
350.	ENSECAG00000005086	EGLN3	Egl-9 Family Hypoxia Inducible Factor 3	1,59144	1,4E-47
351.	ENSECAG00000014774	MMP23	Matrix Metalloproteinase 23	1,59082	3,4E-16
352.	ENSECAG00000003966	GPC4	glypican 4	1,57436	1E-05
353.	ENSECAG00000026688	ENSECAG00000026688	small nucleolar RNA SNORD113/SNORD114 family	1,57293	3,4E-05
354.	ENSECAG00000007872	TCF19	transcription factor 19	1,57288	8,8E-12
355.	ENSECAG00000015967	ASF1B	Anti-Silencing Function 1B Histone Chaperone	1,56902	0,04243
356.	ENSECAG00000017874	SH2D3C	SH2 domain containing 3C	1,56688	4,4E-08
357.	ENSECAG00000036440	RGS16	regulator of G protein signaling 16	1,56421	0,03082
358.	ENSECAG00000036638	SLC6A12	solute carrier family 6 member 12	1,56376	0,00341
359.	ENSECAG00000005719	PRKD1	protein kinase D1	1,56359	4,6E-35
360.	ENSECAG00000020167	RGMA	repulsive guidance molecule BMP co-receptor a	1,56008	2,7E-05
361.	ENSECAG00000020645	ASPM	assembly factor for spindle microtubules	1,55973	7,1E-09
362.	ENSECAG00000013188	CDCA2	cell division cycle associated 2	1,55794	4,3E-05
363.	ENSECAG00000021024	APLP1	amyloid beta precursor like protein 1	1,55308	0,01424
364.	ENSECAG00000032390	TNFRSF6B	TNF Receptor Superfamily Member 6b	1,55134	0,04658
365.	ENSECAG00000015835	NT5DC2	5'-Nucleotidase Domain Containing 2	1,54792	1,3E-13
366.	ENSECAG00000007991	WDR86	WD repeat domain 86	1,54448	3,3E-13
367.	ENSECAG00000014314	POLQ	DNA polymerase theta	1,54427	0,0016
368.	ENSECAG00000015058	ARHGEF3	Rho guanine nucleotide exchange factor 3	1,53767	6,6E-38
369.	ENSECAG00000023484	SKA1	spindle and kinetochore associated complex subunit 1	1,53249	9,2E-05
370.	ENSECAG00000017906	PRC1	Protein Regulator Of Cytokinesis 1	1,53082	6,5E-15
371.	ENSECAG00000012629	MASTL	microtubule associated serine/threonine kinase like	1,53072	3,2E-08
372.	ENSECAG00000023526	PLPP4	phospholipid phosphatase 4	1,5279	4,4E-07
373.	ENSECAG00000032055	PROKR2	prokineticin receptor 2	1,52015	0,00221
374.	ENSECAG00000022418	MAP6D1	MAP6 domain containing 1	1,51852	0,01897
375.	ENSECAG00000006991	PECAM1	platelet and endothelial cell adhesion molecule 1	1,5166	1,6E-55
376.	ENSECAG00000024523	KLRG1	killer cell lectin like receptor G1	1,51347	0,00047
377.	ENSECAG00000013238	FAM83D	family with sequence similarity 83 member D	1,50831	1,1E-09
378.	ENSECAG00000000292	THSD7A	Thrombospondin Type 1 Domain Containing 7A	1,50598	1,7E-06
379.	ENSECAG00000018935	SRPX	sushi repeat containing protein X-linked	1,50476	1E-17
380.	ENSECAG00000034840	TNFSF13	TNF superfamily member 13	1,50351	2,2E-26

381.	ENSECAG00000014346	GBA3	glucosylceramidase beta 3	1,49987	5,7E-07
382.	ENSECAG00000006359	PDP2	pyruvate dehydrogenase phosphatase catalytic subunit 2	1,49957	3,4E-10
383.	ENSECAG00000022278	KNL1	kinetochore scaffold 1	1,49604	4,4E-08
384.	ENSECAG00000018510	RGS20	Regulator Of G Protein Signaling 20	1,49555	5,7E-05
385.	ENSECAG00000017926	TROAP	trophinin associated protein	1,49438	0,00016
386.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,49048	6,7E-28
387.	ENSECAG00000008270	FABP5	fatty acid binding protein 5	1,48298	3,8E-08
388.	ENSECAG00000007388	ADCYAP1R1	ADCYAP receptor type I	1,48173	0,00071
389.	ENSECAG000000013268	AP1S3	adaptor related protein complex 1 subunit sigma 3	1,48162	6,2E-06
390.	ENSECAG00000018438	CEP55	centrosomal protein 55	1,47839	7,1E-06
391.	ENSECAG00000023527	PHF19	PHD finger protein 19	1,47768	0,00011
392.	ENSECAG00000010384	ARSL	arylsulfatase L	1,4771	4,1E-13
393.	ENSECAG00000000281	SHCBP1	SHC Binding And Spindle Associated 1	1,47548	1,4E-05
394.	ENSECAG00000023776	TTK	TTK protein kinase	1,47423	6,3E-05
395.	ENSECAG00000010569	SV2C	synaptic vesicle glycoprotein 2C	1,47409	0,00064
396.	ENSECAG00000020015	BMP6	bone morphogenetic protein 6	1,46527	0,00451
397.	ENSECAG00000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,46438	4,4E-33
398.	ENSECAG00000022142	SRRM3	Serine/Arginine Repetitive Matrix 3	1,45728	1,2E-05
399.	ENSECAG00000017017	LNK1	ligand of numb-protein X 1	1,45629	1,1E-05
400.	ENSECAG00000015822	VDR	vitamin D receptor	1,45306	1,2E-14
401.	ENSECAG00000016578	ENSECAG00000016578	granulocyte-macrophage colony-stimulating factor receptor subunit alpha	1,4504	9,3E-06
402.	ENSECAG00000000426	CENPL	centromere protein L	1,45037	0,02289
403.	ENSECAG00000030219	ENSECAG00000030219		1,44546	8,5E-07
404.	ENSECAG00000003345	ENO1	Enolase 1	1,44166	1,1E-65
405.	ENSECAG00000023046	SORCS1	sortilin related VPS10 domain containing receptor 1	1,43692	0,00011
406.	ENSECAG00000021331	NOTCH3	notch receptor 3	1,4303	7,4E-09
407.	ENSECAG00000022842	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1,42866	5,6E-36
408.	ENSECAG00000015369	NID2	nidogen 2	1,42381	5,3E-57
409.	ENSECAG00000008876	PTPRE	protein tyrosine phosphatase receptor type E	1,42221	0,00562
410.	ENSECAG00000011380	TACC3	transforming acidic coiled-coil containing protein 3	1,42207	9,9E-15
411.	ENSECAG00000018918	TRIP13		1,41659	1,6E-06
412.	ENSECAG00000024182	VSTM4	V-set and transmembrane domain containing 4	1,41139	2,2E-18
413.	ENSECAG00000019161	DIAPH3	diaphanous related formin 3	1,41083	2,5E-07
414.	ENSECAG00000038039	TBXA2R	thromboxane A2 receptor	1,40169	5,3E-05
415.	ENSECAG00000010768	LRBA	LPS responsive beige-like anchor protein	1,39985	3E-12
416.	ENSECAG00000019455	NIPAL1	NIPA like domain containing 1	1,39889	0,00623
417.	ENSECAG00000009370	ORC1	Origin Recognition Complex Subunit 1	1,39783	0,0002
418.	ENSECAG00000008528	ENSECAG00000008528		1,39752	0,00253
419.	ENSECAG00000006771	PRKCA	protein kinase C alpha	1,39715	1,7E-17
420.	ENSECAG00000003783	ENSECAG00000003783	ubiquitin C-terminal hydrolase L3	1,39586	7,5E-14
421.	ENSECAG00000024196	KIFC1	kinesin family member C1	1,38667	2E-09
422.	ENSECAG00000022051	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1,3857	3,2E-38
423.	ENSECAG00000024795	CPVL	carboxypeptidase vitellogenic like	1,38506	1,9E-28
424.	ENSECAG00000020448	UBE2T	ubiquitin conjugating enzyme E2 T	1,38462	0,00924
425.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,38247	4,2E-24
426.	ENSECAG00000033093	VWA1	Von Willebrand Factor A Domain Containing 1	1,38066	5,2E-06
427.	ENSECAG00000009420	NT5E	5'-Nucleotidase Ecto	1,3804	0,02043

428.	ENSECAG00000022901	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	1,37991	0,02666
429.	ENSECAG00000036001	HOXB9	homeobox B9	1,37934	3,8E-10
430.	ENSECAG00000016498	FXVD3	FXVD domain containing ion transport regulator 3	1,37857	0,01814
431.	ENSECAG00000026394	eca-mir-656	microRNA mir-656	1,37597	0,02702
432.	ENSECAG00000019604	LRRIC71	leucine rich repeat containing 71	1,37592	0,04422
433.	ENSECAG00000016383	USP53	Ubiquitin Specific Peptidase 53	1,37412	1,2E-13
434.	ENSECAG00000022722	ESPL1	extra spindle pole bodies like 1, separase	1,37075	4,2E-07
435.	ENSECAG00000000752	EHF	ETS Homologous Factor	1,36828	0,00066
436.	ENSECAG00000008569	TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1	1,36811	5,3E-19
437.	ENSECAG00000020669	LDHA	lactate dehydrogenase A	1,36105	2,3E-27
438.	ENSECAG00000018810	HELLS	helicase, lymphoid specific	1,36	3E-06
439.	ENSECAG00000013106	ESM1	endothelial cell specific molecule 1	1,35749	0,00736
440.	ENSECAG00000020927	NEK10	NIMA related kinase 10	1,35304	0,00039
441.	ENSECAG00000021201	BMP2	bone morphogenetic protein 2	1,35153	1,1E-23
442.	ENSECAG00000000138	ACVR2A	activin A receptor type 2A	1,35098	1,5E-25
443.	ENSECAG00000024419	JADE1	jade family PHD finger 1	1,35029	5,7E-30
444.	ENSECAG00000024851	EDNRB	endothelin receptor type B	1,34966	1,4E-09
445.	ENSECAG00000012858	RASL11A	RAS like family 11 member A	1,34518	1,7E-06
446.	ENSECAG00000000303	SLC2A1	solute carrier family 2 member 1	1,34365	6E-24
447.	ENSECAG00000011878	DTL	denticless E3 ubiquitin protein ligase homolog	1,34045	3,7E-10
448.	ENSECAG00000007709	SEMA3F	semaphorin 3F	1,33834	2,5E-27
449.	ENSECAG00000016036	WVOX	WW domain containing oxidoreductase	1,33829	2,5E-09
450.	ENSECAG00000008466	BIRC5	Baculoviral IAP Repeat Containing 5	1,33671	0,00257
451.	ENSECAG00000020101	SLC24A2	solute carrier family 24 member 2	1,33545	0,0155
452.	ENSECAG00000033960	GALNT16	Polypeptide N-Acetylgalactosaminyltransferase 16	1,33094	1,9E-13
453.	ENSECAG00000004572	CH25H	cholesterol 25-hydroxylase	1,32786	1,1E-09
454.	ENSECAG00000016910	SLC4A8	solute carrier family 4 member 8	1,32695	0,02007
455.	ENSECAG00000013100	PI15	peptidase inhibitor 15	1,32662	0,00049
456.	ENSECAG00000021169	ANKRD6	ankyrin repeat domain 6	1,32537	0,00132
457.	ENSECAG00000012344	PTPRU	Protein Tyrosine Phosphatase Receptor Type U	1,32396	2,4E-06
458.	ENSECAG00000037578	ELFN1	extracellular leucine rich repeat and fibronectin type III domain containing 1	1,32343	0,0004
459.	ENSECAG00000035510	ENSECAG00000035510	serpin B3	1,32221	0,04639
460.	ENSECAG00000018253	FGFRL1	fibroblast growth factor receptor like 1	1,32189	8,6E-20
461.	ENSECAG00000021812	STARD5	StAR Related Lipid Transfer Domain Containing 5	1,32095	2,3E-16
462.	ENSECAG00000010065	OXCT2	3-Oxoacid CoA-Transferase 2	1,32056	0,00033
463.	ENSECAG00000008888	PTH1R	parathyroid hormone 1 receptor	1,32038	0,00029
464.	ENSECAG00000000225	CATSPERG	cation channel sperm associated auxiliary subunit gamma	1,31866	3,1E-13
465.	ENSECAG00000020682	TTL11	tubulin tyrosine ligase like 11	1,31489	8,9E-08
466.	ENSECAG00000017894	CKAP2	Cytoskeleton Associated Protein 2	1,31389	9,7E-07
467.	ENSECAG00000035279	IGFBP2	insulin like growth factor binding protein 2	1,3134	7,6E-27
468.	ENSECAG00000009254	N4BP3	NEDD4 binding protein 3	1,31334	0,01905
469.	ENSECAG0000001653	POLE	DNA polymerase epsilon, catalytic subunit	1,31207	7,9E-13
470.	ENSECAG00000005266	SORD	sorbitol dehydrogenase	1,30756	2,2E-09
471.	ENSECAG00000017458	BNIP3	BCL2 interacting protein 3	1,30598	1,3E-07
472.	ENSECAG00000007647	COL5A3	collagen type V alpha 3 chain	1,30311	5,4E-26

473.	ENSECAG00000012475	SGO1	shugoshin 1	1,30056	0,04433
474.	ENSECAG00000015115	RHBDL1	rhomboid like 1	1,30043	0,00239
475.	ENSECAG00000018699	CHTF18	chromosome transmission fidelity factor 18	1,29882	0,00124
476.	ENSECAG00000005265	NAAA	N-acylethanolamine acid amidase	1,29534	9,8E-16
477.	ENSECAG00000026863	EFS	Embryonal Fyn-Associated Substrate	1,29457	2,9E-24
478.	ENSECAG00000019750	IL6ST	interleukin 6 cytokine family signal transducer	1,29205	4,4E-28
479.	ENSECAG00000017203	BTG2	BTG Anti-Proliferation Factor 2	1,284	5,4E-06
480.	ENSECAG00000019988	RPUSD3	RNA Pseudouridine Synthase D3	1,28395	3,3E-16
481.	ENSECAG00000009452	KLK15	Kallikrein Related Peptidase 15	1,28091	3,9E-10
482.	ENSECAG00000017922	ADAM19	ADAM metallopeptidase domain 19	1,27877	2,7E-46
483.	ENSECAG00000012646	SYNJ2	Synaptojanin 2	1,27631	2,7E-20
484.	ENSECAG00000008634	NCAPH	non-SMC condensin I complex subunit H	1,27363	0,00024
485.	ENSECAG00000014259	TIMP1	TIMP metallopeptidase inhibitor 1	1,27273	2,7E-23
486.	ENSECAG00000004400	RBM47	RNA binding motif protein 47	1,27113	9,3E-05
487.	ENSECAG00000020933	ITPR1	Inositol 1,4,5-Trisphosphate Receptor Type 1	1,26669	2,4E-07
488.	ENSECAG00000023279	GATA6	GATA binding protein 6	1,26651	8,2E-09
489.	ENSECAG00000038338	BCAS4	Breast Carcinoma Amplified Sequence 4	1,2665	2,4E-10
490.	ENSECAG00000035238	IFITM5	interferon induced transmembrane protein 5	1,2561	0,00064
491.	ENSECAG00000015003	PLGRKT	Plasminogen Receptor With A C-Terminal Lysine	1,2544	2,7E-08
492.	ENSECAG00000016661	NR4A1	Nuclear Receptor Subfamily 4 Group A Member 1	1,24667	1,9E-06
493.	ENSECAG00000011641	TVP23A	trans-golgi network vesicle protein 23 homolog A	1,2402	9,6E-05
494.	ENSECAG00000014619	UBE2C	ubiquitin conjugating enzyme E2 C	1,2375	7,2E-07
495.	ENSECAG00000014377	CHAF1A	Chromatin Assembly Factor 1 Subunit A	1,23607	1,4E-10
496.	ENSECAG00000021905	HK2	hexokinase 2	1,23435	1,3E-22
497.	ENSECAG00000009839	VAT1L	vesicle amine transport 1 like	1,2331	0,01104
498.	ENSECAG00000012423	HOXB2	homeobox B2	1,2286	3E-05
499.	ENSECAG00000024138	CREG1	cellular repressor of E1A stimulated genes 1	1,22848	1,6E-15
500.	ENSECAG00000021799	MYRF	myelin regulatory factor	1,21786	2,5E-05
501.	ENSECAG00000019197	TCF21	transcription factor 21	1,2165	0,01628
502.	ENSECAG00000021453	TICRR	TOPBP1 interacting checkpoint and replication regulator	1,21531	9,5E-05
503.	ENSECAG00000016773	NABP1	nucleic acid binding protein 1	1,21351	2,2E-19
504.	ENSECAG00000014501	TMEM54	transmembrane protein 54	1,20724	5,4E-08
505.	ENSECAG00000014732	ATP10A	ATPase phospholipid transporting 10A (putative)	1,20339	5,5E-12
506.	ENSECAG00000035032	NXT1	nuclear transport factor 2 like export factor 1	1,20172	6,5E-24
507.	ENSECAG00000008971	P3H2	prolyl 3-hydroxylase 2	1,20083	0,00104
508.	ENSECAG00000009173	ZNF367	zinc finger protein 367	1,20044	0,00082
509.	ENSECAG00000024817	P4HA2	prolyl 4-hydroxylase subunit alpha 2	1,20021	5E-61
510.	ENSECAG00000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	1,19965	0,00058
511.	ENSECAG00000024121	TCF7L2	Transcription Factor 7 Like 2	1,19653	7,5E-18
512.	ENSECAG00000020036	KRT10A	keratin 10A	1,19617	3E-26
513.	ENSECAG00000038379	ENSECAG00000038379	keratin 18	1,19433	0,00017
514.	ENSECAG00000024190	UCHL3	Ubiquitin C-Terminal Hydrolase L3	1,19389	7E-33
515.	ENSECAG00000016339	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif 1	1,19115	5,8E-40
516.	ENSECAG00000009163	NUF2	NUF2 component of NDC80 kinetochore complex	1,1901	9,5E-05

517.	ENSECAG00000010879	NTS	Neurotensin	1,19007	0,02829
518.	ENSECAG00000028902	SP9	Sp9 transcription factor	1,18915	0,01278
519.	ENSECAG00000024293	AMDHD1	amidohydrolase domain containing 1	1,18713	0,0432
520.	ENSECAG00000000373	LOXL3	lysyl oxidase like 3	1,18652	1,2E-32
521.	ENSECAG00000012742	CXCL6	C-X-C motif chemokine ligand 6	1,18563	0,01181
522.	ENSECAG00000006788	PCSK5	proprotein convertase subtilisin/kexin type 5	1,18333	8,4E-26
523.	ENSECAG00000026887	TSPAN8	tetraspanin 8	1,17958	0,00017
524.	ENSECAG00000017077	IL17RA	interleukin 17 receptor A	1,17792	8,1E-22
525.	ENSECAG00000021192	PEAR1	platelet endothelial aggregation receptor 1	1,17715	3,1E-23
526.	ENSECAG00000016522	SCG3	Secretogranin III	1,17648	7,9E-07
527.	ENSECAG00000007571	PLAT	plasminogen activator, tissue type	1,17626	3,6E-27
528.	ENSECAG00000015194	RHBDL2	rhomboid like 2	1,17549	0,00162
529.	ENSECAG00000013037	ALDOC	Aldolase, Fructose-Bisphosphate C	1,17402	1,1E-14
530.	ENSECAG00000020698	MELK	maternal embryonic leucine zipper kinase	1,174	6,3E-06
531.	ENSECAG00000013883	ICAM1	Intercellular Adhesion Molecule 1	1,17196	4E-06
532.	ENSECAG00000013680	TLE1	TLE Family Member 1, Transcriptional Corepressor	1,16105	2,8E-11
533.	ENSECAG00000006558	RIC1	RIC1 homolog, RAB6A GEF complex partner 1	1,15909	4,8E-14
534.	ENSECAG00000014998	GLCE	glucuronic acid epimerase	1,15828	5,1E-11
535.	ENSECAG00000015298	SYNGR3	synaptogyrin 3	1,15734	0,00441
536.	ENSECAG00000019103	EXD2	exonuclease 3'-5' domain containing 2	1,15348	1,4E-21
537.	ENSECAG00000017771	ATP1B1	ATPase Na ⁺ /K ⁺ transporting subunit beta 1	1,15143	6,4E-11
538.	ENSECAG00000014658	SCD	stearoyl-CoA desaturase	1,14983	3,7E-17
539.	ENSECAG00000008392	SLC8A2	solute carrier family 8 member A2	1,14732	0,04384
540.	ENSECAG00000016337	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	1,1447	0,00415
541.	ENSECAG00000015385	RNF150	ring finger protein 150	1,13644	0,03654
542.	ENSECAG00000020506	MCM3	minichromosome maintenance complex component 3	1,13572	1,6E-10
543.	ENSECAG00000024054	SLC18A2	solute carrier family 18 member A2	1,13464	4,8E-06
544.	ENSECAG00000026677	ENSECAG00000026677	small nucleolar RNA SNORD113/SNORD114 family	1,13343	0,0105
545.	ENSECAG00000017426	FGF11	Fibroblast Growth Factor 11	1,12991	8,2E-07
546.	ENSECAG0000001964	PDHA1	Pyruvate Dehydrogenase E1 Subunit Alpha 1	1,12768	3,5E-37
547.	ENSECAG00000009303	GFPT2	Glutamine-Fructose-6-Phosphate Transaminase 2	1,12739	1,7E-32
548.	ENSECAG00000010786	PGAM1	Phosphoglycerate Mutase 1	1,12715	1,2E-19
549.	ENSECAG00000021634	SLC29A4	solute carrier family 29 member 4	1,12536	3,2E-05
550.	ENSECAG00000018101	FBLN1	fibulin 1	1,12496	2,2E-14
551.	ENSECAG00000010241	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	1,12477	0,00074
552.	ENSECAG00000025101	NELL2	neural EGFL like 2	1,12381	0,03631
553.	ENSECAG00000016417	TBC1D4	TBC1 domain family member 4	1,12134	2,2E-11
554.	ENSECAG00000014891	NRCAM	Neuronal Cell Adhesion Molecule	1,11892	8,5E-07
555.	ENSECAG00000016202	SEMA4C	semaphorin 4C	1,116	5,8E-23
556.	ENSECAG00000009073	ARHGEF39	Rho Guanine Nucleotide Exchange Factor 39	1,11592	0,02948
557.	ENSECAG00000023637	ADAM33	ADAM Metallopeptidase Domain 33	1,11299	5E-06
558.	ENSECAG00000020518	GNA14	G protein subunit alpha 14	1,10917	7,1E-16
559.	ENSECAG00000017109	QSOX1	Quiescin Sulphydryl Oxidase 1	1,10887	3,8E-16
560.	ENSECAG00000012887	CPZ	carboxypeptidase Z	1,10883	1,2E-17

561.	ENSECAG00000014934	ARHGEF9	Cdc42 guanine nucleotide exchange factor 9	1,10486	3,2E-10
562.	ENSECAG00000021428	GYS1	Glycogen Synthase 1	1,10416	4,6E-14
563.	ENSECAG00000008432	HASPIN	histone H3 associated protein kinase	1,10262	0,00202
564.	ENSECAG00000020840	OSBPL11	Oxysterol Binding Protein Like 11	1,10228	1,5E-14
565.	ENSECAG00000023815	PLA2R1	phospholipase A2 receptor 1	1,10194	1,3E-15
566.	ENSECAG00000024106	CHST1	carbohydrate sulfotransferase 1	1,10183	0,00031
567.	ENSECAG00000010914	CHSY1	chondroitin sulfate synthase 1	1,09645	4,4E-14
568.	ENSECAG00000010619	F12	coagulation factor XII	1,09348	0,04088
569.	ENSECAG00000017168	ABCC4	ATP binding cassette subfamily C member 4	1,08774	1,4E-10
570.	ENSECAG00000022553	IRS3	insulin receptor substrate 3	1,08708	6,2E-05
571.	ENSECAG00000017845	GGCT	Gamma-Glutamylcyclotransferase	1,08517	7,5E-05
572.	ENSECAG00000000397	SDHA	succinate dehydrogenase complex flavoprotein subunit A	1,08112	3,1E-32
573.	ENSECAG00000011929	NR4A3	Nuclear Receptor Subfamily 4 Group A Member 3	1,0792	2,9E-06
574.	ENSECAG00000017784	OSR2	odd-skipped related transcription factor 2	1,07887	2,2E-10
575.	ENSECAG00000010022	CYP17A1	Cytochrome P450 Family 17 Subfamily A Member 1	1,07571	0,01457
576.	ENSECAG00000020312	LRIG3	leucine rich repeats and immunoglobulin like domains 3	1,07493	1,2E-08
577.	ENSECAG00000004709	C2	Complement C2	1,0709	0,032
578.	ENSECAG00000006917	P4HA3	prolyl 4-hydroxylase subunit alpha 3	1,06508	2,4E-10
579.	ENSECAG00000023668	RGS5	regulator of G protein signaling 5	1,05863	6,8E-07
580.	ENSECAG00000028292	ENSECAG00000028292		1,05181	1,1E-26
581.	ENSECAG00000012716	RAB42	RAB42, member RAS oncogene family	1,0477	0,03082
582.	ENSECAG00000022063	ABHD5	abhydrolase domain containing 5, lysophosphatidic acid acyltransferase	1,04643	7,1E-36
583.	ENSECAG00000000841	ENSECAG00000000841	heat shock 70 kDa protein 1-like	1,04231	0,01741
584.	ENSECAG00000014526	PPIL6	peptidylprolyl isomerase like 6	1,03932	2,1E-09
585.	ENSECAG00000039655	RARRES1	Retinoic Acid Receptor Responder 1	1,03921	3E-10
586.	ENSECAG00000019713	SRM	Spermidine Synthase	1,03839	6,2E-25
587.	ENSECAG00000017487	MXRA5	matrix remodeling associated 5	1,03807	6E-05
588.	ENSECAG00000009787	SNAI1	Snail Family Transcriptional Repressor 1	1,03432	5,1E-10
589.	ENSECAG00000013425	IGFBP5	insulin like growth factor binding protein 5	1,03418	0,00039
590.	ENSECAG00000017925	CD200	CD200 molecule	1,03282	4,3E-05
591.	ENSECAG00000016360	PDE3A	Phosphodiesterase 3A	1,0322	8,4E-06
592.	ENSECAG00000003462	RUNX1	RUNX family transcription factor 1	1,02848	2,9E-14
593.	ENSECAG00000041907	ENSECAG00000041907		1,02723	4,7E-09
594.	ENSECAG00000002569	FLRT3	fibronectin leucine rich transmembrane protein 3	1,02564	1,6E-10
595.	ENSECAG00000006213	PDK1	Pyruvate Dehydrogenase Kinase 1	1,025	2,2E-08
596.	ENSECAG00000003634	RHNO1	RAD9-HUS1-RAD1 Interacting Nuclear Orphan 1	1,02452	3,4E-06
597.	ENSECAG00000021206	HAS2	hyaluronan synthase 2	1,02246	6,8E-09
598.	ENSECAG00000014953	KIF15	kinesin family member 15	1,0164	0,00222
599.	ENSECAG00000011008	MCOLN2	mucolipin TRP cation channel 2	1,01599	1E-15
600.	ENSECAG00000008700	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	1,01501	0,03868
601.	ENSECAG00000024339	CAMK2D	calcium/calmodulin dependent protein kinase II delta	1,01467	5,3E-32
602.	ENSECAG00000018332	AK4	adenylate kinase 4	1,01276	1,8E-06
603.	ENSECAG00000024107	ROR1	receptor tyrosine kinase like orphan receptor 1	1,01244	8,2E-07

604.	ENSECAG00000000269	CDC37L1	cell division cycle 37 like 1, HSP90 cochaperone	1,01068	9,6E-20
605.	ENSECAG00000004544	HRH1	histamine receptor H1	1,01043	0,00362
606.	ENSECAG00000007942	LMNB1	lamin B1	1,00943	7,3E-07
607.	ENSECAG00000023472	KCNK2	potassium two pore domain channel subfamily K member 2	1,00902	0,00185
608.	ENSECAG00000022780	TTYH2	Tweety Family Member 2	1,00743	1,5E-08
609.	ENSECAG00000016098	ENSECAG00000016098		1,00655	0,00443
610.	ENSECAG00000008624	CCL28	C-C motif chemokine ligand 28	1,00598	0,00187
611.	ENSECAG00000018596	STIMATE	STIM Activating Enhancer	1,00457	1,9E-06
612.	ENSECAG00000038536	CCND1	Cyclin D1	-1,00088	7E-14
613.	ENSECAG00000011246	GLI1	GLI Family Zinc Finger 1	-1,00249	7E-07
614.	ENSECAG00000010522	BACH2	BTB domain and CNC homolog 2	-1,00337	0,03572
615.	ENSECAG00000026969	RIMKLB	ribosomal modification protein rimK like family member B	-1,00557	2,2E-08
616.	ENSECAG00000030081	ENSECAG00000030081	cationic amino acid transporter 4	-1,00578	0,01537
617.	ENSECAG00000015128	CAPG	capping actin protein, gelsolin like	-1,0059	8E-17
618.	ENSECAG00000019478	CCDC158	coiled-coil domain containing 158	-1,01009	2,8E-06
619.	ENSECAG00000015951	PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	-1,01051	2,2E-08
620.	ENSECAG00000007176	ELOVL7	ELOVL fatty acid elongase 7	-1,01173	5,6E-06
621.	ENSECAG00000022821	ZNF570	zinc finger protein 570	-1,01265	2E-06
622.	ENSECAG00000000354	PLK2	Polo Like Kinase 2	-1,01504	4,8E-12
623.	ENSECAG00000012700	JADE3	jade family PHD finger 3	-1,01547	0,03016
624.	ENSECAG00000024139	LONRF3	LON peptidase N-terminal domain and ring finger 3	-1,01622	7,5E-09
625.	ENSECAG00000015134	PELI2	pellino E3 ubiquitin protein ligase family member 2	-1,01722	0,00011
626.	ENSECAG00000017185	ZBP1	Z-DNA binding protein 1	-1,01832	0,00011
627.	ENSECAG00000006554	PRRG4	Proline Rich And Gla Domain 4	-1,0184	2,9E-06
628.	ENSECAG00000015611	ETV4	ETS variant transcription factor 4	-1,01857	0,00631
629.	ENSECAG00000002061	NEURL2	neuralized E3 ubiquitin protein ligase 2	-1,01984	0,00063
630.	ENSECAG00000001399	SAMD9	sterile alpha motif domain containing 9	-1,02144	2,8E-08
631.	ENSECAG00000035548	ENSECAG00000035548	T-lymphocyte surface antigen Ly-9	-1,02159	0,00371
632.	ENSECAG00000037749	ENSECAG00000037749		-1,02188	0,04054
633.	ENSECAG00000021092	KLF15	KLF transcription factor 15	-1,02234	8,9E-08
634.	ENSECAG00000038056	ENSECAG00000038056		-1,02383	3,8E-06
635.	ENSECAG00000018147	ENSECAG00000018147		-1,02473	2,8E-09
636.	ENSECAG00000003619	AFF1	ALF transcription elongation factor 1	-1,02567	3,5E-26
637.	ENSECAG00000016917	TES	testin LIM domain protein	-1,02601	3,2E-21
638.	ENSECAG00000021941	STK4	serine/threonine kinase 4	-1,02727	2,8E-10
639.	ENSECAG00000012012	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5	-1,0281	2,7E-17
640.	ENSECAG00000013633	ARHGAP6	Rho GTPase activating protein 6	-1,02925	7,1E-11
641.	ENSECAG00000012340	RADX	RPA1 related single stranded DNA binding protein, X-linked	-1,02989	0,0361
642.	ENSECAG00000024999	SMC5	structural maintenance of chromosomes 5	-1,03197	3,4E-19
643.	ENSECAG00000010560	MIP-2BETA	CXCL3	-1,03251	0,00112
644.	ENSECAG00000013154	SERAC1	serine active site containing 1	-1,03311	2E-14
645.	ENSECAG00000014382	ZDHHC23	zinc finger DHHC-type palmitoyltransferase 23	-1,03447	6,6E-05
646.	ENSECAG00000011594	KCND3	potassium voltage-gated channel subfamily D member 3	-1,03468	0,02309
647.	ENSECAG00000000158	SPATA6	Spermatogenesis Associated 6	-1,03537	2,2E-08
648.	ENSECAG00000012362	C7	complement C7	-1,03579	2,8E-08
649.	ENSECAG00000012518	ATP10D	ATPase phospholipid transporting 10D (putative)	-1,03806	2,8E-14

650.	ENSECAG00000017878	PPP1R42	protein phosphatase 1 regulatory subunit 42	-1,03887	0,00409
651.	ENSECAG00000011511	PGR		-1,03995	4,1E-18
652.	ENSECAG00000009638	PALS2	protein associated with LIN7 2, MAGUK p55 family member	-1,04008	2,1E-05
653.	ENSECAG00000038389	ENSECAG00000038389		-1,04141	1,2E-05
654.	ENSECAG00000039710	ZNF543	Zinc Finger Protein 543	-1,04242	0,00175
655.	ENSECAG00000007095	PLEKHG1	pleckstrin homology and RhoGEF domain containing G1	-1,04433	6,6E-07
656.	ENSECAG00000000637	STAC2	SH3 and cysteine rich domain 2	-1,04559	9,5E-21
657.	ENSECAG00000007164	EEIG1	estrogen-induced osteoclastogenesis regulator 1	-1,04839	3,3E-12
658.	ENSECAG00000034913	ENSECAG00000034913		-1,0488	1,5E-06
659.	ENSECAG00000024305	RTN1	reticulon 1	-1,04911	3,2E-09
660.	ENSECAG00000019700	TGFBR3	Transforming Growth Factor Beta Receptor 3	-1,05108	1,8E-20
661.	ENSECAG00000032818	ENSECAG00000032818		-1,05173	2,2E-32
662.	ENSECAG00000019343	ALDH1A1	aldehyde dehydrogenase 1 family member A1	-1,05528	0,00014
663.	ENSECAG00000005083	IL1RAP	interleukin 1 receptor accessory protein	-1,05584	1,9E-19
664.	ENSECAG00000039741	ENSECAG00000039741		-1,05914	0,0064
665.	ENSECAG00000024624	MLPH	melanophilin	-1,06046	0,00222
666.	ENSECAG00000007373	SHTN1		-1,06385	8,1E-26
667.	ENSECAG00000016733	PDLIM5	PDZ and LIM domain 5	-1,06415	2,9E-28
668.	ENSECAG00000015608	CRIM1	cysteine rich transmembrane BMP regulator 1	-1,06441	3,7E-19
669.	ENSECAG00000011726	EIF2AK2	Eukaryotic Translation Initiation Factor 2 Alpha Kinase 2	-1,06452	8,9E-11
670.	ENSECAG00000042557	ENSECAG00000042557		-1,06577	6,5E-13
671.	ENSECAG00000012024	TBC1D8	TBC1 domain family member 8	-1,06599	9,9E-10
672.	ENSECAG00000034852	COL4A5	collagen type IV alpha 5 chain	-1,06604	0,00353
673.	ENSECAG00000004762	NRIP1	nuclear receptor interacting protein 1	-1,06687	4,4E-21
674.	ENSECAG00000020473	CTIF	cap binding complex dependent translation initiation factor	-1,06802	1,8E-17
675.	ENSECAG00000021125	TFAP2C	transcription factor AP-2 gamma	-1,06921	5,7E-13
676.	ENSECAG00000011045	SLC29A2	solute carrier family 29 member 2	-1,07102	0,00606
677.	ENSECAG00000011727	RNASE4	ribonuclease A family member 4	-1,07207	9,9E-15
678.	ENSECAG00000024394	SLC6A17	solute carrier family 6 member 17	-1,07312	3,4E-17
679.	ENSECAG00000000910	ENSECAG00000000910	interferon-induced transmembrane protein 1	-1,07347	5,1E-15
680.	ENSECAG00000008259	MASP1	MBL associated serine protease 1	-1,0737	1,9E-09
681.	ENSECAG00000010201	ENSECAG00000010201	feline leukemia virus subgroup C receptor-related protein 2	-1,07438	1,1E-06
682.	ENSECAG00000014504	KIF1A	kinesin family member 1A	-1,07506	2,1E-13
683.	ENSECAG00000017042	ENSECAG00000017042	membrane-spanning 4-domains subfamily A member 6A	-1,07534	0,03253
684.	ENSECAG00000008545	ECM1	Extracellular Matrix Protein 1	-1,07605	4,2E-20
685.	ENSECAG00000009543	EPSTI1	epithelial stromal interaction 1	-1,07708	8,8E-11
686.	ENSECAG00000016958	CXXC5	CXXC finger protein 5	-1,07884	1,8E-15
687.	ENSECAG00000001900	ENSECAG00000001900	pleckstrin homology like domain family A member 1	-1,08047	9,5E-12
688.	ENSECAG00000019512	PDGFC	platelet derived growth factor C	-1,08102	4,8E-10
689.	ENSECAG00000009318	EHBP1	EH domain binding protein 1	-1,084	2,6E-18
690.	ENSECAG00000013450	CORO6	coronin 6	-1,08527	0,00277
691.	ENSECAG00000022007	SCN9A	sodium voltage-gated channel alpha subunit 9	-1,08603	0,00934
692.	ENSECAG00000009280	SPARCL1	SPARC Like 1	-1,08681	1,8E-08
693.	ENSECAG00000020259	SMAD3	SMAD Family Member 3	-1,09063	1,1E-16
694.	ENSECAG00000001100	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	-1,09353	1,5E-06
695.	ENSECAG00000024271	TEX9	Testis Expressed 9	-1,09389	0,00012
696.	ENSECAG00000019199	ENSECAG00000019199		-1,09622	3,8E-11

697.	ENSECAG00000029715	ENSECAG00000029715		-1,09925	0,02124
698.	ENSECAG00000015727	PAK3	p21 (RAC1) activated kinase 3	-1,09931	0,00263
699.	ENSECAG00000013957	PDE5A	phosphodiesterase 5A	-1,10003	5,8E-17
700.	ENSECAG00000019758	TNFSF13B	TNF Superfamily Member 13b	-1,10017	0,00017
701.	ENSECAG00000011551	KLHL31	kelch like family member 31	-1,10268	0,00165
702.	ENSECAG00000022129	HOXD3	homeobox D3	-1,1049	1,1E-08
703.	ENSECAG00000043642	NREP	neuronal regeneration related protein	-1,10546	0,00067
704.	ENSECAG00000037149	ENSECAG00000037149		-1,10803	2,6E-07
705.	ENSECAG00000014416	BTBD8	KIAA1107 ortholog	-1,1083	0,02691
706.	ENSECAG00000017216	EHD4	EH Domain Containing 4	-1,10904	2E-14
707.	ENSECAG00000007210	CTSL	cathepsin L	-1,10968	0,0051
708.	ENSECAG00000012327	IL34	interleukin 34	-1,11017	1,9E-15
709.	ENSECAG00000009291	ENKD1	enkurin domain containing 1	-1,11145	0,00138
710.	ENSECAG00000006315	XYLT1	xylosyltransferase 1	-1,11224	7,8E-19
711.	ENSECAG00000007220	HEYL	hes related family bHLH transcription factor with YRPW motif like	-1,11362	0,00023
712.	ENSECAG00000017147	CCDC9B	coiled-coil domain containing 9B	-1,11436	3,1E-18
713.	ENSECAG00000009060	DIPK2A	divergent protein kinase domain 2A	-1,11461	1,7E-07
714.	ENSECAG00000013515	SEMA3B	semaphorin 3B	-1,11479	6,7E-10
715.	ENSECAG00000006501	FJX1	Four-Jointed Box Kinase 1	-1,11803	0,00047
716.	ENSECAG00000016261	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	-1,11814	1,9E-12
717.	ENSECAG00000018619	FOLR2	folate receptor beta	-1,11957	9,6E-11
718.	ENSECAG00000018067	ITGBL1	integrin subunit beta like 1	-1,12049	1,4E-06
719.	ENSECAG00000014003	TMEM192	transmembrane protein 192	-1,12387	6,1E-19
720.	ENSECAG00000018290	GPD2	glycerol-3-phosphate dehydrogenase 2	-1,12447	4,9E-16
721.	ENSECAG00000007646	NR1D2	nuclear receptor subfamily 1 group D member 2	-1,12489	3,2E-40
722.	ENSECAG00000020468	RELN	Reelin	-1,12507	0,01829
723.	ENSECAG00000016038	ZNF892	zinc finger protein 501	-1,12565	0,00045
724.	ENSECAG00000000026	XG	Xg Glycoprotein	-1,12642	4,9E-20
725.	ENSECAG00000018131	CTNNAL1	catenin alpha like 1	-1,12948	2,9E-19
726.	ENSECAG00000006020	RRAGB	Ras related GTP binding B	-1,12949	8,1E-21
727.	ENSECAG00000005381	LRRN4CL	LRRN4 C-terminal like	-1,12964	8,2E-16
728.	ENSECAG00000019660	TRIB1	tribbles pseudokinase 1	-1,13023	5,5E-08
729.	ENSECAG00000015394	SLC25A35	solute carrier family 25 member 35	-1,13073	0,0097
730.	ENSECAG00000020399	CTHRC1	collagen triple helix repeat containing 1	-1,13098	6E-09
731.	ENSECAG00000010546	KLF5	KLF transcription factor 5	-1,13177	0,00222
732.	ENSECAG00000000709	ENSECAG00000000709	neuroigin 4 X-linked	-1,13283	0,00213
733.	ENSECAG00000010437	TCEA3	transcription elongation factor A3	-1,13295	1,3E-08
734.	ENSECAG00000024705	MAFB	MAF bZIP transcription factor B	-1,1347	1,1E-09
735.	ENSECAG00000026819	NTN1	netrin 1	-1,13565	7,6E-22
736.	ENSECAG00000021480	ZNF573	Zinc Finger Protein 573	-1,13862	0,00227
737.	ENSECAG00000011749	MSX2	msh homeobox 2	-1,13889	0,00036
738.	ENSECAG00000023363	SLC26A2	solute carrier family 26 member 2	-1,14058	9,1E-11
739.	ENSECAG00000026059	MIR10B	MicroRNA 10b	-1,14375	0,0315
740.	ENSECAG00000008793	PGBD1	piggyBac transposable element derived 1	-1,14379	0,00653
741.	ENSECAG00000026951	ARVCF	ARVCF delta catenin family member	-1,146	0,00011
742.	ENSECAG00000000217	MTSS2	MTSS I-BAR domain containing 2	-1,14663	1,9E-19
743.	ENSECAG00000040382	ENSECAG00000040382		-1,14933	3,9E-09
744.	ENSECAG00000031302	ENSECAG00000031302	aldo-keto reductase family 1 member C23-like protein	-1,15197	0,00301
745.	ENSECAG00000000234	GPC6	glypican 6	-1,15315	3,6E-07
746.	ENSECAG00000015878	AMOT	angiomotin	-1,15525	6,6E-08
747.	ENSECAG00000014660	IFNGR2	interferon gamma receptor 2	-1,15613	5,6E-15

748.	ENSECAG00000022924	EEF2K	eukaryotic elongation factor 2 kinase	-1,15625	5,2E-18
749.	ENSECAG00000006567	SLITRK4	SLIT and NTRK like family member 4	-1,15627	0,01694
750.	ENSECAG00000013544	TMEM268	transmembrane protein 268	-1,15784	1,1E-21
751.	ENSECAG00000037336	ENSECAG00000037336	heparan sulfate glucosamine 3-O-sulfotransferase 4	-1,15895	0,0011
752.	ENSECAG00000021989	RIGI	RNA sensor RIG-I	-1,16143	2,6E-22
753.	ENSECAG00000005794	MYRIP	myosin VIIA and Rab interacting protein	-1,16295	0,0042
754.	ENSECAG00000033952	TMEM123	transmembrane protein 123	-1,16311	3,9E-17
755.	ENSECAG00000040532	ENSECAG00000040532		-1,16504	0,00302
756.	ENSECAG00000020162	PRR5L	proline rich 5 like	-1,16652	0,0034
757.	ENSECAG00000013393	AHR	aryl hydrocarbon receptor	-1,16736	2E-14
758.	ENSECAG00000020337	DOCK11	dedicator of cytokinesis 11	-1,16887	1,2E-32
759.	ENSECAG00000013629	ADD3	adducin 3	-1,16898	3,2E-31
760.	ENSECAG00000001652	ITGA6	integrin subunit alpha 6	-1,17237	1E-08
761.	ENSECAG00000006879	PLA2G5	phospholipase A2 group V	-1,17456	0,00965
762.	ENSECAG00000019769	PPARGC1B	PPARG Coactivator 1 Beta	-1,17469	0,00024
763.	ENSECAG00000000480	ABI3BP	ABI Family Member 3 Binding Protein	-1,17584	2,3E-20
764.	ENSECAG00000001445	CHD7	chromodomain helicase DNA binding protein 7	-1,17601	6,8E-06
765.	ENSECAG000000018112	FAM241B	family with sequence similarity 241 member B	-1,17929	0,0106
766.	ENSECAG000000010762	ROBO2	Roundabout Guidance Receptor 2	-1,18141	0,03881
767.	ENSECAG000000021448	PADI1	peptidyl arginine deiminase 1	-1,18148	0,00619
768.	ENSECAG000000014992	JAM2	Junctional Adhesion Molecule 2	-1,18228	0,02501
769.	ENSECAG000000020548	ENSECAG000000020548	caspase-14	-1,18243	0,04995
770.	ENSECAG00000008662	DPYSL2	dihydropyrimidinase like 2	-1,18272	5,4E-31
771.	ENSECAG000000012541	SLC38A4	solute carrier family 38 member 4	-1,18566	2,1E-18
772.	ENSECAG000000000713	MDM1	Mdm1 Nuclear Protein	-1,18658	4,1E-20
773.	ENSECAG000000004219	ZNF831	zinc finger protein 831	-1,18906	0,03239
774.	ENSECAG000000024622	RHOBTB3	Rho related BTB domain containing 3	-1,18913	2,8E-17
775.	ENSECAG000000032860	ENSECAG000000032860		-1,19197	0,00143
776.	ENSECAG000000024448	TRIM63	tripartite motif containing 63	-1,19353	3,5E-16
777.	ENSECAG000000039591	ZNF469	zinc finger protein 469	-1,1952	4,8E-16
778.	ENSECAG000000015144	CADM1	cell adhesion molecule 1	-1,19573	7,2E-08
779.	ENSECAG000000016238	RPS6KA1	ribosomal protein S6 kinase A1	-1,19735	0,00042
780.	ENSECAG000000015715	ADAMTS15	ADAM Metalloproteinase With Thrombospondin Type 1 Motif 15	-1,19755	4,8E-10
781.	ENSECAG000000013382	SLC25A34	Solute Carrier Family 25 Member 34	-1,19844	9,1E-06
782.	ENSECAG000000021621	MOB3B	MOB kinase activator 3B	-1,19952	0,0077
783.	ENSECAG000000005704	CARD11	caspase recruitment domain family member 11	-1,20297	2E-11
784.	ENSECAG000000016605	NR3C2	nuclear receptor subfamily 3 group C member 2	-1,2037	0,00314
785.	ENSECAG000000001634	INSYN1	inhibitory synaptic factor 1	-1,20396	4,2E-19
786.	ENSECAG000000019818	POU2F3	POU class 2 homeobox 3	-1,20403	1,5E-27
787.	ENSECAG000000008565	GPR37	G protein-coupled receptor 37	-1,20497	2,9E-05
788.	ENSECAG000000022513	NPAS1	neuronal PAS domain protein 1	-1,20955	0,00807
789.	ENSECAG000000019648	MID1	midline 1	-1,21151	0,00052
790.	ENSECAG000000019445	MMP12	matrix metalloproteinase 3	-1,21851	0,02489
791.	ENSECAG000000019716	CCDC88C	Coiled-Coil Domain Containing 88C	-1,21997	4E-14
792.	ENSECAG000000010672	PLXDC1	plexin domain containing 1	-1,22008	0,00147
793.	ENSECAG000000013217	ECHDC2	enoyl-CoA hydratase domain containing 2	-1,22132	1,5E-10
794.	ENSECAG000000021066	KLHL24	kelch like family member 24	-1,22253	1E-26
795.	ENSECAG000000013574	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	-1,22506	1,9E-06
796.	ENSECAG000000007386	ENO2	Enolase 2	-1,2251	6,5E-11
797.	ENSECAG000000021996	RALGDS	ral guanine nucleotide dissociation stimulator	-1,22744	2E-20

798.	ENSECAG00000005631	BDKRB1	bradykinin receptor B1	-1,22997	7,7E-06
799.	ENSECAG00000024047	IL6R	interleukin 6 receptor	-1,23144	0,00205
800.	ENSECAG00000021374	TCF23	Transcription Factor 23	-1,23316	3,1E-05
801.	ENSECAG00000024459	MARK1	Microtubule Affinity Regulating Kinase 1	-1,23363	2,5E-45
802.	ENSECAG00000032515	CEBPA	CCAAT enhancer binding protein alpha	-1,23665	5,9E-11
803.	ENSECAG00000035205	ZNF853	zinc finger protein 853	-1,23796	5,3E-12
804.	ENSECAG00000006829	KAZN	Kazrin, Periplakin Interacting Protein	-1,24002	1,1E-09
805.	ENSECAG00000012133	VEGFC	vascular endothelial growth factor C	-1,24113	8,5E-23
806.	ENSECAG00000017090	CLEC2L	C-type lectin domain family 2 member L	-1,24296	0,00209
807.	ENSECAG00000021042	VASH1	vasohibin 1	-1,24421	1,2E-26
808.	ENSECAG00000008199	PDZD2	PDZ domain containing 2	-1,24574	0,03493
809.	ENSECAG00000024593	SLC35G1	solute carrier family 35 member G1	-1,25326	0,00155
810.	ENSECAG00000016217	RNF213	ring finger protein 213	-1,25625	8,2E-23
811.	ENSECAG00000020437	BCL2	BCL2 apoptosis regulator	-1,25703	6,3E-05
812.	ENSECAG00000000751	NEDD4L	NEDD4 like E3 ubiquitin protein ligase	-1,26772	1E-10
813.	ENSECAG00000016171	GRM7	glutamate metabotropic receptor 7	-1,27605	0,00457
814.	ENSECAG00000010531	F2RL2	Coagulation Factor II Thrombin Receptor Like 2	-1,27659	4E-11
815.	ENSECAG00000007658	MGLL	monoglyceride lipase	-1,27673	2,7E-06
816.	ENSECAG00000008564	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1,27864	0,00122
817.	ENSECAG00000012132	ENSECAG00000012132	2'-5'-oligoadenylate synthase- like protein 2	-1,27962	5,1E-18
818.	ENSECAG00000006685	NPFFR2	Neuropeptide FF Receptor 2	-1,28376	0,01387
819.	ENSECAG00000002186	CD68	CD68 Molecule	-1,28426	0,00058
820.	ENSECAG00000017986	AXIN2	axin 2	-1,28596	0,00104
821.	ENSECAG00000019958	ARHGAP20	Rho GTPase activating protein 20	-1,28718	1,3E-12
822.	ENSECAG00000000903	RASGRF2	Ras protein specific guanine nucleotide releasing factor 2	-1,2921	0,00334
823.	ENSECAG00000011747	BCL7A	BAF Chromatin Remodeling Complex Subunit BCL7A	-1,29266	0,00142
824.	ENSECAG00000020606	FAM186B	family with sequence similarity 186 member B	-1,29303	0,0011
825.	ENSECAG00000017209	DAPP1	dual adaptor of phosphotyrosine and 3- phosphoinositides 1	-1,29426	2,9E-07
826.	ENSECAG00000008852	ABCA1	ATP binding cassette subfamily A member 1	-1,29668	3,9E-19
827.	ENSECAG00000024049	S100A13	S100 Calcium Binding Protein A13	-1,29856	7,8E-27
828.	ENSECAG00000033821	ANKRD33B	Ankyrin Repeat Domain 33B	-1,30077	0,00617
829.	ENSECAG00000007173	HMCN1	hemiscentin 1	-1,305	0,00324
830.	ENSECAG00000000203	TRPA1	transient receptor potential cation channel subfamily A member 1	-1,30682	4,6E-10
831.	ENSECAG00000020795	DAGLA	diacylglycerol lipase alpha	-1,30693	0,00268
832.	ENSECAG00000022703	LY5	lymphocyte antigen 75	-1,30773	1,8E-15
833.	ENSECAG00000005659	TPST1	tyrosylprotein sulfotransferase 1	-1,31003	1E-19
834.	ENSECAG00000019391	TNFSF10	TNF Superfamily Member 10	-1,31824	1,3E-19
835.	ENSECAG00000018258	WDR35	WD repeat domain 35	-1,31955	8,2E-13
836.	ENSECAG00000024531	ADM	Adrenomedullin	-1,31976	1E-43
837.	ENSECAG00000000178	RUNX1T1	RUNX1 Partner Transcriptional Co-Repressor 1	-1,32	3,2E-15
838.	ENSECAG00000002716	KDM7A	lysine demethylase 7A	-1,32083	1,4E-10
839.	ENSECAG00000019290	CAMK1D	calcium/calmodulin dependent protein kinase ID	-1,32091	4,8E-11
840.	ENSECAG00000000072	MAP7D2	MAP7 domain containing 2	-1,32188	0,00882
841.	ENSECAG00000020638	NEB	nebulin	-1,324	0,00647
842.	ENSECAG00000016204	SLC31A2	solute carrier family 31 member 2	-1,32779	7,9E-13

843.	ENSECAG00000015387	MYLK	myosin light chain kinase	-1,33227	1,1E-43
844.	ENSECAG00000000731	SPMIP5		-1,33316	0,04479
845.	ENSECAG00000003331	PLEKHH2	pleckstrin homology, MyTH4 and FERM domain containing H2	-1,33496	3,1E-18
846.	ENSECAG00000024143	MYO7A	Myosin VIIA	-1,33689	0,00011
847.	ENSECAG00000015189	FAM216B	family with sequence similarity 216 member B	-1,3393	0,0037
848.	ENSECAG00000043319	ENSECAG00000043319		-1,34065	1,8E-05
849.	ENSECAG00000017381	ENSECAG00000017381	interferon regulatory factor 4	-1,34606	8,5E-08
850.	ENSECAG00000018631	LTBP2	latent transforming growth factor beta binding protein 2	-1,34646	9,6E-16
851.	ENSECAG00000008983	LRRTM1	leucine rich repeat transmembrane neuronal 1	-1,3501	3,6E-07
852.	ENSECAG00000022011	AKAP7	A-kinase anchoring protein 7	-1,35354	0,00132
853.	ENSECAG00000021653	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	-1,35621	6,1E-30
854.	ENSECAG00000005525	GJA1	gap junction protein alpha 1	-1,35631	3,1E-20
855.	ENSECAG00000010288	LRRK2	Leucine Rich Repeat Kinase 2	-1,35667	1,3E-34
856.	ENSECAG00000031607	ENSECAG00000031607		-1,35922	0,00038
857.	ENSECAG00000010004	PRUNE2	prune homolog 2 with BCH domain	-1,36096	7,7E-51
858.	ENSECAG00000009648	CLIP1	CAP-Gly domain containing linker protein 1	-1,36153	3,2E-52
859.	ENSECAG00000008535	DNAH10	dynein axonemal heavy chain 10	-1,3686	4,7E-07
860.	ENSECAG00000018771	PKNOX2	PBX/knotted 1 homeobox 2	-1,36885	3,4E-07
861.	ENSECAG00000000278	FCAMR		-1,36972	0,00252
862.	ENSECAG00000017661	ZC2HC1C	zinc finger C2HC-type containing 1C	-1,3701	4E-05
863.	ENSECAG00000008638	RERE	arginine-glutamic acid dipeptide repeats	-1,37105	7,8E-44
864.	ENSECAG00000015809	ZBTB20	Zinc Finger And BTB Domain Containing 20	-1,37586	0,04377
865.	ENSECAG00000028267	CYP2C11		-1,37658	3,6E-08
866.	ENSECAG00000014947	OPN3	opsin 3	-1,3781	7,5E-11
867.	ENSECAG00000019008	SHROOM3	shroom family member 3	-1,37987	8,3E-28
868.	ENSECAG00000021545	MTSS1	MTSS I-BAR domain containing 1	-1,38269	2,6E-16
869.	ENSECAG00000008906	PARP15	poly(ADP-ribose) polymerase family member 15	-1,38409	8,1E-18
870.	ENSECAG00000002390	ENSECAG00000002390	protein BEX1	-1,39509	1,1E-08
871.	ENSECAG00000007798	ME3	Malic Enzyme 3	-1,39512	0,00713
872.	ENSECAG00000000541	PTCH2	Patched 2	-1,39742	2,5E-08
873.	ENSECAG00000025019	ARHGEF26	Rho guanine nucleotide exchange factor 26	-1,40023	0,0002
874.	ENSECAG00000014275	DBP	D-box binding PAR bZIP transcription factor	-1,4054	3,6E-08
875.	ENSECAG00000033816	ENSECAG00000033816		-1,40983	0,00702
876.	ENSECAG00000016667	ENSECAG00000016667		-1,41264	1,8E-14
877.	ENSECAG00000021162	CDH13	Cadherin 13	-1,41337	2,3E-12
878.	ENSECAG00000021518	SLX1A	SLX1 Homolog A, Structure-Specific Endonuclease Subunit	-1,42087	1,7E-07
879.	ENSECAG00000014993	SCNN1B	sodium channel epithelial 1 subunit beta	-1,42327	1,9E-06
880.	ENSECAG00000009311	SH3TC2	SH3 domain and tetratricopeptide repeats 2	-1,42559	0,03249
881.	ENSECAG00000022441	ESR1	estrogen receptor 1	-1,42955	8,2E-23
882.	ENSECAG00000014888	NEK5	NIMA related kinase 5	-1,43193	0,01119
883.	ENSECAG00000023101	TP53I11	tumor protein p53 inducible protein 11	-1,43223	3,4E-17
884.	ENSECAG00000009813	CD83	CD83 Molecule	-1,43738	1,2E-06
885.	ENSECAG00000001598	IFI35	interferon induced protein 35	-1,4398	1,6E-15
886.	ENSECAG00000020932	SVIL	supervillin	-1,44356	1,6E-25
887.	ENSECAG00000007330	ALS2CL	ALS2 C-terminal like	-1,4454	0,01105
888.	ENSECAG00000019701	ANKFN1	Ankyrin Repeat And Fibronectin Type III Domain Containing 1	-1,44558	0,03576

889.	ENSECAG00000013884	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	-1,44692	0,01745
890.	ENSECAG00000038332	ENSECAG00000038332		-1,44725	8,5E-55
891.	ENSECAG00000009968	SH3PXD2B	SH3 And PX Domains 2B	-1,44737	1,3E-62
892.	ENSECAG00000012962	SAMD12	sterile alpha motif domain containing 12	-1,44852	1,2E-10
893.	ENSECAG00000019617	ATP8B4	ATPase phospholipid transporting 8B4 (putative)	-1,44979	0,00412
894.	ENSECAG00000018663	PLB1	Phospholipase B1	-1,44987	1,6E-06
895.	ENSECAG00000023960	KLHL30	kelch like family member 30	-1,45283	0,00052
896.	ENSECAG00000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,45323	6,7E-20
897.	ENSECAG00000024148	RAB39A	RAB39A, Member RAS Oncogene Family	-1,45931	0,01527
898.	ENSECAG00000009660	PLEKHA6	Pleckstrin Homology Domain Containing A6	-1,46074	8,5E-12
899.	ENSECAG00000034729	ENSECAG00000034729		-1,4614	0,00064
900.	ENSECAG00000035459	BATF2	basic leucine zipper ATF-like transcription factor 2	-1,46333	9E-09
901.	ENSECAG00000017335	CDON	cell adhesion associated, oncogene regulated	-1,46335	1,4E-23
902.	ENSECAG00000026945	HES1	hes family bHLH transcription factor 1	-1,4635	4,2E-05
903.	ENSECAG00000002918	BMP7	bone morphogenetic protein 7	-1,47123	0,00082
904.	ENSECAG00000014313	DCLK2	doublecortin like kinase 2	-1,4737	0,02365
905.	ENSECAG00000021259	SCNN1G	sodium channel epithelial 1 subunit gamma	-1,47372	0,00037
906.	ENSECAG00000016384	RORA	RAR related orphan receptor A	-1,47739	3,4E-08
907.	ENSECAG00000009262	PTGDS	prostaglandin D2 synthase	-1,47848	0,00293
908.	ENSECAG00000013242	ABCA3	ATP binding cassette subfamily A member 3	-1,47957	2,4E-30
909.	ENSECAG00000010436	ENSECAG00000010436	protein BEX1	-1,48086	9,3E-06
910.	ENSECAG00000016047	CPA6	carboxypeptidase A6	-1,48557	7,5E-24
911.	ENSECAG00000012993	JAG1	jagged canonical Notch ligand 1	-1,48657	7E-06
912.	ENSECAG00000032719	ENSECAG00000032719		-1,50159	5E-05
913.	ENSECAG00000006419	C2CD2	C2 Calcium Dependent Domain Containing 2	-1,50167	4,2E-34
914.	ENSECAG00000011358	TMEM86A	transmembrane protein 86A	-1,50249	8,3E-07
915.	ENSECAG00000002211	CD80	CD80 molecule	-1,50467	0,00567
916.	ENSECAG00000000931	TMEM119	transmembrane protein 119	-1,50533	3,6E-27
917.	ENSECAG00000007989	C1QTNF7	C1q and TNF related 7	-1,50846	0,00256
918.	ENSECAG00000006546	ZNF521	zinc finger protein 521	-1,5088	1,3E-18
919.	ENSECAG00000019411	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	-1,50955	3,6E-27
920.	ENSECAG00000011797	SOD2	Superoxide Dismutase 2	-1,50999	0,00025
921.	ENSECAG00000015510	FGF7	fibroblast growth factor 7	-1,51028	0,00021
922.	ENSECAG00000042911	ENSECAG00000042911		-1,51285	0,01829
923.	ENSECAG00000005697	HTR1D	5-hydroxytryptamine receptor 1D	-1,51385	0,01958
924.	ENSECAG00000016559	TNFSF11	TNF superfamily member 11	-1,51947	7,1E-07
925.	ENSECAG00000009618	IFI44L	interferon induced protein 44 like	-1,52591	2,4E-15
926.	ENSECAG00000017346	GCLC	glutamate-cysteine ligase catalytic subunit	-1,52758	1,9E-30
927.	ENSECAG00000027518	ENSECAG00000027518	small nucleolar RNA U109	-1,5291	0,00907
928.	ENSECAG00000015865	GLUL	glutamate-ammonia ligase	-1,53024	1,4E-10
929.	ENSECAG00000017943	ZNF608	zinc finger protein 608	-1,53442	2,5E-08
930.	ENSECAG00000023259	NUDT17	nudix hydrolase 17	-1,53905	0,01337
931.	ENSECAG00000002579	MATN2	matrilin 2	-1,5426	3,2E-13
932.	ENSECAG00000021903	LAMC2	laminin subunit gamma 2	-1,54669	2,2E-29
933.	ENSECAG00000005360	MITF	melanocyte inducing transcription factor	-1,54777	1,3E-32
934.	ENSECAG00000040252	HMGA2	high mobility group AT-hook 2	-1,55177	0,00098
935.	ENSECAG00000017459	ARRB1	arrestin beta 1	-1,55393	4,1E-09
936.	ENSECAG00000014870	CPNE8	copine 8	-1,55601	9E-09
937.	ENSECAG00000028399	DTX1	deltex E3 ubiquitin ligase 1	-1,56689	0,0443
938.	ENSECAG00000010553	NGF	nerve growth factor	-1,57331	6E-10

939.	ENSECAG00000025076	CTTNBP2	cortactin binding protein 2	-1,57744	2,4E-18
940.	ENSECAG00000007542	SH3D19	SH3 domain containing 19	-1,58153	5,2E-56
941.	ENSECAG00000041716	ENSECAG00000041716		-1,58166	0,00455
942.	ENSECAG00000013677	FRY	FRY microtubule binding protein	-1,58258	7,3E-28
943.	ENSECAG00000018359	COL13A1	collagen type XIII alpha 1 chain	-1,583	0,01309
944.	ENSECAG00000016430	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	-1,58425	0,00044
945.	ENSECAG00000021973	NFE2L3	NFE2 like bZIP transcription factor 3	-1,58746	0,01554
946.	ENSECAG00000015845	PLD5	phospholipase D family member 5	-1,58779	1,2E-07
947.	ENSECAG00000007047	ASPN	Asporin	-1,59377	0,00048
948.	ENSECAG00000022071	OTUD7A	OTU Deubiquitinase 7A	-1,59978	0,0187
949.	ENSECAG00000018803	PGM2L1	phosphoglucomutase 2 like 1	-1,60338	3E-12
950.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-1,60426	4,7E-06
951.	ENSECAG00000017701	CELSR2	Cadherin EGF LAG Seven-Pass G-Type Receptor 2	-1,60844	1,7E-07
952.	ENSECAG00000018916	FILIP1	Filamin A Interacting Protein 1	-1,60863	0,01283
953.	ENSECAG00000019137	MAML3	mastermind like transcriptional coactivator 3	-1,61055	5E-08
954.	ENSECAG00000012282	MPP7	MAGUK p55 scaffold protein 7	-1,61183	0,00171
955.	ENSECAG00000010405	TRIB2	tribbles pseudokinase 2	-1,61479	2,6E-14
956.	ENSECAG00000040326	ENSECAG00000040326		-1,61576	0,00267
957.	ENSECAG00000010109	IGF1	insulin like growth factor 1	-1,6209	5,3E-06
958.	ENSECAG00000018280	TACC2	transforming acidic coiled-coil containing protein 2	-1,62255	1,2E-40
959.	ENSECAG00000023958	ADPRH	ADP-ribosylarginine hydrolase	-1,62441	7,2E-33
960.	ENSECAG00000015669	RAB3B	RAB3B, member RAS oncogene family	-1,62725	0,00129
961.	ENSECAG00000007718	TMOD1	Tropomodulin 1	-1,62847	2,8E-34
962.	ENSECAG00000016349	GLIS1	GLIS Family Zinc Finger 1	-1,62925	4,3E-14
963.	ENSECAG00000017186	SLFN5	schlafen family member 5	-1,63207	7,2E-05
964.	ENSECAG00000009020	IFI44	interferon induced protein 44	-1,64041	1,5E-26
965.	ENSECAG00000008809	OAS3	2'-5'-oligoadenylate synthetase 3	-1,64159	2,7E-32
966.	ENSECAG00000008425	LURAP1L	leucine rich adaptor protein 1 like	-1,64302	2E-12
967.	ENSECAG00000014422	OAS2	2'-5'-oligoadenylate synthetase 2	-1,65079	5,5E-68
968.	ENSECAG00000024570	BRINP2	BMP/retinoic acid inducible neural specific 2	-1,65177	2E-14
969.	ENSECAG00000022981	PLEKHN1	Pleckstrin Homology Domain Containing N1	-1,65366	0,019
970.	ENSECAG00000014194	EGFLAM	EGF Like, Fibronectin Type III And Laminin G Domains	-1,6552	0,01175
971.	ENSECAG00000018105	IL4I1	interleukin 4 induced 1	-1,65575	0,00134
972.	ENSECAG00000013079	USP54	ubiquitin specific peptidase 54	-1,65904	1,4E-45
973.	ENSECAG00000013081	MMP9	Matrix Metallopeptidase 9	-1,66732	2,3E-19
974.	ENSECAG00000011111	FMNL2	formin like 2	-1,66964	2,1E-20
975.	ENSECAG00000007183	SEMA3E	semaphorin 3E	-1,67148	0,03476
976.	ENSECAG00000011854	CFB	complement factor B	-1,67877	4,2E-20
977.	ENSECAG00000017907	RNFT2	Ring Finger Protein, Transmembrane 2	-1,6811	0,03513
978.	ENSECAG00000008094	BCL11A	BCL11 transcription factor A	-1,68232	0,01099
979.	ENSECAG00000030878	ENSECAG00000030878	Scm polycomb group protein like 1	-1,68473	0,00465
980.	ENSECAG00000015023	FAM184A	family with sequence similarity 184 member A	-1,68725	1,3E-18
981.	ENSECAG00000042466	AMTN	amelotin	-1,69442	0,00188
982.	ENSECAG00000024358	ZBTB16	zinc finger and BTB domain containing 16	-1,70176	0,01109
983.	ENSECAG00000000420	BANP	BTG3 associated nuclear protein	-1,70787	9,5E-23
984.	ENSECAG00000000343	HACD4	3-hydroxyacyl-CoA dehydratase 4	-1,70938	2,7E-05
985.	ENSECAG00000019193	NCAM1	neural cell adhesion molecule 1	-1,713	2,6E-45
986.	ENSECAG00000026894	CIDEA	Cell Death Inducing DFFA Like Effector A	-1,71598	0,00225

987.	ENSECAG00000012071	TCP11	t-complex 11	-1,7191	0,0409
988.	ENSECAG00000012105	IGSF9B	immunoglobulin superfamily member 9B	-1,72141	0,01702
989.	ENSECAG00000002165	ENSECAG00000002165	uncharacterized protein CXorf21	-1,73568	0,02109
990.	ENSECAG00000010814	ENSECAG00000010814	embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	-1,74503	3,8E-07
991.	ENSECAG00000001279	AGTR1	angiotensin II receptor type 1	-1,7456	0,01519
992.	ENSECAG00000004445	PDE11A	phosphodiesterase 11A	-1,75039	5,5E-23
993.	ENSECAG00000016824	NRP2	neuropilin 2	-1,75524	4,1E-47
994.	ENSECAG00000009948	ADCY5	adenylate cyclase 5	-1,75782	2,8E-18
995.	ENSECAG00000014398	ENSECAG00000014398		-1,76818	0,03197
996.	ENSECAG00000026856	AIF1L	allograft inflammatory factor 1 like	-1,77325	1,5E-09
997.	ENSECAG00000019499	ISG20	Interferon Stimulated Exonuclease Gene 20	-1,78215	1,9E-07
998.	ENSECAG00000015379	FGD4	FYVE, RhoGEF And PH Domain Containing 4	-1,79933	8,1E-13
999.	ENSECAG00000016721	RUBCNL	rubicon like autophagy enhancer	-1,80016	2E-14
1000.	ENSECAG00000017844	OXTR	Oxytocin Receptor	-1,80102	7,7E-24
1001.	ENSECAG00000012539	RASGRP3	RAS guanyl releasing protein 3	-1,80869	0,04955
1002.	ENSECAG00000007385	NIBAN1	niban apoptosis regulator 1	-1,81437	1,8E-41
1003.	ENSECAG00000041748	COL4A3	collagen type IV alpha 3 chain	-1,81533	9,9E-07
1004.	ENSECAG00000036801	ABCC9	ATP-binding cassette sub-family C member 9	-1,81632	0,03004
1005.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	-1,81873	7,9E-44
1006.	ENSECAG00000024715	FIBCD1	fibrinogen C domain containing 1	-1,81933	0,03482
1007.	ENSECAG00000034320	ENSECAG00000034320		-1,82513	0,03493
1008.	ENSECAG00000024757	ENSECAG00000024757	neuronal acetylcholine receptor subunit alpha-7	-1,82624	8,3E-09
1009.	ENSECAG00000023088	BMF	Bcl2 Modifying Factor	-1,8287	0,00201
1010.	ENSECAG00000000650	NPL	N-Acetylneuraminate Pyruvate Lyase	-1,84077	2,3E-68
1011.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-1,84318	6E-33
1012.	ENSECAG00000007881	IFIH1	Interferon Induced With Helicase C Domain 1	-1,84622	6E-23
1013.	ENSECAG00000017937	ENSECAG00000017937		-1,84873	3,8E-10
1014.	ENSECAG00000001481	SAMD9L	sterile alpha motif domain containing 9 like	-1,84906	4E-14
1015.	ENSECAG00000010747	SH3BGR	SH3 domain binding glutamate rich protein	-1,85003	1,2E-17
1016.	ENSECAG00000023765	IGSF9	immunoglobulin superfamily member 9	-1,85129	5,2E-05
1017.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	-1,85167	2,2E-15
1018.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-1,85561	2,5E-18
1019.	ENSECAG00000017743	SESN3	Sestrin 3	-1,85821	4,8E-27
1020.	ENSECAG00000000666	CEP126	centrosomal protein 126	-1,85899	0,03134
1021.	ENSECAG00000011898	SPEF2	sperm flagellar 2	-1,8594	2,4E-10
1022.	ENSECAG00000024011	ADGRF4	adhesion G protein-coupled receptor F4	-1,86064	0,00074
1023.	ENSECAG00000021078	GRB14	growth factor receptor bound protein 14	-1,86675	2,7E-06
1024.	ENSECAG00000032483	GPR85	G protein-coupled receptor 85	-1,87037	4,5E-07
1025.	ENSECAG00000014962	FAXDC2	Fatty Acid Hydroxylase Domain Containing 2	-1,87322	1,1E-10
1026.	ENSECAG00000022823	PLCE1	phospholipase C epsilon 1	-1,87444	7,9E-28
1027.	ENSECAG00000000284	USP18	Ubiquitin Specific Peptidase 18	-1,87478	1,1E-13
1028.	ENSECAG00000000593	PTN	pleiotrophin	-1,88252	5,2E-53
1029.	ENSECAG00000023892	RPS6KA5	ribosomal protein S6 kinase A5	-1,88284	8E-27
1030.	ENSECAG00000000530	EPHA5	EPH receptor A5	-1,88473	0,03659
1031.	ENSECAG00000015745	BLNK	B cell linker	-1,88829	2,1E-31
1032.	ENSECAG00000011887	ADAMTSL2	ADAMTS like 2	-1,89262	7,3E-07
1033.	ENSECAG00000006796	ZSCAN26	Zinc Finger And SCAN Domain Containing 26	-1,89542	6,2E-05

1034.	ENSECAG00000010908	CCDC30	Coiled-Coil Domain Containing 30	-1,89544	0,0104
1035.	ENSECAG00000012889	TMEM108	transmembrane protein 108	-1,9056	0,00058
1036.	ENSECAG00000013376	ENSECAG00000013376	transcription elongation factor A like 2	-1,91934	0,03233
1037.	ENSECAG00000033624	ENSECAG00000033624	contactin-associated protein- like 4	-1,92704	0,00201
1038.	ENSECAG00000012060	MYO3A	myosin IIIA	-1,92797	2,3E-05
1039.	ENSECAG00000012773	CMPK2	cytidine/uridine monophosphate kinase 2	-1,93193	4,1E-13
1040.	ENSECAG00000015000	FAM83G	Family With Sequence Similarity 83 Member G	-1,93635	1,8E-26
1041.	ENSECAG00000017357	DPP4	dipeptidyl peptidase 4	-1,94318	0,00426
1042.	ENSECAG00000009699	DNAH7	dynein axonemal heavy chain 7	-1,9528	0,01356
1043.	ENSECAG00000019940	AKAP6	A-kinase anchoring protein 6	-1,95281	3,9E-18
1044.	ENSECAG00000009218	EGFL6	EGF like domain multiple 6	-1,95953	9,8E-06
1045.	ENSECAG00000015760	ITGA3	integrin subunit alpha 3	-1,95976	2,3E-70
1046.	ENSECAG00000024062	DDX60L	DEAD/H-box 60 like	-1,96613	2,9E-56
1047.	ENSECAG00000010939	ANGPTL1	angiopoietin like 1	-1,96844	6,9E-08
1048.	ENSECAG00000009211	ANGPT4	angiopoietin 4	-1,97377	3,5E-08
1049.	ENSECAG00000015736	ODAPH	odontogenesis associated phosphoprotein	-1,97646	0,00017
1050.	ENSECAG00000017689	ARHGEF28	Rho Guanine Nucleotide Exchange Factor 28	-1,9826	4,9E-43
1051.	ENSECAG00000010880	SOX6	SRY-box transcription factor 6	-1,98769	0,00013
1052.	ENSECAG00000029347	ADAMTS6	centromere protein K	-1,98769	1,4E-32
1053.	ENSECAG00000020311	BCO2	beta-carotene oxygenase 2	-1,99009	9,1E-07
1054.	ENSECAG00000013036	MCAM	melanoma cell adhesion molecule	-1,99588	8,1E-14
1055.	ENSECAG00000022638	PLD1	phospholipase D1	-2,00573	4,5E-18
1056.	ENSECAG00000018716	FGF9	fibroblast growth factor 9	-2,01715	1,3E-32
1057.	ENSECAG00000010881	DPYD	dihydropyrimidine dehydrogenase	-2,0188	2,5E-21
1058.	ENSECAG00000021363	DEPTOR	DEP domain containing MTOR interacting protein	-2,03483	0,00988
1059.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-2,03827	8,7E-07
1060.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-2,03885	5,9E-07
1061.	ENSECAG00000014730	PELI3	pellino E3 ubiquitin protein ligase family member 3	-2,04196	0,00049
1062.	ENSECAG00000022556	ABCA9	ATP binding cassette subfamily A member 9	-2,05125	9E-61
1063.	ENSECAG00000020045	HAPLN4	hyaluronan and proteoglycan link protein 4	-2,05133	5,3E-20
1064.	ENSECAG00000013170	JADE2	jade family PHD finger 2	-2,05423	8E-19
1065.	ENSECAG00000014519	ETV7	ETS variant transcription factor 7	-2,06144	9,9E-10
1066.	ENSECAG00000022329	LRRC4C	leucine rich repeat containing 4C	-2,06315	0,01829
1067.	ENSECAG00000000121	NAV3	neuron navigator 3	-2,07746	1,7E-28
1068.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-2,07754	4,6E-15
1069.	ENSECAG00000003230	AKAP5	A-kinase anchoring protein 5	-2,07881	9,3E-13
1070.	ENSECAG00000008087	ENSECAG00000008087	stabilizer of axonemal microtubules 2	-2,0834	0,00022
1071.	ENSECAG00000013138	RAB27B	RAB27B, member RAS oncogene family	-2,08368	0,00085
1072.	ENSECAG00000013390	ZMAT1	zinc finger matrin-type 1	-2,08634	0,00107
1073.	ENSECAG000000009949	P2RX7	purinergic receptor P2X 7	-2,08882	8,9E-10
1074.	ENSECAG00000000170	MACROD2	Mono-ADP Ribosylhydrolase 2	-2,08988	0,02899
1075.	ENSECAG00000005701	LINGO1	leucine rich repeat and Ig domain containing 1	-2,09819	0,01287
1076.	ENSECAG00000004274	IQGAP2	IQ motif containing GTPase activating protein 2	-2,09893	8,5E-05
1077.	ENSECAG00000019495	C5H1orf141	chromosome 5 C1orf141 homolog	-2,10259	0,00014
1078.	ENSECAG00000011776	MX1	MX dynamin like GTPase 1	-2,10707	7,1E-90
1079.	ENSECAG00000021468	POPCD2	popeye domain containing 2	-2,11031	0,00521

1080.	ENSECAG00000011467	ALPL	alkaline phosphatase, biomineralization associated	-2,1145	3,4E-09
1081.	ENSECAG00000017454	KIAA1755	KIAA1755	-2,11928	4,4E-05
1082.	ENSECAG00000000634	SMPDL3B	Sphingomyelin Phosphodiesterase Acid Like 3B	-2,11931	0,04715
1083.	ENSECAG00000004778	RTN4R	reticulon 4 receptor	-2,12975	0,03889
1084.	ENSECAG00000015388	EDIL3	EGF like repeats and discoidin domains 3	-2,1316	3,7E-14
1085.	ENSECAG00000012507	CRYAB	Crystallin Alpha B	-2,14763	2,6E-36
1086.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-2,15571	8,1E-10
1087.	ENSECAG00000010721	MGP	Matrix Gla Protein	-2,15797	2,1E-37
1088.	ENSECAG00000023963	NMNAT2	Nicotinamide Nucleotide Adenylyltransferase 2	-2,15867	3,4E-45
1089.	ENSECAG00000016735	VCAM1	Vascular Cell Adhesion Molecule 1	-2,16113	0,00131
1090.	ENSECAG00000033029	ENSECAG00000033029	interferon-induced protein with tetratricopeptide repeats 1B	-2,16206	5,4E-19
1091.	ENSECAG00000028632	ENSECAG00000028632		-2,16847	7,3E-10
1092.	ENSECAG00000008518	NPNT	nephronectin	-2,16879	8,4E-05
1093.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-2,17862	4,3E-26
1094.	ENSECAG00000015552	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-2,18405	3,9E-07
1095.	ENSECAG00000009192	SRGN	Serglycin	-2,20419	5,3E-08
1096.	ENSECAG00000039231	ATOH8	atonal bHLH transcription factor 8	-2,21431	0,02322
1097.	ENSECAG00000015952	BDNF	brain derived neurotrophic factor	-2,21653	8E-12
1098.	ENSECAG00000034190	ENSECAG00000034190		-2,22412	0,0009
1099.	ENSECAG00000008560	LRRC56	leucine rich repeat containing 56	-2,22966	0,03004
1100.	ENSECAG00000040468	ENSECAG00000040468		-2,23442	6,6E-10
1101.	ENSECAG00000016984	RANBP3L	RAN binding protein 3 like	-2,23617	0,00109
1102.	ENSECAG00000016957	OLFM1	olfactomedin 1	-2,244	2,6E-38
1103.	ENSECAG00000013486	C4BPA	complement component 4 binding protein alpha	-2,24811	2,4E-15
1104.	ENSECAG00000008221	S100A4	S100 calcium binding protein A4	-2,25822	3,7E-54
1105.	ENSECAG00000011404	ENSECAG00000011404	serum amyloid A protein	-2,26152	3,3E-10
1106.	ENSECAG00000019717	ECM2	extracellular matrix protein 2	-2,2625	2E-31
1107.	ENSECAG00000021844	CALML4	calmodulin like 4	-2,26991	0,02527
1108.	ENSECAG00000034367	ENSECAG00000034367		-2,28281	4,8E-08
1109.	ENSECAG00000010185	IFIT2	Interferon Induced Protein With Tetratricopeptide Repeats 2	-2,28844	3,7E-20
1110.	ENSECAG00000021274	COL4A6	collagen type IV alpha 6 chain	-2,28955	0,01553
1111.	ENSECAG00000012032	KIT	KIT proto-oncogene, receptor tyrosine kinase	-2,29043	0,02386
1112.	ENSECAG00000021174	ACKR4	atypical chemokine receptor 4	-2,30078	8,6E-17
1113.	ENSECAG00000010830	MMP11		-2,30598	1,3E-10
1114.	ENSECAG00000020835	ADAMTS20	ADAM metalloproteinase with thrombospondin type 1 motif 20	-2,30771	9,5E-27
1115.	ENSECAG00000013634	BNIP5	BCL2 Interacting Protein 5	-2,31139	0,02364
1116.	ENSECAG00000000740	C10H6orf58		-2,31534	0,00018
1117.	ENSECAG00000015834	DMD	dystrophin	-2,3337	3,3E-18
1118.	ENSECAG00000012686	SNCAIP	synuclein alpha interacting protein	-2,33843	0,002
1119.	ENSECAG00000030850	FGF18	Fibroblast Growth Factor 18	-2,34196	7,7E-14
1120.	ENSECAG00000006482	CRISP2	Cysteine Rich Secretory Protein 2	-2,3477	1,6E-06
1121.	ENSECAG00000024961	XAF1	XIAP Associated Factor 1	-2,35765	1E-22
1122.	ENSECAG00000019087	CTSK	Cathepsin K	-2,36703	1E-112
1123.	ENSECAG00000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-2,37481	7,9E-05
1124.	ENSECAG00000018016	FAR2	fatty acyl-CoA reductase 2	-2,37707	0,00345
1125.	ENSECAG0000001488	GPR171	G protein-coupled receptor 171	-2,38457	4,2E-20

1126.	ENSECAG00000016784	TDH	L-threonine dehydrogenase	-2,38911	2,5E-06
1127.	ENSECAG00000017443	TRIM14	tripartite motif containing 14	-2,38961	4,2E-06
1128.	ENSECAG00000016234	ANGPTL2	angiopoietin like 2	-2,39288	2,6E-44
1129.	ENSECAG00000030788	DIO2	iodothyronine deiodinase 2	-2,4323	3,8E-08
1130.	ENSECAG00000003266	PIRT	phosphoinositide interacting regulator of transient receptor potential channels	-2,43276	3,9E-06
1131.	ENSECAG00000020093	NPR3	natriuretic peptide receptor 3	-2,45642	1,2E-07
1132.	ENSECAG00000024959	FBXO39	F-box protein 39	-2,45716	4,7E-05
1133.	ENSECAG00000015569	MATCAP2	microtubule associated tyrosine carboxypeptidase 2	-2,46596	2,9E-05
1134.	ENSECAG00000018049	PAMR1	peptidase domain containing associated with muscle regeneration 1	-2,46721	4,4E-25
1135.	ENSECAG00000029465	CHI3L1	chitinase 3 like 1	-2,4735	0,00015
1136.	ENSECAG00000034457	U1	U1 spliceosomal RNA	-2,48452	0,0249
1137.	ENSECAG00000022844	ENSECAG00000022844	tyrosine-protein phosphatase non-receptor type 11	-2,48629	0,00604
1138.	ENSECAG00000012212	LRP1B	LDL Receptor Related Protein 1	-2,4944	1,6E-18
1139.	ENSECAG00000037214	TUBB4A	tubulin beta 4A class IVa	-2,5019	1,2E-30
1140.	ENSECAG00000022047	APOD	apolipoprotein D	-2,5296	8E-22
1141.	ENSECAG00000021165	STAC	SH3 and cysteine rich domain	-2,53375	2,9E-33
1142.	ENSECAG00000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-2,53915	5,6E-93
1143.	ENSECAG00000010869	CAPN6	calpain 6	-2,54799	9E-08
1144.	ENSECAG00000017460	ATP12A	ATPase H+/K+ Transporting Non-Gastric Alpha2 Subunit	-2,54977	0,01754
1145.	ENSECAG00000000324	RASEF	RAS and EF-hand domain containing	-2,553	0,00054
1146.	ENSECAG00000013739	DLGAP1	DLG associated protein 1	-2,56065	1,4E-15
1147.	ENSECAG00000020198	NOTUM	notum, palmitoleoyl-protein carboxylesterase	-2,57079	0,00559
1148.	ENSECAG00000023161	IGSF10	immunoglobulin superfamily member 10	-2,57124	7,6E-34
1149.	ENSECAG00000017924	KCNG1	potassium voltage-gated channel modifier subfamily G member 1	-2,57995	0,01398
1150.	ENSECAG00000008418	RHCG	Rh family C glycoprotein	-2,58692	0,00564
1151.	ENSECAG00000004433	ENSECAG00000004433	interferon-induced protein with tetratricopeptide repeats 1	-2,59127	2,4E-14
1152.	ENSECAG00000018108	VGF	VGF nerve growth factor inducible	-2,59234	3,3E-09
1153.	ENSECAG00000002430	PRKAG3	protein kinase AMP-activated non-catalytic subunit gamma 3	-2,61271	7E-05
1154.	ENSECAG00000038712	TNXB	tenascin XB	-2,63933	2,1E-11
1155.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-2,66159	7,9E-11
1156.	ENSECAG000000041924	COL23A1	collagen type XXIII alpha 1 chain	-2,66191	2,8E-12
1157.	ENSECAG00000032492	ENSECAG00000032492	probable ATP-dependent RNA helicase DDX60	-2,66204	0,00422
1158.	ENSECAG00000012253	CXCL11	C-X-C motif chemokine ligand 11	-2,6682	0,00426
1159.	ENSECAG00000017988	FRMD7	FERM Domain Containing 7	-2,67055	0,00356
1160.	ENSECAG00000024873	CCDC190	Coiled-Coil Domain Containing 190	-2,6743	3,8E-06
1161.	ENSECAG00000006853	UBD	ubiquitin D	-2,68237	4,2E-07
1162.	ENSECAG00000006176	CNTFR	Ciliary Neurotrophic Factor Receptor	-2,68539	0,00575
1163.	ENSECAG00000018004	CA8	carbonic anhydrase 8	-2,68909	0,00366
1164.	ENSECAG00000012990	CALCRL	calcitonin receptor like receptor	-2,69947	3,1E-16
1165.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-2,70462	3,2E-38
1166.	ENSECAG00000037655	GDNF	glial cell derived neurotrophic factor	-2,7063	0,0078
1167.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-2,73344	2,6E-16
1168.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-2,73883	1,1E-22
1169.	ENSECAG00000006511	MCHR1	melanin concentrating hormone receptor 1	-2,74329	0,02154

1170.	ENSECAG00000023039	CCN3	cellular communication network factor 3	-2,74634	8,6E-19
1171.	ENSECAG00000013758	ENSECAG00000013758		-2,75904	1,6E-05
1172.	ENSECAG00000020494	B3GALT2	beta-1,3-galactosyltransferase 2	-2,7613	1,8E-05
1173.	ENSECAG00000031578	ENSECAG00000031578		-2,78235	0,00702
1174.	ENSECAG00000023361	RHPN1	Rhopilin Rho GTPase Binding Protein 1	-2,81713	0,00942
1175.	ENSECAG00000010128	SEMA4D	semaphorin 4D	-2,83325	2,8E-12
1176.	ENSECAG00000015846	VASH2	vasohibin 2	-2,83576	4,1E-30
1177.	ENSECAG00000038866	PTX3	pentraxin 3	-2,85126	8,7E-09
1178.	ENSECAG00000021586	FBP1	fructose-bisphosphatase 1	-2,90546	0,00694
1179.	ENSECAG00000039579	GDF15	growth differentiation factor 15	-2,92057	7,4E-06
1180.	ENSECAG00000021101	LG14	Leucine Rich Repeat LGI Family Member 4	-2,92198	0,00102
1181.	ENSECAG00000017816	ADORA1	adenosine A1 receptor	-2,95523	1,7E-21
1182.	ENSECAG00000012109	SOSTDC1	sclerostin domain containing 1	-3,00429	1,3E-15
1183.	ENSECAG00000023264	RTP4	Receptor Transporter Protein 4	-3,00873	1,7E-09
1184.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-3,00983	1,3E-08
1185.	ENSECAG00000016251	ENSECAG00000016251		-3,01081	3,1E-11
1186.	ENSECAG00000016176	NDP	norrin cystine knot growth factor NDP	-3,01274	0,0012
1187.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-3,01423	1,6E-81
1188.	ENSECAG00000017280	MAPK10	mitogen-activated protein kinase 10	-3,02469	0,00028
1189.	ENSECAG00000004501	FDCSP	follicular dendritic cell secreted protein	-3,04927	7,2E-10
1190.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-3,0583	2E-103
1191.	ENSECAG00000017802	OGN	osteoglycin	-3,05902	4,9E-61
1192.	ENSECAG00000032728	HBQ1	Hemoglobin Subunit Theta 1	-3,06441	3,9E-09
1193.	ENSECAG00000016015	PCDH19	protocadherin 19	-3,08563	7,8E-52
1194.	ENSECAG00000006717	ASS1	argininosuccinate synthase 1	-3,16782	7,2E-22
1195.	ENSECAG00000016639	ADAD1	adenosine deaminase domain containing 1	-3,17221	0,00118
1196.	ENSECAG00000020901	CLCA2	chloride channel accessory 2	-3,19461	2,4E-06
1197.	ENSECAG00000017843	ENSECAG00000017843	calcium-activated chloride channel regulator 4	-3,20526	0,00111
1198.	ENSECAG00000009483	PRLR	prolactin receptor	-3,20885	1,7E-27
1199.	ENSECAG00000040154	ELN	elastin	-3,22778	0,00021
1200.	ENSECAG00000014287	OMD	osteomodulin	-3,25315	4,3E-24
1201.	ENSECAG00000018308	GREB1	growth regulating estrogen receptor binding 1	-3,28214	5,3E-32
1202.	ENSECAG00000021576	SGCG	sarcoglycan gamma	-3,32277	0,00309
1203.	ENSECAG00000024028	PDE6A	phosphodiesterase 6A	-3,3589	5,6E-06
1204.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-3,35947	2,8E-21
1205.	ENSECAG00000024612	SNED1	Sushi, Nidogen And EGF Like Domains 1	-3,36079	4,6E-08
1206.	ENSECAG00000010791	LMCD1	LIM and cysteine rich domains 1	-3,37924	2,1E-11
1207.	ENSECAG00000003067	PWWP3B	PWWP domain containing 3B	-3,39793	0,00216
1208.	ENSECAG00000022629	SLC1A7	Solute Carrier Family 1 Member 7	-3,42017	6,3E-69
1209.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-3,42625	6,8E-16
1210.	ENSECAG00000015484	ATP6V0D2	ATPase H+ transporting V0 subunit d2	-3,43647	1,6E-73
1211.	ENSECAG00000019805	WSCD2	WSC domain containing 2	-3,46366	1,3E-05
1212.	ENSECAG00000009138	MME	membrane metalloendopeptidase	-3,49407	2E-34
1213.	ENSECAG00000023720	SLAMF8	SLAM family member 8	-3,50924	0,00816
1214.	ENSECAG00000014513	TNFSF15	TNF superfamily member 15	-3,58379	1,2E-15
1215.	ENSECAG00000035060	ENSECAG00000035060	calcium-activated chloride channel regulator 4	-3,65636	0,00097
1216.	ENSECAG00000000813	SCN5A	sodium voltage-gated channel alpha subunit 5	-3,68448	1,7E-16
1217.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-3,77462	1,8E-14
1218.	ENSECAG00000031859	ENSECAG00000031859		-3,85529	1,9E-17

1219.	ENSECAG00000009742	S100A12	S100 Calcium Binding Protein A12	-3,98497	2E-07
1220.	ENSECAG00000005126	TRIM22	tripartite motif containing 22	-4,11889	1,7E-17
1221.	ENSECAG00000034702	DEFB1	defensin beta 1	-4,17921	1,5E-06
1222.	ENSECAG00000034955	BHLHE41	basic helix-loop-helix family member e41	-4,20435	1,3E-32
1223.	ENSECAG00000029885	CHST7	carbohydrate sulfotransferase 7	-4,20869	1,8E-66
1224.	ENSECAG00000021534	ASPA	aspartoacylase	-4,3243	5,9E-09
1225.	ENSECAG00000023157	GDPD4	glycerophosphodiester phosphodiesterase domain containing 4	-4,78707	0,00011
1226.	ENSECAG00000012667	RBFOX1	RNA Binding Fox-1 Homolog 1	-4,94492	7,2E-22
1227.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-5,28621	2,9E-56
1228.	ENSECAG00000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-5,4994	4,9E-21

Supplementary Table 7. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category IIB endometria treated with interleukin 4 (IL-4) for 48 hours (Research task 3, Experiment 1).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	Padj
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	15,8087	7E-72
2.	ENSECAG00000013482	SERPINA3	Serpin Family A Member 3	9,65986	1E-54
3.	ENSECAG00000011581	ENSECAG00000011581		9,28008	2E-40
4.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	9,14626	3E-27
5.	ENSECAG00000020578	PDCD1LG2	Programmed Cell Death 1 Ligand 2	9,02259	2E-37
6.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	8,81458	2E-18
7.	ENSECAG00000000706	MEGF11	multiple EGF like domains 11	8,65298	8E-18
8.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	8,63059	6E-35
9.	ENSECAG00000016867	CISH	Cytokine Inducible SH2 Containing Protein	8,5223	1E-18
10.	ENSECAG00000015516	APBA2	amyloid beta precursor protein binding family A member 2	7,96949	3E-15
11.	ENSECAG00000038698	ALOX15	Arachidonate 15-Lipoxygenase	7,96679	3E-38
12.	ENSECAG00000020738	CDH26	cadherin 26	7,73678	4E-174
13.	ENSECAG00000014650	INSRR	insulin receptor related receptor	7,5396	2E-37
14.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	7,47597	4E-25
15.	ENSECAG00000023918	DUOX1	dual oxidase 1	7,43393	3E-12
16.	ENSECAG00000016312	CD274	CD274 molecule	7,3459	4E-25
17.	ENSECAG00000018409	NOX5	NADPH oxidase 5	7,31854	6E-09
18.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	6,81483	2E-13
19.	ENSECAG00000034282	CCL8	C-C motif chemokine 7	6,79425	5E-117
20.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	6,63019	1E-37
21.	ENSECAG00000002249	PLEKHG4B	Pleckstrin Homology And RhoGEF Domain Containing G4B	6,58517	4E-11
22.	ENSECAG00000017764	DUOX2	dual oxidase 2	6,55139	3E-09
23.	ENSECAG000000004201	FETUB	fetuin B	6,34196	2E-23
24.	ENSECAG00000016169	COL6A6	collagen type VI alpha 6 chain	6,09909	0,0001
25.	ENSECAG00000035561	ENSECAG00000035561	ubiquitin conjugating enzyme E2 Q family like 1	6,00716	1E-14
26.	ENSECAG00000023032	AZIN2	Antizyme Inhibitor 2	5,907	5E-58
27.	ENSECAG00000005379	HPGD	15-Hydroxyprostaglandin Dehydrogenase	5,85331	5E-108
28.	ENSECAG00000009034	DUOXA1	dual oxidase maturation factor 1	5,56099	9E-08
29.	ENSECAG00000023841	POSTN	periostin	5,40807	5E-33
30.	ENSECAG00000005241	THBD	thrombomodulin	5,29855	2E-186
31.	ENSECAG00000014916	TNFRSF11B	TNF receptor superfamily member 11b	5,17302	4E-22
32.	ENSECAG00000026965	SOCS1	suppressor of cytokine signaling 1	5,15591	1E-63
33.	ENSECAG00000032667	INA	Interneixin Neuronal Intermediate Filament Protein Alpha	5,14445	5E-09
34.	ENSECAG00000009767	P2RX1	purinergic receptor P2X 1	5,1094	2E-12
35.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	5,00691	2E-211
36.	ENSECAG00000017896	PDLIM3	PDZ and LIM domain 3	4,95338	9E-16
37.	ENSECAG00000023942	ENSECAG00000023942	ras GTPase-activating protein 4	4,92482	2E-113
38.	ENSECAG00000007825	CALCA	calcitonin-related polypeptide alpha	4,8674	3E-14
39.	ENSECAG000000021182	TNFSF4	TNF superfamily member 4	4,81169	3E-09
40.	ENSECAG00000000152	KITLG	KIT ligand	4,80889	6E-50
41.	ENSECAG00000013703	PPP1R3C	Protein Phosphatase 1 Regulatory Subunit 3C	4,79351	2E-59
42.	ENSECAG00000010048	IGSF11	immunoglobulin superfamily member 11	4,74232	1E-05
43.	ENSECAG00000009916	GRIA4	glutamate ionotropic receptor AMPA type subunit 4	4,72888	7E-06
44.	ENSECAG00000018734	GSG1L	GSG1 like	4,72308	0,0008
45.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	4,60621	5E-40
46.	ENSECAG00000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	4,55714	4E-19
47.	ENSECAG00000015842	ANKRD55	ankyrin repeat domain 55	4,4448	3E-19
48.	ENSECAG00000022686	MRAP2	melanocortin 2 receptor accessory protein 2	4,34222	3E-05
49.	ENSECAG00000019800	TSPAN33	Tetraspanin 33	4,33753	1E-89
50.	ENSECAG00000011897	CHRD12	chordin like 2	4,29348	3E-07

51.	ENSECAG00000021604	PDGFRL	platelet derived growth factor receptor like	4,24361	1E-80
52.	ENSECAG00000012830	CHN2	Chimerin 2	4,16901	2E-81
53.	ENSECAG000000008739	ENSECAG000000008739		4,07773	8E-16
54.	ENSECAG000000005307	RNF183	ring finger protein 183	4,05491	5E-30
55.	ENSECAG000000001189	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	4,04411	4E-72
56.	ENSECAG000000021914	PDE1C	phosphodiesterase 1C	4,04131	2E-22
57.	ENSECAG000000010499	TRABD2A	TraB domain containing 2A	3,97097	1E-05
58.	ENSECAG000000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	3,96278	7E-19
59.	ENSECAG000000010750	VWCE	von Willebrand factor C and EGF domains	3,9446	2E-103
60.	ENSECAG000000021057	ADGRV1	adhesion G protein-coupled receptor V1	3,90797	5E-17
61.	ENSECAG000000010805	PGM5	phosphoglucomutase 5	3,86063	1E-46
62.	ENSECAG000000029510	ENSECAG000000029510		3,82021	4E-19
63.	ENSECAG000000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	3,8016	6E-32
64.	ENSECAG000000014126	CFAP161	Cilia And Flagella Associated Protein 161	3,8	4E-16
65.	ENSECAG000000004372	SLC22A3	Solute Carrier Family 22 Member 3	3,77378	1E-19
66.	ENSECAG000000021775	KRT8	keratin 8	3,76393	7E-21
67.	ENSECAG000000000681	ENSECAG000000000681		3,74432	5E-05
68.	ENSECAG000000024719	ENSECAG000000024719	solute carrier family 2 member 3	3,7305	3E-118
69.	ENSECAG000000011407	STON2	Stonin 2	3,72118	1E-05
70.	ENSECAG000000019438	OSMR	oncostatin M receptor	3,69662	3E-32
71.	ENSECAG000000004587	ANKRD34B	ankyrin repeat domain 34B	3,68482	1E-09
72.	ENSECAG000000024845	PI16	peptidase inhibitor 16	3,6309	2E-18
73.	ENSECAG000000023895	EXOC3L2	exocyst complex component 3 like 2	3,61724	2E-19
74.	ENSECAG000000016953	HLF	HLF transcription factor, PAR bZIP family member	3,5797	8E-27
75.	ENSECAG000000012826	CDO1	Cysteine Dioxygenase Type 1	3,53393	1E-16
76.	ENSECAG000000015651	ARSF	arylsulfatase F	3,52761	5E-13
77.	ENSECAG000000010569	SV2C	synaptic vesicle glycoprotein 2C	3,52318	4E-08
78.	ENSECAG000000015657	TNNT1	troponin T1, slow skeletal type	3,4837	4E-24
79.	ENSECAG000000036638	SLC6A12	solute carrier family 6 member 12	3,47773	3E-09
80.	ENSECAG000000010879	NTS	Neurotensin	3,46503	1E-06
81.	ENSECAG000000011893	CNTNAP4	Contactin Associated Protein Family Member 4	3,45565	0,0002
82.	ENSECAG000000017570	SYT4	synaptotagmin 4	3,42323	2E-10
83.	ENSECAG000000014145	TLL2	tolloid like 2	3,3671	9E-09
84.	ENSECAG000000023199	COL24A1	Collagen Type XXIV Alpha 1 Chain	3,34374	5E-11
85.	ENSECAG000000015333	ADAP2	ArfGAP With Dual PH Domains 2	3,32297	4E-10
86.	ENSECAG000000001603	PEG10	Paternally Expressed 10	3,31511	3E-05
87.	ENSECAG000000020238	GRAMD1B	GRAM domain containing 1B	3,30341	5E-21
88.	ENSECAG000000013009	KIF26B	kinesin family member 26B	3,27961	3E-19
89.	ENSECAG000000009700	ANK3	ankyrin 3	3,27279	4E-11
90.	ENSECAG000000024340	TTYH1	tweety family member 1	3,23538	0,0003
91.	ENSECAG000000009046	BIN2	Bridging Integrator 2	3,22458	6E-29
92.	ENSECAG000000016048	ANKRD24	ankyrin repeat domain 24	3,20729	1E-07
93.	ENSECAG000000024750	NCALD	neurocalcin delta	3,20329	2E-10
94.	ENSECAG000000016560	CRABP2	Cellular Retinoic Acid Binding Protein 2	3,18139	7E-18
95.	ENSECAG000000024110	PENK	proenkephalin	3,17264	9E-19
96.	ENSECAG000000013207	SHISA2	shisa family member 2	3,12659	5E-05
97.	ENSECAG000000003201	PRSS35	serine protease 35	3,11793	1E-14
98.	ENSECAG000000021654	SLC10A4	solute carrier family 10 member 4	3,11266	1E-15
99.	ENSECAG000000016934	IL31RA	Interleukin 31 Receptor A	3,08568	4E-08
100.	ENSECAG000000021343	NRG1	neuregulin 1	3,07028	8E-117
101.	ENSECAG0000000024973	CD34	CD34 Molecule	3,04457	4E-05
102.	ENSECAG000000022093	SLC2A5	solute carrier family 2 member 5	3,03267	2E-07
103.	ENSECAG000000009580	LVRN	laeverin	3,02227	1E-11
104.	ENSECAG000000005468	PTPRN	Protein Tyrosine Phosphatase Receptor Type N	3,01868	0,0009
105.	ENSECAG000000014817	RND2	Rho Family GTPase 2	2,97457	1E-17
106.	ENSECAG000000009121	NEIL3	nei like DNA glycosylase 3	2,95716	2E-05

107.	ENSECAG00000030024	MAPK13	mitogen-activated protein kinase 13	2,95628	6E-31
108.	ENSECAG00000021262	MMP7	matrix metalloproteinase 7	2,92929	0,0094
109.	ENSECAG00000002256	ENSECAG00000002256		2,85292	0,0043
110.	ENSECAG00000010445	ST3GAL6	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 6	2,84856	8E-33
111.	ENSECAG00000013035	ENPP1	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1	2,8451	1E-24
112.	ENSECAG00000006229	PIMREG	PICALM interacting mitotic regulator	2,81334	0,0091
113.	ENSECAG00000022731	COL6A1	collagen type VI alpha 1 chain	2,80387	2E-99
114.	ENSECAG00000015449	IRF8	interferon regulatory factor 8	2,80385	2E-05
115.	ENSECAG00000014254	LCTL	Lactase Like	2,79736	0,0012
116.	ENSECAG00000017217	CA12	carbonic anhydrase 12	2,77378	2E-24
117.	ENSECAG00000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	2,76911	7E-43
118.	ENSECAG00000024027	CAPN13	calpain 13	2,75622	0,0013
119.	ENSECAG00000014305	CACNA2D3	Calcium Voltage-Gated Channel Auxiliary Subunit Alpha2delta 3	2,74336	0,0007
120.	ENSECAG00000016576	C1QTNF12	C1q And TNF Related 12	2,73341	1E-21
121.	ENSECAG00000008059	PDE4C	phosphodiesterase 4C	2,70948	0,0007
122.	ENSECAG00000001988	FAT3	FAT atypical cadherin 3	2,70434	5E-09
123.	ENSECAG00000023173	EDN2	Endothelin 2	2,6689	0,0105
124.	ENSECAG00000024406	KCP	kelin cysteine rich BMP regulator	2,6536	3E-05
125.	ENSECAG00000008880	SLC22A16	solute carrier family 22 member 16	2,64753	4E-07
126.	ENSECAG00000015069	BHLHE40	basic helix-loop-helix family member e40	2,63846	6E-92
127.	ENSECAG00000002570	HS3ST1	heparan sulfate-glucosamine 3-sulfotransferase 1	2,62252	3E-11
128.	ENSECAG00000014379	BMP3	bone morphogenetic protein 3	2,60519	5E-11
129.	ENSECAG00000024322	ARSJ	arylsulfatase family member J	2,59709	9E-59
130.	ENSECAG00000000574	NIPAL4	NIPA Like Domain Containing 4	2,58984	1E-31
131.	ENSECAG000000012104	TNFAIP6	TNF Alpha Induced Protein 6	2,58561	4E-114
132.	ENSECAG00000004795	ENSECAG00000004795		2,58492	3E-07
133.	ENSECAG00000003278	TRIM9	tripartite motif containing 9	2,57053	2E-20
134.	ENSECAG00000018841	CGA	Glycoprotein Hormones, Alpha Polypeptide	2,56798	4E-12
135.	ENSECAG00000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	2,55683	4E-50
136.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	2,55551	1E-19
137.	ENSECAG00000016742	TJP2	tight junction protein 2	2,55056	3E-18
138.	ENSECAG00000007964	EBF1	EBF transcription factor 1	2,53023	1E-53
139.	ENSECAG00000007300	DCLK1	doublecortin like kinase 1	2,52057	5E-110
140.	ENSECAG00000014588	CAMK1G	calcium/calmodulin dependent protein kinase 1G	2,51823	3E-06
141.	ENSECAG00000009535	FCER1G	Fc Epsilon Receptor Ig	2,50749	4E-08
142.	ENSECAG00000015967	ASF1B	Anti-Silencing Function 1B Histone Chaperone	2,48725	0,0129
143.	ENSECAG00000024172	ADAMTS4	ADAM Metalloproteinase With Thrombospondin Type 1 Motif 4	2,48456	1E-21
144.	ENSECAG00000012263	RNF19B	Ring Finger Protein 19B	2,48011	3E-183
145.	ENSECAG00000003943	SYT5	synaptotagmin 5	2,4718	8E-42
146.	ENSECAG00000017598	IMPA2	inositol monophosphatase 2	2,45009	2E-26
147.	ENSECAG00000023252	ADGRG2	adhesion G protein-coupled receptor G2	2,44145	0,0006
148.	ENSECAG00000019215	ITGB8	Integrin Subunit Beta 8	2,43895	1E-42
149.	ENSECAG00000013324	TXN	Thioredoxin	2,4361	6E-55
150.	ENSECAG00000033890	CIDEC	cell death inducing DFFA like effector c	2,43603	5E-18
151.	ENSECAG00000015695	PTPRO	protein tyrosine phosphatase receptor type O	2,42627	5E-07
152.	ENSECAG00000023685	GJA4	gap junction protein alpha 4	2,42505	0,008
153.	ENSECAG00000000235	MTBP	MDM2 binding protein	2,4165	2E-67
154.	ENSECAG00000009769	CNTN4	contactin 4	2,40535	4E-05
155.	ENSECAG00000035439	ENSECAG00000035439	RAB6B, member RAS oncogene family	2,39617	0,0005
156.	ENSECAG00000016661	NR4A1	Nuclear Receptor Subfamily 4 Group A Member 1	2,39488	7E-19

157.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	2,39485	1E-09
158.	ENSECAG00000024127	CENPF	centromere protein F	2,37948	5E-05
159.	ENSECAG00000014732	ATP10A	ATPase phospholipid transporting 10A (putative)	2,36898	2E-36
160.	ENSECAG00000020767	IL7	interleukin 7	2,36238	1E-23
161.	ENSECAG00000023908	OLFML2A	olfactomedin like 2A	2,36039	7E-11
162.	ENSECAG00000011099	VAV3	Vav Guanine Nucleotide Exchange Factor 3	2,36033	3E-30
163.	ENSECAG00000000651	SPINK5	serine peptidase inhibitor Kazal type 5	2,35416	0,0301
164.	ENSECAG00000026891	ENSECAG00000026891	PCNA clamp associated factor	2,3535	5E-06
165.	ENSECAG00000011788	CDC45	cell division cycle 45	2,34606	4E-07
166.	ENSECAG00000007432	PTGDR	Prostaglandin D2 Receptor	2,34045	9E-62
167.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	2,32385	6E-121
168.	ENSECAG00000011669	TNN	tenascin N	2,31956	2E-39
169.	ENSECAG00000015593	EGFL7	EGF like domain multiple 7	2,29177	0,0007
170.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	2,28712	4E-52
171.	ENSECAG00000019170	MN1	MN1 Proto-Oncogene, Transcriptional Regulator	2,27366	8E-06
172.	ENSECAG00000019229	STAMBPL1	STAM binding protein like 1	2,26802	2E-56
173.	ENSECAG00000018996	PLEK	pleckstrin	2,26142	0,0023
174.	ENSECAG00000019578	CDCA5	cell division cycle associated 5	2,2459	0,001
175.	ENSECAG00000000532	EPS8L1	EPS8 like 1	2,2455	1E-18
176.	ENSECAG00000006288	SIK1	salt inducible kinase 1	2,23881	1E-38
177.	ENSECAG00000019551	CXCL12	C-X-C motif chemokine ligand 12	2,23565	2E-50
178.	ENSECAG00000039680	ENSECAG00000039680	RecQ mediated genome instability 2	2,22386	0,0007
179.	ENSECAG00000016248	JPH1	junctophilin 1	2,21917	3E-05
180.	ENSECAG00000006763	GPBAR1	G protein-coupled bile acid receptor 1	2,21369	0,0151
181.	ENSECAG00000017826	TMEM26	transmembrane protein 26	2,20433	3E-12
182.	ENSECAG00000019880	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif 9	2,20108	3E-43
183.	ENSECAG00000041708	ENSECAG00000041708		2,19724	1E-17
184.	ENSECAG00000038893	CST3	cystatin C	2,1968	4E-179
185.	ENSECAG00000021799	MYRF	myelin regulatory factor	2,17676	8E-15
186.	ENSECAG00000009403	IL1RAPL2	interleukin 1 receptor accessory protein like 2	2,17202	2E-06
187.	ENSECAG00000015385	RNF150	ring finger protein 150	2,16785	1E-10
188.	ENSECAG00000036105	ENSECAG00000036105		2,15847	1E-11
189.	ENSECAG00000011627	ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6	2,15808	1E-17
190.	ENSECAG00000023800	AK2	adenylate kinase 2	2,1577	4E-92
191.	ENSECAG00000007974	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	2,14911	0,0145
192.	ENSECAG00000010188	ABHD3	abhydrolase domain containing 3, phospholipase	2,1464	2E-58
193.	ENSECAG00000019398	TFPI2	Tissue Factor Pathway Inhibitor 2	2,14	9E-43
194.	ENSECAG00000000292	THSD7A	Thrombospondin Type 1 Domain Containing 7A	2,13346	4E-09
195.	ENSECAG00000032992	TIAM1	TIAM Rac1 associated GEF 1	2,13341	1E-29
196.	ENSECAG00000009081	KIAA1210	KIAA1210	2,11948	2E-09
197.	ENSECAG00000022014	RAVER2	Ribonucleoprotein, PTB Binding 2	2,10933	0,0002
198.	ENSECAG00000024113	ABLIM1	actin binding LIM protein 1	2,09137	3E-06
199.	ENSECAG00000007018	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	2,09064	4E-10
200.	ENSECAG00000017035	SHF	Src homology 2 domain containing F	2,08865	2E-40
201.	ENSECAG00000002377	SPESP1	Sperm Equatorial Segment Protein 1	2,08008	4E-26
202.	ENSECAG00000014794	MIIP	Migration And Invasion Inhibitory Protein	2,07685	4E-36
203.	ENSECAG00000025101	NELL2	neural EGFL like 2	2,07507	7E-10
204.	ENSECAG00000024293	AMDHD1	amidohydrolase domain containing 1	2,07398	3E-09
205.	ENSECAG00000024795	CPVL	carboxypeptidase vitellogenic like	2,07211	6E-56
206.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	2,06581	1E-56
207.	ENSECAG00000011929	NR4A3	Nuclear Receptor Subfamily 4 Group A Member 3	2,0653	5E-13
208.	ENSECAG00000020769	FGF1	fibroblast growth factor 1	2,04976	1E-33
209.	ENSECAG00000018373	FAM234B	family with sequence similarity 234 member B	2,04882	5E-28

210.	ENSECAG00000020927	NEK10	NIMA related kinase 10	2,04643	2E-11
211.	ENSECAG00000016976	RARB	retinoic acid receptor beta	2,04176	2E-08
212.	ENSECAG00000020645	ASPM	assembly factor for spindle microtubules	2,03859	1E-09
213.	ENSECAG00000023019	KIF18B	kinesin family member 18B	2,03818	0,0014
214.	ENSECAG00000013691	MALT1	MALT1 paracaspase	2,03573	6E-73
215.	ENSECAG00000000122	GDA	Guanine Deaminase	2,03197	5E-26
216.	ENSECAG00000021976	LRATD2	LRAT domain containing 2	2,03136	5E-06
217.	ENSECAG00000020258	SSC4D	scavenger receptor cysteine rich family member with 4 domains	2,0097	0,0219
218.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	2,00278	4E-08
219.	ENSECAG00000016360	PDE3A	Phosphodiesterase 3A	1,99843	4E-10
220.	ENSECAG00000008493	SERPINB10	serpin family B member 10	1,98664	0,0031
221.	ENSECAG00000006060	RAI2	retinoic acid induced 2	1,97885	7E-10
222.	ENSECAG00000006827	SEMA6A	semaphorin 6A	1,97338	0,0107
223.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,96733	3E-129
224.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	1,96172	3E-21
225.	ENSECAG00000002992	MID1IP1	MID1 interacting protein 1	1,96139	2E-104
226.	ENSECAG00000010447	EFEMP1	EGF Containing Fibulin Extracellular Matrix Protein 1	1,95678	2E-27
227.	ENSECAG00000024779	SERPINA5	serpin family A member 5	1,94967	0,0006
228.	ENSECAG00000018118	BMERB1	bMERB domain containing 1	1,94558	0,0005
229.	ENSECAG00000005925	MYBL2	MYB Proto-Oncogene Like 2	1,9434	3E-11
230.	ENSECAG00000036575	MACIR	macrophage immunometabolism regulator	1,94218	0,006
231.	ENSECAG00000021694	CYB5D2	cytochrome b5 domain containing 2	1,94122	0,0138
232.	ENSECAG00000016902	PRR16	proline rich 16	1,93612	3E-23
233.	ENSECAG00000010053	HJURP	Holliday junction recognition protein	1,93396	2E-07
234.	ENSECAG00000018874	PRICKLE1	Prickle Planar Cell Polarity Protein 1	1,93238	4E-52
235.	ENSECAG00000008461	DEPDC1	DEP domain containing 1	1,9291	0,0016
236.	ENSECAG00000016860	KIF20A	kinesin family member 20A	1,92538	9E-16
237.	ENSECAG00000030620	ENSECAG00000030620		1,92252	0,0128
238.	ENSECAG00000010963	SERPING1	Serpin Family G Member 1	1,92001	4E-76
239.	ENSECAG00000008655	DLGAP5	DLG Associated Protein 5	1,91836	3E-05
240.	ENSECAG00000023076	GPCPD1	glycerophosphocholine phosphodiesterase 1	1,91512	3E-28
241.	ENSECAG00000017017	LNK1	ligand of numb-protein X 1	1,91025	1E-14
242.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	1,90739	1E-06
243.	ENSECAG00000038379	ENSECAG00000038379	keratin 18	1,90561	1E-09
244.	ENSECAG00000008876	PTPRE	protein tyrosine phosphatase receptor type E	1,90381	0,0027
245.	ENSECAG00000033164	ENSECAG00000033164	NAC alpha domain containing	1,8976	1E-14
246.	ENSECAG00000010500	ITGA4	integrin subunit alpha 4	1,89719	3E-30
247.	ENSECAG00000021746	SHROOM1	Shroom Family Member 1	1,88871	6E-49
248.	ENSECAG00000008569	TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1	1,88829	7E-43
249.	ENSECAG00000019705	CDC20	Cell Division Cycle 20	1,88784	2E-11
250.	ENSECAG00000015835	NT5DC2	5'-Nucleotidase Domain Containing 2	1,87877	7E-25
251.	ENSECAG00000012858	RASL11A	RAS like family 11 member A	1,87446	3E-08
252.	ENSECAG00000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	1,87207	8E-32
253.	ENSECAG00000018322	EXO1	exonuclease 1	1,86688	5E-05
254.	ENSECAG00000014536	KIF23	kinesin family member 23	1,86447	6E-18
255.	ENSECAG00000023134	KCNK5	potassium two pore domain channel subfamily K member 5	1,85967	5E-65
256.	ENSECAG00000020111	IQGAP3	IQ Motif Containing GTPase Activating Protein 3	1,85264	3E-05
257.	ENSECAG00000003789	RASL11B	RAS like family 11 member B	1,84801	5E-23
258.	ENSECAG00000009839	VAT1L	vesicle amine transport 1 like	1,83588	3E-05
259.	ENSECAG00000009501	DAAM2	dishevelled associated activator of morphogenesis 2	1,83463	3E-49
260.	ENSECAG00000001372	SYN1	synapsin I	1,83355	3E-05
261.	ENSECAG00000024853	RSPO2	R-Spondin 2	1,83141	0,0012
262.	ENSECAG00000010587	ISM1	Isthmin 1	1,8288	2E-08
263.	ENSECAG00000014511	IL11	Interleukin 11	1,82504	7E-73

264.	ENSECAG00000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	1,82455	1E-18
265.	ENSECAG00000000752	EHF	ETS Homologous Factor	1,82284	0,0012
266.	ENSECAG00000022404	TRPV6	transient receptor potential cation channel subfamily V member 6	1,81042	4E-08
267.	ENSECAG00000014787	RCAN1	regulator of calcineurin 1	1,80885	1E-113
268.	ENSECAG00000020881	CTSC	cathepsin C	1,803	5E-40
269.	ENSECAG00000015746	SMC1B	structural maintenance of chromosomes 1B	1,79759	0,0049
270.	ENSECAG00000006788	PCSK5	proprotein convertase subtilisin/kexin type 5	1,79349	4E-61
271.	ENSECAG00000036440	RGS16	regulator of G protein signaling 16	1,79098	0,0069
272.	ENSECAG00000008823	CDH11	cadherin 11	1,78901	7E-79
273.	ENSECAG00000014813	CCNB2	Cyclin B2	1,78612	2E-05
274.	ENSECAG00000017671	ROBO1	roundabout guidance receptor 1	1,7821	2E-32
275.	ENSECAG00000015966	SERPINF6	Serpin Family B Member 6	1,78111	6E-71
276.	ENSECAG00000013298	POLE2	dynein axonemal assembly factor 2	1,78067	2E-06
277.	ENSECAG00000000426	CENPL	centromere protein L	1,7792	0,0022
278.	ENSECAG00000019600	GRP	gastrin releasing peptide	1,7769	1E-10
279.	ENSECAG00000009042	ENSECAG00000009042	carcinoembryonic antigen-related cell adhesion molecule 1	1,77515	8E-05
280.	ENSECAG00000005559	GABRA5	gamma-aminobutyric acid type A receptor subunit alpha5	1,77121	0,0013
281.	ENSECAG00000007464	RRM2	ribonucleotide reductase regulatory subunit M2	1,75869	8E-14
282.	ENSECAG00000012179	RGS2	regulator of G protein signaling 2	1,75799	1E-17
283.	ENSECAG00000021015	ATP8B1	ATPase phospholipid transporting 8B1	1,75491	1E-11
284.	ENSECAG00000010525	KEL	Kell metallo-endopeptidase	1,75043	0,0038
285.	ENSECAG00000019433	CDKN3	cyclin dependent kinase inhibitor 3	1,74456	0,0004
286.	ENSECAG00000020563	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1,74049	8E-95
287.	ENSECAG00000023526	PLPP4	phospholipid phosphatase 4	1,73123	3E-09
288.	ENSECAG00000021452	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	1,72911	9E-11
289.	ENSECAG00000019750	IL6ST	interleukin 6 cytokine family signal transducer	1,72747	6E-83
290.	ENSECAG00000015060	PRR11	proline rich 11	1,72615	1E-05
291.	ENSECAG00000005086	EGLN3	Egl-9 Family Hypoxia Inducible Factor 3	1,72234	3E-49
292.	ENSECAG00000030025	ENSECAG00000030025		1,7207	0,0042
293.	ENSECAG00000017864	FMOD	fibromodulin	1,72022	3E-07
294.	ENSECAG00000019455	NIPAL1	NIPA like domain containing 1	1,71627	0,0017
295.	ENSECAG00000013425	IGFBP5	insulin like growth factor binding protein 5	1,71606	5E-07
296.	ENSECAG00000012646	SYNJ2	Synaptojanin 2	1,71527	9E-19
297.	ENSECAG00000024694	KIF14	kinesin family member 14	1,71496	0,0012
298.	ENSECAG00000014137	DOCK3	Dedicator Of Cytokinesis 3	1,70761	0,0161
299.	ENSECAG00000010065	OXCT2	3-Oxoacid CoA-Transferase 2	1,70633	1E-05
300.	ENSECAG00000024121	TCF7L2	Transcription Factor 7 Like 2	1,70517	8E-23
301.	ENSECAG00000005719	PRKD1	protein kinase D1	1,70434	4E-46
302.	ENSECAG00000016121	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif 12	1,70357	1E-10
303.	ENSECAG00000003966	GPC4	glypican 4	1,70357	9E-18
304.	ENSECAG00000015034	PLAC8B	placenta associated 8 B	1,70265	0,0083
305.	ENSECAG00000001290	CABP1	calcium binding protein 1	1,70149	0,0382
306.	ENSECAG00000008827	NDC80	NDC80 kinetochore complex component	1,69902	4E-07
307.	ENSECAG00000020053	SLC4A4	solute carrier family 4 member 4	1,69805	0,0031
308.	ENSECAG00000026863	EFS	Embryonal Fyn-Associated Substrate	1,69462	1E-22
309.	ENSECAG00000010725	STXBP5L	syntaxin binding protein 5L	1,69274	0,0042
310.	ENSECAG00000025159	DNAH9	Dynein Axonemal Heavy Chain 9	1,68879	0,0085
311.	ENSECAG00000024428	PROCR	protein C receptor	1,6885	7E-38
312.	ENSECAG00000024186	KIF21A	kinesin family member 21A	1,68839	9E-07
313.	ENSECAG00000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,68775	2E-114
314.	ENSECAG00000014361	FGF10	fibroblast growth factor 10	1,6779	5E-05
315.	ENSECAG00000035412	ENSECAG00000035412	small nucleolar RNA SNORD113/SNORD114 family	1,67775	0,0005

316.	ENSECAG00000013106	ESM1	endothelial cell specific molecule 1	1,67604	1E-08
317.	ENSECAG00000024473	MCM10	minichromosome maintenance 10 replication initiation factor	1,67547	1E-05
318.	ENSECAG00000020920	NEK2	NIMA related kinase 2	1,67462	3E-05
319.	ENSECAG00000008787	CCNB3	cyclin B3	1,67343	0,0138
320.	ENSECAG00000033207	TWIST1	twist family bHLH transcription factor 1	1,67242	6E-37
321.	ENSECAG00000007165	TRAF5	TNF receptor associated factor 5	1,67195	2E-34
322.	ENSECAG00000014774	MMP23	Matrix Metalloproteinase 23	1,67101	2E-31
323.	ENSECAG00000026688	ENSECAG00000026688	small nucleolar RNA SNORD113/SNORD114 family	1,66613	6E-08
324.	ENSECAG00000011656	DPH5	diphthamide biosynthesis 5	1,66466	1E-70
325.	ENSECAG00000019038	KIF2C	kinesin family member 2C	1,66381	0,0001
326.	ENSECAG00000011878	DTL	denticleless E3 ubiquitin protein ligase homolog	1,66245	1E-11
327.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,64413	9E-06
328.	ENSECAG00000023149	SCIN	scinderin	1,64063	1E-06
329.	ENSECAG00000032416	APC2	APC regulator of WNT signaling pathway 2	1,63997	0,0006
330.	ENSECAG00000024008	SCAI	suppressor of cancer cell invasion	1,63544	1E-06
331.	ENSECAG00000020101	SLC24A2	solute carrier family 24 member 2	1,6339	0,0017
332.	ENSECAG00000017388	CENPT	centromere protein T	1,62744	0,0003
333.	ENSECAG00000015806	CCNB1	cyclin B1	1,62466	1E-12
334.	ENSECAG00000036001	HOXB9	homeobox B9	1,62384	2E-07
335.	ENSECAG00000008506	HMMR	Hyaluronan Mediated Motility Receptor	1,62293	7E-07
336.	ENSECAG00000020682	TTL11	tubulin tyrosine ligase like 11	1,62171	2E-08
337.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	1,61734	3E-31
338.	ENSECAG00000021155	MXD3	MAX dimerization protein 3	1,61726	0,0105
339.	ENSECAG00000016383	USP53	Ubiquitin Specific Peptidase 53	1,61559	7E-07
340.	ENSECAG00000010821	RACGAP1	Rac GTPase activating protein 1	1,60971	8E-09
341.	ENSECAG00000010643	TPD52L1	TPD52 like 1	1,6048	0,0175
342.	ENSECAG00000043057	ENSECAG00000043057		1,60264	0,0052
343.	ENSECAG000000000015	KIAA1217	KIAA1217	1,59307	7E-12
344.	ENSECAG00000002958	LRRC4	leucine rich repeat containing 4	1,5906	0,0387
345.	ENSECAG00000016036	WWOX	WW domain containing oxidoreductase	1,58862	7E-28
346.	ENSECAG00000007918	TNS4	tensin 4	1,579	8E-07
347.	ENSECAG00000015058	ARHGEF3	Rho guanine nucleotide exchange factor 3	1,57852	5E-90
348.	ENSECAG00000028820	HEY1	hes related family bHLH transcription factor with YRPW motif 1	1,5694	5E-05
349.	ENSECAG00000005266	SORD	sorbitol dehydrogenase	1,56903	1E-22
350.	ENSECAG00000022931	TCF7L1	transcription factor 7 like 1	1,56873	2E-39
351.	ENSECAG00000010859	KIF4A	kinesin family member 4A	1,56788	1E-06
352.	ENSECAG00000009913	CDC6	cell division cycle 6	1,56359	2E-08
353.	ENSECAG00000030455	ENSECAG00000030455		1,56099	1E-06
354.	ENSECAG00000024574	GATA3	GATA binding protein 3	1,56044	2E-07
355.	ENSECAG00000018935	SRPX	sushi repeat containing protein X-linked	1,56031	5E-35
356.	ENSECAG00000015822	VDR	vitamin D receptor	1,5573	9E-17
357.	ENSECAG00000018476	TPX2	TPX2 microtubule nucleation factor	1,55605	3E-09
358.	ENSECAG00000014395	PTH2R	parathyroid hormone 2 receptor	1,55422	2E-08
359.	ENSECAG00000001407	CHSY3	chondroitin sulfate synthase 3	1,55344	4E-44
360.	ENSECAG00000018519	FANCD2	FA complementation group D2	1,55329	2E-09
361.	ENSECAG00000024375	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	1,54533	0,0003
362.	ENSECAG00000016495	NUSAP1	nucleolar and spindle associated protein 1	1,54347	2E-10
363.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,53513	5E-47
364.	ENSECAG00000021634	SLC29A4	solute carrier family 29 member 4	1,53082	1E-07
365.	ENSECAG00000032664	GPR27	G protein-coupled receptor 27	1,51921	0,0327
366.	ENSECAG00000017784	OSR2	odd-skipped related transcription factor 2	1,51273	3E-22
367.	ENSECAG00000019129	FOXO1	forkhead box M1	1,51214	0,0003
368.	ENSECAG00000023492	TMC1	Transmembrane Channel Like 1	1,51163	0,016

369.	ENSECAG00000015115	RHBDL1	rhomoid like 1	1,506	1E-07
370.	ENSECAG00000030219	ENSECAG00000030219		1,5044	2E-11
371.	ENSECAG00000036591	APLN	apelin	1,49877	8E-14
372.	ENSECAG00000004400	RBM47	RNA binding motif protein 47	1,49504	3E-09
373.	ENSECAG00000013100	PII5	peptidase inhibitor 15	1,49496	1E-06
374.	ENSECAG000000034739	ADORA2A	adenosine A2a receptor	1,49371	7E-10
375.	ENSECAG000000031932	TMEM63C	transmembrane protein 63C	1,49191	0,0014
376.	ENSECAG000000023668	RGS5	regulator of G protein signaling 5	1,4911	5E-18
377.	ENSECAG00000000281	SHCBP1	SHC Binding And Spindle Associated 1	1,48869	1E-09
378.	ENSECAG000000005265	NAAA	N-acylethanolamine acid amidase	1,48587	1E-05
379.	ENSECAG000000037578	ELFN1	extracellular leucine rich repeat and fibronectin type III domain containing 1	1,48038	3E-08
380.	ENSECAG000000009303	GFPT2	Glutamine-Fructose-6-Phosphate Transaminase 2	1,47951	1E-52
381.	ENSECAG00000015127	SLC13A4	solute carrier family 13 member 4	1,47817	6E-05
382.	ENSECAG000000023279	GATA6	GATA binding protein 6	1,47638	3E-23
383.	ENSECAG000000021206	HAS2	hyaluronan synthase 2	1,47521	4E-13
384.	ENSECAG000000001064	RET	ret proto-oncogene	1,47404	5E-07
385.	ENSECAG00000014646	KNG1	kininogen 1	1,46518	4E-14
386.	ENSECAG000000006558	RIC1	RIC1 homolog, RAB6A GEF complex partner 1	1,46387	1E-14
387.	ENSECAG00000014346	GBA3	glucosylceramidase beta 3	1,46286	4E-08
388.	ENSECAG000000008971	P3H2	prolyl 3-hydroxylase 2	1,46222	8E-05
389.	ENSECAG000000004572	CH25H	cholesterol 25-hydroxylase	1,45792	2E-28
390.	ENSECAG000000006991	PECAM1	platelet and endothelial cell adhesion molecule 1	1,45669	6E-51
391.	ENSECAG000000007571	PLAT	plasminogen activator, tissue type	1,45566	2E-18
392.	ENSECAG00000018101	FBLN1	fibulin 1	1,45198	3E-42
393.	ENSECAG00000017926	TROAP	trophinin associated protein	1,44951	0,0006
394.	ENSECAG0000000024851	EDNRB	endothelin receptor type B	1,44858	2E-35
395.	ENSECAG00000013053	TOP2A	DNA topoisomerase II alpha	1,44222	2E-17
396.	ENSECAG00000015369	NID2	nidogen 2	1,44135	1E-59
397.	ENSECAG00000014259	TIMP1	TIMP metalloproteinase inhibitor 1	1,43542	1E-20
398.	ENSECAG000000024182	VSTM4	V-set and transmembrane domain containing 4	1,43152	7E-38
399.	ENSECAG00000016910	SLC4A8	solute carrier family 4 member 8	1,42861	0,0009
400.	ENSECAG000000022901	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	1,42667	0,0033
401.	ENSECAG000000002675	ZGRF1	zinc finger GRF-type containing 1	1,42542	0,0109
402.	ENSECAG000000005814	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	1,42439	0,002
403.	ENSECAG000000009173	ZNF367	zinc finger protein 367	1,42038	2E-05
404.	ENSECAG00000016339	ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif 1	1,42022	2E-48
405.	ENSECAG000000020270	CCNE2	cyclin E2	1,41693	0,0034
406.	ENSECAG00000017015	MYH11	myosin heavy chain 11	1,41586	3E-05
407.	ENSECAG000000009516	IZUMO4	IZUMO Family Member 4	1,41564	0,0036
408.	ENSECAG00000013434	DLL4	Delta Like Canonical Notch Ligand 4	1,41395	0,0301
409.	ENSECAG00000014891	NRCAM	Neuronal Cell Adhesion Molecule	1,41305	3E-12
410.	ENSECAG00000016080	KCNB1	potassium voltage-gated channel subfamily B member 1	1,41074	0,0018
411.	ENSECAG00000016056	BICDL2	BICD family like cargo adaptor 2	1,40871	0,0045
412.	ENSECAG00000014314	POLQ	DNA polymerase theta	1,40759	0,0058
413.	ENSECAG000000023525	NDUFA4L2	NDUFA4 Mitochondrial Complex Associated Like 2	1,40628	0,0023
414.	ENSECAG00000010768	LRBA	LPS responsive beige-like anchor protein	1,40571	3E-14
415.	ENSECAG000000009370	ORC1	Origin Recognition Complex Subunit 1	1,40546	0,0003
416.	ENSECAG000000020840	OSBPL11	Oxysterol Binding Protein Like 11	1,4045	3E-35
417.	ENSECAG00000014998	GLCE	glucuronic acid epimerase	1,40196	1E-10
418.	ENSECAG000000009472	CLSPN	claspin	1,39737	2E-06
419.	ENSECAG00000010035	SCUBE2	Signal Peptide, CUB Domain And EGF Like Domain Containing 2	1,396	3E-18
420.	ENSECAG000000009568	CENPI	centromere protein I	1,39404	2E-09
421.	ENSECAG00000016522	SCG3	Secretogranin III	1,39254	3E-14

422.	ENSECAG00000009716	CDK1	cyclin dependent kinase 1	1,39204	1E-06
423.	ENSECAG000000021782	DCK	deoxycytidine kinase	1,38979	4E-08
424.	ENSECAG000000001964	PDHA1	Pyruvate Dehydrogenase E1 Subunit Alpha 1	1,38763	2E-36
425.	ENSECAG000000011708	GAREM1	GRB2 associated regulator of MAPK1 subtype 1	1,38006	4E-09
426.	ENSECAG000000022553	IRS3	insulin receptor substrate 3	1,37863	2E-07
427.	ENSECAG000000023026	PAPPA	Pappalysin 1	1,37852	8E-15
428.	ENSECAG000000034840	TNFSF13	TNF superfamily member 13	1,37626	3E-32
429.	ENSECAG000000017168	ABCC4	ATP binding cassette subfamily C member 4	1,37193	3E-31
430.	ENSECAG000000014658	SCD	stearoyl-CoA desaturase	1,36882	1E-06
431.	ENSECAG000000013731	STC1	Stanniocalcin 1	1,36783	0,028
432.	ENSECAG000000005447	GUCY1A1	Guanylate Cyclase 1 Soluble Subunit Alpha 1	1,36388	0,0023
433.	ENSECAG000000014517	CDCA3	cell division cycle associated 3	1,35979	7E-07
434.	ENSECAG000000024106	CHST1	carbohydrate sulfotransferase 1	1,35661	0,0003
435.	ENSECAG000000016773	NABP1	nucleic acid binding protein 1	1,35348	4E-23
436.	ENSECAG000000021370	SCN4B	sodium voltage-gated channel beta subunit 4	1,35322	0,0232
437.	ENSECAG000000005685	RDH10	Retinol Dehydrogenase 10	1,34815	8E-24
438.	ENSECAG000000024668	IGDCC4	immunoglobulin superfamily DCC subclass member 4	1,34622	0,0057
439.	ENSECAG000000015003	PLGRKT	Plasminogen Receptor With A C-Terminal Lysine	1,34602	2E-14
440.	ENSECAG000000006771	PRKCA	protein kinase C alpha	1,3404	2E-14
441.	ENSECAG000000012946	CYP7A1	cytochrome P450 family 7 subfamily A member 1	1,34009	3E-24
442.	ENSECAG000000003345	ENO1	Enolase 1	1,33843	3E-44
443.	ENSECAG000000013268	AP1S3	adaptor related protein complex 1 subunit sigma 3	1,33627	5E-10
444.	ENSECAG000000024419	JADE1	jade family PHD finger 1	1,33593	2E-31
445.	ENSECAG000000021902	SPATA6L	spermatogenesis associated 6 like	1,33317	0,0051
446.	ENSECAG000000011486	ATF3	activating transcription factor 3	1,32758	8E-43
447.	ENSECAG000000032055	PROKR2	prokineticin receptor 2	1,32509	0,0106
448.	ENSECAG000000030001	DIRAS3	DIRAS family GTPase 3	1,32393	2E-05
449.	ENSECAG000000021201	BMP2	bone morphogenetic protein 2	1,31735	6E-09
450.	ENSECAG000000010380	HAP1	huntingtin associated protein 1	1,31607	0,0389
451.	ENSECAG000000023815	PLA2R1	phospholipase A2 receptor 1	1,31246	7E-14
452.	ENSECAG000000010858	ANKRD37	ankyrin repeat domain 37	1,30711	4E-05
453.	ENSECAG000000021024	APLP1	amyloid beta precursor like protein 1	1,30553	0,0081
454.	ENSECAG000000020933	ITPR1	Inositol 1,4,5-Trisphosphate Receptor Type 1	1,30506	4E-07
455.	ENSECAG000000019624	OSTF1	Osteoclast Stimulating Factor 1	1,30367	2E-46
456.	ENSECAG000000000138	ACVR2A	activin A receptor type 2A	1,30345	1E-25
457.	ENSECAG000000018665	RECQL4	RecQ like helicase 4	1,30313	7E-05
458.	ENSECAG000000005547	CDT1	Chromatin Licensing And DNA Replication Factor 1	1,30181	0,0005
459.	ENSECAG000000021905	HK2	hexokinase 2	1,30127	2E-24
460.	ENSECAG000000008270	FABP5	fatty acid binding protein 5	1,30088	2E-07
461.	ENSECAG000000026887	TSPAN8	tetraspanin 8	1,29908	8E-06
462.	ENSECAG000000014384	AURKB	aurora kinase B	1,29584	0,0039
463.	ENSECAG000000024558	ENSECAG000000024558	centromere protein E	1,29034	2E-08
464.	ENSECAG000000023046	SORCS1	sortilin related VPS10 domain containing receptor 1	1,28932	1E-05
465.	ENSECAG000000006359	PDP2	pyruvate dehydrogenase phosphatase catalytic subunit 2	1,28851	6E-17
466.	ENSECAG000000011380	TACC3	transforming acidic coiled-coil containing protein 3	1,28601	2E-10
467.	ENSECAG000000008927	HIPK2	homeodomain interacting protein kinase 2	1,2821	0,0003
468.	ENSECAG000000017458	BNIP3	BCL2 interacting protein 3	1,2792	1E-11
469.	ENSECAG000000038834	MTFR2	Mitochondrial Fission Regulator 2	1,27759	0,0001
470.	ENSECAG000000013988	DLC1	DLC1 Rho GTPase activating protein	1,27685	4E-19
471.	ENSECAG000000020456	ZBTB7C	zinc finger and BTB domain containing 7C	1,26992	0,0036
472.	ENSECAG000000022842	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1,26448	7E-38
473.	ENSECAG000000024817	P4HA2	prolyl 4-hydroxylase subunit alpha 2	1,26441	6E-34

474.	ENSECAG00000017077	IL17RA	interleukin 17 receptor A	1,2609	9E-37
475.	ENSECAG00000008466	BIRC5	Baculoviral IAP Repeat Containing 5	1,25817	0,0002
476.	ENSECAG00000017845	GGCT	Gamma-Glutamylcyclotransferase	1,258	2E-09
477.	ENSECAG00000003944	ENSECAG00000003944		1,25497	0,0072
478.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,25362	2E-28
479.	ENSECAG00000022278	KNL1	kinetochore scaffold 1	1,25285	1E-07
480.	ENSECAG00000002513	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	1,24611	9E-11
481.	ENSECAG00000012887	CPZ	carboxypeptidase Z	1,24144	5E-43
482.	ENSECAG00000013680	TLE1	TLE Family Member 1, Transcriptional Corepressor	1,23871	2E-27
483.	ENSECAG00000018510	RGS20	Regulator Of G Protein Signaling 20	1,23784	0,0002
484.	ENSECAG00000017526	MSI1	musashi RNA binding protein 1	1,22936	0,0051
485.	ENSECAG00000020126	LGI3	leucine rich repeat LGI family member 3	1,2275	0,0026
486.	ENSECAG00000023355	GTSE1	G2 and S-phase expressed 1	1,22683	2E-05
487.	ENSECAG00000017874	SH2D3C	SH2 domain containing 3C	1,22561	0,0003
488.	ENSECAG00000018596	STIMATE	STIM Activating Enhancer	1,22298	7E-08
489.	ENSECAG00000011008	MCOLN2	mucolipin TRP cation channel 2	1,2204	4E-19
490.	ENSECAG00000024889	TDRD6	tudor domain containing 6	1,2156	5E-06
491.	ENSECAG00000028902	SP9	Sp9 transcription factor	1,21267	0,0022
492.	ENSECAG00000022141	TSLP	thymic stromal lymphopoietin	1,20903	0,0004
493.	ENSECAG00000020167	RGMA	repulsive guidance molecule BMP co-receptor a	1,2085	9E-13
494.	ENSECAG00000007709	SEMA3F	semaphorin 3F	1,20647	4E-29
495.	ENSECAG00000011641	TVP23A	trans-golgi network vesicle protein 23 homolog A	1,20605	0,0001
496.	ENSECAG00000018253	FGFRL1	fibroblast growth factor receptor like 1	1,2026	4E-28
497.	ENSECAG00000035279	IGFBP2	insulin like growth factor binding protein 2	1,19976	4E-22
498.	ENSECAG00000013133	GNAO1	G protein subunit alpha o1	1,19847	5E-06
499.	ENSECAG00000007872	TCF19	transcription factor 19	1,19799	3E-09
500.	ENSECAG00000005787	TBX18	T-box transcription factor 18	1,19169	4E-16
501.	ENSECAG00000023771	BCL6B	solute carrier family 16 member 13	1,19154	7E-07
502.	ENSECAG00000020221	KNDC1	kinase non-catalytic C-lobe domain containing 1	1,18867	0,0009
503.	ENSECAG00000010619	F12	coagulation factor XII	1,18438	0,0033
504.	ENSECAG00000015641	DSCC1	DNA Replication And Sister Chromatid Cohesion 1	1,18328	0,0004
505.	ENSECAG00000021269	ETS2	ETS proto-oncogene 2, transcription factor	1,18262	7E-16
506.	ENSECAG00000016974	BRCA1	BRCA1 DNA Repair Associated	1,18055	4E-08
507.	ENSECAG00000019369	CCNF	Cyclin F	1,17793	0,0024
508.	ENSECAG00000022051	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1,17647	2E-40
509.	ENSECAG00000020669	LDHA	lactate dehydrogenase A	1,17298	3E-33
510.	ENSECAG00000035238	IFITM5	interferon induced transmembrane protein 5	1,16933	0,0015
511.	ENSECAG00000010080	PDK3	pyruvate dehydrogenase kinase 3	1,16894	1E-21
512.	ENSECAG00000009281	GLI3	GLI family zinc finger 3	1,16535	2E-07
513.	ENSECAG00000007589	ITGB5	integrin subunit beta 5	1,16486	2E-44
514.	ENSECAG00000009250	RAMP1	receptor activity modifying protein 1	1,16243	6E-05
515.	ENSECAG00000041907	ENSECAG00000041907		1,16241	1E-20
516.	ENSECAG00000024780	RHOF	Ras Homolog Family Member F, Filopodia Associated	1,16098	0,0157
517.	ENSECAG00000024374	ERBB3	erb-b2 receptor tyrosine kinase 3	1,1582	0,003
518.	ENSECAG00000000373	LOXL3	lysyl oxidase like 3	1,14655	6E-43
519.	ENSECAG00000000303	SLC2A1	solute carrier family 2 member 1	1,14627	4E-17
520.	ENSECAG00000019633	IGFBP6	Insulin Like Growth Factor Binding Protein 6	1,14174	4E-23
521.	ENSECAG00000033093	VWA1	Von Willebrand Factor A Domain Containing 1	1,13829	1E-07
522.	ENSECAG00000017922	ADAM19	ADAM metallopeptidase domain 19	1,13763	2E-28
523.	ENSECAG00000017487	MXRA5	matrix remodeling associated 5	1,13641	0,0004
524.	ENSECAG00000021428	GYS1	Glycogen Synthase 1	1,13282	8E-15
525.	ENSECAG00000009452	KLK15	Kallikrein Related Peptidase 15	1,12785	9E-10
526.	ENSECAG00000025871	MIR186	MicroRNA 186	1,12693	0,0375

527.	ENSECAG00000016854	ACSL4	acyl-CoA synthetase long chain family member 4	1,12656	1E-12
528.	ENSECAG00000001041	CENPN	centromere protein N	1,12645	1E-05
529.	ENSECAG00000024523	KLRG1	killer cell lectin like receptor G1	1,12557	0,0008
530.	ENSECAG00000032390	TNFRSF6B	TNF Receptor Superfamily Member 6b	1,1254	0,0465
531.	ENSECAG00000003783	ENSECAG00000003783	ubiquitin C-terminal hydrolase L3	1,12538	2E-12
532.	ENSECAG00000008888	PTH1R	parathyroid hormone 1 receptor	1,12471	0,0144
533.	ENSECAG00000013870	CERCAM	cerebral endothelial cell adhesion molecule	1,12233	1E-24
534.	ENSECAG00000014934	ARHGEF9	Cdc42 guanine nucleotide exchange factor 9	1,12126	4E-11
535.	ENSECAG00000016856	SLC7A2	solute carrier family 7 member 2	1,11744	0,0121
536.	ENSECAG00000009707	PTGS1	prostaglandin-endoperoxide synthase 1	1,11513	0,0057
537.	ENSECAG00000017203	BTG2	BTG Anti-Proliferation Factor 2	1,11442	2E-05
538.	ENSECAG00000025166	MYOCD	myocardin	1,11417	7E-05
539.	ENSECAG00000021812	STARD5	StAR Related Lipid Transfer Domain Containing 5	1,11335	2E-16
540.	ENSECAG00000008281	SPATA20	spermatogenesis associated 20	1,10999	0,0115
541.	ENSECAG00000009783	NRIP3	nuclear receptor interacting protein 3	1,10955	0,0002
542.	ENSECAG00000029466	SHANK1	SH3 and multiple ankyrin repeat domains 1	1,10739	0,0441
543.	ENSECAG00000008517	PNMA2	PNMA family member 2	1,10489	0,0003
544.	ENSECAG00000017213	TULP4	TUB like protein 4	1,10216	3E-08
545.	ENSECAG00000007388	ADCYAP1R1	ADCYAP receptor type I	1,09882	0,0375
546.	ENSECAG00000020036	KRT10A	keratin 10A	1,09858	3E-35
547.	ENSECAG00000003462	RUNX1	RUNX family transcription factor 1	1,09815	3E-08
548.	ENSECAG00000023115	RAB3A	RAB3A, member RAS oncogene family	1,09748	0,0001
549.	ENSECAG00000024980	H1-2	H1.2 Linker Histone, Cluster Member	1,09636	2E-10
550.	ENSECAG00000002569	FLRT3	fibronectin leucine rich transmembrane protein 3	1,09529	2E-15
551.	ENSECAG00000013037	ALDOC	Aldolase, Fructose-Bisphosphate C	1,09083	2E-10
552.	ENSECAG00000009454	PTPRH	Protein Tyrosine Phosphatase Receptor Type H	1,08615	8E-07
553.	ENSECAG00000007647	COL5A3	collagen type V alpha 3 chain	1,08508	3E-08
554.	ENSECAG00000022070	PITPNC1	phosphatidylinositol transfer protein cytoplasmic 1	1,08507	2E-11
555.	ENSECAG00000017728	CAPN12	calpain 12	1,08385	0,0296
556.	ENSECAG00000017925	CD200	CD200 molecule	1,08056	0,0076
557.	ENSECAG00000017968	SLC41A1	Solute Carrier Family 41 Member 1	1,07832	4E-11
558.	ENSECAG00000031983	MTUS1	microtubule associated scaffold protein 1	1,07645	0,0031
559.	ENSECAG00000009167	DACT1	Dishevelled Binding Antagonist Of Beta Catenin 1	1,07618	5E-23
560.	ENSECAG00000014207	TENT5A	terminal nucleotidyltransferase 5A	1,07328	6E-14
561.	ENSECAG00000014526	PPIL6	peptidylprolyl isomerase like 6	1,07254	8E-10
562.	ENSECAG00000014953	KIF15	kinesin family member 15	1,07055	0,0002
563.	ENSECAG00000021310	RND3	Rho family GTPase 3	1,06893	2E-29
564.	ENSECAG00000018810	HELLS	helicase, lymphoid specific	1,0685	9E-05
565.	ENSECAG00000027765	ENSECAG00000027765		1,0662	3E-20
566.	ENSECAG00000021453	TICRR	TOPBP1 interacting checkpoint and replication regulator	1,0644	6E-05
567.	ENSECAG00000033960	GALNT16	Polypeptide N-Acetylgalactosaminyltransferase 16	1,06271	4E-10
568.	ENSECAG00000024339	CAMK2D	calcium/calmodulin dependent protein kinase II delta	1,06189	1E-25
569.	ENSECAG00000010558	PTGFR	prostaglandin F receptor	1,06151	2E-21
570.	ENSECAG00000019952	TRIO	trio Rho guanine nucleotide exchange factor	1,05769	2E-18
571.	ENSECAG00000019485	PPP4R4	protein phosphatase 4 regulatory subunit 4	1,05761	0,0469
572.	ENSECAG00000021364	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1,05555	2E-23
573.	ENSECAG00000023969	PLPP6	Phospholipid Phosphatase 6	1,0539	0,0004
574.	ENSECAG00000018145	NT5DC3	5'-nucleotidase domain containing 3	1,05382	9E-05
575.	ENSECAG00000007767	REEP5	receptor accessory protein 5	1,05079	3E-32
576.	ENSECAG00000009797	PRTFDC1	phosphoribosyl transferase domain containing 1	1,04935	4E-06

577.	ENSECAG00000021331	NOTCH3	notch receptor 3	1,04852	0,0034
578.	ENSECAG00000019382	S100A10	S100 Calcium Binding Protein A10	1,0481	2E-16
579.	ENSECAG00000019565	DLX5	distal-less homeobox 5	1,04756	0,0002
580.	ENSECAG00000024190	UCHL3	Ubiquitin C-Terminal Hydrolase L3	1,04717	9E-39
581.	ENSECAG00000021192	PEAR1	platelet endothelial aggregation receptor 1	1,04505	2E-28
582.	ENSECAG00000039655	RARRES1	Retinoic Acid Receptor Responder 1	1,04494	1E-20
583.	ENSECAG00000009400	ARRDC4	arrestin domain containing 4	1,04191	1E-09
584.	ENSECAG00000000397	SDHA	succinate dehydrogenase complex flavoprotein subunit A	1,04102	8E-56
585.	ENSECAG00000022900	RAP1GAP	RAP1 GTPase activating protein	1,04082	0,008
586.	ENSECAG00000022739	CA4	carbonic anhydrase 4	1,03712	6E-06
587.	ENSECAG00000031899	CDC26	cell division cycle 26	1,03221	1E-20
588.	ENSECAG00000025150	LMO4	LIM domain only 4	1,02395	3E-33
589.	ENSECAG00000024868	DAB2IP	DAB2 interacting protein	1,02104	2E-12
590.	ENSECAG00000009163	NUF2	NUF2 component of NDC80 kinetochore complex	1,01753	0,0009
591.	ENSECAG00000009420	NT5E	5'-Nucleotidase Ecto	1,01469	0,0094
592.	ENSECAG00000017777	PLK1	polo like kinase 1	1,01404	3E-05
593.	ENSECAG00000007072	PRPF4	pre-mRNA processing factor 4	1,01312	4E-12
594.	ENSECAG00000019103	EXD2	exonuclease 3'-5' domain containing 2	1,01272	1E-36
595.	ENSECAG00000024054	SLC18A2	solute carrier family 18 member A2	1,01114	3E-09
596.	ENSECAG00000023527	PHF19	PHD finger protein 19	1,00996	0,0004
597.	ENSECAG00000006607	KIF11	kinesin family member 11	1,00752	1E-10
598.	ENSECAG00000016417	TBC1D4	TBC1 domain family member 4	1,00691	4E-13
599.	ENSECAG00000015461	CACNA1G	calcium voltage-gated channel subunit alpha1 G	1,00634	5E-11
600.	ENSECAG00000008634	NCAPH	non-SMC condensin I complex subunit H	1,00591	0,0002
601.	ENSECAG00000014368	MCM5	minichromosome maintenance complex component 5	1,00446	1E-07
602.	ENSECAG00000024107	ROR1	receptor tyrosine kinase like orphan receptor 1	1,00108	2E-09
603.	ENSECAG00000019533	FGFR3	Fibroblast Growth Factor Receptor 3	1,00033	0,0252
604.	ENSECAG00000039741	ENSECAG00000039741		-1,0002	0,0012
605.	ENSECAG00000000158	SPATA6	Spermatogenesis Associated 6	-1,0008	2E-07
606.	ENSECAG00000018663	PLB1	Phospholipase B1	-1,001	0,0005
607.	ENSECAG00000030809	BICRA	BRD4 Interacting Chromatin Remodeling Complex Associated Protein	-1,0012	8E-17
608.	ENSECAG00000018258	WDR35	WD repeat domain 35	-1,0013	1E-08
609.	ENSECAG00000016958	CXXC5	CXXC finger protein 5	-1,0026	1E-17
610.	ENSECAG00000024200	POU6F1	POU class 6 homeobox 1	-1,0053	0,0015
611.	ENSECAG000000008809	OAS3	2'-5'-oligoadenylate synthetase 3	-1,0063	4E-09
612.	ENSECAG00000009543	EPSTI1	epithelial stromal interaction 1	-1,0066	8E-13
613.	ENSECAG00000013393	AHR	aryl hydrocarbon receptor	-1,0074	4E-14
614.	ENSECAG00000021856	PADI2	Peptidyl Arginine Deiminase 2	-1,0075	0,0012
615.	ENSECAG00000032188	ENSECAG00000032188		-1,0118	4E-28
616.	ENSECAG00000020596	HMGB3	high mobility group box 3	-1,012	2E-12
617.	ENSECAG00000005995	BCOR	BCL6 corepressor	-1,0142	7E-21
618.	ENSECAG00000007373	SHTN1	Shootin 1	-1,0151	3E-30
619.	ENSECAG00000042287	ENSECAG00000042287		-1,0191	0,0085
620.	ENSECAG00000009648	CLIP1	CAP-Gly domain containing linker protein 1	-1,0201	5E-42
621.	ENSECAG00000042273	CACNB1	calcium voltage-gated channel auxiliary subunit beta 1	-1,021	0,0045
622.	ENSECAG00000012839	TMC4	transmembrane channel like 4	-1,0231	0,0066
623.	ENSECAG00000011829	PID1	Phosphotyrosine Interaction Domain Containing 1	-1,0242	3E-17
624.	ENSECAG00000002116	SLC19A1	solute carrier family 19 member 1	-1,0248	2E-08
625.	ENSECAG00000017566	MVB12B	multivesicular body subunit 12B	-1,0264	1E-11
626.	ENSECAG00000022683	RSPO1	R-spondin 1	-1,027	3E-07
627.	ENSECAG00000015144	CADM1	cell adhesion molecule 1	-1,0274	4E-08
628.	ENSECAG00000009418	RASSF7	Ras Association Domain Family Member 7	-1,029	8E-06
629.	ENSECAG00000012132	ENSECAG00000012132	2'-5'-oligoadenylate synthase-like protein 2	-1,0292	3E-07
630.	ENSECAG00000033821	ANKRD33B	Ankyrin Repeat Domain 33B	-1,0301	0,0158

631.	ENSECAG00000011467	ALPL	alkaline phosphatase, biomineralization associated	-1,0309	5E-07
632.	ENSECAG00000019391	TNFSF10	TNF Superfamily Member 10	-1,0318	4E-15
633.	ENSECAG00000000637	STAC2	SH3 and cysteine rich domain 2	-1,0318	2E-13
634.	ENSECAG00000026969	RIMKLB	ribosomal modification protein rimK like family member B	-1,0341	2E-12
635.	ENSECAG00000020259	SMAD3	SMAD Family Member 3	-1,0344	7E-16
636.	ENSECAG00000022839	ENSECAG00000022839		-1,0356	7E-11
637.	ENSECAG00000020473	CTIF	cap binding complex dependent translation initiation factor	-1,0402	6E-12
638.	ENSECAG00000018924	PTK2B	protein tyrosine kinase 2 beta	-1,0415	7E-09
639.	ENSECAG00000020085	RELL2	RELT like 2	-1,0415	0,0026
640.	ENSECAG00000018218	SYNPO2	synaptopodin 2	-1,0423	3E-18
641.	ENSECAG00000025050	CCN4	Cellular Communication Network Factor 4	-1,0429	0,0002
642.	ENSECAG00000004493	MAB21L1	mab-21 like 1	-1,0449	0,006
643.	ENSECAG00000021092	KLF15	KLF transcription factor 15	-1,0454	1E-09
644.	ENSECAG00000008751	ENSECAG00000008751		-1,0469	3E-08
645.	ENSECAG00000018743	EVA1C	eva-1 homolog C	-1,0481	0,0252
646.	ENSECAG00000009650	TSNAXIP1	translin associated factor X interacting protein 1	-1,0483	0,0251
647.	ENSECAG00000015358	STARD10	StAR Related Lipid Transfer Domain Containing 10	-1,049	6E-06
648.	ENSECAG00000018830	DYNLRB2	Dynein Light Chain Roadblock-Type 2	-1,0505	0,0313
649.	ENSECAG00000015180	NEXN	nexilin F-actin binding protein	-1,0519	2E-08
650.	ENSECAG00000003570	PICK1	protein interacting with PRKCA 1	-1,0572	8E-07
651.	ENSECAG00000032860	ENSECAG00000032860		-1,0596	0,0001
652.	ENSECAG00000031250	KLRG2	killer cell lectin like receptor G2	-1,0627	5E-07
653.	ENSECAG00000003331	PLEKHH2	pleckstrin homology, MyTH4 and FERM domain containing H2	-1,0652	6E-11
654.	ENSECAG00000021670	GGT5	gamma-glutamyltransferase 5	-1,0654	0,0009
655.	ENSECAG00000020508	RPS6KA2	ribosomal protein S6 kinase A2	-1,0655	3E-24
656.	ENSECAG00000015840	PODN	podocan	-1,0662	7E-16
657.	ENSECAG00000015444	SLC37A1	solute carrier family 37 member 1	-1,0673	2E-09
658.	ENSECAG00000016613	PHLDB2	Pleckstrin Homology Like Domain Family B Member 2	-1,0687	4E-81
659.	ENSECAG00000032849	ENSECAG00000032849		-1,069	0,0002
660.	ENSECAG00000021653	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	-1,0704	1E-25
661.	ENSECAG00000008564	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1,0708	0,0072
662.	ENSECAG00000026951	ARVCF	ARVCF delta catenin family member	-1,0709	9E-05
663.	ENSECAG00000001128	ASTN2	astrotactin 2	-1,0735	4E-13
664.	ENSECAG00000039591	ZNF469	zinc finger protein 469	-1,075	1E-12
665.	ENSECAG00000024039	HFM1	Helicase For Meiosis 1	-1,0785	2E-05
666.	ENSECAG00000015878	AMOT	angiominin	-1,0791	2E-06
667.	ENSECAG00000023088	BMF	Bcl2 Modifying Factor	-1,0806	0,0112
668.	ENSECAG00000010322	LDHD	lactate dehydrogenase D	-1,0809	0,0002
669.	ENSECAG00000012105	IGSF9B	immunoglobulin superfamily member 9B	-1,0817	0,0381
670.	ENSECAG00000007718	TMOD1	Tropomodulin 1	-1,0821	8E-19
671.	ENSECAG00000040532	ENSECAG00000040532		-1,0831	0,0199
672.	ENSECAG00000033952	TMEM123	transmembrane protein 123	-1,0835	3E-24
673.	ENSECAG00000015510	FGF7	fibroblast growth factor 7	-1,0839	1E-06
674.	ENSECAG00000014382	ZDHHC23	zinc finger DHHC-type palmitoyltransferase 23	-1,0849	3E-06
675.	ENSECAG00000022129	HOXD3	homeobox D3	-1,0898	1E-09
676.	ENSECAG00000015048	CGN	cingulin	-1,0902	0,0008
677.	ENSECAG00000009038	TMEM255A	transmembrane protein 255A	-1,0912	6E-18
678.	ENSECAG00000016973	FILIP1L	filamin A interacting protein 1 like	-1,0919	7E-35
679.	ENSECAG00000014003	TMEM192	transmembrane protein 192	-1,094	8E-22
680.	ENSECAG00000009626	TNFAIP3	TNF alpha induced protein 3	-1,0948	6E-19
681.	ENSECAG00000024705	MAFB	MAF bZIP transcription factor B	-1,0958	2E-19
682.	ENSECAG00000012541	SLC38A4	solute carrier family 38 member 4	-1,0958	2E-14

683.	ENSECAG00000011747	BCL7A	BAF Chromatin Remodeling Complex Subunit BCL7A	-1,0965	0,0028
684.	ENSECAG00000019716	CCDC88C	BAF Chromatin Remodeling Complex Subunit BCL7A	-1,0972	2E-12
685.	ENSECAG00000007508	IRF2	interferon regulatory factor 2	-1,0985	1E-19
686.	ENSECAG00000020587	GM2A	ganglioside GM2 activator	-1,0986	2E-13
687.	ENSECAG00000020411	ENSECAG00000020411	folate receptor alpha	-1,1019	3E-16
688.	ENSECAG00000020932	SVIL	supervillin	-1,1043	3E-10
689.	ENSECAG00000005573	LOXL4	lysyl oxidase like 4	-1,1057	2E-21
690.	ENSECAG00000017743	SESN3	Sestrin 3	-1,1087	4E-06
691.	ENSECAG00000021125	TFAP2C	transcription factor AP-2 gamma	-1,1094	3E-08
692.	ENSECAG00000024271	TEX9	Testis Expressed 9	-1,1101	3E-07
693.	ENSECAG00000008662	DPYSL2	dihydropyrimidinase like 2	-1,1115	2E-37
694.	ENSECAG00000010695	FGF21	fibroblast growth factor 21	-1,1133	0,0021
695.	ENSECAG00000014491	NLRC5	NLR family CARD domain containing 5	-1,1144	1E-19
696.	ENSECAG00000000943	PTGES	Prostaglandin E Synthase	-1,1145	1E-10
697.	ENSECAG00000015865	GLUL	glutamate-ammonia ligase	-1,1156	3E-22
698.	ENSECAG00000012012	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5	-1,1217	7E-20
699.	ENSECAG00000014247	TINAGL1	tubulointerstitial nephritis antigen like 1	-1,1232	2E-08
700.	ENSECAG00000022721	BCAR3	BCAR3 adaptor protein, NSP family member	-1,1247	3E-09
701.	ENSECAG00000017501	TOR4A	torsin family 4 member A	-1,1276	0,0034
702.	ENSECAG00000009911	SLC12A7	solute carrier family 12 member 7	-1,1303	2E-21
703.	ENSECAG00000005108	SMIM29	Small Integral Membrane Protein 29	-1,1308	1E-10
704.	ENSECAG00000014108	TNFRSF8	TNF receptor superfamily member 8	-1,1316	5E-09
705.	ENSECAG00000017147	CCDC9B	coiled-coil domain containing 9B	-1,132	5E-25
706.	ENSECAG00000000541	PTCH2	Patched 2	-1,1386	3E-07
707.	ENSECAG00000007330	ALS2CL	ALS2 C-terminal like	-1,1412	0,0178
708.	ENSECAG00000021368	FGGY	FGGY carbohydrate kinase domain containing	-1,143	3E-07
709.	ENSECAG00000016232	IL22RA1	interleukin 22 receptor subunit alpha 1	-1,1438	0,0338
710.	ENSECAG00000020421	TOMM34	translocase of outer mitochondrial membrane 34	-1,1458	2E-15
711.	ENSECAG00000013956	ROBO3	roundabout guidance receptor 3	-1,1483	9E-05
712.	ENSECAG00000014867	PLBD1	phospholipase B domain containing 1	-1,1521	0,0012
713.	ENSECAG00000019932	ENSECAG00000019932	galectin-9	-1,1537	1E-16
714.	ENSECAG00000016171	GRM7	glutamate metabotropic receptor 7	-1,1544	5E-05
715.	ENSECAG00000021448	PADI1	peptidyl arginine deiminase 1	-1,1546	0,0194
716.	ENSECAG00000015134	PELI2	pellino E3 ubiquitin protein ligase family member 2	-1,1578	5E-07
717.	ENSECAG00000023416	F3	Coagulation Factor III, Tissue Factor	-1,1583	0,0013
718.	ENSECAG00000000386	LRRC23	leucine rich repeat containing 23	-1,1592	0,033
719.	ENSECAG00000015608	CRIM1	cysteine rich transmembrane BMP regulator 1	-1,1592	8E-18
720.	ENSECAG00000002083	KCTD12	potassium channel tetramerization domain containing 12	-1,161	3E-22
721.	ENSECAG00000010004	PRUNE2	prune homolog 2 with BCH domain	-1,1625	3E-10
722.	ENSECAG00000013450	CORO6	coronin 6	-1,1647	0,0027
723.	ENSECAG00000017402	SNX32	sorting nexin 32	-1,1684	0,0218
724.	ENSECAG00000022823	PLCE1	phospholipase C epsilon 1	-1,1698	2E-13
725.	ENSECAG00000028267	CYP2C111	cytochrome P450 family 2 subfamily C member 111	-1,1699	8E-06
726.	ENSECAG00000001312	GPR146	G protein-coupled receptor 146	-1,1718	0,0203
727.	ENSECAG00000006020	RRAGB	Ras related GTP binding B	-1,1722	2E-32
728.	ENSECAG00000009637	OCA2	OCA2 melanosomal transmembrane protein	-1,1735	1E-06
729.	ENSECAG000000037711	DDIT4L	DNA Damage Inducible Transcript 4 Like	-1,1752	0,022
730.	ENSECAG00000019602	DLEC1	DLEC1 cilia and flagella associated protein	-1,1771	0,0004
731.	ENSECAG00000030502	ENSECAG00000030502		-1,1792	4E-08
732.	ENSECAG00000011138	COL4A4	collagen type IV alpha 4 chain	-1,1793	0,0002
733.	ENSECAG00000000026	XG	Xg Glycoprotein	-1,1798	2E-35
734.	ENSECAG00000019974	CFAP298	Cilia And Flagella Associated Protein 298	-1,1813	2E-11

735.	ENSECAG00000013574	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1	-1,1823	3E-07
736.	ENSECAG00000017676	BMP4	Bone Morphogenetic Protein 4	-1,1829	6E-13
737.	ENSECAG00000010546	KLF5	KLF transcription factor 5	-1,1895	0,0006
738.	ENSECAG00000011797	SOD2	Superoxide Dismutase 2	-1,1897	6E-12
739.	ENSECAG00000022441	ESR1	estrogen receptor 1	-1,1903	2E-09
740.	ENSECAG00000014880	CFAP45	V-set and immunoglobulin domain containing 8	-1,1905	3E-05
741.	ENSECAG00000011111	FMNL2	formin like 2	-1,1917	4E-23
742.	ENSECAG00000025138	MARCHF9	membrane associated ring-CH-type finger 9	-1,1926	1E-09
743.	ENSECAG00000019176	KRT80	keratin 80	-1,1942	0,0074
744.	ENSECAG00000009311	SH3TC2	SH3 domain and tetratricopeptide repeats 2	-1,1942	0,0465
745.	ENSECAG00000016733	PDLIM5	PDZ and LIM domain 5	-1,1984	4E-29
746.	ENSECAG00000001716	PLXNA2	Plexin A2	-1,1987	2E-11
747.	ENSECAG00000010667	ERG	ETS transcription factor ERG	-1,2031	0,0013
748.	ENSECAG00000016706	ENC1	ectodermal-neural cortex 1	-1,2034	6E-25
749.	ENSECAG00000000178	RUNX1T1	RUNX1 Partner Transcriptional Co-Repressor 1	-1,2063	4E-26
750.	ENSECAG00000016238	RPS6KA1	ribosomal protein S6 kinase A1	-1,2119	1E-05
751.	ENSECAG00000013170	JADE2	jade family PHD finger 2	-1,2131	4E-08
752.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	-1,2133	0,0003
753.	ENSECAG00000007210	CTSL	cathepsin L	-1,2135	0,0137
754.	ENSECAG00000001598	IFI35	interferon induced protein 35	-1,221	3E-11
755.	ENSECAG00000033234	CBLN2	cerebellin 2 precursor	-1,2221	0,0001
756.	ENSECAG00000015140	LIPG	lipase G, endothelial type	-1,2256	1E-15
757.	ENSECAG00000000713	MDM1	Mdm1 Nuclear Protein	-1,2304	1E-28
758.	ENSECAG00000020702	NPHP1	nephrocystin 1	-1,2336	4E-05
759.	ENSECAG000000007047	ASPN	Asporin	-1,2342	0,0005
760.	ENSECAG00000002390	ENSECAG00000002390	protein BEX1	-1,2387	1E-10
761.	ENSECAG00000019199	ENSECAG00000019199		-1,2399	9E-13
762.	ENSECAG00000009968	SH3PXD2B	SH3 And PX Domains 2B	-1,2417	6E-23
763.	ENSECAG00000032515	CEBPA	CCAAT enhancer binding protein alpha	-1,2431	1E-06
764.	ENSECAG00000008565	GPR37	G protein-coupled receptor 37	-1,2455	9E-06
765.	ENSECAG00000024570	BRINP2	BMP/retinoic acid inducible neural specific 2	-1,2479	2E-10
766.	ENSECAG00000019648	MID1	midline 1	-1,2501	1E-06
767.	ENSECAG00000015023	FAM184A	family with sequence similarity 184 member A	-1,2502	2E-10
768.	ENSECAG00000025076	CTTNBP2	cortactin binding protein 2	-1,2519	1E-18
769.	ENSECAG00000017454	KIAA1755	KIAA1755	-1,2524	0,0165
770.	ENSECAG00000005794	MYRIP	myosin VIIA and Rab interacting protein	-1,2525	5E-05
771.	ENSECAG00000022594	SCEL	sciellin	-1,253	0,0495
772.	ENSECAG00000015766	SNCA	synuclein alpha	-1,2538	0,0016
773.	ENSECAG00000008638	RERE	arginine-glutamic acid dipeptide repeats	-1,2539	2E-51
774.	ENSECAG00000013544	TMEM268	transmembrane protein 268	-1,2539	7E-29
775.	ENSECAG00000015611	ETV4	ETS variant transcription factor 4	-1,2558	3E-05
776.	ENSECAG00000016667	ENSECAG00000016667		-1,2559	4E-13
777.	ENSECAG00000000658	GPNMB	Glycoprotein Nmb	-1,257	9E-18
778.	ENSECAG00000020548	ENSECAG00000020548	caspase-14	-1,2573	0,0037
779.	ENSECAG00000007385	NIBAN1	niban apoptosis regulator 1	-1,2579	2E-15
780.	ENSECAG00000009088	KCNMB2	potassium calcium-activated channel subfamily M regulatory beta subunit 2	-1,2588	3E-12
781.	ENSECAG00000013633	ARHGAP6	Rho GTPase activating protein 6	-1,261	9E-17
782.	ENSECAG00000012340	RADX	RPA1 related single stranded DNA binding protein, X-linked	-1,2664	0,0072
783.	ENSECAG00000010436	ENSECAG00000010436	protein BEX1	-1,2673	0,0001
784.	ENSECAG00000041280	ENSECAG00000041280		-1,2682	0,0442
785.	ENSECAG00000005343	GNAL	G protein subunit alpha L	-1,2756	0,0009
786.	ENSECAG00000019478	CCDC158	coiled-coil domain containing 158	-1,2759	2E-10
787.	ENSECAG00000005525	GJA1	gap junction protein alpha 1	-1,2775	9E-16
788.	ENSECAG00000017191	SPP1	secreted phosphoprotein 1	-1,2792	0,0329
789.	ENSECAG00000021042	VASH1	vasohibin 1	-1,2801	2E-37

790.	ENSECAG00000038536	CCND1	Cyclin D1	-1,2808	2E-44
791.	ENSECAG00000010437	TCEA3	transcription elongation factor A3	-1,2852	1E-13
792.	ENSECAG00000017157	IER3	immediate early response 3	-1,2875	3E-19
793.	ENSECAG00000008738	ID2	Inhibitor Of DNA Binding 2	-1,2881	6E-05
794.	ENSECAG00000000284	USP18	Ubiquitin Specific Peptidase 18	-1,2909	0,0009
795.	ENSECAG00000037336	ENSECAG00000037336	heparan sulfate glucosamine 3-O-sulfotransferase 4	-1,2923	0,0003
796.	ENSECAG00000012660	HLA-DRA	Major Histocompatibility Complex, Class II, DR Alpha	-1,2981	0,0333
797.	ENSECAG00000005563	PRSS23	serine protease 23	-1,2985	2E-08
798.	ENSECAG00000021184	LAT	Linker For Activation Of T Cells	-1,2987	1E-06
799.	ENSECAG00000016917	TES	testin LIM domain protein	-1,2996	3E-29
800.	ENSECAG00000012962	SAMD12	sterile alpha motif domain containing 12	-1,3036	1E-06
801.	ENSECAG00000019660	TRIB1	tribbles pseudokinase 1	-1,3043	1E-12
802.	ENSECAG00000017335	CDON	cell adhesion associated, oncogene regulated	-1,3047	2E-27
803.	ENSECAG00000007173	HMCN1	hemicentin 1	-1,306	3E-09
804.	ENSECAG00000037937	DUSP6	dual specificity phosphatase 6	-1,308	4E-05
805.	ENSECAG00000000234	GPC6	glypican 6	-1,3101	1E-11
806.	ENSECAG00000031322	ENSECAG00000031322		-1,3101	2E-13
807.	ENSECAG00000017937	ENSECAG00000017937		-1,3114	4E-06
808.	ENSECAG00000011776	MX1	MX dynamin like GTPase 1	-1,3116	0,0002
809.	ENSECAG00000010881	DPYD	dihydropyrimidine dehydrogenase	-1,3146	7E-08
810.	ENSECAG00000019781	SERPINE1	Serpin Family E Member 1	-1,3146	6E-16
811.	ENSECAG00000008425	LURAP1L	leucine rich adaptor protein 1 like	-1,3155	6E-10
812.	ENSECAG00000001634	INSYN1	inhibitory synaptic factor 1	-1,3158	3E-26
813.	ENSECAG00000013382	SLC25A34	Solute Carrier Family 25 Member 34	-1,3168	7E-08
814.	ENSECAG00000019193	NCAM1	neural cell adhesion molecule 1	-1,317	1E-37
815.	ENSECAG00000006546	ZNF521	zinc finger protein 521	-1,3177	8E-25
816.	ENSECAG00000019429	KDR	kinase insert domain receptor	-1,3193	0,0067
817.	ENSECAG00000006803	SYTL2	synaptotagmin like 2	-1,3195	1E-22
818.	ENSECAG00000009101	IRAG1	inositol 1,4,5-triphosphate receptor associated 1	-1,3233	5E-16
819.	ENSECAG00000003602	SLC26A7	solute carrier family 26 member 7	-1,3244	0,0017
820.	ENSECAG00000035205	ZNF853	zinc finger protein 853	-1,326	2E-27
821.	ENSECAG00000022556	ABCA9	ATP binding cassette subfamily A member 9	-1,3262	2E-38
822.	ENSECAG00000000709	ENSECAG00000000709	neuroligin 4 X-linked	-1,3275	0,0005
823.	ENSECAG00000016600	PPFIA4	PTPRF interacting protein alpha 4	-1,3288	7E-11
824.	ENSECAG00000019371	SLC1A3	solute carrier family 1 member 3	-1,3322	4E-12
825.	ENSECAG00000013514	DUSP5	dual specificity phosphatase 5	-1,3327	0,0058
826.	ENSECAG00000019818	POU2F3	POU class 2 homeobox 3	-1,3339	8E-20
827.	ENSECAG00000012791	GBP6	guanylate-binding protein 6	-1,3342	6E-17
828.	ENSECAG00000008906	PARP15	poly(ADP-ribose) polymerase family member 15	-1,3381	3E-12
829.	ENSECAG00000039359	CYS1	cystin 1	-1,3406	0,0023
830.	ENSECAG00000009742	S100A12	S100 Calcium Binding Protein A12	-1,3411	0,0168
831.	ENSECAG00000024305	RTN1	reticulon 1	-1,3426	1E-23
832.	ENSECAG00000017927	DOK7	docking protein 7	-1,3445	0,0189
833.	ENSECAG00000012373	PLEKHG6	pleckstrin homology and RhoGEF domain containing G6	-1,3455	0,0114
834.	ENSECAG00000024049	S100A13	S100 Calcium Binding Protein A13	-1,3459	7E-16
835.	ENSECAG00000017986	AXIN2	axin 2	-1,3467	1E-08
836.	ENSECAG00000009291	ENKD1	enkurin domain containing 1	-1,35	1E-07
837.	ENSECAG00000014422	OAS2	2'-5'-oligoadenylate synthetase 2	-1,3511	6E-14
838.	ENSECAG00000005360	MITF	melanocyte inducing transcription factor	-1,3574	2E-19
839.	ENSECAG00000019617	ATP8B4	ATPase phospholipid transporting 8B4 (putative)	-1,3577	0,013
840.	ENSECAG00000013079	USP54	ubiquitin specific peptidase 54	-1,3606	5E-30
841.	ENSECAG00000010560	MIP-2BETA	CXCL3	-1,3611	5E-12
842.	ENSECAG00000023892	RPS6KA5	ribosomal protein S6 kinase A5	-1,3612	3E-20
843.	ENSECAG00000016204	SLC31A2	solute carrier family 31 member 2	-1,3625	3E-08
844.	ENSECAG00000017943	ZNF608	zinc finger protein 608	-1,3636	2E-11
845.	ENSECAG00000041653	DUSP15	dual specificity phosphatase 15	-1,3684	4E-11
846.	ENSECAG00000017381	ENSECAG00000017381	interferon regulatory factor 4	-1,3706	3E-08

847.	ENSECAG00000005659	TPST1	tyrosylprotein sulfotransferase 1	-1,3737	4E-22
848.	ENSECAG00000024062	DDX60L	DEXD/H-box 60 like	-1,3743	3E-09
849.	ENSECAG00000007176	ELOVL7	ELOVL fatty acid elongase 7	-1,3751	1E-18
850.	ENSECAG00000010818	EGR2	early growth response 2	-1,3764	0,0002
851.	ENSECAG00000001159	FOXSI	forkhead box S1	-1,3827	1E-11
852.	ENSECAG00000037214	TUBB4A	tubulin beta 4A class IVa	-1,3835	7E-08
853.	ENSECAG00000026274	eca-mir-143	microRNA mir-143	-1,3855	0,041
854.	ENSECAG00000013243	ANKRD45	ankyrin repeat domain 45	-1,3876	0,0077
855.	ENSECAG00000031302	ENSECAG00000031302	aldo-keto reductase family 1 member C23-like protein	-1,3908	3E-05
856.	ENSECAG00000040382	ENSECAG00000040382		-1,3993	3E-11
857.	ENSECAG00000013081	MMP9	Matrix Metalloproteinase 9	-1,4002	5E-05
858.	ENSECAG00000012799	COL8A2	collagen type VIII alpha 2 chain	-1,4014	0,0318
859.	ENSECAG00000011729	ST6GAL2	ST6 beta-galactoside alpha-2,6-sialyltransferase 2	-1,4018	1E-28
860.	ENSECAG00000012133	VEGFC	vascular endothelial growth factor C	-1,402	2E-16
861.	ENSECAG00000021043	ACP3	acid phosphatase 3	-1,4029	0,0123
862.	ENSECAG00000007542	SH3D19	SH3 domain containing 19	-1,4113	2E-43
863.	ENSECAG00000018191	GUCY1A2	guanylate cyclase 1 soluble subunit alpha 2	-1,42	6E-20
864.	ENSECAG00000036146	PNCK	Pregnancy Up-Regulated Nonubiquitous CaM Kinase	-1,421	0,0134
865.	ENSECAG00000024459	MARK1	Microtubule Affinity Regulating Kinase 1	-1,4221	5E-55
866.	ENSECAG00000012767	C7H11orf52		-1,4226	0,0056
867.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-1,4239	3E-17
868.	ENSECAG00000001100	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1	-1,4272	1E-12
869.	ENSECAG00000010201	ENSECAG00000010201	feline leukemia virus subgroup C receptor-related protein 2	-1,4308	4E-19
870.	ENSECAG00000023089	SLAIN1	SLAIN motif family member 1	-1,4318	0,0042
871.	ENSECAG00000040468	ENSECAG00000040468		-1,4319	5E-05
872.	ENSECAG00000022638	PLD1	phospholipase D1	-1,432	2E-20
873.	ENSECAG00000021174	ACKR4	atypical chemokine receptor 4	-1,4338	2E-05
874.	ENSECAG00000017346	GCLC	glutamate-cysteine ligase catalytic subunit	-1,4344	9E-50
875.	ENSECAG00000019512	PDGFC	platelet derived growth factor C	-1,4386	6E-21
876.	ENSECAG00000009813	CD83	CD83 Molecule	-1,4391	9E-08
877.	ENSECAG00000017443	TRIM14	tripartite motif containing 14	-1,4406	0,0195
878.	ENSECAG00000014708	PTH1H	Parathyroid Hormone Like Hormone	-1,4493	1E-11
879.	ENSECAG00000017701	CELSR2	Cadherin EGF LAG Seven-Pass G-Type Receptor 2	-1,4524	7E-05
880.	ENSECAG00000008237	KLHL13	kelch like family member 13	-1,4528	6E-23
881.	ENSECAG00000009660	PLEKHA6	Pleckstrin Homology Domain Containing A6	-1,4541	1E-13
882.	ENSECAG00000013242	ABCA3	ATP binding cassette subfamily A member 3	-1,4547	4E-61
883.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	-1,4563	2E-18
884.	ENSECAG00000023387	FRRS1	Ferric Chelate Reductase 1	-1,4608	0,0105
885.	ENSECAG00000014275	DBP	D-box binding PAR bZIP transcription factor	-1,4629	6E-18
886.	ENSECAG00000038332	ENSECAG00000038332		-1,4631	8E-32
887.	ENSECAG00000019758	TNFSF13B	TNF Superfamily Member 13b	-1,4637	1E-09
888.	ENSECAG00000015808	DNAI7	dynein axonemal intermediate chain 7	-1,4641	0,0492
889.	ENSECAG00000007183	SEMA3E	semaphorin 3E	-1,4654	0,0175
890.	ENSECAG00000024448	TRIM63	tripartite motif containing 63	-1,4689	8E-23
891.	ENSECAG00000015128	CAPG	capping actin protein, gelsolin like	-1,4702	3E-31
892.	ENSECAG00000035459	BATF2	basic leucine zipper ATF-like transcription factor 2	-1,472	6E-09
893.	ENSECAG00000005704	CARD11	caspase recruitment domain family member 11	-1,4785	9E-16
894.	ENSECAG00000013960	FGFR2	fibroblast growth factor receptor 2	-1,48	0,0013
895.	ENSECAG00000021518	SLX1A	SLX1 Homolog A, Structure-Specific Endonuclease Subunit	-1,4806	8E-08
896.	ENSECAG00000018888	RENBP	renin binding protein	-1,4819	7E-23
897.	ENSECAG00000018147	ENSECAG00000018147		-1,4835	3E-34
898.	ENSECAG00000000217	MTSS2	MTSS I-BAR domain containing 2	-1,4865	5E-36
899.	ENSECAG00000016349	GLIS1	GLIS Family Zinc Finger 1	-1,4899	9E-14

900.	ENSECAG00000014660	IFNGR2	interferon gamma receptor 2	-1,5079	1E-23
901.	ENSECAG00000001279	AGTR1	angiotensin II receptor type 1	-1,5097	0,0149
902.	ENSECAG00000016559	TNFSF11	TNF superfamily member 11	-1,5141	2E-05
903.	ENSECAG000000040252	HMGA2	high mobility group AT-hook 2	-1,5234	1E-07
904.	ENSECAG00000001900	ENSECAG00000001900	pleckstrin homology like domain family A member 1	-1,5242	2E-17
905.	ENSECAG000000035745	TBX1	T-box transcription factor 1	-1,5251	0,0109
906.	ENSECAG000000043642	NREP	neuronal regeneration related protein	-1,5296	5E-09
907.	ENSECAG000000008259	MASP1	MBL associated serine protease 1	-1,5334	1E-23
908.	ENSECAG000000020311	BCO2	beta-carotene oxygenase 2	-1,5367	9E-06
909.	ENSECAG000000018696	PDE2A	phosphodiesterase 2A	-1,5422	0,0441
910.	ENSECAG000000011423	HSD17B1	Hydroxysteroid 17-Beta Dehydrogenase 1	-1,5533	0,0247
911.	ENSECAG000000006796	ZSCAN26	Zinc Finger And SCAN Domain Containing 26	-1,5542	7E-05
912.	ENSECAG000000017661	ZC2HC1C	zinc finger C2HC-type containing 1C	-1,5557	5E-08
913.	ENSECAG000000018292	FZD3	Frizzled Class Receptor 3	-1,5584	9E-05
914.	ENSECAG000000009483	PRLR	prolactin receptor	-1,5715	0,0291
915.	ENSECAG000000006567	SLITRK4	SLIT and NTRK like family member 4	-1,5799	3E-06
916.	ENSECAG000000019137	MAML3	mastermind like transcriptional coactivator 3	-1,5803	2E-10
917.	ENSECAG000000023101	TP53I11	tumor protein p53 inducible protein 11	-1,5816	8E-31
918.	ENSECAG000000012327	IL34	interleukin 34	-1,5844	2E-34
919.	ENSECAG000000000731	SPMIP5	Sperm Microtubule Inner Protein 5	-1,5864	0,0009
920.	ENSECAG000000018359	COL13A1	collagen type XIII alpha 1 chain	-1,5926	0,0095
921.	ENSECAG000000009168	GADD45B	Growth Arrest And DNA Damage Inducible Beta	-1,5971	6E-09
922.	ENSECAG000000019008	SHROOM3	shroom family member 3	-1,5993	1E-54
923.	ENSECAG000000024367	CASP1	Caspase 1	-1,6002	0,0467
924.	ENSECAG000000006829	KAZN	Kazrin, Periplakin Interacting Protein	-1,6006	4E-23
925.	ENSECAG000000013217	ECHDC2	enoyl-CoA hydratase domain containing 2	-1,6014	2E-21
926.	ENSECAG000000020045	HAPLN4	hyaluronan and proteoglycan link protein 4	-1,6025	2E-14
927.	ENSECAG000000013016	TMEM82	Transmembrane Protein 82	-1,6047	0,0467
928.	ENSECAG000000022071	OTUD7A	OTU Deubiquitinase 7A	-1,6052	0,0495
929.	ENSECAG000000016047	CPA6	carboxypeptidase A6	-1,6057	7E-28
930.	ENSECAG000000015927	CABLES1	Cdk5 and Abl enzyme substrate 1	-1,6066	0,006
931.	ENSECAG000000023958	ADPRH	ADP-ribosylarginine hydrolase	-1,6142	2E-32
932.	ENSECAG000000028351	HES6	Hes Family BHLH Transcription Factor 6	-1,6152	0,0005
933.	ENSECAG000000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,6199	2E-18
934.	ENSECAG000000010531	F2RL2	Coagulation Factor II Thrombin Receptor Like 2	-1,6211	7E-30
935.	ENSECAG000000015387	MYLK	myosin light chain kinase	-1,624	6E-67
936.	ENSECAG000000020399	CTHRC1	collagen triple helix repeat containing 1	-1,6257	7E-23
937.	ENSECAG000000008535	DNAH10	dynein axonemal heavy chain 10	-1,6272	8E-08
938.	ENSECAG000000021374	TCF23	Transcription Factor 23	-1,633	2E-11
939.	ENSECAG000000010814	ENSECAG000000010814	embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	-1,6332	0,0007
940.	ENSECAG000000019495	C5H1orf141	chromosome 5 C1orf141 homolog	-1,6337	0,0139
941.	ENSECAG000000012282	MPP7	MAGUK p55 scaffold protein 7	-1,6348	0,001
942.	ENSECAG000000018280	TACC2	transforming acidic coiled-coil containing protein 2	-1,6367	2E-29
943.	ENSECAG000000007881	IFIH1	Interferon Induced With Helicase C Domain 1	-1,6487	3E-16
944.	ENSECAG000000010405	TRIB2	tribbles pseudokinase 2	-1,6493	3E-17
945.	ENSECAG000000013022	ACTC1	actin alpha cardiac muscle 1	-1,6495	0,0456
946.	ENSECAG000000032719	ENSECAG000000032719	piggyBac transposable element derived 1	-1,6497	7E-06
947.	ENSECAG000000008793	PGBD1	piggyBac transposable element derived 1	-1,6498	5E-07
948.	ENSECAG000000000593	PTN	pleiotrophin	-1,6503	2E-49
949.	ENSECAG000000021360	KCNMB1	potassium calcium-activated channel subfamily M regulatory beta subunit 1	-1,6512	1E-14

950.	ENSECAG00000005631	BDKRB1	bradykinin receptor B1	-1,6569	6E-11
951.	ENSECAG00000024148	RAB39A	RAB39A, Member RAS Oncogene Family	-1,6579	1E-06
952.	ENSECAG00000006419	C2CD2	C2 Calcium Dependent Domain Containing 2	-1,6623	6E-49
953.	ENSECAG00000011887	ADAMTSL2	ADAMTS like 2	-1,6648	3E-05
954.	ENSECAG00000041010	SPINK8	serine peptidase inhibitor Kazal type 8 (putative)	-1,666	0,0338
955.	ENSECAG00000026856	AIF1L	allograft inflammatory factor 1 like	-1,6698	3E-09
956.	ENSECAG00000019717	ECM2	extracellular matrix protein 2	-1,6699	6E-21
957.	ENSECAG00000008618	LCA5L	lebercilin LCA5 like	-1,6716	0,0297
958.	ENSECAG00000016784	TDH	L-threonine dehydrogenase	-1,6778	0,0226
959.	ENSECAG00000022724	CYP26B1	cytochrome P450 family 26 subfamily B member 1	-1,6808	0,0056
960.	ENSECAG00000017459	ARRB1	arrestin beta 1	-1,6828	2E-08
961.	ENSECAG00000020437	BCL2	BCL2 apoptosis regulator	-1,6868	8E-07
962.	ENSECAG00000020835	ADAMTS20	ADAM metalloproteinase with thrombospondin type 1 motif 20	-1,6904	2E-17
963.	ENSECAG00000021903	LAMC2	laminin subunit gamma 2	-1,6945	2E-18
964.	ENSECAG00000013176	MEGF6	Multiple EGF Like Domains 6	-1,6968	2E-13
965.	ENSECAG00000006501	FJX1	Four-Jointed Box Kinase 1	-1,7007	4E-13
966.	ENSECAG00000018916	FILIP1	Filamin A Interacting Protein 1	-1,7012	0,0114
967.	ENSECAG00000016129	ABLIM3	actin binding LIM protein family member 3	-1,7096	9E-06
968.	ENSECAG00000000650	NPL	N-Acetylneuraminase Pyruvate Lyase	-1,7097	6E-55
969.	ENSECAG00000018631	LTBP2	latent transforming growth factor beta binding protein 2	-1,715	1E-33
970.	ENSECAG00000025066	PLA2G3	phospholipase A2 group III	-1,717	1E-06
971.	ENSECAG00000015715	ADAMTS15	ADAM Metalloproteinase With Thrombospondin Type 1 Motif 15	-1,717	9E-23
972.	ENSECAG00000001442	RHEBL1	RHEB Like 1	-1,7365	0,0228
973.	ENSECAG00000017812	AHRR	aryl hydrocarbon receptor repressor	-1,7365	7E-07
974.	ENSECAG00000015845	PLD5	phospholipase D family member 5	-1,7377	0,0006
975.	ENSECAG00000020162	PRR5L	proline rich 5 like	-1,7473	1E-07
976.	ENSECAG00000004445	PDE11A	phosphodiesterase 11A	-1,7538	3E-18
977.	ENSECAG00000033029	ENSECAG00000033029	interferon-induced protein with tetratricopeptide repeats 1B	-1,7666	3E-11
978.	ENSECAG00000013228	GLT1D1	glycosyltransferase 1 domain containing 1	-1,7694	0,0007
979.	ENSECAG00000018112	FAM241B	family with sequence similarity 241 member B	-1,7836	8E-05
980.	ENSECAG00000027532	SCARNA10	small nucleolar RNA U85	-1,7961	0,028
981.	ENSECAG00000018803	PGM2L1	phosphoglucomutase 2 like 1	-1,7978	2E-21
982.	ENSECAG00000036801	ABCC9	ATP-binding cassette sub-family C member 9	-1,8032	0,0072
983.	ENSECAG00000042952	GPX3	Glutathione Peroxidase 3	-1,8045	0,0073
984.	ENSECAG00000012993	JAG1	jagged canonical Notch ligand 1	-1,8145	3E-09
985.	ENSECAG00000019940	AKAP6	A-kinase anchoring protein 6	-1,8211	6E-24
986.	ENSECAG00000004778	RTN4R	reticulon 4 receptor	-1,8259	0,0218
987.	ENSECAG00000022513	NPAS1	neuronal PAS domain protein 1	-1,8332	6E-06
988.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-1,8338	6E-05
989.	ENSECAG00000007900	ART3	ADP-ribosyltransferase 3 (inactive)	-1,8433	0,029
990.	ENSECAG00000008518	NPNT	nephronectin	-1,8496	2E-06
991.	ENSECAG00000020494	B3GALT2	beta-1,3-galactosyltransferase 2	-1,8497	0,0007
992.	ENSECAG00000024531	ADM	Glutathione Peroxidase 3	-1,8498	2E-08
993.	ENSECAG00000018105	IL4I1	interleukin 4 induced 1	-1,85	6E-05
994.	ENSECAG00000014992	JAM2	Junctional Adhesion Molecule 2	-1,8511	5E-05
995.	ENSECAG00000030878	ENSECAG00000030878	Scm polycomb group protein like 1	-1,8527	0,0008
996.	ENSECAG00000016957	OLFM1	olfactomedin 1	-1,8553	5E-28
997.	ENSECAG00000010830	MMP11	Matrix Metalloproteinase 11	-1,8618	4E-25
998.	ENSECAG00000010109	IGF1	insulin like growth factor 1	-1,8638	3E-13
999.	ENSECAG00000038712	TNXB	tenascin XB	-1,8639	0,0009
1000.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-1,8641	8E-09
1001.	ENSECAG00000008983	LRRTM1	leucine rich repeat transmembrane neuronal 1	-1,8688	1E-09
1002.	ENSECAG00000023960	KLHL30	kelch like family member 30	-1,874	2E-06

1003.	ENSECAG00000009388	IQCD	IQ motif containing D	-1,8793	0,0091
1004.	ENSECAG00000024961	XAF1	XIAP Associated Factor 1	-1,8813	2E-13
1005.	ENSECAG00000023626	PTGIR	prostaglandin I2 receptor	-1,8815	0,0215
1006.	ENSECAG00000023161	IGSF10	immunoglobulin superfamily member 10	-1,8838	7E-11
1007.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-1,8857	2E-13
1008.	ENSECAG00000012773	CMPK2	cytidine/uridine monophosphate kinase 2	-1,8866	5E-08
1009.	ENSECAG00000019445	MMP12	matrix metalloproteinase 3	-1,8891	0,0069
1010.	ENSECAG00000016721	RUBCNL	rubicon like autophagy enhancer	-1,8961	3E-18
1011.	ENSECAG00000015379	FGD4	FYVE, RhoGEF And PH Domain Containing 4	-1,8964	3E-22
1012.	ENSECAG00000011358	TMEM86A	transmembrane protein 86A	-1,904	5E-15
1013.	ENSECAG00000010721	MGP	Matrix Gla Protein	-1,9048	5E-59
1014.	ENSECAG00000013677	FRY	FRY microtubule binding protein	-1,9061	5E-27
1015.	ENSECAG00000012507	CRYAB	Crystallin Alpha B	-1,9092	4E-22
1016.	ENSECAG00000013138	RAB27B	RAB27B, member RAS oncogene family	-1,9134	0,0005
1017.	ENSECAG00000024358	ZBTB16	zinc finger and BTB domain containing 16	-1,9173	0,0052
1018.	ENSECAG00000014730	PELI3	pellino E3 ubiquitin protein ligase family member 3	-1,9207	0,0062
1019.	ENSECAG00000021973	NFE2L3	NFE2 like bZIP transcription factor 3	-1,9238	0,0047
1020.	ENSECAG00000015952	BDNF	brain derived neurotrophic factor	-1,9366	5E-15
1021.	ENSECAG00000024937	TBC1D21	TBC1 domain family member 21	-1,9367	0,0157
1022.	ENSECAG00000006482	CRISP2	Cysteine Rich Secretory Protein 2	-1,9377	0,0072
1023.	ENSECAG00000018716	FGF9	fibroblast growth factor 9	-1,9494	8E-28
1024.	ENSECAG00000006879	PLA2G5	phospholipase A2 group V	-1,95	1E-06
1025.	ENSECAG00000014519	ETV7	ETS variant transcription factor 7	-1,9532	1E-13
1026.	ENSECAG00000023264	RTP4	Receptor Transporter Protein 4	-1,9548	0,0007
1027.	ENSECAG00000000931	TMEM119	transmembrane protein 119	-1,9563	9E-40
1028.	ENSECAG00000002211	CD80	CD80 molecule	-1,9592	1E-05
1029.	ENSECAG00000018016	FAR2	fatty acyl-CoA reductase 2	-1,9626	0,0023
1030.	ENSECAG00000008087	ENSECAG00000008087	stabilizer of axonemal microtubules 2	-1,9678	0,0081
1031.	ENSECAG00000024757	ENSECAG00000024757	neuronal acetylcholine receptor subunit alpha-7	-1,9738	6E-13
1032.	ENSECAG00000023528	ATP2B2	ATPase plasma membrane Ca2+ transporting 2	-1,978	0,019
1033.	ENSECAG00000028632	ENSECAG00000028632		-1,9784	4E-06
1034.	ENSECAG00000017844	OXTR	Oxytocin Receptor	-1,9863	6E-37
1035.	ENSECAG00000015669	RAB3B	RAB3B, member RAS oncogene family	-1,9932	4E-10
1036.	ENSECAG00000012990	CALCRL	calcitonin receptor like receptor	-2,0022	4E-21
1037.	ENSECAG00000036372	ISLR2	immunoglobulin superfamily containing leucine rich repeat 2	-2,0069	8E-19
1038.	ENSECAG00000025446	ENSECAG00000025446	small nucleolar RNA U2-19	-2,0076	0,0209
1039.	ENSECAG00000026945	HES1	hes family bHLH transcription factor 1	-2,0209	4E-06
1040.	ENSECAG00000016824	NRP2	neuropilin 2	-2,0305	3E-87
1041.	ENSECAG00000014194	EGFLAM	EGF Like, Fibronectin Type III And Laminin G Domains	-2,0307	0,0079
1042.	ENSECAG00000004258	IL17RB	interleukin 17 receptor B	-2,0392	0,0007
1043.	ENSECAG00000009218	EGFL6	EGF like domain multiple 6	-2,0489	1E-12
1044.	ENSECAG00000002874	LRRN1	leucine rich repeat neuronal 1	-2,0521	9E-05
1045.	ENSECAG00000015000	FAM83G	Family With Sequence Similarity 83 Member G	-2,0526	4E-20
1046.	ENSECAG00000022047	APOD	apolipoprotein D	-2,0545	3E-34
1047.	ENSECAG00000020093	NPR3	natriuretic peptide receptor 3	-2,0694	5E-06
1048.	ENSECAG00000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-2,0734	1E-35
1049.	ENSECAG00000000420	BANP	BTG3 associated nuclear protein	-2,0901	3E-75
1050.	ENSECAG00000000121	NAV3	neuron navigator 3	-2,0907	8E-29
1051.	ENSECAG00000015388	EDIL3	EGF like repeats and discoidin domains 3	-2,1106	3E-23
1052.	ENSECAG00000009125	UPK3A	Uroplakin 3A	-2,1158	0,0177
1053.	ENSECAG00000010118	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	-2,121	0,0032
1054.	ENSECAG00000009261	AOAH	acyloxyacyl hydrolase	-2,1221	0,0054

1055.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-2,1306	1E-48
1056.	ENSECAG00000035101	ANOS1	anosmin 1	-2,1392	5E-05
1057.	ENSECAG000000041716	ENSECAG000000041716		-2,1403	1E-06
1058.	ENSECAG00000022525	AREG	amphiregulin	-2,1417	0,0021
1059.	ENSECAG00000033624	ENSECAG00000033624	contactin-associated protein-like 4	-2,1432	0,0077
1060.	ENSECAG00000021576	SGCG	sarcoglycan gamma	-2,1491	0,0022
1061.	ENSECAG00000027244	RNaseP_nuc		-2,1582	0,0033
1062.	ENSECAG00000016430	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	-2,175	4E-06
1063.	ENSECAG00000004433	ENSECAG00000004433	interferon-induced protein with tetratricopeptide repeats 1	-2,1768	2E-06
1064.	ENSECAG00000040154	ELN	elastin	-2,1775	3E-07
1065.	ENSECAG00000019087	CTSK	Cathepsin K	-2,1795	2E-42
1066.	ENSECAG00000015460	HCLS1	Hematopoietic Cell-Specific Lyn Substrate 1	-2,1849	0,0029
1067.	ENSECAG00000023765	IGSF9	immunoglobulin superfamily member 9	-2,1851	2E-06
1068.	ENSECAG00000022015	ALOX12	arachidonate 12-lipoxygenase, 12S-type	-2,1872	0,0008
1069.	ENSECAG00000041748	COL4A3	collagen type IV alpha 3 chain	-2,1901	5E-25
1070.	ENSECAG00000010553	NGF	nerve growth factor	-2,1985	4E-10
1071.	ENSECAG00000006666	CAVIN4	caveolae associated protein 4	-2,2024	0,0092
1072.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-2,2027	2E-14
1073.	ENSECAG00000016735	VCAM1	Vascular Cell Adhesion Molecule 1	-2,2322	2E-05
1074.	ENSECAG00000015760	ITGA3	integrin subunit alpha 3	-2,2419	9E-52
1075.	ENSECAG00000017042	ENSECAG00000017042	membrane-spanning 4-domains subfamily A member 6A	-2,2422	0,0002
1076.	ENSECAG00000021468	POPDC2	popeye domain containing 2	-2,2437	6E-05
1077.	ENSECAG00000009948	ADCY5	adenylate cyclase 5	-2,267	1E-36
1078.	ENSECAG00000015745	BLNK	B cell linker	-2,2696	9E-61
1079.	ENSECAG00000011749	MSX2	msh homeobox 2	-2,2744	2E-31
1080.	ENSECAG00000015569	MATCAP2	microtubule associated tyrosine carboxypeptidase 2	-2,2754	4E-05
1081.	ENSECAG00000011404	ENSECAG00000011404	serum amyloid A protein	-2,2943	3E-10
1082.	ENSECAG00000023963	NMNAT2	Nicotinamide Nucleotide Adenylyltransferase 2	-2,2986	3E-26
1083.	ENSECAG00000035548	ENSECAG00000035548	T-lymphocyte surface antigen Ly-9	-2,2994	4E-10
1084.	ENSECAG00000012514	ENSECAG00000012514		-2,3053	0,0003
1085.	ENSECAG00000026067	RNase_MRP		-2,314	0,0025
1086.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-2,3236	1E-30
1087.	ENSECAG00000015736	ODAPH	odontogenesis associated phosphoprotein	-2,3295	0,0002
1088.	ENSECAG00000014695	RBP5	retinol binding protein 5	-2,3311	1E-13
1089.	ENSECAG00000013758	ENSECAG00000013758		-2,3487	6E-11
1090.	ENSECAG00000021165	STAC	SH3 and cysteine rich domain	-2,3533	4E-39
1091.	ENSECAG00000021078	GRB14	growth factor receptor bound protein 14	-2,3648	9E-15
1092.	ENSECAG00000014398	ENSECAG00000014398		-2,3656	0,0072
1093.	ENSECAG00000003266	PIRT	phosphoinositide interacting regulator of transient receptor potential channels	-2,3667	4E-05
1094.	ENSECAG00000012212	LRP1B	LDL Receptor Related Protein 1B	-2,3697	2E-09
1095.	ENSECAG00000013739	DLGAP1	DLG associated protein 1	-2,3749	1E-07
1096.	ENSECAG00000012539	RASGRP3	RAS guanyl releasing protein 3	-2,3955	0,0094
1097.	ENSECAG00000041924	COL23A1	collagen type XXIII alpha 1 chain	-2,4049	3E-05
1098.	ENSECAG00000017816	ADORA1	adenosine A1 receptor	-2,4327	3E-37
1099.	ENSECAG00000017689	ARHGEF28	Rho Guanine Nucleotide Exchange Factor 28	-2,4386	3E-55
1100.	ENSECAG00000000278	FCAMR	Fc Alpha And Mu Receptor	-2,4545	7E-11
1101.	ENSECAG00000013817	CYP1A1	cytochrome P450 family 1 subfamily A member 1	-2,4552	2E-06
1102.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-2,4613	4E-65
1103.	ENSECAG00000013486	C4BPA	complement component 4 binding protein alpha	-2,4654	4E-32
1104.	ENSECAG00000009949	P2RX7	purinergic receptor P2X 7	-2,4704	6E-13
1105.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-2,4919	3E-13

1106.	ENSECAG00000029347	ADAMTS6	centromere protein K	-2,494	1E-106
1107.	ENSECAG00000009138	MME	membrane metalloendopeptidase	-2,496	6E-12
1108.	ENSECAG00000013036	MCAM	melanoma cell adhesion molecule	-2,5081	2E-31
1109.	ENSECAG00000015552	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-2,518	4E-16
1110.	ENSECAG00000034367	ENSECAG00000034367		-2,5353	1E-10
1111.	ENSECAG00000016234	ANGPTL2	angiopoietin like 2	-2,538	7E-62
1112.	ENSECAG00000034457	U1	U1 spliceosomal RNA	-2,5388	0,0248
1113.	ENSECAG00000019499	ISG20	Interferon Stimulated Exonuclease Gene 20	-2,545	2E-10
1114.	ENSECAG00000005126	TRIM22	tripartite motif containing 22	-2,545	0,0132
1115.	ENSECAG00000023039	CCN3	cellular communication network factor 3	-2,5542	6E-06
1116.	ENSECAG00000037655	GDNF	glial cell derived neurotrophic factor	-2,5638	9E-05
1117.	ENSECAG00000014962	FAXDC2	Fatty Acid Hydroxylase Domain Containing 2	-2,5669	4E-17
1118.	ENSECAG00000010747	SH3BGR	SH3 domain binding glutamate rich protein	-2,5882	2E-48
1119.	ENSECAG00000001488	GPR171	G protein-coupled receptor 171	-2,59	1E-22
1120.	ENSECAG00000018049	PAMR1	peptidase domain containing associated with muscle regeneration 1	-2,5956	1E-63
1121.	ENSECAG00000024873	CCDC190	Coiled-Coil Domain Containing 190	-2,5999	1E-04
1122.	ENSECAG00000017802	OGN	osteoglycin	-2,6021	3E-59
1123.	ENSECAG00000009211	ANGPT4	angiopoietin 4	-2,6045	2E-22
1124.	ENSECAG00000021534	ASPA	aspartoacylase	-2,6431	0,0021
1125.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-2,6724	3E-63
1126.	ENSECAG00000003230	AKAP5	A-kinase anchoring protein 5	-2,6763	1E-28
1127.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-2,6768	2E-15
1128.	ENSECAG00000016015	PCDH19	protocadherin 19	-2,6804	1E-16
1129.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-2,684	2E-16
1130.	ENSECAG00000008221	S100A4	S100 calcium binding protein A4	-2,7001	1E-16
1131.	ENSECAG00000015834	DMD	dystrophin	-2,7107	9E-27
1132.	ENSECAG00000004274	IQGAP2	IQ motif containing GTPase activating protein 2	-2,7139	2E-10
1133.	ENSECAG00000014287	OMD	osteonmodulin	-2,7349	2E-28
1134.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-2,7421	1E-21
1135.	ENSECAG00000018108	VGF	VGF nerve growth factor inducible	-2,7499	1E-08
1136.	ENSECAG00000000343	HACD4	3-hydroxyacyl-CoA dehydratase 4	-2,7689	1E-11
1137.	ENSECAG00000015644	SLC1A2	solute carrier family 1 member 2	-2,7749	0,0002
1138.	ENSECAG00000010185	IFIT2	Interferon Induced Protein With Tetratricopeptide Repeats 2	-2,8052	9E-21
1139.	ENSECAG00000011498	SFRP4	Secreted Frizzled Related Protein 4	-2,8273	8E-06
1140.	ENSECAG00000029465	CHI3L1	chitinase 3 like 1	-2,8959	3E-13
1141.	ENSECAG00000024028	PDE6A	phosphodiesterase 6A	-2,931	0,0002
1142.	ENSECAG00000036921	ENSECAG00000036921		-2,967	0,0007
1143.	ENSECAG00000016176	NDP	norrin cystine knot growth factor NDP	-2,9902	0,0002
1144.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-3,0083	1E-05
1145.	ENSECAG00000007798	ME3	Malic Enzyme 3	-3,0619	9E-12
1146.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-3,1178	1E-80
1147.	ENSECAG00000000740	C10H6orf58		-3,146	2E-12
1148.	ENSECAG00000038866	PTX3	pentraxin 3	-3,1556	5E-10
1149.	ENSECAG00000017988	FRMD7	FERM Domain Containing 7	-3,156	0,0004
1150.	ENSECAG00000000813	SCN5A	sodium voltage-gated channel alpha subunit 5	-3,1659	8E-05
1151.	ENSECAG00000016984	RANBP3L	RAN binding protein 3 like	-3,1681	6E-11
1152.	ENSECAG00000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-3,1704	4E-14
1153.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-3,2597	7E-19
1154.	ENSECAG00000018308	GREB1	growth regulating estrogen receptor binding 1	-3,2672	2E-39
1155.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-3,348	5E-16
1156.	ENSECAG00000030850	FGF18	Fibroblast Growth Factor 18	-3,4031	2E-22
1157.	ENSECAG00000016251	ENSECAG00000016251		-3,4138	4E-14

1158.	ENSECAG00000030969	CHST4	carbohydrate sulfotransferase 4	-3,4337	2E-08
1159.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-3,452	2E-07
1160.	ENSECAG00000015846	VASH2	vasohibin 2	-3,4539	1E-40
1161.	ENSECAG00000010791	LMCD1	LIM and cysteine rich domains 1	-3,4806	4E-13
1162.	ENSECAG00000021101	LG14	Leucine Rich Repeat LGI Family Member 4	-3,4845	2E-05
1163.	ENSECAG00000010465	FRMD1	FERM domain containing 1	-3,4956	9E-05
1164.	ENSECAG00000020901	CLCA2	chloride channel accessory 2	-3,513	4E-10
1165.	ENSECAG00000024612	SNED1	Sushi, Nidogen And EGF Like Domains 1	-3,5925	5E-06
1166.	ENSECAG00000019412	HTR2B	5-hydroxytryptamine receptor 2B	-3,6064	3E-05
1167.	ENSECAG00000023720	SLAMF8	SLAM family member 8	-3,6354	8E-09
1168.	ENSECAG00000022629	SLC1A7	Solute Carrier Family 1 Member 7	-3,6893	1E-78
1169.	ENSECAG00000032728	HBQ1	Hemoglobin Subunit Theta 1	-3,701	5E-13
1170.	ENSECAG00000006717	ASS1	argininosuccinate synthase 1	-3,7164	6E-21
1171.	ENSECAG00000017280	MAPK10	mitogen-activated protein kinase 10	-3,7421	9E-07
1172.	ENSECAG00000010869	CAPN6	calpain 6	-3,7489	8E-07
1173.	ENSECAG00000013893	SCARA5	Scavenger Receptor Class A Member 5	-3,7703	4E-05
1174.	ENSECAG00000015484	ATP6V0D2	ATPase H ⁺ transporting V0 subunit d2	-3,785	2E-43
1175.	ENSECAG00000034955	BHLHE41	basic helix-loop-helix family member e41	-3,8785	7E-41
1176.	ENSECAG00000002430	PRKAG3	protein kinase AMP-activated non-catalytic subunit gamma 3	-3,8919	3E-16
1177.	ENSECAG00000006853	UBD	ubiquitin D	-3,9168	3E-36
1178.	ENSECAG00000014513	TNFSF15	TNF superfamily member 15	-3,9992	1E-13
1179.	ENSECAG00000012109	SOSTDC1	sclerostin domain containing 1	-4,1197	9E-27
1180.	ENSECAG00000010128	SEMA4D	semaphorin 4D	-4,1911	7E-21
1181.	ENSECAG00000039231	ATOX1	atonal bHLH transcription factor 8	-4,2494	2E-05
1182.	ENSECAG00000031859	ENSECAG00000031859		-4,2802	9E-18
1183.	ENSECAG00000029885	CHST7	carbohydrate sulfotransferase 7	-4,3436	2E-34
1184.	ENSECAG00000012667	RBFOX1	RNA Binding Fox-1 Homolog 1	-5,0797	3E-25
1185.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-5,1607	5E-33
1186.	ENSECAG00000009103	MLANA	melan-A	-5,4848	7E-07
1187.	ENSECAG00000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-5,765	2E-13

Supplementary Table 8. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category I endometria treated with interleukin 13 (IL-13) for 48 hours (Research task 3, Experiment 1).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	Padj
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	11,23792	1,1E-24
2.	ENSECAG00000016867	CISH	Cytokine Inducible SH2 Containing Protein	7,801064	1,2E-14
3.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	7,75192	2E-106
4.	ENSECAG00000034282	CCL8	C-C motif chemokine 7	6,53882	5,5E-31
5.	ENSECAG00000038698	ALOX15	Arachidonate 15-Lipoxygenase	6,537912	2E-10
6.	ENSECAG00000013482	SERPINA3	Serpin Family A Member 3	6,329048	5,2E-35
7.	ENSECAG00000020738	CDH26	cadherin 26	6,243501	1,6E-60
8.	ENSECAG00000004201	FETUB	fetuin B	6,104537	3,1E-12
9.	ENSECAG00000020578	PDCD1LG2	Programmed Cell Death 1 Ligand 2	6,072479	7,8E-31
10.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	6,063142	8E-29
11.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	5,515653	1,3E-07
12.	ENSECAG00000018409	NOX5	NADPH oxidase 5	5,478831	7E-09
13.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	5,44063	9,3E-14
14.	ENSECAG00000019282	HDC	histidine decarboxylase	5,427789	1,6E-05
15.	ENSECAG00000002249	PLEKHG4B	Pleckstrin Homology And RhoGEF Domain Containing G4B	5,405328	3,8E-10
16.	ENSECAG00000014650	INSRR	insulin receptor related receptor	5,323572	1,2E-34
17.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	4,99158	1,8E-08
18.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	4,918051	1,6E-05
19.	ENSECAG00000023032	AZIN2	Antizyme Inhibitor 2	4,672365	4,1E-21
20.	ENSECAG00000009916	GRIA4	glutamate ionotropic receptor AMPA type subunit 4	4,644424	7,9E-11
21.	ENSECAG00000008739	ENSECAG00000008739		4,577555	3,7E-06
22.	ENSECAG00000021182	TNFSF4	TNF superfamily member 4	4,484006	1,9E-05
23.	ENSECAG00000017948	BTN1A1	butyrophilin subfamily 1 member A1	4,210765	0,00074
24.	ENSECAG00000023918	DUOX1	dual oxidase 1	4,16479	1,1E-08
25.	ENSECAG00000023942	ENSECAG00000023942	ras GTPase-activating protein 4	4,085458	9,7E-15
26.	ENSECAG00000008034	PLPPR5	phospholipid phosphatase related 5	3,84776	0,0014
27.	ENSECAG00000014916	TNFRSF11B	TNF receptor superfamily member 11b	3,807307	5,4E-05
28.	ENSECAG00000016312	CD274	CD274 molecule	3,790058	1,4E-39
29.	ENSECAG00000026965	SOCS1	suppressor of cytokine signaling 1	3,682413	2,7E-06
30.	ENSECAG00000013703	PPP1R3C	Protein Phosphatase 1 Regulatory Subunit 3C	3,600189	6,8E-18
31.	ENSECAG00000011581	ENSECAG00000011581		3,520255	6,7E-07
32.	ENSECAG00000016169	COL6A6	collagen type VI alpha 6 chain	3,381976	0,02587
33.	ENSECAG00000005241	THBD	thrombomodulin	3,376162	1,8E-16
34.	ENSECAG00000009034	DUOXA1	dual oxidase maturation factor 1	3,355428	0,0053
35.	ENSECAG00000019800	TSPAN33	Tetraspanin 33	3,334165	9E-26
36.	ENSECAG00000023841	POSTN	periostin	3,196832	5,5E-07
37.	ENSECAG00000008880	SLC22A16	solute carrier family 22 member 16	3,179841	0,00032
38.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	3,154791	1,7E-34
39.	ENSECAG00000010805	PGM5	phosphoglucomutase 5	3,146231	5,9E-13
40.	ENSECAG00000021604	PDGFR1	platelet derived growth factor receptor like	3,06868	9,2E-32
41.	ENSECAG00000012830	CHN2	Chimerin 2	3,007202	1E-32
42.	ENSECAG00000001603	PEG10	Paternally Expressed 10	2,982867	0,00048
43.	ENSECAG00000022686	MRAP2	melanocortin 2 receptor accessory protein 2	2,920728	0,01093
44.	ENSECAG00000007825	CALCA	calcitonin-related polypeptide alpha	2,887653	7,2E-07
45.	ENSECAG00000000706	MEGF11	multiple EGF like domains 11	2,842977	4,2E-05
46.	ENSECAG00000009767	P2RX1	purinergic receptor P2X 1	2,802538	6,6E-06
47.	ENSECAG00000005379	HPGD		2,740945	0,00427
48.	ENSECAG00000021057	ADGRV1	adhesion G protein-coupled receptor V1	2,733744	1,8E-15
49.	ENSECAG00000013584	PSAPL1	prosaposin like 1	2,674451	0,04138
50.	ENSECAG00000000574	NIPAL4	NIPA Like Domain Containing 4	2,66374	6,6E-20
51.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	2,62046	0,00063

52.	ENSECAG00000017217	CA12	carbonic anhydrase 12	2,581489	7,7E-22
53.	ENSECAG00000024845	PI16	peptidase inhibitor 16	2,548744	1,3E-05
54.	ENSECAG00000000152	KITLG	KIT ligand	2,542773	1,8E-09
55.	ENSECAG00000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	2,532588	7,5E-25
56.	ENSECAG00000010750	VWCE	von Willebrand factor C and EGF domains	2,510545	7,6E-12
57.	ENSECAG00000032667	INA	Internexin Neuronal Intermediate Filament Protein Alpha	2,469706	0,01266
58.	ENSECAG00000016576	C1QTNF12	C1q And TNF Related 12	2,460054	4,5E-26
59.	ENSECAG00000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	2,451942	4,1E-05
60.	ENSECAG00000014817	RND2	Rho Family GTPase 2	2,444789	1,6E-10
61.	ENSECAG00000020258	SSC4D	scavenger receptor cysteine rich family member with 4 domains	2,427112	0,02498
62.	ENSECAG00000001372	SYN1	synapsin I	2,407594	0,00039
63.	ENSECAG00000013207	SHISA2	shisa family member 2	2,383958	0,00226
64.	ENSECAG00000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	2,362936	0,00096
65.	ENSECAG00000015657	TNNT1	troponin T1, slow skeletal type	2,355911	4,8E-08
66.	ENSECAG00000015842	ANKRD55	ankyrin repeat domain 55	2,314706	0,00017
67.	ENSECAG00000024779	SERPINA5	serpin family A member 5	2,265101	0,0003
68.	ENSECAG00000024694	KIF14	kinesin family member 14	2,254412	0,00038
69.	ENSECAG00000009046	BIN2	Bridging Integrator 2	2,240594	1,6E-10
70.	ENSECAG00000014145	TLL2	tolloid like 2	2,222925	0,02376
71.	ENSECAG00000024719	ENSECAG00000024719	solute carrier family 2 member 3	2,200732	2,1E-63
72.	ENSECAG00000005307	RNF183	ring finger protein 183	2,194748	5E-08
73.	ENSECAG00000023895	EXOC3L2	exocyst complex component 3 like 2	2,168849	1E-09
74.	ENSECAG00000014126	CFAP161	Cilia And Flagella Associated Protein 161	2,110122	3E-05
75.	ENSECAG00000011893	CNTNAP4	Contactin Associated Protein Family Member 4	2,106823	0,00978
76.	ENSECAG00000008059	PDE4C	phosphodiesterase 4C	2,104831	0,00883
77.	ENSECAG00000008787	CCNB3	cyclin B3	2,062228	0,04729
78.	ENSECAG00000001988	FAT3	FAT atypical cadherin 3	2,042267	0,0022
79.	ENSECAG00000014379	BMP3	bone morphogenetic protein 3	2,04012	2,3E-10
80.	ENSECAG00000003943	SYT5	synaptotagmin 5	1,986252	1,2E-24
81.	ENSECAG00000010053	HJURP	Holliday junction recognition protein	1,973326	7,7E-07
82.	ENSECAG00000009769	CNTN4	contactin 4	1,959961	0,00044
83.	ENSECAG00000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	1,957936	1,5E-54
84.	ENSECAG00000033890	CIDEC	cell death inducing DFFA like effector c	1,957627	5E-07
85.	ENSECAG00000013009	KIF26B	kinesin family member 26B	1,951473	9E-26
86.	ENSECAG00000017570	SYT4	synaptotagmin 4	1,948362	0,00065
87.	ENSECAG00000009580	LVRN	laeverin	1,939534	0,00134
88.	ENSECAG00000019438	OSMR	oncostatin M receptor	1,932931	1E-10
89.	ENSECAG00000017826	TMEM26	transmembrane protein 26	1,924033	1,1E-10
90.	ENSECAG00000019229	STAMBPL1	STAM binding protein like 1	1,903897	8,4E-48
91.	ENSECAG00000017598	IMPA2	inositol monophosphatase 2	1,89305	1,4E-06
92.	ENSECAG00000001064	RET	ret proto-oncogene	1,892948	0,02406
93.	ENSECAG00000009081	KIAA1210	KIAA1210	1,884451	2,9E-13
94.	ENSECAG00000023199	COL24A1	Collagen Type XXIV Alpha 1 Chain	1,872719	0,0019
95.	ENSECAG00000015069	BHLHE40	basic helix-loop-helix family member e40	1,86933	9E-13
96.	ENSECAG00000018118	BMERB1	bMERB domain containing 1	1,867149	7,4E-06
97.	ENSECAG00000012061	CES2	carboxylesterase 2	1,849391	0,02516
98.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	1,846288	5E-70
99.	ENSECAG00000010291	LRRC17	leucine rich repeat containing 17	1,844584	0,0024
100.	ENSECAG00000030455	ENSECAG00000030455		1,806666	0,00032
101.	ENSECAG00000011994	CYFIP2	cytoplasmic FMR1 interacting protein 2	1,80481	4,7E-06
102.	ENSECAG00000021976	LRATD2	LRAT domain containing 2	1,795643	0,00147
103.	ENSECAG00000010500	ITGA4	integrin subunit alpha 4	1,795149	5E-66
104.	ENSECAG00000004372	SLC22A3	Solute Carrier Family 22 Member 3	1,776739	2,6E-09
105.	ENSECAG00000015651	ARSF	arylsulfatase F	1,764847	0,00456
106.	ENSECAG00000023083	HGD	homogentisate 1,2-dioxygenase	1,743651	0,00806

107.	ENSECAG00000024322	ARSJ	arylsulfatase family member J	1,70127	1,8E-26
108.	ENSECAG00000022731	COL6A1	collagen type VI alpha 1 chain	1,680793	1E-11
109.	ENSECAG00000008506	HMMR	Hyaluronan Mediated Motility Receptor	1,671846	0,00012
110.	ENSECAG00000019129	FOXM1	forkhead box M1	1,661684	0,00243
111.	ENSECAG00000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	1,65364	9,9E-22
112.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	1,646782	7E-18
113.	ENSECAG00000011669	TNN	tenascin N	1,643931	2,1E-10
114.	ENSECAG00000013106	ESM1	endothelial cell specific molecule 1	1,643624	0,00121
115.	ENSECAG00000019551	CXCL12	C-X-C motif chemokine ligand 12	1,637757	1,1E-06
116.	ENSECAG00000014536	KIF23	kinesin family member 23	1,62729	8,3E-08
117.	ENSECAG00000022404	TRPV6	transient receptor potential cation channel subfamily V member 6	1,626965	1,3E-12
118.	ENSECAG00000001407	CHSY3	chondroitin sulfate synthase 3	1,622221	5E-08
119.	ENSECAG00000024406	KCP	kielin cysteine rich BMP regulator	1,620311	0,002
120.	ENSECAG00000021343	NRG1	neuregulin 1	1,617721	5,5E-06
121.	ENSECAG00000007300	DCLK1	doublecortin like kinase 1	1,617322	2,6E-11
122.	ENSECAG00000020111	IQGAP3	IQ Motif Containing GTPase Activating Protein 3	1,606418	0,00062
123.	ENSECAG00000014646	KNG1	kininogen 1	1,591289	5,9E-05
124.	ENSECAG00000016934	IL31RA	Interleukin 31 Receptor A	1,581472	0,01386
125.	ENSECAG00000010445	ST3GAL6	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 6	1,57737	3,4E-09
126.	ENSECAG00000015127	SLC13A4	solute carrier family 13 member 4	1,571423	2,3E-05
127.	ENSECAG00000009403	IL1RAPL2	interleukin 1 receptor accessory protein like 2	1,557792	0,0056
128.	ENSECAG00000000235	MTBP	MDM2 binding protein	1,544333	4,4E-15
129.	ENSECAG00000020769	FGF1	fibroblast growth factor 1	1,541448	7,6E-43
130.	ENSECAG00000012263	RNF19B	Ring Finger Protein 19B	1,532877	7E-68
131.	ENSECAG00000016742	TJP2	tight junction protein 2	1,531997	1,4E-05
132.	ENSECAG00000014787	RCAN1	regulator of calcineurin 1	1,523234	1E-45
133.	ENSECAG00000007918	TNS4	tensin 4	1,516421	1,1E-16
134.	ENSECAG00000024110	PENK	proenkephalin	1,513839	3,3E-05
135.	ENSECAG00000022931	TCF7L1	transcription factor 7 like 1	1,509841	3,6E-37
136.	ENSECAG00000019398	TFPI2	Tissue Factor Pathway Inhibitor 2	1,504194	1,6E-10
137.	ENSECAG00000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	1,49584	0,00114
138.	ENSECAG00000012826	CDO1	Cysteine Dioxygenase Type 1	1,495535	0,00505
139.	ENSECAG00000020767	IL7	interleukin 7	1,486871	8,6E-07
140.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	1,481408	0,02616
141.	ENSECAG00000022093	SLC2A5	solute carrier family 2 member 5	1,468502	0,04374
142.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	1,454091	3,3E-09
143.	ENSECAG00000024293	AMDHD1	amidohydrolase domain containing 1	1,447775	0,03472
144.	ENSECAG00000019038	KIF2C	kinesin family member 2C	1,445386	0,00036
145.	ENSECAG00000030024	MAPK13	mitogen-activated protein kinase 13	1,439205	1,9E-14
146.	ENSECAG00000016560	CRABP2	Cellular Retinoic Acid Binding Protein 2	1,438009	3,5E-08
147.	ENSECAG00000014511	IL11	Interleukin 11	1,437682	5,6E-30
148.	ENSECAG00000009535	FCER1G	Fc Epsilon Receptor Ig	1,425647	0,02243
149.	ENSECAG00000019705	CDC20	Cell Division Cycle 20	1,424582	3,5E-06
150.	ENSECAG00000011788	CDC45	cell division cycle 45	1,423616	0,00193
151.	ENSECAG00000023800	AK2	adenylate kinase 2	1,413157	5,5E-34
152.	ENSECAG00000032055	PROKR2	prokineticin receptor 2	1,409529	0,01364
153.	ENSECAG00000003789	RASL11B	RAS like family 11 member B	1,39491	1,6E-18
154.	ENSECAG00000023076	GPCPD1	glycerophosphocholine phosphodiesterase 1	1,394909	2E-07
155.	ENSECAG00000013731	STC1	Stanniocalcin 1	1,394885	6E-07
156.	ENSECAG00000006288	SIK1	salt inducible kinase 1	1,390418	8,6E-24
157.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	1,387475	9,1E-10
158.	ENSECAG00000018373	FAM234B	family with sequence similarity 234 member B	1,385098	3,9E-06
159.	ENSECAG00000014384	AURKB	aurora kinase B	1,382191	0,00498
160.	ENSECAG00000007432	PTGDR	Prostaglandin D2 Receptor	1,381209	0,00031

161.	ENSECAG00000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	1,375151	0,00018
162.	ENSECAG00000017015	MYH11	myosin heavy chain 11	1,369731	2E-08
163.	ENSECAG00000015966	SERPINB6	Serpin Family B Member 6	1,369279	3,3E-17
164.	ENSECAG00000034739	ADORA2A	adenosine A2a receptor	1,366526	1,3E-06
165.	ENSECAG00000024127	CENPF	centromere protein F	1,36261	0,00015
166.	ENSECAG00000038893	CST3	cystatin C	1,354582	4E-43
167.	ENSECAG00000020563	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1,339653	9,8E-36
168.	ENSECAG00000018874	PRICKLE1	Prickle Planar Cell Polarity Protein 1	1,331862	5E-34
169.	ENSECAG00000036105	ENSECAG00000036105		1,321426	0,02568
170.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,318413	0,01836
171.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	1,318374	3,3E-06
172.	ENSECAG00000023908	OLFML2A	olfactomedin like 2A	1,318245	0,00871
173.	ENSECAG00000018510	RGS20	Regulator Of G Protein Signaling 20	1,31767	0,002
174.	ENSECAG00000012179	RGS2	regulator of G protein signaling 2	1,310073	3,9E-08
175.	ENSECAG00000020808	TRIL	TLR4 interactor with leucine rich repeats	1,302354	0,00493
176.	ENSECAG00000003278	TRIM9	tripartite motif containing 9	1,301421	0,00019
177.	ENSECAG00000024750	NCALD	neurocalcin delta	1,293996	0,01434
178.	ENSECAG00000018322	EXO1	exonuclease 1	1,292393	0,0068
179.	ENSECAG00000021775	KRT8	keratin 8	1,290839	0,00114
180.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,286443	2E-20
181.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	1,286207	3,2E-07
182.	ENSECAG00000021746	SHROOM1	Shroom Family Member 1	1,284774	1,2E-11
183.	ENSECAG00000009299	ICAM5	intercellular adhesion molecule 5	1,280891	0,0307
184.	ENSECAG00000005719	PRKD1	protein kinase D1	1,273822	1,2E-22
185.	ENSECAG00000020927	NEK10	NIMA related kinase 10	1,273297	0,00235
186.	ENSECAG00000013035	ENPP1	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1	1,273096	0,00125
187.	ENSECAG00000016902	PRR16	proline rich 16	1,264009	6,8E-14
188.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	1,260239	2,4E-26
189.	ENSECAG00000014794	MIIP	Migration And Invasion Inhibitory Protein	1,253963	1E-30
190.	ENSECAG00000009700	ANK3	ankyrin 3	1,251191	0,01079
191.	ENSECAG00000010022	CYP17A1	Cytochrome P450 Family 17 Subfamily A Member 1	1,248566	0,00922
192.	ENSECAG00000015058	ARHGEF3	Rho guanine nucleotide exchange factor 3	1,246395	3,1E-24
193.	ENSECAG00000024574	GATA3	GATA binding protein 3	1,244423	0,03499
194.	ENSECAG00000016860	KIF20A	kinesin family member 20A	1,239107	1,7E-05
195.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	1,235688	0,00286
196.	ENSECAG00000024523	KLRG1	killer cell lectin like receptor G1	1,225112	0,01346
197.	ENSECAG00000015871	CDCA8	cell division cycle associated 8	1,224461	0,00743
198.	ENSECAG00000017017	LNK1	ligand of numb-protein X 1	1,222627	0,0007
199.	ENSECAG00000008569	TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1	1,221444	1,5E-14
200.	ENSECAG00000007964	EBF1	EBF transcription factor 1	1,217335	3,5E-18
201.	ENSECAG00000015806	CCNB1	cyclin B1	1,216213	3E-07
202.	ENSECAG00000032416	APC2	APC regulator of WNT signaling pathway 2	1,214663	0,04391
203.	ENSECAG00000014346	GBA3	glucosylceramidase beta 3	1,213837	0,00032
204.	ENSECAG00000023279	GATA6	GATA binding protein 6	1,209333	1,7E-07
205.	ENSECAG00000021088	GDF9		1,206886	0,01683
206.	ENSECAG00000017864	FMOD	fibromodulin	1,20352	0,0064
207.	ENSECAG00000016953	HLF	HLF transcription factor, PAR bZIP family member	1,202136	9,9E-08
208.	ENSECAG00000033164	ENSECAG00000033164	NAC alpha domain containing	1,196933	0,00852
209.	ENSECAG00000014774	MMP23	Matrix Metalloproteinase 23B	1,196376	1,3E-08
210.	ENSECAG00000019600	GRP	gastrin releasing peptide	1,194897	6,6E-05

211.	ENSECAG00000010188	ABHD3	abhydrolase domain containing 3, phospholipase	1,192658	1,3E-09
212.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,191233	1,4E-17
213.	ENSECAG00000002377	SPESP1	Sperm Equatorial Segment Protein 1	1,169916	5,9E-09
214.	ENSECAG00000000292	THSD7A		1,169761	0,00114
215.	ENSECAG00000013268	AP1S3	adaptor related protein complex 1 subunit sigma 3	1,168963	0,00255
216.	ENSECAG00000021201	BMP2	bone morphogenetic protein 2	1,154834	1,5E-16
217.	ENSECAG00000011008	MCOLN2	mucolipin TRP cation channel 2	1,149214	3,8E-18
218.	ENSECAG00000000225	CATSPERG	cation channel sperm associated auxiliary subunit gamma	1,148891	1,3E-09
219.	ENSECAG00000024851	EDNRB	endothelin receptor type B	1,144496	1,2E-06
220.	ENSECAG00000012104	TNFAIP6	Thrombospondin Type 1 Domain Containing 7A	1,140884	4,6E-15
221.	ENSECAG00000024428	PROCR	protein C receptor	1,140517	9,5E-21
222.	ENSECAG00000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,135494	1,7E-19
223.	ENSECAG00000008823	CDH11	cadherin 11	1,134783	4,5E-24
224.	ENSECAG00000024419	JADE1	jade family PHD finger 1	1,132836	1,6E-20
225.	ENSECAG00000024172	ADAMTS4	ADAM Metalloproteinase With Thrombospondin Type 1 Motif 4	1,131157	0,00378
226.	ENSECAG00000008493	SERPINF10	serpin family B member 10	1,127956	0,00114
227.	ENSECAG000000022780	TTYH2	Tweety Family Member 2	1,123552	3,1E-10
228.	ENSECAG00000014813	CCNB2	Cyclin B2	1,11849	0,04303
229.	ENSECAG00000020312	LRIG3	leucine rich repeats and immunoglobulin like domains 3	1,116164	1,1E-08
230.	ENSECAG00000036591	APLN	apelin	1,116144	0,00058
231.	ENSECAG00000008700	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	1,115838	0,03943
232.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,115796	5,7E-22
233.	ENSECAG00000017035	SHF	Src homology 2 domain containing F	1,115288	0,00229
234.	ENSECAG00000010447	EFEMP1	EGF Containing Fibulin Extracellular Matrix Protein 1	1,114539	0,03869
235.	ENSECAG00000012742	CXCL6	C-X-C motif chemokine ligand 6	1,113153	0,0371
236.	ENSECAG00000023134	KCNK5	potassium two pore domain channel subfamily K member 5	1,108214	5,7E-20
237.	ENSECAG00000006991	PECAM1	platelet and endothelial cell adhesion molecule 1	1,099684	1,4E-28
238.	ENSECAG00000005086	EGLN3	Egl-9 Family Hypoxia Inducible Factor 3	1,097935	1,9E-22
239.	ENSECAG00000018101	FBLN1	fibulin 1	1,096163	3,9E-13
240.	ENSECAG00000000122	GDA	Guanine Deaminase	1,093446	0,00383
241.	ENSECAG00000011099	VAV3	Vav Guanine Nucleotide Exchange Factor 3	1,080552	0,00026
242.	ENSECAG00000015822	VDR	vitamin D receptor	1,076881	1,2E-07
243.	ENSECAG00000014259	TIMP1	TIMP metalloproteinase inhibitor 1	1,069489	4,1E-16
244.	ENSECAG00000011475	ZNF703	Zinc Finger Protein 703	1,066845	3,1E-06
245.	ENSECAG00000002513	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase	1,061195	0,00146
246.	ENSECAG00000007018	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	1,052404	0,01427
247.	ENSECAG00000017922	ADAM19	ADAM metalloproteinase domain 19	1,049282	1,4E-30
248.	ENSECAG00000013691	MALT1	MALT1 paracaspase	1,045528	3,4E-09
249.	ENSECAG00000019750	IL6ST	interleukin 6 cytokine family signal transducer	1,042989	6,4E-18
250.	ENSECAG00000006060	RAI2	retinoic acid induced 2	1,038411	0,00102
251.	ENSECAG00000018476	TPX2	TPX2 microtubule nucleation factor	1,03309	0,00082
252.	ENSECAG00000011656	DPH5	diphthamide biosynthesis 5	1,029768	2,6E-10
253.	ENSECAG00000007991	WDR86	WD repeat domain 86	1,025363	7,4E-06
254.	ENSECAG00000024182	VSTM4	V-set and transmembrane domain containing 4	1,025094	2,3E-09
255.	ENSECAG00000021206	HAS2	hyaluronan synthase 2	1,020803	2E-08
256.	ENSECAG00000016578	ENSECAG00000016578	granulocyte-macrophage colony-stimulating factor receptor subunit alpha	1,017206	0,00708

257.	ENSECAG00000033960	GALNT16	Polypeptide N-Acetylgalactosaminyltransferase 16	1,015856	1,2E-07
258.	ENSECAG00000001189	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	1,014749	1,5E-06
259.	ENSECAG00000023637	ADAM33	ADAM Metallopeptidase Domain 33	1,014687	9,7E-05
260.	ENSECAG00000016974	BRCA1	BRCA1 DNA Repair Associated	1,013524	0,00015
261.	ENSECAG00000024008	SCAI	suppressor of cancer cell invasion	1,013444	0,01981
262.	ENSECAG00000015369	NID2	nidogen 2	1,009397	5,4E-28
263.	ENSECAG00000019215	ITGB8	Integrin Subunit Beta 8	1,009328	3,4E-08
264.	ENSECAG00000005925	MYBL2	MYB Proto-Oncogene Like 2	1,006826	0,01444
265.	ENSECAG00000018253	FGFRL1	fibroblast growth factor receptor like 1	1,00109	4,7E-11
266.	ENSECAG00000014993	SCNN1B	sodium channel epithelial 1 subunit beta	-1,00179	0,0045
267.	ENSECAG00000007658	MGLL	monoglyceride lipase	-1,00473	0,00028
268.	ENSECAG00000008809	OAS3	2'-5'-oligoadenylate synthetase 3	-1,00804	4,1E-12
269.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	-1,01168	2,4E-14
270.	ENSECAG00000024139	LONRF3	LON peptidase N-terminal domain and ring finger 3	-1,01183	5,4E-08
271.	ENSECAG00000015865	GLUL	glutamate-ammonia ligase	-1,01544	0,00011
272.	ENSECAG00000019769	PPARGC1B	PPARG Coactivator 1 Beta	-1,01719	0,00303
273.	ENSECAG00000002874	LRRN1	leucine rich repeat neuronal 1	-1,01912	0,02547
274.	ENSECAG00000007385	NIBAN1	niban apoptosis regulator 1	-1,01983	7,9E-13
275.	ENSECAG00000037336	ENSECAG00000037336	heparan sulfate glucosamine 3-O-sulfotransferase 4	-1,01999	0,01014
276.	ENSECAG00000025076	CTTNBP2	cortactin binding protein 2	-1,02447	2E-07
277.	ENSECAG00000015745	BLNK	B cell linker	-1,03138	5,3E-10
278.	ENSECAG00000031607	ENSECAG00000031607		-1,04017	0,01564
279.	ENSECAG00000002186	CD68	CD68 Molecule	-1,04225	0,01399
280.	ENSECAG00000016824	NRP2	neuropilin 2	-1,05406	1,9E-17
281.	ENSECAG00000011747	BCL7A	BAF Chromatin Remodeling Complex Subunit BCL7A	-1,0549	0,01725
282.	ENSECAG00000022703	LY5	lymphocyte antigen 75	-1,06315	1,2E-10
283.	ENSECAG00000023963	NMNAT2	Nicotinamide Nucleotide Adenylyltransferase 2	-1,06417	9,5E-12
284.	ENSECAG00000007718	TMOD1	Tropomodulin 1	-1,06491	7,3E-15
285.	ENSECAG00000023958	ADPRH	ADP-ribosylarginine hydrolase	-1,06566	2,1E-14
286.	ENSECAG00000015760	ITGA3	integrin subunit alpha 3	-1,06797	1,6E-21
287.	ENSECAG00000002579	MATN2	matrilin 2	-1,07486	3,7E-06
288.	ENSECAG000000022441	ESR1	estrogen receptor 1	-1,07627	1,6E-12
289.	ENSECAG00000015834	DMD	dystrophin	-1,08403	0,0003
290.	ENSECAG00000009949	P2RX7	purinergic receptor P2X 7	-1,08502	0,00198
291.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-1,08684	0,00443
292.	ENSECAG00000025019	ARHGEF26	Rho guanine nucleotide exchange factor 26	-1,09063	0,01126
293.	ENSECAG00000017186	SLFN5	schlafen family member 5	-1,09333	0,01573
294.	ENSECAG00000010721	MGP	Matrix Gla Protein	-1,09358	4,5E-10
295.	ENSECAG00000008564	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1,09364	0,01484
296.	ENSECAG00000013079	USP54	ubiquitin specific peptidase 54	-1,10012	1,5E-20
297.	ENSECAG00000012507	CRYAB	Crystallin Alpha B	-1,10104	1,1E-10
298.	ENSECAG00000000903	RASGRF2	Ras protein specific guanine nucleotide releasing factor 2	-1,1025	0,02337
299.	ENSECAG00000003291	AMIGO1	adhesion molecule with Ig like domain 1	-1,10282	0,04439
300.	ENSECAG00000012993	JAG1	jagged canonical Notch ligand 1	-1,10717	0,00283
301.	ENSECAG00000016430	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6	-1,11941	0,02892
302.	ENSECAG00000009813	CD83	CD83 Molecule	-1,11988	0,00046
303.	ENSECAG00000019940	AKAP6	A-kinase anchoring protein 6	-1,12731	1,9E-06
304.	ENSECAG00000020437	BCL2	BCL2 apoptosis regulator	-1,1282	0,00185
305.	ENSECAG00000011404	ENSECAG00000011404	serum amyloid A protein	-1,1313	0,00619
306.	ENSECAG00000040252	HMGA2	high mobility group AT-hook 2	-1,13519	0,0269
307.	ENSECAG00000013131	PECR	peroxisomal trans-2-enoyl-CoA reductase	-1,13535	0,0333

308.	ENSECAG00000009168	GADD45B	Growth Arrest And DNA Damage Inducible Beta	-1,1356	2,7E-05
309.	ENSECAG00000014992	JAM2	Junctional Adhesion Molecule 2	-1,13817	0,04058
310.	ENSECAG00000001481	SAMD9L	sterile alpha motif domain containing 9 like	-1,14061	1,9E-05
311.	ENSECAG00000011138	COL4A4	collagen type IV alpha 4 chain	-1,14612	0,01416
312.	ENSECAG00000013514	DUSP5	dual specificity phosphatase 5	-1,14636	0,01079
313.	ENSECAG00000000284	USP18	Junctional Adhesion Molecule 2	-1,15552	2,1E-05
314.	ENSECAG00000011749	MSX2	msh homeobox 2	-1,15669	0,00087
315.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	-1,16458	2,7E-06
316.	ENSECAG00000020835	ADAMTS20	ADAM metalloproteinase with thrombospondin type 1 motif 20	-1,16743	5,6E-07
317.	ENSECAG00000020045	HAPLN4	hyaluronan and proteoglycan link protein 4	-1,16758	9,3E-07
318.	ENSECAG00000017459	ARRB1	arrestin beta 1	-1,18688	3E-05
319.	ENSECAG00000013170	JADE2	jade family PHD finger 2	-1,19057	1,4E-07
320.	ENSECAG00000011111	FMNL2	formin like 2	-1,1969	2,4E-10
321.	ENSECAG00000025060	MYH3	myosin heavy chain 3	-1,20263	0,02031
322.	ENSECAG00000033029	ENSECAG00000033029	interferon-induced protein with tetratricopeptide repeats 1B	-1,20595	5,3E-06
323.	ENSECAG00000030850	FGF18	Fibroblast Growth Factor 18	-1,20888	7,6E-05
324.	ENSECAG00000016721	RUBCNL	rubicon like autophagy enhancer	-1,21256	7,2E-08
325.	ENSECAG00000009218	EGFL6	EGF like domain multiple 6	-1,2145	0,01191
326.	ENSECAG00000010405	TRIB2	tribbles pseudokinase 2	-1,23119	4,5E-09
327.	ENSECAG00000017937	ENSECAG00000017937		-1,23296	0,00013
328.	ENSECAG00000023264	RTP4	Receptor Transporter Protein 4	-1,2424	0,00532
329.	ENSECAG00000019617	ATP8B4	ATPase phospholipid transporting 8B4 (putative)	-1,24324	0,03081
330.	ENSECAG00000005360	MITF	melanocyte inducing transcription factor	-1,25268	6,7E-21
331.	ENSECAG00000022638	PLD1	phospholipase D1	-1,26016	3E-07
332.	ENSECAG00000002211	CD80	CD80 molecule	-1,2651	0,04093
333.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-1,26917	3,2E-09
334.	ENSECAG00000026945	HES1	hes family bHLH transcription factor 1	-1,27203	0,00064
335.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-1,2804	1,5E-09
336.	ENSECAG00000021165	STAC	SH3 and cysteine rich domain	-1,28893	2,4E-10
337.	ENSECAG00000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,28973	3,9E-15
338.	ENSECAG00000016384	RORA	RAR related orphan receptor A	-1,29175	7,7E-06
339.	ENSECAG00000015552	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-1,29177	0,00461
340.	ENSECAG00000034367	ENSECAG00000034367		-1,29184	0,0026
341.	ENSECAG00000015845	PLD5	phospholipase D family member 5	-1,29248	4,7E-05
342.	ENSECAG00000010546	KLF5	KLF transcription factor 5	-1,29385	0,00126
343.	ENSECAG00000010762	ROBO2	Roundabout Guidance Receptor 2	-1,29396	0,03428
344.	ENSECAG00000024062	DDX60L	DEXD/H-box 60 like	-1,29674	1,9E-24
345.	ENSECAG00000032483	GPR85	G protein-coupled receptor 85	-1,29739	0,00096
346.	ENSECAG00000012060	MYO3A	myosin IIIA	-1,30663	0,00862
347.	ENSECAG00000013677	FRY	FRY microtubule binding protein	-1,30963	4,9E-19
348.	ENSECAG00000011358	TMEM86A	transmembrane protein 86A	-1,31061	3,3E-05
349.	ENSECAG00000021174	ACKR4	atypical chemokine receptor 4	-1,3138	2,5E-06
350.	ENSECAG00000015952	BDNF	brain derived neurotrophic factor	-1,31491	3,3E-05
351.	ENSECAG00000014962	FAXDC2	Fatty Acid Hydroxylase Domain Containing 2	-1,32685	4,7E-06
352.	ENSECAG00000000121	NAV3	neuron navigator 3	-1,33937	2E-12
353.	ENSECAG00000016234	ANGPTL2	angiopoietin like 2	-1,33938	1E-14
354.	ENSECAG000000043761	AK9	adenylate kinase 9	-1,34087	0,01145
355.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-1,3421	7E-18
356.	ENSECAG00000000343	HACD4	3-hydroxyacyl-CoA dehydratase 4	-1,34307	0,00155
357.	ENSECAG00000011776	MX1	MX dynamin like GTPase 1	-1,34428	2,3E-37
358.	ENSECAG00000015000	FAM83G	Family With Sequence Similarity 83 Member G	-1,34508	1,4E-13
359.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-1,34847	0,00465

360.	ENSECAG00000000593	PTN	pleiotrophin	-1,35195	3,1E-27
361.	ENSECAG00000017689	ARHGEF28	Rho Guanine Nucleotide Exchange Factor 28	-1,35367	8,6E-21
362.	ENSECAG00000019495	C5H1orf141	chromosome 5 C1orf141 homolog	-1,35773	0,0428
363.	ENSECAG00000017454	KIAA1755	KIAA1755	-1,36932	0,00656
364.	ENSECAG00000017743	SESN3	Sestrin 3	-1,37209	3,6E-15
365.	ENSECAG00000015846	VASH2	vasohibin 2	-1,37345	5,2E-10
366.	ENSECAG00000022556	ABCA9	ATP binding cassette subfamily A member 9	-1,37484	8,2E-27
367.	ENSECAG00000018049	PAMR1	peptidase domain containing associated with muscle regeneration 1	-1,37508	2,3E-08
368.	ENSECAG00000016957	OLFM1	olfactomedin 1	-1,37622	1,1E-14
369.	ENSECAG00000012340	RADX	RPA1 related single stranded DNA binding protein, X-linked	-1,37938	0,00802
370.	ENSECAG00000003266	PIRT	phosphoinositide interacting regulator of transient receptor potential channels	-1,38007	0,01506
371.	ENSECAG00000012212	LRP1B	LDL Receptor Related Protein 1B	-1,38447	3,1E-06
372.	ENSECAG00000004433	ENSECAG00000004433	interferon-induced protein with tetratricopeptide repeats 1	-1,38773	2,9E-05
373.	ENSECAG00000024961	XAF1		-1,39428	8,6E-09
374.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-1,41837	3,7E-05
375.	ENSECAG00000012990	CALCRL	calcitonin receptor like receptor	-1,41938	1,6E-05
376.	ENSECAG00000010185	IFIT2	Interferon Induced Protein With Tetratricopeptide Repeats 2	-1,426	6,7E-09
377.	ENSECAG00000023960	KLHL30	kelch like family member 30	-1,43342	0,00123
378.	ENSECAG000000000740	C10H6orf58		-1,43946	0,01364
379.	ENSECAG00000007047	ASPN	Asporin	-1,45249	0,00392
380.	ENSECAG00000021078	GRB14	growth factor receptor bound protein 14	-1,4578	0,00016
381.	ENSECAG00000022823	PLCE1	phospholipase C epsilon 1	-1,45821	1,6E-15
382.	ENSECAG00000038712	TNXB	tenascin XB	-1,45847	0,00108
383.	ENSECAG00000041748	COL4A3	collagen type IV alpha 3 chain	-1,46726	0,00022
384.	ENSECAG00000019499	ISG20	Interferon Stimulated Exonuclease Gene 20	-1,47161	3E-05
385.	ENSECAG00000001488	GPR171	G protein-coupled receptor 171	-1,47168	1,2E-08
386.	ENSECAG00000041924	COL23A1	collagen type XXIII alpha 1 chain	-1,47204	6,6E-06
387.	ENSECAG00000038866	PTX3	pentraxin 3	-1,47493	0,01112
388.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-1,48012	0,00068
389.	ENSECAG00000009192	SRGN	Serglycin	-1,48647	0,00031
390.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-1,50017	0,00113
391.	ENSECAG00000004501	FDCSP	follicular dendritic cell secreted protein	-1,51193	0,00648
392.	ENSECAG00000010880	SOX6	SRY-box transcription factor 6	-1,51682	0,01496
393.	ENSECAG00000019298	FER1L6	fer-1 like family member 6	-1,52786	0,0443
394.	ENSECAG00000008087	ENSECAG00000008087	stabilizer of axonemal microtubules 2	-1,53122	0,00821
395.	ENSECAG00000024959	FBXO39	F-box protein 39	-1,53258	0,02298
396.	ENSECAG00000022047	APOD	apolipoprotein D	-1,54015	4,1E-08
397.	ENSECAG00000019087	CTSK	Cathepsin K	-1,54828	8,4E-48
398.	ENSECAG00000015736	ODAPH	odontogenesis associated phosphoprotein	-1,5644	0,00725
399.	ENSECAG00000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-1,5765	3,4E-34
400.	ENSECAG00000037214	TUBB4A	tubulin beta 4A class IVa	-1,58746	2,6E-12
401.	ENSECAG00000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-1,59137	0,01169
402.	ENSECAG00000017816	ADORA1	adenosine A1 receptor	-1,59268	4,9E-08
403.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-1,6127	3,4E-09
404.	ENSECAG00000018916	FILIP1	Filamin A Interacting Protein 1	-1,61976	0,02539
405.	ENSECAG00000010939	ANGPTL1	angiopoietin like 1	-1,62083	9,4E-06
406.	ENSECAG00000017443	TRIM14	tripartite motif containing 14	-1,62472	0,00278
407.	ENSECAG00000008518	NPNT	nephronectin	-1,63248	0,00816

408.	ENSECAG00000019717	ECM2	extracellular matrix protein 2	-1,63583	1,2E-17
409.	ENSECAG00000014513	TNFSF15	TNF superfamily member 15	-1,6455	2,7E-05
410.	ENSECAG00000013739	DLGAP1	DLG associated protein 1	-1,65259	5,9E-07
411.	ENSECAG00000032728	HBQ1	Hemoglobin Subunit Theta 1	-1,65272	0,00504
412.	ENSECAG00000010830	MMP11	Matrix Metallopeptidase 11	-1,6669	1,6E-05
413.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-1,69082	3,7E-10
414.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-1,71344	2,1E-15
415.	ENSECAG00000033624	ENSECAG00000033624	contactin-associated protein-like 4	-1,72868	0,02385
416.	ENSECAG00000006482	CRISP2	Cysteine Rich Secretory Protein 2	-1,72922	0,00163
417.	ENSECAG00000024612	SNED1	Sushi, Nidogen And EGF Like Domains 1	-1,75609	0,01305
418.	ENSECAG00000011467	ALPL	alkaline phosphatase, biomineralization associated	-1,75883	3,8E-06
419.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-1,77228	1,4E-28
420.	ENSECAG00000015388	EDIL3	EGF like repeats and discoidin domains 3	-1,77547	2,6E-10
421.	ENSECAG00000012889	TMEM108	transmembrane protein 108	-1,80265	0,00202
422.	ENSECAG00000002977	SLC25A53	solute carrier family 25 member 53	-1,81558	0,03507
423.	ENSECAG00000028632	ENSECAG00000028632		-1,82403	4,5E-06
424.	ENSECAG00000010128	SEMA4D	semaphorin 4D	-1,83842	1,1E-05
425.	ENSECAG00000023039	CCN3	cellular communication network factor 3	-1,84522	2,4E-08
426.	ENSECAG00000016171	GRM7	glutamate metabotropic receptor 7	-1,85839	0,00137
427.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-1,87532	4,2E-11
428.	ENSECAG00000016251	ENSECAG00000016251		-1,88032	1,4E-05
429.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-1,88869	0,00054
430.	ENSECAG00000016015	PCDH19	protocadherin 19	-1,88991	2,2E-18
431.	ENSECAG00000031859	ENSECAG00000031859		-1,89161	0,00012
432.	ENSECAG00000020093	NPR3	natriuretic peptide receptor 3	-1,91695	0,00013
433.	ENSECAG00000006717	ASS1	argininosuccinate synthase 1	-1,93746	5,6E-10
434.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-1,95484	7,2E-09
435.	ENSECAG00000018308	GREB1	growth regulating estrogen receptor binding 1	-1,97315	2,1E-11
436.	ENSECAG00000024028	PDE6A	phosphodiesterase 6A	-1,98371	0,00828
437.	ENSECAG00000021363	DEPTOR	DEP domain containing MTOR interacting protein	-2,00346	0,02606
438.	ENSECAG00000021534	ASPA	aspartoacylase	-2,02173	0,01062
439.	ENSECAG00000009483	PRLR	prolactin receptor	-2,02548	2E-11
440.	ENSECAG00000015484	ATP6V0D2	ATPase H+ transporting V0 subunit d2	-2,0925	8,7E-35
441.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-2,10533	6,5E-06
442.	ENSECAG00000017802	OGN	osteoglycin	-2,11656	5,6E-30
443.	ENSECAG00000018108	VGF	VGF nerve growth factor inducible	-2,14332	1,1E-06
444.	ENSECAG00000022629	SLC1A7	Solute Carrier Family 1 Member 7	-2,19412	2,2E-33
445.	ENSECAG00000030788	DIO2	iodothyronine deiodinase 2	-2,25538	1,4E-06
446.	ENSECAG00000014287	OMD	osteonectin	-2,29968	9,4E-14
447.	ENSECAG00000023161	IGSF10	immunoglobulin superfamily member 10	-2,32672	1,5E-23
448.	ENSECAG00000039579	GDF15	growth differentiation factor 15	-2,3457	0,0006
449.	ENSECAG00000017280	MAPK10	mitogen-activated protein kinase 10	-2,34795	0,00668
450.	ENSECAG00000021101	LGI4	Leucine Rich Repeat LGI Family Member 4	-2,35885	0,00623
451.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-2,37449	6,8E-62
452.	ENSECAG00000010791	LMCD1	LIM and cysteine rich domains 1	-2,38362	9,7E-06
453.	ENSECAG00000012109	SOSTDC1	sclerostin domain containing 1	-2,39065	7,4E-11
454.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-2,45801	2,4E-08
455.	ENSECAG00000010869	CAPN6	calpain 6	-2,45827	5,3E-09
456.	ENSECAG00000000813	SCN5A	sodium voltage-gated channel alpha subunit 5	-2,46482	3,4E-09
457.	ENSECAG00000009138	MME	membrane metalloendopeptidase	-2,52995	1,3E-18
458.	ENSECAG00000020901	CLCA2	chloride channel accessory 2	-2,55887	0,00039

459.	ENSECAG00000012667	RBFOX1	RNA Binding Fox-1 Homolog 1	-2,58738	2,1E-10
460.	ENSECAG00000012032	KIT	KIT proto-oncogene, receptor tyrosine kinase	-2,59987	0,03499
461.	ENSECAG00000029885	CHST7	carbohydrate sulfotransferase 7	-2,68946	1,2E-35
462.	ENSECAG00000034702	DEFB1	defensin beta 1	-2,80379	0,00279
463.	ENSECAG00000034955	BHLHE41	basic helix-loop-helix family member e41	-2,81202	5,4E-20
464.	ENSECAG00000000324	RASEF	RAS and EF-hand domain containing	-2,85882	0,00114
465.	ENSECAG00000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-2,87275	8,9E-14
466.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-2,95017	3,6E-18
467.	ENSECAG00000005126	TRIM22	tripartite motif containing 22	-3,05783	5E-12
468.	ENSECAG00000017843	ENSECAG00000017843	calcium-activated chloride channel regulator 4	-3,15483	0,00062
469.	ENSECAG00000035060	ENSECAG00000035060	calcium-activated chloride channel regulator 4	-3,23204	0,00146
470.	ENSECAG00000020198	NOTUM	notum, palmitoleoyl-protein carboxylesterase	-3,34359	0,00116
471.	ENSECAG00000016639	ADAD1	adenosine deaminase domain containing 1	-3,69337	0,00106

Supplementary Table 9. The full list of differentially expressed genes (DEGs) identified in fibroblasts derived from category IIB endometria treated with interleukin 13 (IL-13) for 48 hours (Research task 3, Experiment 2).

No.	Ensembl gene ID	Gene symbol	Gene name	log2FC	P _{adj}
1.	ENSECAG00000012733	COL6A5	collagen type VI alpha 5 chain	10,9464154	5,2743E-34
2.	ENSECAG00000020578	PDCD1LG2	programmed cell death 1 ligand 2	7,557265272	9,3403E-26
3.	ENSECAG00000013482	SERPINA3	Serpin Family A Member 3	7,200407693	7,0284E-30
4.	ENSECAG00000038698	ALOX15	Arachidonate 15-Lipoxygenase	6,9476232	1,4624E-28
5.	ENSECAG00000004201	FETUB	fetuin B	6,892988077	2,8968E-27
6.	ENSECAG00000004408	CMKLR2	chemerin chemokine-like receptor 2	6,552500796	1,1193E-13
7.	ENSECAG00000016867	CISH	Cytokine Inducible SH2 Containing Protein	6,470968709	2,2109E-10
8.	ENSECAG00000014650	INSRR	insulin receptor related receptor	6,345076168	5,397E-26
9.	ENSECAG00000011581	ENSECAG0000011581		6,050803718	9,448E-17
10.	ENSECAG00000020738	CDH26	cadherin 26	6,015968198	1,813E-103
11.	ENSECAG00000031648	PROKR1	prokineticin receptor 1	5,987489411	9,3002E-16
12.	ENSECAG00000022659	CCL26	C-C motif chemokine ligand 26	5,973745644	2,1382E-16
13.	ENSECAG00000002249	PLEKHG4B	Pleckstrin Homology And RhoGEF Domain Containing G4B	5,845883239	2,3056E-08
14.	ENSECAG00000016312	CD274	CD274 molecule	5,823519888	1,8359E-15
15.	ENSECAG00000034282	CCL8	C-C motif chemokine 7	5,632571699	4,3925E-79
16.	ENSECAG00000009460	NTRK1	neurotrophic receptor tyrosine kinase 1	5,555336824	4,6454E-26
17.	ENSECAG00000013457	CSF3R	colony stimulating factor 3 receptor	5,386033696	1,1367E-06
18.	ENSECAG00000018409	NOX5	NADPH oxidase 5	5,14223665	0,00023129
19.	ENSECAG00000015516	APBA2	amyloid beta precursor protein binding family A member 2	5,077093182	7,0113E-06
20.	ENSECAG00000000706	MEGF11	multiple EGF like domains 11	4,454409109	0,00018491
21.	ENSECAG00000039959	ZDBF2	zinc finger DBF-type containing 2	4,313302327	3,0749E-05
22.	ENSECAG00000005379	HPGD	15-Hydroxyprostaglandin Dehydrogenase	3,99363999	7,4008E-49
23.	ENSECAG00000023032	AZIN2	Antizyme Inhibitor 2	3,894831437	3,9769E-24
24.	ENSECAG00000009916	GRIA4	glutamate ionotropic receptor AMPA type subunit 4	3,731679166	0,00182695
25.	ENSECAG00000023841	POSTN	periostin	3,682627622	1,0757E-14
26.	ENSECAG00000023918	DUOX1	dual oxidase 1	3,663912878	0,00422456
27.	ENSECAG00000011626	S1PR1	sphingosine-1-phosphate receptor 1	3,62193037	8,716E-109
28.	ENSECAG00000021182	TNFSF4	TNF superfamily member 4	3,620139178	5,2268E-05
29.	ENSECAG00000000152	KITLG	KIT ligand	3,575151899	4,3074E-27
30.	ENSECAG00000013703	PPP1R3C	Protein Phosphatase 1 Regulatory Subunit 3C	3,501140705	2,3315E-30
31.	ENSECAG00000005241	THBD	thrombomodulin	3,427060228	9,9646E-77
32.	ENSECAG00000014916	TNFRSF11B	TNF receptor superfamily member 11b	3,353884193	4,4225E-09
33.	ENSECAG00000026965	SOCS1	suppressor of cytokine signaling 1	3,351490918	1,6052E-25
34.	ENSECAG00000016407	KCNB2	potassium voltage-gated channel subfamily B member 2	3,227849169	2,3713E-09
35.	ENSECAG00000019800	TSPAN33	Tetraspanin 33	3,220539777	3,1597E-47
36.	ENSECAG00000022686	MRAP2	melanocortin 2 receptor accessory protein 2	3,173060596	0,00839352
37.	ENSECAG00000023942	ENSECAG0000023942	ras GTPase-activating protein 4	3,159449229	7,1825E-45
38.	ENSECAG00000024016	IL13RA2	interleukin 13 receptor subunit alpha 2	3,132213747	1,5407E-11
39.	ENSECAG00000022509	PDE1A	phosphodiesterase 1A	3,076140905	1,8335E-17
40.	ENSECAG00000010805	PGM5	phosphoglucomutase 5	3,058078184	1,6084E-28
41.	ENSECAG00000012830	CHN2	Chimerin 2	2,92828822	1,08E-38

42.	ENSECAG00000007825	CALCA	calcitonin-related polypeptide alpha	2,817662032	0,00015049
43.	ENSECAG000000021057	ADGRV1	adhesion G protein-coupled receptor V1	2,794116489	1,7286E-08
44.	ENSECAG000000014126	CFAP161	Chimerin 2	2,791422384	2,8506E-08
45.	ENSECAG000000014379	BMP3	bone morphogenetic protein 3	2,771671596	5,7488E-12
46.	ENSECAG000000012843	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	2,711105773	1,1741E-15
47.	ENSECAG000000009767	P2RX1	purinergic receptor P2X 1	2,709999423	0,00201104
48.	ENSECAG000000002256	ENSECAG0000002256		2,695218991	0,01526395
49.	ENSECAG000000001988	FAT3	FAT atypical cadherin 3	2,685203246	1,8011E-08
50.	ENSECAG000000011897	CHRD2	chordin like 2	2,640969262	0,00919345
51.	ENSECAG000000001603	PEG10	Paternally Expressed 10	2,599002526	0,00336746
52.	ENSECAG000000000574	NIPAL4	NIPA Like Domain Containing 4	2,589080794	4,0114E-31
53.	ENSECAG000000021775	KRT8	keratin 8	2,586834928	1,0664E-09
54.	ENSECAG000000023199	COL24A1	Collagen Type XXIV Alpha 1 Chain	2,584579654	2,6783E-06
55.	ENSECAG000000015842	ANKRD55	ankyrin repeat domain 55	2,580625743	3,7842E-06
56.	ENSECAG000000021604	PDGFRL	platelet derived growth factor receptor like	2,512261707	7,0756E-27
57.	ENSECAG000000024719	ENSECAG00000024719	solute carrier family 2 member 3	2,471823261	2,3656E-51
58.	ENSECAG000000017217	CA12	carbonic anhydrase 12	2,451767185	1,042E-18
59.	ENSECAG000000010499	TRABD2A	TraB domain containing 2A	2,451642176	0,03237128
60.	ENSECAG000000013207	SHISA2	shisa family member 2	2,44835994	0,00538438
61.	ENSECAG000000008880	SLC22A16	solute carrier family 22 member 16	2,429836323	1,1022E-05
62.	ENSECAG000000017896	PDLIM3	PDZ and LIM domain 3	2,412102203	0,00105469
63.	ENSECAG000000005468	PTPRN	Protein Tyrosine Phosphatase Receptor Type N	2,371318869	0,02682051
64.	ENSECAG000000011893	CNTNAP4	Contactin Associated Protein Family Member 4	2,348772824	0,03556549
65.	ENSECAG000000000681	ENSECAG0000000681		2,336359852	0,04586297
66.	ENSECAG000000015657	TNNT1	troponin T1, slow skeletal type	2,285893738	6,9704E-10
67.	ENSECAG000000019438	OSMR	oncostatin M receptor	2,268151047	5,2514E-12
68.	ENSECAG000000021343	NRG1	neuregulin 1	2,240949741	2,57E-61
69.	ENSECAG000000013009	KIF26B	kinesin family member 26B	2,214022107	1,2458E-08
70.	ENSECAG000000024406	KCP	kielin cysteine rich BMP regulator	2,212457434	0,00188515
71.	ENSECAG000000021914	PDE1C	phosphodiesterase 1C	2,211713419	1,69E-06
72.	ENSECAG000000005307	RNF183	ring finger protein 183	2,205276369	2,0439E-08
73.	ENSECAG000000014646	KNG1	kininogen 1	2,164343279	1,229E-29
74.	ENSECAG000000010750	VWCE	von Willebrand factor C and EGF domains	2,138979959	9,0597E-29
75.	ENSECAG000000030024	MAPK13	mitogen-activated protein kinase 13	2,121946396	1,666E-15
76.	ENSECAG000000025159	DNAH9	Dynein Axonemal Heavy Chain 9	2,103141899	0,0012247
77.	ENSECAG000000021694	CYB5D2	cytochrome b5 domain containing 2	2,096657057	0,01317611
78.	ENSECAG000000010879	NTS	Neurotensin	2,094414392	0,01770292
79.	ENSECAG000000019243	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	2,071675015	8,7378E-32
80.	ENSECAG000000015069	BHLHE40	basic helix-loop-helix family member e40	2,047308611	1,031E-54
81.	ENSECAG000000015942	TRPM6	transient receptor potential cation channel subfamily M member 6	2,018158007	4,4648E-22
82.	ENSECAG000000024845	PI16	peptidase inhibitor 16	2,011772708	2,0722E-05
83.	ENSECAG000000003260	ITIH5	inter-alpha-trypsin inhibitor heavy chain 5	1,970693302	1,0895E-34
84.	ENSECAG000000019170	MN1	MN1 Proto-Oncogene, Transcriptional Regulator	1,963118907	0,00043335

85.	ENSECAG00000007097	CRTAC1	cartilage acidic protein 1	1,950841334	0,04762661
86.	ENSECAG00000000942	ACKR3	atypical chemokine receptor 3	1,942957586	4,8842E-37
87.	ENSECAG000000022731	COL6A1	collagen type VI alpha 1 chain	1,941038762	3,2652E-47
88.	ENSECAG000000024973	CD34	CD34 Molecule	1,92350988	0,03705405
89.	ENSECAG000000010569	SV2C	synaptic vesicle glycoprotein 2C	1,920356151	0,01737618
90.	ENSECAG000000020767	IL7	interleukin 7	1,917469433	6,2214E-15
91.	ENSECAG000000023895	EXOC3L2	exocyst complex component 3 like 2	1,914380952	3,6419E-05
92.	ENSECAG000000023657	FAM20A	FAM20A golgi associated secretory pathway pseudokinase	1,893100279	1,4728E-19
93.	ENSECAG000000014145	TLL2	tolloid like 2	1,871511983	0,00980879
94.	ENSECAG000000007300	DCLK1	doublecortin like kinase 1	1,869091162	1,1564E-59
95.	ENSECAG000000016048	ANKRD24	ankyrin repeat domain 24	1,857625749	0,0132028
96.	ENSECAG000000017826	TMEM26	transmembrane protein 26	1,854106453	3,1247E-08
97.	ENSECAG000000016576	C1QTNF12	C1q And TNF Related 12	1,847631523	2,9775E-09
98.	ENSECAG000000024853	RSPO2	R-Spondin 2	1,840789741	0,00239525
99.	ENSECAG000000019215	ITGB8	Integrin Subunit Beta 8	1,838913112	1,3937E-23
100.	ENSECAG000000024293	AMDHD1	amidohydrolase domain containing 1	1,822568265	9,3024E-07
101.	ENSECAG000000018373	FAM234B	family with sequence similarity 234 member B	1,818357552	1,8268E-21
102.	ENSECAG000000014588	CAMK1G	calcium/calmodulin dependent protein kinase IG	1,818197152	0,00353292
103.	ENSECAG000000017570	SYT4	synaptotagmin 4	1,806886766	0,00587882
104.	ENSECAG000000016976	RARB	retinoic acid receptor beta	1,791975415	3,8774E-06
105.	ENSECAG000000016934	IL31RA	Interleukin 31 Receptor A	1,790253751	0,0089001
106.	ENSECAG000000008876	PTPRE	protein tyrosine phosphatase receptor type E	1,785056874	0,01102207
107.	ENSECAG000000021976	LRATD2	LRAT domain containing 2	1,770211679	0,00025382
108.	ENSECAG000000009046	BIN2	Bridging Integrator 2	1,768825286	4,6343E-08
109.	ENSECAG000000014817	RND2	Rho Family GTPase 2	1,743728509	4,7358E-06
110.	ENSECAG000000013035	ENPP1	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1	1,737860522	7,3158E-09
111.	ENSECAG000000019229	STAMBPL1	STAM binding protein like 1	1,7354283	3,6013E-32
112.	ENSECAG000000019551	CXCL12	C-X-C motif chemokine ligand 12	1,72235291	2,1093E-29
113.	ENSECAG000000020769	FGF1	fibroblast growth factor 1	1,718947558	2,831E-23
114.	ENSECAG000000014787	RCAN1	regulator of calcineurin 1	1,709878699	7,97E-101
115.	ENSECAG000000003943	SYT5	synaptotagmin 5	1,70085248	5,5407E-19
116.	ENSECAG000000010500	ITGA4	integrin subunit alpha 4	1,700721532	6,7055E-24
117.	ENSECAG000000009081	KIAA1210	KIAA1210	1,692926861	6,9211E-06
118.	ENSECAG000000012104	TNFAIP6	TNF Alpha Induced Protein 6	1,67535081	3,2652E-47
119.	ENSECAG000000013106	ESM1	endothelial cell specific molecule 1	1,675241043	3,8468E-08
120.	ENSECAG000000004372	SLC22A3	Solute Carrier Family 22 Member 3	1,666381323	0,00055385
121.	ENSECAG000000021654	SLC10A4	solute carrier family 10 member 4	1,66346207	0,00023537
122.	ENSECAG000000024322	ARSJ	arylsulfatase family member J	1,658234126	1,8238E-23
123.	ENSECAG000000024110	PENK	proenkephalin	1,647851864	8,5014E-05
124.	ENSECAG000000003520	ENSECAG0000003520		1,640759783	0,04765993
125.	ENSECAG000000022093	SLC2A5	solute carrier family 2 member 5	1,628155421	0,02566537
126.	ENSECAG000000004795	ENSECAG0000004795		1,620265836	0,00741677
127.	ENSECAG000000000235	MTBP	MDM2 binding protein	1,619522303	1,0494E-28
128.	ENSECAG000000012826	CDO1	Cysteine Dioxygenase Type 1	1,614833272	0,00185617
129.	ENSECAG000000012263	RNF19B	Ring Finger Protein 19B	1,599323119	1,1354E-74

130.	ENSECAG00000002570	HS3ST1	heparan sulfate-glucosamine 3-sulfotransferase 1	1,597854591	0,00038611
131.	ENSECAG00000016560	CRABP2	Cellular Retinoic Acid Binding Protein 2	1,597213773	0,00012221
132.	ENSECAG00000009580	LVRN	laeverin	1,594291784	0,00332128
133.	ENSECAG00000017017	LNX1	ligand of numb-protein X 1	1,588065116	1,038E-09
134.	ENSECAG00000016902	PRR16	proline rich 16	1,586530199	3,4076E-15
135.	ENSECAG00000009700	ANK3	ankyrin 3	1,578977822	0,00875454
136.	ENSECAG00000007964	EBF1	EBF transcription factor 1	1,578460799	2,7684E-20
137.	ENSECAG00000011929	NR4A3	Nuclear Receptor Subfamily 4 Group A Member 3	1,57570552	2,578E-07
138.	ENSECAG00000011627	ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6	1,568392675	4,8488E-09
139.	ENSECAG00000007918	TNS4	tensin 4	1,566066456	2,6927E-06
140.	ENSECAG00000019436	COL6A2	collagen type VI alpha 2 chain	1,550072998	2,32E-53
141.	ENSECAG00000016248	JPH1	junctophilin 1	1,531338306	0,01415543
142.	ENSECAG00000018874	PRICKLE1	Prickle Planar Cell Polarity Protein 1	1,525887089	6,1328E-32
143.	ENSECAG00000020927	NEK10	NIMA related kinase 10	1,521114541	4,7411E-06
144.	ENSECAG00000022931	TCF7L1	transcription factor 7 like 1	1,519347667	2,2235E-36
145.	ENSECAG00000014732	ATP10A	ATPase phospholipid transporting 10A (putative)	1,519146809	1,8887E-14
146.	ENSECAG00000014099	GARIN5B	golgi associated RAB2 interactor family member 5B	1,518326468	0,00012496
147.	ENSECAG00000022404	TRPV6	transient receptor potential cation channel subfamily V member 6	1,502036246	2,3566E-05
148.	ENSECAG00000011669	TNN	tenascin N	1,499550864	1,1121E-15
149.	ENSECAG00000007432	PTGDR	Prostaglandin D2 Receptor	1,499322712	8,9004E-25
150.	ENSECAG00000021799	MYRF	myelin regulatory factor	1,497300195	9,0652E-07
151.	ENSECAG000000041708	ENSECAG00000041708		1,484730195	1,5294E-07
152.	ENSECAG00000008569	TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1	1,478520613	7,4943E-26
153.	ENSECAG00000016742	TJP2	tight junction protein 2	1,463690795	4,4721E-06
154.	ENSECAG00000033890	CIDEC	cell death inducing DFFA like effector c	1,459889505	4,0411E-06
155.	ENSECAG00000014511	IL11	Interleukin 11	1,456844186	7,7087E-46
156.	ENSECAG00000006288	SIK1	salt inducible kinase 1	1,452710182	7,5314E-16
157.	ENSECAG00000020563	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1,448084673	7,0392E-65
158.	ENSECAG00000010445	ST3GAL6	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 6	1,445037947	3,6389E-08
159.	ENSECAG00000003201	PRSS35	serine protease 35	1,43846975	0,00413951
160.	ENSECAG00000008739	ENSECAG00000008739		1,437361064	0,03501804
161.	ENSECAG00000027808	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1	1,4323853	0,00164113
162.	ENSECAG00000012858	RASL11A	RAS like family 11 member A	1,430533786	0,00010311
163.	ENSECAG00000010447	EFEMP1	EGF Containing Fibulin Extracellular Matrix Protein 1	1,428326704	2,2584E-14
164.	ENSECAG00000019398	TFPI2	Tissue Factor Pathway Inhibitor 2	1,42236538	1,2602E-18
165.	ENSECAG00000009516	IZUMO4	IZUMO Family Member 4	1,422014425	0,0068627
166.	ENSECAG00000011099	VAV3		1,412612631	3,4484E-10
167.	ENSECAG00000038893	CST3	cystatin C	1,411437925	8,0028E-73
168.	ENSECAG00000021642	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3	1,404570538	7,9353E-23
169.	ENSECAG00000000122	GDA	Vav Guanine Nucleotide Exchange Factor 3	1,401510226	4,2888E-12
170.	ENSECAG00000023908	OLFML2A	olfactomedin like 2A	1,388857712	0,00099889

171.	ENSECAG00000003278	TRIM9	tripartite motif containing 9	1,38370752	9,0574E-06
172.	ENSECAG00000001407	CHSY3	chondroitin sulfate synthase 3	1,380303963	3,0992E-34
173.	ENSECAG00000023279	GATA6	GATA binding protein 6	1,379165572	7,6302E-20
174.	ENSECAG00000015058	ARHGEF3	Rho guanine nucleotide exchange factor 3	1,37263612	5,1172E-67
175.	ENSECAG00000000752	EHF	ETS Homologous Factor	1,370311588	0,04060365
176.	ENSECAG00000013193	UHRF1	ubiquitin like with PHD and ring finger domains 1	1,370113315	1,4743E-05
177.	ENSECAG00000018101	FBLN1	fibulin 1	1,368665823	6,0635E-37
178.	ENSECAG00000024121	TCF7L2	Transcription Factor 7 Like 2	1,35146196	5,3535E-14
179.	ENSECAG00000020846	PDE7B	phosphodiesterase 7B	1,344360095	1,0655E-09
180.	ENSECAG00000021206	HAS2	hyaluronan synthase 2	1,34180207	1,8574E-10
181.	ENSECAG00000009707	PTGS1	prostaglandin-endoperoxide synthase 1	1,340090696	0,0012279
182.	ENSECAG00000023076	GPCPD1	glycerophosphocholine phosphodiesterase 1	1,339843849	1,3861E-13
183.	ENSECAG00000015385	RNF150	ring finger protein 150	1,335184524	0,00047107
184.	ENSECAG00000009535	FCER1G	Fc Epsilon Receptor Ig	1,327228719	0,02044497
185.	ENSECAG00000001373	HSPA12B	heat shock protein family A (Hsp70) member 12B	1,318718247	4,8055E-34
186.	ENSECAG00000012484	NAMPT	nicotinamide phosphoribosyltransferase	1,313406506	1,7584E-68
187.	ENSECAG00000000532	EPS8L1	EPS8 like 1	1,313393379	2,9085E-06
188.	ENSECAG00000011708	GAREM1	GRB2 associated regulator of MAPK1 subtype 1	1,304564964	9,4901E-08
189.	ENSECAG00000026891	ENSECAG0000026891	PCNA clamp associated factor	1,303693928	0,04652998
190.	ENSECAG00000002377	SPESP1	Sperm Equatorial Segment Protein 1	1,299220886	5,2993E-10
191.	ENSECAG00000024851	EDNRB	endothelin receptor type B	1,2868869	2,097E-27
192.	ENSECAG00000025871	MIR186	MicroRNA 186	1,279004501	0,026604
193.	ENSECAG00000015822	VDR	vitamin D receptor	1,276798344	7,4716E-11
194.	ENSECAG00000028144	TXNIP	thioredoxin interacting protein	1,275757208	1,3824E-53
195.	ENSECAG00000013298	POLE2	dynein axonemal assembly factor 2	1,268456024	0,00292021
196.	ENSECAG00000005719	PRKD1	protein kinase D1	1,26794252	5,806E-25
197.	ENSECAG00000016661	NR4A1	Nuclear Receptor Subfamily 4 Group A Member 1	1,256430978	4,0614E-05
198.	ENSECAG00000016337	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	1,25427534	0,03744247
199.	ENSECAG00000008823	CDH11	cadherin 11	1,250016906	6,1611E-38
200.	ENSECAG00000017598	IMPA2	inositol monophosphatase 2	1,249412171	1,8662E-06
201.	ENSECAG00000001189	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4	1,248710236	1,3738E-06
202.	ENSECAG00000008190	ADTRP	androgen dependent TFPI regulating protein	1,223114411	0,00189222
203.	ENSECAG00000024106	CHST1	carbohydrate sulfotransferase 1	1,217568117	0,00324338
204.	ENSECAG00000024419	JADE1	jade family PHD finger 1	1,205976391	3,6334E-25
205.	ENSECAG00000006788	PCSK5	proprotein convertase subtilisin/kexin type 5	1,203864364	4,8014E-27
206.	ENSECAG00000015583	TCN1	transcobalamin 1	1,199925463	0,00057062
207.	ENSECAG00000005086	EGLN3	Egl-9 Family Hypoxia Inducible Factor 3	1,197768329	3,8375E-23
208.	ENSECAG00000023134	KCNK5	potassium two pore domain channel subfamily K member 5	1,188750692	1,0743E-25
209.	ENSECAG00000022463	GABRB3	gamma-aminobutyric acid type A receptor subunit beta3	1,185415675	0,01171275
210.	ENSECAG00000019750	IL6ST	interleukin 6 cytokine family signal transducer	1,184456273	1,7354E-38
211.	ENSECAG00000036591	APLN	apelin	1,173891047	3,265E-08
212.	ENSECAG00000020015	BMP6	bone morphogenetic protein 6	1,171436938	0,00012231
213.	ENSECAG00000023800	AK2	adenylate kinase 2	1,168450012	2,0811E-26

214.	ENSECAG00000023668	RGS5	regulator of G protein signaling 5	1,164672036	1,4933E-10
215.	ENSECAG00000011008	MCOLN2	mucolipin TRP cation channel 2	1,162296138	7,4759E-17
216.	ENSECAG00000017671	ROBO1	roundabout guidance receptor 1	1,151764885	2,5799E-13
217.	ENSECAG00000008927	HIPK2	homeodomain interacting protein kinase 2	1,149911893	0,0031165
218.	ENSECAG00000006991	PECAM1	platelet and endothelial cell adhesion molecule 1	1,133463797	2,6572E-30
219.	ENSECAG00000016482	IL6	Interleukin 6	1,132654771	0,00598663
220.	ENSECAG00000014259	TIMP1	TIMP metalloproteinase inhibitor 1	1,130874741	1,6962E-12
221.	ENSECAG00000013691	MALT1	MALT1 paracaspase	1,130692751	1,4574E-21
222.	ENSECAG00000028820	HEY1	hes related family bHLH transcription factor with YRPW motif 1	1,127761502	0,01287927
223.	ENSECAG00000024182	VSTM4	V-set and transmembrane domain containing 4	1,120746122	1,9347E-22
224.	ENSECAG00000003789	RASL11B	RAS like family 11 member B	1,116519564	2,3922E-08
225.	ENSECAG00000009925	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2	1,113811625	5,5803E-22
226.	ENSECAG00000017922	ADAM19	ADAM metalloproteinase domain 19	1,110232845	1,7294E-26
227.	ENSECAG00000016360	PDE3A	Phosphodiesterase 3A	1,105493838	0,00298237
228.	ENSECAG00000019880	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif 9	1,103188974	1,4638E-10
229.	ENSECAG00000009913	CDC6	cell division cycle 6	1,10037319	0,00046871
230.	ENSECAG00000018686	PPA1	inorganic pyrophosphatase 1	1,097661148	1,3044E-15
231.	ENSECAG00000017912	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	1,097100459	0,01944994
232.	ENSECAG00000009524	SLC16A3	solute carrier family 16 member 3	1,091736336	0,01165103
233.	ENSECAG00000024795	CPVL	carboxypeptidase vitellogenic like	1,088683331	2,5313E-15
234.	ENSECAG00000006558	RIC1	RIC1 homolog, RAB6A GEF complex partner 1	1,085692566	7,2799E-08
235.	ENSECAG00000021015	ATP8B1	ATPase phospholipid transporting 8B1	1,083184504	0,000153
236.	ENSECAG00000015369	NID2	nidogen 2	1,078708901	5,953E-33
237.	ENSECAG00000000292	THSD7A	Thrombospondin Type 1 Domain Containing 7A	1,077676839	0,01770292
238.	ENSECAG000000038379	ENSECAG0000038379	keratin 18	1,075385111	0,00339951
239.	ENSECAG00000012179	RGS2	regulator of G protein signaling 2	1,062840606	2,6747E-06
240.	ENSECAG00000012344	PTPRU	Protein Tyrosine Phosphatase Receptor Type U	1,062298412	1,1345E-17
241.	ENSECAG00000034739	ADORA2A	adenosine A2a receptor	1,061235479	6,1277E-05
242.	ENSECAG00000010558	PTGFR	prostaglandin F receptor	1,060882946	6,2086E-21
243.	ENSECAG00000030001	DIRAS3	DIRAS family GTPase 3	1,053097514	0,00221252
244.	ENSECAG00000007571	PLAT	plasminogen activator, tissue type	1,052340201	1,655E-09
245.	ENSECAG00000016953	HLF	HLF transcription factor, PAR bZIP family member	1,050996155	0,01121741
246.	ENSECAG00000032992	TIAM1	TIAM Rac1 associated GEF 1	1,049090005	6,0371E-07
247.	ENSECAG00000013680	TLE1	TLE Family Member 1, Transcriptional Corepressor	1,045690778	4,6281E-19
248.	ENSECAG00000014395	PTH2R	parathyroid hormone 2 receptor	1,045408882	0,00081065
249.	ENSECAG00000015966	SERPINB6	Serpin Family B Member 6	1,041401671	9,1187E-24
250.	ENSECAG00000008485	ITGAL	integrin subunit alpha L	1,040692509	5,0643E-06
251.	ENSECAG00000018841	CGA	Glycoprotein Hormones, Alpha Polypeptide	1,034235796	0,03502588
252.	ENSECAG00000026887	TSPAN8	tetraspanin 8	1,033170802	0,00132885
253.	ENSECAG00000000015	KIAA1217	KIAA1217	1,029913059	6,202E-05
254.	ENSECAG00000008506	HMMR	Hyaluronan Mediated Motility Receptor	1,028432917	0,00787459
255.	ENSECAG00000021746	SHROOM1	Shroom Family Member 1	1,010934784	2,3333E-13

256.	ENSECAG00000024107	ROR1	receptor tyrosine kinase like orphan receptor 1	1,002578516	4,1315E-09
257.	ENSECAG00000010963	SERPING1	Serpin Family G Member 1	1,000781025	2,5914E-20
258.	ENSECAG00000019758	TNFSF13B	TNF Superfamily Member 13b	-1,006207733	5,8427E-05
259.	ENSECAG00000010153	IFIT3	interferon induced protein with tetratricopeptide repeats 3	-1,00921152	0,00690667
260.	ENSECAG00000000121	NAV3	neuron navigator 3	-1,009549495	1,7168E-07
261.	ENSECAG00000016917	TES	testin LIM domain protein	-1,011428806	1,7138E-17
262.	ENSECAG00000018105	IL4I1	interleukin 4 induced 1	-1,015520628	0,04604433
263.	ENSECAG00000007989	C1QTNF7	C1q and TNF related 7	-1,020842242	0,01457936
264.	ENSECAG00000022441	ESR1	estrogen receptor 1	-1,020926684	1,1714E-06
265.	ENSECAG00000010109	IGF1	insulin like growth factor 1	-1,022936922	0,00011564
266.	ENSECAG00000003230	AKAP5	A-kinase anchoring protein 5	-1,028009742	1,0292E-05
267.	ENSECAG00000024045	EFHD1	EF-hand domain family member D1	-1,028930812	0,01089678
268.	ENSECAG00000024531	ADM	Adrenomedullin	-1,03271003	0,00679475
269.	ENSECAG00000024232	A2ML1	alpha-2-macroglobulin like 1	-1,035406393	0,00042735
270.	ENSECAG00000020835	ADAMTS20	ADAM metalloproteinase with thrombospondin type 1 motif 20	-1,047651156	2,4939E-07
271.	ENSECAG00000021165	STAC	SH3 and cysteine rich domain	-1,060499699	2,9858E-09
272.	ENSECAG00000019818	POU2F3	POU class 2 homeobox 3	-1,061214889	2,5876E-12
273.	ENSECAG00000029347	ADAMTS6	centromere protein K	-1,064943457	7,0263E-24
274.	ENSECAG00000005857	FZD8	Frizzled Class Receptor 8	-1,067555605	0,00124466
275.	ENSECAG00000024961	XAF1	XIAP Associated Factor 1	-1,070302262	4,6476E-05
276.	ENSECAG00000035548	ENSECAG0000035548	T-lymphocyte surface antigen Ly-9	-1,075619157	0,0046755
277.	ENSECAG00000008535	DNAH10	dynein axonemal heavy chain 10	-1,08901082	0,0007449
278.	ENSECAG00000015388	EDIL3	EGF like repeats and discoidin domains 3	-1,090416753	3,4316E-07
279.	ENSECAG00000023958	ADPRH	ADP-ribosylarginine hydrolase	-1,090557918	4,6555E-15
280.	ENSECAG00000007330	ALS2CL	ALS2 C-terminal like	-1,09088585	0,04088603
281.	ENSECAG00000016667	ENSECAG0000016667		-1,091838638	6,7982E-10
282.	ENSECAG00000010553	NGF	nerve growth factor	-1,100629156	0,00714358
283.	ENSECAG00000012662	SEMA3A	semaphorin 3A	-1,105433454	1,4933E-10
284.	ENSECAG00000013450	CORO6	coronin 6	-1,106891595	0,00879194
285.	ENSECAG00000009744	IRF7	interferon regulatory factor 7	-1,117229415	5,8938E-11
286.	ENSECAG00000001900	ENSECAG0000001900	pleckstrin homology like domain family A member 1	-1,120871034	1,2502E-09
287.	ENSECAG00000023963	NMNAT2	Nicotinamide Nucleotide Adenylyltransferase 2	-1,122630621	6,6993E-07
288.	ENSECAG00000010939	ANGPTL1	angiopoietin like 1	-1,126524914	0,00179865
289.	ENSECAG00000014295	PI3	peptidase inhibitor 3	-1,128271905	2,968E-05
290.	ENSECAG00000015952	BDNF	brain derived neurotrophic factor	-1,128566908	1,4679E-05
291.	ENSECAG00000006501	FJX1	Four-Jointed Box Kinase 1	-1,149063972	1,2545E-06
292.	ENSECAG00000036372	ISLR2	immunoglobulin superfamily containing leucine rich repeat 2	-1,157202339	1,9237E-07
293.	ENSECAG00000013758	ENSECAG0000013758		-1,159368369	0,00273956
294.	ENSECAG00000032719	ENSECAG0000032719		-1,164854638	0,00273956
295.	ENSECAG00000015915	ABCC13	ATP binding cassette subfamily C member 13	-1,167579384	0,00060628
296.	ENSECAG00000018069	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-1,169186524	0,02089178
297.	ENSECAG00000020437	BCL2	BCL2 apoptosis regulator	-1,170017884	0,00138033
298.	ENSECAG00000006669	ACSM3	acyl-CoA synthetase medium chain family member 3	-1,174056363	0,00212081
299.	ENSECAG00000005704	CARD11	caspase recruitment domain family member 11	-1,174658583	3,3791E-10

300.	ENSECAG00000005360	MITF	melanocyte inducing transcription factor	-1,175127323	1,9063E-14
301.	ENSECAG00000001312	GPR146	G protein-coupled receptor 146	-1,177253853	0,03479459
302.	ENSECAG00000000731	SPMIP5	Sperm Microtubule Inner Protein 5	-1,178285414	0,02335379
303.	ENSECAG00000006846	GFRA1	GDNF family receptor alpha 1	-1,180594145	0,00061692
304.	ENSECAG000000015669	RAB3B	RAB3B, member RAS oncogene family	-1,183702531	0,00033281
305.	ENSECAG00000008983	LRRTM1	leucine rich repeat transmembrane neuronal 1	-1,186917043	0,0002395
306.	ENSECAG000000041716	ENSECAG00000041716		-1,189827043	0,01158646
307.	ENSECAG000000023089	SLAIN1	SLAIN motif family member 1	-1,197763025	0,02941692
308.	ENSECAG000000016957	OLFM1	olfactomedin 1	-1,20102661	4,8315E-12
309.	ENSECAG000000023960	KLHL30	kelch like family member 30	-1,202856247	0,00367384
310.	ENSECAG000000026945	HES1	hes family bHLH transcription factor 1	-1,206572443	0,01363336
311.	ENSECAG000000021518	SLX1A	SLX1 Homolog A, Structure-Specific Endonuclease Subunit	-1,206690005	2,9429E-05
312.	ENSECAG000000013486	C4BPA	complement component 4 binding protein alpha	-1,213323668	3,2474E-09
313.	ENSECAG000000023765	IGSF9	immunoglobulin superfamily member 9	-1,216749755	0,01374085
314.	ENSECAG000000015760	ITGA3	integrin subunit alpha 3	-1,221436336	1,7243E-15
315.	ENSECAG000000028351	HES6	Hes Family BHLH Transcription Factor 6	-1,221821949	0,01640033
316.	ENSECAG000000012993	JAG1	jagged canonical Notch ligand 1	-1,223578228	0,00030768
317.	ENSECAG000000037214	TUBB4A	tubulin beta 4A class IVa	-1,233196603	3,4338E-06
318.	ENSECAG000000011404	ENSECAG00000011404	serum amyloid A protein	-1,236021224	0,00302073
319.	ENSECAG000000010747	SH3BGR	SH3 domain binding glutamate rich protein	-1,236309105	1,441E-12
320.	ENSECAG000000012507	CRYAB	Crystallin Alpha B	-1,237608943	1,0655E-09
321.	ENSECAG000000013677	FRY	FRY microtubule binding protein	-1,237918591	3,7915E-12
322.	ENSECAG000000023720	SLAMF8	SLAM family member 8	-1,240029708	0,02654777
323.	ENSECAG000000030878	ENSECAG00000030878	Scm polycomb group protein like 1	-1,250604102	0,03759961
324.	ENSECAG000000009813	CD83	CD83 Molecule	-1,258050194	7,404E-06
325.	ENSECAG000000006567	SLITRK4	SLIT and NTRK like family member 4	-1,259759532	0,00040642
326.	ENSECAG000000010721	MGP	Matrix Gla Protein	-1,26192299	1,45E-26
327.	ENSECAG000000012652	CHDH	choline dehydrogenase	-1,262264137	0,00073935
328.	ENSECAG000000022129	HOXD3	homeobox D3	-1,264442878	3,8929E-12
329.	ENSECAG000000000593	PTN	pleiotrophin	-1,268782797	3,1301E-30
330.	ENSECAG000000020045	HAPLN4	hyaluronan and proteoglycan link protein 4	-1,27370424	2,4522E-09
331.	ENSECAG000000024624	MLPH	melanophilin	-1,275612925	0,0093081
332.	ENSECAG000000021468	POPDC2	popeye domain containing 2	-1,280558202	0,02844739
333.	ENSECAG000000017816	ADORA1	adenosine A1 receptor	-1,285628145	1,4265E-12
334.	ENSECAG000000000420	BANP	BTG3 associated nuclear protein	-1,289043406	2,011E-30
335.	ENSECAG000000034367	ENSECAG00000034367		-1,289871033	0,00123705
336.	ENSECAG000000024636	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2	-1,298362293	1,129E-11
337.	ENSECAG000000011138	COL4A4	collagen type IV alpha 4 chain	-1,307433699	7,3996E-05
338.	ENSECAG000000016234	ANGPTL2	angiopoietin like 2	-1,308897275	1,3267E-17
339.	ENSECAG000000021602	PARM1	prostate androgen-regulated mucin-like protein 1	-1,315475092	3,8895E-15
340.	ENSECAG000000015000	FAM83G		-1,315584296	4,697E-09
341.	ENSECAG000000004433	ENSECAG0000004433	interferon-induced protein with tetratricopeptide repeats 1	-1,322821469	0,00518319

342.	ENSECAG00000018049	PAMR1	peptidase domain containing associated with muscle regeneration 1	-1,324294576	5,9904E-19
343.	ENSECAG00000000278	FCAMR	Fc Alpha And Mu Receptor	-1,327201515	0,00045893
344.	ENSECAG00000004258	IL17RB	interleukin 17 receptor B	-1,339772624	0,03735562
345.	ENSECAG00000017927	DOK7	docking protein 7	-1,344673698	0,03384271
346.	ENSECAG00000017459	ARRB1	arrestin beta 1	-1,346408378	1,1474E-05
347.	ENSECAG00000009948	ADCY5	adenylate cyclase 5	-1,348807019	1,6013E-14
348.	ENSECAG00000009637	OCA2	OCA2 melanosomal transmembrane protein	-1,350636595	5,2192E-08
349.	ENSECAG00000019717	ECM2	extracellular matrix protein 2	-1,35599309	5,3527E-14
350.	ENSECAG00000033029	ENSECAG0000033029	interferon-induced protein with tetratricopeptide repeats 1B	-1,376271297	9,8985E-07
351.	ENSECAG00000000816	AMPD3	adenosine monophosphate deaminase 3	-1,379407774	1,0895E-22
352.	ENSECAG00000015745	BLNK	B cell linker	-1,382040019	3,3753E-26
353.	ENSECAG00000012773	CMPK2	cytidine/uridine monophosphate kinase 2	-1,382838089	0,0001089
354.	ENSECAG00000000343	HACD4	3-hydroxyacyl-CoA dehydratase 4	-1,394629534	0,00018306
355.	ENSECAG00000029465	CHI3L1	chitinase 3 like 1	-1,40082453	0,00010423
356.	ENSECAG00000004274	IQGAP2	IQ motif containing GTPase activating protein 2	-1,401771238	0,00057392
357.	ENSECAG00000004698	PTGR1	prostaglandin reductase 1	-1,402056414	1,6689E-18
358.	ENSECAG00000016984	RANBP3L	RAN binding protein 3 like	-1,407554328	0,00105469
359.	ENSECAG00000012282	MPP7	MAGUK p55 scaffold protein 7	-1,41490372	0,00769284
360.	ENSECAG00000008518	NPNT	nephronectin	-1,427958452	0,00047995
361.	ENSECAG00000018803	PGM2L1	phosphoglucosmutase 2 like 1	-1,428213182	5,0427E-14
362.	ENSECAG00000015846	VASH2	vasohibin 2	-1,446417487	1,6137E-09
363.	ENSECAG00000038866	PTX3	pentraxin 3	-1,448681648	0,01704427
364.	ENSECAG00000022513	NPAS1	neuronal PAS domain protein 1	-1,449633055	0,00057256
365.	ENSECAG00000000931	TMEM119	transmembrane protein 119	-1,463787884	4,0683E-23
366.	ENSECAG00000015552	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	-1,470905991	6,0371E-07
367.	ENSECAG00000037655	GDNF	glial cell derived neurotrophic factor	-1,473698182	0,03696312
368.	ENSECAG00000016251	ENSECAG0000016251		-1,474483431	0,00041879
369.	ENSECAG00000017689	ARHGEF28	Rho Guanine Nucleotide Exchange Factor 28	-1,481693968	4,4545E-22
370.	ENSECAG00000019087	CTSK	Cathepsin K	-1,487347419	1,4438E-19
371.	ENSECAG00000009168	GADD45B	Growth Arrest And DNA Damage Inducible Beta	-1,501913034	1,2443E-07
372.	ENSECAG00000013781	CRACD	capping protein inhibiting regulator of actin dynamics	-1,503959582	7,7735E-06
373.	ENSECAG00000010830	MMP11	Matrix Metalloproteinase 11	-1,504732395	2,0387E-16
374.	ENSECAG00000022047	APOD	apolipoprotein D	-1,508038762	1,3746E-18
375.	ENSECAG00000012340	RADX	RPA1 related single stranded DNA binding protein, X-linked	-1,509247003	0,00264344
376.	ENSECAG00000011423	HSD17B1	Hydroxysteroid 17-Beta Dehydrogenase	-1,511259931	0,04845652
377.	ENSECAG00000015834	DMD	dystrophin	-1,511794911	3,6401E-10
378.	ENSECAG00000023039	CCN3	cellular communication network factor 3	-1,523923129	0,01449942
379.	ENSECAG00000008221	S100A4	S100 calcium binding protein A4	-1,524926343	2,1288E-05
380.	ENSECAG00000032728	HBQ1	Hemoglobin Subunit Theta 1	-1,530123297	0,00781278
381.	ENSECAG00000020093	NPR3	natriuretic peptide receptor 3	-1,536636555	0,00205949
382.	ENSECAG00000023387	FRRS1	Ferric Chelate Reductase 1	-1,538498177	0,01318667
383.	ENSECAG00000016829	ABTB2	ankyrin repeat and BTB domain containing 2	-1,557435825	3,8895E-15

384.	ENSECAG00000014962	FAXDC2	Fatty Acid Hydroxylase Domain Containing 2	-1,572345253	9,2874E-08
385.	ENSECAG00000002430	PRKAG3	protein kinase AMP-activated non-catalytic subunit gamma 3	-1,577013084	6,495E-05
386.	ENSECAG00000019412	HTR2B	5-hydroxytryptamine receptor 2B	-1,579221835	0,04631055
387.	ENSECAG00000011749	MSX2	msh homeobox 2	-1,593446071	1,9407E-17
388.	ENSECAG00000023264	RTP4	Fatty Acid Hydroxylase Domain Containing 2	-1,595818777	0,00916504
389.	ENSECAG00000024873	CCDC190	Coiled-Coil Domain Containing 190	-1,611953146	0,02023792
390.	ENSECAG00000010185	IFIT2	Interferon Induced Protein With Tetratricopeptide Repeats 2	-1,618184296	8,2315E-09
391.	ENSECAG00000019445	MMP12	matrix metalloproteinase 3	-1,630917013	0,04111421
392.	ENSECAG00000011498	SFRP4	Secreted Frizzled Related Protein 4	-1,636537204	0,01215269
393.	ENSECAG00000009949	P2RX7	purinergic receptor P2X 7	-1,642080437	1,0779E-06
394.	ENSECAG00000001488	GPR171	G protein-coupled receptor 171	-1,657741789	3,1902E-11
395.	ENSECAG00000021101	LGI4	Leucine Rich Repeat LGI Family Member 4	-1,681745879	0,01772494
396.	ENSECAG00000016015	PCDH19	protocadherin 19	-1,686434531	2,7069E-07
397.	ENSECAG00000017802	OGN	osteoglycin	-1,691425881	9,0597E-29
398.	ENSECAG00000007379	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	-1,694043024	7,4716E-11
399.	ENSECAG000000041748	COL4A3	collagen type IV alpha 3 chain	-1,702089579	1,0445E-15
400.	ENSECAG00000030850	FGF18	Fibroblast Growth Factor 18	-1,705165114	6,1965E-07
401.	ENSECAG00000017191	SPP1	secreted phosphoprotein 1	-1,711931423	0,00786261
402.	ENSECAG00000009138	MME	membrane metalloendopeptidase	-1,718191391	3,6357E-06
403.	ENSECAG00000017280	MAPK10	mitogen-activated protein kinase 10	-1,721614492	0,00695667
404.	ENSECAG00000019499	ISG20	Interferon Stimulated Exonuclease Gene 20	-1,724118995	6,3286E-06
405.	ENSECAG00000006853	UBD	ubiquitin D	-1,740758682	2,675E-10
406.	ENSECAG00000014287	OMD	osteomodulin	-1,746871947	2,6303E-13
407.	ENSECAG00000013036	MCAM	melanoma cell adhesion molecule	-1,757732875	9,3434E-17
408.	ENSECAG00000030969	CHST4	carbohydrate sulfotransferase 4	-1,765301671	0,00195569
409.	ENSECAG00000021186	FHOD3	formin homology 2 domain containing 3	-1,7736124	2,6471E-08
410.	ENSECAG00000011467	ALPL	alkaline phosphatase, biomineralization associated	-1,776577608	1,2106E-18
411.	ENSECAG00000004778	RTN4R	reticulon 4 receptor	-1,778834754	0,04338884
412.	ENSECAG00000012212	LRP1B	LDL Receptor Related Protein 1B	-1,80467928	6,3096E-06
413.	ENSECAG00000013739	DLGAP1	DLG associated protein 1	-1,805468264	9,6288E-05
414.	ENSECAG000000041924	COL23A1	collagen type XXIII alpha 1 chain	-1,824255056	0,00194251
415.	ENSECAG00000002874	LRRN1	leucine rich repeat neuronal 1	-1,828059038	0,00094314
416.	ENSECAG00000031859	ENSECAG00000031859		-1,83249001	0,00098659
417.	ENSECAG00000021078	GRB14	growth factor receptor bound protein 14	-1,847800231	2,9144E-10
418.	ENSECAG00000026894	CIDEA	Cell Death Inducing DFFA Like Effector A	-1,849336514	0,0214024
419.	ENSECAG00000007047	ASPN	Asporin	-1,851948357	1,7296E-07
420.	ENSECAG00000011358	TMEM86A	transmembrane protein 86A	-1,855510865	3,061E-14
421.	ENSECAG00000003266	PIRT	phosphoinositide interacting regulator of transient receptor potential channels	-1,873800541	0,0018997
422.	ENSECAG00000010869	CAPN6	calpain 6	-1,934077878	0,00825367
423.	ENSECAG00000014398	ENSECAG00000014398		-1,941533621	0,04745531
424.	ENSECAG00000001554	P2RY14	purinergic receptor P2Y14	-1,94263012	2,4872E-32
425.	ENSECAG000000042952	GPX3	Glutathione Peroxidase 3	-1,979901642	0,00680239
426.	ENSECAG00000009483	PRLR	prolactin receptor	-1,980038459	0,0105371

427.	ENSECAG00000012539	RASGRP3	RAS guanyl releasing protein 3	-1,987566337	0,04862805
428.	ENSECAG00000017407	MOXD1	monooxygenase DBH like 1	-1,988742343	7,1825E-45
429.	ENSECAG00000009164	PPARGC1A	PPARG coactivator 1 alpha	-2,006882656	0,00364973
430.	ENSECAG00000016784	TDH	L-threonine dehydrogenase	-2,034410932	0,01073082
431.	ENSECAG00000018308	GREB1	growth regulating estrogen receptor binding 1	-2,051422939	1,3829E-15
432.	ENSECAG00000006717	ASS1	argininosuccinate synthase 1	-2,054665136	3,9292E-09
433.	ENSECAG00000003776	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-2,071566028	0,00096312
434.	ENSECAG00000017379	CYP27C1	cytochrome P450 family 27 subfamily C member 1	-2,079893884	5,4812E-11
435.	ENSECAG00000010791	LMCD1	LIM and cysteine rich domains 1	-2,105493258	2,6425E-06
436.	ENSECAG00000000740	C10H6orf58		-2,137822519	4,9567E-07
437.	ENSECAG000000022629	SLC1A7	Solute Carrier Family 1 Member 7	-2,145381952	3,8501E-33
438.	ENSECAG00000017988	FRMD7	FERM Domain Containing 7	-2,148240786	0,01863487
439.	ENSECAG00000017812	AHRR	aryl hydrocarbon receptor repressor	-2,150926657	4,0763E-09
440.	ENSECAG00000018108	VGF	VGF nerve growth factor inducible	-2,201149484	3,0447E-06
441.	ENSECAG000000028632	ENSECAG00000028632		-2,210924736	8,2269E-07
442.	ENSECAG00000011293	PTPRZ1	protein tyrosine phosphatase receptor type Z1	-2,211757329	3,2799E-10
443.	ENSECAG00000017042	ENSECAG00000017042	membrane-spanning 4-domains subfamily A member 6A	-2,230992033	0,00052388
444.	ENSECAG00000018674	CEMIP	cell migration inducing hyaluronidase 1	-2,30478441	2,0913E-09
445.	ENSECAG000000024612	SNED1	Sushi, Nidogen And EGF Like Domains 1	-2,325267229	0,00101911
446.	ENSECAG00000012514	ENSECAG00000012514		-2,342613381	0,00052759
447.	ENSECAG00000014513	TNFSF15	TNF superfamily member 15	-2,361318389	1,5251E-06
448.	ENSECAG000000020901	CLCA2	chloride channel accessory 2	-2,392411101	9,2674E-06
449.	ENSECAG00000015484	ATP6V0D2	ATPase H ⁺ transporting V0 subunit d2	-2,407197777	7,3327E-24
450.	ENSECAG000000023161	IGSF10	immunoglobulin superfamily member 10	-2,408162777	9,4372E-16
451.	ENSECAG00000012109	SOSTDC1	sclerostin domain containing 1	-2,433399283	1,2044E-12
452.	ENSECAG00000012667	RBFOX1	RNA Binding Fox-1 Homolog 1	-2,441541404	6,469E-10
453.	ENSECAG00000010465	FRMD1	FERM domain containing 1	-2,485697797	0,00567919
454.	ENSECAG00000013893	SCARA5	Scavenger Receptor Class A Member 5	-2,600693491	0,00249099
455.	ENSECAG000000024028	PDE6A	phosphodiesterase 6A	-2,617850287	0,00104404
456.	ENSECAG000000034955	BHLHE41	basic helix-loop-helix family member e41	-2,640271765	3,0557E-25
457.	ENSECAG00000000813	SCN5A	sodium voltage-gated channel alpha subunit 5	-2,850486895	0,00050728
458.	ENSECAG00000013817	CYP1A1	cytochrome P450 family 1 subfamily A member 1	-2,889707373	1,8475E-07
459.	ENSECAG00000009103	MLANA	melan-A	-2,977417697	0,00180313
460.	ENSECAG000000039231	ATOH8	atonal bHLH transcription factor 8	-3,033819867	0,00109331
461.	ENSECAG000000029885	CHST7	carbohydrate sulfotransferase 7	-3,055492891	2,784E-22
462.	ENSECAG00000010128	SEMA4D	semaphorin 4D	-3,202802246	1,9584E-14
463.	ENSECAG00000014164	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8	-3,472261129	1,1881E-06
464.	ENSECAG000000025597	U2	U2 spliceosomal RNA	-3,547325786	0,00680502
465.	ENSECAG00000012750	SLC6A6	solute carrier family 6 member 6	-3,578232086	9,828E-23