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(71) Applicant (for all designated States except US): **DERMACHIP INC.** [US/US]; 719 2nd Street Suite 10, Davis, CA 95616 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **GIULIANI, Giammaria** [IT/IT]; DERMACHIP INC., 719 2nd Street Suite10, Davis, CA 95616 (US). **RODRIGUEZ, Raymond** [US/US]; DERMACHIP INC., 719 2nd Street Suite 10, Davis, CA 95616 (US). **NANDI, Somen** [US/US]; DERMACHIP INC., 719 2nd Street Suite 10, Davis, CA 95616 (US).(74) Agent: **BELL & ASSOCIATES**; 58 West Portal Ave #121, San Francisco, CA 94127 (US).

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(54) Title: EXPRESSION SIGNATURES OF GENES AND GENE NETWORKS ASSOCIATED WITH SKIN AGING

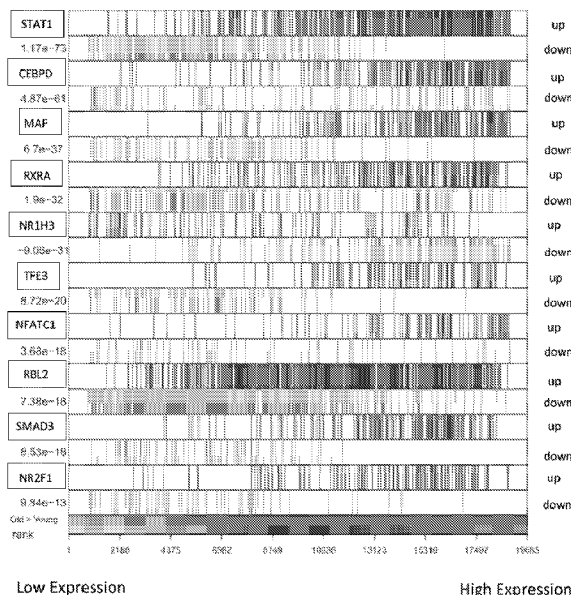


Figure 2. Master regulators correlate with the differential gene expression signatures between old and young cohorts. Low expression level in old cohorts is at the left of the bottom row which shows expression levels gradually increased to the right. The regulator gene symbols are listed at left side of the graph and are inside boxes. Each regulator has two rows of up and down regulated genes that are positioned according to their gene expression levels in the data sets. The P-value of the correlations between the gene expression signature of overall datasets (bottom row) and individual regulation patterns are listed right below each gene symbol. The lower the P-value, the high possibility the regulator has to be responsible for the signature changes.

(57) Abstract: Described herein are expression signatures of genes and coordinately expressed gene networks associated with skin aging, methods used to determine the physiological age of skin, and methods used to screen for compounds used to reduce the visible signs of aging of the skin.



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IN THE PATENT COOPERATION TREATY**INTERNATIONAL PATENT APPLICATION**

Title: Expression signatures of genes and gene networks associated with skin aging

Inventors: Giammaria Giuliani, Raymond Rodriguez, and Somen Nandi

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Assignee: DERMACHIP INC. 719 2nd Street Suite 10, Davis, CA 95616, The USA

Relation to other applications: This application claims the benefit of and priority to US Provisional application No. 61/482,071 filed 03-MAY-2011.

[001] **Field of the invention**

[002] The invention relates to newly discovered expression signatures of coordinately expressed genes and gene networks associated with the physiological and pathological processes of skin aging and to methods for identifying and using compounds that regulate and in some cases recalibrate gene sets and gene pathways associated with skin ageing wherein such regulation and recalibration effectively reverses the effects of ageing of the skin to produce more youthful looking skin so that the skin is more supple, smooth and hydrated and has less wrinkles and fine lines typically associated with ageing.

[003] **Background**

[004] Skin aging is natural process associated with a number of pathophysiologies that can reduce quality of life and longevity. The goal of this study is to gain new insights into how skin ages as a function of time. The working hypothesis for this study is that skin aging results from the dysregulation of key regulatory genes (i.e., gene signatures) that control thousands of genes in multiple, interacting and overlapping networks and pathways. Dysregulation of gene functions leads to physiological aging of tissues, cells and subcellular components. This dysregulation may be the result of damage to the products of key regulatory genes (i.e., oxidative damage to regulatory proteins) or to transcriptional silencing of these genes by mutagenic and/or epigenetic processes. This study is the first of its kind to examine, in a comprehensive fashion, the gene expression profiles in human skin (specifically adult females who self-identified themselves as white) of various age and to identify gene networks and gene signatures associated with the aging process. This information should yield a small number of robust and predictive genes/gene-network whose expression can be used to: (a) understand the relationship between chronological age and physiological age and (b) assess the ability of compounds (e.g., drugs, natural products and dietary factors) to regulate and/or dysregulate genes and gene networks. The present study provides information

that will guide future research and suggest new therapies for preventing, mitigating or treating skin pathologies related to aging.

[005] The skin is the largest human organ comprising about one sixth of total body weight. The skin performs a complex role in human physiology: serves as a barrier to the environment, and the sebum produced by some of its glands (sebaceous) have anti-infective properties. The skin acts as a channel for communication to the outside world, protects us from water loss, friction wounds, and impact wounds and uses specialized pigment cells to protect us from ultraviolet rays of the sun. Skin produces vitamin D in the epidermal layer, when it is exposed to the sun's rays. The skin helps regulate body temperature through sweat glands and helps regulate metabolism. The skin consists of three functional layers: Epidermis, the Dermis (or corium) and the Subcutis (or hypodermis).

[006] Various cell types are present in the skin. Keratinocytes is the most abundant cell type in the epidermis. These cells produce keratin proteins. Fibroblasts differentiate into cells that form the dermis and produce collagen and elastin. Melanocytes produce the pigment melanin that accumulates around the nuclei of the keratinocytes absorbing harmful ultraviolet (UV) light. Langerhans cells (macrophages) reside in the dermis mediating humoral and cellular immune functions. Merkel's cells, which are present in small numbers but are more numerous in the skin of the palms and soles of the feet, are sensory mechanical receptors that respond to certain stimuli such as pressure or touch. The epidermis is the outermost skin layer. As skin cells migrate to the surface, farther away from their source of nourishment, they flatten and shrink. They lose their nuclei, move out of the basal layer to the horny layer (stratum corneum), and die. This process, called keratinization, takes about 4 weeks. About 10 percent of epidermal cells are melanocytes that pigment the skin. The epidermis is differentiated into five layers: horny layer (stratum corneum); clear layer (stratum lucidum); granular layer (stratum granulosum); prickle-cell layer (stratum spinosum); and the basal layer (stratum basale). The dermis is the layer just below the outer keratinized epidermal layer. The dermis contains cells, water, collagen fibers, glycosaminoglycans and fibronectins that form a hydrated gel and are responsible for the high elasticity and tensile strength of the dermis. Embedded in this layer are lymph channels, blood vessels, nerve fibers, muscle cells, hair follicles, sebaceous glands, and sweat glands.

[007] Glycosaminoglycans are mucopolysaccharides present in the dermis that can bind large amounts of water. As the skin ages, the interweaving of the collagen fibers increases and the water-binding capacity diminishes and the skin tends to wrinkle. Glycosaminoglycans bind with the proteins in the connective tissue matrix to form proteoglycans. These proteoglycans form a gel-like material that can absorb and expel water like a sponge. Glycosaminoglycans are subject to a continuous turnover. In contrast, the collagen fibers are only renewed when necessary, such as when injury is sustained. The ability of the skin to store water and thereby remain soft and supple depends in part on the presence of lipids, arginine, and other "natural moisturizing factors" (NMF) that

originate from the cornification (differentiation) of the keratinocytes, for example, pyrrolidine carboxylic acid, and secretions from the sweat and sebaceous glands including urea, salts, and organic acids.

[008] The dermis also contains collagens. Type I collagen is the most abundant protein in skin connective tissue, which also contains other types of collagen (III, V, VII), elastin, proteoglycans, fibronectin, and other extracellular matrix proteins. Newly synthesized type I procollagen is secreted into the dermal extracellular space where it undergoes enzymatic-processing, arranging itself into a triple helix configuration. The triple helix complexes associate with other extracellular matrix proteins such as leucine-rich small proteoglycans, to form regularly arranged fibrillar structures. This process, called fibrillogenesis, results in formation of collagen bundles that are responsible for the strength and resiliency of the skin.

[009] Skin aging is influenced by several factors, including genetics, environmental exposure (ultraviolet (UV) irradiation, xenobiotics, and mechanical stress), hormonal changes, and metabolic processes (generation of reactive chemical compounds such as activated oxygen species, sugars, and aldehydes). Taken together, these factors lead to cumulative alterations of skin structure, function, and appearance. The influence of the environment, especially solar UV irradiation, is of considerable importance for skin aging. Skin aging due to UV exposure (photoaging) is superimposed on chronological skin aging. Historically, scientists considered photoaging and chronological skin aging as two distinct entities. Although the typical appearance of photoaged and chronologically aged human skin can be readily distinguished, recent evidence indicates that chronologically aged and UV-irradiated skin share important molecular features including altered signal transduction pathways that promote matrix-metalloproteinase (MMP) expression, decreased procollagen synthesis, and connective tissue damage. This concordance of molecular mechanisms suggests that UV irradiation accelerates many key aspects of the chronological aging process in human skin. Based on this relationship between UV irradiation and chronological aging, acute UV irradiation of human skin may serve as a useful model to study molecular mechanism of skin chronological aging.

[0010] At the tissue level, chronologically aged skin shows general atrophy of the extracellular matrix reflected by decreased number of fibroblasts, and reduced levels of collagen and elastin. The organization of collagen fibrils and elastin fibers is also impaired. This impairment is thought to result from both decreased protein synthesis that particularly affects types I and III collagens in the dermis and increased breakdown of extracellular matrix proteins.

[0011] Photodamaged skin is associated with increased epidermal thickness and alterations of connective tissue organization. The hallmark of photoaged skin is accumulation of amorphous elastin-containing material that

resides beneath the epidermal dermal junction. Impairment of the fibrillar organization of collagen and elastin is typically more severe in photoaged skin, compared to sun-protected chronologically aged skin. The severity of photoaging is proportional to accumulated sun exposure and inversely related to the degree of skin pigmentation. Individuals with fair skin are more susceptible to solar UV-induced skin damage than darker-skinned individuals.

[0012] At the cellular level, one of the earliest detectable responses of human skin cells to UV irradiation is activation of multiple cytokine and growth factor cell surface receptors, including epidermal growth factor receptor (EGF-R), tumor necrosis factor (TNF) alpha receptor, platelet activating factor (PAF) receptor, insulin receptor, interleukin (IL-1) receptor, and platelet-derived growth factor (PDGF) receptor.

[0013] Activation of cell surface cytokine and growth factor receptors results in recruitment in cytoplasm of adaptor proteins that mediate downstream signaling. Assembly of these signaling complexes results in activation of small GTP-binding protein family members which are key upstream regulators of the certain MAP kinases. The action of certain GTP-binding proteins results in an increased formation of superoxide anions. This increased production of ROS likely participates in amplification of the signal leading to the activation of the downstream enzyme complexes such as MAP kinase. ROS are necessary participants in multiple MAP kinase pathways.

[0014] Increased intracellular ceramide content may also contribute to activation of the MAP kinase pathways by UV irradiation. UV-induced ceramide generation seems to be dependent on increased ROS production, since ceramide and ROS levels rise in parallel, and UV-induced ceramide production is inhibited by the free radical scavenger Vitamin E. MAP kinase activation results in induction of transcription factor AP-1 that is a major effector of the MAP kinase pathways. AP-1 regulates expression of many genes involved in the regulation of cellular growth and differentiation. Transcription of several MMP (matrix-metalloproteinase) family members is strongly regulated by AP-1. Several MMPs are upregulated by AP-1. These include MMP-1 (interstitial collagenase or collagenase 1) which initiates degradation of types I and III fibrillar collagens, MMP-9 (gelatinase B), which further degrades collagen fragments generated by collagenases, and MMP-3 (stromelysin 1), which degrades type IV collagen of the basement membrane and activates pro-MMP-1. MMP induction is, in part, responsible for UV-induced damage to skin connective tissue. Together, MMP-1, MMP-3, and MMP-9 have the capacity to completely degrade mature fibrillar collagen in skin. Consistent with this, increased collagen breakdown has been demonstrated within 24 h after UV irradiation in human skin in vivo. Thus, UV irradiation of human skin causes extracellular matrix degradation via induction of transcription factor AP-1 and subsequent increased MMP production.

[0015] In addition to causing collagen breakdown, UV irradiation impairs new type I collagen synthesis. UV irradiation has been shown to decrease collagen production and impair organization of collagen fibrils in skin *in vivo*. In addition, increased breakdown of extracellular matrix proteins is also observed in UV-irradiated fibroblasts *in vitro* and in human skin *in vivo*. Down-regulation of type I collagen is mediated in part by UV-induced AP-1, which negatively regulates transcription of both genes that encode for type I procollagen (COL1A1 and COL1A2).

[0016] UV-induced down-regulation of collagen synthesis also occurs via paracrine mechanisms involving transforming growth factor-beta (TGF-beta) and other cytokines. TGF-beta is a major profibrotic cytokine, which regulates multiple cellular functions including differentiation, proliferation, and induction of synthesis of extracellular matrix proteins. The biological effects of TGF-beta are diverse and strongly dependent on its expression pattern and cell type. In human skin, TGF-beta inhibits growth of epidermal keratinocytes and stimulates growth of dermal fibroblasts. Moreover, TGF-beta induces synthesis and secretion of the major extracellular matrix proteins collagen and elastin. TGF-beta also inhibits expression of certain specific enzymes involved in the breakdown of collagen, including MMP-1 and MMP-3. TGF-beta also has the ability to affect gene expression by epigenetic modification of DNA. Exogenous TGF-beta was shown to induce and maintain expression of Foxp3 in regulatory T cells by demethylating a highly conserved region of the Foxp3 gene called Treg-specific demethylation region (TSDR) [J.K. Polansky et al., 2008. Eur. J. Immunol. 38: 1654-1663]. Both aging and UV irradiation induce molecular alterations that create skin aging. A major feature of aged skin is the reduction of types I and III procollagen synthesis. This reduction results in skin thinning and increased fragility. Both types I and III procollagen mRNA and protein expression are reduced in aged skin.

[0017] In addition to impaired collagen synthesis, increased production of several MMP family members, including MMP-1, MMP-2 (gelatinase A), MMP-3, and MMP-9 occurs in chronologically aged skin. With the exception of MMP-2, these MMPs are regulated by AP-1 and induced by UV irradiation. Interestingly, AP-1 expression is increased in aged human skin *in vivo* and aged skin fibroblasts *in vitro*. Oxidative stress is thought to be of primary importance in driving the aging process. The free radical theory of aging, first proposed several decades ago, envisions that the molecular basis of aging derives from accumulation, over a lifetime, of oxidative damage to cells resulting from excess ROS, which are produced as a consequence of aerobic metabolism. Although skin possesses extremely efficient anti-oxidant activities, it has been demonstrated that during aging, ROS levels rise and anti-oxidant defenses decline. ROS are necessary participants in multiple MAP kinase pathways. MAPK activation results in induction of AP-1, which in turn, upregulates expression of MMPs. This scenario provides a plausible mechanism for the observed increased collagen degradation in aged human skin.

[0018] In spite of existing differences, many critical molecular features of aged and UV-irradiated human skin bear striking similarities. It could be stated that these similarities reflect the central role that oxidative stress plays in UV irradiation-induced responses and aging in human skin. Viewed in this light, it is not surprising that UV irradiation and aging evoke similar molecular responses, since both are responding to oxidative stress. Nor is it surprising that the consequences of UV irradiation and aging have similar damaging impact on skin connective tissue.

[0019] **Short description of the invention**

[0020] The invention relates to expression signatures of genes and to coordinately expressed gene networks associated with skin aging. Additionally the invention relates to methods used to determine the physiological age of skin, and methods used to screen for compounds used to reduce the visible signs of aging of the skin.

[0021] The inventors have used high throughput expression screening and SAGE (Serial Analysis of Gene Expression) analysis to compare sets of skin tissue from two cohorts of individuals of substantially different ages. The inventors have discovered a large number of previously unknown expression signatures that are related to age. Additionally they have discovered a large and complex network of coordinately expressed genes and pathways that are associated with the physiological and pathological process of skin aging. These expression signatures are used to (i) determine the physiological age of skin, (ii) screen for compounds and compositions that are used to reduce the visible signs of aging of the skin, particularly to the prevention and reduction of skin wrinkles and to the production and maintenance of youthful looking skin.

[0022] Additionally, using the methods of the invention, compounds may be identified by the methods of the invention which compounds affect the expression of various genes within the skin that are involved in chronological-induced and UV-induced skin damage. The invention relates to methods for recalibrating the expression of genes, genetic networks, and cellular pathways in the human skin, primarily in the dermis, that have changed as a result of the chronological aging process. The invention also relates to combinations of natural compounds that produce synergistic effects on the expression of genes relevant to the reversal of skin aging and skin cancer risk reduction.

[0023] **Description of the figures and tables**

[0024] **Figure 1.** A regulatory module responsible for a single gene signature in one aging-related network. White = up-regulated, grey = down-regulated). This network which created using only top 100 up & down regulated genes illustrates the complexity of the aging process. This network is connected to other networks

involved in skin aging as well as to aging in other tissues. It is the gene signatures in different but connected and interacting networks that determine the aging process. It is the genetic regulatory module (e.g., IL-8, IFNG) that will serve as targets for drugs and natural compounds to reverse skin aging. It is believed that the loss of connections between networks reduces the ability of the cell to make coordinated responses to external stimuli and thus the cause of disease and aging.

[0025] **Figure 2.** Master regulators correlate with the differential gene expression signatures between old and young cohorts. The X axis represents age from older (on the left) to younger (on the right). For each regulator (acronym boxed on the left hand side) two rows are shown, one of up-regulated genes and one of downregulated genes. It is very clear from this figure that certain genes and gene sets are upregulated in older skin samples and certain genes and gene sets are upregulated in younger skin samples. Low expression level in old cohorts is at the left of the bottom row which shows expression levels gradually increased to the right. The regulator gene symbols are listed at left side of the graph inside boxes. Each regulator has two rows of up and down regulated genes that are positioned according to their gene expression levels in the data sets. The P-value of the correlations between the gene expression signature of overall datasets (bottom row) and individual regulation patterns are listed right below each gene symbol. The lower the P-value, the high possibility the regulator has to be responsible for the signature changes. STAT1 = a member of the Signal Transducers and Activators of Transcription family of transcription factors. CEBPD = a CCAAT/enhancer-binding protein delta is a protein that in humans is encoded by the CEBPD gene. The protein encoded by this intronless gene is a bZIP transcription factor which can bind as a homodimer to certain DNA regulatory regions. MAF = a transcription factor that in humans is encoded by the MAF gene. RXRA = Retinoid X receptor alpha (RXR-alpha), also known as NR2B1 (nuclear receptor subfamily 2, group B, member 1) is a nuclear receptor. NR1H3 = Liver X receptor alpha (LXR-alpha) is a nuclear receptor protein. TFE3 = Transcription factor E3. NFATC1 = Nuclear factor of activated T-cells, cytoplasmic 1. RBL2 = Retinoblastoma-like protein 2. SMAD3 = Mothers against decapentaplegic homolog 3. NR2F1 = Nuclear Receptor subfamily 2, group F, member 1 is member of nuclear hormone receptor family of steroid hormone receptors.

[0026] **Table 1.** This table lists genes of interest with names and symbol and HGNC ID. Table 1 is used to look up the identity of genes listed on Table 4, which shows the degree of up or down-regulation for these genes.

[0027] **Table 2.** This is a list of cellular pathways and other functional categories based on the up- and down-regulated genes in Table1 showing the degree of enrichment based on the ~2000 up and down regulated genes. A conservative cut-off with FDR of ≤ 0.1 has been used to identify important pathways.

[0028] **Table 3.** This table shows regulatory genes. This table shows a list of gene signatures and regulatory factors controlling the expression of skin-aging-related genes in various pathways and/or gene networks. Note that the gene described in italics at the end of the table are not part of Table 1 (which only includes the top 2000 up and down regulated genes); these italicized genes are part of the gene network regulators.

[0029] **Table 4.** This table shows the 2000 genes showing the greatest degree of up- or down-regulation and differential expression between the two age cohorts. This table shows the degree of differential expression for the top 2000 up and down regulated genes selected out of over 24000 human genes. 'Fc' means Fold Change represented in log 2 scale (these are relative numbers in comparison to expression of other genes so no units are appropriate). The fold-changes in gene expression are all relative to the young subjects. Thus a positive (+) value mean up-regulated in older subject, down-regulated in younger subjects. Negative (-) values means down-regulated in older subjects, up-regulated in younger subjects. HGNC is the standard identification number designated by HUGO Gene Nomenclature Committee. This data was gathered from a total of 32 subjects including 15 samples from the older group (age 59 - 75 year), and 17 samples from younger group (age 19 - 21 years). All samples were collected from healthy volunteer white females from an area of the body unexposed to sun (the buttock cheeks). Rest of the procedure are as described herein.

[0030] **Table 5.** This table shows a list of the top 35 genes/regulators controlling the expression of skin-aging-related genes in various genetic networks. This set of genes is selected from the larger list disclosed herein with the intention of supporting specific claims. The italicized genes were discovered during gene network analysis and are not part of Table 1. The inventors explicitly are not restricting the scope of the invention to these 35 genes.

[0031] **Table 6.** This table is a reduced list of the top 23 gene signatures controlling the expression of skin-aging-related genes in genetic networks.

[0032] **General Representations Concerning the Disclosure**

[0033] In this specification where reference is made to particular features of the invention it is to be understood that the disclosure of the invention in this specification includes all appropriate combinations of such particular features. The embodiments disclosed in this specification are exemplary and do not limit the invention. As used in this specification, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. The term "comprises" and grammatical equivalents thereof are used in this specification to mean that, in addition to the features specifically identified, other features are optionally present. The term "at least" followed by a number is used herein to denote the start of a range beginning with that number. Where

reference is made in this specification to a method comprising two or more defined steps, the defined steps can be carried out in any order or simultaneously.

[0034] This specification incorporates by reference all documents referred to herein and all documents filed concurrently with this specification or filed previously in connection with this application, including but not limited to such documents which are open to public inspection with this specification. Additionally this application incorporates by reference US provisional application No. 61,198,235 filed Nov 3rd 2008, and also to PCT/US09/063137, international filing date Nov 3rd 2009, and also to the following patents and patent publications: US 6,569, 624 US 2004/0142335 US 2006/0275294 US 2003/0152947 US 2005/0089914 US 2007/0059711 US 2005/0250137 US 2005/0250137 US 2005/0053637 US 7,105,292 US 2007/0161022 US 6,692,916 US 2006/0134663 and US 2007/0148106. The specification also incorporates by reference the following: Anuurad, E., Yamasaki, M., Shachter, N., Pearson, T.A. and Berglund, L. (2009). ApoE and ApoC-I polymorphisms: association of genotype with cardiovascular disease phenotype in African Americans. *J Lipid Res* 50(7): 1472-8. Deo, R. C., D. Reich, Tandon, A., Akylbekova, E., Patterson, N., Waliszewska, A., Kathiresan, S., Sarpong, D., Taylor, H.A. Jr. and Wilson, J. G. (2009). Genetic differences between the determinants of lipid profile phenotypes in African and European Americans: the Jackson Heart Study. *PLoS Genet* 5(1): e1000342. Van Dyke, A. L., M. L. Cote, Wenzlaff, A.S., Land, S. and Schwartz, A.G. (2009). Cytokine SNPs: Comparison of allele frequencies by race and implications for future studies. *Cytokine* 46(2): 236-44.

[0035] **Definitions**

[0036] The term "signs of skin aging" refers to any anatomical visible indication that is generally associated with skin as a person gets older, including wrinkles, sagging, discoloration and reduced suppleness.

[0037] The term "recalibrating" when applied to the expression of genes, genetic networks, and cellular pathways refers to a change of adjustment of expression of one or more genes to produce a verisimilitude of a former state, such as the adjustment of expression of one or more genes listed in Table 1 so as to increase the production of glycosaminoglycans, proteoglycans, collagen etc.

[0038] The term "genetic network" or "genetic pathway" refers to two or more genes the expression of which is coordinated or related to a single physiological function such as the production of a particular protein or glycosaminoglycan.

[0039] The term "variant or derivative" when used in conjunction with a species such as a drug or other chemical entity is used to mean said drug or other chemical entity comprising at least one chemical modification, such as, but not limited to, a moiety, a radical group, a reactive group, a charged group, an uncharged group, an ion, or the like. The chemical modification can be either addition or removal of such moiety, group, ion, or the like.

[0040] The term “drug” is used to mean any molecule that alters the physiology of an organism.

[0041] The term “protein” includes peptides.

[0042] The term “environmental stimulus” is used to mean any stimulus that in some way affects the physiology of an organism and that has its origins outside of the organism.

[0043] The term “a therapeutic amount” is used to mean an amount (of a substance) that produces a measurable effect related to the health of an organism.

[0044] The term “gene expression” is used to refer to the transcription of a gene or a part of a gene and is independent from translation. The expression of the gene or part thereof can be increased or it can be decreased. Translation of the expressed gene or part thereof can be increased or it can be decreased.

[0045] The term “gene regulatory network” (GRN) refers to a collection of genes or DNA segments in a cell which interact with each other directly or indirectly through their RNA and protein products. Genes may also interact with other constituents in the cell, thereby governing the rates at which genes in the network are transcribed into mRNA. Some proteins serve only to activate other genes, and these transcription factors that are the main players in regulatory networks or cascades. By binding to the promoter region at the start of other genes they turn them on, initiating the production of another protein, and so on. Some transcription factors are inhibitory.

[0046] The term “genetic regulatory module(s)” refers to a gene or group of genes whose action sets the transcription levels for other genes belonging to a network, which satisfy a certain arbitrary threshold criteria, such as 1.5 fold change with a significance $p < 0.01$.

[0047] “HGNC” is the standard identification number designated by HUGO Gene Nomenclature Committee (<http://www.genenames.org/>). The HUGO Gene Nomenclature Committee is responsible for providing human gene naming guidelines and approving new, unique human gene names and symbols (short form abbreviations of full gene name). In addition to species-specific databases, approved gene names and symbols for human can be located in the National Center for Biotechnology Information's Entrez Gene database (<http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene>). See: Genetic nomenclature guide (1995). Trends Genet and The Trends In Genetics Nomenclature Guide (1998). Elsevier, Cambridge.

[0048] **Detailed description of the invention**

[0049] The invention relates to expression signatures of genes and to coordinately expressed gene networks associated with skin aging. Additionally the invention relates to methods used to determine the physiological age of skin, and methods used to screen for compounds used to reduce the visible signs of aging of the skin.

[0050] The inventors have used high throughput expression screening and SAGE (Serial Analysis of Gene Expression) analysis to compare sets of skin tissue from two cohorts of individuals of substantially different ages. The inventors have discovered a large number of previously unknown expression signatures that are related to age. Additionally they have discovered a large and complex network of coordinately expressed genes and pathways that are associated with the physiological and pathological process of skin aging. The results have identified coordinated gene expression networks and coordination between metabolic pathways that were previously not known to be related to skin ageing. The results have identified a number of transcriptional activators and expression regulators that appear to play key roles in regulation of genes and pathways involved in skin ageing. For example, cholesterol biosynthesis and peroxisome lipid metabolism are both downregulated in the older population, but IL-6 synthesis is upregulated.

[0051] The newly discovered expression signatures may be used to (i) determine the physiological age of skin, (ii) screen for compounds and compositions that are used to reduce the visible signs of aging of the skin. Information determined from SAGE analysis includes (1) a categorization of up- and down regulated genes in the younger and older subjects; (2) categorization of physiological and signal transduction pathways in which these genes are over-represented and (3) categorization of gene networks and genes that constitute hubs within the networks.

[0052] This disclosure further describes a method for reversing signs of skin aging and risk of skin cancer by recalibrating the expression of genes, genetic networks, and cellular pathways in the human skin, primarily in the dermis, that have changed as a result of the chronological aging process. Gene expression patterns, and the pathways they participate in, are restored to levels characteristic of a younger chronological age by treating the skin with specific combinations of natural compounds (e.g., phyto-chemicals, nutrients, minerals, vitamins, etc). Specific combinations of natural compounds are determined using informatic algorithms and high throughput screening. Natural compounds are delivered to the dermis topically with dermo-cosmetics and internally with oral supplements. Combinations of natural compounds are claimed that produce synergistic effects on the expression of genes relevant to the reversal of skin aging and skin cancer risk reduction. Natural compounds can affect gene expression directly (e.g., transcription factor agonists or antagonist) or indirectly (e.g., non-coding RNAs, epigenetic modifications, signalling receptor agonists or antagonist). The invention includes those natural compounds that produce synergistic effects on gene expression when administered both orally and topically. Also disclosed are those genes, gene networks, non-coding RNAs and epigenetic modifications associated with chronologically younger or older skin.

[0053] The invention includes various specific embodiments such as, for example:

[0054] A method for delaying, ceasing or reversing signs of skin aging and risk of skin cancer by recalibrating the expression of genes, genetic networks, and cellular pathways in the human skin, primarily in the dermis, that have changed as a result of the chronological aging process wherein the genes are selected from the group consisting of specific genes are listed in Table 1, cellular pathways, and other functional categories are listed in Table 7, and gene signatures controlling the expression of aging-related genes in gene networks in Table 3.

[0055] The method above wherein the genes recalibrated comprise one or more genes from Table 1 or genes selected from the group consisting of the genes of the functional categories listed in Table 7 and Table 3.

[0056] The method above wherein the genetic networks or cellular pathways recalibrated comprise one or more selected from the groups consisting of the genetic networks or cellular pathways listed in Table 7 and Table 3.

[0057] A method for reducing the signs of aging of the skin the method comprising applying to the skin a compound that was identified as having recalibrating potency with the method above.

[0058] A method for reducing the signs of aging of the skin the method comprising topically applying to the skin a compound "A" having anti-aging properties and further comprising orally administering a compound "B" having anti-aging properties.

[0059] The method above wherein compounds A and B, when administered contemporaneously, provide a synergistic effects on expression of genes of Table 1 or groups of Table 7 and Table 3.

[0060] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that alter the expression of genes involved in the biosynthesis or degradation of a substance selected from the 16 groups listed in Table 7.

[0061] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that increase the expression of genes involved in the biosynthesis of type I or type II collagen.

[0062] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that recalibrate the genes for enzymes listed in Table 1.

[0063] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that decrease production of MMPs.

[0064] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that reduce the rate of degradation of the extracellular matrix proteins in the dermis.

[0065] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of fibroblasts present in the dermis.

[0066] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of collagen fibrils or elastin fibers in the dermis.

[0067] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of collagen fibrils or elastin fibers in the dermis.

[0068] A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the 3-dimensional extracellular matrix structure of collagen, elastin, and other extracellular matrix proteins in the dermis,

[0069] A composition for reducing the signs of aging of the skin the composition comprising combinations of natural compounds including phytochemicals, nutrients, minerals, vitamins, etc.

[0070] The invention also encompasses compositions of natural compounds, for external application to the skin, that reduce, delay, and/or reverse the signs of aging of the skin; composition of natural compounds, for internal application that reduce, delay, and/or reverse the signs of aging of the skin; compositions of natural compounds that produce synergistic effects on the expression of genes and/or gene products relevant to the reversal of skin aging and skin cancer risk reduction; compositions of natural compounds that affect and/or recalibrate the expression of various sets of genes, genetic networks, and/or cellular pathways in the human skin with the effect of reducing, delaying, and/or reversing the signs of aging of the skin; methods for reducing, delaying, and/or reversing the signs of aging of the skin by the external application and internal administration of claimed compounds; and methods for making above compounds and formulations; and methods for evaluating the efficacy of claimed compounds and formulations.

[0071] The present work also includes the identification of genetic regulatory modules responsible for gene signatures in aging-related networks. Fig. 1 shows a graphically displayed network (where white = up-regulated, grey = down-regulated genes) showing the complexity of the aging process. This network is connected to other networks involved in skin aging as well as to general aging in other tissues. Key to this and future work is the identification of nodes (genes) that connect networks together. It is the gene signatures in different but connected and interacting networks that determine the aging process. The genetic regulatory module (e.g. IL-6, IL-8, IFNG, CSF3) will serve as targets for drugs and natural compounds to reverse skin aging. The inventors believe that the loss of connections between networks reduces the ability of the cell to make coordinated responses to external stimuli and thus accelerates disease and aging.

[0072] The present work also includes the identification of genetic regulatory modules responsible for gene signatures in aging-related networks. Fig. 1 shows a graphically displayed network (where white = up-regulated, grey = down-regulated genes) showing the complexity of the aging process. This network is connected to other networks involved in skin aging as well as to general aging in other tissues. Key to this work is the identification of nodes (genes) that connect networks together. It is the gene signatures in different but connected and interacting networks that determine the aging process. The genetic regulatory module (e.g., IL-6, IL-8, IFNG, CSF3) provide targets for drugs and natural compounds to reverse skin aging. The inventors believe that the loss

of connections between networks reduces the ability of the cell to make coordinated responses to external stimuli and thus accelerates disease and aging.

[0073] **Methods of the invention**

[0074] Gene expression analysis was performed on skin samples from a total of 32 subjects including 15 samples from the older group (age 59 - 75 year), and 17 samples from younger group (age 19 - 21 years). All samples were collected from healthy volunteer white females from an area of the body unexposed to sun (the white unexposed buttock cheeks).

[0075] The following steps were performed:

- 1) Obtaining of healthy skin from adult female who self-identified themselves as white of different ages.
- 2) Isolating mRNA from skin tissues for gene expression analysis using microarray technology.
- 3) Isolating DNA from skin tissues to assess DNA methylation status of key aging-related genes identified in specific aims 6.
- 4) Performing bioinformatics analysis of the gene expression dataset using various bio-computational and statistical tools.
- 5) Identification of genes, pathways and networks associated with the skin aging.
- 6) Identified a small number of genes whose expression can serve as predictors (i.e., biomarkers) of skin aging.
- 7) Correlation of chronological age with physiological age by use of biomarker genes/gene-net-works.

[0076] For data analysis the following steps were carried out.

[0077] (1) DNA Sequence fragments from the sequencing experiments were mapped to rna.fa files for *Homo Sapiens* from NCBI (ftp://ftp.ncbi.nih.gov/genomes/H_sapiens/RNA/, rna.fa.gz, Size: 29793 KB, Last Modified: 11/22/10 7:40:00PM).

[0078] (2) BWA and SAMtools were used to map to sequences in rna.fa file (see item 1) and to count number of fragments match the same sequences with no more than two nucleotide differences. BWA algorithm was published at Li H. and Durbin R. (2009) *Fast and accurate short read alignment with Burrows-Wheeler Transform*. *Bioinformatics*, 25:1754- 60. (incorporated by reference) and SAMtools was published at Li H.*, Handsaker B.*, Wysoker A., Fennell T., Ruan J., Homer N., Marth G., Abecasis G., Durbin R. and 1000 Genome Project Data Processing Subgroup (2009) *The Sequence alignment/map (SAM) format and SAMtools*. *Bioinformatics*, 25, 2078-9. (incorporated by reference).

[0079] (3) R package DESeq 1.4.1 was used for statistics analysis. The DESeq algorithm was documented at Anders S. and Huber W. (2010) *Differential expression analysis for sequence count data* *Genome Biology* 11:R106 (incorporated by reference).

[0080] (4) Network analysis used STRING database. STRING database was published at von Mering C., Huynen M., Jaeggi D., Schmidt S., Bork P., Snel B., (2003), *STRING: a database of predicted functional associations between proteins*, Nucleic Acids Res. 2003 Jan 1;31(1):258-61 (incorporated by reference).

[0081] The dermis (inner most layer of the skin) and the epidermis (the outer most layer of the skin) were sampled together in this study. Volunteers, white women at least 18 years of age only, each provided a single, 4 mm deep biopsy of otherwise discarded skin tissue from the buttock.

[0082] Exclusion Criteria: Patients with the following criteria were excluded:

[0083] individuals with atopic dermatitis, psoriasis and other significant skin disorders

[0084] individuals with any serious medical condition

[0085] History of alcohol or drug abuse

[0086] Known hepatitis or HIV

[0087] Pregnant women

[0088] Significant allergic or adverse reaction to local anaesthetics

[0089] Blood clotting disorder

[0090] Faintness or vasovagal reaction with skin biopsies or procedures

[0091] Current smoker

[0092] The sex, race and health criteria were chosen to exclude as many variants as possible. A homogeneous population was chosen to reduce genetic variables.

[0093] **Experimental Design**

[0094] **Identification of genes differentially expressed in healthy skin from subjects of different chronological age**

[0095] Each 4mm buttock skin sample is immediately immersed into RNALater or snap frozen and stored at -80°C until nucleic acid (RNA and DNA) extraction.

[0096] The samples undergo RNA and DNA extraction.

[0097] The extracted RNA is subjected to reverse transcription into cDNA, amplified, and processed for microarray analysis and also by Taqman qRT-PCR.

[0098] RNA sequenced are detected by using New Generation Sequencing (NGS), Illumina procedure, and data output and analysis is performed per standard analytical software.

[0099] Average-linkage hierarchal clustering of data is applied using Gene Cluster software and results are displayed with Java TreeView. Analyses for differential expression include use of appropriate statistical limits for identified gene sets and both paired and multivariate statistical treatment. Gene and pathway identification is assisted by application of interaction gene network analyses for processes such as immune response, inflammation, wound repair, cell growth, apoptosis, cell migration, etc.

[00100] This method has lead to pathway-specific hypothesis testing and aids in identification of regulated genes and gene network modules. This treatment of the microarray data enables us to compare gene expression profiles in skin by age.

[00101] **2. DNA Methylation Status of Aging-Related Gene Signatures.**

[00102] Based on the results of microarray data analysis, the DNA methylation status of candidate genes that are highly correlated with age (i.e., show the greatest change between young and old skin samples) were determined.

[00103] PureLink Genomic DNA Isolation kit (Invitrogen) was used to isolate DNA from half of the nucleic extraction samples.

[00104] This genomic DNA was subjected to bisulfite-specific PCR and sequencing of their 5' promoter regions to determine their DNA methylation status. The DNA is subjected to bisulfite conversion (EZ DNA-Methylation-Direct, Zymo Research).

[00105] Bisulfite-converted genomic DNA is subjected to bisulfite-specific PCR (BSP) using primers specific to the 5' end of the candidate genes. The BSP primers pairs that recognize methylated and unmethylated DNA are designed using Methyl-Primer Express v1.0 (Lifetechnologies).

[00106] PCR is carried out in a 25 ul reaction volume using a Taq PCR Kit (New England BioLabs) and PCR products are resolved in 1.5% agarose gels. PCR bands are excised and purified using a Gel Extraction Kit (Qiagen) before ligating to pCR4-TOPO vector (Invitrogen), and transformed into DH5-alpha E. coli. Insert-containing plasmids are verified by PCR and EcoRI digestion before DNA sequencing.

[00107] Correlations between DNA hypermethylation in the 5'-ends of aging-related gene signatures, gene expression levels and age are examined. DNA hypermethylation and low level expression of gene signatures in older skin samples are suggestive of epigenetic silencing of gene function, leading to aged skin.

[00108] **3. Skin Aging Gene Expression (SAGE) analysis**

[00109] The initial experiment employed the following samples:

15 samples from the older group (age 59 - 75 years)

17 samples from younger group (age 19 - 21 years)

1 Sample has been rejected because of tissue inconsistency

1 Sample has been rejected because of the data quality

[00110] Transcript RNA from the samples was isolated and sequenced in 36bp x 36bp Paired End Reads. This gave about 45M raw reads per sample. About 94% passed quality control. About 84.5% mapped to human transcripts.

[00111] **Results**

[00112] The study has discovered a large number of genes and pathways that are differentially expressed between the old and young cohorts.

[00113] Additionally the study reveals that many genes and pathways display coordinated expression. This suggests that the coordinated pathways are subject to regulation by means of expression regulators such as transcription regulators, translation regulators, siRNAs and other suppressors of protein expression. Such regulators appear to have pleiotropic effects on numerous genes not necessarily linked in series but found at disparate locations in the genome.

[00114] The results of the data analysis is shown Tables 1, 2, 3, 4, 5 and 6.

[00115] For example, cholesterol biosynthesis and peroxisome lipid metabolism are both downregulated in the older population, but IL-6 synthesis is upregulated.

[00116] Another pathway whose regulation is clearly affected by ageing is the T Cell Receptor (TCR) signaling pathway (see Table 7). T Cell Receptor (TCR) activation promotes a number of signaling cascades that ultimately determine cell fate through regulating cytokine production, cell survival, proliferation, and differentiation. An early event in TCR activation is phosphorylation of immunoreceptor tyrosine-base activation motifs (ITAMs) on the cytosolic side of the TCR/CD3 complex by lymphocyte protein-tyrosine kinase (Lck). The CD45 receptor tyrosine phosphatase modulates the phosphorylation and activation of Lck and other Src family tyrosine kinases. z-chain associated protein kinase (Zap-70) is recruited to the TCR/CD3 complex where it becomes activated, promoting recruitment and phosphorylation of downstream adaptor or scaffold proteins. Phosphorylation of SLP-76 by Zap-70 promotes recruitment of Vav (a guanine nucleotide exchange factor), the adaptor proteins NCK and GADS, and an inducible T cell kinase (ITK). Phosphorylation of phospholipase C γ 1 (PLC γ 1) by Itk results in the hydrolysis of phosphatidylinositol 4,5-bisphosphate (PIP2) to produce the second messengers diacylglycerol (DAG) and inositol trisphosphate (IP3). DAG activates PKC θ and the MAPK/Erk pathways, both promoting

transcription factor NF- κ B activation. IP3 triggers the release of Ca²⁺ from the ER, which promotes the entry of extracellular Ca²⁺ into cells through calcium release-activated Ca²⁺(CRAC) channels. Calcium-bound calmodulin (Ca²⁺/CaM) activates the phosphatase calcineurin, which promotes IL-2 gene transcription through the transcription factor NFAT. Feedback regulation at several points within these pathways allows for different outcomes, depending on the cell type and environment. The incorporation of signals from additional cell surface receptors (such as CD28 or LFA-1) further regulates cellular response.

TABLE 1

Symbol	Gene Name	HGNC ID
A2ML1	alpha-2-macroglobulin-like 1	HGNC:23336
AACS	acetoacetyl-CoA synthetase	HGNC:21298
AADACL3	arylacetamide deacetylase-like 3	HGNC:32037
AADACL4	arylacetamide deacetylase-like 4	HGNC:32038
ABCA13	ATP-binding cassette, sub-family A (ABC1), member 13	HGNC:14638
ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	HGNC:34
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	HGNC:36
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	HGNC:38
ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	HGNC:39
ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member	HGNC:46
ABCC11	ATP-binding cassette, sub-family C (CFTR/MRP), 11	HGNC:14639
ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), 4	HGNC:55
ABHD12B	abhydrolase domain containing 12B	HGNC:19837
ABHD3	abhydrolase domain containing 3	HGNC:18718
ABHD5	abhydrolase domain containing 5	HGNC:21396
ABLIM2	actin binding LIM protein family, member 2	HGNC:19195
ABLIM3	actin binding LIM protein family, member 3	HGNC:29132
ACAA1	acetyl-CoA acyltransferase 1	HGNC:82
ACAA2	acetyl-CoA acyltransferase 2	HGNC:83
ACAD8	acyl-CoA dehydrogenase family, member 8	HGNC:87
ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	HGNC:89
ACADVL	acyl-CoA dehydrogenase, very long chain	HGNC:92
ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains1	HGNC:16467
ACAT2	acetyl-CoA acetyltransferase 2	HGNC:94
ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A)1	HGNC:2707
ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A)1	HGNC:13557
ACLY	ATP citrate lyase	HGNC:115
ACO1	aconitase 1, soluble	HGNC:117
ACOT1	acyl-CoA thioesterase 1	HGNC:33128
ACOT2	acyl-CoA thioesterase 2	HGNC:18431
ACOT4	acyl-CoA thioesterase 4	HGNC:19748
ACOT7	acyl-CoA thioesterase 7	HGNC:24157
ACOX2	acyl-CoA oxidase 2, branched chain	HGNC:120
ACP6	acid phosphatase 6, lysophosphatidic	HGNC:29609
ACPP	acid phosphatase, prostate	HGNC:125
ACSBG1	acyl-CoA synthetase bubblegum family member 1	HGNC:29567
ACSL1	acyl-CoA synthetase long-chain family member 1	HGNC:3569
ACSL3	acyl-CoA synthetase long-chain family member 3	HGNC:3570
ACSL5	acyl-CoA synthetase long-chain family member 5	HGNC:16526
ACSM3	acyl-CoA synthetase medium-chain family member 3	HGNC:10522

ACSM5	acyl-CoA synthetase medium-chain family member 5	HGNC:26060
ACSS2	acyl-CoA synthetase short-chain family member 2	HGNC:15814
ACTA1	actin, alpha 1, skeletal muscle	HGNC:129
ACTA2	actin, alpha 2, smooth muscle, aorta	HGNC:130
ACTBL2	actin, beta-like 2	HGNC:17780
ACTC1	actin, alpha, cardiac muscle 1	HGNC:143
ACTG2	actin, gamma 2, smooth muscle, enteric	HGNC:145
ACTN1	actinin, alpha 1	HGNC:163
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	HGNC:24025
ACVR1C	activin A receptor, type IC	HGNC:18123
ACVRL1	activin A receptor type II-like 1	HGNC:175
ACY1	aminoacylase 1	HGNC:177
ADAM33	ADAM metalloproteinase domain 33	HGNC:15478
ADAM8	ADAM metalloproteinase domain 8	HGNC:215
ADAMTS15	ADAM metalloproteinase with thrombospondin type 1 motif, 15	HGNC:16305
ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5	HGNC:221
ADAMTS7	ADAM metalloproteinase with thrombospondin type 1 motif, 7	HGNC:223
ADAMTSL1	ADAMTS-like 1	HGNC:14632
ADAMTSL3	ADAMTS-like 3	HGNC:14633
ADAMTSL5	ADAMTS-like 5	HGNC:27912
ADCK1	aarF domain containing kinase 1	HGNC:19038
ADCY5	adenylate cyclase 5	HGNC:236
ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	HGNC:249
ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	HGNC:250
ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	HGNC:251
ADH6	alcohol dehydrogenase 6 (class V)	HGNC:255
ADHFE1	alcohol dehydrogenase, iron containing, 1	HGNC:16354
ADIPOQ	adiponectin, C1Q and collagen domain containing	HGNC:13633
ADRA2A	adrenergic, alpha-2A-, receptor	HGNC:281
AEBP1	AE binding protein 1	HGNC:303
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	HGNC:324
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	HGNC:326
AGPHD1	aminoglycoside phosphotransferase domain containing 1	HGNC:34403
AGR2	anterior gradient 2 homolog (<i>Xenopus laevis</i>)	HGNC:328
AGRN	Agrin	HGNC:329
AGTRAP	angiotensin II receptor-associated protein	HGNC:13539
AHSP	alpha hemoglobin stabilizing protein	HGNC:18075
AKAP12	A kinase (PRKA) anchor protein 12	HGNC:370
AKAP2	A kinase (PRKA) anchor protein 2	HGNC:372
AKNA	AT-hook transcription factor	HGNC:24108
AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	HGNC:380
ALAS1	aminolevulinate, delta-, synthase 1	HGNC:396

ALAS2	aminolevulinate, delta-, synthase 2	HGNC:397
ALCAM	activated leukocyte cell adhesion molecule	HGNC:400
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	HGNC:407
ALDH1L1	aldehyde dehydrogenase 1 family, member L1	HGNC:3978
ALDH3A1	aldehyde dehydrogenase 3 family, member A1	HGNC:405
ALDH3B2	aldehyde dehydrogenase 3 family, member B2	HGNC:411
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	HGNC:7179
ALDOB	aldolase B, fructose-bisphosphate	HGNC:417
ALDOC	aldolase C, fructose-bisphosphate	HGNC:418
ALG1L	asparagine-linked glycosylation 1-like	HGNC:33721
ALOX15B	arachidonate 15-lipoxygenase, type B	HGNC:434
ALPK2	alpha-kinase 2	HGNC:20565
AMACR	alpha-methylacyl-CoA racemase	HGNC:451
AMICA1	adhesion molecule, interacts with CXADR antigen 1	HGNC:19084
AMOT	angiomotin	HGNC:17810
AMOTL2	angiomotin like 2	HGNC:17812
AMPD1	adenosine monophosphate deaminase 1	HGNC:468
AMTN	amelotin	HGNC:33188
AMY1A	amylase, alpha 1A (salivary)	HGNC:474
AMY1B	amylase, alpha 1B (salivary)	HGNC:475
AMY1C	amylase, alpha 1C (salivary)	HGNC:476
ANGPT1	angiopoietin 1	HGNC:484
ANGPTL2	angiopoietin-like 2	HGNC:490
ANGPTL4	angiopoietin-like 4	HGNC:16039
ANGPTL5	angiopoietin-like 5	HGNC:19705
ANGPTL7	angiopoietin-like 7	HGNC:24078
ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	HGNC:15819
ANKRD22	ankyrin repeat domain 22	HGNC:28321
ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	HGNC:26724
ANPEP	alanyl (membrane) aminopeptidase	HGNC:500
ANTXR2	anthrax toxin receptor 2	HGNC:21732
ANXA3	annexin A3	HGNC:541
ANXA6	annexin A6	HGNC:544
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	HGNC:550
AOX1	aldehyde oxidase 1	HGNC:553
APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	HGNC:17379
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	HGNC:17357
APOC1	apolipoprotein C-I	HGNC:607
APOD	apolipoprotein D	HGNC:612
APOE	apolipoprotein E	HGNC:613
APOL1	apolipoprotein L, 1	HGNC:618
APOL3	apolipoprotein L, 3	HGNC:14868

APOL6	apolipoprotein L, 6	HGNC:14870
AQP4	aquaporin 4	HGNC:637
AQP5	aquaporin 5	HGNC:638
AQP7	aquaporin 7	HGNC:640
AREG	amphiregulin	HGNC:651
AREGB	amphiregulin B	HGNC:34509
ARHGAP20	Rho GTPase activating protein 20	HGNC:18357
ARHGAP29	Rho GTPase activating protein 29	HGNC:30207
ARHGAP30	Rho GTPase activating protein 30	HGNC:27414
ARHGAP6	Rho GTPase activating protein 6	HGNC:676
ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	HGNC:679
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	HGNC:685
ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	HGNC:697
ARR3	arrestin 3, retinal (X-arrestin)	HGNC:710
ARSH	arylsulfatase family, member H	HGNC:32488
ASIP	agouti signaling protein	HGNC:745
ASTN1	astrotactin 1	HGNC:773
ATOH1	atonal homolog 1 (Drosophila)	HGNC:797
ATOH8	atonal homolog 8 (Drosophila)	HGNC:24126
ATP12A	ATPase, H ⁺ /K ⁺ transporting, nongastric, alpha polypeptide	HGNC:13816
ATP1A2	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide	HGNC:800
ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	HGNC:833
ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	HGNC:843
ATP5I	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit E	HGNC:846
ATP6V0A4	ATPase, H ⁺ transporting, lysosomal V0 subunit a4	HGNC:866
ATP6V0B	ATPase, H ⁺ transporting, lysosomal 21kDa, V0 subunit b	HGNC:861
ATP6V0C	ATPase, H ⁺ transporting, lysosomal 16kDa, V0 subunit c	HGNC:855
ATP6V1C2	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	HGNC:18264
AVIL	advillin	HGNC:14188
AWAT1	acyl-CoA wax alcohol acyltransferase 1	HGNC:23252
AWAT2	acyl-CoA wax alcohol acyltransferase 2	HGNC:23251
B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	HGNC:13528
B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	HGNC:24136
BAI1	brain-specific angiogenesis inhibitor 1	HGNC:943
BARX2	BARX homeobox 2	HGNC:956
BCAN	brevican	HGNC:23059
BCAP29	B-cell receptor-associated protein 29	HGNC:24131
BCAP31	B-cell receptor-associated protein 31	HGNC:16695
BCAT1	branched chain amino-acid transaminase 1, cytosolic	HGNC:976
BCAT2	branched chain amino-acid transaminase 2, mitochondrial	HGNC:977
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide	HGNC:987
BDH1	3-hydroxybutyrate dehydrogenase, type 1	HGNC:1027

BEAN1	brain expressed, associated with NEDD4, 1	HGNC:24160
BHMT2	betaine--homocysteine S-methyltransferase 2	HGNC:1048
BICC1	bicaudal C homolog 1 (Drosophila)	HGNC:19351
BIRC3	baculoviral IAP repeat containing 3	HGNC:591
BLNK	B-cell linker	HGNC:14211
BRI3BP	BRI3 binding protein	HGNC:14251
BRP44	brain protein 44	HGNC:24515
BRP44L	brain protein 44-like	HGNC:21606
BSG	basigin (Ok blood group)	HGNC:1116
BST1	bone marrow stromal cell antigen 1	HGNC:1118
BST2	bone marrow stromal cell antigen 2	HGNC:1119
BTN3A1	butyrophilin, subfamily 3, member A1	HGNC:1138
BTN3A2	butyrophilin, subfamily 3, member A2	HGNC:1139
BTN3A3	butyrophilin, subfamily 3, member A3	HGNC:1140
BZW1	basic leucine zipper and W2 domains 1	HGNC:18380
C10orf129	chromosome 10 open reading frame 129	HGNC:31665
C10orf57	chromosome 10 open reading frame 57	HGNC:25804
C11orf96	chromosome 11 open reading frame 96	HGNC:38675
C12orf39	chromosome 12 open reading frame 39	HGNC:28139
C14orf180	chromosome 14 open reading frame 180	HGNC:33795
C14orf2	chromosome 14 open reading frame 2	HGNC:1188
C14orf49	chromosome 14 open reading frame 49	HGNC:19861
C15orf23	chromosome 15 open reading frame 23	HGNC:30767
C15orf43	chromosome 15 open reading frame 43	HGNC:28520
C15orf48	chromosome 15 open reading frame 48	HGNC:29898
C16orf73	chromosome 16 open reading frame 73	HGNC:28569
C16orf74	chromosome 16 open reading frame 74	HGNC:23362
C16orf89	chromosome 16 open reading frame 89	HGNC:28687
C17orf97	chromosome 17 open reading frame 97	HGNC:33800
C19orf46	chromosome 19 open reading frame 46	HGNC:26703
C19orf71	chromosome 19 open reading frame 71	HGNC:34496
C1orf122	chromosome 1 open reading frame 122	HGNC:24789
C1orf158	chromosome 1 open reading frame 158	HGNC:28567
C1orf162	chromosome 1 open reading frame 162	HGNC:28344
C1orf51	chromosome 1 open reading frame 51	HGNC:25200
C1orf53	chromosome 1 open reading frame 53	HGNC:30003
C1orf68	chromosome 1 open reading frame 68	HGNC:29468
C1orf9	chromosome 1 open reading frame 9	HGNC:1240
C1QA	complement component 1, q subcomponent, A chain	HGNC:1241
C1QB	complement component 1, q subcomponent, B chain	HGNC:1242
C1QC	complement component 1, q subcomponent, C chain	HGNC:1245
C1QTNF5	C1q and tumor necrosis factor related protein 5	HGNC:14344
C1QTNF6	C1q and tumor necrosis factor related protein 6	HGNC:14343

C1R	complement component 1, r subcomponent	HGNC:1246
C1S	complement component 1, s subcomponent	HGNC:1247
C2	complement component 2	HGNC:1248
C20orf24	chromosome 20 open reading frame 24	HGNC:15870
C20orf3	chromosome 20 open reading frame 3	HGNC:13238
C21orf33	chromosome 21 open reading frame 33	HGNC:1273
C3	complement component 3	HGNC:1318
C3AR1	complement component 3a receptor 1	HGNC:1319
C5orf4	chromosome 5 open reading frame 4	HGNC:1334
C6orf106	chromosome 6 open reading frame 106	HGNC:21215
C7	complement component 7	HGNC:1346
C7orf58	chromosome 7 open reading frame 58	HGNC:26159
C9orf16	chromosome 9 open reading frame 16	HGNC:17823
CA14	carbonic anhydrase XIV	HGNC:1372
CA6	carbonic anhydrase VI	HGNC:1380
CALCB	calcitonin-related polypeptide beta	HGNC:1438
CALD1	caldesmon 1	HGNC:1441
CALML3	calmodulin-like 3	HGNC:1452
CAMK1G	calcium/calmodulin-dependent protein kinase IG	HGNC:14585
CAMP	cathelicidin antimicrobial peptide	HGNC:1472
CAPN13	calpain 13	HGNC:16663
CAPN3	calpain 3, (p94)	HGNC:1480
CAPN8	calpain 8	HGNC:1485
CARD11	caspase recruitment domain family, member 11	HGNC:16393
CARD18	caspase recruitment domain family, member 18	HGNC:28861
CASQ2	calsequestrin 2 (cardiac muscle)	HGNC:1513
CASS4	Cas scaffolding protein family member 4	HGNC:15878
CBLN1	cerebellin 1 precursor	HGNC:1543
CBLN2	cerebellin 2 precursor	HGNC:1544
CCBP2	chemokine binding protein 2	HGNC:1565
CCDC69	coiled-coil domain containing 69	HGNC:24487
CCDC85A	coiled-coil domain containing 85A	HGNC:29400
CCDC86	coiled-coil domain containing 86	HGNC:28359
CCK	cholecystokinin	HGNC:1569
CCKBR	cholecystokinin B receptor	HGNC:1571
CCL13	chemokine (C-C motif) ligand 13	HGNC:10611
CCL14	chemokine (C-C motif) ligand 14	HGNC:10612
CCL15	chemokine (C-C motif) ligand 15	HGNC:10613
CCL17	chemokine (C-C motif) ligand 17	HGNC:10615
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	HGNC:10616
CCL19	chemokine (C-C motif) ligand 19	HGNC:10617
CCL27	chemokine (C-C motif) ligand 27	HGNC:10626
CCL4	chemokine (C-C motif) ligand 4	HGNC:10630

CCL4L2	chemokine (C-C motif) ligand 4-like 2	HGNC:24066
CCL5	chemokine (C-C motif) ligand 5	HGNC:10632
CCNC	cyclin C	HGNC:1581
CCND1	cyclin D1	HGNC:1582
CCNF	cyclin F	HGNC:1591
CCR1	chemokine (C-C motif) receptor 1	HGNC:1602
CCR2	chemokine (C-C motif) receptor 2	HGNC:1603
CCR4	chemokine (C-C motif) receptor 4	HGNC:1605
CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)	HGNC:1606
CCR7	chemokine (C-C motif) receptor 7	HGNC:1608
CD163	CD163 molecule	HGNC:1631
CD1C	CD1c molecule	HGNC:1636
CD1E	CD1e molecule	HGNC:1638
CD2	CD2 molecule	HGNC:1639
CD207	CD207 molecule, langerin	HGNC:17935
CD209	CD209 molecule	HGNC:1641
CD226	CD226 molecule	HGNC:16961
CD24	CD24 molecule	HGNC:1645
CD247	CD247 molecule	HGNC:1677
CD248	CD248 molecule, endosialin	HGNC:18219
CD27	CD27 molecule	HGNC:11922
CD28	CD28 molecule	HGNC:1653
CD34	CD34 molecule	HGNC:1662
CD36	CD36 molecule (thrombospondin receptor)	HGNC:1663
CD37	CD37 molecule	HGNC:1666
CD38	CD38 molecule	HGNC:1667
CD3D	CD3d molecule, delta (CD3-TCR complex)	HGNC:1673
CD3E	CD3e molecule, epsilon (CD3-TCR complex)	HGNC:1674
CD40LG	CD40 ligand	HGNC:11935
CD48	CD48 molecule	HGNC:1683
CD5	CD5 molecule	HGNC:1685
CD52	CD52 molecule	HGNC:1804
CD53	CD53 molecule	HGNC:1686
CD6	CD6 molecule	HGNC:1691
CD68	CD68 molecule	HGNC:1693
CD74	CD74 molecule, major histocompatibility complex, class II invariant	HGNC:1697
CD84	CD84 molecule	HGNC:1704
CD8A	CD8a molecule	HGNC:1706
CD96	CD96 molecule	HGNC:16892
CD97	CD97 molecule	HGNC:1711
CDA	cytidine deaminase	HGNC:1712
CDH5	cadherin 5, type 2 (vascular endothelium)	HGNC:1764
CDH7	cadherin 7, type 2	HGNC:1766

CDK5	cyclin-dependent kinase 5	HGNC:1774
CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	HGNC:1782
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	HGNC:1784
CDO1	cysteine dioxygenase, type I	HGNC:1795
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1	HGNC:1814
CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6	HGNC:1818
CECR2	cat eye syndrome chromosome region, candidate 2	HGNC:1840
CELF2	CUGBP, Elav-like family member 2	HGNC:2550
CES1	carboxylesterase 1	HGNC:1863
CFB	complement factor B	HGNC:1037
CFD	complement factor D (adipsin)	HGNC:2771
CFH	complement factor H	HGNC:4883
CFHR1	complement factor H-related 1	HGNC:4888
CFHR3	complement factor H-related 3	HGNC:16980
CGA	glycoprotein hormones, alpha polypeptide	HGNC:1885
CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	HGNC:15559
CHGA	chromogranin A (parathyroid secretory protein 1)	HGNC:1929
CHGB	chromogranin B (secretogranin 1)	HGNC:1930
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	HGNC:1932
CHI3L2	chitinase 3-like 2	HGNC:1933
CHIT1	chitinase 1 (chitotriosidase)	HGNC:1936
CHL1	cell adhesion molecule with homology to L1CAM	HGNC:1939
CHRD1	chordin-like 1	HGNC:29861
CHRD2	chordin-like 2	HGNC:24168
CHRNA9	cholinergic receptor, nicotinic, alpha 9 (neuronal)	HGNC:14079
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	HGNC:1970
CIDEA	cell death-inducing DFFA-like effector a	HGNC:1976
CIDEC	cell death-inducing DFFA-like effector c	HGNC:24229
CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	HGNC:1980
CILP2	cartilage intermediate layer protein 2	HGNC:24213
CISH	cytokine inducible SH2-containing protein	HGNC:1984
CKB	creatine kinase, brain	HGNC:1991
CKMT1A	creatine kinase, mitochondrial 1A	HGNC:31736
CKMT1B	creatine kinase, mitochondrial 1B	HGNC:1995
CLC	Charcot-Leyden crystal protein	HGNC:2014
CLCA2	chloride channel accessory 2	HGNC:2016
CLDN10	claudin 10	HGNC:2033
CLDN11	claudin 11	HGNC:8514
CLDN5	claudin 5	HGNC:2047
CLEC10A	C-type lectin domain family 10, member A	HGNC:16916
CLEC12A	C-type lectin domain family 12, member A	HGNC:31713
CLEC2A	C-type lectin domain family 2, member A	HGNC:24191
CLEC3B	C-type lectin domain family 3, member B	HGNC:11891

CLEC4G	C-type lectin domain family 4, member G	HGNC:24591
CLIC2	chloride intracellular channel 2	HGNC:2063
CLIC3	chloride intracellular channel 3	HGNC:2064
CLIC6	chloride intracellular channel 6	HGNC:2065
CLIP2	CAP-GLY domain containing linker protein 2	HGNC:2586
CLIP3	CAP-GLY domain containing linker protein 3	HGNC:24314
CLSTN3	calsyntenin 3	HGNC:18371
CLU	clusterin	HGNC:2095
CMA1	chymase 1, mast cell	HGNC:2097
CMTM8	CKLF-like MARVEL transmembrane domain containing 8	HGNC:19179
CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	HGNC:20675
CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	HGNC:24437
CNIH4	cornichon homolog 4 (Drosophila)	HGNC:25013
CNKSR3	CNKSR family member 3	HGNC:23034
CNN1	calponin 1, basic, smooth muscle	HGNC:2155
CNPY1	canopy 1 homolog (zebrafish)	HGNC:27786
COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	HGNC:2180
COL11A1	collagen, type XI, alpha 1	HGNC:2186
COL12A1	collagen, type XII, alpha 1	HGNC:2188
COL16A1	collagen, type XVI, alpha 1	HGNC:2193
COL1A1	collagen, type I, alpha 1	HGNC:2197
COL1A2	collagen, type I, alpha 2	HGNC:2198
COL3A1	collagen, type III, alpha 1	HGNC:2201
COL4A1	collagen, type IV, alpha 1	HGNC:2202
COL4A2	collagen, type IV, alpha 2	HGNC:2203
COL4A6	collagen, type IV, alpha 6	HGNC:2208
COL5A1	collagen, type V, alpha 1	HGNC:2209
COL7A1	collagen, type VII, alpha 1	HGNC:2214
COL8A1	collagen, type VIII, alpha 1	HGNC:2215
COMP	cartilage oligomeric matrix protein	HGNC:2227
COQ4	coenzyme Q4 homolog (S. cerevisiae)	HGNC:19693
COQ9	coenzyme Q9 homolog (S. cerevisiae)	HGNC:25302
CORO1A	coronin, actin binding protein, 1A	HGNC:2252
COTL1	coactosin-like 1 (Dictyostelium)	HGNC:18304
COX5A	cytochrome c oxidase subunit Va	HGNC:2267
COX6C	cytochrome c oxidase subunit VIc	HGNC:2285
COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	HGNC:2288
COX7B	cytochrome c oxidase subunit VIIb	HGNC:2291
COX7C	cytochrome c oxidase subunit VIIc	HGNC:2292
COX8A	cytochrome c oxidase subunit VIIIA (ubiquitous)	HGNC:2294
CP	ceruloplasmin (ferroxidase)	HGNC:2295
CPA3	carboxypeptidase A3 (mast cell)	HGNC:2298
CPA4	carboxypeptidase A4	HGNC:15740

CPB2	carboxypeptidase B2 (plasma)	HGNC:2300
CPD	carboxypeptidase D	HGNC:2301
CPE	carboxypeptidase E	HGNC:2303
CPEB4	cytoplasmic polyadenylation element binding protein 4	HGNC:21747
CPLX3	complexin 3	HGNC:27652
CPT2	carnitine palmitoyltransferase 2	HGNC:2330
CPVL	carboxypeptidase, vitellogenic-like	HGNC:14399
CPXM1	carboxypeptidase X (M14 family), member 1	HGNC:15771
CPZ	carboxypeptidase Z	HGNC:2333
CRABP1	cellular retinoic acid binding protein 1	HGNC:2338
CRAT	carnitine O-acetyltransferase	HGNC:2342
CREG1	cellular repressor of E1A-stimulated genes 1	HGNC:2351
CRISP3	cysteine-rich secretory protein 3	HGNC:16904
CRYAB	crystallin, alpha B	HGNC:2389
CRYBB2	crystallin, beta B2	HGNC:2398
CS	citrate synthase	HGNC:2422
CSAG3	CSAG family, member 3	HGNC:26237
CSF1	colony stimulating factor 1 (macrophage)	HGNC:2432
CSF1R	colony stimulating factor 1 receptor	HGNC:2433
CSN1S1	casein alpha s1	HGNC:2445
CSPG4	chondroitin sulfate proteoglycan 4	HGNC:2466
CSRP2	cysteine and glycine-rich protein 2	HGNC:2470
CST1	cystatin SN	HGNC:2473
CST6	cystatin E/M	HGNC:2478
CST7	cystatin F (leukocystatin)	HGNC:2479
CSTB	cystatin B (stefin B)	HGNC:2482
CTAG2	cancer/testis antigen 2	HGNC:2492
CTH	cystathionase (cystathionine gamma-lyase)	HGNC:2501
CTHRC1	collagen triple helix repeat containing 1	HGNC:18831
CTNND2	catenin (cadherin-associated protein), delta 2	HGNC:2516
CTSG	cathepsin G	HGNC:2532
CTSK	cathepsin K	HGNC:2536
CTSL2	cathepsin L2	HGNC:2538
CTSS	cathepsin S	HGNC:2545
CUBN	cubilin (intrinsic factor-cobalamin receptor)	HGNC:2548
CUX2	cut-like homeobox 2	HGNC:19347
CXCL10	chemokine (C-X-C motif) ligand 10	HGNC:10637
CXCL11	chemokine (C-X-C motif) ligand 11	HGNC:10638
CXCL9	chemokine (C-X-C motif) ligand 9	HGNC:7098
CXCR3	chemokine (C-X-C motif) receptor 3	HGNC:4540
CXCR7	chemokine (C-X-C motif) receptor 7	HGNC:23692
CYB5A	cytochrome b5 type A (microsomal)	HGNC:2570
CYBB	cytochrome b-245, beta polypeptide	HGNC:2578

CYBRD1	cytochrome b reductase 1	HGNC:20797
CYCS	cytochrome c, somatic	HGNC:19986
CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	HGNC:2594
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	HGNC:2595
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	HGNC:2596
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	HGNC:2597
CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	HGNC:20581
CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	HGNC:2605
CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	HGNC:2606
CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	HGNC:20580
CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	HGNC:2637
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	HGNC:2644
CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	HGNC:2645
CYP4F22	cytochrome P450, family 4, subfamily F, polypeptide 22	HGNC:26820
CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	HGNC:2646
CYP4F8	cytochrome P450, family 4, subfamily F, polypeptide 8	HGNC:2648
CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	HGNC:2649
CYTH4	cytohesin 4	HGNC:9505
DACH1	dachshund homolog 1 (Drosophila)	HGNC:2663
DAPK2	death-associated protein kinase 2	HGNC:2675
DBT	dihydrolipoamide branched chain transacylase E2	HGNC:2698
DCD	dermcidin	HGNC:14669
DCT	dopachrome tautomerase	HGNC:2709
DCXR	dicarbonyl/L-xylulose reductase	HGNC:18985
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	HGNC:2719
DDHD1	DDHD domain containing 1	HGNC:19714
DDIT4	DNA-damage-inducible transcript 4	HGNC:24944
DDO	D-aspartate oxidase	HGNC:2727
DDR2	discoidin domain receptor tyrosine kinase 2	HGNC:2731
DDX43	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43	HGNC:18677
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	HGNC:25942
DEFA6	defensin, alpha 6, Paneth cell-specific	HGNC:2765
DEFB132	defensin, beta 132	HGNC:33806
DENND3	DENN/MADD domain containing 3	HGNC:29134
DES	desmin	HGNC:2770
DGAT2	diacylglycerol O-acyltransferase 2	HGNC:16940
DGAT2L6	diacylglycerol O-acyltransferase 2-like 6	HGNC:23250
DHCR24	24-dehydrocholesterol reductase	HGNC:2859
DHCR7	7-dehydrocholesterol reductase	HGNC:2860
DHRS11	dehydrogenase/reductase (SDR family) member 11	HGNC:28639
DHRS2	dehydrogenase/reductase (SDR family) member 2	HGNC:18349
DHRS7B	dehydrogenase/reductase (SDR family) member 7B	HGNC:24547
DHRS9	dehydrogenase/reductase (SDR family) member 9	HGNC:16888

DIO2	deiodinase, iodothyronine, type II	HGNC:2884
DIRAS1	DIRAS family, GTP-binding RAS-like 1	HGNC:19127
DIRAS3	DIRAS family, GTP-binding RAS-like 3	HGNC:687
DKK1	dickkopf 1 homolog (<i>Xenopus laevis</i>)	HGNC:2891
DLD	dihydrolipoamide dehydrogenase	HGNC:2898
DLK1	delta-like 1 homolog (<i>Drosophila</i>)	HGNC:2907
DMBX1	diencephalon/mesencephalon homeobox 1	HGNC:19026
DMRTA1	DMRT-like family A1	HGNC:13826
DNAH17	dynein, axonemal, heavy chain 17	HGNC:2946
DNAH8	dynein, axonemal, heavy chain 8	HGNC:2952
DNASE1L2	deoxyribonuclease I-like 2	HGNC:2958
DOC2B	double C2-like domains, beta	HGNC:2986
DOCK11	dedicator of cytokinesis 11	HGNC:23483
DOCK2	dedicator of cytokinesis 2	HGNC:2988
DOK2	docking protein 2, 56kDa	HGNC:2991
DOPEY2	dopey family member 2	HGNC:1291
DPEP1	dipeptidase 1 (renal)	HGNC:3002
DPP4	dipeptidyl-peptidase 4	HGNC:3009
DPT	dermatopontin	HGNC:3011
DPYD	dihydropyrimidine dehydrogenase	HGNC:3012
DRAM1	DNA-damage regulated autophagy modulator 1	HGNC:25645
DSC2	desmocollin 2	HGNC:3036
DSE	dermatan sulfate epimerase	HGNC:21144
DSG4	desmoglein 4	HGNC:21307
DTNA	dystrobrevin, alpha	HGNC:3057
DTX4	deltex homolog 4 (<i>Drosophila</i>)	HGNC:29151
DUSP1	dual specificity phosphatase 1	HGNC:3064
DUSP16	dual specificity phosphatase 16	HGNC:17909
DUSP4	dual specificity phosphatase 4	HGNC:3070
DUSP5	dual specificity phosphatase 5	HGNC:3071
DUSP6	dual specificity phosphatase 6	HGNC:3072
EBF1	early B-cell factor 1	HGNC:3126
EBI3	Epstein-Barr virus induced 3	HGNC:3129
EBP	emopamil binding protein (sterol isomerase)	HGNC:3133
ECH1	enoyl CoA hydratase 1, peroxisomal	HGNC:3149
ECHDC1	enoyl CoA hydratase domain containing 1	HGNC:21489
ECHDC2	enoyl CoA hydratase domain containing 2	HGNC:23408
ECM1	extracellular matrix protein 1	HGNC:3153
ECM2	extracellular matrix protein 2, female organ and adipocyte specific	HGNC:3154
EDA2R	ectodysplasin A2 receptor	HGNC:17756
EDDM3B	epididymal protein 3B	HGNC:19223
EFCAB4A	EF-hand calcium binding domain 4A	HGNC:28703
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	HGNC:3218

EFNB2	ephrin-B2	HGNC:3227
EGFL6	EGF-like-domain, multiple 6	HGNC:3235
EGLN3	egl nine homolog 3 (C. elegans)	HGNC:14661
EGR1	early growth response 1	HGNC:3238
EGR2	early growth response 2	HGNC:3239
EGR3	early growth response 3	HGNC:3240
EHD2	EH-domain containing 2	HGNC:3243
EHF	ets homologous factor	HGNC:3246
EI24	etoposide induced 2.4 mRNA	HGNC:13276
ELANE	elastase, neutrophil expressed	HGNC:3309
ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2	HGNC:3313
ELL2	elongation factor, RNA polymerase II, 2	HGNC:17064
ELOVL1	ELOVL fatty acid elongase 1	HGNC:14418
ELOVL3	ELOVL fatty acid elongase 3	HGNC:18047
ELOVL4	ELOVL fatty acid elongase 4	HGNC:14415
ELOVL5	ELOVL fatty acid elongase 5	HGNC:21308
EMID2	EMI domain containing 2	HGNC:18038
EMILIN1	elastin microfibril interfacer 1	HGNC:19880
EMILIN2	elastin microfibril interfacer 2	HGNC:19881
EMILIN3	elastin microfibril interfacer 3	HGNC:16123
EML6	echinoderm microtubule associated protein like 6	HGNC:35412
EN2	engrailed homeobox 2	HGNC:3343
ENC1	ectodermal-neural cortex 1 (with BTB-like domain)	HGNC:3345
ENDOU	endonuclease, polyU-specific	HGNC:14369
ENG	endoglin	HGNC:3349
ENO2	enolase 2 (gamma, neuronal)	HGNC:3353
EOMES	eomesodermin	HGNC:3372
EPB41L2	erythrocyte membrane protein band 4.1-like 2	HGNC:3379
EPPK1	epiplakin 1	HGNC:15577
ERAP1	endoplasmic reticulum aminopeptidase 1	HGNC:18173
ESRRA	estrogen-related receptor alpha	HGNC:3471
ETFDH	electron-transferring-flavoprotein dehydrogenase	HGNC:3483
ETHE1	ethylmalonic encephalopathy 1	HGNC:23287
ETV4	ets variant 4	HGNC:3493
EVI2B	ecotropic viral integration site 2B	HGNC:3500
EYA4	eyes absent homolog 4 (Drosophila)	HGNC:3522
F10	coagulation factor X	HGNC:3528
F13A1	coagulation factor XIII, A1 polypeptide	HGNC:3531
F3	coagulation factor III (thromboplastin, tissue factor)	HGNC:3541
F9	coagulation factor IX	HGNC:3551
FA2H	fatty acid 2-hydroxylase	HGNC:21197
FABP12	fatty acid binding protein 12	HGNC:34524
FABP4	fatty acid binding protein 4, adipocyte	HGNC:3559

FABP6	fatty acid binding protein 6, ileal	HGNC:3561
FABP7	fatty acid binding protein 7, brain	HGNC:3562
FABP9	fatty acid binding protein 9, testis	HGNC:3563
FADS1	fatty acid desaturase 1	HGNC:3574
FADS2	fatty acid desaturase 2	HGNC:3575
FADS6	fatty acid desaturase domain family, member 6	HGNC:30459
FAM108C1	family with sequence similarity 108, member C1	HGNC:26925
FAM126A	family with sequence similarity 126, member A	HGNC:24587
FAM129A	family with sequence similarity 129, member A	HGNC:16784
FAM132A	family with sequence similarity 132, member A	HGNC:32308
FAM150B	family with sequence similarity 150, member B	HGNC:27683
FAM176A	family with sequence similarity 176, member A	HGNC:25816
FAM181A	family with sequence similarity 181, member A	HGNC:20491
FAM196B	family with sequence similarity 196, member B	HGNC:37271
FAM19A2	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	HGNC:21589
FAM26D	family with sequence similarity 26, member D	HGNC:21094
FAM26E	family with sequence similarity 26, member E	HGNC:21568
FAM3C	family with sequence similarity 3, member C	HGNC:18664
FAM3D	family with sequence similarity 3, member D	HGNC:18665
FAM46C	family with sequence similarity 46, member C	HGNC:24712
FAM69C	family with sequence similarity 69, member C	HGNC:31729
FAM70A	family with sequence similarity 70, member A	HGNC:26086
FAM73B	family with sequence similarity 73, member B	HGNC:23621
FAM75D1	family with sequence similarity 75, member D1	HGNC:37283
FAM78A	family with sequence similarity 78, member A	HGNC:25465
FAM82A2	family with sequence similarity 82, member A2	HGNC:25550
FAM83A	family with sequence similarity 83, member A	HGNC:28210
FAM84A	family with sequence similarity 84, member A	HGNC:20743
FAM84B	family with sequence similarity 84, member B	HGNC:24166
FAR2	fatty acyl CoA reductase 2	HGNC:25531
FASN	fatty acid synthase	HGNC:3594
FASTKD1	FAST kinase domains 1	HGNC:26150
FBLN2	fibulin 2	HGNC:3601
FBLN5	fibulin 5	HGNC:3602
FBN1	fibrillin 1	HGNC:3603
FBP1	fructose-1,6-bisphosphatase 1	HGNC:3606
FBP2	fructose-1,6-bisphosphatase 2	HGNC:3607
FBXO9	F-box protein 9	HGNC:13588
FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	HGNC:3612
FCGBP	Fc fragment of IgG binding protein	HGNC:13572
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	HGNC:3616
FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	HGNC:3618
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	HGNC:3619

FCGRT	Fc fragment of IgG, receptor, transporter, alpha	HGNC:3621
FCN1	ficolin (collagen/fibrinogen domain containing) 1	HGNC:3623
FDFT1	farnesyl-diphosphate farnesyltransferase 1	HGNC:3629
FDPS	farnesyl diphosphate synthase	HGNC:3631
FEN1	flap structure-specific endonuclease 1	HGNC:3650
FERMT2	fermitin family member 2	HGNC:15767
FERMT3	fermitin family member 3	HGNC:23151
FETUB	fetuin B	HGNC:3658
FGF16	fibroblast growth factor 16	HGNC:3672
FGF18	fibroblast growth factor 18	HGNC:3674
FGF9	fibroblast growth factor 9 (glia-activating factor)	HGNC:3687
FGFR1	fibroblast growth factor receptor 1	HGNC:3688
FGFR2	fibroblast growth factor receptor 2	HGNC:3689
FHL1	four and a half LIM domains 1	HGNC:3702
FIBIN	fin bud initiation factor homolog (zebrafish)	HGNC:33747
FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	HGNC:3708
FILIP1	filamin A interacting protein 1	HGNC:21015
FITM2	fat storage-inducing transmembrane protein 2	HGNC:16135
FLNA	filamin A, alpha	HGNC:3754
FLNC	filamin C, gamma	HGNC:3756
FLRT2	fibronectin leucine rich transmembrane protein 2	HGNC:3761
FLT4	fms-related tyrosine kinase 4	HGNC:3767
FMNL1	formin-like 1	HGNC:1212
FMO2	flavin containing monooxygenase 2 (non-functional)	HGNC:3770
FMO3	flavin containing monooxygenase 3	HGNC:3771
FMOD	fibromodulin	HGNC:3774
FOS	FBJ murine osteosarcoma viral oncogene homolog	HGNC:3796
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	HGNC:3797
FOSL1	FOS-like antigen 1	HGNC:13718
FOXC1	forkhead box C1	HGNC:3800
FOXQ1	forkhead box Q1	HGNC:20951
FPR2	formyl peptide receptor 2	HGNC:3827
FPR3	formyl peptide receptor 3	HGNC:3828
FREM1	FRAS1 related extracellular matrix 1	HGNC:23399
FRZB	frizzled-related protein	HGNC:3959
FSTL3	folliculin-like 3 (secreted glycoprotein)	HGNC:3973
FTL	ferritin, light polypeptide	HGNC:3999
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	HGNC:4014
FXYD5	FXYD domain containing ion transport regulator 5	HGNC:4029
FYN	FYN oncogene related to SRC, FGR, YES	HGNC:4037
FZD4	frizzled family receptor 4	HGNC:4042
FZD5	frizzled family receptor 5	HGNC:4043
FZD7	frizzled family receptor 7	HGNC:4045

G0S2	G0/G1 switch 2	HGNC:30229
G6PD	glucose-6-phosphate dehydrogenase	HGNC:4057
GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	HGNC:4507
GABRA4	gamma-aminobutyric acid (GABA) A receptor, alpha 4	HGNC:4078
GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	HGNC:4089
GADD45G	growth arrest and DNA-damage-inducible, gamma	HGNC:4097
GAGE12D	G antigen 12D	HGNC:31904
GAGE12G	G antigen 12G	HGNC:31907
GAGE12I	G antigen 12I	HGNC:4105
GAGE2B	G antigen 2B	HGNC:31957
GAGE2C	G antigen 2C	HGNC:31958
GAGE2D	G antigen 2D	HGNC:31959
GAL	galanin prepropeptide	HGNC:4114
GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase-like 1	HGNC:23233
GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase-like 2	HGNC:21531
GALNTL5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase-like 5	HGNC:21725
GALNTL6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase-like 6	HGNC:33844
GAP43	growth associated protein 43	HGNC:4140
GAS1	growth arrest-specific 1	HGNC:4165
GATA2	GATA binding protein 2	HGNC:4171
GATA6	GATA binding protein 6	HGNC:4174
GBP3	guanylate binding protein 3	HGNC:4184
GBP4	guanylate binding protein 4	HGNC:20480
GBP6	guanylate binding protein family, member 6	HGNC:25395
GCLM	glutamate-cysteine ligase, modifier subunit	HGNC:4312
GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2	HGNC:17973
GCSH	glycine cleavage system protein H (aminomethyl carrier)	HGNC:4208
GDA	guanine deaminase	HGNC:4212
GDF10	growth differentiation factor 10	HGNC:4215
GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	HGNC:25974
GFM2	G elongation factor, mitochondrial 2	HGNC:29682
GFRA1	GNDF family receptor alpha 1	HGNC:4243
GGPS1	geranylgeranyl diphosphate synthase 1	HGNC:4249
GGT6	gamma-glutamyltransferase 6	HGNC:26891
GIMAP4	GTPase, IMAP family member 4	HGNC:21872
GJA3	gap junction protein, alpha 3, 46kDa	HGNC:4277
GJB2	gap junction protein, beta 2, 26kDa	HGNC:4284
GJB6	gap junction protein, beta 6, 30kDa	HGNC:4288
GJC2	gap junction protein, gamma 2, 47kDa	HGNC:17494
GK	glycerol kinase	HGNC:4289
GK5	glycerol kinase 5 (putative)	HGNC:28635

GLDC	glycine dehydrogenase (decarboxylating)	HGNC:4313
GLIPR1	GLI pathogenesis-related 1	HGNC:17001
GLRX	glutaredoxin (thioltransferase)	HGNC:4330
GLRX5	glutaredoxin 5	HGNC:20134
GLYAT	glycine-N-acyltransferase	HGNC:13734
GLYATL1	glycine-N-acyltransferase-like 1	HGNC:30519
GLYATL1P4	glycine-N-acyltransferase-like 1 pseudogene 4	HGNC:37864
GNLY	granulysin	HGNC:4414
GNPAT	glyceronephosphate O-acyltransferase	HGNC:4416
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	HGNC:4432
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	HGNC:24865
GPBAR1	G protein-coupled bile acid receptor 1	HGNC:19680
GPC3	glypican 3	HGNC:4451
GPER	G protein-coupled estrogen receptor 1	HGNC:4485
GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	HGNC:24945
GPR124	G protein-coupled receptor 124	HGNC:17849
GPR133	G protein-coupled receptor 133	HGNC:19893
GPR143	G protein-coupled receptor 143	HGNC:20145
GPR15	G protein-coupled receptor 15	HGNC:4469
GPR174	G protein-coupled receptor 174	HGNC:30245
GPR18	G protein-coupled receptor 18	HGNC:4472
GPR182	G protein-coupled receptor 182	HGNC:13708
GPR64	G protein-coupled receptor 64	HGNC:4516
GPR98	G protein-coupled receptor 98	HGNC:17416
GPRC5D	G protein-coupled receptor, family C, group 5, member D	HGNC:13310
GPRIN2	G protein regulated inducer of neurite outgrowth 2	HGNC:23730
GPSM3	G-protein signaling modulator 3	HGNC:13945
GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	HGNC:4552
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	HGNC:18062
GRAP2	GRB2-related adaptor protein 2	HGNC:4563
GREB1	growth regulation by estrogen in breast cancer 1	HGNC:24885
GREM1	gremlin 1	HGNC:2001
GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	HGNC:4585
GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	HGNC:16767
GRK5	G protein-coupled receptor kinase 5	HGNC:4544
GRM3	glutamate receptor, metabotropic 3	HGNC:4595
GRM7	glutamate receptor, metabotropic 7	HGNC:4599
GRP	gastrin-releasing peptide	HGNC:4605
GSDMA	gasdermin A	HGNC:13311
GTSF1	gametocyte specific factor 1	HGNC:26565
GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	HGNC:4688
GYG2	glycogenin 2	HGNC:4700

GYPC	glycophorin C (Gerbich blood group)	HGNC:4704
GYS2	glycogen synthase 2 (liver)	HGNC:4707
GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	HGNC:4708
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	HGNC:4709
GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	HGNC:4710
GZMK	granzyme K (granzyme 3; tryptase II)	HGNC:4711
GZMM	granzyme M (lymphocyte met-ase 1)	HGNC:4712
HACL1	2-hydroxyacyl-CoA lyase 1	HGNC:17856
HADH	hydroxyacyl-CoA dehydrogenase	HGNC:4799
HAO2	hydroxyacid oxidase 2 (long chain)	HGNC:4810
HAPLN1	hyaluronan and proteoglycan link protein 1	HGNC:2380
HBA1	hemoglobin, alpha 1	HGNC:4823
HBA2	hemoglobin, alpha 2	HGNC:4824
HBB	hemoglobin, beta	HGNC:4827
HBD	hemoglobin, delta	HGNC:4829
HBEGF	heparin-binding EGF-like growth factor	HGNC:3059
HBG2	hemoglobin, gamma G	HGNC:4832
HCLS1	hematopoietic cell-specific Lyn substrate 1	HGNC:4844
HEATR4	HEAT repeat containing 4	HGNC:16761
HEPACAM	hepatic and glial cell adhesion molecule	HGNC:26361
HEPACAM2	HEPACAM family member 2	HGNC:27364
HEPHL1	hephaestin-like 1	HGNC:30477
HEPN1	hepatocellular carcinoma, down-regulated 1	HGNC:34400
HGD	homogentisate 1,2-dioxygenase	HGNC:4892
HHATL	hedgehog acyltransferase-like	HGNC:13242
HIBCH	3-hydroxyisobutyryl-CoA hydrolase	HGNC:4908
HIC1	hypermethylated in cancer 1	HGNC:4909
HINT1	histidine triad nucleotide binding protein 1	HGNC:4912
HIP1	huntingtin interacting protein 1	HGNC:4913
HIST1H1C	histone cluster 1, H1c	HGNC:4716
HIST1H1D	histone cluster 1, H1d	HGNC:4717
HIST1H2AE	histone cluster 1, H2ae	HGNC:4724
HIST1H2BC	histone cluster 1, H2bc	HGNC:4757
HIST1H2BK	histone cluster 1, H2bk	HGNC:13954
HIST3H2A	histone cluster 3, H2a	HGNC:20507
HK2	hexokinase 2	HGNC:4923
HLA-A	major histocompatibility complex, class I, A	HGNC:4931
HLA-B	major histocompatibility complex, class I, B	HGNC:4932
HLA-C	major histocompatibility complex, class I, C	HGNC:4933
HLA-DMB	major histocompatibility complex, class II, DM beta	HGNC:4935
HLA-DOA	major histocompatibility complex, class II, DO alpha	HGNC:4936
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	HGNC:4938
HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	HGNC:4942

HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	HGNC:4943
HLA-DRA	major histocompatibility complex, class II, DR alpha	HGNC:4947
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	HGNC:4948
HLA-DRB5	major histocompatibility complex, class II, DR beta 5	HGNC:4953
HLA-E	major histocompatibility complex, class I, E	HGNC:4962
HLA-F	major histocompatibility complex, class I, F	HGNC:4963
HLCS	holocarboxylase synthetase (biotin-(propionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	HGNC:4976
HMCN2	hemicentin 2	HGNC:21293
HMGB3	high mobility group box 3	HGNC:5004
HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase	HGNC:5005
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	HGNC:5006
HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	HGNC:5007
HOMER1	homer homolog 1 (Drosophila)	HGNC:17512
HPGDS	hematopoietic prostaglandin D synthase	HGNC:17890
HPSE2	heparanase 2	HGNC:18374
HRASLS5	HRAS-like suppressor family, member 5	HGNC:24978
HRSP12	heat-responsive protein 12	HGNC:16897
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	HGNC:5208
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	HGNC:5209
HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	HGNC:22960
HSD17B13	hydroxysteroid (17-beta) dehydrogenase 13	HGNC:18685
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	HGNC:5211
HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	HGNC:5217
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	HGNC:5218
HSPA12A	heat shock 70kDa protein 12A	HGNC:19022
HSPB6	heat shock protein, alpha-crystallin-related, B6	HGNC:26511
HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	HGNC:5249
HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	HGNC:5269
HSPG2	heparan sulfate proteoglycan 2	HGNC:5273
HTRA3	HtrA serine peptidase 3	HGNC:30406
HYAL1	hyaluronoglucosaminidase 1	HGNC:5320
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	HGNC:5361
ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	HGNC:5362
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	HGNC:5382
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	HGNC:5383
IDI1	isopentenyl-diphosphate delta isomerase 1	HGNC:5387
IER3	immediate early response 3	HGNC:5392
IFI27	interferon, alpha-inducible protein 27	HGNC:5397
IFI44L	interferon-induced protein 44-like	HGNC:17817
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	HGNC:5409
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	HGNC:5411
IFITM1	interferon induced transmembrane protein 1	HGNC:5412

IFITM3	interferon induced transmembrane protein 3	HGNC:5414
IFNG	interferon, gamma	HGNC:5438
IFRD1	interferon-related developmental regulator 1	HGNC:5456
IGF1	insulin-like growth factor 1 (somatomedin C)	HGNC:5464
IGF2	insulin-like growth factor 2 (somatomedin A)	HGNC:5466
IGFBP3	insulin-like growth factor binding protein 3	HGNC:5472
IGFL2	IGF-like family member 2	HGNC:32929
IGFL4	IGF-like family member 4	HGNC:32931
IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	HGNC:5713
IGLL5	immunoglobulin lambda-like polypeptide 5	HGNC:38476
IGLON5	IgLON family member 5	HGNC:34550
IGSF10	immunoglobulin superfamily, member 10	HGNC:26384
IGSF6	immunoglobulin superfamily, member 6	HGNC:5953
IKZF1	IKAROS family zinc finger 1 (Ikaros)	HGNC:13176
IKZF3	IKAROS family zinc finger 3 (Aiolos)	HGNC:13178
IL10RA	interleukin 10 receptor, alpha	HGNC:5964
IL15RA	interleukin 15 receptor, alpha	HGNC:5978
IL17D	interleukin 17D	HGNC:5984
IL1B	interleukin 1, beta	HGNC:5992
IL2RG	interleukin 2 receptor, gamma	HGNC:6010
IL32	interleukin 32	HGNC:16830
IL33	interleukin 33	HGNC:16028
IL7R	interleukin 7 receptor	HGNC:6024
IL8	interleukin 8	HGNC:6025
ILDR1	immunoglobulin-like domain containing receptor 1	HGNC:28741
INHBB	inhibin, beta B	HGNC:6067
INMT	indolethylamine N-methyltransferase	HGNC:6069
INPPL1	inositol polyphosphate phosphatase-like 1	HGNC:6080
INSIG1	insulin induced gene 1	HGNC:6083
INSM1	insulinoma-associated 1	HGNC:6090
IQCJ	IQ motif containing J	HGNC:32406
IQSEC3	IQ motif and Sec7 domain 3	HGNC:29193
IRF1	interferon regulatory factor 1	HGNC:6116
IRF8	interferon regulatory factor 8	HGNC:5358
IRGM	immunity-related GTPase family, M	HGNC:29597
IRX6	iroquois homeobox 6	HGNC:14675
ISLR	immunoglobulin superfamily containing leucine-rich repeat	HGNC:6133
ISM1	isthmin 1 homolog (zebrafish)	HGNC:16213
ISOC1	isochorismatase domain containing 1	HGNC:24254
ITGA1	integrin, alpha 1	HGNC:6134
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	HGNC:6137
ITGA7	integrin, alpha 7	HGNC:6143

ITGA8	integrin, alpha 8	HGNC:6144
ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	HGNC:6148
ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	HGNC:6149
ITGB1BP1	integrin beta 1 binding protein 1	HGNC:23927
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	HGNC:6155
ITIH5	inter-alpha-trypsin inhibitor heavy chain family, member 5	HGNC:21449
ITK	IL2-inducible T-cell kinase	HGNC:6171
ITSN1	intersectin 1 (SH3 domain protein)	HGNC:6183
IVD	isovaleryl-CoA dehydrogenase	HGNC:6186
IYD	iodotyrosine deiodinase	HGNC:21071
JAM3	junctional adhesion molecule 3	HGNC:15532
JPH2	junctophilin 2	HGNC:14202
KANK2	KN motif and ankyrin repeat domains 2	HGNC:29300
KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	HGNC:6221
KCNA6	potassium voltage-gated channel, shaker-related subfamily, member 6	HGNC:6225
KCNB1	potassium voltage-gated channel, Shab-related subfamily, member 1	HGNC:6231
KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member 5	HGNC:6254
KCNIP2	Kv channel interacting protein 2	HGNC:15522
KCNIP3	Kv channel interacting protein 3, calsenilin	HGNC:15523
KCNJ13	potassium inwardly-rectifying channel, subfamily J, member 13	HGNC:6259
KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	HGNC:6261
KCNK2	potassium channel, subfamily K, member 2	HGNC:6277
KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	HGNC:6284
KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	HGNC:6285
KDEL2	KDEL (Lys-Asp-Glu-Leu) containing 2	HGNC:28496
KIAA0513	KIAA0513	HGNC:29058
KIAA0754	KIAA0754	HGNC:29111
KIAA1191	KIAA1191	HGNC:29209
KIF1A	kinesin family member 1A	HGNC:888
KIF3C	kinesin family member 3C	HGNC:6321
KIRREL	kin of IRRE like (Drosophila)	HGNC:15734
KLHDC8B	kelch domain containing 8B	HGNC:28557
KLHL31	kelch-like 31 (Drosophila)	HGNC:21353
KLK10	kallikrein-related peptidase 10	HGNC:6358
KLK12	kallikrein-related peptidase 12	HGNC:6360
KLK13	kallikrein-related peptidase 13	HGNC:6361
KLK6	kallikrein-related peptidase 6	HGNC:6367
KLRF1	killer cell lectin-like receptor subfamily F, member 1	HGNC:13342
KPRP	keratinocyte proline-rich protein	HGNC:31823
KREMEN2	kringle containing transmembrane protein 2	HGNC:18797
KRT16	keratin 16	HGNC:6423

KRT17	keratin 17	HGNC:6427
KRT20	keratin 20	HGNC:20412
KRT25	keratin 25	HGNC:30839
KRT26	keratin 26	HGNC:30840
KRT27	keratin 27	HGNC:30841
KRT28	keratin 28	HGNC:30842
KRT31	keratin 31	HGNC:6448
KRT32	keratin 32	HGNC:6449
KRT33A	keratin 33A	HGNC:6450
KRT33B	keratin 33B	HGNC:6451
KRT34	keratin 34	HGNC:6452
KRT35	keratin 35	HGNC:6453
KRT36	keratin 36	HGNC:6454
KRT38	keratin 38	HGNC:6456
KRT39	keratin 39	HGNC:32971
KRT4	keratin 4	HGNC:6441
KRT40	keratin 40	HGNC:26707
KRT6A	keratin 6A	HGNC:6443
KRT6B	keratin 6B	HGNC:6444
KRT6C	keratin 6C	HGNC:20406
KRT71	keratin 71	HGNC:28927
KRT72	keratin 72	HGNC:28932
KRT73	keratin 73	HGNC:28928
KRT74	keratin 74	HGNC:28929
KRT75	keratin 75	HGNC:24431
KRT79	keratin 79	HGNC:28930
KRT81	keratin 81	HGNC:6458
KRT82	keratin 82	HGNC:6459
KRT83	keratin 83	HGNC:6460
KRT84	keratin 84	HGNC:6461
KRT85	keratin 85	HGNC:6462
KRT86	keratin 86	HGNC:6463
KRT9	keratin 9	HGNC:6447
KRTAP1-1	keratin associated protein 1-1	HGNC:16772
KRTAP1-3	keratin associated protein 1-3	HGNC:16771
KRTAP1-5	keratin associated protein 1-5	HGNC:16777
KRTAP10-1	keratin associated protein 10-1	HGNC:22966
KRTAP10-10	keratin associated protein 10-10	HGNC:22972
KRTAP10-11	keratin associated protein 10-11	HGNC:20528
KRTAP10-12	keratin associated protein 10-12	HGNC:20533
KRTAP10-2	keratin associated protein 10-2	HGNC:22967
KRTAP10-3	keratin associated protein 10-3	HGNC:22968
KRTAP10-4	keratin associated protein 10-4	HGNC:20521

KRTAP10-5	keratin associated protein 10-5	HGNC:22969
KRTAP10-6	keratin associated protein 10-6	HGNC:20523
KRTAP10-7	keratin associated protein 10-7	HGNC:22970
KRTAP10-8	keratin associated protein 10-8	HGNC:20525
KRTAP10-9	keratin associated protein 10-9	HGNC:22971
KRTAP11-1	keratin associated protein 11-1	HGNC:18922
KRTAP12-1	keratin associated protein 12-1	HGNC:20529
KRTAP12-2	keratin associated protein 12-2	HGNC:20530
KRTAP12-3	keratin associated protein 12-3	HGNC:20531
KRTAP13-1	keratin associated protein 13-1	HGNC:18924
KRTAP13-2	keratin associated protein 13-2	HGNC:18923
KRTAP17-1	keratin associated protein 17-1	HGNC:18917
KRTAP19-1	keratin associated protein 19-1	HGNC:18936
KRTAP19-3	keratin associated protein 19-3	HGNC:18938
KRTAP19-5	keratin associated protein 19-5	HGNC:18940
KRTAP19-7	keratin associated protein 19-7	HGNC:18942
KRTAP2-1	keratin associated protein 2-1	HGNC:16775
KRTAP2-2	keratin associated protein 2-2	HGNC:18905
KRTAP2-4	keratin associated protein 2-4	HGNC:18891
KRTAP20-1	keratin associated protein 20-1	HGNC:18943
KRTAP20-2	keratin associated protein 20-2	HGNC:18944
KRTAP21-2	keratin associated protein 21-2	HGNC:18946
KRTAP24-1	keratin associated protein 24-1	HGNC:33902
KRTAP26-1	keratin associated protein 26-1	HGNC:33760
KRTAP3-1	keratin associated protein 3-1	HGNC:16778
KRTAP3-2	keratin associated protein 3-2	HGNC:16779
KRTAP3-3	keratin associated protein 3-3	HGNC:18890
KRTAP4-1	keratin associated protein 4-1	HGNC:18907
KRTAP4-11	keratin associated protein 4-11	HGNC:18911
KRTAP4-12	keratin associated protein 4-12	HGNC:16776
KRTAP4-2	keratin associated protein 4-2	HGNC:18900
KRTAP4-3	keratin associated protein 4-3	HGNC:18908
KRTAP4-4	keratin associated protein 4-4	HGNC:16928
KRTAP4-5	keratin associated protein 4-5	HGNC:18899
KRTAP4-6	keratin associated protein 4-6	HGNC:18909
KRTAP4-7	keratin associated protein 4-7	HGNC:18898
KRTAP4-8	keratin associated protein 4-8	HGNC:17230
KRTAP4-9	keratin associated protein 4-9	HGNC:18910
KRTAP5-1	keratin associated protein 5-1	HGNC:23596
KRTAP5-10	keratin associated protein 5-10	HGNC:23605
KRTAP5-11	keratin associated protein 5-11	HGNC:23606
KRTAP5-2	keratin associated protein 5-2	HGNC:23597
KRTAP5-3	keratin associated protein 5-3	HGNC:23598

KRTAP5-4	keratin associated protein 5-4	HGNC:23599
KRTAP5-5	keratin associated protein 5-5	HGNC:23601
KRTAP5-6	keratin associated protein 5-6	HGNC:23600
KRTAP5-7	keratin associated protein 5-7	HGNC:23602
KRTAP5-8	keratin associated protein 5-8	HGNC:23603
KRTAP5-9	keratin associated protein 5-9	HGNC:23604
KRTAP7-1	keratin associated protein 7-1 (gene/pseudogene)	HGNC:18934
KRTAP8-1	keratin associated protein 8-1	HGNC:18935
KRTAP9-2	keratin associated protein 9-2	HGNC:16926
KRTAP9-3	keratin associated protein 9-3	HGNC:16927
KRTAP9-4	keratin associated protein 9-4	HGNC:18902
KRTAP9-8	keratin associated protein 9-8	HGNC:17231
KRTAP9-9	keratin associated protein 9-9	HGNC:16773
LAIR1	leukocyte-associated immunoglobulin-like receptor 1	HGNC:6477
LAMA2	laminin, alpha 2	HGNC:6482
LAMA4	laminin, alpha 4	HGNC:6484
LAMB4	laminin, beta 4	HGNC:6491
LAMC1	laminin, gamma 1 (formerly LAMB2)	HGNC:6492
LAPTM5	lysosomal protein transmembrane 5	HGNC:29612
LAT	linker for activation of T cells	HGNC:18874
LAX1	lymphocyte transmembrane adaptor 1	HGNC:26005
LBP	lipopolysaccharide binding protein	HGNC:6517
LCE1A	late cornified envelope 1A	HGNC:29459
LCE2A	late cornified envelope 2A	HGNC:29469
LCE2B	late cornified envelope 2B	HGNC:16610
LCE2C	late cornified envelope 2C	HGNC:29460
LCE5A	late cornified envelope 5A	HGNC:16614
LCK	lymphocyte-specific protein tyrosine kinase	HGNC:6524
LCN2	lipocalin 2	HGNC:6526
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	HGNC:6528
LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	HGNC:6529
LCT	lactase	HGNC:6530
LDHB	lactate dehydrogenase B	HGNC:6541
LDHD	lactate dehydrogenase D	HGNC:19708
LDLR	low density lipoprotein receptor	HGNC:6547
LEP	leptin	HGNC:6553
LEPR	leptin receptor	HGNC:6554
LETM1	leucine zipper-EF-hand containing transmembrane protein 1	HGNC:6556
LGALS9	lectin, galactoside-binding, soluble, 9	HGNC:6570
LGI3	leucine-rich repeat LGI family, member 3	HGNC:18711
LGR5	leucine-rich repeat containing G protein-coupled receptor 5	HGNC:4504
LHFP	lipoma HMGIC fusion partner	HGNC:6586

LHFPL4	lipoma HMGIC fusion partner-like 4	HGNC:29568
LHX2	LIM homeobox 2	HGNC:6594
LHX3	LIM homeobox 3	HGNC:6595
LILRB5	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	HGNC:6609
LIMCH1	LIM and calponin homology domains 1	HGNC:29191
LIPE	lipase, hormone-sensitive	HGNC:6621
LIPG	lipase, endothelial	HGNC:6623
LIPH	lipase, member H	HGNC:18483
LIPK	lipase, family member K	HGNC:23444
LMO3	LIM domain only 3 (rhombotin-like 2)	HGNC:6643
LMOD1	leiomodin 1 (smooth muscle)	HGNC:6647
LOX	lysyl oxidase	HGNC:6664
LPCAT3	lysophosphatidylcholine acyltransferase 3	HGNC:30244
LPHN3	latrophilin 3	HGNC:20974
LPIN1	lipin 1	HGNC:13345
LPL	lipoprotein lipase	HGNC:6677
LPO	lactoperoxidase	HGNC:6678
LRG1	leucine-rich alpha-2-glycoprotein 1	HGNC:29480
LRIT2	leucine-rich repeat, immunoglobulin-like and transmembrane domains 2	HGNC:23443
LRP1	low density lipoprotein receptor-related protein 1	HGNC:6692
LRRC10B	leucine rich repeat containing 10B	HGNC:37215
LRRC31	leucine rich repeat containing 31	HGNC:26261
LRRC32	leucine rich repeat containing 32	HGNC:4161
LRRN4CL	LRRN4 C-terminal like	HGNC:33724
LTB	lymphotoxin beta (TNF superfamily, member 3)	HGNC:6711
LTBP2	latent transforming growth factor beta binding protein 2	HGNC:6715
LTBP3	latent transforming growth factor beta binding protein 3	HGNC:6716
LTF	lactotransferrin	HGNC:6720
LUM	lumican	HGNC:6724
LY6E	lymphocyte antigen 6 complex, locus E	HGNC:6727
LY6G6D	lymphocyte antigen 6 complex, locus G6D	HGNC:13935
LY9	lymphocyte antigen 9	HGNC:6730
LYG2	lysozyme G-like 2	HGNC:29615
LYRM5	LYR motif containing 5	HGNC:27052
LYZ	lysozyme	HGNC:6740
LZTS1	leucine zipper, putative tumor suppressor 1	HGNC:13861
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	HGNC:6776
MAGEA11	melanoma antigen family A, 11	HGNC:6798
MAGEB2	melanoma antigen family B, 2	HGNC:6809
MAN1A1	mannosidase, alpha, class 1A, member 1	HGNC:6821
MAN2B2	mannosidase, alpha, class 2B, member 2	HGNC:29623
MANEAL	mannosidase, endo-alpha-like	HGNC:26452

MAOB	monoamine oxidase B	HGNC:6834
MAP1B	microtubule-associated protein 1B	HGNC:6836
MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	HGNC:6883
MARCKSL1	MARCKS-like 1	HGNC:7142
MARCO	macrophage receptor with collagenous structure	HGNC:6895
MAT1A	methionine adenosyltransferase I, alpha	HGNC:6903
MBOAT2	membrane bound O-acyltransferase domain containing 2	HGNC:25193
MC5R	melanocortin 5 receptor	HGNC:6933
MCAM	melanoma cell adhesion molecule	HGNC:6934
MCCC1	methylcrotonoyl-CoA carboxylase 1 (alpha)	HGNC:6936
MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	HGNC:6937
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	HGNC:6983
MECR	mitochondrial trans-2-enoyl-CoA reductase	HGNC:19691
MEF2A	myocyte enhancer factor 2A	HGNC:6993
MEGF11	multiple EGF-like-domains 11	HGNC:29635
MERTK	c-mer proto-oncogene tyrosine kinase	HGNC:7027
METTL7B	methyltransferase like 7B	HGNC:28276
MFAP3L	microfibrillar-associated protein 3-like	HGNC:29083
MFAP4	microfibrillar-associated protein 4	HGNC:7035
MFAP5	microfibrillar associated protein 5	HGNC:29673
MFGE8	milk fat globule-EGF factor 8 protein	HGNC:7036
MGLL	monoglyceride lipase	HGNC:17038
MGP	matrix Gla protein	HGNC:7060
MGST1	microsomal glutathione S-transferase 1	HGNC:7061
MKX	mohawk homeobox	HGNC:23729
MLANA	melan-A	HGNC:7124
MMD	monocyte to macrophage differentiation-associated	HGNC:7153
MME	membrane metallo-endopeptidase	HGNC:7154
MMP28	matrix metallopeptidase 28	HGNC:14366
MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	HGNC:7174
MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	HGNC:7176
MMRN1	multimerin 1	HGNC:7178
MNDA	myeloid cell nuclear differentiation antigen	HGNC:7183
MOCOS	molybdenum cofactor sulfurase	HGNC:18234
MOGAT1	monoacylglycerol O-acyltransferase 1	HGNC:18210
MOGAT2	monoacylglycerol O-acyltransferase 2	HGNC:23248
MORN2	MORN repeat containing 2	HGNC:30166
MPEG1	macrophage expressed 1	HGNC:29619
MRC1	mannose receptor, C type 1	HGNC:7228
MRPL13	mitochondrial ribosomal protein L13	HGNC:14278
MRPL14	mitochondrial ribosomal protein L14	HGNC:14279
MRPS25	mitochondrial ribosomal protein S25	HGNC:14511

MRV11	murine retrovirus integration site 1 homolog	HGNC:7237
MS4A1	membrane-spanning 4-domains, subfamily A, member 1	HGNC:7315
MS4A18	membrane-spanning 4-domains, subfamily A, member 18	HGNC:37636
MS4A4A	membrane-spanning 4-domains, subfamily A, member 4A	HGNC:13371
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	HGNC:13375
MS4A7	membrane-spanning 4-domains, subfamily A, member 7	HGNC:13378
MSMB	microseminoprotein, beta-	HGNC:7372
MSR1	macrophage scavenger receptor 1	HGNC:7376
MTCH2	mitochondrial carrier 2	HGNC:17587
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	HGNC:3942
MUC1	mucin 1, cell surface associated	HGNC:7508
MUC15	mucin 15, cell surface associated	HGNC:14956
MUC21	mucin 21, cell surface associated	HGNC:21661
MUC7	mucin 7, secreted	HGNC:7518
MUCL1	mucin-like 1	HGNC:30588
MUM1L1	melanoma associated antigen (mutated) 1-like 1	HGNC:26583
MVD	mevalonate (diphospho) decarboxylase	HGNC:7529
MVK	mevalonate kinase	HGNC:7530
MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	HGNC:7532
MX2	myxovirus (influenza virus) resistance 2 (mouse)	HGNC:7533
MXRA7	matrix-remodelling associated 7	HGNC:7541
MXRA8	matrix-remodelling associated 8	HGNC:7542
MYBPC1	myosin binding protein C, slow type	HGNC:7549
MYEOV	myeloma overexpressed (in a subset of t(11;14) positive multiple myelomas)	HGNC:7563
MYH11	myosin, heavy chain 11, smooth muscle	HGNC:7569
MYH3	myosin, heavy chain 3, skeletal muscle, embryonic	HGNC:7573
MYL4	myosin, light chain 4, alkali; atrial, embryonic	HGNC:7585
MYL9	myosin, light chain 9, regulatory	HGNC:15754
MYO1F	myosin IF	HGNC:7600
MYO1G	myosin IG	HGNC:13880
MYOCD	myocardin	HGNC:16067
MYOM2	myomesin (M-protein) 2, 165kDa	HGNC:7614
MYOZ2	myozenin 2	HGNC:1330
NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	HGNC:14526
NADSYN1	NAD synthetase 1	HGNC:29832
NAMPT	nicotinamide phosphoribosyltransferase	HGNC:30092
NCKAP1L	NCK-associated protein 1-like	HGNC:4862
NDRG1	N-myc downstream regulated 1	HGNC:7679
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	HGNC:7687
NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	HGNC:29836
NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown,	HGNC:7706

	2, 14.5kDa	
NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	HGNC:7712
NEFH	neurofilament, heavy polypeptide	HGNC:7737
NEFL	neurofilament, light polypeptide	HGNC:7739
NEGR1	neuronal growth regulator 1	HGNC:17302
NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	HGNC:13823
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	HGNC:14644
NEXN	nexilin (F actin binding protein)	HGNC:29557
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	HGNC:29805
NID1	nidogen 1	HGNC:7821
NIT2	nitrilase family, member 2	HGNC:29878
NKG7	natural killer cell group 7 sequence	HGNC:7830
NLRP10	NLR family, pyrin domain containing 10	HGNC:21464
NOP16	NOP16 nucleolar protein homolog (yeast)	HGNC:26934
NOTCH1	notch 1	HGNC:7881
NOVA1	neuro-oncological ventral antigen 1	HGNC:7886
NOX4	NADPH oxidase 4	HGNC:7891
NPC1	Niemann-Pick disease, type C1	HGNC:7897
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	HGNC:16781
NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	HGNC:7943
NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	HGNC:7944
NQO2	NAD(P)H dehydrogenase, quinone 2	HGNC:7856
NR1H3	nuclear receptor subfamily 1, group H, member 3	HGNC:7966
NRN1	neuritin 1	HGNC:17972
NRP2	neuropilin 2	HGNC:8005
NSDHL	NAD(P) dependent steroid dehydrogenase-like	HGNC:13398
NTAN1	N-terminal asparagine amidase	HGNC:29909
NTM	neurotrimin	HGNC:17941
NTN1	netrin 1	HGNC:8029
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	HGNC:8032
NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	HGNC:8051
NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	HGNC:21042
NXF3	nuclear RNA export factor 3	HGNC:8073
NXPH4	neurexophilin 4	HGNC:8078
OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	HGNC:8086
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	HGNC:8087
OASL	2'-5'-oligoadenylate synthetase-like	HGNC:8090
OC90	otoconin 90	HGNC:8100
OCA2	oculocutaneous albinism II	HGNC:8101
ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)	HGNC:29944

OLAH	oleoyl-ACP hydrolase	HGNC:25625
OLFM4	olfactomedin 4	HGNC:17190
OLFML3	olfactomedin-like 3	HGNC:24956
OLIG3	oligodendrocyte transcription factor 3	HGNC:18003
OR52E8	olfactory receptor, family 52, subfamily E, member 8	HGNC:15217
OR7E24	olfactory receptor, family 7, subfamily E, member 24	HGNC:8396
OSGIN2	oxidative stress induced growth inhibitor family member 2	HGNC:1355
OTUB2	OTU domain, ubiquitin aldehyde binding 2	HGNC:20351
OXCT2	3-oxoacid CoA transferase 2	HGNC:18606
P2RY12	purinergic receptor P2Y, G-protein coupled, 12	HGNC:18124
P2RY4	pyrimidinergic receptor P2Y, G-protein coupled, 4	HGNC:8542
PADI3	peptidyl arginine deiminase, type III	HGNC:18337
PADI4	peptidyl arginine deiminase, type IV	HGNC:18368
PAFAH2	platelet-activating factor acetylhydrolase 2, 40kDa	HGNC:8579
PALM2-AKAP2	PALM2-AKAP2 readthrough	HGNC:33529
PAM	peptidylglycine alpha-amidating monooxygenase	HGNC:8596
PAMR1	peptidase domain containing associated with muscle regeneration 1	HGNC:24554
PANK1	pantothenate kinase 1	HGNC:8598
PAPLN	papilin, proteoglycan-like sulfated glycoprotein	HGNC:19262
PAQR3	progesterone and adipoQ receptor family member III	HGNC:30130
PARP14	poly (ADP-ribose) polymerase family, member 14	HGNC:29232
PARVB	parvin, beta	HGNC:14653
PC	pyruvate carboxylase	HGNC:8636
PCCB	propionyl CoA carboxylase, beta polypeptide	HGNC:8654
PCDH12	protocadherin 12	HGNC:8657
PCDH18	protocadherin 18	HGNC:14268
PCDH9	protocadherin 9	HGNC:8661
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	HGNC:8724
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	HGNC:8725
PCOLCE2	procollagen C-endopeptidase enhancer 2	HGNC:8739
PCP4	Purkinje cell protein 4	HGNC:8742
PCP4L1	Purkinje cell protein 4 like 1	HGNC:20448
PCSK2	proprotein convertase subtilisin/kexin type 2	HGNC:8744
PCSK6	proprotein convertase subtilisin/kexin type 6	HGNC:8569
PCTP	phosphatidylcholine transfer protein	HGNC:8752
PCYT2	phosphate cytidylyltransferase 2, ethanolamine	HGNC:8756
PDCD1	programmed cell death 1	HGNC:8760
PDCD1LG2	programmed cell death 1 ligand 2	HGNC:18731
PDE2A	phosphodiesterase 2A, cGMP-stimulated	HGNC:8777
PDE3B	phosphodiesterase 3B, cGMP-inhibited	HGNC:8779
PDE4DIP	phosphodiesterase 4D interacting protein	HGNC:15580
PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	HGNC:8785

PDGFC	platelet derived growth factor C	HGNC:8801
PDGFD	platelet derived growth factor D	HGNC:30620
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	HGNC:8803
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HGNC:8804
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	HGNC:8806
PDHX	pyruvate dehydrogenase complex, component X	HGNC:21350
PDLIM3	PDZ and LIM domain 3	HGNC:20767
PDZD4	PDZ domain containing 4	HGNC:21167
PDZK1	PDZ domain containing 1	HGNC:8821
PDZRN4	PDZ domain containing ring finger 4	HGNC:30552
PEBP4	phosphatidylethanolamine-binding protein 4	HGNC:28319
PECR	peroxisomal trans-2-enoyl-CoA reductase	HGNC:18281
PENK	proenkephalin	HGNC:8831
PEX11A	peroxisomal biogenesis factor 11 alpha	HGNC:8852
PEX16	peroxisomal biogenesis factor 16	HGNC:8857
PEX3	peroxisomal biogenesis factor 3	HGNC:8858
PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	HGNC:8872
PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	HGNC:8875
PFN2	profilin 2	HGNC:8882
PGBD5	piggyBac transposable element derived 5	HGNC:19405
PGD	phosphogluconate dehydrogenase	HGNC:8891
PGM1	phosphoglucomutase 1	HGNC:8905
PGM5	phosphoglucomutase 5	HGNC:8908
PGRMC1	progesterone receptor membrane component 1	HGNC:16090
PHLDA2	pleckstrin homology-like domain, family A, member 2	HGNC:12385
PHLDB1	pleckstrin homology-like domain, family B, member 1	HGNC:23697
PHLDB2	pleckstrin homology-like domain, family B, member 2	HGNC:29573
PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	HGNC:16865
PI15	peptidase inhibitor 15	HGNC:8946
PI16	peptidase inhibitor 16	HGNC:21245
PID1	phosphotyrosine interaction domain containing 1	HGNC:26084
PIP	prolactin-induced protein	HGNC:8993
PIRT	phosphoinositide-interacting regulator of transient receptor potential channels	HGNC:37239
PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	HGNC:25123
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	HGNC:9018
PKLR	pyruvate kinase, liver and RBC	HGNC:9020
PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	HGNC:9031
PLA2G2F	phospholipase A2, group IIF	HGNC:30040
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	HGNC:9040
PLA2R1	phospholipase A2 receptor 1, 180kDa	HGNC:9042
PLAU	plasminogen activator, urokinase	HGNC:9052
PLCL2	phospholipase C-like 2	HGNC:9064

PLD5	phospholipase D family, member 5	HGNC:26879
PLEK	pleckstrin	HGNC:9070
PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	HGNC:17733
PLEKHO2	pleckstrin homology domain containing, family O member 2	HGNC:30026
PLIN1	perilipin 1	HGNC:9076
PLIN2	perilipin 2	HGNC:248
PLIN4	perilipin 4	HGNC:29393
PLIN5	perilipin 5	HGNC:33196
PLN	phospholamban	HGNC:9080
PLP1	proteolipid protein 1	HGNC:9086
PLXDC1	plexin domain containing 1	HGNC:20945
PLXNA4	plexin A4	HGNC:9102
PLXND1	plexin D1	HGNC:9107
PM20D1	peptidase M20 domain containing 1	HGNC:26518
PMEPA1	prostate transmembrane protein, androgen induced 1	HGNC:14107
PMFBP1	polyamine modulated factor 1 binding protein 1	HGNC:17728
PMM1	phosphomannomutase 1	HGNC:9114
PMVK	phosphomevalonate kinase	HGNC:9141
PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	HGNC:21185
PNLIPRP2	pancreatic lipase-related protein 2	HGNC:9157
PNLIPRP3	pancreatic lipase-related protein 3	HGNC:23492
PNMAL1	paraneoplastic Ma antigen family-like 1	HGNC:25578
PNPLA3	patatin-like phospholipase domain containing 3	HGNC:18590
PNPLA5	patatin-like phospholipase domain containing 5	HGNC:24888
PODN	podocan	HGNC:23174
PODXL2	podocalyxin-like 2	HGNC:17936
PON3	paraoxonase 3	HGNC:9206
POPDC2	popeye domain containing 2	HGNC:17648
POR	P450 (cytochrome) oxidoreductase	HGNC:9208
POSTN	periostin, osteoblast specific factor	HGNC:16953
POU3F1	POU class 3 homeobox 1	HGNC:9214
PPAP2B	phosphatidic acid phosphatase type 2B	HGNC:9229
PPARG	peroxisome proliferator-activated receptor gamma	HGNC:9236
PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	HGNC:9237
PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	HGNC:9240
PPIF	peptidylprolyl isomerase F	HGNC:9259
PPM1K	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K	HGNC:25415
PPP1R12B	protein phosphatase 1, regulatory subunit 12B	HGNC:7619
PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	HGNC:9286
PPP1R3G	protein phosphatase 1, regulatory subunit 3G	HGNC:14945
PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	HGNC:9305
PPP2R2C	protein phosphatase 2, regulatory subunit B, gamma	HGNC:9306

PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	HGNC:9308
PPP4R4	protein phosphatase 4, regulatory subunit 4	HGNC:23788
PPT2	palmitoyl-protein thioesterase 2	HGNC:9326
PRAME	preferentially expressed antigen in melanoma	HGNC:9336
PRB1	proline-rich protein BstNI subfamily 1	HGNC:9337
PRB2	proline-rich protein BstNI subfamily 2	HGNC:9338
PRB3	proline-rich protein BstNI subfamily 3	HGNC:9339
PRDX2	peroxiredoxin 2	HGNC:9353
PRELP	proline/arginine-rich end leucine-rich repeat protein	HGNC:9357
PRF1	perforin 1 (pore forming protein)	HGNC:9360
PRG4	proteoglycan 4	HGNC:9364
PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	HGNC:9392
PRKCB	protein kinase C, beta	HGNC:9395
PRKCQ	protein kinase C, theta	HGNC:9410
PRR4	proline rich 4 (lacrimal)	HGNC:18020
PRR5L	proline rich 5 like	HGNC:25878
PRRT4	proline-rich transmembrane protein 4	HGNC:37280
PRSS22	protease, serine, 22	HGNC:14368
PRSS27	protease, serine 27	HGNC:15475
PRSS8	protease, serine, 8	HGNC:9491
PRUNE2	prune homolog 2 (Drosophila)	HGNC:25209
PSAPL1	prosaposin-like 1 (gene/pseudogene)	HGNC:33131
PSG4	pregnancy specific beta-1-glycoprotein 4	HGNC:9521
PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	HGNC:9533
PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	HGNC:9546
PSME4	proteasome (prosome, macropain) activator subunit 4	HGNC:20635
PSPH	phosphoserine phosphatase	HGNC:9577
PTGDS	prostaglandin D2 synthase 21kDa (brain)	HGNC:9592
PTGER3	prostaglandin E receptor 3 (subtype EP3)	HGNC:9595
PTGFR	prostaglandin F receptor (FP)	HGNC:9600
PTGIS	prostaglandin I2 (prostacyclin) synthase	HGNC:9603
PTHLH	parathyroid hormone-like hormone	HGNC:9607
PTN	pleiotrophin	HGNC:9630
PTPN7	protein tyrosine phosphatase, non-receptor type 7	HGNC:9659
PTPRC	protein tyrosine phosphatase, receptor type, C	HGNC:9666
PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	HGNC:9667
PTPRG	protein tyrosine phosphatase, receptor type, G	HGNC:9671
PTX3	pentraxin 3, long	HGNC:9692
PXDN	peroxidasin homolog (Drosophila)	HGNC:14966
PXMP2	peroxisomal membrane protein 2, 22kDa	HGNC:9716
PXMP4	peroxisomal membrane protein 4, 24kDa	HGNC:15920
PXN	paxillin	HGNC:9718

PYHIN1	pyrin and HIN domain family, member 1	HGNC:28894
RAB15	RAB15, member RAS oncogene family	HGNC:20150
RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	HGNC:9802
RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	HGNC:9803
RAMP2	receptor (G protein-coupled) activity modifying protein 2	HGNC:9844
RARRES1	retinoic acid receptor responder (tazarotene induced) 1	HGNC:9867
RARRES2	retinoic acid receptor responder (tazarotene induced) 2	HGNC:9868
RASA3	RAS p21 protein activator 3	HGNC:20331
RASAL1	RAS protein activator like 1 (GAP1 like)	HGNC:9873
RASEF	RAS and EF-hand domain containing	HGNC:26464
RASSF3	Ras association (RalGDS/AF-6) domain family member 3	HGNC:14271
RBM47	RNA binding motif protein 47	HGNC:30358
RBMS3	RNA binding motif, single stranded interacting protein 3	HGNC:13427
RBP1	retinol binding protein 1, cellular	HGNC:9919
RBP4	retinol binding protein 4, plasma	HGNC:9922
RBP5	retinol binding protein 5, cellular	HGNC:15847
RCL1	RNA terminal phosphate cyclase-like 1	HGNC:17687
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	HGNC:17964
RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	HGNC:9940
RECK	reversion-inducing-cysteine-rich protein with kazal motifs	HGNC:11345
REEP6	receptor accessory protein 6	HGNC:30078
REG3G	regenerating islet-derived 3 gamma	HGNC:29595
RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	HGNC:25991
RFTN1	raftlin, lipid raft linker 1	HGNC:30278
RGL1	ral guanine nucleotide dissociation stimulator-like 1	HGNC:30281
RGS9BP	regulator of G protein signaling 9 binding protein	HGNC:30304
RHCG	Rh family, C glycoprotein	HGNC:18140
RHOXF2	Rhox homeobox family, member 2	HGNC:30011
RIMBP2	RIMS binding protein 2	HGNC:30339
RIMS4	regulating synaptic membrane exocytosis 4	HGNC:16183
RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	HGNC:10044
RND3	Rho family GTPase 3	HGNC:671
RNF133	ring finger protein 133	HGNC:21154
RNF157	ring finger protein 157	HGNC:29402
RNF17	ring finger protein 17	HGNC:10060
RNFT1	ring finger protein, transmembrane 1	HGNC:30206
ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	HGNC:13433
ROBO4	roundabout, axon guidance receptor, homolog 4 (Drosophila)	HGNC:17985
ROS1	c-ros oncogene 1, receptor tyrosine kinase	HGNC:10261
RRAS	related RAS viral (r-ras) oncogene homolog	HGNC:10447
RSAD2	radical S-adenosyl methionine domain containing 2	HGNC:30908
RSPO3	R-spondin 3	HGNC:20866

RTN1	reticulon 1	HGNC:10467
S100A2	S100 calcium binding protein A2	HGNC:10492
S100A3	S100 calcium binding protein A3	HGNC:10493
S100A7	S100 calcium binding protein A7	HGNC:10497
S100A7A	S100 calcium binding protein A7A	HGNC:21657
S100A8	S100 calcium binding protein A8	HGNC:10498
S100A9	S100 calcium binding protein A9	HGNC:10499
S100P	S100 calcium binding protein P	HGNC:10504
S1PR4	sphingosine-1-phosphate receptor 4	HGNC:3170
SAA1	serum amyloid A1	HGNC:10513
SAMD3	sterile alpha motif domain containing 3	HGNC:21574
SAMD5	sterile alpha motif domain containing 5	HGNC:21180
SAMD9L	sterile alpha motif domain containing 9-like	HGNC:1349
SAMHD1	SAM domain and HD domain 1	HGNC:15925
SAMM50	sorting and assembly machinery component 50 homolog (<i>S. cerevisiae</i>)	HGNC:24276
SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	HGNC:10528
SASH3	SAM and SH3 domain containing 3	HGNC:15975
SATB2	SATB homeobox 2	HGNC:21637
SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, <i>S. cerevisiae</i>)-like	HGNC:10547
SCAP	SREBF chaperone	HGNC:30634
SCARA5	scavenger receptor class A, member 5 (putative)	HGNC:28701
SCGB1D2	secretoglobin, family 1D, member 2	HGNC:18396
SCGB2A1	secretoglobin, family 2A, member 1	HGNC:7051
SCGB2A2	secretoglobin, family 2A, member 2	HGNC:7050
SCGB3A1	secretoglobin, family 3A, member 1	HGNC:18384
SCN2A	sodium channel, voltage-gated, type II, alpha subunit	HGNC:10588
SCN7A	sodium channel, voltage-gated, type VII, alpha subunit	HGNC:10594
SCUBE2	signal peptide, CUB domain, EGF-like 2	HGNC:30425
SDPR	serum deprivation response	HGNC:10690
SEC11C	SEC11 homolog C (<i>S. cerevisiae</i>)	HGNC:23400
SEC14L2	SEC14-like 2 (<i>S. cerevisiae</i>)	HGNC:10699
SEC14L4	SEC14-like 4 (<i>S. cerevisiae</i>)	HGNC:20627
SELPLG	selectin P ligand	HGNC:10722
SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	HGNC:10723
SEMA5B	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	HGNC:10737
SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	HGNC:10739
SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	HGNC:10741
SERINC2	serine incorporator 2	HGNC:23231
SERPINA12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	HGNC:18359
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	HGNC:16

SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4	HGNC:8948
SERPINA9	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	HGNC:15995
SERPINB13	serpin peptidase inhibitor, clade B (ovalbumin), member 13	HGNC:8944
SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	HGNC:10569
SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	HGNC:13902
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	HGNC:8951
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	HGNC:8824
SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	HGNC:1228
SETBP1	SET binding protein 1	HGNC:15573
SFRP5	secreted frizzled-related protein 5	HGNC:10779
SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	HGNC:10807
SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	HGNC:10809
SGK2	serum/glucocorticoid regulated kinase 2	HGNC:13900
SGPP2	sphingosine-1-phosphate phosphatase 2	HGNC:19953
SH2B3	SH2B adaptor protein 3	HGNC:29605
SH2D1A	SH2 domain containing 1A	HGNC:10820
SH3KBP1	SH3-domain kinase binding protein 1	HGNC:13867
SHF	Src homology 2 domain containing F	HGNC:25116
SHISA2	shisa homolog 2 (<i>Xenopus laevis</i>)	HGNC:20366
SHISA6	shisa homolog 6 (<i>Xenopus laevis</i>)	HGNC:34491
SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin	HGNC:11127
SIPA1L2	signal-induced proliferation-associated 1 like 2	HGNC:23800
SIT1	signaling threshold regulating transmembrane adaptor 1	HGNC:17710
SLA	Src-like-adaptor	HGNC:10902
SLAMF1	signaling lymphocytic activation molecule family member 1	HGNC:10903
SLAMF6	SLAM family member 6	HGNC:21392
SLAMF8	SLAM family member 8	HGNC:21391
SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	HGNC:10908
SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	HGNC:15595
SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4	HGNC:15827
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	HGNC:10920
SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	HGNC:10921
SLC16A11	solute carrier family 16, member 11 (monocarboxylic acid transporter 11)	HGNC:23093
SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	HGNC:10927
SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	HGNC:23520
SLC24A5	solute carrier family 24, member 5	HGNC:20611
SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	HGNC:10979
SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	HGNC:10981
SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	HGNC:10987
SLC25A18	solute carrier family 25 (glutamate carrier), member 18	HGNC:10988

SLC25A33	solute carrier family 25 (pyrimidine nucleotide carrier), member 33	HGNC:29681
SLC25A34	solute carrier family 25, member 34	HGNC:27653
SLC25A35	solute carrier family 25, member 35	HGNC:31921
SLC25A41	solute carrier family 25, member 41	HGNC:28533
SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	HGNC:10991
SLC26A2	solute carrier family 26 (sulfate transporter), member 2	HGNC:10994
SLC26A3	solute carrier family 26, member 3	HGNC:3018
SLC26A6	solute carrier family 26, member 6	HGNC:14472
SLC26A9	solute carrier family 26, member 9	HGNC:14469
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	HGNC:10996
SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	HGNC:10998
SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	HGNC:11000
SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	HGNC:11005
SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	HGNC:18301
SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	HGNC:13446
SLC30A1	solute carrier family 30 (zinc transporter), member 1	HGNC:11012
SLC30A10	solute carrier family 30, member 10	HGNC:25355
SLC31A1	solute carrier family 31 (copper transporters), member 1	HGNC:11016
SLC31A2	solute carrier family 31 (copper transporters), member 2	HGNC:11017
SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	HGNC:11022
SLC35B1	solute carrier family 35, member B1	HGNC:20798
SLC39A8	solute carrier family 39 (zinc transporter), member 8	HGNC:20862
SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	HGNC:11025
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	HGNC:10909
SLC41A1	solute carrier family 41, member 1	HGNC:19429
SLC43A2	solute carrier family 43, member 2	HGNC:23087
SLC43A3	solute carrier family 43, member 3	HGNC:17466
SLC44A3	solute carrier family 44, member 3	HGNC:28689
SLC45A4	solute carrier family 45, member 4	HGNC:29196
SLC46A3	solute carrier family 46, member 3	HGNC:27501
SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	HGNC:11041
SLC6A14	solute carrier family 6 (amino acid transporter), member 14	HGNC:11047
SLC6A17	solute carrier family 6, member 17	HGNC:31399
SLC7A4	solute carrier family 7 (orphan transporter), member 4	HGNC:11062
SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	HGNC:11063
SLC9A2	solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	HGNC:11072
SLCO4C1	solute carrier organic anion transporter family, member 4C1	HGNC:23612
SLFN5	schlafen family member 5	HGNC:28286
SLIT2	slit homolog 2 (Drosophila)	HGNC:11086
SLIT3	slit homolog 3 (Drosophila)	HGNC:11087
SMAD3	SMAD family member 3	HGNC:6769

SMAD6	SMAD family member 6	HGNC:6772
SMOC1	SPARC related modular calcium binding 1	HGNC:20318
SMOC2	SPARC related modular calcium binding 2	HGNC:20323
SMOX	spermine oxidase	HGNC:15862
SMTN	smoothelin	HGNC:11126
SNCG	synuclein, gamma (breast cancer-specific protein 1)	HGNC:11141
SNED1	sushi, nidogen and EGF-like domains 1	HGNC:24696
SNX10	sorting nexin 10	HGNC:14974
SNX4	sorting nexin 4	HGNC:11175
SOAT1	sterol O-acyltransferase 1	HGNC:11177
SOD3	superoxide dismutase 3, extracellular	HGNC:11181
SORBS1	sorbin and SH3 domain containing 1	HGNC:14565
SORD	sorbitol dehydrogenase	HGNC:11184
SOST	sclerostin	HGNC:13771
SOSTDC1	sclerostin domain containing 1	HGNC:21748
SOX7	SRY (sex determining region Y)-box 7	HGNC:18196
SOX9	SRY (sex determining region Y)-box 9	HGNC:11204
SP5	Sp5 transcription factor	HGNC:14529
SP8	Sp8 transcription factor	HGNC:19196
SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	HGNC:11219
SPEG	SPEG complex locus	HGNC:16901
SP11	spleen focus forming virus (SFFV) proviral integration oncogene spi1	HGNC:11241
SPIRE2	spire homolog 2 (Drosophila)	HGNC:30623
SPNS2	spinster homolog 2 (Drosophila)	HGNC:26992
SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	HGNC:11251
SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	HGNC:13564
SPP1	secreted phosphoprotein 1	HGNC:11255
SPRR1A	small proline-rich protein 1A	HGNC:11259
SPRR1B	small proline-rich protein 1B	HGNC:11260
SPRR2A	small proline-rich protein 2A	HGNC:11261
SPRR2B	small proline-rich protein 2B	HGNC:11262
SPRR2D	small proline-rich protein 2D	HGNC:11264
SPRR4	small proline-rich protein 4	HGNC:23173
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	HGNC:11269
SPTBN5	spectrin, beta, non-erythrocytic 5	HGNC:15680
SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	HGNC:11284
SRD5A3	steroid 5 alpha-reductase 3	HGNC:25812
SREBF1	sterol regulatory element binding transcription factor 1	HGNC:11289
SRGN	serglycin	HGNC:9361
SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	HGNC:11298
SRPRB	signal recognition particle receptor, B subunit	HGNC:24085
SRPX	sushi-repeat containing protein, X-linked	HGNC:11309

SRXN1	sulfiredoxin 1	HGNC:16132
SSPN	sarcospan	HGNC:11322
ST6GALNAC 4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N- acetylgalactosaminide alpha-2,6-sialyltransferase 4	HGNC:17846
STAB2	stabilin 2	HGNC:18629
STAP2	signal transducing adaptor family member 2	HGNC:30430
STARD4	StAR-related lipid transfer (START) domain containing 4	HGNC:18058
STAT1	signal transducer and activator of transcription 1, 91kDa	HGNC:11362
STAT5A	signal transducer and activator of transcription 5A	HGNC:11366
STEAP4	STEAP family member 4	HGNC:21923
STK17B	serine/threonine kinase 17b	HGNC:11396
STRBP	spermatid perinuclear RNA binding protein	HGNC:16462
STS	steroid sulfatase (microsomal), isozyme S	HGNC:11425
STXBP5L	syntaxin binding protein 5-like	HGNC:30757
SULT1C3	sulfotransferase family, cytosolic, 1C, member 3	HGNC:33543
SULT4A1	sulfotransferase family 4A, member 1	HGNC:14903
SUOX	sulfite oxidase	HGNC:11460
SUSD4	sushi domain containing 4	HGNC:25470
SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	HGNC:15985
SYN2	synapsin II	HGNC:11495
SYNE1	spectrin repeat containing, nuclear envelope 1	HGNC:17089
SYNM	synemin, intermediate filament protein	HGNC:24466
SYNPO	synaptopodin	HGNC:30672
SYNPO2	synaptopodin 2	HGNC:17732
SYPL2	synaptophysin-like 2	HGNC:27638
SYT12	synaptotagmin XII	HGNC:18381
SYT4	synaptotagmin IV	HGNC:11512
SYT7	synaptotagmin VII	HGNC:11514
SYTL5	synaptotagmin-like 5	HGNC:15589
TAC1	tachykinin, precursor 1	HGNC:11517
TACC1	transforming, acidic coiled-coil containing protein 1	HGNC:11522
TACR2	tachykinin receptor 2	HGNC:11527
TAGLN	transgelin	HGNC:11553
TAGLN3	transgelin 3	HGNC:29868
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	HGNC:43
TAS1R3	taste receptor, type 1, member 3	HGNC:15661
TBX5	T-box 5	HGNC:11604
TCHH	trichohyalin	HGNC:11791
TCHHL1	trichohyalin-like 1	HGNC:31796
TDRD12	tudor domain containing 12	HGNC:25044
TDRD6	tudor domain containing 6	HGNC:21339
TECR	trans-2,3-enoyl-CoA reductase	HGNC:4551
TECRL	trans-2,3-enoyl-CoA reductase-like	HGNC:27365

TENC1	tensin like C1 domain containing phosphatase (tensin 2)	HGNC:19737
TEX264	testis expressed 264	HGNC:30247
TF	transferrin	HGNC:11740
TFF3	trefoil factor 3 (intestinal)	HGNC:11757
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	HGNC:11760
TFRC	transferrin receptor (p90, CD71)	HGNC:11763
TG	thyroglobulin	HGNC:11764
TGFB1	transforming growth factor, beta 1	HGNC:11766
TGFBR3	transforming growth factor, beta receptor III	HGNC:11774
TGM6	transglutaminase 6	HGNC:16255
TGM7	transglutaminase 7	HGNC:30790
THBS2	thrombospondin 2	HGNC:11786
THEMIS	thymocyte selection associated	HGNC:21569
THRSP	thyroid hormone responsive	HGNC:11800
TIGIT	T cell immunoreceptor with Ig and ITIM domains	HGNC:26838
TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	HGNC:11818
TIMP3	TIMP metalloproteinase inhibitor 3	HGNC:11822
TIMP4	TIMP metalloproteinase inhibitor 4	HGNC:11823
TKT	transketolase	HGNC:11834
TLCD1	TLC domain containing 1	HGNC:25177
TLCD2	TLC domain containing 2	HGNC:33522
TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	HGNC:11838
TLN1	talin 1	HGNC:11845
TLN2	talin 2	HGNC:15447
TM4SF1	transmembrane 4 L six family member 1	HGNC:11853
TM7SF2	transmembrane 7 superfamily member 2	HGNC:11863
TMC2	transmembrane channel-like 2	HGNC:16527
TMC5	transmembrane channel-like 5	HGNC:22999
TMC8	transmembrane channel-like 8	HGNC:20474
TMCC3	transmembrane and coiled-coil domain family 3	HGNC:29199
TMED3	transmembrane emp24 protein transport domain containing 3	HGNC:28889
TMED5	transmembrane emp24 protein transport domain containing 5	HGNC:24251
TMEM132C	transmembrane protein 132C	HGNC:25436
TMEM135	transmembrane protein 135	HGNC:26167
TMEM164	transmembrane protein 164	HGNC:26217
TMEM171	transmembrane protein 171	HGNC:27031
TMEM176A	transmembrane protein 176A	HGNC:24930
TMEM176B	transmembrane protein 176B	HGNC:29596
TMEM189	transmembrane protein 189	HGNC:16735
TMEM33	transmembrane protein 33	HGNC:25541
TMEM37	transmembrane protein 37	HGNC:18216
TMEM41A	transmembrane protein 41A	HGNC:30544

TMEM56	transmembrane protein 56	HGNC:26477
TMEM63C	transmembrane protein 63C	HGNC:23787
TMEM91	transmembrane protein 91	HGNC:32393
TMEM97	transmembrane protein 97	HGNC:28106
TMPRSS11E	transmembrane protease, serine 11E	HGNC:24465
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	HGNC:11895
TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	HGNC:11917
TNMD	tenomodulin	HGNC:17757
TNNT1	troponin T type 1 (skeletal, slow)	HGNC:11948
TNNT2	troponin T type 2 (cardiac)	HGNC:11949
TNR	tenascin R (restrictin, janusin)	HGNC:11953
TNS1	tensin 1	HGNC:11973
TNS3	tensin 3	HGNC:21616
TNXB	tenascin XB	HGNC:11976
TP53INP2	tumor protein p53 inducible nuclear protein 2	HGNC:16104
TPD52L1	tumor protein D52-like 1	HGNC:12006
TPM2	tropomyosin 2 (beta)	HGNC:12011
TPSAB1	tryptase alpha/beta 1	HGNC:12019
TPSB2	tryptase beta 2 (gene/pseudogene)	HGNC:14120
TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	HGNC:29011
TRAT1	T cell receptor associated transmembrane adaptor 1	HGNC:30698
TRIL	TLR4 interactor with leucine-rich repeats	HGNC:22200
TRIM17	tripartite motif containing 17	HGNC:13430
TRIM2	tripartite motif containing 2	HGNC:15974
TRIM22	tripartite motif containing 22	HGNC:16379
TRIM48	tripartite motif containing 48	HGNC:19021
TRIM55	tripartite motif containing 55	HGNC:14215
TRIM58	tripartite motif containing 58	HGNC:24150
TRIM67	tripartite motif containing 67	HGNC:31859
TRIML2	tripartite motif family-like 2	HGNC:26378
TRIO	triple functional domain (PTPRF interacting)	HGNC:12303
TRPS1	trichorhinophalangeal syndrome I	HGNC:12340
TSHZ2	teashirt zinc finger homeobox 2	HGNC:13010
TSPAN2	tetraspanin 2	HGNC:20659
TSPAN6	tetraspanin 6	HGNC:11858
TST	thiosulfate sulfurtransferase (rhodanese)	HGNC:12388
TTC38	tetratricopeptide repeat domain 38	HGNC:26082
TTC39B	tetratricopeptide repeat domain 39B	HGNC:23704
TTLL4	tubulin tyrosine ligase-like family, member 4	HGNC:28976
TTYH3	tweety homolog 3 (Drosophila)	HGNC:22222
TUSC5	tumor suppressor candidate 5	HGNC:29592
TXN	thioredoxin	HGNC:12435
TXNDC9	thioredoxin domain containing 9	HGNC:24110

TYR	tyrosinase (oculocutaneous albinism IA)	HGNC:12442
TYRP1	tyrosinase-related protein 1	HGNC:12450
UBA7	ubiquitin-like modifier activating enzyme 7	HGNC:12471
UBASH3A	ubiquitin associated and SH3 domain containing A	HGNC:12462
UBD	ubiquitin D	HGNC:18795
UBE2L6	ubiquitin-conjugating enzyme E2L 6	HGNC:12490
UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	HGNC:37269
UBE2S	ubiquitin-conjugating enzyme E2S	HGNC:17895
UBIAD1	UbiA prenyltransferase domain containing 1	HGNC:30791
UBR4	ubiquitin protein ligase E3 component n-recognin 4	HGNC:30313
UGT1A4	UDP glucuronosyltransferase 1 family, polypeptide A4	HGNC:12536
UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	HGNC:12538
UGT2A1	UDP glucuronosyltransferase 2 family, polypeptide A1, complex locus	HGNC:12542
UGT2A2	UDP glucuronosyltransferase 2 family, polypeptide A2	HGNC:28183
UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	HGNC:27266
ULK4	unc-51-like kinase 4 (C. elegans)	HGNC:15784
UNC5B	unc-5 homolog B (C. elegans)	HGNC:12568
UPB1	ureidopropionase, beta	HGNC:16297
UQCRC1	ubiquinol-cytochrome c reductase core protein I	HGNC:12585
UQCRH	ubiquinol-cytochrome c reductase hinge protein	HGNC:12590
UQCRCQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	HGNC:29594
USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	HGNC:30889
VCAM1	vascular cell adhesion molecule 1	HGNC:12663
VGLL3	vestigial like 3 (Drosophila)	HGNC:24327
VIP	vasoactive intestinal peptide	HGNC:12693
VIT	vitrin	HGNC:12697
VLDLR	very low density lipoprotein receptor	HGNC:12698
VNN1	vanin 1	HGNC:12705
VNN2	vanin 2	HGNC:12706
VSIG4	V-set and immunoglobulin domain containing 4	HGNC:17032
VSNL1	visinin-like 1	HGNC:12722
VTCN1	V-set domain containing T cell activation inhibitor 1	HGNC:28873
VWF	von Willebrand factor	HGNC:12726
WASF3	WAS protein family, member 3	HGNC:12734
WDFY4	WDFY family member 4	HGNC:29323
WDR72	WD repeat domain 72	HGNC:26790
WFDC5	WAP four-disulfide core domain 5	HGNC:20477
WFDC6	WAP four-disulfide core domain 6	HGNC:16164
WIPF1	WAS/WASL interacting protein family, member 1	HGNC:12736
WNT3	wingless-type MMTV integration site family, member 3	HGNC:12782
WNT4	wingless-type MMTV integration site family, member 4	HGNC:12783
WNT7B	wingless-type MMTV integration site family, member 7B	HGNC:12787

WNT9B	wingless-type MMTV integration site family, member 9B	HGNC:12779
WSCD2	WSC domain containing 2	HGNC:29117
XAGE5	X antigen family, member 5	HGNC:30930
XBP1	X-box binding protein 1	HGNC:12801
XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	HGNC:12823
XYLB	xylulokinase homolog (H. influenzae)	HGNC:12839
ZBED2	zinc finger, BED-type containing 2	HGNC:20710
ZC3H12A	zinc finger CCCH-type containing 12A	HGNC:26259
ZCCHC24	zinc finger, CCHC domain containing 24	HGNC:26911
ZEB1	zinc finger E-box binding homeobox 1	HGNC:11642
ZFHx3	zinc finger homeobox 3	HGNC:777
ZFHx4	zinc finger homeobox 4	HGNC:30939
ZFPM2	zinc finger protein, multitype 2	HGNC:16700
ZG16B	zymogen granule protein 16 homolog B (rat)	HGNC:30456
ZIC1	Zic family member 1	HGNC:12872
ZIC4	Zic family member 4	HGNC:20393
ZNF117	zinc finger protein 117	HGNC:12897
ZNF254	zinc finger protein 254	HGNC:13047
ZNF385B	zinc finger protein 385B	HGNC:26332
ZNF43	zinc finger protein 43	HGNC:13109
ZNF493	zinc finger protein 493	HGNC:23708
ZNF703	zinc finger protein 703	HGNC:25883
ZNF80	zinc finger protein 80	HGNC:13155
ZNF831	zinc finger protein 831	HGNC:16167
ZP1	zona pellucida glycoprotein 1 (sperm receptor)	HGNC:13187
FAM213A	family with sequence similarity 213, member A	HGNC:28651
OTOGL	otogelin-like	HGNC:26901
SERTM1	serine-rich and transmembrane domain containing 1	HGNC:33792
MFS12	major facilitator superfamily domain containing 12	HGNC:28299
RUSC1-AS1	RUSC1 antisense RNA 1 (non-protein coding)	HGNC:26680
SH3D21	SH3 domain containing 21	HGNC:26236
AXDND1	axonemal dynein light chain domain containing 1	HGNC:26564
LAMP5	lysosomal-associated membrane protein family, member 5	HGNC:16097
METTL19	methyltransferase like 19	HGNC:26653
NDNF	neuron-derived neurotrophic factor	HGNC:26256
ADTRP	androgen-dependent TFPI-regulating protein	HGNC:21214
CLPSL2	colipase-like 2	HGNC:21250
SAPCD1	suppressor APC domain containing 1	HGNC:13938
ZC2HC1B	zinc finger, C2HC-type containing 1B	HGNC:21174
HILPDA	hypoxia inducible lipid droplet-associated	HGNC:28859
SAPCD2	suppressor APC domain containing 2	HGNC:28055
CACFD1	calcium channel flower domain containing 1	HGNC:1365
ECI1	enoyl-CoA delta isomerase 1	HGNC:2703

MMRN2	multimerin 2	HGNC:19888
ERV3-1	endogenous retrovirus group 3, member 1	HGNC:3454
FMO4	flavin containing monooxygenase 4	HGNC:3772
IL36RN	interleukin 36 receptor antagonist	HGNC:15561
IL37	interleukin 37	HGNC:15563
KRT6A	keratin 6A	HGNC:6443
CERS4	ceramide synthase 4	HGNC:23747
LHFPL3	lipoma HMGIC fusion partner-like 3	HGNC:6589
LTBP3	latent transforming growth factor beta binding protein 3	HGNC:6716
LTBP2	latent transforming growth factor beta binding protein 2	HGNC:6715
LY6G6F	lymphocyte antigen 6 complex, locus G6F	HGNC:13933
MRC1	mannose receptor, C type 1	HGNC:7228
ODZ1	odz, odd Oz/ten-m homolog 1 (Drosophila)	HGNC:8117
SLC50A1	solute carrier family 50 (sugar transporter), member 1	HGNC:30657
CRABP1	cellular retinoic acid binding protein 1	HGNC:2338
MSMO1	methylsterol monooxygenase 1	HGNC:10545
SCGB2B2	secretoglobin, family 2B, member 2	HGNC:27616
MSRB1	methionine sulfoxide reductase B1	HGNC:14133
SGK3	serum/glucocorticoid regulated kinase family, member 3	HGNC:10812
PMEL	premelanosome protein	HGNC:10880
XBP1P1	X-box binding protein 1 pseudogene 1	HGNC:12802
SOAT2	sterol O-acyltransferase 2	HGNC:11178
CLMP	CXADR-like membrane protein	HGNC:24039
PARD3	par-3 partitioning defective 3 homolog (C. elegans)	HGNC:16051
PGAP1	post-GPI attachment to proteins 1	HGNC:25712
MFRP	membrane frizzled-related protein	HGNC:18121
CXCL10	chemokine (C-X-C motif) ligand 10	HGNC:10637
CHAMP1	chromosome alignment maintaining phosphoprotein 1	HGNC:20311
CCRL1	chemokine (C-C motif) receptor-like 1	HGNC:1611
CNOT6	CCR4-NOT transcription complex, subunit 6	HGNC:14099
CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	HGNC:14254
CTLA4	cytotoxic T-lymphocyte-associated protein 4	HGNC:2505
CDH19	cadherin 19, type 2	HGNC:1758
CDH20	cadherin 20, type 2	HGNC:1760
DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11	HGNC:2736
RHOV	ras homolog family member V	HGNC:18313
CLCF1	cardiotrophin-like cytokine factor 1	HGNC:17412
CPA4	carboxypeptidase A4	HGNC:15740
HOMER2	homer homolog 2 (Drosophila)	HGNC:17513
CSTB	cystatin B (stefin B)	HGNC:2482
VSIG2	V-set and immunoglobulin domain containing 2	HGNC:17149
DSC3	desmocollin 3	HGNC:3037
DUSP12	dual specificity phosphatase 12	HGNC:3067

SH3D19	SH3 domain containing 19	HGNC:30418
GLB1	galactosidase, beta 1	HGNC:4298
CNTN1	contactin 1	HGNC:2171
FADS1	fatty acid desaturase 1	HGNC:3574
KHSRP	KH-type splicing regulatory protein	HGNC:6316
HPLH1	hemophagocytic lymphohistiocytosis 1	HGNC:23824
CFH	complement factor H	HGNC:4883
SLC25A16	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	HGNC:10986
PAEP	progestagen-associated endometrial protein	HGNC:8573
GOLT1B	golgi transport 1B	HGNC:20175
GOLT1A	golgi transport 1A	HGNC:24766
DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase)	HGNC:2995
LGALS1	lectin, galactoside-binding-like	HGNC:25012
KRT123P	keratin 123 pseudogene	HGNC:30196
KRT121P	keratin 121 pseudogene	HGNC:30198
HBB	hemoglobin, beta	HGNC:4827
KCNA5	potassium voltage-gated channel, shaker-related subfamily, member	HGNC:6224
HOOK2	hook homolog 2 (Drosophila)	HGNC:19885
KIF2A	kinesin heavy chain member 2A	HGNC:6318
CAPN5	calpain 5	HGNC:1482
KLK1	kallikrein 1	HGNC:6357
KRTAP5-9	keratin associated protein 5-9	HGNC:23604
KRTAP5-5	keratin associated protein 5-5	HGNC:23601
KRTAP5-8	keratin associated protein 5-8	HGNC:23603
KRTAP5-7	keratin associated protein 5-7	HGNC:23602
KRTAP5-11	keratin associated protein 5-11	HGNC:23606
KRTAP5-2	keratin associated protein 5-2	HGNC:23597
KRTAP5-3	keratin associated protein 5-3	HGNC:23598
SPNS1	spinster homolog 1 (Drosophila)	HGNC:30621
TOX4	TOX high mobility group box family member 4	HGNC:20161
C1D	C1D nuclear receptor corepressor	HGNC:29911
PCDHB16	protocadherin beta 16	HGNC:14546
MS4A2	membrane-spanning 4-domains, subfamily A, member 2	HGNC:7316
MS4A4A	membrane-spanning 4-domains, subfamily A, member 4A	HGNC:13371
NPRL2	nitrogen permease regulator-like 2 (S. cerevisiae)	HGNC:24969
NELL2	NEL-like 2 (chicken)	HGNC:7751
MYCBP2	MYC binding protein 2, E3 ubiquitin protein ligase	HGNC:23386
PODXL	podocalyxin-like	HGNC:9171
PORCN	porcupine homolog (Drosophila)	HGNC:17652
RBL1	retinoblastoma-like 1 (p107)	HGNC:9893
PVRL4	poliovirus receptor-related 4	HGNC:19688
PXDN	peroxidasin homolog (Drosophila)	HGNC:14966

NCOA3	nuclear receptor coactivator 3	HGNC:7670
ARID4A	AT rich interactive domain 4A (RBP1-like)	HGNC:9885
POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	HGNC:9191
SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	HGNC:30605
SLIT3	slit homolog 3 (Drosophila)	HGNC:11087
SLIT1	slit homolog 1 (Drosophila)	HGNC:11085
CXXC1	CXXC finger protein 1	HGNC:24343
DDR2	discoidin domain receptor tyrosine kinase 2	HGNC:2731
CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain	HGNC:23228

Table 2

Database	PathwayName	Pvalue	Fold Enrichment	FDR
KEGG	Valine, leucine and isoleucine degradation	4.39E-09	4.17	5.40E-06
KEGG	PPAR signaling pathway	6.22E-09	3.38	7.64E-06
KEGG	Viral myocarditis	5.98E-08	3.17	7.35E-05
KEGG	Type I diabetes mellitus	4.40E-07	3.77	5.41E-04
KEGG	Allograft rejection	1.07E-06	3.94	1.32E-03
KEGG	Systemic lupus erythematosus	2.41E-06	2.53	2.96E-03
KEGG	Cell adhesion molecules (CAMs)	2.89E-06	2.27	3.55E-03
KEGG	Graft-versus-host disease	3.91E-06	3.63	4.80E-03
KEGG	Steroid biosynthesis	5.01E-06	5.39	6.15E-03
KEGG	Hematopoietic cell lineage	1.39E-05	2.52	1.71E-02
KEGG	ECM-receptor interaction	2.83E-05	2.48	3.48E-02
KEGG	Glycolysis / Gluconeogenesis	4.08E-05	2.78	5.01E-02
KEGG	Autoimmune thyroid disease	4.97E-05	2.94	6.10E-02
REACTOME	Metabolism of lipids and lipoproteins	2.31E-18	3.39	2.26E-15
REACTOME	Signaling in Immune system	1.20E-07	1.93	1.17E-04
REACTOME	Metabolism of carbohydrates	7.72E-07	2.70	7.57E-04
REACTOME	Biological oxidations	6.38E-05	2.19	6.25E-02
PANTHER	Cholesterol biosynthesis	4.79E-05	6.43	5.46E-02
BIOCARTA	T Cytotoxic Cell Surface Molecules	2.05E-05	5.79	2.59E-02

Table 2. Pathway enriched based on the ~2000 up and down regulated genes. The presentation of enriched pathways based on DAVID database along with the source database where the pathways are from and have a enrichment calculation algorithm. We used a conservative cut-off with FDR ≤ 0.1 to filter out important pathways. In case, you need a different cut-off, we have also attached the excel spread-sheet listing all the pathways pass the DAVID cut-off.

Table 3: List of gene signatures/regulatory factors controlling the expression of skinaging-related genes in various pathways and/or gene networks. Note that the gene described in italics at the end of the table are not part of Table 1 (it only includes the top 2000 up and down regulated genes); these italicized genes are part of the gene network regulators.

Symbol	Name	HGNC ID
IL6	interleukin 6 (interferon, beta 2)	HGNC:6018
CSF3	colony stimulating factor 3 (granulocyte)	HGNC:2438
IFNG	interferon, gamma	HGNC:5438
IL8	interleukin 8	HGNC:6025
CXCL2	chemokine (C-X-C motif) ligand 2	HGNC:4603
CXCL9	chemokine (C-X-C motif) ligand 9	HGNC:7098
CCKAR	cholecystokinin A receptor	HGNC:1570
CSN1S1	casein alpha s1	HGNC:2445
CXCL10	chemokine (C-X-C motif) ligand 10	HGNC:10637
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	HGNC:4602
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	HGNC:3797
DEFA6	defensin, alpha 6, Paneth cell-specific	HGNC:2765
NR4A2	nuclear receptor subfamily 4, group A, member 2	HGNC:7981
EGFL6	EGF-like-domain, multiple 6	HGNC:3235
NR4A1	nuclear receptor subfamily 4, group A, member 1	HGNC:7980
CD38	CD38 molecule	HGNC:1667
SOCS3	suppressor of cytokine signaling 3	HGNC:19391
RGS1	regulator of G-protein signaling 1	HGNC:9991
FOSL1	FOS-like antigen 1	HGNC:13718
SAA4	serum amyloid A4, constitutive	HGNC:10516
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	HGNC:8724
LIPE	lipase, hormone-sensitive	HGNC:6621
MMP1	matrix metalloproteinase 1 (interstitial collagenase)	HGNC:7155
LEP	leptin	HGNC:6553
BPIL1	bactericidal/permeability-increasing protein-like 1	HGNC:16177
TUSC5	tumor suppressor candidate 5	HGNC:29592
FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	HGNC:3708
GYS2	glycogen synthase 2 (liver)	HGNC:4707
LHFPL3	lipoma HMGIC fusion partner-like 3	HGNC:6589
CXCL11	chemokine (C-X-C motif) ligand 11	HGNC:10638
ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	HGNC:680
CCL4L2	chemokine (C-C motif) ligand 4-like 2	HGNC:24066
ACVR1C	activin A receptor, type IC	HGNC:18123
NR4A3	nuclear receptor subfamily 4, group A, member 3	HGNC:7982
PLIN1	perilipin 1	HGNC:9076
OSM	oncostatin M	HGNC:8506
FABP12	fatty acid binding protein 12	HGNC:34524
SAA1	serum amyloid A1	HGNC:10513
FABP4	fatty acid binding protein 4, adipocyte	HGNC:3559

IL20	interleukin 20	HGNC:6002
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	HGNC:4709
CD69	CD69 molecule	HGNC:1694
SAA2	serum amyloid A2	HGNC:10514
ATF3	activating transcription factor 3	HGNC:785
PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1	HGNC:8872
CYR61	cysteine-rich, angiogenic inducer, 61	HGNC:2654
JAKMIP1	janus kinase and microtubule interacting protein 1	HGNC:26460
PKLR1	pyruvate kinase, liver and RBC	HGNC:9020
ALDOB	aldolase B, fructose-bisphosphate	HGNC:417
LDHC	lactate dehydrogenase C	HGNC:6544
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	HGNC:5218
HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	HGNC:3283
PDZK1	PDZ domain containing 1	HGNC:5174
SLC26A3	solute carrier family 26, member 3	HGNC:1811
FABP6	fatty acid binding protein 6, ileal	HGNC:2172
FABP7	fatty acid binding protein 7, brain	HGNC:2173
FADS1	fatty acid desaturase 1	HGNC:3992
FADS2	fatty acid desaturase 2	HGNC:9415
CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	HGNC:84735
UBP1	Ureidopropionase, beta (CN hydrolase family)	HGNC:51733
ELOVL3	Elongation of very long chain fatty acids	HGNC:83401
TREH	trehalase (brush-border membrane glycoprotein)	HGNC:11181
AMY1A	Amylase, alpha 1A (salivary)	HGNC:276
MUC7	mucin 7, secreted	HGNC:4589
APOC1	apolipoprotein C-I	HGNC:341
ACSBG1	acyl-CoA synthetase bubblegum family member 1	HGNC:23205
MUC1	mucin 1, cell surface associated	HGNC:4582
GSK3B	glycogen synthase kinase 3 beta	HGNC:2932
EGFR	epidermal growth factor receptor	HGNC:1956
ESR1	estrogen receptor 1	HGNC:2099
ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	HGNC:25
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	HGNC:1499
GAGE2C G	antigen 2C	HGNC:2574
OR52E8	olfactory receptor, family 52, subfamily E, member 8	HGNC:390079
MAPK1	mitogen-activated protein kinase 1	HGNC:5594
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	HGNC:6774
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	HGNC:4790
JUN	an proto-oncogene	HGNC:3725

HGNC: HUGO Gene Nomenclature Committee [url: http://www.genenames.org/](http://www.genenames.org/)

Table 4: up- and down- regulation of genes

		ACSL3	1.757608676
Gene ID	log2FoldChange		
A2ML1	5.232038252		
AACS	4.080550359	ACSL5	1.741815779
AADACL3	3.725566743	ACSM3	1.741500471
AADACL4	3.705855774	ACSM5	1.737979248
ABCA13	3.33791816	ACSS2	1.733440435
ABCA4	3.202673123	ACTA1	1.731120615
ABCA6	2.961209119	ACTA2	1.691612489
ABCA8	2.812579577	ACTBL2	1.686446343
ABCA9	2.760008088	ACTC1	1.673273334
ABCB5	2.568469326	ACTG2	1.672073089
ABCC11	2.501770187	ACTN1	1.659898906
ABCC4	2.413636014	ACTR6	1.655515583
ABHD12B	2.383847689	ACVR1C	1.634133301
ABHD3	2.288932795	ACVRL1	1.620276681
ABHD5	2.253846967	ACY1	1.610307087
ABLM2	2.214099057	ADAM33	1.58406277
ABLM3	2.167263213	ADAM8	1.575793381
ACAA1	2.097514835	ADAMTS15	1.574263825
ACAA2	2.089701582	ADAMTS5	1.574078143
ACAD8	2.084597545	ADAMTS7	1.550685556
ACADM	2.019198644	ADAMTSL1	1.549161629
ACADVL	1.980871868	ADAMTSL3	1.547103771
ACAP1	1.902109447	ADAMTSL5	1.529584451
ACAT2	1.852622907	ADCK1	1.508070416
ACE	1.852383074	ADCY5	1.500080295
ACE2	1.848437824	ADH1A	1.488934892
ACLY	1.843490132	ADH1B	1.479869122
ACO1	1.83798896	ADH1C	1.476996607
ACOT1	1.828371596	ADH6	1.467829493
ACOT2	1.806970784	ADHFE1	1.460316269
ACOT4	1.799871164	ADIPOQ	1.441750612
ACOT7	1.78933249	ADRA2A	1.434237726
ACOX2	1.776943169	AEBP1	1.433240506
ACP6	1.765634945	AGPAT1	1.427009839
ACPP	1.761788468	AGPAT3	1.426814356
ACSBG1	1.761560397	AGPHD1	1.423607062
ACSL1	1.760241809	AGR2	1.422523795

AGRN	1.421273275	ANXA6	1.197184453
AGTRAP	1.418689497	AOC3	1.189948198
AHSP	1.416074982	AOX1	1.188424407
AKAP12	1.412103606	APBB1IP	1.184874211
AKAP2	1.408745781	APOBEC3G	1.18093333
AKNA	1.405734349	APOC1	1.175109861
AKR1A1	1.405058571	APOD	1.167265269
ALAS1	1.391295285	APOE	1.165869476
ALAS2	1.387922866	APOL1	1.163700968
ALCAM	1.375534132	APOL3	1.163133343
ALDH1B1	1.365090643	APOL6	1.159161307
ALDH1L1	1.355041255	AQP4	1.154896716
ALDH3A1	1.354717154	AQP5	1.151012768
ALDH3B2	1.347098017	AQP7	1.144851374
ALDH6A1	1.334078453	AREG	1.144230495
ALDOB	1.325953664	AREGB	1.142744141
ALDOC	1.314987024	ARHGAP20	1.135201358
ALG1L	1.303849161	ARHGAP29	1.126299843
ALOX15B	1.300565313	ARHGAP30	1.125005561
ALPK2	1.290316723	ARHGAP6	1.118435563
AMACR	1.285915698	ARHGDIB	1.116034827
AMICA1	1.283991875	ARHGEF6	1.10244655
AMOT	1.283895871	ARL6IP1	1.098174751
AMOTL2	1.282276837	ARR3	1.097858046
AMPD1	1.263993007	ARSH	1.094469072
AMTN	1.259721834	ASAM	1.091336285
AMY1A	1.254402487	ASIP	1.076112291
AMY1B	1.253325064	ASTN1	1.072358931
AMY1C	1.248710176	ATOH1	1.071959393
ANGPT1	1.239085271	ATOH8	1.06171746
ANGPTL2	1.236238143	ATP12A	1.055952873
ANGPTL4	1.234793741	ATP1A2	1.054836184
ANGPTL5	1.219705692	ATP5C1	1.052303724
ANGPTL7	1.219381934	ATP5G3	1.048297241
ANKRD1	1.211951612	ATP5I	1.048075539
ANKRD22	1.204764559	ATP6V0A4	1.044224499
ANKS6	1.203042217	ATP6V0B	1.042247045
ANPEP	1.201433379	ATP6V0C	1.040727114
ANTXR2	1.200115748	ATP6V1C2	1.039340118
ANXA3	1.197427942	AVIL	1.038198856

AWAT1	1.035847539	C15orf48	0.899742683
AWAT2	1.027746543	C16orf73	0.897654572
B3GNT3	1.026300251	C16orf74	0.897319749
B4GALNT2	1.021337432	C16orf89	0.891418909
BAI1	1.017206262	C17orf97	0.88725701
BARX2	1.016925237	C19orf28	0.884549425
BCAN	1.012246448	C19orf46	0.883918413
BCAP29	1.011200565	C19orf71	0.88287833
BCAP31	1.0103578	C1orf104	0.877772162
BCAT1	1.004877622	C1orf113	0.876792387
BCAT2	1.002735372	C1orf122	0.869490471
BCKDHB	0.998635214	C1orf125	0.868635503
BDH1	0.996523706	C1orf158	0.866593789
BEAN1	0.99308757	C1orf162	0.856422456
BHMT2	0.990062406	C1orf51	0.85361664
BICC1	0.984397677	C1orf53	0.851849469
BIRC3	0.976297686	C1orf68	0.850683059
BLNK	0.975649143	C1orf9	0.848017236
BRI3BP	0.969430675	C1QA	0.842038447
BRP44	0.96917848	C1QB	0.841688189
BRP44L	0.961102823	C1QC	0.840617385
BSG	0.960242752	C1QTNF5	0.83930445
BST1	0.959113336	C1QTNF6	0.835742329
BST2	0.958044351	C1R	0.835366478
BTN3A1	0.950424103	C1S	0.82925104
BTN3A2	0.947981912	C2	0.828081804
BTN3A3	0.943516128	C20orf103	0.827752937
BZW1	0.942613394	C20orf24	0.82673847
C10orf129	0.940311238	C20orf3	0.825665684
C10orf57	0.931744078	C21orf33	0.825016444
C10orf58	0.931389357	C3	0.82319498
C11orf96	0.930836216	C3AR1	0.821201653
C12orf39	0.929331896	C4orf23	0.813087813
C12orf64	0.927058692	C4orf31	0.812533891
C13orf36	0.920042594	C5orf4	0.812098722
C14orf180	0.914186227	C6orf105	0.811577891
C14orf2	0.91385926	C6orf106	0.808618456
C14orf49	0.904358065	C6orf126	0.807958993
C15orf23	0.90410343	C6orf26	0.807917972
C15orf43	0.902489928	C6orf94	0.806442564

C7	0.801725925	CCNF	0.750948895
C7orf58	0.800896147	CCR1	0.749275262
C7orf68	0.798953825	CCR2	0.74901499
C9orf140	0.797269786	CCR4	0.748940725
C9orf16	0.795551973	CCR5	0.748840622
C9orf7	0.793758218	CCR7	0.747443487
CA14	0.793468014	CD163	0.746895014
CA6	0.792626914	CD1C	0.745484678
CALCB	0.791137389	CD1E	0.744287962
CALD1	0.786509848	CD2	0.744059612
CALML3	0.78380644	CD207	0.743132085
CAMK1G	0.782937966	CD209	0.739038868
CAMP	0.780273373	CD226	0.736591855
CAPN13	0.77814649	CD24	0.736216427
CAPN3	0.77638503	CD247	0.735954286
CAPN8	0.775634239	CD248	0.734122479
CARD11	0.772918944	CD27	0.733476618
CARD18	0.770869921	CD28	0.733425584
CASQ2	0.770769276	CD34	0.733371965
CASS4	0.770620159	CD36	0.733005039
CBLN1	0.765830306	CD37	0.731592379
CBLN2	0.765746887	CD38	0.730346031
CCBP2	0.764914593	CD3D	0.730323379
CCDC69	0.764870382	CD3E	0.728577927
CCDC85A	0.763278452	CD40LG	0.725829232
CCDC86	0.762945653	CD48	0.723778399
CCK	0.762709079	CD5	0.723184088
CCKBR	0.76267341	CD52	0.72168319
CCL13	0.762218024	CD53	0.718476028
CCL14	0.76179936	CD6	0.718229421
CCL15	0.761409502	CD68	0.717801714
CCL17	0.76094414	CD74	0.717400398
CCL18	0.758899798	CD84	0.717372863
CCL19	0.757671358	CD8A	0.717216953
CCL27	0.755513617	CD96	0.71571822
CCL4	0.753719824	CD97	0.712842251
CCL4L2	0.753256985	CDA	0.710635861
CCL5	0.75171897	CDH5	0.709367024
CCNC	0.751032062	CDH7	0.708961348
CCND1	0.75100013	CDK5	0.708420828

CDKL2	0.708341515	CLEC12A	0.66019268
CDKN1A	0.708063289	CLEC2A	0.659533948
CDO1	0.707175314	CLEC3B	0.659181375
CEACAM1	0.705976589	CLEC4G	0.657807469
CEACAM6	0.704684521	CLIC2	0.656902749
CECR2	0.70067378	CLIC3	0.654887307
CELF2	0.700594894	CLIC6	0.65439818
CES1	0.699640956	CLIP2	0.653848693
CFB	0.699438037	CLIP3	0.653639962
CFD	0.697056958	CLSTN3	0.652488207
CFH	0.692238866	CLU	0.651219801
CFHR1	0.691912767	CMA1	0.648360441
CFHR3	0.691771062	CMTM8	0.647054101
CGA	0.688193587	CNDP1	0.646608556
CHCHD10	0.686823982	CNDP2	0.646165968
CHGA	0.686256791	CNIH4	0.64556632
CHGB	0.6840037	CNKSR3	0.642491771
CHI3L1	0.683256591	CNN1	0.640289415
CHI3L2	0.681823307	CNPY1	0.637826241
CHIT1	0.681679494	COCH	0.637181915
CHL1	0.681431466	COL11A1	0.636839925
CHP	0.67660651	COL12A1	0.635940089
CHRD1	0.675579307	COL16A1	0.635281955
CHRD2	0.67553655	COL1A1	0.633662888
CHRNA9	0.675076329	COL1A2	0.632689827
CHST2	0.674405775	COL3A1	0.631890797
CIDEA	0.674304617	COL4A1	0.631579102
CIDEC	0.673569412	COL4A2	0.629278808
CILP	0.673553398	COL4A6	0.628472358
CILP2	0.673102173	COL5A1	0.626403674
CISH	0.67068239	COL7A1	0.622171021
CKB	0.66864368	COL8A1	0.621627606
CKMT1A	0.668581748	COMP	0.6213615
CKMT1B	0.667304308	COQ4	0.620432773
CLC	0.667280993	COQ9	0.620139929
CLCA2	0.666510809	CORO1A	0.618806539
CLDN10	0.663957279	COTL1	0.617518298
CLDN11	0.662363671	COX5A	0.617426889
CLDN5	0.661150212	COX6C	0.616145976
CLEC10A	0.660670207	COX7A2	0.615282691

COX7B	0.613751991	CUBN	0.583407172
COX7C	0.612974235	CUX2	0.582747052
COX8A	0.611463404	CXCL10	0.582537857
CP	0.610400505	CXCL11	0.581158017
CPA3	0.608812298	CXCL9	0.580570674
CPA4	0.608183636	CXCR3	0.580561381
CPB2	0.607393505	CXCR7	0.580068749
CPD	0.607164577	CYB5A	0.579131054
CPE	0.6071146	CYBB	0.577935074
CPEB4	0.606576095	CYBRD1	0.576732674
CPLX3	0.604875519	CYCS	0.575502733
CPT2	0.6046887	CYP19A1	0.57529074
CPVL	0.604269631	CYP1A1	0.57340909
CPXM1	0.602189623	CYP1A2	0.572169566
CPZ	0.600586734	CYP1B1	0.571600726
CRABP1	0.597909379	CYP26B1	0.567724157
CRAT	0.596720556	CYP27A1	0.567494882
CREG1	0.595727948	CYP27B1	0.567192991
CRISP3	0.59528462	CYP2R1	0.564830904
CRYAB	0.594419199	CYP3A4	0.563584501
CRYBB2	0.593911532	CYP4B1	0.560296992
CS	0.592384522	CYP4F2	0.558822441
CSAG3	0.591530447	CYP4F22	0.558064138
CSF1	0.591527932	CYP4F3	0.557536701
CSF1R	0.591023422	CYP4F8	0.557400907
CSN1S1	0.590746098	CYP51A1	0.556847797
CSPG4	0.590717207	CYTH4	0.556541709
CSRP2	0.58959508	DACH1	0.556495194
CST1	0.588973383	DAPK2	0.55643176
CST6	0.588296267	DBT	0.556294248
CST7	0.588167494	DCD	0.555938734
CSTB	0.587950682	DCI	0.555202823
CTAG2	0.587238503	DCT	0.554212398
CTH	0.586221894	DCXR	0.553250615
CTHRC1	0.586151017	DDC	0.553206096
CTNND2	0.585631706	DDHD1	0.552844184
CTSG	0.58554417	DDIT4	0.551724084
CTSK	0.585534422	DDO	0.551158736
CTSL2	0.584352618	DDR2	0.550486387
CTSS	0.583898886	DDX43	0.549939754

DDX60	0.549534157	DUSP16	0.519933255
DEFA6	0.548742699	DUSP4	0.517909682
DEFB132	0.547219123	DUSP5	0.517848658
DENND3	0.547156719	DUSP6	0.517792586
DES	0.546995716	EBF1	0.517730154
DGAT2	0.546570087	EBI3	0.517509195
DGAT2L6	0.545608075	EBP	0.516349706
DHCR24	0.544674381	ECH1	0.51518304
DHCR7	0.544444263	ECHDC1	0.514841211
DHRS11	0.54360883	ECHDC2	0.514547832
DHRS2	0.540802501	ECM1	0.514458624
DHRS7B	0.540744778	ECM2	0.514343092
DHRS9	0.540429524	EDA2R	0.513861922
DIO2	0.539530158	EDDM3B	0.513723775
DIRAS1	0.539329212	EFCAB4A	0.513375304
DIRAS3	0.539258665	EFEMP1	0.513258467
DKK1	0.538978494	EFNB2	0.512917839
DLD	0.538656747	EGFL6	0.512838555
DLK1	0.53703431	EGLN3	0.51225525
DMBX1	0.535852296	EGR1	0.51206884
DMRTA1	0.534608355	EGR2	0.511003459
DNAH17	0.532919317	EGR3	0.510778993
DNAH8	0.532281963	EHD2	0.510692469
DNASE1L2	0.531698368	EHF	0.510492657
DOC2B	0.529777062	EI24	0.510489591
DOCK11	0.527318535	ELANE	0.510006127
DOCK2	0.52575	ELAVL2	0.5093179
DOK2	0.5251	ELL2	0.50817644
DOPEY2	0.524154558	ELOVL1	0.507689446
DPEP1	0.524067295	ELOVL3	0.507599462
DPP4	0.523670923	ELOVL4	0.507260864
DPT	0.523544437	ELOVL5	0.506248238
DPYD	0.523378009	EMID2	0.505320796
DRAM1	0.522613629	EMILIN1	0.504268622
DSC2	0.522349227	EMILIN2	0.503644696
DSE	0.522319047	EMILIN3	0.50263856
DSG4	0.521926513	EML6	0.501499895
DTNA	0.521581818	EN2	0.500916685
DTX4	0.521179582	ENC1	0.500012065
DUSP1	0.520864957	ENDOU	0.499665741

ENG	0.497713985	FAM69C	0.467246808
ENO2	0.496499653	FAM70A	0.466978034
EOMES	0.495395643	FAM73B	0.466642696
EPB41L2	0.494925743	FAM75D1	0.463984346
EPPK1	0.49484724	FAM78A	0.463488642
ERAP1	0.494808452	FAM82A2	0.463327022
ERV3	0.493329551	FAM83A	0.463322813
ESRRA	0.492028503	FAM84A	0.463074926
ETFDH	0.490659237	FAM84B	0.463025792
ETHE1	0.490296755	FAR2	0.462953519
ETV4	0.490270215	FASN	0.461857874
EVI2B	0.489841762	FASTKD1	0.461642503
EYA4	0.489352923	FBLN2	0.461224657
F10	0.488597264	FBLN5	0.461090095
F13A1	0.487259535	FBN1	0.460820724
F3	0.48720793	FBP1	0.46071627
F9	0.48673417	FBP2	0.46043014
FA2H	0.486577314	FBXO9	0.460072274
FABP12	0.486303594	FCER2	0.458826422
FABP4	0.485898265	FCGBP	0.4578527
FABP6	0.485222561	FCGR2A	0.45729655
FABP7	0.48519999	FCGR2B	0.456578608
FABP9	0.485179665	FCGR3A	0.45471022
FADS1	0.484857177	FCGRT	0.454024904
FADS2	0.481183487	FCN1	0.452955612
FADS6	0.480742796	FDFT1	0.452776108
FAM108C1	0.479530823	FDPS	0.452041731
FAM126A	0.479034379	FEN1	0.451447394
FAM129A	0.478551739	FERMT2	0.45079544
FAM132A	0.477436416	FERMT3	0.450095285
FAM150B	0.477095654	FETUB	0.447961211
FAM176A	0.476338419	FGF16	0.447692602
FAM181A	0.474180788	FGF18	0.446672685
FAM196B	0.473964863	FGF9	0.446560585
FAM19A2	0.472973712	FGFR1	0.446465742
FAM26D	0.47129739	FGFR2	0.446452184
FAM26E	0.470000202	FHL1	0.446384972
FAM3C	0.469482303	FIBIN	0.44597033
FAM3D	0.46928969	FIGF	0.444818416
FAM46C	0.468636377	FILIP1	0.444473374

FITM2	0.443436285	GALNTL2	0.414588797
FLNA	0.443148116	GALNTL5	0.413987457
FLNC	0.442931256	GALNTL6	0.413809399
FLRT2	0.442875917	GAP43	0.413082067
FLT4	0.442724546	GAS1	0.412393081
FMNL1	0.441949503	GATA2	0.411699719
FMO2	0.439383581	GATA6	0.409777155
FMO3	0.438446633	GBP3	0.409161485
FMOD	0.437783118	GBP4	0.40823574
FOS	0.437656262	GBP6	0.406675827
FOSB	0.436782135	GCLM	0.406199678
FOSL1	0.435456258	GCNT4	0.405426509
FOXC1	0.435229184	GCSH	0.405328259
FOXQ1	0.435068041	GDA	0.402905319
FPR2	0.434717067	GDF10	0.401440696
FPR3	0.433481626	GDPD2	0.400792296
FREM1	0.432798735	GFM2	0.399650739
FRZB	0.432584717	GFRA1	0.399277856
FSTL3	0.432445979	GGPS1	0.398900983
FTL	0.430814667	GGT6	0.397232289
FUT3	0.428448779	GIMAP4	0.397046987
FXYD5	0.427778053	GJA3	0.396442895
FYN	0.426143223	GJB2	0.396112709
FZD4	0.42596125	GJB6	0.395989602
FZD5	0.42562054	GJC2	0.394744395
FZD7	0.423642522	GK	0.393439469
G0S2	0.422234972	GK5	0.393287609
G6PD	0.421332339	GLDC	0.393176377
GABBR2	0.420294908	GLIPR1	0.392739575
GABRA4	0.419568551	GLRX	0.392298676
GABRP	0.41913361	GLRX5	0.391956567
GADD45G	0.419100444	GLYAT	0.391790273
GAGE12D	0.418585219	GLYATL1	0.390655024
GAGE12G	0.418092899	GLYATL1P4	0.389167164
GAGE12I	0.418026024	GNLY	0.389113939
GAGE2B	0.417476314	GNPAT	0.388519224
GAGE2C	0.416885549	GOT1	0.387970871
GAGE2D	0.416232315	GPAM	0.387509463
GAL	0.41616708	GPBAR1	0.387015245
GALNTL1	0.415241439	GPC3	0.386701956

GPGR	0.384885424	HBA1	0.362532603
GPIHBP1	0.384362718	HBA2	0.361731395
GPR124	0.383796053	HBB	0.360550859
GPR133	0.383202367	HBD	0.360135475
GPR143	0.381926676	HBEGF	0.360107409
GPR15	0.381908315	HBG2	0.360077239
GPR174	0.381810225	HCLS1	0.360000847
GPR18	0.381390002	HEATR4	0.359508493
GPR182	0.380192444	HEPACAM	0.358167932
GPR64	0.380024147	HEPACAM2	0.357383769
GPR98	0.379606532	HEPHL1	0.35679072
GPRC5D	0.378717053	HEPN1	0.355941294
GPRIN2	0.378016339	HGD	0.355633389
GPSM3	0.376224592	HHATL	0.355423622
GPT	0.375757779	HIBCH	0.35411249
GPT2	0.375349942	HIC1	0.353743897
GRAP2	0.375167333	HINT1	0.353718189
GREB1	0.374347763	HIP1	0.353451166
GREM1	0.374001977	HIST1H1C	0.353159511
GRIN2A	0.373897381	HIST1H1D	0.352543122
GRIN3A	0.372221995	HIST1H2AE	0.352088356
GRK5	0.371629768	HIST1H2BC	0.351533058
GRM3	0.371205788	HIST1H2BK	0.351383587
GRM7	0.370099769	HIST3H2A	0.351274488
GRP	0.368889749	HK2	0.349778086
GSDMA	0.368563892	HLA-A	0.349061207
GTSF1	0.368482596	HLA-B	0.347048285
GUCY2C	0.367768843	HLA-C	0.346220033
GYG2	0.367257476	HLA-DMB	0.346138368
GYPC	0.367155053	HLA-DOA	0.346099359
GYS2	0.366803828	HLA-DPA1	0.345283862
GZMA	0.366594994	HLA-DQA1	0.344850808
GZMB	0.365585394	HLA-DQA2	0.343963545
GZMH	0.365326339	HLA-DRA	0.343793274
GZMK	0.364726135	HLA-DRB1	0.341012381
GZMM	0.364148823	HLA-DRB5	0.3410012
HACL1	0.363141825	HLA-E	0.340269137
HADH	0.362621929	HLA-F	0.339653035
HAO2	0.362609081	HLCS	0.339327294
HAPLN1	0.362562741	HMCN2	0.338340285

HMGB3	0.338126355	IGFL2	-0.316021513
HMGCL	0.338035254	IGFL4	-0.316638145
HMGCR	0.336684476	IGJ	-0.319191271
HMGCS1	0.334634902	IGLL5	-0.319294922
HOMER1	0.333365411	IGLON5	-0.321538601
HPGDS	0.331206161	IGSF10	-0.32374151
HPSE2	0.330593941	IGSF6	-0.32412571
HRASLS5	0.330425547	IKZF1	-0.325523477
HRSP12	0.330210898	IKZF3	-0.327145557
HSD11B1	0.330077469	IL10RA	-0.32780564
HSD11B2	0.328295015	IL15RA	-0.329459037
HSD17B11	0.328286358	IL17D	-0.32959268
HSD17B13	0.328201223	IL1B	-0.330397817
HSD17B2	0.327136911	IL1F5	-0.331656538
HSD3B1	0.32553856	IL1F7	-0.332343867
HSD3B2	0.324191227	IL2RG	-0.333512614
HSPA12A	0.324023642	IL32	-0.337044685
HSPB6	0.323967547	IL33	-0.337543924
HSPB7	0.323844248	IL7R	-0.3402628
HSPE1	0.323333539	IL8	-0.340327434
HSPG2	0.322286825	ILDR1	-0.344833085
HTRA3	0.322013216	INHBB	-0.345793364
HYAL1	0.321623895	INMT	-0.346780353
ID2	0.321248741	INPPL1	-0.347810097
ID3	0.32121773	INSIG1	-0.348758707
IDH1	0.319935235	INSM1	-0.349648393
IDH2	0.318706745	IQCI	-0.350708871
IDI1	0.315251532	IQSEC3	-0.351774633
IER3	0.314342282	IRF1	-0.352437557
IFI27	0.310739952	IRF8	-0.354239737
IFI44L	0.308630452	IRGM	-0.354786194
IFIT2	0.306903229	IRX6	-0.354863011
IFIT3	0.306597217	ISLR	-0.356012151
IFITM1	0.288684024	ISM1	-0.356364283
IFITM3	-0.300679949	ISOC1	-0.356612572
IFNG	-0.306736602	ITGA1	-0.357737902
IFRD1	-0.309907523	ITGA2	-0.358686744
IGF1	-0.31122826	ITGA7	-0.35885742
IGF2	-0.311737198	ITGA8	-0.359303654
IGFBP3	-0.313895641	ITGAL	-0.359561236

ITGAM	-0.360274694	KRT20	-0.396530359
ITGB1BP1	-0.361124559	KRT25	-0.397452929
ITGB2	-0.362379255	KRT26	-0.399757999
ITIH5	-0.362861158	KRT27	-0.400126125
ITK	-0.364220441	KRT28	-0.401030923
ITSN1	-0.364603478	KRT31	-0.402427006
IVD	-0.364874994	KRT32	-0.403200561
IYD	-0.367247619	KRT33A	-0.403652835
JAM3	-0.369137152	KRT33B	-0.404109387
JPH2	-0.36915775	KRT34	-0.405025997
KANK2	-0.36939919	KRT35	-0.406442519
KCNA3	-0.369814629	KRT36	-0.407149843
KCNA6	-0.370700895	KRT38	-0.40718969
KCNB1	-0.372800404	KRT39	-0.409800723
KCNH5	-0.373558632	KRT4	-0.410615619
KCNIP2	-0.374188703	KRT40	-0.411781704
KCNIP3	-0.37554618	KRT6A	-0.413538794
KCNJ13	-0.375904647	KRT6B	-0.415093538
KCNJ15	-0.376715272	KRT6C	-0.415339343
KCNK2	-0.377005302	KRT71	-0.415595423
KCNMA1	-0.377366219	KRT72	-0.415633737
KCNMB1	-0.378737683	KRT73	-0.417054693
KDELC2	-0.380063597	KRT74	-0.417810039
KIAA0513	-0.380251395	KRT75	-0.418723877
KIAA0754	-0.38043491	KRT79	-0.418809139
KIAA1191	-0.380825884	KRT81	-0.418869716
KIF1A	-0.381197718	KRT82	-0.41909923
KIF3C	-0.383830723	KRT83	-0.420227024
KIRREL	-0.383840228	KRT84	-0.420443314
KLHDC8B	-0.384186674	KRT85	-0.420571265
KLHL31	-0.384530502	KRT86	-0.421084266
KLK10	-0.386465555	KRT9	-0.421204889
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KLK6	-0.389841088	KRTAP1-5	-0.422353098
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LDLR	-0.509358508	LYG2	-0.550622286
LEP	-0.509546106	LYRM5	-0.553750184
LEPR	-0.512238623	LYZ	-0.553908798
LETM1	-0.512551133	LZTS1	-0.55470368
LGALS9	-0.513575251	MAF	-0.555326479
LGI3	-0.514039127	MAGEA11	-0.560324601
LGR5	-0.514482089	MAGEB2	-0.561237931
LHFP	-0.515549919	MAN1A1	-0.564424533
LHFPL4	-0.515645851	MAN2B2	-0.564616419
LHX2	-0.517205628	MANEAL	-0.568102524
LHX3	-0.51886187	MAOB	-0.569761253
LILRB5	-0.519507453	MAP1B	-0.57111945
LIMCH1	-0.520351478	MAPK8IP2	-0.573871012
LIPE	-0.523394371	MARCKSL1	-0.574963966
LIPG	-0.523716319	MARCO	-0.575413522
LIPH	-0.524508068	MAT1A	-0.576230552
LIPK	-0.524701057	MBOAT2	-0.578483541
LMO3	-0.525923847	MC5R	-0.578631006
LMOD1	-0.527767234	MCAM	-0.578789415
LOX	-0.529750106	MCCC1	-0.581881171
LPCAT3	-0.530850216	MCCC2	-0.581966797
LPHN3	-0.532483446	ME1	-0.583729688
LPIN1	-0.535930759	MECR	-0.584619372
LPL	-0.535974399	MEF2A	-0.584700412
LPO	-0.539960832	MEGF11	-0.584921065
LRG1	-0.540227863	MERTK	-0.586178861
LRIT2	-0.540659866	METTL7B	-0.587425188
LRP1	-0.541122408	MFAP3L	-0.588407811
LRRC10B	-0.541382981	MFAP4	-0.588595975
LRRC31	-0.541908609	MFAP5	-0.58896597
LRRC32	-0.542449599	MFGE8	-0.589276627
LRRN4CL	-0.544401271	MGLL	-0.590090765
LTB	-0.545811456	MGP	-0.593019469
LTBP2	-0.546255227	MGST1	-0.5931126
LTBP3	-0.546520759	MKX	-0.594489105
LTF	-0.546576967	MLANA	-0.598565645
LUM	-0.547037791	MMD	-0.600014427
LY6E	-0.547871644	MME	-0.600332202
LY6G6D	-0.548587941	MMP28	-0.600345509
LY9	-0.548592091	MMP7	-0.600647859

MMP9	-0.602399345	MYL9	-0.64852348
MMRN1	-0.603841554	MYO1F	-0.653656081
MNDA	-0.603900561	MYO1G	-0.655947427
MOCOS	-0.604251074	MYOCD	-0.656003739
MOGAT1	-0.604699311	MYOM2	-0.656204738
MOGAT2	-0.605613414	MYOZ2	-0.657402926
MORN2	-0.605797707	NAALAD2	-0.658531502
MPEG1	-0.606068102	NADSYN1	-0.65914615
MRC1	-0.606250609	NAMPT	-0.663321221
MRC1L1	-0.60934354	NCKAP1L	-0.66395007
MRPL13	-0.611878842	NDRG1	-0.665366494
MRPL14	-0.613933735	NDUFA4	-0.667554244
MRPS25	-0.613995035	NDUFA4L2	-0.667734019
MRV11	-0.614302775	NDUFC2	-0.66933108
MS4A1	-0.615988158	NDUFS5	-0.670809021
MS4A18	-0.617064793	NEFH	-0.671330604
MS4A4A	-0.623456154	NEFL	-0.67286048
MS4A6A	-0.623584643	NEGR1	-0.673876365
MS4A7	-0.624896318	NETO1	-0.681627045
MSMB	-0.626182891	NETO2	-0.681765683
MSR1	-0.626658615	NEXN	-0.689608187
MTCH2	-0.62705467	NFKBIZ	-0.690630636
MTOR	-0.628236911	NID1	-0.691279966
MUC1	-0.629292281	NIT2	-0.691320912
MUC15	-0.629668792	NKG7	-0.691603556
MUC21	-0.630097959	NLRP10	-0.694640544
MUC7	-0.630707817	NOP16	-0.696609698
MUCL1	-0.632281702	NOTCH1	-0.700702492
MUMIL1	-0.632890347	NOVA1	-0.703190588
MVD	-0.63377999	NOX4	-0.705313267
MVK	-0.634350771	NPC1	-0.707841851
MX1	-0.637154959	NPL	-0.709858759
MX2	-0.640063673	NPR1	-0.710007842
MXRA7	-0.641897514	NPR2	-0.711393968
MXRA8	-0.642027129	NQO2	-0.714002827
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MYH3	-0.645671444	NSDHL	-0.72289418
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NTM	-0.724714231	PCK1	-0.798762701
NTN1	-0.726146775	PCK2	-0.80093061
NTRK2	-0.72724064	PCOLCE2	-0.805749221
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OAS1	-0.74252223	PCTP	-0.815880263
OAS2	-0.744908106	PCYT2	-0.815967921
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OC90	-0.748786894	PDCD1LG2	-0.819107555
OCA2	-0.749872404	PDE2A	-0.819209688
ODZ3	-0.753954128	PDE3B	-0.819462683
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OLFML3	-0.758876338	PDGFC	-0.824566198
OLIG3	-0.761588941	PDGFD	-0.825600768
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OR7E24	-0.763566491	PDGFRB	-0.827548745
OSGIN2	-0.768662816	PDHA1	-0.827581041
OTUB2	-0.769525642	PDHX	-0.830580639
OXCT2	-0.770343029	PDLIM3	-0.831618564
P2RY12	-0.772886519	PDZD4	-0.832261007
P2RY4	-0.774171979	PDZK1	-0.833857225
PADI3	-0.775142684	PDZRN4	-0.835885008
PADI4	-0.776070731	PEBP4	-0.836770014
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PHLDB1	-0.861641022	PNPLA5	-0.949827267
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PHYHIP	-0.86487347	PODXL2	-0.950993074
PII5	-0.865029734	PON3	-0.953720157
PII6	-0.865665115	POPDC2	-0.958332824
PID1	-0.866498848	POR	-0.962594839
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PLA2G2A	-0.876605146	PPBP	-0.966890036
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PLA2G7	-0.881039596	PPM1K	-0.970342274
PLA2R1	-0.883520743	PPP1R12B	-0.97072505
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PLIN1	-0.897514794	PPT2	-0.981991149
PLIN2	-0.898322981	PRAME	-0.982312375
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PLXDC1	-0.915580511	PRELP	-1.003532216
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PNLDC1	-0.937171756	PRRT4	-1.031008711
PNLIPRP2	-0.937889074	PRSS22	-1.032236383
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PNMAL1	-0.946545491	PRSS8	-1.033578955
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SERPING1	-1.378730149	SLC26A3	-1.547375232
SETBP1	-1.383530305	SLC26A6	-1.548584857
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SLC5A6	-1.694868645	SPRR2A	-1.984424997
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SYT7	-2.246464548	TM4SF1	-2.554078171
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TACC1	-2.262090835	TMC5	-2.597892642
TACR2	-2.269897864	TMC8	-2.601271973
TAGLN	-2.282062492	TMCC3	-2.612083339
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TAP1	-2.289726386	TMED5	-2.62446575
TAS1R3	-2.294200626	TMEM132C	-2.631317468
TBX5	-2.296211382	TMEM135	-2.658803942
TCHH	-2.297991423	TMEM164	-2.66469741
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TF	-2.330864878	TMEM56	-2.758633885
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TNS1	-2.945317659	UBIAD1	-3.568701272
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TPSAB1	-3.066487578	UGT3A2	-3.684967762
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TRIM58	-3.181998773	VIP	-3.79667408
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TRIML2	-3.271088667	VLDLR	-3.815181583
TRIO	-3.29291105	VNN1	-3.834888027
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TST	-3.393068288	VWF	-3.917152093
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TUSC5	-3.455257937	WFDC6	-3.961114641
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TYR	-3.480735135	WNT4	-4.020110524
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XPNPEP2	-4.107938592
XYLB	-4.177052766
ZBED2	-4.205448209
ZC3H12A	-4.239150084
ZCCHC24	-4.392112936
ZEB1	-4.427362372
ZFHX3	-4.485302641
ZFHX4	-4.492516599
ZFPM2	-4.502949665
ZG16B	-4.554145212
ZIC1	-4.592714118
ZIC4	-4.833821498
ZNF117	-4.856367277
ZNF254	-4.971443263
ZNF385B	-5.057326146
ZNF43	-5.186763686
ZNF493	-5.587177539
ZNF703	-5.657126133
ZNF80	-5.722284476
ZNF831	-6.216622384
ZP1	-6.537478789

Table 5: List of TOP 35 gene signatures/regulatory factors controlling the expression of skin-aging-related genes in various genetic networks

Symbol	Name	HGNC ID
IL6	interleukin 6 (interferon, beta 2)	HGNC:6018
CSF3	colony stimulating factor 3 (granulocyte)	HGNC:2438
IFNG	interferon, gamma	HGNC:5438
IL8	interleukin 8	HGNC:6025
CXCL2	chemokine (C-X-C motif) ligand 2	HGNC:4603
CXCL9	chemokine (C-X-C motif) ligand 9	HGNC:7098
CXCL10	chemokine (C-X-C motif) ligand 10	HGNC:10637
	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	HGNC:4602
CXCL1		
NR4A1	nuclear receptor subfamily 4, group A, member 1	HGNC:7980
SOCS3	suppressor of cytokine signaling 3	HGNC:19391
SAA4	serum amyloid A4, constitutive	HGNC:10516
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	HGNC:8724
LIPE	lipase, hormone-sensitive	HGNC:6621
LEP	leptin	HGNC:6553
CXCL11	chemokine (C-X-C motif) ligand 11	HGNC:10638
CCL4L2	chemokine (C-C motif) ligand 4-like 2	HGNC:24066
OSM	oncostatin M	HGNC:8506
SAA1	serum amyloid A1	HGNC:10513
FABP4	fatty acid binding protein 4, adipocyte	HGNC:3559
IL20	interleukin 20	HGNC:6002
	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	HGNC:4709
GZMB		
CD69	CD69 molecule	HGNC:1694
SAA2	serum amyloid A2	HGNC:10514
LDHC	lactate dehydrogenase C	HGNC:6544
FABP6	fatty acid binding protein 6, ileal	HGNC:2172
FABP7	fatty acid binding protein 7, brain	HGNC:2173
MUC7	mucin 7, secreted	HGNC:4589
MUC1	mucin 1, cell surface associated	HGNC:4582
SOAT1	sterol O-acyltransferase 1	HGNC:6646
CTNNA1	catenin (cadherin-associated protein), beta 1, 88kDa	HGNC:1499
GAGE2C G	antigen 2C	HGNC:2574
OR52E8	olfactory receptor, family 52, subfamily E, member 8	HGNC:390079
MAPK1	mitogen-activated protein kinase 1	HGNC:5594
	signal transducer and activator of transcription 3 (acute-phase response factor)	HGNC:6774
STAT3		
	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	HGNC:4790
NFKB1		

Table 6: A reduced List of TOP 23 gene signatures controlling the expression of skin-aging-related genes in genetic networks

Symbol	Name
IL - family	interleukin
CSF3	colony stimulating factor 3 (granulocyte)
IFNG	interferon, gamma
CXCL - family	chemokine (C-X-C motif) ligand
NR4A1	nuclear receptor subfamily 4, group A, member 1
SOCS3	suppressor of cytokine signaling 3
SAA4	serum amyloid A4, constitutive
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)
LIPE	lipase, hormone-sensitive
LEP	leptin
CCL4L2	chemokine (C-C motif) ligand 4-like 2
OSM	oncostatin M
SAA1	serum amyloid A1
FABP4	fatty acid binding protein 4, adipocyte
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
CD69	CD69 molecule
SAA2	serum amyloid A2
LDHC	lactate dehydrogenase C
FABP6	fatty acid binding protein 6, ileal
FABP7	fatty acid binding protein 7, brain
MUC7	mucin 7, secreted
MUC1	mucin 1, cell surface associated
SOAT1	sterol O-acyltransferase 1

Claims

1. A method for reducing or reversing the visible signs of skin ageing, the method comprising up-regulating or down-regulating a specific pathway selected from the group consisting of the pathways listed in Table 2.
2. The method of claim 1 further comprising up-regulating or down-regulating the interaction between different but connected and interacting biosynthetic pathways listed in Table 2.
3. The method of claim 2 comprising up-regulating or down-regulating the interaction between two or more of the following regulators: STAT1, CEBPD, MAF, RXRA, NR2B1, NR1H3, TFE3, NFATC1, RBL, SMAD3, and NR2F1.
4. The method of claim 1 further comprising recalibrating the expression of two or more pathways expressed in human skin tissue the expression of which has changed as a result of aging wherein the pathways are selected from the IL-6 pathway, cholesterol biosynthesis, and proximal lipid metabolism pathway.
5. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that alter the expression of genes/pathways involved in the biosynthesis or degradation of IL-6 or cholesterol.
6. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that decrease or increase the expression of one or more genes selected from the genes listed Table 5.
7. A method for identifying a compound that will up-regulate or down-regulate the activity of one or more metabolic pathways associated with ageing, the method comprising: (i) providing a skin tissue sample, (ii) measuring the expression of a selected plurality of aging-related genes selected from the group consisting of the genes of Table 4, (iii) exposing skin tissue to a test compound, (iv) re-measuring the expression of the genes, (v) identifying a compound that changes the expression of the selected plurality of genes wherein the change in expression is at least two-fold.
8. The method of claim 7 wherein the plurality of aging-related genes comprise at least the genes encoding interleukin, colony stimulating factor 3, and interferon gamma.

9. The method of claim 7 wherein the plurality of aging-related genes comprise at least the genes encoding IL6, BARX1, CFS3, IFNG, CSAG3, PRHOXNB, IP8, LPA, CXCL2, FOXD4L6, OR1L8, IGLL5, and CXCL9.
10. The method of claim 7 wherein the plurality of aging-related genes comprise at least the genes encoding interleukin 6, colony stimulating factor 3, interferon gamma, interleukin 8, chemokine (C-X-C motif) ligand 2, chemokine (C-X-C motif) ligand 9, chemokine (C-X-C motif) ligand 10, and chemokine (C-X-C motif) ligand 1.
11. The method of claim 7 wherein the plurality of aging-related genes are shown in table 4 to be differentially expressed by a factor of at least $fc(\log_2)$ of at least 4.
12. The method of claim 8 wherein the plurality of aging-related genes are shown in table 4 to be differentially expressed by a factor of at least $fc(\log_2)$ of at least 4.
13. The method of claim 9 wherein the plurality of aging-related genes are shown in table 4 to be differentially expressed by a factor of at least $fc(\log_2)$ of at least 4.
14. The method of claim 10 wherein the plurality of aging-related genes are shown in table 4 to be differentially expressed by a factor of at least $fc(\log_2)$ of at least 4.
15. A method for identifying new compounds that alter aging-related gene expression profiles and signatures, the method comprising: (i) providing a skin tissue sample, (ii) measuring the expression of a selected plurality of aging-related genes selected from Table 1, (iii) exposing skin tissue to a test compound, (iv) re-measuring the expression of the genes, (v) identifying a compound that changes the expression of the selected plurality of genes wherein the change in expression is at least two-fold.
16. A method for delaying, ceasing or reversing signs of skin aging and risk of skin cancer by recalibrating the expression of genes, genetic networks, and cellular pathways in the human skin, primarily in the dermis, that have changed as a result of the chronological aging process wherein the genes are selected from the group consisting of specific genes are listed in Table 1, cellular pathways, and other functional categories are listed in Table 2.
17. The method of claim 16 wherein the genes recalibrated comprise one or more genes from Table 1 or genes selected from the group consisting of the genes of the functional categories listed in Table 2 and Table 3.

18. The method of claim 16 wherein the genetic networks or cellular pathways recalibrated comprise one or more selected from the groups consisting of the genetic networks or cellular pathways listed in Table 2 and Table 3.
19. A method for reducing the signs of aging of the skin the method comprising applying to the skin a compound having recalibrating potency according to the method of claim 15.
20. A method for reducing the signs of aging of the skin the method comprising topically applying to the skin a compound "A" having anti-aging properties and further comprising orally administering a compound "B" having anti-aging properties.
21. The method of claim 20 wherein compounds A and B, when administered contemporaneously, provide a synergistic effects on expression of genes of Table 1 or groups of Table 2 and Table 3.
22. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that alter the expression of genes involved in the biosynthesis or degradation of a substance selected from the groups listed in Table 2.
23. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that increase the expression of genes involved in the biosynthesis of type I or type II collagen.
24. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that recalibrate the genes for enzymes listed in Table 1.
25. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that decrease production of MMPs.
26. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that reduce the rate of degradation of the extracellular matrix proteins in the dermis.
27. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of fibroblasts present in the dermis.

28. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of collagen fibrils or elastin fibers in the dermis.

29. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the number of collagen fibrils or elastin fibers in the dermis.

30. A composition for reducing the signs of aging of the skin, the composition comprising one or more substances that maintain or increase the 3-dimensional extracellular matrix structure of collagen, elastin, and other extracellular matrix proteins in the dermis,

31. A composition for reducing the signs of aging of the skin the composition comprising combinations of natural compounds including phytochemicals, nutrients, minerals, and vitamins.

32. A method for reversing skin ageing by targeting a genetic regulatory module selected from the group consisting of IL-6, IL-8, IFNG, and CSF3.

33. A method for delaying, ceasing or reversing signs of skin aging and risk of skin cancer by recalibrating the expression of genes, genetic networks, and cellular pathways in the human skin, primarily in the dermis, that have changed as a result of the chronological aging process wherein the genes are selected from the group consisting of specific genes are listed in Table 1, cellular pathways, and other functional categories are listed in Table 7, and a list of gene signatures controlling the expression of aging-related genes in various gene networks in Table 3, the method comprising applying to the skin one of more natural compounds selected from the group consisting of: Acerola, Vitamin C, Algae Extract, Alginate, Allantoin, Aloe Vera, Apricot Seed Oil, Arbutin, Arnica Extract, Ascorbic Acid, Avocado Oil, Barley Extract, and Bearberry Extract.

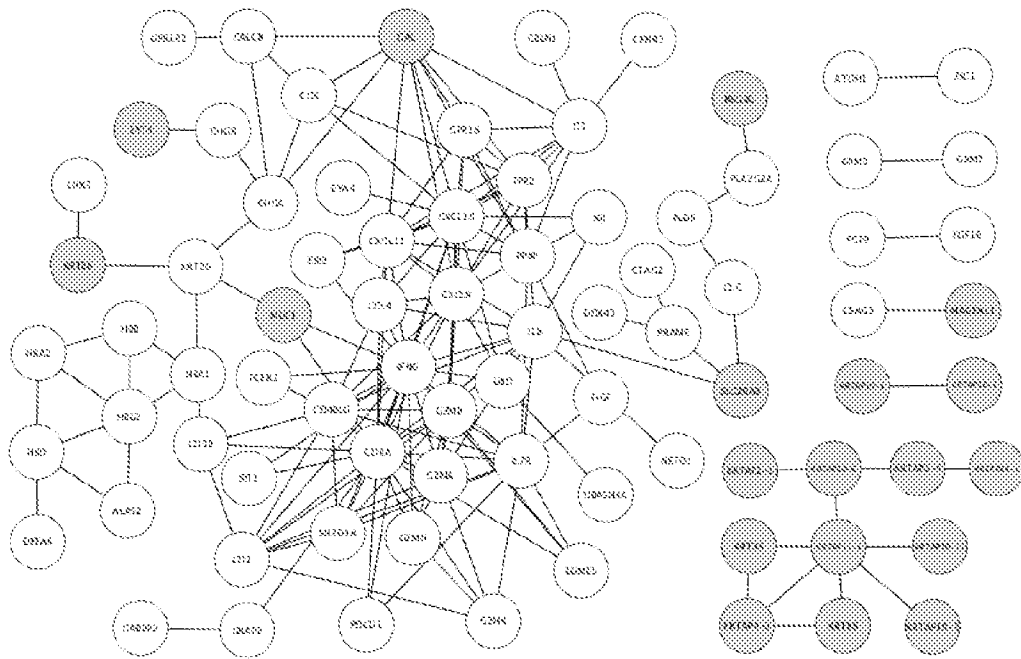


Figure 1. A genetic regulatory module responsible for a single gene signature in one aging-related network.

White = up-regulated, grey = down-regulated). This network which created using only top 100 up & down regulated genes illustrates the complexity of the aging process. This network is connected to other networks involved in skin aging as well as to aging in other tissues. It is the gene signatures in different but connected and interacting networks that determine the aging process. It is the genetic regulatory module (e.g., IL-8, IFNG) that will serve as targets for drugs and natural compounds to reverse skin aging. It is believed that the loss of connections between networks reduces the ability of the cell to make coordinated responses to external stimuli and thus the cause of disease and aging.

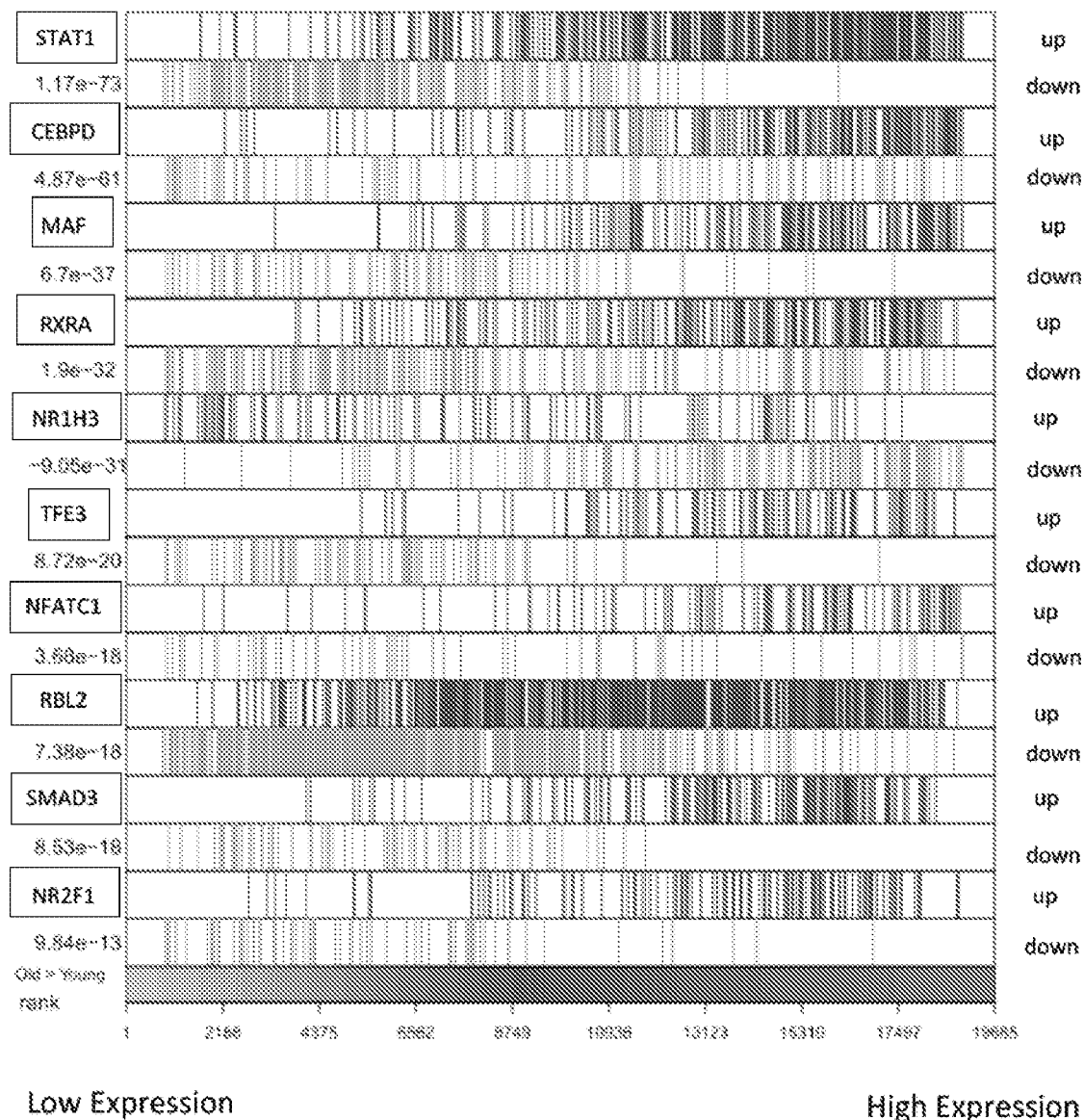


Figure 2. Master regulators correlate with the differential gene expression signatures between old and young cohorts. Low expression level in old cohorts is at the left of the bottom row which shows expression levels gradually increased to the right. The regulator gene symbols are listed at left side of the graph and are inside boxes. Each regulator has two rows of up and down regulated genes that are positioned according to their gene expression levels in the data sets. The P-value of the correlations between the gene expression signature of overall datasets (bottom row) and individual regulation patterns are listed right below each gene symbol. The lower the P-value, the high possibility the regulator has to be responsible for the signature changes.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/036226

A. CLASSIFICATION OF SUBJECT MATTER		<i>A61K 33/00 (2006.01)</i> <i>A61K 35/00 (2006.01)</i> <i>A61K 36/00 (2006.01)</i> <i>A61K 38/00 (2006.01)</i> <i>A61K 45/00 (2006.01)</i> <i>A61P 17/00 (2006.01)</i>										
According to International Patent Classification (IPC) or to both national classification and IPC												
B. FIELDS SEARCHED												
Minimum documentation searched (classification system followed by classification symbols)												
A61K 33/00, 35/00, 36/00, 38/00, 45/00, A61P 17/00												
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched												
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)												
ARIPO, ATPO AUPO, CH, DPMA DWPI, EBI, EPO, Esp@cenet, France, GBPO, Google, KR, NCBI, OAPI, PAJ, USPTO, WIPO, BD neopublikovannie zayavki												
C. DOCUMENTS CONSIDERED TO BE RELEVANT												
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.										
X	US 20070031356 A1 (PETRA BUCHWALD HUNZIKER et al.) 08.02.2007, claims 9, 10, 19, 27, table 1	1-3, 5, 6, 16-18, 22, 32										
X	WO 2010/062762 A2 (DERMACHIP INC.) 03.06.2010, tables 1, 3, claims 1, 2, 4	1-2, 16-18, 32										
X	KNOTT A. et al. Natural Arctium lappa fruit extract improves the clinical signs of aging skin. J Cosmet Dermatol, 2008 Dec; 7(4):281-9, abstract, [on-line], [retrieved on 04.06.2012], PubMed, PMID: 19146605	1, 5, 6, 16-18, 22, 32										
☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.												
* Special categories of cited documents: <table border="0"> <tr> <td>“A” document defining the general state of the art which is not considered to be of particular relevance</td> <td>“T” later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>“E” earlier document but published on or after the international filing date</td> <td>“X” document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>“L” document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>“Y” document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>“O” document referring to an oral disclosure, use, exhibition or other means</td> <td>“&” document member of the same patent family</td> </tr> <tr> <td>“P” document published prior to the international filing date but later than the priority date claimed</td> <td></td> </tr> </table>			“A” document defining the general state of the art which is not considered to be of particular relevance	“T” later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	“E” earlier document but published on or after the international filing date	“X” document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	“L” document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	“Y” document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	“O” document referring to an oral disclosure, use, exhibition or other means	“&” document member of the same patent family	“P” document published prior to the international filing date but later than the priority date claimed	
“A” document defining the general state of the art which is not considered to be of particular relevance	“T” later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention											
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“O” document referring to an oral disclosure, use, exhibition or other means	“&” document member of the same patent family											
“P” document published prior to the international filing date but later than the priority date claimed												
Date of the actual completion of the international search		Date of mailing of the international search report										
04 June 2012 (04.06.2012)		23 August 2012 (23.08.2012)										
Name and mailing address of the ISA/ FIPS Russia, 123995, Moscow, G-59, GSP-5, Berezhkovskaya nab., 30-1		Authorized officer M. Kuptsova										
Facsimile No. +7 (499) 243-33-37		Telephone No. (495)531-65-15										

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/036226

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2010/0316720 A1 (MILBELLE AG) 16.12.2010, claims, table 5	1, 5, 6, 16-18, 22, 32, 33
X	US 2006/0275294 A1 (OSEMWOTA SOTA OMOIGUI) 07.12.2006, abstract, claims 97, 106, 107, 125, p. 34	1, 4, 16-18, 32
X	KR 2009046504 A (DONG H S et al.) 11.05.2009	5, 6, 22
X	US 7485315 B2 (L'OREAL) 03.02.2009, claims 1, 4, 5	33
X	US 2010/0247563 A1 (MARY KAY INC.) 30.09.2010, abstract, claims 1, 11	33
X	US 2006/0251608 A1 (RWACHSBERG HOLDINGS INC.) 09.11.2006, claims 1, 6	33
X	EP 1593372 A1 (L'OREAL) 09.11.2005, claims 2, 13	33
X	WO 2006/137100 A2 (MEDCARE S.R.L.) 28.12.2006, abstract, claims 1, 16, 33, 68	33
X	JP 2007230916 A (MARUZEN PHARMA) 03.09.2007, abstract	33
X	US 2002/0025303 A1 (ALAIN E FRUCTUS et al.) 28.02.2002, claims 1	33

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/036226

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see extra sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-6, 16-18, 22, 32, 33

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

Continuation of Box III

According to Rule 13 of the Regulations under the PCT the claimed invention does not meet the requirement of unity of invention *a priori*, therefore independent claims 1, 5, 6, 7, 15, 16, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33 form several groups of inventions, which are not so linked as to form a single general inventive concept.

The special technical feature of independent claims 1, 5, 6, 16, 22, 32, 33 is regulating IL-6 gene, which is a member of signaling pathway of immune system. This special technical feature is absent in claims 7, 15, 19, 20, 23, 24, 25, 26, 27, 28, 29, 30.

Tables 1, 4, 5, comprise IL-8 gene, which is also a gene of signaling pathway of immune system. Regulating said gene is provided only in claims 1, 6, 7, 15, 16, 19, 24, 32 and 33.

Tables 1 and 4 comprise collagen types 1 and 2 genes. Regulating said genes is provided only in claims 7, 15, 16, 19, 23, 24 and 33.

Tables 1 and 4 comprise MMPs genes. Regulating said genes is provided only in claims 7, 15, 16, 19, 24, 25 and 33.

Tables 1 and 4 comprise IFGN gene. Regulating said gene is provided only in claims 6, 7, 15, 16, 19, 24, 32 and 33.

There is no the same or corresponding special technical feature between compositions of claims 20, 26, 27, 30, 31 and claims 28, 29 or between them and the subject-matter of the above-mentioned claims.

Hence, claims comprise 11 groups of inventions, namely:

1 invention – claims 1, 5, 6, 16, 22, 32, 33, for which the special technical feature is regulating IL-6 gene;

2 invention – claims 1, 6, 7, 15, 16, 19, 24, 32, 33, for which the special technical feature is regulating IL-8 gene;

3 invention – claims 7, 15, 16, 19, 23, 24, 33, for which the special technical feature is regulating collagen types 1 and 2 genes;

4 invention – claims 7, 15, 16, 19, 24, 25, 33, for which the special technical feature is regulating MMPs genes;

5 invention – claims 6, 7, 15, 16, 19, 24, 32 and 33, for which the special technical feature is regulating IFGN gene;

6 invention – claim 20;

7 invention – claim 26;

8 invention – claim 27;

9 invention – identical claims 28 and 29;

10 invention – claim 30;

11 inventions – claim 31.