On-line Table: Differentially expressed genes in aneurysm tissue compared with those in control tissue

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
AADAC	Arylacetamide deacetylase	Positive regulation of triglyceride catabolic process	4.46	1.33E-05	2.60E-04	Up-regulated
ABCA6	ATP-binding cassette, subfamily A (ABC1), member 6	Integral component of membrane	3.79	9.15E-14	8.88E-12	Up-regulated
ABCC3	ATP-binding cassette, subfamily C (CFTR/MRP), member 3	ATPase activity, coupled to transmembrane movement of substances	6.63	1.21E-10	7.33E-09	Up-regulated
ABI3	*ABI* family, member 3	Peptidyl-tyrosine phosphorylation	6.47	2.47E-05	4.56E-04	Up-regulated
ACKR1	Atypical chemokine receptor 1 (Duffy blood group)	G-protein–coupled receptor signaling pathway	3.80	7.95E-10	4.18E-08	Up-regulated
ACKR2	Atypical chemokine receptor 2	G-protein–coupled receptor signaling pathway	0.42	3.29E-04	4.41E-03	Down-regulated
ACSM1	Acyl-CoA synthetase medium-chain family member 1	Energy derivation by oxidation of organic compounds	9.87	1.70E-08	6.52E-07	Up-regulated
ACTC1	Actin, α, cardiac muscle 1	Negative regulation of apoptotic process	0.30	7.96E-06	1.65E-04	Down-regulated
ACTG2	Actin, γ2, smooth muscle, enteric	Blood microparticle	0.29	1.61E-16	2.36E-14	Down-regulated
ADAM33	ADAM domain 33	Integral component of membrane	0.23	9.74E-09	3.95E-07	Down-regulated
ADAM8	ADAM domain 8	Positive regulation of tumor necrosis factor (ligand) superfamily member 11 production	4.69	2.93E-04	4.01E-03	Up-regulated
ADAMTS18	ADAM with thrombospondin type 1 motif 18	Negative regulation of platelet aggregation	6.27	4.37E-06	9.85E-05	Up-regulated
ADAMTS20	ADAM with thrombospondin type 1 motif 20	Positive regulation of melanocyte differentiation	0.18	1.50E-04	2.29E-03	Down-regulated
ADAMTS3	ADAM with thrombospondin type 1 motif 3	Positive regulation of vascular endothelial growth factor signaling pathway	3.14	1.67E-06	4.23E-05	Up-regulated
ADAMTS6	ADAM with thrombospondin type 1 motif 6	Proteinaceous extracellular matrix	0.48	1.25E-04	1.96E-03	Down-regulated
ADAMTS8	ADAM with thrombospondin type 1 motif 8	Low-affinity phosphate transmembrane transporter activity	0.40	4.42E-07	1.31E-05	Down-regulated
ADAMTSL1	ADAMTS-like 1	Proteinaceous extracellular matrix	3.13	7.12E-09	3.01E-07	Up-regulated
ADAP2	ArfGAP with dual PH domains 2	Phosphatidylinositol-3,4,5-trisphosphate binding	10.88	5.26E-14	5.21E-12	Up-regulated
ADCYAP1R1	Adenylate cyclase-activating polypeptide 1 (pituitary) receptor type I	Transmembrane receptor protein tyrosine kinase signaling pathway	2.12	4.27E-05	7.45E-04	Up-regulated
ADORA3	Adenosine A3 receptor	Positive regulation of phosphatidylinositol 3-kinase signaling	12.30	1.95E-07	6.14E-06	Up-regulated
ADRA1A	Adrenoceptor α1A	Negative regulation of heart rate involved in baroreceptor response to increased systemic arterial blood pressure	0.39	1.79E-05	3.39E-04	Down-regulated
AIF1	Allograft inflammatory factor 1	Positive regulation of G_1/S transition of mitotic cell cycle	12.40	1.81E-22	6.08E-20	Up-regulated
ALDH1A2	Aldehyde dehydrogenase 1 family, member A2	3-Chloroallyl aldehyde dehydrogenase activity	2.46	2.46E-10	1.42E-08	Up-regulated
ALOX5	Arachidonate 5-lipoxygenase	Leukotriene production involved in inflammatory response	5.22	7.56E-15	9.12E-13	Up-regulated
AMOTL2	Angiomotin-like 2	Identical protein binding	2.63	1.14E-12	9.56E-11	Up-regulated
AMPH	Amphiphysin	Synaptic vesicle endocytosis	0.45	3.64E-05	6.44E-04	Down-regulated
ANGPT4	Angiopoietin 4	Activation of transmembrane receptor protein tyrosine kinase activity	2.37	5.52E-05	9.32E-04	Up-regulated
ANKRD1	Ankyrin repeat domain 1 (cardiac muscle)	Positive regulation of DNA damage response, signal transduction by p53 class mediator	206.36	1.13E-18	2.48E-16	Up-regulated
ANO3	Anoctamin 3	Intracellular calcium-activated chloride channel activity	9.30	4.58E-07	1.35E-05	Up-regulated
AOAH	Acyloxyacyl hydrolase (neutrophil)	Negative regulation of inflammatory response	12.42	7.97E-07	2.21E-05	Up-regulated
APBA2	Amyloid β (A4) precursor protein-binding, family A, member 2	In utero embryonic development	3.77	4.55E-06	1.02E-04	Up-regulated
APLNR	Apelin receptor	G-protein–coupled receptor signaling pathway	3.53	1.40E-05	2.72E-04	Up-regulated
APOBEC1	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	Negative regulation of methylation-dependent chromatin silencing	8.02	4.81E-07	1.41E-05	Up-regulated
ARG1	Arginase 1	Cellular response to transforming growth factor β stimulus	12.10	1.70E-05	3.25E-04	Up-regulated
ARHGAP18	Rho GTPase-activating protein 18	Regulation of small GTPase-mediated signal transduction	2.79	5.98E-07	1.71E-05	Up-regulated
ARHGAP30	Rho GTPase-activating protein 30	Regulation of small GTPase-mediated signal transduction	6.44	8.32E-06	1.70E-04	Up-regulated
ARHGDIB	Rho GDP-dissociation inhibitor (GDI) β	Regulation of small GTPase-mediated signal transduction	2.27	5.35E-04	6.67E-03	Up-regulated
ARHGEF26	Rho guanine nucleotide exchange factor (GEF) 26	ρ-Guanyl-nucleotide exchange factor activity	0.46	6.31E-06	1.37E-04	Down-regulated
ARNTL2	Aryl hydrocarbon receptor nuclear translocator-like 2	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity	15.63	3.60E-21	1.09E-18	Up-regulated
ASGR1	Asialoglycoprotein receptor 1	Cellular response to extracellular stimulus	16.83	3.43E-24	1.54E-21	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
ATF3	Activating transcription factor 3	RNA polymerase II transcription regulatory region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	0.43	1.06E-06	2.85E-05	Down-regulated
ATP10B	ATPase, class V, type 10B	Phospholipid-translocating ATPase activity	0.12	5.81E-05	9.67E-04	Down-regulated
ATP1A2	ATPase, Na^+/K^+ transporting, $\alpha 2$ polypeptide	Regulation of respiratory gaseous exchange by neurologic system process	0.46	3.44E-07	1.04E-05	Down-regulated
ATP2A3	ATPase, Ca^{++} transporting, ubiquitous	Platelet-dense tubular network membrane	0.37	1.07E-12	9.10E-11	Down-regulated
ATP6V0D2	ATPase, H^+ transporting, lysosomal 38 kDa, V0 subunit d2	Vacuolar proton-transporting V-type ATPase complex	6.09	4.10E-05	7.16E-04	Up-regulated
ATP8B4	ATPase, class I, type 8B, member 4	Phospholipid-translocating ATPase activity	6.21	8.22E-06	1.69E-04	Up-regulated
BAG3	BCL2-associated athanogene 3	Extrinsic apoptotic signaling pathway via death-domain receptors	0.50	1.33E-06	3.49E-05	Down-regulated
BASP1	Brain-abundant, membrane-attached signal protein 1	Positive regulation of metanephric ureteric bud development	4.18	6.71E-08	2.36E-06	Up-regulated
BATF	Basic leucine zipper transcription factor, ATF-like	DNA damage response, signal transduction by p53 class mediator	11.20	1.40E-04	2.15E-03	Up-regulated
BCHE	Butyrylcholinesterase	Negative regulation of synaptic transmission	0.23	2.09E-12	1.73E-10	Down-regulated
BHLHE22	Basic helix-loop-helix family, member e22	Sequence-specific DNA binding RNA polymerase II transcription factor activity	3.21	6.64E-04	7.97E-03	Up-regulated
BIN2	Bridging integrator 2	Phagocytosis, engulfment	6.63	4.30E-05	7.47E-04	Up-regulated
BIRC3	Baculoviral IAP repeat containing 3	Regulation of nucleotide-binding oligomerization domain containing signaling pathway	2.18	7.96E-04	9.39E-03	Up-regulated
BLNK	B-cell linker	Transmembrane receptor protein tyrosine kinase signaling pathway	14.87	3.80E-08	1.38E-06	Up-regulated
BMPR1B	Bone morphogenetic protein receptor, type IB	Positive regulation of extrinsic apoptotic signaling pathway via death-domain receptors	3.03	7.27E-08	2.54E-06	Up-regulated
BMX	BMX nonreceptor tyrosine kinase	Cellular component disassembly involved in execution phase of apoptosis	0.46	2.41E-04	3.43E-03	Down-regulated
BNIPL	BCL2/adenovirus E1B 19 kDa interacting protein-like	Negative regulation of cell proliferation	9.55	1.92E-06	4.75E-05	Up-regulated
BOC	BOC cell adhesion associated, oncogene regulated	Positive regulation of muscle cell differentiation	2.46	2.82E-10	1.61E-08	Up-regulated
BTK	Bruton agammaglobulinemia tyrosine kinase	Positive regulation of NF-κB transcription factor activity	7.30	9.06E-07	2.47E-05	Up-regulated
BVES	Blood vessel epicardial substance	Substrate adhesion-dependent cell spreading	0.34	1.20E-07	4.02E-06	Down-regulated
C11orf16	Chromosome 11 open reading frame 16	—	7.33	2.48E-04	3.51E-03	Up-regulated
C1orf110	Chromosome 1 open reading frame 110	—	2.35	1.16E-04	1.84E-03	Up-regulated
C1orf162	Chromosome 1 open reading frame 162	Integral component of membrane	60.67	2.05E-12	1.71E-10	Up-regulated
C1orf54	Chromosome 1 open reading frame 54	Extracellular region	3.66	5.77E-08	2.04E-06	Up-regulated
C1QA	Complement component 1, q subcomponent, A chain	Complement activation, classic pathway	4.20	1.24E-15	1.64E-13	Up-regulated
C1QB	Complement component 1, q subcomponent, B chain	Complement activation, classic pathway	5.21	1.19E-11	8.50E-10	Up-regulated
C1QC	Complement component 1, q subcomponent, C chain	Negative regulation of granulocyte differentiation	5.26	3.69E-14	3.87E-12	Up-regulated
C1QTNF3	C1q and tumor necrosis factor–related protein 3	Negative regulation of monocyte chemotactic protein 1 production	0.49	2.70E-06	6.41E-05	Down-regulated
C1QTNF9	C1q and tumor necrosis factor–related protein 9	Extracellular region	2.65	8.54E-04	9.97E-03	Up-regulated
C1RL	Complement component 1, r subcomponent-like	Complement activation, classic pathway	2.01	3.41E-06	7.88E-05	Up-regulated
C1S	Complement component 1, s subcomponent	Complement activation, classic pathway	2.01	3.39E-06	7.84E-05	Up-regulated
C2orf40	Chromosome 2 open reading frame 40	Cyclin catabolic process	4.57	5.21E-09	2.29E-07	Up-regulated
C3AR1	Complement component 3a receptor 1	Positive regulation vascular endothelial growth factor production	7.28	3.84E-09	1.74E-07	Up-regulated
C8orf34	Chromosome 8 open reading frame 34	—	13.83	1.13E-09	5.81E-08	Up-regulated
CA3	Carbonic anhydrase III, muscle specific	Small molecule metabolic process	0.20	5.66E-05	9.52E-04	Down-regulated
CA9	Carbonic anhydrase IX	Regulation of transcription from RNA polymerase II promoter in response to hypoxia	0.15	1.63E-16	2.36E-14	Down-regulated
CABLES1	Cdk5 and Abl enzyme substrate 1	Cyclin-dependent protein serine/threonine kinase regulator activity	2.23	4.16E-04	5.38E-03	Up-regulated
CADM1	Cell adhesion molecule 1	Positive regulation of natural killer cell–mediated cytotoxicity	2.26	2.76E-04	3.84E-03	Up-regulated
CADM3	Cell adhesion molecule 3	Protein homodimerization activity	0.37	1.92E-09	9.28E-08	Down-regulated
CAPG	Capping protein (actin filament), gelsolin-like	Barbed-end actin filament capping	2.17	9.52E-06	1.92E-04	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
CASP1	Caspase 1, apoptosis-related cysteine peptidase	Nucleotide-binding domain, leucine-rich repeat containing receptor signaling pathway	11.56	1.02E-05	2.05E-04	Up-regulated
CASP8	Caspase 8, apoptosis-related cysteine peptidase	Positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	4.88	7.45E-05	1.22E-03	Up-regulated
CASQ2	Calsequestrin 2 (cardiac muscle)	Regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	0.21	3.21E-15	3.93E-13	Down-regulated
CCBE1	Collagen and calcium binding EGF domains 1	Positive regulation of vascular endothelial growth factor signaling pathway	4.05	6.12E-07	1.74E-05	Up-regulated
CCDC102B	Coiled-coil domain containing 102B	—	3.75	2.20E-06	5.33E-05	Up-regulated
CCDC126	Coiled-coil domain containing 126	α-1,6-Mannosylglycoprotein 6-β-*N*-acetylglucosaminyltransferase activity	2.03	1.30E-04	2.03E-03	Up-regulated
CCL13	Chemokine (C-C motif) ligand 13	Cellular calcium ion homeostasis	8.67	6.98E-06	1.48E-04	Up-regulated
CCL14	Chemokine (C-C motif) ligand 14	Positive regulation of cell proliferation	2.43	1.30E-06	3.45E-05	Up-regulated
CCL19	Chemokine (C-C motif) ligand 19	Positive regulation of dendritic cell antigen processing and presentation	7.04	1.37E-05	2.67E-04	Up-regulated
CCL2	Chemokine (C-C motif) ligand 2	G-protein–coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	5.38	1.58E-10	9.30E-09	Up-regulated
CCL21	Chemokine (C-C motif) ligand 21	Positive regulation of dendritic cell antigen processing and presentation	8.19	2.35E-50	7.39E-47	Up-regulated
CCR1	Chemokine (C-C motif) receptor 1	G-protein–coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	32.11	8.32E-14	8.16E-12	Up-regulated
CCR2	Chemokine (C-C motif) receptor 2	Positive regulation of immune complex clearance by monocytes and macrophages	13.14	8.62E-07	2.36E-05	Up-regulated
CCR5	Chemokine (C-C motif) receptor 5 (gene/pseudogene)	Release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	24.10	9.71E-12	7.09E-10	Up-regulated
CD14	CD14 molecule	Positive regulation of tumor necrosis factor production	9.22	1.39E-17	2.33E-15	Up-regulated
CD163	CD163 molecule	Integral component of plasma membrane	2.73	2.43E-07	7.48E-06	Up-regulated
CD180	CD180 molecule	Positive regulation of lipopolysaccharide-mediated signaling pathway	13.45	2.66E-11	1.80E-09	Up-regulated
CD1C	CD1c molecule	T-cell activation involved in immune response	7.40	3.69E-04	4.90E-03	Up-regulated
CD200	CD200 molecule	Integral component of plasma membrane	2.30	2.80E-09	1.31E-07	Up-regulated
CD300LG	CD300 molecule-like family member g	Extracellular vesicular exosome	2.82	3.48E-05	6.21E-04	Up-regulated
CD34	CD34 molecule	Positive regulation of glial cell line–derived neurotrophic factor secretion	0.44	2.10E-08	7.96E-07	Down-regulated
CD48	CD48 molecule	Anchored component of plasma membrane	8.55	3.47E-08	1.27E-06	Up-regulated
CD53	CD53 molecule	Positive regulation of myoblast fusion	5.49	1.65E-06	4.20E-05	Up-regulated
CD68	CD68 molecule	Cellular response to organic substance	4.46	8.29E-09	3.43E-07	Up-regulated
CD74	CD74 molecule, MHC class II invariant chain	Negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	39.56	7.67E-18	1.36E-15	Up-regulated
CD80	CD80 molecule	Positive regulation of granulocyte-macrophage colony-stimulating factor biosynthetic process	15.17	1.39E-16	2.07E-14	Up-regulated
CD83	CD83 molecule	Positive regulation of CD4-positive, α-β T-cell differentiation	13.66	4.69E-09	2.08E-07	Up-regulated
CD84	CD84 molecule	Integral component of plasma membrane	11.44	1.40E-14	1.59E-12	Up-regulated
CD86	CD86 molecule	Positive regulation of interleukin-2 biosynthetic process	12.86	8.56E-11	5.24E-09	Up-regulated
CD93	CD93 molecule	Cytoplasmic membrane-bounded vesicle	2.67	2.17E-10	1.26E-08	Up-regulated
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)	Corticospinal tract morphogenesis	4.57	1.32E-27	8.90E-25	Up-regulated
CDH19	Cadherin 19, type 2	Integral component of membrane	0.36	1.73E-04	2.59E-03	Down-regulated
CDH2	Cadherin 2, type 1, N-cadherin (neuronal)	Negative regulation of canonical Wnt signaling pathway	6.97	4.46E-12	3.50E-10	Up-regulated
CDH20	Cadherin 20, type 2	Integral component of membrane	3.71	4.35E-05	7.51E-04	Up-regulated
CDH3	Cadherin 3, type 1, P-cadherin (placental)	Positive regulation of insulin-like growth factor receptor signaling pathway	9.70	8.01E-05	1.30E-03	Up-regulated
CDH6	Cadherin 6, type 2, K-cadherin (fetal kidney)	Cell–cell junction organization	3.83	3.09E-06	7.21E-05	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
CDH8	Cadherin 8, type 2	Synaptic transmission, glutamatergic	0.34	2.55E-04	3.59E-03	Down-regulated
CDK15	Cyclin-dependent kinase 15	Cyclin-dependent protein serine/threonine kinase activity	0.36	6.08E-04	7.47E-03	Down-regulated
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	DNA-damage response, signal transduction by p53 class mediator resulting in cell-cycle arrest	3.78	3.89E-14	4.02E-12	Up-regulated
CDKN2A	Cyclin-dependent kinase inhibitor 2A	Positive regulation of DNA-damage response, signal transduction by p53 class mediator	54.19	1.81E-20	4.88E-18	Up-regulated
CDKN2B	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	Positive regulation of transforming growth factor β receptor signaling pathway	4.87	5.35E-10	2.91E-08	Up-regulated
CELSR2	Cadherin, EGF LAG seven-pass G-type receptor 2	Neural plate anterior/posterior regionalization	0.49	2.92E-04	4.01E-03	Down-regulated
CFH	Complement factor H	Complement activation, alternative pathway	6.34	2.41E-26	1.33E-23	Up-regulated
CFP	Complement factor properdin	Complement activation, alternative pathway	5.33	4.32E-06	9.76E-05	Up-regulated
CH25H	Cholesterol 25-hydroxylase	Cholesterol 25-hydroxylase activity	4.67	7.58E-11	4.73E-09	Up-regulated
CHAC1	ChaC, cation transport regulator homolog 1 (*Escherichia coli*)	Intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	4.45	3.16E-05	5.70E-04	Up-regulated
CHI3L1	Chitinase 3-like 1 (cartilage glycoprotein 39)	Positive regulation of peptidyl-threonine phosphorylation	7.97	5.85E-13	5.10E-11	Up-regulated
CHI3L2	Chitinase 3-like 2	Carbohydrate metabolic process	55.72	1.47E-07	4.77E-06	Up-regulated
CHIT1	Chitinase 1 (chitotriosidase)	Polysaccharide catabolic process	24.30	2.13E-11	1.47E-09	Up-regulated
CHMP4C	Charged multivesicular body protein 4C	Positive regulation of viral release from host cell	0.34	1.35E-04	2.09E-03	Down-regulated
CHN2	Chimerin 2	Regulation of small GTPase-mediated signal transduction	3.47	7.42E-05	1.22E-03	Up-regulated
CHP2	Calcineurin-like EF-hand protein 2	Positive regulation of transcription from RNA polymerase II promoter	2.64	2.30E-05	4.29E-04	Up-regulated
CHRDL2	Chordin-like 2	Cartilage development	6.46	1.29E-05	2.54E-04	Up-regulated
CLEC12A	C-type lectin domain family 12, member A	Integral component of membrane	20.14	7.62E-10	4.05E-08	Up-regulated
CLEC4A	C-type lectin domain family 4, member A	Transmembrane signaling receptor activity	8.82	1.34E-07	4.39E-06	Up-regulated
CLEC4D	C-type lectin domain family 4, member D	Integral component of membrane	8.99	5.31E-08	1.89E-06	Up-regulated
CLEC4E	C-type lectin domain family 4, member E	Positive regulation of cytokine secretion	21.53	5.81E-13	5.10E-11	Up-regulated
CLEC7A	C-type lectin domain family 7, member A	Cell surface pattern recognition receptor signaling pathway	13.53	1.16E-17	2.00E-15	Up-regulated
CMTM1	CKLF-like MARVEL transmembrane domain containing 1	Integral component of membrane	3.59	5.48E-04	6.82E-03	Up-regulated
COL10A1	Collagen, type X, α1	Proteinaceous extracellular matrix	163.48	3.66E-26	1.91E-23	Up-regulated
COL11A1	Collagen, type XI, α1	Detection of mechanical stimulus involved in sensory perception of sound	29.94	7.85E-45	1.48E-41	Up-regulated
COL12A1	Collagen, type XII, α1	Extracellular matrix structural constituent conferring tensile strength	3.28	1.11E-16	1.68E-14	Up-regulated
COL1A1	Collagen, type I, α1	Cartilage development involved in endochondral bone morphogenesis	2.09	1.04E-04	1.66E-03	Up-regulated
COL1A2	Collagen, type I, α2	Transforming growth factor β receptor signaling pathway	2.05	4.84E-05	8.26E-04	Up-regulated
COL23A1	Collagen, type XXIII, α1	Extracellular matrix organization	8.57	1.65E-23	6.49E-21	Up-regulated
COL25A1	Collagen, type XXV, α1	Integral component of plasma membrane	2.30	7.73E-04	9.15E-03	Up-regulated
COL28A1	Collagen, type XXVIII, α1	Negative regulation of endopeptidase activity	0.29	6.27E-06	1.36E-04	Down-regulated
COL4A3	Collagen, type IV, α3 (Goodpasture antigen)	Activation of cysteine-type endopeptidase activity involved in apoptotic process	3.97	1.21E-11	8.56E-10	Up-regulated
COL4A4	Collagen, type IV, α4	Extracellular matrix structural constituent	5.86	8.57E-15	1.01E-12	Up-regulated
COL8A1	Collagen, type VIII, α1	Positive regulation of cell-substrate adhesion	2.26	1.36E-07	4.45E-06	Up-regulated
COLQ	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	Acetylcholine catabolic process in synaptic cleft	3.56	1.09E-04	1.74E-03	Up-regulated
CORO1A	Coronin, actin-binding protein 1A	Homeostasis of number of cells within a tissue	10.29	4.18E-06	9.53E-05	Up-regulated
CP	Ceruloplasmin (ferroxidase)	Extracellular vesicular exosome	4.48	1.54E-24	7.24E-22	Up-regulated
CREB5	cAMP-responsive element-binding protein 5	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	0.49	2.71E-04	3.78E-03	Down-regulated
CRTAC1	Cartilage acidic protein 1	Proteinaceous extracellular matrix	2.20	4.42E-05	7.60E-04	Up-regulated
CSF1R	Colony-stimulating factor 1 receptor	Cellular response to macrophage colony-stimulating factor stimulus	5.68	9.51E-30	7.47E-27	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
CSF2RB	Colony-stimulating factor 2 receptor, β, low affinity (granulocyte-macrophage)	Granulocyte-macrophage colony-stimulating factor receptor complex	4.70	3.84E-07	1.15E-05	Up-regulated
CTBS	Chitobiase, di-*N*-acetyl-	Oligosaccharide catabolic process	2.10	2.31E-05	4.30E-04	Up-regulated
CTGF	Connective tissue growth factor	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	4.44	2.47E-19	5.96E-17	Up-regulated
CTSB	Cathepsin B	Proteolysis involved in cellular protein catabolic process	2.43	1.39E-08	5.40E-07	Up-regulated
CTSE	Cathepsin E	Antigen processing and presentation of exogenous peptide antigen via MHC class II	3.77	6.26E-04	7.65E-03	Up-regulated
CTSK	Cathepsin K	Proteolysis involved in cellular protein catabolic process	2.04	1.33E-06	3.49E-05	Up-regulated
CTSS	Cathepsin S	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP independent	5.95	4.79E-21	1.41E-18	Up-regulated
CX3CR1	Chemokine (C-X3-C motif) receptor 1	Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	61.52	1.33E-23	5.45E-21	Up-regulated
CXCL16	Chemokine (C-X-C motif) ligand 16	Low-density lipoprotein receptor activity	2.31	2.63E-06	6.27E-05	Up-regulated
CXCL6	Chemokine (C-X-C motif) ligand 6	Defense response to bacterium	5.29	5.34E-06	1.18E-04	Up-regulated
CXCL8	Chemokine (C-X-C motif) ligand 8	Regulation of single-stranded viral RNA replication via double-stranded DNA intermediate	12.37	4.62E-07	1.36E-05	Up-regulated
CXCR4	Chemokine (C-X-C motif) receptor 4	Positive regulation of cytosolic calcium ion concentration	7.52	2.09E-04	3.03E-03	Up-regulated
CXorf21	Chromosome X open reading frame 21	—	9.42	1.23E-05	2.44E-04	Up-regulated
CXorf36	Chromosome X open reading frame 36	Extracellular region	3.63	9.52E-06	1.92E-04	Up-regulated
CYBB	Cytochrome b-245, β polypeptide	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP dependent	3.99	2.08E-10	1.21E-08	Up-regulated
CYP26A1	Cytochrome P450, family 26, subfamily A, polypeptide 1	Negative regulation of retinoic acid receptor signaling pathway	86.52	3.30E-14	3.50E-12	Up-regulated
CYR61	Cysteine-rich, angiogenic inducer 61	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	3.18	3.15E-15	3.90E-13	Up-regulated
CYSLTR1	Cysteinyl leukotriene receptor 1	Positive regulation of cytosolic calcium ion concentration	4.17	7.78E-04	9.19E-03	Up-regulated
DAAM2	Dishevelled-associated activator of morphogenesis 2	Actin cytoskeleton organization	2.47	1.38E-10	8.29E-09	Up-regulated
DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (*Drosophila*)	Positive regulation of transforming growth factor β receptor signaling pathway	2.44	3.78E-11	2.51E-09	Up-regulated
DAPK2	Death-associated protein kinase 2	Regulation of intrinsic apoptotic signaling pathway	3.41	3.45E-08	1.26E-06	Up-regulated
DAPL1	Death-associated protein-like 1	Cell differentiation	2.25	6.95E-04	8.32E-03	Up-regulated
DAPP1	Dual adaptor of phosphotyrosine and 3-phosphoinositides	Phosphatidylinositol-3,4,5-trisphosphate binding	9.11	7.08E-06	1.49E-04	Up-regulated
DCBLD2	Discoidin, CUB and LCCL domain containing 2	Intracellular receptor signaling pathway	0.44	1.24E-07	4.12E-06	Down-regulated
DCHS2	Dachsous cadherin-related 2	Integral component of membrane	0.35	2.79E-04	3.86E-03	Down-regulated
DDAH1	Dimethylarginine dimethylaminohydrolase 1	Positive regulation of nitric-oxide biosynthetic process	2.24	7.24E-05	1.19E-03	Up-regulated
DES	Desmin	Structural constituent of cytoskeleton	0.35	2.39E-12	1.96E-10	Down-regulated
DHRS7C	Dehydrogenase/reductase (SDR family) member 7C	Regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	8.28	1.43E-06	3.73E-05	Up-regulated
DKK3	Dickkopf Wnt signaling pathway inhibitor 3	Negative regulation of aldosterone biosynthetic process	3.18	7.14E-12	5.42E-10	Up-regulated
DLG2	Discs, large homolog 2 (Drosophila)	Negative regulation of phosphatase activity	0.14	3.48E-12	2.76E-10	Down-regulated
DLX1	Distal-less homeobox 1	Regulation of transcription from RNA polymerase II promoter involved in forebrain neuron fate commitment	3.28	3.75E-05	6.61E-04	Up-regulated
DLX5	Distal-less homeobox 5	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	19.90	3.84E-36	4.52E-33	Up-regulated
DLX6	Distal-less homeobox 6	Transcription regulatory region sequence-specific DNA binding	30.78	1.10E-19	2.79E-17	Up-regulated
DNAH11	Dynein, axonemal, heavy-chain 11	Cilium or flagellum-dependent cell motility	0.09	1.52E-18	3.25E-16	Down-regulated
DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	Negative regulation of transcription from RNA polymerase II promoter	0.50	2.12E-07	6.65E-06	Down-regulated
DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	Post-Golgi vesicle-mediated transport	2.13	2.33E-04	3.32E-03	Up-regulated
DNER	Delta/notch-like EGF repeat containing	Transmembrane signaling receptor activity	0.27	6.92E-09	2.94E-07	Down-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
DOCK2	Dedicator of cytokinesis 2	Myeloid dendritic cell activation involved in immune response	5.33	1.16E-04	1.84E-03	Up-regulated
DOK3	Docking protein 3	Ras protein signal transduction	14.55	5.03E-10	2.76E-08	Up-regulated
DPYSL3	Dihydropyrimidinase-like 3	Hydrolase activity, acting on carbon—nitrogen (but not peptide) bonds, in cyclic amides	2.14	3.65E-09	1.67E-07	Up-regulated
DUSP6	Dual-specificity phosphatase 6	Regulation of fibroblast growth factor receptor signaling pathway	2.61	1.27E-07	4.21E-06	Up-regulated
DYNC1I1	Dynein, cytoplasmic 1, intermediate-chain 1	Antigen processing and presentation of exogenous peptide antigen via MHC class II	3.31	2.60E-06	6.21E-05	Up-regulated
EGR1	Early growth response 1	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	2.85	4.04E-11	2.66E-09	Up-regulated
EMCN	Endomucin	Integral component of membrane	4.16	1.44E-14	1.62E-12	Up-regulated
EMP1	Epithelial membrane protein 1	Multicellular organismal development	2.36	1.01E-08	4.06E-07	Up-regulated
ENPEP	Glutamyl aminopeptidase (aminopeptidase A)	Regulation of systemic arterial blood pressure by renin–angiotensin	5.79	2.40E-18	4.75E-16	Up-regulated
ENPP2	Ectonucleotide pyrophosphatase/ phosphodiesterase 2	Alkyl glycerophosphoethanolamine phosphodiesterase activity	4.18	1.29E-21	4.06E-19	Up-regulated
ENPP3	Ectonucleotide pyrophosphatase/ phosphodiesterase 3	Phosphate-containing compound metabolic process	3.97	3.35E-06	7.76E-05	Up-regulated
EPHA5	Eph receptor A5	Regulation of insulin secretion involved in cellular response to glucose stimulus	0.36	1.20E-05	2.39E-04	Down-regulated
EPSTI1	Epithelial stromal interaction 1 (breast)	—	3.79	6.98E-04	8.34E-03	Up-regulated
ESM1	Endothelial cell-specific molecule 1	Positive regulation of hepatocyte growth factor receptor signaling pathway	0.45	2.16E-05	4.06E-04	Down-regulated
ETV5	ETS variant 5	RNA polymerase II transcription regulatory region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	2.05	1.78E-05	3.37E-04	Up-regulated
EVI2A	Ecotropic viral integration site 2A	Transmembrane signaling receptor activity	9.44	6.68E-12	5.11E-10	Up-regulated
EVI2B	Ecotropic viral integration site 2B	Integral component of plasma membrane	14.52	5.18E-06	1.15E-04	Up-regulated
EXOC3L1	Exocyst complex component 3-like 1	Peptide hormone secretion	5.87	1.50E-06	3.87E-05	Up-regulated
F5	Coagulation factor V (proaccelerin, labile factor)	Serine-type endopeptidase activity	4.24	1.69E-09	8.31E-08	Up-regulated
FABP5	Fatty acid–binding protein 5 (psoriasis associated)	Phosphatidylcholine biosynthetic process	2.66	1.65E-06	4.20E-05	Up-regulated
FAM13C	Family with sequence similarity 13, member C	—	0.20	3.30E-14	3.50E-12	Down-regulated
FAM43A	Family with sequence similarity 43, member A	—	2.07	6.27E-04	7.65E-03	Up-regulated
FAM46A	Family with sequence similarity 46, member A	Regulation of blood coagulation	2.08	3.85E-08	1.40E-06	Up-regulated
FAM46B	Family with sequence similarity 46, member B	—	0.45	5.78E-09	2.52E-07	Down-regulated
FAM83D	Family with sequence similarity 83, member D	Mitotic nuclear division	0.08	1.17E-17	2.00E-15	Down-regulated
FAR2	Fatty acyl CoA reductase 2	Fatty-acyl-CoA reductase (alcohol-forming) activity	0.27	1.56E-04	2.36E-03	Down-regulated
FBLN7	Fibulin 7	Proteinaceous extracellular matrix	5.86	5.88E-31	5.03E-28	Up-regulated
FBN2	Fibrillin 2	Positive regulation of osteoblast differentiation	6.43	1.52E-04	2.31E-03	Up-regulated
FCER1A	Fc fragment of IgE, high-affinity I, receptor for α polypeptide	Positive regulation of granulocyte-macrophage colony-stimulating factor biosynthetic process	5.57	2.26E-04	3.23E-03	Up-regulated
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP dependent	11.13	1.06E-22	3.69E-20	Up-regulated
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	Fc-γ receptor signaling pathway involved in phagocytosis	5.14	4.97E-20	1.30E-17	Up-regulated
FGD2	FYVE, RhoGEF and PH domain containing 2	Regulation of small GTPase-mediated signal transduction	18.24	1.95E-09	9.37E-08	Up-regulated
FGF1	Fibroblast growth factor 1 (acidic)	Positive regulation of transcription from RNA polymerase II promoter	5.08	7.70E-23	2.79E-20	Up-regulated
FGFR4	Fibroblast growth factor receptor 4	Fibroblast growth factor–activated receptor activity	2.49	1.88E-05	3.55E-04	Up-regulated
FHL1	Four and a half LIM domains 1	Regulation of potassium ion transmembrane transporter activity	0.44	2.13E-07	6.65E-06	Down-regulated
FHL2	Four and a half LIM domains 2	Negative regulation of transcription from RNA polymerase II promoter	4.23	3.18E-22	1.03E-19	Up-regulated
FHOD3	Formin homology 2 domain containing 3	Negative regulation of actin filament polymerization	0.24	2.88E-16	4.11E-14	Down-regulated
FLNC	Filamin C, γ	Cytoskeletal protein binding	0.45	2.89E-07	8.78E-06	Down-regulated
FMNL3	Formin-like 3	GTPase-activating protein binding	2.79	3.69E-11	2.47E-09	Up-regulated
FN1	Fibronectin 1	Endoplasmic reticulum–Golgi intermediate compartment	2.80	3.30E-09	1.53E-07	Up-regulated
FOLR2	Folate receptor 2 (fetal)	Anchored component of external side of plasma membrane	4.44	2.72E-10	1.56E-08	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
FOS	FBJ murine osteosarcoma viral oncogene homolog	Regulation of sequence-specific DNA-binding transcription factor activity	2.66	2.11E-06	5.16E-05	Up-regulated
FST	Follistatin	Negative regulation of transcription from RNA polymerase II promoter	5.23	2.54E-25	1.26E-22	Up-regulated
FYB	FYN-binding protein	NLS-bearing protein import into nucleus	7.84	5.02E-05	8.55E-04	Up-regulated
GADD45A	Growth arrest and DNA-damage inducible, α	Regulation of cyclin-dependent protein serine/threonine kinase activity	2.11	8.01E-08	2.75E-06	Up-regulated
GAREM	GRB2 associated, regulator of MAPK1	Cellular response to EGF stimulus	0.48	4.92E-04	6.18E-03	Down-regulated
GAS2L2	Growth arrest-specific 2-like 2	Negative regulation of microtubule depolymerization	0.22	1.46E-04	2.24E-03	Down-regulated
GCNT1	Glucosaminyl (*N*-acetyl) transferase 1, core 2	β-1,3-Galactosyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase activity	4.46	6.44E-04	7.81E-03	Up-regulated
GDF6	Growth-differentiation factor 6	Positive regulation of pathway-restricted SMAD protein phosphorylation	3.30	3.21E-04	4.34E-03	Up-regulated
GGH	γ-Glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	γ-Glutamyl-peptidase activity	3.99	1.90E-06	4.73E-05	Up-regulated
GLB1	Galactosidase, β1	Glycosaminoglycan catabolic process	2.84	1.78E-13	1.66E-11	Up-regulated
GLDN	Gliomedin	Protein binding involved in heterotypic cell–cell adhesion	11.50	3.83E-18	7.07E-16	Up-regulated
GLP2R	Glucagon-like peptide 2 receptor	Adenylate cyclase-modulating G-protein–coupled receptor signaling pathway	17.27	7.00E-11	4.39E-09	Up-regulated
GMFG	Glia maturation factor, γ	Negative regulation of protein kinase activity	7.59	3.41E-05	6.13E-04	Up-regulated
GNAO1	Guanine nucleotide-binding protein (G protein), α-activating activity polypeptide O	Adenylate cyclase-modulating G-protein–coupled receptor signaling pathway	0.32	4.31E-09	1.92E-07	Down-regulated
GNG2	Guanine nucleotide-binding protein (G protein), γ2	Adenylate cyclase-activating dopamine receptor signaling pathway	3.18	6.50E-05	1.08E-03	Up-regulated
GNGT2	Guanine nucleotide-binding protein (G protein), γ-transducing activity polypeptide 2	G-protein–coupled receptor signaling pathway	4.22	4.35E-05	7.51E-04	Up-regulated
GPNMB	Glycoprotein (transmembrane) nmb	Negative regulation of cell proliferation	4.26	4.65E-08	1.66E-06	Up-regulated
GPR183	G-protein–coupled receptor 183	Mature B-cell differentiation involved in immune response	9.42	9.95E-09	4.02E-07	Up-regulated
GPR34	G-protein–coupled receptor 34	G-protein–coupled receptor signaling pathway	8.01	1.59E-18	3.34E-16	Up-regulated
GPR65	G-protein–coupled receptor 65	Positive regulation of cAMP biosynthetic process	19.44	2.00E-06	4.94E-05	Up-regulated
GPR97	G-protein–coupled receptor 97	G-protein–coupled receptor activity	7.16	6.86E-10	3.67E-08	Up-regulated
GREM1	Gremlin 1, DAN family BMP antagonist	Positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation	3.65	1.98E-15	2.49E-13	Up-regulated
GREM2	Gremlin 2, DAN family BMP antagonist	Cytokine-mediated signaling pathway	3.39	5.02E-06	1.11E-04	Up-regulated
GRN	Granulin	Positive regulation of epithelial cell proliferation	2.10	1.02E-06	2.75E-05	Up-regulated
HAVCR1	Hepatitis A virus cellular receptor 1	Integral component of membrane	11.58	2.28E-08	8.58E-07	Up-regulated
HCK	Hematopoietic cell kinase	Regulation of sequence-specific DNA-binding transcription factor activity	26.15	2.11E-11	1.46E-09	Up-regulated
HCLS1	Hematopoietic cell-specific Lyn substrate 1	Negative regulation of transcription from RNA polymerase II promoter	14.90	1.37E-09	6.83E-08	Up-regulated
HEXA	Hexosaminidase A (α polypeptide)	Cell morphogenesis involved in neuron differentiation	2.30	6.41E-09	2.75E-07	Up-regulated
HHATL	Hedgehog acyltransferase-like	Negative regulation of N-terminal protein palmitoylation	0.29	4.69E-04	5.93E-03	Down-regulated
HHIP	Hedgehog-interacting protein	Oxidoreductase activity, acting on the CH—OH group of donors, quinone or similar compound as acceptor	0.28	2.91E-10	1.64E-08	Down-regulated
HK3	Hexokinase 3 (white cell)	Glucose 6-phosphate metabolic process	11.49	1.02E-05	2.05E-04	Up-regulated
HLA-A	MHC class I, A	Antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP independent	2.71	6.59E-06	1.42E-04	Up-regulated
HLA-DMA	MHC class II, DMα	Antigen processing and presentation of exogenous peptide antigen via MHC class II	26.08	4.57E-14	4.63E-12	Up-regulated
HLA-DMB	MHC class II, DMβ	Positive regulation of T-cell activation via T-cell receptor contact with antigen bound to MHC molecule on antigen-presenting cell	26.50	3.74E-13	3.35E-11	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
HLA-DOB	MHC class II, DOβ	Negative regulation of antigen processing and presentation of peptide antigen via MHC class II	11.08	8.39E-07	2.31E-05	Up-regulated
HLA-DPA1	MHC class II, DPα1	Antigen processing and presentation of exogenous peptide antigen via MHC class II	10.98	8.71E-08	2.96E-06	Up-regulated
HLA-DPB1	MHC class II, DPβ1	Antigen processing and presentation of exogenous peptide antigen via MHC class II	8.04	1.97E-05	3.71E-04	Up-regulated
HLA-DQA1	MHC class II, DQα1	Antigen processing and presentation of exogenous peptide antigen via MHC class II	46.24	1.33E-19	3.30E-17	Up-regulated
HLA-DQB2	MHC class II, DQβ2	Antigen processing and presentation of exogenous peptide antigen via MHC class II	12.42	2.69E-12	2.17E-10	Up-regulated
HLA-DRA	MHC class II, DR α	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	41.87	2.42E-18	4.75E-16	Up-regulated
HLA-DRB1	MHC class II, DRβ1	Positive regulation of insulin secretion involved in cellular response to glucose stimulus	44.42	2.50E-18	4.80E-16	Up-regulated
HLA-DRB5	MHC class II, DRβ5	Positive regulation of insulin secretion involved in cellular response to glucose stimulus	14.96	1.13E-09	5.81E-08	Up-regulated
HMCN1	Hemicentin 1	Extracellular vesicular exosome	0.48	4.28E-08	1.54E-06	Down-regulated
HMGCLL1	3-Hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	Hydroxymethylglutaryl-CoA lyase activity	0.23	7.21E-06	1.51E-04	Down-regulated
HMOX1	Heme oxygenase (decycling) 1	Regulation of transcription from RNA polymerase II promoter in response to oxidative stress	9.52	7.20E-12	5.43E-10	Up-regulated
HNMT	Histamine *N*-methyltransferase	Histamine *N*-methyltransferase activity	3.22	7.34E-09	3.09E-07	Up-regulated
HP	Haptoglobin	Negative regulation of hydrogen peroxide catabolic process	3.00	5.08E-14	5.09E-12	Up-regulated
HPGD	Hydroxyprostaglandin dehydrogenase 15 (NAD)	Transforming growth factor β receptor signaling pathway	0.20	8.68E-12	6.44E-10	Down-regulated
HPSE	Heparanase	Positive regulation vascular endothelial growth factor production	3.66	5.44E-05	9.20E-04	Up-regulated
HPSE2	Heparanase 2	Heparan sulfate proteoglycan binding	0.38	3.26E-04	4.39E-03	Down-regulated
HRH1	Histamine receptor H1	Phospholipase C-activating G-protein–coupled receptor signaling pathway	0.31	2.03E-09	9.72E-08	Down-regulated
HS3ST1	Heparan sulfate (glucosamine) 3-*O*-sulfotransferase 1	[heparan sulfate]-Glucosamine 3-sulfotransferase 1 activity	0.45	3.73E-04	4.92E-03	Down-regulated
HSPA1A/HSPA1B	Heat shock 70-kDa protein 1A	—	0.44	1.16E-07	3.89E-06	Down-regulated
HSPA1A/HSPA1B	Heat shock 70-kDa protein 1A	—	0.42	1.02E-05	2.05E-04	Down-regulated
HSPA1A/HSPA1B	Heat shock 70kDa protein 1A	—	0.41	9.44E-10	4.91E-08	Down-regulated
HTRA1	HtrA serine peptidase 1	Negative regulation of transforming growth factor β receptor signaling pathway	2.11	3.75E-07	1.13E-05	Up-regulated
IFIT3	Interferon-induced protein with tetratricopeptide repeats 3	Negative regulation of cell proliferation	2.82	2.41E-05	4.47E-04	Up-regulated
IGFALS	Insulin-like growth factor-binding protein, acid-labile subunit	Cellular protein metabolic process	5.93	9.25E-05	1.49E-03	Up-regulated
IGJ	IgJ polypeptide, linker protein for Igα and Igμ polypeptides	Positive regulation of protein oligomerization	4.93	2.92E-04	4.01E-03	Up-regulated
IGSF3	Ig superfamily, member 3	Integral component of membrane	0.48	2.46E-07	7.53E-06	Down-regulated
IGSF6	Ig superfamily, member 6	Transmembrane signaling receptor activity	12.07	3.04E-16	4.27E-14	Up-regulated
IL13RA2	Interleukin 13 receptor, α2	Cytokine-mediated signaling pathway	4.28	8.25E-07	2.29E-05	Up-regulated
IL15	Interleukin 15	Positive regulation of tyrosine phosphorylation of Stat3 protein	3.91	4.11E-04	5.33E-03	Up-regulated
IL1B	Interleukin 1β	Positive regulation of vascular endothelial growth factor receptor signaling pathway	23.09	1.70E-08	6.52E-07	Up-regulated
IL1R1	Interleukin 1 receptor type I	Interleukin 1, type I, activating receptor activity	2.09	1.77E-07	5.69E-06	Up-regulated
IL1RL2	Interleukin 1 receptor-like 2	Interleukin-1, type I, activating receptor activity	7.24	7.60E-08	2.64E-06	Up-regulated
IL1RN	Interleukin 1 receptor antagonist	Negative regulation of interleukin 1–mediated signaling pathway	24.95	1.40E-10	8.32E-09	Up-regulated
IL21R	Interleukin 21 receptor	Interleukin 21–mediated signaling pathway	24.86	2.36E-06	5.69E-05	Up-regulated
IL3RA	Interleukin 3 receptor, α (low affinity)	Interleukin 3–mediated signaling pathway	4.80	5.73E-04	7.09E-03	Up-regulated
IL7	Interleukin 7	Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	3.61	1.49E-04	2.27E-03	Up-regulated
INPP4A	Inositol polyphosphate-4-phosphatase, type I, 107 kDa	Phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity	0.49	1.87E-07	5.96E-06	Down-regulated
IRF5	Interferon regulatory factor 5	Positive regulation of transcription from RNA polymerase II promoter	18.44	1.42E-15	1.81E-13	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
IRG1	Immunoresponsive 1 homolog (mouse)	Positive regulation of reactive oxygen species metabolic process	9.95	3.75E-05	6.61E-04	Up-regulated
IRGC	Immunity-related GTPase family, cinema	Hydrolase activity, acting on acid anhydrides	4.34	3.18E-04	4.31E-03	Up-regulated
IRX5	Iroquois homeobox 5	Sequence-specific DNA-binding transcription factor activity	11.81	4.03E-09	1.82E-07	Up-regulated
IRX6	Iroquois homeobox 6	Sequence-specific DNA-binding transcription factor activity	3.38	3.56E-04	4.74E-03	Up-regulated
ITGA10	Integrin, α10	Integrin-mediated signaling pathway	3.51	4.98E-19	1.14E-16	Up-regulated
ITGA2B	Integrin, α2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	Positive regulation of leukocyte migration	0.33	5.64E-06	1.24E-04	Down-regulated
ITGA3	Integrin, α3 (antigen CD49C, α3 subunit of VLA-3 receptor)	Positive regulation of neuron projection development	2.67	8.05E-08	2.76E-06	Up-regulated
ITGA5	Integrin, α5 (fibronectin receptor, α polypeptide)	Positive regulation of vascular endothelial growth factor receptor signaling pathway	0.43	1.59E-08	6.13E-07	Down-regulated
ITGBL1	Integrin, β-like 1 (with EGF-like repeat domains)	Extracellular region	2.06	8.84E-06	1.80E-04	Up-regulated
ITIH3	Inter-α-trypsin inhibitor heavy-chain 3	Negative regulation of endopeptidase activity	5.61	4.99E-13	4.43E-11	Up-regulated
KANK4	KN motif and ankyrin repeat domains 4	Cytoplasm	7.44	2.67E-27	1.68E-24	Up-regulated
KCNAB1	Potassium voltage-gated channel, shaker-related subfamily, β member 1	Regulation of potassium ion transmembrane transporter activity	0.25	6.83E-19	1.53E-16	Down-regulated
KCNH1	Potassium voltage-gated channel, subfamily H (eag-related), member 1	Delayed rectifier potassium channel activity	0.24	9.79E-07	2.66E-05	Down-regulated
KCNK3	Potassium channel, subfamily K, member 3	Negative regulation of cytosolic calcium ion concentration	0.45	3.43E-05	6.14E-04	Down-regulated
KCNQ4	Potassium voltage-gated channel, KQT-like subfamily, member 4	Delayed rectifier potassium channel activity	0.41	1.81E-05	3.42E-04	Down-regulated
KCNQ5	Potassium voltage-gated channel, KQT-like subfamily, member 5	Delayed rectifier potassium channel activity	2.08	2.17E-04	3.11E-03	Up-regulated
KCTD12	Potassium channel tetramerization domain containing 12	Extracellular vesicular exosome	2.70	2.67E-09	1.26E-07	Up-regulated
KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	Positive regulation of nitric-oxide synthase biosynthetic process	3.25	1.18E-09	6.00E-08	Up-regulated
KIAA1598	KIAA1598	Kinase binding	3.29	2.99E-05	5.44E-04	Up-regulated
KIF21B	Kinesin family member 21B	Microtubule motor activity	7.76	4.04E-05	7.07E-04	Up-regulated
KIF5C	Kinesin family member 5C	Microtubule motor activity	0.42	3.32E-06	7.73E-05	Down-regulated
KIRREL3	Kin of IRRE-like 3 (*Drosophila*)	Principal sensory nucleus of trigeminal nerve development	0.44	4.47E-04	5.71E-03	Down-regulated
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	Positive regulation of sequence-specific DNA-binding transcription factor activity	2.85	1.77E-04	2.64E-03	Up-regulated
KLHL40	Kelch-like family member 40	Multicellular organismal development	0.23	7.91E-06	1.64E-04	Down-regulated
KLHL6	Kelch-like family member 6	B-cell receptor signaling pathway	7.70	1.66E-04	2.50E-03	Up-regulated
LAPTM5	Lysosomal protein transmembrane 5	Integral component of plasma membrane	9.60	5.95E-13	5.15E-11	Up-regulated
LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	Transmembrane receptor protein tyrosine kinase signaling pathway	12.68	3.91E-06	8.93E-05	Up-regulated
LECT1	Leukocyte-cell–derived chemotaxin 1	Negative regulation of vascular endothelial growth factor receptor signaling pathway	0.31	1.87E-08	7.11E-07	Down-regulated
LEF1	Lymphoid-enhancer–binding factor 1	RNA polymerase II transcription regulatory region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	11.03	2.13E-07	6.65E-06	Up-regulated
LGALS9B	Lectin, galactoside binding, soluble 9B	Carbohydrate binding	79.40	3.66E-09	1.67E-07	Up-regulated
LGMN	Legumain	Antigen processing and presentation of exogenous peptide antigen via MHC class II	2.22	4.14E-09	1.86E-07	Up-regulated
LIPA	Lipase A, lysosomal acid, cholesterol esterase	Homeostasis of number of cells within a tissue	2.63	1.61E-11	1.13E-09	Up-regulated
LMO2	LIM domain only 2 (rhombotin-like 1)	RNA polymerase II transcription regulatory region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	2.13	1.41E-05	2.74E-04	Up-regulated
LNP1	Leukemia NUP98 fusion partner 1	—	0.24	3.75E-05	6.61E-04	Down-regulated
LPCAT2	Lysophosphatidylcholine acyltransferase 2	1-Alkylglycerophosphocholine *O*-acetyltransferase activity	6.26	1.02E-11	7.38E-10	Up-regulated
LPXN	Leupaxin	Negative regulation of B-cell receptor signaling pathway	6.17	4.73E-05	8.10E-04	Up-regulated
LRRTM3	Leucine-rich repeat transmembrane neuronal 3	Positive regulation of β-amyloid formation	3.85	1.82E-04	2.68E-03	Up-regulated
LY86	Lymphocyte antigen 86	Positive regulation of lipopolysaccharide-mediated signaling pathway	18.71	5.28E-09	2.31E-07	Up-regulated
LYN	v-yes-1 Yamaguchi sarcoma viral-related oncogene homolog	Positive regulation of Fc receptor-mediated stimulatory signaling pathway	5.48	1.11E-13	1.06E-11	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
LYPD6	LY6/PLAUR domain-containing 6	Extracellular region	0.44	5.81E-06	1.27E-04	Down-regulated
LYZ	Lysozyme	Cell wall macromolecule catabolic process	10.44	1.16E-08	4.60E-07	Up-regulated
LZTS1	Leucine zipper, putative tumor suppressor 1	Sequence-specific DNA-binding transcription factor activity	2.10	8.45E-04	9.88E-03	Up-regulated
MAL2	Mal, T-cell differentiation protein 2 (gene/pseudogene)	Extracellular vesicular exosome	0.11	2.65E-08	9.91E-07	Down-regulated
MAN1C1	Mannosidase, α, class 1C, member 1	Mannosyl-oligosaccharide 1,2-α-mannosidase activity	2.05	8.13E-06	1.67E-04	Up-regulated
MAP4K1	MAPK kinase kinase kinase 1	MAPK kinase kinase kinase activity	6.25	4.73E-04	5.97E-03	Up-regulated
MAPK4	MAPK4	Protein heterodimerization activity	0.27	7.85E-17	1.21E-14	Down-regulated
MARCKS	Myristoylated alanine-rich protein kinase C substrate	Energy-reserve metabolic process	2.15	4.29E-05	7.47E-04	Up-regulated
MARCO	Macrophage receptor with collagenous structure	Signaling pattern-recognition receptor activity	45.60	4.33E-09	1.93E-07	Up-regulated
MATN3	Matrilin 3	Extracellular matrix structural constituent	35.90	2.59E-18	4.88E-16	Up-regulated
MB21D1	Mab-21 domain containing 1	Positive regulation of defense response to virus by host	7.26	2.92E-06	6.89E-05	Up-regulated
MCOLN2	Mucolipin 2	Calcium ion transmembrane transport	23.65	3.00E-08	1.11E-06	Up-regulated
ME3	Malic enzyme 3, NADP(+) dependent, mitochondrial	Malate dehydrogenase (decarboxylating) (NADP$^+$) activity	0.33	8.31E-11	5.12E-09	Down-regulated
MEGF10	Multiple EGF-like domains 10	Regulation of skeletal muscle tissue development	2.48	5.60E-04	6.96E-03	Up-regulated
MEIS2	Meis homeobox 2	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	0.36	5.94E-09	2.58E-07	Down-regulated
MFAP3 L	Microfibrillar-associated protein 3-like	Integral component of membrane	0.32	7.80E-10	4.13E-08	Down-regulated
MFAP5	Microfibrillar-associated protein 5	Extracellular matrix structural constituent	0.37	1.35E-08	5.29E-07	Down-regulated
MFI2	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	Negative regulation of substrate adhesion-dependent cell spreading	12.28	5.50E-10	2.98E-08	Up-regulated
MGP	Matrix Gla protein	Extracellular matrix structural constituent	4.74	1.80E-18	3.70E-16	Up-regulated
MILR1	Mast cell Ig-like receptor 1	Negative regulation of mast cell activation	15.14	1.46E-07	4.75E-06	Up-regulated
miR-1 (and other miRNAs with seed GGAAUGU)		—	0.48	4.62E-05	1.01E-03	Down-regulated
miR-10a-5p (and other miRNAs with seed ACCCUGU)		—	2.66	8.83E-09	4.66E-07	Up-regulated
miR-10a-5p (and other miRNAs with seed ACCCUGU)		—	2.45	3.47E-07	1.47E-05	Up-regulated
miR-146a-5p (and other miRNAs with seed GAGAACU)		—	3.32	9.08E-11	6.39E-09	Up-regulated
miR-146a-5p (and other miRNAs with seed GAGAACU)		—	3.68	1.45E-06	4.38E-05	Up-regulated
miR-204-5p (and other miRNAs with seed UCCCUUU)		—	0.48	7.32E-06	1.93E-04	Down-regulated
miR-21-5p (and other miRNAs with seed AGCUUAU)		—	3.51	4.43E-11	4.67E-09	Up-regulated
miR-223-3p (miRNAs with seed GUCAGUU)		—	3.95	6.79E-12	1.43E-09	Up-regulated
miR-34a-5p (and other miRNAs with seed GGCAGUG)		—	3.79	1.28E-06	4.38E-05	Up-regulated
miR-34a-5p (and other miRNAs with seed GGCAGUG)		—	2.34	1.15E-04	2.02E-03	Up-regulated
miR-9-5p (and other miRNAs with seed CUUUGGU)		—	0.43	4.80E-05	1.01E-03	Down-regulated
MLANA	Melan-A	Integral component of plasma membrane	13.86	1.25E-09	6.32E-08	Up-regulated
MMP12	Matrix metallopeptidase 12 (macrophage elastase)	Positive regulation of epithelial cell proliferation involved in wound healing	44.11	2.61E-17	4.23E-15	Up-regulated
MMRN1	Multimerin 1	Platelet α granule lumen	3.94	9.16E-09	3.77E-07	Up-regulated
MPEG1	Macrophage expressed 1	Integral component of membrane	17.10	1.16E-14	1.35E-12	Up-regulated
MRC1	Mannose receptor, C type 1	Integral component of plasma membrane	2.55	1.86E-09	9.02E-08	Up-regulated
MS4A4A	Membrane-spanning 4 domains, subfamily A, member 4A	Integral component of membrane	3.67	2.36E-08	8.86E-07	Up-regulated
MS4A6A	Membrane-spanning 4-domains, subfamily A, member 6A	Integral component of membrane	4.63	2.66E-11	1.80E-09	Up-regulated
MSR1	Macrophage scavenger receptor 1	Positive regulation of macrophage-derived foam cell differentiation	28.78	1.13E-29	8.20E-27	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
MST4	Serine/threonine protein kinase MST4	Cellular component disassembly involved in execution phase of apoptosis	3.08	5.76E-04	7.12E-03	Up-regulated
MSX2	Msh homeobox 2	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity	2.38	1.93E-04	2.82E-03	Up-regulated
MT1E	Metallothionein 1E	Cellular response to cadmium ion	2.46	2.78E-07	8.47E-06	Up-regulated
MT2A	Metallothionein 2A	Interferon γ-mediated signaling pathway	2.71	7.68E-06	1.60E-04	Up-regulated
MYCT1	myc target 1	Nucleus	2.29	8.37E-04	9.82E-03	Up-regulated
MYLK2	Myosin light-chain kinase 2	Skeletal muscle satellite cell differentiation	0.23	2.21E-04	3.16E-03	Down-regulated
MYO10	Myosin X	Fc-γ receptor signaling pathway involved in phagocytosis	2.97	6.43E-10	3.46E-08	Up-regulated
MYO1B	Myosin IB	Phosphatidylinositol-3,4,5-trisphosphate binding	0.47	2.42E-05	4.49E-04	Down-regulated
MYO1G	Myosin IG	Extracellular vesicular exosome	6.58	3.00E-05	5.44E-04	Up-regulated
MYO7A	Myosin VIIA	Auditory receptor cell stereocilium organization	4.25	4.63E-16	6.32E-14	Up-regulated
MYO7B	Myosin VIIB	Extracellular vesicular exosome	0.44	6.49E-04	7.82E-03	Down-regulated
MYOCD	Myocardin	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	0.45	2.34E-07	7.26E-06	Down-regulated
NAGLU	*N*-Acetylglucosaminidase, α	Cerebellar Purkinje cell layer development	2.46	5.04E-10	2.76E-08	Up-regulated
NALCN	Sodium leak channel, nonselective	Membrane depolarization during action potential	3.33	1.68E-06	4.23E-05	Up-regulated
NAV3	Neuron navigator 3	Nucleoside-triphosphatase activity	4.76	1.31E-14	1.51E-12	Up-regulated
NCF4	Neutrophil cytosolic factor 4, 40 kDa	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP dependent	6.95	6.64E-06	1.43E-04	Up-regulated
NCKAP5	NCK-associated protein 5	Biologic process	3.65	1.43E-06	3.72E-05	Up-regulated
NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	Lens development in camera-type eye	2.01	3.20E-04	4.34E-03	Up-regulated
NOD1	Nucleotide-binding oligomerization domain containing 1	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.03	1.37E-05	2.67E-04	Up-regulated
NOS3	Nitric-oxide synthase 3 (endothelial cell)	Negative regulation of extrinsic apoptotic signaling pathway via death-domain receptors	0.32	6.53E-11	4.13E-09	Down-regulated
NRG1	Neuregulin 1	Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	5.92	2.77E-09	1.30E-07	Up-regulated
NRROS	Negative regulator of reactive oxygen species	Endoplasmic reticulum membrane	5.62	3.96E-05	6.94E-04	Up-regulated
NTN1	Netrin 1	Positive regulation of cell proliferation	0.48	7.40E-05	1.22E-03	Down-regulated
NUAK1	NUAK family, SNF1-like kinase 1	Regulation of myosin-light-chain-phosphatase activity	4.54	2.22E-14	2.46E-12	Up-regulated
NUAK2	NUAK family, SNF1-like kinase 2	Negative regulation of apoptotic process	4.28	1.31E-04	2.04E-03	Up-regulated
NYAP2	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	Phosphatidylinositol 3-kinase signaling	12.62	1.44E-09	7.14E-08	Up-regulated
OAS2	2′-5′-Oligoadenylate synthetase 2, 69/71 kDa	Nucleobase-containing compound metabolic process	5.79	2.86E-05	5.21E-04	Up-regulated
OLFM3	Olfactomedin 3	α-Amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex	0.32	7.43E-09	3.11E-07	Down-regulated
OLR1	Oxidized low-density lipoprotein (lectin-like) receptor 1	Low-density lipoprotein receptor activity	91.52	6.29E-47	1.48E-43	Up-regulated
OMD	Osteomodulin	Keratan sulfate biosynthetic process	6.50	9.11E-37	1.23E-33	Up-regulated
OSBP2	Oxysterol-binding protein 2	Cholesterol binding	7.67	1.30E-15	1.71E-13	Up-regulated
P2RX1	Purinergic receptor P2X, ligand-gated ion channel 1	Activation of cysteine-type endopeptidase activity involved in apoptotic process	0.29	7.55E-17	1.18E-14	Down-regulated
P2RY12	Purinergic receptor P2Y, G protein coupled 12	Adenylate cyclase-inhibiting G-protein–coupled receptor signaling pathway	6.84	1.55E-10	9.19E-09	Up-regulated
P2RY14	Purinergic receptor P2Y, G protein coupled 14	G-protein–coupled purinergic nucleotide receptor signaling pathway	0.27	1.68E-06	4.23E-05	Down-regulated
P4HA3	Prolyl 4-hydroxylase, α polypeptide III	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of 2 atoms of oxygen	6.02	6.09E-12	4.70E-10	Up-regulated
PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	Regulation of transcription, DNA templated	0.40	1.32E-04	2.05E-03	Down-regulated
PALD1	Phosphatase domain containing, paladin 1	Protein binding	2.47	7.55E-06	1.57E-04	Up-regulated
PALMD	Palmdelphin	Regulation of cell shape	3.73	2.51E-13	2.29E-11	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
PAMR1	Peptidase domain containing associated with muscle regeneration 1	Extracellular region	0.44	1.63E-05	3.11E-04	Down-regulated
PCDH12	Protocadherin 12	Integral component of plasma membrane	3.37	6.77E-07	1.92E-05	Up-regulated
PCP4L1	Purkinje cell protein 4–like 1	—	3.13	1.71E-05	3.26E-04	Up-regulated
PCSK2	Proprotein convertase subtilisin/kexin type 2	Islet amyloid polypeptide processing	0.34	4.41E-05	7.59E-04	Down-regulated
PCSK6	Proprotein convertase subtilisin/kexin type 6	Zygotic determination of anterior/posterior axis, embryo	0.50	2.38E-05	4.44E-04	Down-regulated
PDE1B	Phosphodiesterase 1B, calmodulin-dependent	Cellular response to granulocyte-macrophage colony-stimulating factor stimulus	2.17	4.47E-04	5.71E-03	Up-regulated
PDE1C	Phosphodiesterase 1C, calmodulin-dependent 70 kDa	Calmodulin-dependent cyclic-nucleotide phosphodiesterase activity	0.18	9.60E-12	7.07E-10	Down-regulated
PDE7B	Phosphodiesterase 7B	3′,5′-cAMP phosphodiesterase activity	3.75	1.76E-09	8.59E-08	Up-regulated
PDGFB	Platelet-derived growth factor β polypeptide	Positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor β signaling pathway	2.75	1.30E-05	2.55E-04	Up-regulated
PDGFC	Platelet-derived growth factor C	Activation of transmembrane receptor protein tyrosine kinase activity	2.77	9.57E-09	3.90E-07	Up-regulated
PDGFD	Platelet-derived growth factor D	Platelet-derived growth factor receptor signaling pathway	2.19	7.91E-08	2.73E-06	Up-regulated
PDGFRL	Platelet-derived growth factor receptor-like	Platelet-derived growth factor receptor-β signaling pathway	2.15	1.48E-07	4.79E-06	Up-regulated
PDZD2	PDZ domain containing 2	Endoplasmic reticulum	0.45	1.75E-08	6.66E-07	Down-regulated
PDZRN4	PDZ domain containing ring finger 4	Ubiquitin-protein transferase activity	0.41	7.60E-08	2.64E-06	Down-regulated
PGF	Placental growth factor	Vascular endothelial growth factor receptor signaling pathway	2.34	3.73E-04	4.92E-03	Up-regulated
PGM5	Phosphoglucomutase 5	Dystrophin-associated glycoprotein complex	0.32	4.53E-12	3.53E-10	Down-regulated
PIEZO2	Piezo-type mechanosensitive ion channel component 2	Detection of mechanical stimulus involved in sensory perception	3.44	1.26E-07	4.17E-06	Up-regulated
PIK3CG	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit γ	1-Phosphatidylinositol-4-phosphate 3-kinase, class IB complex	4.90	1.56E-04	2.36E-03	Up-regulated
PIK3R5	Phosphoinositide-3-kinase, regulatory subunit 5	1-Phosphatidylinositol-4-phosphate 3-kinase, class IB complex	8.14	4.22E-06	9.59E-05	Up-regulated
PILRB	Paired Ig-like type 2 receptor β	Activation of transmembrane receptor protein tyrosine kinase activity	28.07	7.51E-16	1.01E-13	Up-regulated
PITPNM3	PITPNM family member 3	Phosphatidylinositol transporter activity	3.91	1.62E-04	2.44E-03	Up-regulated
PKDCC	Protein kinase domain containing, cytoplasmic	Negative regulation of Golgi to plasma membrane protein transport	2.04	3.14E-07	9.52E-06	Up-regulated
PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor α	Negative regulation of transcription from RNA polymerase II promoter	0.31	8.17E-04	9.61E-03	Down-regulated
PKIB	Protein kinase (cAMP-dependent, catalytic) inhibitor β	Negative regulation of protein serine/threonine kinase activity	7.12	1.08E-13	1.03E-11	Up-regulated
PLA1A	Phospholipase A1 member A	Phosphatidylcholine 1-acylhydrolase activity	8.09	1.81E-13	1.67E-11	Up-regulated
PLA2G7	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	1-Alkyl-2-acetylglycerophosphocholine esterase activity	3.07	4.30E-14	4.40E-12	Up-regulated
PLA2R1	Phospholipase A2 receptor 1, 180 kDa	Positive regulation of DNA-damage response, signal transduction by p53 class mediator	3.33	6.41E-17	1.02E-14	Up-regulated
PLAC8	Placenta-specific 8	Positive regulation of transcription from RNA polymerase II promoter	17.30	6.09E-09	2.62E-07	Up-regulated
PLBD2	Phospholipase B domain containing 2	Extracellular vesicular exosome	2.03	5.03E-06	1.11E-04	Up-regulated
PLCB2	Phospholipase Cβ2	Phosphatidylinositol phospholipase C activity	3.12	6.99E-07	1.97E-05	Up-regulated
PLCB4	Phospholipase Cβ4	Phosphatidylinositol phospholipase C activity	0.47	1.64E-06	4.20E-05	Down-regulated
PLCL1	Phospholipase C-like 1	Regulation of synaptic transmission, GABAergic	0.30	3.36E-12	2.68E-10	Down-regulated
PLCXD2	Phosphatidylinositol-specific phospholipase C, X domain containing 2	Phosphoric diester hydrolase activity	0.20	7.24E-05	1.19E-03	Down-regulated
PLEK	Pleckstrin	Negative regulation of G-protein–coupled receptor protein signaling pathway	3.93	3.04E-06	7.11E-05	Up-regulated
PLK2	Polo-like kinase 2	Positive regulation of proteasomal ubiquitin-dependent protein catabolic process	2.27	1.78E-04	2.64E-03	Up-regulated
PLK3	Polo-like kinase 3	Positive regulation of proteasomal ubiquitin-dependent protein catabolic process involved in cellular response to hypoxia	2.54	7.59E-04	9.02E-03	Up-regulated
PLXDC1	Plexin domain containing 1	Integral component of membrane	0.27	1.12E-07	3.78E-06	Down-regulated
PLXNC1	Plexin C1	Integral component of membrane	3.61	1.79E-04	2.65E-03	Up-regulated
PODXL	Podocalyxin-like	Positive regulation of cell–cell adhesion mediated by integrin	0.47	3.92E-04	5.13E-03	Down-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
PPAPDC1A	Phosphatidic acid phosphatase type 2 domain containing 1A	Fc-γ receptor signaling pathway involved in phagocytosis	7.26	2.89E-08	1.07E-06	Up-regulated
PRCP	Prolylcarboxypeptidase (angiotensinase C)	Serine-type carboxypeptidase activity	2.37	9.33E-06	1.89E-04	Up-regulated
PRDM1	PR domain containing 1, with ZNF domain	Negative regulation of lipopolysaccharide-mediated signaling pathway	13.93	2.46E-07	7.53E-06	Up-regulated
PRKG2	Protein kinase, cGMP dependent, type II	Regulation of nitric-oxide synthase activity	0.23	7.31E-04	8.69E-03	Down-regulated
PRR15	Proline-rich 15	Multicellular organismal development	7.19	2.02E-06	4.98E-05	Up-regulated
PRR5 L	Proline-rich 5-like	Positive regulation of phosphatidylinositol 3-kinase signaling	3.05	1.11E-05	2.21E-04	Up-regulated
PRUNE2	Prune homolog 2 (*Drosophila*)	Pyrophosphatase activity	0.46	2.05E-06	5.04E-05	Down-regulated
PTAFR	Platelet-activating factor receptor	Lipopolysaccharide-mediated signaling pathway	11.09	7.66E-09	3.18E-07	Up-regulated
PTGER4	Prostaglandin E receptor 4 (subtype EP4)	Adenylate cyclase-modulating G-protein–coupled receptor signaling pathway	2.86	3.45E-08	1.26E-06	Up-regulated
PTK2B	Protein tyrosine kinase 2β	Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	3.11	3.70E-04	4.91E-03	Up-regulated
PTPN18	Protein tyrosine phosphatase, nonreceptor type 18 (brain derived)	Non–membrane-spanning protein tyrosine phosphatase activity	9.65	3.60E-06	8.28E-05	Up-regulated
PTPN6	Protein tyrosine phosphatase, nonreceptor type 6	Negative regulation of humoral immune response mediated by circulating Ig	7.66	2.27E-06	5.49E-05	Up-regulated
PTPRC	Protein tyrosine phosphatase, receptor type, C	Negative regulation of cell adhesion involved in substrate-bound cell migration	5.21	2.14E-04	3.08E-03	Up-regulated
PTPRO	Protein tyrosine phosphatase, receptor type, O	Transmembrane receptor protein tyrosine phosphatase activity	5.50	2.50E-06	6.01E-05	Up-regulated
PTX3	Pentraxin 3, long	Positive regulation of nitric-oxide biosynthetic process	5.65	1.25E-06	3.32E-05	Up-regulated
QPCT	Glutaminyl-peptide cyclotransferase	Peptidyl-pyroglutamic acid biosynthetic process, using glutaminyl-peptide cyclotransferase	2.40	1.32E-06	3.48E-05	Up-regulated
QSOX1	Quiescin Q6 sulfhydryl oxidase 1	Flavin-linked sulfhydryl oxidase activity	2.58	1.72E-11	1.20E-09	Up-regulated
RARRES1	Retinoic acid receptor responder (tazarotene induced) 1	Negative regulation of cell proliferation	3.48	1.20E-20	3.32E-18	Up-regulated
RASL10B	RAS-like, family 10, member B	Regulation of systemic arterial blood pressure by atrial natriuretic peptide	0.25	1.29E-05	2.54E-04	Down-regulated
RBM47	RNA-binding motif protein 47	Poly(A) RNA binding	5.06	6.03E-06	1.32E-04	Up-regulated
RBP1	Retinol-binding protein 1, cellular	Phototransduction, visible light	2.32	2.64E-05	4.85E-04	Up-regulated
RBP4	Retinol-binding protein 4, plasma	Detection of light stimulus involved in visual perception	0.50	2.94E-06	6.91E-05	Down-regulated
RBPMS2	RNA-binding protein with multiple splicing 2	Nucleic acid binding	0.46	7.03E-06	1.48E-04	Down-regulated
RELN	Reelin	Positive regulation of α-amino-3-hydroxy-5-methyl-4-isoxazole propionate-selective glutamate receptor activity	2.84	2.51E-06	6.01E-05	Up-regulated
RFTN1	Raftlin, lipid raft linker 1	T-cell antigen processing and presentation	2.06	2.32E-04	3.31E-03	Up-regulated
RGS1	Regulator of G-protein signaling 1	Adenylate cyclase-inhibiting G-protein–coupled receptor signaling pathway	14.98	8.82E-07	2.41E-05	Up-regulated
RGS10	Regulator of G-protein signaling 10	Termination of G-protein–coupled receptor signaling pathway	2.74	5.36E-05	9.09E-04	Up-regulated
RHOBTB1	Rho-related BTB domain containing 1	Regulation of small GTPase-mediated signal transduction	2.17	8.49E-07	2.33E-05	Up-regulated
RNASE6	Ribonuclease, RNase A family, k6	Endoribonuclease activity, producing 3′-phosphomonoesters	8.06	3.62E-09	1.66E-07	Up-regulated
RNU1-1	RNA, U1 small nuclear 1	—	0.23	2.78E-11	1.87E-09	Down-regulated
ROBO2	Roundabout, axon guidance receptor, homolog 2 (*Drosophila*)	Negative regulation of negative chemotaxis	2.83	7.02E-05	1.16E-03	Up-regulated
ROBO4	Roundabout, axon guidance receptor, homolog 4 (*Drosophila*)	Negative regulation of cell migration	2.15	9.35E-06	1.89E-04	Up-regulated
RPS6KA1	Ribosomal protein S6 kinase, 90 kDa, polypeptide 1	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	5.19	6.71E-06	1.44E-04	Up-regulated
RRAD	Ras-related associated with diabetes	Small GTPase-mediated signal transduction	0.34	2.16E-04	3.11E-03	Down-regulated
RSPO2	R-spondin 2	Epithelial tube branching involved in lung morphogenesis	20.75	3.97E-19	9.35E-17	Up-regulated
RTP4	Receptor (chemosensory) transporter protein 4	Detection of chemical stimulus involved in sensory perception of bitter taste	2.33	1.11E-05	2.21E-04	Up-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
RUNX2	Runt-related transcription factor 2	RNA polymerase II core promoter proximal region sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	8.63	9.23E-09	3.78E-07	Up-regulated
RUNX3	Runt-related transcription factor 3	Sequence-specific DNA-binding RNA polymerase II transcription factor activity	6.08	8.08E-04	9.51E-03	Up-regulated
S100A1	S100 calcium-binding protein A1	Negative regulation of transcription from RNA polymerase II promoter	2.89	4.11E-04	5.33E-03	Up-regulated
S100A14	S100 calcium-binding protein A14	Positive regulation of granulocyte chemotaxis	0.09	6.28E-04	7.65E-03	Down-regulated
SALL1	Spalt-like transcription factor 1	Mesenchymal to epithelial transition involved in metanephros morphogenesis	7.04	6.22E-06	1.35E-04	Up-regulated
SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	Negative regulation of peptidyl-tyrosine phosphorylation	5.52	5.34E-04	6.66E-03	Up-regulated
SBSPON	Somatomedin B and thrombospondin, type 1 domain containing	Proteinaceous extracellular matrix	0.34	3.31E-09	1.53E-07	Down-regulated
SCARA5	Scavenger receptor class A, member 5 (putative)	Integral component of plasma membrane	0.42	1.12E-07	3.78E-06	Down-regulated
SCIN	Scinderin	Positive regulation of megakaryocyte differentiation	5.43	5.38E-11	3.42E-09	Up-regulated
SCN7A	Sodium channel, voltage gated, type VII, α subunit	Membrane depolarization during action potential	0.42	6.49E-04	7.82E-03	Down-regulated
SDC3	Syndecan 3	Glycosaminoglycan biosynthetic process	2.96	3.13E-10	1.74E-08	Up-regulated
SDS	Serine dehydratase	L-Threonine ammonia-lyase activity	2.09	1.15E-04	1.82E-03	Up-regulated
SEL1L3	Sel-1 suppressor of lin-12-like 3 (*Caenorhabditis elegans*)	Integral component of membrane	2.65	2.54E-04	3.58E-03	Up-regulated
SELE	Selectin E	Leukocyte migration involved in inflammatory response	13.59	1.31E-09	6.56E-08	Up-regulated
SEMA3A	Sema domain, Ig domain, short basic domain, secreted, (semaphorin) 3A	Dichotomous subdivision of terminal units involved in salivary gland branching	4.90	7.74E-11	4.79E-09	Up-regulated
SEMA4A	Sema domain, Ig domain, transmembrane domain and short cytoplasmic domain, (semaphorin) 4A	Regulation of endothelial cell migration	5.12	1.84E-06	4.60E-05	Up-regulated
SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	Detection of mechanical stimulus involved in sensory perception	10.25	3.17E-55	1.49E-51	Up-regulated
SESN2	Sestrin 2	Regulation of response to reactive oxygen species	3.25	2.05E-04	2.98E-03	Up-regulated
SFRP2	Secreted frizzled-related protein 2	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.59	8.31E-10	4.35E-08	Up-regulated
SGCD	Sarcoglycan, delta (35-kDa dystrophin-associated glycoprotein)	Dystrophin-associated glycoprotein complex	0.47	1.56E-06	4.02E-05	Down-regulated
SGK1	Serum/glucocorticoid-regulated kinase 1	Regulation of sequence-specific DNA-binding transcription factor activity	2.72	4.99E-11	3.24E-09	Up-regulated
SH2D1B	SH2 domain containing 1B	Positive regulation of natural killer cell–mediated immunity	6.25	2.26E-07	7.02E-06	Up-regulated
SHF	Src homology 2 domain containing F	Apoptotic process	2.62	4.19E-06	9.53E-05	Up-regulated
SHOX2	Short stature homeobox 2	Negative regulation of transcription from RNA polymerase II promoter	4.86	4.95E-06	1.10E-04	Up-regulated
SIGLEC15	Sialic acid-binding Ig-like lectin 15	Cellular response to lipoprotein particle stimulus	16.81	3.12E-10	1.74E-08	Up-regulated
SIRPB2	Signal-regulatory protein β2	Integral component of membrane	3.48	1.43E-04	2.19E-03	Up-regulated
SIX1	SIX homeobox 1	Positive regulation of mesenchymal cell proliferation involved in ureter development	2.24	1.74E-04	2.60E-03	Up-regulated
SKAP2	Src kinase associated phosphoprotein 2	Positive regulation of signal transduction	3.44	7.44E-07	2.08E-05	Up-regulated
SLA	Src-like adaptor	Positive regulation of signal transduction	7.77	3.76E-04	4.95E-03	Up-regulated
SLAMF8	SLAM family member 8	Regulation of NAD(P)H oxidase activity	11.28	3.22E-06	7.50E-05	Up-regulated
SLC15A2	Solute carrier family 15 (oligopeptide transporter), member 2	High-affinity oligopeptide transporter activity	15.30	3.13E-14	3.38E-12	Up-regulated
SLC15A3	Solute carrier family 15 (oligopeptide transporter), member 3	Integral component of membrane	2.70	2.06E-09	9.81E-08	Up-regulated
SLC37A2	Solute carrier family 37 (glucose-6-phosphate transporter), member 2	Extracellular vesicular exosome	7.88	5.12E-18	9.28E-16	Up-regulated
SLC39A8	Solute carrier family 39 (zinc transporter), member 8	Metal ion transmembrane transporter activity	2.31	3.56E-05	6.34E-04	Up-regulated
SLC40A1	Solute carrier family 40 (iron-regulated transporter), member 1	Multicellular organismal iron ion homeostasis	2.21	3.92E-07	1.17E-05	Up-regulated
SLC44A4	Solute carrier family 44, member 4	Glycerophospholipid biosynthetic process	4.97	4.52E-04	5.75E-03	Up-regulated
SLC46A1	Solute carrier family 46 (folate transporter), member 1	Water-soluble vitamin metabolic process	2.68	4.29E-04	5.50E-03	Up-regulated
SLC6A1	Solute carrier family 6 (neurotransmitter transporter), member 1	Positive regulation of γ-aminobutyric acid secretion	0.09	1.85E-07	5.94E-06	Down-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
SLC7A7	Solute carrier family 7 (amino acid transporter light-chain, y+L system), member 7	Amino acid transmembrane transporter activity	7.02	5.97E-09	2.58E-07	Up-regulated
SLC9A9	Solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9	Hydrogen ion transmembrane transport	3.30	4.40E-08	1.58E-06	Up-regulated
SLCO2A1	Solute carrier organic anion transporter family, member 2A1	Prostaglandin transmembrane transporter activity	0.45	4.87E-06	1.09E-04	Down-regulated
SLCO2B1	Solute carrier organic anion transporter family, member 2B1	Sodium-independent organic anion transmembrane transporter activity	4.92	8.03E-12	6.00E-10	Up-regulated
SLITRK5	SLIT and NTRK-like family, member 5	Cardiovascular system development	0.18	1.02E-05	2.05E-04	Down-regulated
SMAD6	SMAD family member 6	Transforming growth factor β receptor, inhibitory cytoplasmic mediator activity	2.03	1.01E-04	1.62E-03	Up-regulated
SMAP2	Small ArfGAP2	Positive regulation of GTPase activity	2.07	1.55E-05	2.98E-04	Up-regulated
SMTNL1	Smoothelin-like 1	Positive regulation of vasoconstriction	0.28	4.54E-11	2.97E-09	Down-regulated
SNX10	Sorting nexin 10	Extrinsic component of endosome membrane	3.10	1.01E-08	4.05E-07	Up-regulated
SP100	SP100 nuclear antigen	DNA-damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	3.13	1.21E-04	1.91E-03	Up-regulated
SP7	Sp7 transcription factor	Positive regulation of transcription from RNA polymerase II promoter	7.02	4.30E-06	9.73E-05	Up-regulated
SPARC	Secreted protein, acidic, cysteine rich (osteonectin)	Cellular response to growth factor stimulus	2.00	2.45E-05	4.54E-04	Up-regulated
SPI1	Spleen focus forming virus (SFFV) proviral integration oncogene	RNA polymerase II distal enhancer sequence-specific DNA-binding transcription factor activity involved in positive regulation of transcription	8.91	2.68E-13	2.43E-11	Up-regulated
SPINK8	Serine peptidase inhibitor, Kazal type 8 (putative)	Negative regulation of endopeptidase activity	0.31	1.17E-07	3.93E-06	Down-regulated
SPP1	Secreted phosphoprotein 1	Negative regulation of collateral sprouting of intact axon in response to injury	17.18	6.48E-43	1.02E-39	Up-regulated
SPRY4	Sprouty homolog 4 (*Drosophila*)	Negative regulation of MAPK activity	4.88	6.54E-09	2.79E-07	Up-regulated
SSX2IP	Synovial sarcoma, X breakpoint 2-interacting protein	Regulation of Rac protein signal transduction	0.48	1.50E-07	4.85E-06	Down-regulated
ST3GAL5	ST3 β-galactoside α-2,3-sialyltransferase 5	Neolactotetraosylceramide α-2,3-sialyltransferase activity	2.90	3.51E-05	6.26E-04	Up-regulated
ST8SIA4	ST8 α-*N*-acetyl-neuraminide α-2,8-sialyltransferase 4	α-*N*-Acetylneuraminate α-2,8-sialyltransferase activity	3.98	2.53E-04	3.58E-03	Up-regulated
STAB1	Stabilin 1	Low-density lipoprotein receptor activity	4.75	4.48E-27	2.64E-24	Up-regulated
STAG3	Stromal antigen 3	Chromosome, centromeric region	8.44	1.91E-07	6.07E-06	Up-regulated
STARD8	StAR-related lipid transfer domain containing 8	Regulation of small GTPase-mediated signal transduction	2.54	1.62E-05	3.11E-04	Up-regulated
STC1	Stanniocalcin 1	Cellular response to glucocorticoid stimulus	5.14	2.98E-06	7.00E-05	Up-regulated
STC2	Stanniocalcin 2	Negative regulation of multicellular organism growth	3.38	1.28E-08	5.03E-07	Up-regulated
STEAP3	STEAP family member 3, metalloreductase	Positive regulation of apoptotic process	3.86	1.83E-04	2.69E-03	Up-regulated
SUCNR1	Succinate receptor 1	G-protein–coupled receptor signaling pathway	3.98	5.70E-05	9.57E-04	Up-regulated
SUSD3	Sushi domain containing 3	Integral component of membrane	4.47	5.04E-04	6.32E-03	Up-regulated
SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	Extracellular region	2.13	7.03E-07	1.98E-05	Up-regulated
SYK	Spleen tyrosine kinase	Positive regulation of granulocyte-macrophage colony-stimulating factor biosynthetic process	10.92	1.77E-06	4.44E-05	Up-regulated
SYTL2	Synaptotagmin-like 2	Phosphatidylinositol-4,5-bisphosphate binding	2.38	2.20E-06	5.33E-05	Up-regulated
TACC2	Transforming, acidic coiled-coil containing protein 2	Regulation of microtubule-based process	0.45	4.85E-07	1.42E-05	Down-regulated
TACR1	Tachykinin receptor 1	Phospholipase C-activating G-protein–coupled receptor signaling pathway	0.04	7.60E-24	3.25E-21	Down-regulated
TAGAP	T-cell activation Rho-GTPase-activating protein	Regulation of small GTPase-mediated signal transduction	8.00	7.07E-06	1.49E-04	Up-regulated
TBX15	T-box 15	Negative regulation of transcription from RNA polymerase II promoter	0.38	1.94E-07	6.13E-06	Down-regulated
TES	Testis-derived transcript (3 LIM domains)	Negative regulation of cell proliferation	0.46	2.42E-07	7.46E-06	Down-regulated
TFEC	Transcription factor EC	Sequence-specific DNA-binding transcription factor activity	6.13	1.74E-06	4.37E-05	Up-regulated
THBS1	Thrombospondin 1	Negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	14.05	6.53E-32	6.15E-29	Up-regulated
THBS4	Thrombospondin 4	Positive regulation of peptidyl-tyrosine phosphorylation	8.33	6.50E-13	5.56E-11	Up-regulated
THEMIS	Thymocyte selection associated	T-cell receptor signaling pathway	0.23	2.04E-04	2.97E-03	Down-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	*P* Value	False Discovery Rate (*q* Value)	Direction of Expression
THSD4	Thrombospondin, type I, domain containing 4	Extracellular vesicular exosome	3.88	3.11E-14	3.38E-12	Up-regulated
TIFAB	TRAF-interacting protein with forkhead-associated domain, family member B	—	72.91	2.45E-17	4.05E-15	Up-regulated
TIMP1	TIMP metallopeptidase inhibitor 1	Negative regulation of membrane protein ectodomain proteolysis	2.57	5.08E-11	3.25E-09	Up-regulated
TJP2	Tight junction protein 2	Cellular component disassembly involved in execution phase of apoptosis	2.04	3.12E-05	5.64E-04	Up-regulated
TLR1	Toll-like receptor 1	Positive regulation of tumor necrosis factor biosynthetic process	9.43	1.57E-08	6.10E-07	Up-regulated
TLR8	Toll-like receptor 8	Pathogen-associated molecular pattern-dependent induction by symbiont of host innate immune response	7.67	1.39E-15	1.80E-13	Up-regulated
TM4SF18	Transmembrane 4 L 6 family member 18	Integral component of membrane	2.53	7.55E-05	1.23E-03	Up-regulated
TMEM56	Transmembrane protein 56	Integral component of membrane	0.40	4.01E-08	1.45E-06	Down-regulated
TMEM98	Transmembrane protein 98	Integral component of membrane	4.18	4.21E-07	1.25E-05	Up-regulated
TMOD1	Tropomodulin 1	Adult locomotory behavior	0.46	4.92E-06	1.10E-04	Down-regulated
TMTC2	Transmembrane and tetratricopeptide repeat containing 2	Integral component of membrane	3.00	1.16E-09	5.94E-08	Up-regulated
TNFAIP8L2	Tumor necrosis factor, α-induced protein 8-like 2	Negative regulation of inflammatory response	7.39	9.97E-07	2.70E-05	Up-regulated
TNFRSF11A	Tumor necrosis factor receptor superfamily, member 11a, NF-κB activator	Positive regulation of fever generation by positive regulation of prostaglandin secretion	3.14	6.86E-06	1.46E-04	Up-regulated
TNFRSF21	Tumor necrosis factor receptor superfamily member 21	Negative regulation of interleukin 10 secretion	2.47	6.48E-08	2.29E-06	Up-regulated
TNFSF10	Tumor necrosis factor (ligand) superfamily member 10	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	4.06	1.14E-13	1.08E-11	Up-regulated
TNFSF13B	Tumor necrosis factor (ligand) superfamily member 13b	Positive regulation of germinal center formation	9.22	8.41E-15	1.00E-12	Up-regulated
TNN	Tenascin N	Proteinaceous extracellular matrix	2.85	2.28E-04	3.26E-03	Up-regulated
TNNC1	Troponin C type 1 (slow)	Ventricular cardiac muscle tissue morphogenesis	0.27	2.63E-12	2.14E-10	Down-regulated
TNNT2	Troponin T type 2 (cardiac)	Ventricular cardiac muscle tissue morphogenesis	0.23	6.64E-21	1.90E-18	Down-regulated
TNXA	Tenascin XA (pseudogene)	Biologic process	0.43	3.63E-06	8.34E-05	Down-regulated
TPBG	Trophoblast glycoprotein	Integral component of plasma membrane	0.30	2.12E-06	5.18E-05	Down-regulated
TPD52	Tumor protein D52	Protein heterodimerization activity	2.14	1.62E-05	3.11E-04	Up-regulated
TPD52L1	Tumor protein D52-like 1	Regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.37	1.37E-04	2.11E-03	Down-regulated
TPP1	Tripeptidyl peptidase I	Activation of signaling protein activity involved in unfolded protein response	2.02	6.72E-06	1.44E-04	Up-regulated
TRABD2A	TraB domain containing 2A	Negative regulation of Wnt signaling pathway	4.98	1.21E-06	3.22E-05	Up-regulated
TREM2	Triggering receptor expressed on myeloid cells 2	Positive regulation of antigen processing and presentation of peptide antigen via MHC class II	43.80	1.10E-58	1.03E-54	Up-regulated
TRIB3	Tribbles pseudokinase 3	Intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	4.85	1.83E-04	2.69E-03	Up-regulated
TRIM63	Tripartite motif containing 63, E3 ubiquitin protein ligase	Response to electrical stimulus involved in regulation of muscle adaptation	0.39	1.54E-05	2.98E-04	Down-regulated
TRPM1	Transient receptor potential cation channel, subfamily M, member 1	G-protein–coupled glutamate receptor signaling pathway	6.94	3.18E-04	4.31E-03	Up-regulated
TRPM3	Transient receptor potential cation channel, subfamily M, member 3	Calcium ion transmembrane transport	0.37	1.82E-04	2.68E-03	Down-regulated
TSPAN15	Tetraspanin 15	Establishment of protein localization to plasma membrane	0.38	6.94E-07	1.96E-05	Down-regulated
TSPAN2	Tetraspanin 2	Integral component of membrane	0.42	1.26E-08	4.98E-07	Down-regulated
TUSC3	Tumor suppressor candidate 3	Dolichyl-diphosphooligosaccharide-protein glycotransferase activity	0.49	3.63E-04	4.83E-03	Down-regulated
TYR	Tyrosinase	Melanin biosynthetic process from tyrosine	0.15	7.33E-06	1.53E-04	Down-regulated
UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)	Negative regulation of insulin secretion involved in cellular response to glucose stimulus	3.80	1.33E-04	2.07E-03	Up-regulated
UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	Glucuronosyltransferase activity	4.76	3.15E-04	4.28E-03	Up-regulated
UNC5B	Unc-5 homolog B (*C elegans*)	Negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	4.16	4.11E-23	1.55E-20	Up-regulated
VCAM1	Vascular cell adhesion molecule 1	Cellular response to vascular endothelial growth factor stimulus	2.75	5.07E-11	3.25E-09	Up-regulated
VIM	Vimentin	Cellular component disassembly involved in execution phase of apoptosis	0.50	5.76E-05	9.61E-04	Down-regulated

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On-line Table: Continued

Gene	Entrez Gene Name	Function	Fold Change	P Value	False Discovery Rate (q Value)	Direction of Expression
VNN1	Vanin 1	Negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	2.04	8.70E-05	1.41E-03	Up-regulated
VSIG4	V-set and Ig domain containing 4	Negative regulation of interleukin 2 production	8.55	3.52E-32	3.69E-29	Up-regulated
VWF	von Willebrand factor	Blood coagulation, intrinsic pathway	3.23	3.99E-16	5.53E-14	Up-regulated
WAS	Wiskott-Aldrich syndrome	Positive regulation of Arp2/3 complex-mediated actin nucleation	4.60	1.40E-04	2.15E-03	Up-regulated
WIF1	Wnt inhibitory factor 1	Positive regulation of fat cell differentiation	3.99	1.06E-11	7.65E-10	Up-regulated
WNT2	Wingless-type MMTV integration site family member 2	Positive regulation of epithelial cell proliferation involved in lung morphogenesis	0.20	3.58E-07	1.08E-05	Down-regulated
XIRP1	Xin actin-binding repeat containing 1	Negative regulation of cell proliferation	3.75	9.74E-11	5.92E-09	Up-regulated
ZCCHC5	Zinc finger, CCHC domain containing 5	Nucleic acid binding	2.12	3.29E-04	4.41E-03	Up-regulated
ZCWPW1	Zinc finger, CW type with PWWP domain 1	Zinc ion binding	7.02	1.37E-08	5.34E-07	Up-regulated
ZDHHC14	Zinc finger, DHHC-type containing 14	Protein–cysteine *S*-palmitoyltransferase activity	2.65	1.27E-04	1.99E-03	Up-regulated
ZDHHC23	Zinc finger, DHHC-type containing 23	Protein–cysteine *S*-palmitoyltransferase activity	0.28	7.28E-04	8.68E-03	Down-regulated
ZNF608	Zinc finger protein 608	Metal ion binding	3.00	1.15E-08	4.58E-07	Up-regulated

Note:—ABI indicates Abelson interactor; ADAM, a disintegrin and metalloproteinase; ADAMTS, a disintegrin and metalloproteinase with thrombospondin motifs; ATP, adenosine triphosphate; cAMP, cyclic adenosine monophosphate; CFTR, cystic fibrosis transmembrane conductance regulator; cGMP, cyclic guanosine monophosphate; CoA, coenzyme A; EGF, epidermal growth factor; ER, estrogen receptor; FBJ, Finkel-Biskis-Jinkins; IAP, inhibitor of apoptosis; Ig, immunoglobulin; MAPK, mitogen-activated protein kinase; MRP, multidrug resistance-associated protein; NAD, nicotinamide adenine dinucleotide; NADP, nicotinamide adenine dinucleotide phosphate; NAD(P)H, reduced nicotinamide adenine dinucleotide phosphate; NF-κB, nuclear factor κB; PH, Pleckstrin homology; SAM, sterile alpha motif; SDR, short-chain dehydrogenase/reductase; STEAP, six transmembrane epithelial antigen of prostate; TAP, transporter associated with antigen presentation; UDP, uridine 5′-diphosphate.

[a] Genes were determined to be differentially expressed if the P value was $<.05$, the false discovery rate was <0.01, and the fold change was >2 or <0.5.