On-line Table 1: Up- and down-regulated molecules comparing coiled versus untreated aneurysms, determined by IPA[a]

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6 (Langereis blood group)	Integral component of mitochondrial outer membrane	2.541	4.28E-05	5.90E-04	Up-regulated
ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	ATPase activity, coupled to transmembrane movement of substances	3.132	4.94E-10	6.17E-08	Up-regulated
ACOT11	Acyl-coa thioesterase 11	Carboxylic ester hydrolase activity	3.973	2.58E-04	2.42E-03	Up-regulated
ADAM10	ADAM metallopeptidase domain 10	*PMA*-inducible membrane protein ectodomain proteolysis	3.425	1.33E-04	1.44E-03	Up-regulated
ADAM8	ADAM metallopeptidase domain 8	Positive regulation of tumor necrosis factor (ligand) superfamily member 11 production	3.417	1.42E-13	6.74E-11	Up-regulated
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	Proteinaceous extracellular matrix	2.134	2.49E-08	1.52E-06	Up-regulated
ADH4	Alcohol dehydrogenase 4 (class II), pi polypeptide	Oxidoreductase activity, acting on the aldehyde or oxo group of donors, *NAD* or *NADP* as acceptor	−2.657	4.44E-05	6.04E-04	Down-regulated
ADORA2B	Adenosine A2b receptor	Positive regulation of chronic inflammatory response to non-antigenic stimulus	2.056	1.95E-05	3.22E-04	Up-regulated
AK4	Adenylate kinase 4	Nucleoside triphosphate adenylate kinase activity	2.074	1.96E-08	1.25E-06	Up-regulated
ALCAM	Activated leukocyte cell adhesion molecule	External side of plasma membrane	2.575	5.08E-12	1.38E-09	Up-regulated
ANLN	Anillin, actin binding protein	Hematopoietic progenitor cell differentiation	2.981	1.65E-07	6.90E-06	Up-regulated
AOAH	Acyloxyacyl hydrolase (neutrophil)	Acyloxyacyl hydrolase activity	2.388	2.34E-06	5.68E-05	Up-regulated
APLN	Apelin	Positive regulation of corticotropin-releasing hormone secretion	4.238	2.53E-08	1.52E-06	Up-regulated
APOBR	Apolipoprotein B receptor	Very-low-density lipoprotein particle receptor activity	3.469	5.03E-11	9.14E-09	Up-regulated
AQP4	Aquaporin 4	Multicellular organismal water homeostasis	−2.236	1.10E-06	3.10E-05	Down-regulated
AQP9	Aquaporin 9	Pyrimidine nucleobase transmembrane transporter activity	3.773	8.71E-08	4.21E-06	Up-regulated
ARG1	Arginase 1	Cellular response to transforming growth factor β stimulus	4.363	1.46E-09	1.49E-07	Up-regulated
ARHGAP25	Rho GTPase activating protein 25	Regulation of small GTPase mediated signal transduction	2.275	2.28E-09	2.21E-07	Up-regulated
ART3	ADP-ribosyltransferase 3	NAD(P) ± protein-arginine ADP-ribosyltransferase activity	−2.691	5.08E-08	2.68E-06	Down-regulated
ASB5	Ankyrin repeat and SOCS box containing 5	Intracellular signal transduction	5.114	5.83E-11	1.04E-08	Up-regulated
ASPM	Asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	Positive regulation of canonical Wnt signaling pathway	3.715	1.08E-09	1.16E-07	Up-regulated
ATP6V0D2	Atpase, H+ transporting, lysosomal 38kDa, V0 subunit d2	Vacuolar proton-transporting V-type ATPase complex	5.247	1.19E-15	2.38E-12	Up-regulated
ATP6V1A	Atpase, H+ transporting, lysosomal 70kDa, V1 subunit A	Proton-transporting ATPase activity, rotational mechanism	2.036	1.04E-09	1.15E-07	Up-regulated
ATP8B4	Atpase, class I, type 8B, member 4	Phospholipid-translocating ATPase activity	2.028	3.58E-08	2.03E-06	Up-regulated
AURKB	Aurora kinase B	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	3.068	1.52E-05	2.64E-04	Up-regulated
B3GALNT1	Beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	Galactosylgalactosylglucosylceramide β-D-acetylgalactosaminyltransferase activity	2.588	2.05E-05	3.34E-04	Up-regulated
BANK1	B-cell scaffold protein with ankyrin repeats 1	Negative regulation of protein kinase B signaling	2.906	6.26E-09	5.01E-07	Up-regulated
BASP1	Brain abundant, membrane attached signal protein 1	Positive regulation of metanephric ureteric bud development	2.576	4.77E-10	6.11E-08	Up-regulated
BATF	Basic leucine zipper transcription factor, ATF-like	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.041	1.23E-04	1.35E-03	Up-regulated
BCL2L15	BCL2-like 15	Apoptotic process	2.39	2.79E-04	2.57E-03	Up-regulated
BLK	BLK proto-oncogene, Src family tyrosine kinase	Transmembrane receptor protein tyrosine kinase signaling pathway	3.377	1.91E-05	3.16E-04	Up-regulated
BUB1	BUB1 mitotic checkpoint serine/threonine kinase	Positive regulation of intrinsic apoptotic signaling pathway	2.613	2.96E-05	4.43E-04	Up-regulated
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	2.989	1.34E-08	9.08E-07	Up-regulated
C11orf16	Chromosome 11 open reading frame 16	Unknown	2.305	1.14E-07	5.16E-06	Up-regulated
C12orf40	Chromosome 12 open reading frame 40	Protein binding	−2.078	1.46E-04	1.55E-03	Down-regulated
C1orf162	Chromosome 1 open reading frame 162	Integral component of membrane	2.949	3.55E-08	2.03E-06	Up-regulated
C1orf228	Chromosome 1 open reading frame 228	Unknown	3.692	3.18E-08	1.86E-06	Up-regulated
C4orf47	Chromosome 4 open reading frame 47	Centrosome	2.351	5.23E-06	1.10E-04	Up-regulated
CA2	Carbonic anhydrase II	Positive regulation of dipeptide transmembrane transport	5.324	2.67E-14	2.14E-11	Up-regulated
CA9	Carbonic anhydrase IX	Regulation of transcription from RNA polymerase II promoter in response to hypoxia	2.045	2.16E-06	5.30E-05	Up-regulated
CAPG	Capping protein (actin filament), gelsolin-like	Positive regulation of podosome assembly	2.042	2.38E-07	9.24E-06	Up-regulated
CASC5	Cancer susceptibility candidate 5	Attachment of spindle microtubules to kinetochore	2.901	1.95E-05	3.22E-04	Up-regulated
CCDC68	Coiled-coil domain containing 68	Protein binding	−2.216	5.51E-06	1.14E-04	Down-regulated
CCL20	Chemokine (C-C motif) ligand 20	Positive regulation of nitric-oxide synthase biosynthetic process	2.926	3.64E-07	1.35E-05	Up-regulated
CCL4	Chemokine (C-C motif) ligand 4	Positive regulation of natural killer cell chemotaxis	2.307	1.99E-06	4.97E-05	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
CCL5	Chemokine (C-C motif) ligand 5	Negative regulation of G-protein coupled receptor protein signaling pathway	4.023	2.98E-10	4.26E-08	Up-regulated
CCNB1	Cyclin B1	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.835	4.02E-07	1.45E-05	Up-regulated
CCNB2	Cyclin B2	G2/M transition of mitotic cell cycle	3.617	6.36E-07	2.04E-05	Up-regulated
CCR1	Chemokine (C-C motif) receptor 1	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	4.059	7.57E-14	4.02E-11	Up-regulated
CCR5	Chemokine (C-C motif) receptor 5 (gene/pseudogene)	Release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	2.797	8.41E-11	1.42E-08	Up-regulated
CCR8	Chemokine (C-C motif) receptor 8	Positive regulation of cytosolic calcium ion concentration	3.355	4.70E-04	3.86E-03	Up-regulated
CCRL2	Chemokine (C-C motif) receptor-like 2	G-protein coupled receptor signaling pathway	3.088	5.46E-06	1.13E-04	Up-regulated
CD101	CD101 molecule	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides	2.892	4.71E-06	1.01E-04	Up-regulated
CD14	CD14 molecule	Activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	2.059	1.68E-05	2.85E-04	Up-regulated
CD163	CD163 molecule	Integral component of plasma membrane	2.478	6.36E-06	1.28E-04	Up-regulated
CD19	CD19 molecule	Positive regulation of release of sequestered calcium ion into cytosol	2.589	2.83E-04	2.59E-03	Up-regulated
CD1C	CD1c molecule	Antigen processing and presentation, exogenous lipid antigen via *MHC* class Ib	2.843	6.48E-08	3.25E-06	Up-regulated
CD27	CD27 molecule	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.146	1.24E-05	2.21E-04	Up-regulated
CD38	CD38 molecule	Positive regulation of cytosolic calcium ion concentration	2.384	9.01E-06	1.71E-04	Up-regulated
CD48	CD48 molecule	Integral component of plasma membrane	2.297	8.12E-09	6.19E-07	Up-regulated
CD53	CD53 molecule	Positive regulation of myoblast fusion	2.295	4.80E-07	1.65E-05	Up-regulated
CD68	CD68 molecule	Cellular response to organic substance	2.852	6.07E-09	4.89E-07	Up-regulated
CD69	CD69 molecule	Transmembrane signaling receptor activity	2.086	1.87E-04	1.88E-03	Up-regulated
CD72	CD72 molecule	Transmembrane signaling receptor activity	4.449	1.11E-11	2.58E-09	Up-regulated
CD79B	CD79b molecule, immunoglobulin-associated β	Transmembrane signaling receptor activity	2.731	2.67E-05	4.13E-04	Up-regulated
CD84	CD84 molecule	Homophilic cell adhesion via plasma membrane adhesion molecules	2.222	5.36E-07	1.77E-05	Up-regulated
CDA	Cytidine deaminase	Nucleobase-containing small molecule metabolic process	2.095	4.82E-08	2.60E-06	Up-regulated
CDC20	Cell division cycle 20	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.244	6.07E-05	7.67E-04	Up-regulated
CDCA2	Cell division cycle associated 2	Positive regulation of protein dephosphorylation	2.411	6.72E-05	8.36E-04	Up-regulated
CDCA7	Cell division cycle associated 7	Regulation of transcription, DNA-templated	3.452	1.43E-05	2.50E-04	Up-regulated
CDH18	Cadherin 18 type 2	Homophilic cell adhesion via plasma membrane adhesion molecules	−2.039	1.72E-04	1.77E-03	Down-regulated
CDH19	Cadherin 19 type 2	Calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	−2.025	9.47E-06	1.78E-04	Down-regulated
CDK1	Cyclin-dependent kinase 1	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.666	4.48E-07	1.57E-05	Up-regulated
CELSR3	Cadherin, EGF LAG seven-pass G-type receptor 3	Homophilic cell adhesion via plasma membrane adhesion molecules	2.031	3.61E-05	5.19E-04	Up-regulated
CENPA	Centromere protein A	Protein localization to chromosome, centromeric region	3.417	5.63E-07	1.84E-05	Up-regulated
CENPE	Centromere protein E, 312kDa	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	3.006	4.88E-06	1.03E-04	Up-regulated
CENPF	Centromere protein F, 350/400kDa	Negative regulation of transcription, DNA-templated	2.959	6.77E-06	1.35E-04	Up-regulated
CEP55	Centrosomal protein 55kDa	Establishment of protein localization	3.098	2.71E-06	6.44E-05	Up-regulated
CERKL	Ceramide kinase-like	Negative regulation of apoptotic process	2.374	8.82E-08	4.23E-06	Up-regulated
CHI3L1	Chitinase 3-like 1 (cartilage glycoprotein-39)	Positive regulation of peptidyl-threonine phosphorylation	5.602	1.11E-17	1.10E-13	Up-regulated
CHI3L2	Chitinase 3-like 2	Carbohydrate metabolic process	2.777	8.73E-06	1.66E-04	Up-regulated
CHIT1	Chitinase 1 (chitotriosidase)	Polysaccharide catabolic process	4.887	6.77E-12	1.76E-09	Up-regulated
CKS2	CDC28 protein kinase regulatory subunit 2	Regulation of cyclin-dependent protein serine/threonine kinase activity	3.33	1.86E-08	1.20E-06	Up-regulated
CLDN19	Claudin 19	Calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	−2.28	3.53E-04	3.06E-03	Down-regulated
CLEC4A	C-type lectin domain family 4 member A	Stimulatory C-type lectin receptor signaling pathway	3.273	1.56E-11	3.40E-09	Up-regulated
CLEC4D	C-type lectin domain family 4 member D	Stimulatory C-type lectin receptor signaling pathway	4.201	8.63E-15	1.02E-11	Up-regulated
CLEC4E	C-type lectin domain family 4 member E	Stimulatory C-type lectin receptor signaling pathway	3.776	2.30E-17	1.15E-13	Up-regulated
CLEC9A	C-type lectin domain family 9 member A	Positive regulation of cytokine secretion	2.474	1.53E-04	1.61E-03	Up-regulated
CLIP4	CAP-GLY domain containing linker protein family, member 4	Negative regulation of T cell receptor signaling pathway	−2.572	6.89E-08	3.44E-06	Down-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
CLSTN2	Calsyntenin 2	Homophilic cell adhesion via plasma membrane adhesion molecules	4.223	2.43E-10	3.63E-08	Up-regulated
CNR2	Cannabinoid receptor 2 (macrophage)	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	2.199	3.56E-04	3.08E-03	Up-regulated
COCH	Cochlin	Positive regulation of innate immune response	2.861	4.37E-08	2.44E-06	Up-regulated
CPA5	Carboxypeptidase A5	Metallocarboxypeptidase activity	3.777	2.89E-14	2.14E-11	Up-regulated
CPPED1	Calcineurin-like phosphoesterase domain containing 1	Phosphoprotein phosphatase activity	2.068	9.46E-13	3.63E-10	Up-regulated
CPVL	Carboxypeptidase, vitellogenic-like	Serine-type carboxypeptidase activity	2.233	1.14E-06	3.17E-05	Up-regulated
CSF2RB	Colony stimulating factor 2 receptor, β, low-affinity (granulocyte-macrophage)	Granulocyte macrophage colony-stimulating factor receptor complex	2.367	3.05E-06	7.14E-05	Up-regulated
CTSB	Cathepsin B	Proteolysis involved in cellular protein catabolic process	2.15	1.77E-08	1.15E-06	Up-regulated
CTSE	Cathepsin E	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	4.164	2.35E-14	2.14E-11	Up-regulated
CTSS	Cathepsin S	Antigen processing and presentation of exogenous peptide antigen via *MHC* class I, *TAP*-independent	2.432	2.67E-09	2.51E-07	Up-regulated
CTSV	Cathepsin V	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.803	3.38E-11	6.49E-09	Up-regulated
CXCL11	Chemokine (C-X-C motif) ligand 11	Positive regulation of release of sequestered calcium ion into cytosol	2.203	2.11E-05	3.43E-04	Up-regulated
CXCL13	Chemokine (C-X-C motif) ligand 13	Negative regulation of endothelial cell chemotaxis to fibroblast growth factor	6.286	9.57E-14	4.78E-11	Up-regulated
CXCL13	Chemokine (C-X-C motif) ligand 13	Negative regulation of endothelial cell chemotaxis to fibroblast growth factor	2.92	1.34E-06	3.67E-05	Up-regulated
CXCL13	Chemokine (C-X-C motif) ligand 13	Negative regulation of endothelial cell chemotaxis to fibroblast growth factor	2.471	3.65E-06	8.11E-05	Up-regulated
CXCL13	Chemokine (C-X-C motif) ligand 13	Negative regulation of endothelial cell chemotaxis to fibroblast growth factor	6.49	5.49E-09	4.53E-07	Up-regulated
CXCL8	Chemokine (C-X-C motif) ligand 8	Regulation of single-stranded viral RNA replication via double-stranded DNA intermediate	5.463	2.09E-10	3.21E-08	Up-regulated
CXCR4	Chemokine (C-X-C motif) receptor 4	Positive regulation of cytosolic calcium ion concentration	3.211	9.02E-10	1.01E-07	Up-regulated
CYBB	Cytochrome b-245 β polypeptide	Antigen processing and presentation of exogenous peptide antigen via *MHC* class I, *TAP*-dependent	2.643	3.20E-09	2.95E-07	Up-regulated
CYP2D6	Cytochrome P450, family 2 subfamily D, polypeptide 6	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	−2.991	4.23E-06	9.28E-05	Down-regulated
DAPL1	Death associated protein-like 1	Cellular response to amino acid starvation	−3.922	2.45E-12	7.41E-10	Down-regulated
DCHS2	Dachsous cadherin-related 2	Homophilic cell adhesion via plasma membrane adhesion molecules	−2.599	3.27E-08	1.89E-06	Down-regulated
DCSTAMP	Dendrocyte expressed seven transmembrane protein	Cellular response to macrophage colony-stimulating factor stimulus	5.363	3.91E-10	5.43E-08	Up-regulated
DDIAS	DNA damage-induced apoptosis suppressor	Negative regulation of fibroblast apoptotic process	2.475	4.89E-07	1.67E-05	Up-regulated
DEPDC1B	DEP domain containing 1B	Regulation of small GTPase mediated signal transduction	2.134	7.09E-05	8.74E-04	Up-regulated
DHRS9	Dehydrogenase/reductase (SDR family) member 9	Integral component of endoplasmic reticulum membrane	3.533	1.41E-09	1.45E-07	Up-regulated
DKK3	Dickkopf WNT signaling pathway inhibitor 3	Negative regulation of aldosterone biosynthetic process	−2.125	2.65E-09	2.51E-07	Down-regulated
DLGAP5	Discs, large (Drosophila) homolog-associated protein 5	Positive regulation of mitotic metaphase/anaphase transition	3.329	9.92E-08	4.61E-06	Up-regulated
DOK3	Docking protein 3	Ras protein signal transduction	2.136	1.69E-06	4.41E-05	Up-regulated
DRP2	Dystrophin related protein 2	Nucleobase-containing compound metabolic process	−2.492	8.65E-06	1.66E-04	Down-regulated
DSC2	Desmocollin 2	Cell adhesive protein binding involved in bundle of His cell-Purkinje myocyte communication	−2.182	1.46E-06	3.92E-05	Down-regulated
DSG2	Desmoglein 2	Cell adhesive protein binding involved in bundle of His cell-Purkinje myocyte communication	3.073	5.42E-06	1.12E-04	Up-regulated
DSP	Desmoplakin	Cell adhesive protein binding involved in bundle of His cell-Purkinje myocyte communication	−2.382	5.40E-07	1.78E-05	Down-regulated
DUSP5	Dual specificity phosphatase 5	*MAP* kinase tyrosine/serine/threonine phosphatase activity	2.151	1.84E-07	7.46E-06	Up-regulated
E2F1	E2F transcription factor 1	Positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2.147	3.23E-05	4.75E-04	Up-regulated
E2F8	E2F transcription factor 8	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	2.332	1.35E-04	1.46E-03	Up-regulated
ECT2	Epithelial cell transforming 2	Regulation of attachment of spindle microtubules to kinetochore	3.077	7.67E-07	2.34E-05	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
EGLN3	Egl-9 family hypoxia-inducible factor 3	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	4.415	9.82E-12	2.39E-09	Up-regulated
EMILIN2	Elastin microfibril interfacer 2	Extracellular matrix constituent conferring elasticity	2.493	1.80E-08	1.17E-06	Up-regulated
ENO2	Enolase 2 (γ, neuronal)	Phosphopyruvate hydratase activity	3.632	9.22E-15	1.02E-11	Up-regulated
EPCAM	Epithelial cell adhesion molecule	Positive regulation of transcription from RNA polymerase II promoter	2.012	3.20E-06	7.36E-05	Up-regulated
EPHA6	EPH receptor A6	Integral component of plasma membrane	−2.681	6.10E-06	1.24E-04	Down-regulated
EPHX4	Epoxide hydrolase 4	Integral component of membrane	2.876	4.31E-09	3.69E-07	Up-regulated
EPX	Eosinophil peroxidase	Negative regulation of interleukin-10 production	−2.128	3.95E-04	3.34E-03	Down-regulated
ERBB3	Erb-b2 receptor tyrosine kinase 3	Transmembrane receptor protein tyrosine kinase signaling pathway	−2.192	2.01E-07	8.09E-06	Down-regulated
ERCC6 L	Excision repair cross-complementation group 6-like	Small GTPase mediated signal transduction	2.505	1.37E-05	2.41E-04	Up-regulated
ERO1 L	ERO1-like (S. Cerevisiae)	Oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	2.47	7.94E-11	1.37E-08	Up-regulated
ESCO2	Establishment of sister chromatid cohesion N-acetyltransferase 2	Lysine N-acetyltransferase activity, acting on acetyl phosphate as donor	2.366	3.58E-04	3.09E-03	Up-regulated
ETV4	Ets variant 4	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.198	5.31E-05	6.91E-04	Up-regulated
EVI2B	Ecotropic viral integration site 2B	Integral component of plasma membrane	2.132	7.67E-07	2.34E-05	Up-regulated
EXO1	Exonuclease 1	Humoral immune response mediated by circulating immunoglobulin	2.993	3.09E-06	7.19E-05	Up-regulated
F3	Coagulation factor III (thromboplastin, tissue factor)	Activation of cysteine-type endopeptidase activity involved in apoptotic process	−2.058	1.09E-08	7.74E-07	Down-regulated
FABP5	Fatty acid binding protein 5 (psoriasis-associated)	Phosphatidylcholine biosynthetic process	3.9	6.86E-14	4.02E-11	Up-regulated
FADS1	Fatty acid desaturase 1	Unsaturated fatty acid biosynthetic process	2.073	1.37E-04	1.47E-03	Up-regulated
FADS1	Fatty acid desaturase 1	Unsaturated fatty acid biosynthetic process	2.138	3.32E-06	7.55E-05	Up-regulated
FAIM2	Fas apoptotic inhibitory molecule 2	Negative regulation of apoptotic signaling pathway	2.91	9.48E-04	6.85E-03	Up-regulated
FAIM3	Fas apoptotic inhibitory molecule 3	Negative regulation of apoptotic process	2.952	2.35E-04	2.25E-03	Up-regulated
FAM150A	Family with sequence similarity 150, member A	Extracellular region	−2.532	3.46E-05	5.01E-04	Down-regulated
FAM46C	Family with sequence similarity 46, member C	Protein binding	2.024	1.25E-05	2.22E-04	Up-regulated
FBP1	Fructose-16-bisphosphatase 1	Negative regulation of Ras protein signal transduction	2.021	3.45E-04	3.02E-03	Up-regulated
FCRL1	Fc receptor-like 1	Integral component of membrane	3.566	2.64E-04	2.46E-03	Up-regulated
FCRL3	Fc receptor-like 3	Integral component of membrane	2.054	5.07E-05	6.66E-04	Up-regulated
FCRLA	Fc receptor-like A	Cell differentiation	3.344	2.09E-04	2.06E-03	Up-regulated
FGF23	Fibroblast growth factor 23	Positive regulation of *MAPKKK* cascade by fibroblast growth factor receptor signaling pathway	7.423	9.83E-12	2.39E-09	Up-regulated
FGF7	Fibroblast growth factor 7	Regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	2.551	3.25E-08	1.89E-06	Up-regulated
FGL1	Fibrinogen-like 1	Extracellular exosome	3.707	4.16E-06	9.14E-05	Up-regulated
FLVCR2	Feline leukemia virus subgroup C cellular receptor family, member 2	Integral component of membrane	2.29	2.52E-06	6.03E-05	Up-regulated
FMN1	Formin 1	Microtubule binding	2.028	1.43E-05	2.50E-04	Up-regulated
FNTB	Farnesyltransferase, CAAX box, β	Positive regulation of nitric-oxide synthase biosynthetic process	2.317	7.65E-14	4.02E-11	Up-regulated
FOLR2	Folate receptor 2 (fetal)	Regulation of thymidylate synthase biosynthetic process	2.325	7.52E-06	1.48E-04	Up-regulated
FOXM1	Forkhead box M1	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	2.688	9.37E-06	1.77E-04	Up-regulated
FRMPD1	FERM and PDZ domain containing 1	Extracellular exosome	−2.298	9.03E-08	4.27E-06	Down-regulated
FRRS1	Ferric-chelate reductase 1	Ferric-chelate reductase activity	2.436	5.53E-08	2.83E-06	Up-regulated
FTL	Ferritin, light polypeptide	Post-Golgi vesicle-mediated transport	3.393	4.20E-10	5.66E-08	Up-regulated
GALNT6	Polypeptide N-acetylgalactosaminyltransferase 6	Polypeptide N-acetylgalactosaminyltransferase activity	3.685	5.19E-10	6.39E-08	Up-regulated
GAPT	GRB2-binding adaptor protein, transmembrane	Immunoglobulin production involved in immunoglobulin mediated immune response	2.689	6.80E-04	5.21E-03	Up-regulated
GGH	γ-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	γ-glutamyl-peptidase activity	2.62	4.43E-08	2.44E-06	Up-regulated
GLRX	Glutaredoxin (thioltransferase)	Positive regulation of sodium ion transmembrane transporter activity	2.955	1.78E-06	4.55E-05	Up-regulated
GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	Glycerol-3-phosphate dehydrogenase (*NAD+*)activity	−2.568	1.08E-07	4.93E-06	Down-regulated
GPI	Glucose-6-phosphate isomerase	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.093	1.12E-09	1.19E-07	Up-regulated
GPNMB	Glycoprotein (transmembrane) nmb	Negative regulation of tumor necrosis factor production	2.746	2.32E-06	5.66E-05	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
GPR158	G protein-coupled receptor 158	Regulation of G-protein coupled receptor protein signaling pathway	5.884	1.27E-09	1.34E-07	Up-regulated
GPR171	G protein-coupled receptor 171	G-protein coupled purinergic nucleotide receptor signaling pathway	2.211	1.56E-04	1.63E-03	Up-regulated
GPR18	G protein-coupled receptor 18	G-protein coupled receptor signaling pathway	3.07	7.58E-09	5.83E-07	Up-regulated
GPR84	G protein-coupled receptor 84	Phospholipase C-activating G-protein coupled receptor signaling pathway	3.628	2.07E-05	3.37E-04	Up-regulated
GPRC5D	G protein-coupled receptor, class C, group 5 member D	G-protein coupled receptor signaling pathway	2.051	1.16E-03	8.03E-03	Up-regulated
GPRIN3	GPRIN family member 3	Unknown	2.444	6.77E-05	8.40E-04	Up-regulated
GSG2	Germ cell associated 2 (haspin)	Histone H3-T3 phosphorylation involved in chromosome passenger complex localization to kinetochore	2.477	1.71E-04	1.77E-03	Up-regulated
GTF3C6	General transcription factor IIIC, polypeptide 6 α 35kDa	5S class ribosomal RNA transcription from RNA polymerase III type 1 promoter	4.617	6.18E-13	2.57E-10	Up-regulated
HAAO	3-hydroxyanthranilate 34-dioxygenase	"De novo" *NAD* biosynthetic process from tryptophan	2.565	3.85E-07	1.40E-05	Up-regulated
HAS2	Hyaluronan synthase 2	Positive regulation of substrate adhesion-dependent cell spreading	2.676	3.13E-11	6.24E-09	Up-regulated
HAVCR1	Hepatitis A virus cellular receptor 1	Integral component of membrane	2.297	3.83E-05	5.43E-04	Up-regulated
HCK	HCK proto-oncogene, Src family tyrosine kinase	Regulation of sequence-specific DNA binding transcription factor activity	2.154	6.94E-07	2.20E-05	Up-regulated
HELLS	Helicase, lymphoid-specific	Methylation-dependent chromatin silencing	2.417	1.22E-07	5.38E-06	Up-regulated
HHIP	Hedgehog interacting protein	Oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor	−3.512	4.82E-15	6.88E-12	Down-regulated
HILS1	Histone linker H1 domain, spermatid-specific 1 pseudogene	Regulation of transcription, DNA-templated	2.327	4.35E-05	5.95E-04	Up-regulated
HK3	Hexokinase 3 (white cell)	Early endosome to late endosome transport	2.099	4.66E-05	6.27E-04	Up-regulated
HLA-DRA	Major histocompatibility complex, class II, DR α	Antigen processing and presentation of peptide or polysaccharide antigen via *MHC* class II	2.073	2.53E-08	1.52E-06	Up-regulated
HMGA2	High mobility group AT-hook 2	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	3.322	7.53E-09	5.83E-07	Up-regulated
HMMR	Hyaluronan-mediated motility receptor (RHAMM)	Glycosaminoglycan metabolic process	3.965	1.21E-08	8.43E-07	Up-regulated
HMOX1	Heme oxygenase 1	Regulation of transcription from RNA polymerase II promoter in response to oxidative stress	4.416	5.12E-08	2.69E-06	Up-regulated
HNMT	Histamine N-methyltransferase	Positive regulation of protein targeting to mitochondrion	2.28	4.04E-10	5.53E-08	Up-regulated
HOOK1	Hook microtubule-tethering protein 1	Early endosome to late endosome transport	2.098	3.70E-04	3.17E-03	Up-regulated
HRH1	Histamine receptor H1	Positive regulation of adenylate cyclase activity involved in G-protein coupled receptor signaling pathway	−2.394	7.10E-07	2.23E-05	Down-regulated
HS3ST3B1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Heparan sulfate proteoglycan biosynthetic process, enzymatic modification	2.026	1.55E-04	1.63E-03	Up-regulated
HSPB3	Heat shock 27kDa protein 3	Response to unfolded protein	2.298	2.42E-04	2.31E-03	Up-regulated
IBSP	Integrin-binding sialoprotein	Cellular response to growth factor stimulus	6.221	6.88E-12	1.76E-09	Up-regulated
ICOS	Inducible T-cell co-stimulator	Integral component of plasma membrane	2.105	8.52E-05	1.01E-03	Up-regulated
IGF2BP3	Insulin-like growth factor 2 mRNA binding protein 3	Regulation of cytokine biosynthetic process	2.684	6.51E-06	1.31E-04	Up-regulated
IGHV3–23	Immunoglobulin heavy variable 3–23	Fc-γ receptor signaling pathway involved in phagocytosis	2.1	6.12E-06	1.24E-04	Up-regulated
IGHV3–23	Immunoglobulin heavy variable 3–23	Fc-γ receptor signaling pathway involved in phagocytosis	2.326	6.85E-07	2.18E-05	Up-regulated
IGSF6	Immunoglobulin superfamily, member 6	Transmembrane signaling receptor activity	3.615	4.48E-14	2.80E-11	Up-regulated
IKZF3	IKAROS family zinc finger 3 (Aiolos)	RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.782	1.22E-05	2.19E-04	Up-regulated
IL10	Interleukin 10	Positive regulation of sequence-specific DNA binding transcription factor activity	2.12	4.41E-05	6.01E-04	Up-regulated
IL18BP	Interleukin 18 binding protein	Extracellular negative regulation of signal transduction	2.181	2.81E-13	1.28E-10	Up-regulated
IL18R1	Interleukin 18 receptor 1	Positive regulation of nuclear factor-κb import into nucleus	2.517	1.18E-05	2.13E-04	Up-regulated
IL18RAP	Interleukin 18 receptor accessory protein	Cell surface receptor signaling pathway	2.351	4.44E-04	3.67E-03	Up-regulated
IL1B	Interleukin 1 β	Positive regulation of vascular endothelial growth factor receptor signaling pathway	3.209	7.84E-06	1.53E-04	Up-regulated
IL1RAP	Interleukin 1 receptor accessory protein	Integral component of plasma membrane	2.577	4.25E-10	5.66E-08	Up-regulated
IL1RN	Interleukin 1 receptor antagonist	Negative regulation of interleukin-1-mediated signaling pathway	3.248	4.45E-08	2.44E-06	Up-regulated
IL23A	Interleukin 23 α subunit p19	Positive regulation of granulocyte macrophage colony-stimulating factor production	3.604	1.63E-07	6.82E-06	Up-regulated
IL2RG	Interleukin 2 receptor, γ	Interleukin-2-mediated signaling pathway	2.185	6.27E-06	1.27E-04	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
IL6	Interleukin 6	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	3.778	6.67E-09	5.25E-07	Up-regulated
IL7R	Interleukin 7 receptor	Positive regulation of T cell differentiation in thymus	3.702	2.60E-16	6.79E-13	Up-regulated
INHBB	Inhibin, β B	Positive regulation of pathway-restricted *SMAD* protein phosphorylation	3.305	2.28E-09	2.21E-07	Up-regulated
IRG1	Immunoresponsive 1 homolog (mouse)	Positive regulation of reactive oxygen species metabolic process	4.375	1.11E-10	1.84E-08	Up-regulated
ITGA4	Integrin, α 4 (antigen CD49D, α 4 subunit of VLA-4 receptor)	Heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	2.695	2.87E-08	1.70E-06	Up-regulated
JCHAIN	Joining chain of multimeric IgA and IgM	Positive regulation of protein oligomerization	5.132	1.42E-08	9.55E-07	Up-regulated
KANK4	KN motif and ankyrin repeat domains 4	Cytoplasm	−2.066	2.45E-04	2.32E-03	Down-regulated
KCNIP1	Kv channel interacting protein 1	Extrinsic component of cytoplasmic side of plasma membrane	2.307	1.78E-05	2.97E-04	Up-regulated
KIAA0101	Kiaa0101	Cellular response to DNA damage stimulus	3.592	1.28E-08	8.82E-07	Up-regulated
KIAA1598	Kiaa1598	Regulation of establishment of cell polarity	2.119	2.43E-08	1.49E-06	Up-regulated
KIF11	Kinesin family member 11	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.931	3.70E-06	8.21E-05	Up-regulated
KIF14	Kinesin family member 14	*SCF*-dependent proteasomal ubiquitin-dependent protein catabolic process	2.541	4.87E-08	2.60E-06	Up-regulated
KIF18B	Kinesin family member 18B	ATP-dependent microtubule motor activity, plus-end-directed	2.962	8.08E-07	2.44E-05	Up-regulated
KIF20A	Kinesin family member 20A	Cell separation after cytokinesis	2.58	2.09E-07	8.27E-06	Up-regulated
KIF24	Kinesin family member 24	Microtubule depolymerization	2.502	6.33E-07	2.03E-05	Up-regulated
KIFC1	Kinesin family member C1	ATP-dependent microtubule motor activity, minus-end-directed	2.352	2.03E-07	8.10E-06	Up-regulated
KLC1	Kinesin light chain 1	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.125	1.35E-04	1.46E-03	Up-regulated
KLC1	Kinesin light chain 1	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.618	3.36E-05	4.90E-04	Up-regulated
KLHL6	Kelch-like family member 6	*Cul3-RING* ubiquitin ligase complex	2.582	5.48E-10	6.59E-08	Up-regulated
KRT32	Keratin 32 type I	Structural molecule activity	2.387	8.07E-05	9.72E-04	Up-regulated
KRT8	Keratin 8 type II	Cell differentiation involved in embryonic placenta development	2.138	1.14E-03	7.92E-03	Up-regulated
LANCL3	Lanc lantibiotic synthetase component C-like 3 (bacterial)	Catalytic activity	2.389	4.00E-05	5.63E-04	Up-regulated
LAT	Linker for activation of T cells	Nuclear origin of replication recognition complex	2.113	3.19E-06	7.36E-05	Up-regulated
LCP1	Lymphocyte cytosolic protein 1 (L-plastin)	Regulation of intracellular protein transport	2.276	6.00E-08	3.03E-06	Up-regulated
LECT1	Leukocyte cell derived chemotaxin 1	Negative regulation of vascular endothelial growth factor receptor signaling pathway	−2.176	2.26E-04	2.18E-03	Down-regulated
LEP	Leptin	Positive regulation of peroxisome proliferator activated receptor signaling pathway	−2.371	1.20E-06	3.32E-05	Down-regulated
LGALS3	Lectin, galactoside-binding, soluble, 3	Negative regulation of T-cell activation via T-cell receptor contact with antigen bound to *MHC* molecule on antigen presenting cell	3.583	2.72E-16	6.79E-13	Up-regulated
LGALS7/LGALS7B	Lectin, galactoside-binding, soluble, 7	Heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	3.084	4.99E-06	1.05E-04	Up-regulated
LIPA	Lipase A, lysosomal acid, cholesterol esterase	Homeostasis of number of cells within a tissue	3.589	1.78E-07	7.29E-06	Up-regulated
LIPA	Lipase A, lysosomal acid, cholesterol esterase	Homeostasis of number of cells within a tissue	5.181	7.73E-10	8.98E-08	Up-regulated
LPAR3	Lysophosphatidic acid receptor 3	Positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	3.454	1.16E-07	5.23E-06	Up-regulated
LPCAT2	Lysophosphatidylcholine acyltransferase 2	1-alkylglycerophosphocholine O-acetyltransferase activity	2.074	3.12E-07	1.18E-05	Up-regulated
LPXN	Leupaxin	Negative regulation of B cell receptor signaling pathway	2.25	2.29E-07	8.94E-06	Up-regulated
LTA	Lymphotoxin α	Positive regulation of humoral immune response mediated by circulating immunoglobulin	2.109	9.99E-05	1.14E-03	Up-regulated
LY86	Lymphocyte antigen 86	Positive regulation of lipopolysaccharide-mediated signaling pathway	2.762	2.16E-08	1.36E-06	Up-regulated
MAP3K19	Mitogen-activated protein kinase kinase kinase 19	Activation of protein kinase activity	7.854	1.13E-10	1.85E-08	Up-regulated
MAPK13	Mitogen-activated protein kinase 13	Vascular endothelial growth factor receptor signaling pathway	2.389	3.92E-07	1.42E-05	Up-regulated
MBNL3	Muscleblind-like splicing regulator 3	Negative regulation of myoblast differentiation	2.542	6.87E-07	2.18E-05	Up-regulated
MC5R	Melanocortin 5 receptor	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	−2.426	1.31E-07	5.70E-06	Down-regulated
MCM8	Minichromosome maintenance complex component 8	Double-strand break repair via homologous recombination	2.144	2.69E-04	2.50E-03	Up-regulated
MCOLN2	Mucolipin 2	Calcium ion transmembrane transport	2.947	1.73E-07	7.15E-06	Up-regulated
MELK	Maternal embryonic leucine zipper kinase	Intrinsic apoptotic signaling pathway in response to oxidative stress	3.825	6.19E-07	2.00E-05	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
MFSD8	Major facilitator superfamily domain containing 8	Substrate-specific transmembrane transporter activity	3.658	4.01E-14	2.67E-11	Up-regulated
MILR1	Mast cell immunoglobulin-like receptor 1	Negative regulation of mast cell activation	2.481	8.78E-07	2.60E-05	Up-regulated
MLANA	Melan-A	Integral component of plasma membrane	2.085	5.42E-05	7.01E-04	Up-regulated
MMP1	Matrix metallopeptidase 1	Positive regulation of protein oligomerization	8.407	1.93E-10	3.06E-08	Up-regulated
MMP12	Matrix metallopeptidase 12	Positive regulation of epithelial cell proliferation involved in wound healing	6.206	1.97E-10	3.07E-08	Up-regulated
MMP13	Matrix metallopeptidase 13	Low-density lipoprotein particle receptor binding	7.201	6.86E-13	2.74E-10	Up-regulated
MMP3	Matrix metallopeptidase 3	Negative regulation of hydrogen peroxide metabolic process	4.084	1.22E-05	2.19E-04	Up-regulated
MOGAT1	Monoacylglycerol O-acyltransferase 1	2-Acylglycerol O-acyltransferase activity	2.101	3.32E-04	2.93E-03	Up-regulated
MPEG1	Macrophage expressed 1	Integral component of membrane	2.847	1.03E-06	2.95E-05	Up-regulated
MPZ	Myelin protein zero	Negative regulation of apoptotic process	−3.4	1.33E-09	1.38E-07	Down-regulated
MREG	Melanoregulin	Melanocyte differentiation	3.746	1.45E-15	2.42E-12	Up-regulated
MS4A1	Membrane-spanning 4-domains, subfamily A, member 1	Protein kinase C-activating G-protein coupled receptor signaling pathway	4.07	4.19E-07	1.48E-05	Up-regulated
MSR1	Macrophage scavenger receptor 1	Positive regulation of macrophage derived foam cell differentiation	3.213	9.40E-09	6.86E-07	Up-regulated
MTFP1	Mitochondrial fission process 1	Integral component of membrane	3.372	1.06E-08	7.54E-07	Up-regulated
MTTP	Microsomal triglyceride transfer protein	Small molecule metabolic process	2.753	1.49E-03	9.73E-03	Up-regulated
MYH7	Myosin, heavy chain 7, cardiac muscle, β	Regulation of slow-twitch skeletal muscle fiber contraction	4.158	1.24E-07	5.44E-06	Up-regulated
MYH7B	Myosin, heavy chain 7B, cardiac muscle, β	Metabolic process	−3.342	1.79E-07	7.29E-06	Down-regulated
MYO1G	Myosin IG	Fc-γ receptor signaling pathway involved in phagocytosis	2.815	1.66E-12	5.72E-10	Up-regulated
MYOZ2	Myozenin 2	Protein phosphatase 2B binding	−2.448	1.95E-05	3.22E-04	Down-regulated
MZB1	Marginal zone B and B1 cell-specific protein	Negative regulation of glucose import in response to insulin stimulus	4.437	5.72E-08	2.91E-06	Up-regulated
NCAPG	Non-SMC condensin I complex, subunit G	Mitotic chromosome condensation	2.443	3.72E-05	5.32E-04	Up-regulated
NCMAP	Noncompact myelin associated protein	Peripheral nervous system myelin formation	−2.569	3.34E-06	7.58E-05	Down-regulated
NDUFA5	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 5	Mitochondrial electron transport, NADH to ubiquinone	2.865	2.17E-11	4.51E-09	Up-regulated
NEIL3	Nei endonuclease VIII-like 3 (E. coli)	DNA-(apurinic or apyrimidinic site) lyase activity	2.628	1.08E-03	7.61E-03	Up-regulated
NEK2	NIMA-related kinase 2	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	3.178	1.02E-07	4.71E-06	Up-regulated
NFASC	Neurofascin	Protein binding involved in heterotypic cell-cell adhesion	−2.249	2.29E-04	2.21E-03	Down-regulated
NIPAL4	NIPA-like domain containing 4	Magnesium ion transmembrane transporter activity	−2.161	3.23E-05	4.75E-04	Down-regulated
NKAIN1	Na+/K+ transporting ATPase interacting 1	Regulation of sodium ion transport	3.565	8.48E-09	6.42E-07	Up-regulated
NPM1	Nucleophosmin (nucleolar phosphoprotein B23 numatrin)	Negative regulation of protein kinase activity by regulation of protein phosphorylation	3.607	8.01E-06	1.55E-04	Up-regulated
NUF2	NUF2 NDC80 kinetochore complex component	Small GTPase-mediated signal transduction	3.212	7.47E-07	2.30E-05	Up-regulated
NYAP2	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	Phosphatidylinositol 3-kinase signaling	2.779	2.43E-10	3.63E-08	Up-regulated
OGDHL	Oxoglutarate dehydrogenase-like	Oxoglutarate dehydrogenase (succinyl-transferring) activity	−2.099	1.15E-05	2.09E-04	Down-regulated
OVGP1	Oviductal glycoprotein 1 120kDa	Negative regulation of binding of sperm to zona pellucida	2.855	8.14E-08	3.95E-06	Up-regulated
P2RX1	Purinergic receptor P2X, ligand gated ion channel, 1	Activation of cysteine-type endopeptidase activity involved in apoptotic process	−2.211	1.94E-06	4.87E-05	Down-regulated
P2RY10	Purinergic receptor P2Y, G-protein coupled, 10	G-protein coupled purinergic nucleotide receptor signaling pathway	2.564	4.54E-05	6.15E-04	Up-regulated
PARPBP	PARP1 binding protein	Negative regulation of double-strand break repair via homologous recombination	2.383	2.57E-04	2.42E-03	Up-regulated
PAX5	Paired box 5	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.793	1.73E-05	2.91E-04	Up-regulated
PBK	PDZ binding kinase	Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	2.934	3.12E-06	7.21E-05	Up-regulated
PCDHAC2	Protocadherin α subfamily C, 2	Homophilic cell adhesion via plasma membrane adhesion molecules	−3.112	7.76E-11	1.36E-08	Down-regulated
PDE4B	Phosphodiesterase 4B, camp-specific	Regulation of high voltage-gated calcium channel activity	2.299	1.45E-04	1.54E-03	Up-regulated
PDE6A	Phosphodiesterase 6A, camp-specific, rod, α	Regulation of rhodopsin mediated signaling pathway	2.271	8.55E-06	1.64E-04	Up-regulated
PFKFB1	6-phosphofructo-2-kinase/fructose-26-biphosphatase 1	6-phosphofructo-2-kinase/fructose-26-biphosphatase complex	−2.417	5.80E-07	1.89E-05	Down-regulated
PGBD5	PiggyBac transposable element derived 5	Integral component of membrane	4.221	3.32E-11	6.49E-09	Up-regulated
PIGR	Polymeric immunoglobulin receptor	Immunoglobulin transcytosis in epithelial cells mediated by polymeric immunoglobulin receptor	3.309	1.73E-05	2.91E-04	Up-regulated
PIGR	Polymeric immunoglobulin receptor	Immunoglobulin transcytosis in epithelial cells mediated by polymeric immunoglobulin receptor	3.876	1.71E-06	4.41E-05	Up-regulated
PKIB	Protein kinase (camp-dependent, catalytic) inhibitor β	Negative regulation of cyclin-dependent protein kinase activity	2.442	4.66E-10	6.11E-08	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
PLB1	Phospholipase B1	Phosphatidylcholine acyl-chain remodeling	2.755	4.24E-12	1.21E-09	Up-regulated
PLEK	Pleckstrin	Negative regulation of G-protein coupled receptor protein signaling pathway	2.5	1.54E-11	3.40E-09	Up-regulated
PLEKHM1	Pleckstrin homology domain containing, family M (with RUN domain) member 1	Intracellular signal transduction	2.181	2.35E-11	4.78E-09	Up-regulated
PLIN2	Perilipin 2	Response to organic cyclic compound	3.099	3.90E-09	3.42E-07	Up-regulated
PLP1	Proteolipid protein 1	Long-chain fatty acid biosynthetic process	−2.244	3.60E-09	3.24E-07	Down-regulated
PLXNC1	Plexin C1	Semaphorin-plexin signaling pathway	2.155	3.79E-08	2.12E-06	Up-regulated
POU2AF1	POU class 2 associating factor 1	Transcription from RNA polymerase II promoter	4.23	1.89E-08	1.21E-06	Up-regulated
PRDM1	PR domain containing 1 with ZNF domain	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	2.611	3.39E-08	1.94E-06	Up-regulated
PRND	Prion protein 2 (dublet)	Anchored component of membrane	5.761	1.44E-08	9.56E-07	Up-regulated
PRR11	Proline rich 11	Regulation of cell cycle	2.744	1.86E-05	3.10E-04	Up-regulated
PRTG	Protogenin	Multicellular organismal development	2.802	1.18E-07	5.27E-06	Up-regulated
PSG4	Pregnancy specific β-1-glycoprotein 4	Extracellular exosome	5.119	4.50E-05	6.11E-04	Up-regulated
PSG4	Pregnancy specific β-1-glycoprotein 4	Extracellular exosome	4.975	7.50E-08	3.69E-06	Up-regulated
PSG4	Pregnancy specific β-1-glycoprotein 4	Extracellular exosome	4.979	2.73E-08	1.62E-06	Up-regulated
PTGER3	Prostaglandin E receptor 3 (subtype EP3)	Ligand-activated sequence-specific DNA binding RNA polymerase II transcription factor activity	−2.149	1.66E-07	6.90E-06	Down-regulated
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/h synthase and cyclooxygenase)	Positive regulation of cell migration involved in sprouting angiogenesis	2.685	1.78E-12	5.72E-10	Up-regulated
PTPN22	Protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	Negative regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway	2.464	4.14E-07	1.47E-05	Up-regulated
PTPRC	Protein tyrosine phosphatase, receptor type, C	Negative regulation of cell adhesion involved in substrate-bound cell migration	2.396	4.32E-09	3.69E-07	Up-regulated
PTPRO	Protein tyrosine phosphatase, receptor type, O	Transmembrane receptor protein tyrosine phosphatase signaling pathway	2.288	9.59E-09	6.94E-07	Up-regulated
PTX3	Pentraxin 3 long	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.131	3.07E-06	7.16E-05	Up-regulated
PVR	Poliovirus receptor	Positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	4.28	1.31E-07	5.70E-06	Up-regulated
PVR	Poliovirus receptor	Positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	3.815	1.41E-12	5.21E-10	Up-regulated
RAB27B	RAB27B, member RAS oncogene family	Vesicle docking involved in exocytosis	−2.289	6.02E-05	7.63E-04	Down-regulated
RACGAP1	Rac GTPase activating protein 1	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.232	5.39E-06	1.12E-04	Up-regulated
RAD23A	RAD23 homolog A (S. Cerevisiae)	Regulation of proteasomal ubiquitin-dependent protein catabolic process	4.195	8.31E-07	2.48E-05	Up-regulated
RAD51	*RAD51* recombinase	Replication-born double-strand break repair via sister chromatid exchange	2.416	2.93E-05	4.40E-04	Up-regulated
RAD51AP1	*RAD51* associated protein 1	Regulation of double-strand break repair via homologous recombination	2.404	1.01E-05	1.88E-04	Up-regulated
RAD9A	RAD9 homolog A (S. Pombe)	Positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage	2.398	5.81E-04	4.60E-03	Up-regulated
RASSF6	Ras association (ralgds/AF-6) domain family member 6	Positive regulation of apoptotic process	3.185	4.90E-07	1.67E-05	Up-regulated
RBM47	RNA binding motif protein 47	Poly(A) RNA binding	2.039	7.37E-08	3.64E-06	Up-regulated
RGR	Retinal G protein coupled receptor	G-protein coupled receptor signaling pathway	2.506	5.54E-07	1.82E-05	Up-regulated
RGS1	Regulator of G-protein signaling 1	Adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	3.944	1.77E-12	5.72E-10	Up-regulated
RGS18	Regulator of G-protein signaling 18	Termination of G-protein coupled receptor signaling pathway	2.003	3.13E-05	4.62E-04	Up-regulated
RHOH	Ras homolog family member H	Negative regulation of I-κb kinase/nuclear factor-κb signaling	2.159	6.89E-04	5.27E-03	Up-regulated
RMI2	Recq mediated genome instability 2	DNA replication	2.708	6.58E-06	1.32E-04	Up-regulated
RNF128	Ring finger protein 128 E3 ubiquitin protein ligase	Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	3.244	1.03E-11	2.45E-09	Up-regulated
RPS24	Ribosomal protein S24	Maturation of *SSU*-rRNA from tricistronic rRNA transcript (*SSU*-rRNA, 5.8S rRNA, *LSU*-rRNA)	2.617	1.10E-03	7.69E-03	Up-regulated
RS1	Retinoschisin 1	Phosphatidylinositol-345-trisphosphate binding	2.487	1.52E-04	1.61E-03	Up-regulated
RTN4RL2	Reticulon 4 receptor-like 2	Anchored component of plasma membrane	4.082	3.00E-14	2.14E-11	Up-regulated
S100A12	S100 calcium binding protein A12	Positive regulation of nuclear factor-κb transcription factor activity	3.974	1.55E-05	2.68E-04	Up-regulated
S100A8	S100 calcium binding protein A8	Activation of cysteine-type endopeptidase activity involved in apoptotic process	4.471	8.81E-10	1.00E-07	Up-regulated
S100A9	S100 calcium binding protein A9	Activation of cysteine-type endopeptidase activity involved in apoptotic process	3.88	4.40E-07	1.55E-05	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
S100B	S100 calcium binding protein B	Negative regulation of skeletal muscle cell differentiation	−2.304	1.68E-12	5.72E-10	Down-regulated
S1PR3	Sphingosine-1-phosphate receptor 3	Adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	3.312	4.08E-07	1.45E-05	Up-regulated
SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	Negative regulation of peptidyl-tyrosine phosphorylation	2.718	6.50E-10	7.64E-08	Up-regulated
SAPCD1	Suppressor APC domain containing 1	Unknown	−2.205	1.57E-10	2.53E-08	Down-regulated
SCG2	Secretogranin II	Negative regulation of sequence-specific DNA binding transcription factor activity	3.773	3.93E-04	3.34E-03	Up-regulated
SCIMP	*SLP* adaptor and *CSK* interacting membrane protein	Positive regulation of *ERK1* and *ERK2* cascade	5.091	5.28E-09	4.40E-07	Up-regulated
SCN4A	Sodium channel, voltage gated, type IV α subunit	Membrane depolarization during action potential	2.368	3.47E-05	5.02E-04	Up-regulated
SCN7A	Sodium channel, voltage gated, type VII α subunit	Membrane depolarization during action potential	−2.228	4.81E-06	1.02E-04	Down-regulated
SERPINB2	Serpin peptidase inhibitor, clade B (ovalbumin), member 2	Negative regulation of endopeptidase activity	3.195	6.47E-05	8.09E-04	Up-regulated
SFRP5	Secreted frizzled-related protein 5	Negative regulation of Wnt signaling pathway involved in digestive tract morphogenesis	−2.394	4.40E-08	2.44E-06	Down-regulated
SGOL1	Shugoshin-like 1 (S. Pombe)	Attachment of spindle microtubules to kinetochore	2.318	3.17E-04	2.82E-03	Up-regulated
SGPL1	Sphingosine-1-phosphate lyase 1	Platelet-derived growth factor receptor signaling pathway	2.051	1.78E-07	7.29E-06	Up-regulated
SH2D1B	SH2 domain containing 1B	Positive regulation of natural killer cell mediated immunity	2.482	9.19E-07	2.68E-05	Up-regulated
SIGLEC15	Sialic acid binding Ig-like lectin 15	Cellular response to lipoprotein particle stimulus	3.027	2.86E-07	1.10E-05	Up-regulated
SIRPB1	Signal-regulatory protein β 1	Cell surface receptor signaling pathway	3.985	1.78E-04	1.82E-03	Up-regulated
SIRPB1	Signal-regulatory protein β 1	Cell surface receptor signaling pathway	5.665	5.54E-09	4.53E-07	Up-regulated
SIRPB2	Signal-regulatory protein β 2	Positive regulation of cell-cell adhesion	2.091	5.04E-08	2.68E-06	Up-regulated
SLAMF1	Signaling lymphocytic activation molecule family member 1	Positive regulation of cell proliferation	2.893	7.33E-07	2.27E-05	Up-regulated
SLAMF6	SLAM family member 6	Integral component of membrane	3.339	3.93E-09	3.42E-07	Up-regulated
SLAMF7	SLAM family member 7	Natural killer cell mediated cytotoxicity	6.67	2.89E-14	2.14E-11	Up-regulated
SLAMF8	SLAM family member 8	Regulation of NAD(P)H oxidase activity	2.166	1.01E-05	1.88E-04	Up-regulated
SLC11A1	Solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1	Positive regulation of dendritic cell antigen processing and presentation	4.39	1.37E-08	9.22E-07	Up-regulated
SLC16A6	Solute carrier family 16 member 6	Monocarboxylic acid transmembrane transporter activity	3.28	1.01E-09	1.13E-07	Up-regulated
SLC35D2	Solute carrier family 35 (*UDP*-glcnac/*UDP*-glucose transporter), member D2	Pyrimidine nucleotide–sugar transmembrane transporter activity	2.056	1.37E-07	5.90E-06	Up-regulated
SLC35D3	Solute carrier family 35 member D3	Pyrimidine nucleotide-sugar transmembrane transporter activity	2.987	1.17E-05	2.11E-04	Up-regulated
SLC35F1	Solute carrier family 35 member F1	Integral component of membrane	−2.288	3.95E-07	1.43E-05	Down-regulated
SLC36A2	Solute carrier family 36 (proton/amino acid symporter), member 2	Hydrogen ion transmembrane transporter activity	−2.072	4.47E-05	6.08E-04	Down-regulated
SLC44A4	Solute carrier family 44 member 4	Glycerophospholipid biosynthetic process	2.198	4.23E-05	5.84E-04	Up-regulated
SLC6A15	Solute carrier family 6 (neutral amino acid transporter), member 15	Neurotransmitter: sodium symporter activity	3.409	4.83E-08	2.60E-06	Up-regulated
SLC6A7	Solute carrier family 6 (neurotransmitter transporter), member 7	L-proline transmembrane transporter activity	2.689	1.62E-06	4.28E-05	Up-regulated
SLC7A10	Solute carrier family 7 (neutral amino acid transporter light chain, asc system), member 10	Neutral amino acid transmembrane transporter activity	−2.088	4.76E-04	3.89E-03	Down-regulated
SLC7A11	Solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	Integral component of plasma membrane	3.344	3.59E-06	8.02E-05	Up-regulated
SLC7A7	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	Basic amino acid transmembrane transporter activity	2.097	4.66E-07	1.62E-05	Up-regulated
SLCO4C1	Solute carrier organic anion transporter family, member 4C1	Sodium-independent organic anion transport	4.099	1.31E-08	8.96E-07	Up-regulated
SMPDL3B	Sphingomyelin phosphodiesterase, acid-like 3B	Hydrolase activity, acting on glycosyl bonds	2.57	5.66E-05	7.28E-04	Up-regulated
SNX10	Sorting nexin 10	Extrinsic component of endosome membrane	2.372	2.34E-09	2.25E-07	Up-regulated
SORCS1	Sortilin-related VPS10 domain containing receptor 1	Integral component of membrane	−2.703	3.77E-07	1.38E-05	Down-regulated
SOST	Sclerostin	Negative regulation of Wnt signaling pathway involved in dorsal/ventral axis specification	−2.05	9.65E-04	6.95E-03	Down-regulated
SPAG5	Sperm associated antigen 5	Regulation of attachment of spindle microtubules to kinetochore	3.271	1.92E-06	4.87E-05	Up-regulated
SPI1	Spi-1 proto-oncogene	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	2.178	1.22E-08	8.47E-07	Up-regulated
SPOCK1	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	Negative regulation of neuron projection development	2.393	1.29E-04	1.41E-03	Up-regulated
SRCIN1	*SRC* kinase signaling inhibitor 1	Negative regulation of protein tyrosine kinase activity	−4.21	7.90E-08	3.85E-06	Down-regulated
SRGN	Serglycin	Maintenance of protease location in mast cell secretory granule	3.309	3.29E-10	4.63E-08	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
SSTR1	Somatostatin receptor 1	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	−2.067	3.72E-04	3.18E-03	Down-regulated
ST3GAL5	ST3 β-galactoside α-23-sialyltransferase 5	Neolactotetraosylceramide α-23-sialyltransferase activity	2.093	2.02E-07	8.09E-06	Up-regulated
STAP1	Signal transducing adaptor family member 1	Positive regulation of non-membrane spanning protein tyrosine kinase activity	2.109	1.19E-04	1.32E-03	Up-regulated
STIL	*SCL/TAL1* interrupting locus	Positive regulation of cyclin-dependent protein serine/threonine kinase activity	3.181	6.65E-06	1.33E-04	Up-regulated
STX11	Syntaxin 11	Synaptic vesicle fusion to presynaptic membrane	3.049	2.42E-08	1.49E-06	Up-regulated
SUCNR1	Succinate receptor 1	G-protein coupled receptor signaling pathway	3.843	1.59E-07	6.76E-06	Up-regulated
SUSD3	Sushi domain containing 3	Integral component of membrane	2.1	9.75E-08	4.55E-06	Up-regulated
TCF19	Transcription factor 19	Regulation of transcription from RNA polymerase II promoter	2.048	9.95E-05	1.14E-03	Up-regulated
TCN1	Transcobalamin I (vitamin B12 binding protein, R binder family)	Water-soluble vitamin metabolic process	3.345	1.77E-05	2.96E-04	Up-regulated
TESPA1	Thymocyte expressed, positive selection associated 1	Positive regulation of T cell receptor signaling pathway	2.938	8.77E-09	6.59E-07	Up-regulated
TFEC	Transcription factor EC	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.519	2.49E-07	9.66E-06	Up-regulated
TGFA	Transforming growth factor, α	Positive regulation of epidermal growth factor-activated receptor activity	4.673	1.17E-11	2.65E-09	Up-regulated
THRSP	Thyroid hormone responsive	Regulation of triglyceride biosynthetic process	−3.089	1.78E-06	4.55E-05	Down-regulated
TIAM1	T-cell lymphoma invasion and metastasis 1	Extrinsic component of cytoplasmic side of plasma membrane	2.143	5.87E-08	2.98E-06	Up-regulated
TLR10	Toll-like receptor 10	*Myd88*-dependent toll-like receptor signaling pathway	2.209	1.58E-05	2.72E-04	Up-regulated
TLR2	Toll-like receptor 2	Induction by symbiont of defense-related host nitric oxide production	2.165	1.22E-07	5.38E-06	Up-regulated
TMEM156	Transmembrane protein 156	Integral component of membrane	2.456	4.77E-06	1.02E-04	Up-regulated
TMEM233	Transmembrane protein 233	Integral component of membrane	−2.646	2.31E-05	3.68E-04	Down-regulated
TMEM26	Transmembrane protein 26	Integral component of membrane	2.509	1.56E-06	4.13E-05	Up-regulated
TMEM37	Transmembrane protein 37	Regulation of ion transmembrane transport	2.096	1.52E-06	4.06E-05	Up-regulated
TMPRSS11D	Transmembrane protease, serine 11D	Integral component of plasma membrane	2.239	9.63E-04	6.94E-03	Up-regulated
TNFRSF17	Tumor necrosis factor receptor superfamily, member 17	Multicellular organismal development	3.411	5.91E-06	1.21E-04	Up-regulated
TNFSF11	Tumor necrosis factor (ligand) superfamily, member 11	Positive regulation of fever generation by positive regulation of prostaglandin secretion	2.237	2.91E-04	2.63E-03	Up-regulated
TNFSF13B	Tumor necrosis factor (ligand) superfamily, member 13b	Positive regulation of germinal center formation	2.231	2.23E-08	1.39E-06	Up-regulated
TNIP3	TNFAIP3 interacting protein 3	Negative regulation of I-κb kinase/ nuclear factor-κb signaling	3.007	2.67E-08	1.60E-06	Up-regulated
TOP2A	Topoisomerase (DNA) II α 170kDa	Positive regulation of single-stranded viral RNA replication via double-stranded DNA intermediate	2.336	1.03E-05	1.91E-04	Up-regulated
TREM1	Triggering receptor expressed on myeloid cells 1	Activation of mitophagy in response to mitochondrial depolarization	4.346	4.86E-10	6.14E-08	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.572	2.79E-06	6.59E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.098	1.28E-04	1.39E-03	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.275	1.97E-06	4.95E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.991	5.24E-10	6.39E-08	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.421	2.42E-04	2.31E-03	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.149	9.33E-07	2.70E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.487	1.12E-06	3.13E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4	5.31E-08	2.75E-06	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.191	3.80E-09	3.36E-07	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.02	3.35E-06	7.60E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.547	1.67E-04	1.73E-03	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.839	1.01E-05	1.88E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.332	9.17E-09	6.79E-07	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.417	9.11E-09	6.79E-07	Up-regulated

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On-line Table 1: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.139	8.77E-07	2.60E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.754	1.27E-05	2.26E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.665	5.03E-07	1.70E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.579	1.50E-05	2.61E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.251	2.09E-06	5.16E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	6.037	6.86E-09	5.35E-07	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.1	5.23E-08	2.72E-06	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.996	2.68E-05	4.14E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	7.583	1.06E-06	3.01E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	6.054	2.37E-08	1.47E-06	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.771	2.79E-04	2.57E-03	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.355	2.88E-05	4.34E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	5.873	3.82E-11	7.20E-09	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.231	8.54E-06	1.64E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.745	1.62E-07	6.82E-06	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.894	1.76E-05	2.95E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.291	3.87E-05	5.47E-04	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	7.083	1.36E-07	5.87E-06	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	6.245	1.16E-06	3.22E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.9	1.73E-06	4.47E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.671	1.08E-06	3.07E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	4.948	7.10E-07	2.23E-05	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	3.039	3.98E-04	3.36E-03	Up-regulated
TREML3P	Triggering receptor expressed on myeloid cells-like 3 pseudogene	Unknown	4.932	4.66E-08	2.53E-06	Up-regulated
TROAP	Trophinin associated protein	Protein binding	2.021	4.90E-04	3.97E-03	Up-regulated
TTK	TTK protein kinase	Positive regulation of pathway-restricted *SMAD* protein phosphorylation	2.88	2.66E-04	2.48E-03	Up-regulated
TUBA4A	Tubulin. α 4a	"De novo" posttranslational protein folding	3.153	4.56E-08	2.49E-06	Up-regulated
TXLNB	Taxilin β	Syntaxin binding	2.408	4.68E-06	1.00E-04	Up-regulated
UBASH3B	Ubiquitin associated and SH3 domain containing B	Regulation of release of sequestered calcium ion into cytosol	2.427	6.47E-09	5.13E-07	Up-regulated
UBE2T	Ubiquitin-conjugating enzyme E2T	Cellular response to DNA damage stimulus	2.217	2.81E-05	4.27E-04	Up-regulated
USH2A	Usher syndrome 2A (autosomal recessive, mild)	Inner ear receptor cell differentiation	−2.932	9.33E-08	4.39E-06	Down-regulated
VSIG4	V-set and immunoglobulin domain containing 4	Negative regulation of interleukin-2 production	2174	3.88E-05	5.49E-04	Up-regulated
VSTM2A	V-set and transmembrane domain containing 2A	Extracellular region	−2.366	2.43E-06	5.89E-05	Down-regulated
VTN	Vitronectin	Positive regulation of vascular endothelial growth factor receptor signaling pathway	2.774	9.01E-04	6.56E-03	Up-regulated
XCR1	Chemokine (C motif) receptor 1	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	2.505	8.06E-05	9.71E-04	Up-regulated
XDH	Xanthine dehydrogenase	Activation of cysteine-type endopeptidase activity involved in apoptotic process	6.298	2.62E-10	3.85E-08	Up-regulated
XIRP1	Xin actin-binding repeat containing 1	Actin cytoskeleton organization	−2.233	4.43E-04	3.67E-03	Down-regulated
XPR1	Xenotropic and polytropic retrovirus receptor 1	G-protein coupled receptor signaling pathway	2.217	1.80E-11	3.82E-09	Up-regulated
ZWILCH	Zwilch kinetochore protein	Small GTPase mediated signal transduction	2.427	2.05E-06	5.08E-05	Up-regulated

[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 (up-regulated) or ≤ 2 (down-regulated). Gene variations were determined by IPA software. The main functions of genes were determined using gene ontology (http://geneontology.org/).

On-line Table 2: Most involved canonical pathways, coil versus control, determined by IPA

Canonical Biologic Pathway	No. of Genes Up-Regulated	Genes	No. of Genes Down-Regulated	Genes
Altered T-cell and B-cell signaling in rheumatoid arthritis	15	*CD79B, CXCL13, HLA-DRA, IL6, IL10, IL1B, IL1RN, IL23A, LTA, SLAMF1, TLR2, TLR10, TNFRSF17, TNFSF11, TNFSF13B*	0	NA
Granulocyte adhesion and diapedesis	16	*CCL4, CCL5, CCL20, CXCL8, CXCL13, CXCR4, IL18RAP, IL1B, IL1RAP, IL1RN, ITGA4, MMP1, MMP3, MMP12, MMP13*	2	*CLDN19, HRH1*
Agranulocyte adhesion and diapedesis	15	*CCL4, CCL5, CCL20, CXCL8, CXCL11, CXCL13, CXCR4, IL1B, IL1RN, ITGA4, MMP1, MMP3, MMP12, MMP13, MYH7*	3	*CDN19, HRH1, MYH7B*
Interleukin-10 signaling	11	*CCR1, CCR5, CD14, HMOX1, IL6, IL10, IL18RAP, IL18, IL1RAP, IL1RN, MAPK13*	0	NA
Communication between innate and adaptive immune cells	12	*CCL4, CCL5, CXCL8, HLA-DRA, IL6, IL10, IL1B, IL1RN, TLR2, TLR10,TNFRSF17, TNFSF13B*	0	NA

Note:—NA indicates not applicable.

On-line Table 3: Up- and down-regulated molecules comparing flow-diverted versus untreated aneurysms, determined by IPA[a]

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	Proteinaceous extracellular matrix	2.265	6.43E-04	3.81E-02	Up-regulated
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	Proteinaceous extracellular matrix	3.275	4.22E-07	1.41E-03	Up-regulated
ALAS2	5′-aminolevulinate synthase 2	Porphyrin-containing compound metabolic process	2.34	1.19E-03	4.90E-02	Up-regulated
APLN	Apelin	Positive regulation of corticotropin-releasing hormone secretion	4.412	2.37E-05	9.93E-03	Up-regulated
ARG1	Arginase 1	Cellular response to transforming growth factor β stimulus	2.451	2.42E-03	6.91E-02	Up-regulated
ASPM	Asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	Positive regulation of canonical Wnt signaling pathway	2.623	3.22E-04	2.69E-02	Up-regulated
ATP6V0D2	Atpase, H+ transporting, lysosomal 38kDa, V0 subunit d2	Vacuolar proton-transporting V-type ATPase complex	2.422	4.02E-03	9.07E-02	Up-regulated
AURKB	Aurora kinase B	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	3.335	9.08E-04	4.41E-02	Up-regulated
BCL6B	B-cell CLL/lymphoma 6 member B	RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	2.615	1.56E-04	2.06E-02	Up-regulated
BUB1	BUB1 mitotic checkpoint serine/threonine kinase	Positive regulation of intrinsic apoptotic signaling pathway	2.934	8.31E-04	4.17E-02	Up-regulated
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	2.734	2.27E-04	2.43E-02	Up-regulated
C17orf53	Chromosome 17 open reading frame 53	Unknown	2.01	4.21E-04	3.13E-02	Up-regulated
CA1	Carbonic anhydrase I	Small molecule metabolic process	2.999	2.45E-04	2.48E-02	Up-regulated
CA12	Carbonic anhydrase XII	Small molecule metabolic process	2.38	3.49E-04	2.78E-02	Up-regulated
CA2	Carbonic anhydrase II	Positive regulation of dipeptide transmembrane transport	2.728	5.05E-04	3.47E-02	Up-regulated
CA9	Carbonic anhydrase IX	Regulation of transcription from RNA polymerase II promoter in response to hypoxia	2.561	1.36E-04	1.90E-02	Up-regulated
CAMK1G	Calcium/calmodulin-dependent protein kinase IG	Calcium- and calmodulin-dependent protein kinase complex	2.953	2.50E-04	2.49E-02	Up-regulated
CCDC163P	Coiled-coil domain containing 163 pseudogene	Unknown	2.131	4.99E-04	3.46E-02	Up-regulated
CCL2	Chemokine (C-C motif) ligand 2	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	2.062	1.08E-03	4.68E-02	Up-regulated
CCNB1	Cyclin B1	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	3.289	6.76E-05	1.31E-02	Up-regulated
CCNB2	Cyclin B2	G2/M transition of mitotic cell cycle	3.441	5.43E-04	3.58E-02	Up-regulated
CD72	CD72 molecule	Transmembrane signaling receptor activity	2.52	2.62E-03	7.19E-02	Up-regulated
CDC20	Cell division cycle 20	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.792	3.88E-04	2.97E-02	Up-regulated
CDC25A	Cell division cycle 25A	Regulation of cyclin-dependent protein serine/threonine kinase activity	2.54	7.99E-04	4.11E-02	Up-regulated
CDC45	Cell division cycle 45	Pre-replicative complex assembly involved in nuclear cell cycle DNA replication	3.057	6.27E-04	3.81E-02	Up-regulated
CDCA2	Cell division cycle associated 2	Positive regulation of protein dephosphorylation	2.488	2.53E-03	7.04E-02	Up-regulated
CDCA3	Cell division cycle associated 3	Mitotic nuclear division	2.028	4.82E-05	1.18E-02	Up-regulated
CDCA7	Cell division cycle associated 7	Regulation of transcription. DNA-templated	3.687	5.54E-04	3.61E-02	Up-regulated
CDH5	Cadherin 5 type 2 (vascular endothelium)	Homophilic cell adhesion via plasma membrane adhesion molecules	2.032	4.80E-04	3.34E-02	Up-regulated
CDK1	Cyclin-dependent kinase 1	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.41	6.59E-04	3.81E-02	Up-regulated
CELSR3	Cadherin, EGF LAG seven-pass G-type receptor 3	Homophilic cell adhesion via plasma membrane adhesion molecules	2.625	1.69E-03	5.80E-02	Up-regulated
CENPA	Centromere protein A	Protein localization to chromosome, centromeric region	3.83	1.36E-04	1.90E-02	Up-regulated
CENPE	Centromere protein E, 312kDa	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.257	2.74E-03	7.33E-02	Up-regulated
CENPT	Centromere protein T	Small GTPase mediated signal transduction	2.089	1.24E-03	4.96E-02	Up-regulated
CEP55	Centrosomal protein 55kDa	Establishment of protein localization	2.791	1.32E-03	5.15E-02	Up-regulated
CFAP52	Cilia and flagella associated protein 52	Cell projection	3.426	1.07E-06	2.03E-03	Up-regulated
CHI3L1	Chitinase 3-like 1 (cartilage glycoprotein-39)	Positive regulation of peptidyl-threonine phosphorylation	4.249	3.04E-06	3.05E-03	Up-regulated
CHRDL2	Chordin-like 2	Negative regulation of BMP signaling pathway	3.005	6.76E-05	1.31E-02	Up-regulated
CHTOP	Chromatin target of PRMT1	Regulation of transcription, DNA-templated	3.228	8.12E-04	4.16E-02	Up-regulated
CKS2	CDC28 protein kinase regulatory subunit 2	Regulation of cyclin-dependent protein serine/threonine kinase activity	3.405	2.11E-05	9.21E-03	Up-regulated
CLSTN2	Calsyntenin 2	Homophilic cell adhesion via plasma membrane adhesion molecules	4.168	7.91E-05	1.42E-02	Up-regulated
COL9A1	Collagen, type IX, α 1	Extracellular matrix structural constituent conferring tensile strength	3.882	2.65E-03	7.19E-02	Up-regulated

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On-line Table 3: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
CTSE	Cathepsin E	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.614	7.10E-04	3.84E-02	Up-regulated
CXCL13	Chemokine (C-X-C motif) ligand 13	Negative regulation of endothelial cell chemotaxis to fibroblast growth factor	2.257	2.84E-04	2.64E-02	Up-regulated
CXCL8	Chemokine (C-X-C motif) ligand 8	Regulation of single-stranded viral RNA replication via double-stranded DNA intermediate	4.781	1.32E-05	8.84E-03	Up-regulated
CXCL8	Chemokine (C-X-C motif) ligand 8	Regulation of single-stranded viral RNA replication via double-stranded DNA intermediate	3.11	2.45E-04	2.48E-02	Up-regulated
CXCR4	Chemokine (C-X-C motif) receptor 4	Positive regulation of cytosolic calcium ion concentration	2.16	1.53E-03	5.58E-02	Up-regulated
DAPL1	Death associated protein-like 1	Cellular response to amino acid starvation	−3.752	6.45E-13	6.48E-09	Down-regulated
DLGAP5	Discs, large (Drosophila) homolog-associated protein 5	Positive regulation of mitotic metaphase/anaphase transition	2.864	2.02E-04	2.30E-02	Up-regulated
DLL4	Delta-like 4 (Drosophila)	Negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	2.073	5.57E-05	1.20E-02	Up-regulated
DNASE2B	Deoxyribonuclease II β	Deoxyribonuclease II activity	2.515	2.77E-03	7.36E-02	Up-regulated
DRD1	Dopamine receptor D1	Positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	2.061	2.97E-03	7.56E-02	Up-regulated
DUSP5	Dual specificity phosphatase 5	*MAP* kinase tyrosine/serine/threonine phosphatase activity	2.072	1.64E-04	2.13E-02	Up-regulated
E2F1	E2F transcription factor 1	Positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2.319	9.77E-04	4.49E-02	Up-regulated
E2F8	E2F transcription factor 8	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	2.583	2.51E-03	7.03E-02	Up-regulated
EGLN3	Egl-9 family hypoxia-inducible factor 3	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	3.25	3.50E-05	1.13E-02	Up-regulated
ENO2	Enolase 2 (γ, neuronal)	Phosphopyruvate hydratase activity	2.914	4.91E-06	4.11E-03	Up-regulated
ERO1 L	ERO1-like (S. Cerevisiae)	Oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	2.039	4.96E-05	1.18E-02	Up-regulated
ETV4	Ets variant 4	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	3.485	8.91E-05	1.46E-02	Up-regulated
EXO1	Exonuclease 1	Humoral immune response mediated by circulating immunoglobulin	2.971	5.88E-04	3.71E-02	Up-regulated
EXOC3L1	Exocyst complex component 3-like 1	Peptide hormone secretion	2.521	2.78E-05	1.03E-02	Up-regulated
EZH2	Enhancer of zeste 2 polycomb repressive complex 2 subunit	Skeletal muscle satellite cell maintenance involved in skeletal muscle regeneration	2.197	3.91E-04	2.97E-02	Up-regulated
FABP5	Fatty acid binding protein 5 (psoriasis-associated)	Phosphatidylcholine biosynthetic process	2.436	7.69E-05	1.42E-02	Up-regulated
FAM150A	Family with sequence similarity 150, member A	Extracellular region	−2.555	1.97E-05	9.21E-03	Down-regulated
FAM179A	Family with sequence similarity 179, member A	Unknown	2.649	2.22E-03	6.79E-02	Up-regulated
FAM64A	Family with sequence similarity 64, member A	Mitotic nuclear division	3.601	5.17E-05	1.18E-02	Up-regulated
FGB	Fibrinogen β chain	Negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	2.824	1.35E-03	5.18E-02	Up-regulated
FGF23	Fibroblast growth factor 23	Positive regulation of *MAPKKK* cascade by fibroblast growth factor receptor signaling pathway	5.662	3.01E-06	3.05E-03	Up-regulated
FGFBP1	Fibroblast growth factor binding protein 1	Activation of mitophagy in response to mitochondrial depolarization	−2.183	3.00E-05	1.04E-02	Down-regulated
FOXM1	Forkhead box M1	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	3.239	2.11E-04	2.33E-02	Up-regulated
FTL	Ferritin, light polypeptide	Post-Golgi vesicle-mediated transport	2.047	1.46E-03	5.39E-02	Up-regulated
GDF6	Growth differentiation factor 6	Positive regulation of pathway-restricted *SMAD* protein phosphorylation	2.114	4.38E-03	9.42E-02	Up-regulated
GPR158	G protein-coupled receptor 158	Regulation of G-protein coupled receptor protein signaling pathway	4.747	5.18E-05	1.18E-02	Up-regulated
GSG2	Germ cell associated 2 (haspin)	Histone H3-T3 phosphorylation involved in chromosome passenger complex localization to kinetochore	2.725	7.60E-04	3.95E-02	Up-regulated
HAS2	Hyaluronan synthase 2	Positive regulation of substrate adhesion-dependent cell spreading	2.285	3.71E-05	1.16E-02	Up-regulated
HBB	Hemoglobin, β	Positive regulation of nitric oxide biosynthetic process	2.46	1.27E-03	5.03E-02	Up-regulated
HMGA2	High mobility group AT-hook 2	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription	4.412	6.98E-07	1.75E-03	Up-regulated

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On-line Table 3: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
HMMR	Hyaluronan-mediated motility receptor (RHAMM)	Glycosaminoglycan metabolic process	3.534	5.77E-05	1.20E-02	Up-regulated
HMOX1	Heme oxygenase 1	Regulation of transcription from RNA polymerase II promoter in response to oxidative stress	3.643	2.77E-04	2.62E-02	Up-regulated
HP	Haptoglobin	Activation of cysteine-type endopeptidase activity involved in apoptotic process	2.553	4.27E-05	1.18E-02	Up-regulated
IBSP	Integrin-binding sialoprotein	Cellular response to growth factor stimulus	2.789	1.73E-03	5.85E-02	Up-regulated
ICAM2	Intercellular adhesion molecule 2	Stimulatory C-type lectin receptor signaling pathway	2.222	2.98E-04	2.69E-02	Up-regulated
IGF2BP3	Insulin-like growth factor 2 mRNA binding protein 3	Regulation of cytokine biosynthetic process	2.095	1.61E-03	5.68E-02	Up-regulated
IL12RB2	Interleukin 12 receptor, β 2	Positive regulation of interferon-γ production	2.027	1.60E-03	5.68E-02	Up-regulated
IL23A	Interleukin 23 α subunit p19	Positive regulation of granulocyte macrophage colony-stimulating factor production	2.748	6.82E-04	3.81E-02	Up-regulated
IL6	Interleukin 6	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	4.375	2.86E-05	1.03E-02	Up-regulated
INHBB	Inhibin, β B	Positive regulation of pathway-restricted *SMAD* protein phosphorylation	2.545	3.85E-04	2.97E-02	Up-regulated
IQGAP3	IQ motif containing GTPase activating protein 3	Positive regulation of mammary gland epithelial cell proliferation	2.343	4.39E-04	3.17E-02	Up-regulated
IRG1	Immunoresponsive 1 homolog (mouse)	Positive regulation of reactive oxygen species metabolic process	2.668	1.16E-03	4.85E-02	Up-regulated
IYD	Iodotyrosine deiodinase	Cellular nitrogen compound metabolic process	2.745	7.77E-05	1.42E-02	Up-regulated
KIAA0101	Kiaa0101	Cellular response to DNA damage stimulus	3.426	8.88E-05	1.46E-02	Up-regulated
KIF11	Kinesin family member 11	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.42	1.62E-03	5.68E-02	Up-regulated
KIF14	Kinesin family member 14	*SCF*-dependent proteasomal ubiquitin-dependent protein catabolic process	2.574	2.67E-04	2.55E-02	Up-regulated
KIF18B	Kinesin family member 18B	ATP-dependent microtubule motor activity, plus-end-directed	4.077	1.64E-05	9.21E-03	Up-regulated
KIF20A	Kinesin family member 20A	Cell separation after cytokinesis	2.645	1.25E-04	1.88E-02	Up-regulated
KIF21A	Kinesin family member 21A	Microtubule-based movement	2.216	2.35E-03	6.84E-02	Up-regulated
KIF2A	Kinesin heavy chain member 2A	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.807	1.18E-03	4.90E-02	Up-regulated
KIFC1	Kinesin family member C1	ATP-dependent microtubule motor activity, minus-end-directed	2.816	5.70E-05	1.20E-02	Up-regulated
KIT	V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	Positive regulation of sequence-specific DNA binding transcription factor activity	2.278	1.80E-04	2.18E-02	Up-regulated
KLHL3	Kelch-like family member 3	Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	2.011	4.94E-05	1.18E-02	Up-regulated
KRT32	Keratin 32 type I	Structural molecule activity	2.815	1.23E-03	4.96E-02	Up-regulated
KRT8	Keratin 8 type II	Cell differentiation involved in embryonic placenta development	6.233	1.21E-06	2.03E-03	Up-regulated
LCTL	Lactase-like	Hydrolase activity, hydrolyzing O-glycosyl compounds	2.614	1.02E-03	4.51E-02	Up-regulated
LECT1	Leukocyte cell derived chemotaxin 1	Negative regulation of vascular endothelial growth factor receptor signaling pathway	−2.373	4.32E-04	3.17E-02	Down-regulated
MAGEL2	Melanoma antigen family L2	Negative regulation of transcription, DNA-templated	2.199	2.21E-03	6.78E-02	Up-regulated
MAPK13	Mitogen-activated protein kinase 13	Vascular endothelial growth factor receptor signaling pathway	2.134	1.59E-03	5.68E-02	Up-regulated
MARCO	Macrophage receptor with collagenous structure	Signaling pattern recognition receptor activity	−2.396	2.94E-04	2.69E-02	Down-regulated
MCM8	Minichromosome maintenance complex component 8	Double-strand break repair via homologous recombination	2.348	1.83E-03	6.02E-02	Up-regulated
MELK	Maternal embryonic leucine zipper kinase	Intrinsic apoptotic signaling pathway in response to oxidative stress	3.352	7.12E-04	3.84E-02	Up-regulated
MFSD5	Major facilitator superfamily domain containing 5	Substrate-specific transmembrane transporter activity	3.465	3.53E-06	3.23E-03	Up-regulated
MMP1	Matrix metallopeptidase 1	Positive regulation of protein oligomerization	4.467	5.20E-04	3.50E-02	Up-regulated
MOGAT1	Monoacylglycerol O-acyltransferase 1	2-Acylglycerol O-acyltransferase activity	2.672	4.51E-04	3.21E-02	Up-regulated
MRPL32	Mitochondrial ribosomal protein L32	Mitochondrial translational termination	2.448	2.07E-05	9.21E-03	Up-regulated
MSH5	Muts homolog 5	Homologous chromosome segregation	2.293	1.90E-03	6.13E-02	Up-regulated
MTFP1	Mitochondrial fission process 1	Integral component of membrane	2.889	3.11E-04	2.69E-02	Up-regulated
MYH7B	Myosin, heavy chain 7B, cardiac muscle, β	Metabolic process	−2.107	4.66E-04	3.27E-02	Down-regulated
NCAPG	Non-SMC condensin I complex, subunit G	Mitotic chromosome condensation	2.472	1.55E-03	5.61E-02	Up-regulated
NEK2	NIMA-related kinase 2	Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	3.311	5.83E-05	1.20E-02	Up-regulated
NKAIN1	Na+/K+ transporting ATPase interacting 1	Regulation of sodium ion transport	3.127	1.27E-04	1.88E-02	Up-regulated
NUF2	NUF2 NDC80 kinetochore complex component	Small GTPase mediated signal transduction	2.809	4.32E-04	3.17E-02	Up-regulated
PBK	PDZ binding kinase	Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	2.589	2.36E-03	6.84E-02	Up-regulated

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On-line Table 3: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
PDE4B	Phosphodiesterase 4B, camp-specific	Regulation of high voltage-gated calcium channel activity	2.371	2.92E-03	7.52E-02	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	2.094	2.09E-04	2.33E-02	Up-regulated
PIGR	Polymeric immunoglobulin receptor	Immunoglobulin transcytosis in epithelial cells mediated by polymeric immunoglobulin receptor	2.808	2.84E-03	7.44E-02	Up-regulated
PLA2G4F	Phospholipase A2 group IVF	Phosphatidylethanolamine acyl-chain remodeling	2.094	2.56E-03	7.10E-02	Up-regulated
PLK1	Polo-like kinase 1	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	2.09	1.07E-04	1.65E-02	Up-regulated
POU2AF1	POU class 2 associating factor 1	Transcription from RNA polymerase II promoter	2.267	2.78E-03	7.36E-02	Up-regulated
PRND	Prion protein 2 (dublet)	Anchored component of membrane	8.719	2.78E-06	3.05E-03	Up-regulated
PRR11	Proline rich 11	Regulation of cell cycle	3.068	7.26E-04	3.88E-02	Up-regulated
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/h synthase and cyclooxygenase)	Positive regulation of cell migration involved in sprouting angiogenesis	3.434	3.07E-08	1.54E-04	Up-regulated
PTX3	Pentraxin 3 long	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	2.42	1.95E-04	2.25E-02	Up-regulated
PVRL2	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	Positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target	2.069	4.62E-03	9.68E-02	Up-regulated
RACGAP1	Rac GTPase activating protein 1	Antigen processing and presentation of exogenous peptide antigen via *MHC* class II	2.331	4.38E-04	3.17E-02	Up-regulated
RAD51AP1	*RAD51* associated protein 1	Regulation of double-strand break repair via homologous recombination	2.328	1.76E-03	5.90E-02	Up-regulated
RELT	RELT tumor necrosis factor receptor	Integral component of membrane	2.375	3.14E-04	2.69E-02	Up-regulated
RMI2	Recq mediated genome instability 2	DNA replication	2.847	7.08E-04	3.84E-02	Up-regulated
RPS6KL1	Ribosomal protein S6 kinase-like 1	Intracellular membrane-bounded organelle	2.792	3.61E-04	2.85E-02	Up-regulated
RTN4RL2	Reticulon 4 receptor-like 2	Anchored component of plasma membrane	2.414	1.27E-04	1.88E-02	Up-regulated
S100A8	S100 calcium binding protein A8	Activation of cysteine-type endopeptidase activity involved in apoptotic process	2.915	9.91E-04	4.49E-02	Up-regulated
S1PR3	Sphingosine-1-phosphate receptor 3	Adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	2.149	4.05E-03	9.11E-02	Up-regulated
SCG2	Secretogranin II	Negative regulation of sequence-specific DNA binding transcription factor activity	3.446	6.64E-04	3.81E-02	Up-regulated
SCIMP	*SLP* adaptor and *CSK* interacting membrane protein	Positive regulation of *ERK1* and *ERK2* cascade	2.813	3.97E-03	9.05E-02	Up-regulated
SCIN	Scinderin	Positive regulation of megakaryocyte differentiation	−2.287	1.20E-05	8.63E-03	Down-regulated
SCN4A	Sodium channel, voltage gated, type IV α subunit	Membrane depolarization during action potential	3.215	6.10E-04	3.81E-02	Up-regulated
SELE	Selectin E	Heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	2.299	1.69E-04	2.13E-02	Up-regulated
SERPINF2	Serpin peptidase inhibitor, clade F (α-2 antiplasmin, pigment epithelium derived factor), member 2	Positive regulation of transcription from RNA polymerase II promoter	2.666	3.25E-04	2.69E-02	Up-regulated
SIRPB1	Signal-regulatory protein β 1	Cell surface receptor signaling pathway	2.393	2.90E-03	7.51E-02	Up-regulated
SIRPB1	Signal-regulatory protein β 1	Cell surface receptor signaling pathway	3.979	3.31E-04	2.73E-02	Up-regulated
SIRPB1	Signal-regulatory protein β 1	Cell surface receptor signaling pathway	5.463	9.20E-05	1.47E-02	Up-regulated
SLC11A1	Solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1	Positive regulation of dendritic cell antigen processing and presentation	3.851	4.68E-05	1.18E-02	Up-regulated
SLC16A6	Solute carrier family 16 member 6	Monocarboxylic acid transmembrane transporter activity	2.335	6.66E-04	3.81E-02	Up-regulated
SLC45A1	Solute carrier family 45 member 1	Glucose transmembrane transporter activity	2.059	1.38E-03	5.26E-02	Up-regulated
SLC4A2	Solute carrier family 4 (anion exchanger), member 2	Anion transmembrane transporter activity	2.497	8.88E-05	1.46E-02	Up-regulated
SMCO2	Single-pass membrane protein with coiled-coil domains 2	Integral component of membrane	2.498	1.35E-03	5.18E-02	Up-regulated
SNORA7B	Small nucleolar RNA, H/ACA box 7B	Unknown	2.601	5.27E-04	3.53E-02	Up-regulated
SNORD10	Small nucleolar RNA, C/D box 10	Unknown	2.58	2.57E-05	1.03E-02	Up-regulated
SPAG5	Sperm associated antigen 5	Regulation of attachment of spindle microtubules to kinetochore	3.315	3.73E-04	2.90E-02	Up-regulated
SRCIN1	*SRC* kinase signaling inhibitor 1	Negative regulation of protein tyrosine kinase activity	−3.295	1.98E-05	9.21E-03	Down-regulated
STIL	*SCL/TAL1* interrupting locus	Positive regulation of cyclin-dependent protein serine/threonine kinase activity	3.04	8.47E-04	4.21E-02	Up-regulated
STMN1	Stathmin 1	Positive regulation of cellular component movement	2.375	2.46E-03	6.98E-02	Up-regulated
TCF19	Transcription factor 19	Regulation of transcription from RNA polymerase II promoter	2.509	5.69E-04	3.61E-02	Up-regulated
TDRD5	Tudor domain containing 5	DNA methylation involved in gamete generation	2.201	4.27E-05	1.18E-02	Up-regulated
TIMP1	*TIMP* metallopeptidase inhibitor 1	Negative regulation of membrane protein ectodomain proteolysis	2.104	6.23E-04	3.81E-02	Up-regulated

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On-line Table 3: Continued

Gene Name	Description	Gene Main Function Determined by Gene Ontology	Fold Change	*P* Value	False Discovery Rate (q Value)	Direction of Expression
TM4SF18	Transmembrane 4 L six family member 18	Integral component of membrane	2.77	8.79E-05	1.46E-02	Up-regulated
TMEM151B	Transmembrane protein 151B	Integral component of membrane	3.543	3.14E-04	2.69E-02	Up-regulated
TREML2	Triggering receptor expressed on myeloid cells-like 2	Integral component of membrane	2.352	4.73E-03	9.82E-02	Up-regulated
TRIML2	Tripartite motif family-like 2	Response to retinoic acid	3.336	1.35E-03	5.18E-02	Up-regulated
TROAP	Trophinin associated protein	Protein binding	3.307	3.13E-04	2.69E-02	Up-regulated
TTC7A	Tetratricopeptide repeat domain 7A	Cellular iron ion homeostasis	2.378	4.50E-05	1.18E-02	Up-regulated
TUBA4A	Tubulin, α 4a	“De novo” posttranslational protein folding	3.447	2.11E-05	9.21E-03	Up-regulated
TVP23A	Trans-Golgi network vesicle protein 23 homolog A (*Saccharomyces Cerevisiae*)	Integral component of Golgi membrane	2.283	2.84E-03	7.44E-02	Up-regulated
UBE2T	Ubiquitin-conjugating enzyme E2T	Cellular response to DNA damage stimulus	2.696	5.67E-04	3.61E-02	Up-regulated
UGGT2	*UDP*-glucose glycoprotein glucosyltransferase 2	*UDP*-glucose: glycoprotein glucosyltransferase activity	2.213	2.19E-03	6.78E-02	Up-regulated
VEGFA	Vascular endothelial growth factor A	Positive regulation of endothelial cell chemotaxis by *VEGF*-activated vascular endothelial growth factor receptor signaling pathway	2.741	1.63E-06	2.33E-03	Up-regulated
WSCD1	*WSC* domain containing 1	Integral component of membrane	2.752	3.83E-05	1.16E-02	Up-regulated
ZMYND15	Zinc finger, MYND-type containing 15	Negative regulation of transcription, DNA-templated	2.43	1.69E-03	5.80E-02	Up-regulated
ZWILCH	Zwilch kinetochore protein	Small GTPase mediated signal transduction	3.099	3.48E-05	1.13E-02	Up-regulated

[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 (up-regulated) or ≤ 2 (down-regulated). Gene variations were determined by IPA software. The main functions of genes were determined using gene ontology (http://geneontology.org/).

On-line Table 4: Most involved canonical pathways, flow-diverted versus control, determined by IPA

Canonical Biologic Pathway	No. of Genes Up-Regulated	Genes	No. of Genes Down-Regulated	Genes
Atherosclerosis signaling	9	*CCL2, CXCL8, CXCR4, IL6, MMP1, PDGFB, PLA2G4F, S100A8, SELE*	0	NA
Mitotic roles of pololike kinase	7	*CCNB1, CCNB2, CDC20, CDC25A, CDK1, KIF11, PLK1*	0	NA
Hepatic fibrosis/hepatic stellate cell activation	8	*CCL2, COL9A1, CXCL8, IL6, MMP1, PDGFB, TIMP1, VEGFA*	1	*MYH7B*
Agranulocyte adhesion and diapedesis	8	*CCL2, CDH5, CXCL8, CXCL13, CXCR4, ICAM2, MMP1, SELE*	1	*MYH7B*
Interleukin-17 signaling	6	*CCL2, CXCL8, IL6, MAPK13, PTGS2, TIMP1*	0	NA

Note:—NA indicates not applicable.

On-line Table 5: Results of RT-PCR and RNA-seq for selected molecules in coiled and flow-diverted aneurysms[a]

	Coils versus Untreated Aneurysm		Flow-Diverted versus Untreated Aneurysm	
Molecule	RT-PCR	RNA-Seq	RT-PCR	RNA-Seq
PRND	5.8	3.6	8.7	4.3
FGF23	7.4	6.5	5.7	3.7
MMP1	8.1	8.0	4.5	3.9
SRCIN1	−4.2	−3.3	−3.3	−2.4
DAPL1	−3.9	−4.2	−3.8	−4.2
HHIP	−3.5	−4.1	x	x

Note:—RT-PCR indicates reverse transcription polymerase chain reaction.

[a] Values are expressed as log-fold changes.