

RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture

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Background and Purpose—Analyzing genes involved in development and rupture of intracranial aneurysms can enhance knowledge about the pathogenesis of aneurysms, and identify new treatment strategies. We compared gene expression between ruptured and unruptured aneurysms and control intracranial arteries.

Methods—We determined expression levels with RNA sequencing. Applying a multivariate negative binomial model, we identified genes that were differentially expressed between 44 aneurysms and 16 control arteries, and between 22 ruptured and 21 unruptured aneurysms. The differential expression of 8 relevant and highly significant genes was validated using digital polymerase chain reaction. Pathway analysis was used to identify enriched pathways. We also analyzed genes with an extreme pattern of differential expression: only expressed in 1 condition without any expression in the other.

Results—We found 229 differentially expressed genes in aneurysms versus controls and 1489 in ruptured versus unruptured aneurysms. The differential expression of all 8 genes selected for digital polymerase chain reaction validation was confirmed. Extracellular matrix pathways were enriched in aneurysms versus controls, whereas pathways involved in immune response and the lysosome pathway were enriched in ruptured versus unruptured aneurysms. Immunoglobulin genes were expressed in aneurysms, but showed no expression in controls.

Conclusions—For rupture of intracranial aneurysms, we identified the lysosome pathway as a new pathway and found further evidence for the role of the immune response. Our results also point toward a role for immunoglobulins in the pathogenesis of aneurysms. Immune-modifying drugs are, therefore, interesting candidate treatment strategies in the prevention of aneurysm development and rupture. (*Stroke*. 2016;47:1286-1293. DOI: 10.1161/STROKEAHA.116.012541.)

Key Words: aneurysm ■ extracellular matrix ■ gene expression ■ lysosomes ■ subarachnoid hemorrhage

Intracranial aneurysms are common with a prevalence of 3%.¹ The availability of noninvasive imaging techniques has increased, which coincided with an increase in incidental detection of aneurysms.² Although only a minority of aneurysms ruptures, the consequences of aneurysmal subarachnoid hemorrhage are enormous, because of the young age at which it occurs, and the high case fatality and morbidity.³ Preventive treatment of unruptured aneurysms carries a risk of complications.⁴ New treatment strategies, therefore, inhibiting

the formation, growth, and rupture of aneurysms are needed. To develop such treatment strategies, we need more insight into the pathogenesis of aneurysm development and rupture. Studies investigating differences in gene expression in aneurysms versus controls and in ruptured versus unruptured aneurysms may identify genes and pathways involved in development and rupture of aneurysms. Previous studies were small and, used microarray techniques,^{5–12} and extracranial instead of intracranial arteries as control.^{6–9,11,12} Recent advances in

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sequencing methodology, such as next-generation sequencing-based RNA profiling methods, provide more accurate, sensitive, comprehensive, and reliable gene expression data than microarrays.¹³ We compared differential expression of genes of a large sample of intracranial aneurysm tissue samples (n=44) to a unique control sample of intracranial arteries (n=16), and compared ruptured (n=22) to unruptured (n=21) aneurysms tissue samples using RNA sequencing, to gain insight in the pathogenesis of the development and the subsequent rupture of intracranial aneurysms.

Methods

Patient Selection and Tissue Collection

Aneurysm tissue samples were excised after complete obliteration of the aneurysm with a clip in patients aged ≥ 18 years undergoing neurosurgical clipping of a ruptured, or unruptured saccular intracranial aneurysm at the department of Neurology and Neurosurgery of the University Medical Center Utrecht, The Netherlands between 2010 and 2013. As controls, a tissue sample of an intracranial cortical artery was obtained from the resected brain tissue of patients aged ≥ 16 years who underwent surgery because of intractable epilepsy. Tissue samples were snap frozen in liquid nitrogen (<1 minute after excision) and stored at -80°C until further use. We collected characteristics for all patients and for those with aneurysms also aneurysm characteristics, including the largest diameter of the lumen of the aneurysm and the location of the aneurysm from the available imaging studies (mostly computed tomographic angiography). This study was approved by the Institutional Review Board of the University Medical Center Utrecht. For further details see the Methods section in the online-only Data Supplement.

Library Preparation and RNA Sequencing

An initial quality check of the extracted RNA of the samples was performed by capillary electrophoresis and RNA quantification using the LabChip GX (PerkinElmer, Waltham, MA). Please see the Methods section in the online-only Data Supplement for further details. The median RNA quality score of the samples was 6.7 (range, 4.2–9.3) with a score of 7.2 (4.2–9.0) in controls, 6.7 (4.8–8.9) in ruptured aneurysm samples, and 6.3 (5.1–9.3) in unruptured aneurysm samples (Table I in the online-only Data Supplement). Sequence libraries were generated from 44 aneurysms (22 ruptured, 21 unruptured, and 1 with unknown rupture status) and 16 control samples using the TruSeq mRNA sample preparation kit from Illumina (San Diego, CA) using the Sciclone NGS Liquid Handler (Perkin Elmer). After an extra purification step of the libraries with the automated agarose gel separation system Labchip XT (PerkinElmer), 9 picomoles of the obtained cDNA fragment libraries were sequenced on an Illumina HiSeq2500 using default parameters (single read 1×100 bp) in randomly arranged pools of 10 or 11 samples. On an average, 14 209 239 reads were generated per sample. The quality of the sequencing data were good (Figure I in the online-only Data Supplement). The average alignment of the reads to the human reference genome (uniquely mapped reads) was 86% (range, 73%–90%). For further details, see the Methods section in the online-only Data Supplement.

Gene Expression Quantification

We used R version 3.1.0¹⁴ and Bioconductor (version 2.14) packages edge R (version 3.6.2)¹⁵ and limma (version 3.20.2)¹⁶ for analysis of the gene expression data (for more details see the Methods section in the online-only Data Supplement). A generalized linear model was used to test the null hypothesis that there is no differential expression of genes between analysis groups. Age and sex of the patients were added to the model. In the model comparing aneurysms and controls, we added the rupture status, to control for genes with strong expression differences between ruptured and unruptured aneurysms.

Common and tagwise dispersion estimates were calculated with the Cox–Reid profile-adjusted likelihood method to be able to correct for the technical and biological variation when fitting the multivariate negative binomial model. A negative binomial generalized log-linear model, using the tagwise dispersion estimates, was fitted to the read counts for each gene and a genewise statistical test was performed for the given coefficient (either aneurysms to controls or ruptured to unruptured aneurysms). Then, a likelihood ratio test for the given coefficient in the model was performed. To correct for multiple testing, we calculated Benjamini Hochberg false discovery rates (FDR) and considered genes with an FDR-adjusted P value <0.05 differentially expressed. Although the genes with low counts (genes with <1 read per million in n of the samples, where n is the size of the smallest group of replicates) are not likely to show significant results in the differential expression analysis, they can still be biologically relevant for the disease in case such genes are only expressed in 1 condition and have 0 counts in the other. We therefore performed a subanalysis of the raw count data and selected those genes that had >200 counts versus 0 counts in aneurysms versus controls and ruptured versus unruptured aneurysms.

Validation of RNA Sequencing Data With Digital Droplet Polymerase Chain Reaction

Eight genes were selected for validation by selecting the 2 most biologically relevant top genes with overexpression and the 2 most biologically relevant top genes with underexpression in the aneurysms versus control tissue analysis and in the ruptured versus unruptured aneurysms analysis. Their expression was studied by digital polymerase chain reaction in the remaining extracted RNA of the samples included in the differential expression experiment (for more details see the Methods section and Figure II in the online-only Data Supplement). In 2 aneurysm samples, the amount of RNA left after RNA sequencing was insufficient leaving 20 ruptured, 21 unruptured aneurysm samples, and 16 control tissue samples for further analysis in this validation step. The relative difference in gene expression between aneurysms and controls or ruptured and unruptured aneurysms was analyzed with the Mann–Whitney U test. Genes with a P value of <0.05 were considered statistically significant differentially expressed.

In addition, we reviewed the existing literature investigating differences in gene expression in aneurysms for the 8 selected genes for further validation.^{5–12} Furthermore, we compared the list of differentially expressed genes in our study to the full lists of differentially expressed genes in the previous studies,^{5–12} when these lists were available online or could be obtained from the authors. The results of this comparison are shown in the Results section and Tables II and III in the online-only Data Supplement.

Functional Network Analysis

To identify the biological functional pathways that were significantly over-represented by differentially expressed genes between aneurysm and control tissue samples as well as between ruptured and unruptured aneurysm samples, we analyzed which Kyoto Encyclopedia of Genes and Genomes functional pathways, and which Gene Ontology categories were enriched in our data set. We used the Bioconductor package goseq (version 1.18.0),¹⁷ which enabled correction for gene length bias in the analysis. We used all genes with differential expression with an FDR-adjusted P value <0.05 as input for the analysis. Kyoto Encyclopedia of Genes and Genome pathways with an FDR-adjusted P value <0.05 were considered significantly enriched. Highly correlated terms were removed from the enriched Gene Ontology lists using the Gotrimming software (for further details see the online-only Data Supplement).¹⁸

Results

We analyzed the transcripts of 44 aneurysm biopsies (22 ruptured, 21 unruptured, and 1 with unknown rupture status) of

Table 1. Baseline Characteristics of the 38 Patients With Aneurysm and 16 Controls

	Patients With Aneurysm (n=38)*	Ruptured (n=22)	Unruptured (n=21)	Control Patients (n=16)
Mean age, y	53	54	53	30
Females	26	17	14	7
Current or former smoker	33	19	19	3
Aneurysm location				
MCA	...	9	17	...
ACA/ACOM	...	11	3	...
PCOM	...	2	0	...
ICA	...	0	1	...
Mean aneurysm size (range)	9 mm (3–25)	8 mm (3–25)	11 mm (5–23)	...
Mean time between rupture and surgery	...	6 d (0–20)

ACA indicates anterior cerebral artery; ACOM, anterior communicating artery; ICA, internal carotid artery; MCA, middle cerebral artery; and PCOM, posterior communicating artery.

*In 6 of the 38 patients, two biopsies of different aneurysms were obtained and analyzed, in 1 patient, the rupture status of the aneurysm was unknown.

38 aneurysm patients (6 patients had two aneurysms treated) and 16 control biopsies of 38 patients with aneurysm and 16 control patients. Baseline characteristics of the patients and controls are shown in Table 1.

Aneurysm Versus Control Tissue

Differentially Expressed Genes

The differential expression analysis yielded 51 genes with over-expression in aneurysms compared with controls (Figure 1; Table IV in the online-only Data Supplement). These included the top 5 genes collagen type X (*COL10A1*), cartilage intermediate layer protein 2 (*CILP2*), 1 RNA gene affiliated with the long noncoding RNA class (ENSG00000206195), secreted frizzled-related protein 2 (*SFRP2*), and muscle excess 3 RNA-binding family member B (*MEX3B*; Table 2). We found 178 genes that were underexpressed in aneurysm tissue (Table IV in the online-only Data Supplement), including the top 5 genes family with sequence similarity 134, member B (*FAM134B*), a gene of the solute carrier family (*SLC13A3*) which code for transporter proteins in the cell membrane, a gene involved in coagulation (*SERPIND1*), the growth regulation by estrogen in breast cancer 1 gene (*GREB1*) and a gap junction protein (*GJB6*; Table 2). The overexpression of *COL10A1* and *CILP2* in aneurysm tissue, seeming the 2 most biologically relevant top genes, was confirmed in the validation experiment ($P<0.0001$), as was the underexpression of *GJB6* ($P<0.0001$) and *SERPIND1* ($P=0.0015$; Table 2; Figure 2). The 4 relevant and highly significant genes in aneurysms versus controls were not found differentially expressed in the 4 previous studies of which a full lists of differentially expressed genes was available,^{6–9} nor in the one in which an incomplete list was available.¹¹

Functional Network Analysis

Functional network analysis of the 229 differentially expressed genes with an FDR-adjusted P value <0.05 did not identify any significant Kyoto Encyclopedia of Genes and

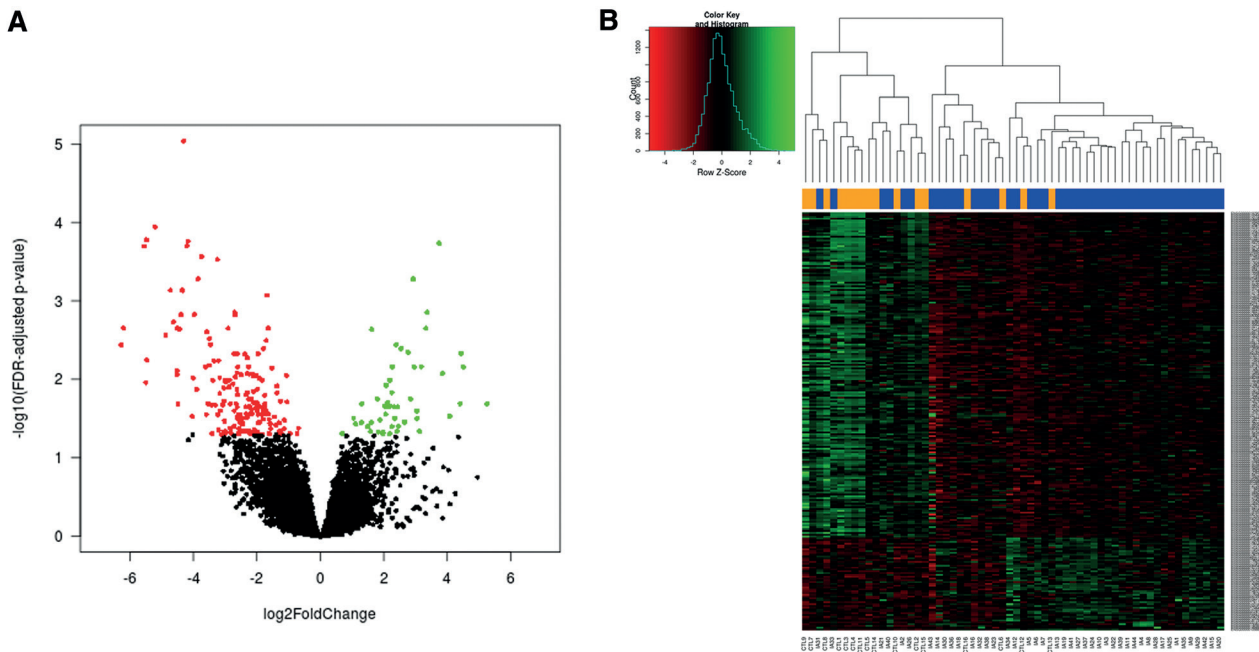


Figure 1. Differential expression in aneurysms versus controls visualized in a volcano plot (A) and a heatmap (B). A, Log2-fold changes and their corresponding P values of each gene were taken for construction of the volcano plot. Green dots represent upregulated genes ($n=51$) with false discovery rates (FDR) <0.05 , whereas downregulated genes ($n=178$) with identical FDR are depicted in red. All other genes whose expression levels were not found to be significantly altered are in black dots. B, Heatmap comparison of the differentially expressed genes across the 60 patients samples (16 controls and 44 aneurysms). Hierarchical clustering is shown on the top.

Table 2. Top 10 of Differentially Expressed Genes in Aneurysms Versus Controls and Ruptured Versus Unruptured Aneurysms

Ensembl ID	Gene ID (HGNC)	Location	logFC	FDR-Adjusted <i>P</i> Value	Validation Experiment <i>P</i> Value
Overexpression in aneurysms versus controls					
ENSG00000123500	COL10A1	6q21-q22	3.7	1.8 E-4	<0.0001
ENSG00000160161	CILP2	19p13.11	2.9	5.2 E-4	<0.0001
ENSG00000206195			3.7	1.3 E-3	
ENSG00000145423	SFRP2	4q31.3	3.3	2.2 E-3	
ENSG00000183496	MEX3B	15q25.2	1.6	2.3 E-3	
ENSG00000260396			2.4	3.6 E-3	
ENSG00000087494	PTHLH	12p12.1-p11.2	2.5	4.0 E-3	
ENSG00000249119	MTND6P4	5q31.1	2.8	4.5 E-3	
ENSG00000130300	PLVAP	19p13.2	4.4	4.6 E-3	
ENSG00000225210			3.2	6.9 E-3	
Underexpression in aneurysms versus controls					
ENSG00000154153	FAM134B	5p15.1	-4.3	9.2 E-6	
ENSG00000158296	SLC13A3	20q13.12	-5.2	1.1 E-4	
ENSG00000099937	SERPIND1	22q11.21	-5.5	1.7 E-4	0.0015
ENSG00000196208	GREB1	2p25.1	-4.2	1.7 E-4	
ENSG00000121742	GJB6	13q12	-5.6	2.0 E-4	<0.0001
ENSG00000107147	KCNT1	9q34.3	-4.2	2.0 E-4	
ENSG00000151715	TMEM45B	11q24.3	-3.7	2.7 E-4	
ENSG00000164309	CMYA5	5q14.1	-3.2	3.0 E-4	
ENSG00000144550	CPNE9	3p25.3	-3.9	5.3 E-4	
ENSG00000107317	PTGDS	9q34.2-q34.3	-4.7	7.3 E-4	
Overexpression in ruptured versus unruptured aneurysms					
ENSG00000019169	MARCO	2q14.2	3.0	2.2 E-6	0.0006
ENSG00000120708	TGFBI	5q31	2.0	1.1 E-5	
ENSG00000173083	HPSE	4q21.3	2.8	4.5 E-5	
ENSG00000167850	CD300C	17q25.1	2.5	7.3 E-5	
ENSG00000186407	CD300E	17q25.1	3.2	8.4 E-5	0.0039
ENSG00000258227	CLEC5A	7q33	2.8	8.4 E-5	
ENSG00000173391	OLR1	12p13.2-p12.3	2.7	8.4 E-5	
ENSG00000170909	OSCAR	19q13.42	2.6	8.4 E-5	
ENSG00000203306			2.1	8.4 E-5	
ENSG00000268802			2.0	8.4 E-5	
Underexpression in ruptured versus unruptured aneurysms					
ENSG00000206052	DOK6	18q22.2	-2.0	1.1 E-4	
ENSG00000070808	CAMK2A	5q32	-3.1	2.0 E-4	0.1085
ENSG00000164591	MYOZ3	5q33.1	-1.8	2.8 E-4	
ENSG00000211892	IGHG4	14q32.33	-6.1	2.9 E-4	
ENSG00000129167	TPH1	11p15.3-p14	-2.7	3.3 E-4	
ENSG00000184731	FAM110C	2p25.3	-2.2	3.3 E-4	
ENSG00000128422	KRT17	17q21.2	-3.2	3.3 E-4	0.06
ENSG00000260396			-2.0	3.3 E-4	
ENSG00000124507	PACIN1	6p21.3	-3.1	4.7 E-4	
ENSG00000181418	DDN	12q13.12	-2.9	5.2 E-4	

FDR indicates Benjamini Hochberg false discovery rates; HGNC, HUGO Gene Nomenclature Committee; and logFC, log fold change.

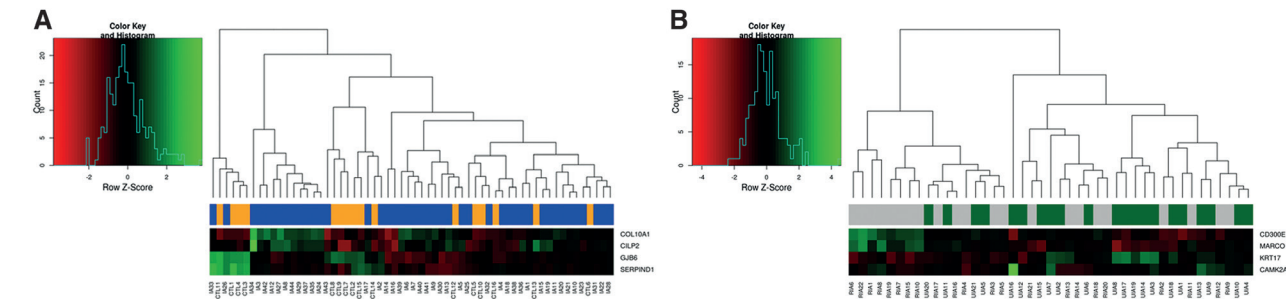


Figure 2. Heatmap showing the differential expression of the 8 genes used in the validation experiment. **A**, Aneurysm versus controls. **B**, Ruptured versus unruptured aneurysms.

Genome pathways. After removal of redundant classes, 51 Gene Ontology terms were identified (Table V in the online-only Data Supplement for the full list), including terms related to the extracellular matrix (ECM) and transmembrane transporter activity, and terms involving blood vessel regulation.

Low-Count Gene Analysis

The subanalysis of low-count genes in the raw count data yielded 3 immunoglobulin κ variable region genes (*IGKV1D-42*, *IGKV3D-15*, and *IGKV1-6*), 5 immunoglobulin heavy chain variable region genes (*IGHV3-20*, *IGHV3OR16-15*, *IGHV3-60*, *IGHV1OR15-4*, and *IGHV3-66*), and 2 other genes (tyrosinase [*TYR*] and a gene with Ensemble ID ENSG00000198229 but without an associated gene name) with >200 counts in aneurysm tissue and 0 counts in control tissue. None of the genes had 0 counts in aneurysms and >200 counts in control tissue.

Ruptured Versus Unruptured Aneurysm Tissue

Differentially Expressed Genes

The differential expression analysis identified 958 genes with overexpression in ruptured aneurysm tissue compared with unruptured aneurysm tissue (Figure 3; Table VI in the online-only Data Supplement). The top 5 overexpressed genes included the macrophage receptor with collagenous structure gene (*MARCO*), genes involved in ECM structure (transforming growth factor β -induced [*TGFBI*], heparanase [*HPSE*]), and 2 members of CD family (*CD300C* and *CD300E*; Table 2). Five hundred thirty-one genes were underexpressed in ruptured aneurysms (Table VI in the online-only Data Supplement). Top 5 underexpressed genes included the docking protein 6 (*DOK6*), calcium/calmodulin-dependent protein kinase type II α chain gene (*CAMK2A*), myozenin 3 (*MYOZ3*), an immunoglobulin gene (*IGHG4*), and tryptophan hydroxylase 1 (*TPHI*; Table 2). We also found keratin 17

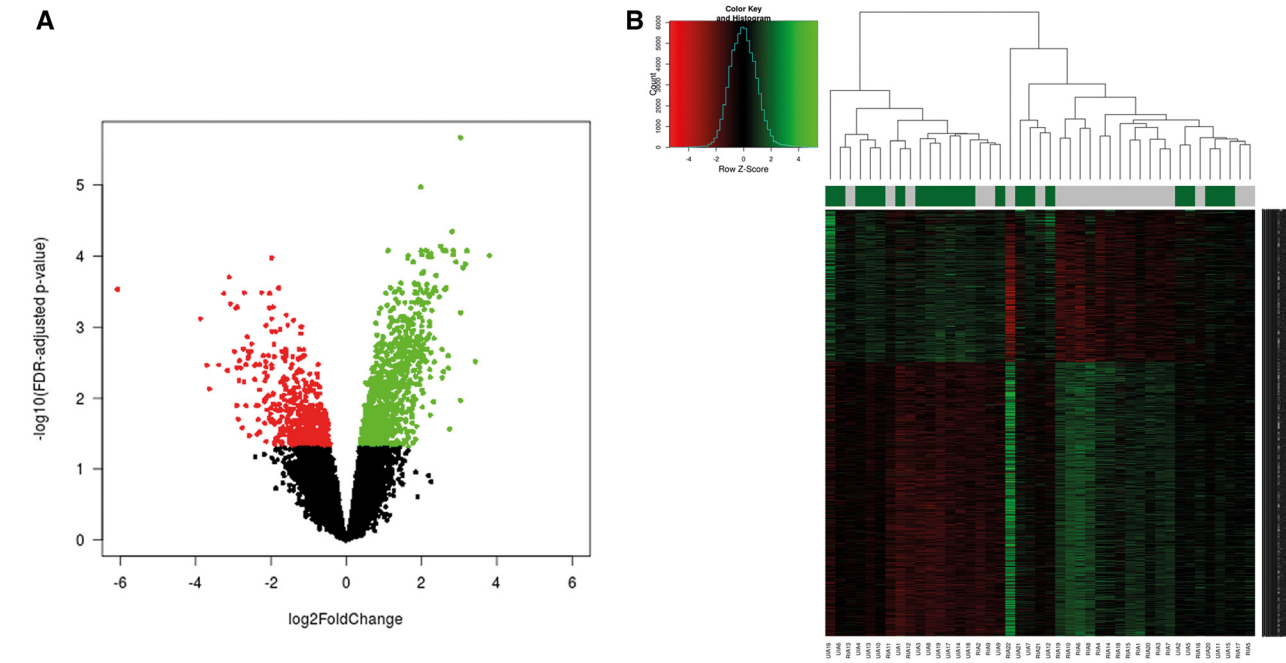


Figure 3. Differential expression in ruptured versus unruptured aneurysms visualized in a volcano plot (**A**) and a heatmap (**B**). **A**, Log2-fold changes and their corresponding *P* values of each gene were taken for construction of the volcano plot. Green dots represent upregulated genes ($n=958$) with false discovery rates (FDR) <0.05 , whereas downregulated genes ($n=531$) with identical FDR are depicted in red. All other genes whose expression levels were not found to be significantly altered are in black dots. **B**, Heatmap comparison of the differentially expressed genes across the 43 aneurysm samples (22 ruptured and 21 unruptured aneurysms). Hierarchical clustering is shown on the top.

(*KRT17*), a cytoskeleton protein expressed in skin, but also in blood and brain, among the top 10 genes with underexpression in ruptured versus unruptured aneurysms (Table 2). The overexpression of *CD300E* ($P=0.0039$) and *MARCO* ($P=0.0006$) in ruptured aneurysm tissue was confirmed in the validation experiment. Comparable to the findings in the RNA sequencing analysis, we again showed underexpression of *KRT17* ($P=0.06$) and *CAMK2A* ($P=0.1085$), although for these genes the relative expression differences were not statistically significant in the validation experiment (Table 2; Figure 2). Of the 4 relevant and highly significant genes in ruptured versus unruptured aneurysms, the *MARCO* gene was also found to be overexpressed in 1 previous study,¹⁰ and the *KRT17* gene was also found to be underexpressed in the 2 most recent gene expression studies.^{10,12} The other 2 relevant and highly significant genes were not found to be differentially expressed before.

Functional Network Analysis

Functional analysis of the 1489 differentially expressed genes with an FDR-adjusted P value <0.05 yielded 6 significant Kyoto Encyclopedia of Genes and Genome pathways: lysosome, osteoclast differentiation, *Staphylococcus aureus* infection, phagosome, leishmaniasis, and Fc γ R-mediated phagocytosis (Table VII in the online-only Data Supplement). After trimming, 306 Gene Ontology terms were identified (Table VIII in the online-only Data Supplement), including many terms involved in immune response, the terms lysosome, lysosome organization, and lysosomal membrane and lumen, and terms involved in cell–cell interaction and in-cell regulation.

Low-Count Gene Analysis

The subanalysis of low-count genes found immunoglobulin κ variable 1D-42 to have >200 counts in unruptured aneurysms and 0 counts in ruptured aneurysms. None of the genes had 0 counts in ruptured aneurysm tissue and >200 counts in unruptured aneurysm tissue.

Discussion

This study found ECM pathways to play a role in aneurysms and pathways involved in immune response in rupture of aneurysms, and identified lysosomes as a new pathway to play a role in rupture. In addition, our results point toward a role for immunoglobulins in the pathogenesis of aneurysms because we found that immunoglobulin κ and heavy chain variable region genes were expressed in aneurysm tissue, but showed no expression in control tissue. One immunoglobulin κ variable region gene was expressed in unruptured and not in ruptured aneurysms. The differences in gene expression found in aneurysms and controls can be the cause, but also be the result of the development of aneurysms. Because intracranial aneurysms are associated with heritable disorders of connective tissue and ECM,¹⁹ changes in the ECM are more likely the cause of the development of aneurysms than its result. As in aneurysms and controls, the differences found in ruptured and unruptured aneurysms can be the cause, but also the result of rupture. Because the time between subarachnoid hemorrhage and clipping was >48 hours in half of our patients, the

overexpression of immune response genes in ruptured versus unruptured aneurysms might also be the result of an inflammatory reaction in response to the event of rupture, instead of the cause of rupture. However, 2 previous studies compared biopsies obtained within a range of 2.6 to 24 hours¹⁰ or 6 to 24 hours after rupture²⁰ and those biopsies obtained later showed no differences in gene expression,¹⁰ nor in the degree of inflammatory cell invasion into the wall.²⁰ Furthermore, in a study of ruptured aneurysms from autopsy cases inflammatory cell infiltration was always found to be accompanied by fibrosis, and fibrosis was never present without an inflammatory cell infiltration, even in unruptured aneurysms.²¹ Because fibrosis is considered the end result of chronic inflammatory reactions,²² this strongly suggests that the inflammatory reaction is present before rupture.

Our study identified the expression of both light (ie, of the κ subtype) and heavy chain immunoglobulin genes in aneurysm tissue and its complete absence in control tissue. Two previous immunohistochemistry studies already showed heavy chain immunoglobulins subtypes IgG and IgM to be present in the majority of the investigated aneurysm walls,^{23,24} whereas these were only rarely found in control arteries.²³ One of these studies also found sporadic B lymphocytes (which produce immunoglobulins) in unruptured aneurysm tissue, whereas these cells were absent in control arteries.²³ The presence of immunoglobulins and B lymphocytes in the aneurysm wall suggest that the inflammatory reaction in the aneurysm wall, which is not seen in healthy control arteries, is initiated by the humoral immune response, through attraction of inflammatory cells and through complement activation.²⁴ Our study underlines the importance of involvement of genes of the ECM pathway in aneurysms, which was also found in a previous meta-analysis of 5 microarray studies.²⁵ Furthermore, several histopathologic studies have shown degradation of the ECM in intracranial aneurysm tissue.²⁶ We found enrichment of the lysosome pathway in ruptured aneurysms. Lysosomes digest the degradation material from the cell. Phagosomes, another enriched pathway in ruptured aneurysms in our study, fuse with lysosomes after phagocytosis of degradation material. Enrichment of these pathways supports the notion that degradation of the components of the unruptured aneurysm wall is a process leading to rupture,²⁷ but may also be a response to rupture. In a previous genome-wide expression study on blood from patients with aneurysmal subarachnoid hemorrhage taken several years after the subarachnoid hemorrhage compared with blood of healthy controls the lysosome pathway was also found enriched.²⁸ This finding strengthens the idea that the lysosome pathway does not reflect an acute and short-lasting reaction to aneurysm rupture. Pathways found to be involved in rupture in previous studies were inflammation and immune response pathways, ECM degradation, cell adhesion, vascular remodeling, oxidative stress, turbulent bloodflow, proteases, and apoptosis.^{8–10,12} Our study also found immune response pathways to be involved in rupture and identified lysosomes as a new pathway. Furthermore, inflammation was a predominant characteristic of ruptured aneurysms in immunohistochemistry studies.²⁶

This study has some limitations. First, aneurysm biopsies could only be taken from aneurysms treated with microneurosurgical techniques, which may induce a selection bias because certain aneurysm characteristics might make aneurysms more suitable for clipping while these characteristics are also associated with rupture.²⁹ Second, as controls we used cortical intracranial arteries obtained from patients with intractable epilepsy. However, we cannot be sure that the composition of these cortical arteries is similar to the composition of the basal arteries of the circle of Willis on which aneurysms arise. Furthermore, we cannot exclude the possibility that the seizures or the epileptogenic focus have altered the cortical vessels, although we found no data supporting such an influence. There are several strengths of this study. First, we did not find larger studies investigating gene expression differences in intracranial aneurysms to date. The large sample size increased power of our study and enabled correction for possible confounders in our analysis, including sex, age, and rupture status of the aneurysm. Furthermore, we used RNA-sequencing methodology, which compared with the previously used microarray technique, has the advantage of requiring less tissue mass as input material (crucial in aneurysm studies because of the small size of the biopsies) and of a genome-wide coverage, enabling the discovery of not yet identified genes involved in the disease. Finally, we used healthy intracranial arteries as controls, which are preferred above extracranial arterial tissue because of the differences in vessel wall composition between intra- and extracranial arteries.

In conclusion, we identified the lysosome pathway as a new pathway for rupture of intracranial aneurysms and found further evidence for the role of the immune response in aneurysmal rupture. Our results also point toward a role for immunoglobulins in the pathogenesis of aneurysms. Our finding that immune response pathways play a role in aneurysm rupture suggest that anti-inflammatory and immune-modifying drugs are interesting candidate therapeutics in the prevention of aneurysm rupture. The presence of immunoglobulins in aneurysm and its absence in control tissue highlights the potential role of immunoglobulin-mediated inhibition of B lymphocytes as an interesting therapeutic intervention in aneurysm development or growth. To identify patients with aneurysms showing signs of increased aneurysm wall inflammation, an imaging technique is required that is able to correctly identify those aneurysms subject to inflammation, for example, by using magnetic resonance imaging with a suitable contrast agent or high resolution vessel wall magnetic resonance imaging.^{30,31}

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Disclosures

None.

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RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture

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SUPPLEMENTAL MATERIAL

ONLINE SUPPLEMENT

RNA sequencing analysis of intracranial aneurysm walls reveals involvement of lysosomes and immunoglobulins in rupture.

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SUPPLEMENTAL METHODS

Patient selection

We included patients who were to undergo neurosurgical clipping of a ruptured, or unruptured saccular intracranial aneurysm. Patients with fusiform, mycotic and dissection aneurysms were excluded, as were patients with previous treatment of the same aneurysm. Patients with underlying diseases such as connective tissue disorders, polycystic kidney disease and arteriovenous malformations were also excluded. As controls, patients who were to undergo surgery because of intractable epilepsy were included. Exclusion criteria for these control patients were a (family) history of intracranial aneurysm, SAH or other cerebrovascular diseases, the presence of a connective tissue disease or polycystic kidney disease, and a pathological diagnosis of a low or high grade glioma after resection.

Sample collection and preparation

When complete obliteration of the aneurysm was confirmed by visual inspection and, if indicated, intraoperative IndoCyanine Green angiography, a part of the aneurysm dome distal to the clip was excised, only when this procedure was assessed to be safe by the neurosurgeon. In the controls, a part of a superficial cortical artery in the resected part of the brain was excised. There were no complications of the excision of the tissue samples. After excision, the samples were snap frozen in liquid nitrogen (< 1 minute after excision) and stored at – 80 °C until further use. The intra-operative judgment on the rupture status of the aneurysm was considered the golden standard in case of SAH and multiple aneurysms. Aneurysms in which the rupture status was unclear and in which the whole aneurysm could not be inspected during surgery in order to identify recent rupture, were excluded for the analysis comparing ruptured and unruptured aneurysms (n=1).

Tissue samples were homogenized with zirconia/silica beads in the BeadBeater machine (BioSpec products, Inc). After homogenization, total RNA was extracted and purified using an RNeasy microkit (Catalog No. 74004, Qiagen, Valencia, CA, USA) according to the manufacturer's instructions.

Quality of the extracted RNA of the samples

A total of 82 tissue samples (60 aneurysm samples and 22 control samples) were homogenized, but only the samples with a minimum of 7 ng non-degraded RNA were selected for subsequent sequencing analysis. A total of 16 aneurysm samples (four ruptured and twelve unruptured) and six control samples had to be excluded due to insufficient amounts of RNA.

Of the 60 samples included, the mean total RNA concentration was 18 ng/ul (range 1-109), and 13 ng/ul (2-35) in controls, 19 ng/ul (3-109) in ruptured aneurysms and 19 ng/ul (1-77) in unruptured aneurysms (Supplementary table I). The mean RNA quality score was 6.8 (range 4.2-9.3), and 7.2 (4.2-9.0) in controls, 6.7 (4.8-8.9) in ruptured aneurysm samples and 6.5 (5.1-9.3) in unruptured aneurysm samples (Supplementary table I). Of two samples, the RNA quality score was not available. The RNA concentration of these samples was 5.0 and 1.2 ng/ul, and both were unruptured aneurysm samples.

Quality control of reads

The number of reads passing filter ranged from 68.43 to 118.25 million. The yield ranged between 3.4 and 5.8 gigabases. We summarized the quality of the reads by using the R/Bioconductor package Rqc^{1,2} producing one bar plot showing an overview of the range of quality values across all bases at each position in the reads from all the samples included in our analysis (Supplementary figure I, panel A). This plot shows that the quality of our reads per position is above 30 at each position, which indicates good quality. A

second plot showing the average quality pattern of reads of all the samples that were included in our analysis shows that more than 90% of the reads exceed a quality score of 30, also indicating good quality of the data (Supplementary figure I, panel B).

Reads mapping

Processing of the raw data including a demultiplexing step was performed using Casava software (Illumina) with standard settings. The trimmed fastQ files were aligned to build 37 human reference genome using STAR 2.3.1³ allowing for two mismatches. Before gene quantification SAMtools 0.1.18⁴ was used to sort the aligned reads. The gene level quantification was performed by HTSeq-0.5.4⁵ using --mode=union --stranded=no using Ensembl version 71 as gene annotation database. The average alignment of the reads to the human reference genome (uniquely mapped reads) was 86% (range 73-90%).

Gene expression quantification

We used R version 3.1.0 for analysis of the gene expression data.¹ The counts per gene for each sample obtained after alignment were used as input for the differential expression analysis. Low count genes (genes with less than 1 read per million in n of the samples, where n is the size of the smallest group of replicates) were filtered out since they have no, or little change of showing significant results in the differential expression analysis.⁶ For the analysis in aneurysms versus control tissue, n was set at 16 (equivalent to the number of replicates in the smallest group, the controls), while n was set at 21 in the analysis of ruptured versus unruptured aneurysms (with unruptured aneurysms being the smallest group). The Bioconductor (version 2.14) packages edgeR (version 3.6.2)⁷ and the for edgeR required package limma (version 3.20.2)⁸ were used for subsequent steps of the differential expression analysis. To correct for technical influences, edgeR adjusts any differential expression analysis for varying sequencing depths between samples as represented by differing library sizes. Furthermore, it calculates scale factors with the trimmed mean of M-values method, thereby normalizing for RNA composition of the sample, and creating an effective library size which is used in downstream analysis.

Age and sex of the patients were added to the model, as was the rupture status of the aneurysms in the comparison of aneurysms and controls. In the process of sequencing, after the first sequencing run of the samples, three pools yielded an insufficient amount of reads due to contamination of adapter-duplexes. These pools were sequenced again in a second run, and the count data of the second run was used for the differential gene expression analysis for the samples involved. Therefore, the sequencing run number was also added to the generalized linear model to correct for possible influences on the data of the different runs.

Validation of RNA sequencing data with digital droplet polymerase chain reaction.

The QX200 Droplet Digital PCR system (Bio-Rad) was used to determine mRNA expression in the samples. First-strand complementary DNA (cDNA) was synthesized using the SuperScript[®] III First-Strand Synthesis Supermix for qRT-PCR kit (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions. Resulting cDNA was diluted by adding 79 μ l nuclease-free water. Thermal cycling was performed using a 20 μ l ddPCR reaction (ddPCR 2X PCR Master Mix, Bio-Rad) with 5 μ l of cDNA template. Each reaction was run in duplicate and droplet counts were merged to increase the precision. Droplet counts were all within expected range (~16,000 - 18,000). Primary data processing was done using the QuantaSoft software. The number of positive and negative droplets is used to calculate the concentration (cDNA copies/ μ l ddPCR reaction) of the targets and their Poisson-based 95% confidence intervals. Further data-analysis was performed in Microsoft Excel. Two reference genes (*SCLY* and *ENOX*) were included for multi-gene normalization.⁹ The normalization factor (NF) was calculated as the geometric mean of reference targets *SCLY* and *UBE4A*, and displayed high expression stability (geNorm M value of 0.49) given the heterogeneity of the samples. The absolute (cDNA copies/ μ l in ddPCR reaction) and relative (unit-less) concentration values and 95% confidence intervals were calculated with the QuantaSoft software in all samples and a non-template control sample. Supplemental figure II shows the results of the validation experiment for each of the selected genes. For validation of the underexpressed genes in ruptured versus unruptured aneurysms we initially chose the immunoglobulin gene *IGHG4*, but due to problems with the specificity of the assay of this gene, we chose keratin 17 (*KRT17*) instead.

Comparison of differential expression results to results of previous studies

The list of differentially expressed genes in aneurysms versus controls and in ruptured versus unruptured aneurysms was compared to the full lists of differentially expressed genes found in previous gene expression studies.¹⁰⁻¹⁷ We used the Gene Symbol, and if available the ENSEMBL ID or the Entrez gene ID to compare the lists.

Trimming of gene ontology (GO) categories

To make interpretation of the enriched GO categories possible, we reduced the number of categories by only selecting the GO terms with a total number of genes greater than 20 and smaller than 400 with a p-value <0.01, since too small or too large categories are not very informative. Then we removed all categories with less than 5 differentially expressed genes, to remove overly-specific terms enriched by only a few genes. The resulting list of GO terms was inputted on a GOtrimming tool¹⁸ using a strong trim threshold (which removes related terms with identical gene content) of 0.40, which calculates the similarity between a parent and child term to be able to remove a parent term with a threshold of 40%. This parent term will be removed if it contains less than or equal to 40% more genes than a child term. The results of the GOtrimming are shown in Supplementary table V and VII.

SUPPLEMENTAL RESULTS

Comparison of differential expression results to results of previous studies

We were able to obtain the full lists of differentially expressed genes in aneurysms versus controls in four of the six previous gene expression studies.¹¹⁻¹⁴ In one more study, we could only compare our results to the (incomplete) list of differentially expressed genes as published in the article.¹⁶ For one study full data was not available online and could not be obtained from the authors.¹⁰

Of the total list of 229 differentially expressed genes in aneurysm versus controls identified in our study ten differentially expressed genes were previously found differentially expressed in three other studies (Supplementary table II).^{11,12,16} One of these genes, *COL4A6*, was found underexpressed in our and two other studies.^{11,16}

The full data from four previous gene expression studies comparing expression in ruptured versus unruptured aneurysms was all available.^{13,14,15,17}

Of the total list of the 1489 differentially expressed genes in ruptured versus unruptured aneurysms identified in our study 463 genes were also found differentially expressed in one or more of the previous studies.^{13,14,15,17} Of these 463 genes, 68 were found in our and in at least two of the four previous studies. The results are shown in Supplementary table III.

SUPPLEMENTARY TABLES

Supplementary Table I. RNA quality values for each of the samples included.

Sample number	Sample type	Total Conc. (ng/ul)	rRNA Height Ratio [28S/18S]	RNA Quality Score
CO1	Control	26.6	1.7	8.1
CO2	Control	5.1	1.3	6.4
CO3	Control	8.0	1.6	7.8
CO4	Control	4.6	1.0	4.2
CO5	Control	13.1	1.7	6.5
CO6	Control	23.4	1.8	6.6
CO7	Control	5.2	1.6	7.7
CO8	Control	2.5	1.4	7.2
CO9	Control	1.9	2.3	8.7
CO10	Control	7.8	2.0	9.0
CO11	Control	13.6	1.3	6.7
CO12	Control	35.0	2.4	8.5
CO13	Control	17.1	1.7	7.4
CO14	Control	10.3	1.7	6.7
CO15	Control	15.3	1.7	7.4
CO16	Control	12.6	1.4	7.2
IA1	Ruptured	3.3	1.8	7.5
IA2	Unruptured	8.9	1.7	6.6
IA3	Ruptured	3.0	1.7	7.1
IA4	Unruptured	77.4	1.9	5.4
IA5	Unruptured	22.1	1.4	6.3
IA6	Unknown	50.8	1.9	7.1
IA7	Unruptured	4.1	2.2	8.9
IA8	Unruptured	71.8	1.8	6.1
IA9	Unruptured	4.2	1.6	5.7
IA10	Unruptured	5.0	0.0	NA
IA11	Ruptured	23.2	1.6	7.9
IA12	Unruptured	14.5	0.8	5.1
IA13	Unruptured	13.9	1.9	5.7
IA14	Ruptured	108.9	1.9	8.0
IA15	Ruptured	39.7	1.6	6.5

IA16	Ruptured	6.7	1.5	4.9
IA17	Ruptured	3.3	1.4	6.3
IA18	Ruptured	6.7	1.0	5.7
IA19	Unruptured	20.7	2.3	7.1
IA20	Unruptured	19.2	1.8	5.8
IA21	Unruptured	2.0	1.4	7.9
IA22	Ruptured	22.1	1.8	8.9
IA23	Ruptured	6.1	1.9	7.2
IA24	Unruptured	15.0	2.0	6.5
IA25	Ruptured	12.6	2.0	6.7
IA26	Ruptured	39.1	1.8	7.3
IA27	Unruptured	1.2	0.0	NA
IA28	Unruptured	4.3	2.0	8.0
IA29	Ruptured	34.4	1.2	7.0
IA30	Ruptured	17.1	2.2	7.6
IA31	Unruptured	24.4	1.0	5.1
IA32	Ruptured	6.3	3.1	6.0
IA33	Ruptured	11.3	1.6	6.9
IA34	Unruptured	22.9	1.8	6.5
IA35	Ruptured	15.9	1.1	4.8
IA36	Ruptured	5.4	1.6	6.6
IA37	Unruptured	6.5	1.6	6.8
IA38	Ruptured	6.9	1.9	5.9
IA39	Ruptured	16.8	1.5	6.0
IA41	Unruptured	2.3	2.1	9.3
IA42	Unruptured	6.9	2.3	6.0
IA43	Ruptured	9.6	3.0	6.7
IA44	Unruptured	51.0	1.7	5.3

Supplementary Table II. Differentially expressed genes in aneurysms versus controls in the current study and in previous studies.

	Current study		Shi ¹¹		Li ¹²		Yu ¹⁶
Hgnc symbol	logFC	FDR adj. Pvalue	Fold Change	FDR adj. Pvalue	Fold Change	P value	Fold Change
LOC440157	3.2	0.00690	41.025	0.0033398	-	-	-
SLC13A4	-4.4	7.3E-04	26.065	0.007781	-	-	-
RGMA	-2.2	8.5E-03	-2.8568	0.00080461	-	-	-
ANKS1B	-2.1	2.0E-02	-2.1774	0.0014819	-	-	-
PPL	-1.6	2.8E-02	-3.4247	0.0025509	-	-	-
COL4A6	-2.3	3.1E-02	-3.5101	0.00011175	-	-	0.0467
FZD3	-1.6	4.2E-02	-2.2943	0.005822	-	-	-
H19	4.4	0.02043	-	-	-3.946855	0.041134	-
PLVAP	4.4	0.00464	-	-	-2.069474	0.031437	-
SLC4A4	-2.1	4.6E-02	-	-	2.524201	2.04E-04	-

Hgnc indicates Human genome nomenclature committee; FDR, false discovery rate.

Supplementary Table III. Differentially expressed genes in ruptured versus unruptured aneurysms in the current study and in previous studies.

	Current study		Kurki ¹⁵		Nakaoka ¹⁷		Marchese ¹⁴		Pera ¹³	
Hgnc symbol	Log FC	FDR adj. Pvalue	FC	FDR adj. Pvalue	Log2 FC	P value	FC	Pvalue	RA/MMA ratio	Pvalue
CD14	1.5	7.3E-04	7.32	2.86E-03	-	-	-	-	2.04	2.30E-04
BCL2	-0.5	4.5E-02	-	-	-0.77078941	0.002095	-4.1	0.0000124	-	-
C19orf59	3.8	9.9E-05	5.54	4.61E-03	3.61989006	5.05091E-05	-	-	-	-
KRT17	-3.2	3.4E-04	0.32	7.34E-03	-2.8813939	7.58407E-05	-	-	-	-
SLC11A1	3.2	1.3E-04	2.75	7.34E-03	2.19960194	0.000205552	-	-	-	-
CCL20	3.0	1.1E-02	5.03	1.60E-03	1.06231547	0.005100282	-	-	-	-
ANPEP	2.8	9.6E-05	4.01	3.41E-03	2.36864509	0.000147943	-	-	-	-
TMEM130	-2.4	5.5E-03	0.39	3.62E-02	-3.8922697	0.000123461	-	-	-	-
IL10	2.4	2.8E-04	1.52	3.63E-02	1.19652507	0.00022704	-	-	-	-
NOD2	2.3	3.0E-04	2.17	4.47E-02	1.33445661	0.001669892	-	-	-	-
MYO1G	2.3	3.4E-04	2.14	1.16E-02	1.19165627	0.00047316	-	-	-	-
AQP9	2.2	4.0E-03	6.28	4.56E-04	2.02862627	0.000720348	-	-	-	-
SPOCD1	2.2	2.3E-03	2.64	3.07E-03	1.11150197	0.001191277	-	-	-	-
VEGFA	2.1	3.1E-03	2.17	3.91E-02	2.31442847	7.19968E-05	-	-	-	-
CD300A	2.1	3.3E-04	1.91	3.88E-02	0.8836525	0.005752949	-	-	-	-

PFKFB4	2.1	2.9E-04	1.63	4.39E-02	1.56404602	5.2061E-06	-	-	-	-
CD163	2.0	4.5E-04	49.46	1.88E-06	1.91839648	0.000215555	-	-	-	-
PPBP	2.0	1.3E-02	23.95	4.85E-03	2.99785242	0.002193543	-	-	-	-
BCL2A1	2.0	5.4E-03	10.50	3.98E-05	1.29681738	0.004379909	-	-	-	-
CCR1	2.0	1.8E-04	5.33	3.42E-03	0.64304855	0.001162229	-	-	-	-
TGFBI	2.0	1.1E-05	2.20	4.05E-02	1.58356982	8.08296E-05	-	-	-	-
SLA	1.9	2.6E-03	8.31	1.06E-03	1.19299423	0.004191646	-	-	-	-
TNFRSF1B	1.9	7.2E-04	4.22	3.06E-03	1.14749978	0.001334608	-	-	-	-
PF4	1.8	4.3E-02	21.47	3.78E-03	2.77937533	0.003445737	-	-	-	-
C1orf162	1.8	7.5E-04	8.33	2.02E-04	1.33842881	0.004622647	-	-	-	-
LILRB2	1.8	3.4E-04	3.56	1.59E-03	1.61717589	0.004887457	-	-	-	-
MPP1	1.8	1.2E-04	3.35	5.79E-04	1.1955788	0.003212891	-	-	-	-
SLC16A3	1.7	1.7E-03	1.72	2.66E-02	0.89601931	0.000170998	-	-	-	-
FPR1	1.6	8.6E-03	7.86	1.72E-03	1.98844243	1.58202E-05	-	-	-	-
MXD1	1.6	3.6E-03	2.04	2.11E-02	1.87017439	0.001407839	-	-	-	-
RASL11B	-1.5	4.0E-02	0.26	1.35E-03	-1.7047446	0.000152165	-	-	-	-
MYO1F	1.5	5.4E-03	3.66	2.20E-03	0.84744758	0.003780601	-	-	-	-
VDR	1.5	1.6E-02	1.98	1.02E-02	1.55757147	0.002004403	-	-	-	-
SLC25A37	1.4	2.0E-02	2.03	3.19E-02	1.84983699	6.55986E-05	-	-	-	-
AMOT	-1.3	7.0E-03	0.37	1.45E-02	-0.7944984	0.002731114	-	-	-	-

FXVD1	-1.3	3.0E-02	0.36	7.67E-03	-1.1909223	0.000445242	-	-	-	-
ANK3	-1.3	5.9E-03	0.26	5.99E-04	-1.9271457	0.000314526	-	-	-	-
ID4	-1.3	2.5E-02	0.23	5.82E-03	-2.0902873	0.002134281	-	-	-	-
ABCA1	1.2	1.2E-02	3.33	7.06E-03	0.63997538	0.004841696	-	-	-	-
MMP19	1.2	4.3E-02	1.82	1.22E-02	1.14294992	0.003151796	-	-	-	-
CTDSPL	-1.1	1.3E-02	0.43	4.34E-02	-1.4233772	8.56397E-05	-	-	-	-
CYB5R4	1.1	9.8E-04	2.02	2.11E-02	0.85768478	0.004507212	-	-	-	-
ZDHC14	-1.0	4.6E-03	0.54	4.63E-02	-0.8869169	0.002897896	-	-	-	-
LYN	1.0	1.9E-02	3.64	1.84E-02	1.08008271	0.002195089	-	-	-	-
HIF1A	1.0	1.9E-02	2.80	5.85E-06	0.66468801	0.002810988	-	-	-	-
RAB40B	-0.9	2.4E-02	0.33	1.41E-02	-0.8858774	0.000377964	-	-	-	-
GPRASP1	-0.9	5.0E-02	0.30	4.16E-03	-1.2385568	0.000753349	-	-	-	-
EFHD2	0.9	3.4E-02	2.73	1.38E-03	0.95900317	0.004198203	-	-	-	-
CD44	0.9	3.5E-02	2.14	2.36E-03	0.85643837	0.000694951	-	-	-	-
IL6R	0.9	4.5E-02	2.09	3.67E-02	1.29242918	0.00018973	-	-	-	-
TPI1	0.9	6.6E-03	1.65	3.03E-02	0.91182332	0.004355477	-	-	-	-
STX6	0.9	4.4E-03	1.46	1.91E-02	0.70358438	0.002064819	-	-	-	-
SSPN	-0.8	3.7E-02	0.24	3.92E-03	-1.6111152	0.001854423	-	-	-	-
GRB2	0.8	4.5E-03	2.21	5.86E-03	1.0165082	0.001142618	-	-	-	-
AMPD2	0.8	4.4E-02	1.89	1.35E-03	0.88547556	0.005474133	-	-	-	-

SRA1	0.8	3.4E-02	1.73	1.12E-02	0.68469927	0.005720202	-	-	-	-
LIMS1	0.8	1.8E-02	1.62	1.63E-02	0.99607243	0.000745811	-	-	-	-
HCFC1R1	-0.7	4.1E-02	0.58	8.01E-03	-1.3353445	0.000827403	-	-	-	-
BDH2	-0.7	3.2E-02	0.57	1.73E-02	-1.2585832	0.003386328	-	-	-	-
MAP3K5	-0.7	8.6E-03	0.33	5.10E-04	-1.0167485	0.002567164	-	-	-	-
BAMBI	-0.7	2.2E-02	0.30	2.01E-02	-1.6762808	0.004827369	-	-	-	-
C20orf24	0.7	2.5E-02	2.03	1.09E-02	0.77446193	0.001361679	-	-	-	-
HIST1H2BK	0.7	2.5E-02	1.85	3.69E-02	0.81477113	0.005521873	-	-	-	-
ACADVL	0.7	1.2E-02	1.80	4.07E-02	0.48951659	0.002955074	-	-	-	-
PPP4C	0.7	3.7E-02	1.57	9.57E-03	0.71281835	0.001344653	-	-	-	-
DNM2	0.7	2.9E-02	1.39	4.84E-02	0.66097063	0.003541809	-	-	-	-
WIPF1	0.6	2.3E-02	2.07	1.59E-02	0.78536415	0.004242081	-	-	-	-
CXorf38	0.6	1.7E-02	1.85	8.67E-03	1.06393771	0.001532792	-	-	-	-
ST14	3.1	1.5E-04	2.75	1.27E-02	-	-	-	-	-	-
MARCO	3.0	2.2E-06	4.10	1.41E-02	-	-	-	-	-	-
CLEC5A	2.8	8.4E-05	6.59	5.60E-03	-	-	-	-	-	-
HPSE	2.8	4.5E-05	4.71	8.00E-03	-	-	-	-	-	-
C15orf48	2.7	2.6E-03	21.66	4.92E-08	-	-	-	-	-	-
OLR1	2.7	8.4E-05	3.19	3.19E-03	-	-	-	-	-	-
EREG	2.7	3.8E-03	1.76	1.20E-02	-	-	-	-	-	-

ALOX5AP	2.6	2.9E-04	4.34	1.52E-02	-	-	-	-	-	-
SLC16A10	2.5	2.1E-03	8.57	5.97E-07	-	-	-	-	-	-
FBP1	2.5	3.8E-04	3.00	7.92E-03	-	-	-	-	-	-
GNA15	2.3	2.9E-04	3.37	1.23E-03	-	-	-	-	-	-
HMOX1	2.2	5.1E-03	10.06	2.60E-04	-	-	-	-	-	-
IFI30	2.2	8.5E-04	8.83	6.68E-04	-	-	-	-	-	-
CD300LF	2.2	3.4E-04	2.48	3.34E-02	-	-	-	-	-	-
ABCC3	2.2	8.6E-05	2.46	2.32E-04	-	-	-	-	-	-
HAVCR2	2.2	1.0E-04	1.76	3.48E-02	-	-	-	-	-	-
CDCP1	2.2	9.7E-04	1.57	2.12E-02	-	-	-	-	-	-
SLC14A1	-2.1	1.5E-02	0.24	2.22E-02	-	-	-	-	-	-
RRM2	2.1	3.0E-03	3.77	2.65E-03	-	-	-	-	-	-
HK3	2.1	4.5E-04	3.46	2.83E-03	-	-	-	-	-	-
SLC37A2	2.1	2.5E-04	1.65	2.65E-02	-	-	-	-	-	-
ADAM8	2.1	1.5E-03	1.54	4.94E-02	-	-	-	-	-	-
ITGAX	2.0	2.3E-03	4.68	6.25E-04	-	-	-	-	-	-
SDS	2.0	7.7E-03	3.04	1.37E-03	-	-	-	-	-	-
LAIR1	2.0	9.6E-05	2.61	1.76E-02	-	-	-	-	-	-
SERPINA1	2.0	1.2E-03	2.08	4.98E-02	-	-	-	-	-	-
KYNU	2.0	7.3E-04	1.89	4.83E-03	-	-	-	-	-	-

SPP1	1.9	2.5E-02	16.62	5.28E-03	-	-	-	-	-	-
CSTA	1.9	1.4E-03	11.69	7.42E-05	-	-	-	-	-	-
CD36	1.9	3.4E-03	6.74	5.10E-04	-	-	-	-	-	-
RNASET2	1.9	1.8E-03	2.65	2.72E-02	-	-	-	-	-	-
FPR3	1.9	1.7E-03	2.43	3.06E-03	-	-	-	-	-	-
MAPK13	1.9	3.4E-04	2.34	2.13E-02	-	-	-	-	-	-
GPR160	1.9	3.7E-03	1.98	2.23E-02	-	-	-	-	-	-
ALOX5	1.9	6.5E-04	1.91	4.88E-02	-	-	-	-	-	-
DLX1	-1.8	1.4E-02	0.45	1.32E-03	-	-	-	-	-	-
LAPTM5	1.8	1.2E-03	8.58	9.31E-03	-	-	-	-	-	-
TYROBP	1.8	3.2E-04	6.54	1.13E-02	-	-	-	-	-	-
FCER1G	1.8	4.5E-04	3.06	7.69E-03	-	-	-	-	-	-
GK	1.8	2.1E-03	2.86	3.57E-02	-	-	-	-	-	-
SYTL3	1.8	2.2E-02	2.85	1.14E-02	-	-	-	-	-	-
CD86	1.8	2.4E-04	2.67	1.52E-02	-	-	-	-	-	-
PLA2G7	1.8	1.0E-02	2.14	1.60E-02	-	-	-	-	-	-
NCF2	1.7	2.5E-03	9.76	1.35E-03	-	-	-	-	-	-
FGR	1.7	6.9E-03	5.52	4.69E-03	-	-	-	-	-	-
NPL	1.7	8.2E-04	4.83	5.02E-03	-	-	-	-	-	-
VSIG4	1.7	1.2E-03	4.60	4.34E-02	-	-	-	-	-	-

TYMP	1.7	5.4E-04	4.31	1.83E-03	-	-	-	-	-	-
TREM1	1.7	1.9E-02	2.58	8.15E-03	-	-	-	-	-	-
MS4A14	1.7	3.4E-03	2.34	2.72E-02	-	-	-	-	-	-
DOK2	1.7	9.2E-04	2.24	1.46E-02	-	-	-	-	-	-
MELK	1.7	1.5E-02	1.93	3.47E-02	-	-	-	-	-	-
IL4I1	1.7	4.5E-04	1.60	4.63E-02	-	-	-	-	-	-
SIGLEC10	1.7	6.2E-03	1.55	4.88E-02	-	-	-	-	-	-
CD53	1.6	2.4E-03	6.20	1.12E-02	-	-	-	-	-	-
MAFB	1.6	1.1E-03	6.15	5.03E-04	-	-	-	-	-	-
TLR2	1.6	6.4E-03	5.41	1.79E-02	-	-	-	-	-	-
CXCR4	1.6	2.1E-02	5.04	1.26E-02	-	-	-	-	-	-
BCAT1	1.6	4.3E-03	3.76	1.21E-02	-	-	-	-	-	-
RNASE6	1.6	1.5E-03	2.89	4.10E-02	-	-	-	-	-	-
PIK3AP1	1.6	1.4E-03	2.44	3.94E-02	-	-	-	-	-	-
SASH3	1.6	1.8E-03	2.39	2.12E-02	-	-	-	-	-	-
NUSAP1	1.6	4.9E-03	1.93	2.01E-02	-	-	-	-	-	-
ODF3B	1.6	2.3E-03	1.81	2.90E-02	-	-	-	-	-	-
CD84	1.6	1.0E-03	1.63	4.36E-02	-	-	-	-	-	-
INMT	-1.5	3.0E-02	0.28	4.89E-02	-	-	-	-	-	-
LYZ	1.5	4.8E-03	6.53	1.60E-03	-	-	-	-	-	-

SYK	1.5	1.4E-03	3.84	3.45E-02	-	-	-	-	-	-
G0S2	1.5	4.5E-02	3.67	1.21E-02	-	-	-	-	-	-
ARHGAP30	1.5	3.5E-03	3.09	1.12E-02	-	-	-	-	-	-
CCRL2	1.5	2.1E-03	2.41	5.24E-03	-	-	-	-	-	-
STAB1	1.5	8.2E-04	2.41	3.91E-02	-	-	-	-	-	-
NCKAP1L	1.5	1.5E-03	1.93	2.64E-02	-	-	-	-	-	-
SLC25A19	1.5	9.8E-04	1.80	1.46E-02	-	-	-	-	-	-
SLC43A3	1.5	1.5E-03	1.79	3.16E-02	-	-	-	-	-	-
PTAFR	1.5	2.6E-03	1.70	3.29E-02	-	-	-	-	-	-
THRB	-1.4	1.2E-02	0.50	1.73E-02	-	-	-	-	-	-
PRRT2	-1.4	3.5E-02	0.46	2.72E-02	-	-	-	-	-	-
KCNS3	-1.4	3.4E-02	0.25	1.04E-02	-	-	-	-	-	-
RGS5	-1.4	4.9E-02	0.20	1.85E-02	-	-	-	-	-	-
RCAN2	-1.4	4.8E-02	0.10	3.25E-02	-	-	-	-	-	-
COTL1	1.4	2.6E-03	7.42	7.19E-05	-	-	-	-	-	-
VAMP8	1.4	1.9E-03	5.17	4.45E-02	-	-	-	-	-	-
PLAUR	1.4	2.2E-02	4.69	3.09E-04	-	-	-	-	-	-
CXorf21	1.4	3.4E-03	4.65	4.74E-02	-	-	-	-	-	-
AIF1	1.4	1.2E-03	3.24	6.17E-03	-	-	-	-	-	-
MS4A4A	1.4	2.3E-03	2.85	1.62E-02	-	-	-	-	-	-

CSF1R	1.4	4.5E-04	2.48	1.99E-02	-	-	-	-	-	-
CCR5	1.4	2.5E-03	2.15	3.50E-02	-	-	-	-	-	-
EMR2	1.4	1.1E-02	1.91	6.07E-03	-	-	-	-	-	-
AMPD3	1.4	3.8E-03	1.84	1.61E-03	-	-	-	-	-	-
ZMYND15	1.4	2.9E-04	1.47	2.44E-02	-	-	-	-	-	-
DTNA	-1.3	2.4E-02	0.57	5.53E-03	-	-	-	-	-	-
ZNF540	-1.3	5.5E-03	0.56	5.69E-03	-	-	-	-	-	-
SMOC2	-1.3	1.3E-02	0.16	1.14E-02	-	-	-	-	-	-
UPP1	1.3	4.5E-02	5.92	2.69E-04	-	-	-	-	-	-
C5AR1	1.3	9.6E-03	4.84	4.33E-03	-	-	-	-	-	-
CCDC109B	1.3	5.1E-03	4.61	3.98E-04	-	-	-	-	-	-
ITGAM	1.3	4.3E-03	4.34	1.74E-02	-	-	-	-	-	-
HCK	1.3	6.2E-03	3.41	1.92E-02	-	-	-	-	-	-
LCP1	1.3	1.5E-02	3.35	1.04E-02	-	-	-	-	-	-
CXCL16	1.3	1.1E-03	3.22	2.01E-02	-	-	-	-	-	-
ADAP2	1.3	8.2E-04	3.04	1.12E-02	-	-	-	-	-	-
SLC7A7	1.3	3.8E-03	3.03	1.69E-02	-	-	-	-	-	-
CAPG	1.3	9.5E-03	2.94	9.82E-03	-	-	-	-	-	-
DPEP2	1.3	1.6E-02	2.60	7.54E-03	-	-	-	-	-	-
STK10	1.3	1.0E-02	2.50	3.35E-03	-	-	-	-	-	-

RBM47	1.3	5.9E-03	2.10	6.37E-03	-	-	-	-	-	-
IRAK1	1.3	1.7E-03	2.09	3.43E-03	-	-	-	-	-	-
ME2	1.3	3.2E-04	1.84	9.01E-03	-	-	-	-	-	-
ERO1L	1.3	2.1E-02	1.72	1.76E-02	-	-	-	-	-	-
EIF4EBP1	1.3	4.1E-04	1.69	4.78E-02	-	-	-	-	-	-
KCNE3	1.3	4.3E-03	1.58	4.63E-02	-	-	-	-	-	-
PLCL1	-1.2	1.2E-03	0.39	3.34E-02	-	-	-	-	-	-
MAMDC2	-1.2	3.4E-02	0.28	1.71E-02	-	-	-	-	-	-
HCLS1	1.2	1.7E-02	8.38	5.27E-03	-	-	-	-	-	-
SLC16A6	1.2	3.0E-02	7.46	7.10E-05	-	-	-	-	-	-
MS4A7	1.2	9.2E-03	4.69	1.41E-03	-	-	-	-	-	-
UCP2	1.2	7.3E-03	4.58	1.04E-02	-	-	-	-	-	-
TCIRG1	1.2	3.5E-03	4.39	1.80E-03	-	-	-	-	-	-
DOCK4	1.2	9.1E-03	3.90	2.57E-02	-	-	-	-	-	-
CTSB	1.2	6.6E-03	3.53	9.53E-03	-	-	-	-	-	-
C3AR1	1.2	5.4E-03	3.13	9.57E-03	-	-	-	-	-	-
FTL	1.2	5.7E-03	3.04	7.65E-03	-	-	-	-	-	-
SH3BGRL3	1.2	8.6E-04	3.03	1.66E-03	-	-	-	-	-	-
CFD	1.2	1.4E-02	2.92	8.47E-03	-	-	-	-	-	-
CMTM7	1.2	7.0E-03	2.83	1.12E-02	-	-	-	-	-	-

ITGB2	1.2	9.8E-03	2.56	4.44E-02	-	-	-	-	-	-
DOCK2	1.2	9.2E-03	2.42	4.31E-02	-	-	-	-	-	-
S100A10	1.2	8.6E-03	2.36	1.73E-03	-	-	-	-	-	-
GLIPR2	1.2	9.7E-04	2.06	2.89E-03	-	-	-	-	-	-
RHBDF2	1.2	9.9E-03	2.05	2.01E-02	-	-	-	-	-	-
MCOLN1	1.2	7.3E-04	2.01	1.22E-02	-	-	-	-	-	-
TACC3	1.2	6.6E-03	1.94	3.90E-02	-	-	-	-	-	-
MYLIP	-1.1	6.4E-03	0.27	2.83E-02	-	-	-	-	-	-
ANKRD6	-1.1	7.8E-03	0.26	1.72E-02	-	-	-	-	-	-
SERPINI1	-1.1	3.4E-02	0.25	9.83E-03	-	-	-	-	-	-
CTSS	1.1	1.4E-02	5.47	8.03E-03	-	-	-	-	-	-
GLUL	1.1	9.6E-03	4.91	2.53E-04	-	-	-	-	-	-
LCP2	1.1	2.2E-02	4.29	5.38E-03	-	-	-	-	-	-
FERMT3	1.1	9.5E-03	4.15	1.93E-03	-	-	-	-	-	-
MS4A6A	1.1	1.8E-02	3.43	2.76E-02	-	-	-	-	-	-
MPEG1	1.1	1.5E-02	3.14	2.31E-02	-	-	-	-	-	-
PLEK	1.1	1.7E-02	2.89	2.43E-02	-	-	-	-	-	-
LPXN	1.1	3.1E-03	2.28	2.64E-02	-	-	-	-	-	-
GSTO1	1.1	2.3E-03	2.19	1.32E-03	-	-	-	-	-	-
TLR1	1.1	1.0E-02	2.18	3.75E-02	-	-	-	-	-	-

GRN	1.1	2.6E-03	1.70	3.69E-02	-	-	-	-	-	-
CD82	1.1	9.5E-04	1.69	2.31E-02	-	-	-	-	-	-
RIN3	1.1	1.3E-02	1.62	2.23E-02	-	-	-	-	-	-
TMEM106A	1.1	4.9E-04	1.56	4.74E-02	-	-	-	-	-	-
LNP1	-1.0	2.2E-02	0.50	1.21E-04	-	-	-	-	-	-
TSPAN2	-1.0	1.4E-02	0.30	2.63E-02	-	-	-	-	-	-
HSPA2	-1.0	3.9E-02	0.24	4.34E-02	-	-	-	-	-	-
ENPP2	-1.0	1.6E-02	0.22	2.22E-02	-	-	-	-	-	-
SCO2	1.0	1.8E-02	3.75	1.49E-04	-	-	-	-	-	-
C4orf48	1.0	3.4E-02	3.48	7.72E-04	-	-	-	-	-	-
BMP2K	1.0	2.0E-02	3.26	4.47E-03	-	-	-	-	-	-
CTSC	1.0	1.8E-02	3.21	2.37E-03	-	-	-	-	-	-
IL10RA	1.0	1.5E-02	3.10	3.62E-02	-	-	-	-	-	-
LGMN	1.0	4.2E-03	3.01	9.17E-03	-	-	-	-	-	-
LHFPL2	1.0	7.7E-03	2.83	1.65E-02	-	-	-	-	-	-
FYB	1.0	4.8E-02	2.78	1.87E-02	-	-	-	-	-	-
SRGN	1.0	3.1E-02	2.68	1.38E-03	-	-	-	-	-	-
HN1	1.0	6.8E-03	2.56	1.10E-03	-	-	-	-	-	-
H2AFY	1.0	3.2E-03	2.52	4.73E-04	-	-	-	-	-	-
ATP6V0B	1.0	3.4E-03	2.49	2.21E-03	-	-	-	-	-	-

VAV1	1.0	3.4E-02	2.44	3.07E-02	-	-	-	-	-	-
SMPDL3A	1.0	7.1E-03	2.33	4.41E-02	-	-	-	-	-	-
MGAT4A	1.0	1.8E-02	2.31	2.60E-02	-	-	-	-	-	-
CKLF	1.0	6.4E-03	2.22	2.86E-03	-	-	-	-	-	-
CYBB	1.0	5.8E-03	2.11	4.54E-02	-	-	-	-	-	-
CYBA	1.0	1.4E-02	2.06	2.31E-02	-	-	-	-	-	-
NRIP3	1.0	1.5E-02	2.05	3.27E-03	-	-	-	-	-	-
QSOX1	1.0	4.3E-03	2.04	8.46E-03	-	-	-	-	-	-
ZNF267	1.0	2.8E-02	1.94	4.71E-02	-	-	-	-	-	-
ADCY7	1.0	6.0E-03	1.83	1.53E-02	-	-	-	-	-	-
SDSL	1.0	6.2E-03	1.78	2.66E-02	-	-	-	-	-	-
PSAP	1.0	1.5E-03	1.71	4.86E-02	-	-	-	-	-	-
LYL1	1.0	9.9E-03	1.70	4.43E-02	-	-	-	-	-	-
TWF2	1.0	1.4E-03	1.58	1.50E-02	-	-	-	-	-	-
ADPGK	1.0	3.0E-03	1.52	2.53E-02	-	-	-	-	-	-
FAM110A	1.0	6.4E-03	1.47	3.00E-02	-	-	-	-	-	-
PLAC9	-0.9	4.4E-02	0.52	4.31E-02	-	-	-	-	-	-
TEX9	-0.9	3.3E-02	0.45	6.85E-03	-	-	-	-	-	-
MN1	-0.9	4.1E-02	0.40	1.64E-02	-	-	-	-	-	-
NHS	-0.9	4.5E-02	0.35	1.76E-02	-	-	-	-	-	-

MYH10	-0.9	2.2E-02	0.34	3.07E-02	-	-	-	-	-	-
INPP4B	-0.9	2.7E-02	0.27	3.27E-03	-	-	-	-	-	-
RGS10	0.9	3.0E-02	4.37	2.06E-02	-	-	-	-	-	-
TNFSF13B	0.9	2.5E-02	3.95	2.94E-02	-	-	-	-	-	-
CPVL	0.9	1.9E-02	3.71	1.82E-02	-	-	-	-	-	-
IMPDH1	0.9	7.0E-03	2.73	2.20E-03	-	-	-	-	-	-
MYD88	0.9	6.1E-03	2.70	1.38E-03	-	-	-	-	-	-
IFNGR2	0.9	2.0E-02	2.20	4.73E-04	-	-	-	-	-	-
DENND4B	0.9	9.5E-03	2.19	2.90E-02	-	-	-	-	-	-
FCGRT	0.9	2.2E-03	2.05	9.75E-03	-	-	-	-	-	-
SOAT1	0.9	5.0E-03	1.94	3.01E-02	-	-	-	-	-	-
NPC2	0.9	4.9E-03	1.83	3.42E-02	-	-	-	-	-	-
MAPKAPK3	0.9	7.2E-03	1.82	1.11E-02	-	-	-	-	-	-
KCNN4	0.9	1.4E-02	1.78	2.57E-02	-	-	-	-	-	-
HOMER3	0.9	4.6E-03	1.71	1.20E-02	-	-	-	-	-	-
KCNK6	0.9	1.2E-02	1.69	3.48E-02	-	-	-	-	-	-
FAM20A	0.9	4.8E-02	1.68	1.63E-02	-	-	-	-	-	-
P2RX4	0.9	1.7E-03	1.65	9.19E-03	-	-	-	-	-	-
IL10RB	0.9	8.2E-03	1.63	1.89E-02	-	-	-	-	-	-
SAMHD1	0.9	2.8E-03	1.56	4.79E-02	-	-	-	-	-	-

BCKDK	0.9	2.1E-02	1.47	1.97E-02	-	-	-	-	-	-
HABP4	-0.8	4.2E-02	0.51	2.06E-03	-	-	-	-	-	-
TRIM2	-0.8	4.7E-02	0.48	1.40E-03	-	-	-	-	-	-
SASH1	-0.8	1.7E-02	0.47	3.05E-02	-	-	-	-	-	-
PRICKLE2	-0.8	3.7E-02	0.33	1.23E-02	-	-	-	-	-	-
CECR1	0.8	3.9E-02	3.26	3.08E-02	-	-	-	-	-	-
EMP3	0.8	6.2E-03	2.54	1.58E-02	-	-	-	-	-	-
MAN2B1	0.8	7.1E-03	2.36	6.22E-03	-	-	-	-	-	-
ATP6V0D1	0.8	5.8E-03	2.10	3.16E-02	-	-	-	-	-	-
PNPLA6	0.8	5.6E-03	2.09	2.05E-02	-	-	-	-	-	-
CIB1	0.8	1.3E-02	2.08	3.51E-04	-	-	-	-	-	-
RHOG	0.8	1.5E-02	2.03	6.22E-03	-	-	-	-	-	-
S100A11	0.8	5.2E-03	1.97	2.64E-02	-	-	-	-	-	-
ARAP1	0.8	7.3E-03	1.83	8.63E-04	-	-	-	-	-	-
ACP2	0.8	3.4E-03	1.78	3.43E-02	-	-	-	-	-	-
HEATR3	0.8	3.2E-03	1.61	3.00E-02	-	-	-	-	-	-
AP1B1	0.8	6.4E-03	1.48	4.87E-02	-	-	-	-	-	-
LRRCC1	-0.7	3.6E-02	0.47	3.37E-04	-	-	-	-	-	-
SMARCD3	-0.7	3.2E-02	0.47	3.91E-02	-	-	-	-	-	-
RIMKLB	-0.7	8.8E-03	0.36	4.69E-03	-	-	-	-	-	-

NFYB	-0.7	1.4E-02	0.36	4.53E-03	-	-	-	-	-	-
SETMAR	-0.7	2.1E-02	0.35	1.19E-02	-	-	-	-	-	-
OSTF1	0.7	1.3E-02	3.10	2.76E-05	-	-	-	-	-	-
ATP6V1B2	0.7	2.2E-02	2.19	3.91E-02	-	-	-	-	-	-
MGAT1	0.7	2.1E-02	2.04	6.29E-03	-	-	-	-	-	-
SUSD1	0.7	9.3E-03	2.02	1.99E-02	-	-	-	-	-	-
TYK2	0.7	2.0E-02	2.00	2.90E-02	-	-	-	-	-	-
CTSA	0.7	7.1E-03	1.96	8.15E-03	-	-	-	-	-	-
SPPL2A	0.7	2.0E-02	1.96	1.90E-02	-	-	-	-	-	-
RPL22L1	0.7	4.7E-02	1.96	1.50E-02	-	-	-	-	-	-
NEK6	0.7	1.9E-02	1.94	7.34E-03	-	-	-	-	-	-
PLEKHO2	0.7	3.6E-02	1.93	4.19E-03	-	-	-	-	-	-
RGS19	0.7	5.0E-02	1.87	8.57E-03	-	-	-	-	-	-
NOP10	0.7	1.4E-02	1.78	5.19E-03	-	-	-	-	-	-
C7orf43	0.7	2.0E-02	1.71	3.00E-02	-	-	-	-	-	-
PLA2G15	0.7	2.4E-02	1.68	4.44E-02	-	-	-	-	-	-
GARS	0.7	1.5E-02	1.67	1.40E-02	-	-	-	-	-	-
C19orf10	0.7	1.8E-02	1.67	1.84E-02	-	-	-	-	-	-
RNPEP	0.7	3.7E-03	1.65	4.11E-02	-	-	-	-	-	-
GGA1	0.7	5.3E-03	1.64	2.27E-02	-	-	-	-	-	-

RIT1	0.7	3.4E-02	1.63	4.12E-02	-	-	-	-	-	-
GALE	0.7	9.6E-03	1.63	1.79E-02	-	-	-	-	-	-
DBNL	0.7	2.8E-02	1.58	5.75E-03	-	-	-	-	-	-
DPP3	0.7	8.6E-03	1.55	4.33E-03	-	-	-	-	-	-
HM13	0.7	8.5E-03	1.51	8.57E-03	-	-	-	-	-	-
C5	-0.6	4.4E-02	0.70	3.69E-02	-	-	-	-	-	-
KIF3A	-0.6	2.1E-02	0.52	1.12E-02	-	-	-	-	-	-
TCF7L2	-0.6	2.0E-02	0.50	3.06E-03	-	-	-	-	-	-
AEBP2	-0.6	1.7E-02	0.44	2.86E-02	-	-	-	-	-	-
ZSCAN18	-0.6	4.9E-02	0.44	1.91E-02	-	-	-	-	-	-
TSPYL4	-0.6	3.9E-02	0.36	8.90E-03	-	-	-	-	-	-
ARHGAP22	0.6	4.6E-02	2.19	2.52E-02	-	-	-	-	-	-
C17orf62	0.6	2.2E-02	2.17	1.30E-02	-	-	-	-	-	-
CSK	0.6	3.0E-02	2.15	1.08E-02	-	-	-	-	-	-
C6orf62	0.6	2.8E-02	2.11	2.98E-03	-	-	-	-	-	-
PLEKHB2	0.6	4.0E-02	2.07	1.04E-02	-	-	-	-	-	-
RPN2	0.6	3.6E-02	1.88	2.44E-03	-	-	-	-	-	-
WIP1	0.6	3.9E-02	1.83	6.07E-03	-	-	-	-	-	-
STX4	0.6	4.9E-02	1.83	1.76E-02	-	-	-	-	-	-
NAGK	0.6	5.6E-03	1.68	2.44E-02	-	-	-	-	-	-

OAZ1	0.6	3.0E-02	1.66	2.04E-02	-	-	-	-	-	-
WDR81	0.6	1.5E-02	1.64	2.57E-02	-	-	-	-	-	-
AP2S1	0.6	1.4E-02	1.63	3.69E-02	-	-	-	-	-	-
RAB32	0.6	2.7E-02	1.63	1.12E-02	-	-	-	-	-	-
SLC25A20	0.6	2.9E-02	1.59	2.91E-02	-	-	-	-	-	-
NAB1	-0.5	4.7E-02	0.57	4.63E-03	-	-	-	-	-	-
AMN1	-0.5	3.9E-02	0.39	2.41E-03	-	-	-	-	-	-
PLOD3	0.5	4.0E-02	1.78	1.61E-03	-	-	-	-	-	-
EFTUD2	0.5	1.7E-02	1.77	9.82E-03	-	-	-	-	-	-
RPN1	0.5	3.9E-02	1.71	1.12E-02	-	-	-	-	-	-
GUSB	0.5	4.7E-02	1.61	6.82E-03	-	-	-	-	-	-
ACTR2	0.5	2.2E-02	1.60	2.19E-02	-	-	-	-	-	-
ACTR3	0.5	4.7E-02	1.55	3.12E-02	-	-	-	-	-	-
ARPC5	0.5	3.0E-02	1.51	2.09E-02	-	-	-	-	-	-
CHFR	0.5	2.3E-02	1.49	1.11E-02	-	-	-	-	-	-
TUBE1	-0.4	4.9E-02	0.52	2.83E-02	-	-	-	-	-	-
FAM8A1	-0.4	4.7E-02	0.35	8.76E-03	-	-	-	-	-	-
COMP	-2.9	5.6E-03	-	-	-3.725943251	0.000173456	-	-	-	-
CHIT1	-2.9	3.7E-03	-	-	-2.336546425	0.001242162	-	-	-	-
KRT16	-2.8	3.8E-03	-	-	-2.030185232	0.001342918	-	-	-	-

GPR97	2.6	4.3E-03	-	-	1.228717139	0.001812378	-	-	-	-
MASP1	-2.5	1.7E-03	-	-	-1.406181514	0.004838805	-	-	-	-
RNASE2	2.3	5.8E-04	-	-	1.135841115	0.005059273	-	-	-	-
STXBP2	2.2	3.7E-04	-	-	0.735546732	0.004766677	-	-	-	-
XG	-2.1	4.0E-02	-	-	-0.98482217	0.002005825	-	-	-	-
ADAMTSL2	-2.1	3.6E-03	-	-	-1.29831655	0.002710339	-	-	-	-
ADAM12	2.1	2.8E-03	-	-	1.1586482	0.001533028	-	-	-	-
NLRC4	2.1	1.7E-04	-	-	1.213638906	0.005376219	-	-	-	-
CPXM2	-2.0	5.3E-04	-	-	-3.438130675	6.49948E-06	-	-	-	-
CRTAC1	-2.0	8.8E-03	-	-	-2.251833634	0.00506222	-	-	-	-
PPIF	2.0	3.3E-04	-	-	1.425520676	0.002029743	-	-	-	-
MPO	2.0	1.5E-03	-	-	0.804525425	0.005133307	-	-	-	-
CSF3R	1.9	6.4E-03	-	-	1.84941776	4.88281E-06	-	-	-	-
SLC43A2	1.9	4.5E-04	-	-	1.53564897	0.000169894	-	-	-	-
MAOB	-1.8	2.1E-02	-	-	-0.966847686	0.001599502	-	-	-	-
MYOZ3	-1.8	2.8E-04	-	-	-1.056684104	0.002627385	-	-	-	-
LILRB3	1.8	2.9E-03	-	-	1.273139122	0.001558399	-	-	-	-
COL10A1	-1.7	3.0E-02	-	-	-2.507437734	9.26831E-07	-	-	-	-
SFRP2	-1.7	4.4E-02	-	-	-3.662179695	0.000632003	-	-	-	-
MYBPC3	1.7	2.6E-03	-	-	1.132586505	0.000140393	-	-	-	-

DGAT2	1.7	1.6E-02	-	-	1.525628038	0.001682551	-	-	-	-
OMD	-1.6	6.4E-03	-	-	-1.704658455	0.000115032	-	-	-	-
NDRG2	-1.6	7.1E-03	-	-	-2.291415574	0.001599458	-	-	-	-
SYT12	-1.6	2.9E-02	-	-	-1.986897645	0.00292464	-	-	-	-
HS3ST1	1.6	9.9E-05	-	-	2.13128276	0.00077811	-	-	-	-
CTSL	1.6	1.1E-04	-	-	1.153850993	0.003075763	-	-	-	-
FGFR3	-1.5	2.1E-02	-	-	-1.562000028	0.001263699	-	-	-	-
KLF15	-1.5	4.0E-02	-	-	-0.970045893	0.001380248	-	-	-	-
SAMD11	-1.5	2.3E-02	-	-	-1.680363434	0.003408976	-	-	-	-
DNASE1L3	-1.5	1.6E-02	-	-	-2.180805845	0.004996852	-	-	-	-
FCN1	1.5	1.9E-02	-	-	2.076703896	0.003986775	-	-	-	-
PRR15	-1.4	1.4E-02	-	-	-2.115263202	3.46529E-05	-	-	-	-
NKD2	-1.4	2.3E-02	-	-	-1.771689943	0.001413014	-	-	-	-
HMGA1	1.4	3.8E-03	-	-	0.961717248	0.001804392	-	-	-	-
ITGA2B	1.4	4.2E-02	-	-	0.509049061	0.002876747	-	-	-	-
CLEC7A	1.4	2.6E-03	-	-	0.510463821	0.0050238	-	-	-	-
PRELP	-1.3	4.2E-02	-	-	-2.618045259	0.001130902	-	-	-	-
SH3BP2	1.3	3.5E-03	-	-	0.887892435	0.002122874	-	-	-	-
BFSP1	-1.2	9.7E-03	-	-	-1.816283939	2.39445E-05	-	-	-	-
SMAD9	-1.2	4.3E-03	-	-	-1.388627301	3.19202E-05	-	-	-	-

ANTXR1	-1.2	2.0E-02	-	-	-1.031427341	5.99916E-05	-	-	-	-
GNG7	-1.2	4.0E-03	-	-	-1.000716732	0.000158784	-	-	-	-
IGSF21	-1.2	4.4E-02	-	-	-3.383143107	0.000354932	-	-	-	-
CCDC3	-1.2	3.2E-02	-	-	-2.364678142	0.000474041	-	-	-	-
LEPR	-1.2	2.7E-03	-	-	-1.792029654	0.000642462	-	-	-	-
CA5B	-1.2	9.8E-04	-	-	-1.259885524	0.00146828	-	-	-	-
ATOH8	-1.2	3.7E-02	-	-	-1.488505509	0.002058554	-	-	-	-
GZMK	-1.2	2.7E-02	-	-	-1.548498194	0.003964833	-	-	-	-
ADAMTS5	-1.2	3.7E-02	-	-	-1.152082912	0.003993117	-	-	-	-
AATK	1.2	5.0E-02	-	-	1.863435465	0.000150626	-	-	-	-
ST8SIA4	1.2	2.0E-02	-	-	0.825214761	0.000548881	-	-	-	-
FGD3	1.2	4.3E-02	-	-	1.091183348	0.000756714	-	-	-	-
BEST1	1.2	1.2E-02	-	-	0.929378316	0.00099713	-	-	-	-
ACRBP	1.2	1.0E-02	-	-	1.018254496	0.004023699	-	-	-	-
FZD1	-1.1	2.1E-03	-	-	-1.385756527	6.62213E-05	-	-	-	-
LTBP4	-1.1	4.2E-02	-	-	-2.349455615	0.000115598	-	-	-	-
EPB41L1	-1.1	6.1E-03	-	-	-1.850653388	0.000508759	-	-	-	-
MYO1D	-1.1	1.9E-02	-	-	-1.877889361	0.00063888	-	-	-	-
SHF	-1.1	2.5E-03	-	-	-0.749097253	0.001986291	-	-	-	-
RGS11	-1.1	2.7E-02	-	-	-1.280368243	0.002539737	-	-	-	-

ZNF704	-1.1	2.6E-02	-	-	-1.43458341	0.002808357	-	-	-	-
PALM	-1.1	9.4E-03	-	-	-1.774565332	0.00563285	-	-	-	-
SOX8	-1.1	1.1E-02	-	-	0.81800597	0.004143692	-	-	-	-
TLR6	1.1	9.6E-03	-	-	0.800917834	6.50215E-05	-	-	-	-
SHKBP1	1.1	6.7E-03	-	-	0.859250299	0.00040708	-	-	-	-
VAV3	1.1	1.4E-02	-	-	0.863170895	0.001681301	-	-	-	-
SLC25A27	-1.0	4.1E-02	-	-	-0.873213734	0.000457378	-	-	-	-
THSD4	-1.0	4.6E-02	-	-	-2.142899156	0.00074772	-	-	-	-
CNKS3	-1.0	1.5E-02	-	-	-1.200294751	0.001439927	-	-	-	-
KIAA1324L	-1.0	1.5E-02	-	-	-1.249588318	0.002339125	-	-	-	-
KALRN	-1.0	1.6E-02	-	-	-0.817930831	0.002419456	-	-	-	-
ID1	-1.0	4.3E-02	-	-	-2.337084849	0.002905381	-	-	-	-
ARID3A	1.0	6.8E-03	-	-	0.990679101	0.000694596	-	-	-	-
SLC36A4	1.0	1.8E-02	-	-	0.742240243	0.001939219	-	-	-	-
SECTM1	1.0	1.8E-02	-	-	0.879345039	0.002328038	-	-	-	-
GSN	-0.9	2.4E-02	-	-	-1.638813247	8.47482E-05	-	-	-	-
RAI2	-0.9	3.2E-02	-	-	-1.588364088	0.000492023	-	-	-	-
DMD	-0.9	2.6E-02	-	-	-1.802744532	0.000499973	-	-	-	-
STON1	-0.9	4.2E-02	-	-	-1.287573755	0.001152904	-	-	-	-
PARD3B	-0.9	3.2E-02	-	-	-0.75073942	0.001438849	-	-	-	-

CRIM1	-0.9	2.2E-02	-	-	-1.095728788	0.003312081	-	-	-	-
GPBAR1	0.9	4.8E-02	-	-	1.247247011	0.001133398	-	-	-	-
ARHGAP27	0.9	4.9E-02	-	-	0.731073352	0.004478153	-	-	-	-
SATB1	0.9	2.0E-02	-	-	1.320048497	0.005529337	-	-	-	-
ST6GAL1	-0.8	4.5E-03	-	-	-1.62573984	0.000273951	-	-	-	-
TJP2	-0.8	6.4E-03	-	-	-1.054279136	0.004193213	-	-	-	-
SYNPO	-0.8	2.8E-02	-	-	1.071534003	0.001860919	-	-	-	-
MMP28	-0.8	4.7E-02	-	-	-0.820032711	0.005793043	-	-	-	-
POR	0.8	1.5E-02	-	-	1.177954893	0.001240103	-	-	-	-
CAPS2	-0.7	4.7E-02	-	-	-0.848907288	0.000365394	-	-	-	-
NEIL1	-0.7	1.7E-02	-	-	-1.276754792	0.003754504	-	-	-	-
FNDC3B	0.7	4.7E-02	-	-	0.818315266	0.001365805	-	-	-	-
PGAM1	0.7	7.8E-03	-	-	0.593447792	0.001773581	-	-	-	-
PNKD	0.7	3.3E-02	-	-	0.725754918	0.005297558	-	-	-	-
KIAA0355	-0.6	4.6E-02	-	-	-1.167393606	0.000838558	-	-	-	-
TCF4	-0.6	4.1E-02	-	-	-0.996127485	0.000878643	-	-	-	-
ACYP2	-0.6	3.8E-02	-	-	-0.713577098	0.00132868	-	-	-	-
TNRC6C	-0.6	3.6E-02	-	-	-0.986382969	0.001909397	-	-	-	-
PCGF5	-0.6	2.8E-02	-	-	-1.145127155	0.002383835	-	-	-	-
SGPL1	0.6	6.5E-03	-	-	0.651649638	0.001591136	-	-	-	-

C6orf48	-0.5	2.9E-02	-	-	-1.080490071	1.57352E-05	-	-	-	-
SAV1	-0.5	3.2E-02	-	-	-0.785571752	0.00194551	-	-	-	-
ZNF529	-0.5	4.6E-02	-	-	-0.6457765	0.002742189	-	-	-	-
ISCU	-0.5	2.2E-02	-	-	-0.63086254	0.002962466	-	-	-	-
MBNL2	-0.5	4.9E-02	-	-	-0.819486495	0.004155075	-	-	-	-
TRPC4AP	0.5	3.0E-02	-	-	0.495100458	0.003055297	-	-	-	-
CTSD	1.4	1.4E-03	-	-	-	-	3.1	0.00635	-	-
TIMP3	-1.0	2.0E-02	-	-	-	-	-6.8	3.48E-05	-	-

Hgnc indicates Human gene nomenclature committee; FC, fold change; FDR, false discovery rate; RA/MMA, ruptured aneurysms/meningeal medial artery.

Supplementary Table IV. Differential expression in intracranial aneurysms versus controls.

Overexpression

hgnc_symbol	logFC	logCPM	LR	PValue	FDR	ensembl	entrez
COL10A1	3.7	3.6	29.5	5.6E-08	0.00019	ENSG00000123500	1300
CILP2	2.9	1.6	26.0	3.4E-07	0.00053	ENSG00000160161	148113
	3.4	2.1	23.2	1.4E-06	0.00140	ENSG00000206195	NA
SFRP2	3.3	7.5	21.5	3.5E-06	0.00223	ENSG00000145423	6423
MEX3B	1.6	2.9	21.3	3.9E-06	0.00231	ENSG00000183496	84206
	2.4	1.6	20.0	7.7E-06	0.00363	ENSG00000260396	NA
PTHLH	2.5	2.9	19.7	9.1E-06	0.00403	ENSG00000087494	5744
MTND6P4	2.8	2.3	19.4	1.0E-05	0.00450	ENSG00000249119	NA
PLVAP	4.4	5.1	19.3	1.1E-05	0.00464	ENSG00000130300	83483
	3.2	0.6	18.1	2.1E-05	0.00690	ENSG00000225210	440157
	3.0	1.0	18.0	2.2E-05	0.00690	ENSG00000244306	NA
GDF7	2.3	2.2	18.0	2.2E-05	0.00690	ENSG00000143869	151449
PMEL	4.5	4.0	17.9	2.3E-05	0.00693	ENSG00000185664	6490
PENK	3.8	4.0	17.4	3.1E-05	0.00848	ENSG00000181195	5179
IL21R	2.2	2.8	16.7	4.5E-05	0.01026	ENSG00000103522	50615
MATN3	2.1	3.8	16.2	5.8E-05	0.01185	ENSG00000132031	4148
	2.3	2.2	15.6	8.0E-05	0.01475	ENSG00000261425	NA
SELP	2.8	5.2	15.1	1.0E-04	0.01765	ENSG00000174175	6403
LMO7	1.8	6.8	15.0	1.1E-04	0.01778	ENSG00000136153	4008
RBP4	2.1	2.7	14.7	1.3E-04	0.01985	ENSG00000138207	5950
COMP	5.3	7.3	14.5	1.4E-04	0.02043	ENSG00000105664	1311
H19	4.4	3.3	14.5	1.4E-04	0.02043	ENSG00000130600	100033819
SLC29A1	1.3	6.7	14.5	1.4E-04	0.02056	ENSG00000112759	2030
ELN	2.0	10.3	14.3	1.6E-04	0.02195	ENSG00000049540	2006
HTR7	2.2	1.9	14.2	1.6E-04	0.02203	ENSG00000148680	3363
ENPEP	2.4	4.0	14.1	1.8E-04	0.02249	ENSG00000138792	2028
PRR15	2.3	1.9	14.1	1.7E-04	0.02249	ENSG00000176532	222171
HOXD-AS1	2.1	-0.2	14.1	1.7E-04	0.02249	ENSG00000224189	401022
SLCO2A1	3.0	5.0	13.7	2.1E-04	0.02525	ENSG00000174640	6578
PRRX2	2.1	4.0	13.5	2.4E-04	0.02782	ENSG00000167157	51450
C3orf36	4.1	0.4	13.3	2.7E-04	0.02958	ENSG00000221972	80111
DAPL1	3.1	1.0	13.0	3.1E-04	0.03143	ENSG00000163331	92196
RIPK4	2.3	3.3	13.0	3.1E-04	0.03143	ENSG00000183421	54101
USP35	1.0	5.5	13.1	3.0E-04	0.03143	ENSG00000118369	57558
CDH3	1.9	2.2	12.9	3.3E-04	0.03301	ENSG00000062038	1001
SLC6A3	2.7	1.1	12.8	3.5E-04	0.03490	ENSG00000142319	6531
CLEC11A	1.6	5.2	12.6	3.8E-04	0.03575	ENSG00000105472	6320
AHR	1.3	6.5	12.7	3.7E-04	0.03575	ENSG00000106546	196
EXT1	1.1	6.8	12.5	4.0E-04	0.03695	ENSG00000182197	2131
SDC1	2.5	3.5	12.4	4.3E-04	0.03944	ENSG00000115884	6382

CBX8	1.5	3.3	12.3	4.4E-04	0.03993	ENSG00000141570	57332
TNN	2.3	1.9	12.3	4.5E-04	0.04002	ENSG00000120332	63923
TRAV39	3.1	0.5	12.0	5.4E-04	0.04586	ENSG00000211818	NA
RSPO3	2.4	1.8	12.0	5.4E-04	0.04586	ENSG00000146374	84870
CTGF	1.6	10.4	11.9	5.6E-04	0.04605	ENSG00000118523	1490
WDR65	1.8	0.4	11.8	5.8E-04	0.04655	ENSG00000243710	149465
ITGBL1	2.0	7.6	11.8	5.9E-04	0.04686	ENSG00000198542	9358
CPXM2	2.0	6.2	11.6	6.5E-04	0.04888	ENSG00000121898	119587
HOXB2	2.0	1.8	11.6	6.6E-04	0.04888	ENSG00000173917	3212
C6orf48	0.7	6.3	11.6	6.7E-04	0.04888	ENSG00000204387	50854
	2.2	0.4	11.6	6.7E-04	0.04931	ENSG00000260604	NA

Underexpression

hgnc_symbol	logFC	logCPM	LR	PValue	FDR	ensembl	entrez
FAM134B	-4.3	4.9	38.5	5.6E-10	9.2E-06	ENSG00000154153	54463
SLC13A3	-5.2	6.2	32.2	1.4E-08	1.1E-04	ENSG00000158296	64849
SERPIND1	-5.5	5.9	30.7	3.0E-08	1.7E-04	ENSG00000099937	3053
GREB1	-4.2	4.3	30.0	4.2E-08	1.7E-04	ENSG00000196208	9687
GJB6	-5.6	4.9	28.7	8.5E-08	2.0E-04	ENSG00000121742	10804
KCNT1	-4.2	4.4	28.9	7.7E-08	2.0E-04	ENSG00000107147	57582
TMEM45B	-3.7	1.9	27.8	1.3E-07	2.7E-04	ENSG00000151715	120224
CMYA5	-3.2	2.7	27.4	1.6E-07	3.0E-04	ENSG00000164309	202333
CPNE9	-3.9	1.2	25.9	3.5E-07	5.3E-04	ENSG00000144550	151835
PTGDS	-4.7	11.6	25.0	5.8E-07	7.3E-04	ENSG00000107317	5730
SLC13A4	-4.4	7.3	25.1	5.6E-07	7.3E-04	ENSG00000164707	26266
LPAR3	-4.3	1.4	24.8	6.3E-07	7.4E-04	ENSG00000171517	23566
RAB3IP	-1.7	3.8	24.4	7.7E-07	8.5E-04	ENSG00000127328	117177
SLC2A12	-2.7	4.1	23.3	1.4E-06	1.4E-03	ENSG00000146411	154091
	-4.4	4.3	22.8	1.8E-06	1.5E-03	ENSG00000168824	27065
NNAT	-4.0	6.4	22.8	1.8E-06	1.5E-03	ENSG00000053438	4826
STAC2	-2.7	2.2	22.9	1.7E-06	1.5E-03	ENSG00000141750	342667
WFIKK2	-4.6	3.6	22.3	2.4E-06	1.9E-03	ENSG00000173714	124857
SLC5A5	-6.2	5.5	21.6	3.4E-06	2.2E-03	ENSG00000105641	6528
RSPO2	-4.5	2.7	21.7	3.2E-06	2.2E-03	ENSG00000147655	340419
TRPM3	-2.9	2.0	21.5	3.5E-06	2.2E-03	ENSG00000083067	80036
AK4	-1.6	4.7	21.8	3.1E-06	2.2E-03	ENSG00000162433	100507855
SLC6A13	-4.4	6.3	21.3	3.9E-06	2.3E-03	ENSG0000010379	6540
WNK4	-3.6	2.5	21.1	4.4E-06	2.5E-03	ENSG00000126562	65266
SLC6A20	-4.9	6.1	20.8	5.0E-06	2.7E-03	ENSG00000163817	54716
IGSF10	-3.5	2.7	20.6	5.7E-06	3.0E-03	ENSG00000152580	285313
MTMR7	-1.7	1.8	20.4	6.2E-06	3.2E-03	ENSG00000003987	9108
ATP1A4	-3.5	2.3	20.1	7.3E-06	3.6E-03	ENSG00000132681	480
SLC22A6	-6.3	5.3	20.0	7.6E-06	3.6E-03	ENSG00000197901	9356
PFKFB2	-1.8	4.9	19.7	8.9E-06	4.0E-03	ENSG00000123836	5208

PCDH19	-2.7	3.0	19.2	1.2E-05	4.7E-03	ENSG00000165194	57526
SLC7A11	-2.6	6.4	19.1	1.2E-05	4.7E-03	ENSG00000151012	23657
KLHL41	-2.4	0.5	19.2	1.2E-05	4.7E-03	ENSG00000239474	10324
PHKA1	-2.0	3.6	19.1	1.2E-05	4.7E-03	ENSG00000067177	5255
TPD52	-2.3	3.8	18.8	1.4E-05	5.3E-03	ENSG00000076554	7163
SLC22A8	-5.5	5.2	18.7	1.5E-05	5.6E-03	ENSG00000149452	9376
AIFM3	-3.2	4.9	18.6	1.6E-05	5.7E-03	ENSG00000183773	150209
OGDHL	-3.4	2.7	18.5	1.7E-05	5.8E-03	ENSG00000197444	55753
GJB2	-3.5	4.6	18.3	1.9E-05	6.6E-03	ENSG00000165474	2706
GPC5	-3.6	1.5	18.1	2.1E-05	6.9E-03	ENSG00000179399	2262
SLC1A3	-2.6	7.1	18.0	2.2E-05	6.9E-03	ENSG00000079215	6507
PAQR8	-2.3	5.5	17.9	2.3E-05	6.9E-03	ENSG00000170915	85315
SLC18B1	-1.5	3.9	17.8	2.4E-05	7.2E-03	ENSG00000146409	116843
SLC9A2	-4.5	2.7	17.6	2.7E-05	7.8E-03	ENSG00000115616	6549
FGFR2	-2.6	4.6	17.5	2.9E-05	8.2E-03	ENSG00000066468	2263
MPP6	-2.3	2.7	17.4	3.0E-05	8.4E-03	ENSG00000105926	51678
LRP4	-2.2	5.3	17.3	3.2E-05	8.5E-03	ENSG00000134569	4038
RGMA	-2.2	4.5	17.3	3.2E-05	8.5E-03	ENSG00000182175	56963
COCH	-4.5	3.1	17.2	3.3E-05	8.7E-03	ENSG00000100473	1690
PCDH9	-2.5	3.0	17.2	3.4E-05	8.8E-03	ENSG00000184226	5101
NAALAD2	-2.0	2.4	17.1	3.5E-05	8.9E-03	ENSG00000077616	10003
NCOA1	-1.1	6.5	17.1	3.6E-05	8.9E-03	ENSG00000084676	8648
TUB	-2.1	5.6	17.0	3.7E-05	9.1E-03	ENSG00000166402	7275
BAI1	-2.7	4.8	16.9	3.9E-05	9.4E-03	ENSG00000181790	575
LCNL1	-4.0	6.4	16.9	4.0E-05	9.6E-03	ENSG00000214402	401562
SLC6A12	-3.2	4.8	16.8	4.1E-05	9.6E-03	ENSG00000111181	6539
PEG3	-1.9	4.7	16.8	4.2E-05	9.7E-03	ENSG00000198300	5178
ATP1A2	-3.4	10.1	16.6	4.7E-05	1.0E-02	ENSG00000018625	477
C2orf82	-2.9	2.5	16.6	4.6E-05	1.0E-02	ENSG00000182600	389084
SLC15A2	-1.8	3.4	16.6	4.7E-05	1.0E-02	ENSG00000163406	6565
ALDH1L1	-3.0	4.4	16.5	4.9E-05	1.0E-02	ENSG00000144908	10840
KCNA2	-2.9	1.3	16.5	4.9E-05	1.0E-02	ENSG00000177301	3737
ATP1B2	-3.0	6.4	16.4	5.1E-05	1.1E-02	ENSG00000129244	482
NCAN	-5.5	6.5	16.3	5.3E-05	1.1E-02	ENSG00000130287	1463
CXADR	-2.7	1.8	16.2	5.6E-05	1.1E-02	ENSG00000154639	1525
KIAA1958	-1.4	2.7	16.1	6.1E-05	1.2E-02	ENSG00000165185	158405
ABCD2	-2.9	1.1	16.0	6.4E-05	1.3E-02	ENSG00000173208	225
LINC00925	-3.0	1.6	15.9	6.6E-05	1.3E-02	ENSG00000255571	254559
CA8	-3.9	1.1	15.8	7.0E-05	1.3E-02	ENSG00000178538	767
SLC6A4	-2.6	1.4	15.8	7.0E-05	1.3E-02	ENSG00000108576	6532
ITM2C	-2.0	8.4	15.8	7.0E-05	1.3E-02	ENSG00000135916	81618
MCF2	-2.1	0.6	15.6	7.6E-05	1.4E-02	ENSG00000101977	4168
EDA	-2.3	3.2	15.5	8.1E-05	1.5E-02	ENSG00000158813	1896
ANKRD32	-1.4	3.0	15.5	8.2E-05	1.5E-02	ENSG00000133302	84250
LYPD6	-3.2	1.2	15.5	8.4E-05	1.5E-02	ENSG00000187123	130574

	-2.6	1.1	15.4	8.9E-05	1.6E-02	ENSG00000257894	NA
GATM	-2.3	5.1	15.3	9.0E-05	1.6E-02	ENSG00000171766	2628
ALDH1A1	-1.8	5.2	15.3	9.2E-05	1.6E-02	ENSG00000165092	216
ASTN2	-2.3	3.9	15.0	1.1E-04	1.8E-02	ENSG00000148219	23245
COLEC12	-2.2	6.4	15.0	1.1E-04	1.8E-02	ENSG00000158270	81035
MYO16	-3.0	0.8	14.9	1.2E-04	1.9E-02	ENSG00000041515	23026
RRAGD	-1.3	4.1	14.9	1.2E-04	1.9E-02	ENSG00000025039	58528
PGRMC1	-1.0	6.6	14.8	1.2E-04	1.9E-02	ENSG00000101856	10857
ANKS1B	-2.1	3.0	14.7	1.2E-04	2.0E-02	ENSG00000185046	56899
MACROD2	-2.0	1.5	14.7	1.3E-04	2.0E-02	ENSG00000172264	140733
NLGN3	-2.0	3.7	14.7	1.3E-04	2.0E-02	ENSG00000196338	54413
PTPRZ1	-3.5	5.2	14.6	1.3E-04	2.0E-02	ENSG00000106278	5803
TAC1	-2.7	1.7	14.6	1.3E-04	2.0E-02	ENSG00000006128	6863
SLC16A12	-2.8	3.7	14.5	1.4E-04	2.0E-02	ENSG00000152779	387700
TM7SF2	-1.8	3.3	14.5	1.4E-04	2.0E-02	ENSG00000149809	7108
GPR37L1	-4.5	4.0	14.5	1.4E-04	2.1E-02	ENSG00000170075	9283
SLC22A2	-3.4	3.5	14.4	1.5E-04	2.1E-02	ENSG00000112499	6582
MUM1L1	-3.3	1.8	14.4	1.5E-04	2.1E-02	ENSG00000157502	139221
NCAM1	-3.1	5.4	14.4	1.5E-04	2.1E-02	ENSG00000149294	4684
TP53I11	-2.0	7.8	14.4	1.5E-04	2.1E-02	ENSG00000175274	9537
PPFIA4	-2.3	4.3	14.1	1.8E-04	2.2E-02	ENSG00000143847	8497
MEGF10	-2.3	3.2	14.1	1.7E-04	2.2E-02	ENSG00000145794	84466
CADM4	-2.3	4.4	14.2	1.7E-04	2.2E-02	ENSG00000105767	199731
CGN	-2.2	0.4	14.1	1.7E-04	2.2E-02	ENSG00000143375	57530
REPS2	-1.9	3.6	14.1	1.7E-04	2.2E-02	ENSG00000169891	9185
PHKG1	-1.8	2.6	14.2	1.7E-04	2.2E-02	ENSG00000164776	5260
TMEM132B	-2.6	3.2	14.0	1.8E-04	2.3E-02	ENSG00000139364	114795
RYR1	-2.0	4.0	14.0	1.8E-04	2.3E-02	ENSG00000196218	6261
GLDC	-2.2	1.7	13.9	1.9E-04	2.4E-02	ENSG00000178445	2731
TNFSF18	-2.7	2.8	13.8	2.0E-04	2.5E-02	ENSG00000120337	8995
CADM2	-3.2	2.5	13.8	2.1E-04	2.5E-02	ENSG00000175161	253559
IGLON5	-2.0	2.5	13.8	2.1E-04	2.5E-02	ENSG00000142549	402665
SIDT1	-1.7	2.9	13.7	2.1E-04	2.5E-02	ENSG00000072858	54847
LINC00173	-1.8	0.5	13.7	2.1E-04	2.5E-02	ENSG00000196668	100287569
RHBDL3	-2.2	2.0	13.5	2.3E-04	2.8E-02	ENSG00000141314	162494
SLCO1C1	-2.3	3.1	13.5	2.4E-04	2.8E-02	ENSG00000139155	53919
PSAT1	-2.2	4.3	13.5	2.4E-04	2.8E-02	ENSG00000135069	29968
VWA7	-1.7	0.9	13.5	2.4E-04	2.8E-02	ENSG00000204396	80737
PPL	-1.6	2.0	13.5	2.4E-04	2.8E-02	ENSG00000118898	5493
SLC1A2	-3.6	7.2	13.4	2.5E-04	2.8E-02	ENSG00000110436	6506
MAP2K6	-2.0	1.7	13.4	2.5E-04	2.8E-02	ENSG00000108984	5608
SPTBN4	-1.8	3.5	13.4	2.5E-04	2.8E-02	ENSG00000160460	57731
TRIM9	-3.2	3.5	13.4	2.6E-04	2.8E-02	ENSG00000100505	114088
CNTN3	-2.5	1.7	13.4	2.5E-04	2.8E-02	ENSG00000113805	5067
KDR	-2.6	6.3	13.3	2.6E-04	2.9E-02	ENSG00000128052	3791

SHISA6	-4.0	2.5	13.2	2.8E-04	3.0E-02	ENSG00000188803	388336
SNAP91	-2.6	2.9	13.2	2.8E-04	3.0E-02	ENSG00000065609	9892
OSBPL6	-1.4	2.3	13.2	2.8E-04	3.0E-02	ENSG00000079156	114880
COL4A6	-2.3	3.3	13.1	2.9E-04	3.1E-02	ENSG00000197565	1288
BEX2	-2.6	2.7	13.0	3.0E-04	3.1E-02	ENSG00000133134	84707
CPAMD8	-2.6	5.2	13.0	3.0E-04	3.1E-02	ENSG00000160111	27151
SHC3	-2.4	1.0	13.0	3.1E-04	3.1E-02	ENSG00000148082	53358
WDR17	-1.8	1.9	13.0	3.2E-04	3.2E-02	ENSG00000150627	116966
MREG	-1.6	1.1	12.9	3.2E-04	3.3E-02	ENSG00000118242	55686
DHCR7	-1.1	4.1	12.9	3.3E-04	3.3E-02	ENSG00000172893	1717
PRKG2	-3.0	0.6	12.8	3.4E-04	3.4E-02	ENSG00000138669	5593
FLRT1	-2.5	1.4	12.7	3.6E-04	3.5E-02	ENSG00000126500	23769
KBTBD11	-1.9	4.6	12.7	3.6E-04	3.5E-02	ENSG00000176595	9920
SLC6A1	-2.5	7.7	12.7	3.7E-04	3.6E-02	ENSG00000157103	6529
CABLES1	-2.0	5.4	12.6	3.8E-04	3.6E-02	ENSG00000134508	91768
BDH1	-1.6	3.0	12.6	3.8E-04	3.6E-02	ENSG00000161267	622
HSD17B14	-1.3	3.8	12.6	3.8E-04	3.6E-02	ENSG00000087076	51171
GLUL	-1.6	10.2	12.6	3.9E-04	3.7E-02	ENSG00000135821	2752
KCNK2	-2.5	5.0	12.5	4.0E-04	3.7E-02	ENSG00000082482	3776
SDC3	-1.4	7.5	12.5	4.1E-04	3.8E-02	ENSG00000162512	9672
CHGB	-2.7	2.7	12.4	4.3E-04	3.9E-02	ENSG00000089199	1114
SLC25A18	-2.8	3.7	12.2	4.7E-04	4.2E-02	ENSG00000182902	83733
GBAS	-0.7	5.1	12.2	4.7E-04	4.2E-02	ENSG00000146729	2631
PKP2	-2.6	5.5	12.2	4.8E-04	4.2E-02	ENSG00000057294	5318
FZD3	-1.6	3.4	12.2	4.8E-04	4.2E-02	ENSG00000104290	7976
ARHGAP32	-1.1	4.8	12.2	4.9E-04	4.2E-02	ENSG00000134909	9743
KLKB1	-2.1	2.2	12.1	5.0E-04	4.3E-02	ENSG00000164344	3818
PMP2	-3.2	5.5	12.1	5.1E-04	4.4E-02	ENSG00000147588	5375
ZNF536	-2.5	1.4	12.0	5.2E-04	4.5E-02	ENSG00000198597	9745
APC2	-2.4	4.7	12.0	5.3E-04	4.5E-02	ENSG00000115266	10297
CRYGN	-2.3	1.0	12.0	5.3E-04	4.5E-02	ENSG00000127377	155051
CRABP1	-3.0	5.7	11.9	5.5E-04	4.6E-02	ENSG00000166426	1381
SLC24A4	-2.3	2.3	11.9	5.5E-04	4.6E-02	ENSG00000140090	123041
SLC4A4	-2.1	4.6	11.9	5.6E-04	4.6E-02	ENSG00000080493	8671
SCUBE2	-1.3	2.9	11.9	5.6E-04	4.6E-02	ENSG00000175356	57758
USP54	-1.2	5.2	11.9	5.6E-04	4.6E-02	ENSG00000166348	159195
ACSBG1	-3.0	3.1	11.9	5.8E-04	4.7E-02	ENSG00000103740	23205
GPM6A	-2.8	6.1	11.8	5.8E-04	4.7E-02	ENSG00000150625	2823
ELMOD1	-2.5	1.4	11.8	5.8E-04	4.7E-02	ENSG00000110675	643923
PRKCA	-1.2	6.3	11.8	5.8E-04	4.7E-02	ENSG00000154229	5578
	-2.0	1.5	11.8	5.9E-04	4.7E-02	ENSG00000264514	NA
SV2B	-3.0	2.0	11.7	6.2E-04	4.9E-02	ENSG00000185518	9899
KIF1B	-0.9	6.7	11.7	6.2E-04	4.9E-02	ENSG00000054523	23095
MAPK4	-3.4	5.8	11.7	6.3E-04	4.9E-02	ENSG00000141639	5596
ELOVL2	-2.6	3.1	11.7	6.3E-04	4.9E-02	ENSG00000197977	54898

CHDH	-2.0	1.9	11.7	6.3E-04	4.9E-02	ENSG00000016391	55349
BMP7	-2.8	3.3	11.6	6.6E-04	4.9E-02	ENSG000000101144	655
CSPG5	-2.6	3.3	11.6	6.6E-04	4.9E-02	ENSG000000114646	10675
	-2.2	2.3	11.6	6.6E-04	4.9E-02	ENSG000000241732	NA
ASIC1	-2.0	2.5	11.6	6.6E-04	4.9E-02	ENSG000000110881	41
CLCN2	-1.6	4.3	11.6	6.6E-04	4.9E-02	ENSG000000114859	1181
SSPO	-1.3	2.9	11.6	6.7E-04	4.9E-02	ENSG000000197558	NA
PHLPP1	-1.2	4.6	11.6	6.6E-04	4.9E-02	ENSG000000081913	23239
MTHFR	-0.7	6.1	11.6	6.5E-04	4.9E-02	ENSG000000177000	4524
CACNA1A	-1.8	3.8	11.5	6.9E-04	5.0E-02	ENSG000000141837	100507353
RIC3	-1.6	3.4	11.5	6.9E-04	5.0E-02	ENSG000000166405	79608
CLMN	-1.6	5.3	11.5	6.9E-04	5.0E-02	ENSG000000165959	79789
ALDH1L1-AS2	-3.1	0.5	11.5	6.9E-04	5.0E-02	ENSG000000246022	100862662

Hgnc indicates Human gene nomenclature committee; FC, fold change; CPM, counts per million, LR, likelihood ratio, FDR, false discovery rate.

Supplementary Table V. Enriched Gene Ontology categories in aneurysms versus controls after trimming.

Category	Description	Over represented P-value
GO:0015698	inorganic anion transport	< 0.001
GO:0001501	skeletal system development	0.005
GO:0048638	regulation of developmental growth	0.009
GO:0098590	plasma membrane region	< 0.001
GO:0001503	ossification	0.003
GO:0007601	visual perception	0.002
GO:0007600	sensory perception	< 0.001
GO:0032941	secretion by tissue	< 0.001
GO:0030324	lung development	0.006
GO:0015079	potassium ion transmembrane transporter activity	< 0.001
GO:0015077	monovalent inorganic cation transmembrane transporter activity	< 0.001
GO:0046873	metal ion transmembrane transporter activity	< 0.001
GO:0015081	sodium ion transmembrane transporter activity	< 0.001
GO:0030198	extracellular matrix organization	0.005
GO:0044057	regulation of system process	0.001
GO:0005911	cell-cell junction	0.001
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	0.008
GO:0004930	G-protein coupled receptor activity	0.006
GO:0009152	purine ribonucleotide biosynthetic process	0.009
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	0.001
GO:0005578	proteinaceous extracellular matrix	< 0.001
GO:0015370	solute:sodium symporter activity	< 0.001
GO:0015672	monovalent inorganic cation transport	0.001
GO:0003014	renal system process	< 0.001
GO:0033267	axon part	0.008
GO:0045121	membrane raft	0.008
GO:0048511	rhythmic process	0.009
GO:0007423	sensory organ development	0.009
GO:0048598	embryonic morphogenesis	0.009
GO:0006820	anion transport	< 0.001
GO:0051216	cartilage development	0.001
GO:0008015	blood circulation	0.003
GO:0051047	positive regulation of secretion	< 0.001
GO:0023061	signal release	0.004
GO:0008509	anion transmembrane transporter activity	< 0.001
GO:0046887	positive regulation of hormone secretion	0.001
GO:0010817	regulation of hormone levels	0.008
GO:0007589	body fluid secretion	< 0.001

GO:0016323	basolateral plasma membrane	< 0.001
GO:0015297	antiporter activity	< 0.001
GO:0016324	apical plasma membrane	< 0.001
GO:0015296	anion:cation symporter activity	< 0.001
GO:0046943	carboxylic acid transmembrane transporter activity	< 0.001
GO:0050880	regulation of blood vessel size	0.005
GO:0015711	organic anion transport	0.002
GO:0015291	secondary active transmembrane transporter activity	< 0.001
GO:0043010	camera-type eye development	0.009
GO:0042476	odontogenesis	0.004
GO:0006813	potassium ion transport	0.007
GO:0015294	solute:cation symporter activity	< 0.001
GO:0006814	sodium ion transport	0.002

Supplementary Table VI. Differential expression in ruptured aneurysms versus unruptured aneurysms.

Overexpression

hgnc_symbol	logFC	logCPM	LR	PValue	FDR	ensembl	entrez
MARCO	3.0	6.0	41.1	1.4E-10	2.2E-06	ENSG00000019169	8685
TGFB1	2.0	10.1	36.6	1.4E-09	1.1E-05	ENSG00000120708	7045
HPSE	2.8	4.9	33.0	9.1E-09	4.5E-05	ENSG00000173083	10855
CD300C	2.5	3.7	31.5	1.9E-08	7.3E-05	ENSG00000167850	10871
CD300E	3.2	7.4	29.6	5.3E-08	8.4E-05	ENSG00000186407	342510
CLEC5A	2.8	6.0	29.9	4.5E-08	8.4E-05	ENSG00000258227	23601
OLR1	2.7	7.5	29.5	5.7E-08	8.4E-05	ENSG00000173391	4973
OSCAR	2.6	5.1	30.3	3.7E-08	8.4E-05	ENSG00000170909	126014
	2.1	2.8	29.7	5.0E-08	8.4E-05	ENSG00000203306	NA
	2.0	2.2	29.8	4.8E-08	8.4E-05	ENSG00000268802	NA
SMS	1.1	4.7	29.3	6.2E-08	8.4E-05	ENSG00000102172	6611
ABCC3	2.2	5.9	29.1	6.9E-08	8.6E-05	ENSG00000108846	8714
TMEM150B	2.3	2.4	28.8	8.0E-08	9.2E-05	ENSG00000180061	284417
ANPEP	2.8	8.6	28.5	9.6E-08	9.6E-05	ENSG00000166825	290
LAIR1	2.0	6.6	28.5	9.5E-08	9.6E-05	ENSG00000167613	3903
C19orf59	3.8	4.8	28.2	1.1E-07	9.9E-05	ENSG00000183019	199675
HS3ST1	1.6	3.6	28.2	1.1E-07	9.9E-05	ENSG00000002587	9957
HAVCR2	2.2	5.8	28.0	1.2E-07	1.0E-04	ENSG00000135077	84868
CD300LB	2.3	4.1	27.9	1.3E-07	1.0E-04	ENSG00000178789	124599
CTSL	1.6	8.6	27.7	1.4E-07	1.1E-04	ENSG00000135047	1514
	2.9	2.0	27.2	1.9E-07	1.2E-04	ENSG00000261222	101928343
MPP1	1.8	6.6	27.2	1.8E-07	1.2E-04	ENSG00000130830	4354
SLC11A1	3.2	9.5	27.0	2.1E-07	1.3E-04	ENSG00000018280	6556
ST14	3.1	6.3	26.7	2.4E-07	1.5E-04	ENSG00000149418	6768
NLRC4	2.1	3.5	26.3	2.9E-07	1.7E-04	ENSG00000091106	58484
CCR1	2.0	5.3	26.1	3.2E-07	1.8E-04	ENSG00000163823	1230
LILRA3	2.4	2.5	25.9	3.5E-07	1.9E-04	ENSG00000170866	11026
CD86	1.8	5.4	25.3	5.0E-07	2.4E-04	ENSG00000114013	942
ITGAE	1.4	4.3	25.3	4.9E-07	2.4E-04	ENSG00000083457	3682
SLC37A2	2.1	4.7	25.0	5.7E-07	2.5E-04	ENSG00000134955	219855
TFEC	1.9	4.1	25.1	5.5E-07	2.5E-04	ENSG00000105967	22797
TMEM180	1.8	3.7	25.1	5.4E-07	2.5E-04	ENSG00000138111	79847
	2.7	4.7	24.7	6.6E-07	2.8E-04	ENSG00000224397	NA
IL10	2.4	3.4	24.6	6.9E-07	2.8E-04	ENSG00000136634	3586
RACGAP1	1.2	3.5	24.6	6.9E-07	2.8E-04	ENSG00000161800	29127
ALOX5AP	2.6	6.6	24.2	8.6E-07	2.9E-04	ENSG00000132965	241
GNA15	2.3	5.1	24.3	8.2E-07	2.9E-04	ENSG00000060558	2769
PFKFB4	2.1	5.9	24.3	8.1E-07	2.9E-04	ENSG00000114268	5210
DOK3	2.0	5.9	24.2	8.5E-07	2.9E-04	ENSG00000146094	79930

ZMYND15	1.4	4.0	24.3	8.2E-07	2.9E-04	ENSG00000141497	84225
NOD2	2.3	5.2	24.1	9.0E-07	3.0E-04	ENSG00000167207	64127
LILRA6	2.4	4.4	24.0	9.6E-07	3.1E-04	ENSG00000244482	NA
TYROBP	1.8	7.5	23.9	1.0E-06	3.2E-04	ENSG00000011600	7305
ME2	1.3	5.5	23.9	1.0E-06	3.2E-04	ENSG00000082212	4200
CD300A	2.1	5.6	23.7	1.1E-06	3.3E-04	ENSG00000167851	11314
PPIF	2.0	7.0	23.7	1.1E-06	3.3E-04	ENSG00000108179	10105
DMXL2	1.3	5.6	23.8	1.1E-06	3.3E-04	ENSG00000104093	23312
CD33	1.5	3.7	23.6	1.2E-06	3.3E-04	ENSG00000105383	945
MYO1G	2.3	6.5	23.3	1.4E-06	3.4E-04	ENSG00000136286	64005
TMEM52B	2.3	2.3	23.3	1.4E-06	3.4E-04	ENSG00000165685	120939
CD300LF	2.2	3.8	23.3	1.4E-06	3.4E-04	ENSG00000186074	146722
MAPK13	1.9	4.6	23.4	1.3E-06	3.4E-04	ENSG00000156711	5603
LILRB2	1.8	5.9	23.3	1.4E-06	3.4E-04	ENSG00000131042	10288
KNSTRN	1.1	2.5	23.3	1.4E-06	3.4E-04	ENSG00000128944	90417
STXBP2	2.2	5.9	23.1	1.6E-06	3.7E-04	ENSG00000076944	6813
FBP1	2.5	4.3	23.0	1.6E-06	3.8E-04	ENSG00000165140	2203
LRRC25	1.9	4.7	22.8	1.8E-06	4.1E-04	ENSG00000175489	126364
EIF4EBP1	1.3	4.1	22.8	1.8E-06	4.1E-04	ENSG00000187840	1978
	2.0	2.2	22.7	1.9E-06	4.2E-04	ENSG00000233038	100506585
PRAM1	2.0	4.4	22.6	1.9E-06	4.3E-04	ENSG00000133246	84106
IL4I1	1.7	2.8	22.5	2.1E-06	4.5E-04	ENSG00000104951	259307
APOBR	2.2	6.1	22.4	2.2E-06	4.5E-04	ENSG00000184730	55911
HK3	2.1	6.3	22.4	2.3E-06	4.5E-04	ENSG00000160883	3101
CD163	2.0	8.5	22.4	2.2E-06	4.5E-04	ENSG00000177575	9332
SLC43A2	1.9	6.7	22.4	2.2E-06	4.5E-04	ENSG00000167703	124935
FCER1G	1.8	6.5	22.4	2.2E-06	4.5E-04	ENSG00000158869	2207
	1.6	1.8	22.3	2.3E-06	4.5E-04	ENSG00000264456	NA
CSF1R	1.4	7.5	22.3	2.3E-06	4.5E-04	ENSG00000182578	1436
SIGLEC9	2.0	4.5	22.1	2.5E-06	4.9E-04	ENSG00000129450	27180
TMEM106A	1.1	4.0	22.1	2.6E-06	4.9E-04	ENSG00000184988	113277
TYMP	1.7	7.8	21.8	3.1E-06	5.4E-04	ENSG00000025708	1890
REEP4	1.3	4.6	21.8	3.1E-06	5.4E-04	ENSG00000168476	80346
COLGALT1	0.9	7.7	21.8	3.1E-06	5.4E-04	ENSG00000130309	79709
PIK3R5	2.1	6.4	21.6	3.3E-06	5.7E-04	ENSG00000141506	23533
RNASE2	2.3	2.3	21.6	3.4E-06	5.8E-04	ENSG00000169385	6036
COQ2	1.2	2.8	21.5	3.5E-06	5.9E-04	ENSG00000173085	27235
CXCL5	3.0	4.1	21.4	3.7E-06	6.2E-04	ENSG00000163735	6374
SLC38A7	0.9	4.8	21.3	3.9E-06	6.4E-04	ENSG00000103042	55238
ZMIZ1-AS1	1.9	2.2	21.3	4.0E-06	6.5E-04	ENSG00000224596	283050
ALOX5	1.9	6.8	21.3	4.0E-06	6.5E-04	ENSG00000012779	240
TNFRSF1B	1.9	8.2	21.0	4.6E-06	7.2E-04	ENSG00000028137	7133
LFNG	1.5	5.2	21.0	4.6E-06	7.2E-04	ENSG00000106003	3955
SH3BP1	1.4	4.1	21.0	4.6E-06	7.2E-04	ENSG00000100092	23616
KYNU	2.0	3.9	20.9	4.8E-06	7.3E-04	ENSG00000115919	8942

CD14	1.5	8.0	20.9	4.8E-06	7.3E-04	ENSG00000170458	929
MCOLN1	1.2	5.5	20.9	4.9E-06	7.3E-04	ENSG00000090674	57192
C1orf162	1.8	5.7	20.8	5.1E-06	7.5E-04	ENSG00000143110	128346
IRF5	1.6	4.6	20.8	5.2E-06	7.6E-04	ENSG00000128604	3663
LILRB4	1.8	5.4	20.7	5.3E-06	7.6E-04	ENSG00000186818	11006
LINC00900	2.0	1.1	20.4	6.1E-06	8.2E-04	ENSG00000246100	283143
NPL	1.7	5.5	20.5	6.1E-06	8.2E-04	ENSG00000135838	80896
CCNB1	1.5	2.9	20.4	6.1E-06	8.2E-04	ENSG00000134057	891
GCHFR	1.5	3.7	20.4	6.2E-06	8.2E-04	ENSG00000137880	2644
STAB1	1.5	9.4	20.4	6.2E-06	8.2E-04	ENSG00000010327	23166
FCGR2B	1.4	3.6	20.5	6.1E-06	8.2E-04	ENSG00000072694	2213
ADAP2	1.3	5.3	20.5	5.8E-06	8.2E-04	ENSG00000184060	55803
SGOL2	1.2	1.5	20.5	6.1E-06	8.2E-04	ENSG00000163535	151246
IFI30	2.2	4.0	20.3	6.5E-06	8.5E-04	ENSG00000216490	10437
SH3BGRL3	1.2	7.8	20.3	6.7E-06	8.6E-04	ENSG00000142669	83442
CDCA4	0.8	2.9	20.2	6.9E-06	8.8E-04	ENSG00000170779	55038
	1.8	1.8	20.1	7.2E-06	9.2E-04	ENSG00000248996	NA
DOK2	1.7	4.9	20.1	7.3E-06	9.2E-04	ENSG00000147443	9046
ARRB2	1.7	7.5	20.1	7.4E-06	9.3E-04	ENSG00000141480	409
CD82	1.1	5.9	20.0	7.8E-06	9.5E-04	ENSG00000085117	3732
TNFSF8	2.0	3.9	19.9	8.0E-06	9.7E-04	ENSG00000106952	944
GLIPR2	1.2	6.3	19.9	8.0E-06	9.7E-04	ENSG00000122694	152007
CDCP1	2.2	4.6	19.9	8.1E-06	9.7E-04	ENSG00000163814	64866
SNX20	1.6	3.9	19.8	8.5E-06	9.8E-04	ENSG00000167208	124460
SLC25A19	1.5	4.1	19.8	8.5E-06	9.8E-04	ENSG00000125454	60386
CYB5R4	1.1	4.5	19.9	8.3E-06	9.8E-04	ENSG00000065615	51167
IMPA2	1.4	3.7	19.7	9.0E-06	1.0E-03	ENSG00000141401	3613
CD84	1.6	5.4	19.7	9.3E-06	1.0E-03	ENSG00000066294	8832
CATSPER1	1.8	1.8	19.5	1.0E-05	1.1E-03	ENSG00000175294	117144
CXCL16	1.3	6.7	19.5	1.0E-05	1.1E-03	ENSG00000161921	58191
MAFB	1.6	6.0	19.4	1.0E-05	1.1E-03	ENSG00000204103	9935
UBE2C	2.0	1.7	19.4	1.1E-05	1.1E-03	ENSG00000175063	11065
AIF1	1.4	6.1	19.4	1.1E-05	1.2E-03	ENSG00000204472	199
SERPINA1	2.0	7.0	19.3	1.1E-05	1.2E-03	ENSG00000197249	5265
VSIG4	1.7	6.5	19.3	1.1E-05	1.2E-03	ENSG00000155659	11326
LAPTM5	1.8	9.2	19.2	1.2E-05	1.2E-03	ENSG00000162511	7805
LINC00854	1.2	2.4	19.2	1.2E-05	1.2E-03	ENSG00000236383	100874261
OSM	2.2	6.8	19.1	1.3E-05	1.3E-03	ENSG00000099985	5008
PPARG	1.6	3.4	19.1	1.3E-05	1.3E-03	ENSG00000132170	5468
PLIN3	0.8	6.7	19.0	1.3E-05	1.3E-03	ENSG00000105355	10226
GPR84	1.9	3.2	18.9	1.4E-05	1.4E-03	ENSG00000139572	53831
TWF2	1.0	4.9	18.9	1.4E-05	1.4E-03	ENSG00000247596	11344
CSTA	1.9	2.9	18.9	1.4E-05	1.4E-03	ENSG00000121552	1475
CTSD	1.4	9.6	18.9	1.4E-05	1.4E-03	ENSG00000117984	1509
DSG2	2.2	4.0	18.8	1.5E-05	1.4E-03	ENSG00000046604	1829

FCGR3A	1.7	7.2	18.8	1.5E-05	1.4E-03	ENSG00000203747	2214
PIK3AP1	1.6	5.6	18.8	1.5E-05	1.4E-03	ENSG00000155629	118788
NLRP12	2.2	3.9	18.7	1.5E-05	1.4E-03	ENSG00000142405	91662
SYK	1.5	5.7	18.7	1.5E-05	1.4E-03	ENSG00000165025	6850
SIGLEC14	2.3	3.4	18.7	1.6E-05	1.5E-03	ENSG00000254415	100049587
PSAP	1.0	11.5	18.7	1.6E-05	1.5E-03	ENSG00000197746	5660
ADAM8	2.1	7.1	18.5	1.7E-05	1.5E-03	ENSG00000151651	101
MPO	2.0	1.0	18.5	1.7E-05	1.5E-03	ENSG00000005381	4353
NCAPG	1.9	1.8	18.6	1.6E-05	1.5E-03	ENSG00000109805	64151
FTLP2	1.6	0.9	18.6	1.6E-05	1.5E-03	ENSG00000232368	NA
	1.6	0.9	18.6	1.6E-05	1.5E-03	ENSG00000237604	NA
SLC43A3	1.5	5.1	18.6	1.7E-05	1.5E-03	ENSG00000134802	29015
NCKAP1L	1.5	6.1	18.5	1.7E-05	1.5E-03	ENSG00000123338	3071
ARHGAP11A	1.3	2.4	18.6	1.6E-05	1.5E-03	ENSG00000198826	9824
LILRB1	1.6	4.5	18.5	1.7E-05	1.5E-03	ENSG00000104972	10859
RNASE6	1.6	4.5	18.4	1.8E-05	1.5E-03	ENSG00000169413	6039
LSP1	1.8	7.0	18.4	1.8E-05	1.6E-03	ENSG00000130592	4046
SLC15A3	1.0	6.0	18.3	1.9E-05	1.7E-03	ENSG00000110446	51296
DSC2	1.6	3.8	18.2	1.9E-05	1.7E-03	ENSG00000134755	1824
FPR3	1.9	5.9	18.2	2.0E-05	1.7E-03	ENSG00000187474	2359
ASGR2	1.7	2.2	18.2	2.0E-05	1.7E-03	ENSG00000161944	433
SLC16A3	1.7	7.6	18.2	2.0E-05	1.7E-03	ENSG00000141526	102465472
TBXAS1	1.5	5.3	18.2	2.0E-05	1.7E-03	ENSG00000059377	6916
IRAK1	1.3	7.5	18.2	2.0E-05	1.7E-03	ENSG00000184216	3654
CARD9	1.3	4.0	18.2	2.0E-05	1.7E-03	ENSG00000187796	728489
P2RX4	0.9	5.1	18.2	2.0E-05	1.7E-03	ENSG00000135124	5025
	2.1	2.8	18.1	2.1E-05	1.7E-03	ENSG00000235027	NA
GAB3	1.2	4.4	18.1	2.1E-05	1.7E-03	ENSG00000160219	139716
POLD1	0.9	4.3	18.1	2.1E-05	1.7E-03	ENSG00000062822	5424
SMCO4	1.1	3.6	18.0	2.2E-05	1.8E-03	ENSG00000166002	56935
RNASET2	1.9	6.3	18.0	2.2E-05	1.8E-03	ENSG00000026297	8635
SASH3	1.6	5.6	17.9	2.3E-05	1.8E-03	ENSG00000122122	54440
CDCA8	1.5	1.4	17.9	2.3E-05	1.8E-03	ENSG00000134690	55143
FERMT1	1.7	2.6	17.9	2.3E-05	1.8E-03	ENSG00000101311	55612
LILRA5	1.9	4.3	17.9	2.4E-05	1.8E-03	ENSG00000187116	353514
BUB1	2.0	1.8	17.9	2.4E-05	1.8E-03	ENSG00000169679	699
PPP1R14B	0.8	5.1	17.8	2.4E-05	1.9E-03	ENSG00000173457	26472
	1.8	4.3	17.8	2.4E-05	1.9E-03	ENSG00000267121	339192
VAMP8	1.4	5.5	17.8	2.4E-05	1.9E-03	ENSG00000118640	8673
GINS4	1.2	1.5	17.7	2.5E-05	1.9E-03	ENSG00000147536	84296
TTYH3	1.0	7.2	17.7	2.6E-05	1.9E-03	ENSG00000136295	80727
LGALS9	1.1	5.7	17.6	2.7E-05	2.0E-03	ENSG00000168961	3965
OASL	2.1	4.4	17.6	2.7E-05	2.0E-03	ENSG00000135114	8638
TOP2A	2.2	3.7	17.6	2.7E-05	2.0E-03	ENSG00000131747	7153
SLC46A2	1.5	1.1	17.6	2.8E-05	2.0E-03	ENSG00000119457	57864

GK	1.8	3.7	17.5	2.8E-05	2.1E-03	ENSG00000198814	2710
SLC16A10	2.5	4.0	17.5	2.8E-05	2.1E-03	ENSG00000112394	117247
BLVRB	0.8	5.6	17.5	2.8E-05	2.1E-03	ENSG00000090013	645
CCRL2	1.5	3.4	17.5	2.9E-05	2.1E-03	ENSG00000121797	9034
FTLP3	1.4	1.6	17.5	2.9E-05	2.1E-03	ENSG00000226608	NA
IQGAP3	2.0	3.3	17.4	3.0E-05	2.1E-03	ENSG00000183856	128239
FCGR2C	1.2	3.2	17.3	3.1E-05	2.2E-03	ENSG00000244682	9103
TPP1	0.8	7.8	17.3	3.1E-05	2.2E-03	ENSG00000166340	1200
TPX2	1.7	3.1	17.3	3.2E-05	2.2E-03	ENSG00000088325	22974
FCGRT	0.9	8.0	17.3	3.2E-05	2.2E-03	ENSG00000104870	2217
GTSE1	1.8	1.6	17.2	3.3E-05	2.2E-03	ENSG00000075218	51512
E2F7	1.9	1.4	17.2	3.3E-05	2.2E-03	ENSG00000165891	144455
ITGAX	2.0	8.6	17.2	3.4E-05	2.3E-03	ENSG00000140678	3687
TRIP13	1.6	1.8	17.2	3.4E-05	2.3E-03	ENSG00000071539	9319
DDX60L	1.5	6.0	17.2	3.4E-05	2.3E-03	ENSG00000181381	91351
GSTO1	1.1	6.5	17.2	3.4E-05	2.3E-03	ENSG00000148834	9446
SPOCD1	2.2	5.5	17.1	3.6E-05	2.3E-03	ENSG00000134668	90853
	1.8	1.4	17.1	3.5E-05	2.3E-03	ENSG00000231964	NA
ODF3B	1.6	5.2	17.1	3.6E-05	2.3E-03	ENSG00000177989	440836
ARL11	1.5	2.3	17.1	3.5E-05	2.3E-03	ENSG00000152213	115761
LAT2	1.5	5.5	17.1	3.5E-05	2.3E-03	ENSG00000086730	7462
MS4A4A	1.4	4.8	17.1	3.5E-05	2.3E-03	ENSG00000110079	51338
RAP2B	1.0	5.1	17.1	3.5E-05	2.3E-03	ENSG00000181467	5912
SHCBP1	1.5	2.4	17.0	3.6E-05	2.3E-03	ENSG00000171241	79801
CD53	1.6	7.0	17.0	3.8E-05	2.4E-03	ENSG00000143119	963
LGMNP1	1.1	2.7	16.9	3.9E-05	2.4E-03	ENSG00000214269	NA
BUB1B	2.0	1.4	16.9	3.9E-05	2.5E-03	ENSG00000156970	701
DNAH17	1.8	4.0	16.9	4.0E-05	2.5E-03	ENSG00000187775	8632
	1.3	1.9	16.9	4.0E-05	2.5E-03	ENSG00000225331	101928576
CCR5	1.4	3.8	16.8	4.1E-05	2.5E-03	ENSG00000160791	1234
FAM96A	0.8	4.1	16.8	4.1E-05	2.5E-03	ENSG00000166797	84191
NCF2	1.7	6.8	16.8	4.1E-05	2.5E-03	ENSG00000116701	4688
ASGR1	1.4	2.7	16.8	4.1E-05	2.5E-03	ENSG00000141505	432
C15orf48	2.7	3.1	16.7	4.3E-05	2.6E-03	ENSG00000166920	84419
MYBPC3	1.7	2.0	16.7	4.3E-05	2.6E-03	ENSG00000134571	4607
SPI1	1.4	6.3	16.7	4.3E-05	2.6E-03	ENSG00000066336	6688
IL1RN	1.8	5.7	16.7	4.3E-05	2.6E-03	ENSG00000136689	3557
CLEC7A	1.4	5.9	16.7	4.4E-05	2.6E-03	ENSG00000172243	64581
GRN	1.1	8.8	16.7	4.4E-05	2.6E-03	ENSG00000030582	2896
PTAFR	1.5	5.5	16.7	4.4E-05	2.6E-03	ENSG00000169403	5724
SLA	1.9	7.0	16.6	4.5E-05	2.6E-03	ENSG00000155926	6503
COTL1	1.4	8.0	16.6	4.6E-05	2.6E-03	ENSG00000103187	23406
SIGLEC1	1.8	6.3	16.6	4.6E-05	2.6E-03	ENSG00000088827	6614
ZWINT	1.3	3.0	16.6	4.6E-05	2.6E-03	ENSG00000122952	11130
RALA	0.8	5.5	16.6	4.7E-05	2.6E-03	ENSG00000006451	5898

KIF11	1.4	2.3	16.6	4.7E-05	2.7E-03	ENSG00000138160	3832
FAH	0.8	4.3	16.6	4.7E-05	2.7E-03	ENSG00000103876	2184
FHAD1	1.8	2.1	16.5	4.8E-05	2.7E-03	ENSG00000142621	114827
COL22A1	1.6	3.0	16.5	4.9E-05	2.7E-03	ENSG00000169436	169044
RPS6KA1	1.7	6.0	16.5	5.0E-05	2.7E-03	ENSG00000117676	6195
ADAM12	2.1	7.0	16.4	5.2E-05	2.8E-03	ENSG00000148848	8038
UNC93B1	0.9	4.8	16.4	5.1E-05	2.8E-03	ENSG00000110057	81622
SAMHD1	0.9	7.1	16.4	5.1E-05	2.8E-03	ENSG00000101347	25939
TNNI2	1.8	1.0	16.4	5.2E-05	2.8E-03	ENSG00000130598	7136
TLDC2	1.2	1.9	16.3	5.4E-05	2.9E-03	ENSG00000101342	140711
SIGLEC7	1.7	2.5	16.3	5.4E-05	2.9E-03	ENSG00000168995	27036
MYO7A	1.3	4.2	16.3	5.4E-05	2.9E-03	ENSG00000137474	4647
LILRB3	1.8	3.4	16.3	5.5E-05	2.9E-03	ENSG00000204577	101929809
TANC2	1.1	5.6	16.2	5.6E-05	3.0E-03	ENSG00000170921	26115
RRM2	2.1	3.2	16.2	5.7E-05	3.0E-03	ENSG00000171848	6241
HOTAIRM1	2.0	1.3	16.2	5.8E-05	3.0E-03	ENSG00000233429	100506311
ADPGK	1.0	6.6	16.2	5.8E-05	3.0E-03	ENSG00000159322	83440
MTRNR2L1	3.4	5.5	16.1	5.9E-05	3.0E-03	ENSG00000256618	100462977
VEGFA	2.1	9.3	16.1	5.9E-05	3.1E-03	ENSG00000112715	7422
ORC1	1.5	1.1	16.1	6.0E-05	3.1E-03	ENSG00000085840	4998
CD1D	1.6	3.4	16.1	6.1E-05	3.1E-03	ENSG00000158473	912
DLGAP5	2.3	1.4	16.1	6.1E-05	3.1E-03	ENSG00000126787	9787
EMR4P	1.6	1.7	16.1	6.2E-05	3.1E-03	ENSG00000268758	326342
LPXN	1.1	4.9	16.0	6.2E-05	3.1E-03	ENSG00000110031	9404
DIAPH3	1.9	2.1	16.0	6.3E-05	3.2E-03	ENSG00000139734	81624
H2AFY	1.0	7.2	16.0	6.4E-05	3.2E-03	ENSG00000113648	9555
HEATR3	0.8	4.5	16.0	6.4E-05	3.2E-03	ENSG00000155393	55027
UHRF1	1.7	2.0	15.9	6.8E-05	3.4E-03	ENSG00000034063	NA
GGA2	1.1	6.9	15.9	6.8E-05	3.4E-03	ENSG00000103365	23062
ATP6V0B	1.0	7.0	15.9	6.8E-05	3.4E-03	ENSG00000117410	533
CXorf21	1.4	3.0	15.8	6.9E-05	3.4E-03	ENSG00000120280	80231
MS4A14	1.7	3.7	15.8	7.0E-05	3.4E-03	ENSG00000166928	84689
TNFRSF8	1.4	2.4	15.8	7.0E-05	3.4E-03	ENSG00000120949	943
ACP2	0.8	5.5	15.8	7.0E-05	3.4E-03	ENSG00000134575	53
CD36	1.9	5.8	15.8	7.2E-05	3.4E-03	ENSG00000135218	948
STAC3	1.1	2.8	15.8	7.1E-05	3.4E-03	ENSG00000185482	246329
TRIM14	1.0	4.7	15.8	7.2E-05	3.4E-03	ENSG00000106785	9830
NT5DC2	0.8	6.6	15.7	7.3E-05	3.4E-03	ENSG00000168268	64943
WAS	1.5	5.6	15.7	7.4E-05	3.5E-03	ENSG00000015285	7454
ARHGAP30	1.5	6.7	15.7	7.4E-05	3.5E-03	ENSG00000186517	257106
TCIRG1	1.2	8.2	15.7	7.6E-05	3.5E-03	ENSG00000110719	10312
SCIMP	1.3	3.0	15.7	7.6E-05	3.5E-03	ENSG00000161929	388325
SH3BP2	1.3	7.2	15.6	7.6E-05	3.5E-03	ENSG00000087266	6452
MXD1	1.6	7.5	15.6	7.9E-05	3.6E-03	ENSG00000059728	4084
RMI1	0.9	2.0	15.6	7.9E-05	3.6E-03	ENSG00000178966	80010

PKM	0.8	10.1	15.6	7.9E-05	3.6E-03	ENSG00000067225	5315
CACNA2D4	1.4	3.6	15.6	8.0E-05	3.6E-03	ENSG00000151062	93589
GPR160	1.9	2.9	15.5	8.2E-05	3.7E-03	ENSG00000173890	26996
RNPEP	0.7	5.8	15.5	8.2E-05	3.7E-03	ENSG00000176393	6051
THEMIS2	1.4	6.9	15.5	8.2E-05	3.7E-03	ENSG00000130775	9473
CLPB	0.7	3.7	15.5	8.2E-05	3.7E-03	ENSG00000162129	81570
APBB1IP	1.5	5.3	15.5	8.3E-05	3.7E-03	ENSG00000077420	54518
KCNK13	1.5	1.4	15.4	8.5E-05	3.8E-03	ENSG00000152315	56659
HMGA1	1.4	5.7	15.4	8.6E-05	3.8E-03	ENSG00000137309	3159
ADAM19	1.3	6.3	15.4	8.5E-05	3.8E-03	ENSG00000135074	8728
ARPC3	0.7	6.2	15.4	8.6E-05	3.8E-03	ENSG00000111229	10094
SLC7A7	1.3	5.2	15.4	8.7E-05	3.8E-03	ENSG00000155465	9056
EREG	2.7	5.5	15.4	8.7E-05	3.8E-03	ENSG00000124882	2069
AMPD3	1.4	5.0	15.4	8.8E-05	3.8E-03	ENSG00000133805	100130460
TMEM170B	1.3	4.3	15.4	8.8E-05	3.8E-03	ENSG00000205269	100113407
ALDH3B1	0.9	5.0	15.3	9.1E-05	3.9E-03	ENSG00000006534	221
AQP9	2.2	6.4	15.3	9.2E-05	4.0E-03	ENSG00000103569	366
	1.6	0.9	15.3	9.2E-05	4.0E-03	ENSG00000259807	101928188
NUP62	0.7	5.7	15.3	9.3E-05	4.0E-03	ENSG00000213024	23636
FAM64A	1.8	1.0	15.2	9.5E-05	4.0E-03	ENSG00000129195	54478
ASF1B	1.4	1.9	15.2	9.5E-05	4.0E-03	ENSG00000105011	55723
CASC5	1.8	1.4	15.2	9.9E-05	4.2E-03	ENSG00000137812	57082
FMNL1	1.6	7.2	15.1	9.9E-05	4.2E-03	ENSG00000184922	752
HSPA7	1.5	4.3	15.1	9.9E-05	4.2E-03	ENSG00000225217	3311
	0.9	1.3	15.2	9.9E-05	4.2E-03	ENSG00000228106	NA
LGMN	1.0	8.1	15.1	1.0E-04	4.2E-03	ENSG00000100600	5641
BCAT1	1.6	6.0	15.1	1.0E-04	4.3E-03	ENSG00000060982	586
QSOX1	1.0	8.1	15.1	1.0E-04	4.3E-03	ENSG00000116260	5768
ITGAM	1.3	6.1	15.1	1.0E-04	4.3E-03	ENSG00000169896	3684
GPR97	2.6	6.1	15.1	1.0E-04	4.3E-03	ENSG00000182885	222487
KCNE3	1.3	3.2	15.1	1.0E-04	4.3E-03	ENSG00000175538	10008
C9orf72	1.2	5.5	15.1	1.0E-04	4.3E-03	ENSG00000147894	203228
BTK	1.2	4.2	15.1	1.0E-04	4.3E-03	ENSG00000010671	695
	1.9	4.0	15.0	1.1E-04	4.3E-03	ENSG00000197146	NA
MIR142	1.4	4.2	15.0	1.1E-04	4.3E-03	ENSG00000265206	406934
ABRACL	1.0	3.8	15.0	1.1E-04	4.3E-03	ENSG00000146386	58527
FUOM	0.8	3.3	15.0	1.1E-04	4.3E-03	ENSG00000148803	282969
CEP85	0.7	3.5	15.0	1.1E-04	4.3E-03	ENSG00000130695	64793
VENTX	1.4	3.8	15.0	1.1E-04	4.4E-03	ENSG00000151650	27287
STX6	0.9	5.6	15.0	1.1E-04	4.4E-03	ENSG00000135823	10228
GSAP	1.1	4.4	15.0	1.1E-04	4.4E-03	ENSG00000186088	54103
GRB2	0.8	6.5	14.9	1.1E-04	4.5E-03	ENSG00000177885	2885
B3GNTL1	1.2	4.2	14.9	1.2E-04	4.5E-03	ENSG00000175711	146712
SIRPB2	1.4	4.3	14.8	1.2E-04	4.6E-03	ENSG00000196209	284759
HOMER3	0.9	4.6	14.8	1.2E-04	4.6E-03	ENSG00000051128	9454

LYZ	1.5	7.7	14.7	1.2E-04	4.8E-03	ENSG00000090382	4069
	1.8	2.0	14.7	1.3E-04	4.9E-03	ENSG00000260997	NA
ZNF697	1.1	3.0	14.7	1.3E-04	4.9E-03	ENSG00000143067	90874
ABCD1	0.9	4.7	14.7	1.3E-04	4.9E-03	ENSG00000101986	215
CCR2	1.8	3.5	14.7	1.3E-04	4.9E-03	ENSG00000121807	729230
NUSAP1	1.6	2.6	14.7	1.3E-04	4.9E-03	ENSG00000137804	51203
NPC2	0.9	7.3	14.7	1.3E-04	4.9E-03	ENSG00000119655	10577
GAS2L3	1.3	2.2	14.6	1.3E-04	5.0E-03	ENSG00000139354	283431
	1.1	1.5	14.6	1.3E-04	5.0E-03	ENSG00000240859	100507642
GAPDH	0.9	10.1	14.6	1.3E-04	5.0E-03	ENSG00000111640	2597
LTA4H	0.8	6.4	14.6	1.3E-04	5.0E-03	ENSG00000111144	101928830
SOAT1	0.9	5.8	14.6	1.3E-04	5.0E-03	ENSG00000057252	6646
	1.2	2.9	14.6	1.3E-04	5.0E-03	ENSG00000270055	NA
CCDC109B	1.3	4.7	14.6	1.4E-04	5.1E-03	ENSG00000005059	55013
DSE	0.9	6.6	14.6	1.4E-04	5.1E-03	ENSG00000111817	29940
HMOX1	2.2	8.9	14.6	1.4E-04	5.1E-03	ENSG00000100292	3162
RNF135	0.8	4.9	14.5	1.4E-04	5.1E-03	ENSG00000181481	84282
S100A11	0.8	8.1	14.5	1.4E-04	5.2E-03	ENSG00000163191	6282
PLIN2	2.6	8.9	14.5	1.4E-04	5.2E-03	ENSG00000147872	123
GGA1	0.7	6.8	14.4	1.4E-04	5.3E-03	ENSG00000100083	26088
MYO1F	1.5	7.5	14.4	1.5E-04	5.4E-03	ENSG00000142347	4542
PGK1	0.9	8.4	14.4	1.5E-04	5.4E-03	ENSG00000102144	5230
	2.0	2.3	14.4	1.5E-04	5.4E-03	ENSG00000241732	NA
MYO9B	0.9	8.4	14.4	1.5E-04	5.4E-03	ENSG00000099331	4650
BCL2A1	2.0	5.4	14.4	1.5E-04	5.4E-03	ENSG00000140379	597
C3AR1	1.2	5.5	14.4	1.5E-04	5.4E-03	ENSG00000171860	719
MARCH1	1.2	4.3	14.3	1.5E-04	5.5E-03	ENSG00000145416	55016
TNFSF4	1.5	3.2	14.3	1.5E-04	5.5E-03	ENSG00000117586	7292
FAM49B	1.2	6.0	14.3	1.5E-04	5.5E-03	ENSG00000153310	51571
TOM1	1.1	6.8	14.3	1.6E-04	5.5E-03	ENSG00000100284	10043
LRR1	0.8	2.0	14.3	1.5E-04	5.5E-03	ENSG00000165501	122769
ZNF710	0.7	4.8	14.3	1.6E-04	5.5E-03	ENSG00000140548	374655
PARVG	1.3	6.3	14.3	1.6E-04	5.5E-03	ENSG00000138964	64098
TMEM206	0.9	2.8	14.3	1.6E-04	5.6E-03	ENSG00000065600	55248
PNPLA6	0.8	6.8	14.3	1.6E-04	5.6E-03	ENSG00000032444	10908
PLAC8	1.7	2.0	14.2	1.6E-04	5.6E-03	ENSG00000145287	51316
NAGK	0.6	7.0	14.2	1.6E-04	5.6E-03	ENSG00000124357	55577
FTL	1.2	11.5	14.2	1.6E-04	5.7E-03	ENSG00000087086	2512
	1.5	1.4	14.2	1.7E-04	5.8E-03	ENSG00000218422	NA
ATP6V0D1	0.8	6.8	14.2	1.7E-04	5.8E-03	ENSG00000159720	9114
CYBB	1.0	6.4	14.1	1.7E-04	5.8E-03	ENSG00000165168	1536
PRR11	1.5	1.8	14.1	1.7E-04	5.9E-03	ENSG00000068489	55771
CDC20	1.7	1.9	14.1	1.8E-04	5.9E-03	ENSG00000117399	991
RBM47	1.3	4.5	14.1	1.8E-04	5.9E-03	ENSG00000163694	54502
WNT5A	1.3	3.8	14.1	1.7E-04	5.9E-03	ENSG00000114251	7474

CLN6	0.9	4.6	14.1	1.8E-04	5.9E-03	ENSG00000128973	54982
CREG1	0.8	6.8	14.1	1.8E-04	5.9E-03	ENSG00000143162	8804
ADCY7	1.0	5.1	14.0	1.8E-04	6.0E-03	ENSG00000121281	113
MFS1	0.9	6.8	14.0	1.8E-04	6.0E-03	ENSG00000118855	64747
MTCH2	0.5	5.3	14.0	1.8E-04	6.1E-03	ENSG00000109919	23788
GAL3ST4	0.9	5.2	14.0	1.8E-04	6.1E-03	ENSG00000197093	79690
MYD88	0.9	6.4	14.0	1.8E-04	6.1E-03	ENSG00000172936	4615
SDSL	1.0	4.2	14.0	1.9E-04	6.2E-03	ENSG00000139410	113675
SIGLEC10	1.7	4.3	14.0	1.9E-04	6.2E-03	ENSG00000142512	89790
PLEK2	1.5	2.2	13.9	1.9E-04	6.2E-03	ENSG00000100558	26499
HCK	1.3	6.2	13.9	1.9E-04	6.2E-03	ENSG00000101336	3055
EMP3	0.8	7.1	13.9	1.9E-04	6.2E-03	ENSG00000142227	2014
ARAP1-AS2	1.3	1.0	13.9	1.9E-04	6.3E-03	ENSG00000245148	NA
	1.1	1.0	13.9	2.0E-04	6.4E-03	ENSG00000265743	NA
TLR2	1.6	6.6	13.8	2.0E-04	6.4E-03	ENSG00000137462	7097
CKLF	1.0	2.5	13.8	2.0E-04	6.4E-03	ENSG00000217555	51192
CENPH	1.0	1.1	13.8	2.0E-04	6.4E-03	ENSG00000153044	64946
FAM110A	1.0	2.3	13.8	2.0E-04	6.4E-03	ENSG00000125898	83541
KIF20A	1.9	2.1	13.8	2.1E-04	6.4E-03	ENSG00000112984	10112
LINC00937	1.9	1.8	13.8	2.0E-04	6.4E-03	ENSG00000226091	389634
CSF3R	1.9	8.8	13.8	2.0E-04	6.4E-03	ENSG00000119535	1441
BRIP1	1.6	1.5	13.8	2.0E-04	6.4E-03	ENSG00000136492	83990
LOX	1.5	6.9	13.8	2.0E-04	6.4E-03	ENSG00000113083	4015
AP1B1	0.8	7.2	13.8	2.0E-04	6.4E-03	ENSG00000100280	162
MCM5	0.7	5.2	13.8	2.0E-04	6.4E-03	ENSG00000100297	4174
TXNDC17	0.7	4.2	13.8	2.0E-04	6.4E-03	ENSG00000129235	84817
SGPL1	0.6	6.1	13.8	2.1E-04	6.5E-03	ENSG00000166224	8879
C19orf38	1.5	3.0	13.7	2.1E-04	6.5E-03	ENSG00000214212	255809
TACC3	1.2	4.6	13.7	2.1E-04	6.6E-03	ENSG0000013810	10460
CTSB	1.2	10.9	13.7	2.1E-04	6.6E-03	ENSG00000164733	1508
TPI1	0.9	7.7	13.7	2.1E-04	6.6E-03	ENSG00000111669	7167
SHKBP1	1.1	6.7	13.7	2.2E-04	6.7E-03	ENSG00000160410	92799
CKAP4	0.9	7.5	13.7	2.2E-04	6.7E-03	ENSG00000136026	10970
ARID3A	1.0	4.5	13.6	2.2E-04	6.8E-03	ENSG00000116017	1820
HN1	1.0	5.1	13.6	2.2E-04	6.8E-03	ENSG00000189159	51155
ENO1	1.0	10.0	13.6	2.2E-04	6.9E-03	ENSG00000074800	2023
FGR	1.7	7.1	13.6	2.3E-04	6.9E-03	ENSG00000000938	2268
PTTG1	1.3	2.0	13.6	2.3E-04	6.9E-03	ENSG00000164611	9232
AURKA	1.3	1.8	13.6	2.3E-04	6.9E-03	ENSG00000087586	6790
GALNT6	1.5	3.5	13.6	2.3E-04	7.0E-03	ENSG00000139629	11226
CMTM7	1.2	4.1	13.6	2.3E-04	7.0E-03	ENSG00000153551	112616
IMPDH1	0.9	6.1	13.6	2.3E-04	7.0E-03	ENSG00000106348	3614
ADAM9	0.7	7.5	13.6	2.3E-04	7.0E-03	ENSG00000168615	8754
DAGLB	0.9	5.2	13.5	2.3E-04	7.0E-03	ENSG00000164535	221955
ANLN	1.6	3.6	13.5	2.3E-04	7.0E-03	ENSG00000011426	54443

SMPDL3A	1.0	3.7	13.5	2.4E-04	7.1E-03	ENSG00000172594	10924
MAN2B1	0.8	6.5	13.5	2.4E-04	7.1E-03	ENSG00000104774	4125
CTSA	0.7	7.6	13.5	2.4E-04	7.1E-03	ENSG00000064601	5476
MAPKAPK3	0.9	5.4	13.5	2.4E-04	7.2E-03	ENSG00000114738	7867
TDP2	0.7	5.5	13.5	2.4E-04	7.2E-03	ENSG00000111802	51567
FKBP15	0.7	6.2	13.5	2.4E-04	7.2E-03	ENSG00000119321	23307
KIF4A	1.4	1.6	13.4	2.5E-04	7.3E-03	ENSG00000090889	24137
UCP2	1.2	6.0	13.4	2.5E-04	7.3E-03	ENSG00000175567	7351
ARAP1	0.8	7.9	13.4	2.5E-04	7.3E-03	ENSG00000186635	116985
GIN51	1.1	1.2	13.4	2.5E-04	7.4E-03	ENSG00000101003	9837
SIRPA	1.1	6.7	13.3	2.6E-04	7.7E-03	ENSG00000198053	140885
LHFPL2	1.0	6.9	13.3	2.6E-04	7.7E-03	ENSG00000145685	10184
SDS	2.0	6.7	13.3	2.7E-04	7.7E-03	ENSG00000135094	10993
ADAMTSL4	0.9	6.1	13.3	2.7E-04	7.7E-03	ENSG00000143382	54507
RAD54L	0.9	1.7	13.3	2.7E-04	7.7E-03	ENSG00000085999	8438
FTH1	1.0	7.1	13.3	2.7E-04	7.7E-03	ENSG00000167996	2495
CDCA5	1.4	2.2	13.3	2.7E-04	7.7E-03	ENSG00000146670	113130
IDH1	0.7	5.5	13.2	2.7E-04	7.8E-03	ENSG00000138413	3417
DENND1B	0.9	3.3	13.2	2.7E-04	7.8E-03	ENSG00000213047	163486
PGAM1	0.7	3.8	13.2	2.8E-04	7.8E-03	ENSG00000171314	5223
LIPA	1.1	6.8	13.2	2.8E-04	8.0E-03	ENSG00000107798	3988
CLN3	1.0	2.9	13.2	2.9E-04	8.0E-03	ENSG00000188603	1201
AURKB	1.6	1.5	13.2	2.9E-04	8.0E-03	ENSG00000178999	9212
C11orf89	1.7	2.8	13.1	2.9E-04	8.2E-03	ENSG00000184682	NA
IL10RB	0.9	5.2	13.1	2.9E-04	8.2E-03	ENSG00000243646	3588
UBXN11	1.1	6.4	13.1	3.0E-04	8.2E-03	ENSG00000158062	91544
GNPDA1	0.6	4.9	13.1	3.0E-04	8.3E-03	ENSG00000113552	10007
RAD51AP1	1.4	1.3	13.1	3.0E-04	8.3E-03	ENSG00000111247	10635
FOXM1	1.3	2.6	13.0	3.0E-04	8.4E-03	ENSG00000111206	2305
LUCAT1	2.0	4.3	13.0	3.1E-04	8.5E-03	ENSG00000248323	100505994
HM13	0.7	7.0	13.0	3.1E-04	8.5E-03	ENSG00000101294	81502
DPP3	0.7	4.8	13.0	3.1E-04	8.6E-03	ENSG00000254986	10072
LY86	1.1	3.6	13.0	3.2E-04	8.6E-03	ENSG00000112799	9450
CD52	1.6	4.8	13.0	3.2E-04	8.6E-03	ENSG00000169442	1043
FPR1	1.6	6.7	13.0	3.2E-04	8.6E-03	ENSG00000171051	2357
PIK3R6	1.2	2.6	13.0	3.2E-04	8.6E-03	ENSG00000174083	146850
S100A10	1.2	7.4	13.0	3.2E-04	8.6E-03	ENSG00000197747	6281
PILRA	1.2	4.6	12.9	3.4E-04	9.0E-03	ENSG00000085514	29992
DOCK4	1.2	5.5	12.8	3.4E-04	9.1E-03	ENSG00000128512	9732
PGD	0.9	6.5	12.8	3.4E-04	9.1E-03	ENSG00000142657	5226
P4HB	0.8	9.1	12.8	3.4E-04	9.1E-03	ENSG00000185624	5034
MS4A7	1.2	5.9	12.8	3.5E-04	9.2E-03	ENSG00000166927	58475
DOCK2	1.2	6.1	12.8	3.5E-04	9.2E-03	ENSG00000134516	1794
P4HA1	1.1	6.3	12.8	3.5E-04	9.2E-03	ENSG00000122884	5033
CORO7	1.0	4.5	12.8	3.5E-04	9.2E-03	ENSG00000262246	79585

CYTH4	1.3	6.8	12.8	3.5E-04	9.2E-03	ENSG00000100055	27128
BMF	0.9	4.7	12.8	3.5E-04	9.3E-03	ENSG00000104081	90427
HCST	1.2	3.8	12.7	3.6E-04	9.3E-03	ENSG00000126264	10870
ADRBK2	1.0	4.7	12.7	3.6E-04	9.3E-03	ENSG00000100077	157
SUSD1	0.7	4.4	12.7	3.6E-04	9.3E-03	ENSG00000106868	64420
PFN1	0.6	8.3	12.7	3.6E-04	9.3E-03	ENSG00000108518	5216
ASPM	1.8	1.5	12.7	3.6E-04	9.4E-03	ENSG00000066279	259266
GPCPD1	1.3	7.4	12.7	3.6E-04	9.4E-03	ENSG00000125772	56261
DENND4B	0.9	7.0	12.7	3.7E-04	9.5E-03	ENSG00000198837	9909
FEN1	0.7	3.6	12.7	3.7E-04	9.5E-03	ENSG00000168496	2237
CAPG	1.3	7.1	12.7	3.7E-04	9.5E-03	ENSG00000042493	822
FERMT3	1.1	6.8	12.7	3.7E-04	9.5E-03	ENSG00000149781	83706
GALE	0.7	3.8	12.7	3.7E-04	9.6E-03	ENSG00000117308	2582
TREML1	1.5	2.4	12.6	3.8E-04	9.6E-03	ENSG00000161911	340205
C5AR1	1.3	7.6	12.6	3.8E-04	9.6E-03	ENSG00000197405	728
TLR6	1.1	3.6	12.6	3.8E-04	9.6E-03	ENSG00000174130	10333
GLUL	1.1	10.1	12.6	3.8E-04	9.6E-03	ENSG00000135821	2752
EEPD1	1.0	4.3	12.6	3.8E-04	9.7E-03	ENSG00000122547	80820
ITGB2	1.2	7.9	12.6	3.9E-04	9.8E-03	ENSG00000160255	3689
RHBDP2	1.2	6.0	12.6	3.9E-04	9.9E-03	ENSG00000129667	79651
LYL1	1.0	3.6	12.6	3.9E-04	9.9E-03	ENSG00000104903	4066
STK10	1.3	6.8	12.5	4.1E-04	1.0E-02	ENSG00000072786	6793
ACRBP	1.2	2.7	12.5	4.1E-04	1.0E-02	ENSG00000111644	84519
PLA2G7	1.8	3.8	12.5	4.2E-04	1.0E-02	ENSG00000146070	7941
TLR1	1.1	4.1	12.5	4.2E-04	1.0E-02	ENSG00000174125	7096
TROAP	1.6	1.5	12.4	4.2E-04	1.0E-02	ENSG00000135451	10024
DAPK1	1.0	5.9	12.4	4.2E-04	1.0E-02	ENSG00000196730	1612
ATP6V1F	0.7	5.7	12.4	4.2E-04	1.0E-02	ENSG00000128524	101927180
FBN2	1.8	3.3	12.4	4.3E-04	1.0E-02	ENSG00000138829	2201
HIST1H2BD	1.0	1.0	12.4	4.3E-04	1.1E-02	ENSG00000158373	3017
KLHDC7B	1.5	1.0	12.4	4.3E-04	1.1E-02	ENSG00000130487	113730
CCL20	3.0	4.0	12.4	4.4E-04	1.1E-02	ENSG00000115009	6364
PTPN6	1.1	6.1	12.3	4.5E-04	1.1E-02	ENSG00000111679	5777
RIPK3	1.1	3.3	12.3	4.5E-04	1.1E-02	ENSG00000129465	11035
PDIA6	0.6	6.9	12.3	4.5E-04	1.1E-02	ENSG00000143870	10130
EMR2	1.4	5.3	12.3	4.5E-04	1.1E-02	ENSG00000127507	30817
P4HA2	0.9	6.1	12.3	4.5E-04	1.1E-02	ENSG00000072682	101927705
MKI67	1.7	3.6	12.3	4.6E-04	1.1E-02	ENSG00000148773	4288
MIR210HG	2.3	3.8	12.2	4.7E-04	1.1E-02	ENSG00000247095	100506211
YIF1B	0.7	5.4	12.2	4.7E-04	1.1E-02	ENSG00000167645	90522
FANCA	1.1	2.7	12.2	4.8E-04	1.2E-02	ENSG00000187741	2175
ACADVL	0.7	9.0	12.1	5.0E-04	1.2E-02	ENSG00000072778	37
BEST1	1.2	4.6	12.1	5.0E-04	1.2E-02	ENSG00000167995	7439
RAB42	1.5	1.9	12.1	5.1E-04	1.2E-02	ENSG00000188060	115273
ABCA1	1.2	6.5	12.1	5.1E-04	1.2E-02	ENSG00000165029	19

DEF6	1.1	5.0	12.1	5.1E-04	1.2E-02	ENSG00000023892	50619
KCNK6	0.9	4.2	12.1	5.1E-04	1.2E-02	ENSG00000099337	9424
GNS	0.6	7.4	12.1	5.1E-04	1.2E-02	ENSG00000135677	2799
CEP55	1.8	2.2	12.1	5.2E-04	1.2E-02	ENSG00000138180	55165
NLRP3	1.4	5.1	12.1	5.2E-04	1.2E-02	ENSG00000162711	114548
FTH1P7	1.1	0.7	12.0	5.2E-04	1.2E-02	ENSG00000232187	NA
RASGRP4	1.4	4.4	12.0	5.2E-04	1.2E-02	ENSG00000171777	115727
LST1	1.2	5.0	12.0	5.2E-04	1.2E-02	ENSG00000204482	7940
ARPC4	0.6	6.5	12.0	5.3E-04	1.2E-02	ENSG00000241553	10093
	1.1	0.7	12.0	5.5E-04	1.3E-02	ENSG00000256546	100506691
RIN3	1.1	6.0	11.9	5.5E-04	1.3E-02	ENSG00000100599	79890
GAPT	1.3	2.6	11.9	5.5E-04	1.3E-02	ENSG00000175857	202309
EFTUD1	0.5	4.0	11.9	5.5E-04	1.3E-02	ENSG00000140598	79631
GAPDHP1	1.0	1.1	11.9	5.6E-04	1.3E-02	ENSG00000228232	NA
SLC35F6	0.5	5.4	11.9	5.6E-04	1.3E-02	ENSG00000213699	54978
EMR1	1.3	1.9	11.9	5.7E-04	1.3E-02	ENSG00000174837	2015
GMIP	1.1	5.7	11.9	5.7E-04	1.3E-02	ENSG00000089639	51291
TBC1D7	1.0	3.5	11.9	5.7E-04	1.3E-02	ENSG00000145979	51256
CENPF	1.8	2.8	11.9	5.7E-04	1.3E-02	ENSG00000117724	1063
ST20	1.3	1.8	11.9	5.7E-04	1.3E-02	ENSG00000180953	400410
PLCB2	1.0	6.6	11.8	5.8E-04	1.3E-02	ENSG00000137841	5330
GPX1	0.8	7.2	11.8	5.9E-04	1.3E-02	ENSG00000233276	2876
CIB1	0.8	6.5	11.8	5.8E-04	1.3E-02	ENSG00000185043	10519
CSMD2	1.5	3.0	11.8	5.9E-04	1.3E-02	ENSG00000121904	114784
OSTF1	0.7	5.3	11.7	6.1E-04	1.3E-02	ENSG00000134996	26578
PPBP	2.0	4.6	11.7	6.1E-04	1.3E-02	ENSG00000163736	5473
TMEM86A	1.0	3.4	11.7	6.2E-04	1.4E-02	ENSG00000151117	144110
NCAPH	1.3	1.3	11.7	6.2E-04	1.4E-02	ENSG00000121152	23397
TEC	0.9	1.7	11.7	6.3E-04	1.4E-02	ENSG00000135605	7006
	1.0	2.9	11.7	6.3E-04	1.4E-02	ENSG00000262580	101929888
AP2S1	0.6	5.9	11.7	6.4E-04	1.4E-02	ENSG00000042753	1175
COL6A3	1.4	10.1	11.6	6.5E-04	1.4E-02	ENSG00000163359	1293
KCNN4	0.9	5.2	11.6	6.5E-04	1.4E-02	ENSG00000104783	3783
LGALS1	0.7	9.6	11.6	6.5E-04	1.4E-02	ENSG00000100097	3956
CTSS	1.1	7.5	11.6	6.5E-04	1.4E-02	ENSG00000163131	1520
TMEM45B	1.7	1.7	11.6	6.6E-04	1.4E-02	ENSG00000151715	120224
CFD	1.2	3.0	11.6	6.6E-04	1.4E-02	ENSG00000197766	1675
VAV3	1.1	3.4	11.6	6.7E-04	1.4E-02	ENSG00000134215	10451
CYBA	1.0	6.9	11.6	6.7E-04	1.4E-02	ENSG00000051523	1535
C17orf53	0.9	0.9	11.6	6.7E-04	1.4E-02	ENSG00000125319	78995
NOP10	0.7	5.5	11.6	6.7E-04	1.4E-02	ENSG00000182117	55505
DOK1	0.6	4.8	11.5	6.8E-04	1.5E-02	ENSG00000115325	1796
MELK	1.7	1.9	11.5	6.9E-04	1.5E-02	ENSG00000165304	9833
GPSM3	1.2	6.0	11.5	6.9E-04	1.5E-02	ENSG00000213654	63940
MPEG1	1.1	6.3	11.5	6.9E-04	1.5E-02	ENSG00000197629	219972

RHOG	0.8	6.1	11.5	6.9E-04	1.5E-02	ENSG00000177105	391
GLB1	0.6	5.6	11.5	7.0E-04	1.5E-02	ENSG00000170266	643853
SPC24	1.5	0.9	11.5	7.0E-04	1.5E-02	ENSG00000161888	147841
CDC6	1.4	2.3	11.5	7.1E-04	1.5E-02	ENSG00000094804	990
IL10RA	1.0	6.6	11.5	7.1E-04	1.5E-02	ENSG00000110324	3587
TMEM171	1.3	0.9	11.4	7.2E-04	1.5E-02	ENSG00000157111	134285
ATF5	0.9	4.8	11.5	7.1E-04	1.5E-02	ENSG00000169136	22809
RNASEH2A	0.7	2.6	11.4	7.2E-04	1.5E-02	ENSG00000104889	10535
RNF130	0.6	6.5	11.5	7.1E-04	1.5E-02	ENSG00000113269	55819
PFN1P1	0.6	5.2	11.4	7.2E-04	1.5E-02	ENSG00000233328	NA
IRF8	1.1	5.0	11.4	7.2E-04	1.5E-02	ENSG00000140968	3394
M6PR	0.5	5.9	11.4	7.2E-04	1.5E-02	ENSG00000003056	4074
	1.3	2.7	11.4	7.3E-04	1.5E-02	ENSG00000269609	100505761
CALR	0.5	9.1	11.4	7.3E-04	1.5E-02	ENSG00000179218	811
CD180	1.4	3.0	11.4	7.3E-04	1.5E-02	ENSG00000134061	4064
BRI3	0.7	5.9	11.4	7.3E-04	1.5E-02	ENSG00000164713	25798
EPHB2	1.2	3.3	11.4	7.4E-04	1.5E-02	ENSG00000133216	2048
LCP1	1.3	8.1	11.4	7.5E-04	1.5E-02	ENSG00000136167	3936
NRIP3	1.0	3.6	11.4	7.5E-04	1.5E-02	ENSG00000175352	56675
MPDU1	0.7	5.2	11.3	7.5E-04	1.5E-02	ENSG00000129255	9526
POR	0.8	6.7	11.3	7.6E-04	1.5E-02	ENSG00000127948	5447
EDEM2	0.6	5.0	11.3	7.7E-04	1.5E-02	ENSG00000088298	55741
SESN2	0.8	5.3	11.3	7.7E-04	1.5E-02	ENSG00000130766	83667
WDR81	0.6	5.4	11.3	7.7E-04	1.5E-02	ENSG00000167716	124997
GARS	0.7	6.7	11.3	7.8E-04	1.5E-02	ENSG00000106105	2617
FAM214B	0.8	6.2	11.3	7.8E-04	1.6E-02	ENSG00000005238	80256
DPEP2	1.3	4.4	11.3	7.8E-04	1.6E-02	ENSG00000167261	64174
PYCARD	1.0	3.4	11.3	7.9E-04	1.6E-02	ENSG00000103490	29108
DGAT2	1.7	3.3	11.3	7.9E-04	1.6E-02	ENSG00000062282	84649
KCNE1	1.6	2.0	11.3	7.9E-04	1.6E-02	ENSG00000180509	3753
VDR	1.5	4.6	11.3	7.9E-04	1.6E-02	ENSG00000111424	7421
DYNLT1	0.6	5.8	11.2	8.0E-04	1.6E-02	ENSG00000146425	6993
MLX	0.5	5.3	11.2	8.0E-04	1.6E-02	ENSG00000108788	6945
NAGA	0.6	5.8	11.2	8.0E-04	1.6E-02	ENSG00000198951	4668
ESRRA	0.5	4.9	11.2	8.1E-04	1.6E-02	ENSG00000173153	2101
TOR2A	0.7	3.8	11.2	8.1E-04	1.6E-02	ENSG00000160404	27433
FAM195A	0.8	3.4	11.2	8.1E-04	1.6E-02	ENSG00000172366	84331
LILRA2	1.5	3.9	11.2	8.2E-04	1.6E-02	ENSG00000239998	11027
DTL	1.5	1.3	11.2	8.3E-04	1.6E-02	ENSG00000143476	51514
C5orf66	1.3	1.3	11.2	8.4E-04	1.6E-02	ENSG00000224186	100996485
HEXB	0.6	6.7	11.1	8.5E-04	1.6E-02	ENSG00000049860	3074
	1.0	1.5	11.1	8.5E-04	1.6E-02	ENSG00000224950	NA
RNASE1	1.3	7.7	11.1	8.6E-04	1.7E-02	ENSG00000129538	6035
CXorf38	0.6	3.5	11.1	8.8E-04	1.7E-02	ENSG00000185753	159013
SFXN1	0.5	4.9	11.1	8.8E-04	1.7E-02	ENSG00000164466	94081

CENPW	0.9	1.3	11.0	8.9E-04	1.7E-02	ENSG00000203760	387103
CYB561D2	0.7	3.8	11.1	8.9E-04	1.7E-02	ENSG00000114395	11068
DOCK8	1.1	6.3	11.0	8.9E-04	1.7E-02	ENSG00000107099	81704
P2RY1	1.7	1.7	11.0	9.0E-04	1.7E-02	ENSG00000169860	5028
	1.3	1.0	11.0	9.0E-04	1.7E-02	ENSG00000268518	100506114
HCLS1	1.2	7.4	11.0	9.0E-04	1.7E-02	ENSG00000180353	3059
PLEK	1.1	6.3	11.0	9.0E-04	1.7E-02	ENSG00000115956	5341
PRR13	0.8	4.3	11.0	9.0E-04	1.7E-02	ENSG00000205352	54458
UBE2T	1.0	1.7	11.0	9.0E-04	1.7E-02	ENSG00000077152	29089
CCNF	0.9	2.1	11.0	9.1E-04	1.7E-02	ENSG00000162063	899
ERI1	0.7	3.9	11.0	9.1E-04	1.7E-02	ENSG00000104626	90459
TMEM51	1.0	4.5	11.0	9.2E-04	1.7E-02	ENSG00000171729	55092
EFTUD2	0.5	6.2	11.0	9.2E-04	1.7E-02	ENSG00000108883	9343
ALDOA	0.7	9.5	11.0	9.3E-04	1.7E-02	ENSG00000149925	226
TDP1	0.6	3.3	11.0	9.3E-04	1.7E-02	ENSG00000042088	55775
MIOS	0.6	4.3	11.0	9.3E-04	1.7E-02	ENSG00000164654	54468
PRG4	2.2	8.5	10.9	9.4E-04	1.7E-02	ENSG00000116690	10216
MAD2L1	1.0	1.8	11.0	9.4E-04	1.7E-02	ENSG00000164109	4085
RNF166	0.9	5.6	10.9	9.4E-04	1.7E-02	ENSG00000158717	115992
VASH1	0.7	6.3	10.9	9.4E-04	1.7E-02	ENSG00000071246	22846
KIAA1524	0.8	1.8	10.9	9.7E-04	1.8E-02	ENSG00000163507	57650
NID2	1.2	6.6	10.9	9.7E-04	1.8E-02	ENSG00000087303	22795
CDCA7	1.3	1.2	10.9	9.8E-04	1.8E-02	ENSG00000144354	83879
SLC36A4	1.0	4.2	10.9	9.8E-04	1.8E-02	ENSG00000180773	120103
SLC31A1	0.6	5.4	10.9	9.8E-04	1.8E-02	ENSG00000136868	1317
CTSC	1.0	7.3	10.9	9.9E-04	1.8E-02	ENSG00000109861	1075
MGAT4A	1.0	5.5	10.8	9.9E-04	1.8E-02	ENSG00000071073	11320
C19orf10	0.7	6.3	10.8	1.0E-03	1.8E-02	ENSG00000074842	56005
MFSD7	0.7	4.3	10.8	1.0E-03	1.8E-02	ENSG00000169026	84179
WDR62	1.0	2.1	10.8	1.0E-03	1.8E-02	ENSG00000075702	284403
	0.9	1.4	10.8	1.0E-03	1.8E-02	ENSG00000268913	NA
MS4A6A	1.1	6.1	10.8	1.0E-03	1.8E-02	ENSG00000110077	64231
AMMECR1	0.7	3.1	10.8	1.0E-03	1.8E-02	ENSG00000101935	9949
H3F3AP4	0.8	2.4	10.8	1.0E-03	1.8E-02	ENSG00000235655	440926
NCLN	0.5	6.1	10.8	1.0E-03	1.8E-02	ENSG00000125912	56926
SECTM1	1.0	4.6	10.8	1.0E-03	1.8E-02	ENSG00000141574	6398
SCO2	1.0	6.1	10.8	1.0E-03	1.8E-02	ENSG00000130489	9997
LIMS1	0.8	6.3	10.8	1.0E-03	1.8E-02	ENSG00000169756	100288695
IFNAR2	0.6	4.5	10.8	1.0E-03	1.9E-02	ENSG00000159110	3455
TREM1	1.7	6.1	10.8	1.0E-03	1.9E-02	ENSG00000124731	54210
XPNPEP1	0.5	5.9	10.8	1.0E-03	1.9E-02	ENSG00000108039	7511
HIF1A	1.0	8.3	10.7	1.1E-03	1.9E-02	ENSG00000100644	3091
CPVL	0.9	5.7	10.7	1.1E-03	1.9E-02	ENSG00000106066	54504
LYN	1.0	6.0	10.7	1.1E-03	1.9E-02	ENSG00000254087	4067
NEK6	0.7	5.9	10.7	1.1E-03	1.9E-02	ENSG00000119408	10783

FANCI	0.9	3.2	10.6	1.1E-03	1.9E-02	ENSG00000140525	55215
CKAP2	0.8	3.3	10.6	1.1E-03	1.9E-02	ENSG00000136108	26586
RENBP	0.7	4.8	10.6	1.1E-03	1.9E-02	ENSG00000102032	5973
FCN1	1.5	6.0	10.6	1.1E-03	1.9E-02	ENSG00000085265	2219
ST8SIA4	1.2	3.9	10.6	1.1E-03	2.0E-02	ENSG00000113532	7903
ESPL1	1.1	2.4	10.6	1.1E-03	2.0E-02	ENSG00000135476	9700
EZH2	0.8	3.1	10.6	1.1E-03	2.0E-02	ENSG00000106462	2146
SPPL2A	0.7	5.0	10.6	1.1E-03	2.0E-02	ENSG00000138600	84888
SLC25A37	1.4	7.7	10.6	1.1E-03	2.0E-02	ENSG00000147454	51312
OPN3	0.8	2.0	10.6	1.1E-03	2.0E-02	ENSG00000054277	23596
BMP2K	1.0	3.9	10.6	1.1E-03	2.0E-02	ENSG00000138756	55589
PCK2	0.7	4.4	10.6	1.1E-03	2.0E-02	ENSG00000100889	5106
SIRPB1	1.6	3.6	10.6	1.2E-03	2.0E-02	ENSG00000101307	100653194
IFNGR2	0.9	6.4	10.6	1.2E-03	2.0E-02	ENSG00000159128	3460
CENPE	1.3	1.6	10.5	1.2E-03	2.0E-02	ENSG00000138778	1062
CRYBB1	1.3	0.9	10.5	1.2E-03	2.0E-02	ENSG00000100122	1414
	1.1	0.7	10.5	1.2E-03	2.0E-02	ENSG00000254419	NA
SATB1	0.9	5.6	10.5	1.2E-03	2.0E-02	ENSG00000182568	6304
TYK2	0.7	7.4	10.5	1.2E-03	2.0E-02	ENSG00000105397	7297
C7orf43	0.7	4.9	10.5	1.2E-03	2.0E-02	ENSG00000146826	55262
SSR1	0.5	7.1	10.5	1.2E-03	2.0E-02	ENSG00000124783	6745
TRPM2	1.0	4.5	10.5	1.2E-03	2.1E-02	ENSG00000142185	7226
RTCA	0.5	4.7	10.5	1.2E-03	2.1E-02	ENSG00000137996	8634
LONP1	0.7	6.5	10.4	1.2E-03	2.1E-02	ENSG00000196365	9361
ORC6	1.0	1.5	10.4	1.2E-03	2.1E-02	ENSG00000091651	23594
MGAT1	0.7	8.1	10.4	1.3E-03	2.1E-02	ENSG00000131446	4245
GBA	0.5	5.0	10.4	1.3E-03	2.1E-02	ENSG00000177628	2629
CCDC167	0.7	2.9	10.4	1.3E-03	2.1E-02	ENSG00000198937	154467
ERO1L	1.3	6.4	10.4	1.3E-03	2.1E-02	ENSG00000197930	30001
VDAC1	0.5	6.1	10.4	1.3E-03	2.1E-02	ENSG00000213585	7416
XRCC4	0.7	3.1	10.4	1.3E-03	2.1E-02	ENSG00000152422	7518
UBXN2B	0.8	4.9	10.4	1.3E-03	2.1E-02	ENSG00000215114	137886
IKBKE	0.8	3.9	10.4	1.3E-03	2.1E-02	ENSG00000143466	9641
VIM-AS1	1.0	2.8	10.4	1.3E-03	2.1E-02	ENSG00000229124	100507347
BCKDK	0.9	6.0	10.4	1.3E-03	2.1E-02	ENSG00000103507	10295
RNPEPL1	0.7	6.5	10.4	1.3E-03	2.1E-02	ENSG00000142327	57140
CXCR4	1.6	8.0	10.3	1.3E-03	2.1E-02	ENSG00000121966	7852
CD72	1.2	3.6	10.3	1.3E-03	2.2E-02	ENSG00000137101	971
TK1	1.2	3.4	10.3	1.3E-03	2.2E-02	ENSG00000167900	7083
ATP6V1B2	0.7	7.3	10.3	1.3E-03	2.2E-02	ENSG00000147416	526
PTPRJ	0.8	5.1	10.3	1.3E-03	2.2E-02	ENSG00000149177	5795
LCP2	1.1	6.0	10.3	1.3E-03	2.2E-02	ENSG00000043462	3937
EVI2A	1.2	3.7	10.3	1.3E-03	2.2E-02	ENSG00000126860	2123
C17orf62	0.6	6.7	10.3	1.4E-03	2.2E-02	ENSG00000178927	79415
RELT	1.3	5.4	10.3	1.4E-03	2.2E-02	ENSG00000054967	84957

	1.1	2.0	10.2	1.4E-03	2.2E-02	ENSG00000235245	NA
FTH1P8	1.1	0.6	10.2	1.4E-03	2.2E-02	ENSG00000219507	NA
PLAUR	1.4	8.1	10.2	1.4E-03	2.2E-02	ENSG00000011422	5329
ACTR2	0.5	7.8	10.2	1.4E-03	2.2E-02	ENSG00000138071	10097
SYTL3	1.8	5.0	10.2	1.4E-03	2.2E-02	ENSG00000164674	94120
	1.0	1.1	10.2	1.4E-03	2.2E-02	ENSG00000261827	NA
NBEAL2	1.0	7.3	10.2	1.4E-03	2.2E-02	ENSG00000160796	23218
CISD2	0.6	3.5	10.2	1.4E-03	2.3E-02	ENSG00000145354	493856
CHFR	0.5	5.3	10.1	1.5E-03	2.3E-02	ENSG00000072609	55743
GNA13	0.8	6.8	10.1	1.5E-03	2.3E-02	ENSG00000120063	10672
TREM2	1.4	4.9	10.1	1.5E-03	2.3E-02	ENSG00000095970	54209
CCNA2	0.8	2.3	10.1	1.5E-03	2.3E-02	ENSG00000145386	890
NA	0.6	3.6	10.1	1.5E-03	2.3E-02	ENSG00000172070	NA
WIPF1	0.6	6.9	10.1	1.5E-03	2.3E-02	ENSG00000115935	7456
TET3	0.9	3.7	10.1	1.5E-03	2.3E-02	ENSG00000187605	200424
CAPZA1	0.7	6.8	10.1	1.5E-03	2.3E-02	ENSG00000116489	829
CEP170	0.7	4.9	10.1	1.5E-03	2.3E-02	ENSG00000143702	9859
TOR4A	0.8	4.1	10.1	1.5E-03	2.4E-02	ENSG00000198113	54863
GAA	0.8	7.0	10.1	1.5E-03	2.4E-02	ENSG00000171298	2548
CLIC1	0.6	8.4	10.1	1.5E-03	2.4E-02	ENSG00000213719	1192
HLA-DMB	1.0	5.8	10.0	1.6E-03	2.4E-02	ENSG00000242574	3109
EPB41L3	1.0	6.3	10.0	1.6E-03	2.4E-02	ENSG00000082397	23136
GSS	0.5	5.1	10.0	1.6E-03	2.4E-02	ENSG00000100983	2937
SH3D21	1.4	5.0	10.0	1.6E-03	2.4E-02	ENSG00000214193	79729
PLA2G15	0.7	5.0	10.0	1.6E-03	2.4E-02	ENSG00000103066	23659
SPOCK1	1.2	6.0	10.0	1.6E-03	2.4E-02	ENSG00000152377	6695
SIPA1	0.7	6.6	10.0	1.6E-03	2.4E-02	ENSG00000213445	6494
CCDC88B	1.1	6.0	10.0	1.6E-03	2.4E-02	ENSG00000168071	283234
BTG1	1.0	7.7	10.0	1.6E-03	2.4E-02	ENSG00000133639	694
NFAM1	1.2	5.7	9.9	1.6E-03	2.5E-02	ENSG00000235568	150372
PDIA4	0.6	7.1	9.9	1.6E-03	2.5E-02	ENSG00000155660	9601
SPP1	1.9	9.6	9.9	1.6E-03	2.5E-02	ENSG00000118785	6696
INPP5D	1.1	6.3	9.9	1.6E-03	2.5E-02	ENSG00000168918	3635
HIST1H2BK	0.7	3.2	9.9	1.7E-03	2.5E-02	ENSG00000197903	85236
CNEP1R1	0.6	4.1	9.9	1.7E-03	2.5E-02	ENSG00000205423	255919
FGD2	1.0	5.0	9.9	1.7E-03	2.5E-02	ENSG00000146192	221472
TNFSF13B	0.9	4.2	9.9	1.7E-03	2.5E-02	ENSG00000102524	10673
C20orf24	0.7	1.5	9.9	1.7E-03	2.5E-02	ENSG00000101084	55969
PCED1B-AS1	0.9	3.4	9.9	1.7E-03	2.5E-02	ENSG00000247774	100233209
SFT2D1	0.5	4.8	9.9	1.7E-03	2.5E-02	ENSG00000198818	113402
FAM102B	0.9	5.0	9.9	1.7E-03	2.5E-02	ENSG00000162636	284611
TMEM251	0.6	2.5	9.9	1.7E-03	2.5E-02	ENSG00000153485	26175
STK32B	1.0	2.3	9.8	1.8E-03	2.6E-02	ENSG00000152953	55351
PLK1	0.9	2.6	9.8	1.8E-03	2.6E-02	ENSG00000166851	5347
CDK1	1.2	2.5	9.8	1.8E-03	2.6E-02	ENSG00000170312	983

ADORA3	1.4	3.7	9.8	1.8E-03	2.7E-02	ENSG00000121933	140
TPRG1	0.8	1.8	9.7	1.8E-03	2.7E-02	ENSG00000188001	285386
CDKN3	1.1	0.9	9.7	1.8E-03	2.7E-02	ENSG00000100526	1033
TLR5	0.8	2.9	9.7	1.8E-03	2.7E-02	ENSG00000187554	7100
IGF2BP2	0.9	4.2	9.7	1.8E-03	2.7E-02	ENSG00000073792	10644
	0.9	0.4	9.7	1.8E-03	2.7E-02	ENSG00000235609	NA
PI15	2.7	4.8	9.7	1.8E-03	2.7E-02	ENSG00000137558	51050
FPR2	1.6	4.1	9.7	1.8E-03	2.7E-02	ENSG00000171049	2358
RAB32	0.6	5.0	9.7	1.8E-03	2.7E-02	ENSG00000118508	10981
SPG21	0.4	5.9	9.7	1.9E-03	2.7E-02	ENSG00000090487	51324
MPHOSPH6	0.5	3.6	9.7	1.9E-03	2.8E-02	ENSG00000135698	10200
RAD51	1.1	1.2	9.6	1.9E-03	2.8E-02	ENSG00000051180	5888
CSF2RA	1.0	4.4	9.6	1.9E-03	2.8E-02	ENSG00000198223	1438
DHX34	0.9	5.6	9.6	1.9E-03	2.8E-02	ENSG00000134815	9704
RASGEF1B	0.9	5.3	9.6	1.9E-03	2.8E-02	ENSG00000138670	153020
C6orf62	0.6	7.4	9.6	1.9E-03	2.8E-02	ENSG00000112308	81688
SNX10	1.3	3.9	9.6	1.9E-03	2.8E-02	ENSG00000086300	29887
SLC4A8	1.1	1.9	9.6	1.9E-03	2.8E-02	ENSG00000050438	9498
NABP1	1.0	5.6	9.6	1.9E-03	2.8E-02	ENSG00000173559	64859
ZNF267	1.0	2.3	9.6	1.9E-03	2.8E-02	ENSG00000185947	10308
DARS2	0.5	3.5	9.6	2.0E-03	2.8E-02	ENSG00000117593	55157
DBNL	0.7	7.6	9.6	2.0E-03	2.8E-02	ENSG00000136279	102466985
PKMYT1	1.3	1.3	9.6	2.0E-03	2.8E-02	ENSG00000127564	9088
SLC8B1	0.6	6.2	9.6	2.0E-03	2.8E-02	ENSG00000089060	80024
CNDP2	0.7	6.8	9.5	2.0E-03	2.8E-02	ENSG00000133313	55748
GBGT1	0.8	3.9	9.5	2.0E-03	2.9E-02	ENSG00000148288	26301
TUBGCP2	0.7	6.5	9.5	2.0E-03	2.9E-02	ENSG00000130640	10844
GBP5	1.2	4.7	9.5	2.0E-03	2.9E-02	ENSG00000154451	115362
GRINA	0.7	7.2	9.5	2.0E-03	2.9E-02	ENSG00000178719	2907
SIGLEC16	1.4	1.5	9.5	2.1E-03	2.9E-02	ENSG00000161643	NA
SH2B2	1.2	2.2	9.5	2.1E-03	2.9E-02	ENSG00000160999	10603
ADM2	1.5	2.2	9.5	2.1E-03	2.9E-02	ENSG00000128165	79924
NDC80	1.3	1.5	9.5	2.1E-03	2.9E-02	ENSG00000080986	10403
PLD2	0.6	6.0	9.5	2.1E-03	2.9E-02	ENSG00000129219	5338
SLC25A20	0.6	4.2	9.5	2.1E-03	2.9E-02	ENSG00000178537	788
DNM2	0.7	7.7	9.5	2.1E-03	2.9E-02	ENSG00000079805	1785
	1.8	2.4	9.4	2.1E-03	2.9E-02	ENSG00000230838	NA
CASP7	0.5	4.5	9.4	2.1E-03	2.9E-02	ENSG00000165806	840
DNASE2	0.6	5.4	9.4	2.1E-03	2.9E-02	ENSG00000105612	1777
KIF14	1.7	1.0	9.4	2.1E-03	3.0E-02	ENSG00000118193	9928
RN7SL138P	1.0	0.4	9.4	2.1E-03	3.0E-02	ENSG00000266274	NA
RGS10	0.9	4.2	9.4	2.1E-03	3.0E-02	ENSG00000148908	6001
LPCAT1	1.0	7.1	9.4	2.2E-03	3.0E-02	ENSG00000153395	79888
MSR1	1.2	6.6	9.4	2.2E-03	3.0E-02	ENSG00000038945	4481
KLHL17	0.5	4.3	9.4	2.2E-03	3.0E-02	ENSG00000187961	339451

ARID3B	0.8	3.0	9.4	2.2E-03	3.0E-02	ENSG00000179361	10620
AGTRAP	0.7	5.4	9.4	2.2E-03	3.0E-02	ENSG00000177674	57085
CSK	0.6	6.2	9.4	2.2E-03	3.0E-02	ENSG00000103653	1445
SLC16A6	1.2	4.4	9.4	2.2E-03	3.0E-02	ENSG00000108932	9120
ARPC5	0.5	7.3	9.4	2.2E-03	3.0E-02	ENSG00000162704	10092
PLK4	0.9	1.3	9.3	2.2E-03	3.0E-02	ENSG00000142731	10733
OAZ1	0.6	8.8	9.3	2.2E-03	3.0E-02	ENSG00000104904	4946
MOB3A	0.8	6.3	9.3	2.2E-03	3.0E-02	ENSG00000172081	126308
TRPC4AP	0.5	7.0	9.3	2.2E-03	3.0E-02	ENSG00000100991	26133
SCAMP2	0.5	6.3	9.3	2.3E-03	3.0E-02	ENSG00000140497	10066
C1orf85	0.6	5.0	9.3	2.3E-03	3.1E-02	ENSG00000198715	112770
C9orf139	1.3	1.2	9.3	2.3E-03	3.1E-02	ENSG00000180539	401563
PPP1CA	0.5	6.2	9.3	2.3E-03	3.1E-02	ENSG00000172531	5499
KIF15	1.0	1.0	9.3	2.3E-03	3.1E-02	ENSG00000163808	56992
TBL2	0.5	5.1	9.3	2.3E-03	3.1E-02	ENSG00000106638	26608
WRAP53	0.5	3.4	9.3	2.3E-03	3.1E-02	ENSG00000141499	55135
MYBL2	1.6	2.5	9.3	2.3E-03	3.1E-02	ENSG00000101057	4605
SRGN	1.0	9.3	9.3	2.3E-03	3.1E-02	ENSG00000122862	5552
CFL1	0.5	9.0	9.2	2.4E-03	3.1E-02	ENSG00000172757	1072
SGK3	0.6	3.2	9.2	2.4E-03	3.1E-02	ENSG00000104205	100533105
LBR	0.8	5.4	9.2	2.4E-03	3.2E-02	ENSG00000143815	3930
CENPO	0.6	2.7	9.2	2.4E-03	3.2E-02	ENSG00000138092	79172
TTLL4	0.6	4.6	9.2	2.4E-03	3.2E-02	ENSG00000135912	9654
YIPF1	0.5	4.5	9.2	2.4E-03	3.2E-02	ENSG00000058799	54432
APEX2	0.4	4.3	9.2	2.4E-03	3.2E-02	ENSG00000169188	27301
GPR137B	0.8	4.9	9.2	2.5E-03	3.2E-02	ENSG00000077585	7107
ATG16L2	0.9	7.4	9.1	2.5E-03	3.3E-02	ENSG00000168010	89849
PNKD	0.7	5.9	9.1	2.5E-03	3.3E-02	ENSG00000127838	25953
GPX7	0.7	4.1	9.1	2.5E-03	3.3E-02	ENSG00000116157	2882
FMN1	1.1	3.6	9.1	2.5E-03	3.3E-02	ENSG00000248905	342184
NCAPG2	0.6	3.5	9.1	2.5E-03	3.3E-02	ENSG00000146918	54892
SPDL1	0.7	3.3	9.1	2.6E-03	3.3E-02	ENSG00000040275	54908
RREB1	0.6	5.4	9.1	2.6E-03	3.3E-02	ENSG00000124782	6239
	1.0	0.8	9.1	2.6E-03	3.3E-02	ENSG00000269899	NA
NACC1	0.5	5.7	9.1	2.6E-03	3.3E-02	ENSG00000160877	112939
SSR2	0.5	7.2	9.1	2.6E-03	3.4E-02	ENSG00000163479	6746
PLOD1	0.9	8.2	9.1	2.6E-03	3.4E-02	ENSG00000083444	5351
RASAL3	1.2	5.2	9.1	2.6E-03	3.4E-02	ENSG00000105122	64926
EFHD2	0.9	6.8	9.1	2.6E-03	3.4E-02	ENSG00000142634	79180
ZDHHC12	0.5	3.9	9.1	2.6E-03	3.4E-02	ENSG00000160446	84885
ZNF511	0.6	3.6	9.1	2.6E-03	3.4E-02	ENSG00000198546	118472
DCP2	0.6	5.3	9.0	2.6E-03	3.4E-02	ENSG00000172795	167227
VAV1	1.0	4.9	9.0	2.6E-03	3.4E-02	ENSG00000141968	7409
RIT1	0.7	5.6	9.0	2.6E-03	3.4E-02	ENSG00000143622	6016
C4orf48	1.0	0.7	9.0	2.7E-03	3.4E-02	ENSG00000243449	401115

FLNC	0.8	7.7	9.0	2.7E-03	3.4E-02	ENSG00000128591	2318
SRA1	0.8	6.4	9.0	2.7E-03	3.4E-02	ENSG00000213523	10011
OSTC	0.7	5.8	9.0	2.7E-03	3.4E-02	ENSG00000198856	646567
DHRS3	1.0	6.4	9.0	2.7E-03	3.4E-02	ENSG00000162496	9249
FUCA2	0.5	5.2	9.0	2.7E-03	3.4E-02	ENSG00000001036	2519
ARHGAP4	0.8	6.7	9.0	2.8E-03	3.5E-02	ENSG00000089820	393
CD44	0.9	8.5	8.9	2.8E-03	3.5E-02	ENSG00000026508	960
OCIAD2	0.6	3.6	8.9	2.8E-03	3.5E-02	ENSG00000145247	132299
	1.0	0.6	8.9	2.8E-03	3.5E-02	ENSG00000259668	NA
PRSS36	1.1	2.0	8.9	2.8E-03	3.5E-02	ENSG00000178226	146547
PPP1R14BP3	0.7	1.4	8.9	2.8E-03	3.5E-02	ENSG00000179967	NA
BIN2	1.1	5.2	8.9	2.8E-03	3.5E-02	ENSG00000110934	51411
ACP5	1.6	6.0	8.9	2.9E-03	3.6E-02	ENSG00000102575	54
	1.1	2.6	8.9	2.9E-03	3.6E-02	ENSG00000225313	NA
RPN2	0.6	7.8	8.9	2.9E-03	3.6E-02	ENSG00000118705	6185
WNT5B	1.0	3.8	8.9	2.9E-03	3.6E-02	ENSG00000111186	81029
KIFC1	1.1	2.3	8.9	2.9E-03	3.6E-02	ENSG00000237649	3833
CECR5	0.6	4.9	8.9	2.9E-03	3.6E-02	ENSG00000069998	27440
ATP6AP1	0.5	7.3	8.9	2.9E-03	3.6E-02	ENSG00000071553	537
PLEKH02	0.7	6.8	8.8	2.9E-03	3.6E-02	ENSG00000241839	80301
PPP4C	0.7	6.2	8.8	3.0E-03	3.7E-02	ENSG00000149923	5531
SQRL	0.6	4.6	8.8	3.0E-03	3.7E-02	ENSG00000137767	58472
PI4K2B	0.5	4.1	8.8	3.0E-03	3.7E-02	ENSG00000038210	285540
UAP1L1	0.7	5.5	8.8	3.1E-03	3.7E-02	ENSG00000197355	91373
COMMD9	0.5	4.5	8.8	3.1E-03	3.7E-02	ENSG00000110442	29099
RER1	0.4	6.3	8.8	3.1E-03	3.7E-02	ENSG00000157916	11079
RARS	0.4	5.5	8.8	3.1E-03	3.7E-02	ENSG00000113643	5917
TBC1D2	0.8	5.9	8.7	3.1E-03	3.8E-02	ENSG00000095383	55357
	1.8	2.7	8.7	3.2E-03	3.8E-02	ENSG00000268734	NA
CASP1	0.7	4.5	8.7	3.2E-03	3.8E-02	ENSG00000137752	834
ULBP2	1.0	1.3	8.7	3.2E-03	3.8E-02	ENSG00000131015	80328
MCM2	0.6	3.3	8.7	3.2E-03	3.8E-02	ENSG00000073111	4171
SLC36A1	0.6	5.5	8.7	3.2E-03	3.8E-02	ENSG00000123643	206358
TREX1	0.7	3.9	8.7	3.2E-03	3.8E-02	ENSG00000213689	84126
PLBD2	0.6	5.9	8.7	3.2E-03	3.8E-02	ENSG00000151176	196463
AMDHD2	0.6	3.9	8.7	3.2E-03	3.9E-02	ENSG00000162066	752014
SPINT1	1.0	2.9	8.7	3.3E-03	3.9E-02	ENSG00000166145	6692
KDM2B	0.7	4.9	8.7	3.3E-03	3.9E-02	ENSG00000089094	84678
HSPA6	1.5	5.3	8.6	3.3E-03	3.9E-02	ENSG00000173110	3310
DTX2	0.6	3.8	8.6	3.3E-03	3.9E-02	ENSG00000091073	113878
CECR1	0.8	6.3	8.6	3.3E-03	3.9E-02	ENSG00000093072	51816
RPN1	0.5	7.6	8.6	3.3E-03	3.9E-02	ENSG00000163902	6184
GNGT2	0.8	1.0	8.6	3.3E-03	3.9E-02	ENSG00000167083	2793
WIP1	0.6	5.3	8.6	3.3E-03	3.9E-02	ENSG00000070540	55062
CNPY3	0.6	6.1	8.6	3.4E-03	4.0E-02	ENSG00000137161	10695

PLEKHB2	0.6	7.0	8.6	3.4E-03	4.0E-02	ENSG00000115762	55041
CTNS	0.5	4.6	8.6	3.4E-03	4.0E-02	ENSG00000040531	1497
SOX11	1.3	1.8	8.6	3.4E-03	4.0E-02	ENSG00000176887	6664
GBE1	0.7	5.8	8.6	3.4E-03	4.0E-02	ENSG00000114480	2632
PLOD3	0.5	6.5	8.6	3.4E-03	4.0E-02	ENSG00000106397	8985
DTYMK	0.6	3.7	8.6	3.4E-03	4.0E-02	ENSG00000168393	1841
OSBPL11	0.5	4.6	8.6	3.4E-03	4.0E-02	ENSG00000144909	114885
PTPN7	1.0	4.4	8.6	3.4E-03	4.0E-02	ENSG00000143851	5778
NCF1	1.4	2.8	8.6	3.4E-03	4.0E-02	ENSG00000158517	653361
AGPAT2	0.7	5.0	8.5	3.5E-03	4.0E-02	ENSG00000169692	10555
GTF2E1	0.5	3.1	8.5	3.5E-03	4.0E-02	ENSG00000153767	2960
TUBB	0.5	8.4	8.5	3.5E-03	4.0E-02	ENSG00000196230	203068
CD37	0.9	5.4	8.5	3.5E-03	4.0E-02	ENSG00000104894	951
ZEB2	0.6	7.2	8.5	3.5E-03	4.0E-02	ENSG00000169554	9839
MED11	0.5	3.1	8.5	3.5E-03	4.1E-02	ENSG00000161920	400569
DCBLD2	0.8	6.0	8.5	3.5E-03	4.1E-02	ENSG00000057019	131566
G6PD	0.4	5.7	8.5	3.6E-03	4.1E-02	ENSG00000160211	2539
MANBA	0.6	5.6	8.5	3.6E-03	4.1E-02	ENSG00000109323	4126
HLA-DMA	0.8	6.3	8.5	3.6E-03	4.1E-02	ENSG00000204257	3108
LINC00106	0.6	2.0	8.5	3.6E-03	4.1E-02	ENSG00000236871	NA
DPP9	0.4	5.9	8.5	3.6E-03	4.1E-02	ENSG00000142002	91039
WHSC1	0.4	5.7	8.4	3.7E-03	4.1E-02	ENSG00000109685	7468
ITGA2B	1.4	3.8	8.4	3.7E-03	4.2E-02	ENSG00000005961	3674
	0.8	1.1	8.4	3.7E-03	4.2E-02	ENSG00000257605	NA
EDEM1	0.7	6.4	8.4	3.7E-03	4.2E-02	ENSG00000134109	9695
AGPAT6	0.7	6.8	8.4	3.7E-03	4.2E-02	ENSG00000158669	137964
GPR1	1.6	2.5	8.4	3.7E-03	4.2E-02	ENSG00000183671	2825
SEC61G	0.5	5.5	8.4	3.7E-03	4.2E-02	ENSG00000132432	23480
FAM78A	0.9	3.9	8.4	3.8E-03	4.2E-02	ENSG00000126882	101927137
IRF7	1.1	6.0	8.4	3.8E-03	4.3E-02	ENSG00000185507	3665
FGD3	1.2	5.5	8.4	3.8E-03	4.3E-02	ENSG00000127084	89846
PRC1	0.8	3.5	8.4	3.8E-03	4.3E-02	ENSG00000198901	9055
PSMB3	0.4	5.6	8.4	3.8E-03	4.3E-02	ENSG00000108294	5691
MMP19	1.2	7.7	8.4	3.8E-03	4.3E-02	ENSG00000123342	4327
PF4	1.8	3.1	8.4	3.9E-03	4.3E-02	ENSG00000163737	5196
CCNB2	0.9	1.7	8.3	3.9E-03	4.3E-02	ENSG00000157456	9133
HIST1H1C	0.8	2.9	8.3	3.9E-03	4.3E-02	ENSG00000187837	3006
PSD4	1.0	5.3	8.3	3.9E-03	4.3E-02	ENSG00000125637	23550
CEACAM3	1.5	2.3	8.3	3.9E-03	4.3E-02	ENSG00000170956	1084
ZNF467	1.1	3.1	8.3	4.0E-03	4.4E-02	ENSG00000181444	168544
FCGR2A	0.9	6.3	8.3	4.0E-03	4.4E-02	ENSG00000143226	2212
MT-TT	1.1	2.6	8.3	4.0E-03	4.4E-02	ENSG00000210195	NA
AMPD2	0.8	7.5	8.3	4.0E-03	4.4E-02	ENSG00000116337	271
ACAA2	0.5	4.4	8.2	4.1E-03	4.5E-02	ENSG00000167315	10449
MCTS1	0.5	4.0	8.2	4.1E-03	4.5E-02	ENSG00000232119	28985

ADAMTS6	1.0	4.1	8.2	4.2E-03	4.5E-02	ENSG00000049192	11174
CENPM	1.3	0.7	8.2	4.2E-03	4.5E-02	ENSG00000100162	79019
UPP1	1.3	7.1	8.2	4.2E-03	4.5E-02	ENSG00000183696	7378
IL6R	0.9	6.3	8.2	4.2E-03	4.5E-02	ENSG00000160712	3570
CMTM3	0.6	5.9	8.2	4.2E-03	4.5E-02	ENSG00000140931	123920
G0S2	1.5	6.0	8.2	4.2E-03	4.5E-02	ENSG00000123689	50486
BRCA1	0.6	2.5	8.2	4.2E-03	4.6E-02	ENSG00000012048	672
TCF19	0.7	2.2	8.2	4.2E-03	4.6E-02	ENSG00000137310	6941
ZNF124	0.7	2.0	8.2	4.3E-03	4.6E-02	ENSG00000196418	7678
LAMTOR2	0.5	4.6	8.2	4.3E-03	4.6E-02	ENSG00000116586	28956
C11orf82	1.0	0.9	8.2	4.3E-03	4.6E-02	ENSG00000165490	220042
ABHD12	0.6	5.7	8.2	4.3E-03	4.6E-02	ENSG00000100997	26090
ARHGAP22	0.6	4.4	8.1	4.3E-03	4.6E-02	ENSG00000128805	58504
RNFT1	0.6	3.6	8.1	4.3E-03	4.6E-02	ENSG00000189050	51136
TMED9	0.5	7.5	8.1	4.4E-03	4.7E-02	ENSG00000184840	54732
	0.6	2.4	8.1	4.4E-03	4.7E-02	ENSG00000226328	100506714
ANXA2	0.5	8.9	8.1	4.4E-03	4.7E-02	ENSG00000182718	302
ACTR3	0.5	7.7	8.1	4.4E-03	4.7E-02	ENSG00000115091	10096
JARID2	1.0	5.5	8.1	4.4E-03	4.7E-02	ENSG00000008083	3720
POC1A	0.8	1.5	8.1	4.4E-03	4.7E-02	ENSG00000164087	25886
CHEK1	0.7	2.6	8.1	4.4E-03	4.7E-02	ENSG00000149554	1111
HPS1	0.4	6.3	8.1	4.4E-03	4.7E-02	ENSG00000107521	3257
INTS4	0.4	3.9	8.1	4.4E-03	4.7E-02	ENSG00000149262	92105
CCDC88A	0.5	5.7	8.1	4.4E-03	4.7E-02	ENSG00000115355	55704
ASPH	0.5	6.9	8.1	4.4E-03	4.7E-02	ENSG00000198363	444
TMEM8A	0.5	6.5	8.1	4.5E-03	4.7E-02	ENSG00000129925	58986
RPL22L1	0.7	4.4	8.1	4.5E-03	4.7E-02	ENSG00000163584	200916
GM2A	0.7	6.1	8.1	4.5E-03	4.7E-02	ENSG00000196743	2760
GUSB	0.5	6.1	8.1	4.5E-03	4.7E-02	ENSG00000169919	2990
E2F1	0.9	2.5	8.1	4.5E-03	4.7E-02	ENSG00000101412	1869
MRRF	0.5	4.0	8.1	4.5E-03	4.7E-02	ENSG00000148187	92399
FNDC3B	0.7	6.8	8.1	4.5E-03	4.7E-02	ENSG00000075420	101928615
MMP16	1.0	3.6	8.1	4.5E-03	4.7E-02	ENSG00000156103	4325
IFNGR1	0.7	7.0	8.1	4.5E-03	4.7E-02	ENSG00000027697	3459
GPBAR1	0.9	1.5	8.0	4.6E-03	4.8E-02	ENSG00000179921	151306
ATP2B1	0.8	6.1	8.0	4.6E-03	4.8E-02	ENSG00000070961	490
WDHD1	0.7	2.2	8.0	4.6E-03	4.8E-02	ENSG00000198554	11169
FYB	1.0	4.5	8.0	4.6E-03	4.8E-02	ENSG00000082074	2533
CLIP4	0.6	4.6	8.0	4.6E-03	4.8E-02	ENSG00000115295	79745
ACTB	0.4	11.9	8.0	4.6E-03	4.8E-02	ENSG00000075624	60
PTK2B	1.0	6.8	8.0	4.6E-03	4.8E-02	ENSG00000120899	2185
FAM20A	0.9	6.0	8.0	4.6E-03	4.8E-02	ENSG00000108950	54757
PIF1	0.9	2.4	8.0	4.6E-03	4.8E-02	ENSG00000140451	80119
PRKCSH	0.4	7.6	8.0	4.6E-03	4.8E-02	ENSG00000130175	5589
USB1	0.5	5.7	8.0	4.6E-03	4.8E-02	ENSG00000103005	79650

ACER3	0.5	4.5	8.0	4.7E-03	4.8E-02	ENSG00000078124	55331
LOXL2	1.2	7.5	8.0	4.7E-03	4.8E-02	ENSG00000134013	4017
	0.9	0.6	8.0	4.7E-03	4.8E-02	ENSG00000243155	NA
APOC1	1.6	6.0	8.0	4.7E-03	4.9E-02	ENSG00000130208	341
TRABD	0.7	6.0	8.0	4.7E-03	4.9E-02	ENSG00000170638	80305
GTPBP2	0.6	6.6	8.0	4.7E-03	4.9E-02	ENSG00000172432	54676
ATG7	0.4	4.8	8.0	4.8E-03	4.9E-02	ENSG00000197548	10533
ARHGAP27	0.9	5.7	7.9	4.8E-03	4.9E-02	ENSG00000159314	201176
BNIP3	1.1	4.5	7.9	4.8E-03	4.9E-02	ENSG00000176171	664
TALDO1	0.5	6.7	7.9	4.9E-03	4.9E-02	ENSG00000177156	6888
CFP	1.2	4.5	7.9	4.9E-03	4.9E-02	ENSG00000126759	5199
STX4	0.6	6.6	7.9	4.9E-03	4.9E-02	ENSG00000103496	6810
GGCX	0.4	5.2	7.9	4.9E-03	5.0E-02	ENSG00000115486	2677
ACADS	0.5	3.5	7.9	4.9E-03	5.0E-02	ENSG00000122971	35
AATK	1.2	5.0	7.9	4.9E-03	5.0E-02	ENSG00000181409	9625
GCNT1	0.7	3.5	7.9	4.9E-03	5.0E-02	ENSG00000187210	2650
AP3B1	0.4	5.6	7.9	4.9E-03	5.0E-02	ENSG00000132842	8546
RGS19	0.7	5.0	7.9	5.0E-03	5.0E-02	ENSG00000171700	10287
LINC00847	0.7	3.9	7.9	5.0E-03	5.0E-02	ENSG00000245060	729678

Hgnc indicates Human gene nomenclature committee; FC, fold change; CPM, counts per million, LR, likelihood ratio, FDR, false discovery rate.

Underexpression

hgnc_symbol	logFC	logCPM	LR	PValue	FDR	ensembl	entrez
DOK6	-2.0	2.0	27.6	1.5E-07	1.1E-04	ENSG00000206052	220164
CAMK2A	-3.1	4.9	25.8	3.9E-07	2.0E-04	ENSG00000070808	815
MYOZ3	-1.8	2.4	24.6	7.1E-07	2.8E-04	ENSG00000164591	91977
IGHG4	-6.1	8.8	24.3	8.3E-07	2.9E-04	ENSG00000211892	NA
TPH1	-2.7	3.4	23.7	1.1E-06	3.3E-04	ENSG00000129167	7166
FAM110C	-2.2	1.1	23.7	1.1E-06	3.3E-04	ENSG00000184731	642273
KRT17	-3.2	2.7	23.3	1.4E-06	3.4E-04	ENSG00000128422	3872
	-2.0	1.8	23.3	1.4E-06	3.4E-04	ENSG00000260396	NA
PACSLN1	-3.1	4.0	22.2	2.4E-06	4.7E-04	ENSG00000124507	29993
DDN	-2.9	3.9	21.9	2.8E-06	5.2E-04	ENSG00000181418	23109
HMCN2	-1.9	2.8	21.9	2.8E-06	5.2E-04	ENSG00000148357	101060175
SLC17A7	-2.9	4.0	21.9	2.9E-06	5.3E-04	ENSG00000104888	57030
CPXM2	-2.0	6.3	21.9	2.9E-06	5.3E-04	ENSG00000121898	119587
OLFM1	-1.6	4.4	21.1	4.3E-06	6.8E-04	ENSG00000130558	10439
IGHG1	-3.9	9.9	20.7	5.3E-06	7.6E-04	ENSG00000211896	102466889
PRSS12	-2.0	2.2	20.7	5.3E-06	7.6E-04	ENSG00000164099	8492
LIMCH1	-1.4	5.8	20.6	5.7E-06	8.0E-04	ENSG00000064042	22998
CCDC85A	-2.1	1.6	20.0	7.6E-06	9.4E-04	ENSG00000055813	114800
LAMA3	-1.6	4.4	20.0	7.6E-06	9.4E-04	ENSG00000053747	3909
WFIKKN1	-1.2	0.6	19.8	8.5E-06	9.8E-04	ENSG00000127578	117166
CA5B	-1.2	5.3	19.8	8.6E-06	9.8E-04	ENSG00000169239	11238
GDF7	-1.8	2.4	19.6	9.5E-06	1.1E-03	ENSG00000143869	151449
ZCCHC12	-2.0	2.0	19.4	1.1E-05	1.1E-03	ENSG00000174460	170261
VWA3A	-1.9	1.2	19.3	1.1E-05	1.2E-03	ENSG00000175267	146177
PLCL1	-1.2	3.6	19.2	1.2E-05	1.2E-03	ENSG00000115896	5334
PKHD1L1	-2.6	1.6	18.9	1.4E-05	1.4E-03	ENSG00000205038	93035
MASP1	-2.5	5.4	18.1	2.1E-05	1.7E-03	ENSG00000127241	5648
ZDHHC11B	-1.9	1.8	18.0	2.2E-05	1.7E-03	ENSG00000206077	653082
BSN	-1.6	2.9	17.6	2.7E-05	2.0E-03	ENSG00000164061	8927
FBXL16	-2.7	4.8	17.6	2.8E-05	2.0E-03	ENSG00000127585	146330
TPD52L1	-1.3	3.4	17.5	2.9E-05	2.1E-03	ENSG00000111907	7164
FZD1	-1.1	5.8	17.4	3.0E-05	2.1E-03	ENSG00000157240	8321
PMEL	-3.0	4.4	17.3	3.2E-05	2.2E-03	ENSG00000185664	6490
FBXO2	-2.6	3.9	17.3	3.2E-05	2.2E-03	ENSG00000116661	26232
PSD2	-2.5	2.7	17.3	3.2E-05	2.2E-03	ENSG00000146005	84249
MATN3	-1.7	3.9	17.3	3.1E-05	2.2E-03	ENSG00000132031	4148
ST8SIA6	-1.6	1.0	17.2	3.3E-05	2.2E-03	ENSG00000148488	338596
SHF	-1.1	3.1	16.9	4.0E-05	2.5E-03	ENSG00000138606	90525
RYR3	-1.6	2.9	16.8	4.1E-05	2.5E-03	ENSG00000198838	6263
SELP	-1.6	5.5	16.8	4.2E-05	2.5E-03	ENSG00000174175	6403
CHD5	-2.2	3.8	16.8	4.2E-05	2.5E-03	ENSG00000116254	101928723
FAM107A	-2.1	7.1	16.8	4.2E-05	2.6E-03	ENSG00000168309	11170

RIMS4	-1.9	2.4	16.6	4.5E-05	2.6E-03	ENSG00000101098	140730
PTCH2	-1.2	3.7	16.6	4.5E-05	2.6E-03	ENSG00000117425	8643
BCAN	-2.6	3.6	16.6	4.6E-05	2.6E-03	ENSG00000132692	63827
GALNT3	-1.4	3.1	16.6	4.6E-05	2.6E-03	ENSG00000115339	2591
WNT10B	-1.7	2.2	16.5	4.8E-05	2.7E-03	ENSG00000169884	7480
CTNNA2	-2.6	2.8	16.5	5.0E-05	2.7E-03	ENSG00000066032	1496
LEPR	-1.2	5.8	16.4	5.0E-05	2.7E-03	ENSG00000116678	54741
ITM2A	-1.3	6.4	16.4	5.2E-05	2.8E-03	ENSG00000078596	9452
RERG	-1.6	2.9	16.2	5.6E-05	3.0E-03	ENSG00000134533	85004
ADCYAP1R1	-2.8	3.6	16.2	5.7E-05	3.0E-03	ENSG00000078549	117
MAPT	-2.1	3.5	16.1	5.9E-05	3.1E-03	ENSG00000186868	4137
IL33	-1.4	5.0	15.9	6.7E-05	3.3E-03	ENSG00000137033	90865
PLP1	-2.3	5.2	15.9	6.8E-05	3.4E-03	ENSG00000123560	5354
C4orf32	-0.8	3.7	15.8	6.9E-05	3.4E-03	ENSG00000174749	132720
HPCAL4	-2.7	3.2	15.8	7.0E-05	3.4E-03	ENSG00000116983	51440
ATP1A3	-2.4	3.1	15.8	7.0E-05	3.4E-03	ENSG00000105409	101927137
IGHG3	-3.4	7.3	15.8	7.1E-05	3.4E-03	ENSG00000211897	NA
CASKIN1	-2.0	1.6	15.8	7.2E-05	3.4E-03	ENSG00000167971	57524
IGHV1-69	-3.7	4.6	15.7	7.2E-05	3.4E-03	ENSG00000211973	NA
DLX3	-2.4	1.8	15.7	7.3E-05	3.5E-03	ENSG00000064195	1747
ADAMTSL2	-2.1	5.4	15.6	8.0E-05	3.6E-03	ENSG00000197859	100996396
CHIT1	-2.9	3.3	15.5	8.4E-05	3.7E-03	ENSG00000133063	1118
VWFP1	-1.5	2.6	15.5	8.4E-05	3.7E-03	ENSG00000241717	100289038
CRLF1	-2.0	5.5	15.5	8.4E-05	3.8E-03	ENSG00000006016	9244
KRT16	-2.8	5.9	15.5	8.5E-05	3.8E-03	ENSG00000186832	3868
GNG7	-1.2	4.0	15.3	9.4E-05	4.0E-03	ENSG00000176533	2788
IGLC2	-3.2	5.4	15.2	9.6E-05	4.1E-03	ENSG00000211677	NA
SMAD9	-1.2	4.9	15.1	1.0E-04	4.3E-03	ENSG00000120693	4093
BZRAP1	-1.3	5.3	15.0	1.1E-04	4.3E-03	ENSG00000005379	9256
TMEM74B	-2.2	2.1	15.0	1.1E-04	4.4E-03	ENSG00000125895	55321
PTCHD4	-1.3	1.6	14.9	1.1E-04	4.5E-03	ENSG00000244694	442213
ST6GAL1	-0.8	6.3	14.9	1.1E-04	4.5E-03	ENSG00000073849	6480
ZDHHC14	-1.0	4.4	14.8	1.2E-04	4.6E-03	ENSG00000175048	79683
S100B	-2.1	5.0	14.6	1.3E-04	5.0E-03	ENSG00000160307	6285
	-1.4	2.5	14.6	1.3E-04	5.0E-03	ENSG00000223855	441307
BRMS1L	-0.8	3.6	14.6	1.3E-04	5.0E-03	ENSG00000100916	84312
DLG2	-1.7	2.7	14.5	1.4E-04	5.1E-03	ENSG00000150672	1740
GJA3	-1.7	1.3	14.5	1.4E-04	5.3E-03	ENSG00000121743	2700
LINC00475	-1.6	2.2	14.4	1.5E-04	5.4E-03	ENSG00000225511	158314
ZNF540	-1.3	2.7	14.3	1.5E-04	5.5E-03	ENSG00000171817	163255
TMEM130	-2.4	6.3	14.3	1.6E-04	5.5E-03	ENSG00000166448	222865
TMEM150C	-1.1	1.6	14.3	1.6E-04	5.6E-03	ENSG00000249242	441027
COMP	-2.9	7.5	14.2	1.6E-04	5.6E-03	ENSG00000105664	1311
B3GAT1	-2.2	3.1	14.2	1.6E-04	5.7E-03	ENSG00000109956	27087
NDRG4	-1.7	4.5	14.1	1.7E-04	5.8E-03	ENSG00000103034	65009

WSCD2	-2.7	2.5	14.1	1.7E-04	5.9E-03	ENSG00000075035	9671
KIAA1456	-1.7	3.7	14.1	1.7E-04	5.9E-03	ENSG00000250305	101927137
KLF9	-0.9	7.4	14.1	1.8E-04	5.9E-03	ENSG00000119138	687
ANK3	-1.3	4.8	14.1	1.8E-04	5.9E-03	ENSG00000151150	288
EPB41L1	-1.1	5.6	14.0	1.9E-04	6.1E-03	ENSG00000088367	2036
	-1.1	2.4	14.0	1.9E-04	6.2E-03	ENSG00000260391	NA
OMD	-1.6	5.5	13.8	2.0E-04	6.4E-03	ENSG00000127083	4958
MYLIP	-1.1	6.0	13.8	2.0E-04	6.4E-03	ENSG00000007944	29116
HMG5	-0.9	2.8	13.8	2.1E-04	6.4E-03	ENSG00000198157	79366
TJP2	-0.8	6.1	13.8	2.0E-04	6.4E-03	ENSG00000119139	9414
EPB41L4A	-0.8	2.9	13.8	2.0E-04	6.4E-03	ENSG00000129595	64097
EPB41L4A-AS1	-0.7	3.4	13.6	2.3E-04	7.0E-03	ENSG00000224032	114915
AMOT	-1.3	4.1	13.5	2.3E-04	7.0E-03	ENSG00000126016	154796
GATA2	-1.0	3.9	13.5	2.3E-04	7.0E-03	ENSG00000179348	2624
NDRG2	-1.6	7.1	13.5	2.4E-04	7.1E-03	ENSG00000165795	57447
RAPGEF4	-1.4	4.6	13.5	2.4E-04	7.1E-03	ENSG00000091428	11069
IGLV3-21	-3.6	4.9	13.4	2.5E-04	7.4E-03	ENSG00000211662	NA
TPPP	-1.6	4.0	13.3	2.6E-04	7.6E-03	ENSG00000171368	11076
PIWIL2	-1.1	1.2	13.3	2.6E-04	7.6E-03	ENSG00000197181	55124
WDR78	-1.0	2.0	13.3	2.6E-04	7.6E-03	ENSG00000152763	79819
PLEKHB1	-2.3	5.4	13.3	2.7E-04	7.7E-03	ENSG00000021300	58473
VWF	-1.4	9.5	13.3	2.7E-04	7.7E-03	ENSG00000110799	7450
	-0.9	3.7	13.3	2.7E-04	7.7E-03	ENSG00000236304	NA
ANKRD6	-1.1	4.6	13.2	2.8E-04	7.8E-03	ENSG00000135299	22881
C12orf60	-0.9	0.9	13.2	2.8E-04	7.9E-03	ENSG00000182993	144608
MYL3	-1.5	1.1	13.2	2.8E-04	8.0E-03	ENSG00000160808	4634
DNAJC6	-1.1	2.9	13.2	2.8E-04	8.0E-03	ENSG00000116675	9829
COL9A2	-1.0	3.7	13.1	3.0E-04	8.3E-03	ENSG00000049089	1298
FAM189A2	-1.4	3.0	13.0	3.1E-04	8.6E-03	ENSG00000135063	9413
PARM1	-1.5	7.2	13.0	3.2E-04	8.6E-03	ENSG00000169116	25849
SLC25A18	-1.9	2.1	13.0	3.2E-04	8.6E-03	ENSG00000182902	83733
SMAD6	-1.2	4.9	13.0	3.2E-04	8.6E-03	ENSG00000137834	4091
	-0.8	2.5	12.9	3.2E-04	8.6E-03	ENSG00000260966	NA
MAP3K5	-0.7	6.2	12.9	3.2E-04	8.6E-03	ENSG00000197442	4217
RIMKLB	-0.7	6.1	12.9	3.3E-04	8.8E-03	ENSG00000166532	57494
CRTAC1	-2.0	5.6	12.9	3.3E-04	8.8E-03	ENSG00000095713	55118
CCNO	-1.7	1.3	12.8	3.4E-04	9.1E-03	ENSG00000152669	10309
NDNF	-2.1	3.2	12.7	3.6E-04	9.3E-03	ENSG00000173376	79625
ADCY1	-1.4	3.3	12.7	3.6E-04	9.4E-03	ENSG00000164742	107
PALM	-1.1	6.0	12.7	3.6E-04	9.4E-03	ENSG00000099864	5064
LRRC16A	-0.8	4.3	12.7	3.7E-04	9.5E-03	ENSG00000079691	55604
CDH4	-1.7	1.9	12.7	3.7E-04	9.5E-03	ENSG00000179242	1002
HID1	-1.1	3.9	12.6	3.8E-04	9.6E-03	ENSG00000167861	283987
BFSP1	-1.2	2.6	12.6	3.8E-04	9.7E-03	ENSG00000125864	631
CAMK2B	-2.1	2.8	12.5	4.0E-04	1.0E-02	ENSG00000058404	816

GLIPR1L2	-1.4	0.9	12.5	4.1E-04	1.0E-02	ENSG00000180481	144321
RXFP1	-2.2	3.1	12.4	4.2E-04	1.0E-02	ENSG00000171509	59350
CD200	-1.3	5.1	12.4	4.2E-04	1.0E-02	ENSG00000091972	4345
FAM65C	-1.4	4.8	12.4	4.3E-04	1.1E-02	ENSG00000042062	140876
CCDC68	-1.6	3.9	12.4	4.3E-04	1.1E-02	ENSG00000166510	80323
C1orf95	-2.2	3.5	12.3	4.4E-04	1.1E-02	ENSG00000203685	375057
SOX8	-1.1	2.8	12.3	4.5E-04	1.1E-02	ENSG00000005513	30812
INHBA-AS1	-1.5	1.6	12.3	4.6E-04	1.1E-02	ENSG00000224116	285954
CYP46A1	-1.5	2.3	12.3	4.6E-04	1.1E-02	ENSG00000036530	10858
SEPT3	-2.2	3.2	12.3	4.6E-04	1.1E-02	ENSG00000100167	55964
C1orf115	-1.2	3.7	12.3	4.6E-04	1.1E-02	ENSG00000162817	79762
SYN2	-2.2	2.8	12.2	4.7E-04	1.1E-02	ENSG00000157152	NA
THRB	-1.4	4.1	12.2	4.9E-04	1.2E-02	ENSG00000151090	7068
PRKAA2	-1.2	3.5	12.1	4.9E-04	1.2E-02	ENSG00000162409	5563
LGR6	-1.9	3.6	12.1	5.1E-04	1.2E-02	ENSG00000133067	59352
	-1.8	2.4	12.0	5.2E-04	1.2E-02	ENSG00000267466	NA
ZNF83	-0.7	6.2	12.0	5.3E-04	1.2E-02	ENSG00000167766	55769
CCDC146	-0.7	3.0	12.0	5.3E-04	1.2E-02	ENSG00000135205	57639
TNNC1	-1.9	2.1	12.0	5.5E-04	1.3E-02	ENSG00000114854	7134
IGHG2	-2.9	6.9	11.9	5.6E-04	1.3E-02	ENSG00000211893	NA
C1orf61	-2.7	4.0	11.9	5.6E-04	1.3E-02	ENSG00000125462	10485
SMOC2	-1.3	7.0	11.9	5.6E-04	1.3E-02	ENSG00000112562	64094
PDZD7	-0.9	1.4	11.9	5.6E-04	1.3E-02	ENSG00000186862	79955
SLC1A2	-2.4	5.3	11.9	5.6E-04	1.3E-02	ENSG00000110436	6506
LINC00630	-0.8	0.6	11.9	5.7E-04	1.3E-02	ENSG00000223546	100287765
MLC1	-2.3	4.8	11.9	5.7E-04	1.3E-02	ENSG00000100427	23209
SYNGR3	-1.6	1.6	11.9	5.7E-04	1.3E-02	ENSG00000127561	9143
HERC2P2	-1.0	6.4	11.9	5.7E-04	1.3E-02	ENSG00000140181	101930157
ERG	-1.0	6.1	11.8	5.8E-04	1.3E-02	ENSG00000157554	2078
CTDSPL	-1.1	6.0	11.8	5.8E-04	1.3E-02	ENSG00000144677	10217
OXER1	-1.0	2.7	11.8	6.0E-04	1.3E-02	ENSG00000162881	165140
ADRA1B	-1.1	2.0	11.8	6.0E-04	1.3E-02	ENSG00000170214	147
	-1.2	1.9	11.7	6.1E-04	1.3E-02	ENSG00000235257	101928187
MFSD4	-1.2	1.5	11.7	6.2E-04	1.4E-02	ENSG00000174514	148808
NFYB	-0.7	5.0	11.7	6.3E-04	1.4E-02	ENSG00000120837	4801
ART4	-2.0	2.5	11.6	6.4E-04	1.4E-02	ENSG00000111339	420
PRR15	-1.4	2.1	11.6	6.5E-04	1.4E-02	ENSG00000176532	222171
SYP	-1.5	3.5	11.6	6.5E-04	1.4E-02	ENSG00000102003	6855
DLX1	-1.8	2.1	11.6	6.6E-04	1.4E-02	ENSG00000144355	1745
TSPAN2	-1.0	4.7	11.6	6.7E-04	1.4E-02	ENSG00000134198	10100
NMNAT2	-1.2	4.3	11.6	6.7E-04	1.4E-02	ENSG00000157064	23057
BAIAP2L2	-0.9	2.1	11.6	6.8E-04	1.4E-02	ENSG00000128298	80115
SLCO2A1	-1.7	5.3	11.5	6.9E-04	1.5E-02	ENSG00000174640	6578
ZNF660	-0.8	2.4	11.5	6.8E-04	1.5E-02	ENSG00000144792	285349
BAIAP3	-1.9	3.7	11.5	6.9E-04	1.5E-02	ENSG00000007516	8938

SRCIN1	-1.5	1.9	11.5	6.9E-04	1.5E-02	ENSG00000017373	101929513
FAM81A	-1.2	1.0	11.5	6.9E-04	1.5E-02	ENSG000000157470	145773
SLC14A1	-2.1	5.8	11.5	7.0E-04	1.5E-02	ENSG000000141469	6563
RND1	-1.6	5.0	11.5	7.0E-04	1.5E-02	ENSG000000172602	27289
ZFP2	-1.0	1.5	11.4	7.2E-04	1.5E-02	ENSG000000198939	80108
CNKSR3	-1.0	4.4	11.4	7.2E-04	1.5E-02	ENSG000000153721	154043
CD302	-0.6	5.5	11.4	7.2E-04	1.5E-02	ENSG000000241399	9936
POU6F2	-1.6	2.0	11.4	7.3E-04	1.5E-02	ENSG000000106536	11281
PRKAR1B	-0.9	5.0	11.4	7.3E-04	1.5E-02	ENSG000000188191	5575
HERC2P9	-0.8	4.0	11.4	7.4E-04	1.5E-02	ENSG000000206149	101930157
KIAA1324L	-1.0	3.1	11.4	7.4E-04	1.5E-02	ENSG000000164659	222223
JPH4	-1.8	3.2	11.4	7.5E-04	1.5E-02	ENSG000000092051	84502
ADCY2	-1.7	3.8	11.3	7.6E-04	1.5E-02	ENSG000000078295	108
FN3K	-1.1	3.7	11.3	7.6E-04	1.5E-02	ENSG000000167363	64122
	-0.8	1.6	11.3	7.7E-04	1.5E-02	ENSG000000182873	NA
LINC00312	-1.3	2.8	11.3	7.7E-04	1.5E-02	ENSG000000237697	29931
BMPR2	-0.6	6.8	11.3	7.9E-04	1.6E-02	ENSG000000204217	659
ENPP2	-1.0	6.2	11.3	7.9E-04	1.6E-02	ENSG000000136960	5168
	-0.8	1.0	11.2	8.1E-04	1.6E-02	ENSG000000261098	NA
DNASE1L3	-1.5	1.0	11.2	8.3E-04	1.6E-02	ENSG000000163687	1776
PRRT1	-1.1	3.5	11.2	8.3E-04	1.6E-02	ENSG000000204314	100507547
PLA1A	-1.0	3.6	11.2	8.3E-04	1.6E-02	ENSG000000144837	51365
MTURN	-1.0	6.6	11.2	8.3E-04	1.6E-02	ENSG000000180354	222166
KALRN	-1.0	5.7	11.2	8.3E-04	1.6E-02	ENSG000000160145	8997
RFTN1	-0.8	6.8	11.1	8.4E-04	1.6E-02	ENSG000000131378	23180
	-0.8	2.5	11.1	8.4E-04	1.6E-02	ENSG000000254615	NA
FAM198B	-0.7	6.6	11.1	8.6E-04	1.7E-02	ENSG000000164125	51313
	-1.3	2.0	11.1	8.7E-04	1.7E-02	ENSG000000224376	NA
CUX2	-2.0	1.9	11.1	8.7E-04	1.7E-02	ENSG000000111249	23316
AEBP2	-0.6	4.8	11.1	8.7E-04	1.7E-02	ENSG000000139154	121536
PLXNA4	-1.0	3.2	11.1	8.8E-04	1.7E-02	ENSG000000221866	91584
	-0.8	2.3	11.1	8.8E-04	1.7E-02	ENSG000000260912	NA
RBMXL1	-0.6	4.2	11.0	8.9E-04	1.7E-02	ENSG000000213516	494115
ADRA2A	-1.1	3.1	11.0	9.0E-04	1.7E-02	ENSG000000150594	150
LIFR	-0.9	4.4	11.0	9.0E-04	1.7E-02	ENSG000000113594	3977
DDX24	-0.5	7.4	11.0	9.0E-04	1.7E-02	ENSG000000089737	57062
SASH1	-0.8	7.2	11.0	9.3E-04	1.7E-02	ENSG000000111961	23328
PDGFD	-1.2	2.7	10.9	9.4E-04	1.7E-02	ENSG000000170962	80310
NEIL1	-0.7	4.7	10.9	9.4E-04	1.7E-02	ENSG000000140398	693216
LGI2	-1.0	3.3	10.9	9.6E-04	1.8E-02	ENSG000000153012	55203
CILP2	-1.5	2.0	10.9	9.7E-04	1.8E-02	ENSG000000160161	148113
	-1.0	0.8	10.9	9.7E-04	1.8E-02	ENSG000000255471	NA
PHYHIP	-1.7	3.6	10.8	1.0E-03	1.8E-02	ENSG000000168490	9796
CCND2	-0.8	6.6	10.8	1.0E-03	1.8E-02	ENSG000000118971	894
SLC38A1	-0.9	5.3	10.7	1.0E-03	1.9E-02	ENSG000000111371	81539

MYO1D	-1.1	8.3	10.7	1.1E-03	1.9E-02	ENSG00000176658	4642
KLHL29	-0.7	4.0	10.7	1.1E-03	1.9E-02	ENSG00000119771	114818
CNTN1	-2.1	2.9	10.7	1.1E-03	1.9E-02	ENSG00000018236	1272
LURAP1L	-1.1	4.0	10.7	1.1E-03	1.9E-02	ENSG00000153714	286343
CACNG8	-1.6	1.8	10.6	1.1E-03	1.9E-02	ENSG00000142408	59283
AQP4	-2.9	5.4	10.6	1.1E-03	2.0E-02	ENSG00000171885	361
ICA1L	-0.9	3.3	10.6	1.1E-03	2.0E-02	ENSG00000163596	130026
TXLNG	-0.6	4.4	10.6	1.1E-03	2.0E-02	ENSG00000086712	55787
TCF7L2	-0.6	4.6	10.6	1.2E-03	2.0E-02	ENSG00000148737	6934
TTYH1	-2.0	3.7	10.6	1.2E-03	2.0E-02	ENSG00000167614	57348
GFAP	-2.3	10.6	10.5	1.2E-03	2.0E-02	ENSG00000131095	2670
H1FX-AS1	-0.9	2.4	10.5	1.2E-03	2.0E-02	ENSG00000206417	NA
TIMP3	-1.0	10.1	10.5	1.2E-03	2.0E-02	ENSG00000100234	7078
TRABD2B	-1.5	1.5	10.5	1.2E-03	2.0E-02	ENSG00000269113	388630
ZFP28	-0.7	3.6	10.5	1.2E-03	2.0E-02	ENSG00000196867	140612
ANTXR1	-1.2	9.4	10.5	1.2E-03	2.0E-02	ENSG00000169604	84168
ARHGEF26	-1.1	2.9	10.5	1.2E-03	2.0E-02	ENSG00000114790	26084
TRMT11	-0.5	3.7	10.5	1.2E-03	2.0E-02	ENSG00000066651	60487
RGS9	-1.4	3.1	10.5	1.2E-03	2.0E-02	ENSG00000108370	8787
FSCN2	-0.8	0.7	10.5	1.2E-03	2.0E-02	ENSG00000186765	25794
SETMAR	-0.7	3.6	10.5	1.2E-03	2.1E-02	ENSG00000170364	6419
IDS	-0.6	7.9	10.5	1.2E-03	2.1E-02	ENSG00000010404	3423
PLCD3	-0.8	5.9	10.4	1.2E-03	2.1E-02	ENSG00000161714	113026
ERBB4	-1.8	1.4	10.4	1.2E-03	2.1E-02	ENSG00000178568	2066
RPS6KL1	-0.9	3.4	10.4	1.3E-03	2.1E-02	ENSG00000198208	83694
URGCP	-0.6	5.8	10.4	1.3E-03	2.1E-02	ENSG00000106608	55665
PPP2R2C	-2.0	2.5	10.4	1.3E-03	2.1E-02	ENSG00000074211	5522
MAOB	-1.8	4.3	10.3	1.3E-03	2.1E-02	ENSG00000069535	4129
SH3BGRL2	-0.7	4.5	10.3	1.3E-03	2.1E-02	ENSG00000198478	83699
KIF3A	-0.6	4.2	10.3	1.3E-03	2.1E-02	ENSG00000131437	11127
FGFR3	-1.5	5.1	10.3	1.3E-03	2.1E-02	ENSG00000068078	2261
FBXW7	-0.6	4.9	10.3	1.3E-03	2.2E-02	ENSG00000109670	55294
ARVCF	-1.5	6.3	10.3	1.3E-03	2.2E-02	ENSG00000099889	421
GALNT15	-1.6	4.8	10.3	1.3E-03	2.2E-02	ENSG00000131386	117248
LNP1	-1.0	1.8	10.3	1.3E-03	2.2E-02	ENSG00000206535	348801
ANKRD29	-1.0	2.8	10.3	1.3E-03	2.2E-02	ENSG00000154065	147463
GOLGA7B	-1.4	2.3	10.3	1.4E-03	2.2E-02	ENSG00000155265	401647
COBL	-1.9	2.9	10.3	1.4E-03	2.2E-02	ENSG00000106078	23242
BAMBI	-0.7	4.8	10.3	1.4E-03	2.2E-02	ENSG00000095739	25805
ISCU	-0.5	6.5	10.2	1.4E-03	2.2E-02	ENSG00000136003	23479
GNAO1	-1.6	3.7	10.2	1.4E-03	2.2E-02	ENSG00000087258	2775
ZNF204P	-1.2	3.0	10.2	1.4E-03	2.2E-02	ENSG00000204789	7754
PITPNM3	-1.2	4.6	10.2	1.4E-03	2.2E-02	ENSG00000091622	83394
CRIM1	-0.9	8.4	10.2	1.4E-03	2.2E-02	ENSG00000150938	101929500
DHRS11	-0.7	2.4	10.2	1.4E-03	2.2E-02	ENSG00000108272	79154

GLI1	-0.8	2.4	10.2	1.4E-03	2.2E-02	ENSG00000111087	2735
MYH10	-0.9	6.7	10.2	1.4E-03	2.2E-02	ENSG00000133026	4628
KIF1A	-2.2	5.5	10.2	1.4E-03	2.3E-02	ENSG00000130294	547
SAMD11	-1.5	4.8	10.1	1.4E-03	2.3E-02	ENSG00000187634	148398
EMX2OS	-1.4	2.5	10.1	1.4E-03	2.3E-02	ENSG00000229847	196047
CNTN2	-1.9	1.9	10.1	1.5E-03	2.3E-02	ENSG00000184144	6900
SAMD5	-1.0	3.0	10.1	1.5E-03	2.3E-02	ENSG00000203727	389432
NKD2	-1.4	1.7	10.1	1.5E-03	2.3E-02	ENSG00000145506	85409
EPS8L2	-1.0	5.5	10.1	1.5E-03	2.3E-02	ENSG00000177106	64787
LINC00657	-0.5	7.8	10.1	1.5E-03	2.3E-02	ENSG00000260032	647979
RAB40B	-0.9	4.1	10.0	1.5E-03	2.4E-02	ENSG00000141542	10966
GSN	-0.9	10.2	10.0	1.5E-03	2.4E-02	ENSG00000148180	2934
DTNA	-1.3	5.9	10.0	1.6E-03	2.4E-02	ENSG00000134769	1837
CDH3	-1.2	2.4	10.0	1.6E-03	2.4E-02	ENSG00000062038	1001
RAB11FIP3	-0.6	6.5	10.0	1.6E-03	2.4E-02	ENSG00000090565	9727
ST6GALNAC6	-0.6	7.1	9.9	1.6E-03	2.5E-02	ENSG00000160408	30815
ID4	-1.3	7.1	9.9	1.6E-03	2.5E-02	ENSG00000172201	3400
AMT	-0.9	5.4	9.9	1.6E-03	2.5E-02	ENSG00000145020	275
NSMF	-0.7	7.0	9.9	1.6E-03	2.5E-02	ENSG00000165802	102466223
MAP7	-1.1	2.5	9.9	1.7E-03	2.5E-02	ENSG00000135525	9053
DCLK2	-1.0	4.7	9.9	1.7E-03	2.5E-02	ENSG00000170390	166614
MOAP1	-0.5	5.0	9.8	1.7E-03	2.5E-02	ENSG00000165943	64112
SNAP25	-1.7	3.8	9.8	1.7E-03	2.6E-02	ENSG00000132639	6616
DMD	-0.9	6.0	9.8	1.7E-03	2.6E-02	ENSG00000198947	1756
IGKV3-20	-2.8	4.2	9.8	1.8E-03	2.6E-02	ENSG00000239951	NA
ZNF704	-1.1	5.9	9.8	1.8E-03	2.6E-02	ENSG00000164684	619279
SYT1	-1.5	2.7	9.8	1.8E-03	2.6E-02	ENSG00000067715	6857
FGF14	-1.5	5.1	9.8	1.8E-03	2.6E-02	ENSG00000102466	2259
PWAR6	-0.9	3.3	9.8	1.8E-03	2.7E-02	ENSG00000257151	NA
TREX2	-1.1	2.1	9.7	1.8E-03	2.7E-02	ENSG00000183479	11219
CITED4	-0.9	2.5	9.7	1.8E-03	2.7E-02	ENSG00000179862	163732
INPP4B	-0.9	4.3	9.7	1.8E-03	2.7E-02	ENSG00000109452	8821
GZMK	-1.2	1.4	9.7	1.9E-03	2.7E-02	ENSG00000113088	3003
RGS11	-1.1	5.1	9.7	1.9E-03	2.7E-02	ENSG00000076344	8786
POU6F1	-0.6	4.7	9.7	1.9E-03	2.7E-02	ENSG00000184271	5463
SNAP91	-1.8	2.0	9.6	1.9E-03	2.8E-02	ENSG00000065609	9892
HDAC9	-1.0	4.3	9.6	1.9E-03	2.8E-02	ENSG00000048052	9734
LETM2	-0.7	3.2	9.6	1.9E-03	2.8E-02	ENSG00000165046	137994
PLA2G5	-1.3	2.1	9.6	1.9E-03	2.8E-02	ENSG00000127472	5322
ACSM5	-1.1	1.7	9.6	1.9E-03	2.8E-02	ENSG00000183549	54988
JMY	-0.5	4.9	9.6	1.9E-03	2.8E-02	ENSG00000152409	133746
	-0.9	1.2	9.6	1.9E-03	2.8E-02	ENSG00000244300	101927167
PCGF5	-0.6	6.7	9.6	1.9E-03	2.8E-02	ENSG00000180628	84333
MTSS1L	-1.0	4.8	9.6	2.0E-03	2.8E-02	ENSG00000132613	92154
CHURC1	-0.7	5.8	9.6	2.0E-03	2.8E-02	ENSG00000258289	91612

	-0.9	2.3	9.6	2.0E-03	2.8E-02	ENSG00000235501	729970
SYNPO	-0.8	9.0	9.6	2.0E-03	2.8E-02	ENSG00000171992	11346
TMCC2	-1.1	3.9	9.5	2.0E-03	2.8E-02	ENSG00000133069	9911
ZNF667	-0.6	3.0	9.5	2.0E-03	2.9E-02	ENSG00000198046	63934
C6orf48	-0.5	6.4	9.5	2.0E-03	2.9E-02	ENSG00000204387	50854
CHN2	-0.7	3.7	9.5	2.0E-03	2.9E-02	ENSG00000106069	644086
SYT12	-1.6	5.8	9.5	2.0E-03	2.9E-02	ENSG00000173227	91683
GPR17	-1.3	4.1	9.5	2.0E-03	2.9E-02	ENSG00000144230	2840
KIF5C	-1.7	4.4	9.5	2.1E-03	2.9E-02	ENSG00000168280	3800
TCEAL3	-0.6	5.0	9.5	2.1E-03	2.9E-02	ENSG00000196507	85012
ZNF880	-0.6	3.3	9.5	2.1E-03	2.9E-02	ENSG00000221923	400713
PRX	-0.7	4.3	9.5	2.1E-03	2.9E-02	ENSG00000105227	57716
SRRM3	-1.1	2.7	9.5	2.1E-03	2.9E-02	ENSG00000177679	222183
	-0.9	1.1	9.5	2.1E-03	2.9E-02	ENSG00000266718	NA
LINC00087	-1.3	2.4	9.5	2.1E-03	2.9E-02	ENSG00000196972	644596
DPT	-1.4	2.1	9.5	2.1E-03	2.9E-02	ENSG00000143196	1805
INMT	-1.5	5.3	9.4	2.1E-03	3.0E-02	ENSG00000241644	11185
TM4SF1	-1.0	8.5	9.4	2.1E-03	3.0E-02	ENSG00000169908	4071
HAUS7	-0.8	3.3	9.4	2.1E-03	3.0E-02	ENSG00000213397	55559
COL10A1	-1.7	3.9	9.4	2.1E-03	3.0E-02	ENSG00000123500	1300
TBX1	-1.3	2.6	9.4	2.2E-03	3.0E-02	ENSG00000184058	6899
SGCA	-1.2	6.0	9.4	2.2E-03	3.0E-02	ENSG00000108823	6442
GALNT18	-1.0	5.6	9.4	2.2E-03	3.0E-02	ENSG00000110328	374378
ITGA10	-1.1	7.8	9.4	2.2E-03	3.0E-02	ENSG00000143127	8515
FXYD1	-1.3	0.9	9.4	2.2E-03	3.0E-02	ENSG00000266964	5348
CTNND2	-2.3	4.0	9.4	2.2E-03	3.0E-02	ENSG00000169862	1501
C8orf46	-1.4	2.4	9.3	2.2E-03	3.0E-02	ENSG00000169085	254778
STX1B	-1.3	2.5	9.3	2.2E-03	3.0E-02	ENSG00000099365	112755
GSG1L	-1.7	1.3	9.3	2.3E-03	3.1E-02	ENSG00000169181	146395
C2CD4C	-1.4	1.4	9.3	2.3E-03	3.1E-02	ENSG00000183186	126567
RGS16	-1.0	6.8	9.3	2.3E-03	3.1E-02	ENSG00000143333	6004
TACC1	-0.6	8.1	9.3	2.3E-03	3.1E-02	ENSG00000147526	6867
PPP1R3F	-0.8	3.3	9.3	2.3E-03	3.1E-02	ENSG00000049769	89801
TMEM178A	-1.1	2.1	9.2	2.4E-03	3.2E-02	ENSG00000152154	130733
NPR1	-1.2	3.9	9.2	2.4E-03	3.2E-02	ENSG00000169418	4881
RNF180	-0.8	3.0	9.2	2.4E-03	3.2E-02	ENSG00000164197	285671
SAV1	-0.5	4.9	9.2	2.4E-03	3.2E-02	ENSG00000151748	60485
C14orf132	-0.9	5.8	9.2	2.4E-03	3.2E-02	ENSG00000227051	101929186
BDH2	-0.7	4.8	9.2	2.4E-03	3.2E-02	ENSG00000164039	56898
FAHD2CP	-0.9	1.3	9.2	2.4E-03	3.2E-02	ENSG00000231584	729234
GPM6B	-1.7	5.5	9.2	2.4E-03	3.2E-02	ENSG00000046653	2824
RAI2	-0.9	4.0	9.2	2.4E-03	3.2E-02	ENSG00000131831	10742
ABCA2	-0.6	6.9	9.2	2.4E-03	3.2E-02	ENSG00000107331	20
GNB5	-0.5	4.6	9.2	2.4E-03	3.2E-02	ENSG00000069966	10681
MT3	-2.4	4.5	9.2	2.5E-03	3.2E-02	ENSG00000087250	4504

LGI1	-1.7	1.6	9.2	2.4E-03	3.2E-02	ENSG00000108231	9211
PSD	-1.7	4.3	9.2	2.5E-03	3.2E-02	ENSG00000059915	5662
CCDC3	-1.2	7.4	9.2	2.5E-03	3.2E-02	ENSG00000151468	83643
TPPP3	-1.2	5.7	9.2	2.4E-03	3.2E-02	ENSG00000159713	51673
BMP4	-1.2	4.5	9.2	2.4E-03	3.2E-02	ENSG00000125378	652
PARD3B	-0.9	5.1	9.2	2.5E-03	3.2E-02	ENSG00000116117	117583
SMARCD3	-0.7	6.6	9.2	2.4E-03	3.2E-02	ENSG00000082014	6604
HSPA4L	-0.8	2.8	9.1	2.6E-03	3.3E-02	ENSG00000164070	22824
TEX9	-0.9	1.3	9.1	2.6E-03	3.3E-02	ENSG00000151575	374618
WDFY3-AS2	-0.9	2.2	9.1	2.6E-03	3.3E-02	ENSG00000180769	404201
HMCES	-0.5	5.1	9.1	2.6E-03	3.3E-02	ENSG00000183624	56941
IGLC3	-2.6	5.4	9.1	2.6E-03	3.4E-02	ENSG00000211679	NA
EFCAB6	-0.8	1.0	9.1	2.6E-03	3.4E-02	ENSG00000186976	64800
LMO3	-1.8	2.3	9.0	2.6E-03	3.4E-02	ENSG00000048540	55885
SERPINI1	-1.1	3.3	9.0	2.6E-03	3.4E-02	ENSG00000163536	5274
NA	-0.6	6.3	9.0	2.6E-03	3.4E-02	ENSG00000259850	NA
TSPYL2	-0.7	8.2	9.0	2.7E-03	3.4E-02	ENSG00000184205	64061
FAM180A	-1.5	4.5	9.0	2.7E-03	3.4E-02	ENSG00000189320	389558
MAMDC2	-1.2	3.8	9.0	2.7E-03	3.4E-02	ENSG00000165072	256691
NEURL1	-1.3	2.3	9.0	2.7E-03	3.4E-02	ENSG00000107954	9148
FBXO27	-0.9	1.3	9.0	2.7E-03	3.4E-02	ENSG00000161243	126433
KCNS3	-1.4	4.8	9.0	2.7E-03	3.4E-02	ENSG00000170745	3790
RAB3A	-1.2	2.8	9.0	2.7E-03	3.4E-02	ENSG00000105649	5864
AQP1	-1.3	8.5	9.0	2.7E-03	3.4E-02	ENSG00000240583	358
	-1.4	4.4	9.0	2.7E-03	3.4E-02	ENSG00000223764	NA
PRRT2	-1.4	5.8	8.9	2.8E-03	3.5E-02	ENSG00000167371	112476
EXD3	-0.7	4.8	8.9	2.8E-03	3.5E-02	ENSG00000187609	54932
PKP4	-0.5	6.2	8.9	2.8E-03	3.5E-02	ENSG00000144283	8502
	-1.5	2.9	8.9	2.9E-03	3.6E-02	ENSG00000267506	100507351
NA	-1.5	1.7	8.9	2.9E-03	3.6E-02	ENSG00000260124	NA
PDZD4	-1.2	6.2	8.9	2.9E-03	3.6E-02	ENSG00000067840	57595
THRA	-0.9	6.4	8.9	2.9E-03	3.6E-02	ENSG00000126351	7067
CNKSR1	-0.8	1.6	8.9	2.9E-03	3.6E-02	ENSG00000142675	10256
ARID5B	-0.7	7.4	8.9	2.9E-03	3.6E-02	ENSG00000150347	84159
TNRC6C	-0.6	4.9	8.9	2.9E-03	3.6E-02	ENSG00000078687	57690
SBDS	-0.6	6.5	8.9	2.9E-03	3.6E-02	ENSG00000126524	51119
RBP4	-1.2	2.8	8.9	2.9E-03	3.6E-02	ENSG00000138207	5950
TMEM184A	-1.2	2.9	8.9	2.9E-03	3.6E-02	ENSG00000164855	101927064
LRRCC1	-0.7	3.4	8.9	2.9E-03	3.6E-02	ENSG00000133739	85444
GPR126	-1.2	3.3	8.8	3.0E-03	3.6E-02	ENSG00000112414	57211
ABLIM1	-0.8	7.1	8.8	3.0E-03	3.6E-02	ENSG00000099204	3983
DENND5B	-0.6	3.8	8.8	3.0E-03	3.7E-02	ENSG00000170456	160518
MORN4	-0.8	2.9	8.8	3.0E-03	3.7E-02	ENSG00000171160	118812
LINC00702	-0.9	1.3	8.8	3.0E-03	3.7E-02	ENSG00000233117	100652988
NPTXR	-1.3	4.9	8.8	3.0E-03	3.7E-02	ENSG00000221890	23467

ATOH8	-1.2	5.5	8.8	3.0E-03	3.7E-02	ENSG00000168874	84913
SLC25A25	-0.7	6.4	8.8	3.0E-03	3.7E-02	ENSG00000148339	114789
TLE1	-0.7	4.8	8.8	3.0E-03	3.7E-02	ENSG00000196781	7088
DOCK9	-0.8	6.1	8.8	3.1E-03	3.7E-02	ENSG00000088387	23348
RUNDC3A	-1.9	3.2	8.8	3.1E-03	3.7E-02	ENSG00000108309	10900
RAMP3	-1.4	4.4	8.8	3.1E-03	3.7E-02	ENSG00000122679	10268
ADAMTS5	-1.2	3.9	8.8	3.1E-03	3.7E-02	ENSG00000154736	11096
ZNF483	-1.0	0.5	8.8	3.1E-03	3.7E-02	ENSG00000173258	158399
PRICKLE2	-0.8	4.8	8.8	3.1E-03	3.7E-02	ENSG00000163637	166336
SSPN	-0.8	3.2	8.8	3.1E-03	3.7E-02	ENSG00000123096	8082
DMTN	-1.0	4.7	8.7	3.1E-03	3.8E-02	ENSG00000158856	2039
MAGI2-AS3	-0.7	5.3	8.7	3.1E-03	3.8E-02	ENSG00000234456	100505881
UNC13A	-1.2	5.1	8.7	3.1E-03	3.8E-02	ENSG00000130477	23025
ACYP2	-0.6	2.7	8.7	3.2E-03	3.8E-02	ENSG00000170634	101927144
PAX6	-1.0	2.0	8.7	3.2E-03	3.8E-02	ENSG00000007372	5080
EDN3	-1.8	2.3	8.7	3.2E-03	3.8E-02	ENSG00000124205	1908
ZNF630	-0.6	1.9	8.7	3.2E-03	3.8E-02	ENSG00000221994	57232
	-1.2	4.1	8.7	3.2E-03	3.9E-02	ENSG00000257337	283335
TSPYL4	-0.6	5.7	8.7	3.2E-03	3.9E-02	ENSG00000187189	23270
RIPK4	-1.5	3.6	8.6	3.3E-03	3.9E-02	ENSG00000183421	54101
TCEAL4	-0.6	6.5	8.6	3.3E-03	3.9E-02	ENSG00000133142	79921
	-0.5	2.6	8.6	3.3E-03	3.9E-02	ENSG00000245958	101926979
AMN1	-0.5	2.0	8.6	3.3E-03	3.9E-02	ENSG00000151743	196394
HSPA2	-1.0	5.7	8.6	3.4E-03	3.9E-02	ENSG00000126803	3306
KLF15	-1.5	2.9	8.6	3.4E-03	4.0E-02	ENSG00000163884	28999
HEYL	-1.2	6.8	8.6	3.4E-03	4.0E-02	ENSG00000163909	26508
PLXNA2	-0.7	6.7	8.6	3.4E-03	4.0E-02	ENSG00000076356	5362
CYBRD1	-0.8	8.2	8.6	3.4E-03	4.0E-02	ENSG00000071967	79901
ZMYND11	-0.5	6.4	8.6	3.4E-03	4.0E-02	ENSG00000015171	10771
	-1.4	1.5	8.6	3.4E-03	4.0E-02	ENSG00000232415	NA
HIP1	-0.8	7.2	8.6	3.4E-03	4.0E-02	ENSG00000127946	3092
MARC2	-0.9	3.8	8.6	3.4E-03	4.0E-02	ENSG00000117791	54996
RASL11B	-1.5	3.2	8.6	3.4E-03	4.0E-02	ENSG00000128045	65997
ANO2	-1.1	3.0	8.6	3.4E-03	4.0E-02	ENSG00000047617	57101
FBXL17	-0.5	4.4	8.5	3.5E-03	4.0E-02	ENSG00000145743	64839
XG	-2.1	2.4	8.5	3.5E-03	4.0E-02	ENSG00000124343	100132596
KIF5A	-1.9	5.6	8.5	3.5E-03	4.0E-02	ENSG00000155980	3798
PHACTR3	-1.8	1.8	8.5	3.5E-03	4.0E-02	ENSG00000087495	116154
ABLIM2	-1.1	3.2	8.5	3.5E-03	4.1E-02	ENSG00000163995	84448
HCFC1R1	-0.7	6.2	8.5	3.5E-03	4.1E-02	ENSG00000103145	54985
TCF4	-0.6	7.3	8.5	3.6E-03	4.1E-02	ENSG00000196628	6925
UBE2E2	-0.5	5.0	8.5	3.5E-03	4.1E-02	ENSG00000182247	7325
SLC25A27	-1.0	3.6	8.5	3.6E-03	4.1E-02	ENSG00000153291	9481
LINC00865	-1.1	1.8	8.5	3.6E-03	4.1E-02	ENSG00000232229	643529
MN1	-0.9	5.6	8.5	3.6E-03	4.1E-02	ENSG00000169184	4330

DCST2	-0.6	1.2	8.5	3.6E-03	4.1E-02	ENSG00000163354	127579
ACSL6	-1.5	1.6	8.5	3.6E-03	4.1E-02	ENSG00000164398	23305
TSPAN7	-1.3	3.9	8.5	3.6E-03	4.1E-02	ENSG00000156298	7102
AXIN2	-0.8	4.4	8.5	3.6E-03	4.1E-02	ENSG00000168646	8313
MCF2L2	-1.2	1.4	8.5	3.6E-03	4.1E-02	ENSG00000053524	23101
C6	-1.7	1.9	8.5	3.6E-03	4.1E-02	ENSG00000039537	729
ACTR3B	-0.7	2.2	8.5	3.6E-03	4.1E-02	ENSG00000133627	57180
POT1-AS1	-1.0	1.1	8.4	3.7E-03	4.2E-02	ENSG00000224897	NA
DKK3	-1.1	9.2	8.4	3.7E-03	4.2E-02	ENSG00000050165	27122
STON1	-0.9	3.9	8.4	3.7E-03	4.2E-02	ENSG00000243244	11037
HABP4	-0.8	5.7	8.4	3.7E-03	4.2E-02	ENSG00000130956	22927
LTBP4	-1.1	9.0	8.4	3.8E-03	4.2E-02	ENSG00000090006	8425
AJUBA	-0.9	4.3	8.4	3.8E-03	4.2E-02	ENSG00000129474	84962
PRELP	-1.3	9.6	8.4	3.8E-03	4.2E-02	ENSG00000188783	5549
MVB12B	-0.6	4.4	8.4	3.8E-03	4.2E-02	ENSG00000196814	89853
ID1	-1.0	6.0	8.4	3.8E-03	4.3E-02	ENSG00000125968	3397
SOD3	-1.1	7.2	8.4	3.8E-03	4.3E-02	ENSG00000109610	6649
NA	-1.2	1.0	8.3	3.9E-03	4.3E-02	ENSG00000262359	NA
MAP6	-1.0	3.8	8.3	3.9E-03	4.3E-02	ENSG00000171533	4135
IGSF21	-1.2	2.5	8.3	3.9E-03	4.4E-02	ENSG00000117154	84966
LCA5	-0.6	3.2	8.3	4.0E-03	4.4E-02	ENSG00000135338	167691
SOX7	-1.2	3.2	8.3	4.0E-03	4.4E-02	ENSG00000171056	83595
C5	-0.6	3.2	8.3	4.0E-03	4.4E-02	ENSG00000106804	727
FBXL3	-0.4	5.8	8.3	4.0E-03	4.4E-02	ENSG00000005812	26224
SEMA5B	-1.5	3.7	8.3	4.0E-03	4.4E-02	ENSG00000082684	54437
SLC6A3	-1.5	1.4	8.3	4.0E-03	4.4E-02	ENSG00000142319	6531
TCEAL1	-0.6	4.4	8.3	4.0E-03	4.4E-02	ENSG00000172465	9338
SFRP2	-1.7	7.9	8.3	4.1E-03	4.4E-02	ENSG00000145423	6423
PLAC9	-0.9	4.6	8.3	4.1E-03	4.4E-02	ENSG00000189129	219348
RAVER2	-0.8	4.1	8.3	4.1E-03	4.4E-02	ENSG00000162437	55225
MICU3	-0.7	3.1	8.3	4.1E-03	4.5E-02	ENSG00000155970	286097
BCL2	-0.5	4.5	8.2	4.1E-03	4.5E-02	ENSG00000171791	596
PTPRZ1	-1.9	4.2	8.2	4.1E-03	4.5E-02	ENSG00000106278	5803
PRDM11	-0.7	3.4	8.2	4.1E-03	4.5E-02	ENSG00000019485	101060179
	-1.4	4.8	8.2	4.1E-03	4.5E-02	ENSG00000261685	NA
NHS	-0.9	5.5	8.2	4.1E-03	4.5E-02	ENSG00000188158	4810
ATP2B2	-1.5	2.1	8.2	4.1E-03	4.5E-02	ENSG00000157087	491
TMEM30B	-1.2	4.1	8.2	4.1E-03	4.5E-02	ENSG00000182107	161291
NA	-0.8	2.5	8.2	4.1E-03	4.5E-02	ENSG00000205873	NA
TLE2	-0.9	4.7	8.2	4.2E-03	4.5E-02	ENSG00000065717	7089
SBDSP1	-0.5	5.0	8.2	4.2E-03	4.5E-02	ENSG00000225648	155370
	-1.1	1.4	8.2	4.2E-03	4.5E-02	ENSG00000259426	NA
ATRNL1	-1.5	2.2	8.2	4.2E-03	4.6E-02	ENSG00000107518	26033
THSD4	-1.0	6.7	8.2	4.3E-03	4.6E-02	ENSG00000187720	79875
FAM222A	-0.8	1.2	8.2	4.3E-03	4.6E-02	ENSG00000139438	84915

KIAA0355	-0.6	6.3	8.2	4.3E-03	4.6E-02	ENSG00000166398	9710
LRRC23	-0.6	3.1	8.2	4.3E-03	4.6E-02	ENSG00000010626	10233
NELL2	-1.3	2.2	8.1	4.3E-03	4.6E-02	ENSG00000184613	4753
ZNF529	-0.5	4.2	8.1	4.3E-03	4.6E-02	ENSG00000186020	57711
FBXO44	-0.7	4.6	8.1	4.3E-03	4.6E-02	ENSG00000132879	93611
C1QTNF1	-1.2	8.0	8.1	4.4E-03	4.7E-02	ENSG00000173918	114897
ELOVL2	-1.4	2.0	8.1	4.4E-03	4.7E-02	ENSG00000197977	54898
MMP28	-0.8	4.3	8.1	4.4E-03	4.7E-02	ENSG00000129270	79148
APC2	-1.2	3.4	8.1	4.4E-03	4.7E-02	ENSG00000115266	10297
FAM155A	-0.9	2.1	8.1	4.4E-03	4.7E-02	ENSG00000204442	728215
LNK1	-0.8	1.3	8.1	4.4E-03	4.7E-02	ENSG00000072201	84708
CAPS2	-0.7	2.1	8.1	4.4E-03	4.7E-02	ENSG00000180881	84698
FAM8A1	-0.4	5.4	8.1	4.5E-03	4.7E-02	ENSG00000137414	51439
TRIM2	-0.8	4.0	8.1	4.5E-03	4.7E-02	ENSG00000109654	23321
NAB1	-0.5	6.3	8.1	4.5E-03	4.7E-02	ENSG00000138386	4664
ARHGEF9	-0.8	5.8	8.1	4.5E-03	4.7E-02	ENSG00000131089	23229
GLS2	-0.8	1.5	8.1	4.5E-03	4.7E-02	ENSG00000135423	27165
CHADL	-1.0	1.2	8.0	4.6E-03	4.8E-02	ENSG00000100399	150356
PAGR1	-0.9	5.3	8.0	4.6E-03	4.8E-02	ENSG00000185928	79447
ZNF521	-0.8	3.0	8.0	4.6E-03	4.8E-02	ENSG00000198795	25925
	-0.7	1.1	8.0	4.6E-03	4.8E-02	ENSG00000247081	101927343
TMEM116	-0.6	2.3	8.0	4.6E-03	4.8E-02	ENSG00000198270	89894
DLX5	-1.7	1.2	8.0	4.7E-03	4.8E-02	ENSG00000105880	1749
	-0.6	2.9	8.0	4.7E-03	4.8E-02	ENSG00000269834	NA
RCAN2	-1.4	7.1	8.0	4.7E-03	4.8E-02	ENSG00000172348	10231
RGS5	-1.4	9.1	8.0	4.7E-03	4.9E-02	ENSG00000143248	8490
ZSCAN18	-0.6	5.6	8.0	4.7E-03	4.9E-02	ENSG00000121413	65982
B4GALNT4	-1.3	2.8	8.0	4.8E-03	4.9E-02	ENSG00000182272	338707
RGN	-1.0	3.1	8.0	4.8E-03	4.9E-02	ENSG00000130988	9104
FAM66C	-0.8	0.7	8.0	4.8E-03	4.9E-02	ENSG00000226711	101928910
MYO7B	-0.9	3.8	8.0	4.8E-03	4.9E-02	ENSG00000169994	4648
PODXL2	-0.9	2.6	8.0	4.8E-03	4.9E-02	ENSG00000114631	50512
EVA1C	-0.8	3.9	8.0	4.8E-03	4.9E-02	ENSG00000166979	59271
MBNL2	-0.5	5.6	7.9	4.8E-03	4.9E-02	ENSG00000139793	10150
FBXO36	-0.6	1.4	7.9	4.8E-03	4.9E-02	ENSG00000153832	130888
TUBE1	-0.4	3.8	7.9	4.9E-03	4.9E-02	ENSG00000074935	51175
STK32A	-1.2	2.2	7.9	4.9E-03	4.9E-02	ENSG00000169302	202374
GPRASP1	-0.9	5.3	7.9	4.9E-03	5.0E-02	ENSG00000198932	9737
STON2	-1.6	2.2	7.9	5.0E-03	5.0E-02	ENSG00000140022	85439

Hgnc indicates Human gene nomenclature committee; FC, fold change; CPM, counts per million, LR, likelihood ratio, FDR, false discovery rate.

Supplementary Table VII. Enriched Kyoto Encyclopedia of Genes and Genomes pathways in ruptured versus unruptured aneurysms.

KEGG-pathway		Number of genes DE in term/total number of genes in pathway	P-value
hsa 04142	<i>Lysosome</i>	41/111	6.1E-12
hsa 04380	<i>Osteoclast differentiation</i>	34/117	4.9E-7
hsa 05150	<i>Staphylococcus aureus infection</i>	19/49	1.8E-6
hsa 04145	<i>Phagosome</i>	35/131	2.8E-6
hsa 05140	<i>Leishmaniasis</i>	18/64	4.0E-4
hsa 04666	<i>Fc gamma R-mediated phagocytosis</i>	21/88	1.3E-3

KEGG indicates Kyoto Encyclopedia of Genes and Genomes; DE, differentially expressed.

Supplementary Table VIII. Enriched Gene Ontology categories in ruptured versus unruptured aneurysms after trimming

Category	Description	Over represented P-value
GO:0007067	mitosis	5.7E-05
GO:0010720	positive regulation of cell development	3.9E-04
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	1.1E-04
GO:0031589	cell-substrate adhesion	6.0E-03
GO:0070228	regulation of lymphocyte apoptotic process	2.0E-03
GO:0045335	phagocytic vesicle	9.0E-05
GO:0048638	regulation of developmental growth	2.2E-03
GO:0010324	membrane invagination	6.8E-04
GO:0045839	negative regulation of mitosis	4.5E-03
GO:0007265	Ras protein signal transduction	1.8E-03
GO:0009620	response to fungus	1.1E-03
GO:0014013	regulation of gliogenesis	6.5E-06
GO:0017157	regulation of exocytosis	7.1E-04
GO:0009617	response to bacterium	2.3E-09
GO:0002521	leukocyte differentiation	2.7E-03
GO:0007088	regulation of mitosis	3.3E-04
GO:0055065	metal ion homeostasis	8.3E-04
GO:0007186	G-protein coupled receptor signaling pathway	1.9E-05
GO:0009311	oligosaccharide metabolic process	1.7E-04
GO:0006897	endocytosis	3.5E-08
GO:0006898	receptor-mediated endocytosis	6.2E-03
GO:0045121	membrane raft	7.2E-03
GO:0045664	regulation of neuron differentiation	5.2E-03
GO:0014003	oligodendrocyte development	6.4E-04
GO:0002768	immune response-regulating cell surface receptor signaling pathway	1.3E-04
GO:0009118	regulation of nucleoside metabolic process	1.0E-03
GO:0009306	protein secretion	5.8E-06
GO:0002685	regulation of leukocyte migration	2.8E-08
GO:2000106	regulation of leukocyte apoptotic process	4.2E-04
GO:2000107	negative regulation of leukocyte apoptotic process	7.1E-03
GO:0019915	lipid storage	5.7E-03
GO:0055072	iron ion homeostasis	9.2E-03
GO:0045860	positive regulation of protein kinase activity	2.1E-04
GO:0007589	body fluid secretion	4.4E-03
GO:0000793	condensed chromosome	7.2E-04
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	8.5E-03
GO:0030335	positive regulation of cell migration	1.4E-03
GO:2000177	regulation of neural precursor cell proliferation	7.7E-04
GO:0051701	interaction with host	8.5E-03

GO:0002548	monocyte chemotaxis	8.3E-03
GO:0050670	regulation of lymphocyte proliferation	3.3E-03
GO:0050672	negative regulation of lymphocyte proliferation	3.7E-03
GO:0045785	positive regulation of cell adhesion	2.5E-03
GO:0031349	positive regulation of defense response	1.1E-06
GO:0045202	synapse	1.5E-03
GO:0007229	integrin-mediated signaling pathway	1.6E-05
GO:0050663	cytokine secretion	3.7E-06
GO:0030833	regulation of actin filament polymerization	5.3E-04
GO:0031334	positive regulation of protein complex assembly	1.8E-03
GO:0002757	immune response-activating signal transduction	7.4E-11
GO:0050767	regulation of neurogenesis	1.8E-04
GO:0030838	positive regulation of actin filament polymerization	1.2E-03
GO:0050766	positive regulation of phagocytosis	5.2E-05
GO:0070374	positive regulation of ERK1 and ERK2 cascade	2.3E-03
GO:0050764	regulation of phagocytosis	4.9E-07
GO:0050867	positive regulation of cell activation	2.3E-03
GO:0050864	regulation of B cell activation	8.0E-03
GO:0050865	regulation of cell activation	7.9E-04
GO:0070372	regulation of ERK1 and ERK2 cascade	2.9E-04
GO:0002429	immune response-activating cell surface receptor signaling pathway	1.5E-06
GO:0004896	cytokine receptor activity	4.0E-04
GO:0003206	cardiac chamber morphogenesis	8.7E-03
GO:0045766	positive regulation of angiogenesis	7.2E-03
GO:0002526	acute inflammatory response	8.3E-03
GO:0002532	production of molecular mediator involved in inflammatory response	3.7E-03
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	2.6E-05
GO:0045088	regulation of innate immune response	6.3E-08
GO:0006518	peptide metabolic process	9.8E-03
GO:0000070	mitotic sister chromatid segregation	9.4E-05
GO:0051046	regulation of secretion	1.4E-05
GO:0051047	positive regulation of secretion	1.4E-04
GO:0051048	negative regulation of secretion	3.0E-03
GO:0050885	neuromuscular process controlling balance	3.5E-03
GO:0006096	glycolysis	9.6E-04
GO:0030855	epithelial cell differentiation	1.3E-03
GO:0002444	myeloid leukocyte mediated immunity	1.0E-05
GO:0002443	leukocyte mediated immunity	7.0E-04
GO:0042742	defense response to bacterium	6.7E-11
GO:0048708	astrocyte differentiation	4.6E-03
GO:0048709	oligodendrocyte differentiation	3.6E-05
GO:0051051	negative regulation of transport	4.4E-03

GO:0043303	mast cell degranulation	3.9E-05
GO:0006833	water transport	9.0E-03
GO:0002702	positive regulation of production of molecular mediator of immune response	2.7E-03
GO:0002703	regulation of leukocyte mediated immunity	2.7E-03
GO:0002700	regulation of production of molecular mediator of immune response	1.5E-03
GO:0061134	peptidase regulator activity	7.0E-03
GO:0006826	iron ion transport	2.5E-04
GO:0019751	polyol metabolic process	8.4E-03
GO:0030666	endocytic vesicle membrane	2.1E-03
GO:0002718	regulation of cytokine production involved in immune response	6.8E-04
GO:0010001	glial cell differentiation	2.2E-04
GO:0060627	regulation of vesicle-mediated transport	2.4E-05
GO:0046651	lymphocyte proliferation	4.9E-04
GO:0009986	cell surface	1.6E-05
GO:0046173	polyol biosynthetic process	1.9E-03
GO:0006066	alcohol metabolic process	1.7E-03
GO:0005819	spindle	1.6E-05
GO:0033124	regulation of GTP catabolic process	3.5E-03
GO:0032612	interleukin-1 production	3.3E-03
GO:0006801	superoxide metabolic process	1.1E-03
GO:0033628	regulation of cell adhesion mediated by integrin	7.2E-03
GO:0006691	leukotriene metabolic process	2.7E-05
GO:0006820	anion transport	7.1E-05
GO:0021983	pituitary gland development	6.7E-03
GO:0033121	regulation of purine nucleotide catabolic process	9.3E-04
GO:0043410	positive regulation of MAPK cascade	6.2E-05
GO:0097285	cell-type specific apoptotic process	3.1E-03
GO:0046847	filopodium assembly	7.9E-03
GO:0005044	scavenger receptor activity	6.8E-03
GO:0007015	actin filament organization	2.0E-03
GO:0006816	calcium ion transport	2.3E-03
GO:0021700	developmental maturation	1.8E-03
GO:0032602	chemokine production	7.2E-03
GO:0019722	calcium-mediated signaling	6.7E-03
GO:0016051	carbohydrate biosynthetic process	6.9E-03
GO:0000226	microtubule cytoskeleton organization	7.0E-04
GO:0006040	amino sugar metabolic process	6.0E-03
GO:0032680	regulation of tumor necrosis factor production	1.7E-04
GO:0006687	glycosphingolipid metabolic process	1.2E-03
GO:0014069	postsynaptic density	2.0E-03
GO:0006875	cellular metal ion homeostasis	3.4E-04
GO:0065004	protein-DNA complex assembly	5.2E-03
GO:0043547	positive regulation of GTPase activity	7.9E-03

GO:0032675	regulation of interleukin-6 production	1.4E-08
GO:0000777	condensed chromosome kinetochore	3.5E-04
GO:0019897	extrinsic component of plasma membrane	5.3E-03
GO:0019898	extrinsic component of membrane	1.0E-03
GO:0006968	cellular defense response	1.5E-03
GO:0006672	ceramide metabolic process	5.2E-03
GO:0045576	mast cell activation	3.9E-04
GO:0008528	G-protein coupled peptide receptor activity	1.6E-03
GO:0006887	exocytosis	1.5E-05
GO:0010038	response to metal ion	2.5E-04
GO:0045685	regulation of glial cell differentiation	1.0E-03
GO:0048168	regulation of neuronal synaptic plasticity	3.3E-03
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	1.4E-03
GO:0048029	monosaccharide binding	2.7E-03
GO:0033559	unsaturated fatty acid metabolic process	6.0E-03
GO:0007040	lysosome organization	6.2E-04
GO:0032655	regulation of interleukin-12 production	4.2E-03
GO:0032651	regulation of interleukin-1 beta production	7.3E-03
GO:0008017	microtubule binding	1.1E-03
GO:0034502	protein localization to chromosome	4.6E-03
GO:0006865	amino acid transport	2.8E-03
GO:0007059	chromosome segregation	2.8E-05
GO:0003774	motor activity	2.1E-04
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	4.2E-03
GO:0046942	carboxylic acid transport	2.3E-04
GO:0007051	spindle organization	5.3E-04
GO:0098542	defense response to other organism	1.7E-06
GO:0007052	mitotic spindle organization	6.3E-03
GO:0005200	structural constituent of cytoskeleton	1.5E-03
GO:0051480	cytosolic calcium ion homeostasis	7.2E-03
GO:0016042	lipid catabolic process	8.2E-03
GO:0071248	cellular response to metal ion	1.9E-04
GO:0042116	macrophage activation	1.5E-03
GO:0001503	ossification	6.6E-03
GO:0042119	neutrophil activation	9.4E-04
GO:0032755	positive regulation of interleukin-6 production	4.8E-06
GO:0033028	myeloid cell apoptotic process	6.3E-03
GO:0005788	endoplasmic reticulum lumen	4.0E-03
GO:0005884	actin filament	3.2E-04
GO:0051493	regulation of cytoskeleton organization	3.3E-04
GO:0006323	DNA packaging	1.1E-03
GO:0043623	cellular protein complex assembly	2.3E-03
GO:0000910	cytokinesis	2.7E-03
GO:0050920	regulation of chemotaxis	5.5E-03

GO:0003779	actin binding	3.2E-08
GO:0032956	regulation of actin cytoskeleton organization	3.6E-03
GO:0003777	microtubule motor activity	8.7E-03
GO:0032760	positive regulation of tumor necrosis factor production	3.8E-04
GO:0001101	response to acid	6.4E-03
GO:0042379	chemokine receptor binding	7.7E-03
GO:0044273	sulfur compound catabolic process	4.5E-03
GO:1901880	negative regulation of protein depolymerization	2.5E-03
GO:0051495	positive regulation of cytoskeleton organization	1.8E-03
GO:0000922	spindle pole	9.4E-06
GO:0008237	metallopeptidase activity	9.1E-03
GO:0002274	myeloid leukocyte activation	1.6E-07
GO:0002275	myeloid cell activation involved in immune response	1.3E-07
GO:0072503	cellular divalent inorganic cation homeostasis	1.3E-03
GO:0005764	lysosome	5.9E-12
GO:0005765	lysosomal membrane	8.1E-03
GO:0071900	regulation of protein serine/threonine kinase activity	9.4E-03
GO:0001817	regulation of cytokine production	3.0E-05
GO:0001818	negative regulation of cytokine production	8.6E-03
GO:0001819	positive regulation of cytokine production	3.7E-04
GO:0002886	regulation of myeloid leukocyte mediated immunity	1.5E-05
GO:0050900	leukocyte migration	7.2E-12
GO:0006007	glucose catabolic process	3.6E-04
GO:0043202	lysosomal lumen	2.3E-08
GO:0046364	monosaccharide biosynthetic process	5.6E-03
GO:1902105	regulation of leukocyte differentiation	6.7E-03
GO:0030595	leukocyte chemotaxis	2.6E-09
GO:0070098	chemokine-mediated signaling pathway	2.4E-03
GO:0030097	hemopoiesis	7.8E-03
GO:0030193	regulation of blood coagulation	1.2E-03
GO:0071346	cellular response to interferon-gamma	5.8E-04
GO:0007601	visual perception	7.4E-03
GO:0015909	long-chain fatty acid transport	4.2E-03
GO:0008360	regulation of cell shape	1.7E-03
GO:0005539	glycosaminoglycan binding	3.8E-03
GO:0021782	glial cell development	3.2E-03
GO:0002224	toll-like receptor signaling pathway	7.7E-05
GO:0048469	cell maturation	6.9E-03
GO:0030198	extracellular matrix organization	1.0E-04
GO:0030593	neutrophil chemotaxis	7.9E-04
GO:0005834	heterotrimeric G-protein complex	4.5E-03
GO:0002366	leukocyte activation involved in immune response	7.5E-06
GO:0001726	ruffle	3.2E-03
GO:0005871	kinesin complex	1.9E-03
GO:0005126	cytokine receptor binding	1.7E-03

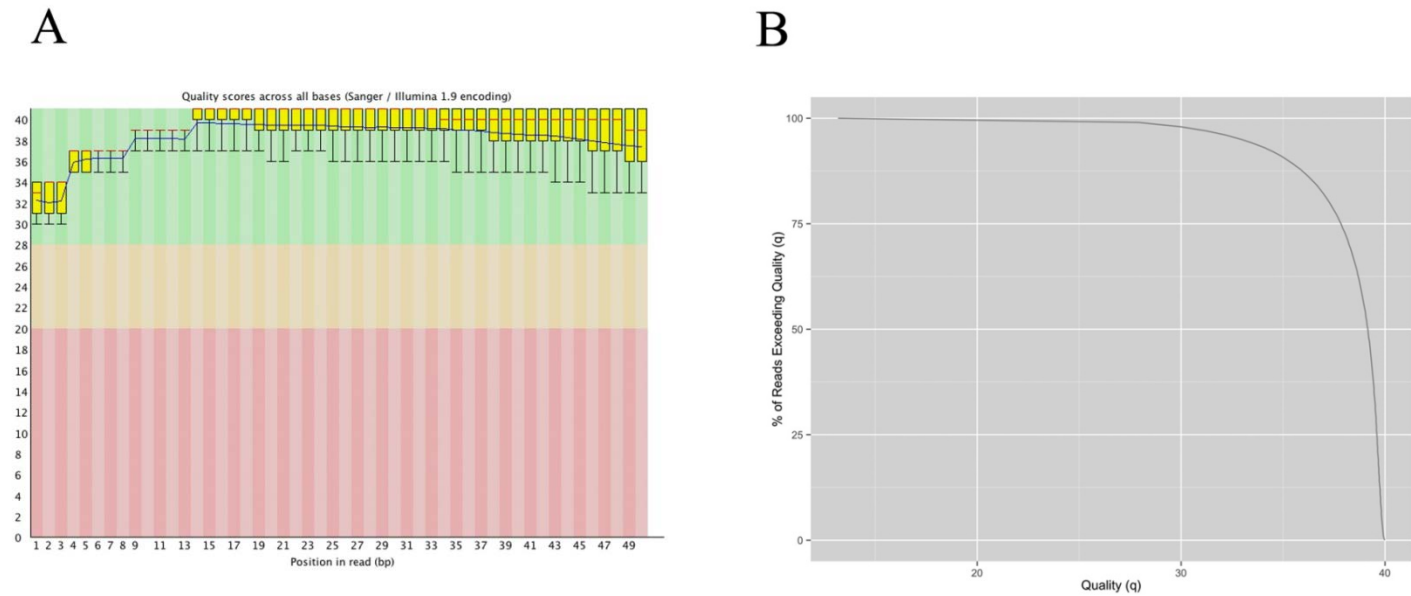
GO:0005125	cytokine activity	3.8E-04
GO:0030071	regulation of mitotic metaphase/anaphase transition	1.0E-03
GO:0042035	regulation of cytokine biosynthetic process	8.1E-04
GO:0071222	cellular response to lipopolysaccharide	8.4E-05
GO:0043235	receptor complex	1.9E-03
GO:0022604	regulation of cell morphogenesis	8.1E-03
GO:0071229	cellular response to acid	4.5E-03
GO:0022411	cellular component disassembly	7.0E-03
GO:0032535	regulation of cellular component size	2.3E-04
GO:0006909	phagocytosis	2.0E-09
GO:0043254	regulation of protein complex assembly	2.0E-03
GO:0033003	regulation of mast cell activation	7.1E-04
GO:0015629	actin cytoskeleton	3.6E-06
GO:0016323	basolateral plasma membrane	5.6E-04
GO:0022617	extracellular matrix disassembly	4.5E-03
GO:0031091	platelet alpha granule	4.7E-03
GO:0043406	positive regulation of MAP kinase activity	5.5E-03
GO:0031256	leading edge membrane	8.6E-04
GO:0001894	tissue homeostasis	7.5E-03
GO:0044304	main axon	9.9E-03
GO:0050727	regulation of inflammatory response	3.9E-03
GO:0030246	carbohydrate binding	4.8E-08
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	6.4E-04
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	1.1E-03
GO:0030261	chromosome condensation	1.8E-03
GO:0050830	defense response to Gram-positive bacterium	3.6E-07
GO:0043269	regulation of ion transport	3.8E-03
GO:0030155	regulation of cell adhesion	7.4E-04
GO:0032103	positive regulation of response to external stimulus	2.9E-03
GO:0061351	neural precursor cell proliferation	4.0E-05
GO:0018108	peptidyl-tyrosine phosphorylation	1.7E-03
GO:0090382	phagosome maturation	6.1E-04
GO:0071173	spindle assembly checkpoint	8.0E-03
GO:0030027	lamellipodium	2.5E-03
GO:0030168	platelet activation	2.6E-06
GO:0051222	positive regulation of protein transport	6.5E-04
GO:0005578	proteinaceous extracellular matrix	8.7E-06
GO:0043087	regulation of GTPase activity	3.3E-03
GO:0051223	regulation of protein transport	4.8E-04
GO:0050701	interleukin-1 secretion	7.6E-04
GO:0051129	negative regulation of cellular component organization	4.0E-04
GO:0050708	regulation of protein secretion	1.8E-05
GO:0050709	negative regulation of protein secretion	5.0E-03
GO:0002478	antigen processing and presentation of exogenous peptide antigen	8.6E-03

GO:0030225	macrophage differentiation	5.4E-04
GO:0050853	B cell receptor signaling pathway	2.6E-05
GO:0097529	myeloid leukocyte migration	8.7E-08
GO:0038032	termination of G-protein coupled receptor signaling pathway	8.5E-03
GO:0002576	platelet degranulation	3.6E-05
GO:0002573	myeloid leukocyte differentiation	7.1E-03
GO:0050715	positive regulation of cytokine secretion	3.6E-05
GO:0034381	plasma lipoprotein particle clearance	8.5E-03
GO:0032386	regulation of intracellular transport	1.9E-03
GO:0001755	neural crest cell migration	6.1E-03
GO:0031252	cell leading edge	1.8E-05
GO:0031253	cell projection membrane	5.0E-03
GO:0051241	negative regulation of multicellular organismal process	5.4E-04
GO:0032496	response to lipopolysaccharide	3.0E-04
GO:0030100	regulation of endocytosis	3.7E-05
GO:2000401	regulation of lymphocyte migration	1.5E-03
GO:0038024	cargo receptor activity	3.1E-04
GO:0002699	positive regulation of immune effector process	4.0E-03
GO:0051235	maintenance of location	8.2E-04
GO:0017124	SH3 domain binding	9.5E-05
GO:0010543	regulation of platelet activation	3.2E-04
GO:0002687	positive regulation of leukocyte migration	1.1E-05
GO:0002697	regulation of immune effector process	3.5E-03
GO:0001948	glycoprotein binding	1.9E-03
GO:0002694	regulation of leukocyte activation	6.2E-03
GO:0044456	synapse part	3.3E-03
GO:0002690	positive regulation of leukocyte chemotaxis	5.5E-04
GO:0051783	regulation of nuclear division	3.1E-05
GO:0042098	T cell proliferation	5.0E-03
GO:0004930	G-protein coupled receptor activity	5.1E-03
GO:0045926	negative regulation of growth	1.7E-03
GO:0051785	positive regulation of nuclear division	2.3E-03
GO:0001664	G-protein coupled receptor binding	3.0E-03
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	1.6E-04
GO:0007568	aging	1.8E-03
GO:0004620	phospholipase activity	7.0E-04
GO:0010638	positive regulation of organelle organization	4.6E-04
GO:0044724	single-organism carbohydrate catabolic process	1.8E-04
GO:0010639	negative regulation of organelle organization	8.6E-05
GO:0051653	spindle localization	7.0E-03
GO:0004715	non-membrane spanning protein tyrosine kinase activity	6.3E-03
GO:0030139	endocytic vesicle	5.2E-04
GO:0030282	bone mineralization	8.4E-03
GO:0071396	cellular response to lipid	6.3E-04

GO:0016459	myosin complex	4.9E-03
GO:0010564	regulation of cell cycle process	2.7E-03
GO:0045807	positive regulation of endocytosis	1.2E-03
GO:0030278	regulation of ossification	8.5E-03
GO:0044437	vacuolar part	1.1E-06

SUPPLEMENTAL FIGURES

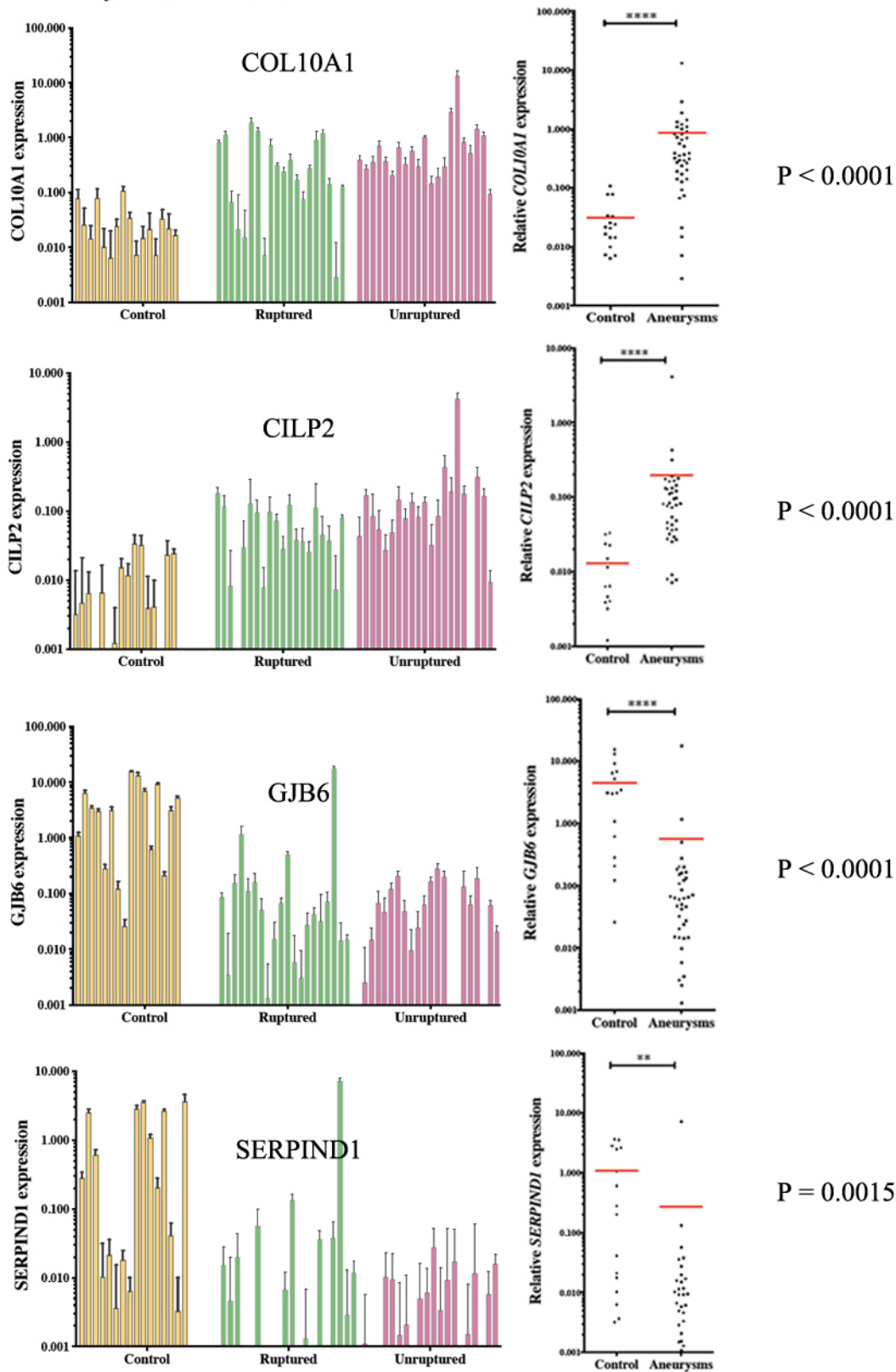
Figure I. Summary of the per base sequencing plots of the control and aneurysm samples.



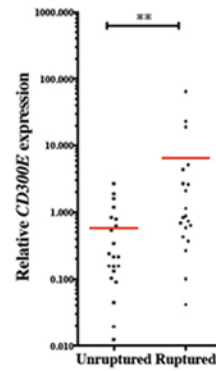
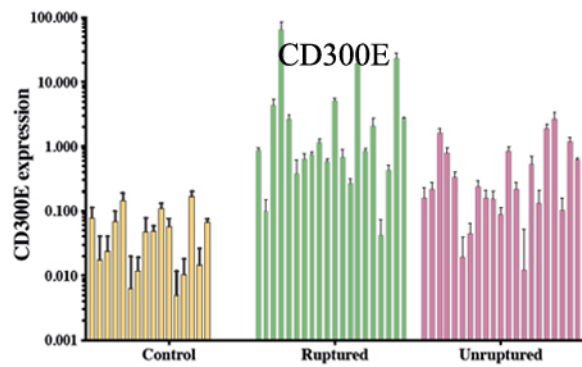
Panel A represents an overview of the range of quality values across all bases at each position in the reads from all the samples studied. Panel B shows the average quality pattern from all the samples studied (e.g. the quality thresholds plotted against the percentage of reads exceeding a quality threshold of 30).

Figure II. Normalized expression of the genes in the validation experiment.

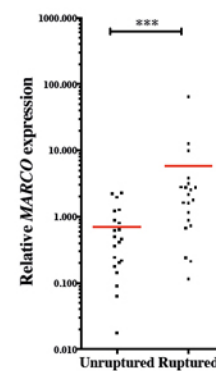
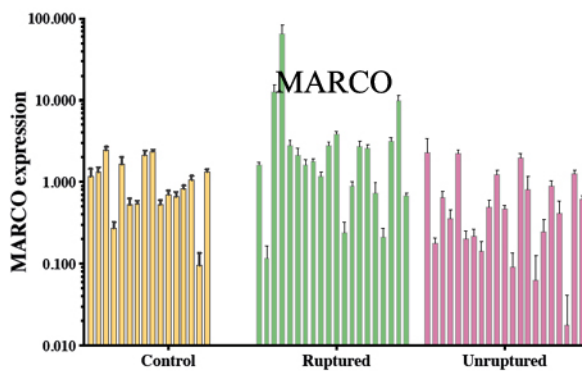
A. Aneurysm versus Controls



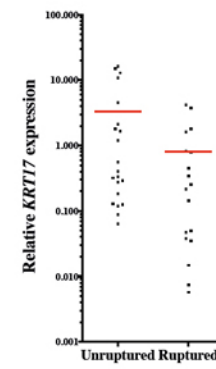
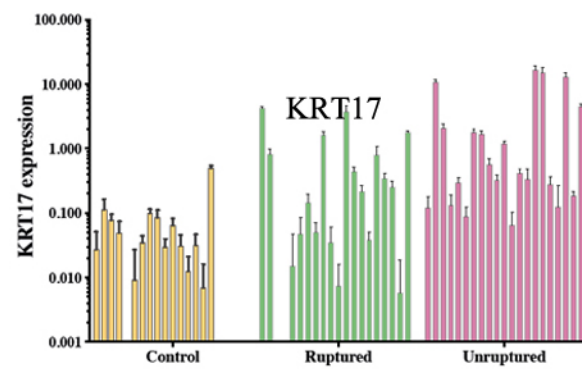
B. Ruptured versus Unruptured Aneurysms



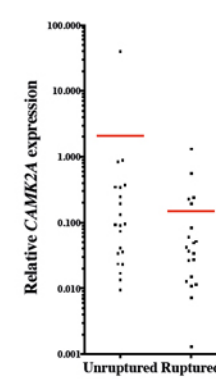
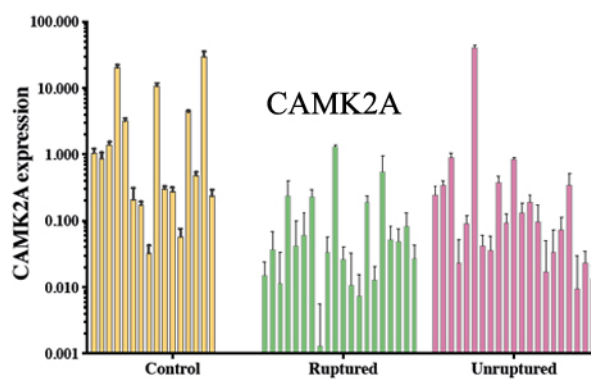
$P = 0.0039$



$P = 0.0006$



$P = 0.06$



$P = 0.1085$

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