

SUPPLEMENTAL MATERIALS

Figures S1 – S6

Tables S1 – S5

SUPPLEMENTAL FIGURES

Supplemental Figure S1. Schematic workflow for RNA-sequencing and phosphoproteomics.

Experimental and bioinformatics details for samples utilized in this study for RNA-sequencing (Top Panel) and phosphoproteomics (Bottom Panel) analysis, including the number of tissue samples, transcript and phosphopeptides identified and computational analysis and filtering. Two main comparisons were carried out between all heart failure and donor samples (comparison 1) and between responders and non-responders (comparison 2) for these two analyses platforms.

Supplemental Figure S2. Assessment of normality and equal variance in proteomics data.

To assess the phosphopeptide data for normality and equal variance we pooled the data for all identified peptides (blue) for each patient sample, graphed on individual histograms, into 22 bins and plotted the log₂ intensities for all phosphopeptides (x-axis) against the count (y-axis). Red shows data plotted for only the phosphopeptides that were identified as differentially abundant between Control, Responders and Non-Responders. X-axis label also includes a unique identifier code for each patient sample. **A**, One representative histogram is enlarged for each of the three groups to allow easy visualization and comparison for: Control, Non-Responder and Responder. **B**, Histograms for every sample analyzed in this study are included to compare normality and variance. These histograms show that in the total phosphopeptide dataset there are very little overall differences in the total number and intensity of phosphopeptides identified (blue), which is to be expected, however, when examining only the phosphopeptides which are differential abundant between groups (red) there are discernable differences which reflect the quantitative changes observed in this subfraction of the data, which is to be expected. **C**, Normal Q-Q plot generated in Prism 9.3.1. further confirmed normality and equal variance across all samples in the phosphoproteomic data set. When looking at sorted sample values on the x-axis (log₂ intensities

for all phosphopeptides) compared to theoretical (predicted) values on the y-axis for a normal Gaussian distribution, we can see an overall linear trend in the association of actual and predicted values, indicating a normal distribution of the data.

Supplemental Figure S3. Phosphopeptide enrichment from myocardial tissue.

Phosphopeptides were enriched with titanium dioxide beads from myocardial tissue lysates and analyzed on an Orbitrap Velos Pro mass spectrometer. The percent enrichment for each sample was calculated as the ratio of phosphorylated peptides identified to all peptides identified.

Supplemental Figure S4. Comparisons of studies examining cardiac tissue from heart failure patients. Comparison between differentially abundant transcripts and phosphopeptides identified in this study and previously published data sets utilizing **A**, RNA-sequencing, **B**, microarrays and **C**, proteomics to interrogate tissue samples from heart failure patients.

Supplemental Figure S5. Patient demographics incorporated into proteomics data. We utilized principal component analysis (PCA) to compare the molecular differences in each patient sample, between responders and non-responders, with their, **A**, age (\geq or $<$ 50 years), or **B**, sex, and shows no clustering between biological replicates (although technical replicates should and do cluster). This data suggests that the molecular differences identified in the proteomics data are consistent and reproducible regardless of the sex or age of the patient in this dataset.

Supplemental Figure S6. Binary comparisons of enriched processes and pathways in both – omics datasets. We performed binary comparisons of the top enriched processes and pathways (p-value <0.01) in both RNA-sequencing and phosphoproteomics data to identify the terms common in both analyses. This is not a comparison of individual transcripts or phosphorylated proteins instead it compares the gene ontology and pathways terms enriched after bioinformatics

analyses of the data using the DAVID platform. This included comparisons of terms from donor vs non-responder, donor vs responder and non-responder vs responder.

SUPPLEMENTAL TABLES

Supplemental Table S1. Clinical characteristics of heart failure patients (A) and donors (B) used in the RNA-Sequencing analysis. RNA Sequencing analysis was performed on 84 heart failure patients and 9 donor hearts not allocated for heart transplantation due to non-cardiac reasons were used as normal controls. Clinical characteristics were captured for the 84 heart failure patients at the time of LVAD implantation. In addition, serial monitoring by echocardiography assessed LVEF (left ventricular ejection fraction) and LVEDD (left ventricular end diastolic dimension) values prior to device implantation (pre-LVAD) and 6 months post-implantation (post-LVAD) to differentiate between responders (n=25) and non-responders (n=59) in the heart failure patients. Demographic information for the normal controls is also presented. P-values were calculated using the Student's t-test with equal or unequal variances as appropriate for continuous variables, and the chi-squared test or Fisher's exact test as appropriate for categorical variables. +/- values indicate standard error of the mean (SEM).

Supplemental Table S2. Clinical characteristics of heart failure patients (A) and donors (B) used in the proteomics analysis Proteomics analysis was performed on 29 heart failure patients and 10 donor hearts not allocated for heart transplantation due to non-cardiac reasons were used as normal controls. Clinical characteristics were captured for the 29 heart failure patients at the time of LVAD implantation. In addition, serial monitoring by echocardiography assessed LVEF (left ventricular ejection fraction) and LVEDD (left ventricular end diastolic dimension) values prior to device implantation (pre-LVAD) and 6 months post-implantation (post-LVAD) to differentiate between responders (n=6) and non-responders (n=23) in the heart failure patients. Demographic information for the normal controls is also presented. P-values were calculated using the Student's t-test with equal or unequal variances as appropriate for continuous variables, and

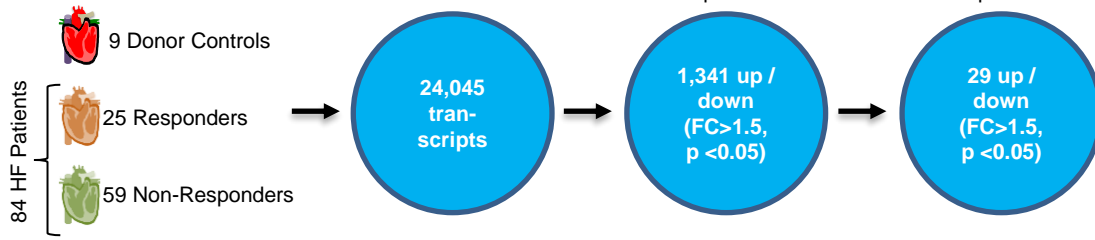
the chi-squared test or Fisher's exact test as appropriate for categorical variables. +/- values indicate standard error of the mean (SEM).

Supplemental Table S3. Transcripts differentially abundant in heart failure patients identified by RNA-Sequencing analysis.

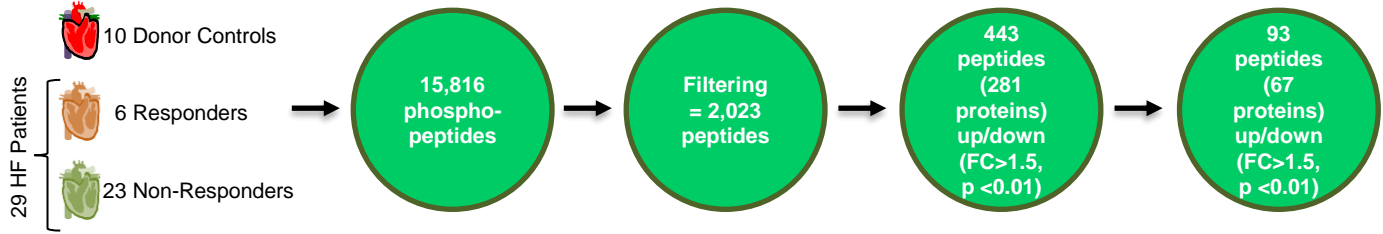
Supplemental Table S4. Phosphorylated peptides differentially abundant in heart failure patients identified by mass spectrometry.

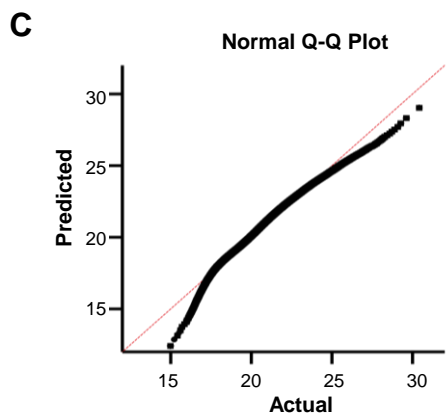
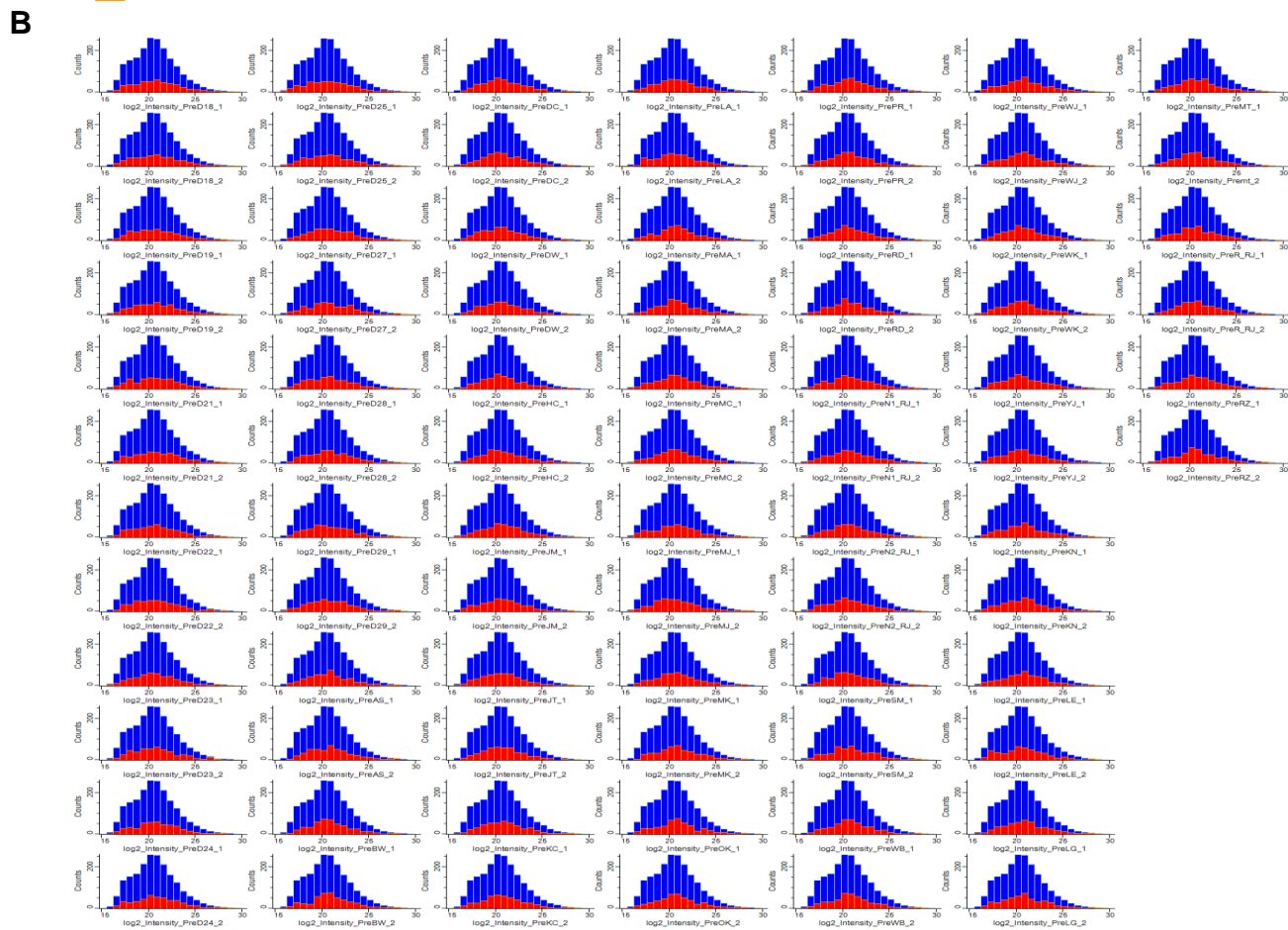
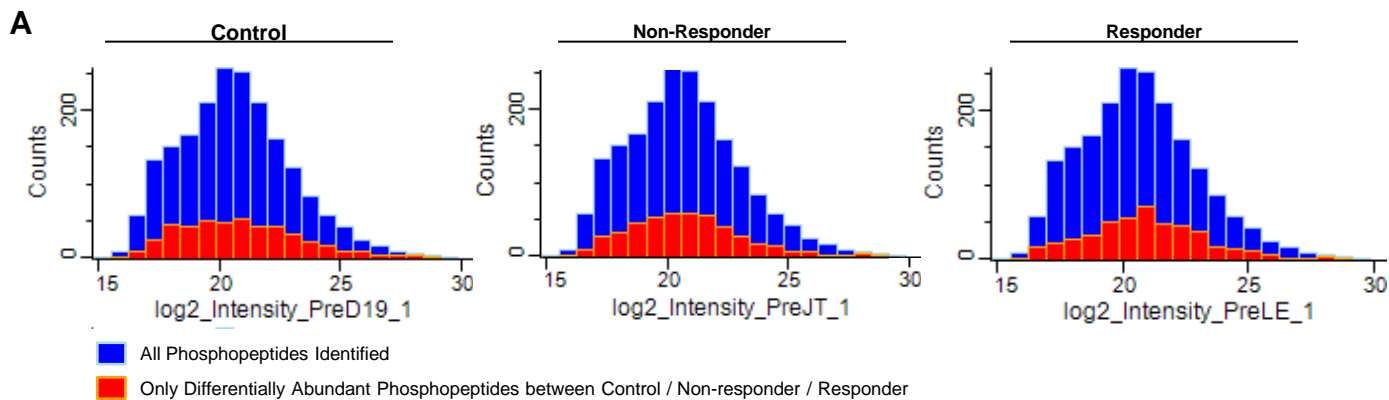
Supplemental Table S5. Phosphorylated peptides differentially abundant in patients who respond positively to LVAD unloading (responders).

RNA-Sequencing

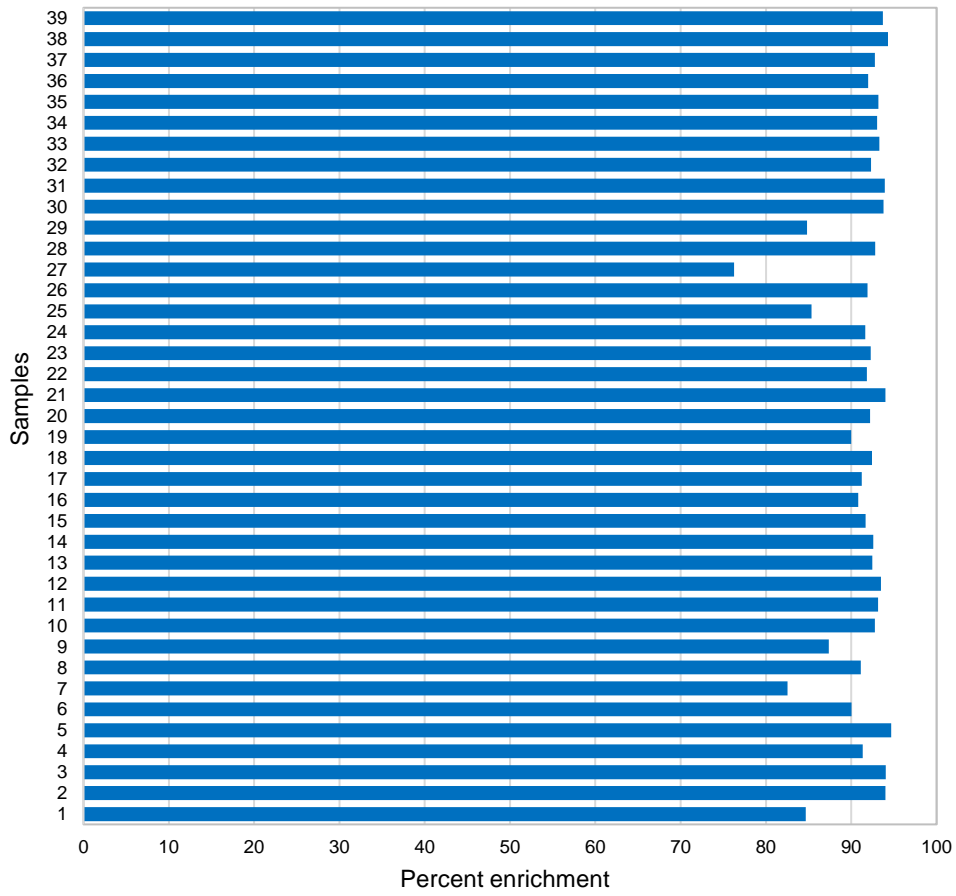


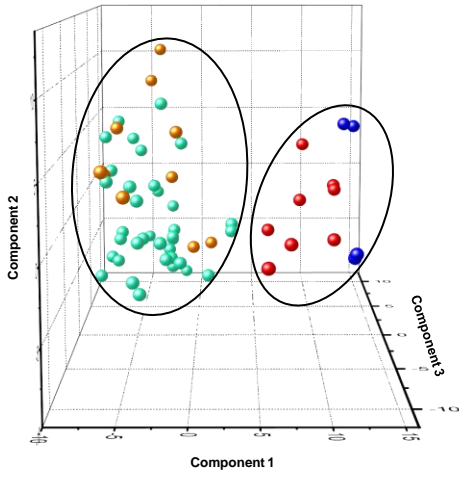
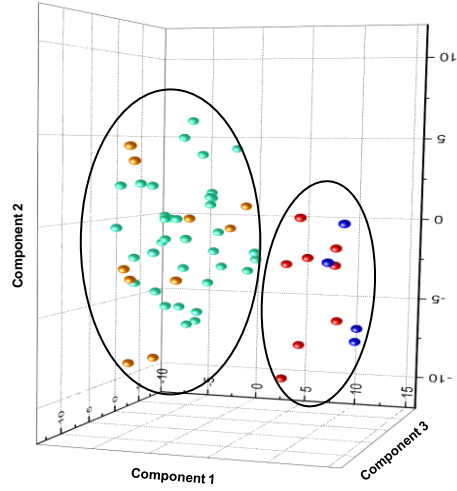
Phosphoproteomics



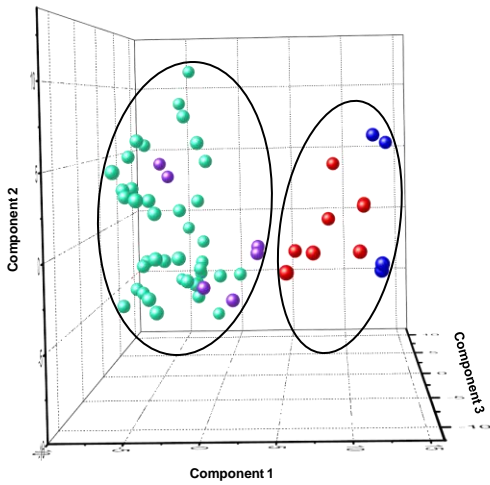
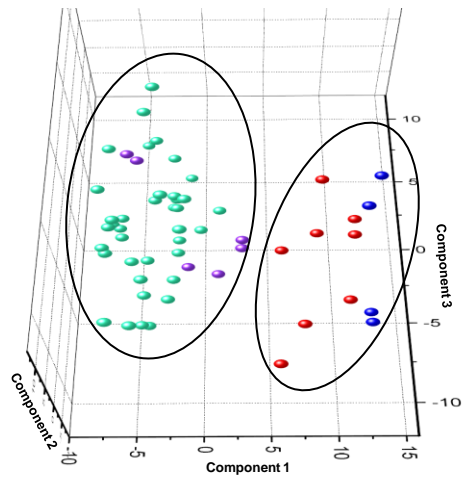


Phosphopeptide Enrichment

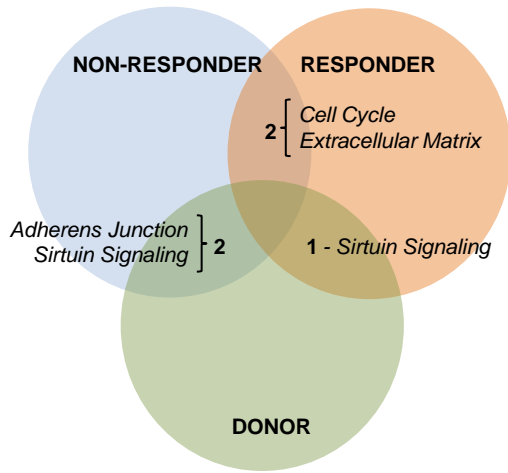


A**Top View**

- Non-Responder Age ≤49
- Non-Responder Age ≥50
- Responder Age ≤49
- Responder Age ≥50

B**Top View**

- Non-Responder Male
- Non-Responder Female
- Responder Male
- Responder Female



Variable	Responders N=25 (mean ± SE)	Non-Responders N=59 (mean ± SE)	p-value
Male sex, n (%)	17 (68)	53 (90)	0.01
Age at LVAD implantation, years	50±4	59±2	0.06
Pre-LVAD			
LVEDD, cm	6.4±0.2	7.0±0.1	0.04
LVEF, %	20±1	19±1	0.38
Post-LVAD			
LVEDD, cm	4.5±0.1	6.3±0.1	<0.001
LVEF, %	47±2	21±1	<0.001
HF Etiology			
Ischemic cardiomyopathy, n (%)	6 (24)	22 (37)	
Non-ischemic cardiomyopathy, n (%)	19 (76)	37 (63)	
New York Heart Association Functional Class			
III, n (%)	8 (32)	13 (22)	
IV, n (%)	17 (68)	46 (78)	
Duration of HF symptoms, months	36±12	106±12	<0.001
Systolic Blood Pressure, mmHg	105±3	104±2	0.69
Diastolic Blood Pressure, mmHg	66±3	68±1	0.53
Mean Right Atrial Pressure, mmHg	11±1	11±1	0.53
Systolic Pulmonary Artery Pressure, mmHg	52±3	54±2	0.65
Diastolic Pulmonary Artery Pressure, mmHg	24±2	26±1	0.50
Pulmonary Capillary Wedge Pressure, mmHg	24±2	25±1	0.80
Cardiac Index, L/min/m ²	2.0±0.1	1.8±0.1	0.25
Pulmonary Vascular Resistance, Wood units	3.5±0.5	3.9±0.4	0.57
B-type Natriuretic Peptide, pg/mL	1710±337	1338±134	0.31
Creatinine, mg/dL	1.2±0.1	1.4±0.1	0.06
Sodium, mmol/L	134±1	135±1	0.79
Hemoglobin, g/dL	13.0±0.5	12.6±0.3	0.48

P-values were calculated using the Student's t-test with equal or unequal variances as appropriate for continuous variables, and the chi-squared test or Fisher's exact test as appropriate for categorical variables. +/- values indicate standard error of the mean (SEM).

Variable	Donors N=9 (mean ± SE)
Male, n (%)	3 (33.3)
Age, years	44.7±2.3
Weight, Kg	68.6±6.2
Cause of death	
Head trauma, n (%)	6 (66.7)
CVA-Stroke/ ICH-Stroke, n (%)	2 (22.2)
CNS Tumor/Intracerebral Hemorrhage, n (%)	1 (11.1)

Variable	Responders N=6 (mean ± SE)	Non-Responders N=23 (mean ± SE)	p-value
Male sex, n (%)	4 (66.7)	20 (86.9)	0.27
Age at LVAD implantation, years	44±12	59±3	0.27
Pre-LVAD			
LVEDD, cm	6.1±0.3	7.1±0.3	0.07
LVEF, %	17±1	16±1	0.86
Post-LVAD			
LVEDD, cm	4.2±0.2	6.5±0.3	<0.001
LVEF, %	45±5	21±2	<0.001
HF Etiology			
Ischemic cardiomyopathy, n (%)	1 (16.7)	5 (21.7)	
Non-ischemic cardiomyopathy, n (%)	5 (83.3)	18 (78.3)	
New York Heart Association Functional Class			
III, n (%)	2 (33.3)	5 (21.7)	
IV, n (%)	4 (66.7)	18 (78.3)	
Duration of HF symptoms, months	36±22	89±12	0.05
Systolic Blood Pressure, mmHg	102±4	102±3	0.96
Diastolic Blood Pressure, mmHg	64±4	70±2	0.20
Mean Right Atrial Pressure, mmHg	13±3	12±1	0.93
Systolic Pulmonary Artery Pressure, mmHg	53±7	61±3	0.18
Diastolic Pulmonary Artery Pressure, mmHg	28±3	27±2	0.72
Pulmonary Capillary Wedge Pressure, mmHg	27±4	28±2	0.91
Cardiac Index, L/min/m ²	2.4±0.4	1.5±0.1	0.09
Pulmonary Vascular Resistance, Wood units	3.0±1.0	4.7±0.7	0.21
B-type Natriuretic Peptide, pg/mL	2442±765	1475±232	0.11
Creatinine, mg/dL	1.1±0.2	1.4±0.1	0.16
Sodium, mmol/L	133±3	133±1	0.93
Hemoglobin, g/dL	11.5±0.8	12.5±0.5	0.34

P-values were calculated using the Student's t-test with equal or unequal variances as appropriate for continuous variables, and the chi-squared test or Fisher's exact test as appropriate for categorical variables. +/- values indicate standard error of the mean (SEM).

Variable	Donors N=10 (mean ± SE)
Male, n (%)	3 (30)
Age, years	45±2
Weight, Kg	73±6
Cause of death	
Head trauma, n (%)	7 (70)
CVA-Stroke/ ICH-Stroke, n (%)	2 (20)
Anoxia/ Drug intoxication, n (%)	1 (10)

Supplemental Table S3

Gene	Gene Name	log2 Fold Change	p-value	adj p-value
ENSG00000145416	March1	-0.840128912	0.000272	0.002227476
ENSG00000107331	ABCA2	0.757229265	4.32E-09	2.03E-07
ENSG00000167972	ABCA3	0.672803358	1.27E-10	9.58E-09
ENSG00000154258	ABCA9	-0.796829823	5.20E-10	3.24E-08
ENSG00000006071	ABCC8	1.696712767	2.14E-11	2.13E-09
ENSG00000118777	ABCG2	1.599469414	7.87E-19	5.46E-16
ENSG00000164074	ABHD18	0.736702737	1.80E-05	0.000240614
ENSG00000140526	ABHD2	0.96422667	1.37E-15	4.32E-13
ENSG00000166016	ABTB2	0.660785726	0.00030933	0.002477265
ENSG00000227249	AC000374.1	-1.154709655	1.56E-07	4.30E-06
ENSG00000283399	AC004381.8	-0.80394707	0.00030044	0.002418472
ENSG00000250497	AC007126.1	-1.528696558	2.95E-09	1.46E-07
ENSG00000267216	AC010642.1	0.602605558	0.00057167	0.004075712
ENSG00000231013	AC013275.2	-1.39019808	3.43E-05	0.00040577
ENSG00000235978	AC018816.3	1.011079564	3.40E-07	8.34E-06
ENSG00000224713	AC025165.8	-0.881295173	0.00074883	0.00503998
ENSG00000225649	AC064875.2	0.595178547	0.01218351	0.046233813
ENSG00000229023	AC067945.3	-0.65439111	0.00037856	0.002919599
ENSG00000237753	AC079922.3	0.592231224	0.00370074	0.018215525
ENSG00000157766	ACAN	1.140577224	3.75E-05	0.000437336
ENSG00000159640	ACE	1.003574611	9.67E-07	2.05E-05
ENSG00000151726	ACSL1	-0.723235521	1.36E-06	2.71E-05
ENSG00000005187	ACSM3	-0.922406497	2.10E-05	0.000271383
ENSG00000148848	ADAM12	1.246536331	1.69E-05	0.000228242
ENSG00000135074	ADAM19	0.900450692	1.43E-07	4.03E-06
ENSG00000160323	ADAMTS13	0.865022557	1.33E-07	3.79E-06
ENSG00000138316	ADAMTS14	1.133548906	1.26E-05	0.000177737
ENSG00000154736	ADAMTS5	-0.726916257	0.00046922	0.003473402
ENSG00000203804	ADAMTSL4-AS	0.599198119	0.0003587	0.00279483
ENSG00000105963	ADAP1	1.025303836	3.01E-06	5.35E-05
ENSG00000174233	ADCY6	0.708163043	4.65E-11	4.11E-09
ENSG00000078549	ADCYAP1R1	-0.97051694	6.92E-06	0.000107889
ENSG00000135298	ADGRB3	-0.761588732	6.79E-08	2.14E-06
ENSG00000112414	ADGRG6	-1.086495235	2.38E-10	1.64E-08
ENSG00000196616	ADH1B	-1.62868427	7.92E-11	6.46E-09
ENSG00000248144	ADH1C	-0.969968963	0.00025933	0.002146118
ENSG00000181092	ADIPOQ	0.820056933	0.0010009	0.00640105
ENSG00000106624	AEBP1	1.593809531	2.78E-09	1.39E-07
ENSG00000232855	AF131217.1	-0.990384081	1.61E-08	6.20E-07
ENSG00000196526	AFAP1	0.614676073	2.27E-05	0.000289436
ENSG00000144218	AFF3	0.594768249	1.04E-05	0.000151047
ENSG00000169692	AGPAT2	0.620483181	1.45E-05	0.000201118

ENSG00000188157	AGRN	0.944499998	3.10E-07	7.72E-06
ENSG00000144891	AGTR1	-0.865538373	6.69E-05	0.000705437
ENSG00000204472	AIF1	-0.657775008	0.0049363	0.022766675
ENSG00000155085	AK9	-0.732662572	8.07E-13	1.18E-10
ENSG00000197976	AKAP17A	0.701800601	1.01E-11	1.15E-09
ENSG00000187134	AKR1C1	-0.765152776	2.00E-05	0.000261622
ENSG00000196139	AKR1C3	-0.735296566	4.64E-07	1.10E-05
ENSG00000170017	ALCAM	-0.810183447	0.00095484	0.00615578
ENSG00000165092	ALDH1A1	-0.70655352	0.00019362	0.00169449
ENSG00000159423	ALDH4A1	0.60519983	5.14E-05	0.000566725
ENSG00000012779	ALOX5	-0.620758902	0.00370348	0.018221665
ENSG00000132965	ALOX5AP	-1.361138083	3.86E-09	1.85E-07
ENSG00000136383	ALPK3	0.705125533	1.22E-07	3.54E-06
ENSG00000162551	ALPL	-0.681086653	0.00015565	0.00141203
ENSG00000155754	ALS2CR11	-1.032923769	2.03E-05	0.000264881
ENSG00000123505	AMD1	-0.844775961	1.30E-21	1.62E-18
ENSG00000214274	ANG	-0.590583388	0.00059157	0.004174622
ENSG00000154188	ANGPT1	-0.720952025	0.00027886	0.002275739
ENSG00000091879	ANGPT2	0.587726914	0.01072641	0.041987898
ENSG00000171819	ANGPTL7	0.895156007	0.00211806	0.011636667
ENSG00000148677	ANKRD1	0.609810995	0.00085508	0.005615659
ENSG00000165887	ANKRD2	-0.882858705	0.00432795	0.020605814
ENSG00000164236	ANKRD33B	1.356878627	1.34E-15	4.32E-13
ENSG00000131620	ANO1	0.827778082	9.23E-06	0.000136923
ENSG00000074855	ANO8	0.751534385	3.65E-08	1.25E-06
ENSG00000166825	ANPEP	-0.878709811	0.00042163	0.003182103
ENSG00000169604	ANTXR1	0.711099483	0.00097107	0.006243501
ENSG00000138772	ANXA3	-0.80980952	8.43E-07	1.83E-05
ENSG00000131471	AOC3	0.797087451	0.00015933	0.001438709
ENSG00000138356	AOX1	-1.15425274	6.62E-06	0.00010387
ENSG00000184441	AP001062.7	0.588173864	0.00075828	0.005089117
ENSG00000113108	APBB3	0.747481342	4.16E-12	5.11E-10
ENSG00000105290	APLP1	1.442891709	3.29E-15	9.82E-13
ENSG00000124701	APOBEC2	-0.639942429	2.00E-07	5.33E-06
ENSG00000189058	APOD	-1.10367275	5.19E-06	8.51E-05
ENSG00000165272	AQP3	-0.722714747	0.00125885	0.007705084
ENSG00000171885	AQP4	-0.921667813	0.00865433	0.035443517
ENSG00000112379	ARFGEF3	0.871055062	1.76E-05	0.000236151
ENSG00000175220	ARHGAP1	0.925885291	6.47E-19	4.76E-16
ENSG00000004777	ARHGAP33	0.961129155	1.43E-06	2.82E-05
ENSG00000147799	ARHGAP39	0.769194177	0.00045965	0.003414346
ENSG00000136002	ARHGEF4	1.16081035	1.75E-08	6.68E-07
ENSG00000140691	ARMC5	0.675204779	1.61E-07	4.42E-06

ENSG00000125449	ARMC7	0.666624998	2.53E-06	4.60E-05
ENSG00000135931	ARMC9	0.762057391	2.50E-07	6.45E-06
ENSG00000133794	ARNTL	-0.615575748	0.0052189	0.023800005
ENSG00000029153	ARNTL2	1.157705475	2.10E-08	7.89E-07
ENSG00000281357	ARRDC3-AS1	0.807932898	8.11E-06	0.000123275
ENSG00000164291	ARSK	-0.604624397	1.24E-11	1.36E-09
ENSG00000156219	ART3	-1.708427143	2.34E-23	3.24E-20
ENSG00000111339	ART4	-0.67468809	0.00193965	0.010870233
ENSG00000239388	ASB14	-0.987176927	4.50E-07	1.07E-05
ENSG00000146809	ASB15	-0.784738674	6.61E-06	0.000103755
ENSG00000005981	ASB4	-1.053180105	8.79E-07	1.89E-05
ENSG00000102048	ASB9	0.879037262	0.00207686	0.011459409
ENSG00000169093	ASMTL	0.61082656	9.40E-10	5.43E-08
ENSG00000106819	ASPN	0.946407666	5.25E-06	8.58E-05
ENSG00000110046	ATG2A	0.626559208	2.53E-09	1.28E-07
ENSG00000206190	ATP10A	0.831446648	2.06E-05	0.000267202
ENSG00000133657	ATP13A3	0.615804856	0.00029004	0.002350765
ENSG00000166896	ATP23	-0.741021956	0.00027906	0.002275831
ENSG00000171130	ATP6V0E2	0.603868627	7.03E-06	0.000109263
ENSG00000204934	ATP6V0E2-AS1	0.601073072	0.00024068	0.002022973
ENSG00000123191	ATP7B	0.638567082	2.36E-09	1.21E-07
ENSG00000107518	ATRNL1	2.004659406	5.69E-14	1.18E-11
ENSG00000160862	AZGP1	-1.276176225	1.87E-09	1.00E-07
ENSG00000162630	B3GALT2	-0.92540825	1.16E-07	3.38E-06
ENSG00000176597	B3GNT5	0.838471956	2.54E-05	0.000316931
ENSG00000237172	B3GNT9	0.627766063	5.97E-07	1.35E-05
ENSG00000118276	B4GALT6	-0.60142445	8.15E-05	0.000828894
ENSG00000112182	BACH2	0.880622506	2.01E-12	2.64E-10
ENSG00000278910	BANCR	1.022258693	0.00031569	0.002518794
ENSG00000163093	BBS5	0.812219828	2.71E-08	9.86E-07
ENSG00000122507	BBS9	-0.919262459	6.79E-28	2.29E-24
ENSG00000114200	BCHE	-0.815818864	1.50E-06	2.95E-05
ENSG00000113916	BCL6	-0.842164527	4.02E-10	2.62E-08
ENSG00000161940	BCL6B	0.920936249	8.66E-07	1.87E-05
ENSG00000151917	BEND6	1.120845893	3.55E-06	6.18E-05
ENSG00000182492	BGN	0.778999373	0.00312971	0.01596479
ENSG00000134107	BHLHE40	0.638146654	0.00211241	0.011619453
ENSG00000132840	BHMT2	-0.589538258	0.00114814	0.00712923
ENSG00000151746	BICD1	0.647217037	2.82E-07	7.14E-06
ENSG0000023445	BIRC3	-0.872251035	1.30E-06	2.63E-05
ENSG00000197299	BLM	-1.586534954	4.55E-15	1.32E-12
ENSG00000101144	BMP7	-1.31954231	4.59E-05	0.000517235
ENSG00000164619	BMPER	-1.245695593	6.99E-06	0.000108896

ENSG00000144857	BOC	0.756853131	2.95E-06	5.24E-05
ENSG00000176720	BOK	0.780323634	0.00015866	0.001434342
ENSG00000185024	BRF1	0.625312151	3.28E-11	3.07E-09
ENSG00000162670	BRINP3	-1.034843171	0.00116908	0.007232571
ENSG00000160469	BRSK1	1.54133441	7.11E-17	3.22E-14
ENSG00000148655	C10orf11	-1.254372032	1.39E-15	4.32E-13
ENSG00000173715	C11orf80	0.90539667	7.24E-06	0.00011219
ENSG00000227051	C14orf132	0.722483194	0.00142669	0.008509273
ENSG00000179476	C14orf28	-0.631146152	5.35E-09	2.43E-07
ENSG00000185347	C14orf80	0.847111384	0.00036492	0.002836575
ENSG00000261652	C15orf65	-0.844989232	6.05E-08	1.94E-06
ENSG00000153446	C16orf89	1.388718002	3.11E-08	1.11E-06
ENSG00000279020	C18orf15	0.754376898	0.00021405	0.001843853
ENSG00000180999	C1orf105	-2.074166823	1.01E-18	6.63E-16
ENSG00000162817	C1orf115	-0.758975961	3.00E-10	2.01E-08
ENSG00000131591	C1orf159	0.637962571	1.02E-05	0.000148645
ENSG00000143110	C1orf162	-0.592216213	5.25E-05	0.000575808
ENSG00000173369	C1QB	-0.959103269	0.00028565	0.002321329
ENSG00000159189	C1QC	-0.783887158	0.00089615	0.005842141
ENSG00000139178	C1RL	-0.732766875	5.08E-07	1.18E-05
ENSG00000174403	C20orf166-AS1	0.632351918	2.76E-05	0.000338514
ENSG00000160298	C21orf58	0.60381027	0.00177828	0.010156615
ENSG00000188511	C22orf34	0.707896736	0.00021712	0.00186216
ENSG00000187699	C2orf88	-0.662751003	5.25E-11	4.49E-09
ENSG00000125730	C3	-1.036067808	2.17E-05	0.000277959
ENSG00000171860	C3AR1	-0.64736795	0.00516834	0.023605979
ENSG00000112936	C7	-1.024942449	2.39E-07	6.22E-06
ENSG00000186354	C9orf47	-0.641422441	7.75E-05	0.000795739
ENSG00000063180	CA11	-0.747969221	8.92E-05	0.000891186
ENSG00000164879	CA3	1.069531209	0.00015379	0.00139848
ENSG00000007402	CACNA2D2	0.69449463	0.00022728	0.001929667
ENSG00000175161	CADM2	-0.767063568	0.0034831	0.017321469
ENSG00000162706	CADM3	-1.310160082	6.41E-10	3.90E-08
ENSG00000081803	CADPS2	-0.637162065	5.24E-10	3.25E-08
ENSG00000058404	CAMK2B	0.693598847	8.40E-11	6.80E-09
ENSG00000132357	CARD6	-0.623296657	2.17E-13	3.60E-11
ENSG00000172508	CARNS1	0.833417772	5.86E-07	1.33E-05
ENSG00000103021	CCDC113	1.175491089	1.72E-24	2.89E-21
ENSG00000233098	CCDC144NL-AS1	0.845557294	0.00059056	0.00417116
ENSG00000256304	CCDC150P1	0.606591174	1.72E-05	0.000231594
ENSG00000175820	CCDC168	1.160672467	1.04E-08	4.27E-07
ENSG00000109881	CCDC34	0.70739788	0.00074064	0.005000582
ENSG00000145075	CCDC39	-1.024495243	8.56E-07	1.86E-05

ENSG00000104983	CCDC61	0.634462081	5.29E-05	0.000579998
ENSG00000198624	CCDC69	-0.880782354	6.86E-26	1.24E-22
ENSG00000091986	CCDC80	1.075709844	1.32E-07	3.78E-06
ENSG00000175602	CCDC85B	0.701025449	0.00050013	0.003656295
ENSG00000172156	CCL11	-1.131066923	4.24E-05	0.000484472
ENSG00000110092	CCND1	0.941493012	6.26E-24	9.84E-21
ENSG00000113328	CCNG1	-0.601133667	2.27E-10	1.57E-08
ENSG00000163823	CCR1	-1.118467908	2.13E-05	0.000274018
ENSG00000170458	CD14	-0.974716322	2.01E-05	0.000262574
ENSG00000177575	CD163	-1.397706164	7.38E-08	2.30E-06
ENSG00000134061	CD180	-1.183616688	1.32E-06	2.66E-05
ENSG00000091972	CD200	0.748784258	0.00431817	0.020567574
ENSG00000215039	CD27-AS1	0.629087718	2.08E-08	7.81E-07
ENSG00000161649	CD300LG	-0.598739765	0.004256	0.02033309
ENSG00000241399	CD302	-0.664519779	1.34E-06	2.68E-05
ENSG00000174059	CD34	-0.689544609	2.20E-08	8.22E-07
ENSG00000135218	CD36	-0.803156013	2.07E-13	3.47E-11
ENSG00000004468	CD38	-1.309039491	1.53E-14	3.81E-12
ENSG00000066294	CD84	-0.792903947	5.17E-05	0.000569192
ENSG00000167617	CDC42EP5	0.631886819	0.00189162	0.010644096
ENSG00000097046	CDC7	-0.813764276	0.00041289	0.003127184
ENSG00000107736	CDH23	1.041798808	1.58E-11	1.70E-09
ENSG00000128536	CDHR3	-0.754809628	0.007065	0.030143231
ENSG00000176749	CDK5R1	0.765818012	7.86E-05	0.000805634
ENSG00000129596	CDO1	-0.614561081	0.00041396	0.003133235
ENSG00000245848	CEBPA	0.856434717	0.00246694	0.013162033
ENSG00000218739	CEBPZOS	-0.635917181	7.94E-09	3.39E-07
ENSG00000075275	CELSR1	0.913481835	1.59E-10	1.15E-08
ENSG00000143126	CELSR2	0.615795881	0.00020885	0.001806967
ENSG00000115163	CENPA	0.890995003	0.00249025	0.013268397
ENSG00000138778	CENPE	-0.622458837	0.00227575	0.012334588
ENSG00000166582	CENPV	-0.634314599	0.00072285	0.004914262
ENSG00000111860	CEP85L	-1.285647849	1.10E-35	1.29E-31
ENSG00000172831	CES2	-0.74896607	6.17E-08	1.97E-06
ENSG00000163075	CFAP221	0.593640354	0.00388691	0.018891316
ENSG00000227082	CH17-437K3.1	1.103479081	1.79E-06	3.42E-05
ENSG00000275993	CH507-42P11.1	0.828897478	0.00539389	0.024442013
ENSG00000016391	CHDH	-1.190575276	8.42E-09	3.57E-07
ENSG00000089199	CHGB	-0.798639732	0.00049353	0.003621499
ENSG00000134121	CHL1	-1.970686559	1.26E-15	4.25E-13
ENSG00000033100	CHPF2	0.597064762	9.12E-09	3.82E-07
ENSG00000104472	CHRAC1	-0.888146803	8.90E-13	1.29E-10
ENSG00000101938	CHRD1	1.075320605	0.00014752	0.001351239

ENSG00000108556	CHRNE	1.041042925	0.00034648	0.002718478
ENSG00000175040	CHST2	0.636589536	0.00361044	0.017845555
ENSG00000122863	CHST3	0.586758717	4.30E-07	1.03E-05
ENSG00000183196	CHST6	1.167105465	1.23E-05	0.000174466
ENSG00000147119	CHST7	0.790113134	0.00128763	0.007842546
ENSG00000154080	CHST9	-0.79741714	0.01086129	0.042403813
ENSG00000198108	CHSY3	0.607238224	0.00283821	0.01479144
ENSG00000179583	CIITA	0.604010325	0.00084591	0.005567831
ENSG00000114737	CISH	1.320121367	1.22E-10	9.26E-09
ENSG00000184113	CLDN5	0.708642488	0.00613976	0.027032133
ENSG00000105472	CLEC11A	0.724131901	0.0004993	0.003654512
ENSG00000069493	CLEC2D	-0.674324574	3.32E-07	8.20E-06
ENSG00000172243	CLEC7A	-0.602661675	0.01298243	0.04850416
ENSG00000070371	CLTCL1	0.754468935	5.30E-13	7.95E-11
ENSG00000132361	CLUH	0.645093949	9.02E-08	2.70E-06
ENSG00000144619	CNTN4	0.709817219	0.0001256	0.001177956
ENSG00000108797	CNTNAP1	0.738212723	4.33E-07	1.04E-05
ENSG00000106714	CNTNAP3	-0.834729157	0.00026801	0.002200143
ENSG00000187955	COL14A1	1.353167998	6.15E-09	2.73E-07
ENSG00000084636	COL16A1	1.06439366	7.00E-10	4.24E-08
ENSG00000108821	COL1A1	1.206754113	1.74E-05	0.000234497
ENSG00000164692	COL1A2	1.071888837	2.02E-06	3.80E-05
ENSG00000171502	COL24A1	0.886209639	9.66E-05	0.000949032
ENSG00000188517	COL25A1	0.647463347	0.00780404	0.032623379
ENSG00000215018	COL28A1	-0.901702019	6.15E-05	0.000656705
ENSG00000168542	COL3A1	0.890614027	0.00015171	0.001382852
ENSG00000130635	COL5A1	0.901946025	7.37E-05	0.00076314
ENSG00000171812	COL8A2	1.04323032	1.44E-05	0.000200096
ENSG00000112280	COL9A1	0.826118417	0.0029374	0.01519086
ENSG00000118004	COLEC11	-0.631918896	0.00237369	0.012759797
ENSG00000198756	COLGALT2	1.276264808	2.64E-16	1.06E-13
ENSG00000206561	COLQ	0.670922885	0.00211675	0.011635959
ENSG00000105664	COMP	1.504532437	1.30E-13	2.35E-11
ENSG00000138495	COX17	-0.692102227	1.82E-08	6.90E-07
ENSG00000160111	CPAMD8	-0.597573963	0.00606478	0.026797083
ENSG00000214575	CPEB1	0.813188327	0.00019352	0.001694286
ENSG00000135678	CPM	-0.838041233	8.72E-06	0.000130809
ENSG00000196353	CPNE4	-1.136075477	7.45E-06	0.000114892
ENSG00000124772	CPNE5	1.094972414	1.55E-05	0.000212386
ENSG00000121898	CPXM2	0.844854465	0.00058761	0.004160373
ENSG00000203710	CR1	-0.791437804	0.00494247	0.022774119
ENSG00000134376	CRB1	0.880617131	0.00017919	0.001584682
ENSG00000157613	CREB3L1	-0.778359734	3.78E-05	0.000439977

ENSG00000121005	CRISPLD1	1.525724883	3.96E-08	1.34E-06
ENSG00000215908	CROCCP2	0.757772983	4.61E-06	7.71E-05
ENSG00000121671	CRY2	0.668605626	9.94E-10	5.72E-08
ENSG00000109846	CRYAB	-0.666451278	1.52E-05	0.000209446
ENSG00000103316	CRYM	0.779332316	5.83E-08	1.88E-06
ENSG00000141551	CSNK1D	0.616473896	3.57E-08	1.23E-06
ENSG00000173546	CSPG4	0.787424555	4.77E-06	7.93E-05
ENSG00000260139	CSPG4P13	0.877116809	7.23E-05	0.000751659
ENSG00000273237	CTB-119C2.1	-1.51117559	3.19E-19	2.59E-16
ENSG00000267385	CTB-50L17.14	-0.665149768	0.00101825	0.006476193
ENSG00000280061	CTD-2001J20.1	0.649626631	0.00694694	0.029736397
ENSG00000278934	CTD-2006M22	-0.856134382	1.07E-08	4.36E-07
ENSG00000261434	CTD-2083E4.7	-0.779129237	0.00081199	0.005377602
ENSG00000249116	CTD-2194D22.	-1.039562807	1.83E-11	1.90E-09
ENSG00000250891	CTD-2281M20	-0.664226824	0.00315124	0.016053752
ENSG00000268518	CTD-2545M3.8	0.817084631	0.0049289	0.022750338
ENSG00000267577	CTD-2587H24.	1.160775892	1.53E-07	4.25E-06
ENSG00000232098	CTD-2619J13.1	0.591574602	0.00060044	0.004228334
ENSG00000180458	CTD-3064H18.	0.637449844	0.00055943	0.004007319
ENSG00000271959	CTD-3064M3.7	0.990825782	1.43E-06	2.83E-05
ENSG00000188897	CTD-3088G3.8	0.898755735	4.97E-06	8.19E-05
ENSG00000118523	CTGF	1.375511395	2.97E-07	7.45E-06
ENSG00000164932	CTHRC1	1.035949218	0.00025411	0.002110293
ENSG00000143387	CTSK	0.847334135	1.17E-06	2.41E-05
ENSG00000142544	CTU1	0.822110284	0.00052725	0.003813163
ENSG00000121966	CXCR4	0.949279575	0.00023303	0.001967127
ENSG00000165168	CYBB	-1.092114002	2.21E-06	4.08E-05
ENSG00000003137	CYP26B1	0.876343012	9.65E-05	0.000948483
ENSG00000142973	CYP4B1	-1.155936654	0.00028215	0.002297807
ENSG00000001630	CYP51A1	0.678334768	0.00040349	0.003070749
ENSG00000142871	CYR61	0.677480739	0.01286003	0.048148924
ENSG00000205795	CYS1	1.184744069	1.77E-08	6.74E-07
ENSG00000152207	CYSLTR2	-0.655801511	9.60E-07	2.04E-05
ENSG00000166265	CYYR1	-0.730553447	9.31E-15	2.49E-12
ENSG00000276644	DACH1	-0.888965703	2.30E-07	6.02E-06
ENSG00000164488	DACT2	1.266890552	1.58E-06	3.07E-05
ENSG00000167657	DAPK3	0.595750349	6.05E-07	1.37E-05
ENSG00000155368	DBI	-0.677097745	1.99E-09	1.05E-07
ENSG00000105516	DBP	0.745767085	0.00030287	0.002435487
ENSG00000166341	DCHS1	0.594699133	8.01E-07	1.76E-05
ENSG00000204580	DDR1	0.805993058	6.69E-08	2.12E-06
ENSG00000185163	DDX51	0.720333017	2.37E-10	1.64E-08
ENSG00000205593	DENND6B	0.745229608	0.0002152	0.001849954

ENSG00000077044	DGKD	0.608589496	1.60E-09	8.67E-08
ENSG00000157680	DGKI	0.664834169	0.002348	0.012656341
ENSG00000145214	DGKQ	0.82937389	2.09E-07	5.53E-06
ENSG00000278535	DHRS11	0.887611326	1.96E-14	4.67E-12
ENSG00000176124	DLEU1	-0.877410176	1.90E-12	2.50E-10
ENSG00000151208	DLG5	0.661499914	7.06E-09	3.07E-07
ENSG00000080845	DLGAP4	0.677331193	0.0003031	0.002436507
ENSG00000128917	DLL4	0.822190533	5.57E-06	9.02E-05
ENSG00000100206	DMC1	0.652151075	0.00274292	0.014393458
ENSG00000114841	DNAH1	0.773137925	5.01E-15	1.42E-12
ENSG00000158486	DNAH3	-1.654990293	4.98E-11	4.34E-09
ENSG00000224165	DNAJC27-AS1	0.717399428	0.00015868	0.001434342
ENSG00000235370	DNM1P51	0.780758318	0.00048317	0.003558816
ENSG00000272636	DOC2B	0.983028273	2.30E-09	1.19E-07
ENSG00000206052	DOK6	1.261321605	4.93E-11	4.31E-09
ENSG00000104885	DOT1L	0.599991558	4.47E-05	0.000507487
ENSG00000167261	DPEP2	0.602326889	0.00822577	0.033970737
ENSG00000143196	DPT	0.635245836	0.00066331	0.004587551
ENSG00000173852	DPY19L1	-0.69032601	7.83E-28	2.31E-24
ENSG00000235436	DPY19L2P4	-0.761302198	0.00023382	0.001972402
ENSG00000113657	DPYSL3	0.649891048	2.30E-05	0.000292208
ENSG00000137857	DUOX1	0.712298836	0.00328281	0.016517035
ENSG00000079393	DUSP13	-0.909122326	1.02E-07	3.03E-06
ENSG00000149599	DUSP15	1.501584919	1.17E-08	4.70E-07
ENSG00000138166	DUSP5	1.078684287	4.62E-07	1.09E-05
ENSG00000184545	DUSP8	0.597532101	0.00178771	0.010198098
ENSG00000125971	DYNLRB1	-0.611791491	3.65E-05	0.00042804
ENSG00000105204	DYRK1B	1.17972237	1.01E-18	6.63E-16
ENSG00000106823	ECM2	0.629545756	0.00032816	0.002594599
ENSG00000131080	EDA2R	1.316818041	1.48E-10	1.07E-08
ENSG00000164176	EDIL3	1.163288465	4.35E-07	1.04E-05
ENSG00000136160	EDNRB	-0.613396794	2.16E-05	0.000276992
ENSG00000232472	EEF1B2P3	-0.594760105	0.0010463	0.006622599
ENSG00000183690	EFHC2	-1.097365503	2.83E-14	6.47E-12
ENSG00000129521	EGLN3	0.667462573	1.22E-06	2.50E-05
ENSG00000120738	EGR1	1.195874064	1.88E-05	0.000249254
ENSG00000122877	EGR2	1.040672131	0.00028572	0.002321329
ENSG00000179388	EGR3	0.915563532	0.00162539	0.009443546
ENSG00000161960	EIF4A1	0.69987149	1.60E-06	3.11E-05
ENSG00000187840	EIF4EBP1	-1.005972874	2.69E-13	4.37E-11
ENSG00000170571	EMB	-0.625922733	0.00116182	0.007191454
ENSG00000164035	EMCN	-0.74392439	3.22E-11	3.04E-09
ENSG00000125746	EML2	0.653412733	1.06E-09	6.01E-08

ENSG00000214595	EML6	0.615808865	0.00019045	0.001669889
ENSG00000167280	ENGASE	0.634625666	1.45E-07	4.05E-06
ENSG00000197594	ENPP1	-0.778623483	1.25E-08	4.99E-07
ENSG00000095203	EPB41L4B	-0.812154372	1.20E-05	0.000170947
ENSG00000142627	EPHA2	0.619489965	1.37E-07	3.88E-06
ENSG00000106123	EPHB6	-0.759191543	2.09E-06	3.91E-05
ENSG00000049283	EPN3	-0.742544511	0.00044946	0.003365162
ENSG00000065361	ERBB3	-0.866943037	0.00065853	0.004557165
ENSG00000187672	ERC2	0.600966295	0.00385111	0.018786358
ENSG00000226887	ERVMER34-1	-0.613108042	0.00122655	0.007536722
ENSG00000164283	ESM1	0.74553433	0.0065553	0.0284421
ENSG00000205707	ETFRF1	-0.699416265	5.07E-11	4.38E-09
ENSG00000143845	ETNK2	-1.179850147	4.42E-11	3.95E-09
ENSG00000175832	ETV4	1.005299888	0.00035524	0.002771494
ENSG00000244405	ETV5	0.635439334	0.00032241	0.002562829
ENSG00000072840	EVC	0.600193309	6.27E-05	0.000666276
ENSG00000185862	EVI2B	-0.867053033	0.00060418	0.004245815
ENSG00000196405	EVL	0.839952714	6.77E-19	4.84E-16
ENSG00000179044	EXOC3L1	0.669636671	0.00061905	0.0043258
ENSG00000110723	EXPH5	-1.058032198	0.00025702	0.002131486
ENSG00000182197	EXT1	0.79123254	9.65E-16	3.34E-13
ENSG00000158008	EXTL1	1.138004391	1.23E-07	3.57E-06
ENSG00000124491	F13A1	-1.082686647	2.48E-05	0.00031163
ENSG00000181104	F2R	0.917920242	7.77E-07	1.71E-05
ENSG00000164220	F2RL2	0.927269277	0.00100215	0.006404891
ENSG00000127533	F2RL3	0.751435417	0.01131839	0.043803962
ENSG00000198734	F5	-1.330176916	7.54E-05	0.000777362
ENSG00000185010	F8	-1.091094777	6.51E-12	7.71E-10
ENSG00000170323	FABP4	-0.940184108	7.85E-07	1.73E-05
ENSG00000164687	FABP5	-0.844220471	0.00055709	0.003994693
ENSG00000167106	FAM102A	0.596580797	6.32E-07	1.42E-05
ENSG00000203950	FAM127B	-0.594688688	0.00037605	0.002905986
ENSG00000158863	FAM160B2	0.673477105	2.47E-12	3.13E-10
ENSG00000122378	FAM213A	-0.648514941	9.49E-12	1.09E-09
ENSG00000099290	FAM21A	-0.6090001	3.17E-10	2.11E-08
ENSG00000184949	FAM227A	0.671066866	2.56E-05	0.000318147
ENSG00000158246	FAM46B	-0.664720573	0.00493352	0.022758298
ENSG00000183508	FAM46C	-0.625604369	1.51E-06	2.96E-05
ENSG00000262919	FAM58A	-0.751571386	1.11E-09	6.22E-08
ENSG00000111913	FAM65B	0.590183505	0.00156325	0.00915697
ENSG00000042062	FAM65C	-0.645567137	0.00065329	0.004526159
ENSG00000187773	FAM69C	0.732668404	0.00064408	0.004474204
ENSG00000157470	FAM81A	-1.028896331	5.22E-08	1.71E-06

ENSG00000133477	FAM83F	-0.785763467	0.0007383	0.004989092
ENSG00000162981	FAM84A	-0.976950058	0.00025004	0.002083835
ENSG00000078098	FAP	1.315084443	3.69E-08	1.26E-06
ENSG00000152767	FARP1	0.687436128	4.77E-07	1.12E-05
ENSG00000165323	FAT3	1.209270626	2.56E-05	0.000318147
ENSG00000188878	FBF1	0.797798384	9.69E-07	2.05E-05
ENSG00000155034	FBXL18	0.866236775	2.32E-09	1.20E-07
ENSG00000099364	FBXL19	0.670459871	1.47E-06	2.90E-05
ENSG00000135722	FBXL8	0.680047489	0.00026539	0.002182484
ENSG00000158869	FCER1G	-1.071459481	8.67E-06	0.000130123
ENSG00000275395	FCGBP	-1.668758345	2.91E-07	7.30E-06
ENSG00000244682	FCGR2C	-0.634660526	0.00560282	0.02515668
ENSG00000203747	FCGR3A	-1.194304588	2.13E-05	0.000274018
ENSG00000142748	FCN3	-2.073364404	4.55E-14	9.67E-12
ENSG00000114279	FGF12	-0.625473625	0.00076388	0.005119359
ENSG00000243319	FGF14-IT1	0.792354974	0.00217582	0.011872089
ENSG00000140285	FGF7	-1.238393795	1.07E-13	2.03E-11
ENSG00000096060	FKBP5	-0.982875587	1.50E-06	2.95E-05
ENSG00000037280	FLT4	0.882763322	3.44E-11	3.13E-09
ENSG00000059122	FLYWCH1	0.626834904	9.73E-07	2.06E-05
ENSG00000248905	FMN1	-0.735948883	4.20E-06	7.10E-05
ENSG00000131781	FMO5	-0.657405472	3.81E-05	0.000443009
ENSG00000122176	FMOD	1.447890496	2.47E-08	9.07E-07
ENSG00000164694	FNDC1	1.466434132	5.09E-09	2.33E-07
ENSG00000170345	FOS	0.920106756	0.00115625	0.007162584
ENSG00000125740	FOSB	1.041860225	1.92E-07	5.15E-06
ENSG00000164916	FOXK1	0.685975457	4.29E-09	2.02E-07
ENSG00000179772	FOXS1	0.657412602	0.00595828	0.026410695
ENSG00000277737	FP325317.1	-0.804668435	0.00520403	0.02374139
ENSG00000164946	FREM1	0.711400094	8.61E-07	1.87E-05
ENSG00000126391	FRMD8	0.656711967	5.72E-08	1.85E-06
ENSG00000162998	FRZB	1.566907433	1.35E-10	9.94E-09
ENSG00000075618	FSCN1	0.875029973	5.50E-06	8.93E-05
ENSG00000186628	FSD2	-0.59445681	0.00043321	0.003257984
ENSG00000165775	FUNDC2	-0.664588355	1.11E-13	2.10E-11
ENSG00000180340	FZD2	0.634608705	0.00685034	0.029419038
ENSG00000155760	FZD7	0.601131124	2.13E-05	0.000274018
ENSG00000177283	FZD8	0.771122904	8.54E-05	0.000861523
ENSG00000105325	FZR1	0.68506968	3.79E-11	3.42E-09
ENSG00000123689	GOS2	-0.888927942	1.51E-06	2.96E-05
ENSG00000163288	GABRB1	0.65740309	5.15E-05	0.000567131
ENSG00000131386	GALNT15	-1.202993558	9.00E-06	0.000134074
ENSG00000110328	GALNT18	0.627179202	1.09E-07	3.21E-06

ENSG00000172020	GAP43	1.356446532	4.62E-07	1.09E-05
ENSG00000136895	GARNL3	0.607898213	2.20E-07	5.78E-06
ENSG00000183087	GAS6	0.618928271	5.73E-08	1.85E-06
ENSG00000171766	GATM	0.721270349	0.00304469	0.015615531
ENSG00000156466	GDF6	1.535879473	1.11E-07	3.27E-06
ENSG00000143869	GDF7	1.134487131	1.53E-06	2.99E-05
ENSG00000158555	GDPD5	0.738544078	0.00024329	0.002039146
ENSG00000239857	GET4	0.885417891	1.42E-05	0.000198413
ENSG00000151892	GFRA1	-1.263482534	4.90E-09	2.28E-07
ENSG00000121743	GJA3	0.618380968	2.48E-08	9.09E-07
ENSG00000074047	GLI2	0.634294688	0.00539927	0.024452275
ENSG00000139278	GLIPR1	-0.65424704	0.00131605	0.007988789
ENSG00000111664	GNB3	0.732826825	4.18E-05	0.000480042
ENSG00000135052	GOLM1	0.65940487	6.15E-06	9.78E-05
ENSG00000063660	GPC1	0.660482241	1.59E-07	4.38E-06
ENSG00000125772	GPCPD1	0.731045064	9.18E-17	4.01E-14
ENSG00000152642	GPD1L	-0.843999962	5.10E-12	6.20E-10
ENSG00000277494	GPIHBP1	-0.948687229	1.25E-05	0.000177703
ENSG00000046653	GPM6B	-0.95406331	0.00010744	0.001032629
ENSG00000184194	GPR173	0.79567903	4.93E-05	0.000546911
ENSG00000166073	GPR176	0.807680925	3.80E-05	0.000441841
ENSG00000170837	GPR27	1.272907742	4.75E-15	1.37E-12
ENSG00000119714	GPR68	1.157191014	4.28E-05	0.00048815
ENSG00000164604	GPR85	0.799786545	0.00100982	0.006443095
ENSG00000121957	GPSM2	-1.034698136	7.35E-09	3.17E-07
ENSG00000211445	GPX3	-1.219548731	2.00E-15	6.03E-13
ENSG00000178075	GRAMD1C	-0.857469297	1.26E-05	0.000178793
ENSG00000115290	GRB14	-1.100333227	8.85E-08	2.66E-06
ENSG00000125675	GRIA3	0.784732708	0.00457856	0.021439676
ENSG00000164418	GRIK2	-0.979262223	0.00022054	0.001885531
ENSG00000163873	GRIK3	-1.114388148	5.40E-05	0.00058979
ENSG00000183454	GRIN2A	-1.108265712	3.13E-05	0.000375173
ENSG00000204928	GRXCR2	-3.26484638	1.37E-28	5.39E-25
ENSG00000230189	GS1-124K5.2	0.669554704	1.93E-05	0.000253511
ENSG00000073605	GSDMB	0.674359364	4.45E-08	1.49E-06
ENSG00000168765	GSTM4	-0.746553704	4.23E-16	1.61E-13
ENSG00000122034	GTF3A	-0.621150486	3.84E-13	5.92E-11
ENSG00000152402	GUCY1A2	-0.628794751	3.35E-07	8.23E-06
ENSG00000189060	H1F0	-0.648093533	4.45E-08	1.49E-06
ENSG00000206417	H1FX-AS1	0.680315181	0.00032764	0.002592213
ENSG00000246705	H2AFJ	-0.599809653	3.27E-08	1.15E-06
ENSG00000162882	HA AO	0.856340867	5.20E-06	8.51E-05
ENSG00000084754	HADHA	-0.697370417	1.35E-10	9.95E-09

ENSG00000138029	HADHB	-0.809301777	7.84E-10	4.64E-08
ENSG00000145681	HAPLN1	0.981845735	0.00014407	0.001323744
ENSG00000140511	HAPLN3	0.651638451	0.00143355	0.008539357
ENSG00000170961	HAS2	-0.72585878	0.00203585	0.011278017
ENSG00000206172	HBA1	0.779167753	0.00785009	0.032775186
ENSG00000188536	HBA2	0.900102145	0.00186895	0.010556861
ENSG00000244734	HBB	1.112846967	8.40E-05	0.000850111
ENSG00000103145	HCFC1R1	-0.712435695	1.07E-09	6.08E-08
ENSG00000099822	HCN2	0.792646033	0.00172566	0.00990888
ENSG00000173706	HEG1	0.613517372	2.76E-13	4.46E-11
ENSG00000130589	HELZ2	0.762692365	6.67E-06	0.000104705
ENSG00000276550	HERC2P2	-0.719299332	9.53E-05	0.00093883
ENSG00000180229	HERC2P3	-0.758132266	0.01201757	0.045803143
ENSG00000188290	HES4	1.233264318	7.39E-08	2.30E-06
ENSG00000182218	HHIPL1	0.722412543	4.26E-06	7.19E-05
ENSG00000167861	HID1	0.625783428	1.08E-08	4.40E-07
ENSG00000124440	HIF3A	-0.677015488	0.00075669	0.005081325
ENSG00000184357	HIST1H1B	-1.212194524	6.14E-05	0.000656198
ENSG00000187837	HIST1H1C	-0.830664777	3.35E-11	3.09E-09
ENSG00000124575	HIST1H1D	-1.257550271	1.57E-07	4.33E-06
ENSG00000168298	HIST1H1E	-0.981512161	2.16E-14	5.03E-12
ENSG00000158373	HIST1H2BD	-0.622834812	8.83E-08	2.66E-06
ENSG00000277224	HIST1H2BF	-0.860668915	3.62E-06	6.27E-05
ENSG00000124635	HIST1H2BJ	-0.598602012	0.00085013	0.005589384
ENSG00000274267	HIST1H3B	-0.821979286	0.01222145	0.046313136
ENSG00000204632	HLA-G	1.034423022	1.23E-05	0.000174858
ENSG00000148357	HMCN2	1.450668795	1.58E-12	2.16E-10
ENSG00000134240	HMGCS2	-2.317701031	3.74E-09	1.80E-07
ENSG00000100292	HMOX1	-0.741849669	0.0043673	0.020746952
ENSG00000103415	HMOX2	-0.804472361	8.77E-18	4.81E-15
ENSG00000241935	HOGA1	-1.029098038	2.12E-08	7.94E-07
ENSG00000134709	HOOK1	-1.049884492	5.67E-06	9.16E-05
ENSG00000168453	HR	0.947221175	7.01E-05	0.000732133
ENSG00000234520	HRAT17	-0.741020132	6.34E-05	0.000673034
ENSG00000135116	HRK	0.697622144	0.01298341	0.04850416
ENSG00000002587	HS3ST1	-0.962929652	2.57E-07	6.60E-06
ENSG00000198189	HSD17B11	-0.613442421	4.87E-07	1.15E-05
ENSG00000119471	HSDL2	-0.644617161	7.54E-09	3.24E-07
ENSG00000205940	HSP90AB2P	0.725719473	0.00707422	0.03016619
ENSG00000126803	HSPA2	0.817849104	0.00014073	0.001297076
ENSG00000164070	HSPA4L	0.677427431	7.50E-10	4.48E-08
ENSG00000169271	HSPB3	-0.770703114	4.69E-08	1.56E-06
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ENSG00000166033	HTRA1	1.062470722	2.37E-27	5.58E-24
ENSG00000181873	IBA57	0.772293006	2.35E-11	2.33E-09
ENSG00000172201	ID4	0.879752592	0.0014663	0.008697108
ENSG00000127415	IDUA	0.665647872	7.43E-05	0.000767518
ENSG00000160888	IER2	1.293881922	4.37E-12	5.34E-10
ENSG00000188483	IER5L	0.716231912	0.00067528	0.004649839
ENSG00000169991	IFFO2	0.670837129	4.11E-08	1.39E-06
ENSG00000185201	IFITM2	-0.709653499	5.03E-05	0.00055713
ENSG00000142089	IFITM3	-0.620193912	3.34E-06	5.83E-05
ENSG00000140443	IGF1R	0.592778705	4.34E-10	2.80E-08
ENSG00000115457	IGFBP2	1.070702524	3.14E-06	5.53E-05
ENSG00000144847	IGSF11	-0.595689365	0.00051525	0.00374522
ENSG00000134470	IL15RA	-0.782650426	2.35E-07	6.14E-06
ENSG00000172458	IL17D	1.429553803	3.01E-08	1.07E-06
ENSG00000115604	IL18R1	-0.951943577	1.85E-07	4.97E-06
ENSG00000115602	IL1RL1	-1.446889614	1.24E-07	3.59E-06
ENSG0000016402	IL20RA	-1.064207133	4.62E-05	0.000519447
ENSG00000143195	ILDR2	0.860551333	1.32E-08	5.25E-07
ENSG00000141401	IMPA2	-0.633025782	4.62E-07	1.09E-05
ENSG00000257704	INAFM1	1.032267148	3.23E-07	7.99E-06
ENSG00000163083	INHBB	0.938638121	0.00099115	0.006350123
ENSG00000164880	INTS1	0.633827371	7.47E-08	2.31E-06
ENSG00000120645	IQSEC3	0.885041654	0.00015116	0.001379184
ENSG00000128604	IRF5	-0.618205563	0.00282772	0.014746558
ENSG00000167378	IRGQ	0.626360994	2.88E-16	1.11E-13
ENSG00000129009	ISLR	0.79349912	3.69E-06	6.39E-05
ENSG00000164171	ITGA2	-0.904878981	7.62E-05	0.000783637
ENSG00000169896	ITGAM	-0.684956087	0.00171258	0.009845746
ENSG00000140678	ITGAX	1.062173744	2.26E-05	0.000288448
ENSG00000115221	ITGB6	-0.593802758	0.00029129	0.0023592
ENSG00000198542	ITGBL1	1.212317866	9.25E-06	0.000137009
ENSG00000148841	ITPRIP	0.706635252	3.63E-05	0.000426282
ENSG00000162434	JAK1	-0.621845952	5.55E-20	5.45E-17
ENSG00000168970	JMJD7-PLA2G4	0.609536312	1.06E-05	0.000153181
ENSG00000177606	JUN	0.639228466	1.18E-06	2.42E-05
ENSG00000171223	JUNB	0.688776642	0.00643106	0.028047545
ENSG00000114166	KAT2B	-0.613022381	8.42E-16	2.96E-13
ENSG00000107821	KAZALD1	0.692633011	7.22E-05	0.000751204
ENSG00000163376	KBTBD8	1.001166963	1.62E-07	4.44E-06
ENSG00000130037	KCNA5	0.727041661	0.00095806	0.006171604
ENSG00000168135	KCNJ4	1.252675751	1.14E-14	2.89E-12
ENSG00000099337	KCNK6	0.763768537	0.00016051	0.001448871
ENSG00000156113	KCNMA1	0.673861466	0.00748395	0.031593387

ENSG00000197584	KCNMB2	0.684091536	0.00068878	0.004733159
ENSG00000143603	KCNN3	0.670028637	5.60E-06	9.05E-05
ENSG00000117013	KCNQ4	1.243692744	2.46E-08	9.04E-07
ENSG00000178695	KCTD12	-0.637561336	8.70E-10	5.08E-08
ENSG00000128052	KDR	-0.646589221	2.85E-07	7.21E-06
ENSG00000235750	KIAA0040	-0.731684573	1.11E-11	1.25E-09
ENSG00000047578	KIAA0556	0.839527999	2.62E-19	2.21E-16
ENSG00000109265	KIAA1211	1.665641885	4.20E-09	1.98E-07
ENSG00000250305	KIAA1456	-0.707815213	2.84E-08	1.03E-06
ENSG00000149633	KIAA1755	0.943064781	1.22E-06	2.50E-05
ENSG00000130294	KIF1A	1.357057384	4.97E-07	1.16E-05
ENSG00000116852	KIF21B	1.150174479	1.68E-07	4.56E-06
ENSG00000166813	KIF7	1.289144852	9.79E-16	3.34E-13
ENSG00000162755	KLHDC9	0.609723908	0.00047056	0.003482242
ENSG00000213160	KLHL23	-0.59661612	4.30E-13	6.49E-11
ENSG00000119771	KLHL29	0.765927458	5.66E-05	0.000614238
ENSG00000185915	KLHL34	0.858850722	4.66E-06	7.78E-05
ENSG00000239474	KLHL41	-0.903208559	1.08E-12	1.52E-10
ENSG00000133247	KMT5C	0.711312526	1.40E-06	2.78E-05
ENSG00000133619	KRBA1	1.023314148	7.20E-10	4.34E-08
ENSG00000198910	L1CAM	-0.816678791	0.00172363	0.009899655
ENSG00000262312	LA16c-390H2.4	0.68974926	0.00026994	0.002212945
ENSG00000147592	LACTB2	-0.646464814	1.61E-07	4.41E-06
ENSG00000159166	LAD1	-1.924818605	2.11E-12	2.75E-10
ENSG00000196878	LAMB3	-0.6568675	0.00024543	0.002052716
ENSG00000162511	LAPTM5	-0.939809628	7.25E-06	0.000112256
ENSG00000162194	LBHD1	0.684632847	1.55E-05	0.000212011
ENSG00000213398	LCAT	0.641610969	1.08E-09	6.11E-08
ENSG00000184925	LCN12	1.625319454	2.96E-11	2.85E-09
ENSG00000267206	LCN6	-1.757013918	1.04E-10	8.01E-09
ENSG00000136167	LCP1	-0.62937573	0.00672291	0.02902274
ENSG00000167615	LENG8	0.633788813	1.15E-07	3.36E-06
ENSG00000106003	LFNG	0.885073963	2.16E-05	0.00027739
ENSG00000186818	LILRB4	-0.646114084	0.00553473	0.024912631
ENSG00000136490	LIMD2	0.638190614	0.00200234	0.011139505
ENSG00000179406	LINC00174	0.823267911	1.97E-07	5.28E-06
ENSG00000223768	LINC00205	0.881310374	1.23E-05	0.000175287
ENSG00000232977	LINC00327	0.646566093	0.00051531	0.00374522
ENSG00000229246	LINC00377	1.441352172	6.76E-08	2.14E-06
ENSG00000237945	LINC00649	-0.622960709	0.00094238	0.006092286
ENSG00000179136	LINC00670	0.865826185	6.45E-05	0.000683157
ENSG00000237949	LINC00844	-0.855027635	0.00084871	0.005581612
ENSG00000251209	LINC00923	-0.679576761	0.00020397	0.001769983

ENSG00000281205	LINC00950	0.88106052	8.00E-09	3.41E-07
ENSG00000203999	LINC01270	1.015985865	2.40E-05	0.000303163
ENSG00000246223	LINC01550	-0.99144351	3.72E-08	1.27E-06
ENSG00000079435	LIPE	0.651466878	9.41E-05	0.000930652
ENSG00000163898	LIPH	0.89759043	0.00021601	0.001855963
ENSG00000139636	LMBR1L	0.692291181	2.39E-14	5.52E-12
ENSG00000167210	LOXHD1	1.133877859	5.26E-07	1.21E-05
ENSG00000129038	LOXL1	0.909437702	9.43E-06	0.000139357
ENSG00000134013	LOXL2	0.732048469	0.00060495	0.004248692
ENSG00000198121	LPAR1	-0.599046783	3.84E-05	0.000445155
ENSG00000171517	LPAR3	-0.735398165	0.00029254	0.002366309
ENSG00000087253	LPCAT2	-0.600492076	2.93E-08	1.05E-06
ENSG00000111684	LPCAT3	-0.642273032	8.78E-07	1.89E-05
ENSG00000176454	LPCAT4	-0.757943898	1.36E-10	9.95E-09
ENSG00000130881	LRP3	0.710729137	1.10E-06	2.29E-05
ENSG00000162337	LRP5	0.643652337	3.21E-13	5.05E-11
ENSG00000100068	LRP5L	0.61381752	1.83E-05	0.000243541
ENSG00000137269	LRRC1	0.803964942	8.09E-10	4.78E-08
ENSG00000185028	LRRC14B	-0.595506261	0.00769875	0.032269067
ENSG00000128606	LRRC17	0.610541283	0.00267253	0.014077355
ENSG00000122477	LRRC39	-0.627136292	5.85E-07	1.33E-05
ENSG00000129295	LRRC6	0.670777184	0.00160458	0.009341021
ENSG00000173114	LRRN3	-2.210034436	5.03E-19	3.83E-16
ENSG00000185565	LSAMP	-1.224106498	5.89E-07	1.33E-05
ENSG00000119681	LTBP2	1.282801789	4.01E-08	1.36E-06
ENSG00000168056	LTBP3	0.853293379	6.94E-07	1.54E-05
ENSG00000090006	LTBP4	0.794264442	8.03E-05	0.000819714
ENSG00000139329	LUM	1.170964393	2.66E-10	1.81E-08
ENSG00000133800	LYVE1	-1.590639876	3.67E-09	1.78E-07
ENSG00000088899	LZTS3	-0.636413594	3.45E-10	2.27E-08
ENSG00000198517	MAFK	1.109171278	2.04E-16	8.44E-14
ENSG00000204740	MALRD1	0.655074008	0.01048567	0.041219843
ENSG00000140400	MAN2C1	0.593796543	1.49E-08	5.81E-07
ENSG00000172469	MANEA	-0.840890733	1.37E-18	8.27E-16
ENSG00000261366	MANEA-AS1	-0.937646272	2.33E-08	8.64E-07
ENSG00000034152	MAP2K3	0.707308155	7.26E-05	0.000753349
ENSG00000156265	MAP3K7CL	1.047517433	3.82E-05	0.000443087
ENSG00000047849	MAP4	0.592613106	4.94E-06	8.16E-05
ENSG00000171533	MAP6	0.652866854	4.11E-09	1.95E-07
ENSG00000141639	MAPK4	0.66890655	0.00055307	0.003968268
ENSG00000121653	MAPK8IP1	0.660913313	9.10E-07	1.95E-05
ENSG00000138834	MAPK8IP3	0.678511128	1.61E-13	2.82E-11
ENSG00000186868	MAPT	0.802608489	5.68E-05	0.000615519

ENSG00000019169	MARCO	-1.00576422	0.00345965	0.017233936
ENSG00000099308	MAST3	0.599496282	1.92E-05	0.000253209
ENSG00000143797	MBOAT2	0.742803987	2.68E-07	6.86E-06
ENSG00000076706	MCAM	0.842842916	4.02E-13	6.12E-11
ENSG00000053524	MCF2L2	0.778965047	9.55E-05	0.000940552
ENSG00000215424	MCM3AP-AS1	-0.981690291	6.08E-09	2.71E-07
ENSG00000140563	MCTP2	-1.139343008	1.06E-06	2.23E-05
ENSG00000110492	MDK	0.802406296	0.00041551	0.003143923
ENSG00000144893	MED12L	1.470524385	1.36E-11	1.49E-09
ENSG00000214548	MEG3	0.813231975	2.06E-08	7.76E-07
ENSG00000105429	MEGF8	0.611274208	3.97E-07	9.61E-06
ENSG00000164024	METAP1	-0.719525916	1.31E-18	8.12E-16
ENSG00000250878	METTL21EP	0.669505128	0.00105087	0.006644235
ENSG00000170439	METTL7B	-0.827467133	0.00085584	0.005619097
ENSG00000128268	MGAT3	0.615251019	0.00205017	0.011341712
ENSG00000182050	MGAT4C	-0.641546202	0.00146516	0.008692496
ENSG00000008394	MGST1	-1.28090266	2.68E-06	4.82E-05
ENSG00000133816	MICAL2	0.709994355	1.92E-09	1.02E-07
ENSG00000164877	MICALL2	0.792692986	1.65E-05	0.000224363
ENSG00000141741	MIEN1	-0.79032632	2.53E-13	4.14E-11
ENSG00000265142	MIR133A1HG	-0.750193733	2.66E-05	0.000327764
ENSG00000267519	MIR24-2	0.890985802	2.87E-05	0.000349763
ENSG00000228526	MIR34A	0.736804545	5.51E-05	0.000599249
ENSG00000267532	MIR497HG	0.646723835	8.92E-06	0.000133175
ENSG00000148773	MKI67	-0.961334091	0.0026319	0.01390685
ENSG00000178053	MLF1	-0.629038578	2.73E-05	0.000335328
ENSG00000089693	MLF2	-0.590915605	1.24E-12	1.73E-10
ENSG00000196549	MME	1.373462067	6.43E-12	7.66E-10
ENSG00000164172	MOCS2	-0.700626658	2.03E-13	3.44E-11
ENSG00000204655	MOG	-1.754871587	3.03E-08	1.08E-06
ENSG00000171160	MORN4	0.609623847	2.57E-06	4.65E-05
ENSG00000079931	MOXD1	0.934221069	4.11E-06	6.97E-05
ENSG00000197629	MPEG1	-0.67077183	0.00090486	0.005891699
ENSG00000158887	MPZ	-1.058922737	2.16E-08	8.10E-07
ENSG00000260314	MRC1	-1.006862943	7.69E-06	0.000117848
ENSG00000011028	MRC2	0.662078783	5.20E-05	0.000571612
ENSG00000175581	MRPL48	-0.593049075	1.12E-10	8.57E-09
ENSG00000243927	MRPS6	-0.703742069	1.46E-12	2.01E-10
ENSG00000110079	MS4A4A	-0.745858252	0.00201022	0.011170177
ENSG00000110077	MS4A6A	-0.828754607	0.00015176	0.001382852
ENSG00000057468	MSH4	0.782175669	8.44E-05	0.00085363
ENSG00000135097	MSI1	0.841345196	4.71E-05	0.00052683
ENSG00000166343	MSS51	1.218478574	1.32E-10	9.75E-09

ENSG00000164078	MST1R	0.602800903	0.00364056	0.017971812
ENSG00000187193	MT1X	-1.025969421	3.75E-05	0.000437336
ENSG00000248527	MTATP6P1	-0.866572739	0.00523112	0.023837303
ENSG00000168502	MTCL1	0.606732885	0.00104223	0.006603766
ENSG00000198712	MT-CO2	-0.730862034	0.00912255	0.036917678
ENSG00000198727	MT-CYB	-0.824627475	0.00836344	0.034454812
ENSG00000120254	MTHFD1L	0.863402423	8.52E-05	0.000860572
ENSG00000122033	MTIF3	-0.73263858	9.41E-15	2.49E-12
ENSG00000198888	MT-ND1	-0.851777889	0.01090944	0.042535467
ENSG00000198763	MT-ND2	-0.88960606	0.00422401	0.020221231
ENSG00000225630	MTND2P28	-0.915024344	0.0015377	0.009045499
ENSG00000198840	MT-ND3	-0.715738639	0.00211094	0.011614827
ENSG00000211459	MT-RNR1	-0.941382333	0.00595068	0.026386902
ENSG00000210082	MT-RNR2	-0.873572679	0.01157276	0.044459971
ENSG00000210176	MT-TH	-0.922085169	0.00436624	0.020746251
ENSG00000210100	MT-TI	-1.115764631	0.00052388	0.003795806
ENSG00000210112	MT-TM	-0.84501348	0.00384184	0.018757325
ENSG00000138823	MTTP	-0.589571596	0.00077866	0.005191879
ENSG00000210184	MT-TS2	-1.292765893	6.14E-06	9.78E-05
ENSG00000210195	MT-TT	-0.961364243	0.00084855	0.005581612
ENSG00000180354	MTURN	0.717005916	3.25E-10	2.16E-08
ENSG00000132938	MTUS2	-1.157483791	7.58E-24	1.12E-20
ENSG00000030304	MUSK	-0.606751431	0.00071731	0.004887193
ENSG00000101825	MXRA5	1.626913124	9.22E-11	7.27E-09
ENSG00000162576	MXRA8	0.622021594	0.00045618	0.003400366
ENSG00000185697	MYBL1	0.652549461	1.96E-05	0.000257324
ENSG00000196091	MYBPC1	-1.03584272	3.60E-05	0.000423276
ENSG00000133026	MYH10	0.760829725	2.06E-05	0.000267202
ENSG00000133392	MYH11	0.849721557	0.00035008	0.002741962
ENSG00000197616	MYH6	-1.96331138	5.20E-11	4.46E-09
ENSG00000160808	MYL3	-0.609845127	1.20E-06	2.48E-05
ENSG00000266714	MYO15B	0.618009009	3.54E-06	6.16E-05
ENSG00000041515	MYO16	-0.638219051	0.00134371	0.008114944
ENSG00000196535	MYO18A	0.588279244	8.78E-09	3.70E-07
ENSG00000133454	MYO18B	0.70510473	3.62E-09	1.76E-07
ENSG00000176658	MYO1D	0.740848004	0.00024186	0.002032227
ENSG00000167306	MYO5B	0.875427101	0.00042024	0.003174609
ENSG00000137474	MYO7A	-0.649451053	6.67E-05	0.000704116
ENSG00000034971	MYOC	0.91461134	0.00088709	0.005790769
ENSG00000120729	MYOT	-1.40291721	3.62E-15	1.07E-12
ENSG00000177791	MYOZ1	0.900694358	0.00169329	0.009751831
ENSG00000249437	NAIP	-0.867182649	0.00028928	0.002346216
ENSG00000254759	NAP1L1P1	0.621196027	0.00270098	0.014198663

ENSG00000186310	NAP1L3	0.616848335	6.90E-05	0.000724274
ENSG00000166833	NAV2	0.819589526	9.08E-10	5.26E-08
ENSG00000273136	NBPF26	0.648482228	0.0126967	0.047705202
ENSG00000104490	NCALD	-0.6091889	7.72E-08	2.37E-06
ENSG00000154654	NCAM2	-0.810357345	4.41E-09	2.06E-07
ENSG00000020129	NCDN	0.857954296	7.64E-15	2.12E-12
ENSG00000100365	NCF4	-0.818249881	9.96E-06	0.000146038
ENSG00000188211	NCR3LG1	1.215309269	1.17E-16	5.00E-14
ENSG00000107130	NCS1	0.615841707	0.00016926	0.0015156
ENSG00000072864	NDE1	0.592197361	1.43E-09	7.85E-08
ENSG00000165795	NDRG2	-0.725617775	4.73E-29	2.79E-25
ENSG00000261624	NDUFB10P2	-0.86731159	9.60E-05	0.000944736
ENSG00000172260	NEGR1	-0.87318288	4.44E-10	2.84E-08
ENSG00000163491	NEK10	-0.731464504	1.86E-06	3.55E-05
ENSG00000197168	NEK5	0.853885962	1.16E-05	0.000166248
ENSG00000132688	NES	0.798202173	1.19E-06	2.44E-05
ENSG00000134259	NGF	-0.896797472	3.50E-08	1.21E-06
ENSG00000116962	NID1	-0.650500815	6.13E-06	9.77E-05
ENSG00000146938	NLGN4X	-0.782289071	5.61E-05	0.000608766
ENSG00000165246	NLGN4Y	0.759891177	0.00868535	0.035551146
ENSG00000243678	NME2	-0.59523782	2.31E-06	4.24E-05
ENSG00000148400	NOTCH1	0.773408723	7.35E-08	2.30E-06
ENSG00000074181	NOTCH3	0.664826131	0.00052765	0.003814894
ENSG00000136999	NOV	0.799570251	0.00198896	0.011083369
ENSG00000107281	NPDC1	0.61764978	7.20E-05	0.000750197
ENSG00000131697	NPHP4	0.863363021	2.46E-10	1.69E-08
ENSG00000175206	NPPA	1.831385102	1.79E-14	4.31E-12
ENSG00000242349	NPPA-AS1	1.19260701	5.07E-05	0.000560465
ENSG00000120937	NPPB	1.875502549	6.19E-17	2.98E-14
ENSG00000106236	NPTX2	-0.748635644	0.00982139	0.039137496
ENSG00000181019	NQO1	-1.062952756	1.69E-13	2.94E-11
ENSG00000119508	NR4A3	1.066675994	0.00010451	0.001008852
ENSG00000198435	NRARP	1.186441682	1.09E-08	4.43E-07
ENSG00000137404	NRM	-0.631852515	7.54E-05	0.000777362
ENSG00000118257	NRP2	0.645165011	5.10E-05	0.000562961
ENSG00000179915	NRXN1	-0.905557927	3.09E-05	0.000372302
ENSG00000168824	NSG1	-2.08874623	7.83E-21	9.23E-18
ENSG00000182667	NTM	0.640384351	0.00897783	0.036438339
ENSG00000196358	NTNG2	1.139064493	3.53E-08	1.22E-06
ENSG00000198088	NUP62CL	1.160542596	2.04E-07	5.41E-06
ENSG00000154358	OBSCN	0.735762195	4.69E-09	2.19E-07
ENSG00000115758	ODC1	0.878241946	4.36E-19	3.43E-16
ENSG00000177989	ODF3B	0.670628529	0.00188254	0.010601648

ENSG00000197444	OGDHL	2.048045351	1.11E-14	2.85E-12
ENSG00000106809	OGN	0.874858274	0.00011075	0.00106145
ENSG00000185585	OLFML2A	0.621017307	3.14E-05	0.000375768
ENSG00000127083	OMD	0.634596699	0.00287847	0.014945113
ENSG00000054277	OPN3	-0.714589035	3.79E-08	1.29E-06
ENSG00000079156	OSBPL6	0.772748082	8.28E-11	6.74E-09
ENSG00000006025	OSBPL7	0.65719213	5.73E-09	2.57E-07
ENSG00000165899	OTOGL	-0.598881138	0.00079968	0.005314028
ENSG00000165312	OTUD1	0.689999695	0.00135265	0.008154315
ENSG00000108405	P2RX1	1.194756062	4.17E-05	0.000479417
ENSG00000099957	P2RX6	0.912071298	4.26E-05	0.000486817
ENSG00000169860	P2RY1	-0.600798926	1.02E-05	0.00014857
ENSG00000182162	P2RY8	0.589278395	0.00614415	0.027046429
ENSG00000090530	P3H2	1.5078638	2.46E-09	1.26E-07
ENSG00000110811	P3H3	0.86349644	5.07E-11	4.38E-09
ENSG00000178467	P4HTM	0.865447168	1.30E-15	4.27E-13
ENSG00000101104	PABPC1L	0.644899565	0.00040216	0.003062478
ENSG00000158006	PAFAH2	0.663313014	2.12E-11	2.12E-09
ENSG00000107719	PALD1	0.647469752	2.40E-07	6.24E-06
ENSG00000129116	PALLD	-0.594505987	1.78E-08	6.75E-07
ENSG00000100767	PAPLN	0.793540158	0.00050355	0.0036756
ENSG00000182752	PAPPA	0.604041594	0.00029231	0.002365881
ENSG00000178184	PARD6G	0.689648122	0.00017505	0.001553868
ENSG00000178685	PARP10	0.619822596	2.53E-05	0.000315393
ENSG00000188677	PARVB	-0.843809215	5.04E-10	3.18E-08
ENSG00000135749	PCNX2	0.730914806	1.25E-05	0.000176889
ENSG00000163710	PCOLCE2	0.864105806	2.88E-08	1.04E-06
ENSG00000125851	PCSK2	-0.925477904	0.00125762	0.007701528
ENSG00000140479	PCSK6	0.683205822	1.21E-05	0.000172436
ENSG00000152270	PDE3B	0.672628988	1.02E-10	7.89E-09
ENSG00000184588	PDE4B	0.990709	3.76E-06	6.48E-05
ENSG00000113231	PDE8B	1.166122879	8.01E-06	0.000122244
ENSG00000134853	PDGFRA	-0.681700506	1.53E-05	0.000209807
ENSG00000067840	PDZD4	1.030335273	2.90E-07	7.29E-06
ENSG00000134020	PEBP4	-0.843174563	1.26E-06	2.55E-05
ENSG00000141456	PELP1	0.692165111	7.65E-10	4.55E-08
ENSG00000181195	PENK	1.907453476	2.03E-11	2.05E-09
ENSG00000132326	PER2	1.038148788	3.44E-10	2.27E-08
ENSG00000101132	PFDN4	-0.677786054	2.74E-07	6.95E-06
ENSG00000177614	PGBD5	0.780894562	2.36E-07	6.14E-06
ENSG00000119630	PGF	0.832528043	8.12E-05	0.000826291
ENSG00000087495	PHACTR3	-1.3889323	3.11E-07	7.73E-06
ENSG00000116273	PHF13	0.671986058	8.92E-08	2.68E-06

ENSG00000139289	PHLDA1	1.237355751	2.48E-11	2.42E-09
ENSG00000174307	PHLDA3	0.689831218	2.70E-05	0.000331742
ENSG00000168490	PHYHIP	1.331656608	3.36E-07	8.26E-06
ENSG00000164530	PI16	1.290981247	7.04E-09	3.07E-07
ENSG00000153823	PID1	-0.786817397	1.92E-11	1.97E-09
ENSG00000154864	PIEZO2	1.144080248	9.84E-05	0.000962628
ENSG00000173947	PIFO	-0.765285696	7.15E-06	0.000110925
ENSG00000155629	PIK3AP1	-0.607630825	0.00061305	0.004291518
ENSG00000100100	PIK3IP1	0.691839276	1.04E-05	0.000151098
ENSG00000276231	PIK3R6	0.82318808	0.0005993	0.004222883
ENSG00000008710	PKD1	0.8541145	5.65E-11	4.79E-09
ENSG00000250251	PKD1P6	0.701637389	2.98E-05	0.000361339
ENSG00000205038	PKHD1L1	-1.193224429	0.00013352	0.001240808
ENSG00000144837	PLA1A	-0.772487285	0.00022057	0.001885531
ENSG00000188257	PLA2G2A	-1.322008587	0.00021764	0.001863872
ENSG00000138193	PLCE1	1.145355579	9.20E-15	2.49E-12
ENSG00000114805	PLCH1	-0.872498492	0.00074637	0.005028242
ENSG00000178209	PLEC	0.724706733	4.12E-07	9.92E-06
ENSG00000115956	PLEK	-0.652640911	0.00664538	0.028743008
ENSG00000171680	PLEKHG5	0.737646982	3.35E-12	4.14E-10
ENSG00000152527	PLEKHH2	0.943173145	8.11E-07	1.77E-05
ENSG00000166819	PLIN1	0.867475423	0.00159579	0.009305951
ENSG00000147872	PLIN2	-0.752384226	2.76E-05	0.000338737
ENSG00000214456	PLIN5	-0.61430795	0.00039295	0.003008124
ENSG00000173846	PLK3	1.052123738	2.91E-08	1.05E-06
ENSG00000102934	PLLP	-0.812090178	1.07E-06	2.24E-05
ENSG00000198523	PLN	-0.775310436	9.57E-09	3.97E-07
ENSG00000123560	PLP1	-1.521310211	3.31E-11	3.08E-09
ENSG00000102007	PLP2	-0.800066804	3.45E-08	1.20E-06
ENSG00000117600	PLPPR4	1.251366375	8.33E-06	0.000126115
ENSG00000100979	PLTP	-0.897495832	4.62E-05	0.000519648
ENSG00000161381	PLXDC1	0.730764777	1.44E-07	4.04E-06
ENSG00000176903	PNMA1	0.616139262	1.12E-06	2.32E-05
ENSG00000183837	PNMA3	-0.673069896	0.00856967	0.035187604
ENSG00000141744	PNMT	-0.62705713	0.00031773	0.002532528
ENSG00000114631	PODXL2	1.388937897	9.41E-11	7.40E-09
ENSG00000137054	POLR1E	0.645640971	1.06E-08	4.31E-07
ENSG00000224897	POT1-AS1	-0.973690454	1.48E-08	5.79E-07
ENSG00000143847	PPFIA4	0.676507739	0.00011341	0.001081655
ENSG00000118898	PPL	-0.828074461	6.77E-06	0.000105923
ENSG00000204619	PPP1R11	-0.651585884	6.51E-07	1.46E-05
ENSG00000135447	PPP1R1A	-0.968855403	1.98E-07	5.30E-06
ENSG00000150722	PPP1R1C	-0.685937478	3.78E-06	6.50E-05

ENSG00000104866	PPP1R37	0.590938594	6.89E-08	2.17E-06
ENSG00000156475	PPP2R2B	0.776928846	0.00401875	0.019419961
ENSG00000214140	PRCD	0.665814004	0.00026134	0.002158174
ENSG00000186314	PRELID2	-2.076682134	5.89E-39	1.39E-34
ENSG00000116690	PRG4	1.062555001	0.00017501	0.001553868
ENSG00000282961	PRNCR1	-0.805284197	3.42E-06	5.97E-05
ENSG00000101000	PROCR	-0.595873713	0.00016554	0.001487968
ENSG00000007062	PROM1	1.187737249	8.00E-07	1.76E-05
ENSG00000155066	PROM2	0.910575735	9.59E-07	2.04E-05
ENSG00000184500	PROS1	0.595276901	0.00061875	0.0043258
ENSG00000135362	PRR5L	0.872936615	3.62E-06	6.28E-05
ENSG00000130962	PRRG1	-0.680071685	3.88E-14	8.55E-12
ENSG00000205155	PSENEEN	-0.606802854	1.09E-10	8.35E-09
ENSG00000244694	PTCHD4	0.75470316	0.00339485	0.016980554
ENSG00000156471	PTDSS1	-0.826204489	1.58E-06	3.08E-05
ENSG00000122420	PTGFR	1.315095212	1.98E-07	5.29E-06
ENSG00000134247	PTGFRN	0.783221041	8.87E-11	7.09E-09
ENSG00000095303	PTGS1	-0.759697579	9.50E-06	0.000140059
ENSG00000112655	PTK7	0.749979816	0.00011795	0.001115896
ENSG00000105894	PTN	0.77376098	1.54E-05	0.000210665
ENSG00000142949	PTPRF	0.616368505	0.0118171	0.045168811
ENSG00000080031	PTPRH	0.863930545	0.000124	0.001164315
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ENSG00000163661	PTX3	1.001455057	0.00077335	0.005165256
ENSG00000177192	PUS1	0.804476137	1.03E-08	4.23E-07
ENSG00000147485	PXDNL	0.716710674	1.60E-07	4.39E-06
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ENSG00000171016	PYGO1	-0.721078649	2.15E-06	3.99E-05
ENSG00000115828	QPCT	0.786161931	0.00014577	0.00133678
ENSG00000213339	QTRT1	0.629661663	3.24E-09	1.59E-07
ENSG00000090565	RAB11FIP3	0.633076879	6.62E-09	2.91E-07
ENSG00000139832	RAB20	0.660538916	3.31E-05	0.000393827
ENSG00000276600	RAB7B	0.592250587	0.00217363	0.011862903
ENSG00000152061	RABGAP1L	0.619329449	7.85E-08	2.39E-06
ENSG00000214842	RAD51AP2	1.035309715	6.94E-06	0.000108182
ENSG00000116191	RALGPS2	-0.843589646	9.25E-15	2.49E-12
ENSG00000164188	RANBP3L	-0.602488652	0.00710686	0.030283476
ENSG00000225125	RANP4	0.923937374	1.33E-07	3.79E-06
ENSG00000165917	RAPSN	0.685789793	0.0024191	0.012959582
ENSG00000118849	RARRES1	-1.849228389	1.08E-08	4.40E-07
ENSG00000172575	RASGRP1	0.934349959	0.00028058	0.002286227
ENSG00000105538	RASIP1	0.688583022	8.77E-07	1.89E-05
ENSG00000270885	RASL10B	-0.815945009	6.38E-08	2.03E-06

ENSG00000128045	RASL11B	0.61543853	0.00684257	0.029407071
ENSG00000163694	RBM47	-0.785035012	0.00027904	0.002275831
ENSG00000114115	RBP1	-0.662969673	1.43E-05	0.000199042
ENSG00000173653	RCE1	0.670374794	3.00E-06	5.33E-05
ENSG00000100918	REC8	0.767594665	5.51E-06	8.94E-05
ENSG00000168476	REEP4	0.627966781	0.00029316	0.002369515
ENSG00000054967	RELT	0.8147377	1.06E-05	0.000153249
ENSG00000169891	REPS2	-0.752083362	4.98E-05	0.00055263
ENSG00000135945	REV1	-0.759080681	1.10E-28	5.17E-25
ENSG00000076344	RGS11	1.107467537	7.05E-17	3.22E-14
ENSG00000117152	RGS4	1.311263224	5.01E-07	1.17E-05
ENSG00000186326	RGS9BP	-0.900247112	1.40E-06	2.79E-05
ENSG00000174791	RIN1	0.731739899	0.00022849	0.001937147
ENSG00000200783	RN7SKP180	-0.616051027	0.00146129	0.008673942
ENSG00000199683	RN7SKP185	0.906445992	0.0023941	0.012851957
ENSG00000201315	RN7SKP227	-1.456057115	5.27E-07	1.22E-05
ENSG00000201793	RN7SKP9	-0.614499175	0.00144505	0.008590504
ENSG00000263426	RN7SL471P	-1.654654615	7.54E-08	2.33E-06
ENSG00000275803	RN7SL736P	-0.79062372	0.01031223	0.040711879
ENSG00000129538	RNASE1	-1.068706637	6.09E-09	2.71E-07
ENSG00000169413	RNASE6	-1.044517862	2.04E-05	0.000265271
ENSG00000101695	RNF125	-0.797462186	6.09E-08	1.95E-06
ENSG00000137393	RNF144B	-0.84560787	4.12E-11	3.69E-09
ENSG00000200795	RNU4-1	-0.822408075	0.00073347	0.004965751
ENSG00000202538	RNU4-2	-0.665213534	0.00307183	0.015720524
ENSG00000262877	RP11-1055B8.4	0.637417291	0.00070397	0.004827691
ENSG00000259370	RP11-1069G1C	0.639798483	0.00167386	0.009670319
ENSG00000253369	RP11-1081M5.	-1.277427158	2.08E-05	0.000269541
ENSG00000224886	RP11-119F19.4	0.716348679	0.00040228	0.003062478
ENSG00000282917	RP11-121C2.3	-1.717879349	2.29E-06	4.20E-05
ENSG00000250775	RP11-12K22.1	0.812208134	0.00360681	0.017831337
ENSG00000260807	RP11-161M6.2	1.211734927	2.95E-08	1.06E-06
ENSG00000261428	RP11-16P6.1	-0.860959171	3.86E-09	1.85E-07
ENSG00000278291	RP11-172H24.4	0.932142543	6.41E-07	1.44E-05
ENSG00000279608	RP11-182N22.1	0.728713894	1.82E-12	2.43E-10
ENSG00000238102	RP11-19D2.1	-0.738596657	7.42E-05	0.000766658
ENSG00000261997	RP11-212I21.4	-0.65989986	6.20E-06	9.83E-05
ENSG00000225032	RP11-228B15.4	1.060216632	4.86E-09	2.27E-07
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ENSG00000260862	RP11-22H5.2	-0.887414204	1.65E-06	3.19E-05
ENSG00000262903	RP11-235E17.6	0.788831553	0.00010366	0.001002882
ENSG00000272129	RP11-250B2.6	-0.784476892	2.97E-08	1.06E-06
ENSG00000270194	RP11-259K5.2	0.76696586	5.97E-06	9.54E-05

ENSG00000262155	RP11-266L9.5	0.845273695	4.86E-08	1.61E-06
ENSG00000242588	RP11-274B21.1	1.20230007	4.57E-06	7.66E-05
ENSG00000245293	RP11-286E11.1	-0.966741918	5.07E-10	3.19E-08
ENSG00000234106	RP11-288E14.2	-0.7819948	4.04E-07	9.75E-06
ENSG00000279970	RP11-299G20.1	0.739946999	0.00058898	0.004165078
ENSG00000274995	RP11-321F6.2	0.892593621	9.19E-06	0.000136516
ENSG00000281106	RP11-327P2.7	0.597703743	0.00938185	0.037740299
ENSG00000280152	RP11-331F4.5	0.871467897	1.71E-08	6.56E-07
ENSG00000271833	RP11-356B19.1	0.621135599	0.00081575	0.005396326
ENSG00000250303	RP11-356J5.12	-0.95887054	1.22E-13	2.21E-11
ENSG00000258676	RP11-386M24.1	-0.984200369	0.00724007	0.030784352
ENSG00000279476	RP11-391L3.3	0.606296476	0.00074431	0.00501875
ENSG00000273597	RP11-392A14.1	0.699391811	0.0012384	0.007597675
ENSG00000237807	RP11-400K9.4	-1.113075606	3.09E-09	1.53E-07
ENSG00000230102	RP11-407B7.1	0.800141876	2.67E-05	0.00032899
ENSG00000261606	RP11-414J4.2	-0.727817637	0.01248755	0.047099514
ENSG00000226900	RP11-432J24.5	-0.731171619	7.49E-05	0.000773341
ENSG00000260267	RP11-452L6.5	0.744950884	2.48E-11	2.42E-09
ENSG00000278864	RP11-45M22.2	0.845857714	4.16E-09	1.97E-07
ENSG00000259877	RP11-46C24.7	0.794388321	5.65E-09	2.54E-07
ENSG00000259953	RP11-4O1.2	-0.681523082	4.11E-06	6.98E-05
ENSG00000260300	RP11-505K9.4	0.607816731	0.0033479	0.016776512
ENSG00000225339	RP11-513I15.6	0.683312804	0.0011224	0.007006321
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ENSG00000248713	RP11-766F14.2	-2.030609133	2.58E-12	3.26E-10
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ENSG00000260276	RP11-77H9.2	0.587875059	0.00372123	0.018285836
ENSG00000229065	RP11-8O115.4	-0.606552966	0.00487772	0.02255825

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ENSG00000234869	RP3-439F8.1	-0.685558471	1.58E-05	0.000216437
ENSG00000260000	RP3-467N11.1	0.833304367	8.60E-05	0.00086564
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ENSG00000230910	RP3-525N10.2	-0.63411225	0.00062351	0.004350578
ENSG00000244560	RP4-800G7.2	0.820042454	4.30E-06	7.24E-05
ENSG00000218018	RP4-800J21.3	0.651995615	0.00053691	0.0038712
ENSG00000236908	RP5-1063M23.	1.70044317	4.02E-10	2.62E-08
ENSG00000237686	RP5-1120P11.2	0.641031897	0.00105637	0.006673614
ENSG00000272894	RP5-1159O4.1	0.721471715	7.94E-05	0.000812834
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ENSG00000276649	RP5-858L17.1	0.629551802	0.00064044	0.004455494
ENSG00000228436	RP5-864K19.4	0.689930055	8.87E-05	0.000887476
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ENSG00000230629	RPS23P8	-0.758564545	4.37E-10	2.80E-08
ENSG00000240616	RPS6P25	-0.878628059	3.16E-10	2.11E-08
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ENSG00000132881	RSG1	0.765345621	2.10E-05	0.000271371
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ENSG00000101347	SAMHD1	-0.779250108	2.02E-07	5.37E-06
ENSG00000004139	SARM1	0.786489103	8.62E-17	3.83E-14
ENSG00000122122	SASH3	-0.751411097	0.00085218	0.005599732
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ENSG00000198794	SCAMP5	0.78990095	5.72E-06	9.20E-05
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ENSG00000171951	SCG2	1.32887905	2.71E-07	6.90E-06
ENSG00000144285	SCN1A	-0.852144812	0.00386076	0.018810736
ENSG00000149575	SCN2B	0.93517716	3.07E-13	4.86E-11
ENSG00000164106	SCRG1	1.37673266	1.55E-06	3.02E-05
ENSG00000180900	SCRIB	0.587432749	6.76E-05	0.000711378
ENSG00000136193	SCRN1	0.608522155	2.52E-06	4.59E-05
ENSG00000175356	SCUBE2	1.486395654	1.37E-11	1.49E-09
ENSG00000069188	SDK2	1.05052685	5.11E-06	8.40E-05
ENSG00000139410	SDSL	1.708655411	7.35E-18	4.12E-15
ENSG00000141574	SECTM1	-0.632332608	0.00790586	0.03294972
ENSG00000143416	SELENBP1	-1.036445234	9.25E-13	1.33E-10
ENSG00000250722	SELENOP	-0.640127047	3.82E-05	0.000443379
ENSG00000153993	SEMA3D	0.634923196	0.00532419	0.024186588
ENSG0000010319	SEMA3G	0.671930241	1.97E-07	5.28E-06
ENSG00000168758	SEMA4C	0.630780281	5.83E-06	9.34E-05
ENSG00000082684	SEMA5B	0.71145073	4.69E-05	0.000524803
ENSG00000135919	SERPINE2	1.14153026	5.15E-07	1.19E-05
ENSG00000149131	SERPING1	-0.945609402	2.05E-05	0.000266307
ENSG00000197019	SERTAD1	0.68531164	0.00014092	0.001298342
ENSG00000130766	SESN2	0.624941292	6.36E-06	0.000100311
ENSG00000100095	SEZ6L	1.885419395	1.95E-11	1.98E-09
ENSG00000104332	SFRP1	1.039027835	1.49E-05	0.000205695
ENSG00000106483	SFRP4	2.176016862	2.10E-16	8.55E-14
ENSG00000214193	SH3D21	0.846107648	7.12E-08	2.23E-06
ENSG00000107295	SH3GL2	0.752529984	0.00498159	0.022908313
ENSG00000147010	SH3KBP1	-0.658743067	2.09E-07	5.52E-06
ENSG00000156463	SH3RF2	-1.284854285	1.41E-16	5.94E-14

ENSG00000172985	SH3RF3	0.749581997	1.28E-09	7.05E-08
ENSG00000125089	SH3TC1	0.590419845	0.00157821	0.009222854
ENSG00000251322	SHANK3	0.608258647	1.45E-05	0.000201047
ENSG00000107338	SHB	0.991646858	1.39E-12	1.93E-10
ENSG00000178343	SHISA3	-0.894892548	0.00010209	0.000991328
ENSG00000198892	SHISA4	-0.980124422	1.45E-15	4.44E-13
ENSG00000105738	SIPA1L3	0.636508483	5.00E-07	1.17E-05
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ENSG00000113504	SLC12A7	0.65052074	1.55E-06	3.03E-05
ENSG00000163406	SLC15A2	-0.593607575	0.00137683	0.008264112
ENSG00000112394	SLC16A10	0.601350325	0.00037396	0.002892758
ENSG00000170190	SLC16A5	0.772014023	2.02E-07	5.37E-06
ENSG00000108932	SLC16A6	1.385300703	1.85E-06	3.53E-05
ENSG00000165449	SLC16A9	1.469837189	4.49E-14	9.62E-12
ENSG00000106688	SLC1A1	-0.87409396	6.28E-08	2.00E-06
ENSG00000197208	SLC22A4	0.800413082	0.0001081	0.001038588
ENSG00000162461	SLC25A34	-0.820190754	0.00014812	0.001355178
ENSG00000005022	SLC25A5	0.591658165	3.41E-06	5.95E-05
ENSG00000181045	SLC26A11	0.625236034	4.81E-06	7.97E-05
ENSG00000174502	SLC26A9	-1.434718036	2.48E-17	1.27E-14
ENSG00000133460	SLC2A11	0.641267176	2.02E-10	1.42E-08
ENSG00000185031	SLC2A3P2	0.605525634	0.00019735	0.001723928
ENSG00000158014	SLC30A2	1.327835724	5.83E-08	1.88E-06
ENSG00000136867	SLC31A2	-0.634711116	6.17E-06	9.80E-05
ENSG00000215790	SLC35E2	0.650957777	0.00083901	0.005530132
ENSG00000196376	SLC35F1	-0.960105892	6.69E-07	1.49E-05
ENSG00000180773	SLC36A4	-0.763420944	1.04E-18	6.65E-16
ENSG00000160190	SLC37A1	0.691725536	6.85E-12	8.07E-10
ENSG00000169507	SLC38A11	0.717019592	0.00912447	0.03691909
ENSG00000133065	SLC41A1	-0.63658264	5.63E-07	1.29E-05
ENSG00000167703	SLC43A2	1.049497194	8.67E-10	5.07E-08
ENSG00000142494	SLC47A1	0.782107826	3.32E-07	8.20E-06
ENSG00000050438	SLC4A8	1.284761422	3.06E-07	7.64E-06
ENSG00000100170	SLC5A1	-0.857350002	1.38E-05	0.000192811
ENSG00000157103	SLC6A1	0.80293473	1.17E-05	0.000167605
ENSG00000010379	SLC6A13	0.809213461	3.20E-06	5.61E-05
ENSG00000131389	SLC6A6	1.023389459	1.04E-05	0.000151394
ENSG00000103257	SLC7A5	0.745492762	0.00327172	0.016471775
ENSG00000155465	SLC7A7	-0.894630782	3.91E-05	0.000451858
ENSG00000092068	SLC7A8	-0.75233253	8.79E-06	0.000131557
ENSG00000090020	SLC9A1	0.698922168	0.00077808	0.005189464

ENSG00000135740	SLC9A5	0.737332034	8.62E-05	0.000867511
ENSG00000065923	SLC9A7	-0.794041825	5.79E-11	4.89E-09
ENSG00000181804	SLC9A9	-0.695298802	1.53E-05	0.000209831
ENSG00000139155	SLCO1C1	0.8724247	4.51E-05	0.000510235
ENSG00000101187	SLCO4A1	-1.086453311	0.00022099	0.001888498
ENSG00000179542	SLITRK4	0.900312015	0.00151757	0.008944965
ENSG00000184564	SLITRK6	-1.169212706	2.66E-05	0.000327593
ENSG00000170290	SLN	-1.182304114	0.00013404	0.00124416
ENSG00000137834	SMAD6	0.842760387	8.07E-07	1.77E-05
ENSG00000101665	SMAD7	0.751746519	1.08E-06	2.25E-05
ENSG00000120693	SMAD9	0.629531054	0.0007136	0.004870851
ENSG00000270332	SMC2-AS1	-1.13223998	2.15E-10	1.51E-08
ENSG00000214097	SMCO1	-0.895262025	5.64E-07	1.29E-05
ENSG00000237296	SMG1P1	0.620241779	0.00140632	0.008415437
ENSG00000180747	SMG1P3	0.60406791	0.00019009	0.001667311
ENSG00000183604	SMG1P5	0.803591923	0.00082137	0.005427558
ENSG00000256235	SMIM3	-0.680499299	4.29E-10	2.78E-08
ENSG00000198732	SMOC1	-0.996697792	0.00178126	0.010168728
ENSG00000112562	SMOC2	1.502335938	1.98E-27	5.19E-24
ENSG00000088826	SMOX	0.715525595	0.00011171	0.001069132
ENSG00000188176	SMTNL2	-0.758023371	0.00020188	0.001756377
ENSG00000115593	SMYD1	-0.783496245	2.61E-11	2.54E-09
ENSG00000124216	SNAI1	0.818279433	0.00571444	0.02553626
ENSG00000143740	SNAP47	1.364918512	1.09E-12	1.52E-10
ENSG00000145335	SNCA	0.94204262	5.56E-06	9.02E-05
ENSG00000212443	SNORA53	-1.034515695	1.12E-06	2.33E-05
ENSG00000200959	SNORA74A	-0.954921107	7.61E-06	0.000116814
ENSG00000212402	SNORA74B	-0.646442947	0.00351143	0.017425612
ENSG00000207279	SNORD116-24	-0.648378226	0.00080035	0.005316961
ENSG00000207445	SNORD15B	-0.728605864	0.00707667	0.030171187
ENSG00000120833	SOCS2	0.926552635	5.86E-11	4.92E-09
ENSG00000246985	SOCS2-AS1	0.995339888	5.60E-08	1.82E-06
ENSG00000109610	SOD3	0.699217249	0.00104361	0.006610759
ENSG00000108018	SORCS1	-1.181534994	9.98E-08	2.97E-06
ENSG00000137642	SORL1	0.662699083	1.23E-05	0.000174977
ENSG00000164736	SOX17	0.616557439	0.0067236	0.02902274
ENSG00000203883	SOX18	0.967214524	2.99E-05	0.000362862
ENSG00000005513	SOX8	1.225479578	1.02E-07	3.02E-06
ENSG00000165698	SPACA9	0.798108184	2.53E-08	9.26E-07
ENSG00000152583	SPARCL1	-0.89395926	9.04E-20	8.52E-17
ENSG00000163071	SPATA18	0.771181103	5.85E-05	0.000630974
ENSG00000158792	SPATA2L	0.702590804	0.00119669	0.007382111
ENSG00000106686	SPATA6L	0.60230233	0.00058005	0.004117026

ENSG00000161888	SPC24	-0.657095953	0.00305141	0.015639804
ENSG00000070182	SPTB	0.617191218	8.95E-09	3.77E-07
ENSG00000173898	SPTBN2	0.814325572	0.00151287	0.008920756
ENSG00000160460	SPTBN4	1.05287966	6.86E-13	1.00E-10
ENSG00000165389	SPTSSA	-0.658841587	3.40E-11	3.12E-09
ENSG00000122862	SRGN	-0.68600445	0.00010568	0.001017791
ENSG00000130511	SSBP4	0.672629005	2.00E-05	0.000261622
ENSG00000179954	SSC5D	1.246395183	5.77E-07	1.31E-05
ENSG00000115525	ST3GAL5	-0.831876834	7.25E-11	5.98E-09
ENSG00000144057	ST6GAL2	0.750688587	0.01037099	0.040875445
ENSG00000184005	ST6GALNAC3	-0.76541321	3.70E-09	1.79E-07
ENSG00000140557	ST8SIA2	0.77042017	0.00024709	0.002061471
ENSG00000101638	ST8SIA5	1.471570636	2.79E-10	1.88E-08
ENSG00000148488	ST8SIA6	-0.821428344	1.09E-10	8.33E-09
ENSG00000214530	STARD10	-0.694157403	5.21E-12	6.26E-10
ENSG00000138378	STAT4	1.327858615	1.62E-06	3.13E-05
ENSG00000159167	STC1	1.099768453	9.99E-05	0.000974479
ENSG00000127954	STEAP4	-0.772096317	1.38E-05	0.00019373
ENSG00000134602	STK26	-0.949619167	3.47E-07	8.50E-06
ENSG00000203685	STUM	-0.687766868	3.39E-05	0.000402402
ENSG00000137573	SULF1	0.893071307	1.76E-05	0.000236636
ENSG00000173705	SUSD5	1.098344468	1.91E-05	0.000251948
ENSG00000165124	SVEP1	0.709224976	5.13E-06	8.42E-05
ENSG00000166111	SVOP	-0.778878204	0.00555749	0.024991213
ENSG00000008056	SYN1	-0.785514291	0.00322931	0.016324501
ENSG00000162520	SYNC	-0.5861885	6.17E-06	9.80E-05
ENSG00000102003	SYP	-0.679091933	4.05E-06	6.91E-05
ENSG00000103528	SYT17	0.809706173	7.23E-05	0.000751242
ENSG00000137501	SYTL2	0.699487129	4.15E-05	0.000477117
ENSG00000147041	SYTL5	1.075130089	0.00020038	0.001745202
ENSG00000183597	TANGO2	0.610621196	2.50E-08	9.17E-07
ENSG00000141556	TBCD	0.620670152	5.81E-09	2.60E-07
ENSG00000121068	TBX2	0.598178413	8.16E-07	1.78E-05
ENSG00000165929	TC2N	-1.595854257	1.63E-14	3.96E-12
ENSG00000185339	TCN2	-0.651640407	1.04E-05	0.000151558
ENSG00000145022	TCTA	0.618501646	3.24E-11	3.04E-09
ENSG00000074219	TEAD2	-0.769673714	3.24E-20	3.47E-17
ENSG00000135605	TEC	0.587801239	3.77E-05	0.000438825
ENSG00000167074	TEF	0.631555166	1.65E-05	0.000224788
ENSG00000100726	TELO2	0.783120509	3.95E-07	9.55E-06
ENSG00000149256	TENM4	1.385412305	6.89E-16	2.46E-13
ENSG00000091513	TF	0.81899214	0.00447873	0.021105234
ENSG00000105967	TFEC	-0.68975715	0.00179595	0.010240171

ENSG00000003436	TFPI	-0.861779628	6.80E-11	5.64E-09
ENSG00000105825	TFPI2	-0.742427847	0.00103627	0.006578367
ENSG00000072274	TFRC	-0.967510496	2.69E-09	1.35E-07
ENSG00000163235	TGFA	-1.105013717	0.00022307	0.001902786
ENSG00000092969	TGFB2	0.97234993	5.82E-06	9.32E-05
ENSG00000163513	TGFBR2	-0.604627962	1.02E-14	2.63E-12
ENSG00000069702	TGFBR3	-0.933468843	6.47E-14	1.32E-11
ENSG00000129028	THAP10	0.63737669	1.28E-06	2.59E-05
ENSG00000186340	THBS2	1.514420673	9.12E-12	1.05E-09
ENSG00000113296	THBS4	1.472559858	1.54E-10	1.11E-08
ENSG00000154096	THY1	1.640739483	2.50E-09	1.27E-07
ENSG00000221995	TIAF1	0.737730202	9.91E-06	0.000145522
ENSG00000100234	TIMP3	-0.624727055	3.22E-05	0.000384673
ENSG00000157150	TIMP4	-0.979718121	4.83E-06	8.01E-05
ENSG00000007350	TKTL1	-0.862143954	8.18E-06	0.000124047
ENSG00000095587	TLL2	0.894704426	0.00013987	0.001289686
ENSG00000137462	TLR2	-0.864208931	8.54E-05	0.000861523
ENSG00000196664	TLR7	-0.633064146	0.00908312	0.036777052
ENSG00000163762	TM4SF18	-0.601543378	0.00045661	0.003400366
ENSG00000141524	TMC6	0.631099637	0.00017272	0.001539859
ENSG00000166292	TMEM100	-0.748136969	0.00045211	0.003380532
ENSG00000144868	TMEM108	-0.734260409	0.00142964	0.008524718
ENSG00000183160	TMEM119	1.092345851	5.91E-05	0.000635986
ENSG00000139364	TMEM132B	-1.594073238	2.60E-09	1.31E-07
ENSG00000181234	TMEM132C	-0.980251124	7.32E-05	0.00075909
ENSG00000178826	TMEM139	-0.990499773	5.48E-07	1.26E-05
ENSG00000236144	TMEM147-AS1	0.589100762	1.37E-08	5.40E-07
ENSG00000261115	TMEM178B	-0.864884928	3.33E-07	8.21E-06
ENSG00000187824	TMEM220	-0.830840826	7.50E-14	1.50E-11
ENSG00000205084	TMEM231	0.601178696	1.03E-08	4.25E-07
ENSG00000224982	TMEM233	1.7011006	1.53E-09	8.31E-08
ENSG00000148483	TMEM236	-1.038480629	1.55E-08	6.02E-07
ENSG00000182107	TMEM30B	1.324157217	2.10E-06	3.92E-05
ENSG00000095209	TMEM38B	-0.696299896	6.96E-12	8.16E-10
ENSG00000164983	TMEM65	-0.814162639	1.23E-17	6.43E-15
ENSG00000159596	TMEM69	-0.672585403	1.01E-12	1.44E-10
ENSG00000165071	TMEM71	0.599127791	0.00045275	0.003381183
ENSG00000137103	TMEM8B	0.609520304	1.73E-07	4.69E-06
ENSG00000125827	TMX4	-0.661651398	1.99E-13	3.42E-11
ENSG00000041982	TNC	1.215360876	9.54E-06	0.000140439
ENSG00000141655	TNFRSF11A	-0.828248568	7.96E-06	0.000121654
ENSG00000164761	TNFRSF11B	1.130175837	4.44E-07	1.06E-05
ENSG00000215788	TNFRSF25	0.904391921	1.65E-11	1.76E-09

ENSG00000186827	TNFRSF4	1.191684468	9.04E-06	0.000134526
ENSG00000105048	TNNT1	0.834178773	2.37E-06	4.33E-05
ENSG00000182095	TNRC18	0.637485445	5.11E-05	0.000564219
ENSG00000204282	TNRC6C-AS1	0.86449752	3.62E-05	0.000425391
ENSG00000168477	TNXB	0.805575743	8.85E-06	0.000132385
ENSG00000160949	TONSL	0.642241283	0.00037618	0.002906
ENSG00000115129	TP53I3	0.71191737	2.27E-05	0.00028947
ENSG00000078804	TP53INP2	0.875237041	7.61E-06	0.000116814
ENSG00000162341	TPCN2	0.618808761	6.41E-07	1.44E-05
ENSG00000111907	TPD52L1	0.788782349	3.35E-09	1.64E-07
ENSG00000141933	TPGS1	0.766962193	5.37E-05	0.000587736
ENSG00000144034	TPRKB	-0.817974167	5.83E-13	8.65E-11
ENSG00000128294	TPST2	-0.702159928	4.61E-11	4.11E-09
ENSG00000076604	TRAF4	0.703770179	0.00057685	0.004101466
ENSG00000072657	TRHDE	-1.613345054	5.49E-08	1.79E-06
ENSG00000173334	TRIB1	0.652407225	0.00021394	0.001843853
ENSG00000255690	TRIL	0.682698406	0.00032541	0.002578213
ENSG00000146054	TRIM7	0.888611157	8.27E-09	3.51E-07
ENSG00000205133	TRIQK	-0.658477771	7.55E-08	2.33E-06
ENSG00000137672	TRPC6	0.875352192	4.85E-05	0.000538571
ENSG00000196689	TRPV1	0.851446512	2.10E-11	2.12E-09
ENSG00000196428	TSC22D2	0.586771927	1.09E-08	4.40E-07
ENSG00000145777	TSLP	-1.023339489	1.68E-12	2.27E-10
ENSG00000064201	TSPAN32	0.718558392	2.11E-07	5.56E-06
ENSG00000168785	TSPAN5	0.736921643	0.00019748	0.001724254
ENSG00000011105	TSPAN9	0.881888526	3.80E-14	8.46E-12
ENSG00000128311	TST	-0.675525875	0.00011152	0.001067932
ENSG00000233864	TTY15	0.656605717	0.01332541	0.049522878
ENSG00000167553	TUBA1C	-0.630510818	0.00010562	0.001017626
ENSG00000075886	TUBA3D	-2.21300499	2.82E-13	4.49E-11
ENSG00000152086	TUBA3E	-2.388724218	1.99E-14	4.69E-12
ENSG00000188229	TUBB4B	-0.78634873	1.67E-09	9.03E-08
ENSG00000131462	TUBG1	-0.637648792	5.85E-08	1.88E-06
ENSG00000074966	TXK	0.622055174	0.00159389	0.009298918
ENSG00000011600	TYROBP	-0.680687528	0.00755411	0.031775783
ENSG00000230454	U73166.2	0.686162471	3.09E-05	0.000372193
ENSG00000108106	UBE2S	0.637969513	0.00211899	0.011637404
ENSG00000154277	UCHL1	0.878291979	0.0003967	0.003029678
ENSG00000143179	UCK2	0.729781626	4.74E-10	3.00E-08
ENSG00000177169	ULK1	0.747792878	2.05E-07	5.44E-06
ENSG00000107731	UNC5B	0.882408629	6.50E-09	2.87E-07
ENSG00000144406	UNC80	2.313663941	9.41E-18	5.04E-15
ENSG00000005007	UPF1	0.663441442	2.27E-12	2.91E-10

ENSG00000183696	UPP1	0.698533531	1.56E-14	3.84E-12
ENSG00000142207	URB1	0.599747036	1.19E-09	6.59E-08
ENSG00000102226	USP11	0.780224641	3.20E-20	3.47E-17
ENSG00000136878	USP20	0.634986405	1.76E-11	1.85E-09
ENSG00000124422	USP22	0.624218969	6.33E-18	3.64E-15
ENSG00000163945	UVSSA	0.653091094	6.76E-09	2.97E-07
ENSG00000162738	VANGL2	-0.779187042	2.14E-06	3.98E-05
ENSG00000071246	VASH1	0.65701036	4.90E-07	1.15E-05
ENSG00000143494	VASH2	-0.738513978	0.00244579	0.013081734
ENSG00000150630	VEGFC	0.599844201	0.00045716	0.003403352
ENSG00000165197	VEGFD	-1.209172809	1.67E-07	4.54E-06
ENSG00000205221	VIT	-1.209205044	1.47E-07	4.10E-06
ENSG00000112303	VNN2	-0.753580609	0.00114741	0.007128744
ENSG0000019102	VSIG2	0.675225295	0.0001588	0.001434492
ENSG00000155659	VSIG4	-1.593314028	1.43E-10	1.05E-08
ENSG00000163032	VSNL1	1.022202201	8.20E-14	1.59E-11
ENSG00000132821	VSTM2L	-1.037027452	0.0002142	0.001844185
ENSG00000109072	VTN	0.720390517	2.74E-05	0.000335835
ENSG00000179403	VWA1	0.585259677	0.00091699	0.005955901
ENSG00000204396	VWA7	0.65585401	0.00020515	0.001778883
ENSG00000239779	WBP1	0.660763516	3.12E-06	5.50E-05
ENSG00000174776	WDR49	-0.930802531	3.93E-06	6.73E-05
ENSG00000075702	WDR62	-0.745968781	0.00065215	0.004520981
ENSG00000158023	WDR66	0.733835457	5.35E-05	0.000586332
ENSG00000161996	WDR90	0.703055922	2.08E-05	0.000268794
ENSG00000215861	WI2-1896O14.	0.620518473	0.00512119	0.023422367
ENSG00000064205	WISP2	-0.761979524	0.00090614	0.005898421
ENSG00000196632	WNK3	-1.150860871	2.20E-09	1.15E-07
ENSG00000114251	WNT5A	-0.839306374	2.89E-07	7.28E-06
ENSG00000143816	WNT9A	2.386811792	5.36E-20	5.45E-17
ENSG00000142279	WTIP	0.620294847	1.75E-06	3.35E-05
ENSG00000206579	XKR4	-0.766180713	0.00592844	0.026317971
ENSG00000143324	XPR1	0.787677823	2.21E-09	1.15E-07
ENSG00000126215	XRCC3	0.637131935	9.15E-05	0.00090911
ENSG00000152422	XRCC4	-0.795488469	8.33E-10	4.89E-08
ENSG00000093100	XXbac-B461K1	0.628029735	0.00245499	0.013119082
ENSG00000175048	ZDHHC14	0.743911555	1.12E-09	6.28E-08
ENSG00000155256	ZFYVE27	0.6171893	7.02E-10	4.24E-08
ENSG00000158805	ZNF276	0.613668199	4.50E-10	2.87E-08
ENSG00000205903	ZNF316	0.738648901	1.52E-07	4.23E-06
ENSG00000138311	ZNF365	1.340796032	1.21E-06	2.49E-05
ENSG00000181444	ZNF467	0.655158965	0.00150848	0.008904757
ENSG00000225614	ZNF469	0.979858532	4.19E-05	0.000480523

ENSG00000197363	ZNF517	0.67609261	2.05E-06	3.84E-05
ENSG00000198597	ZNF536	0.759400468	0.00016117	0.001453681
ENSG00000168916	ZNF608	0.655491974	3.24E-06	5.68E-05
ENSG00000196109	ZNF676	0.771245954	1.04E-08	4.27E-07
ENSG00000267254	ZNF790-AS1	0.67354693	2.34E-05	0.000296327
ENSG00000213973	ZNF99	0.760568493	0.00026409	0.002174794
ENSG00000174276	ZNHIT2	0.629721349	0.00098893	0.006339317
ENSG00000121413	ZSCAN18	0.700326835	9.50E-15	2.49E-12
ENSG00000132003	ZSWIM4	0.658417697	0.00024658	0.002059412

Supplemental Table S4

Gene names	Sequence window	FC	p-value
NRAP	GVGMDRRTLHAMKVGSLASNVAYKADYKHDI	-1.887794206	0.002274013
TNS1	ALPEKRMSVGDRAAGSLPNYATINGKVSSPV	-2.247670462	0.006901013
TNS1	SLGRHLGGSGSVVPGSPCLDRHVAYGGYSTP	1.617300322	0.000521025
TNS1	MLDLEPASAAAPLHKSQSVPGAWPGASPLSS	-2.326999423	0.002254274
TNS1	VSVDYNTSDPLIRWDSYDNFSGHRDDGMEEV	2.140347535	1.68E-05
C10orf54	QAASNRRRAQELVRMDSNIQGIENPGFEASPP	-2.615814099	8.02E-07
ADD1	___MNGDSRAAVVTSPPTTAPHKERYFDR	1.541756425	0.009549895
ADD1;LA04NCO	LLNPEKYKAKSRSPGSPVGEETGSPKQWQIG	4.97564703	9.03E-06
CLASP1	GTTTKAEGRIIRTRRQSSGSATNVASTPDNRG;PGSYA	-2.569656177	3.51E-09
HIST1H1E	_____MSETAPAAPAAPAPAEK	-3.28839855	3.31E-05
PTPN12	ESTIEQIDKKLERNLSFEIKKVPLQEGPKSF	-2.60762991	0.000469018
KIAA0415;FOXk	GVSCFRTPFGPLSSRSAPASPTHGMLMSPRS	-1.599872401	0.002973894
KIAA0415;FOXk	FRTPFGLSSRSAPASPTHGMLMSPRSGGLQ	-1.724448756	0.003952206
CAMK2B	SPLPAPSPRISDILNSVRRGSGTPEAEGPLS	2.270656703	0.000523486
CAMK2B	EDEDAKAPRVPDILSSVRRGSGAPEAEGPLP	2.13350756	0.000937747
XIRP2	QFDESIHKFQIIRGISAQEIQTGNVKSAKWL	-1.933719627	0.00069494
APOL1	ASASRPRVTEPISAESGEQVERVNEPSILEM	2.735150589	0.005335391
tmp_locus_29;I	LSSPVFPRAGFGSKGSSSVTSRVYQVSRST	-2.020189066	0.003820303
tmp_locus_29;I	MRQMRELEDRFASEASGYQDNIARLEEEIRH	2.083870719	0.00025821
CEP170	PTRTSLRRARLGEASDSELADADKASVASE	2.143399596	0.000973711
	EPVGMETGLGQAPGRSAVLSASEHKRSGAA_	-6.750950586	0.000279148
SPTAN1;DKFZp	VATFNSIKELNERWRSLQQLAEERSQLLGSA	-2.425573594	0.003859032
MYOM3	VLVRDAEENPGAGSPLNVRCLDVNRDCLI	-2.056708278	0.002898414
MYOM3	CTYKEDEGLYMVRVPSFGPREQSTYVLVRD	2.105655813	3.33E-17
TP53BP1	GDCKLMLSTSEYSQSPKMESLSSHRIDEDG	1.724605372	0.000357261
TP53BP1	LTVECKTSEIEPKNSPEDLGLSLTGDSCKL	1.766746696	0.000285398
PRKAR1A;PRKA	LQKAGTRTDSREDEISPPPPNPVVKGRRRRG	1.873749103	2.31E-05
ATG9A	QAQAEPERHVWHRRESDESSESAPDEGGEGA	-2.79996149	3.63E-07
FILIP1	GEAAEEETPAVFIKRSFQENHIMSNLRQVG	-2.382178335	1.94E-08
ACTA2;ACTC1;A	VGMGQKDSYVGDQAQSKRGILTKYPIEHGI	-7.112553768	6.95E-09
ACTA2;ACTC1;A	GIADRMQKEITALAPSTMKIKIAPPERKYS;GIADRM	-3.073305014	0.000973868
MYBPC3	APARPAPDAPEDTGDSDEWVFDKLLCETEG	-2.683191832	0.003175127
	SAFRRTSLAGGRRISDSHEDTGILNFSSLL	-3.073203916	0.002889164
GYS1	AAQGYRYPRPASVPPSPSLSRHSSPHQSEDE	3.242273598	0.001316447
PRKAR2A	EDLEVPVPSRFNRRVSVCAETYNPDEEEEDT	-1.724391818	5.71E-07
MLLT4	LPGDDRLMKNRADHRSSPNVANQPSPGGKS	-1.735480141	0.001095593
SYNRG	NSTAASKYDVFRQLSLEGSGLGVEDLKDNT	-1.532132676	0.004189432
MYOM1	DSEAIEVKAAIGGGVSPDVCALSDEPGGLT	3.35672244	5.39E-06
MYOM1	SSAAHRRESEAFRRASASSSQQASQHALSS	-3.868091003	4.83E-06
BCKDK	PLRPLLGPALALRARSTSATDTHHVEMARER	-2.96011804	6.49E-05
TJP1;DKFZp686	WRFRLRSSKRNLKRSREDLAQPVQTKFPA	1.635955962	3.95E-07
SRRM1	RLSPSASPPRRRHRPSPATPPPKTRHSPTP	-2.399341606	0.000838982
DKFZp781D221	NNFPKNQTPVRMRRNSFTLSSSNTIRRPRN	-2.467061138	6.74E-11
NEBL	KKDLENEIKGKGMQVSMIPDILRAKRTSEI	-3.353369668	1.24E-05
NEBL	TVKYTQDQHKQMKGRPSLILDTPAMRHVKEAQ	-6.288776043	3.36E-11
NEBL	EKVYKEDFEKEIKGRSSLDLTKTPEFLHVKY	-2.864504562	0.00079528

NEBL	QGYGYMHQTSVSSMRSMQHSPNLRTRYAMYD	-1.763767281	0.004969043
ATP1A2;ATP1A	DIRILAAQGCKVDNSSLTGESEPQTRSPECT;DLRIISAF	-2.669089458	0.002857657
TGOLN2	SHPEPQTPKDSPSKSSAEQTPEDTPNKSGA	1.50982815	0.008443804
CDC42EP4	TEEAVPRRNGAAGPHSPDLLDEQAFGLDLD	2.760274739	2.92E-05
SSR1	MSWIPQETLNQINKASPRRLPRKRAQKRSVG	-1.789590437	0.003578436
NCK1	NLKDTLIGIKVKRKPSVPDSASPADDSDVDP	-2.087422378	8.74E-05
HARS2	KPNFIIKTPKGTDLSPQHMMVVREKILDVLI	1.979497727	0.000225321
CSDC2	SRVWERGGVPPRDLPSPLPTKRTRTYSATAR	-1.721080603	2.22E-05
CSDC2	MTSESTSPVVPPLHSPKSPVWPTFPFHREG	-2.051237625	0.000341946
MYOZ2	SQQAPLTPPNTDPSPNPNDIAPGYSGPL	1.792079012	6.85E-07
SLC9A1	AHKLDSPTMSRARIGSDPLAYEPKEDLPVIT	3.14074322	3.33E-05
UGP2	____MSRFVQDLKAMSQDGASQFQEVIRQEL	2.139590372	0.000102175
CCNY;CCNYL1	NPSDHPRASTIFLSKQTDVREKRKSLFINH;NPSDHPF	-2.438714694	3.33E-06
ANKRD2	AALQKVKGQERVRKTSLDLRREIDVGGIQN	-14.04320325	8.11E-06
CAST	TAISGKPGDKKKEKSLTAPVPEVKPDKPS;TAISGKP	-2.785638456	9.47E-05
SPTBN1	KGEQVSQNGLPAEQGSPRMAETVDTSEMVNG	1.76493394	0.000393727
PPP1R13B	RRKLANAPRPLKKRSSITEPEGGPNIQKL	-1.833999799	0.000164457
SORBS2	PRSGAPTPSSRAPALSPTRPPKKPLDYVQDH	2.257792723	2.55E-17
SORBS2	SKSHSDNSPNAFKDASSPVPVPPVPPVPL	2.704780552	0.003145956
SORBS2	SPPSRAKDRESRYSSTLTDMGRSAPRERR;SSPSRAI	-1.935095643	0.005601414
SORBS2	GRKPLSSSRLGEVTGSPSPPPRSGAPTSSR	2.114388187	0.000321541
SORBS2	KPLSSSRLGEVTGSPSPPPRSGAPTSSRAP	1.970543068	0.000108387
CCNL2	LLPGGTQVLDGTSGFSPAPKLAWSAVALSGI	-2.184850749	8.19E-06
PCDH1	YQDRGGQEPAGAGSPSPEDRNTKTAPVRL	1.781880781	0.00456674
PCDH1	GDSPRIHLPLNYPPGSPDLGRHYRSNSPLPS	1.689960277	0.00191093
SMTN	SSKKMGSIFDREDQASPRAGSLAALEKQAE	-1.946699936	0.000618704
NAGLT1	PTFQDLATNVNRNIISSLSFIFVGRALGYLSG	-3.994814283	9.94E-07
NAGLT1	FQDLATNVNRNIISSLSFIFVGRALGYLSGSV	-3.766609813	3.88E-06
ABLIM1	LPDGHMPAMRMDRGVSMPNMLEPKIFPYEML	-2.18105085	0.000190478
ABLIM1	GPPSFAVVGPDMKRRSSGREEDDEELLRRRQ	-4.793011307	1.99E-09
ABLIM1	PPSFAVVGPDMKRRSSGREEDDEELLRRRQL	-3.013477475	0.00726124
AARSD1;PTGES	NEKIRDRLPVNVRELSLDDPEVEQVSGRGLP	-1.859244584	0.000834635
TJAP1	PQPNGECHSLGTARGSPPEELPLPAFEKLN	2.734875394	0.001251642
ABLIM1	GRDCLCQLCAQPMSSSPKETTSSNCAGCGR	1.783982414	2.02E-05
PXN	GERCWAAGWPRDGGRSSPGGQDEGGFMAQGK	1.891015895	2.80E-05
PXN	ERCWAAGWPRDGGRSSPGGQDEGGFMAQGKT	1.884624456	3.40E-05
FAM122A	ASPKRIDFIPVSPAPSPTRGIGKQCFSPSLQ	-2.207418901	0.000805173
DBNL	AVHPREIFKQKERAMSTTSISSPQPGKLRSP	3.749911862	1.31E-05
GORASP2	SEKPVSAAVDANASESP_____	1.5170002	0.005426058
SMARCC2	REEEQEDLTKDMDEPSPVPNVVEVTLPKTVN	2.433430388	2.44E-06
HNRPK;HNRNPI	QGGSGYDYSYAGGRGSYGLDGGPIITQVTI	-2.095566423	2.22E-05
PGM1	IIRKIKAIIGGIILTASHNPGGPNDFGIKFN	-3.723439494	1.77E-05
CANX	EDRKPKAEDEILNRSPNRKPRRE_____	1.536340925	0.003228217
	_____MSRDISPEEIDLKNEPWYKFF	2.604205146	2.34E-08
PLEKHA5	REKKKGLNVIGASDQSPLOSPSNLRDNPFR	-1.532068683	0.000153704
GJA1	GDRNNSSCRNYNKQASEQNWANYSAEQNRMG	-2.368491957	0.001615528
SYNPO2L	DEPIWRTELASAPVPSAPPPEAPRGLGASP	3.107906143	1.05E-13

SYNPO2L	GRGVQLFEQQRQRADSSTQELARVEPAAMLN	-3.420818797	2.48E-08
SYNPO2L	MELARAGSRASEGQGSGLGGQLSEVSGRGVQ	1.757640779	8.08E-07
SYNPO2L	PRAQSAPPEAAVLPPSPLPAPVASPRPFQPG	3.869223148	1.29E-09
SYNPO2L	EAAVLPPSPLPAPVASPRPFQGGGAPTAP	2.979803984	0.001487693
SYNPO2L	PPSRGLLDGLVNGAASSAGIPEPPRLQGRGG	3.084634769	7.59E-05
SYNPO2L	PSRGLLDGLVNGAASSAGIPEPPRLQGRGGE	2.155800461	0.00934987
SYNPO2L	ARVEPAAMLNGEGLQSPRAQSAPPEAAVL	2.97283805	3.25E-14
VDAC2	YQLDPTASISAKVNNSSLIGVGYTQLRPGV	-2.010372776	6.97E-06
SLC16A1	IDVAGKPNEVTKAAESPDQKDTDGGPKKEES	-2.547996904	6.99E-05
SLC16A1	SPDQKDTDGGPKKEESPV	-3.607043467	4.46E-05
CTNNB1	HQLSKKEASRHAIMRSPQMVAIVRTMQNTN	1.923967369	1.67E-05
CTNNB1	FRMSEDKPQDYKKRLSVELTSSLRTEPMAW	-3.423274547	7.42E-05
CTNNB1	VQLLVRAHQDTQRRTSMGGTQQQFVEGVRME	-2.117092065	9.99E-05
SKIV2L;SKI2W	TVSASPCSAPLARASSLEDLVLKEASTAVST	1.73825215	0.001002715
MAP4	VAPSTVKEVGLLKDMSPLSETEMALGKDVT	2.436056926	0.004594481
MAP4	ISSTEISSAEKVALSSETEVALARDMTLPE	2.285391618	6.57E-07
DKFZp564A228	DDIYKTHLENNRFGGSGSQVDSARMNLASSF	2.333962033	4.92E-12
PPP1R12C	ERRTAEGAPGAGLQRSASSSWLEGTSTQAKE	-2.686280535	3.96E-05
PKM	MADTFLEHMCRLDIDSPITARNTGIICTIG	2.529771914	0.006742413
ABC1	PKPAKPEKNRINKAVSEEQQPALKGKKGKEE	3.019991022	0.000448699
HNRNPA1;HNR	_____MSKSESPKEPEQLRKLFIG	-2.055147218	2.19E-07
DKFZp586F042	ARIAATTGNGQPRRRSIQDLTVTGTEPGQVS	2.607996883	7.41E-07
LMOD2	_____MSTFGYRRGLSKYESIDEDELLASLSAEEL	2.45233936	9.88E-05
LMOD2	TKVWQRGTPSSSPYVSPRHSPWSSPKLPKKV	4.528752813	0.001721675
DPF2	PLEKRGAPDRVDDDSLGEFPVNSRARKRI	-1.571562546	0.007506526
LSM14A	TASAHLPAPAAVGRRSPVSTRPLPSASQKAG	1.824916672	6.54E-08
MYLK;DKFZp68	LSSMAMISGLSRKSSTGSPTSPLNAEKLES	1.834715488	0.001162254
PACSIN3	FHELHRDLHQGIEAASDEEDLRWWRSTHGPG	2.65753852	3.52E-06
EIF3J	_____MAAAAAAGDSDSWDADAFSVEDPVR	-2.22105828	0.001032398
ENO3;ENO2;EN	FTSKGLFRAAVPSGASTGIYEALERDNDKT;HTAKGRI	-2.615518715	4.07E-05
EIF3C;EIF3CL	TKPVGGNYGKQPLLLSEDEEDTKRVVRSKD	2.299360573	0.000245661
SORBS3	EPRLRLCDDGPQLPTSPRLTAAARSARHPSS	2.107717503	0.003032617
EVL	_____MKPAGSVNDMALDAFDLDRMK;EKPV	-1.732345725	0.004093077
PLEKHF1	AAQQRQEAEQAGAGSPGQPAHLARPICGAS	1.723710414	0.004347076
SH3RF2	NGIEKQVKTFRFQNYSPPTKHYTSHPTSGK	-2.063441779	8.18E-08
ACTN3;ACTN1;	GMIWTIILRFAIQDISVEETSAKEGLLLWCQ	5.094270295	1.35E-13
SIPA1	PHTFEPVRGPELLRSGSDAGEARPPTPASP	-1.533822255	0.000363571
SIPA1	TFEPRPVRGPELLRSGSDAGEARPPTPASPRA	-1.557807137	0.000371977
CTNNA1	QLPQEQKAKIAEQVASFQEEKSKLDAEVSKW	2.569618224	2.76E-07
AKAP2	GPPEDSGASAAKGQKSPGALETSAAGSQGN	1.903268093	0.00021993
PLXDC2	ERRPSRWPAMKFRRGSGHPAYAEVEPVGEKE	3.005643347	0.000905278
HRC	HRHQGHRDEEDEDVSTERWHQGPQHVVHGL	-2.743751124	0.003271004
CAMK2D	LKGAILTTMLATRNFSAAKSLKKPDGVKIN	1.894498908	0.001229792
LIMCH1	ATVETTIARASVLDTSMSAGSGSPKTVTPK	2.549588529	0.000373622
DKFZp686G032	ERSDSLSPRHRGDDSFDSLDFGSRSRQTP	1.75802876	0.00127332
LIMCH1	TLPLDKSINHQIESPERRKKSREHFQAGP	1.649753379	0.001470249
LIMCH1	GKVELVLSQKVVKPKSPEPEATLTFPFLDKM	2.786297496	1.23E-05

ALDOC	LRIVAPGKGILAADES VGSMARLSQIGVEN	-1.912052589	0.009981084
RRAS2	LVRVIRKFQEQECPSPETRKEKDKKGCHC	1.630850935	1.20E-05
PPHLN1	RERSPYKRDNTFFRESPVGRKDSPHSRSGSS	-2.076561083	0.00324148
CRIP2	ARAEERKASGPPKGPSRASSVTTFTGEPNTC	-2.450835621	3.04E-06
ARHGEF7	TMKKLLPKRKPERSDEEFASRKSTAALEE	-2.315734408	0.003493969
SORBS1	AVTLRASSYRETPSSSPASPQETRQHESKP	-2.647234044	0.000866269
SORBS1	AIEKRAKDDSRVVKSTQDLSVSMDEVGIP	-1.774012987	0.000533736
CAMSAP1	ERGEGRPRSIVSRPSEGPQLVRRKMTGSR	-4.289440639	7.19E-10
SUMO1	_____MSDQEAKPSTEDLGDKK	1.809398824	1.28E-05
SYNPO2	AKPFPGSVNQPATPFSPTRNMTSPIADFPAP	1.546277772	0.001690643
SYNPO2	IIQISSGRELRVIQESEAGDAGLPRVEILD	2.073661816	3.28E-05
ARVCF	GFPEGPEPRDPSYGSLSRGLGMRPPRAGPL	2.022743896	0.002153086
PDLIM4	AQAHRIHIDPEIQDGSPTTSRRPSGTGTGPE	2.74349522	0.002924027
SYNM	VAENIVTSILKQFTQSPETEASADSFDPDKV	3.330860795	0.004326357
SYNM	VVRESLSRQRSPAGSPDEEGGAEAPAAGIR	1.669380683	1.96E-07
APEH	KAESFFQTKALDVSASDDEIARLKKPDQAIK	-2.028675544	0.000127237
SORBS2	SGGAVSPMSYYQRPFSPSAY_____	2.564769858	0.000789266
TNS2;TENC1	QERSPGGHSDGASPRSPVPTTLPLGRHAPWQ	3.155856114	2.09E-11
MYH11	SRRSGGRRVIENADGSEETDTRDADFNGTK	1.734127143	0.001722437
TTN	LDARLHGDLVTIRAGSDLVLDAVGGKPEPK	-1.537543252	0.004506025
TTN	PKRVKSPEPSHPKAVSPTETKPTTEKVQHL	-9.956217769	0.000448459
TTN	ARVTEKAVTSPRVKSPEPRVKSPEAVKSPK	-3.470365846	1.09E-06
TTN	VVTEEKITIVTQREESPPPAVPEIPKKKVPPE	1.840365602	6.16E-05
TTN	EGILMPEEPETQAVLSDTEKIFPSAMSIEQI	1.685798841	0.002765198
TTN	VQEEEPFVPLTQRLSIDNSKKGESQLRVRD	-2.522150261	0.001400887
TTN	QAVLSDTEKIFPSAMSIEQINSLTVEPLKTL	2.292339635	0.000666078
TTN	LSPSMEAPKIFERIQSQTVGQGSDAHFRVRV	-1.52777557	0.004985658
TTN	GSKITGYVIEAQRKGSQWTHITTVKGLECV	-1.867812538	0.008137272
TTN	TPSPIEAERRLRPGSGGKPPDEAPFTYQL	-2.552796387	1.03E-05
TTN	VPEKKVPEAIPKPEPPPEVPEVLPKPEVV	1.628443075	0.006669667
TTN	EKEFEELVFSFIQRLSQTEPVTLIKDIENQT	-5.560657906	8.61E-09
TTN	SPARMSPARMSPARMSPGRRLEETDESQLER	-2.895358158	4.85E-05
TTN	PEVPPPWKQEGYVASSSEAEMRETTLTSTQ	2.11812384	0.001081135
TTN	QDDLEIVRPARRRTPSPDYDFYRPRRRSLG	2.276382694	3.20E-05
TTN	QTRIEKKIEAHFDARSATVEMVIDGAAGQQ	-1.736696657	0.007674023
TTN	PVSRIRLSRSPRSRSPIRMSPARMSPARMS	2.558521624	0.009900996
ARHGEF2	AEAPWARRPVDPRRRSLPAGDALYLSFNPPQ	-1.594056173	0.009160486
NES	ESLTALEKENQEPLRSPEVGDEEALRPLTKE	1.997591859	0.00913311
NES	ETLRTLEKETQRRRSLGEQDQMTLRPPEKV	3.039202759	9.85E-09
PDLIM5	DNTKKAKEKIPLHVFSKYTKLRDWHHEVSA	-1.794312338	0.000544652
PDLIM5	ATLSKVATTYSSLSSTGNVEDSFEGFRNFS	2.119865642	0.003770119
MYH6;MYH7;M	TEAKAELQRVLSKANSEVAQWRKYETDAIQ	-3.711926684	0.001020068
MYH6;MYH7	LEEISERLEEAGGATSVQIEMNKKREAEFQK	2.828311219	0.002974845
HBB	GRLLVVYPWTQRFESFGDLSTPDAVMGNPK	2.575672805	0.00074117
TPM1	DRKYEEVARKLVIIESDLERAERAELSEGK	1.779715347	0.000220357
DKFZp434I243E	GSSAEQLGGRLRKLKSLGQYDNDAGGLPFS	-1.677919714	0.005660274
CAST	_____MSQPGQKPAASPRPRRAAAARRTHEH	-3.966781938	6.83E-05

MAP4	KGSDSLNKKVDLTLSPKSENDKLKEISLAC	2.470262797	6.66E-08
MAP4	PSKRSNDGKSKKVKNSPEKHILENKIDATK	2.531841922	0.000524293
MAP4	VSGSSSCGGPGNQKRSIHVDSLEPQRDLGRE	-4.844351001	4.02E-17
MAP4	PQPAPHLKTPVDKSQSVGPLNLKGPLAEVSA	1.787628958	0.003523658
PROB1	LALAGRTAPAQPRAASAPPTDRSPQSPSQGA	-3.414155347	1.57E-06
PROB1	APAQPRAASAPPTDRSPQSPSQGARRQPGAA	-2.894206975	9.14E-05
PROB1	PRQTPNGAVRGPSPQNLSPWDRTRRRVS	-2.395192368	0.002871409
PROB1	QAAAGFVQTALARKLSPEAPAPSSATFGSTG	-1.642353484	1.33E-05
PROB1	RAAGAPRPRLLLRTGSLDESLGPLQAAAGFV	-5.708629553	0.000100301
MAST4	APKLGGRYRSGRRKSAGNIPLSPLARTPSP	-3.145637601	1.76E-06
NACA	SLSFQGSKDSPATTHSPTPPSPKGAPTPSAV	-1.655194912	0.00874561
KIF13A	QSIPEKNSKSLCRTGSCSELDACPSKISQPA	1.625205977	0.001150555
LRBA	_____MASEDNRVSPPTGDDGGGGGREE	1.782701723	2.82E-06
MAP1A	VTKAPSLDSSLPQLPSPSSPGAPLLSNLPRP	2.970719462	6.60E-05
MAP1A	EEGTLEKEEKVPPRSPQAQAEVNIIDEGLT	1.799631225	0.000695595
CALD1	DKEKEEEEEKPKRGSIGENQIKDEKIKKDK	1.906566421	1.22E-05
LMO7	TSGLDLMSESGEISQREVSRSQDQFSDM	2.491408779	1.48E-05
LMO7	QKEVAATEEDVTRLPSPTSPFSSLSQDQAAT	1.866811215	0.001495648
LMO7	TTGVATTQSPTPRSHSPSASQSGSQRNRSV	-2.878493415	0.00073372
C11orf58;SMAF	SAARESHPHGVKRSASPDDDLGSSNWEAADL	-2.09220843	0.002679387
TPD52L1	ISKKFGDMRNSPTFKSFEERVETTVTSLKTK	2.220016228	0.000247672
TPD52L1;hD53	TSLKTKVGGTNPNGGSFEEVLSSTAHASAQS	1.688136333	0.009969764
CRYAB	LSPFYLRPPSFLRAPSWFDTGLSEMRLEKDR	-2.676194485	3.78E-06
CADPS	GGLQPSSRAGGRPSSPSPVSEKEKEELE	1.724771629	0.004132127
MYPN	TFSIPSGNQFQPRCVSIPVSPTRSRIQNPVA	2.33151114	0.001790565
PCDH7	SPSMGRYRSVNGGPGSPDLARHYKSSSPLPT	2.272497788	7.06E-05
MYO18B;DKFz	LAVQRKSTERLEPASSPLASRSTNTSPLSRE	1.672451358	9.21E-05
LDB3	ASPGTPGTPELRPTFSPAFSRPSAFSSLAEA	2.898112544	0.000187687
LDB3	PVIPHQKDPALDTNGSLVAPSPPEARASPG	3.141328956	0.004863031
LDB3	QKDPALDTNGSLVAPSPPEARASPGTGP	2.486355607	0.000207191
LDB3	DPALDTNGSLVAPSPPEARASPGTGPTEL	3.148757729	2.55E-09
PARVA	_____MATSPQKSPSPKSPKSPSRKK	2.931747629	0.005243216
CLASP2	RLSSSVSAMRVLNTGSDVEEAVADALKKPAR	1.995658054	0.008130895
CLIP1	SATPPISNLTKTASESISNLSEAGSIKKGER	-1.810859878	0.000443423
RPTOR	QRVLDTSSTLQSAPASPTNKGVHIHQAGGSP	1.899025803	7.58E-07
CNOT4	SNPVIPISSNHSARSPFEGAVTESQSLFSD	2.263843499	9.33E-08
UBE4B	SNSLETQSQSLRSQSMIDIGVSCSMSQV	1.570463623	0.002115603
ACSS2	RGQEEAGAGGRARSWSPPEVSRSAHVPSLQ	-2.867854709	0.000558881
CEP170	RGGHGVPHGKLLKQKSEEPSVIPFLQTALL	2.01776075	0.001099639
SIK3;KIAA0999	TLQLLNGMGPLGRRASDGGANIQLHAQQLLK	-2.364256869	0.000463086
LMO7	_____XDVTRLPSPTSPFSSLSQDQAAT	1.82336661	0.000692605
KLC1;KNS2	SRESEPKNPGMKRASSLNLVVGKAAEDRF	-1.501725338	0.000186993
RYR2	REGDSMALYNRTRRISQTSQVSVDAAHGYSP	-1.935412025	0.000994116
RYR2	DSMALYNRTRRISQTSQVSVDAAHGYSPRAI	3.855062303	5.25E-08
PPP1R1A	EDRIPNPHLKSTLAMSPRQRKKMTRITPTMK	-5.545933387	2.97E-06
CARHSP1	SSEPPPPQPPTHQASVGLLDTPRSRRERSPS	-1.696756519	0.006803536
CARHSP1	NVVPSPLPTRRTRTFSATVRASQGPVYKVC	2.799211258	0.00476465

OBSCN	CELSRAGASVEWRKGSLLQFPCAQYQMVQDG	1.868041147	0.007142253
OBSCN	IEEGTERRLTVRNVSADDDAVYICETPEGS	1.52328187	0.002335192
ZFYVE19	QDPERVTLQDYRLPDSDDDEDEETAIQRLVQ	-1.68221302	0.00622022
STARD13	HIPKDHKPGTFPKALSIESLPTDSSNGVNW	-2.341938642	3.56E-06
SRCIN1	AELPLGFSRMNRFRQSLPLRSASQTKLRSP	2.483123288	6.21E-09
PRKCA	KTKTIRSTLNPQWNESTFKLKPDKDRRLS	-1.580451788	0.004471422
FXYD1	QRTGEPDEEEGTFRSSIRRLSTRRR_____	-2.470978803	0.00425237
COPE	____MAPPAPGPASGGSGEDELFDVKNAFYI	2.186078091	3.17E-05
BIN1	AQPSDNAPAKGNKSPSPDGDSPAATPEIRVN	1.793925675	0.002674009
HSPB6	MEIPVPVQPSWLRRASAPLPLGLSAPGRFLDQ	-2.288014352	1.45E-05
SCAMP3	LDNPFQDPAVIQHRPSRQYATLDVYNPFETR	-6.075863112	2.31E-10
STX7	REKEFVARVRASSRVSGSPEDSSKERNLVS	2.129940887	5.32E-06
TGFB111	SGDKDHLYSTVCKPRSPKPAAPAAPPFSSSS	2.638510953	6.74E-05
PPP1R12B	VPATEAGEGQQPWGRSLDEEPICHRLRCPAQ	2.355001054	9.54E-05
DKC1	AKAGLESGAEPGDGSDTTKKKKKKKKAKEV	-1.878277828	0.000650934
COBL	MHSRSLTLGPSLSLGSISGVSVKSEMKKRRA	1.977451773	0.000606566
DNAJB6	GVQREAAVEQAQSETSLGARGQRGHK_____	1.534126018	3.13E-05
SEC22B	TKKLYIDSCARRNLGSINTELQDVQRIMVAN	-2.880183174	9.07E-06
SORBS2	RVSQITVNGNSGGAVSPMSYYQRPFSAYS	2.440695432	0.000710522
SORBS2	_____MNTGRDSQSPDSAKGFRSVRPNLQ	-2.78009975	0.002394763
ABLIM3	WTYHGSPKVPRARRFSSGGEEDDFDRSMHKL	-1.509410074	7.88E-06
STBD1	DRVDHEEWEMVPRHSSWGDVGVGSLKAPVL	-5.003662956	0.000219059
STBD1	DLGKLQAASWRLQNPSREVCDNSREHVPSGQ	2.470124492	1.17E-06
TACC2	PKMKKTPEKLDNTPASPPRSPAEPNDIPIAK	2.448557864	1.35E-07
SVIL;DKFZp586	VTLAGLASKENFSNVSLRSVNLTEQNSNSA	2.277428095	2.19E-17
SVIL	GHNREASKKRKVRTRSLSDFTGPPQLQALKY	1.616377529	0.001629224
SVIL	PKHAHSSSLQQAASRSPSFGDPQLSPEARPR;PKHAH!	3.334599303	0.000224983
SVIL	QQAASRSPSFGDPQLSPEARPRCTSHSETPT;QQAASI	2.844606238	0.000152644
AIFM1	VRREGVKVMPNAIVQSVGVSSGKLLIKLDG	-2.818968382	0.000351493
MB	GAMNKALELFRKDMASNYKELGFQG_____	-3.650185248	7.84E-11
ALDOA	VAPGKGILAADESTGSIKRLQSIGTENTEE	-1.692711929	4.69E-05
HSPB1	IESPAVAAPAYSRALSRQLSSGVSEIRHTAD	-15.40801477	8.69E-08
CKM	LQKRGTTGGVDTAAVGSVFDVSNADRLGSSEV	-1.827153875	3.36E-05
LDHB	SLFLQTPKIVADKDYSVTANSKIVVVTAGVR	-2.183325394	5.38E-07
VIM	RTYSLGSALRPSTSRSLYASSPGGVYATRSS	-1.97757071	0.005664176
MYH3;MYH1;M	QEAKAELQRALSKANSEVAQWRKYETDAIQ;QEAK/	-3.563627555	0.000787874
SPTB	STAINESQSIRVKAQSLPLPSLSPDASLGK	-2.904724968	2.53E-07
IGF2R	KSVKALSSHLHGDDQDSEDEVLTIPVVKVHSG	-1.576786095	0.000928246
MYH7	DQMNEHRSKAETQRSVNDLTSQRAKLQ TEN	1.559875481	0.001882597
MYH7	RILNPAAIPEGQFIDSRKGAEKLLSLDIDH	-2.162736455	0.00291514
MYH7	ETVVGLYQKSSLLKLLSTLFANYAGADAPIEK	2.024181501	0.006018698
DSP;DSP varian	VRRASSKGGGGYTCQSGSGWDEFTKHTVSEC	-2.294407475	1.26E-05
HIST1H1C	_____MSETAPAAPAAAPPAEK	-2.496216503	0.00269425
VCL	ENACTKLVQAAQMLQSDPYSPVARDYLIDGS	1.728597859	0.002012899
VCL	VEKMTGLVDEAIDTKSLLDASEEAIKDKLDK	3.336464562	5.49E-06
FLNA;FLJ00119	KIPEISIQDMTAQVTSPSGKTHEAEIVEGEN	1.737766966	0.009384761
VDAC1	YQIDPDACFSAKVNNSLIGLYTQTLKPGI	-1.89295373	0.000158919

TNXB;TNXA	LSAEGTTGLAPAGQTSEESRPRLSQLSVTDV	2.625506687	0.002525007
PLN	MEKVQYLTRSARRASTIEMPQQARQKLQNL	-5.03708535	5.55E-10
ACTN2	TKWVKVQLVPIRDQSLQEELARQHANERLR	-2.836052141	0.000300204
TXLNA	GPERRPEGPGAQAPSSPRVTEAPCYPGAPST	-3.307738437	0.000214183
MAP1B	PTPVVKQTKLKQRADSRESLKPAAKPLPSKS	3.623587952	0.000262008
MAP1B;DKFZp6	FEFSDAKDENERASVSPMDEPVPDSESPIEK	1.720961595	0.002188696
RBM25	HRPKIGLSLKLGNASNSPGQNSVVRKRLPVD	-2.545685827	0.004641818
RANBP2	GSSTKCAACQNPRKQSLPATS IPTASFKFG	-2.434241998	7.52E-08
HNRNPM;HNR	GIERMGLAMGGGGGASFDRAIEMERGNFGGS	2.639901197	0.000429116
RRAD	GGSRGGGQERERRRGSTPWGPAPPLHRRSMP	-5.683289596	9.80E-08
CDK18	QNQRFRSMEDVSKRLSLPMDIRLPQEFLLQL	-2.273388222	0.000182973
DMTN	SSLPAYGRTTSLRQLQSTEFSPSGSETGSPGL	-1.613622098	0.005550761
AHNAK	FDIKSPKFKAELPSPKLEGELQAPDLELS	2.827187322	1.29E-06
AHNAK	VDVTGREGAKDIDISSPEFKIKIPRHELTEI	2.778554817	0.000550012
AHNAK	PDWNLKMPKMKMPKFSVSGLKAEGPDVAVDL	-2.904969411	2.02E-05
AHNAK	GKGGVTGSPEASISGSKGDLKSSKASLGSLE	-3.68587059	5.87E-05
AHNAK	VEGDLKGPEIDIKGPSLDIDTPDVNIEGPEG	2.65769328	3.06E-06
AHNAK	VDVETQSGKTVIRLPSGSGAASPTGSAVDIR	1.870651099	0.002894342
AHNAK	PRLDFEGPDAKLSGPSLKMPLEISAPKVTA	-2.306073515	3.63E-05
CGNL1	TKKTRPDVLPFRRQDSAGPVLGDARSRRSSS	1.532701553	0.008202179
AKAP13	LCQVSHPHTKLMRIPSFPPSPPEPPSPSAPS	-2.448036237	0.003006491
SNTB2	GDSLPGSPSRGLGPPSPAPPGRPAGEAGAS	1.924193438	7.44E-11
SNTB2	SPPAPPGRPAGEAGASPPVRRVRVVKQEAGG	2.071051621	9.75E-09
SNTB1	AGAGHPGAGGAQPPDSPAGVRTAFTDLPEQV	1.588028493	0.000449314
SCRIB	TAKAERRHQERLRVQSPEPPAPERALSAPL	1.501608282	0.004320467
DPYSL3	RRGQGREESREPAPASPAPAGVEIRSATGKE	2.442526439	6.10E-06
CTTN	KLEEQARAKTQTPPVSPAPQPTTEERLPSSPV	1.715808551	0.000841518
PDE3A	SAEMSGCSSKSHRRTSLPCIPREQLMGHSEW	-2.19843255	2.15E-05
LTBP1	EYVLKPKYFPAQKGISGEQSTEGSFPLRYVQ	2.02910331	0.000600892
NUMA1 variant	PRTQPDGTSVPGEPASPISQLPCKVESLES	1.814330315	0.000131432
PLCL1	EVTDEDEEAEMSRMSVDYNGEQKQIRLCRE	-2.944327266	1.51E-06
PLCL1	DCVTAASGGRMRDRRSGVALPGAAGTPADSE	-4.433287259	2.45E-09
PCBP1	QGRVMTIPYQPMPASSPVICAGGQDRCSDA	-1.722272379	1.35E-05
TRIP10	PLGGPVPSALPNGPPSPRSGRDPLAILSEIS	-1.723075385	0.002905644
SPEG	DQFPLTRSRAIQECRSPVPPPAADPPEARTEK	1.769138852	0.00355755
SPEG	PLFSRPSTPKTSRAVSPAAAQPPSPSSAEKP	1.85916749	0.004494924
SPEG	QPKSERGAPWGTGASQEELRAPGSVAERRR	-2.445352977	0.00351961
SPEG	PAAGASPRRGELRRGSSAESALPRAGPRELG	-2.056208181	0.008908071
SPEG	IPVARLGARRLQESPLSALSEAQSPSPARP	2.324033515	3.30E-05
SPEG	SSARGSPVLAMRRRLSFTLERLSSRLQRSGS	-1.654783447	0.004749033
ZYX	QHPVPPPAQNQNQVRSPPGAPGLTLKEVEEL	4.150097718	2.80E-08
SGCB	____MAAAAAAAAAEQSSNGPVKSMREKAVE	2.064709354	0.00613071
SMTNL2	GKGKGEARARLKRSQSFQVASSIKILLE	-4.606851282	4.77E-08
MYLK3	GTEPGEQTPEGARELSPLQESSPPGGVKAEE	2.016336207	0.002982787
MAP7D1;RPRC:	SKRRASNEKESAAPASPAPSPAPSPPTAPPQ	1.904900839	8.87E-06
MAP7D1;RPRC:	MGPRDARPPRRSSQPSPTAVPASDSPTKQE	2.402806844	7.99E-08
GNG12	KASADLMSYCEEHARSPELLIGIPTSENPFK	1.883526944	0.002132442

PDLIM3	QSGSFRVLQGMVDDGSDDRPAGTRSVRAPVT	2.491035757	4.37E-05
TEX264	GSRETSAAATLSPGASSRGWDDGDTRSEHSYS	2.269299005	0.000385115
SH3KBP1	FGDIFKDKPIKLRPRSIEVENDFLPVEKTIG	1.9815109	0.00314546
PLEKHA1	GPGRSASSMRQARRLSNPCIQRSIPPVLQNP	-2.394672409	1.51E-05
PERM1	ELGPGPAGAPEPGPRSPVQEDRPGPGLGLST	2.349263609	0.00010395
KANK2	PRLSSLPRGPGSWWTSTESLCSNASGDSRHS	-2.00161168	0.002589576
KANK3	SPGRGVPRSPRSGRSPAPNLAPASPGPAQ	2.35435615	3.27E-07
KANK3	PGRGVPRSPRSGRSPAPNLAPASPGPAQL	1.746974878	0.005005869
FIP1L1	RERERTRERERERDHSPTPSVFNSDEERYRY	1.77506603	0.004577323
XIRP1	GGGSDPRIPAAPRKVSREEQALPRGLPGGWV	-1.861705023	0.0006012
XIRP1	GTRMLFETRPLDRLGSRPSLQEQSPLELRSE	-2.133278838	6.87E-06
XIRP1	MLFETRPLDRLGSRPSLQEQSPLELRSEIQE	-2.309237472	2.26E-09
TAOK1	YREEGDPTRASDPQSPQVSRHKSHYRNRE	3.207351232	2.91E-07
HUWE1	LTHPPPIMGGVVRDLMSSEEDQMMRAIAMSL	-1.688413543	0.004413574
PHLDB2;DKFZp1	LAGESDRVFATRNFSCGSVEFDEADLESLR	-2.324189441	0.000113619
PHLDB1;KIAA06	TFSDGLATRTLQPPESPRLGRRGLDSMRELP	2.833513615	1.53E-07
PACS2	LKERQAARPQNERANSLDNERCPDARSQLQI	-2.144447199	3.47E-07
P2RY8	GCRRVPRDTLDRRESLFSARTTTSVRSEAGA	1.983130921	0.002509547
PPFIBP1	GSKALEYSNGIFDCQSPTSPFMGSLRALHLV	-1.764335623	0.000493539
CMYA5	KLPPERFFQKPVSGLSVEQVKSETISSSVKT	1.782162866	0.002617551
SYNPO	LKENAALLTANGLHLSQNREAQQSSPAPPPA	5.392838502	8.41E-12
DCLK2;MGC454	SSSNVNGGPELDRCSPEGVNGNRCSESSTL	1.878651137	0.000132135
FAM160A2	LQGRDGLGAGLGLSGGSPGASTPVLLTRGGAP	-1.726306268	0.000286943
BVES	SDSDDGLHQFLRGTSMSLHVSSPHQRASA	-2.731774142	0.000186396
NAV1	KSSGIPVKPVNGRKTSLDVSNSAEPGFLAPG	-2.426919409	1.04E-05
TPM3	KAISEELDHALNDMTS_____	1.714988938	0.009358663
PPP1R13L	ARVLAIEIPRPLKRRGSMEQAPAVALPPTHKK	-2.458423646	0.001949186
PALLD	ESKNTDFFPGLSAFLSQEINKSLDLARRAI	2.804573532	0.001689967
PALLD	SGHPHVRRPRSRSDSGDENEPQERFFRPH	-2.992353548	1.11E-07
CASKIN2	SLADNLSHRPLANCRSGEQIFTQDVRPEQLL	1.603950657	0.000227076
CASKIN2	PRVGLSPDSPAGDRNSVSGSESVGSIRSAGS	-2.008634661	0.003255205
TTN;DKFZp451f	ETREQQEIHKEKIPSPETLQPDTHNISKS	-1.684583529	0.000210661
TTN;DKFZp451f	HRGDVQEADTLHRQLSLSQCFLLMTEEQQN	-4.113761054	1.30E-06
PHKB	SWKVLERRARTKRSGSVYEPLKSINLPRPDN	-3.161259507	8.19E-05
IRS2	MDRPLSHCGRSYRRVSGDAAQDLDRGLRKRT	-3.415955612	1.44E-06
FAM129B	APAGESPQKAAPEASSPPASPLQHLLPGKA	1.813101345	0.003932352
FAM129B	SPQKAAPEASSPPASPLQHLLPGKAVDLGP	2.1353939	0.000107017
PKP2	EGRWGRGTAQYSSQKSVEERSLRHPLRLEI	-1.549499548	0.005248754
PKP2	ERAHYTHSDYQYSQRSQAGHTLHHQESRRAA	-2.695103157	0.00275447
PKP2	YSQRSQAGHTLHHQESRRAALLVPPRYARSE	-3.339514235	2.61E-05
	PGPGGPYPRPLRRIISVEEDPLPQLLDGGFE	1.937584833	0.004187405
FUNDC2	_____METSAPRAGSQVVATTARHSAAYRA	-2.053918031	0.000562801
SORBS1	ASIYNTDHLALSPRASPSLSLPHLSWSDR	-4.117764948	0.001925283
SORBS1	GKSSVLTNEKMSRDISPEIDLKNEPWYKFF	2.729450559	7.70E-08
SORBS1	RGGEQAGRKAARRGGSQSHSLRAGPDLTE	3.026786653	0.000800604
TNKS1BP1	VSQCPEPGLRHNGSLSPGLEARDPLEARELG	1.702332324	0.001058247
NUCKS1;NUCKS	PVRNRKVVDYSQFQESDDADEDYGRDSGPPT	2.058439371	2.43E-05

DCTPP1	_____MSVAGGEIRGDTGGEDT	-1.734000356	0.004223817
RTN4	PPSTPAAPKRRGSSGSVDETLFALPAASEPV	2.159557438	0.001117595
SERINC1	SNNSQVNKLTLSDESTLIEDGGARSDGSLE	-1.900314473	0.001262649
C9orf78	RPLRVGDTEKPEPERSPPNRKRPAANEKATDD	-1.76606633	0.004782188
SIPA1L2	AVNPNTGAALHREYGSTSSIDRQGLSGENFF	2.67898288	0.000506066
TJP2	FGPSRDRDRDRSRGRSIDQDYERAYHRAYPD	-1.877164974	5.41E-07
TJP2	VVKRPRKVQVAALQASPLDQDDRAFEVMDE	-1.746828808	1.11E-05
TJP2	SRLNSHGGRSRWEDSPERGRPHERARSRER	-2.675108703	0.000100947
PLCL2	NKPGTENADVQKPRRSLEVIPEKANDETGE_	-2.295805984	3.13E-08
SRRM2;KIAA03	PRVPLSAYERVSGRTSPPLDRARSRTPPSA	1.846370244	5.59E-06
TLN1	VLVEDTKVLVQNAAGSQEKLAQAAQSSVATI	2.475617245	0.000490124
TLN1	SQLVACTKVVAPTISSPVCQEQLVEAGRLVA	2.625421423	9.20E-06
LRRFIP2	VVSAADYFSRSNRRGSVVSEVDDISIPDLSS	-1.64981079	0.00619502
ARFGEF2	IQSKPQSPVIQAAVSPKFVRLKHSQAQSKP	1.950250049	0.003582029
TNS1	ESLVASRSPQPLAETPIPSLPEFPRAASQQ	1.758762776	4.66E-05
CAMK2B	VCQRSTVASMMHRQETVECKKFNARRKLGK	-1.752010315	0.000224358
ACTA2;ACTC1;A	SSLEKSYELPDGQVITIGNERFRCPEALFQP;SSLEKSYE	-2.068083967	0.001847056
SYNRG	ANRTTPGKLTKEELYTVLAMIAVTQRGVPAM	1.900445381	0.00482415
SRRM1	SASPPRRRHRPSPPATPPPKTRHSPTPQQSN	-2.408998012	0.000850291
PCYT1A	ERSPSPSFRWPFSGKTSPPCSPANLSRHKAA	-1.868242499	0.001723485
SORBS2	AVGPPRGLGDQASARTSPGRVDLPGSSTTLT	2.225088809	0.00856326
	SRTSPGRVDLPGSSTTLTKSFTSSSPSPSR	3.530075106	0.005020146
MAPK3;DKFzP6	LARIADPEHDHTGFLTEYVATRWRAPAEIML	2.677519576	0.000768179
PGM1	SCIIRKIKAIIGGIILTASHNPGGPNDFGIK	-4.486660993	0.002268711
SYNPO2L	PLPMAPKTPPMTPKTPPPVAPKPPSRGLLD;PPPM#	3.119518596	3.07E-16
C2orf18;SLC35F	LAESEQERLLGGTRTPINDAS_____	-2.740808517	0.004124446
SORBS2	SRTSPGRVDLPGSSTTLTKSFTSSSPSPSR	4.773294578	0.000626263
SORBS1	SQPARASGSFAPISQTPPSFPPPLVPPAP	4.515628963	0.002204205
FARP1	TPGSRLGAPENSGISTLERGQKPPPTPSGKL	2.023332328	0.001995405
TTN	PIRHSPSPVRHVRAPTSPVRSVSPAARIST	-3.427838368	0.000407728
TTN	FTLIQKARVTEKAVTSPPRVKSPPEPRVKSP	-3.474443879	1.06E-06
MYH6;MYH7	KMRRDLEEATLQHEATAAALRKKHADSV AEL	-3.110109225	6.50E-07
MYH6;MYH7	QARIEELEELEAERTARAKVEKLRSDLSRE	-1.879897053	0.000434507
MYH6;MYH7;M	NSSRFGKFIRIHFGATGKLASADIETYLLEK	-7.980209021	7.35E-06
MYH6;MYH3;M	HAELEASQKESRSLSTELFKIKNAYEESLDQ;QAELEAA	-2.102696217	3.43E-06
MAP1A;M1LP	SRAIRGEKELSSEPQTTPPAQKGTVPLPTISG	1.730790859	0.003897752
LDB3	PSPSPEARASPGTGPTELPTFSPAFSRPS	2.074362181	0.000106753
OBSCN	LWEALARKRRMSREPTLDSISELPEEDGRSQ	3.54938228	1.48E-05
LMNB2	ATMATPLPGRAGGPATPLSPTRLRLQEKEE	1.941852599	0.004542641
KIF1C	YPAQRPPGPRYPPTYTPPRMRRQRSAPDLKE	2.452497339	5.60E-07
PPP1R12B	LRKARSRQARQTRRSTQGVTLTDLQEAERTF	-3.459884854	8.34E-07
SPAG9	ISLGIFPLPAGDGLLTPDAQKGETPGSEQW	-2.211553679	0.003857814
STK10	MFFKLSEEAECNPSTPSKAAKFFPYSSADA	2.145003815	1.34E-06
MB	MKASEDLKKHGATVLTALGGILKKKGHHEAE	-3.305011865	1.84E-05
CKM	KFEEILTRLRLQKRGTTGGVDTAAVGSVFDVS	-1.90096217	0.000451705
CKM	RRAVEKLSVEALNSLTGEFKGKYYPKSMTE	-2.169246557	0.007037034
MYH7	TVVGLYQKSSLKLLSTLFANYAGADAPIEKG	-3.046181946	0.000552465

CKMT2	RFSKILENLRQKRGTTGGVDTAAVADVYDIS	-1.896207735	6.09E-05
CKMT2	LKGDLAGRYKLESEMTEQDQQLIDDHFLFD	-3.148481638	1.85E-07
PLN	EKVQYLTRSAIRRASTIEMPQQARQKLQNL	-2.095979742	0.000183583
PLEC;PLEC1	SDARKLTFRGLRQKITMEELVRSQVMDEATA	-2.307034957	0.000271342
MURC	AARPVYPPHEGREIPTPEPLKVTFKSQVKVE	2.413886569	0.004806476
XIRP1	QATSRKFEEGFSANSTDQEPTRPQGGGDVR	-2.34131538	0.00023581
RRAGC	VFHKMSPNETLFLESTNKIYKDDISNSSFVN	-2.639784529	0.000639989
RRAGD	VFHKMSPNETLFLESTNKICREDVSNSSFVN	-2.613655345	0.001291004
MAPK1	RVADPDHDHTGFLTEYVATRWYRAPEIMLNS	5.468904752	1.34E-07
ACTA2;ACTC1;A	RDLDYLMKILTERGYSFVTTAEREIVRDIK	-2.811088739	3.91E-09
HEL-S-54e;PHB	GLIELRKLEAAEDIAYQLSRNRNITYLPAGQ	-4.517673167	6.26E-08
MAPK3;DKFZp6	RIADPEHDHTGFLTEYVATRWYRAPEIMLNS	3.256974744	0.000188087
	_____MGNHELYMRRRKPDITIEVQQMK	2.184030725	6.47E-08
TTN	KTSWKVDQLQEGCSYYFRVLAENEYIGLPA	-2.015949958	0.000356239
VPS13A	_____LYSILAFIDNFQAAKQA	2.032878375	0.000618983
ANK2	SLPSSQFLDGMNYLRYSLGGRSDSLRSFSS	3.014544092	4.69E-08
MYH7	EKEALISQLTRGKLYTQQLDLKRQLEEEV	-3.104335115	2.13E-09
CKMT2	KRGTGGVDTAAVADVYDISNIDRIGRSEVEL	-1.888042662	1.98E-09
USP48	ERRLVSKAWSKLQYFPKAPFPYKECCS	-2.048568764	0.006013615
DYRK2;DYRK4	IDFGSSCYEHQRVYTYIQSRFYRAPEVILGA	3.51465102	7.84E-08

Supplemental Table S5

Gene	Sequence	FC	p-value
ABLIM1	RQSLGESPRTLSPTPSAEGYQDVRDRMIHRS	-1.54016165	0.0044773
ACIN1	ASLVALPEQTASEEETPPPLLTKEASSPPPH	1.518451472	0.0023391
ACTC1	SSLEKSYELPDGQVITIGNERFRCPEALFQP;SSLEKSYELPDGQVITIGNE	2.491970069	0.0057501
AHNAK	VDIKAPDVEGQGLDWSLKIPKMKMPKFSMPS	2.153547875	0.0086724
AHNAK	SGSKGDLKSSKASLGSLEGEAEAEASSPKGK	1.57410079	2.29E-05
AHNAK	PKADIDVSGPKVDIDTPDIDIHGPEGKLGKGP	-2.64786859	0.0008281
BRD3	TTTTPTTSAITASRSESPPLSDPKQAKVVAR	2.948331636	7.966E-05
C5AR1	RKSLPSLLRNVLTEESVRESKSFTRSTVDT	2.66674505	0.0002993
CACNA1C	LRTLHDIGPEIRRAISGDLTAEELDKAMKE	3.621025874	6.391E-05
CALD1	DKEKEEEEEKPKRGSIGENQIKDEKIKKDK	3.784544831	0.0001845
CAST	_____MSQPGQKPAASPRPRAAAARRTHEH	-3.86178751	0.0013695
CAV1	_____MSGGKYVDSEGHLYTVP	1.94879169	0.0081726
CAV1	_____MADELSEKQVYDAHTKEIDL	1.63354092	0.0003383
CDK18	_____MNKMKNFKRRFSLVPRTEIEESLAE	2.297244314	0.0012044
CDK18	QNQRFSMEDVSKRLSLPMDIRLPQEFQLKL	2.428522652	0.0066386
cDNA	TPPDFFFPEPTCLSASPPNAPPRQSKRQGR	1.505543215	0.004946
cDNA	RRIGTNLPLKPCARASFETLPNISDLCLRDV	3.421981955	0.0012043
CLASP1	SLRGVTEAIEKFSFRSQEDLNEPIKRDGKKE;SLRGVTEAIEKFSFRSQEDI	2.394451841	0.0078506
CLASP1	GTTTKAEGRIRTRRQSSGSATNVASTPDNRG;PGSYASLGRIRTRRQSS	-2.07183475	0.0006222
COBL	VNKRSNSKGCLTTPNSPSMHSRSLTLGPSLS	-2.54939231	0.0024835
CPEB4	QQEQQDPLEKQQLSPSPGQEAGILPETEKAK	2.000732745	0.0049171
CTNNA1	ELDDSDFETEDFDVRSRTSVQTEDDQLIAGQ;LEDDSDFEQEDYDVRSF	-2.73150382	0.0011938
CTNNA1	DSDFEQEDYDVRSRTSVQTEDDQLIAGQSAR;DSDFETEDFDVRSRTSV	-2.28716236	0.0012315
CTNNA1	FEQEDYDVRSRTSVQTEDDQLIAGQSARAIM;FETEDFDVRSRTSVQTE	-2.44250726	0.0003752
DIP2C	_____MADRSLGEMALPLEVRARLA	1.668328037	0.0071208
DNAJB6	SAAGVQREAAVEQAQSETSLGARGQRGHKPR	-5.07292175	2.999E-05
DPYSL3	RRGQGREESREPAPASPAPAGVEIRSATGKE	-2.12926071	0.0043994
DTX3L	_____MASHLRPPSPLLVRVYKSGPRVRR	2.219650982	0.0085004
DYRK2	IDFGSSCYEHQRVYTYIQSRFYRAPEVILGA	2.116905067	0.00041
EBAG9	FLKRLICRSGRGRKLSGDQITLPTTVDYSSV	1.885982647	0.0005482
FLNC	PYTVAVKYADQEVPRSPFKIKVLPADHASKV	2.307129732	0.0001125
FLNC	TRGETKREVRVEESTQVGGDPFPAVFGDFL	-3.52425721	0.000914
GIGYF1	RSRGRGRGDSCFYQRSIEEGDGAFGRSPREI	1.995042765	0.0002794
GOSR1	CTSYSHSSTRDGRRDSSDTPLLNGSSQDRM	-1.60005739	0.0065201
GPS1	SARVDSHSKSPPREGSQGELTPANSQSRMST	1.903417261	0.004036
HDAC7	LPLAQGGHRPLSRAQSSPAAPASLSAPEPAS	2.040621936	0.0075275
HRC	HHHHHRVPREEDEEVSaelGHQAPSHRQSHQ	-4.52326455	0.0006806
HSPH1	NTCEPVVTQPKPKIESPKLERTPNGPNIDKK	-6.09503773	0.0006071
JUN	DGLLASPDGLLLKLASPELERLIQSNGLVT;SDLLTSPDVGLLKLASPELE	1.723460454	0.0033274
LDB3	LRPTFSPAFSRPSAFSSLAEASDPGPPRASL	-3.6241252	0.0025356
LDB3	PVIPHQKDPALDTNGSLVAPSPSPEARASPG	-3.3438338	0.0038156
LDB3	SSNLQSRFRILAQMTGTEFMQDPDEEALRR	-2.12759936	0.0047944
LIMCH1	RRKKSPREHFQAGPFSPCSPTPPGQSPNRSI	2.050409014	0.0019123
LMO7	TTGVATTQSPTPRSHSPASQSGSQLRNRSV;TTGVATTQSPTPRSHSP	-3.0418378	0.0069079
LRRC10	KVAKGVRVGRWAEETPEPDPKARRYLVR	3.21443751	0.0047642
MAP1A	AGRNTSAEKELSSPISPKSLQSDTPTFSYAA	2.185956476	0.0003688

MAP4	TRPKPARVPPELLGGSPWKTLDHRLGHCSL	2.168495886	0.0047227
MAPK14	LDFGLARHTDDEMTGYVATRWRRAPEIMLNW	-2.93744985	0.0085231
MOT2	SKHSEDVNVKVSNAQSVTSETNI_____	-2.07325563	0.0057389
OBSCN	TDTVSYVFRNMMKLSSIDLNDQVEGDDRAFE	3.291823972	0.0053965
PALLD	ESKNTDFFPGLSAFLSQEEINKSLDLARRAI	-2.41001281	0.0078956
PCDH7	SQPKLSTFMPVDERGSQEKLANGEAAIMGDR	-1.96821492	0.0058484
PDLIM2	RSSYSSPTLSPRAGSPFPPSSSSLTGEA	2.577056208	0.0069223
PEAK1	NAYDNLAIYKSFLGTSGELSVKEKTTSVISH	2.390188529	3.9E-06
PGRMC1	LYKIVRGDQPAASGSDDDDEPPPLPRLKRRD	-2.03103445	0.0010997
PKP2	PVTQNRASRSSHQSSFHSTRTLREAGPSVA	2.994297674	0.0076825
PKP2	TATYEGRWGRGTAQYSSQKSVEERSLRHPLR	-3.93606777	3.375E-05
PKP2	ATYEGRWGRGTAQYSSQKSVEERSLRHPLRR	-3.44831711	0.002791
PKP2	VEERSLRHPLRRLEISPDSSPERAHYTHSDY	-2.08331617	0.0079287
PKP2	YQLEAELPEKYSQNIYIQNRNIQTDNNSIG	-3.18370999	0.0010427
PLEKHF1	AAQQRQEEAEEQGAGSPGQPAHLARPICGAS	2.123755999	0.0088387
PLN	MEKVQYLTRSAIRRASTIEMPQQARQKLQNL	-3.46551782	7.654E-06
PLN	EKVQYLTRSAIRRASTIEMPQQARQKLQNLF	-3.52910591	0.0035961
PROB1	RAAGAPRPRLLLRTGSLDESGLPLQAAAGFV	-3.82485758	0.009781
PTPN21	ANSTPDLRHLIYSSSNPDLITRRVHHSVQT	2.148004156	0.008291
RBM20	QMSSPKPAERARQSPFVDDCKTRGTPEDG	2.621305531	5.229E-05
RBM25	HRPKIGLSLKLKASNSPGQNSVKRKKLPVD	-3.66651252	0.0019576
RBM39	SRRRSRSKSPFRKDKSPVREPIDNLTPEERD	5.695442054	0.0003854
SHRM3	SSEPEREPEWRDRPGSPESPLLDAPFSRAYR	3.248687505	2.085E-07
SKIV2L	TVSASPCSAPLARASSLEDLVLKEASTAVST	2.306059859	0.0005897
SLC25A46	RDEQGFGGAFPARSFSTGSDLGHWVTTPPDI	3.579270124	0.006923
SLTM	SEASKPKDGQDAIAQSPEKESKDYEMNANHK	-1.64159549	0.0072128
SORBS1	ASGSFAPISQTPPSFSPPPPLVPPAPEDLRR	1.722244942	0.0090703
SORBS3	_____MADGGSPFLGRRDFVYPSSTR	2.237728096	0.0026207
SPTAN1	VATFNSIKELNERWRSLQQLAEERSQLLGSA	2.166070767	0.0081811
SPTBN1	KGEQVSQNGLPAEQGSPRMAETVDTSEMVNG	-1.57419682	0.0060635
SRRM1	PSPPRRRRSPSPRRYSPPIQRRYSPSPPKR	3.611219376	0.0013217
SYNPO2	SPIADFPAPPYSAVTPPPDAFSRGVSSPIA	2.53823614	0.0074763
TJAP1	PQPNGECHSLGTARGSPPEELPLPAFEKLN	2.312887084	0.0080029
TJP1	RSPDQRSEPSDHSRHSPPQPSNGSLRSRDEE	-1.80567004	0.009641
TLR3	KIQALKSEELDIFANSSLKKLELSSNIKEF	-2.01196571	0.0014027
TNS1	PLRRRAASDGQYENQSPEATSPRSPGVRSPV	2.042624773	9.696E-07
TNS1	SPQARHRTVGTNTPPSPGFRRAINSSMAAP	6.133154098	0.0032638
TPM2	KAISEELDNALNDITSL_____	3.769615665	0.0006977
TTN	TPSPIEAERRKLRPGSGGKPPDEAPFTYQL	1.996450752	0.0071223
TTN	KAQLARQQSPSPIRHSPSPVRHVRAPTSPV	-4.16266032	0.0080773
TTN	QLPHKTPPRIPPKRSPTPPSIAAKAQLA	-11.864028	0.0004072
TTN	KTPPRIPPKRSPTPPSIAAKAQLARQQS	-1.61577152	0.0029269
TXLNA	GPERRPEGPGAQAPSSPRVTEAPCYPGAPST	-2.98204452	0.0082844
WDR44	TFKETENTAYKVGNESPVQELKQDVSKKIIIE	2.203541486	0.0046304
YAP1	VRAHSSPASLQLGAVSPGTLTPTGVVSGPAA	1.991670092	0.0076527
ZYX	QHPVPPPAQNQNQVRSPGAPGPLTLKEVEEL	2.350837417	0.0041595
	YKTAPGKIEKVKPPSPPTTEGPSLQPDLAPE	1.779699986	0.0021601