

Supplemental Figures and Tables

Transcriptomic analysis of fumarate compounds identifies unique effects of isosorbide di-(methyl fumarate) on NRF2, NF-kappaB and IRF1 pathway genes

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Supplemental figure legends

Figure S1. Differential expression analyses. (A-C) P-value distributions. Plots show the raw p-value distribution among all genes for each differential expression analysis. The number of DEGs identified is shown (top margin; $P < 0.05$ with $FC > 1.25$ or $FC < 0.80$). (D-F) QQ plots for moderated T statistics. Deviation of sample quantiles (black points) from a straight line (null) reflects more differential expression among genes tested. (G) P-value empirical cumulative distribution functions (CDFs). CDF curves are shown for each comparison (to the CTL treatment). Deviation from a straight line indicates a non-uniform p-value distribution. (H-J) Number of DEGs identified at varying FC thresholds ($P < 0.05$; yellow arrow: $FC > 1.25$ or $FC < 0.80$). (K-M) Volcano plots. The $-\log_{10}$ -transformed p-value (vertical axis) is plotted with respect to the estimated FC (horizontal axis). (N-P) MA plots. The FC (vertical axis) is plotted against average expression (horizontal axis) for each gene. The solid green line is the LOESS curve fit. In (K) - (P), red and blue symbols correspond to genes significantly increased or decreased, respectively ($P < 0.05$, $FC > 1.25$ or $FC < 0.80$).

Figure S2. Motifs enriched in 5 kb sequences upstream of DEGs. (A) Z statistic interpretation. Z statistics were calculated using semiparametric generalized additive logistic models. Positive Z statistics indicate a relative increase in the frequency of a binding site in DEG upstream sequences (as compared to all non-DEGs). Negative Z statistics indicate a relative decrease in the frequency of a binding site in DEG upstream sequences (as compared to all non-DEGs). (B - G) Top motifs enriched in DEG upstream sequences. The primary and reverse complement sequence logos are shown for each motif along with the enrichment Z statistic (* $P < 0.05$; **FDR < 0.05).

Figure S3. NF- κ B motif enrichment. (A) NF- κ B motif sequence logos. (B, C) NF- κ B motif enrichment. The Z statistic (vertical axis) quantifies enrichment of each motif in 5 kb upstream regions (positive value: motif enrichment; negative value: motif depletion; black asterisk: $P < 0.05$; red asterisk: FDR < 0.05). (D) NF- κ B subunits. NF- κ B signaling occurs through both canonical and non-canonical pathways. The canonical pathway is activated by stimuli such as TNF- α and IL-1 and leads to formation of p50/p65 dimers. The non-canonical pathway is triggered by stimuli such as lymphotoxin beta (LT- β) and B-cell activating factor (BAFF) to promote p52/RELB dimer formation. (E - I) NF- κ B subunit gene expression. Average expression (\log_2 scale) is shown for each treatment (± 1 standard error; * $P < 0.05$, comparison to CTL treatment). Expression is normalized to the average value in the CTL treatment for each gene.

Figure S4. Niacin-HCAR2 pathway genes. (A) *HCAR2*. (B) *PTGDS*. (C) *SREBF1*. (D) *ABCA1*. In (A) - (D), average expression (\log_2 scale) is shown for each treatment (± 1 standard error; * $P < 0.05$, comparison to CTL treatment). Expression is normalized to the average value in the CTL treatment for each gene. (E) Niacin-activated genes. (F) Niacin-suppressed genes. In (E) and (F), the value of $|FC|_{\max}$ was calculated for each gene, where $|FC|_{\max}$ is defined as $\max[\text{abs}(FC_{\text{MMF}}, FC_{\text{DRF}}, FC_{\text{IDMF}})]$, and the 23 niacin-activated or niacin-suppressed genes with highest value of $|FC|_{\max}$ are shown. Non-black gene labels are used if there is significant differential expression ($P < 0.05$) for any of the three comparisons, in which case the label color matches the comparison associated with the lowest differential expression p-value. (G, H, K, L,

O, P) FC estimates for niacin-activated genes. FC estimates are plotted and the proportion of fumarate-increased (red) fumarate-decreased (blue) genes is shown (P-value: Fisher's exact test). The percentage of increased/decreased genes is also indicated (see legend). (I, J, M, N, Q, R) The cumulative overlap is shown between niacin-activated genes and genes ranked based upon their response to each fumarate compound. A positive area statistic denotes enrichment among fumarate-increased genes, and a negative area statistic indicates enrichment among fumarate-decreased genes (P-value: Wilcoxon rank sum test).

Figure S5. Interferon regulatory factor (IRF) motif enrichment. (A) IRF motif sequence logos. (B, C) IRF motif enrichment. The Z statistic (vertical axis) quantifies enrichment of each motif in 5 kb upstream regions (positive value: motif enrichment; negative value: motif depletion; black asterisk: $P < 0.05$; red asterisk: $FDR < 0.05$). (D-F, H-J) IRF factor gene expression. Average expression (\log_2 scale) is shown for each treatment (± 1 standard error; * $P < 0.05$, comparison to CTL treatment). Expression is normalized to the average value in the CTL treatment for each gene. (G) IRF1 predicted targets (motif #1 in part A). (K) IRF1 binding sites in regions upstream of IDMF-decreased genes. Motif sequence matches are shown at varying degrees of stringency (60-90%, see legend). The FC (IDMF/CTL) and differential expression p-value are shown (right margin).

Figure S6. Genes associated with A1/A2 reactive astrocyte polarization. (A) *C3*. (B) *GBP2*. (C) *S100A10*. (D) *TGFB1*. In (A) - (D), average expression (\log_2 scale) is shown for each treatment (± 1 standard error; * $P < 0.05$, comparison to CTL treatment). Expression is normalized to the average value in the CTL treatment for each gene. (E, H, K) Median expression of genes associated with the A1 phenotype ($n = 161$ genes), A2 phenotype ($n = 75$), and pan-reactive astrogliosis (A1 + A2) ($n = 127$). Boxes outline FC estimates for the middle 50% of genes (middle line: median) and whiskers span the 10th to 90th percentiles. (F, G, I, J, L, M) Genes associated with A1 and A2 phenotypes. Figures show marker genes most strongly altered by (F, G) MMF, (I, J) DRF, or (L, M) IDMF. Genes shown in red and blue font are significantly up- and down-regulated by (F, G) MMF, (I, J) DRF, or (L, M) IDMF, respectively. (N, O, P) Gene ontology (GO) biological process (BP), molecular function (MF), and cell component (CC) terms associated with IDMF-decreased A1 astrocyte marker genes ($P < 0.05$). Enrichment is shown on the horizontal axis ($-\log_{10}(p\text{-value})$, conditional Fisher's Exact Test) and the number of genes associated with each term is given in parentheses (left margin). The single gene associated with each term and most strongly down-regulated by IDMF is listed within each figure.

Figure S7. Genes altered in MS patient astrocytes (GSE83670) and their overlap with DEGs. (A, E, I) Fold-change scatterplots. Plots compare FC estimates from the current analysis (horizontal axis) with those from MS astrocytes (vertical axis). Each point represents an individual gene. The proportion of genes within each quadrant is indicated in the top margin (red font: $P < 0.05$, Fisher's Exact Test). The yellow ellipse outlines the middle 90% of genes closest to the bivariate mean. (B, C, F, G, J, K) Venn diagrams. Diagrams show the overlap between genes altered by MMF, DRF or IDMF and those altered in astrocytes from MS patients ($P < 0.05$, $FC > 1.25$ or $FC < 0.80$). (D, H, L) GSEA analysis. Genes were ranked based upon expression change in MS astrocytes (horizontal axis) and cumulative overlap is shown (vertical axis) with respect to the top 100 genes increased (red) or decreased (blue) by each compound.

The area between each cumulative overlap curve and the diagonal is indicated (Area > 0: enrichment among MS-increased genes; Area < 0: enrichment among MS-decreased genes; p-value: two-sample Mann Whitney U test). (M, N) Genes altered in the same direction by IDMF ($P < 0.05$) and in astrocytes from MS patients ($P < 0.15$). (O, P) GO BP terms enriched among genes (O) increased by IDMF and in MS astrocytes or (P) decreased by IDMF and in MS astrocytes. The number of genes associated with each term is given in parentheses (left margin) and example genes for each term are listed within each figure.

Figure S8. *In vitro* kinetics of IDMF hydrolysis by carboxylesterase-2. (A) High-performance liquid chromatography (HPLC) chromatograms. Overlaid chromatograms are shown for IDMF and the metabolites MMF and IMMF. (B - D) Calibration curves. Calibration curves are shown for IDMF and its MMF and IMMF derivatives. The least-squares regression line is shown (dotted line) with associated R^2 value (top-left) and estimated regression equation (top margin). (E) IDMF degradation and product accumulation during hydrolysis. Estimated concentrations for each compound following hydrolysis are shown over two hours.

Figure S9. Microarray quality control. (A – L) Microarray pseudoimages. Darker colors correspond to regions of increased hybridization. (M) 260/280 absorbance ratios. (N) Eukaryotic hybridization controls. Controls were spiked into the hybridization cocktail at different relative concentrations (cre > BioD > BioC > BioB). The average expression of control probes is shown for each array. (O) Labeling controls. Poly-A RNA control probes target *B. subtilis* genes absent in eukaryotic samples, which were spiked into the RNA sample at varying concentrations during sample preparation (dap > thr > phe > lys). (P) Positive vs. negative AUC. Area under the curve (AUC) values were calculated from receiver operator curves (ROC), which were generated by evaluating how well probe set signals separate exons (positive control) from introns (negative control). A value of 1.00 is consistent with complete separation between exon- and intron-derived signals, whereas a value of 0.50 suggests overlap between these two probe set groups. (Q) Probe-level model (PLM) residuals. Boxplots outline the middle 50% of residual values for each array (whiskers: 10th to 90th percentiles). (R) Normalized unscaled standard error (NUSE) median. (S) NUSE interquartile range (IQR). (T) Relative log expression (RLE) median. (U) RLE IQR. (V) Hierarchical cluster analysis. Samples were clustered based upon the Euclidean distance with groups joined by average linkage. (W) Principal component (PC) analysis. Samples are plotted with respect to the first two PC axes. The percentage of variation accounted for by each PC axis is indicated in axis labels. (X) PC axis 1 standard score (Z-score). The p-value obtained from the univariate maximum normalized residual test for outliers is shown (i.e., Grubb's test).

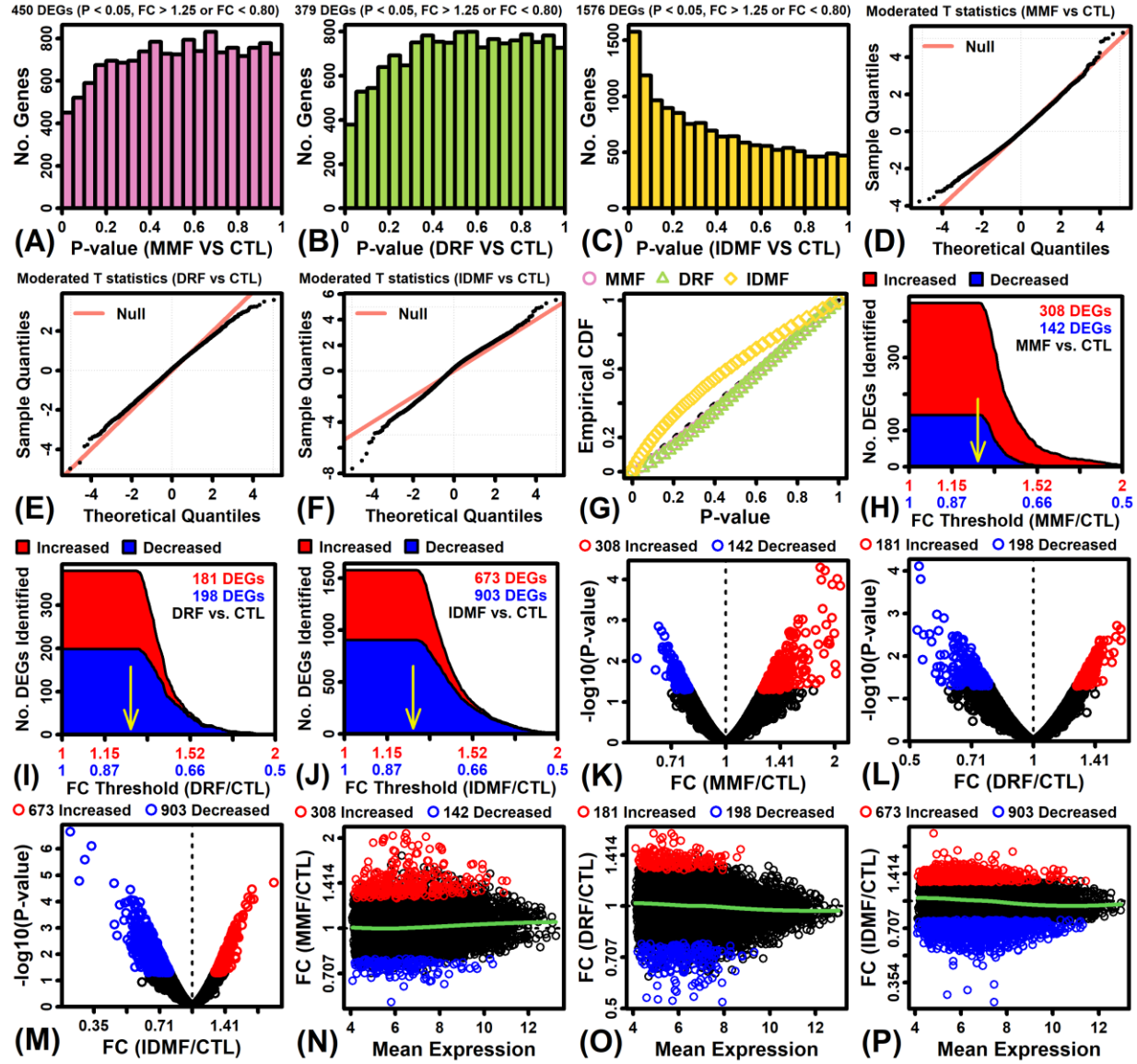


Figure S1. Differential expression analyses.

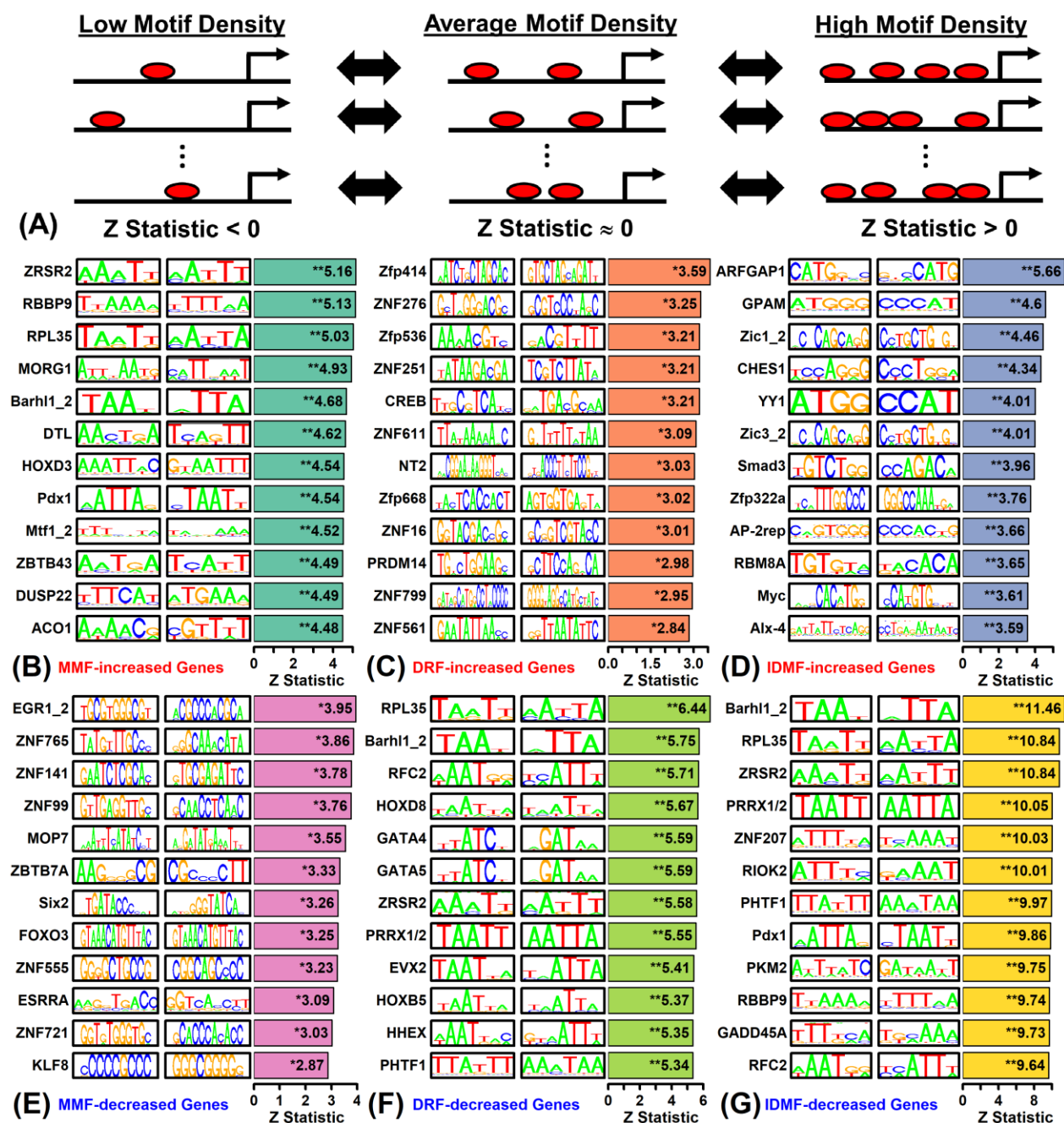


Figure S2. Motifs enriched in 5 kb sequences upstream of DEGs.

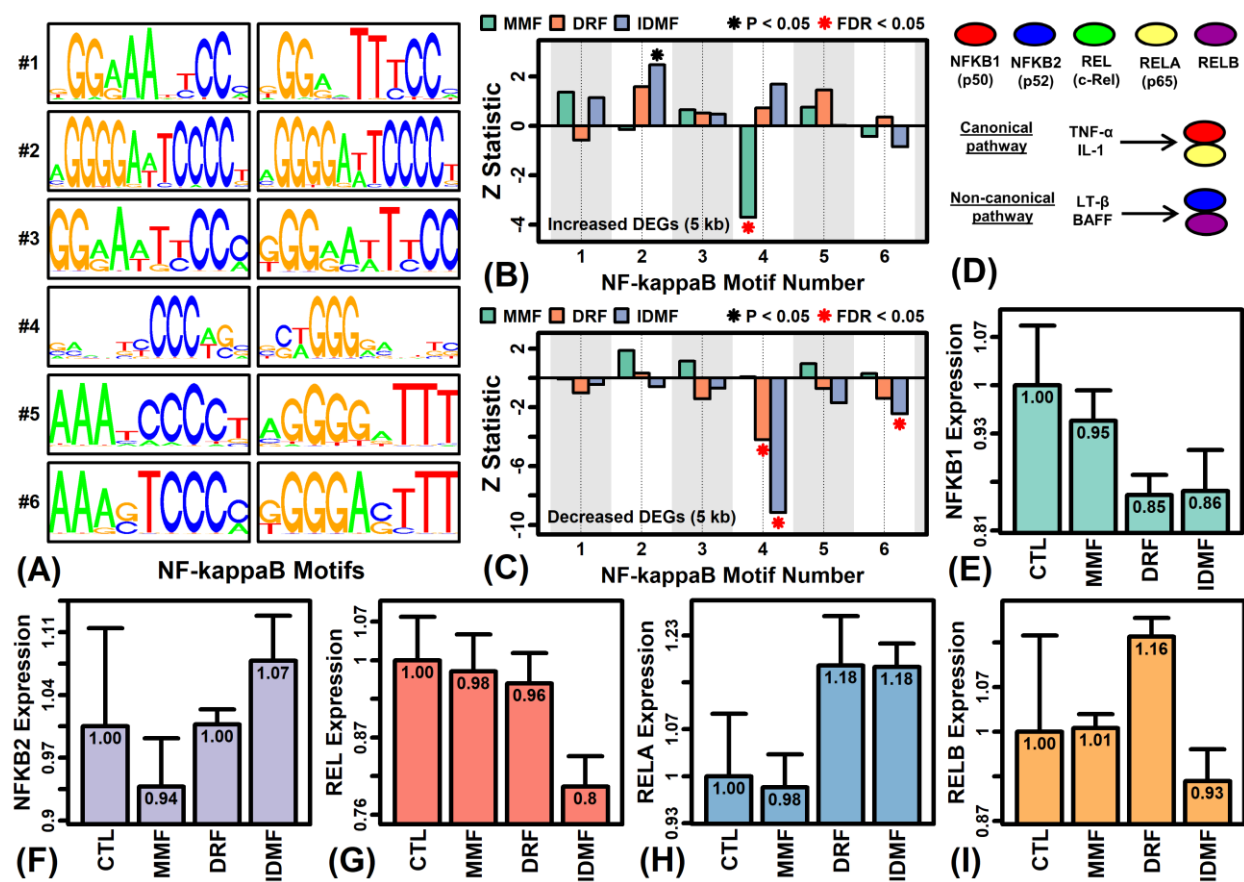


Figure S3. NF- κ B motif enrichment.

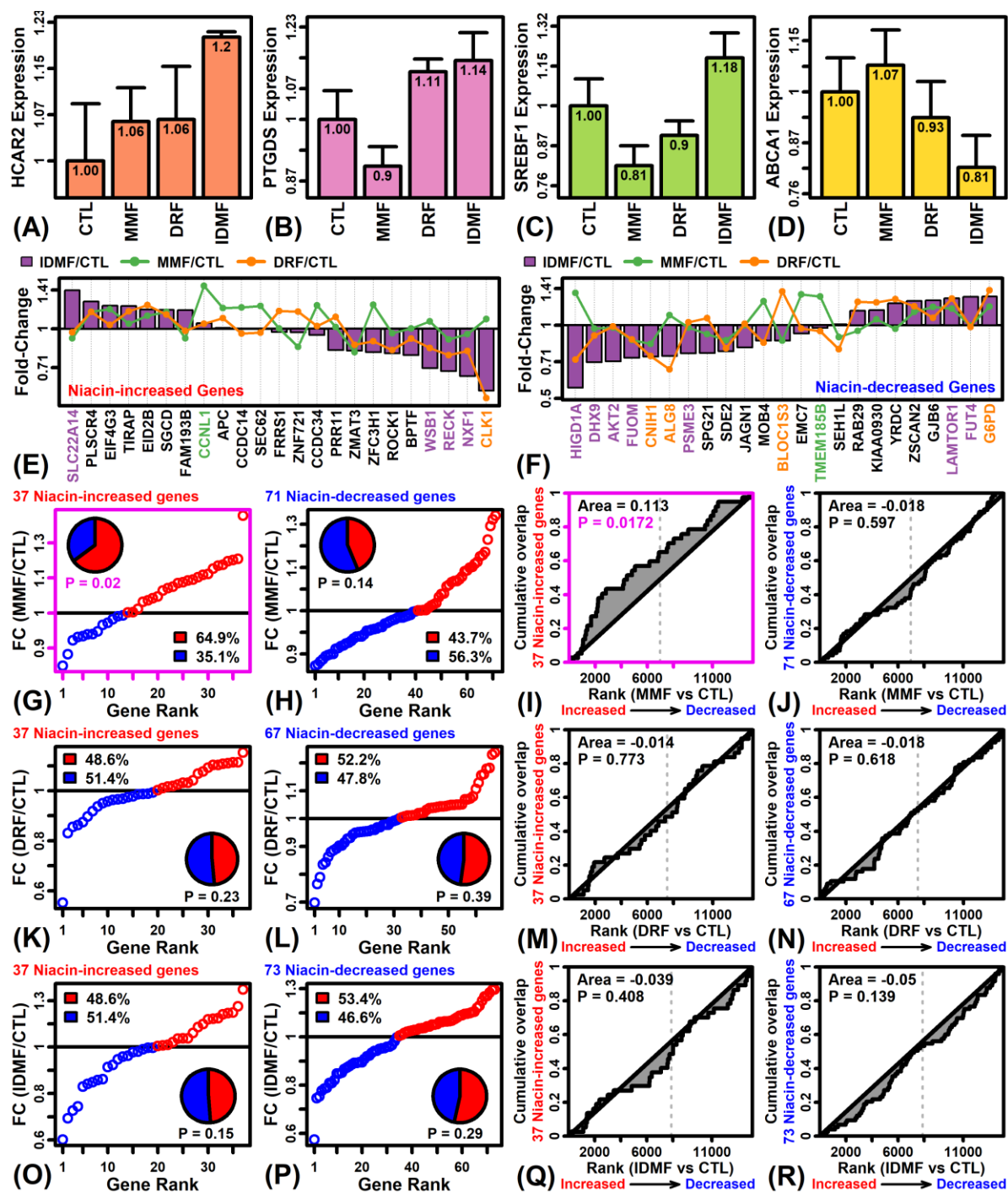


Figure S4. Niacin-HCAR2 pathway genes.

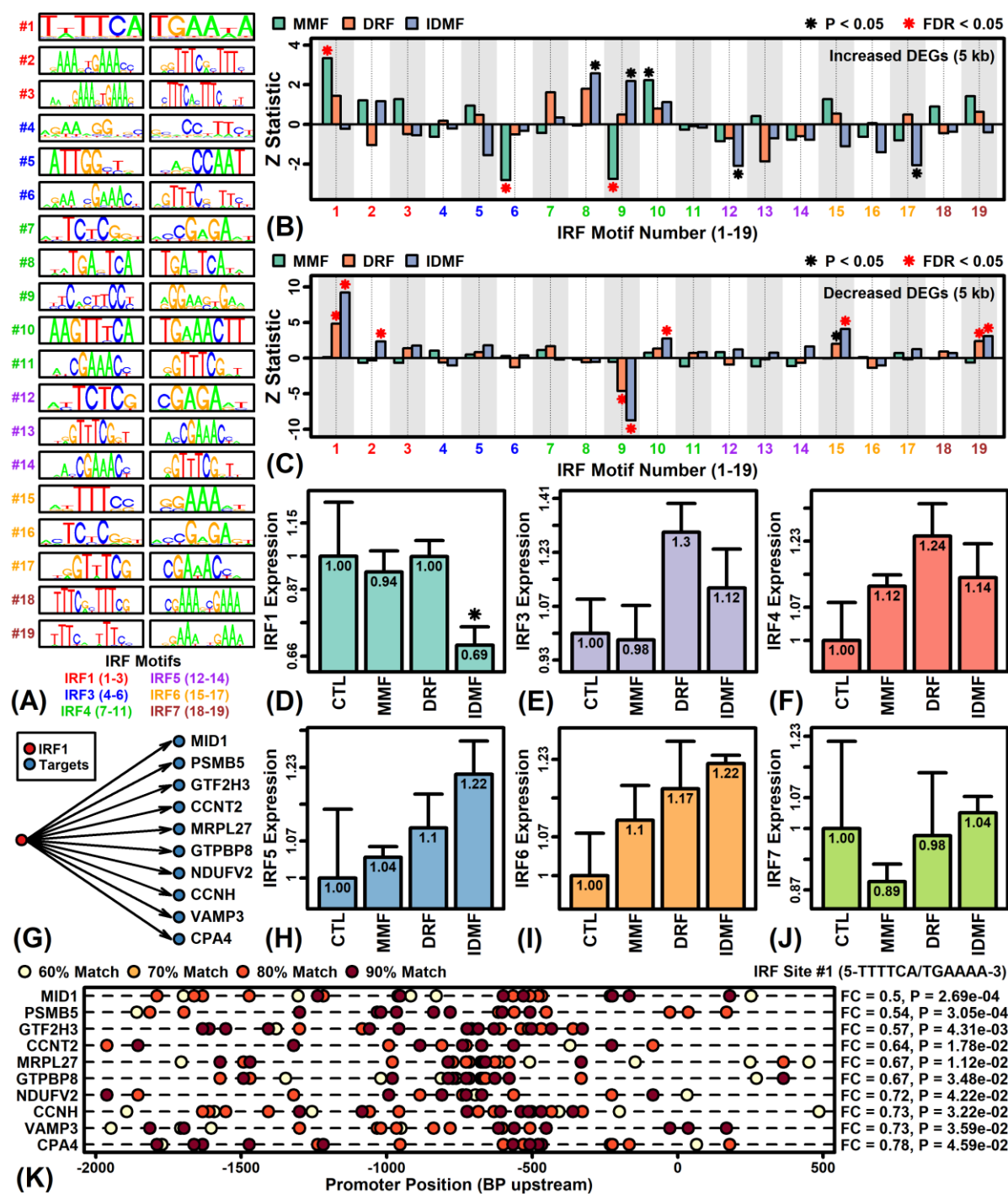


Figure S5. Interferon regulatory factor (IRF) motif enrichment.

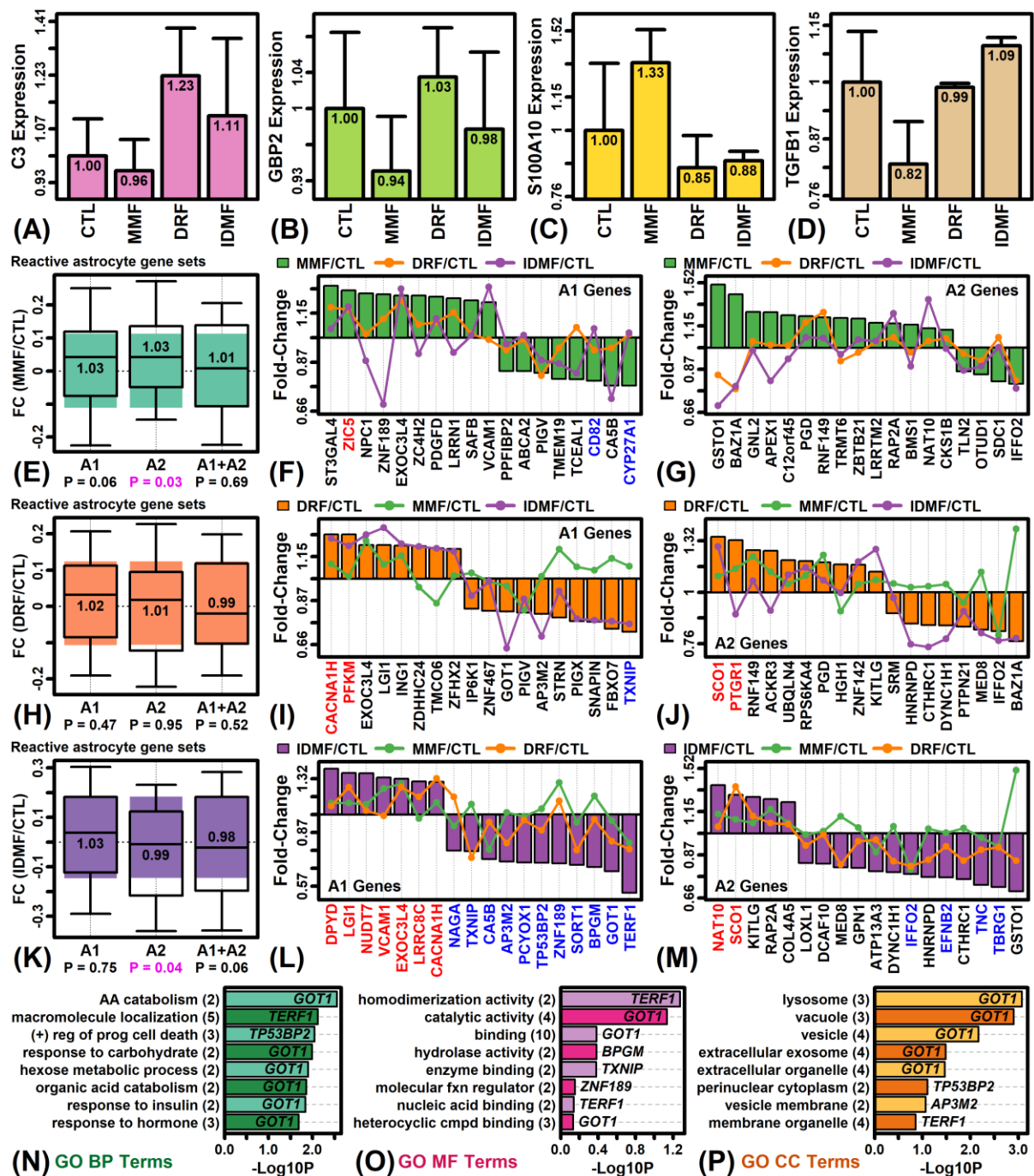


Figure S6. Genes associated with A1/A2 reactive astrocyte polarization.

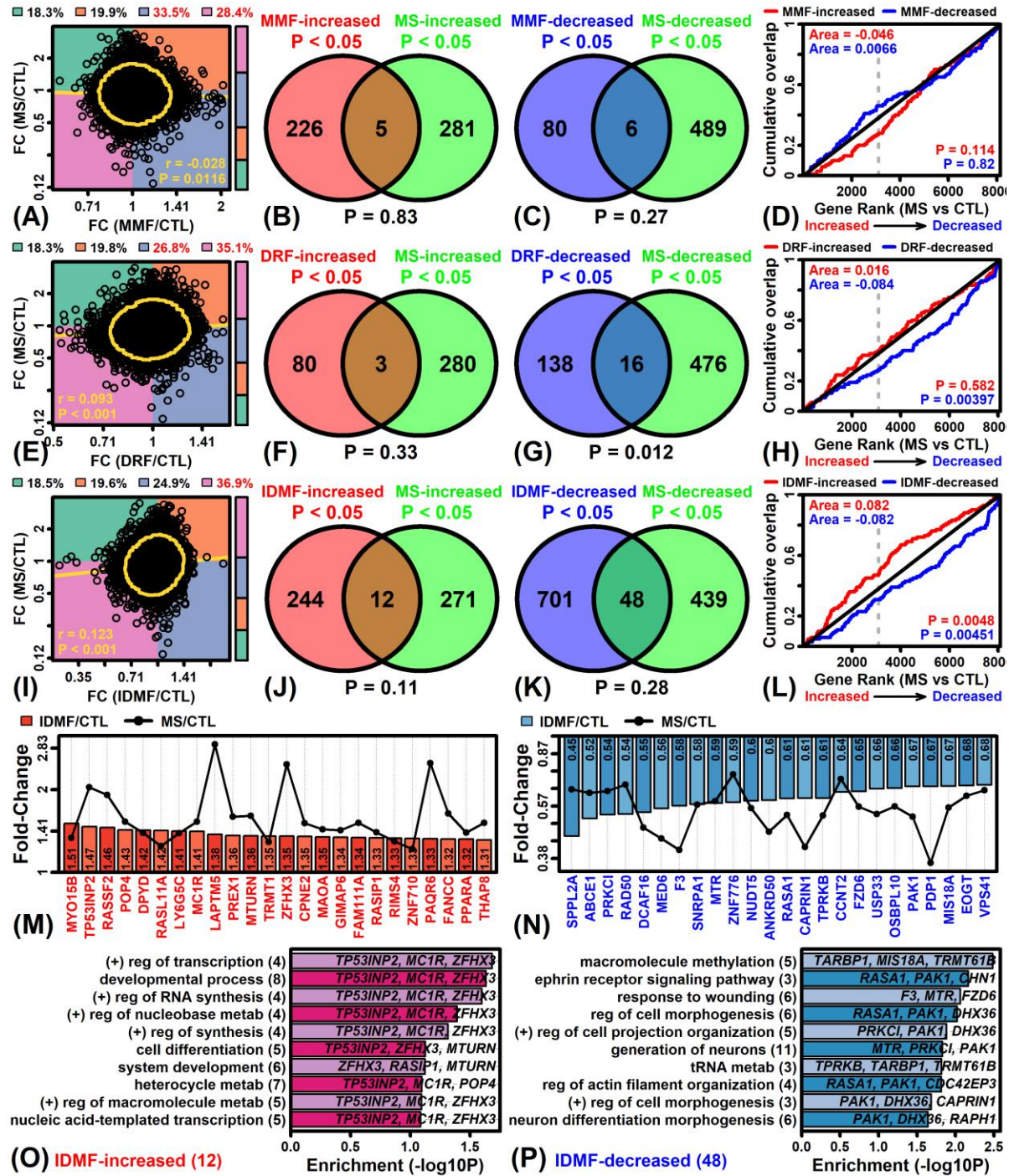


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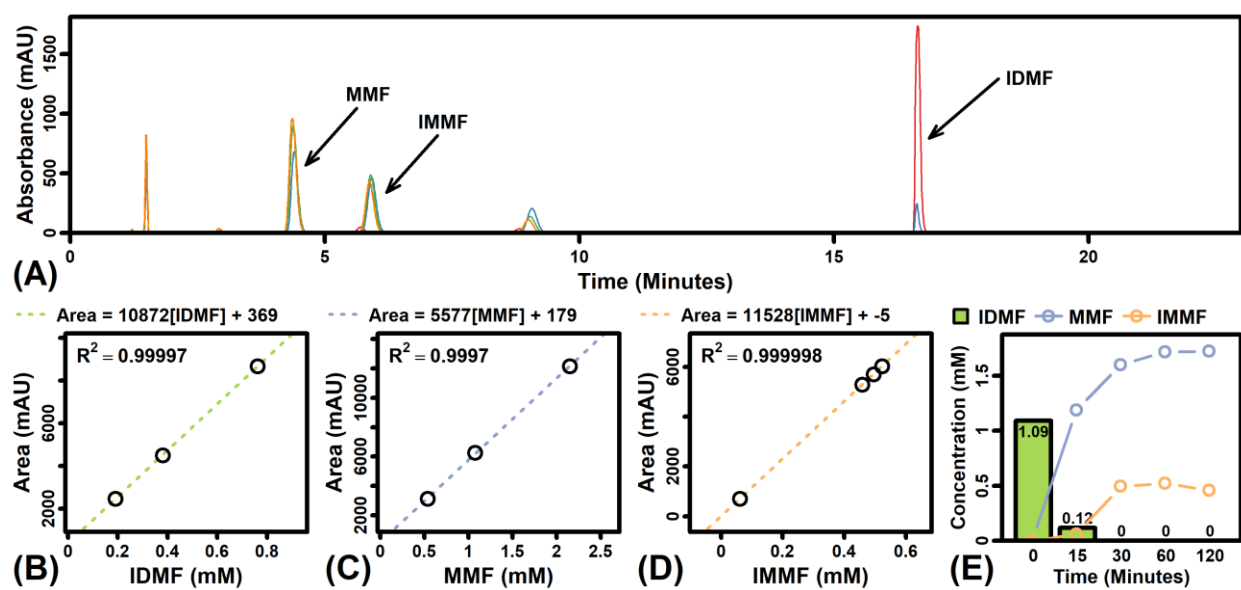


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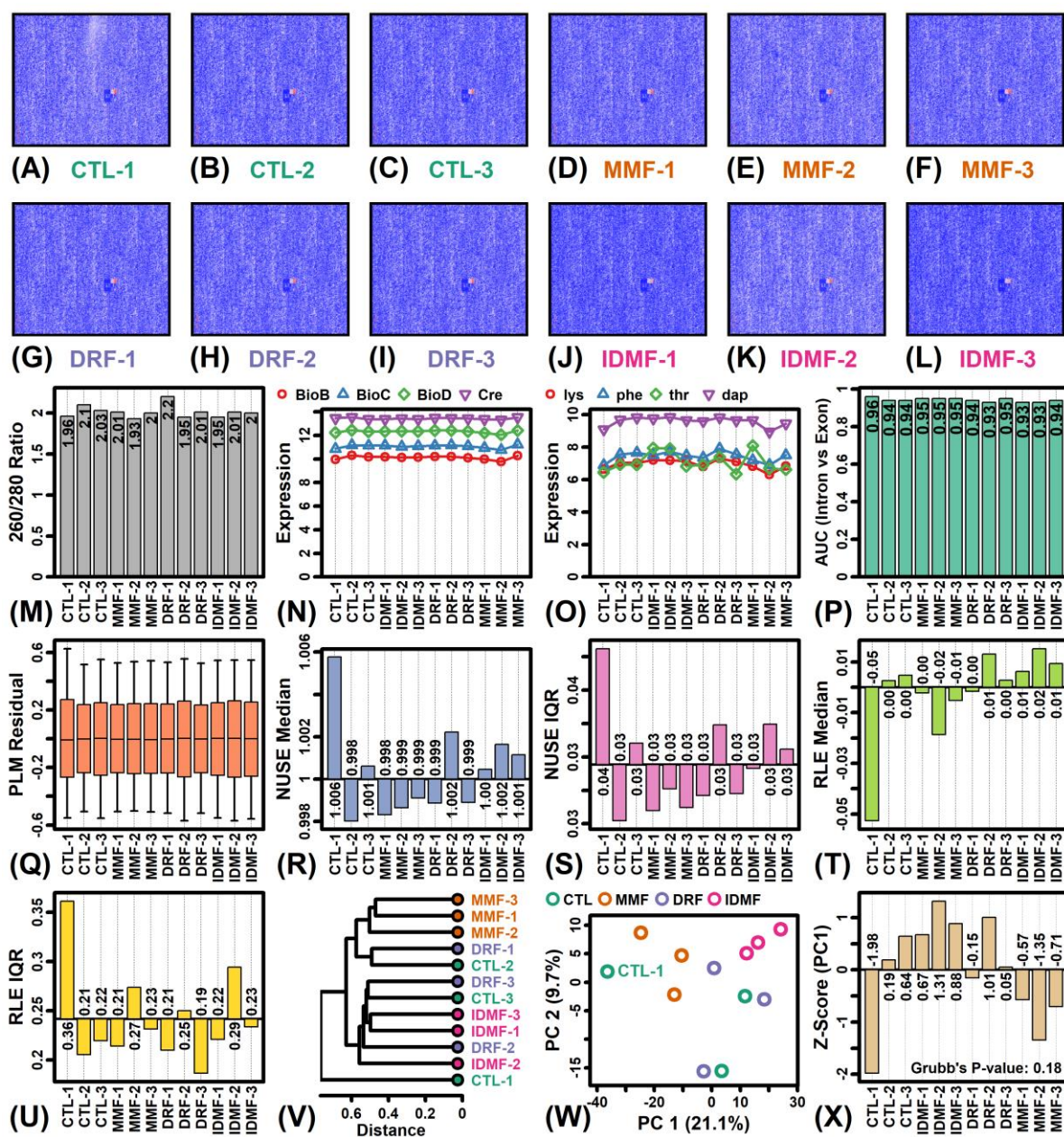


Figure S9. Microarray quality control.

Table S1. MMF-increased genes ($P < 0.05$ with $FC > 1.25$). The table lists 308 MMF-increased genes ranked by estimated fold-change (FC) (MMF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group).

Symbol	Description	FC	P-value
<i>BSCL2</i>	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	2.07	0.000143
<i>C1orf54</i>	chromosome 1 open reading frame 54	2.03	0.0000967
<i>PSMA3</i>	proteasome subunit alpha 3	2.02	0.0204
<i>COA5</i>	cytochrome c oxidase assembly factor 5	2.01	0.0123
<i>PROSER1</i>	proline and serine rich 1	2.00	0.00211
<i>NEFM</i>	neurofilament, medium polypeptide	1.97	0.000135
<i>LSAMP</i>	limbic system-associated membrane protein	1.97	0.000873
<i>PARN</i>	poly(A)-specific ribonuclease	1.94	0.00384
<i>UPF3B</i>	UPF3 regulator of nonsense transcripts homolog B (yeast)	1.93	0.00309
<i>NTPCR</i>	nucleoside-triphosphatase, cancer-related	1.91	0.00363
<i>ZNF106</i>	zinc finger protein 106	1.90	0.0013
<i>SCPEP1</i>	serine carboxypeptidase 1	1.88	0.0000603
<i>CNIH4</i>	cornichon family AMPA receptor auxiliary protein 4	1.87	0.00665
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	1.85	0.000523
<i>ATF3</i>	activating transcription factor 3	1.84	0.000103
<i>NFATC2</i>	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1.83	0.0000509
<i>HADH</i>	hydroxyacyl-CoA dehydrogenase	1.82	0.0291
<i>LPCAT3</i>	lysophosphatidylcholine acyltransferase 3	1.80	0.00394
<i>CD47</i>	CD47 molecule	1.78	0.035
<i>SRPRB</i>	signal recognition particle receptor, B subunit	1.77	0.00173
<i>EEF1D</i>	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange	1.72	0.0275
<i>NDUFAF5</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	1.69	0.0092
<i>RRAGC</i>	Ras-related GTP binding C	1.68	0.0354
<i>MED31</i>	mediator complex subunit 31	1.68	0.00612
<i>VWA8</i>	von Willebrand factor A domain containing 8	1.67	0.017
<i>VPS18</i>	VPS18 CORVET/HOPS core subunit	1.66	0.00201
<i>PLAA</i>	phospholipase A2-activating protein	1.66	0.0234
<i>PHLDB1</i>	pleckstrin homology-like domain, family B, member 1	1.65	0.00822
<i>PIK3C3</i>	phosphatidylinositol 3-kinase, catalytic subunit type 3	1.65	0.016
<i>RBMS1</i>	RNA binding motif, single stranded interacting protein 1	1.64	0.00499
<i>LAMTOR5</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5	1.64	0.0185
<i>CENPP</i>	centromere protein P	1.63	0.00096
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	1.63	0.00846
<i>MRPS16</i>	mitochondrial ribosomal protein S16	1.63	0.00893
<i>TTLL7</i>	tubulin tyrosine ligase-like family member 7	1.62	0.0129
<i>PIN4</i>	peptidylprolyl cis/trans isomerase, NIMA-interacting 4	1.62	0.00668
<i>SRSF7</i>	serine/arginine-rich splicing factor 7	1.60	0.0373
<i>ZNF385D</i>	zinc finger protein 385D	1.59	0.000949
<i>DCAF17</i>	DDB1 and CUL4 associated factor 17	1.58	0.00125
<i>EIF4A3</i>	eukaryotic translation initiation factor 4A3	1.58	0.0193
<i>RPS13</i>	ribosomal protein S13	1.58	0.0307
<i>ZC3H12C</i>	zinc finger CCCH-type containing 12C	1.57	0.00215
<i>SLC50A1</i>	solute carrier family 50 (sugar efflux transporter), member 1	1.55	0.00534
<i>AHSA1</i>	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	1.55	0.0365
<i>TEN1</i>	TEN1 CST complex subunit	1.55	0.00264
<i>KLHL15</i>	kelch-like family member 15	1.54	0.00228
<i>NCAM1</i>	neural cell adhesion molecule 1	1.54	0.00441
<i>ALG5</i>	ALG5, dolichyl-phosphate beta-glucosyltransferase	1.54	0.0217
<i>NDUFA5</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1.53	0.00837
<i>MRPL3</i>	mitochondrial ribosomal protein L3	1.53	0.0156
<i>RRAD</i>	Ras-related associated with diabetes	1.53	0.00202
<i>DEPDC1</i>	DEP domain containing 1	1.52	0.00215
<i>SMDT1</i>	single-pass membrane protein with aspartate-rich tail 1	1.52	0.00901
<i>SDF2</i>	stromal cell-derived factor 2	1.52	0.0188
<i>NR4A2</i>	nuclear receptor subfamily 4, group A, member 2	1.51	0.00759

<i>BAIAP2</i>	BAI1-associated protein 2	1.51	0.013
<i>SLC1A3</i>	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.51	0.0019
<i>ERP29</i>	endoplasmic reticulum protein 29	1.51	0.00239
<i>PSMD9</i>	proteasome 26S subunit, non-ATPase 9	1.51	0.0148
<i>SOX5</i>	SRY box 5	1.51	0.00191
<i>THEM4</i>	thioesterase superfamily member 4	1.51	0.0181
<i>LARP7</i>	La ribonucleoprotein domain family, member 7	1.51	0.0356
<i>NQO1</i>	NAD(P)H dehydrogenase, quinone 1	1.51	0.00473
<i>ANKRD28</i>	ankyrin repeat domain 28	1.50	0.0208
<i>RSPH3</i>	radial spoke 3 homolog (Chlamydomonas)	1.50	0.00968
<i>STRADB</i>	STE20-related kinase adaptor beta	1.50	0.0278
<i>CERS2</i>	ceramide synthase 2	1.50	0.0164
<i>CLEC2D</i>	C-type lectin domain family 2, member D	1.50	0.00198
<i>MED15</i>	mediator complex subunit 15	1.49	0.0408
<i>TLCD1</i>	TLC domain containing 1	1.49	0.00956
<i>MRPL14</i>	mitochondrial ribosomal protein L14	1.48	0.0233
<i>PSMB5</i>	proteasome subunit beta 5	1.48	0.025
<i>SNRPE</i>	small nuclear ribonucleoprotein polypeptide E	1.48	0.0444
<i>MAP4K5</i>	mitogen-activated protein kinase kinase kinase 5	1.48	0.0197
<i>NFIA</i>	nuclear factor I/A	1.47	0.00413
<i>ERI3</i>	ERI1 exoribonuclease family member 3	1.47	0.0118
<i>CTPS2</i>	CTP synthase 2	1.47	0.00692
<i>PPP6C</i>	protein phosphatase 6, catalytic subunit	1.47	0.0383
<i>PPP3CC</i>	protein phosphatase 3, catalytic subunit, gamma isozyme	1.47	0.00471
<i>CCNL1</i>	cyclin L1	1.47	0.0207
<i>TRAPPC2</i>	trafficking protein particle complex 2	1.47	0.0103
<i>MTIF2</i>	mitochondrial translational initiation factor 2	1.47	0.0113
<i>MRPL33</i>	mitochondrial ribosomal protein L33	1.47	0.0187
<i>AFF2</i>	AF4/FMR2 family, member 2	1.46	0.00892
<i>CYB5A</i>	cytochrome b5 type A (microsomal)	1.46	0.0189
<i>ZSWIM7</i>	zinc finger, SWIM-type containing 7	1.46	0.0389
<i>ZNF280B</i>	zinc finger protein 280B	1.46	0.0175
<i>SCML1</i>	sex comb on midleg-like 1 (Drosophila)	1.46	0.0144
<i>FAM200B</i>	family with sequence similarity 200, member B	1.46	0.0152
<i>ABCD3</i>	ATP binding cassette subfamily D member 3	1.45	0.0155
<i>PLPP1</i>	phospholipid phosphatase 1	1.45	0.00896
<i>TIGD5</i>	tigger transposable element derived 5	1.45	0.0204
<i>PRPF40A</i>	PRP40 pre-mRNA processing factor 40 homolog A	1.45	0.0305
<i>VPS33A</i>	vacuolar protein sorting 33 homolog A (S. cerevisiae)	1.45	0.00916
<i>TMEM126A</i>	transmembrane protein 126A	1.45	0.0364
<i>LUM</i>	lumican	1.45	0.0349
<i>OSGEP</i>	O-sialoglycoprotein endopeptidase	1.44	0.0175
<i>SNRPF</i>	small nuclear ribonucleoprotein polypeptide F	1.44	0.0251
<i>NDUFA4</i>	NDUFA4, mitochondrial complex associated	1.44	0.0295
<i>SETDB1</i>	SET domain, bifurcated 1	1.44	0.0215
<i>SOD1</i>	superoxide dismutase 1, soluble	1.44	0.0188
<i>SDHA</i>	succinate dehydrogenase complex subunit A, flavoprotein (Fp)	1.43	0.023
<i>MOXD1</i>	monooxygenase, DBH-like 1	1.43	0.00694
<i>ZCCHC7</i>	zinc finger, CCHC domain containing 7	1.43	0.0104
<i>KLHL2</i>	kelch-like family member 2	1.43	0.0168
<i>ANKHD1</i>	ankyrin repeat and KH domain containing 1	1.43	0.0213
<i>IGFBP7</i>	insulin like growth factor binding protein 7	1.42	0.0248
<i>TMED5</i>	transmembrane p24 trafficking protein 5	1.42	0.00845
<i>PPP1CC</i>	protein phosphatase 1, catalytic subunit, gamma isozyme	1.42	0.0217
<i>ORC5</i>	origin recognition complex subunit 5	1.42	0.0145
<i>MTHFS</i>	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	1.42	0.0266
<i>FBXW2</i>	F-box and WD repeat domain containing 2	1.42	0.00852
<i>ITPA</i>	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	1.42	0.0257
<i>TFPI</i>	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	1.42	0.0102

<i>SLC3A2</i>	solute carrier family 3 (amino acid transporter heavy chain), member 2	1.41	0.0112
<i>LATS1</i>	large tumor suppressor kinase 1	1.41	0.0335
<i>EPB41L5</i>	erythrocyte membrane protein band 4.1 like 5	1.41	0.00772
<i>ALDH1L2</i>	aldehyde dehydrogenase 1 family, member L2	1.41	0.0498
<i>YARS2</i>	tyrosyl-tRNA synthetase 2, mitochondrial	1.41	0.0301
<i>EIF3L</i>	eukaryotic translation initiation factor 3, subunit L	1.41	0.0167
<i>MCM6</i>	minichromosome maintenance complex component 6	1.41	0.00692
<i>KNDC1</i>	Transcript Identified by AceView, Entrez Gene ID(s) 85442	1.41	0.0485
<i>ZNF451</i>	zinc finger protein 451	1.40	0.0448
<i>FBXW7</i>	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	1.40	0.0123
<i>NPLOC4</i>	NPL4 homolog, ubiquitin recognition factor	1.40	0.0161
<i>ZNF267</i>	zinc finger protein 267	1.40	0.0149
<i>HTATSF1</i>	HIV-1 Tat specific factor 1	1.40	0.0135
<i>ACSF2</i>	acyl-CoA synthetase family member 2	1.40	0.0134
<i>TTLL4</i>	tubulin tyrosine ligase-like family member 4	1.40	0.0297
<i>EIF2B3</i>	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	1.40	0.0163
<i>RSRC1</i>	arginine/serine-rich coiled-coil 1	1.40	0.0103
<i>TSPAN4</i>	tetraspanin 4	1.40	0.0106
<i>RBM27</i>	RNA binding motif protein 27	1.40	0.033
<i>VPS26B</i>	VPS26 retromer complex component B	1.40	0.0144
<i>DDX56</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 56	1.40	0.0301
<i>TACC1</i>	transforming, acidic coiled-coil containing protein 1	1.39	0.0268
<i>RPS19BP1</i>	ribosomal protein S19 binding protein 1	1.39	0.00984
<i>TYW3</i>	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	1.39	0.016
<i>TECR</i>	trans-2,3-enoyl-CoA reductase	1.39	0.0134
<i>RNASET2</i>	ribonuclease T2	1.39	0.012
<i>TPD52L1</i>	tumor protein D52-like 1	1.39	0.0242
<i>LMO3</i>	LIM domain only 3 (rhombotin-like 2)	1.39	0.0175
<i>PRDX2</i>	peroxiredoxin 2	1.38	0.0231
<i>TBXAS1</i>	thromboxane A synthase 1 (platelet)	1.38	0.0221
<i>ZDHC15</i>	zinc finger, DHHC-type containing 15	1.38	0.0181
<i>SAP130</i>	Sin3A associated protein 130kDa	1.38	0.0458
<i>POPDC3</i>	popeye domain containing 3	1.38	0.0215
<i>TMX3</i>	thioredoxin-related transmembrane protein 3	1.38	0.0252
<i>OGFOD3</i>	2-oxoglutarate and iron-dependent oxygenase domain containing 3	1.38	0.0123
<i>PFN2</i>	profilin 2	1.38	0.0136
<i>MGLL</i>	monoglyceride lipase	1.38	0.0155
<i>RAB31</i>	RAB31, member RAS oncogene family	1.38	0.0377
<i>ARL3</i>	ADP-ribosylation factor like GTPase 3	1.38	0.0247
<i>IFT27</i>	intraflagellar transport 27	1.38	0.0109
<i>LDAH</i>	lipid droplet associated hydrolase	1.38	0.0196
<i>RNF24</i>	ring finger protein 24	1.38	0.0133
<i>KIZ</i>	kizuna centrosomal protein	1.37	0.0428
<i>FXR1</i>	fragile X mental retardation, autosomal homolog 1	1.37	0.0188
<i>ANAPC16</i>	anaphase promoting complex subunit 16	1.37	0.0272
<i>LRRC27</i>	leucine rich repeat containing 27	1.37	0.00979
<i>TEX10</i>	testis expressed 10	1.37	0.0293
<i>CPEB1</i>	cytoplasmic polyadenylation element binding protein 1	1.36	0.0179
<i>POP4</i>	POP4 homolog, ribonuclease P/MRP subunit	1.36	0.0402
<i>FAXDC2</i>	fatty acid hydroxylase domain containing 2	1.36	0.0131
<i>TRMT10C</i>	tRNA methyltransferase 10C, mitochondrial RNase P subunit	1.36	0.0192
<i>ZNF101</i>	zinc finger protein 101	1.36	0.0183
<i>VPS52</i>	vacuolar protein sorting 52 homolog (S. cerevisiae)	1.36	0.0186
<i>GSTM3</i>	glutathione S-transferase mu 3 (brain)	1.36	0.0167
<i>RCN3</i>	reticulocalbin 3, EF-hand calcium binding domain	1.36	0.0177
<i>AOX1</i>	aldehyde oxidase 1	1.36	0.0306
<i>KCMF1</i>	potassium channel modulatory factor 1	1.36	0.0144
<i>PRKAG2</i>	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.36	0.0189
<i>B3GAT2</i>	beta-1,3-glucuronyltransferase 2	1.36	0.0294

<i>MAPK6</i>	mitogen-activated protein kinase 6	1.36	0.0231
<i>INAFM2</i>	InaF-motif containing 2	1.36	0.0384
<i>INIP</i>	INTS3 and NABP interacting protein	1.36	0.0226
<i>SREBF2</i>	sterol regulatory element binding transcription factor 2	1.35	0.0139
<i>PPP4R1</i>	protein phosphatase 4, regulatory subunit 1	1.35	0.0438
<i>EIF2D</i>	eukaryotic translation initiation factor 2D	1.35	0.0477
<i>ISCA2</i>	iron-sulfur cluster assembly 2	1.35	0.0391
<i>FNIP2</i>	folliculin interacting protein 2	1.35	0.0241
<i>UROD</i>	uroporphyrinogen decarboxylase	1.35	0.0477
<i>LZIC</i>	leucine zipper and CTNNBIP1 domain containing	1.35	0.0354
<i>VWA5A</i>	von Willebrand factor A domain containing 5A	1.35	0.036
<i>TAF15</i>	TATA box binding protein associated factor 15	1.35	0.0141
<i>RPAIN</i>	RPA interacting protein	1.35	0.0489
<i>HSD17B4</i>	hydroxysteroid (17-beta) dehydrogenase 4	1.35	0.0463
<i>GSTT2</i>	glutathione S-transferase theta 2 (gene/pseudogene)	1.35	0.0151
<i>INPP5A</i>	inositol polyphosphate-5-phosphatase A	1.35	0.0205
<i>PRPSAP2</i>	phosphoribosyl pyrophosphate synthetase-associated protein 2	1.35	0.046
<i>KLHL3</i>	kelch-like family member 3	1.35	0.0329
<i>NPRL2</i>	NPR2-like, GATOR1 complex subunit	1.35	0.0166
<i>JUN</i>	jun proto-oncogene	1.34	0.0265
<i>CCDC12</i>	coiled-coil domain containing 12	1.34	0.0261
<i>CXCL14</i>	chemokine (C-X-C motif) ligand 14	1.34	0.0205
<i>DUSP10</i>	dual specificity phosphatase 10	1.34	0.0151
<i>ZNF366</i>	zinc finger protein 366	1.34	0.0172
<i>PSTK</i>	phosphoserine-tRNA kinase	1.34	0.0193
<i>ERGIC2</i>	ERGIC and golgi 2	1.34	0.0248
<i>RNF7</i>	ring finger protein 7	1.34	0.0443
<i>MAP3K12</i>	mitogen-activated protein kinase kinase kinase 12	1.34	0.0201
<i>S100A7A</i>	S100 calcium binding protein A7A	1.34	0.0335
<i>TMEM97</i>	transmembrane protein 97	1.34	0.0284
<i>YME1L1</i>	YME1-like 1 ATPase	1.34	0.0339
<i>EGR3</i>	early growth response 3	1.34	0.0225
<i>KIAA1328</i>	KIAA1328	1.34	0.0288
<i>PFDN4</i>	prefoldin subunit 4	1.34	0.0476
<i>CCNDBP1</i>	cyclin D-type binding-protein 1	1.34	0.0239
<i>STEAP1</i>	six transmembrane epithelial antigen of the prostate 1	1.34	0.0387
<i>PREB</i>	prolactin regulatory element binding	1.34	0.0245
<i>CDK10</i>	cyclin-dependent kinase 10	1.34	0.0368
<i>PSMD8</i>	proteasome 26S subunit, non-ATPase 8	1.33	0.0229
<i>LRRC69</i>	leucine rich repeat containing 69	1.33	0.0443
<i>GNAI1</i>	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide	1.33	0.0264
<i>EMC4</i>	ER membrane protein complex subunit 4	1.33	0.0468
<i>CHCHD4</i>	coiled-coil-helix-coiled-coil-helix domain containing 4	1.33	0.0259
<i>VAV3</i>	vav 3 guanine nucleotide exchange factor	1.33	0.0238
<i>STPG1</i>	sperm-tail PG-rich repeat containing 1	1.33	0.0309
<i>FAM50A</i>	family with sequence similarity 50, member A	1.33	0.0381
<i>GTPBP10</i>	GTP-binding protein 10 (putative)	1.33	0.0375
<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	1.33	0.0346
<i>CMTM4</i>	CKLF-like MARVEL transmembrane domain containing 4	1.33	0.0201
<i>BNC1</i>	basonuclin 1	1.33	0.0208
<i>MPEG1</i>	macrophage expressed 1	1.33	0.0396
<i>OSCP1</i>	organic solute carrier partner 1	1.33	0.0253
<i>FBXO27</i>	F-box protein 27	1.33	0.0353
<i>JMJD1C</i>	jumonji domain containing 1C	1.33	0.0223
<i>ZNF583</i>	zinc finger protein 583	1.33	0.0336
<i>KIF3B</i>	kinesin family member 3B	1.33	0.042
<i>RPEL1</i>	ribulose-5-phosphate-3-epimerase-like 1	1.33	0.0288
<i>KDM2B</i>	lysine (K)-specific demethylase 2B	1.33	0.0462
<i>ATAD2B</i>	ATPase family, AAA domain containing 2B	1.33	0.0394

<i>TANGO6</i>	transport and golgi organization 6 homolog	1.33	0.0227
<i>COMMD3-</i>	COMMD3-BMI1 readthrough	1.33	0.0322
<i>PDE8A</i>	phosphodiesterase 8A	1.33	0.0422
<i>RBBP6</i>	retinoblastoma binding protein 6	1.33	0.0412
<i>EXD2</i>	exonuclease 3-5 domain containing 2	1.33	0.0212
<i>URM1</i>	ubiquitin related modifier 1	1.33	0.0444
<i>NSF</i>	N-ethylmaleimide-sensitive factor	1.33	0.0476
<i>OLFM4</i>	olfactomedin 4	1.33	0.0338
<i>TMEM184C</i>	transmembrane protein 184C	1.33	0.0478
<i>GPBP1</i>	GC-rich promoter binding protein 1	1.32	0.0429
<i>STEAP1B</i>	STEAP family member 1B	1.32	0.0369
<i>RNF170</i>	ring finger protein 170	1.32	0.0241
<i>COQ7</i>	coenzyme Q7 homolog, ubiquinone (yeast)	1.32	0.0321
<i>ELOVL6</i>	ELOVL fatty acid elongase 6	1.32	0.0372
<i>ARL15</i>	ADP-ribosylation factor like GTPase 15	1.32	0.0223
<i>PRRX1</i>	paired related homeobox 1	1.32	0.0481
<i>LMAN2</i>	lectin, mannose-binding 2	1.32	0.0421
<i>SEMA6C</i>	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin)	1.32	0.049
<i>UNC119B</i>	unc-119 lipid binding chaperone B	1.32	0.0435
<i>HK1</i>	hexokinase 1	1.32	0.028
<i>NRP1</i>	neuropilin 1	1.31	0.0484
<i>FAM3D</i>	family with sequence similarity 3, member D	1.31	0.0231
<i>C11orf68</i>	chromosome 11 open reading frame 68	1.31	0.0262
<i>PSMB4</i>	proteasome subunit beta 4	1.31	0.0491
<i>ADH1</i>	acireductone dioxygenase 1	1.31	0.0418
<i>TMEM185B</i>	transmembrane protein 185B	1.31	0.0275
<i>SH3BGRL2</i>	SH3 domain binding glutamate-rich protein like 2	1.31	0.047
<i>RNASE13</i>	ribonuclease, RNase A family, 13 (non-active)	1.31	0.023
<i>SIN3A</i>	SIN3 transcription regulator family member A	1.31	0.0263
<i>MSRA</i>	methionine sulfoxide reductase A	1.31	0.0414
<i>SLC24A1</i>	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	1.31	0.0326
<i>BTBD3</i>	BTB (POZ) domain containing 3	1.31	0.035
<i>PPP4R3B</i>	protein phosphatase 4, regulatory subunit 3B	1.31	0.0344
<i>HDHD2</i>	haloacid dehalogenase-like hydrolase domain containing 2	1.31	0.0306
<i>ZIC5</i>	Zic family member 5	1.31	0.0292
<i>CCDC151</i>	coiled-coil domain containing 151	1.31	0.0479
<i>ICE1</i>	interactor of little elongation complex ELL subunit 1	1.30	0.043
<i>F2RL2</i>	coagulation factor II (thrombin) receptor-like 2	1.30	0.0346
<i>SART3</i>	squamous cell carcinoma antigen recognized by T-cells 3	1.30	0.0464
<i>GPRC5A</i>	G protein-coupled receptor, class C, group 5, member A	1.30	0.0426
<i>CES3</i>	carboxylesterase 3	1.30	0.0367
<i>RAB8A</i>	RAB8A, member RAS oncogene family	1.30	0.0487
<i>UBIAD1</i>	UbiA prenyltransferase domain containing 1	1.30	0.0361
<i>TOMM40L</i>	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	1.30	0.046
<i>ARL6IP5</i>	ADP-ribosylation factor like GTPase 6 interacting protein 5	1.30	0.0359
<i>GFM1</i>	G elongation factor, mitochondrial 1	1.30	0.0477
<i>NETO1</i>	neuropilin (NRP) and tolloid (TLL)-like 1	1.30	0.0451
<i>FMO5</i>	flavin containing monooxygenase 5	1.30	0.0314
<i>PITPNC1</i>	phosphatidylinositol transfer protein, cytoplasmic 1	1.29	0.0389
<i>APIP</i>	APAF1 interacting protein	1.29	0.0424
<i>HSPBP1</i>	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	1.29	0.0304
<i>SGCZ</i>	sarcoglycan zeta	1.29	0.0451
<i>GMPR</i>	guanosine monophosphate reductase	1.29	0.0404
<i>GUF1</i>	GUF1 homolog, GTPase	1.29	0.0482
<i>COG6</i>	component of oligomeric golgi complex 6	1.29	0.048
<i>HDAC5</i>	histone deacetylase 5	1.29	0.0387
<i>STARD3</i>	StAR-related lipid transfer domain containing 3	1.29	0.035
<i>GPR15</i>	G protein-coupled receptor 15	1.29	0.034
<i>MICA</i>	MHC class I polypeptide-related sequence A	1.29	0.0407

<i>SLC25A15</i>	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	1.29	0.0475
<i>PARD3</i>	par-3 family cell polarity regulator	1.29	0.0426
<i>ZFP64</i>	ZFP64 zinc finger protein	1.29	0.0399
<i>FRG2B</i>	FSHD region gene 2 family, member B	1.28	0.0488
<i>OXSM</i>	3-oxoacyl-ACP synthase, mitochondrial	1.28	0.0401
<i>C12orf76</i>	chromosome 12 open reading frame 76	1.28	0.0383
<i>MOV10</i>	Mov10 RISC complex RNA helicase	1.28	0.0385
<i>GLT8D2</i>	glycosyltransferase 8 domain containing 2	1.28	0.0484
<i>BMP6</i>	bone morphogenetic protein 6	1.28	0.0373
<i>ARMCX2</i>	armadillo repeat containing, X-linked 2	1.28	0.05
<i>EPHA1</i>	EPH receptor A1	1.27	0.0484
<i>TOX</i>	thymocyte selection-associated high mobility group box	1.27	0.0436
<i>ZFP82</i>	ZFP82 zinc finger protein	1.27	0.0477
<i>TRIM24</i>	tripartite motif containing 24	1.27	0.0484
<i>NEB</i>	nebulin	1.27	0.0472
<i>KIF20A</i>	kinesin family member 20A	1.26	0.0497
<i>FAM111A</i>	family with sequence similarity 111, member A	1.26	0.0472

Table S2. MMF-decreased genes (P < 0.05 with FC < 0.80). The table lists 142 MMF-decreased genes ranked by estimated fold-change (FC) (MMF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group).

Symbol	Description	FC	P-value
<i>TP53INP1</i>	tumor protein p53 inducible nuclear protein 1	0.57	0.00853
<i>TCEA1</i>	transcription elongation factor A (SII), 1	0.64	0.0166
<i>F3</i>	coagulation factor III (thromboplastin, tissue factor)	0.65	0.00141
<i>ZC3H4</i>	zinc finger CCCH-type containing 4	0.66	0.00186
<i>SLC20A2</i>	solute carrier family 20 (phosphate transporter), member 2	0.67	0.00457
<i>ATP6V1E2</i>	ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E2	0.67	0.00524
<i>OSBPL10</i>	oxysterol binding protein-like 10	0.68	0.00243
<i>CCDC81</i>	coiled-coil domain containing 81	0.68	0.0051
<i>IRAK4</i>	interleukin 1 receptor associated kinase 4	0.68	0.0231
<i>TSSC4</i>	tumor suppressing subtransferable candidate 4	0.69	0.00458
<i>SFXN1</i>	sideroflexin 1	0.69	0.0064
<i>PIGU</i>	Salzman2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL,	0.69	0.00843
<i>GPR157</i>	G protein-coupled receptor 157	0.69	0.00439
<i>TOP2A</i>	topoisomerase (DNA) II alpha	0.70	0.0084
<i>GLIS2</i>	GLIS family zinc finger 2	0.70	0.00901
<i>KLHL18</i>	kelch-like family member 18	0.70	0.00659
<i>PHLPP1</i>	PH domain and leucine rich repeat protein phosphatase 1	0.70	0.00874
<i>PGM3</i>	phosphoglucomutase 3	0.70	0.0189
<i>YPEL2</i>	yippee like 2	0.71	0.0241
<i>CCNF</i>	cyclin F	0.71	0.00704
<i>PRR5L</i>	proline rich 5 like	0.71	0.0154
<i>CTSL</i>	cathepsin L	0.71	0.0139
<i>KLHL20</i>	kelch-like family member 20	0.71	0.0108
<i>ATP6V1C2</i>	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	0.71	0.0171
<i>TGDS</i>	TDP-glucose 4,6-dehydratase	0.72	0.00897
<i>IMPACT</i>	impact RWD domain protein	0.72	0.0114
<i>DDR2</i>	discoidin domain receptor tyrosine kinase 2	0.72	0.0085
<i>FES</i>	FES proto-oncogene, tyrosine kinase	0.72	0.028
<i>FCER1G</i>	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	0.72	0.0195
<i>SMARCD1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	0.72	0.0402
<i>NUTM2G</i>	NUT family member 2G	0.73	0.0258
<i>UBE2W</i>	ubiquitin-conjugating enzyme E2W (putative)	0.73	0.0236
<i>CDKN1B</i>	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	0.73	0.0196
<i>GRIN2C</i>	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	0.73	0.0201
<i>SPTLC1</i>	serine palmitoyltransferase, long chain base subunit 1	0.73	0.0264
<i>KRTAP2-1</i>	keratin associated protein 2-1	0.73	0.0129
<i>C11orf96</i>	chromosome 11 open reading frame 96	0.73	0.0122
<i>ZNF616</i>	zinc finger protein 616	0.73	0.0492
<i>EIF2S3</i>	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	0.73	0.0324
<i>ABHD14A</i>	abhydrolase domain containing 14A	0.73	0.0412
<i>PRSS27</i>	protease, serine 27	0.73	0.0157
<i>ARFGEF2</i>	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-	0.73	0.0241
<i>RASL10A</i>	RAS-like, family 10, member A	0.74	0.0124
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recognin 5	0.74	0.039
<i>MIB1</i>	mindbomb E3 ubiquitin protein ligase 1	0.74	0.0283
<i>C8G</i>	complement component 8, gamma polypeptide	0.74	0.0151
<i>FAM114A2</i>	family with sequence similarity 114, member A2	0.74	0.0239
<i>SNX11</i>	sorting nexin 11	0.74	0.0273
<i>RALGPS1</i>	Ral GEF with PH domain and SH3 binding motif 1	0.74	0.0145
<i>MTMR2</i>	myotubularin related protein 2	0.74	0.0165
<i>CIQTNF3</i>	C1q and tumor necrosis factor related protein 3	0.74	0.0154
<i>ENHO</i>	energy homeostasis associated	0.74	0.023
<i>PTPRJ</i>	protein tyrosine phosphatase, receptor type, J	0.74	0.0317
<i>LRFN3</i>	leucine rich repeat and fibronectin type III domain containing 3	0.74	0.0186
<i>NUAK1</i>	NUAK family, SNF1-like kinase, 1	0.74	0.026

<i>ZNF548</i>	zinc finger protein 548	0.74	0.0149
<i>MAPK8IP2</i>	mitogen-activated protein kinase 8 interacting protein 2	0.75	0.0174
<i>NKX2-1</i>	NK2 homeobox 1	0.75	0.0242
<i>SIM2</i>	single-minded family bHLH transcription factor 2	0.75	0.0457
<i>CAND2</i>	cullin-associated and neddylation-dissociated 2 (putative)	0.75	0.0166
<i>TBX15</i>	T-box 15	0.75	0.0359
<i>KRTAP2-2</i>	keratin associated protein 2-2	0.75	0.018
<i>ACSL4</i>	acyl-CoA synthetase long-chain family member 4	0.75	0.0239
<i>NOX4</i>	NADPH oxidase 4	0.75	0.0422
<i>KDM8</i>	lysine (K)-specific demethylase 8	0.75	0.0239
<i>LUZP1</i>	leucine zipper protein 1	0.75	0.0268
<i>CDC23</i>	cell division cycle 23	0.75	0.0371
<i>USP25</i>	ubiquitin specific peptidase 25	0.75	0.0394
<i>ANKRD61</i>	ankyrin repeat domain 61	0.75	0.0345
<i>WWC1</i>	WW and C2 domain containing 1	0.76	0.0266
<i>SACM1L</i>	SAC1 suppressor of actin mutations 1-like (yeast)	0.76	0.0284
<i>PLEC</i>	plectin	0.76	0.0369
<i>ANKLE2</i>	ankyrin repeat and LEM domain containing 2	0.76	0.0311
<i>FADS6</i>	fatty acid desaturase 6	0.76	0.0456
<i>CEMIP</i>	cell migration inducing protein, hyaluronan binding	0.76	0.0232
<i>ZNF250</i>	zinc finger protein 250	0.76	0.026
<i>TSPAN13</i>	tetraspanin 13	0.76	0.0448
<i>TMEM177</i>	transmembrane protein 177	0.76	0.0313
<i>XAGE5</i>	X antigen family, member 5	0.76	0.0287
<i>BPIFB6</i>	BPI fold containing family B, member 6	0.76	0.0347
<i>DMWD</i>	dystrophia myotonica, WD repeat containing	0.76	0.0314
<i>CACNA1G</i>	calcium channel, voltage-dependent, T type, alpha 1G subunit	0.76	0.0411
<i>RCAN1</i>	regulator of calcineurin 1	0.76	0.0479
<i>USP21</i>	ubiquitin specific peptidase 21	0.76	0.0483
<i>CYP27A1</i>	cytochrome P450, family 27, subfamily A, polypeptide 1	0.76	0.0341
<i>TNPO1</i>	transportin 1	0.76	0.0244
<i>SMCR8</i>	Smith-Magenis syndrome chromosome region, candidate 8	0.76	0.0324
<i>PELI2</i>	pellino E3 ubiquitin protein ligase family member 2	0.76	0.0367
<i>YAP1</i>	Yes-associated protein 1	0.76	0.0388
<i>DNAJC9</i>	DnaJ (Hsp40) homolog, subfamily C, member 9	0.76	0.0369
<i>SDHB</i>	succinate dehydrogenase complex subunit B, iron sulfur (Ip)	0.76	0.0366
<i>CFAP73</i>	cilia and flagella associated protein 73	0.76	0.0315
<i>MRS2</i>	MRS2 magnesium transporter	0.76	0.0355
<i>SP5</i>	Sp5 transcription factor	0.77	0.0303
<i>METTL15</i>	methyltransferase like 15	0.77	0.0499
<i>GPT</i>	glutamic-pyruvate transaminase (alanine aminotransferase)	0.77	0.0301
<i>CCDC190</i>	coiled-coil domain containing 190	0.77	0.0413
<i>ATP6AP1L</i>	ATPase, H ⁺ transporting, lysosomal accessory protein 1-like	0.77	0.0366
<i>ST6GAL2</i>	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	0.77	0.0467
<i>FLOT2</i>	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript	0.77	0.0303
<i>PARBP</i>	PARP1 binding protein	0.77	0.0477
<i>RGL3</i>	ral guanine nucleotide dissociation stimulator-like 3	0.77	0.0424
<i>FSTL3</i>	folliculin-like 3 (secreted glycoprotein)	0.77	0.0373
<i>TBC1D3</i>	TBC1 domain family, member 3	0.77	0.0361
<i>SSRP1</i>	structure specific recognition protein 1	0.77	0.0351
<i>KCNH1</i>	potassium channel, voltage gated eag related subfamily H, member 1	0.77	0.0488
<i>AHDC1</i>	AT hook, DNA binding motif, containing 1	0.77	0.0314
<i>CEACAM19</i>	carcinoembryonic antigen-related cell adhesion molecule 19	0.77	0.0473
<i>ZNF816</i>	zinc finger protein 816	0.77	0.0369
<i>DOLPP1</i>	dolichyldiphosphatase 1	0.77	0.0336
<i>SLC44A5</i>	solute carrier family 44, member 5	0.77	0.035
<i>CHST14</i>	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 14	0.77	0.036
<i>UPF2</i>	UPF2 regulator of nonsense transcripts homolog (yeast)	0.77	0.03
<i>CREB3L3</i>	cAMP responsive element binding protein 3-like 3	0.77	0.0331

<i>SLC26A11</i>	solute carrier family 26 (anion exchanger), member 11	0.77	0.037
<i>HIBCH</i>	Transcript Identified by AceView, Entrez Gene ID(s) 26275	0.77	0.0499
<i>ERCC6</i>	excision repair cross-complementation group 6	0.77	0.0449
<i>ATF7IP</i>	activating transcription factor 7 interacting protein	0.77	0.0454
<i>STK11IP</i>	serine/threonine kinase 11 interacting protein	0.77	0.0412
<i>ARHGAP22</i>	Rho GTPase activating protein 22	0.77	0.0318
<i>MFSD14A</i>	major facilitator superfamily domain containing 14A	0.78	0.0428
<i>GPR4</i>	G protein-coupled receptor 4	0.78	0.0463
<i>SETD9</i>	SET domain containing 9	0.78	0.0396
<i>NMB</i>	neuromedin B	0.78	0.0401
<i>REPS1</i>	RALBP1 associated Eps domain containing 1	0.78	0.0373
<i>ERCC5</i>	excision repair cross-complementation group 5	0.78	0.0424
<i>C12orf50</i>	chromosome 12 open reading frame 50	0.78	0.0392
<i>PLEKHG3</i>	pleckstrin homology domain containing, family G (with RhoGef domain)	0.78	0.0372
<i>LTB</i>	lymphotoxin beta (TNF superfamily, member 3)	0.78	0.0488
<i>DTWD2</i>	DTW domain containing 2	0.78	0.0466
<i>ZNF439</i>	zinc finger protein 439	0.78	0.0395
<i>GPRIN1</i>	G protein regulated inducer of neurite outgrowth 1	0.78	0.0472
<i>CD82</i>	CD82 molecule	0.78	0.0398
<i>LYN</i>	LYN proto-oncogene, Src family tyrosine kinase	0.78	0.0467
<i>MAP6D1</i>	MAP6 domain containing 1	0.78	0.0474
<i>MPZ</i>	myelin protein zero	0.79	0.046
<i>DCLK2</i>	doublecortin-like kinase 2	0.79	0.0435
<i>NDST2</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	0.79	0.0444
<i>TRNP1</i>	TMF1-regulated nuclear protein 1	0.79	0.0466
<i>MC2R</i>	melanocortin 2 receptor (adrenocorticotrophic hormone)	0.79	0.0433
<i>PTP4A2</i>	protein tyrosine phosphatase type IVA, member 2	0.79	0.0439
<i>EMID1</i>	EMI domain containing 1	0.79	0.0484

Table S3. DRF-increased genes ($P < 0.05$ with $FC > 1.25$). The table lists 181 DRF-increased genes ranked by estimated fold-change (FC) (DRF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group).

Symbol	Description	FC	P-value
<i>TIGD5</i>	tigger transposable element derived 5	1.64	0.00427
<i>ABI3BP</i>	ABI family, member 3 (NESH) binding protein	1.64	0.00234
<i>SPATA25</i>	spermatogenesis associated 25	1.60	0.00194
<i>NEFM</i>	neurofilament, medium polypeptide	1.59	0.00353
<i>ZDHHC15</i>	zinc finger, DHHC-type containing 15	1.57	0.0083
<i>NDUFAF6</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	1.56	0.0141
<i>FAM83D</i>	family with sequence similarity 83, member D	1.53	0.00922
<i>ACSL6</i>	acyl-CoA synthetase long-chain family member 6	1.52	0.00427
<i>TPPP3</i>	tubulin polymerization-promoting protein family member 3	1.49	0.0131
<i>ZNF180</i>	zinc finger protein 180	1.49	0.00439
<i>SCN2A</i>	sodium channel, voltage gated, type II alpha subunit	1.48	0.0384
<i>PSIP1</i>	PC4 and SFRS1 interacting protein 1	1.48	0.00735
<i>SLITRK5</i>	SLIT and NTRK-like family, member 5	1.47	0.00546
<i>TXNRD1</i>	thioredoxin reductase 1	1.47	0.00951
<i>GHRHR</i>	growth hormone releasing hormone receptor	1.46	0.0101
<i>GSAP</i>	gamma-secretase activating protein	1.45	0.00431
<i>CD33</i>	CD33 molecule	1.45	0.00473
<i>ALDH1L1</i>	aldehyde dehydrogenase 1 family, member L1	1.45	0.00857
<i>HLA-DRB5</i>	major histocompatibility complex, class II, DR beta 5	1.45	0.00685
<i>CLRN2</i>	clarin 2	1.45	0.00786
<i>SIX3</i>	SIX homeobox 3	1.44	0.00659
<i>SLC50A1</i>	solute carrier family 50 (sugar efflux transporter), member 1	1.44	0.0101
<i>SLA</i>	Src-like-adaptor	1.44	0.0129
<i>BCDIN3D</i>	BCDIN3 domain containing	1.43	0.0407
<i>RPEL1</i>	ribulose-5-phosphate-3-epimerase-like 1	1.43	0.0125
<i>OR2L3</i>	olfactory receptor, family 2, subfamily L, member 3	1.43	0.0155
<i>ULK3</i>	unc-51 like kinase 3	1.43	0.0165
<i>SCPEP1</i>	serine carboxypeptidase 1	1.43	0.00789
<i>FAM216B</i>	family with sequence similarity 216, member B	1.43	0.00999
<i>GUF1</i>	GUF1 homolog, GTPase	1.43	0.0159
<i>WDR4</i>	WD repeat domain 4	1.42	0.00767
<i>RAP2C</i>	RAP2C, member of RAS oncogene family	1.42	0.0217
<i>FAT2</i>	FAT atypical cadherin 2	1.42	0.0171
<i>GJB7</i>	gap junction protein beta 7	1.42	0.0074
<i>ATF3</i>	activating transcription factor 3	1.42	0.00823
<i>FBXO27</i>	F-box protein 27	1.42	0.0129
<i>METTL25</i>	methyltransferase like 25	1.42	0.026
<i>GP9</i>	glycoprotein IX (platelet)	1.41	0.014
<i>CST9</i>	cystatin 9 (testatin)	1.41	0.0166
<i>AANAT</i>	aralkylamine N-acetyltransferase	1.41	0.00922
<i>OSGIN1</i>	oxidative stress induced growth inhibitor 1	1.41	0.0105
<i>TACC2</i>	transforming, acidic coiled-coil containing protein 2	1.41	0.0203
<i>MCEMP1</i>	mast cell-expressed membrane protein 1	1.41	0.0337
<i>RNF40</i>	ring finger protein 40, E3 ubiquitin protein ligase	1.40	0.0125
<i>STX3</i>	syntaxin 3	1.40	0.0278
<i>PRDM1</i>	PR domain containing 1, with ZNF domain	1.40	0.0103
<i>OR4F17</i>	olfactory receptor, family 4, subfamily F, member 17	1.40	0.0107
<i>RAD18</i>	RAD18 E3 ubiquitin protein ligase	1.40	0.0392
<i>GPAT2</i>	glycerol-3-phosphate acyltransferase 2, mitochondrial	1.40	0.0142
<i>C2orf68</i>	chromosome 2 open reading frame 68	1.40	0.0287
<i>B3GNT4</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	1.40	0.0125
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	1.40	0.0194
<i>SHISA6</i>	shisa family member 6	1.40	0.0141
<i>TBXAS1</i>	thromboxane A synthase 1 (platelet)	1.39	0.0189
<i>INAFM1</i>	InaF-motif containing 1	1.39	0.0143

<i>NQO1</i>	NAD(P)H dehydrogenase, quinone 1	1.39	0.0247
<i>G6PD</i>	glucose-6-phosphate dehydrogenase	1.39	0.015
<i>OPRL1</i>	opiate receptor-like 1	1.39	0.0226
<i>PIK3CG</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.39	0.0256
<i>LRFN5</i>	leucine rich repeat and fibronectin type III domain containing 5	1.39	0.0172
<i>PRDM15</i>	PR domain containing 15	1.38	0.0229
<i>TBX2</i>	T-box 2	1.38	0.0142
<i>BMP10</i>	bone morphogenetic protein 10	1.38	0.0279
<i>CENPP</i>	centromere protein P	1.38	0.0227
<i>OR2Z1</i>	olfactory receptor, family 2, subfamily Z, member 1	1.38	0.0465
<i>FAM221A</i>	family with sequence similarity 221, member A	1.38	0.039
<i>UNC93B1</i>	unc-93 homolog B1 (C. elegans)	1.38	0.0233
<i>BCKDHB</i>	branched chain keto acid dehydrogenase E1, beta polypeptide	1.38	0.034
<i>GPR153</i>	G protein-coupled receptor 153	1.38	0.013
<i>BLOC1S3</i>	biogenesis of lysosomal organelles complex-1, subunit 3	1.38	0.0225
<i>SEMA4D</i>	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript	1.37	0.033
<i>SLC12A5</i>	solute carrier family 12 (potassium/chloride transporter), member 5	1.37	0.0205
<i>HS3ST2</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	1.37	0.0209
<i>CELA2B</i>	chymotrypsin-like elastase family, member 2B	1.37	0.0243
<i>FOXO6</i>	forkhead box O6	1.37	0.0187
<i>TTL4</i>	tubulin tyrosine ligase-like family member 4	1.37	0.037
<i>TACC1</i>	transforming, acidic coiled-coil containing protein 1	1.37	0.0417
<i>RAPGEF3</i>	Rap guanine nucleotide exchange factor 3	1.37	0.021
<i>RCBTB1</i>	regulator of chromosome condensation (RCC1) and BTB (POZ) domain	1.37	0.0197
<i>STK4</i>	serine/threonine kinase 4	1.37	0.016
<i>GIPC2</i>	GIPC PDZ domain containing family, member 2	1.37	0.0321
<i>IFT81</i>	intraflagellar transport 81	1.36	0.0234
<i>ZNF366</i>	zinc finger protein 366	1.36	0.0183
<i>NFATC2</i>	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1.36	0.0179
<i>PAPSS2</i>	3-phosphoadenosine 5-phosphosulfate synthase 2	1.36	0.0206
<i>MGST1</i>	microsomal glutathione S-transferase 1	1.36	0.0266
<i>MAN2A2</i>	mannosidase, alpha, class 2A, member 2	1.35	0.0401
<i>CHRNA2</i>	cholinergic receptor, nicotinic beta 2	1.35	0.024
<i>SOX30</i>	SRY box 30	1.35	0.0293
<i>UBL4A</i>	ubiquitin-like 4A	1.35	0.02
<i>LY6G6C</i>	lymphocyte antigen 6 complex, locus G6C	1.35	0.0286
<i>GSR</i>	glutathione reductase	1.35	0.0171
<i>PLAC8L1</i>	PLAC8-like 1	1.35	0.036
<i>ZNF341</i>	zinc finger protein 341	1.35	0.0238
<i>CPXM2</i>	carboxypeptidase X (M14 family), member 2	1.35	0.0194
<i>RHD</i>	Rh blood group, D antigen	1.35	0.0202
<i>GRK6</i>	G protein-coupled receptor kinase 6	1.35	0.0221
<i>DUOXA2</i>	dual oxidase maturation factor 2	1.35	0.0353
<i>NANOG</i>	Nanog homeobox	1.35	0.0182
<i>FAM71A</i>	family with sequence similarity 71, member A	1.35	0.0246
<i>DAGLB</i>	diacylglycerol lipase, beta	1.35	0.0493
<i>EGFR</i>	epidermal growth factor receptor	1.35	0.0403
<i>HCAR3</i>	hydroxycarboxylic acid receptor 3	1.35	0.0219
<i>RNF113A</i>	ring finger protein 113A	1.35	0.0223
<i>FRG2</i>	FSHD region gene 2	1.35	0.0441
<i>SCO1</i>	SCO1 cytochrome c oxidase assembly protein	1.35	0.02
<i>P2RX2</i>	purinergic receptor P2X, ligand gated ion channel, 2	1.35	0.027
<i>PAQR6</i>	progesterone and adipoQ receptor family member VI	1.35	0.0382
<i>CNR2</i>	cannabinoid receptor 2	1.35	0.0199
<i>RNF111</i>	ring finger protein 111	1.35	0.0297
<i>PRG3</i>	proteoglycan 3	1.34	0.025
<i>WDFY3</i>	WD repeat and FYVE domain containing 3	1.34	0.0249
<i>ZACN</i>	zinc activated ligand-gated ion channel	1.34	0.0269
<i>NFIA</i>	nuclear factor I/A	1.34	0.0371

<i>TRIM6</i>	tripartite motif containing 6	1.34	0.0469
<i>RPUSD4</i>	RNA pseudouridylate synthase domain containing 4	1.34	0.0424
<i>RNF170</i>	ring finger protein 170	1.34	0.0218
<i>PBRM1</i>	polybromo 1	1.34	0.0331
<i>NLRP12</i>	NLR family, pyrin domain containing 12	1.34	0.0219
<i>CFAP46</i>	cilia and flagella associated protein 46	1.34	0.0242
<i>EPHA8</i>	EPH receptor A8	1.33	0.0382
<i>GCLC</i>	glutamate-cysteine ligase, catalytic subunit	1.33	0.0369
<i>IKZF4</i>	IKAROS family zinc finger 4	1.33	0.029
<i>SYNGR4</i>	synaptogyrin 4	1.33	0.033
<i>CAPN3</i>	calpain 3	1.33	0.0396
<i>GMPR</i>	guanosine monophosphate reductase	1.33	0.0294
<i>EID3</i>	EP300 interacting inhibitor of differentiation 3	1.33	0.0298
<i>CYP11B2</i>	cytochrome P450, family 11, subfamily B, polypeptide 2	1.33	0.0263
<i>ZNF385D</i>	zinc finger protein 385D	1.33	0.0445
<i>APIP</i>	APAF1 interacting protein	1.33	0.0349
<i>CDC42EP4</i>	CDC42 effector protein (Rho GTPase binding) 4	1.33	0.0266
<i>TRIM73</i>	tripartite motif containing 73	1.33	0.0363
<i>PTGR1</i>	prostaglandin reductase 1	1.32	0.04
<i>MYOZ3</i>	myozenin 3	1.32	0.045
<i>TMEM97</i>	transmembrane protein 97	1.32	0.0379
<i>GPR6</i>	G protein-coupled receptor 6	1.32	0.0374
<i>SLC22A8</i>	solute carrier family 22 (organic anion transporter), member 8	1.32	0.0417
<i>PCID2</i>	PCI domain containing 2	1.32	0.0404
<i>CACNA1H</i>	calcium channel, voltage-dependent, T type, alpha 1H subunit	1.32	0.047
<i>GMPR2</i>	guanosine monophosphate reductase 2	1.32	0.0313
<i>PFKM</i>	phosphofructokinase, muscle	1.32	0.035
<i>IL2RG</i>	interleukin 2 receptor, gamma	1.32	0.0392
<i>PIK3R5</i>	phosphoinositide-3-kinase, regulatory subunit 5	1.32	0.0298
<i>FMO5</i>	flavin containing monooxygenase 5	1.32	0.0279
<i>FBXO34</i>	F-box protein 34	1.32	0.0382
<i>TRIOBP</i>	TRIO and F-actin binding protein	1.31	0.0459
<i>PPARA</i>	peroxisome proliferator-activated receptor alpha	1.31	0.0361
<i>C2orf83</i>	chromosome 2 open reading frame 83	1.31	0.041
<i>GSKIP</i>	GSK3B interacting protein	1.31	0.0378
<i>ACTRT3</i>	actin-related protein T3	1.31	0.0449
<i>MYLK4</i>	myosin light chain kinase family member 4	1.31	0.0374
<i>TRIM49D1</i>	tripartite motif containing 49D1	1.31	0.0379
<i>NR1D1</i>	nuclear receptor subfamily 1, group D, member 1	1.31	0.0468
<i>C10orf95</i>	chromosome 10 open reading frame 95	1.31	0.0479
<i>TAS2R10</i>	taste receptor, type 2, member 10	1.31	0.0409
<i>PRAMEF9</i>	---	1.31	0.0425
<i>LCE5A</i>	late cornified envelope 5A	1.31	0.0411
<i>ARL4D</i>	ADP-ribosylation factor like GTPase 4D	1.31	0.0435
<i>ELAC1</i>	elaC ribonuclease Z 1	1.31	0.0468
<i>OR52M1</i>	olfactory receptor, family 52, subfamily M, member 1	1.30	0.0422
<i>TP53INP2</i>	tumor protein p53 inducible nuclear protein 2	1.30	0.0459
<i>ISX</i>	intestine-specific homeobox	1.30	0.0426
<i>AOX1</i>	aldehyde oxidase 1	1.30	0.0414
<i>FETUB</i>	fetuin B	1.30	0.0345
<i>FGF6</i>	fibroblast growth factor 6	1.30	0.0384
<i>SVEP1</i>	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.30	0.0383
<i>GPR161</i>	G protein-coupled receptor 161	1.30	0.04
<i>AGPAT5</i>	1-acylglycerol-3-phosphate O-acyltransferase 5	1.30	0.0385
<i>C17orf97</i>	chromosome 17 open reading frame 97	1.30	0.0362
<i>ALDH3A2</i>	aldehyde dehydrogenase 3 family, member A2	1.30	0.0389
<i>KIF25</i>	kinesin family member 25	1.30	0.0495
<i>ST3GAL5</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.30	0.0441
<i>BEST1</i>	bestrophin 1	1.30	0.0386

<i>BCAS1</i>	breast carcinoma amplified sequence 1	1.29	0.0385
<i>PAFAH2</i>	platelet-activating factor acetylhydrolase 2	1.29	0.0449
<i>CRYGA</i>	crystallin gamma A	1.29	0.0461
<i>ROM1</i>	retinal outer segment membrane protein 1	1.29	0.0468
<i>APOBEC2</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	1.29	0.0416
<i>SLC1A3</i>	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.28	0.0497
<i>LIMD1</i>	LIM domains containing 1	1.28	0.0499
<i>RASSF8</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	1.28	0.0494

Table S4. DRF-decreased genes ($P < 0.05$ with $FC < 0.80$). The table lists 198 DRF-decreased genes ranked by estimated fold-change (FC) (DRF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group).

Symbol	Description	FC	P-value
<i>ACTR3</i>	ARP3 actin-related protein 3 homolog (yeast)	0.52	0.00245
<i>SACM1L</i>	SAC1 suppressor of actin mutations 1-like (yeast)	0.53	0.0000774
<i>NOX4</i>	NADPH oxidase 4	0.53	0.000157
<i>CLK1</i>	CDC like kinase 1	0.54	0.0121
<i>RAP1B</i>	RAP1B, member of RAS oncogene family	0.54	0.00318
<i>TIMM9</i>	translocase of inner mitochondrial membrane 9 homolog (yeast)	0.56	0.00304
<i>MOCS2</i>	molybdenum cofactor synthesis 2	0.57	0.00457
<i>PRKCI</i>	protein kinase C, iota	0.58	0.0255
<i>FCHSD2</i>	FCH and double SH3 domains 2	0.58	0.00106
<i>KLHDC2</i>	kelch domain containing 2	0.58	0.0179
<i>TAF9</i>	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated	0.59	0.00255
<i>REXO2</i>	RNA exonuclease 2	0.59	0.00941
<i>WDR41</i>	WD repeat domain 41	0.59	0.0369
<i>LYPLAL1</i>	lysophospholipase-like 1	0.59	0.0174
<i>UCHL3</i>	ubiquitin C-terminal hydrolase L3	0.60	0.0398
<i>LNPEP</i>	leucyl/cystinyl aminopeptidase	0.61	0.0193
<i>NAE1</i>	NEDD8 activating enzyme E1 subunit 1	0.61	0.00129
<i>CCT2</i>	chaperonin containing TCP1, subunit 2 (beta)	0.61	0.00926
<i>LSM1</i>	LSM1 homolog, mRNA degradation associated	0.61	0.0284
<i>TANK</i>	TRAF family member-associated NFkB activator	0.63	0.0486
<i>RIOK1</i>	RIO kinase 1	0.63	0.0216
<i>ZNF24</i>	zinc finger protein 24	0.64	0.00344
<i>HACD3</i>	3-hydroxyacyl-CoA dehydratase 3	0.64	0.0218
<i>SFT2D1</i>	SFT2 domain containing 1	0.64	0.0359
<i>C20orf194</i>	chromosome 20 open reading frame 194	0.64	0.0176
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recogin 5	0.64	0.0104
<i>ZZZ3</i>	zinc finger, ZZ-type containing 3	0.64	0.018
<i>RAP1A</i>	RAP1A, member of RAS oncogene family	0.64	0.00542
<i>NUP50</i>	nucleoporin 50kDa	0.64	0.0252
<i>RAD50</i>	RAD50 homolog, double strand break repair protein	0.64	0.00656
<i>RPL22L1</i>	ribosomal protein L22-like 1	0.64	0.0418
<i>METTL8</i>	methyltransferase like 8	0.65	0.00365
<i>CUL2</i>	cullin 2	0.65	0.0378
<i>RC3H1</i>	ring finger and CCCH-type domains 1	0.65	0.011
<i>TMEM59</i>	transmembrane protein 59	0.65	0.0299
<i>PSMG1</i>	proteasome (prosome, macropain) assembly chaperone 1	0.65	0.0494
<i>MFSD14A</i>	major facilitator superfamily domain containing 14A	0.65	0.00637
<i>DHX36</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 36	0.65	0.00403
<i>ANO4</i>	anoctamin 4	0.65	0.00339
<i>TP53INP1</i>	tumor protein p53 inducible nuclear protein 1	0.66	0.0392
<i>ALG8</i>	ALG8, alpha-1,3-glucosyltransferase	0.66	0.0151
<i>CHSY3</i>	chondroitin sulfate synthase 3	0.66	0.0264
<i>ZNF766</i>	zinc finger protein 766	0.66	0.00564
<i>ANXA5</i>	annexin A5	0.66	0.0276
<i>MRPL14</i>	mitochondrial ribosomal protein L14	0.66	0.048
<i>CMC1</i>	C-x(9)-C motif containing 1	0.67	0.0304
<i>OLA1</i>	Obg-like ATPase 1	0.67	0.0239
<i>SENp6</i>	SUMO1/sentrin specific peptidase 6	0.67	0.0285
<i>TRAPPC6B</i>	trafficking protein particle complex 6B	0.67	0.042
<i>CFAP36</i>	cilia and flagella associated protein 36	0.67	0.00751
<i>ARFGEF1</i>	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-	0.67	0.0208
<i>ZNF567</i>	zinc finger protein 567	0.67	0.00456
<i>MAMLD1</i>	mastermind-like domain containing 1	0.67	0.009
<i>SETD9</i>	SET domain containing 9	0.67	0.00429
<i>ZNF616</i>	zinc finger protein 616	0.67	0.0066

<i>LUM</i>	lumican	0.67	0.0425
<i>COA7</i>	cytochrome c oxidase assembly factor 7 (putative)	0.67	0.0041
<i>CHD1</i>	chromodomain helicase DNA binding protein 1	0.67	0.0276
<i>XRCC4</i>	X-ray repair complementing defective repair in Chinese hamster cells 4	0.68	0.0123
<i>EEA1</i>	early endosome antigen 1	0.68	0.0345
<i>DPP8</i>	dipeptidyl-peptidase 8	0.68	0.00616
<i>GAPVD1</i>	GTPase activating protein and VPS9 domains 1	0.68	0.0355
<i>NDUFA8</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	0.68	0.034
<i>CDK8</i>	cyclin-dependent kinase 8	0.68	0.0269
<i>DCAF16</i>	DDB1 and CUL4 associated factor 16	0.68	0.0119
<i>PMPCA</i>	peptidase (mitochondrial processing) alpha	0.68	0.0258
<i>UBXN8</i>	UBX domain protein 8	0.68	0.0148
<i>RASA1</i>	RAS p21 protein activator (GTPase activating protein) 1	0.69	0.0111
<i>BIN3</i>	bridging integrator 3	0.69	0.0167
<i>GTPBP8</i>	GTP-binding protein 8 (putative)	0.69	0.0373
<i>RHOT1</i>	ras homolog family member T1	0.69	0.015
<i>ERCC6</i>	excision repair cross-complementation group 6	0.69	0.0115
<i>GRSF1</i>	G-rich RNA sequence binding factor 1	0.69	0.0395
<i>CDC123</i>	cell division cycle 123	0.70	0.02
<i>GBP1</i>	guanylate binding protein 1, interferon-inducible	0.70	0.0282
<i>SEC11C</i>	SEC11 homolog C, signal peptidase complex subunit	0.70	0.0235
<i>IDH1</i>	isocitrate dehydrogenase 1 (NADP+)	0.70	0.0289
<i>PXMP4</i>	peroxisomal membrane protein 4	0.70	0.0134
<i>NSL1</i>	NSL1, MIS12 kinetochore complex component	0.70	0.0153
<i>WDR37</i>	WD repeat domain 37	0.70	0.0217
<i>EOGT</i>	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	0.70	0.0198
<i>PPP2R5E</i>	protein phosphatase 2, regulatory subunit B, epsilon isoform	0.70	0.0208
<i>HSD17B7</i>	hydroxysteroid (17-beta) dehydrogenase 7	0.70	0.0218
<i>UPF2</i>	UPF2 regulator of nonsense transcripts homolog (yeast)	0.70	0.00801
<i>MOSPD2</i>	motile sperm domain containing 2	0.70	0.0147
<i>HOXD4</i>	homeobox D4	0.71	0.00645
<i>PIGL</i>	phosphatidylinositol glycan anchor biosynthesis class L	0.71	0.0199
<i>GLRX3</i>	glutaredoxin 3	0.71	0.0253
<i>KDM5B</i>	lysine (K)-specific demethylase 5B	0.71	0.0164
<i>BMPR2</i>	bone morphogenetic protein receptor type II	0.71	0.0403
<i>BMPR1B</i>	bone morphogenetic protein receptor type IB	0.71	0.013
<i>PFDN4</i>	prefoldin subunit 4	0.71	0.0286
<i>HACD2</i>	3-hydroxyacyl-CoA dehydratase 2	0.71	0.0437
<i>CYP51A1</i>	cytochrome P450, family 51, subfamily A, polypeptide 1	0.71	0.0282
<i>MTA3</i>	metastasis associated 1 family member 3	0.71	0.0209
<i>CHSY1</i>	chondroitin sulfate synthase 1	0.71	0.021
<i>PDGFC</i>	platelet derived growth factor C	0.71	0.0265
<i>TXNIP</i>	thioredoxin interacting protein	0.72	0.0194
<i>EFR3A</i>	EFR3 homolog A	0.72	0.0106
<i>ARMC9</i>	armadillo repeat containing 9	0.72	0.0388
<i>TMEM203</i>	transmembrane protein 203	0.72	0.0494
<i>FKTN</i>	fukutin	0.72	0.0313
<i>RHOBTB3</i>	Rho-related BTB domain containing 3	0.72	0.0254
<i>SDHAF1</i>	succinate dehydrogenase complex assembly factor 1	0.72	0.0319
<i>ANKRD1</i>	ankyrin repeat domain 1 (cardiac muscle)	0.72	0.0405
<i>EXT1</i>	exostosin glycosyltransferase 1	0.72	0.0159
<i>CFAP20</i>	cilia and flagella associated protein 20	0.72	0.0225
<i>ZMYM2</i>	zinc finger, MYM-type 2	0.72	0.0474
<i>APPBP2</i>	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	0.72	0.0439
<i>MANSC1</i>	MANSC domain containing 1	0.72	0.0143
<i>GREB1L</i>	growth regulation by estrogen in breast cancer-like	0.72	0.0264
<i>ACYPI</i>	acylphosphatase 1, erythrocyte (common) type	0.72	0.0424
<i>EPPK1</i>	epiplakin 1	0.72	0.0142
<i>PPP3CB</i>	protein phosphatase 3, catalytic subunit, beta isozyme	0.72	0.044

<i>TRIM16</i>	tripartite motif containing 16	0.72	0.0314
<i>IWS1</i>	IWS1 homolog (S. cerevisiae)	0.72	0.0247
<i>UBE2W</i>	ubiquitin-conjugating enzyme E2W (putative)	0.72	0.023
<i>TBC1D19</i>	TBC1 domain family, member 19	0.72	0.035
<i>PARP4</i>	poly(ADP-ribose) polymerase family member 4	0.72	0.0225
<i>OSBPL10</i>	oxysterol binding protein-like 10	0.72	0.0118
<i>GLO1</i>	glyoxalase I	0.72	0.0251
<i>PARP1</i>	poly(ADP-ribose) polymerase 1	0.72	0.0229
<i>PPP1CB</i>	protein phosphatase 1, catalytic subunit, beta isozyme	0.72	0.0469
<i>HCN1</i>	hyperpolarization activated cyclic nucleotide gated potassium channel 1	0.72	0.0194
<i>GPNTB</i>	glycoprotein (transmembrane) nmb	0.72	0.034
<i>TRUB1</i>	TruB pseudouridine (psi) synthase family member 1	0.73	0.0221
<i>TOP2A</i>	topoisomerase (DNA) II alpha	0.73	0.0379
<i>KIF9</i>	kinesin family member 9	0.73	0.0247
<i>PARP14</i>	poly(ADP-ribose) polymerase family member 14	0.73	0.0403
<i>UCP2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	0.73	0.0234
<i>RAD51AP1</i>	RAD51 associated protein 1	0.73	0.0165
<i>FAM216A</i>	family with sequence similarity 216, member A	0.73	0.031
<i>MPRIIP</i>	myosin phosphatase Rho interacting protein	0.73	0.0293
<i>PCDH12</i>	protocadherin 12	0.73	0.0311
<i>PPID</i>	peptidylprolyl isomerase D	0.73	0.0177
<i>HDAC1</i>	histone deacetylase 1	0.73	0.021
<i>LZTR1</i>	leucine-zipper-like transcription regulator 1	0.73	0.0295
<i>TAF7</i>	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated	0.73	0.03
<i>TNNI3K</i>	TNNI3 interacting kinase	0.73	0.0258
<i>ACTC1</i>	actin, alpha, cardiac muscle 1	0.73	0.0264
<i>VAMP3</i>	vesicle associated membrane protein 3	0.73	0.0254
<i>ARPC4</i>	actin related protein 2/3 complex subunit 4	0.74	0.0322
<i>TPRKB</i>	TP53RK binding protein	0.74	0.0246
<i>IAH1</i>	isoamyl acetate-hydrolyzing esterase 1 homolog	0.74	0.0483
<i>CCT3</i>	chaperonin containing TCP1, subunit 3 (gamma)	0.74	0.0331
<i>GPC4</i>	glypican 4	0.74	0.0234
<i>ARL4A</i>	ADP-ribosylation factor like GTPase 4A	0.74	0.0437
<i>LMO1</i>	LIM domain only 1 (rhombotin 1)	0.74	0.0262
<i>RNF13</i>	ring finger protein 13	0.74	0.0472
<i>CCNL2</i>	cyclin L2	0.74	0.0303
<i>IFNAR2</i>	interferon (alpha, beta and omega) receptor 2	0.74	0.0385
<i>STK38</i>	serine/threonine kinase 38	0.74	0.0228
<i>C2orf49</i>	chromosome 2 open reading frame 49	0.74	0.0458
<i>NEO1</i>	neogenin 1	0.74	0.0402
<i>SNX27</i>	sorting nexin family member 27	0.74	0.031
<i>ING5</i>	inhibitor of growth family member 5	0.74	0.0364
<i>SERGEF</i>	secretion regulating guanine nucleotide exchange factor	0.74	0.049
<i>TRIM52</i>	tripartite motif containing 52	0.74	0.0449
<i>ANKRD42</i>	ankyrin repeat domain 42	0.74	0.0365
<i>SIMC1</i>	SUMO-interacting motifs containing 1	0.75	0.0408
<i>CNIH1</i>	connexin family AMPA receptor auxiliary protein 1	0.75	0.0453
<i>PPP1R2</i>	protein phosphatase 1, regulatory (inhibitor) subunit 2	0.75	0.0382
<i>TGDS</i>	TDP-glucose 4,6-dehydratase	0.75	0.0251
<i>TM2D1</i>	TM2 domain containing 1	0.75	0.0348
<i>PRPF18</i>	pre-mRNA processing factor 18	0.75	0.0237
<i>SNCAIP</i>	synuclein alpha interacting protein	0.75	0.0434
<i>JMY</i>	junction mediating and regulatory protein, p53 cofactor	0.75	0.0263
<i>DIRAS3</i>	DIRAS family, GTP-binding RAS-like 3	0.75	0.0493
<i>INPP1</i>	inositol polyphosphate-1-phosphatase	0.75	0.0471
<i>C1orf116</i>	chromosome 1 open reading frame 116	0.75	0.0333
<i>CEMP1</i>	cell migration inducing protein, hyaluronan binding	0.75	0.0382
<i>ARL8B</i>	ADP-ribosylation factor like GTPase 8B	0.75	0.0382
<i>PTPRG</i>	protein tyrosine phosphatase, receptor type, G	0.75	0.0359

<i>ZRANB1</i>	zinc finger, RAN-binding domain containing 1	0.76	0.0329
<i>SEPHS2</i>	selenophosphate synthetase 2	0.76	0.0373
<i>CISD2</i>	CDGSH iron sulfur domain 2	0.76	0.0396
<i>RIPK1</i>	receptor (TNFRSF)-interacting serine-threonine kinase 1	0.76	0.0377
<i>ASCC3</i>	activating signal cointegrator 1 complex subunit 3	0.76	0.0326
<i>DMWD</i>	dystrophia myotonica, WD repeat containing	0.76	0.0366
<i>NRIP3</i>	nuclear receptor interacting protein 3	0.76	0.0315
<i>PHGDH</i>	phosphoglycerate dehydrogenase	0.76	0.0279
<i>NSD1</i>	nuclear receptor binding SET domain protein 1	0.76	0.0487
<i>ELMO2</i>	engulfment and cell motility 2	0.76	0.0365
<i>DIXDC1</i>	DIX domain containing 1	0.76	0.0373
<i>ATP6V1C2</i>	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	0.76	0.0466
<i>VTI1B</i>	vesicle transport through interaction with t-SNAREs 1B	0.76	0.0484
<i>METTL2B</i>	methyltransferase like 2B	0.76	0.0407
<i>OCRL</i>	oculocerebrorenal syndrome of Lowe	0.77	0.0384
<i>PHLPP2</i>	PH domain and leucine rich repeat protein phosphatase 2	0.77	0.0415
<i>EDA2R</i>	ectodysplasin A2 receptor	0.77	0.0446
<i>B3GALT4</i>	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 4	0.77	0.0338
<i>TMEM25</i>	transmembrane protein 25	0.77	0.0351
<i>ZNF880</i>	zinc finger protein 880	0.77	0.0404
<i>PHLDB2</i>	pleckstrin homology-like domain, family B, member 2	0.77	0.0403
<i>TUBAL3</i>	tubulin, alpha-like 3	0.77	0.0422
<i>PTPN3</i>	protein tyrosine phosphatase, non-receptor type 3	0.77	0.0408
<i>SKIL</i>	SKI-like proto-oncogene	0.78	0.0497
<i>PHF6</i>	PHD finger protein 6	0.78	0.0416

Table S5. IDMF-increased genes (P < 0.05 with FC > 1.25). The table lists 673 IDMF-increased genes ranked by estimated fold-change (FC) (IDMF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group; *FDR < 0.10).

Symbol	Description	FC	P-value
<i>ALDH1L1</i>	aldehyde dehydrogenase 1 family, member L1	2.37	1.93e-05*
<i>C9orf24</i>	chromosome 9 open reading frame 24	1.91	8.14e-05*
<i>OSGIN1</i>	oxidative stress induced growth inhibitor 1	1.88	3.46e-05*
<i>ZDHHC11B</i>	zinc finger, DHHC-type containing 11B	1.85	8.42e-05*
<i>OIT3</i>	oncoprotein induced transcript 3	1.81	6.88e-05*
<i>LPAR2</i>	lysophosphatidic acid receptor 2	1.79	0.000161*
<i>CDRT1</i>	CMT1A duplicated region transcript 1	1.76	0.000131*
<i>OR2M7</i>	olfactory receptor, family 2, subfamily M, member 7	1.71	0.000324
<i>LY6G6C</i>	lymphocyte antigen 6 complex, locus G6C	1.70	0.000394
<i>ALG1</i>	ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase	1.69	0.000793
<i>C9orf131</i>	chromosome 9 open reading frame 131	1.65	0.000398
<i>SMIM6</i>	small integral membrane protein 6	1.63	0.00235
<i>ATF3</i>	activating transcription factor 3	1.62	0.000446
<i>KNDC1</i>	Transcript Identified by AceView, Entrez Gene ID(s) 85442	1.60	0.00765
<i>HCAR3</i>	hydroxycarboxylic acid receptor 3	1.60	0.00216
<i>ULK3</i>	unc-51 like kinase 3	1.60	0.00113
<i>P4HTM</i>	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	1.60	0.00227
<i>TYR</i>	tyrosinase	1.60	0.00171
<i>MCEMP1</i>	mast cell-expressed membrane protein 1	1.59	0.000766
<i>SPATA25</i>	spermatogenesis associated 25	1.59	0.0018
<i>LSMEM1</i>	leucine-rich single-pass membrane protein 1	1.59	0.000802
<i>ALPI</i>	alkaline phosphatase, intestinal	1.59	0.00108
<i>MXD1</i>	MAX dimerization protein 1	1.58	0.00104
<i>TLX1</i>	T-cell leukemia homeobox 1	1.58	0.0145
<i>TMEM174</i>	transmembrane protein 174	1.58	0.00195
<i>ISX</i>	intestine-specific homeobox	1.58	0.0122
<i>CCL16</i>	chemokine (C-C motif) ligand 16	1.58	0.00133
<i>NLRP9</i>	NLR family, pyrin domain containing 9	1.57	0.0017
<i>LRRC46</i>	leucine rich repeat containing 46	1.57	0.00222
<i>DOK4</i>	docking protein 4	1.57	0.00185
<i>GATA4</i>	GATA binding protein 4	1.57	0.000767
<i>TRIM73</i>	tripartite motif containing 73	1.57	0.000989
<i>TMEM39B</i>	transmembrane protein 39B	1.56	0.00181
<i>KCTD21</i>	potassium channel tetramerization domain containing 21	1.55	0.00177
<i>BEST1</i>	bestrophin 1	1.55	0.00152
<i>SLC5A5</i>	solute carrier family 5 (sodium/iodide cotransporter), member 5	1.55	0.00454
<i>JPH3</i>	junctophilin 3	1.54	0.00311
<i>DMRTC1</i>	DMRT-like family C1	1.54	0.00479
<i>CYP17A1</i>	cytochrome P450, family 17, subfamily A, polypeptide 1	1.53	0.00187
<i>HMOX1</i>	heme oxygenase 1	1.53	0.0014
<i>CD33</i>	CD33 molecule	1.53	0.00116
<i>ISG20</i>	interferon stimulated exonuclease gene 20kDa	1.53	0.0043
<i>CST9</i>	cystatin 9 (testatin)	1.53	0.00217
<i>RASL10B</i>	RAS-like, family 10, member B	1.52	0.00329
<i>ARHGEF38</i>	Rho guanine nucleotide exchange factor 38	1.52	0.00141
<i>SEMA4D</i>	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript	1.52	0.00429
<i>OR9A2</i>	olfactory receptor, family 9, subfamily A, member 2	1.52	0.00289
<i>SH2B2</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.51	0.0286
<i>MYO15B</i>	myosin XVB	1.51	0.00219
<i>SIRT7</i>	sirtuin 7	1.51	0.00185
<i>FAM89A</i>	family with sequence similarity 89, member A	1.51	0.00318
<i>ALDH4A1</i>	aldehyde dehydrogenase 4 family, member A1	1.51	0.00586
<i>RBM39</i>	RNA binding motif protein 39	1.51	0.00429
<i>USP17L21</i>	ubiquitin specific peptidase 17-like family member 21	1.50	0.00242

<i>GSR</i>	glutathione reductase	1.50	0.00203
<i>PTH1H</i>	parathyroid hormone-like hormone	1.50	0.00336
<i>NBL1</i>	neuroblastoma 1, DAN family BMP antagonist	1.50	0.00457
<i>TGFBR3L</i>	transforming growth factor beta receptor III like	1.50	0.00458
<i>CENPP</i>	centromere protein P	1.50	0.00674
<i>SHCBP1</i>	SHC SH2-domain binding protein 1	1.49	0.00307
<i>MCM4</i>	minichromosome maintenance complex component 4	1.49	0.0102
<i>NEURL2</i>	neuralized E3 ubiquitin protein ligase 2	1.49	0.00547
<i>WFDC6</i>	WAP four-disulfide core domain 6	1.49	0.00498
<i>LRRC38</i>	leucine rich repeat containing 38	1.49	0.00498
<i>SLC39A2</i>	solute carrier family 39 (zinc transporter), member 2	1.49	0.00769
<i>NDUFAF6</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	1.48	0.0159
<i>OR10R2</i>	olfactory receptor, family 10, subfamily R, member 2	1.48	0.00387
<i>GHRHR</i>	growth hormone releasing hormone receptor	1.48	0.00324
<i>SLC7A11</i>	solute carrier family 7 (anionic amino acid transporter light chain, xc- system),	1.48	0.00305
<i>CFAP46</i>	cilia and flagella associated protein 46	1.48	0.00556
<i>MEGF6</i>	multiple EGF-like-domains 6	1.48	0.00417
<i>CPEB1</i>	cytoplasmic polyadenylation element binding protein 1	1.48	0.00754
<i>SHANK2</i>	SH3 and multiple ankyrin repeat domains 2	1.48	0.00644
<i>TMED9</i>	transmembrane p24 trafficking protein 9	1.48	0.012
<i>PRSS58</i>	protease, serine, 58	1.48	0.00286
<i>FAM156A</i>	family with sequence similarity 156, member A	1.48	0.00416
<i>SMNDC1</i>	survival motor neuron domain containing 1	1.48	0.00739
<i>MCCC1</i>	methylenecrotonyl-CoA carboxylase 1	1.48	0.0115
<i>CMTM2</i>	CKLF-like MARVEL transmembrane domain containing 2	1.47	0.00761
<i>CDK2</i>	cyclin-dependent kinase 2	1.47	0.0338
<i>POTEB</i>	POTE ankyrin domain family, member B	1.47	0.0103
<i>MYL3</i>	myosin, light chain 3, alkali; ventricular, skeletal, slow	1.47	0.00477
<i>MICAL1</i>	Jeck2013 ANTISENSE, coding, INTERNAL, intronic best transcript	1.47	0.00776
<i>TRIM49C</i>	tripartite motif containing 49C	1.47	0.00283
<i>PPM1G</i>	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1G	1.47	0.0101
<i>RNF40</i>	ring finger protein 40, E3 ubiquitin protein ligase	1.47	0.00307
<i>SVEP1</i>	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.47	0.00279
<i>NCS1</i>	neuronal calcium sensor 1	1.47	0.00664
<i>TP53INP2</i>	tumor protein p53 inducible nuclear protein 2	1.47	0.00724
<i>USP17L24</i>	ubiquitin specific peptidase 17-like family member 24	1.46	0.00608
<i>USP17L25</i>	ubiquitin specific peptidase 17-like family member 25	1.46	0.00608
<i>GUCY1A2</i>	guanylate cyclase 1, soluble, alpha 2	1.46	0.00774
<i>HAPLN3</i>	hyaluronan and proteoglycan link protein 3	1.46	0.00677
<i>L3MBTL4</i>	l(3)mbt-like 4 (Drosophila)	1.46	0.0155
<i>COLGALT2</i>	collagen beta(1-O)galactosyltransferase 2	1.46	0.00676
<i>RASSF2</i>	Memczak2013 ANTISENSE, coding, INTERNAL, UTR3 best transcript	1.46	0.00643
<i>LRRC43</i>	leucine rich repeat containing 43	1.46	0.0197
<i>DOC2B</i>	double C2-like domains, beta	1.46	0.0179
<i>OR2L2</i>	olfactory receptor, family 2, subfamily L, member 2	1.46	0.00782
<i>UBL4A</i>	ubiquitin-like 4A	1.45	0.00477
<i>IGSF8</i>	immunoglobulin superfamily, member 8	1.45	0.00833
<i>AFF2</i>	AF4/FMR2 family, member 2	1.45	0.0203
<i>PLA2G2D</i>	phospholipase A2, group IID	1.45	0.00478
<i>CST7</i>	cystatin F (leukocystatin)	1.45	0.00512
<i>OR52D1</i>	olfactory receptor, family 52, subfamily D, member 1	1.45	0.00863
<i>FER1L5</i>	fer-1-like family member 5	1.45	0.00704
<i>OR1B1</i>	olfactory receptor, family 1, subfamily B, member 1 (gene/pseudogene)	1.45	0.00785
<i>MTFP1</i>	mitochondrial fission process 1	1.45	0.00902
<i>SNRNP70</i>	small nuclear ribonucleoprotein, U1 70kDa subunit	1.45	0.00435
<i>RPEL1</i>	ribulose-5-phosphate-3-epimerase-like 1	1.45	0.0217
<i>ITGA9</i>	integrin alpha 9	1.45	0.0108
<i>POLE</i>	polymerase (DNA directed), epsilon, catalytic subunit	1.45	0.00577
<i>TNP1</i>	transition protein 1 (during histone to protamine replacement)	1.44	0.0249

<i>KIAA1614</i>	KIAA1614	1.44	0.00539
<i>SLC6A6</i>	solute carrier family 6 (neurotransmitter transporter), member 6	1.44	0.0053
<i>SCYL3</i>	SCY1-like, kinase-like 3	1.44	0.00711
<i>TMEM175</i>	transmembrane protein 175	1.44	0.00566
<i>CDH18</i>	cadherin 18, type 2	1.44	0.00983
<i>ACSL6</i>	acyl-CoA synthetase long-chain family member 6	1.44	0.011
<i>SERPINE3</i>	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1),	1.44	0.00791
<i>TRIOBP</i>	TRIO and F-actin binding protein	1.44	0.0113
<i>EGR1</i>	early growth response 1	1.44	0.00911
<i>KIF26A</i>	kinesin family member 26A	1.44	0.0087
<i>GPR101</i>	G protein-coupled receptor 101	1.44	0.0111
<i>USP17L27</i>	ubiquitin specific peptidase 17-like family member 27	1.43	0.00939
<i>USP17L29</i>	ubiquitin specific peptidase 17-like family member 29	1.43	0.00939
<i>HLA-DRB5</i>	major histocompatibility complex, class II, DR beta 5	1.43	0.00696
<i>CAV3</i>	caveolin 3	1.43	0.0246
<i>BMP7</i>	bone morphogenetic protein 7	1.43	0.0113
<i>TRPV6</i>	transient receptor potential cation channel, subfamily V, member 6	1.43	0.00579
<i>PPP1R10</i>	protein phosphatase 1, regulatory subunit 10	1.43	0.00599
<i>DYRK1A</i>	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	1.43	0.00797
<i>POP4</i>	POP4 homolog, ribonuclease P/MRP subunit	1.43	0.0142
<i>FAT2</i>	FAT atypical cadherin 2	1.43	0.0106
<i>BTNL2</i>	butyrophilin-like 2	1.43	0.0158
<i>ZNF778</i>	zinc finger protein 778	1.43	0.0164
<i>RFFL</i>	ring finger and FYVE-like domain containing E3 ubiquitin protein ligase	1.43	0.0113
<i>DPYD</i>	dihydropyrimidine dehydrogenase	1.42	0.0103
<i>PKNOX2</i>	PBX/knotted 1 homeobox 2	1.42	0.00893
<i>FOXC2</i>	forkhead box C2	1.42	0.0175
<i>APOBEC2</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	1.42	0.00709
<i>TLCD2</i>	TLC domain containing 2	1.42	0.0159
<i>CCL3</i>	chemokine (C-C motif) ligand 3	1.42	0.0172
<i>EVPL</i>	envoplakin	1.42	0.00828
<i>WFDC12</i>	WAP four-disulfide core domain 12	1.42	0.00653
<i>FRG2B</i>	FSHD region gene 2 family, member B	1.42	0.00842
<i>GP9</i>	glycoprotein IX (platelet)	1.42	0.0107
<i>ABCA4</i>	ATP binding cassette subfamily A member 4	1.42	0.013
<i>SAMD4A</i>	sterile alpha motif domain containing 4A	1.42	0.0119
<i>RASL11A</i>	RAS-like, family 11, member A	1.42	0.00866
<i>OR4K14</i>	olfactory receptor, family 4, subfamily K, member 14	1.42	0.0143
<i>DMRTC1B</i>	DMRT-like family C1B	1.42	0.0185
<i>KLHL33</i>	kelch-like family member 33	1.42	0.00636
<i>DNLZ</i>	DNL-type zinc finger	1.42	0.00762
<i>C10orf95</i>	chromosome 10 open reading frame 95	1.42	0.0121
<i>SNAPC4</i>	Zhang2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic	1.42	0.0161
<i>CD14</i>	CD14 molecule	1.41	0.0249
<i>GAGE4</i>	G antigen 4	1.41	0.0158
<i>ZFP62</i>	ZFP62 zinc finger protein	1.41	0.0155
<i>TCP11X2</i>	t-complex 11 family, X-linked 2	1.41	0.0106
<i>TIGD5</i>	tigger transposable element derived 5	1.41	0.0227
<i>ADAP1</i>	ArfGAP with dual PH domains 1	1.41	0.00872
<i>ZNF671</i>	zinc finger protein 671	1.41	0.0121
<i>SLC5A2</i>	solute carrier family 5 (sodium/glucose cotransporter), member 2	1.41	0.0133
<i>LY6G5C</i>	lymphocyte antigen 6 complex, locus G5C	1.41	0.0118
<i>LMX1A</i>	LIM homeobox transcription factor 1, alpha	1.41	0.00677
<i>TRIM49B</i>	tripartite motif containing 49B	1.41	0.0135
<i>TMIE</i>	transmembrane inner ear	1.41	0.0164
<i>SLC22A14</i>	solute carrier family 22, member 14	1.41	0.0177
<i>APOC2</i>	apolipoprotein C-II	1.41	0.0124
<i>HSPBP1</i>	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	1.41	0.00832
<i>RPRML</i>	reprimo-like	1.41	0.0073

<i>DCX</i>	doublecortin	1.41	0.00841
<i>OR52M1</i>	olfactory receptor, family 52, subfamily M, member 1	1.41	0.0146
<i>MC1R</i>	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	1.41	0.0128
<i>SLC24A1</i>	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	1.41	0.00838
<i>FGF10</i>	fibroblast growth factor 10	1.41	0.00839
<i>CLDN18</i>	claudin 18	1.41	0.0151
<i>CNPPD1</i>	cyclin Pas1/PHO80 domain containing 1	1.41	0.00864
<i>CES1</i>	carboxylesterase 1	1.41	0.0218
<i>FAM13A</i>	family with sequence similarity 13, member A	1.41	0.00736
<i>TBX5</i>	T-box 5	1.41	0.00905
<i>GTSF1L</i>	gametocyte specific factor 1-like	1.41	0.0098
<i>SLC39A7</i>	solute carrier family 39 (zinc transporter), member 7	1.41	0.00901
<i>CIQA</i>	complement component 1, q subcomponent, A chain	1.41	0.0129
<i>CARD14</i>	caspase recruitment domain family, member 14	1.41	0.0189
<i>TAZ</i>	tafazzin	1.41	0.00645
<i>KRTAP20-1</i>	keratin associated protein 20-1	1.40	0.0133
<i>COA1</i>	cytochrome c oxidase assembly factor 1 homolog	1.40	0.0386
<i>RBM26</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.40	0.028
<i>BCAT2</i>	branched chain amino-acid transaminase 2, mitochondrial	1.40	0.0087
<i>MYCL</i>	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	1.40	0.012
<i>KRTAP23-1</i>	keratin associated protein 23-1	1.40	0.021
<i>CDK5R1</i>	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	1.40	0.0192
<i>NUP35</i>	nucleoporin 35kDa	1.40	0.012
<i>ZNF366</i>	zinc finger protein 366	1.40	0.014
<i>NR1D1</i>	nuclear receptor subfamily 1, group D, member 1	1.40	0.011
<i>CADM4</i>	cell adhesion molecule 4	1.40	0.0126
<i>TRIM74</i>	tripartite motif containing 74	1.40	0.0098
<i>SNX8</i>	sorting nexin 8	1.40	0.0147
<i>HES3</i>	hes family bHLH transcription factor 3	1.40	0.0183
<i>FOXI1</i>	forkhead box I1	1.40	0.0217
<i>SLC29A4</i>	solute carrier family 29 (equilibrative nucleoside transporter), member 4	1.40	0.023
<i>AQP7</i>	aquaporin 7	1.40	0.0125
<i>KDM4E</i>	lysine (K)-specific demethylase 4E	1.40	0.0103
<i>C3orf35</i>	chromosome 3 open reading frame 35	1.40	0.0242
<i>BMP10</i>	bone morphogenetic protein 10	1.40	0.0154
<i>ETV2</i>	ets variant 2	1.40	0.0161
<i>PRB1</i>	proline-rich protein BstNI subfamily 1	1.39	0.0184
<i>PTPRN</i>	protein tyrosine phosphatase, receptor type, N	1.39	0.0256
<i>SLC7A6</i>	solute carrier family 7 (amino acid transporter light chain, y+L system), member	1.39	0.0115
<i>HNRNPF</i>	heterogeneous nuclear ribonucleoprotein F	1.39	0.0162
<i>ADAM22</i>	ADAM metalloproteinase domain 22	1.39	0.0293
<i>ESRRG</i>	estrogen-related receptor gamma	1.39	0.00989
<i>SPNS1</i>	spinster homolog 1 (Drosophila)	1.39	0.0119
<i>OLFM4</i>	olfactomedin 4	1.39	0.0104
<i>DNASE1</i>	deoxyribonuclease I	1.39	0.0123
<i>CHST5</i>	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	1.39	0.014
<i>PLAC8L1</i>	PLAC8-like 1	1.39	0.0198
<i>CNP</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.39	0.0139
<i>SLC1A2</i>	solute carrier family 1 (glial high affinity glutamate transporter), member 2	1.39	0.0105
<i>SRXN1</i>	sulfiredoxin 1	1.39	0.0143
<i>SMCO2</i>	single-pass membrane protein with coiled-coil domains 2	1.39	0.0213
<i>FAM166A</i>	family with sequence similarity 166, member A	1.39	0.0167
<i>MC2R</i>	melanocortin 2 receptor (adrenocorticotrophic hormone)	1.39	0.0143
<i>SLC17A6</i>	solute carrier family 17 (vesicular glutamate transporter), member 6	1.39	0.0122
<i>PRRG2</i>	proline rich Gla (G-carboxyglutamic acid) 2	1.39	0.0363
<i>KLHL3</i>	kelch-like family member 3	1.39	0.0139
<i>PDE3A</i>	phosphodiesterase 3A, cGMP-inhibited	1.39	0.018
<i>LMO3</i>	LIM domain only 3 (rhombotin-like 2)	1.39	0.0143
<i>PIK3R5</i>	phosphoinositide-3-kinase, regulatory subunit 5	1.39	0.0238

<i>DUX4</i>	double homeobox 4	1.39	0.0217
<i>BEAN1</i>	brain expressed, associated with NEDD4, 1	1.39	0.0255
<i>SCAF1</i>	SR-related CTD-associated factor 1	1.39	0.0179
<i>MDC1</i>	mediator of DNA-damage checkpoint 1	1.39	0.0204
<i>CBFA2T3</i>	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1.39	0.0162
<i>TKT</i>	transketolase	1.39	0.00914
<i>APOBEC3H</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H	1.38	0.016
<i>LOC730183</i>	uncharacterized LOC730183	1.38	0.0312
<i>CSAD</i>	cysteine sulfinic acid decarboxylase	1.38	0.0224
<i>C8orf34</i>	chromosome 8 open reading frame 34	1.38	0.0147
<i>OSBP2</i>	oxysterol binding protein 2	1.38	0.0292
<i>CHRNA1</i>	cholinergic receptor, nicotinic alpha 1	1.38	0.0226
<i>CIQTNF8</i>	C1q and tumor necrosis factor related protein 8	1.38	0.0104
<i>ALKBH4</i>	alkB homolog 4, lysine demethylase	1.38	0.0461
<i>MRRF</i>	mitochondrial ribosome recycling factor	1.38	0.0118
<i>MST1L</i>	macrophage stimulating 1-like	1.38	0.0141
<i>PLA2G5</i>	phospholipase A2, group V	1.38	0.0149
<i>LGII</i>	leucine-rich, glioma inactivated 1	1.38	0.0161
<i>FAM71F1</i>	family with sequence similarity 71, member F1	1.38	0.0234
<i>PTOV1</i>	prostate tumor overexpressed 1	1.38	0.0233
<i>ZNF233</i>	zinc finger protein 233	1.38	0.0173
<i>AVP11</i>	arginine vasopressin-induced 1	1.38	0.0138
<i>SLC6A4</i>	solute carrier family 6 (neurotransmitter transporter), member 4	1.38	0.0144
<i>F10</i>	coagulation factor X	1.38	0.0278
<i>CST2</i>	cystatin SA	1.38	0.0163
<i>SYT4</i>	synaptotagmin IV	1.38	0.0215
<i>SELPLG</i>	selectin P ligand	1.38	0.0183
<i>RAB3IL1</i>	RAB3A interacting protein (rabin3)-like 1	1.38	0.0128
<i>CKMT1A</i>	creatine kinase, mitochondrial 1A	1.38	0.0329
<i>C1orf53</i>	chromosome 1 open reading frame 53	1.38	0.0126
<i>HSFX2</i>	heat shock transcription factor family, X-linked 2	1.38	0.0104
<i>LAPTM5</i>	lysosomal protein transmembrane 5	1.38	0.0123
<i>ST6GALNAC1</i>	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-	1.38	0.0137
<i>AOC2</i>	amine oxidase, copper containing 2 (retina-specific)	1.38	0.0144
<i>NUDT7</i>	nudix hydrolase 7	1.38	0.0114
<i>OR4A5</i>	olfactory receptor, family 4, subfamily A, member 5	1.37	0.022
<i>TSPAN7</i>	tetraspanin 7	1.37	0.0161
<i>SPRR2E</i>	small proline-rich protein 2E	1.37	0.019
<i>PBXIP1</i>	pre-B-cell leukemia homeobox interacting protein 1	1.37	0.0133
<i>XAGE1B</i>	X antigen family, member 1B	1.37	0.0131
<i>ALAD</i>	aminolevulinate dehydratase	1.37	0.019
<i>DAPL1</i>	death associated protein like 1	1.37	0.0203
<i>IDH3A</i>	isocitrate dehydrogenase 3 (NAD+) alpha	1.37	0.0241
<i>IGSF22</i>	immunoglobulin superfamily, member 22	1.37	0.0294
<i>TPPP3</i>	tubulin polymerization-promoting protein family member 3	1.37	0.0452
<i>MUC16</i>	mucin 16, cell surface associated	1.37	0.0227
<i>OTOL1</i>	otolin 1	1.37	0.0163
<i>ACVR1</i>	activin A receptor type I	1.37	0.0185
<i>SCGB1D4</i>	secretoglobin, family 1D, member 4	1.37	0.0212
<i>ELOVL5</i>	ELOVL fatty acid elongase 5	1.37	0.0162
<i>SPP1</i>	secreted phosphoprotein 1	1.37	0.0123
<i>USP17L28</i>	ubiquitin specific peptidase 17-like family member 28	1.37	0.0216
<i>LDHC</i>	lactate dehydrogenase C	1.37	0.0261
<i>FAM219A</i>	family with sequence similarity 219, member A	1.37	0.0322
<i>TEX9</i>	testis expressed 9	1.37	0.0159
<i>ADPRHL1</i>	ADP-ribosylhydrolase like 1	1.37	0.0119
<i>POLR2D</i>	polymerase (RNA) II (DNA directed) polypeptide D	1.37	0.0253
<i>FGF8</i>	fibroblast growth factor 8 (androgen-induced)	1.37	0.0304
<i>TMEM128</i>	transmembrane protein 128	1.37	0.0236

<i>OR2T27</i>	olfactory receptor, family 2, subfamily T, member 27	1.37	0.0172
<i>MAGEB10</i>	MAGE family member B10	1.37	0.0155
<i>LY6D</i>	lymphocyte antigen 6 complex, locus D	1.37	0.018
<i>USP17L26</i>	ubiquitin specific peptidase 17-like family member 26	1.37	0.0214
<i>SRD5A1</i>	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-	1.37	0.0395
<i>DEGS2</i>	delta(4)-desaturase, sphingolipid 2	1.36	0.0168
<i>MYLK3</i>	myosin light chain kinase 3	1.36	0.018
<i>FABP6</i>	fatty acid binding protein 6, ileal	1.36	0.0178
<i>MLLT11</i>	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11	1.36	0.0185
<i>ACSM2B</i>	acyl-CoA synthetase medium-chain family member 2B	1.36	0.0248
<i>RIBC1</i>	RIB43A domain with coiled-coils 1	1.36	0.0143
<i>IL1R2</i>	interleukin 1 receptor, type II	1.36	0.0214
<i>GPR6</i>	G protein-coupled receptor 6	1.36	0.0196
<i>ELAC1</i>	elaC ribonuclease Z 1	1.36	0.029
<i>PCSK6</i>	proprotein convertase subtilisin/kexin type 6	1.36	0.0414
<i>CCDC154</i>	coiled-coil domain containing 154	1.36	0.0159
<i>OR52E8</i>	olfactory receptor, family 52, subfamily E, member 8	1.36	0.0149
<i>ISL1</i>	Transcript Identified by AceView, Entrez Gene ID(s) 3670	1.36	0.022
<i>ARHGEF39</i>	Rho guanine nucleotide exchange factor 39	1.36	0.0187
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	1.36	0.0263
<i>CBY3</i>	chibby homolog 3 (Drosophila)	1.36	0.021
<i>PREX1</i>	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic	1.36	0.0298
<i>NAT10</i>	N-acetyltransferase 10 (GCN5-related)	1.36	0.0199
<i>DISC1</i>	disrupted in schizophrenia 1	1.36	0.0233
<i>DEFA3</i>	defensin, alpha 3, neutrophil-specific	1.36	0.0426
<i>HNRNPCL2</i>	heterogeneous nuclear ribonucleoprotein C-like 2	1.36	0.0175
<i>PGS1</i>	phosphatidylglycerophosphate synthase 1	1.36	0.0258
<i>RARRES2</i>	retinoic acid receptor responder (tazarotene induced) 2	1.36	0.0224
<i>CSF3</i>	colony stimulating factor 3	1.36	0.0278
<i>COQ2</i>	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase	1.36	0.0387
<i>SLC4A8</i>	solute carrier family 4, sodium bicarbonate cotransporter, member 8	1.36	0.0218
<i>RAPGEF3</i>	Rap guanine nucleotide exchange factor 3	1.36	0.0176
<i>AVPR1B</i>	arginine vasopressin receptor 1B	1.36	0.0235
<i>SERTAD3</i>	SERTA domain containing 3	1.36	0.0236
<i>DEFB106A</i>	defensin, beta 106A	1.36	0.0364
<i>KRT38</i>	keratin 38, type I	1.36	0.0273
<i>MTURN</i>	maturin, neural progenitor differentiation regulator homolog (Xenopus)	1.36	0.0286
<i>PCP2</i>	Purkinje cell protein 2	1.36	0.0318
<i>CEP170B</i>	centrosomal protein 170B	1.36	0.0224
<i>ADGRE2</i>	adhesion G protein-coupled receptor E2	1.36	0.0153
<i>ASAP3</i>	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	1.36	0.0354
<i>ANGPTL4</i>	angiopoietin like 4	1.36	0.0222
<i>TRMT1</i>	tRNA methyltransferase 1	1.35	0.0449
<i>LCE5A</i>	late cornified envelope 5A	1.35	0.0203
<i>HDAC10</i>	histone deacetylase 10	1.35	0.0246
<i>ZFHX3</i>	zinc finger homeobox 3	1.35	0.0185
<i>NUBP2</i>	nucleotide binding protein 2	1.35	0.016
<i>USP17L22</i>	ubiquitin specific peptidase 17-like family member 22	1.35	0.0214
<i>EPHA10</i>	EPH receptor A10	1.35	0.0183
<i>SLC28A2</i>	solute carrier family 28 (concentrative nucleoside transporter), member 2	1.35	0.0185
<i>HNRNPA1L2</i>	heterogeneous nuclear ribonucleoprotein A1-like 2	1.35	0.0185
<i>IL20RB</i>	interleukin 20 receptor beta	1.35	0.0213
<i>DAND5</i>	DAN domain family member 5, BMP antagonist	1.35	0.0217
<i>CNR2</i>	cannabinoid receptor 2	1.35	0.0153
<i>DTX2</i>	deltex 2, E3 ubiquitin ligase	1.35	0.0303
<i>PROP1</i>	PROP paired-like homeobox 1	1.35	0.0253
<i>OR7D2</i>	olfactory receptor, family 7, subfamily D, member 2	1.35	0.0275
<i>ENO4</i>	enolase family member 4	1.35	0.0178
<i>FGB</i>	fibrinogen beta chain	1.35	0.0198

<i>SPACA5B</i>	sperm acrosome associated 5B	1.35	0.0311
<i>AKNA</i>	AT-hook transcription factor	1.35	0.0471
<i>CPNE2</i>	copine II	1.35	0.0258
<i>LRP1B</i>	LDL receptor related protein 1B	1.35	0.0475
<i>VSIG8</i>	V-set and immunoglobulin domain containing 8	1.35	0.027
<i>OPA3</i>	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	1.35	0.0284
<i>GMPR</i>	guanosine monophosphate reductase	1.35	0.02
<i>CNIH2</i>	cornichon family AMPA receptor auxiliary protein 2	1.35	0.0369
<i>XYLT2</i>	xylosyltransferase II	1.35	0.0212
<i>LCE3B</i>	late cornified envelope 3B	1.35	0.0345
<i>ITLN1</i>	intelectin 1 (galactofuranose binding)	1.35	0.0306
<i>GNG8</i>	guanine nucleotide binding protein (G protein), gamma 8	1.35	0.0344
<i>GREB1</i>	growth regulation by estrogen in breast cancer 1	1.35	0.034
<i>ZNF582</i>	zinc finger protein 582	1.35	0.0162
<i>OR4K13</i>	olfactory receptor, family 4, subfamily K, member 13	1.35	0.019
<i>PLA2G10</i>	phospholipase A2, group X	1.35	0.0352
<i>SLC22A9</i>	solute carrier family 22 (organic anion transporter), member 9	1.35	0.0308
<i>MAOA</i>	monoamine oxidase A	1.35	0.0355
<i>LIMCH1</i>	LIM and calponin homology domains 1	1.35	0.0431
<i>FAM71A</i>	family with sequence similarity 71, member A	1.35	0.0432
<i>ARID1B</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.35	0.0499
<i>KRTAP3-2</i>	keratin associated protein 3-2	1.35	0.0451
<i>IGFN1</i>	immunoglobulin-like and fibronectin type III domain containing 1	1.35	0.0242
<i>FUT9</i>	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	1.35	0.0288
<i>FOLH1</i>	folate hydrolase (prostate-specific membrane antigen) 1	1.35	0.028
<i>SLC35F3</i>	solute carrier family 35, member F3	1.35	0.0393
<i>CCDC42</i>	coiled-coil domain containing 42	1.35	0.0409
<i>ZNF831</i>	zinc finger protein 831	1.34	0.039
<i>GRK7</i>	G protein-coupled receptor kinase 7	1.34	0.0211
<i>DPH5</i>	diphthamide biosynthesis 5	1.34	0.0278
<i>TBXAS1</i>	thromboxane A synthase 1 (platelet)	1.34	0.0243
<i>ULBP2</i>	UL16 binding protein 2	1.34	0.0193
<i>MEX3B</i>	mex-3 RNA binding family member B	1.34	0.0169
<i>OR6B2</i>	olfactory receptor, family 6, subfamily B, member 2	1.34	0.0353
<i>CREG2</i>	cellular repressor of E1A-stimulated genes 2	1.34	0.0261
<i>PTMS</i>	parathymosin	1.34	0.0259
<i>ZPBP2</i>	zona pellucida binding protein 2	1.34	0.0247
<i>MLN</i>	motilin	1.34	0.032
<i>ARNT</i>	aryl hydrocarbon receptor nuclear translocator	1.34	0.0278
<i>MTMR11</i>	myotubularin related protein 11	1.34	0.0265
<i>GIMAP6</i>	GTPase, IMAF family member 6	1.34	0.0471
<i>FANCA</i>	Fanconi anemia complementation group A	1.34	0.0186
<i>HAP1</i>	huntingtin-associated protein 1	1.34	0.0332
<i>DPEP2</i>	dipeptidase 2	1.34	0.0286
<i>TMBIM1</i>	transmembrane BAX inhibitor motif containing 1	1.34	0.0299
<i>CAPN12</i>	calpain 12	1.34	0.0237
<i>WDR7</i>	WD repeat domain 7	1.34	0.0266
<i>TBATA</i>	thymus, brain and testes associated	1.34	0.0209
<i>ZNF284</i>	zinc finger protein 284	1.34	0.0295
<i>ZNF214</i>	zinc finger protein 214	1.34	0.0324
<i>ADGRF3</i>	adhesion G protein-coupled receptor F3	1.34	0.0319
<i>AANAT</i>	aralkylamine N-acetyltransferase	1.34	0.0175
<i>MED14</i>	mediator complex subunit 14	1.34	0.0437
<i>FXYP7</i>	FXYP domain containing ion transport regulator 7	1.34	0.0237
<i>PNPLA1</i>	patatin-like phospholipase domain containing 1	1.34	0.047
<i>ACTR5</i>	ARP5 actin-related protein 5 homolog (yeast)	1.34	0.0231
<i>SOX30</i>	SRY box 30	1.34	0.0326
<i>OMP</i>	olfactory marker protein	1.34	0.0197
<i>ZBED9</i>	zinc finger, BED-type containing 9	1.34	0.0286

<i>GAGE1</i>	G antigen 1	1.34	0.0427
<i>CFC1B</i>	cripto, FRL-1, cryptic family 1B	1.34	0.026
<i>FAM111A</i>	family with sequence similarity 111, member A	1.34	0.0203
<i>PC</i>	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic	1.34	0.0304
<i>ORAI1</i>	ORAI calcium release-activated calcium modulator 1	1.34	0.0256
<i>ANKMY1</i>	ankyrin repeat and MYND domain containing 1	1.34	0.0262
<i>IL19</i>	interleukin 19	1.34	0.0255
<i>FAAH</i>	fatty acid amide hydrolase	1.34	0.0264
<i>MIXL1</i>	Mix paired-like homeobox	1.34	0.0311
<i>C4orf47</i>	chromosome 4 open reading frame 47	1.34	0.0493
<i>DEFB106B</i>	defensin, beta 106B	1.34	0.0303
<i>MSH6</i>	mutS homolog 6	1.34	0.0289
<i>GRK6</i>	G protein-coupled receptor kinase 6	1.34	0.0275
<i>OXER1</i>	oxoeicosanoid (OXE) receptor 1	1.33	0.0323
<i>IQCH</i>	IQ motif containing H	1.33	0.0257
<i>ACSM6</i>	acyl-CoA synthetase medium-chain family member 6	1.33	0.0235
<i>PHF24</i>	PHD finger protein 24	1.33	0.0394
<i>KANSL1</i>	KAT8 regulatory NSL complex subunit 1	1.33	0.0303
<i>SCNN1A</i>	sodium channel, non voltage gated 1 alpha subunit	1.33	0.0288
<i>RASIP1</i>	Ras interacting protein 1	1.33	0.0239
<i>UBN2</i>	ubiquitin 2	1.33	0.0288
<i>DEFB132</i>	defensin, beta 132	1.33	0.0275
<i>DMBX1</i>	diencephalon/mesencephalon homeobox 1	1.33	0.0218
<i>ITIH4</i>	inter-alpha-trypsin inhibitor heavy chain family, member 4	1.33	0.0227
<i>C1QL1</i>	complement component 1, q subcomponent-like 1	1.33	0.023
<i>S100A3</i>	S100 calcium binding protein A3	1.33	0.0199
<i>KLK3</i>	kallikrein related peptidase 3	1.33	0.0358
<i>MALL</i>	mal, T-cell differentiation protein-like	1.33	0.0382
<i>SUPT20HL2</i>	SPT20 homolog, SAGA complex component-like 2	1.33	0.0418
<i>CYP3A7</i>	cytochrome P450, family 3, subfamily A, polypeptide 7	1.33	0.0256
<i>RIMS4</i>	regulating synaptic membrane exocytosis 4	1.33	0.0349
<i>KRTAP19-1</i>	keratin associated protein 19-1	1.33	0.0242
<i>C6</i>	complement component 6	1.33	0.0283
<i>POU6F1</i>	POU class 6 homeobox 1	1.33	0.0307
<i>VCAM1</i>	vascular cell adhesion molecule 1	1.33	0.0232
<i>OR1S2</i>	olfactory receptor, family 1, subfamily S, member 2	1.33	0.0324
<i>C19orf33</i>	chromosome 19 open reading frame 33	1.33	0.0341
<i>EYA1</i>	EYA transcriptional coactivator and phosphatase 1	1.33	0.0345
<i>OR2G2</i>	olfactory receptor, family 2, subfamily G, member 2	1.33	0.0423
<i>OR4F5</i>	olfactory receptor, family 4, subfamily F, member 5	1.33	0.0392
<i>C19orf84</i>	chromosome 19 open reading frame 84	1.33	0.0429
<i>VCY</i>	variable charge, Y-linked	1.33	0.0299
<i>NTF4</i>	neurotrophin 4	1.33	0.0234
<i>SLC22A13</i>	solute carrier family 22 (organic anion/urate transporter), member 13	1.33	0.0224
<i>MSMP</i>	microseminoprotein, prostate associated	1.33	0.0296
<i>IPO7</i>	importin 7	1.33	0.0313
<i>ZNF710</i>	zinc finger protein 710	1.33	0.0434
<i>FEV</i>	FEV (ETS oncogene family)	1.33	0.0251
<i>REG3G</i>	regenerating islet-derived 3 gamma	1.33	0.0302
<i>OTP</i>	orthopedia homeobox	1.33	0.0334
<i>NTSR1</i>	neurotensin receptor 1 (high affinity)	1.33	0.0418
<i>TPRX1</i>	tetra-peptide repeat homeobox 1	1.33	0.0388
<i>CDH9</i>	cadherin 9, type 2 (T1-cadherin)	1.33	0.0372
<i>MTHFSD</i>	methenyltetrahydrofolate synthetase domain containing	1.33	0.0285
<i>PELP1</i>	proline, glutamate and leucine rich protein 1	1.33	0.0433
<i>BCL11B</i>	B-cell CLL/lymphoma 11B (zinc finger protein)	1.33	0.0347
<i>SPEM1</i>	spermatid maturation 1	1.33	0.0255
<i>GPR15</i>	G protein-coupled receptor 15	1.33	0.0415
<i>SPACA5</i>	sperm acrosome associated 5	1.33	0.0321

<i>ANGPTL7</i>	angiopoietin like 7	1.33	0.0272
<i>ZNF561</i>	zinc finger protein 561	1.33	0.0238
<i>YLPM1</i>	YLP motif containing 1	1.33	0.0342
<i>ANKRD23</i>	ankyrin repeat domain 23	1.33	0.0474
<i>TMEM145</i>	transmembrane protein 145	1.33	0.0239
<i>PAQR6</i>	progesterone and adipoQ receptor family member VI	1.33	0.0477
<i>LYG1</i>	lysozyme G-like 1	1.32	0.0309
<i>PRSS53</i>	protease, serine 53	1.32	0.0262
<i>ACTRT2</i>	actin-related protein T2	1.32	0.0371
<i>MLANA</i>	melan-A	1.32	0.0259
<i>HOXD8</i>	homeobox D8	1.32	0.0342
<i>ZSCAN25</i>	zinc finger and SCAN domain containing 25	1.32	0.0265
<i>EID3</i>	EP300 interacting inhibitor of differentiation 3	1.32	0.0339
<i>SPANXA2</i>	SPANX family, member A2	1.32	0.0428
<i>ADGRG6</i>	adhesion G protein-coupled receptor G6	1.32	0.0275
<i>GM2A</i>	GM2 ganglioside activator	1.32	0.0408
<i>TUBA4B</i>	tubulin, alpha 4b	1.32	0.0337
<i>CDC42BPG</i>	CDC42 binding protein kinase gamma (DMPK-like)	1.32	0.024
<i>TRPM2</i>	transient receptor potential cation channel, subfamily M, member 2	1.32	0.0454
<i>LRRC27</i>	leucine rich repeat containing 27	1.32	0.0408
<i>FANCC</i>	Fanconi anemia complementation group C	1.32	0.0294
<i>VWA5B1</i>	von Willebrand factor A domain containing 5B1	1.32	0.027
<i>GPRI37C</i>	G protein-coupled receptor 137C	1.32	0.0253
<i>SMIM24</i>	small integral membrane protein 24	1.32	0.0447
<i>TSSK1B</i>	testis-specific serine kinase 1B	1.32	0.0473
<i>OR7A17</i>	olfactory receptor, family 7, subfamily A, member 17	1.32	0.0315
<i>CELA2A</i>	chymotrypsin-like elastase family, member 2A	1.32	0.0382
<i>TNFSF12-</i>	TNFSF12-TNFSF13 readthrough	1.32	0.0257
<i>PPARA</i>	peroxisome proliferator-activated receptor alpha	1.32	0.0374
<i>KRTAP9-1</i>	keratin associated protein 9-1	1.32	0.0261
<i>MAPT</i>	microtubule associated protein tau	1.32	0.038
<i>GDF2</i>	growth differentiation factor 2	1.32	0.0353
<i>EPHX1</i>	epoxide hydrolase 1, microsomal (xenobiotic)	1.32	0.0411
<i>ZNF358</i>	zinc finger protein 358	1.32	0.0233
<i>RINL</i>	Ras and Rab interactor like	1.32	0.0298
<i>ZNF324B</i>	zinc finger protein 324B	1.32	0.0289
<i>PLB1</i>	phospholipase B1	1.32	0.0495
<i>SCNN1D</i>	sodium channel, non voltage gated 1 delta subunit	1.32	0.0271
<i>PRAMEF2</i>	PRAME family member 2	1.32	0.0444
<i>EXOC3L4</i>	exocyst complex component 3-like 4	1.32	0.0429
<i>ADRA2A</i>	adrenoceptor alpha 2A	1.32	0.0312
<i>SCPEP1</i>	serine carboxypeptidase 1	1.32	0.0309
<i>TMEM100</i>	transmembrane protein 100	1.32	0.0298
<i>CD207</i>	CD207 molecule, langerin	1.32	0.0313
<i>UVSSA</i>	UV stimulated scaffold protein A	1.32	0.0309
<i>AIMP1</i>	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	1.32	0.0316
<i>GJC2</i>	gap junction protein gamma 2	1.32	0.0283
<i>ZNF530</i>	zinc finger protein 530	1.32	0.0324
<i>LACTBL1</i>	lactamase, beta-like 1	1.32	0.0431
<i>LMNTD2</i>	lamin tail domain containing 2	1.32	0.0378
<i>KLHL15</i>	kelch-like family member 15	1.32	0.044
<i>SLIT1</i>	slit guidance ligand 1	1.32	0.0414
<i>C11orf95</i>	chromosome 11 open reading frame 95	1.32	0.0389
<i>C10orf82</i>	chromosome 10 open reading frame 82	1.32	0.0288
<i>KNCN</i>	kinocilin	1.32	0.0407
<i>IL15RA</i>	interleukin 15 receptor, alpha	1.32	0.0342
<i>SLC22A11</i>	solute carrier family 22 (organic anion/urate transporter), member 11	1.32	0.0446
<i>CYTH2</i>	cytohesin 2	1.32	0.0388
<i>ZNF546</i>	zinc finger protein 546	1.32	0.033

<i>B4GALNT2</i>	beta-1,4-N-acetyl-galactosaminyl transferase 2	1.31	0.042
<i>FAM102B</i>	family with sequence similarity 102, member B	1.31	0.0336
<i>B3GALT5</i>	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 5	1.31	0.0332
<i>TSC22D4</i>	TSC22 domain family, member 4	1.31	0.0279
<i>MARS2</i>	methionyl-tRNA synthetase 2, mitochondrial	1.31	0.0327
<i>C9orf50</i>	chromosome 9 open reading frame 50	1.31	0.0351
<i>G6PD</i>	glucose-6-phosphate dehydrogenase	1.31	0.0353
<i>DUSP5</i>	dual specificity phosphatase 5	1.31	0.0325
<i>GLE1</i>	GLE1 RNA export mediator	1.31	0.0488
<i>HAL</i>	histidine ammonia-lyase	1.31	0.0413
<i>LGALS4</i>	lectin, galactoside-binding, soluble, 4	1.31	0.0483
<i>KRT28</i>	keratin 28, type I	1.31	0.0327
<i>GRID1</i>	glutamate receptor, ionotropic, delta 1	1.31	0.0341
<i>NLRX1</i>	NLR family member X1	1.31	0.043
<i>CLDN23</i>	claudin 23	1.31	0.0407
<i>TMEM239</i>	transmembrane protein 239	1.31	0.045
<i>THRA</i>	thyroid hormone receptor, alpha	1.31	0.0489
<i>THAP8</i>	THAP domain containing 8	1.31	0.0458
<i>SH3GL2</i>	SH3-domain GRB2-like 2	1.31	0.0383
<i>RHBDL1</i>	rhomboid, veinlet-like 1 (Drosophila)	1.31	0.0478
<i>PRAM1</i>	PML-RARA regulated adaptor molecule 1	1.31	0.0349
<i>CDC42EP4</i>	CDC42 effector protein (Rho GTPase binding) 4	1.31	0.0301
<i>USP7</i>	ubiquitin specific peptidase 7 (herpes virus-associated)	1.31	0.0485
<i>TMPRSS11D</i>	transmembrane protease, serine 11D	1.31	0.0358
<i>BHLHA15</i>	basic helix-loop-helix family, member a15	1.31	0.0469
<i>ZNF32</i>	zinc finger protein 32	1.31	0.0432
<i>FUT4</i>	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	1.31	0.0357
<i>GYS2</i>	glycogen synthase 2 (liver)	1.31	0.0295
<i>BCKDHB</i>	branched chain keto acid dehydrogenase E1, beta polypeptide	1.31	0.0466
<i>GSDMB</i>	gasdermin B	1.31	0.0366
<i>CSAG1</i>	chondrosarcoma associated gene 1	1.31	0.0398
<i>STXBP6</i>	syntaxin binding protein 6 (amisyn)	1.31	0.0412
<i>RWDD2A</i>	RWD domain containing 2A	1.31	0.0448
<i>DMRT1</i>	doublesex and mab-3 related transcription factor 1	1.31	0.0306
<i>PDLIM7</i>	PDZ and LIM domain 7 (enigma)	1.31	0.0464
<i>CCHCR1</i>	coiled-coil alpha-helical rod protein 1	1.31	0.0364
<i>BCL2L2-</i>	BCL2L2-PABPN1 readthrough	1.31	0.0466
<i>IFNA4</i>	interferon, alpha 4	1.31	0.0499
<i>LGI4</i>	leucine-rich repeat LGI family, member 4	1.31	0.0346
<i>HSD11B1L</i>	hydroxysteroid (11-beta) dehydrogenase 1-like	1.31	0.0481
<i>LZTS3</i>	leucine zipper, putative tumor suppressor family member 3	1.31	0.047
<i>MPP7</i>	membrane protein, palmitoylated 7	1.31	0.0394
<i>FNDC9</i>	fibronectin type III domain containing 9	1.31	0.0366
<i>ROM1</i>	retinal outer segment membrane protein 1	1.31	0.0353
<i>SPAG11A</i>	sperm associated antigen 11A	1.31	0.039
<i>MVP</i>	major vault protein	1.31	0.046
<i>SEC31B</i>	SEC31 homolog B, COPII coat complex component	1.30	0.0306
<i>ZFP82</i>	ZFP82 zinc finger protein	1.30	0.0456
<i>FUT11</i>	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	1.30	0.037
<i>RNF213</i>	ring finger protein 213	1.30	0.0407
<i>SLC23A3</i>	solute carrier family 23, member 3	1.30	0.0365
<i>PTPN18</i>	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	1.30	0.04
<i>GABPB2</i>	GA binding protein transcription factor, beta subunit 2	1.30	0.0305
<i>EPN1</i>	epsin 1	1.30	0.0352
<i>ART5</i>	ADP-ribosyltransferase 5	1.30	0.0412
<i>SERP2</i>	stress-associated endoplasmic reticulum protein family member 2	1.30	0.0429
<i>ADM</i>	adrenomedullin	1.30	0.0386
<i>CTRB1</i>	chymotrypsinogen B1	1.30	0.049
<i>MROH5</i>	maestro heat-like repeat family member 5	1.30	0.0336

<i>UBTD1</i>	ubiquitin domain containing 1	1.30	0.0429
<i>B3GALNT2</i>	beta-1,3-N-acetylgalactosaminyltransferase 2	1.30	0.0489
<i>CD19</i>	CD19 molecule	1.30	0.0314
<i>NFIA</i>	nuclear factor I/A	1.30	0.0424
<i>MFSD9</i>	major facilitator superfamily domain containing 9	1.30	0.0423
<i>BPIFB1</i>	BPI fold containing family B, member 1	1.30	0.0468
<i>KIF25</i>	kinesin family member 25	1.30	0.0437
<i>ZNF619</i>	zinc finger protein 619	1.30	0.0458
<i>ARID3B</i>	AT rich interactive domain 3B (BRIGHT-like)	1.30	0.0316
<i>SLC52A1</i>	solute carrier family 52 (riboflavin transporter), member 1	1.30	0.0371
<i>KIF2C</i>	Jeck2013 ALT_DONOR, coding, INTERNAL, intronic best transcript	1.30	0.0342
<i>PLA2G4D</i>	phospholipase A2, group IVD (cytosolic)	1.30	0.0439
<i>DMRTB1</i>	DMRT-like family B with proline-rich C-terminal, 1	1.30	0.042
<i>TPD52L3</i>	tumor protein D52-like 3	1.30	0.0385
<i>LAT2</i>	linker for activation of T-cells family member 2	1.30	0.0416
<i>MEN1</i>	Jeck2013 ANTISENSE, CDS, coding, INTERNAL, OVCODE, OVEXON best	1.30	0.0497
<i>OR4M2</i>	Homo sapiens olfactory receptor, family 4, subfamily M, member 2 (OR4M2),	1.30	0.0364
<i>LITAF</i>	lipopolysaccharide-induced TNF factor	1.30	0.0439
<i>LRRN4</i>	leucine rich repeat neuronal 4	1.30	0.0387
<i>FKBP9</i>	FK506 binding protein 9	1.30	0.0434
<i>NOTCH4</i>	notch 4	1.30	0.0425
<i>RBFOX1</i>	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic	1.30	0.0445
<i>ST6GALNAC6</i>	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-	1.30	0.0477
<i>CLDN4</i>	claudin 4	1.30	0.0426
<i>RASSF4</i>	Ras association (RalGDS/AF-6) domain family member 4	1.30	0.041
<i>CFAP52</i>	cilia and flagella associated protein 52	1.30	0.0346
<i>TLL8</i>	tubulin tyrosine ligase-like family member 8	1.30	0.0432
<i>BRINP2</i>	bone morphogenetic protein/retinoic acid inducible neural-specific 2	1.30	0.0394
<i>GDAP1L1</i>	ganglioside induced differentiation associated protein 1-like 1	1.30	0.0427
<i>C19orf38</i>	chromosome 19 open reading frame 38	1.30	0.0376
<i>RIC3</i>	RIC3 acetylcholine receptor chaperone	1.29	0.0436
<i>IL9R</i>	interleukin 9 receptor	1.29	0.0457
<i>WDR97</i>	WD repeat domain 97	1.29	0.0422
<i>SEL1L</i>	sel-1 suppressor of lin-12-like (C. elegans)	1.29	0.0427
<i>ABO</i>	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase;	1.29	0.0465
<i>RAPSN</i>	receptor-associated protein of the synapse	1.29	0.0408
<i>DMRT3</i>	doublesex and mab-3 related transcription factor 3	1.29	0.0487
<i>OR2V1</i>	olfactory receptor, family 2, subfamily V, member 1	1.29	0.0471
<i>HR</i>	hair growth associated	1.29	0.0479
<i>GEM</i>	GTP binding protein overexpressed in skeletal muscle	1.29	0.049
<i>GP2</i>	glycoprotein 2 (zymogen granule membrane)	1.29	0.0426
<i>PPP1R15A</i>	protein phosphatase 1, regulatory subunit 15A	1.29	0.0462
<i>ARMCX2</i>	armadillo repeat containing, X-linked 2	1.29	0.0384
<i>NPRL2</i>	NPR2-like, GATOR1 complex subunit	1.29	0.0393
<i>NCAN</i>	neurocan	1.29	0.0443
<i>NR1H3</i>	nuclear receptor subfamily 1, group H, member 3	1.29	0.0474
<i>SFTPA1</i>	surfactant protein A1	1.29	0.038
<i>KCNA7</i>	potassium channel, voltage gated shaker related subfamily A, member 7	1.29	0.0449
<i>FTL</i>	ferritin, light polypeptide	1.29	0.0419
<i>LRRC8C</i>	leucine rich repeat containing 8 family, member C	1.29	0.0429
<i>NAIF1</i>	nuclear apoptosis inducing factor 1	1.29	0.0414
<i>AK8</i>	adenylate kinase 8	1.29	0.0414
<i>GGT1</i>	gamma-glutamyltransferase 1	1.29	0.0466
<i>ITPKA</i>	inositol-trisphosphate 3-kinase A	1.29	0.0469
<i>FAM199X</i>	family with sequence similarity 199, X-linked	1.29	0.0395
<i>CD1B</i>	CD1b molecule	1.29	0.0433
<i>LAMTOR1</i>	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1	1.29	0.0445
<i>NIPA1</i>	non imprinted in Prader-Willi/Angelman syndrome 1	1.29	0.0488
<i>CACNA1H</i>	calcium channel, voltage-dependent, T type, alpha 1H subunit	1.29	0.0471

<i>MEGF11</i>	multiple EGF-like-domains 11	1.29	0.0452
<i>TRPM8</i>	transient receptor potential cation channel, subfamily M, member 8	1.29	0.0453
<i>AFAP1L1</i>	actin filament associated protein 1-like 1	1.29	0.047
<i>OR10G7</i>	olfactory receptor, family 10, subfamily G, member 7	1.29	0.0485
<i>FLI1</i>	Fli-1 proto-oncogene, ETS transcription factor	1.28	0.0423
<i>GYPE</i>	glycophorin E (MNS blood group)	1.28	0.0436
<i>SLC6A15</i>	solute carrier family 6 (neutral amino acid transporter), member 15	1.28	0.0448
<i>ITIH1</i>	inter-alpha-trypsin inhibitor heavy chain 1	1.28	0.0494
<i>SLC2A4RG</i>	SLC2A4 regulator	1.28	0.0428
<i>SLC26A6</i>	solute carrier family 26 (anion exchanger), member 6	1.28	0.0481
<i>CTNS</i>	cystinosin, lysosomal cystine transporter	1.28	0.0424
<i>IFNA10</i>	interferon, alpha 10	1.28	0.0462
<i>CGA</i>	glycoprotein hormones, alpha polypeptide	1.28	0.0475
<i>ST6GALNAC2</i>	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	1.28	0.0495
<i>FAM78B</i>	family with sequence similarity 78, member B	1.28	0.0435
<i>MBD3L3</i>	methyl-CpG binding domain protein 3-like 3	1.28	0.0491
<i>PIK3CG</i>	Memczak2013 ANTISENSE, CDS, coding, INTERNAL best transcript	1.28	0.0442
<i>SCO1</i>	SCO1 cytochrome c oxidase assembly protein	1.28	0.0475
<i>CLDN16</i>	claudin 16	1.28	0.0434
<i>PRAMEF7</i>	PRAME family member 7	1.28	0.0489
<i>ZNF341</i>	zinc finger protein 341	1.28	0.0448
<i>NGFR</i>	nerve growth factor receptor	1.28	0.0483
<i>ELFN2</i>	extracellular leucine-rich repeat and fibronectin type III domain containing 2	1.28	0.0496
<i>DGCR8</i>	DGCR8 microprocessor complex subunit	1.28	0.0437
<i>GJB7</i>	gap junction protein beta 7	1.28	0.0447
<i>BCAS1</i>	breast carcinoma amplified sequence 1	1.28	0.0474
<i>EML5</i>	echinoderm microtubule associated protein like 5	1.27	0.0487
<i>FBXO36</i>	Transcript Identified by AceView, Entrez Gene ID(s) 130888	1.27	0.0444
<i>GPX8</i>	glutathione peroxidase 8 (putative)	1.27	0.0478

Table S6. IDMF-decreased genes (P < 0.05 with FC < 0.80). The table lists 903 IDMF-decreased genes ranked by estimated fold-change (FC) (IDMF/CTL). The gene symbol and description are shown. The raw p-value is listed in the final column (generalized least square linear models with moderated t-statistics; $n = 3$ samples per group; *FDR < 0.10).

Symbol	Description	FC	P-value
<i>ACTR3</i>	ARP3 actin-related protein 3 homolog (yeast)	0.28	2.22e-07*
<i>KPNB1</i>	karyopherin (importin) beta 1	0.30	1.65e-05*
<i>RAP1B</i>	RAP1B, member of RAS oncogene family	0.32	2.58e-06*
<i>TNFAIP3</i>	tumor necrosis factor, alpha-induced protein 3	0.34	7.89e-07*
<i>COPA</i>	coatamer protein complex subunit alpha	0.44	2.03e-05*
<i>WDR41</i>	WD repeat domain 41	0.44	0.00075
<i>SPPL2A</i>	signal peptide peptidase like 2A	0.45	0.00198
<i>TP53INP1</i>	tumor protein p53 inducible nuclear protein 1	0.46	0.000133*
<i>TMEM138</i>	transmembrane protein 138	0.49	0.000517
<i>METTL9</i>	methyltransferase like 9	0.49	0.000113*
<i>MID1</i>	midline 1	0.50	0.000269
<i>PSMB1</i>	proteasome subunit beta 1	0.50	0.00276
<i>EFEMP1</i>	EGF containing fibulin-like extracellular matrix protein 1	0.51	9.98e-05*
<i>SMURF2</i>	SMAD specific E3 ubiquitin protein ligase 2	0.52	0.00369
<i>CSF1</i>	colony stimulating factor 1 (macrophage)	0.52	3.52e-05*
<i>ABCE1</i>	ATP binding cassette subfamily E member 1	0.52	0.000479
<i>ARFGEF1</i>	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-	0.52	8.62e-05*
<i>PARL</i>	presenilin associated, rhomboid-like	0.53	0.00536
<i>EXOC1</i>	exocyst complex component 1	0.53	0.00192
<i>SLC30A9</i>	solute carrier family 30 (zinc transporter), member 9	0.53	0.000355
<i>MAPK8</i>	mitogen-activated protein kinase 8	0.53	0.00477
<i>NABP1</i>	nucleic acid binding protein 1	0.53	9.89e-05*
<i>PSMD12</i>	proteasome 26S subunit, non-ATPase 12	0.53	0.000864
<i>UCHL3</i>	ubiquitin C-terminal hydrolase L3	0.53	0.00942
<i>MRPS28</i>	mitochondrial ribosomal protein S28	0.54	0.00691
<i>PSMB5</i>	proteasome subunit beta 5	0.54	0.000305
<i>PRKCI</i>	protein kinase C, iota	0.54	0.00562
<i>RAD50</i>	RAD50 homolog, double strand break repair protein	0.54	0.000363
<i>PACSLN2</i>	protein kinase C and casein kinase substrate in neurons 2	0.54	9.17e-05*
<i>DICER1</i>	dicer 1, ribonuclease type III	0.54	0.000986
<i>SNAP23</i>	synaptosome associated protein 23kDa	0.54	0.00169
<i>TERF1</i>	telomeric repeat binding factor (NIMA-interacting) 1	0.55	0.00515
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recogin 5	0.55	0.000334
<i>GTF3C6</i>	general transcription factor IIIC subunit 6	0.55	0.0313
<i>DCAF16</i>	DDB1 and CUL4 associated factor 16	0.55	0.000159*
<i>WDR61</i>	WD repeat domain 61	0.55	0.00064
<i>CORO1C</i>	coronin, actin binding protein, 1C	0.55	0.00187
<i>PDZD8</i>	PDZ domain containing 8	0.55	0.00126
<i>NUP50</i>	nucleoporin 50kDa	0.55	0.00359
<i>ACTC1</i>	actin, alpha, cardiac muscle 1	0.55	0.000128*
<i>ANKRD13A</i>	ankyrin repeat domain 13A	0.55	0.00663
<i>KCTD10</i>	potassium channel tetramerization domain containing 10	0.55	0.00519
<i>SFT2D1</i>	SFT2 domain containing 1	0.55	0.00619
<i>HIGD1A</i>	HIG1 hypoxia inducible domain family, member 1A	0.55	0.0114
<i>PGRMC2</i>	progesterone receptor membrane component 2	0.56	0.00164
<i>ENY2</i>	enhancer of yellow 2 homolog (Drosophila)	0.56	0.00346
<i>SYNRG</i>	synergin, gamma	0.56	0.00317
<i>IFNAR2</i>	interferon (alpha, beta and omega) receptor 2	0.56	0.000452
<i>GSPT1</i>	G1 to S phase transition 1	0.56	0.0109
<i>APBB2</i>	amyloid beta (A4) precursor protein-binding, family B, member 2	0.56	0.00233
<i>ITGAE</i>	integrin alpha E	0.56	0.000965
<i>CNDP2</i>	CNDP dipeptidase 2 (metallopeptidase M20 family)	0.56	0.00143
<i>TAPT1</i>	transmembrane anterior posterior transformation 1	0.56	0.0038
<i>MED6</i>	mediator complex subunit 6	0.56	0.000154*

<i>TANK</i>	TRAF family member-associated NFKB activator	0.57	0.016
<i>LNPEP</i>	leucyl/cystinyl aminopeptidase	0.57	0.00662
<i>NDUFB5</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	0.57	0.0119
<i>GBP1</i>	guanylate binding protein 1, interferon-inducible	0.57	0.00133
<i>CPEB4</i>	cytoplasmic polyadenylation element binding protein 4	0.57	0.000303
<i>NTM</i>	neurotrimin	0.57	0.0134
<i>DBNL</i>	drebrin-like	0.57	0.000746
<i>ARV1</i>	ARV1 homolog, fatty acid homeostasis modulator	0.57	0.00157
<i>GTF2H3</i>	general transcription factor IIH subunit 3	0.57	0.00431
<i>ANK3</i>	ankyrin 3, node of Ranvier (ankyrin G)	0.57	0.00147
<i>RCN2</i>	reticulocalbin 2, EF-hand calcium binding domain	0.57	0.00566
<i>LTBP1</i>	latent transforming growth factor beta binding protein 1	0.57	0.00542
<i>MRPL46</i>	mitochondrial ribosomal protein L46	0.57	0.00523
<i>APLP2</i>	amyloid beta (A4) precursor-like protein 2	0.57	0.00527
<i>MFSD14B</i>	major facilitator superfamily domain containing 14B	0.58	0.00286
<i>CLK1</i>	CDC like kinase 1	0.58	0.0256
<i>F3</i>	coagulation factor III (thromboplastin, tissue factor)	0.58	0.000108*
<i>PTP4A1</i>	protein tyrosine phosphatase type IVA, member 1	0.58	0.0018
<i>TIMM9</i>	translocase of inner mitochondrial membrane 9 homolog (yeast)	0.58	0.0013
<i>MED20</i>	mediator complex subunit 20	0.58	0.000308
<i>LUM</i>	lumican	0.58	0.00367
<i>KCTD4</i>	potassium channel tetramerization domain containing 4	0.58	0.00331
<i>DUSP11</i>	dual specificity phosphatase 11	0.58	0.00625
<i>TWF1</i>	twinfilin actin binding protein 1	0.58	0.000796
<i>ENC1</i>	ectodermal-neural cortex 1 (with BTB domain)	0.58	0.000268
<i>NEDD4L</i>	neural precursor cell expressed, developmentally down-regulated 4-like, E3	0.58	0.0066
<i>AMD1</i>	adenosylmethionine decarboxylase 1	0.58	0.00508
<i>EPB41L3</i>	erythrocyte membrane protein band 4.1-like 3	0.58	0.000336
<i>SNRPA1</i>	small nuclear ribonucleoprotein polypeptide A	0.58	0.0306
<i>NBAS</i>	neuroblastoma amplified sequence	0.58	0.00194
<i>MDH1</i>	malate dehydrogenase 1	0.58	0.000985
<i>EFCAB11</i>	EF-hand calcium binding domain 11	0.58	0.0314
<i>KBTBD2</i>	kelch repeat and BTB (POZ) domain containing 2	0.58	0.00645
<i>SNX5</i>	sorting nexin 5	0.59	0.00888
<i>ZBTB38</i>	zinc finger and BTB domain containing 38	0.59	0.0235
<i>GRSF1</i>	G-rich RNA sequence binding factor 1	0.59	0.00597
<i>METTL23</i>	methyltransferase like 23	0.59	0.00464
<i>MTR</i>	5-methyltetrahydrofolate-homocysteine methyltransferase	0.59	0.000263
<i>MAGI1</i>	membrane associated guanylate kinase, WW and PDZ domain containing 1	0.59	0.00381
<i>ANKRD1</i>	ankyrin repeat domain 1 (cardiac muscle)	0.59	0.00192
<i>PPP2R5C</i>	protein phosphatase 2, regulatory subunit B, gamma	0.59	0.0112
<i>HNRNPA2B1</i>	heterogeneous nuclear ribonucleoprotein A2/B1	0.59	0.0119
<i>EBAG9</i>	estrogen receptor binding site associated, antigen, 9	0.59	0.00335
<i>ZNF776</i>	zinc finger protein 776	0.59	0.00225
<i>FARP2</i>	FERM, ARH/RhoGEF and pleckstrin domain protein 2	0.59	0.00359
<i>TARDBP</i>	TAR DNA binding protein	0.59	0.0037
<i>IFT46</i>	intraflagellar transport 46	0.59	0.0051
<i>P3H2</i>	prolyl 3-hydroxylase 2	0.59	0.00128
<i>COX4I1</i>	cytochrome c oxidase subunit IV isoform 1	0.59	0.00326
<i>PRKACB</i>	protein kinase, cAMP-dependent, catalytic, beta	0.60	0.00459
<i>TMEM59</i>	transmembrane protein 59	0.60	0.0053
<i>LSM5</i>	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated	0.60	0.00887
<i>PLOD2</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0.60	0.00241
<i>NUDT5</i>	nudix hydrolase 5	0.60	0.00088
<i>BCCIP</i>	BRCA2 and CDKN1A interacting protein	0.60	0.00504
<i>SEC23IP</i>	SEC23 interacting protein	0.60	0.0154
<i>RPS27A</i>	ribosomal protein S27a	0.60	0.00697
<i>ANKRD50</i>	ankyrin repeat domain 50	0.60	0.00175
<i>CCNB1</i>	cyclin B1	0.60	0.00581

<i>SEC11A</i>	SEC11 homolog A, signal peptidase complex subunit	0.60	0.00642
<i>SF3A3</i>	splicing factor 3a subunit 3	0.60	0.00565
<i>ZNF148</i>	zinc finger protein 148	0.60	0.00553
<i>CETN3</i>	centrin 3	0.60	0.0235
<i>XRCC5</i>	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-	0.60	0.0116
<i>PSMC5</i>	proteasome 26S subunit, ATPase 5	0.60	0.0055
<i>TOMM5</i>	translocase of outer mitochondrial membrane 5 homolog (yeast)	0.60	0.0133
<i>NDUFA8</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	0.61	0.00451
<i>ZSWIM7</i>	zinc finger, SWIM-type containing 7	0.61	0.0055
<i>PDGFC</i>	platelet derived growth factor C	0.61	0.00171
<i>GTF2H2</i>	general transcription factor IIH subunit 2	0.61	0.00118
<i>LYPLAL1</i>	lysophospholipase-like 1	0.61	0.0161
<i>NRDC</i>	nardilysin convertase	0.61	0.0102
<i>MELK</i>	maternal embryonic leucine zipper kinase	0.61	0.00388
<i>RASA1</i>	RAS p21 protein activator (GTPase activating protein) 1	0.61	0.00103
<i>WNT5A</i>	wingless-type MMTV integration site family, member 5A	0.61	0.00107
<i>USP25</i>	ubiquitin specific peptidase 25	0.61	0.00808
<i>VPS72</i>	vacuolar protein sorting 72 homolog (S. cerevisiae)	0.61	0.000476
<i>CAPRIN1</i>	cell cycle associated protein 1	0.61	0.0261
<i>TPRKB</i>	TP53RK binding protein	0.61	0.00127
<i>ATAD1</i>	ATPase family, AAA domain containing 1	0.61	0.00366
<i>ARL4A</i>	ADP-ribosylation factor like GTPase 4A	0.61	0.00224
<i>GORASP2</i>	golgi reassembly stacking protein 2	0.61	0.0034
<i>ARIH1</i>	ariadne RBR E3 ubiquitin protein ligase 1	0.61	0.018
<i>ANO10</i>	anoctamin 10	0.61	0.00281
<i>TM4SF1</i>	transmembrane 4 L six family member 1	0.61	0.000588
<i>TMEM45A</i>	transmembrane protein 45A	0.62	0.0199
<i>ARPC2</i>	actin related protein 2/3 complex subunit 2	0.62	0.00122
<i>ZZZ3</i>	zinc finger, ZZ-type containing 3	0.62	0.00878
<i>TM2D1</i>	TM2 domain containing 1	0.62	0.00409
<i>ANAPC7</i>	anaphase promoting complex subunit 7	0.62	0.00366
<i>AGO3</i>	argonaute RISC catalytic component 3	0.62	0.00724
<i>CBWD3</i>	COBW domain containing 3	0.62	0.0212
<i>NUP155</i>	nucleoporin 155kDa	0.62	0.00194
<i>FCHSD2</i>	FCH and double SH3 domains 2	0.62	0.00604
<i>NFKBIA</i>	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.62	0.00227
<i>YTHDF2</i>	YTH N(6)-methyladenosine RNA binding protein 2	0.62	0.00369
<i>C18orf21</i>	chromosome 18 open reading frame 21	0.62	0.00196
<i>MLH1</i>	mutL homolog 1	0.62	0.0311
<i>UQCRHL</i>	ubiquinol-cytochrome c reductase hinge protein like	0.62	0.00477
<i>CLDN1</i>	claudin 1	0.62	0.00144
<i>COPZ1</i>	coatamer protein complex subunit zeta 1	0.62	0.0117
<i>MYL12A</i>	myosin light chain 12A	0.62	0.0141
<i>ZNF616</i>	zinc finger protein 616	0.62	0.00194
<i>PSMG1</i>	proteasome (prosome, macropain) assembly chaperone 1	0.62	0.0299
<i>OXCT1</i>	3-oxoacid CoA-transferase 1	0.62	0.013
<i>CBR4</i>	carbonyl reductase 4	0.62	0.00762
<i>SRI</i>	sorcin	0.62	0.0048
<i>PAPOLA</i>	poly(A) polymerase alpha	0.62	0.00393
<i>PCNA</i>	proliferating cell nuclear antigen	0.62	0.00815
<i>TMEM234</i>	transmembrane protein 234	0.63	0.00423
<i>TDRD3</i>	tudor domain containing 3	0.63	0.00178
<i>SENP6</i>	SUMO1/sentrin specific peptidase 6	0.63	0.0159
<i>NOX4</i>	NADPH oxidase 4	0.63	0.00273
<i>MTA3</i>	metastasis associated 1 family member 3	0.63	0.00109
<i>CFAP20</i>	cilia and flagella associated protein 20	0.63	0.0016
<i>PPP1R7</i>	protein phosphatase 1, regulatory subunit 7	0.63	0.00719
<i>LSM1</i>	LSM1 homolog, mRNA degradation associated	0.63	0.0167
<i>POLR2H</i>	polymerase (RNA) II (DNA directed) polypeptide H	0.63	0.00246

<i>CTNNA1</i>	catenin (cadherin-associated protein), alpha 1	0.63	0.00387
<i>SF3B1</i>	splicing factor 3b, subunit 1, 155kDa	0.63	0.0194
<i>OSTF1</i>	osteoclast stimulating factor 1	0.63	0.0265
<i>DEGS1</i>	delta(4)-desaturase, sphingolipid 1	0.63	0.00632
<i>PSMD9</i>	proteasome 26S subunit, non-ATPase 9	0.63	0.00628
<i>UCP2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	0.63	0.000996
<i>EEF1D</i>	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange	0.63	0.0499
<i>PFDN4</i>	prefoldin subunit 4	0.63	0.00294
<i>CYP51A1</i>	cytochrome P450, family 51, subfamily A, polypeptide 1	0.63	0.00354
<i>NBPF9</i>	neuroblastoma breakpoint family, member 9	0.63	0.00907
<i>MRPS17</i>	mitochondrial ribosomal protein S17	0.63	0.00692
<i>UBLCP1</i>	ubiquitin-like domain containing CTD phosphatase 1	0.63	0.0408
<i>ADNP2</i>	ADNP homeobox 2	0.63	0.0487
<i>ATP2B1</i>	ATPase, Ca++ transporting, plasma membrane 1	0.63	0.00115
<i>BMPR2</i>	bone morphogenetic protein receptor type II	0.63	0.00253
<i>SEC14L1</i>	SEC14-like lipid binding 1	0.63	0.0149
<i>KLHDC2</i>	kelch domain containing 2	0.63	0.0326
<i>PSMG2</i>	proteasome (prosome, macropain) assembly chaperone 2	0.63	0.000872
<i>MFS1D1</i>	major facilitator superfamily domain containing 1	0.63	0.00793
<i>BCL6</i>	B-cell CLL/lymphoma 6	0.63	0.00103
<i>ZNF433</i>	zinc finger protein 433	0.63	0.00304
<i>MAPRE1</i>	microtubule-associated protein, RP/EB family, member 1	0.63	0.00906
<i>PDSS1</i>	prenyl (decaprenyl) diphosphate synthase, subunit 1	0.64	0.00275
<i>XPR1</i>	xenotropic and polytropic retrovirus receptor 1	0.64	0.00453
<i>IKZF5</i>	IKAROS family zinc finger 5	0.64	0.0269
<i>NRG1</i>	neuregulin 1	0.64	0.0057
<i>DCAF6</i>	DDB1 and CUL4 associated factor 6	0.64	0.0016
<i>BROX</i>	BRO1 domain and CAAX motif containing	0.64	0.0192
<i>IFNAR1</i>	interferon (alpha, beta and omega) receptor 1	0.64	0.00251
<i>EIF2AK1</i>	eukaryotic translation initiation factor 2-alpha kinase 1	0.64	0.0096
<i>PSMD2</i>	proteasome 26S subunit, non-ATPase 2	0.64	0.00248
<i>SNRNP25</i>	small nuclear ribonucleoprotein, U11/U12 25kDa subunit	0.64	0.00278
<i>ERH</i>	enhancer of rudimentary homolog (Drosophila)	0.64	0.0115
<i>SPTLC2</i>	serine palmitoyltransferase, long chain base subunit 2	0.64	0.00656
<i>FAM229B</i>	family with sequence similarity 229, member B	0.64	0.00343
<i>VEGFA</i>	vascular endothelial growth factor A	0.64	0.00229
<i>CCNT2</i>	cyclin T2	0.64	0.0178
<i>TATDN1</i>	TatD DNase domain containing 1	0.64	0.0154
<i>BAG1</i>	BCL2-associated athanogene	0.64	0.0457
<i>PARP1</i>	poly(ADP-ribose) polymerase 1	0.64	0.00294
<i>PLAA</i>	phospholipase A2-activating protein	0.64	0.038
<i>MORN2</i>	MORN repeat containing 2	0.64	0.0256
<i>GDI1</i>	GDP dissociation inhibitor 1	0.64	0.00157
<i>GOT1</i>	glutamic-oxaloacetic transaminase 1, soluble	0.64	0.00274
<i>CCZ1</i>	CCZ1 homolog, vacuolar protein trafficking and biogenesis associated	0.64	0.00396
<i>FZD6</i>	frizzled class receptor 6	0.65	0.00464
<i>NDUFAB1</i>	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	0.65	0.0177
<i>CCDC82</i>	coiled-coil domain containing 82	0.65	0.0159
<i>COPS3</i>	COP9 signalosome subunit 3	0.65	0.00904
<i>CFLAR</i>	CASP8 and FADD like apoptosis regulator	0.65	0.00277
<i>GNPNAT1</i>	glucosamine-phosphate N-acetyltransferase 1	0.65	0.0215
<i>ITGAV</i>	integrin alpha V	0.65	0.00818
<i>CCNC</i>	cyclin C	0.65	0.0131
<i>RPF2</i>	ribosome production factor 2 homolog	0.65	0.0385
<i>TMEM50A</i>	transmembrane protein 50A	0.65	0.003
<i>PLCG1</i>	phospholipase C, gamma 1	0.65	0.00742
<i>RNASEH2B</i>	ribonuclease H2, subunit B	0.65	0.0191
<i>CDS2</i>	CDP-diacylglycerol synthase 2	0.65	0.00511
<i>AP3S1</i>	adaptor-related protein complex 3, sigma 1 subunit	0.65	0.0164

<i>CASD1</i>	CAS1 domain containing 1	0.65	0.0161
<i>IAH1</i>	isoamyl acetate-hydrolyzing esterase 1 homolog	0.65	0.00888
<i>MFAP5</i>	microfibrillar associated protein 5	0.65	0.0175
<i>CHEK1</i>	checkpoint kinase 1	0.65	0.0218
<i>KIAA0100</i>	KIAA0100	0.65	0.00297
<i>STRADB</i>	STE20-related kinase adaptor beta	0.65	0.0156
<i>SENPI</i>	SUMO1/sentrin specific peptidase 1	0.65	0.0302
<i>ADCY3</i>	adenylate cyclase 3	0.65	0.0014
<i>SUMO1</i>	small ubiquitin-like modifier 1	0.65	0.0067
<i>RAB23</i>	RAB23, member RAS oncogene family	0.65	0.005
<i>NXF1</i>	nuclear RNA export factor 1	0.65	0.00303
<i>RRM2B</i>	ribonucleotide reductase M2 B (TP53 inducible)	0.65	0.00365
<i>COG7</i>	component of oligomeric golgi complex 7	0.66	0.00422
<i>TMCC1</i>	transmembrane and coiled-coil domain family 1	0.66	0.00531
<i>PIEZO1</i>	piezo-type mechanosensitive ion channel component 1	0.66	0.00226
<i>EDIL3</i>	EGF-like repeats and discoidin I-like domains 3	0.66	0.00652
<i>ERLEC1</i>	endoplasmic reticulum lectin 1	0.66	0.00832
<i>TTC14</i>	tetratricopeptide repeat domain 14	0.66	0.00269
<i>LPCAT2</i>	lysophosphatidylcholine acyltransferase 2	0.66	0.015
<i>MSN</i>	moesin	0.66	0.0104
<i>SCRN1</i>	secernin 1	0.66	0.00393
<i>FGD6</i>	FYVE, RhoGEF and PH domain containing 6	0.66	0.00274
<i>DCAF5</i>	DDB1 and CUL4 associated factor 5	0.66	0.0045
<i>HERPUD1</i>	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like	0.66	0.0077
<i>USP33</i>	ubiquitin specific peptidase 33	0.66	0.0296
<i>STIM2</i>	stromal interaction molecule 2	0.66	0.00615
<i>CASP4</i>	caspase 4	0.66	0.00197
<i>PTAR1</i>	protein prenyltransferase alpha subunit repeat containing 1	0.66	0.0103
<i>REST</i>	RE1-silencing transcription factor	0.66	0.0157
<i>STYXL1</i>	serine/threonine/tyrosine interacting-like 1	0.66	0.0117
<i>PAWR</i>	PRKC, apoptosis, WT1, regulator	0.66	0.00383
<i>VTI1B</i>	vesicle transport through interaction with t-SNAREs 1B	0.66	0.00438
<i>PMS2</i>	PMS1 homolog 2, mismatch repair system component	0.66	0.0124
<i>PRDX4</i>	peroxiredoxin 4	0.66	0.0105
<i>OSBPL10</i>	oxysterol binding protein-like 10	0.66	0.00178
<i>LIMS1</i>	LIM and senescent cell antigen-like domains 1	0.66	0.00275
<i>RTN4</i>	reticulon 4	0.66	0.00573
<i>ANXA5</i>	annexin A5	0.66	0.0198
<i>ERCC8</i>	excision repair cross-complementation group 8	0.66	0.012
<i>CWC27</i>	CWC27 spliceosome-associated protein homolog	0.66	0.0123
<i>IWS1</i>	IWS1 homolog (S. cerevisiae)	0.66	0.0064
<i>HACD3</i>	3-hydroxyacyl-CoA dehydratase 3	0.66	0.0153
<i>POLR2G</i>	polymerase (RNA) II (DNA directed) polypeptide G	0.66	0.00372
<i>PMPCA</i>	peptidase (mitochondrial processing) alpha	0.66	0.00383
<i>IQCI</i>	IQ motif containing J	0.66	0.0113
<i>FMR1</i>	fragile X mental retardation 1	0.66	0.0142
<i>BTBD3</i>	BTB (POZ) domain containing 3	0.67	0.00362
<i>USP21</i>	ubiquitin specific peptidase 21	0.67	0.00328
<i>RSPRY1</i>	ring finger and SPRY domain containing 1	0.67	0.00747
<i>BPGM</i>	2,3-bisphosphoglycerate mutase	0.67	0.0181
<i>APPBP2</i>	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	0.67	0.0137
<i>EXT1</i>	exostosin glycosyltransferase 1	0.67	0.00298
<i>KANK1</i>	KN motif and ankyrin repeat domains 1	0.67	0.00369
<i>UBR2</i>	ubiquitin protein ligase E3 component n-recogin 2	0.67	0.00818
<i>MRPL27</i>	mitochondrial ribosomal protein L27	0.67	0.0112
<i>OGFRL1</i>	opioid growth factor receptor-like 1	0.67	0.00702
<i>CHMP2B</i>	charged multivesicular body protein 2B	0.67	0.0275
<i>CALM2</i>	calmodulin 2 (phosphorylase kinase, delta)	0.67	0.0248
<i>STAT3</i>	signal transducer and activator of transcription 3 (acute-phase response factor)	0.67	0.00513

<i>MAP4K5</i>	mitogen-activated protein kinase kinase kinase 5	0.67	0.0194
<i>GTPBP8</i>	GTP-binding protein 8 (putative)	0.67	0.0348
<i>PARP4</i>	poly(ADP-ribose) polymerase family member 4	0.67	0.00551
<i>CSTF3</i>	cleavage stimulation factor, 3 pre-RNA, subunit 3	0.67	0.0459
<i>STC1</i>	stanniocalcin 1	0.67	0.0381
<i>TMEM254</i>	transmembrane protein 254	0.67	0.00406
<i>VPS36</i>	vacuolar protein sorting 36 homolog (S. cerevisiae)	0.67	0.00485
<i>PAK1</i>	p21 protein (Cdc42/Rac)-activated kinase 1	0.67	0.00633
<i>RAB34</i>	RAB34, member RAS oncogene family	0.67	0.0275
<i>TAB2</i>	TGF-beta activated kinase 1/MAP3K7 binding protein 2	0.67	0.00938
<i>REXO2</i>	RNA exonuclease 2	0.67	0.0279
<i>SEC11C</i>	SEC11 homolog C, signal peptidase complex subunit	0.67	0.0124
<i>PFDN5</i>	prefoldin subunit 5	0.67	0.00937
<i>RTN4IP1</i>	reticulon 4 interacting protein 1	0.67	0.004
<i>PDP1</i>	pyruvate dehydrogenase phosphatase catalytic subunit 1	0.67	0.00347
<i>FAM122B</i>	family with sequence similarity 122B	0.67	0.00331
<i>TMEM147</i>	transmembrane protein 147	0.67	0.00939
<i>ANO4</i>	anoctamin 4	0.67	0.00538
<i>MIS18A</i>	MIS18 kinetochore protein A	0.67	0.0133
<i>GHITM</i>	growth hormone inducible transmembrane protein	0.67	0.0107
<i>ZNF639</i>	zinc finger protein 639	0.67	0.00404
<i>AP2B1</i>	adaptor-related protein complex 2, beta 1 subunit	0.67	0.00588
<i>MRPL14</i>	mitochondrial ribosomal protein L14	0.68	0.0171
<i>EOGT</i>	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	0.68	0.012
<i>TTC37</i>	tetratricopeptide repeat domain 37	0.68	0.045
<i>KDM2A</i>	lysine (K)-specific demethylase 2A	0.68	0.011
<i>SORT1</i>	sortilin 1	0.68	0.0319
<i>EXOC6B</i>	exocyst complex component 6B	0.68	0.00511
<i>RIOK1</i>	RIO kinase 1	0.68	0.0259
<i>CCDC90B</i>	coiled-coil domain containing 90B	0.68	0.0423
<i>WDR43</i>	WD repeat domain 43	0.68	0.0134
<i>PTPRJ</i>	protein tyrosine phosphatase, receptor type, J	0.68	0.00656
<i>CCNJ</i>	cyclin J	0.68	0.00537
<i>CCT3</i>	chaperonin containing TCP1, subunit 3 (gamma)	0.68	0.00943
<i>UPF2</i>	UPF2 regulator of nonsense transcripts homolog (yeast)	0.68	0.00395
<i>UGGT1</i>	UDP-glucose glycoprotein glucosyltransferase 1	0.68	0.00437
<i>MYLK</i>	myosin light chain kinase	0.68	0.0188
<i>VPS41</i>	vacuolar protein sorting 41 homolog (S. cerevisiae)	0.68	0.00737
<i>NOTCH2</i>	notch 2	0.68	0.00605
<i>DSEL</i>	dermatan sulfate epimerase-like	0.68	0.0194
<i>TXNL4B</i>	thioredoxin-like 4B	0.68	0.0172
<i>AZI2</i>	5-azacytidine induced 2	0.68	0.0262
<i>EEA1</i>	early endosome antigen 1	0.68	0.0389
<i>RGS2</i>	regulator of G-protein signaling 2	0.68	0.00357
<i>CAV2</i>	caveolin 2	0.68	0.00411
<i>FBXL20</i>	F-box and leucine-rich repeat protein 20	0.68	0.0211
<i>ADPRM</i>	ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent	0.68	0.00418
<i>TIMM10</i>	translocase of inner mitochondrial membrane 10 homolog (yeast)	0.68	0.00362
<i>LAMP2</i>	lysosomal-associated membrane protein 2	0.68	0.0111
<i>MOCS2</i>	molybdenum cofactor synthesis 2	0.68	0.0465
<i>EML4</i>	echinoderm microtubule associated protein like 4	0.68	0.00817
<i>MGAT2</i>	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	0.68	0.00797
<i>CASP6</i>	caspase 6	0.68	0.0235
<i>DIABLO</i>	diablo, IAP-binding mitochondrial protein	0.68	0.0329
<i>TRIM16</i>	tripartite motif containing 16	0.68	0.00858
<i>RECK</i>	reversion-inducing-cysteine-rich protein with kazal motifs	0.68	0.00798
<i>HNRNPU</i>	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.68	0.0169
<i>TARBP1</i>	TAR (HIV-1) RNA binding protein 1	0.68	0.00564
<i>TMEM183A</i>	transmembrane protein 183A	0.68	0.00595

<i>TXNL4A</i>	thioredoxin-like 4A	0.68	0.0377
<i>SYNJ2BP-</i>	SYNJ2BP-COX16 readthrough	0.68	0.0195
<i>ZNF189</i>	zinc finger protein 189	0.68	0.0128
<i>LSM8</i>	LSM8 homolog, U6 small nuclear RNA associated	0.68	0.0219
<i>RNF26</i>	ring finger protein 26	0.69	0.00469
<i>BDH2</i>	3-hydroxybutyrate dehydrogenase, type 2	0.69	0.0072
<i>CMC1</i>	C-x(9)-C motif containing 1	0.69	0.0315
<i>GAB3</i>	GRB2-associated binding protein 3	0.69	0.0131
<i>EIF3E</i>	eukaryotic translation initiation factor 3, subunit E	0.69	0.0113
<i>NPIPB4</i>	nuclear pore complex interacting protein family, member B4	0.69	0.0172
<i>RCOR1</i>	REST corepressor 1	0.69	0.0085
<i>TSPAN13</i>	tetraspanin 13	0.69	0.00722
<i>DIXDC1</i>	DIX domain containing 1	0.69	0.00529
<i>RPL5</i>	ribosomal protein L5	0.69	0.0187
<i>C6orf62</i>	chromosome 6 open reading frame 62	0.69	0.0148
<i>MAMLD1</i>	mastermind-like domain containing 1	0.69	0.00751
<i>GALNT1</i>	polypeptide N-acetylgalactosaminyltransferase 1	0.69	0.0111
<i>ID1</i>	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	0.69	0.0098
<i>NT5DC3</i>	5-nucleotidase domain containing 3	0.69	0.00445
<i>SETD9</i>	SET domain containing 9	0.69	0.00459
<i>GLRX3</i>	glutaredoxin 3	0.69	0.00904
<i>EDN1</i>	endothelin 1	0.69	0.0068
<i>TP53BP2</i>	tumor protein p53 binding protein 2	0.69	0.0055
<i>PCYOX1</i>	prenylcysteine oxidase 1	0.69	0.013
<i>HSD17B10</i>	hydroxysteroid (17-beta) dehydrogenase 10	0.69	0.00735
<i>GLS</i>	glutaminase	0.69	0.0102
<i>TAF9</i>	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor,	0.69	0.0151
<i>BTN3A2</i>	butyrophilin, subfamily 3, member A2	0.69	0.0245
<i>GAS6</i>	growth arrest-specific 6	0.69	0.0165
<i>XPC</i>	xeroderma pigmentosum, complementation group C	0.69	0.0173
<i>MMAA</i>	methylmalonic aciduria (cobalamin deficiency) cblA type	0.69	0.00483
<i>TGM2</i>	transglutaminase 2	0.69	0.00372
<i>PTX3</i>	pentraxin 3, long	0.69	0.00426
<i>RNF128</i>	ring finger protein 128, E3 ubiquitin protein ligase	0.69	0.0453
<i>IRF1</i>	interferon regulatory factor 1	0.69	0.0258
<i>SAP18</i>	Sin3A associated protein 18kDa	0.69	0.0375
<i>DHX36</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 36	0.69	0.00875
<i>EIF2AK4</i>	eukaryotic translation initiation factor 2 alpha kinase 4	0.69	0.0418
<i>COA3</i>	cytochrome c oxidase assembly factor 3	0.69	0.0162
<i>INAFM1</i>	InaF-motif containing 1	0.69	0.024
<i>SIPA1L1</i>	signal-induced proliferation-associated 1 like 1	0.69	0.0131
<i>ZBED5</i>	zinc finger, BED-type containing 5	0.69	0.00724
<i>NAE1</i>	NEDD8 activating enzyme E1 subunit 1	0.69	0.00867
<i>PPP3CB</i>	protein phosphatase 3, catalytic subunit, beta isozyme	0.69	0.0247
<i>SEMA5A</i>	sema domain, seven thrombospondin repeats (type 1 and type 1-like),	0.69	0.00773
<i>HIVEP2</i>	human immunodeficiency virus type I enhancer binding protein 2	0.69	0.00709
<i>SPCS3</i>	signal peptidase complex subunit 3	0.69	0.0116
<i>ACTR8</i>	ARP8 actin-related protein 8 homolog (yeast)	0.69	0.00825
<i>MTDH</i>	metadherin	0.69	0.0446
<i>MATR3</i>	matrin 3	0.69	0.0426
<i>CD24</i>	CD24 molecule	0.69	0.0215
<i>TXNDC5</i>	thioredoxin domain containing 5 (endoplasmic reticulum)	0.69	0.0105
<i>POMGNT1</i>	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)	0.69	0.0172
<i>MALT1</i>	MALT1 paracaspase	0.69	0.0349
<i>SRSF5</i>	serine/arginine-rich splicing factor 5	0.69	0.00624
<i>MFSD14A</i>	major facilitator superfamily domain containing 14A	0.69	0.00644
<i>DAP3</i>	death associated protein 3	0.69	0.0194
<i>CGGBP1</i>	CGG triplet repeat binding protein 1	0.69	0.0353
<i>AP3M2</i>	adaptor-related protein complex 3, mu 2 subunit	0.69	0.0176

<i>AZIN1</i>	antizyme inhibitor 1	0.69	0.022
<i>SLC35A3</i>	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter),	0.70	0.0078
<i>MEDAG</i>	mesenteric estrogen-dependent adipogenesis	0.70	0.00658
<i>CCDC96</i>	coiled-coil domain containing 96	0.70	0.00863
<i>AASDHPPT</i>	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.70	0.0131
<i>DNAJC13</i>	DnaJ (Hsp40) homolog, subfamily C, member 13	0.70	0.0296
<i>MYL12B</i>	myosin light chain 12B	0.70	0.0417
<i>LY96</i>	lymphocyte antigen 96	0.70	0.00734
<i>MYOF</i>	myoferlin	0.70	0.0112
<i>ICAM1</i>	intercellular adhesion molecule 1	0.70	0.00804
<i>LTA4H</i>	leukotriene A4 hydrolase	0.70	0.0377
<i>SECISBP2L</i>	SECIS binding protein 2-like	0.70	0.0226
<i>SUB1</i>	SUB1 homolog, transcriptional regulator	0.70	0.0227
<i>BIN3</i>	bridging integrator 3	0.70	0.0123
<i>BBX</i>	bobby sox homolog (Drosophila)	0.70	0.0165
<i>CALM1</i>	calmodulin 1 (phosphorylase kinase, delta)	0.70	0.0246
<i>ANAPC1</i>	anaphase promoting complex subunit 1	0.70	0.0286
<i>TGDS</i>	TDP-glucose 4,6-dehydratase	0.70	0.0222
<i>RAP1A</i>	RAP1A, member of RAS oncogene family	0.70	0.0214
<i>BAG5</i>	BCL2-associated athanogene 5	0.70	0.0237
<i>FBXO22</i>	F-box protein 22	0.70	0.0317
<i>RCN1</i>	reticulocalbin 1, EF-hand calcium binding domain	0.70	0.00794
<i>NFU1</i>	NFU1 iron-sulfur cluster scaffold	0.70	0.0202
<i>OGFOD1</i>	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0.70	0.0434
<i>HGSNAT</i>	heparan-alpha-glucosaminide N-acetyltransferase	0.70	0.00593
<i>MCUR1</i>	mitochondrial calcium uniporter regulator 1	0.70	0.0337
<i>ZNF302</i>	zinc finger protein 302	0.70	0.0124
<i>AGO2</i>	argonaute RISC catalytic component 2	0.70	0.00853
<i>USP9X</i>	ubiquitin specific peptidase 9, X-linked	0.70	0.0138
<i>SP100</i>	SP100 nuclear antigen	0.70	0.0252
<i>SNRNPB</i>	small nuclear ribonucleoprotein polypeptides B and B1	0.70	0.0094
<i>ATP11C</i>	ATPase, class VI, type 11C	0.70	0.0363
<i>ZNF28</i>	zinc finger protein 28	0.70	0.00694
<i>ZNF532</i>	zinc finger protein 532	0.70	0.0146
<i>VAPA</i>	VAMP associated protein A	0.70	0.0109
<i>GNAZ</i>	guanine nucleotide binding protein (G protein), alpha z polypeptide	0.70	0.0405
<i>DHX15</i>	DEAH (Asp-Glu-Ala-His) box helicase 15	0.70	0.0491
<i>FBXL4</i>	F-box and leucine-rich repeat protein 4	0.70	0.0067
<i>WSB1</i>	WD repeat and SOCS box containing 1	0.70	0.0195
<i>HIF1A</i>	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription	0.70	0.0179
<i>C1orf21</i>	chromosome 1 open reading frame 21	0.70	0.0293
<i>FYN</i>	FYN proto-oncogene, Src family tyrosine kinase	0.70	0.00669
<i>ZBTB80S</i>	zinc finger and BTB domain containing 8 opposite strand	0.70	0.043
<i>UTP23</i>	UTP23, small subunit (SSU) processome component, homolog (yeast)	0.70	0.0145
<i>MTF2</i>	metal response element binding transcription factor 2	0.70	0.0165
<i>DGKI</i>	diacylglycerol kinase, iota	0.70	0.0296
<i>KLHL5</i>	kelch-like family member 5	0.70	0.0247
<i>GEMIN7</i>	gem nuclear organelle associated protein 7	0.70	0.0301
<i>DHX9</i>	DEAH (Asp-Glu-Ala-His) box helicase 9	0.70	0.0337
<i>IRAK4</i>	interleukin 1 receptor associated kinase 4	0.70	0.04
<i>CIR1</i>	corepressor interacting with RBPJ, 1	0.70	0.0172
<i>ERRFI1</i>	ERBB receptor feedback inhibitor 1	0.70	0.0146
<i>CDC42BPB</i>	CDC42 binding protein kinase beta (DMPK-like)	0.70	0.017
<i>RBX1</i>	ring-box 1, E3 ubiquitin protein ligase	0.70	0.0238
<i>TRMT112</i>	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	0.70	0.00708
<i>WBP2</i>	WW domain binding protein 2	0.70	0.0257
<i>HIVEP1</i>	human immunodeficiency virus type I enhancer binding protein 1	0.71	0.0145
<i>IL13RA1</i>	interleukin 13 receptor, alpha 1	0.71	0.0101
<i>EID1</i>	EP300 interacting inhibitor of differentiation 1	0.71	0.0312

<i>RAD54L2</i>	RAD54-like 2 (<i>S. cerevisiae</i>)	0.71	0.0107
<i>KCNH1</i>	potassium channel, voltage gated eag related subfamily H, member 1	0.71	0.00787
<i>USP15</i>	ubiquitin specific peptidase 15	0.71	0.0347
<i>STK17A</i>	serine/threonine kinase 17a	0.71	0.033
<i>NCKAP1</i>	NCK-associated protein 1	0.71	0.0177
<i>PGAM1</i>	Homo sapiens phosphoglycerate mutase 1 (brain), mRNA (cDNA clone	0.71	0.0129
<i>ZNF26</i>	zinc finger protein 26	0.71	0.0115
<i>MBTPS1</i>	membrane bound transcription factor peptidase, site 1	0.71	0.00945
<i>OCRL</i>	oculocerebrorenal syndrome of Lowe	0.71	0.0103
<i>NT5DC2</i>	5-nucleotidase domain containing 2	0.71	0.0143
<i>PGK1</i>	phosphoglycerate kinase 1	0.71	0.00833
<i>NTAN1</i>	N-terminal asparagine amidase	0.71	0.0111
<i>TMEM8B</i>	transmembrane protein 8B	0.71	0.0192
<i>CCNK</i>	cyclin K	0.71	0.0139
<i>CA5B</i>	carbonic anhydrase VB, mitochondrial	0.71	0.028
<i>B4GALT3</i>	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3	0.71	0.0143
<i>PSMD11</i>	proteasome 26S subunit, non-ATPase 11	0.71	0.0254
<i>TBRG1</i>	transforming growth factor beta regulator 1	0.71	0.00925
<i>SP110</i>	SP110 nuclear body protein	0.71	0.0199
<i>CBWD2</i>	COBW domain containing 2	0.71	0.0441
<i>NDUFS5</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q	0.71	0.0112
<i>ACYP1</i>	acylphosphatase 1, erythrocyte (common) type	0.71	0.0324
<i>ITFG1</i>	integrin alpha FG-GAP repeat containing 1	0.71	0.0127
<i>RAB7A</i>	RAB7A, member RAS oncogene family	0.71	0.0137
<i>DDX3X</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	0.71	0.01
<i>PPP2CA</i>	protein phosphatase 2, catalytic subunit, alpha isozyme	0.71	0.0319
<i>AKT2</i>	v-akt murine thymoma viral oncogene homolog 2	0.71	0.0114
<i>POLR2C</i>	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	0.71	0.0242
<i>FUS</i>	FUS RNA binding protein	0.71	0.0157
<i>KIAA0586</i>	KIAA0586	0.71	0.03
<i>ATG9A</i>	autophagy related 9A	0.71	0.00935
<i>MYO5A</i>	myosin VA	0.71	0.0141
<i>TCTN3</i>	tectonic family member 3	0.71	0.00893
<i>JAG1</i>	jagged 1	0.71	0.0263
<i>TNNI3K</i>	TNNI3 interacting kinase	0.71	0.0127
<i>ANKRD12</i>	ankyrin repeat domain 12	0.71	0.0328
<i>MRPL20</i>	mitochondrial ribosomal protein L20	0.71	0.0243
<i>RHOT1</i>	ras homolog family member T1	0.71	0.0253
<i>PIP5K1A</i>	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	0.71	0.0192
<i>SGTB</i>	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	0.71	0.0276
<i>WDR45</i>	WD repeat domain 45	0.71	0.0191
<i>DSN1</i>	DSN1 homolog, MIS12 kinetochore complex component	0.71	0.0171
<i>TPP2</i>	tripeptidyl peptidase II	0.71	0.0245
<i>S100A16</i>	S100 calcium binding protein A16	0.71	0.0323
<i>CXCL8</i>	chemokine (C-X-C motif) ligand 8	0.71	0.0491
<i>MKNK1</i>	MAP kinase interacting serine/threonine kinase 1	0.71	0.0447
<i>ZNF879</i>	zinc finger protein 879	0.71	0.0106
<i>CFAP36</i>	cilia and flagella associated protein 36	0.71	0.0225
<i>ADAMTS12</i>	ADAM metalloproteinase with thrombospondin type 1 motif 12	0.71	0.0105
<i>RBMS1</i>	RNA binding motif, single stranded interacting protein 1	0.71	0.0415
<i>CUL5</i>	cullin 5	0.72	0.023
<i>TRPC1</i>	transient receptor potential cation channel, subfamily C, member 1	0.72	0.019
<i>IBTK</i>	inhibitor of Bruton agammaglobulinemia tyrosine kinase	0.72	0.0371
<i>EIF6</i>	eukaryotic translation initiation factor 6	0.72	0.00836
<i>MSMO1</i>	methylsterol monooxygenase 1	0.72	0.0189
<i>AP3S2</i>	adaptor-related protein complex 3, sigma 2 subunit	0.72	0.0275
<i>ARL3</i>	ADP-ribosylation factor like GTPase 3	0.72	0.0181
<i>ARID2</i>	AT rich interactive domain 2 (ARID, RFX-like)	0.72	0.00889
<i>TCTN1</i>	tectonic family member 1	0.72	0.00903

<i>KRT18</i>	keratin 18, type I	0.72	0.00962
<i>MARVELD1</i>	MARVEL domain containing 1	0.72	0.0136
<i>SLC25A36</i>	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	0.72	0.0342
<i>TOP2A</i>	topoisomerase (DNA) II alpha	0.72	0.0158
<i>SGPL1</i>	sphingosine-1-phosphate lyase 1	0.72	0.0155
<i>NR3C1</i>	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	0.72	0.0129
<i>IFT80</i>	intraflagellar transport 80	0.72	0.0114
<i>RAB8B</i>	RAB8B, member RAS oncogene family	0.72	0.0127
<i>DDX17</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 17	0.72	0.0122
<i>PTBP2</i>	polypyrimidine tract binding protein 2	0.72	0.025
<i>FTO</i>	fat mass and obesity associated	0.72	0.0199
<i>MOSPD2</i>	motile sperm domain containing 2	0.72	0.00981
<i>NDUFV2</i>	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	0.72	0.0422
<i>PARBP</i>	PARP1 binding protein	0.72	0.0131
<i>CREBBP</i>	CREB binding protein	0.72	0.0212
<i>MOGS</i>	mannosyl-oligosaccharide glucosidase	0.72	0.0111
<i>SYNCRIP</i>	synaptotagmin binding, cytoplasmic RNA interacting protein	0.72	0.0251
<i>POLR2B</i>	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.72	0.024
<i>TNC</i>	tenascin C	0.72	0.0114
<i>FRMD4A</i>	FERM domain containing 4A	0.72	0.0196
<i>CTNNB1</i>	catenin (cadherin-associated protein), beta 1	0.72	0.0184
<i>CYB5A</i>	cytochrome b5 type A (microsomal)	0.72	0.0267
<i>PRPF40A</i>	PRP40 pre-mRNA processing factor 40 homolog A	0.72	0.0462
<i>SUDS3</i>	SDS3 homolog, SIN3A corepressor complex component	0.72	0.0198
<i>NRXN3</i>	neurexin 3	0.72	0.0158
<i>PPP1CA</i>	protein phosphatase 1, catalytic subunit, alpha isozyme	0.72	0.0288
<i>PGM3</i>	phosphoglucomutase 3	0.72	0.0222
<i>TYK2</i>	tyrosine kinase 2	0.72	0.0109
<i>CTBP2</i>	C-terminal binding protein 2	0.72	0.0126
<i>RNMT</i>	RNA (guanine-7-) methyltransferase	0.72	0.0191
<i>NGLY1</i>	N-glycanase 1	0.72	0.0196
<i>PWP1</i>	PWP1 homolog, endonuclease	0.72	0.0234
<i>MYDGF</i>	myeloid-derived growth factor	0.72	0.0175
<i>MTMR10</i>	myotubularin related protein 10	0.72	0.0384
<i>COPB2</i>	coatamer protein complex subunit beta 2 (beta prime)	0.72	0.0145
<i>TRAPPC3</i>	trafficking protein particle complex 3	0.72	0.0153
<i>SMARCAD1</i>	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin,	0.72	0.0125
<i>BDNF</i>	brain-derived neurotrophic factor	0.72	0.0243
<i>NME1</i>	NME/NM23 nucleoside diphosphate kinase 1	0.72	0.0272
<i>TJP1</i>	tight junction protein 1	0.72	0.015
<i>FDX1</i>	ferredoxin 1	0.72	0.0145
<i>PTPRD</i>	protein tyrosine phosphatase, receptor type, D	0.72	0.0264
<i>USP30</i>	ubiquitin specific peptidase 30	0.72	0.0291
<i>GLO1</i>	glyoxalase I	0.72	0.0314
<i>ACTN1</i>	actinin, alpha 1	0.72	0.0236
<i>ZFR</i>	zinc finger RNA binding protein	0.72	0.0241
<i>BHLHE40</i>	basic helix-loop-helix family, member e40	0.72	0.0109
<i>UBL3</i>	ubiquitin-like 3	0.72	0.0321
<i>EIF2B1</i>	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	0.72	0.0123
<i>ACBD6</i>	acyl-CoA binding domain containing 6	0.72	0.0315
<i>TUBB2A</i>	tubulin, beta 2A class IIa	0.72	0.0135
<i>DNAJA1</i>	DnaJ (Hsp40) homolog, subfamily A, member 1	0.72	0.0468
<i>IMPACT</i>	impact RWD domain protein	0.72	0.0167
<i>MALSU1</i>	mitochondrial assembly of ribosomal large subunit 1	0.72	0.0346
<i>ARMC1</i>	armadillo repeat containing 1	0.72	0.0249
<i>C20orf194</i>	chromosome 20 open reading frame 194	0.72	0.0456
<i>TRIM9</i>	tripartite motif containing 9	0.72	0.0125
<i>NDUFB2</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	0.72	0.026
<i>TRAPPC1</i>	trafficking protein particle complex 1	0.72	0.0152

<i>MCFD2</i>	multiple coagulation factor deficiency 2	0.72	0.0289
<i>CCDC80</i>	coiled-coil domain containing 80	0.72	0.0303
<i>YPEL2</i>	yippee like 2	0.73	0.0241
<i>FAM120AOS</i>	family with sequence similarity 120A opposite strand	0.73	0.0123
<i>UFC1</i>	ubiquitin-fold modifier conjugating enzyme 1	0.73	0.034
<i>GALNT2</i>	polypeptide N-acetylgalactosaminyltransferase 2	0.73	0.0249
<i>MTMR12</i>	myotubularin related protein 12	0.73	0.0236
<i>PLCB4</i>	phospholipase C, beta 4	0.73	0.0399
<i>SYT17</i>	synaptotagmin XVII	0.73	0.016
<i>GATAD1</i>	GATA zinc finger domain containing 1	0.73	0.0299
<i>MRPL44</i>	mitochondrial ribosomal protein L44	0.73	0.0448
<i>PTPMT1</i>	protein tyrosine phosphatase, mitochondrial 1	0.73	0.0204
<i>LANCL2</i>	LanC lantibiotic synthetase component C-like 2 (bacterial)	0.73	0.0226
<i>CCZ1B</i>	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated	0.73	0.0172
<i>GANAB</i>	glucosidase, alpha; neutral AB	0.73	0.0138
<i>PIK3C2A</i>	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	0.73	0.0222
<i>MASTL</i>	microtubule associated serine/threonine kinase-like	0.73	0.0109
<i>AAMDC</i>	adipogenesis associated, Mth938 domain containing	0.73	0.0357
<i>REV1</i>	REV1, DNA directed polymerase	0.73	0.0223
<i>AHCYL1</i>	adenosylhomocysteinase like 1	0.73	0.0202
<i>ZNF439</i>	zinc finger protein 439	0.73	0.0115
<i>AP2M1</i>	adaptor-related protein complex 2, mu 1 subunit	0.73	0.0123
<i>SPECC1</i>	sperm antigen with calponin homology and coiled-coil domains 1	0.73	0.0416
<i>GPBP1L1</i>	GC-rich promoter binding protein 1-like 1	0.73	0.0312
<i>RYK</i>	receptor-like tyrosine kinase	0.73	0.0312
<i>ANLN</i>	anillin actin binding protein	0.73	0.0411
<i>PLXDC2</i>	plexin domain containing 2	0.73	0.0211
<i>ATP6V1C1</i>	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	0.73	0.0273
<i>PCYT2</i>	phosphate cytidyltransferase 2, ethanolamine	0.73	0.0144
<i>SKIL</i>	SKI-like proto-oncogene	0.73	0.0131
<i>PDE1C</i>	phosphodiesterase 1C, calmodulin-dependent 70kDa	0.73	0.0172
<i>DMD</i>	dystrophin	0.73	0.0404
<i>WEE1</i>	WEE1 G2 checkpoint kinase	0.73	0.0194
<i>TBC1D19</i>	TBC1 domain family, member 19	0.73	0.0406
<i>MRPS14</i>	mitochondrial ribosomal protein S14	0.73	0.0143
<i>ZNF644</i>	zinc finger protein 644	0.73	0.0273
<i>TRMT61B</i>	tRNA methyltransferase 61B	0.73	0.0144
<i>RABEPK</i>	Rab9 effector protein with kelch motifs	0.73	0.0449
<i>KHDRBS3</i>	KH domain containing, RNA binding, signal transduction associated 3	0.73	0.0237
<i>CCNH</i>	cyclin H	0.73	0.0322
<i>GPN2</i>	GPN-loop GTPase 2	0.73	0.0142
<i>ASIC1</i>	acid sensing ion channel 1	0.73	0.0235
<i>HDAC1</i>	histone deacetylase 1	0.73	0.0153
<i>GTF2H2C_2</i>	GTF2H2 family member C, copy 2	0.73	0.0366
<i>CHCHD1</i>	coiled-coil-helix-coiled-coil-helix domain containing 1	0.73	0.0203
<i>INSIG2</i>	insulin induced gene 2	0.73	0.0184
<i>SLC30A7</i>	solute carrier family 30 (zinc transporter), member 7	0.73	0.0196
<i>ZDHHC2</i>	zinc finger, DHHC-type containing 2	0.73	0.0248
<i>ZDHHC21</i>	zinc finger, DHHC-type containing 21	0.73	0.019
<i>EXOSC7</i>	exosome component 7	0.73	0.0369
<i>GPR107</i>	G protein-coupled receptor 107	0.73	0.0164
<i>MMADHC</i>	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	0.73	0.0487
<i>KIAA2026</i>	KIAA2026	0.73	0.0214
<i>CFI</i>	complement factor I	0.73	0.0398
<i>COX7A2</i>	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	0.73	0.0204
<i>CLTC</i>	clathrin, heavy chain (Hc)	0.73	0.0379
<i>TAF2</i>	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor,	0.73	0.0412
<i>TRPM7</i>	transient receptor potential cation channel, subfamily M, member 7	0.73	0.0429
<i>VAMP3</i>	vesicle associated membrane protein 3	0.73	0.0359

<i>RTF1</i>	RTF1 homolog, Paf1/RNA polymerase II complex component	0.73	0.0394
<i>TMED2</i>	transmembrane p24 trafficking protein 2	0.73	0.029
<i>FUOM</i>	fucose mutarotase	0.73	0.0147
<i>ZNF558</i>	zinc finger protein 558	0.73	0.0247
<i>GPR137B</i>	G protein-coupled receptor 137B	0.73	0.0206
<i>ZNF24</i>	zinc finger protein 24	0.73	0.0232
<i>NRAS</i>	neuroblastoma RAS viral (v-ras) oncogene homolog	0.73	0.0292
<i>FUCA1</i>	fucosidase, alpha-L- 1, tissue	0.73	0.0393
<i>TMED7-</i>	TMED7-TICAM2 readthrough	0.73	0.037
<i>AREL1</i>	apoptosis resistant E3 ubiquitin protein ligase 1	0.73	0.0347
<i>RAN</i>	RAN, member RAS oncogene family	0.73	0.0364
<i>DDX6</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 6	0.73	0.0309
<i>ARHGEF28</i>	Rho guanine nucleotide exchange factor 28	0.73	0.0483
<i>NREP</i>	neuronal regeneration related protein	0.73	0.0331
<i>BMP2K</i>	BMP2 inducible kinase	0.73	0.0335
<i>FEZ1</i>	fasciculation and elongation protein zeta 1	0.73	0.0356
<i>MLC1</i>	megalencephalic leukoencephalopathy with subcortical cysts 1	0.73	0.0326
<i>RRP36</i>	ribosomal RNA processing 36	0.74	0.0283
<i>CREB3</i>	cAMP responsive element binding protein 3	0.74	0.0202
<i>GLT8D2</i>	glycosyltransferase 8 domain containing 2	0.74	0.019
<i>NUAK1</i>	NUAK family, SNF1-like kinase, 1	0.74	0.0162
<i>CDKN1C</i>	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0.74	0.0233
<i>PLK2</i>	polo-like kinase 2	0.74	0.0342
<i>DNMBP</i>	dynamamin binding protein	0.74	0.0342
<i>OPHN1</i>	oligophrenin 1	0.74	0.0199
<i>SERINC1</i>	serine incorporator 1	0.74	0.023
<i>PDCD2L</i>	programmed cell death 2-like	0.74	0.0393
<i>NDUFA12</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	0.74	0.0325
<i>KCTD20</i>	potassium channel tetramerization domain containing 20	0.74	0.0141
<i>TIMM23</i>	translocase of inner mitochondrial membrane 23 homolog (yeast)	0.74	0.0305
<i>SCARB2</i>	scavenger receptor class B, member 2	0.74	0.0269
<i>RBFOX2</i>	RNA binding protein, fox-1 homolog (C. elegans) 2	0.74	0.0168
<i>ATIC</i>	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP	0.74	0.0453
<i>RPL39</i>	ribosomal protein L39	0.74	0.0377
<i>EIF4A2</i>	eukaryotic translation initiation factor 4A2	0.74	0.0341
<i>PEX12</i>	peroxisomal biogenesis factor 12	0.74	0.0215
<i>NSL1</i>	NSL1, MIS12 kinetochore complex component	0.74	0.0162
<i>ZNF548</i>	zinc finger protein 548	0.74	0.0166
<i>PGAM4</i>	phosphoglycerate mutase family member 4	0.74	0.0452
<i>RNF10</i>	ring finger protein 10	0.74	0.0347
<i>RAPH1</i>	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	0.74	0.0191
<i>KDM5B</i>	lysine (K)-specific demethylase 5B	0.74	0.0326
<i>MRPS27</i>	mitochondrial ribosomal protein S27	0.74	0.0444
<i>EXOC6</i>	exocyst complex component 6	0.74	0.0254
<i>PHF12</i>	PHD finger protein 12	0.74	0.0322
<i>DGUOK</i>	deoxyguanosine kinase	0.74	0.0388
<i>NAGK</i>	N-acetylglucosamine kinase	0.74	0.0328
<i>MMP1</i>	matrix metalloproteinase 1	0.74	0.0422
<i>GTF2E2</i>	general transcription factor IIE subunit 2	0.74	0.0228
<i>FKBP14</i>	FK506 binding protein 14	0.74	0.0249
<i>ESCO1</i>	establishment of sister chromatid cohesion N-acetyltransferase 1	0.74	0.0241
<i>ZDHHC7</i>	zinc finger, DHHC-type containing 7	0.74	0.0317
<i>UBXN8</i>	UBX domain protein 8	0.74	0.0435
<i>PHACTR4</i>	phosphatase and actin regulator 4	0.74	0.0239
<i>TOMM22</i>	translocase of outer mitochondrial membrane 22 homolog (yeast)	0.74	0.0263
<i>CNIH1</i>	cornichon family AMPA receptor auxiliary protein 1	0.74	0.0479
<i>SAMD9L</i>	sterile alpha motif domain containing 9-like	0.74	0.0245
<i>DDX58</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0.74	0.0216
<i>SPAG7</i>	sperm associated antigen 7	0.74	0.0321

<i>LIX1L</i>	limb and CNS expressed 1 like	0.74	0.0307
<i>COQ10B</i>	coenzyme Q10B	0.74	0.0356
<i>CHSY1</i>	chondroitin sulfate synthase 1	0.74	0.0409
<i>CHN1</i>	chimerin 1	0.74	0.0355
<i>MPV17</i>	MpV17 mitochondrial inner membrane protein	0.74	0.019
<i>BNC2</i>	basonuclin 2	0.74	0.0212
<i>SH2D4A</i>	SH2 domain containing 4A	0.74	0.0388
<i>FAM83G</i>	family with sequence similarity 83, member G	0.75	0.0325
<i>CHD2</i>	chromodomain helicase DNA binding protein 2	0.75	0.022
<i>TAF9B</i>	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor,	0.75	0.024
<i>MAGOH</i>	mago homolog, exon junction complex core component	0.75	0.0429
<i>FBN1</i>	fibrillin 1	0.75	0.0356
<i>RNPEP</i>	arginyl aminopeptidase (aminopeptidase B)	0.75	0.0331
<i>XRCC6</i>	X-ray repair complementing defective repair in Chinese hamster cells 6	0.75	0.0257
<i>HADHA</i>	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase	0.75	0.0427
<i>HHIP</i>	hedgehog interacting protein	0.75	0.0203
<i>ALG8</i>	ALG8, alpha-1,3-glucosyltransferase	0.75	0.0341
<i>RPP30</i>	ribonuclease P/MRP 30kDa subunit	0.75	0.0249
<i>TSEN2</i>	TSEN2 tRNA splicing endonuclease subunit	0.75	0.0353
<i>TUBGCP2</i>	tubulin, gamma complex associated protein 2	0.75	0.0295
<i>EIF2B2</i>	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	0.75	0.025
<i>DMTF1</i>	cyclin D binding myb-like transcription factor 1	0.75	0.0279
<i>BPHL</i>	biphenyl hydrolase-like (serine hydrolase)	0.75	0.0417
<i>SLC16A9</i>	solute carrier family 16, member 9	0.75	0.0223
<i>UTP18</i>	UTP18 small subunit (SSU) processome component	0.75	0.0375
<i>ZYG11B</i>	zyg-11 family member B, cell cycle regulator	0.75	0.0396
<i>SPOPL</i>	speckle-type POZ protein-like	0.75	0.04
<i>TPX2</i>	TPX2, microtubule-associated	0.75	0.0453
<i>TAF12</i>	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor,	0.75	0.0354
<i>ZFHx4</i>	zinc finger homeobox 4	0.75	0.0325
<i>ARMC9</i>	armadillo repeat containing 9	0.75	0.0404
<i>FAF1</i>	Fas (TNFRSF6) associated factor 1	0.75	0.0299
<i>TUBB2B</i>	tubulin, beta 2B class IIb	0.75	0.0475
<i>ZCCHC9</i>	zinc finger, CCHC domain containing 9	0.75	0.0277
<i>STK32B</i>	serine/threonine kinase 32B	0.75	0.0497
<i>SMAD1</i>	SMAD family member 1	0.75	0.0202
<i>RAB21</i>	RAB21, member RAS oncogene family	0.75	0.031
<i>QSOX1</i>	quiescin Q6 sulfhydryl oxidase 1	0.75	0.0231
<i>TADA1</i>	transcriptional adaptor 1	0.75	0.0413
<i>DCTN2</i>	dynactin 2 (p50)	0.75	0.0275
<i>OTUB1</i>	OTU deubiquitinase, ubiquitin aldehyde binding 1	0.75	0.0208
<i>GALNT5</i>	polypeptide N-acetylgalactosaminyltransferase 5	0.75	0.0447
<i>MRPS18A</i>	mitochondrial ribosomal protein S18A	0.75	0.0252
<i>DENND4C</i>	DENN/MADD domain containing 4C	0.75	0.04
<i>LRP12</i>	LDL receptor related protein 12	0.75	0.0305
<i>GOLPH3</i>	golgi phosphoprotein 3 (coat-protein)	0.75	0.0304
<i>TXNIP</i>	thioredoxin interacting protein	0.75	0.0312
<i>TBC1D1</i>	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	0.75	0.0379
<i>CDC23</i>	cell division cycle 23	0.75	0.0381
<i>GNPAT</i>	glyceronephosphate O-acyltransferase	0.75	0.0493
<i>GPR89A</i>	G protein-coupled receptor 89A	0.75	0.0362
<i>FBXO32</i>	F-box protein 32	0.75	0.0264
<i>GNAI3</i>	guanine nucleotide binding protein (G protein), alpha inhibiting activity	0.75	0.0494
<i>DERL1</i>	derlin 1	0.75	0.0246
<i>TMEM205</i>	transmembrane protein 205	0.75	0.0321
<i>APIG1</i>	adaptor-related protein complex 1, gamma 1 subunit	0.75	0.0299
<i>UBE3A</i>	ubiquitin protein ligase E3A	0.75	0.0316
<i>ARPC4</i>	actin related protein 2/3 complex subunit 4	0.75	0.0256
<i>EFNB2</i>	ephrin-B2	0.75	0.0315

<i>ITGA2</i>	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	0.75	0.0334
<i>GABRG3</i>	gamma-aminobutyric acid (GABA) A receptor, gamma 3	0.75	0.0282
<i>IDH3B</i>	isocitrate dehydrogenase 3 (NAD+) beta	0.75	0.0321
<i>PPRC1</i>	peroxisome proliferator-activated receptor gamma, coactivator-related 1	0.75	0.0277
<i>ACTR10</i>	actin-related protein 10 homolog (S. cerevisiae)	0.75	0.0372
<i>LRRC8B</i>	leucine rich repeat containing 8 family, member B	0.75	0.034
<i>CEMIP</i>	cell migration inducing protein, hyaluronan binding	0.75	0.0241
<i>IFNGR2</i>	interferon gamma receptor 2 (interferon gamma transducer 1)	0.75	0.0263
<i>TMEM168</i>	transmembrane protein 168	0.76	0.0284
<i>BIRC3</i>	baculoviral IAP repeat containing 3	0.76	0.0253
<i>NSFL1C</i>	NSFL1 (p97) cofactor (p47)	0.76	0.0413
<i>NDUFB8</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	0.76	0.0306
<i>PITPNB</i>	phosphatidylinositol transfer protein, beta	0.76	0.0417
<i>MAP1B</i>	microtubule associated protein 1B	0.76	0.0384
<i>NAGA</i>	N-acetylgalactosaminidase, alpha-	0.76	0.0267
<i>ZNF280B</i>	zinc finger protein 280B	0.76	0.0452
<i>TGS1</i>	trimethylguanosine synthase 1	0.76	0.0425
<i>MAP3K3</i>	mitogen-activated protein kinase kinase kinase 3	0.76	0.0285
<i>FKTN</i>	fukutin	0.76	0.0456
<i>ARHGEF25</i>	Rho guanine nucleotide exchange factor 25	0.76	0.0352
<i>STK38</i>	serine/threonine kinase 38	0.76	0.037
<i>COMMD1</i>	copper metabolism (Murr1) domain containing 1	0.76	0.0448
<i>NCBP2</i>	nuclear cap binding protein subunit 2	0.76	0.0334
<i>MAPKAP1</i>	mitogen-activated protein kinase associated protein 1	0.76	0.0491
<i>RNF214</i>	ring finger protein 214	0.76	0.0307
<i>IRAK2</i>	interleukin 1 receptor associated kinase 2	0.76	0.0379
<i>CCM2</i>	cerebral cavernous malformation 2	0.76	0.039
<i>PDE5A</i>	phosphodiesterase 5A, cGMP-specific	0.76	0.0296
<i>GMDS</i>	GDP-mannose 4,6-dehydratase	0.76	0.027
<i>BCAR3</i>	breast cancer anti-estrogen resistance 3	0.76	0.0393
<i>SRRD</i>	SRR1 domain containing	0.76	0.0289
<i>LMNA</i>	lamin A/C	0.76	0.035
<i>XRNI</i>	5-3 exoribonuclease 1	0.76	0.028
<i>FAM155A</i>	family with sequence similarity 155, member A	0.76	0.034
<i>MAN1A2</i>	mannosidase, alpha, class 1A, member 2	0.76	0.0373
<i>GDE1</i>	glycerophosphodiester phosphodiesterase 1	0.76	0.0419
<i>VAMP1</i>	vesicle associated membrane protein 1	0.76	0.0341
<i>SNRNP35</i>	small nuclear ribonucleoprotein, U11/U12 35kDa subunit	0.76	0.0487
<i>PATZ1</i>	POZ (BTB) and AT hook containing zinc finger 1	0.76	0.0488
<i>DDX39B</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	0.76	0.0375
<i>RECQL5</i>	RecQ helicase-like 5	0.76	0.0414
<i>TINF2</i>	TERF1 (TRF1)-interacting nuclear factor 2	0.76	0.0329
<i>RRP8</i>	ribosomal RNA processing 8, methyltransferase, homolog (yeast)	0.76	0.037
<i>MFF</i>	mitochondrial fission factor	0.76	0.0417
<i>PRKG1</i>	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic	0.76	0.033
<i>FAM120B</i>	family with sequence similarity 120B	0.76	0.0354
<i>POLR2E</i>	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	0.76	0.0426
<i>SLC25A43</i>	solute carrier family 25, member 43	0.76	0.0264
<i>DHRS1</i>	dehydrogenase/reductase (SDR family) member 1	0.76	0.0378
<i>CCNG1</i>	cyclin G1	0.76	0.0432
<i>SH3RF1</i>	SH3 domain containing ring finger 1	0.76	0.0435
<i>RNF145</i>	ring finger protein 145	0.76	0.0416
<i>ILF3</i>	interleukin enhancer binding factor 3	0.76	0.0348
<i>SHOC2</i>	SHOC2 leucine-rich repeat scaffold protein	0.76	0.0378
<i>UTP4</i>	UTP4 small subunit (SSU) processome component	0.76	0.0389
<i>CMIP</i>	c-Maf inducing protein	0.76	0.0297
<i>TMEM192</i>	transmembrane protein 192	0.76	0.0391
<i>BRAP</i>	BRCA1 associated protein	0.76	0.0392
<i>TUBGCP5</i>	tubulin, gamma complex associated protein 5	0.76	0.0297

<i>EPHA2</i>	EPH receptor A2	0.76	0.0359
<i>SPTAN1</i>	spectrin, alpha, non-erythrocytic 1	0.76	0.0405
<i>N6AMT1</i>	N-6 adenine-specific DNA methyltransferase 1 (putative)	0.76	0.047
<i>IL6</i>	interleukin 6	0.76	0.0374
<i>MEIS1</i>	Meis homeobox 1	0.76	0.0409
<i>MRPL36</i>	mitochondrial ribosomal protein L36	0.76	0.0367
<i>SLC11A2</i>	solute carrier family 11 (proton-coupled divalent metal ion transporter), member	0.77	0.0361
<i>COMMD8</i>	COMM domain containing 8	0.77	0.049
<i>GDF5</i>	growth differentiation factor 5	0.77	0.0498
<i>PDZD11</i>	PDZ domain containing 11	0.77	0.0429
<i>PLPP3</i>	phospholipid phosphatase 3	0.77	0.0474
<i>MON2</i>	MON2 homolog, regulator of endosome-to-Golgi trafficking	0.77	0.044
<i>EDA2R</i>	ectodysplasin A2 receptor	0.77	0.0363
<i>SHB</i>	Src homology 2 domain containing adaptor protein B	0.77	0.0361
<i>RSL1D1</i>	ribosomal L1 domain containing 1	0.77	0.0335
<i>MLXIP</i>	MLX interacting protein	0.77	0.0372
<i>CDC42EP3</i>	CDC42 effector protein (Rho GTPase binding) 3	0.77	0.0324
<i>PXYLP1</i>	2-phosphoxylose phosphatase 1	0.77	0.0353
<i>ATP6V1E2</i>	ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E2	0.77	0.0495
<i>CDC42</i>	cell division cycle 42	0.77	0.0432
<i>LMCD1</i>	LIM and cysteine-rich domains 1	0.77	0.0348
<i>MLF2</i>	myeloid leukemia factor 2	0.77	0.0405
<i>PSME3</i>	proteasome activator subunit 3	0.77	0.0321
<i>RPS4X</i>	ribosomal protein S4, X-linked	0.77	0.0423
<i>POLR3A</i>	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	0.77	0.0493
<i>NOL11</i>	nucleolar protein 11	0.77	0.0359
<i>PIGG</i>	phosphatidylinositol glycan anchor biosynthesis class G	0.77	0.0338
<i>GID8</i>	GID complex subunit 8	0.77	0.0404
<i>C1D</i>	C1D nuclear receptor corepressor	0.77	0.0431
<i>S100A6</i>	S100 calcium binding protein A6	0.77	0.0491
<i>HP1BP3</i>	heterochromatin protein 1, binding protein 3	0.77	0.0459
<i>NEO1</i>	neogenin 1	0.77	0.0482
<i>ZNF322</i>	zinc finger protein 322	0.77	0.0394
<i>IGF2BP2</i>	insulin-like growth factor 2 mRNA binding protein 2	0.77	0.0429
<i>CDC27</i>	cell division cycle 27	0.77	0.0406
<i>IFFO2</i>	intermediate filament family orphan 2	0.77	0.0404
<i>XIAP</i>	X-linked inhibitor of apoptosis, E3 ubiquitin protein ligase	0.77	0.0454
<i>SUGP2</i>	SURP and G-patch domain containing 2	0.77	0.0411
<i>FAM3C</i>	family with sequence similarity 3, member C	0.77	0.0361
<i>UBE2K</i>	ubiquitin conjugating enzyme E2K	0.77	0.0481
<i>SPAG9</i>	sperm associated antigen 9	0.77	0.0396
<i>UAP1</i>	UDP-N-acetylglucosamine pyrophosphorylase 1	0.77	0.0484
<i>HTRA1</i>	HtrA serine peptidase 1	0.77	0.0393
<i>RAP1GAP2</i>	RAP1 GTPase activating protein 2	0.77	0.0479
<i>ANKFY1</i>	ankyrin repeat and FYVE domain containing 1	0.77	0.0407
<i>FER</i>	fer (fps/fes related) tyrosine kinase	0.77	0.0402
<i>GDI2</i>	GDP dissociation inhibitor 2	0.77	0.0452
<i>BTN2A1</i>	butyrophilin, subfamily 2, member A1	0.77	0.0351
<i>NUAK2</i>	NUAK family, SNF1-like kinase, 2	0.77	0.0489
<i>DAW1</i>	dynein assembly factor with WDR repeat domains 1	0.77	0.0488
<i>SUCO</i>	SUN domain containing ossification factor	0.77	0.0499
<i>RPL10</i>	ribosomal protein L10	0.77	0.0441
<i>ZC3H14</i>	zinc finger CCCH-type containing 14	0.77	0.0446
<i>ZNF398</i>	zinc finger protein 398	0.77	0.0451
<i>FMNL3</i>	formin like 3	0.77	0.0339
<i>CITED2</i>	Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain,	0.77	0.0459
<i>STX8</i>	syntaxin 8	0.78	0.048
<i>PHLDB2</i>	pleckstrin homology-like domain, family B, member 2	0.78	0.0469
<i>IYD</i>	iodotyrosine deiodinase	0.78	0.0438

<i>KCMF1</i>	potassium channel modulatory factor 1	0.78	0.046
<i>FAM114A2</i>	family with sequence similarity 114, member A2	0.78	0.0468
<i>NOL9</i>	nucleolar protein 9	0.78	0.0467
<i>PIGB</i>	phosphatidylinositol glycan anchor biosynthesis class B	0.78	0.0386
<i>CPA4</i>	carboxypeptidase A4	0.78	0.0459
<i>TTLL5</i>	tubulin tyrosine ligase-like family member 5	0.78	0.0433
<i>PRKA</i>	protein kinase C, alpha	0.78	0.0446
<i>ZNF608</i>	zinc finger protein 608	0.78	0.0408
<i>ZDHHC23</i>	zinc finger, DHHC-type containing 23	0.78	0.0442
<i>APOBEC3C</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	0.78	0.0457
<i>ARRDC4</i>	arrestin domain containing 4	0.78	0.0487
<i>TMEM265</i>	transmembrane protein 265	0.78	0.0406
<i>CAPZB</i>	capping protein (actin filament) muscle Z-line, beta	0.78	0.0493
<i>STAU1</i>	staufen double-stranded RNA binding protein 1	0.78	0.0434
<i>SEMA3C</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted,	0.78	0.0471
<i>VEZF1</i>	vascular endothelial zinc finger 1	0.78	0.0474
<i>BEX4</i>	brain expressed X-linked 4	0.78	0.0432
<i>LCAT</i>	lecithin-cholesterol acyltransferase	0.78	0.0445
<i>SOCS4</i>	suppressor of cytokine signaling 4	0.78	0.0489
<i>TMBIM4</i>	transmembrane BAX inhibitor motif containing 4	0.78	0.0461
<i>NDST2</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	0.78	0.0467
<i>PCCB</i>	propionyl-CoA carboxylase beta subunit	0.79	0.0448
<i>VCL</i>	vinculin	0.79	0.0464