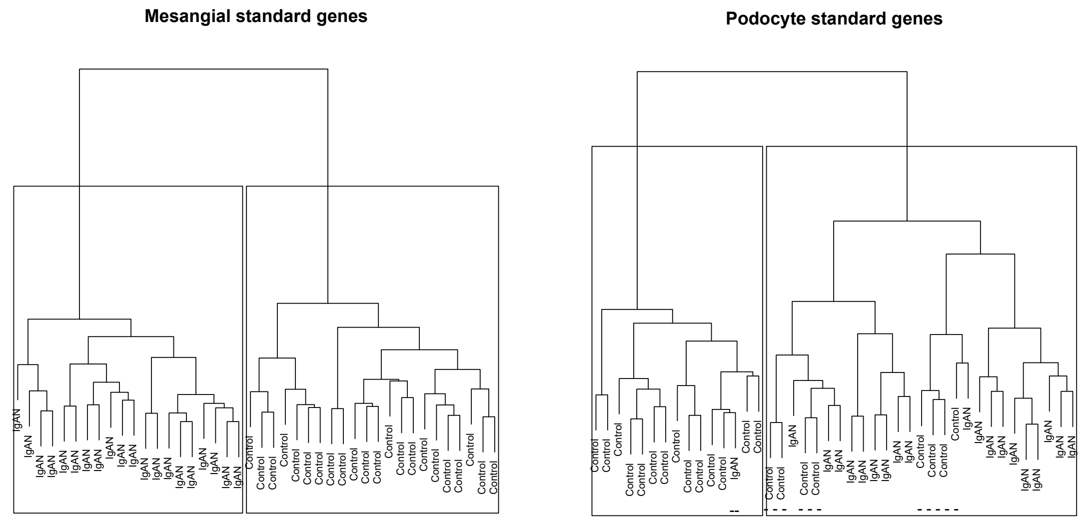
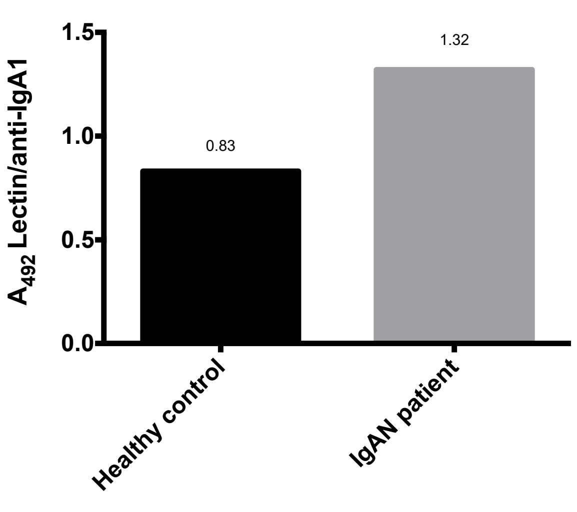
Supplement

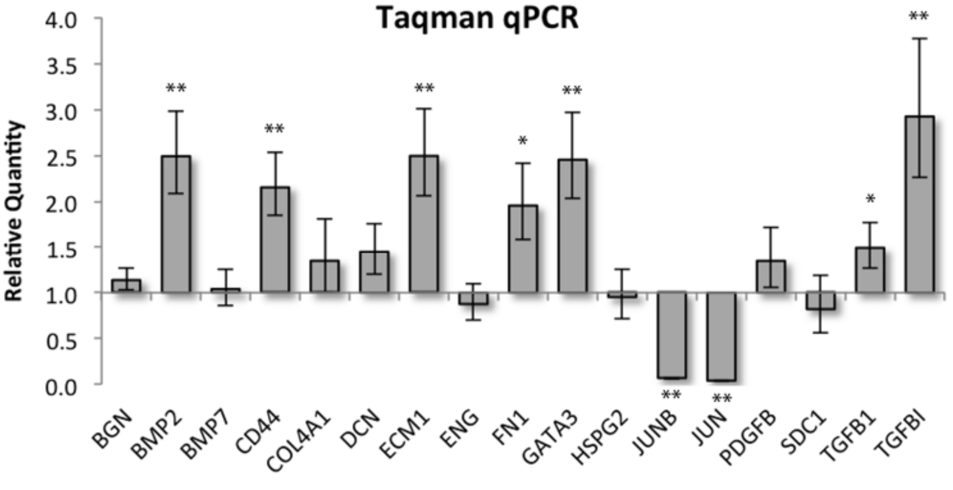
Supplemental Figure 1: Hierarchical clustering using “Ward” averaging method based only on cell-type positive standard genes from mesangial cells or podocytes. Using mesangial cell positive standard genes the IgAN patient samples can be separated from the control group samples, while using podocyte positive standard genes yields overlapping results.



Supplemental Figure 2: ELISA showing the ratio of gd-IgA content in the serum of an IgAN patient compared to that of healthy control. Lectin *Helix Aspersa* was used to detect gd-IgA. The ratio of gd-IgA in patient serum is 1.32 compared to healthy control 0.83, indicating a much higher gd-IgA content in the IgAN patient.



Supplemental Figure 3: Taqman® Q-PCR evaluation of microarray data. Bar graph represents confirmed expression of significantly regulated genes. Up and down regulation is also confirmed in agreement with the microarray data.



Supplemental Table 1: List of all significantly differentially expressed genes identified in microarray analysis. Genes are sorted according to q-values and fold change is considered up regulation if the q-value is >1.5 and down regulation if the q-value is <0.67.

Entrez ID	Fold change (Unlogged)	Fold change (log2)	Q-value	Symbol	Description
3627	2.3914	1.2579	0.00E+00	CXCL10	chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:HGNC:10637]
10516	1.9331	0.9509	0.00E+00	FBLN5	fibulin 5 [Source:HGNC Symbol;Acc:HGNC:3602]
7097	1.5844	0.6639	0.00E+00	TLR2	toll-like receptor 2 [Source:HGNC Symbol;Acc:HGNC:11848]
6039	1.6594	0.7307	0.00E+00	RNASE6	ribonuclease, RNase A family, k6 [Source:HGNC Symbol;Acc:HGNC:10048]
1043	1.5658	0.6469	0.00E+00	CD52	CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
3043	1.9514	0.9645	0.00E+00	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
23015	1.5353	0.6186	0.00E+00	GOLGA8B	golgin A8 family, member B [Source:HGNC Symbol;Acc:HGNC:31973]
221303	1.5654	0.6465	0.00E+00	FAM162B	family with sequence similarity 162, member B [Source:HGNC Symbol;Acc:HGNC:21549]
6351	2.4230	1.2768	0.00E+00	CCL4	chemokine (C-C motif) ligand 4 [Source:HGNC Symbol;Acc:HGNC:10630]
3394	1.6520	0.7242	0.00E+00	IRF8	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:HGNC:5358]
4057	1.6081	0.6854	0.00E+00	LTF	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
1759	1.5543	0.6363	0.00E+00	DNM1	dynamin 1 [Source:HGNC Symbol;Acc:HGNC:2972]
10288	1.7345	0.7945	0.00E+00	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 [Source:HGNC Symbol;Acc:HGNC:6606]
4050	1.5094	0.5940	0.00E+00	LTB	lymphotoxin beta (TNF superfamily, member 3) [Source:HGNC Symbol;Acc:HGNC:6711]
3620	2.1099	1.0772	0.00E+00	IDO1	indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:HGNC:6059]
1520	1.5858	0.6653	0.00E+00	CTSS	cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
2162	1.8440	0.8828	0.00E+00	F13A1	coagulation factor XIII, A1 polypeptide [Source:HGNC Symbol;Acc:HGNC:3531]
2268	1.5315	0.6150	0.00E+00	FGR	FGR proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:3697]
963	1.7540	0.8107	0.00E+00	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
3908	1.5794	0.6593	0.00E+00	LAMA2	laminin, alpha 2 [Source:HGNC Symbol;Acc:HGNC:6482]
962	1.6889	0.7561	0.00E+00	CD48	CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]

9770	1.5077	0.5924	0.00E+00	RASSF2	Ras association (RalGDS/AF-6) domain family member 2 [Source:HGNC Symbol;Acc:HGNC:9883]
6422	1.6381	0.7121	0.00E+00	SFRP1	secreted frizzled-related protein 1 [Source:HGNC Symbol;Acc:HGNC:10776]
348094	1.5023	0.5872	0.00E+00	ANKDD1A	ankyrin repeat and death domain containing 1A [Source:HGNC Symbol;Acc:HGNC:28002]
3561	1.5313	0.6148	0.00E+00	IL2RG	interleukin 2 receptor, gamma [Source:HGNC Symbol;Acc:HGNC:6010]
4907	1.7807	0.8325	0.00E+00	NT5E	5'-nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:HGNC:8021]
3936	1.7666	0.8210	0.00E+00	LCP1	lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:HGNC:6528]
2687	1.5054	0.5901	0.00E+00	GGT5	gamma-glutamyltransferase 5 [Source:HGNC Symbol;Acc:HGNC:4260]
6876	1.7099	0.7739	0.00E+00	TAGLN	transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
3689	1.6183	0.6945	0.00E+00	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:HGNC:6155]
7276	1.6219	0.6977	0.00E+00	TTR	transthyretin [Source:HGNC Symbol;Acc:HGNC:12405]
10417	1.5646	0.6458	0.00E+00	SPON2	spondin 2, extracellular matrix protein [Source:HGNC Symbol;Acc:HGNC:11253]
200316	1.5090	0.5936	0.00E+00	APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F [Source:HGNC Symbol;Acc:HGNC:17356]
4938	1.5206	0.6046	0.00E+00	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa [Source:HGNC Symbol;Acc:HGNC:8086]
9232	1.5753	0.6557	0.00E+00	PTTG1	pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:HGNC:9690]
140578	3.1165	1.6399	0.00E+00	CHODL	chondrolectin [Source:HGNC Symbol;Acc:HGNC:17807]
11098	1.5355	0.6187	0.00E+00	PRSS23	protease, serine, 23 [Source:HGNC Symbol;Acc:HGNC:14370]
64231	1.9938	0.9955	0.00E+00	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A [Source:HGNC Symbol;Acc:HGNC:13375]
3371	1.5718	0.6524	0.00E+00	TNC	tenascin C [Source:HGNC Symbol;Acc:HGNC:5318]
51058	1.5211	0.6051	0.00E+00	ZNF691	zinc finger protein 691 [Source:HGNC Symbol;Acc:HGNC:28028]
30845	1.5549	0.6369	0.00E+00	EHD3	EH-domain containing 3 [Source:HGNC Symbol;Acc:HGNC:3244]
10201	1.5190	0.6031	0.00E+00	NME6	NME/NM23 nucleoside diphosphate kinase 6 [Source:HGNC Symbol;Acc:HGNC:20567]

6275	1.7170	0.7799	0.00E+00	S100A4	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:HGNC:10494]
1259	1.9399	0.9560	0.00E+00	CNGA1	cyclic nucleotide gated channel alpha 1 [Source:HGNC Symbol;Acc:HGNC:2148]
8605	1.5090	0.5936	0.00E+00	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent) [Source:HGNC Symbol;Acc:HGNC:9037]
170685	1.5303	0.6138	0.00E+00	NUDT10	nudix (nucleoside diphosphate linked moiety X)-type motif 10 [Source:HGNC Symbol;Acc:HGNC:17621]
51365	1.8290	0.8711	0.00E+00	PLA1A	phospholipase A1 member A [Source:HGNC Symbol;Acc:HGNC:17661]
650	1.8616	0.8966	0.00E+00	BMP2	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:HGNC:1069]
5198	1.5342	0.6175	0.00E+00	PFAS	phosphoribosylformylglycinamidine synthase [Source:HGNC Symbol;Acc:HGNC:8863]
387758	1.8248	0.8677	0.00E+00	FIBIN	fin bud initiation factor homolog (zebrafish) [Source:HGNC Symbol;Acc:HGNC:33747]
2331	1.7533	0.8101	0.00E+00	FMOD	fibromodulin [Source:HGNC Symbol;Acc:HGNC:3774]
2350	1.7110	0.7749	0.00E+00	FOLR2	folate receptor 2 (fetal) [Source:HGNC Symbol;Acc:HGNC:3793]
10537	2.5424	1.3462	0.00E+00	UBD	ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
146722	1.5148	0.5991	0.00E+00	CD300LF	CD300 molecule-like family member f [Source:HGNC Symbol;Acc:HGNC:29883]
652	1.8416	0.8810	0.00E+00	BMP4	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:HGNC:1071]
7980	1.9089	0.9327	0.00E+00	TFPI2	tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:11761]
64091	1.6074	0.6847	0.00E+00	POPDC2	popeye domain containing 2 [Source:HGNC Symbol;Acc:HGNC:17648]
122786	1.5183	0.6025	0.00E+00	FRMD6	FERM domain containing 6 [Source:HGNC Symbol;Acc:HGNC:19839]
56670	2.2346	1.1600	0.00E+00	SUCNR1	succinate receptor 1 [Source:HGNC Symbol;Acc:HGNC:4542]
54440	1.6264	0.7017	0.00E+00	SASH3	SAM and SH3 domain containing 3 [Source:HGNC Symbol;Acc:HGNC:15975]
3553	2.2845	1.1919	0.00E+00	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:HGNC:5992]
83541	1.6571	0.7286	0.00E+00	FAM110A	family with sequence similarity 110, member A [Source:HGNC Symbol;Acc:HGNC:16188]
4069	2.0589	1.0419	0.00E+00	LYZ	lysozyme [Source:HGNC Symbol;Acc:HGNC:6740]

5880	1.5967	0.6751	0.00E+00	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) [Source:HGNC Symbol;Acc:HGNC:9802]
23378	1.5014	0.5863	0.00E+00	RRP8	ribosomal RNA processing 8, methyltransferase, homolog (yeast) [Source:HGNC Symbol;Acc:HGNC:29030]
9133	1.5263	0.6100	0.00E+00	CCNB2	cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
85377	1.6049	0.6825	0.00E+00	MICALL1	MICAL-like 1 [Source:HGNC Symbol;Acc:HGNC:29804]
253264	1.5705	0.6512	0.00E+00	ZNF503-AS1	ZNF503 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:27370]
7075	1.6341	0.7085	0.00E+00	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1 [Source:HGNC Symbol;Acc:HGNC:11809]
126375	1.6286	0.7037	0.00E+00	ZNF792	zinc finger protein 792 [Source:HGNC Symbol;Acc:HGNC:24751]
9603	1.5594	0.6410	0.00E+00	NFE2L3	nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:HGNC:7783]
4125	1.5590	0.6406	0.00E+00	MAN2B1	mannosidase, alpha, class 2B, member 1 [Source:HGNC Symbol;Acc:HGNC:6826]
3119	1.9625	0.9727	0.00E+00	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:4944]
4092	1.6715	0.7411	0.00E+00	SMAD7	SMAD family member 7 [Source:HGNC Symbol;Acc:HGNC:6773]
84281	1.5310	0.6145	0.00E+00	C2ORF88	chromosome 2 open reading frame 88 [Source:HGNC Symbol;Acc:HGNC:28191]
2207	1.9536	0.9662	0.00E+00	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide [Source:HGNC Symbol;Acc:HGNC:3611]
187	2.1982	1.1363	0.00E+00	APLNR	apelin receptor [Source:HGNC Symbol;Acc:HGNC:339]
11010	1.5155	0.5998	0.00E+00	GLIPR1	GLI pathogenesis-related 1 [Source:HGNC Symbol;Acc:HGNC:17001]
10974	1.5283	0.6119	0.00E+00	ADIRF	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:HGNC:24043]
4237	1.5569	0.6387	0.00E+00	MFAP2	microfibrillar-associated protein 2 [Source:HGNC Symbol;Acc:HGNC:7033]
55900	1.5448	0.6274	0.00E+00	ZNF302	zinc finger protein 302 [Source:HGNC Symbol;Acc:HGNC:13848]
10718	1.6048	0.6824	0.00E+00	NRG3	neuregulin 3 [Source:HGNC Symbol;Acc:HGNC:7999]
8490	1.5941	0.6728	0.00E+00	RGS5	regulator of G-protein signaling 5 [Source:EntrezGene;Acc:8490]
79778	1.6285	0.7036	0.00E+00	MICALL2	MICAL-like 2 [Source:HGNC Symbol;Acc:HGNC:29672]

7058	2.3112	1.2087	0.00E+00	THBS2	thrombospondin 2 [Source:HGNC Symbol;Acc:HGNC:11786]
1524	2.3199	1.2140	0.00E+00	CX3CR1	chemokine (C-X3-C motif) receptor 1 [Source:HGNC Symbol;Acc:HGNC:2558]
5156	1.5183	0.6025	0.00E+00	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide [Source:HGNC Symbol;Acc:HGNC:8803]
727936	1.5399	0.6228	0.00E+00	GXYLT2	glucoside xylosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:33383]
59	1.9215	0.9422	0.00E+00	ACTA2	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Acc:HGNC:130]
60676	1.5898	0.6688	0.00E+00	PAPPA2	pappalysin 2 [Source:HGNC Symbol;Acc:HGNC:14615]
5507	1.8404	0.8800	0.00E+00	PPP1R3C	protein phosphatase 1, regulatory subunit 3C [Source:HGNC Symbol;Acc:HGNC:9293]
10631	2.1573	1.1092	0.00E+00	POSTN	periostin, osteoblast specific factor [Source:HGNC Symbol;Acc:HGNC:16953]
7133	1.5402	0.6231	0.00E+00	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:HGNC:11917]
595	1.6085	0.6857	0.00E+00	CCND1	cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
2615	1.6683	0.7384	0.00E+00	LRRC32	leucine rich repeat containing 32 [Source:HGNC Symbol;Acc:HGNC:4161]
641700	1.5180	0.6021	0.00E+00	ECSCR	endothelial cell surface expressed chemotaxis and apoptosis regulator [Source:HGNC Symbol;Acc:HGNC:35454]
3429	1.5561	0.6380	0.00E+00	IFI27	interferon, alpha-inducible protein 27 [Source:HGNC Symbol;Acc:HGNC:5397]
2633	1.9519	0.9648	0.00E+00	GBP1	guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:HGNC:4182]
185	1.7520	0.8090	0.00E+00	AGTR1	angiotensin II receptor, type 1 [Source:HGNC Symbol;Acc:HGNC:336]
6659	1.5640	0.6452	0.00E+00	SOX4	SRY (sex determining region Y)-box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
84171	1.7251	0.7867	0.00E+00	LOXL4	lysyl oxidase-like 4 [Source:HGNC Symbol;Acc:HGNC:17171]
25939	1.5904	0.6694	0.00E+00	SAMHD1	SAM domain and HD domain 1 [Source:HGNC Symbol;Acc:HGNC:15925]
7805	1.9044	0.9294	0.00E+00	LAPTM5	lysosomal protein transmembrane 5 [Source:HGNC Symbol;Acc:HGNC:29612]
3687	1.5723	0.6529	0.00E+00	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit) [Source:HGNC Symbol;Acc:HGNC:6152]
127281	1.5130	0.5974	0.00E+00	FAM213B	family with sequence similarity 213, member B [Source:HGNC Symbol;Acc:HGNC:28390]

5738	1.5797	0.6597	0.00E+00	PTGFRN	prostaglandin F2 receptor inhibitor [Source:HGNC Symbol;Acc:HGNC:9601]
58189	1.8035	0.8508	0.00E+00	WFDC1	WAP four-disulfide core domain 1 [Source:HGNC Symbol;Acc:HGNC:15466]
27242	1.7091	0.7732	0.00E+00	TNFRSF21	tumor necrosis factor receptor superfamily, member 21 [Source:HGNC Symbol;Acc:HGNC:13469]
83643	1.9292	0.9480	0.00E+00	CCDC3	coiled-coil domain containing 3 [Source:HGNC Symbol;Acc:HGNC:23813]
219972	2.1736	1.1201	0.00E+00	MPEG1	macrophage expressed 1 [Source:HGNC Symbol;Acc:HGNC:29619]
9034	1.7018	0.7671	0.00E+00	CCRL2	chemokine (C-C motif) receptor-like 2 [Source:HGNC Symbol;Acc:HGNC:1612]
63895	1.5231	0.6070	0.00E+00	PIEZO2	piezo-type mechanosensitive ion channel component 2 [Source:HGNC Symbol;Acc:HGNC:26270]
3113	1.6352	0.7095	0.00E+00	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:HGNC:4938]
54863	1.6563	0.7280	0.00E+00	TOR4A	torsin family 4, member A [Source:HGNC Symbol;Acc:HGNC:25981]
10875	1.6015	0.6794	0.00E+00	FGL2	fibrinogen-like 2 [Source:HGNC Symbol;Acc:HGNC:3696]
7298	1.7130	0.7765	0.00E+00	TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12441]
5764	1.9146	0.9371	0.00E+00	PTN	pleiotrophin [Source:HGNC Symbol;Acc:HGNC:9630]
140628	1.6388	0.7127	0.00E+00	GATA5	GATA binding protein 5 [Source:HGNC Symbol;Acc:HGNC:15802]
55920	1.5089	0.5935	0.00E+00	RCC2	regulator of chromosome condensation 2 [Source:HGNC Symbol;Acc:HGNC:30297]
1909	1.7598	0.8154	0.00E+00	EDNRA	endothelin receptor type A [Source:HGNC Symbol;Acc:HGNC:3179]
10184	1.5553	0.6372	0.00E+00	LHFPL2	lipoma HMGIC fusion partner-like 2 [Source:HGNC Symbol;Acc:HGNC:6588]
1009	1.6923	0.7590	0.00E+00	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC Symbol;Acc:HGNC:1750]
4886	1.6339	0.7083	0.00E+00	NPY1R	neuropeptide Y receptor Y1 [Source:HGNC Symbol;Acc:HGNC:7956]
3560	1.5807	0.6606	0.00E+00	IL2RB	interleukin 2 receptor, beta [Source:HGNC Symbol;Acc:HGNC:6009]
7345	2.3543	1.2353	0.00E+00	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) [Source:HGNC Symbol;Acc:HGNC:12513]
284611	1.6277	0.7029	0.00E+00	FAM102B	family with sequence similarity 102, member B [Source:HGNC Symbol;Acc:HGNC:27637]

1234	1.6617	0.7327	0.00E+00	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:1606]
60490	1.5215	0.6055	0.00E+00	PPCDC	phosphopantothenoylcysteine decarboxylase [Source:HGNC Symbol;Acc:HGNC:28107]
3489	1.8255	0.8683	0.00E+00	IGFBP6	insulin-like growth factor binding protein 6 [Source:HGNC Symbol;Acc:HGNC:5475]
221184	1.5552	0.6371	0.00E+00	CPNE2	copine II [Source:HGNC Symbol;Acc:HGNC:2315]
2701	1.9765	0.9830	0.00E+00	GJA4	gap junction protein, alpha 4, 37kDa [Source:HGNC Symbol;Acc:HGNC:4278]
23500	1.5337	0.6170	0.00E+00	DAAM2	dishevelled associated activator of morphogenesis 2 [Source:HGNC Symbol;Acc:HGNC:18143]
1307	1.6672	0.7374	0.00E+00	COL16A1	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2193]
9046	1.5783	0.6584	0.00E+00	DOK2	docking protein 2, 56kDa [Source:HGNC Symbol;Acc:HGNC:2991]
23166	1.5178	0.6020	0.00E+00	STAB1	stabilin 1 [Source:HGNC Symbol;Acc:HGNC:18628]
25927	1.5718	0.6524	0.00E+00	CNRIP1	cannabinoid receptor interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:24546]
375387	1.5093	0.5939	0.00E+00	NRROS	negative regulator of reactive oxygen species [Source:HGNC Symbol;Acc:HGNC:24613]
7837	1.6257	0.7011	0.00E+00	PXDN	peroxidasin [Source:HGNC Symbol;Acc:HGNC:14966]
168537	1.5872	0.6665	0.00E+00	GIMAP7	GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:HGNC:22404]
109	1.6325	0.7070	0.00E+00	ADCY3	adenylate cyclase 3 [Source:HGNC Symbol;Acc:HGNC:234]
51285	1.5799	0.6598	0.00E+00	RASL12	RAS-like, family 12 [Source:HGNC Symbol;Acc:HGNC:30289]
9902	1.7759	0.8285	0.00E+00	MRC2	mannose receptor, C type 2 [Source:HGNC Symbol;Acc:HGNC:16875]
10437	2.1764	1.1220	0.00E+00	IFI30	interferon, gamma-inducible protein 30 [Source:HGNC Symbol;Acc:HGNC:5398]
7424	1.9287	0.9476	0.00E+00	VEGFC	vascular endothelial growth factor C [Source:HGNC Symbol;Acc:HGNC:12682]
25902	1.5103	0.5949	0.00E+00	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like [Source:HGNC Symbol;Acc:HGNC:21055]
2487	1.7761	0.8287	0.00E+00	FRZB	frizzled-related protein [Source:HGNC Symbol;Acc:HGNC:3959]
100628315	1.7406	0.7996	0.00E+00	DNM3OS	DNM3 opposite strand/antisense RNA [Source:HGNC Symbol;Acc:HGNC:41228]
1879	1.5975	0.6758	0.00E+00	EBF1	early B-cell factor 1 [Source:HGNC Symbol;Acc:HGNC:3126]
196883	1.6064	0.6839	0.00E+00	ADCY4	adenylate cyclase 4 [Source:HGNC Symbol;Acc:HGNC:235]

3594	1.5051	0.5899	0.00E+00	IL12RB1	interleukin 12 receptor, beta 1 [Source:HGNC Symbol;Acc:HGNC:5971]
1289	1.6446	0.7178	0.00E+00	COL5A1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2209]
25805	1.7787	0.8308	0.00E+00	BAMBI	BMP and activin membrane-bound inhibitor [Source:HGNC Symbol;Acc:HGNC:30251]
3587	2.2059	1.1414	0.00E+00	IL10RA	interleukin 10 receptor, alpha [Source:HGNC Symbol;Acc:HGNC:5964]
79572	1.6250	0.7004	0.00E+00	ATP13A3	ATPase type 13A3 [Source:HGNC Symbol;Acc:HGNC:24113]
3087	2.0343	1.0245	0.00E+00	HHEX	hematopoietically expressed homeobox [Source:HGNC Symbol;Acc:HGNC:4901]
94274	1.9355	0.9527	0.00E+00	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A [Source:HGNC Symbol;Acc:HGNC:14871]
23604	1.5857	0.6651	0.00E+00	DAPK2	death-associated protein kinase 2 [Source:HGNC Symbol;Acc:HGNC:2675]
79690	1.6062	0.6836	0.00E+00	GAL3ST4	galactose-3-O-sulfotransferase 4 [Source:HGNC Symbol;Acc:HGNC:24145]
57608	1.5089	0.5935	0.00E+00	KIAA1462	KIAA1462 [Source:HGNC Symbol;Acc:HGNC:29283]
7305	2.3836	1.2532	0.00E+00	TYROBP	TYRO protein tyrosine kinase binding protein [Source:HGNC Symbol;Acc:HGNC:12449]
5549	1.7605	0.8160	0.00E+00	PRELP	proline/arginine-rich end leucine-rich repeat protein [Source:HGNC Symbol;Acc:HGNC:9357]
55076	1.5630	0.6443	0.00E+00	TMEM45A	transmembrane protein 45A [Source:HGNC Symbol;Acc:HGNC:25480]
138311	1.5042	0.5890	0.00E+00	FAM69B	family with sequence similarity 69, member B [Source:HGNC Symbol;Acc:HGNC:28290]
2634	1.6814	0.7497	0.00E+00	GBP2	guanylate binding protein 2, interferon-inducible [Source:HGNC Symbol;Acc:HGNC:4183]
3768	1.5924	0.6712	0.00E+00	KCNJ12	potassium channel, inwardly rectifying subfamily J, member 12 [Source:HGNC Symbol;Acc:HGNC:6258]
5341	2.0594	1.0422	0.00E+00	PLEK	pleckstrin [Source:HGNC Symbol;Acc:HGNC:9070]
170575	1.5405	0.6234	0.00E+00	GIMAP1	GTPase, IMAP family member 1 [Source:HGNC Symbol;Acc:HGNC:23237]
112464	1.5888	0.6680	0.00E+00	PRKCDBP	protein kinase C, delta binding protein [Source:HGNC Symbol;Acc:HGNC:9400]
3059	2.0214	1.0154	0.00E+00	HCLS1	hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:HGNC:4844]
389119	1.5553	0.6372	0.00E+00	FAM212A	family with sequence similarity 212, member A [Source:HGNC Symbol;Acc:HGNC:32480]

55803	1.6342	0.7086	0.00E+00	ADAP2	ArfGAP with dual PH domains 2 [Source:HGNC Symbol;Acc:HGNC:16487]
23240	2.1274	1.0891	0.00E+00	KIAA0922	KIAA0922 [Source:HGNC Symbol;Acc:HGNC:29146]
55281	1.5670	0.6480	0.00E+00	TMEM140	transmembrane protein 140 [Source:HGNC Symbol;Acc:HGNC:21870]
7978	1.5666	0.6476	0.00E+00	MTERF1	mitochondrial transcription termination factor 1 [Source:HGNC Symbol;Acc:HGNC:21463]
140706	1.8214	0.8650	0.00E+00	CCM2L	cerebral cavernous malformation 2-like [Source:HGNC Symbol;Acc:HGNC:16153]
9535	1.5168	0.6010	0.00E+00	GMFG	glia maturation factor, gamma [Source:HGNC Symbol;Acc:HGNC:4374]
79064	1.5987	0.6769	0.00E+00	TMEM223	transmembrane protein 223 [Source:HGNC Symbol;Acc:HGNC:28464]
219699	1.5184	0.6025	0.00E+00	UNC5B	unc-5 homolog B (C. elegans) [Source:HGNC Symbol;Acc:HGNC:12568]
55619	1.7970	0.8456	0.00E+00	DOCK10	dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:HGNC:23479]
79834	1.5450	0.6276	0.00E+00	PEAK1	pseudopodium-enriched atypical kinase 1 [Source:HGNC Symbol;Acc:HGNC:29431]
56944	2.2274	1.1554	0.00E+00	OLFML3	olfactomedin-like 3 [Source:HGNC Symbol;Acc:HGNC:24956]
976	1.7135	0.7769	0.00E+00	ADGRE5	adhesion G protein-coupled receptor E5 [Source:HGNC Symbol;Acc:HGNC:1711]
965	1.5254	0.6092	0.00E+00	CD58	CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688]
5228	2.0013	1.0009	0.00E+00	PGF	placental growth factor [Source:HGNC Symbol;Acc:HGNC:8893]
55106	1.6632	0.7339	0.00E+00	SLFN12	schlafen family member 12 [Source:HGNC Symbol;Acc:HGNC:25500]
974	1.5653	0.6465	0.00E+00	CD79B	CD79b molecule, immunoglobulin-associated beta [Source:HGNC Symbol;Acc:HGNC:1699]
1303	1.6306	0.7054	0.00E+00	COL12A1	collagen, type XII, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2188]
200942	1.5001	0.5850	0.00E+00	KLHDC8B	kelch domain containing 8B [Source:HGNC Symbol;Acc:HGNC:28557]
1284	1.6852	0.7529	0.00E+00	COL4A2	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:HGNC:2203]
126669	1.5571	0.6389	0.00E+00	SHE	Src homology 2 domain containing E [Source:HGNC Symbol;Acc:HGNC:27004]
2702	1.5902	0.6692	0.00E+00	GJA5	gap junction protein, alpha 5, 40kDa [Source:HGNC Symbol;Acc:HGNC:4279]
79974	1.5612	0.6427	0.00E+00	CPED1	cadherin-like and PC-esterase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:26159]

114801	2.5820	1.3685	0.00E+00	TMEM200A	transmembrane protein 200A [Source:HGNC Symbol;Acc:HGNC:21075]
1396	2.0772	1.0546	0.00E+00	CRIP1	cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:HGNC:2360]
10544	1.6174	0.6937	0.00E+00	PROCR	protein C receptor, endothelial [Source:HGNC Symbol;Acc:HGNC:9452]
55303	1.5405	0.6234	0.00E+00	GIMAP4	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:HGNC:21872]
4162	1.5216	0.6056	0.00E+00	MCAM	melanoma cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:6934]
87	1.8147	0.8597	0.00E+00	ACTN1	actinin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:163]
7351	2.1194	1.0837	0.00E+00	UCP2	uncoupling protein 2 (mitochondrial, proton carrier) [Source:HGNC Symbol;Acc:HGNC:12518]
784	1.5677	0.6486	0.00E+00	CACNB3	calcium channel, voltage-dependent, beta 3 subunit [Source:HGNC Symbol;Acc:HGNC:1403]
1193	1.6124	0.6892	0.00E+00	CLIC2	chloride intracellular channel 2 [Source:HGNC Symbol;Acc:HGNC:2063]
4242	1.6402	0.7139	0.00E+00	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [Source:HGNC Symbol;Acc:HGNC:7038]
2791	1.5439	0.6266	0.00E+00	GNG11	guanine nucleotide binding protein (G protein), gamma 11 [Source:HGNC Symbol;Acc:HGNC:4403]
8829	1.5104	0.5949	0.00E+00	NRP1	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
162394	1.5043	0.5891	0.00E+00	SLFN5	schlafen family member 5 [Source:HGNC Symbol;Acc:HGNC:28286]
10266	1.8763	0.9079	0.00E+00	RAMP2	receptor (G protein-coupled) activity modifying protein 2 [Source:HGNC Symbol;Acc:HGNC:9844]
89849	1.5407	0.6236	0.00E+00	ATG16L2	autophagy related 16-like 2 (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:25464]
285382	1.8770	0.9084	0.00E+00	C3ORF70	chromosome 3 open reading frame 70 [Source:HGNC Symbol;Acc:HGNC:33731]
5924	1.6641	0.7347	0.00E+00	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2 [Source:HGNC Symbol;Acc:HGNC:9876]
9710	1.5178	0.6019	0.00E+00	KIAA0355	KIAA0355 [Source:HGNC Symbol;Acc:HGNC:29016]
10312	1.6836	0.7515	0.00E+00	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3 [Source:HGNC Symbol;Acc:HGNC:11647]
29941	1.6680	0.7381	0.00E+00	PKN3	protein kinase N3 [Source:HGNC Symbol;Acc:HGNC:17999]
165	2.1521	1.1058	0.00E+00	AEBP1	AE binding protein 1 [Source:HGNC Symbol;Acc:HGNC:303]

126282	1.8706	0.9035	0.00E+00	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1 [Source:HGNC Symbol;Acc:HGNC:28279]
79258	1.5797	0.6596	0.00E+00	MMEL1	membrane metallo-endopeptidase-like 1 [Source:HGNC Symbol;Acc:HGNC:14668]
58191	1.5642	0.6454	0.00E+00	CXCL16	chemokine (C-X-C motif) ligand 16 [Source:HGNC Symbol;Acc:HGNC:16642]
4846	1.6690	0.7389	0.00E+00	NOS3	nitric oxide synthase 3 (endothelial cell) [Source:HGNC Symbol;Acc:HGNC:7876]
3714	1.7767	0.8292	0.00E+00	JAG2	jagged 2 [Source:HGNC Symbol;Acc:HGNC:6189]
29108	1.8500	0.8875	0.00E+00	PYCARD	PYD and CARD domain containing [Source:HGNC Symbol;Acc:HGNC:16608]
4854	1.5192	0.6033	0.00E+00	NOTCH3	notch 3 [Source:HGNC Symbol;Acc:HGNC:7883]
2	1.5218	0.6058	0.00E+00	A2M	alpha-2-macroglobulin [Source:HGNC Symbol;Acc:HGNC:7]
10161	2.2051	1.1409	0.00E+00	LPAR6	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:HGNC:15520]
344558	1.6497	0.7222	0.00E+00	SH3RF3	SH3 domain containing ring finger 3 [Source:HGNC Symbol;Acc:HGNC:24699]
1281	2.4930	1.3179	0.00E+00	COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2201]
26031	1.6512	0.7235	0.00E+00	OSBPL3	oxysterol binding protein-like 3 [Source:HGNC Symbol;Acc:HGNC:16370]
93109	1.6657	0.7361	0.00E+00	TMEM44	transmembrane protein 44 [Source:HGNC Symbol;Acc:HGNC:25120]
27253	1.9630	0.9731	0.00E+00	PCDH17	protocadherin 17 [Source:HGNC Symbol;Acc:HGNC:14267]
4330	2.2264	1.1547	0.00E+00	MN1	meningioma (disrupted in balanced translocation) 1 [Source:HGNC Symbol;Acc:HGNC:7180]
83706	1.6440	0.7172	0.00E+00	FERMT3	fermitin family member 3 [Source:HGNC Symbol;Acc:HGNC:23151]
23336	1.7215	0.7837	0.00E+00	SYNM	synemin, intermediate filament protein [Source:HGNC Symbol;Acc:HGNC:24466]
929	2.1953	1.1344	0.00E+00	CD14	CD14 molecule [Source:HGNC Symbol;Acc:HGNC:1628]
1436	2.5557	1.3537	0.00E+00	CSF1R	colony stimulating factor 1 receptor [Source:HGNC Symbol;Acc:HGNC:2433]
2037	1.5566	0.6384	0.00E+00	EPB41L2	erythrocyte membrane protein band 4.1-like 2 [Source:HGNC Symbol;Acc:HGNC:3379]
441478	2.5758	1.3650	0.00E+00	NRARP	NOTCH-regulated ankyrin repeat protein [Source:HGNC Symbol;Acc:HGNC:33843]
5118	1.9377	0.9543	0.00E+00	PCOLCE	procollagen C-endopeptidase enhancer [Source:HGNC Symbol;Acc:HGNC:8738]

22808	1.5497	0.6320	0.00E+00	MRAS	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7227]
51155	1.5240	0.6079	0.00E+00	HN1	hematological and neurological expressed 1 [Source:HGNC Symbol;Acc:HGNC:14569]
57182	1.6178	0.6940	0.00E+00	ANKRD50	ankyrin repeat domain 50 [Source:HGNC Symbol;Acc:HGNC:29223]
5547	1.5198	0.6039	0.00E+00	PRCP	prolylcarboxypeptidase (angiotensinase C) [Source:HGNC Symbol;Acc:HGNC:9344]
91010	1.6556	0.7273	0.00E+00	FMNL3	formin-like 3 [Source:HGNC Symbol;Acc:HGNC:23698]
2200	1.6202	0.6962	0.00E+00	FBN1	fibrillin 1 [Source:HGNC Symbol;Acc:HGNC:3603]
3216	1.8879	0.9168	0.00E+00	HOXB6	homeobox B6 [Source:HGNC Symbol;Acc:HGNC:5117]
56654	1.7018	0.7670	0.00E+00	NPDC1	neural proliferation, differentiation and control, 1 [Source:HGNC Symbol;Acc:HGNC:7899]
157285	2.0651	1.0462	0.00E+00	SGK223	Tyrosine-protein kinase SgK223 [Source:UniProtKB/Swiss-Prot;Acc:Q86YV5]
719	2.4013	1.2638	0.00E+00	C3AR1	complement component 3a receptor 1 [Source:HGNC Symbol;Acc:HGNC:1319]
1036	2.0980	1.0690	0.00E+00	CDO1	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:HGNC:1795]
79047	1.5451	0.6277	0.00E+00	KCTD15	potassium channel tetramerization domain containing 15 [Source:HGNC Symbol;Acc:HGNC:23297]
947	1.9840	0.9884	0.00E+00	CD34	CD34 molecule [Source:HGNC Symbol;Acc:HGNC:1662]
151887	1.9647	0.9743	0.00E+00	CCDC80	coiled-coil domain containing 80 [Source:HGNC Symbol;Acc:HGNC:30649]
3142	2.3118	1.2090	0.00E+00	HLX	H2.0-like homeobox [Source:HGNC Symbol;Acc:HGNC:4978]
1893	3.2799	1.7137	0.00E+00	ECM1	extracellular matrix protein 1 [Source:HGNC Symbol;Acc:HGNC:3153]
79888	1.5127	0.5971	0.00E+00	LPCAT1	lysophosphatidylcholine acyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:25718]
25960	1.7276	0.7887	0.00E+00	ADGRA2	adhesion G protein-coupled receptor A2 [Source:HGNC Symbol;Acc:HGNC:17849]
54751	1.5169	0.6011	0.00E+00	FBLIM1	filamin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGNC:24686]
4313	2.2424	1.1650	0.00E+00	MMP2	matrix metallopeptidase 2 [Source:HGNC Symbol;Acc:HGNC:7166]
83742	1.6249	0.7004	0.00E+00	MARVELD1	MARVEL domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28674]
6926	1.7748	0.8277	0.00E+00	TBX3	T-box 3 [Source:HGNC Symbol;Acc:HGNC:11602]

4082	2.0256	1.0183	0.00E+00	MARCKS	myristoylated alanine-rich protein kinase C substrate [Source:HGNC Symbol;Acc:HGNC:6759]
2022	1.7843	0.8354	0.00E+00	ENG	endoglin [Source:HGNC Symbol;Acc:HGNC:3349]
9262	1.8833	0.9132	0.00E+00	STK17B	serine/threonine kinase 17b [Source:HGNC Symbol;Acc:HGNC:11396]
1282	1.8867	0.9159	0.00E+00	COL4A1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2202]
7045	2.3436	1.2287	0.00E+00	TGFBI	transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:HGNC:11771]
10800	2.1932	1.1330	0.00E+00	CYSLTR1	cysteinyl leukotriene receptor 1 [Source:HGNC Symbol;Acc:HGNC:17451]
2122	2.2532	1.1720	0.00E+00	MECOM	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:HGNC:3498]
1050	1.9230	0.9434	0.00E+00	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HGNC Symbol;Acc:HGNC:1833]
6591	2.2864	1.1931	0.00E+00	SNAI2	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:11094]
1290	2.1905	1.1313	0.00E+00	COL5A2	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:HGNC:2210]
23208	2.2482	1.1688	0.00E+00	SYT11	synaptotagmin XI [Source:HGNC Symbol;Acc:HGNC:19239]
4921	1.5727	0.6533	0.00E+00	DDR2	discoidin domain receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:2731]
84674	1.6669	0.7372	0.00E+00	CARD6	caspase recruitment domain family, member 6 [Source:HGNC Symbol;Acc:HGNC:16394]
171024	2.0447	1.0319	0.00E+00	SYNPO2	synaptopodin 2 [Source:HGNC Symbol;Acc:HGNC:17732]
874	1.9107	0.9341	0.00E+00	CBR3	carbonyl reductase 3 [Source:HGNC Symbol;Acc:HGNC:1549]
65059	1.8226	0.8660	0.00E+00	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 [Source:HGNC Symbol;Acc:HGNC:14436]
2335	2.8077	1.4894	0.00E+00	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
26119	1.8511	0.8884	0.00E+00	LDLRAP1	low density lipoprotein receptor adaptor protein 1 [Source:HGNC Symbol;Acc:HGNC:18640]
22899	1.9415	0.9572	0.00E+00	ARHGEF15	Rho guanine nucleotide exchange factor (GEF) 15 [Source:HGNC Symbol;Acc:HGNC:15590]
753	1.7709	0.8245	0.00E+00	LDLRAD4	low density lipoprotein receptor class A domain containing 4 [Source:HGNC Symbol;Acc:HGNC:1224]
81831	2.0668	1.0474	0.00E+00	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Symbol;Acc:HGNC:14644]
960	2.1239	1.0867	0.00E+00	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1681]

5742	2.9247	1.5483	0.00E+00	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:HGNC:9604]
2982	2.0331	1.0237	0.00E+00	GUCY1A3	guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol;Acc:HGNC:4685]
53827	2.2068	1.1420	0.00E+00	FXYD5	FXYD domain containing ion transport regulator 5 [Source:HGNC Symbol;Acc:HGNC:4029]
2014	2.0619	1.0440	0.00E+00	EMP3	epithelial membrane protein 3 [Source:HGNC Symbol;Acc:HGNC:3335]
51063	1.9641	0.9738	0.00E+00	CALHM2	calcium homeostasis modulator 2 [Source:HGNC Symbol;Acc:HGNC:23493]
56892	2.9758	1.5733	0.00E+00	C8ORF4	chromosome 8 open reading frame 4 [Source:HGNC Symbol;Acc:HGNC:1357]
2625	3.5510	1.8282	0.00E+00	GATA3	GATA binding protein 3 [Source:HGNC Symbol;Acc:HGNC:4172]
64321	3.3012	1.7230	0.00E+00	SOX17	SRY (sex determining region Y)-box 17 [Source:HGNC Symbol;Acc:HGNC:18122]
1278	5.3537	2.4205	0.00E+00	COL1A2	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:HGNC:2198]
4066	2.2891	1.1948	0.00E+00	LYL1	lymphoblastic leukemia associated hematopoiesis regulator 1 [Source:HGNC Symbol;Acc:HGNC:6734]
54510	3.0890	1.6271	0.00E+00	PCDH18	protocadherin 18 [Source:HGNC Symbol;Acc:HGNC:14268]
1843	0.1954	-2.3553	0.00E+00	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:3064]
1958	0.1452	-2.7843	0.00E+00	EGR1	early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3238]
7538	0.1903	-2.3940	0.00E+00	ZFP36	ZFP36 ring finger protein [Source:HGNC Symbol;Acc:HGNC:12862]
54546	0.2433	-2.0395	0.00E+00	RNF186	ring finger protein 186 [Source:HGNC Symbol;Acc:HGNC:25978]
1052	0.1985	-2.3328	0.00E+00	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta [Source:HGNC Symbol;Acc:HGNC:1835]
3725	0.1893	-2.4012	0.00E+00	JUN	jun proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6204]
64651	0.2167	-2.2064	0.00E+00	CSRNP1	cysteine-serine-rich nuclear protein 1 [Source:HGNC Symbol;Acc:HGNC:14300]
54206	0.2894	-1.7887	0.00E+00	ERRFI1	ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:18185]
81575	0.0764	-3.7101	0.00E+00	APOLD1	apolipoprotein L domain containing 1 [Source:HGNC Symbol;Acc:HGNC:25268]
9314	0.2100	-2.2512	0.00E+00	KLF4	Kruppel-like factor 4 (gut) [Source:HGNC Symbol;Acc:HGNC:6348]

467	0.2170	-2.2043	0.00E+00	ATF3	activating transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:785]
5514	0.4808	-1.0566	0.00E+00	PPP1R10	protein phosphatase 1, regulatory subunit 10 [Source:HGNC Symbol;Acc:HGNC:9284]
10560	0.3069	-1.7043	0.00E+00	SLC19A2	solute carrier family 19 (thiamine transporter), member 2 [Source:HGNC Symbol;Acc:HGNC:10938]
25976	0.2754	-1.8607	0.00E+00	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase [Source:HGNC Symbol;Acc:HGNC:23696]
5187	0.3029	-1.7230	0.00E+00	PER1	period circadian clock 1 [Source:HGNC Symbol;Acc:HGNC:8845]
359948	0.5742	-0.8005	0.00E+00	IRF2BP2	interferon regulatory factor 2 binding protein 2 [Source:HGNC Symbol;Acc:HGNC:21729]
3726	0.2641	-1.9211	0.00E+00	JUNB	jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6205]
51655	0.1563	-2.6775	0.00E+00	RASD1	RAS, dexamethasone-induced 1 [Source:HGNC Symbol;Acc:HGNC:15828]
7050	0.6053	-0.7244	0.00E+00	TGIF1	TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Acc:HGNC:11776]
55224	0.5089	-0.9745	0.00E+00	ETNK2	ethanolamine kinase 2 [Source:HGNC Symbol;Acc:HGNC:25575]
969	0.1282	-2.9641	0.00E+00	CD69	CD69 molecule [Source:HGNC Symbol;Acc:HGNC:1694]
3164	0.1906	-2.3915	0.00E+00	NR4A1	nuclear receptor subfamily 4, group A, member 1 [Source:HGNC Symbol;Acc:HGNC:7980]
1316	0.3491	-1.5183	0.00E+00	KLF6	Kruppel-like factor 6 [Source:HGNC Symbol;Acc:HGNC:2235]
8553	0.2864	-1.8040	0.00E+00	BHLHE40	basic helix-loop-helix family, member e40 [Source:HGNC Symbol;Acc:HGNC:1046]
8645	0.2906	-1.7829	0.00E+00	KCNK5	potassium channel, two pore domain subfamily K, member 5 [Source:HGNC Symbol;Acc:HGNC:6280]
5144	0.5749	-0.7986	0.00E+00	PDE4D	phosphodiesterase 4D, cAMP-specific [Source:HGNC Symbol;Acc:HGNC:8783]
22822	0.3087	-1.6955	0.00E+00	PHLDA1	pleckstrin homology-like domain, family A, member 1 [Source:HGNC Symbol;Acc:HGNC:8933]
7832	0.3816	-1.3897	0.00E+00	BTG2	BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:1131]
5105	0.2694	-1.8922	0.00E+00	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble) [Source:HGNC Symbol;Acc:HGNC:8724]
5142	0.4300	-1.2176	0.00E+00	PDE4B	phosphodiesterase 4B, cAMP-specific [Source:HGNC Symbol;Acc:HGNC:8781]
388	0.5843	-0.7752	0.00E+00	RHOB	ras homolog family member B [Source:HGNC Symbol;Acc:HGNC:668]

4783	0.3036	-1.7198	0.00E+00	NFIL3	nuclear factor, interleukin 3 regulated [Source:HGNC Symbol;Acc:HGNC:7787]
9099	0.5444	-0.8773	0.00E+00	USP2	ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HGNC:12618]
10253	0.3354	-1.5761	0.00E+00	SPRY2	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:11270]
5166	0.2532	-1.9815	0.00E+00	PDK4	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC Symbol;Acc:HGNC:8812]
65997	0.4087	-1.2909	0.00E+00	RASL11B	RAS-like, family 11, member B [Source:HGNC Symbol;Acc:HGNC:23804]
4128	0.4972	-1.0082	0.00E+00	MAOA	monoamine oxidase A [Source:HGNC Symbol;Acc:HGNC:6833]
687	0.4424	-1.1764	0.00E+00	KLF9	Kruppel-like factor 9 [Source:HGNC Symbol;Acc:HGNC:1123]
57669	0.6630	-0.5928	0.00E+00	EPB41L5	erythrocyte membrane protein band 4.1 like 5 [Source:HGNC Symbol;Acc:HGNC:19819]
84913	0.3292	-1.6031	0.00E+00	ATOH8	atonal homolog 8 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:24126]
157506	0.4576	-1.1278	0.00E+00	RDH10	retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:HGNC:19975]
11082	0.2145	-2.2210	0.00E+00	ESM1	endothelial cell-specific molecule 1 [Source:HGNC Symbol;Acc:HGNC:3466]
1428	0.3467	-1.5281	0.00E+00	CRYM	crystallin, mu [Source:HGNC Symbol;Acc:HGNC:2418]
84612	0.6036	-0.7282	0.00E+00	PARD6B	par-6 family cell polarity regulator beta [Source:HGNC Symbol;Acc:HGNC:16245]
64332	0.2857	-1.8072	0.00E+00	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta [Source:HGNC Symbol;Acc:HGNC:29805]
2938	0.2334	-2.0991	0.00E+00	GSTA1	glutathione S-transferase alpha 1 [Source:HGNC Symbol;Acc:HGNC:4626]
4739	0.5139	-0.9605	0.00E+00	NEDD9	neural precursor cell expressed, developmentally down-regulated 9 [Source:HGNC Symbol;Acc:HGNC:7733]
3727	0.6388	-0.6465	0.00E+00	JUND	jun D proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6206]
131034	0.3384	-1.5633	0.00E+00	CPNE4	copine IV [Source:HGNC Symbol;Acc:HGNC:2317]
201164	0.4391	-1.1875	0.00E+00	PLD6	phospholipase D family, member 6 [Source:HGNC Symbol;Acc:HGNC:30447]
6584	0.5388	-0.8921	0.00E+00	SLC22A5	solute carrier family 22 (organic cation/carnitine transporter), member 5 [Source:HGNC Symbol;Acc:HGNC:10969]
65124	0.3730	-1.4228	0.00E+00	SOWAHC	sosondowah ankyrin repeat domain family member C [Source:HGNC Symbol;Acc:HGNC:26149]
205	0.4391	-1.1875	0.00E+00	AK4	adenylate kinase 4 [Source:HGNC Symbol;Acc:HGNC:363]

55422	0.3212	-1.6386	0.00E+00	ZNF331	zinc finger protein 331 [Source:HGNC Symbol;Acc:HGNC:15489]
3621	0.5172	-0.9511	0.00E+00	ING1	inhibitor of growth family, member 1 [Source:HGNC Symbol;Acc:HGNC:6062]
3242	0.2060	-2.2796	0.00E+00	HPD	4-hydroxyphenylpyruvate dioxygenase [Source:HGNC Symbol;Acc:HGNC:5147]
23014	0.6016	-0.7332	0.00E+00	FBXO21	F-box protein 21 [Source:HGNC Symbol;Acc:HGNC:13592]
22941	0.5513	-0.8590	0.00E+00	SHANK2	SH3 and multiple ankyrin repeat domains 2 [Source:HGNC Symbol;Acc:HGNC:14295]
4036	0.4056	-1.3020	0.00E+00	LRP2	low density lipoprotein receptor-related protein 2 [Source:HGNC Symbol;Acc:HGNC:6694]
4616	0.3538	-1.4991	0.00E+00	GADD45B	growth arrest and DNA-damage-inducible, beta [Source:HGNC Symbol;Acc:HGNC:4096]
651746	0.3753	-1.4140	0.00E+00	ANKRD33B	ankyrin repeat domain 33B [Source:HGNC Symbol;Acc:HGNC:35240]
85415	0.5495	-0.8637	0.00E+00	RHPN2	rhophilin, Rho GTPase binding protein 2 [Source:HGNC Symbol;Acc:HGNC:19974]
4329	0.4673	-1.0977	0.00E+00	ALDH6A1	aldehyde dehydrogenase 6 family, member A1 [Source:HGNC Symbol;Acc:HGNC:7179]
134147	0.4228	-1.2419	0.00E+00	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas) [Source:HGNC Symbol;Acc:HGNC:25090]
1644	0.4483	-1.1576	0.00E+00	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase) [Source:HGNC Symbol;Acc:HGNC:2719]
51733	0.5176	-0.9502	0.00E+00	UPB1	ureidopropionase, beta [Source:HGNC Symbol;Acc:HGNC:16297]
384	0.4377	-1.1921	0.00E+00	ARG2	arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]
28970	0.4989	-1.0031	0.00E+00	C11ORF54	chromosome 11 open reading frame 54 [Source:HGNC Symbol;Acc:HGNC:30204]
4257	0.3779	-1.4039	0.00E+00	MGST1	microsomal glutathione S-transferase 1 [Source:HGNC Symbol;Acc:HGNC:7061]
1051	0.3274	-1.6108	0.00E+00	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:HGNC:1834]
256764	0.4644	-1.1065	0.00E+00	WDR72	WD repeat domain 72 [Source:HGNC Symbol;Acc:HGNC:26790]
79799	0.3682	-1.4413	0.00E+00	UGT2A3	UDP glucuronosyltransferase 2 family, polypeptide A3 [Source:HGNC Symbol;Acc:HGNC:28528]
3400	0.4884	-1.0338	0.00E+00	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein [Source:HGNC Symbol;Acc:HGNC:5363]

130013	0.2678	-1.9005	0.00E+00	ACMSD	aminocarboxymuconate semialdehyde decarboxylase [Source:HGNC Symbol;Acc:HGNC:19288]
11136	0.2670	-1.9052	0.00E+00	SLC7A9	solute carrier family 7 (amino acid transporter light chain, bo,+ system), member 9 [Source:HGNC Symbol;Acc:HGNC:11067]
7128	0.2492	-2.0044	0.00E+00	TNFAIP3	tumor necrosis factor, alpha-induced protein 3 [Source:HGNC Symbol;Acc:HGNC:11896]
2355	0.4473	-1.1607	0.00E+00	FOSL2	FOS-like antigen 2 [Source:HGNC Symbol;Acc:HGNC:3798]
4792	0.4976	-1.0071	0.00E+00	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha [Source:HGNC Symbol;Acc:HGNC:7797]
3337	0.1854	-2.4315	0.00E+00	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1 [Source:HGNC Symbol;Acc:HGNC:5270]
1831	0.4687	-1.0931	0.00E+00	TSC22D3	TSC22 domain family, member 3 [Source:HGNC Symbol;Acc:HGNC:3051]
26353	0.5581	-0.8415	0.00E+00	HSPB8	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGNC:30171]
64577	0.3431	-1.5432	0.00E+00	ALDH8A1	aldehyde dehydrogenase 8 family, member A1 [Source:HGNC Symbol;Acc:HGNC:15471]
2168	0.2946	-1.7634	0.00E+00	FABP1	fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:3555]
6470	0.4402	-1.1839	0.00E+00	SHMT1	serine hydroxymethyltransferase 1 (soluble) [Source:HGNC Symbol;Acc:HGNC:10850]
51361	0.5777	-0.7917	0.00E+00	HOOK1	hook microtubule-tethering protein 1 [Source:HGNC Symbol;Acc:HGNC:19884]
23743	0.3883	-1.3648	0.00E+00	BHMT2	betaine--homocysteine S-methyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:1048]
4170	0.5567	-0.8450	0.00E+00	MCL1	myeloid cell leukemia 1 [Source:HGNC Symbol;Acc:HGNC:6943]
6819	0.4466	-1.1629	0.00E+00	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2 [Source:HGNC Symbol;Acc:HGNC:11456]
287	0.4322	-1.2103	0.00E+00	ANK2	ankyrin 2, neuronal [Source:HGNC Symbol;Acc:HGNC:493]
10370	0.5868	-0.7691	0.00E+00	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 [Source:HGNC Symbol;Acc:HGNC:1987]
445	0.4681	-1.0951	0.00E+00	ASS1	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:HGNC:758]
23764	0.2343	-2.0934	0.00E+00	MAFF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F [Source:HGNC Symbol;Acc:HGNC:6780]

23767	0.6124	-0.7074	0.00E+00	FLRT3	fibronectin leucine rich transmembrane protein 3 [Source:HGNC Symbol;Acc:HGNC:3762]
116154	0.2152	-2.2160	0.00E+00	PHACTR3	phosphatase and actin regulator 3 [Source:HGNC Symbol;Acc:HGNC:15833]
23414	0.5319	-0.9108	0.00E+00	ZFPM2	zinc finger protein, FOG family member 2 [Source:HGNC Symbol;Acc:HGNC:16700]
8382	0.5658	-0.8217	0.00E+00	NME5	NME/NM23 family member 5 [Source:HGNC Symbol;Acc:HGNC:7853]
343990	0.6096	-0.7141	0.00E+00	KIAA1211L	KIAA1211-like [Source:HGNC Symbol;Acc:HGNC:33454]
26751	0.6112	-0.7104	0.00E+00	SH3YL1	SH3 and SYLF domain containing 1 [Source:HGNC Symbol;Acc:HGNC:29546]
50507	0.4974	-1.0074	0.00E+00	NOX4	NADPH oxidase 4 [Source:HGNC Symbol;Acc:HGNC:7891]
229	0.3540	-1.4980	0.00E+00	ALDOB	aldolase B, fructose-bisphosphate [Source:HGNC Symbol;Acc:HGNC:417]
10140	0.6571	-0.6058	0.00E+00	TOB1	transducer of ERBB2, 1 [Source:HGNC Symbol;Acc:HGNC:11979]
2104	0.4965	-1.0102	0.00E+00	ESRRG	estrogen-related receptor gamma [Source:HGNC Symbol;Acc:HGNC:3474]
9476	0.4648	-1.1054	0.00E+00	NAPSA	napsin A aspartic peptidase [Source:HGNC Symbol;Acc:HGNC:13395]
84803	0.3514	-1.5088	0.00E+00	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC Symbol;Acc:HGNC:28157]
11001	0.2694	-1.8924	0.00E+00	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2 [Source:HGNC Symbol;Acc:HGNC:10996]
5264	0.6013	-0.7338	0.00E+00	PHYH	phytanoyl-CoA 2-hydroxylase [Source:HGNC Symbol;Acc:HGNC:8940]
123	0.5365	-0.8983	0.00E+00	PLIN2	perilipin 2 [Source:HGNC Symbol;Acc:HGNC:248]
3795	0.4746	-1.0752	0.00E+00	KHK	ketohexokinase (fructokinase) [Source:HGNC Symbol;Acc:HGNC:6315]
9531	0.4336	-1.2055	0.00E+00	BAG3	BCL2-associated athanogene 3 [Source:HGNC Symbol;Acc:HGNC:939]
1154	0.6021	-0.7319	0.00E+00	CISH	cytokine inducible SH2-containing protein [Source:HGNC Symbol;Acc:HGNC:1984]
118980	0.5362	-0.8990	0.00E+00	SFXN2	sideroflexin 2 [Source:HGNC Symbol;Acc:HGNC:16086]
1807	0.2574	-1.9579	0.00E+00	DPYS	dihydropyrimidinase [Source:HGNC Symbol;Acc:HGNC:3013]
7743	0.4617	-1.1148	0.00E+00	ZNF189	zinc finger protein 189 [Source:HGNC Symbol;Acc:HGNC:12980]
64081	0.4685	-1.0940	0.00E+00	PBLD	phenazine biosynthesis-like protein domain containing [Source:HGNC Symbol;Acc:HGNC:23301]

401548	0.6287	-0.6696	0.00E+00	SNX30	sorting nexin family member 30 [Source:HGNC Symbol;Acc:HGNC:23685]
23428	0.6526	-0.6157	0.00E+00	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8 [Source:HGNC Symbol;Acc:HGNC:11066]
7071	0.5308	-0.9138	0.00E+00	KLF10	Kruppel-like factor 10 [Source:HGNC Symbol;Acc:HGNC:11810]
4494	0.4827	-1.0509	0.00E+00	MT1F	metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]
169693	0.4213	-1.2471	0.00E+00	TMEM252	transmembrane protein 252 [Source:HGNC Symbol;Acc:HGNC:28537]
51585	0.5764	-0.7950	0.00E+00	PCF11	PCF11 cleavage and polyadenylation factor subunit [Source:HGNC Symbol;Acc:HGNC:30097]
1848	0.4868	-1.0385	0.00E+00	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:HGNC:3072]
114789	0.5168	-0.9523	0.00E+00	SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 [Source:HGNC Symbol;Acc:HGNC:20663]
3081	0.4639	-1.1080	0.00E+00	HGD	homogentisate 1,2-dioxygenase [Source:HGNC Symbol;Acc:HGNC:4892]
64762	0.6435	-0.6360	0.00E+00	GAREM	GRB2 associated, regulator of MAPK1 [Source:HGNC Symbol;Acc:HGNC:26136]
54541	0.3512	-1.5098	0.00E+00	DDIT4	DNA-damage-inducible transcript 4 [Source:HGNC Symbol;Acc:HGNC:24944]
25925	0.6059	-0.7228	0.00E+00	ZNF521	zinc finger protein 521 [Source:HGNC Symbol;Acc:HGNC:24605]
6382	0.4640	-1.1077	0.00E+00	SDC1	syndecan 1 [Source:HGNC Symbol;Acc:HGNC:10658]
353189	0.3888	-1.3629	0.00E+00	SLCO4C1	solute carrier organic anion transporter family, member 4C1 [Source:HGNC Symbol;Acc:HGNC:23612]
130271	0.6108	-0.7113	0.00E+00	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2 [Source:HGNC Symbol;Acc:HGNC:30506]
4501	0.3985	-1.3274	0.00E+00	MT1X	metallothionein 1X [Source:HGNC Symbol;Acc:HGNC:7405]
57393	0.3376	-1.5665	0.00E+00	TMEM27	transmembrane protein 27 [Source:HGNC Symbol;Acc:HGNC:29437]
163882	0.6367	-0.6512	0.00E+00	CNST	consortin, connexin sorting protein [Source:HGNC Symbol;Acc:HGNC:26486]
10158	0.5403	-0.8883	0.00E+00	PDZK1IP1	PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:16887]
2878	0.5718	-0.8063	0.00E+00	GPX3	glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:4555]
55937	0.4346	-1.2023	0.00E+00	APOM	apolipoprotein M [Source:HGNC Symbol;Acc:HGNC:13916]

1410	0.6670	-0.5843	0.00E+00	CRYAB	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
23645	0.4484	-1.1571	0.00E+00	PPP1R15A	protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:HGNC:14375]
80318	0.5992	-0.7389	0.00E+00	GKAP1	G kinase anchoring protein 1 [Source:HGNC Symbol;Acc:HGNC:17496]
83758	0.4311	-1.2139	0.00E+00	RBP5	retinol binding protein 5, cellular [Source:HGNC Symbol;Acc:HGNC:15847]
2203	0.4109	-1.2832	0.00E+00	FBP1	fructose-1,6-bisphosphatase 1 [Source:HGNC Symbol;Acc:HGNC:3606]
79960	0.6601	-0.5993	0.00E+00	JADE1	jade family PHD finger 1 [Source:HGNC Symbol;Acc:HGNC:30027]
57291	0.6263	-0.6751	0.00E+00	DANCR	differentiation antagonizing non-protein coding RNA [Source:HGNC Symbol;Acc:HGNC:28964]
84919	0.5396	-0.8899	0.00E+00	PPP1R15B	protein phosphatase 1, regulatory subunit 15B [Source:HGNC Symbol;Acc:HGNC:14951]
7465	0.6206	-0.6883	0.00E+00	WEE1	WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:HGNC:12761]
642273	0.5528	-0.8552	0.00E+00	FAM110C	family with sequence similarity 110, member C [Source:HGNC Symbol;Acc:HGNC:33340]
11080	0.5733	-0.8026	0.00E+00	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4 [Source:HGNC Symbol;Acc:HGNC:14886]
7803	0.6658	-0.5868	0.00E+00	PTP4A1	protein tyrosine phosphatase type IVA, member 1 [Source:HGNC Symbol;Acc:HGNC:9634]
220963	0.3408	-1.5532	0.00E+00	SLC16A9	solute carrier family 16, member 9 [Source:HGNC Symbol;Acc:HGNC:23520]
1195	0.5341	-0.9048	0.00E+00	CLK1	CDC-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
3033	0.6480	-0.6260	0.00E+00	HADH	hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc:HGNC:4799]
51084	0.5641	-0.8261	0.00E+00	CRYL1	crystallin, lambda 1 [Source:HGNC Symbol;Acc:HGNC:18246]
27106	0.2741	-1.8674	0.00E+00	ARRDC2	arrestin domain containing 2 [Source:HGNC Symbol;Acc:HGNC:25225]
3491	0.4272	-1.2269	0.00E+00	CYR61	cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol;Acc:HGNC:2654]
10083	0.5099	-0.9718	0.00E+00	USH1C	Usher syndrome 1C [Source:HGNC Symbol;Acc:HGNC:12597]
64849	0.4741	-1.0766	0.00E+00	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 [Source:HGNC Symbol;Acc:HGNC:14430]
8671	0.4674	-1.0971	0.00E+00	SLC4A4	solute carrier family 4 (sodium bicarbonate cotransporter), member 4 [Source:HGNC Symbol;Acc:HGNC:11030]

29958	0.3874	-1.3679	0.00E+00	DMGDH	dimethylglycine dehydrogenase [Source:HGNC Symbol;Acc:HGNC:24475]
2805	0.5633	-0.8281	0.00E+00	GOT1	glutamic-oxaloacetic transaminase 1, soluble [Source:HGNC Symbol;Acc:HGNC:4432]
10891	0.4759	-1.0712	0.00E+00	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha [Source:HGNC Symbol;Acc:HGNC:9237]
9592	0.4796	-1.0601	0.00E+00	IER2	immediate early response 2 [Source:HGNC Symbol;Acc:HGNC:28871]
7430	0.6611	-0.5971	0.00E+00	EZR	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
48	0.6223	-0.6843	0.00E+00	ACO1	aconitase 1, soluble [Source:HGNC Symbol;Acc:HGNC:117]
55586	0.2903	-1.7842	0.00E+00	MIOX	myo-inositol oxygenase [Source:HGNC Symbol;Acc:HGNC:14522]
22981	0.6164	-0.6980	0.00E+00	NINL	ninein-like [Source:HGNC Symbol;Acc:HGNC:29163]
36	0.6485	-0.6247	0.00E+00	ACADSB	acyl-CoA dehydrogenase, short/branched chain [Source:HGNC Symbol;Acc:HGNC:91]
8424	0.3554	-1.4926	0.00E+00	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 [Source:HGNC Symbol;Acc:HGNC:964]
730091	0.6062	-0.7222	0.00E+00	LINC00886	long intergenic non-protein coding RNA 886 [Source:HGNC Symbol;Acc:HGNC:48572]
2690	0.6413	-0.6410	0.00E+00	GHR	growth hormone receptor [Source:HGNC Symbol;Acc:HGNC:4263]
2628	0.3970	-1.3328	0.00E+00	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Source:HGNC Symbol;Acc:HGNC:4175]
7512	0.3769	-1.4079	0.00E+00	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound [Source:HGNC Symbol;Acc:HGNC:12823]
217	0.6496	-0.6225	0.00E+00	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:404]
94234	0.3370	-1.5691	0.00E+00	FOXQ1	forkhead box Q1 [Source:HGNC Symbol;Acc:HGNC:20951]
6519	0.4661	-1.1013	0.00E+00	SLC3A1	solute carrier family 3 (amino acid transporter heavy chain), member 1 [Source:HGNC Symbol;Acc:HGNC:11025]
51268	0.3120	-1.6804	0.00E+00	PIPOX	pipecolic acid oxidase [Source:HGNC Symbol;Acc:HGNC:17804]
132299	0.6474	-0.6272	0.00E+00	OCIAD2	OCIA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:28685]
34	0.6635	-0.5917	0.00E+00	ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Source:HGNC Symbol;Acc:HGNC:89]

160760	0.6659	-0.5866	0.00E+00	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:30695]
29950	0.5018	-0.9947	0.00E+00	SERTAD1	SERTA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:17932]
1844	0.4078	-1.2941	0.00E+00	DUSP2	dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:HGNC:3068]
80311	0.6303	-0.6658	0.00E+00	KLHL15	kelch-like family member 15 [Source:HGNC Symbol;Acc:HGNC:29347]
54790	0.6158	-0.6995	0.00E+00	TET2	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc:HGNC:25941]
8660	0.6568	-0.6064	0.00E+00	IRS2	insulin receptor substrate 2 [Source:HGNC Symbol;Acc:HGNC:6126]
159963	0.3878	-1.3667	0.00E+00	SLC5A12	solute carrier family 5 (sodium/monocarboxylate cotransporter), member 12 [Source:HGNC Symbol;Acc:HGNC:28750]
10912	0.3904	-1.3571	0.00E+00	GADD45G	growth arrest and DNA-damage-inducible, gamma [Source:HGNC Symbol;Acc:HGNC:4097]
23086	0.6339	-0.6577	0.00E+00	EXPH5	exophilin 5 [Source:HGNC Symbol;Acc:HGNC:30578]
5340	0.3398	-1.5572	0.00E+00	PLG	plasminogen [Source:HGNC Symbol;Acc:HGNC:9071]
3273	0.3999	-1.3224	0.00E+00	HRG	histidine-rich glycoprotein [Source:HGNC Symbol;Acc:HGNC:5181]
10766	0.5099	-0.9718	0.00E+00	TOB2	transducer of ERBB2, 2 [Source:HGNC Symbol;Acc:HGNC:11980]
10249	0.3546	-1.4957	0.00E+00	GLYAT	glycine-N-acyltransferase [Source:HGNC Symbol;Acc:HGNC:13734]
1800	0.4381	-1.1906	0.00E+00	DPEP1	dipeptidase 1 (renal) [Source:HGNC Symbol;Acc:HGNC:3002]
8864	0.6307	-0.6649	0.00E+00	PER2	period circadian clock 2 [Source:HGNC Symbol;Acc:HGNC:8846]
9356	0.4084	-1.2918	0.00E+00	SLC22A6	solute carrier family 22 (organic anion transporter), member 6 [Source:HGNC Symbol;Acc:HGNC:10970]
6505	0.5513	-0.8591	0.00E+00	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 [Source:HGNC Symbol;Acc:HGNC:10939]
3303	0.5786	-0.7894	0.00E+00	HSPA1A	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:HGNC:5232]
57733	0.3670	-1.4463	0.00E+00	GBA3	glucosidase, beta, acid 3 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:19069]
56704	0.5503	-0.8617	0.00E+00	JPH1	junctophilin 1 [Source:HGNC Symbol;Acc:HGNC:14201]
83660	0.5137	-0.9611	0.00E+00	TLN2	talin 2 [Source:HGNC Symbol;Acc:HGNC:15447]

10840	0.5266	-0.9253	0.00E+00	ALDH1L1	aldehyde dehydrogenase 1 family, member L1 [Source:HGNC Symbol;Acc:HGNC:3978]
55664	0.6366	-0.6516	0.00E+00	CDC37L1	cell division cycle 37-like 1 [Source:HGNC Symbol;Acc:HGNC:17179]
8436	0.3870	-1.3696	0.00E+00	SDPR	serum deprivation response [Source:HGNC Symbol;Acc:HGNC:10690]
90007	0.6527	-0.6155	0.00E+00	MIDN	midnolin [Source:HGNC Symbol;Acc:HGNC:16298]
284422	0.3947	-1.3412	0.00E+00	SMIM24	small integral membrane protein 24 [Source:HGNC Symbol;Acc:HGNC:37244]
3613	0.4824	-1.0516	0.00E+00	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2 [Source:HGNC Symbol;Acc:HGNC:6051]
57396	0.6103	-0.7123	0.00E+00	CLK4	CDC-like kinase 4 [Source:HGNC Symbol;Acc:HGNC:13659]
23235	0.6099	-0.7134	0.00E+00	SIK2	salt-inducible kinase 2 [Source:HGNC Symbol;Acc:HGNC:21680]
9021	0.4206	-1.2494	0.00E+00	SOCS3	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:HGNC:19391]
85450	0.4477	-1.1593	0.00E+00	ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein [Source:HGNC Symbol;Acc:HGNC:29370]
8972	0.3957	-1.3375	0.00E+00	MGAM	maltase-glucoamylase [Source:HGNC Symbol;Acc:HGNC:7043]
9317	0.6402	-0.6434	0.00E+00	PTER	phosphotriesterase related [Source:HGNC Symbol;Acc:HGNC:9590]
23580	0.6626	-0.5939	0.00E+00	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4 [Source:HGNC Symbol;Acc:HGNC:17147]
4129	0.6616	-0.5960	0.00E+00	MAOB	monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:6834]
55151	0.6645	-0.5897	0.00E+00	TMEM38B	transmembrane protein 38B [Source:HGNC Symbol;Acc:HGNC:25535]
11067	0.4077	-1.2945	0.00E+00	C10ORF10	chromosome 10 open reading frame 10 [Source:HGNC Symbol;Acc:HGNC:23355]
64902	0.3813	-1.3909	0.00E+00	AGXT2	alanine--glyoxylate aminotransferase 2 [Source:HGNC Symbol;Acc:HGNC:14412]
55244	0.3886	-1.3635	0.00E+00	SLC47A1	solute carrier family 47 (multidrug and toxin extrusion), member 1 [Source:HGNC Symbol;Acc:HGNC:25588]
79814	0.3805	-1.3942	0.00E+00	AGMAT	agmatine ureohydrolase (agmatinase) [Source:HGNC Symbol;Acc:HGNC:18407]
10053	0.6224	-0.6841	0.00E+00	AP1M2	adaptor-related protein complex 1, mu 2 subunit [Source:HGNC Symbol;Acc:HGNC:558]
9376	0.3963	-1.3353	0.00E+00	SLC22A8	solute carrier family 22 (organic anion transporter), member 8 [Source:HGNC Symbol;Acc:HGNC:10972]

5932	0.5403	-0.8881	0.00E+00	RBBP8	retinoblastoma binding protein 8 [Source:HGNC Symbol;Acc:HGNC:9891]
5357	0.5638	-0.8267	0.00E+00	PLS1	plastin 1 [Source:HGNC Symbol;Acc:HGNC:9090]
130	0.5159	-0.9550	0.00E+00	ADH6	alcohol dehydrogenase 6 (class V) [Source:HGNC Symbol;Acc:HGNC:255]
4609	0.3208	-1.6404	0.00E+00	MYC	v-myc avian myelocytomatosis viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7553]
58510	0.5344	-0.9040	0.00E+00	PRODH2	proline dehydrogenase (oxidase) 2 [Source:HGNC Symbol;Acc:HGNC:17325]
29953	0.5362	-0.8993	0.00E+00	TRHDE	thyrotropin-releasing hormone degrading enzyme [Source:HGNC Symbol;Acc:HGNC:30748]
27283	0.4350	-1.2009	0.00E+00	TINAG	tubulointerstitial nephritis antigen [Source:HGNC Symbol;Acc:HGNC:14599]
1026	0.3883	-1.3647	0.00E+00	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HGNC Symbol;Acc:HGNC:1784]
146802	0.4068	-1.2978	0.00E+00	SLC47A2	solute carrier family 47 (multidrug and toxin extrusion), member 2 [Source:HGNC Symbol;Acc:HGNC:26439]
87769	0.6183	-0.6937	0.00E+00	GGACT	gamma-glutamylamine cyclotransferase [Source:HGNC Symbol;Acc:HGNC:25100]
4502	0.5765	-0.7946	0.00E+00	MT2A	metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
4291	0.5053	-0.9849	0.00E+00	MLF1	myeloid leukemia factor 1 [Source:HGNC Symbol;Acc:HGNC:7125]
5053	0.3498	-1.5154	0.00E+00	PAH	phenylalanine hydroxylase [Source:HGNC Symbol;Acc:HGNC:8582]
92292	0.3914	-1.3534	0.00E+00	GLYATL1	glycine-N-acyltransferase-like 1 [Source:HGNC Symbol;Acc:HGNC:30519]
85027	0.4872	-1.0375	0.00E+00	SMIM3	small integral membrane protein 3 [Source:HGNC Symbol;Acc:HGNC:30248]
22936	0.5586	-0.8401	0.00E+00	ELL2	elongation factor, RNA polymerase II, 2 [Source:HGNC Symbol;Acc:HGNC:17064]
23087	0.5210	-0.9406	0.00E+00	TRIM35	tripartite motif containing 35 [Source:HGNC Symbol;Acc:HGNC:16285]
3773	0.5933	-0.7532	0.00E+00	KCNJ16	potassium channel, inwardly rectifying subfamily J, member 16 [Source:HGNC Symbol;Acc:HGNC:6262]
2180	0.6689	-0.5801	0.00E+00	ACSL1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:HGNC:3569]
57821	0.6188	-0.6924	0.00E+00	CCDC181	coiled-coil domain containing 181 [Source:HGNC Symbol;Acc:HGNC:28051]
2710	0.5197	-0.9441	0.00E+00	GK	glycerol kinase [Source:HGNC Symbol;Acc:HGNC:4289]

2326	0.3510	-1.5105	0.00E+00	FMO1	flavin containing monooxygenase 1 [Source:HGNC Symbol;Acc:HGNC:3769]
390	0.5955	-0.7478	0.00E+00	RND3	Rho family GTPase 3 [Source:HGNC Symbol;Acc:HGNC:671]
3570	0.4814	-1.0545	0.00E+00	IL6R	interleukin 6 receptor [Source:HGNC Symbol;Acc:HGNC:6019]
8029	0.3729	-1.4230	0.00E+00	CUBN	cubilin (intrinsic factor-cobalamin receptor) [Source:HGNC Symbol;Acc:HGNC:2548]
5184	0.6080	-0.7177	0.00E+00	PEPD	peptidase D [Source:HGNC Symbol;Acc:HGNC:8840]
9920	0.6695	-0.5788	0.00E+00	KBTBD11	kelch repeat and BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc:HGNC:29104]
171425	0.6502	-0.6210	0.00E+00	CLYBL	citrate lyase beta like [Source:HGNC Symbol;Acc:HGNC:18355]
10247	0.4931	-1.0201	0.00E+00	HRSP12	heat-responsive protein 12 [Source:HGNC Symbol;Acc:HGNC:16897]
23221	0.6439	-0.6352	0.00E+00	RHOBTB2	Rho-related BTB domain containing 2 [Source:HGNC Symbol;Acc:HGNC:18756]
60370	0.5889	-0.7640	0.00E+00	AVPI1	arginine vasopressin-induced 1 [Source:HGNC Symbol;Acc:HGNC:30898]
1610	0.4577	-1.1276	0.00E+00	DAO	D-amino-acid oxidase [Source:HGNC Symbol;Acc:HGNC:2671]
94081	0.6275	-0.6724	0.00E+00	SFXN1	sideroflexin 1 [Source:HGNC Symbol;Acc:HGNC:16085]
116842	0.5630	-0.8289	0.00E+00	LEAP2	liver expressed antimicrobial peptide 2 [Source:HGNC Symbol;Acc:HGNC:29571]
183	0.4127	-1.2769	0.00E+00	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8) [Source:HGNC Symbol;Acc:HGNC:333]
3772	0.4828	-1.0506	0.00E+00	KCNJ15	potassium channel, inwardly rectifying subfamily J, member 15 [Source:HGNC Symbol;Acc:HGNC:6261]
9027	0.3774	-1.4059	0.00E+00	NAT8	N-acetyltransferase 8 (GCN5-related, putative) [Source:HGNC Symbol;Acc:HGNC:18069]
118471	0.5458	-0.8736	0.00E+00	PRAP1	proline-rich acidic protein 1 [Source:HGNC Symbol;Acc:HGNC:23304]
635	0.4131	-1.2754	0.00E+00	BHMT	betaine--homocysteine S-methyltransferase [Source:HGNC Symbol;Acc:HGNC:1047]
91694	0.6012	-0.7341	0.00E+00	LONRF1	LON peptidase N-terminal domain and ring finger 1 [Source:HGNC Symbol;Acc:HGNC:26302]
6299	0.6308	-0.6648	0.00E+00	SALL1	spalt-like transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:10524]
203328	0.6439	-0.6350	0.00E+00	SUSD3	sushi domain containing 3 [Source:HGNC Symbol;Acc:HGNC:28391]
55777	0.6693	-0.5793	0.00E+00	MBD5	methyl-CpG binding domain protein 5 [Source:HGNC Symbol;Acc:HGNC:20444]

79589	0.5257	-0.9276	0.00E+00	RNF128	ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:21153]
340024	0.5414	-0.8851	0.00E+00	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19 [Source:HGNC Symbol;Acc:HGNC:27960]
83992	0.6308	-0.6647	0.00E+00	CTTNBP2	cortactin binding protein 2 [Source:HGNC Symbol;Acc:HGNC:15679]
957	0.5545	-0.8507	0.00E+00	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5 [Source:HGNC Symbol;Acc:HGNC:3367]
23761	0.6619	-0.5953	0.00E+00	PISD	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:HGNC:8999]
6540	0.6042	-0.7269	0.00E+00	SLC6A13	solute carrier family 6 (neurotransmitter transporter), member 13 [Source:HGNC Symbol;Acc:HGNC:11046]
29126	0.6162	-0.6985	0.00E+00	CD274	CD274 molecule [Source:HGNC Symbol;Acc:HGNC:17635]
3304	0.3067	-1.7052	0.00E+00	HSPA1B	heat shock 70kDa protein 1B [Source:HGNC Symbol;Acc:HGNC:5233]
5577	0.6376	-0.6493	0.00E+00	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta [Source:HGNC Symbol;Acc:HGNC:9392]
10103	0.4910	-1.0261	0.00E+00	TSPAN1	tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
22977	0.5154	-0.9563	0.00E+00	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) [Source:HGNC Symbol;Acc:HGNC:390]
58480	0.6210	-0.6872	0.00E+00	RHOU	ras homolog family member U [Source:HGNC Symbol;Acc:HGNC:17794]
1645	0.4561	-1.1324	0.00E+00	AKR1C1	aldo-keto reductase family 1, member C1 [Source:HGNC Symbol;Acc:HGNC:384]
80176	0.5242	-0.9317	0.00E+00	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1 [Source:HGNC Symbol;Acc:HGNC:30628]
91860	0.6140	-0.7036	0.00E+00	CALML4	calmodulin-like 4 [Source:HGNC Symbol;Acc:HGNC:18445]
5106	0.5681	-0.8158	0.00E+00	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial) [Source:HGNC Symbol;Acc:HGNC:8725]
222484	0.6022	-0.7318	0.00E+00	LNX2	ligand of numb-protein X 2 [Source:HGNC Symbol;Acc:HGNC:20421]
5326	0.6609	-0.5975	0.00E+00	PLAGL2	pleiomorphic adenoma gene-like 2 [Source:HGNC Symbol;Acc:HGNC:9047]
23475	0.6553	-0.6097	0.00E+00	QPRT	quinolinate phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:9755]

84706	0.6034	-0.7289	0.00E+00	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:HGNC Symbol;Acc:HGNC:18062]
25924	0.5080	-0.9772	0.00E+00	MYRIP	myosin VIIA and Rab interacting protein [Source:HGNC Symbol;Acc:HGNC:19156]
10808	0.4398	-1.1850	0.00E+00	HSPH1	heat shock 105kDa/110kDa protein 1 [Source:HGNC Symbol;Acc:HGNC:16969]
130502	0.6201	-0.6895	0.00E+00	TTC32	tetratricopeptide repeat domain 32 [Source:HGNC Symbol;Acc:HGNC:32954]
1839	0.3857	-1.3743	0.00E+00	HBEGF	heparin-binding EGF-like growth factor [Source:HGNC Symbol;Acc:HGNC:3059]
78989	0.6108	-0.7113	0.00E+00	COLEC11	collectin sub-family member 11 [Source:HGNC Symbol;Acc:HGNC:17213]
493861	0.6197	-0.6903	0.00E+00	EID3	EP300 interacting inhibitor of differentiation 3 [Source:HGNC Symbol;Acc:HGNC:32961]
4499	0.2787	-1.8431	0.00E+00	MT1M	metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296]
3957	0.5045	-0.9870	0.00E+00	LGALS2	lectin, galactoside-binding, soluble, 2 [Source:HGNC Symbol;Acc:HGNC:6562]
10365	0.5271	-0.9239	0.00E+00	KLF2	Kruppel-like factor 2 [Source:HGNC Symbol;Acc:HGNC:6347]
100288413	0.5917	-0.7571	0.00E+00	ERVMER34-1	endogenous retrovirus group MER34, member 1 [Source:HGNC Symbol;Acc:HGNC:42970]
5997	0.6183	-0.6935	0.00E+00	RGS2	regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc:HGNC:9998]
8870	0.4966	-1.0098	0.00E+00	IER3	immediate early response 3 [Source:HGNC Symbol;Acc:HGNC:5392]
5265	0.3740	-1.4191	0.00E+00	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:HGNC Symbol;Acc:HGNC:8941]
81932	0.6139	-0.7040	0.00E+00	HDHD3	haloacid dehalogenase-like hydrolase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:28171]
4072	0.5321	-0.9103	0.00E+00	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:11529]
57584	0.6684	-0.5812	0.00E+00	ARHGAP21	Rho GTPase activating protein 21 [Source:HGNC Symbol;Acc:HGNC:23725]
5054	0.3703	-1.4333	0.00E+00	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 [Source:HGNC Symbol;Acc:HGNC:8583]
1579	0.5268	-0.9246	0.00E+00	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22 [Source:HGNC Symbol;Acc:HGNC:20575]

2706	0.5165	-0.9531	0.00E+00	GJB2	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;Acc:HGNC:4284]
84251	0.6408	-0.6421	0.00E+00	SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:25412]
283375	0.6236	-0.6814	0.00E+00	SLC39A5	solute carrier family 39 (zinc transporter), member 5 [Source:HGNC Symbol;Acc:HGNC:20502]
7678	0.5390	-0.8917	0.00E+00	ZNF124	zinc finger protein 124 [Source:HGNC Symbol;Acc:HGNC:12907]
64798	0.6349	-0.6553	0.00E+00	DEPTOR	DEP domain containing MTOR-interacting protein [Source:HGNC Symbol;Acc:HGNC:22953]
9929	0.6458	-0.6308	0.00E+00	JOSD1	Josephin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28953]
387882	0.5970	-0.7441	0.00E+00	C12ORF75	chromosome 12 open reading frame 75 [Source:HGNC Symbol;Acc:HGNC:35164]
125206	0.5458	-0.8736	0.00E+00	SLC5A10	solute carrier family 5 (sodium/sugar cotransporter), member 10 [Source:HGNC Symbol;Acc:HGNC:23155]
57018	0.6530	-0.6148	0.00E+00	CCNL1	cyclin L1 [Source:HGNC Symbol;Acc:HGNC:20569]
9075	0.4711	-1.0860	0.00E+00	CLDN2	claudin 2 [Source:HGNC Symbol;Acc:HGNC:2041]
4495	0.4134	-1.2743	0.00E+00	MT1G	metallothionein 1G [Source:HGNC Symbol;Acc:HGNC:7399]
9365	0.6523	-0.6163	0.00E+00	KL	klotho [Source:HGNC Symbol;Acc:HGNC:6344]
64284	0.6223	-0.6844	0.00E+00	RAB17	RAB17, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:16523]
18	0.6018	-0.7326	0.00E+00	ABAT	4-aminobutyrate aminotransferase [Source:HGNC Symbol;Acc:HGNC:23]
26	0.4376	-1.1924	0.00E+00	AOC1	amine oxidase, copper containing 1 [Source:HGNC Symbol;Acc:HGNC:80]
5770	0.6388	-0.6465	0.00E+00	PTPN1	protein tyrosine phosphatase, non-receptor type 1 [Source:HGNC Symbol;Acc:HGNC:9642]
28959	0.5401	-0.8886	0.00E+00	TMEM176B	transmembrane protein 176B [Source:HGNC Symbol;Acc:HGNC:29596]
8858	0.5902	-0.7608	0.00E+00	PROZ	protein Z, vitamin K-dependent plasma glycoprotein [Source:HGNC Symbol;Acc:HGNC:9460]
639	0.5863	-0.7702	0.00E+00	PRDM1	PR domain containing 1, with ZNF domain [Source:HGNC Symbol;Acc:HGNC:9346]
84457	0.6656	-0.5872	0.00E+00	PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like [Source:HGNC Symbol;Acc:HGNC:29378]
2731	0.5939	-0.7518	0.00E+00	GLDC	glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:HGNC:4313]

6582	0.5673	-0.8177	0.00E+00	SLC22A2	solute carrier family 22 (organic cation transporter), member 2 [Source:HGNC Symbol;Acc:HGNC:10966]
151295	0.4023	-1.3137	0.00E+00	SLC23A3	solute carrier family 23, member 3 [Source:HGNC Symbol;Acc:HGNC:20601]
9056	0.5545	-0.8506	0.00E+00	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7 [Source:HGNC Symbol;Acc:HGNC:11065]
55603	0.6674	-0.5834	0.00E+00	FAM46A	family with sequence similarity 46, member A [Source:HGNC Symbol;Acc:HGNC:18345]
9104	0.6430	-0.6372	0.00E+00	RGN	regucalcin [Source:HGNC Symbol;Acc:HGNC:9989]
9353	0.6196	-0.6907	0.00E+00	SLIT2	slit homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:11086]
6242	0.6270	-0.6735	0.00E+00	RTKN	rhotekin [Source:HGNC Symbol;Acc:HGNC:10466]
51181	0.6493	-0.6232	0.00E+00	DCXR	dicarbonyl/L-xylulose reductase [Source:HGNC Symbol;Acc:HGNC:18985]
83716	0.4318	-1.2116	0.00E+00	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:HGNC:25248]
387763	0.4699	-1.0896	0.00E+00	C11ORF96	chromosome 11 open reading frame 96 [Source:HGNC Symbol;Acc:HGNC:38675]
1999	0.6219	-0.6853	0.00E+00	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific) [Source:HGNC Symbol;Acc:HGNC:3318]
55647	0.6582	-0.6034	0.00E+00	RAB20	RAB20, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:18260]
6569	0.5532	-0.8542	0.00E+00	SLC34A1	solute carrier family 34 (type II sodium/phosphate cotransporter), member 1 [Source:HGNC Symbol;Acc:HGNC:11019]
1969	0.6411	-0.6415	0.00E+00	EPHA2	EPH receptor A2 [Source:HGNC Symbol;Acc:HGNC:3386]
3310	0.3316	-1.5923	0.00E+00	HSPA6	heat shock 70kDa protein 6 (HSP70B') [Source:HGNC Symbol;Acc:HGNC:5239]
79746	0.6626	-0.5938	0.00E+00	ECHDC3	enoyl CoA hydratase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:23489]
124044	0.6073	-0.7196	0.00E+00	SPATA2L	spermatogenesis associated 2-like [Source:HGNC Symbol;Acc:HGNC:28393]
2329	0.6164	-0.6980	0.00E+00	FMO4	flavin containing monooxygenase 4 [Source:HGNC Symbol;Acc:HGNC:3772]
100507650	0.4217	-1.2458	0.00E+00	RNF212B	ring finger protein 212B [Source:HGNC Symbol;Acc:HGNC:20438]
3305	0.6288	-0.6694	0.00E+00	HSPA1L	heat shock 70kDa protein 1-like [Source:HGNC Symbol;Acc:HGNC:5234]

84275	0.6536	-0.6134	0.00E+00	SLC25A33	solute carrier family 25 (pyrimidine nucleotide carrier), member 33 [Source:HGNC Symbol;Acc:HGNC:29681]
9456	0.4723	-1.0822	0.00E+00	HOMER1	homer scaffolding protein 1 [Source:HGNC Symbol;Acc:HGNC:17512]
1962	0.6554	-0.6095	0.00E+00	EHHADH	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase [Source:HGNC Symbol;Acc:HGNC:3247]
8644	0.5501	-0.8624	0.00E+00	AKR1C3	aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:HGNC:386]
1184	0.6628	-0.5935	0.00E+00	CLCN5	chloride channel, voltage-sensitive 5 [Source:HGNC Symbol;Acc:HGNC:2023]
2348	0.6306	-0.6651	0.00E+00	FOLR1	folate receptor 1 (adult) [Source:HGNC Symbol;Acc:HGNC:3791]
6590	0.5543	-0.8513	0.00E+00	SLPI	secretory leukocyte peptidase inhibitor [Source:HGNC Symbol;Acc:HGNC:11092]
8836	0.5886	-0.7647	0.00E+00	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) [Source:HGNC Symbol;Acc:HGNC:4248]
10615	0.6573	-0.6053	0.00E+00	SPAG5	sperm associated antigen 5 [Source:HGNC Symbol;Acc:HGNC:13452]
80339	0.6365	-0.6517	0.00E+00	PNPLA3	patatin-like phospholipase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:18590]
91947	0.6681	-0.5818	0.00E+00	ARRDC4	arrestin domain containing 4 [Source:HGNC Symbol;Acc:HGNC:28087]
83481	0.6229	-0.6829	0.00E+00	EPPK1	epiplakin 1 [Source:HGNC Symbol;Acc:HGNC:15577]
4860	0.6534	-0.6140	0.00E+00	PNP	purine nucleoside phosphorylase [Source:HGNC Symbol;Acc:HGNC:7892]
6515	0.4773	-1.0669	0.00E+00	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3 [Source:HGNC Symbol;Acc:HGNC:11007]
55365	0.5720	-0.8058	0.00E+00	TMEM176A	transmembrane protein 176A [Source:HGNC Symbol;Acc:HGNC:24930]
4482	0.6447	-0.6332	0.00E+00	MSRA	methionine sulfoxide reductase A [Source:HGNC Symbol;Acc:HGNC:7377]
130589	0.6380	-0.6483	0.00E+00	GALM	galactose mutarotase (aldose 1-epimerase) [Source:HGNC Symbol;Acc:HGNC:24063]
1014	0.6683	-0.5814	0.00E+00	CDH16	cadherin 16, KSP-cadherin [Source:HGNC Symbol;Acc:HGNC:1755]
84451	0.6159	-0.6993	0.00E+00	MLK4	Mitogen-activated protein kinase kinase kinase MLK4 [Source:UniProtKB/Swiss-Prot;Acc:Q5TCX8]

7748	0.6512	-0.6188	0.00E+00	ZNF195	zinc finger protein 195 [Source:HGNC Symbol;Acc:HGNC:12986]
121506	0.4706	-1.0874	0.00E+00	ERP27	endoplasmic reticulum protein 27 [Source:HGNC Symbol;Acc:HGNC:26495]
2289	0.4933	-1.0193	0.00E+00	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3721]
9131	0.6534	-0.6139	0.00E+00	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1 [Source:HGNC Symbol;Acc:HGNC:8768]
51267	0.5326	-0.9088	0.00E+00	CLEC1A	C-type lectin domain family 1, member A [Source:HGNC Symbol;Acc:HGNC:24355]
3249	0.6004	-0.7361	0.00E+00	HPN	hepsin [Source:HGNC Symbol;Acc:HGNC:5155]
866	0.5504	-0.8614	0.00E+00	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 [Source:HGNC Symbol;Acc:HGNC:1540]
134288	0.5448	-0.8763	0.00E+00	TMEM174	transmembrane protein 174 [Source:HGNC Symbol;Acc:HGNC:28187]
80221	0.6438	-0.6354	0.00E+00	ACSF2	acyl-CoA synthetase family member 2 [Source:HGNC Symbol;Acc:HGNC:26101]
2215	0.4888	-1.0328	0.00E+00	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b) [Source:HGNC Symbol;Acc:HGNC:3620]
27294	0.6521	-0.6168	0.00E+00	DHDH	dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;Acc:HGNC:17887]
84560	0.6615	-0.5961	0.00E+00	MT4	metallothionein 4 [Source:HGNC Symbol;Acc:HGNC:18705]
6279	0.4539	-1.1395	0.00E+00	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:HGNC:10498]
9071	0.5645	-0.8251	0.00E+00	CLDN10	claudin 10 [Source:HGNC Symbol;Acc:HGNC:2033]
10245	0.6633	-0.5923	0.00E+00	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast) [Source:HGNC Symbol;Acc:HGNC:17310]
83959	0.5834	-0.7776	0.00E+00	SLC4A11	solute carrier family 4, sodium borate transporter, member 11 [Source:HGNC Symbol;Acc:HGNC:16438]
5243	0.5822	-0.7805	0.00E+00	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1 [Source:HGNC Symbol;Acc:HGNC:40]
115749	0.6642	-0.5903	0.00E+00	C12ORF56	chromosome 12 open reading frame 56 [Source:HGNC Symbol;Acc:HGNC:26967]
112817	0.6477	-0.6266	0.00E+00	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1 [Source:HGNC Symbol;Acc:HGNC:25155]
55753	0.6478	-0.6264	0.00E+00	OGDHL	oxoglutarate dehydrogenase-like [Source:HGNC Symbol;Acc:HGNC:25590]

8793	0.6654	-0.5876	0.00E+00	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain [Source:HGNC Symbol;Acc:HGNC:11907]
1164	0.5851	-0.7732	0.00E+00	CKS2	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Symbol;Acc:HGNC:2000]
330	0.5211	-0.9403	0.00E+00	BIRC3	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:HGNC:591]
2018	0.6163	-0.6983	0.00E+00	EMX2	empty spiracles homeobox 2 [Source:HGNC Symbol;Acc:HGNC:3341]
10841	0.6383	-0.6478	0.00E+00	FTCD	formimidoyltransferase cyclodeaminase [Source:HGNC Symbol;Acc:HGNC:3974]
316	0.5561	-0.8465	0.00E+00	AOX1	aldehyde oxidase 1 [Source:HGNC Symbol;Acc:HGNC:553]
23670	0.6388	-0.6465	0.00E+00	TMEM2	transmembrane protein 2 [Source:HGNC Symbol;Acc:HGNC:11869]
6273	0.3675	-1.4443	0.00E+00	S100A2	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:HGNC:10492]
5950	0.5178	-0.9495	0.00E+00	RBP4	retinol binding protein 4, plasma [Source:HGNC Symbol;Acc:HGNC:9922]
222643	0.5398	-0.8895	0.00E+00	UNC5CL	unc-5 homolog C (C. elegans)-like [Source:HGNC Symbol;Acc:HGNC:21203]
359	0.6048	-0.7254	0.00E+00	AQP2	aquaporin 2 (collecting duct) [Source:HGNC Symbol;Acc:HGNC:634]
9547	0.5479	-0.8681	0.00E+00	CXCL14	chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Acc:HGNC:10640]
7074	0.6577	-0.6045	0.00E+00	TIAM1	T-cell lymphoma invasion and metastasis 1 [Source:HGNC Symbol;Acc:HGNC:11805]
54886	0.5547	-0.8501	0.00E+00	RP11-35N6.1	Lipid phosphate phosphatase-related protein type 1 [Source:UniProtKB/Swiss-Prot;Acc:Q8TBJ4]
117854	0.6076	-0.7189	0.00E+00	TRIM6	tripartite motif containing 6 [Source:HGNC Symbol;Acc:HGNC:16277]
81563	0.6684	-0.5813	0.00E+00	C1ORF21	chromosome 1 open reading frame 21 [Source:HGNC Symbol;Acc:HGNC:15494]
347	0.4042	-1.3069	0.00E+00	APOD	apolipoprotein D [Source:HGNC Symbol;Acc:HGNC:612]
55195	0.6467	-0.6288	0.00E+00	C14ORF105	chromosome 14 open reading frame 105 [Source:HGNC Symbol;Acc:HGNC:20189]
80896	0.6256	-0.6766	0.00E+00	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) [Source:HGNC Symbol;Acc:HGNC:16781]
23136	0.6501	-0.6213	1.52E-04	EPB41L3	erythrocyte membrane protein band 4.1-like 3 [Source:HGNC Symbol;Acc:HGNC:3380]

25878	2.0623	1.0443	1.57E-04	MXRA5	matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:HGNC:7539]
11130	1.5527	0.6348	1.57E-04	ZWINT	ZW10 interacting kinetochore protein [Source:HGNC Symbol;Acc:HGNC:13195]
2170	0.5962	-0.7461	1.61E-04	FABP3	fatty acid binding protein 3, muscle and heart [Source:HGNC Symbol;Acc:HGNC:3557]
29119	0.6433	-0.6364	2.77E-04	CTNNA3	catenin (cadherin-associated protein), alpha 3 [Source:HGNC Symbol;Acc:HGNC:2511]
11013	2.0052	1.0037	2.80E-04	TMSB15A	thymosin beta 15a [Source:HGNC Symbol;Acc:HGNC:30744]
100170765	0.6168	-0.6971	2.83E-04	ERICH4	glutamate-rich 4 [Source:HGNC Symbol;Acc:HGNC:34497]
163782	1.5197	0.6038	2.87E-04	KANK4	KN motif and ankyrin repeat domains 4 [Source:HGNC Symbol;Acc:HGNC:27263]
6574	0.5955	-0.7478	2.87E-04	SLC20A1	solute carrier family 20 (phosphate transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10946]
81788	0.6668	-0.5847	2.94E-04	NUAK2	NUAK family, SNF1-like kinase, 2 [Source:HGNC Symbol;Acc:HGNC:29558]
164832	0.5990	-0.7394	2.94E-04	LONRF2	LON peptidase N-terminal domain and ring finger 2 [Source:HGNC Symbol;Acc:HGNC:24788]
2888	0.5879	-0.7664	3.98E-04	GRB14	growth factor receptor-bound protein 14 [Source:HGNC Symbol;Acc:HGNC:4565]
3684	1.6066	0.6840	4.03E-04	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:HGNC:6149]
50486	0.6591	-0.6014	4.03E-04	G0S2	G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]
91752	0.6467	-0.6288	4.03E-04	ZNF804A	zinc finger protein 804A [Source:HGNC Symbol;Acc:HGNC:21711]
8547	1.5572	0.6389	4.57E-04	FCN3	ficolin (collagen/fibrinogen domain containing) 3 [Source:HGNC Symbol;Acc:HGNC:3625]
290	0.6349	-0.6554	5.03E-04	ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:HGNC:500]
4023	0.5767	-0.7942	5.10E-04	LPL	lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
54988	0.6453	-0.6320	5.10E-04	ACSM5	acyl-CoA synthetase medium-chain family member 5 [Source:HGNC Symbol;Acc:HGNC:26060]
2357	0.6219	-0.6853	6.20E-04	FPR1	formyl peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:3826]
6402	0.5642	-0.8257	6.20E-04	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
3291	0.6600	-0.5996	8.12E-04	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:HGNC:5209]
718	1.6945	0.7608	8.26E-04	C3	complement component 3 [Source:HGNC Symbol;Acc:HGNC:1318]

80271	0.5948	-0.7494	8.26E-04	ITPKC	inositol-trisphosphate 3-kinase C [Source:HGNC Symbol;Acc:HGNC:14897]
57007	0.6049	-0.7251	9.18E-04	ACKR3	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:HGNC:23692]
5649	0.5736	-0.8020	1.02E-03	RELN	reelin [Source:HGNC Symbol;Acc:HGNC:9957]
415	0.5931	-0.7536	1.02E-03	ARSE	arylsulfatase E (chondrodysplasia punctata 1) [Source:HGNC Symbol;Acc:HGNC:719]
9358	1.5386	0.6216	1.12E-03	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains) [Source:HGNC Symbol;Acc:HGNC:6164]
84417	1.6012	0.6792	1.12E-03	C2ORF40	chromosome 2 open reading frame 40 [Source:HGNC Symbol;Acc:HGNC:24642]
122416	1.5859	0.6653	1.22E-03	ANKRD9	ankyrin repeat domain 9 [Source:HGNC Symbol;Acc:HGNC:20096]
25928	1.5967	0.6751	1.22E-03	SOSTDC1	sclerostin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:21748]
1950	0.6131	-0.7057	1.26E-03	EGF	epidermal growth factor [Source:HGNC Symbol;Acc:HGNC:3229]
1672	0.5737	-0.8017	1.26E-03	DEFB1	defensin, beta 1 [Source:HGNC Symbol;Acc:HGNC:2766]
6280	0.6519	-0.6173	1.26E-03	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:HGNC:10499]
730	1.6223	0.6980	1.59E-03	C7	complement component 7 [Source:HGNC Symbol;Acc:HGNC:1346]
57211	0.6349	-0.6554	1.71E-03	ADGRG6	adhesion G protein-coupled receptor G6 [Source:HGNC Symbol;Acc:HGNC:13841]
4745	1.6089	0.6861	1.94E-03	NELL1	NEL-like 1 (chicken) [Source:HGNC Symbol;Acc:HGNC:7750]
283120	1.5322	0.6156	2.12E-03	H19	H19, imprinted maternally expressed transcript (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:4713]
7704	0.4457	-1.1657	2.59E-03	ZBTB16	zinc finger and BTB domain containing 16 [Source:HGNC Symbol;Acc:HGNC:12930]
4283	1.6440	0.7172	3.35E-03	CXCL9	chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:HGNC:7098]
825	0.6223	-0.6844	3.35E-03	CAPN3	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
1959	0.4784	-1.0636	4.12E-03	EGR2	early growth response 2 [Source:HGNC Symbol;Acc:HGNC:3239]
4316	1.5317	0.6152	5.12E-03	MMP7	matrix metallopeptidase 7 [Source:HGNC Symbol;Acc:HGNC:7174]
6785	0.6415	-0.6404	5.12E-03	ELOVL4	ELOVL fatty acid elongase 4 [Source:HGNC Symbol;Acc:HGNC:14415]
51330	0.6611	-0.5971	8.00E-03	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A [Source:HGNC Symbol;Acc:HGNC:18152]

1008	0.6631	-0.5928	9.08E-03	CDH10	cadherin 10, type 2 (T2-cadherin) [Source:HGNC Symbol;Acc:HGNC:1749]
8838	0.6454	-0.6317	9.72E-03	WISP3	WNT1 inducible signaling pathway protein 3 [Source:HGNC Symbol;Acc:HGNC:12771]
1803	0.5642	-0.8258	9.72E-03	DPP4	dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:HGNC:3009]

Supplemental Table 2: List of positive standard genes from different cell types. Genes with underline are standard genes found in the current dataset. Bold genes with underline are significantly regulated standard genes found in the current dataset.

Cell type	Standard genes
Mesangial cell	**ACTA2**, **AGTR1**, **AKR1C3**, ANGPT2, **BMP4**, **CAD**, **CALD1**, **CD34**, **ETS1**, **F2R**, F5, **FBN1**, GAS6, **IGFBP5**, ITGA8, **ITGAV**, ITGB1, **KLF6**, NES, **Nox4**, **SERPINE1**, **PCDH12**, PDGFRA, PDGFRB, PTGS1/COX1, SERPINB7, SERPINE2, SOX9, **TAGLN**, TG2, THY1, **TNS1**, **TNS3**, **TXNIP**, **USP2**
Podocyte	**ACTN4**, NPHS1, NPHS2, SYNPO, PTPRO, NES, DDN, LRRC7, WT1, **TCF21**, MAGI1, **MAGI2**, RAB3A, **KIRREL**, KIRREL2, KIRREL3, CD2AP, **CASK**, IQGAP1, **TJP1**, TRPC6, NCK2, DES, PDPN, PODXL, LMX1B, FAT1, CDH3, PLCE1, **CLIC5**, CDH13, **MME**, **UCHL1**, CD80, Sv2b, **PALLD**, **FYN**, **PLAUR**, **DAG1**, AGRN, EFNB1, **EZR**, FOXC2, **MAFB**, UTRN, MYOC, BASP1, SULF1, SCEL, CX3CL1

Supplemental Table 3: List of all significantly regulated proteins identified in mass spectrometry data analysis. Proteins are sorted according to BH p-values (Benjamin-Hochberg adjustment) and fold change is considered up regulation if p-value >1.15 and down regulation if p-value <0.85.

Accession	**Fold change (unlogged)**	**Fold change (log2)**	**BH p-value**	**Symbol**	**Description**
O60613	2.9924	1.5813	3.86E-08	SEP15	15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3 - [SEP15_HUMAN]
Q9BQE4	3.2495	1.7002	6.81E-08	SELS	Selenoprotein S OS=Homo sapiens GN=VIMP PE=1 SV=3 - [SELS_HUMAN]
Q8WWX9	3.5669	1.8347	7.18E-08	SELM	Selenoprotein M OS=Homo sapiens GN=SELM PE=1 SV=3 - [SELM_HUMAN]
Q01581	0.4902	-1.0286	2.62E-07	HMCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2 - [HMCS1_HUMAN]
P35222	1.2434	0.3142	2.62E-07	CTNB1	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]
P05121	0.4930	-1.0203	3.22E-07	PAI1	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1 - [PAI1_HUMAN]
Q9Y6K8	0.7200	-0.4739	3.22E-07	KAD5	Adenylate kinase isoenzyme 5 OS=Homo sapiens GN=AK5 PE=1 SV=2 - [KAD5_HUMAN]
Q9HBL0	1.1681	0.2242	3.35E-07	TENS1	Tensin-1 OS=Homo sapiens GN=TNS1 PE=1 SV=2 - [TENS1_HUMAN]
Q96M96	0.7510	-0.4130	3.42E-07	FGD4	FYVE, RhoGEF and PH domain-containing protein 4 OS=Homo sapiens GN=FGD4 PE=1 SV=2 - [FGD4_HUMAN]
P07203	3.3710	1.7532	4.95E-07	GPX1	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 - [GPX1_HUMAN]
Q16850	0.5173	-0.9509	4.95E-07	CP51A	Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 PE=1 SV=3 - [CP51A_HUMAN]
Q96BY6	1.2392	0.3094	4.95E-07	DOC10	Dedicator of cytokinesis protein 10 OS=Homo sapiens GN=DOCK10 PE=1 SV=3 - [DOC10_HUMAN]
Q92626	1.9732	0.9806	5.92E-07	PXDN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2 - [PXDN_HUMAN]
Q15582	7.7023	2.9453	6.65E-07	BGH3	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]
Q7Z7A1	35.7000	5.1579	6.65E-07	CNTRL	Centriolin OS=Homo sapiens GN=CNTRL PE=1 SV=2 - [CNTRL_HUMAN]
P49748	1.3184	0.3988	6.65E-07	ACADV	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]

Q9H845	1.1832	0.2427	7.28E-07	ACAD9	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1 - [ACAD9_HUMAN]
P23634	1.2109	0.2761	7.28E-07	AT2B4	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2 - [AT2B4_HUMAN]
P06756	1.4495	0.5356	7.28E-07	ITAV	Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2 - [ITAV_HUMAN]
P48735	1.2617	0.3354	7.59E-07	IDHP	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 - [IDHP_HUMAN]
P52292	0.6128	-0.7065	7.59E-07	IMA1	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 - [IMA1_HUMAN]
P08243	0.7390	-0.4363	7.59E-07	ASNS	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4 - [ASNS_HUMAN]
P04004	4.2041	2.0718	7.59E-07	VTNC	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 - [VTNC_HUMAN]
P42892	0.6320	-0.6619	7.59E-07	ECE1	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2 - [ECE1_HUMAN]
Q9UKX5	1.3103	0.3899	8.36E-07	ITA11	Integrin alpha-11 OS=Homo sapiens GN=ITGA11 PE=1 SV=2 - [ITA11_HUMAN]
Q10472	1.2719	0.3470	8.36E-07	GALT1	Polypeptide N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=GALNT1 PE=1 SV=1 - [GALT1_HUMAN]
P13804	1.1532	0.2057	8.36E-07	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN]
O95379	1.5370	0.6201	9.30E-07	TFIP8	Tumor necrosis factor alpha-induced protein 8 OS=Homo sapiens GN=TNFAIP8 PE=1 SV=1 - [TFIP8_HUMAN]
Q9NSV4	0.5950	-0.7489	1.13E-06	DIAP3	Protein diaphanous homolog 3 OS=Homo sapiens GN=DIAPH3 PE=1 SV=4 - [DIAP3_HUMAN]
Q9HCU0	1.4961	0.5812	1.24E-06	CD248	Endosialin OS=Homo sapiens GN=CD248 PE=1 SV=1 - [CD248_HUMAN]
P37268	0.6853	-0.5451	1.39E-06	FDFT	Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 - [FDFT_HUMAN]
Q53EL6	1.4191	0.5050	1.39E-06	PDCD4	Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 PE=1 SV=2 - [PDCD4_HUMAN]
P05090	31.2738	4.9669	1.39E-06	APOD	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1 - [APOD_HUMAN]
P43121	1.3164	0.3966	1.39E-06	MUC18	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2 - [MUC18_HUMAN]
Q6XZF7	0.8141	-0.2968	1.54E-06	DNMBP	Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=1 SV=1 - [DNMBP_HUMAN]

Q13740	1.2400	0.3104	1.54E-06	CD166	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2 - [CD166_HUMAN]
Q16881	2.0173	1.0124	1.60E-06	TRXR1	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3 - [TRXR1_HUMAN]
Q99715	1.1750	0.2327	1.69E-06	COCA1	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]
P24821	2.1394	1.0972	1.69E-06	TENA	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]
Q53GA4	0.4652	-1.1041	1.69E-06	PHLA2	Pleckstrin homology-like domain family A member 2 OS=Homo sapiens GN=PHLDA2 PE=1 SV=2 - [PHLA2_HUMAN]
Q9H425	1.2644	0.3384	1.69E-06	CA198	Uncharacterized protein C1orf198 OS=Homo sapiens GN=C1orf198 PE=1 SV=1 - [CA198_HUMAN]
Q63ZY3	1.2919	0.3695	1.69E-06	KANK2	KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1 - [KANK2_HUMAN]
P80723	1.3008	0.3794	1.78E-06	BASP1	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 - [BASP1_HUMAN]
Q9H3M7	2.1120	1.0786	2.01E-06	TXNIP	Thioredoxin-interacting protein OS=Homo sapiens GN=TXNIP PE=1 SV=1 - [TXNIP_HUMAN]
P07996	1.2896	0.3669	2.03E-06	TSP1	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]
P29323	1.3810	0.4657	2.24E-06	EPHB2	Ephrin type-B receptor 2 OS=Homo sapiens GN=EPHB2 PE=1 SV=5 - [EPHB2_HUMAN]
Q13011	1.2811	0.3574	2.24E-06	ECH1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2 - [ECH1_HUMAN]
Q9UL42	0.5957	-0.7474	2.24E-06	PNMA2	Paraneoplastic antigen Ma2 OS=Homo sapiens GN=PNMA2 PE=1 SV=2 - [PNMA2_HUMAN]
Q12884	1.3866	0.4716	2.30E-06	SEPR	Seprase OS=Homo sapiens GN=FAP PE=1 SV=5 - [SEPR_HUMAN]
P05413	0.5977	-0.7426	2.39E-06	FABPH	Fatty acid-binding protein, heart OS=Homo sapiens GN=FABP3 PE=1 SV=4 - [FABPH_HUMAN]
Q02952	0.7592	-0.3974	2.39E-06	AKA12	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4 - [AKA12_HUMAN]
Q15848	59.0665	5.8843	2.66E-06	ADIPO	Adiponectin OS=Homo sapiens GN=ADIPOQ PE=1 SV=1 - [ADIPO_HUMAN]
Q9Y4K0	0.6475	-0.6271	2.74E-06	LOXL2	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1 - [LOXL2_HUMAN]
Q01813	1.2020	0.2654	2.89E-06	K6PP	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]
P05997	0.7931	-0.3345	2.95E-06	CO5A2	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3 - [CO5A2_HUMAN]

P07099	1.4352	0.5213	2.95E-06	HYEP	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]
P17813	1.4295	0.5155	3.37E-06	EGLN	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2 - [EGLN_HUMAN]
Q99959	0.8206	-0.2853	3.41E-06	PKP2	Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 - [PKP2_HUMAN]
P09936	1.1774	0.2356	3.42E-06	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2 - [UCHL1_HUMAN]
P50151	1.4437	0.5298	3.50E-06	GBG10	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-10 OS=Homo sapiens GN=GNG10 PE=1 SV=1 - [GBG10_HUMAN]
P06737	1.1781	0.2365	3.54E-06	PYGL	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]
P00748	10.7906	3.4317	3.60E-06	FA12	Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3 - [FA12_HUMAN]
P35442	1.4740	0.5597	3.71E-06	TSP2	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 - [TSP2_HUMAN]
O95833	1.3575	0.4409	3.71E-06	CLIC3	Chloride intracellular channel protein 3 OS=Homo sapiens GN=CLIC3 PE=1 SV=2 - [CLIC3_HUMAN]
O14682	0.4046	-1.3056	3.71E-06	ENC1	Ectoderm-neural cortex protein 1 OS=Homo sapiens GN=ENC1 PE=1 SV=2 - [ENC1_HUMAN]
O43520	0.6445	-0.6337	4.06E-06	AT8B1	Probable phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3 - [AT8B1_HUMAN]
Q9NP74	0.6202	-0.6891	4.06E-06	PALMD	Palmdelphin OS=Homo sapiens GN=PALMD PE=1 SV=1 - [PALMD_HUMAN]
P63218	1.3184	0.3988	4.06E-06	GBG5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3 - [GBG5_HUMAN]
P18084	1.3303	0.4118	4.09E-06	ITB5	Integrin beta-5 OS=Homo sapiens GN=ITGB5 PE=1 SV=1 - [ITB5_HUMAN]
Q15437	0.7522	-0.4109	4.21E-06	SC23B	Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2 - [SC23B_HUMAN]
Q96I59	1.7556	0.8120	4.21E-06	SYNM	Probable asparagine--tRNA ligase, mitochondrial OS=Homo sapiens GN=NARS2 PE=1 SV=3 - [SYNM_HUMAN]
P07951	1.2672	0.3416	4.33E-06	TPM2	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1 - [TPM2_HUMAN]
P05546	28.0465	4.8098	4.33E-06	HEP2	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3 - [HEP2_HUMAN]

P12277	1.2972	0.3754	4.42E-06	KCRB	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]
P48681	0.7892	-0.3416	4.54E-06	NEST	Nestin OS=Homo sapiens GN=NES PE=1 SV=2 - [NEST_HUMAN]
Q01082	0.8525	-0.2302	5.20E-06	SPTB2	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN]
Q9C0C2	0.8185	-0.2889	5.20E-06	TB182	182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 - [TB182_HUMAN]
Q99685	0.7670	-0.3828	5.24E-06	MGLL	Monoglyceride lipase OS=Homo sapiens GN=MGLL PE=1 SV=2 - [MGLL_HUMAN]
P00747	9.6580	3.2717	5.35E-06	PLMN	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2 - [PLMN_HUMAN]
Q02818	1.1637	0.2187	5.40E-06	NUCB1	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4 - [NUCB1_HUMAN]
P02671	2.7706	1.4702	5.44E-06	FIBA	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2 - [FIBA_HUMAN]
Q8WWI1	0.8266	-0.2747	5.45E-06	LMO7	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 - [LMO7_HUMAN]
Q6UVK1	1.1959	0.2581	5.63E-06	CSPG4	Chondroitin sulfate proteoglycan 4 OS=Homo sapiens GN=CSPG4 PE=1 SV=2 - [CSPG4_HUMAN]
Q9P0V3	0.7184	-0.4772	5.63E-06	SH3B4	SH3 domain-binding protein 4 OS=Homo sapiens GN=SH3BP4 PE=1 SV=1 - [SH3B4_HUMAN]
P11413	1.2042	0.2681	5.72E-06	G6PD	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]
P04003	37.5267	5.2298	5.72E-06	C4BPA	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2 - [C4BPA_HUMAN]
P19823	19.2516	4.2669	5.79E-06	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2 - [ITIH2_HUMAN]
P51911	1.3864	0.4714	6.24E-06	CNN1	Calponin-1 OS=Homo sapiens GN=CNN1 PE=1 SV=2 - [CNN1_HUMAN]
P53814	0.7766	-0.3648	6.24E-06	SMTN	Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=7 - [SMTN_HUMAN]
P78324	1.4400	0.5261	6.24E-06	SHPS1	Tyrosine-protein phosphatase non-receptor type substrate 1 OS=Homo sapiens GN=SIRPA PE=1 SV=2 - [SHPS1_HUMAN]
Q14624	12.8356	3.6821	6.31E-06	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4 - [ITIH4_HUMAN]
Q6ZMP0	0.5430	-0.8810	6.33E-06	THSD4	Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4 PE=2 SV=2 - [THSD4_HUMAN]

P26447	1.4116	0.4973	6.41E-06	S10A4	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]
P13611	1.3275	0.4087	6.44E-06	CSPG2	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]
P55287	1.1839	0.2436	6.44E-06	CAD11	Cadherin-11 OS=Homo sapiens GN=CDH11 PE=1 SV=2 - [CAD11_HUMAN]
P00403	1.1539	0.2065	6.63E-06	COX2	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 - [COX2_HUMAN]
P20020	0.6994	-0.5158	6.63E-06	AT2B1	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]
P19827	42.2616	5.4013	6.76E-06	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]
Q99985	2.0239	1.0172	6.86E-06	SEM3C	Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=1 SV=2 - [SEM3C_HUMAN]
Q13308	1.5116	0.5961	7.66E-06	PTK7	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2 - [PTK7_HUMAN]
Q53FA7	1.2259	0.2939	8.94E-06	QORX	Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2 - [QORX_HUMAN]
P04792	1.2906	0.3680	9.14E-06	HSPB1	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]
Q8NCN5	2.2584	1.1753	9.29E-06	PDPR	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2 - [PDPR_HUMAN]
O95999	0.7718	-0.3737	9.45E-06	BCL10	B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1 - [BCL10_HUMAN]
P21399	1.3716	0.4558	9.56E-06	ACOC	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]
Q9UGM5	2.0233	1.0167	1.02E-05	FETUB	Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2 - [FETUB_HUMAN]
P01591	3.4344	1.7801	1.05E-05	IGJ	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4 - [IGJ_HUMAN]
Q96BZ9	1.7841	0.8352	1.05E-05	TBC20	TBC1 domain family member 20 OS=Homo sapiens GN=TBC1D20 PE=1 SV=1 - [TBC20_HUMAN]
P02649	4.6000	2.2016	1.08E-05	APOE	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]
Q9UI42	0.5842	-0.7755	1.08E-05	CBPA4	Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=1 SV=2 - [CBPA4_HUMAN]
P29401	1.1810	0.2400	1.08E-05	TKT	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN]
P20337	1.2429	0.3137	1.08E-05	RAB3B	Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2 - [RAB3B_HUMAN]

P02647	38.7522	5.2762	1.10E-05	APOA1	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 - [APOA1_HUMAN]
O94925	1.4083	0.4940	1.14E-05	GLSK	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 - [GLSK_HUMAN]
P01625	8.5705	3.0994	1.16E-05	KV402	Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2 - [KV402_HUMAN]
Q13620	0.8216	-0.2834	1.22E-05	CUL4B	Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4 - [CUL4B_HUMAN]
Q9H3K2	1.3528	0.4359	1.22E-05	GHITM	Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2 - [GHITM_HUMAN]
P80748	63.9019	5.9978	1.23E-05	LV302	Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1 - [LV302_HUMAN]
P10909	2.9266	1.5492	1.23E-05	CLUS	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 - [CLUS_HUMAN]
Q8N568	1.4794	0.5650	1.24E-05	DCLK2	Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 PE=2 SV=4 - [DCLK2_HUMAN]
P02790	21.8555	4.4499	1.25E-05	HEMO	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]
Q16706	0.7132	-0.4876	1.25E-05	MA2A1	Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 - [MA2A1_HUMAN]
Q9UBB4	0.7681	-0.3807	1.25E-05	ATX10	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 - [ATX10_HUMAN]
P50454	1.1711	0.2279	1.25E-05	SERPH	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]
Q9NZN4	0.7275	-0.4589	1.25E-05	EHD2	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2 - [EHD2_HUMAN]
P47985	1.1496	0.2011	1.25E-05	UCRI	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2 - [UCRI_HUMAN]
P04035	0.3540	-1.4983	1.25E-05	HMDH	3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Homo sapiens GN=HMGCR PE=1 SV=1 - [HMDH_HUMAN]
P17936	2.0903	1.0637	1.28E-05	IBP3	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2 - [IBP3_HUMAN]
P06280	1.2545	0.3271	1.30E-05	AGAL	Alpha-galactosidase A OS=Homo sapiens GN=GLA PE=1 SV=1 - [AGAL_HUMAN]
P36776	1.1743	0.2317	1.34E-05	LONM	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]
P83881	0.8317	-0.2659	1.34E-05	RL36A	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2 - [RL36A_HUMAN]

O14495	2.6670	1.4152	1.38E-05	LPP3	Lipid phosphate phosphohydrolase 3 OS=Homo sapiens GN=PPAP2B PE=1 SV=1 - [LPP3_HUMAN]
Q5TCZ1	1.2490	0.3208	1.38E-05	SPD2A	SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1 - [SPD2A_HUMAN]
P30837	1.2653	0.3395	1.38E-05	AL1B1	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]
P36969	2.6278	1.3939	1.40E-05	GPX4	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3 - [GPX4_HUMAN]
P35221	1.1693	0.2257	1.50E-05	CTNA1	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]
P16989	0.8178	-0.2902	1.51E-05	YBOX3	Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4 - [YBOX3_HUMAN]
P17812	1.3060	0.3851	1.51E-05	PYRG1	CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN]
P02760	10.7832	3.4307	1.51E-05	AMBP	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1 - [AMBP_HUMAN]
Q92974	0.8018	-0.3187	1.53E-05	ARHG2	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4 - [ARHG2_HUMAN]
P46060	0.8002	-0.3216	1.56E-05	RAGP1	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]
Q15392	1.3659	0.4498	1.56E-05	DHC24	Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 - [DHC24_HUMAN]
O15254	1.3133	0.3932	1.60E-05	ACOX3	Peroxisomal acyl-coenzyme A oxidase 3 OS=Homo sapiens GN=ACOX3 PE=1 SV=2 - [ACOX3_HUMAN]
P01617	6.4992	2.7003	1.64E-05	KV204	Ig kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1 - [KV204_HUMAN]
O96000	1.1733	0.2306	1.66E-05	NDUBA	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3 - [NDUBA_HUMAN]
Q9UL41	0.5690	-0.8135	1.73E-05	PNMA3	Paraneoplastic antigen Ma3 OS=Homo sapiens GN=PNMA3 PE=2 SV=2 - [PNMA3_HUMAN]
O94851	0.7941	-0.3326	1.73E-05	MICA2	Protein-methionine sulfoxide oxidase MICAL2 OS=Homo sapiens GN=MICAL2 PE=1 SV=1 - [MICA2_HUMAN]
P0C0L5	8.3044	3.0539	1.74E-05	CO4B	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2 - [CO4B_HUMAN]
Q9BV36	0.4762	-1.0705	1.74E-05	MELPH	Melanophilin OS=Homo sapiens GN=MLPH PE=1 SV=1 - [MELPH_HUMAN]

P00738	4.1512	2.0535	1.80E-05	HPT	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1 - [HPT_HUMAN]
O95163	0.8034	-0.3159	1.80E-05	ELP1	Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3 - [ELP1_HUMAN]
Q76M96	1.5819	0.6617	1.80E-05	CCD80	Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1 - [CCD80_HUMAN]
P55058	1.7552	0.8117	1.84E-05	PLTP	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1 - [PLTP_HUMAN]
P42330	1.7337	0.7939	1.86E-05	AK1C3	Aldo-keto reductase family 1 member C3 OS=Homo sapiens GN=AKR1C3 PE=1 SV=4 - [AK1C3_HUMAN]
P01766	28.2087	4.8181	1.87E-05	HV305	Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1 - [HV305_HUMAN]
Q6IQ49	0.7161	-0.4818	1.89E-05	SDE2	Protein SDE2 homolog OS=Homo sapiens GN=SDE2 PE=1 SV=1 - [SDE2_HUMAN]
P01859	20.5097	4.3582	1.89E-05	IGHG2	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]
P01834	49.4669	5.6284	1.91E-05	IGKC	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 - [IGKC_HUMAN]
P01024	8.8622	3.1477	1.93E-05	CO3	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HUMAN]
P01876	58.2074	5.8631	1.95E-05	IGHA1	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2 - [IGHA1_HUMAN]
P0CG05	55.1186	5.7845	2.00E-05	LAC2	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1 - [LAC2_HUMAN]
P04114	23.4051	4.5488	2.00E-05	APOB	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2 - [APOB_HUMAN]
O43854	1.3117	0.3915	2.01E-05	EDIL3	EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1 - [EDIL3_HUMAN]
P15121	1.3110	0.3906	2.08E-05	ALDR	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 - [ALDR_HUMAN]
Q13884	0.8505	-0.2337	2.18E-05	SNTB1	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3 - [SNTB1_HUMAN]
P02787	3.2018	1.6789	2.22E-05	TRFE	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]
Q9BYN0	1.4997	0.5847	2.24E-05	SRXN1	Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2 - [SRXN1_HUMAN]
P42765	1.2330	0.3022	2.28E-05	THIM	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]
P07339	1.1945	0.2564	2.29E-05	CATD	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 - [CATD_HUMAN]

Q8N5W9	2.0546	1.0389	2.30E-05	F101B	Protein FAM101B OS=Homo sapiens GN=FAM101B PE=1 SV=1 - [F101B_HUMAN]
O95983	0.8337	-0.2624	2.36E-05	MBD3	Methyl-CpG-binding domain protein 3 OS=Homo sapiens GN=MBD3 PE=1 SV=1 - [MBD3_HUMAN]
P33992	0.6815	-0.5533	2.45E-05	MCM5	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN]
Q5JRX3	1.1491	0.2005	2.48E-05	PREP	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3 - [PREP_HUMAN]
Q9BWD1	0.7763	-0.3654	2.48E-05	THIC	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]
O14791	17.1240	4.0979	2.67E-05	APOL1	Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5 - [APOL1_HUMAN]
P04278	13.3612	3.7400	2.68E-05	SHBG	Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=1 SV=2 - [SHBG_HUMAN]
P05155	14.4334	3.8513	2.70E-05	IC1	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2 - [IC1_HUMAN]
P0C0L4	7.6905	2.9431	2.72E-05	CO4A	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2 - [CO4A_HUMAN]
P47914	0.7141	-0.4859	2.81E-05	RL29	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]
P00966	1.2734	0.3487	2.81E-05	ASSY	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]
P07602	1.1994	0.2624	2.81E-05	SAP	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]
O43491	0.8347	-0.2607	2.84E-05	E41L2	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 - [E41L2_HUMAN]
P52895	1.8118	0.8575	2.84E-05	AK1C2	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]
P17301	1.2175	0.2839	3.10E-05	ITA2	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 - [ITA2_HUMAN]
Q86TX2	1.1871	0.2475	3.24E-05	ACOT1	Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1 - [ACOT1_HUMAN]
Q08357	0.7320	-0.4502	3.24E-05	S20A2	Sodium-dependent phosphate transporter 2 OS=Homo sapiens GN=SLC20A2 PE=1 SV=1 - [S20A2_HUMAN]
P48507	1.2878	0.3650	3.24E-05	GSH0	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 - [GSH0_HUMAN]

Q07817	0.7231	-0.4678	3.29E-05	B2CL1	Bcl-2-like protein 1 OS=Homo sapiens GN=BCL2L1 PE=1 SV=1 - [B2CL1_HUMAN]
Q8IWU6	0.7998	-0.3224	3.30E-05	SULF1	Extracellular sulfatase Sulf-1 OS=Homo sapiens GN=SULF1 PE=1 SV=1 - [SULF1_HUMAN]
P12111	0.7228	-0.4683	3.39E-05	CO6A3	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5 - [CO6A3_HUMAN]
Q9NUQ6	0.8267	-0.2746	3.39E-05	SPS2L	SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 - [SPS2L_HUMAN]
Q15327	0.4854	-1.0427	3.39E-05	ANKR1	Ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=ANKRD1 PE=1 SV=2 - [ANKR1_HUMAN]
Q9HAV4	0.8095	-0.3049	3.44E-05	XPO5	Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 - [XPO5_HUMAN]
Q9UG63	0.8462	-0.2409	3.44E-05	ABCF2	ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 - [ABCF2_HUMAN]
P05106	1.3463	0.4291	3.48E-05	ITB3	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2 - [ITB3_HUMAN]
Q14690	0.8276	-0.2730	3.50E-05	RRP5	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN]
P13073	1.1545	0.2073	3.53E-05	COX41	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]
Q3KQU3	0.8321	-0.2652	3.55E-05	MA7D1	MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1 - [MA7D1_HUMAN]
P12235	1.2377	0.3076	3.61E-05	ADT1	ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 - [ADT1_HUMAN]
Q9BZF9	0.7826	-0.3536	3.61E-05	UACA	Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=1 SV=2 - [UACA_HUMAN]
P17844	0.8317	-0.2659	3.62E-05	DDX5	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]
Q9Y6Q2	1.5825	0.6622	3.67E-05	STON1	Stonin-1 OS=Homo sapiens GN=STON1 PE=1 SV=2 - [STON1_HUMAN]
Q70E73	0.7855	-0.3483	3.70E-05	RAPH1	Ras-associated and pleckstrin homology domains-containing protein 1 OS=Homo sapiens GN=RAPH1 PE=1 SV=3 - [RAPH1_HUMAN]
Q2NL82	0.8386	-0.2539	3.70E-05	TSR1	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 - [TSR1_HUMAN]
P19022	1.3053	0.3843	3.72E-05	CADH2	Cadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4 - [CADH2_HUMAN]

Q16134	1.1569	0.2102	3.73E-05	ETFD	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]
Q9NVU7	0.8140	-0.2968	3.73E-05	SDA1	Protein SDA1 homolog OS=Homo sapiens GN=SDAD1 PE=1 SV=3 - [SDA1_HUMAN]
Q86V21	0.8143	-0.2963	3.73E-05	AACS	Acetoacetyl-CoA synthetase OS=Homo sapiens GN=AACS PE=1 SV=1 - [AACS_HUMAN]
Q02388	1.5683	0.6492	3.81E-05	CO7A1	Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2 - [CO7A1_HUMAN]
Q6EMK4	1.6275	0.7026	3.82E-05	VASN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1 - [VASN_HUMAN]
O95980	1.3310	0.4125	3.98E-05	RECK	Reversion-inducing cysteine-rich protein with Kazal motifs OS=Homo sapiens GN=RECK PE=1 SV=1 - [RECK_HUMAN]
P10619	1.1818	0.2410	4.07E-05	PPGB	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]
Q9H857	1.2493	0.3212	4.21E-05	NT5D2	5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=1 SV=1 - [NT5D2_HUMAN]
Q52LW3	0.7895	-0.3411	4.26E-05	RHG29	Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=1 SV=2 - [RHG29_HUMAN]
P00390	1.2038	0.2676	4.28E-05	GSHR	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]
Q9BWS9	1.1863	0.2464	4.33E-05	CHID1	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1 - [CHID1_HUMAN]
P28065	0.8432	-0.2460	4.49E-05	PSB9	Proteasome subunit beta type-9 OS=Homo sapiens GN=PSMB9 PE=1 SV=2 - [PSB9_HUMAN]
P07093	1.3555	0.4388	4.49E-05	GDN	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1 - [GDN_HUMAN]
Q9UHG3	1.1509	0.2027	4.49E-05	PCYOX	Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=1 SV=3 - [PCYOX_HUMAN]
P60891	1.3180	0.3984	4.49E-05	PRPS1	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]
Q96PD2	0.6643	-0.5901	4.53E-05	DCBD2	Discoidin, CUB and LCCL domain-containing protein 2 OS=Homo sapiens GN=DCBLD2 PE=1 SV=1 - [DCBD2_HUMAN]
Q9P265	1.1616	0.2161	4.61E-05	DIP2B	Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3 - [DIP2B_HUMAN]
P09601	1.8412	0.8806	4.70E-05	HMOX1	Heme oxygenase 1 OS=Homo sapiens GN=HMOX1 PE=1 SV=1 - [HMOX1_HUMAN]

P05091	1.2488	0.3206	4.70E-05	ALDH2	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2 - [ALDH2_HUMAN]
Q96CM8	1.2167	0.2830	4.74E-05	ACSF2	Acyl-CoA synthetase family member 2, mitochondrial OS=Homo sapiens GN=ACSF2 PE=1 SV=2 - [ACSF2_HUMAN]
P37837	1.1940	0.2558	4.82E-05	TALDO	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]
Q96SB4	0.7642	-0.3879	4.82E-05	SRPK1	SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2 - [SRPK1_HUMAN]
P48163	1.2341	0.3034	4.95E-05	MAOX	NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1 - [MAOX_HUMAN]
Q9Y6C2	1.2533	0.3257	5.14E-05	EMIL1	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2 - [EMIL1_HUMAN]
P15144	1.2899	0.3673	5.15E-05	AMPN	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]
Q14118	1.1822	0.2415	5.34E-05	DAG1	Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2 - [DAG1_HUMAN]
P08729	1.2086	0.2733	5.42E-05	K2C7	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]
Q9NR19	0.7878	-0.3440	5.46E-05	ACSA	Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2 PE=1 SV=1 - [ACSA_HUMAN]
P01871	5.6268	2.4923	5.56E-05	IGHM	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]
Q96IG2	1.2162	0.2824	5.58E-05	FXL20	F-box/LRR-repeat protein 20 OS=Homo sapiens GN=FBXL20 PE=1 SV=2 - [FXL20_HUMAN]
Q9Y5Q0	1.2184	0.2850	5.70E-05	FADS3	Fatty acid desaturase 3 OS=Homo sapiens GN=FADS3 PE=2 SV=1 - [FADS3_HUMAN]
Q99650	1.3529	0.4360	5.74E-05	OSMR	Oncostatin-M-specific receptor subunit beta OS=Homo sapiens GN=OSMR PE=1 SV=1 - [OSMR_HUMAN]
Q96J92	0.7124	-0.4891	5.74E-05	WNK4	Serine/threonine-protein kinase WNK4 OS=Homo sapiens GN=WNK4 PE=1 SV=1 - [WNK4_HUMAN]
Q9Y394	1.1600	0.2141	5.74E-05	DHRS7	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1 - [DHRS7_HUMAN]
Q9NR30	0.6855	-0.5448	5.75E-05	DDX21	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]
Q8TC76	1.7179	0.7806	5.75E-05	F110B	Protein FAM110B OS=Homo sapiens GN=FAM110B PE=1 SV=1 - [F110B_HUMAN]
P15559	1.3118	0.3915	5.88E-05	NQO1	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]

O75027	1.1797	0.2385	5.88E-05	ABCB7	ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens GN=ABCB7 PE=1 SV=2 - [ABCB7_HUMAN]
Q8N5K1	0.7531	-0.4091	6.01E-05	CISD2	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 - [CISD2_HUMAN]
Q9UH99	1.1566	0.2099	6.21E-05	SUN2	SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3 - [SUN2_HUMAN]
O15231	1.1716	0.2285	6.27E-05	ZN185	Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3 - [ZN185_HUMAN]
Q13907	0.7412	-0.4320	6.45E-05	IDI1	Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens GN=IDI1 PE=1 SV=2 - [IDI1_HUMAN]
P04211	4.4398	2.1505	6.45E-05	LV001	Ig lambda chain V region 4A OS=Homo sapiens PE=4 SV=1 - [LV001_HUMAN]
Q6DKJ4	0.8278	-0.2727	6.50E-05	NXN	Nucleoredoxin OS=Homo sapiens GN=NXN PE=1 SV=2 - [NXN_HUMAN]
P61927	0.7420	-0.4306	6.50E-05	RL37	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]
P01042	24.9053	4.6384	6.75E-05	KNG1	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 - [KNG1_HUMAN]
P01857	9.3843	3.2302	6.75E-05	IGHG1	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 - [IGHG1_HUMAN]
P11310	1.1759	0.2338	6.89E-05	ACADM	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]
Q14914	1.2934	0.3712	7.05E-05	PTGR1	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]
O43665	0.8465	-0.2404	7.25E-05	RGS10	Regulator of G-protein signaling 10 OS=Homo sapiens GN=RGS10 PE=1 SV=2 - [RGS10_HUMAN]
Q7LBR1	1.2685	0.3432	7.25E-05	CHM1B	Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1 - [CHM1B_HUMAN]
Q12929	0.8447	-0.2436	7.25E-05	EPS8	Epidermal growth factor receptor kinase substrate 8 OS=Homo sapiens GN=EPS8 PE=1 SV=1 - [EPS8_HUMAN]
Q96HH9	1.2280	0.2963	7.25E-05	GRAM3	GRAM domain-containing protein 3 OS=Homo sapiens GN=GRAMD3 PE=1 SV=1 - [GRAM3_HUMAN]
Q9NPR9	1.3081	0.3874	7.38E-05	GP108	Protein GPR108 OS=Homo sapiens GN=GPR108 PE=2 SV=3 - [GP108_HUMAN]
Q96PD5	11.5942	3.5353	7.39E-05	PGRP2	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1 - [PGRP2_HUMAN]

O95864	0.7632	-0.3900	7.62E-05	FADS2	Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=1 SV=1 - [FADS2_HUMAN]
Q9BPW8	1.1739	0.2313	7.65E-05	NIPS1	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]
Q5T4B2	1.3592	0.4427	7.79E-05	GT253	Probable inactive glycosyltransferase 25 family member 3 OS=Homo sapiens GN=CERCAM PE=2 SV=1 - [GT253_HUMAN]
P61812	0.8164	-0.2927	7.83E-05	TGFB2	Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2 PE=1 SV=1 - [TGFB2_HUMAN]
O00468	1.1760	0.2339	7.93E-05	AGRIN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5 - [AGRIN_HUMAN]
O60218	1.6985	0.7642	8.08E-05	AK1BA	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]
P02511	1.2262	0.2942	8.34E-05	CRYAB	Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2 - [CRYAB_HUMAN]
Q5T9L3	0.7723	-0.3728	8.87E-05	WLS	Protein wntless homolog OS=Homo sapiens GN=WLS PE=1 SV=2 - [WLS_HUMAN]
O14530	0.8021	-0.3182	8.90E-05	TXND9	Thioredoxin domain-containing protein 9 OS=Homo sapiens GN=TXNDC9 PE=1 SV=2 - [TXND9_HUMAN]
P14324	0.8453	-0.2424	8.99E-05	FPPS	Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4 - [FPPS_HUMAN]
P16112	0.7318	-0.4504	9.10E-05	PGCA	Aggrecan core protein OS=Homo sapiens GN=ACAN PE=1 SV=2 - [PGCA_HUMAN]
Q15113	1.4027	0.4882	9.31E-05	PCOC1	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2 - [PCOC1_HUMAN]
Q7Z3E5	1.1819	0.2411	9.36E-05	ARMC9	LisH domain-containing protein ARMC9 OS=Homo sapiens GN=ARMC9 PE=1 SV=2 - [ARMC9_HUMAN]
Q10713	1.1624	0.2170	9.36E-05	MPPA	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2 - [MPPA_HUMAN]
Q9NVT9	1.1797	0.2385	9.36E-05	ARMC1	Armadillo repeat-containing protein 1 OS=Homo sapiens GN=ARMC1 PE=1 SV=1 - [ARMC1_HUMAN]
P57077	0.7121	-0.4899	9.54E-05	M3KCL	MAP3K7 C-terminal-like protein OS=Homo sapiens GN=MAP3K7CL PE=1 SV=1 - [M3KCL_HUMAN]
Q53EP0	0.8397	-0.2521	9.54E-05	FND3B	Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B PE=1 SV=2 - [FND3B_HUMAN]
Q6P1J9	0.8364	-0.2577	9.56E-05	CDC73	Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1 - [CDC73_HUMAN]

P01023	1.8991	0.9253	9.56E-05	A2MG	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3 - [A2MG_HUMAN]
P23743	1.1581	0.2118	9.58E-05	DGKA	Diacylglycerol kinase alpha OS=Homo sapiens GN=DGKA PE=1 SV=3 - [DGKA_HUMAN]
Q16222	0.8356	-0.2592	9.89E-05	UAP1	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3 - [UAP1_HUMAN]
Q14566	0.7630	-0.3903	9.89E-05	MCM6	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]
Q9UBG0	1.1539	0.2065	9.94E-05	MRC2	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2 - [MRC2_HUMAN]
O15533	0.8355	-0.2593	9.99E-05	TPSN	Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 - [TPSN_HUMAN]
P62341	1.5811	0.6609	9.99E-05	SELT	Selenoprotein T OS=Homo sapiens GN=SELT PE=2 SV=2 - [SELT_HUMAN]
P50443	1.4180	0.5038	1.01E-04	S26A2	Sulfate transporter OS=Homo sapiens GN=SLC26A2 PE=1 SV=2 - [S26A2_HUMAN]
P07738	1.1976	0.2601	1.01E-04	PMGE	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2 - [PMGE_HUMAN]
Q6DKI1	0.8173	-0.2911	1.02E-04	RL7L	60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 - [RL7L_HUMAN]
Q15434	0.8098	-0.3043	1.04E-04	RBMS2	RNA-binding motif, single-stranded-interacting protein 2 OS=Homo sapiens GN=RBMS2 PE=1 SV=1 - [RBMS2_HUMAN]
Q14123	0.8399	-0.2517	1.06E-04	PDE1C	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C OS=Homo sapiens GN=PDE1C PE=1 SV=1 - [PDE1C_HUMAN]
Q8NB16	0.8214	-0.2839	1.07E-04	MLKL	Mixed lineage kinase domain-like protein OS=Homo sapiens GN=MLKL PE=1 SV=1 - [MLKL_HUMAN]
P40261	1.2875	0.3646	1.08E-04	NNMT	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]
Q06830	1.1769	0.2349	1.15E-04	PRDX1	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]
O76021	0.8094	-0.3050	1.17E-04	RL1D1	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3 - [RL1D1_HUMAN]
P80303	1.1523	0.2046	1.19E-04	NUCB2	Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2 - [NUCB2_HUMAN]
Q7Z3B1	1.1570	0.2104	1.19E-04	NEGR1	Neuronal growth regulator 1 OS=Homo sapiens GN=NEGR1 PE=1 SV=3 - [NEGR1_HUMAN]
O75112	1.4843	0.5698	1.19E-04	LDB3	LIM domain-binding protein 3 OS=Homo sapiens GN=LDB3 PE=1 SV=2 - [LDB3_HUMAN]

Q9BZM5	1.2807	0.3569	1.19E-04	N2DL2	NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1 - [N2DL2_HUMAN]
Q92871	0.7521	-0.4110	1.22E-04	PMM1	Phosphomannomutase 1 OS=Homo sapiens GN=PMM1 PE=1 SV=2 - [PMM1_HUMAN]
P0CG04	3.0748	1.6205	1.23E-04	LAC1	Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1 - [LAC1_HUMAN]
P17275	0.6258	-0.6762	1.25E-04	JUNB	Transcription factor jun-B OS=Homo sapiens GN=JUNB PE=1 SV=1 - [JUNB_HUMAN]
Q5M775	1.2434	0.3143	1.29E-04	CYTSB	Cytospin-B OS=Homo sapiens GN=SPECC1 PE=1 SV=1 - [CYTSB_HUMAN]
P16401	0.7235	-0.4668	1.30E-04	H15	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]
Q8NI36	0.7518	-0.4116	1.31E-04	WDR36	WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 - [WDR36_HUMAN]
Q3KQV9	1.1844	0.2442	1.35E-04	UAP1L	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Homo sapiens GN=UAP1L1 PE=1 SV=2 - [UAP1L_HUMAN]
Q9NUJ1	1.2453	0.3165	1.35E-04	ABHDA	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1 - [ABHDA_HUMAN]
O14981	0.8447	-0.2435	1.37E-04	BTAF1	TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2 - [BTAF1_HUMAN]
Q68CQ7	1.1775	0.2357	1.43E-04	GL8D1	Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2 - [GL8D1_HUMAN]
Q14534	0.7931	-0.3345	1.45E-04	ERG1	Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=1 SV=3 - [ERG1_HUMAN]
P35520	0.7860	-0.3473	1.45E-04	CBS	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]
Q92503	0.6513	-0.6185	1.49E-04	S14L1	SEC14-like protein 1 OS=Homo sapiens GN=SEC14L1 PE=1 SV=2 - [S14L1_HUMAN]
P04179	1.1685	0.2247	1.53E-04	SODM	Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]
Q16832	1.2573	0.3303	1.53E-04	DDR2	Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2 - [DDR2_HUMAN]
Q9BQE5	0.8440	-0.2447	1.55E-04	APOL2	Apolipoprotein L2 OS=Homo sapiens GN=APOL2 PE=1 SV=1 - [APOL2_HUMAN]
Q9H773	0.8325	-0.2645	1.56E-04	DCTP1	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1 - [DCTP1_HUMAN]

Q9NZJ7	1.2076	0.2721	1.57E-04	MTCH1	Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1 - [MTCH1_HUMAN]
Q15269	0.8188	-0.2884	1.60E-04	PWP2	Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2 - [PWP2_HUMAN]
Q8IX30	0.7786	-0.3611	1.62E-04	SCUB3	Signal peptide, CUB and EGF-like domain-containing protein 3 OS=Homo sapiens GN=SCUBE3 PE=1 SV=1 - [SCUB3_HUMAN]
Q96RU3	0.8021	-0.3181	1.65E-04	FNBP1	Formin-binding protein 1 OS=Homo sapiens GN=FNBP1 PE=1 SV=2 - [FNBP1_HUMAN]
Q6NUM9	1.2168	0.2831	1.72E-04	RETST	All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=1 SV=2 - [RETST_HUMAN]
O95084	0.8278	-0.2726	1.73E-04	PRS23	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1 - [PRS23_HUMAN]
Q9Y2R0	1.1885	0.2491	1.73E-04	COA3	Cytochrome c oxidase assembly protein 3 homolog, mitochondrial OS=Homo sapiens GN=COA3 PE=1 SV=1 - [COA3_HUMAN]
Q14978	0.7979	-0.3258	1.74E-04	NOLC1	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HUMAN]
Q5BJF2	0.6181	-0.6941	1.75E-04	TMM97	Transmembrane protein 97 OS=Homo sapiens GN=TMEM97 PE=1 SV=1 - [TMM97_HUMAN]
Q9UBM7	0.8488	-0.2365	1.81E-04	DHCR7	7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1 - [DHCR7_HUMAN]
Q9HD26	1.1663	0.2219	1.81E-04	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein OS=Homo sapiens GN=GOPC PE=1 SV=1 - [GOPC_HUMAN]
Q13938	1.3429	0.4254	1.81E-04	CAYP1	Calcyphosin OS=Homo sapiens GN=CAPS PE=1 SV=1 - [CAYP1_HUMAN]
P08519	2.9234	1.5476	1.84E-04	APOA	Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1 - [APOA_HUMAN]
Q9Y6H1	1.1507	0.2025	1.86E-04	CHCH2	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1 - [CHCH2_HUMAN]
P04181	1.1608	0.2152	1.90E-04	OAT	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 - [OAT_HUMAN]
Q96QV1	0.7726	-0.3722	1.94E-04	HHIP	Hedgehog-interacting protein OS=Homo sapiens GN=HHIP PE=1 SV=3 - [HHIP_HUMAN]
P08493	0.6307	-0.6649	1.96E-04	MGP	Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2 - [MGP_HUMAN]
P35240	0.8382	-0.2546	1.97E-04	MERL	Merlin OS=Homo sapiens GN=NF2 PE=1 SV=1 - [MERL_HUMAN]

P62910	0.7873	-0.3450	1.98E-04	RL32	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]
P35568	1.5925	0.6713	2.03E-04	IRS1	Insulin receptor substrate 1 OS=Homo sapiens GN=IRS1 PE=1 SV=1 - [IRS1_HUMAN]
O75153	0.8300	-0.2689	2.03E-04	CLU	Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2 - [CLU_HUMAN]
P02765	4.1146	2.0407	2.05E-04	FETUA	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]
P23142	1.3153	0.3954	2.09E-04	FBLN1	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]
P01623	9.8898	3.3059	2.12E-04	KV305	Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1 - [KV305_HUMAN]
Q15262	1.2873	0.3644	2.12E-04	PTPRK	Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapiens GN=PTPRK PE=1 SV=2 - [PTPRK_HUMAN]
P07942	0.8486	-0.2368	2.12E-04	LAMB1	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2 - [LAMB1_HUMAN]
P00568	1.1690	0.2253	2.13E-04	KAD1	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]
P26022	0.7176	-0.4787	2.13E-04	PTX3	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3 - [PTX3_HUMAN]
Q16540	1.2793	0.3554	2.13E-04	RM23	39S ribosomal protein L23, mitochondrial OS=Homo sapiens GN=MRPL23 PE=1 SV=1 - [RM23_HUMAN]
O95801	0.7812	-0.3563	2.17E-04	TTC4	Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 - [TTC4_HUMAN]
Q15147	1.4646	0.5505	2.22E-04	PLCB4	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4 OS=Homo sapiens GN=PLCB4 PE=1 SV=3 - [PLCB4_HUMAN]
O00767	0.7643	-0.3878	2.26E-04	ACOD	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 - [ACOD_HUMAN]
Q8IVM0	0.8187	-0.2887	2.26E-04	CCD50	Coiled-coil domain-containing protein 50 OS=Homo sapiens GN=CCDC50 PE=1 SV=1 - [CCD50_HUMAN]
Q16527	1.1521	0.2043	2.26E-04	CSRP2	Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=1 SV=3 - [CSRP2_HUMAN]
Q9BUE6	1.3325	0.4142	2.32E-04	ISCA1	Iron-sulfur cluster assembly 1 homolog, mitochondrial OS=Homo sapiens GN=ISCA1 PE=2 SV=1 - [ISCA1_HUMAN]
Q96NE9	0.8059	-0.3114	2.36E-04	FRMD6	FERM domain-containing protein 6 OS=Homo sapiens GN=FRMD6 PE=1 SV=1 - [FRMD6_HUMAN]
P50148	1.1638	0.2188	2.49E-04	GNAQ	Guanine nucleotide-binding protein G(q) subunit alpha

					OS=Homo sapiens GN=GNAQ PE=1 SV=4 - [GNAQ_HUMAN]
P11233	1.1718	0.2288	2.59E-04	RALA	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1 - [RALA_HUMAN]
P52943	1.1654	0.2209	2.59E-04	CRIP2	Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1 - [CRIP2_HUMAN]
Q8NE86	1.1835	0.2431	2.64E-04	MCU	Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU PE=1 SV=1 - [MCU_HUMAN]
P54652	0.7676	-0.3816	2.76E-04	HSP72	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
P53602	0.8166	-0.2923	2.78E-04	MVD1	Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1 SV=1 - [MVD1_HUMAN]
Q9BZE4	0.8265	-0.2750	2.84E-04	NOG1	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]
Q08209	1.1750	0.2326	2.95E-04	PP2BA	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA PE=1 SV=1 - [PP2BA_HUMAN]
Q969X6	0.8135	-0.2978	2.95E-04	CIR1A	Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1 - [CIR1A_HUMAN]
Q16762	1.2377	0.3076	3.00E-04	THTR	Thiosulfate sulfurtransferase OS=Homo sapiens GN=TST PE=1 SV=4 - [THTR_HUMAN]
P04062	1.2005	0.2636	3.02E-04	GLCM	Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3 - [GLCM_HUMAN]
O15075	0.7831	-0.3527	3.03E-04	DCLK1	Serine/threonine-protein kinase DCLK1 OS=Homo sapiens GN=DCLK1 PE=1 SV=2 - [DCLK1_HUMAN]
Q9BTD8	1.4728	0.5586	3.07E-04	RBM42	RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1 - [RBM42_HUMAN]
Q9HB63	1.3667	0.4507	3.13E-04	NET4	Netrin-4 OS=Homo sapiens GN=NTN4 PE=2 SV=2 - [NET4_HUMAN]
O00625	1.2458	0.3171	3.13E-04	PIR	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1 - [PIR_HUMAN]
Q00537	0.8103	-0.3035	3.18E-04	CDK17	Cyclin-dependent kinase 17 OS=Homo sapiens GN=CDK17 PE=1 SV=2 - [CDK17_HUMAN]
O14879	0.7390	-0.4364	3.25E-04	IFIT3	Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 - [IFIT3_HUMAN]
Q8IXK0	0.7541	-0.4072	3.27E-04	PHC2	Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 - [PHC2_HUMAN]
Q71RC2	0.8180	-0.2898	3.27E-04	LARP4	La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3 - [LARP4_HUMAN]

O14494	1.4608	0.5467	3.28E-04	LPP1	Lipid phosphate phosphohydrolase 1 OS=Homo sapiens GN=PPAP2A PE=1 SV=1 - [LPP1_HUMAN]
Q07352	1.3993	0.4847	3.29E-04	TISB	Zinc finger protein 36, C3H1 type-like 1 OS=Homo sapiens GN=ZFP36L1 PE=1 SV=1 - [TISB_HUMAN]
Q15397	0.8256	-0.2764	3.35E-04	K0020	Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3 - [K0020_HUMAN]
P49407	1.1583	0.2120	3.37E-04	ARRB1	Beta-arrestin-1 OS=Homo sapiens GN=ARRB1 PE=1 SV=2 - [ARRB1_HUMAN]
Q8TDB4	0.7054	-0.5035	3.39E-04	HUMMR	Protein MGARP OS=Homo sapiens GN=MGARP PE=1 SV=1 - [HUMMR_HUMAN]
P48506	1.2280	0.2963	3.49E-04	GSH1	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 - [GSH1_HUMAN]
Q04941	1.1745	0.2321	3.49E-04	PLP2	Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1 - [PLP2_HUMAN]
O75326	1.2157	0.2818	3.60E-04	SEM7A	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1 - [SEM7A_HUMAN]
P49736	0.6935	-0.5280	3.71E-04	MCM2	DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN]
Q9GZM8	0.7797	-0.3590	3.74E-04	NDEL1	Nuclear distribution protein nudE-like 1 OS=Homo sapiens GN=NDEL1 PE=1 SV=1 - [NDEL1_HUMAN]
P33993	0.7516	-0.4120	3.74E-04	MCM7	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]
Q9Y697	1.1637	0.2187	3.74E-04	NFS1	Cysteine desulfurase, mitochondrial OS=Homo sapiens GN=NFS1 PE=1 SV=3 - [NFS1_HUMAN]
A6NDU8	0.7188	-0.4764	4.00E-04	CE051	UPF0600 protein C5orf51 OS=Homo sapiens GN=C5orf51 PE=1 SV=1 - [CE051_HUMAN]
Q13228	1.1816	0.2408	4.07E-04	SBP1	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]
Q96QD8	1.3391	0.4213	4.34E-04	S38A2	Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2 - [S38A2_HUMAN]
Q6P158	0.8325	-0.2645	4.52E-04	DHX57	Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens GN=DHX57 PE=1 SV=2 - [DHX57_HUMAN]
P30825	0.7722	-0.3730	4.55E-04	CTR1	High affinity cationic amino acid transporter 1 OS=Homo sapiens GN=SLC7A1 PE=1 SV=1 - [CTR1_HUMAN]

Q9BZX2	0.7846	-0.3499	4.65E-04	UCK2	Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1 - [UCK2_HUMAN]
Q06203	0.8055	-0.3121	4.67E-04	PUR1	Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1 - [PUR1_HUMAN]
O43166	1.2104	0.2755	4.69E-04	SI1L1	Signal-induced proliferation-associated 1-like protein 1 OS=Homo sapiens GN=SIPA1L1 PE=1 SV=4 - [SI1L1_HUMAN]
Q9UIF9	1.1786	0.2370	4.69E-04	BAZ2A	Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=1 SV=4 - [BAZ2A_HUMAN]
Q9Y6R0	1.1741	0.2316	4.79E-04	NUMBL	Numb-like protein OS=Homo sapiens GN=NUMBL PE=1 SV=1 - [NUMBL_HUMAN]
Q7Z7M9	0.7461	-0.4226	4.88E-04	GALT5	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1 - [GALT5_HUMAN]
P24385	0.6148	-0.7018	4.88E-04	CCND1	G1/S-specific cyclin-D1 OS=Homo sapiens GN=CCND1 PE=1 SV=1 - [CCND1_HUMAN]
O95865	1.1578	0.2114	4.93E-04	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1 - [DDAH2_HUMAN]
P02792	0.5992	-0.7388	4.94E-04	FRIL	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]
Q13823	0.7364	-0.4414	4.99E-04	NOG2	Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 - [NOG2_HUMAN]
Q08397	0.7895	-0.3410	5.06E-04	LOXL1	Lysyl oxidase homolog 1 OS=Homo sapiens GN=LOXL1 PE=1 SV=2 - [LOXL1_HUMAN]
P42771	0.8083	-0.3070	5.28E-04	CD2A1	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3 OS=Homo sapiens GN=CDKN2A PE=1 SV=2 - [CD2A1_HUMAN]
O15066	0.8482	-0.2376	5.29E-04	KIF3B	Kinesin-like protein KIF3B OS=Homo sapiens GN=KIF3B PE=1 SV=1 - [KIF3B_HUMAN]
Q6ZNB6	1.1963	0.2585	5.33E-04	NFXL1	NF-X1-type zinc finger protein NFXL1 OS=Homo sapiens GN=NFXL1 PE=1 SV=2 - [NFXL1_HUMAN]
Q9HB40	1.2052	0.2692	5.38E-04	RISC	Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1 - [RISC_HUMAN]
P15924	0.8182	-0.2895	5.38E-04	DESP	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]
P02794	0.7023	-0.5097	5.41E-04	FRIH	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2 - [FRIH_HUMAN]
O75683	0.8285	-0.2715	5.53E-04	SURF6	Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3 - [SURF6_HUMAN]
Q96BA8	0.7162	-0.4816	5.55E-04	CR3L1	Cyclic AMP-responsive element-binding protein 3-like protein 1

					OS=Homo sapiens GN=CREB3L1 PE=1 SV=1 - [CR3L1_HUMAN]
Q9BQ61	0.8447	-0.2435	5.61E-04	CS043	Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1 - [CS043_HUMAN]
O95183	0.8383	-0.2544	5.63E-04	VAMP5	Vesicle-associated membrane protein 5 OS=Homo sapiens GN=VAMP5 PE=1 SV=1 - [VAMP5_HUMAN]
P17931	0.8426	-0.2471	5.64E-04	LEG3	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]
Q63HR2	1.1864	0.2466	5.70E-04	TENC1	Tensin-like C1 domain-containing phosphatase OS=Homo sapiens GN=TENC1 PE=1 SV=2 - [TENC1_HUMAN]
Q6PK04	0.8069	-0.3095	5.86E-04	CC137	Coiled-coil domain-containing protein 137 OS=Homo sapiens GN=CCDC137 PE=1 SV=1 - [CC137_HUMAN]
Q08431	1.1932	0.2549	5.87E-04	MFGM	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2 - [MFGM_HUMAN]
Q9GZR7	0.7840	-0.3510	5.88E-04	DDX24	ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1 - [DDX24_HUMAN]
Q13433	1.2156	0.2817	5.90E-04	S39A6	Zinc transporter ZIP6 OS=Homo sapiens GN=SLC39A6 PE=1 SV=3 - [S39A6_HUMAN]
Q16363	1.8468	0.8850	5.90E-04	LAMA4	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=4 - [LAMA4_HUMAN]
O75208	1.1875	0.2479	5.94E-04	COQ9	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens GN=COQ9 PE=1 SV=1 - [COQ9_HUMAN]
Q4J6C6	0.8384	-0.2543	6.28E-04	PPCEL	Prolyl endopeptidase-like OS=Homo sapiens GN=PREPL PE=1 SV=1 - [PPCEL_HUMAN]
O14949	1.1591	0.2130	6.38E-04	QCR8	Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRQ PE=1 SV=4 - [QCR8_HUMAN]
Q9H4G0	1.2091	0.2740	6.55E-04	E41L1	Band 4.1-like protein 1 OS=Homo sapiens GN=EPB41L1 PE=1 SV=2 - [E41L1_HUMAN]
O14556	0.8454	-0.2423	6.56E-04	G3PT	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 - [G3PT_HUMAN]
Q15061	0.8272	-0.2736	6.62E-04	WDR43	WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3 - [WDR43_HUMAN]
P02748	2.5803	1.3675	6.62E-04	CO9	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2 - [CO9_HUMAN]
Q92597	1.1490	0.2004	6.93E-04	NDRG1	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1 - [NDRG1_HUMAN]
Q6ICB0	0.7892	-0.3415	7.13E-04	DESI1	Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 - [DESI1_HUMAN]

P50213	1.1891	0.2499	7.20E-04	IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 - [IDH3A_HUMAN]
P11166	0.8262	-0.2754	7.27E-04	GTR1	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2 - [GTR1_HUMAN]
P34096	1.2400	0.3104	7.37E-04	RNAS4	Ribonuclease 4 OS=Homo sapiens GN=RNASE4 PE=1 SV=3 - [RNAS4_HUMAN]
Q16822	1.1640	0.2191	7.41E-04	PCKGM	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]
Q9P2E7	0.8017	-0.3188	7.41E-04	PCD10	Protocadherin-10 OS=Homo sapiens GN=PCDH10 PE=2 SV=2 - [PCD10_HUMAN]
Q9ULF5	1.2147	0.2806	7.45E-04	S39AA	Zinc transporter ZIP10 OS=Homo sapiens GN=SLC39A10 PE=1 SV=2 - [S39AA_HUMAN]
Q9Y580	0.8177	-0.2903	7.59E-04	RBM7	RNA-binding protein 7 OS=Homo sapiens GN=RBM7 PE=1 SV=1 - [RBM7_HUMAN]
E9PRG8	0.8471	-0.2393	7.65E-04	CK098	Uncharacterized protein C11orf98 OS=Homo sapiens GN=C11orf98 PE=4 SV=1 - [CK098_HUMAN]
P62891	0.8239	-0.2794	7.66E-04	RL39	60S ribosomal protein L39 OS=Homo sapiens GN=RPL39 PE=1 SV=2 - [RL39_HUMAN]
Q9Y3D2	1.1712	0.2280	7.75E-04	MSRB2	Methionine-R-sulfoxide reductase B2, mitochondrial OS=Homo sapiens GN=MSRB2 PE=2 SV=2 - [MSRB2_HUMAN]
P51884	1.1831	0.2426	7.86E-04	LUM	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]
Q14137	0.8393	-0.2527	7.94E-04	BOP1	Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2 - [BOP1_HUMAN]
P10599	1.2365	0.3063	8.23E-04	THIO	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]
Q5W0Z9	1.1881	0.2486	8.27E-04	ZDH20	Probable palmitoyltransferase ZDHHC20 OS=Homo sapiens GN=ZDHHC20 PE=1 SV=1 - [ZDH20_HUMAN]
Q9NY61	0.7440	-0.4266	8.27E-04	AATF	Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1 - [AATF_HUMAN]
O43426	1.3383	0.4204	8.37E-04	SYNJ1	Synaptojanin-1 OS=Homo sapiens GN=SYNJ1 PE=1 SV=2 - [SYNJ1_HUMAN]
Q15067	1.2098	0.2747	8.80E-04	ACOX1	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]
Q96JA1	0.5337	-0.9058	8.82E-04	LRIG1	Leucine-rich repeats and immunoglobulin-like domains protein 1 OS=Homo sapiens GN=LRIG1 PE=1 SV=2 - [LRIG1_HUMAN]

Q53F39	1.2898	0.3671	8.95E-04	MPPE1	Metallophosphoesterase 1 OS=Homo sapiens GN=MPPE1 PE=1 SV=2 - [MPPE1_HUMAN]
Q96BR5	1.2871	0.3641	9.04E-04	SELR1	Sel1 repeat-containing protein 1 OS=Homo sapiens GN=SELRC1 PE=1 SV=2 - [SELR1_HUMAN]
P84022	0.7218	-0.4703	9.14E-04	SMAD3	Mothers against decapentaplegic homolog 3 OS=Homo sapiens GN=SMAD3 PE=1 SV=1 - [SMAD3_HUMAN]
Q53HC0	0.8293	-0.2700	9.16E-04	CCD92	Coiled-coil domain-containing protein 92 OS=Homo sapiens GN=CCDC92 PE=1 SV=2 - [CCD92_HUMAN]
Q9H4G4	1.2278	0.2961	9.18E-04	GAPR1	Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3 - [GAPR1_HUMAN]
Q13642	0.7510	-0.4131	9.39E-04	FHL1	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4 - [FHL1_HUMAN]
Q9H1K1	1.2296	0.2982	9.43E-04	ISCU	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial OS=Homo sapiens GN=ISCU PE=1 SV=2 - [ISCU_HUMAN]
Q9BQI0	0.7501	-0.4147	9.48E-04	AIF1L	Allograft inflammatory factor 1-like OS=Homo sapiens GN=AIF1L PE=1 SV=1 - [AIF1L_HUMAN]
Q86U70	1.2254	0.2933	9.53E-04	LDB1	LIM domain-binding protein 1 OS=Homo sapiens GN=LDB1 PE=1 SV=2 - [LDB1_HUMAN]
Q9UDY8	1.2785	0.3545	9.62E-04	MALT1	Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens GN=MALT1 PE=1 SV=1 - [MALT1_HUMAN]
P00441	1.1489	0.2003	9.80E-04	SODC	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]
Q8TDR0	1.6741	0.7434	1.02E-03	MIPT3	TRAF3-interacting protein 1 OS=Homo sapiens GN=TRAF3IP1 PE=1 SV=1 - [MIPT3_HUMAN]
P46087	0.8459	-0.2414	1.02E-03	NOP2	Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2 - [NOP2_HUMAN]
Q9UBN6	0.7256	-0.4627	1.03E-03	TR10D	Tumor necrosis factor receptor superfamily member 10D OS=Homo sapiens GN=TNFRSF10D PE=1 SV=1 - [TR10D_HUMAN]
O14683	0.8432	-0.2460	1.03E-03	P5I11	Tumor protein p53-inducible protein 11 OS=Homo sapiens GN=TP53I11 PE=1 SV=2 - [P5I11_HUMAN]
Q14644	0.8178	-0.2901	1.04E-03	RASA3	Ras GTPase-activating protein 3 OS=Homo sapiens GN=RASA3 PE=1 SV=3 - [RASA3_HUMAN]
Q13510	1.1534	0.2059	1.04E-03	ASAH1	Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5 - [ASAH1_HUMAN]
Q9BV79	1.1838	0.2435	1.04E-03	MECR	Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2 - [MECR_HUMAN]

Q9UKD2	0.8075	-0.3084	1.05E-03	MRT4	mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2 - [MRT4_HUMAN]
O60507	1.2204	0.2874	1.06E-03	TPST1	Protein-tyrosine sulfotransferase 1 OS=Homo sapiens GN=TPST1 PE=2 SV=1 - [TPST1_HUMAN]
Q3MIP1	0.7324	-0.4493	1.07E-03	IPIL2	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 OS=Homo sapiens GN=ITPRIPL2 PE=1 SV=1 - [IPIL2_HUMAN]
Q8IXS6	0.8502	-0.2342	1.08E-03	PALM2	Paralemmin-2 OS=Homo sapiens GN=PALM2 PE=2 SV=3 - [PALM2_HUMAN]
P35052	1.3421	0.4245	1.09E-03	GPC1	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2 - [GPC1_HUMAN]
Q8WWI5	1.2037	0.2674	1.09E-03	CTL1	Choline transporter-like protein 1 OS=Homo sapiens GN=SLC44A1 PE=1 SV=1 - [CTL1_HUMAN]
Q86WK6	1.1589	0.2128	1.09E-03	AMGO1	Amphoterin-induced protein 1 OS=Homo sapiens GN=AMIGO1 PE=1 SV=1 - [AMGO1_HUMAN]
P55061	1.4184	0.5042	1.10E-03	BI1	Bax inhibitor 1 OS=Homo sapiens GN=TMBIM6 PE=1 SV=2 - [BI1_HUMAN]
Q9UHY7	0.8213	-0.2841	1.10E-03	ENOPH	Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1 - [ENOPH_HUMAN]
Q6KF10	0.7637	-0.3890	1.12E-03	GDF6	Growth/differentiation factor 6 OS=Homo sapiens GN=GDF6 PE=1 SV=1 - [GDF6_HUMAN]
P10915	2.5432	1.3466	1.12E-03	HPLN1	Hyaluronan and proteoglycan link protein 1 OS=Homo sapiens GN=HAPLN1 PE=2 SV=2 - [HPLN1_HUMAN]
Q9Y4C8	0.8497	-0.2350	1.13E-03	RBM19	Probable RNA-binding protein 19 OS=Homo sapiens GN=RBM19 PE=1 SV=3 - [RBM19_HUMAN]
Q9BVP2	0.7977	-0.3260	1.13E-03	GNL3	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3_HUMAN]
P24941	1.1637	0.2187	1.14E-03	CDK2	Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 - [CDK2_HUMAN]
Q15800	0.6306	-0.6652	1.16E-03	MSMO1	Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1 PE=1 SV=1 - [MSMO1_HUMAN]
Q13303	1.2851	0.3618	1.16E-03	KCAB2	Voltage-gated potassium channel subunit beta-2 OS=Homo sapiens GN=KCNAB2 PE=1 SV=2 - [KCAB2_HUMAN]
P78524	1.2193	0.2861	1.19E-03	ST5	Suppression of tumorigenicity 5 protein OS=Homo sapiens GN=ST5 PE=1 SV=3 - [ST5_HUMAN]
Q9H7S9	0.7192	-0.4755	1.22E-03	ZN703	Zinc finger protein 703 OS=Homo sapiens GN=ZNF703 PE=1 SV=1 - [ZN703_HUMAN]
P49916	1.1637	0.2187	1.24E-03	DNLI3	DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2 - [DNLI3_HUMAN]
Q9UDW1	1.1775	0.2357	1.24E-03	QCR9	Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3 - [QCR9_HUMAN]

Q6WKZ4	0.8099	-0.3041	1.24E-03	RFIP1	Rab11 family-interacting protein 1 OS=Homo sapiens GN=RAB11FIP1 PE=1 SV=3 - [RFIP1_HUMAN]
P29373	1.2625	0.3363	1.24E-03	RABP2	Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=CRABP2 PE=1 SV=2 - [RABP2_HUMAN]
P10253	1.1491	0.2006	1.25E-03	LYAG	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]
Q7Z7L8	1.4534	0.5394	1.25E-03	CK096	Uncharacterized protein C11orf96 OS=Homo sapiens GN=C11orf96 PE=1 SV=3 - [CK096_HUMAN]
P05412	0.7970	-0.3273	1.26E-03	JUN	Transcription factor AP-1 OS=Homo sapiens GN=JUN PE=1 SV=2 - [JUN_HUMAN]
Q6ULP2	0.8496	-0.2351	1.26E-03	AFTIN	Aftiphilin OS=Homo sapiens GN=AFTPH PE=1 SV=2 - [AFTIN_HUMAN]
Q6PD62	0.8326	-0.2644	1.30E-03	CTR9	RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens GN=CTR9 PE=1 SV=1 - [CTR9_HUMAN]
Q99523	0.8262	-0.2754	1.33E-03	SORT	Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3 - [SORT_HUMAN]
O75815	0.8456	-0.2420	1.33E-03	BCAR3	Breast cancer anti-estrogen resistance protein 3 OS=Homo sapiens GN=BCAR3 PE=1 SV=1 - [BCAR3_HUMAN]
Q29983	0.7877	-0.3443	1.33E-03	MICA	MHC class I polypeptide-related sequence A OS=Homo sapiens GN=MICA PE=1 SV=1 - [MICA_HUMAN]
O60437	1.5076	0.5923	1.35E-03	PEPL	Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4 - [PEPL_HUMAN]
Q3SXM5	1.2597	0.3331	1.38E-03	HSDL1	Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 PE=1 SV=3 - [HSDL1_HUMAN]
A1L390	0.6985	-0.5176	1.39E-03	PKHG3	Pleckstrin homology domain-containing family G member 3 OS=Homo sapiens GN=PLEKHG3 PE=1 SV=1 - [PKHG3_HUMAN]
P10620	1.1611	0.2154	1.39E-03	MGST1	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]
Q16890	1.1778	0.2361	1.40E-03	TPD53	Tumor protein D53 OS=Homo sapiens GN=TPD52L1 PE=1 SV=1 - [TPD53_HUMAN]
Q96LJ7	1.2125	0.2780	1.40E-03	DHRS1	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]
P14921	0.8439	-0.2448	1.45E-03	ETS1	Protein C-ets-1 OS=Homo sapiens GN=ETS1 PE=1 SV=1 - [ETS1_HUMAN]
Q8N6G6	0.8416	-0.2488	1.45E-03	ATL1	ADAMTS-like protein 1 OS=Homo sapiens GN=ADAMTSL1 PE=1 SV=4 - [ATL1_HUMAN]

Q8IWA0	0.8488	-0.2365	1.46E-03	WDR75	WD repeat-containing protein 75 OS=Homo sapiens GN=WDR75 PE=1 SV=1 - [WDR75_HUMAN]
P55268	1.1883	0.2489	1.49E-03	LAMB2	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2 - [LAMB2_HUMAN]
Q969X1	0.7506	-0.4138	1.49E-03	LFG3	Protein lifeguard 3 OS=Homo sapiens GN=TMBIM1 PE=1 SV=2 - [LFG3_HUMAN]
O75781	1.2367	0.3065	1.50E-03	PALM	Paralemmin-1 OS=Homo sapiens GN=PALM PE=1 SV=2 - [PALM_HUMAN]
P07711	1.2554	0.3281	1.52E-03	CATL1	Cathepsin L1 OS=Homo sapiens GN=CTSL PE=1 SV=2 - [CATL1_HUMAN]
Q6YHK3	1.2185	0.2851	1.52E-03	CD109	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2 - [CD109_HUMAN]
Q86Y56	0.8288	-0.2709	1.55E-03	HEAT2	HEAT repeat-containing protein 2 OS=Homo sapiens GN=HEATR2 PE=1 SV=4 - [HEAT2_HUMAN]
O60279	1.1613	0.2158	1.56E-03	SUSD5	Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 PE=1 SV=3 - [SUSD5_HUMAN]
O00488	0.7139	-0.4861	1.57E-03	ZN593	Zinc finger protein 593 OS=Homo sapiens GN=ZNF593 PE=1 SV=2 - [ZN593_HUMAN]
P48061	1.2105	0.2756	1.58E-03	SDF1	Stromal cell-derived factor 1 OS=Homo sapiens GN=CXCL12 PE=1 SV=1 - [SDF1_HUMAN]
Q8TDX6	0.8001	-0.3217	1.59E-03	CGAT1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=CSGALNACT1 PE=1 SV=2 - [CGAT1_HUMAN]
Q96SL4	1.1505	0.2023	1.60E-03	GPX7	Glutathione peroxidase 7 OS=Homo sapiens GN=GPX7 PE=1 SV=1 - [GPX7_HUMAN]
O75298	1.2034	0.2671	1.61E-03	RTN2	Reticulon-2 OS=Homo sapiens GN=RTN2 PE=1 SV=1 - [RTN2_HUMAN]
Q16877	0.7507	-0.4138	1.69E-03	F264	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 OS=Homo sapiens GN=PFKFB4 PE=2 SV=6 - [F264_HUMAN]
Q9H583	0.8479	-0.2381	1.70E-03	HEAT1	HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3 - [HEAT1_HUMAN]
P17900	1.2254	0.2932	1.77E-03	SAP3	Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4 - [SAP3_HUMAN]
Q9C035	0.8422	-0.2478	1.77E-03	TRIM5	Tripartite motif-containing protein 5 OS=Homo sapiens GN=TRIM5 PE=1 SV=1 - [TRIM5_HUMAN]
Q6PCB0	1.2145	0.2803	1.80E-03	VWA1	von Willebrand factor A domain-containing protein 1 OS=Homo sapiens GN=VWA1 PE=2 SV=1 - [VWA1_HUMAN]
Q8N5M1	1.2478	0.3194	1.83E-03	ATPF2	ATP synthase mitochondrial F1 complex assembly factor 2 OS=Homo sapiens GN=ATPAF2 PE=1 SV=1 - [ATPF2_HUMAN]

O75845	0.6951	-0.5247	1.83E-03	SC5D	Lathosterol oxidase OS=Homo sapiens GN=SC5D PE=1 SV=2 - [SC5D_HUMAN]
O60565	1.7279	0.7890	1.84E-03	GREM1	Gremlin-1 OS=Homo sapiens GN=GREM1 PE=1 SV=1 - [GREM1_HUMAN]
O00244	1.3201	0.4006	1.85E-03	ATOX1	Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1 - [ATOX1_HUMAN]
P15153	0.8153	-0.2947	1.87E-03	RAC2	Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [RAC2_HUMAN]
P36021	1.4016	0.4871	1.88E-03	MOT8	Monocarboxylate transporter 8 OS=Homo sapiens GN=SLC16A2 PE=1 SV=2 - [MOT8_HUMAN]
Q13247	0.8235	-0.2802	1.93E-03	SRSF6	Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN]
Q86YS7	0.7666	-0.3835	1.93E-03	C2CD5	C2 domain-containing protein 5 OS=Homo sapiens GN=C2CD5 PE=1 SV=1 - [C2CD5_HUMAN]
Q5T5C0	1.2466	0.3180	1.94E-03	STXB5	Syntaxin-binding protein 5 OS=Homo sapiens GN=STXBP5 PE=1 SV=1 - [STXB5_HUMAN]
P33991	0.7901	-0.3399	1.94E-03	MCM4	DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN]
P11182	1.2041	0.2679	1.94E-03	ODB2	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3 - [ODB2_HUMAN]
Q6RFH5	0.7660	-0.3845	1.96E-03	WDR74	WD repeat-containing protein 74 OS=Homo sapiens GN=WDR74 PE=1 SV=1 - [WDR74_HUMAN]
Q96JG8	0.6670	-0.5842	1.96E-03	MAGD4	Melanoma-associated antigen D4 OS=Homo sapiens GN=MAGED4 PE=1 SV=3 - [MAGD4_HUMAN]
Q15154	0.8277	-0.2728	1.97E-03	PCM1	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 - [PCM1_HUMAN]
Q9H6X2	1.7232	0.7851	1.97E-03	ANTR1	Anthrax toxin receptor 1 OS=Homo sapiens GN=ANTXR1 PE=1 SV=2 - [ANTR1_HUMAN]
P34741	0.8456	-0.2420	1.99E-03	SDC2	Syndecan-2 OS=Homo sapiens GN=SDC2 PE=1 SV=2 - [SDC2_HUMAN]
P42766	0.8286	-0.2713	2.08E-03	RL35	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]
Q9BS40	1.1577	0.2112	2.11E-03	LXN	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2 - [LXN_HUMAN]
Q9Y5U2	1.4592	0.5452	2.14E-03	TSSC4	Protein TSSC4 OS=Homo sapiens GN=TSSC4 PE=1 SV=3 - [TSSC4_HUMAN]
Q9NQ55	0.8259	-0.2760	2.18E-03	SSF1	Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN PE=1 SV=1 - [SSF1_HUMAN]
Q9H089	0.8509	-0.2330	2.21E-03	LSG1	Large subunit GTPase 1 homolog OS=Homo sapiens GN=LSG1 PE=1 SV=2 - [LSG1_HUMAN]

Q96IZ0	1.2186	0.2853	2.29E-03	PAWR	PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 - [PAWR_HUMAN]
Q6NW40	0.5176	-0.9500	2.29E-03	RGMB	RGM domain family member B OS=Homo sapiens GN=RGMB PE=1 SV=3 - [RGMB_HUMAN]
P60033	1.1518	0.2039	2.32E-03	CD81	CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1 - [CD81_HUMAN]
Q9UMY1	0.8090	-0.3057	2.34E-03	NOL7	Nucleolar protein 7 OS=Homo sapiens GN=NOL7 PE=1 SV=2 - [NOL7_HUMAN]
Q6UXV4	1.1734	0.2307	2.41E-03	APOOL	Apolipoprotein O-like OS=Homo sapiens GN=APOOL PE=1 SV=1 - [APOOL_HUMAN]
Q13454	1.1522	0.2044	2.61E-03	TUSC3	Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=1 SV=1 - [TUSC3_HUMAN]
P63096	1.2791	0.3551	2.69E-03	GNAI1	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2 - [GNAI1_HUMAN]
P08727	1.1644	0.2196	2.77E-03	K1C19	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]
O43159	0.8301	-0.2686	2.80E-03	RRP8	Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 - [RRP8_HUMAN]
Q92947	1.1709	0.2276	2.81E-03	GCDH	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1 - [GCDH_HUMAN]
O95478	0.7827	-0.3535	2.94E-03	NSA2	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1 - [NSA2_HUMAN]
P08651	1.1946	0.2566	2.95E-03	NFIC	Nuclear factor 1 C-type OS=Homo sapiens GN=NFIC PE=1 SV=2 - [NFIC_HUMAN]
Q9H7B2	0.8517	-0.2317	2.98E-03	RPF2	Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1 SV=2 - [RPF2_HUMAN]
P28347	1.1597	0.2137	2.99E-03	TEAD1	Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2 - [TEAD1_HUMAN]
Q9BV19	1.3945	0.4797	3.04E-03	CA050	Uncharacterized protein C1orf50 OS=Homo sapiens GN=C1orf50 PE=1 SV=2 - [CA050_HUMAN]
Q9UBU8	0.8328	-0.2640	3.05E-03	MO4L1	Mortality factor 4-like protein 1 OS=Homo sapiens GN=MORF4L1 PE=1 SV=2 - [MO4L1_HUMAN]
Q9P0P0	0.8137	-0.2974	3.06E-03	RN181	E3 ubiquitin-protein ligase RNF181 OS=Homo sapiens GN=RNF181 PE=1 SV=1 - [RN181_HUMAN]
Q92484	1.1843	0.2440	3.07E-03	ASM3A	Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2 - [ASM3A_HUMAN]
A1A4S6	0.8398	-0.2520	3.08E-03	RHG10	Rho GTPase-activating protein 10 OS=Homo sapiens GN=ARHGAP10 PE=1 SV=1 - [RHG10_HUMAN]

A6NJ78	1.3680	0.4520	3.09E-03	MET15	Probable methyltransferase-like protein 15 OS=Homo sapiens GN=METTL15 PE=2 SV=1 - [MET15_HUMAN]
Q9NRA1	1.3210	0.4016	3.12E-03	PDGFC	Platelet-derived growth factor C OS=Homo sapiens GN=PDGFC PE=1 SV=2 - [PDGFC_HUMAN]
Q96CB9	1.1630	0.2178	3.24E-03	NSUN4	5-methylcytosine rRNA methyltransferase NSUN4 OS=Homo sapiens GN=NSUN4 PE=1 SV=2 - [NSUN4_HUMAN]
Q9NUM4	1.1515	0.2035	3.25E-03	T106B	Transmembrane protein 106B OS=Homo sapiens GN=TMEM106B PE=1 SV=2 - [T106B_HUMAN]
Q9BYC9	0.8274	-0.2733	3.37E-03	RM20	39S ribosomal protein L20, mitochondrial OS=Homo sapiens GN=MRPL20 PE=1 SV=1 - [RM20_HUMAN]
Q9Y312	0.4902	-1.0286	3.46E-03	AAR2	Protein AAR2 homolog OS=Homo sapiens GN=AAR2 PE=1 SV=2 - [AAR2_HUMAN]
Q9HD67	0.7001	-0.5144	3.52E-03	MYO10	Unconventional myosin-X OS=Homo sapiens GN=MYO10 PE=1 SV=3 - [MYO10_HUMAN]
Q96RW7	1.1768	0.2348	3.56E-03	HMCN1	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2 - [HMCN1_HUMAN]
Q99538	1.1625	0.2172	3.56E-03	LGMN	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1 - [LGMN_HUMAN]
Q9Y2V2	1.1762	0.2341	3.64E-03	CHSP1	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CARHSP1 PE=1 SV=2 - [CHSP1_HUMAN]
Q6FIF0	0.8312	-0.2668	3.64E-03	ZFAN6	AN1-type zinc finger protein 6 OS=Homo sapiens GN=ZFAND6 PE=1 SV=2 - [ZFAN6_HUMAN]
P20674	1.1867	0.2469	3.66E-03	COX5A	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 - [COX5A_HUMAN]
Q9BXS4	1.3215	0.4021	3.70E-03	TMM59	Transmembrane protein 59 OS=Homo sapiens GN=TMEM59 PE=1 SV=1 - [TMM59_HUMAN]
P08697	1.8276	0.8700	3.72E-03	A2AP	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3 - [A2AP_HUMAN]
Q68D10	0.8142	-0.2965	3.73E-03	SPT2	Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 PE=1 SV=3 - [SPT2_HUMAN]
Q15118	0.8018	-0.3187	3.79E-03	PDK1	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial OS=Homo sapiens GN=PDK1 PE=1 SV=1 - [PDK1_HUMAN]
P78316	0.8350	-0.2601	3.84E-03	NOP14	Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3 - [NOP14_HUMAN]
Q9Y3C1	0.7940	-0.3329	3.87E-03	NOP16	Nucleolar protein 16 OS=Homo sapiens GN=NOP16 PE=1 SV=2 - [NOP16_HUMAN]
P42677	0.8489	-0.2363	3.90E-03	RS27	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]

P09758	0.7563	-0.4029	3.95E-03	TACD2	Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3 - [TACD2_HUMAN]
O60306	0.8499	-0.2347	3.96E-03	AQR	Intron-binding protein aquarius OS=Homo sapiens GN=AQR PE=1 SV=4 - [AQR_HUMAN]
Q9H7C9	1.1689	0.2251	3.96E-03	AAMDC	Mth938 domain-containing protein OS=Homo sapiens GN=AAMDC PE=1 SV=1 - [AAMDC_HUMAN]
P29972	0.7048	-0.5047	4.00E-03	AQP1	Aquaporin-1 OS=Homo sapiens GN=AQP1 PE=1 SV=3 - [AQP1_HUMAN]
P62861	0.8507	-0.2332	4.16E-03	RS30	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]
Q8NCS4	1.3194	0.3998	4.18E-03	ZMYNB	Uncharacterized protein ZMYM6NB OS=Homo sapiens GN=ZMYM6NB PE=2 SV=1 - [ZMYNB_HUMAN]
P56937	0.7719	-0.3735	4.28E-03	DHB7	3-keto-steroid reductase OS=Homo sapiens GN=HSD17B7 PE=1 SV=1 - [DHB7_HUMAN]
Q5T0D9	0.7969	-0.3276	4.32E-03	TPRGL	Tumor protein p63-regulated gene 1-like protein OS=Homo sapiens GN=TPRG1L PE=1 SV=1 - [TPRGL_HUMAN]
P27658	1.1746	0.2322	4.34E-03	CO8A1	Collagen alpha-1(VIII) chain OS=Homo sapiens GN=COL8A1 PE=1 SV=2 - [CO8A1_HUMAN]
Q15678	0.7553	-0.4049	4.37E-03	PTN14	Tyrosine-protein phosphatase non-receptor type 14 OS=Homo sapiens GN=PTPN14 PE=1 SV=2 - [PTN14_HUMAN]
Q99805	1.1491	0.2005	4.37E-03	TM9S2	Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1 - [TM9S2_HUMAN]
Q9NQ89	1.4543	0.5403	4.67E-03	CL004	Uncharacterized protein C12orf4 OS=Homo sapiens GN=C12orf4 PE=2 SV=1 - [CL004_HUMAN]
O60739	0.8470	-0.2396	4.72E-03	EIF1B	Eukaryotic translation initiation factor 1b OS=Homo sapiens GN=EIF1B PE=1 SV=2 - [EIF1B_HUMAN]
P17676	1.4754	0.5611	4.87E-03	CEBPB	CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB PE=1 SV=2 - [CEBPB_HUMAN]
Q9P0J1	0.7593	-0.3973	5.05E-03	PDP1	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial OS=Homo sapiens GN=PDP1 PE=1 SV=3 - [PDP1_HUMAN]
Q04727	1.2221	0.2894	5.11E-03	TLE4	Transducin-like enhancer protein 4 OS=Homo sapiens GN=TLE4 PE=1 SV=3 - [TLE4_HUMAN]
P10606	1.4280	0.5140	5.12E-03	COX5B	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2 - [COX5B_HUMAN]
Q8N2Y8	1.1501	0.2018	5.13E-03	RUSC2	Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=3 - [RUSC2_HUMAN]

P28161	1.2017	0.2651	5.23E-03	GSTM2	Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=1 SV=2 - [GSTM2_HUMAN]
Q8WU10	0.7895	-0.3410	5.53E-03	PYRD1	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=PYROXD1 PE=1 SV=1 - [PYRD1_HUMAN]
Q9H8H0	0.8190	-0.2881	5.64E-03	NOL11	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 - [NOL11_HUMAN]
Q9Y4J8	0.8517	-0.2316	5.82E-03	DTNA	Dystrobrevin alpha OS=Homo sapiens GN=DTNA PE=1 SV=2 - [DTNA_HUMAN]
Q15031	1.1536	0.2062	5.92E-03	SYLM	Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2 - [SYLM_HUMAN]
O95169	1.1689	0.2252	6.06E-03	NDUB8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUFB8 PE=1 SV=1 - [NDUB8_HUMAN]
P19634	1.1790	0.2376	6.06E-03	SL9A1	Sodium/hydrogen exchanger 1 OS=Homo sapiens GN=SLC9A1 PE=1 SV=2 - [SL9A1_HUMAN]
O15397	0.7674	-0.3819	6.08E-03	IPO8	Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2 - [IPO8_HUMAN]
Q9Y5V0	0.8411	-0.2496	6.21E-03	ZN706	Zinc finger protein 706 OS=Homo sapiens GN=ZNF706 PE=1 SV=1 - [ZN706_HUMAN]
Q8N1W1	0.8282	-0.2720	6.28E-03	ARG28	Rho guanine nucleotide exchange factor 28 OS=Homo sapiens GN=ARHGEF28 PE=1 SV=3 - [ARG28_HUMAN]
Q9NZV1	1.1510	0.2029	6.38E-03	CRIM1	Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 - [CRIM1_HUMAN]
P49674	0.8055	-0.3120	6.42E-03	KC1E	Casein kinase I isoform epsilon OS=Homo sapiens GN=CSNK1E PE=1 SV=1 - [KC1E_HUMAN]
P78504	0.8427	-0.2470	6.43E-03	JAG1	Protein jagged-1 OS=Homo sapiens GN=JAG1 PE=1 SV=3 - [JAG1_HUMAN]
O95273	0.8439	-0.2449	6.62E-03	CCDB1	Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2 - [CCDB1_HUMAN]
P03915	1.1620	0.2166	6.70E-03	NU5M	NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens GN=MT-ND5 PE=1 SV=2 - [NU5M_HUMAN]
Q8TF72	0.7752	-0.3673	6.82E-03	SHRM3	Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2 - [SHRM3_HUMAN]
O95476	1.2895	0.3669	6.82E-03	CNEP1	CTD nuclear envelope phosphatase 1 OS=Homo sapiens GN=CTDNEP1 PE=1 SV=2 - [CNEP1_HUMAN]
Q96PU5	0.7786	-0.3610	6.88E-03	NED4L	E3 ubiquitin-protein ligase NEDD4-like OS=Homo sapiens GN=NEDD4L PE=1 SV=2 - [NED4L_HUMAN]
P53611	0.8317	-0.2659	6.89E-03	PGTB2	Geranylgeranyl transferase type-2 subunit beta OS=Homo sapiens

					GN=RABGGTB PE=1 SV=2 - [PGTB2_HUMAN]
Q03013	1.2407	0.3111	6.94E-03	GSTM4	Glutathione S-transferase Mu 4 OS=Homo sapiens GN=GSTM4 PE=1 SV=3 - [GSTM4_HUMAN]
O15061	1.1953	0.2574	6.98E-03	SYNEM	Synemin OS=Homo sapiens GN=SYNM PE=1 SV=2 - [SYNEM_HUMAN]
Q01484	0.7708	-0.3756	7.38E-03	ANK2	Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4 - [ANK2_HUMAN]
Q9NX00	1.1669	0.2226	7.40E-03	TM160	Transmembrane protein 160 OS=Homo sapiens GN=TMEM160 PE=1 SV=1 - [TM160_HUMAN]
P22415	1.1944	0.2563	7.67E-03	USF1	Upstream stimulatory factor 1 OS=Homo sapiens GN=USF1 PE=1 SV=1 - [USF1_HUMAN]
P02768	1.5007	0.5857	7.67E-03	ALBU	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]
P01344	0.8198	-0.2867	7.85E-03	IGF2	Insulin-like growth factor II OS=Homo sapiens GN=IGF2 PE=1 SV=1 - [IGF2_HUMAN]
P49366	0.8462	-0.2409	7.95E-03	DHYS	Deoxyhypusine synthase OS=Homo sapiens GN=DHPS PE=1 SV=1 - [DHYS_HUMAN]
P35914	0.7598	-0.3963	8.02E-03	HMGCL	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]
P25205	0.7732	-0.3711	8.28E-03	MCM3	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 - [MCM3_HUMAN]
O60287	0.7271	-0.4597	8.41E-03	NPA1P	Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4 - [NPA1P_HUMAN]
Q8N8Z6	0.7744	-0.3689	8.47E-03	DCBD1	Discoidin, CUB and LCCL domain-containing protein 1 OS=Homo sapiens GN=DCBLD1 PE=1 SV=2 - [DCBD1_HUMAN]
P09038	1.1889	0.2496	9.01E-03	FGF2	Fibroblast growth factor 2 OS=Homo sapiens GN=FGF2 PE=1 SV=3 - [FGF2_HUMAN]
P08574	1.2189	0.2856	9.01E-03	CY1	Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3 - [CY1_HUMAN]
Q8N264	0.7404	-0.4337	9.19E-03	RHG24	Rho GTPase-activating protein 24 OS=Homo sapiens GN=ARHGAP24 PE=1 SV=2 - [RHG24_HUMAN]
Q9Y5G0	1.1519	0.2040	9.24E-03	PCDGH	Protocadherin gamma-B5 OS=Homo sapiens GN=PCDHGB5 PE=2 SV=1 - [PCDGH_HUMAN]
Q8TCT7	1.2757	0.3512	9.27E-03	SPP2B	Signal peptide peptidase-like 2B OS=Homo sapiens GN=SPPL2B PE=1 SV=2 - [SPP2B_HUMAN]
Q9NW13	0.8432	-0.2461	9.73E-03	RBM28	RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3 - [RBM28_HUMAN]
Q9NV31	0.8261	-0.2756	1.02E-02	IMP3	U3 small nucleolar ribonucleoprotein protein IMP3

					OS=Homo sapiens GN=IMP3 PE=1 SV=1 - [IMP3_HUMAN]
Q92633	1.3243	0.4053	1.10E-02	LPAR1	Lysophosphatidic acid receptor 1 OS=Homo sapiens GN=LPAR1 PE=1 SV=3 - [LPAR1_HUMAN]
P41221	0.8245	-0.2785	1.10E-02	WNT5A	Protein Wnt-5a OS=Homo sapiens GN=WNT5A PE=1 SV=2 - [WNT5A_HUMAN]
Q9Y3B9	0.8189	-0.2882	1.12E-02	RRP15	RRP15-like protein OS=Homo sapiens GN=RRP15 PE=1 SV=2 - [RRP15_HUMAN]
Q96J84	1.1521	0.2043	1.12E-02	KIRR1	Kin of IRRE-like protein 1 OS=Homo sapiens GN=KIRREL PE=1 SV=2 - [KIRR1_HUMAN]
Q8NBZ7	0.7784	-0.3615	1.14E-02	UXS1	UDP-glucuronic acid decarboxylase 1 OS=Homo sapiens GN=UXS1 PE=1 SV=1 - [UXS1_HUMAN]
Q8NHP6	0.8309	-0.2673	1.16E-02	MSPD2	Motile sperm domain-containing protein 2 OS=Homo sapiens GN=MOSPD2 PE=1 SV=1 - [MSPD2_HUMAN]
O95450	1.2296	0.2981	1.16E-02	ATS2	A disintegrin and metalloproteinase with thrombospondin motifs 2 OS=Homo sapiens GN=ADAMTS2 PE=2 SV=2 - [ATS2_HUMAN]
P78314	1.3438	0.4263	1.18E-02	3BP2	SH3 domain-binding protein 2 OS=Homo sapiens GN=SH3BP2 PE=1 SV=2 - [3BP2_HUMAN]
Q8TEB9	1.2581	0.3312	1.19E-02	RHBL4	Rhomboid-related protein 4 OS=Homo sapiens GN=RHBDD1 PE=1 SV=1 - [RHBL4_HUMAN]
O75147	1.1812	0.2403	1.24E-02	OBSL1	Obscurin-like protein 1 OS=Homo sapiens GN=OBSL1 PE=1 SV=4 - [OBSL1_HUMAN]
P38571	0.8341	-0.2617	1.24E-02	LICH	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2 - [LICH_HUMAN]
Q9ULG6	1.2598	0.3332	1.25E-02	CCPG1	Cell cycle progression protein 1 OS=Homo sapiens GN=CCPG1 PE=2 SV=3 - [CCPG1_HUMAN]
Q6PID8	0.8066	-0.3101	1.26E-02	KLD10	Kelch domain-containing protein 10 OS=Homo sapiens GN=KLHDC10 PE=2 SV=1 - [KLD10_HUMAN]
Q9Y6M7	1.1638	0.2189	1.27E-02	S4A7	Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=1 SV=2 - [S4A7_HUMAN]
P51636	1.2677	0.3423	1.32E-02	CAV2	Caveolin-2 OS=Homo sapiens GN=CAV2 PE=1 SV=2 - [CAV2_HUMAN]
Q9Y5J1	0.7947	-0.3315	1.33E-02	UTP18	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 - [UTP18_HUMAN]
Q9UPU7	0.8004	-0.3211	1.33E-02	TBD2B	TBC1 domain family member 2B OS=Homo sapiens GN=TBC1D2B PE=1 SV=2 - [TBD2B_HUMAN]
P13747	1.1630	0.2178	1.35E-02	HLAE	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens GN=HLA-E PE=1 SV=3 - [HLAE_HUMAN]

P13796	1.2054	0.2695	1.37E-02	PLSL	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 - [PLSL_HUMAN]
Q92845	0.8398	-0.2519	1.37E-02	KIFA3	Kinesin-associated protein 3 OS=Homo sapiens GN=KIFAP3 PE=1 SV=2 - [KIFA3_HUMAN]
Q9UNN8	1.3733	0.4576	1.37E-02	EPCR	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1 - [EPCR_HUMAN]
O95757	0.8510	-0.2327	1.38E-02	HS74L	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]
P09914	0.7241	-0.4658	1.40E-02	IFIT1	Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 - [IFIT1_HUMAN]
P27169	1.4525	0.5385	1.41E-02	PON1	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]
Q9UBK8	0.8283	-0.2718	1.43E-02	MTRR	Methionine synthase reductase OS=Homo sapiens GN=MTRR PE=1 SV=3 - [MTRR_HUMAN]
Q8TDW7	0.8334	-0.2629	1.43E-02	FAT3	Protocadherin Fat 3 OS=Homo sapiens GN=FAT3 PE=2 SV=2 - [FAT3_HUMAN]
O75380	1.1932	0.2548	1.47E-02	NDUS6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Homo sapiens GN=NDUFS6 PE=1 SV=1 - [NDUS6_HUMAN]
Q9H0X4	1.2316	0.3006	1.49E-02	ITFG3	Protein ITFG3 OS=Homo sapiens GN=ITFG3 PE=1 SV=1 - [ITFG3_HUMAN]
O60220	1.2119	0.2773	1.53E-02	TIM8A	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1 - [TIM8A_HUMAN]
Q5QJE6	0.8384	-0.2543	1.58E-02	TDIF2	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=1 SV=2 - [TDIF2_HUMAN]
Q6P1Q9	0.8049	-0.3131	1.62E-02	MET2B	Methyltransferase-like protein 2B OS=Homo sapiens GN=METTL2B PE=1 SV=3 - [MET2B_HUMAN]
Q9ULP9	1.2202	0.2871	1.62E-02	TBC24	TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 - [TBC24_HUMAN]
Q99424	1.1562	0.2094	1.62E-02	ACOX2	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]
Q8WUH6	0.8415	-0.2490	1.71E-02	CL023	UPF0444 transmembrane protein C12orf23 OS=Homo sapiens GN=C12orf23 PE=1 SV=1 - [CL023_HUMAN]
Q9NQ92	0.8164	-0.2927	1.73E-02	COPRS	Coordinator of PRMT5 and differentiation stimulator OS=Homo sapiens GN=COPRS PE=1 SV=3 - [COPRS_HUMAN]
Q9BRS2	0.8501	-0.2343	1.80E-02	RIOK1	Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2 - [RIOK1_HUMAN]

O75061	0.8355	-0.2593	1.81E-02	AUXI	Putative tyrosine-protein phosphatase auxilin OS=Homo sapiens GN=DNAJC6 PE=1 SV=3 - [AUXI_HUMAN]
O75420	1.2596	0.3329	1.82E-02	PERQ1	PERQ amino acid-rich with GYF domain-containing protein 1 OS=Homo sapiens GN=GIGYF1 PE=1 SV=2 - [PERQ1_HUMAN]
P04921	0.8490	-0.2362	1.84E-02	GLPC	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1 - [GLPC_HUMAN]
Q9UFF9	0.7750	-0.3677	1.90E-02	CNOT8	CCR4-NOT transcription complex subunit 8 OS=Homo sapiens GN=CNOT8 PE=1 SV=1 - [CNOT8_HUMAN]
P02788	1.1932	0.2548	1.91E-02	TRFL	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]
O15213	0.8041	-0.3146	1.93E-02	WDR46	WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 - [WDR46_HUMAN]
Q15059	1.2099	0.2749	1.99E-02	BRD3	Bromodomain-containing protein 3 OS=Homo sapiens GN=BRD3 PE=1 SV=1 - [BRD3_HUMAN]
Q4G0N4	1.2679	0.3425	2.01E-02	NAKD2	NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=1 SV=2 - [NAKD2_HUMAN]
Q9UN70	0.7879	-0.3439	2.02E-02	PCDGK	Protocadherin gamma-C3 OS=Homo sapiens GN=PCDHGC3 PE=1 SV=1 - [PCDGK_HUMAN]
Q9NP58	1.2197	0.2865	2.06E-02	ABCB6	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1 - [ABCB6_HUMAN]
Q12891	1.1844	0.2441	2.07E-02	HYAL2	Hyaluronidase-2 OS=Homo sapiens GN=HYAL2 PE=1 SV=4 - [HYAL2_HUMAN]
P58397	0.8412	-0.2494	2.15E-02	ATS12	A disintegrin and metalloproteinase with thrombospondin motifs 12 OS=Homo sapiens GN=ADAMTS12 PE=1 SV=2 - [ATS12_HUMAN]
O75746	1.1804	0.2393	2.15E-02	CMC1	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2 - [CMC1_HUMAN]
Q9Y5R8	1.2205	0.2875	2.20E-02	TPPC1	Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 - [TPPC1_HUMAN]
Q7Z6K3	0.8496	-0.2351	2.26E-02	PTAR1	Protein prenyltransferase alpha subunit repeat-containing protein 1 OS=Homo sapiens GN=PTAR1 PE=2 SV=2 - [PTAR1_HUMAN]
P09234	1.2230	0.2905	2.32E-02	RU1C	U1 small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1 - [RU1C_HUMAN]
P51805	1.1944	0.2563	2.45E-02	PLXA3	Plexin-A3 OS=Homo sapiens GN=PLXNA3 PE=1 SV=2 - [PLXA3_HUMAN]
Q15291	1.4857	0.5712	2.50E-02	RBBP5	Retinoblastoma-binding protein 5 OS=Homo sapiens GN=RBBP5 PE=1 SV=2 - [RBBP5_HUMAN]

Q12983	0.8118	-0.3008	2.50E-02	BNIP3	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Homo sapiens GN=BNIP3 PE=1 SV=2 - [BNIP3_HUMAN]
Q9HAU4	0.8248	-0.2778	2.57E-02	SMUF2	E3 ubiquitin-protein ligase SMURF2 OS=Homo sapiens GN=SMURF2 PE=1 SV=1 - [SMUF2_HUMAN]
Q15025	0.8179	-0.2900	2.65E-02	TNIP1	TNFAIP3-interacting protein 1 OS=Homo sapiens GN=TNIP1 PE=1 SV=2 - [TNIP1_HUMAN]
P02774	1.2988	0.3772	2.72E-02	VTDB	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 - [VTDB_HUMAN]
Q9Y4H2	1.3380	0.4201	2.74E-02	IRS2	Insulin receptor substrate 2 OS=Homo sapiens GN=IRS2 PE=1 SV=2 - [IRS2_HUMAN]
P15408	0.8206	-0.2853	2.75E-02	FOSL2	Fos-related antigen 2 OS=Homo sapiens GN=FOSL2 PE=1 SV=1 - [FOSL2_HUMAN]
Q5TBB1	0.8110	-0.3022	2.78E-02	RNH2B	Ribonuclease H2 subunit B OS=Homo sapiens GN=RNASEH2B PE=1 SV=1 - [RNH2B_HUMAN]
Q96FX8	0.7054	-0.5035	2.84E-02	PERP	p53 apoptosis effector related to PMP-22 OS=Homo sapiens GN=PERP PE=2 SV=1 - [PERP_HUMAN]
P21731	1.2946	0.3725	2.93E-02	TA2R	Thromboxane A2 receptor OS=Homo sapiens GN=TBXA2R PE=1 SV=3 - [TA2R_HUMAN]
P17405	1.1657	0.2212	3.01E-02	ASM	Sphingomyelin phosphodiesterase OS=Homo sapiens GN=SMPD1 PE=1 SV=4 - [ASM_HUMAN]
P05165	1.3033	0.3822	3.03E-02	PCCA	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]
Q9BVG3	0.6984	-0.5178	3.07E-02	TRI62	Tripartite motif-containing protein 62 OS=Homo sapiens GN=TRIM62 PE=2 SV=1 - [TRI62_HUMAN]
Q9Y618	0.8026	-0.3173	3.11E-02	NCOR2	Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2 PE=1 SV=2 - [NCOR2_HUMAN]
Q13572	0.8322	-0.2649	3.28E-02	ITPK1	Inositol-tetrakisphosphate 1-kinase OS=Homo sapiens GN=ITPK1 PE=1 SV=2 - [ITPK1_HUMAN]
P50607	1.2113	0.2765	3.33E-02	TUB	Tubby protein homolog OS=Homo sapiens GN=TUB PE=1 SV=1 - [TUB_HUMAN]
O60292	0.8207	-0.2851	3.37E-02	SI1L3	Signal-induced proliferation-associated 1-like protein 3 OS=Homo sapiens GN=SIPA1L3 PE=1 SV=3 - [SI1L3_HUMAN]
Q96A19	1.1962	0.2584	3.45E-02	C102A	Coiled-coil domain-containing protein 102A OS=Homo sapiens GN=CCDC102A PE=1 SV=2 - [C102A_HUMAN]
Q96S19	0.8493	-0.2356	3.47E-02	CP013	UPF0585 protein C16orf13 OS=Homo sapiens GN=C16orf13 PE=1 SV=2 - [CP013_HUMAN]
Q14678	1.1957	0.2578	3.52E-02	KANK1	KN motif and ankyrin repeat domain-containing protein 1

					OS=Homo sapiens GN=KANK1 PE=1 SV=3 - [KANK1_HUMAN]
Q8IY63	0.7723	-0.3728	3.54E-02	AMOL1	Angiomotin-like protein 1 OS=Homo sapiens GN=AMOTL1 PE=1 SV=1 - [AMOL1_HUMAN]
Q92793	1.2024	0.2659	3.54E-02	CBP	CREB-binding protein OS=Homo sapiens GN=CREBBP PE=1 SV=3 - [CBP_HUMAN]
P14543	1.1776	0.2359	3.68E-02	NID1	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3 - [NID1_HUMAN]
Q9NRQ2	1.1580	0.2117	3.72E-02	PLS4	Phospholipid scramblase 4 OS=Homo sapiens GN=PLSCR4 PE=1 SV=2 - [PLS4_HUMAN]
Q8NI35	1.3989	0.4843	3.87E-02	INADL	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3 - [INADL_HUMAN]
Q7Z6J0	0.8352	-0.2598	3.89E-02	SH3R1	E3 ubiquitin-protein ligase SH3RF1 OS=Homo sapiens GN=SH3RF1 PE=1 SV=2 - [SH3R1_HUMAN]
P51784	0.7343	-0.4456	3.89E-02	UBP11	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=3 - [UBP11_HUMAN]
Q9UPY5	1.2886	0.3658	4.03E-02	XCT	Cystine/glutamate transporter OS=Homo sapiens GN=SLC7A11 PE=1 SV=1 - [XCT_HUMAN]
P26358	0.7605	-0.3949	4.04E-02	DNMT1	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 - [DNMT1_HUMAN]
P06732	1.4730	0.5588	4.36E-02	KCRM	Creatine kinase M-type OS=Homo sapiens GN=CKM PE=1 SV=2 - [KCRM_HUMAN]
Q9BSW2	0.8325	-0.2645	4.37E-02	EFC4B	EF-hand calcium-binding domain-containing protein 4B OS=Homo sapiens GN=EFCAB4B PE=1 SV=1 - [EFC4B_HUMAN]
P06400	0.8262	-0.2754	4.37E-02	RB	Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 - [RB_HUMAN]
Q8TEW0	1.1753	0.2330	4.57E-02	PARD3	Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2 - [PARD3_HUMAN]
Q9UPN9	1.2435	0.3144	4.66E-02	TRI33	E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33 PE=1 SV=3 - [TRI33_HUMAN]
Q9BWW4	1.4414	0.5274	4.68E-02	SSBP3	Single-stranded DNA-binding protein 3 OS=Homo sapiens GN=SSBP3 PE=1 SV=1 - [SSBP3_HUMAN]
Q8N5I4	1.1876	0.2481	4.84E-02	DHRSX	Dehydrogenase/reductase SDR family member on chromosome X OS=Homo sapiens GN=DHRSX PE=2 SV=2 - [DHRSX_HUMAN]
O60925	1.2340	0.3034	4.89E-02	PFD1	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2 - [PFD1_HUMAN]

Supplemental Table 4: List of regulated genes and proteins in the common regulated pathways from microarray and proteomic analysis. Common transcriptional regulators (transcripts or proteins) in each pathway are underlined.

Ingenuity Canonical Pathways	**Dataset**	**Transcripts/proteins**
Acute Phase Response Signaling	Array	JUN, C3, IL1B, SOCS3, TNFRSF1B, MRAS, IL6R, RBP4, NFKBIA, PLG, A2M, AGT, FN1, HRG, CEBPB, SERPINA1, SERPINE1, RBP5, TTR,
	Cell MS	JUN, FTL, TF, C3, CRABP2, PLG, A2M, C4A/C4B, HP, SERPINF2, C9, AMBP, ITIH2, ALB, ITIH4, FGA, HMOX1, OSMR, SOD2, NOLC1, CEBPB, APOA1, C4BPA, SERPINE1, HPX, AHSG, SERPING1, SERPIND1
Agrin Interactions at Neuromuscular Junction	Array	JUN, MRAS, NRG3, ITGB2, ACTA2, RAC2, LAMA2
	Cell MS	JUN, ITGA2, LAMB1, AGRN, ITGB3, RAC2, DAG1
Aryl Hydrocarbon Receptor Signaling	Array	JUN, MYC, ALDH1L1, IL1B, CCND1, CDKN1A, ALDH6A1, GSTA1, MGST1, ALDH8A1
	Cell MS	JUN, NCOR2, MCM7, CDK2, CDKN2A, TGFB2, NQO1, MGST1, NFIC, HSPB1, CCND1, GSTM2, GSTM4, ALDH1B1, RB1, CTSD
Atherosclerosis Signaling	Array	S100A8, IL1B, APOD, COL3A1, COL1A2, ITGB2, RBP4, APOM, PLA2G4C, LYZ, PNPLA3, LPL, SERPINA1, TNFRSF12A
	Cell MS	PON1, LPA, CXCL12, APOB, CLU, APOD, APOA1, PCYOX1, APOE, APOL1, ALB, PDGFC
Caveolar-mediated Endocytosis Signaling	Array	ITGAM, EGF, CD48, ITGAX, ITGB2, ACTA2, PTPN1
	Cell MS	ITGB5, ITGAV, ITGA2, ITGA11, ITGB3, ALB
Clathrin-mediated Endocytosis Signaling	Array	LDLRAP1, S100A8, APOD, UBD, PGF, ITGB2, ACTA2, RBP4, DNM1, APOM, LYZ, EGF, SERPINA1, VEGFC
	Cell MS	PON1, TF, ITGB5, APOD, PCYOX1, FGF2, EPHB2, PPP3CA, PDGFC, ARRB1, LPA, APOB, CLU, APOA1, SH3BP4, ITGB3, APOE, SYNJ1, APOL1, ALB
Coagulation System	Array	A2M, SERPINA1, F13A1, SERPINE1, PLG
	Cell MS	A2M, F12, KNG1, SERPINF2, FGA, SERPINE1, PLG, SERPIND1
Complement System	Array	ITGAM, C3, C7, ITGAX, ITGB2, C3AR1
	Cell MS	C4A/C4B, C3, C4BPA, C9, SERPING1
FXR/RXR Activation	Array	PCK2, C3, IL1B, APOD, RBP4, APOM, SDC1, AGT, PPARGC1A, LPL, SERPINA1, FBP1, TTR
	Cell MS	GC, TF, C3, C4A/C4B, KNG1, SERPINF2, CREBBP, C9, AMBP, APOL1, ALB, PON1, PCK2, ITIH4, APOD, PCYOX1, FGA, APOB, VTN, CLU, FETUB, APOA1, APOE, HPX, AHSG, PLTP
Glioma Invasiveness Signaling	Array	MMP2, RHOB, MRAS, PLG, RND3, RHOU, CD44
	Cell MS	VTN, ITGB5, ITGAV, ITGB3, PLG, FNBP1
Glutathione Redox Reactions I	Array	CLIC2, GPX3, MGST1
	Cell MS	GPX4, GSR, GPX7, GPX1, MGST1
Glutathione-mediated Detoxification	Array	GGH, ANPEP, GSTA1, MGST1, NAT8
	Cell MS	GSTM2, GSTM4, ANPEP, MGST1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	Array	CXCL9, EDNRA, MMP2, PGF, IL6R, ACTA2, AGTR1, IL10RA, A2M, CCR5, COL12A1, FN1, SMAD7, VEGFC, COL4A1, BAMBI, IL1B, KLF6, PDGFRA, TNFRSF1B, CD14, COL3A1, COL1A2, COL5A1, AGT, EGF, COL16A1, COL5A2, COL4A2, SERPINE1
	Cell MS	COL7A1, COL6A3, TGFB2, FGF2, COL8A1, IGF2, PDGFC, A2M, COL12A1, COL5A2, SMAD3, ECE1, IGFBP3, SERPINE1

IL-12 Signaling and Production in Macrophages	Array	JUN, LYZ, S100A8, IRF8, APOD, CEBPB, SERPINA1, RBP4, TLR2, APOM, IL12RB1
	Cell MS	PON1, JUN, APOD, TGFB2, PCYOX1, LPA, APOB, CLU, CEBPB, APOA1, APOE, APOL1, ALB
IL-8 Signaling	Array	JUN, HBEGF, ITGAM, MMP2, GNG11, MRAS, PGF, ITGAX, NOX4, ITGB2, RAC2, EGF, PLD6, CCND1, RHOB, VEGFC, RND3, RHOU
	Cell MS	GNAI1, JUN, ITGB5, ITGAV, GNG10, RAC2, HMOX1, PDGFC, GNG5, CCND1, ITGB3, BCL2L1, FNBP1
Inhibition of Matrix Metalloproteases	Array	MMP7, A2M, MMP2, THBS2, TFPI2, SDC1
	Cell MS	A2M, RECK, THBS2, SDC2
LXR/RXR Activation	Array	S100A8, C3, IL1B, CD14, TNFRSF1B, APOD, HADH, RBP4, APOM, AGT, LYZ, ARG2, LPL, SERPINA1, TTR
	Cell MS	GC, NCOR2, TF, C3, HMGCR, LPA, C4A/C4B, SCD, KNG1, SERPINF2, C9, AMBP, APOL1, ALB, PON1, ITIH4, APOD, PCYOX1, FGA, FDFT1, APOB, VTN, CLU, CYP51A1, APOA1, APOE, HPX, AHSG, PLTP
Methylglyoxal Degradation III	Array	AKR7A3, AKR1C3, FAM213B, AKR1C1/AKR1C2
	Cell MS	AKR1C3, AKR1B1, AKR1B10, AKR1C1/AKR1C2
NRF2-mediated Oxidative Stress Response	Array	JUN, DNAJB1, MRAS, HSPB8, FMO1, ACTA2, MGST1, MAFF, AKR7A3, JUND, FKBP5, AOX1, DNAJB4, GSTA1, JUNB
	Cell MS	JUN, DNAJC6, GCLC, FTL, TXN, SOD1, TXNRD1, NQO1, MGST1, PRDX1, HMOX1, ENC1, SOD2, GSR, GSTM2, GSTM4, CREBBP, EPHX1, GCLM, FTH1, JUNB
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	Array	JUN, PPP1R14A, S100A8, TNFRSF1B, APOD, RBP4, NFKBIA, APOM, LYZ, IRF8, PPP1R10, PPP1R3C, RHOB, ARG2, SERPINA1, TLR2, RND3, RHOU
	Cell MS	PON1, JUN, APOD, PCYOX1, LPA, APOB, CLU, APOA1, CREBBP, APOE, SIRPA, APOL1, ALB, FNBP1
Superpathway of Citrulline Metabolism	Array	ASS1, ARG2, NOS3
	Cell MS	OAT, ASS1, GLS
γ-glutamyl Cycle	Array	GGT5, ANPEP, GGACT
	Cell MS	GCLC, ANPEP, GCLM