

Supplementary Table 9. Functional enrichment and PPI hub-protein analyses for the updated transcriptomic workflow.

(A) FDR-controlled GO enrichment results for the 155 overlapping DEGs.

ONTOLOID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count	source_gene_set
BP	GO:0030198 extracellular matrix organization	12/135	339/18805	0.03539823	4.930842347	6.210390461	6.16966E-06	0.005389506	0.00484827	IL6/ADAMTS2/MYH11/MMP14/MMP16/THSD4/ADAMTS20/MMP28/PLOD3/IBSP/COL1A1	12	overlap_155_DEGs
BP	GO:0043062 extracellular structure organization	12/135	340/18805	0.035294118	4.916339869	6.196764946	6.35666E-06	0.005389506	0.00484827	IL6/ADAMTS2/MYH11/MMP14/MMP16/THSD4/ADAMTS20/MMP28/PLOD3/IBSP/COL1A1	12	overlap_155_DEGs
BP	GO:0045229 external encapsulating structure organization	12/135	341/18805	0.035190616	4.90192245	6.183192592	6.54861E-06	0.005389506	0.00484827	IL6/ADAMTS2/MYH11/MMP14/MMP16/THSD4/ADAMTS20/MMP28/PLOD3/IBSP/COL1A1	12	overlap_155_DEGs
BP	GO:0032963 collagen metabolic process	7/135	112/18805	0.0625	8.706018519	6.955356634	1.62748E-05	0.010045643	0.009036817	IL6/ADAMTS2/MMP14/MMP16/MMP28/PLOD3/CBX8	7	overlap_155_DEGs
BP	GO:0001952 regulation of cell-matrix adhesion	7/135	125/18805	0.056	7.800592593	6.486839837	3.31604E-05	0.011830532	0.01064246	CSF1/MMP14/RRAS/PIK3R1/ROCK2/BCL2/MAP4K4	7	overlap_155_DEGs
BP	GO:0010810 regulation of cell-substrate adhesion	9/135	224/18805	0.040178571	5.59672619	5.885155593	3.50651E-05	0.011830532	0.01064246	CSF1/MMP14/RRAS/PIK3R1/ROCK2/BCL2/PTPRO/MAP4K4/ANGPT2	9	overlap_155_DEGs
BP	GO:0050871 positive regulation of B cell activation	6/135	86/18805	0.069767442	9.718346253	6.89067653	3.59524E-05	0.011830532	0.01064246	IL6/MMP14/TNIP2/BCL2/IRS2/TNFSF4	6	overlap_155_DEGs
BP	GO:1904035 regulation of epithelial cell apoptotic process	5/135	53/18805	0.094339623	13.14116003	7.526519091	3.85224E-05	0.011830532	0.01064246	IL6/WNT11/GSN/ITGB3BP/BCL2	5	overlap_155_DEGs
BP	GO:0042113 B cell activation	10/135	287/18805	0.034843206	4.853529488	5.59399737	4.31247E-05	0.011830532	0.01064246	IL6/MMP14/KLF6/PIK3R1/TNIP2/ITM2A/BCL2/IRS2/TPD52/TNFSF4	10	overlap_155_DEGs
BP	GO:0048251 elastic fiber assembly	3/135	11/18805	0.272727273	37.98989899	10.4349344	5.72402E-05	0.01413261	0.012713353	MYH11/THSD4/LTBPA	3	overlap_155_DEGs
BP	GO:0030183 B cell differentiation	7/135	141/18805	0.04964539	6.915418965	5.995322496	7.14677E-05	0.01604125	0.01443032	IL6/MMP14/KLF6/PIK3R1/ITM2A/BCL2/TPD52	7	overlap_155_DEGs
BP	GO:0150115 cell-substrate junction organization	6/135	103/18805	0.058252427	8.114347357	6.156437832	9.89791E-05	0.020364957	0.018319822	MMP14/PIK3R1/ROCK2/IQSEC1/BCL2/MAP4K4	6	overlap_155_DEGs
BP	GO:0010812 negative regulation of cell-substrate adhesion	5/135	66/18805	0.075757576	10.55274972	6.610693291	0.000111343	0.021146598	0.019022968	MMP14/PIK3R1/PTPRO/MAP4K4/ANGPT2	5	overlap_155_DEGs
BP	GO:0150116 regulation of cell-substrate junction organization	5/135	68/18805	0.073529412	10.24237473	6.492438543	0.000128391	0.022642637	0.020368768	MMP14/PIK3R1/ROCK2/IQSEC1/MAP4K4	5	overlap_155_DEGs
BP	GO:0060562 epithelial tube morphogenesis	10/135	337/18805	0.029673591	4.133421255	4.935641976	0.000162654	0.026772807	0.024084169	ST14/FZD3/CSF1/MMP14/WNT11/WNT2B/BCL2/HS2ST1/FKBPL/COL4A1	10	overlap_155_DEGs
BP	GO:1904019 epithelial cell apoptotic process	5/135	80/18805	0.0625	8.706018519	5.873324216	0.000276424	0.042644775	0.038362208	IL6/WNT11/GSN/ITGB3BP/BCL2	5	overlap_155_DEGs
BP	GO:0030574 collagen catabolic process	4/135	45/18805	0.088888889	12.381893	6.500162069	0.000301256	0.042644775	0.038362208	ADAMTS2/MMP16/MMP28	4	overlap_155_DEGs
BP	GO:1904037 positive regulation of epithelial cell apoptotic process	3/135	19/18805	0.157894737	21.99415205	7.785344346	0.000322304	0.042644775	0.038362208	IL6/WNT11/GSN	3	overlap_155_DEGs
BP	GO:0061333 renal tubule morphogenesis	5/135	83/18805	0.060240964	8.39134315	5.738602426	0.00032817	0.042644775	0.038362208	WNT11/WNT2B/BCL2/HS2ST1/COL4A1	5	overlap_155_DEGs
MF	GO:004222 metalloendopeptidase activity	6/137	110/18639	0.054545455	7.420968812	5.811945208	0.00016178	0.007237719	0.006399668	ADAMTS2/MMP16/ADAMTS20/MMP28/ECE2	6	overlap_155_DEGs
MF	GO:0106310 protein serine kinase activity	10/137	361/18639	0.027700831	3.76872839	4.571094686	0.000340892	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/MAPK4/STK16/HIPK2/MAPK13/MAP4K4	10	overlap_155_DEGs
MF	GO:0004674 protein serine/threonine kinase activity	11/137	433/18639	0.025404157	3.456263381	4.450022548	0.000360175	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/MAPK4/STK16/HIPK2/MAPK13/MAP4K4	11	overlap_155_DEGs
MF	GO:0004694 eukaryotic translation initiation factor 2alpha kinase activity	8/137	243/18639	0.032921811	4.479048391	4.697345502	0.000438556	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0004676 3-phosphoinositide-dependent protein kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0004711 ribosomal protein S6 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0035175 histone H3S10 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0035979 histone H2AXS139 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0044022 histone H3S28 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0044023 histone H4S1 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0044024 histone H2AS1 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0044025 histone H2BS14 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0072354 histone H3T3 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0072371 histone H2AS121 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0072518 Rho-dependent protein serine/threonine kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140823 histone H2BS36 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140855 histone H3S57 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140995 histone H2A kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140997 histone H4 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140998 histone H2B kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:1990244 histone H2AT120 kinase activity	8/137	245/18639	0.032653061	4.442484731	4.667319944	0.000463031	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0004677 DNA-dependent protein kinase activity	8/137	246/18639	0.032520325	4.42442585	4.652427711	0.000475679	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0140857 histone H3T45 kinase activity	8/137	246/18639	0.032520325	4.42442585	4.652427711	0.000475679	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0035402 histone H3T11 kinase activity	8/137	247/18639	0.032388664	4.406513195	4.637614785	0.000488605	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0035403 histone H3T6 kinase activity	8/137	247/18639	0.032388664	4.406513195	4.637614785	0.000488605	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0004679 AMP-activated protein kinase activity	8/137	248/18639	0.032258065	4.388744996	4.622880386	0.000501815	0.007237719	0.006399668	LIMK2/CSNK1A1L/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	8	overlap_155_DEGs
MF	GO:0043548 phosphatidylinositol 3-kinase binding	3/137	26/18639	0.115384615	15.69820326	6.453470558	0.000892375	0.0123941	0.010958994	PIK3R1/GSN/IRS2	3	overlap_155_DEGs
MF	GO:0141003 histone H2AX kinase activity	9/137	354/18639	0.025423729	3.458926141	4.019298229	0.001236057	0.016554337	0.014637519	LIMK2/CSNK1A1L/NTRK3/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	9	overlap_155_DEGs
MF	GO:0140996 histone H3 kinase activity	9/137	357/18639	0.025210084	3.429859535	3.988908033	0.001310382	0.016944599	0.014982593	LIMK2/CSNK1A1L/NTRK3/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	9	overlap_155_DEGs
MF	GO:0035173 histone kinase activity	9/137	360/18639	0.025	3.401277372	3.958840106	0.001388277	0.017353467	0.015344118	LIMK2/CSNK1A1L/NTRK3/CHEK1/NUAK1/ROCK2/STK16/HIPK2/MAP4K4	9	overlap_155_DEGs
MF	GO:0017147 Wnt-protein binding	3/137	31/18639	0.096774194	13.16623499	5.833615458	0.001501957	0.018168833	0.016065073	FZD3/FZD1/PTPRO	3	overlap_155_DEGs
MF	GO:0005125 cytokine activity	7/137	234/18639	0.02991453	4.069904548	4.06645049	0.001737977	0.020366916	0.018008641	IL6/CSF1/WNT11/WNT2B/IL17D/CCL27/TNFSF4	7	overlap_155_DEGs
MF	GO:0008237 metalloproteinase activity	6/137	184/18639	0.032608696	4.436448746	4.030995902	0.002411119	0.027399076	0.024226551	ADAMTS2/MMP14/MMP16/ADAMTS20/MMP28/ECE2	6	overlap_155_DEGs
MF	GO:0005109 frizzled binding	3/137	38/18639	0.078947368	10.74087591	5.172163699	0.00271514	0.029946401	0.026478923	FZD1/WNT11/WNT2B	3	overlap_155_DEGs
MF	GO:0004175 endopeptidase activity	9/137	405/18639	0.022222222	3.023357664	3.542499471	0.00307515	0.032948035	0.029132999	CFB/ST14/ADAMTS2/MMP14/MMP16/ADAMTS20/MMP28/ECE2/PREPL	9	overlap_155_DEGs
MF	GO:0035014 phosphatidylinositol 3-kinase regulator activity	2/137	12/18639	0.166666667	22.67518248	6.462975762	0.003372967	0.03513507	0.031066799	PIK3R1/IRS2	2	overlap_155_DEGs
MF	GO:0004705 JUN kinase activity	2/137	14/18639	0.142857143	19.4358707	5.937862404	0.004606065	0.045454588	0.040191426	MAPK4/MAPK13	2	overlap_155_DEGs
MF	GO:0042813 Wnt receptor activity	2/137	14/18639	0.142857143	19.4358707	5.937862404	0.004606065	0.045454588	0.040191426	FZD3/FZD1	2	overlap_155_DEGs

(B) FDR-controlled KEGG enrichment results for the 155 overlapping DEGs.

category	subcategory	ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count	source_gene_set
Human Diseases	Cancer: specific types	hsa05226	Gastric cancer	7/74	150/9400	0.046666667	5.927927928	5.419361102	0.000168537	0.013301418	0.010210696	122011/7976/8321/7481/5295/7482/596	7	overlap_155_DEGs
Human Diseases	Cancer: overview	hsa05205	Proteoglycans in cancer	8/74	204/9400	0.039215686	4.98145204	5.12113318	0.000189328	0.013301418	0.010210696	7976/8321/6237/7481/5295/9475/7482/5603	8	overlap_155_DEGs
Cellular Processes	Cell growth and death	hsa04218	Cellular senescence	7/74	157/9400	0.044585987	5.663625409	5.24899294	0.000223437	0.013301418	0.010210696	3569/890/6237/1111/5295/28996/5603	7	overlap_155_DEGs
Environmental Information Processing	Signal transduction	hsa04150	mTOR signaling pathway	7/74	158/9400	0.044303797	5.627779678	5.225492337	0.000232339	0.013301418	0.010210696	7976/6520/64900/8321/7481/5295/7482	7	overlap_155_DEGs
		hsa04519	Cadherin signaling	11/74	404/9400	0.027227723	3.458656676	4.499588799	0.000292886	0.013414163	0.010297243	122011/7976/8321/1674/1006/6237/7481/4542/9475/74	11	overlap_155_DEGs
Human Diseases	Cancer: specific types	hsa05225	Hepatocellular carcinoma	7/74	170/9400	0.041176471	5.230524642	4.958231708	0.000363337	0.013867356	0.010645132	122011/7976/8321/7481/5295/7482/2949	7	overlap_155_DEGs
Environmental Information Processing	Signal transduction	hsa04310	Wnt signaling pathway	7/74	178/9400	0.039325843	4.995444883	4.793707879	0.000479615	0.015690249	0.012044457	122011/7976/8321/7481/9475/7482/80319	7	overlap_155_DEGs
Cellular Processes	Cellular community - eukaryotes	hsa04550	Signaling pathways regulating pluripotency of stem cells	6/74	144/9400	0.041666667	5.292792793	4.624006952	0.000916667	0.024181133	0.018562396	7976/8321/7481/5295/7482/5603	6	overlap_155_DEGs
Human Diseases	Cancer: specific types	hsa05224	Breast cancer	6/74	148/9400	0.040540541	5.149744339	4.532557955	0.001057128	0.024181133	0.018562396	122011/7976/8321/7481/5295/7482	6	overlap_155_DEGs
Human Diseases	Infectious disease: viral	hsa05165	Human papillomavirus infection	9/74	333/9400	0.027027027	3.433162893	4.026896547	0.001145183	0.024181133	0.018562396	122011/7976/890/8321/7481/5295/7482/3381/1282	9	overlap_155_DEGs
Human Diseases	Endocrine and metabolic disease	hsa04933	AGE-RAGE signaling pathway in diabetic complications	5/74	101/9400	0.04950495	6.288466685	4.75971901	0.001161539	0.024181133	0.018562396	3569/5295/596/1282/5603	5	overlap_155_DEGs
Organismal Systems	Immune system	hsa04625	C-type lectin receptor signaling pathway	5/74	105/9400	0.047619048	6.048906049	4.634215452	0.001381973	0.024497501	0.018805252	3569/6237/5295/53342/5603	5	overlap_155_DEGs
Human Diseases	Cancer: specific types	hsa05217	Basal cell carcinoma	4/74	63/9400	0.063492063	8.065208065	5.011878458	0.001484212	0.024497501	0.018805252	7976/8321/7481/7482	4	overlap_155_DEGs
Human Diseases	Cardiovascular disease	hsa05417	Lipid and atherosclerosis	7/74	216/9400	0.032407407	4.116616617	4.127654128	0.001497664	0.024497501	0.018805252	3569/4973/5295/9475/6403/596/5603	7	overlap_155_DEGs
Environmental Information Processing	Signal transduction	hsa04010	MAPK signaling pathway	8/74	300/9400	0.026666667	3.387387387	3.743448006	0.002372456	0.034362069	0.026377685	1435/6237/9254/10235/5603/9448/285/3164	8	overlap_155_DEGs
Environmental Information Processing	Signal transduction	hsa04668	TNF signaling pathway	5/74	119/9400	0.042016807	5.337270043	4.241324841	0.002400843	0.034362069	0.026377685	3569/1435/4323/5295/5603	5	overlap_155_DEGs
Human Diseases	Neurodegenerative disease	hsa05010	Alzheimer disease	9/74	388/9400	0.023195876	2.946503204	3.487942954	0.003258003	0.043887221	0.03368957	3569/122011/7976/1435/8321/7481/5295/7482/8660	9	overlap_155_DEGs
Environmental Information Processing	Signal transduction	hsa04068	FoxO signaling pathway	5/74	133/9400	0.037593985	4.775452144	3.906017528	0.003881153	0.049376886	0.037903654	3569/5295/26260/8660/5603	5	overlap_155_DEGs

(C) FDR-controlled GO enrichment results for the 29 FDR-defined overlapping DEGs.

ONTOLOGY	ID	Descriptio	GeneRatio	BgRatio	RichFacte	FoldEnrichm	zScore	pvalue	p.adjust	qvalue	geneID	Count	source_gene_set
BP	GO:0030198	extracellul	5/27	339/18805	0.014749	10.27258822	6.532760603	0.000107674	0.023023516	0.016933625	ADAMTS2/M	5	strict_29_overlap_DEGs
BP	GO:0043062	extracellul	5/27	340/18805	0.014706	10.24237473	6.521247921	0.000109174	0.023023516	0.016933625	ADAMTS2/M	5	strict_29_overlap_DEGs
BP	GO:0045229	external er	5/27	341/18805	0.014663	10.21233844	6.509783035	0.00011069	0.023023516	0.016933625	ADAMTS2/M	5	strict_29_overlap_DEGs
BP	GO:0060047	heart contr	4/27	254/18805	0.015748	10.96821231	6.065028008	0.000446694	0.048318021	0.035537546	DES/GSN/ME	4	strict_29_overlap_DEGs
BP	GO:0003012	muscle sys	5/27	467/18805	0.010707	7.456975176	5.357891428	0.000474957	0.048318021	0.035537546	SLMAP/DES/	5	strict_29_overlap_DEGs
BP	GO:0003015	heart proct	4/27	263/18805	0.015209	10.59287424	5.940604953	0.000509359	0.048318021	0.035537546	DES/GSN/ME	4	strict_29_overlap_DEGs
BP	GO:0032963	collagen m	3/27	112/18805	0.026786	18.65575397	7.106211231	0.000542029	0.048318021	0.035537546	ADAMTS2/M	3	strict_29_overlap_DEGs
MF	GO:0004705	JUN kinas	2/26	14/18639	0.142857	102.4120879	14.18677694	0.000168523	0.011757873	0.009224151	MAPK4/MAP	2	strict_29_overlap_DEGs
MF	GO:0004707	MAP kina	2/26	16/18639	0.125	89.61057692	13.25253234	0.000221847	0.011757873	0.009224151	MAPK4/MAP	2	strict_29_overlap_DEGs

(D) STRING PPI hub proteins from the 155 overlapping DEGs, ranked by network degree.

gene	degree	logFC_ski	logFC_aorta	concordance
IL6	18	6.175009		4.254405042 same_direction
BCL2	13	-0.87035		-0.800452309 same_direction
CCNA2	9	-1.90713		2.254186737 opposite_direction
NPM1	8	-0.86637		-1.523085683 same_direction
PIK3R1	8	0.987652		-2.294336685 opposite_direction
CENPI	7	-0.9416		2.057244097 opposite_direction
MMP14	7	1.34731		2.717136765 same_direction
CDC25C	6	-1.40063		2.573087212 opposite_direction
CHEK1	6	-0.94257		3.005359611 opposite_direction
FZD1	6	-1.01345		-0.985203826 same_direction
FZD3	5	2.937878		-1.072124225 opposite_direction
RRAS	5	-1.08214		-0.917817608 same_direction
ZWINT	5	1.519435		4.662356483 same_direction
CSF1	4	-1.58509		1.390332193 opposite_direction
MAPK13	4	-0.87098		1.798195473 opposite_direction
NR4A1	4	-0.83052		1.518056226 opposite_direction
SELP	4	0.967416		-2.660312602 opposite_direction
CCL27	3	-1.1066		1.566317824 opposite_direction
COL4A1	3	-0.82088		0.887386392 opposite_direction
CXXC4	3	0.813472		-3.077651926 opposite_direction
GMNN	3	-0.97933		1.495458681 opposite_direction
IRS2	3	-0.81956		-0.967425211 same_direction
ITGB3BP	3	1.261104		1.246769676 same_direction
KLF6	3	-0.97414		1.807983135 opposite_direction
MYH11	3	-1.816		-2.966708606 same_direction
NTRK3	3	-0.81659		-1.195116231 same_direction
ROCK2	3	-1.22789		-0.817914607 same_direction
WNT11	3	1.097773		-2.527318521 opposite_direction
WNT2B	3	-1.27847		1.237282171 opposite_direction
ADAMTS2	2	2.371069		1.00125459 same_direction
ANGPT2	2	-0.81286		2.052382849 opposite_direction
BCL2L12	2	-1.46181		0.867793934 opposite_direction
CBX8	2	-1.16496		1.308148943 opposite_direction
CD300C	2	-0.97653		2.272145901 opposite_direction
CDS2	2	-0.81797		-0.970420878 same_direction
CEBPD	2	3.447004		1.334831102 same_direction
COQ2	2	-1.05513		1.054559031 opposite_direction
MAP4K4	2	-0.9106		0.847767932 opposite_direction
MEF2A	2	1.080543		-1.235881804 opposite_direction
OLR1	2	-1.63037		3.65272434 opposite_direction
PTPRO	2	-0.84268		-1.542118523 same_direction
RASGRP2	2	1.287536		-1.785102728 opposite_direction
SLMAP	2	1.806038		-2.361701057 opposite_direction
SMURF2	2	0.846052		-1.58851058 opposite_direction
STRN4	2	-0.97122		0.814887353 opposite_direction
TNRC6A	2	-1.41757		-0.986367442 same_direction
UGDH	2	-0.94086		1.218737963 opposite_direction
ADH5	1	-0.96792		-1.016678548 same_direction
ARID4A	1	1.056634		-0.955657656 opposite_direction
CACNA2D2	1	-1.17754		-1.806528781 same_direction
CFB	1	2.534775		0.847606608 same_direction
CLEC10A	1	-1.03981		-2.320601983 same_direction
CRBN	1	1.050076		-0.803141867 opposite_direction
DES	1	-1.13279		-3.57319701 same_direction
FBXO25	1	0.839479		-1.627649539 opposite_direction
FBXO9	1	-0.96056		-2.645400584 same_direction
GGH	1	1.166852		1.368167226 same_direction
GRP65	1	-0.95286		0.88313799 opposite_direction
GSN	1	-0.83969		-1.361295689 same_direction
GSTM5	1	-1.04421		-2.193662332 same_direction
ICA1L	1	0.80589		-1.510538742 opposite_direction

IFI27	1	1.040363	-2.026290808	opposite_direction
IL17D	1	-1.22523	-1.563079808	same_direction
IQSEC1	1	1.772734	-0.880573729	opposite_direction
JAM2	1	1.017227	-1.020631684	opposite_direction
KREMEN1	1	-0.9114	-1.508927059	same_direction
LIMK2	1	4.618528	1.513104741	same_direction
LPIN3	1	-1.21063	-1.368597872	same_direction
MAF	1	-0.86459	-0.866153324	same_direction
MALL	1	1.271487	1.210835369	same_direction
MMP16	1	-1.04235	-2.446835517	same_direction
MPP2	1	-1.26878	-1.337297672	same_direction
MRPS12	1	-1.08597	0.824930454	opposite_direction
PHF1	1	-1.36209	-0.812982413	same_direction
PLOD3	1	1.155249	0.822633691	same_direction
RNASE2	1	-1.19151	3.809748592	opposite_direction
RPS15	1	-1.03449	1.233686229	opposite_direction
SLC3A2	1	-1.84181	0.896922628	opposite_direction
SPO11	1	-1.35856	2.572697689	opposite_direction
TNFSF4	1	-0.92603	0.927980751	opposite_direction
TOM1L2	1	1.796066	-0.940989102	opposite_direction
TPD52	1	-1.16259	-1.212109966	same_direction