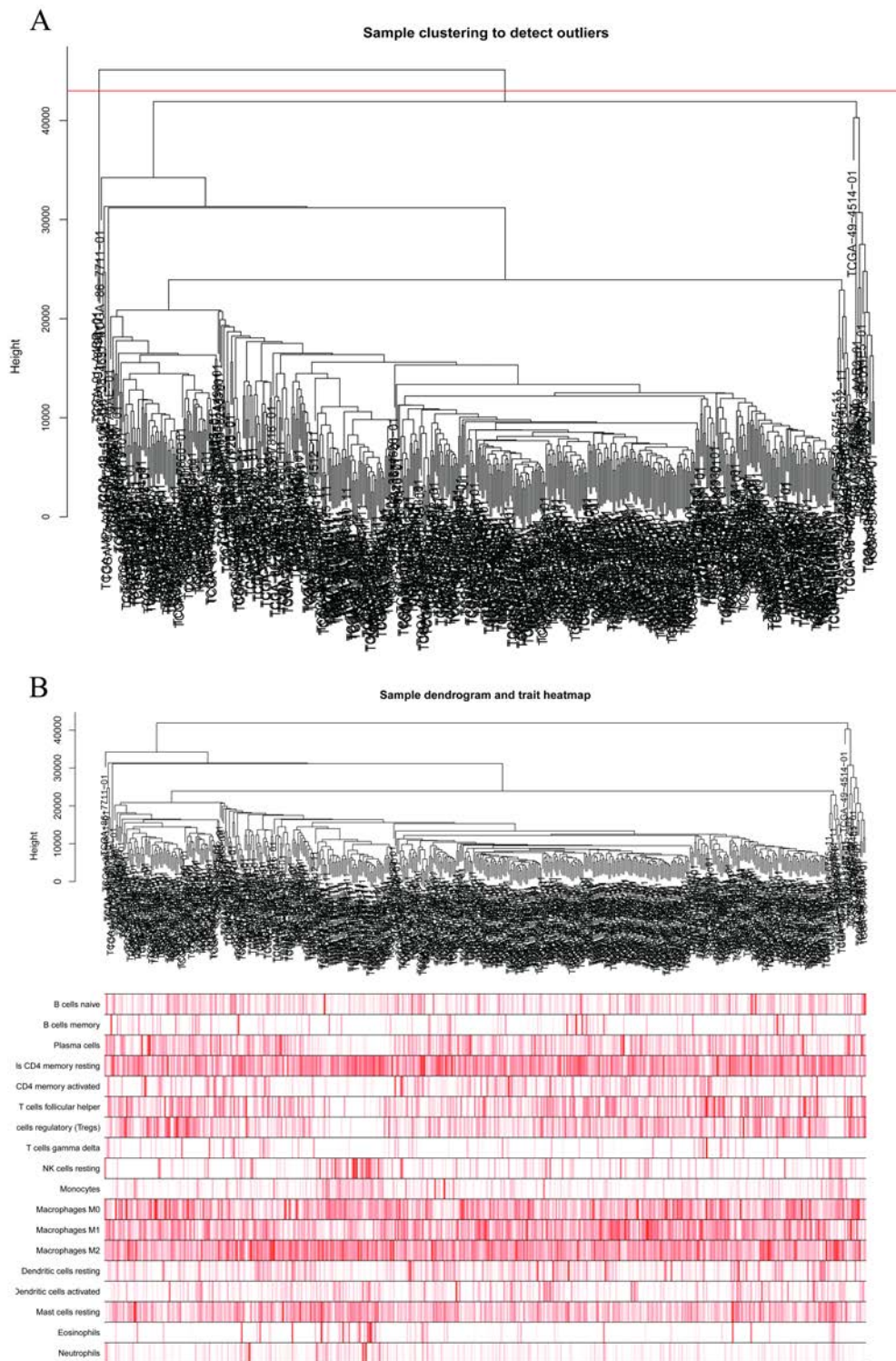
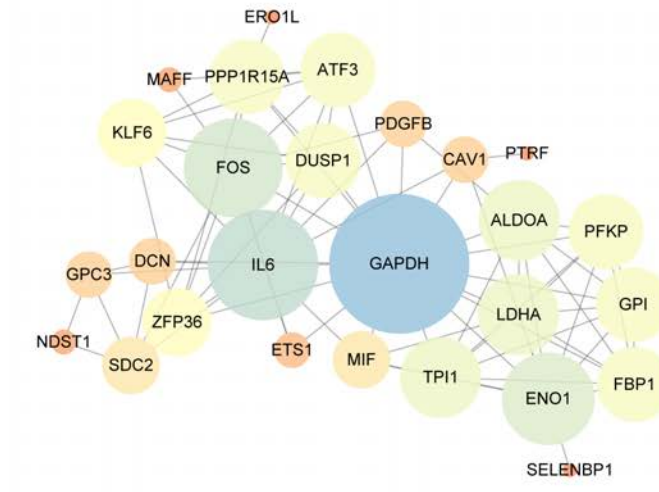


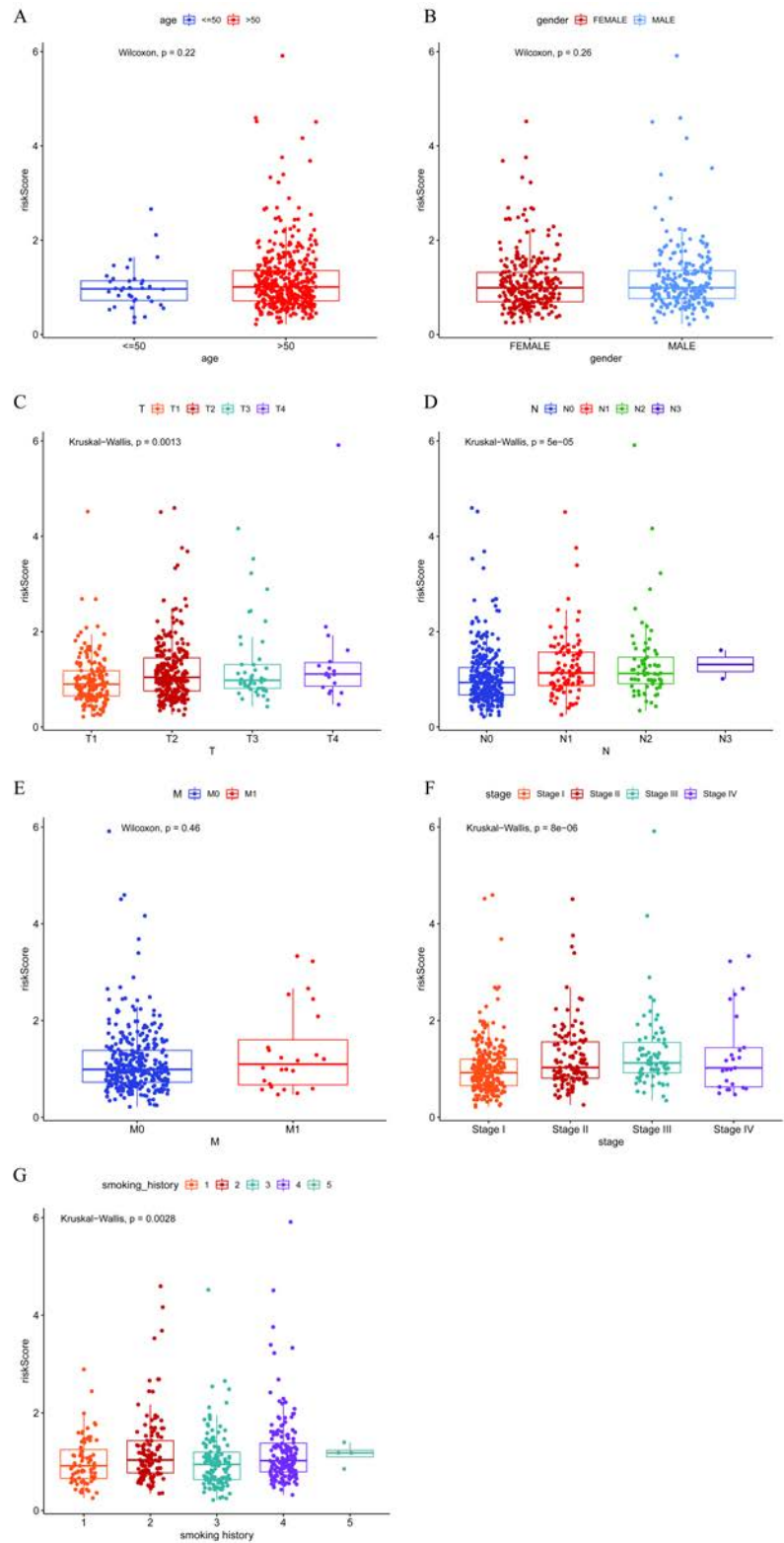
Supplementary Material



Supplementary Figure 1. Detection of abnormal samples. (A). Clustering dendrogram of 496 TCGA samples. (B). Clustering dendrogram of samples based on their Euclidean distance. The clustering was based on the TCGA-LUAD RNA-seq data. TCGA: the Cancer Genome Atlas; LUAD: lung adenocarcinoma.



Supplementary Figure 2. PPI network of the 30 H&IIRGs. The PPI network of H&IIRGs was constructed using Cytoscape. The larger the circle, the more important the gene is in the PPI network. PPI: protein-protein interaction; H&IIRGs: hypoxia- and infiltrating immune cell-related genes.



Supplementary Figure 3. Box plots showing the relationships between risk scores and clinical characteristics.

Supplementary Table 1. List of 200 hypoxia-related genes obtained from the MSigDB database

ACKR3	BNIP3L	CSRP2	FAM162A	HDLBP	KDM3A	NDRG1	PGM1	S100A4	TES
ADM	BRS3	CXCR4	FBP1	HEXA	KIF5A	NDST1	PGM2	SAP30	TGFB3
ADORA2B	BTG1	DCN	FOS	HK1	KLF6	NDST2	PHKG1	SCARB1	TGFBI
AK4	CA12	DDIT3	FOSL2	HK2	KLF7	NEDD4L	PIM1	SDC2	TGM2
AKAP12	CASP6	DDIT4	FOXO3	HMOX1	KLHL24	NFIL3	PKLR	SDC3	TIPARP
ALDOA	CAV1	DPYSL4	GAA	HOXB9	LALBA	NOCT	PKP1	SDC4	TKTL1
ALDOB	CAVIN1	DTNA	GALK1	HS3ST1	LARGE1	NR3C1	PLAC8	SELENBP1	TMEM45A
ALDOC	CAVIN3	DUSP1	GAPDH	HSPA5	LDHA	P4HA1	PLAUR	SERPINE1	TNFAIP3
AMPD3	CCN1	EDN2	GAPDHS	IDS	LDHC	P4HA2	PLIN2	SIAH2	TPBG
ANGPTL4	CCN2	EFNA1	GBE1	IER3	LOX	PAM	PNRC1	SLC25A1	TPD52
ANKZF1	CCN5	EFNA3	GCK	IGFBP1	LXN	PCK1	PPARGC1A	SLC2A1	TPI1
ANXA2	CCNG2	EGFR	GCNT2	IGFBP3	MAFF	PDGFB	PPFIA4	SLC2A3	TPST2
ATF3	CDKN1A	ENO1	GLRX	IL6	MAP3K1	PDK1	PPP1R15A	SLC2A5	UGP2
ATP7A	CDKN1B	ENO2	GPC1	ILVBL	MIF	PDK3	PPP1R3C	SLC37A4	VEGFA
B3GALT6	CDKN1C	ENO3	GPC3	INHA	MT1E	PFKFB3	PRDX5	SLC6A6	VHL
B4GALNT2	CHST2	ERO1A	GPC4	IRS2	MT2A	PFKL	PRKCA	SRPX	VLDLR
BCAN	CHST3	ERRFI1	GPI	ISG20	MXI1	PFKP	PYGM	STBD1	WSB1
BCL2	CITED2	ETS1	GRHPR	JMJD6	MYH9	PGAM2	RBPJ	STC1	XPNPEP1
BGN	COL5A1	EXT1	GYS1	JUN	NAGK	PGF	RORA	STC2	ZFP36
BHLHE40	CP	F3	HAS1	KDELR3	NCAN	PGK1	RRAGD	SULT2B1	ZNF292

Supplementary Table 2. Risk scores for tumor samples in the training set

id	futime	fustat	FBP1	LDHA	MAFF	PDGFB	GPC3	riskScore	risk
TCGA-50-	3.528767	1	4.876352	7.336842	2.089679	2.693871	0.51802	1.463932	high
TCGA-69-	0.353425	0	4.782257	7.562368	3.024292	2.369239	4.211943	1.356427	high
TCGA-73-	3.257534	0	6.800206	6.003484	2.396301	3.361	3.953668	0.544844	low
TCGA-78-	1.715068	1	5.777301	7.565209	2.921827	2.952801	2.506125	1.50019	high
TCGA-95-	1.515068	0	5.938112	7.387048	2.3767	3.235266	2.383434	1.294425	high
TCGA-78-	3.328767	1	6.365983	6.755566	2.348318	2.052785	1.308449	0.783937	low
TCGA-MP	0.841096	1	5.851654	6.170017	3.047475	2.765337	4.084634	0.674247	low
TCGA-55-	0.512329	1	4.338993	7.611766	2.826457	2.319918	2.405394	1.642491	high
TCGA-44-	1.276712	0	6.493556	7.648423	2.212169	1.834624	2.079115	1.012167	high
TCGA-97-	1.479452	0	5.962941	6.654964	3.449632	3.138677	3.366203	1.030187	high
TCGA-67-	1.169863	0	5.58228	7.426379	2.369446	2.111454	2.565137	1.089542	high
TCGA-50-	0.920548	1	7.287102	6.843853	2.321151	2.546231	2.62632	0.701467	low
TCGA-73-	1.947945	1	5.53714	7.005483	2.500774	3.115248	3.958608	1.006102	high
TCGA-38-	2.939726	1	3.322861	6.891799	2.185399	3.792317	3.514695	1.463652	high
TCGA-78-	3.279452	1	6.320074	6.216527	4.175327	2.752709	2.58976	0.915779	low
TCGA-J2-	1.506849	1	5.325744	6.915489	2.946523	3.111456	3.324474	1.147983	high
TCGA-44-	5.106849	0	5.667546	6.823854	2.559117	3.507559	4.843292	0.921402	low
TCGA-38-	0.364384	0	6.202171	6.981085	3.581192	3.750969	3.746715	1.298926	high
TCGA-50-	2.128767	1	4.568198	7.571607	2.852658	3.03059	1.331865	1.98173	high
TCGA-44-	1.931507	0	6.686418	6.914122	2.511573	2.014196	2.758365	0.729429	low
TCGA-95-	0.230137	0	6.812571	7.823423	2.109828	2.188859	1.281837	1.179775	high
TCGA-44-	3.915068	0	7.270885	7.351618	2.382765	2.646971	2.672322	0.913781	low
TCGA-50-	5.013699	1	5.361662	6.320851	2.78477	3.029805	2.294143	0.903754	low
TCGA-75-	3.652055	0	5.755454	8.248012	2.564142	2.030779	5.8643	1.196431	high
TCGA-86-	2.586301	0	5.345802	7.03103	2.195638	1.862938	1.685274	0.931116	low
TCGA-05-	0.331507	1	5.312753	8.099419	3.310187	3.239823	2.15834	2.41794	high
TCGA-4B-	0.821918	1	7.142268	6.975853	4.065044	1.863911	0.910863	1.091599	high
TCGA-86-	3.169863	0	4.671402	7.193505	3.472537	2.288876	5.515762	1.120052	high
TCGA-91-	1.652055	0	6.404043	7.21704	1.901926	1.895838	2.377093	0.779521	low
TCGA-78-	10.79452	0	5.557829	5.926994	1.847386	3.759903	2.250565	0.705287	low
TCGA-78-	2.6	1	6.202418	6.197923	1.875668	2.157657	1.469169	0.568818	low
TCGA-49-	1.336986	1	4.917358	7.585629	2.731818	3.702599	2.762373	1.873499	high
TCGA-05-	4.172603	0	5.918084	6.749955	1.594324	2.328876	3.259921	0.640711	low
TCGA-64-	6.816438	0	4.992802	7.295534	2.016682	3.698679	3.349567	1.335008	high
TCGA-69-	0.553425	0	6.205446	7.359248	1.580792	1.536894	2.460112	0.741967	low
TCGA-05-	1.671233	0	6.521937	6.405059	2.775615	2.485411	3.266837	0.655388	low
TCGA-55-	5.854795	0	6.143663	7.296302	1.813672	2.651432	2.687141	0.933586	low
TCGA-05-	1.835616	0	5.418646	7.300952	2.158697	1.228197	1.273276	0.945048	low
TCGA-55-	1.931507	0	5.791547	7.055285	2.020928	2.999262	5.302456	0.785041	low
TCGA-97-	0.049315	1	6.091187	6.581061	3.14872	1.358086	4.314575	0.594676	low
TCGA-75-	7.09589	0	6.459245	6.298282	3.068148	2.417536	3.376603	0.652541	low
TCGA-05-	0.750685	1	4.00243	9.434903	2.836641	1.843649	0.809694	4.164509	high
TCGA-44-	3.175342	0	6.347094	6.642516	1.878714	1.871768	3.473839	0.544139	low
TCGA-80-	7.758904	0	6.101585	7.211035	3.243906	1.828622	4.681956	0.860818	low
TCGA-55-	2.082192	1	5.63396	7.376013	4.65726	3.827105	2.069048	2.458331	high
TCGA-99-	0.120548	0	4.728166	6.870986	2.926116	2.909554	3.20931	1.183664	high
TCGA-55-	1.663014	1	5.475818	5.203917	3.735863	2.191994	3.368806	0.496758	low
TCGA-97-	1.709589	0	8.051662	5.456613	2.644361	3.067068	3.760612	0.356844	low
TCGA-50-	0.060274	1	5.131546	6.465677	3.190357	3.267174	5.367618	0.872867	low
TCGA-67-	1.569863	0	5.355627	7.346572	2.407681	2.1222	3.997488	0.969183	low
TCGA-86-	1.657534	0	5.139007	6.576879	1.768458	2.538717	4.677015	0.632771	low
TCGA-L9-	1.819178	0	6.762633	7.176765	3.289676	3.461859	2.107821	1.343568	high
TCGA-05-	2	0	6.372305	6.168722	3.481141	2.231744	3.695113	0.634148	low
TCGA-91-	0.120548	0	5.129187	6.726935	1.824143	3.219854	4.608092	0.791243	low

TCGA-91-	3.446575	1	4.464259	6.89516	1.684549	2.918275	5.081593	0.826727	low
TCGA-44-	1.369863	1	3.679349	8.46539	3.281704	2.686499	0.351988	3.757557	high
TCGA-05-	2.084932	0	5.589521	6.853248	2.185867	2.776384	5.316367	0.727182	low
TCGA-05-	3.920548	0	6.52091	7.769334	2.927041	3.0258	1.708244	1.611034	high
TCGA-L4-	1.583562	0	5.748732	6.172218	2.230406	2.500931	1.286519	0.700737	low
TCGA-53-	2.857534	1	4.062342	7.612219	3.127387	3.599778	0.927006	2.660698	high
TCGA-55-	3.542466	1	5.754532	6.652428	1.863771	2.030877	3.86519	0.592247	low
TCGA-93-	1.583562	0	6.25451	5.79055	2.889346	4.07995	5.990526	0.571838	low
TCGA-44-	3.627397	0	5.574543	6.98932	2.609821	2.319562	3.139338	0.929113	low
TCGA-55-	3.227397	0	4.325734	7.054744	3.691861	2.59285	3.73655	1.427818	high
TCGA-50-	4.038356	0	5.786677	7.399424	2.193846	2.613258	2.568774	1.114822	high
TCGA-49-	1.854795	0	5.656098	6.886922	2.201529	2.411973	0.451572	1.034917	high
TCGA-78-	2.167123	0	6.512467	5.690917	2.874862	1.587134	1.656549	0.462468	low
TCGA-55-	1.786301	0	3.334299	7.658972	3.943577	5.063962	1.536564	4.519451	high
TCGA-78-	8.682192	1	6.052557	6.042728	1.779269	4.269159	4.414816	0.628685	low
TCGA-55-	0.649315	1	6.335062	6.954669	2.439282	3.756895	2.340635	1.130529	high
TCGA-86-	2.569863	0	6.71162	6.350115	2.830873	2.30502	3.750485	0.581984	low
TCGA-44-	2.838356	0	6.321784	7.755533	2.229741	2.708502	4.262058	1.080095	high
TCGA-75-	4.153425	1	5.982295	8.161973	2.30465	2.75808	2.775331	1.59182	high
TCGA-44-	2.334247	0	4.172002	5.773093	1.23776	1.238721	3.868226	0.373204	low
TCGA-44-	3.09589	0	5.897617	7.607121	2.972355	2.574168	1.540704	1.529355	high
TCGA-50-	3.082192	0	5.963412	6.39044	3.009475	2.666982	4.43507	0.693462	low
TCGA-49-	3.367123	1	4.81864	6.923667	2.567869	2.863669	0.953807	1.339016	high
TCGA-49-	2.342466	1	5.322194	6.91868	2.404899	3.14848	3.400614	1.032644	high
TCGA-44-	1.80274	0	4.844608	6.541975	2.281581	3.270367	3.676148	0.9078	low
TCGA-L9-	0.158904	1	3.818759	7.933744	3.602912	2.921615	0.348343	3.225203	high
TCGA-69-	1.167123	0	5.309468	7.858916	2.761304	2.328049	2.629174	1.553053	high
TCGA-L9-	1.547945	0	5.936056	4.733354	2.365119	2.219569	4.598468	0.257431	low
TCGA-97-	1.493151	0	6.676909	6.100824	2.430994	2.602944	5.192522	0.451456	low
TCGA-86-	1.136986	0	5.962794	6.409896	2.579289	3.839623	5.096784	0.766496	low
TCGA-55-	2.726027	1	5.403044	6.589871	2.561016	3.30224	3.086113	0.959128	low
TCGA-NJ-	0.010959	1	7.694432	5.971472	1.575532	1.477937	1.302041	0.345149	low
TCGA-44-	2.084932	1	5.081613	7.463844	2.742729	3.618391	1.504221	1.899077	high
TCGA-55-	1.027397	1	5.224956	7.979015	3.280101	3.202272	3.232615	2.084628	high
TCGA-55-	1.928767	0	8.062231	6.506414	3.635186	2.457789	1.561347	0.753128	low
TCGA-62-	6.024658	0	5.74612	7.404048	1.827097	2.025847	0.89977	1.071053	high
TCGA-55-	1.726027	0	5.242945	7.268451	2.23514	2.957969	2.524964	1.230256	high
TCGA-71-	0.70137	0	8.628896	6.277428	2.387206	2.307074	0.868061	0.500925	low
TCGA-55-	6.709589	0	5.054499	7.261602	2.240058	2.916693	1.81821	1.328881	high
TCGA-78-	5.408219	0	5.086231	7.319707	2.444897	3.024237	3.261553	1.278286	high
TCGA-55-	3.835616	0	5.629557	7.288887	2.325459	2.609263	3.463293	1.02983	high
TCGA-50-	6.556164	1	7.337901	7.59128	2.56983	3.037995	1.204463	1.286313	high
TCGA-95-	1.783562	0	6.200897	7.349212	3.367884	3.578191	2.365541	1.603186	high
TCGA-64-	2.367123	0	4.146298	7.043579	3.669265	2.953988	6.006579	1.283909	high
TCGA-44-	0.961644	0	6.196662	7.102412	2.454415	2.593107	2.914728	0.934262	low
TCGA-97-	1.191781	0	6.244225	6.017889	2.54678	3.812892	3.922459	0.671752	low
TCGA-78-	3.208219	1	2.17886	6.808859	0.633503	1.578852	7.740296	0.544115	low
TCGA-49-	1.172603	1	5.638862	7.649667	2.960307	2.940299	2.747434	1.566495	high
TCGA-97-	1.715068	0	6.89178	5.23493	2.269842	1.952652	4.951976	0.255144	low
TCGA-MP	0.928767	1	5.420642	6.896154	3.092727	2.721111	3.225784	1.0783	high
TCGA-73-	0.358904	0	3.712364	7.908257	3.447017	4.042159	2.253882	3.332659	high
TCGA-55-	0.076712	0	6.027373	8.003294	2.499296	3.744592	0.981494	2.17074	high
TCGA-69-	0.630137	0	4.656863	7.07407	2.50168	2.937605	3.422308	1.190527	high
TCGA-50-	3.383562	1	5.755108	6.525443	2.829039	2.308275	2.881961	0.779605	low
TCGA-05-	2.084932	0	6.29874	6.574647	2.518367	3.297814	4.220163	0.753051	low
TCGA-49-	6.350685	1	6.449108	6.641371	2.338973	1.764274	2.368867	0.632459	low

TCGA-78-	9.208219	1	6.365684	5.977983	3.759812	4.05613	4.406908	0.832749	low
TCGA-95-	2.273973	0	6.345995	6.087156	2.534589	2.700909	3.668466	0.558057	low
TCGA-MP	2.60274	1	4.829001	7.171124	3.295015	2.612233	1.19032	1.615746	high
TCGA-55-	0.665753	1	6.319528	6.416121	3.734352	3.354569	4.037131	0.915396	low
TCGA-69-	1.134247	0	6.257683	6.827837	2.002642	2.270073	2.983872	0.694791	low
TCGA-44-	1.120548	1	5.597986	6.66438	1.852355	2.505263	5.608124	0.575378	low
TCGA-49-	2.736986	1	3.127944	7.825465	1.568766	1.193554	0.514008	1.572423	high
TCGA-78-	0.79726	1	4.956222	6.761127	3.649904	2.774253	2.476765	1.305288	high
TCGA-49-	1.854795	1	5.668335	7.103395	3.144106	2.662654	3.278254	1.13811	high
TCGA-62-	1.627397	1	5.484218	6.545525	2.444312	2.649404	1.977618	0.875807	low
TCGA-49-	0.969863	0	6.330128	7.742238	2.275646	3.8015	1.879395	1.650687	high
TCGA-44-	2.810959	1	6.037201	7.518667	1.959488	2.333088	4.102325	0.898838	low
TCGA-69-	1.126027	0	4.850989	6.067405	3.521625	2.927129	3.821117	0.862495	low
TCGA-93-	1.454795	0	5.499271	6.735801	3.553813	2.708378	2.335355	1.169565	high
TCGA-86-	0.065753	0	5.427912	7.968944	3.060328	2.589153	3.396367	1.682578	high
TCGA-MP	2.454795	1	5.615457	6.894466	2.593645	1.631739	1.734669	0.866486	low
TCGA-55-	1.191781	0	6.419912	7.819611	2.587248	2.815827	3.905955	1.241291	high
TCGA-49-	5.186301	0	5.612765	6.127657	2.542877	3.079432	0.438834	0.899582	low
TCGA-38-	3.717808	1	5.910349	6.993853	2.11376	2.399363	1.224164	0.961542	low
TCGA-62-	4.528767	1	6.2699	6.288533	3.259295	2.943534	3.106994	0.788391	low
TCGA-99-	1.79726	1	5.015731	8.50783	3.185033	2.034537	1.620171	2.444028	high
TCGA-55-	5.778082	0	5.980251	7.946208	2.924118	3.107751	5.313024	1.408893	high
TCGA-91-	1.189041	1	6.7165	5.80294	2.306423	2.686789	3.905125	0.433442	low
TCGA-64-	3.084932	0	5.477544	6.772864	2.386423	1.305844	2.815985	0.684726	low
TCGA-86-	2.731507	0	6.63435	6.822884	2.828434	2.343723	2.932113	0.790196	low
TCGA-55-	0.131507	0	6.537254	6.276217	2.964027	2.18364	3.284088	0.601767	low
TCGA-86-	0.339726	1	5.573697	7.388177	2.892587	3.19184	4.187746	1.285565	high
TCGA-73-	1.279452	0	5.388729	7.262398	3.032162	2.519277	2.73555	1.268631	high
TCGA-55-	2.726027	1	5.60453	7.610553	2.571083	2.456558	1.574296	1.435488	high
TCGA-67-	1.156164	0	5.869784	6.503506	2.117094	1.761182	5.753323	0.461392	low
TCGA-44-	1.994521	0	5.648399	5.710361	4.272279	1.835416	2.759558	0.668465	low
TCGA-49-	2.479452	1	7.847109	6.921058	2.370397	2.263279	2.173618	0.665544	low
TCGA-64-	7.331507	0	4.45927	7.384523	3.338354	2.488674	2.572483	1.643138	high
TCGA-97-	1.367123	0	7.147705	7.594602	3.182357	2.728127	3.830509	1.123894	high
TCGA-78-	19.34795	0	5.689659	6.892452	2.219015	2.710334	2.546044	0.919238	low
TCGA-95-	1.306849	0	6.36231	6.690715	3.284305	2.438355	2.63613	0.885562	low
TCGA-44-	2.70411	1	6.4075	7.557028	2.260149	3.713742	3.094922	1.323397	high
TCGA-55-	1.282192	1	5.749684	6.682361	1.022962	2.925582	3.774666	0.611533	low
TCGA-49-	2.408219	1	5.073644	6.910971	2.882498	2.733442	1.002561	1.326503	high
TCGA-55-	0.939726	1	5.299613	6.358099	3.16503	3.018144	1.952586	1.028481	high
TCGA-86-	1.216438	1	5.736751	6.94779	2.708781	2.054817	1.365879	1.003003	high
TCGA-50-	1.309589	1	7.527061	7.09142	2.741967	2.625006	2.404815	0.855629	low
TCGA-05-	0.668493	1	5.764759	7.740291	2.268199	2.571053	3.617338	1.203621	high
TCGA-50-	3.065753	0	7.019249	6.772177	3.410939	3.811654	2.492688	1.143041	high
TCGA-NJ-	1.690411	0	6.445401	7.021345	3.101047	1.751887	1.796148	0.920094	low
TCGA-49-	2.380822	1	5.908954	8.109727	2.353357	2.579892	2.380352	1.583091	high
TCGA-64-	2.372603	0	6.514419	7.879549	3.038484	3.362534	2.555194	1.725609	high
TCGA-86-	0.380822	0	5.37349	5.820064	2.985416	2.958017	2.611296	0.715737	low
TCGA-49-	1.430137	0	6.650542	7.29722	2.411475	2.653413	2.679034	0.980369	low
TCGA-38-	0.969863	1	3.798576	8.043163	2.930347	2.698703	2.870217	2.290453	high
TCGA-38-	10.06575	0	6.678997	6.244698	2.899192	4.329951	4.558847	0.789503	low
TCGA-44-	2.315068	0	3.17866	6.266767	1.635252	2.484152	3.906801	0.747451	low
TCGA-55-	2.608219	1	6.434431	7.537534	2.385129	2.527692	2.83879	1.080695	high
TCGA-55-	1.49589	0	5.386033	5.86804	2.706268	3.533251	4.420804	0.663443	low
TCGA-69-	1.117808	0	5.690775	6.547177	2.878698	1.774782	2.254993	0.76139	low
TCGA-44-	1.136986	0	5.060409	6.044419	2.804074	3.642193	1.830286	0.980862	low

TCGA-05-	2.50137	0	5.928434	6.005114	2.543455	3.022255	4.079639	0.588327	low
TCGA-MN	0.230137	0	6.357876	6.93599	2.460916	2.939139	2.411106	0.947309	low
TCGA-99-	3.063014	0	7.005667	6.784418	2.9793	3.194968	3.155157	0.882292	low
TCGA-75-	6.487671	0	5.381934	6.943142	3.127205	2.442022	3.591458	1.022688	high
TCGA-55-	5.657534	0	6.049212	6.171057	2.317216	3.257978	1.569915	0.77499	low
TCGA-55-	2.849315	0	5.256939	7.028248	2.374517	1.958183	2.118015	0.958825	low
TCGA-80-	7.109589	0	7.374186	7.570502	2.381953	2.097689	2.280489	0.922597	low
TCGA-91-	0.884932	0	5.799592	6.55083	3.200123	3.154523	3.034652	0.986799	low
TCGA-69-	0.509589	0	5.31316	7.20992	2.812718	2.992753	1.307884	1.487878	high
TCGA-91-	0.09589	0	6.802404	7.104465	3.907311	2.062904	2.110515	1.106096	high
TCGA-MP	2.030137	0	6.146829	6.111212	2.809106	2.021723	3.025849	0.566003	low
TCGA-44-	1.572603	1	5.168835	7.765044	2.938573	3.349654	4.218836	1.683084	high
TCGA-44-	3.506849	0	5.802033	7.43944	2.294195	2.716895	1.080603	1.340664	high
TCGA-73-	4.194521	1	6.412675	6.724548	2.50802	1.902411	4.589274	0.580844	low
TCGA-55-	1.205479	0	4.068	7.074542	2.315907	3.901113	1.652788	1.76046	high
TCGA-86-	2.29863	0	6.554367	6.345018	1.850018	3.147016	3.118177	0.60909	low
TCGA-95-	1.30411	0	1.841754	6.228393	2.157161	2.55319	1.304524	1.251324	high
TCGA-95-	1.378082	1	3.910355	7.019822	1.05679	2.505425	1.906049	1.009936	high
TCGA-50-	1.709589	1	4.674579	8.167385	2.361026	2.714555	1.774133	2.102437	high
TCGA-J2-	2.706849	0	5.713903	6.527001	3.49411	2.381704	3.683216	0.849778	low
TCGA-86-	2.936986	0	4.32645	7.582093	2.50689	2.588031	2.537549	1.587914	high
TCGA-78-	0.490411	1	5.996218	6.864884	2.274499	1.676489	0.716596	0.835745	low
TCGA-05-	2.416438	0	4.851128	6.791533	2.992021	2.440238	3.111397	1.043277	high
TCGA-91-	0.849315	0	5.010029	7.498169	2.251266	1.983443	4.002545	1.028815	high
TCGA-97-	1.509589	0	6.033228	7.771007	3.016923	2.706366	1.775641	1.642173	high
TCGA-86-	0.052055	1	5.616564	7.802317	2.968915	2.719468	1.562053	1.78852	high
TCGA-50-	1.013699	1	6.880869	7.269473	1.739881	2.322398	0.705378	0.9071	low
TCGA-86-	1.712329	1	5.307378	7.151272	1.596615	1.288921	2.135828	0.752768	low
TCGA-86-	1.030137	1	6.067705	7.323069	2.994863	4.025598	3.335069	1.507531	high
TCGA-55-	1.638356	1	5.884013	7.753534	3.645214	3.252619	2.684088	1.947927	high
TCGA-55-	1.471233	0	5.660952	7.376686	1.454994	2.601872	2.138143	1.002527	high
TCGA-55-	1.145205	0	6.123248	6.496016	2.488373	2.688243	3.10457	0.721198	low
TCGA-93-	0.509589	0	4.63715	7.040698	3.232297	2.738254	1.97817	1.480534	high
TCGA-97-	5.123288	0	7.413808	5.918441	2.877655	2.901035	4.780283	0.449208	low
TCGA-55-	1.641096	0	6.51819	8.45663	2.27043	2.801428	2.33792	1.755692	high
TCGA-05-	3.084932	0	5.315499	7.819735	3.226824	1.99181	4.499273	1.333131	high
TCGA-86-	1.158904	0	5.073487	6.608469	1.774137	3.120849	3.230901	0.824862	low
TCGA-62-	1.216438	1	4.606492	7.518659	3.428934	3.158703	1.465609	2.190095	high
TCGA-55-	2.167123	0	6.402278	5.458253	2.542268	3.076401	4.175673	0.428464	low
TCGA-83-	2.257534	0	4.006784	6.590359	2.571743	2.770838	1.3731	1.222982	high
TCGA-05-	1	0	6.785655	6.605614	2.109526	1.822332	1.354046	0.624763	low
TCGA-50-	5.956164	1	6.407593	7.247253	2.97697	3.046914	2.913393	1.17824	high
TCGA-44-	2.213699	1	3.710064	6.80387	1.91509	2.243118	2.677415	0.993167	high
TCGA-91-	1.142466	0	4.92891	6.380117	2.698006	2.112259	3.175468	0.749759	low
TCGA-55-	0.323288	1	3.515277	7.96116	2.474833	5.205538	3.089802	3.393505	high
TCGA-55-	1.715068	0	5.919669	7.455272	2.712382	3.187627	2.012881	1.464769	high
TCGA-93-	1.871233	0	6.609214	6.578334	1.88666	2.384916	2.099539	0.635143	low
TCGA-MP	3.465753	1	5.524527	6.382082	3.059447	4.897413	3.367195	1.270941	high
TCGA-49-	0.712329	1	3.773466	7.750503	2.319741	5.138213	0.548754	3.528888	high
TCGA-55-	1.643836	0	5.189783	7.255941	3.307551	2.61841	1.963378	1.498808	high
TCGA-97-	5.383562	0	5.76147	5.83255	2.912239	1.568504	4.289882	0.440374	low
TCGA-05-	1.246575	0	5.740568	6.705368	2.784201	3.562882	2.327435	1.132965	high
TCGA-62-	4.726027	1	7.418257	6.400061	2.65582	1.369829	0.785728	0.555672	low
TCGA-49-	1.054795	1	5.393751	7.012978	3.906898	3.287406	3.896717	1.421953	high
TCGA-62-	1.134247	1	6.471808	7.77644	1.898722	2.526914	2.402705	1.129385	high
TCGA-97-	1.723288	0	5.22842	6.453662	2.583548	3.471673	5.585174	0.774917	low

TCGA-78-	6.465753	0	6.538195	7.014167	2.533993	3.276797	3.604849	0.937872	low
TCGA-MP	0.920548	1	4.144047	7.631643	2.88664	3.018473	1.096888	2.218611	high
TCGA-55-	1.49863	0	5.859045	7.832796	2.22014	2.016584	1.468365	1.320535	high
TCGA-91-	0.613699	0	4.940869	7.142398	3.382613	2.543379	3.422848	1.301124	high
TCGA-86-	2.027397	0	5.404316	6.102023	2.59741	2.791905	3.646907	0.664377	low
TCGA-78-	2.210959	1	3.688342	7.236476	1.803435	2.496549	2.790474	1.238298	high
TCGA-L9-	1.30411	0	5.353664	6.353732	2.71502	3.096263	2.044383	0.937746	low
TCGA-35-	0.723288	0	4.270524	7.026747	1.451934	1.484103	7.272334	0.536539	low
TCGA-50-	1.260274	1	4.914725	7.299812	3.837698	3.095408	2.468995	1.863818	high
TCGA-55-	1.476712	0	6.270717	5.954504	2.222787	3.182848	3.059607	0.578242	low
TCGA-38-	1.227397	0	4.083271	7.156586	2.524152	2.908625	3.885315	1.288675	high
TCGA-MN	3.219178	0	6.749856	6.775571	2.27094	4.727551	2.048948	1.180394	high
TCGA-44-	0.59726	0	5.338765	6.602683	2.682927	3.867804	2.464096	1.178241	high
TCGA-MP	7.169863	1	6.046137	6.149056	2.942812	2.431044	1.459915	0.744776	low
TCGA-95-	1.657534	0	5.491148	6.487843	3.457468	4.086516	3.977318	1.172281	high
TCGA-55-	2.432877	0	6.795054	6.002572	2.286012	1.884284	4.899369	0.366088	low
TCGA-86-	0.967123	0	6.339191	7.523069	2.821441	3.16275	1.545428	1.506404	high
TCGA-95-	0.238356	1	6.121692	8.629313	1.996738	2.233252	4.588466	1.402157	high
TCGA-05-	2.167123	0	5.519904	8.217312	2.449048	2.400176	2.113677	1.769634	high
TCGA-55-	1.690411	0	4.95927	7.299851	2.699411	2.211675	3.475375	1.133302	high
TCGA-99-	2.90411	0	7.25363	7.181534	2.862429	3.093961	1.538807	1.123752	high
TCGA-44-	1.969863	0	7.302336	7.007638	2.878303	2.843604	4.381033	0.770697	low
TCGA-NJ-	6.194521	0	7.161031	6.427573	2.38916	1.922279	2.649483	0.526823	low
TCGA-44-	1.054795	0	7.043083	6.782545	3.246539	3.064048	1.737449	1.017605	high
TCGA-62-	3.983562	1	3.557201	8.793832	1.125657	2.317399	1.429042	2.443887	high
TCGA-93-	0.090411	1	6.160289	6.300559	2.310774	3.018096	3.438626	0.656749	low
TCGA-44-	0.265753	1	5.984472	6.783011	2.318649	2.061604	3.777453	0.675873	low
TCGA-67-	1.054795	0	6.269498	6.739451	3.807179	2.730638	4.115668	0.952006	low
TCGA-86-	1.789041	0	4.952511	7.715419	1.801527	4.081678	2.86256	1.755606	high
TCGA-62-	0.380822	1	5.092795	7.003794	3.196327	2.758309	4.196761	1.124067	high
TCGA-MP	4.90411	1	5.680428	6.023144	2.426973	1.773507	3.070775	0.510199	low
TCGA-55-	1.424658	0	5.243497	6.794429	3.266419	2.418582	2.794001	1.067608	high
TCGA-64-	3.19726	1	6.579679	6.827529	2.570998	2.678614	6.845328	0.579608	low
TCGA-50-	4.794521	0	6.354945	6.096874	2.422119	1.590424	5.661303	0.369711	low
TCGA-44-	0.786301	0	5.802128	6.92911	2.640782	2.267309	0.995659	1.046565	high
TCGA-L4-	1.191781	0	6.742098	5.696443	1.901108	3.766945	4.675397	0.44029	low
TCGA-49-	13.67671	0	5.783628	5.628129	3.77871	4.261843	4.54384	0.796599	low
TCGA-49-	0.734247	1	4.09138	7.504951	2.659863	1.921212	0.272375	1.737002	high
TCGA-75-	8.380822	0	4.131559	7.16747	2.788499	3.632136	1.942322	1.850754	high
TCGA-38-	8.145205	0	3.407159	8.12607	3.04903	4.06935	1.898731	3.682631	high
TCGA-44-	0.712329	0	5.784395	7.190739	3.065691	3.352893	4.569008	1.17875	high
TCGA-44-	7.167123	0	5.853209	6.637588	1.773752	2.554208	3.079657	0.676298	low
TCGA-62-	4.10411	1	5.051941	7.00248	3.832601	2.503549	2.647408	1.393392	high
TCGA-75-	5.553425	1	5.57293	7.054012	2.118254	2.321731	1.800176	0.973244	low
TCGA-64-	3.257534	0	3.969411	8.040362	5.251591	0.633083	3.629039	2.206937	high
TCGA-95-	1.556164	0	5.167524	6.74343	3.079415	2.350395	1.959265	1.075913	high
TCGA-99-	1.80274	0	6.301102	5.61166	3.236271	4.385263	4.856395	0.656953	low
TCGA-97-	0.449315	1	5.073352	5.437936	2.185918	3.83961	4.79682	0.527907	low
TCGA-55-	1.923288	1	5.639864	6.966082	2.365793	3.285861	2.162909	1.143356	high
TCGA-69-	1.619178	0	7.175727	6.486481	2.208228	2.422634	2.823876	0.567076	low
TCGA-55-	0.482192	1	4.826201	7.593934	2.454157	3.727752	1.655301	1.991255	high
TCGA-78-	9.958904	0	7.109649	7.015619	2.305764	1.812494	4.808479	0.556225	low
TCGA-05-	0.169863	0	6.268126	6.680547	2.105949	2.352508	2.584876	0.696265	low
TCGA-69-	1.120548	0	7.029785	6.097832	4.011695	2.28367	3.536589	0.636461	low
TCGA-J2-	2.956164	0	6.055036	6.113257	3.844341	2.139895	4.278346	0.64993	low
TCGA-78-	1.824658	1	3.460808	8.821105	3.050782	3.569593	2.018553	4.508404	high

TCGA-93-	1.967123	0	4.725459	5.750935	2.94949	2.858524	5.629234	0.571848	low
TCGA-J2-	1.983562	0	5.9797	7.043507	2.813912	3.505727	3.055198	1.195234	high
TCGA-55-	0.468493	1	5.817168	7.841353	2.516029	2.889205	2.0046	1.609102	high
TCGA-55-	2.117808	0	5.131159	7.395489	1.703464	1.627666	1.076667	1.033917	high
TCGA-50-	8.476712	0	5.858148	7.036504	2.429289	3.440167	3.861512	1.033747	high
TCGA-49-	2.454795	1	5.998178	5.724496	3.010349	3.183851	2.799454	0.647961	low
TCGA-73-	2.191781	0	7.374414	7.460309	2.433483	2.569153	1.719804	1.021429	high
TCGA-MP	6.158904	0	6.603077	5.914542	2.404449	2.72267	1.932271	0.564035	low
TCGA-55-	1.652055	0	6.43589	7.231878	2.041607	1.720993	1.286658	0.851881	low
TCGA-95-	3.484932	0	7.402686	6.859989	2.450399	3.247328	2.730333	0.813259	low
TCGA-78-	2.673973	1	6.995356	5.99078	1.997153	2.844709	3.135011	0.470402	low
TCGA-55-	1.284932	1	5.595698	8.468865	2.856994	4.270227	3.794013	2.683135	high
TCGA-44-	1.526027	1	6.308577	8.71594	2.917118	3.875703	3.285802	2.651984	high
TCGA-97-	2.123288	0	7.018388	7.710843	2.353736	3.534395	5.917899	1.00469	high
TCGA-78-	7.345205	1	5.749198	6.335032	2.177117	2.15425	2.513321	0.627656	low
TCGA-50-	0.517808	1	4.499855	7.570326	2.677959	4.698007	2.279205	2.484031	high
TCGA-64-	1.720548	1	4.45058	7.501683	1.761758	1.852373	4.085702	0.97885	low
TCGA-97-	1.556164	0	6.523798	6.420957	3.210807	1.994486	4.434954	0.590875	low
TCGA-97-	1.8	0	5.288845	7.15214	2.279138	2.499162	2.242036	1.09265	high
TCGA-62-	3.271233	1	6.284609	7.372508	2.299031	2.406779	2.784134	0.986514	low
TCGA-97-	1.556164	0	6.283075	7.349248	1.70213	2.004902	0.283951	0.990013	low
TCGA-44-	1.928767	0	5.817032	4.609666	2.558156	2.585805	7.469142	0.216367	low
TCGA-MP	0.457534	1	5.847507	7.145818	3.55579	3.108644	2.899776	1.387227	high
TCGA-49-	4.657534	0	5.679476	7.630922	2.497353	2.382306	1.681844	1.37892	high
TCGA-50-	4.430137	0	4.505271	6.119322	2.305998	2.348941	4.487642	0.611977	low
TCGA-55-	1.410959	0	7.589174	6.534992	2.209155	3.969402	5.092577	0.612961	low
TCGA-55-	1.468493	0	4.253398	6.571492	3.621563	4.499197	6.668499	1.296501	high
TCGA-71-	0.575342	1	4.98733	7.091211	2.486065	3.291897	5.596956	1.016454	high
TCGA-69-	0.367123	0	5.349656	7.549533	2.620921	2.917833	2.093884	1.533518	high
TCGA-L9-	0.528767	1	6.897651	7.315219	2.89571	2.836907	2.98699	1.062393	high
TCGA-55-	1.334247	0	5.36585	5.994325	1.86891	2.335911	4.960118	0.448133	low
TCGA-78-	1.624658	1	4.425645	6.527671	2.941983	2.704559	3.616803	0.981587	low
TCGA-S2-	1.405479	0	5.782882	6.104396	4.133518	2.990433	1.933985	1.033173	high
TCGA-05-	0.413699	0	7.98578	7.097943	2.225746	1.164644	3.687707	0.48496	low
TCGA-50-	0.326027	1	2.179074	7.784535	2.168021	2.606393	7.600891	1.440934	high
TCGA-62-	3.331507	0	6.277117	6.719016	2.142565	3.219607	3.189128	0.805016	low
TCGA-55-	0.326027	0	5.249793	7.473811	2.454139	1.585847	3.463772	0.990378	low
TCGA-49-	2.961644	1	5.767646	8.016749	2.22121	1.905171	2.422254	1.312634	high
TCGA-49-	3.893151	1	5.057737	6.895792	2.295433	1.885633	3.794475	0.780094	low
TCGA-91-	2.306849	0	2.745877	6.823414	2.467922	2.790159	5.416287	1.134237	high
TCGA-86-	2.019178	1	6.423719	7.091518	2.582307	2.416491	2.235461	0.944627	low
TCGA-49-	6.093151	0	5.812233	6.348489	1.64347	1.899427	0.785102	0.619633	low
TCGA-73-	2.526027	1	7.198133	7.088671	3.457002	3.152218	1.578045	1.233117	high
TCGA-38-	4.087671	1	6.876125	6.251418	2.184904	1.792253	4.628294	0.399517	low
TCGA-O1-	4.926027	1	8.017182	7.331674	1.821528	2.27163	3.543733	0.625945	low
TCGA-05-	0.830137	1	6.014425	7.088707	2.435161	2.718	1.467969	1.101597	high
TCGA-44-	1.621918	0	4.742059	6.512563	1.502141	2.736475	4.107986	0.673269	low
TCGA-86-	2.6	0	7.278774	7.219695	2.67366	2.33715	2.664055	0.856653	low
TCGA-97-	1.545205	0	7.167651	7.221993	1.975722	2.323896	1.132014	0.861294	low
TCGA-05-	1.252055	0	6.532458	7.779505	1.884429	1.899736	2.343002	0.991457	high
TCGA-78-	0.879452	1	3.637223	8.513377	3.241059	3.611819	0.39448	4.59431	high
TCGA-67-	1.671233	0	4.713908	7.141874	3.350416	2.748572	2.804739	1.466586	high
TCGA-38-	2.191781	1	5.566049	6.1418	2.960815	2.805708	4.845327	0.643593	low
TCGA-78-	19.85753	0	6.154993	8.287703	2.178694	0.399489	1.457767	1.121431	high
TCGA-73-	4.383562	1	6.807931	6.937561	2.850991	3.240214	2.897304	0.979116	low
TCGA-78-	1.909589	1	6.233193	6.519192	2.463156	2.954925	3.056933	0.75603	low

TCGA-49-	4.441096	0	5.006197	6.828976	2.680901	3.469551	3.084562	1.200468	high
TCGA-05-	1.832877	0	6.155208	8.579187	2.6623	2.89206	0.417004	2.540828	high
TCGA-78-	13.59178	1	6.557467	6.920013	2.970674	1.463971	5.128727	0.597524	low
TCGA-55-	1.265753	0	6.808738	5.996944	2.44212	0.980428	3.27195	0.360886	low
TCGA-55-	8.934247	0	5.325001	7.893315	3.089359	2.242567	2.917709	1.612692	high
TCGA-69-	0.452055	0	5.53169	7.53884	2.407206	2.911632	2.50758	1.373	high
TCGA-55-	2.389041	0	7.269786	6.576163	3.112813	2.688507	1.744556	0.80865	low
TCGA-50-	3.473973	1	7.426761	6.466292	2.798578	1.787544	2.828247	0.537315	low
TCGA-73-	0.10411	1	5.321837	6.737118	3.293706	2.689022	2.17391	1.150737	high
TCGA-05-	1.252055	1	5.875201	6.972342	3.594699	2.798437	3.247176	1.173134	high
TCGA-MP	4.871233	1	7.624503	6.67351	2.394905	2.062426	1.897161	0.606152	low
TCGA-55-	4.471233	1	5.900872	5.512758	1.937855	1.354311	2.350127	0.346638	low
TCGA-78-	4.186301	1	5.132941	5.898733	2.485988	3.959842	3.120418	0.812504	low
TCGA-44-	3.745205	0	6.326723	6.938019	1.692183	2.814979	2.258444	0.806722	low
TCGA-55-	7.734247	0	6.130825	7.018826	2.491952	2.017055	2.250945	0.862736	low
TCGA-97-	1.786301	0	5.739718	6.947189	2.006497	1.574677	2.078082	0.744135	low
TCGA-50-	4.106849	1	5.511271	7.690475	2.253545	0.958937	2.270723	0.989306	low
TCGA-86-	2.205479	0	7.077697	5.151729	2.829161	4.483737	5.228888	0.433039	low
TCGA-86-	0.317808	1	5.305799	6.91244	5.027218	3.718395	3.490781	1.942751	high
TCGA-55-	2.476712	0	5.39084	7.555853	2.279815	2.376838	1.595531	1.337438	high
TCGA-50-	1.789041	1	7.020532	7.231726	2.037124	2.601403	4.58704	0.703367	low
TCGA-53-	1.161644	0	5.825443	7.92223	2.134174	1.020055	1.617628	1.09965	high
TCGA-73-	6.890411	0	7.284572	6.478675	2.532155	1.889711	2.346366	0.556033	low
TCGA-62-	7.386301	0	4.394539	6.911303	4.257285	3.275299	3.377318	1.752132	high
TCGA-44-	2.435616	0	5.104582	6.878552	2.615387	2.742046	2.881169	1.051729	high
TCGA-97-	5.293151	0	6.228407	6.226815	2.640071	2.496759	3.926956	0.580466	low
TCGA-44-	1.630137	0	4.907109	7.82281	2.670493	2.16538	2.472369	1.558909	high
TCGA-44-	2.416438	0	4.081487	6.782639	4.007872	3.555108	3.634395	1.699422	high
TCGA-49-	10.29863	0	6.806577	7.354657	2.840949	4.430089	2.075176	1.61103	high
TCGA-44-	3.70137	0	5.806007	6.503622	1.931828	2.281424	5.102018	0.526305	low
TCGA-55-	1.410959	0	3.058639	7.40012	2.795983	3.759461	4.671246	1.953425	high
TCGA-64-	4.734247	0	6.516659	7.472757	2.224927	0.748179	1.745206	0.772772	low
TCGA-91-	1.383562	0	7.422707	6.31609	2.097977	1.651517	4.145049	0.378993	low
TCGA-35-	0.038356	0	5.016349	7.062364	1.847978	1.789154	1.447269	0.928764	low
TCGA-55-	1.969863	1	6.342971	7.365512	2.366451	3.17963	3.64885	1.071043	high
TCGA-67-	0.476712	0	7.357129	7.789087	1.473477	1.789701	2.244898	0.803803	low
TCGA-53-	2.934247	0	5.673355	6.046394	1.685567	1.526506	1.259338	0.494459	low
TCGA-MP	4.112329	1	5.867742	7.725698	1.965897	2.04743	1.479223	1.199276	high
TCGA-73-	0.769863	1	5.678252	7.525553	2.258045	2.901765	2.889909	1.252617	high
TCGA-86-	1.90137	1	5.24359	7.188909	3.02889	2.982731	5.619809	1.072328	high
TCGA-78-	0.879452	1	5.133841	7.206065	2.317105	3.244687	2.527767	1.306847	high
TCGA-91-	1.019178	0	4.008196	4.585186	2.305395	3.457216	8.962418	0.275961	low
TCGA-44-	3.564384	0	4.717362	7.678885	2.713995	2.454909	1.884597	1.685126	high
TCGA-75-	9.054795	0	5.700748	6.009645	2.217417	1.949423	4.904413	0.429114	low
TCGA-44-	1.331507	0	4.342916	6.791672	3.212688	2.534702	2.205489	1.291725	high
TCGA-44-	3.241096	0	3.417776	6.25457	1.140004	1.272402	3.813974	0.514604	low
TCGA-62-	2.493151	0	6.464262	7.528623	1.85769	2.082162	2.260899	0.926705	low
TCGA-MP	7.178082	1	6.621413	7.222516	2.514353	2.354965	1.473226	1.014408	high
TCGA-49-	3.109589	1	5.348823	6.269269	2.832423	2.71421	2.097019	0.852445	low
TCGA-50-	0.684932	1	4.778824	7.27618	2.606789	3.868355	2.934196	1.646422	high
TCGA-55-	2.547945	0	5.241186	6.319577	2.46741	3.181342	0.56521	1.030522	high
TCGA-97-	1.682192	0	6.276214	6.919831	2.478666	3.238859	2.861226	0.975308	low
TCGA-L9-	0.841096	0	7.295108	6.225293	2.448987	3.068782	1.00245	0.689905	low
TCGA-55-	1.221918	0	6.071842	6.570444	2.661964	2.234098	1.542509	0.81277	low
TCGA-50-	0.843836	1	5.977386	7.430566	2.422315	2.705199	4.251292	1.015972	high
TCGA-91-	1.347945	0	5.961898	6.733091	3.374319	3.093805	3.983873	0.988919	low

TCGA-97-	1.646575	0	7.277557	5.216568	1.915946	2.63895	5.27926	0.248653	low
TCGA-44-	2.364384	0	4.246559	6.541149	3.680343	1.681186	4.101532	0.919138	low
TCGA-78-	0.668493	1	6.012031	7.584561	1.513855	1.98838	3.354228	0.846231	low
TCGA-MP	1.175342	1	7.329915	7.888928	2.562088	4.292493	2.216884	1.7368	high
TCGA-05-	1.583562	0	6.762661	6.785602	3.516791	3.420371	4.11266	0.981226	low
TCGA-99-	2.046575	0	6.792249	7.698109	1.830721	3.014191	3.260761	1.051157	high
TCGA-64-	3.575342	0	6.606666	6.904012	2.806849	1.429576	2.404168	0.714746	low
TCGA-78-	2.263014	1	7.352428	7.64225	2.883166	2.981491	2.556429	1.232444	high
TCGA-NJ-	0.136986	0	5.517733	7.045798	2.732037	2.931231	0.498075	1.395722	high
TCGA-55-	1.668493	0	6.653006	6.711593	2.358234	2.789023	4.480475	0.652196	low
TCGA-55-	1.846575	0	6.071233	6.913058	2.741215	3.428219	2.782102	1.10356	high
TCGA-55-	1.309589	0	5.411473	7.268356	3.069427	3.52279	1.777329	1.694355	high
TCGA-05-	1.167123	0	6.346317	6.340611	2.138482	3.575732	3.779939	0.683063	low
TCGA-55-	1.512329	0	5.937127	6.273872	3.227429	4.557381	1.359707	1.308131	high
TCGA-97-	1.326027	0	6.735218	6.476484	3.158577	2.801474	4.389921	0.686315	low
TCGA-62-	3.531507	0	6.486691	6.888632	2.589323	1.354937	0.958348	0.770681	low
TCGA-91-	0.164384	0	5.255078	7.80452	3.043522	3.846628	4.832082	1.811594	high
TCGA-44-	3.186301	0	5.935121	8.254185	2.669985	3.612863	4.043001	1.91459	high
TCGA-55-	1.536986	1	5.237527	7.168454	3.526051	2.233737	0.839113	1.523365	high
TCGA-55-	1.920548	1	6.020384	6.817365	2.500682	3.059631	4.909864	0.784852	low
TCGA-64-	0.169863	1	4.522005	7.922485	2.246673	2.395159	0.760408	1.920131	high
TCGA-44-	1.893151	0	6.035977	7.346823	2.968737	1.499403	1.402704	1.085249	high
TCGA-55-	1.665753	0	6.437023	5.412912	2.26817	1.742166	3.513896	0.32042	low
TCGA-55-	3.378082	0	5.489061	6.9933	3.482768	2.570986	4.226593	1.075622	high
TCGA-86-	3.145205	0	3.558921	8.17582	2.706855	2.009679	4.075379	1.893599	high
TCGA-38-	2.367123	1	6.016389	8.205077	2.44432	3.542425	1.222291	2.219841	high
TCGA-78-	1.605479	1	5.258573	6.455538	2.474953	1.737315	5.195079	0.552601	low
TCGA-55-	0.421918	1	3.549534	7.188121	3.566779	2.546419	2.087001	1.88811	high
TCGA-86-	2.454795	0	6.399824	6.045978	3.851821	2.480541	3.150151	0.708134	low
TCGA-05-	0.753425	1	6.275836	8.631493	4.04127	2.644556	1.644568	2.89091	high
TCGA-55-	1.887671	0	5.772213	6.344395	2.499345	2.538199	3.656533	0.656193	low
TCGA-86-	2.361644	0	5.196167	7.149024	2.555226	2.641576	1.746546	1.254501	high
TCGA-86-	2.208219	0	6.38329	7.711708	2.963255	2.300889	0.493111	1.547561	high
TCGA-49-	4.610959	0	6.578005	7.102985	2.460876	2.626819	3.546225	0.844999	low
TCGA-44-	2.775342	0	3.003046	6.852689	2.689418	1.773505	4.688288	1.006427	high
TCGA-05-	1.663014	0	5.496814	7.371251	3.317234	3.732897	3.79837	1.617758	high
TCGA-49-	18.44384	0	4.981249	6.610681	2.016384	1.270379	1.358323	0.712643	low
TCGA-55-	1.482192	0	3.76205	6.913566	2.946384	2.42238	2.976228	1.288385	high
TCGA-MP	0.20274	1	6.76019	7.137385	3.047658	3.118388	1.851025	1.200088	high
TCGA-49-	13.05479	0	6.397867	6.551568	2.771481	3.112987	5.386548	0.674083	low
TCGA-05-	2.167123	0	7.520989	6.920508	2.583824	2.018785	2.009867	0.702843	low
TCGA-75-	3.054795	1	4.312633	7.343807	3.160863	2.288797	0.370035	1.844011	high
TCGA-69-	1.890411	0	5.257698	6.565397	3.092299	3.592195	3.927811	1.062167	high
TCGA-86-	2.720548	0	6.62966	7.05947	2.490084	2.247694	2.479279	0.840041	low
TCGA-78-	4.443836	1	6.405612	6.252586	2.186745	2.463243	1.284546	0.651227	low
TCGA-78-	0.706849	1	5.41068	7.691036	3.180261	2.661953	0.818699	1.923798	high
TCGA-55-	2.435616	0	5.604453	7.474606	1.915156	2.31817	2.74846	1.039912	high
TCGA-35-	0.49863	0	5.131874	8.370708	2.177584	2.222723	1.19281	1.985463	high
TCGA-55-	1.835616	0	6.245693	6.458999	2.330358	2.124514	2.534296	0.633275	low
TCGA-64-	4.271233	0	2.89337	6.99748	2.89462	2.05488	1.813411	1.540733	high
TCGA-L9-	1.210959	1	6.8759	6.899833	2.704563	2.739023	1.873177	0.913965	low
TCGA-97-	1.736986	0	5.696473	6.621614	2.422814	3.551913	4.511457	0.844408	low
TCGA-35-	0.616438	0	6.436948	8.089147	1.991642	2.392397	2.51734	1.287217	high
TCGA-55-	1.783562	0	5.914096	7.341312	2.375968	2.721715	3.841328	1.013042	high
TCGA-86-	0.490411	0	5.286438	6.957817	2.177606	2.391186	2.166111	0.964767	low
TCGA-NJ-	5.920548	0	5.696072	7.888181	2.206952	2.200141	1.50625	1.42992	high

TCGA-05-	3.750685	0	5.686953	6.342973	1.760758	1.81182	2.19011	0.561318	low
TCGA-NJ-	3.923288	0	5.567193	6.386768	1.524712	2.549662	1.48852	0.683748	low
TCGA-55-	3.778082	1	5.250912	8.082035	2.837781	3.71996	3.756577	2.112663	high
TCGA-97-	3.520548	0	6.193872	6.507718	3.297829	2.59352	6.054146	0.643681	low
TCGA-MN	2.265753	0	5.77837	6.064416	3.107745	3.414428	3.315777	0.798751	low
TCGA-62-	3.413699	0	4.342282	7.594337	3.017369	2.949364	0.604583	2.238754	high
TCGA-55-	2.257534	0	3.367041	6.833859	1.705433	3.345641	1.218549	1.431945	high
TCGA-55-	1.205479	1	6.040227	8.103938	2.817405	1.963702	6.563369	1.051128	high
TCGA-78-	3.312329	1	6.319131	6.318898	3.509697	3.903675	4.875456	0.869084	low
TCGA-67-	1.671233	0	6.190763	7.175719	2.349023	1.445349	4.914386	0.634468	low
TCGA-50-	0.70411	1	4.973782	7.906527	2.734598	2.879969	1.581075	2.023433	high
TCGA-67-	0.386301	0	5.691493	7.677611	2.200757	1.419278	1.795418	1.082765	high
TCGA-69-	0.50411	0	7.851521	7.615733	2.694804	3.218151	2.834234	1.117326	high
TCGA-93-	1.441096	0	5.392129	6.775609	2.279987	3.237759	2.138825	1.058748	high
TCGA-55-	2.676712	0	6.569223	6.775109	3.185506	2.376981	3.694062	0.790541	low
TCGA-97-	1.282192	1	5.566564	7.022489	1.921508	2.374154	2.024285	0.914911	low
TCGA-86-	1.920548	0	6.076279	6.648832	2.707624	2.626228	4.8587	0.691847	low
TCGA-MP	0.441096	1	5.211064	7.044547	2.829954	3.540874	2.09078	1.464875	high
TCGA-55-	1.632877	0	6.828519	5.823362	1.717671	2.89354	2.949599	0.432683	low
TCGA-J2-	2.024658	0	5.930221	7.135162	2.886016	2.492774	3.939065	0.96478	low
TCGA-50-	2.271233	0	5.500612	7.000915	1.967162	2.853791	2.461891	0.978291	low
TCGA-NJ-	0.041096	0	4.926179	5.837768	2.371584	2.568683	4.264636	0.546217	low
TCGA-55-	1.30411	0	6.458778	5.775495	2.909904	2.440338	5.218789	0.426462	low
TCGA-55-	0.271233	1	6.180893	7.013834	2.858571	2.420557	1.113734	1.099021	high
TCGA-86-	2.865753	1	2.296871	7.182313	2.41731	4.764932	2.502027	2.688588	high
TCGA-MP	1.594521	1	6.718081	6.83542	2.350647	3.427125	2.525572	0.917125	low
TCGA-50-	3.950685	0	4.634088	7.756302	2.219703	1.93572	1.671844	1.46919	high
TCGA-50-	5.060274	0	6.009767	6.380088	2.053969	1.686782	4.215255	0.474185	low
TCGA-69-	2.227397	0	7.92199	6.320629	4.173539	2.839539	3.683519	0.707298	low
TCGA-44-	0.780822	0	4.226054	7.989867	3.215573	2.714207	1.856663	2.435445	high
TCGA-78-	0.473973	1	5.035252	8.299785	2.422201	2.056285	1.592096	1.913174	high
TCGA-91-	0.09863	0	4.108657	7.984688	4.2852	2.595428	3.106171	2.687453	high
TCGA-55-	1.271233	1	4.483699	7.50565	2.685984	2.948943	3.004441	1.604417	high
TCGA-05-	2.49863	0	5.380057	7.019307	1.943997	2.115768	4.64643	0.715146	low
TCGA-86-	2.594521	0	5.04179	7.285596	1.603228	2.02939	1.919928	0.983624	low
TCGA-NJ-	1.652055	0	4.399639	7.089749	2.634456	3.091391	3.271202	1.334772	high
TCGA-05-	2.00274	1	4.007143	6.819157	3.559801	1.942867	3.454077	1.175087	high
TCGA-53-	2.545205	1	6.471556	6.322083	3.419509	3.52358	4.297756	0.814472	low
TCGA-95-	1.032877	0	4.904804	7.425116	2.495961	2.164394	1.561652	1.35546	high
TCGA-73-	0.931507	1	4.215651	6.021947	3.126984	1.952322	0.600105	0.926964	low
TCGA-44-	3.005479	0	4.875563	7.416904	1.877455	2.239246	3.572015	1.023459	high
TCGA-NJ-	0.035616	0	6.15387	6.520217	3.037002	3.113799	2.980828	0.891901	low
TCGA-55-	1.463014	0	6.638468	7.582839	2.042007	2.974158	1.319265	1.245548	high
TCGA-05-	0.249315	1	3.024066	10.11061	2.874998	1.728473	1.806304	5.911782	high
TCGA-91-	0.216438	0	5.190742	5.981906	1.847659	2.706665	5.198192	0.480024	low
TCGA-55-	1.210959	0	6.252633	7.485959	2.307047	1.688555	3.877071	0.825156	low
TCGA-55-	0.030137	0	7.406104	6.929269	2.742501	2.416845	1.113347	0.865856	low
TCGA-50-	1.189041	1	3.19969	6.930773	3.388164	3.152818	4.165243	1.607352	high
TCGA-55-	1.317808	0	5.927685	6.819325	3.000824	2.70769	0.845967	1.161887	high
TCGA-50-	0.772603	1	4.933891	6.360063	2.295472	3.208193	2.566542	0.8978	low
TCGA-38-	3.142466	1	4.333425	7.409998	2.741801	2.98767	3.649234	1.512889	high
TCGA-67-	1.227397	0	5.573538	6.376686	2.414025	3.008511	3.413948	0.755451	low
TCGA-55-	1.553425	0	5.623411	7.220081	1.949837	1.84941	2.786369	0.843224	low
TCGA-55-	1.139726	0	6.961034	6.471799	3.559494	3.392109	4.587208	0.794998	low

Supplementary Table 3. Risk scores for tumor samples in the validation set

id	futime	fustat	FBP1	LDHA	MAFF	PDGFB	GPC3	riskScore	risk
GSM16721	8.8	0	10.23664	13.11122	8.646784	6.884643	8.166213	4.325975	low
GSM16721	2.1	0	10.83464	12.89049	7.997888	6.883573	9.281536	2.861791	low
GSM16721	5.4	1	10.77148	13.39059	9.039159	6.641892	7.116905	5.137969	low
GSM16721	5.766667	0	11.83647	13.3319	9.147113	7.642683	8.849912	4.618899	low
GSM16721	2.825	1	10.68013	13.58215	10.30089	8.289862	8.09097	9.363013	high
GSM16721	6.916667	0	11.74969	13.49703	8.647976	6.933517	8.050202	4.242839	low
GSM16721	5.766667	0	12.1164	13.46796	8.955215	7.044571	7.93124	4.363869	low
GSM16721	2.258333	0	11.79235	13.10019	9.298403	7.243354	8.727492	4.018988	low
GSM16721	0.483333	1	10.25709	13.50329	9.947683	6.729303	7.897023	6.654161	high
GSM16721	4.183333	1	9.767272	12.97642	8.920777	7.104896	9.832979	4.162628	low
GSM16721	6.083333	0	11.86706	13.17559	9.047973	6.908714	8.298842	3.79858	low
GSM16721	2.9	1	11.10124	13.53598	8.026369	6.857812	8.273469	4.043206	low
GSM16721	2.3	1	10.08363	13.38624	9.977208	7.063604	8.116432	6.82192	high
GSM16721	4.066667	1	10.4335	13.1349	8.537721	7.568422	9.881555	4.116748	low
GSM16721	5.55	0	9.970509	14.00822	9.075898	7.128015	8.412718	7.606331	high
GSM16721	0.841667	1	9.962753	14.29485	9.020055	6.345003	7.905182	7.674102	high
GSM16721	0.725	1	9.611065	13.87019	9.547438	7.087655	6.550714	9.612268	high
GSM16721	5.1	1	11.58099	13.79167	9.033303	6.809187	7.646271	5.4306	low
GSM16721	11.01667	0	9.232723	13.97437	9.472688	6.433875	6.432899	9.297286	high
GSM16721	10.73333	1	10.62038	13.97768	8.635259	6.199078	9.475034	4.744263	low
GSM16721	3.65	1	11.7598	13.20908	8.469324	6.533501	8.335645	3.225768	low
GSM16721	0.491667	1	9.534455	13.82287	9.188562	6.796346	7.899315	7.43775	high
GSM16721	0.2	1	10.33134	14.39411	9.934056	6.463413	8.166705	9.165373	high
GSM16721	1.466667	1	10.24659	13.71347	8.356333	6.812329	7.411697	5.652432	low
GSM16721	1.358333	1	9.245051	14.03855	9.007505	7.310513	8.0329	9.044039	high
GSM16721	2.466667	1	10.1193	13.77391	8.815279	6.038775	6.539528	5.992447	high
GSM16721	6.766667	1	9.697913	13.5765	9.813667	6.318593	7.901929	6.683965	high
GSM16721	4.916667	1	10.22308	13.31155	9.297134	6.853771	8.377558	5.285803	low
GSM16721	7.716667	1	9.680994	13.83898	8.949328	6.533442	7.611408	6.801326	high
GSM16721	0.333333	1	8.867943	13.48531	9.597351	6.835623	7.694421	7.801046	high
GSM16721	1.4	1	12.38898	13.63615	8.424	6.586265	7.994054	3.699283	low
GSM16721	5.166667	0	10.40729	13.65673	8.964142	6.664111	9.511925	4.931042	low
GSM16721	5.191667	1	11.27802	13.22738	8.43859	6.673934	6.827933	4.05353	low
GSM16721	5.983333	0	10.09604	13.49987	9.521168	7.11462	8.024347	6.666838	high
GSM16721	7	0	9.258778	13.87002	8.976086	6.68813	11.60443	5.399106	low
GSM16721	1.55	1	11.18161	13.15343	9.798458	7.087861	9.245945	4.608856	low
GSM16721	3.816667	1	12.57888	14.54573	8.840189	6.766672	8.950075	5.680327	low
GSM16721	1.716667	1	9.189657	13.58856	9.310237	6.540466	7.710786	6.942651	high
GSM16721	9.208333	0	10.68718	13.49957	9.015164	6.284437	7.59963	4.861505	low
GSM16721	11.13333	0	11.50863	13.57631	8.917004	6.444939	8.342706	4.253128	low
GSM16721	5.875	1	10.35576	13.36216	8.605824	6.736999	7.939773	4.686492	low
GSM16721	4.341667	0	10.96967	13.05588	9.560924	6.012553	10.67871	3.090766	low
GSM16721	1.466667	1	10.64392	13.59453	8.471417	6.613888	8.075832	4.697664	low
GSM16721	1.408333	1	10.83351	13.463	9.253272	6.658953	7.132793	5.507481	low
GSM16721	7.233333	0	11.13842	13.60495	9.399261	6.906341	8.469011	5.430283	low
GSM16721	8.616667	0	9.652825	13.44928	8.701897	5.786457	8.019702	4.518314	low
GSM16721	9.8	0	10.87393	13.75174	9.545243	6.131628	7.304584	5.881137	high
GSM16721	9.65	1	10.61884	13.77977	9.348066	6.104501	7.257888	5.930988	high
GSM16721	1.583333	1	11.38853	13.46235	9.913167	6.173554	8.507585	4.683895	low
GSM16721	7.008333	1	11.00076	13.29868	8.57861	6.62501	6.781229	4.456878	low
GSM16721	12.775	0	9.379298	12.98927	9.482085	6.618116	9.720364	4.539379	low
GSM16721	12.825	0	9.838244	13.71252	9.501845	6.540139	8.493599	6.508681	high
GSM16721	13.55	0	11.0913	13.42832	9.827883	6.540254	9.816036	4.549956	low
GSM16721	5.316667	0	10.87523	13.79455	8.920596	6.564537	7.677889	5.586294	low

GSM1672:	11.04167	1	10.30951	13.5432	8.369004	6.406476	7.950113	4.572976	low
GSM1672:	10.9	0	9.790373	13.66995	10.05715	6.209516	7.668275	7.217849	high
GSM1672:	13.3	0	10.24166	13.9239	8.525141	6.43438	7.277604	6.04659	high
GSM1672:	13.14167	0	11.48404	13.75048	9.66512	6.503652	7.339405	5.924571	high
GSM1672:	6.358333	0	9.363732	13.13323	9.763088	6.576229	7.481129	6.17818	high
GSM1672:	8.825	0	10.81048	13.64576	9.943385	6.68832	7.277734	6.858339	high
GSM1672:	2.35	1	9.310558	14.0167	9.662096	7.428707	7.720107	10.63833	high
GSM1672:	0.6	1	12.61921	14.53855	8.89281	6.897091	8.85079	5.888675	high
GSM1672:	6.625	1	10.29763	14.09823	9.473477	7.022064	7.484767	8.685309	high
GSM1672:	6.858333	0	11.0007	13.39087	8.798332	6.180994	8.014489	4.001707	low
GSM1672:	8.433333	0	9.824849	13.66238	8.605931	6.634566	7.83576	5.739192	low
GSM1672:	14.00833	0	8.356338	13.74776	9.6649	6.338124	8.578192	8.059386	high
GSM1672:	1.241667	1	10.07755	13.97031	9.057821	6.652031	7.560944	7.174155	high
GSM1672:	0.8	1	11.42364	13.42418	9.33035	6.947088	7.891583	5.011439	low
GSM1672:	7.916667	0	10.18651	13.53769	8.936528	6.294929	8.981813	4.657944	low
GSM1672:	5.2	0	9.548263	13.40922	9.566558	6.974933	7.248696	7.254177	high
GSM1672:	5.358333	0	10.6429	13.42549	9.095028	6.762051	5.572232	6.287783	high
GSM1672:	1.741667	1	11.55131	13.62879	8.522833	6.723227	7.979991	4.363022	low
GSM1672:	1.858333	1	9.633836	13.78137	9.654351	6.801796	7.498753	8.183637	high
GSM1672:	5.658333	1	11.40926	13.82303	8.510392	6.81843	8.320245	4.807783	low
GSM1672:	3.025	0	9.826957	13.5652	9.027502	7.039274	7.39315	6.723765	high
GSM1672:	1.891667	1	10.29361	14.09431	9.32478	6.106198	10.06206	5.623835	low
GSM1672:	2.741667	0	11.10679	13.66247	8.822227	6.190136	7.418122	4.730989	low
GSM1672:	3.175	0	10.10106	13.64471	8.885292	5.842692	7.47209	5.097461	low
GSM1672:	4.516667	1	11.44769	13.73706	8.860837	6.359652	10.90996	3.604541	low
GSM1672:	8.008333	1	11.16404	13.578	9.096929	7.099415	9.549228	4.764917	low
GSM1672:	4.433333	0	10.98504	13.49927	9.251226	6.087459	9.431069	4.013944	low
GSM1672:	1.041667	1	11.35247	13.50576	7.710641	6.045422	6.289012	3.638201	low
GSM1672:	2.458333	0	10.31094	13.58159	10.27902	6.640451	7.249588	7.597025	high
GSM1672:	8.958333	0	11.88741	13.98265	9.111471	6.811631	7.484082	5.847756	high
GSM1672:	4.475	0	9.054862	13.54488	8.857846	7.001636	7.986326	6.783984	high
GSM1672:	1.816667	0	10.71536	13.7892	8.807994	6.773563	8.035184	5.636676	low
GSM1672:	4.65	0	11.09585	13.65928	9.424411	6.900535	8.051753	5.828158	low
GSM1672:	1.75	1	9.43346	14.05322	9.763756	6.856435	7.255699	10.07011	high
GSM1672:	0.608333	1	10.75507	13.62651	10.78391	6.872956	8.902025	7.323332	high
GSM1672:	13.325	0	10.10809	13.31417	8.815784	6.93275	7.095218	5.538069	low
GSM1672:	5.066667	0	11.04129	13.46829	9.141139	6.66065	9.424044	4.307703	low
GSM1672:	1.766667	1	10.8709	13.51427	8.95551	6.338065	8.656486	4.349327	low
GSM1672:	4.466667	0	10.34351	13.17686	9.28541	6.092368	8.969873	3.977811	low
GSM1672:	1.933333	0	10.19922	13.50784	8.600482	6.72895	7.921668	5.119168	low
GSM1672:	3.939167	0	11.57482	13.73855	9.240432	6.309562	7.132279	5.22964	low
GSM1672:	4.925833	1	10.34712	13.89125	9.117411	6.351663	6.743717	6.803703	high
GSM1672:	4.298333	0	10.7134	13.99182	8.077641	6.727052	6.447091	6.066925	high
GSM1672:	3.020833	1	10.58077	13.54841	8.253117	6.593149	7.799346	4.52949	low
GSM1672:	0.55	1	11.09463	13.52992	9.296853	7.301487	7.500834	6.07991	high
GSM1672:	4.5775	1	9.315881	14.02991	9.245603	6.518323	7.856861	8.106728	high
GSM1672:	0.811667	1	10.13923	13.02138	9.905838	6.720839	9.325775	4.74951	low
GSM1672:	4.906667	0	11.61065	13.47634	8.830006	6.603075	9.294988	3.74201	low
GSM1672:	4.3175	0	9.879076	14.17776	9.568671	6.249565	6.887355	8.795335	high
GSM1672:	1.79	1	10.93424	12.90593	9.417367	6.514308	7.749568	4.001607	low
GSM1672:	0.531667	1	10.39078	13.54764	9.670546	6.735839	8.487313	5.999102	high
GSM1672:	5.750833	1	10.19377	13.61503	9.389892	6.48572	6.954976	6.525816	high
GSM1672:	5.345	0	10.66403	13.40332	9.128082	6.764122	10.13928	4.226467	low
GSM1672:	2.686667	1	12.1401	13.42369	8.671368	5.94478	7.196951	3.441541	low
GSM1672:	0	0	9.195399	13.73867	9.737639	6.862909	6.812973	9.327445	high
GSM1672:	4.695833	0	13.01347	13.52853	9.599295	6.662137	6.231636	4.812245	low

GSM1672:	5.754167	0	9.683379	13.59148	8.602634	6.714642	8.841492	5.281355	low
GSM1672:	4.693333	0	12.19222	13.92229	9.253852	6.466861	7.466725	5.237548	low
GSM1672:	5.104167	0	9.261456	13.85147	8.183017	6.420163	7.752775	6.015944	high
GSM1672:	4.2025	0	11.7264	13.12567	8.482328	6.750683	9.319796	3.002038	low
GSM1672:	6.113333	0	9.906963	13.47193	8.851829	6.820375	7.697496	5.73309	low
GSM1672:	5.561667	0	10.98216	13.35732	8.701033	7.106227	8.996654	4.284638	low
GSM1672:	6.066667	0	10.65832	13.7476	8.514197	7.08638	7.135289	6.042763	high
GSM1672:	1.658333	1	11.24861	13.03294	9.88307	6.664809	9.217509	4.04676	low
GSM1672:	2.606667	1	11.22576	13.94626	9.373345	6.579931	7.096135	6.57748	high
GSM1672:	3.7775	1	11.23562	13.2132	8.974541	6.26503	6.984908	4.102737	low
GSM1672:	6.995833	0	10.56245	13.8818	9.332188	6.601871	7.072342	7.009033	high
GSM1672:	1.0525	1	10.64683	13.89941	8.436095	7.247592	7.611003	6.33513	high
GSM1672:	6.490833	0	10.66509	13.38664	8.644316	7.409518	8.248132	5.089681	low
GSM1672:	0.931667	0	9.095845	13.79578	9.598555	6.353108	8.096246	7.643868	high
GSM1672:	2.544167	0	10.78283	13.34841	9.078145	7.439762	9.433919	4.876142	low
GSM1672:	6.1325	0	10.51316	13.0641	8.734423	7.052467	8.794864	4.057708	low
GSM1672:	0.973333	1	10.07097	13.65093	10.03189	7.578982	9.137988	7.925612	high
GSM1672:	6.2175	0	8.194166	13.85151	9.626494	7.700281	11.42288	8.832654	high
GSM1672:	2.661667	1	11.64015	12.94139	9.459748	6.829772	9.461025	3.410324	low
GSM1672:	0.186667	1	10.87902	13.49049	9.62743	7.49495	7.753932	6.693013	high
GSM1672:	0.7375	1	8.109455	13.8784	9.844497	6.942241	7.077307	11.7927	high
GSM1672:	7.683333	0	10.02029	13.32853	10.10978	7.015652	8.873401	6.391049	high
GSM1672:	7.505833	0	10.39709	13.6769	10.28645	8.015727	8.557693	9.237855	high
GSM1672:	2.080833	1	9.880049	14.33752	8.950244	7.077262	7.869285	9.066449	high
GSM1672:	3.503333	1	10.84968	13.15193	8.395538	5.957874	7.760567	3.30287	low
GSM1672:	1.016667	1	9.546487	14.02453	9.952484	7.542638	6.852324	12.05657	high
GSM1672:	0.225	1	10.47591	13.78316	8.640042	7.084215	7.704388	6.156191	high
GSM1672:	8	1	9.491222	13.70985	9.863025	6.822207	7.81405	8.237055	high
GSM1672:	5.508333	1	10.29247	13.68138	8.878227	6.373564	6.702214	5.981521	high
GSM1672:	5.716667	1	12.50527	13.7547	8.683295	6.604808	7.558926	4.216564	low
GSM1672:	4	1	9.402217	14.1596	9.342117	6.578752	7.602795	8.963616	high
GSM1672:	1.333333	1	9.713715	14.1663	8.581991	6.751339	6.818889	8.171095	high
GSM1672:	6	0	8.544605	13.23076	9.394057	7.231624	6.508952	8.358346	high
GSM1672:	3.916667	0	10.69058	13.00584	9.915607	7.642129	8.950894	5.418887	low
GSM1672:	4.333333	1	13.12604	13.29054	9.99278	7.307444	8.692246	4.232113	low
GSM1672:	3.25	1	9.15496	13.43472	9.180347	6.932043	5.709357	8.128476	high
GSM1672:	5.5	0	10.66035	13.13135	9.361725	7.289216	10.06554	4.370396	low
GSM1672:	3.666667	0	11.01766	13.46777	9.405143	7.323162	8.577421	5.591877	low
GSM1672:	5.833333	0	10.45672	12.94044	9.84327	7.23721	7.369658	5.659588	low
GSM1672:	6.25	0	11.51286	13.62614	9.004263	6.964022	8.270991	4.939501	low
GSM1672:	7.666667	0	11.78731	13.44324	9.824863	7.38661	8.066654	5.699728	low
GSM1672:	5.416667	0	10.77529	14.43504	8.40937	6.556544	9.819681	5.706542	low
GSM1672:	3.583333	0	8.461721	13.86459	8.924364	6.580423	7.388655	8.390008	high
GSM1672:	5.75	0	8.670589	13.96886	9.683291	7.338638	7.459473	11.50459	high
GSM1672:	3.333333	1	12.19213	13.69954	9.548	6.684444	7.632217	5.164115	low
GSM1672:	1.75	1	10.79569	13.78795	9.023817	6.110148	8.121186	5.056756	low
GSM1672:	2.416667	1	10.17521	13.61881	8.918337	7.340451	7.14176	6.959792	high
GSM1672:	2.166667	1	10.22607	13.3895	9.22584	6.96058	8.730497	5.350763	low
GSM1672:	6.416667	0	8.028094	14.26086	9.958566	7.017146	6.809414	15.11745	high
GSM1672:	0.166667	1	9.163675	14.21678	9.01463	6.825177	6.739619	10.08466	high
GSM1672:	5.5	0	10.7098	13.50865	9.79887	6.709923	8.974165	5.511655	low
GSM1672:	1.166667	1	9.421417	14.24372	9.23135	7.311598	7.928027	10.23018	high
GSM1672:	2.75	0	10.28023	13.02762	10.73325	7.763131	9.058717	6.943283	high
GSM1672:	7.083333	0	8.558264	14.22037	9.673936	6.575887	7.629349	11.08747	high
GSM1672:	5.5	0	10.56797	13.3885	8.289839	7.703421	7.498841	5.439354	low
GSM1672:	1.25	0	11.38266	13.22138	9.314609	6.74245	6.436885	4.977168	low

GSM1672 ⁴	7.583333	0	10.26952	13.98355	9.177295	7.044116	6.450797	8.553913	high
GSM1672 ⁴	5.666667	1	11.71854	13.30081	9.196608	7.499046	7.99749	4.889085	low
GSM1672 ⁴	2.75	0	9.405601	13.28882	9.675517	7.11932	8.400303	6.677426	high
GSM1672 ⁴	2	1	10.52925	13.70035	9.093843	7.627714	8.97113	6.442195	high
GSM1672 ⁴	5.166667	0	11.30457	13.48629	9.232204	6.77164	8.145132	4.859388	low
GSM1672 ⁴	9.5	1	10.7287	14.4924	9.538339	6.999324	7.293748	10.03427	high
GSM1672 ⁴	0.333333	1	11.92496	13.70661	9.552733	7.037358	8.239799	5.488485	low
GSM1672 ⁴	1.666667	1	10.24017	13.39123	10.27605	6.536381	7.832681	6.547197	high
GSM1672 ⁴	4.333333	1	9.910367	13.62228	10.25755	7.213979	6.059706	10.13454	high
GSM1672 ⁴	7.75	0	8.662992	13.90869	9.735669	6.983619	7.264733	10.72383	high
GSM1672 ⁴	1.166667	1	9.825437	13.87944	8.936214	7.202806	7.878701	7.562112	high
GSM1672 ⁴	8.333333	0	10.85361	13.47738	9.657683	7.382135	8.272821	6.282659	high
GSM1672 ⁴	2.75	0	10.75181	13.44261	9.214636	6.841336	8.082804	5.236969	low
GSM1672 ⁴	2.666667	1	10.81336	13.1859	8.705159	7.359575	9.118347	4.226472	low
GSM1672 ⁴	5	0	11.70651	13.6525	8.961869	6.779154	8.781101	4.448386	low
GSM1672 ⁴	4.166667	0	11.29758	13.93842	9.447734	7.465848	7.324595	7.706014	high
GSM1672 ⁴	1.25	1	10.02752	13.64511	9.121637	6.896911	7.790974	6.488795	high
GSM1672 ⁴	3.083333	0	10.49067	13.4133	9.190163	7.02172	9.747466	4.798188	low
GSM1672 ⁴	4.5	0	11.15596	13.13204	9.932012	7.043704	8.654461	4.905994	low
GSM1672 ⁴	2.583333	0	10.97264	12.8957	8.126983	7.38663	9.592066	3.107534	low
GSM1672 ⁴	3.166667	0	9.404316	13.76542	8.484563	6.889538	8.747324	6.070574	high
GSM1672 ⁴	9.583333	0	10.41059	12.73242	9.088853	7.113853	13.02367	2.675293	low
GSM1672 ⁴	3	0	11.87996	13.08655	9.402032	7.196711	8.09593	4.21132	low
GSM1672 ⁴	4	1	11.43288	12.83763	10.64298	6.788006	9.071259	4.355124	low
GSM1672 ⁴	1.583333	1	10.95396	13.50348	8.963525	6.954583	8.596507	4.869481	low
GSM1672 ⁴	7.583333	0	10.17939	13.67032	9.776331	7.346018	8.47656	7.555739	high
GSM1672 ⁴	17	1	9.425434	13.63572	9.757093	6.806795	7.745338	7.889342	high
GSM1672 ⁴	4.166667	0	10.96851	13.99967	8.607066	6.718207	7.889924	5.759664	low
GSM1672 ⁴	6.666667	0	10.19383	13.49061	8.924214	6.715632	7.108326	5.799745	low
GSM1672 ⁴	3.5	1	10.88886	13.46182	8.632065	6.887212	9.637377	4.071606	low
GSM1672 ⁴	5	0	9.529106	14.65644	7.770085	6.769531	9.649148	7.03425	high
GSM1672 ⁴	2.166667	0	10.62125	13.9356	9.348613	7.228455	7.092091	8.086718	high
GSM1672 ⁴	5.166667	1	10.66076	13.5072	9.217941	6.985932	6.551128	6.418499	high
GSM1672 ⁴	1.833333	0	7.431055	12.74805	9.588744	7.406949	9.23425	6.696003	high
GSM1672 ⁴	5.25	0	11.85485	13.48286	9.831234	6.789059	8.980288	4.724251	low
GSM1672 ⁴	5.666667	0	10.81913	12.74618	8.500035	7.124281	8.658476	3.285468	low
GSM1672 ⁴	0.583333	0	10.84554	13.88093	9.521638	7.132533	8.115673	7.105578	high
GSM1672 ⁴	4.333333	1	10.66205	12.88231	9.106962	6.870133	8.261009	3.973973	low
GSM1672 ⁴	3	0	10.68764	12.99961	9.004187	7.002897	9.051709	3.928355	low
GSM1672 ⁴	1.25	1	9.872025	13.49026	9.056947	6.982961	7.80013	6.199961	high
GSM1672 ⁴	1.666667	1	12.009	13.50587	8.791531	6.413375	6.584746	4.317182	low
GSM1672 ⁴	3.416667	0	9.975963	13.03908	9.879164	7.333301	8.724991	5.800476	low
GSM1672 ⁴	2.083333	1	10.5195	13.51838	8.984601	6.649817	8.080327	5.153509	low
GSM1672 ⁴	3.5	0	9.844789	13.30869	9.306912	6.771833	7.826548	5.758631	low
GSM1672 ⁴	4.25	1	11.41864	13.55379	8.701298	7.50352	9.002326	4.767154	low
GSM1672 ⁴	4.166667	0	9.218217	13.5401	9.148339	7.042988	7.501805	7.367098	high
GSM1672 ⁴	4.75	1	9.794305	13.287	9.949663	7.193942	10.03382	5.884122	high
GSM1672 ⁴	1.083333	1	9.597846	13.74543	8.441336	7.125145	7.35086	6.851494	high
GSM1672 ⁴	6.5	1	9.837797	13.75956	8.457272	7.269173	7.684707	6.685559	high
GSM1672 ⁴	4	0	10.92575	12.74525	9.301541	6.570791	7.818192	3.655222	low
GSM1672 ⁴	2.75	1	11.46172	13.31497	9.641666	7.186222	9.478612	4.619936	low
GSM1672 ⁴	3.083333	0	10.51283	12.5022	9.98498	7.760654	10.98171	3.847407	low
GSM1672 ⁴	1.416667	1	10.24067	13.79224	9.954353	7.381325	8.406779	8.317535	high
GSM1672 ⁴	2	1	9.764671	13.57387	8.863111	7.294126	6.54147	7.458609	high
GSM1672 ⁴	3.666667	0	11.45277	13.54035	8.35764	6.814872	8.859479	3.882313	low
GSM1672 ⁴	2.5	0	10.71009	13.80342	9.475599	7.081332	8.180009	6.818661	high

GSM1672: 4.166667	0	11.65523	13.73671	9.833926	8.34709	8.254438	7.939304	high
GSM1672: 7.333333	0	9.829068	13.87495	8.751788	6.822305	9.540909	5.843002	high
GSM1672: 3.5	0	11.39339	13.40668	9.496696	8.034519	8.969493	5.848657	high
GSM1672: 3.833333	0	11.23118	13.32418	9.396176	7.085475	7.842174	5.146818	low
GSM1672: 4.666667	0	11.07661	12.75691	9.354037	7.032805	10.21369	3.246454	low
GSM1672: 3.333333	0	12.24782	12.79101	8.397506	6.95814	9.650982	2.379005	low
GSM1672: 3.166667	0	11.38901	13.98352	8.776696	6.98404	8.221075	5.708604	low
GSM1672: 3.583333	0	9.333759	14.23835	9.463519	6.58523	7.466244	9.743123	high
GSM1672: 4.583333	0	9.408977	13.3335	9.428134	7.612965	8.944618	6.828367	high
GSM1672: 1.416667	1	11.71576	13.96259	9.036459	7.104013	7.694191	6.090603	high
GSM1672: 3	0	10.57874	13.34202	10.63132	7.556898	8.541538	7.555383	high
GSM1672: 0.833333	1	10.15898	13.52977	8.996692	7.352891	10.02849	5.325747	low
GSM1672: 1.916667	1	9.423696	14.40667	8.423358	7.064486	8.125238	8.771724	high
GSM1672: 5.166667	0	8.701026	13.61605	8.867354	7.327908	7.996276	7.878972	high
GSM1672: 7.083333	0	10.1121	12.69134	9.078971	6.860292	9.452132	3.529469	low
GSM1672: 3.916667	1	8.996982	13.71111	10.66205	7.639034	7.589876	12.46245	high
GSM1672: 4	1	10.83218	13.28705	9.607374	7.058104	8.325278	5.333646	low
GSM1672: 4.75	0	11.74177	13.59695	9.324985	6.97778	7.809974	5.246945	low
GSM1672: 3.583333	0	11.09126	13.06855	9.264091	7.477738	9.098308	4.415349	low
GSM1672: 3.416667	0	10.1032	12.70684	9.386267	7.646945	9.814554	4.294202	low
GSM1672: 3.583333	0	10.92568	12.69085	8.672851	7.040069	8.801996	3.17206	low
GSM1672: 2.666667	0	8.836884	13.03201	9.326753	7.536984	5.834858	8.126563	high
GSM1672: 5.333333	0	11.15826	12.78731	8.973319	7.538116	9.374059	3.582995	low
GSM1672: 8.916667	0	12.72963	13.34423	9.114061	6.930394	8.864056	3.517672	low
GSM1672: 2.083333	1	12.16569	13.39977	8.636362	7.031788	8.981005	3.591178	low
GSM1672: 8	0	10.38849	13.76455	9.307362	7.570374	8.918416	7.018131	high
GSM1672: 8.166667	0	10.64834	13.30786	9.158896	7.53506	8.965836	5.260828	low
GSM1672: 3.083333	1	11.43987	14.14156	9.048521	6.896455	9.183286	5.824497	low
GSM1672: 7.5	0	11.13974	13.29866	8.92161	8.137558	8.135873	5.637112	low
GSM1672: 3.333333	0	10.73217	13.50596	9.561196	7.020416	8.224629	5.935078	high
GSM1672: 5.916667	1	12.55388	13.314	9.677739	7.345864	9.511055	4.095083	low
GSM1672: 0.75	1	11.1781	14.36357	8.563414	7.470195	8.722049	7.087596	high
GSM1672: 9.166667	0	9.99291	13.60771	9.431092	7.006891	7.62511	7.071835	high
GSM1672: 9.166667	0	10.63841	12.89084	9.213477	7.126527	9.795911	3.774305	low
GSM1672: 0.5	1	9.140096	14.51327	11.23142	7.372007	7.026025	19.69665	high
GSM1672: 7.916667	1	10.62316	13.94021	9.716885	7.090928	7.904309	7.916888	high
GSM1672: 3.166667	1	10.48316	13.66532	9.47039	7.319842	7.808913	7.149245	high
GSM1672: 0.75	1	7.611401	14.31456	10.44315	7.752249	8.224677	18.59913	high
GSM1672: 7.25	0	9.888393	14.55427	10.00258	7.928672	13.70484	8.887453	high
GSM1672: 7.333333	0	11.38398	13.49629	9.674404	7.082604	8.02412	5.670924	low
GSM1672: 6.166667	0	12.51205	14.37282	8.788963	7.023406	8.359504	5.804262	low
GSM1672: 0.666667	1	9.198511	14.3438	10.79045	7.614459	8.336413	15.51495	high
GSM1672: 4.916667	0	11.30775	13.24625	8.371088	7.001575	10.16587	3.222158	low
GSM1672: 4.583333	0	12.2652	13.64796	8.955303	6.893122	7.52621	4.661297	low
GSM1672: 3	0	10.11749	13.03409	8.596736	7.187623	8.629783	4.292979	low
GSM1672: 1.25	1	10.68624	13.24439	7.660984	7.709349	9.584621	3.694204	low
GSM1672: 7.083333	0	11.1311	14.57814	9.070067	6.804507	7.371289	8.569824	high
GSM1672: 0.75	1	8.337778	14.39472	7.722671	7.072853	5.097935	11.49436	high
GSM1672: 0.916667	1	9.540475	14.42326	9.309696	7.362109	6.610572	12.54704	high
GSM1672: 6.583333	1	12.47333	13.11072	9.832258	7.195145	9.215654	3.873083	low
GSM1672: 8.75	0	12.17405	13.39797	9.091297	6.899351	9.130609	3.775496	low
GSM1672: 8.083333	0	8.260092	14.22919	9.334613	7.124705	4.363437	16.01773	high
GSM1672: 0.333333	1	10.21203	14.18859	9.374267	7.551202	7.765488	9.748819	high
GSM1672: 3	1	10.08144	14.06307	9.450069	6.847646	7.871363	8.197368	high
GSM1672: 3.666667	1	10.61113	13.4163	8.954166	6.534581	10.43452	3.853157	low
GSM1672: 6.166667	1	12.1525	14.23705	8.63519	7.55249	7.800648	6.490098	high

GSM1672:	1.083333	1	9.478499	13.21228	8.414119	7.283133	9.630655	4.60529	low
GSM1672:	7.5	0	10.20429	13.98806	9.009728	6.511627	7.743979	6.733739	high
GSM1672:	7.083333	0	10.99111	14.25918	8.729194	7.348681	8.264246	7.281557	high
GSM1672:	5.916667	1	11.1745	13.26788	8.327398	7.238336	7.414804	4.362974	low
GSM1672:	5.333333	1	11.13096	14.07371	8.537385	7.290604	7.219933	6.816315	high
GSM1672:	5.416667	1	9.501286	13.06468	8.876066	7.545447	8.123258	5.641952	low
GSM1672:	5.666667	0	10.2516	13.91148	9.594756	7.36665	7.662882	8.673053	high
GSM1672:	5.333333	0	10.61787	13.89109	9.998346	6.219314	8.50042	6.544371	high
GSM1672:	5.25	0	11.1731	13.37407	9.671392	7.76354	7.283977	6.740084	high
GSM1672:	1.083333	1	11.05511	13.32324	9.234698	7.436514	7.597673	5.594454	low
GSM1672:	7.916667	0	9.33985	14.61468	8.809985	6.652474	7.025583	10.68395	high
GSM1672:	6.166667	0	11.30327	13.8923	8.958312	6.839386	6.537386	6.449805	high
GSM1672:	4.75	1	10.39539	13.11529	9.220156	7.614937	8.262076	5.454636	low
GSM1672:	4.666667	1	11.84993	14.23393	9.304645	6.569041	8.197841	6.148669	high
GSM1672:	4	0	10.5789	13.96467	10.11136	6.275907	7.537141	7.648466	high
GSM1672:	4.083333	0	11.39568	13.62122	9.423014	7.001418	9.082628	5.123419	low
GSM1672:	2.333333	0	12.06366	13.54208	9.20413	7.149356	6.697538	5.427801	low
GSM1672:	3	0	10.57496	13.64664	8.833072	6.678931	8.389674	5.153246	low
GSM1672:	3.333333	0	10.25099	13.89974	9.379116	7.082187	9.050611	6.930982	high
GSM1672:	3.083333	0	9.932256	14.04563	9.171462	7.23269	7.760906	8.563994	high
GSM1672:	3.333333	0	11.8265	13.28516	10.18856	6.987986	9.225767	4.74109	low
GSM1672:	1.916667	1	11.5663	13.6331	9.818621	7.329281	9.078519	5.812842	low
GSM1672:	6.333333	0	10.47671	13.52338	9.967379	7.522309	7.505097	7.91573	high
GSM1672:	2.833333	1	12.13321	13.71696	9.583	7.557787	8.409976	5.888368	high
GSM1672:	5.5	0	12.90515	13.66615	10.04632	7.64452	7.524871	6.203545	high
GSM1672:	2.416667	1	9.420967	14.51495	9.941646	7.232283	10.66304	10.40959	high
GSM1672:	0.583333	1	7.652135	13.92556	8.871645	6.290863	12.66475	5.75985	low
GSM1672:	4.416667	0	11.28464	13.64515	9.008959	6.81823	7.701868	5.255504	low
GSM1672:	5.25	0	11.1285	13.74741	9.618723	7.333306	8.770178	6.439504	high
GSM1672:	1.916667	0	11.1745	13.38322	9.281783	6.934856	8.51728	4.772222	low
GSM1672:	5.166667	0	9.212248	13.85528	9.674806	6.51443	7.8009	8.309494	high
GSM1672:	0.583333	1	12.23345	13.55012	9.700622	7.417169	7.603708	5.734242	low
GSM1672:	2.166667	0	10.67195	13.98859	8.493974	7.073521	7.558153	6.455411	high
GSM1672:	3.333333	0	11.23857	13.83902	8.744398	7.34902	8.929847	5.489069	low
GSM1672:	2.5	0	10.7519	14.11018	8.997412	7.250487	8.305756	7.255603	high
GSM1672:	3.333333	0	11.82605	14.03872	8.847638	7.288561	8.316549	5.880308	high
GSM1672:	7	0	11.27508	13.26429	9.064158	7.083538	9.133194	4.165989	low
GSM1672:	1.5	1	10.52761	13.86191	9.261015	7.160161	7.433711	7.457894	high
GSM1672:	2.083333	1	11.31591	13.71729	9.380775	7.406243	8.700381	6.016559	high
GSM1672:	6.666667	0	10.70501	13.34593	9.098989	7.317325	6.561438	6.172275	high
GSM1672:	1	1	8.899303	13.67598	9.548895	7.171915	7.421518	9.191173	high
GSM1672:	2.666667	0	11.23138	13.26271	9.03292	6.617132	8.800761	3.902291	low
GSM1672:	8.75	0	11.35912	13.4039	9.650622	7.42471	8.805689	5.435883	low
GSM1672:	6.75	0	10.80746	13.85589	9.391647	6.785586	8.753417	6.079031	high
GSM1672:	6.25	0	10.72183	13.36669	8.518584	6.807396	9.755967	3.801293	low
GSM1672:	8.083333	0	11.27999	13.01776	8.87681	7.14141	10.0561	3.34603	low
GSM1672:	1.5	1	12.8806	13.60628	8.764973	6.931472	7.849536	3.949964	low
GSM1672:	2.666667	1	11.54049	13.85291	9.840856	7.468954	9.246926	6.571885	high
GSM1672:	0.833333	1	9.896591	14.25396	9.718263	7.063437	7.620366	10.34511	high
GSM1672:	3.745	1	10.6597	13.50798	8.89949	6.354485	8.398774	4.53347	low
GSM1672:	2.896667	1	10.20256	13.87869	9.902162	7.035795	7.965548	8.347058	high
GSM1672:	1.653333	1	9.518384	13.50217	10.04774	6.932755	6.970658	8.504535	high
GSM1672:	0.7175	1	10.77661	13.40582	9.25992	6.923349	8.835779	4.934533	low
GSM1672:	0.044167	1	10.01456	12.61092	9.66817	6.924272	8.750988	4.175478	low
GSM1672:	3.129167	1	8.446703	13.20473	10.03495	6.515771	8.83106	6.768104	high
GSM1672:	8.881667	0	10.29708	14.2055	10.02034	6.795222	7.824456	9.454239	high

GSM16720	10.275	0	9.759068	13.59756	8.873596	6.757341	8.931479	5.536455	low
GSM16720	4.733333	1	10.09015	13.5216	9.202221	7.04242	7.656225	6.430558	high
GSM16720	2.51	1	9.445298	13.81217	8.763285	6.588833	7.734764	6.697301	high
GSM16720	1.110833	1	11.13401	13.17149	9.230368	6.951666	8.064468	4.495316	low
GSM16720	8.8325	1	11.29109	13.25591	9.049384	7.017784	10.11253	3.746625	low
GSM16720	3.701667	1	9.403947	13.26645	9.088152	7.017222	7.605702	6.162122	high
GSM16720	1.738333	1	9.860207	13.47468	10.17482	7.2771	7.305852	8.538082	high
GSM16720	2.3025	1	10.33985	13.37104	8.457063	6.403485	6.596792	4.804694	low
GSM16720	6.181667	1	10.55199	13.18903	9.533138	6.529731	7.345254	5.117279	low
GSM16720	8	1	10.68788	12.97496	9.126519	6.331565	10.64276	3.037809	low
GSM16720	3.444167	1	10.59521	13.37907	10.21954	6.546479	7.548814	6.281133	high
GSM16720	0.470833	1	11.05547	13.68637	11.0759	7.478686	7.97994	9.33775	high
GSM16720	0.035833	1	10.00913	13.80597	8.927131	6.413807	7.246285	6.409884	high
GSM16720	1.38	1	9.963422	13.43832	9.590349	6.750478	7.950935	6.267094	high
GSM16720	5.100833	1	10.85514	13.70383	10.30676	6.517364	7.476698	7.15317	high
GSM16720	8.705833	0	9.593348	13.71091	9.661812	7.35193	7.849687	8.643552	high
GSM16720	5.883333	1	10.29692	13.18303	9.509512	7.001468	7.973026	5.485414	low
GSM16720	0.293333	1	9.853238	13.74978	9.699364	6.983706	7.726661	8.020558	high
GSM16720	1.461667	1	10.29531	14.11635	8.857969	6.612215	7.247225	7.280856	high
GSM16720	2.296667	1	9.197536	14.04926	10.6183	7.441791	7.551724	13.52615	high
GSM16720	1.365833	1	9.219628	13.69921	8.530566	6.78808	7.224513	6.813031	high
GSM16720	6.475	0	11.33854	13.6518	10.24132	6.770231	7.698774	6.637236	high
GSM16720	7.846667	0	10.96521	12.86279	8.676997	6.752429	8.84404	3.214294	low
GSM16720	6.116667	0	9.933865	13.54774	9.745544	6.77768	6.914254	7.502446	high
GSM16720	3.77	1	12.12028	13.75037	9.127662	6.927215	7.252315	5.322927	low
GSM16720	0.0025	1	9.664616	13.34206	8.493485	5.933766	7.755816	4.33751	low
GSM16720	6.310833	1	11.5517	13.37356	9.083604	7.033268	8.891276	4.272333	low
GSM16720	3.255	1	11.57317	13.61708	9.170879	6.237831	7.841929	4.525182	low
GSM16720	6.466667	1	9.26407	13.57395	8.73421	6.420638	7.389231	6.099906	high
GSM16720	0.189167	1	9.682099	13.88205	10.33581	6.616208	7.967601	9.035276	high
GSM16720	7.036667	0	10.85802	13.27758	8.459659	5.771461	7.864799	3.380834	low
GSM16720	3.515	1	10.03461	13.29805	9.088542	6.699911	7.712032	5.313302	low
GSM16720	7.1375	1	10.80796	13.88126	9.700764	6.114904	7.465101	6.391134	high
GSM16720	7.71	0	10.11022	13.88993	9.450813	6.393629	9.938393	5.769363	low
GSM16720	3.28	1	9.39508	13.82756	8.679776	6.206974	8.753066	5.673367	low
GSM16720	6.875	0	10.57574	13.20346	9.236864	6.451521	7.308312	4.777543	low
GSM16720	2.641667	0	10.48075	13.64946	8.663713	6.914731	7.839292	5.554614	low
GSM16720	3.501667	1	11.37577	13.47151	9.11585	6.695326	7.638414	4.800425	low
GSM16720	0.481667	1	11.49399	13.5887	9.031019	6.158681	6.752655	4.746201	low
GSM16720	0.640833	1	9.738314	13.18889	10.54915	7.219407	9.642729	6.646432	high
GSM16720	3.991667	1	11.00504	13.35184	9.009133	6.63649	7.714884	4.60462	low
GSM16720	4.903333	0	10.03466	13.27031	9.434036	6.735122	7.721222	5.657887	low
GSM16720	6.795	0	11.8253	13.32639	8.870235	6.33767	6.871745	3.984768	low
GSM16720	2.0425	1	10.73451	13.39669	9.410471	6.55412	7.65839	5.235247	low
GSM16720	0.585833	1	10.09936	13.42738	8.703698	6.900993	7.803995	5.341113	low
GSM16720	0.8025	1	11.02692	13.6714	9.351163	6.774354	6.630028	6.423687	high
GSM16720	3.350833	1	10.14186	13.4879	9.356892	6.576657	8.527731	5.482652	low
GSM16720	5.5575	0	10.85497	13.26225	8.80176	6.581928	9.018729	3.831245	low
GSM16720	3.414167	1	9.191804	14.25636	9.833119	6.600759	7.825544	10.50357	high
GSM16720	6.343333	0	8.897192	13.38372	9.814095	6.454896	8.106825	6.927674	high
GSM16720	6.053333	1	10.9847	13.41379	10.5878	7.063419	7.729403	7.09496	high
GSM16720	0.999167	1	9.389081	13.84266	9.084042	6.703674	7.763292	7.453362	high
GSM16720	0.52	1	9.271643	14.44802	9.664447	6.966936	7.541135	12.08581	high
GSM16720	1.823333	1	11.07748	13.5074	9.037595	6.647194	7.874164	4.86684	low
GSM16720	6.570833	0	10.3777	13.35541	8.578739	6.788817	8.139014	4.601031	low
GSM16720	6.004167	0	10.43283	14.03936	9.18633	6.3527	7.295741	6.959351	high

GSM1672(2.354167	1	9.578546	14.01793	8.524826	7.137704	8.388779	7.26424	high
GSM1672(4.449167	0	10.29178	13.2918	9.416806	5.991994	9.754153	3.975681	low
GSM1672(3.2525	0	9.860805	13.68163	9.528015	6.745291	7.568154	7.251118	high
GSM1672(4.35	1	11.13868	13.41133	7.909263	6.2241	7.248165	3.568344	low
GSM1672(1.314167	1	10.05708	13.77252	8.94928	6.552031	7.232661	6.480491	high
GSM1672(2.305	1	9.088955	13.85531	8.137396	6.175033	9.298072	5.106311	low
GSM1672(2.4725	1	9.538086	13.34452	9.720131	6.625447	8.693271	5.993264	high
GSM1672(1.001667	1	8.717114	13.32203	10.75298	7.450068	6.811702	11.37046	high
GSM1672(12.515	0	8.864452	13.84807	9.654853	6.385511	7.779726	8.465368	high
GSM1672(1.289167	1	10.94766	13.52066	8.589108	7.181636	7.279778	5.337223	low
GSM1672(2.061667	1	10.1941	13.48438	9.659636	6.449348	8.544478	5.620443	low
GSM1672(1.374167	1	9.642248	13.76207	9.686569	6.519499	7.908945	7.441245	high
GSM1672(0.745	1	8.891161	13.82577	10.39996	7.066849	6.485544	12.40789	high
GSM1672(2.198333	1	9.271052	13.32445	9.825975	6.795661	7.312157	7.33868	high
GSM1672(1.516667	1	9.18912	13.27605	8.607499	7.116434	7.007812	6.222216	high
GSM1672(6.628333	1	11.74459	13.28285	8.548951	7.266447	9.250623	3.637327	low
GSM1672(2.558333	1	9.807571	13.54761	8.662127	7.151238	7.903954	6.083613	high
GSM1672(6.741667	1	8.958698	12.89867	8.779396	6.888509	6.778051	5.453402	low
GSM1672(0.975	1	11.79693	13.64532	9.647061	6.381261	6.913895	5.442751	low
GSM1672(2.766667	1	10.10287	13.02798	9.301353	6.20955	12.24089	2.98392	low
GSM1672(3.541667	1	11.40467	13.33223	8.950578	6.982011	7.229992	4.756594	low
GSM1672(10.2	1	10.29609	13.75634	10.46526	6.672373	8.00449	8.079933	high
GSM1672(2.516667	1	9.76147	13.5272	8.561513	7.015145	5.870777	6.886362	high
GSM1672(6.541667	1	10.67859	13.82443	8.717053	7.121185	7.334819	6.435862	high
GSM1672(6.1	1	10.39067	13.53898	8.311866	7.013257	8.404631	4.842088	low
GSM1672(5.433333	1	10.5339	13.77525	8.890673	6.407761	7.957056	5.469215	low
GSM1672(12.15	0	9.949282	13.32293	8.728002	6.926077	6.921972	5.665003	low
GSM1672(6.141667	1	11.89042	13.48559	9.661296	6.528298	7.408848	4.939441	low
GSM1672(0.275	1	10.46043	14.03403	8.760954	6.529216	6.569107	6.998827	high
GSM1672'	1.625	1	12.08345	13.58088	9.299111	7.151721	8.507485	4.81197	low
GSM1672'	0.7	1	10.54453	14.33546	9.40095	6.027434	7.349091	7.643474	high
GSM1672'	2.241667	1	10.35991	13.8578	9.986419	6.839278	8.171202	7.766528	high
GSM1672'	10.81667	0	9.571753	13.44065	10.20467	7.514217	10.09059	7.279739	high
GSM1672'	1.633333	1	11.61083	13.90659	9.221077	6.851635	7.328747	6.13489	high
GSM1672'	8.783333	1	11.25051	13.67184	8.982245	6.444634	7.291364	5.112252	low
GSM1672'	13.125	1	11.82468	14.06699	9.310539	6.573801	7.133851	6.27332	high
GSM1672'	10.04167	1	10.08265	13.72403	9.395726	6.633888	6.78326	7.295665	high
GSM1672'	3.983333	1	9.425103	13.61159	10.24872	6.590959	6.714039	9.010343	high
GSM1672'	10.83333	1	9.533273	13.79561	9.867554	6.768855	7.243555	8.856696	high
GSM1672'	4.358333	0	10.31858	14.0195	9.038871	6.509675	8.65854	6.248654	high
GSM1672'	5.783333	0	11.38607	13.965	8.434845	6.269313	7.874182	4.722121	low
GSM1672'	2.1625	1	10.30359	13.47355	8.569164	6.997279	8.051301	5.147186	low
GSM1672'	10.15	0	8.875884	13.57784	9.434168	7.797763	7.527141	9.672961	high
GSM1672'	2.716667	1	10.23867	14.20297	10.17545	6.983793	6.596026	11.33212	high
GSM1672'	3.35	1	11.5447	13.88874	9.015206	6.403298	6.897253	5.592159	low
GSM1672'	1.208333	1	11.08977	14.12294	10.2424	7.880195	8.000648	10.39178	high
GSM1672'	0.766667	1	8.332475	13.96682	8.677193	6.86839	7.017833	9.320397	high
GSM1672'	1.583333	1	9.380777	13.45495	9.479924	6.266213	6.662419	6.806822	high
GSM1672'	10.1	0	10.52668	13.70252	8.831578	6.524764	8.482421	5.120375	low
GSM1672'	0.75	1	9.862549	13.58151	8.991739	6.13729	8.792045	4.958017	low
GSM1672'	8.133333	0	10.17404	14.01596	9.387608	6.792386	8.699736	7.202106	high
GSM1672'	14.65833	0	9.932507	13.55284	10.32233	6.626217	8.347644	7.246972	high
GSM1672'	3.775	1	10.27785	14.18509	9.284231	6.277908	6.698982	8.04574	high

Supplementary Table 4. List of DEGs between normal than tumor in TCGA database

gene	logFC	AveExpr	t	P.Value	adj.P.Val	B
GPM6A	2.778249624	0.647571565	37.90264944	5.14E-158	1.01E-153	350.523958
SERTM1	2.358019267	0.406679703	37.15232536	1.74E-154	1.71E-150	342.4378591
SH3GL3	1.26346089	0.250475837	36.17924803	7.29E-150	4.78E-146	331.8479095
SLC6A4	3.868215395	0.714455861	36.02657162	3.92E-149	1.92E-145	330.1758682
SGCG	1.731139528	0.464160961	34.82466249	2.39E-143	9.41E-140	316.9155697
C10orf67	1.185393219	0.258976412	34.55784188	4.72E-142	1.54E-138	313.9486644
RS1	1.122518642	0.249868526	34.46973963	1.26E-141	3.55E-138	312.9671936
ANGPT4	1.142097943	0.237410404	34.38276341	3.35E-141	8.22E-138	311.9973848
ITLN2	3.821337902	0.904781456	33.05470008	1.08E-134	2.35E-131	297.0821825
WNT3A	2.170047747	0.550873829	32.82250538	1.51E-133	2.96E-130	294.4542855
GYPE	1.269367035	0.396059965	32.48104905	7.38E-132	1.32E-128	290.5792089
CD300LG	1.895147017	0.351103705	32.11254826	4.99E-130	8.17E-127	286.3832902
RTKN2	3.467985356	1.61367099	31.53501581	3.79E-127	5.72E-124	279.7788606
SPAAR	1.389070749	0.741946757	30.38366528	2.31E-121	3.02E-118	266.5137089
SCUBE1	1.751724264	0.528060763	30.02325826	1.53E-119	1.88E-116	262.3356916
MYZAP	2.187791222	0.987360241	29.72577948	4.92E-118	5.69E-115	258.8784471
LGI3	3.631298255	1.018603097	29.66000255	1.06E-117	1.16E-114	258.1129599
CA4	3.313336157	1.041610122	29.56382437	3.27E-117	3.38E-114	256.9930079
FABP4	4.938887641	2.010070834	29.40349609	2.13E-116	2.09E-113	255.1243168
FAM107A	3.850324817	1.745860279	29.36076655	3.52E-116	3.29E-113	254.6259237
GRIA1	1.606153719	0.416324595	29.08606498	8.80E-115	7.52E-112	251.4182523
RXFP1	1.138069298	0.384584015	28.99211692	2.65E-114	2.17E-111	250.319829
NECAB1	1.740646454	0.650561461	28.59660196	2.77E-112	2.09E-109	245.6879786
CNTN6	1.679879974	0.47524594	28.45598184	1.45E-111	1.06E-108	244.0383242
FXYD1	1.333944386	0.541476891	28.19937246	2.99E-110	2.10E-107	241.0242467
TEK	2.731336454	1.840121231	27.87160322	1.44E-108	9.73E-106	237.1676155
NCKAP5	2.266772615	0.785614956	27.68093007	1.37E-107	8.68E-105	234.9207785
CHRM1	1.122962741	0.21436312	27.50267975	1.13E-106	6.94E-104	232.8182144
TAL1	1.387480677	0.659809693	27.30517184	1.17E-105	6.99E-103	230.4861986
CCDC85A	1.183151619	0.480055462	27.20926217	3.66E-105	2.12E-102	229.3529315
STX11	2.711212989	2.330854137	27.17861495	5.27E-105	2.96E-102	228.9906912
GPD1	3.076602923	1.227096937	27.10384075	1.28E-104	6.98E-102	228.1066573
STXBP6	2.147766194	0.81880504	27.03024107	3.06E-104	1.63E-101	227.2361997
ST8SIA6	1.653732584	0.56884088	26.80180325	4.62E-103	2.39E-100	224.5325867
KANK3	2.040225706	1.322255434	26.62318492	3.87E-102	1.95E-99	222.4166815
EDNRB	3.160259667	2.140779244	26.56436464	7.78E-102	3.82E-99	221.7195462
LIMS2	2.218423936	1.698588259	26.26795695	2.65E-100	1.27E-97	218.2040142
HSPA12B	2.115101298	1.660449672	25.74619985	1.33E-97	6.09E-95	212.0064637
ADRB2	2.455109244	1.48696329	25.74273119	1.39E-97	6.20E-95	211.9652264
ADAMTS8	2.703389294	1.139870429	25.69400855	2.48E-97	1.08E-94	211.3859414
PYCR1	-3.283780832	4.889937575	-25.61873502	6.10E-97	2.61E-94	210.4908161
GPIHBP1	3.157099298	1.452853366	25.51557248	2.09E-96	8.74E-94	209.2637315
ANKRD1	3.761272051	1.30544266	25.4930456	2.74E-96	1.12E-93	208.995735
UPK3B	4.371805848	1.857261596	25.47934053	3.22E-96	1.29E-93	208.8326813
PRX	2.694422553	1.76999014	25.29547479	2.90E-95	1.14E-92	206.64461
RSPO1	1.358194895	0.40359631	25.25773554	4.55E-95	1.75E-92	206.1953753
OTUD1	1.816942355	2.973790402	25.23349505	6.07E-95	2.29E-92	205.9068039
JAM2	1.966513551	1.639567177	25.22820665	6.47E-95	2.40E-92	205.843846
MYOC	1.401821514	0.271048018	25.22162358	7.00E-95	2.55E-92	205.765474
SEMA3G	2.292854247	1.578701378	25.1253386	2.21E-94	7.90E-92	204.6190596
HBA1	1.553886186	0.375441542	25.01544747	8.22E-94	2.88E-91	203.3103542
ARHGAP6	1.23854606	0.724634528	24.8175561	8.76E-93	3.02E-90	200.9529391
PTPN21	2.000397366	1.953631753	24.79152503	1.20E-92	4.05E-90	200.642778
LDB2	2.181375454	2.068855224	24.73565326	2.33E-92	7.64E-90	199.9770194

ACADL	2.178089599	0.909454599	24.64805428	6.65E-92	2.14E-89	198.9330898
TMEM100	3.838353317	1.831766901	24.54846667	2.19E-91	6.94E-89	197.7461335
CLEC1A	1.413729513	1.037760385	24.52892415	2.77E-91	8.62E-89	197.5131938
ACVRL1	2.304306377	3.010416936	24.5135742	3.32E-91	1.02E-88	197.330224
NOVA2	1.129172166	0.649206948	24.48762677	4.53E-91	1.37E-88	197.0209258
ROBO4	2.369279485	2.107097328	24.4841316	4.73E-91	1.41E-88	196.979262
WWC2	2.002202132	2.198864706	24.38433776	1.56E-90	4.57E-88	195.7896132
CCM2L	1.686337621	1.166753626	24.26209705	6.73E-90	1.92E-87	194.3322162
BTNL9	2.515343221	1.147319896	24.17886032	1.82E-89	5.12E-87	193.3397566
ANGPTL7	1.058446518	0.230219638	24.1627194	2.21E-89	6.12E-87	193.1472964
S1PR1	2.634631932	3.194938906	24.15392478	2.46E-89	6.70E-87	193.0424308
CLEC3B	3.850323912	3.067279813	24.09047277	5.25E-89	1.39E-86	192.2858242
FHL1	3.451676005	2.690965106	24.07533709	6.29E-89	1.65E-86	192.1053414
ECSCR	1.92850358	2.014902517	24.05541164	7.99E-89	2.06E-86	191.867742
AGER	6.216060798	4.397378457	24.032187	1.05E-88	2.69E-86	191.5907992
CLIC5	3.670915492	2.177540909	23.94390197	3.03E-88	7.64E-86	190.5380211
RAMP2	2.719361691	3.716599827	23.85992405	8.29E-88	2.06E-85	189.5365837
NMUR1	1.102508144	0.514465201	23.83897538	1.06E-87	2.61E-85	189.2867689
TCF21	2.477477622	1.305948501	23.82269852	1.29E-87	3.14E-85	189.0926657
PRKG2	1.302019449	0.613618536	23.76404198	2.61E-87	6.18E-85	188.3931806
ODAM	1.290163936	0.363969545	23.63312987	1.25E-86	2.89E-84	186.8320589
ALKAL2	1.470133887	0.541947438	23.56392778	2.86E-86	6.54E-84	186.0068497
PECAM1	2.24606215	4.744001265	23.39604452	2.13E-85	4.82E-83	184.0050237
LYVE1	2.614262495	1.665014604	23.36924903	2.94E-85	6.57E-83	183.6855372
EPAS1	2.584988366	5.835388532	23.32677767	4.89E-85	1.08E-82	183.1791593
CD101	1.708316015	1.149842184	23.2951516	7.14E-85	1.56E-82	182.8021
FOXF1	2.182746652	1.84524006	23.25929362	1.10E-84	2.37E-82	182.3745996
RGCC	2.834389397	5.543240482	23.21444318	1.87E-84	4.00E-82	181.8399128
GPR146	1.010522176	0.622247747	23.15338632	3.89E-84	8.22E-82	181.1120629
SIRPB1	1.78480254	0.975690206	23.14807101	4.15E-84	8.67E-82	181.0487024
FRMD3	1.329757535	0.733034753	23.04661202	1.40E-83	2.89E-81	179.8393551
RAMP3	2.893488664	3.425102015	23.0079791	2.22E-83	4.53E-81	179.3789119
EMP2	2.762032308	4.944441504	22.9795933	3.11E-83	6.30E-81	179.040615
FCN3	4.041817547	2.360519379	22.97298019	3.37E-83	6.68E-81	178.9618033
FHL5	1.936739353	1.121997427	22.96782468	3.58E-83	7.04E-81	178.9003631
ABCA8	1.927415826	0.910063954	22.94420893	4.75E-83	9.15E-81	178.6189314
MCEMP1	4.12744108	2.338709552	22.86186992	1.27E-82	2.43E-80	177.6377741
ARHGEF26	2.326275391	2.038262505	22.82035665	2.09E-82	3.95E-80	177.1431531
GSTM5	1.21036648	0.682347837	22.78921072	3.03E-82	5.67E-80	176.7720816
USHBP1	1.109373638	0.691665142	22.77208762	3.72E-82	6.90E-80	176.5680871
SPOCK2	3.24116707	3.622837393	22.76245621	4.18E-82	7.67E-80	176.4533472
SCN4B	1.959427509	1.138970132	22.75495349	4.57E-82	8.31E-80	176.363968
GRK5	2.148635477	2.115757696	22.70483442	8.31E-82	1.50E-79	175.7669397
MGAT3	2.589605246	1.35153487	22.68736826	1.02E-81	1.83E-79	175.558894
SLC19A3	1.84798736	0.847170935	22.66965626	1.27E-81	2.24E-79	175.3479279
VEGFD	3.330330068	1.568848271	22.66290268	1.37E-81	2.41E-79	175.2674888
FGFBP2	1.848374198	0.645934394	22.59107148	3.24E-81	5.58E-79	174.4120115
RGS9	1.045885491	0.574070524	22.59038538	3.27E-81	5.58E-79	174.403841
FGD5	1.839823456	1.953271941	22.48174366	1.20E-80	2.03E-78	173.1102449
CAV1	3.884710949	4.883969083	22.47594831	1.28E-80	2.15E-78	173.0412496
TNNC1	3.642776143	2.644135741	22.47543336	1.29E-80	2.15E-78	173.035119
STARD13	1.469334986	1.502211342	22.46245005	1.51E-80	2.49E-78	172.8805529
FMO2	3.137443483	2.608085891	22.45645986	1.62E-80	2.65E-78	172.8092415
GDF10	2.583716903	1.191186855	22.3535407	5.53E-80	8.91E-78	171.5841996
ARHGEF15	1.861194991	1.655338997	22.32878106	7.44E-80	1.19E-77	171.2895391
CALCRL	2.503008974	2.677390296	22.32022655	8.24E-80	1.30E-77	171.1877381

PLAC9	2.25830011	2.155378944	22.31166035	9.12E-80	1.42E-77	171.0858006
NXPB3	1.13558764	0.630537674	22.21034726	3.06E-79	4.73E-77	169.8803758
C14orf132	2.180884126	1.634973485	22.20255551	3.36E-79	5.15E-77	169.787685
EMCN	2.288697787	1.825078702	22.19760777	3.56E-79	5.42E-77	169.7288277
CDH5	2.355735272	3.194904055	22.1463629	6.57E-79	9.92E-77	169.1192849
PDLIM2	1.442511367	1.607063662	22.07104067	1.61E-78	2.42E-76	168.2235361
LRRN3	1.634841753	0.6989486	22.05831616	1.88E-78	2.79E-76	168.0722361
SH2D3C	1.922876977	2.372233712	22.02463785	2.81E-78	4.15E-76	167.6718186
EFCC1	1.898454852	1.382034651	21.94481579	7.27E-78	1.07E-75	166.722969
PTPRB	2.180041445	1.963064984	21.93583415	8.10E-78	1.18E-75	166.6162211
CAVIN2	3.432926396	3.694935249	21.84265242	2.46E-77	3.55E-75	165.5089611
ADGRE3	1.135885948	0.470984673	21.83979037	2.54E-77	3.65E-75	165.4749582
MYCT1	1.82911315	1.9522529	21.8176501	3.31E-77	4.72E-75	165.211932
LIN7A	1.548050783	0.741764272	21.79891132	4.14E-77	5.86E-75	164.9893338
SOX7	2.045984835	1.365895669	21.74438038	7.94E-77	1.11E-74	164.341657
TENT5B	2.410831848	1.816873691	21.66604074	2.02E-76	2.81E-74	163.4114584
CDO1	1.739917374	0.95017665	21.65170591	2.39E-76	3.31E-74	163.2412818
PRKCE	1.330948603	1.575514728	21.60695699	4.08E-76	5.61E-74	162.7101126
CYYR1	1.906327499	2.338014548	21.53644072	9.45E-76	1.29E-73	161.8733033
SEMA6A	1.566677281	0.9285801	21.52302776	1.11E-75	1.50E-73	161.714164
CD36	2.76741359	1.789115957	21.47985485	1.85E-75	2.49E-73	161.2020034
TGFBR3	2.096706333	1.545503836	21.38141815	5.98E-75	8.00E-73	160.0346491
ALDH18A1	-1.56475399	4.749827392	-21.37157885	6.73E-75	8.93E-73	159.9179969
GIMAP8	2.160551749	2.373685981	21.35712591	7.99E-75	1.05E-72	159.7466571
CTXND1	1.137541271	0.32241917	21.30238146	1.53E-74	2.01E-72	159.0977761
THSD1	1.497718018	1.288391063	21.25717133	2.62E-74	3.41E-72	158.5620444
RASIP1	1.880497124	1.909883933	21.24035805	3.20E-74	4.14E-72	158.3628429
VIPR1	2.486166947	1.725313325	21.21714042	4.22E-74	5.42E-72	158.0877934
SOSTDC1	2.810817902	0.992108267	21.21662105	4.25E-74	5.42E-72	158.081641
SOX17	1.663734883	1.074550622	21.18796559	5.97E-74	7.57E-72	157.7422206
FAM189A2	2.658959604	1.991847586	21.17092734	7.31E-74	9.21E-72	157.5404301
STARD8	1.623052893	1.688633232	21.15349309	9.00E-74	1.13E-71	157.3339693
FEZ1	1.409150319	1.222359554	21.12171836	1.31E-73	1.63E-71	156.9577368
HIGD1B	2.375949095	2.057973946	21.04040919	3.45E-73	4.23E-71	155.9952971
ERG	1.642458515	1.738598308	20.97560362	7.45E-73	9.03E-71	155.2285358
AGRP	1.694327992	0.771124829	20.97270977	7.71E-73	9.29E-71	155.1943036
NPR1	2.34540126	1.878630564	20.88569714	2.16E-72	2.56E-70	154.1652864
PHACTR1	1.698810016	1.306745267	20.84405013	3.55E-72	4.17E-70	153.6729637
INMT	3.649635753	2.950345013	20.82931055	4.23E-72	4.91E-70	153.4987536
FPR2	1.792765769	0.883904727	20.8172009	4.88E-72	5.64E-70	153.3556395
ADRB1	2.395255994	1.197613025	20.79236985	6.55E-72	7.52E-70	153.0622165
NLRC4	1.392332211	1.219951263	20.72880082	1.39E-71	1.58E-69	152.3112528
IGSF10	1.651753882	0.732087297	20.72005776	1.54E-71	1.74E-69	152.2079927
COL6A6	1.850668418	0.913772356	20.69786219	2.01E-71	2.25E-69	151.9458787
SMAD6	1.662173805	1.417345543	20.65242168	3.44E-71	3.84E-69	151.409381
FAM110D	1.353220304	0.98202959	20.61674391	5.25E-71	5.79E-69	150.9882656
LRRC36	2.140826829	0.912944988	20.6093064	5.73E-71	6.29E-69	150.9004916
HBA2	4.119652558	2.894734473	20.51862229	1.68E-70	1.80E-68	149.8306511
PKNOX2	1.262912909	0.70073378	20.29654371	2.32E-69	2.45E-67	147.2137036
HTR3C	1.001336	0.184958293	20.22228142	5.58E-69	5.86E-67	146.3396044
DNASE1L3	2.026707083	0.88758609	20.21475011	6.10E-69	6.37E-67	146.2509865
PPP1R14B	-2.036646497	5.557289591	-20.11583524	1.96E-68	2.04E-66	145.087601
ARC	1.523525852	0.59186087	20.08520712	2.81E-68	2.91E-66	144.7275621
SLC39A8	2.612334346	4.260009452	20.08029748	2.98E-68	3.07E-66	144.669857
TMEM177	-1.185835843	2.319181457	-20.06811145	3.44E-68	3.52E-66	144.5266398
ANOS1	2.685973324	2.465483659	20.00511285	7.24E-68	7.29E-66	143.7864818

GOLM1	-2.428754504	5.727232768	-19.98487339	9.19E-68	9.16E-66	143.5487777
SLIT2	2.035324614	1.829328272	19.91924417	1.99E-67	1.97E-65	142.7782796
RBP2	1.683205665	0.5629709	19.90175807	2.45E-67	2.40E-65	142.5730654
DACH1	1.523468714	0.834785634	19.85261665	4.36E-67	4.24E-65	141.996522
ADAMTSL3	1.343544828	0.817850351	19.74881988	1.48E-66	1.43E-64	140.7795963
ANGPTL1	1.528154238	0.825204443	19.7411163	1.62E-66	1.55E-64	140.6893256
CLEC14A	2.139864226	3.576678034	19.69197854	2.89E-66	2.74E-64	140.1136826
DPEP2	1.638834356	1.418890293	19.63823328	5.43E-66	5.13E-64	139.4843737
CLDN18	5.61496127	2.997589546	19.6342535	5.69E-66	5.33E-64	139.4377871
SEMA5A	2.096199542	1.547479025	19.63421386	5.70E-66	5.33E-64	139.437323
MMRN2	1.811023469	2.477861216	19.58552794	1.01E-65	9.40E-64	138.867561
GRASP	1.905492022	2.111128942	19.56354045	1.31E-65	1.21E-63	138.6103354
KCNT2	1.004184307	0.392431132	19.53060956	1.92E-65	1.77E-63	138.2251914
CAT	1.893481379	4.939457027	19.45146073	4.87E-65	4.41E-63	137.3000289
GLDN	1.551210278	0.953930566	19.44712324	5.12E-65	4.62E-63	137.24935
LMO2	1.599536481	2.311896443	19.39279643	9.69E-65	8.69E-63	136.6147937
ACKR4	1.292570984	0.640209008	19.3881863	1.02E-64	9.13E-63	136.5609623
GPA33	1.948491176	0.755986856	19.26445918	4.36E-64	3.87E-62	135.1172148
PTCRA	1.041497951	0.569062134	19.24921303	5.21E-64	4.61E-62	134.9394436
HHIP	2.455850786	1.073383764	19.19110808	1.03E-63	9.05E-62	134.2622085
RASGRP4	1.05656848	0.863747847	19.17855872	1.19E-63	1.04E-61	134.1159983
MME	2.292179282	1.376489626	19.13015427	2.10E-63	1.83E-61	133.5522393
ADGRE1	1.500978413	0.758202038	19.10120187	2.94E-63	2.53E-61	133.2151826
ARHGAP31	1.94076621	2.404849115	19.07157299	4.16E-63	3.56E-61	132.8703657
PLA2G4F	2.455578521	1.673641279	19.05099205	5.28E-63	4.51E-61	132.6309166
EFNA4	-1.894199656	3.786891761	-19.04868576	5.43E-63	4.62E-61	132.6040876
SRPK1	-1.415479406	3.678654	-19.00351977	9.20E-63	7.79E-61	132.0788181
VEPH1	2.426837805	1.624122294	19.00158043	9.41E-63	7.93E-61	132.0562702
TGM1	1.230254907	0.718309683	18.99265844	1.04E-62	8.77E-61	131.9525447
PAICS	-1.655271121	3.965222434	-18.90149494	3.02E-62	2.51E-60	130.8933226
SBSPON	1.61353991	0.896382182	18.77079394	1.39E-61	1.13E-59	129.3767545
CLDN5	2.571441412	2.955065089	18.75659651	1.64E-61	1.33E-59	129.2121645
GIMAP1	1.423081801	1.456641465	18.7338368	2.13E-61	1.73E-59	128.9483735
SLC14A1	1.141331841	0.471329081	18.73000986	2.23E-61	1.80E-59	128.9040257
ATIC	-1.230856646	4.593150728	-18.72380128	2.40E-61	1.93E-59	128.8320833
AOC3	2.668243462	3.600893246	18.68142147	3.92E-61	3.14E-59	128.341155
RAI2	1.905023466	2.288325148	18.66029222	5.01E-61	3.99E-59	128.0964928
C1QTNF7	1.412230219	0.778563732	18.617997	8.19E-61	6.49E-59	127.6069433
RHOJ	1.497864623	2.013265456	18.61062455	8.93E-61	7.04E-59	127.5216378
RCC1	-1.565705646	3.946704655	-18.58204476	1.24E-60	9.78E-59	127.1910228
UBE2T	-2.551983139	3.692285321	-18.54775983	1.85E-60	1.44E-58	126.7945739
SULT1C4	1.345370162	0.862753072	18.53995742	2.03E-60	1.57E-58	126.704377
PEAR1	1.34317875	1.249698761	18.52210828	2.49E-60	1.92E-58	126.4980736
DKK2	1.396318428	1.021059164	18.50851176	2.92E-60	2.24E-58	126.3409556
LRRC32	1.996264889	3.141279926	18.50270859	3.12E-60	2.39E-58	126.2739044
ABI3BP	2.182547782	1.828511195	18.49111576	3.57E-60	2.72E-58	126.1399735
NME1	-1.949818827	3.922778987	-18.49000925	3.62E-60	2.75E-58	126.1271912
CGNL1	2.039546025	2.446520409	18.44480802	6.11E-60	4.62E-58	125.6051937
CXCR2	1.253827198	0.676933913	18.44220991	6.30E-60	4.74E-58	125.5751998
CORO2B	1.289521796	0.900075056	18.44151193	6.35E-60	4.76E-58	125.5671421
OR7E47P	1.652176055	1.496483138	18.43176061	7.11E-60	5.31E-58	125.454578
PIP5K1B	1.863824265	1.428879685	18.42110822	8.05E-60	5.99E-58	125.3316294
CFP	1.202024442	0.904677367	18.41972474	8.18E-60	6.06E-58	125.3156628
TNXB	2.111125026	1.310745786	18.37649122	1.35E-59	9.93E-58	124.8168613
ADPRH	1.312044345	2.206057915	18.36700024	1.51E-59	1.10E-57	124.7074001
TMEM88	1.668171466	1.794195643	18.32725985	2.39E-59	1.74E-57	124.2492241

F11	1.383127234	0.502024208	18.2842782	3.92E-59	2.83E-57	123.7539663
SFXN1	-1.208412119	2.735811263	-18.25468921	5.52E-59	3.97E-57	123.4132013
PI16	1.659836321	0.604176679	18.24137998	6.44E-59	4.62E-57	123.2599708
CASQ2	1.130527618	0.498834738	18.21050992	9.20E-59	6.57E-57	122.9046737
HBB	4.559863442	4.423530307	18.20812905	9.46E-59	6.73E-57	122.8772777
MAMDC2	2.447973615	1.783639094	18.19010595	1.16E-58	8.23E-57	122.6699222
SASH1	1.516435684	2.256703966	18.1783656	1.33E-58	9.39E-57	122.5348788
THBD	2.354528617	3.452272707	18.16240986	1.60E-58	1.13E-56	122.3513848
ADH1B	3.729448555	2.577024817	18.14532756	1.95E-58	1.37E-56	122.1549827
PALMD	1.470334992	1.346630019	18.13283474	2.26E-58	1.57E-56	122.0113788
CSRN1P1	2.078583696	4.073050046	18.12531298	2.46E-58	1.70E-56	121.9249296
DES	3.046914526	2.22555282	18.12478205	2.48E-58	1.71E-56	121.9188278
CPED1	1.484706144	1.286480207	18.12105554	2.59E-58	1.78E-56	121.8760021
RSPO2	1.22107655	0.477601771	18.10003787	3.29E-58	2.26E-56	121.6345076
GIMAP6	1.918746732	2.795449309	18.0913375	3.64E-58	2.48E-56	121.5345617
KL	1.511027627	0.799713117	18.08479238	3.93E-58	2.67E-56	121.4593829
TIE1	1.684026242	2.339568077	18.0639572	4.99E-58	3.38E-56	121.2201139
FAM162B	1.79603594	1.672826932	18.06359072	5.02E-58	3.39E-56	121.215906
CCL23	1.921907748	1.316580188	18.05907985	5.28E-58	3.55E-56	121.1641137
TCEAL2	1.631713034	0.687017217	18.0438409	6.30E-58	4.22E-56	120.9891713
CNOT11	-1.130503611	4.755154151	-18.03460042	7.01E-58	4.68E-56	120.8831106
SELP	1.843247503	1.704795041	17.94552607	1.95E-57	1.30E-55	119.8614927
OCIAD2	-1.989893229	5.166357077	-17.93543739	2.19E-57	1.45E-55	119.7458707
GLIPR2	2.123072663	3.653123697	17.89383271	3.54E-57	2.33E-55	119.2692486
SPN	1.968243303	2.128463724	17.88737789	3.81E-57	2.51E-55	119.19533
KANK2	1.477169571	3.669800024	17.88602571	3.87E-57	2.54E-55	119.1798462
PEAK1	1.207154879	1.610201708	17.87987202	4.16E-57	2.71E-55	119.1093844
ODF3L1	1.023303887	0.608303302	17.86143304	5.14E-57	3.34E-55	118.898293
ABCG2	1.238589037	1.042621122	17.85628908	5.45E-57	3.54E-55	118.8394153
AFF3	1.358053925	0.71349624	17.8384131	6.70E-57	4.33E-55	118.6348442
RADIL	1.046442805	0.574469284	17.81754598	8.51E-57	5.48E-55	118.3961159
PLPP2	-2.13061408	3.403271569	-17.80691782	9.62E-57	6.17E-55	118.2745558
ST6GALNAC5	1.771379222	1.454129477	17.77858173	1.33E-56	8.49E-55	117.9505614
CD93	2.11940134	3.845143724	17.74914387	1.87E-56	1.18E-54	117.6141253
ANGPT1	1.762034358	1.391043489	17.74808421	1.89E-56	1.19E-54	117.6020177
TBX3	1.598885472	1.540149554	17.74434219	1.97E-56	1.24E-54	117.5592636
SPRYD7	1.028528714	2.467243613	17.74371279	1.99E-56	1.24E-54	117.5520727
DENND3	1.415834088	2.109581992	17.73975718	2.08E-56	1.30E-54	117.5068814
ETV4	-2.666047015	3.30271815	-17.73290855	2.25E-56	1.40E-54	117.4286454
FAM136A	-1.138616322	3.939460909	-17.70989126	2.93E-56	1.81E-54	117.1657687
CTHRC1	-3.225755602	4.547802017	-17.62365809	7.87E-56	4.84E-54	116.1817955
HBEGF	2.37374159	3.205889556	17.61042327	9.15E-56	5.62E-54	116.0309024
SLIT3	2.046092694	1.656367148	17.59565297	1.08E-55	6.63E-54	115.8625422
CAVIN1	2.107728821	5.668370694	17.59484302	1.09E-55	6.67E-54	115.8533112
CAV2	2.516286009	3.635209125	17.58967633	1.16E-55	7.06E-54	115.7944289
SYNM	1.243881563	1.379119076	17.57685933	1.34E-55	8.15E-54	115.6483821
CPB2	3.22074962	1.476286894	17.57127721	1.43E-55	8.66E-54	115.5847849
HEG1	1.997772822	3.13756596	17.53132562	2.26E-55	1.36E-53	115.1297908
PDZD2	1.777695545	1.399472553	17.52083756	2.55E-55	1.53E-53	115.0103973
B3GNT3	-3.087249218	3.643926637	-17.50628944	3.01E-55	1.80E-53	114.8448203
PDIA4	-1.718717887	6.933460156	-17.47500459	4.31E-55	2.57E-53	114.4888967
GUCY1A2	1.170405249	0.833955749	17.41903865	8.16E-55	4.84E-53	113.8526591
HSPB6	2.422520834	2.26109319	17.40422436	9.66E-55	5.72E-53	113.6843495
SPTBN1	1.658617436	4.552085949	17.38969646	1.14E-54	6.71E-53	113.5193361
PNPLA6	1.324313371	3.49549958	17.35766543	1.64E-54	9.60E-53	113.1556643
KIAA1324L	1.709792862	1.768848007	17.34941392	1.80E-54	1.05E-52	113.0620123

SESN1	1.395953445	2.325435095	17.33459909	2.14E-54	1.24E-52	112.893903
BCHE	1.60401386	0.916572082	17.3244933	2.40E-54	1.39E-52	112.7792542
FXYD6	1.591082033	2.11223796	17.29250012	3.45E-54	1.99E-52	112.4164327
SCN7A	2.036708149	1.542612062	17.28644737	3.70E-54	2.13E-52	112.3478144
RETN	2.990416316	1.871634388	17.2774248	4.10E-54	2.35E-52	112.2455419
SNX22	1.13917776	1.117252906	17.23798083	6.42E-54	3.68E-52	111.7986329
RAPGEF4	1.0027703	0.852804419	17.17085339	1.38E-53	7.84E-52	111.0388022
TNS1	2.150775539	4.084453552	17.15733158	1.61E-53	9.11E-52	110.8858593
TSPAN18	1.645713468	1.973141295	17.14986644	1.75E-53	9.89E-52	110.8014387
JCAD	1.836548551	2.560323707	17.14934578	1.76E-53	9.92E-52	110.7955513
TOP2A	-2.805612445	3.640280117	-17.13744001	2.01E-53	1.13E-51	110.6609387
P2RY1	1.056698248	0.996723345	17.12770911	2.25E-53	1.26E-51	110.5509385
LMCD1	1.37924201	2.186918272	17.08815739	3.52E-53	1.97E-51	110.1040429
DUOX1	2.718431446	2.313852746	17.08656639	3.58E-53	2.00E-51	110.086073
COX4I2	2.056741547	2.723427343	17.07548866	4.06E-53	2.26E-51	109.9609687
GPM6B	1.510657017	1.397044508	17.06281757	4.69E-53	2.60E-51	109.8179022
DNASE2B	1.238352492	0.559623952	17.05063762	5.39E-53	2.98E-51	109.6804134
ADARB1	1.302963779	1.77450085	17.02400827	7.28E-53	4.01E-51	109.3799285
COX7A1	1.61465377	2.586819795	16.97874505	1.22E-52	6.67E-51	108.8695302
WFS1	1.591771753	3.912573375	16.97194589	1.31E-52	7.19E-51	108.7928997
CD300C	1.660282933	1.73514325	16.95977972	1.51E-52	8.23E-51	108.6558049
LAMP3	3.17192509	4.550376803	16.94627432	1.76E-52	9.56E-51	108.5036568
LTBP4	2.095891344	3.723944654	16.87207816	4.06E-52	2.19E-50	107.6684972
FFAR4	1.294527106	0.792982435	16.86816329	4.25E-52	2.28E-50	107.6244648
CCT3	-1.333805367	6.194610273	-16.85722206	4.81E-52	2.57E-50	107.5014216
F8	1.213714452	1.54388633	16.83191873	6.40E-52	3.41E-50	107.2169668
CAMP	1.547188522	0.740731386	16.81261584	7.95E-52	4.23E-50	107.000064
PAFAH1B3	-1.970221817	4.390111561	-16.80587913	8.58E-52	4.56E-50	106.9243845
DAPK2	1.405479873	1.357109004	16.78257325	1.12E-51	5.91E-50	106.6626477
CASKIN2	1.349900094	2.936966853	16.74567451	1.69E-51	8.91E-50	106.2485072
LGR4	-2.002717391	3.189827376	-16.73508808	1.91E-51	9.99E-50	106.1297453
FGFR4	2.283133381	1.914617153	16.72749316	2.08E-51	1.08E-49	106.0445589
GFOD1	1.006426557	0.922260288	16.71710406	2.33E-51	1.22E-49	105.9280535
IL3RA	1.485630329	2.928720092	16.68309706	3.42E-51	1.77E-49	105.5468656
TACC1	1.753889671	3.212568782	16.66109318	4.38E-51	2.26E-49	105.3003636
NOTCH4	1.360167775	1.852682162	16.62003935	6.96E-51	3.57E-49	104.8407511
PRAM1	1.480234935	1.362321605	16.61445515	7.41E-51	3.79E-49	104.7782643
NDST1	1.40834628	3.613774713	16.59374714	9.35E-51	4.77E-49	104.5466065
SFTPC	7.721358434	5.952172636	16.58605448	1.02E-50	5.19E-49	104.4605753
FOLR3	1.396999087	0.479735983	16.52093099	2.12E-50	1.07E-48	103.732822
TRPV2	1.722825822	3.104892803	16.49472519	2.84E-50	1.43E-48	103.4402564
SFXN4	-1.272307196	3.734730811	-16.4924958	2.91E-50	1.46E-48	103.4153747
SLC5A9	1.274809375	0.590841451	16.48792354	3.07E-50	1.54E-48	103.3643485
TBX4	1.837753973	1.773066422	16.47744501	3.45E-50	1.72E-48	103.2474274
ITGA8	1.747408428	1.694099734	16.47728701	3.45E-50	1.72E-48	103.2456647
FLAD1	-1.265773579	3.701169011	-16.44915516	4.73E-50	2.35E-48	102.9318964
MANF	-1.356988105	5.203198428	-16.44297951	5.07E-50	2.52E-48	102.8630419
GYPC	1.594854675	2.809876211	16.44041726	5.22E-50	2.58E-48	102.8344771
CDC20	-2.734346343	3.49765086	-16.43767012	5.38E-50	2.66E-48	102.8038529
GPX3	2.497723706	5.844887537	16.43542885	5.52E-50	2.72E-48	102.7788693
FGF2	1.115947575	0.744496349	16.43231105	5.72E-50	2.81E-48	102.744117
TMEM204	1.599694698	3.269418771	16.41171938	7.20E-50	3.52E-48	102.5146527
CXCR1	1.124581521	0.504310051	16.39803691	8.39E-50	4.09E-48	102.3622381
MS4A7	2.100838375	3.092661375	16.39450775	8.73E-50	4.24E-48	102.3229328
FGR	1.913977543	2.864268183	16.36815789	1.17E-49	5.68E-48	102.0295622
TMEM184A	-1.904262886	2.41246472	-16.34481619	1.52E-49	7.36E-48	101.7698252

FLI1	1.343132281	1.930623043	16.29160997	2.76E-49	1.32E-47	101.1782689
TRAP1	-1.070703029	3.549902627	-16.27769215	3.22E-49	1.54E-47	101.0236436
GGCT	-1.563604763	4.841963286	-16.23081106	5.43E-49	2.58E-47	100.5031556
AMOTL1	1.573704342	2.347452658	16.2149221	6.48E-49	3.07E-47	100.3268764
EIF2AK1	-1.026979509	5.397519038	-16.19044258	8.51E-49	4.02E-47	100.055414
PPP1R15A	1.647220498	4.857138428	16.18171889	9.38E-49	4.42E-47	99.95871041
ESAM	1.979760365	4.026063323	16.16450096	1.14E-48	5.34E-47	99.76790322
EML1	1.176439773	1.298714377	16.13660603	1.55E-48	7.27E-47	99.45893453
BCL6B	1.356094237	2.049177001	16.11822652	1.90E-48	8.88E-47	99.25546861
AFAP1L1	1.319043534	1.933036945	16.05951357	3.65E-48	1.70E-46	98.60608193
CCNB1	-2.255850506	3.566228797	-16.03361847	4.87E-48	2.26E-46	98.31995559
ITIH5	1.566500654	1.158729215	16.0302293	5.06E-48	2.34E-46	98.28252008
DOCK4	1.274169262	1.875056957	16.02338712	5.45E-48	2.50E-46	98.20695294
ADCY4	1.030268066	1.115490792	16.00712973	6.53E-48	2.99E-46	98.02745035
VSIR	1.474073182	3.487524695	16.00339818	6.81E-48	3.10E-46	97.98625892
LHFPL6	1.584147309	3.741487546	15.99677999	7.33E-48	3.33E-46	97.91321181
ZWINT	-2.041359149	3.406035479	-15.98474326	8.37E-48	3.79E-46	97.78038785
CBLC	-2.29277326	3.251644434	-15.97456164	9.37E-48	4.22E-46	97.66806441
WASF3	1.440087292	1.480764618	15.96859816	1.00E-47	4.50E-46	97.6022881
RCAN1	1.481436273	2.689423827	15.95331959	1.19E-47	5.31E-46	97.43381044
KAT2A	-1.549180987	4.031726343	-15.95007596	1.23E-47	5.49E-46	97.39805065
CASS4	1.335278592	1.400465296	15.94939985	1.24E-47	5.52E-46	97.3905971
MSRB3	1.667029266	2.334935076	15.93940924	1.38E-47	6.15E-46	97.28047376
PDE5A	1.297275174	1.645368138	15.93474589	1.46E-47	6.46E-46	97.2290801
RECK	1.122804277	1.531904987	15.92829067	1.56E-47	6.92E-46	97.15794823
RILPL2	1.087497658	2.431185433	15.91798818	1.75E-47	7.74E-46	97.04444499
PTH1R	1.151580719	0.956978608	15.91752437	1.76E-47	7.76E-46	97.03933581
SPP1	-4.295400461	6.472260592	-15.90940339	1.93E-47	8.48E-46	96.94988739
SERINC1	1.094233846	6.000432611	15.89198919	2.34E-47	1.03E-45	96.75813798
GNL3	-1.101819834	4.587184342	-15.87112075	2.95E-47	1.29E-45	96.52846005
SEMA6D	1.219392733	0.746344894	15.85965748	3.34E-47	1.46E-45	96.40234502
LILRA5	1.610118595	1.629965622	15.85416275	3.55E-47	1.55E-45	96.34190628
MSR1	2.287443077	3.033771744	15.8520142	3.64E-47	1.58E-45	96.31827578
NIM1K	1.006832289	0.522189381	15.84385977	3.98E-47	1.73E-45	96.22860171
OLR1	2.639353836	3.433958585	15.83940522	4.18E-47	1.81E-45	96.17962258
KDELR3	-1.951738142	4.416793805	-15.82747084	4.77E-47	2.06E-45	96.04842709
FAM83A	-3.469759275	3.37473065	-15.81588334	5.42E-47	2.33E-45	95.9210815
TRAF4	-1.301452879	4.503495347	-15.81494141	5.48E-47	2.34E-45	95.91073139
ROR1	1.330584556	1.292404864	15.78636984	7.51E-47	3.20E-45	95.59689504
KLF6	1.671909274	4.886624659	15.78514568	7.61E-47	3.24E-45	95.58345362
HMGB3	-2.887154911	5.380731087	-15.780954	7.97E-47	3.38E-45	95.53743126
CBX7	1.392889579	2.221466295	15.77670863	8.35E-47	3.54E-45	95.49082433
MSTO1	-1.044032356	2.133173779	-15.75339184	1.08E-46	4.54E-45	95.2349335
MDK	-2.741909291	6.497307706	-15.74988701	1.12E-46	4.71E-45	95.19648241
VWF	2.329393995	4.278190327	15.74388987	1.20E-46	5.03E-45	95.13069637
OSCAR	2.027561007	2.679988329	15.73861247	1.27E-46	5.30E-45	95.07281364
SPAG4	-1.894459799	2.617081607	-15.72649972	1.45E-46	6.05E-45	94.93998953
QKI	1.200541369	2.824774649	15.71308517	1.68E-46	7.00E-45	94.79293729
MRPL3	-1.053246911	5.002027961	-15.71233749	1.70E-46	7.04E-45	94.78474262
RXRG	1.278393826	0.574491572	15.71047825	1.73E-46	7.17E-45	94.76436566
ADTRP	1.442204149	1.069457452	15.70353206	1.87E-46	7.72E-45	94.68824495
SLC50A1	-1.648180651	5.280930181	-15.69649018	2.02E-46	8.33E-45	94.61108919
MMRN1	1.685593442	1.382356989	15.69511268	2.05E-46	8.44E-45	94.59599798
PCOLCE2	2.028741366	1.452013395	15.68167983	2.38E-46	9.76E-45	94.44886146
NPM3	-1.560513858	4.404692308	-15.66831622	2.76E-46	1.13E-44	94.30253294
MARCO	3.630981515	4.341736525	15.66669486	2.81E-46	1.15E-44	94.2847827

CCL14	1.01073776	0.557956704	15.66383902	2.90E-46	1.18E-44	94.25351968
S100A3	1.664094423	1.478793663	15.6560334	3.16E-46	1.28E-44	94.1680825
CRYAB	1.787582372	2.10810248	15.64809977	3.44E-46	1.39E-44	94.08126146
CRTAC1	3.148589836	2.688029967	15.64479803	3.57E-46	1.44E-44	94.04513435
TGFBR2	1.706209798	5.308585055	15.63347483	4.04E-46	1.63E-44	93.92126075
ST6GALNAC6	1.216980174	3.62382749	15.63313049	4.06E-46	1.63E-44	93.91749427
C2orf40	1.954385659	1.030012802	15.63186862	4.12E-46	1.65E-44	93.90369205
DLC1	2.2447873	2.929226039	15.62028083	4.68E-46	1.87E-44	93.77696607
NARF	-1.11314857	3.23559849	-15.62024586	4.68E-46	1.87E-44	93.77658363
RMI2	-1.584846586	2.462427613	-15.61071612	5.19E-46	2.07E-44	93.67239315
WIF1	4.012511172	2.430572082	15.60750296	5.38E-46	2.14E-44	93.63726877
RNF144B	1.60931535	2.936900692	15.60534706	5.51E-46	2.19E-44	93.61370337
NLN	-1.010648747	2.085087124	-15.60083669	5.79E-46	2.29E-44	93.56440627
SPTBN2	-1.705841699	2.518073391	-15.58796297	6.67E-46	2.63E-44	93.42373138
LDLR	1.854102096	3.79381509	15.57608338	7.60E-46	2.98E-44	93.29396108
ZBED2	1.81043272	1.516730611	15.57551424	7.64E-46	3.00E-44	93.28774495
MARCKSL1	-1.923069871	6.576507922	-15.56930701	8.18E-46	3.20E-44	93.21995521
PREX2	1.062152814	0.788264724	15.55087648	1.00E-45	3.91E-44	93.01873781
ADM2	-1.757496056	1.989217892	-15.53823038	1.15E-45	4.49E-44	92.88072815
AQP4	3.751311263	3.32574673	15.53234469	1.23E-45	4.77E-44	92.81651183
DENND2A	1.314629567	1.479872317	15.53214997	1.23E-45	4.78E-44	92.81438745
SLC1A1	2.184043979	2.410385065	15.5059179	1.64E-45	6.33E-44	92.52830131
POLR2H	-1.117123746	4.006638387	-15.49436477	1.86E-45	7.17E-44	92.40236557
LGALS1	1.605393938	2.62374623	15.49190406	1.91E-45	7.35E-44	92.37554729
ANKRD29	2.051548177	1.771074121	15.4812406	2.15E-45	8.24E-44	92.25935078
IQANK1	-1.836468879	3.381906823	-15.47790412	2.23E-45	8.53E-44	92.22300088
BMPR2	1.139131591	3.359580468	15.45924093	2.73E-45	1.04E-43	92.01972999
SVEP1	1.593629376	1.358603811	15.44622538	3.15E-45	1.20E-43	91.87802984
PPAT	-1.237364095	2.096846457	-15.44349684	3.25E-45	1.24E-43	91.84833049
CDCA8	-2.014922209	2.716002154	-15.43727702	3.48E-45	1.32E-43	91.78063746
NHSL1	1.457152852	1.945986342	15.4334938	3.62E-45	1.37E-43	91.73946858
KIF1C	1.206703445	4.183570742	15.43023078	3.75E-45	1.42E-43	91.7039638
ADAMTS1	2.017604526	2.675584014	15.41405508	4.48E-45	1.69E-43	91.52800206
B4GALT2	-1.169871915	3.99919832	-15.40706595	4.84E-45	1.82E-43	91.45199658
IL1RL1	1.957473233	0.914361454	15.40639014	4.87E-45	1.83E-43	91.44464803
UBE2C	-3.075236614	4.034769084	-15.40052133	5.19E-45	1.95E-43	91.38083802
SLC35F2	-1.58251516	3.378551755	-15.39702104	5.40E-45	2.02E-43	91.34278505
JPT2	-1.130042456	5.035590446	-15.39648111	5.43E-45	2.03E-43	91.33691557
SLC25A10	-1.57877635	2.697929321	-15.35663706	8.39E-45	3.12E-43	90.9040137
MYO19	-1.133460359	2.125951599	-15.3559029	8.46E-45	3.14E-43	90.89604144
WISP2	1.664575117	1.645963591	15.35259812	8.77E-45	3.24E-43	90.86015693
BZW2	-1.266481257	4.586127416	-15.33434377	1.07E-44	3.95E-43	90.66200172
NUSAP1	-1.926384473	3.10780278	-15.31910466	1.26E-44	4.65E-43	90.49665256
LEPR	1.525530662	1.429030122	15.31874537	1.27E-44	4.66E-43	90.49275498
KRT4	2.561245234	1.251902558	15.30086475	1.54E-44	5.64E-43	90.2988338
MFAP4	2.960712434	5.120389421	15.29208281	1.70E-44	6.19E-43	90.2036254
TNFRSF21	-1.846619043	5.481722012	-15.28291311	1.87E-44	6.83E-43	90.10423747
TFB2M	-1.097269825	3.675691042	-15.2573176	2.48E-44	8.97E-43	89.82694639
FERMT2	1.212190185	2.742539149	15.25399183	2.57E-44	9.29E-43	89.79093072
PLPP3	1.261052571	3.793610415	15.24917599	2.71E-44	9.77E-43	89.73878447
PHACTR2	1.282345608	2.147338848	15.24878381	2.72E-44	9.79E-43	89.73453817
AGTR2	2.447079917	1.14877273	15.23788264	3.06E-44	1.10E-42	89.6165264
CNRIP1	1.097564752	1.656033704	15.23327358	3.22E-44	1.16E-42	89.56664117
METTL7A	1.963379385	4.222195824	15.23144275	3.28E-44	1.18E-42	89.54682733
IQGAP3	-1.861622291	2.100781365	-15.20783321	4.24E-44	1.52E-42	89.29140688
KCNK3	2.056714161	1.467516211	15.20573707	4.34E-44	1.55E-42	89.26873773

SLC25A39	-1.232010221	5.545074202	-15.20541883	4.35E-44	1.55E-42	89.26529625
PCDH12	1.280186599	1.967796588	15.2023054	4.50E-44	1.60E-42	89.23162816
KIF20A	-1.788270751	2.199906503	-15.18187525	5.62E-44	2.00E-42	89.010773
FUT2	-1.977582445	2.529005785	-15.18089631	5.68E-44	2.02E-42	89.00019352
DKC1	-1.084121647	4.133852325	-15.15430317	7.59E-44	2.68E-42	88.71291115
EPCAM	-1.580118468	7.291320955	-15.1367934	9.17E-44	3.23E-42	88.52387209
TEDC2	-1.358738034	1.461265403	-15.13197764	9.67E-44	3.40E-42	88.47189647
SNRPE	-1.136990587	5.00366581	-15.1287735	1.00E-43	3.51E-42	88.43731861
GAB1	1.053917048	1.786150292	15.12073712	1.09E-43	3.82E-42	88.35060696
C8B	1.799660431	0.738919709	15.11969878	1.10E-43	3.86E-42	88.3394049
TK1	-2.281665258	4.528039841	-15.11076188	1.22E-43	4.25E-42	88.2430026
CDH13	1.14050776	1.032758133	15.09818544	1.39E-43	4.86E-42	88.10738197
PEBP4	3.800566444	3.159245566	15.08082413	1.68E-43	5.85E-42	87.92024202
CD34	1.41560492	2.680643749	15.06835659	1.93E-43	6.69E-42	87.78590976
SYNPO	1.649158409	3.687668526	15.06531359	1.99E-43	6.89E-42	87.75312998
P4HB	-1.156163793	7.815653048	-15.06529071	1.99E-43	6.89E-42	87.75288346
MYADM	1.792856336	5.288122082	15.04869864	2.38E-43	8.23E-42	87.57420083
TPX2	-2.545373583	3.374743192	-15.0416462	2.57E-43	8.86E-42	87.49827764
ITM2A	1.890243606	3.268178285	15.02893339	2.95E-43	1.02E-41	87.36145638
KLF4	2.247334213	3.208955639	15.02332795	3.14E-43	1.08E-41	87.30114384
GNAQ	1.098800373	3.897598098	15.01877517	3.29E-43	1.13E-41	87.25216476
GPBR1	1.339816282	1.02526874	15.00554998	3.80E-43	1.30E-41	87.10992358
FRY	1.111921036	1.481229838	14.96940169	5.61E-43	1.92E-41	86.72141441
CCBE1	1.69040212	0.981208242	14.9336646	8.26E-43	2.81E-41	86.33772555
PLK1	-1.860138561	2.288314146	-14.92898346	8.68E-43	2.95E-41	86.2874964
GKN2	3.426195868	1.815995891	14.92285612	9.28E-43	3.14E-41	86.22175984
CD52	2.398466081	5.315052281	14.92046851	9.52E-43	3.22E-41	86.19614776
CFD	2.548557581	4.129219539	14.91927774	9.64E-43	3.25E-41	86.183375
BMPER	1.124225824	0.556051718	14.91649923	9.94E-43	3.35E-41	86.15357301
C5AR1	1.834476697	3.259067728	14.91541319	1.01E-42	3.38E-41	86.14192491
C1orf162	1.668825871	3.054993745	14.91349639	1.03E-42	3.44E-41	86.12136762
SGCA	1.517019353	1.424598634	14.91139721	1.05E-42	3.51E-41	86.09885573
TBX2	1.613748505	2.373322444	14.90220023	1.16E-42	3.87E-41	86.00024214
RASGEF1B	1.089812953	1.719565488	14.89548891	1.25E-42	4.16E-41	85.92829763
RASGRF1	1.904589438	1.257772174	14.88822361	1.35E-42	4.49E-41	85.85043053
IL33	2.311515951	2.942731221	14.88516364	1.39E-42	4.63E-41	85.81763982
STAC	1.637392058	1.383816762	14.87562715	1.54E-42	5.12E-41	85.71546542
SERINC2	-1.882017096	5.441450294	-14.86879229	1.66E-42	5.50E-41	85.64225408
ADGRL2	1.709161357	2.530936176	14.85950334	1.84E-42	6.07E-41	85.54277972
EZH2	-1.556894733	2.206138401	-14.85018038	2.03E-42	6.70E-41	85.44296873
TMOD1	1.083732321	0.990461239	14.84179016	2.22E-42	7.31E-41	85.35316721
SEC14L6	1.817354577	1.45046555	14.81945104	2.82E-42	9.26E-41	85.11417827
SSTR1	1.5775211	0.892743968	14.81486852	2.97E-42	9.72E-41	85.06517318
HSD17B6	2.803543239	2.963017451	14.81066397	3.10E-42	1.01E-40	85.02021597
ACE	1.524404096	2.527251248	14.80399187	3.34E-42	1.09E-40	84.94888604
SYNPO2	1.22155128	1.166664801	14.79929289	3.51E-42	1.14E-40	84.89865882
HACD4	1.135178211	1.72642272	14.79625532	3.62E-42	1.17E-40	84.86619416
ARHGEF16	-1.36350973	2.808788171	-14.78312144	4.17E-42	1.35E-40	84.72585713
SPAG5	-1.837859615	2.357438706	-14.76580294	5.03E-42	1.61E-40	84.54089169
CBX3	-1.061745978	5.389165779	-14.74850269	6.05E-42	1.94E-40	84.35621779
SAPCD2	-1.824737788	2.014826901	-14.74777486	6.10E-42	1.95E-40	84.34845063
CCNB2	-1.930713836	2.576795185	-14.74393876	6.36E-42	2.03E-40	84.30751559
BIRC5	-2.370923691	2.919745798	-14.74271287	6.44E-42	2.05E-40	84.29443519
RRM2	-2.220054338	2.996420045	-14.74189239	6.50E-42	2.07E-40	84.28568079
PSMG3	-1.4121402	4.231989499	-14.73407673	7.06E-42	2.25E-40	84.20229985
EPN3	-1.6937576	2.057361467	-14.73137121	7.27E-42	2.31E-40	84.17344081

E2F3	-1.115605512	2.624715728	-14.730686	7.33E-42	2.32E-40	84.16613224
PLEK2	-1.950631404	3.17845226	-14.72714393	7.61E-42	2.41E-40	84.12835428
PPP1R14A	1.720989243	2.577469637	14.71803906	8.39E-42	2.65E-40	84.03126489
SOX4	-1.625617958	5.118795328	-14.70892006	9.25E-42	2.92E-40	83.93405189
MFNG	1.341767698	2.746115171	14.70563811	9.58E-42	3.01E-40	83.89907132
HIST1H2BD	-2.10797325	4.101209585	-14.67662619	1.31E-41	4.09E-40	83.59000135
PID1	1.882555266	2.403545651	14.67080696	1.39E-41	4.35E-40	83.52804096
RSPO4	1.432984005	0.872630475	14.66885781	1.42E-41	4.42E-40	83.50728986
SFRP5	1.555631644	0.695961682	14.66881911	1.42E-41	4.42E-40	83.50687788
GIMAP7	1.753167783	3.488998925	14.66066722	1.55E-41	4.81E-40	83.42010442
ITPRIP	1.347586485	2.589801032	14.66023828	1.56E-41	4.82E-40	83.41553918
JDP2	1.106862881	2.570070405	14.65988148	1.56E-41	4.83E-40	83.4117417
SPARCL1	1.990679302	5.516190266	14.65900318	1.58E-41	4.87E-40	83.40239407
TOM1L2	1.170285463	2.849656702	14.65396367	1.67E-41	5.13E-40	83.34876422
HSPB8	2.000757654	3.304184779	14.64659043	1.80E-41	5.53E-40	83.27031425
GAPDH	-1.641912542	9.201819891	-14.63365348	2.07E-41	6.34E-40	83.13271034
COL10A1	-2.896412109	3.150328306	-14.63106591	2.13E-41	6.50E-40	83.10519431
TMEM47	1.566450856	2.505814909	14.58117984	3.63E-41	1.10E-39	82.57514095
IQC�	1.224158111	0.8169441	14.57566795	3.85E-41	1.16E-39	82.51662608
VSIG4	2.536894482	4.342840272	14.5709345	4.05E-41	1.22E-39	82.4663834
S1PR4	1.464574458	2.22942944	14.56223898	4.44E-41	1.34E-39	82.37410501
JPT1	-1.561177978	5.254781871	-14.5565818	4.72E-41	1.42E-39	82.31408361
CAB39L	1.059153342	1.838961607	14.53951645	5.66E-41	1.69E-39	82.13308864
P3H4	-1.634969387	3.265277929	-14.53757448	5.77E-41	1.73E-39	82.11249835
ASF1B	-1.751235414	2.857528202	-14.51867756	7.06E-41	2.10E-39	81.91220364
NECTIN4	-1.979654395	3.940879802	-14.49528117	9.06E-41	2.69E-39	81.6643835
MYL9	1.7688912	5.78551909	14.48732647	9.86E-41	2.92E-39	81.5801673
ANXA3	2.002924042	3.447738993	14.47406533	1.14E-40	3.35E-39	81.43981938
TMEM273	1.300169673	1.934693276	14.4682545	1.21E-40	3.56E-39	81.3783398
SAMD10	-1.265488318	2.457222499	-14.46360709	1.27E-40	3.74E-39	81.32917756
SLC2A1	-2.685092176	4.343977819	-14.45387285	1.41E-40	4.14E-39	81.22622852
C11orf80	-1.134452855	2.684894187	-14.4450492	1.55E-40	4.54E-39	81.13293751
PDK4	2.459319156	3.225384995	14.444012	1.56E-40	4.58E-39	81.1219731
RECQL4	-1.804895144	2.367386171	-14.44282245	1.58E-40	4.63E-39	81.10939864
MCM4	-1.738525844	3.454486731	-14.43467197	1.73E-40	5.04E-39	81.02325451
ACOXL	1.243028228	0.920238858	14.42005803	2.02E-40	5.88E-39	80.86885331
CEP55	-1.993486845	2.538335103	-14.41839334	2.05E-40	5.97E-39	80.8512699
PAK1	-1.076897613	3.75003386	-14.41415713	2.15E-40	6.24E-39	80.80652892
ENG	1.532755074	5.262354759	14.41358405	2.16E-40	6.27E-39	80.80047682
ADAMTSL4	1.719111642	2.275056995	14.40407341	2.39E-40	6.92E-39	80.70005379
GPT2	-2.179002818	2.982437719	-14.38429613	2.95E-40	8.48E-39	80.49132393
SLC39A11	-1.183890469	3.600481338	-14.37839579	3.14E-40	9.00E-39	80.42907749
HSPE1	-1.257125192	5.300321674	-14.3777595	3.16E-40	9.05E-39	80.42236558
GALNT7	-1.391846518	3.399988509	-14.36521997	3.61E-40	1.03E-38	80.29012056
HSPD1	-1.253350025	6.116359854	-14.35427386	4.05E-40	1.16E-38	80.1747242
MYBL2	-2.791798881	3.456381947	-14.34458516	4.49E-40	1.28E-38	80.07261812
GAS6	1.798282386	4.1086514	14.34422891	4.51E-40	1.28E-38	80.06886433
DBNDD1	-1.474947203	2.721881028	-14.34336281	4.55E-40	1.29E-38	80.05973851
ZNF106	1.133040717	2.767354492	14.33248542	5.10E-40	1.44E-38	79.94514831
PGM5	1.3766833	1.223958931	14.32626382	5.45E-40	1.54E-38	79.87962389
ERO1A	-1.70753232	4.578420034	-14.31914683	5.88E-40	1.65E-38	79.80468583
FIBIN	1.946651025	2.294205622	14.31206943	6.34E-40	1.78E-38	79.73018207
VAR5	-1.148873477	4.362856744	-14.30507034	6.82E-40	1.91E-38	79.65651964
PHKA1	-1.121706257	2.159086915	-14.29345764	7.71E-40	2.16E-38	79.53433846
HYAL2	1.046306619	4.131222479	14.27835399	9.05E-40	2.53E-38	79.37549779
CHRDL1	2.409702694	2.322293919	14.27409965	9.47E-40	2.63E-38	79.33077042

KIF2C	-2.01108069	2.38541272	-14.26052248	1.09E-39	3.03E-38	79.18807124
RBMS2	1.100522336	3.183752768	14.25976605	1.10E-39	3.05E-38	79.18012288
KLF9	1.500946883	3.531903743	14.23587864	1.42E-39	3.91E-38	78.92922302
MRC1	2.666053775	3.886488671	14.22412844	1.60E-39	4.42E-38	78.80587886
SHC3	1.141185402	0.963009504	14.21675482	1.73E-39	4.77E-38	78.72850127
DOK2	1.776133877	3.04539862	14.19567816	2.17E-39	5.95E-38	78.50743142
ILF2	-1.089481453	6.540694874	-14.18799922	2.35E-39	6.44E-38	78.42692701
GATA6	1.716497751	2.118866759	14.18157925	2.51E-39	6.87E-38	78.35963747
CXorf36	1.136614477	1.588663601	14.17980917	2.56E-39	6.99E-38	78.34108723
DCAF13	-1.056241238	2.679214049	-14.17079322	2.82E-39	7.66E-38	78.24661865
IRAK1	-1.207710468	5.335694018	-14.1670834	2.93E-39	7.96E-38	78.20775563
NDRG4	1.229424528	0.990665583	14.14949937	3.52E-39	9.56E-38	78.023617
HMGAI1	-2.026148042	6.318118345	-14.13363973	4.16E-39	1.12E-37	77.85763004
FBLN5	1.861979088	3.308984089	14.12689978	4.47E-39	1.20E-37	77.7871168
WNT7A	1.453065306	0.663885411	14.12568475	4.53E-39	1.22E-37	77.77440699
PCLAF	-1.632850164	2.142251083	-14.09319773	6.37E-39	1.71E-37	77.43476955
KDELR2	-1.023948371	6.471121114	-14.07578988	7.65E-39	2.05E-37	77.25293354
GATA2	1.440811879	1.961117155	14.07200865	7.96E-39	2.13E-37	77.21345053
OLFML1	1.314432314	1.937753443	14.06774025	8.32E-39	2.22E-37	77.16888672
PCDH17	1.29025814	1.820786939	14.06577053	8.50E-39	2.26E-37	77.14832429
ANLN	-2.145919432	2.543506217	-14.06156882	8.88E-39	2.36E-37	77.10446608
JAML	1.476033905	1.953681834	14.0486127	1.02E-38	2.70E-37	76.96926799
CTNNAL1	1.268581887	3.673171313	14.04242561	1.09E-38	2.87E-37	76.90472648
FKBP11	-1.471470944	3.240343992	-14.03178357	1.21E-38	3.21E-37	76.79374491
RBMS3	1.206961577	1.400687214	14.03118284	1.22E-38	3.23E-37	76.78748137
GPC3	2.607174134	3.20060258	14.02849394	1.26E-38	3.31E-37	76.75944697
SORBS1	1.235351359	1.725507923	14.01957063	1.38E-38	3.63E-37	76.6664314
PLA2G1B	2.932088632	2.120062865	14.01288414	1.48E-38	3.89E-37	76.59675113
UQC2	-1.22085423	3.135028136	-14.01197938	1.49E-38	3.92E-37	76.58732387
KIF11	-1.648839059	2.326048014	-14.0111878	1.51E-38	3.95E-37	76.57907603
CSF3	2.172106149	0.937463759	14.00880666	1.54E-38	4.04E-37	76.55426746
PLEKHN1	-1.398382554	1.625247276	-14.00074261	1.68E-38	4.39E-37	76.47026498
PSAT1	-2.335690669	3.121460378	-13.99601296	1.77E-38	4.61E-37	76.42100755
NEK2	-1.880641563	2.124154084	-13.98303369	2.02E-38	5.27E-37	76.28587559
SLC52A2	-1.355204895	4.662105756	-13.97767595	2.14E-38	5.56E-37	76.23011196
DUS1L	-1.141619962	4.117767227	-13.97566977	2.19E-38	5.67E-37	76.20923422
OGN	1.885360225	1.291683049	13.94711834	2.95E-38	7.63E-37	75.91226709
FABP5	1.894562261	2.886041794	13.9406532	3.15E-38	8.16E-37	75.84506372
MRM1	-1.005194643	2.427160336	-13.93529405	3.33E-38	8.62E-37	75.78936828
CFL2	1.178299559	2.329966784	13.91446616	4.14E-38	1.07E-36	75.57301286
CRABP2	-4.176198048	5.664933194	-13.91191048	4.26E-38	1.10E-36	75.54647602
AHNAK	2.077118468	4.972260574	13.91138662	4.28E-38	1.10E-36	75.54103689
EFNA3	-1.429257176	1.725867415	-13.91052842	4.32E-38	1.11E-36	75.5321265
TMEM150B	1.372000658	1.53441934	13.90808831	4.43E-38	1.13E-36	75.50679304
DUOXA1	2.047152674	2.070649623	13.89802638	4.92E-38	1.25E-36	75.40235268
FERMT1	-1.803100273	2.282513179	-13.89418434	5.12E-38	1.30E-36	75.36248312
UHRF1	-1.506256919	1.707131517	-13.88425585	5.68E-38	1.44E-36	75.25947843
SRPX	1.749924583	2.263775437	13.88161763	5.84E-38	1.48E-36	75.23211393
LDHA	-1.316126874	6.845356035	-13.86749601	6.76E-38	1.71E-36	75.08568332
CACNA2D2	3.020610775	2.839214813	13.86234107	7.14E-38	1.80E-36	75.03224885
ARHGAP44	1.376464671	1.808911845	13.85773241	7.49E-38	1.89E-36	74.98448524
SHMT2	-1.33900769	4.334893235	-13.85471281	7.73E-38	1.95E-36	74.95319475
NEBL	1.527497333	2.440518692	13.83622992	9.37E-38	2.36E-36	74.76174025
CHPF2	-1.00778075	4.584396038	-13.83353669	9.64E-38	2.42E-36	74.73385312
TMPRSS4	-2.669659908	2.859660994	-13.82965109	1.00E-37	2.52E-36	74.69362419
FZD4	1.386834607	2.371445419	13.82146487	1.09E-37	2.73E-36	74.60888806

TINCR	1.314912192	0.732421969	13.80194273	1.34E-37	3.34E-36	74.40691376
RBP4	2.359920403	1.948014518	13.79256137	1.48E-37	3.68E-36	74.30990558
KPNA2	-1.761206956	4.749148221	-13.79141084	1.49E-37	3.71E-36	74.29801082
PRC1	-1.628043564	2.448562213	-13.78951754	1.52E-37	3.78E-36	74.27843797
SHROOM4	1.389953483	1.752102441	13.78734738	1.56E-37	3.87E-36	74.25600455
ITPRID2	1.106691229	3.73444121	13.78057708	1.67E-37	4.14E-36	74.18602979
KIF26B	-1.51683174	1.789736182	-13.77938114	1.69E-37	4.18E-36	74.17367088
MS4A15	3.320694898	2.127069237	13.77599891	1.75E-37	4.32E-36	74.13872161
RUSC1	-1.022575009	3.354536377	-13.75937638	2.08E-37	5.12E-36	73.96702016
CBX4	-1.038765367	3.894262487	-13.75691209	2.14E-37	5.24E-36	73.94157426
MT1M	2.193846868	1.840125523	13.75416701	2.20E-37	5.38E-36	73.91323163
DPYSL2	1.619770821	4.497087627	13.74283937	2.47E-37	6.05E-36	73.79630512
CDC6	-1.709984082	1.996010334	-13.72840587	2.87E-37	7.01E-36	73.6473892
KIF4A	-1.809503509	1.987226507	-13.72615954	2.94E-37	7.16E-36	73.6242201
CALCOCO1	1.07646623	3.304931169	13.72607627	2.94E-37	7.16E-36	73.62336127
KLF13	1.243048819	3.508334466	13.71119879	3.44E-37	8.32E-36	73.46996
AURKB	-1.965054492	2.350576872	-13.70090434	3.82E-37	9.25E-36	73.36386338
PDCD2L	-1.140014565	2.633428909	-13.69428369	4.09E-37	9.88E-36	73.29565085
KIAA0040	1.079443731	3.519490428	13.67872754	4.81E-37	1.16E-35	73.13544126
PPIF	-1.091712856	4.456513009	-13.67546107	4.98E-37	1.20E-35	73.10181229
DONSON	-1.066241143	2.273682847	-13.6752539	4.99E-37	1.20E-35	73.09967953
TLCD1	-1.513241145	3.839643056	-13.67145412	5.19E-37	1.24E-35	73.06056539
GINS1	-1.559756638	1.928174622	-13.66597233	5.49E-37	1.32E-35	73.00414668
TIMP3	1.548156816	1.748433404	13.66465367	5.56E-37	1.33E-35	72.99057674
ALG3	-1.058723928	3.959848052	-13.63358802	7.67E-37	1.83E-35	72.67108045
CYBRD1	1.962917627	4.61430125	13.62040037	8.79E-37	2.09E-35	72.53556295
MVB12B	1.210598385	2.09512306	13.59613328	1.13E-36	2.67E-35	72.28636643
SECISBP2L	1.360735812	3.246812666	13.59163992	1.18E-36	2.80E-35	72.24024943
UBASH3B	1.137714935	1.364198793	13.59140983	1.19E-36	2.80E-35	72.23788814
ZFYVE9	1.048929719	2.17852087	13.58032039	1.33E-36	3.13E-35	72.12410722
ACSS3	1.007686875	0.842289992	13.58016627	1.33E-36	3.13E-35	72.12252622
TPPP3	2.672196151	3.644341396	13.57989123	1.34E-36	3.14E-35	72.11970489
AGTR1	1.075154112	0.670660915	13.57760006	1.37E-36	3.21E-35	72.09620309
RTN1	1.062070295	1.106803449	13.57688852	1.38E-36	3.23E-35	72.08890486
KHDC4	-1.267175415	3.256035901	-13.57551216	1.40E-36	3.27E-35	72.07478818
CLEC12A	1.363131902	1.249630176	13.5745556	1.41E-36	3.30E-35	72.06497755
CCDC167	-1.352477978	4.546210695	-13.57226019	1.45E-36	3.37E-35	72.04143698
PHLDA2	-2.174197991	4.450133337	-13.5592875	1.65E-36	3.84E-35	71.90843399
IGSF9	-1.730101257	2.025805574	-13.55788405	1.68E-36	3.89E-35	71.89404897
DLGAP5	-1.794446342	2.018078721	-13.55761679	1.68E-36	3.90E-35	71.8913097
ICAM2	1.128202053	2.21854454	13.55038382	1.81E-36	4.19E-35	71.81718642
LMOD1	1.598280694	2.37494363	13.54764238	1.86E-36	4.30E-35	71.78909744
FGFR2	1.701149838	2.022558955	13.54570578	1.90E-36	4.38E-35	71.76925673
CCDC69	1.512458588	3.338945301	13.54382662	1.94E-36	4.46E-35	71.75000583
CCNA2	-1.838006379	2.582152582	-13.53737273	2.07E-36	4.75E-35	71.68389993
A2M	2.045268772	7.292606046	13.5328593	2.17E-36	4.97E-35	71.63767946
PTGER4	1.42454661	2.189794187	13.52697218	2.31E-36	5.27E-35	71.5774033
ENO1	-1.23051055	8.709841981	-13.51389548	2.64E-36	6.01E-35	71.44356383
FOXM1	-1.993044338	2.503246977	-13.49321389	3.26E-36	7.41E-35	71.23202453
LPL	2.700382218	3.203424145	13.49098463	3.34E-36	7.58E-35	71.20923278
BUB1B	-1.564056144	1.783550194	-13.47622774	3.89E-36	8.80E-35	71.05840857
CYP4B1	3.73946263	3.876006151	13.47550623	3.92E-36	8.85E-35	71.0510365
ZEB2	1.105475657	1.651266729	13.46964267	4.16E-36	9.39E-35	70.9911327
TLR8	1.36605529	1.427672939	13.46755283	4.25E-36	9.58E-35	70.96978553
PKP3	-1.421197548	4.269715899	-13.46049421	4.57E-36	1.03E-34	70.89769632
ACP5	1.735092978	5.300810071	13.44736196	5.23E-36	1.17E-34	70.76362955

SLC11A1	1.536655238	2.220955455	13.42807502	6.37E-36	1.43E-34	70.56685263
HYAL1	2.168754204	2.482033895	13.42295404	6.72E-36	1.50E-34	70.51462993
PRKCQ	1.14195271	1.333027392	13.40105842	8.41E-36	1.88E-34	70.29145975
SCARA5	1.736979409	1.012408179	13.39804339	8.67E-36	1.93E-34	70.26074395
STX1A	-1.647151785	2.117127263	-13.39528823	8.92E-36	1.99E-34	70.23267876
MND1	-1.205322021	1.429450812	-13.38722493	9.69E-36	2.16E-34	70.15056014
CD300LF	1.612530313	2.317478861	13.37563215	1.09E-35	2.42E-34	70.03254146
RASL12	1.332113876	2.437169868	13.369339	1.16E-35	2.58E-34	69.96849726
SLC46A2	1.952937336	1.40580267	13.36769285	1.18E-35	2.62E-34	69.95174731
ARHGEF6	1.2606138	2.322553449	13.36450325	1.22E-35	2.70E-34	69.9192954
PLSCR4	1.290760553	2.707600656	13.3601956	1.28E-35	2.82E-34	69.87547458
MELK	-1.849842594	2.128215752	-13.3499621	1.42E-35	3.12E-34	69.771401
MS4A2	1.246870912	1.013423103	13.34123051	1.55E-35	3.40E-34	69.6826347
TLR4	1.44127509	2.186188625	13.33237029	1.70E-35	3.72E-34	69.59259178
LHFPL3	1.119304078	0.547421345	13.32272116	1.87E-35	4.09E-34	69.49456724
02-Mar	1.3972209	2.897811318	13.32074805	1.91E-35	4.17E-34	69.47452713
CCRL2	1.268858554	1.812154741	13.31068886	2.12E-35	4.60E-34	69.37238435
ECT2	-1.588293933	3.02988804	-13.30720101	2.20E-35	4.76E-34	69.33697757
CDT1	-1.634766129	2.219203698	-13.30543416	2.24E-35	4.84E-34	69.31904326
PROM2	-1.983477664	3.461403642	-13.300763	2.35E-35	5.08E-34	69.27163514
HJURP	-1.763741643	1.918010589	-13.29630659	2.46E-35	5.31E-34	69.22641461
LMNB1	-1.55514753	3.450758534	-13.29326546	2.53E-35	5.47E-34	69.19556
LIMCH1	1.646699518	3.829083464	13.29001318	2.62E-35	5.65E-34	69.16256716
TIMELESS	-1.326344405	2.931722256	-13.28264435	2.82E-35	6.07E-34	69.08782969
HDGF	-1.038805326	6.61653596	-13.27521684	3.04E-35	6.54E-34	69.01251908
CENPF	-1.738607626	2.038939436	-13.25872888	3.60E-35	7.73E-34	68.84542026
CCNF	-1.130693126	1.853549067	-13.25790943	3.63E-35	7.78E-34	68.83711831
FEN1	-1.357283751	3.606058942	-13.25537872	3.73E-35	7.98E-34	68.81148106
P3H2	2.216128017	2.383876576	13.24765214	4.03E-35	8.61E-34	68.73322352
RHBDL2	-1.442338849	1.945767801	-13.24138221	4.30E-35	9.17E-34	68.66973718
CHAF1B	-1.064287026	1.684728009	-13.23638768	4.52E-35	9.64E-34	68.61917622
ZEB1	1.083826376	1.892094799	13.22915773	4.87E-35	1.03E-33	68.54600352
CDCA5	-1.777106114	2.34128255	-13.22836889	4.91E-35	1.04E-33	68.53802105
NEXN	1.21944225	1.891943566	13.20828062	6.02E-35	1.27E-33	68.33482981
BOP1	-1.448250541	3.856746031	-13.2065797	6.13E-35	1.29E-33	68.31763261
PTTG1	-1.767604292	3.258192361	-13.20023441	6.53E-35	1.38E-33	68.25348892
ALOX5	1.821209458	3.793817786	13.19986752	6.56E-35	1.38E-33	68.2497806
PRDX4	-1.368071092	5.777726995	-13.19813616	6.68E-35	1.41E-33	68.23228158
BYSL	-1.127493841	3.490243002	-13.1941879	6.95E-35	1.46E-33	68.19238081
MKI67	-1.827632535	2.347469374	-13.19389791	6.97E-35	1.46E-33	68.18945045
COL1A1	-2.814205891	7.348223859	-13.19278292	7.05E-35	1.48E-33	68.17818371
GPR4	1.046613401	1.717104799	13.18817014	7.39E-35	1.55E-33	68.131578
CENPU	-1.515957987	2.340569495	-13.18269645	7.81E-35	1.64E-33	68.07628529
KIF22	-1.055528079	3.510651776	-13.17893177	8.11E-35	1.69E-33	68.03826325
NME4	-1.303099158	4.451007694	-13.17169513	8.73E-35	1.82E-33	67.96519189
VAMP2	1.049488598	4.288635137	13.15471469	1.04E-34	2.16E-33	67.79381728
IL7R	1.980480046	3.219076041	13.14574021	1.14E-34	2.36E-33	67.70329021
NTN4	1.711709137	3.688539794	13.12105759	1.46E-34	3.01E-33	67.45448296
LRRK2	2.504548577	2.607652591	13.11520698	1.55E-34	3.19E-33	67.39554399
TMEM139	1.811299702	1.56036316	13.11484129	1.56E-34	3.20E-33	67.3918605
KIFC1	-1.805922615	2.652037625	-13.10645724	1.69E-34	3.47E-33	67.3074255
METTL1	-1.153662456	3.176911129	-13.09616844	1.88E-34	3.84E-33	67.20384753
C1orf198	1.124396407	4.567383553	13.08516854	2.10E-34	4.28E-33	67.09315917
ACKR1	2.24004857	2.564964115	13.06336468	2.62E-34	5.32E-33	66.87390196
PCYOX1	1.026717777	4.554996053	13.05347336	2.89E-34	5.86E-33	66.77450089
ID4	1.99860811	2.868806296	13.04481528	3.16E-34	6.38E-33	66.68752635

DTYMK	-1.16120953	3.623025788	-13.03510087	3.49E-34	7.02E-33	66.58997757
HS6ST2	-2.235884343	2.67691342	-13.02647019	3.80E-34	7.65E-33	66.50334425
AURKA	-1.755190213	2.728231659	-13.01727389	4.17E-34	8.38E-33	66.41106738
STIL	-1.037481938	1.306853939	-12.99855527	5.04E-34	1.01E-32	66.22335141
HMMR	-1.537192189	1.898939511	-12.99757419	5.09E-34	1.02E-32	66.21351682
PCDHGC3	1.25744965	1.899418081	12.99739698	5.10E-34	1.02E-32	66.21174048
PROS1	1.568082264	3.411409864	12.99564671	5.19E-34	1.04E-32	66.19419657
ALOX5AP	2.041124469	4.47199094	12.99549429	5.20E-34	1.04E-32	66.19266886
TONSL	-1.217860808	1.868974794	-12.99149916	5.41E-34	1.08E-32	66.15262859
NUF2	-1.659237482	1.838643292	-12.98128046	6.00E-34	1.19E-32	66.05024436
KCNJ5	1.314359887	1.159121927	12.97942911	6.11E-34	1.21E-32	66.03169974
TXNDC17	-1.429674873	4.099064978	-12.96970046	6.74E-34	1.33E-32	65.93427374
FAM49A	1.197625259	2.092232767	12.96227345	7.27E-34	1.43E-32	65.85992381
HMBS	-1.005994225	2.848620335	-12.95914906	7.50E-34	1.48E-32	65.82865331
GARS	-1.01999241	4.909610076	-12.95538019	7.79E-34	1.53E-32	65.79093792
ORC6	-1.123435639	1.280577914	-12.9441565	8.72E-34	1.71E-32	65.678657
KLF2	1.727366289	3.613671619	12.93374549	9.68E-34	1.90E-32	65.57455344
GIMAP4	1.47036403	3.878076295	12.9208265	1.10E-33	2.16E-32	65.44543523
HLA-E	1.32176116	8.242592023	12.91914199	1.12E-33	2.19E-32	65.42860469
PC	-1.308458502	2.686913222	-12.91829763	1.13E-33	2.21E-32	65.4201689
UBL3	1.061716084	4.156606681	12.91512308	1.17E-33	2.28E-32	65.38845513
AP1S1	-1.108762749	5.121636468	-12.90832696	1.25E-33	2.43E-32	65.32057641
EPB41L2	1.22988644	2.409765057	12.90473922	1.30E-33	2.52E-32	65.28475044
GIPC2	1.080096489	0.794986136	12.90050676	1.35E-33	2.62E-32	65.24249347
NCAPH	-1.60250704	2.012443601	-12.89599736	1.42E-33	2.74E-32	65.19747987
AARD	1.299658817	0.77615742	12.88593525	1.57E-33	3.02E-32	65.09706927
PTPRM	1.320714264	2.651238811	12.88217224	1.63E-33	3.14E-32	65.05952899
NCF2	1.660812494	3.902936593	12.87822956	1.69E-33	3.26E-32	65.02020271
E2F8	-1.177170846	1.320440886	-12.87433176	1.76E-33	3.38E-32	64.98133057
GINS2	-1.469317934	1.878885971	-12.87355863	1.77E-33	3.40E-32	64.97362105
MYOZ1	1.302787736	1.123364993	12.8697637	1.84E-33	3.53E-32	64.93578227
INAVA	-1.583315826	2.826698061	-12.8586925	2.06E-33	3.94E-32	64.82542777
LAD1	-1.777814278	5.165926018	-12.85374883	2.16E-33	4.13E-32	64.77616748
FANCI	-1.230432935	2.074756163	-12.84926785	2.26E-33	4.32E-32	64.73152664
GFPT1	-1.057279059	4.309663873	-12.8474175	2.30E-33	4.40E-32	64.7130955
SCIMP	1.18630622	1.569440289	12.84298265	2.41E-33	4.59E-32	64.6689261
CA3	1.383325171	1.121944589	12.82988053	2.75E-33	5.21E-32	64.53848334
GPI	-1.093442915	5.203407151	-12.82781697	2.80E-33	5.32E-32	64.51794552
VMP1	-1.240377013	5.101301117	-12.82771938	2.81E-33	5.32E-32	64.51697433
TIMP1	-1.602943692	7.957053244	-12.82757752	2.81E-33	5.32E-32	64.51556243
C1QTNF6	-1.389952093	2.139467756	-12.81572751	3.17E-33	5.97E-32	64.39766047
FAM167A	1.718334967	1.688000146	12.80030456	3.69E-33	6.96E-32	64.24429946
XPR1	-1.532774038	3.932491637	-12.79874619	3.75E-33	7.06E-32	64.22880916
SLC25A25	1.146468581	2.583654498	12.79584832	3.86E-33	7.25E-32	64.20000697
DECR2	-1.059517848	2.565189604	-12.79347729	3.96E-33	7.42E-32	64.17644379
UTRN	1.298593314	3.107357494	12.78896568	4.14E-33	7.76E-32	64.13161427
ST14	-1.425924751	5.923263549	-12.78323409	4.38E-33	8.20E-32	64.07467516
GALNT18	1.341271781	3.151188204	12.77347347	4.83E-33	9.00E-32	63.97774299
SOCS2	1.59596268	1.987661699	12.77101329	4.95E-33	9.22E-32	63.9533176
CDC45	-1.558117111	1.867539691	-12.76641819	5.18E-33	9.64E-32	63.90770306
SPC24	-1.3304746	1.72623708	-12.76196368	5.42E-33	1.01E-31	63.8634928
GTSE1	-1.349053375	1.562792118	-12.73359493	7.19E-33	1.33E-31	63.5821389
NRN1	1.621188187	1.979198572	12.72387809	7.93E-33	1.46E-31	63.48584982
TDRKH	-1.081565019	2.698427231	-12.7021514	9.84E-33	1.81E-31	63.27069754
PKMYT1	-1.281425719	1.498475355	-12.70140181	9.92E-33	1.83E-31	63.26327825
NPR3	1.340735561	1.559251903	12.69460431	1.06E-32	1.95E-31	63.19600918

MEX3A	-1.878242599	2.018237411	-12.68352731	1.19E-32	2.17E-31	63.08643272
CDCA7	-1.83372175	2.436078291	-12.67316806	1.31E-32	2.40E-31	62.98400479
HOXA5	1.269677303	2.015672834	12.67178569	1.33E-32	2.43E-31	62.97034002
KHDRBS2	1.287513481	0.869755351	12.66221913	1.46E-32	2.67E-31	62.87579727
C19orf48	-1.25740923	3.644299944	-12.66107855	1.48E-32	2.70E-31	62.86452805
GMFG	1.431557962	3.955299176	12.65957263	1.50E-32	2.74E-31	62.84964997
THBS2	-2.326970529	4.299536842	-12.65252038	1.61E-32	2.93E-31	62.77998904
TBX5	1.09058203	1.581334158	12.64947597	1.66E-32	3.02E-31	62.74992358
RALGPS2	-1.083193726	2.07000046	-12.64240635	1.78E-32	3.23E-31	62.68012234
UNC5CL	-1.727883677	2.19510103	-12.63899845	1.85E-32	3.33E-31	62.64648258
LMO7	1.409055064	4.093411034	12.62765688	2.07E-32	3.72E-31	62.53456545
MOCS1	1.041671835	1.828097793	12.62094936	2.21E-32	3.97E-31	62.46840307
NPNT	2.113697426	3.492809013	12.61633436	2.31E-32	4.15E-31	62.42289266
GNG11	1.797889181	3.473692213	12.6023486	2.66E-32	4.75E-31	62.28503038
ZBTB16	1.355983483	0.827121607	12.60040592	2.71E-32	4.84E-31	62.26588762
TYMS	-1.459895265	3.071635683	-12.59736396	2.79E-32	4.98E-31	62.235916
TNS2	1.316186246	3.411863439	12.59173291	2.95E-32	5.26E-31	62.18044565
COLEC12	1.769190794	2.655177509	12.58428237	3.18E-32	5.65E-31	62.10707334
FCGR3B	1.21580136	0.843378335	12.57502835	3.48E-32	6.18E-31	62.01597463
SKA3	-1.279067134	1.455610346	-12.56680466	3.78E-32	6.69E-31	61.93505056
MMP11	-2.831142225	2.953316459	-12.56170919	3.97E-32	7.02E-31	61.88492433
LIFR	1.555754455	2.647071987	12.54528571	4.67E-32	8.23E-31	61.72343808
HGH1	-1.051715385	3.615082775	-12.54185471	4.83E-32	8.50E-31	61.68971739
ITLN1	2.072443363	0.765641995	12.53753831	5.05E-32	8.87E-31	61.64730223
TOX2	1.220737945	1.67139189	12.53426727	5.21E-32	9.15E-31	61.61516477
DCSTAMP	1.026185172	0.758375415	12.52266305	5.85E-32	1.02E-30	61.50119375
EFEMP1	1.846410287	4.708886158	12.51886794	6.07E-32	1.06E-30	61.46393296
TSTA3	-1.264292942	4.775702477	-12.5111882	6.55E-32	1.14E-30	61.38855226
NIPSNAP1	-1.047024471	4.625031357	-12.49098969	7.99E-32	1.38E-30	61.19041867
SLC7A7	1.349609968	2.998677805	12.48509238	8.47E-32	1.46E-30	61.1326045
TMED3	-1.000676299	2.906892748	-12.48334147	8.62E-32	1.49E-30	61.11544253
TPI1	-1.115182652	7.494514251	-12.47614013	9.25E-32	1.59E-30	61.04487102
RRAS	1.318503742	5.398960511	12.47105201	9.73E-32	1.67E-30	60.99502264
BRIX1	-1.029344122	3.133926346	-12.47041972	9.79E-32	1.68E-30	60.98882888
FOSB	3.261142763	3.20427074	12.46316957	1.05E-31	1.80E-30	60.91782123
MCM2	-1.53836371	3.242915579	-12.45767627	1.11E-31	1.90E-30	60.86403576
SLC7A5	-2.121804387	4.184366901	-12.45591013	1.13E-31	1.93E-30	60.84674617
PILRA	1.386033728	2.691759841	12.45107966	1.18E-31	2.02E-30	60.79946558
NEDD9	1.686818294	3.779293176	12.44762327	1.23E-31	2.09E-30	60.76564087
TSPAN7	2.240167498	2.731395175	12.43994785	1.32E-31	2.24E-30	60.69054739
SEMA4B	-1.464103051	4.57772259	-12.4205836	1.60E-31	2.71E-30	60.50121274
PAPSS2	1.581285135	4.343880668	12.4194949	1.62E-31	2.73E-30	60.49057301
SRM	-1.056042757	4.976011606	-12.41297092	1.72E-31	2.91E-30	60.42682586
CLIC3	2.258924218	3.705658972	12.39841605	1.99E-31	3.35E-30	60.28467653
HSH2D	-1.162330456	2.742259467	-12.39514724	2.05E-31	3.46E-30	60.25276499
SH3BP5	1.125871912	2.00982861	12.39296104	2.10E-31	3.53E-30	60.23142513
TNFSF12	1.10161237	3.923476245	12.38333868	2.31E-31	3.88E-30	60.13752534
CCT5	-1.172547665	5.168652155	-12.38158714	2.35E-31	3.94E-30	60.12043746
TROAP	-1.622050445	1.760014389	-12.37197325	2.58E-31	4.32E-30	60.02666981
RIPOR1	1.090681163	3.231267942	12.36704029	2.71E-31	4.53E-30	59.97857326
APBB1	1.19033574	2.348160134	12.35582471	3.02E-31	5.05E-30	59.86926208
TACC3	-1.296212924	2.888996729	-12.35263227	3.12E-31	5.20E-30	59.83815781
GJB2	-2.54867456	2.934205948	-12.34732896	3.29E-31	5.47E-30	59.78649737
MIS18A	-1.021171663	2.924691888	-12.34677312	3.30E-31	5.49E-30	59.78108359
ABCC3	-2.073026026	4.200590406	-12.33992775	3.53E-31	5.87E-30	59.7144224
SSR4	-1.31522775	5.869970185	-12.3376444	3.61E-31	5.99E-30	59.69219157

KNTC1	-1.102618904	1.659577967	-12.33408061	3.74E-31	6.20E-30	59.65749906
FILIP1	1.29185711	1.376060745	12.33175293	3.83E-31	6.34E-30	59.63484291
KRT80	-1.891943646	3.404506961	-12.32946489	3.91E-31	6.48E-30	59.61257489
CYP27A1	1.786207798	4.406359044	12.32571078	4.06E-31	6.71E-30	59.57604387
NDC80	-1.456367098	1.748938315	-12.32009348	4.29E-31	7.07E-30	59.52139424
AATK	1.508013584	1.487764131	12.31391007	4.56E-31	7.51E-30	59.46125369
SHANK3	1.050068893	2.125218652	12.30976779	4.75E-31	7.81E-30	59.42097525
DARS2	-1.027509786	3.273326742	-12.30899969	4.78E-31	7.86E-30	59.41350726
GNPNAT1	-1.190449865	3.258048892	-12.30741669	4.86E-31	7.97E-30	59.39811724
SELENOP	1.816336363	4.043921402	12.30482408	4.98E-31	8.16E-30	59.37291414
SUSD2	3.132964981	4.247928564	12.30295925	5.08E-31	8.31E-30	59.35478776
APOLD1	1.291817033	1.937172826	12.30222302	5.11E-31	8.36E-30	59.34763196
ARHGAP18	1.104294581	3.625814626	12.29845564	5.30E-31	8.67E-30	59.3110187
TPBG	-1.267174058	2.595429842	-12.29181909	5.66E-31	9.23E-30	59.24653737
HDHD3	-1.075613064	3.767863567	-12.28893632	5.82E-31	9.49E-30	59.21853443
CDK1	-1.678251018	2.82869654	-12.28374202	6.12E-31	9.97E-30	59.168087
ATAD3A	-1.03953017	3.136078131	-12.2810606	6.29E-31	1.02E-29	59.14204972
COL3A1	-2.410043904	7.503594766	-12.27621802	6.59E-31	1.07E-29	59.09503546
PLLP	1.408321524	2.118994089	12.27253872	6.83E-31	1.11E-29	59.05932211
CRIM1	1.325107824	3.649434128	12.25635895	8.00E-31	1.30E-29	58.90234607
CKS1B	-1.379330173	3.41880212	-12.25334378	8.24E-31	1.33E-29	58.87310622
ALDOA	-1.179803158	7.603397459	-12.24917687	8.59E-31	1.39E-29	58.83270414
FLRT3	1.979906628	3.033159695	12.24366242	9.06E-31	1.46E-29	58.77924883
BCL9	-1.108911004	3.032732099	-12.2341453	9.94E-31	1.60E-29	58.68702589
HK3	1.65126965	2.396116636	12.2301482	1.03E-30	1.66E-29	58.64830566
SLC15A2	1.592744043	2.262469957	12.22356612	1.10E-30	1.77E-29	58.58456052
TTYH3	-1.344450044	4.477564347	-12.22017427	1.14E-30	1.82E-29	58.55171949
NOSTRIN	1.241050156	1.770925136	12.21712635	1.17E-30	1.88E-29	58.52221295
MYH10	1.410519135	3.65453229	12.2168932	1.18E-30	1.88E-29	58.51995606
NDRG2	1.425031466	2.608005536	12.21668165	1.18E-30	1.88E-29	58.51790826
CDC25C	-1.059820197	1.102204945	-12.20622909	1.31E-30	2.08E-29	58.41675343
SLC27A3	1.167834637	2.868055738	12.2003128	1.38E-30	2.20E-29	58.35952096
GPRIN1	-1.228769077	1.550137128	-12.19609932	1.44E-30	2.29E-29	58.31877084
STK39	-1.299767332	3.74794758	-12.18874331	1.55E-30	2.45E-29	58.24764786
MCM6	-1.249421762	3.608033649	-12.18323055	1.63E-30	2.58E-29	58.19436328
TUBG1	-1.080782654	4.123722794	-12.18301029	1.64E-30	2.59E-29	58.1922346
PPBP	1.823351989	1.05632082	12.16431523	1.96E-30	3.09E-29	58.01164114
JUND	1.284171031	6.177969534	12.16019395	2.04E-30	3.22E-29	57.97185162
GJA5	1.500091112	3.123854018	12.15503664	2.15E-30	3.38E-29	57.92207086
KIF18B	-1.476335869	1.575787377	-12.15436443	2.16E-30	3.39E-29	57.91558321
BAIAP2L1	-1.119687989	4.147822233	-12.15207989	2.21E-30	3.46E-29	57.89353646
RFC4	-1.256407959	2.591239014	-12.12158408	2.97E-30	4.62E-29	57.59947261
STOM	1.268415344	6.383594817	12.11999692	3.02E-30	4.69E-29	57.58417992
EXO1	-1.30363832	1.411798065	-12.11954157	3.03E-30	4.71E-29	57.57979272
ABCG1	1.289811395	2.935807823	12.11483874	3.17E-30	4.92E-29	57.5344877
ABHD11	-1.290512071	4.289639968	-12.09889977	3.70E-30	5.73E-29	57.38101588
PPIL1	-1.014674652	4.297585429	-12.09704644	3.77E-30	5.83E-29	57.36317837
CDCA3	-1.187344081	1.346481661	-12.09229337	3.95E-30	6.09E-29	57.31743965
BUB1	-1.445793174	1.977197225	-12.078003	4.54E-30	6.97E-29	57.17998772
APOBR	1.395961338	2.476581511	12.07121876	4.84E-30	7.43E-29	57.11476711
PYCR3	-1.104718283	2.853248992	-12.06798867	5.00E-30	7.66E-29	57.08372212
FAM167B	1.097089495	2.499593827	12.06449275	5.17E-30	7.91E-29	57.05012778
FAM111B	-1.34273854	1.726316771	-12.05622181	5.60E-30	8.56E-29	56.97067041
POC1A	-1.080130265	2.208712455	-12.05546901	5.64E-30	8.61E-29	56.96344
CD83	1.446755365	3.538049916	12.05412472	5.72E-30	8.72E-29	56.95052921
CDKN3	-1.619178937	2.130901035	-12.04020566	6.54E-30	9.92E-29	56.81689819

FPR1	1.612122251	2.541626893	12.03848975	6.65E-30	1.01E-28	56.80043082
PFKP	-1.791559785	4.649134371	-12.03687072	6.75E-30	1.02E-28	56.78489452
CENPA	-1.52299607	1.682668696	-12.03301677	7.01E-30	1.06E-28	56.74791662
ABCA3	2.569829151	4.623970229	12.01854887	8.06E-30	1.22E-28	56.60916306
PTGES	-2.125385956	3.810539822	-12.01758066	8.14E-30	1.23E-28	56.59988106
ADCK5	-1.165997156	2.395631328	-12.017573	8.14E-30	1.23E-28	56.59980758
C17orf53	-1.15999768	1.443982442	-12.0136042	8.46E-30	1.27E-28	56.56176425
C1orf115	1.56715173	2.891042234	12.00261982	9.40E-30	1.41E-28	56.45651138
NCAPG	-1.421964719	1.665016751	-11.99691597	9.93E-30	1.49E-28	56.40187942
ARRB1	1.216357003	3.408830849	11.99651965	9.97E-30	1.49E-28	56.39808393
SIX4	-1.122538177	1.698998077	-11.99262808	1.04E-29	1.55E-28	56.36081981
EDN1	1.922866624	3.519857579	11.99197436	1.04E-29	1.56E-28	56.35456072
EXOSC5	-1.096703925	3.707772439	-11.98712555	1.09E-29	1.63E-28	56.30814199
SHCBP1	-1.132123686	1.586209289	-11.98258735	1.14E-29	1.70E-28	56.26470695
GPRIN2	1.699401005	2.299329078	11.98206003	1.15E-29	1.70E-28	56.25966068
MRPL24	-1.047506802	5.081939473	-11.98109224	1.16E-29	1.72E-28	56.25039945
PRG4	1.851974881	1.196445676	11.96668352	1.33E-29	1.97E-28	56.11256927
H2AFX	-1.23041665	4.583902169	-11.96032928	1.41E-29	2.09E-28	56.05181777
DOCK11	1.177125404	2.228017857	11.94990695	1.56E-29	2.30E-28	55.95221389
SELPLG	1.457100379	3.985728816	11.93893313	1.74E-29	2.55E-28	55.84739581
ST6GALNAC2	1.276782413	1.568678113	11.9378657	1.75E-29	2.57E-28	55.83720311
GJA4	1.204201019	2.592214791	11.93765293	1.76E-29	2.58E-28	55.83517149
MMP19	1.461996406	2.222076609	11.93719637	1.77E-29	2.59E-28	55.83081219
CD302	1.266778266	2.238780542	11.93504334	1.80E-29	2.64E-28	55.81025568
PGM2L1	-1.226514028	2.303970378	-11.93083243	1.88E-29	2.74E-28	55.77005775
F10	1.103690332	1.228278477	11.92544718	1.98E-29	2.89E-28	55.71866178
CRY2	1.041112114	3.130502374	11.9146365	2.19E-29	3.19E-28	55.61552836
SMAD9	1.172107415	1.270285823	11.90623471	2.38E-29	3.45E-28	55.53541458
MYRF	1.800390424	1.929409971	11.89119319	2.75E-29	3.99E-28	55.39207358
PHLDB2	1.203985495	1.637555796	11.89014363	2.77E-29	4.02E-28	55.38207567
EGR2	1.416696144	2.248437114	11.88858835	2.82E-29	4.08E-28	55.36726134
RAD54L	-1.18843612	1.320411923	-11.88392231	2.95E-29	4.25E-28	55.32282343
CARD16	1.17139499	2.471521414	11.87340545	3.26E-29	4.70E-28	55.22270278
PDGFB	1.228524964	2.817479419	11.85682652	3.82E-29	5.50E-28	55.06497975
MYH11	1.879791898	2.602665902	11.83998812	4.49E-29	6.44E-28	54.90492451
SERPINH1	-1.11595713	5.688294496	-11.80501864	6.27E-29	8.93E-28	54.57296657
EPHA10	-1.069552072	1.115772732	-11.8046786	6.29E-29	8.95E-28	54.56974156
FIGNL1	-1.008322816	2.001389866	-11.80373203	6.35E-29	9.03E-28	54.56076442
DEPDC1B	-1.222942969	1.311500208	-11.8033473	6.37E-29	9.06E-28	54.55711585
SORBS3	1.068952452	3.670926788	11.7964971	6.80E-29	9.66E-28	54.49216368
ZNF692	-1.291688689	2.866888817	-11.79417742	6.95E-29	9.86E-28	54.47017417
TUBB3	-1.268897292	1.231689265	-11.79130643	7.15E-29	1.01E-27	54.44296208
LAMC3	1.295722425	1.671238417	11.78902077	7.31E-29	1.03E-27	54.42130083
ZNF385B	1.913886801	1.549471381	11.7881394	7.37E-29	1.04E-27	54.41294871
ESRP1	-1.058111031	4.49998055	-11.75914418	9.71E-29	1.36E-27	54.13839434
FLVCR2	1.038607931	2.138805014	11.75642711	9.97E-29	1.40E-27	54.11268768
H1FO	-1.148494306	6.923423037	-11.74346388	1.13E-28	1.58E-27	53.99008992
SCD5	1.562667363	2.220011642	11.74166375	1.15E-28	1.60E-27	53.97307205
BMP2	1.796613434	2.742695302	11.72591327	1.33E-28	1.85E-27	53.8242393
CA2	2.064178009	3.10085922	11.72539359	1.34E-28	1.86E-27	53.81933073
SLC16A11	1.172796481	1.117767773	11.72265505	1.38E-28	1.91E-27	53.7934663
CEACAM21	1.053188771	1.306629005	11.72103665	1.40E-28	1.94E-27	53.77818293
NR4A3	1.640010724	1.4752533	11.72061816	1.40E-28	1.95E-27	53.7742311
SOX18	1.184028093	2.185028134	11.71341007	1.50E-28	2.08E-27	53.7061784
BTK	1.150325282	2.0134437	11.71119894	1.53E-28	2.12E-27	53.68530798
POLE2	-1.055578384	1.444481553	-11.70749666	1.59E-28	2.19E-27	53.65036821

TNFSF13	1.119122755	3.385809134	11.69531478	1.78E-28	2.45E-27	53.53545096
CKAP2L	-1.180719558	1.345415688	-11.69311842	1.82E-28	2.50E-27	53.51473954
CHEK1	-1.108103643	1.607191142	-11.68613473	1.95E-28	2.66E-27	53.4488998
YDJC	-1.106035935	3.599661794	-11.68520021	1.96E-28	2.69E-27	53.44009136
STYK1	-1.236855316	1.663910726	-11.68399315	1.99E-28	2.71E-27	53.42871461
MAD2L1	-1.310946446	1.819304103	-11.67934599	2.08E-28	2.83E-27	53.38492114
PBK	-1.642331842	1.942757446	-11.6748645	2.17E-28	2.95E-27	53.34269906
NES	1.522978039	3.222977377	11.67439176	2.18E-28	2.96E-27	53.33824578
SERPING1	1.449896615	6.386293067	11.66645059	2.35E-28	3.19E-27	53.2634548
KCNN4	-2.283106218	3.375286105	-11.66563876	2.36E-28	3.21E-27	53.25581061
PPARG	1.527071002	2.271094674	11.64584181	2.85E-28	3.86E-27	53.06950453
PAQR5	1.22537324	1.583221039	11.64454452	2.89E-28	3.90E-27	53.05730269
ZNF217	-1.127103915	3.751829218	-11.63493753	3.16E-28	4.26E-27	52.96696908
MFSD2A	1.744281629	3.421945597	11.62688768	3.41E-28	4.59E-27	52.89131244
ORC1	-1.180078596	1.464750167	-11.62299664	3.54E-28	4.76E-27	52.85475406
RAD51	-1.053948758	1.492574508	-11.61641056	3.77E-28	5.06E-27	52.79289153
ATAD2	-1.295353388	2.668910752	-11.61446586	3.84E-28	5.15E-27	52.7746292
PDIA6	-1.032107527	6.026500455	-11.61411651	3.85E-28	5.16E-27	52.77134874
MRPL15	-1.080792851	5.264508499	-11.61184428	3.94E-28	5.27E-27	52.75001349
ASPM	-1.217268325	1.293785369	-11.59537121	4.60E-28	6.15E-27	52.5954154
S100A12	1.361129252	0.948503318	11.58463158	5.09E-28	6.78E-27	52.49469811
SPI1	1.576120714	4.296585455	11.57385063	5.64E-28	7.49E-27	52.39365139
CLEC4E	1.204046879	1.287701963	11.57169151	5.75E-28	7.64E-27	52.37342164
IL20RA	1.312743087	1.460446395	11.56518791	6.12E-28	8.11E-27	52.31250043
RAB5IF	-1.091171083	4.328449801	-11.55289644	6.87E-28	9.07E-27	52.19742059
WNT3	-1.053112416	1.602202024	-11.54786277	7.20E-28	9.50E-27	52.15031436
CKAP4	-1.047449919	5.254567413	-11.54590892	7.34E-28	9.67E-27	52.13203322
RAB11FIP1	1.425877367	3.648195366	11.53398216	8.21E-28	1.08E-26	52.0204825
RFLNB	1.061133332	2.578517855	11.52646126	8.81E-28	1.16E-26	51.95017643
LRRC20	-1.016874105	3.090795289	-11.52303742	9.10E-28	1.19E-26	51.91817951
GMNN	-1.078307774	2.880763407	-11.51262462	1.00E-27	1.31E-26	51.82090481
ABLIM3	1.24875038	1.747136709	11.51089212	1.02E-27	1.33E-26	51.80472545
MAOB	1.608994562	2.753607972	11.50858601	1.04E-27	1.36E-26	51.78319151
HRCT1	1.182065787	1.348929502	11.50623731	1.07E-27	1.39E-26	51.76126274
SYT7	-2.111597916	2.876695396	-11.48849656	1.26E-27	1.64E-26	51.59571492
NCAPG2	-1.151387568	2.200262107	-11.4869314	1.28E-27	1.66E-26	51.58111729
SFTPD	3.581199738	6.194822311	11.48174031	1.34E-27	1.74E-26	51.53271081
SLCO2A1	1.762080118	3.583129752	11.46076524	1.63E-27	2.10E-26	51.33725942
MTHFD2	-1.340772927	3.888746607	-11.43847448	2.01E-27	2.58E-26	51.129793
KIF23	-1.245889747	1.675629073	-11.41661679	2.47E-27	3.16E-26	50.92660301
TUBB6	1.338965697	3.630188911	11.41289717	2.56E-27	3.27E-26	50.89204952
CYGB	1.023921408	2.659433615	11.4119195	2.58E-27	3.30E-26	50.88296865
TPPP	1.544517841	1.979964791	11.40902	2.65E-27	3.38E-26	50.85604004
C11orf96	1.66949463	3.569977815	11.40797171	2.68E-27	3.42E-26	50.84630533
KCTD12	1.419061979	4.302079561	11.4068598	2.71E-27	3.45E-26	50.83598035
ADGRE5	1.258425399	4.531514795	11.39582661	3.00E-27	3.81E-26	50.73356302
CDCA4	-1.126598567	2.917171548	-11.39258654	3.10E-27	3.93E-26	50.70349834
NAXE	-1.07531907	5.833932668	-11.38506574	3.32E-27	4.20E-26	50.63373358
CCNE1	-1.4438082	1.728811702	-11.38053439	3.47E-27	4.38E-26	50.59171357
FCN1	1.398080957	1.712276977	11.37823846	3.54E-27	4.47E-26	50.57042709
SPC25	-1.160555914	1.604796086	-11.37111569	3.78E-27	4.77E-26	50.50440611
PLEKHO2	1.050009876	3.826186918	11.36942341	3.84E-27	4.84E-26	50.48872426
FAM83D	-1.514867732	2.403214255	-11.36554937	3.99E-27	5.02E-26	50.45283002
ADGRL4	1.025654685	2.526372072	11.36356004	4.06E-27	5.10E-26	50.43440131
RASAL1	-1.30597779	1.346988547	-11.35600334	4.36E-27	5.47E-26	50.36441608
HYOU1	-1.078653456	4.968781853	-11.35391531	4.44E-27	5.56E-26	50.34508328

NFIX	1.574075215	3.612726715	11.34444348	4.85E-27	6.07E-26	50.25741298
SNX25	1.212558874	3.058741633	11.33117741	5.49E-27	6.86E-26	50.13470133
CREB3L4	-1.119449292	3.108724436	-11.33072965	5.52E-27	6.88E-26	50.1305611
PPP1R35	-1.134728571	3.831854447	-11.32502761	5.82E-27	7.25E-26	50.07784617
ADAM8	-1.63170119	3.466315393	-11.3199059	6.10E-27	7.58E-26	50.03051068
GMDS	-1.098271246	2.812739676	-11.31580767	6.34E-27	7.86E-26	49.9926441
FHL2	-1.651421807	2.941219383	-11.30579919	6.96E-27	8.62E-26	49.90020476
P2RY6	-1.580426824	2.043704741	-11.28469038	8.47E-27	1.04E-25	49.70541164
NDNF	2.293773404	3.963982044	11.27791053	9.02E-27	1.11E-25	49.6428958
TTK	-1.244838443	1.410601581	-11.25899875	1.08E-26	1.32E-25	49.46863974
TRIP13	-1.590699241	2.372144268	-11.24596459	1.21E-26	1.48E-25	49.34864921
TMEM132A	-1.456498842	2.797444453	-11.24225066	1.26E-26	1.53E-25	49.3144755
MROH6	-1.698118691	2.972243266	-11.2411594	1.27E-26	1.54E-25	49.30443563
DTL	-1.141304898	1.866544114	-11.23720003	1.32E-26	1.60E-25	49.26801371
PODXL2	-2.327385126	3.831293492	-11.20078797	1.84E-26	2.22E-25	48.93344574
SPDEF	-2.297363252	3.643242227	-11.19720047	1.91E-26	2.29E-25	48.90051988
SFTPA1	4.784181136	8.388364267	11.1909557	2.02E-26	2.42E-25	48.84322193
SLC15A3	1.252168079	3.093852651	11.18970303	2.04E-26	2.45E-25	48.83173071
FBP1	1.588750237	5.863903244	11.18638711	2.11E-26	2.52E-25	48.80131651
CENPM	-1.225952658	2.245655848	-11.176141	2.32E-26	2.76E-25	48.70737368
SCGB1A1	5.13775958	5.129010696	11.17422833	2.36E-26	2.81E-25	48.68984322
LARGE2	-1.746170807	3.138035637	-11.16153092	2.65E-26	3.14E-25	48.5735146
ZDHHC9	-1.228264994	5.050491404	-11.15367794	2.85E-26	3.37E-25	48.50161114
MEST	-1.194981244	3.782415157	-11.15162743	2.90E-26	3.43E-25	48.48284158
CHTF18	-1.052569907	1.793860716	-11.14932228	2.97E-26	3.51E-25	48.46174381
GRTP1	-1.03644509	2.308358961	-11.14529707	3.08E-26	3.63E-25	48.42491002
GADD45B	1.421708165	4.811807062	11.13559251	3.37E-26	3.96E-25	48.33614081
COA6	-1.067699349	4.151005468	-11.13374521	3.43E-26	4.03E-25	48.31924887
LSR	-1.274006969	6.174933924	-11.12922485	3.57E-26	4.19E-25	48.27792181
ASNS	-1.223705159	3.012904245	-11.12628431	3.67E-26	4.30E-25	48.25104393
PABPC1	-1.020075024	8.16113819	-11.1135592	4.13E-26	4.82E-25	48.13478304
KIF14	-1.002916444	1.036184387	-11.11171168	4.20E-26	4.89E-25	48.11791067
IDH2	-1.095308139	5.544324423	-11.09491779	4.90E-26	5.70E-25	47.96462364
DEPDC1	-1.172107727	1.222297749	-11.08070203	5.58E-26	6.48E-25	47.83498548
CP	-2.702493254	4.572565737	-11.07816387	5.71E-26	6.62E-25	47.81185039
ALG1L	-1.934179431	2.521994435	-11.07125138	6.09E-26	7.04E-25	47.74886124
CPAMD8	1.585774451	1.758625935	11.06239893	6.60E-26	7.63E-25	47.66823147
RNASEH2A	-1.092514057	3.350969038	-11.05717976	6.93E-26	7.99E-25	47.62071383
TSPAN6	-1.04058528	3.8098121	-11.04107243	8.03E-26	9.24E-25	47.47415692
VIM	1.278239673	7.157110234	11.04090526	8.04E-26	9.25E-25	47.47263663
TNS3	1.042516019	3.855585421	11.02055384	9.69E-26	1.11E-24	47.2876635
ANKRD22	-1.857510083	2.937786922	-11.01414428	1.03E-25	1.17E-24	47.22945304
FBXO32	-1.406372945	2.839511851	-11.00979789	1.07E-25	1.22E-24	47.18999244
GYG2	-1.264685743	1.879650813	-11.00551688	1.11E-25	1.27E-24	47.15113534
FUT8	-1.118741062	3.158502083	-10.99649775	1.21E-25	1.38E-24	47.06930423
RASSF8	1.192673882	2.005776323	10.99232258	1.26E-25	1.43E-24	47.03143736
PMP22	1.20845576	4.661085629	10.99148512	1.26E-25	1.44E-24	47.02384318
F2RL3	1.07035046	1.401480102	10.98024496	1.40E-25	1.59E-24	46.92195167
SLCO2B1	1.461588498	3.228157275	10.97883395	1.42E-25	1.61E-24	46.90916571
MCM10	-1.101023956	1.176082513	-10.97523866	1.47E-25	1.66E-24	46.87659163
SAMHD1	1.204511604	4.694295289	10.96193158	1.66E-25	1.87E-24	46.75608724
FUT3	-1.612042331	2.935027611	-10.95727626	1.73E-25	1.95E-24	46.7139527
NET1	-1.209562262	5.114964979	-10.95529112	1.76E-25	1.99E-24	46.695989
MSMO1	1.034025548	4.812865257	10.9447919	1.94E-25	2.18E-24	46.60101633
CEACAM1	-1.500257328	3.095580858	-10.91809385	2.47E-25	2.77E-24	46.35978199
CYS1	1.463933273	1.449488543	10.90947519	2.67E-25	2.98E-24	46.28198893

MAFF	1.00179792	2.745158585	10.8931791	3.10E-25	3.44E-24	46.1350084
TSPAN12	1.293898134	3.705565426	10.88211573	3.43E-25	3.80E-24	46.03530583
MATN3	1.40268094	1.887542115	10.88055334	3.48E-25	3.85E-24	46.02123095
MNDA	1.486406127	3.203003019	10.86574443	3.98E-25	4.38E-24	45.88789022
RAC3	-1.572626635	2.90619622	-10.85189636	4.51E-25	4.96E-24	45.7633089
SFTPA2	4.580828173	8.646648369	10.84635793	4.74E-25	5.21E-24	45.71351282
RETREG1	1.343004083	1.789488582	10.83003847	5.50E-25	6.03E-24	45.56688152
DERL3	-1.69427154	3.044858089	-10.82953169	5.52E-25	6.05E-24	45.5623304
SEMA3B	1.772577899	2.626240276	10.82385226	5.82E-25	6.35E-24	45.51133608
TPSAB1	1.875079974	3.163307662	10.81840162	6.11E-25	6.66E-24	45.46241252
PCSK9	1.725472725	1.472318979	10.81740467	6.17E-25	6.71E-24	45.45346594
BCL2L15	-1.445626575	1.652459471	-10.81155004	6.50E-25	7.08E-24	45.40093757
SKA1	-1.127852981	1.309274658	-10.80744681	6.75E-25	7.33E-24	45.36413417
APOL3	1.230344647	2.791043645	10.80138556	7.13E-25	7.73E-24	45.30978538
DNAJB4	1.071968282	2.487747307	10.78058802	8.60E-25	9.30E-24	45.12345529
PIMREG	-1.222669719	1.40560818	-10.77270634	9.24E-25	9.96E-24	45.05290349
IL6	1.834434473	1.976961823	10.76492465	9.91E-25	1.07E-23	44.98328012
MMP1	-3.065893268	3.703366321	-10.75452694	1.09E-24	1.17E-23	44.89030312
MTURN	1.20311589	2.732376196	10.75054014	1.13E-24	1.21E-23	44.85466868
ESPL1	-1.061435796	1.197908758	-10.74983277	1.14E-24	1.22E-23	44.84834701
VGLL3	1.124427972	1.467894614	10.73790586	1.26E-24	1.35E-23	44.74179996
NSMF	-1.048901956	3.41632492	-10.73503344	1.30E-24	1.38E-23	44.71615139
STEAP1	-1.949658345	3.235327203	-10.7259564	1.41E-24	1.50E-23	44.63513009
B3GALNT1	1.159433811	2.095958911	10.72257393	1.45E-24	1.54E-23	44.60495
ARHGAP29	1.011690316	2.124614001	10.72227321	1.46E-24	1.55E-23	44.60226713
CHPF	-1.182303795	5.335279751	-10.7122289	1.59E-24	1.69E-23	44.51268552
KCNJ8	1.304689002	2.516601633	10.69805878	1.81E-24	1.91E-23	44.38640217
AK1	1.205818754	2.903693924	10.687541	1.99E-24	2.09E-23	44.29274026
RHBDL1	-1.314553862	1.563028948	-10.68641459	2.01E-24	2.11E-23	44.28271312
AQP9	1.458190866	2.135801691	10.68591675	2.02E-24	2.12E-23	44.27828156
PAQR4	-1.07490751	2.579527777	-10.68245711	2.08E-24	2.19E-23	44.24748969
SLFN13	-1.165574106	2.341891954	-10.67588602	2.21E-24	2.32E-23	44.18902313
PKIG	1.168904939	3.929247696	10.65778465	2.60E-24	2.71E-23	44.02808934
ALDH2	1.271583692	4.537669167	10.64481226	2.92E-24	3.04E-23	43.91286799
SOX12	-1.080961078	2.838256118	-10.64228449	2.98E-24	3.11E-23	43.89042706
SELE	1.021798264	0.696599291	10.61992903	3.65E-24	3.79E-23	43.69211642
C11orf97	1.236571748	0.613881304	10.60963643	4.00E-24	4.14E-23	43.60090677
LAGE3	-1.085149862	4.408226801	-10.60925229	4.01E-24	4.15E-23	43.59750373
SULF1	-1.894352401	3.57054792	-10.60878287	4.03E-24	4.17E-23	43.5933454
CCND2	1.215385372	2.691746485	10.59498067	4.56E-24	4.69E-23	43.47113441
ZFP36	1.684379938	6.752455844	10.58445697	5.01E-24	5.14E-23	43.37802443
MYLK	1.136781697	2.43675302	10.57498719	5.45E-24	5.58E-23	43.29429227
SMPDL3B	-1.553123595	4.223277745	-10.57406981	5.49E-24	5.63E-23	43.28618346
SIRPA	1.223828375	3.592084217	10.57148715	5.62E-24	5.75E-23	43.26335755
PTPRH	-1.667357945	1.629457312	-10.55464466	6.53E-24	6.66E-23	43.11459322
MAPK4	1.03507427	0.522017887	10.5529772	6.63E-24	6.76E-23	43.09987368
CTGF	1.653962024	6.143291919	10.54336782	7.22E-24	7.34E-23	43.01507767
RASSF2	1.13633208	2.827481163	10.54226602	7.29E-24	7.41E-23	43.00535833
ARHGEF19	-1.243486435	3.214402642	-10.54129779	7.35E-24	7.47E-23	42.99681789
IHH	1.208918442	0.583247307	10.52934295	8.18E-24	8.29E-23	42.89141129
RHPN1	-1.42458701	2.915160854	-10.52919349	8.19E-24	8.30E-23	42.890094
LY86	1.372996147	3.024804202	10.51944609	8.93E-24	9.02E-23	42.8042111
PCNA	-1.039566827	5.714736764	-10.51656463	9.16E-24	9.24E-23	42.77883324
LIMK1	-1.030760533	3.715645381	-10.51349228	9.42E-24	9.48E-23	42.75177935
MRPL12	-1.134474837	4.363559322	-10.5064048	1.00E-23	1.01E-22	42.68939015
DUSP1	1.789879794	7.023695321	10.50368861	1.03E-23	1.03E-22	42.66548776

C11orf88	1.158441005	0.60289551	10.50103406	1.05E-23	1.05E-22	42.64213184
COL5A2	-1.734932855	4.279200348	-10.49331368	1.13E-23	1.13E-22	42.57422715
AQP1	2.496954327	6.216926485	10.48747565	1.19E-23	1.18E-22	42.52290115
C1QA	1.75209706	7.091776016	10.47946212	1.27E-23	1.27E-22	42.45248036
ADCY9	1.015092858	2.380407616	10.47430431	1.33E-23	1.32E-22	42.40717411
RAD51AP1	-1.194496289	1.966349642	-10.47270411	1.35E-23	1.34E-22	42.39312101
EMP1	1.37940884	4.1244083	10.47030704	1.38E-23	1.37E-22	42.37207243
SLC51B	1.399079413	1.326720076	10.46794796	1.41E-23	1.40E-22	42.35136063
PRR11	-1.286733196	2.053315144	-10.46446438	1.45E-23	1.44E-22	42.32078202
CCL24	1.500983087	1.393715309	10.45889838	1.53E-23	1.51E-22	42.27193825
PREX1	1.075731661	2.991091962	10.45723703	1.55E-23	1.53E-22	42.25736273
ATOH8	1.829866617	2.239167549	10.45246836	1.62E-23	1.60E-22	42.21553435
TYROBP	1.576718025	6.271591731	10.44447696	1.74E-23	1.71E-22	42.14546689
C7	2.29106285	3.582781099	10.44091206	1.79E-23	1.76E-22	42.11422205
NCKAP1L	1.158702615	2.465095809	10.43971031	1.81E-23	1.78E-22	42.10369093
CADM1	1.609151568	3.13025425	10.41883193	2.18E-23	2.13E-22	41.92086061
PTGFRN	-1.052416051	3.765614187	-10.40366026	2.49E-23	2.43E-22	41.78815958
IGFBP3	-1.926899012	5.520419165	-10.39438752	2.70E-23	2.63E-22	41.70711922
EHD2	1.32270158	5.25641632	10.39399738	2.71E-23	2.64E-22	41.70371062
ARRDC4	1.083133109	2.710187794	10.39353089	2.72E-23	2.65E-22	41.69963503
JAM3	1.0337253	2.261813007	10.38867528	2.84E-23	2.76E-22	41.65722081
PTGDS	1.968515308	4.49880194	10.3868797	2.89E-23	2.80E-22	41.64153958
BICDL1	-1.244246712	2.057901627	-10.38117913	3.04E-23	2.94E-22	41.5917676
SBK1	-1.563970421	2.430352237	-10.37917949	3.09E-23	2.99E-22	41.57431303
DCN	1.583655099	4.781792259	10.37820178	3.12E-23	3.01E-22	41.56577958
DTX2	-1.033254698	3.026041001	-10.36086098	3.63E-23	3.49E-22	41.41452037
MICALL2	-1.145049475	2.553254569	-10.3575763	3.74E-23	3.59E-22	41.38588837
ETS1	1.139513637	3.963820129	10.35344809	3.88E-23	3.71E-22	41.34991237
TUBA1C	-1.005458807	4.650482024	-10.35324595	3.88E-23	3.72E-22	41.34815101
PABPC1L	-1.492103548	2.606872447	-10.32206709	5.11E-23	4.86E-22	41.07675735
F12	-1.054135442	1.27246379	-10.3149503	5.44E-23	5.16E-22	41.01488847
RPL39L	-1.687853582	3.337210486	-10.31029825	5.66E-23	5.37E-22	40.97446223
SEC14L4	1.179391319	1.315995947	10.28952582	6.79E-23	6.40E-22	40.79410294
WISP1	-1.20362785	1.81148159	-10.27776115	7.53E-23	7.08E-22	40.6920654
CELF2	1.187226827	3.060526796	10.26629159	8.33E-23	7.81E-22	40.5926646
FAM216B	1.677264196	1.073538686	10.26050149	8.76E-23	8.19E-22	40.5425138
OIP5	-1.021168423	1.396817873	-10.26017926	8.78E-23	8.21E-22	40.53972343
CPA3	1.979023979	3.448482454	10.24955438	9.64E-23	8.99E-22	40.4477489
NQO1	-2.271201602	5.465820844	-10.22966522	1.15E-22	1.07E-21	40.27575432
ARHGAP11A	-1.04787891	1.655531593	-10.22301156	1.22E-22	1.13E-21	40.21826722
GREM1	-1.686796917	1.682058072	-10.21934186	1.25E-22	1.16E-21	40.18657231
CYP27B1	-1.020177259	1.415384076	-10.20992361	1.36E-22	1.26E-21	40.10526368
PDPN	1.460760292	2.984230793	10.20277688	1.45E-22	1.34E-21	40.04359976
FAM83H	-1.090288386	4.408438576	-10.191425	1.60E-22	1.47E-21	39.94571406
PRELP	1.622808679	3.695467895	10.19116583	1.60E-22	1.47E-21	39.94348013
CNN1	1.302831193	2.335401092	10.18451398	1.70E-22	1.56E-21	39.88615824
LST1	1.326131707	2.994446826	10.18399226	1.71E-22	1.56E-21	39.88166341
C9orf24	1.821310221	1.334358509	10.17462112	1.85E-22	1.69E-21	39.80095493
CERCAM	-1.187372365	3.135529864	-10.17380974	1.87E-22	1.70E-21	39.79396933
SLC22A18	-1.06654383	2.734147389	-10.16873001	1.95E-22	1.78E-21	39.75024437
DBN1	-1.096729179	4.253666972	-10.16416994	2.03E-22	1.85E-21	39.71100536
C1QB	1.780343132	6.995843444	10.16086244	2.09E-22	1.90E-21	39.68255217
COL5A1	-1.697524723	4.332137109	-10.15670192	2.16E-22	1.97E-21	39.64676995
GABARAPL1	1.027537586	4.156610224	10.14164934	2.47E-22	2.24E-21	39.5173964
HCK	1.373020689	3.501726771	10.11646261	3.07E-22	2.77E-21	39.30122005
GRAMD2A	1.304135436	2.254846624	10.1162669	3.07E-22	2.78E-21	39.29954173

LAPTM4B	-1.301474632	6.379896993	-10.11271726	3.17E-22	2.86E-21	39.26910577
SDF2L1	-1.055938613	4.736259912	-10.11028371	3.24E-22	2.92E-21	39.24824396
MCM7	-1.09898589	4.599031895	-10.10866912	3.28E-22	2.96E-21	39.23440462
IRF7	-1.122760235	4.150881128	-10.10363366	3.43E-22	3.09E-21	39.19125354
ETV5	1.070928119	3.232332393	10.1005864	3.52E-22	3.17E-21	39.16514739
AADAC	1.70423263	1.271233001	10.09868213	3.58E-22	3.21E-21	39.14883622
TNFRSF18	-1.526442035	2.288958338	-10.09625782	3.65E-22	3.28E-21	39.1280736
DAB2	1.066808567	3.2810039	10.09033066	3.85E-22	3.45E-21	39.07732616
CHI3L2	1.696583038	2.317170246	10.08478356	4.03E-22	3.61E-21	39.0298515
KRT8	-1.282766094	7.489288144	-10.07922846	4.23E-22	3.78E-21	38.98232657
HPGDS	1.159991711	1.518804124	10.07417758	4.42E-22	3.95E-21	38.93913118
NFAM1	1.019543697	1.915095447	10.04820826	5.53E-22	4.91E-21	38.71727898
PRR36	-1.337357697	2.245818485	-10.01557037	7.33E-22	6.46E-21	38.43902595
C15orf48	-2.267828855	4.365873775	-10.00605802	7.95E-22	6.99E-21	38.35804808
CNFN	-1.367845486	1.909093642	-9.998197976	8.51E-22	7.46E-21	38.29117689
HLF	1.494611132	1.787824688	9.987805567	9.30E-22	8.15E-21	38.20281758
FAP	-1.155672856	1.738882336	-9.981041138	9.86E-22	8.63E-21	38.14533906
CES1	2.518662563	4.163117735	9.96323892	1.15E-21	1.00E-20	37.99420132
TPSB2	1.907163715	3.113757391	9.942327138	1.37E-21	1.19E-20	37.81690632
IRX1	1.277323134	0.841602341	9.930279713	1.52E-21	1.32E-20	37.71488452
MMP12	-2.443871408	2.970614618	-9.913580814	1.76E-21	1.52E-20	37.57361664
CYR61	1.59624998	6.025423648	9.909953788	1.81E-21	1.56E-20	37.54295521
HNF4G	-1.080157706	1.180353334	-9.907549308	1.85E-21	1.59E-20	37.52263307
XDH	-1.454906848	1.599795808	-9.903824841	1.91E-21	1.64E-20	37.49116155
ADAM28	-1.21450908	1.903967373	-9.901865961	1.94E-21	1.67E-20	37.47461249
CILP2	-1.353564884	1.47792776	-9.900371879	1.97E-21	1.69E-20	37.46199171
PLXNB3	-1.394582595	1.623363697	-9.888585593	2.17E-21	1.86E-20	37.36247793
TFAP2A	-1.158033318	1.226851315	-9.871754168	2.51E-21	2.14E-20	37.22051246
RACGAP1	-1.099539688	2.880140686	-9.867789049	2.60E-21	2.21E-20	37.18709338
CXCL16	1.029680064	5.659321468	9.865328765	2.65E-21	2.25E-20	37.16636223
CDH3	-2.009935363	3.51604381	-9.86426968	2.67E-21	2.27E-20	37.15743916
PXDC1	1.036359166	3.909869778	9.863719946	2.69E-21	2.28E-20	37.15280778
PLEKHH2	1.030498941	1.591240277	9.863559769	2.69E-21	2.28E-20	37.15145836
TNNI2	1.221485793	1.383229292	9.860071131	2.77E-21	2.35E-20	37.12207197
ARHGAP40	-1.479358873	1.63432664	-9.851740009	2.98E-21	2.51E-20	37.05192493
CDKN2B	1.323302856	2.711298853	9.846882592	3.10E-21	2.61E-20	37.01104546
ETV1	1.198053645	2.255686878	9.842674657	3.21E-21	2.71E-20	36.97564352
SMIM22	-1.579549962	4.226861572	-9.838392126	3.33E-21	2.80E-20	36.939625
CXCL2	1.960743925	4.235488213	9.835699759	3.41E-21	2.86E-20	36.91698636
C1orf21	1.012485711	2.180514118	9.828190475	3.64E-21	3.04E-20	36.85386815
THY1	-1.371840236	3.615402138	-9.8165339	4.01E-21	3.35E-20	36.75595829
GALNT14	-1.601206163	1.860542423	-9.814292105	4.09E-21	3.41E-20	36.73713771
SRD5A3	-1.279925971	3.875534301	-9.803561331	4.48E-21	3.72E-20	36.64709178
CXCL13	-2.365811748	3.484838415	-9.799011711	4.66E-21	3.86E-20	36.60893536
ADGRG1	-1.249832851	4.193397277	-9.791342031	4.97E-21	4.11E-20	36.5446404
BIK	-1.352508764	2.71722549	-9.777735472	5.57E-21	4.59E-20	36.43066475
EVI2B	1.231853748	3.680966601	9.769860618	5.96E-21	4.90E-20	36.36475245
VSIG2	2.279888866	3.472899383	9.763602067	6.28E-21	5.15E-20	36.31239557
PKDCC	1.247529109	2.021023796	9.758109003	6.58E-21	5.39E-20	36.26646221
KCNJ15	1.702924499	2.284558219	9.750817293	7.00E-21	5.72E-20	36.20551695
CXCL12	1.278312422	2.720876672	9.744723363	7.37E-21	6.01E-20	36.15460787
ITM2C	-1.135563261	5.583728957	-9.741185038	7.59E-21	6.18E-20	36.12505891
CX3CR1	1.036133358	1.173019012	9.740001058	7.67E-21	6.24E-20	36.11517306
FOXF2	1.120049261	2.009073761	9.732729533	8.15E-21	6.63E-20	36.05447706
TEKT1	1.369730548	0.833911301	9.730782446	8.29E-21	6.73E-20	36.03823007
DHCR24	1.05726738	7.187552294	9.723318154	8.83E-21	7.15E-20	35.97596764

SLC22A18AS	-1.093984104	1.509126218	-9.717805097	9.25E-21	7.48E-20	35.93000312
MANEAL	-1.238346656	2.546164971	-9.706705955	1.02E-20	8.19E-20	35.83752183
ADGRD1	1.24091957	1.645088874	9.703936831	1.04E-20	8.37E-20	35.81446047
CPXM1	-1.401268996	2.361163523	-9.701959742	1.06E-20	8.51E-20	35.7979981
PITX1	-1.661225282	1.70455808	-9.689532966	1.17E-20	9.42E-20	35.69458066
CABCOCO1	1.189465217	1.043269603	9.678049609	1.29E-20	1.03E-19	35.599099
TNFRSF25	-1.17120291	1.970650937	-9.669562591	1.39E-20	1.11E-19	35.52858347
KLF15	1.288313742	1.731051474	9.660740721	1.49E-20	1.19E-19	35.45533285
CYP24A1	-2.665548314	2.666937136	-9.649574803	1.64E-20	1.30E-19	35.3626878
ARHGAP30	1.054887522	3.110542126	9.649187657	1.65E-20	1.31E-19	35.35947698
DNTTIP1	-1.205947941	4.777428082	-9.640196078	1.77E-20	1.40E-19	35.28493085
ATF3	1.568854984	3.557185953	9.637915702	1.81E-20	1.43E-19	35.26603297
ZP3	-1.000067722	1.526211701	-9.629074154	1.95E-20	1.54E-19	35.19279193
HCAR2	1.448729486	1.8306792	9.621311929	2.08E-20	1.64E-19	35.12853161
CST1	-2.671866206	2.560018398	-9.616421072	2.17E-20	1.70E-19	35.08806136
UBE2S	-1.194664234	2.650613368	-9.608369712	2.32E-20	1.82E-19	35.02147128
IER5L	-1.178816424	2.411281151	-9.599322069	2.50E-20	1.95E-19	34.94668927
TMEM45B	-1.427166019	3.903021042	-9.599281506	2.50E-20	1.95E-19	34.94635413
TEF	1.003409156	2.803145487	9.570309335	3.18E-20	2.47E-19	34.70723174
SLC17A9	-1.367833904	2.067297242	-9.560066761	3.47E-20	2.69E-19	34.62281945
SCEL	1.799742301	3.491215441	9.559549763	3.48E-20	2.70E-19	34.61856044
SDC2	1.15523074	3.457780945	9.553253414	3.67E-20	2.84E-19	34.56670472
TSKU	-1.345609634	3.789831602	-9.547062519	3.86E-20	2.98E-19	34.51574162
GBP4	1.370009211	3.275787288	9.521684771	4.77E-20	3.67E-19	34.30708361
GCNT3	-1.975666878	2.048732315	-9.520906419	4.80E-20	3.69E-19	34.30069029
RHOV	-2.06928009	2.964249497	-9.518848962	4.88E-20	3.75E-19	34.28379236
SIGLEC14	1.014689051	1.669005878	9.511844314	5.18E-20	3.97E-19	34.2262829
OTULINL	1.394133992	3.061620009	9.507666451	5.36E-20	4.11E-19	34.1919965
PPP1R14D	-2.502866995	2.525814655	-9.506946356	5.39E-20	4.13E-19	34.18608802
MAL	1.322423236	2.051473302	9.499822983	5.72E-20	4.37E-19	34.12765719
ITGA11	-1.386095948	1.813908251	-9.494711401	5.97E-20	4.56E-19	34.08574808
TBC1D2	1.103924323	3.862968137	9.492729032	6.06E-20	4.63E-19	34.06949933
COL4A3	1.306409537	1.683876828	9.488652925	6.27E-20	4.78E-19	34.03609674
DNAJC12	-2.114934613	2.543169303	-9.440597254	9.33E-20	7.03E-19	33.64308101
EGR3	1.067354734	1.415728828	9.41134175	1.19E-19	8.88E-19	33.4045323
NR4A1	1.801855559	3.673454094	9.402977911	1.27E-19	9.49E-19	33.33643318
SNTN	1.174150711	0.824023296	9.392748948	1.38E-19	1.03E-18	33.25320825
GPRC5A	1.543881512	5.981848386	9.388459889	1.43E-19	1.07E-18	33.21833132
AK4	-1.273976549	1.778836862	-9.382146732	1.51E-19	1.12E-18	33.16701643
METTL7B	-1.697586754	2.912009139	-9.38073092	1.53E-19	1.13E-18	33.15551184
C6	1.040266283	0.684307784	9.378143293	1.56E-19	1.15E-18	33.13448859
EGR1	1.696101329	5.868262006	9.372584649	1.63E-19	1.21E-18	33.08934162
PTGIS	1.28561253	2.34142298	9.368206953	1.69E-19	1.25E-18	33.05380004
DAPK1	1.115699693	3.399040554	9.362012924	1.78E-19	1.31E-18	33.00353284
FCER1G	1.300835446	5.682806051	9.361844044	1.78E-19	1.31E-18	33.00216265
FBLN1	1.387583911	4.387893553	9.360634496	1.80E-19	1.33E-18	32.99234962
SGK1	1.108553484	3.471488931	9.355630024	1.88E-19	1.38E-18	32.95175838
ITGAL	1.15578126	2.746830083	9.35023212	1.96E-19	1.44E-18	32.90799386
NECTIN1	-1.128252259	2.659648726	-9.347891368	2.00E-19	1.47E-18	32.88902154
SLCO4C1	1.360545676	1.829200381	9.345866977	2.03E-19	1.49E-18	32.8726162
GOLGA7B	-1.337241233	1.876742761	-9.344152818	2.06E-19	1.51E-18	32.85872698
ADAM12	-1.239434241	1.515286556	-9.338311443	2.16E-19	1.58E-18	32.81141043
KRT18	-1.107629399	7.620402757	-9.321399135	2.49E-19	1.81E-18	32.67453923
MB	-1.524319893	1.836623068	-9.319676372	2.52E-19	1.84E-18	32.66060716
TUBA1A	1.15731831	5.332952225	9.316094107	2.60E-19	1.89E-18	32.63164326
TUBA4B	1.196480576	0.79314722	9.302511971	2.90E-19	2.11E-18	32.52190123

MMP9	-1.938400993	4.303706496	-9.298432743	3.00E-19	2.18E-18	32.48896458
KRTCAP3	-1.302637937	4.814701268	-9.296366359	3.05E-19	2.21E-18	32.47228416
APLN	1.308113946	2.125102802	9.290735141	3.19E-19	2.31E-18	32.42684129
CFAP77	1.016353339	0.615239206	9.288058684	3.26E-19	2.36E-18	32.40524989
TMSB15A	1.032452691	0.837198753	9.285370186	3.34E-19	2.41E-18	32.38356598
MORN5	1.38992138	0.949718408	9.281227683	3.45E-19	2.49E-18	32.35016394
SIX1	-1.448101739	2.122801121	-9.249832363	4.46E-19	3.20E-18	32.09737315
C20orf85	2.471320076	2.091297415	9.244513116	4.65E-19	3.33E-18	32.05460597
CFAP52	1.049436428	0.721230942	9.235116394	5.02E-19	3.59E-18	31.97910001
EPHX3	-1.463189497	2.811935583	-9.223089484	5.54E-19	3.94E-18	31.88254243
MIF	-1.143895387	5.148043088	-9.214733043	5.93E-19	4.21E-18	31.8155079
STOML3	1.060573019	0.64373254	9.206654934	6.33E-19	4.48E-18	31.7507489
CPNE7	-1.208389493	1.429687548	-9.19449293	6.99E-19	4.93E-18	31.65333032
FCGR3A	1.460006571	5.001396578	9.19372311	7.03E-19	4.96E-18	31.64716722
ID3	1.104122243	4.567812635	9.188779967	7.32E-19	5.16E-18	31.60760202
NRGN	1.862935716	3.937535406	9.182857615	7.68E-19	5.40E-18	31.56021996
GJA1	1.490488593	4.926881445	9.170956041	8.45E-19	5.92E-18	31.46506942
EPHB2	-1.116488814	1.705605561	-9.170402555	8.49E-19	5.94E-18	31.46064664
GSDMB	-1.116991797	2.208948492	-9.162250457	9.07E-19	6.34E-18	31.39552817
C2CD4A	-1.573562884	1.721780563	-9.152016563	9.85E-19	6.87E-18	31.31384137
DSP	-1.789416889	4.566149978	-9.145160397	1.04E-18	7.25E-18	31.25915352
EFCAB1	1.023840694	0.650067876	9.130737271	1.17E-18	8.11E-18	31.14420777
SGCE	1.168795288	3.372614009	9.116211275	1.31E-18	9.10E-18	31.02857879
MAP1LC3C	1.150912293	1.34565265	9.112153302	1.36E-18	9.39E-18	30.99630126
SRPX2	-1.531665652	3.096601356	-9.111789705	1.36E-18	9.42E-18	30.9934097
SGMS2	1.035790552	3.309408709	9.107724731	1.41E-18	9.71E-18	30.96108819
DEPTOR	-1.20747595	3.225891123	-9.103338868	1.46E-18	1.00E-17	30.92622729
ATP13A4	1.716700809	2.42211963	9.092923395	1.59E-18	1.09E-17	30.84349042
AOX1	1.069640657	1.294396977	9.04536142	2.32E-18	1.58E-17	30.46657451
CD44	1.123583935	5.027394259	9.036041298	2.50E-18	1.70E-17	30.39288839
LAPTM5	1.206115679	6.464235976	9.031976008	2.58E-18	1.75E-17	30.36076549
SELENBP1	1.681174717	5.475719643	9.030582122	2.61E-18	1.77E-17	30.34975384
ACY3	-1.218538096	1.550037154	-9.028524945	2.66E-18	1.80E-17	30.33350456
FMO3	1.045815228	1.943972622	9.025383823	2.72E-18	1.85E-17	30.30869874
EGLN3	-1.654909126	2.507467908	-9.014586022	2.97E-18	2.00E-17	30.22347655
CYBB	1.485704059	4.485357858	9.010479289	3.07E-18	2.07E-17	30.19108404
CLDN4	-1.118649253	6.313973985	-9.001236544	3.30E-18	2.22E-17	30.11822097
MS4A4A	1.200791436	3.2055312	8.998087666	3.39E-18	2.28E-17	30.09341033
OLFML2A	1.000567136	2.16881339	8.992742156	3.53E-18	2.37E-17	30.05130691
COL11A1	-1.997399573	1.924110771	-8.989630546	3.62E-18	2.43E-17	30.02680727
RAMP1	-1.670105723	4.15471389	-8.982487763	3.84E-18	2.57E-17	29.97059177
PANX2	-1.356821728	2.160213472	-8.96878744	4.28E-18	2.86E-17	29.86286084
MMP28	1.932802395	2.704966326	8.967905169	4.31E-18	2.87E-17	29.85592744
RTN4RL2	-1.499206768	2.173562702	-8.967473085	4.32E-18	2.88E-17	29.85253206
DYNLRB2	1.00822178	0.788654174	8.95796511	4.66E-18	3.10E-17	29.77784817
PLAU	-1.841908013	5.022285302	-8.941825671	5.30E-18	3.52E-17	29.65121164
EFNB2	1.15067676	3.526160681	8.93423937	5.63E-18	3.73E-17	29.59174593
DNAJC22	-1.110601759	1.230403104	-8.930036929	5.82E-18	3.85E-17	29.55882122
ITPKA	-1.830745144	1.878309974	-8.926731459	5.97E-18	3.95E-17	29.53293218
DKK3	1.176459178	3.889653574	8.926239347	6.00E-18	3.97E-17	29.52907849
SIGLEC1	1.143430643	2.23586021	8.917510234	6.43E-18	4.24E-17	29.46074812
FA2H	-1.438180595	2.54169293	-8.912545395	6.68E-18	4.40E-17	29.42190651
NMU	-1.668438291	1.768751529	-8.911158854	6.76E-18	4.44E-17	29.41106206
NEIL3	-1.004896291	1.017065497	-8.901069809	7.32E-18	4.80E-17	29.33219169
CCNO	-1.36367935	2.171632428	-8.899820222	7.39E-18	4.85E-17	29.32242783
CSTA	1.271539658	2.566339461	8.88600877	8.25E-18	5.39E-17	29.2145788

THEM5	-1.228575169	2.539955685	-8.871259014	9.27E-18	6.03E-17	29.09954281
C1orf194	1.445968593	1.215970372	8.867782339	9.52E-18	6.19E-17	29.07244867
SLC29A4	-1.439343534	1.912130908	-8.829240307	1.29E-17	8.32E-17	28.77262551
DEPP1	1.268325997	5.149966865	8.821283139	1.37E-17	8.84E-17	28.71084916
C1orf189	1.212663557	0.960428938	8.81190623	1.48E-17	9.49E-17	28.63810481
DRAM1	1.297487565	4.921118002	8.803706479	1.58E-17	1.01E-16	28.57454084
DPT	1.551640726	3.493939407	8.79945366	1.63E-17	1.04E-16	28.54159097
BTG2	1.335166376	5.636699615	8.799069253	1.64E-17	1.05E-16	28.53861327
TOX3	-1.490010726	2.138988933	-8.796207285	1.67E-17	1.07E-16	28.51644695
COL4A4	1.079700853	1.937719404	8.790315065	1.75E-17	1.12E-16	28.4708282
IL4I1	-1.311457228	2.536837856	-8.788262222	1.78E-17	1.14E-16	28.45494014
WFDC3	-1.507908523	1.712980431	-8.787729068	1.79E-17	1.14E-16	28.45081424
ZMYND10	1.331036185	1.348594893	8.777476403	1.94E-17	1.23E-16	28.37150931
SLC39A4	-1.093861282	3.217182637	-8.771832732	2.02E-17	1.29E-16	28.32788529
NGEF	-1.109970499	1.324159294	-8.770536417	2.04E-17	1.30E-16	28.31786815
GGTLC1	2.162010404	2.767097738	8.770060638	2.05E-17	1.30E-16	28.3141919
CYB5A	1.182367719	4.058878417	8.767079004	2.10E-17	1.33E-16	28.29115688
CAPSL	1.441550748	1.085000265	8.75889946	2.24E-17	1.42E-16	28.22799533
SPINK1	-3.437455397	3.946219601	-8.750283983	2.40E-17	1.52E-16	28.16151619
AXL	1.042597097	3.524833873	8.744677737	2.50E-17	1.58E-16	28.11828382
ALDH1A1	1.828656636	4.707749317	8.732371209	2.76E-17	1.74E-16	28.02345666
UGDH	-1.361607913	4.757529271	-8.729944829	2.81E-17	1.77E-16	28.00477238
S100A4	1.51204431	7.064488053	8.728119818	2.85E-17	1.79E-16	27.99072154
CARD11	-1.259072592	2.587456414	-8.725671672	2.90E-17	1.83E-16	27.97187668
TFRC	1.142402327	4.201081733	8.724415966	2.93E-17	1.84E-16	27.96221233
ENC1	-1.031211593	3.861828139	-8.721252459	3.01E-17	1.89E-16	27.93786957
EMP3	1.033959724	4.522534614	8.718790317	3.06E-17	1.92E-16	27.91892839
RSPH4A	1.191117738	1.052678855	8.715299526	3.15E-17	1.97E-16	27.89208085
BHLHA15	-1.290403289	1.741281806	-8.696272384	3.65E-17	2.27E-16	27.74588846
BARX2	-1.308859855	1.435116645	-8.693581106	3.73E-17	2.32E-16	27.72523014
SPRY4	1.021261043	3.405485219	8.678808097	4.18E-17	2.59E-16	27.61191939
LYPD1	-1.138427776	1.20607163	-8.677217594	4.23E-17	2.62E-16	27.59972885
APOC1	1.56037921	6.01728666	8.677039041	4.24E-17	2.63E-16	27.59836042
C4orf48	-1.146638633	2.667140462	-8.673868895	4.34E-17	2.69E-16	27.57406807
CFTR	1.232056494	1.420429752	8.669348174	4.50E-17	2.78E-16	27.53943823
KIFC2	-1.100145336	2.135402184	-8.660523487	4.82E-17	2.97E-16	27.47187885
ANO9	-1.121023144	2.506235394	-8.660283824	4.83E-17	2.98E-16	27.47004479
PRF1	1.217489715	2.703613401	8.65780731	4.92E-17	3.04E-16	27.45109516
LIPA	1.040096902	4.936494224	8.657669525	4.93E-17	3.04E-16	27.45004099
SNX30	1.049651705	2.767759378	8.656828794	4.96E-17	3.06E-16	27.44360896
DSG2	-1.160385824	4.69905906	-8.653744521	5.08E-17	3.13E-16	27.42001679
PXMP4	1.06693248	2.891152607	8.624216371	6.38E-17	3.91E-16	27.19447745
BCL2A1	1.175529793	3.197736305	8.624188887	6.38E-17	3.91E-16	27.19426781
WDR38	1.44233728	1.13380402	8.622584431	6.46E-17	3.95E-16	27.18202979
ALOX15	1.449862334	1.101059221	8.609873799	7.13E-17	4.35E-16	27.08514117
LCPI	1.204060141	5.276605616	8.592711567	8.14E-17	4.95E-16	26.95449419
LGSN	-1.496320368	1.537155796	-8.591225744	8.23E-17	5.00E-16	26.94319285
CFB	-1.267214338	2.500242333	-8.588991601	8.38E-17	5.09E-16	26.92620254
NKD2	1.028631046	2.146010509	8.587555741	8.47E-17	5.14E-16	26.91528485
POSTN	-1.546142244	4.998573463	-8.579825207	8.99E-17	5.45E-16	26.8565292
STK32A	-1.039939119	1.675057091	-8.577299011	9.17E-17	5.56E-16	26.83733778
ROPN1L	1.146089761	0.987959556	8.558913083	1.06E-16	6.38E-16	26.69779193
FAM92B	1.293303552	1.116416002	8.550937222	1.12E-16	6.76E-16	26.63732849
TBX15	-1.243224936	1.374263168	-8.54153007	1.21E-16	7.25E-16	26.56607069
CITED2	1.127979318	5.452316997	8.514029367	1.49E-16	8.89E-16	26.3581048
TMEM190	1.615251866	1.28687977	8.512246811	1.51E-16	9.00E-16	26.34464266

EFNB1	1.040631697	3.259269018	8.505810213	1.59E-16	9.44E-16	26.29605065
PDGFRL	-1.076138504	2.633540169	-8.492418286	1.76E-16	1.04E-15	26.19504182
MUC20	-1.515724667	3.07102866	-8.481855937	1.91E-16	1.13E-15	26.11546218
E2F1	-1.086259882	2.993572373	-8.480040526	1.93E-16	1.14E-15	26.10179211
EIF4EBP1	-1.259064386	4.866731384	-8.477356358	1.97E-16	1.16E-15	26.08158445
NTM	1.099928951	1.608913305	8.474482104	2.02E-16	1.19E-15	26.05995124
CEACAM5	-3.287249477	5.291847641	-8.471081489	2.07E-16	1.22E-15	26.03436369
SRGN	1.238949897	6.747237205	8.469723158	2.09E-16	1.23E-15	26.02414531
MMP17	-1.0006824	1.285111297	-8.466792834	2.14E-16	1.26E-15	26.00210556
ERICH2	1.097398073	2.258815469	8.451480767	2.40E-16	1.41E-15	25.88703575
ALPL	2.081743226	4.472069805	8.451411557	2.40E-16	1.41E-15	25.88651601
SLC16A3	-1.13122575	4.117969113	-8.450466758	2.42E-16	1.42E-15	25.87942121
RCN3	-1.323308459	3.896887799	-8.440130727	2.62E-16	1.53E-15	25.80184495
PLAC8	1.369944001	2.160618172	8.437396183	2.67E-16	1.57E-15	25.7813334
CD37	1.057248025	3.165838861	8.433017023	2.76E-16	1.61E-15	25.74849651
CAMK2N1	1.396848372	3.600530982	8.429050082	2.85E-16	1.66E-15	25.71876208
PLEKHA6	-1.13731901	2.721676354	-8.428624435	2.86E-16	1.67E-15	25.71557226
MACROD2	1.146959258	1.248754299	8.40873792	3.32E-16	1.93E-15	25.56668176
EEF1A2	-2.720378176	2.881551127	-8.408046291	3.34E-16	1.94E-15	25.56150846
PER1	1.181171232	3.854805499	8.388085401	3.89E-16	2.24E-15	25.41234634
PODNL1	-1.243326861	1.705391269	-8.37721129	4.22E-16	2.43E-15	25.33120355
ENTPD8	-1.062479148	1.050186111	-8.365090939	4.62E-16	2.66E-15	25.24085814
SLC2A3	1.197281094	3.2915233	8.363411953	4.68E-16	2.69E-15	25.22835099
HES6	-1.520122463	2.706345627	-8.362491759	4.72E-16	2.70E-15	25.22149709
NDN	1.015166177	3.165876909	8.359565054	4.82E-16	2.76E-15	25.19970196
FOS	1.574830286	6.265473452	8.358596828	4.86E-16	2.78E-15	25.19249291
CBX2	-1.134661884	1.644302877	-8.358208883	4.87E-16	2.79E-15	25.1896046
ACTG2	1.19267233	2.208569362	8.355721456	4.96E-16	2.84E-15	25.17108781
ESPN	-1.242443173	1.803566586	-8.34862221	5.24E-16	2.99E-15	25.11826361
COMP	-1.911654673	2.840356696	-8.346771346	5.31E-16	3.03E-15	25.10449744
FKBP10	-1.403236622	4.487941935	-8.343735003	5.43E-16	3.10E-15	25.0819192
PLBD1	1.239073326	3.864329844	8.343368783	5.45E-16	3.11E-15	25.07919642
SCNN1G	1.317657862	2.077920871	8.338302223	5.66E-16	3.22E-15	25.04153709
SOD3	1.221286156	4.089920376	8.315795269	6.71E-16	3.80E-15	24.87446122
B4GALNT4	-1.392294331	1.403111809	-8.310374247	6.98E-16	3.95E-15	24.83427221
ARNTL2	-1.237219673	2.02510678	-8.271667529	9.34E-16	5.24E-15	24.54791558
C5orf38	1.445198858	2.043486885	8.265046801	9.81E-16	5.50E-15	24.49903983
SLPI	2.249885165	8.266410291	8.263605901	9.92E-16	5.56E-15	24.48840684
ADGRF5	1.606211307	4.772366388	8.258848212	1.03E-15	5.75E-15	24.45330828
SLC6A8	-1.199622435	2.655553346	-8.244889292	1.14E-15	6.36E-15	24.35042186
LRRC4	1.040624281	1.529206416	8.240879183	1.18E-15	6.55E-15	24.32089003
MFAP2	-1.172101811	3.039650406	-8.23800369	1.20E-15	6.68E-15	24.29972088
BEX5	1.086901416	1.853524803	8.234500596	1.23E-15	6.85E-15	24.27393922
ASPHD1	-1.339461923	1.935125234	-8.226304534	1.31E-15	7.27E-15	24.21365255
HCST	1.018416778	3.279601675	8.220126615	1.37E-15	7.61E-15	24.16824173
BEX4	1.041470364	4.314909424	8.207656669	1.51E-15	8.33E-15	24.07666322
REEP6	-1.379364223	2.678928866	-8.191262922	1.70E-15	9.37E-15	23.95643541
SCG5	-1.423780385	1.955579346	-8.182301506	1.82E-15	9.99E-15	23.89079473
SPATA18	1.148021187	1.533490694	8.163304055	2.09E-15	1.14E-14	23.75182969
AKAP12	1.364937947	2.335599024	8.161325223	2.13E-15	1.16E-14	23.73736936
CABYR	-1.379584376	1.434095855	-8.137324242	2.54E-15	1.38E-14	23.56220275
CENPW	-1.076333609	2.94695934	-8.133609544	2.61E-15	1.41E-14	23.53512821
CLDN3	-1.631637625	5.556536297	-8.120136647	2.88E-15	1.55E-14	23.43701335
CSF3R	1.338291839	2.679424012	8.095324902	3.46E-15	1.86E-14	23.25666203
TMEM63C	-1.090041742	1.132508749	-8.087965746	3.65E-15	1.96E-14	23.20325411
STRA6	-1.119339273	1.126321956	-8.080885297	3.85E-15	2.06E-14	23.15190525

SGPP2	-1.280489398	4.232414514	-8.05934559	4.51E-15	2.40E-14	22.99591468
PLOD2	-1.327557792	3.454314542	-8.053059283	4.72E-15	2.51E-14	22.95045164
HIST1H3H	-1.14418221	1.670283533	-8.048641853	4.88E-15	2.59E-14	22.91852135
FAM166B	1.114278007	1.142591131	8.030288336	5.58E-15	2.95E-14	22.7860069
CD163	1.319188746	3.87504243	8.013767055	6.30E-15	3.31E-14	22.66692753
NFE2L3	-1.018216159	3.23978098	-8.005618352	6.69E-15	3.51E-14	22.60826667
CNTD2	-1.091628991	1.118574163	-8.003390021	6.80E-15	3.56E-14	22.59223365
CA9	-2.051286	2.0869596	-7.99672876	7.14E-15	3.73E-14	22.54432659
CPD	-1.065050825	4.41446006	-7.982405284	7.92E-15	4.13E-14	22.44142159
PRSS22	-1.213505363	3.295695827	-7.982198269	7.93E-15	4.13E-14	22.4399354
LYZ	1.758096469	7.551724291	7.976567321	8.27E-15	4.30E-14	22.39952183
CFAP73	1.058410205	0.951081044	7.974486725	8.39E-15	4.36E-14	22.38459507
GLB1L2	-1.024568452	2.38995043	-7.967507901	8.83E-15	4.58E-14	22.33454981
FAXDC2	1.257666709	2.564386414	7.956017546	9.60E-15	4.98E-14	22.25222861
IGLL5	-1.895818758	4.739618387	-7.954879301	9.68E-15	5.01E-14	22.24407898
CD53	1.072338591	4.98001285	7.947949391	1.02E-14	5.26E-14	22.19448214
HSD17B13	1.01303474	0.744429458	7.920209618	1.24E-14	6.39E-14	21.99629735
XKRX	-1.297417706	1.861064192	-7.911641862	1.32E-14	6.79E-14	21.93519788
CAPN5	-1.193683541	2.766962585	-7.875179343	1.72E-14	8.75E-14	21.67576543
CXCL3	1.111776798	1.742048484	7.870159918	1.79E-14	9.07E-14	21.64012739
TMEM156	-1.020777329	1.439497509	-7.866703539	1.83E-14	9.29E-14	21.61559763
MELTF	-1.104189811	1.501199536	-7.861989579	1.90E-14	9.59E-14	21.58215684
BAIAP2L2	-1.183873043	1.371841503	-7.855187835	1.99E-14	1.01E-13	21.53393374
ADA2	1.016436978	3.997241244	7.852980679	2.02E-14	1.02E-13	21.51829263
DDIT4L	-1.263823384	1.604153824	-7.830049248	2.39E-14	1.20E-13	21.35599742
CD69	1.026546169	2.162295344	7.826673321	2.44E-14	1.23E-13	21.33213687
JSRP1	-1.119849578	1.41360937	-7.826043367	2.46E-14	1.23E-13	21.32768537
HLA-DOA	1.276993273	3.92652492	7.818679834	2.59E-14	1.30E-13	21.27567317
S100P	-2.980312971	5.030169511	-7.796241655	3.04E-14	1.52E-13	21.11742494
CACHD1	1.075990089	1.983668354	7.789738286	3.18E-14	1.59E-13	21.07162768
OASL	1.02296487	2.14068229	7.776100166	3.51E-14	1.74E-13	20.97568715
TRIM2	-1.042816916	3.404482782	-7.775364767	3.53E-14	1.75E-13	20.97051768
TGFB2	1.027039143	1.747691376	7.772363284	3.61E-14	1.79E-13	20.9494229
LRRC46	1.103976968	1.386640525	7.750682231	4.21E-14	2.08E-13	20.7972415
ALDH3B2	-1.225748905	1.696575934	-7.748037088	4.29E-14	2.11E-13	20.77869852
HSF4	-1.075873889	1.96793388	-7.745500024	4.37E-14	2.15E-13	20.76091802
HIST1H4H	-1.221035234	2.446086098	-7.727356823	4.97E-14	2.43E-13	20.63390246
AOC1	-1.943943317	2.144360216	-7.721861114	5.17E-14	2.53E-13	20.59547613
MZB1	-1.619422682	3.515248781	-7.719005548	5.27E-14	2.58E-13	20.57551859
SFN	-1.255605896	6.636598455	-7.701246675	5.98E-14	2.91E-13	20.45153627
C1QC	1.294026567	6.987472136	7.684963197	6.71E-14	3.25E-13	20.33805799
MMP13	-1.867035446	1.859431965	-7.684938866	6.71E-14	3.25E-13	20.33788858
RAB15	-1.056997579	3.469516102	-7.679555198	6.97E-14	3.37E-13	20.30041322
SYT12	-1.279267073	1.221780941	-7.671840414	7.37E-14	3.56E-13	20.24674831
CGREF1	-1.000909164	1.037149023	-7.670670599	7.43E-14	3.58E-13	20.23861477
ATP6V1C2	-1.096301633	1.473176644	-7.669821712	7.47E-14	3.60E-13	20.23271322
LYPD3	-1.476468825	2.051859618	-7.658140002	8.11E-14	3.90E-13	20.15155477
LAMA3	1.368636394	2.49290419	7.642572738	9.06E-14	4.35E-13	20.04355792
BATF	-1.007635672	3.561559054	-7.638578313	9.31E-14	4.46E-13	20.01587569
APOBEC3B	-1.154760457	1.928926886	-7.633387001	9.66E-14	4.62E-13	19.9799164
IFT57	1.062829618	4.428463761	7.612244653	1.12E-13	5.35E-13	19.83367288
LOXL2	-1.168872977	2.911744102	-7.607341356	1.16E-13	5.53E-13	19.79980356
TXNIP	1.015439937	7.506342358	7.547742353	1.76E-13	8.29E-13	19.38955109
NOXA1	-1.018754132	2.951814211	-7.543948823	1.81E-13	8.51E-13	19.36352745
ADGRF4	-1.015755231	1.021380967	-7.529889613	1.99E-13	9.35E-13	19.2671746
SLC7A11	-1.310107229	1.7125276	-7.516217054	2.19E-13	1.02E-12	19.17361281

AGR2	-1.784630135	6.723592748	-7.51529002	2.21E-13	1.03E-12	19.16727412
B3GNT6	-1.687929038	1.653499856	-7.495907829	2.53E-13	1.17E-12	19.03489341
MT1A	1.376378496	1.61381914	7.486635999	2.69E-13	1.25E-12	18.97166581
PLA1A	1.062841972	2.016154059	7.477753581	2.86E-13	1.33E-12	18.9111154
SCD	1.055545164	6.151535467	7.470730795	3.01E-13	1.39E-12	18.86335276
CTSH	1.331506545	6.11243132	7.467253548	3.08E-13	1.42E-12	18.83969822
MYEOV	-1.549017745	1.486051326	-7.466314609	3.10E-13	1.43E-12	18.83331248
RARRES2	1.122654802	5.127676907	7.457929376	3.29E-13	1.52E-12	18.77631368
FNDC4	-1.132790371	2.377696337	-7.455996024	3.33E-13	1.53E-12	18.76317915
HLA-DRA	1.264630963	9.958801052	7.45220248	3.42E-13	1.57E-12	18.73741525
SHE	1.081785056	1.937969697	7.445380603	3.58E-13	1.65E-12	18.69111151
DMBT1	2.144420164	3.209123404	7.444438148	3.61E-13	1.66E-12	18.68471731
TMPRSS11E	-1.656152252	1.567248864	-7.424264945	4.15E-13	1.89E-12	18.54800943
SOCS3	1.053802905	5.73047037	7.420668921	4.25E-13	1.94E-12	18.52367231
HLA-DPA1	1.268098807	6.306606271	7.416357962	4.38E-13	2.00E-12	18.49450947
SEZ6L2	-1.292494233	4.124703644	-7.412211002	4.50E-13	2.05E-12	18.46646922
PTK6	-1.132424244	3.00660826	-7.402678363	4.81E-13	2.19E-12	18.40206196
HILPDA	-1.103596655	3.272558292	-7.398445666	4.95E-13	2.25E-12	18.37348566
MS4A8	1.460397766	1.367175284	7.374603643	5.83E-13	2.63E-12	18.21277242
CD79A	-1.563461609	3.600342303	-7.342016679	7.29E-13	3.27E-12	17.99380482
VCAN	-1.211207696	3.580864852	-7.327071414	8.07E-13	3.61E-12	17.89364861
MAP7D2	-1.062865719	1.233220987	-7.323198537	8.29E-13	3.70E-12	17.86772195
C2	1.134044409	3.741194907	7.321696062	8.37E-13	3.74E-12	17.85766668
VMO1	1.016445053	2.571368792	7.31231819	8.92E-13	3.97E-12	17.79494509
S100A2	-1.727928427	3.200099944	-7.311350883	8.98E-13	4.00E-12	17.78847927
HIST1H2BK	-1.052723158	5.862807149	-7.310362922	9.04E-13	4.02E-12	17.78187612
MUC3A	-1.487174268	1.625691541	-7.307897349	9.20E-13	4.08E-12	17.76540041
FOXA3	-1.236235968	1.576579948	-7.304406977	9.42E-13	4.18E-12	17.74208456
CDHR3	1.107894205	1.122995672	7.303257082	9.49E-13	4.21E-12	17.73440523
PMAIP1	-1.135057658	2.884584367	-7.286717763	1.06E-12	4.69E-12	17.62406177
PRSS12	1.095264036	1.53046453	7.282908703	1.09E-12	4.81E-12	17.5986787
FOXA1	-1.101581884	3.984070461	-7.274756876	1.15E-12	5.06E-12	17.54439301
COL17A1	-1.717093629	2.028108946	-7.269077735	1.20E-12	5.26E-12	17.50660358
HIST1H2BC	-1.184474916	2.581367513	-7.267303291	1.21E-12	5.32E-12	17.49480131
MGP	1.178888008	6.070119649	7.251165797	1.35E-12	5.90E-12	17.38757675
GALNT6	-1.171029207	2.933034247	-7.246706605	1.39E-12	6.07E-12	17.35798285
HLA-DRB5	1.542953919	7.458446326	7.229255693	1.57E-12	6.80E-12	17.24231358
FAM183A	1.291493235	1.759175927	7.216145716	1.71E-12	7.40E-12	17.15556981
FNDC1	-1.215726944	2.068035486	-7.200204724	1.91E-12	8.21E-12	17.05027092
RSPH1	1.116036899	1.572138945	7.174362236	2.27E-12	9.72E-12	16.87997968
C5orf49	1.066319773	1.396428644	7.16780001	2.37E-12	1.01E-11	16.83681865
PTN	1.213392307	2.212038646	7.16052481	2.49E-12	1.06E-11	16.78900678
MAOA	1.218015446	4.335704209	7.160071779	2.49E-12	1.07E-11	16.78603085
IRX2	1.603011219	2.753702311	7.150816262	2.65E-12	1.13E-11	16.72526636
HTR3A	-1.207014786	1.15010292	-7.132601798	3.00E-12	1.27E-11	16.60587621
COL1A2	-1.277481878	6.801417864	-7.121606575	3.22E-12	1.36E-11	16.53392916
HLA-DRB1	1.259714279	9.082676101	7.116668727	3.33E-12	1.41E-11	16.50164865
AIM2	-1.251255623	1.856765101	-7.114569583	3.38E-12	1.42E-11	16.48793146
PTPN13	1.203933738	2.756235615	7.109918543	3.48E-12	1.47E-11	16.45755056
AKR7A3	-1.49279104	1.585097398	-7.104743061	3.61E-12	1.52E-11	16.42376351
ADAMDEC1	-1.216444996	1.899523682	-7.099255617	3.74E-12	1.57E-11	16.38796239
CDKN2A	-1.395128235	1.815877743	-7.093487761	3.89E-12	1.63E-11	16.35035678
LRRN4	1.47786185	2.432122913	7.093029448	3.90E-12	1.64E-11	16.34736974
KCNK1	-1.044782679	3.276468272	-7.081402099	4.21E-12	1.76E-11	16.27164301
HLA-DPB1	1.154624988	7.043851746	7.078104425	4.31E-12	1.80E-11	16.25018484
AHNAK2	-1.185960143	2.165396979	-7.077996646	4.31E-12	1.80E-11	16.24948365

NKG7	1.182901207	3.394332521	7.048190434	5.25E-12	2.18E-11	16.05591561
SPNS2	1.08988681	2.859452593	7.00893832	6.80E-12	2.81E-11	15.8020507
HIST1H2BG	-1.156684908	1.350210078	-7.00816898	6.83E-12	2.82E-11	15.79708687
MXRA5	-1.156041604	3.297239004	-7.002812359	7.08E-12	2.92E-11	15.76253831
ALDH3B1	1.073901102	4.053013257	6.995519157	7.43E-12	3.06E-11	15.71553514
COL7A1	-1.002711455	1.244832095	-6.976145747	8.43E-12	3.46E-11	15.59087784
FCER1A	1.288582742	2.036843171	6.954336869	9.73E-12	3.97E-11	15.45089826
ID1	1.254952124	5.169348827	6.9384474	1.08E-11	4.39E-11	15.34914503
LCN2	-1.930803231	5.459666504	-6.920444596	1.21E-11	4.91E-11	15.23409587
BMP5	1.027741103	2.01713281	6.860905406	1.79E-11	7.15E-11	14.85540414
CEBPA	1.037766457	3.053806196	6.849533231	1.92E-11	7.67E-11	14.78338804
ATP1B1	-1.001628816	7.314059826	-6.846619856	1.96E-11	7.80E-11	14.76495492
XAGE2	1.358794081	1.110188616	6.846187813	1.96E-11	7.82E-11	14.76222193
GPR87	-1.529225275	1.724315421	-6.82661614	2.23E-11	8.83E-11	14.63856976
C4BPA	2.013555013	5.413328962	6.805415161	2.55E-11	1.01E-10	14.50496289
CXCL14	-2.196128433	3.946928016	-6.801935595	2.61E-11	1.03E-10	14.48306867
KRT15	-1.296429477	2.192107519	-6.793333359	2.76E-11	1.08E-10	14.42898229
BASP1	-1.213128042	4.668611202	-6.789793877	2.82E-11	1.11E-10	14.40674476
ST6GALNAC1	-1.419153837	3.652576821	-6.781959606	2.97E-11	1.16E-10	14.35755939
PGC	3.16908021	4.821031022	6.776239359	3.08E-11	1.20E-10	14.32167687
SLC16A9	-1.304672459	1.85305115	-6.756831459	3.49E-11	1.35E-10	14.20012513
SPAG6	1.042794463	1.094725802	6.754702831	3.53E-11	1.37E-10	14.18681159
HIST1H2AE	-1.18440875	1.455402611	-6.720520768	4.39E-11	1.69E-10	13.97350903
KCNK5	-1.092703542	3.700919526	-6.716712507	4.50E-11	1.73E-10	13.9498019
TESC	-1.914582905	3.820676263	-6.710834291	4.67E-11	1.80E-10	13.91323142
SCGB3A2	2.704210374	5.998479355	6.705715732	4.83E-11	1.85E-10	13.8814093
CT83	-1.720581646	1.636830492	-6.678663474	5.73E-11	2.19E-10	13.71356966
SMKR1	-1.081232594	1.567157123	-6.647676092	6.97E-11	2.64E-10	13.52202833
LDLRAD1	1.13045002	1.467121306	6.642881312	7.18E-11	2.72E-10	13.49245861
QPCT	-1.476052171	3.148090683	-6.631575539	7.71E-11	2.92E-10	13.42280751
RRAD	1.354564485	3.520643781	6.629263796	7.83E-11	2.96E-10	13.40857815
RHOBTB2	1.009528866	3.949931005	6.599469007	9.44E-11	3.55E-10	13.22556437
PRRX2	-1.049022853	1.807011923	-6.585789746	1.03E-10	3.85E-10	13.14177673
HGD	-1.46123898	1.945330291	-6.554626827	1.25E-10	4.64E-10	12.95145656
COL6A3	-1.019395218	4.794610397	-6.535761161	1.40E-10	5.19E-10	12.83661611
PRAME	-1.561868945	1.444250396	-6.531614549	1.44E-10	5.33E-10	12.81141274
S100A8	1.51213427	4.026172064	6.525291534	1.50E-10	5.53E-10	12.77300754
CACNG4	1.304546384	1.960411503	6.502155495	1.73E-10	6.35E-10	12.63275525
LRRC15	-1.137086129	1.83378591	-6.499048312	1.76E-10	6.47E-10	12.61395199
PLA2G4A	-1.349088867	3.408730483	-6.481945964	1.96E-10	7.17E-10	12.51059503
PCP4	-1.756952617	1.944075738	-6.469916229	2.11E-10	7.71E-10	12.43803484
CST2	-1.041242401	1.472362257	-6.465576692	2.17E-10	7.91E-10	12.41188845
AC007906.2	1.387497822	1.988674247	6.465375773	2.17E-10	7.92E-10	12.41067825
MAB21L4	1.095104722	2.516109347	6.437567108	2.58E-10	9.34E-10	12.24349087
TNS4	-1.422061046	1.816732103	-6.428348501	2.73E-10	9.86E-10	12.18820551
HOXB7	-1.137614477	2.402318107	-6.421569054	2.84E-10	1.03E-09	12.14759187
MUC4	-1.266982414	2.129933075	-6.418914537	2.89E-10	1.04E-09	12.13169955
IER3	-1.013970653	5.593316371	-6.410938779	3.03E-10	1.09E-09	12.08398372
CX3CL1	1.237908455	3.67729877	6.402592225	3.19E-10	1.15E-09	12.03410455
GPX2	-2.514161871	3.223178207	-6.39944245	3.25E-10	1.17E-09	12.01529605
WFDC2	-1.380749352	7.354064111	-6.396621369	3.31E-10	1.19E-09	11.99845711
CLDN10	-1.418396859	1.671836793	-6.386653673	3.52E-10	1.26E-09	11.93901176
MT-ND6	1.129307065	10.39441835	6.384204926	3.57E-10	1.28E-09	11.92442022
TRIM31	-1.004782464	1.13545737	-6.38162177	3.63E-10	1.30E-09	11.90903301
UCHL1	-1.790201525	3.201559697	-6.373436242	3.81E-10	1.36E-09	11.86030954
HIST1H1C	-1.097535712	5.766138082	-6.355556626	4.25E-10	1.51E-09	11.75407165

DUSP4	-1.295746712	3.014797485	-6.353473616	4.30E-10	1.53E-09	11.74171157
KRT16	-1.303258895	1.364246837	-6.339280229	4.69E-10	1.66E-09	11.65758502
CEMIP	-1.134966323	2.555452797	-6.326680454	5.06E-10	1.79E-09	11.58304097
FOLR1	1.707505401	5.710771403	6.319856819	5.28E-10	1.86E-09	11.54272407
SCGB3A1	2.577286325	5.663899543	6.318057017	5.34E-10	1.88E-09	11.53209639
COL9A2	-1.06894202	2.408896286	-6.279778974	6.72E-10	2.35E-09	11.3066911
MUC21	-1.810030324	2.934333856	-6.229025121	9.11E-10	3.16E-09	11.00966031
ROS1	1.22229078	2.94852946	6.228088716	9.16E-10	3.18E-09	11.00419986
SLC16A14	-1.242237126	2.057976052	-6.21812377	9.72E-10	3.36E-09	10.94613574
PAEP	-2.28810612	2.355393898	-6.215158604	9.90E-10	3.42E-09	10.92887387
ITGB4	-1.190469545	4.51104278	-6.209572828	1.02E-09	3.54E-09	10.8963755
RNASE1	1.213885323	8.035512453	6.207597229	1.04E-09	3.58E-09	10.88488746
TREM1	1.176763724	3.430376673	6.202621072	1.07E-09	3.68E-09	10.85596542
CIT	-1.149724765	2.746352811	-6.188456949	1.16E-09	3.99E-09	10.77375273
SCNN1B	1.219794757	3.629034713	6.185765061	1.18E-09	4.05E-09	10.7581468
PGGHG	-1.335870686	3.983597945	-6.176518447	1.25E-09	4.27E-09	10.70458579
HIST3H2A	-1.255669264	2.528509785	-6.168611013	1.31E-09	4.46E-09	10.65883756
SFTPB	2.258564658	9.815290369	6.162501015	1.35E-09	4.62E-09	10.62352346
HLA-DQA1	1.107032665	5.027997685	6.153961109	1.42E-09	4.85E-09	10.57421647
CD24	-1.162621912	5.975198508	-6.14257395	1.52E-09	5.17E-09	10.50856338
CILP	-1.023025705	1.542021561	-6.128263514	1.66E-09	5.61E-09	10.42620707
HHIPL2	-1.097597871	1.04617209	-6.127295206	1.67E-09	5.64E-09	10.42064056
GCLC	-1.174741161	2.938206817	-6.126557254	1.67E-09	5.66E-09	10.41639881
MUC13	-1.84099206	1.955785507	-6.092920798	2.04E-09	6.85E-09	10.22353201
RNF128	1.161638841	2.634073826	6.091972798	2.05E-09	6.89E-09	10.21810981
SIX2	-1.000455723	1.244376116	-5.972511202	4.11E-09	1.34E-08	9.540775394
FGL1	-1.738119833	1.681771785	-5.965230736	4.29E-09	1.40E-08	9.499878058
HORMAD1	-1.025056035	1.072409266	-5.949753405	4.69E-09	1.52E-08	9.413081892
MUC15	1.131147823	2.255948196	5.946893303	4.76E-09	1.55E-08	9.397064365
GJB3	-1.183116629	1.657872289	-5.941636756	4.91E-09	1.60E-08	9.367643689
PFN2	-1.053990462	4.275997825	-5.930210763	5.24E-09	1.70E-08	9.303772146
TNNT1	-1.438485506	2.245554834	-5.915171046	5.71E-09	1.85E-08	9.219865473
PPP1R14C	1.054770264	2.856688472	5.896873308	6.35E-09	2.04E-08	9.118036395
ACHE	-1.037226943	1.775391427	-5.879816694	6.99E-09	2.25E-08	9.023365783
TMEM59L	-1.414887842	1.771037071	-5.837460361	8.90E-09	2.83E-08	8.789323274
ISG15	-1.08662804	5.956584338	-5.833418996	9.10E-09	2.89E-08	8.767070882
NT5E	-1.132256748	3.390808914	-5.825192834	9.53E-09	3.02E-08	8.721818586
BARX1	-1.534894381	1.438220198	-5.822399455	9.69E-09	3.07E-08	8.706465036
VSTM2L	-1.401415107	4.29752174	-5.815444966	1.01E-08	3.18E-08	8.668268737
MUC5B	-1.957713496	2.954107759	-5.807881276	1.05E-08	3.32E-08	8.626772527
KLK10	1.194309728	1.767783748	5.806442481	1.06E-08	3.34E-08	8.618884387
LY6K	-1.000037584	1.152648691	-5.790267507	1.16E-08	3.64E-08	8.530325153
SLC22A3	1.064918587	2.997786392	5.785742306	1.19E-08	3.73E-08	8.505588638
IL37	-1.511505199	1.528840214	-5.774160656	1.27E-08	3.97E-08	8.44235714
BMP6	1.04550887	1.832092719	5.770038591	1.30E-08	4.06E-08	8.419879389
TMPRSS2	1.011506107	3.947990909	5.683145038	2.11E-08	6.48E-08	7.949374976
TUBB2B	-1.216449795	1.556295548	-5.678830275	2.16E-08	6.62E-08	7.926177694
FOXA2	1.143173535	3.122961786	5.660815574	2.39E-08	7.28E-08	7.829496008
VIL1	-1.172707661	1.092401695	-5.64210206	2.65E-08	8.04E-08	7.729354618
LY6D	-1.244947162	1.250260426	-5.59505148	3.43E-08	1.03E-07	7.478884319
IL20RB	-1.01518651	1.254734761	-5.580804473	3.70E-08	1.11E-07	7.403411976
ALOX15B	1.300245972	3.694713375	5.578940598	3.74E-08	1.12E-07	7.393551008
TCN1	-1.607438838	1.646659254	-5.57420009	3.84E-08	1.15E-07	7.368484309
TFF1	-2.067743294	2.042357297	-5.491413936	6.01E-08	1.77E-07	6.933815291
C1orf116	1.144218527	4.945848592	5.429071479	8.39E-08	2.44E-07	6.610348857
FDCSP	-1.225581617	2.007736053	-5.428260457	8.43E-08	2.45E-07	6.606162767

AKR1B10	-1.930432409	1.987379205	-5.42641335	8.51E-08	2.47E-07	6.59663102
ANGPTL4	-1.200026044	3.519173927	-5.389423857	1.04E-07	2.99E-07	6.406367993
HOXC10	-1.048010713	0.995990455	-5.388686425	1.04E-07	3.00E-07	6.402586807
UBD	-1.089957748	2.872955319	-5.375869654	1.11E-07	3.20E-07	6.336943346
HPGD	1.268673726	3.553224771	5.346785275	1.30E-07	3.70E-07	6.188506403
SLC34A2	1.376597815	8.043219433	5.327117273	1.44E-07	4.09E-07	6.088540313
CRLF1	-1.717304855	3.120698479	-5.325878287	1.45E-07	4.11E-07	6.082254111
HLA-DQB1	1.002545696	5.721263445	5.284224948	1.80E-07	5.07E-07	5.871689718
AGT	-1.146196357	2.315159439	-5.20734824	2.68E-07	7.43E-07	5.487005306
CCL21	1.037380104	5.115779716	5.15739269	3.46E-07	9.52E-07	5.239779919
FGB	-2.010364754	1.977817706	-5.112397413	4.35E-07	1.19E-06	5.018961074
KRT6A	-1.572869	1.852206368	-5.041407044	6.21E-07	1.67E-06	4.674161301
ADGRF1	-1.07172463	2.009925742	-5.041212387	6.22E-07	1.67E-06	4.673221912
ARSE	-1.051935721	2.671436411	-4.999202207	7.67E-07	2.04E-06	4.471262952
KLK11	1.301431037	2.316278392	4.982591756	8.33E-07	2.21E-06	4.391837176
CCL19	-1.159650416	4.026207057	-4.960100212	9.31E-07	2.46E-06	4.284676143
SPRR1B	-1.31132821	1.363446388	-4.93228204	1.07E-06	2.80E-06	4.152751671
CDA	-1.176233372	2.954028982	-4.908929959	1.20E-06	3.13E-06	4.04253314
SFTA3	1.070645567	4.526044444	4.902007615	1.24E-06	3.23E-06	4.009953001
SERPINB5	-1.005392367	1.1285634	-4.882701739	1.36E-06	3.53E-06	3.919312842
HABP2	-1.053353945	2.016759373	-4.833403305	1.73E-06	4.44E-06	3.68935253
CCL18	1.106253437	5.586063113	4.831974187	1.74E-06	4.47E-06	3.682718237
PCSK1N	-1.056980064	2.210780096	-4.799696666	2.03E-06	5.18E-06	3.533360193
C16orf89	1.479726506	5.553843458	4.783041342	2.20E-06	5.59E-06	3.456651988
CST6	1.09614902	3.365727603	4.775679143	2.28E-06	5.79E-06	3.422822869
PRSS2	-1.303780762	1.493819559	-4.774649452	2.29E-06	5.81E-06	3.418095299
INHA	-1.043850817	1.053992062	-4.750952701	2.56E-06	6.48E-06	3.30955767
SMOC1	-1.021357889	1.372756124	-4.746265333	2.62E-06	6.62E-06	3.28814733
PIGR	1.638866246	6.007079717	4.648659586	4.15E-06	1.03E-05	2.846760325
TFPI2	-1.510631513	3.491618553	-4.610934744	4.95E-06	1.22E-05	2.67844061
NAPSA	1.447940292	7.811215462	4.541323608	6.82E-06	1.66E-05	2.371195447
VSIG1	-1.204193548	1.866580495	-4.496452355	8.37E-06	2.01E-05	2.175450205
CXCL5	1.000272124	2.061809339	4.491167322	8.58E-06	2.06E-05	2.152514056
GFRA3	-1.138028273	2.071589811	-4.421379742	1.17E-05	2.78E-05	1.85200704
SERPINA1	1.052962419	6.903284399	4.41950357	1.18E-05	2.80E-05	1.843988819
KRT81	-1.014895831	1.112820587	-4.413441929	1.22E-05	2.88E-05	1.818104815
CLDN6	-1.155673932	1.263404814	-4.343704934	1.66E-05	3.86E-05	1.522707615
MMP7	-1.129636827	4.162042128	-4.286936446	2.13E-05	4.89E-05	1.285495498
SFRP2	-1.058278394	5.099654523	-4.276563857	2.22E-05	5.10E-05	1.24246875
BPIFA1	-1.986837828	3.938633125	-4.210351524	2.96E-05	6.71E-05	0.970117606
AGR3	1.156140185	4.874459036	4.173142016	3.47E-05	7.82E-05	0.818816428
MAGEA3	-1.002835156	0.921754194	-4.124471012	4.27E-05	9.53E-05	0.622818479
CCL20	-1.055346072	3.439546816	-4.08708432	4.99E-05	0.000110681	0.473733623
KRT17	-1.140366309	3.627033715	-3.939823407	9.16E-05	0.000196988	-0.101015674
CPS1	-1.256223735	1.419309141	-3.917838947	0.000100169	0.00021443	-0.185107558
SAA1	-1.037448893	3.010703781	-3.854154744	0.000129315	0.000273691	-0.426185174
TM4SF4	-1.01280689	1.321289799	-3.717667615	0.00022089	0.000454338	-0.930210896
AKR1C2	-1.159502906	2.523867683	-3.092894696	0.002079	0.003793253	-3.014883411
TFF3	-1.01779631	4.335422995	-2.907222479	0.003788187	0.006671352	-3.563219679
CALCA	-1.01717155	1.22840469	-2.794251405	0.005376756	0.009258973	-3.880727664
MSMB	-1.021104209	3.06997048	-2.578881861	0.010161232	0.016786706	-4.452060948

Supplementary Table 5. Expression patterns of genes shared by HRGs and DEGs in the TCGA database

	gene	logFC	AveExpr	t	P.Value	adj.P.Val	B
Up	CAV1	3.884711	4.883969	22.47595	1.28E-80	2.15E-78	173.0412
	CAVIN1	2.107729	5.668371	17.59484	1.09E-55	6.67E-54	115.8533
	NDST1	1.408346	3.613775	16.59375	9.35E-51	4.77E-49	104.5466
	PPP1R15A	1.64722	4.857138	16.18172	9.38E-49	4.42E-47	99.95871
	KLF6	1.671909	4.886625	15.78515	7.61E-47	3.24E-45	95.58345
	GPC3	2.607174	3.200603	14.02849	1.26E-38	3.31E-37	76.75945
	SRPX	1.749925	2.263775	13.88162	5.84E-38	1.48E-36	75.23211
	PDGFB	1.228525	2.817479	11.85683	3.82E-29	5.50E-28	55.06498
	FBP1	1.58875	5.863903	11.18639	2.11E-26	2.52E-25	48.80132
	MAFF	1.001798	2.745159	10.89318	3.10E-25	3.44E-24	46.13501
	IL6	1.834434	1.976962	10.76492	9.91E-25	1.07E-23	44.98328
	ZFP36	1.68438	6.752456	10.58446	5.01E-24	5.14E-23	43.37802
	DUSP1	1.78988	7.023695	10.50369	1.03E-23	1.03E-22	42.66549
	DCN	1.583655	4.781792	10.3782	3.12E-23	3.01E-22	41.56578
	ETS1	1.139514	3.96382	10.35345	3.88E-23	3.71E-22	41.34991
	ATF3	1.568855	3.557186	9.637916	1.81E-20	1.43E-19	35.26603
	SDC2	1.155231	3.457781	9.553253	3.67E-20	2.84E-19	34.5667
	SELENBP1	1.681175	5.47572	9.030582	2.61E-18	1.77E-17	30.34975
	S100A4	1.512044	7.064488	8.72812	2.85E-17	1.79E-16	27.99072
	CITED2	1.127979	5.452317	8.514029	1.49E-16	8.89E-16	26.3581
	PLAC8	1.369944	2.160618	8.437396	2.67E-16	1.57E-15	25.78133
	SLC2A3	1.197281	3.291523	8.363412	4.68E-16	2.69E-15	25.22835
	FOS	1.57483	6.265473	8.358597	4.86E-16	2.78E-15	25.19249
	AKAP12	1.364938	2.335599	8.161325	2.13E-15	1.16E-14	23.73737
	KDELR3	-1.95174	4.416794	-15.8275	4.77E-47	2.06E-45	96.04843
	GAPDH	-1.64191	9.20182	-14.6337	2.07E-41	6.34E-40	83.13271
	SLC2A1	-2.68509	4.343978	-14.4539	1.41E-40	4.14E-39	81.22623
	ERO1A	-1.70753	4.57842	-14.3191	5.88E-40	1.65E-38	79.80469
	EFNA3	-1.42926	1.725867	-13.9105	4.32E-38	1.11E-36	75.53213
	LDHA	-1.31613	6.845356	-13.8675	6.76E-38	1.71E-36	75.08568
	ENO1	-1.23051	8.709842	-13.5139	2.64E-36	6.01E-35	71.44356
	GPI	-1.09344	5.203407	-12.8278	2.80E-33	5.32E-32	64.51795
	TPI1	-1.11518	7.494514	-12.4761	9.25E-32	1.59E-30	61.04487
TPBG	-1.26717	2.59543	-12.2918	5.66E-31	9.23E-30	59.24654	
Down	ALDOA	-1.1798	7.603397	-12.2492	8.59E-31	1.39E-29	58.8327
	PFKP	-1.79156	4.649134	-12.0369	6.75E-30	1.02E-28	56.78489
	CP	-2.70249	4.572566	-11.0782	5.71E-26	6.62E-25	47.81185
	IGFBP3	-1.9269	5.520419	-10.3944	2.70E-23	2.63E-22	41.70712
	COL5A1	-1.69752	4.332137	-10.1567	2.16E-22	1.97E-21	39.64677
	AK4	-1.27398	1.778837	-9.38215	1.51E-19	1.12E-18	33.16702
	MIF	-1.1439	5.148043	-9.21473	5.93E-19	4.21E-18	31.81551
	IER3	-1.01397	5.593316	-6.41094	3.03E-10	1.09E-09	12.08398
	ANGPTL4	-1.20003	3.519174	-5.38942	1.04E-07	2.99E-07	6.406368
	INHA	-1.04385	1.053992	-4.75095	2.56E-06	6.48E-06	3.309558

NRROS	STOM	FAM78A	CLNS1A	PPARG	ETV4	NELFE	OVCH2	TIMM17A	TJP1	SLC4A1	WDR4	NMUR1	STARD8
TSPAN32	SYNE3	EMC8	VPS39	TOMM401	KAT2B	CNR1	FFAR4	PRICKLE2	KRT79	MFAP4	SYT15	MRPS26	IFFO1
CYBRD1	DPYS	TPK1	WDR74	FAM167B	PRELP	STYXL1	TIMP3	RIPOR1	GPI	ATP5MC2	SEC14L6	INAFM2	SPINT1
TACO1	PEAR1	MRPS10	NHSL2	ROMO1	CD34	DLG3	DPEP2	FOS	LRRC25	TSPAN17	RETREG1	DOK2	CORO1C
FAM162B	CD244	VIP	SOX13	WWP2	DTX2	GLDN	APH1A	GPRC5A	DIXDC1	PHKA1	EPAS1	LMO2	PSMD4
N4BP2L1	AHNAK	SNX25	PDZD2	STYK1	KLF6	RNF122	IGSF6	ADIPOQ	TLR4	MRPS34	RGS9	TNNC1	MME
EFNB1	SLC15A3	GALK1	SOX5	MYBL2	CDK7	SGPL1	ADRA1A	MAFF	APOLD1	ATP5MC1	RCN1	CCT3	CSF2RB
TSACC	STAC3	CASP3	TBRG4	ARHGEF6	MAD2L2	ADGRA2	NR4A3	FBXW4	PAFAH1B	MAP3K15	CACNA1C	PSMD7	C18orf63
COASY	RHOA	CNTN6	ADRB2	PKP3	RAPGEF2	LRRC36	ITGB2	SLC39A8	NIP7	CACNA1S	ATXN1L	TBXA2R	CHMP3
RPS6KA2	PLPPR4	C11orf96	SOX4	MED19	SYVN1	LIG3	LAMA2	UNC5C	CASP1	KRTCAP3	GNAI2	GIPC2	KCNA4
SMARCA5	METTL5	PAPSS1	PDCD6IP	ATP5MPL	P3H2	CHPF2	THOP1	IL18R1	KDF1	ABTB1	KIF22	ST6GALN	CPED1
POLR2H	DOCK8	TMEM88	ATP1B2	TUBB6	H2AFX	GOLGA5	KRT27	MRPL13	PKHD1L1	PEBP4	ANKRD29	ABHD11	TPSAB1
TBC1D9	POP5	ARHGEF3	ARHGAP1	GP9	LAT2	PDLIM2	CRTAM	GIMAP2	ITGAL	MSTO1	SESN1	RSPO4	PYCR1
HSPA5	CSTF2	TRIOBP	UBE2M	RAB5IF	FREM3	ITPRIP	ERH	FCGR3B	CD4	TNR	TMSB10	IARS	CTU2
FOXRED1	SIGLEC1	ALG8	PTGIS	MEOX2	EFTUD2	FRMD3	CMTM5	MAGI2	ECI1	CYP7A1	TPSB2	FLVCR2	SELP
MYZAP	TIMM10	PIK3IP1	ARHGEF2	ERIC4	MBOAT7	EMCN	LTC4S	TGFB2	NABP2	HLF	S1PR4	RMDN3	OCIAD2
CARS	ARF4	EGR3	SF3B6	FRMD4A	HDHD3	SIGMAR1	NATD1	KIAA1324	NPLOC4	RPN1	RNF187	PSMG3	DUOXA1
SLC27A3	UPK3B	PPP6C	STAP2	SRPK1	STX12	LBH	CASP5	MDK	CNP	TIMM13	ZDHHHC3	ARPC3	BOLA1
TEF	PDE4B	SULT1A1	TRIAP1	MLF2	EXOSC4	AKAP13	MLST8	HLA.E	AIFM1	FBXL5	PHF2	PFDN4	MRPL52
CTNNAL1	PRKD1	DCHS1	RCC1L	UBL3	JUNB	ABCA9	TMED9	CDK5	SECISBP2	CCDC102I	LSM5	GALNT15	CCT4
	TPBG	EGFL6	CD300LF	LIMS2	CXorf36	FIG4	RAVER2	ZNF25	PRKG1	TNFAIP1	ENOPH1	EFEMP2	RGS18

Supplementary Table 7. List of identified H&IRGs

CAV1
CAVIN1
NDST1
PPP1R15A
KDEL3
KLF6
GAPDH
ERO1A
GPC3
EFNA3
LDHA
ENO1
GPI
TPI1
TPBG
ALDOA
PFKP
PDGFB
FBP1
MAFF
IL6
ZFP36
DUSP1
DCN
ETS1
ATF3
SDC2
MIF
SELENBP1
FOS

Supplementary Table 8. Univariate Cox regression analysis in LUAD

id	HR	HR.95L	HR.95H	pvalue
ALDOA	1.391452	1.133078	1.708743	0.001621
ATF3	0.975586	0.859145	1.107807	0.703089
CAV1	1.092619	0.978841	1.219621	0.114385
DCN	0.887511	0.787653	1.00003	0.050057
DUSP1	0.978273	0.875857	1.092664	0.697034
EFNA3	1.159426	0.969638	1.386361	0.104823
ENO1	1.319533	1.034696	1.682781	0.025425
FBP1	0.784737	0.688243	0.894761	0.000293
FOS	0.924302	0.831852	1.027027	0.143198
GAPDH	1.505493	1.256657	1.803602	9.06E-06
GPC3	0.871319	0.780128	0.973169	0.0146
GPI	1.481849	1.196988	1.834501	0.000305
IL6	0.996136	0.886896	1.118832	0.947918
KDEL3	1.024022	0.869449	1.206076	0.776157
KLF6	0.995781	0.829349	1.195611	0.963857
LDHA	1.723769	1.396164	2.128245	4.12E-07
MAFF	1.269663	1.008218	1.598903	0.042403
MIF	1.24081	1.051325	1.464446	0.010712
NDST1	0.950424	0.760915	1.18713	0.654055
PDGFB	1.242008	1.040918	1.481946	0.016174
PFKP	1.273511	1.116267	1.452904	0.000323
SDC2	1.005794	0.867701	1.165865	0.938884
SELENBP1	0.838131	0.755863	0.929353	0.000808
TPI1	1.480293	1.17544	1.864211	0.000857
ZFP36	0.97745	0.860363	1.110473	0.726075

Supplementary Table 9. List of DEGs identified between high- and low-risk groups

Gene	logFC	AveExpr	t	P-value	adj. P-value	B
LDHA	0.922942	6.974682	18.60254	4.62E-59	9.01E-55	122.7628
GAPDH	0.850257	9.362282	12.93322	3.36E-33	3.28E-29	64.4427
LOXL2	1.147576	3.03805	12.65719	4.87E-32	3.17E-28	61.82197
SLC2A1	1.326628	4.622609	11.82959	1.24E-28	6.05E-25	54.14166
STC1	1.139023	2.590905	11.68366	4.80E-28	1.87E-24	52.81672
ERO1A	0.845268	4.75534	11.6276	8.05E-28	2.62E-24	52.31024
PLOD2	1.165533	3.586983	11.5908	1.13E-27	3.15E-24	51.97855
GPD1L	-0.79155	3.731824	-11.4299	4.93E-27	1.20E-23	50.53547
SPHK1	0.810664	1.98649	11.1233	7.92E-26	1.56E-22	47.81736
ACSS1	-0.80766	2.605283	-11.1226	7.97E-26	1.56E-22	47.81131
SELENBP1	-1.27271	5.303556	-11.085	1.12E-25	1.98E-22	47.48122
EGLN3	1.229307	2.678203	10.86653	7.83E-25	1.27E-21	45.57536
ESYT3	-0.71279	1.36614	-10.82	1.18E-24	1.78E-21	45.17216
TMPRSS2	-1.1848	3.844384	-10.7732	1.79E-24	2.49E-21	44.76862
CCNB1	0.930251	3.795787	10.72482	2.74E-24	3.56E-21	44.35167
SFTA3	-1.43596	4.42333	-10.6051	7.80E-24	9.52E-21	43.32592
PGK1	0.652392	6.752186	10.55302	1.23E-23	1.41E-20	42.8816
ADH1B	-1.33573	2.188533	-10.5424	1.35E-23	1.46E-20	42.7911
C1orf116	-1.36517	4.816248	-10.5075	1.83E-23	1.88E-20	42.49442
VIPR1	-0.67745	1.468733	-10.4245	3.75E-23	3.66E-20	41.79125
ATP13A4	-1.20976	2.234654	-10.338	7.89E-23	7.34E-20	41.06281
CTSH	-1.13974	5.976605	-10.2973	1.12E-22	9.93E-20	40.72104
IL6R	-0.71536	3.149635	-10.2865	1.23E-22	1.04E-19	40.63038
INMT	-1.09643	2.572217	-10.2439	1.77E-22	1.42E-19	40.2745
TNFAIP6	0.75449	1.949226	10.21549	2.25E-22	1.69E-19	40.0373
PLA2G4F	-0.80126	1.425447	-10.1108	5.48E-22	3.82E-19	39.16723
RRM2	0.943143	3.224588	10.07041	7.72E-22	5.20E-19	38.83313
ARNTL2	0.917475	2.138183	10.01161	1.27E-21	8.25E-19	38.34831
CYP4B1	-1.73301	3.485559	-10.0028	1.36E-21	8.60E-19	38.2758
ADGRF5	-1.21817	4.60606	-9.99648	1.44E-21	8.78E-19	38.22384
VEGFD	-0.89639	1.220933	-9.96983	1.80E-21	1.07E-18	38.00494
SUSD2	-1.59319	3.92636	-9.96202	1.92E-21	1.10E-18	37.94088
DLGAP5	0.827168	2.205371	9.922644	2.67E-21	1.45E-18	37.61835
TMEM158	0.749001	1.434108	9.916128	2.82E-21	1.49E-18	37.56505
TMEM125	-0.86587	5.204755	-9.85194	4.83E-21	2.36E-18	37.0413
BUB1B	0.71763	1.947708	9.817498	6.43E-21	3.06E-18	36.76122
FBP1	-0.84478	5.688654	-9.74477	1.17E-20	5.33E-18	36.17192
NCAPG	0.727578	1.813076	9.732288	1.30E-20	5.78E-18	36.07112
KPNA2	0.770084	4.928798	9.634083	2.92E-20	1.27E-17	35.28082
LYPD3	1.169224	2.205543	9.630469	3.01E-20	1.28E-17	35.25184
CCNB2	0.792082	2.77867	9.618999	3.31E-20	1.37E-17	35.15991
ANLN	0.925484	2.761223	9.6076	3.63E-20	1.48E-17	35.06863
TPX2	1.022113	3.635697	9.599532	3.88E-20	1.52E-17	35.00407
FAM189A	-0.74408	1.722085	-9.59939	3.89E-20	1.52E-17	35.00293
C16orf89	-1.87371	5.392011	-9.59379	4.07E-20	1.56E-17	34.95818
KIF4A	0.799928	2.175688	9.590408	4.18E-20	1.57E-17	34.9311
CLIC5	-0.91572	1.796515	-9.58517	4.37E-20	1.61E-17	34.88924
FAM83D	0.794692	2.555747	9.538517	6.39E-20	2.27E-17	34.51701
MTHFD2	0.687285	4.025153	9.464615	1.17E-19	4.06E-17	33.92994
SMOX	0.690834	2.331715	9.462347	1.19E-19	4.07E-17	33.91198
MAD2L1	0.671107	1.950988	9.4454	1.36E-19	4.51E-17	33.77782
CDC45	0.800078	2.521235	9.436644	1.46E-19	4.76E-17	33.70857
ARHGAP1	0.614092	1.766105	9.423383	1.63E-19	5.21E-17	33.60377
ABCC6	-0.62608	1.759492	-9.40708	1.86E-19	5.85E-17	33.4751

CCNA2	0.802635	2.770297	9.363304	2.64E-19	7.94E-17	33.13028
GREM1	0.979669	1.857621	9.350707	2.93E-19	8.66E-17	33.03127
CDC6	0.737764	2.173298	9.323219	3.65E-19	1.06E-16	32.81554
BTBD9	-0.59372	2.730217	-9.31325	3.95E-19	1.14E-16	32.73739
CACNA2D	-1.27731	2.531727	-9.30529	4.21E-19	1.19E-16	32.67511
CDKN3	0.790975	2.299901	9.278932	5.20E-19	1.45E-16	32.4689
STC2	0.786308	1.700869	9.276545	5.31E-19	1.46E-16	32.45025
SKA1	0.616556	1.427355	9.268715	5.65E-19	1.53E-16	32.38909
BIRC5	0.940798	3.164282	9.265311	5.80E-19	1.55E-16	32.36253
GGTLC1	-1.44076	2.546767	-9.2414	7.03E-19	1.85E-16	32.17606
SNX30	-0.70251	2.652872	-9.20753	9.20E-19	2.36E-16	31.91248
EXO1	0.630538	1.5465	9.187509	1.08E-18	2.74E-16	31.757
PLK1	0.725498	2.478948	9.18455	1.10E-18	2.77E-16	31.73404
ABCA3	-1.23785	4.351847	-9.17662	1.18E-18	2.91E-16	31.67256
HLF	-0.86615	1.634243	-9.15538	1.39E-18	3.29E-16	31.50801
CDC20	0.960707	3.777043	9.133987	1.65E-18	3.83E-16	31.34254
FOXM1	0.853833	2.701786	9.132467	1.67E-18	3.84E-16	31.33079
ECT2	0.694692	3.19277	9.105939	2.06E-18	4.62E-16	31.12602
CD302	-0.61132	2.104538	-9.10104	2.14E-18	4.75E-16	31.08824
CTHRC1	1.04334	4.887631	9.092379	2.29E-18	4.97E-16	31.02152
CGNL1	-0.624	2.23795	-9.0841	2.45E-18	5.25E-16	30.95774
KIF23	0.632306	1.806421	9.070544	2.72E-18	5.78E-16	30.85348
SLC16A3	0.760406	4.228423	9.04665	3.29E-18	6.83E-16	30.66992
PLPP4	0.656617	0.964836	9.033703	3.64E-18	7.40E-16	30.5706
PRR11	0.706783	2.182773	9.030582	3.73E-18	7.51E-16	30.54668
C1QTNF6	0.619862	2.285277	8.993279	5.00E-18	9.95E-16	30.26116
CEP55	0.790209	2.743194	8.991651	5.06E-18	9.98E-16	30.24872
HMMR	0.674488	2.053813	8.978992	5.59E-18	1.09E-15	30.15203
HSD17B6	-1.07461	2.672274	-8.97605	5.72E-18	1.10E-15	30.12956
HJURP	0.758142	2.103634	8.941298	7.50E-18	1.42E-15	29.86472
NUSAP1	0.711653	3.308997	8.933768	7.95E-18	1.49E-15	29.80743
PBK	0.802442	2.118148	8.91609	9.13E-18	1.68E-15	29.67305
CFAP221	-0.63388	1.210609	-8.90615	9.86E-18	1.80E-15	29.59759
ATP8A1	-0.71892	2.294049	-8.90165	1.02E-17	1.85E-15	29.56344
NCAPH	0.70456	2.180231	8.864978	1.36E-17	2.41E-15	29.28565
SPOCK1	0.842373	1.258565	8.822068	1.89E-17	3.27E-15	28.96164
MAMDC2	-0.73769	1.53598	-8.80252	2.20E-17	3.70E-15	28.81441
PFKP	0.832288	4.825851	8.784937	2.52E-17	4.10E-15	28.6822
ADAM12	0.74547	1.645666	8.778429	2.65E-17	4.25E-15	28.63331
BUB1	0.671308	2.128179	8.769409	2.84E-17	4.51E-15	28.5656
CDC45	0.685968	2.030416	8.765056	2.94E-17	4.63E-15	28.53294
CDK1	0.762874	3.004714	8.745778	3.41E-17	5.32E-15	28.38843
RASGRF1	-0.70564	1.06476	-8.73576	3.68E-17	5.70E-15	28.31346
ITGA5	0.68966	3.627662	8.726636	3.95E-17	6.04E-15	28.24517
VEPH1	-0.70435	1.375904	-8.71732	4.24E-17	6.33E-15	28.17552
KIF2C	0.787132	2.594228	8.717095	4.25E-17	6.33E-15	28.17386
LAMP3	-1.03726	4.220923	-8.70808	4.55E-17	6.73E-15	28.10655
COL11A1	1.238915	2.137247	8.697542	4.93E-17	7.18E-15	28.02788
VSIG2	-1.29228	3.243461	-8.69461	5.04E-17	7.23E-15	28.006
AK1	-0.62656	2.776513	-8.69438	5.05E-17	7.23E-15	28.00431
UCK2	0.680442	2.205755	8.678445	5.71E-17	7.96E-15	27.88554
UBE2C	1.105141	4.356292	8.673784	5.91E-17	8.19E-15	27.85084
KIF20A	0.650701	2.383569	8.66135	6.50E-17	8.92E-15	27.75832
LMO3	-1.04697	3.088905	-8.62541	8.55E-17	1.16E-14	27.49141
SHH	-0.59993	1.070961	-8.61775	9.06E-17	1.21E-14	27.43469
SERPINE1	1.011093	4.531727	8.591909	1.10E-16	1.44E-14	27.24343

NDC80	0.652398	1.90347	8.589377	1.12E-16	1.46E-14	27.22471
FOSL1	0.989546	2.212335	8.574632	1.26E-16	1.62E-14	27.1158
TMEM163	-0.83523	2.292071	-8.55216	1.49E-16	1.91E-14	26.95006
PXMP4	-0.66629	2.781622	-8.54622	1.56E-16	1.97E-14	26.90632
PRR15L	-0.94133	5.064927	-8.52045	1.89E-16	2.37E-14	26.71674
FNIP2	-0.61515	2.776098	-8.51898	1.91E-16	2.38E-14	26.70598
CPAMD8	-0.77612	1.611009	-8.51273	2.01E-16	2.47E-14	26.66009
KLF15	-0.7126	1.596427	-8.51222	2.01E-16	2.47E-14	26.65635
TUBB3	0.586762	1.367247	8.484237	2.49E-16	3.03E-14	26.45113
PLA2G1B	-1.13072	1.822874	-8.46396	2.89E-16	3.44E-14	26.30277
SCN7A	-0.62098	1.335542	-8.46105	2.96E-16	3.50E-14	26.28146
PRC1	0.641282	2.617065	8.456895	3.05E-16	3.59E-14	26.25112
CENPA	0.688752	1.84157	8.443589	3.37E-16	3.92E-14	26.15396
C7	-1.17536	3.341665	-8.43754	3.53E-16	4.07E-14	26.10981
MMP12	1.322584	3.217694	8.435849	3.57E-16	4.10E-14	26.09749
DUOX1	-0.84959	2.032929	-8.42217	3.96E-16	4.52E-14	25.99778
FSCN1	0.917044	4.506128	8.421068	3.99E-16	4.53E-14	25.98976
KIF11	0.636695	2.500135	8.417562	4.10E-16	4.58E-14	25.96423
DLC1	-0.75986	2.701866	-8.4144	4.19E-16	4.65E-14	25.94125
RACGAP1	0.60145	2.989398	8.407125	4.43E-16	4.86E-14	25.88828
DUOXA1	-0.7845	1.858684	-8.40303	4.57E-16	4.98E-14	25.85848
AURKA	0.728142	2.914967	8.400727	4.64E-16	4.98E-14	25.84175
CDKL2	-0.72128	1.667209	-8.39097	4.99E-16	5.30E-14	25.77082
ADAMTS1	0.610946	1.727419	8.38801	5.11E-16	5.39E-14	25.74934
MMP14	0.725271	5.958977	8.386029	5.18E-16	5.42E-14	25.73496
MELK	0.746045	2.316667	8.368005	5.93E-16	6.12E-14	25.6042
NEK2	0.721382	2.317009	8.35441	6.56E-16	6.74E-14	25.50571
HMGA1	0.762041	6.518265	8.336753	7.48E-16	7.56E-14	25.37798
NKX2-1	-1.14154	5.282582	-8.32613	8.09E-16	8.14E-14	25.30122
RHOV	1.154341	3.183901	8.317233	8.64E-16	8.65E-14	25.237
POSTN	0.924639	5.165232	8.30058	9.77E-16	9.68E-14	25.11693
SLC15A2	-0.69368	2.102868	-8.29866	9.91E-16	9.77E-14	25.10311
ADM	0.853708	2.771472	8.297381	1.00E-15	9.82E-14	25.09388
RAD51AP	0.606441	2.091234	8.285777	1.09E-15	1.06E-13	25.01034
SULF1	0.946416	3.770381	8.281114	1.13E-15	1.09E-13	24.9768
SCTR	-1.06107	2.099028	-8.26618	1.26E-15	1.21E-13	24.86947
PRDM16	-0.61391	1.147115	-8.25221	1.40E-15	1.32E-13	24.76917
LRRK2	-1.00695	2.344896	-8.24894	1.43E-15	1.35E-13	24.74572
DAPK1	-0.6258	3.282066	-8.22428	1.71E-15	1.59E-13	24.56911
COL4A3	-0.71096	1.557345	-8.21212	1.88E-15	1.73E-13	24.48216
TWIST1	0.609377	0.969815	8.197728	2.08E-15	1.89E-13	24.37936
GPC6	0.709752	1.663052	8.183539	2.31E-15	2.08E-13	24.27816
TOP2A	0.859033	3.927017	8.1697	2.56E-15	2.28E-13	24.17958
GFPT2	0.593251	1.957962	8.165734	2.63E-15	2.33E-13	24.15135
MKI67	0.729118	2.53614	8.165668	2.63E-15	2.33E-13	24.15088
EMP2	-0.61967	4.652927	-8.13042	3.41E-15	2.89E-13	23.90047
AQP4	-1.26256	2.934779	-8.12581	3.52E-15	2.98E-13	23.86778
CENPW	0.68942	3.06228	8.111572	3.91E-15	3.28E-13	23.7669
LOX	0.687659	2.802323	8.110872	3.93E-15	3.28E-13	23.76195
COL5A2	0.851208	4.46397	8.09689	4.35E-15	3.60E-13	23.66303
KIFC1	0.720787	2.844094	8.095897	4.38E-15	3.61E-13	23.65601
SCGB3A2	-2.09188	5.715086	-8.08804	4.64E-15	3.80E-13	23.60048
ITGA9	-0.61144	2.231255	-8.08382	4.78E-15	3.91E-13	23.57069
AGER	-1.32649	3.74982	-8.06499	5.48E-15	4.42E-13	23.43782
PCLAF	0.60221	2.316115	8.060886	5.65E-15	4.54E-13	23.4089
PEBP4	-1.30498	2.764375	-8.05315	5.97E-15	4.76E-13	23.35441

NAMPT	0.761417	4.47097	8.048744	6.16E-15	4.89E-13	23.3234
PTTG1	0.691999	3.436654	8.041486	6.50E-15	5.11E-13	23.27234
SEC14L6	-0.62536	1.265521	-7.99731	8.93E-15	6.95E-13	22.96232
GJB2	1.067127	3.1945	7.99495	9.09E-15	7.04E-13	22.94576
PLAUR	0.689874	4.119753	7.984052	9.83E-15	7.55E-13	22.8695
PMAIP1	0.787686	2.982881	7.976655	1.04E-14	7.93E-13	22.81778
MYBL2	0.998513	3.747806	7.964539	1.13E-14	8.56E-13	22.73315
NFIX	-0.70756	3.458955	-7.95528	1.21E-14	9.11E-13	22.66852
PIGR	-1.80658	5.832103	-7.93987	1.35E-14	1.01E-12	22.56114
UBE2S	0.634778	2.776711	7.912003	1.65E-14	1.21E-12	22.3673
CDC4A8	0.666683	2.925218	7.906636	1.71E-14	1.25E-12	22.33004
NAPSA	-1.62886	7.662918	-7.89724	1.83E-14	1.32E-12	22.26483
SFTPB	-1.88067	9.55676	-7.89138	1.91E-14	1.37E-12	22.22422
ANGPTL4	1.102754	3.627126	7.872084	2.19E-14	1.56E-12	22.09058
KIF18B	0.620566	1.729671	7.858262	2.41E-14	1.71E-12	21.99502
NUF2	0.652348	2.014769	7.855991	2.45E-14	1.73E-12	21.97933
LIFR	-0.61482	2.489257	-7.8519	2.53E-14	1.77E-12	21.95107
RNASE1	-0.99615	7.909878	-7.8493	2.57E-14	1.80E-12	21.93314
METTL7A	-0.64956	4.013381	-7.84185	2.71E-14	1.88E-12	21.88173
AURKB	0.728181	2.555211	7.834798	2.85E-14	1.97E-12	21.83309
ST3GAL5	-0.7582	3.67318	-7.80312	3.57E-14	2.38E-12	21.61509
CD1C	-0.75584	1.871032	-7.79296	3.83E-14	2.54E-12	21.5453
SLC7A5	0.852248	4.397569	7.786421	4.01E-14	2.62E-12	21.50042
DSG2	0.667551	4.821206	7.782555	4.12E-14	2.68E-12	21.47391
COL12A1	0.953547	2.910077	7.778662	4.24E-14	2.73E-12	21.44722
HOPX	-1.1353	4.642892	-7.76655	4.62E-14	2.96E-12	21.36428
CXCL8	1.041102	3.829151	7.764971	4.67E-14	2.98E-12	21.35344
ICAM5	-0.64962	1.546893	-7.7605	4.82E-14	3.06E-12	21.32285
TK1	0.751594	4.761218	7.75711	4.93E-14	3.13E-12	21.29965
PIFO	-0.71791	1.885539	-7.74675	5.31E-14	3.34E-12	21.2288
CAVIN2	-0.77841	3.330876	-7.72914	6.01E-14	3.75E-12	21.10861
KRT6A	1.532579	1.978503	7.72537	6.17E-14	3.82E-12	21.08291
ZWINT	0.635051	3.625237	7.705069	7.11E-14	4.35E-12	20.94464
CHRDL1	-0.82549	2.071768	-7.68507	8.18E-14	4.96E-12	20.80869
SFTPC	-2.31342	5.152663	-7.67513	8.76E-14	5.26E-12	20.74124
ALDH2	-0.59298	4.401797	-7.67433	8.81E-14	5.28E-12	20.73579
TNNC1	-0.79867	2.275905	-7.65067	1.04E-13	6.15E-12	20.57557
SPAG5	0.618391	2.549771	7.646241	1.07E-13	6.32E-12	20.54559
MDFI	0.744761	3.063786	7.641	1.11E-13	6.50E-12	20.51015
B3GNT8	-0.7982	3.07348	-7.63521	1.16E-13	6.72E-12	20.47103
STEAP1	0.893483	3.431295	7.621668	1.27E-13	7.25E-12	20.37961
ZNF385B	-0.80056	1.350001	-7.61942	1.29E-13	7.33E-12	20.36448
TDRD10	-0.66344	1.292001	-7.60969	1.38E-13	7.77E-12	20.29885
MCM4	0.595462	3.636753	7.606416	1.41E-13	7.93E-12	20.27681
SFTPD	-1.53842	5.824874	-7.59938	1.48E-13	8.28E-12	20.22943
CYP24A1	1.356082	2.933751	7.581459	1.68E-13	9.29E-12	20.10893
CYB5A	-0.66048	3.925475	-7.57601	1.74E-13	9.60E-12	20.07231
GJB3	0.975003	1.771724	7.575871	1.75E-13	9.60E-12	20.07141
SCGB3A1	-1.97816	5.395648	-7.56077	1.94E-13	1.05E-11	19.97007
CLEC3B	-0.77058	2.671113	-7.55348	2.04E-13	1.10E-11	19.92124
CCNE1	0.623479	1.878211	7.549907	2.09E-13	1.13E-11	19.89732
FAM83A	1.073681	3.717893	7.547533	2.12E-13	1.14E-11	19.88143
IFT57	-0.67785	4.319374	-7.54397	2.18E-13	1.16E-11	19.8576
TRIP13	0.679341	2.527445	7.532396	2.36E-13	1.25E-11	19.78019
GPR160	-0.64285	3.194564	-7.52479	2.48E-13	1.30E-11	19.72935
INHBA	0.688777	2.577999	7.521407	2.54E-13	1.32E-11	19.70679

COL4A4	-0.59065	1.832125	-7.52082	2.55E-13	1.32E-11	19.70285
CLDN18	-1.38177	2.415768	-7.48548	3.25E-13	1.66E-11	19.4674
DRAM1	-0.714	4.794067	-7.46952	3.62E-13	1.83E-11	19.36136
ZDHHC11	-0.64659	1.24892	-7.4657	3.72E-13	1.87E-11	19.33604
UNC13B	-0.62002	4.072646	-7.45358	4.04E-13	2.02E-11	19.25566
WIF1	-1.23548	2.023215	-7.43056	4.73E-13	2.30E-11	19.10323
FMO5	-0.85349	2.921446	-7.39813	5.89E-13	2.80E-11	18.8892
NPC2	-0.74297	7.404507	-7.38555	6.42E-13	3.02E-11	18.80639
MS4A15	-1.15203	1.785124	-7.35841	7.71E-13	3.57E-11	18.62809
STRIP2	0.591851	1.266443	7.354163	7.94E-13	3.65E-11	18.60025
RAP1GAP	-0.87086	3.611509	-7.35278	8.01E-13	3.67E-11	18.59115
AHNAK2	0.796761	2.284732	7.348237	8.26E-13	3.78E-11	18.56141
THBS2	0.867956	4.551828	7.319843	1.00E-12	4.47E-11	18.37564
SLC6A8	0.692218	2.7927	7.311384	1.06E-12	4.71E-11	18.32041
SLC47A1	-0.60796	1.501516	-7.30446	1.11E-12	4.91E-11	18.27522
IGFBP3	0.85908	5.725137	7.28408	1.27E-12	5.58E-11	18.14249
CXCL17	-1.17986	7.040542	-7.27338	1.37E-12	5.94E-11	18.07294
CD109	0.666765	1.933074	7.25746	1.52E-12	6.54E-11	17.96954
CEBPA	-0.70763	2.955524	-7.22407	1.90E-12	7.99E-11	17.75335
TMEM130	-0.76526	1.619612	-7.21168	2.06E-12	8.54E-11	17.6733
C5orf38	-0.80946	1.878268	-7.1706	2.71E-12	1.10E-10	17.40879
SLC34A2	-1.20911	7.903006	-7.16334	2.84E-12	1.15E-10	17.36215
PARM1	-0.84212	4.790917	-7.14873	3.13E-12	1.25E-10	17.26846
LAMC2	0.936206	4.784413	7.146845	3.17E-12	1.27E-10	17.25636
COL3A1	0.886755	7.756234	7.143921	3.23E-12	1.29E-10	17.23762
PLAU	0.954808	5.209179	7.131167	3.52E-12	1.39E-10	17.15599
DOK4	-0.64135	3.509914	-7.12752	3.60E-12	1.41E-10	17.13267
SCNN1B	-0.91703	3.5034	-7.11839	3.82E-12	1.49E-10	17.07436
VCAN	0.761943	3.710208	7.114453	3.92E-12	1.52E-10	17.04919
FHL2	0.675369	3.118772	7.106712	4.13E-12	1.59E-10	16.9998
MYBPHL	-0.72449	1.166634	-7.09032	4.60E-12	1.75E-10	16.89534
SLC16A1	0.699228	2.049733	7.08814	4.67E-12	1.77E-10	16.88147
SLC26A9	-1.01897	2.48465	-7.08436	4.78E-12	1.81E-10	16.85742
FOLR1	-1.25077	5.529289	-7.08105	4.89E-12	1.85E-10	16.83637
TROAP	0.607677	1.929396	7.062505	5.52E-12	2.04E-10	16.71856
PCDH7	0.60808	1.408585	7.000768	8.26E-12	2.88E-10	16.3282
UBE2T	0.626483	3.961279	6.978157	9.56E-12	3.30E-10	16.18592
KRT16	0.933001	1.503077	6.97509	9.75E-12	3.35E-10	16.16666
SLCO4C1	-0.65893	1.693994	-6.96871	1.02E-11	3.48E-10	16.1266
SLC22A31	-1.14934	4.605144	-6.9572	1.10E-11	3.70E-10	16.05439
C4BPA	-1.34294	5.21102	-6.94569	1.18E-11	3.94E-10	15.98227
ADGRF4	0.616102	1.125398	6.940465	1.22E-11	4.05E-10	15.94961
DUSP5	0.623946	3.945123	6.935793	1.26E-11	4.17E-10	15.92039
SLC22A3	-0.83726	2.88427	-6.93216	1.29E-11	4.24E-10	15.89767
MT2A	0.784735	6.09618	6.906456	1.52E-11	4.90E-10	15.73729
DNALI1	-0.65046	2.61443	-6.9028	1.56E-11	5.00E-10	15.71449
IRX2	-1.00727	2.576296	-6.90214	1.56E-11	5.01E-10	15.71043
EIF4EBP1	0.666432	4.997646	6.893969	1.65E-11	5.24E-10	15.65954
HILPDA	0.664954	3.398209	6.888469	1.70E-11	5.37E-10	15.62534
HLA-DMA	-0.64607	5.804636	-6.8773	1.83E-11	5.71E-10	15.55594
COL1A2	0.788892	6.935085	6.860901	2.03E-11	6.27E-10	15.45422
RHOBTB2	-0.6751	3.846003	-6.84296	2.28E-11	6.95E-10	15.34315
PGC	-2.10189	4.505488	-6.83904	2.34E-11	7.10E-10	15.31894
MBIP	-0.60863	4.426332	-6.83027	2.47E-11	7.48E-10	15.26476
CERS4	-0.6283	3.296529	-6.80588	2.89E-11	8.56E-10	15.11442
MLPH	-0.70516	4.431552	-6.80221	2.96E-11	8.72E-10	15.09183

SHE	-0.64367	1.826389	-6.79514	3.09E-11	9.07E-10	15.04831
MXRA5	0.725696	3.424311	6.781725	3.37E-11	9.77E-10	14.96593
GGT6	-0.80026	1.843327	-6.78081	3.39E-11	9.81E-10	14.96032
GPC3	-0.81847	2.941852	-6.77668	3.48E-11	1.00E-09	14.93497
HOXD1	-0.65918	1.204294	-6.771	3.60E-11	1.03E-09	14.90014
FOXA2	-0.90017	3.001813	-6.76773	3.68E-11	1.05E-09	14.8801
COL1A1	0.915062	7.644074	6.751395	4.08E-11	1.16E-09	14.78013
ACSL5	-0.72263	5.115936	-6.73008	4.67E-11	1.31E-09	14.64999
SLC40A1	-0.65409	5.188408	-6.70918	5.32E-11	1.48E-09	14.52267
FCER1A	-0.80671	1.89648	-6.7087	5.34E-11	1.48E-09	14.51975
ACKR1	-0.72784	2.328775	-6.70513	5.46E-11	1.51E-09	14.49803
IRX5	-0.68198	2.418061	-6.70084	5.61E-11	1.55E-09	14.47196
PTPN13	-0.73877	2.634418	-6.69549	5.80E-11	1.59E-09	14.43944
ZNF750	-0.68368	1.921752	-6.68041	6.38E-11	1.73E-09	14.34798
MMP1	1.241549	4.016607	6.668824	6.86E-11	1.85E-09	14.27781
C15orf48	0.980271	4.599305	6.656468	7.41E-11	1.96E-09	14.20308
MYEOV	0.908057	1.629274	6.647462	7.84E-11	2.07E-09	14.14869
CDA	1.032771	3.050658	6.640971	8.16E-11	2.15E-09	14.10952
PRG4	-0.6197	1.008973	-6.63514	8.46E-11	2.22E-09	14.07434
C9orf152	-0.72392	2.778167	-6.63388	8.53E-11	2.23E-09	14.0668
MGP	-0.70376	5.951468	-6.63233	8.61E-11	2.25E-09	14.05743
SFRP2	1.049648	5.213651	6.630034	8.73E-11	2.28E-09	14.0436
CLIC6	-1.03521	4.546789	-6.61491	9.60E-11	2.48E-09	13.95261
TNS4	0.955574	1.956546	6.603435	1.03E-10	2.64E-09	13.88366
CYP27A1	-0.61438	4.226054	-6.59529	1.08E-10	2.77E-09	13.83478
COL7A1	0.61863	1.35844	6.593707	1.09E-10	2.79E-09	13.82531
ALOX15B	-0.99491	3.558383	-6.59055	1.12E-10	2.83E-09	13.80638
AK4	0.587213	1.902197	6.573501	1.24E-10	3.09E-09	13.70432
SUSD4	-0.60386	1.845605	-6.56465	1.31E-10	3.24E-09	13.6514
SELENOP	-0.62766	3.849257	-6.51514	1.78E-10	4.21E-09	13.3566
BMP3	-0.78586	1.964947	-6.4859	2.13E-10	4.94E-09	13.18339
KCNK5	-0.6929	3.807591	-6.47826	2.23E-10	5.13E-09	13.13826
A2M	-0.6379	7.081351	-6.46038	2.48E-10	5.62E-09	13.03276
TMEM45	0.645304	2.199651	6.439732	2.82E-10	6.30E-09	12.91124
COL5A1	0.693882	4.515635	6.438212	2.84E-10	6.35E-09	12.9023
GGH	0.657177	2.859242	6.419056	3.19E-10	7.06E-09	12.78988
TCEA3	-0.63242	4.014463	-6.41829	3.21E-10	7.09E-09	12.7854
LGALS1	0.609149	7.389476	6.399099	3.61E-10	7.87E-09	12.67306
NDNF	-0.85371	3.727096	-6.3648	4.43E-10	9.57E-09	12.473
MMP11	0.934943	3.251725	6.360464	4.55E-10	9.78E-09	12.44778
PTGDS	-0.78956	4.300786	-6.3599	4.57E-10	9.80E-09	12.4445
MFSD2A	-0.62002	3.24231	-6.35786	4.62E-10	9.89E-09	12.43265
CPXM1	0.585259	2.508784	6.357191	4.64E-10	9.92E-09	12.42874
TLR2	-0.59172	3.320283	-6.33422	5.33E-10	1.12E-08	12.2954
PTHLH	0.590348	1.125977	6.32043	5.79E-10	1.20E-08	12.21556
AQP3	-1.00742	6.628751	-6.31894	5.84E-10	1.21E-08	12.20691
PI3	0.993948	2.017437	6.29677	6.67E-10	1.36E-08	12.0789
COL15A1	0.616175	3.023044	6.290192	6.94E-10	1.41E-08	12.04099
KYNU	0.595069	1.194366	6.28408	7.19E-10	1.46E-08	12.00578
HLA-DPB1	-0.67201	6.911599	-6.27995	7.37E-10	1.49E-08	11.98202
ABO	-0.63053	2.452745	-6.27952	7.39E-10	1.49E-08	11.97953
DES	-0.68199	1.91941	-6.27427	7.63E-10	1.53E-08	11.94935
TPPP3	-0.80715	3.365675	-6.27409	7.64E-10	1.53E-08	11.94834
FHL1	-0.5875	2.334896	-6.26608	8.01E-10	1.59E-08	11.90231
CYP4X1	-0.68408	2.227706	-6.26063	8.27E-10	1.63E-08	11.87103
PALM3	-0.67097	1.963056	-6.23477	9.65E-10	1.88E-08	11.7229

GZMB	0.683415	2.642897	6.229794	9.93E-10	1.92E-08	11.69443
CPE	0.850001	4.910169	6.221881	1.04E-09	1.99E-08	11.64923
DDIT4	0.647912	5.553565	6.217913	1.07E-09	2.03E-08	11.62659
APOD	-0.98617	3.655639	-6.18467	1.30E-09	2.44E-08	11.43739
SFTA2	-1.05102	6.980478	-6.17941	1.34E-09	2.51E-08	11.40751
SFTPA1	-1.74891	7.890994	-6.17822	1.35E-09	2.53E-08	11.40078
ATOH8	-0.70591	2.035062	-6.16507	1.46E-09	2.71E-08	11.3262
EPHX1	-0.69264	6.719632	-6.1631	1.47E-09	2.73E-08	11.31508
FKBP10	0.679537	4.631596	6.146625	1.62E-09	2.97E-08	11.22189
SPINK5	-0.81071	1.776021	-6.13154	1.77E-09	3.21E-08	11.13675
RSPO3	0.623383	1.106954	6.123232	1.86E-09	3.36E-08	11.08996
ITGA11	0.588816	1.965686	6.119725	1.90E-09	3.42E-08	11.07022
GPC4	-0.60574	4.374668	-6.11967	1.90E-09	3.42E-08	11.0699
ROS1	-0.79157	2.82116	-6.11848	1.91E-09	3.44E-08	11.06318
IGF2BP2	0.617326	2.357728	6.111262	1.99E-09	3.58E-08	11.02262
PLA2G12I	-0.68429	1.265944	-6.0955	2.19E-09	3.90E-08	10.93409
PITX1	0.68823	1.858782	6.088839	2.27E-09	4.03E-08	10.89677
CCL20	0.998004	3.52549	6.045357	2.92E-09	5.02E-08	10.65388
CHIA	-0.69052	1.127761	-6.02773	3.24E-09	5.50E-08	10.55586
PFN2	0.702446	4.390118	6.020248	3.38E-09	5.70E-08	10.5143
FGFR3	-0.75096	2.510927	-6.0149	3.48E-09	5.85E-08	10.48464
HHIPL2	0.709068	1.14948	5.987447	4.08E-09	6.75E-08	10.33272
MFAP4	-0.75938	4.823565	-5.98559	4.12E-09	6.81E-08	10.32246
CRYM	-0.81061	2.153629	-5.97866	4.29E-09	7.06E-08	10.28421
IL20RB	0.703891	1.326008	5.974628	4.39E-09	7.21E-08	10.26199
BTG2	-0.58717	5.498168	-5.96303	4.69E-09	7.67E-08	10.19811
HLA-DPA	-0.66793	6.154963	-5.96001	4.77E-09	7.80E-08	10.18149
SFTPA2	-1.66521	8.171622	-5.9459	5.17E-09	8.38E-08	10.10394
DKK1	0.913831	1.680335	5.916611	6.11E-09	9.71E-08	9.943509
LPCAT1	-0.66928	6.482401	-5.89406	6.94E-09	1.09E-07	9.820453
FCGBP	-0.73016	2.172071	-5.88859	7.16E-09	1.12E-07	9.790679
S100A9	1.035851	7.56635	5.867602	8.06E-09	1.25E-07	9.67658
MAOA	-0.66003	4.194613	-5.84816	9.00E-09	1.37E-07	9.571247
CD207	-0.83908	1.832868	-5.84621	9.10E-09	1.39E-07	9.560692
IER3	0.590088	5.700201	5.84065	9.38E-09	1.42E-07	9.530608
BCAM	-0.59879	5.676284	-5.84034	9.40E-09	1.42E-07	9.52896
HTRA3	0.633878	4.015319	5.782809	1.30E-08	1.88E-07	9.21932
TGFBI	0.650708	4.749924	5.778982	1.33E-08	1.91E-07	9.198815
CAPN8	-0.78216	3.667178	-5.77285	1.37E-08	1.97E-07	9.166014
GAL	0.606611	0.863638	5.753933	1.52E-08	2.17E-07	9.064925
COL9A2	-0.64844	2.544048	-5.74715	1.58E-08	2.25E-07	9.02874
NR0B2	-0.75437	1.429779	-5.7253	1.78E-08	2.50E-07	8.912472
SCGB1A1	-1.68871	4.599986	-5.71224	1.92E-08	2.66E-07	8.84317
PLA2G10	-0.69082	1.805746	-5.7098	1.94E-08	2.69E-07	8.830246
HLA-DOA	-0.61136	3.780978	-5.70805	1.96E-08	2.71E-07	8.821003
LRRC31	-0.5867	1.147135	-5.70077	2.04E-08	2.80E-07	8.782459
CA9	0.96863	2.303403	5.68059	2.28E-08	3.11E-07	8.675815
ELN	-0.67045	3.614379	-5.67048	2.41E-08	3.27E-07	8.622529
APOH	-0.76961	1.65993	-5.61802	3.21E-08	4.23E-07	8.347319
DSP	0.719052	4.758125	5.607468	3.40E-08	4.45E-07	8.292234
SPP1	0.988257	6.907102	5.603241	3.48E-08	4.54E-07	8.270196
MMP9	0.746384	4.520265	5.600679	3.53E-08	4.59E-07	8.256846
PHYHD1	-0.59694	2.434522	-5.59047	3.73E-08	4.82E-07	8.20368
INHA	0.81062	1.164755	5.582104	3.91E-08	5.01E-07	8.160205
KIF12	-0.61494	1.955026	-5.56751	4.23E-08	5.38E-07	8.084466
CAPS	-0.59766	3.076306	-5.56554	4.27E-08	5.42E-07	8.074253

ANKRD65	-0.63392	3.328894	-5.53013	5.17E-08	6.42E-07	7.891307
IRX3	-0.62881	3.795443	-5.50025	6.07E-08	7.39E-07	7.73772
AGR3	-1.0033	4.76487	-5.47945	6.78E-08	8.11E-07	7.631241
SERPINB5	0.745407	1.219127	5.460173	7.51E-08	8.89E-07	7.532874
CPB2	-0.65305	1.149337	-5.45972	7.53E-08	8.90E-07	7.530575
LRRC15	0.628952	1.958141	5.447579	8.03E-08	9.44E-07	7.468776
SRPX2	0.609524	3.246509	5.44301	8.23E-08	9.63E-07	7.445559
KIAA1324	-0.80184	2.764178	-5.42964	8.83E-08	1.02E-06	7.377685
AQP1	-0.85343	5.939965	-5.40668	9.97E-08	1.14E-06	7.261543
BNIP1	-0.58976	1.936918	-5.38406	1.12E-07	1.27E-06	7.147522
SLC7A11	0.617627	1.836614	5.356353	1.30E-07	1.44E-06	7.00841
FNDC1	0.596186	2.202283	5.344322	1.38E-07	1.52E-06	6.948209
CIT	-0.65521	2.864518	-5.31945	1.57E-07	1.71E-06	6.824132
KRT17	1.004206	3.76689	5.281339	1.92E-07	2.04E-06	6.63504
SLC44A4	-0.66388	4.981685	-5.25432	2.21E-07	2.31E-06	6.501712
CHIT1	-0.77525	2.47215	-5.22398	2.58E-07	2.66E-06	6.352701
HLA-DQB	-0.65187	5.600328	-5.22168	2.61E-07	2.69E-06	6.341439
GDF15	-0.73801	4.697503	-5.21229	2.74E-07	2.81E-06	6.29553
CRTAC1	-0.68858	2.370421	-5.19571	2.98E-07	3.03E-06	6.214606
LPL	-0.68981	2.92338	-5.19169	3.04E-07	3.08E-06	6.195015
HABP2	-0.7476	2.123986	-5.16389	3.50E-07	3.52E-06	6.059897
CPA3	-0.65289	3.234999	-5.12229	4.32E-07	4.25E-06	5.858987
ABCC2	0.667381	0.884855	5.112967	4.53E-07	4.44E-06	5.814157
S100A8	0.78328	3.87029	5.106163	4.69E-07	4.58E-06	5.781485
GKN2	-0.77494	1.457565	-5.09917	4.85E-07	4.72E-06	5.747968
C2CD4A	0.589438	1.887702	5.090254	5.07E-07	4.92E-06	5.705247
CLU	-0.70565	5.17618	-5.07489	5.48E-07	5.24E-06	5.631847
HAS3	-0.63935	2.511107	-5.06917	5.64E-07	5.39E-06	5.604526
HLA-DRB	-0.70706	7.287705	-5.03679	6.63E-07	6.21E-06	5.450626
MFSD4A	-0.67501	2.64285	-5.03054	6.84E-07	6.38E-06	5.421016
DMBT1	-0.95551	2.994242	-5.02762	6.94E-07	6.46E-06	5.407187
HLA-DRB	-0.58876	8.93724	-4.99851	8.01E-07	7.32E-06	5.269808
B3GNT7	-0.63423	4.073286	-4.97173	9.14E-07	8.25E-06	5.144047
SAA1	0.867016	3.083627	4.939104	1.07E-06	9.51E-06	4.991644
KLK6	0.684835	0.992476	4.87909	1.44E-06	1.23E-05	4.713705
STEAP4	-0.61642	3.715663	-4.87033	1.50E-06	1.28E-05	4.673406
NRGN	-0.65087	3.746222	-4.83059	1.81E-06	1.51E-05	4.491352
SLC1A7	-0.72316	1.48294	-4.78511	2.25E-06	1.83E-05	4.284653
CPS1	1.040116	1.574015	4.779615	2.31E-06	1.88E-05	4.25982
HLA-DQB	-0.70263	4.389584	-4.77844	2.33E-06	1.88E-05	4.254517
CD1A	-0.602	1.659486	-4.7671	2.46E-06	1.97E-05	4.203297
KRT81	0.725071	1.209519	4.756016	2.59E-06	2.07E-05	4.153389
MUC1	-0.59496	7.335829	-4.74407	2.74E-06	2.18E-05	4.099678
TMPRSS1	0.710647	1.73552	4.71865	3.09E-06	2.41E-05	3.985861
GPR87	0.705873	1.875853	4.708743	3.23E-06	2.52E-05	3.941643
FOXJ1	-0.64728	3.416103	-4.68386	3.63E-06	2.79E-05	3.830958
NTS	0.815121	0.913102	4.679396	3.71E-06	2.85E-05	3.811164
DPP4	-0.69943	4.046902	-4.67048	3.87E-06	2.94E-05	3.77166
DUSP4	0.637654	3.14587	4.665372	3.96E-06	3.00E-05	3.749073
MUCL3	-0.58533	0.973781	-4.6595	4.07E-06	3.07E-05	3.723138
MAGEA3	0.76585	1.037185	4.649332	4.27E-06	3.20E-05	3.67827
AC007906	-0.62219	1.838392	-4.58226	5.82E-06	4.21E-05	3.384616
ALPL	-0.75336	4.259763	-4.57545	6.00E-06	4.33E-05	3.355003
FABP3	-0.59495	3.423731	-4.57288	6.07E-06	4.37E-05	3.343848
CXCL5	0.664112	1.960822	4.547189	6.83E-06	4.85E-05	3.232629
PPP1R1B	-0.74889	2.910064	-4.53337	7.28E-06	5.11E-05	3.173044

LRRN4	-0.62908	2.267732	-4.51889	7.77E-06	5.41E-05	3.110772
GJB1	-0.71778	2.389376	-4.51538	7.89E-06	5.48E-05	3.095727
GSTA2	-0.58598	1.146541	-4.49802	8.54E-06	5.88E-05	3.021356
ALDH1A1	-0.62959	4.516309	-4.49394	8.70E-06	5.98E-05	3.003898
TNNT1	0.731735	2.390884	4.48307	9.14E-06	6.23E-05	2.957535
MAGEA6	0.683037	0.908561	4.459869	1.01E-05	6.81E-05	2.858879
MUC3A	-0.6022	1.78719	-4.37421	1.48E-05	9.54E-05	2.498733
QPCT	0.651933	3.292415	4.362127	1.57E-05	9.99E-05	2.448456
MMP28	-0.62431	2.481916	-4.32412	1.85E-05	0.000116	2.291136
WFDC2	-0.62276	7.511644	-4.31339	1.94E-05	0.000121	2.246957
FGFBP1	0.632795	2.048329	4.312273	1.95E-05	0.000122	2.242359
ADGRF1	-0.61038	2.117827	-4.29114	2.14E-05	0.000132	2.15567
MUC21	-0.82774	3.127787	-4.27863	2.25E-05	0.000139	2.104521
CEACAM6	-0.79423	8.301433	-4.27597	2.28E-05	0.00014	2.09368
PCP4L1	-0.71145	2.97201	-4.25545	2.49E-05	0.000151	2.010136
CLDN2	-0.79183	2.025824	-4.23621	2.71E-05	0.000162	1.932131
S100A2	0.656408	3.355875	4.191444	3.28E-05	0.000192	1.751981
CLDN10	0.615357	1.816579	4.100067	4.82E-05	0.000268	1.38975
CXCL10	0.58768	4.234281	4.072932	5.40E-05	0.000296	1.28362
TNC	0.610036	4.293037	4.050957	5.91E-05	0.000321	1.198155
SNCG	0.61397	3.368975	3.959171	8.61E-05	0.000447	0.845858
C20orf85	-0.65195	1.828936	-3.87089	0.000123	0.000607	0.514158
PRAME	0.624869	1.616681	3.857058	0.00013	0.000636	0.462835
AQP5	-0.86706	3.235528	-3.85314	0.000132	0.000645	0.448345
UCHL1	0.717958	3.391937	3.798424	0.000164	0.000775	0.24716
TFF1	0.930404	2.250193	3.645478	0.000295	0.001298	-0.30074
CTSE	-0.80043	5.044177	-3.58259	0.000374	0.001593	-0.51984
TCN1	0.694402	1.811844	3.536152	0.000444	0.001848	-0.67929
IL37	-0.61635	1.666167	-3.47457	0.000556	0.002241	-0.88772
GFRA3	-0.59908	2.194553	-3.45545	0.000596	0.002381	-0.95169
SLPI	-0.62972	8.026117	-3.39791	0.000733	0.002853	-1.14229
BARX1	0.604154	1.608971	3.357815	0.000846	0.003228	-1.27326
GSTA1	-0.6386	2.915065	-3.35615	0.000851	0.003245	-1.27867
FGA	0.86359	2.823366	3.28934	0.001075	0.003963	-1.49353
FGB	0.876382	2.19619	3.264155	0.001173	0.004272	-1.57345
CXCL14	-0.66683	4.209872	-3.04373	0.00246	0.008073	-2.24777
PAEP	0.752756	2.582415	2.984453	0.00298	0.009538	-2.42136
AKR1B10	0.702227	2.168768	2.913586	0.003733	0.011547	-2.62457
SPINK1	-0.7387	4.294496	-2.76845	0.005842	0.016866	-3.02602
S100P	0.677093	5.347798	2.614378	0.009209	0.024865	-3.43041
BPIFA1	0.785628	4.112323	2.476388	0.013602	0.03443	-3.77346

Supplementary Table 11. KEGG analysis results for risk score-related DEGs

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
hsa04974	Protein digestion and absorption	17/252	103/8104	1.46E-08	3.63E-06	2.98E-06	COL11A1/COL4A3/COL5A2/COL12A1/COL4A4/COL3A1/COL1A2/COL1A1/COL7A1/KCNK5/COL5A1/COL15A1/COL9A2/ELN/CPB2/CPA3/DPP4
hsa04512	ECM-receptor interaction	13/252	88/8104	2.80E-06	0.000275392	0.000225855	HMMR/ITGA5/COL4A3/ITGA9/COL4A4/THBS2/LAMC2/COL1A2/COL1A1/ITGA11/COL9A2/SPP1/TNC
hsa05310	Asthma	8/252	31/8104	3.32E-06	0.000275392	0.000225855	HLA-DMA/FCER1A/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04940	Type I diabetes mellitus	9/252	43/8104	5.27E-06	0.000327844	0.000268873	HLA-DMA/HLA-DPB1/GZMB/CPE/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa05330	Allograft rejection	8/252	38/8104	1.70E-05	0.000848082	0.000695532	HLA-DMA/HLA-DPB1/GZMB/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa05323	Rheumatoid arthritis	12/252	93/8104	2.80E-05	0.001006154	0.00082517	CXCL8/HLA-DMA/MMP1/TLR2/HLA-DPB1/CCL20/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1/CXCL5
hsa04110	Cell cycle	14/252	124/8104	2.83E-05	0.001006154	0.00082517	CCNB1/BUB1B/CCNB2/MAD2L1/CCNA2/CDC6/PLK1/CDC20/BUB1/CDC45/CDK1/PTTG1/MCM4/CCNE1
hsa05332	Graft-versus-host disease	8/252	42/8104	3.69E-05	0.001148657	0.00094204	HLA-DMA/HLA-DPB1/GZMB/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04672	Intestinal immune network for IgA production	8/252	49/8104	0.000116819	0.003231991	0.002650629	PIGR/HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa05320	Autoimmune thyroid disease	8/252	53/8104	0.000206218	0.005134837	0.004211196	HLA-DMA/HLA-DPB1/GZMB/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04640	Hematopoietic cell lineage	11/252	99/8104	0.000236804	0.005360392	0.004396179	IL6R/ITGA5/CD1C/HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1/CD1A
hsa04145	Phagosome	14/252	152/8104	0.00026041	0.005403501	0.004431534	ITGA5/TUBB3/SFTPD/THBS2/HLA-DMA/TLR2/HLA-DPB1/SFTPA1/HLA-DPA1/SFTPA2/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04610	Complement and coagulation cascades	10/252	85/8104	0.000284235	0.005444199	0.00446491	SERPINE1/C7/PLAUR/PLAU/C4BPA/A2M/CPB2/CLU/FGA/FGB
hsa04115	p53 signaling pathway	9/252	73/8104	0.000401955	0.007149061	0.005863106	CCNB1/RRM2/CCNB2/CDK1/SERPINE1/PMAIP1/CCNE1/IGFBP3/SERPIN5
hsa05321	Inflammatory bowel disease	8/252	65/8104	0.000851735	0.014138794	0.011595545	HLA-DMA/TLR2/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa00010	Glycolysis / Gluconeogenesis	8/252	67/8104	0.001043397	0.016237866	0.013317041	LDHA/GAPDH/ACSS1/PGK1/ADH1B/FBP1/PFKP/ALDH2
hsa05146	Amoebiasis	10/252	102/8104	0.001219207	0.017745371	0.01455338	COL4A3/CD1C/CXCL8/COL4A4/LAMC2/COL3A1/COL1A2/COL1A1/TLR2/CD1A
hsa05166	Human T-cell leukemia virus 1 infection	16/252	219/8104	0.001282798	0.017745371	0.01455338	SLC2A1/BUB1B/CCNB2/MAD2L1/CCNA2/CDC20/FOSL1/PTTG1/CCNE1/HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04514	Cell adhesion molecules	12/252	149/8104	0.002286845	0.029187459	0.023937295	ITGA9/CLDN18/VCAN/HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1/CLDN2/CLDN10
hsa05416	Viral myocarditis	7/252	60/8104	0.002446983	0.029187459	0.023937295	HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04657	IL-17 signaling pathway	9/252	94/8104	0.002501728	0.029187459	0.023937295	FOSL1/CXCL8/MMP1/CCL20/S100A9/MMP9/S100A8/CXCL5/CXCL10
hsa05140	Leishmaniasis	8/252	77/8104	0.002578812	0.029187459	0.023937295	HLA-DMA/TLR2/HLA-DPB1/HLA-DPA1/HLA-DOA/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa05150	Staphylococcus aureus infection	9/252	96/8104	0.002890062	0.031288058	0.025660043	KRT16/HLA-DMA/HLA-DPB1/HLA-DPA1/HLA-DOA/KRT17/HLA-DQB1/HLA-DRB5/HLA-DRB1
hsa04933	AGE-RAGE signaling pathway in diabetic complications	9/252	100/8104	0.003808975	0.039162093	0.032117718	VEGFD/SERPINE1/COL4A3/AGER/CXCL8/COL4A4/COL3A1/COL1A2/COL1A1
hsa04510	Focal adhesion	14/252	201/8104	0.003931937	0.039162093	0.032117718	VEGFD/RASGRF1/ITGA5/COL4A3/ITGA9/COL4A4/THBS2/LAMC2/COL1A2/COL1A1/ITGA11/COL9A2/SPP1/TNC