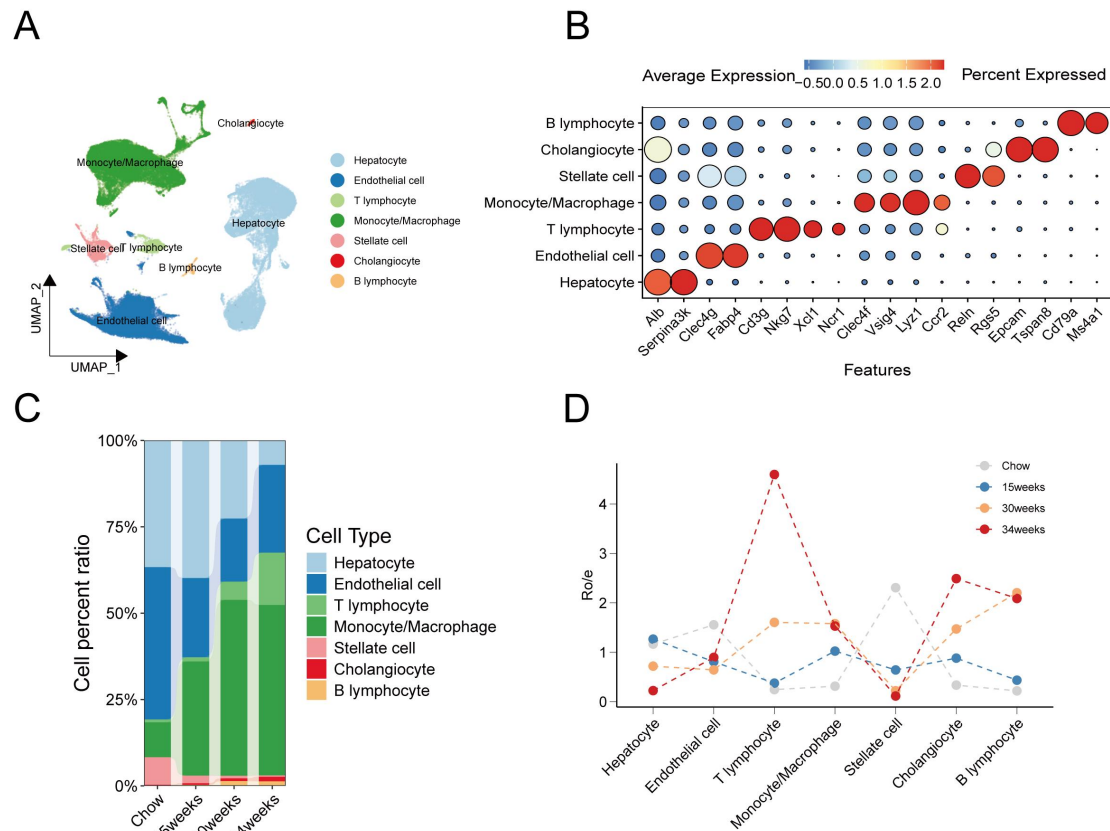
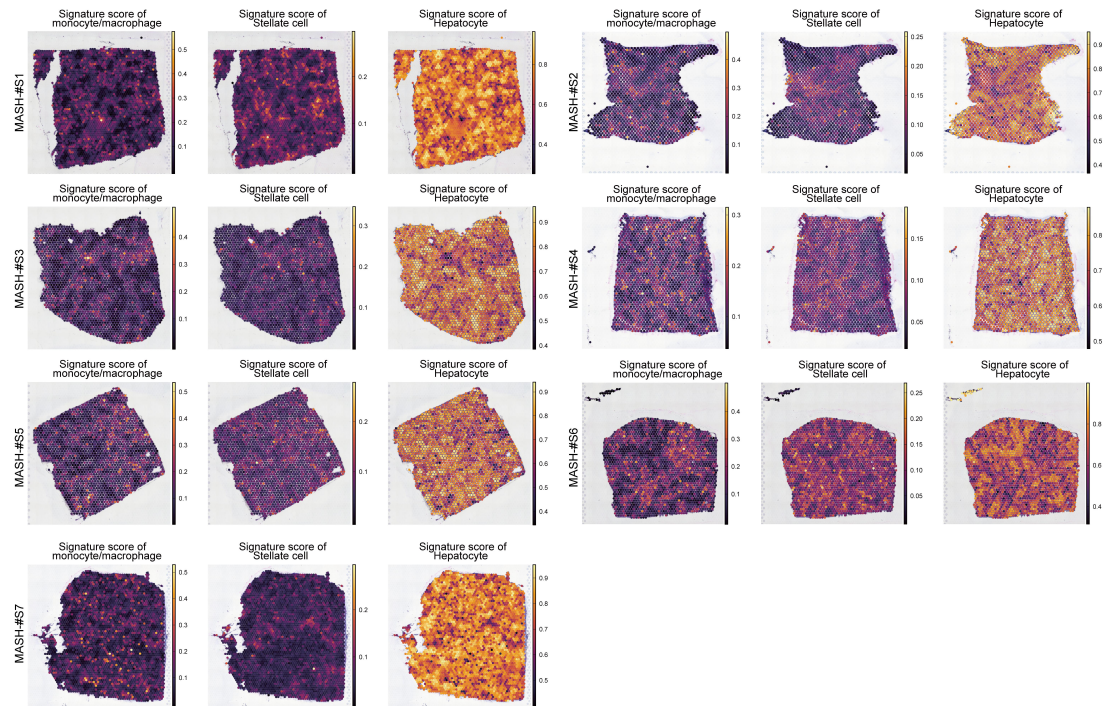


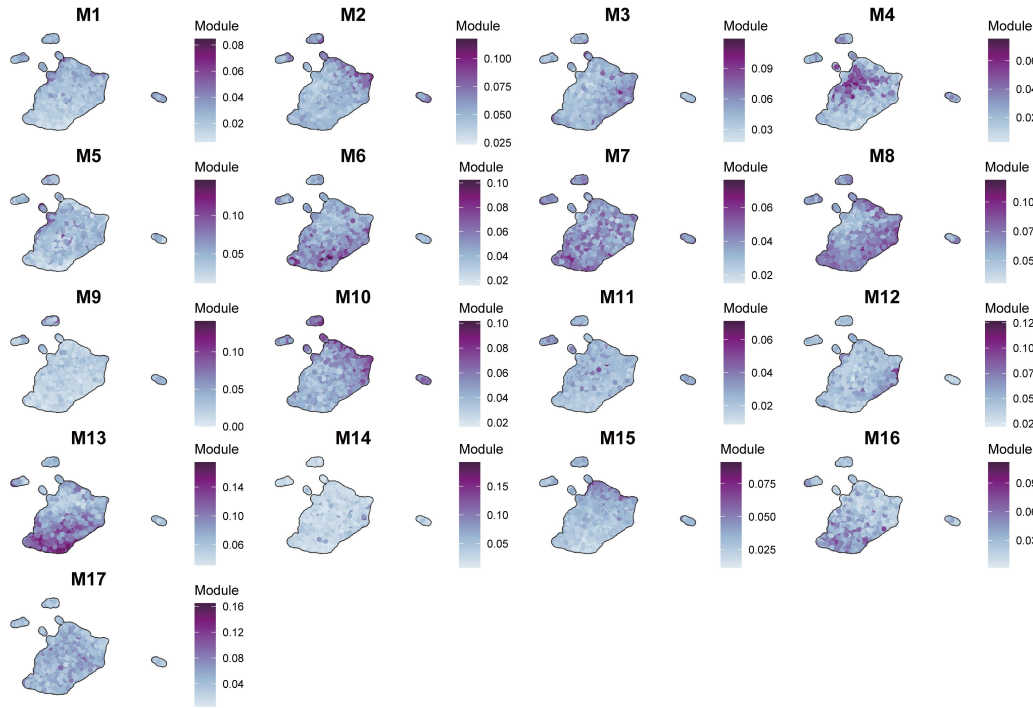


Supplementary Figure 1 | Validation of cell types and dynamics in murine MASLD progression. (A) UMAP plot color-coded by the seven major cell types identified in the validation dataset. (B) Dot plot displaying mean expression and percentage of expressing cells for canonical marker genes across cell types in the validation cohort. (C) Stacked bar chart of major cell-type proportions at indicated time points (control, 15 w, 30 w, 34 w) in HFHFD-fed mice. (D) Relative abundance (Ro/e) of each major cell type across control, 15-w, 30-w, and 34-w groups.

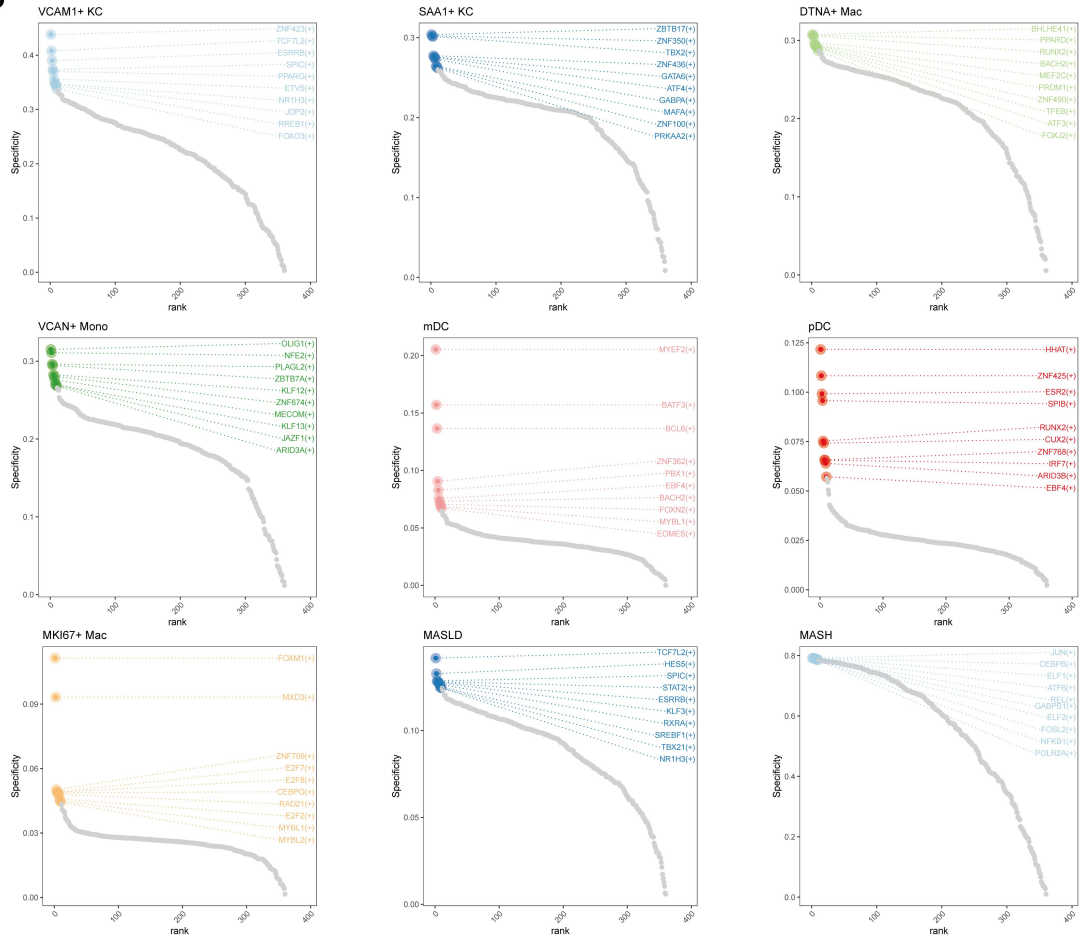


Supplementary Figure 2 | Spatial co-localization of monocytes/macrophages and hepatic stellate cells in MASH. Spatial transcriptomic images from seven MASH samples illustrate the spatial distribution of monocytes/macrophages and hepatic stellate cells, highlighting their extensive co-localization.

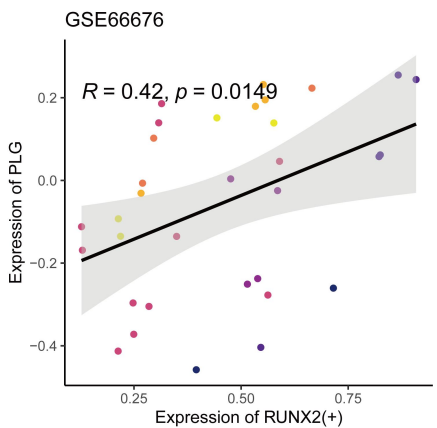
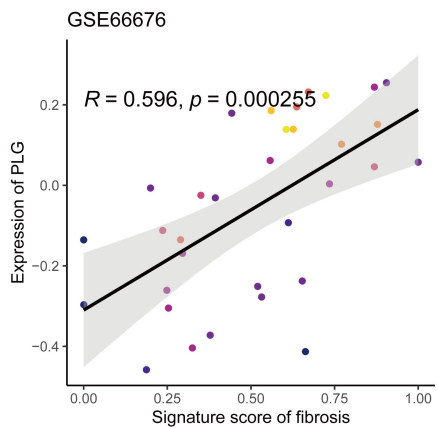
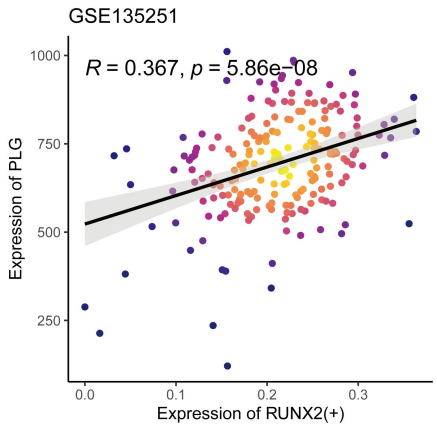
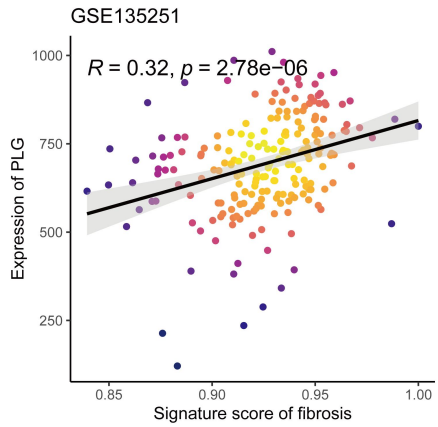
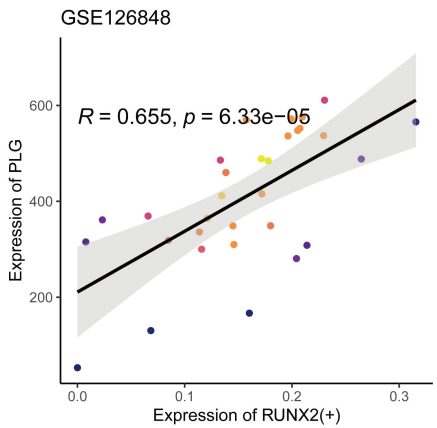
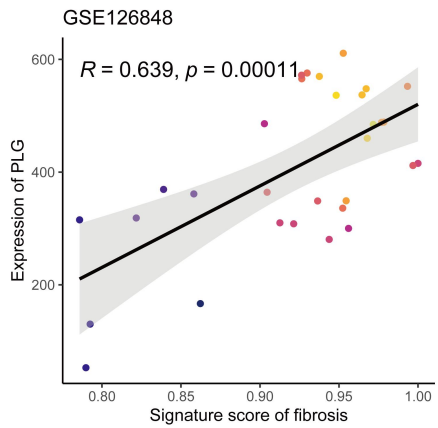
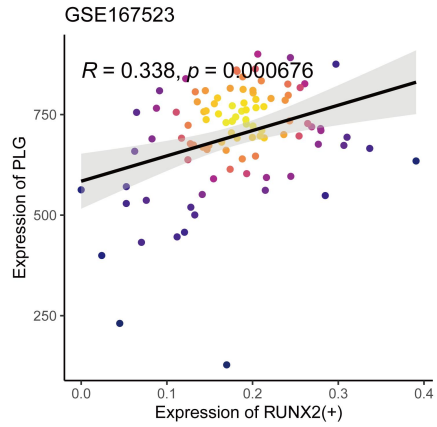
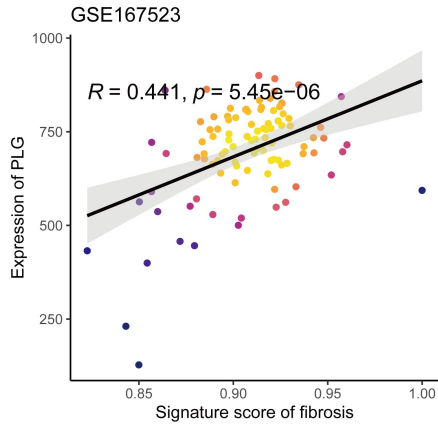
A



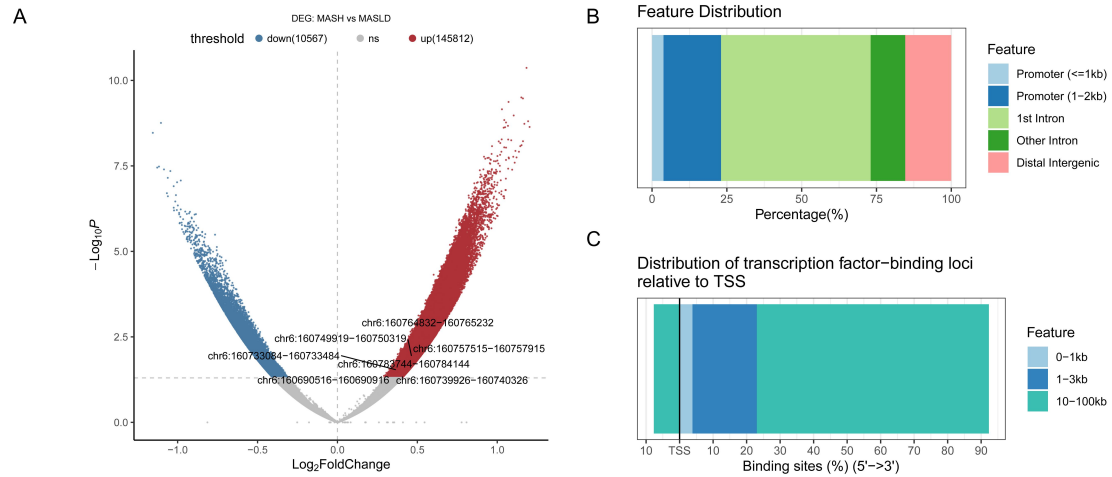
B



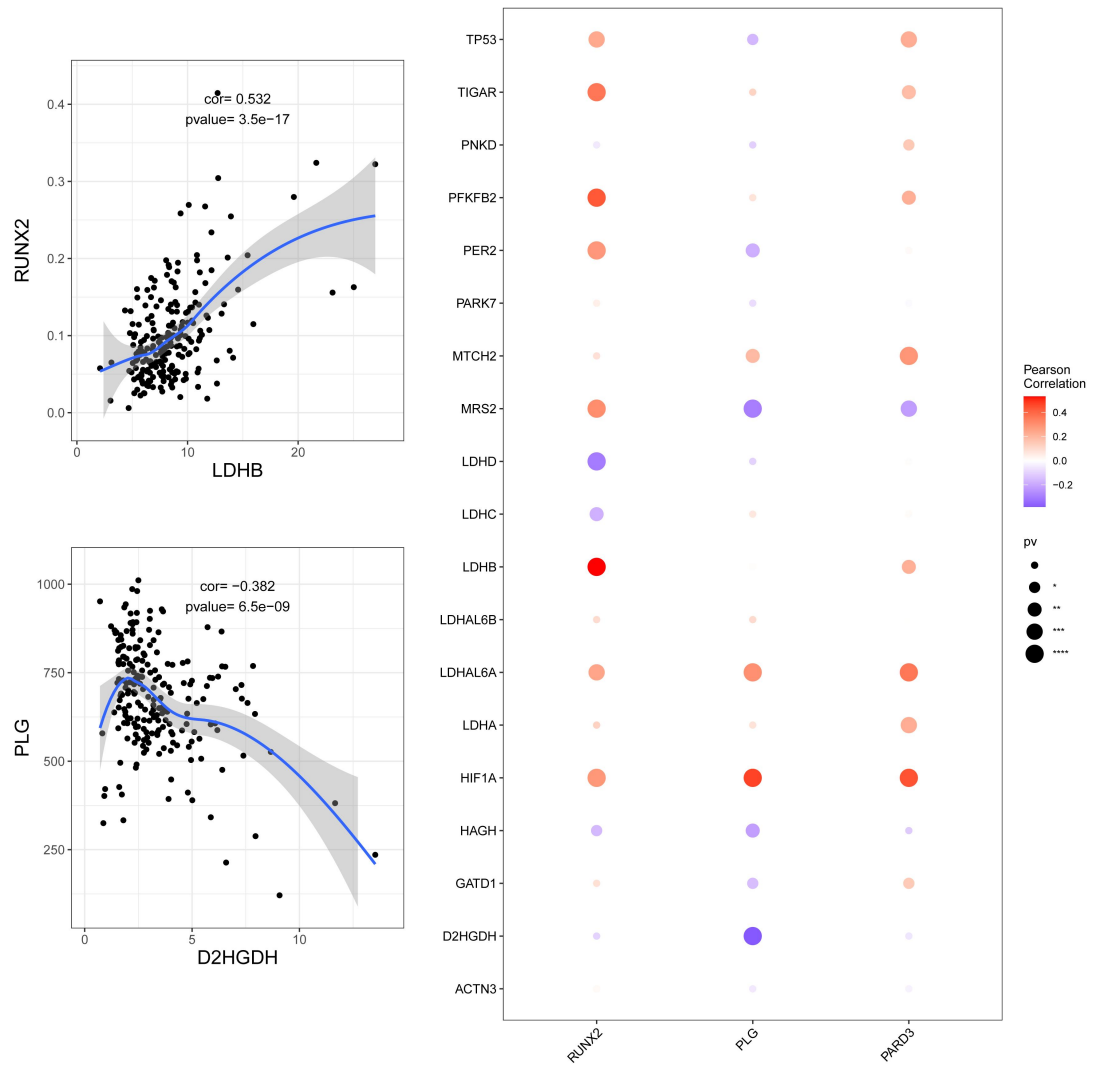
Supplementary Figure 3 | Supplementary transcription-factor analyses of DTNA⁺ macrophages. (A) Density plots depicting activity of each CSI module within monocytes/macrophages. **(B)** Top 10 transcription factors (TFs) ranked by regulon specificity score (RSS) across indicated cell types.



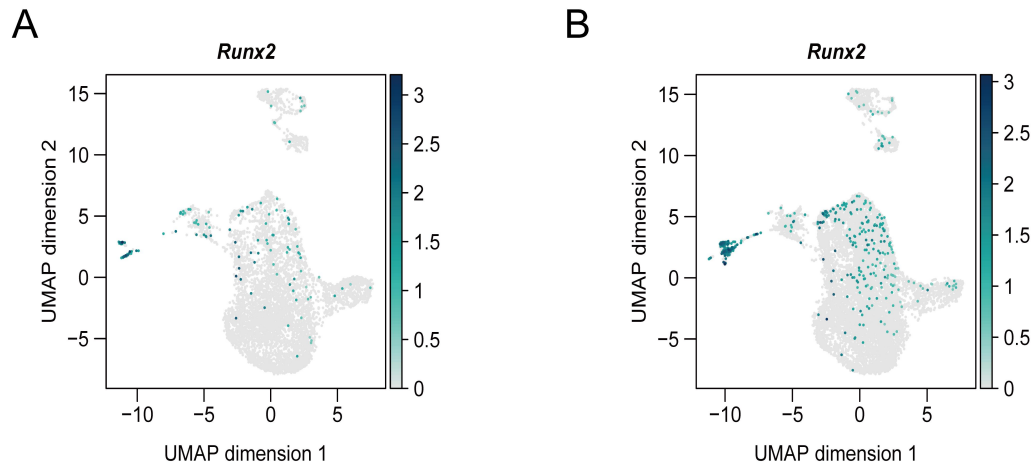
Supplementary Figure 4 | RUNX2 and PLG expression are positively correlated across four independent bulk RNA-seq datasets. Scatter plots demonstrate that PLG expression is significantly positively correlated with hepatic fibrosis, and RUNX2 expression is significantly positively correlated with PLG expression in all four datasets.



Supplementary Figure 5 | ATAC-seq analysis reveals chromatin accessibility differences between MASH and MASLD and validates the RUNX2-PLG regulatory axis. (A) Volcano plot of differential accessibility regions (DARs) between MASH and MASLD. Seven PLG-associated peaks (highlighted with red arrows) are significantly upregulated, indicating enriched chromatin accessibility in MASH. **(B)** Stacked bar plot of RUNX2 transcription factor binding site (TFBS) annotation at the PLG locus, showing the proportion of TFBS located in proximal promoters (≤ 1 kb, light blue), distal promoters (1–2 kb, dark blue), first introns (light green), other introns (dark green), and distal intergenic regions (pink). **(C)** Stacked bar plot of RUNX2 binding site distribution relative to the PLG transcription start site (TSS). The plot shows the proportion of TFBS located within 0–1 kb (light blue), 1–3 kb (dark blue), and 10–100 kb (green) of the TSS.

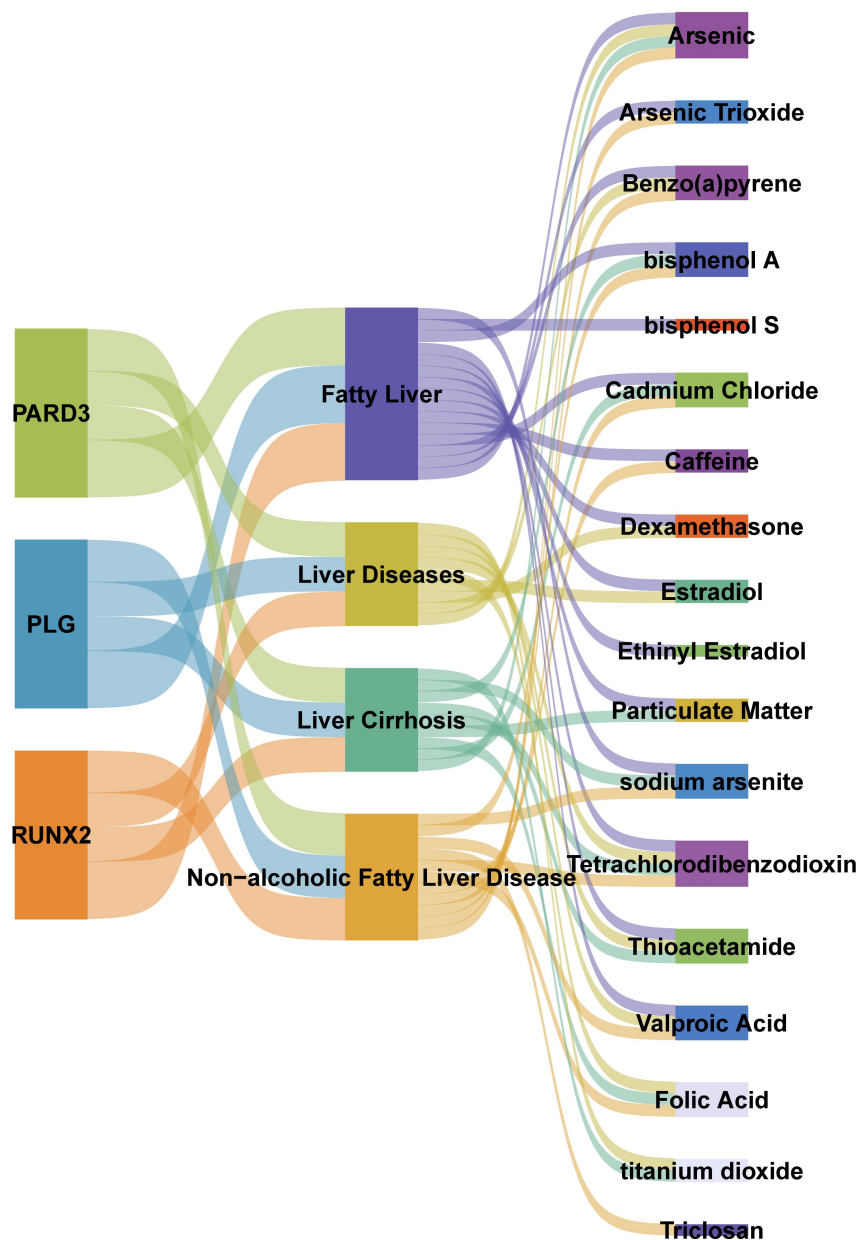


Supplementary Figure 6 | Correlation analysis of the RUNX2-PLG-PARD3 axis with lactate-metabolism-related genes. Lactate-metabolism-related genes were obtained from the Molecular Signatures Database (MsigDB). Pearson correlation analysis was performed to assess the association between these genes and the RUNX2-PLG-PARD3 axis.

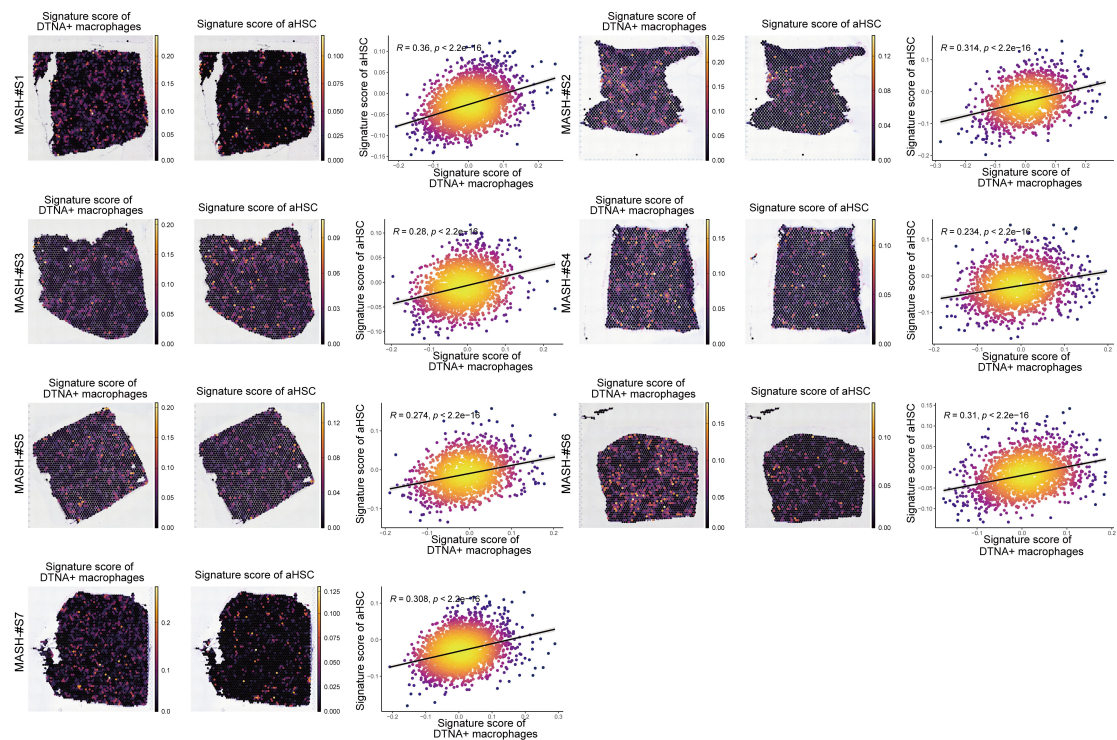


Supplementary Figure 7 | *Runx2* expression during murine MASLD progression.

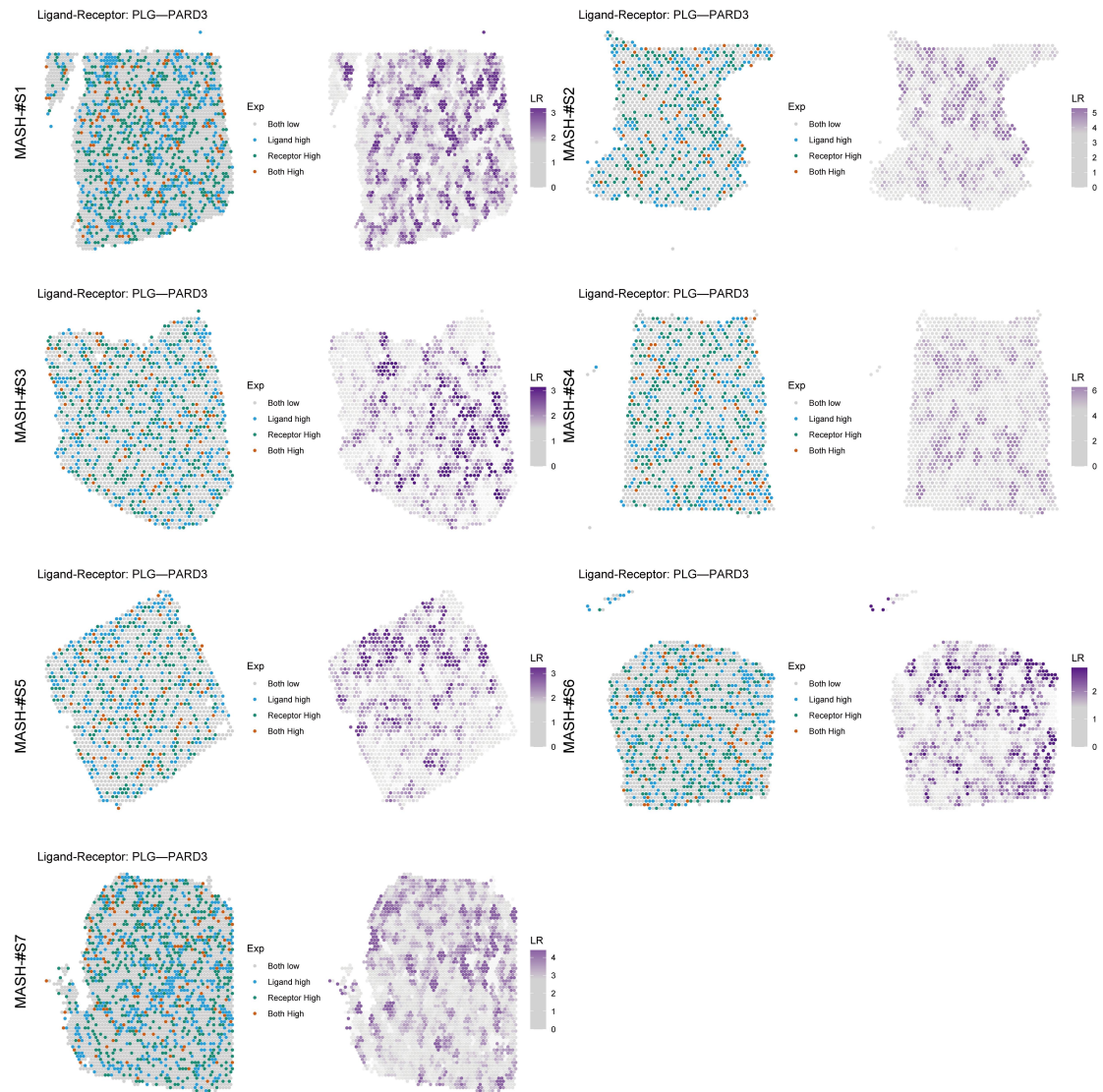
(A) UMAP projection of myeloid cells from HFHFD-fed 15-w samples, colored by *Runx2* expression level. **(B)** UMAP projection of myeloid cells from HFHFD-fed 30-w samples, colored by *Runx2* expression level.



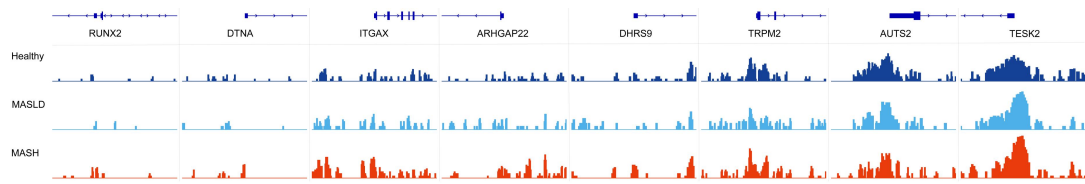
Supplementary Figure 8 | Drug prediction for the RUNX2-PLG-PARD3 axis based on the Comparative Toxicogenomics Database (CTD). The morula plot displays 18 candidate drugs that simultaneously target these three molecules. All listed drugs have been reported for the treatment of fatty liver, liver diseases, cirrhosis, and non-alcoholic fatty liver disease (NAFLD)-related disorders.



Supplementary Figure 9 | Extended spatial correlation of DTNA⁺ macrophages and aHSCs. Spatial transcriptomic images from additional MASH samples show extensive co-localization of DTNA⁺ macrophages and aHSCs; accompanying scatter plots confirm a significant positive correlation ($p < 0.001$).



Supplementary Figure 10 | Co-expression of the PLG–PARD3 axis in situ. Spatial transcriptomic images from MASH specimens illustrate the expression patterns of PLG and PARD3, underscoring their pronounced spatial co-expression.



Supplementary Figure 11 | ATAC-seq signal tracks of promoter regions (± 2 kb) for eight model genes, showing normalized signal intensity in Healthy (blue), MASLD (cyan), and MASH (red) groups.

Supplementary Table 1

DataSet	Sample	Group	Species	tissue
GSE189600	GSM6808755	disease state: healthy	Homo sapiens	liver
GSE189600	GSM6808756	disease state: healthy	Homo sapiens	liver
GSE189600	GSM6808757	disease state: healthy	Homo sapiens	liver
GSE189600	GSM6808758	disease state: NASH	Homo sapiens	liver
GSE189600	GSM6808759	disease state: NASH	Homo sapiens	liver
GSE189600	GSM6808760	disease state: NASH	Homo sapiens	liver
GSE202379	GSM6112209	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112210	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112211	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112212	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112213	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112216	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112217	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112218	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112219	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112220	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112221	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112222	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112223	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112224	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112225	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver

DataSet	Sample	Group	Species	tissue
GSE202379	GSM6112226	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112229	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112230	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112231	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112232	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112233	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112234	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112235	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112236	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112237	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112239	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112241	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112243	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112244	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112251	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112252	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112253	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112255	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112256	disease status: NAFLD	Homo sapiens	tissue: liver
GSE202379	GSM6112257	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112259	disease status: NASH w/o cirrhosis	Homo sapiens	tissue: liver
GSE202379	GSM6112260	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112261	disease status: NASH	Homo	tissue: liver

DataSet	Sample	Group	Species	tissue
		w/o cirrhosis	sapiens	
GSE202379	GSM6112263	disease status: Healthy control	Homo sapiens	tissue: liver
GSE202379	GSM6112266	disease status: NAFLD	Homo sapiens	tissue: liver
GSE189175	GSM5695736	condition: NAFLD	Homo sapiens	tissue: Adjacent non-tumor
GSE189175	GSM5695738	condition: NASH	Homo sapiens	tissue: Adjacent non-tumor
GSE189175	GSM5695740	condition: NASH	Homo sapiens	tissue: Adjacent non-tumor
GSE212837	GSM6556449	disease state: Control	Homo sapiens	tissue: Liver
GSE212837	GSM6556450	disease state: Control	Homo sapiens	tissue: Liver
GSE212837	GSM6556451	disease state: Control	Homo sapiens	tissue: Liver
GSE212837	GSM6556452	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556453	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556454	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556455	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556456	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556457	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556458	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556459	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556460	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556461	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556462	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556463	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556464	disease state: NASH	Homo sapiens	tissue: Liver
GSE212837	GSM6556465	disease state: NASH	Homo sapiens	tissue: Liver

DataSet	Sample	Group	Species	tissue
GSE212837	GSM6556466	disease state: NASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785686	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785687	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785688	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785689	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785690	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785691	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785692	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785693	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785694	disease group: MASL	Homo sapiens	tissue: Liver
GSE289173	GSM8785695	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785696	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785697	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785698	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785699	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785700	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785701	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785702	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785703	disease group: eMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785704	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785705	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785706	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785707	disease group: aMASH	Homo	tissue: Liver

DataSet	Sample	Group	Species	tissue
			sapiens	
GSE289173	GSM8785708	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785709	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785710	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785711	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785712	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785713	disease group: aMASH	Homo sapiens	tissue: Liver
GSE289173	GSM8785714	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785715	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785716	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785717	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785718	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785719	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785720	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785722	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785724	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785726	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785729	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785731	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785733	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785735	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785738	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785740	disease group: ctrl	Homo sapiens	tissue: Liver

DataSet	Sample	Group	Species	tissue
GSE289173	GSM8785742	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785745	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785747	disease group: ctrl	Homo sapiens	tissue: Liver
GSE289173	GSM8785749	disease group: ctrl	Homo sapiens	tissue: Liver

Supplementary Table 2

Series	Platforms	Group	Type
GSE126848	GPL18573	MASLD/MASH	bulk RNA-seq
GSE135251	GPL18573	MASLD/MASH	bulk RNA-seq
GSE162694	GPL21290	MASH	bulk RNA-seq
GSE164760	GPL13667	MASH	bulk RNA-seq
GSE167523	GPL21290	MASLD/MASH	bulk RNA-seq
GSE24807	GPL2895	MASH	Affymetrix microarray
GSE48452	GPL11532	MASLD/MASH	Affymetrix microarray
GSE66676	GPL6244	MASLD/MASH	Affymetrix microarray
GSE89632	GPL14951	MASLD/MASH	Affymetrix microarray

Series	Sample	Group	Type
GSE248077	GSM7905578	MASH	Spatial transcriptome
GSE248077	GSM7905579	MASH	Spatial transcriptome
GSE248077	GSM7905580	MASH	Spatial transcriptome
GSE248077	GSM7905581	MASH	Spatial transcriptome
GSE248077	GSM7905582	MASH	Spatial transcriptome
GSE248077	GSM7905583	MASH	Spatial transcriptome
GSE248077	GSM7905584	MASH	Spatial transcriptome

BioProject	BioSample	group	Type
PRJNA725028	SAMN18868094	MASH	ATAC-seq
PRJNA725028	SAMN18868058	MASLD	ATAC-seq
PRJNA725028	SAMN18868093	MASH	ATAC-seq
PRJNA725028	SAMN18868092	MASH	ATAC-seq
PRJNA725028	SAMN18868091	MASH	ATAC-seq
PRJNA725028	SAMN18868090	MASH	ATAC-seq
PRJNA725028	SAMN18868089	MASH	ATAC-seq
PRJNA725028	SAMN18868088	MASH	ATAC-seq
PRJNA725028	SAMN18868087	MASH	ATAC-seq
PRJNA725028	SAMN18868086	MASH	ATAC-seq
PRJNA725028	SAMN18868085	MASH	ATAC-seq
PRJNA725028	SAMN18868084	MASH	ATAC-seq
PRJNA725028	SAMN18868057	Healthy	ATAC-seq
PRJNA725028	SAMN18868083	MASH	ATAC-seq
PRJNA725028	SAMN18868082	MASH	ATAC-seq
PRJNA725028	SAMN18868081	MASH	ATAC-seq
PRJNA725028	SAMN18868080	MASH	ATAC-seq
PRJNA725028	SAMN18868079	MASH	ATAC-seq
PRJNA725028	SAMN18868078	MASH	ATAC-seq
PRJNA725028	SAMN18868077	MASH	ATAC-seq

PRJNA725028	SAMN18868076	MASLD	ATAC-seq
PRJNA725028	SAMN18868075	MASLD	ATAC-seq
PRJNA725028	SAMN18868074	MASLD	ATAC-seq
PRJNA725028	SAMN18868056	Healthy	ATAC-seq
PRJNA725028	SAMN18868073	MASLD	ATAC-seq
PRJNA725028	SAMN18868072	MASLD	ATAC-seq
PRJNA725028	SAMN18868071	MASLD	ATAC-seq
PRJNA725028	SAMN18868070	MASLD	ATAC-seq
PRJNA725028	SAMN18868069	MASLD	ATAC-seq
PRJNA725028	SAMN18868068	MASLD	ATAC-seq
PRJNA725028	SAMN18868067	MASLD	ATAC-seq
PRJNA725028	SAMN18868066	MASLD	ATAC-seq
PRJNA725028	SAMN18868065	MASLD	ATAC-seq
PRJNA725028	SAMN18868064	MASLD	ATAC-seq
PRJNA725028	SAMN18868055	Healthy	ATAC-seq
PRJNA725028	SAMN18868054	Healthy	ATAC-seq
PRJNA725028	SAMN18868063	MASLD	ATAC-seq
PRJNA725028	SAMN18868062	MASLD	ATAC-seq
PRJNA725028	SAMN18868061	MASLD	ATAC-seq
PRJNA725028	SAMN18868060	MASLD	ATAC-seq
PRJNA725028	SAMN18868059	MASLD	ATAC-seq
PRJNA725028	SAMN18868097	MASH	ATAC-seq
PRJNA725028	SAMN18868096	MASH	ATAC-seq
PRJNA725028	SAMN18868095	MASH	ATAC-seq

Supplementary Table 3

Cluster	Sample	Number	Percentage
Hepatocyte	Healthy	149021	0.625224461711447
Endothelial cell	Healthy	43381	0.182006981388558
T lymphocyte	Healthy	16467	0.0690880561196234
Monocyte/Macrophage	Healthy	14665	0.0615276822125631
Stellate cell	Healthy	9368	0.0393038750062933
Cholangiocyte	Healthy	4141	0.0173737560206085
B lymphocyte	Healthy	1305	0.00547518754090657
Hepatocyte	MASLD	19180	0.52919103851672
Endothelial cell	MASLD	6341	0.174953095684803
T lymphocyte	MASLD	6011	0.165848140381856
Monocyte/Macrophage	MASLD	1906	0.0525880145679285
Stellate cell	MASLD	1373	0.0378821322149873
Cholangiocyte	MASLD	981	0.0270665489460324
B lymphocyte	MASLD	452	0.0124710296876724
Hepatocyte	MASH	154345	0.522137874574597
Endothelial cell	MASH	43650	0.147664765461668
T lymphocyte	MASH	41727	0.14115939675645
Monocyte/Macrophage	MASH	21336	0.0721781314064181
Stellate cell	MASH	15332	0.0518670374354707
Cholangiocyte	MASH	15788	0.0534096521674414
B lymphocyte	MASH	3424	0.0115831421979554

Supplementary Table 4

p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
0	1.968447388	0.807	0.21	0	qHSC	COL25A1
0	1.904327988	0.908	0.285	0	qHSC	RELN
0	1.862038302	0.72	0.169	0	qHSC	SYT1
0	1.828129889	0.744	0.213	0	qHSC	HHIP
0	1.744011557	0.962	0.422	0	qHSC	DACH1
0	1.680122067	0.937	0.409	0	qHSC	ADAMTSL1
0	1.506883806	0.521	0.086	0	qHSC	RSPO3
0	1.494860277	0.663	0.256	0	qHSC	ANO3
0	1.484097075	0.634	0.186	0	qHSC	CADM2
0	1.41212899	0.57	0.118	0	qHSC	CAMK4
0	1.401742282	0.749	0.257	0	qHSC	ATRNL1
0	1.395627772	0.736	0.22	0	qHSC	COLEC10
0	1.394378191	0.532	0.18	0	qHSC	SGCZ
0	1.335699489	0.856	0.344	0	qHSC	MASP1
0	1.308903811	0.969	0.683	0	qHSC	NR1H4
0	1.293135564	0.415	0.138	0	qHSC	FGF13
0	1.290507883	0.751	0.287	0	qHSC	IGFBP3
0	1.272558739	0.513	0.118	0	qHSC	LINC01695
0	1.270887807	0.551	0.131	0	qHSC	NLGN4X
0	1.249657541	0.737	0.318	0	qHSC	FGFR2
0	1.248837277	0.562	0.123	0	qHSC	RXFP1
0	1.239098526	0.342	0.048	0	qHSC	SYT10
0	1.233224504	0.704	0.244	0	qHSC	PAMR1
0	1.232306457	0.402	0.076	0	qHSC	EGFLAM
0	1.232255016	0.902	0.491	0	qHSC	ARHGAP15
0	1.20891103	0.783	0.226	0	qHSC	IFITM10
0	1.198180283	0.557	0.136	0	qHSC	PDE8B
0	1.176084227	0.819	0.382	0	qHSC	SEMA5A
0	1.168056842	0.914	0.509	0	qHSC	HGF
0	1.16249724	0.517	0.133	0	qHSC	SYTL5
0	1.15186101	0.822	0.374	0	qHSC	AGTR1
0	1.148226571	0.724	0.237	0	qHSC	BMPER
0	1.133941746	0.578	0.163	0	qHSC	P3H2
0	1.127902332	0.557	0.183	0	qHSC	EFNA5
0	1.124706361	0.609	0.2	0	qHSC	BMPR1B
0	1.123247651	0.931	0.529	0	qHSC	PWRN1
0	1.101471847	0.7	0.367	0	qHSC	CHSY3
0	1.07497496	0.87	0.498	0	qHSC	HMCN1
0	1.054104329	0.956	0.668	0	qHSC	LIFR
0	1.051501776	0.844	0.345	0	qHSC	ADAMTS13

0	1.042924561	0.979	0.709	0	qHSC	ANKS1A
0	1.029138199	0.762	0.289	0	qHSC	VIPR1
0	1.019577179	0.292	0.05	0	qHSC	CXCL14
0	1.003980932	0.521	0.177	0	qHSC	ESRRG
0	1.001554888	0.66	0.244	0	qHSC	SEMA6D
0	1.00154134	0.816	0.404	0	qHSC	KAZN
0	0.996577962	0.833	0.454	0	qHSC	ARHGAP42
0	0.990948358	0.451	0.106	0	qHSC	GRIA3
0	0.98705783	0.474	0.128	0	qHSC	ECM1
0	0.975502632	0.835	0.444	0	qHSC	PAG1
0	0.975087839	0.63	0.242	0	qHSC	ST6GAL2
0	0.966604463	0.639	0.244	0	qHSC	STEAP4
0	0.966042884	0.528	0.169	0	qHSC	SLC1A2
0	0.951634516	0.318	0.056	0	qHSC	COL6A6
0	0.940736723	0.694	0.302	0	qHSC	ABCB11
0	0.940177544	0.973	0.703	0	qHSC	PDE4D
0	0.939811891	0.735	0.353	0	qHSC	ETS1
0	0.938854782	0.688	0.293	0	qHSC	PDE7B
0	0.937138	0.477	0.147	0	qHSC	PRLR
0	0.93222169	0.873	0.551	0	qHSC	ARHGAP24
0	0.91761055	0.62	0.268	0	qHSC	FHOD3
0	0.91626385	0.854	0.487	0	qHSC	FRMD4A
0	0.903182256	0.858	0.504	0	qHSC	KANK1
0	0.894434474	0.77	0.386	0	qHSC	FERMT2
0	0.892212679	0.948	0.678	0	qHSC	ADGRL2
0	0.873926789	0.879	0.495	0	qHSC	PTH1R
0	0.87330164	0.534	0.186	0	qHSC	MIR503HG
0	0.871321584	0.562	0.232	0	qHSC	ZNF385B
0	0.870169237	0.722	0.35	0	qHSC	CXCL12
0	0.867813606	0.869	0.495	0	qHSC	PLCB1
0	0.864766336	0.79	0.459	0	qHSC	ZFPM2-AS1
0	0.860760154	0.315	0.071	0	qHSC	VIPR1-AS1
0	0.855526384	0.999	0.94	0	qHSC	RBMS3
0	0.852793804	0.71	0.35	0	qHSC	MEG8
0	0.844036484	0.744	0.368	0	qHSC	PLEKHH2
0	0.841825845	0.347	0.082	0	qHSC	GNG2
0	0.83871755	0.817	0.496	0	qHSC	SPATS2L
0	0.838366487	0.888	0.568	0	qHSC	CNTN4
0	0.837427471	0.582	0.253	0	qHSC	EDNRB
0	0.833669574	0.959	0.668	0	qHSC	ITGA9
0	0.832524464	0.375	0.112	0	qHSC	NCAM1
0	0.822709349	0.677	0.326	0	qHSC	FILIP1
0	0.817800829	0.411	0.118	0	qHSC	HS3ST3B1

0	0.813798348	0.886	0.593	0	qHSC	PSD3
0	0.803190176	0.807	0.46	0	qHSC	GNA14
0	0.801119492	0.453	0.157	0	qHSC	NID2
0	0.793386203	0.545	0.209	0	qHSC	TUSC3
0	0.776832384	0.558	0.227	0	qHSC	RAI14
0	0.770756215	0.407	0.127	0	qHSC	FLVCR2
0	0.762123652	0.987	0.821	0	qHSC	ZFPM2
0	0.755000324	0.435	0.149	0	qHSC	ZNF160
0	0.753688937	0.96	0.752	0	qHSC	DMD
0	0.748716193	0.461	0.15	0	qHSC	RBP1
0	0.744850402	0.677	0.351	0	qHSC	HMBOX1
0	0.732493262	0.982	0.835	0	qHSC	PARD3
0	0.730022764	0.799	0.43	0	qHSC	MEG3
0	0.729741231	0.753	0.429	0	qHSC	ROBO1
0	0.729566088	0.782	0.436	0	qHSC	C1orf21
0	0.726119469	0.898	0.575	0	qHSC	MYO10
0	0.724468486	0.495	0.182	0	qHSC	ALLC
0	0.717531249	0.294	0.06	0	qHSC	CCDC88C
0	0.71068328	0.275	0.052	0	qHSC	ZNF503-AS1
0	0.704697092	0.768	0.435	0	qHSC	EPAS1
0	0.693037942	0.289	0.059	0	qHSC	LHX2
0	0.688273467	0.744	0.418	0	qHSC	HAND2-AS1
0	0.687589174	0.266	0.06	0	qHSC	LRAT
0	0.675919349	0.746	0.43	0	qHSC	APP
0	0.664257158	0.603	0.282	0	qHSC	TRANK1
0	0.652179791	0.287	0.06	0	qHSC	PRAM1
0	0.643431613	0.732	0.412	0	qHSC	DENND1A
7.74E-308	0.708761645	0.664	0.341	1.59E-303	qHSC	SAMD5
1.80E-305	0.680541383	0.453	0.175	3.70E-301	qHSC	STIM2
8.51E-305	0.709363854	0.739	0.419	1.75E-300	qHSC	ST5
2.08E-303	0.801379579	0.531	0.237	4.28E-299	qHSC	EDA
3.85E-299	0.619305173	0.573	0.258	7.92E-295	qHSC	ADCY5
7.30E-298	0.819032041	0.534	0.248	1.50E-293	qHSC	RBMS3-AS2
3.94E-297	0.681775643	0.287	0.077	8.12E-293	qHSC	PRKAR2B
4.97E-296	0.749941688	0.603	0.302	1.02E-291	qHSC	CALCRL
4.53E-295	0.603082082	0.348	0.111	9.32E-291	qHSC	RWDD3
1.46E-293	0.771636853	0.344	0.112	3.00E-289	qHSC	ADAMTS5
1.70E-291	0.604099693	0.75	0.433	3.49E-287	qHSC	FARP1
3.57E-290	0.613447725	0.826	0.516	7.35E-286	qHSC	NR2F1-AS1
3.97E-289	0.718513953	0.603	0.299	8.17E-285	qHSC	ADRA1B
5.92E-285	0.706057365	0.69	0.381	1.22E-280	qHSC	MAP2
4.03E-284	0.618707435	0.956	0.781	8.30E-280	qHSC	EXT1
8.49E-281	0.813419772	0.412	0.163	1.75E-276	qHSC	GNA14-AS1

8.00E-278	0.767652532	0.547	0.267	1.65E-273	qHSC	PIGN
1.01E-277	0.6416168	0.825	0.518	2.07E-273	qHSC	GPM6A
1.22E-276	0.674196215	0.466	0.195	2.51E-272	qHSC	BCAR3
3.68E-276	0.666697563	0.441	0.178	7.57E-272	qHSC	SFMBT2
7.92E-275	0.678826988	0.346	0.116	1.63E-270	qHSC	FREM1
6.00E-272	0.636783646	0.686	0.381	1.23E-267	qHSC	CDH2
7.49E-271	0.680419231	0.577	0.286	1.54E-266	qHSC	ELMO1
1.06E-270	0.630235482	0.62	0.319	2.18E-266	qHSC	DSE
1.72E-267	0.623212934	0.687	0.378	3.55E-263	qHSC	SLC9A9
1.01E-266	0.608243392	0.653	0.346	2.07E-262	qHSC	OSBPL10
1.33E-266	0.646422681	0.587	0.295	2.74E-262	qHSC	ABCC9
1.21E-264	0.651423551	0.584	0.293	2.48E-260	qHSC	NR2F1
6.88E-255	0.595424708	0.832	0.552	1.42E-250	qHSC	PDLIM5
5.58E-254	0.665665081	0.89	0.659	1.15E-249	qHSC	PCDH9
1.13E-238	0.631106475	0.417	0.177	2.33E-234	qHSC	SUCLG2-AS1
2.29E-238	0.606262458	0.531	0.26	4.72E-234	qHSC	CNKSR3
4.39E-238	0.818871171	0.277	0.088	9.04E-234	qHSC	NCAM2
1.33E-237	0.636091424	0.357	0.135	2.74E-233	qHSC	STAC
2.00E-235	0.683043095	0.757	0.482	4.12E-231	qHSC	SLC8A1
5.70E-220	0.629930037	0.256	0.08	1.17E-215	qHSC	PIK3R3
3.39E-215	0.710285228	0.337	0.133	6.97E-211	qHSC	EYS
1.22E-208	0.624089207	0.374	0.159	2.50E-204	qHSC	AHR
5.71E-204	0.679660855	0.608	0.353	1.17E-199	qHSC	AC007319.1
4.52E-203	0.615229622	0.314	0.121	9.31E-199	qHSC	MBOAT2
1.50E-200	0.66843807	0.547	0.294	3.09E-196	qHSC	FGD4
3.97E-199	0.622475257	0.609	0.353	8.18E-195	qHSC	GUCY1A2
1.10E-197	0.59423466	0.398	0.18	2.26E-193	qHSC	AC007098.1
8.11E-192	0.675492501	0.359	0.157	1.67E-187	qHSC	KIF26B
1.95E-188	0.604061099	0.538	0.293	4.02E-184	qHSC	ITGA9-AS1
8.04E-185	1.082052668	0.6	0.401	1.66E-180	qHSC	KIAA1217
1.43E-174	0.652812527	0.33	0.142	2.94E-170	qHSC	CHRM2
6.97E-131	0.670877524	0.286	0.133	1.44E-126	qHSC	ROBO2
3.06E-134	1.009753746	0.667	0.595	6.29E-130	inHSC	PTH1R
5.62E-132	0.61728047	0.729	0.524	1.16E-127	inHSC	ADAMTSL1
1.96E-120	0.944514018	0.581	0.472	4.03E-116	inHSC	ADAMTS13
1.79E-116	0.638677944	0.618	0.433	3.68E-112	inHSC	RELN
8.16E-89	0.850800588	0.51	0.409	1.68E-84	inHSC	VIPR1
1.55E-82	0.938754932	0.473	0.371	3.20E-78	inHSC	IFITM10
1.51E-41	0.674900405	0.544	0.522	3.11E-37	inHSC	KAZN
1.73E-41	0.648915865	0.473	0.413	3.55E-37	inHSC	IGFBP3
1.16E-34	0.770459471	0.462	0.458	2.38E-30	inHSC	COL27A1
2.09E-29	0.60346891	0.476	0.434	4.31E-25	inHSC	FGFR2
0	2.01475025	0.574	0.113	0	aHSC	MGAT4C

0	1.906856618	0.775	0.273	0	aHSC	KALRN
0	1.71956217	0.57	0.151	0	aHSC	ITGBL1
0	1.663589354	0.84	0.35	0	aHSC	NAV3
0	1.541289979	0.727	0.265	0	aHSC	PLCXD3
0	1.507824006	0.35	0.058	0	aHSC	SCN7A
0	1.455620103	0.875	0.487	0	aHSC	C7
0	1.447084804	0.263	0.051	0	aHSC	NEGR1
0	1.410210091	0.561	0.137	0	aHSC	MIR100HG
0	1.378860007	0.521	0.113	0	aHSC	LAMC3
0	1.369255758	0.795	0.339	0	aHSC	BICC1
0	1.25601056	0.627	0.272	0	aHSC	NAV2
0	1.249052672	0.406	0.093	0	aHSC	DEPTOR
0	1.223623206	0.596	0.187	0	aHSC	FBLN5
0	1.144567845	0.318	0.04	0	aHSC	SPON1
0	1.092118691	0.6	0.232	0	aHSC	NALCN
0	1.091093515	0.393	0.118	0	aHSC	MAMDC2
0	1.07309477	0.448	0.12	0	aHSC	ROR2
0	1.036993768	0.342	0.078	0	aHSC	LMCD1
0	1.032758104	0.329	0.05	0	aHSC	CDH11
0	1.03257377	0.6	0.287	0	aHSC	COL4A4
0	1.027687204	0.408	0.151	0	aHSC	LRRC7
0	0.977759172	0.464	0.158	0	aHSC	KIAA1211
0	0.941228528	0.503	0.214	0	aHSC	CYP7B1
0	0.937538174	0.284	0.042	0	aHSC	EFEMP1
0	0.933692127	0.476	0.184	0	aHSC	CTIF
0	0.933434644	0.273	0.054	0	aHSC	SMOC2
0	0.926470787	0.775	0.286	0	aHSC	CACNA1C
0	0.909822924	0.488	0.2	0	aHSC	CELF2
0	0.88894582	0.474	0.18	0	aHSC	DOK6
0	0.826296347	0.624	0.283	0	aHSC	NFASC
0	0.824901624	0.412	0.151	0	aHSC	MITF
0	0.728047553	0.872	0.627	0	aHSC	PARD3B
3.75E-307	0.740148299	0.807	0.526	7.71E-303	aHSC	MIR99AHG
4.19E-305	0.933065153	0.373	0.125	8.63E-301	aHSC	PRR16
1.72E-304	0.833041191	0.564	0.267	3.53E-300	aHSC	ZNF704
9.96E-304	0.805783624	0.378	0.132	2.05E-299	aHSC	ADARB1
2.25E-301	0.831056056	0.763	0.464	4.62E-297	aHSC	EPHA3
4.24E-300	0.754438319	0.364	0.12	8.73E-296	aHSC	ARHGEF26
4.88E-297	1.034117352	0.436	0.177	1.00E-292	aHSC	ELN
2.12E-291	0.806051408	0.311	0.093	4.37E-287	aHSC	COL4A3
4.54E-290	0.683751581	0.416	0.157	9.35E-286	aHSC	ITGB5
6.25E-287	0.677387785	0.323	0.101	1.29E-282	aHSC	PODN
6.90E-283	0.807584749	0.427	0.17	1.42E-278	aHSC	DAB1

1.52E-282	0.734875255	0.797	0.517	3.12E-278	aHSC	DLG2
1.83E-282	0.707230892	0.334	0.109	3.76E-278	aHSC	AEBP1
2.96E-281	0.869955423	0.545	0.271	6.09E-277	aHSC	LINC00924
3.09E-274	0.932038164	0.586	0.309	6.36E-270	aHSC	SLIT2
4.12E-274	0.739016069	0.739	0.466	8.48E-270	aHSC	UACA
4.25E-274	0.613163034	0.313	0.097	8.74E-270	aHSC	CLIP4
6.43E-270	0.638401382	0.341	0.115	1.32E-265	aHSC	ART4
1.38E-262	0.659260228	0.267	0.075	2.83E-258	aHSC	TC2N
7.67E-261	0.778890885	0.34	0.119	1.58E-256	aHSC	TIAM1
1.55E-257	0.789382761	0.496	0.233	3.19E-253	aHSC	KLHL29
1.09E-250	0.741110296	0.526	0.26	2.24E-246	aHSC	BNC2
6.19E-249	0.673139107	0.256	0.072	1.27E-244	aHSC	DPYSL3
6.20E-241	1.072239945	0.3	0.105	1.28E-236	aHSC	GEM
8.70E-237	0.636081939	0.389	0.156	1.79E-232	aHSC	ATP10A
4.70E-232	0.769946396	0.433	0.193	9.67E-228	aHSC	CARMIL1
2.91E-231	0.733331388	0.624	0.357	5.99E-227	aHSC	PID1
8.13E-231	0.628493803	0.404	0.172	1.67E-226	aHSC	RNF217
3.04E-230	0.735645222	0.737	0.49	6.26E-226	aHSC	FBXL7
2.29E-228	0.689311339	0.431	0.195	4.72E-224	aHSC	FHL2
1.68E-225	0.936621335	0.515	0.264	3.46E-221	aHSC	FGF14
8.61E-223	0.735295997	0.566	0.31	1.77E-218	aHSC	SETBP1
3.02E-222	0.662644494	0.518	0.265	6.22E-218	aHSC	HIVEP3
7.19E-222	0.815711742	0.442	0.202	1.48E-217	aHSC	TIMP3
3.81E-220	0.699268062	0.523	0.27	7.84E-216	aHSC	COL1A2
1.05E-214	0.661067374	0.257	0.082	2.15E-210	aHSC	ANKS1B
1.10E-208	0.61594279	0.428	0.194	2.26E-204	aHSC	MAP3K5
7.34E-206	0.631612923	0.306	0.116	1.51E-201	aHSC	PVT1
5.41E-202	0.623818988	0.296	0.109	1.11E-197	aHSC	MID1
1.77E-201	0.627625373	0.782	0.557	3.65E-197	aHSC	PDGFRA
2.32E-200	0.802205543	0.257	0.089	4.77E-196	aHSC	SEMA3D
5.82E-197	0.590407498	0.621	0.368	1.20E-192	aHSC	MYH10
7.43E-197	0.646534955	0.339	0.141	1.53E-192	aHSC	SAMHD1
1.16E-194	0.76091273	0.536	0.306	2.39E-190	aHSC	PALM2-AKAP2
4.34E-193	0.592323516	0.267	0.095	8.94E-189	aHSC	THBS2
2.13E-189	0.608533865	0.562	0.321	4.39E-185	aHSC	TSC22D1
3.53E-188	0.597911486	0.846	0.64	7.27E-184	aHSC	PLXDC2
2.46E-184	0.78630027	0.465	0.247	5.06E-180	aHSC	CLSTN2
1.01E-182	0.61009625	0.483	0.253	2.08E-178	aHSC	RERG
6.22E-181	0.6185932	0.356	0.158	1.28E-176	aHSC	MYO1E
1.48E-174	0.637714344	0.254	0.093	3.04E-170	aHSC	PAPPA
5.19E-167	0.723155803	0.682	0.465	1.07E-162	aHSC	COL4A2
6.20E-163	0.667460911	0.289	0.12	1.28E-158	aHSC	XYLT1
7.12E-157	0.748559901	0.585	0.375	1.47E-152	aHSC	CRISPLD2

1.44E-139	0.60591042	0.887	0.739	2.97E-135	aHSC	LAMA2
3.96E-119	0.827072603	0.533	0.354	8.15E-115	aHSC	COL4A1
5.12E-85	0.674789913	0.316	0.183	1.05E-80	aHSC	THBS1
7.35E-78	0.60371587	0.484	0.342	1.51E-73	aHSC	CDH19
1.03E-93	0.719828155	0.736	0.584	2.12E-89	hep-like HSC	C7
1.45E-91	0.72209952	0.957	0.943	2.98E-87	hep-like HSC	ALB
6.11E-73	0.790941461	0.759	0.738	1.26E-68	hep-like HSC	APOA1
9.92E-66	0.730848563	0.758	0.731	2.04E-61	hep-like HSC	APOC3
1.96E-53	0.748990167	0.691	0.684	4.04E-49	hep-like HSC	APOC1
3.35E-53	0.777975222	0.518	0.386	6.89E-49	hep-like HSC	PLCXD3
5.05E-52	0.91062023	0.674	0.627	1.04E-47	hep-like HSC	SERPINA1
1.44E-51	0.895353245	0.679	0.633	2.96E-47	hep-like HSC	HP
5.96E-49	0.901871404	0.338	0.22	1.23E-44	hep-like HSC	LAMC3
3.71E-47	0.775317102	0.689	0.683	7.63E-43	hep-like HSC	APOA2
9.50E-41	0.871230862	0.637	0.604	1.95E-36	hep-like HSC	FGB
1.53E-40	0.733540768	0.612	0.596	3.15E-36	hep-like HSC	APOE
2.93E-39	0.738117305	0.566	0.507	6.04E-35	hep-like HSC	APOH
2.88E-37	0.67902697	0.6	0.583	5.92E-33	hep-like HSC	RBP4
4.19E-37	0.76738474	0.569	0.534	8.63E-33	hep-like HSC	AMBP
1.31E-35	0.667784341	0.642	0.626	2.70E-31	hep-like HSC	TTR
1.43E-34	0.897070409	0.595	0.559	2.94E-30	hep-like HSC	FGA
5.42E-31	0.88792445	0.564	0.534	1.12E-26	hep-like HSC	FGG
6.52E-31	0.810628564	0.588	0.558	1.34E-26	hep-like HSC	APOB
6.47E-30	0.736315056	0.622	0.616	1.33E-25	hep-like HSC	TF
1.65E-29	0.800868375	0.527	0.498	3.40E-25	hep-like HSC	C3
3.63E-26	0.69193766	0.507	0.491	7.47E-22	hep-like HSC	APOC2
4.92E-26	0.722005343	0.488	0.459	1.01E-21	hep-like HSC	VTN
5.71E-25	0.820420777	0.425	0.366	1.17E-20	hep-like HSC	FGL1
4.48E-23	0.733997487	0.482	0.455	9.23E-19	hep-like HSC	CP
9.47E-21	1.025483753	0.337	0.271	1.95E-16	hep-like HSC	SERPINA3
9.33E-19	0.938998596	0.29	0.224	1.92E-14	hep-like HSC	SAA1
1.57E-17	0.781086935	0.365	0.323	3.24E-13	hep-like HSC	ORM2
8.99E-17	0.696395846	0.253	0.19	1.85E-12	hep-like HSC	CRP
1.63E-16	0.710406822	0.381	0.352	3.36E-12	hep-like HSC	HPX
2.48E-16	0.907954495	0.441	0.423	5.10E-12	hep-like HSC	ORM1
2.71E-16	0.672584669	0.391	0.364	5.58E-12	hep-like HSC	KNG1
6.46E-16	0.605331742	0.458	0.461	1.33E-11	hep-like HSC	SELENOP
1.77E-15	0.710278016	0.405	0.38	3.64E-11	hep-like HSC	GC
8.03E-14	0.623755465	0.43	0.409	1.65E-09	hep-like HSC	CLU
2.37E-13	0.664455372	0.386	0.374	4.88E-09	hep-like HSC	CYP2C8
4.22E-13	0.596013605	0.511	0.512	8.69E-09	hep-like HSC	CPS1
5.84E-13	0.627452421	0.344	0.307	1.20E-08	hep-like HSC	C9
1.13E-12	0.685197382	0.381	0.369	2.32E-08	hep-like HSC	CYP3A5

1.47E-12	0.642829884	0.328	0.292	3.02E-08	hep-like HSC	CFB
1.92E-12	0.595410111	0.351	0.329	3.95E-08	hep-like HSC	MGST1
3.34E-12	0.615763967	0.272	0.235	6.87E-08	hep-like HSC	F2
6.33E-12	0.618464248	0.361	0.34	1.30E-07	hep-like HSC	SERPING1
8.62E-12	0.685913574	0.277	0.24	1.77E-07	hep-like HSC	SAA4
1.22E-11	0.648617386	0.352	0.33	2.52E-07	hep-like HSC	AHSG
1.89E-11	0.586978338	0.292	0.261	3.89E-07	hep-like HSC	A1BG
2.33E-11	0.625677599	0.333	0.305	4.80E-07	hep-like HSC	TAT
9.34E-11	0.788521918	0.499	0.529	1.92E-06	hep-like HSC	ADAMTSL2
2.95E-10	0.586676203	0.371	0.355	6.07E-06	hep-like HSC	FABP1
3.88E-10	0.601315315	0.382	0.377	7.99E-06	hep-like HSC	PLG
6.80E-10	0.612888057	0.393	0.398	1.40E-05	hep-like HSC	CYP2C9
2.87E-09	0.665702452	0.25	0.218	5.90E-05	hep-like HSC	AGT
1.62E-08	0.622272247	0.252	0.221	0.000333712	hep-like HSC	IGFBP1
2.67E-08	0.597082081	0.26	0.235	0.000550089	hep-like HSC	APCS
4.64E-08	0.592260997	0.284	0.27	0.000955067	hep-like HSC	AZGP1
9.81E-08	0.592936016	0.327	0.32	0.002020162	hep-like HSC	C5
3.33E-07	0.606125089	0.3	0.284	0.006844333	hep-like HSC	CES1
0	3.232273978	0.55	0.038	0	SMC	MYH11
0	3.215459398	0.525	0.017	0	SMC	RGS6
0	3.095794039	0.809	0.078	0	SMC	EBF1
0	2.634769436	0.528	0.065	0	SMC	SPARCL1
0	2.51834569	0.508	0.056	0	SMC	NTRK3
0	2.464886759	0.638	0.132	0	SMC	SLIT3
0	2.164724672	0.786	0.309	0	SMC	RCAN2
0	2.089459476	0.88	0.385	0	SMC	CACNA1C
0	2.054018772	0.476	0.067	0	SMC	DGKG
0	1.990683302	0.367	0.022	0	SMC	LAMA3
0	1.980968628	0.434	0.025	0	SMC	NOTCH3
0	1.921981464	0.6	0.155	0	SMC	CLMN
0	1.758478815	0.467	0.093	0	SMC	PPM1L
0	1.695952681	0.302	0.005	0	SMC	LDB3
0	1.6728893	0.397	0.085	0	SMC	LMOD1
0	1.662203721	0.343	0.06	0	SMC	AKAP6
0	1.656333745	0.678	0.305	0	SMC	FRY
0	1.60545934	0.313	0.012	0	SMC	MCAM
0	1.565885027	0.297	0.045	0	SMC	PPARG
0	1.532685086	0.285	0.021	0	SMC	MYOCD
0	1.52878405	0.296	0.033	0	SMC	ADGRF5
0	1.48795558	0.268	0.027	0	SMC	CPE
0	1.460318233	0.305	0.046	0	SMC	CDH13
0	1.392349148	0.257	0.011	0	SMC	GJC1
0	1.363581924	0.277	0.014	0	SMC	ITGA7

0	1.282777568	0.257	0.033	0	SMC	SIPA1L2
4.27E-284	1.344517117	0.373	0.091	8.78E-280	SMC	MRVI1
1.56E-279	1.639558848	0.367	0.092	3.22E-275	SMC	PLCE1
4.61E-278	1.498552412	0.688	0.339	9.48E-274	SMC	PDGFRB
1.99E-263	1.230856624	0.251	0.043	4.09E-259	SMC	CDH6
1.09E-258	1.419225008	0.395	0.11	2.25E-254	SMC	DTNA
2.33E-247	1.609956841	0.533	0.21	4.80E-243	SMC	PLCL1
1.26E-231	1.386712997	0.386	0.113	2.60E-227	SMC	PLCB4
7.39E-218	1.758522263	0.337	0.096	1.52E-213	SMC	RGS5
7.57E-212	1.268136444	0.617	0.286	1.56E-207	SMC	SLC7A2
8.79E-212	1.432437264	0.579	0.285	1.81E-207	SMC	TBC1D1
8.56E-206	1.577476876	0.697	0.443	1.76E-201	SMC	CARMN
3.10E-202	1.569606479	0.714	0.471	6.38E-198	SMC	ZFHX3
1.05E-197	1.782249783	0.305	0.084	2.17E-193	SMC	KCNMA1
5.53E-195	1.543814065	0.388	0.129	1.14E-190	SMC	AKAP12
5.40E-190	1.713883041	0.447	0.179	1.11E-185	SMC	ENPEP
6.12E-184	1.071492163	0.261	0.063	1.26E-179	SMC	TMTC1
3.62E-173	1.19847457	0.407	0.153	7.46E-169	SMC	SPECC1
4.06E-171	1.360624552	0.62	0.34	8.37E-167	SMC	CTNNA3
5.58E-164	1.276571429	0.431	0.179	1.15E-159	SMC	NHS
5.20E-161	1.424752506	0.426	0.183	1.07E-156	SMC	ADCY3
1.67E-156	1.089420343	0.518	0.238	3.45E-152	SMC	CARMIL1
4.16E-155	1.010024914	0.315	0.102	8.56E-151	SMC	ASAP2
1.10E-153	1.324560661	0.541	0.293	2.25E-149	SMC	HIPK2
9.05E-150	1.13736667	0.391	0.154	1.86E-145	SMC	MYOM1
4.61E-149	1.277525398	0.564	0.308	9.50E-145	SMC	CACNB2
3.76E-145	1.564843535	0.497	0.248	7.73E-141	SMC	ADGRL3
6.80E-141	1.090933832	0.378	0.151	1.40E-136	SMC	EDNRA
8.42E-141	1.06864809	0.394	0.162	1.73E-136	SMC	JAG1
1.21E-138	1.28103555	0.449	0.204	2.49E-134	SMC	RYR2
2.26E-136	1.04238807	0.386	0.163	4.65E-132	SMC	UBA2
3.10E-132	1.074142028	0.348	0.138	6.38E-128	SMC	KLHL23
1.62E-131	1.192517216	0.507	0.281	3.32E-127	SMC	ARHGEF7
1.23E-128	1.242380704	0.459	0.222	2.54E-124	SMC	MAP1B
2.87E-124	0.872889536	0.28	0.095	5.90E-120	SMC	FAT1
2.31E-119	1.097004387	0.535	0.3	4.74E-115	SMC	MAML3
3.02E-118	1.034603454	0.261	0.09	6.21E-114	SMC	SORT1
3.37E-118	1.037933685	0.362	0.159	6.93E-114	SMC	DGKD
6.90E-116	1.345167308	0.443	0.226	1.42E-111	SMC	ACTA2
6.03E-115	0.860534434	0.759	0.6	1.24E-110	SMC	UTRN
8.83E-114	0.794434298	0.62	0.362	1.82E-109	SMC	SETBP1
4.96E-110	0.90775236	0.32	0.129	1.02E-105	SMC	COL4A5
5.28E-109	0.972857419	0.286	0.109	1.09E-104	SMC	HEYL

1.80E-106	0.975792344	0.419	0.205	3.71E-102	SMC	ATP10A
3.47E-105	0.907760525	0.786	0.625	7.15E-101	SMC	PDE3A
4.96E-105	0.995738154	0.398	0.195	1.02E-100	SMC	ECE1
4.15E-104	0.928481658	0.432	0.217	8.53E-100	SMC	TLE1
1.56E-98	0.952606711	0.393	0.188	3.22E-94	SMC	SDK1
3.97E-98	0.91188169	0.41	0.208	8.18E-94	SMC	PACSIN2
4.63E-97	0.928029703	0.649	0.453	9.53E-93	SMC	HIP1
1.31E-93	0.682119023	0.894	0.842	2.69E-89	SMC	LPP
1.43E-88	1.049854818	0.333	0.156	2.94E-84	SMC	MACROD2
1.95E-87	0.787982507	0.348	0.163	4.01E-83	SMC	SNTB1
7.53E-87	0.875528814	0.373	0.189	1.55E-82	SMC	SLC39A11
1.19E-85	0.845586995	0.315	0.144	2.46E-81	SMC	ATP8B1
2.85E-85	0.830070131	0.419	0.228	5.87E-81	SMC	MAP3K20
8.78E-85	1.102482908	0.514	0.329	1.81E-80	SMC	SORBS2
1.94E-84	1.053926387	0.595	0.417	4.00E-80	SMC	MEF2C
2.97E-84	0.931359472	0.323	0.152	6.12E-80	SMC	TTLL7
1.55E-80	0.8294974	0.438	0.252	3.20E-76	SMC	ITPR1
2.39E-80	0.899403986	0.277	0.119	4.92E-76	SMC	ANKS1B
2.21E-78	0.922134175	0.424	0.245	4.54E-74	SMC	COL18A1
6.88E-76	0.904533101	0.367	0.196	1.42E-71	SMC	DSTN
4.55E-75	0.861259437	0.323	0.159	9.36E-71	SMC	CDC14B
6.13E-74	0.962782161	0.299	0.142	1.26E-69	SMC	ADAMTS1
4.15E-71	1.72025911	0.329	0.174	8.53E-67	SMC	ATP1B3
2.90E-69	0.702762926	0.623	0.445	5.96E-65	SMC	A2M
3.00E-67	0.663093701	0.634	0.471	6.16E-63	SMC	MAGI1
7.39E-67	0.651223747	0.564	0.366	1.52E-62	SMC	NFASC
2.33E-65	0.756425334	0.442	0.268	4.79E-61	SMC	ADRA1A
4.17E-64	0.943016674	0.316	0.169	8.59E-60	SMC	TBX2
3.86E-63	0.916557498	0.523	0.366	7.95E-59	SMC	RNF152
3.86E-62	0.777295219	0.376	0.22	7.94E-58	SMC	ARHGAP17
5.29E-62	0.681242127	0.762	0.646	1.09E-57	SMC	IMMP2L
1.68E-59	0.661687347	0.648	0.491	3.46E-55	SMC	TACC1
1.40E-56	0.84169654	0.815	0.767	2.88E-52	SMC	DLC1
1.51E-56	0.729462186	0.356	0.205	3.10E-52	SMC	ATP2B4
6.31E-56	0.686854576	0.264	0.131	1.30E-51	SMC	MARK1
6.81E-56	1.310144448	0.52	0.395	1.40E-51	SMC	PLA2G5
1.53E-55	0.615098402	0.408	0.248	3.15E-51	SMC	ST6GAL1
3.19E-54	0.915693276	0.275	0.143	6.56E-50	SMC	PITPNC1
2.01E-53	0.730907696	0.464	0.306	4.14E-49	SMC	RERG
5.41E-53	0.799452414	0.312	0.175	1.11E-48	SMC	AXL
2.85E-51	0.795183206	0.346	0.208	5.86E-47	SMC	FLNA
8.74E-50	0.682891559	0.688	0.579	1.80E-45	SMC	BCAS3
1.57E-49	1.119078375	0.339	0.206	3.23E-45	SMC	IGFBP5

5.73E-49	0.625237017	0.55	0.409	1.18E-44	SMC	KLF12
3.29E-48	0.710228823	0.476	0.343	6.78E-44	SMC	RABGAP1
5.49E-47	0.597644325	0.401	0.258	1.13E-42	SMC	ABHD2
6.15E-47	0.964270892	0.264	0.142	1.27E-42	SMC	TAGLN
9.65E-46	1.071416898	0.471	0.347	1.99E-41	SMC	ESYT2
1.20E-45	0.66162531	0.325	0.185	2.48E-41	SMC	PRR16
2.19E-45	0.737396255	0.254	0.136	4.52E-41	SMC	NMD3
1.87E-44	0.612657896	0.367	0.23	3.85E-40	SMC	ATP2A2
6.79E-44	0.709684109	0.424	0.291	1.40E-39	SMC	DGKH
4.55E-42	0.618205243	0.595	0.475	9.36E-38	SMC	SSBP2
6.25E-42	0.624000142	0.299	0.176	1.29E-37	SMC	PDE5A
1.72E-41	0.601850064	0.522	0.397	3.54E-37	SMC	MSRB3
9.64E-41	0.593530844	0.35	0.22	1.98E-36	SMC	LDLRAD3
1.00E-39	0.636508624	0.394	0.271	2.07E-35	SMC	CRTC3
3.17E-39	0.67255419	0.606	0.503	6.52E-35	SMC	SIK3
3.33E-39	0.807716267	0.365	0.246	6.85E-35	SMC	ANGPT1
9.81E-39	0.605467987	0.388	0.261	2.02E-34	SMC	WDFY2
1.23E-37	0.661139278	0.436	0.313	2.53E-33	SMC	ARHGAP29
2.35E-37	0.627954418	0.391	0.261	4.83E-33	SMC	TIMP3
9.29E-35	1.021562192	0.437	0.321	1.91E-30	SMC	PDK4
1.18E-34	0.611990526	0.402	0.289	2.44E-30	SMC	MPRIIP
1.37E-33	0.609138571	0.599	0.494	2.82E-29	SMC	ARHGAP6
2.39E-28	0.616156129	0.342	0.237	4.91E-24	SMC	ARHGAP26
9.64E-28	0.635511898	0.473	0.362	1.98E-23	SMC	FGL1
6.68E-27	0.803118069	0.363	0.27	1.37E-22	SMC	MYL9
4.97E-26	0.613115049	0.259	0.169	1.02E-21	SMC	ARHGAP44
1.09E-24	0.742144978	0.407	0.315	2.23E-20	SMC	PPP1CB
1.48E-19	0.727654201	0.631	0.556	3.05E-15	SMC	FGA
6.98E-19	1.127942416	0.392	0.333	1.44E-14	SMC	ADAMTS9
9.28E-19	0.735666022	0.598	0.531	1.91E-14	SMC	FGG
6.51E-18	0.645336907	0.623	0.555	1.34E-13	SMC	APOB
1.15E-17	0.706969518	0.25	0.173	2.36E-13	SMC	SAA2
1.93E-16	0.641052457	0.419	0.351	3.97E-12	SMC	PLCG2
6.55E-16	0.662346761	0.664	0.602	1.35E-11	SMC	FGB
7.76E-16	0.793442138	0.675	0.627	1.60E-11	SMC	SERPINA1
3.09E-14	0.929854188	0.459	0.435	6.35E-10	SMC	CRISPLD2
2.59E-13	0.609768622	0.292	0.225	5.32E-09	SMC	SAA1
2.85E-13	0.58957721	0.342	0.282	5.86E-09	SMC	SVIL
6.61E-13	0.629680146	0.259	0.197	1.36E-08	SMC	CMSS1
9.90E-13	0.776928629	0.336	0.273	2.04E-08	SMC	SERPINA3
2.23E-11	0.645557244	0.465	0.421	4.60E-07	SMC	ORM1
6.54E-11	0.610322254	0.662	0.636	1.35E-06	SMC	HP

Supplementary Table 5

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
PTH1R	3.08E-199	-1.551796879	0.55	0.858	6.33E-195
ADAMTS13	1.30E-190	-1.3824963	0.427	0.789	2.68E-186
VIPR1	8.46E-167	-1.246102606	0.343	0.724	1.74E-162
CADM2	1.10E-155	-1.521070282	0.198	0.535	2.26E-151
NID2	9.04E-152	-1.123446539	0.179	0.506	1.86E-147
GPC5	2.00E-143	-1.536406867	0.075	0.31	4.12E-139
CAMK4	7.28E-141	-1.131731382	0.195	0.528	1.50E-136
POSTN	1.79E-134	-1.008523585	0.059	0.27	3.69E-130
NR1H4	2.11E-131	-0.987496708	0.746	0.912	4.34E-127
ECM1	2.38E-128	-1.060806408	0.175	0.479	4.89E-124
KIAA1217	1.73E-123	-1.761047609	0.408	0.675	3.56E-119
FRMD4A	1.31E-120	-1.010322038	0.55	0.814	2.69E-116
IFITM10	1.86E-118	-1.211267844	0.373	0.675	3.83E-114
CP	2.50E-116	2.214947121	0.558	0.245	5.15E-112
FKBP5	2.91E-116	1.513032745	0.556	0.201	5.99E-112
FGL1	3.94E-115	2.56771507	0.483	0.145	8.11E-111
CCDC88C	2.43E-114	-0.947292943	0.113	0.361	5.00E-110
MASP1	1.24E-110	-0.99898156	0.461	0.748	2.56E-106
PAMR1	2.15E-109	-0.972965529	0.328	0.649	4.43E-105
FREM1	7.47E-107	-0.844388028	0.137	0.396	1.54E-102
NGFR	4.24E-105	-0.838221219	0.1	0.327	8.74E-101
SEMA5A	1.43E-102	-0.976256578	0.471	0.736	2.94E-98
CFH	1.11E-101	1.097723745	0.78	0.627	2.28E-97
ETS1	3.11E-101	-0.857686271	0.419	0.724	6.40E-97
EGFLAM	6.22E-101	-1.027972456	0.125	0.364	1.28E-96
COL25A1	3.53E-99	-1.145497612	0.327	0.616	7.27E-95
ZEB2	3.24E-97	-0.751990817	0.721	0.894	6.68E-93
COL6A1	3.39E-97	-0.889935594	0.417	0.72	6.98E-93
KAZN	8.25E-97	-1.058467172	0.487	0.743	1.70E-92
GNG2	1.70E-94	-0.830421428	0.123	0.355	3.51E-90
SAA1	2.39E-93	4.820637087	0.34	0.041	4.91E-89
PARD3	5.48E-91	-0.659776296	0.861	0.94	1.13E-86
PRAM1	9.95E-91	-0.810909404	0.1	0.308	2.05E-86
ARHGAP42	3.51E-90	-0.864604181	0.559	0.784	7.23E-86
ADAMTS5	1.92E-88	-0.876888951	0.144	0.382	3.94E-84
CRP	3.12E-88	2.434983405	0.308	0.021	6.43E-84
CALM2	1.98E-87	-0.817553396	0.332	0.621	4.07E-83
SAA2	3.65E-87	3.874182167	0.289	0.008	7.51E-83
FGA	8.27E-87	3.436637695	0.577	0.367	1.70E-82
COL27A1	2.36E-86	-0.85382744	0.425	0.716	4.85E-82

NEAT1	2.83E-86	0.841222376	0.95	0.95	5.82E-82
IGFBP3	5.34E-86	-0.679621187	0.344	0.645	1.10E-81
VWDE	6.14E-86	-0.694648181	0.037	0.173	1.26E-81
C9	3.41E-84	1.851464259	0.402	0.116	7.01E-80
RGS5	4.91E-84	-0.843955822	0.096	0.292	1.01E-79
ZBTB16	4.23E-82	1.101386651	0.674	0.477	8.70E-78
APOB	7.59E-82	2.853713025	0.6	0.42	1.56E-77
NWD2	1.50E-81	-0.912607536	0.035	0.163	3.09E-77
CPS1	4.16E-81	1.391880803	0.601	0.354	8.56E-77
EDA	1.61E-80	-0.854667205	0.302	0.576	3.31E-76
SERPINA3	4.31E-79	3.588987163	0.36	0.096	8.87E-75
FGB	4.93E-79	3.120548313	0.613	0.442	1.02E-74
FN1	5.01E-79	1.430273102	0.518	0.255	1.03E-74
GPR158	5.25E-79	-0.680413403	0.027	0.141	1.08E-74
NNMT	1.94E-78	1.340010228	0.374	0.091	3.99E-74
GNA14	2.76E-78	-0.7507478	0.527	0.781	5.68E-74
DACH1	2.20E-77	-0.785890189	0.574	0.796	4.54E-73
KALRN	2.97E-77	1.786199569	0.495	0.222	6.11E-73
RELN	6.74E-76	-0.984716481	0.448	0.679	1.39E-71
TRANK1	4.94E-75	-0.767453046	0.331	0.598	1.02E-70
ABI3BP	5.29E-75	-0.811323325	0.254	0.506	1.09E-70
COLEC10	4.10E-74	-0.807136244	0.342	0.605	8.43E-70
BMP1	4.79E-74	-0.901803432	0.21	0.445	9.87E-70
SON	6.31E-74	-0.647445724	0.598	0.828	1.30E-69
SLC1A2	3.06E-73	-0.834726317	0.232	0.478	6.30E-69
RXFP1	4.14E-73	-0.782992084	0.23	0.476	8.53E-69
ZNF160	1.73E-72	-0.833754322	0.216	0.461	3.56E-68
CXCL12	1.73E-71	-0.690685779	0.385	0.661	3.57E-67
PLEKHH2	1.46E-70	-0.667201872	0.425	0.686	3.01E-66
MEF2C	2.04E-70	-0.9519386	0.401	0.625	4.20E-66
TF	3.55E-70	2.215928742	0.647	0.538	7.30E-66
TRERF1	6.44E-70	-0.760490044	0.323	0.578	1.32E-65
PRLR	1.20E-69	-0.799932486	0.207	0.439	2.48E-65
PCDH9	1.66E-69	-0.777612611	0.673	0.823	3.42E-65
PEG3	1.75E-69	-0.628892786	0.066	0.22	3.60E-65
SEMA6D	2.84E-69	-0.669819397	0.319	0.593	5.84E-65
SYT10	8.29E-68	-0.768404036	0.107	0.293	1.71E-63
ESRRG	2.98E-67	-0.835589958	0.247	0.483	6.14E-63
AGT	5.23E-67	1.751553074	0.297	0.058	1.08E-62
FGG	2.28E-66	2.944035059	0.549	0.372	4.69E-62
DLC1	4.18E-66	-0.619410884	0.754	0.881	8.61E-62
ATRNL1	5.18E-66	-0.922290601	0.367	0.608	1.07E-61
RSPO3	1.12E-65	-0.860992157	0.193	0.416	2.31E-61

BMPER	5.90E-65	-0.67950489	0.327	0.583	1.21E-60
CTNNA3	9.31E-65	-0.905597923	0.289	0.523	1.92E-60
ROBO2	1.68E-64	-0.929707582	0.136	0.33	3.46E-60
CACNB2	1.03E-63	-0.804317196	0.289	0.531	2.11E-59
LHX2	7.75E-63	-0.597651111	0.11	0.291	1.60E-58
SLC7A2	1.58E-62	1.076567038	0.394	0.135	3.26E-58
SYT1	1.86E-62	-0.84036164	0.295	0.535	3.82E-58
TAT	1.92E-62	1.294707177	0.364	0.116	3.96E-58
ARHGAP15	8.65E-61	-0.716148061	0.587	0.778	1.78E-56
C3	2.32E-60	1.71835375	0.564	0.409	4.77E-56
C5	7.97E-60	1.322010682	0.409	0.181	1.64E-55
ELL2	1.69E-59	1.001275039	0.396	0.147	3.48E-55
CIRBP	4.02E-59	-0.622184316	0.228	0.452	8.28E-55
C1S	2.62E-58	1.106921943	0.566	0.377	5.39E-54
HMGCLL1	3.38E-57	-0.691678551	0.227	0.443	6.95E-53
MAPK10	2.19E-56	-0.592504508	0.631	0.812	4.51E-52
PRKCA	2.38E-56	-0.652492383	0.529	0.739	4.90E-52
BMP5	2.39E-56	-0.704019	0.351	0.585	4.92E-52
TBC1D9	2.65E-56	-0.628179521	0.206	0.414	5.45E-52
BCAR3	7.50E-55	-0.65356605	0.247	0.469	1.54E-50
FERMT2	1.98E-54	-0.642841661	0.483	0.694	4.07E-50
C4BPA	5.02E-54	1.291073815	0.317	0.104	1.03E-49
SLC25A48	5.73E-54	-0.755349537	0.072	0.208	1.18E-49
CRISPLD2	9.90E-54	1.138868143	0.461	0.249	2.04E-49
CLU	1.48E-53	1.732764818	0.426	0.239	3.05E-49
ADARB2	2.65E-53	-0.878340253	0.045	0.157	5.46E-49
EFNA5	2.95E-53	-0.889995421	0.288	0.491	6.08E-49
GC	4.64E-53	1.789849964	0.422	0.236	9.55E-49
RHOBTB3	5.21E-53	-0.646352219	0.3	0.519	1.07E-48
SERPINA1	1.87E-52	3.263961427	0.596	0.501	3.85E-48
PDE7B	2.66E-52	-0.722588393	0.383	0.596	5.47E-48
MGST1	2.84E-52	1.23052595	0.405	0.19	5.84E-48
IGFBP1	6.41E-52	1.468641078	0.241	0.042	1.32E-47
CPB2	1.09E-51	1.111691902	0.316	0.102	2.25E-47
ROBO1	1.25E-51	-0.646196706	0.522	0.725	2.57E-47
NAMPT	4.08E-51	0.868033827	0.358	0.133	8.40E-47
ARRB1	5.17E-51	-0.608418499	0.281	0.501	1.07E-46
FAM110B	5.47E-51	-0.639585753	0.18	0.369	1.13E-46
XIST	2.01E-50	-0.665484519	0.348	0.571	4.15E-46
EPB41L2	2.96E-50	-0.675146254	0.456	0.655	6.10E-46
RCS1	3.24E-49	-0.601002101	0.138	0.308	6.66E-45
CYP3A5	3.43E-49	0.956536134	0.454	0.238	7.05E-45
ADCY5	1.39E-48	-0.658538409	0.318	0.533	2.87E-44

SERPING1	1.74E-48	1.44648142	0.393	0.204	3.58E-44
PDE3B	4.11E-48	1.108279097	0.333	0.121	8.46E-44
CFB	4.22E-48	1.560887622	0.36	0.172	8.69E-44
PLG	7.89E-48	1.220803294	0.437	0.242	1.62E-43
HS3ST3B1	2.84E-47	-0.631462282	0.21	0.407	5.85E-43
DOCK6	4.99E-47	-0.652391945	0.202	0.39	1.03E-42
MAGI1	5.05E-47	0.828924981	0.539	0.327	1.04E-42
LBP	7.56E-47	1.035138158	0.21	0.03	1.56E-42
HPX	2.56E-46	1.433994599	0.408	0.23	5.28E-42
A2M	2.57E-46	1.161812563	0.518	0.359	5.29E-42
CARMIL1	2.79E-46	1.169937738	0.317	0.113	5.75E-42
ZBTB46	4.81E-46	-0.666255012	0.317	0.528	9.90E-42
ABCB4	4.99E-46	1.00339188	0.253	0.062	1.03E-41
KNG1	5.98E-46	1.435961207	0.412	0.238	1.23E-41
HP	7.73E-46	2.466079818	0.588	0.509	1.59E-41
KANK2	1.58E-45	-0.651329139	0.3	0.505	3.25E-41
ARHGAP24	1.62E-45	-0.636843409	0.648	0.794	3.34E-41
COLEC11	2.05E-45	-0.613602902	0.363	0.572	4.21E-41
EPAS1	2.67E-45	-0.590005667	0.523	0.709	5.50E-41
NGF	4.50E-45	-0.629181442	0.264	0.468	9.26E-41
ORM2	1.07E-44	1.821913786	0.364	0.195	2.20E-40
BAAT	1.58E-44	1.065022627	0.325	0.127	3.25E-40
F9	2.23E-44	1.014352894	0.214	0.038	4.58E-40
APOH	3.59E-44	1.753400855	0.508	0.388	7.40E-40
MTRNR2L12	1.05E-43	1.152508921	0.309	0.12	2.17E-39
LRG1	1.51E-43	1.076570919	0.182	0.018	3.11E-39
TARID	1.99E-43	-0.620323772	0.129	0.286	4.10E-39
P4HB	5.77E-42	1.06456633	0.311	0.125	1.19E-37
UGT2B4	1.09E-41	0.998724329	0.219	0.047	2.25E-37
TM4SF4	4.35E-41	0.893759912	0.208	0.038	8.95E-37
VTN	3.40E-40	1.539423806	0.463	0.337	6.99E-36
INSIG1	7.15E-40	0.970247489	0.243	0.069	1.47E-35
APCS	2.32E-39	1.085270315	0.285	0.109	4.77E-35
CYP3A7	3.03E-39	0.919893519	0.162	0.013	6.24E-35
C7	2.13E-38	0.669632622	0.617	0.422	4.38E-34
PPARGC1A	1.10E-37	0.716972669	0.221	0.052	2.25E-33
ALB	1.40E-37	2.054404726	0.923	0.92	2.88E-33
IL1RAPL1	5.00E-37	-0.731540299	0.136	0.278	1.03E-32
SLC39A14	7.14E-37	0.798330334	0.285	0.109	1.47E-32
FOXO1	8.83E-37	0.784377927	0.47	0.289	1.82E-32
SULT2A1	2.92E-36	0.841954679	0.241	0.075	6.02E-32
COL4A1	1.07E-35	1.296995257	0.484	0.349	2.20E-31
APOA1	1.45E-35	1.459079651	0.679	0.63	2.99E-31

SLC38A4	1.66E-35	0.945791235	0.318	0.149	3.42E-31
LEPR	4.72E-35	0.846187139	0.346	0.168	9.72E-31
MYO15B	4.72E-35	-0.594535608	0.192	0.353	9.72E-31
TIMP3	6.23E-35	1.052358343	0.283	0.111	1.28E-30
CFI	7.21E-35	0.842568579	0.314	0.143	1.48E-30
SCD	1.20E-34	1.095731696	0.178	0.034	2.48E-30
PALM2-AKAP2	2.43E-34	0.961030616	0.431	0.274	5.00E-30
KLF9	2.62E-34	0.752306246	0.225	0.068	5.40E-30
LPP	2.86E-34	0.600950694	0.851	0.848	5.89E-30
ANGPTL3	2.94E-34	0.929729009	0.233	0.077	6.05E-30
ITIH2	3.62E-34	1.098522167	0.273	0.115	7.46E-30
VMP1	5.91E-34	0.901760574	0.41	0.242	1.22E-29
PRG4	6.99E-34	0.847911941	0.181	0.038	1.44E-29
METTL7A	9.27E-34	0.959979101	0.264	0.106	1.91E-29
SAA4	1.33E-33	1.163249845	0.299	0.143	2.74E-29
PCK1	1.47E-33	0.962555767	0.3	0.134	3.02E-29
ADAMTS1	1.67E-33	0.902421783	0.191	0.044	3.44E-29
DUSP1	1.73E-33	0.863706585	0.161	0.024	3.55E-29
ERRFI1	1.93E-33	0.803357982	0.353	0.185	3.97E-29
RASAL2	2.00E-33	0.706339748	0.613	0.477	4.12E-29
ARHGAP10	6.61E-33	0.837858319	0.639	0.563	1.36E-28
C1R	7.75E-33	0.888501412	0.432	0.28	1.59E-28
POR	9.82E-33	0.744957051	0.301	0.132	2.02E-28
HSP90B1	1.15E-32	0.992067816	0.379	0.229	2.36E-28
SORBS2	1.72E-32	0.897979443	0.414	0.25	3.54E-28
CLSTN2	3.03E-32	1.040171059	0.369	0.202	6.24E-28
SERPINE1	4.19E-32	1.730774044	0.164	0.029	8.62E-28
AMBP	2.11E-31	1.485041627	0.501	0.42	4.35E-27
CTIF	2.14E-31	0.834739823	0.335	0.175	4.41E-27
CFHR2	2.76E-31	0.877086533	0.249	0.098	5.69E-27
AOX1	2.89E-31	0.846321495	0.275	0.118	5.96E-27
TAGLN	3.88E-31	0.753982353	0.161	0.029	7.98E-27
SERPINC1	7.68E-31	1.104412344	0.304	0.16	1.58E-26
ACSL1	1.92E-30	0.865934647	0.367	0.207	3.94E-26
F2	2.65E-30	0.942754104	0.289	0.139	5.46E-26
FGF13	2.79E-30	-0.785025427	0.209	0.354	5.75E-26
APOE	2.95E-30	1.257390314	0.567	0.5	6.08E-26
PPP1CB	1.02E-29	0.790817177	0.348	0.198	2.10E-25
NALCN	1.13E-29	0.595850568	0.399	0.212	2.32E-25
CACNA1C	2.74E-29	0.668884795	0.468	0.291	5.65E-25
DEPTOR	4.08E-29	0.925773008	0.233	0.088	8.40E-25
SPINK1	5.73E-29	0.68276643	0.105	0	1.18E-24
C8A	9.35E-29	0.749416145	0.224	0.083	1.92E-24

MAP1B	1.14E-28	0.837961154	0.286	0.13	2.34E-24
PLCG2	2.18E-28	1.096630707	0.394	0.263	4.48E-24
MERTK	2.44E-28	0.715989758	0.192	0.058	5.03E-24
ORM1	6.20E-28	2.136355209	0.441	0.362	1.28E-23
ATP13A3	1.87E-27	0.760698157	0.326	0.178	3.85E-23
ALDOB	2.17E-27	1.174498035	0.553	0.458	4.47E-23
MTTP	4.49E-27	0.725587238	0.174	0.049	9.24E-23
UGT2B7	7.95E-27	1.160811738	0.212	0.082	1.64E-22
MYO1E	2.59E-26	0.717542016	0.266	0.12	5.33E-22
HRG	2.82E-26	1.138696679	0.249	0.115	5.81E-22
ITGB5	3.10E-26	0.667474937	0.279	0.132	6.37E-22
SRPX2	3.75E-26	0.804104712	0.299	0.164	7.72E-22
CYP2C8	4.47E-26	0.680118464	0.437	0.291	9.20E-22
PRR16	1.24E-25	0.672909224	0.223	0.083	2.55E-21
SH3BP5	1.26E-25	0.823621026	0.196	0.071	2.60E-21
ITIH3	1.75E-25	0.747683568	0.262	0.122	3.60E-21
ROR2	2.11E-25	0.715969724	0.273	0.13	4.35E-21
TSC22D1	2.83E-25	0.733447069	0.414	0.276	5.83E-21
CALR	3.29E-25	0.778806114	0.226	0.096	6.77E-21
MAT1A	3.42E-25	0.980981548	0.306	0.173	7.05E-21
SLC2A2	4.88E-25	0.712907287	0.249	0.113	1.00E-20
C6	9.82E-25	0.665504488	0.284	0.143	2.02E-20
EFEMP1	1.21E-24	0.607936971	0.159	0.043	2.49E-20
FOXO3	2.65E-24	0.73495517	0.517	0.399	5.46E-20
PALLD	3.11E-24	0.809698484	0.443	0.314	6.41E-20
SDC1	3.44E-24	0.673341083	0.131	0.026	7.09E-20
CTSB	4.01E-24	0.6833898	0.21	0.084	8.26E-20
PVT1	4.39E-24	0.615642859	0.223	0.091	9.03E-20
ARG1	8.06E-24	0.703055525	0.217	0.091	1.66E-19
MYOM1	9.75E-24	0.649322357	0.227	0.097	2.01E-19
SLCO1B1	9.82E-24	0.72253965	0.306	0.172	2.02E-19
TMEM123	1.53E-23	0.718603938	0.232	0.105	3.15E-19
LAMA2	2.14E-23	0.731417655	0.797	0.802	4.40E-19
ATP1B3	3.57E-23	0.959756799	0.236	0.109	7.35E-19
PDK4	6.40E-23	1.02311138	0.359	0.236	1.32E-18
HGD	1.03E-22	0.720466496	0.254	0.125	2.12E-18
AASS	1.06E-22	0.695052909	0.385	0.255	2.18E-18
UGT2B15	1.08E-22	0.837955695	0.173	0.06	2.23E-18
PCSK6	1.31E-22	0.632896815	0.284	0.149	2.70E-18
LAMC3	1.48E-22	0.719351221	0.285	0.148	3.05E-18
PLIN2	1.50E-22	0.684543619	0.206	0.087	3.08E-18
ZFAND5	1.93E-22	0.708792322	0.283	0.154	3.97E-18
ABHD2	2.67E-22	0.658265106	0.323	0.194	5.50E-18

SELENOP	3.65E-22	0.974291085	0.469	0.384	7.50E-18
DDAH1	4.55E-22	0.841537583	0.268	0.14	9.36E-18
PKHD1	6.71E-22	0.645796965	0.16	0.051	1.38E-17
DHCR24	1.04E-21	0.670951206	0.178	0.067	2.14E-17
A1BG	1.08E-21	0.824002607	0.297	0.177	2.23E-17
WNK3	1.13E-21	0.623538459	0.139	0.037	2.33E-17
MTHFD1L	1.28E-21	0.710994555	0.204	0.084	2.64E-17
TMBIM6	1.29E-21	0.906168268	0.409	0.308	2.66E-17
PDLIM3	1.59E-21	0.693254831	0.171	0.06	3.27E-17
COL4A2	1.66E-21	0.764426614	0.583	0.506	3.41E-17
G6PC	2.15E-21	0.678711845	0.196	0.082	4.42E-17
GDA	2.24E-21	0.622929546	0.158	0.051	4.61E-17
B2M	2.90E-21	0.863223306	0.512	0.444	5.96E-17
SAMHD1	3.36E-21	0.671673589	0.219	0.1	6.91E-17
LMCD1	3.88E-21	0.724795715	0.182	0.069	7.98E-17
PIK3C2G	5.57E-21	0.595869623	0.232	0.109	1.15E-16
TIMP1	5.63E-21	0.714455068	0.184	0.072	1.16E-16
FTL	1.42E-20	0.692868466	0.549	0.434	2.91E-16
RUNX1	1.54E-20	0.610230834	0.238	0.115	3.18E-16
DEFB1	1.82E-20	0.596718825	0.112	0.022	3.74E-16
FOS	2.10E-20	0.678861754	0.113	0.021	4.32E-16
ARHGEF26	2.20E-20	0.641630408	0.201	0.086	4.53E-16
ASGR2	3.27E-20	0.607098748	0.173	0.066	6.74E-16
KLF6	5.36E-20	0.645287636	0.215	0.101	1.10E-15
HIF3A	8.81E-20	0.677950585	0.229	0.114	1.81E-15
STOM	1.37E-19	0.655830651	0.257	0.142	2.83E-15
CANX	1.52E-19	0.663588655	0.251	0.137	3.13E-15
NEXN	2.73E-19	0.597429435	0.347	0.221	5.62E-15
SLC38A2	4.62E-19	0.59598571	0.603	0.539	9.51E-15
NR4A1	1.72E-18	0.598370217	0.111	0.025	3.54E-14
SOD2	2.56E-18	0.630573793	0.303	0.187	5.26E-14
KLHL29	3.51E-18	0.613646848	0.348	0.224	7.22E-14
MYOF	5.45E-18	0.672811431	0.177	0.077	1.12E-13
CEBPD	9.58E-18	0.601197214	0.199	0.096	1.97E-13
ANOS1	1.29E-17	0.618042798	0.1	0.021	2.65E-13
KIF26B	1.70E-17	-0.762013858	0.225	0.33	3.50E-13
HSD17B6	1.88E-17	0.775641147	0.278	0.168	3.87E-13
THBS1	4.88E-17	0.849476731	0.245	0.14	1.00E-12
CTSD	4.95E-17	0.643058749	0.226	0.123	1.02E-12
SIPA1L1	1.68E-16	0.617828685	0.421	0.317	3.45E-12
SERPINF2	2.24E-16	0.670704365	0.249	0.147	4.61E-12
LINC00907	2.38E-16	0.835780926	0.187	0.092	4.90E-12
EEF1A1	3.43E-16	0.825659469	0.423	0.351	7.05E-12

MAMDC2	8.13E-16	0.651401288	0.201	0.101	1.67E-11
IL18R1	1.18E-15	0.585552219	0.147	0.06	2.44E-11
HAMP	1.66E-15	0.733229429	0.235	0.139	3.42E-11
CREB5	1.82E-15	0.676409496	0.116	0.038	3.74E-11
PAH	6.35E-15	0.58593976	0.304	0.201	1.31E-10
ACTB	1.17E-14	0.641418318	0.262	0.168	2.40E-10
ANG	3.69E-14	0.626518906	0.185	0.098	7.60E-10
CES1	6.68E-14	0.872827286	0.31	0.224	1.37E-09
FABP1	4.83E-13	0.659461989	0.356	0.262	9.93E-09
USP53	1.15E-12	0.590091013	0.462	0.389	2.38E-08
ITGAV	3.07E-12	0.613289704	0.313	0.231	6.32E-08
AZGP1	8.76E-12	0.67634748	0.293	0.217	1.80E-07
APOC3	1.94E-11	0.775177801	0.671	0.648	3.99E-07
APOC2	1.21E-10	0.708867781	0.487	0.458	2.49E-06
AHSG	1.30E-10	1.015321627	0.327	0.263	2.68E-06
FGFR2	2.79E-10	-0.621186056	0.476	0.545	5.73E-06
CDH19	2.39E-08	1.033324513	0.393	0.352	0.000492566
HPD	4.74E-08	0.600804294	0.25	0.186	0.000974717
RBP4	6.88E-08	0.641367833	0.533	0.517	0.001416311
GEM	8.12E-08	0.645619678	0.156	0.099	0.001672223

Supplementary Table 6

p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
0	2.047941777	0.91	0.235	0	VCAM1+ KC	NDST3
0	1.783595189	0.825	0.204	0	VCAM1+ KC	DSCAM
0	1.613944195	0.526	0.097	0	VCAM1+ KC	FGF13
0	1.567768348	0.667	0.132	0	VCAM1+ KC	CD5L
0	1.548067485	0.972	0.607	0	VCAM1+ KC	EXT1
0	1.47659686	0.642	0.144	0	VCAM1+ KC	VCAM1
0	1.406281036	0.803	0.217	0	VCAM1+ KC	KIAA1217
0	1.405874722	0.903	0.338	0	VCAM1+ KC	RBMS3
0	1.405520863	0.916	0.375	0	VCAM1+ KC	RGL1
0	1.402507332	0.864	0.328	0	VCAM1+ KC	CCDC26
0	1.368918706	0.925	0.422	0	VCAM1+ KC	MYO9A
0	1.355751818	0.497	0.074	0	VCAM1+ KC	UNC5C
0	1.331887569	0.772	0.226	0	VCAM1+ KC	EDA
0	1.31423081	0.968	0.614	0	VCAM1+ KC	SLC9A9
0	1.274531258	0.56	0.111	0	VCAM1+ KC	MPPED2
0	1.272375593	0.834	0.268	0	VCAM1+ KC	ME1
0	1.263639341	0.55	0.093	0	VCAM1+ KC	TMEM26
0	1.213692265	0.707	0.194	0	VCAM1+ KC	MARCO
0	1.203214319	0.937	0.457	0	VCAM1+ KC	EPB41L2
0	1.195569344	0.561	0.115	0	VCAM1+ KC	PIEZO2
0	1.18709616	0.978	0.627	0	VCAM1+ KC	FRMD4B
0	1.177813477	0.9	0.375	0	VCAM1+ KC	NCKAP5
0	1.161796256	0.845	0.283	0	VCAM1+ KC	ITGA9
0	1.160393641	0.954	0.452	0	VCAM1+ KC	CD163
0	1.146882263	0.891	0.426	0	VCAM1+ KC	PDE4B
0	1.142963605	0.713	0.251	0	VCAM1+ KC	PLD1
0	1.134128412	0.67	0.192	0	VCAM1+ KC	STON2
0	1.124339065	0.383	0.042	0	VCAM1+ KC	TIMD4
0	1.113019338	0.404	0.058	0	VCAM1+ KC	SOBP
0	1.11179285	0.587	0.14	0	VCAM1+ KC	ETV5
0	1.09882548	0.744	0.301	0	VCAM1+ KC	SLC40A1
0	1.098249071	0.465	0.085	0	VCAM1+ KC	ROR1
0	1.086487434	0.69	0.214	0	VCAM1+ KC	CR1
0	1.069032852	0.517	0.109	0	VCAM1+ KC	ITGAD
0	1.056637869	0.776	0.326	0	VCAM1+ KC	SPATS2L
0	1.053343935	0.689	0.24	0	VCAM1+ KC	SNX24
0	1.048301734	0.517	0.115	0	VCAM1+ KC	PIK3R3
0	1.047138931	0.867	0.46	0	VCAM1+ KC	WWP1
0	1.044470064	0.917	0.465	0	VCAM1+ KC	ITSN1
0	1.036155861	0.655	0.263	0	VCAM1+ KC	ANKRD36C

0	1.028879485	0.883	0.391	0	VCAM1+ KC	MRC1
0	1.023676384	0.816	0.407	0	VCAM1+ KC	ZFYVE16
0	1.022612229	0.979	0.599	0	VCAM1+ KC	FMNL2
0	1.005876157	0.829	0.372	0	VCAM1+ KC	PDGFC
0	1.003459475	0.778	0.285	0	VCAM1+ KC	PTPRM
0	1.003076068	0.678	0.23	0	VCAM1+ KC	GCNT1
0	1.001837819	0.824	0.396	0	VCAM1+ KC	NRP1
0	0.999110755	0.551	0.127	0	VCAM1+ KC	CXCL12
0	0.99123395	0.374	0.046	0	VCAM1+ KC	LINC01645
0	0.989323093	0.791	0.341	0	VCAM1+ KC	SAMSN1
0	0.980418471	0.574	0.16	0	VCAM1+ KC	RHOBTB1
0	0.976452074	0.657	0.211	0	VCAM1+ KC	CD163L1
0	0.971658428	0.47	0.142	0	VCAM1+ KC	HMOX1
0	0.964868901	0.419	0.096	0	VCAM1+ KC	LYVE1
0	0.960641643	0.623	0.236	0	VCAM1+ KC	LINC00342
0	0.960348091	0.759	0.337	0	VCAM1+ KC	ETNK1
0	0.95874304	0.947	0.442	0	VCAM1+ KC	KCNMA1
0	0.956669679	0.644	0.205	0	VCAM1+ KC	SLC22A23
0	0.951941694	0.336	0.079	0	VCAM1+ KC	PCAT1
0	0.943101699	0.634	0.212	0	VCAM1+ KC	MCOLN1
0	0.936973519	0.821	0.381	0	VCAM1+ KC	EXOC6B
0	0.934699506	0.612	0.196	0	VCAM1+ KC	CD38
0	0.934597779	0.834	0.422	0	VCAM1+ KC	ADAP2
0	0.931774298	0.961	0.558	0	VCAM1+ KC	TCF7L2
0	0.930275563	0.663	0.246	0	VCAM1+ KC	IL18
0	0.925523573	0.879	0.409	0	VCAM1+ KC	MERTK
0	0.922142732	0.769	0.418	0	VCAM1+ KC	PDK4
0	0.916347763	0.811	0.412	0	VCAM1+ KC	DLEU1
0	0.915558905	0.82	0.382	0	VCAM1+ KC	SNX9
0	0.915065343	0.435	0.111	0	VCAM1+ KC	NHS
0	0.91163519	0.68	0.272	0	VCAM1+ KC	LIPA
0	0.897912027	0.936	0.476	0	VCAM1+ KC	FRMD4A
0	0.88531816	0.829	0.384	0	VCAM1+ KC	TPRG1
0	0.88360682	0.76	0.324	0	VCAM1+ KC	MS4A4E
0	0.880927562	0.612	0.152	0	VCAM1+ KC	ADAMTS2
0	0.873440959	0.388	0.055	0	VCAM1+ KC	PHKA1
0	0.868348793	0.637	0.23	0	VCAM1+ KC	RAB20
0	0.864010757	0.34	0.045	0	VCAM1+ KC	SLC16A9
0	0.86220207	0.65	0.222	0	VCAM1+ KC	SPIRE1
0	0.858207201	0.84	0.392	0	VCAM1+ KC	PSD3
0	0.855472412	0.684	0.19	0	VCAM1+ KC	LILRB5
0	0.854378406	0.514	0.15	0	VCAM1+ KC	ANK3
0	0.85169395	0.927	0.623	0	VCAM1+ KC	WSB1

0	0.847553972	0.908	0.48	0	VCAM1+ KC	ABCA1
0	0.845790241	0.691	0.224	0	VCAM1+ KC	DYSF
0	0.845178417	0.558	0.187	0	VCAM1+ KC	MS4A4A
0	0.831471553	0.345	0.065	0	VCAM1+ KC	ZBTB7C
0	0.830653839	0.545	0.169	0	VCAM1+ KC	PYGL
0	0.828376831	0.522	0.133	0	VCAM1+ KC	TRPV4
0	0.828050549	0.703	0.273	0	VCAM1+ KC	TTC28
0	0.825874187	0.72	0.261	0	VCAM1+ KC	AXL
0	0.823361456	0.638	0.255	0	VCAM1+ KC	BASP1
0	0.8192518	0.423	0.118	0	VCAM1+ KC	PLEKHG1
0	0.81717367	0.266	0.038	0	VCAM1+ KC	ANKS1B
0	0.808833621	0.952	0.578	0	VCAM1+ KC	DST
0	0.804708575	0.667	0.233	0	VCAM1+ KC	PPARG
0	0.800304281	0.886	0.512	0	VCAM1+ KC	WDFY3
0	0.798211363	0.74	0.285	0	VCAM1+ KC	PTK2
0	0.797702088	0.658	0.25	0	VCAM1+ KC	THRB
0	0.794047559	0.723	0.316	0	VCAM1+ KC	ANKH
0	0.793687556	0.332	0.041	0	VCAM1+ KC	SPSB4
0	0.7906162	0.513	0.129	0	VCAM1+ KC	AC023590.1
0	0.78989629	0.469	0.138	0	VCAM1+ KC	VSIG4
0	0.789292124	0.823	0.394	0	VCAM1+ KC	MS4A7
0	0.779915835	0.359	0.082	0	VCAM1+ KC	ZNF704
0	0.777193198	0.557	0.18	0	VCAM1+ KC	DTNB
0	0.775925885	0.627	0.219	0	VCAM1+ KC	FARP1
0	0.770545361	0.89	0.521	0	VCAM1+ KC	MS4A6A
0	0.77038945	0.524	0.168	0	VCAM1+ KC	NR3C2
0	0.760342863	0.567	0.189	0	VCAM1+ KC	CMKLR1
0	0.756011469	0.936	0.608	0	VCAM1+ KC	DAPK1
0	0.752727352	0.943	0.556	0	VCAM1+ KC	MTSS1
0	0.752602176	0.447	0.128	0	VCAM1+ KC	HRH1
0	0.751926896	0.272	0.074	0	VCAM1+ KC	AGBL4
0	0.7513558	0.743	0.388	0	VCAM1+ KC	NRIP1
0	0.749964172	0.434	0.127	0	VCAM1+ KC	SPATA7
0	0.742220863	0.659	0.273	0	VCAM1+ KC	SAMD4A
0	0.740454876	0.763	0.376	0	VCAM1+ KC	SGMS1
0	0.738974623	0.675	0.281	0	VCAM1+ KC	TRIM14
0	0.73456826	0.886	0.469	0	VCAM1+ KC	FCHO2
0	0.733868173	0.332	0.054	0	VCAM1+ KC	KREMEN1
0	0.733129839	0.668	0.264	0	VCAM1+ KC	LGMN
0	0.732189242	0.679	0.279	0	VCAM1+ KC	C2CD5
0	0.731686684	0.423	0.118	0	VCAM1+ KC	SLC7A8
0	0.731338796	0.44	0.142	0	VCAM1+ KC	IFI44L
0	0.721018009	0.781	0.361	0	VCAM1+ KC	EPB41L3

0	0.720181462	0.308	0.091	0	VCAM1+ KC	CHSY3
0	0.717430835	0.722	0.25	0	VCAM1+ KC	SIGLEC1
0	0.71519987	0.81	0.364	0	VCAM1+ KC	SASH1
0	0.714798491	0.811	0.423	0	VCAM1+ KC	RAPGEF2
0	0.708353755	0.855	0.428	0	VCAM1+ KC	MSR1
0	0.708063358	0.506	0.171	0	VCAM1+ KC	MFHAS1
0	0.706554725	0.699	0.297	0	VCAM1+ KC	NPL
0	0.706336616	0.894	0.554	0	VCAM1+ KC	FHIT
0	0.701630242	0.663	0.303	0	VCAM1+ KC	GTDC1
0	0.699119954	0.335	0.089	0	VCAM1+ KC	TCF7L1
0	0.694959043	0.716	0.307	0	VCAM1+ KC	MVB12B
0	0.694778764	0.274	0.067	0	VCAM1+ KC	PTCH2
0	0.691501077	0.558	0.214	0	VCAM1+ KC	TMEM117
0	0.687005038	0.824	0.465	0	VCAM1+ KC	PHACTR2
0	0.674726447	0.428	0.123	0	VCAM1+ KC	BMPR1A
0	0.674707681	0.761	0.339	0	VCAM1+ KC	SLCO2B1
0	0.674298853	0.561	0.205	0	VCAM1+ KC	BLVRB
0	0.671195379	0.947	0.647	0	VCAM1+ KC	FNBP1
0	0.669487645	0.425	0.094	0	VCAM1+ KC	RGL3
0	0.666481682	0.803	0.406	0	VCAM1+ KC	CNTLN
0	0.666471476	0.403	0.083	0	VCAM1+ KC	SIGLEC11
0	0.663680838	0.79	0.4	0	VCAM1+ KC	ATP8B4
0	0.661156826	0.476	0.179	0	VCAM1+ KC	PLAC8
0	0.660539973	0.524	0.168	0	VCAM1+ KC	NR1H3
0	0.656326999	0.387	0.115	0	VCAM1+ KC	P2RY12
0	0.65412562	0.516	0.149	0	VCAM1+ KC	SDC3
0	0.639110067	0.718	0.362	0	VCAM1+ KC	STARD13
0	0.635913485	0.628	0.249	0	VCAM1+ KC	MKNK1
0	0.634918874	0.533	0.199	0	VCAM1+ KC	FAM20A
0	0.634039905	0.29	0.086	0	VCAM1+ KC	ABTB2
0	0.632546868	0.261	0.054	0	VCAM1+ KC	ITGA9-AS1
0	0.626073367	0.435	0.132	0	VCAM1+ KC	SH3PXD2A
0	0.623112637	0.685	0.333	0	VCAM1+ KC	LRCH1
0	0.621887693	0.389	0.124	0	VCAM1+ KC	LARGE1
0	0.620181849	0.492	0.189	0	VCAM1+ KC	FUT8
0	0.618239627	0.848	0.501	0	VCAM1+ KC	ANKS1A
0	0.614886355	0.62	0.266	0	VCAM1+ KC	APPL2
0	0.612625397	0.556	0.209	0	VCAM1+ KC	ARHGAP12
0	0.611707725	0.514	0.194	0	VCAM1+ KC	JDP2
0	0.610317174	0.77	0.399	0	VCAM1+ KC	SNX6
0	0.609930595	0.81	0.412	0	VCAM1+ KC	NFIA
0	0.609582419	0.945	0.67	0	VCAM1+ KC	TCF12
0	0.609193967	0.288	0.082	0	VCAM1+ KC	TNFRSF21

0	0.608283207	0.444	0.153	0	VCAM1+ KC	CREG1
0	0.606083697	0.643	0.289	0	VCAM1+ KC	ZNF124
0	0.600950542	0.755	0.412	0	VCAM1+ KC	HCLS1
0	0.592231264	0.45	0.151	0	VCAM1+ KC	TBC1D16
0	0.591642258	0.497	0.179	0	VCAM1+ KC	ITGB5
0	0.590112101	0.45	0.166	0	VCAM1+ KC	SRGAP3
0	0.588943186	0.935	0.659	0	VCAM1+ KC	ITPR2
0	0.587554302	0.871	0.549	0	VCAM1+ KC	ZNF609
0	0.587505413	0.703	0.341	0	VCAM1+ KC	SPRED1
0	0.586467043	0.803	0.439	0	VCAM1+ KC	AAK1
5.13E-200	0.71158108	0.933	0.95	1.06E-195	SAA1+ KC	ALB
1.39E-125	0.801089035	0.619	0.568	2.86E-121	SAA1+ KC	FGA
5.25E-122	0.754005625	0.748	0.8	1.08E-117	SAA1+ KC	APOC3
5.55E-110	0.769335766	0.633	0.607	1.14E-105	SAA1+ KC	FGB
9.59E-81	0.616183885	0.659	0.683	1.97E-76	SAA1+ KC	SERPINA1
2.12E-75	0.701838361	0.728	0.797	4.37E-71	SAA1+ KC	APOA1
4.22E-72	0.656721736	0.65	0.679	8.68E-68	SAA1+ KC	HP
4.90E-69	0.635433797	0.693	0.776	1.01E-64	SAA1+ KC	APOC1
3.34E-67	0.72882385	0.607	0.602	6.87E-63	SAA1+ KC	TF
4.14E-59	0.843685998	0.366	0.301	8.53E-55	SAA1+ KC	FGL1
6.17E-48	1.480946294	0.276	0.21	1.27E-43	SAA1+ KC	SAA1
2.31E-44	0.585982053	0.553	0.544	4.76E-40	SAA1+ KC	APOB
3.01E-43	0.859506044	0.413	0.372	6.20E-39	SAA1+ KC	MARCO
1.68E-40	0.673981823	0.554	0.585	3.47E-36	SAA1+ KC	AMBP
3.76E-38	0.754342895	0.324	0.273	7.74E-34	SAA1+ KC	SERPINA3
1.91E-37	0.869604253	0.417	0.423	3.94E-33	SAA1+ KC	SIGLEC1
3.32E-36	0.748851631	0.457	0.448	6.83E-32	SAA1+ KC	CPS1
8.88E-33	0.654925712	0.434	0.418	1.83E-28	SAA1+ KC	CP
3.48E-28	0.717895607	0.339	0.314	7.17E-24	SAA1+ KC	C9
7.50E-27	0.620715413	0.427	0.432	1.54E-22	SAA1+ KC	CFH
1.18E-26	0.737623784	0.321	0.293	2.43E-22	SAA1+ KC	TAT
1.31E-26	0.696350818	0.469	0.499	2.70E-22	SAA1+ KC	VTN
2.76E-26	0.605817432	0.587	0.671	5.68E-22	SAA1+ KC	APOE
3.02E-26	0.669222511	0.438	0.449	6.21E-22	SAA1+ KC	CLU
2.07E-22	0.586623057	0.474	0.493	4.26E-18	SAA1+ KC	C3
1.54E-21	0.734248874	0.362	0.372	3.17E-17	SAA1+ KC	LILRB5
1.66E-20	0.588945814	0.51	0.548	3.41E-16	SAA1+ KC	APOH
1.52E-19	0.633076213	0.455	0.495	3.13E-15	SAA1+ KC	CYP2E1
7.99E-19	0.665265756	0.459	0.514	1.64E-14	SAA1+ KC	MT2A
2.12E-16	0.683036887	0.317	0.315	4.36E-12	SAA1+ KC	CYP2C8
1.27E-15	0.641438044	0.359	0.366	2.61E-11	SAA1+ KC	PLG
3.10E-15	0.592375926	0.416	0.449	6.39E-11	SAA1+ KC	ADH1B
1.04E-14	0.688617909	0.313	0.318	2.15E-10	SAA1+ KC	CYP3A4

1.53E-14	0.695220259	0.301	0.299	3.15E-10	SAA1+ KC	SOX5
2.89E-14	0.627820369	0.355	0.364	5.95E-10	SAA1+ KC	HPX
4.49E-13	0.654299632	0.316	0.32	9.23E-09	SAA1+ KC	MGST1
2.01E-12	0.654277258	0.43	0.467	4.14E-08	SAA1+ KC	ORM1
3.42E-11	0.645123138	0.289	0.291	7.04E-07	SAA1+ KC	MAT1A
5.49E-10	0.738186934	0.311	0.322	1.13E-05	SAA1+ KC	RORA
1.79E-09	0.633122108	0.316	0.329	3.68E-05	SAA1+ KC	C1S
2.46E-09	0.695626819	0.272	0.285	5.06E-05	SAA1+ KC	SDC3
9.57E-09	0.599628826	0.276	0.278	0.000196887	SAA1+ KC	PCK1
4.26E-08	0.598025572	0.334	0.359	0.000876243	SAA1+ KC	CYP2C9
2.66E-07	0.595452549	0.253	0.255	0.005484771	SAA1+ KC	SLC38A4
0	1.61033975	0.415	0.047	0	ITGAX+ Mac	DTNA
0	1.539486915	0.611	0.262	0	ITGAX+ Mac	ALCAM
0	1.517678726	0.368	0.041	0	ITGAX+ Mac	ADAM28
0	1.376839057	0.511	0.156	0	ITGAX+ Mac	RTN1
0	1.374140285	0.568	0.194	0	ITGAX+ Mac	ITGAX
0	1.367624364	0.447	0.085	0	ITGAX+ Mac	ARHGAP22
0	1.356173402	0.526	0.228	0	ITGAX+ Mac	MYO1E
0	1.327914823	0.623	0.295	0	ITGAX+ Mac	SFMBT2
0	1.266507066	0.259	0.039	0	ITGAX+ Mac	BNC2
0	1.232098107	0.389	0.148	0	ITGAX+ Mac	HLA-DQA1
0	1.213032867	0.3	0.058	0	ITGAX+ Mac	ZNF804A
0	1.198664512	0.269	0.053	0	ITGAX+ Mac	DHRS9
0	1.174141393	0.906	0.705	0	ITGAX+ Mac	PLXDC2
0	1.166887178	0.409	0.18	0	ITGAX+ Mac	ARHGAP10
0	1.148899856	0.586	0.338	0	ITGAX+ Mac	HLA-DRA
0	1.121871025	0.285	0.048	0	ITGAX+ Mac	PCNX2
0	1.116039776	0.757	0.561	0	ITGAX+ Mac	CD74
0	1.114832134	0.517	0.243	0	ITGAX+ Mac	TANC2
0	1.113684995	0.392	0.114	0	ITGAX+ Mac	MGAT4A
0	1.091814243	0.474	0.232	0	ITGAX+ Mac	HLA-DPA1
0	1.054239502	0.596	0.345	0	ITGAX+ Mac	CIITA
0	1.043505838	0.507	0.228	0	ITGAX+ Mac	CSF2RA
0	1.026971525	0.352	0.084	0	ITGAX+ Mac	SPECC1
0	1.019725158	0.491	0.247	0	ITGAX+ Mac	HLA-DPB1
0	0.99716559	0.705	0.421	0	ITGAX+ Mac	FMN1
0	0.978186481	0.33	0.118	0	ITGAX+ Mac	HLA-DQB1
0	0.940105428	0.447	0.143	0	ITGAX+ Mac	XYLT1
0	0.916289782	0.359	0.128	0	ITGAX+ Mac	JAML
0	0.906566233	0.307	0.082	0	ITGAX+ Mac	TRPM2
0	0.890687805	0.33	0.093	0	ITGAX+ Mac	NAV1
0	0.88729236	0.325	0.119	0	ITGAX+ Mac	MYO1D
0	0.838950277	0.32	0.065	0	ITGAX+ Mac	RUNX2

0	0.825059974	0.319	0.094	0	ITGAX+ Mac	FCGR2A
0	0.7737017	0.387	0.161	0	ITGAX+ Mac	ITPR1
0	0.758549704	0.306	0.091	0	ITGAX+ Mac	TRERF1
0	0.757670491	0.309	0.11	0	ITGAX+ Mac	PCED1B
0	0.724927488	0.369	0.134	0	ITGAX+ Mac	PLXNC1
0	0.678233074	0.484	0.238	0	ITGAX+ Mac	CCSER1
7.47E-296	0.753913774	0.35	0.139	1.54E-291	ITGAX+ Mac	CDK14
5.40E-293	0.799000318	0.492	0.263	1.11E-288	ITGAX+ Mac	ARHGAP18
7.96E-287	0.743509965	0.439	0.215	1.64E-282	ITGAX+ Mac	ST3GAL6
1.43E-286	0.643651625	0.297	0.106	2.95E-282	ITGAX+ Mac	EMILIN2
1.99E-283	0.836454835	0.257	0.088	4.09E-279	ITGAX+ Mac	PALD1
4.54E-277	1.160997155	0.535	0.328	9.35E-273	ITGAX+ Mac	HLA-DRB1
4.99E-276	0.734748836	0.39	0.177	1.03E-271	ITGAX+ Mac	AHR
2.64E-256	0.794673262	0.507	0.28	5.44E-252	ITGAX+ Mac	ITGA4
3.30E-239	0.776561985	0.467	0.26	6.80E-235	ITGAX+ Mac	ZFP36L2
1.86E-226	0.615938791	0.287	0.121	3.82E-222	ITGAX+ Mac	BLNK
3.38E-225	0.696497112	0.444	0.244	6.96E-221	ITGAX+ Mac	GPRIN3
4.49E-224	0.602020983	0.342	0.154	9.23E-220	ITGAX+ Mac	AUTS2
1.94E-223	0.625621359	0.25	0.093	3.99E-219	ITGAX+ Mac	CREB5
4.28E-217	0.605855917	0.711	0.519	8.80E-213	ITGAX+ Mac	ANKRD44
4.06E-198	0.665108508	0.276	0.119	8.36E-194	ITGAX+ Mac	PALM2-AKAP2
3.38E-197	0.629987534	0.367	0.192	6.96E-193	ITGAX+ Mac	HLA-DMB
1.15E-195	0.689801065	0.551	0.361	2.37E-191	ITGAX+ Mac	ENTPD1
1.50E-195	0.700554682	0.272	0.121	3.10E-191	ITGAX+ Mac	VASH1
6.84E-187	0.645057415	0.423	0.245	1.41E-182	ITGAX+ Mac	SMURF2
3.11E-180	0.590816835	0.272	0.125	6.41E-176	ITGAX+ Mac	HLA-DMA
3.75E-180	0.687534967	0.752	0.594	7.71E-176	ITGAX+ Mac	CHST11
9.50E-175	0.801081941	0.289	0.141	1.95E-170	ITGAX+ Mac	HLA-DRB5
2.73E-172	0.644717317	0.355	0.193	5.61E-168	ITGAX+ Mac	OGFRL1
2.64E-171	1.14914527	0.303	0.162	5.42E-167	ITGAX+ Mac	GPNMB
3.09E-171	0.629380198	0.253	0.113	6.36E-167	ITGAX+ Mac	TESK2
1.13E-165	0.626853347	0.254	0.114	2.32E-161	ITGAX+ Mac	SH3PXD2B
1.25E-164	0.735407932	0.312	0.162	2.56E-160	ITGAX+ Mac	SGK1
7.39E-159	0.666809312	0.354	0.199	1.52E-154	ITGAX+ Mac	SLC39A10
3.54E-158	0.602739783	0.29	0.143	7.30E-154	ITGAX+ Mac	SLC41A2
1.26E-156	0.592048657	0.36	0.201	2.58E-152	ITGAX+ Mac	IL13RA1
1.62E-152	0.615012324	0.45	0.287	3.34E-148	ITGAX+ Mac	FPR3
2.00E-152	0.591271217	0.462	0.299	4.12E-148	ITGAX+ Mac	PDE7A
3.10E-152	0.680367164	0.28	0.142	6.37E-148	ITGAX+ Mac	CKLF
9.51E-148	0.63729853	0.689	0.559	1.96E-143	ITGAX+ Mac	MEF2C
8.34E-147	0.613435509	0.552	0.393	1.72E-142	ITGAX+ Mac	DENND4C
1.57E-143	0.679804812	0.252	0.122	3.23E-139	ITGAX+ Mac	CD83
2.02E-139	0.66456729	0.442	0.289	4.15E-135	ITGAX+ Mac	ENTPD1-AS1

2.80E-129	0.614776765	0.362	0.215	5.77E-125	ITGAX+ Mac	ATP13A3
2.12E-118	0.60412128	0.428	0.287	4.36E-114	ITGAX+ Mac	PAK1
3.91E-103	0.913215432	0.514	0.403	8.06E-99	ITGAX+ Mac	AFF3
2.01E-93	0.604399822	0.495	0.374	4.13E-89	ITGAX+ Mac	SRGAP1
7.00E-89	0.724359722	0.312	0.202	1.44E-84	ITGAX+ Mac	MGLL
4.84E-75	0.724633502	0.361	0.249	9.96E-71	ITGAX+ Mac	CST3
3.17E-47	0.586192061	0.255	0.173	6.52E-43	ITGAX+ Mac	ATP1B3
0	3.337913198	0.451	0.037	0	VCAN+ Mono	VCAN
0	2.73845815	0.506	0.022	0	VCAN+ Mono	FCN1
0	1.860239885	0.469	0.147	0	VCAN+ Mono	RAP1GAP2
0	1.84727231	0.694	0.467	0	VCAN+ Mono	LYST
0	1.770212832	0.429	0.192	0	VCAN+ Mono	PLCB1
0	1.704452115	0.465	0.096	0	VCAN+ Mono	SLC11A1
0	1.653738081	0.359	0.093	0	VCAN+ Mono	TMTC2
0	1.619339108	0.586	0.274	0	VCAN+ Mono	SLCO3A1
0	1.608030216	0.352	0.091	0	VCAN+ Mono	S100Z
0	1.598233219	0.277	0.033	0	VCAN+ Mono	GLT1D1
0	1.54969105	0.545	0.281	0	VCAN+ Mono	LRRK2
0	1.546529622	0.469	0.151	0	VCAN+ Mono	XYLT1
0	1.539479585	0.346	0.077	0	VCAN+ Mono	MNDA
0	1.440062024	0.504	0.266	0	VCAN+ Mono	CPPED1
0	1.433996788	0.339	0.118	0	VCAN+ Mono	SVIL
0	1.433942993	0.44	0.146	0	VCAN+ Mono	FYN
0	1.427729489	0.399	0.129	0	VCAN+ Mono	FGR
0	1.41432876	0.451	0.216	0	VCAN+ Mono	MEGF9
0	1.368950057	0.43	0.22	0	VCAN+ Mono	ITGAL
0	1.366837728	0.311	0.071	0	VCAN+ Mono	PRAM1
0	1.299925321	0.375	0.135	0	VCAN+ Mono	MAP4K4
0	1.268880612	0.727	0.537	0	VCAN+ Mono	ARHGAP26
0	1.26884508	0.327	0.116	0	VCAN+ Mono	LYZ
0	1.24524201	0.278	0.058	0	VCAN+ Mono	TRAF3IP3
0	1.233029662	0.446	0.232	0	VCAN+ Mono	STK38
0	1.220605847	0.287	0.091	0	VCAN+ Mono	CREB5
0	1.213241309	0.383	0.141	0	VCAN+ Mono	PLXNC1
0	1.193210568	0.343	0.112	0	VCAN+ Mono	SULF2
0	1.176987062	0.428	0.188	0	VCAN+ Mono	RTN1
0	1.142528789	0.366	0.136	0	VCAN+ Mono	JAML
0	1.107559187	0.69	0.594	0	VCAN+ Mono	CTSS
0	1.001792101	0.799	0.743	0	VCAN+ Mono	PTPRC
1.93E-307	1.121415492	0.274	0.092	3.98E-303	VCAN+ Mono	KSR1
5.69E-300	1.291456546	0.406	0.194	1.17E-295	VCAN+ Mono	SORL1
8.29E-299	1.207904699	0.401	0.193	1.71E-294	VCAN+ Mono	IL17RA
2.07E-297	0.944264917	0.682	0.532	4.26E-293	VCAN+ Mono	ANKRD44

3.74E-277	1.167316732	0.494	0.292	7.69E-273	VCAN+ Mono	ITGA4
7.18E-277	0.891506658	0.775	0.719	1.48E-272	VCAN+ Mono	SSH2
4.00E-270	1.335752224	0.443	0.252	8.24E-266	VCAN+ Mono	FRY
5.33E-269	1.321755176	0.465	0.273	1.10E-264	VCAN+ Mono	CLEC12A
3.94E-247	0.993037489	0.61	0.438	8.11E-243	VCAN+ Mono	SIPA1L1
9.15E-241	1.061314995	0.378	0.193	1.88E-236	VCAN+ Mono	VSIR
1.45E-237	1.137360129	0.417	0.231	2.98E-233	VCAN+ Mono	NLRP1
5.05E-235	1.153135424	0.45	0.271	1.04E-230	VCAN+ Mono	COTL1
2.50E-234	1.210590861	0.305	0.132	5.14E-230	VCAN+ Mono	ST6GALNAC3
1.93E-232	0.995757487	0.614	0.473	3.97E-228	VCAN+ Mono	IRAK3
5.00E-230	0.610989537	0.955	0.946	1.03E-225	VCAN+ Mono	NEAT1
5.06E-225	0.939106201	0.658	0.557	1.04E-220	VCAN+ Mono	NUMB
7.41E-223	0.955095043	0.256	0.1	1.53E-218	VCAN+ Mono	LILRB3
1.10E-221	0.992274566	0.331	0.157	2.26E-217	VCAN+ Mono	FMNL1
7.11E-216	1.20077432	0.483	0.322	1.46E-211	VCAN+ Mono	POU2F2
5.02E-214	1.099797439	0.515	0.361	1.03E-209	VCAN+ Mono	TNFRSF1B
1.16E-205	0.987940934	0.253	0.104	2.39E-201	VCAN+ Mono	CCDC88C
2.84E-197	1.046436589	0.406	0.241	5.84E-193	VCAN+ Mono	PILRA
3.86E-197	0.831721505	0.652	0.545	7.95E-193	VCAN+ Mono	SMAP2
2.55E-194	0.842428869	0.426	0.239	5.26E-190	VCAN+ Mono	ITGAX
1.07E-189	0.994177119	0.316	0.16	2.21E-185	VCAN+ Mono	NCF2
4.57E-184	0.877441368	0.72	0.68	9.40E-180	VCAN+ Mono	LYN
1.50E-183	0.66964073	0.775	0.736	3.09E-179	VCAN+ Mono	FOXP1
2.36E-183	0.796837247	0.271	0.119	4.86E-179	VCAN+ Mono	EMILIN2
1.79E-179	0.922290181	0.281	0.131	3.68E-175	VCAN+ Mono	RASSF2
9.53E-179	0.909150681	0.28	0.132	1.96E-174	VCAN+ Mono	KIAA0513
6.99E-172	0.972433405	0.416	0.258	1.44E-167	VCAN+ Mono	ADGRE2
3.01E-162	0.732548826	0.717	0.687	6.21E-158	VCAN+ Mono	USP15
1.02E-154	0.890837018	0.53	0.422	2.11E-150	VCAN+ Mono	USP3
5.64E-150	0.827877657	0.325	0.177	1.16E-145	VCAN+ Mono	AHNAK
5.07E-149	0.863440307	0.419	0.269	1.04E-144	VCAN+ Mono	JAZF1
4.26E-146	0.724321556	0.692	0.634	8.77E-142	VCAN+ Mono	VMP1
1.13E-141	0.672088444	0.814	0.83	2.32E-137	VCAN+ Mono	AOAH
4.58E-130	0.913354882	0.483	0.379	9.43E-126	VCAN+ Mono	AGTPBP1
5.12E-130	0.784781794	0.255	0.131	1.05E-125	VCAN+ Mono	ITGB2
1.59E-128	0.788628077	0.351	0.217	3.28E-124	VCAN+ Mono	DIAPH1
2.21E-127	0.822167345	0.599	0.545	4.56E-123	VCAN+ Mono	BACH1
2.23E-127	0.595527116	0.756	0.76	4.60E-123	VCAN+ Mono	MED13L
1.92E-126	0.705059959	0.654	0.597	3.95E-122	VCAN+ Mono	SIK3
5.36E-125	0.899031783	0.584	0.534	1.10E-120	VCAN+ Mono	SCLT1
1.36E-119	0.829495804	0.256	0.138	2.80E-115	VCAN+ Mono	PIGX
3.60E-119	0.865684104	0.422	0.299	7.40E-115	VCAN+ Mono	ALOX5
4.12E-119	0.799462254	0.454	0.325	8.48E-115	VCAN+ Mono	TXNIP

1.19E-118	0.903426618	0.423	0.313	2.44E-114	VCAN+ Mono	FBXL5
1.82E-116	0.78691441	0.353	0.223	3.75E-112	VCAN+ Mono	TIAM1
7.46E-116	0.829504818	0.331	0.204	1.54E-111	VCAN+ Mono	PELI2
1.23E-115	0.950256944	0.275	0.155	2.52E-111	VCAN+ Mono	WARS
8.93E-114	0.974454355	0.367	0.252	1.84E-109	VCAN+ Mono	LILRB2
1.77E-100	0.882189201	0.436	0.345	3.65E-96	VCAN+ Mono	MAP3K1
3.99E-98	0.761872243	0.457	0.36	8.22E-94	VCAN+ Mono	SH3KBP1
1.26E-97	0.838970881	0.461	0.371	2.60E-93	VCAN+ Mono	PHF21A
9.54E-95	0.866857839	0.402	0.3	1.96E-90	VCAN+ Mono	TYMP
3.63E-94	0.723479575	0.464	0.377	7.46E-90	VCAN+ Mono	NOTCH2
3.93E-90	0.938327735	0.258	0.157	8.08E-86	VCAN+ Mono	RNF24
8.84E-90	0.970652303	0.422	0.343	1.82E-85	VCAN+ Mono	PECAM1
2.57E-89	0.801683749	0.295	0.191	5.30E-85	VCAN+ Mono	SEMA4D
1.20E-88	0.821433061	0.375	0.277	2.48E-84	VCAN+ Mono	DENND5A
1.73E-87	0.660000026	0.262	0.156	3.56E-83	VCAN+ Mono	BTG1
2.26E-83	0.776809871	0.548	0.504	4.65E-79	VCAN+ Mono	HCK
2.87E-80	0.651818755	0.258	0.16	5.91E-76	VCAN+ Mono	HK1
1.51E-78	0.705659593	0.371	0.273	3.11E-74	VCAN+ Mono	ZDHHC20
2.27E-76	0.783162806	0.375	0.283	4.66E-72	VCAN+ Mono	TBL1X
1.60E-69	0.72359103	0.37	0.281	3.29E-65	VCAN+ Mono	PCNX1
3.20E-68	0.668814141	0.339	0.249	6.58E-64	VCAN+ Mono	MYH9
4.07E-68	0.706390679	0.405	0.328	8.37E-64	VCAN+ Mono	ERICH1
8.01E-68	0.651094938	0.444	0.365	1.65E-63	VCAN+ Mono	CHST15
2.69E-67	0.655726853	0.345	0.255	5.54E-63	VCAN+ Mono	CSGALNACT2
3.69E-66	0.706092071	0.405	0.324	7.60E-62	VCAN+ Mono	CTBP2
9.42E-66	0.587764791	0.576	0.551	1.94E-61	VCAN+ Mono	LRRFIP1
1.11E-64	0.720213942	0.435	0.366	2.29E-60	VCAN+ Mono	RASSF3
4.12E-64	0.664298555	0.47	0.415	8.48E-60	VCAN+ Mono	UBE2R2
1.95E-62	0.671296886	0.432	0.366	4.02E-58	VCAN+ Mono	HIPK3
2.23E-62	0.596398123	0.278	0.187	4.59E-58	VCAN+ Mono	TTC39C
9.16E-60	0.708481205	0.281	0.2	1.88E-55	VCAN+ Mono	RYBP
3.14E-59	0.773506163	0.323	0.238	6.47E-55	VCAN+ Mono	MTRNR2L12
4.15E-59	0.70079986	0.253	0.169	8.54E-55	VCAN+ Mono	GCH1
3.29E-58	0.633035915	0.405	0.334	6.78E-54	VCAN+ Mono	PSEN1
1.65E-57	0.688093613	0.36	0.284	3.39E-53	VCAN+ Mono	SPI1
2.13E-57	0.633357641	0.285	0.204	4.38E-53	VCAN+ Mono	FGD3
2.50E-57	0.701846505	0.354	0.28	5.14E-53	VCAN+ Mono	MTMR3
2.95E-57	0.953238709	0.455	0.417	6.08E-53	VCAN+ Mono	CSF3R
1.42E-56	0.729485598	0.318	0.241	2.92E-52	VCAN+ Mono	HDAC4
6.22E-56	0.611073827	0.434	0.375	1.28E-51	VCAN+ Mono	ATP11A
3.04E-54	0.67900225	0.481	0.432	6.27E-50	VCAN+ Mono	NEDD9
5.88E-53	0.608085201	0.416	0.347	1.21E-48	VCAN+ Mono	PITPNC1
7.12E-52	0.654755201	0.43	0.367	1.46E-47	VCAN+ Mono	ACTB

4.28E-50	0.589027073	0.272	0.198	8.82E-46	VCAN+ Mono	PTP4A2
2.62E-49	0.869714125	0.699	0.673	5.39E-45	VCAN+ Mono	SERPINA1
2.71E-47	0.634285711	0.425	0.369	5.57E-43	VCAN+ Mono	PRKCE
1.14E-46	0.703993601	0.28	0.211	2.34E-42	VCAN+ Mono	TTC7A
2.87E-43	0.627466279	0.316	0.248	5.90E-39	VCAN+ Mono	ZMIZ1
1.94E-42	0.631449396	0.268	0.202	4.00E-38	VCAN+ Mono	KCNQ1
3.04E-42	0.602380055	0.31	0.241	6.26E-38	VCAN+ Mono	SLC43A2
7.79E-41	0.612108613	0.294	0.229	1.60E-36	VCAN+ Mono	ZNF516
2.19E-39	0.65173498	0.352	0.296	4.52E-35	VCAN+ Mono	ADGRE5
8.60E-39	0.654457982	0.388	0.346	1.77E-34	VCAN+ Mono	MAPK14
5.30E-38	0.586883348	0.478	0.455	1.09E-33	VCAN+ Mono	FBXW7
9.30E-36	1.090988189	0.277	0.213	1.92E-31	VCAN+ Mono	SAA1
5.58E-31	0.777129384	0.373	0.343	1.15E-26	VCAN+ Mono	LST1
5.05E-20	0.587703131	0.489	0.497	1.04E-15	VCAN+ Mono	IKZF1
8.54E-20	0.734337978	0.646	0.678	1.76E-15	VCAN+ Mono	HP
1.03E-19	0.64829202	0.28	0.235	2.11E-15	VCAN+ Mono	ZBTB16
3.35E-16	0.765388146	0.454	0.46	6.89E-12	VCAN+ Mono	ORM1
4.16E-16	0.807679326	0.557	0.583	8.57E-12	VCAN+ Mono	FGA
2.91E-15	0.734954773	0.584	0.619	5.99E-11	VCAN+ Mono	FGB
6.20E-14	0.883048953	0.306	0.279	1.28E-09	VCAN+ Mono	SERPINA3
1.60E-12	0.672441338	0.529	0.549	3.29E-08	VCAN+ Mono	APOB
4.22E-12	0.773862345	0.522	0.547	8.69E-08	VCAN+ Mono	FGG
3.98E-09	0.692400276	0.322	0.313	8.20E-05	VCAN+ Mono	FGL1
0	5.036536926	0.951	0.016	0	mDC	CLNK
0	4.292798361	0.978	0.273	0	mDC	CCSER1
0	3.969326281	0.985	0.392	0	mDC	WDFY4
0	3.950747452	0.654	0.036	0	mDC	SDK1
0	3.617843939	0.866	0.051	0	mDC	NEGR1
0	3.570181446	0.915	0.081	0	mDC	FLT3
0	3.355631185	0.888	0.139	0	mDC	CADM1
0	3.277147083	0.937	0.176	0	mDC	AUTS2
0	3.251249732	0.798	0.034	0	mDC	NCALD
0	2.93069511	0.766	0.039	0	mDC	TOX
0	2.617156044	0.618	0.013	0	mDC	IDO1
0	2.576474437	0.912	0.4	0	mDC	CAMK2D
0	2.538017477	0.672	0.05	0	mDC	P2RY14
0	2.446004616	0.703	0.079	0	mDC	SLC24A4
0	2.441207532	0.551	0.008	0	mDC	ENOX1
0	2.425583095	0.582	0.007	0	mDC	CLEC9A
0	2.359758594	0.654	0.102	0	mDC	ZNF366
0	2.310259837	0.552	0.03	0	mDC	RAB7B
0	2.271840409	0.745	0.1	0	mDC	ZEB1
0	2.188326966	0.852	0.292	0	mDC	DENND1B

0	2.187836313	0.602	0.058	0	mDC	SLAMF7
0	2.166006931	0.711	0.171	0	mDC	VAC14
0	2.153923213	0.568	0.026	0	mDC	KCND3
0	2.098302385	0.637	0.132	0	mDC	DNASE1L3
0	2.096612722	0.777	0.228	0	mDC	NUBPL
0	2.087629062	0.638	0.088	0	mDC	ENPP1
0	2.05614111	0.563	0.031	0	mDC	IDO2
0	2.020987845	0.672	0.123	0	mDC	TRERF1
0	1.942289172	0.654	0.096	0	mDC	ADAM28
0	1.934137136	0.4	0.001	0	mDC	XCR1
0	1.893191238	0.597	0.079	0	mDC	CPNE3
0	1.881445394	0.509	0.042	0	mDC	C1orf21
0	1.731684431	0.497	0.041	0	mDC	ADAM19
0	1.645543135	0.354	0.004	0	mDC	SLCO5A1
0	1.594678932	0.402	0.008	0	mDC	BTLA
0	1.580166996	0.48	0.058	0	mDC	ST18
0	1.571911817	0.463	0.053	0	mDC	AKAP6
0	1.543692294	0.32	0.017	0	mDC	ARHGAP20
0	1.533683384	0.548	0.086	0	mDC	PCNX2
0	1.474576784	0.472	0.055	0	mDC	MCOLN2
0	1.451113655	0.403	0.048	0	mDC	CBFA2T3
0	1.388455545	0.3	0.011	0	mDC	AP000462.1
0	1.377138963	0.269	0.004	0	mDC	PAK3
0	1.37608636	0.418	0.056	0	mDC	AIM2
0	1.333007812	0.34	0.024	0	mDC	LINC00299
0	1.293155818	0.295	0.012	0	mDC	PARM1
0	1.284263816	0.351	0.028	0	mDC	CCDC122
0	1.254894456	0.252	0.004	0	mDC	PDE1C
0	1.196433907	0.323	0.032	0	mDC	BATF3
0	1.169963552	0.277	0.014	0	mDC	MYEF2
0	1.082116192	0.268	0.016	0	mDC	CYYR1
2.95E-307	1.598143002	0.665	0.14	6.07E-303	mDC	SULF2
3.99E-303	1.577895846	0.437	0.062	8.20E-299	mDC	LDLRAD3
2.35E-296	2.038138409	0.991	0.744	4.84E-292	mDC	HDAC9
4.32E-295	1.515795976	0.5	0.084	8.88E-291	mDC	SLC9A7
1.77E-293	1.859576106	0.638	0.149	3.65E-289	mDC	SNX3
2.94E-288	0.930579146	0.292	0.029	6.04E-284	mDC	DPP4
2.15E-276	1.228511037	0.403	0.056	4.43E-272	mDC	SLC38A1
1.43E-274	2.035635401	0.669	0.18	2.94E-270	mDC	PLEKHM3
4.49E-272	1.84330303	0.655	0.162	9.25E-268	mDC	BCL6
5.75E-270	1.196534341	0.382	0.051	1.18E-265	mDC	IL18R1
4.99E-269	0.979444276	0.269	0.026	1.03E-264	mDC	LGALS2
2.71E-265	2.160339162	0.943	0.569	5.58E-261	mDC	CPVL

2.08E-264	1.168402402	0.326	0.04	4.29E-260	mDC	AP3M2
2.02E-263	1.511705692	0.469	0.082	4.17E-259	mDC	GNG7
8.05E-257	1.084367829	0.338	0.043	1.66E-252	mDC	NET1
9.19E-254	1.630003813	0.56	0.123	1.89E-249	mDC	SAMD12
3.05E-250	1.186105957	0.371	0.052	6.27E-246	mDC	CARD11
3.54E-249	1.576609004	0.603	0.146	7.29E-245	mDC	PPM1H
1.77E-243	1.808441477	0.772	0.273	3.63E-239	mDC	KIF16B
5.07E-242	1.652527312	0.614	0.151	1.04E-237	mDC	MYO1D
8.92E-242	1.990080517	0.718	0.237	1.84E-237	mDC	IRF8
5.19E-237	1.57074464	0.558	0.126	1.07E-232	mDC	ZBTB46
1.80E-235	1.494010873	0.489	0.099	3.70E-231	mDC	INPP5F
2.07E-231	1.103713265	0.308	0.039	4.26E-227	mDC	DAPK2
1.68E-222	1.808572778	0.665	0.192	3.46E-218	mDC	PLPP1
5.75E-220	1.330295918	0.48	0.097	1.18E-215	mDC	PTPN22
2.71E-218	1.676701413	0.698	0.226	5.58E-214	mDC	CCDC6
6.56E-218	1.050266552	0.397	0.067	1.35E-213	mDC	PAWR
2.94E-210	0.987532582	0.331	0.049	6.06E-206	mDC	MYLK
4.30E-210	1.336739206	0.531	0.124	8.86E-206	mDC	ELOVL5
2.38E-208	1.641805604	0.769	0.286	4.89E-204	mDC	HLA-DPB1
6.30E-207	1.514097103	0.545	0.132	1.30E-202	mDC	NAV1
5.73E-203	0.84011835	0.254	0.031	1.18E-198	mDC	RAB30
7.84E-203	1.662409284	0.792	0.316	1.61E-198	mDC	LRRK2
2.50E-199	0.914992618	0.303	0.043	5.14E-195	mDC	HSH2D
4.25E-196	1.360355637	0.654	0.186	8.75E-192	mDC	FYN
9.89E-195	1.25900771	0.455	0.099	2.04E-190	mDC	RGS10
1.40E-193	1.561369463	0.683	0.237	2.88E-189	mDC	FAM135A
1.47E-191	1.596848735	0.875	0.524	3.02E-187	mDC	SHTN1
2.54E-189	1.238218924	0.382	0.072	5.24E-185	mDC	MAP2K6
3.90E-189	1.105131595	0.426	0.085	8.03E-185	mDC	NUP210
8.68E-188	1.57549554	0.582	0.164	1.79E-183	mDC	SLC41A2
6.91E-184	1.384997712	0.949	0.672	1.42E-179	mDC	ASAP1
7.31E-184	1.202062674	0.38	0.074	1.50E-179	mDC	TSPAN33
1.88E-182	1.655761558	0.551	0.16	3.87E-178	mDC	C1orf54
1.52E-180	1.635123102	0.817	0.387	3.13E-176	mDC	CIITA
5.10E-178	1.369788727	0.503	0.13	1.05E-173	mDC	KCNK6
3.23E-173	1.052085173	0.334	0.06	6.64E-169	mDC	CCDC126
9.82E-171	1.520242917	0.777	0.378	2.02E-166	mDC	PIK3CB
3.53E-166	1.395974041	0.932	0.731	7.26E-162	mDC	ETV6
1.78E-165	0.954764478	0.328	0.059	3.67E-161	mDC	LINC00877
4.51E-160	1.51298064	0.812	0.432	9.28E-156	mDC	SPPL3
1.47E-157	1.173481052	0.432	0.101	3.02E-153	mDC	ANPEP
1.91E-155	1.272572182	0.952	0.792	3.93E-151	mDC	LPP
3.48E-155	1.458157028	0.748	0.326	7.17E-151	mDC	PACS1

3.69E-153	0.90091212	0.357	0.072	7.60E-149	mDC	BCL11A
1.44E-152	1.453011904	0.835	0.442	2.97E-148	mDC	PTK2
2.21E-152	1.119946869	0.348	0.071	4.55E-148	mDC	PRELID2
4.13E-152	1.208187127	0.512	0.143	8.50E-148	mDC	PALM2-AKAP2
1.06E-151	1.587986569	0.9	0.595	2.18E-147	mDC	CD74
2.46E-149	0.926084954	0.355	0.074	5.07E-145	mDC	FLNB
2.50E-149	0.997318541	0.391	0.088	5.15E-145	mDC	USP53
1.19E-148	1.258452873	0.529	0.159	2.44E-144	mDC	OFD1
2.67E-146	1.114771759	0.442	0.116	5.50E-142	mDC	LY75
1.06E-144	1.442096733	0.682	0.273	2.18E-140	mDC	HLA-DPA1
3.75E-144	1.227842753	0.525	0.162	7.72E-140	mDC	DAPP1
3.63E-143	1.115877156	0.935	0.699	7.48E-139	mDC	RABGAP1L
5.21E-143	1.298248271	0.512	0.153	1.07E-138	mDC	HLA-DQB1
1.24E-142	1.364348601	0.445	0.118	2.55E-138	mDC	SERPINB9
1.32E-142	1.342690032	0.569	0.189	2.73E-138	mDC	HLA-DQA1
8.48E-142	1.033746581	0.335	0.07	1.75E-137	mDC	LINC01725
1.98E-140	1.466245078	0.8	0.432	4.07E-136	mDC	NEDD9
6.59E-140	1.135263043	0.463	0.126	1.36E-135	mDC	SCMH1
2.54E-139	1.428335125	0.706	0.298	5.23E-135	mDC	SIPA1L3
7.04E-138	0.924583033	0.354	0.077	1.45E-133	mDC	PATJ
1.43E-137	1.485213988	0.845	0.503	2.95E-133	mDC	VAV3
4.77E-137	1.08821732	0.852	0.416	9.82E-133	mDC	AFF3
1.04E-136	1.297650722	0.657	0.255	2.14E-132	mDC	PLEKHA5
3.19E-136	1.196101213	0.695	0.276	6.56E-132	mDC	CSF2RA
2.07E-135	0.866099797	0.298	0.058	4.26E-131	mDC	AP1S3
2.83E-135	1.106815233	0.474	0.131	5.84E-131	mDC	SPECC1
3.86E-131	1.302072727	0.849	0.507	7.94E-127	mDC	RUNX1
4.31E-131	1.128638197	0.878	0.551	8.88E-127	mDC	ANKRD44
2.69E-130	1.271739092	0.64	0.253	5.54E-126	mDC	KIAA1958
3.92E-129	0.867737749	0.329	0.071	8.06E-125	mDC	LSP1
6.73E-128	1.204970476	0.606	0.232	1.39E-123	mDC	ZNF516
1.83E-127	1.260212218	0.629	0.246	3.78E-123	mDC	RUBCNL
3.00E-125	1.239524879	0.595	0.23	6.17E-121	mDC	NLRC5
4.16E-125	1.219208611	0.492	0.158	8.57E-121	mDC	MIR4435-2HG
1.47E-123	0.823990083	0.285	0.057	3.03E-119	mDC	ITGB2-AS1
1.12E-122	1.177968792	0.502	0.165	2.30E-118	mDC	CD226
2.67E-122	1.160752624	0.454	0.139	5.49E-118	mDC	SUB1
2.18E-120	1.005170971	0.272	0.055	4.49E-116	mDC	IPO9-AS1
2.56E-119	1.028933143	0.414	0.115	5.28E-115	mDC	ST3GAL2
1.28E-117	0.836404291	0.331	0.076	2.63E-113	mDC	CYFIP2
1.79E-116	0.985568427	0.345	0.086	3.68E-112	mDC	NIPAL2
3.68E-116	1.011457667	0.466	0.144	7.57E-112	mDC	CEP128
3.79E-115	0.960611061	0.314	0.073	7.81E-111	mDC	MED12L

3.93E-114	0.840267116	0.32	0.076	8.09E-110	mDC	TAP2
1.83E-111	0.820898341	0.305	0.069	3.77E-107	mDC	GPT2
3.88E-111	0.981396452	0.286	0.064	7.99E-107	mDC	BCL2L11
1.66E-110	1.114659977	0.811	0.52	3.43E-106	mDC	LRBA
3.17E-110	1.268915715	0.689	0.319	6.52E-106	mDC	ITGA4
1.67E-106	1.244486917	0.714	0.378	3.44E-102	mDC	FARS2
1.31E-104	1.168559157	0.751	0.38	2.70E-100	mDC	HLA-DRA
1.69E-100	1.135945788	0.566	0.239	3.48E-96	mDC	NSMAF
8.29E-100	0.9608948	0.949	0.752	1.71E-95	mDC	FNBP1
1.02E-99	0.748537412	0.302	0.073	2.09E-95	mDC	STK39
1.06E-98	1.032844082	0.871	0.607	2.18E-94	mDC	UVRAG
1.46E-96	1.122668574	0.709	0.363	3.01E-92	mDC	HLA-DRB1
2.71E-96	1.019016358	0.651	0.308	5.58E-92	mDC	PAK1
3.88E-96	0.844861505	0.292	0.072	7.99E-92	mDC	CASS4
5.01E-96	0.906753111	0.9	0.652	1.03E-91	mDC	FAM49B
8.54E-95	0.997716155	0.508	0.197	1.76E-90	mDC	HPS5
5.68E-94	1.105203557	0.597	0.271	1.17E-89	mDC	DSE
1.09E-92	1.232749722	0.509	0.2	2.24E-88	mDC	HIVEP2
2.61E-92	0.985551774	0.409	0.135	5.37E-88	mDC	BICD1
2.82E-90	0.95458618	0.658	0.314	5.80E-86	mDC	MAP4
2.67E-89	0.850573091	0.346	0.103	5.50E-85	mDC	CDKL5
3.20E-89	0.991619841	0.818	0.511	6.59E-85	mDC	FNIP2
4.05E-89	0.969991812	0.525	0.212	8.34E-85	mDC	RFTN1
4.82E-89	1.019768765	0.852	0.516	9.91E-85	mDC	CCDC26
1.47E-88	1.1940681	0.632	0.314	3.02E-84	mDC	OSBPL3
3.52E-88	0.915878913	0.905	0.676	7.24E-84	mDC	DOCK10
1.42E-87	0.94564202	0.671	0.325	2.91E-83	mDC	APBA1
2.37E-87	0.744068851	0.335	0.094	4.87E-83	mDC	GPAT3
8.12E-87	0.979242922	0.462	0.175	1.67E-82	mDC	MAP3K4
2.22E-86	1.086011581	0.474	0.188	4.57E-82	mDC	SLC46A3
2.39E-86	0.710835226	0.277	0.071	4.91E-82	mDC	ATP6V0A2
2.98E-86	0.993630094	0.588	0.262	6.13E-82	mDC	FARP2
2.63E-85	0.931241268	0.425	0.146	5.40E-81	mDC	LYZ
1.69E-84	0.890187887	0.368	0.116	3.48E-80	mDC	SMAD3
8.16E-84	0.739825804	0.26	0.065	1.68E-79	mDC	NBEAL2
5.07E-81	0.796630634	0.286	0.079	1.04E-76	mDC	THEM4
5.67E-80	0.921007334	0.411	0.144	1.17E-75	mDC	LINC01374
2.09E-79	0.985175276	0.437	0.164	4.31E-75	mDC	CKLF
7.82E-79	0.999308935	0.266	0.071	1.61E-74	mDC	ROBO1
3.05E-78	0.853203974	0.372	0.126	6.27E-74	mDC	STK17A
5.13E-76	0.673242079	0.266	0.071	1.06E-71	mDC	CYB5R3
6.81E-76	0.925033483	0.289	0.084	1.40E-71	mDC	C12orf45
4.23E-75	0.93200317	0.378	0.133	8.72E-71	mDC	APOL3

2.53E-74	0.918578231	0.752	0.457	5.20E-70	mDC	VOPP1
3.70E-74	0.881201426	0.498	0.213	7.61E-70	mDC	NAP1L1
1.75E-73	0.845130849	0.457	0.181	3.60E-69	mDC	DENND5B
1.85E-73	0.742386624	0.654	0.32	3.80E-69	mDC	SLCO3A1
9.54E-72	0.841402164	0.546	0.248	1.96E-67	mDC	PKP4
2.18E-71	0.653395737	0.3	0.089	4.48E-67	mDC	PON2
9.01E-71	0.950287648	0.497	0.22	1.86E-66	mDC	NAAA
8.39E-70	0.898625832	0.405	0.155	1.73E-65	mDC	CASK
1.92E-69	0.850797203	0.714	0.391	3.94E-65	mDC	THRB
2.35E-69	0.838503275	0.343	0.118	4.83E-65	mDC	N4BP2
1.29E-68	1.180517294	0.363	0.132	2.65E-64	mDC	MACROD2
2.95E-67	0.899085866	0.585	0.293	6.07E-63	mDC	FUT8
4.54E-67	0.842213083	0.622	0.329	9.34E-63	mDC	CTNNB1
6.68E-67	0.891298622	0.422	0.171	1.38E-62	mDC	REEP3
8.13E-66	0.790555971	0.317	0.105	1.67E-61	mDC	PAM
1.37E-65	0.7959074	0.472	0.197	2.81E-61	mDC	TTC39C
7.34E-65	1.025691894	0.525	0.253	1.51E-60	mDC	KAT2B
3.37E-64	0.885798815	0.726	0.447	6.93E-60	mDC	RBPJ
4.90E-64	0.881567095	0.7	0.429	1.01E-59	mDC	CLASP2
5.19E-64	1.263784508	0.542	0.266	1.07E-59	mDC	CST3
2.43E-62	0.829363453	0.452	0.195	5.01E-58	mDC	GALNT7
3.51E-62	0.850379494	0.795	0.554	7.23E-58	mDC	INPP5D
6.78E-62	0.708985632	0.358	0.133	1.40E-57	mDC	ERAP2
1.08E-61	0.701898618	0.457	0.197	2.23E-57	mDC	ZDHHC17
2.01E-59	0.781494219	0.308	0.109	4.14E-55	mDC	ST7
3.96E-59	0.756568047	0.525	0.254	8.15E-55	mDC	EPB41
4.63E-59	0.860549258	0.729	0.472	9.52E-55	mDC	MBP
1.74E-58	0.781770237	0.505	0.242	3.58E-54	mDC	HEATR5A
1.97E-58	0.621759216	0.268	0.085	4.05E-54	mDC	TRIT1
3.59E-58	0.802192682	0.638	0.353	7.39E-54	mDC	PITPNC1
1.15E-57	0.763574198	0.483	0.22	2.36E-53	mDC	FGL2
1.73E-56	0.66779974	0.308	0.11	3.56E-52	mDC	EDEM1
2.41E-56	0.599811334	0.311	0.107	4.97E-52	mDC	P2RY8
4.57E-56	0.858881965	0.7	0.443	9.41E-52	mDC	ATF7IP
1.84E-55	0.707846713	0.842	0.639	3.78E-51	mDC	TRIO
2.72E-55	0.748295716	0.392	0.165	5.59E-51	mDC	ENSA
3.33E-55	0.645546886	0.28	0.095	6.86E-51	mDC	FGFR1OP
3.94E-55	0.69803691	0.575	0.293	8.10E-51	mDC	TANC2
6.41E-55	0.782719096	0.688	0.423	1.32E-50	mDC	ZCCHC7
1.40E-54	0.754229294	0.794	0.542	2.88E-50	mDC	CMIP
2.55E-54	0.73227473	0.377	0.155	5.25E-50	mDC	DMD
6.71E-53	0.590948649	0.272	0.092	1.38E-48	mDC	FLOT2
8.89E-53	0.976980868	0.495	0.251	1.83E-48	mDC	FAR2

4.01E-52	0.59920199	0.286	0.101	8.25E-48	mDC	HACD2
6.39E-52	0.80573574	0.52	0.269	1.32E-47	mDC	SNX30
1.20E-51	0.611035472	0.292	0.104	2.46E-47	mDC	MTHFD1L
1.26E-51	0.663347462	0.452	0.208	2.59E-47	mDC	TAPBP
5.54E-51	0.758967402	0.463	0.224	1.14E-46	mDC	MAP4K5
1.43E-50	0.711920507	0.606	0.348	2.94E-46	mDC	TRAK1
4.04E-50	0.695058953	0.557	0.3	8.32E-46	mDC	CHD6
4.71E-50	0.734611194	0.602	0.352	9.69E-46	mDC	HTT
6.13E-50	0.63677397	0.286	0.104	1.26E-45	mDC	DLGAP4
2.68E-49	0.75540332	0.502	0.257	5.52E-45	mDC	SPATS2
1.58E-48	0.89404261	0.428	0.208	3.25E-44	mDC	P2RY6
2.47E-48	0.701795903	0.783	0.549	5.07E-44	mDC	KDM2A
3.63E-48	0.768951998	0.708	0.45	7.48E-44	mDC	MVB12B
1.62E-47	0.751737148	0.506	0.265	3.33E-43	mDC	ARHGAP5
1.83E-47	0.693261089	0.348	0.144	3.76E-43	mDC	CD83
6.20E-47	0.673762953	0.374	0.163	1.28E-42	mDC	GNA12
8.84E-47	0.718142168	0.38	0.167	1.82E-42	mDC	HLA-DRB5
1.17E-46	0.736253691	0.729	0.514	2.40E-42	mDC	PTPRE
3.40E-46	0.607365611	0.322	0.13	6.99E-42	mDC	MAP3K13
6.06E-46	0.631004261	0.386	0.171	1.25E-41	mDC	AHI1
8.47E-46	0.809995885	0.56	0.328	1.74E-41	mDC	PDE7A
8.63E-46	0.669813104	0.331	0.135	1.78E-41	mDC	FAM118A
1.12E-45	0.617208921	0.268	0.097	2.31E-41	mDC	IRAK2
1.17E-45	0.678892564	0.674	0.427	2.40E-41	mDC	NFAT5
1.83E-45	0.69749872	0.349	0.149	3.76E-41	mDC	MTMR1
2.77E-45	0.701012311	0.683	0.428	5.71E-41	mDC	NCOA7
3.90E-45	0.585696879	0.282	0.107	8.04E-41	mDC	GOLGA8B
1.19E-44	0.667777672	0.62	0.371	2.45E-40	mDC	ATAD2B
1.39E-44	0.795500985	0.548	0.321	2.85E-40	mDC	STIM2
2.07E-44	0.727968467	0.554	0.317	4.26E-40	mDC	STX12
3.56E-44	0.774986996	0.374	0.174	7.32E-40	mDC	MPEG1
3.75E-44	0.601100598	0.86	0.682	7.73E-40	mDC	ARID1B
6.72E-44	0.639945649	0.392	0.178	1.38E-39	mDC	CDK14
1.12E-43	0.678011128	0.657	0.422	2.31E-39	mDC	CBL
1.41E-43	0.618514535	0.728	0.475	2.91E-39	mDC	HLA-B
3.42E-43	0.675580549	0.371	0.168	7.05E-39	mDC	TMEM65
6.26E-43	0.7147804	0.454	0.23	1.29E-38	mDC	ID2
2.54E-42	0.665264422	0.443	0.215	5.24E-38	mDC	AHR
2.11E-41	0.727412198	0.492	0.26	4.35E-37	mDC	ADD3
3.53E-41	0.685039913	0.351	0.159	7.26E-37	mDC	KLHL22
4.67E-41	0.641622185	0.828	0.633	9.62E-37	mDC	1-Mar
6.97E-41	0.599494774	0.288	0.116	1.43E-36	mDC	BIRC3
7.35E-41	0.703847656	0.318	0.139	1.51E-36	mDC	LYRM4

8.89E-41	0.737373643	0.314	0.132	1.83E-36	mDC	CSGALNACT1
5.06E-40	0.59249473	0.506	0.276	1.04E-35	mDC	AKNA
8.83E-40	0.659166136	0.62	0.392	1.82E-35	mDC	UPF2
1.34E-39	0.626024039	0.817	0.623	2.76E-35	mDC	CCDC88A
3.95E-39	0.608214044	0.335	0.151	8.13E-35	mDC	CYTOR
5.06E-39	0.617247586	0.446	0.229	1.04E-34	mDC	NMT1
1.20E-38	0.640398864	0.354	0.164	2.48E-34	mDC	KIF2A
2.98E-38	0.611024749	0.278	0.115	6.14E-34	mDC	EFCAB2
8.27E-38	0.626500145	0.343	0.16	1.70E-33	mDC	PPT1
2.29E-37	0.599747928	0.365	0.171	4.71E-33	mDC	PHLPP1
3.12E-37	0.709625013	0.622	0.395	6.43E-33	mDC	MIR181A1HG
4.95E-37	0.613353296	0.303	0.132	1.02E-32	mDC	GABPB1-AS1
2.45E-36	0.606459366	0.478	0.269	5.05E-32	mDC	SFT2D2
2.40E-35	0.62205485	0.682	0.48	4.94E-31	mDC	TET2
2.82E-34	0.610948896	0.312	0.144	5.81E-30	mDC	CAMK2G
4.20E-34	0.629229149	0.635	0.414	8.64E-30	mDC	ST8SIA4
5.51E-34	0.726781059	0.591	0.373	1.13E-29	mDC	ACTB
5.48E-32	0.587408171	0.597	0.378	1.13E-27	mDC	ARHGAP31
7.42E-32	0.768296224	0.265	0.116	1.53E-27	mDC	PDE7B
1.71E-28	0.616304864	0.622	0.441	3.53E-24	mDC	LCP1
5.12E-26	0.60993793	0.289	0.143	1.05E-21	mDC	ADGRA3
1.10E-24	0.676005898	0.302	0.158	2.26E-20	mDC	CPB2-AS1
7.01E-24	0.633669827	0.562	0.383	1.44E-19	mDC	TMSB4X
9.50E-24	0.850235822	0.274	0.141	1.95E-19	mDC	PPARGC1A
3.39E-22	0.627436288	0.528	0.363	6.97E-18	mDC	FOXO1
4.18E-15	0.832327183	0.358	0.243	8.60E-11	mDC	SORBS2
7.16E-15	0.611897713	0.392	0.268	1.47E-10	mDC	HRG
1.55E-14	0.671443431	0.297	0.188	3.20E-10	mDC	HGD
2.68E-14	0.847729482	0.558	0.447	5.52E-10	mDC	CPS1
5.83E-14	0.748491903	0.431	0.317	1.20E-09	mDC	RORA
0	4.455945789	0.839	0.007	0	pDC	LINC01478
0	4.025030621	0.902	0.067	0	pDC	BCL11A
0	3.83377725	0.899	0.14	0	pDC	LINC01374
0	3.765381792	0.873	0.098	0	pDC	ZFAT
0	3.727699882	0.772	0.009	0	pDC	PLXNA4
0	3.681323444	0.817	0.026	0	pDC	FAM160A1
0	3.674710389	0.881	0.108	0	pDC	RUNX2
0	3.653408089	0.749	0.006	0	pDC	RGS7
0	3.601302128	0.815	0.013	0	pDC	PTPRS
0	3.557292747	0.804	0.005	0	pDC	CLEC4C
0	3.445508694	0.873	0.107	0	pDC	CUX2
0	3.33359317	0.635	0.018	0	pDC	LINC00996
0	3.300138999	0.799	0.05	0	pDC	CARD11

0	3.247322033	0.939	0.26	0	pDC	AC023590.1
0	3.177772032	0.754	0.041	0	pDC	EPHB1
0	3.093230594	0.648	0.006	0	pDC	COL24A1
0	3.002519066	0.683	0.018	0	pDC	SLC35F3
0	2.89353864	0.741	0.055	0	pDC	P2RY14
0	2.799919536	0.854	0.186	0	pDC	APP
0	2.726454024	0.601	0.028	0	pDC	DACH1
0	2.694569677	0.603	0.006	0	pDC	PHEX
0	2.685640506	0.68	0.037	0	pDC	SCN9A
0	2.514858083	0.616	0.044	0	pDC	IL3RA
0	2.496683321	0.558	0.002	0	pDC	LINC01226
0	2.343333612	0.611	0.074	0	pDC	IRF7
0	2.230191482	0.638	0.087	0	pDC	STRBP
0	2.172183147	0.587	0.044	0	pDC	ADAM19
0	2.150802837	0.622	0.057	0	pDC	MCOLN2
0	2.146985246	0.37	0.008	0	pDC	COL26A1
0	2.113663639	0.487	0.005	0	pDC	SPIB
0	2.109349362	0.466	0.001	0	pDC	PACSIN1
0	2.088252949	0.32	0.009	0	pDC	PTGDS
0	2.076340962	0.481	0.004	0	pDC	KCNK10
0	2.023808155	0.519	0.037	0	pDC	PPP1R16B
0	2.003182846	0.484	0.016	0	pDC	C12orf75
0	1.886279173	0.418	0.003	0	pDC	MZB1
0	1.660003774	0.381	0.015	0	pDC	IFNLR1
0	1.628744323	0.368	0.022	0	pDC	GPM6B
0	1.613855406	0.368	0.011	0	pDC	ADGRG5
0	1.591738549	0.36	0.02	0	pDC	BCL7A
0	1.56166252	0.36	0.008	0	pDC	CYP46A1
0	1.559341438	0.341	0.003	0	pDC	LILRA4
0	1.501556096	0.328	0.002	0	pDC	LRRC36
0	1.477421432	0.315	0.017	0	pDC	CYYR1
0	1.477181085	0.347	0.021	0	pDC	ATP2A3
0	1.447683617	0.325	0	0	pDC	LAMP5
0	1.443321529	0.262	0.001	0	pDC	VIPR2
0	1.43438942	0.31	0.002	0	pDC	DERL3
0	1.298555398	0.275	0.005	0	pDC	SLC12A3
0	1.244357478	0.272	0.01	0	pDC	PLD4
0	1.166171089	0.267	0.014	0	pDC	SMPD3
5.82E-307	3.026213682	0.812	0.176	1.20E-302	pDC	CCDC50
7.50E-298	2.034963435	0.376	0.03	1.54E-293	pDC	ADGRB3
2.18E-297	1.813735612	0.397	0.034	4.50E-293	pDC	SYCP2L
5.72E-295	1.43855696	0.259	0.014	1.18E-290	pDC	IRF4
5.29E-290	2.25443278	0.778	0.143	1.09E-285	pDC	SULF2

2.31E-289	2.523897172	0.854	0.184	4.76E-285	pDC	AUTS2
4.04E-281	2.94570998	0.899	0.263	8.32E-277	pDC	UGCG
2.80E-272	2.07471271	0.587	0.084	5.76E-268	pDC	GNG7
2.46E-270	2.516810627	0.799	0.174	5.06E-266	pDC	COBLL1
8.37E-269	1.757527102	0.471	0.053	1.72E-264	pDC	HS3ST3B1
1.55E-268	1.473626684	0.373	0.033	3.18E-264	pDC	SCAMP5
1.84E-268	1.238903982	0.278	0.018	3.78E-264	pDC	FAM81A
1.03E-257	1.698839137	0.487	0.058	2.12E-253	pDC	SLC38A1
5.79E-256	1.966949379	0.532	0.073	1.19E-251	pDC	MED12L
3.11E-255	2.535969688	0.714	0.147	6.39E-251	pDC	BLNK
6.38E-252	1.522920059	0.392	0.039	1.31E-247	pDC	ST3GAL4
5.35E-239	2.494473894	0.704	0.148	1.10E-234	pDC	ERN1
1.31E-237	1.758154761	0.476	0.061	2.69E-233	pDC	ATP10A
8.88E-235	1.776782424	0.405	0.044	1.83E-230	pDC	KHDRBS2
3.89E-234	1.608696518	0.389	0.041	8.00E-230	pDC	DAPK2
1.89E-230	3.216794922	0.981	0.561	3.88E-226	pDC	TCF4
4.06E-229	2.465533012	0.831	0.24	8.36E-225	pDC	IRF8
2.19E-218	2.414794942	0.976	0.418	4.51E-214	pDC	AFF3
9.35E-212	1.982364125	0.611	0.115	1.92E-207	pDC	ST3GAL2
3.27E-210	1.147885866	0.299	0.026	6.74E-206	pDC	SELL
8.71E-208	1.693968299	0.489	0.074	1.79E-203	pDC	PPM1K
7.28E-201	2.26634688	0.733	0.196	1.50E-196	pDC	ZDHHC17
2.49E-196	1.732107212	0.481	0.075	5.13E-192	pDC	FLNB
8.47E-196	1.520135427	0.466	0.067	1.74E-191	pDC	SH2D3C
4.84E-195	1.465018625	0.415	0.054	9.97E-191	pDC	IL18R1
6.99E-195	1.506159578	0.495	0.076	1.44E-190	pDC	CYFIP2
3.68E-194	2.501375328	0.974	0.701	7.57E-190	pDC	RABGAP1L
1.01E-187	2.290479635	0.974	0.74	2.09E-183	pDC	FCHSD2
3.76E-185	1.207337982	0.333	0.038	7.73E-181	pDC	CYB561A3
1.52E-180	1.509222336	0.323	0.037	3.14E-176	pDC	GRIP1
6.09E-180	1.431465838	0.405	0.057	1.25E-175	pDC	HHAT
1.85E-179	1.976011565	0.661	0.161	3.80E-175	pDC	OFD1
5.50E-177	1.472343039	0.407	0.059	1.13E-172	pDC	STAMBPL1
9.53E-176	1.662509841	0.511	0.093	1.96E-171	pDC	TEX2
9.60E-174	2.024333928	0.595	0.132	1.98E-169	pDC	MAPKAPK2
6.34E-173	1.318656296	0.54	0.094	1.30E-168	pDC	FLT3
9.97E-172	2.190192103	0.579	0.127	2.05E-167	pDC	SAMD12
5.40E-171	1.636709464	0.601	0.129	1.11E-166	pDC	ANTXR2
5.76E-170	1.702254279	0.556	0.108	1.19E-165	pDC	ZEB1
2.12E-168	1.813022688	0.524	0.104	4.35E-164	pDC	CCDC186
1.84E-160	1.224983019	0.296	0.034	3.79E-156	pDC	EPDR1
2.35E-160	1.467904909	0.437	0.07	4.84E-156	pDC	GLT1D1
8.78E-154	1.379903761	0.413	0.066	1.81E-149	pDC	SLAMF7

9.45E-154	1.393447505	0.251	0.026	1.94E-149	pDC	SLC7A5
3.19E-151	1.727178903	0.601	0.145	6.57E-147	pDC	CEP128
3.06E-149	1.922374757	0.754	0.261	6.29E-145	pDC	CD2AP
3.25E-148	1.325973035	0.344	0.048	6.69E-144	pDC	SEMA3C
3.41E-148	1.69007926	0.548	0.127	7.03E-144	pDC	SLC15A4
4.25E-148	1.19913893	0.315	0.04	8.75E-144	pDC	P2RX1
4.50E-147	2.068234905	0.81	0.321	9.27E-143	pDC	SEL1L3
3.79E-146	1.312199649	0.394	0.063	7.81E-142	pDC	CCDC69
6.77E-143	1.419043472	0.402	0.065	1.39E-138	pDC	NEGR1
3.84E-139	1.354955565	0.347	0.052	7.90E-135	pDC	CBFA2T3
5.38E-138	1.509400997	0.439	0.084	1.11E-133	pDC	C12orf45
5.79E-137	1.634810328	0.683	0.196	1.19E-132	pDC	RAP1GAP2
5.48E-134	1.051945398	0.251	0.029	1.13E-129	pDC	C11orf80
2.21E-132	1.572099026	0.471	0.101	4.55E-128	pDC	LAIR1
5.68E-132	1.947846511	0.693	0.241	1.17E-127	pDC	GRAMD1B
2.33E-131	1.664710653	0.759	0.294	4.79E-127	pDC	OGT
2.78E-129	1.278075187	0.349	0.056	5.73E-125	pDC	TRG-AS1
3.24E-129	1.746078242	0.598	0.171	6.67E-125	pDC	AHI1
2.80E-128	1.868297645	0.733	0.279	5.76E-124	pDC	CDYL
3.75E-128	0.961194306	0.27	0.034	7.72E-124	pDC	UCK2
7.11E-125	1.830818165	0.833	0.392	1.46E-120	pDC	SETBP1
1.26E-123	1.308307151	0.437	0.088	2.60E-119	pDC	SLC9A7
1.87E-122	1.654099797	0.556	0.145	3.84E-118	pDC	PCED1B
5.34E-122	1.34204244	0.394	0.075	1.10E-117	pDC	MAP2K6
8.15E-119	1.335763718	0.616	0.171	1.68E-114	pDC	MAP4K4
8.65E-117	1.594137797	0.537	0.146	1.78E-112	pDC	SMC6
1.79E-116	1.814839821	0.728	0.281	3.69E-112	pDC	PLAC8
2.85E-115	1.131737574	0.344	0.06	5.87E-111	pDC	EMB
7.38E-115	1.286011248	0.458	0.102	1.52E-110	pDC	ATP2B4
6.24E-114	0.977986993	0.257	0.035	1.28E-109	pDC	GAS6
9.49E-114	1.283074396	0.423	0.089	1.95E-109	pDC	NUP210
1.08E-112	1.558472473	0.529	0.139	2.22E-108	pDC	DNASE1L3
2.09E-112	1.352210445	0.81	0.4	4.30E-108	pDC	WDFY4
6.89E-112	1.470620849	0.362	0.07	1.42E-107	pDC	CCDC102B
1.92E-110	1.692587061	0.725	0.283	3.95E-106	pDC	MYO1E
2.68E-107	1.42399239	0.444	0.105	5.52E-103	pDC	SLC7A6
2.44E-104	1.610934738	0.471	0.121	5.02E-100	pDC	GLCCI1
7.45E-103	1.266495508	0.468	0.115	1.53E-98	pDC	SERPINF1
2.28E-102	1.647202928	0.638	0.237	4.69E-98	pDC	NPC1
5.34E-101	1.511825185	0.653	0.248	1.10E-96	pDC	NGLY1
1.09E-100	1.081800883	0.259	0.04	2.24E-96	pDC	TP53I13
2.69E-96	1.555257066	0.508	0.148	5.54E-92	pDC	LHFPL2
5.22E-95	1.141616979	0.579	0.17	1.08E-90	pDC	JAML

1.47E-92	1.404394245	0.442	0.117	3.02E-88	pDC	MCC
1.14E-91	1.093489532	0.352	0.076	2.34E-87	pDC	IDH3A
3.37E-91	1.473201487	0.643	0.249	6.93E-87	pDC	RUBCNL
1.40E-89	1.659093482	0.646	0.262	2.88E-85	pDC	TBC1D4
3.19E-89	1.436034966	0.762	0.357	6.56E-85	pDC	SFMBT2
4.45E-89	1.357605482	0.447	0.119	9.16E-85	pDC	SH3D19
1.49E-88	1.140529249	0.339	0.071	3.07E-84	pDC	SPATA13
3.48E-87	0.920091851	0.302	0.057	7.16E-83	pDC	ETS1
7.04E-87	1.528331102	0.696	0.317	1.45E-82	pDC	MDFIC
8.16E-87	1.400115433	0.458	0.128	1.68E-82	pDC	P3H2
4.98E-86	1.410690311	0.579	0.203	1.02E-81	pDC	ITPR1
1.21E-85	1.376783045	0.45	0.128	2.49E-81	pDC	TBC1D32
1.96E-84	1.140311542	0.376	0.089	4.04E-80	pDC	ULK1
7.27E-84	1.117758297	0.357	0.084	1.50E-79	pDC	VEGFB
2.71E-82	1.426287583	0.587	0.218	5.58E-78	pDC	TTC7A
6.57E-78	1.350229158	0.513	0.174	1.35E-73	pDC	MPEG1
5.17E-77	1.292353513	0.688	0.29	1.06E-72	pDC	JAZF1
5.02E-76	1.30986501	0.556	0.204	1.03E-71	pDC	ASPH
2.24E-74	1.3646459	0.466	0.152	4.61E-70	pDC	CREB3L2
4.13E-74	1.318308119	0.429	0.127	8.50E-70	pDC	DAAM1
1.13E-73	1.217435254	0.505	0.169	2.33E-69	pDC	SLC41A2
1.41E-73	1.177690326	0.429	0.125	2.90E-69	pDC	TRPM2
4.17E-73	1.314191158	0.503	0.176	8.58E-69	pDC	CDC14A
7.84E-71	1.646401654	0.587	0.243	1.61E-66	pDC	GAB1
2.54E-70	1.232362915	0.386	0.108	5.23E-66	pDC	POLB
3.48E-70	1.346019746	0.611	0.265	7.17E-66	pDC	FAM214A
4.25E-69	1.311720746	0.669	0.324	8.74E-65	pDC	ZNRF2
6.09E-69	1.020229881	0.28	0.062	1.25E-64	pDC	CCDC138
9.24E-68	1.198573723	0.452	0.15	1.90E-63	pDC	MTMR1
1.51E-67	1.212461717	0.725	0.384	3.11E-63	pDC	RAP1GDS1
2.57E-67	1.263171192	0.545	0.214	5.29E-63	pDC	HERPUD1
2.98E-67	1.359206663	0.561	0.227	6.14E-63	pDC	LINC01684
3.56E-67	1.226877357	0.728	0.403	7.34E-63	pDC	USP24
7.87E-67	1.173888566	0.437	0.137	1.62E-62	pDC	BICD1
8.01E-67	0.901014971	0.257	0.054	1.65E-62	pDC	NIPA1
8.84E-67	1.052915092	0.384	0.109	1.82E-62	pDC	ARID3A
2.09E-66	1.208325863	0.421	0.13	4.30E-62	pDC	SCMH1
3.85E-65	1.164505635	0.746	0.438	7.92E-61	pDC	ITCH
5.23E-65	1.243753091	0.799	0.492	1.08E-60	pDC	IKZF1
1.04E-63	1.315879877	0.532	0.214	2.13E-59	pDC	INTS6
1.58E-63	1.045393118	0.399	0.118	3.25E-59	pDC	MSI2
1.74E-63	1.160652995	0.455	0.158	3.59E-59	pDC	TARBP1
4.62E-63	1.134103077	0.392	0.12	9.50E-59	pDC	N4BP2

7.66E-63	1.182426741	0.751	0.444	1.58E-58	pDC	TGFBR2
7.45E-62	1.186765556	0.606	0.269	1.53E-57	pDC	NIN
1.47E-61	1.208839682	0.45	0.153	3.02E-57	pDC	TNFRSF21
1.94E-61	1.193868293	0.524	0.21	3.99E-57	pDC	TASP1
3.28E-61	1.211066397	0.569	0.245	6.76E-57	pDC	MNAT1
3.94E-61	1.327274886	0.516	0.204	8.12E-57	pDC	SUPT3H
4.52E-61	1.087336756	0.336	0.094	9.30E-57	pDC	CRIM1
3.07E-60	1.070271088	0.524	0.199	6.32E-56	pDC	TTC39C
3.99E-60	1.132003888	0.638	0.292	8.22E-56	pDC	PCNX1
4.63E-60	1.305969394	0.746	0.457	9.53E-56	pDC	CERS6
6.14E-60	1.244418713	0.587	0.258	1.26E-55	pDC	CYTH4
1.76E-59	0.923982641	0.894	0.683	3.63E-55	pDC	ARID1B
3.99E-59	0.977566366	0.257	0.06	8.22E-55	pDC	PFKFB2
1.24E-58	1.192583896	0.434	0.152	2.56E-54	pDC	FMNL3
1.46E-58	1.231257336	0.481	0.183	3.00E-54	pDC	DENND5B
3.00E-58	1.002051935	0.32	0.087	6.17E-54	pDC	AVEN
3.16E-58	1.22733864	0.659	0.347	6.51E-54	pDC	PI4KA
2.62E-57	1.253405328	0.516	0.216	5.39E-53	pDC	CLCN5
1.18E-55	1.128155196	0.796	0.527	2.43E-51	pDC	INPP4A
2.23E-53	1.025980676	0.865	0.592	4.59E-49	pDC	PDE4B
1.85E-52	1.048013313	0.437	0.162	3.81E-48	pDC	UBE2J1
2.66E-52	0.796335076	0.251	0.062	5.48E-48	pDC	FYCO1
3.78E-52	1.071851624	0.587	0.27	7.78E-48	pDC	ZHX2
9.22E-52	1.137659375	0.669	0.373	1.90E-47	pDC	SH3KBP1
1.52E-51	1.185338469	0.463	0.184	3.14E-47	pDC	CORO1C
1.54E-51	1.036903958	0.466	0.183	3.16E-47	pDC	MDN1
3.19E-51	1.142832307	0.444	0.174	6.57E-47	pDC	TATDN3
1.37E-50	1.185372385	0.651	0.345	2.81E-46	pDC	HIP1
2.16E-50	0.812392591	0.28	0.076	4.45E-46	pDC	CD37
9.05E-50	1.005923955	0.68	0.385	1.86E-45	pDC	ARID2
1.51E-49	1.125412605	0.423	0.161	3.11E-45	pDC	ATP8A1
2.70E-49	1.130323505	0.492	0.212	5.56E-45	pDC	CLN8
4.17E-49	1.020857072	0.362	0.121	8.58E-45	pDC	SELENOS
5.59E-48	0.966240411	0.817	0.601	1.15E-43	pDC	TNRC6B
5.66E-48	0.961109931	0.312	0.097	1.16E-43	pDC	LINC01176
6.14E-48	0.829755061	0.307	0.091	1.26E-43	pDC	TRABD
1.38E-47	0.969590335	0.418	0.157	2.85E-43	pDC	DHTKD1
7.47E-47	0.991581998	0.78	0.515	1.54E-42	pDC	PTPRE
2.61E-46	0.888057801	0.32	0.101	5.38E-42	pDC	SEC61B
4.75E-46	0.868347776	0.32	0.102	9.79E-42	pDC	SLC37A1
7.24E-46	1.138259624	0.513	0.237	1.49E-41	pDC	HIVEP1
1.12E-45	0.922604988	0.333	0.106	2.31E-41	pDC	VCL
5.79E-43	0.829065805	0.304	0.097	1.19E-38	pDC	MEF2D

5.88E-43	0.889351348	0.857	0.662	1.21E-38	pDC	CHD9
6.17E-43	0.94783976	0.474	0.206	1.27E-38	pDC	LIMD1
7.03E-43	0.84489483	0.283	0.086	1.45E-38	pDC	ZNF589
1.55E-42	0.886927004	0.839	0.632	3.19E-38	pDC	CUX1
2.58E-42	0.784536163	0.886	0.694	5.31E-38	pDC	PRKCB
2.35E-41	0.970588093	0.577	0.304	4.83E-37	pDC	NFX1
7.33E-41	0.775805001	0.299	0.097	1.51E-36	pDC	FGFR1OP
2.92E-40	0.794447981	0.265	0.08	6.02E-36	pDC	SCYL3
4.29E-40	1.024239064	0.354	0.133	8.82E-36	pDC	CYSLTR1
7.27E-40	0.896436574	0.817	0.669	1.50E-35	pDC	ANKRD12
1.14E-39	0.927369653	0.794	0.583	2.35E-35	pDC	MEF2C
4.15E-39	0.972446673	0.582	0.32	8.55E-35	pDC	BTAF1
2.29E-38	0.892775297	0.368	0.144	4.72E-34	pDC	TMEM63A
2.43E-38	0.85554167	0.267	0.085	5.01E-34	pDC	ARHGAP9
3.67E-37	0.87356559	0.571	0.301	7.55E-33	pDC	B4GALT1
3.94E-37	1.028017586	0.431	0.197	8.12E-33	pDC	RUBCN
8.17E-37	0.892320194	0.341	0.128	1.68E-32	pDC	PPCDC
8.58E-36	0.853854997	0.362	0.146	1.77E-31	pDC	C18orf25
1.46E-35	0.802573363	0.77	0.559	3.01E-31	pDC	SYK
1.47E-35	1.006985347	0.532	0.287	3.03E-31	pDC	R3HDM1
2.00E-35	0.789274791	0.384	0.154	4.12E-31	pDC	RASSF2
3.27E-35	0.774893125	0.741	0.492	6.73E-31	pDC	SND1
7.38E-35	0.861630285	0.259	0.085	1.52E-30	pDC	MEF2C-AS1
1.04E-34	0.904889255	0.767	0.537	2.15E-30	pDC	ANKRD11
3.03E-34	0.799928768	0.402	0.176	6.23E-30	pDC	NUP160
3.78E-34	0.946212235	0.389	0.17	7.79E-30	pDC	RFX3-AS1
1.17E-33	0.896304533	0.466	0.228	2.41E-29	pDC	SLC39A10
1.74E-33	0.847795011	0.45	0.214	3.58E-29	pDC	S100PBP
8.43E-33	0.987573072	0.513	0.274	1.73E-28	pDC	CRLF3
3.09E-32	1.010303102	0.505	0.275	6.36E-28	pDC	RRBP1
3.59E-32	0.760492849	0.254	0.086	7.38E-28	pDC	L3MBTL3
3.97E-32	0.930783553	0.447	0.213	8.16E-28	pDC	SLC20A1
4.64E-32	0.844590281	0.421	0.195	9.56E-28	pDC	ANKRD36
5.35E-32	0.898472318	0.481	0.253	1.10E-27	pDC	PIP5K1A
7.95E-32	0.827497791	0.593	0.355	1.64E-27	pDC	PTPN2
8.45E-32	0.839761757	0.55	0.307	1.74E-27	pDC	GLS
8.75E-32	0.843001394	0.534	0.293	1.80E-27	pDC	SNHG14
9.59E-32	0.731456357	0.392	0.169	1.97E-27	pDC	MGAT4A
2.19E-31	0.763458772	0.791	0.611	4.50E-27	pDC	DDX17
2.24E-31	0.8518379	0.283	0.104	4.60E-27	pDC	PTPN22
2.53E-31	0.902874338	0.632	0.421	5.22E-27	pDC	PHC3
4.44E-31	0.728821713	0.786	0.611	9.15E-27	pDC	UVRAG
4.59E-31	0.871918042	0.632	0.398	9.44E-27	pDC	GLG1

5.10E-31	0.703526765	0.28	0.1	1.05E-26	pDC	AR
8.12E-31	0.721004268	0.328	0.131	1.67E-26	pDC	ABI2
8.07E-30	0.773990546	0.701	0.495	1.66E-25	pDC	FRYL
1.60E-29	0.797086865	0.328	0.135	3.28E-25	pDC	GLCE
1.66E-29	0.744316927	0.725	0.508	3.41E-25	pDC	VAV3
3.18E-29	0.804653726	0.455	0.231	6.54E-25	pDC	NMT1
4.32E-29	0.670135701	0.267	0.099	8.89E-25	pDC	ENTPD4
8.49E-29	0.783908316	0.606	0.376	1.75E-24	pDC	MDM4
1.22E-28	0.610121422	0.839	0.665	2.52E-24	pDC	IQGAP2
2.91E-28	0.729812296	0.307	0.125	5.98E-24	pDC	RABL6
5.51E-28	0.762926642	0.783	0.597	1.13E-23	pDC	DDX5
5.84E-28	0.654204026	0.304	0.119	1.20E-23	pDC	SMAD3
9.67E-28	1.060156183	0.328	0.145	1.99E-23	pDC	USP9Y
1.02E-27	0.843459055	0.323	0.137	2.09E-23	pDC	FAM118A
1.05E-27	0.811423584	0.339	0.149	2.17E-23	pDC	SOGA1
1.72E-27	0.821889911	0.55	0.329	3.54E-23	pDC	DNM2
2.57E-27	0.763437952	0.661	0.461	5.30E-23	pDC	TBL1XR1
3.30E-27	0.680268093	0.712	0.492	6.79E-23	pDC	ZMYM2
1.09E-26	0.89223011	0.471	0.257	2.24E-22	pDC	KAT2B
1.87E-26	0.803262409	0.262	0.101	3.85E-22	pDC	CCS
1.93E-26	0.704148853	0.278	0.109	3.97E-22	pDC	IVD
1.01E-25	0.742067703	0.251	0.097	2.07E-21	pDC	PRMT7
1.84E-25	0.743636899	0.265	0.104	3.78E-21	pDC	FBRSL1
2.46E-25	0.730281709	0.344	0.16	5.06E-21	pDC	ZFYVE26
2.79E-25	0.637922587	0.291	0.12	5.75E-21	pDC	IRF2BP2
5.46E-25	0.803302799	0.611	0.421	1.12E-20	pDC	NRDC
5.57E-25	0.824151774	0.347	0.164	1.15E-20	pDC	DBNL
5.58E-25	0.615377919	0.799	0.625	1.15E-20	pDC	CCDC88A
1.32E-24	0.70557442	0.508	0.282	2.72E-20	pDC	CSF2RA
1.41E-24	0.830921958	0.407	0.214	2.90E-20	pDC	TDRD3
2.88E-24	0.731074982	0.421	0.215	5.92E-20	pDC	KDM4B
8.54E-24	0.753660475	0.646	0.444	1.76E-19	pDC	ZRANB2
1.71E-23	0.671323182	0.299	0.131	3.52E-19	pDC	LEMD3
2.04E-23	0.713941677	0.257	0.104	4.20E-19	pDC	PARP10
2.14E-23	0.606115218	0.257	0.102	4.40E-19	pDC	FBXW5
2.19E-23	0.772301893	0.468	0.271	4.50E-19	pDC	SFT2D2
2.54E-23	0.808618421	0.439	0.244	5.22E-19	pDC	RHBDD1
2.73E-23	0.632433989	0.378	0.184	5.61E-19	pDC	RALGPS2
3.94E-23	0.698549005	0.286	0.121	8.11E-19	pDC	PALD1
4.27E-23	0.677071932	0.341	0.16	8.78E-19	pDC	PACS2
4.99E-23	0.749390594	0.54	0.333	1.03E-18	pDC	PHYKPL
5.78E-23	0.772485716	0.458	0.259	1.19E-18	pDC	GGA2
6.52E-23	0.681974543	0.69	0.495	1.34E-18	pDC	TRAPPC9

1.16E-22	0.703640141	0.513	0.313	2.39E-18	pDC	TRIM22
1.23E-22	1.007470574	0.45	0.263	2.53E-18	pDC	SUSD1
1.38E-22	0.754248261	0.497	0.293	2.85E-18	pDC	EXOC6
1.51E-22	0.631486938	0.362	0.179	3.10E-18	pDC	CCDC14
1.90E-22	0.634029475	0.251	0.102	3.92E-18	pDC	PRPSAP1
2.15E-22	0.668632019	0.344	0.163	4.42E-18	pDC	DGKD
2.31E-22	0.675214115	0.347	0.166	4.75E-18	pDC	KIF2A
3.13E-22	0.783679731	0.712	0.542	6.45E-18	pDC	IFNAR2
3.45E-22	0.696937183	0.497	0.292	7.10E-18	pDC	UBE2D2
4.07E-22	0.736981241	0.447	0.253	8.37E-18	pDC	GGNBP2
4.17E-22	0.65499695	0.291	0.129	8.58E-18	pDC	ZNF506
5.84E-22	0.816289008	0.532	0.346	1.20E-17	pDC	CCDC18-AS1
7.57E-22	0.671738176	0.275	0.12	1.56E-17	pDC	ZNF706
7.72E-22	0.652663114	0.579	0.374	1.59E-17	pDC	ATAD2B
7.84E-22	0.688827524	0.556	0.359	1.61E-17	pDC	GTF2I
8.97E-22	0.670035875	0.431	0.239	1.85E-17	pDC	MAP3K14
1.40E-21	0.632291784	0.743	0.6	2.89E-17	pDC	ADK
1.47E-21	0.632462324	0.601	0.4	3.03E-17	pDC	HNRNPU
1.78E-21	0.626151033	0.296	0.136	3.65E-17	pDC	CNPY3
2.11E-21	0.798278651	0.447	0.264	4.35E-17	pDC	MOB1B
3.37E-21	0.70915442	0.378	0.199	6.94E-17	pDC	UNC93B1
5.46E-21	0.593661816	0.254	0.108	1.12E-16	pDC	BTG2
5.81E-21	0.746756277	0.394	0.211	1.20E-16	pDC	TAPBP
6.66E-21	0.621381043	0.635	0.433	1.37E-16	pDC	CLASP2
6.74E-21	0.723892596	0.347	0.178	1.39E-16	pDC	STX18
7.93E-21	0.694740953	0.296	0.137	1.63E-16	pDC	LINC00513
1.17E-20	0.663755536	0.69	0.515	2.40E-16	pDC	CDC42SE2
2.32E-20	0.717891899	0.627	0.455	4.78E-16	pDC	ARGLU1
2.55E-20	0.652326269	0.288	0.133	5.26E-16	pDC	DGKZ
3.73E-20	0.774048707	0.333	0.166	7.68E-16	pDC	GNA12
3.96E-20	0.688048218	0.347	0.175	8.16E-16	pDC	NFATC2IP
6.08E-20	0.728870857	0.397	0.216	1.25E-15	pDC	PPARA
7.11E-20	0.718190639	0.5	0.308	1.46E-15	pDC	LRRC8D
1.03E-19	0.883945987	0.526	0.348	2.12E-15	pDC	PIK3CD
2.28E-19	0.604718772	0.606	0.418	4.68E-15	pDC	FNBP4
2.51E-19	0.733908387	0.368	0.201	5.17E-15	pDC	FIP1L1
4.56E-19	0.722923366	0.54	0.349	9.38E-15	pDC	C22orf34
5.07E-19	0.655626868	0.267	0.123	1.04E-14	pDC	SAP30BP
5.76E-19	0.707503456	0.434	0.261	1.19E-14	pDC	NUTM2B-AS1
6.84E-19	0.60817793	0.312	0.154	1.41E-14	pDC	TEP1
7.72E-19	0.714466918	0.386	0.216	1.59E-14	pDC	YLPM1
1.33E-18	0.602881211	0.333	0.168	2.75E-14	pDC	ACTN4
1.63E-18	0.674440384	0.352	0.187	3.35E-14	pDC	LPXN

2.94E-18	0.622243739	0.611	0.423	6.06E-14	pDC	MAP3K2
3.31E-18	0.639294475	0.471	0.291	6.81E-14	pDC	ZNF652
5.42E-18	0.750672862	0.556	0.39	1.12E-13	pDC	SP110
6.31E-18	0.592387538	0.278	0.134	1.30E-13	pDC	PPP1R2
1.13E-17	0.649950017	0.519	0.34	2.32E-13	pDC	PHF14
1.13E-17	0.611842145	0.283	0.137	2.33E-13	pDC	SCAI
2.22E-17	0.59861243	0.302	0.151	4.57E-13	pDC	NBEA
3.29E-17	0.595271464	0.349	0.188	6.77E-13	pDC	CCDC18
5.32E-17	0.618573244	0.288	0.14	1.09E-12	pDC	RAB11FIP1
5.70E-17	0.828971354	0.339	0.188	1.17E-12	pDC	CCDC146
7.94E-17	0.639096642	0.598	0.43	1.63E-12	pDC	NFAT5
8.54E-17	0.605201245	0.347	0.189	1.76E-12	pDC	SUZ12
1.02E-16	0.625079093	0.365	0.205	2.09E-12	pDC	UBE2E3
1.05E-16	0.627187116	0.728	0.588	2.16E-12	pDC	RBM6
2.75E-16	0.705096816	0.299	0.154	5.65E-12	pDC	EEF2K
2.77E-16	0.59533018	0.563	0.403	5.71E-12	pDC	ASCC3
4.77E-16	0.612904767	0.434	0.27	9.82E-12	pDC	SMG7
5.44E-16	0.646617539	0.275	0.14	1.12E-11	pDC	EDRF1
7.95E-16	0.589754034	0.299	0.156	1.64E-11	pDC	LILRB4
9.26E-16	0.59630772	0.468	0.302	1.91E-11	pDC	HEATR5B
9.29E-16	0.709378581	0.534	0.385	1.91E-11	pDC	PTBP3
1.37E-15	0.617898401	0.291	0.151	2.83E-11	pDC	MARS
1.41E-15	0.727314127	0.37	0.217	2.91E-11	pDC	RFTN1
1.72E-15	0.616791283	0.415	0.253	3.54E-11	pDC	ANAPC16
2.30E-15	0.748983143	0.28	0.144	4.73E-11	pDC	ZMIZ2
3.18E-15	0.637474194	0.492	0.338	6.54E-11	pDC	SYNRG
3.42E-15	0.599565862	0.497	0.331	7.05E-11	pDC	CD4
3.60E-15	0.61417462	0.37	0.218	7.40E-11	pDC	PRIM2
4.42E-15	0.609564851	0.291	0.152	9.10E-11	pDC	ZRANB3
5.17E-15	0.63793829	0.384	0.227	1.06E-10	pDC	CLASRP
8.88E-15	0.586915072	0.323	0.182	1.83E-10	pDC	RBBP4
2.14E-14	0.594484832	0.439	0.279	4.41E-10	pDC	N4BP2L1
3.15E-14	0.605769386	0.579	0.427	6.48E-10	pDC	ZCCHC7
3.37E-14	0.592442669	0.466	0.311	6.93E-10	pDC	TM9SF2
1.29E-13	0.613110776	0.299	0.17	2.66E-09	pDC	KIAA0100
1.35E-13	0.680751023	0.463	0.307	2.77E-09	pDC	GALNT2
2.64E-13	0.598234157	0.331	0.193	5.43E-09	pDC	TULP4
2.75E-13	0.58748891	0.365	0.222	5.67E-09	pDC	MGA
5.34E-13	0.586307863	0.347	0.212	1.10E-08	pDC	CD164
6.22E-13	0.593921219	0.36	0.222	1.28E-08	pDC	PCNX4
7.19E-13	0.613448569	0.392	0.25	1.48E-08	pDC	ECHDC1
4.73E-10	0.651971349	0.317	0.206	9.73E-06	pDC	ATP8B1
6.30E-10	0.618743947	0.302	0.187	1.30E-05	pDC	NAALADL2

6.00E-08	0.653601002	0.659	0.587	0.001234569	pDC	WVOX
0	2.48833623	0.585	0.012	0	MKI67+ Mac	DIAPH3
0	2.350577024	0.5	0.004	0	MKI67+ Mac	RRM2
0	2.311729071	0.596	0.019	0	MKI67+ Mac	BRIP1
0	2.154541774	0.569	0.011	0	MKI67+ Mac	POLQ
0	2.025432622	0.418	0.006	0	MKI67+ Mac	ASPM
0	2.002255315	0.561	0.056	0	MKI67+ Mac	LINC01572
0	1.999222534	0.386	0.004	0	MKI67+ Mac	TOP2A
0	1.886572209	0.42	0.004	0	MKI67+ Mac	MKI67
0	1.857807493	0.457	0.009	0	MKI67+ Mac	CIT
0	1.739338632	0.428	0.026	0	MKI67+ Mac	HELLS
0	1.719081001	0.354	0.01	0	MKI67+ Mac	CENPF
0	1.706155498	0.455	0.018	0	MKI67+ Mac	KNL1
0	1.703162656	0.463	0.015	0	MKI67+ Mac	CENPK
0	1.681987828	0.439	0.006	0	MKI67+ Mac	MELK
0	1.625177213	0.42	0.014	0	MKI67+ Mac	NUSAP1
0	1.594339826	0.42	0.031	0	MKI67+ Mac	ARHGAP11B
0	1.574493254	0.343	0.001	0	MKI67+ Mac	KIF18B
0	1.566540573	0.402	0.016	0	MKI67+ Mac	C21orf58
0	1.557636873	0.375	0.002	0	MKI67+ Mac	DTL
0	1.539789619	0.457	0.03	0	MKI67+ Mac	FANCI
0	1.502552951	0.441	0.037	0	MKI67+ Mac	NCAPG2
0	1.461037125	0.463	0.043	0	MKI67+ Mac	BRCA1
0	1.448925997	0.354	0.008	0	MKI67+ Mac	KIF11
0	1.415537971	0.303	0.003	0	MKI67+ Mac	GTSE1
0	1.405610769	0.407	0.028	0	MKI67+ Mac	LMNB1
0	1.399654145	0.346	0.006	0	MKI67+ Mac	CLSPN
0	1.360531856	0.324	0.005	0	MKI67+ Mac	BUB1B
0	1.358271874	0.322	0.006	0	MKI67+ Mac	KIF15
0	1.349025916	0.322	0.002	0	MKI67+ Mac	ANLN
0	1.335634451	0.314	0.004	0	MKI67+ Mac	TPX2
0	1.305176881	0.327	0.011	0	MKI67+ Mac	STIL
0	1.185192516	0.332	0.008	0	MKI67+ Mac	ZNF367
0	1.166706772	0.282	0.012	0	MKI67+ Mac	WDR76
0	1.164801335	0.266	0.001	0	MKI67+ Mac	FAM111B
0	1.160756185	0.298	0.003	0	MKI67+ Mac	NCAPG
0	1.157553639	0.277	0.004	0	MKI67+ Mac	NDC80
0	1.127005473	0.309	0.014	0	MKI67+ Mac	CENPU
0	1.111724537	0.322	0.02	0	MKI67+ Mac	BLM
0	1.101024535	0.287	0.009	0	MKI67+ Mac	PRC1
0	1.07783439	0.266	0.01	0	MKI67+ Mac	CENPI
0	1.049027567	0.263	0.004	0	MKI67+ Mac	DEPDC1B
0	1.043219611	0.282	0.002	0	MKI67+ Mac	KIF4A

0	0.995425869	0.266	0.011	0	MKI67+ Mac	GINS1
1.95E-272	2.018724482	0.596	0.087	4.02E-268	MKI67+ Mac	EZH2
4.88E-264	1.082299941	0.279	0.018	1.01E-259	MKI67+ Mac	UHRF1
2.30E-258	1.891027533	0.426	0.044	4.74E-254	MKI67+ Mac	APOLD1
1.11E-254	1.465914766	0.457	0.052	2.28E-250	MKI67+ Mac	KNTC1
5.91E-254	1.2007542	0.367	0.033	1.22E-249	MKI67+ Mac	FANCA
8.67E-240	1.088352628	0.34	0.03	1.79E-235	MKI67+ Mac	LIG1
4.10E-239	1.834480399	0.58	0.09	8.43E-235	MKI67+ Mac	ATAD2
4.40E-236	0.854289997	0.258	0.017	9.05E-232	MKI67+ Mac	MCM8
8.17E-236	1.051404685	0.282	0.021	1.68E-231	MKI67+ Mac	PARPBP
1.64E-235	0.964886109	0.285	0.021	3.38E-231	MKI67+ Mac	WDHD1
1.01E-233	1.813506438	0.561	0.086	2.08E-229	MKI67+ Mac	SMC4
5.20E-228	1.191507663	0.356	0.034	1.07E-223	MKI67+ Mac	FANCD2
1.56E-221	1.568668472	0.529	0.079	3.21E-217	MKI67+ Mac	ATAD5
4.04E-207	1.457514968	0.471	0.066	8.31E-203	MKI67+ Mac	RFC3
2.63E-206	0.941448608	0.271	0.022	5.42E-202	MKI67+ Mac	SGO2
1.80E-204	1.322235041	0.375	0.043	3.70E-200	MKI67+ Mac	ZGRF1
4.03E-196	1.89664546	0.697	0.161	8.30E-192	MKI67+ Mac	NSD2
8.84E-193	0.923133917	0.25	0.02	1.82E-188	MKI67+ Mac	NUF2
3.63E-187	1.421817499	0.434	0.062	7.48E-183	MKI67+ Mac	BARD1
2.08E-167	1.400562016	0.495	0.087	4.28E-163	MKI67+ Mac	BRCA2
5.82E-161	0.941787327	0.279	0.03	1.20E-156	MKI67+ Mac	POLE2
1.76E-151	1.463453614	0.364	0.053	3.62E-147	MKI67+ Mac	CENPE
3.89E-151	1.505405496	0.532	0.11	8.01E-147	MKI67+ Mac	MMS22L
9.67E-149	1.342990039	0.505	0.1	1.99E-144	MKI67+ Mac	RBL1
3.75E-134	1.429268126	0.593	0.145	7.71E-130	MKI67+ Mac	CEP128
1.37E-129	0.883051569	0.266	0.032	2.82E-125	MKI67+ Mac	HMGB2
1.30E-122	1.033686498	0.367	0.063	2.68E-118	MKI67+ Mac	GEN1
2.88E-122	0.772664582	0.261	0.033	5.94E-118	MKI67+ Mac	DDX11
4.76E-122	0.868186324	0.29	0.04	9.81E-118	MKI67+ Mac	SMC2
3.47E-121	1.131876801	0.41	0.077	7.15E-117	MKI67+ Mac	CEP152
2.97E-111	1.708922694	0.731	0.286	6.12E-107	MKI67+ Mac	CENPP
2.06E-108	1.403352046	0.612	0.184	4.23E-104	MKI67+ Mac	CCDC18
4.06E-108	1.104444844	0.423	0.089	8.35E-104	MKI67+ Mac	NUP210
1.64E-105	0.772101978	0.25	0.035	3.39E-101	MKI67+ Mac	PRIM1
4.46E-102	0.904140449	0.348	0.065	9.19E-98	MKI67+ Mac	VRK1
2.45E-96	1.006549527	0.386	0.083	5.04E-92	MKI67+ Mac	ITGB3BP
2.12E-95	1.125189782	0.367	0.077	4.37E-91	MKI67+ Mac	KIF20B
2.96E-93	0.863542728	0.266	0.043	6.08E-89	MKI67+ Mac	NCAPD2
1.42E-91	1.096297377	0.415	0.098	2.91E-87	MKI67+ Mac	FANCC
8.44E-91	1.135693623	0.404	0.096	1.74E-86	MKI67+ Mac	NCAPD3
5.00E-90	0.837751081	0.271	0.046	1.03E-85	MKI67+ Mac	POLE
3.27E-88	1.081642941	0.378	0.086	6.73E-84	MKI67+ Mac	TACC3

1.85E-85	1.196280394	0.471	0.13	3.81E-81	MKI67+ Mac	SCMH1
3.85E-83	1.302578744	0.476	0.144	7.92E-79	MKI67+ Mac	POLA1
5.55E-82	0.746326046	0.269	0.048	1.14E-77	MKI67+ Mac	CENPJ
2.01E-80	1.104725815	0.489	0.148	4.14E-76	MKI67+ Mac	NASP
2.70E-73	0.911638297	0.396	0.105	5.55E-69	MKI67+ Mac	RFWD3
4.60E-71	0.794043805	0.394	0.104	9.46E-67	MKI67+ Mac	TTF2
1.00E-70	0.996776029	0.484	0.154	2.06E-66	MKI67+ Mac	FAM111A
2.97E-70	1.082891249	0.513	0.175	6.12E-66	MKI67+ Mac	TMPO
1.23E-67	0.965687447	0.471	0.148	2.53E-63	MKI67+ Mac	DNMT1
1.74E-67	0.910245364	0.431	0.129	3.59E-63	MKI67+ Mac	TOPBP1
9.38E-67	0.872548133	0.359	0.094	1.93E-62	MKI67+ Mac	LIN54
6.23E-66	1.184424676	0.553	0.215	1.28E-61	MKI67+ Mac	PRIM2
5.10E-63	0.655386351	0.253	0.052	1.05E-58	MKI67+ Mac	CHEK2
1.53E-59	1.035647268	0.566	0.226	3.15E-55	MKI67+ Mac	DEK
4.96E-54	0.735273377	0.37	0.11	1.02E-49	MKI67+ Mac	LIN52
6.38E-54	0.890812241	0.423	0.141	1.31E-49	MKI67+ Mac	HMGN2
9.16E-54	0.92009367	0.402	0.131	1.89E-49	MKI67+ Mac	MPHOSPH9
6.22E-51	0.937348052	0.471	0.178	1.28E-46	MKI67+ Mac	CCDC14
1.95E-49	0.662119225	0.269	0.07	4.02E-45	MKI67+ Mac	RAD18
2.26E-49	0.851905908	0.428	0.152	4.64E-45	MKI67+ Mac	CEP295
4.13E-49	1.005459401	0.604	0.287	8.50E-45	MKI67+ Mac	CEP192
7.39E-49	0.773028035	0.375	0.122	1.52E-44	MKI67+ Mac	RTTN
1.38E-48	0.702766943	0.258	0.066	2.84E-44	MKI67+ Mac	TFDP1
1.67E-48	0.827913113	0.332	0.097	3.44E-44	MKI67+ Mac	FLT3
2.98E-48	0.917811001	0.439	0.165	6.13E-44	MKI67+ Mac	CKAP5
8.47E-48	0.653218499	0.271	0.072	1.74E-43	MKI67+ Mac	POLA2
8.75E-48	0.769304424	0.311	0.09	1.80E-43	MKI67+ Mac	DDB2
1.37E-47	0.82886369	0.463	0.172	2.82E-43	MKI67+ Mac	PHLPP1
5.59E-47	0.631178169	0.348	0.109	1.15E-42	MKI67+ Mac	ANP32B
1.19E-45	0.892169467	0.569	0.264	2.46E-41	MKI67+ Mac	SPATA5
1.72E-44	0.632113062	0.253	0.067	3.54E-40	MKI67+ Mac	RBBP8
2.09E-44	0.675210887	0.335	0.106	4.31E-40	MKI67+ Mac	H2AFV
2.85E-44	0.713223088	0.25	0.066	5.86E-40	MKI67+ Mac	ST18
8.70E-44	0.794959332	0.314	0.099	1.79E-39	MKI67+ Mac	MYO19
1.58E-41	0.730904341	0.33	0.106	3.25E-37	MKI67+ Mac	ADAM28
3.53E-40	0.797339277	0.42	0.163	7.27E-36	MKI67+ Mac	ST3GAL3
1.19E-39	0.856477889	0.793	0.554	2.44E-35	MKI67+ Mac	FAF1
2.97E-39	0.750454087	0.463	0.197	6.12E-35	MKI67+ Mac	SRSF10
1.32E-38	0.862952648	0.468	0.207	2.71E-34	MKI67+ Mac	CDK5RAP2
1.33E-38	0.732468297	0.295	0.095	2.73E-34	MKI67+ Mac	PCNT
9.47E-38	0.608425006	0.354	0.125	1.95E-33	MKI67+ Mac	RAD21
1.00E-37	0.814366465	0.668	0.363	2.06E-33	MKI67+ Mac	CNTRL
1.39E-37	0.731065135	0.303	0.1	2.86E-33	MKI67+ Mac	TUBB

3.68E-37	0.84166813	0.33	0.118	7.57E-33	MKI67+ Mac	TUBA1B
8.90E-37	0.72516961	0.527	0.243	1.83E-32	MKI67+ Mac	NUCKS1
1.19E-36	0.762417025	0.402	0.164	2.45E-32	MKI67+ Mac	FANCL
7.61E-36	0.926764804	0.447	0.19	1.57E-31	MKI67+ Mac	AUTS2
7.78E-36	0.617001414	0.303	0.103	1.60E-31	MKI67+ Mac	SAE1
4.44E-35	0.681812985	0.354	0.134	9.14E-31	MKI67+ Mac	SLF1
7.78E-35	0.73375992	0.362	0.138	1.60E-30	MKI67+ Mac	BICD1
1.70E-34	0.645892405	0.388	0.157	3.50E-30	MKI67+ Mac	USP37
2.97E-34	0.718997767	0.359	0.136	6.11E-30	MKI67+ Mac	SPECC1
8.54E-34	0.72907087	0.274	0.092	1.76E-29	MKI67+ Mac	RANBP17
8.59E-34	0.90340973	0.327	0.12	1.77E-29	MKI67+ Mac	DTNA
1.40E-33	0.716258576	0.426	0.18	2.87E-29	MKI67+ Mac	SFMBT1
1.78E-33	0.646528456	0.282	0.094	3.65E-29	MKI67+ Mac	PCNX2
3.17E-33	0.739293921	0.423	0.179	6.53E-29	MKI67+ Mac	CDK14
6.96E-33	0.594904526	0.309	0.111	1.43E-28	MKI67+ Mac	GMPS
1.54E-32	0.649979756	0.359	0.142	3.18E-28	MKI67+ Mac	CASP8AP2
1.40E-31	0.762588061	0.569	0.313	2.88E-27	MKI67+ Mac	PRKDC
1.56E-31	0.681498375	0.295	0.106	3.22E-27	MKI67+ Mac	MTHFD1L
3.25E-31	0.898318474	0.476	0.226	6.69E-27	MKI67+ Mac	RTN1
9.08E-31	0.665878911	0.388	0.163	1.87E-26	MKI67+ Mac	MIR4435-2HG
1.29E-30	0.700185282	0.569	0.295	2.65E-26	MKI67+ Mac	PDS5B
1.58E-30	0.701558227	0.402	0.174	3.25E-26	MKI67+ Mac	NDUFAF6
3.28E-30	0.66244722	0.391	0.168	6.74E-26	MKI67+ Mac	MAST2
5.36E-30	0.59606059	0.346	0.139	1.10E-25	MKI67+ Mac	NUP107
6.89E-30	1.07464336	0.649	0.422	1.42E-25	MKI67+ Mac	AFF3
3.38E-29	0.657654223	0.415	0.188	6.96E-25	MKI67+ Mac	SUZ12
1.18E-28	0.728496698	0.497	0.252	2.43E-24	MKI67+ Mac	PKP4
3.64E-28	0.659584488	0.391	0.174	7.50E-24	MKI67+ Mac	AHI1
4.27E-27	0.604249952	0.356	0.153	8.80E-23	MKI67+ Mac	CYTOR
1.21E-26	0.586275368	0.367	0.161	2.48E-22	MKI67+ Mac	KLHL22
1.82E-26	0.663077435	0.378	0.167	3.75E-22	MKI67+ Mac	CKLF
1.86E-25	0.597266689	0.316	0.13	3.84E-21	MKI67+ Mac	ELOVL5
1.94E-25	0.659527147	0.402	0.187	4.00E-21	MKI67+ Mac	CTCF
7.43E-25	0.594488355	0.465	0.239	1.53E-20	MKI67+ Mac	NAP1L4
7.73E-25	0.619877142	0.261	0.097	1.59E-20	MKI67+ Mac	GPAT3
9.95E-25	0.691303871	0.574	0.335	2.05E-20	MKI67+ Mac	XPO1
2.35E-24	0.630149339	0.364	0.168	4.83E-20	MKI67+ Mac	IPO9
2.99E-24	0.695296001	0.378	0.178	6.14E-20	MKI67+ Mac	UBAP2
5.77E-24	0.602156915	0.316	0.133	1.19E-19	MKI67+ Mac	TRERF1
6.49E-24	0.604619385	0.362	0.165	1.34E-19	MKI67+ Mac	ZNF83
9.84E-24	0.611761068	0.452	0.232	2.03E-19	MKI67+ Mac	RIF1
9.92E-24	0.683401539	0.699	0.471	2.04E-19	MKI67+ Mac	PBX3
3.01E-23	0.596375887	0.497	0.27	6.20E-19	MKI67+ Mac	CTDSPL2

3.93E-23	0.65275628	0.731	0.507	8.10E-19	MKI67+ Mac	RAD51B
4.60E-23	0.626637223	0.811	0.627	9.47E-19	MKI67+ Mac	STAG1
8.75E-23	0.621025772	0.556	0.33	1.80E-18	MKI67+ Mac	PDE7A
8.86E-23	0.627350647	0.263	0.104	1.82E-18	MKI67+ Mac	HNRNPLL
3.16E-21	0.679510351	0.702	0.462	6.50E-17	MKI67+ Mac	HNRNPH1
3.17E-21	0.723214341	0.59	0.359	6.53E-17	MKI67+ Mac	SFMBT2
1.80E-18	0.598008607	0.513	0.313	3.70E-14	MKI67+ Mac	PAK1
1.43E-17	0.608509443	0.654	0.462	2.94E-13	MKI67+ Mac	MIS18BP1
6.29E-17	0.64302886	0.609	0.415	1.29E-12	MKI67+ Mac	HP1BP3
3.43E-16	0.588109665	0.582	0.393	7.06E-12	MKI67+ Mac	LCORL
1.92E-14	0.588055528	0.449	0.28	3.96E-10	MKI67+ Mac	HLA-DPA1
4.19E-13	0.599141104	0.559	0.386	8.62E-09	MKI67+ Mac	HLA-DRA
9.72E-09	0.590733531	0.415	0.287	0.000200138	MKI67+ Mac	CCSER1

Supplementary Table 7

regulons	Module
ARID3A(+)	M1
ARID3B(+)	M1
ARNT2(+)	M2
ATF3(+)	M3
ATF4(+)	M4
ATF5(+)	M5
ATF6(+)	M6
ATF6B(+)	M7
ATF7(+)	M7
ATOH8(+)	M5
BACH1(+)	M8
BACH2(+)	M2
BATF3(+)	M9
BBX(+)	M10
BCL11A(+)	M2
BCL11B(+)	M1
BCL3(+)	M2
BCL6(+)	M10
BCLAF1(+)	M2
BDP1(+)	M7
BHLHE40(+)	M6
BHLHE41(+)	M3
BRCA1(+)	M11
BRF2(+)	M5
CEBPA(+)	M1
CEBPB(+)	M12
CEBPD(+)	M13
CEBPG(+)	M1
CEBPZ(+)	M11
CERS3(+)	M1
CHD1(+)	M12
CHD2(+)	M8
CLOCK(+)	M8
CREB1(+)	M8
CREB3(+)	M4
CREB3L2(+)	M3
CREM(+)	M12
CTCF(+)	M10
CUX1(+)	M8
CUX2(+)	M1

DBP(+)	M9
DDIT3(+)	M14
DMRTA1(+)	M13
E2F1(+)	M15
E2F2(+)	M11
E2F3(+)	M13
E2F4(+)	M13
E2F6(+)	M7
E2F7(+)	M11
E2F8(+)	M11
EBF4(+)	M10
EGR2(+)	M12
EGR3(+)	M6
ELF1(+)	M13
ELF2(+)	M13
ELF3(+)	M1
ELF4(+)	M11
ELF5(+)	M7
ELK1(+)	M6
ELK3(+)	M10
ELK4(+)	M12
EOMES(+)	M1
EP300(+)	M8
ERF(+)	M16
ERG(+)	M15
ESR1(+)	M4
ESR2(+)	M9
ESRRA(+)	M5
ESRRB(+)	M16
ETS1(+)	M5
ETS2(+)	M12
ETV1(+)	M16
ETV2(+)	M5
ETV3L(+)	M13
ETV4(+)	M11
ETV5(+)	M13
ETV6(+)	M8
ETV7(+)	M8
EZH2(+)	M2
FLI1(+)	M8
FOS(+)	M12
FOSB(+)	M6
FOSL1(+)	M12

FOSL2(+)	M12
FOXA1(+)	M6
FOXA2(+)	M6
FOXA3(+)	M5
FOXJ2(+)	M10
FOXJ3(+)	M10
FO XK1(+)	M2
FOXM1(+)	M5
FOXN2(+)	M2
FOXO1(+)	M5
FOXO3(+)	M6
FOXO4(+)	M1
FOXP1(+)	M2
FOXP4(+)	M5
GABPA(+)	M4
GABPB1(+)	M10
GATA2(+)	M15
GATA4(+)	M5
GATA6(+)	M5
GBX1(+)	M15
GLI3(+)	M6
GLIS2(+)	M5
GMEB1(+)	M13
GMEB2(+)	M1
GRHL1(+)	M4
GRHL2(+)	M5
GTF2B(+)	M16
GTF2F1(+)	M15
GTF3C2(+)	M2
HES5(+)	M16
HEY2(+)	M5
HHAT(+)	M1
HIC1(+)	M4
HINFP(+)	M11
HIVEP1(+)	M8
HIVEP2(+)	M3
HIVEP3(+)	M8
HLF(+)	M5
HMGB1(+)	M1
HMGB3(+)	M5
HMGN3(+)	M4
HNF1A(+)	M5
HNF1B(+)	M5

HN4A(+)	M5
HN4G(+)	M5
HOXB2(+)	M3
HOXB6(+)	M16
HSF1(+)	M6
ID1(+)	M5
IKZF1(+)	M8
IKZF2(+)	M6
IRF1(+)	M2
IRF2(+)	M8
IRF4(+)	M10
IRF7(+)	M2
IRF8(+)	M8
IRF9(+)	M7
JAZF1(+)	M10
JDP2(+)	M13
JUN(+)	M12
JUNB(+)	M12
JUND(+)	M5
KDM5A(+)	M8
KLF10(+)	M10
KLF11(+)	M1
KLF12(+)	M15
KLF13(+)	M15
KLF2(+)	M10
KLF3(+)	M7
KLF4(+)	M5
KLF5(+)	M3
KLF6(+)	M12
KLF8(+)	M15
LEF1(+)	M1
LHX4(+)	M11
LMO2(+)	M10
MAFA(+)	M5
MAFB(+)	M13
MAFF(+)	M6
MAFK(+)	M1
MAX(+)	M7
MAZ(+)	M4
MECOM(+)	M1
MEF2B(+)	M5
MEF2C(+)	M2
MEF2D(+)	M10

MITF(+)	M13
MLX(+)	M7
MNT(+)	M1
MTA3(+)	M2
MXD3(+)	M1
MXI1(+)	M1
MYB(+)	M1
MYBL1(+)	M10
MYBL2(+)	M11
MYC(+)	M8
MYEF2(+)	M9
NELFE(+)	M1
NEUROG3(+)	M13
NFE2(+)	M1
NFE2L1(+)	M5
NFE2L2(+)	M8
NFE2L3(+)	M10
NFIL3(+)	M12
NFKB1(+)	M8
NFKB2(+)	M8
NFYA(+)	M12
NFYB(+)	M15
NFYC(+)	M2
NHLH1(+)	M7
NPDC1(+)	M11
NR1D2(+)	M5
NR1H3(+)	M13
NR1H4(+)	M5
NR1I2(+)	M5
NR1I3(+)	M5
NR2C1(+)	M4
NR2F1(+)	M1
NR2F2(+)	M5
NR2F6(+)	M5
NR3C1(+)	M8
NUAK2(+)	M10
OLIG1(+)	M15
ONECUT1(+)	M5
PATZ1(+)	M6
PBX1(+)	M1
PHF8(+)	M5
PKM(+)	M1
PKNOX1(+)	M12

PLAGL2(+)	M15
POLE3(+)	M1
POLR2A(+)	M14
POLR3A(+)	M1
POU1F1(+)	M16
POU6F2(+)	M5
PPARA(+)	M5
PPARD(+)	M8
PPARG(+)	M13
PPARGC1A(+)	M5
PRDM1(+)	M8
PRDM16(+)	M10
PRKAA2(+)	M4
PURA(+)	M1
RAD21(+)	M10
RARA(+)	M8
RARB(+)	M8
RARG(+)	M3
RBBP5(+)	M15
RCOR1(+)	M8
REL(+)	M3
RELA(+)	M1
RELB(+)	M8
RFX1(+)	M5
RFX3(+)	M7
RFX4(+)	M7
RFX5(+)	M11
RFXAP(+)	M1
RORC(+)	M9
RREB1(+)	M13
RUNX2(+)	M10
RUNX3(+)	M10
RXRA(+)	M7
SETDB1(+)	M7
SHOX2(+)	M17
SIN3A(+)	M10
SMAD3(+)	M1
SMAD6(+)	M7
SMARCA4(+)	M2
SOX10(+)	M4
SOX13(+)	M7
SOX18(+)	M15
SOX30(+)	M11

SOX4(+)	M10
SOX9(+)	M5
SP1(+)	M11
SP4(+)	M15
SPI1(+)	M2
SPIB(+)	M10
SPIC(+)	M13
SREBF1(+)	M13
SREBF2(+)	M8
SRF(+)	M12
STAT1(+)	M8
STAT2(+)	M7
STAT3(+)	M6
STAT4(+)	M5
STAT5A(+)	M17
SUPT20H(+)	M8
TAF1(+)	M10
TAF7(+)	M15
TBP(+)	M7
TBX1(+)	M13
TBX19(+)	M7
TBX2(+)	M4
TBX20(+)	M3
TBX21(+)	M7
TBX3(+)	M5
TBX4(+)	M11
TCF12(+)	M13
TCF7L1(+)	M16
TCF7L2(+)	M13
TEAD1(+)	M5
TEAD4(+)	M9
TEF(+)	M5
TFDP1(+)	M10
TFE3(+)	M13
TFEB(+)	M2
TFEC(+)	M13
TGIF1(+)	M12
THAP1(+)	M5
THRA(+)	M6
TP53(+)	M7
UBTF(+)	M16
USF1(+)	M11
USF2(+)	M8

VAX2(+)	M1
VDR(+)	M10
VENTX(+)	M5
XBP1(+)	M5
XRCC4(+)	M8
YY1(+)	M15
ZBTB17(+)	M4
ZBTB2(+)	M16
ZBTB7A(+)	M15
ZBTB7B(+)	M1
ZC3H11A(+)	M4
ZEB1(+)	M2
ZFHX2(+)	M7
ZFP64(+)	M7
ZFY(+)	M7
ZKSCAN8(+)	M9
ZMIZ1(+)	M8
ZNF100(+)	M4
ZNF121(+)	M11
ZNF143(+)	M14
ZNF224(+)	M4
ZNF236(+)	M10
ZNF254(+)	M7
ZNF266(+)	M16
ZNF274(+)	M6
ZNF287(+)	M1
ZNF296(+)	M1
ZNF304(+)	M16
ZNF316(+)	M12
ZNF329(+)	M9
ZNF345(+)	M15
ZNF35(+)	M9
ZNF350(+)	M4
ZNF362(+)	M10
ZNF384(+)	M7
ZNF394(+)	M15
ZNF423(+)	M16
ZNF425(+)	M9
ZNF426(+)	M7
ZNF436(+)	M4
ZNF44(+)	M11
ZNF490(+)	M2
ZNF549(+)	M10

ZNF639(+)	M16
ZNF658(+)	M15
ZNF672(+)	M6
ZNF674(+)	M15
ZNF687(+)	M1
ZNF696(+)	M4
ZNF709(+)	M9
ZNF71(+)	M4
ZNF713(+)	M10
ZNF740(+)	M9
ZNF768(+)	M9
ZNF770(+)	M15
ZNF772(+)	M6
ZNF8(+)	M5
ZNF814(+)	M4
ZNF821(+)	M4
ZNF846(+)	M16
ZNF92(+)	M14
ZXDB(+)	M5

Supplementary Table 8

seqnames	start	end	width	strand	Conc	Conc. MASH	Conc. MASLD	Fold	p.value	FDR	type
chr6	160764832	160765232	401	*	3.210373556	3.477098819	2.843665073	0.510840479	0.002087318	0.021227548	sigUp
chr6	160749919	160750319	401	*	3.375210936	3.630360905	3.028135189	0.463916005	0.011846536	0.054909746	sigUp
chr6	160757515	160757915	401	*	4.653090608	4.9210307	4.284296866	0.465683569	0.011903585	0.055060985	sigUp
chr6	160783744	160784144	401	*	2.779517802	2.994598919	2.497268133	0.39335697	0.020617197	0.075981981	sigUp
chr6	160733084	160733484	401	*	3.557601346	3.751881102	3.307218337	0.369698755	0.029181749	0.093661598	sigUp
chr6	160739926	160740326	401	*	4.036030366	4.273417533	3.718275274	0.399923508	0.033527266	0.102026065	sigUp
chr6	160690516	160690916	401	*	3.199676913	3.387225191	2.959360997	0.348494905	0.033584675	0.102128699	sigUp

Supplementary Table 9

[illegible]

Supplementary Table 10

ID	name	seqnames	start	end	width	strand	score
MA0511.2	RUNX2	chr6	160764929	160764937	9	-	9.49357754717842
MA0511.2	RUNX2	chr6	160764940	160764948	9	-	7.06830428769327
MA0511.2	RUNX2	chr6	160764969	160764977	9	-	3.20869188382545
MA0511.2	RUNX2	chr6	160765023	160765031	9	-	7.05961806161014
MA0511.2	RUNX2	chr6	160765034	160765042	9	-	3.29326675914408
MA0511.2	RUNX2	chr6	160765041	160765049	9	-	3.56829909545862
MA0511.2	RUNX2	chr6	160765081	160765089	9	-	7.89674864907033
MA0511.2	RUNX2	chr6	160765090	160765098	9	-	6.84498301043702
MA0511.2	RUNX2	chr6	160765144	160765152	9	-	7.05961806161014
MA0511.2	RUNX2	chr6	160750004	160750012	9	+	5.86003932861242
MA0511.2	RUNX2	chr6	160750011	160750019	9	+	7.64315647849457
MA0511.2	RUNX2	chr6	160750188	160750196	9	-	2.04472964959184
MA0511.2	RUNX2	chr6	160757571	160757579	9	+	2.12220162146564
MA0511.2	RUNX2	chr6	160757625	160757633	9	+	9.64424930018837
MA0511.2	RUNX2	chr6	160757634	160757642	9	+	2.41852033472734
MA0511.2	RUNX2	chr6	160757642	160757650	9	+	2.3716720463506
MA0511.2	RUNX2	chr6	160783927	160783935	9	+	1.93568473981511
MA0511.2	RUNX2	chr6	160784023	160784031	9	-	0.479037818319499
MA0511.2	RUNX2	chr6	160733110	160733118	9	+	0.467780905403947
MA0511.2	RUNX2	chr6	160733111	160733119	9	+	3.19422445718704
MA0511.2	RUNX2	chr6	160733180	160733188	9	+	6.27904993054596
MA0511.2	RUNX2	chr6	160733430	160733438	9	+	1.73562650057478
MA0511.2	RUNX2	chr6	160740304	160740312	9	+	2.98590231497178
MA0511.2	RUNX2	chr6	160740062	160740070	9	-	5.99285750812367
MA0511.2	RUNX2	chr6	160690652	160690660	9	+	6.8014427240983
MA0511.2	RUNX2	chr6	160690759	160690767	9	-	5.26645000083251

Supplementary Table 11

seqnames	start	end	width	strand	score	annotation	geneChr	geneStart	geneEnd	geneLength	geneStrand	geneId	transcriptId	distanceToSS	ENSEMBL	SYMBOL	GENENAME
chr6	160764529	160764587	9	-	9493877547	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25769	ENSG00000122194	PLG	plasminogen
chr6	160764540	160764549	9	-	7088904380	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25780	ENSG00000122194	PLG	plasminogen
chr6	160764569	160764577	9	-	3208691884	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25809	ENSG00000122194	PLG	plasminogen
chr6	160765023	160765021	9	-	7056418052	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25863	ENSG00000122194	PLG	plasminogen
chr6	160765034	160765042	9	-	2352907576	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25874	ENSG00000122194	PLG	plasminogen
chr6	160765041	160765049	9	-	358299056	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25881	ENSG00000122194	PLG	plasminogen
chr6	160765081	160765089	9	-	7896749548	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25921	ENSG00000122194	PLG	plasminogen
chr6	160765090	160765098	9	-	684498203	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25930	ENSG00000122194	PLG	plasminogen
chr6	160765144	160765152	9	-	7056418052	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		25984	ENSG00000122194	PLG	plasminogen
chr6	160765004	160765002	9	+	5890028229	Intron ENST00000418964.2/ENST00000418964.2, intron 17 of 18)	6	160739108	160753215	14148	1	ENST000000461414.2		10838	ENSG00000122194	PLG	plasminogen
chr6	160765011	160765019	9	+	7642156478	Intron ENST00000418964.2/ENST00000418964.2, intron 17 of 18)	6	160739108	160753215	14148	1	ENST000000461414.2		10843	ENSG00000122194	PLG	plasminogen
chr6	160765188	160765196	9	-	204472965	Intron ENST00000418964.2/ENST00000418964.2, intron 17 of 18)	6	160739108	160753215	14148	1	ENST000000461414.2		11028	ENSG00000122194	PLG	plasminogen
chr6	160767671	160767679	9	+	2122201621	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		18403	ENSG00000122194	PLG	plasminogen
chr6	160767625	160767633	9	+	944024502	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		18457	ENSG00000122194	PLG	plasminogen
chr6	160767634	160767642	9	+	2418523235	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		18466	ENSG00000122194	PLG	plasminogen
chr6	160767642	160767650	9	+	2371672046	Intron ENST000000659713.1/ENST000000659713.1, intron 1 of 1)	6	160739108	160753215	14148	1	ENST000000461414.2		18474	ENSG00000122194	PLG	plasminogen
chr6	160782857	160782865	9	+	153858474	Distal Intergenic	6	160739108	160753215	14148	1	ENST000000461414.2		44789	ENSG00000122194	PLG	plasminogen
chr6	160784022	160784031	9	-	0479027818	Distal Intergenic	6	160739108	160753215	14148	1	ENST000000461414.2		44983	ENSG00000122194	PLG	plasminogen
chr6	160732110	160732118	9	+	0467789505	Promoter (1-34)	6	160731831	160739843	8012	1	ENST000000706907.1		1279	ENSG00000122194	PLG	plasminogen
chr6	160732111	160732119	9	+	3194234487	Promoter (1-34)	6	160731831	160739843	8012	1	ENST000000706907.1		1280	ENSG00000122194	PLG	plasminogen
chr6	160732180	160732188	9	+	6278049601	Promoter (1-34)	6	160731831	160739843	8012	1	ENST000000706907.1		1349	ENSG00000122194	PLG	plasminogen
chr6	160732430	160732438	9	+	1736626501	Promoter (1-34)	6	160731831	160739843	8012	1	ENST000000706907.1		1599	ENSG00000122194	PLG	plasminogen
chr6	160740304	160740312	9	+	2586902315	Promoter (1-34)	6	160739108	160753215	14148	1	ENST000000461414.2		1136	ENSG00000122194	PLG	plasminogen
chr6	160740362	160740370	9	+	5592857508	Promoter (-34)	6	160739108	160753215	14148	1	ENST000000461414.2		802	ENSG00000122194	PLG	plasminogen
chr6	160690662	160690660	9	+	6901442724	Distal Intergenic	6	160702194	160764046	51853	1	ENST000000418964.2		-11534	ENSG00000122194	PLG	plasminogen
chr6	160690759	160690767	9	+	6296450001	Distal Intergenic	6	160702194	160764046	51853	1	ENST000000418964.2		-11435	ENSG00000122194	PLG	plasminogen

Supplementary Table 12

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
APOB	0	2.382425019	0.896	0.425	0
TF	0	2.488690437	0.923	0.521	0
ALB	0	2.456477814	0.989	0.945	0
FGB	0	2.389953175	0.921	0.467	0
FGA	0	2.396400707	0.907	0.422	0
FGG	0	2.413367502	0.897	0.392	0
PLG	0	3.050074657	1	0.192	0
AMBP	0	2.067159422	0.906	0.454	0
ORM2	0	2.121207456	0.816	0.248	0
APOH	1.55E-306	2.132280273	0.887	0.432	3.18E-302
CLU	2.69E-300	2.022311818	0.851	0.33	5.54E-296
SERPINA1	2.72E-296	2.391514194	0.917	0.549	5.59E-292
GC	2.11E-290	2.042028155	0.817	0.275	4.35E-286
MALAT1	1.60E-287	-1.720952622	1	1	3.29E-283
VTN	6.36E-285	1.929727054	0.869	0.381	1.31E-280
FN1	3.44E-283	1.916545105	0.799	0.252	7.08E-279
HP	4.67E-277	2.12031981	0.915	0.545	9.61E-273
C3	2.50E-276	1.913848583	0.874	0.401	5.14E-272
KNG1	7.37E-276	1.974135286	0.81	0.293	1.52E-271
APOA1	1.89E-272	1.966469065	0.94	0.727	3.88E-268
CP	3.03E-269	2.02219043	0.832	0.341	6.25E-265
CFB	4.92E-266	1.906695594	0.749	0.222	1.01E-261
CFH	2.99E-262	1.827361144	0.82	0.317	6.16E-258
HPX	5.11E-257	1.844850943	0.781	0.269	1.05E-252
APOC3	5.90E-253	1.730108943	0.939	0.732	1.21E-248
SERPING1	7.90E-253	1.835858666	0.74	0.23	1.63E-248
SERPINA3	4.10E-245	2.334084943	0.706	0.191	8.44E-241
C9	5.83E-242	1.871576113	0.711	0.208	1.20E-237
APOE	1.78E-238	1.665334793	0.915	0.623	3.66E-234
AGT	6.89E-231	1.817548362	0.63	0.15	1.42E-226
C4BPA	2.63E-229	1.720556774	0.64	0.162	5.40E-225
ALDOB	1.35E-228	2.116700986	0.847	0.447	2.77E-224
UGT2B7	1.37E-225	2.067081428	0.611	0.146	2.83E-221
FGL1	5.68E-219	1.969239705	0.701	0.217	1.17E-214
TMBIM6	4.94E-216	1.727030079	0.752	0.306	1.02E-211
C1S	2.29E-214	1.613574907	0.728	0.256	4.72E-210
AHSG	6.64E-210	2.029914631	0.715	0.266	1.37E-205
RBP4	5.28E-208	1.560576355	0.888	0.552	1.09E-203
ITIH2	5.14E-206	1.724805199	0.621	0.172	1.06E-201
CES1	1.64E-205	1.855449208	0.693	0.242	3.38E-201

HRG	4.85E-198	1.994129721	0.621	0.187	9.98E-194
APCS	1.01E-197	1.620055973	0.611	0.171	2.08E-193
SERPINC1	2.63E-195	1.575907402	0.639	0.193	5.41E-191
ORM1	2.65E-195	1.981781575	0.781	0.361	5.46E-191
TAT	1.78E-188	1.791651751	0.622	0.191	3.65E-184
CPS1	1.61E-186	1.617968256	0.788	0.369	3.32E-182
MAT1A	2.87E-186	1.682334532	0.614	0.187	5.91E-182
IGFBP1	8.28E-185	1.831496376	0.531	0.125	1.70E-180
MGST1	2.02E-181	1.533593649	0.694	0.262	4.16E-177
CYP2E1	2.68E-181	1.837213286	0.77	0.408	5.52E-177
APOC1	1.60E-180	1.315697439	0.93	0.725	3.29E-176
C1R	7.23E-176	1.507935096	0.579	0.167	1.49E-171
A1BG	1.72E-174	1.575974244	0.614	0.205	3.54E-170
SCD	1.61E-173	1.798997467	0.553	0.158	3.32E-169
P4HB	5.03E-171	1.460508458	0.63	0.218	1.03E-166
CFHR2	1.27E-170	1.468518837	0.533	0.139	2.62E-166
SAA4	1.55E-170	1.569147801	0.613	0.197	3.18E-166
TTR	3.31E-169	1.487559624	0.882	0.627	6.82E-165
F2	2.18E-168	1.528327119	0.55	0.153	4.48E-164
ADH1B	6.48E-165	1.719520388	0.717	0.34	1.33E-160
HSD17B6	2.65E-163	1.59494944	0.587	0.188	5.46E-159
UGT2B15	3.39E-163	1.550222313	0.484	0.113	6.97E-159
SELENOP	2.04E-156	1.295891156	0.841	0.505	4.20E-152
FKBP5	1.47E-155	1.195724806	0.877	0.591	3.03E-151
SLC2A2	4.34E-155	1.455771075	0.502	0.135	8.94E-151
PRG4	1.84E-154	1.324683752	0.433	0.09	3.79E-150
CPB2	9.38E-154	1.344389048	0.55	0.161	1.93E-149
APOC2	9.50E-150	1.229252627	0.825	0.494	1.96E-145
UGT2B4	1.68E-149	1.377372857	0.489	0.13	3.45E-145
C5	9.77E-146	1.385673395	0.617	0.233	2.01E-141
PCK1	1.21E-144	1.405000536	0.56	0.183	2.49E-140
SULT2A1	3.03E-142	1.376488516	0.482	0.132	6.24E-138
F9	1.72E-141	1.255304104	0.447	0.106	3.54E-137
SERPINF2	3.37E-138	1.353570243	0.504	0.151	6.94E-134
CRP	2.50E-137	1.611867471	0.454	0.113	5.15E-133
CYP2C9	1.04E-135	1.291329002	0.658	0.29	2.14E-131
CFI	2.28E-135	1.296124462	0.469	0.128	4.69E-131
APOA2	1.21E-133	1.042833678	0.914	0.712	2.48E-129
BAAT	1.41E-131	1.409289915	0.536	0.185	2.90E-127
SLC38A4	2.55E-130	1.307999331	0.54	0.184	5.26E-126
ANGPTL3	9.75E-130	1.269631348	0.493	0.152	2.01E-125
CYP2C8	3.37E-129	1.197374173	0.619	0.253	6.93E-125
FABP1	5.11E-129	1.28498761	0.692	0.337	1.05E-124

EPHX1	6.25E-128	1.46277109	0.512	0.18	1.29E-123
C6	2.38E-125	1.215333898	0.428	0.111	4.89E-121
HSP90B1	2.97E-124	1.237275531	0.698	0.375	6.12E-120
SLC7A2	2.46E-122	1.311190974	0.45	0.126	5.07E-118
IGFBP4	7.75E-122	1.282407707	0.449	0.131	1.60E-117
ZBTB16	1.83E-121	1.155408183	0.536	0.173	3.76E-117
METTL7A	5.33E-121	1.252658501	0.544	0.211	1.10E-116
SAA2	3.16E-120	2.050909776	0.414	0.107	6.50E-116
FTL	5.08E-120	0.898538356	0.922	0.741	1.05E-115
ITIH4	1.76E-119	1.223637093	0.606	0.269	3.63E-115
MTPP	3.89E-117	1.193343977	0.365	0.082	8.00E-113
ITIH3	1.20E-116	1.247729514	0.425	0.117	2.46E-112
LRG1	2.03E-116	1.212188461	0.35	0.073	4.17E-112
SAA1	3.09E-115	2.133594344	0.489	0.17	6.37E-111
TDO2	1.05E-114	1.229109932	0.483	0.161	2.15E-110
TM4SF4	1.06E-111	1.196480399	0.392	0.102	2.19E-107
PEBP1	3.18E-111	1.39091722	0.597	0.279	6.54E-107
SERPIND1	7.45E-109	1.183746816	0.372	0.096	1.53E-104
HPD	1.21E-108	1.38382065	0.508	0.197	2.48E-104
NNMT	2.00E-107	1.127073705	0.391	0.103	4.11E-103
SLCO1B1	6.97E-107	1.186646629	0.488	0.173	1.43E-102
AZGP1	1.19E-106	1.238624037	0.516	0.202	2.45E-102
AOX1	1.48E-106	1.134846384	0.418	0.123	3.05E-102
DHCR24	5.52E-105	1.126372931	0.378	0.101	1.14E-100
F5	6.28E-105	1.061604483	0.388	0.103	1.29E-100
EEF1A1	6.54E-103	1.026448458	0.769	0.503	1.35E-98
SPTBN1	1.39E-102	1.129587281	0.451	0.152	2.86E-98
SLC39A14	2.51E-102	1.037108845	0.385	0.105	5.16E-98
LBP	3.65E-102	1.081623022	0.321	0.069	7.52E-98
PON1	5.39E-101	1.086324177	0.359	0.093	1.11E-96
TPT1	7.34E-101	1.090753023	0.704	0.419	1.51E-96
ERRF1	6.86E-100	1.126521925	0.463	0.162	1.41E-95
ASGR2	7.48E-100	1.083471578	0.388	0.112	1.54E-95
INSIG1	3.64E-97	1.181797252	0.491	0.188	7.49E-93
CYP3A4	9.17E-97	1.192898497	0.489	0.194	1.89E-92
PPARGC1A	1.78E-96	1.07961475	0.331	0.08	3.66E-92
PGRMC1	3.62E-96	1.133249634	0.339	0.088	7.46E-92
ACSL1	1.01E-95	1.003497548	0.718	0.412	2.07E-91
SLC22A1	1.97E-95	1.104014589	0.425	0.143	4.06E-91
HSD11B1	3.37E-93	0.955501603	0.318	0.076	6.95E-89
C8A	1.64E-92	0.958593411	0.374	0.11	3.37E-88
RDH16	4.59E-91	1.135377921	0.289	0.065	9.45E-87
NAMPT	7.24E-91	1.068178773	0.634	0.319	1.49E-86

MSMO1	2.46E-90	1.114703744	0.379	0.118	5.06E-86
EGFR	4.15E-89	1.074753354	0.358	0.104	8.54E-85
CFHR1	2.18E-88	1.013016065	0.399	0.13	4.49E-84
HGD	3.30E-88	1.174617584	0.379	0.12	6.79E-84
SLC27A2	1.46E-87	0.948488484	0.299	0.072	3.00E-83
ITIH1	1.86E-87	1.027565059	0.393	0.131	3.83E-83
TMEM176A	4.26E-87	1.03681967	0.358	0.107	8.78E-83
G6PC	3.45E-86	1.042396018	0.355	0.105	7.10E-82
A2M	1.26E-85	0.912165465	0.778	0.549	2.60E-81
CALR	1.35E-85	1.116133836	0.435	0.169	2.78E-81
CYP8B1	9.44E-85	0.888205731	0.28	0.063	1.94E-80
TFR2	1.61E-84	0.962712735	0.325	0.089	3.31E-80
HAMP	1.62E-84	1.017952922	0.428	0.156	3.33E-80
GATM	5.75E-84	1.273593183	0.434	0.175	1.18E-79
SDC1	2.72E-83	0.958757593	0.299	0.075	5.60E-79
A1CF	8.18E-83	0.974052924	0.436	0.164	1.68E-78
SERPINA6	8.01E-82	0.909085892	0.269	0.06	1.65E-77
SERPINA4	2.39E-81	0.943173835	0.236	0.044	4.93E-77
PAH	1.33E-80	1.111631218	0.437	0.175	2.74E-76
NRG1	3.94E-80	1.040793359	0.29	0.073	8.11E-76
ANG	7.85E-80	1.039882546	0.401	0.146	1.62E-75
TNFAIP2	1.11E-79	-1.227789767	0.22	0.546	2.28E-75
HABP2	1.12E-79	0.907334266	0.269	0.062	2.31E-75
GSTA2	1.17E-79	1.109869458	0.247	0.052	2.40E-75
CCND3	1.41E-79	1.025660838	0.539	0.262	2.90E-75
CES2	7.38E-78	1.043795148	0.354	0.118	1.52E-73
RHOB	2.74E-77	1.129182039	0.321	0.098	5.64E-73
CYP3A5	4.37E-77	1.035883259	0.511	0.234	9.00E-73
APOA5	2.28E-76	0.954361227	0.289	0.078	4.69E-72
RBMS3	9.23E-76	0.987209008	0.465	0.191	1.90E-71
C8B	1.40E-75	0.928126652	0.297	0.082	2.88E-71
SLC38A6	1.42E-75	-1.255216132	0.202	0.513	2.92E-71
AASS	1.73E-75	0.996414146	0.273	0.068	3.55E-71
SC5D	7.79E-75	0.992497515	0.318	0.098	1.60E-70
UGT2B10	1.86E-74	1.050505996	0.3	0.087	3.83E-70
PERP	1.96E-74	0.736408104	0.203	0.034	4.04E-70
CSGALNACT1	1.11E-73	0.990407091	0.406	0.147	2.29E-69
AADAC	1.29E-73	0.858627484	0.27	0.068	2.66E-69
RNASE4	1.50E-73	0.828890667	0.225	0.045	3.09E-69
SLC13A5	1.55E-72	0.908430652	0.264	0.066	3.20E-68
CLDN1	3.53E-72	0.942435997	0.306	0.091	7.27E-68
GPC6	1.21E-71	0.936287641	0.481	0.211	2.48E-67
MYO1B	3.10E-71	0.904167635	0.338	0.111	6.39E-67

AFM	1.66E-70	0.961215533	0.374	0.138	3.42E-66
ST6GALNAC3	1.98E-68	0.969003768	0.34	0.114	4.08E-64
PRDX4	3.36E-68	0.82553255	0.254	0.065	6.92E-64
EGR1	4.01E-68	0.886160179	0.222	0.048	8.25E-64
CYP2A6	1.14E-67	1.070153983	0.314	0.103	2.34E-63
RORA	1.57E-67	0.800729713	0.518	0.247	3.23E-63
PRAP1	1.73E-67	0.863496191	0.328	0.11	3.56E-63
HSD17B13	2.27E-67	0.989340352	0.287	0.087	4.67E-63
RARRES2	6.36E-67	0.923233423	0.411	0.173	1.31E-62
DUSP1	2.02E-66	1.02514154	0.369	0.14	4.15E-62
ARG1	2.44E-66	0.924015952	0.359	0.132	5.02E-62
LEPR	2.60E-66	0.922833666	0.483	0.238	5.34E-62
SORBS2	2.78E-66	0.865813714	0.456	0.203	5.73E-62
IGFBP2	1.18E-65	0.703199214	0.206	0.041	2.44E-61
CCDC88A	3.72E-65	-0.903440854	0.492	0.739	7.66E-61
ABCB11	9.49E-65	0.858366435	0.326	0.111	1.95E-60
GHR	1.84E-64	0.89070527	0.466	0.215	3.79E-60
CYP51A1	2.20E-64	0.972045611	0.304	0.102	4.52E-60
STOM	2.24E-64	0.967113401	0.375	0.155	4.61E-60
SERPINA11	3.65E-64	0.723673481	0.2	0.041	7.50E-60
SERPINF1	5.47E-63	0.911535176	0.295	0.097	1.13E-58
ECHS1	1.23E-62	0.970996412	0.328	0.12	2.53E-58
RSRP1	2.12E-62	-0.911828218	0.354	0.633	4.36E-58
TFPI	2.64E-62	0.807800372	0.451	0.204	5.43E-58
ITGA1	4.76E-62	0.846559692	0.291	0.093	9.79E-58
ABCC5	6.11E-62	-1.118112718	0.261	0.53	1.26E-57
HPGD	3.28E-61	0.868015097	0.259	0.075	6.76E-57
BHMT	4.19E-61	0.945698788	0.383	0.161	8.62E-57
SRSF7	4.59E-61	-0.887259628	0.155	0.442	9.44E-57
ZFYVE16	5.18E-61	-0.992999912	0.289	0.567	1.07E-56
TMEM176B	9.38E-61	0.914773001	0.45	0.22	1.93E-56
REEP6	1.83E-60	0.796371202	0.21	0.049	3.77E-56
TGFB3	5.47E-60	0.750760354	0.219	0.053	1.13E-55
COL18A1	6.26E-60	0.832682893	0.322	0.118	1.29E-55
WSB1	8.83E-60	-0.782265385	0.47	0.72	1.82E-55
DHRS9	1.96E-59	-1.231940196	0.082	0.336	4.03E-55
B2M	2.96E-59	0.631366689	0.872	0.749	6.09E-55
PKP2	4.57E-59	0.876318108	0.205	0.047	9.41E-55
UBB	8.14E-59	0.955291174	0.328	0.127	1.68E-54
SH3PXD2B	9.15E-59	0.826758772	0.452	0.209	1.88E-54
SRRM2	1.13E-58	-0.810452344	0.37	0.66	2.32E-54
SRGAP1	1.20E-58	0.897926236	0.661	0.446	2.47E-54
CMBL	1.94E-58	0.876988341	0.238	0.067	3.99E-54

PROS1	2.57E-58	0.850636161	0.375	0.157	5.28E-54
ADAP2	3.09E-58	-0.944410107	0.304	0.585	6.37E-54
GPX3	1.33E-57	0.736293677	0.206	0.049	2.75E-53
ADGRA3	1.49E-57	0.861596507	0.297	0.103	3.06E-53
ASS1	2.02E-57	0.869930776	0.293	0.099	4.15E-53
NPL	2.48E-57	-1.004233241	0.261	0.525	5.10E-53
IL6ST	2.74E-57	0.839719199	0.528	0.301	5.64E-53
C8G	3.57E-57	0.777157786	0.239	0.068	7.34E-53
ARGLU1	4.06E-57	-0.781657315	0.263	0.559	8.35E-53
MAN1A1	5.59E-57	0.83620771	0.633	0.407	1.15E-52
SAT1	6.00E-57	-0.906889487	0.784	0.885	1.23E-52
ADH4	1.41E-56	1.163877343	0.468	0.264	2.91E-52
SERPINA10	2.09E-56	0.709017274	0.185	0.04	4.31E-52
ZNF385D	5.35E-56	0.769197494	0.267	0.084	1.10E-51
EBP	2.48E-55	0.756849554	0.212	0.055	5.10E-51
SRGN	2.59E-55	0.946509469	0.489	0.26	5.34E-51
ZEB2	3.08E-55	-0.73299515	0.781	0.884	6.34E-51
SERPINA7	3.66E-55	0.646516445	0.177	0.037	7.54E-51
GPNMB	7.06E-55	-1.310302445	0.164	0.414	1.45E-50
INSR	7.38E-55	0.921152371	0.536	0.313	1.52E-50
SCP2	7.82E-55	0.954387831	0.559	0.359	1.61E-50
PTMS	1.02E-54	0.944656212	0.355	0.155	2.09E-50
KLF9	6.99E-54	0.744099955	0.273	0.091	1.44E-49
ARHGAP17	7.66E-54	-0.855111986	0.187	0.457	1.58E-49
HMGCS2	1.35E-53	0.882210537	0.366	0.158	2.78E-49
PCSK6	4.04E-53	0.778928703	0.311	0.116	8.32E-49
TMEM123	4.14E-53	0.892704036	0.483	0.281	8.51E-49
LMAN1	7.90E-53	0.784990939	0.317	0.125	1.63E-48
LST1	1.24E-52	-1.025607666	0.115	0.356	2.56E-48
SOX5	1.80E-52	0.811139787	0.471	0.244	3.71E-48
PON3	1.90E-52	0.725326444	0.224	0.064	3.92E-48
N4BP2L2	1.95E-52	-0.66909641	0.573	0.762	4.02E-48
C2	2.91E-52	0.786865857	0.271	0.094	5.98E-48
F13B	3.41E-52	0.674494814	0.191	0.046	7.03E-48
SYK	4.35E-52	-0.765187965	0.465	0.697	8.96E-48
NFIB	6.51E-52	0.812660292	0.316	0.122	1.34E-47
CALD1	7.11E-52	0.769015119	0.322	0.127	1.46E-47
CANX	1.13E-51	0.832234496	0.478	0.264	2.32E-47
TTPA	2.65E-51	0.767347733	0.232	0.07	5.45E-47
MRC1	2.68E-51	0.799048158	0.606	0.375	5.52E-47
FMO5	2.98E-51	0.893735822	0.342	0.15	6.13E-47
OOEP	3.40E-51	0.586465098	0.123	0.016	7.00E-47
IFITM3	3.83E-51	0.763957123	0.351	0.15	7.88E-47

PDK4	3.96E-51	0.684729076	0.64	0.42	8.15E-47
ATP10D	8.19E-51	-0.766839129	0.133	0.384	1.69E-46
CELF2	8.91E-51	0.709762587	0.858	0.786	1.83E-46
STARD10	1.29E-50	0.785074211	0.226	0.068	2.66E-46
EEF2	2.47E-50	0.800823814	0.319	0.132	5.08E-46
CYB5A	3.16E-50	0.857020781	0.43	0.223	6.50E-46
F12	5.98E-50	0.790315335	0.251	0.084	1.23E-45
MYO5A	6.01E-50	-0.760553936	0.451	0.685	1.24E-45
AKAP13	8.13E-50	0.737489358	0.857	0.795	1.67E-45
CFHR3	8.72E-50	0.755504176	0.284	0.105	1.79E-45
PCYOX1	1.04E-49	0.769188826	0.233	0.073	2.15E-45
SERPINA5	1.32E-49	0.675816061	0.205	0.056	2.72E-45
SLC1A2	1.86E-49	0.62105861	0.128	0.019	3.83E-45
HLA-B	4.48E-49	0.851644212	0.663	0.498	9.21E-45
NABP1	6.97E-49	-0.929235159	0.254	0.505	1.43E-44
APOA4	7.16E-49	0.612397946	0.138	0.024	1.47E-44
ARHGAP25	8.05E-49	-0.777608273	0.294	0.546	1.66E-44
ACSM2B	9.79E-49	0.759662957	0.327	0.135	2.01E-44
FOS	9.82E-49	0.739480674	0.32	0.129	2.02E-44
MIF	1.67E-48	0.802883588	0.316	0.129	3.43E-44
SON	2.03E-48	-0.767695993	0.449	0.685	4.18E-44
PLEK	2.79E-48	-0.838716653	0.106	0.342	5.74E-44
GSTA1	3.87E-48	1.028766949	0.398	0.21	7.97E-44
SPINK1	7.77E-48	0.620701519	0.155	0.032	1.60E-43
ZRANB2	1.61E-47	-0.680767651	0.269	0.533	3.31E-43
IGSF6	1.65E-47	-0.886452323	0.09	0.314	3.39E-43
PROX1	2.14E-47	0.750256912	0.25	0.086	4.40E-43
ITGAX	3.18E-47	-0.798624049	0.347	0.612	6.54E-43
PROC	5.03E-47	0.684925564	0.228	0.073	1.04E-42
UBA52	5.50E-47	0.802919487	0.35	0.159	1.13E-42
DOCK10	1.22E-46	-0.695193916	0.614	0.793	2.51E-42
HMGCS1	1.62E-46	0.89509788	0.338	0.154	3.33E-42
FADS2	3.27E-46	0.793558245	0.23	0.077	6.73E-42
AC007952.4	4.05E-46	0.661693494	0.177	0.046	8.33E-42
LGALS3	4.82E-46	-0.902724248	0.105	0.329	9.93E-42
MAGI1	5.32E-46	0.775647936	0.371	0.172	1.10E-41
HSD17B2	6.07E-46	0.58843538	0.169	0.04	1.25E-41
MRC2	6.19E-46	-0.961539709	0.118	0.343	1.27E-41
LIMD2	6.38E-46	-0.828742399	0.07	0.282	1.31E-41
TSC22D3	6.58E-46	0.781573593	0.272	0.102	1.35E-41
H19	6.67E-46	0.789637985	0.211	0.065	1.37E-41
UBE2E2	6.68E-46	-0.64560778	0.701	0.845	1.38E-41
IL1RAP	7.69E-46	0.791762261	0.37	0.176	1.58E-41

HNRNPDL	7.92E-46	-0.792248582	0.243	0.491	1.63E-41
AQP9	9.32E-46	0.704003127	0.251	0.088	1.92E-41
FUS	9.68E-46	-0.707640349	0.312	0.562	1.99E-41
MTRNR2L12	1.13E-45	0.738760404	0.448	0.241	2.32E-41
APOF	3.16E-45	0.621931067	0.149	0.032	6.50E-41
PKN2	3.44E-45	-0.675394371	0.362	0.609	7.08E-41
ALDH1A1	3.80E-45	0.805571648	0.417	0.219	7.81E-41
PNISR	4.24E-45	-0.707028693	0.359	0.612	8.73E-41
FBP1	4.33E-45	0.875424585	0.379	0.192	8.92E-41
ABCA6	6.75E-45	0.67747461	0.229	0.076	1.39E-40
ATG7	8.86E-45	-0.691588263	0.617	0.789	1.82E-40
ADI1	9.75E-45	0.82553718	0.293	0.123	2.01E-40
DDX5	1.04E-44	-0.649122152	0.523	0.73	2.14E-40
TFEC	2.77E-44	-0.87972676	0.274	0.508	5.71E-40
MCOLN1	3.01E-44	-0.942085315	0.12	0.34	6.20E-40
UPF2	3.07E-44	-0.73394824	0.218	0.467	6.32E-40
DEFB1	4.91E-44	0.720384262	0.207	0.063	1.01E-39
MT2A	6.07E-44	0.82124879	0.616	0.438	1.25E-39
LEAP2	9.24E-44	0.758562421	0.26	0.1	1.90E-39
TCF25	1.29E-43	-0.707051022	0.287	0.546	2.65E-39
ASAP1	1.89E-43	-0.645909296	0.568	0.763	3.90E-39
GJB1	2.15E-43	0.632844942	0.165	0.042	4.42E-39
TOB1	2.69E-43	0.699520877	0.201	0.062	5.54E-39
PDIA4	2.87E-43	0.666046204	0.274	0.109	5.92E-39
CYP2B6	2.99E-43	0.725258461	0.254	0.092	6.15E-39
MITF	4.13E-43	-0.816998075	0.372	0.601	8.50E-39
CYP1A2	5.39E-43	0.790504675	0.18	0.05	1.11E-38
LIFR	8.79E-43	0.690319695	0.229	0.079	1.81E-38
SETDB2	1.09E-42	-0.744006475	0.166	0.398	2.23E-38
SDS	1.09E-42	0.649729644	0.402	0.202	2.23E-38
GAS2L3	1.16E-42	-0.814105825	0.146	0.374	2.40E-38
TNFRSF14	1.24E-42	-0.767857977	0.165	0.4	2.56E-38
SLC39A10	1.54E-42	-0.814504468	0.15	0.375	3.18E-38
PPP1R21	2.05E-42	-0.740717688	0.217	0.457	4.22E-38
PPARG	3.01E-42	-0.94055015	0.232	0.461	6.20E-38
XRRA1	3.29E-42	-0.696161847	0.072	0.274	6.76E-38
TSHZ2	3.32E-42	0.657035909	0.306	0.127	6.83E-38
AK4	5.42E-42	0.662265132	0.172	0.047	1.11E-37
DGAT2	7.64E-42	0.618377388	0.154	0.037	1.57E-37
SOD1	8.71E-42	0.835964017	0.346	0.169	1.79E-37
PGLYRP2	8.78E-42	0.673622718	0.158	0.04	1.81E-37
LY86	9.66E-42	-0.806459496	0.176	0.406	1.99E-37
ABLM1	1.26E-41	0.646084724	0.239	0.086	2.60E-37

PNN	2.61E-41	-0.664564257	0.182	0.416	5.36E-37
SLC27A5	4.34E-41	0.740650193	0.236	0.087	8.94E-37
IGFBP7	6.68E-41	0.666767432	0.261	0.102	1.38E-36
TIMP1	1.41E-40	0.675686603	0.249	0.094	2.89E-36
SIPA1L1	1.48E-40	0.798090387	0.643	0.475	3.04E-36
RAPGEF5	1.76E-40	0.754298176	0.238	0.088	3.63E-36
THBS1	2.36E-40	0.658580961	0.159	0.04	4.86E-36
ARHGAP10	2.65E-40	-0.944094142	0.274	0.503	5.46E-36
CYP3A7	4.24E-40	0.720983117	0.192	0.059	8.72E-36
PDE7B	7.24E-40	0.731506183	0.233	0.084	1.49E-35
ZNF124	7.90E-40	-0.81695789	0.228	0.453	1.63E-35
VKORC1	8.35E-40	0.592213003	0.187	0.057	1.72E-35
SORD	1.03E-39	0.854158447	0.248	0.099	2.12E-35
MPHOSPH8	1.30E-39	-0.652227742	0.19	0.42	2.69E-35
MYO9B	2.05E-39	-0.597134953	0.525	0.737	4.23E-35
BMP2K	2.30E-39	-0.625027126	0.462	0.664	4.74E-35
HLF	3.16E-39	0.590471262	0.147	0.036	6.50E-35
GAMT	4.66E-39	0.653228516	0.18	0.054	9.59E-35
ADH1A	6.15E-39	0.89811957	0.305	0.145	1.27E-34
MAML2	1.09E-38	-0.695760709	0.649	0.793	2.25E-34
TEAD1	2.33E-38	0.607446439	0.21	0.072	4.80E-34
LIPA	3.23E-38	-0.84692815	0.266	0.469	6.65E-34
NAGK	3.73E-38	-0.730497656	0.16	0.374	7.67E-34
FKBP15	6.90E-38	-0.643835287	0.206	0.435	1.42E-33
NRP1	1.10E-37	-0.877060702	0.428	0.61	2.26E-33
C4BPB	1.12E-37	0.634199216	0.218	0.078	2.30E-33
MYO1E	1.53E-37	-0.92086988	0.376	0.593	3.16E-33
NR5A2	2.01E-37	0.649893283	0.221	0.08	4.13E-33
DMXL2	2.28E-37	-0.700599738	0.359	0.569	4.69E-33
SORBS1	3.06E-37	0.62233597	0.215	0.077	6.31E-33
ATF5	3.25E-37	0.757559276	0.377	0.205	6.69E-33
CUX2	3.30E-37	0.695840243	0.225	0.084	6.79E-33
ACAA2	3.67E-37	0.720550796	0.327	0.162	7.54E-33
ABHD2	6.04E-37	0.742228935	0.516	0.348	1.24E-32
CDH1	7.86E-37	0.590043891	0.172	0.052	1.62E-32
NRP2	7.94E-37	-0.755925836	0.158	0.366	1.63E-32
CHD9	8.73E-37	-0.605783452	0.544	0.742	1.80E-32
AKR1D1	1.58E-36	0.723292283	0.194	0.067	3.26E-32
HS3ST2	1.60E-36	-1.59999186	0.072	0.249	3.28E-32
EVL	1.60E-36	-0.649108259	0.252	0.475	3.29E-32
PLEKHM2	2.13E-36	-0.666696791	0.197	0.416	4.39E-32
SRGAP3	2.88E-36	-0.776884137	0.126	0.323	5.92E-32
LDB2	2.94E-36	0.67354917	0.314	0.15	6.05E-32

FMO3	3.23E-36	0.747950164	0.264	0.115	6.65E-32
SEC11C	3.95E-36	0.616402723	0.194	0.066	8.13E-32
RNPC3	3.97E-36	-0.622788031	0.193	0.416	8.17E-32
IRS2	4.68E-36	0.623637195	0.294	0.133	9.64E-32
VNN1	5.25E-36	0.708676814	0.198	0.07	1.08E-31
APOC4	6.48E-36	0.701584803	0.274	0.122	1.33E-31
TST	6.88E-36	0.675523711	0.208	0.076	1.42E-31
SLC25A24	9.10E-36	-0.673065469	0.099	0.289	1.87E-31
STX7	9.34E-36	-0.632660047	0.408	0.621	1.92E-31
ATG4C	1.20E-35	-0.666345503	0.157	0.368	2.46E-31
COX6A1	1.29E-35	0.660556089	0.267	0.118	2.66E-31
WWP1	1.57E-35	-0.781116731	0.394	0.584	3.24E-31
UGCG	1.67E-35	-0.744971932	0.196	0.408	3.45E-31
ADRA1A	2.21E-35	0.643548665	0.292	0.131	4.56E-31
CHKB	2.34E-35	-0.624871609	0.056	0.226	4.82E-31
WDFY4	2.36E-35	-0.643035691	0.304	0.52	4.86E-31
LAMP1	4.44E-35	0.726717787	0.354	0.192	9.15E-31
ACAT1	5.01E-35	0.77458232	0.374	0.211	1.03E-30
MCL1	5.83E-35	0.744581218	0.376	0.209	1.20E-30
TYROBP	6.23E-35	-0.727334195	0.138	0.335	1.28E-30
PRMT2	1.02E-34	-0.636475414	0.321	0.55	2.10E-30
PARVG	1.06E-34	-0.661160898	0.246	0.464	2.18E-30
PDIA3	1.29E-34	0.710215134	0.392	0.224	2.66E-30
CERS2	1.67E-34	0.642547986	0.221	0.086	3.45E-30
LY6E	2.19E-34	0.630401255	0.195	0.069	4.50E-30
SNX24	2.52E-34	-0.766664943	0.172	0.37	5.19E-30
RUFY3	4.61E-34	-0.598039707	0.381	0.599	9.49E-30
RIDA	4.70E-34	0.709654575	0.256	0.114	9.68E-30
ZNF710	5.36E-34	-0.620722769	0.398	0.609	1.10E-29
ST3GAL5	7.50E-34	-0.659186291	0.145	0.345	1.54E-29
MIR99AHG	1.04E-33	0.683142815	0.423	0.247	2.13E-29
OSBPL11	1.99E-33	-0.645280258	0.245	0.459	4.10E-29
DDX46	2.32E-33	-0.625072107	0.223	0.432	4.77E-29
ADH1C	2.61E-33	0.720578713	0.253	0.113	5.37E-29
HIPK2	3.37E-33	0.621243739	0.518	0.355	6.94E-29
CHKA	3.39E-33	0.776670608	0.531	0.381	6.97E-29
EML4	4.62E-33	-0.654723354	0.389	0.595	9.52E-29
PAXBP1	4.98E-33	-0.617559641	0.157	0.358	1.02E-28
EHHADH	6.75E-33	0.693315798	0.294	0.145	1.39E-28
H2AFY	7.37E-33	-0.598087873	0.447	0.642	1.52E-28
P2RY6	1.01E-32	-0.756934251	0.06	0.221	2.09E-28
PIK3C2G	1.11E-32	0.641224679	0.239	0.099	2.29E-28
LGMN	1.24E-32	-0.906258865	0.25	0.442	2.55E-28

PBX3	1.34E-32	-0.680315636	0.379	0.581	2.76E-28
PLA2G7	1.38E-32	-0.700318364	0.146	0.338	2.84E-28
BHMT2	1.72E-32	0.612302524	0.289	0.138	3.54E-28
KALRN	2.07E-32	0.595960869	0.176	0.06	4.26E-28
HPN	2.53E-32	0.629861081	0.254	0.114	5.21E-28
RAP2B	2.86E-32	-0.614445335	0.084	0.257	5.88E-28
AKAP12	3.25E-32	0.628329578	0.144	0.042	6.70E-28
CYP4A11	3.41E-32	0.606878562	0.197	0.074	7.01E-28
P2RX7	3.48E-32	-0.723194393	0.129	0.316	7.16E-28
DSP	4.08E-32	0.588906753	0.162	0.053	8.40E-28
ACIN1	4.35E-32	-0.590153663	0.194	0.399	8.94E-28
CCDC18-AS1	4.36E-32	-0.634888217	0.232	0.441	8.98E-28
GGA1	4.67E-32	-0.586115422	0.123	0.311	9.62E-28
TAF1D	5.37E-32	-0.602109261	0.228	0.439	1.11E-27
PABPC4	5.82E-32	0.758281342	0.438	0.28	1.20E-27
SAMD4A	8.37E-32	-0.91859335	0.275	0.461	1.72E-27
XAF1	9.26E-32	-0.679554425	0.193	0.394	1.91E-27
PBLD	9.42E-32	0.631848192	0.19	0.071	1.94E-27
CD200R1	1.73E-31	-0.663701107	0.038	0.184	3.55E-27
RASAL2	2.71E-31	-0.683712341	0.381	0.569	5.58E-27
ZNF438	3.26E-31	-0.686621981	0.304	0.504	6.72E-27
NHSL1	3.71E-31	0.799032049	0.609	0.474	7.64E-27
C20orf194	5.86E-31	-0.597765908	0.458	0.635	1.21E-26
RNF111	5.90E-31	-0.592460118	0.336	0.544	1.21E-26
DHRS7	8.48E-31	0.58507817	0.218	0.091	1.75E-26
SMURF2	1.11E-30	-0.671697499	0.283	0.486	2.29E-26
RNF213	1.51E-30	-0.597950661	0.485	0.674	3.12E-26
NDUFA4	2.02E-30	0.624490865	0.249	0.115	4.16E-26
ATP6V0A1	2.28E-30	-0.592706804	0.261	0.464	4.69E-26
LRRK1	2.71E-30	-0.65592879	0.296	0.499	5.57E-26
XIST	5.69E-30	-0.683061747	0.299	0.497	1.17E-25
SNHG12	5.78E-30	-0.629915836	0.064	0.218	1.19E-25
FASN	5.98E-30	0.586412913	0.166	0.057	1.23E-25
ITGAL	7.63E-30	-0.638446214	0.119	0.296	1.57E-25
RAB32	7.71E-30	-0.610900934	0.065	0.221	1.59E-25
CAT	8.95E-30	0.796581018	0.432	0.292	1.84E-25
EPB41L2	1.05E-29	-0.667406895	0.464	0.637	2.16E-25
IL1R2	1.47E-29	0.786734505	0.206	0.082	3.04E-25
RNF169	1.57E-29	-0.58970643	0.148	0.33	3.24E-25
ACMSD	1.66E-29	0.588163089	0.183	0.069	3.42E-25
LILRB2	1.67E-29	-0.603198037	0.076	0.237	3.43E-25
ACADSB	2.57E-29	0.638182612	0.231	0.104	5.28E-25
CD36	3.13E-29	-1.128890537	0.183	0.362	6.44E-25

RASA1	4.92E-29	-0.594172849	0.38	0.578	1.01E-24
ITGA4	6.73E-29	-0.753064878	0.329	0.514	1.39E-24
ARPC1B	7.89E-29	-0.614788264	0.265	0.46	1.62E-24
SPATA7	8.49E-29	-0.653659666	0.086	0.246	1.75E-24
MSR1	1.34E-28	-0.677682448	0.571	0.708	2.75E-24
BLNK	1.60E-28	-0.587548425	0.139	0.319	3.30E-24
PER1	1.70E-28	0.604216539	0.229	0.103	3.49E-24
CXCL2	2.17E-28	0.600880826	0.162	0.058	4.46E-24
TPRG1	2.19E-28	-1.008232603	0.362	0.527	4.51E-24
ZC3H12C	3.08E-28	-0.762261735	0.143	0.315	6.34E-24
SLC36A1	3.30E-28	-0.702557106	0.142	0.309	6.79E-24
PHYKPL	3.30E-28	-0.606519608	0.205	0.393	6.80E-24
MAFB	3.44E-28	-0.723976983	0.183	0.362	7.09E-24
ANKRD10	6.58E-28	-0.62200739	0.212	0.397	1.35E-23
MDFIC	8.30E-28	-0.596332493	0.316	0.513	1.71E-23
SPI1	1.38E-27	-0.5868795	0.176	0.36	2.85E-23
ZFAND5	1.77E-27	0.795897652	0.418	0.286	3.65E-23
PDE3B	1.89E-27	0.601222973	0.532	0.381	3.89E-23
HULC	1.90E-27	0.589538674	0.257	0.124	3.92E-23
APP	2.66E-27	0.61103415	0.409	0.255	5.48E-23
SIGLEC1	4.00E-27	-0.650810351	0.143	0.316	8.23E-23
FADS1	4.41E-27	0.611610089	0.179	0.071	9.09E-23
RAB31	4.84E-27	0.678759515	0.668	0.569	9.96E-23
C1QA	6.56E-27	0.64810321	0.35	0.207	1.35E-22
NR1H3	7.88E-27	-0.624636731	0.103	0.263	1.62E-22
SLAMF7	8.13E-27	-0.648645726	0.031	0.155	1.67E-22
HTR7	1.42E-26	-0.659757604	0.072	0.216	2.92E-22
SPRED1	1.43E-26	-0.600049608	0.353	0.531	2.94E-22
IL1R1	2.96E-26	0.649981445	0.235	0.112	6.08E-22
ZNF804A	3.99E-26	-0.799116311	0.193	0.362	8.21E-22
SAMD9L	4.55E-26	-0.590685666	0.122	0.288	9.36E-22
TMCC3	5.46E-26	0.674674182	0.295	0.162	1.12E-21
HLA-DQA1	1.19E-25	-0.817851163	0.196	0.366	2.45E-21
DCXR	1.23E-25	0.706898694	0.361	0.227	2.52E-21
HLA-DRB1	1.55E-25	-0.794185889	0.349	0.524	3.19E-21
ATP1B3	1.96E-25	1.012156204	0.366	0.233	4.03E-21
ARL6IP1	6.57E-25	0.62853958	0.229	0.112	1.35E-20
BCAR3	6.63E-25	-0.625180556	0.095	0.241	1.36E-20
DOCK3	7.89E-25	-0.914289608	0.077	0.215	1.62E-20
DAB2	1.14E-24	-0.59217355	0.196	0.37	2.34E-20
SLC18B1	1.22E-24	-0.626916214	0.086	0.229	2.51E-20
EI24	3.14E-24	0.617436698	0.197	0.09	6.47E-20
PTCH2	3.33E-24	-0.737318577	0.029	0.143	6.86E-20

MGLL	3.86E-24	-0.857277971	0.236	0.394	7.95E-20
SH3BP5	6.23E-24	0.596370759	0.415	0.275	1.28E-19
ME1	2.60E-23	-0.664396651	0.216	0.38	5.35E-19
TBC1D2	3.27E-23	-0.619960487	0.102	0.244	6.74E-19
PRKCH	3.38E-23	0.643634785	0.449	0.315	6.96E-19
CARMIL1	5.02E-23	-0.589191955	0.264	0.434	1.03E-18
USP53	1.06E-22	0.686015231	0.306	0.18	2.18E-18
BBS5	1.31E-22	-0.790314443	0.068	0.195	2.69E-18
PRDX1	1.94E-22	0.591866571	0.241	0.129	4.00E-18
HRH1	2.00E-22	-0.604481692	0.082	0.215	4.11E-18
FABP5	2.31E-22	-0.616964509	0.062	0.186	4.75E-18
PRDX6	3.63E-21	0.632921048	0.241	0.131	7.48E-17
SYAP1	1.39E-20	0.775628373	0.262	0.152	2.86E-16
PSTPIP2	3.38E-20	0.667555795	0.375	0.255	6.97E-16
MT1X	7.35E-20	0.64690563	0.302	0.183	1.51E-15
LINC01374	8.42E-20	-0.649454076	0.183	0.327	1.73E-15
HGF	1.19E-19	-0.588503162	0.098	0.224	2.45E-15
FAM20A	2.77E-19	-0.590094682	0.196	0.34	5.70E-15
IGSF21	1.08E-18	0.629095742	0.222	0.118	2.22E-14
ANK3	1.57E-17	0.69049773	0.21	0.114	3.23E-13
CD55	6.76E-17	0.586258922	0.237	0.139	1.39E-12
SYTL3	1.15E-14	0.623097095	0.235	0.146	2.37E-10
PLCL1	6.80E-14	-0.594904895	0.165	0.274	1.40E-09
RTN1	8.47E-14	-0.622323673	0.405	0.519	1.74E-09
CD163L1	5.21E-11	-0.646050881	0.192	0.289	1.07E-06