

Supplementary Materials

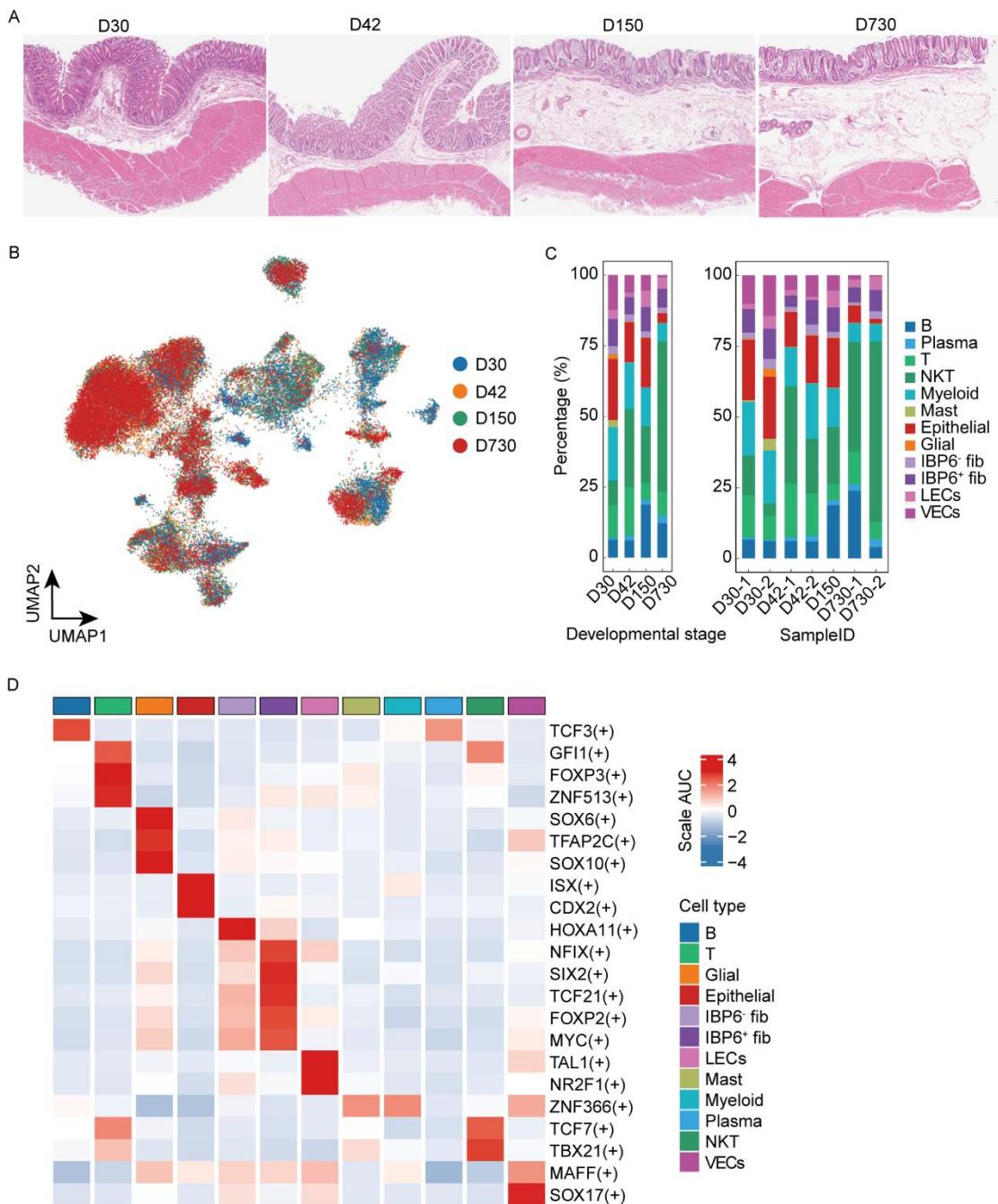
Single-cell profiling of the pig cecum at various developmental stages

Yan-Yuan Xiao¹, Qing Zhang¹, Fei Huang¹, Lin Rao¹, Tian-Xiong Yao¹, Si-Yu Yang¹,
Lei Xie¹, Xiao-Xiao Zou¹, Li-Ping Cai¹, Jia-Wen Yang¹, Bin Yang^{1,*}, Lu-Sheng
Huang^{1,*}

¹ National Key Laboratory for Swine Genetic Improvement and Germplasm Innovation, Ministry of Science and Technology of China, Jiangxi Agricultural University,

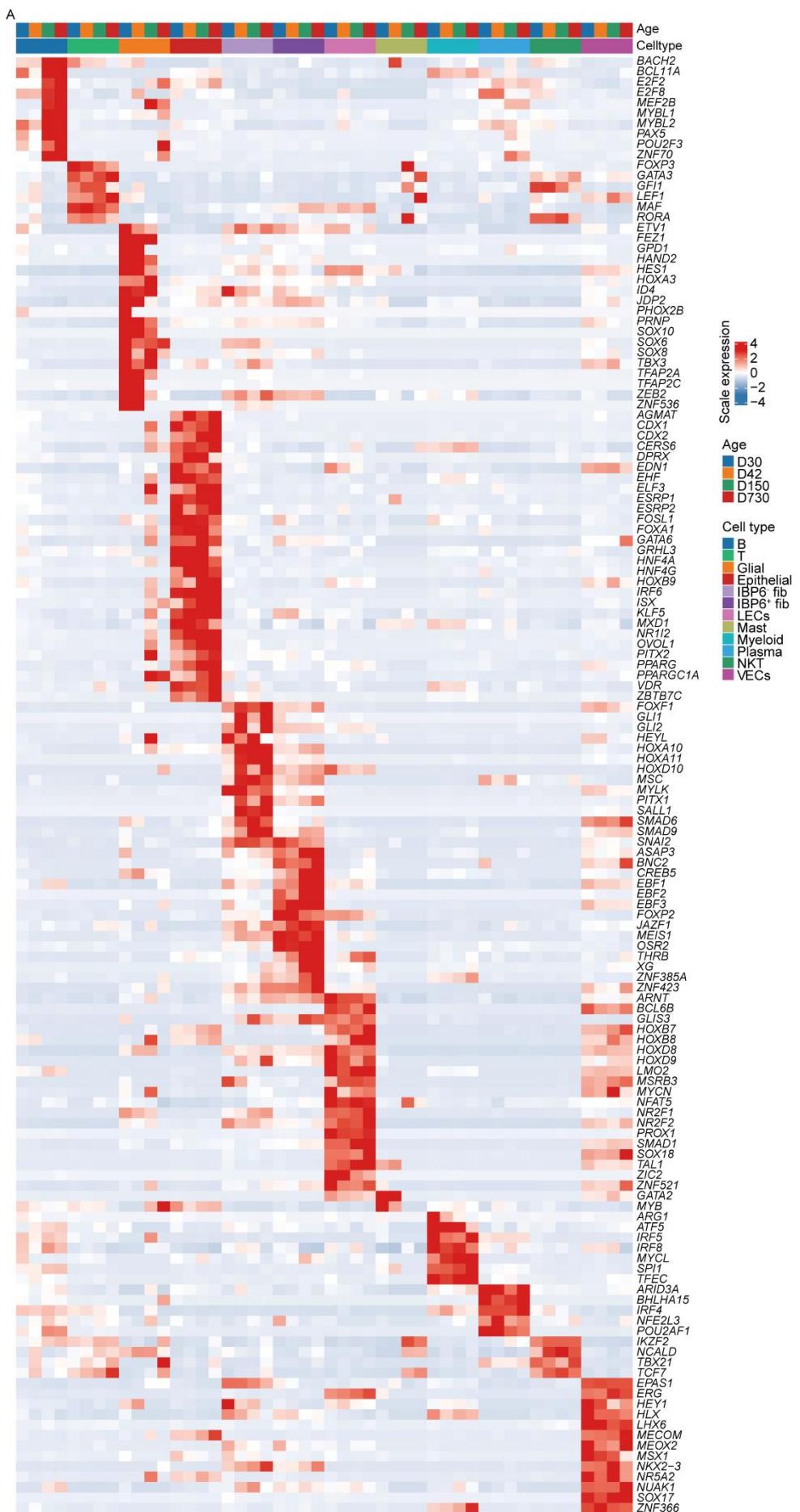
Nanchang, Jiangxi 330045, China

*Corresponding authors, E-mail: binyang@live.cn; lushenghuang@hotmail.com



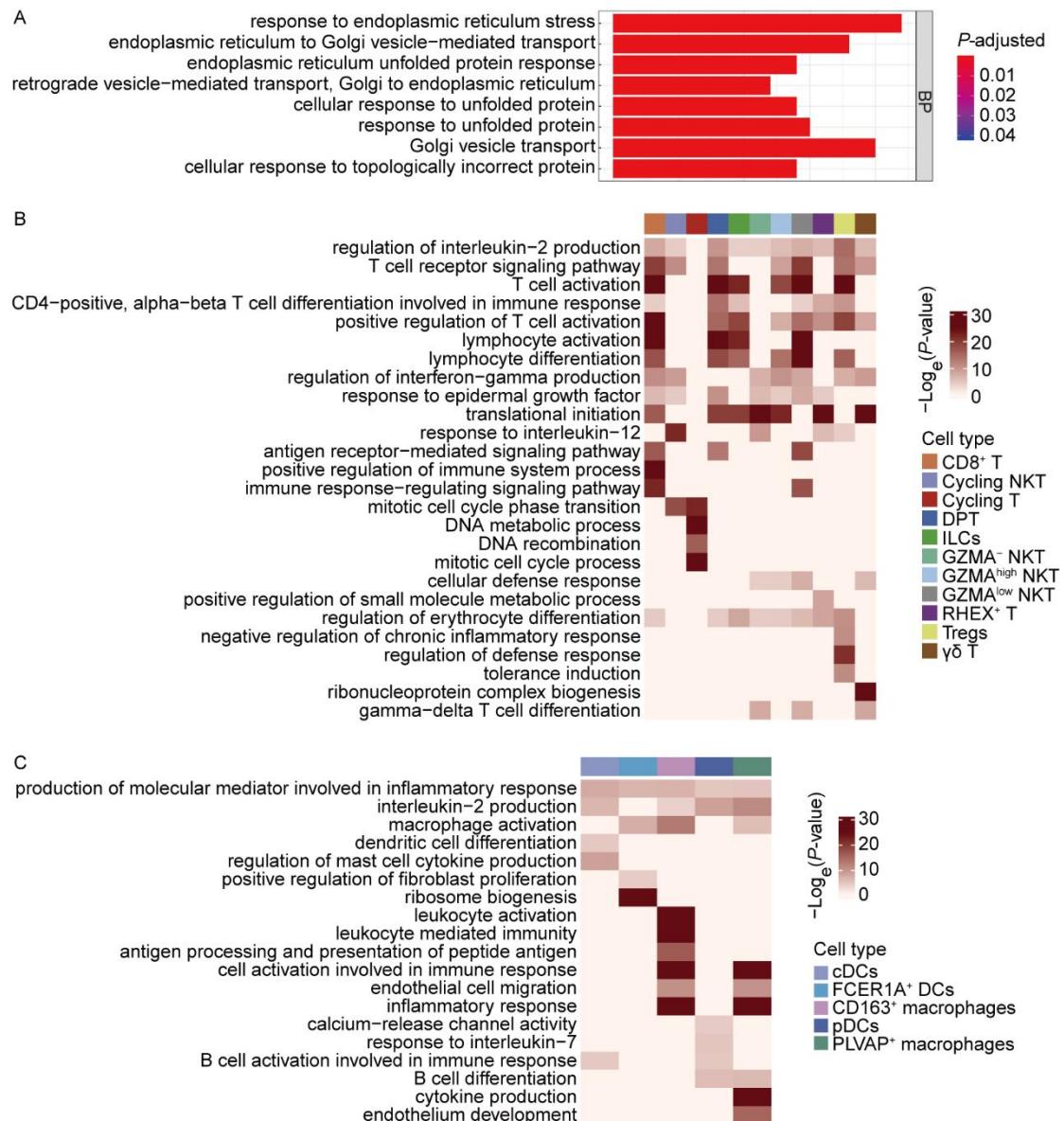
Supplementary Figure S1 Characteristics of major cell types

A: Histological sections of Bama Xiang cecum at each sampling site. B: UMAP of 45,572 cells, colored by developmental stage C: Relative proportions of major cell types at each developmental stage (left) and in each sample (right). D: Regulon heatmap showing cell-type-specific regulons.



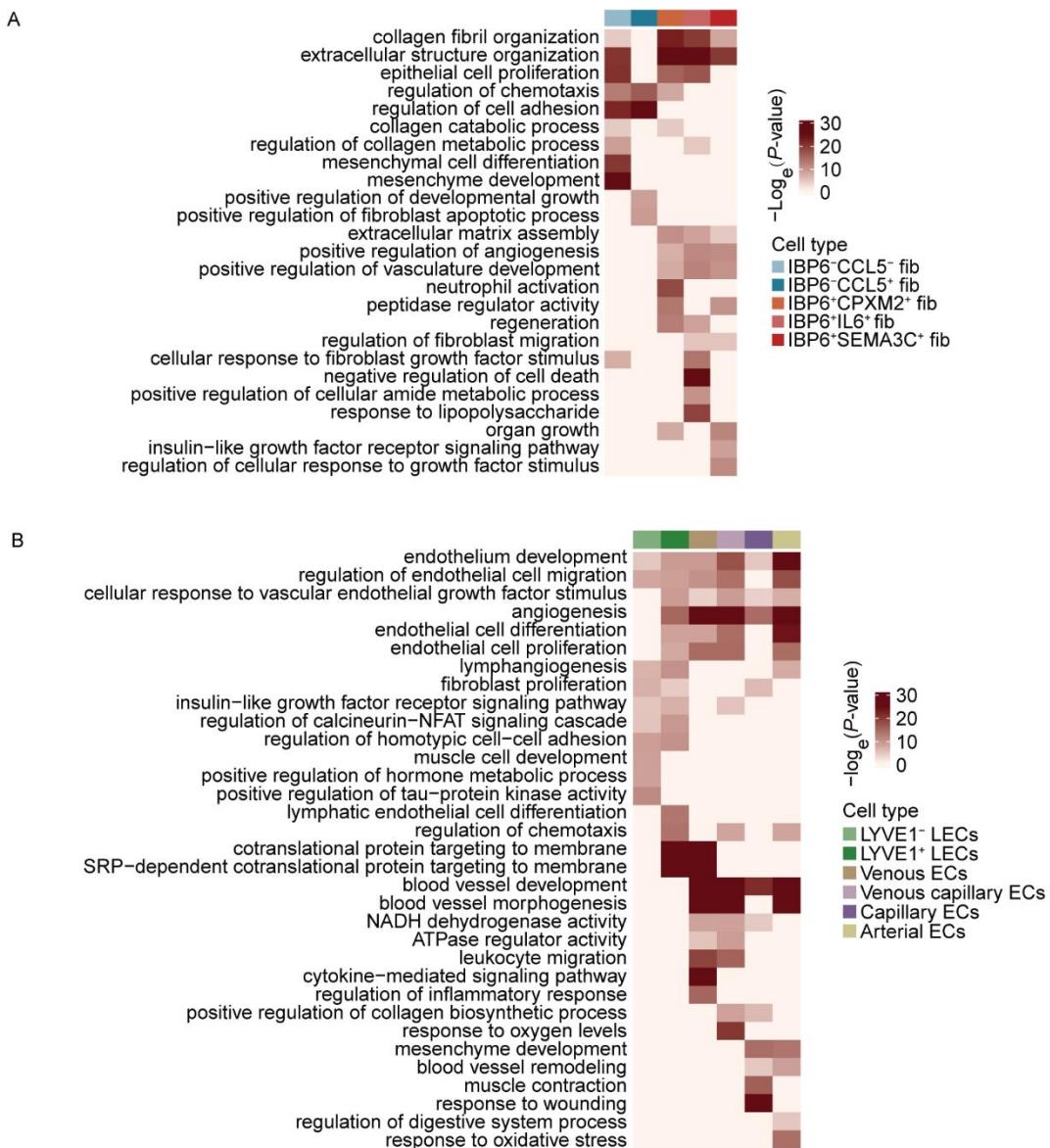
Supplementary Figure S2 Cell-type-specific TFs at four developmental stages

A: Heatmap showing expression of 140 cell-type-specific TFs at different developmental stages.



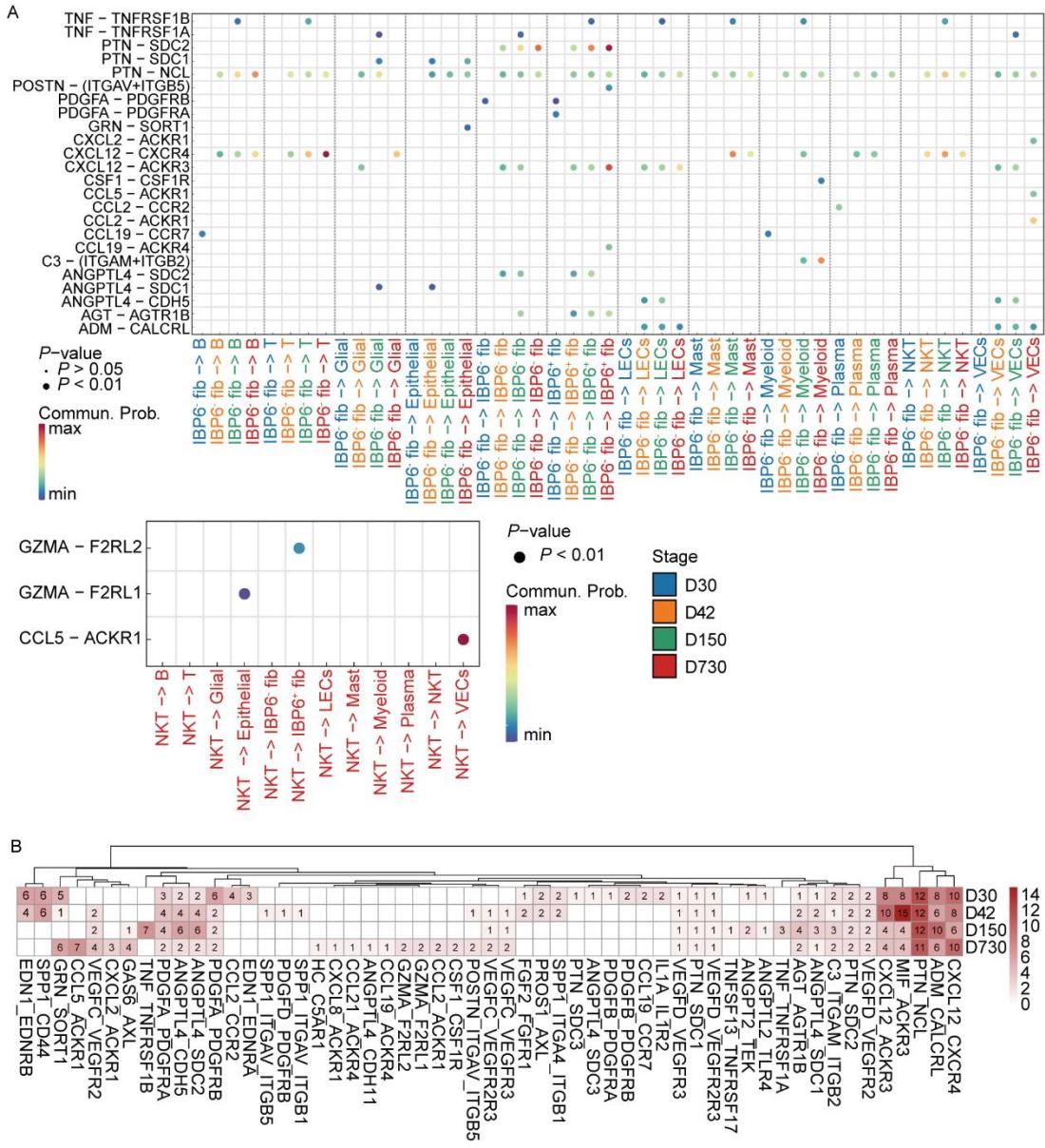
Supplementary Figure S3 Goblet cells, subpopulations of T lymphocytes, and their characteristics

GO analysis of top 200 highly expressed genes in goblet cells (A), T cell subtypes (B), and myeloid cell subtypes (C).



Supplementary Figure S4 Subpopulations of fibroblasts, endothelial cells, and their characteristics

GO analysis of top 200 highly expressed genes in fibroblast subtypes (A) and endothelial cell subtypes (B).



Supplementary Figure S5 Cell-cell communication across different cell types

A: Bubble plot showing significant receptor-ligand pairs of IBP6⁻ fibroblasts (upper) and NKT cells (below) for communication with other cell types at different developmental stages. **B:** Number of occurrences of receptor-ligand pairs at each developmental stage.

Supplementary Table S1 sample information

Sample	Breed	Stage	Sex
210504A-B01M38aW	Bama Xiang	D30	M
210504A-B01F38aW	Bama Xiang	D30	F
210504A-B02M38aW	Bama Xiang	D42	M
210504A-B02F38aW	Bama Xiang	D42	F
210504B-B03M38aW	Bama Xiang	D150	M
210504C-B04M38aW	Bama Xiang	D730	M
210504C-B04F38aW	Bama Xiang	D730	F

Supplementary Table S2 Top200 highly expressed genes in stem cells

gene	pvals	logfoldchanges
OLFM4	0	5.245
CPSF6	0	4.966
C3	1.8E-242	4.264
ENSSSCG00000048603-C4BPA	2.5E-210	3.779
RPS6	2.3E-205	1.439
RPS2	2E-201	1.264
RPL5	9E-193	1.652
ENSSSCG00000033019-RL12	4.9E-188	1.573
NPM1	9.1E-185	2.002
ENSSSCG00000037274	1.3E-184	1.267
RPL21	5.2E-178	1.240
RPS4X	1.9E-176	1.261
RPL7	2.6E-173	1.293
BPI	3.7E-173	3.490
RPL4	1.9E-170	1.292
ENSSSCG00000016737	5.2E-159	1.184
RPSA	2.9E-158	1.411
ENSSSCG00000011272-RL14	8E-153	1.161
RPL15	1.5E-148	1.217
RPS3A	4.5E-143	1.259
ENSSSCG00000035053-ELAF	8.6E-141	2.743
RPL6	1.6E-139	1.139
ENSSSCG00000009327	6.1E-139	1.843
ENSSSCG00000035080-RL23A	9.2E-138	0.996
RPL17-C18orf32	1.5E-136	1.004
ENSSSCG00000035768-RS15A	1.5E-134	1.322
RPS12	8.4E-133	1.079
RPL32	1.9E-130	0.895
ENSSSCG00000033733	3.7E-128	2.085

EEF1B2	2.3E-127	1.357
FCN2	4.5E-126	2.907
RPL3	1.2E-124	1.135
EEF1A1	1.3E-124	0.869
ENSSSCG00000031088	4.6E-123	1.025
RPL27A	6.2E-123	1.110
ENSSSCG0000009138-CFAI	9.7E-121	3.757
CXCL2	5.6E-120	2.603
RPS20	1.5E-118	0.985
PIGR	1.4E-114	1.937
ENSSSCG00000024914-CFAB	6.8E-114	2.244
DAB2	1.1E-110	2.709
RPS17	1.5E-108	0.987
RACK1	1.1E-107	1.193
HNRNPA1	4.6E-106	1.665
RPL35	2.1E-105	1.006
RPS8	5.6E-105	0.757
SPINK1	3.2E-104	2.842
RPLP0	5.3E-104	1.019
RPL26	5.7E-104	0.983
RPL37	3.1E-100	0.807
ENSSSCG00000039544	7.2E-99	0.653
ENSSSCG00000014855	1.19E-97	1.010
ENSSSCG00000012427-RL9	1.44E-95	1.189
RPL27	2.46E-95	0.949
ENSSSCG00000038606	2.85E-95	2.343
RPL34	1.29E-92	0.969
YBX3	1.77E-92	1.580
RPL22L1	1E-91	1.438
RPL10	1.9E-87	0.918
RPL38	3.83E-86	0.844
RPS27A	1.89E-85	1.016
RPS23	4.22E-84	0.925
RPS11	1.32E-82	0.874
RPL36A-HNRNPH2	2.61E-82	1.044
ERBB3	1.36E-80	1.075
RPL37A	6.37E-80	0.744
RPL31	6.86E-80	0.711
RPL24	1.43E-79	0.970
CXCL8	2.65E-79	2.011
RPS5	2.73E-78	1.129
EEF2	3.81E-78	0.869
ENSSSCG00000034448-RL13A	1.98E-77	0.935
TUBA1B	8.79E-77	1.429

NME2	2.44E-76	1.197
H2AFZ	6.25E-76	1.559
RPL23	2.54E-75	0.837
EEF1G	2.1E-73	1.097
RPS13	3.37E-73	0.816
RPL11	2.48E-72	0.759
DUT	8.75E-72	1.927
ENSSSCG00000005656-SETLP	1.51E-71	1.226
C6	1.87E-71	2.346
HMGB2	1.94E-71	1.848
RPL19	7.43E-71	0.853
RPS15	8.16E-71	0.681
RPS25	2.64E-69	0.667
ENSSSCG00000010893-CFAH	7.44E-69	1.858
C5	6.55E-68	1.648
ENSSSCG00000020830-NACA	7.16E-68	0.925
RPL30	1.21E-67	0.851
RPS18	1.49E-67	0.992
NAP1L1	1.93E-67	1.840
PRDX1	2.44E-66	1.154
NANS	9.13E-65	1.173
ENSSSCG00000015988	2.16E-64	1.352
ENSSSCG00000009746	1.34E-60	1.385
ENSSSCG00000033310	5.08E-60	0.673
ENSSSCG00000024776	5.19E-60	1.477
S100A11	2.57E-59	1.578
RPL22	3.79E-59	0.983
HSD11B1L	3.98E-59	1.045
NUDT3	1.23E-58	1.022
FBL	1.58E-58	2.111
NOP58	2.3E-58	1.582
NPM3	9.96E-58	2.225
ENSSSCG0000000377-PA2G4	5.45E-57	1.466
TUBB	1.11E-55	1.367
ENSSSCG00000024974-RL13	2.36E-54	1.024
SLC12A2	4.33E-54	2.392
C4BPB	7.8E-54	2.418
ENSSSCG00000040857-RSMB	2.15E-53	1.303
RPL39	1.05E-52	0.705
PDIA4	1.54E-52	1.533
HNRNPA2B1	2.1E-52	0.770
NCL	6.83E-52	1.223
HNRNPH1	9.03E-52	1.295
ENSSSCG00000013318-RCN1	9.16E-52	2.729

ENSSCG00000006063	1.63E-51	1.046
RPL8	9.04E-51	0.902
PRDX4	2.32E-50	1.839
FABP3	4.01E-50	1.494
ENSSCG00000039731-GLRX1	5.25E-50	1.007
ENO1	7.63E-50	0.670
ENSSCG00000003042-RS19	1.11E-48	0.889
NUTF2	2.55E-48	1.309
SNRPF	3.77E-48	1.447
OSTC	4.2E-48	1.743
PLIN2	1.77E-47	1.430
SNRPE	8.2E-47	1.355
PDIA6	1.12E-46	1.262
RPL18A	1.24E-46	0.910
ENSSCG00000040273	1.85E-46	0.627
ENSSCG00000031838-RS27	2.19E-46	0.703
BTF3	2.92E-46	0.796
RPL29	4.49E-45	0.853
DDX39A	7.46E-45	1.687
HNRNPM	9.05E-45	1.156
RANBP1	1.55E-44	1.638
ENSSCG00000021591-RBM3	2.13E-44	1.305
MCM7	3.96E-44	2.427
CBX3	5.3E-44	1.584
SYNCRIP	1.26E-43	1.336
CFP	1.32E-43	1.911
SSR4	1.82E-43	1.201
DDX21	1.02E-42	1.394
ILF2	1.69E-42	1.375
HSPA8	6.15E-42	0.392
SOD1	2.98E-41	0.981
ENSSCG00000033734-TYB4	6.69E-41	1.568
TOMM20	1.2E-40	1.401
NUDT21	2.36E-40	1.356
ILF3	2.53E-40	1.251
HNRNPK	8.23E-40	0.886
C1QBP	2.41E-39	1.297
HNRNPDL	2.54E-39	1.173
NONO	4.73E-39	1.201
RPN1	1.2E-38	1.047
CLINT1	1.75E-38	1.208
CDK2AP1	2.39E-38	1.251
RBMX	3.65E-38	1.169
YWHAQ	4.62E-38	1.078

ENSSSCG00000011850-MUC4	5.11E-38	1.724
SEC61B	5.82E-38	0.942
ENSSSCG00000009772-TMED2	2.21E-36	1.053
AHCY	3.34E-36	1.205
ERH	1.12E-35	1.054
UBE2C	1.22E-35	2.592
CCT6A	1.49E-35	1.124
GPX1	2.55E-35	1.044
HNRNPD	2.99E-35	1.080
S100G	6.52E-35	1.284
TRMT112	8.04E-35	1.403
ENSSSCG00000001930-PARP6	1.14E-34	0.554
AKR1B1	2.85E-34	2.908
NOP56	3.87E-34	1.307
SRSF3	6.42E-34	0.908
PTPMT1	6.78E-34	1.813
CCT5	1.15E-33	0.998
KARS1	1.2E-33	0.808
HDGF	1.21E-33	0.840
PTBP1	1.27E-33	0.899
CCT4	2.65E-33	1.034
PCLAF	3.51E-33	2.517
KPNB1	4.3E-33	1.287
RPS28	4.79E-33	0.614
STEAP1	5.35E-33	2.782
PLAUR	1.49E-32	1.223
JPT2	1.81E-32	1.360
RPN2	1.94E-32	1.005
ACTG1	2.04E-32	0.470
EIF3I	2.32E-32	1.118
ENSSSCG00000037645	2.94E-32	1.170
HSP90AB1	3.59E-32	0.572
ENSSSCG00000026064-LSM5	4.39E-32	1.450
ENSSSCG00000017032-PTTG1	4.66E-32	2.553
SSRP1	1.82E-31	1.331
LBP	1.84E-31	2.935
CCNB1	1.85E-31	2.540
PCNA	2.95E-31	1.348
SMC2	6.47E-31	1.905

Supplementary Table S3 Transcription factors that change significantly over pseudotime in BEST4⁺ epithelial cell lineage

gene	Estimate	Std.Error	tvalue	Pvalue	qvalue
PRDM1	0.107	0.006	16.853	4.29E-61	2.86E-59
KLF4	0.073	0.005	15.170	3.15E-50	1.53E-48
PPARG	0.099	0.007	15.015	2.81E-49	1.30E-47
SPIB	0.313	0.021	14.833	3.62E-48	1.58E-46
ISX	0.159	0.011	14.265	8.62E-45	3.34E-43
STAT1	0.080	0.006	13.102	3.14E-38	8.94E-37
STAT2	0.117	0.009	12.803	1.26E-36	3.35E-35
MAFF	0.061	0.005	11.559	2.68E-30	4.93E-29
HNF4G	0.119	0.010	11.394	1.67E-29	2.96E-28
IRF6	0.063	0.006	10.986	1.41E-27	2.24E-26
ATF3	0.070	0.007	10.299	1.72E-24	2.41E-23
CDX2	0.073	0.007	10.264	2.46E-24	3.41E-23
MXD1	0.051	0.005	10.234	3.33E-24	4.57E-23
UGP2	0.082	0.008	10.233	3.34E-24	4.58E-23
MEF2D	0.085	0.009	8.918	7.87E-19	7.71E-18
KLF13	0.067	0.008	8.897	9.49E-19	9.25E-18
FOSB	0.043	0.005	8.684	6.04E-18	5.58E-17
EGR1	0.047	0.005	8.679	6.29E-18	5.80E-17
KLF5	0.047	0.005	8.573	1.56E-17	1.39E-16
NR1I2	0.067	0.008	8.557	1.78E-17	1.59E-16
HSPA5	0.052	0.006	8.403	6.50E-17	5.52E-16
STAT3	0.052	0.006	8.182	4.00E-16	3.22E-15
PRDX5	0.049	0.006	7.962	2.33E-15	1.76E-14
HES4	0.224	0.028	7.953	2.51E-15	1.88E-14
ELF4	0.087	0.011	7.847	5.79E-15	4.24E-14
CYCS	0.042	0.005	7.768	1.07E-14	7.64E-14
SP110	0.082	0.011	7.747	1.25E-14	8.90E-14
NFE2L2	0.051	0.007	7.689	1.96E-14	1.38E-13
KLF3	0.051	0.007	7.543	5.96E-14	4.05E-13
MAF	0.115	0.016	7.367	2.21E-13	1.44E-12
DPRX	0.068	0.009	7.256	5.00E-13	3.15E-12
MEIS1	0.343	0.048	7.070	1.90E-12	1.13E-11
HNF4A	0.037	0.005	6.932	5.00E-12	2.90E-11
PIR	0.079	0.011	6.922	5.38E-12	3.12E-11
NR3C2	0.096	0.014	6.857	8.44E-12	4.80E-11
BHLHE40	0.038	0.006	6.748	1.77E-11	9.73E-11
ZNF133	0.077	0.011	6.719	2.16E-11	1.18E-10
HTATIP2	0.053	0.008	6.666	3.09E-11	1.65E-10
OVOL1	0.069	0.011	6.551	6.63E-11	3.43E-10
ZMIZ1	0.076	0.012	6.544	6.97E-11	3.60E-10
SSBP3	0.059	0.009	6.527	7.79E-11	3.99E-10

NR1H4	0.156	0.024	6.523	7.99E-11	4.08E-10
YOD1	0.052	0.008	6.511	8.67E-11	4.41E-10
AGMAT	0.111	0.017	6.499	9.35E-11	4.73E-10
ETV3	0.039	0.006	6.253	4.58E-10	2.17E-09
ID4	0.076	0.012	6.121	1.05E-09	4.79E-09
FOS	0.029	0.005	6.061	1.51E-09	6.79E-09
KLF6	0.032	0.005	5.984	2.42E-09	1.06E-08
BHLHE41	0.212	0.036	5.829	6.16E-09	2.57E-08
NFE2L1	0.054	0.009	5.774	8.50E-09	3.50E-08
ZNF654	0.090	0.016	5.759	9.25E-09	3.79E-08
NR4A2	0.071	0.012	5.721	1.16E-08	4.70E-08
VPS4B	0.042	0.007	5.679	1.48E-08	5.90E-08
NR1D1	0.189	0.033	5.654	1.71E-08	6.78E-08
SP6	0.471	0.084	5.632	1.94E-08	7.64E-08
HBP1	0.054	0.010	5.400	7.14E-08	2.64E-07
PBX3	0.061	0.011	5.361	8.88E-08	3.23E-07
SREBF1	0.051	0.010	5.313	1.15E-07	4.12E-07
FOXO1	0.081	0.015	5.309	1.18E-07	4.20E-07
TOB2	0.037	0.007	5.051	4.64E-07	1.53E-06
PPARD	0.083	0.017	4.975	6.89E-07	2.22E-06
ETV7	0.178	0.036	4.970	7.06E-07	2.28E-06
SP100	0.076	0.015	4.931	8.62E-07	2.74E-06
PBX1	0.083	0.017	4.885	1.09E-06	3.42E-06
ANXA1	0.033	0.007	4.840	1.36E-06	4.23E-06
TEAD3	0.050	0.011	4.689	2.87E-06	8.49E-06
ELF3	0.057	0.012	4.630	3.80E-06	1.10E-05

Supplementary Table S4 Top20 up-regulated and down-regulated DEGs in different cell types of the D42 cecum compared to the D30 cecum

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	group	celltype
CD247	2.050E-25	1.622	0.355	0.124	3.48E-21	up	B
ENSSSCG00000024973-GBP2	3.045E-40	1.620	0.456	0.138	5.17E-36	up	B
CCL5	2.456E-22	1.590	0.252	0.060	4.17E-18	up	B
ENSSSCG00000029668-IL2RB	3.544E-29	1.340	0.422	0.144	6.01E-25	up	B
CD3E	7.561E-25	1.257	0.382	0.133	1.28E-20	up	B
BAG3	3.706E-15	1.213	0.437	0.267	6.29E-11	up	B
ENSSSCG00000008214	2.971E-17	1.210	0.275	0.101	5.04E-13	up	B
ENSSSCG00000029160	1.376E-21	1.078	0.804	0.686	2.33E-17	up	B
CD2	7.078E-15	1.068	0.268	0.107	1.20E-10	up	B
ENSSSCG00000034570	2.710E-12	1.031	0.259	0.113	4.60E-08	up	B
SERPINB9	3.691E-17	0.957	0.427	0.221	6.26E-13	up	B
IKZF3	2.943E-11	0.914	0.252	0.115	4.99E-07	up	B
NKG7	1.390E-14	0.905	0.250	0.092	2.36E-10	up	B
LCK	8.770E-17	0.864	0.285	0.106	1.49E-12	up	B
FYN	9.006E-12	0.862	0.292	0.146	1.53E-07	up	B
FYB1	2.204E-15	0.843	0.303	0.127	3.74E-11	up	B
ENSSSCG00000030801-GBP6	3.894E-11	0.841	0.313	0.169	6.61E-07	up	B
PCLAF	3.289E-11	0.840	0.279	0.137	5.58E-07	up	B
ARHGDIIB	6.771E-21	0.833	0.728	0.574	1.15E-16	up	B
ENSSSCG00000037645	2.900E-14	0.806	0.502	0.327	4.92E-10	up	B
KLF2	2.934E-37	-1.609	0.243	0.546	4.98E-33	down	B
PHACTR1	1.030E-33	-1.439	0.219	0.521	1.75E-29	down	B
TMEM123	1.019E-22	-1.272	0.328	0.538	1.73E-18	down	B

ENSSCG00000001456-DQA2	2.860E-24	-1.222	0.423	0.623	4.85E-20	down	B
ENSSCG00000021576-CD83	1.414E-23	-1.222	0.241	0.488	2.40E-19	down	B
SLA-DQB1	1.241E-27	-1.163	0.651	0.753	2.11E-23	down	B
TP53I11	4.318E-19	-1.147	0.209	0.414	7.33E-15	down	B
CD40	3.847E-20	-1.069	0.111	0.307	6.53E-16	down	B
CD19	7.228E-19	-1.035	0.080	0.258	1.23E-14	down	B
PLEK	1.132E-12	-1.033	0.155	0.304	1.92E-08	down	B
LYN	4.218E-22	-1.026	0.119	0.331	7.16E-18	down	B
PEA15	1.397E-18	-0.998	0.214	0.419	2.37E-14	down	B
DUSP1	2.137E-26	-0.938	0.297	0.574	3.63E-22	down	B
ENSSCG00000031023	8.091E-16	-0.938	0.091	0.252	1.37E-11	down	B
ENSSCG00000039658-CDNF	8.975E-18	-0.925	0.307	0.508	1.52E-13	down	B
NR4A1	1.201E-18	-0.920	0.194	0.403	2.04E-14	down	B
TSC22D3	3.272E-12	-0.900	0.237	0.393	5.55E-08	down	B
SMC6	1.116E-12	-0.886	0.284	0.443	1.89E-08	down	B
PDE4B	2.548E-15	-0.845	0.306	0.494	4.32E-11	down	B
FOS	3.591E-15	-0.814	0.499	0.675	6.09E-11	down	B
ISG12(A)	1.164E-231	2.512	0.717	0.267	1.98E-227	up	Epithelial
ENSSCG00000024911	1.563E-97	2.409	0.388	0.124	2.65E-93	up	Epithelial
ENSSCG00000034570	8.663E-146	2.253	0.456	0.113	1.47E-141	up	Epithelial
ENSSCG00000008214	9.713E-166	1.868	0.877	0.630	1.65E-161	up	Epithelial
HSPA6	9.993E-124	1.762	0.548	0.214	1.70E-119	up	Epithelial
ENSSCG00000001229-HLAA	0.000E+00	1.672	0.992	0.901	0.00E+00	up	Epithelial
ENSSCG00000030300	8.370E-93	1.604	0.351	0.094	1.42E-88	up	Epithelial
B2M	2.645E-298	1.388	0.971	0.853	4.49E-294	up	Epithelial
MX1	1.898E-113	1.375	0.381	0.091	3.22E-109	up	Epithelial

KRT20	6.841E-145	1.375	0.813	0.523	1.16E-140	up	Epithelial
ENSSCG00000017754-LEG9	8.783E-132	1.366	0.751	0.472	1.49E-127	up	Epithelial
ENSSCG00000039095-ZNT10	2.983E-145	1.351	0.384	0.059	5.06E-141	up	Epithelial
OAS2	2.574E-122	1.247	0.360	0.064	4.37E-118	up	Epithelial
S100G	6.169E-80	1.207	0.613	0.323	1.05E-75	up	Epithelial
OASL	6.321E-139	1.194	0.277	0.009	1.07E-134	up	Epithelial
SELENBP1	1.235E-100	1.163	0.757	0.520	2.10E-96	up	Epithelial
INSIG1	8.599E-46	1.105	0.435	0.245	1.46E-41	up	Epithelial
MS4A12	6.537E-68	1.100	0.459	0.212	1.11E-63	up	Epithelial
ENSSCG00000024973-GBP2	4.580E-97	1.073	0.573	0.259	7.77E-93	up	Epithelial
STAT1	2.152E-90	1.067	0.589	0.324	3.65E-86	up	Epithelial
BPI	1.927E-142	-2.630	0.084	0.461	3.27E-138	down	Epithelial
ENSSCG00000035053-ELAF	3.200E-203	-2.621	0.152	0.608	5.43E-199	down	Epithelial
CPSF6	1.332E-142	-2.175	0.549	0.800	2.26E-138	down	Epithelial
C3	8.115E-148	-2.089	0.117	0.505	1.38E-143	down	Epithelial
FCN2	4.040E-101	-1.804	0.126	0.441	6.85E-97	down	Epithelial
AGR2	2.138E-44	-1.758	0.165	0.364	3.63E-40	down	Epithelial
OLFM4	1.387E-142	-1.603	0.469	0.814	2.35E-138	down	Epithelial
ENSSCG00000024914-CFAB	2.422E-73	-1.519	0.241	0.496	4.11E-69	down	Epithelial
SPINK4	2.106E-23	-1.479	0.193	0.326	3.57E-19	down	Epithelial
ENSSCG00000048603-C4BPA	1.112E-121	-1.452	0.136	0.490	1.89E-117	down	Epithelial
CXCL2	8.468E-61	-1.401	0.344	0.567	1.44E-56	down	Epithelial
CXCL8	4.269E-25	-1.229	0.432	0.534	7.24E-21	down	Epithelial
ENSSCG00000022258-SLPI	1.519E-44	-1.029	0.231	0.412	2.58E-40	down	Epithelial
NPM1	4.597E-96	-0.990	0.603	0.781	7.80E-92	down	Epithelial
ENSSCG00000038606	9.586E-49	-0.976	0.267	0.475	1.63E-44	down	Epithelial

C4BPB	1.830E-69	-0.945	0.065	0.287	3.10E-65	down	Epithelial
ENSSCG00000009138-CFAI	4.286E-54	-0.922	0.108	0.310	7.27E-50	down	Epithelial
S100A11	3.547E-68	-0.919	0.275	0.529	6.02E-64	down	Epithelial
ENSSCG00000033733	9.346E-69	-0.908	0.384	0.612	1.59E-64	down	Epithelial
YBX3	1.222E-62	-0.879	0.454	0.652	2.07E-58	down	Epithelial
HSPA6	2.690E-24	2.566	0.541	0.184	4.56E-20	up	IBP6- fib
AGT	3.753E-30	2.550	0.469	0.060	6.37E-26	up	IBP6- fib
ENSSCG00000039926-MXRA5	1.441E-31	2.431	0.525	0.100	2.45E-27	up	IBP6- fib
ENSSCG00000009672-SCAR5	4.733E-33	2.384	0.508	0.067	8.03E-29	up	IBP6- fib
ADM	2.408E-23	2.211	0.489	0.134	4.09E-19	up	IBP6- fib
ECM1	9.104E-32	2.118	0.623	0.184	1.54E-27	up	IBP6- fib
ALDH1A1	1.572E-31	2.071	0.416	0.020	2.67E-27	up	IBP6- fib
COL6A5	2.657E-26	2.055	0.482	0.097	4.51E-22	up	IBP6- fib
DPT	2.395E-29	2.015	0.515	0.094	4.06E-25	up	IBP6- fib
LUM	1.609E-28	1.999	0.564	0.137	2.73E-24	up	IBP6- fib
DUSP1	5.013E-21	1.898	0.649	0.344	8.51E-17	up	IBP6- fib
ENSSCG00000008214	1.235E-12	1.885	0.298	0.070	2.10E-08	up	IBP6- fib
NT5E	9.247E-26	1.861	0.361	0.023	1.57E-21	up	IBP6- fib
C7	1.177E-24	1.842	0.502	0.110	2.00E-20	up	IBP6- fib
ENSSCG00000009182	5.284E-24	1.833	0.361	0.030	8.97E-20	up	IBP6- fib
RARRES1	2.901E-25	1.821	0.413	0.054	4.92E-21	up	IBP6- fib
PLAC9	3.263E-24	1.779	0.489	0.114	5.54E-20	up	IBP6- fib
COL15A1	9.220E-22	1.767	0.593	0.247	1.56E-17	up	IBP6- fib
DCN	4.856E-20	1.654	0.623	0.301	8.24E-16	up	IBP6- fib
FBLN1	9.660E-23	1.647	0.466	0.107	1.64E-18	up	IBP6- fib
ACTG2	5.984E-11	-1.753	0.141	0.365	1.02E-06	down	IBP6- fib

RGS16	2.712E-23	-1.488	0.200	0.612	4.60E-19	down	IBP6- fib
FABP4	3.684E-09	-1.275	0.148	0.355	6.25E-05	down	IBP6- fib
ENSSCG00000005316	2.603E-17	-1.242	0.321	0.645	4.42E-13	down	IBP6- fib
ACTA2	4.788E-28	-1.186	0.482	0.903	8.12E-24	down	IBP6- fib
FABP5	1.575E-07	-1.145	0.095	0.254	2.67E-03	down	IBP6- fib
MGP	2.319E-15	-1.077	0.374	0.676	3.93E-11	down	IBP6- fib
RPL10	1.810E-20	-1.060	0.761	0.870	3.07E-16	down	IBP6- fib
NET1	6.048E-07	-1.060	0.233	0.398	1.03E-02	down	IBP6- fib
AOPEP	1.025E-08	-1.048	0.220	0.408	1.74E-04	down	IBP6- fib
CSRP2	1.501E-08	-1.040	0.308	0.492	2.55E-04	down	IBP6- fib
PKIG	5.936E-08	-1.032	0.128	0.304	1.01E-03	down	IBP6- fib
MYH11	6.866E-15	-1.014	0.269	0.595	1.17E-10	down	IBP6- fib
TPM1	6.903E-24	-0.983	0.541	0.866	1.17E-19	down	IBP6- fib
FJX1	3.694E-09	-0.978	0.256	0.455	6.27E-05	down	IBP6- fib
GJA4	1.859E-10	-0.941	0.285	0.548	3.16E-06	down	IBP6- fib
ITIH4	9.192E-10	-0.933	0.220	0.468	1.56E-05	down	IBP6- fib
MYL9	9.905E-08	-0.891	0.200	0.391	1.68E-03	down	IBP6- fib
MYL6	6.027E-14	-0.874	0.728	0.839	1.02E-09	down	IBP6- fib
TAGLN	3.780E-15	-0.859	0.387	0.722	6.41E-11	down	IBP6- fib
ENSSCG00000031292	3.535E-103	1.972	0.686	0.206	6.00E-99	up	IBP6+ fib
HSPA6	9.655E-61	1.864	0.665	0.344	1.64E-56	up	IBP6+ fib
ENSSCG00000001229-HLAA	5.866E-113	1.529	0.964	0.887	9.95E-109	up	IBP6+ fib
OMD	2.321E-62	1.496	0.681	0.355	3.94E-58	up	IBP6+ fib
AGT	1.021E-52	1.261	0.783	0.556	1.73E-48	up	IBP6+ fib
CRYAB	4.821E-08	1.057	0.438	0.334	8.18E-04	up	IBP6+ fib
ENSSCG00000008214	1.568E-15	0.981	0.281	0.126	2.66E-11	up	IBP6+ fib

ENSSCG00000009182	7.332E-23	0.901	0.282	0.100	1.24E-18	up	IBP6+ fib
ADGRD1	1.166E-32	0.893	0.533	0.282	1.98E-28	up	IBP6+ fib
PI16	1.837E-11	0.881	0.615	0.519	3.12E-07	up	IBP6+ fib
EFEMP1	1.940E-22	0.877	0.549	0.346	3.29E-18	up	IBP6+ fib
CYP1B1	7.679E-20	0.842	0.265	0.101	1.30E-15	up	IBP6+ fib
FBLN2	3.889E-16	0.825	0.521	0.378	6.60E-12	up	IBP6+ fib
ENSSCG00000029160	1.420E-36	0.812	0.968	0.951	2.41E-32	up	IBP6+ fib
B2M	1.206E-49	0.791	0.925	0.845	2.05E-45	up	IBP6+ fib
TXNIP	1.121E-26	0.782	0.831	0.684	1.90E-22	up	IBP6+ fib
GJA1	1.183E-23	0.779	0.369	0.162	2.01E-19	up	IBP6+ fib
ENSSCG00000009672-SCAR5	1.622E-26	0.750	0.731	0.551	2.75E-22	up	IBP6+ fib
GHSR	2.869E-11	0.747	0.461	0.322	4.87E-07	up	IBP6+ fib
ENSSCG00000000261-IBP6	2.486E-11	0.745	0.500	0.369	4.22E-07	up	IBP6+ fib
SFRP2	7.114E-33	-1.208	0.399	0.626	1.21E-28	down	IBP6+ fib
NREP	1.065E-47	-1.073	0.564	0.770	1.81E-43	down	IBP6+ fib
NR4A1	1.497E-35	-1.068	0.504	0.728	2.54E-31	down	IBP6+ fib
IER3	1.612E-20	-0.856	0.278	0.482	2.73E-16	down	IBP6+ fib
CCN2	3.135E-15	-0.853	0.308	0.486	5.32E-11	down	IBP6+ fib
PCOLCE	8.312E-19	-0.802	0.618	0.714	1.41E-14	down	IBP6+ fib
RPL10	1.615E-56	-0.755	0.921	0.965	2.74E-52	down	IBP6+ fib
IL6	2.788E-07	-0.752	0.278	0.386	4.73E-03	down	IBP6+ fib
BGN	9.556E-19	-0.735	0.193	0.383	1.62E-14	down	IBP6+ fib
ENSSCG00000035293-IGF2	3.874E-21	-0.735	0.668	0.798	6.57E-17	down	IBP6+ fib
PLIN2	6.943E-14	-0.712	0.308	0.467	1.18E-09	down	IBP6+ fib
CXCL2	6.212E-09	-0.712	0.261	0.387	1.05E-04	down	IBP6+ fib
GEM	3.267E-18	-0.706	0.515	0.681	5.54E-14	down	IBP6+ fib

ENSSCG00000022925-GTR3	4.501E-16	-0.701	0.492	0.636	7.64E-12	down	IBP6+ fib
CXCL14	9.509E-12	-0.659	0.129	0.267	1.61E-07	down	IBP6+ fib
LSAMP	3.112E-15	-0.658	0.249	0.414	5.28E-11	down	IBP6+ fib
ENSSCG00000024974-RL13	1.931E-16	-0.586	0.551	0.686	3.28E-12	down	IBP6+ fib
CBX4	2.022E-08	-0.570	0.206	0.319	3.43E-04	down	IBP6+ fib
PTX3	4.408E-07	-0.560	0.228	0.328	7.48E-03	down	IBP6+ fib
ATF4	3.132E-12	-0.559	0.656	0.729	5.32E-08	down	IBP6+ fib
SERPINE1	1.378E-10	2.199	0.404	0.185	2.34E-06	up	LECs
LYVE1	1.113E-19	1.815	0.677	0.313	1.89E-15	up	LECs
CCN3	7.162E-16	1.589	0.384	0.101	1.22E-11	up	LECs
ENSSCG00000008214	1.795E-08	1.440	0.258	0.084	3.05E-04	up	LECs
TSC22D3	1.429E-08	1.232	0.439	0.242	2.42E-04	up	LECs
ENSSCG00000001455	3.280E-15	1.190	0.561	0.248	5.57E-11	up	LECs
GHSR	2.482E-08	1.041	0.697	0.579	4.21E-04	up	LECs
HLA-DRA	5.172E-07	1.033	0.348	0.170	8.78E-03	up	LECs
CYYR1	4.893E-07	1.001	0.384	0.206	8.30E-03	up	LECs
SLA-DQB1	3.719E-09	0.949	0.505	0.263	6.31E-05	up	LECs
ENSSCG00000033262-HG2A	8.758E-07	0.949	0.404	0.221	1.49E-02	up	LECs
TGM2	3.428E-07	0.887	0.485	0.284	5.82E-03	up	LECs
MMRN1	1.034E-07	0.733	0.773	0.627	1.76E-03	up	LECs
CAVIN2	8.409E-08	0.673	0.833	0.684	1.43E-03	up	LECs
ENSSCG00000008137-LIMS1	9.002E-07	0.650	0.646	0.481	1.53E-02	up	LECs
ENSSCG00000001229-HLAA	7.077E-14	0.510	1.000	0.973	1.20E-09	up	LECs
RPS16	9.416E-08	0.498	0.854	0.800	1.60E-03	up	LECs
RPL11	8.191E-07	0.494	0.869	0.851	1.39E-02	up	LECs
B2M	2.605E-11	0.489	0.995	0.943	4.42E-07	up	LECs

RPS25	2.177E-07	0.377	0.944	0.919	3.69E-03	up	LECs
MGP	3.680E-14	-2.173	0.192	0.507	6.24E-10	down	LECs
PLAT	1.333E-15	-1.868	0.192	0.528	2.26E-11	down	LECs
APOA1	7.879E-12	-1.658	0.071	0.316	1.34E-07	down	LECs
MAFF	6.288E-22	-1.511	0.369	0.740	1.07E-17	down	LECs
IRF1	5.156E-12	-1.319	0.197	0.478	8.75E-08	down	LECs
CLU	9.422E-09	-1.224	0.081	0.290	1.60E-04	down	LECs
IL33	1.680E-06	-1.211	0.237	0.418	2.85E-02	down	LECs
ENSSSCG00000016646-IFRD1	5.014E-09	-1.170	0.328	0.549	8.51E-05	down	LECs
ICAM1	8.263E-07	-1.126	0.278	0.451	1.40E-02	down	LECs
ENSSSCG00000013260	3.418E-12	-1.114	0.394	0.660	5.80E-08	down	LECs
TM4SF1	2.109E-13	-1.056	0.525	0.761	3.58E-09	down	LECs
SCG3	6.231E-07	-1.038	0.242	0.457	1.06E-02	down	LECs
AMOTL2	1.161E-07	-1.033	0.116	0.316	1.97E-03	down	LECs
GADD45A	8.582E-10	-1.002	0.162	0.421	1.46E-05	down	LECs
NREP	1.105E-08	-1.000	0.414	0.639	1.88E-04	down	LECs
CCN2	2.244E-09	-0.999	0.333	0.597	3.81E-05	down	LECs
CXCL2	1.195E-07	-0.985	0.616	0.770	2.03E-03	down	LECs
ENSSSCG00000003079-PVR	2.365E-06	-0.961	0.131	0.310	4.01E-02	down	LECs
TMSB10	7.188E-20	-0.946	0.914	0.976	1.22E-15	down	LECs
SPRY1	6.177E-07	-0.930	0.096	0.275	1.05E-02	down	LECs
ENSSSCG00000008214	2.993E-09	1.819	0.409	0.055	5.08E-05	up	Mast
ENSSSCG00000001229-HLAA	5.186E-07	1.215	1.000	0.926	8.80E-03	up	Mast
RPL10	1.015E-07	-1.437	0.727	0.980	1.72E-03	down	Mast
FCER1A	1.786E-92	1.977	0.408	0.136	3.03E-88	up	Myeloid
GSN	4.214E-101	1.590	0.454	0.155	7.15E-97	up	Myeloid

SERPINE1	7.455E-69	1.394	0.345	0.113	1.27E-64	up	Myeloid
ENSSCG00000024973-GBP2	1.199E-138	1.376	0.592	0.194	2.03E-134	up	Myeloid
BAG3	5.277E-67	1.007	0.780	0.610	8.95E-63	up	Myeloid
ACTN1	1.501E-52	1.006	0.401	0.188	2.55E-48	up	Myeloid
HSPA6	6.549E-48	0.982	0.404	0.193	1.11E-43	up	Myeloid
ENSSCG00000030801-GBP6	2.784E-72	0.953	0.356	0.112	4.72E-68	up	Myeloid
ITGAE	2.407E-79	0.951	0.251	0.038	4.08E-75	up	Myeloid
TAP1	2.772E-50	0.836	0.578	0.363	4.70E-46	up	Myeloid
ENSSCG00000033089-GVIN1	8.076E-36	0.824	0.352	0.178	1.37E-31	up	Myeloid
ANXA6	5.148E-50	0.818	0.307	0.117	8.74E-46	up	Myeloid
ENSSCG00000008214	2.262E-36	0.800	0.262	0.102	3.84E-32	up	Myeloid
FLT3	4.883E-51	0.785	0.373	0.161	8.29E-47	up	Myeloid
ENSSCG00000001398-HLAB	4.708E-59	0.783	0.434	0.193	7.99E-55	up	Myeloid
SPINT2	2.520E-33	0.777	0.483	0.311	4.28E-29	up	Myeloid
MX1	1.028E-31	0.765	0.277	0.128	1.74E-27	up	Myeloid
ARHGAP18	3.455E-37	0.758	0.314	0.146	5.86E-33	up	Myeloid
ENSSCG00000017754-LEG9	9.042E-33	0.742	0.492	0.318	1.53E-28	up	Myeloid
ENSSCG00000029160	9.438E-66	0.729	0.967	0.917	1.60E-61	up	Myeloid
ENSSCG00000039214	2.894E-87	-2.095	0.432	0.656	4.91E-83	down	Myeloid
CXCL8	2.349E-38	-1.773	0.288	0.453	3.99E-34	down	Myeloid
CXCL2	1.232E-48	-1.658	0.486	0.637	2.09E-44	down	Myeloid
THBS1	5.843E-50	-1.651	0.165	0.362	9.91E-46	down	Myeloid
CPSF6	5.739E-48	-1.364	0.150	0.342	9.74E-44	down	Myeloid
CXCL14	9.513E-19	-1.302	0.176	0.283	1.61E-14	down	Myeloid
ENSSCG00000008088	2.846E-70	-1.297	0.084	0.300	4.83E-66	down	Myeloid
CD163	2.925E-56	-1.253	0.135	0.348	4.96E-52	down	Myeloid

ENSSSCG00000014540	1.559E-127	-1.248	0.983	0.990	2.65E-123	down	Myeloid
HBEGF	1.367E-73	-1.246	0.413	0.624	2.32E-69	down	Myeloid
SOD2	4.712E-44	-1.234	0.366	0.533	8.00E-40	down	Myeloid
AREG	1.352E-38	-1.139	0.367	0.520	2.29E-34	down	Myeloid
ENSSSCG00000026043-TGM3	8.107E-28	-1.113	0.153	0.287	1.38E-23	down	Myeloid
ENSSSCG00000028461-SHPS1	2.946E-63	-1.104	0.311	0.530	5.00E-59	down	Myeloid
PHF11	1.879E-46	-1.039	0.306	0.484	3.19E-42	down	Myeloid
IL1R2	1.348E-19	-0.972	0.214	0.328	2.29E-15	down	Myeloid
SRGN	1.520E-68	-0.962	0.834	0.866	2.58E-64	down	Myeloid
IL1A	6.009E-38	-0.940	0.160	0.322	1.02E-33	down	Myeloid
ENSSSCG00000033909-GIMA1	2.150E-63	-0.940	0.788	0.840	3.65E-59	down	Myeloid
PLIN2	3.283E-32	-0.882	0.138	0.283	5.57E-28	down	Myeloid
ENSSSCG00000034570	4.754E-73	1.652	0.450	0.119	8.07E-69	up	NKT
ENSSSCG00000050093	2.042E-41	1.392	0.347	0.119	3.46E-37	up	NKT
CD247	2.490E-57	1.185	0.739	0.522	4.22E-53	up	NKT
BAG3	6.661E-29	1.080	0.527	0.342	1.13E-24	up	NKT
XCL1	2.953E-33	1.026	0.485	0.256	5.01E-29	up	NKT
FSCN1	1.122E-32	0.886	0.347	0.138	1.90E-28	up	NKT
ENSSSCG00000024973-GBP2	3.721E-32	0.838	0.518	0.298	6.31E-28	up	NKT
ENSSSCG00000001455	1.698E-29	0.790	0.519	0.303	2.88E-25	up	NKT
HLA-DRA	6.312E-25	0.771	0.376	0.190	1.07E-20	up	NKT
ITGAE	2.164E-28	0.745	0.465	0.255	3.67E-24	up	NKT
VMP1	6.732E-18	0.730	0.355	0.208	1.14E-13	up	NKT
GPR18	2.556E-20	0.700	0.502	0.327	4.34E-16	up	NKT
CCNYL1	5.308E-15	0.694	0.262	0.137	9.01E-11	up	NKT
FYB1	5.518E-26	0.688	0.485	0.287	9.36E-22	up	NKT

ENSSSCG00000004670	2.483E-19	0.673	0.371	0.210	4.21E-15	up	NKT
TCF7	6.389E-15	0.647	0.400	0.265	1.08E-10	up	NKT
ATP8	1.356E-36	0.620	0.707	0.480	2.30E-32	up	NKT
SLA-DQB1	2.206E-19	0.616	0.580	0.388	3.74E-15	up	NKT
ANXA6	2.465E-17	0.588	0.252	0.118	4.18E-13	up	NKT
ABLIM1	5.834E-17	0.575	0.313	0.169	9.90E-13	up	NKT
SATB1	1.912E-23	-0.850	0.274	0.422	3.24E-19	down	NKT
PCED1B	3.427E-22	-0.845	0.209	0.350	5.81E-18	down	NKT
ADGRE5	1.172E-28	-0.804	0.109	0.253	1.99E-24	down	NKT
BHLHE40	2.301E-19	-0.753	0.226	0.360	3.90E-15	down	NKT
ADGRG1	3.634E-11	-0.657	0.198	0.293	6.17E-07	down	NKT
SMC4	6.284E-10	-0.641	0.305	0.383	1.07E-05	down	NKT
ENSSSCG00000002918	8.946E-11	-0.560	0.168	0.255	1.52E-06	down	NKT
AHSA1	1.182E-08	-0.534	0.244	0.321	2.00E-04	down	NKT
PLK3	5.969E-08	-0.527	0.197	0.269	1.01E-03	down	NKT
NKG7	5.308E-08	-0.496	0.630	0.640	9.01E-04	down	NKT
SH2D2A	4.638E-16	-0.493	0.299	0.432	7.87E-12	down	NKT
RPS12	8.302E-46	-0.491	0.898	0.932	1.41E-41	down	NKT
PCBP1	4.560E-14	-0.489	0.511	0.588	7.74E-10	down	NKT
CYCS	8.098E-10	-0.481	0.412	0.488	1.37E-05	down	NKT
PDE4D	5.725E-12	-0.471	0.368	0.470	9.71E-08	down	NKT
CTSW	1.346E-07	-0.465	0.526	0.581	2.28E-03	down	NKT
CHORDC1	1.796E-09	-0.460	0.245	0.335	3.05E-05	down	NKT
ENSSSCG00000011272-RL14	5.087E-36	-0.458	0.871	0.930	8.63E-32	down	NKT
ENSSSCG00000034448-RL13A	3.866E-36	-0.456	0.861	0.918	6.56E-32	down	NKT
TUBA1B	1.617E-14	-0.455	0.606	0.679	2.74E-10	down	NKT

ATF4	5.69E-08	-0.969	0.62	0.87	9.66E-04	down	Plasma
ENSSCG00000034570	1.027E-54	1.483	0.411	0.158	1.74E-50	up	T
ENSSCG00000036618-FCG3A	1.485E-84	1.442	0.643	0.308	2.52E-80	up	T
ENSSCG00000024973-GBP2	3.225E-76	1.428	0.559	0.248	5.47E-72	up	T
ATP1B2	1.746E-27	1.036	0.263	0.105	2.96E-23	up	T
BHLHE40	1.362E-19	0.895	0.342	0.203	2.31E-15	up	T
FYB1	4.320E-27	0.856	0.424	0.251	7.33E-23	up	T
RGS1	1.506E-29	0.843	0.596	0.425	2.56E-25	up	T
BAG3	3.965E-11	0.807	0.370	0.276	6.73E-07	up	T
CD2	1.728E-26	0.780	0.456	0.283	2.93E-22	up	T
ENSSCG00000030801-GBP6	1.621E-25	0.753	0.475	0.298	2.75E-21	up	T
CD4	5.982E-22	0.686	0.466	0.305	1.02E-17	up	T
ENSSCG00000007743-CHCH2	3.340E-13	0.644	0.497	0.391	5.67E-09	up	T
CYTIP	7.027E-18	0.644	0.485	0.345	1.19E-13	up	T
VMP1	7.963E-12	0.632	0.305	0.203	1.35E-07	up	T
ENSSCG00000048856	3.560E-21	0.599	0.927	0.873	6.04E-17	up	T
ICOS	1.375E-10	0.572	0.383	0.285	2.33E-06	up	T
SPNS1	2.964E-13	0.562	0.416	0.299	5.03E-09	up	T
CTSB	8.902E-12	0.553	0.549	0.444	1.51E-07	up	T
UBB	1.359E-14	0.533	0.989	0.988	2.31E-10	up	T
ENSSCG00000029160	1.716E-06	0.512	0.878	0.874	2.91E-02	up	T
YBX3	1.362E-71	-1.856	0.067	0.294	2.31E-67	down	T
TP53I11	2.439E-58	-1.657	0.165	0.400	4.14E-54	down	T
ENSSCG00000032017	4.436E-39	-1.289	0.108	0.279	7.53E-35	down	T
KLF2	2.282E-37	-1.238	0.189	0.378	3.87E-33	down	T
SERPINB1	3.411E-14	-0.860	0.333	0.435	5.79E-10	down	T

SERPINB9	6.388E-18	-0.829	0.344	0.467	1.08E-13	down	T
YWHAQ	2.949E-19	-0.794	0.159	0.281	5.00E-15	down	T
NET1	4.820E-19	-0.771	0.212	0.347	8.18E-15	down	T
S100A11	3.338E-23	-0.746	0.191	0.340	5.66E-19	down	T
CYCS	1.463E-19	-0.661	0.384	0.523	2.48E-15	down	T
KLF13	1.795E-16	-0.613	0.431	0.554	3.05E-12	down	T
CTSW	1.425E-08	-0.609	0.196	0.274	2.42E-04	down	T
IL6R	7.855E-11	-0.599	0.204	0.294	1.33E-06	down	T
ADGRE5	7.179E-13	-0.591	0.172	0.276	1.22E-08	down	T
TUBA1B	6.582E-19	-0.565	0.472	0.594	1.12E-14	down	T
EIF3L	3.786E-12	-0.529	0.218	0.324	6.42E-08	down	T
APEX1	6.670E-07	-0.516	0.188	0.256	1.13E-02	down	T
ATP2B4	3.796E-08	-0.511	0.186	0.263	6.44E-04	down	T
ENSSCG00000040294-TCP4	1.181E-08	-0.497	0.174	0.253	2.00E-04	down	T
RPL10	3.467E-31	-0.493	0.823	0.895	5.88E-27	down	T
HSPA6	1.859E-23	1.255	0.539	0.375	3.15E-19	up	VECs
ENSSCG00000008214	3.152E-27	1.235	0.316	0.123	5.35E-23	up	VECs
ENSSCG00000034570	1.397E-31	1.038	0.710	0.538	2.37E-27	up	VECs
ISG12(A)	4.905E-23	0.937	0.599	0.438	8.32E-19	up	VECs
STEAP3	2.289E-16	0.735	0.484	0.320	3.88E-12	up	VECs
ENSSCG00000017754-LEG9	6.308E-16	0.721	0.525	0.379	1.07E-11	up	VECs
ENSSCG00000024973-GBP2	8.753E-16	0.715	0.389	0.229	1.49E-11	up	VECs
MX1	1.999E-09	0.651	0.340	0.233	3.39E-05	up	VECs
OAS2	5.891E-11	0.631	0.259	0.147	1.00E-06	up	VECs
IFITM3	1.535E-21	0.597	0.861	0.772	2.60E-17	up	VECs
ENSSCG00000029160	9.811E-21	0.580	0.982	0.985	1.66E-16	up	VECs

HERC6	2.676E-10	0.565	0.501	0.382	4.54E-06	up	VECs
MGST3	1.280E-09	0.555	0.446	0.332	2.17E-05	up	VECs
CDH13	7.734E-08	0.550	0.286	0.193	1.31E-03	up	VECs
TGFBR2	5.743E-09	0.544	0.562	0.474	9.75E-05	up	VECs
STAT1	3.720E-08	0.539	0.418	0.319	6.31E-04	up	VECs
GHSR	4.604E-11	0.520	0.580	0.477	7.81E-07	up	VECs
FKBP5	2.051E-10	0.520	0.264	0.151	3.48E-06	up	VECs
ENSSCG00000048856	1.173E-11	0.491	0.901	0.865	1.99E-07	up	VECs
HSPH1	9.198E-09	0.477	0.797	0.775	1.56E-04	up	VECs
ENSSCG00000014565-IFM1	3.121E-34	-1.183	0.060	0.284	5.30E-30	down	VECs
ENSSCG00000030300	2.946E-20	-1.152	0.197	0.384	5.00E-16	down	VECs
NREP	1.702E-25	-1.050	0.154	0.366	2.89E-21	down	VECs
CCL4	1.403E-12	-0.902	0.210	0.349	2.38E-08	down	VECs
ACTA2	8.697E-08	-0.772	0.200	0.309	1.48E-03	down	VECs
CCL2	7.346E-14	-0.765	0.543	0.652	1.25E-09	down	VECs
RPL10	1.652E-45	-0.754	0.789	0.912	2.80E-41	down	VECs
S100A11	3.814E-18	-0.725	0.356	0.533	6.47E-14	down	VECs
TMSB10	8.450E-32	-0.719	0.872	0.933	1.43E-27	down	VECs
FABP4	1.640E-08	-0.708	0.268	0.388	2.78E-04	down	VECs
RGS16	1.089E-08	-0.673	0.229	0.337	1.85E-04	down	VECs
PDK4	7.900E-14	-0.662	0.135	0.278	1.34E-09	down	VECs
APLNR	5.413E-12	-0.645	0.156	0.291	9.19E-08	down	VECs
LXN	2.234E-12	-0.643	0.214	0.360	3.79E-08	down	VECs
IL6	1.718E-10	-0.633	0.313	0.463	2.92E-06	down	VECs
ENSSCG00000013260	3.625E-11	-0.617	0.178	0.308	6.15E-07	down	VECs
SOD2	1.799E-08	-0.607	0.396	0.504	3.05E-04	down	VECs

IL33	3.913E-11	-0.590	0.388	0.527	6.64E-07	down	VECs
ENSSSCG00000043175	2.452E-07	-0.553	0.199	0.299	4.16E-03	down	VECs
PLIN2	1.035E-11	-0.551	0.171	0.307	1.76E-07	down	VECs

Supplementary Table S5 cell-cell communication at different developmental stages

source_target	ligand_receptor	stage
Epithelial_LECs	ADM_CALCRL	D30
IBP6+ fib_LECs	ADM_CALCRL	D30
LECs_LECs	ADM_CALCRL	D30
Myeloid_LECs	ADM_CALCRL	D30
Epithelial_VECs	ADM_CALCRL	D30
IBP6+ fib_VECs	ADM_CALCRL	D30
LECs_VECs	ADM_CALCRL	D30
Myeloid_VECs	ADM_CALCRL	D30
IBP6+ fib_IBP6+ fib	AGT_AGTR1B	D30
LECs_VECs	ANGPT2_TEK	D30
IBP6+ fib_Myeloid	ANGPTL2_TLR4	D30
IBP6+ fib_LECs	ANGPTL4_CDH5	D30
IBP6+ fib_VECs	ANGPTL4_CDH5	D30
IBP6+ fib_Epithelial	ANGPTL4_SDC1	D30
IBP6+ fib_IBP6- fib	ANGPTL4_SDC2	D30
IBP6+ fib_IBP6+ fib	ANGPTL4_SDC2	D30
IBP6+ fib_Glial	ANGPTL4_SDC3	D30
Epithelial_Myeloid	C3_ITGAM_ITGB2	D30
IBP6+ fib_Myeloid	C3_ITGAM_ITGB2	D30
IBP6- fib_B	CCL19_CCR7	D30
IBP6- fib_Myeloid	CCL19_CCR7	D30
Glial_Plasma	CCL2_CCR2	D30
IBP6- fib_Plasma	CCL2_CCR2	D30
IBP6+ fib_Plasma	CCL2_CCR2	D30
VECs_Plasma	CCL2_CCR2	D30
IBP6+ fib_Glial	CXCL12_ACKR3	D30
VECs_Glial	CXCL12_ACKR3	D30
IBP6+ fib_IBP6+ fib	CXCL12_ACKR3	D30
VECs_IBP6+ fib	CXCL12_ACKR3	D30
IBP6+ fib_LECs	CXCL12_ACKR3	D30
VECs_LECs	CXCL12_ACKR3	D30
IBP6+ fib_VECs	CXCL12_ACKR3	D30
VECs_VECs	CXCL12_ACKR3	D30
IBP6+ fib_B	CXCL12_CXCR4	D30
VECs_B	CXCL12_CXCR4	D30
IBP6+ fib_T	CXCL12_CXCR4	D30
VECs_T	CXCL12_CXCR4	D30
IBP6+ fib_Myeloid	CXCL12_CXCR4	D30
VECs_Myeloid	CXCL12_CXCR4	D30
IBP6+ fib_Plasma	CXCL12_CXCR4	D30
VECs_Plasma	CXCL12_CXCR4	D30

IBP6+ fib_NKT	CXCL12_CXCR4	D30
VECs_NKT	CXCL12_CXCR4	D30
Epithelial_IBP6- fib	EDN1_EDNRA	D30
LECs_IBP6- fib	EDN1_EDNRA	D30
VECs_IBP6- fib	EDN1_EDNRA	D30
Epithelial_Glial	EDN1_EDNRB	D30
LECs_Glial	EDN1_EDNRB	D30
VECs_Glial	EDN1_EDNRB	D30
Epithelial_IBP6- fib	EDN1_EDNRB	D30
LECs_IBP6- fib	EDN1_EDNRB	D30
VECs_IBP6- fib	EDN1_EDNRB	D30
Glial_IBP6+ fib	FGF2_FGFR1	D30
Epithelial_Epithelial	GRN_SORT1	D30
IBP6+ fib_Epithelial	GRN_SORT1	D30
LECs_Epithelial	GRN_SORT1	D30
Myeloid_Epithelial	GRN_SORT1	D30
VECs_Epithelial	GRN_SORT1	D30
Epithelial_Myeloid	IL1A_IL1R2	D30
Myeloid_Myeloid	IL1A_IL1R2	D30
Epithelial_Glial	MIF_ACKR3	D30
Plasma_Glial	MIF_ACKR3	D30
Epithelial_IBP6+ fib	MIF_ACKR3	D30
Plasma_IBP6+ fib	MIF_ACKR3	D30
Epithelial_LECs	MIF_ACKR3	D30
Plasma_LECs	MIF_ACKR3	D30
Epithelial_VECs	MIF_ACKR3	D30
Plasma_VECs	MIF_ACKR3	D30
Glial_IBP6+ fib	PDGFA_PDGFRA	D30
Epithelial_IBP6+ fib	PDGFA_PDGFRA	D30
IBP6- fib_IBP6+ fib	PDGFA_PDGFRA	D30
Glial_IBP6- fib	PDGFA_PDGFRA	D30
Epithelial_IBP6- fib	PDGFA_PDGFRA	D30
IBP6- fib_IBP6- fib	PDGFA_PDGFRA	D30
Glial_IBP6+ fib	PDGFA_PDGFRA	D30
Epithelial_IBP6+ fib	PDGFA_PDGFRA	D30
IBP6- fib_IBP6+ fib	PDGFA_PDGFRA	D30
Myeloid_IBP6+ fib	PDGFB_PDGFRA	D30
Myeloid_IBP6- fib	PDGFB_PDGFRA	D30
Myeloid_IBP6+ fib	PDGFB_PDGFRA	D30
IBP6+ fib_IBP6- fib	PROS1_AXL	D30
IBP6+ fib_IBP6+ fib	PROS1_AXL	D30
IBP6+ fib_B	PTN_NCL	D30
IBP6+ fib_T	PTN_NCL	D30
IBP6+ fib_Glial	PTN_NCL	D30

IBP6+ fib_Epithelial	PTN_NCL	D30
IBP6+ fib_IBP6- fib	PTN_NCL	D30
IBP6+ fib_IBP6+ fib	PTN_NCL	D30
IBP6+ fib_LECs	PTN_NCL	D30
IBP6+ fib_Mast	PTN_NCL	D30
IBP6+ fib_Myeloid	PTN_NCL	D30
IBP6+ fib_Plasma	PTN_NCL	D30
IBP6+ fib_NKT	PTN_NCL	D30
IBP6+ fib_VECs	PTN_NCL	D30
IBP6+ fib_Epithelial	PTN_SDC1	D30
IBP6+ fib_IBP6- fib	PTN_SDC2	D30
IBP6+ fib_IBP6+ fib	PTN_SDC2	D30
IBP6+ fib_Glial	PTN_SDC3	D30
Glial_Myeloid	SPP1_ITGA4_ITGB1	D30
Glial_Plasma	SPP1_ITGA4_ITGB1	D30
Glial_T	SPP1_CD44	D30
Glial_Glial	SPP1_CD44	D30
Glial_Epithelial	SPP1_CD44	D30
Glial_Myeloid	SPP1_CD44	D30
Glial_Plasma	SPP1_CD44	D30
Glial_NKT	SPP1_CD44	D30
IBP6+ fib_LECs	VEGFD_VEGFR2	D30
IBP6+ fib_VECs	VEGFD_VEGFR2	D30
IBP6+ fib_LECs	VEGFD_VEGFR2R3	D30
IBP6+ fib_LECs	VEGFD_VEGFR3	D30
Epithelial_LECs	ADM_CALCRL	D42
IBP6- fib_LECs	ADM_CALCRL	D42
IBP6+ fib_LECs	ADM_CALCRL	D42
Epithelial_VECs	ADM_CALCRL	D42
IBP6- fib_VECs	ADM_CALCRL	D42
IBP6+ fib_VECs	ADM_CALCRL	D42
IBP6- fib_IBP6+ fib	AGT_AGTR1B	D42
IBP6+ fib_IBP6+ fib	AGT_AGTR1B	D42
IBP6- fib_LECs	ANGPTL4_CDH5	D42
IBP6+ fib_LECs	ANGPTL4_CDH5	D42
IBP6- fib_VECs	ANGPTL4_CDH5	D42
IBP6+ fib_VECs	ANGPTL4_CDH5	D42
IBP6- fib_Epithelial	ANGPTL4_SDC1	D42
IBP6+ fib_Epithelial	ANGPTL4_SDC1	D42
IBP6- fib_IBP6- fib	ANGPTL4_SDC2	D42
IBP6+ fib_IBP6- fib	ANGPTL4_SDC2	D42
IBP6- fib_IBP6+ fib	ANGPTL4_SDC2	D42
IBP6+ fib_IBP6+ fib	ANGPTL4_SDC2	D42
IBP6+ fib_Myeloid	C3_ITGAM_ITGB2	D42

IBP6- fib_Glial	CXCL12_ACKR3	D42
IBP6+ fib_Glial	CXCL12_ACKR3	D42
IBP6- fib_IBP6- fib	CXCL12_ACKR3	D42
IBP6+ fib_IBP6- fib	CXCL12_ACKR3	D42
IBP6- fib_IBP6+ fib	CXCL12_ACKR3	D42
IBP6+ fib_IBP6+ fib	CXCL12_ACKR3	D42
IBP6- fib_LECs	CXCL12_ACKR3	D42
IBP6+ fib_LECs	CXCL12_ACKR3	D42
IBP6- fib_VECs	CXCL12_ACKR3	D42
IBP6+ fib_VECs	CXCL12_ACKR3	D42
IBP6- fib_B	CXCL12_CXCR4	D42
IBP6+ fib_B	CXCL12_CXCR4	D42
IBP6- fib_T	CXCL12_CXCR4	D42
IBP6+ fib_T	CXCL12_CXCR4	D42
IBP6- fib_Plasma	CXCL12_CXCR4	D42
IBP6+ fib_Plasma	CXCL12_CXCR4	D42
IBP6- fib_NKT	CXCL12_CXCR4	D42
IBP6+ fib_NKT	CXCL12_CXCR4	D42
Epithelial_Glial	EDN1_EDNRB	D42
VECs_Glial	EDN1_EDNRB	D42
Epithelial_IBP6- fib	EDN1_EDNRB	D42
VECs_IBP6- fib	EDN1_EDNRB	D42
Glial_IBP6- fib	FGF2_FGFR1	D42
Glial_IBP6+ fib	FGF2_FGFR1	D42
Myeloid_Epithelial	GRN_SORT1	D42
Epithelial_Glial	MIF_ACKR3	D42
Myeloid_Glial	MIF_ACKR3	D42
Plasma_Glial	MIF_ACKR3	D42
Epithelial_IBP6- fib	MIF_ACKR3	D42
Myeloid_IBP6- fib	MIF_ACKR3	D42
Plasma_IBP6- fib	MIF_ACKR3	D42
Epithelial_IBP6+ fib	MIF_ACKR3	D42
Myeloid_IBP6+ fib	MIF_ACKR3	D42
Plasma_IBP6+ fib	MIF_ACKR3	D42
Epithelial_LECs	MIF_ACKR3	D42
Myeloid_LECs	MIF_ACKR3	D42
Plasma_LECs	MIF_ACKR3	D42
Epithelial_VECs	MIF_ACKR3	D42
Myeloid_VECs	MIF_ACKR3	D42
Plasma_VECs	MIF_ACKR3	D42
Glial_IBP6- fib	PDGFA_PDGFR α	D42
Epithelial_IBP6- fib	PDGFA_PDGFR α	D42
Glial_IBP6+ fib	PDGFA_PDGFR α	D42
Epithelial_IBP6+ fib	PDGFA_PDGFR α	D42

Glial_IBP6- fib	PDGFA_PDGFRB	D42
Epithelial_IBP6- fib	PDGFA_PDGFRB	D42
Glial_IBP6- fib	PDGFD_PDGFRB	D42
IBP6+ fib_IBP6+ fib	POSTN_ITGAV_ITGB5	D42
IBP6+ fib_IBP6- fib	PROS1_AXL	D42
IBP6+ fib_IBP6+ fib	PROS1_AXL	D42
IBP6- fib_B	PTN_NCL	D42
IBP6- fib_T	PTN_NCL	D42
IBP6- fib_Glial	PTN_NCL	D42
IBP6- fib_Epithelial	PTN_NCL	D42
IBP6- fib_IBP6- fib	PTN_NCL	D42
IBP6- fib_IBP6+ fib	PTN_NCL	D42
IBP6- fib_LECs	PTN_NCL	D42
IBP6- fib_Mast	PTN_NCL	D42
IBP6- fib_Myeloid	PTN_NCL	D42
IBP6- fib_Plasma	PTN_NCL	D42
IBP6- fib_NKT	PTN_NCL	D42
IBP6- fib_VECs	PTN_NCL	D42
IBP6- fib_Epithelial	PTN_SDC1	D42
IBP6- fib_IBP6- fib	PTN_SDC2	D42
IBP6- fib_IBP6+ fib	PTN_SDC2	D42
Glial_Myeloid	SPP1_ITGA4_ITGB1	D42
Glial_NKT	SPP1_ITGA4_ITGB1	D42
Glial_IBP6+ fib	SPP1_ITGAV_ITGB1	D42
Glial_IBP6+ fib	SPP1_ITGAV_ITGB5	D42
Glial_T	SPP1_CD44	D42
Glial_Glial	SPP1_CD44	D42
Glial_Epithelial	SPP1_CD44	D42
Glial_Myeloid	SPP1_CD44	D42
Glial_Plasma	SPP1_CD44	D42
Glial_NKT	SPP1_CD44	D42
IBP6+ fib_LECs	VEGFC_VEGFR2	D42
IBP6+ fib_VECs	VEGFC_VEGFR2	D42
IBP6+ fib_LECs	VEGFC_VEGFR2R3	D42
IBP6+ fib_LECs	VEGFC_VEGFR3	D42
IBP6+ fib_LECs	VEGFD_VEGFR2	D42
IBP6+ fib_VECs	VEGFD_VEGFR2	D42
IBP6+ fib_LECs	VEGFD_VEGFR2R3	D42
IBP6+ fib_LECs	VEGFD_VEGFR3	D42
Glial_LECs	ADM_CALCRL	D150
Epithelial_LECs	ADM_CALCRL	D150
IBP6- fib_LECs	ADM_CALCRL	D150
IBP6+ fib_LECs	ADM_CALCRL	D150
LECs_LECs	ADM_CALCRL	D150

Glial_VECs	ADM_CALCRL	D150
Epithelial_VECs	ADM_CALCRL	D150
IBP6- fib_VECs	ADM_CALCRL	D150
IBP6+ fib_VECs	ADM_CALCRL	D150
LECs_VECs	ADM_CALCRL	D150
IBP6- fib_IBP6- fib	AGT_AGTR1B	D150
IBP6+ fib_IBP6- fib	AGT_AGTR1B	D150
IBP6- fib_IBP6+ fib	AGT_AGTR1B	D150
IBP6+ fib_IBP6+ fib	AGT_AGTR1B	D150
LECs_LECs	ANGPT2_TEK	D150
LECs_VECs	ANGPT2_TEK	D150
IBP6+ fib_Myeloid	ANGPTL2_TLR4	D150
IBP6- fib_LECs	ANGPTL4_CDH5	D150
IBP6+ fib_LECs	ANGPTL4_CDH5	D150
LECs_LECs	ANGPTL4_CDH5	D150
IBP6- fib_VECs	ANGPTL4_CDH5	D150
IBP6+ fib_VECs	ANGPTL4_CDH5	D150
LECs_VECs	ANGPTL4_CDH5	D150
IBP6- fib_Glial	ANGPTL4_SDC1	D150
IBP6+ fib_Glial	ANGPTL4_SDC1	D150
LECs_Glial	ANGPTL4_SDC1	D150
IBP6- fib_IBP6- fib	ANGPTL4_SDC2	D150
IBP6+ fib_IBP6- fib	ANGPTL4_SDC2	D150
LECs_IBP6- fib	ANGPTL4_SDC2	D150
IBP6- fib_IBP6+ fib	ANGPTL4_SDC2	D150
IBP6+ fib_IBP6+ fib	ANGPTL4_SDC2	D150
LECs_IBP6+ fib	ANGPTL4_SDC2	D150
Glial_Myeloid	C3_ITGAM_ITGB2	D150
IBP6- fib_Myeloid	C3_ITGAM_ITGB2	D150
IBP6+ fib_Myeloid	C3_ITGAM_ITGB2	D150
IBP6- fib_IBP6- fib	CXCL12_ACKR3	D150
IBP6- fib_IBP6+ fib	CXCL12_ACKR3	D150
IBP6- fib_LECs	CXCL12_ACKR3	D150
IBP6- fib_VECs	CXCL12_ACKR3	D150
IBP6- fib_B	CXCL12_CXCR4	D150
IBP6- fib_T	CXCL12_CXCR4	D150
IBP6- fib_Mast	CXCL12_CXCR4	D150
IBP6- fib_Myeloid	CXCL12_CXCR4	D150
IBP6- fib_Plasma	CXCL12_CXCR4	D150
IBP6- fib_NKT	CXCL12_CXCR4	D150
LECs_IBP6+ fib	GAS6_AXL	D150
Epithelial_IBP6- fib	MIF_ACKR3	D150
Epithelial_IBP6+ fib	MIF_ACKR3	D150
Epithelial_LECs	MIF_ACKR3	D150

Epithelial_VECs	MIF_ACKR3	D150
Glial_IBP6- fib	PDGFA_PDGFR A	D150
Epithelial_IBP6- fib	PDGFA_PDGFR A	D150
Glial_IBP6+ fib	PDGFA_PDGFR A	D150
Epithelial_IBP6+ fib	PDGFA_PDGFR A	D150
Glial_IBP6- fib	PDGFA_PDGFR B	D150
Epithelial_IBP6- fib	PDGFA_PDGFR B	D150
IBP6- fib_B	PTN_NCL	D150
IBP6- fib_T	PTN_NCL	D150
IBP6- fib_Glial	PTN_NCL	D150
IBP6- fib_Epithelial	PTN_NCL	D150
IBP6- fib_IBP6- fib	PTN_NCL	D150
IBP6- fib_IBP6+ fib	PTN_NCL	D150
IBP6- fib_LECs	PTN_NCL	D150
IBP6- fib_Mast	PTN_NCL	D150
IBP6- fib_Myeloid	PTN_NCL	D150
IBP6- fib_Plasma	PTN_NCL	D150
IBP6- fib_NKT	PTN_NCL	D150
IBP6- fib_VECs	PTN_NCL	D150
IBP6- fib_Glial	PTN_SDC1	D150
IBP6- fib_IBP6- fib	PTN_SDC2	D150
IBP6- fib_IBP6+ fib	PTN_SDC2	D150
IBP6- fib_Glial	TNF_TNFRSF1A	D150
IBP6- fib_IBP6- fib	TNF_TNFRSF1A	D150
IBP6- fib_VECs	TNF_TNFRSF1A	D150
IBP6- fib_B	TNF_TNFRSF1B	D150
IBP6- fib_T	TNF_TNFRSF1B	D150
IBP6- fib_IBP6+ fib	TNF_TNFRSF1B	D150
IBP6- fib_LECs	TNF_TNFRSF1B	D150
IBP6- fib_Mast	TNF_TNFRSF1B	D150
IBP6- fib_Myeloid	TNF_TNFRSF1B	D150
IBP6- fib_NKT	TNF_TNFRSF1B	D150
Glial_Plama	TNFSF13_TNFRSF17	D150
IBP6+ fib_LECs	VEGFC_VEGFR2	D150
IBP6+ fib_VECs	VEGFC_VEGFR2	D150
IBP6+ fib_LECs	VEGFC_VEGFR2R3	D150
IBP6+ fib_LECs	VEGFC_VEGFR3	D150
IBP6+ fib_LECs	VEGFD_VEGFR2	D150
IBP6+ fib_VECs	VEGFD_VEGFR2	D150
IBP6+ fib_LECs	VEGFD_VEGFR2R3	D150
IBP6+ fib_LECs	VEGFD_VEGFR3	D150
Epithelial_LECs	ADM_CALCRL	D730
IBP6- fib_LECs	ADM_CALCRL	D730
IBP6+ fib_LECs	ADM_CALCRL	D730

Epithelial_VECs	ADM_CALCRL	D730
IBP6- fib_VECs	ADM_CALCRL	D730
IBP6+ fib_VECs	ADM_CALCRL	D730
IBP6- fib_IBP6+ fib	AGT_AGTR1B	D730
IBP6+ fib_IBP6+ fib	AGT_AGTR1B	D730
LECs_IBP6- fib	ANGPTL4_CDH11	D730
LECs_LECs	ANGPTL4_CDH5	D730
LECs_VECs	ANGPTL4_CDH5	D730
LECs_Epithelial	ANGPTL4_SDC1	D730
LECs_IBP6- fib	ANGPTL4_SDC2	D730
LECs_IBP6+ fib	ANGPTL4_SDC2	D730
IBP6- fib_Myeloid	C3_ITGAM_ITGB2	D730
IBP6+ fib_Myeloid	C3_ITGAM_ITGB2	D730
IBP6- fib_IBP6+ fib	CCL19_ACKR4	D730
IBP6- fib_VECs	CCL2_ACKR1	D730
IBP6+ fib_VECs	CCL2_ACKR1	D730
LECs_IBP6+ fib	CCL21_ACKR4	D730
Glial_VECs	CCL5_ACKR1	D730
Epithelial_VECs	CCL5_ACKR1	D730
IBP6- fib_VECs	CCL5_ACKR1	D730
LECs_VECs	CCL5_ACKR1	D730
Mast_VECs	CCL5_ACKR1	D730
Myeloid_VECs	CCL5_ACKR1	D730
NKT_VECs	CCL5_ACKR1	D730
IBP6- fib_Myeloid	CSF1_CSF1R	D730
IBP6+ fib_Myeloid	CSF1_CSF1R	D730
IBP6- fib_IBP6+ fib	CXCL12_ACKR3	D730
IBP6+ fib_IBP6+ fib	CXCL12_ACKR3	D730
IBP6- fib_LECs	CXCL12_ACKR3	D730
IBP6+ fib_LECs	CXCL12_ACKR3	D730
IBP6- fib_B	CXCL12_CXCR4	D730
IBP6+ fib_B	CXCL12_CXCR4	D730
IBP6- fib_T	CXCL12_CXCR4	D730
IBP6+ fib_T	CXCL12_CXCR4	D730
IBP6- fib_Glial	CXCL12_CXCR4	D730
IBP6+ fib_Glial	CXCL12_CXCR4	D730
IBP6- fib_Mast	CXCL12_CXCR4	D730
IBP6+ fib_Mast	CXCL12_CXCR4	D730
IBP6- fib_NKT	CXCL12_CXCR4	D730
IBP6+ fib_NKT	CXCL12_CXCR4	D730
IBP6- fib_VECs	CXCL2_ACKR1	D730
LECs_VECs	CXCL2_ACKR1	D730
Myeloid_VECs	CXCL2_ACKR1	D730
Epithelial_VECs	CXCL8_ACKR1	D730

LECs_IBP6- fib	GAS6_AXL	D730
VECs_IBP6- fib	GAS6_AXL	D730
LECs_IBP6+ fib	GAS6_AXL	D730
VECs_IBP6+ fib	GAS6_AXL	D730
Epithelial_Epithelial	GRN_SORT1	D730
IBP6- fib_Epithelial	GRN_SORT1	D730
IBP6+ fib_Epithelial	GRN_SORT1	D730
LECs_Epithelial	GRN_SORT1	D730
Myeloid_Epithelial	GRN_SORT1	D730
VECs_Epithelial	GRN_SORT1	D730
Glial_Epithelial	GZMA_F2RL1	D730
NKT_Epithelial	GZMA_F2RL1	D730
Glial_IBP6+ fib	GZMA_F2RL2	D730
NKT_IBP6+ fib	GZMA_F2RL2	D730
Epithelial_Myeloid	HC_C5AR1	D730
Epithelial_IBP6+ fib	MIF_ACKR3	D730
Myeloid_IBP6+ fib	MIF_ACKR3	D730
Epithelial_LECs	MIF_ACKR3	D730
Myeloid_LECs	MIF_ACKR3	D730
Epithelial_IBP6- fib	PDGFA_PDGFR	D730
Epithelial_IBP6+ fib	PDGFA_PDGFR	D730
Epithelial_IBP6- fib	PDGFA_PDGFRB	D730
Epithelial_IBP6+ fib	PDGFA_PDGFRB	D730
IBP6- fib_IBP6+ fib	POSTN_ITGAV_ITGB5	D730
IBP6+ fib_IBP6+ fib	POSTN_ITGAV_ITGB5	D730
IBP6- fib_B	PTN_NCL	D730
IBP6- fib_T	PTN_NCL	D730
IBP6- fib_Epithelial	PTN_NCL	D730
IBP6- fib_IBP6- fib	PTN_NCL	D730
IBP6- fib_IBP6+ fib	PTN_NCL	D730
IBP6- fib_LECs	PTN_NCL	D730
IBP6- fib_Mast	PTN_NCL	D730
IBP6- fib_Myeloid	PTN_NCL	D730
IBP6- fib_Plasma	PTN_NCL	D730
IBP6- fib_NKT	PTN_NCL	D730
IBP6- fib_VECs	PTN_NCL	D730
IBP6- fib_Epithelial	PTN_SDC1	D730
IBP6- fib_IBP6- fib	PTN_SDC2	D730
IBP6- fib_IBP6+ fib	PTN_SDC2	D730
IBP6+ fib_LECs	VEGFC_VEGFR2	D730
VECs_LECs	VEGFC_VEGFR2	D730
IBP6+ fib_VECs	VEGFC_VEGFR2	D730
VECs_VECs	VEGFC_VEGFR2	D730
IBP6+ fib_LECs	VEGFC_VEGFR2R3	D730

VECs_LECs	VEGFC_VEGFR2R3	D730
IBP6+ fib_LECs	VEGFC_VEGFR3	D730
VECs_LECs	VEGFC_VEGFR3	D730
IBP6+ fib_LECs	VEGFD_VEGFR2	D730
IBP6+ fib_VECs	VEGFD_VEGFR2	D730
IBP6+ fib_LECs	VEGFD_VEGFR2R3	D730
IBP6+ fib_LECs	VEGFD_VEGFR3	D730