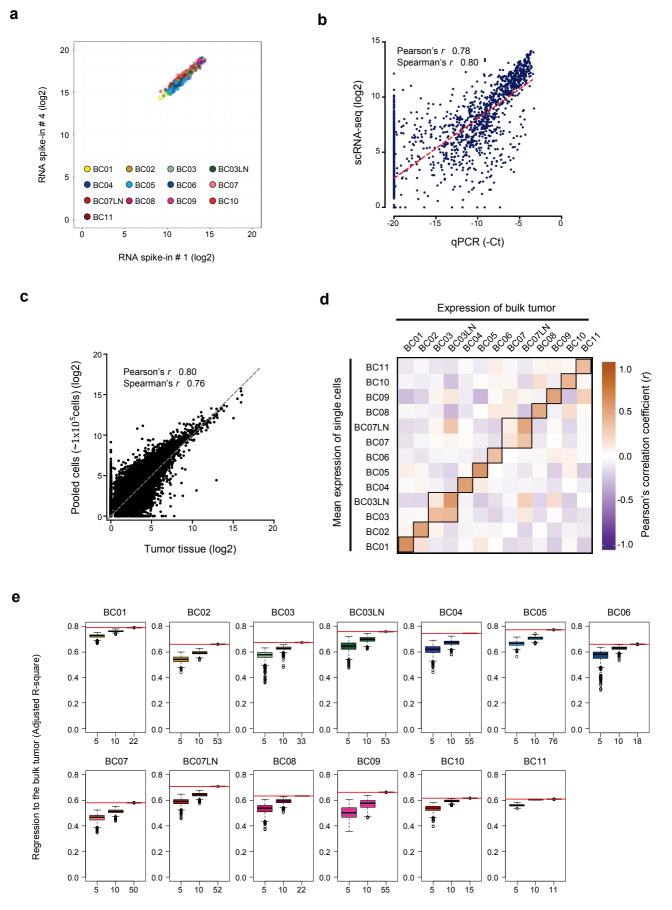
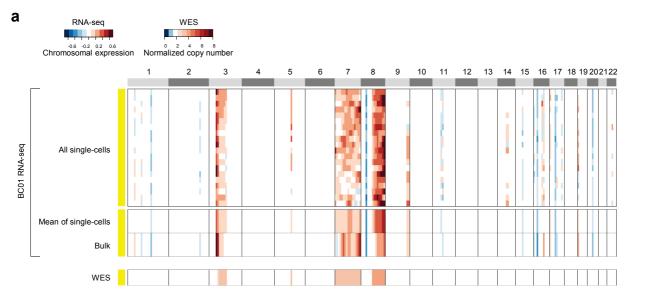


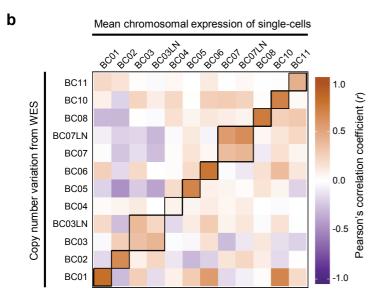
Supplementary Figure 1. Genomic profiles of breast cancer specimens. Copy number variations (CNV) and single nucleotide variations (SNV) were detected from whole exome sequencing data for the bulk tumors. SNV and CNV are marked for significantly mutated genes in breast cancer for each tumor specimen.



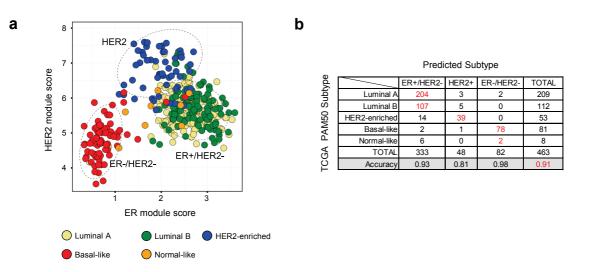
Cell number of random sampling (permutation = 1000)

Supplementary Figure 2. Reliability and representativeness of single-cell RNA sequencing data. (a) Consistent detection of normalized read counts for two array control RNA spike-ins in all single-cell samples. (b) Single-cell RNA-seq data showing a significant correlation with the matched qPCR results (Pearson's r 0.78). The linear regression result is drawn as a dashed line. (c) Significant correlation in the RNA-seq data between the tumor tissues and pooled tumor tissue isolates (Pearson's r 0.8). (d) Centered correlations between the averages of tumor single cells and their matching bulk samples (bulk tissue for BC07 or pooled tissue isolates for all others) showing significant but partial representation of the bulk tumor by single cells (Pearson's r 0.16-0.63 with average 0.47, p < 0.001). (e) Multiple regression analysis was performed using expression levels of each single cell as the explanatory variable to predict the expression level of bulk tumors. Adjusted R-squares of multiple regression analysis were calculated by random sampling of single cells with 1,000 iterations. Horizontal red lines represent maximum adjusted R-square values.



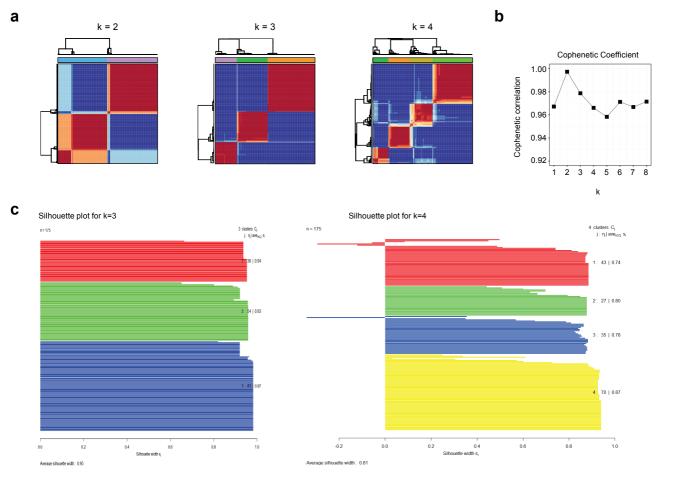


Supplementary Figure 3. The correlation between inferred CNVs from single-cell RNA-seq and CNVs estimated from WES. (a) Heatmaps of estimated CNVs from WES and inferred CNVs from RNA-seq in a 10-Mb genomic window size. In the representative BC01 tumor, the inferred CNVs from RNA-seq has a high correlation with the CNVs from WES (Pearson's r 0.82). (b) Correlations between averaged inferred CNVs from single-cells and CNVs estimated from WES. Most tumors show a higher correlation with the matched single cell averages than with the unmatched ones (Pearson's r 0.08-0.82 with average 0.52).

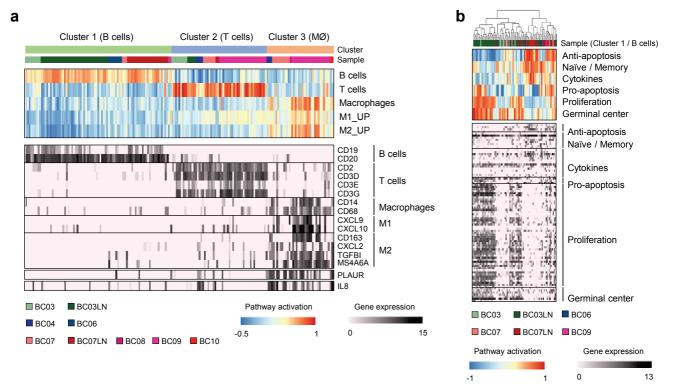


Supplementary Figure 4. Subtyping validation using TCGA data. (a) Subtyping of TCGA breast cancer samples with the ER and HER2 module scores. **(b)** Subtyping using ER and HER2 module scores predicted the breast cancer subtype for TCGA RNA sequencing data with 91% accuracy.

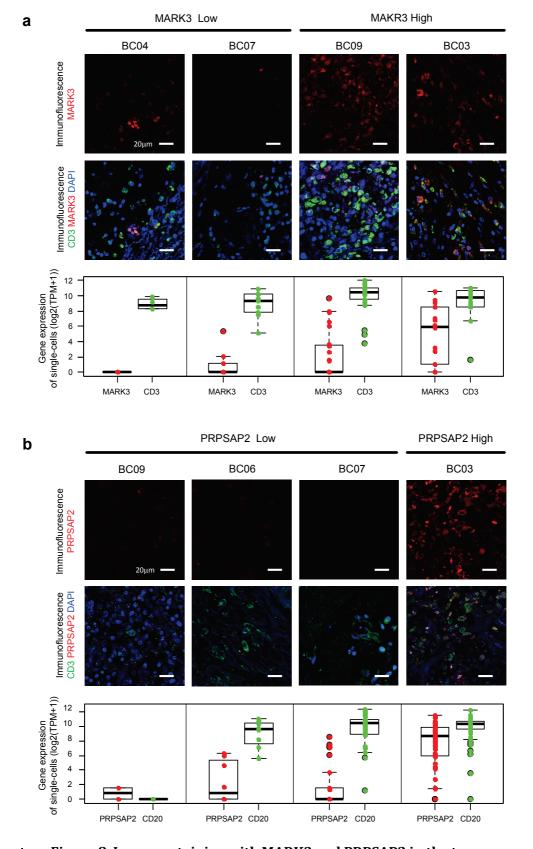
Supplementary Figure 5. Heterogeneity in cancer-related pathway activation. (a) GSVA enrichment scores in core cancer-related pathways and recurrence scores from MammaPrint³ (R software package genefu) are plotted for individual tumor cells in four breast cancer subtypes from 10 patient tumors. (b) Gene expression signatures in (a) were compared between the four subtypes. Tumor cells from the TNBC subtype showed higher stemness, EMT, and recurrence scores compared to the Luminal subtypes. Each box shows the median and IQR (interquartile range, 25^{th} to 75^{th} percentiles), whiskers indicate the highest and lowest value within 1.5 times the IQR, and outliers are marked as dots. *P* value, Student's *t*-test (***, p < 0.001; **, p < 0.01; *, p < 0.05).



Supplementary Figure 6. NMF clustering for classification of non-tumor cells. (a) NMF clustering analysis with immune gene sets for k = 2, k = 3, and k = 4. **(b)** The curve of cophenetic correlation coefficients. A peak was detected at k = 3, suggesting an optimal cluster of 3. **(c)** The silhouette width of each single cell for the k = 3 and k = 4 clusters. The k = 3 cluster had highest average silhouette width relative to the other clusters.



Supplementary Figure 7. Immune signatures in the tumor microenvironment. (a) GSVA analysis using immune genesets (upper panel) shows characteristics of 3 immune clusters. The third cluster, expected as tumor associated macrophages expressed high levels of M2-type genes. **(b)** Hierarchical clustering using GSVA enrichment scores (upper panel) for B lymphocytes³⁸ classified cells into two groups. One group, mostly from TNBC tumors (BC07, BC07LN, and BC09), showed naïve/memory B cell gene expression signatures. Another group, mostly derived from the BC03 (luminal B tumor) lymph node, showed proliferation signatures associated with germinal center B cells. Gene expression profiles for the used gene sets are presented in the lower panel.



Supplementary Figure 8. Immunostaining with MARK3 and PRPSAP2 in the tumor microenvironment. (a) MARK3 or **(b)** PRPSAP2 were co-stained with the T cell marker CD3 or B cell marker CD20 respectively. Single cell level gene expression is presented at the bottom for comparison. Each box shows the mean and IQR (interquartile range, 25th to 75th percentiles), whiskers indicate the highest and lowest value within 1.5 times the IQR, and outliers are marked as dots. Scale bar, 20µm

Supplementary Table 1. Clinical and histological profiles of the breast cancer specimens

Patient index	BC01 ER+	BC02 ER+	BC03 ER+/HER+	BC04 HER2+	BC05 HER2+	BC06 HER2+	BC07 TNBC	BC08 TNBC	BC09 TNBC	BC10 TNBC	BC11 TNBC
Age	66	72	72	67	46	67	71	67	53	82	47
Pathologic stage	pT1N0 (IA)	pT3N1 (IIIA)	pT2N1 (IIB)	pT2N0 (IIA)	ypT1N1mi (IB)	T2N1 (IIB)	pT1N3 (IIIC)	pT2N0 (IIA)	pT2N0 (IIA)	pT2N2 (IIIA)	T2N0 (IIA)
Molecular subtype	Luminal A	Luminal A	Luminal B	HER2-enriched	HER2-enriched	HER2-enriched	Basal-like	Basal-like	Basal-like	Basal-like	Basal-like
Immunohistochemistry											
ER	positive	positive	positive	negative	negative	negative (weak positive)	negative	negative	negative	negative	negative
PR	negative	positive	positive	negative	negative	negative (weak positive)	negative	negative	negative	negative	negative
HER2	2+/3	1+/3	3+/3	3+/3	3+/3	3+/3	1+/3	2+/3	1+/3	1+/3	1+/3
HER2 FISH	negative	-	-	-	-	-	-	negative	-	-	-
No. of single cells											
*Tumor	26 (22)	56 (53)	37 (33)	59 (55)	77 (76)	25 (18)	51 (50)	23 (22)	60 (55)	16 (15)	11 (11)
Lymph node	-	-	55 (53)	-	-	-	53 (52)	-	-	-	-
Lymph node metastasis	0/18	1/13	2/18	0/11	1/4	1/18	16/35	0/3	0/3	9/21	0/6

ER, estrogen receptor; IDC, invasive ductal carcinoma; HER2, human epidermal growth factor receptor 2; PR, progesterone receptor; FISH, fluorescence in situ hybridization

^{*} the number of total cells (the number of analysed cells)

Supplementary Table 2. Tumor-specific gene lists identified at a single cell resolution

a. ER+ tumor marker gene

Gene symbol	Fold change	P-value	AUC
Gene symbol	Fold change	(LRT test)	(ROC test)
CPB1	11.76	0.0.E+00	0.81
RP11-53O19.1	8.51	0.0.E+00	0.82
TFF1	7.82	0.0.E+00	0.73
PVALB	7.79	0.0.E+00	0.81
ANKRD30B	6.86	0.0.E+00	0.78
LINC00173	6.83	0.0.E+00 0.0.E+00	0.73
DSCAM-AS1	6.70	4.9.E-14	0.70
IGHG1 SERPINA5	6.26 6.23	4.9.E-14 0.0.E+00	0.76 0.75
ESR1	5.60	0.0.E+00	0.75
LRP2	5.30	0.0.E+00	0.80
IGLC3	5.24	5.9.E-13	0.72
CA12	5.23	0.0.E+00	0.96
RP11-64B16.2	5.23	0.0.E+00	0.72
SLC7A2	5.01	0.0.E+00	0.79
AFF3	4.83	0.0.E+00	0.85
IGFBP4	4.13	0.0.E+00	0.76
GSTM3	3.97	0.0.E+00	0.83
ANKRD30A	3.85	0.0.E+00	0.73
GSTT1	3.82	3.3.E-16	0.71
GSTM1	3.78	3.6.E-14	0.71
AC026806.2	3.66	0.0.E+00	0.74
C19orf33	3.55	0.0.E+00	0.91
STC2	3.53	1.1.E-14	0.75
HSPB8	3.45	0.0.E+00	0.92
RPL29P11	3.42	0.0.E+00	0.74
FBP1	3.36	0.0.E+00	0.78
AGR3	3.25	0.0.E+00	0.85
TCEAL1	3.23	0.0.E+00	0.83
CYP4B1	3.18	4.9.E-12	0.71
SYT1	3.13	2.1.E-12	0.70
COX6C	3.04	0.0.E+00	0.95
MT1E	3.01	0.0.E+00	0.88
SYTL2	3.00	3.6.E-15	0.76
THSD4	2.94	2.1.E-15	0.72
IFI6	2.86	3.5.E-12	0.72
KIAA1467	2.81	1.1.E-16	0.75
SLC39A6	2.76	0.0.E+00	0.86
ABCD3	2.74	1.3.E-13	0.74
SERPINA3	2.71	0.0.E+00	0.82
DEGS2	2.70	1.1.E-16	0.78
ERLIN2	2.69	1.5.E-10	0.73
HEBP1	2.69	1.8.E-12	0.71
BCL2	2.50	5.1.E-15	0.74
TCEAL3	2.47	5.8.E-15	0.78
PPT1	2.45	0.0.E+00	0.85
SLC7A8	2.43	0.0.E+00	0.82
RP11-96D1.10	2.41	3.9.E-12	0.74
HIST1H4H	2.41	6.7.E-12	0.74
PI15	2.41	0.0.E+00	0.77
PPAPDC1B	2.37	1.7.E-13	0.72
RARRES3	2.37	1.8.E-09	0.71
GALNT6	2.27	1.6.E-13	0.79
IL6ST	2.23	0.0.E+00	0.82
MYC BST2	2.21	5.3.E-12	0.76
	2.20	1.1.E-16	0.76
RP11-658F2.8	2.19	9.7.E-09	0.71
MRPS30	2.17	1.5.E-13	0.76
MAPT AMFR	2.17 2.16	1.1.E-11 4.8.E-14	0.70 0.82
TCEAL4	2.16	4.6.E-14 0.0.E+00	0.82
MED13L	2.14	2.1.E-15	0.80
ISG15	2.12	1.2.E-13	0.79
NDUFC2	2.07	0.0.E+00	0.79
TIMP3	2.03	2.2.E-11	0.80
RP13-39P12.3	2.02	2.2.E-11 2.9.E-12	0.73
PARD6B	2.02	0.0.E+00	0.74
	2.01	0.0.2	0.01

b. HER2+ tumor marker genes

b. HER2+ tum	ioi illaikei	genes	
Gene symbol	Fold change	P-value	AUC
,			(ROC test)
MUC19	8.80	0.0.E+00	0.71
RPS12P26	8.18	0.0.E+00	0.78
CEACAM5	7.67	0.0.E+00	0.79
UBD	7.58	0.0.E+00	0.83
H19	6.97	0.0.E+00	0.80
NDST4	6.86	0.0.E+00	0.76
KRT20* RP11-483P21.2	6.70 6.64	0.0.E+00 0.0.E+00	0.71 0.75
BPIFB2		0.0.E+00 0.0.E+00	0.75
EREG	6.62	0.0.E+00 0.0.E+00	
RP11-697E2.7	5.95 4.78	0.0.E+00 0.0.E+00	0.76 0.78
IL8	4.76	0.0.E+00	0.78
ZNF710	4.07	0.0.E+00	0.79
MTND2P28	4.39	0.0.E+00	0.74
RP11-617F23.1	4.28	0.0.E+00	0.74
TFPI	4.26 4.26	0.0.E+00 0.0.E+00	0.79
KRT86		0.0.E+00 0.0.E+00	
NR1D1*	4.20 3.96	0.0.E+00 0.0.E+00	0.72 0.77
NGRN	3.80	0.0.E+00	0.77
CXCL1	3.76	0.0.E+00	0.82
GRB7*	3.70	0.0.E+00	0.76
IGF2BP2	3.01	0.0.E+00 1.8.E-13	0.95
SEMA4B	3.16	0.0.E+00	0.72
CIB1	3.08	0.0.E+00	0.73
MIEN1*	3.06	0.0.E+00	0.74
CDC6*	2.95	0.0.E+00	0.93
SIX4	2.93	0.0.E+00	0.81
PTPN13	2.93	2.2.E-16	0.76
MSL1*	2.90	0.0.E+00	0.76
CEACAM6	2.86	5.0.E-13	0.77
CAPS	2.60	6.2.E-14	0.74
PPP1R1B*	2.56	8.5.E-14	0.74
AREG	2.54	0.0.E+00	0.79
ERBB2*	2.48	0.0.E+00	0.95
PEG10	2.47	0.0.E+00	0.80
MED1*	2.43	7.8.E-16	0.77
AP3S2	2.41	1.5.E-10	0.74
IDH2	2.32	3.5.E-14	0.74
RP11-889L3.1	2.32	0.0.E+00	0.83
RPL19*	2.30	0.0.E+00	0.79
CDK12*	2.28	0.0.E+00	0.83
RP11-690G19.3*	2.26	7.4.E-14	0.74
NLK	2.18	0.0.E+00	0.77
CASC3*	2.13	0.0.E+00	0.87
STARD3*	2.12	6.3.E-15	0.70
MED31*	2.09	1.7.E-09	0.76
TXNDC17*	2.08	0.0.E+00	0.78
KPNA2*	2.01	1.4.E-11	0.78

* Genes located in HER2 amplification region (17q12-q21)

c. TNBC tumor marker genes

FABPT			P-value	AUC
FABP7 TSPAN8 8.13 0.0.E+00 0.78 CYP421 7.44 0.0.E+00 0.78 CYP421 7.44 0.0.E+00 0.78 0.0.E+00 0.78 CYP421 7.44 0.0.E+00 0.74 HOXA10 7.28 0.0.E+00 0.70 0.83 CLDN1 7.11 0.0.E+00 0.71 TMSB15A 6.78 0.0.E+00 0.70 C10orf10 5.67 0.0.E+00 0.75 HOXA9 5.63 0.0.E+00 0.71 ATP13A4 5.57 0.0.E+00 0.72 GLYATL2 5.12 2.1.E-15 0.74 RP11-48020.4 5.09 0.0.E+00 0.70 MUCL1 4.75 0.0.E+00 0.70 SHOX2 4.38 0.0.E+00 0.71 SHOX2 4.38 0.0.E+00 0.71 SHOX2 283851.1 4.29 3.3.E-16 0.72 CD82 4.14 1.1.E-16 0.78 CGL6A1 3.89 2.2.E-16 0.70 KRT23 3.87 0.0.E+00 0.71 PRICKLE1 3.67 3.3.E-16 0.71 GCNT2 3.65 1.1.E-15 0.74 KHDRBS3 3.57 3.3.E-14 0.71 SIPA1L2 3.55 4.4.E-14 0.75 LMO4 3.53 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.77 ELF5 3.40 C10rf116 3.19 3.7.E-10 0.71 ADD3 3.14 2.2.E-16 0.76 SPNMB 2.93 2.0.E-13 0.75 SPNMB 2.93 2.0.E-13 0.75 SPNMB 2.93 2.0.E-13 0.75 SPNMB 2.93 2.0.E-13 0.75 SPR12 SRP1-35NA.6 2.71 1.3.E-10 0.71 CXADR CXADR SSFA2 2.51 7.1.E-13 0.75 SFRP1 2.74 1.4.E-09 0.71 ADCS SFRP1 2.74 1.4.E-09 0.71 RPIL-15-10 0.77 RPIL-15-10 0.70 RALL 2.75 0.0.E+00 0.76 CTD-2314B22.3 0.75 SRP1 2.76 CNT2 SRP11 2.77 CNRB SRP1 2.74 1.4.E-19 0.77 RPIL-15-10 0.77 RPIL-25-10 0.77 RPIL-25-10 0.77 RPIL-25-10 0.77 RPIL-35-10 0.77 RPIL-36-10 0	Gene symbol	Fold change		
CYP4Z1 7.44 0.0.E+00 0.74 HOXA10 7.28 0.0.E+00 0.83 CLDN1 7.11 0.E+00 0.71 TMSB15A 6.78 0.0.E+00 0.70 C10orf10 5.67 0.0.E+00 0.70 TRPV6 5.65 0.0.E+00 0.75 HOXA9 5.63 0.0.E+00 0.71 ATP13A4 5.57 0.0.E+00 0.72 GLYATL2 5.12 21.E-15 0.74 RP11-48020.4 5.09 0.0.E+00 0.72 ID4 4.75 0.0.E+00 0.72 ID4 4.76 0.0.E+00 0.70 MUCL1 4.75 0.0.E+00 0.70 ID4 4.74 0.E+00 0.72 SHOX2 4.38 0.0.E+00 0.71 SHOX2 4.38 0.0.E+00 0.71 Z83851.1 4.29 3.3.E-16 0.72 CD82 4.14 1.1.E-16 0.78 COL6A1 3.89 2.2.E-16 0.70 KRT23 3.87 0.0.E+00 0.85 GCHFR 3.79 1.4.E-12 0.71 PRICKLE1 3.67 3.3.E-16 0.71 GCNT2 3.65 1.1.E-15 0.74 KHDRBS3 3.57 3.3.E-14 0.71 SIPA1L2 3.55 4.4.E-14 0.75 LMO4 3.53 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.77 ELF5 3.40 1.9.E-13 0.74 C10f116 3.19 3.7.E-10 0.71 ADD3 3.14 2.2.E-16 0.76 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.71 MALL 1.75 0.0.E+00 0.74 SCABAHA 3.11 3.7.E-14 0.71 LTF 1.76 0.76 CDNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.71 MALL 2.75 0.0.E+00 0.74 SPICAL 1 0.71 ADD3 3.14 2.2.E-16 0.76 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 6.3.E-12 0.72 RP1-257A7.5 2.72 1.8.E-12 0.71 PRDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 SCABAH 2.55 1.1.E-15 0.70 RP1-257A7.5 2.72 1.8.E-12 0.71 RP1-1-353N4.6 2.71 1.3.E-10 0.71 ADM 2.46 3.6.E-13 0.75 ADM 2.46 3.6.E-13 0.77 ADM 2.46 3.6.E-13	FABP7	9.57		
CYP4Z1 7.44 0.0.E+00 0.74 HOXA10 7.28 0.0.E+00 0.83 CLDN1 7.11 0.E+00 0.71 TMSB15A 6.78 0.0.E+00 0.70 C10orf10 5.67 0.0.E+00 0.70 TRPV6 5.65 0.0.E+00 0.75 HOXA9 5.63 0.0.E+00 0.71 ATP13A4 5.57 0.0.E+00 0.72 GLYATL2 5.12 21.E-15 0.74 RP11-48020.4 5.09 0.0.E+00 0.72 ID4 4.75 0.0.E+00 0.72 ID4 4.76 0.0.E+00 0.70 MUCL1 4.75 0.0.E+00 0.70 ID4 4.74 0.E+00 0.72 SHOX2 4.38 0.0.E+00 0.71 SHOX2 4.38 0.0.E+00 0.71 Z83851.1 4.29 3.3.E-16 0.72 CD82 4.14 1.1.E-16 0.78 COL6A1 3.89 2.2.E-16 0.70 KRT23 3.87 0.0.E+00 0.85 GCHFR 3.79 1.4.E-12 0.71 PRICKLE1 3.67 3.3.E-16 0.71 GCNT2 3.65 1.1.E-15 0.74 KHDRBS3 3.57 3.3.E-14 0.71 SIPA1L2 3.55 4.4.E-14 0.75 LMO4 3.53 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.77 ELF5 3.40 1.9.E-13 0.74 C10f116 3.19 3.7.E-10 0.71 ADD3 3.14 2.2.E-16 0.76 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.71 MALL 1.75 0.0.E+00 0.74 SCABAHA 3.11 3.7.E-14 0.71 LTF 1.76 0.76 CDNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.71 MALL 2.75 0.0.E+00 0.74 SPICAL 1 0.71 ADD3 3.14 2.2.E-16 0.76 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 6.3.E-12 0.72 RP1-257A7.5 2.72 1.8.E-12 0.71 PRDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 SCABAH 2.55 1.1.E-15 0.70 RP1-257A7.5 2.72 1.8.E-12 0.71 RP1-1-353N4.6 2.71 1.3.E-10 0.71 ADM 2.46 3.6.E-13 0.75 ADM 2.46 3.6.E-13 0.77 ADM 2.46 3.6.E-13	TSPAN8	8.13	0.0.E+00	0.78
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CD82	SHOX2	4.38	0.0.E+00	0.71
COL6A1 3.89 2.2.E-16 0.70 KRT23 3.87 0.0.E+00 0.85 GCHFR 3.79 1.4.E-12 0.71 PRICKLE1 3.67 3.3.E-16 0.71 GCNT2 3.65 1.1.E-15 0.74 KHDRBS3 3.57 3.3.E-14 0.71 SIPA1L2 3.55 4.4.E-14 0.75 LMO4 3.53 0.0.E+00 0.80 TFAP2B 3.49 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.77 ELF5 3.40 1.9.E-13 0.74 C1orf116 3.19 3.7.E-10 0.71 ADD3 3.14 2.2.E-16 0.76 EFNA3 3.12 5.9.E-15 0.71 EFCAB4A 3.11 3.7.E-14 0.74 LTF 3.07 3.6.E-14 0.73 LRRC31 3.02 2.2.E-14 0.71 ARL4C 2.95 1.2.E-13 0.75 GPNMB 2.93 2.0.E-13 0.75 GPNMB 2.93 2.0.E-13 0.75 SDR16C5 2.81 6.3.E-12 0.72 RHOV 2.80 1.0.E-10 0.71 MALL 2.75 0.0.E+00 0.74 PXDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 AZML1 2.74 1.4.E-09 0.71 AZML1 2.74 1.4.E-09 0.71 AZML1 2.74 1.4.E-09 0.71 AZML1 2.74 1.3.E-10 0.70 GALNT3 2.65 8.6.E-09 0.71 CXADR 2.55 1.1.E-16 0.70 SFRP2 2.51 7.1.E-13 0.75 SFA2 2.51 7.1.E-13 0.75 SFRP1 2.24 1.7.E-14 0.71 ADCK3 2.37 5.7.E-10 0.70 RPNP 2.55 7.5.E-10 0.70 RPNP 2.51 1.2.E-13 0.75 SFRP1 2.24 1.7.E-14 0.71 RPNP 2.21 1.2.E-13 0.78 SIVA1 2.09 2.7.E-12 0.74 AL589743.1 2.10 2.6.E-13 0.77	Z83851.1	4.29	3.3.E-16	0.72
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GCHFR PRICKLE1 3.67 3.3.E-16 0.71 PRICKLE1 3.67 3.3.E-16 0.71 CONT2 3.65 1.1.E-15 0.74 KHDRBS3 3.57 S.IPA1L2 3.55 4.4.E-14 0.75 LMO4 3.53 0.0.E+00 0.80 TFAP2B 3.49 0.0.E+00 0.74 SLC43A3 3.44 1.0.E-11 0.71 FURIN 3.40 0.0.E+00 0.77 ELF5 3.40 1.9.E-13 0.74 C1orf116 3.19 3.T.E-10 0.71 ADD3 3.14 2.2.E-16 0.76 EFNA3 3.12 5.9.E-15 0.71 EFCAB4A 3.11 3.7.E-14 0.73 LRRC31 3.02 2.2.E-14 0.71 ARL4C 2.95 1.2.E-13 0.75 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 63.E-12 0.72 RHOV 2.80 1.0.E-10 0.71 MALL 2.75 0.0.E+00 0.74 YAP1 2.74 1.4.E-09 0.71 AZML1 2.75 0.0.E+00 0.74 YAP1 2.74 1.4.E-09 0.71 RP1-257A7.5 2.72 1.8.E-12 0.71 RP11-353N4.6 2.71 1.3.E-10 0.71 RP11-353N4.6 2.71 1.3.E-10 0.71 CXADR 2.55 1.1.E-16 0.76 CTD-2314B22.3 C65 8.6.E-09 0.71 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 ADM 2.46 3.6.E-13 0.75 SSFA2 2.51 ADM 3.6.E-14 0.71 RPNP 2.21 2.24 1.7.E-14 0.71 RPNP 2.21 1.2.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 ALE89743.1 2.10 2.6.E-13 0.77 ALE89743.1 2.10 2.6.E-13 0.77 ALE89743.1 2.10 2.6.E-13 0.77 ALES9743.1 2.10 2.6.E-13 0.77 ALES9143.1 2.10 2.6.E-13 0.71 ALES9143.1 2.10 2.6.E-13 0.71 ALES9143.1 2.10 2.6.E-13 0.71	COL6A1	3.89	2.2.E-16	0.70
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ARL4C 2.95 1.2.E-13 0.75 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 6.3.E-12 0.72 RHOV 2.80 1.0.E-10 0.71 PXDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 YAP1 2.74 1.4.E-09 0.71 A2ML1 2.74 1.0.E-15 0.70 RP1-257A7.5 2.72 1.8.E-12 0.71 RP11-353N4.6 2.71 1.3.E-10 0.71 ZBTB18 2.66 0.0.E+00 0.76 CTD-2314B22.3 2.65 2.1.E-10 0.74 GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SFRP1 2.39 1.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SFRP1 2.39 1.0.E+00 0.85 ADCK3 2.37 5.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RBMS1 2.14 4.2.E-09 0.72 RBMS1 2.14 4.2.E-09 0.72 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	LTF	3.07	3.6.E-14	0.73
ARL4C 2.95 1.2.E-13 0.75 GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 6.3.E-12 0.72 RHOV 2.80 1.0.E-10 0.71 PXDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 YAP1 2.74 1.4.E-09 0.71 A2ML1 2.74 1.0.E-15 0.70 RP1-257A7.5 2.72 1.8.E-12 0.71 RP11-353N4.6 2.71 1.3.E-10 0.71 ZBTB18 2.66 0.0.E+00 0.76 CTD-2314B22.3 2.65 2.1.E-10 0.74 GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SCASA37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-610G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RBMS1 2.14 4.2.E-09 0.72 RBMS1 2.14 4.2.E-09 0.72 RBMS1 2.14 4.2.E-09 0.72 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	LRRC31	3.02	2.2.E-14	0.71
GPNMB 2.93 2.0.E-13 0.75 VIM 2.82 3.7.E-12 0.76 SDR16C5 2.81 6.3.E-12 0.72 RHOV 2.80 1.0.E-10 0.71 PXDC1 2.77 1.7.E-10 0.70 MALL 2.75 0.0.E+00 0.74 YAP1 2.74 1.0.E-15 0.70 RP1-257A7.5 2.72 1.8.E-12 0.71 RP11-353N4.6 2.71 1.3.E-10 0.74 ZBTB18 2.66 0.0.E+00 0.76 CTD-2314B22.3 2.65 2.1.E-10 0.74 GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 <tr< td=""><td>ARL4C</td><td>2.95</td><td>1.2.E-13</td><td></td></tr<>	ARL4C	2.95	1.2.E-13	
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ZBTB18 2.66 0.0.E+00 0.76 CTD-2314B22.3 2.65 2.1.E-10 0.74 GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 1.8 6.E-15 0.74 RBMS1 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
CTD-2314B22.3 2.65 2.1.E-10 0.74 GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.6.E-15 0.74 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 AL589743.1 2.09 2.7.E-12 0.74				
GALNT3 2.65 8.6.E-09 0.71 BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
BCL11A 2.57 6.1.E-13 0.70 CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.74 SIVA1 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81 <td></td> <td></td> <td></td> <td></td>				
CXADR 2.55 1.1.E-16 0.77 SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.6.E-15 0.74 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.74 SIVA1 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	GALNT3		8.6.E-09	
SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	BCL11A	2.57	6.1.E-13	0.70
SSFA2 2.51 7.1.E-13 0.75 ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	CXADR	2.55	1.1.E-16	0.77
ADM 2.46 3.6.E-13 0.73 GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 18.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	SSFA2		7.1.E-13	
GUCY1A3 2.43 7.3.E-10 0.72 GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	ADM	2.46		
GSTP1 2.39 0.0.E+00 0.85 ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
ADCK3 2.37 5.7.E-10 0.70 SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
SLC25A37 2.32 0.0.E+00 0.82 SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
SFRP1 2.24 1.7.E-14 0.71 PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
PRNP 2.21 1.2.E-13 0.78 DEGS1 2.18 7.8.E-13 0.76 RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
DEGS1 2.18 7.8.E-13 0.76 RP11.110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11.640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81	-			
RP11-110G21.2 2.14 4.6.E-15 0.74 RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
RBMS1 2.14 4.2.E-09 0.72 RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
RP11-640M9.1 2.12 1.8.E-12 0.77 AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
AL589743.1 2.10 2.6.E-13 0.77 ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
ATF3 2.09 2.7.E-12 0.74 SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				
SIVA1 2.09 4.3.E-11 0.71 TACSTD2 2.04 1.1.E-16 0.81				0.77
TACSTD2 2.04 1.1.E-16 0.81	ATF3	2.09	2.7.E-12	0.74
	SIVA1	2.09	4.3.E-11	0.71
	TACSTD2	2.04	1.1.E-16	0.81
	HEBP2	2.03	0.0.E+00	0.86

Supplementary Table 3. Immune gene sets

Cons set name	P. collo	Taolla	T holper colle	CD9 T collo	Cutotovio collo	NK collo	Dondritio collo	Eccinophila	Macrophagos	Most collo	Noutrophila
Gene set name Genes	B cells MS4A1	T cells PRKCQ	T helper cells ICOS	CD8 T cells CD8B	Cytotoxic cells KLRD1	NK cells LOC643313	CD209	IL5RA	Macrophages MARCO	Mast cells PRG2	Neutrophils CSF3R
Genes	TCL1A	CD3D	LRBA	CD8A	KLRF1	GAGE2	CCL17	KCNH2	CXCL5	CTSG	CYP4F3
	HLA-DOB	CD3G	ITM2A	PF4	GNLY	ZNF747	HSD11B1	TKTL1	SCG5	TPSAB1	VNN3
	PNOC	CD28	FAM111A	PRR5	CTSW	XCL1	CCL13	EMR1	SULT1C2	SLC18A2	FPRL1
	KIAA0125	LCK	PHF10	SF1	KLRB1	XCL2	CCL22	CCR3	MSR1	MS4A2	KCNJ15
	CD19	TRAT1	NUP107	LIME1	KLRK1	AF107846	PPFIBP2	ACACB	CTSK	CPA3	MME
	CR2	BCL11B	SEC24C	DNAJB1	NKG7	SLC30A5	NPR1	THBS1	PTGDS	TPSB2	IL8RA
	IGHG1	CD2	NAP1L4	ARHGAP8	GZMH	SGMS1	CD1B	GALC	COLEC12	TPSB2	IL8RB
	FCRL2 BLK	TRBC1 TRAC	BATF ASF1A	GZMM SLC16A7	SIGIRR ZBTB16	MCM3AP TBXA2R	VASH1 F13A1	RNU2 CLC	GPC4 PCOLCE2	GATA2 HDC	FCGR3B DYSF
	COCH	ITM2A	FRYL	SFRS7	RUNX3	CDC5L	CD1E	HIST1H1C	CHIT1	LOH11CR2A	FCAR
	OSBPL10	SH2D1A	FUSIP1	APBA2	APOL3	LOC730096	MMP12	CYSLTR2	KAL1	SIGLEC6	CEACAM3
	IGHA1	CD6	YME1L1	C4orf15	RORA	FUT5	FABP4	HRH4	CLEC5A	ELA2	HIST1H2BC
	TNFRSF17	CD96	TRA	LEPROTL1	APBA2	FGF18	CLEC10A	RNASE2	ME1	CMA1	HPSE
	ABCB4	NCALD	RPA1	ZFP36L2	WHDC1L1	MRC2	SYT17	CAT	DNASE2B	PGDS	CPPED1
	BLNK	GIMAP5	UBE2L3	GADD45A	DUSP2	RP5-886K2.1		LRP5L	CCL7	MLPH	CREB5
	GLDC	TRA	ANP32B	MYST3	GZMA	SPN	CTNS	SYNJ1	FN1	ADCYAP1	S100A12
	MEF2C IGHM	CD3E SKAP1	DDX50 C13orf34	ZEB1 ZNF609		PSMD4 PRX	GUCA1A CARD9	THBS4 GPR44	CD163 GM2A	SLC24A3	TNFRSF10C
	FAM30A	SKAFI	PPP2R5C	C12orf47		FZR1	ABCG2	KBTBD11	SCARB2	CALB2 KIT	SLC22A4 TECPR2
	SPIB		SLC25A12	THUMPD1		ZNF205	CD1A	HES1	BCAT1	TAL1	SLC25A37
	BCL11A		ATF2	VAMP2		AL080130	PPARG	ABHD2	RAI14	ABCC4	BST1
	GNG7		CD28	ZNF91		ZNF528	RAP1GAP	TIPARP	COL8A2	PPM1H	CRISPLD2
	IGKC		GOLGA8A	ZNF22		MAPRE3	SLC7A8	SMPD3	APOE	MAOB	G0S2
	CD72		IFNG	TMC6		BCL2	GSTT1	MYO15B	CHI3L1	HPGD	SIGLEC5
	MICAL3 BACH2		LTA APBB2	FLT3LG CDKN2AIP		NM_017616 ARL6IP2	PDXK FZD2	TGIF1 RRP12	ATG7 CD84	SCG2 PTGS1	CD93 MGAM
	IGL		DOK5	TSC22D3		PDLIM4	CSF1R	IGSF2	FDX1	CEACAM8	ALPL
	CCR9		IL12RB2	TBCC		TRPV6	HS3ST2	RCOR3	MS4A4A	MPO	FPR1
	QRSL1		APOD	RBM3		LDB3	CH25H	EPN2	SGMS1	NR0B1	PDE4B
	DTNB		ZBTB32	ABT1		ADARB1	LMAN2L	C9orf156	EMP1	LOC339524	LILRB2
	HLA-DQA1		CD38	C19orf6		SMEK1	SLC26A6	SIAH1	CYBB		
	SCN3A SLC15A2		CSF2 CTLA4	CAMLG PPP1R2		TCTN2 TINAGL1	BLVRB NUDT9		CD68		
	SECTOAL		CD70	AES		IGFBP5	PREP				
			DPP4	KLF9		ALDH1B1	TM7SF4				
			EGFL6	PRF1		NCR1	TACSTD2				
			BST2			KIR3DL2	CD1C				
			DUSP5			SPON2	CCL1				
			LRP8			KIR2DL3	EBI3				
			IL22 DGKI			GZMB KIR3DS1	INDO LAMP3				
			CCL4			KIR3DS1	OAS3				
			GGT1			TCC38	IL3RA				
			LRRN3			PMEPA1					
			SYNGR3			IL21R					
			ATP9A			KIR3DL3					
			BTG3			KIR2DS5					
			CMAH HBEGF			KIR2DS2 GTF3C1					
			SGCB			KIR2DS1					
			PMCH			S1PR5					
			AHI1			DUSP4					
			PTGIS			RRAD					
			CXCR6			PLA2G6					
			EVI5			NIBP					
			IL26			FOXJ1					l
			MB NEIL3			MARCH6 MADD					l
			GSTA4			LPCAT4					l
			PHEX			MPPED1					l
			SMAD2			MUC3B					l
			CENPF								l
			ANK1								l
			ADCY1								
			LOC728210 LAIR2								l
			SNRPD1								l
			MICAL2								l
			DHFR								l
			WDHD1								
			BIRC5								l
			SLC39A14								
			HELLS LIMA1								
			CDC25C								
			CDC7								
			GATA3								

Supplementary Table 4. Immune-specific gene lists identified at a single cell resolution

a. B cell upregulated

u. B con uprog		P-value	AUC			P-value	AUC			P-value	AUC
Gene symbol	Fold change		(ROC test)	Gene symbol	Fold change		(ROC test)	Gene symbol	Fold change		(ROC test)
IGLC1	12.37	3.9.E-12	0.70	DCAF12	4.43	1.6.E-11	0.71	SEL1L3	2.69	4.9.E-11	0.79
FCRLA	8.11	0.0.E+00	0.84	ABCA6	4.26	1.8.E-11	0.72	BCAR3	2.67	4.9.E-10	0.73
RN7SL627P	7.98	3.7.E-15	0.74	GPR18	4.16	8.9.E-16	0.81	SSBP2	2.66	3.3.E-12	0.75
RN7SL639P	7.98	3.7.E-15	0.74	PAX5	4.11	0.0.E+00	0.89	BCAS4	2.66	4.2.E-15	0.77
GCSAM	7.81	7.8.E-16	0.75	CTA-250D10.23	4.09	0.0.E+00	0.77	FAM3C	2.65	2.0.E-08	0.72
VNN2	7.78	0.0.E+00	0.77	MCTP2	4.06	1.6.E-12	0.71	TMED8	2.65	2.7.E-11	0.75
AICDA	7.77	0.0.E+00	0.78	CDK14	4.04	7.7.E-12	0.74	FAM210A	2.64	3.0.E-08	0.70
IGHG4	7.68	0.0.E+00	0.80	BRI3BP	4.01	2.5.E-11	0.72	KIAA0922	2.64	2.1.E-12	0.80
VPREB3	7.17	0.0.E+00	0.84	LPP	3.93	5.1.E-14	0.76	PTK2	2.60	3.4.E-08	0.73
RGS13	7.16	0.0.E+00	0.85	NCF1	3.84	1.7.E-12	0.71	MZB1	2.60	5.5.E-08	0.71
SNX29P1	7.05	0.0.E+00	0.80	ENTPD4	3.83	6.1.E-10	0.72	KBTBD8	2.55	1.8.E-13	0.78
E2F5	6.77	1.8.E-13	0.70	DTX1	3.81	7.9.E-13	0.72	FAM208B	2.49	1.7.E-08	0.73
PNOC	6.68	7.2.E-14	0.72	POU2AF1	3.75	0.0.E+00	0.82	LAT2	2.46	4.0.E-11	0.79
FCRL1	6.65	2.4.E-14	0.72	RRM2B	3.70	2.1.E-10	0.72	BIK	2.40	9.7.E-14	0.77
AC079767.4	6.55	2.2.E-12	0.70	RAB30	3.70	0.0.E+00	0.87	HLA-DOB	2.37	6.9.E-09	0.72
ELL3	6.48	0.0.E+00	0.78	FAM3C2	3.51	1.7.E-11	0.70	ADAM28	2.35	7.0.E-10	0.76
IGHG1	6.37	0.0.E+00	0.86	RRAS2	3.51	4.3.E-14	0.79	SEC14L1	2.34	1.4.E-07	0.75
EBF1	6.11	0.0.E+00	0.82	SHCBP1	3.50	4.0.E-10	0.72	PHF6	2.33	3.3.E-08	0.73
CCDC144B	6.09	0.0.E+00	0.80	CTD-2369P2.2	3.44	1.7.E-14	0.82	MEF2C	2.33	0.0.E+00	0.88
IGKC	6.09	5.6.E-16	0.85	DNAJC10	3.39	1.6.E-12	0.77	UBE2J1	2.31	4.0.E-09	0.76
CD79A	6.02	0.0.E+00	0.92	PRKD3	3.35	2.5.E-14	0.82	CLIC4	2.29	3.0.E-06	0.71
CD19	5.89	0.0.E+00	0.78	HAUS8	3.23	1.0.E-07	0.71	TRAK1	2.25	7.9.E-07	0.70
LINC00877	5.87	2.1.E-13	0.71	KLHL6	3.22	2.6.E-10	0.75	RPRD1B	2.22	2.0.E-08	0.72
CCDC144A	5.86	4.4.E-16	0.76	LRMP	3.10	0.0.E+00	0.86	SWAP70	2.12	0.0.E+00	0.87
STAG3	5.85	1.6.E-11	0.71	HDAC9	3.10	7.8.E-16	0.82	LY9	2.12	1.9.E-10	0.75
RALGPS2	5.80	3.3.E-16	0.76	P2RX5	3.09	6.3.E-12	0.72	FAM76B	2.08	2.3.E-09	0.74
ZNF608	5.64	0.0.E+00	0.78	COBLL1	3.06	7.5.E-15	0.79	PIK3C2B	2.07	1.0.E-10	0.71
CD22	5.57	0.0.E+00	0.89	ST6GAL1	3.04	0.0.E+00	0.84	RHOH	2.04	2.1.E-12	0.81
PRPSAP2	5.40	5.6.E-16	0.80	DGKD	2.97	6.1.E-09	0.72	CCNB1	2.04	1.0.E-06	0.72
MS4A1	5.39	0.0.E+00	0.97	BLNK	2.91	6.4.E-12	0.79	MRPS27	2.03	2.6.E-08	0.72
P2RY8	5.33	1.1.E-13	0.71	BANK1	2.81	5.2.E-13	0.74	SPATS2	2.03	2.5.E-07	0.71
IGHG3	5.11	0.0.E+00	0.86	SMIM14	2.79	0.0.E+00	0.81	SNX22	2.02	2.8.E-12	0.72
GMDS	5.06	2.3.E-11	0.71	EIF2AK3	2.75	2.7.E-13	0.79	TMEM156	2.02	4.9.E-07	0.72
NEIL1	4.96	1.1.E-12	0.74	EAF2	2.74	0.0.E+00	0.85	IGLC3	2.01	1.9.E-08	0.71
SNX29P2	4.93	0.0.E+00	0.91	LYPLAL1	2.73	1.6.E-07	0.71	NR4A1	2.00	6.6.E-06	0.71
PLCG2	4.85	0.0.E+00	0.83	TEX9	2.72	3.2.E-12	0.71				
CD79B	4.55	0.0.E+00	0.89	FANCA	2.72	2.3.E-09	0.71				

b. T cell upregulated

_	b. I cell apreg	uiatea										
	Gene symbol	Fold change	P-value (LRT test)	AUC (ROC test)	Gene symbol	Fold change	P-value (LRT test)	AUC (ROC test)	Gene symbol	Fold change	P-value (LRT test) (AUC (ROC test)
1	IFNG	6.19	7.7.E-10	0.71	RORA	3.63	3.7.E-10	0.75	CD96	2.78	6.0.E-14	0.81
	CD3G	5.06	0.0.E+00	0.90	SH2D1A	3.43	1.1.E-16	0.79	MAF	2.77	1.0.E-07	0.73
	CD3D	4.46	0.0.E+00	0.94	PRKCH	3.30	1.0.E-09	0.75	CCL5	2.75	3.8.E-06	0.72
	INPP4B	4.07	3.0.E-11	0.72	TRAT1	3.24	5.0.E-10	0.71	TIGIT	2.73	1.1.E-09	0.75
	CD2	4.06	0.0.E+00	0.95	FYN	3.07	2.7.E-13	0.82	SLA	2.68	6.8.E-09	0.74
	ITK	3.90	8.9.E-10	0.73	ARAP2	2.93	5.3.E-09	0.75	TRAC	2.66	2.2.E-16	0.87
	STAT4	3.77	9.6.E-12	0.77	ITM2A	2.82	1.1.E-16	0.82	TRBC2	2.35	0.0.E+00	0.91
	II 32	3 64	0.0 F+00	0.91	CD3F	2 81	22 F-15	0.78	RARRES3	2 01	3 2 F-06	0.73

Table continued on next page

Supplementary Table 4 cont.

c. Macrophage upregulated

Gene symbol	Fold change	P-value	AUC (ROC test)	Gene symbol	Fold change	P-value (LRT test)	AUC (ROC test)	Gene symbol	Fold change	P-value (LRT test)	AUC (ROC test)
C1QB	9.79	2.3.E-12	0.72	PLXDC2	3.73	4.6.E-11	0.74	CST3	2.64	0.0.E+00	0.93
CD163	9.28	1.1.E-15	0.73	CREG1	3.70	3.8.E-11	0.75	VAMP3	2.62	9.5.E-09	0.74
IL1B	9.14	2.8.E-14	0.72	MNDA	3.69	8.1.E-13	0.81	VAMP5	2.61	1.6.E-06	0.74
FCGR3A	8.61	4.5.E-14	0.75	KIAA1598	3.68	2.1.E-08	0.73	BEST1	2.60	6.4.E-09	0.79
CCL2	8.52	1.9.E-11	0.72	GPNMB	3.67	7.3.E-09	0.72	RBM47	2.58	2.1.E-07	0.76
TMEM176B	8.24	0.0.E+00	0.80	MYOF	3.66	9.3.E-10	0.77	CEBPB	2.52	2.0.E-07	0.70
CXCL9	7.97	7.3.E-12	0.73	TIMP1	3.65	2.0.E-07	0.75	PSAP	2.51	1.7.E-09	0.82
FCGR1A	7.69	1.4.E-11	0.71	AXL	3.65	3.6.E-15	0.80	TGFBI	2.50	6.9.E-14	0.83
APOC1	7.59	5.2.E-15	0.79	LAIR1	3.60	1.4.E-10	0.75	CXCL16	2.49	1.0.E-08	0.73
FN1	7.51	3.3.E-16	0.83	CD68	3.60	1.6.E-14	0.85	TIMP2	2.48	2.3.E-12	0.78
TMEM176A	7.09	3.9.E-12	0.72	MS4A6A	3.60	1.1.E-16	0.84	ITM2B	2.47	2.2.E-08	0.80
S100A9	6.72	2.1.E-10	0.73	TYROBP	3.55	0.0.E+00	0.88	CPVL	2.44	2.2.E-07	0.70
APOE	6.68	1.4.E-12	0.71	RASSF4	3.54	3.0.E-11	0.77	IGSF6	2.44	9.8.E-12	0.75
SLAMF8	6.66	2.9.E-11	0.71	DSE	3.51	3.3.E-16	0.78	HEXB	2.42	1.5.E-09	0.79
CD14	6.35	4.2.E-13	0.76	FTL	3.50	0.0.E+00	0.88	CTSC	2.41	8.6.E-10	0.81
CXCL10	6.05	5.4.E-10	0.75	KCTD12	3.23	1.2.E-13	0.77	BRI3	2.39	1.9.E-07	0.73
FCGR2A	5.72	7.2.E-12	0.75	FCER1G	3.21	0.0.E+00	0.87	GPX1	2.36	7.1.E-11	0.84
RP11-1143G9.4	5.63	1.3.E-15	0.81	FCGRT	3.21	5.3.E-11	0.79	MARCKS	2.36	1.6.E-07	0.77
HNMT	5.55	4.4.E-12	0.71	CTSB	3.17	3.3.E-13	0.85	CAPG	2.33	7.8.E-08	0.79
PLBD1	5.48	7.3.E-14	0.70	HLA-DQB2	3.09	5.4.E-05	0.72	IFITM3	2.33	1.1.E-10	0.83
A2M	5.35	0.0.E+00	0.82	SLC8A1	3.05	2.8.E-07	0.70	S100A11	2.31	1.8.E-11	0.88
CXCL2	5.06	1.8.E-10	0.74	IER3	3.04	4.2.E-08	0.72	HLA-DQA2	2.29	1.3.E-07	0.77
MAFB	5.02	1.1.E-16	0.80	MFSD1	3.03	2.7.E-11	0.82	LST1	2.28	6.4.E-10	0.80
MSR1	4.87	1.8.E-12	0.75	PLAUR	3.00	5.4.E-13	0.81	TNFSF13B	2.25	4.4.E-11	0.80
PLAU	4.81	1.6.E-09	0.72	IL18	3.00	2.8.E-10	0.74	RNASET2	2.23	1.7.E-07	0.77
CTSL	4.69	3.1.E-14	0.82	ANKRD22	2.96	1.5.E-09	0.72	FTLP3	2.23	2.4.E-10	0.80
SIRPA	4.66	1.9.E-13	0.76	ATP6AP1	2.93	9.2.E-07	0.71	LPCAT2	2.20	2.6.E-11	0.71
FGL2	4.62	6.2.E-12	0.76	SOD2	2.90	9.7.E-08	0.77	CD63	2.20	1.8.E-07	0.78
LYZ	4.55	2.3.E-15	0.82	GLUL	2.86	8.5.E-09	0.79	CCL4	2.20	2.7.E-04	0.70
SERPING1	4.51	0.0.E+00	0.88	IFIT1	2.83	4.4.E-06	0.71	LILRB4	2.19	1.5.E-09	0.75
SCARB2	4.40	4.2.E-11	0.76	IFI27	2.82	1.5.E-13	0.87	HLA-DRB6	2.16	6.2.E-08	0.72
CLEC7A	4.36	7.9.E-15	0.84	CCND1	2.79	7.4.E-08	0.71	MS4A7	2.13	2.2.E-06	0.72
AIF1	4.20	6.1.E-14	0.83	IFIT3	2.71	4.5.E-05	0.71	ATOX1	2.12	3.0.E-06	0.75
PILRA	4.19	6.1.E-11	0.71	GNAQ	2.71	4.1.E-11	0.77	DAB2	2.09	2.2.E-15	0.81
C15orf48	4.00	4.0.E-12	0.76	IL8	2.71	8.8.E-08	0.76	NAGK	2.02	5.2.E-07	0.76
FAM26F	3.97	3.0.E-09	0.71	NPC2	2.70	1.0.E-15	0.90	IFI30	2.02	6.6.E-09	0.81
SERPINA1	3.80	9.7.E-11	0.75	NRP1	2.70	1.7.E-08	0.73				
RIN2	3.77	5.6.E-10	0.73	RNASE6	2.66	4.3.E-07	0.73				

$Supplementary\ Table\ 5.\ Immune\ signature\ gene\ sets$

a. M1/M2 gene sets

b. B cell signature gene sets

a. M1/M2 gen	e sets		. !	b. B cell signa	ature gene sets	3				
Gene set name	M1_UP	M2_UP		Gene set name	Anti-apoptosis	Naïve / Memory	Cytokines	Pro-apoptosis	Proliferation	Germinal center
Genes	CCR7	GPR86		Genes	BCL2	BMI1	CCL5	BIK	ASK	BCL7A
	IL2RA	P2RY5			CASP8	CD24	CCR1	FAS	AURKA	CD27
	IL15RA	TGFBR2			FAIM3	CD69	CCR6	LGALS1	AURKB	CD36
	IL7R	HRH1			TNFSF10	CR1	CCR7		AURKC	CD80
	CXCL11	TLR5				ENTPD1	CLR1		BUB1B	HGF
	CCL19	DCL-1				FCER2	GPR9		CCNA2	MME
	CXCL10	MSR1				FCGR2B	IFNGR1		CCNB1	MYBL1
	CXCL9	CXCR4				FCGRT	IL10RB		CCNB2	RGS13
	TNF	DECTIN1				IGHD	IL15		CCNE2	TNFSF8
	CCL5	P2RY14					IL24		CCNF	
	CCL15	DCSIGN					IL2RB		CDC20	
	IL12B	CLECSF13					IL2RG		CDC25B	
	IL15	MS4A6A					IL4R		CDC45	
	TRAIL	CD36					IL6		CDC6	
	IL6	MS4A4A					IL8		CDK1	
	CCL20	MRC1					TGFB1		CDK5	
	PBEF1	IGF1					TGFB3		CDKN2C	
	ECGF1	CCL23					TGFBR2		CENPA	
	BCL2A1	CCL18					TNFRSF1B		CENPE	
	FAS	CCL13					TNFSF11		CENPF	
	BIRC3	SLC21A9					XCL1		CHEK1	
	GADD45G	SLC4A7					XOLI		CIP2	
	HSXIAPAF1	SLC38A6							DEEPEST	
	SLC7A5	CTSC							E2F5	
	SLC21A15	HEXB							ECA39	
	SLC21A13	LIPA							FOXA1	
	SLC2A0	ADK							GADD45A	
	INDO	HNMT							GADD45A GADD45B	
	PLA1A	TPST2							GTSE1	
	OASL	CERK							HEC1	
	CHI3L2	HS3ST2							KIF11	
	HSD11B1	LTA4H							KIF22	
	AK3	CA2							KIF22 KIF23	
	SPHK1	ALOX15							MAD2L1	
	PFKFB3	HS3ST1							MCM3	
	PSME2	TGFBI							MCM4	
	PFKP	SEPP1							MCM6	
	PSMB9	CHN2							MCM7	
	PSMA2	FN1							MKI67	
	OAS2	FGL2							NCAPD2	
	PTX3	GAS7							NDN	
	CSPG2	EGR2							NEK2	
	APOL3	MAF							PCNA	
	IGFBP4	IVIAF							PLK4	
	APOL1								PTTG1 RABGAP1	
	PDGFA									
	EDN1 APOL2								RAD17	
	INHBA								RFC3 RGL2	
	APOL6								RGL2 RPA3	
	HESX1								SIL-TAL1	
	IRF1								TFDP1	
	ATF3								TMPO	
	IRF7								TPX2	
	INF <i>I</i>								TTK	
									UBE2C	
									WEE1	
									ZW10	
			L						∠vv 10	

Supplementary Table 5 cont.

c. T cell signature gene sets

Gene set name	Cytotoxic	Exhausted	Regulatory	Naïve	Costimulatory	G1/S	G2/M
Genes	CST7	BTLA	IL2RA	CCR7	ICOS	ATAD2	ANLN
	GZMA	CTLA4	IL4R	LEF1	CD226	BLM	ANP32E
	GZMB	HAVCR2	IL7	SELL	SLAMF1	BRIP1	AURKA
	IFNG	LAG3	TGFB1	TCF7	TNFRSF14	CASP8AP2	AURKB
	NKG7	PDCD1	TGFB3		TNFRSF25	CCNE2	BIRC5
	PRF1	TIGIT	TGFBI		TNFRSF9	CDC45	BUB1
	TNFSF10		TGFBR1			CDC6	CBX5
						CDCA7	CCNB2
						CHAF1B	CDC20
						CLSPN	CDC25C
						DSCC1	CDCA2
						DTL	CDCA3
						E2F8	CDCA8
						EXO1	CDK1
						FEN1	CENPA
						GINS2	CENPE
						GMNN	CENPF
						HELLS	CKAP2
						MCM2	CKAP2L
						MCM4	CKAP5
						MCM5	CKS1B
						MCM6	CKS2
						MLF1IP	CTCF
						MSH2	DLGAPS
						NASP	ECT2
						PCNA	FAM64A
						POLA1	G2E3
						POLD3	GAS2L3
						PRIM1	GTSE1
						RAD51	HJURP
						RAD51AP1	HJURP
						RFC2	HMGB2
						RPA2	HMMR
						RRM1	HN1
						RRM2	KIF11
						SLBP	KIF20B
						TIPIN	KIF23
						TYMS	KIF2C
						UBR7	LBR
						UHRF1	MKI67
						UNG	NCAPD2
						USP1	NDC80
						WDR76	NEK2
							NUF2
							NUSAP1
							PSRC1
							RANGAP
							SMC4
							TACC3
							TMPO
							TOP2A
							TPX2
							TTK
							TUBB4B
							UBE2C

Supplementary Table 6. Quantitative PCR primers

RefSeq ID	Gene Symbol	Forward Primer	Reverse Primer
NM_002046	GAPDH	AGGTCGGAGTCAACGGATTT	TGACGGTGCCATGGAATTTG
NM_001101	ACTB	ACTCTTCCAGCCTTCCTTCC	CGTACAGGTCTTTGCGGATG
NM_000125	ESR1	GACAGGGAGCTGGTTCACA	GACCTGATCATGGAGGGTCAAA
NM_000926	PGR	AGCCAAGAAGAGTTCCTCTGTA	TTGACTTCGTAGCCCTTCCA
NM_004448	ERBB2	ACAGGGAAAGCTGTGGGAAA	TACGCCTCCAACACACTGAA
NM_005228	EGFR	AGGTGAAAACAGCTGCAAGG	CCAGAAGGTTGCACTTGTCC
NM_000633	BCL2	ATGTGTGGGGGGGCGTCAA	GTGCCGGTTCAGGTACTCA
NM_002417	MKI67	AGAGTAACGCGGAGTGTCA	CTTGACACACACATTGTCCTCA
NM_000044	AR	CTTTGCAGCCTTGCTCTCTA	TCTGGTCGTCCACGTGTAA
NM_000546	TP53	GACTGTACCACCATCCACTACA	AAAGCTGTTCCGTCCCAGTA
NM_001012270	BIRC5	GGACCACCGCATCTCTACAT	GAAACACTGGGCCAAGTCTG
NM_018014	BCL11A	AACCCCAGCACTTAAGCAAAC	GGCCGTGGTCTGGTTCA
NM_000224	KRT18	TCCCATGTCCCAGTCAATTCC	TACCTGGGAGGGGATGTTCA
NM_002276	KRT19	GGAGGTGTCATTGGAGCTGAA	AGCAGCTTCCACCACTTCAA
NM_002051	GATA3	CACGGTGCAGAGGTACCC	AGGGTAGGGATCCATGAAGCA
NM_004360	CDH1	AGTGCCAACTGGACCATTCA	TCTAAGGCCATCTTTGGCTTCA
NM 001067	TOP2A	GGTGTGGAACTAGAAGGCCT	TCTGTTTCTCGTGGAGGGAC
 NM_000201	ICAM1	AACCCCACAGTCACCTATGG	TTCTGAGACCTCTGGCTTCG
NM 001432	EREG	TTGTTTGCATGGACAGTGCA	GCTTAAAGGTTGGTGGACGG
NM 080921	PTPRC	GTGGCTTAAACTCTTGGCATTT	GGGAAGGTGTTGGGCTTT
_ NM_002354	EPCAM	CGTCAATGCCAGTGTACTTCA	TTCTGCCTTCATCACCAAACA
_ NM_201442.2	C1S	TACGGGGTTTGCTGCATACTA	AGTGGCTACAAGGGACATCTAC
 NM_000064.3	C3	GGCGTGTTCGTGCTGAATAA	CCGATGTCTGCCTTCTCCA
NM 000346	SOX9	GTGCTCAAAGGCTACGACTG	AGAAGTCTCCAGAGCTTGCC