Figure S1 Cell score difference between breast cancer tissues and adjacent normal tissues in TCGA cohort. Red: breast cancer tissues; green: adjacent normal tissues. aDC, activated dendritic cell; cDC, conventional dendritic cell; CLP, common lymphoid progenitor; CMP, common myeloid progenitor; DC, dendritic cell; GMP, granulocyte–macrophage progenitor; HSC, hematopoietic stem cell; iDC, immature dendritic cell; MEP, megakaryocyte–erythroid progenitor; MPP, multipotent rogenitor; MSC, mesenchymal stem cell; NKT, natural killer T cell; pDC, plasmacytoid dendritic cell; TCGA, The Cancer Genome Atlas.
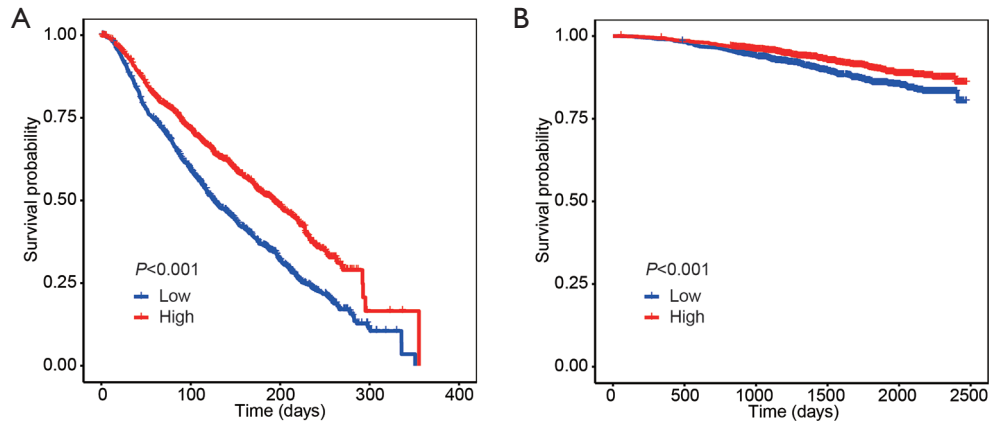
Figure S2 High cDC score is associated with a better overall survival. (A) METABRIC (HR =0.65; 95% CI: 0.58–0.73; P<0.001); (B) GSE96058 (HR =0.70, 95% CI: 0.57–0.87; P<0.001). cDC, conventional dendritic cell; CI, confidence interval; HR, hazard ratio.
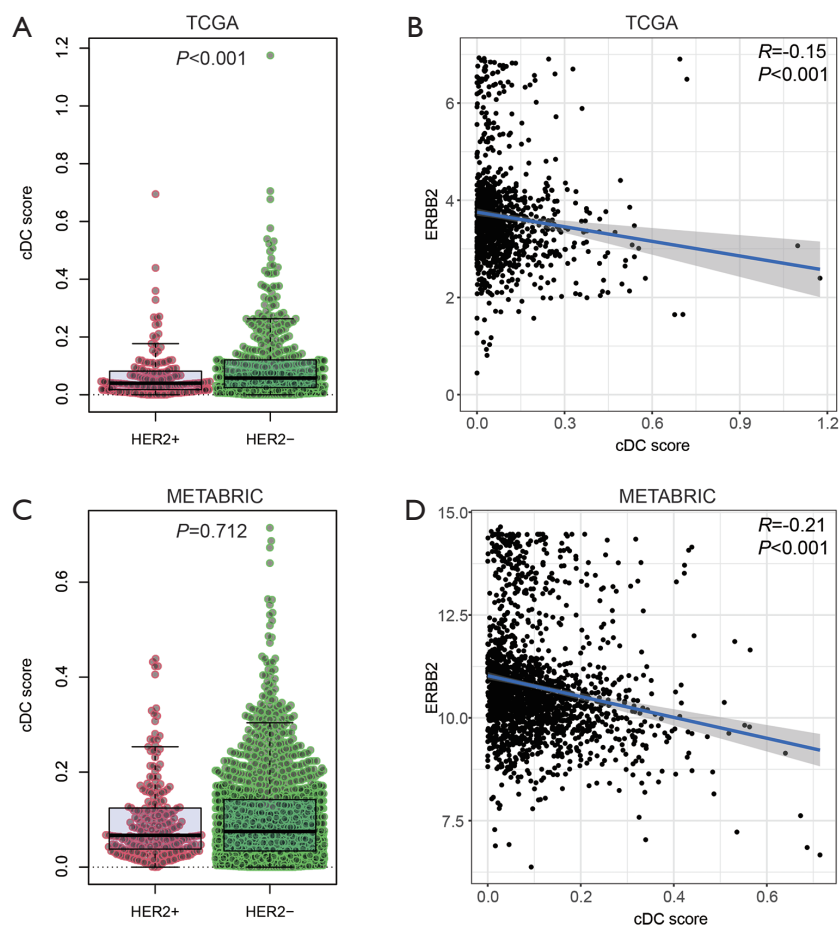

Figure S3 cDC score is inversely correlated with the expression level of HER2. (A) Distribution of cDC score according to HER2 status in TCGA; (B) distribution of cDC score according to HER2 status in METABRIC; (C) Spearman's correlation analysis between cDC score and expression level of HER2 in TCGA; (D) Spearman's correlation analysis between cDC score and expression level of HER2 in METABRIC. cDC, conventional dendritic cell; TCGA, The Cancer Genome Atlas.
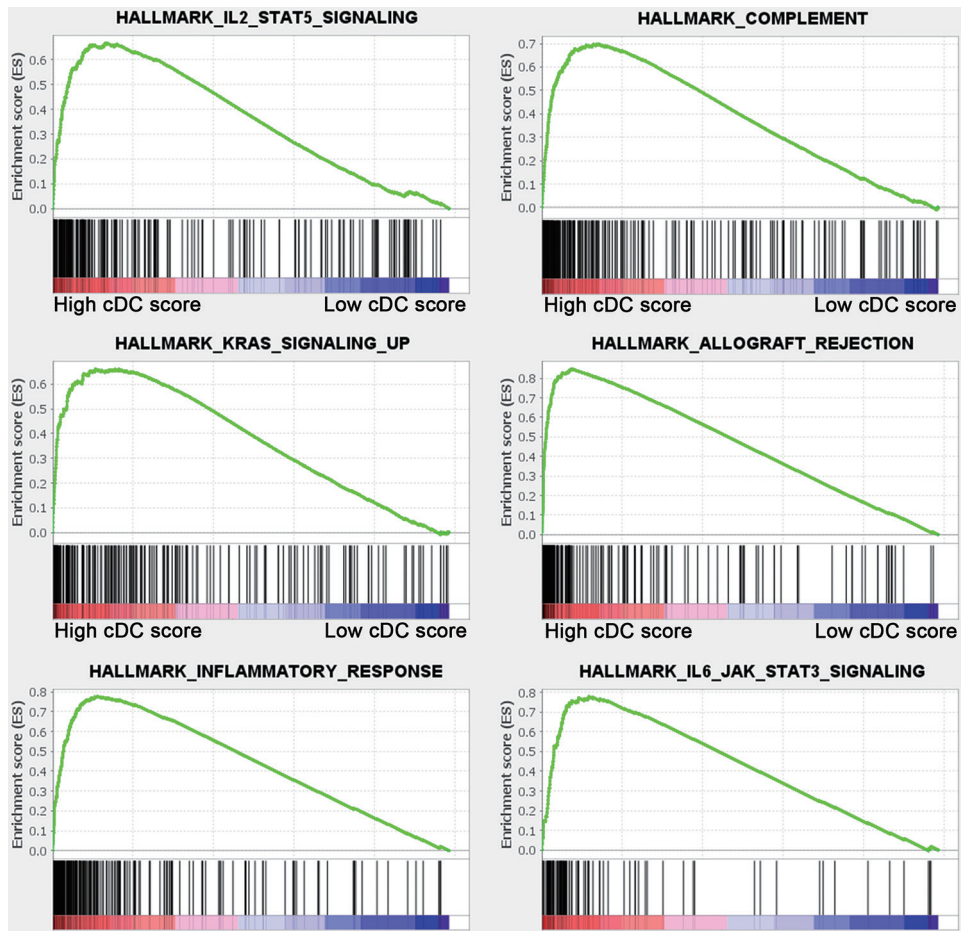
Figure S4 Gene set enrichment analysis (GSEA) with Hallmarks gene sets for which highly enriched in the high cDC tumors compared to low tumors in the TCGA. cDC, conventional dendritic cell; TCGA, The Cancer Genome Atlas.

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Table S1 Characteristics of breast cancer patients

Characteristic	All (n=1,056)	Training set (n=528)	Test set (n=528)	P value
Age, years, mean ± SD	58.05±12.93	58.15±13.13	57.94±12.74	0.781
Age, n (%)				
≤65 years	759 (71.88)	375 (71.02)	384 (72.73)	0.538
>65 years	297 (28.12)	153 (28.98)	144 (27.27)	
Race, n (%)				
White	736 (69.70)	373 (70.64)	363 (8.75)	0.503
Others	320 (30.30)	155 (29.36)	165 (31.25)	
Stage, n (%)				
I	181 (17.50)	94 (18.18)	87 (16.83)	0.513
II	597 (57.74)	289 (55.90)	308 (59.57)	
III	237 (22.92)	126 (24.37)	111 (21.47)	
IV	19 (1.84)	8 (1.55)	11 (2.13)	
Tumor size, n (%)				
T1	278 (26.40)	141 (26.76)	137 (26.05)	0.137
T2	606 (57.55)	290 (55.03)	316 (60.08)	
T3	132 (12.54)	72 (13.66)	60 (11.41)	
T4	37 (3.51)	44 (4.55)	13 (2.47)	
Node status, n (%)				
N0	498 (47.93)	262 (50.38)	236 (45.47)	0.070
N1	350 (33.69)	165 (31.73)	185 (35.65)	
N2	119 (11.45)	65 (12.50)	54 (10.40)	
N3	72 (6.93)	28 (5.38)	44 (8.48)	
Metastases, n (%)				
M0	873 (97.65)	436 (98.20)	437 (97.11)	0.283
M1	21 (2.34)	8 (1.80)	13 (2.89)	
Status, n (%)				
Alive	908 (85.98)	457 (86.55)	451 (85.41)	0.595
Death	148 (14.02)	71 (13.45)	77 (15.58)	
Survival time (days), mean ± SD	1,259.53±1,193.34	1,237.46±1,239.282	1,281.60±1,146.32	0.548

SD, standard deviation.

Table S2 Gene set enrichment analysis (GSEA) with Hallmarks gene sets for which highly enriched in the high cDC tumors compared to low tumors in the TCGA cohort

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Genes of core enrichment
HALLMARK_IL2_STAT5_SIGNALING	199	0.667	2.779	0.000	0.000	0.000	IL10RA, TNFRSF1B, FGL2, CCR4, CD48, CD86, IL18R1, TNFRSF9, IRF8, GPR65, CST7, TRAF1, TNFRSF8, ICOS, CTLA4, EOMES, SELP, SYT11, CDC42SE2, TLR7, IRF4, ABCB1, LRRC8C, CD83, PRKCH, IL3RA, CD79B, IL10, IFNGR1, IL4R, BATF3, LTB, ADAM19, CSF1, TNFRSF4, SLC2A3, F2RL2, FLT3LG, PIM1, CTSZ, NRP1, MYO1E, SOCS1, GBP4, SWAP70, TGM2, SHE, PRNP, AHR, ITGAE, KLF6, IL2RA, RORA, NFIL3, CXCL10, IL13, NT5E, GALM, IL2RB, PLPP1, PTCH1, IL1RL1, DENND5A, GUCY1B1, CSF2, LIF, GLIPR2, RGS16, GABARAPL1, BMPR2, PLSCR1, GADD45B, COL6A1, ANXA4, MAP3K8, EMP1, IKZF4, PLIN2, IGF2R, ITGAV, TNFRSF21, BMP2, GATA1, HOPX, GSTO1, ARL4A, CD81, CAPG, IKZF2, WLS, SELL, CYFIP1
HALLMARK_INFLAMMATORY_RESPONSE	200	0.776	2.743	0.000	0.000	0.000	GPR183, NLRP3, PTAFR, IL7R, SLAMF1, EBI3, CYBB, IL12B, CD69, LTA, C3AR1, IL18RAP, PTGER4, KCNA3, CD40, FPR1, CXCL9, CMKLR1, TLR1, SEMA4D, RGS1, IL15, IL15RA, SCARF1, P2RX7, EMP3, STAB1, PTPRE, CCL22, AXL, MEFV, C5AR1, CCL17, CCL2, IL1B, IL18, GPR132, APLNR, MSR1, NFKBIA, NMI, TACR1, ADGRE1, TLR2, ICAM1, HBEGF, NFKB1, PTGIR, PDPN, HRH1, CD82, OSMR, CXCL11, CCRL2, IFNGR2, AQP9, SELE, HAS2, IRAK2, CALCRL, IL1R1, CHST2, SLC31A2, OSM, CD14, ACVR2A, BEST1, ABCA1, TLR3, CLEC5A, CCL24, LAMP3, NAMPT, CCR7, TNFAIP6, TAPBP, LPAR1, EDN1, ITGA5, CX3CL1, TNFSF15, HIF1A, MARCO, GCH1, PDE4B, MEP1A, IFNAR1, ITGB8, ITGB3, GNA15
HALLMARK_COMPLEMENT	200	0.697	2.739	0.000	0.000	0.000	LCP2, PLEK, PIK3R5, WAS, GNGT2, FCN1, LCK, PIK3CG, TNFAIP3, CTSS, GZMK, CD40LG, GZMA, SH2B3, FCER1G, APOBEC3G, CCL5, C1QA, LYN, C3, C1QC, SPOCK2, CASP4, SERPING1, IRF1, CR1, CASP10, CASP1, DOCK10, GZMB, C1S, C1R, CTSC, PLA2G7, LGMN, JAK2, FYN, CFH, GP1BA, GNG2, GNAI2, RHOG, CTSB, LIPA, PSMB9, CASP5, LAP3, DOCK4, OLR1, APOC1, DPP4, ITGAM, LRP1, ZEB1, F10, CTSL, ERAP2, CTSH, IRF2, TIMP2, APOBEC3F, CTSO, MMP8, CBLB, C2, DGKG, CR2, MMP12, EHD1, ITIH1, XPNPEP1, IL6, FDX1, NOTCH4, ANXA5, SERPINE1, PLAUR, PDP1, F3, LTF, USP15, L3MBTL4, GCA, GNB4, DGKH, HPCAL4, COL4A2, CPM, ZFPM2, LGALS3, MMP14, CEBPB, CXCL1, PRCP, LTA4H, KIF2A, CASP7, CD59, DOCK9
HALLMARK_KRAS_SIGNALING_UP	200	0.660	2.655	0.000	0.000	0.000	CLEC4A, DOCK2, IKZF1, LAPTM5, ITGB2, ETS1, IL2RG, LAT2, TLR8, MAP4K1, PDCD1LG2, LY96, PRDM1, CD37, MAFB, LCP1, CSF2RA, BIRC3, ENG, ADAMDEC1, PECAM1, GYPC, ADGRA2, IL33, GFPT2, ADGRL4, SPARCL1, CXCR4, TSPAN7, GPNMB, CBL, PLVAP, TMEM176B, EPHB2, PRRX1, NIN, ADAM8, HSD11B1, FLT4, PPP1R15A, GNG11, SPRY2, F13A1, ST6GAL1, PSMB8, GUCY1A1, MALL, KLF4, AKAP12, TMEM176A, ANKH, SPON1, GPRC5B, ADAM17
HALLMARK_ALLOGRAFT_REJECTION	200	0.847	2.621	0.000	0.000	0.000	CD4, HCLS1, HLA-DRA, HLA-DMB, SRGN, PTPRC, CCR5, CD3G, CD2, HLA-DQA1, HLA-DOA, NCF4, PRKCB, CRTAM, CD1D, ITK, CD247, CD96, IL16, FGR, HLA-DMA, CD3E, FYB1, SPI1, CCR2, CD3D, STAT4, CD28, CXCR3, IGSF6, CD74, ST8SIA4, CD8A, SIT1, LY86, ITGAL, HLA-E, PRF1, CFP, KLRD1, ZAP70, FASLG, NCR1, IL2, CD7, CCL19, FCGR2B, IFNAR2, CD8B, CD79A, B2M, HLA-DOB, LY75, TRAT1, TLR6, F2R, GBP2, IFNG, CCL13, TAP2, PSMB10, NCK1, PTPN6, WARS1, CSK, SOCS5, FLNA, HLA-A, ELF4, CD47, IL27RA
HALLMARK_IL6_JAK_STAT3_SIGNALING	87	0.779	2.596	0.000	0.000	0.000	IL12RB1, CSF2RB, CD38, FAS, ACVRL1, IL9R, CCR1, IL17RA, ITGA4, TGFB1, IL7, IL10RB, CRLF2, MYD88, STAT1, STAT2, A2M, TNFRSF1A, LEPR, PTPN2, HMOX1, BAK1, TYK2
HALLMARK_TNFA_SIGNALING_VIA_NFKB	200	0.734	2.543	0.000	0.000	0.000	TNFAIP8, CCL4, CFLAR, GEM, RNF19B, CD80, SGK1, ETS2, RELB, SOD2, FUT4, NFKBIE, SERPINB8, EGR2, DUSP2, PNRC1, PLPP3, CCN1, NFKB2, TAP1, MCL1, STAT5A, KLF2, SOCS3, SLC2A6, TANK, B4GALT5, CXCL3, KLF9, BIRC2, DUSP1, NR4A3, MSC, ZFP36, TNF, DNAJB4, TNIP1, CCNL1, ATF3, BTG1, EGR3, DRAM1, NFE2L2, CXCL2, JUN, TNFAIP2, TRIP10, MARCKS, JUNB, EGR1, SPSB1, NR4A1, PER1, JAG1, FOS, NFAT5, FOSL2, RCAN1, TIPARP, LAMB3, SAT1, ZC3H12A, TNC, FOSB, CEBPD, IFIH1, LITAF, BCL6, RIPK2, FOSL1, BCL2A1, MAP2K3, KDM6B, IL23A, TSC22D1, BTG2, BTG3

Table S2 (*continued*)

Table S2 (*continued*)

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Genes of core enrichment
HALLMARK_INTERFERON_GAMMA_RESPONSE	200	0.791	2.325	0.000	0.000	0.001	HLA-DRB1, CIITA, ITGB7, SAMHD1, IL18BP, SLAMF7, P2RY14, KLRK1, XCL1, MARCHF1, FCGR1A, EPSTI1, NLRC5, CD274, GPR18, IFI30, VAMP5, APOL6, BANK1, LATS2, SAMD9L, NOD1, ARID5B, IRF5, HLA-B, PML, PELI1, CASP8, VCAM1, TXNIP, TRIM21, ZBP1, SP110, LYSMD2, TRIM14, SSPN, UPP1, PARP14, IDO1, XAF1, MX2, ISG20, RIPK1, GBP6, BATF2, ST3GAL5, ZNFX1, EIF4E3, PARP12
HALLMARK_APOPTOSIS	161	0.521	2.296	0.000	0.000	0.001	PLCB2, DPYD, HGF, CYLD, MMP2, NEDD9, PDGFRB, DCN, ANXA1, ROCK1, GSN, LUM, BGN, GPX1, FEZ1, AVPR1A, BCL10, GPX3, SATB1, CAV1, CTNNB1, CCND2, APP, IL1A
HALLMARK_COAGULATION	137	0.578	2.250	0.000	0.000	0.001	PROS1, CFI, VWF, CTSK, KLF7, THBD, ISCU, P2RY1, GNG12, RAPGEF3
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	0.677	2.209	0.000	0.000	0.002	WIPF1, GLIPR1, ABI3BP, DAB2, SLIT2, IL32, FSTL1, LAMA2, CXCL12, FBLN2, SFRP4, VIM, DPYSL3, NNMT, CCN2, ADAM12, GAS1, CALD1, HTRA1, COL16A1, COL6A3, MXRA5, LAMC1, SNAI2, FBLN1, COL3A1, MMP3, FBN1, FBLN5, LOX, SERPINE2, NID2, EFEMP2, COL6A2, BMP1, FAP, MYLK, ELN, DST, CTHRC1, SLIT3, FERMT2, VCAN, GPX7, ITGB1, P3H1, SPARC, COL1A1, COLGALT1, SGCD, FOXC2, LAMC2, CDH11, THY1, LOXL1, COL5A1, FUCA1, PCOLCE, COL1A2, TNFRSF11B, POSTN, TGFBI, VEGFC, SFRP1, COL5A2, NOTCH2, ECM2, CALU, WNT5A, IGFBP3, CDH6, TPM1, PDLIM4, MATN2, LRRC15, CXCL8, PMP22, TAGLN
HALLMARK_APICAL_JUNCTION	200	0.521	2.162	0.000	0.000	0.004	RAC2, MSN, SYK, ICAM2, ARPC2, SIRPA, CD209, EPB41L2, ZYX, CNN2, RHOF, CADM3, CLDN11, CD34, SKAP2, SDC3, CLDN15, ACTB, AKT3, CLDN5, CAP1, ITGA9, ADAM23, JAM3, ACTN1, CDH3, LAYN, NECTIN3, NRXN2, ADAMTS5, MYH9, CD99, VCL, MAPK11, TSPAN4, DSC1, MAPK14, DSC3, PARVA, ITGB4, NECTIN1, MPZL1, SGCE, YWHAH, GNAI1, PARD6G, RSU1, COL17A1, IKBKG, VASP, MMP9, CLDN19, NLGN3, PFN1, FSCN1
HALLMARK_UV_RESPONSE_DN	144	0.522	1.955	0.006	0.007	0.052	PIK3CD, CELF2, TGFBR2, NR3C1, GRK5, ADD3, RND3, PRDM2, RASA2, SYNE1, DLC1, PTPRM, PTGFR, PTPN21, PRKCA, ATXN1, ID1, KIT, SCHIP1, EFEMP1, RUNX1, KALRN, TFPI, ATP2B4, NFIB, WDR37, MAP1B
HALLMARK_INTERFERON_ALPHA_RESPONSE	97	0.725	1.947	0.010	0.007	0.055	TMEM140, LPAR6, NCOA7, HLA-C, UBA7, NUB1, PROCR, TRIM5, UBE2L6, PSME2
HALLMARK_ANGIOGENESIS	36	0.567	1.873	0.002	0.013	0.102	SLCO2A1, PRG2, S100A4, SPP1, TIMP1, PDGFA
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	0.433	1.839	0.002	0.016	0.126	SLA, CAMK4, DAPP1, RPS6KA3, ACTR3, MKNK1, CAB39, PIK FYVE, ACTR2, RALB, RPS6KA1
HALLMARK_P53_PATHWAY	199	0.410	1.816	0.004	0.019	0.151	TCN2, RAP2B, DGKA, GM2A, PLK3, DEF6, ADA, ZFP36L1, NOTCH1, ZMAT3, EPHA2, PTPN14, TP63, RALGDS, RB1, VDR, FBXW7, TAX1BP3, RHBDF2, STEAP3, POLH, POM121, HDAC3, ZBTB16, TGFA, VWA5A, IRAK1, TNFSF9, CEBPA, CCND3, CLCA2, PRMT2, SPHK1
HALLMARK_HYPOXIA	200	0.434	1.805	0.004	0.020	0.158	PLAC8, AMPD3, SLC2A5, HS3ST1, SRPX, CHST3, TES, NDST2, CAVIN1, TGFB3, CAVIN3, NAGK, SLC6A6, HAS1, TPST2, CCN5, PGF, EXT1, GLRX, RBPJ, NDST1, KLHL24, HEXA, MAFF, PGM2, ERRFI1
HALLMARK_TGF_BETA_SIGNALING	54	0.477	1.689	0.021	0.041	0.282	WWTR1, LTBP2, ACVR1, SKI, ID3, TGFBR1, SMURF1, FKBP1A, SPTBN1, KLF10, NOG, TJP1, MAP3K7, SMAD1, SMURF2, RHOA

cDC, conventional dendritic cell; ES, enrichment score; FDR, false discovery rate; FWER, family-wise error rate; NES, normalized enrichment score; NOM, normal; TCGA, The Cancer Genome Atlas.

Table S3 Survival analysis with the key genes associated with high cDC score in gene set enrichment analysis

Genes	P	HR (95% CI)
PDP1	0.000	1.969 (1.403–2.763)
RAC2	0.000	0.531 (0.380–0.741)
CEBPD	0.000	0.533 (0.382–0.744)
IL2	0.000	0.557 (0.401–0.774)
SPOCK2	0.001	0.579 (0.416–0.805)
CD3E	0.001	0.577 (0.414–0.804)
DEF6	0.001	0.576 (0.412–0.804)
CD3D	0.001	0.577 (0.413–0.805)
APOBEC3G	0.001	0.585 (0.421–0.812)
CD247	0.002	0.587 (0.421–0.819)
APOBEC3F	0.002	0.593 (0.426–0.825)
IL27RA	0.002	0.595 (0.428–0.826)
HLA-DRA	0.002	0.596 (0.428–0.831)
EGR3	0.002	0.601 (0.434–0.834)
BTG1	0.002	0.602 (0.435–0.834)
UBA7	0.002	0.595 (0.426–0.832)
TRAT1	0.002	0.599 (0.430–0.835)
IFNG	0.003	0.601 (0.432–0.836)
ITIH1	0.003	0.604 (0.435–0.838)
TNIP1	0.003	0.602 (0.433–0.838)
FLT3LG	0.003	0.600 (0.430–0.838)
TAPBP	0.003	0.608 (0.438–0.844)
PSME2	0.003	0.607 (0.437–0.845)
STAT4	0.003	0.606 (0.433–0.846)
CXCL1	0.003	0.613 (0.443–0.850)
GZMA	0.003	0.609 (0.438–0.849)
IL12B	0.004	0.613 (0.442–0.852)
IRF2	0.004	0.618 (0.446–0.854)
CD40LG	0.004	0.612 (0.439–0.854)
CD79A	0.004	0.618 (0.445–0.858)
PSMB8	0.004	0.621 (0.447–0.862)
CD96	0.005	0.619 (0.444–0.863)
FASLG	0.005	0.620 (0.444–0.865)
NFKBIA	0.005	0.628 (0.453–0.872)
MAP4K1	0.005	0.625 (0.448–0.871)
IGF2R	0.006	1.594 (1.145–2.218)
CD2	0.006	0.628 (0.451–0.874)
CD48	0.006	0.628 (0.451–0.875)
GSTO1	0.006	0.630 (0.453–0.876)
TGFBR1	0.006	1.580 (1.138–2.194)
HLA-DQA1	0.007	0.638 (0.459–0.887)
LAMB3	0.007	0.638 (0.458–0.887)
RPS6KA1	0.008	0.639 (0.460–0.887)
RUNX1	0.008	0.639 (0.460–0.888)
CD8B	0.008	0.638 (0.458–0.888)

Table S3 (continued)

Genes	P	HR (95% CI)
HLA-DOB	0.008	0.642 (0.463–0.889)
SOCS3	0.008	0.643 (0.464–0.890)
CXCL3	0.008	0.644 (0.465–0.893)
IL18RAP	0.008	0.638 (0.458–0.891)
CD74	0.009	0.645 (0.465–0.895)
WLS	0.009	0.646 (0.466–0.895)
CCR7	0.009	0.644 (0.463–0.895)
CST7	0.009	0.645 (0.464–0.897)
CAB39	0.009	1.561 (1.117–2.181)
PLAC8	0.009	0.647 (0.466–0.898)
SELL	0.009	0.648 (0.468–0.899)
CCL19	0.010	0.652 (0.470–0.903)
BIRC3	0.011	0.653 (0.471–0.906)
NFKBIE	0.011	0.653 (0.470–0.906)
CAMK4	0.011	0.651 (0.468–0.906)
CXCL2	0.011	0.655 (0.473–0.908)
HLA-DMA	0.011	0.655 (0.471–0.909)
CXCL9	0.012	0.654 (0.470–0.909)
SOCS1	0.013	0.659 (0.475–0.914)
PDLIM4	0.013	0.661 (0.477–0.916)
IL7	0.013	0.660 (0.475–0.916)
CD3G	0.013	0.659 (0.473–0.917)
EMP3	0.013	0.661 (0.476–0.918)
IRF1	0.014	0.665 (0.480–0.922)
ERRFI1	0.015	0.667 (0.482–0.924)
GBP2	0.016	0.668 (0.481–0.927)
IL2RB	0.016	0.667 (0.480–0.928)
WAS	0.017	0.668 (0.481–0.929)
TP63	0.017	0.672 (0.486–0.931)
SFRP1	0.017	0.673 (0.487–0.931)
IL2RG	0.017	0.670 (0.482–0.930)
ITK	0.019	0.674 (0.485–0.937)
LTF	0.019	0.678 (0.489–0.938)
CD8A	0.020	0.676 (0.486–0.941)
C1S	0.022	0.680 (0.489–0.945)
DST	0.022	0.682 (0.492–0.947)
IKZF1	0.022	0.680 (0.488–0.947)
DENND5A	0.022	0.684 (0.494–0.948)
PRF1	0.023	0.680 (0.488–0.948)
GPR18	0.023	0.685 (0.494–0.949)
CCNL1	0.023	0.685 (0.495–0.950)
CLCA2	0.024	0.685 (0.494–0.951)
NT5E	0.024	1.457 (1.051–2.019)
TACR1	0.024	0.689 (0.498–0.953)
OSMR	0.026	0.690 (0.499–0.956)
DGKA	0.026	0.690 (0.497–0.957)

Table S3 (continued)

Table S3 (*continued*)

Genes	P	HR (95% CI)
IL18	0.027	0.691 (0.498–0.958)
CD83	0.027	0.691 (0.498–0.959)
L3MBTL4	0.028	0.693 (0.500–0.961)
LTA4H	0.028	0.695 (0.502–0.962)
PIK3CD	0.030	0.696 (0.502–0.965)
ISG20	0.030	0.695 (0.500–0.965)
EOMES	0.030	0.693 (0.498–0.966)
IL7R	0.031	0.695 (0.499–0.967)
SIT1	0.032	0.698 (0.503–0.970)
GSN	0.032	0.696 (0.499–0.970)
ITGB4	0.033	0.700 (0.504–0.971)
ZAP70	0.033	0.700 (0.504–0.972)
FBLN5	0.034	0.702 (0.507–0.973)
HLA–DRB1	0.034	0.699 (0.503–0.973)
PTAFR	0.034	0.700 (0.503–0.974)
CD37	0.035	0.700 (0.503–0.975)
IL16	0.035	0.701 (0.503–0.976)
NCF4	0.036	0.704 (0.507–0.977)
CXCR3	0.036	0.704 (0.507–0.978)
EIF4E3	0.037	0.709 (0.512–0.980)
GP1BA	0.037	0.703 (0.504–0.979)
CLDN11	0.039	0.710 (0.513–0.982)
STAT5A	0.039	0.709 (0.512–0.982)
XCL1	0.039	0.709 (0.512–0.982)
MAFF	0.039	0.711 (0.514–0.983)
IFNAR1	0.039	1.412 (1.017–1.959)
MKNK1	0.040	0.708 (0.509–0.984)
CCL5	0.040	0.710 (0.512–0.985)
NEDD9	0.041	0.712 (0.514–0.986)
LAMP3	0.042	0.714 (0.516–0.988)
CCR5	0.042	0.710 (0.511–0.988)
AHR	0.042	0.714 (0.516–0.989)
GNAI2	0.043	0.714 (0.515–0.989)
ITGAL	0.043	0.713 (0.514–0.990)
BCL10	0.044	0.716 (0.518–0.990)
PLPP3	0.044	0.714 (0.515–0.991)
ICAM1	0.044	0.715 (0.516–0.991)
CTSO	0.046	0.715 (0.514–0.994)
GPR183	0.046	0.714 (0.513–0.995)
LCP1	0.047	0.720 (0.520–0.996)
KLRK1	0.048	0.718 (0.518–0.996)
IL10	0.048	1.394 (1.002–1.938)
LAT2	0.049	0.718 (0.516–0.999)
GZMB	0.049	0.719 (0.517–0.999)

cDC, conventional dendritic cell; HR, hazard ratio; CI, confidence interval.

Table S4 Spearman's correlation analysis between IL-2 and cells

Cell type	P value*	R
CD8+ Tcm	9.65E-106	0.599
aDC	9.75E-105	0.596
DC	4.04E-78	0.527
cDC	8.65E-78	0.526
CD8+ T-cells	3.29E-66	0.490
CD4+ memory T-cells	1.49E-44	0.408
CD4+ Tem	3.09E-42	0.398
B-cells	5.24E-37	0.373
Megakaryocytes	1.99E-35	0.366
CD4+ naive T-cells	5.46E-35	0.363
CD8+ naive T-cells	3.13E-29	0.332
Class-switched memory B-cells	5.30E-29	0.331
Stroma score	3.20E-27	0.321
Tregs	4.75E-25	0.308
Macrophages M1	7.49E-25	0.306
Fibroblasts	3.28E-22	0.289
iDC	2.70E-20	0.276
Adipocytes	2.95E-20	0.276
CD4+ T-cells	3.05E-20	0.276
Mesangial cells	5.71E-20	0.274
Endothelial cells	1.65E-18	0.263
Memory B-cells	3.04E-18	0.261
pDC	1.94E-17	0.255
HSC	2.62E-17	0.254
ly Endothelial cells	3.28E-17	0.253
mv Endothelial cells	5.23E-16	0.243
Macrophages	6.96E-15	0.234
CD8+ Tem	7.64E-15	0.234
Monocytes	9.99E-12	0.205
Tgd cells	1.26E-10	0.194
Macrophages M2	1.75E-10	0.193
naive B-cells	3.55E-10	0.190
Chondrocytes	8.00E-10	0.186
Plasma cells	7.14E-09	0.175
Astrocytes	1.07E-07	0.161
Basophils	6.28E-05	0.122
Th2 cells	7.39E-05	0.120
Keratinocytes	3.79E-04	0.108
Sebocytes	4.53E-04	0.107
Melanocytes	7.04E-04	0.103
GMP	1.14E-02	0.077
MEP	1.31E-03	−0.098
MSC	1.68E-04	−0.114
Th1 cells	1.11E-05	−0.133

Table S4 (*continued*)

Table S4 (*continued*)

Cell type	P value*	R
Smooth muscle	1.38E-11	−0.204
CLP	1.22E-16	−0.249
Myocytes	5.38E-23	−0.294
Neurons	1.96E-25	−0.310
Osteoblast	5.08E-41	−0.392

*, only cells with a P value <0.05 are listed. aDC, activated dendritic cell; cDC, conventional dendritic cell; CLP, common lymphoid progenitor; DC, dendritic cell; GMP, granulocyte-macrophage progenitor; HSC, hematopoietic stem cell; iDC, immature dendritic cell; MEP, megakaryocyte-erythroid progenitor; MSC, mesenchymal stem cell; pDC, plasmacytoid dendritic cell.