

Supplemental Table 1. Patient demographics

Characteristic, n (%)	Late stage VSCC (n=45)	Early stage VSCC (n=64)	p-value
Age (years) - median (range)	67 (42-98)	69 (40-91)	0.682
Smoking			0.876
No	22 (48.9%)	30 (46.9%)	
Current	12 (26.7%)	21 (32.8%)	
Stopped	4 (8.9%)	4 (6.2%)	
Unknown	7 (15.5%)	9 (14.1%)	
Immunosuppression			0.347
HIV	-		
Immunosuppressive medication	-	2 (3.1%)	
HPV/p53 status			<0.001
HPV positive	6 (13.3%)	23 (35.9%)	
HPV negative, p53 wild type	7 (15.6%)	20 (31.3%)	
HPV negative, p53 mutant	32 (71.1%)	21 (32.8%)	
FIGO stadium			<0.001
IA	-	3 (4.7%)	
IB	-	61 (95.3%)	
II	-	-	
IIIA	39 (86.7%)	-	
IIIB	6 (13.3%)	-	
Tumor size in cm			0.144
≤ 2cm	15 (33.3%)	34 (53.1%)	
2-4 cm	17 (37.8%)	18 (28.1%)	
≥ 4 cm	13 (28.9%)	11 (17.2%)	
Unknown		1 (1.6%)	
Invasion depth in mm			0.015
≤4mm	13 (28.9%)	33 (51.6%)	
>4mm	31 (68.9%)	29 (45.3%)	
Unknown	1 (2.2%)	2 (3.1%)	
Lymphovascular space invasion			0.149
No	35 (77.8%)	57 (89.0%)	
Yes	7 (15.5%)	3 (4.7%)	
Unknown	3 (6.7%)	4 (6.3%)	
Perineural growth			0.010
No	17 (37.8%)	31 (48.4%)	
Yes	8 (17.8%)	1 (1.6%)	
Unknown	20 (44.4%)	32 (50.0%)	
Primary treatment modality			<0.001
Surgery	21 (46.7%)	62 (96.8%)	
Surgery & (chemo)radiotherapy	24 (53.3%)	1 (1.6%)	
Unknown	-	1 (1.6%)	
Recurrence (60 months)			0.412
No	35 (77.8%)	44 (68.7%)	
Yes	10 (22.2%)	20 (31.3%)	
Overall survival (60 months)			0.004
Alive	27 (60.0%)	55 (85.9%)	
Dead	18 (40.0%)	9 (14.1%)	
Follow-up (median, IQR range)	Late stage VSCC (n=45)	Early stage VSCC (n=64)	p-value
Follow-up time, months	76.0 (7-134)	40.5 (1-201)	0.073
Time to recurrence, months	26.0 (6-84)	32.5 (7-125)	0.514

Supplemental Table 2. Study cohort gene expression profiling

Sample	FIGO stage	Molecular subtype	CD3 intraepithelial count (cells/mm ²)	Immunoscore	Infiltration
Sample 1	FIGO I/II	HPVpos	110,04	D	low
Sample 2	FIGO I/II	HPVneg/p53mut	34,27	D	low
Sample 3	FIGO I/II	HPVneg/p53wt	36,03	D	low
Sample 4	FIGO I/II	HPVneg/p53mut	13,78	D	low
Sample 5	FIGO I/II	HPVpos	119,38	D	low
Sample 6	FIGO I/II	HPVneg/p53mut	12,55	D	low
Sample 7	FIGO I/II	HPVneg/p53wt	35,19	D	low
Sample 8	FIGO I/II	HPVneg/p53wt	89,58	D	low
Sample 9	FIGO I/II	HPVneg/p53mut	33,74	AI	low
Sample 10	FIGO I/II	HPVpos	149,64	AI	low
Sample 11	FIGO I/II	HPVneg/p53wt	60,61	AI	low
Sample 12	FIGO I/II	HPVneg/p53wt	198,15	AI	low
Sample 13	FIGO I/II	HPVneg/p53mut	39,76	AI	low
Sample 14	FIGO I/II	HPVpos	35,47	AI	low
Sample 15	FIGO I/II	HPVpos	198,73	AI	low
Sample 16	FIGO I/II	HPVneg/p53mut	600,36	AE	high
Sample 17	FIGO I/II	HPVneg/p53mut	580,32	AE	high
Sample 18	FIGO I/II	HPVneg/p53mut	340,2	AE	high
Sample 19	FIGO I/II	HPVneg/p53wt	188,1	AE	high
Sample 20	FIGO I/II	HPVpos	573,49	AE	high
Sample 21	FIGO I/II	HPVneg/p53mut	248,5	AE	high
Sample 22	FIGO I/II	HPVneg/p53wt	1720,56	AE	high
Sample 23	FIGO I/II	HPVneg/p53wt	948,03	AE	high
Sample 24	FIGO I/II	HPVneg/p53mut	641,09	AE	high
Sample 25	FIGO I/II	HPVpos	607,1	AE	high
Sample 26*	FIGO I/II	HPVneg/p53wt	2719,33	AE	high
Sample 27	FIGO I/II	HPVpos	1140,16	I	high
Sample 28	FIGO I/II	HPVpos	637,84	I	high
Sample 29	FIGO I/II	HPVpos	611,58	I	high
Sample 30	FIGO I/II	HPVneg/p53wt	1895,25	I	high
Sample 31	FIGO III	HPVneg/p53mut	12,02	D	low
Sample 32	FIGO III	HPVneg/p53mut	13,07	D	low
Sample 33	FIGO III	HPVneg/p53mut	23,28	D	low
Sample 34	FIGO III	HPVneg/p53mut	31,61	D	low
Sample 35	FIGO III	HPVneg/p53mut	35,5	D	low
Sample 36*	FIGO III	HPVneg/p53mut	23,28	D	low
Sample 37	FIGO III	HPVneg/p53mut	30,1	AI	low
Sample 38	FIGO III	HPVpos	524,47	AI	low
Sample 39	FIGO III	HPVneg/p53mut	320,03	AE	high
Sample 40	FIGO III	HPVneg/p53mut	571,46	AE	high
Sample 41	FIGO III	HPVpos	584,39	I	high
Sample 42	FIGO III	HPVneg/p53wt	661,54	I	high

* excluded for further nanotraining analysis due to poor RNA quality.

D: deserted, AI: altered-immunosuppressed, AE: altered-excluded, I: inflamed

Supplemental Table 3. Gene lists

IO360 panel	Pancaner panel
A2M	ABL1
ACVR1C	ACVR1B
ADAM12	ACVR1C
ADGRE1	ACVR2A
ADM	AKT1
ADORA2A	AKT2
AKT1	AKT3
ALDOA	ALK
ALDOC	ALKBH2
ANGPT1	ALKBH3
ANGPT2	AMER1
ANGPTL4	AMH
ANLN	ANGPT1
APC	APC
APH1B	APH1B
API5	AR
APLNR	ARID1A
APOE	ARID1B
APOL6	ARID2
AQP9	ARNT2
AREG	ASXL1
ARG1	ATM
ARG2	ATR
ARID1A	ATRX
ARNT2	AXIN1
ATF3	AXIN2
ATM	B2M
AXIN1	BAD
AXL	BAIAP3
B2M	BAMBI
BAD	BAP1
BAMBI	BAX
BATF3	BCL2
BAX	BCL2A1
BBC3	BCL2L1
BBS1	BCOR
BCAT1	BDNF
BCL2	BID
BCL2L1	BIRC3
BCL6B	BIRC7
BID	BMP2
BIRC3	BMP4
BIRC5	BMP5
BLK	BMP6
BLM	BMP7
BMP2	BMP8A
BNIP3	BMPR1B
BNIP3L	BNIP3

BRCA1	BRAF
BRCA2	BRCA1
BRD3	BRCA2
BRD4	BRIP1
BRIP1	C19orf40
BTLA	CACNA1C
C1QA	CACNA1D
C1QB	CACNA1E
C2	CACNA1G
C5	CACNA1H
C5AR1	CACNA2D1
C7	CACNA2D2
CASP1	CACNA2D3
CASP3	CACNA2D4
CASP8	CACNB2
CASP9	CACNB3
CBLC	CACNB4
CCL13	CACNG1
CCL14	CACNG4
CCL18	CACNG6
CCL19	CALML3
CCL2	CALML5
CCL20	CALML6
CCL21	CAMK2B
CCL22	CAPN2
CCL3/L1	CARD11
CCL4	CASP10
CCL5	CASP12
CCL7	CASP3
CCL8	CASP7
CCNA1	CASP8
CCNB1	CASP9
CCND1	CBL
CCND2	CBLC
CCND3	CCNA1
CCNE1	CCNA2
CCNO	CCNB1
CCR2	CCNB3
CCR4	CCND1
CCR5	CCND2
CD14	CCND3
CD163	CCNE1
CD19	CCNE2
CD1C	CCNO
CD2	CCR7
CD209	CD14
CD244	CD19
CD247	CD40
CD27	CDC14A
CD274	CDC14B

CD276	CDC25A
CD28	CDC25B
CD300A	CDC25C
CD36	CDC6
CD38	CDC7
CD3D	CDH1
CD3E	CDK2
CD3G	CDK4
CD4	CDK6
CD40	CDKN1A
CD40LG	CDKN1B
CD44	CDKN1C
CD45RA	CDKN2A
CD45RB	CDKN2B
CD45RO	CDKN2C
CD47	CDKN2D
CD48	CEBPA
CD5	CEBPE
CD58	CHAD
CD6	CHEK1
CD68	CHEK2
CD69	CHUK
CD7	CIC
CD70	CLCF1
CD74	CNTRF
CD79A	COL11A1
CD79B	COL11A2
CD80	COL1A1
CD84	COL1A2
CD86	COL24A1
CD8A	COL27A1
CD8B	COL2A1
CD96	COL3A1
CDC20	COL4A3
CDC25C	COL4A4
CDH1	COL4A5
CDH11	COL4A6
CDH2	COL5A1
CDH5	COL5A2
CDK2	COL6A6
CDK6	COMP
CDKN1A	CREB3L1
CDKN1C	CREB3L3
CDKN2A	CREB3L4
CDKN2B	CREB5
CEACAM3	CREBBP
CEBPB	CRLF2
CENPF	CSF1R
CEP55	CSF2
CES3	CSF3

CHUK	CSF3R
CLEC14A	CTNNB1
CLEC4E	CUL1
CLEC5A	CXXC4
CLEC7A	CYLD
CLECL1	DAXX
CMKLR1	DDB2
CNTFR	DDIT3
COL11A1	DDIT4
COL11A2	DKK1
COL17A1	DKK2
COL4A5	DKK4
COL5A1	DLL1
COL6A3	DLL3
COMP	DLL4
CPA3	DNMT1
CRABP2	DNMT3A
CSF1	DTX1
CSF1R	DTX3
CSF2	DTX4
CSF2RB	DUSP10
CSF3	DUSP2
CSF3R	DUSP4
CST2	DUSP5
CTAG1B	DUSP6
CTLA4	DUSP8
CTNNB1	E2F1
CTSS	E2F5
CTSW	EFNA1
CX3CL1	EFNA2
CX3CR1	EFNA3
CXCL1	EFNA5
CXCL10	EGF
CXCL11	EGFR
CXCL12	EIF4EBP1
CXCL13	ENDOG
CXCL14	EP300
CXCL16	EPHA2
CXCL2	EPO
CXCL3	EPOR
CXCL5	ERBB2
CXCL6	ERCC2
CXCL8	ERCC6
CXCL9	ETS2
CXCR2	ETV1
CXCR3	ETV4
CXCR4	ETV7
CXCR6	EYA1
CXorf36	EZH2
CYBB	FANCA

DAB2	FANCB
DDB2	FANCC
DEFB134	FANCE
DEPTOR	FANCF
DKK1	FANCG
DLL1	FANCL
DLL4	FAS
DNMT1	FASLG
DPP4	FBXW7
DTX3L	FEN1
DTX4	FGF1
DUSP1	FGF10
DUSP2	FGF11
DUSP5	FGF12
E2F3	FGF13
EDN1	FGF14
EGF	FGF16
EGFR	FGF17
EGR1	FGF18
EIF2AK2	FGF19
EIF2B4	FGF2
EIF4EBP1	FGF20
EIF5AL1	FGF21
ELOB	FGF22
ENO1	FGF23
ENTPD1	FGF3
EOMES	FGF4
EPCAM	FGF5
EPM2AIP1	FGF6
ERBB2	FGF7
ERO1A	FGF8
ESR1	FGF9
EXO1	FGFR1
EZH2	FGFR2
F2RL1	FGFR3
FADD	FGFR4
FAM124B	FIGF
FAM30A	FLNA
FANCA	FLNC
FAP	FLT1
FAS	FLT3
FASLG	FN1
FBP1	FOS
FCAR	FOSL1
FCGR1A	FOXL2
FCGR2A	FOXO4
FCGR2B	FST
FCGR3A/B	FUBP1
FCGRT	FUT8
FCN1	FZD10

FCRL2	FZD2
FGF13	FZD3
FGF18	FZD7
FGF9	FZD8
FGFR1	FZD9
FLNB	GADD45A
FLT1	GADD45B
FOSL1	GADD45G
FOXP3	GAS1
FPR1	GATA1
FPR3	GATA2
FSTL3	GATA3
FUT4	GDF6
FYN	GHR
FZD8	GLI1
FZD9	GLI3
GAS1	GNA11
GBP1	GNAQ
GBP2	GNAS
GBP4	GNG12
GHR	GNG4
GIMAP4	GNG7
GIMAP6	GNGT1
GLI1	GPC4
GLS	GRB2
GLUD1	GRIA3
GLUL	GRIN1
GMIP	GRIN2A
GNG4	GRIN2B
GPLY	GSK3B
GOT1	GTF2H3
GOT2	GZMB
GPC4	H2AFX
GPR160	H3F3A
GPSM3	H3F3C
GZMA	HDAC1
GZMB	HDAC10
GZMH	HDAC11
GZMK	HDAC2
GZMM	HDAC4
H2AFX	HDAC5
HAVCR2	HDAC6
HCK	HELLS
HDAC11	HES1
HDAC3	HES5
HDAC4	HGF
HDAC5	HHEX
HDC	HHIP
HELLS	HIST1H3B
HERC6	HIST1H3G

HES1	HIST1H3H
HEY1	HMGA1
HIF1A	HMGA2
HK1	HNF1A
HK2	HOXA10
HLA-A	HOXA11
HLA-B	HOXA9
HLA-C	HPGD
HLA-DMA	HRAS
HLA-DMB	HSP90B1
HLA-DOA	HSPA1A
HLA-DOB	HSPA2
HLA-DPA1	HSPA6
HLA-DPB1	HSPB1
HLA-DQA1	IBSP
HLA-DQA2	ID1
HLA-DQB1	ID2
HLA-DRA	ID4
HLA-DRB1	IDH1
HLA-DRB5	IDH2
HLA-E	IFNA17
HLA-F	IFNA2
HMGA1	IFNA7
HMGB1	IFNG
HNF1A	IGF1
HRAS	IGF1R
HSD11B1	IGFBP3
ICAM1	IKBKB
ICAM2	IKBKG
ICAM3	IL10
ICAM5	IL11
ICOS	IL11RA
ICOSLG	IL12A
ID4	IL12B
IDO1	IL12RB2
IER3	IL13
IFI16	IL13RA2
IFI27	IL15
IFI35	IL19
IFI6	IL1A
IFIH1	IL1B
IFIT1	IL1R1
IFIT2	IL1R2
IFIT3	IL1RAP
IFITM1	IL20RA
IFITM2	IL20RB
IFNA1	IL22RA1
IFNAR1	IL22RA2
IFNG	IL23A
IFNGR1	IL23R

IFNGR2	IL24
IGF2R	IL2RA
IHH	IL2RB
IKBKB	IL3
IKBKG	IL3RA
IL10	IL5RA
IL10RA	IL6
IL11	IL6R
IL11RA	IL7
IL12RB2	IL7R
IL15	IL8
IL16	INHBA
IL17A	INHBB
IL18	IRAK2
IL18R1	IRAK3
IL1A	IRS1
IL1B	ITGA2
IL1R2	ITGA3
IL1RN	ITGA6
IL2	ITGA7
IL21R	ITGA8
IL22RA1	ITGA9
IL24	ITGB3
IL2RA	ITGB4
IL2RB	ITGB6
IL2RG	ITGB7
IL32	ITGB8
IL33	JAG1
IL34	JAG2
IL4	JAK1
IL6	JAK2
IL6R	JAK3
IL7R	JUN
INHBA	KAT2B
IRF1	KDM5C
IRF2	KDM6A
IRF3	KIT
IRF4	KITLG
IRF5	KLF4
IRF7	KMT2C
IRF8	KMT2D
IRF9	KRAS
ISG15	LAMA1
ITGA1	LAMA3
ITGA2	LAMA5
ITGA4	LAMB3
ITGA6	LAMB4
ITGAE	LAMC2
ITGAL	LAMC3
ITGAM	LAT

ITGAV	LEF1
ITGAX	LEFTY1
ITGB2	LEFTY2
ITGB3	LEP
ITGB8	LEPR
ITPK1	LFNG
JAG1	LIF
JAG2	LIFR
JAK1	LIG4
JAK2	LRP2
JAK3	LTBP1
KAT2B	MAD2L2
KDR	MAML2
KIF2C	MAP2K1
KIR2DL3	MAP2K2
KIR3DL1	MAP2K4
KIR3DL2	MAP2K6
KIT	MAP3K1
KLRB1	MAP3K12
KLRD1	MAP3K13
KLRK1	MAP3K14
KRAS	MAP3K5
LAG3	MAP3K8
LAIR1	MAPK1
LAMA1	MAPK10
LAMB3	MAPK12
LAMC2	MAPK3
LCK	MAPK8
LDHA	MAPK8IP1
LDHB	MAPK8IP2
LGALS9	MAPK9
LIF	MAPT
LILRA1	MCM2
LILRA3	MCM4
LILRA5	MCM5
LILRB2	MCM7
LILRB4	MDC1
LOXL2	MDM2
LRRC32	MECOM
LTB	MED12
LTBP1	MEN1
LY9	MET
LY96	MFNG
LYZ	MGMT
MAGEA1	MLF1
MAGEA12	MLH1
MAGEA3/A6	MLLT3
MAGEA4	MLLT4
MAGEB2	MMP3
MAGEC1	MMP7

MAGEC2	MMP9
MAML2	MNAT1
MAP3K12	MPL
MAP3K5	MPO
MAP3K7	MSH2
MAP3K8	MSH6
MAPK10	MTOR
MARCO	MUTYH
MB21D1	MYB
MELK	MYC
MET	MYCN
MFGE8	MYD88
MFNG	NASP
MGMT	NBN
MICA	NCOR1
MICB	NF1
MKI67	NF2
MLANA	NFATC1
MLH1	NFE2L2
MMP1	NFKB1
MMP7	NFKBIA
MMP9	NFKBIZ
MMRN2	NGF
MRC1	NGFR
MRE11	NKD1
MS4A1	NODAL
MS4A2	NOG
MS4A4A	NOS3
MS4A6A	NOTCH1
MSH2	NOTCH2
MSH6	NOTCH3
MTOR	NPM1
MX1	NPM2
MXI1	NR4A1
MYC	NR4A3
MYCT1	NRAS
MYD88	NSD1
NBN	NTF3
NCAM1	NTHL1
NCR1	NTRK1
NDUFA4L2	NTRK2
NECTIN1	NUMBL
NECTIN2	NUPR1
NEIL1	OSM
NF1	PAK3
NFAM1	PAK7
NFATC2	PAX3
NFIL3	PAX5
NFKB1	PAX8
NFKB2	PBRM1

NFKBIA	PBX1
NFKBIE	PBX3
NGFR	PCK1
NID2	PCNA
NKG7	PDGFA
NLRC5	PDGFB
NLRP3	PDGFC
NOD2	PDGFD
NOS2	PDGFRA
NOTCH1	PDGFRB
NOTCH2	PGF
NRAS	PHF6
NT5E	PIK3CA
OAS1	PIK3CB
OAS2	PIK3CD
OAS3	PIK3CG
OASL	PIK3R1
OLFML2B	PIK3R2
OLR1	PIK3R3
OTOA	PIK3R5
P2RY13	PIM1
P4HA1	PITX2
P4HA2	PKMYT1
PALMD	PLA1A
PARP12	PLA2G10
PARP4	PLA2G2A
PARP9	PLA2G3
PC	PLA2G4A
PCK2	PLA2G4C
PDCD1	PLA2G4E
PDCD1LG2	PLA2G4F
PDGFA	PLA2G5
PDGFB	PLAT
PDGFRB	PLAU
PDK1	PLCB1
PDZK1IP1	PLCB4
PECAM1	PLCE1
PF4	PLCG2
PFKFB3	PLD1
PFKM	PML
PGPEP1	POLB
PIAS4	POLD1
PIK3CA	POLD4
PIK3CD	POLE2
PIK3CG	POLR2D
PIK3R1	POLR2H
PIK3R2	POLR2J
PIK3R5	PPARG
PKM	PPARGC1A
PLA1A	PPP2CB

PLA2G2A	PPP2R1A
PLOD2	PPP2R2B
PMS2	PPP2R2C
PNOC	PPP3CA
POLD1	PPP3CB
PPARG	PPP3CC
PPARGC1B	PPP3R1
PRF1	PPP3R2
PRKAA2	PRDM1
PRKACB	PRKAA2
PRKCA	PRKACA
PRKX	PRKACB
PRLR	PRKACG
PROM1	PRKAR1B
PRR5	PRKAR2A
PSMB10	PRKAR2B
PSMB5	PRKCA
PSMB8	PRKCB
PSMB9	PRKCG
PTCD2	PRKDC
PTEN	PRKX
PTGER4	PRL
PTGS2	PRLR
PTPN11	PRMT8
PTPRC	PROM1
PVR	PTCH1
PVRIG	PTCRA
RAD50	PTEN
RAD51	PTPN11
RAD51C	PTPN5
RASAL1	PTPRR
RASGRF1	PTTG2
RB1	RAC1
RBL2	RAC2
RELA	RAC3
RELB	RAD21
RELN	RAD50
REN	RAD51
RICTOR	RAD52
RIPK1	RAF1
RIPK2	RASA4
RIPK3	RASAL1
RNLS	RASGRF1
ROBO4	RASGRF2
ROCK1	RASGRP1
ROR2	RASGRP2
RORC	RB1
RPL23	RBX1
RPL7A	RELA
RPS6KB1	RELN

RPTOR	RET
RRM2	RFC3
RSAD2	RFC4
RUNX3	RHOA
S100A12	RIN1
S100A8	RNF43
S100A9	RPA3
SAMD9	RPS27A
SAMSN1	RPS6KA5
SBNO2	RPS6KA6
SELE	RRAS2
SELL	RUNX1
SELP	RUNX1T1
SERPINA1	RXRG
SERPINB5	SETBP1
SERPINH1	SETD2
SFRP1	SF3B1
SFRP4	SFN
SFXN1	SFRP1
SGK1	SFRP2
SH2D1A	SFRP4
SHC2	SGK2
SIGLEC1	SHC1
SIGLEC5	SHC2
SIGLEC8	SHC3
SIRPA	SHC4
SIRPB2	SIN3A
SLAMF7	SIRT4
SLC11A1	SIX1
SLC16A1	SKP1
SLC1A5	SKP2
SLC2A1	SMAD2
SLC7A5	SMAD3
SMAD5	SMAD4
SMAP1	SMAD9
SNAI1	SMARCA4
SNCA	SMARCB1
SOCS1	SMC1A
SOX10	SMC1B
SOX11	SMC3
SOX2	SMO
SPIB	SOCS1
SPP1	SOCS2
SPRY4	SOCS3
SREBF1	SOS1
SRP54	SOS2
STAT1	SOST
STAT2	SOX17
STAT3	SOX9
STAT4	SP1

STC1	SPOP
SYK	SPP1
TAF3	SPRY1
TAP1	SPRY2
TAP2	SPRY4
TAPBP	SRSF2
TAPBPL	SSX1
TBX21	STAG2
TBXAS1	STAT1
TCF3	STAT3
TCL1A	STAT4
TDO2	STK11
TGFB1	STMN1
TGFB2	SUV39H2
TGFB3	SYK
TGFBR1	TBL1XR1
TGFBR2	TCF3
THBD	TCF7L1
THBS1	TCL1B
THY1	TET2
TICAM1	TFDP1
TIE1	TGFB1
TIGIT	TGFB2
TLR1	TGFB3
TLR2	TGFBR2
TLR3	THBS1
TLR4	THBS4
TLR5	THEM4
TLR7	TIAM1
TLR8	TLR2
TLR9	TLR4
TMEM140	TLX1
TMEM173	TMPRSS2
TNF	TNC
TNFAIP3	TNF
TNFAIP6	TNFAIP3
TNFRSF10B	TNFRSF10A
TNFRSF10C	TNFRSF10B
TNFRSF10D	TNFRSF10C
TNFRSF11A	TNFRSF10D
TNFRSF11B	TNFSF10
TNFRSF14	TNN
TNFRSF17	TNR
TNFRSF18	TP53
TNFRSF1A	TPO
TNFRSF1B	TRAF7
TNFRSF25	TSC1
TNFRSF4	TSHR
TNFRSF8	TSLP
TNFRSF9	TSPAN7

TNFSF10	TTK
TNFSF12	U2AF1
TNFSF13	UBB
TNFSF13B	UBE2T
TNFSF18	UTY
TNFSF4	VEGFA
TNFSF8	VEGFC
TNFSF9	VHL
TNKS	WEE1
TP53	WHSC1
TPI1	WHSC1L1
TPM1	WIF1
TPSAB1/B2	WNT10A
TRAF1	WNT10B
TRAT1	WNT11
TREM1	WNT16
TREM2	WNT2
TRIM21	WNT2B
TSLP	WNT3
TTC30A	WNT4
TWF1	WNT5A
TWIST1	WNT5B
TWIST2	WNT6
TYMP	WNT7A
TYMS	WNT7B
UBA7	WT1
UBE2C	XPA
UBE2T	XRCC4
ULBP2	ZAK
VCAM1	ZBTB16
VCAN	ZBTB32
VEGFA	ZIC2
VEGFB	Internal Reference Genes
VEGFC	ACAD9
VHL	AGK
VSIR	AMMECR1L
VTCN1	C10orf76
WDR76	CC2D1B
WNT10A	CNOT10
WNT11	CNOT4
WNT2	COG7
WNT2B	DDX50
WNT3A	DHX16
WNT4	DNAJC14
WNT5A	EDC3
WNT5B	EIF2B4
WNT7B	ERCC3
XCL1/2	FCF1
ZAP70	FTSJ2
ZC3H12A	GPATCH3

ZEB1	HDAC3
ZEB2	MRPS5
Internal Reference Genes	MTMR14
ABCF1	NOL7
DNAJC14	NUBP1
ERCC3	PIAS1
G6PD	PIK3R4
GUSB	PRPF38A
MRPL19	RBM45
NRDE2	SAP130
OAZ1	SF3A3
POLR2A	SLC4A1AP
PSMC4	TLK2
PUM1	TMUB2
SDHA	TRIM39
SF3A1	TTC31
STK11IP	USP39
TBC1D10B	VPS33B
TBP	ZC3H14
TFRC	ZKSCAN5
TLK2	ZNF143
TMUB2	ZNF346
UBB	ZNF384

Supplemental table 4. Automated cell type profiling

Cell type	Number of genes	Genes
B cells	8	<i>FCRL2, TNFRSF17, PNOX, MS4A1, TCL1A, CD19, SPIB, FAM30A</i>
CD45 ⁺ cells	1	<i>CD45RA, PTPRC, CD45RO</i>
CD8 ⁺ T cells	2	<i>CD8A, CD8B</i>
Cytotoxic cells	10	<i>CTSW, NKG7, KLRK1, PRF1, GZMA, GZMB, GZMH, KLRD1, KLRB1, GNLY</i>
DCs	3	<i>CCL13, CD209, HSD11B1</i>
Exhausted CD8 ⁺ cells	4	<i>CD244, LAG3, EOMES, PTGER4</i>
Macrophages	4	<i>CD68, CD84, MS4A4A, CD163</i>
Mast cells	3	<i>HDC, TPSAB1/B2, MS4A2, CPA3</i>
Neutrophils	6	<i>FPR1, FCAR, FCGR3A/B, CSF3R, CEACAM3, S100A12</i>
NK CD56dim cells	4	<i>IL21R</i>
NK cells	1	<i>XCL1/2, NCR1</i>
T cells	6	<i>TRAT1, CD3D, CD3G, CD6, CD3E, SH2D1A</i>
<i>TBX21</i> ⁺ cells	1	<i>TBX21</i>
Tregs	1	<i>FOXP3</i>

Supplemental Table 5. Uni- and multivariate analysis for overall survival and recurrence-free period.

Variable	5-years overall survival				5-years recurrence-free period			
	HR crude	p-value	HR adjusted	p-value	HR crude	p-value	HR adjusted	p-value
Intraepithelial CD3+ (low/high)	12.504	0.001	8.310	0.005	2.615	0.014	2.573	0.025
Stage (early/late)			1.936	0.116	0.811	0.589	0.533	0.119
Molecular subtype								
HPVpos	REF	0.056	REF	0.452	REF	0.192	REF	0.402
HPVneg/p53wt	5.944	0.096	3.364	0.262	2.194	0.246	2.034	0.298
HPVneg/p53mut	9.843	0.026	3.747	0.208	3.012	0.076	2.413	0.177
Intraepithelial CD3+CD8-Foxp3- (low/high)	17.17	0.005	12.146	0.015	3.490	0.006	3.213	0.013
Stage (early/late)			2.287	0.050	0.811	0.589	0.589	0.184
Molecular subtype								
HPVpos	REF	0.056	REF	0.404	REF	0.192	REF	0.354
HPVneg/p53wt	5.944	0.096	3.551	0.240	2.194	0.246	2.005	0.308
HPVneg/p53mut	9.843	0.026	4.086	0.180	3.012	0.076	2.508	0.153
Intraepithelial CD3+CD8+ Foxp3- (low/high)	4.052	0.001	3.061	0.008	2.685	0.017	2.168	0.069
Stage (early/late)			2.298	0.053	0.811	0.589	0.685	0.342
Molecular subtype								
HPVpos	REF	0.056	REF	0.276	REF	0.192	REF	0.258
HPVneg/p53wt	5.944	0.096	4.988	0.134	2.194	0.246	1.979	0.320
HPVneg/p53mut	9.843	0.026	5.319	0.110	3.012	0.076	2.168	0.112

HR = hazard ratio

Supplemental table 6A. List of single gene RNA that significantly differ between molecular subtypes using oncogenic pathway panel in 29 early-stage V5CC.

	Gene	Log2 fold change	std error (log2)	Lower confidence limit (log2)	Upper confidence limit (log2)	Linear fold change	Lower confidence limit (linear)	Upper confidence limit (linear)	BH p-value	Pathways	
HPV/posV5CC vs HPV/negV5CC/p53wt	<i>BRIP1</i>	-1.04	0.305	-1.64	-0.447	0.485	0.321	0.734	0.0359	DNA Damage - Repair	
	<i>CACNA2D3</i>	-2.01	0.612	-3.21	-0.81	0.248	0.108	0.57	0.0403	MAPK	
	<i>CACNG4</i>	-2.02	0.647	-3.29	-0.755	0.246	0.102	0.592	0.0496	MAPK	
	<i>CCNE2</i>	-1.45	0.246	-1.93	-0.965	0.367	0.262	0.512	0.000564	Cell Cycle - Apoptosis, PI3K	
	<i>CDC25C</i>	-1.01	0.257	-1.51	-0.509	0.496	0.35	0.703	0.0138	Cell Cycle - Apoptosis	
	<i>CDKN1C</i>	-1.45	0.442	-2.31	-0.58	0.367	0.201	0.669	0.0403	Cell Cycle - Apoptosis	
	<i>CDKN2A</i>	-2.64	0.574	-3.76	-1.51	0.161	0.0737	0.35	0.00376	Cell Cycle - Apoptosis, Driver Gene	
	<i>CREB3L4</i>	-1.03	0.319	-1.65	-0.4	0.491	0.318	0.758	0.0437	PI3K	
	<i>E2F1</i>	-1.22	0.265	-1.74	-0.704	0.428	0.298	0.614	0.00376	Cell Cycle - Apoptosis	
	<i>FANCA</i>	-1.07	0.206	-1.47	-0.661	0.478	0.361	0.632	0.0015	DNA Damage - Repair	
	<i>FANCB</i>	-1.21	0.256	-1.71	-0.71	0.432	0.305	0.611	0.00294	DNA Damage - Repair	
	<i>GADD45B</i>	1.26	0.266	0.744	1.79	2.4	1.68	3.45	0.00294	Cell Cycle - Apoptosis, MAPK	
	<i>MCM2</i>	-1.25	0.238	-1.72	-0.785	0.42	0.304	0.581	0.00133	Cell Cycle - Apoptosis	
	<i>MCM5</i>	-1.1	0.219	-1.53	-0.672	0.466	0.346	0.628	0.00175	Cell Cycle - Apoptosis	
	<i>MECOM</i>	-4.49	0.833	-6.13	-2.86	0.0443	0.0143	0.137	0.00103	MAPK	
	<i>MMP3</i>	2.42	0.715	1.02	3.82	5.36	2.03	14.2	0.0375	Transcriptional Misregulation	
	<i>MYB</i>	-2.34	0.643	-3.6	-1.08	0.198	0.0826	0.474	0.0273	PI3K	
	<i>NASP</i>	-1.12	0.223	-1.56	-0.686	0.459	0.339	0.621	0.00175	Chromatin Modification	
	<i>POLE2</i>	-1.27	0.178	-1.62	-0.918	0.416	0.326	0.529	9.00E-05	DNA Damage - Repair	
	<i>STMN1</i>	-1.06	0.321	-1.69	-0.434	0.478	0.309	0.74	0.0398	MAPK	
	<i>TGFB1</i>	1.19	0.218	0.76	1.61	2.28	1.69	3.06	0.00103	Cell Cycle - Apoptosis, MAPK, TGF-beta	
	<i>WNT5A</i>	1.03	0.295	0.457	1.61	2.05	1.37	3.06	0.0337	Hedgehog, Wnt	
	HPV/posV5CC vs HPV/negV5CC/p53mut	<i>BRIP1</i>	-1.23	0.297	-1.81	-0.644	0.428	0.286	0.64	0.00837	DNA Damage - Repair
		<i>CALML3</i>	1.59	0.485	0.641	2.54	3.01	1.56	5.83	0.0334	Ras
		<i>CCNE2</i>	-1.26	0.239	-1.73	-0.791	0.417	0.302	0.578	0.00114	Cell Cycle - Apoptosis, PI3K
		<i>CDC25C</i>	-1.05	0.25	-1.54	-0.557	0.484	0.345	0.68	0.0079	Cell Cycle - Apoptosis
<i>CDC7</i>		-1.11	0.214	-1.53	-0.688	0.464	0.347	0.621	0.0013	Cell Cycle - Apoptosis	
<i>CDKN1C</i>		-1.36	0.43	-2.2	-0.517	0.389	0.217	0.699	0.0404	Cell Cycle - Apoptosis	
<i>CDKN2A</i>		-1.99	0.558	-3.08	-0.893	0.252	0.118	0.539	0.0214	Cell Cycle - Apoptosis, Driver Gene	
<i>CDKN2C</i>		-1.17	0.279	-1.72	-0.626	0.443	0.303	0.648	0.0079	Cell Cycle - Apoptosis, Transcriptional Misregulation	
<i>COL4A5</i>		1.73	0.419	0.905	2.55	3.31	1.87	5.84	0.00837	PI3K	
<i>COL4A6</i>		1.77	0.545	0.699	2.84	3.4	1.62	7.14	0.0355	PI3K	
<i>E2F1</i>		-1.37	0.259	-1.87	-0.859	0.388	0.273	0.551	0.00114	Cell Cycle - Apoptosis	
<i>EGFR</i>		2.13	0.548	1.05	3.2	4.36	2.07	9.18	0.0145	Driver Gene, MAPK, PI3K, Ras	
<i>FANCC</i>		-1	0.204	-1.4	-0.603	0.499	0.379	0.658	0.00232	DNA Damage - Repair	
<i>GRIA3</i>		1.34	0.42	0.514	2.16	2.53	1.43	4.47	0.0391	Transcriptional Misregulation	
<i>IL24</i>		1.73	0.58	0.595	2.87	3.32	1.51	7.31	0.0493	JAK-STAT	
<i>MECOM</i>		-4.63	0.811	-6.22	-3.04	0.0403	0.0134	0.121	0.000525	MAPK	
<i>MMP3</i>		2.46	0.696	1.09	3.82	5.5	2.14	14.1	0.0223	Transcriptional Misregulation	
<i>MYB</i>		-2.96	0.626	-4.18	-1.73	0.129	0.0551	0.302	0.00335	PI3K	
<i>NASP</i>		-1.33	0.217	-1.76	-0.907	0.397	0.295	0.533	0.000214	Chromatin Modification	
<i>NKD1</i>		1.06	0.321	0.436	1.69	2.09	1.35	3.23	0.0323	Wnt	
<i>PLAU</i>		1.33	0.396	0.556	2.11	2.52	1.47	4.32	0.0306	Transcriptional Misregulation	
<i>POLD4</i>		1.04	0.241	0.566	1.51	2.05	1.48	2.85	0.00671	DNA Damage - Repair	
<i>POLE2</i>		-1.18	0.173	-1.52	-0.841	0.441	0.349	0.558	6.1e-05	DNA Damage - Repair	
<i>SFN</i>		1.12	0.336	0.46	1.78	2.17	1.38	3.43	0.0323	Cell Cycle - Apoptosis	
<i>SPRY4</i>		1.11	0.327	0.473	1.76	2.16	1.39	3.38	0.0289	JAK-STAT	
<i>STMN1</i>		-1.45	0.313	-2.06	-0.833	0.367	0.24	0.561	0.00372	MAPK	
<i>TMPPSS2</i>		-3.88	1.11	-6.06	-1.7	0.0679	0.0149	0.309	0.0248	Transcriptional Misregulation	
<i>UBE2T</i>		-1.03	0.16	-1.34	-0.714	0.491	0.395	0.609	0.000124	DNA Damage - Repair	
<i>WNT3</i>		1.69	0.499	0.714	2.67	3.23	1.64	6.37	0.0292	Hedgehog, Wnt	
<i>WNT7A</i>		1.59	0.527	0.562	2.63	3.02	1.48	6.18	0.0471	Hedgehog, Wnt	
<i>ZBTB16</i>		-2.84	0.75	-4.31	-1.37	0.14	0.0505	0.388	0.0169	Transcriptional Misregulation	

MECOM was excluded from analysis due to overlap between the median and 95%CI.

BH p-value = Benjamini-Hochberg adjusted p-value

Supplemental table 6B. List of single gene RNA that significantly differ between molecular subtypes using IO360 panel in 40 early- and late-stage VSCC.

	Gene	Log2 fold change	std error (log2)	Lower confidence limit (log2)	Upper confidence limit (log2)	Linear fold change	Lower confidence limit (linear)	Upper confidence limit (linear)	BH p-value	Pathways
HPVpos vs HPVneg/p53w	CDKN2A	-2,46	0,565	-3,57	-1,35	0,182	0,0845	0,392	0,0348	Cell Proliferation, Metabolic Stress
	MMP1	3,22	0,596	2,05	4,39	9,34	4,15	21	0,00365	Matrix Remodeling and Metastasis, Myeloid Compartment
HPVpos vs HPVneg/p53mut	MMP1	-1,12	0,168	-1,45	-0,788	0,461	0,367	0,579	0,0000776	Matrix Remodeling and Metastasis, Myeloid Compartment
	COL4A5	3,01	0,495	2,04	3,98	8,08	4,13	15,8	0,000157	Matrix Remodeling and Metastasis, Myeloid Compartment
	COL4A5	1,46	0,29	0,895	2,03	2,76	1,86	4,09	0,00151	Matrix Remodeling and Metastasis, PI3K-Akt
	PC	1,59	0,311	0,977	2,2	3	1,97	4,58	0,00151	Metabolic Stress
	COL17A1	2,04	0,423	1,21	2,87	4,11	2,31	7,29	0,0023	Matrix Remodeling and Metastasis, Myeloid Compartment
	MELK	-1,04	0,224	-1,48	-0,6	0,487	0,359	0,66	0,00251	Cell Proliferation
	SPRY4	1,07	0,243	0,597	1,55	2,1	1,51	2,93	0,00411	Cytotoxicity
	LTBP1	1,07	0,256	0,565	1,57	2,09	1,48	2,97	0,00719	Matrix Remodeling and Metastasis, TGF-beta Signaling
	CDKN2A	-1,94	0,468	-2,86	-1,02	0,261	0,138	0,492	0,00732	Cell Proliferation, Metabolic Stress
	CXCL14	1,74	0,427	0,899	2,57	3,33	1,87	5,95	0,00773	Cytokine and Chemokine Signaling
	TDO2	1,79	0,445	0,918	2,66	3,46	1,89	6,33	0,00833	
	SLC7A5	1,01	0,259	0,502	1,52	2,01	1,42	2,86	0,0103	Metabolic Stress
	IFI27	1,21	0,31	0,604	1,82	2,32	1,52	3,53	0,0103	Cytotoxicity, Interferon Signaling, Lymphoid Compartment
	FADD	1,36	0,347	0,676	2,04	2,56	1,6	4,1	0,0103	Apoptosis
	DUSP2	-1,11	0,289	-1,68	-0,544	0,463	0,313	0,686	0,0113	MAPK
	BCL2	-1,38	0,365	-2,1	-0,663	0,385	0,234	0,632	0,013	Apoptosis, Autophagy, Hypoxia, JAK-STAT Signaling, PI3K-Akt
	EGFR	1,51	0,404	0,719	2,3	2,85	1,65	4,94	0,0135	Hypoxia, MAPK, Metabolic Stress, PI3K-Akt
	WNT10A	1,02	0,276	0,481	1,56	2,03	1,4	2,95	0,0139	Hedgehog Signaling, Wnt Signaling
	CD70	-1,8	0,498	-2,77	-0,821	0,288	0,146	0,566	0,0171	Costimulatory Signaling, Lymphoid Compartment, NF-kappaB Signaling
	COL5A1	1,08	0,302	0,489	1,67	2,11	1,4	3,18	0,0179	Matrix Remodeling and Metastasis
	IFI1	1,63	0,465	0,721	2,54	3,1	1,65	5,83	0,0207	Cytotoxicity, Interferon Signaling, Lymphoid Compartment
	GLUL	-1,02	0,295	-1,6	-0,441	0,493	0,33	0,737	0,0229	
	TGFB3	1,15	0,34	0,487	1,82	2,22	1,4	3,53	0,0254	MAPK, Matrix Remodeling and Metastasis, TGF-beta Signaling
	CCL21	1,26	0,38	0,515	2	2,39	1,43	4,01	0,0306	Cytokine and Chemokine Signaling
	IER3	1,11	0,348	0,432	1,8	2,16	1,35	3,47	0,0376	Myeloid Compartment
	HERC6	1,13	0,358	0,433	1,84	2,2	1,35	3,57	0,039	
	WNT2B	-1,46	0,469	-2,38	-0,544	0,362	0,192	0,686	0,0439	Hedgehog Signaling, Wnt Signaling

Supplemental table 7. List of single gene RNA that significantly differ between 40 high and low infiltrated tumors using IO360 panel.

Gene	Lower		Upper		Lower		Upper		BH p-value	Pathways
	Log2 fold change	std error	confidence limit (log2)	confidence limit (log2)	Linear fold change	confidence limit (linear)	confidence limit (linear)			
DKK1	-1.83	0.485	-2.78	-0.877	0.282	0.146	0.544	0.00464		Wnt Signaling
NDUFA4L2	-1.24	0.373	-1.97	-0.507	0.424	0.256	0.704	0.0121		
EGFR	-1.22	0.336	-1.88	-0.564	0.429	0.272	0.677	0.0062		Hypoxia, MAPK, Metabolic Stress, PI3K-Akt
CDKN2B	-1.1	0.416	-1.91	-0.285	0.467	0.265	0.821	0.00492		Cell Proliferation, Metabolic Stress, TGF-beta Signaling
CD2	1.01	0.325	0.367	1.64	2.01	1.29	3.12	0.0199		Costimulatory Signaling, Immune Cell Adhesion and Migration, Lymphoid Compartment
HLA-DRA	1.01	0.22	0.577	1.44	2.01	1.49	2.71	0.000893		Antigen Presentation, Costimulatory Signaling, Immune Cell Adhesion and Migration, Interferon Signaling
JAK3	1.03	0.262	0.521	1.55	2.05	1.43	2.92	0.00335		Cytokine and Chemokine Signaling, Cytotoxicity, JAK-STAT Signaling, PI3K-Akt
C10B	1.04	0.342	0.366	1.71	2.05	1.29	3.26	0.0226		
CD5	1.04	0.262	0.531	1.56	2.06	1.44	2.94	0.00319		Lymphoid Compartment
CD84	1.04	0.214	0.624	1.46	2.06	1.54	2.75	0.000469		
LTB	1.04	0.331	0.393	1.69	2.06	1.31	3.22	0.0176		NF-kappaB Signaling
CD48	1.05	0.294	0.474	1.63	2.07	1.39	3.09	0.00713		Costimulatory Signaling, Lymphoid Compartment
SELL	1.05	0.344	0.373	1.72	2.07	1.3	3.3	0.022		Immune Cell Adhesion and Migration
HLA-DMB	1.06	0.235	0.597	1.52	2.08	1.51	2.87	0.00106		Antigen Presentation, Immune Cell Adhesion and Migration
LILRB2	1.07	0.273	0.534	1.6	2.1	1.45	3.04	0.00353		Costimulatory Signaling, Myeloid Compartment
CD84	1.08	0.272	0.545	1.61	2.11	1.46	3.06	0.00332		
IL2RA	1.09	0.283	0.537	1.65	2.13	1.45	3.13	0.004		Costimulatory Signaling, Cytokine and Chemokine Signaling, JAK-STAT Signaling, PI3K-Akt
CD45RB	1.1	0.287	0.535	1.66	2.14	1.45	3.16	0.00412		
P2RY13	1.1	0.26	0.585	1.61	2.14	1.5	3.04	0.00188		Myeloid Compartment
HLA-DPB1	1.12	0.224	0.678	1.56	2.17	1.6	2.94	0.000361		Antigen Presentation, Costimulatory Signaling, Immune Cell Adhesion and Migration, Interferon Signaling
PDCD1LG2	1.13	0.266	0.606	1.65	2.18	1.52	3.13	0.00181		Costimulatory Signaling, Immune Cell Adhesion and Migration
BIRC3	1.15	0.261	0.638	1.66	2.22	1.56	3.16	0.00122		Antigen Presentation, Hypoxia, Immune Cell Adhesion and Migration, Myeloid Compartment
STAT4	1.15	0.215	0.725	1.57	2.22	1.65	2.97	0.000197		Costimulatory Signaling, JAK-STAT Signaling
CCL3L1	1.16	0.305	0.565	1.76	2.24	1.48	3.39	0.00419		Cytokine and Chemokine Signaling
CD80	1.16	0.242	0.684	1.63	2.23	1.61	3.1	0.000592		Costimulatory Signaling, Immune Cell Adhesion and Migration, Lymphoid Compartment
PTPRC	1.16	0.285	0.602	1.72	2.24	1.52	3.29	0.00258		Costimulatory Signaling, Immune Cell Adhesion and Migration
BIRC3	1.17	0.316	0.555	1.79	2.26	1.47	3.47	0.00524		Apoptosis, NF-kappaB Signaling
CD28	1.17	0.329	0.803	1.65	2.25	1.62	3.14	0.000587		Antigen Presentation, Cytokine and Chemokine Signaling, Myeloid Compartment
CTLA4	1.17	0.265	0.647	1.69	2.25	1.57	3.22	0.00122		Costimulatory Signaling, Immune Cell Adhesion and Migration, Lymphoid Compartment
FBP1	1.17	0.405	0.381	1.97	2.26	1.3	3.91	0.0296		Metabolic Stress
HAVCR2	1.18	0.288	0.615	1.74	2.26	1.53	3.35	0.00244		Costimulatory Signaling
KLRF1	1.18	0.308	0.58	1.79	2.27	1.5	3.45	0.00405		Cytotoxicity, Lymphoid Compartment
TIGIT	1.19	0.267	0.667	1.72	2.28	1.59	3.28	0.00112		Costimulatory Signaling, Immune Cell Adhesion and Migration, Lymphoid Compartment
CCL4	1.2	0.315	0.735	1.57	2.3	1.5	3.52	0.00418		Antigen Presentation, Cytokine and Chemokine Signaling, Myeloid Compartment
HLA-DRB1	1.21	0.333	0.553	1.86	2.31	1.47	3.63	0.00649		Antigen Presentation, Costimulatory Signaling, Immune Cell Adhesion and Migration, Interferon Signaling
IRF8	1.21	0.265	0.69	1.73	2.31	1.61	3.32	0.000929		Antigen Presentation, Interferon Signaling
CD45RO	1.24	0.226	0.797	1.68	2.36	1.74	3.21	0.00015		
LILRB4	1.24	0.365	0.527	1.96	2.37	1.44	3.89	0.00996		
IL2RG	1.25	0.227	0.785	1.71	2.38	1.72	3.28	0.000201		Costimulatory Signaling, Cytokine and Chemokine Signaling, JAK-STAT Signaling, Lymphoid Compartment, PI3K-Akt
CD5	1.27	0.25	0.783	1.76	2.41	1.72	3.39	0.000288		Immune Cell Adhesion and Migration, Lymphoid Compartment
GBP4	1.29	0.3	0.704	1.88	2.45	1.63	3.68	0.00155		Interferon Signaling
IL2RB	1.32	0.251	0.826	1.81	2.49	1.77	3.51	0.000206		Costimulatory Signaling, Cytokine and Chemokine Signaling, JAK-STAT Signaling, PI3K-Akt
ITGAL	1.35	0.258	0.841	1.85	2.54	1.79	3.61	0.000206		Immune Cell Adhesion and Migration, Matrix Remodeling and Metastasis
MS4A1	1.36	0.436	0.502	2.21	2.56	1.42	4.63	0.0189		Lymphoid Compartment
FCGR1A	1.38	0.334	0.728	2.04	2.61	1.66	4.11	0.00221		Antigen Presentation, Interferon Signaling, Myeloid Compartment
LOK	1.39	0.266	0.868	1.91	2.62	1.82	3.76	0.000206		Costimulatory Signaling, Lymphoid Compartment
CD96	1.42	0.255	0.922	1.92	2.68	1.9	3.78	0.000119		Lymphoid Compartment
CCR5	1.43	0.234	0.972	1.89	2.7	1.96	3.71	4.51e-05		Antigen Presentation, Cytokine and Chemokine Signaling
CD7	1.43	0.263	0.915	1.95	2.7	1.89	3.86	0.000157		Lymphoid Compartment
CD30	1.44	0.244	0.962	1.92	2.71	1.95	3.78	6.05e-05		Costimulatory Signaling, Lymphoid Compartment
CD274	1.45	0.329	0.803	2.09	2.73	1.74	4.26	0.00122		Costimulatory Signaling, Immune Cell Adhesion and Migration, Lymphoid Compartment
GZMK	1.46	0.296	0.879	2.04	2.75	1.84	4.11	0.000414		Cytotoxicity, Lymphoid Compartment
LYZ	1.46	0.308	0.859	2.07	2.76	1.81	4.19	0.000613		Myeloid Compartment
TNFRSF9	1.48	0.245	0.996	1.96	2.78	2	3.88	5.13e-05		
TRAT1	1.48	0.354	0.785	2.17	2.79	1.72	4.51	0.00201		Costimulatory Signaling
CXCL11	1.51	0.529	0.473	2.55	2.85	1.39	5.84	0.0329		Cytokine and Chemokine Signaling, Lymphoid Compartment
SH2D1A	1.52	0.283	0.962	2.07	2.86	1.95	4.2	0.000187		
ZAP70	1.53	0.257	1.03	2.04	2.89	2.04	4.1	5.7e-05		Costimulatory Signaling, Lymphoid Compartment, MAPK
CD3E	1.56	0.305	0.964	2.16	2.95	1.95	4.47	0.000267		Costimulatory Signaling, Lymphoid Compartment
CXCL10	1.61	0.451	0.724	2.49	3.05	1.65	5.63	0.00722		Cytokine and Chemokine Signaling, Lymphoid Compartment
CD8B	1.7	0.265	1.18	2.22	3.25	2.27	4.65	4.06e-05		Antigen Presentation, Immune Cell Adhesion and Migration, Lymphoid Compartment
CTSW	1.75	0.351	1.11	2.4	3.37	2.15	5.29	0.000197		Antigen Presentation
CXCL9	1.76	0.416	0.94	2.57	3.38	1.92	5.94	0.00186		Cytokine and Chemokine Signaling, Lymphoid Compartment
KLRF1	1.76	0.306	1.17	2.36	3.4	2.24	5.15	7.61e-05		Cytotoxicity, Lymphoid Compartment
KLRD1	1.77	0.338	1.1	2.43	3.4	2.15	5.38	0.000206		Antigen Presentation, Cytotoxicity, Lymphoid Compartment
CXCR6	1.78	0.279	1.24	2.33	3.44	2.36	5.03	4.06e-05		Cytokine and Chemokine Signaling
CXCL13	1.8	0.425	0.965	2.63	3.48	1.95	6.2	0.00183		Cytokine and Chemokine Signaling, Lymphoid Compartment
LAD3	1.81	0.33	1.16	2.45	3.5	2.23	5.47	0.00015		Costimulatory Signaling, Lymphoid Compartment
IDO1	1.84	0.414	1.02	2.65	3.57	2.03	6.26	0.00116		Lymphoid Compartment
IFNG	1.84	0.586	0.689	2.98	3.57	1.61	7.91	0.0181		Antigen Presentation, Cytotoxicity, Hypoxia, Interferon Signaling, JAK-STAT Signaling, Lymphoid Compartment, TGF-beta Signaling
GZMA	1.89	0.333	1.24	2.54	3.71	2.36	5.84	9.37e-05		Cytotoxicity, Lymphoid Compartment
CCL5	1.9	0.272	1.36	2.43	3.73	2.58	5.4	2.57e-05		Cytokine and Chemokine Signaling, Myeloid Compartment
CD8A	1.91	0.301	1.32	2.5	3.77	2.5	5.67	4.06e-05		Antigen Presentation, Immune Cell Adhesion and Migration, Lymphoid Compartment
NKG7	1.95	0.31	1.34	2.56	3.87	2.54	5.91	4.06e-05		
GNLY	1.98	0.32	1.35	2.6	3.93	2.55	6.07	4.16e-05		Cytotoxicity, Lymphoid Compartment
GZMB	2.03	0.402	1.24	2.81	4.07	2.36	7.03	0.000316		Apoptosis, Cytotoxicity, Lymphoid Compartment, Notch Signaling
PRF1	2.03	0.329	1.39	2.68	4.09	2.61	6.39	4.16e-05		Cytotoxicity, Lymphoid Compartment
GZMH	2.25	0.422	1.42	3.08	4.75	2.68	8.43	0.000197		Cytotoxicity, Lymphoid Compartment
HLA-DQA2	3.1	0.533	2.06	4.15	8.6	4.17	17.7	7.12e-05		Antigen Presentation, Costimulatory Signaling, Immune Cell Adhesion and Migration, Interferon Signaling

BH p-value = Benjamini-Hochberg adjusted p-value