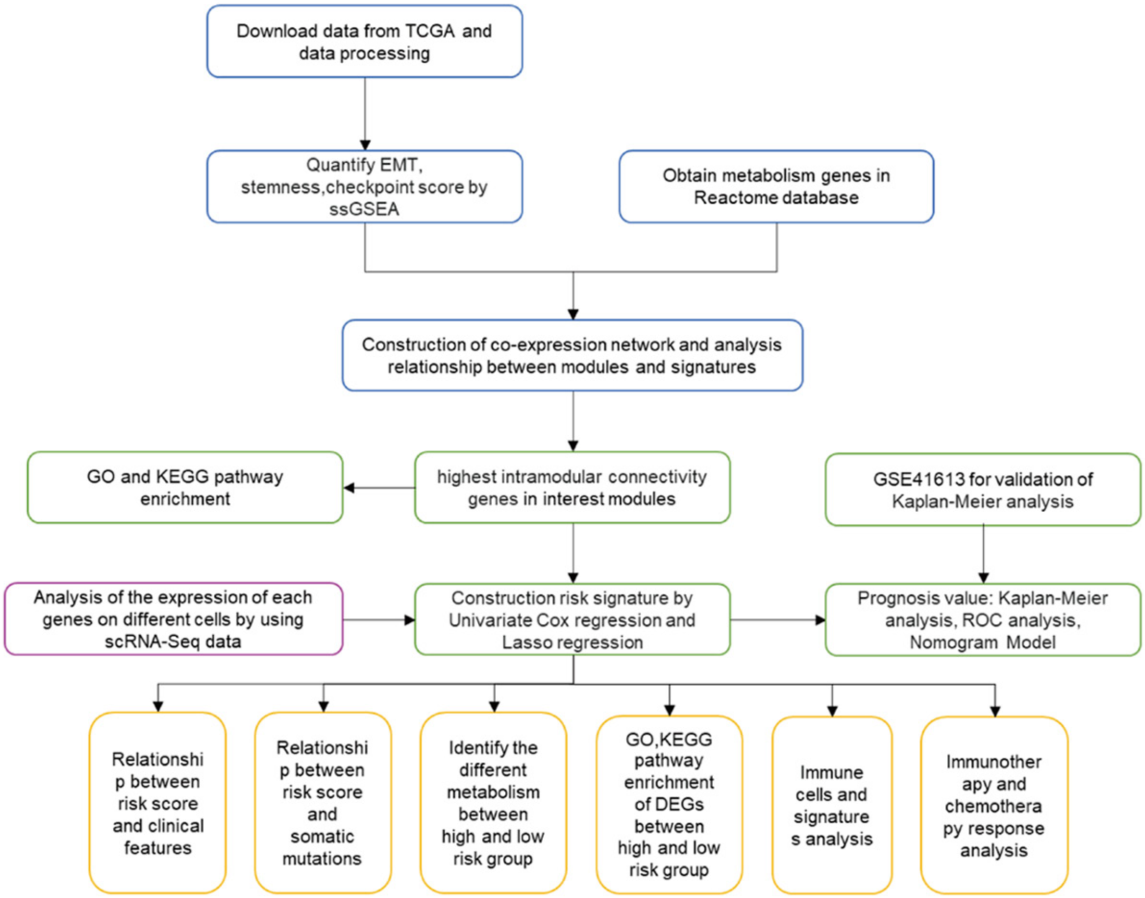


Figure S1. The flow chart of this study.

Table S1. 330 OSCC patients information in TCGA cohort

Clinical characteristics		Number	n (%)
Age	< 65	126	38.18
	> 65	204	61.82
Gender	male	229	69.39
	female	101	30.61
T	TX-T1	26	7.88
	T2	107	32.42
	T3	83	25.15
	T4	101	30.61
	Null	13	3.94
N	NX-N0	183	55.45
	N1	56	16.97
	N2	85	25.76
	N3	6	1.82
M	MX	19	5.76
	M0	309	93.64
	M1	2	0.61
	Null	3	0.91

Tumor Stage	I	12	3.64
	II	79	23.94
	III	67	20.30
	IV	162	49.09
	Null	10	3.03
HPV	+	10	3.03
	-	58	17.58
	Null	262	79.39
Origin tissue	Tongue	144	43.64
	Mouth Floor	72	21.82
	Cheek	19	5.76
	Pharynx	11	3.33
	Gum	10	3.03
	Plate	5	1.52
	others	69	20.91

Table S2. EMT, stemness, checkpoint signatures

signature	genes
EMT	ANLN, APLP2, CD63, CDH2, CLIC4, VCAN, CTSB, CX3CR1, DSG2, EDNRB, EMP1, ENC1, FGG, FZD1, TUBA4A, HMMR, ITGAV, LUM, L1CAM, MFAP1, MMP2, PFN1, PRKCA, RAB1A, RAN, RRAGA, SDCBP, SELENOP, SERPINA3, SMARCA1, SPA17, SPARC, TUBA4A, TUBA3C, TUBA1A, TUBB3
stemness	DNMT3B, PFAS, XRCC5, HAUS6, TET1, IGF2BP1, PLAA, TEX10, MSH6, DLGAP5, SKIV2L2, SOHLH2, RRAS2, PAICS, CPSF3, LIN28B, IPO5, BMPR1A, ZNF788, ASCC3, FANCB, HMGA2, TRIM24, ORC1, HDAC2, HESX1, INHBE, MIS18A, DCUN1D5, MRPL3, CENPH, MYCN, HAUS1, GDF3, TBCE, RIOK2, BCKDHB, RAD1, NREP, ADH5, PLRG1, ROR1, RAB3B, DIAPH3, GNL2, FGF2, NMNAT2, KIF20A, CENPI, DDX1, XXYLT1, GPR176, BBS9, C14orf166, BOD1, CDC123, SNRPD3, FAM118B, DPH3, EIF2B3, RPF2, APLP1, DACT1, PDHB, C14orf119, DTD1, SAMM50, CCL26, MED20, UTP6, RARS2, ARMCX2, RARS, MTHFD2, DHX15, HTR7, MTHFD1L, ARMC9, XPOT, IARS, HDX, ACTRT3, ERCC2, TBC1D16, GARS, KIF7, UBE2K, SLC25A3, ICMT, UGGT2, ATP11C, SLC24A1, EIF2AK4, GPX8, ALX1, OSTC, TRPC4, HAS2, FZD2, TRNT1, MMADHC, SNX8, CDH6, HAT1, SEC11A, DIMT1, TM2D2, FST, GBE1
checkpoint	IDO1, LAG3, CTLA4, TNFRSF9, ICOS, CD80, PDCD1LG2, TIGIT, CD70, TNFSF9, ICOSLG, KIR3DL1, CD86, PDCD1, LAIR1, TNFRSF8, TNFSF15, TNFRSF14, IDO2, CD276, CD40, TNFRSF4, TNFSF14, HHLA2, CD244, CD274, HAVCR2, CD27, BTLA, LGALS9, TMIGD2, CD28, CD48, TNFRSF25, CD40LG, ADORA2A, VTCN1, CD160, CD44, TNFSF18, TNFRSF18, BTNL2, C10orf54, CD200R1, TNFSF4, CD200, NRP1

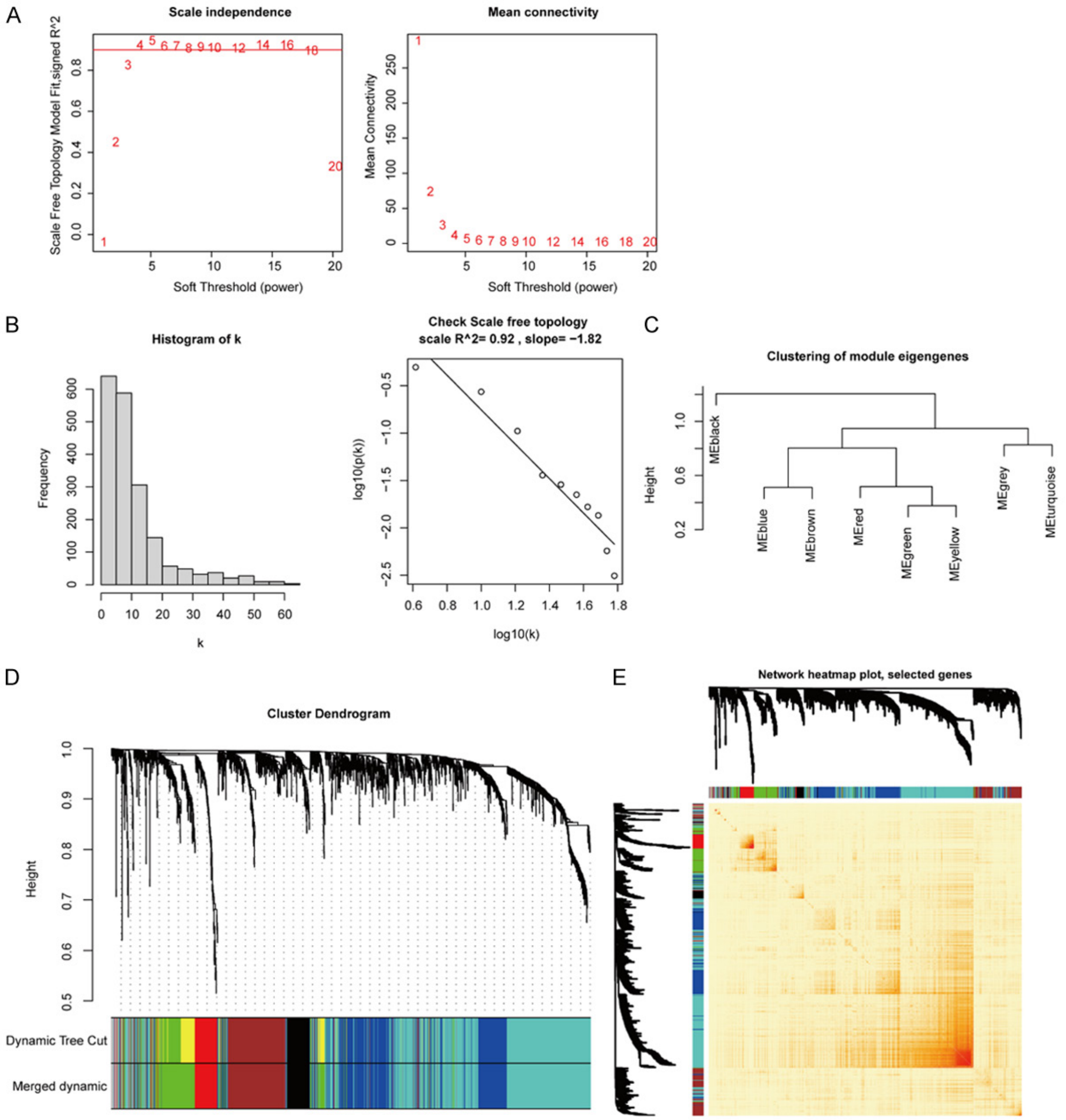
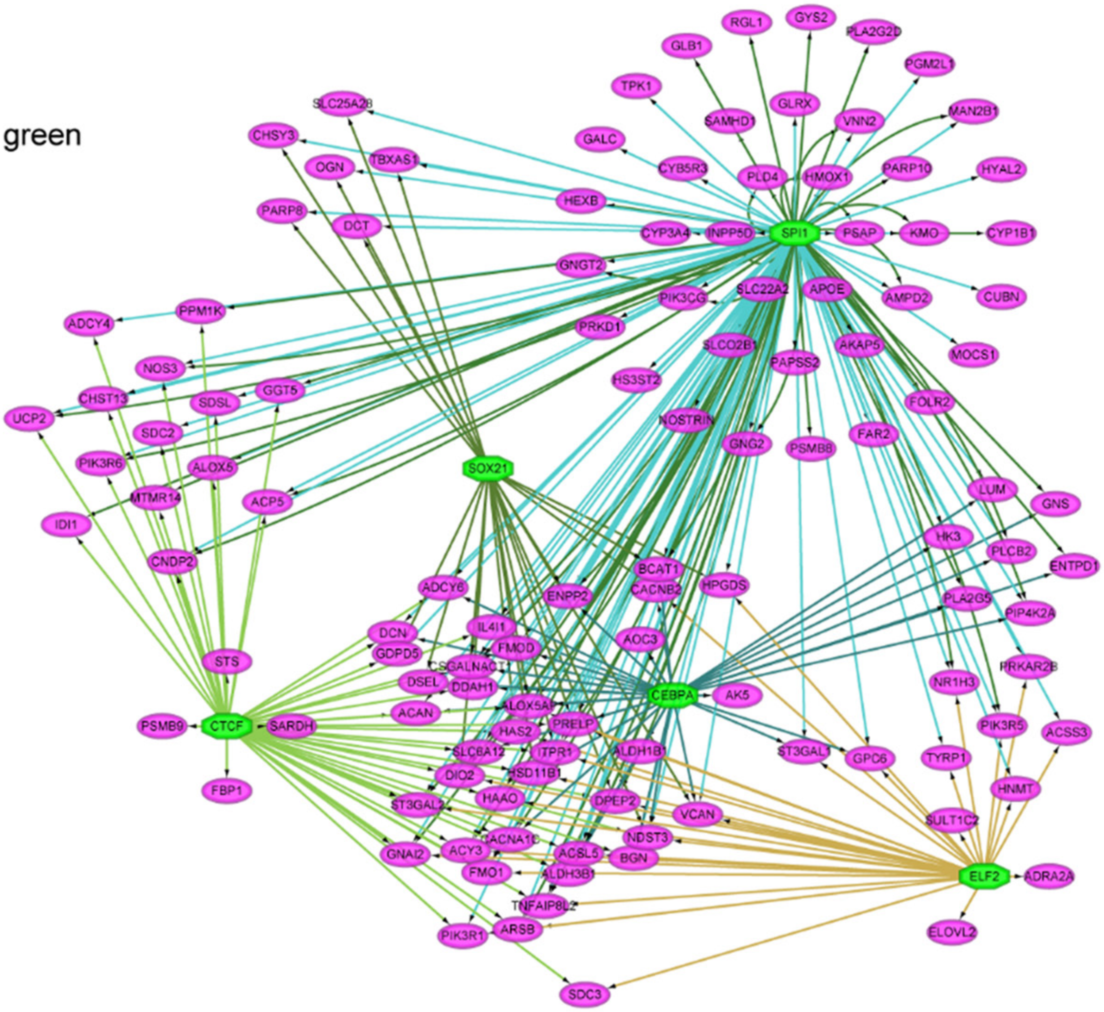


Figure S2. Construction of gene co-expression network. A. Analysis the scale-free fit index and mean connectivity of soft threshold of power. B. The distribution of k and liner model of fitting of R2 index. C. The dendrogram of gene modules. D. Gene dendrogram, the cut height was set as 0.4 to merge modules. E. Eigengene adjacency heatmap of 800 genes.


green
RGL1
GYS2
PLA2G2D
GLB1
PGM2L1
TPK1
GLRX
SAMHD1
VNN2
MAN2B1
SLC25A28
CHSY3
GALC
CYB5R3
PLD4
HMOX1
PARP10
HYAL2
OGN
TBXAS1
HEXB
PARP8
DCT
CYP3A4
INPP5D
SPI1
PSAP
KMO
CYP1B1
GNGT2
SLC22A2
APOE
AMPD2
CUBN
PPM1K
PIK3CG
ADCY4
PRKD1
AKAP5
MOCS1
SLCO2B1
NOS3
PAPSS2
HS3ST2
CHST13
GGT5
SDSL
UCP2
FOLR2
NOSTRIN
SDC2
FAR2
GNG2
PSMB8
PIK3R6
ALOX5
SOX21
LUM
GNS
MTMR14
ACP5
IDI1
HK3
PLCB2
ENTPD1
CNDP2
BCAT1
CACNB2
HPGDS
ADCY6
ENPP2
PLA2G5
PIP4K2A
DCN
IL4I1
AOC3
FMOD
GDPD5
CSGALNACT1
STS
DSEL
DDAH1
NR1H3
PRKAR2B
CEBPA
AK5
ALOX5AP
ACAN
PSMB9
CTCF
SARDH
HAS2
PRELP
PIK3R5
ACSS3
SLC6A12
TPR1
ALDH1B1
ST3GAL1
GPC6
TYRP1
DIO2
HSD11B1
FBP1
HNMT
HAAO
DPEP2
ST3GAL2
VCAN
SULT1C2
CACNA1C
NDST3
GNAI2
ACY3
ACSL5
BGN
ELF2
ADRA2A
FMO1
ALDH3B1
TNFAIP8L2
ELOVL2
PIK3R1
ARSB
SDC3

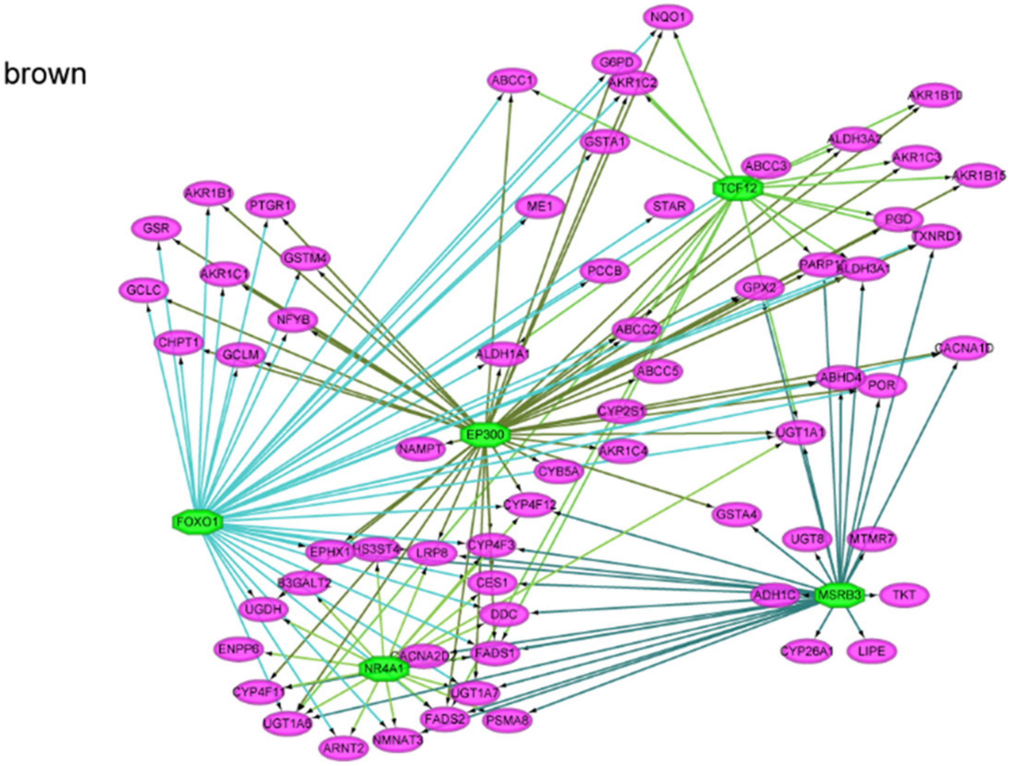

brown
NQO1
G6PD
ABCC1
AKR1C2
AKR1B10
GSTA1
ALDH3A2
AKR1C3
ABCC3
TCF12
AKR1B15
AKR1B1
PTGR1
ME1
STAR
GSR
PGD
GSTM4
TXNRD1
PCCB
PARP1
ALDH3A1
AKR1C1
GCLC
GPX2
NFYB
ABCC2
CHPT1
GCLM
ALDH1A1
CACNA1D
ABCC5
ABHD4
POR
CYP2S1
EP300
UGT1A1
NAMPT
AKR1C4
CYB5A
FOXO1
CYP4F12
GSTA4
UGT8
MTMR7
EPHX1
HS3ST4
LRP8
CYP4F3
CES1
ADH1C
MSRB3
TKT
B3GALT2
UGDH
DDC
ENPP6
CACNA2D
FADS1
CYP26A1
LIPE
NR4A1
UGT1A7
CYP4F11
FADS2
PSMA8
UGT1A6
NMNAT3
ARNT2

Figure S3. Transcription factors of genes in green and brown modules predicted by iRegulon.

Table S3. The 12 genes signature and coefficient

Gene	Coef
PTGR1	0.006695
FUT7	0.006255
ALDH1B1	0.307717
FMOD	-0.17457
MCCC1	0.084753
SLC2A3	0.276657
UGT1A10	0.032856
INPP5D	-0.1686
HK1	0.464965
PRKCA	0.245153
CSGALNACT1	-0.53195
NADSYN1	0.243603
NADSYN1	0.243603

Table S4. KEGG metabolic pathways

	Pathways	statistic	*p*.value
1	2-Oxocarboxylic acid metabolism - Homo sapiens (human)	5.110798	5.47E-07
2	Alanine, aspartate and glutamate metabolism - Homo sapiens (human)	4.916578	1.39E-06
3	alpha-Linolenic acid metabolism - Homo sapiens (human)	-6.06745	3.59E-09
4	Amino sugar and nucleotide sugar metabolism - Homo sapiens (human)	2.567315	0.010711
5	Arachidonic acid metabolism - Homo sapiens (human)	-5.05392	7.22E-07
6	Arginine and proline metabolism - Homo sapiens (human)	0.578506	0.563321
7	Arginine biosynthesis - Homo sapiens (human)	-0.23138	0.817162
8	Ascorbate and aldarate metabolism - Homo sapiens (human)	3.877937	0.000128
9	beta-Alanine metabolism - Homo sapiens (human)	-0.36899	0.712372
10	Biosynthesis of amino acids - Homo sapiens (human)	6.769541	5.97E-11
11	Biosynthesis of unsaturated fatty acids - Homo sapiens (human)	-1.04469	0.296937
12	Biotin metabolism - Homo sapiens (human)	-1.83431	0.067514
13	Butanoate metabolism - Homo sapiens (human)	0.351868	0.725168
14	Caffeine metabolism - Homo sapiens (human)	-1.66422	0.097038
15	Carbon metabolism - Homo sapiens (human)	4.715426	3.62E-06
16	Citrate cycle (TCA cycle) - Homo sapiens (human)	0.085758	0.931713
17	Cysteine and methionine metabolism - Homo sapiens (human)	2.376877	0.01804
18	D-Arginine and D-ornithine metabolism - Homo sapiens (human)	-1.85745	0.064143
19	D-Glutamine and D-glutamate metabolism - Homo sapiens (human)	1.691564	0.091706
20	Drug metabolism - cytochrome P450 - Homo sapiens (human)	1.332127	0.183755
21	Drug metabolism - other enzymes - Homo sapiens (human)	3.482113	0.000565
22	Ether lipid metabolism - Homo sapiens (human)	-5.70615	2.59E-08
23	Fatty acid biosynthesis - Homo sapiens (human)	-2.89668	0.004025
24	Fatty acid degradation - Homo sapiens (human)	0.338237	0.735408
25	Fatty acid elongation - Homo sapiens (human)	-2.79499	0.005496
26	Fatty acid metabolism - Homo sapiens (human)	-1.02522	0.306018
27	Folate biosynthesis - Homo sapiens (human)	-0.29924	0.764948
28	Fructose and mannose metabolism - Homo sapiens (human)	5.032899	8.03E-07

29	Galactose metabolism - Homo sapiens (human)	2.088841	0.037496
30	Glutathione metabolism - Homo sapiens (human)	3.517366	0.000498
31	Glycerolipid metabolism - Homo sapiens (human)	-1.42396	0.155408
32	Glycerophospholipid metabolism - Homo sapiens (human)	-1.26808	0.20567
33	Glycine, serine and threonine metabolism - Homo sapiens (human)	1.570814	0.117192
34	Glycolysis/Gluconeogenesis - Homo sapiens (human)	3.694357	0.000258
35	Glycosaminoglycan biosynthesis - chondroitin sulfate/dermatan sulfate - Homo sapiens (human)	1.517116	0.130202
36	Glycosaminoglycan biosynthesis - heparan sulfate/heparin - Homo sapiens (human)	1.350717	0.177728
37	Glycosaminoglycan biosynthesis - keratan sulfate - Homo sapiens (human)	1.484128	0.138735
38	Glycosaminoglycan degradation - Homo sapiens (human)	-0.71578	0.474636
39	Glycosphingolipid biosynthesis - ganglio series - Homo sapiens (human)	2.67079	0.007947
40	Glycosphingolipid biosynthesis - globo and isoglobo series - Homo sapiens (human)	-0.20665	0.836411
41	Glycosphingolipid biosynthesis - lacto and neolacto series - Homo sapiens (human)	-1.46715	0.143298
42	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis - Homo sapiens (human)	1.936882	0.053618
43	Glyoxylate and dicarboxylate metabolism - Homo sapiens (human)	2.579394	0.010345
44	Histidine metabolism - Homo sapiens (human)	-3.73655	0.00022
45	Inositol phosphate metabolism - Homo sapiens (human)	-2.509	0.012593
46	Linoleic acid metabolism - Homo sapiens (human)	-5.93368	7.59E-09
47	Lipoic acid metabolism - Homo sapiens (human)	1.082252	0.279937
48	Lysine degradation - Homo sapiens (human)	1.825642	0.068813
49	Mannose type O-glycan biosynthesis - Homo sapiens (human)	4.115939	4.90E-05
50	Metabolic pathways - Homo sapiens (human)	0.329685	0.741849
51	Metabolism of xenobiotics by cytochrome P450 - Homo sapiens (human)	2.643925	0.008599
52	Mucin type O-glycan biosynthesis - Homo sapiens (human)	-0.23394	0.81518
53	N-Glycan biosynthesis - Homo sapiens (human)	0.638976	0.523286
54	Neomycin, kanamycin and gentamicin biosynthesis - Homo sapiens (human)	4.040443	6.67E-05
55	Nicotinate and nicotinamide metabolism - Homo sapiens (human)	0.820551	0.412499
56	Nitrogen metabolism - Homo sapiens (human)	0.442635	0.658322
57	One carbon pool by folate - Homo sapiens (human)	2.410379	0.016486
58	Other glycan degradation - Homo sapiens (human)	0.884766	0.376937
59	Other types of O-glycan biosynthesis - Homo sapiens (human)	3.175186	0.00164
60	Oxidative phosphorylation - Homo sapiens (human)	0.190115	0.849337
61	Pantothenate and CoA biosynthesis - Homo sapiens (human)	-5.84823	1.23E-08
62	Pentose and glucuronate interconversions - Homo sapiens (human)	2.829573	0.004956
63	Pentose phosphate pathway - Homo sapiens (human)	4.044598	6.56E-05
64	Phenylalanine metabolism - Homo sapiens (human)	-0.29081	0.771388
65	Phenylalanine, tyrosine and tryptophan biosynthesis - Homo sapiens (human)	0.122598	0.902501
66	Phosphonate and phosphinate metabolism - Homo sapiens (human)	3.727206	0.000228
67	Porphyrin and chlorophyll metabolism - Homo sapiens (human)	3.366537	0.000854
68	Primary bile acid biosynthesis - Homo sapiens (human)	-3.37802	0.000818
69	Propanoate metabolism - Homo sapiens (human)	1.604057	0.1097
70	Purine metabolism - Homo sapiens (human)	0.847311	0.39745
71	Pyrimidine metabolism - Homo sapiens (human)	-1.04799	0.29542
72	Pyruvate metabolism - Homo sapiens (human)	2.582007	0.010257
73	Retinol metabolism - Homo sapiens (human)	-0.59925	0.549423
74	Riboflavin metabolism - Homo sapiens (human)	-0.95403	0.340774
75	Selenocompound metabolism - Homo sapiens (human)	3.339217	0.000938
76	Sphingolipid metabolism - Homo sapiens (human)	-3.30776	0.00105

77	Starch and sucrose metabolism - Homo sapiens (human)	0.724978	0.468983
78	Steroid biosynthesis - Homo sapiens (human)	0.555455	0.578964
79	Steroid hormone biosynthesis - Homo sapiens (human)	1.646613	0.100607
80	Sulfur metabolism - Homo sapiens (human)	-1.58328	0.114323
81	Synthesis and degradation of ketone bodies - Homo sapiens (human)	-0.49565	0.620471
82	Taurine and hypotaurine metabolism - Homo sapiens (human)	-1.06229	0.288888
83	Terpenoid backbone biosynthesis - Homo sapiens (human)	-1.99851	0.046487
84	Thiamine metabolism - Homo sapiens (human)	0.457475	0.647634
85	Tryptophan metabolism - Homo sapiens (human)	-1.53283	0.126328
86	Tyrosine metabolism - Homo sapiens (human)	0.226162	0.82122
87	Ubiquinone and other terpenoid-quinone biosynthesis - Homo sapiens (human)	2.923608	0.003705
88	Valine, leucine and isoleucine biosynthesis - Homo sapiens (human)	3.22197	0.001401
89	Valine, leucine and isoleucine degradation - Homo sapiens (human)	2.326173	0.020629
90	Vitamin B6 metabolism - Homo sapiens (human)	0.122998	0.902184

Table S5. Immune related process and ICB-response signatures

signature	genes
APC co inhibition	C10orf54, CD274, LGALS9, PDCD1LG2, PVRL3, CD40, CD58, CD70, ICOSLG, SLAMF1, TNFSF14, TNFSF15, TNFSF18, TNFSF4, TNFSF8, TNFSF9
CCR	CCL16, TPO, TGFBR2, CXCL2, CCL14, TGFBR3, IL11RA, CCL11, IL4I1, IL33, CXCL12, CXCL10, BMPER, BMP8A, CXCL11, IL21R, IL17B, TNFRSF9, ILF2, CX3CR1, CCR8, TNFSF12, CSF3, TNFSF4, BMP3, CX3CL1, BMP5, CXCR2, TNFRSF10D, BMP2, CXCL14, CCL28, CXCL3, BMP6, CCL21, CXCL9, CCL23, IL6, TNFRSF18, IL17RD, IL17D, IL27, CCL7, IL1R1, CXCR4, CXCR2P1, TGFB1I1, IFNGR1, IL9R, IL1RAPL1, IL11, CSF1, IL20RA, IL25, TNFRSF4, IL18, ILF3, CCL20, TNFRSF12A, IL6ST, CXCL13, IL12B, TNFRSF8, IL6R, BMPR2, IFNE, IL1RAPL2, IL3RA, BMP4, CCL24, TNFSF13B, CCR4, IL2RA, IL32, TNFRSF10C, IL22RA1, BMPR1A, CXCR5, CXCR3, IFNA8, IL17REL, IFNB1, IFNAR1, TNFRSF1B, CCL17, IFNL1, IL16, IL1RL1, ILK, CCL25, ILDR2, CXCR1, IL36RN, IL34, TGFB1, IFNG, IL19, ILKAP, BMP2K, CCR10, ILDR1, EPO, CCR7, IL17C, IL23A, CCR5, IL7, EPOR, CCL13, IL2RG, IL31RA, TNFAIP6, IFNL2, BMP1, IL12RB1, TNFAIP8, IL4R, TNFRSF6B, TNFAIP8L1, TNFRSF10B, IFNL3, CCL5, CXCL6, CXCL1, CCR3, TNFSF11, CSF1R, IL21, IL1RAP, IL12RB2, CCL1, IL17RA, CCR1, IL1RN, TNFRSF11B, TNFRSF14, IL13, IL2RB, BMP8B, CCL2, IL24, IL18RAP, TGFBI, TNFSF10, TNFRSF11A, CXCL5, IL5RA, TNFSF9, IL1RL2, TNFRSF13C, IL36G, IL15RA, TNFRSF21, CXCL8, IL22RA2, TNFAIP8L2, IL18R1, IFNLR1, CXCR6, CCL3L3, TNFRSF1A, IL17RE, IFNGR2, IL17RC, TNFAIP8L3, ILVBL, TGFBRAP1, CCL4L1, CSF2RA, CCRN4L, CCL26, TNFAIP1, CCRL2, IFNA10, TNFRSF17, IFNA13, IL20, IL18BP, CCL3L1, TNFSF12-TNFSF13, IL5, IL23R, IL26, TNF, TGFA, CSF2, IL1F10, CXCL17, TNFSF13, IFNA4, IL37, IL12A, IL7R, IFNA1, IL1A, IL4, IL2, CCL22, CSF3R, IL10, IFNK, TGFB2, IL1R2, IL1B, IL17F, IL27RA, IL15, TNFSF8, IL36B, XCL1, CXCL16, TNFRSF19, IL3, CCL3, IFNA2, BMPR1B, IFNA21, TNFSF18, CCL8, IL17RB, TNFRSF25, IL22, IL10RB, IFNAR2, CCL18, IFNA16, CSF2RB, IL36A, TNFAIP3, IL13RA2, IL13RA1, CCR9, TNFRSF10A, IFNA7, IFNW1, XCL2, TNFSF14, CCR2, BMP15, BMP10, CCL15-CCL14, TGFBR1, IFNA5, BMP7, IFNA14, IL20RB, IL10RA, IFNA17, CCR6, TGFB3, CCL15, CCL4, CCL27, TNFRSF13B, TNFAIP2, IL31, IL17A, TNFSF15, CCL19, IFNA6, IL9
checkpoint	IDO1, LAG3, CTLA4, TNFRSF9, ICOS, CD80, PDCD1LG2, TIGIT, CD70, TNFSF9, ICOSLG, KIR3DL1, CD86, PDCD1, LAIR1, TNFRSF8, TNFSF15, TNFRSF14, IDO2, CD276, CD40, TNFRSF4, TNFSF14, HHLA2, CD244, CD274, HAVCR2, CD27, BTLA, LGALS9, TMIGD2, CD28, CD48, TNFRSF25, CD40LG, ADORA2A, VTCN1, CD160, CD44, TNFSF18, TNFRSF18, BTNL2, C10orf54, CD200R1, TNFSF4, CD200, NRP1
Cytolytic activity	PRF1, GZMB, GZMA
HLA	HLA-E, HLA-DPB2, HLA-C, HLA-J, HLA-DQB1, HLA-DQB2, HLA-DQA2, HLA-DQA1, HLA-A, HLA-DMA, HLA-DOB, HLA-DRB1, HLA-H, HLA-B, HLA-DRB5, HLA-DOA, HLA-DPB1, HLA-DRA, HLA-DRB6, HLA-L, HLA-F, HLA-G, HLA-DMB, HLA-DPA1
Inflammation-promoting	CCL5, CD19, CD8B, CXCL10, CXCL13, CXCL9, GNLY, GZMB, IFNG, IL12A, IL12B, IRF1, PRF1, STAT1, TBX21
Parainflammation	CXCL10, PLAT, CCND1, LGMN, PLAUR, AIM2, MMP7, ICAM1, MX2, CXCL9, ANXA1, TLR2, PLA2G2D, ITGA2, MX1, HMOX1, CD276, TIRAP, IL33, PTGES, TNFRSF12A, SCARB1, CD14, BLNK, IFIT3, RETNLB, IFIT2, ISG15, OAS2, REL, OAS3, CD44, PPARG, BST2, OAS1, NOX1, PLA2G2A, IFIT1, IFITM3, IL1RN

T cell co-inhibition	BTLA, C10orf54, CD160, CD244, CD274, CTLA4, HAVCR2, LAG3, LAIR1, TIGIT
T cell co-stimulation	CD2, CD226, CD27, CD28, CD40LG, ICOS, SLAMF1, TNFRSF18, TNFRSF25, TNFRSF4, TNFRSF8, TNFRSF9, TNFSF14
Type I IFN Reponse	DDX4, IFIT1, IFIT2, IFIT3, IRF7, ISG20, MX1, MX2, RSAD2, TNFSF10
Type II IFN Reponse	GPR146, SELP, AHR
ICB-response	AKR1C4, KCNA1, CREB3L3, NEU4, PIGR, ACOD1, CPN2, CCL16, HGD, DEFA1, TAT, PDCD1, GLYATL1, MT1H, COLEC10, THRSP, HS3ST3B1, IL24, IFNG, SMCO2, TMEM155, DBH
CD8 T effector	CD8A, CXCL10, CXCL9, GZMA, GZMB, IFNG, PRF1, TBX21
DNA damage repair	ALKBH2, ALKBH3, APEX1, APEX2, APLF, ATM, ATR, ATRIP, BLM, BRCA1, BRCA2, BRIP1, CCNH, CDK7, CETN2, CHAF1A, CHEK1, CHEK2, CLK2, DCLRE1C, DDB1, DDB2, DUT, ENDOV, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ERCC6, ERCC8, FAN1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCL, FANCM, GTF2H1, GTF2H2, GTF2H3, GTF2H4, GTF2H5, H2AFX, HLTF, HUS1, LIG1, LIG3, LIG4, MBD4, MDC1, MGMT, MLH1, MLH3, MMS19, MNAT1, MPG, MSH2, MSH3, MSH4, MSH5, MSH6, MUTYH, NEIL1, NEIL2, NEIL3, NHEJ1, NTHL1, NUDT1, OGG1, PALB2, PARP1, PARP2, PARP3, PCNA, PER1, PMS1, PMS2, PNKP, POLB, POLD1, POLE, POLG, POLH, POLL, POLM, POLQ, PRKDC, RAD1, RAD17, RAD18, RAD23A, RAD23B, RAD51C, RAD9A, RECQL4, RECQL5, RIF1, RNF168, RNF4, RNF8, RPA1, RPA2, RPA3, RPA4, RRM2B, SETMAR, SHPRH, SMUG1, TDP1, TDP2, TOPBP1, TP53, TREX1, UBE2A, UBE2B, UBE2N, UBE2V2, UNG, UVSSA, WRN, XAB2, XPA, XPC, XRCC1, XRCC4, XRCC5, XRCC6
Pan-F-TBRS	ACTA2, ACTG2, ADAM12, ADAM19, CNN1, COL4A1, CTGF, CTPS1, FAM101B, FSTL3, HSPB1, IGFBP3, PXDC1, SEMA7A, SH3PXD2A, TAGLN, TGFBI, TNS1, TPM1
Antigen processing machinery	B2M, HLA-A, HLA-B, HLA-C, TAP1, TAP2
Immune checkpoint	CD274, CTLA4, HAVCR2, LAG3, PDCD1, PDCD1LG2, TIGIT
EMT (1)	CLDN3, CLDN7, CLDN4, CDH1, VIM, TWIST1, ZEB1, ZEB2
FGFR3-related genees	FGFR3, TP63, WNT7B
KEGG discovered histones	HIST1H2AG, HIST1H2AI, HIST1H2BL, HIST2H2BF
Angiogenesis	CDH5, SOX17, SOX18, TEK
Fanconi anemia	APITD1, ATR, ATRIP, BLM, BRCA1, BRCA2, BRIP1, C17orf70, C19orf40, EME1, EME2, ERCC1, ERCC4, FAN1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, HES1, MLH1, MUS81, PALB2, PMS2, POLH, POLI, POLK, POLN, RAD51, RAD51C, REV1, REV3L, RMI1, RMI2, RPA1, RPA2, RPA3, RPA4, SLX4, STRA13, TELO2, TOP3A, TOP3B, UBE2T, USP1, WDR48
Cell cycle	ABL1, ANAPC1, ANAPC10, ANAPC11, ANAPC13, ANAPC2, ANAPC4, ANAPC5, ANAPC7, ATM, ATR, BUB1, BUB1B, BUB3, CCNA1, CCNA2, CCNB1, CCNB2, CCNB3, CCND1, CCND2, CCND3, CCNE1, CCNE2, CCNH, CDC14A, CDC14B, CDC16, CDC20, CDC23, CDC25A, CDC25B, CDC25C, CDC26, CDC27, CDC45, CDC6, CDC7, CDK1, CDK2, CDK4, CDK6, CDK7, CDKN1A, CDKN1B, CDKN1C, CDKN2A, CDKN2B, CDKN2C, CDKN2D, CHEK1, CHEK2, CREBBP, CUL1, DBF4, E2F1, E2F2, E2F3, E2F4, E2F5, EP300, ESPL1, FZR1, GADD45A, GADD45B, GADD45G, GSK3B, HDAC1, HDAC2, MAD1L1, MAD2L1, MAD2L2, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, MDM2, MYC, ORC1, ORC2, ORC3, ORC4, ORC5, ORC6, PCNA, PKMYT1, PLK1, PRKDC, PTTG1, PTTG2, RAD21, RB1, RBL1, RBL2, RBX1, SFN, SKP1, SKP2, SMAD2, SMAD3, SMAD4, SMC1A, SMC1B, SMC3, STAG1, STAG2, TFDP1, TFDP2, TGFB1, TGFB2, TGFB3, TP53, TTK, WEE1, YWHAB, YWHAE, YWHAG, YWHAH, YWHAQ, YWHAZ, ZBTB17
DNA replication	DNA2, FEN1, LIG1, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLA2, POLD1, POLD2, POLD3, POLD4, POLE, POLE2, POLE3, POLE4, PRIM1, PRIM2, RFC1, RFC2, RFC3, RFC4, RFC5, RNASEH1, RNASEH2A, RNASEH2B, RNASEH2C, RPA1, RPA2, RPA3, RPA4, SSBP1
Nucleotide excision repair	CCNH, CDK7, CETN2, CUL4A, CUL4B, DDB1, DDB2, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ERCC6, ERCC8, GTF2H1, GTF2H2, GTF2H3, GTF2H4, GTF2H5, LIG1, MNAT1, PCNA, POLD1, POLD2, POLD3, POLD4, POLE, POLE2, POLE3, POLE4, RAD23A, RAD23B, RBX1, RFC1, RFC2, RFC3, RFC4, RFC5, RPA1, RPA2, RPA3, RPA4, XPA, XPC
Homologous recombination	BLM, BRCA2, EME1, MRE11A, MUS81, NBN, POLD1, POLD2, POLD3, POLD4, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54B, RAD54L, RPA1, RPA2, RPA3, RPA4, SHFM1, SSBP1, TOP3A, TOP3B, XRCC2, XRCC3
Mismatch repair	EXO1, LIG1, MLH1, MLH3, MSH2, MSH3, MSH6, PCNA, PMS2, POLD1, POLD2, POLD3, POLD4, RFC1, RFC2, RFC3, RFC4, RFC5, RPA1, RPA2, RPA3, RPA4, SSBP1
EMT2	AXL, FAP, LOXL2, ROR2, TAGLN, TWIST2, WNT5A
EMT3	FOXF1, GATA6, SOX9, TWIST1, ZEB1, ZEB2
WNT target	EFNB3, MYC, TCF12, VEGFA
Cell cycle regulators	ATM, CCND1, CCNE1, CDKN1A, CDKN2A, E2F3, FBXW7, MDM2, RB1, TP53

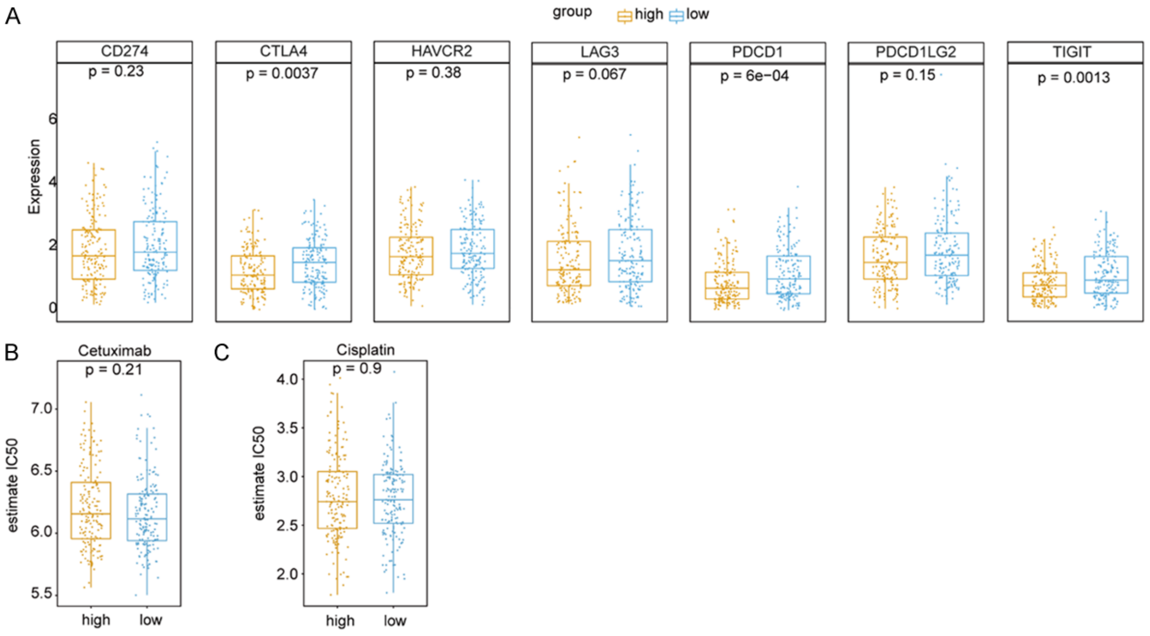


Figure S4. Checkpoints and IC50 of drugs. A. The 7 checkpoints expression in different risk group. B, C. IC50 of Cetuximab and Cisplatin estimated by "pRRophetic" package.

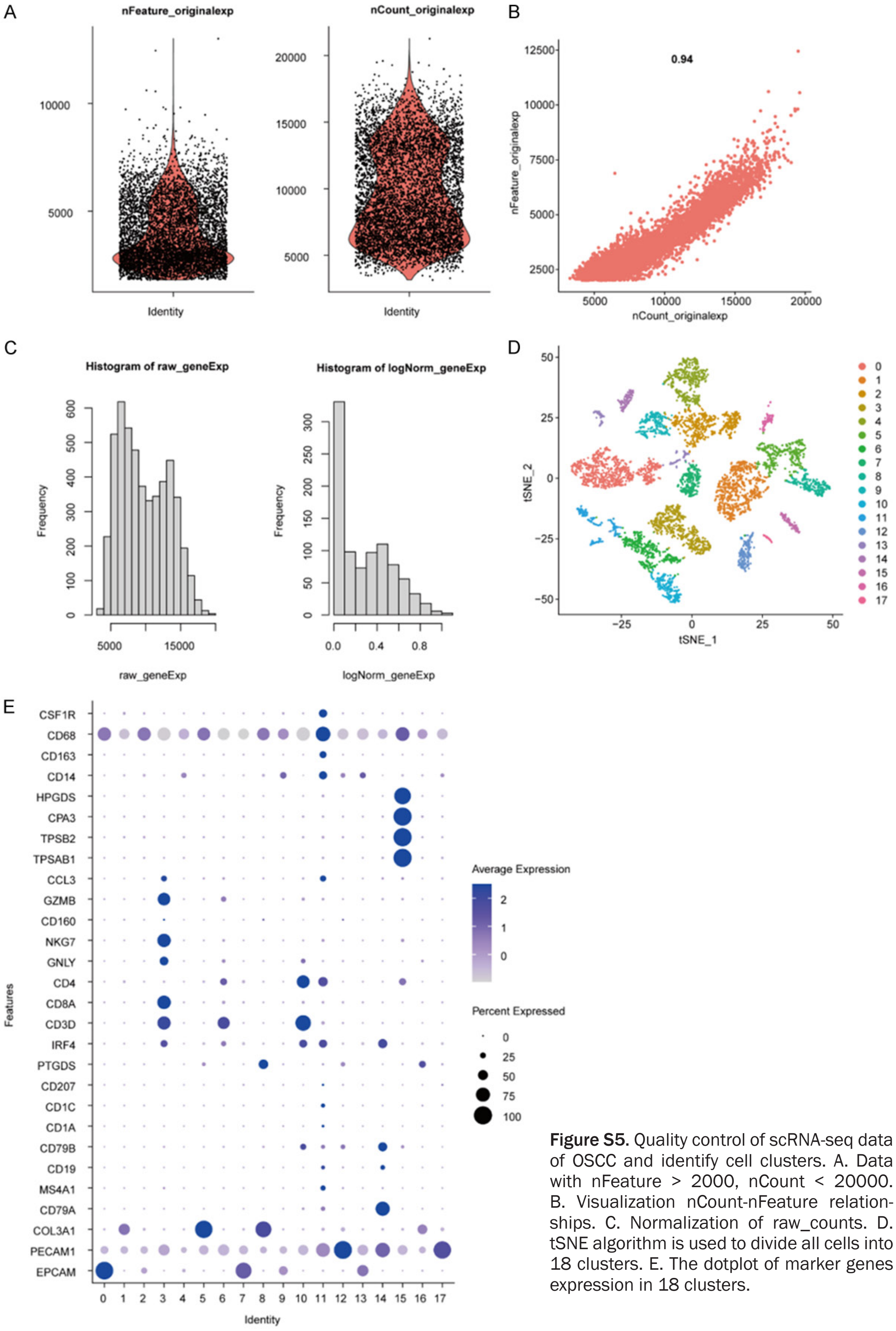


Figure S5. Quality control of scRNA-seq data of OSCC and identify cell clusters. A. Data with nFeature > 2000, nCount < 20000. B. Visualization nCount-nFeature relationships. C. Normalization of raw_counts. D. tSNE algorithm is used to divide all cells into 18 clusters. E. The dotplot of marker genes expression in 18 clusters.

Table S6. Markers used to identify cell types in 18 cell clusters

Cells	Maker genes
Tumor cells	EPCAM
Endothelial cells	PECAM1
Fibroblasts	COL3A1
B cells	CD79A, MS4A1, IGHM, CD19, CD79B
Dendritic cells	CD1A, CD1C, CD207, PTGDS, IRF4
T cell	CD3D, CD8A, CD4
NK cells	GNLY, NKG7, CD160, GZMB, CCL3
Mast cells	TPSAB1, TPSB2, CPA3, HPGDS
Macrophages	CD14, CD163, CD68, CSF1R

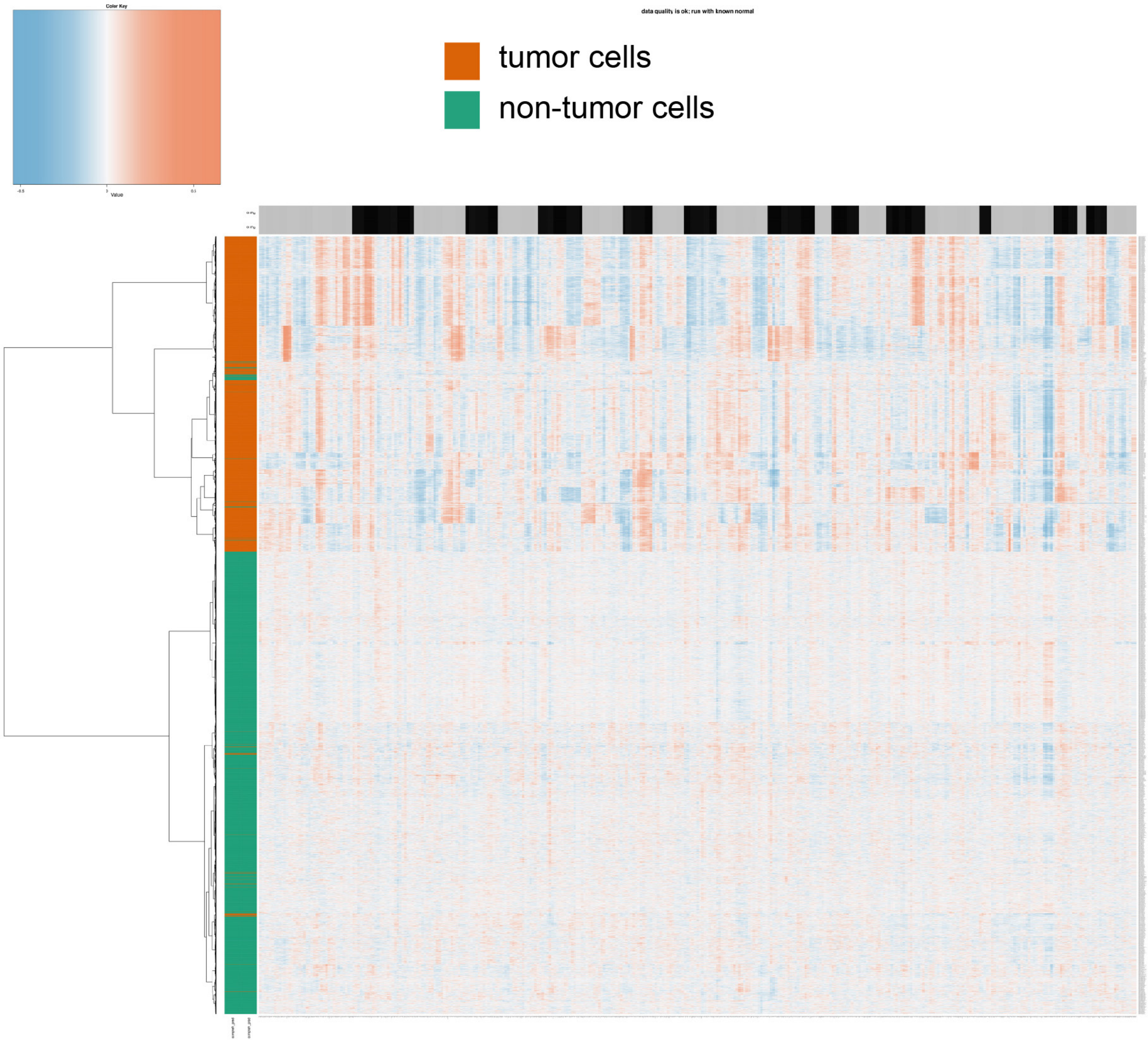


Figure S6. The estimated CNVs of 5746 cells analyzed by CopyKAT.

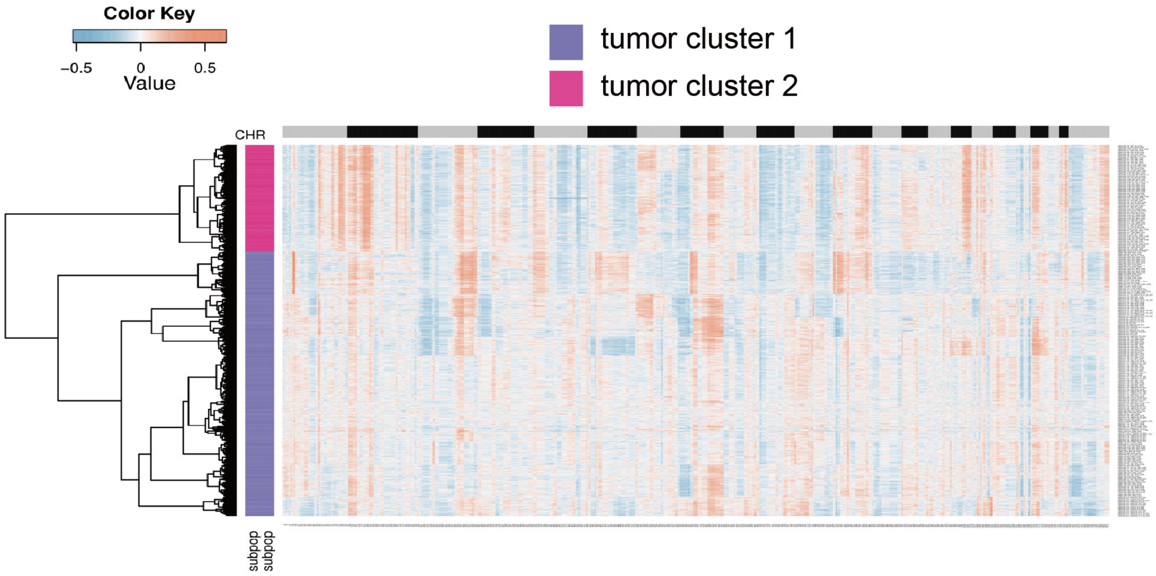


Figure S7. The estimated CNVs of tumor cells analyzed by CopyKAT.