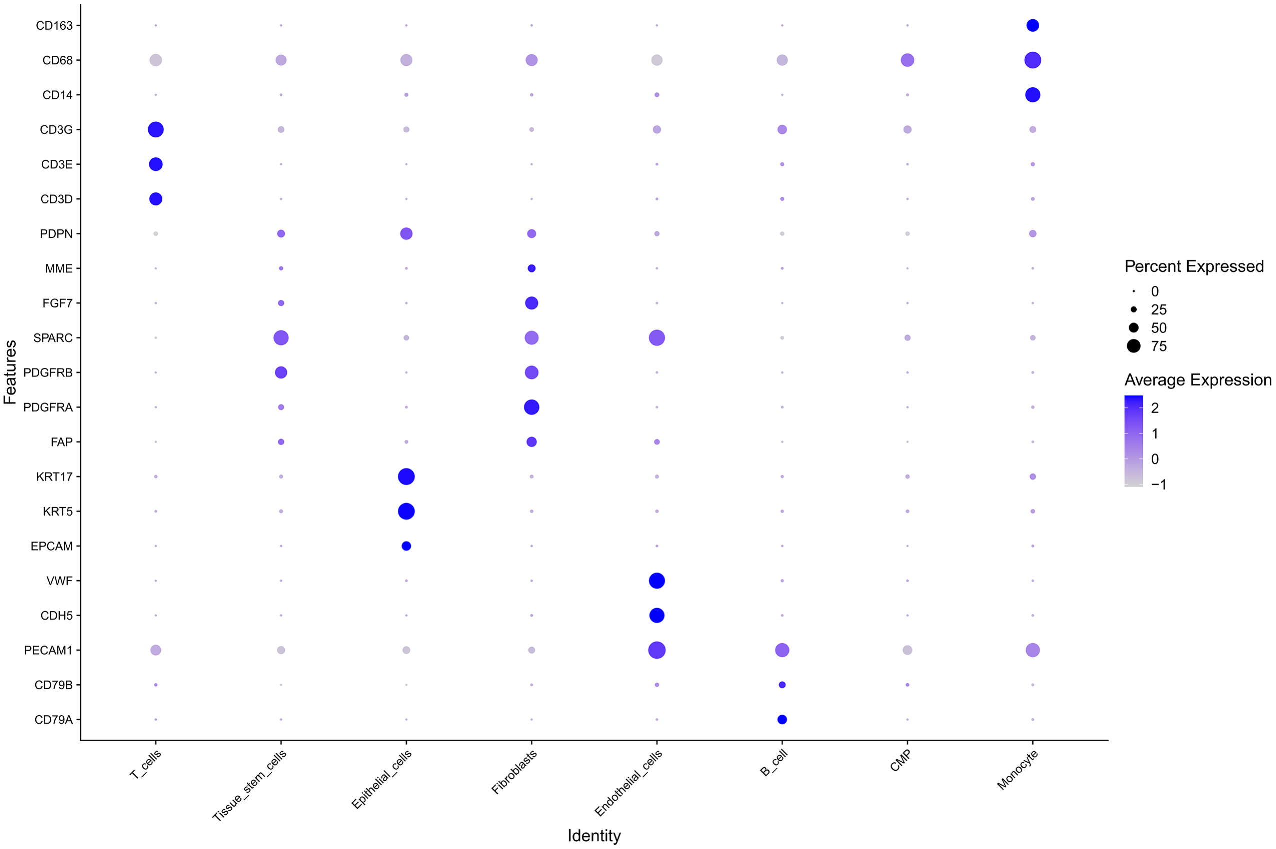

Figure S1 Bubble plot of marker genes for eight annotated cell types. CMP, common myeloid progenitor.

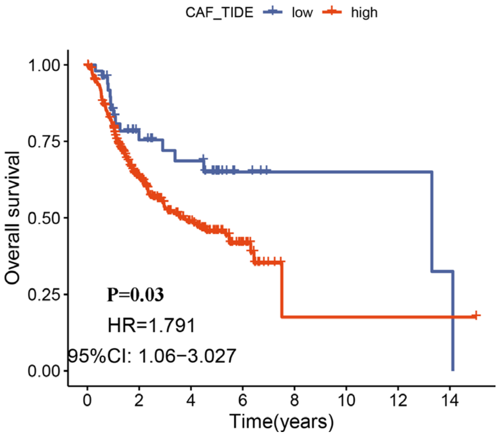

Figure S2 Kaplan-Meier curves for OS of patients with OSCC in high CAF and low CAF scores. CAF, cancer-associated fibroblast; CI, confidence interval; HR, hazard ratio; OS, overall survival; OSCC, oral squamous cell carcinoma; TIDE, Tumor Immune Dysfunction and Exclusion.

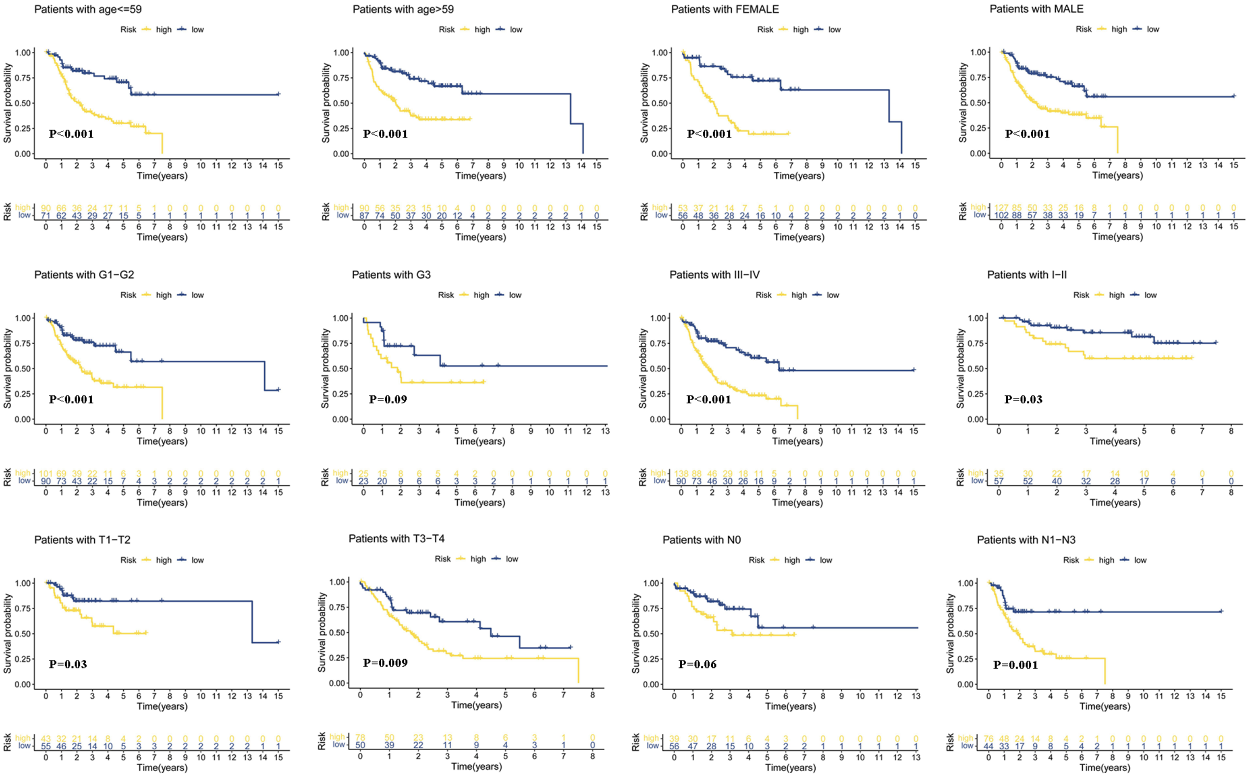

Figure S3 Kaplan-Meier curves for OS between the high- and low-risk groups stratified by clinical features. G, grade; N, node; OS, overall survival; T, tumor.

https://dx.doi.org/10.21037/tcr-2025-2129

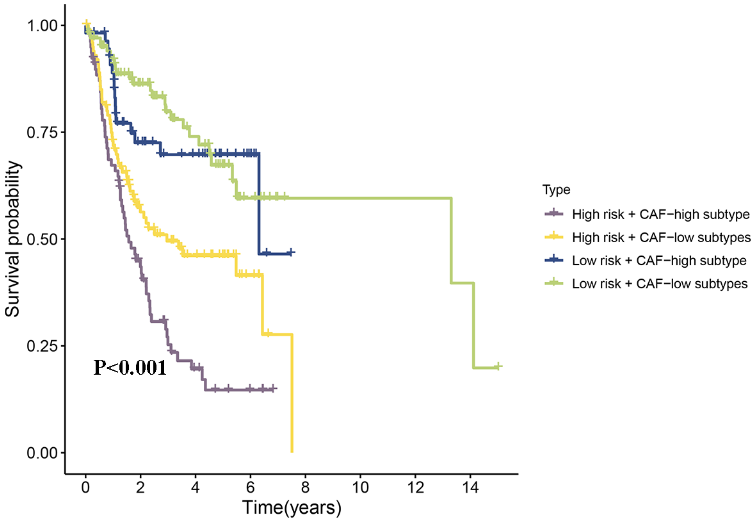

Figure S4 Survival curves combining CAF subtypes with risk scores. CAF, cancer-associated fibroblast.

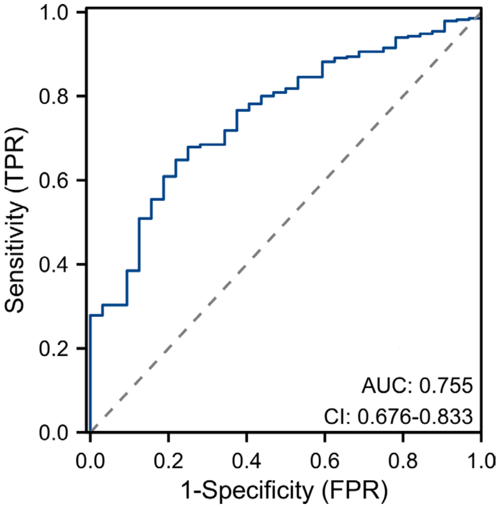

Figure S5 ROC curve analysis of risk score to validate the response to immunotherapy in patients with TCGA-OSCC. AUC, area under the curve; CI, confidence interval; FPR, false positive rate; OSCC, oral squamous cell carcinoma; ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas; TPR, true positive rate.

https://dx.doi.org/10.21037/tcr-2025-2129

Table S1 Clinicopathologic features of 30 OSCC patients

ID	Age (years)	Gender	Grade	Stage	T	N	M
84	37	Male	G1	II	T2	N0	M0
87	32	Female	G2	II	T2	N0	M0
102	55	Male	G3	IV	T3	N2	M0
108	60	Female	G2	IV	T4	N1	M0
119	32	Female	G2	II	T2	N0	M0
154	51	Female	G3	IV	T4	N0	M0
155	65	Female	G2	III	T3	N0	M0
163	50	Female	G1	III	T3	N0	M0
173	51	Female	G1	IV	T2	N3	MX
176	53	Male	G3	IV	T4	N3	M0
179	57	Male	G2	I	T1	N0	M0
192	66	Male	G1	III	T3	N1	MX
198	68	Male	G3	IV	T3	N3	M0
199	56	Male	G1	I	T1	N0	M0
201	74	Female	G3	III	T2	N1	MX
210	38	Male	G2	I	T1	N0	MX
212	57	Male	G3	III	T3	N1	MX
221	51	Male	G1	II	T2	N0	M0
237	36	Female	G1	II	T2	N0	M0
239	38	Male	G3	III	T3	N1	M0
241	58	Female	G3	II	T2	N0	M0
244	31	Male	G1	II	T2	N0	M0
245	39	Male	G1	I	T1	N0	M0
248	44	Male	G1	I	T1	N0	M0
249	53	Female	G2	II	T2	N0	M0
250	32	Male	G2	III	T3	N1	M0
251	46	Male	G1	III	T3	N1	M0
258	67	Male	G1	IV	T3	N2	M0
259	36	Male	G2	III	T3	N1	M0
263	55	Male	G2	IV	T2	N2	MX

G, grade; M, metastasis; N, node; OSCC, oral squamous cell carcinoma; T, tumor.

Table S2 Three hundred and twenty marker genes from fibroblast cluster

APOD, OGN, PDGFRB, CTSF, MIR205HG, SFRP2, MMP2, PRELP, LAMB1, KRT5, PLA2G2A, COLEC12, ADAM33, RASD1, KRT17, PODN, CD248, TENC1, EZR, DSP, ABCA8, SRPX, C1R, TGFB3, SDC1, PDGFRL, EBF2, PDK4, TSPAN4, KRT19, ADH1B, PCOLCE, HSD11B1, ALDH1A1, KRT6A, ABI3BP, RNASE4, FN1, TIMP3, PMAIP1, PDGFRA, CD34, NFIA, FMOD, TP63, VIT, COL1A2, SPON1, LAMC1, CDC42SE2, PI16, FIBIN, MIR100HG, IGFBP6, KRT14, TNXB, CFH, FSTL1, C5orf4, SERPINB5, ABCA6, CFD, FHL1, A2M, MPZL2, LAMA2, GALNT16, GPX3, PCDHGC3, PTPRC, CILP, SERPINF1, ELN, RND3, TRIM29, CHRDL1, PCDH18, F10, SERPINA3, TUBA4A, GFRA1, PDGFD, PLAGL1, COL5A2, S100A2, SVEP1, CYBRD1, FMO1, CXCL14, STXBP2, GDF10, LRP1, IGFBP5, ANTXR2, LAMB3, AOX1, COL6A2, AKAP12, SH3D19, FABP5, OLFML3, DIO2, SSPN, DPYSL2, BST2, MAMDC2, PRRX1, FXYD6, NT5E, RGS1, COL6A3, FBLN1, TMEM176A, ABCA9, KRT18, DPT, OMD, SERPING1, MXRA5, CALML3, CAPN6, EFEMP1, EPB41L2, SYNGR2, CLCA2, MFAP4, NID1, TMEM176B, ADAMTS1, CDH3, ABCA10, LHFP, EFEMP2, NUPR1, IDH2, MYOC, COL3A1, GSN, ANG, PTTG1, FIGF, GSTM5, SPON2, CRISPLD2, BIRC3, CDO1, RAMP2, TCEAL7, PLTP, PIM2, FBLN5, CD302, RARRES1, PLXDC2, LGALS7, ADH1C, CTGF, SDC2, NRP1, SRGN, FBLN2, VCAN, GFPT2, F11R, ANXA8L1, CXCL12, OSR1, PPAP2B, LAMB2, PDCL3, PLAC9, EBF1, MITF, ADD3, LYPD3, GPR133, FMO2, ZBTB16, FGL2, KRT16, THBS4, COL14A1, MME, BDH2, CD3G, ANGPTL1, SEPP1, COL1A1, FCGRT, DEF6, NEGR1, DDR2, IGF1, VAT1, RAC2, FGF7, RBMS3, RCN3, PTGIS, IL2RG, C3, COL15A1, LTBP2, VAMP8, LAPTM5, TNXA, RUNX1T1, RECK, DDAH2, CAPG, PTGFR, LPAR1, HTRA3, SLC38A1, COL17A1, MGST1, CYP1B1, TMEM204, OCIAD2, CKS2, SFRP1, GLT8D2, NNMT, INMT, KRT6B, MGP, COL6A1, BGN, MFAP5, CXCR4, PTGDS, PMP22, LAMA4, DSG3, LCP1, ISLR, RARRES2, SGCE, SLC7A5, ISG20, MXRA8, TIMP2, CYR61, PLXDC1, SAMSN1, SCARA5, TFPI, FAP, LEPR, TNFAIP3, HSPB6, SOD3, CPQ, FAM60A, CORO1A, BOC, CPED1, GPNMB, METTL7A, COTL1, FGF10, OLFML1, PHLDB1, SPINT2, DUSP4, GPC3, DAB2, ANGPTL2, CD82, DUSP2, SFRP4, FAM198B, SPARCL1, SLC9A3R1, STK17B, ANK2, C1S, THBS2, PPP1CA, CARD16, DCN, MRC2, AEBP1, STEAP1, CD96, CCDC80, IGFBP4, SMOC2, FXYD3, PRKCH, WISP2, FBN1, PLSCR4, HN1, FYB, RSPO3, PID1, OLFML2B, ARHGDIB, HMHA1, CTSK, COL8A1, CYP27A1, SFN, C7, NOVA1, MEG3, GGT5, F3, C16orf54, LUM, LTBP4, C1orf21, SLC2A1, CREM, LOC339524, BMP4, TGFBR3, TACSTD2, RGCC

Table S3 Twenty-four CAF marker genes associated with the prognosis of patients with OSCC

ID	HR	HR.95L	HR.95H	P value
SVEP1	1.295869	1.019446	1.647245	0.034235
FGF7	1.195208	1.008124	1.417010	0.040060
SRPX	1.150000	1.034705	1.278141	0.009517
PDGFD	1.177992	1.008066	1.376563	0.039299
CYP1B1	1.123493	1.011480	1.247910	0.029782
AKAP12	1.181869	1.028324	1.358342	0.018607
GFPT2	1.226501	1.073743	1.400992	0.002627
MME	1.121531	1.004763	1.251868	0.040887
NNMT	1.124148	1.001840	1.261387	0.046454
SGCE	1.200622	1.024736	1.406698	0.023678
C1orf21	0.738149	0.547642	0.994927	0.046223
CXCL14	0.921895	0.850420	0.999378	0.048260
NT5E	1.183819	1.050963	1.333469	0.005463
NRP1	1.204708	1.006654	1.441727	0.042119
OCIAD2	1.278301	1.045312	1.563221	0.016774
LEPR	1.268570	1.011091	1.591618	0.039854
TRIM29	0.864001	0.753919	0.990155	0.035532
LAMB3	1.200785	1.050974	1.371951	0.007119
KRT18	1.215836	1.074262	1.376068	0.001974
PTTG1	1.247360	1.013076	1.535826	0.037310
RAC2	1.190864	1.008600	1.406066	0.039304
IL2RG	0.815425	0.700071	0.949787	0.008743
CKS2	1.404869	1.174970	1.679751	0.000193
TNFAIP3	1.193899	1.033438	1.379276	0.016102

CAF, cancer-associated fibroblast; HR, hazard ratio; HR.95H, upper limit of the 95% confidence interval; HR.95L, lower limit of the 95% confidence interval; OSCC, oral squamous cell carcinoma.