

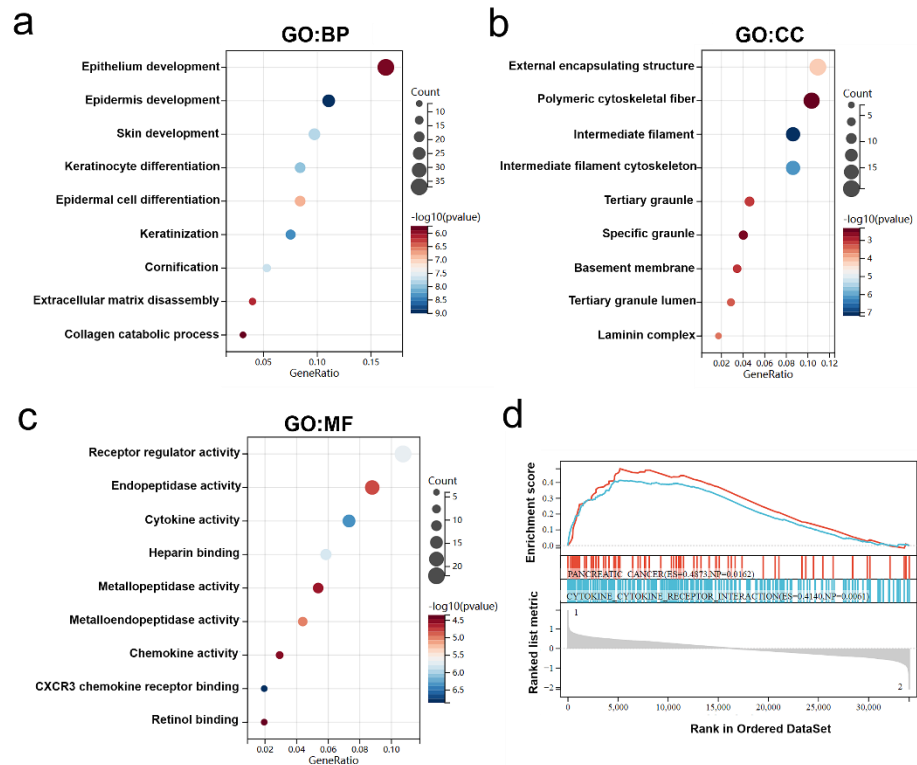


Fig. S1 GO and GSEA functional enrichment analysis. A-C GO analysis demonstrates the enrichment of differentially expressed genes in biological processes (BP), cellular components (CC), and molecular functions (MF). D GSEA analysis highlights the significant role of cytokines and their receptors in HNSCC.

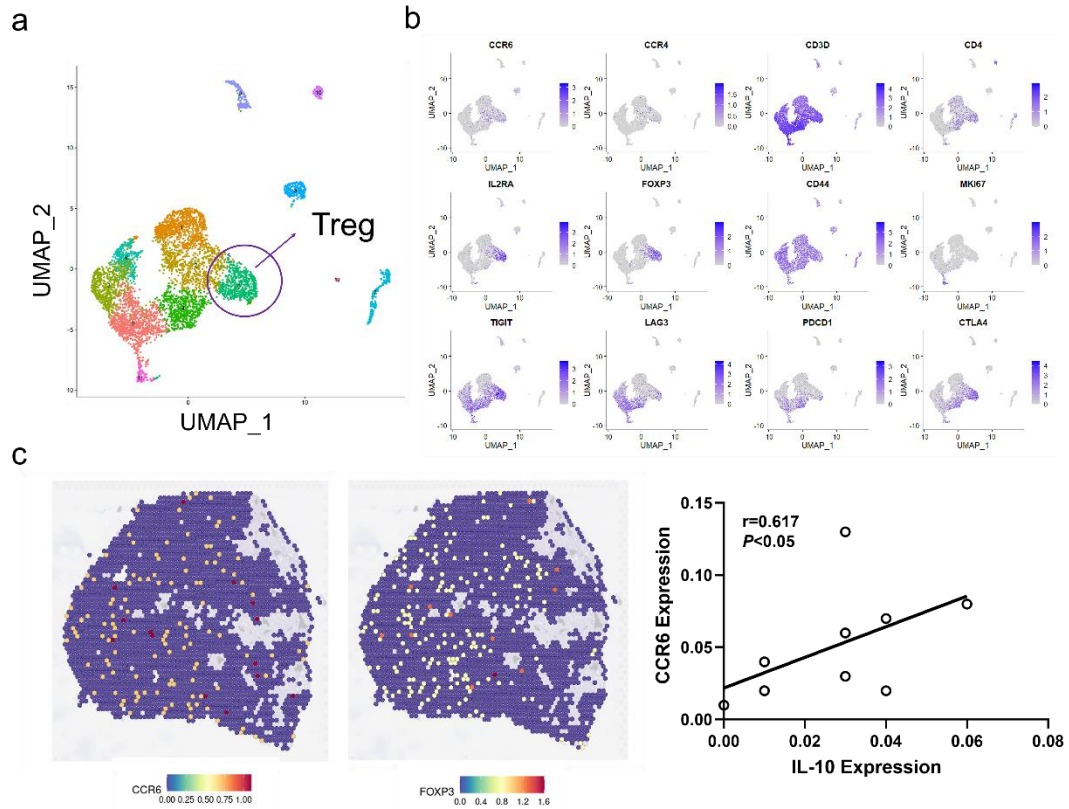


Fig. S2 CCR6 is predominantly localized on Treg cells. A-B CCR6 is primarily expressed on CD4+CD25+FOXP3+ Treg cells and is associated with the effector molecule CD44 and the proliferation marker Ki67. It also shows a co-expression trend with immune checkpoints such as PD1, TIGIT, LAG3, and CTLA4. C Spatial transcriptomic analysis reveals a correlation between CCR6 and FOXP3 expression in OSCC ($P<0.05$, $r=0.617$).

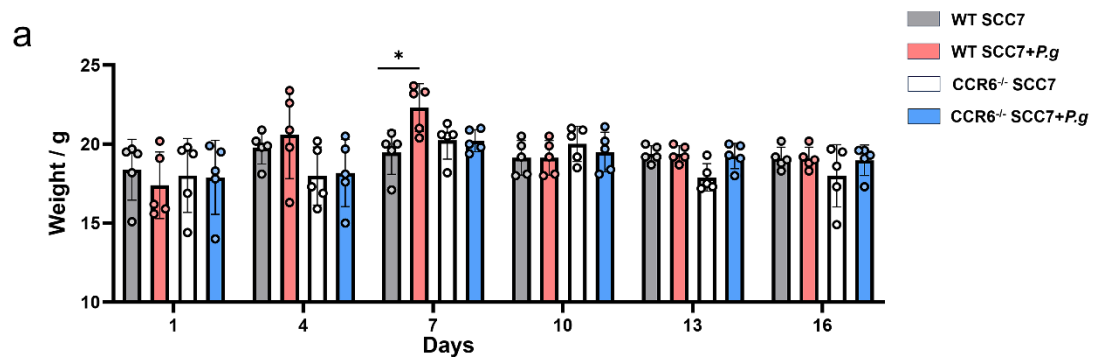


Fig. S3 Body weight curves of the mouse model. A No significant differences in body weight were observed among the three groups of mice during the modeling period, $*P < 0.05$. Data are presented as means $\pm$ SEM. Two-way ANOVA was used for statistical analysis.

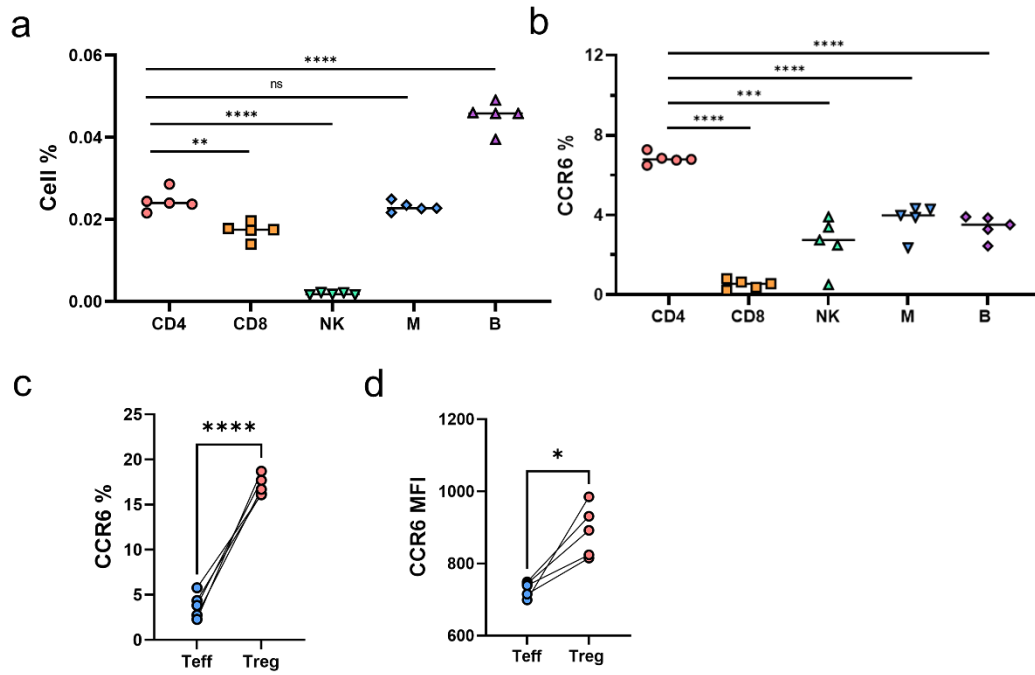


Fig. S4 Expression of CCR6 in lymphocytes. A B cells constitute the largest proportion of the tumor microenvironment, followed by CD4⁺ T cells, $**P < 0.01$, $****P < 0.0001$. Data are presented as means $\pm$ SEM. One-way ANOVA was used for statistical analysis. B CCR6 is predominantly localized on CD4⁺ T cells, $***P < 0.001$, $****P < 0.0001$. Data are presented as means $\pm$ SEM. One-way ANOVA was used for statistical analysis. C Among CD4⁺ T cells, CCR6 is most abundantly expressed on Treg cells, $****P < 0.0001$. T-test was used for statistical analysis. D Compared to CD8⁺ T cells, CCR6 is mainly expressed on Treg cells within the CD4⁺ T cell population, $*P < 0.05$. T-test was used for statistical analysis.

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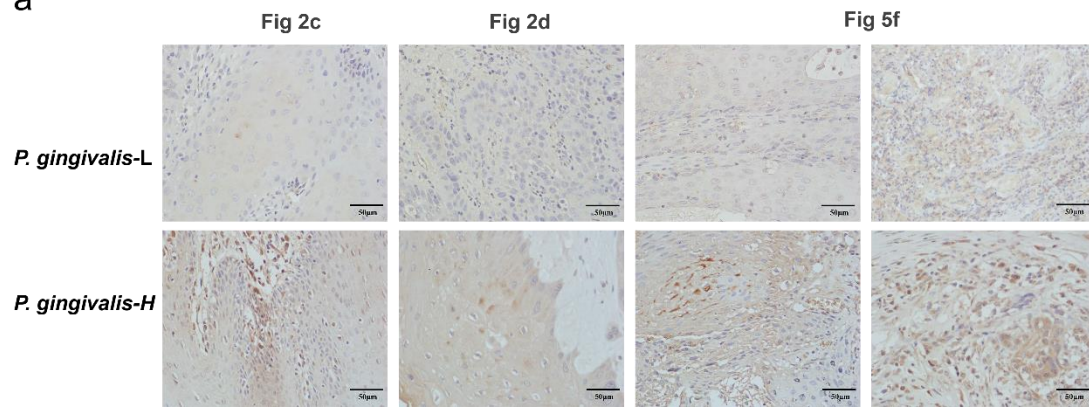


Fig S5. Expression of *P. gingivalis* in OSCC patients. Scale bar = 50μm.

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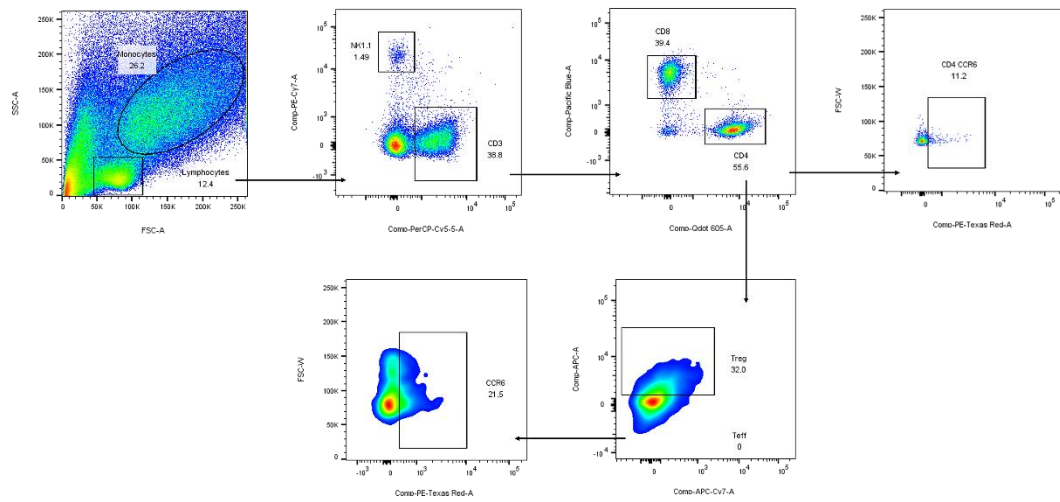


Fig S6. The gating strategy used for FACS.

supplementary table 1. Univariate and multivariate analysis of prognostic parameters in TCGA database overall survival (OS)

Variable	Univariate analysis		Multivariate analysis	
	HR (95% CI)	<i>P</i> -value	HR (95% CI)	<i>P</i> -value
CCL20	1.400(1.068-1.834)	0.015	1.409(1.076-1.846)	0.013
Age	1.021(1.008-1.034)	0.001	1.019(1.006-1.032)	0.004
Gender	1.369(1.026-1.826)	0.033	1.242(0.922-1.673)	0.154
T	1.230(0.920-1.644)	0.161		
N	1.240(0.945-1.627)	0.121		
Clinical stage	1.123(0.854-1.477)	0.406		

Abbreviations: CI, confidence interval; HR, hazard ratio.