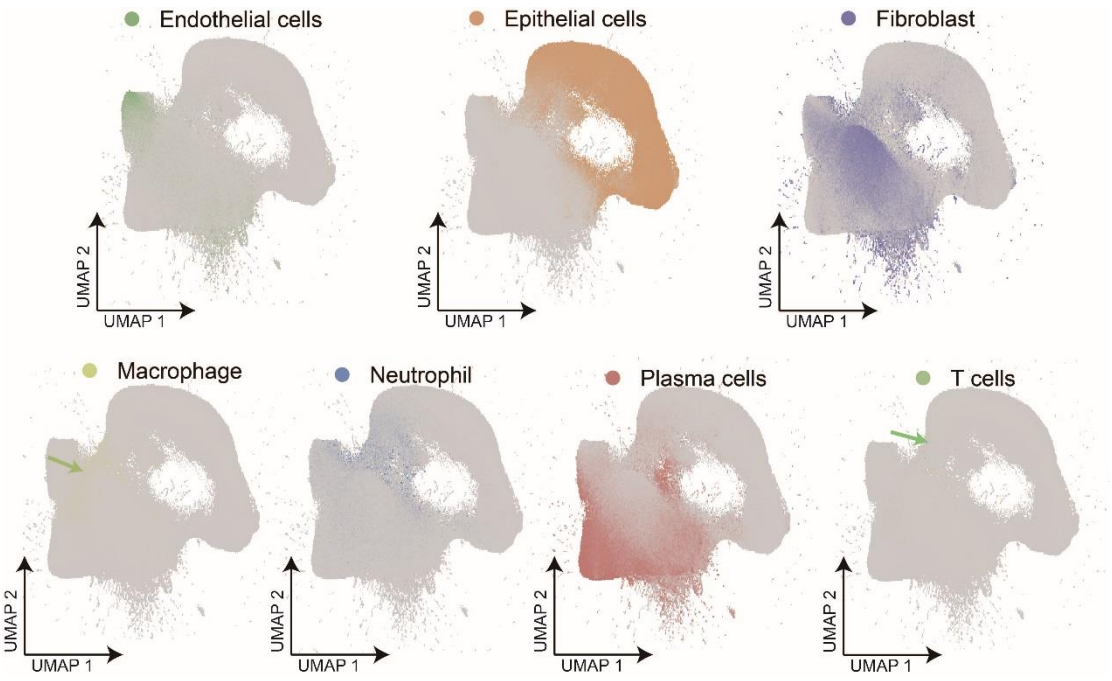
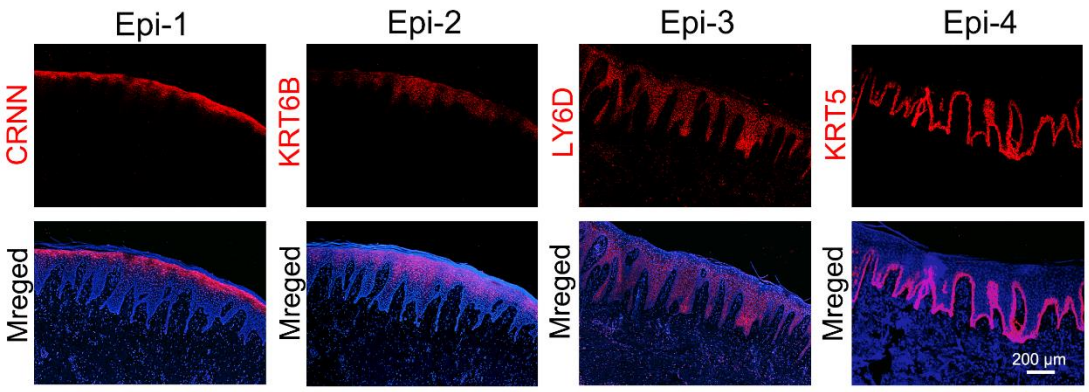
Supplemental Information

Table 1 Primers used in this study

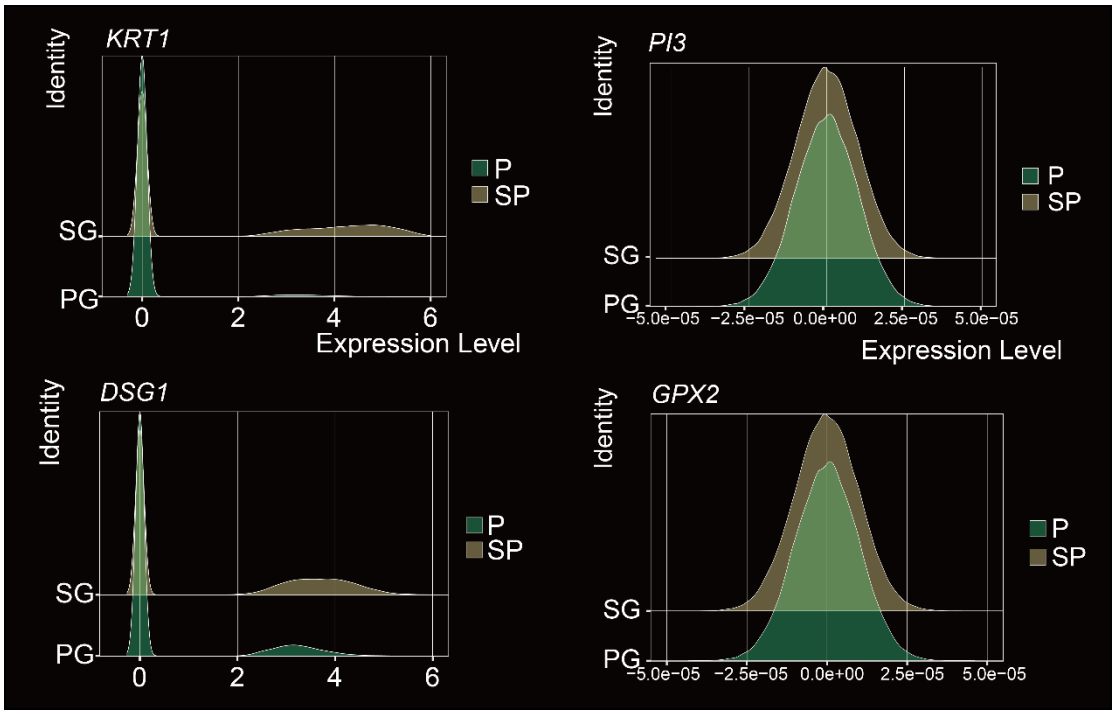
GENE	PRIMER SEQUENCE (5'-3')
KRT1	AAGGAGAGTGGACCAACTGA
	AAGCACCATCCACATCCTTC
PI3	GTTCCCCAGTGAGAGGGA
	TGGGAGGAAGAATGGACAGT
DSG1	ACCCAATCGCCAAAATTCAC
	TTGGCCCATTGAGTTCAGAG
GPX2	CTGGATGGGGAGAAGGTAGAT
	ATTCTGACAGTTCTCCTGATGTC
GAPDH	AGATCCCTCCAAAATCAAGTGG
	GGCAGAGATGATGACCCTTTT
Cxcl12	CACTTGCCAAGCTCCAACTT
	ACCCAGCTAAAGGTCCTCAC
Gapdh	AGGTCGGTGTGAACGGATTTG
	TGTAGACCATGTAGTTGAGGTCA



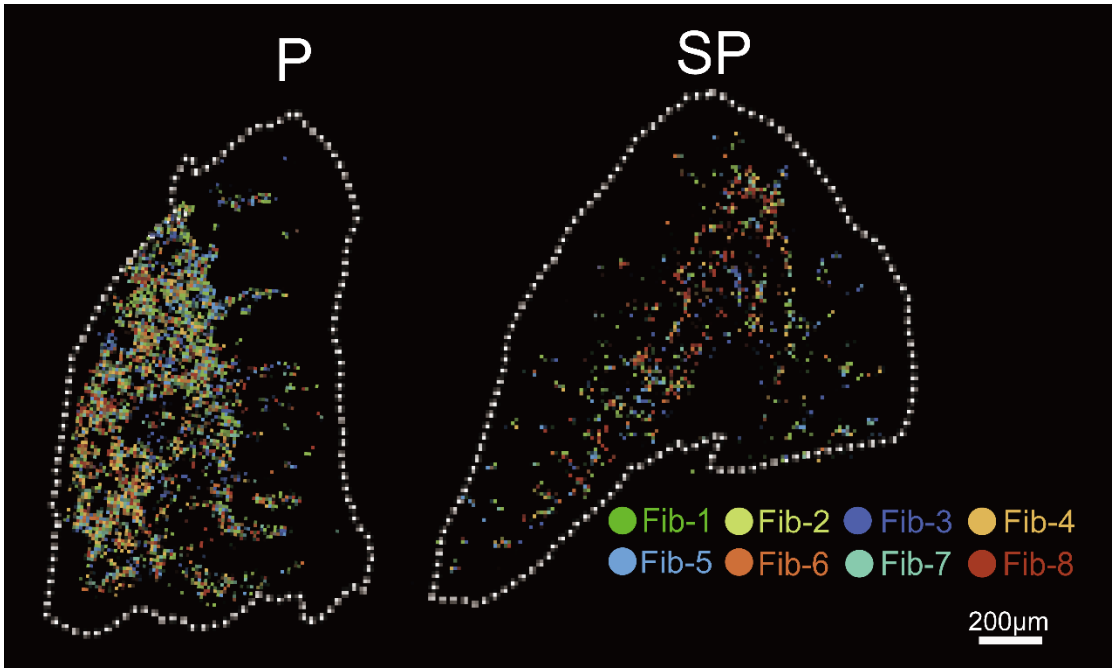
Sup Fig.1 Dot plots showing the expression of marker genes for the 7 major clusters (Epithelial cell, Macrophage, Endothelial cell, Plasma cell, Fibroblast, Neutrophil and T cell).



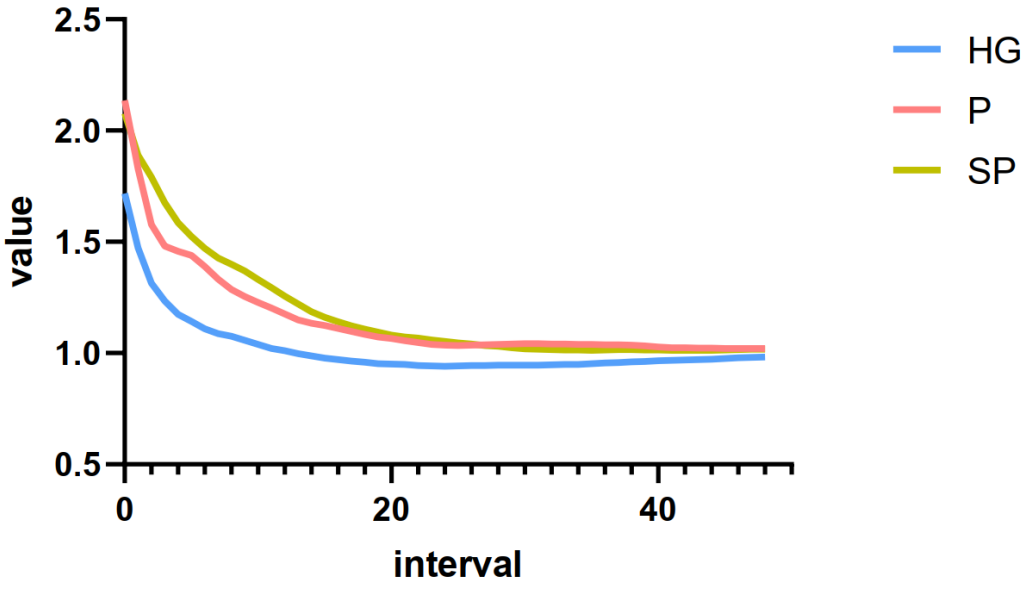
Sup Fig.2 Immunofluorescence staining shows different epithelial layers with single-cell genes markers (CRNN, KRT6B, LY6D, KRT5). Scale bar=200 μm.



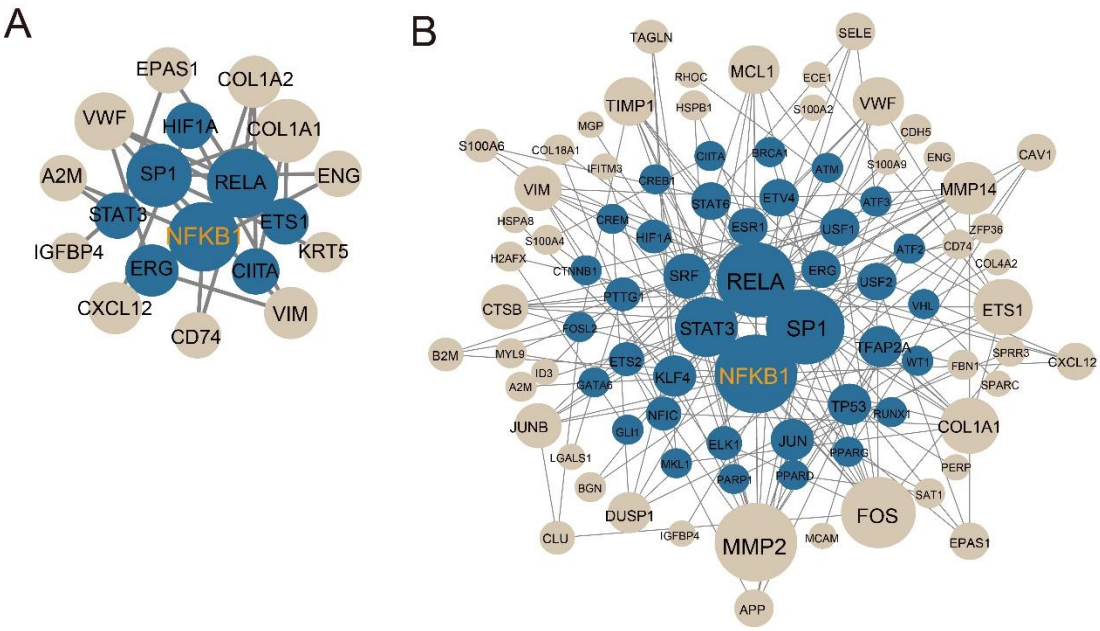
Sup Fig.3 Visium HD data analysis revealing the relative expression levels of *KRT1*, *DSG1*, *PI3*, and *GPX2* in the gingival tissue.



Sup Fig.4 Spatial map of the eight subgroups of fibroblasts in the Visium HD date. Scale bar=200 μm.



Sup Fig.5 The cell spatial relationship of macrophages and endothelial cells in the three group (HG、P、SP).



Sup Fig.6 (A). Gene regulatory network showing key transcription factors and upregulated genes in endothelial cells from the SP group compared with the HG group. (B). Gene regulatory network showing key transcription factors and upregulated genes in endothelial cells from the SP group compared with the P group.