

Integrated analysis of Single-cell RNA-seq, Mendelian randomization and eQTL reveals immune cell-related nomogram model and subtypes in periodontitis

Running title: Immune Cell Subtypes and Nomogram Model in Periodontitis

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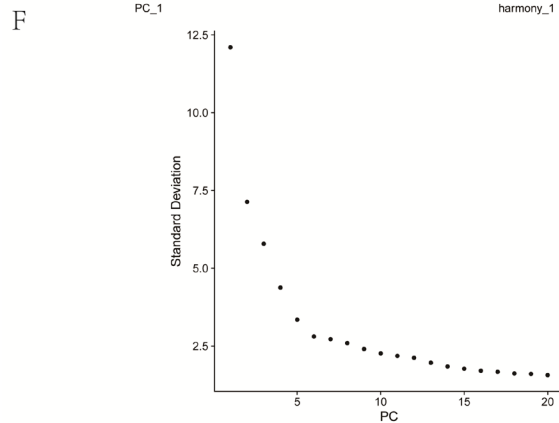
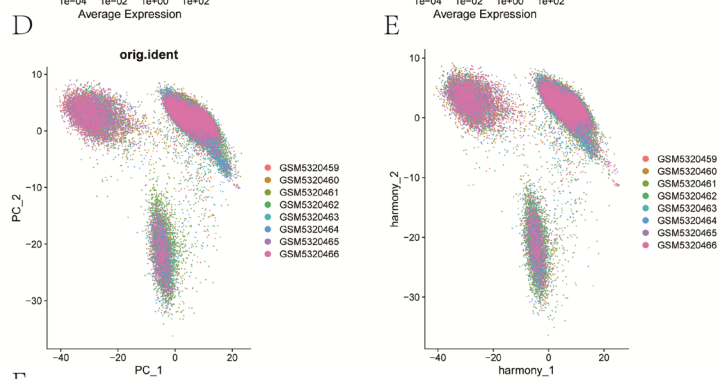
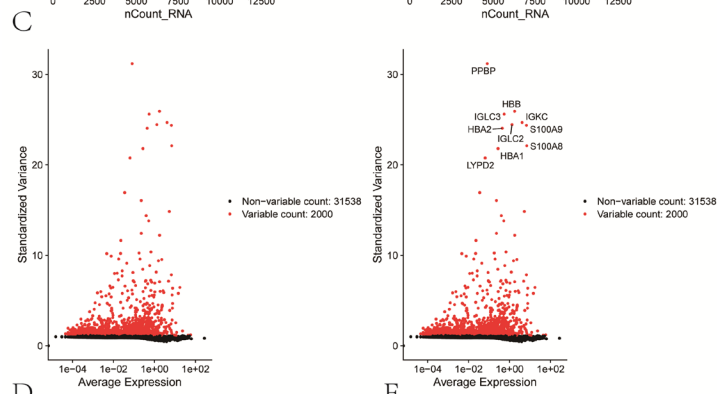
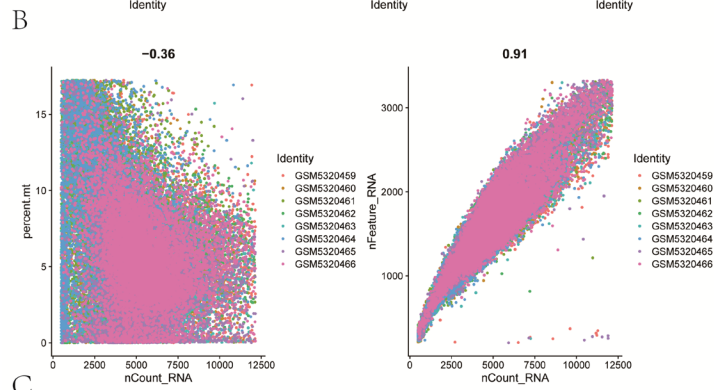
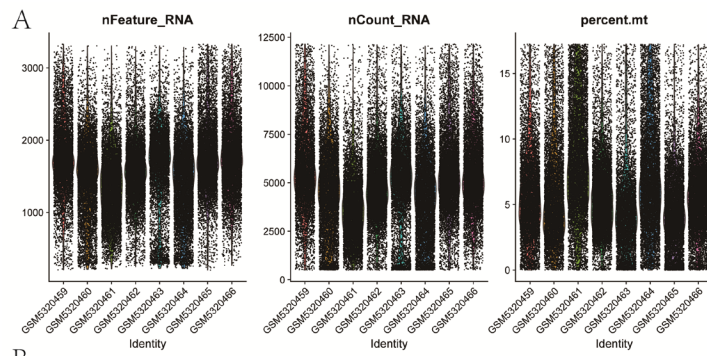
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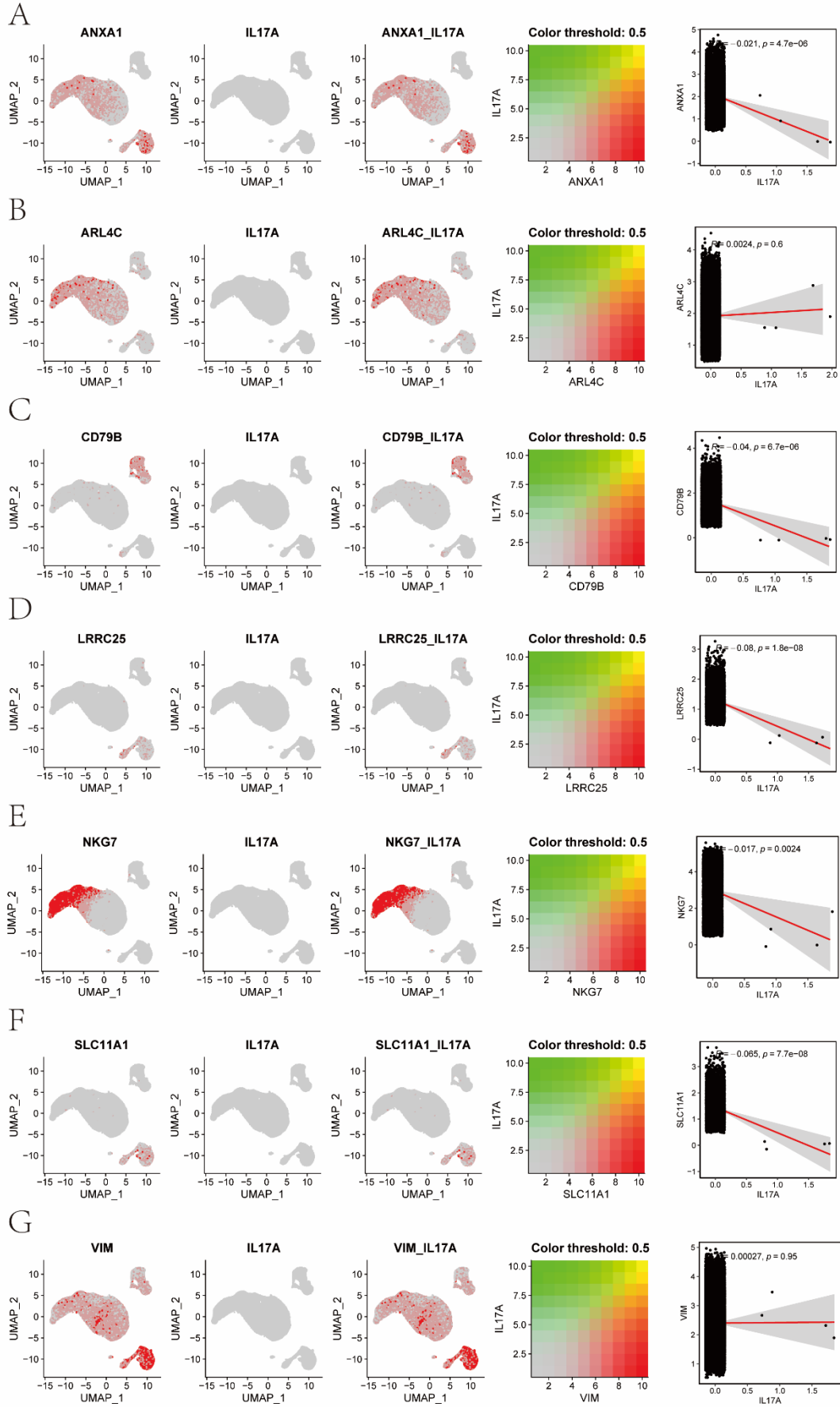
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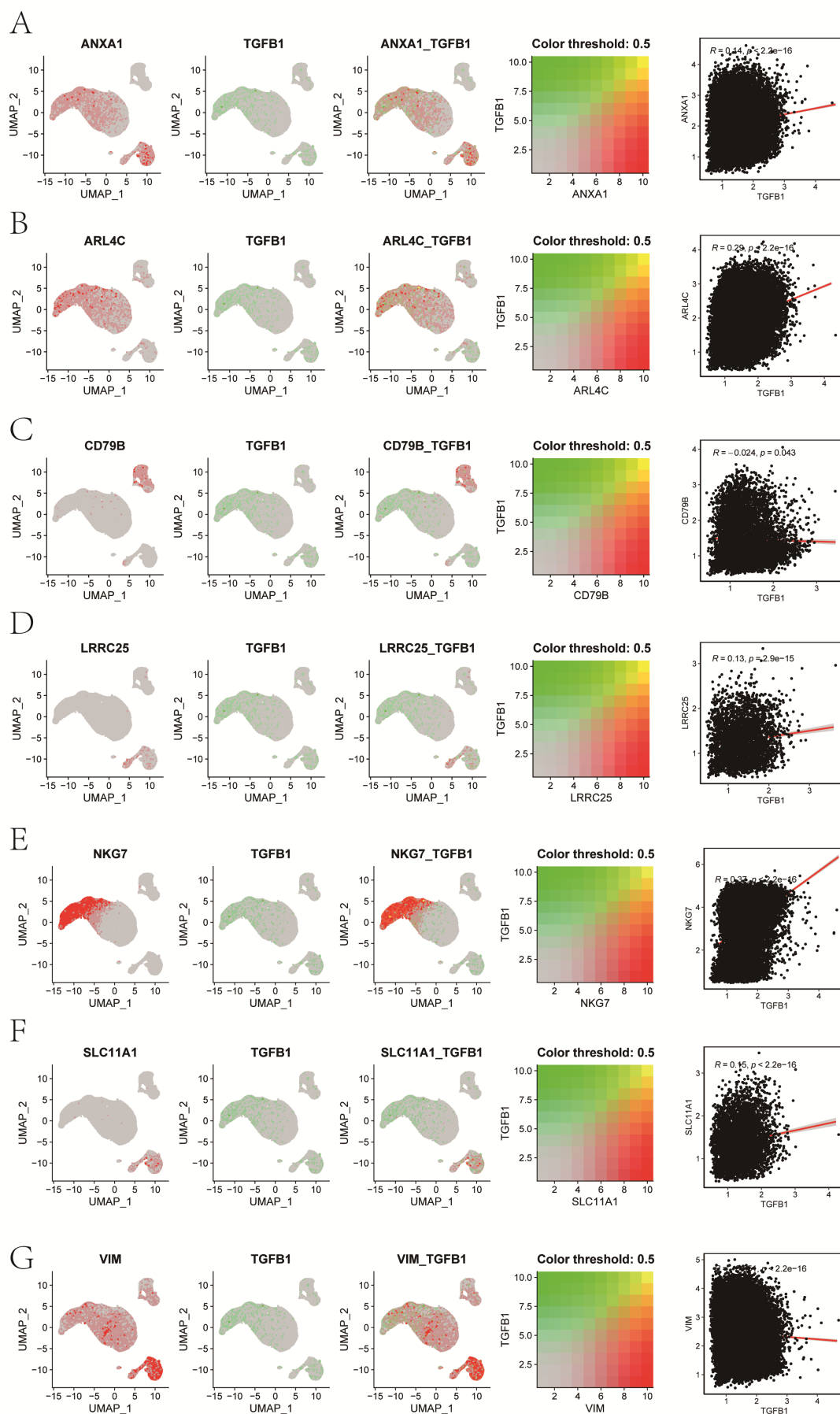
Xuedi Qiu and Fan Yang contributed equally first co-author for this work.



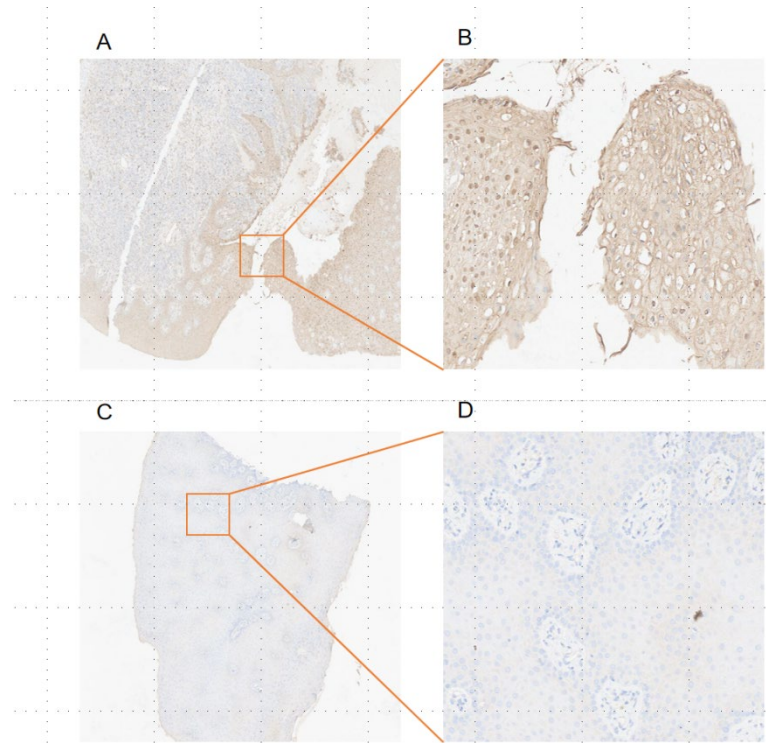
S1 Fig. sc-RNA seq analysis and DEGs analysis.(A)DEGs expression in datasets. (B)Scatter plot of DEGs count vs. feature. (C)Volcano plot of DEGs in datasets. (D) and (E)Screening of differentially expressed DEGs in datasets. (F)Analysis of various soft-thresholding powers.



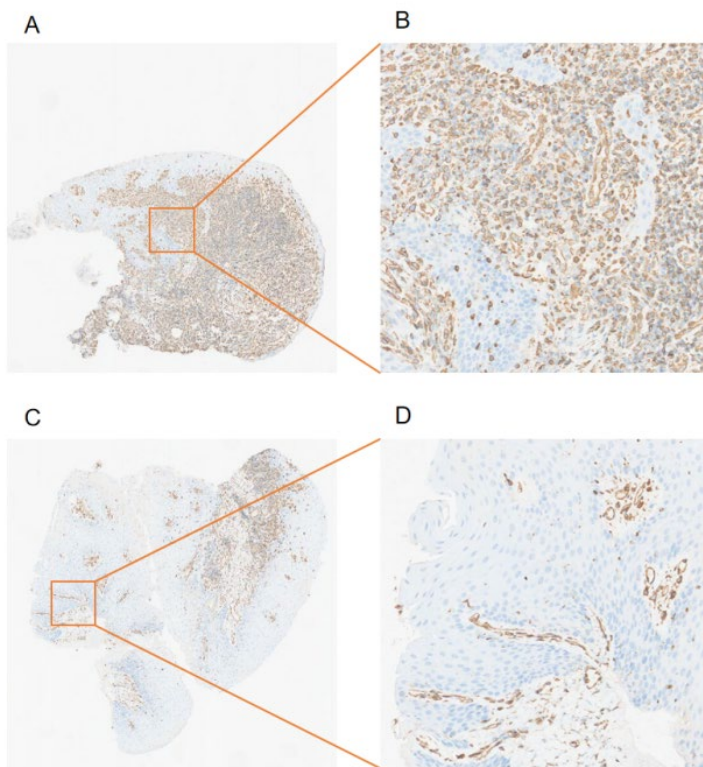
S2 Fig. Correlationship between hub genes and IL17A. (A~G) Correlations between TGF- β and hub genes(ANXA1, ARL4C, CD79B, LRRC25, NKG7, SLC11A1, and VIM)



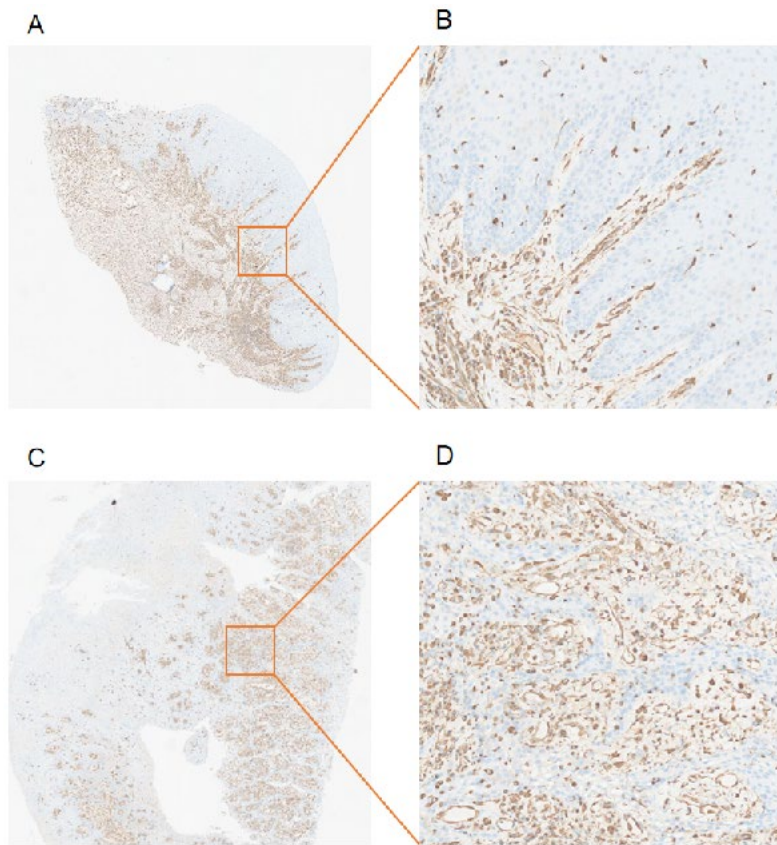
S3 Fig. Correlationship between hub genes and TGF- β . (A~G) Correlations between TGF- β and hub genes(ANXA1, ARL4C, CD79B, LRRC25, NKG7, SLC11A1, and VIM)



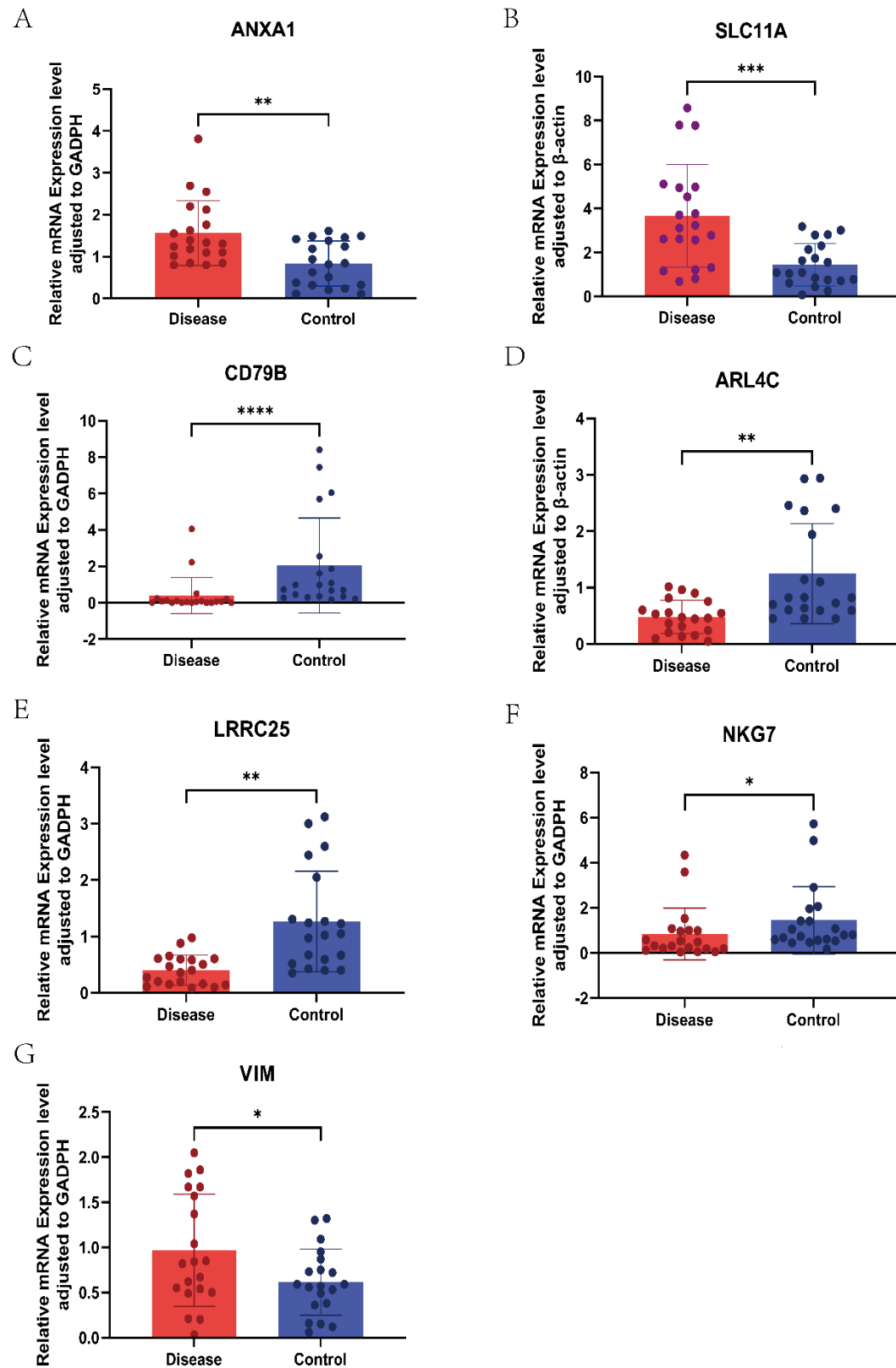
S4 Fig. Expression of ANXA1 protein in periodontitis tissues and normal gingival tissues.A. Periodontitis tissue ($\times 10$);B. Periodontitis tissue ($\times 40$);C. Normal gingival tissue ($\times 10$);D. Normal gingival tissue ($\times 40$).



S5 Fig. Expression of SLC11A1 protein in periodontitis tissues and normal gingival tissues. A. Periodontitis tissue ($\times 10$); B. Periodontitis tissue ($\times 40$); C. Normal gingival tissue ($\times 10$); D. Normal gingival tissue ($\times 40$).



S6 Fig. Expression of CD79B protein in periodontitis tissues and normal gingival tissues. A. Periodontitis tissue ($\times 10$); B. Periodontitis tissue ($\times 40$); C. Normal gingival tissue ($\times 10$); D. Normal gingival tissue ($\times 40$).



S7 Fig. Transcriptional levels of Genes mRNA in gingival tissues