Figure S1 Workflow of data collection and analysis.
Figure S2 ROC Analysis of clinical prognostic markers and in combination with the four prognostic genes in HNSCC, using TCGA data. (A-B) ROC curves of HPV status, identified by p16 staining (A) or in situ hybridization (ISH) (B), with AUC scores. (C) ROC curves for CD8+ T-cell abundance, with AUC scores. (D-I) ROC curves for the model including the four prognostic genes combined with p16 staining (D), in situ hybridization (ISH) (E), CD8+ T-cell abundance (F), pathological T-classification (G), tumor stage (H) and tumor grade (I). (J) ROC curves for the model including the four prognostic genes combined with CD8+ T-cell abundance and Path_N stage.
Figure S3 IHC validations of the four immune-related genes associated with HNSCC, from the HPA database. Representative images showing the expression of each gene in HNSCC tissues and normal oral cavity mucosal tissues. The fractions of samples with high, medium, low, or undetectable antibody staining levels are presented by the blue color-coded scale. (A-D) Expression levels of all four proteins encoded by the prognostic genes, PVR, TNFRSF12A, IL21R, and SOCS1, in HNSCC tissues were higher than in normal oral tissues.
Figure S4 Representative images from TMA-IHC staining of PVR, TNFRSF12A, IL21R, and SOCS1 protein expression in matched HNSCC tumors and adjacent normal tissues.
Figure S5 Correlations between the four immune-related genes and 22 immune-cell types. Correlation between the four prognostic-associated immune genes and 22 immune-cell types, by Pearson’s correlation analysis. The correlation coefficients are shown in each cell and the asterisks represent significance. (*p < 0.05; **p < 0.01; ***p < 0.001)