

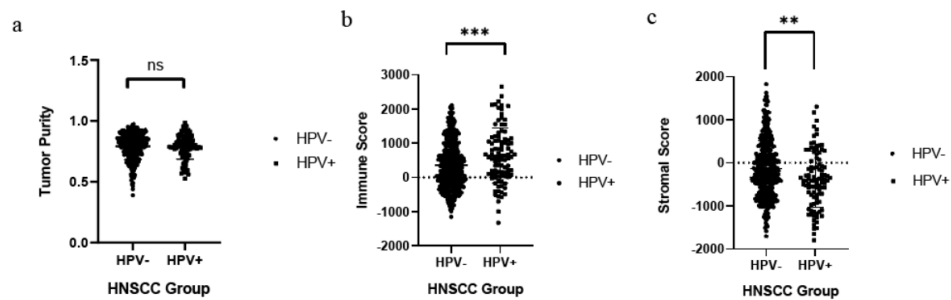


FIGURE 1 The immune cell score, stromal cell score, and tumor purity of each sample

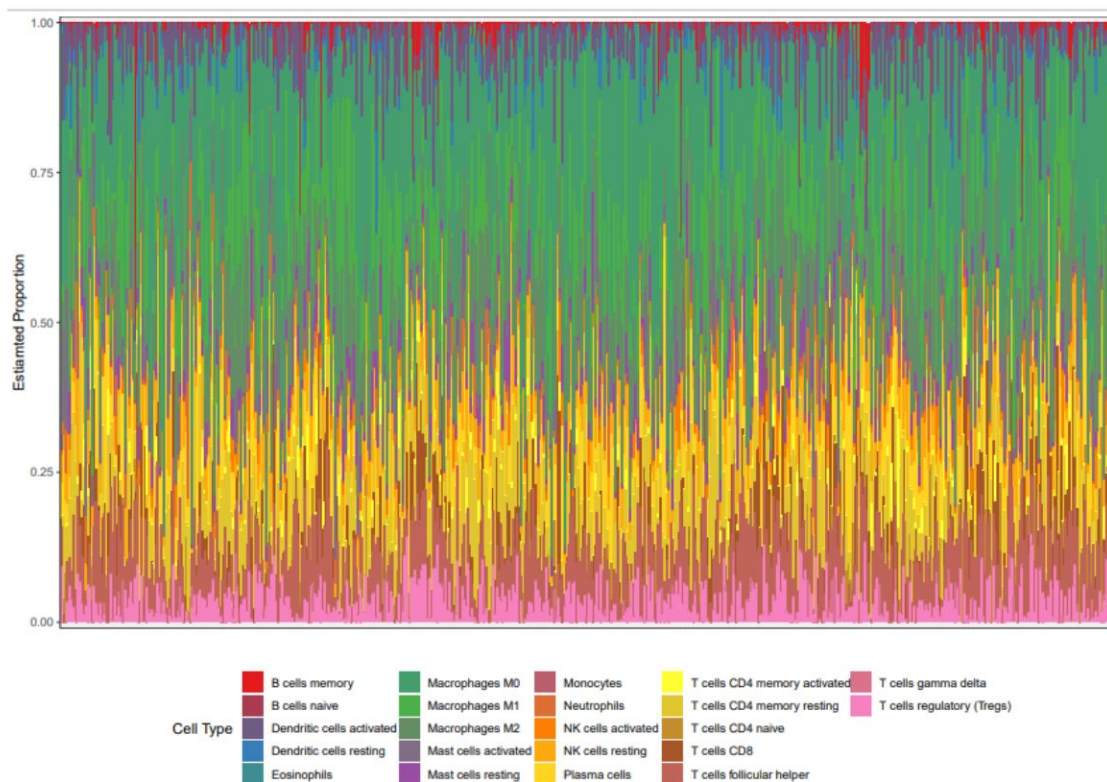


FIGURE 2 The types of immune cell infiltration in the sample

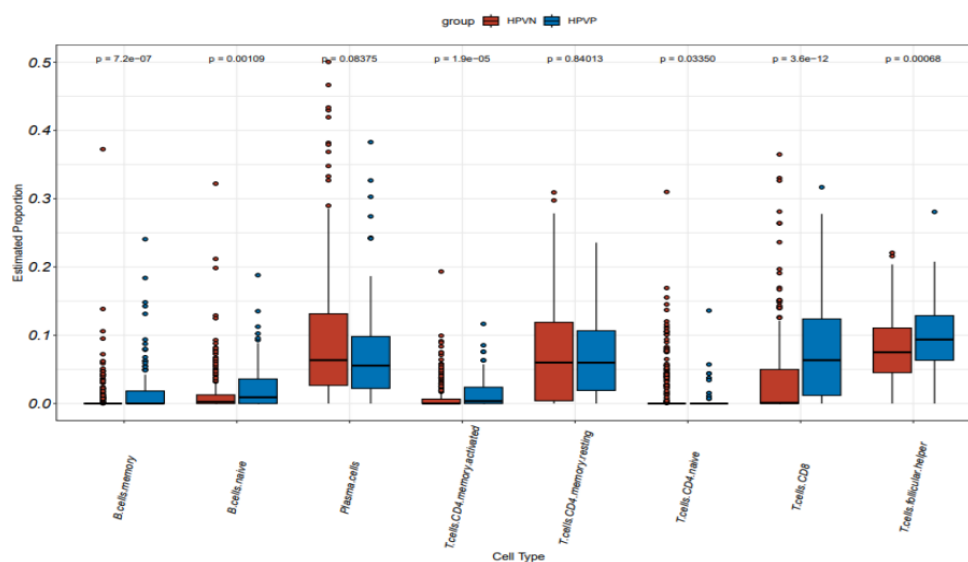


FIGURE 3 The types and proportions of immune cell infiltration in the sample

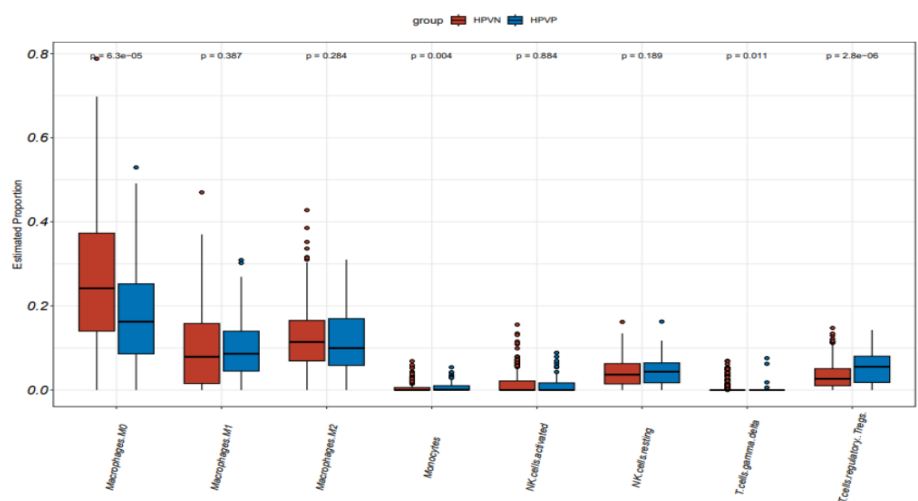


FIGURE 4 The types and proportions of immune cell infiltration in the sample

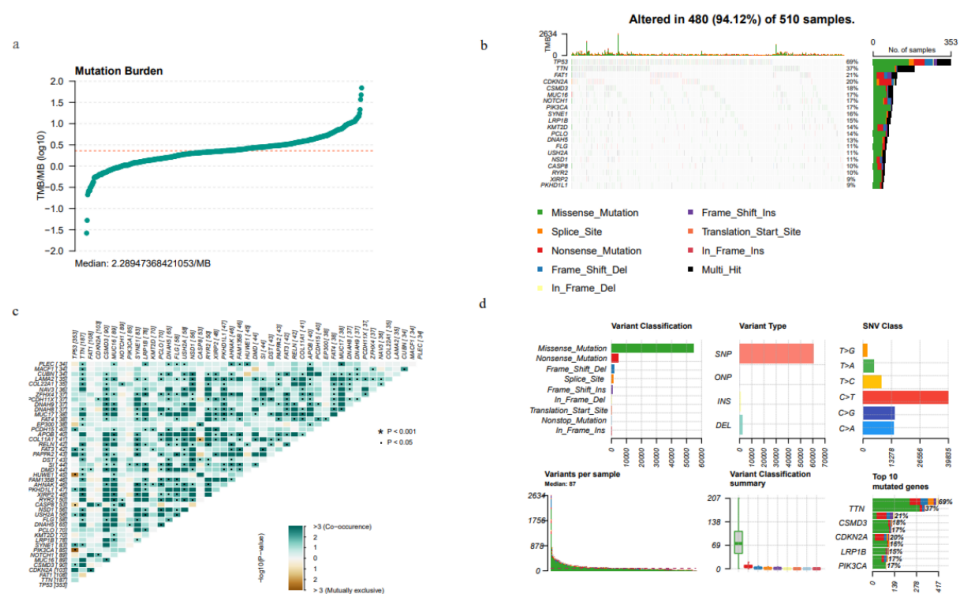


FIGURE 5 The tumor mutation burden of patients

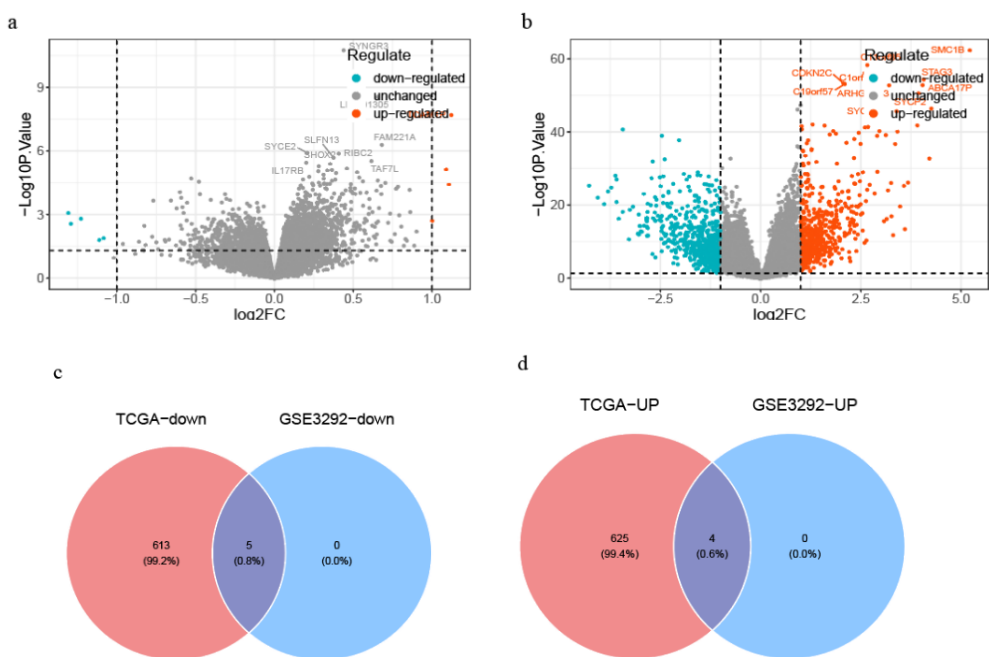


FIGURE 6 Comparison of differential genes between HPV+ and HPV- HNSCC patients in TCGA and GEO databases.

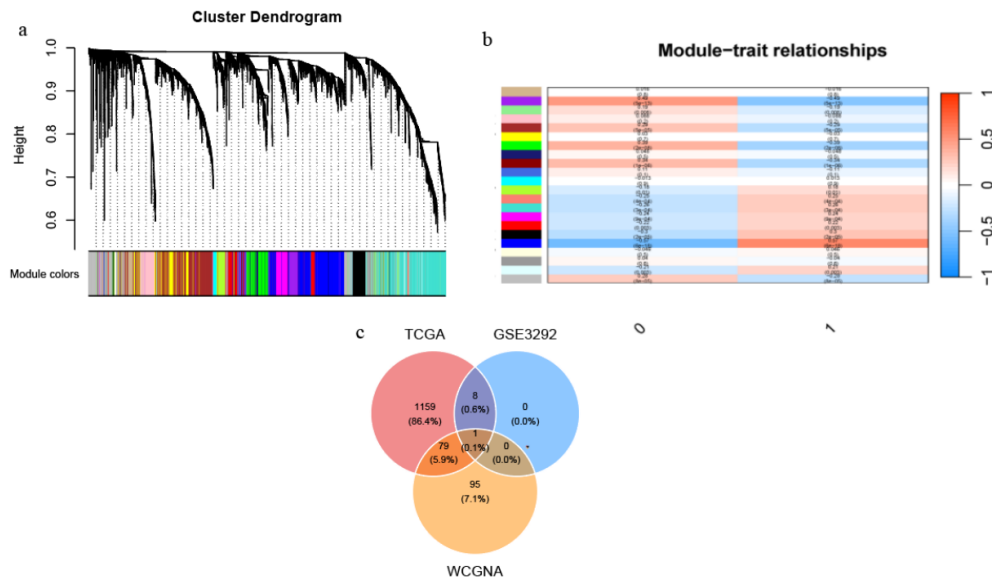


FIGURE 7 Weighted gene co-expression network analysis of HPV+ HNSCC patients to identify potential gene modules.

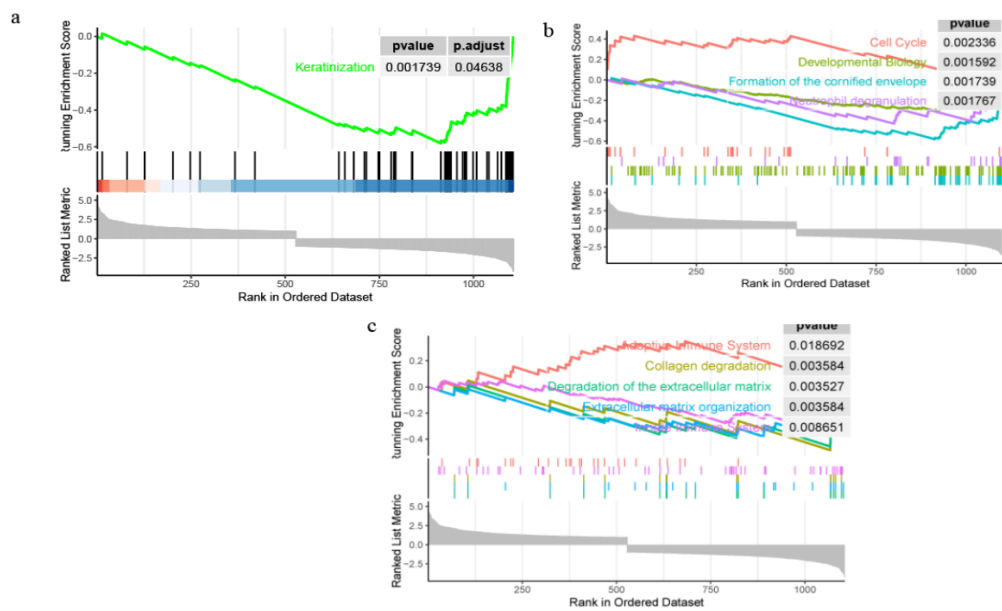


FIGURE 8 Gene set enrichment analysis (GSEA) of DEGs

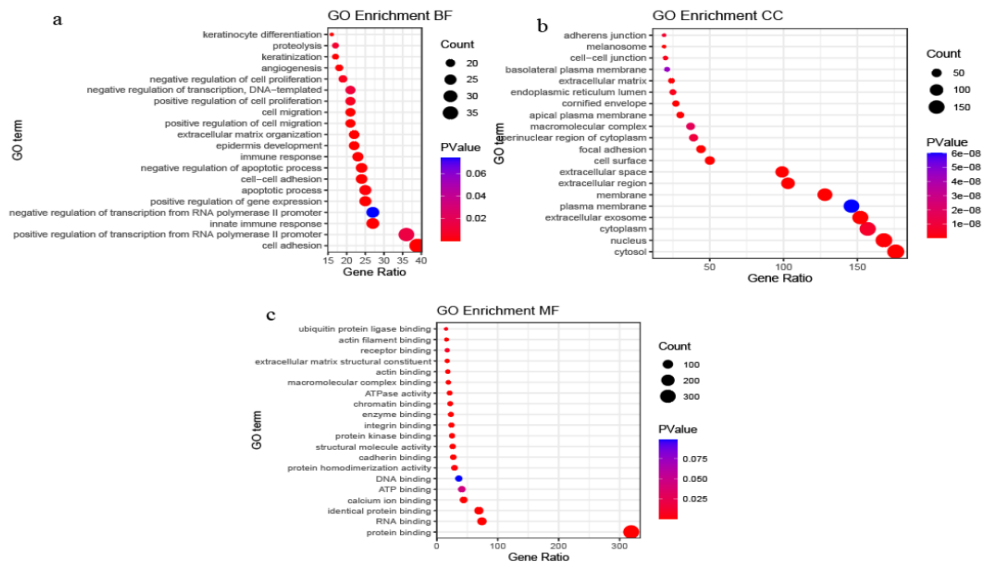


FIGURE 9 GO and KEGG pathway enrichment analyses of genes in module link to HPV+ HNSCC

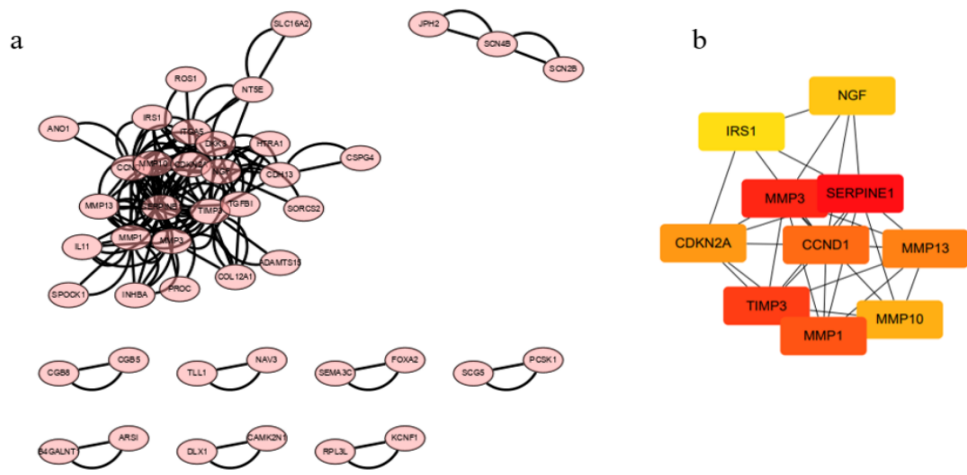


FIGURE 10 Protein-protein interaction network construction and identification of hub genes (a: The result of whole potential hub genes; b: 10 most Critical Genes Selected Based on Connection Tightness)

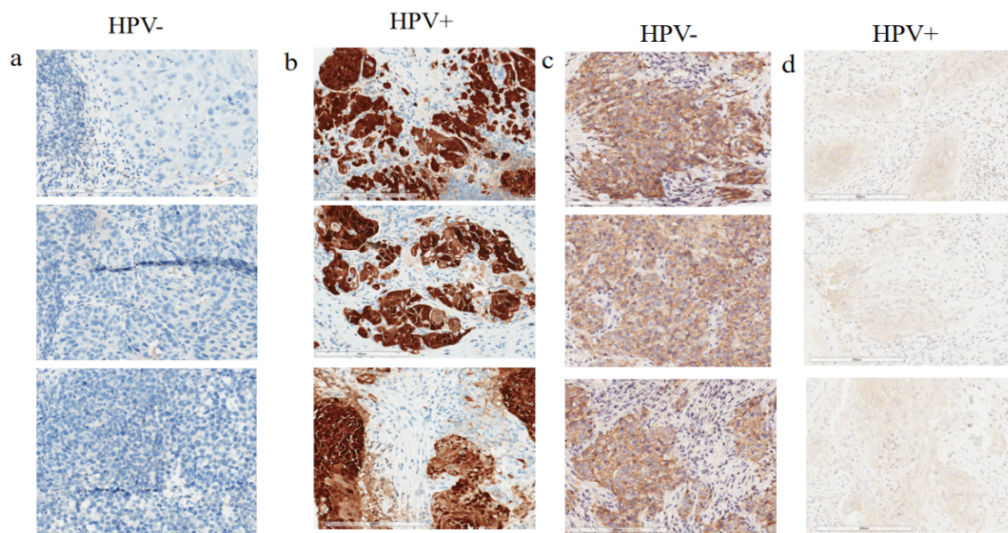


FIGURE 11 Immunohistochemistry of HPV and SERPINE1 in HNSCC samples (laryngeal, oral cavity, and nasal cavity cancers). The SERPINE1 was expressed in nucleus and cytoplasm. (a: HPV- staining group; b: HPV+ staining group; c: SERPINE1 is strongly positively expressed in HPV- HNSCC group; d: SERPINE1 is positively expressed in HPV- group HNSCC)

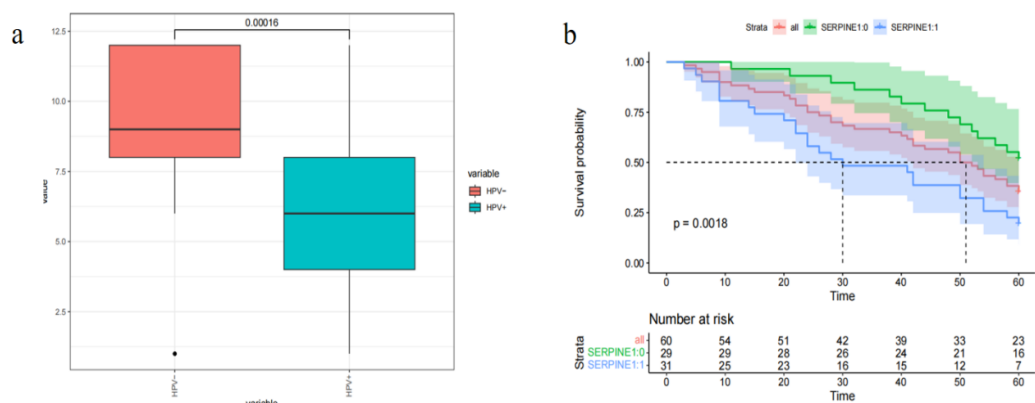


FIGURE 12 a: Comparison of SEPRINE1 expression between HPV+ HNSCC and HPV- HNSCC patients; b: KM

survival curves according to the level of SEPRINE1 expression.

