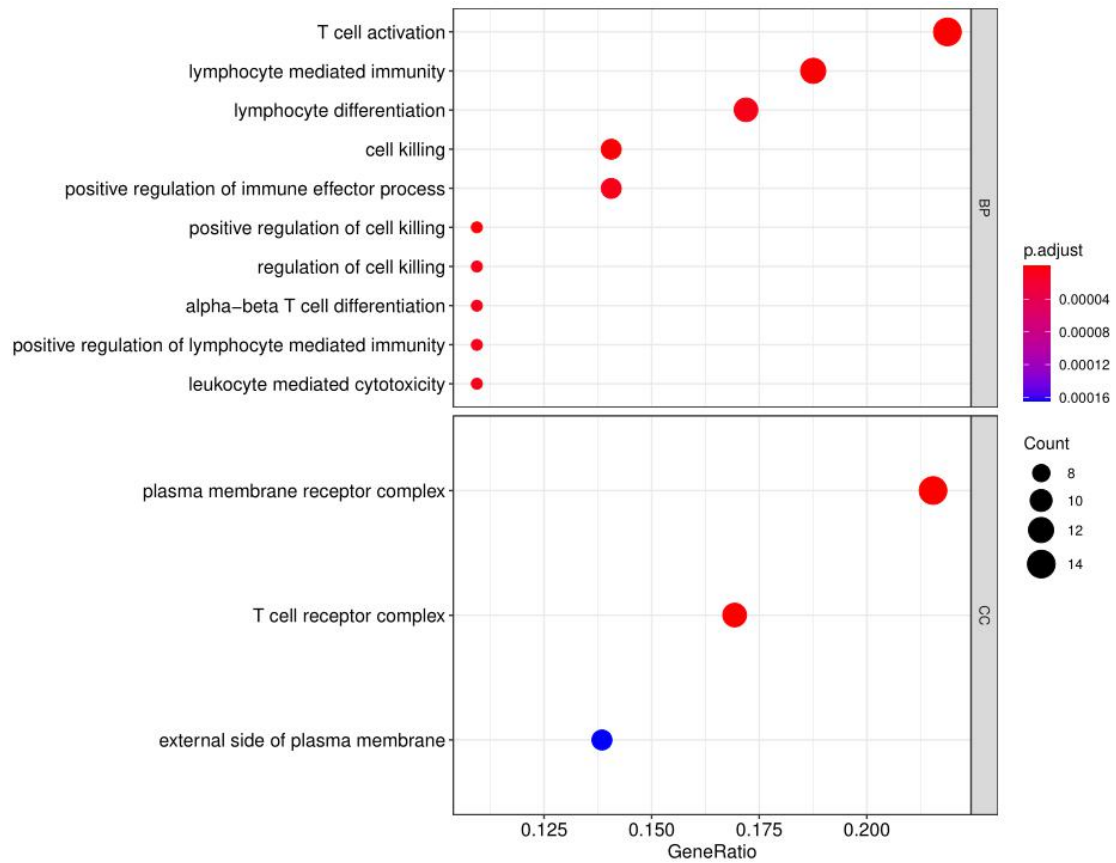
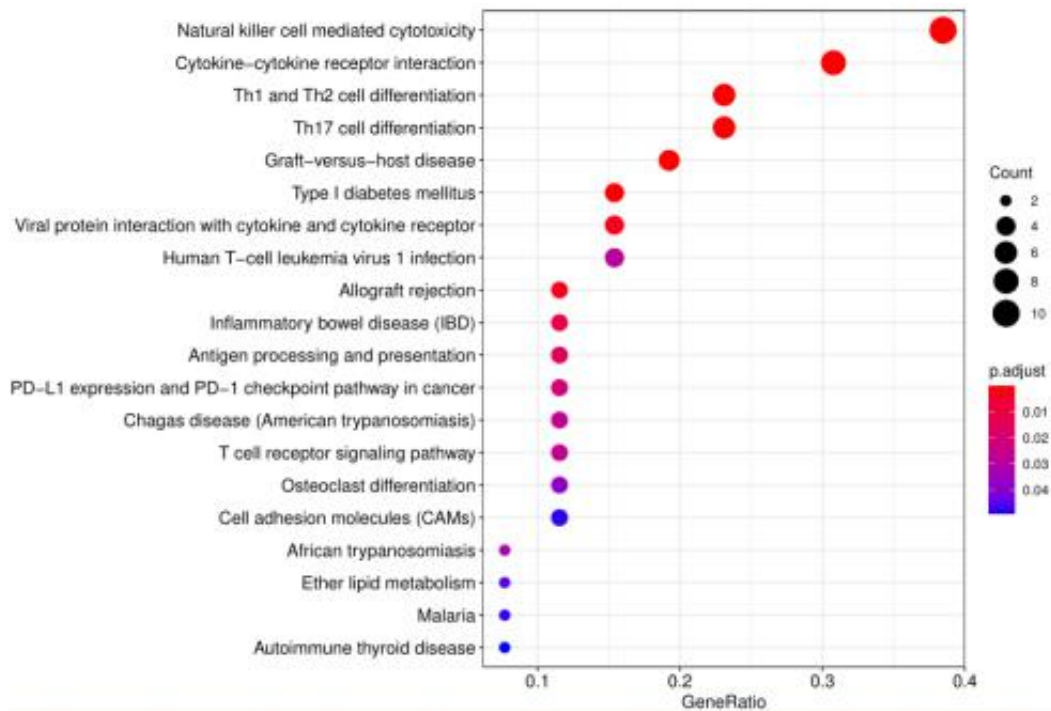


FigureS1 WCGNA to identify modules related with risk score and risk group. Differentially expressed genes between HPV+ and normal-adjacent tissues were used to perform WCGNA. We identified MEred module significantly associated with both risk score and risk group for further enrichment analysis.



FigureS2 GO enrichment analysis of risk-related MERed module.



FigureS3 KEGG enrichment analysis of risk-related MERed module.