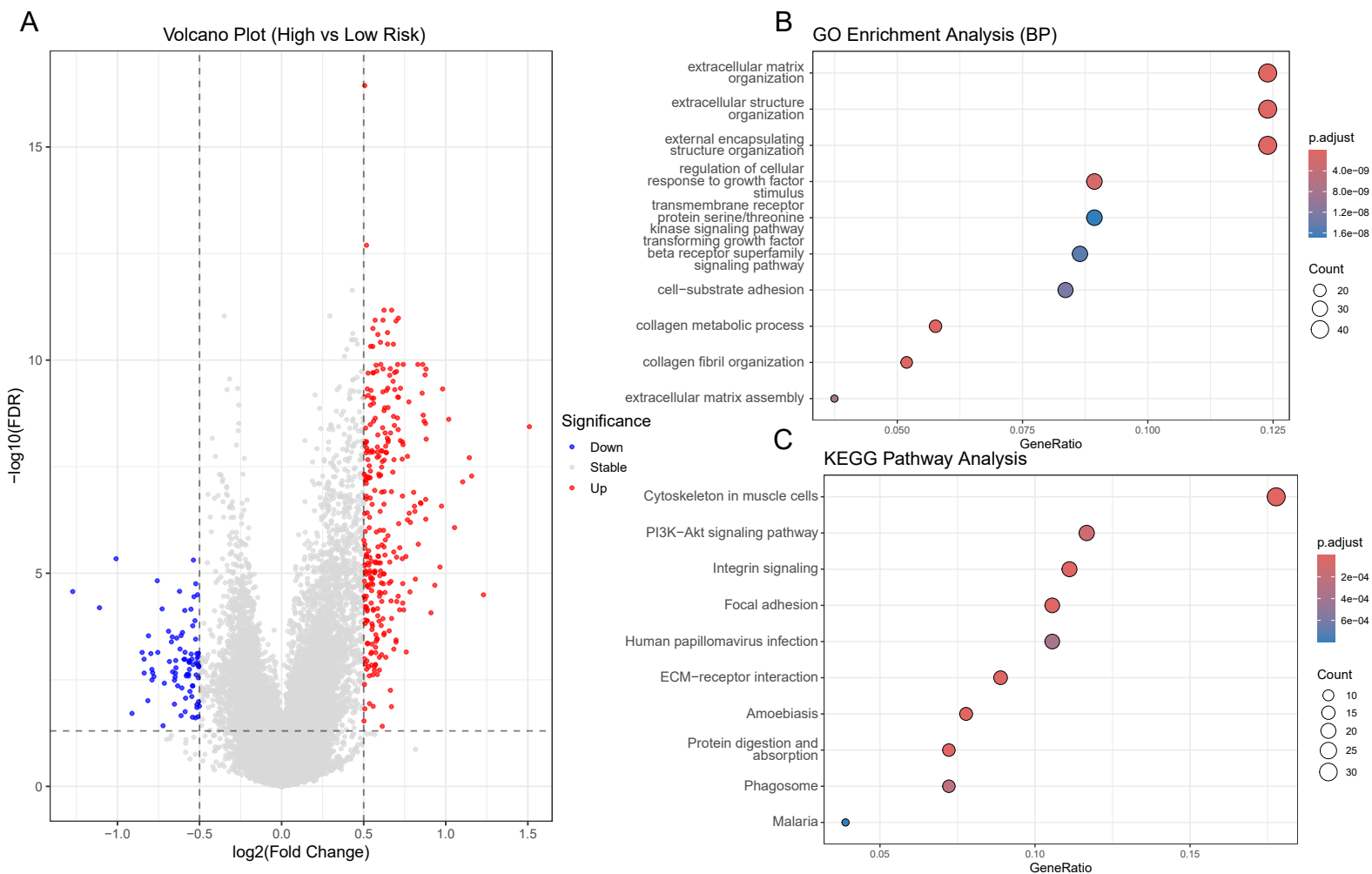




Supplementary Figure S5. Differential expression and pathway enrichment analyses between high- and low-risk patients in the TCGA-COAD cohort. (A) Volcano plot of the differentially expressed genes (DEGs) between the high- and low-risk groups. (B) Bubble plot illustrating the top enriched Gene Ontology (GO) biological processes for the identified DEGs. (C) Bubble plot displaying the top enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways for the DEGs. For both (B) and (C), the size of the dots represents the number of enriched genes (Count), and the color gradient indicates the statistical significance (adjusted P-value).