Supplementary

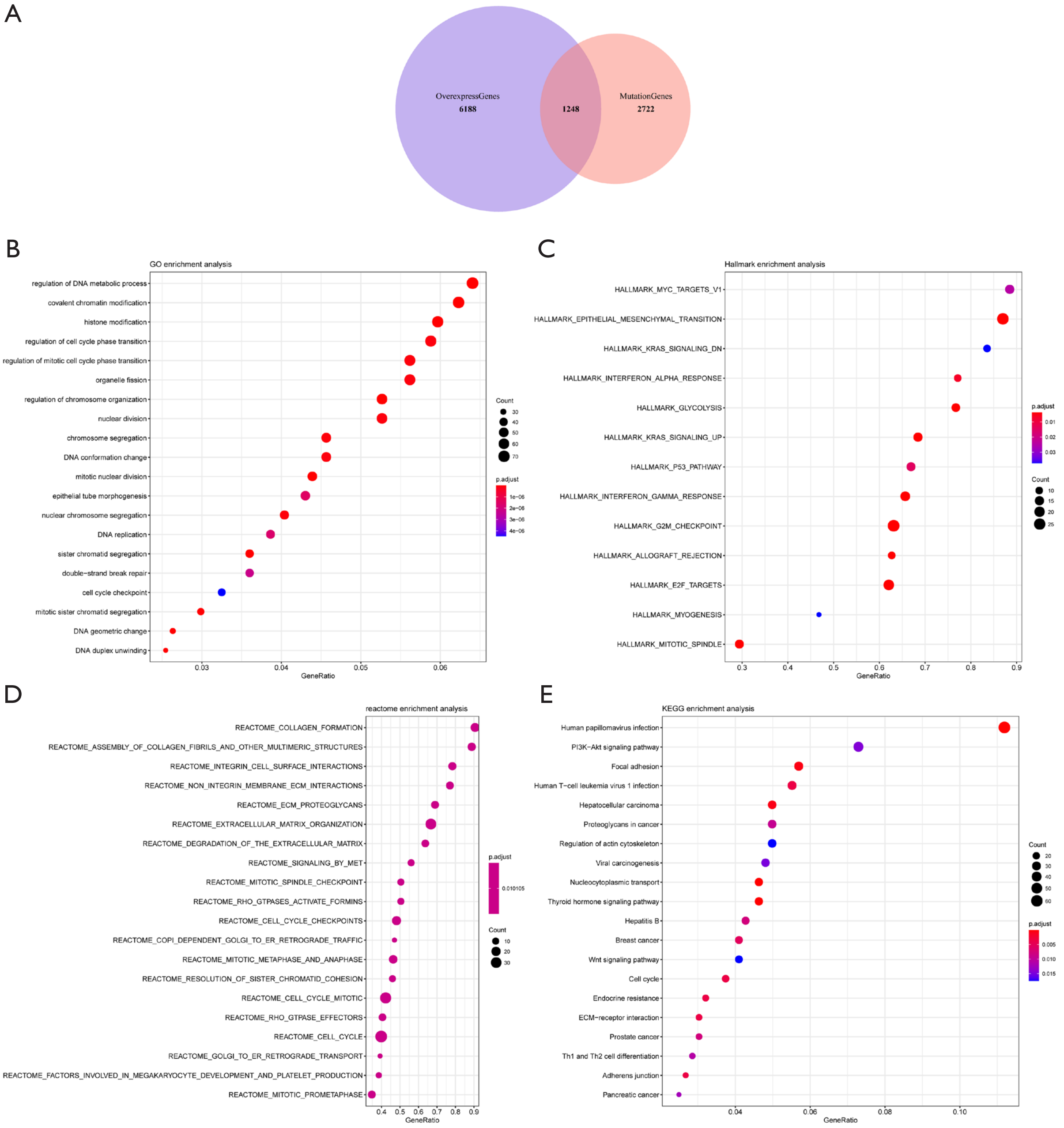
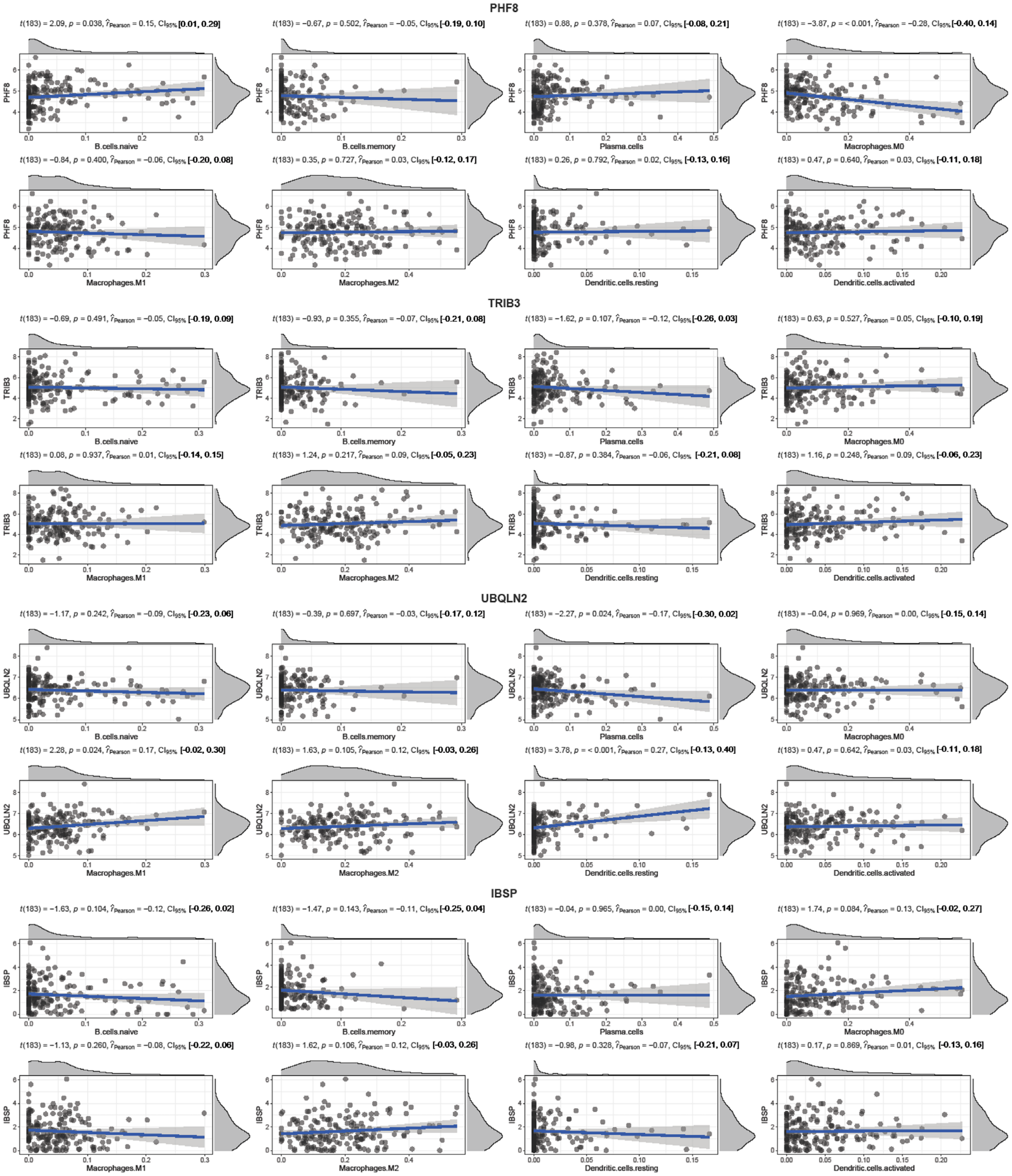


Figure S1 Functional enrichment analysis of overexpressed and mutated genes as antigen candidates. (A) Overexpressed and mutant gene sets and their gene intersections. (B) GO enrichment analyses. (C) Hallmark, (D) Reactome, and (E) KEGG enrichment analyses. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.



© AME Publishing Company.
https://dx.doi.org/10.21037/jtd-2025-233

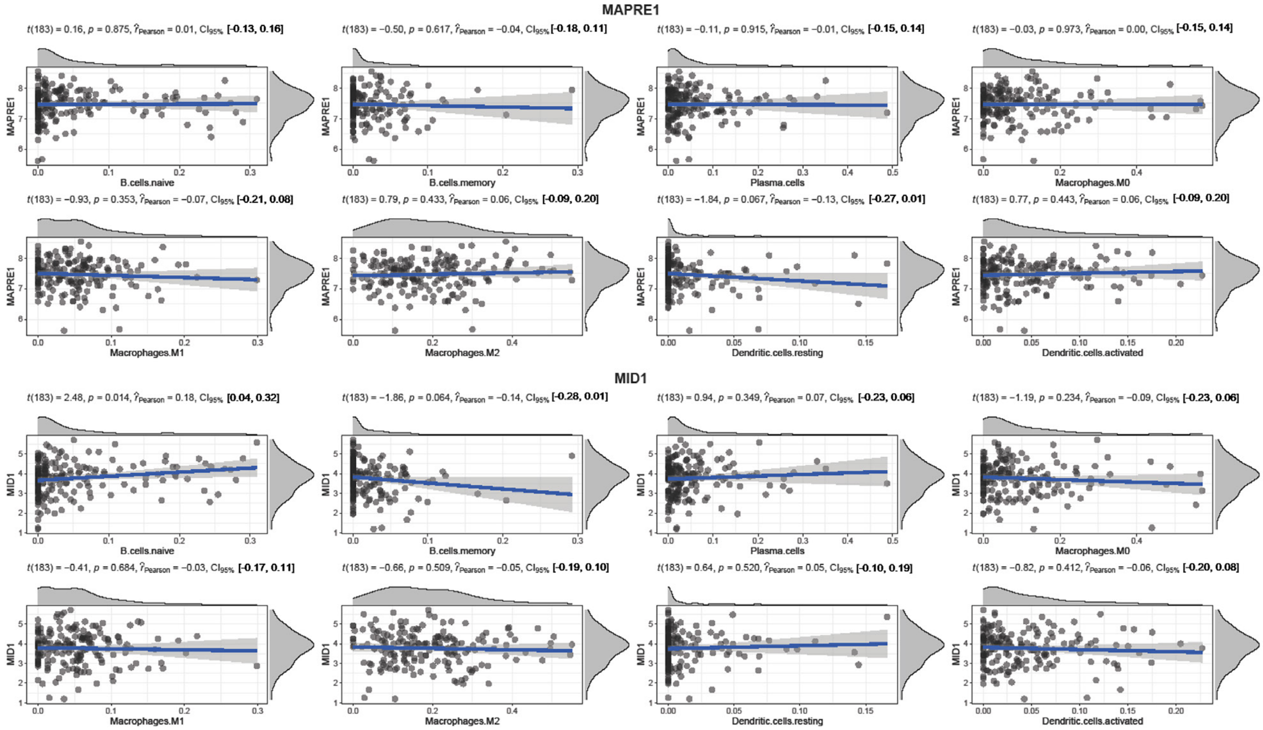


Figure S2 Relevance of six potential antigens to APCs. APCs, Antigen-Presenting Cells.

© AME Publishing Company.

https://dx.doi.org/10.21037/jtd-2025-233

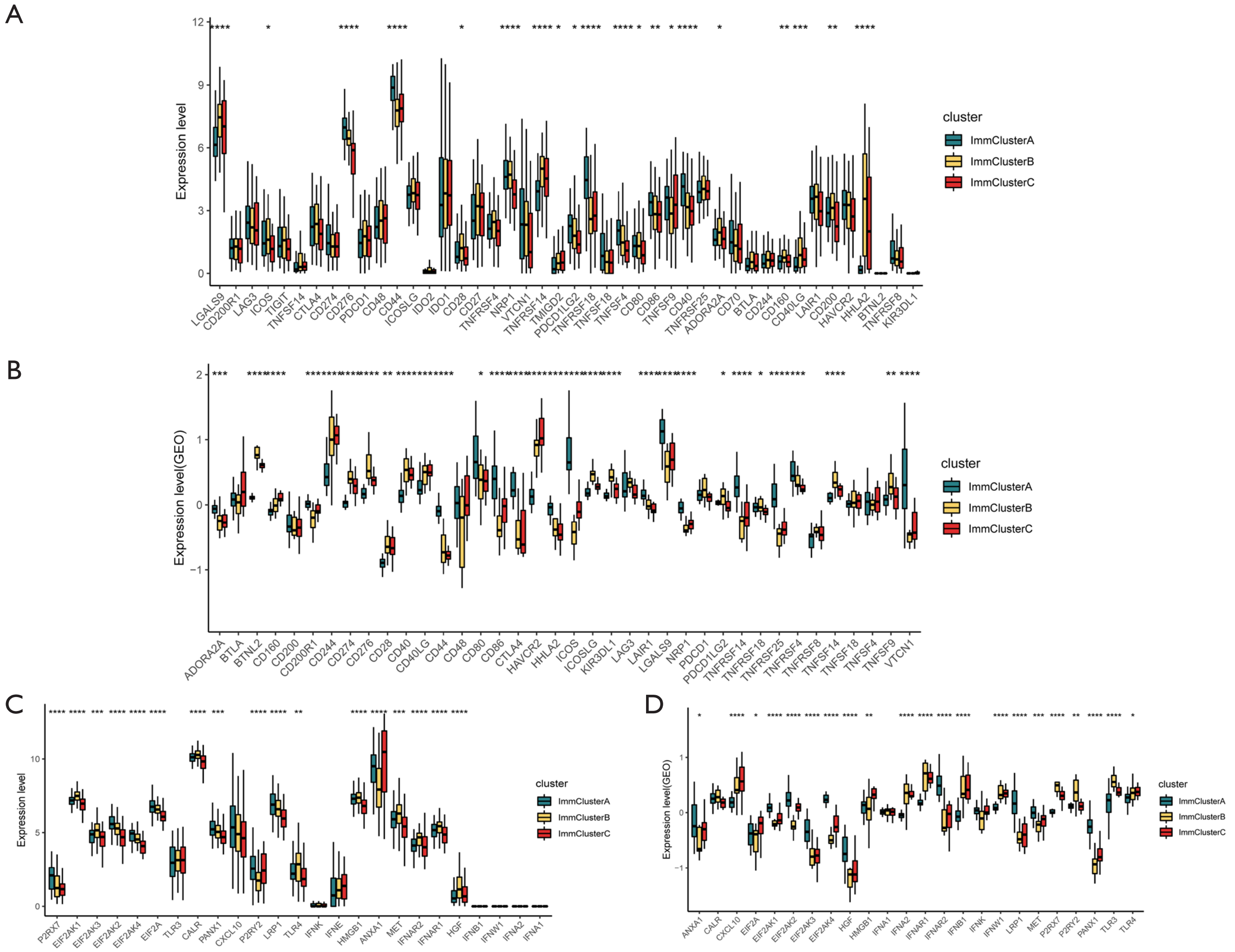


Figure S3 ICPs and ICDs expressed in different immune subtypes. (A) Differential expression of ICPs within different immune subtypes in TCGA data. (B) Differential expression of ICPs within different immune subtypes in GEO data. (C) Differential expression of ICDs within different immune subtypes in TCGA data. (D) Differential expression of ICDs within different immune subtypes in GEO data. *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001. ICPs, immune checkpoint proteins; ICD, immune cell death; KEGG, Kyoto Encyclopedia of Genes and Genomes; GEO, Gene Expression Omnibus.

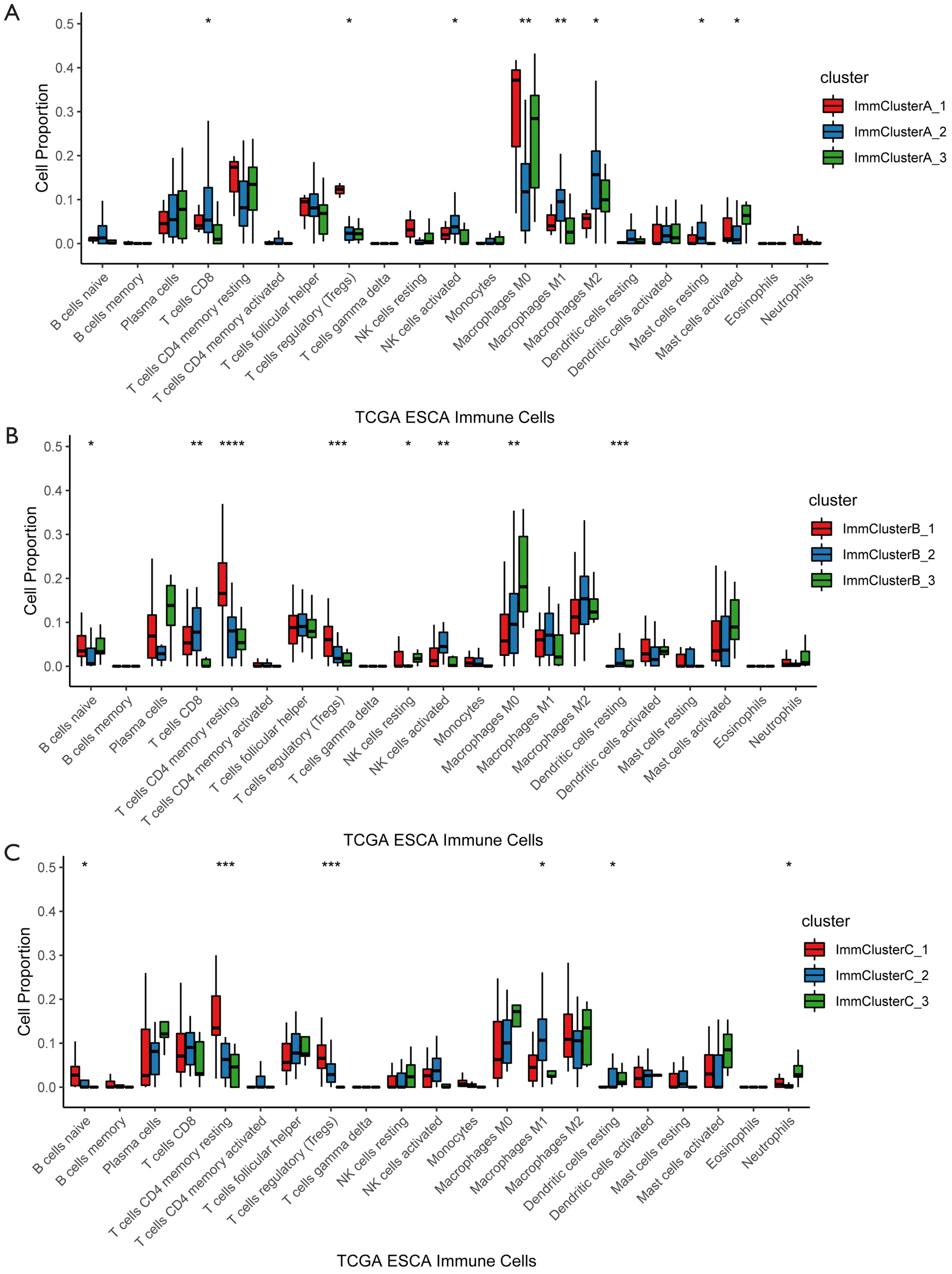


Figure S4 The relationship between the proportion of immune cells in the three clusters (A-C). *, P<0.05; **, P<0.01; ***, P<0.001; ****P<0.0001. TCGA, The Cancer Genome Atlas; ESCA, esophageal cancer.