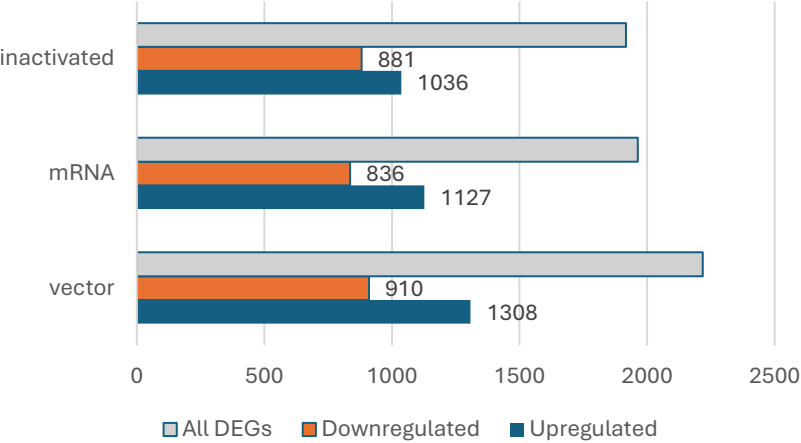
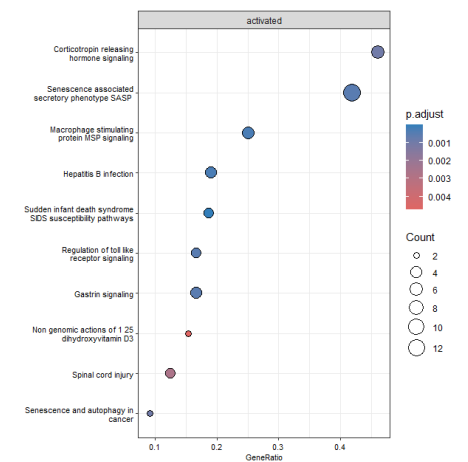
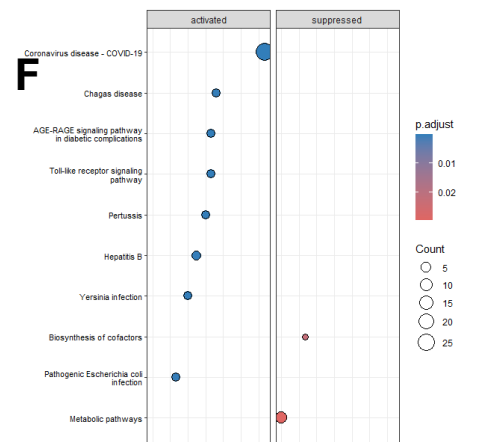
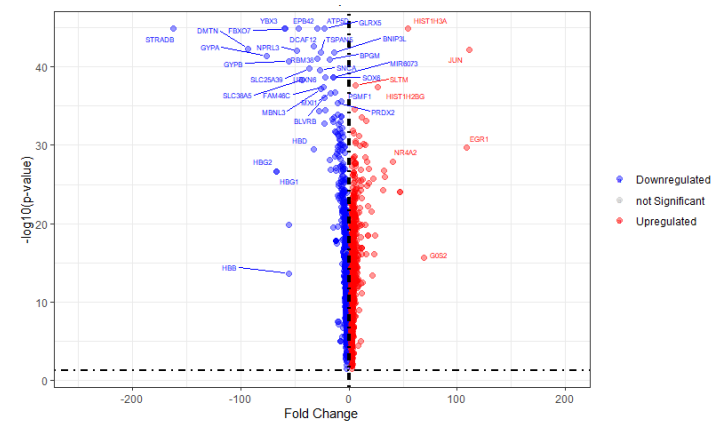
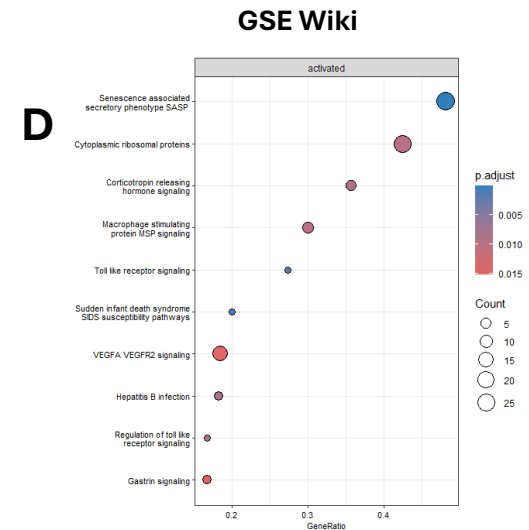
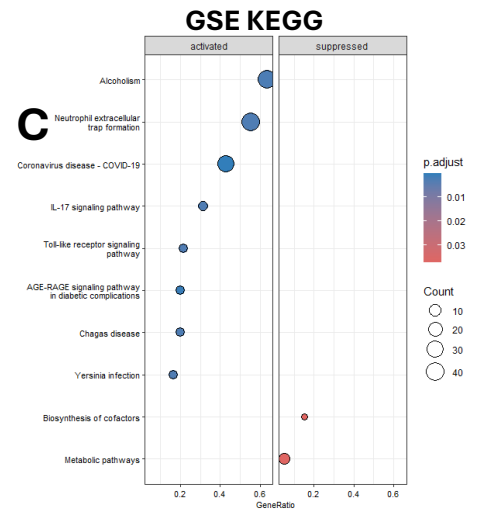
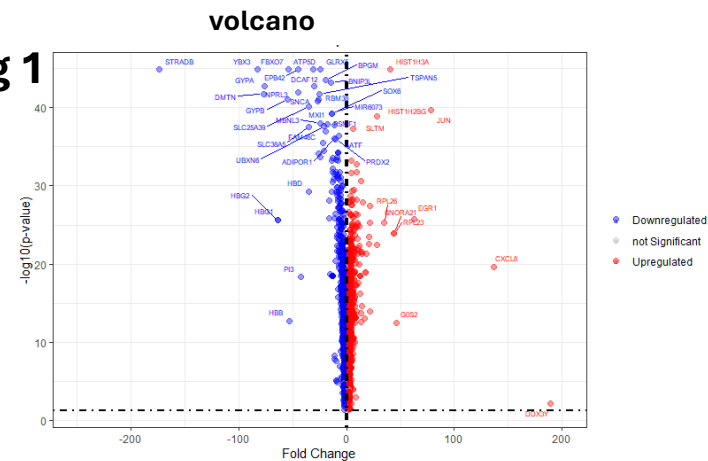


S Fig 1. Comparison of DEGs between different post-pandemic groups as per the vaccines received.

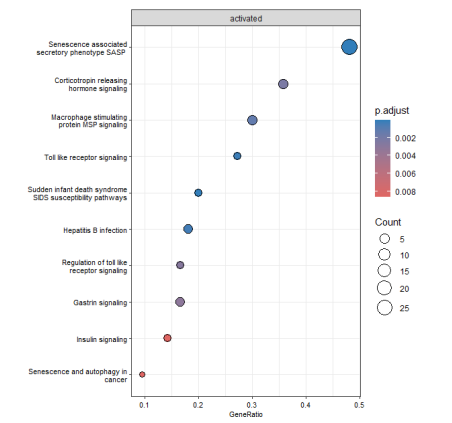
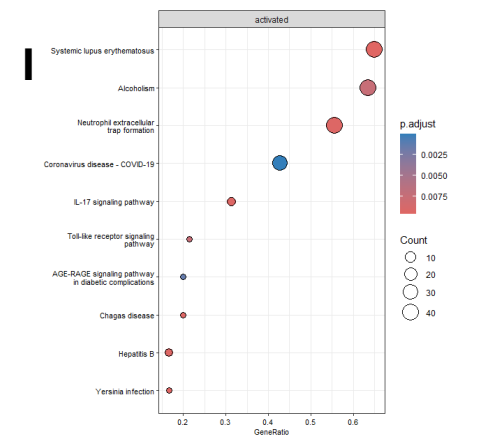
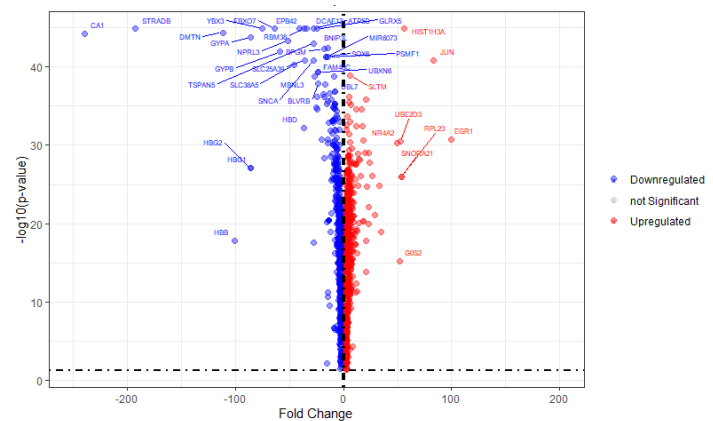
A.



B



H



S Fig 1. Comparison of DEGs between different post-pandemic groups as per the vaccines received. The graphs the analysis of the T3 cohort vaccine sub-groups and the comparison of their transcriptional profiles with healthy pre-pandemic controls (EC). The plots display analysis of DEGs between T3 sub-groups and EC.

A, The barplot depicts the 2,030 differentially expressed genes (DEGs) between vaccinated and healthy control groups as up-regulated, down-regulated, and total genes for each T3 group comparison against EC. Each gene set was analysed through a volcano plot, GSE KEGG and GSE Wiki pathways. Figures for GSE dotplot for Wiki pathways show top 10 activated pathways with the pathways on the Y-axis and the gene ratio on the X-axis in each case. B-D, T3 inactivated vaccine group analysis of 1,917 DEGs. E-G, T3 mRNA group analysis of 1963 DEGs. H-J, vector vaccine group analysis of 2218 DEGs. Permission for use of KEGG analysis and imagery was taken from Kanehisa Laboratories.