

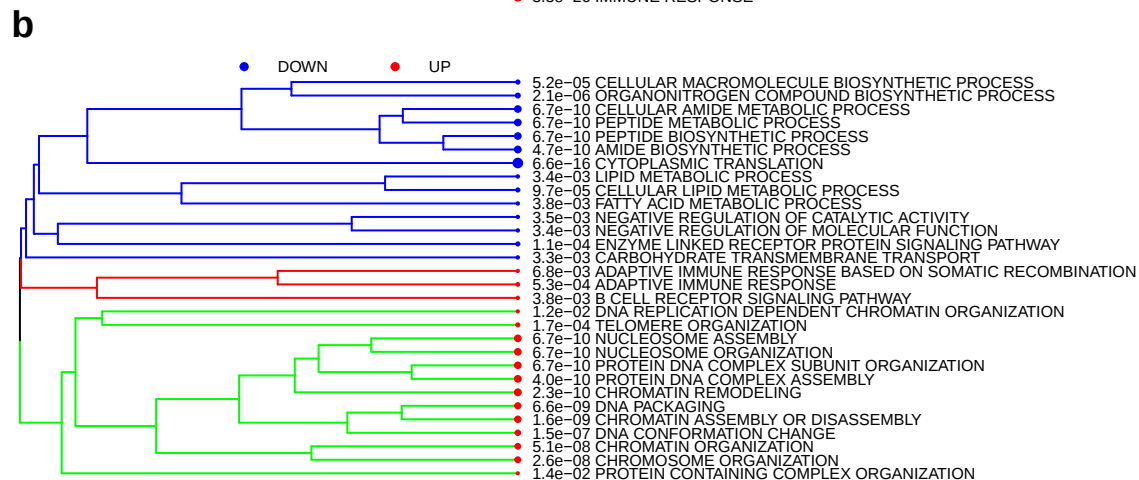
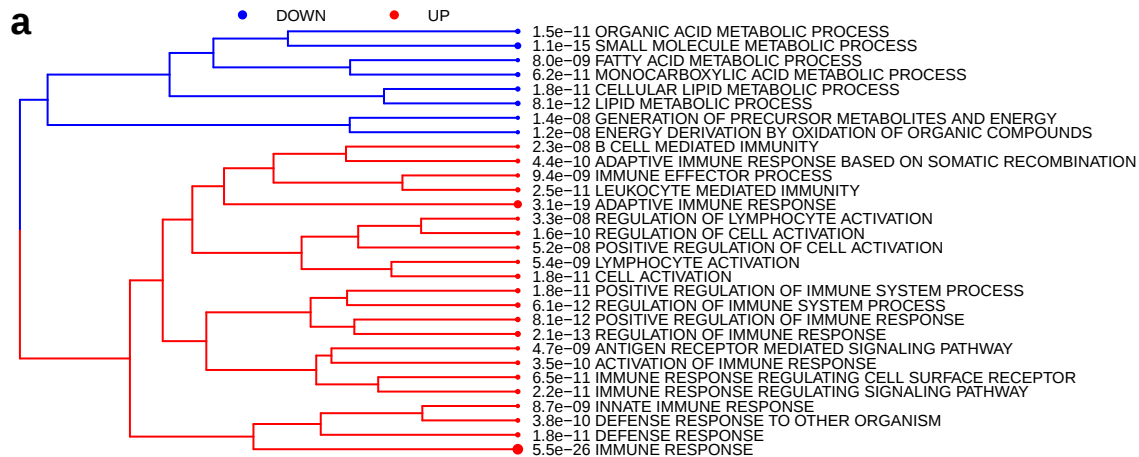


Figure S3. Gene set enrichment analysis of differentially expressed genes between tumor and normal tissues from the HIIT and Ctrl groups.

a Hierarchical clustering of enriched gene sets based on the DEGs between HIIT-T vs HIIT-N.

Blue dots designate pathways that are upregulated in the HIIT-N and red dots – pathways that are upregulated in the HIIT-T; dot size is proportional to p-values.

b Hierarchical clustering of enriched gene sets based on the DEGs between Ctrl-T and vs Ctrl-N.