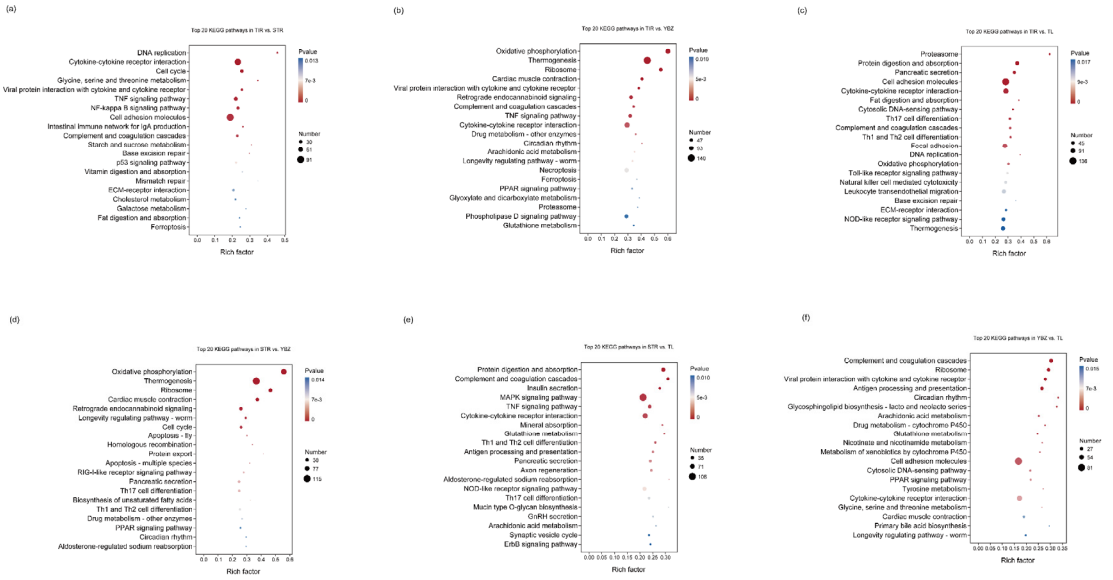


Figure S1 Enrichment analysis of the top 20 KEGG pathways in the four comparison groups under the reference transcriptome. (a) Top 20 pathways in TIR vs. STR; (b) Top 20 pathways in TIR vs. YBZ; (c) Top 20 pathways in TIR vs. TL; (d) Top 20 pathways in STR vs. YBZ; (e) Top 20 pathways in STR vs. TL; (f) Top 20 pathways in YBZ vs. TL. Rich factor is number of DEGs enriched into the pathway/total genes enriched into the pathway. P value $<$ 0.05.