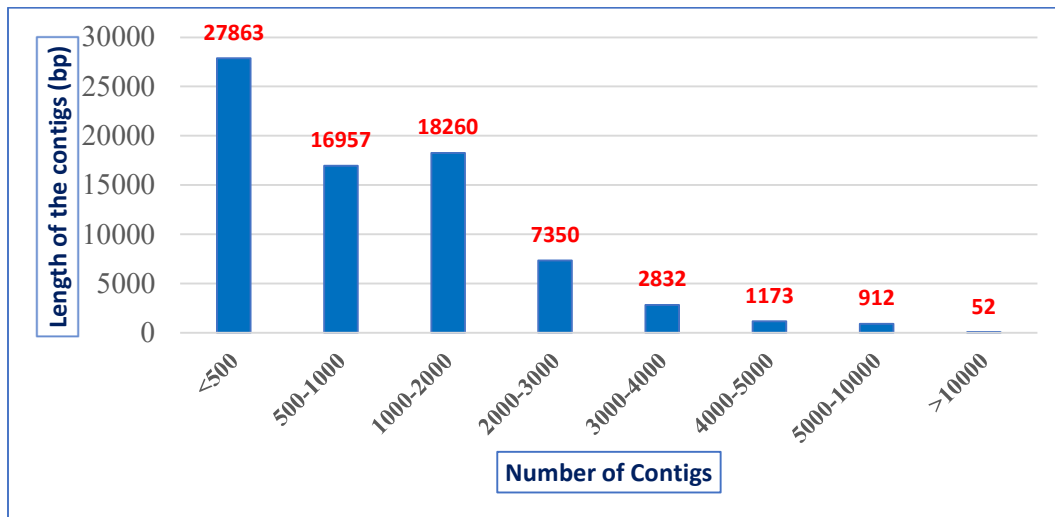


**Supplementary Figure S1: BUSCO completeness assessment of denovo assembly against Eudicots lineage with 2326 BUSCOs**

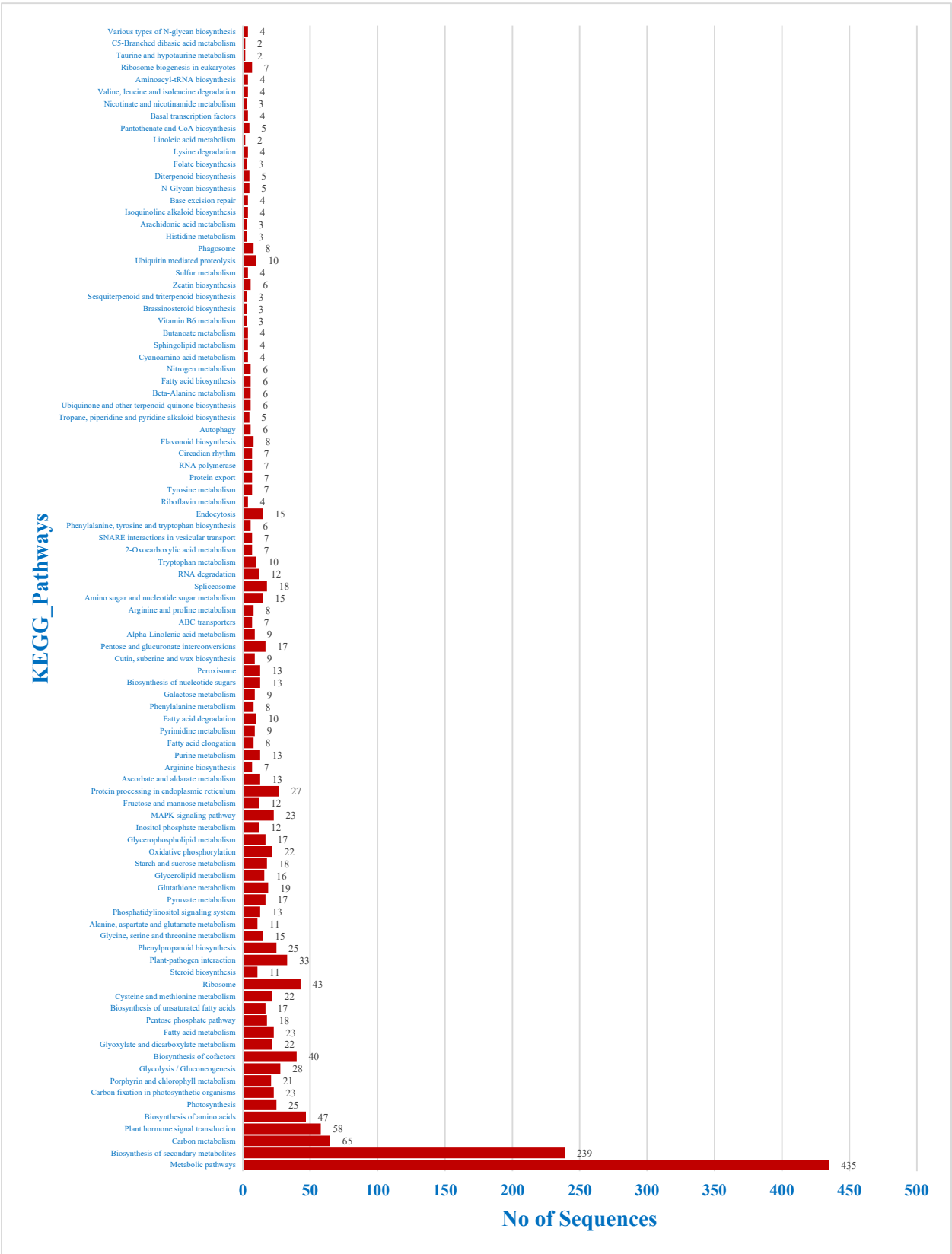


**Supplementary Figure S2: Details of the Contig length of *De novo* assembly**

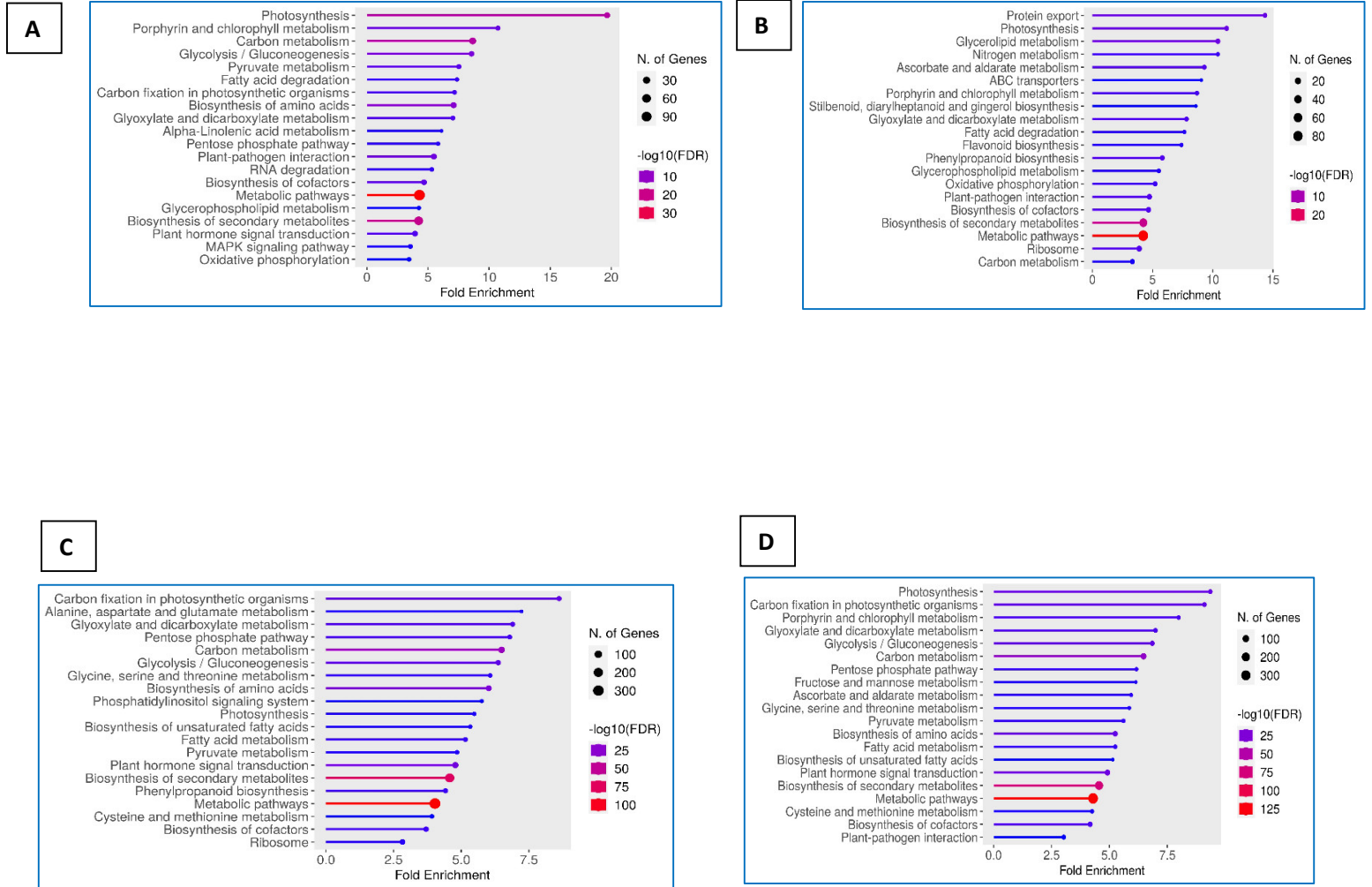


**Supplementary Figure S3: Gene ontology classification of 17566 common DEGs identified across**

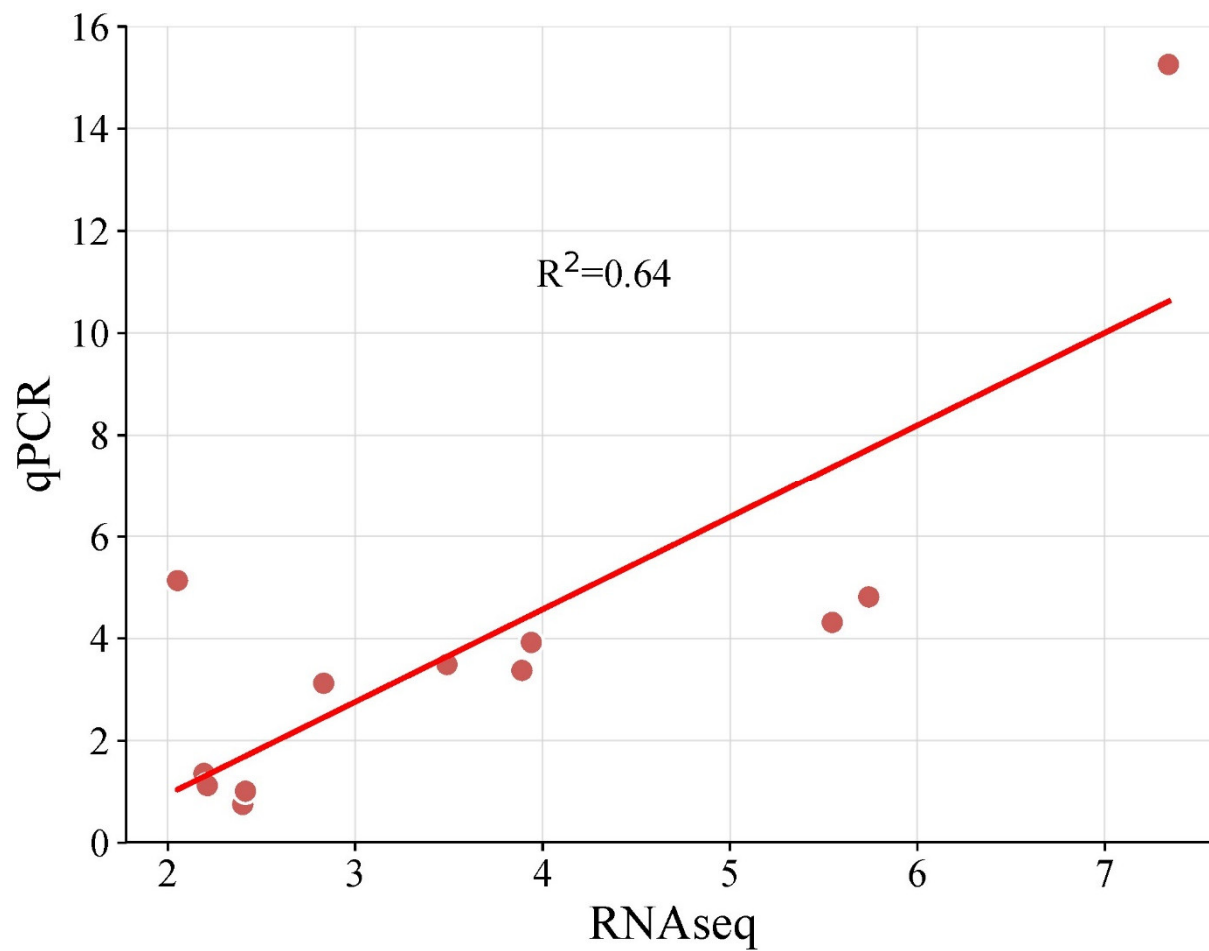
tissues and cultivars



**Supplementary Figure S4: KEGG Pathway analysis of total DEGs across tissues and cultivars**



**Supplementary Figure S5: Top 20 KEGG pathways enriched in different tissues A) Root tissue B) FPL Tissue] and among cultivars [C) Western tissue D) Eastern cv drawn in shinyGO.77 using *Daucus carota* subsp *sativus* as a reference**



**Supplementary Figure S6: Validation of DEGs identified in RNA seq by quantitative real-time PCR (qRT-PCR) based on Log<sub>2</sub>FC and linear regression method**