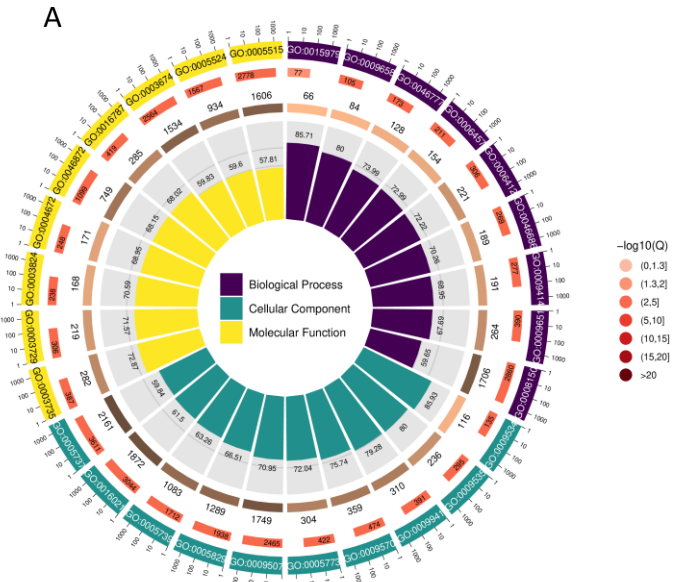
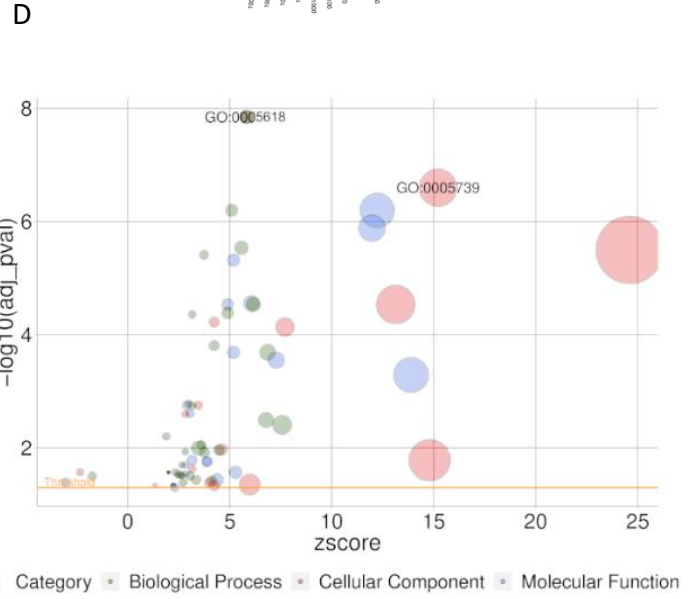
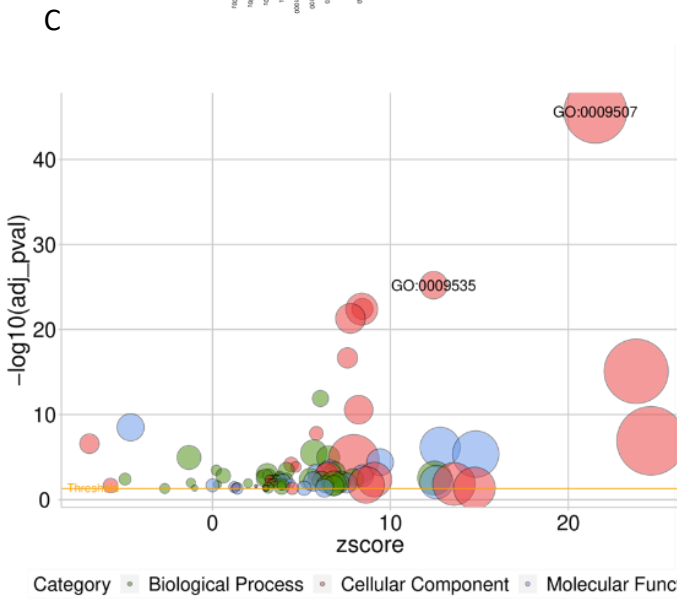
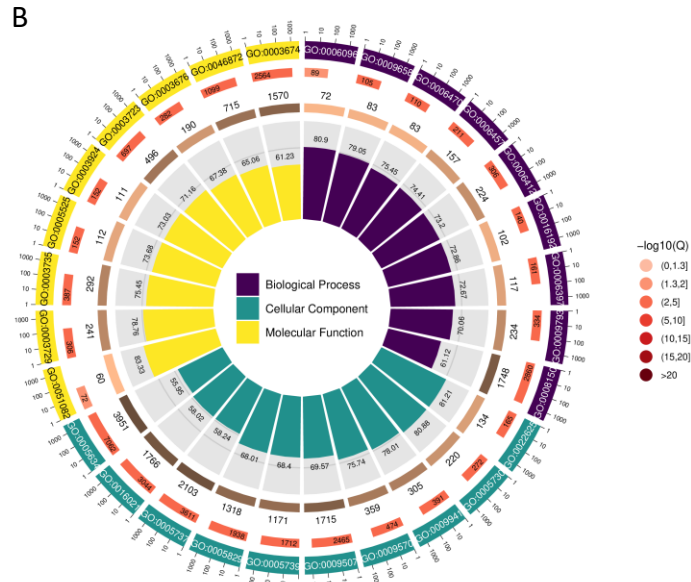


WT vs N2_1 vs N2_2 GO enrichment

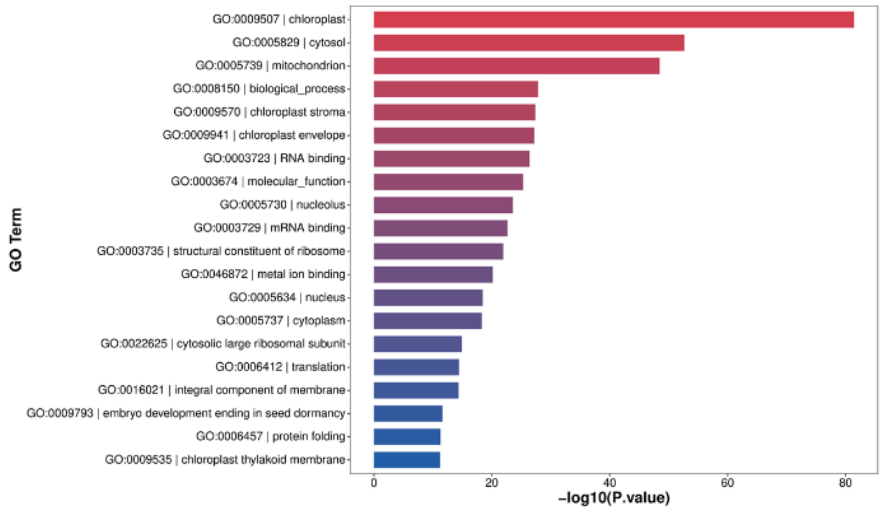


WT vs N3_1 vs N3_3 GO enrichment



E

Top 20 of GO Enrichment



S9 Fig. The GO enrichment of DEGs in N2/ N3 vs WT

S9 Fig. The GO enrichment of DEGs in N2/ N3 mutant vs WT

The gene enrichments of the GO analysis including 3 indexes: the top 9 GO pathways of the biological process (purple), the cellular component (green), the molecular function (yellow).

(A) The top 9 pathways of GO enrichment in **N2 vs WT**

(B) The top 9 pathways of GO enrichment in **N3 vs WT**.

(C) The GO bubble Statistics includes biological process (blue), cellular component (red), molecular function (green), which were in accordance with results in **fig A** and **fig E**.

In the cellular component (red), the two GO pathways :GO :0009507- the chloroplast pathway and GO:0009535- the chloroplast thylakoid membrane pathway were significantly enriched in **N2 vs WT**.

(D) The bubble analysis of Go pathways in the **N3 vs WT** . In molecular function (green), the GO:0005618- cell wall pathway is the most significantly enriched pathway. While less genes are enriched in the other cellular component (red) GO:0005739- mitochondrion pathway.

(E) The results represents the top 20 GO pathways of seed transcriptome including the GO significantly enriched pathways as appearing in **fig C** and **fig D**.