Figure S1 GO-BP enrichment of different expressed genes, the volcano figure above represents the distribution of different pathway. Where the X-axis represents the enrichment rate and Y-axis represents the difference level (FDR value). The bar chart in middle represents the distribution of DEGs screened in GO-BP function, and the network below represents the correlation between the GO-BP screened. GO, Genetic Ontology; BP, biological process; FDR, false discovery rate; DEG, differentially expressed gene.
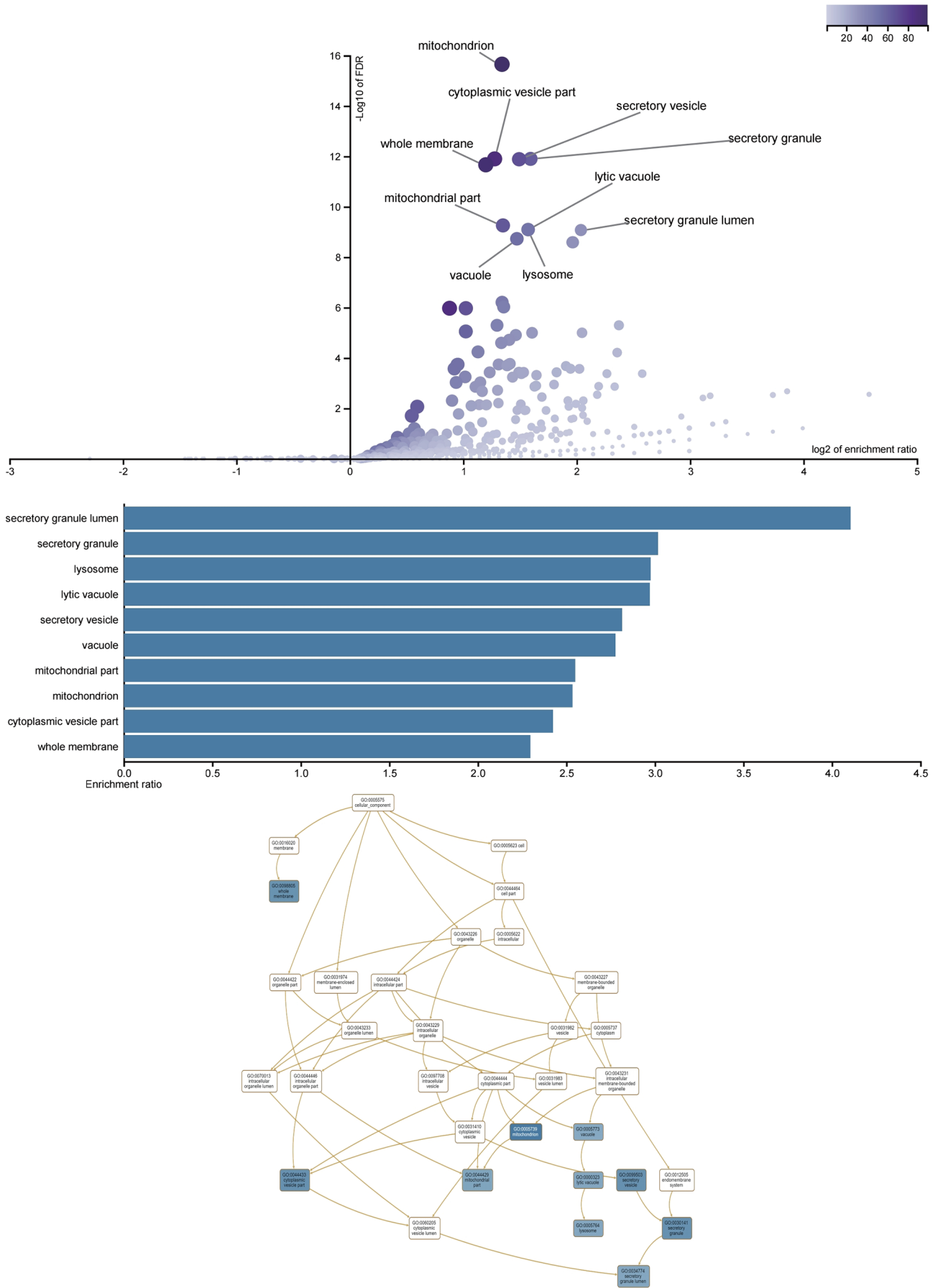
Figure S2 GO-CC enrichment of different expressed genes, the volcano figure above represents the distribution of different pathway. Where the X-axis represents the enrichment rate and Y-axis represents the difference level (FDR value). The bar chart in middle represents the distribution of DEGs screened in GO-CC function, and the network below represents the correlation between the GO-CC screened. GO, Genetic Ontology; CC, cellular component; FDR, false discovery rate; DEG, differentially expressed gene.
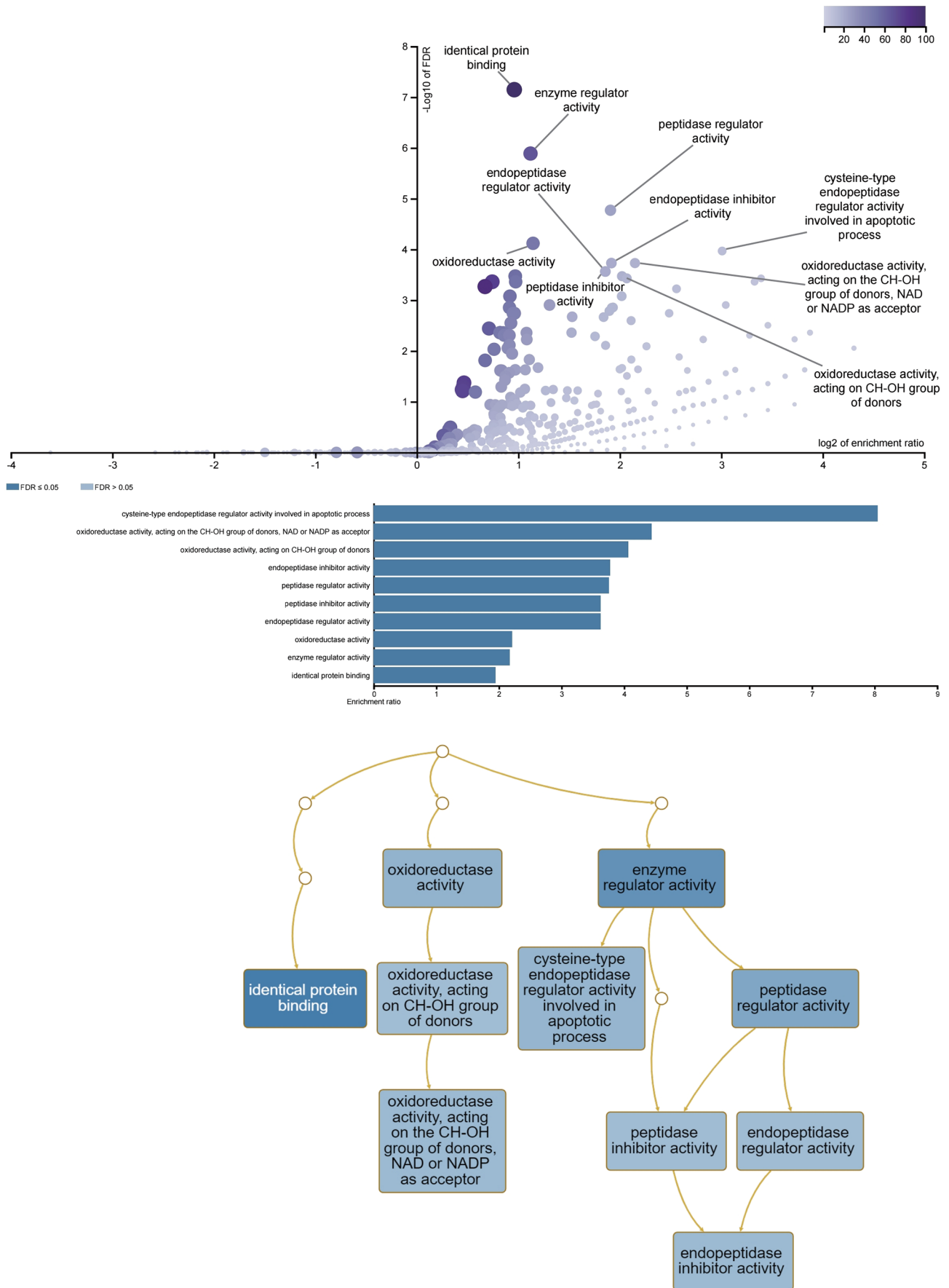
Figure S3 GO-MF enrichment of different expressed genes, the volcano figure above represents the distribution of different pathway. Where the X-axis represents the enrichment rate and Y-axis represents the difference level (FDR value). The bar chart in middle represents the distribution of DEGs screened in GO-MF, and the network below represents the correlation between the GO-MF screened. GO, Genetic Ontology; MF, molecular function; FDR, false discovery rate; DEG, differentially expressed gene.