

Figure S1. Gene ontology (GO) functional classification of genes. The results are summarized in three main categories: biological processes (brown), cellular components (blue), and molecular functions (green). The x -axis indicates the number of genes.

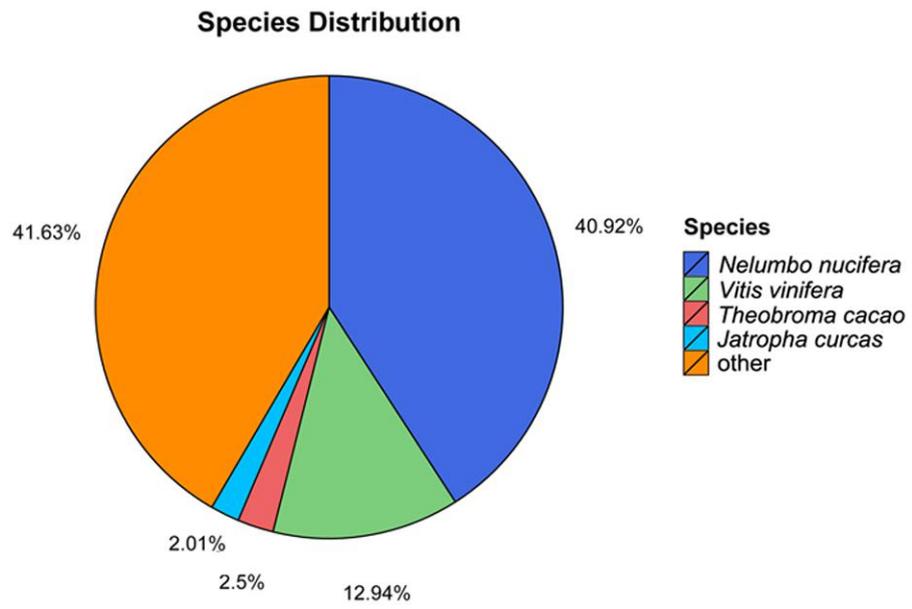


Figure S2. Species distribution of the top BLAST hits.

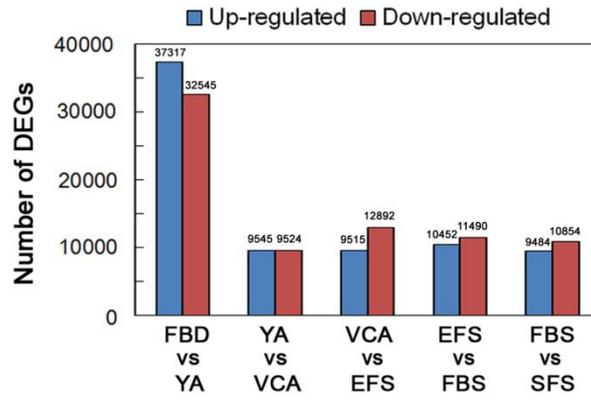


Figure S3. The number of up- or down-regulated genes in FBD vs YA, YA vs VCA, VCA vs EFS, EFS vs FBS, and FBS vs SFS in *A. amurensis*. We used a false discovery rate of ≤ 0.001 and an absolute \log_2 ratio of ≥ 1 as the threshold to determine significant differences in gene expression.

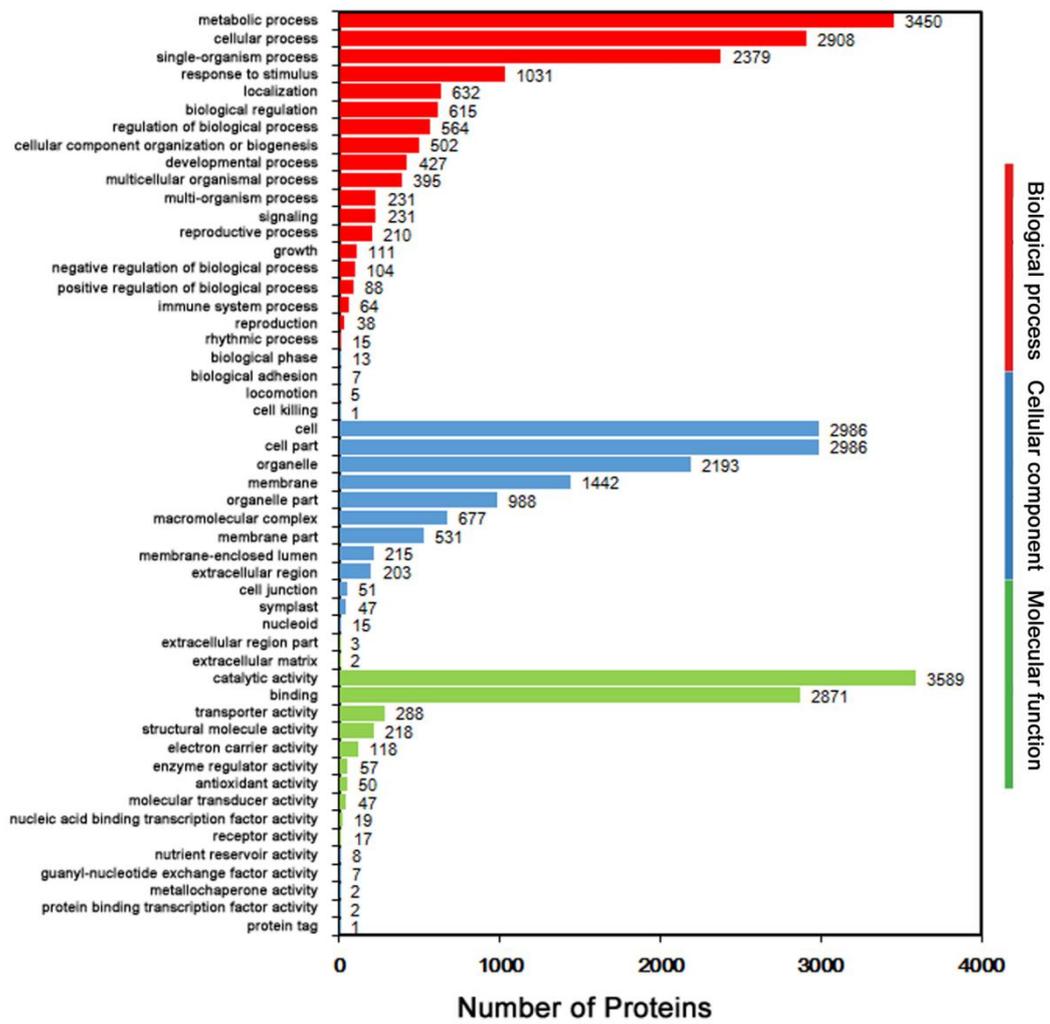


Figure S4. Gene ontology (GO) functional classification of proteins. The results are summarized under three main categories: biological processes (brown), cellular components (blue), and molecular functions (green). The x -axis indicates the number of proteins.