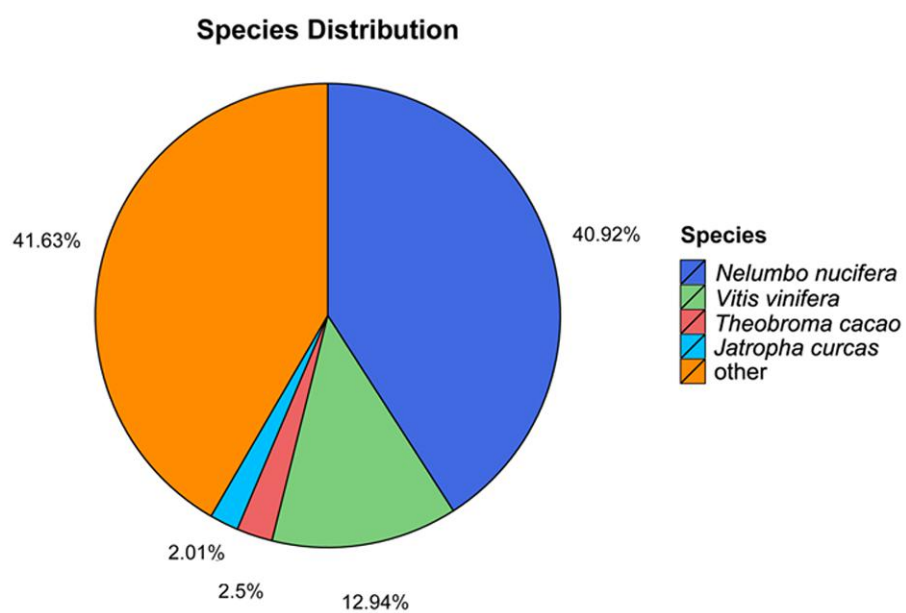
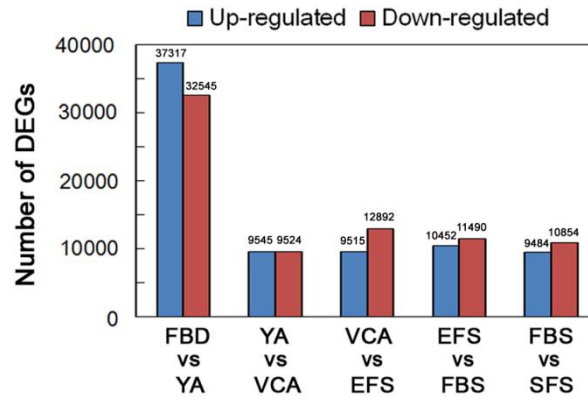


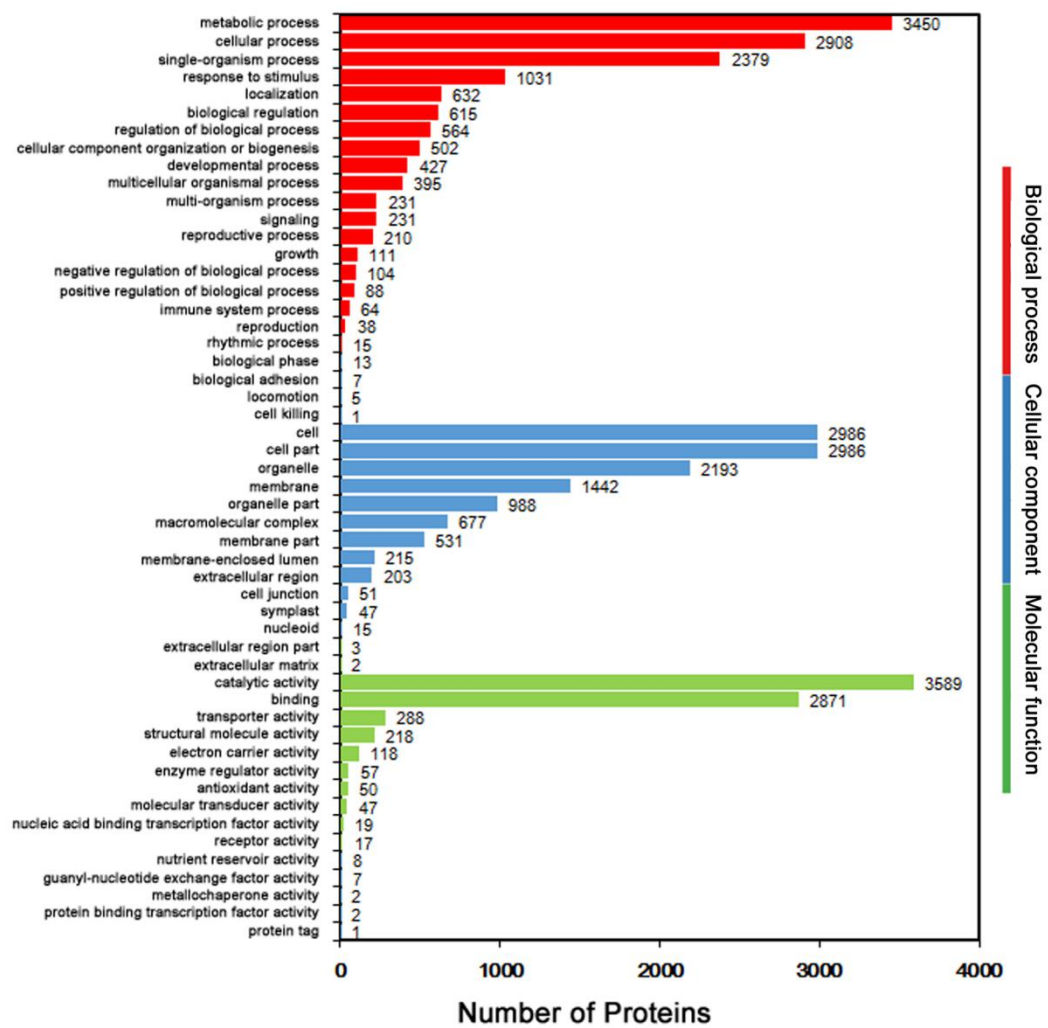
**Figure S1.** Gene ontology (GO) functional classification of genes. The results are summarized in three main categories: biological processes (brown), cellular components (blue), and molecular functions (green). The  $x$ -axis indicates the number of genes.



**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  $\leq 0.001$  and an absolute log2 ratio of  $\geq 1$  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.