

Figure S1. POD and SOD activity assays of *S. japonica* roots under four PEG-6000 concentrations (0%, 10%, 20%, 30%) across four time points (0, 6, 12 and 24 h). (A) POD activity (U·g⁻¹min⁻¹); (B) SOD activity (U·g⁻¹Fw). CK denotes without PEG-6000.

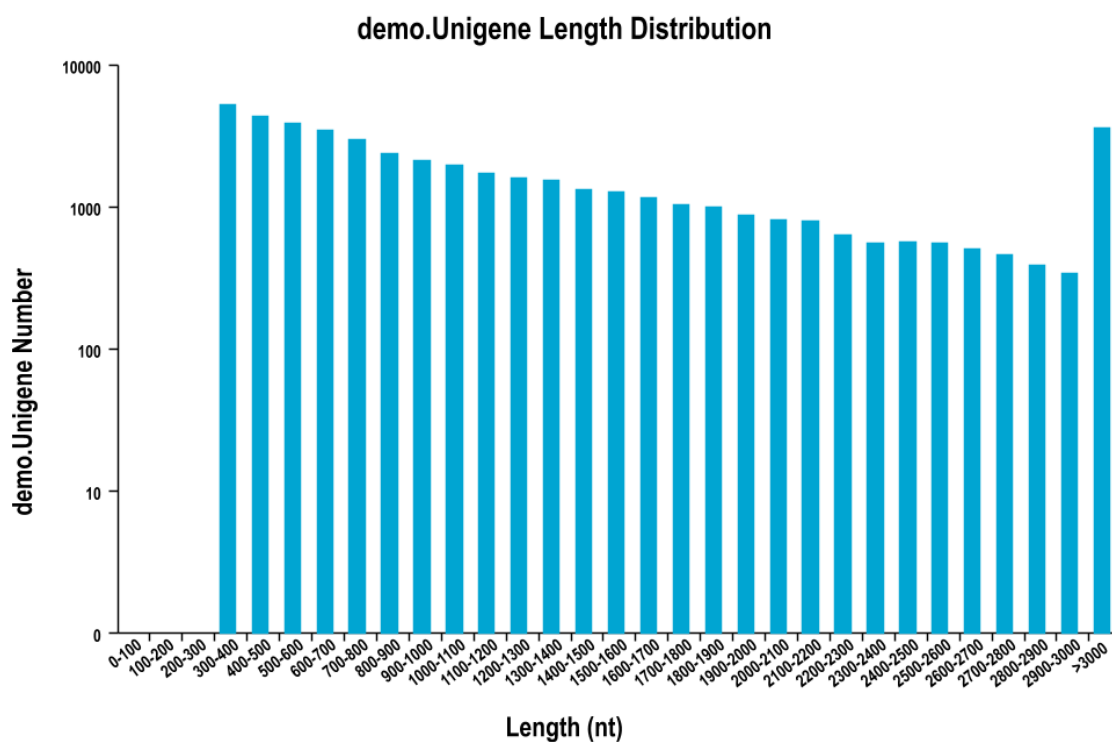


Figure S2. Length distribution of assembled unigenes.

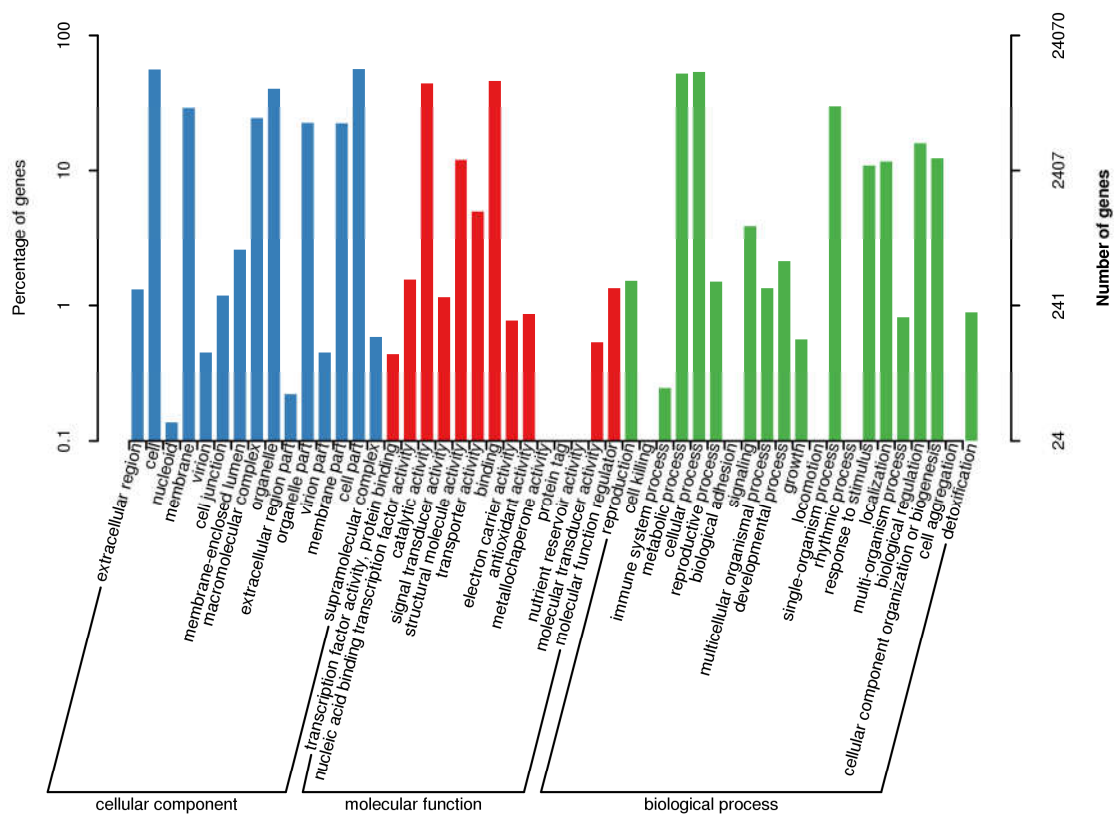
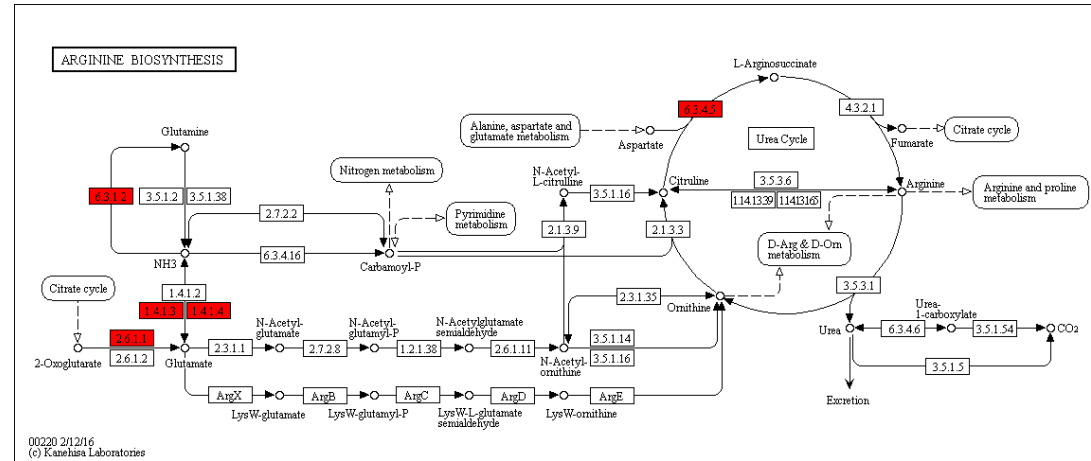


Figure S3. Functional annotation of assembled sequences based on Gene Ontology (GO) categorization.

A



B

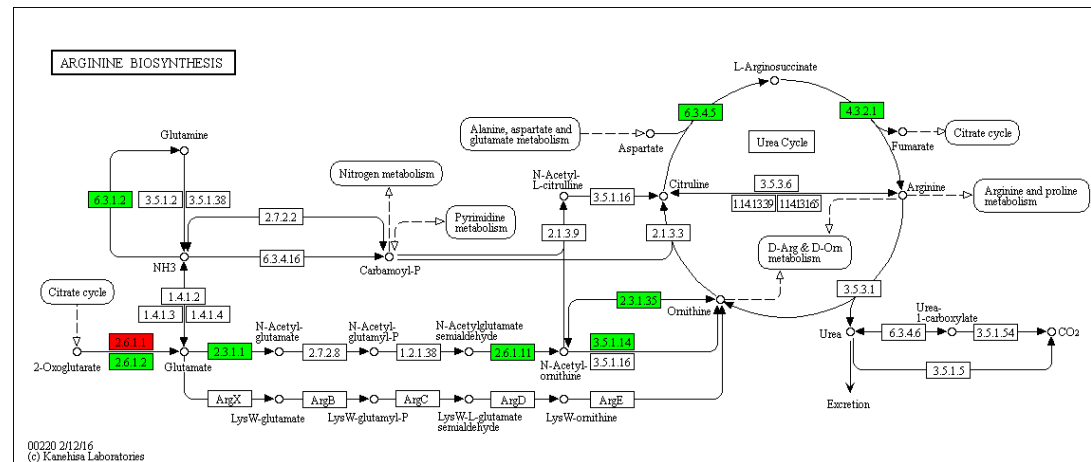
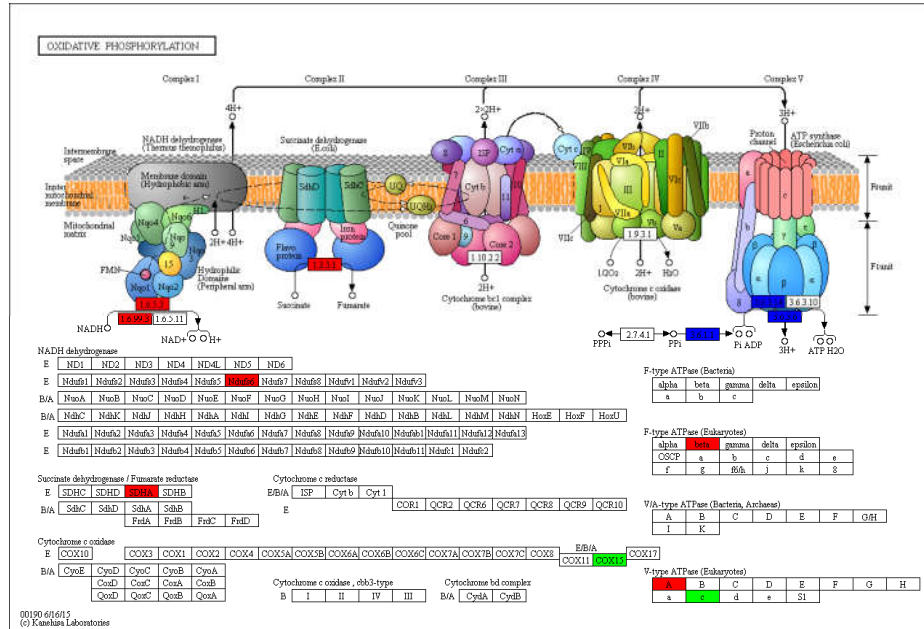


Figure S6. DEGs involved in arginine biosynthesis pathway upon drought. (A) Under normal N condition, NN vs NL; (B) Under N starvation condition, LN vs LL. Transcripts significantly up-regulated are highlighted in red, significantly down-regulated are highlighted in green. Blue indicates both significantly up- and down-regulated genes exist.

A



B

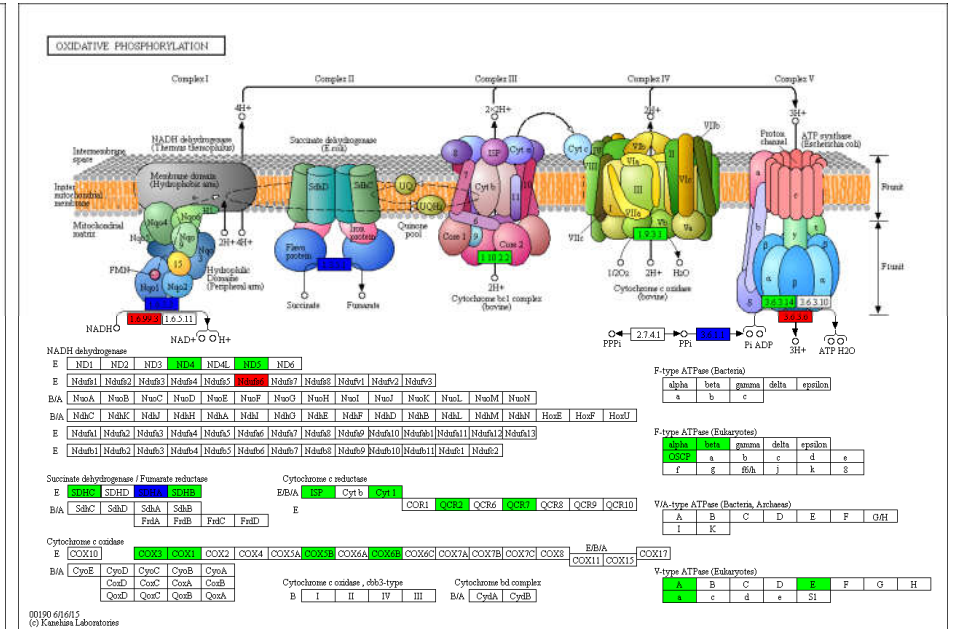
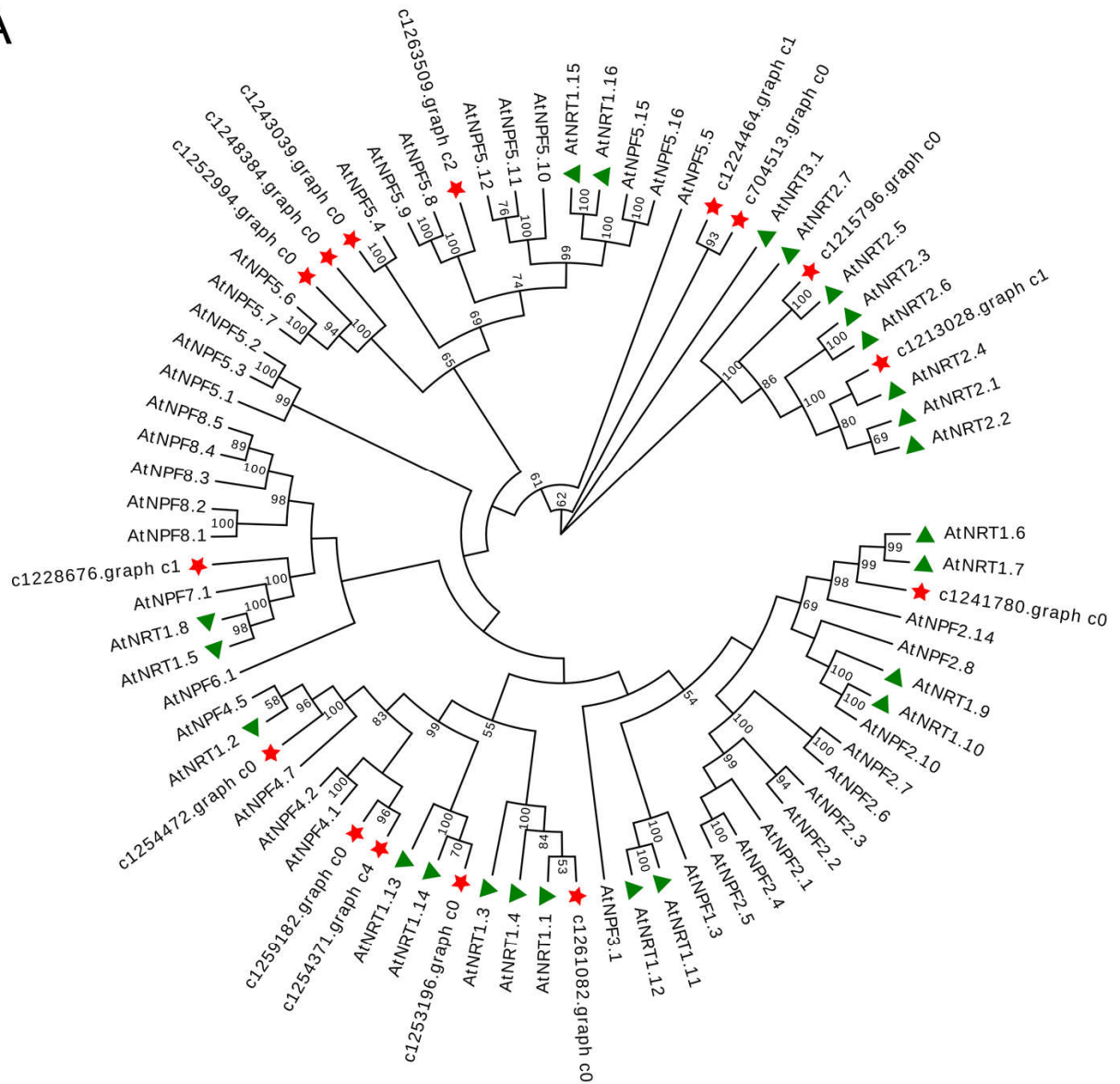


Figure S7. DEGs involved in oxidative phosphorylation pathway upon drought. (A) Under normal N condition, NN vs NL; (B) Under N starvation condition, LN vs LL. Transcripts significantly up-regulated are highlighted in red, significantly down-regulated are highlighted in green. Blue indicates both significantly up- and down-regulated genes exist.

A

B

A



B

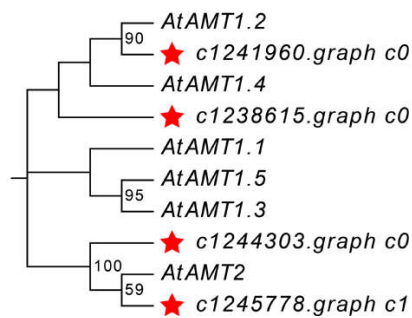


Figure S9. Neighbor-joining phylogenetic analysis of (A) NTRs and (B) AMTs with related genes in Arabidopsis. The trees were constructed by neighbor-joining phylogeny test, and 1000bootstrao replicates. The protein sequences are provided in Table S13. The green triangles represent the genes proved to have functions to transports nitrate in Arabidopsis. The red stars represent the identified genes involved in N uptake and metabolism at present study.

