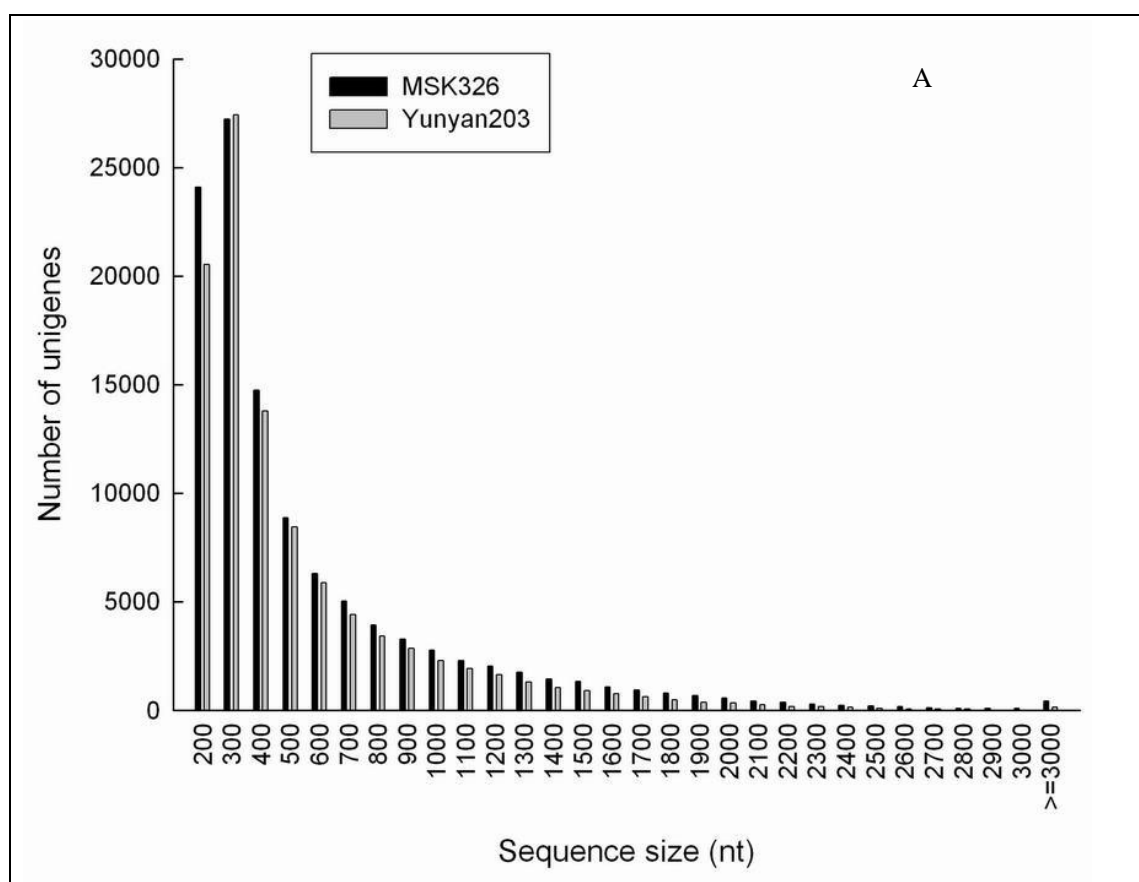
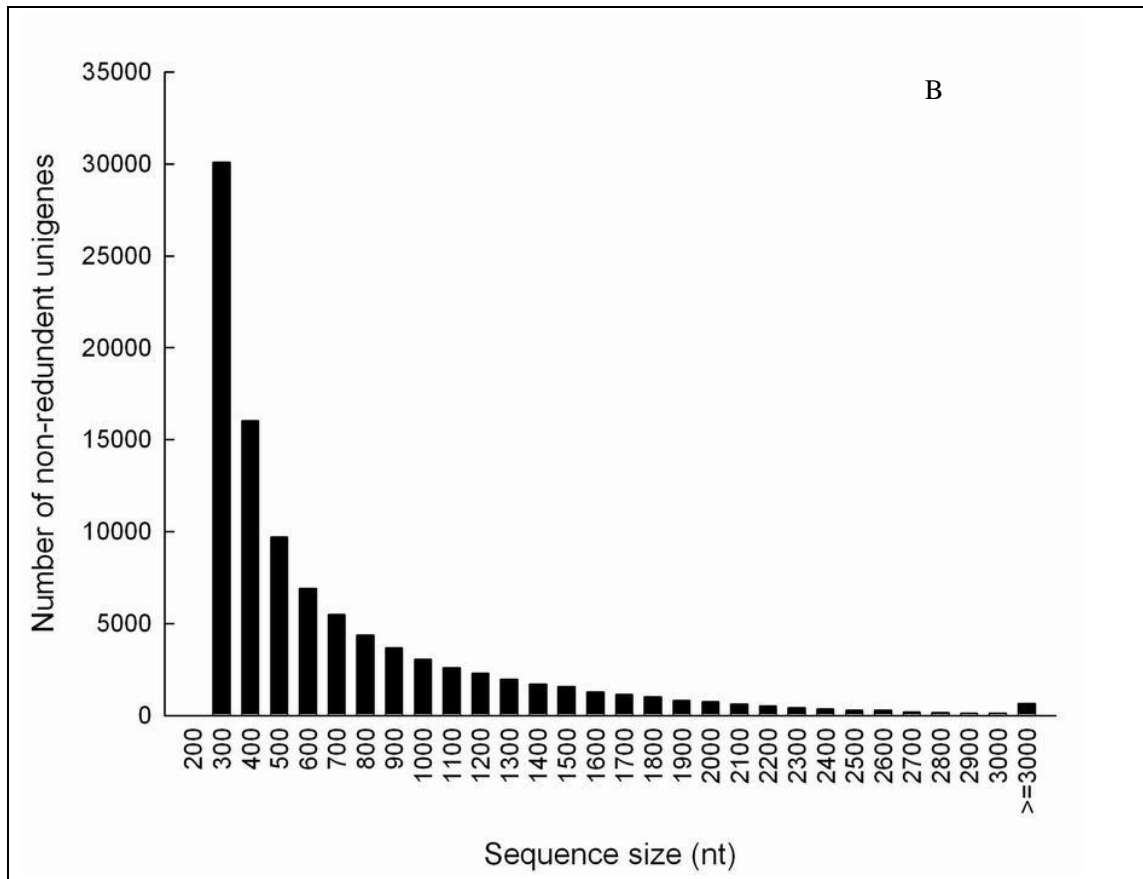


Comparison of transcriptomes of chilling- and drought-tolerant and intolerant *Nicotiana tabacum* varieties and identification of genes associated with stress tolerance**Dahai Hao, Wenguang Ma, Yelong Sheng, Jianbo Zhang, Yunfeng Jin, Huiqin Yang, Zhongguang Li, Shasha Wang, Ming Gong***

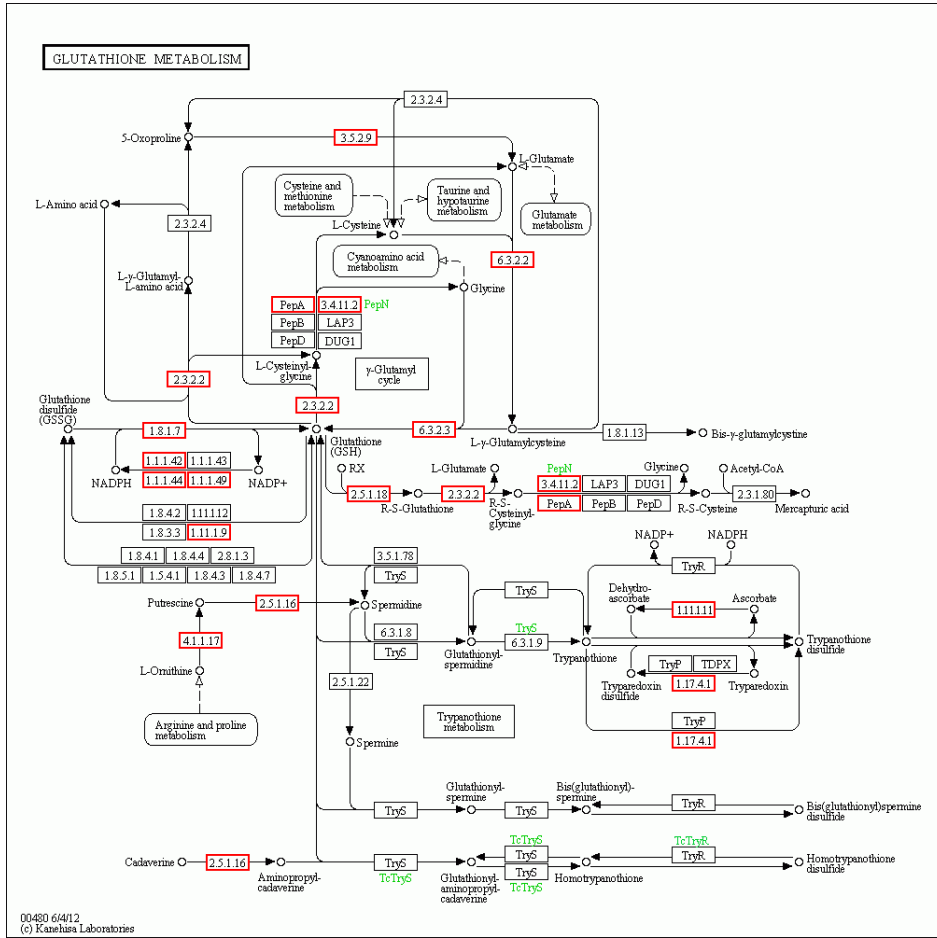
Supplementary Figures



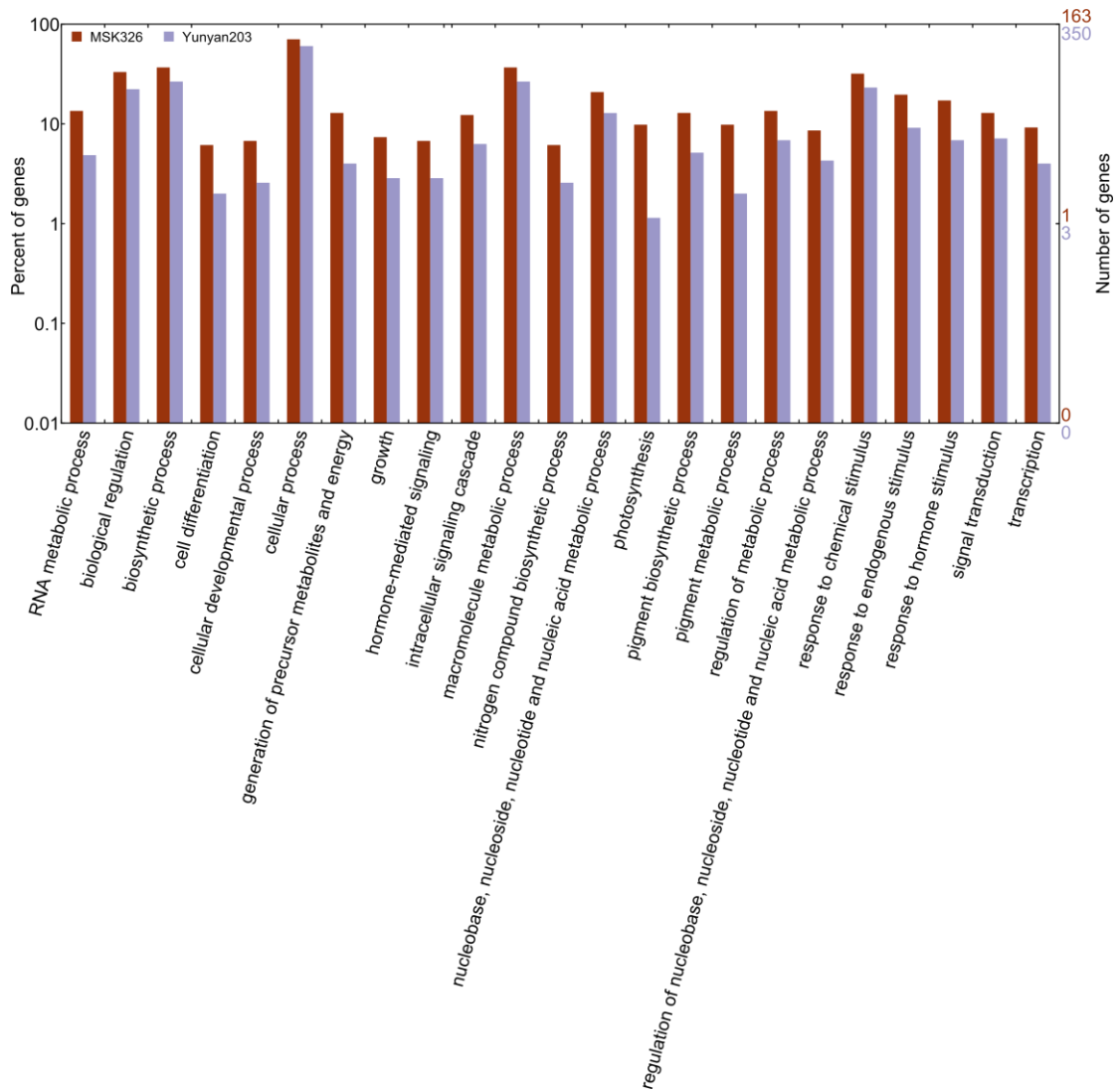


Supplementary Figure 1 The length distribution of unigenes (A) and non-redundant unigenes (B) of *Nicotiana*.

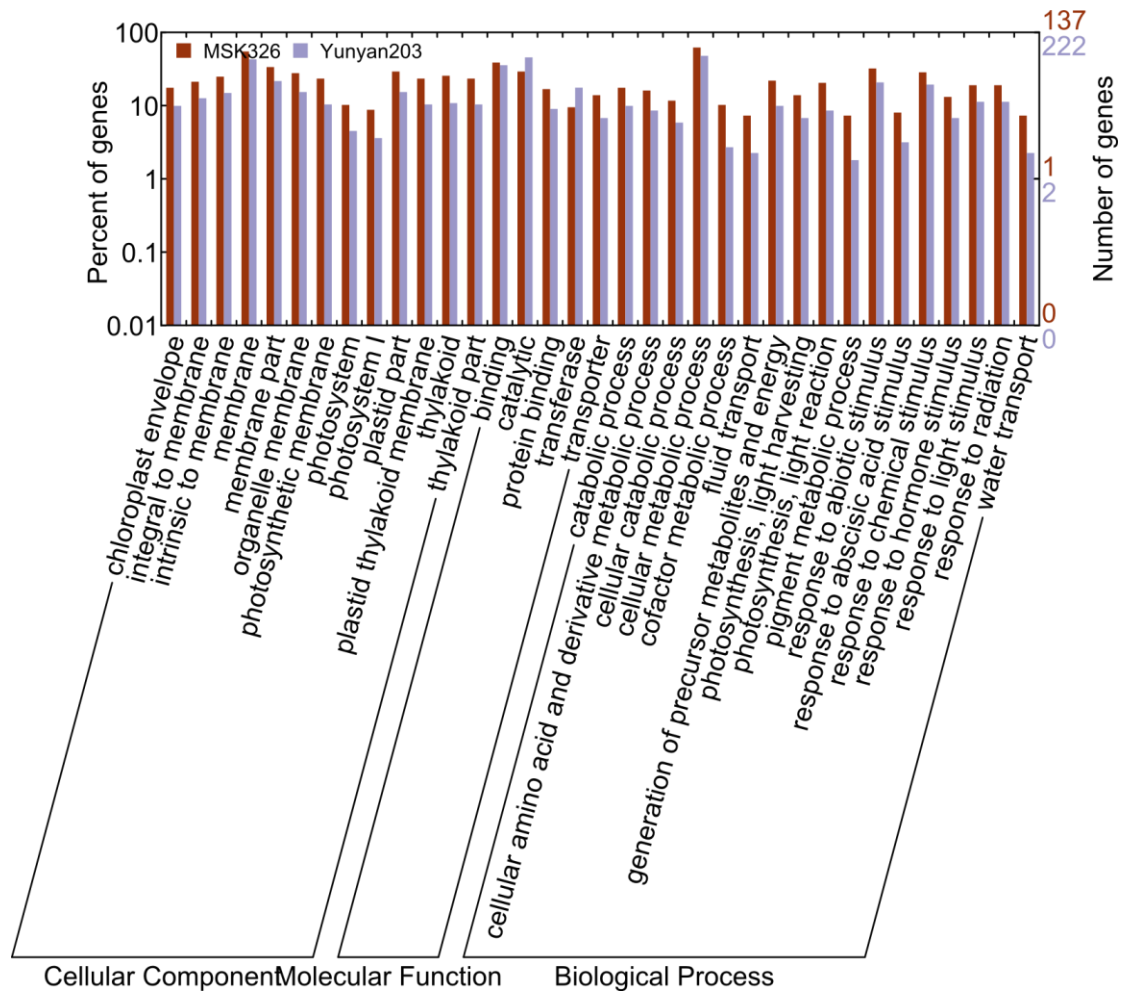
tabacum cv. Yunyan203 and MSK326.



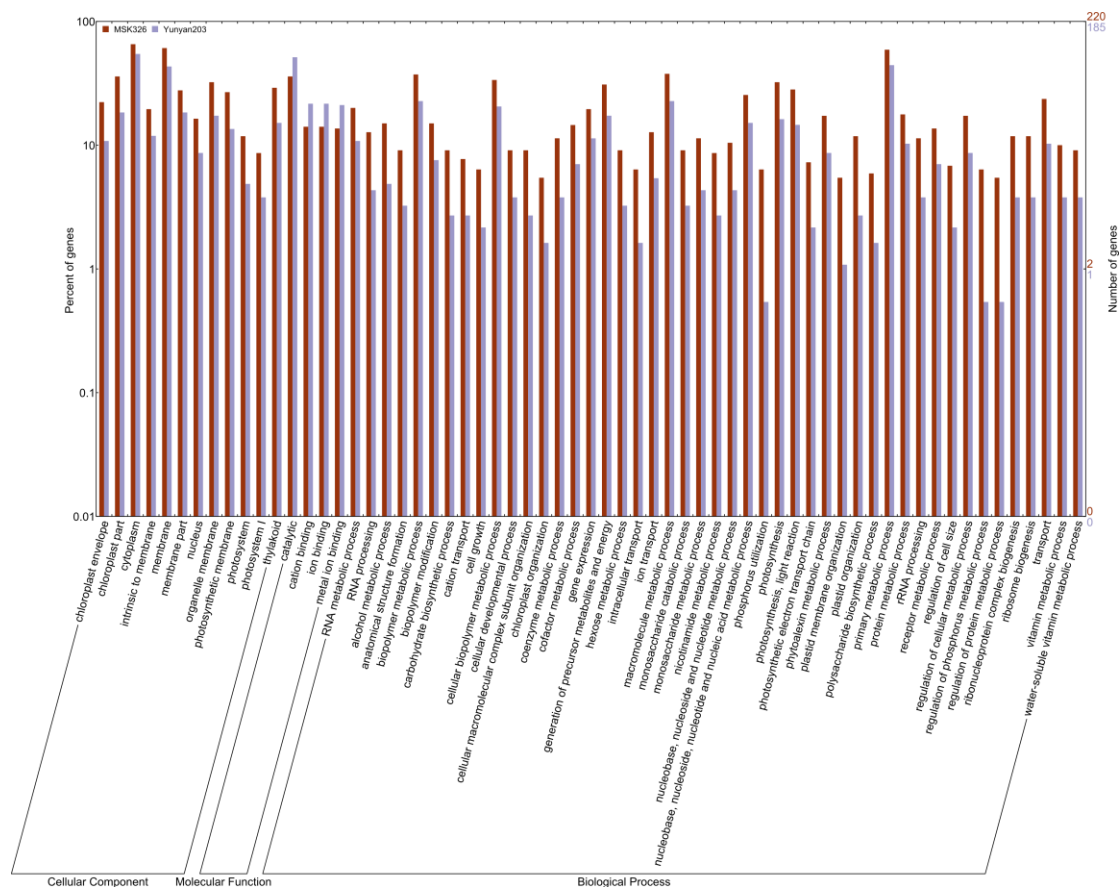
Supplementary Figure 2. Unigenes of chilling and drought stressed *N. tobacco* associated with glutathione metabolic pathway for revealed unigenes by KEGG (from: <http://www.genome.jp/kegg/kegg1.html>).



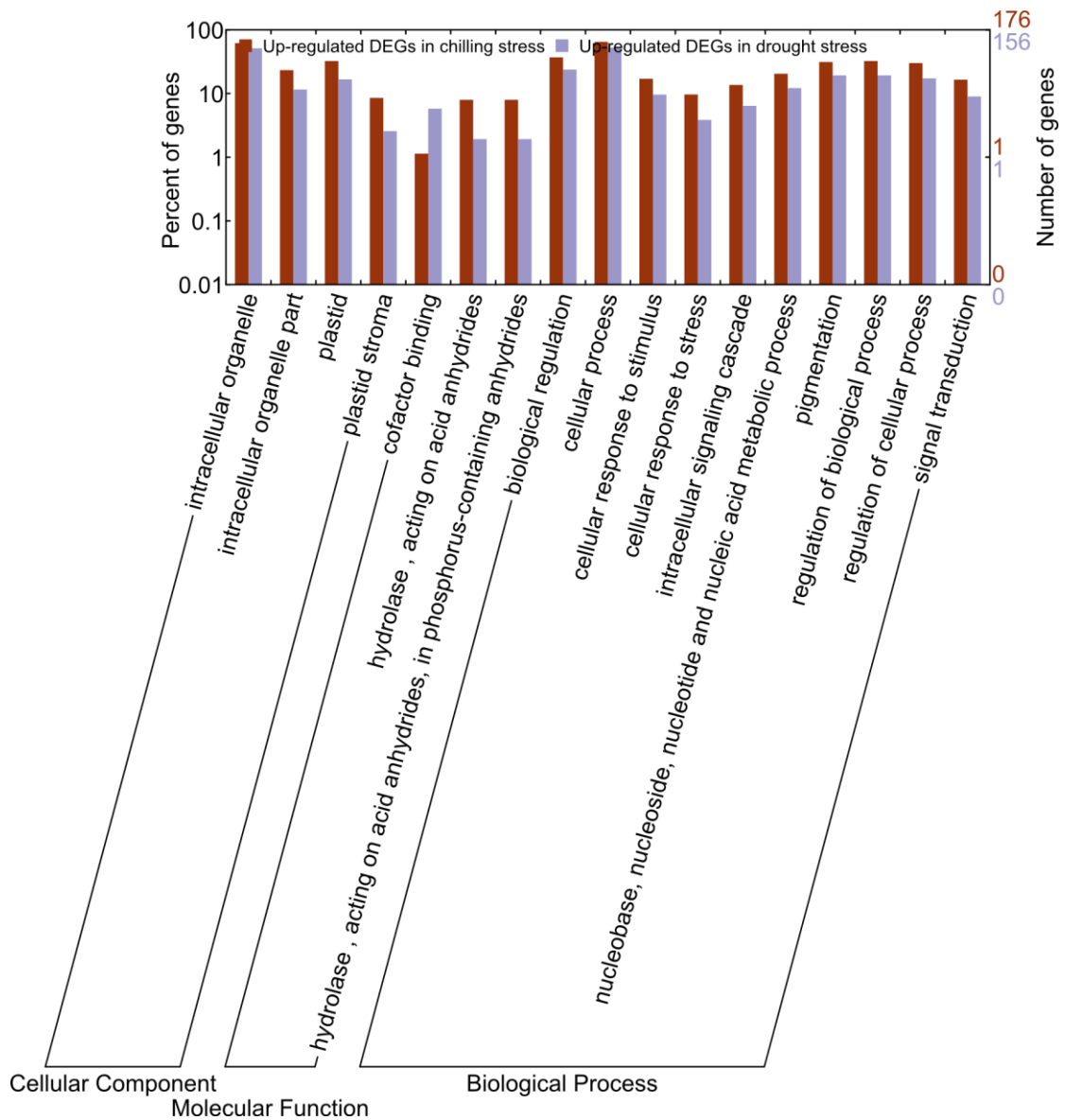
Supplementary Figure 3. Gene ontology (GO) enrichment analysis. The digital gene expressions (DGEs) of MSK326 (stress tolerance) and Yunyan203 (stress intolerance) cultured under control conditions. In this plot, the p values of all GO terms were obtained using Pearson chi-square test; the gene numbers between these two DGE libraries and were all significant.



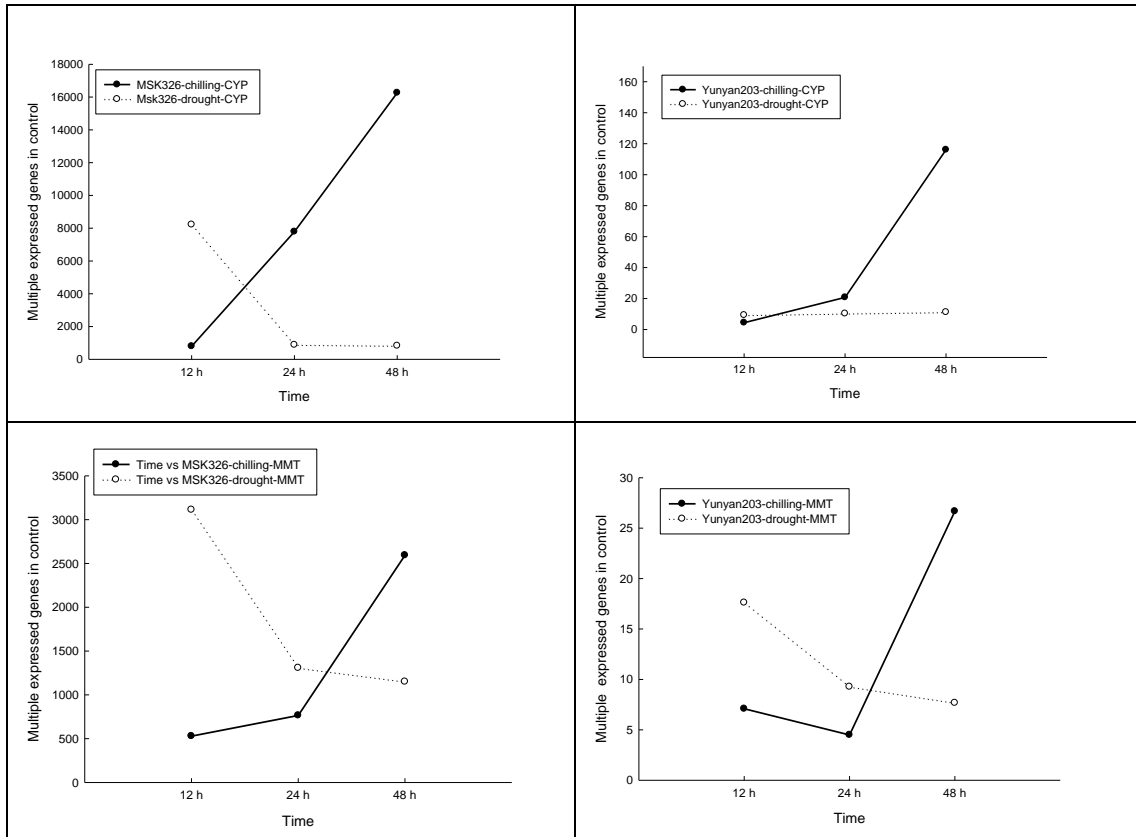
Supplementary Figure 4. Gene ontology (GO) enrichment analysis of common down-regulated differentially expressed genes (DEGs) under chilling stress. Comparison of GO enrichment between the chilling stress-tolerant MSK326 and chilling stress-intolerant Yunyan203. The *p* values of all GO terms were obtained using Pearson chi-square test; the gene numbers of the two digital gene expression (DGE) libraries were all significant.



Supplementary Figure 5. Gene ontology (GO) enrichment analysis of common differentially expressed genes (DEGs) of drought-stressed samples. Comparison of GO enrichment analysis of drought-tolerant MSK326 and drought-intolerant Yunyan203. The p values of all GO terms were obtained using Pearson chi-square test; the gene numbers of the two digital gene expression (DGE) libraries were all significant.

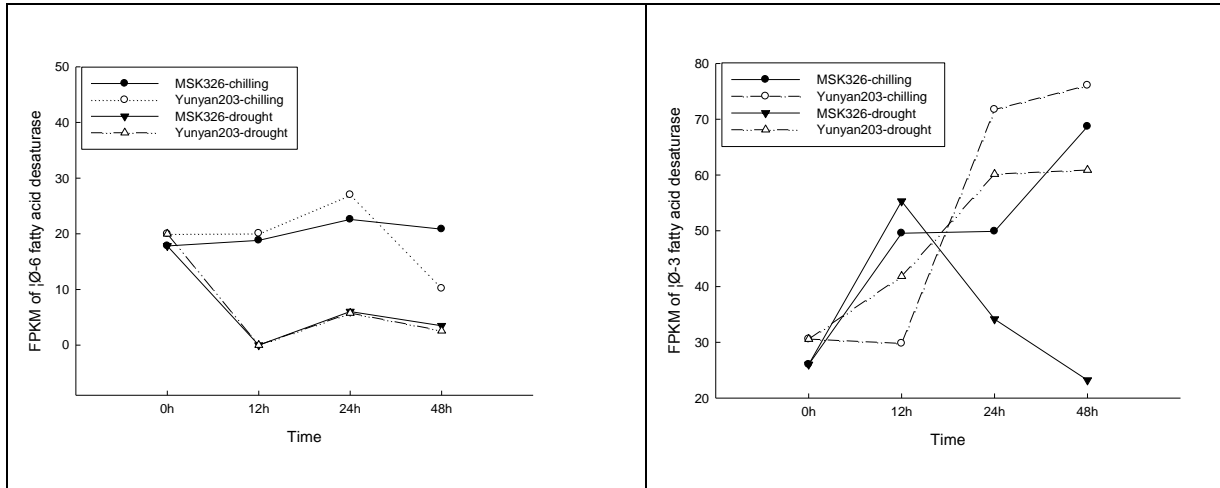


Supplementary Figure 6. Differences between common differentially expressed genes (DEGs) of chilling and drought stress samples. The *p* values of all gene ontology (GO) terms were obtained using Pearson chi-square test; the gene numbers of the two digital gene expression (DGE) libraries and were all significant.

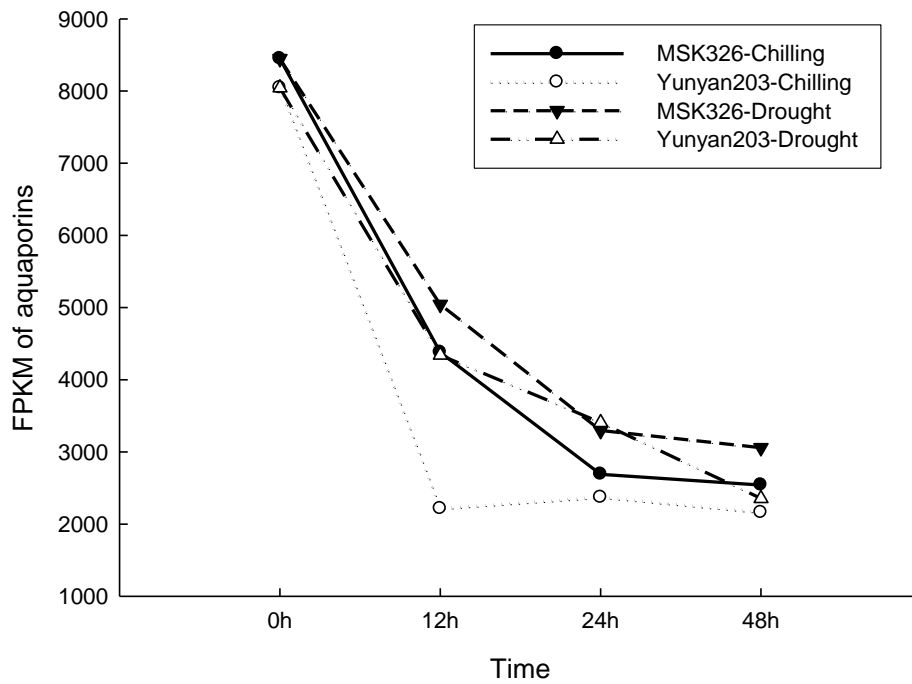


Supplementary Figure 7. Comparison of cytochrome P450 (CYP) and myricetin O-methyltransferase 2 (MMT)

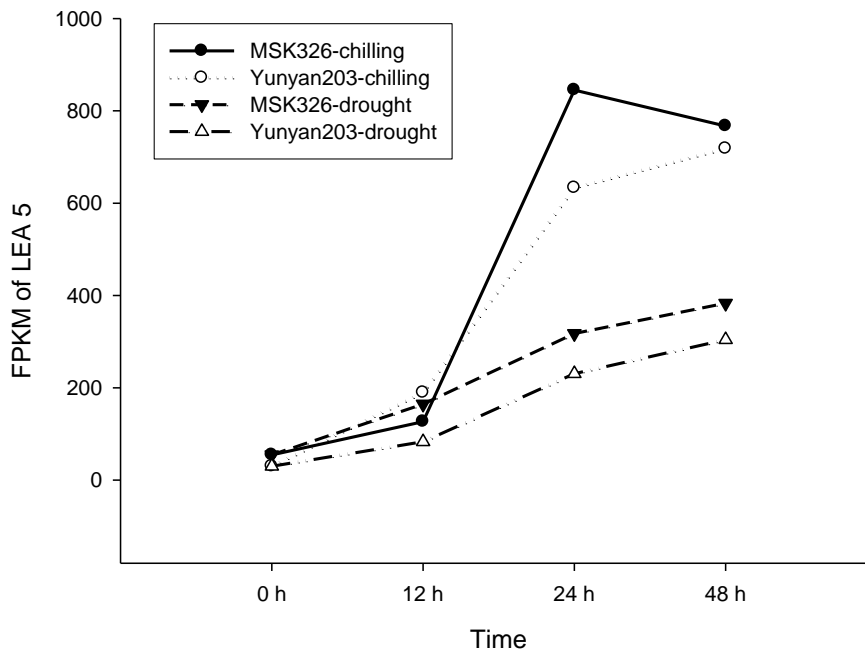
expression between control and stress-treated *N. tabacum* samples.



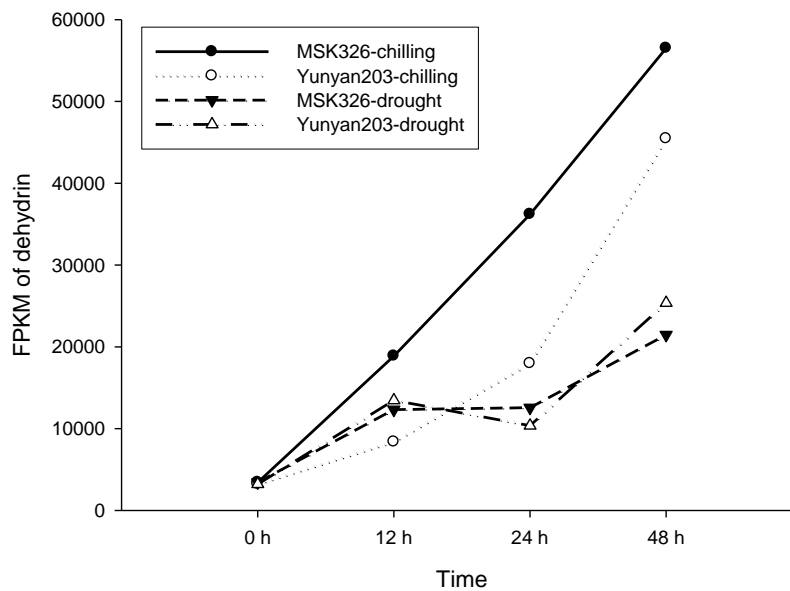
Supplementary Figure 8. Expression pattern of fatty acid desaturase (FAD)6 and FAD3 of in chilling- and drought-treated *N. tabacum* samples.



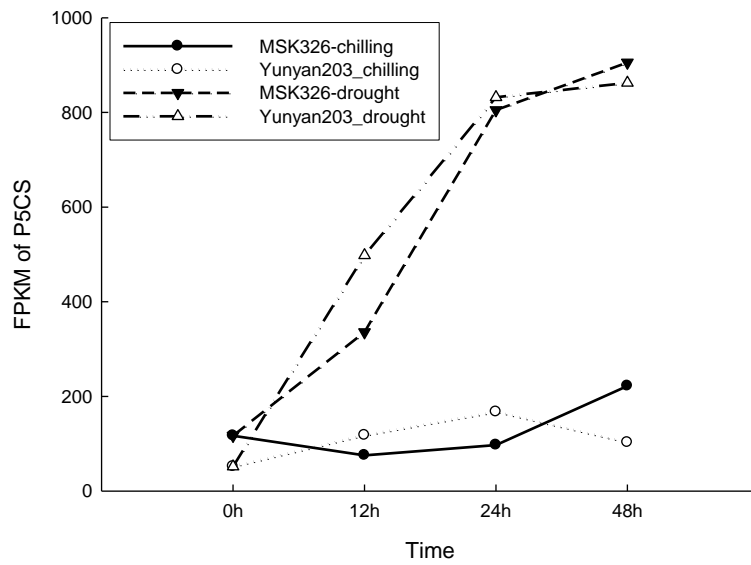
Supplementary Figure 9. The sum of FPKM for aquaporins in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



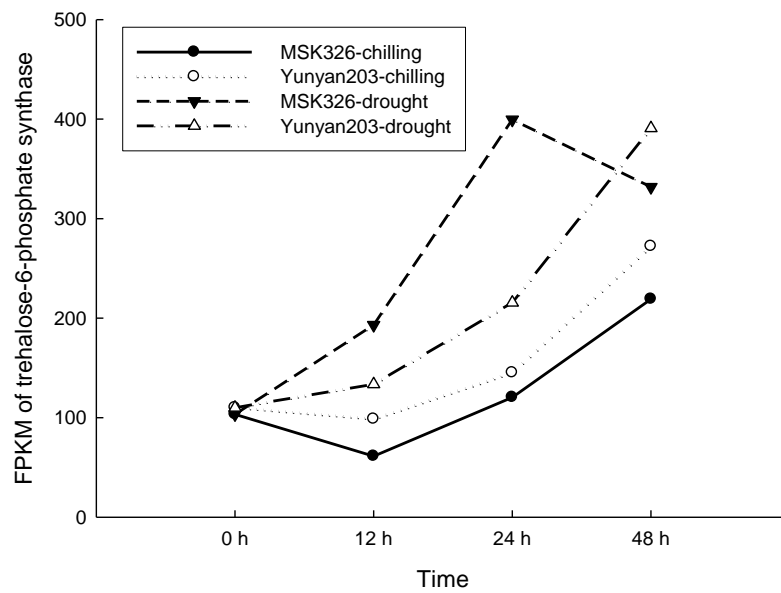
Supplementary Figure 10. The sum of FPKM for late embryogenesis abundant (LEA) 5 proteins in 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



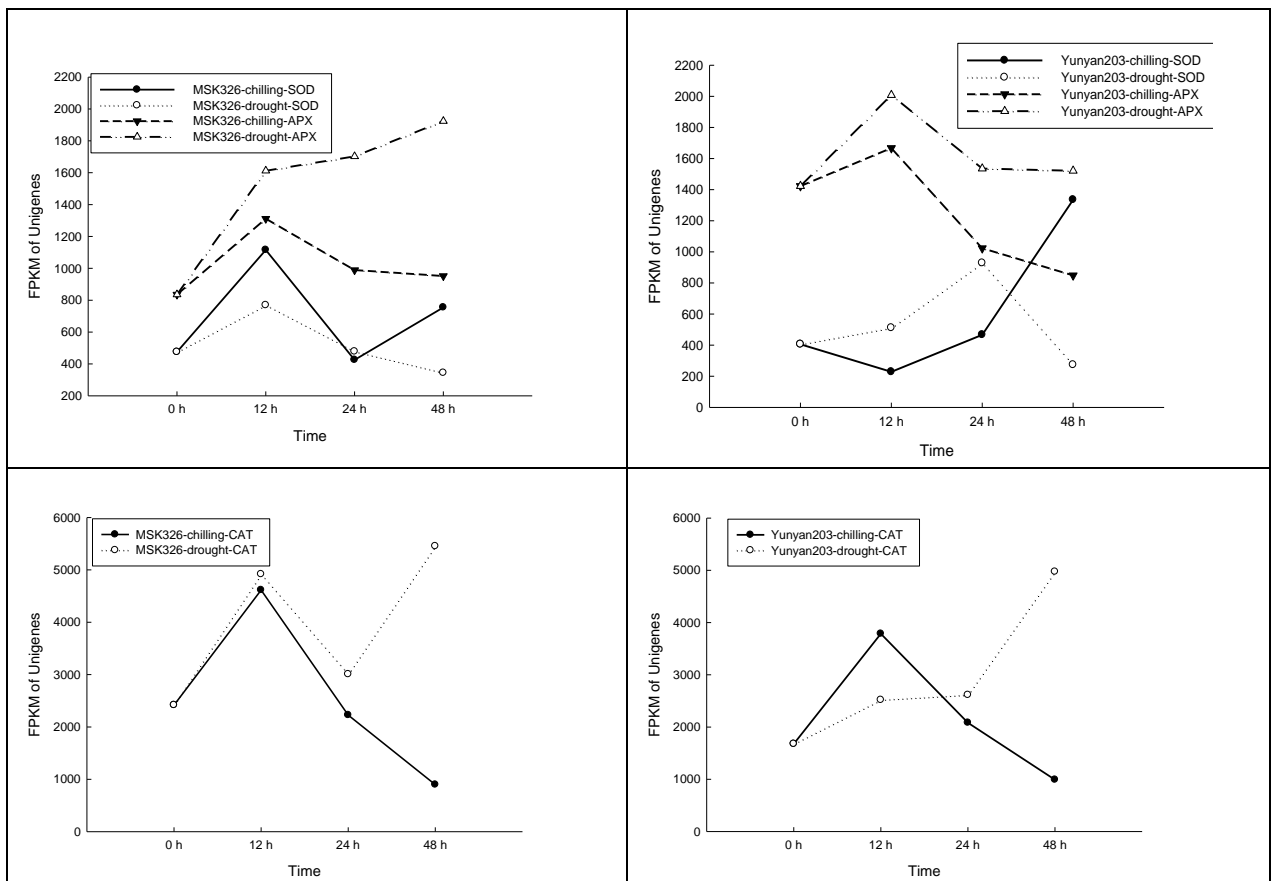
Supplementary Figure 11. The sum of FPKM for dehydrin (DHN) proteins in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



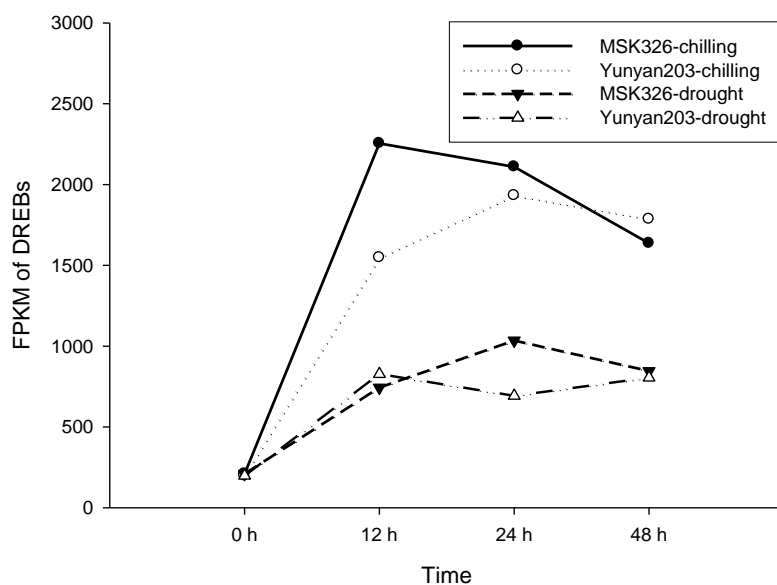
Supplementary Figure 12. The FPKM for Δ^1 -pyrroline-5-carboxylate synthase (P5CS) in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



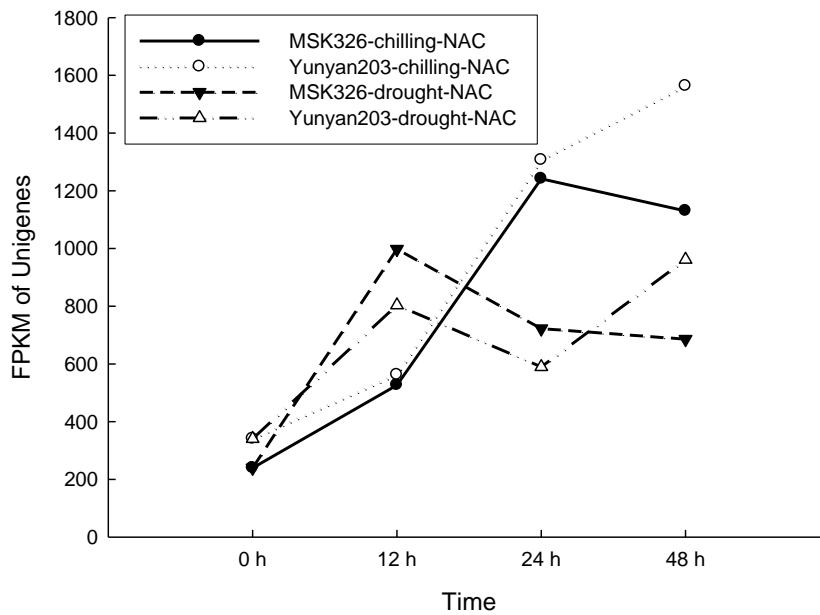
Supplementary Figure 13. The FPKM for trehalose-6-phosphate synthase in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



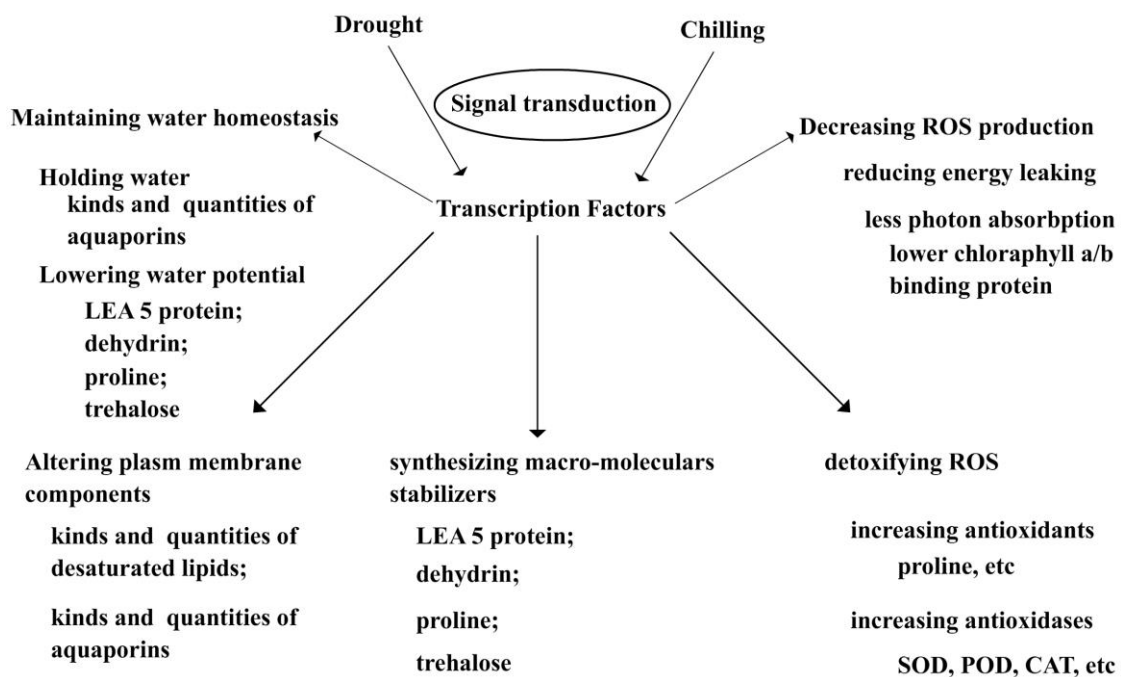
Supplementary Figure 14. The FPKM for superoxide dismutase (SOD), ascorbate peroxidase (APX), and catalase (CAT) in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



Supplementary Figure 15. The FPKM for dehydration responsive element binding (DREB) proteins in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



Supplementary Figure 16. The FPKM of NAC in the 14 digital gene expressions (DGEs) of *N. tabacum*. FPKM, fragments per kilobase of exon per million fragments mapped.



Supplementary Figure 17. Some common reaction of *N. tabacum* cv. Yunyan203 (intolerant) and MSK326 (tolerant) to drought/chilling stress.