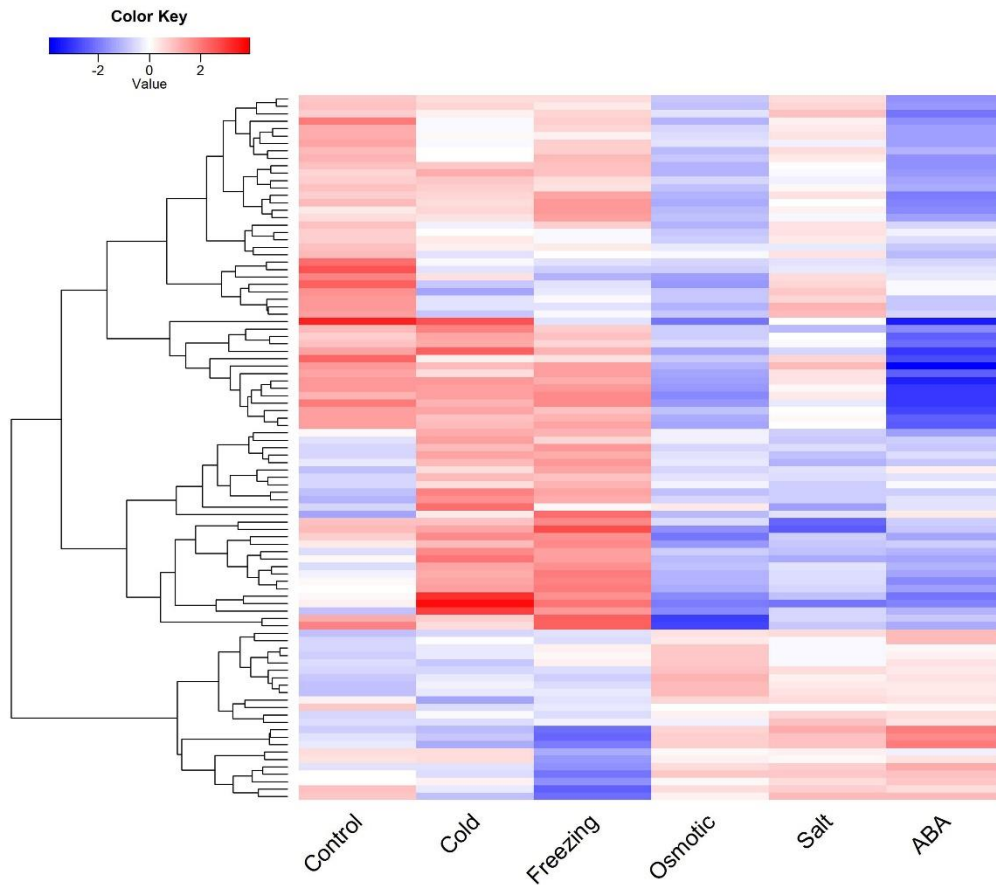


## Supplementary Material to “Transcriptome sequencing and expression profiling of genes involved in the response to abiotic stress in *Medicago ruthenica*”



**Figure S3** - Heatmap showing the expression profiles of transcription factor genes that are differentially expressed in response to abiotic stress in *Medicago ruthenica*. The heatmap was generated using the R gplots package, the FPKM values for each transcript were normalized and used as input; red represents high levels of expression, while blue represents low expression levels.