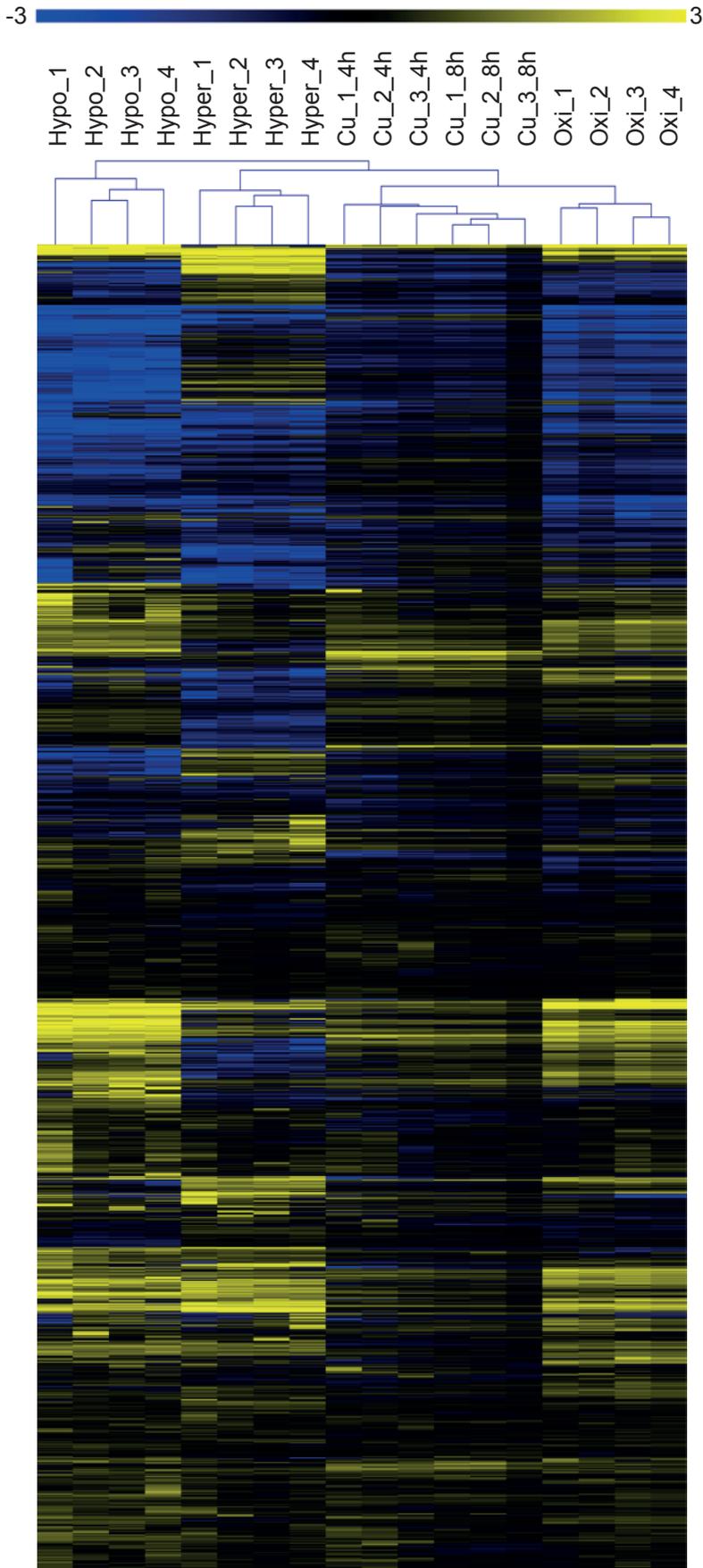# Additional file 4

Additional file 4. Hierarchical clustering of gene expression data obtained by microarray in *E. siliculosus* submitted to different abiotic stress conditions: Hypo_1-4 = hyposaline stress (salinity of 4 ppt, 6 h), Hyper_1-4=hypersaline stress (salinity of 96 ppt, 6 h), Oxi_1-4=oxidative stress (10mM H_2O_2, 6 h, see Dittami *et al*. 2009 for experimental details for these stressors), and Cu_1_4h - Cu_3_8h (250 µg L^{-1} copper stress, 4-8 h, this study). The heat map shows log2-ratios of gene expression in stress compared to control conditions. Gene trees and sample trees were obtained by hierarchical clustering and "Euclidean distance" as metric.