Supplementary Fig. S1 Expression levels of nine genes from daylily transcriptome data. Transcript levels of candidate genes in the highly tolerant cultivar 'Here Lies Butch' and highly sensitive cultivar 'Bonibrae Sharky' at 0h and 24h under submergence were used for the comparison of RNA-seq and RT-qPCR. Error bars indicate standard deviation (SD) of the means from three biological replicates.