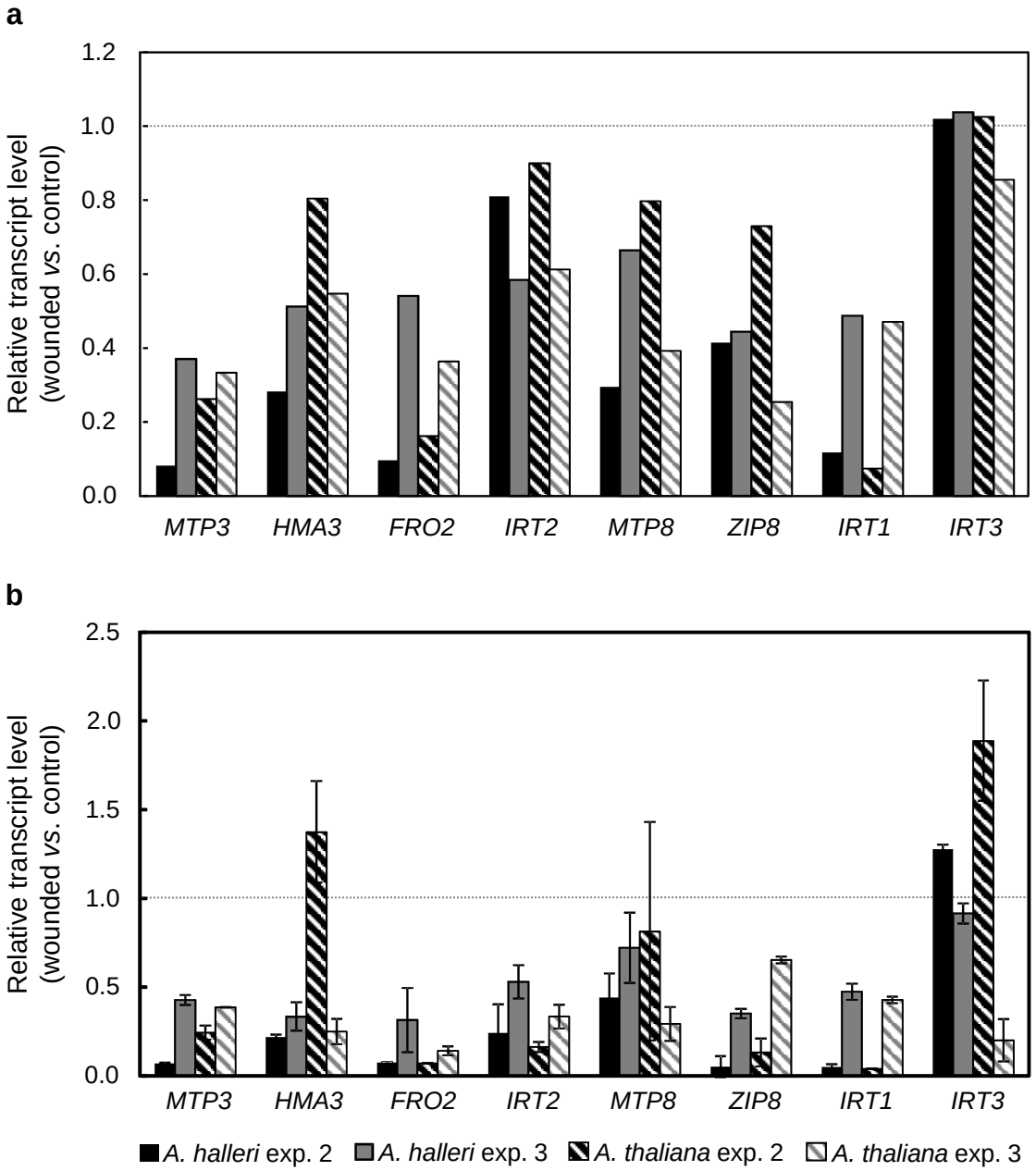


**Supplementary Figure 1: Real-time RT-PCR (qPCR) validation of gene expression determined by microarray hybridization.** For seven selected iron deficiency response metal homeostasis genes (*MTP3*, *HMA3*, *FRO2*, *IRT2*, *MTP8*, *ZIP8*, *IRT1*) and one Zn-deficiency response metal homeostasis gene as a negative control (IRT3), bars show transcript levels in leaves of wounded relative to non-wounded *A. halleri* and *A. thaliana* plants based on **(a)** CATMA microarray hybridization and **(b)** quantitative real-time RT-PCR, using the same RNA. For qPCR, values represent fold changes in gene expression calculated by dividing relative transcript levels (RTL) of wounding treatments by RTL of controls (see Talke *et al.*, 2006). Across all four replicates, average microarray values for *IRT1* (*A.h.* fold change: 0.44, $P = 0.073$, *A.t.* fold change: 0.39, $P = 0.069$) did not pass the stringent cut-off values. According to the microarray data, *IRT3* transcript levels showed no wounding-dependent regulation and served as a negative control (*A.h.* fold change: 1.02, $P = 0.631$, *A.t.* fold change: 1.05, $P = 0.482$). *A.h., A. halleri*; *A.t., A. thaliana*.