



Figure S4. Detecting *in planta* changes in mRNA stability between conditions

(A) Scatter plot relating the half-life ratio (HL/US) to mean mRNA abundance for the 3,960 modelled transcripts. Points represent individual genes.

(B) Scatter plot presenting the fold-change in mRNA abundance (20 min REC/ 10 min HL), in mock-treated samples, versus the half-life ratio (REC/HL) determined for 3,960 modelled transcripts. Points denote individual genes, line denotes fitted linear model, 'm' denotes regression coefficient, and 'r' denotes Pearson's correlation coefficient.