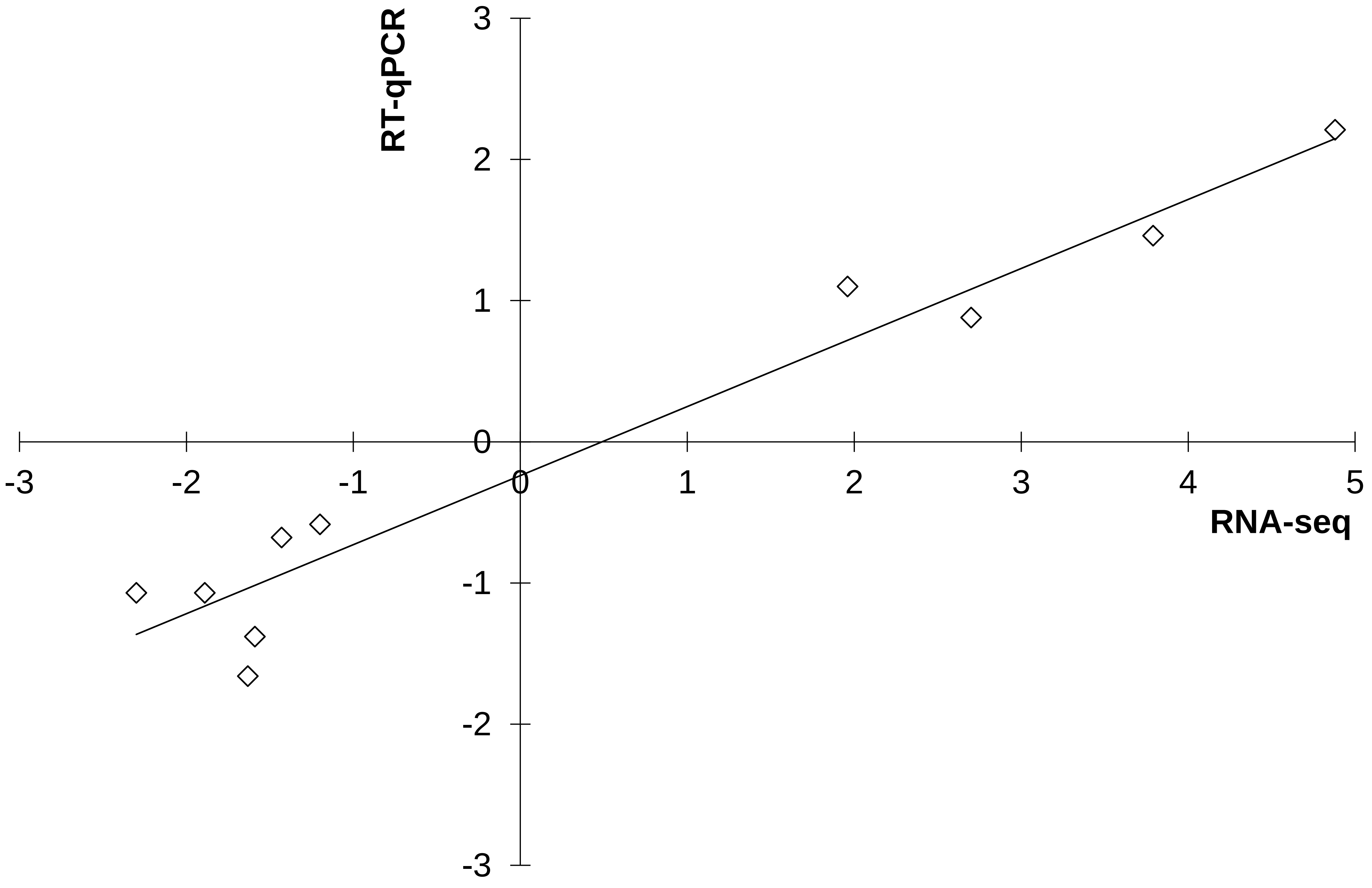

Figure S2 Scatter plot: RNA-seq vs. RT-qPCR

RNA-seq and RT-qPCR relative level of expression are presented as log2fold-change

Triticum aestivum genes presented in the scatter plot: TaS_37759224**, TaS_52545880**, contig_4027***, TaS_52541981*, TaS_22370925*, TaS_37846208*, TaS_17890143*, TaS_26026646*, TaS552541449** and contig_2766**. RNA-seq data represent biological duplicates of colonized and non-inoculated wheat roots. RT-qPCR data represent biological duplicates of colonized and non-inoculated wheat roots, obtained independently from RNA-seq samples, and each sample was run in triplicate. Significant differences in the RT-qPCR (*p < 0.05, ** p < 0.01, and *** p < 0.001) were determined using one-tailed t-test. Pearson coefficient correlation between RNA-seq and qRT-PCR was >0.97, p-value<0.0001.