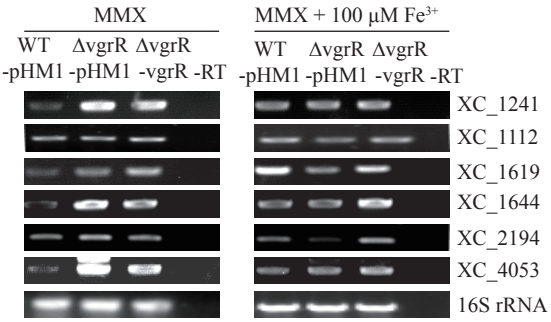

S3 Fig. Verification of the expression of genes identified by comparative proteomics. Semi-quantitative RT-PCR was used to compare the expression levels of genes between different bacterial strains under iron-deplete (MMX) and replete conditions (MMX + 100 μM Fe^{3+}), respectively. cDNAs synthesized from total RNA of bacterial strains were used as template. Amplification of cDNA of 16S RNA was used as loading control. –RT: negative control, in which reverse transcriptase was absent when synthesizing cDNA. The experiment was repeated 3 times.