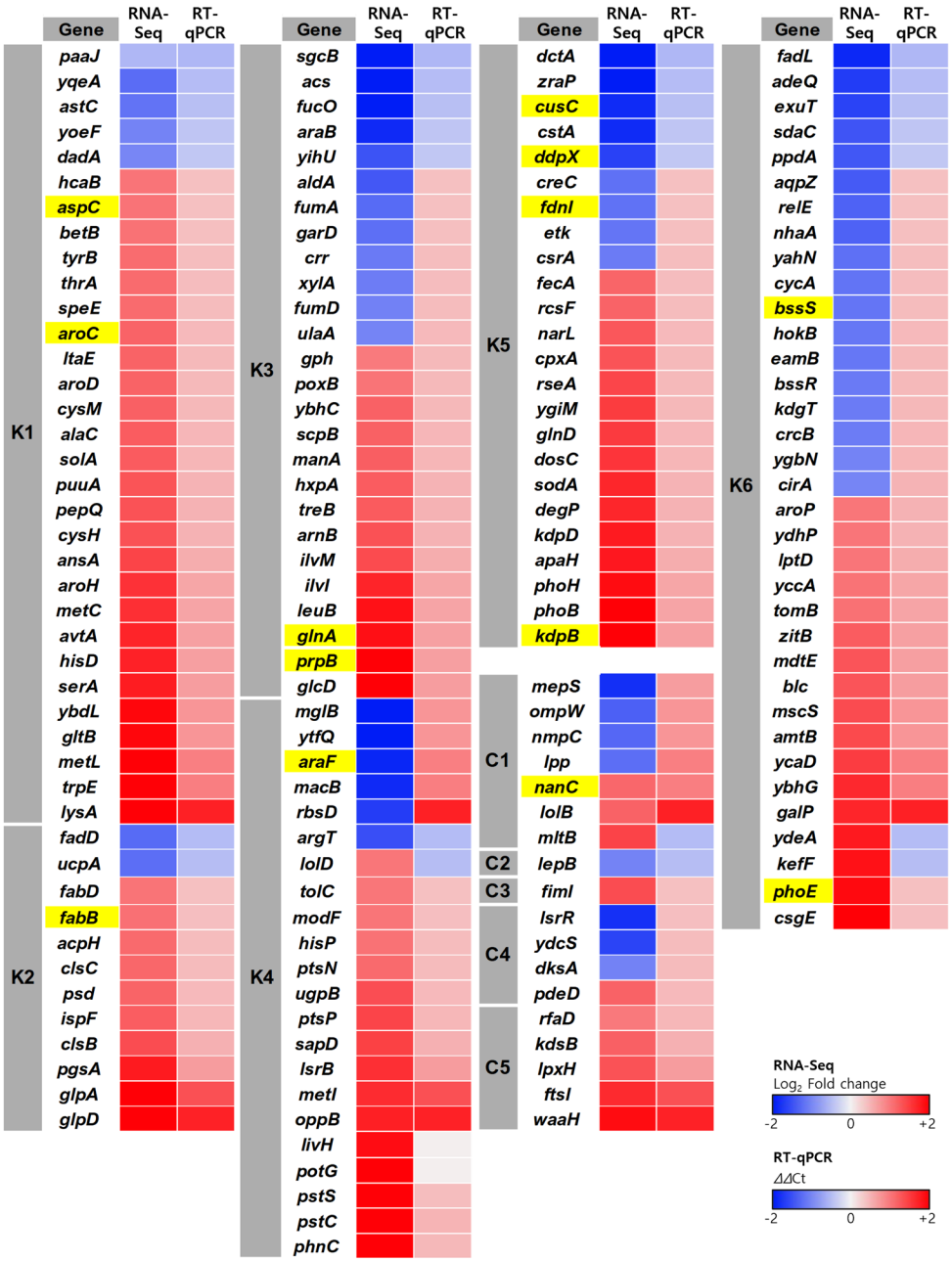

Fig. S5. Comparison of expression patterns between RNA-seq and RT-qPCR. Heat maps illustrate the expression profiles of 168 differentially expressed genes (DEGs) determined by RNA-seq (left column of each pair) and RT-qPCR (right column of each pair). Genes are organized according to their KEGG and COG functional categories, with each row corresponding to a single gene. Expression changes induced by LNT113 treatment are represented by color intensity, where red denotes upregulated genes and blue denotes downregulated genes. RT-qPCR expression levels are reported as $\Delta\Delta$Ct values, calculated by subtracting the ΔCt of the control group (Tris buffer, 15 min) from that of the LNT113-treated group (15 min), with ΔCt defined as $Ct_{[rpoD]} - Ct_{[\text{target gene}]}$ (n = 2 per group). RNA-seq results are shown as fold changes between the LNT113-treated (15 min) and control (Tris buffer, 15 min) samples. Genes highlighted in yellow exhibited statistically significant differences in RT-qPCR analysis ($p < 0.05$) and were subsequently selected for functional validation.