

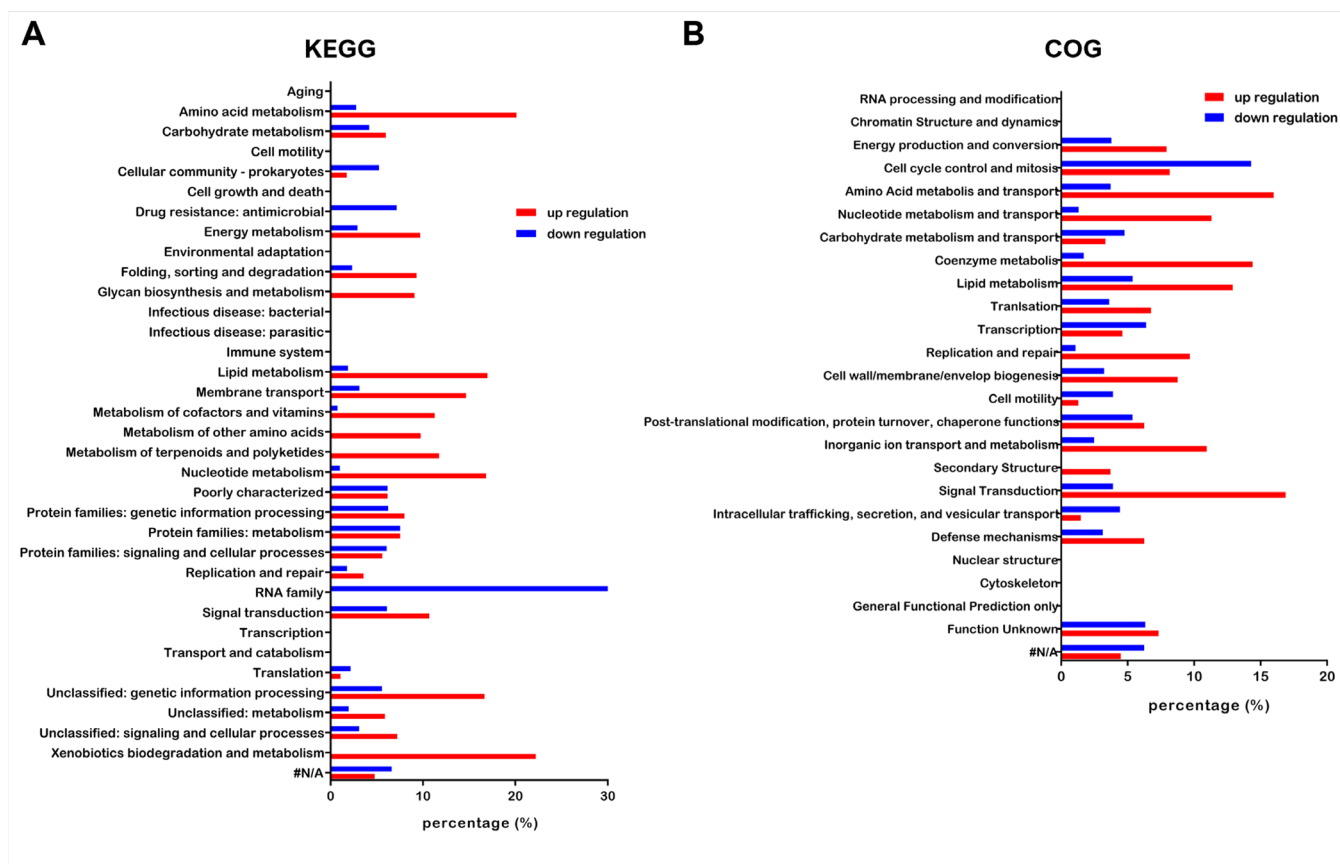


Fig. S3. Functional categorization of genes with altered mRNA levels following LNT113 treatment. Differentially expressed genes (DEGs) were grouped based on (A) Kyoto Encyclopedia of Genes and Genomes (KEGG) classification and (B) Clusters of Orthologous Groups (COG) analysis. Red and blue bars represent the percentages of genes with upregulated and downregulated expressions, respectively, in each functional category.