Supplementary Figures

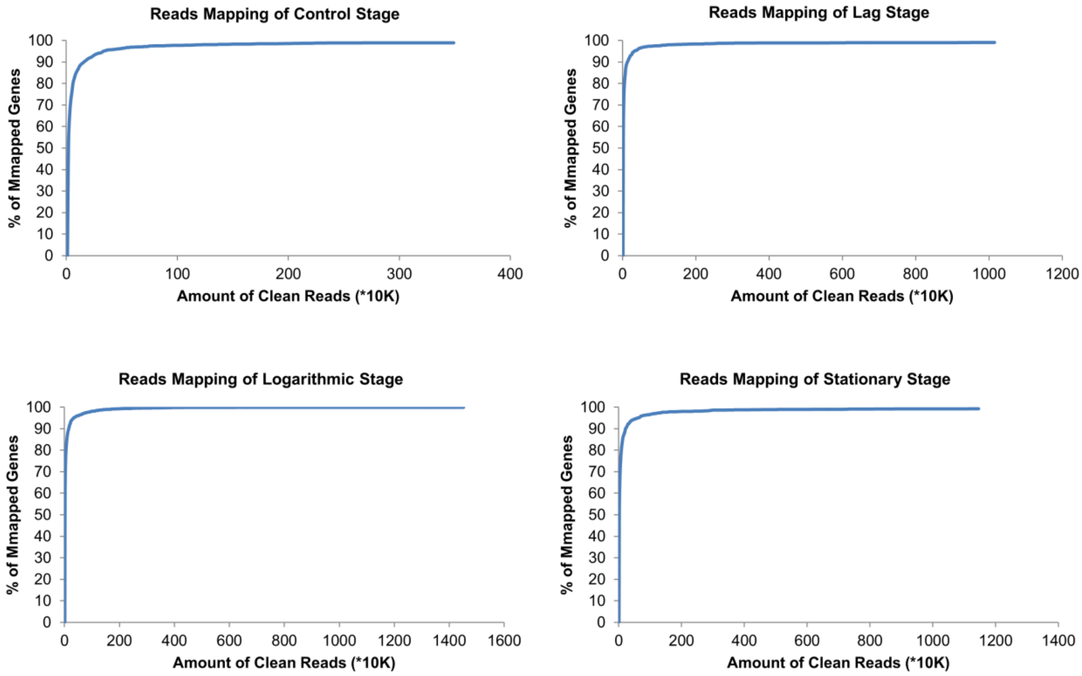

Figure S1. The sequencing saturation analysis of RNA-seq data in the four growth stages.

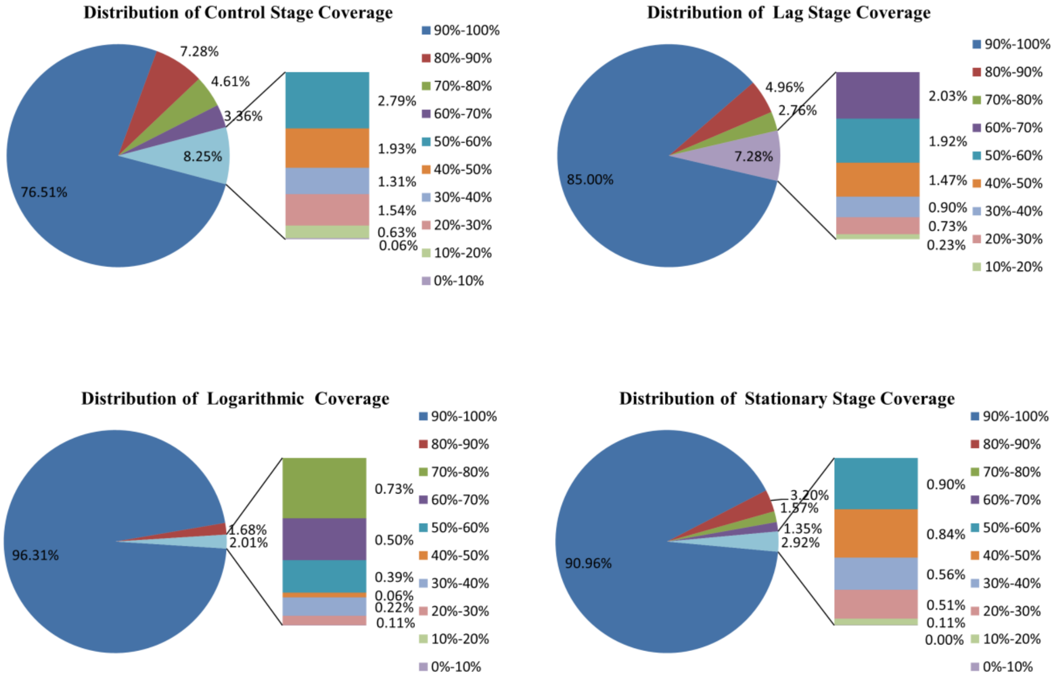

Figure S2. Gene coverage distribution of RNA-seq data in the four growth stages.

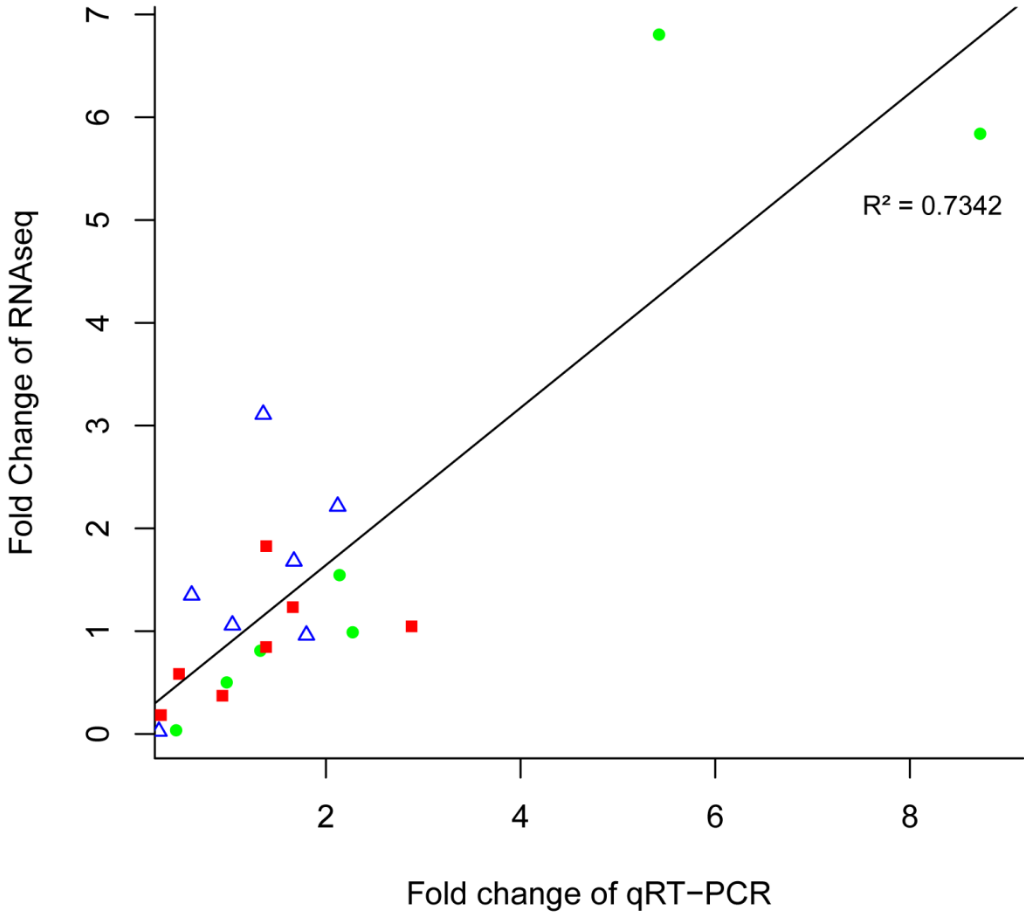

Figure S3. Correlation of fold-changes between RNAseq and real time PCR (qRT-PCR). The fold-change between lag phase and control phase was represented by red rectangles, the fold-change between logarithmic phase and control phase was indicated by blue triangles, and the fold-change between stationary phase and control phase was indicated by green dots.

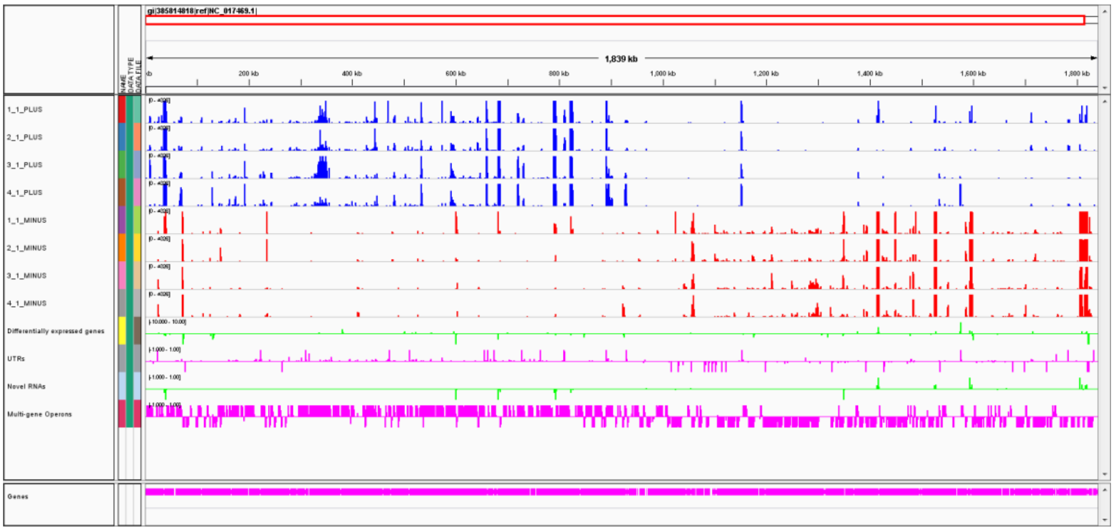

Figure S4. The snapshot of Rockhopper analysis of *Lb.bulgaricus* 2038 transcriptome. The number 1,2,3,4 on the left represented control, lag, logarithmic, and stationary stages, respectively.

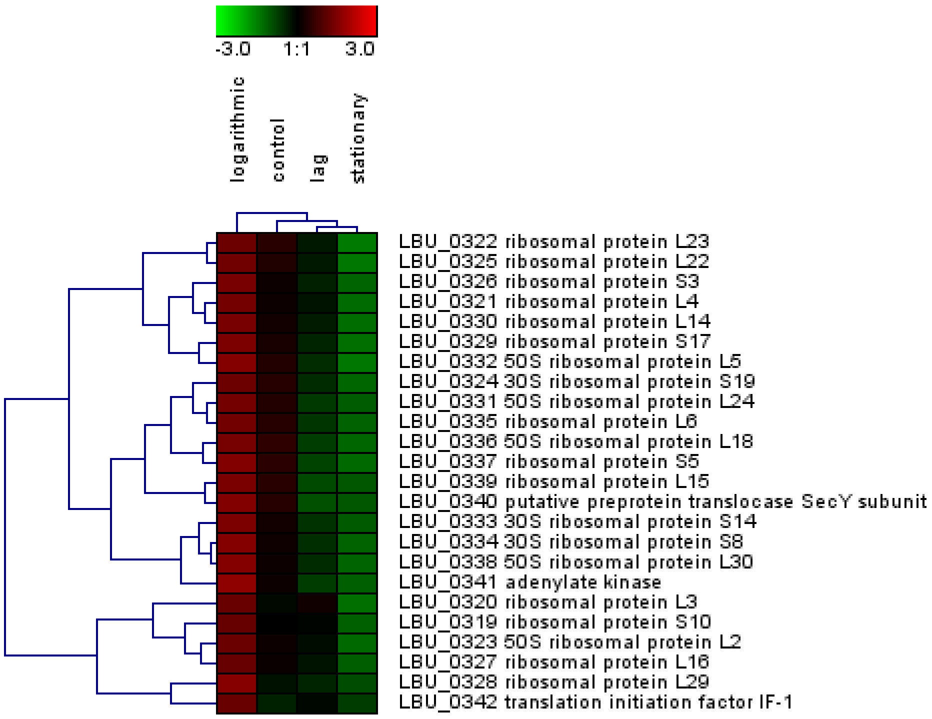

Figure S5. Hierarchical clustering of the 24 genes in the largest operon (Operon_072). All these genes were involved in COG Class of ‘Translation, ribosomal structure and biogenesis’.

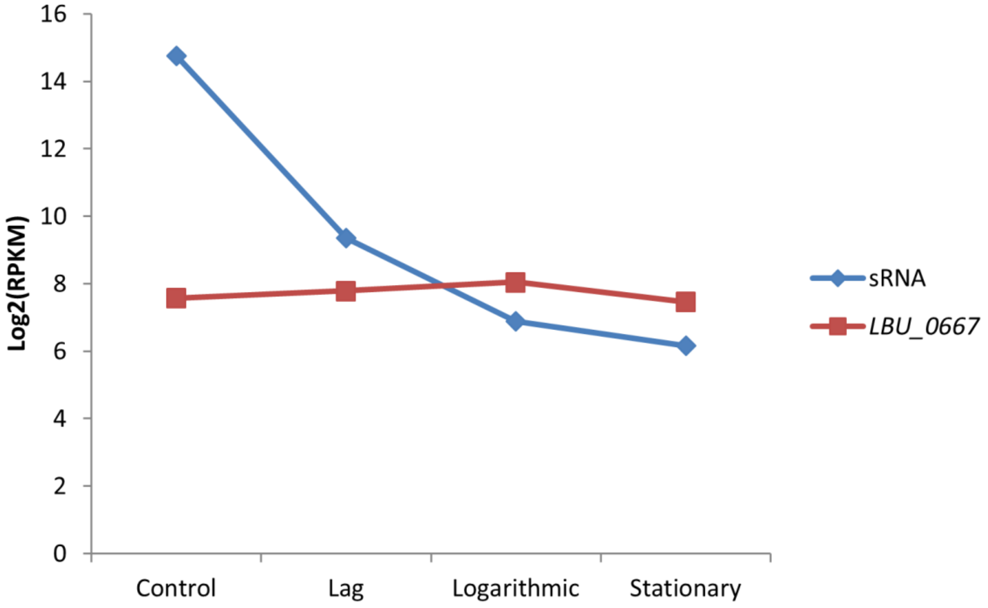

Figure S6. Expression profile of the sRNA and its target in *Lb.bulgaricus* 2038. The four growing stages were isted in the x-axis.Numbers on the y-axis represents log 2 transformed RPKM values.