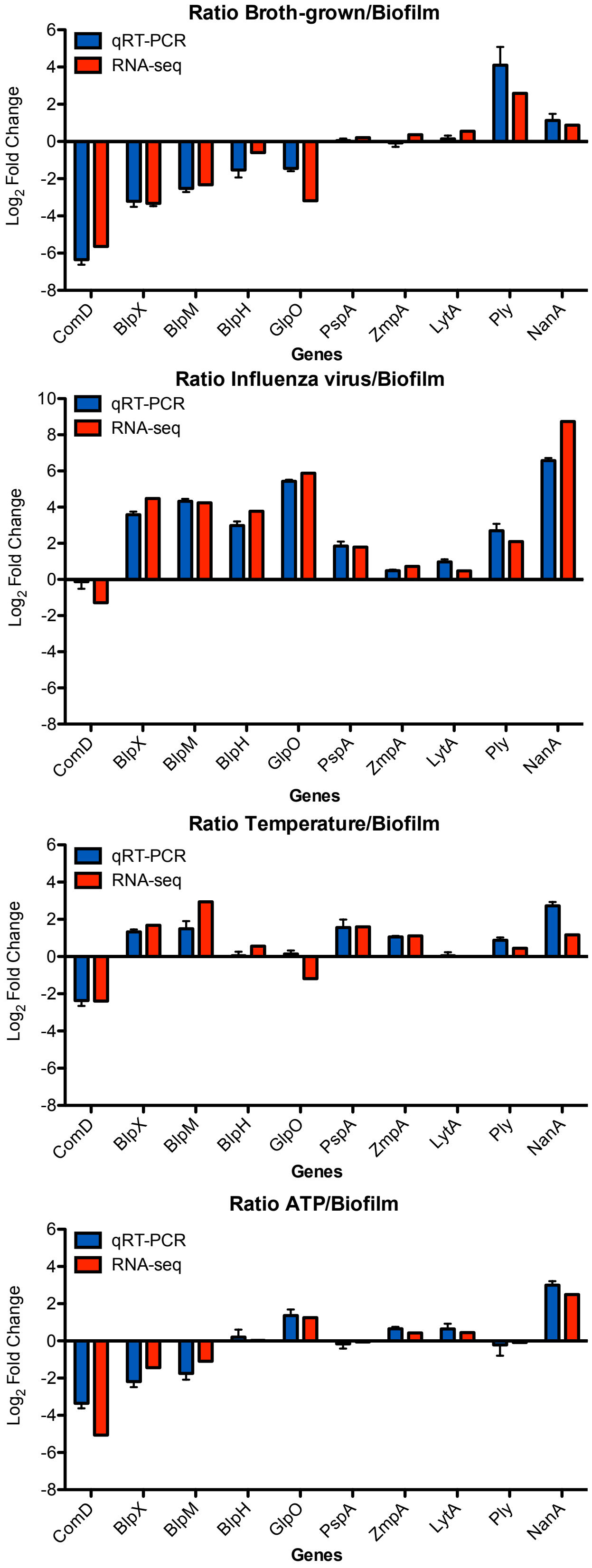
## SUPLEMENTARY FIGURES

**Figure S1. Correlation of gene expression by RNA-seq and qRT-PCR.**



Ratio Broth-grown/Biofilm

Ratio Influenza virus/Biofilm

Ratio Temperature/Biofilm

Ratio ATP/Biofilm

The RNA from Broth-grown bacteria and bacteria actively dispersed from biofilms were used to measure the gene expression by qRT-PCR normalized to gyrA, that was not shown to change in the RNA-seq analysis. Genes shown by RNA-seq to be down-regualted, up-regauted or unchanged were selected for the comparison. The expression levels measured by RNA seq (red bars) correlated well with those measured by qRT-PCR. Each experiment was repeated at least three times in duplicate.

**Figure S2. Genes differentially expressed in IAV, heat, and ATP compared to biofilm bacteria**. Heatmap of $\log_2$-transformed fold changes of 90 genes significantly differentially expressed in each of the three conditions (i.e., IAV, heat, and ATP) compared to biofilm. Complete linkage hierarchical clustering was used to identify and group similarly regulated genes close to each other. A color key is located in the top left corner.