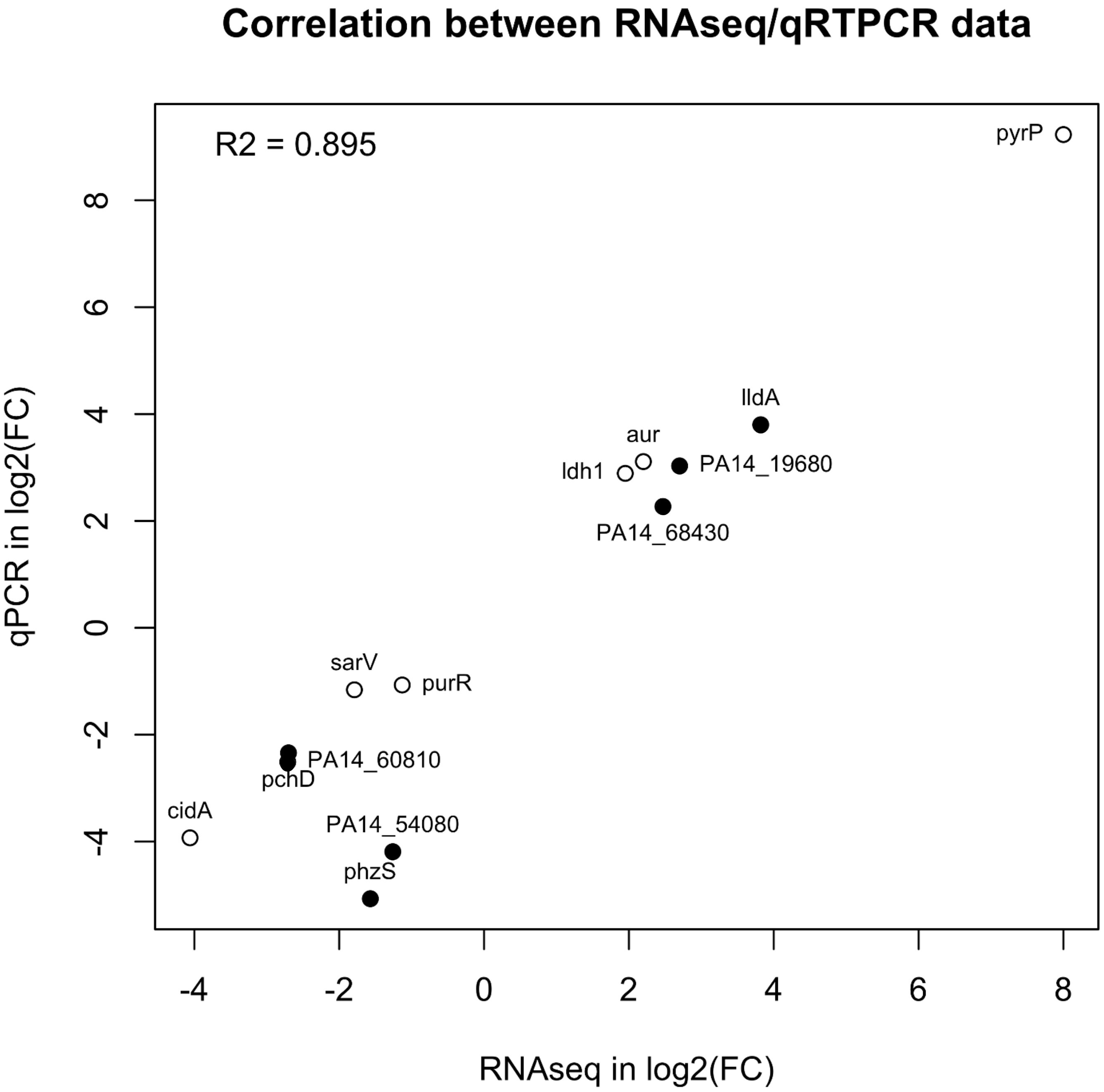

Fig. S2 Comparison of the fold-changes ($\log_2$ base) obtained by RNA sequencing and qRT-PCR for three genes that were up- or down-regulated in each organism in response to the competitor. A statistically significant correlation ($R^2 = 0.895$, $p < 0.05$) was found for the 12 genes tested. *P. aeruginosa* genes (filled symbols), *S. aureus* genes (open symbols). Data points represent the average of the three replicate samples. The package 'gplots' of R (https://cran.r-project.org/web/packages/gplots/index.html) was used for the regression analysis.