



Suppl. Fig. S2 — Gene expression changes in response to vancomycin stress by qRT-PCR. The title of the graphs indicate control. Only genes showing significant changes, indicated by * are plotted in A-D. E shows transcriptional changes between ATCC 700699 and treated samples were mostly non-significant. Relative normalized mRNA expression of (A) *pbp2*, *vraS*, *tagA*, *ureC*, *pbp4*, *pflA*, *pflB*, *recR*, *atl*, *ureB*, *tagX* and *rsbW* in control (untreated V26) and treated V26 (V26_VISA2); (B) *pbp4*, *tagX*, *vraS*, *recR*, *recF*, *rsbW*, *pflB*, *pflA*, *tagA*, and *pbp2* in control (untreated V29) and treated V29 at two different time points (V29_VISA2: at MIC = 4 μ g/mL and V29_VISA3: at MIC = 8 μ g/mL); (C) *pbp2*, *recF*, *tagX*, *pflA*, *pflB*, *tagA*, *ureC*, *pbp4*, *ureB*, *atl*, *rsbW* and *vraS* in control (untreated V30) and treated V30 at two different time points (V30_VISA2: at MIC = 4 μ g/mL and V30_VISA3: at MIC = 8 μ g/mL); (D) *recR*, *rsbW*, *tagA*, *ureC*, and *atl* in control (untreated B11) and treated B11 at two different time points (B11_VISA: at MIC = 8 μ g/mL and B11_VRSA: at MIC = 16 μ g/mL); and (E) *pflB*, *pbp4*, *vraS*, *pflA*, *tagA*, *ureB*, *ureC*, *atl*, *rsbW*, *recR*, *pbp2*, *recF*, and *tagX*, in control (ATCC_700699) and treated V26, V29, V30 and B11