



Supplemental Figure S3. Correlation analysis of read allele frequency and genome coverage. Overall sequence data from all derivative strains obtained during vancomycin (VAN), daptomycin (DAP) resistance selection, or antibiotic-free passaging (CON) from all collection time points are presented. Linear estimation (red line) was used. Red points are matched to key SNPs involved in vancomycin or daptomycin resistance.