Figure S2  Size distribution of detected duplications and deletions. Duplications and deletions (≥ 2kb) were detected by comparing the read coverage in each of the 103 strains to the coverage of the resequenced reference strain (PS312) using the program cnv-seq (P<0.01). The boxplots show median and interquartile range of the size distribution of duplications (A) and deletions (B) across all 103 strains.