

## Appendix B

Tables that have been deposited in Duke Data Repository:

**Table B1:** List of mutations in parent and knockout strains, detected by Breseq

**Table B2:** Raw growth data for parental and  $\Delta hpyA$  cells in optimal and reduced salt (9 biological replicates), measured as optical density (OD600).

**Table B3:** List of peaks obtained by HpyA ChIP-seq; arranged by peak (**B3\_simplified**) and by overlap of peak and genomic feature (**B3\_full**)

**Table B4:** List of genes differentially expressed in  $\Delta hpyA$  in reduced and optimal salt conditions.

**Table B5:** List of genes in each subcluster obtained by clustering of expression patterns of differentially expressed genes.

**Table B6:** arCOG enrichments for genes nearest the HpyA ChIP-seq peaks, and for genes differentially expressed in  $\Delta hpyA$

**Table B7:** List of ChIP-seq peaks within 500 bp of differentially expressed genes.

**Table B8:** Growth data (OD600) for  $\Delta hstA$  and  $\Delta pyrE$  parent strain in optimal conditions.

**Table B9:** Manually curated list of ChIP-seq peaks for HstA.

**Table B10:** Details of characteristics (number of peaks, average width, total area covered by peaks) of ChIP-seq peaks for HpyA, HstA, and other DNA-binding proteins (shown graphically in main text figures).

**Table B11:** List of ChIP-seq datasets used for start site occupancy and peak width/coverage analysis, (with SRA trace where available), and genomes analyzed for periodicity (with link to the relevant NCBI assembly).

**Table B12:** Results of all rRNA removal experiments, including species, removal method, %rRNA (5S, 16S, 23S) remaining, total and non-rRNA aligned reads. Tabs within the table use the same data and are made for convenience of figure generation.

**Table B13:** Data downloaded from NCBI regarding number of publications per year mentioning “Archaea”, “RNA-Seq”, and “Archaea RNA-Seq”.

**Table B14:** Effect of probe specificity on rRNA removal: %age alignment of each custom-designed probe to *Hbt sal* 16S, 23S, and 5S rRNA sequences, and results of removal using these custom probes and non-targeted probes.

**Table B15:** Correlations between gene counts for different rRNA removal methods.