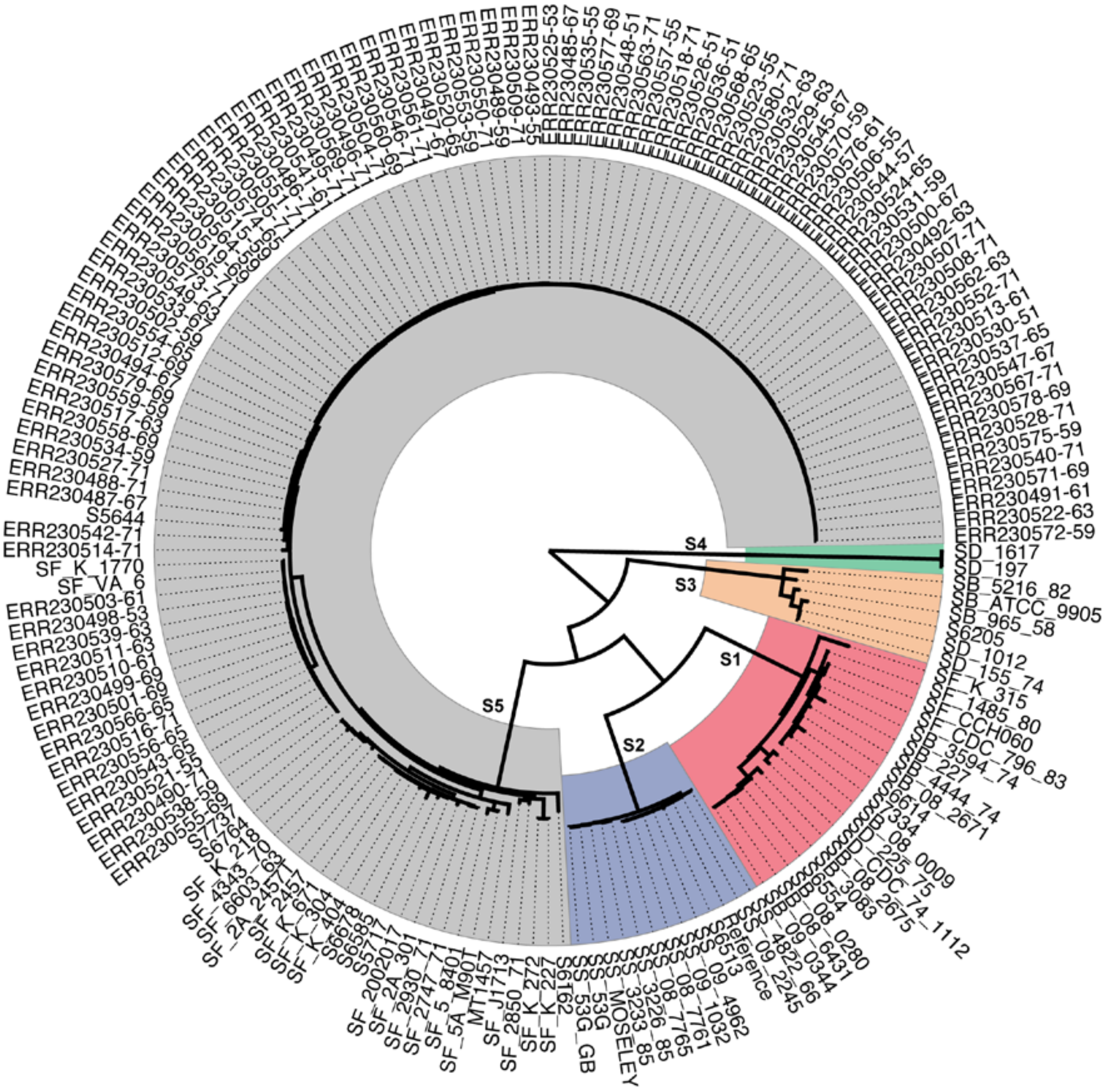
Supplemental Figure Legends

Supplemental Figure 1. A whole genome phylogeny of 164 *Shigella* genomes. The tree was inferred with FastTree2 (2) on a Mugsy (1) whole-genome alignment. Labels at branch nodes indicate the clade naming convention developed in this study. This phylogeny illustrates the placement of 96 *S. flexneri* genomes, assembled from raw read data in the Sequence Read Archive (http://www.ncbi.nlm.nih.gov/sra), compared to the 69 *Shigella* genomes shown in Figure 3.

Figure S1.



Supplemental References

1. **Angiuoli, S. V., and S. L. Salzberg.** 2010. Mugsy: Fast multiple alignment of closely related whole genomes. Bioinformatics.
2. **Price, M. N., P. S. Dehal, and A. P. Arkin.** 2010. FastTree 2--approximately maximum-likelihood trees for large alignments. PLoS One **5:**e9490.