

## **Supplementary Data Files**

**Supplementary Data 1.** List of metagenomic samples and metadata used in this study.

**Supplementary Data 2.** Results of sweep-detection pipeline applied to all non-redundant pairs of quasi-phaseable timepoints.

**Supplementary Data 3.** Locations of SNVs for all detected sweeps in Supplementary Data 2.

**Supplementary Data 4.** Species relative abundance estimates for each of the samples in Supplementary Data 1.

**Supplementary Code 1.** Analysis code and figure generation scripts for Figures 1-3.