

Figure S1: Rarefaction curves. These curves are the expected accumulation of phylogenetic diversity (Faith, 1992) as rarefaction depth (D) is increased (sample is randomly downsampled to contain D sequences). In this figure, curves are binned by their phylogenetic diversity (Faith, 1992) at the rarefaction depth of D=1500 sequences per sample into 6 bins of even width (but varying numbers of curves within), to create averages (heavy lines). Binning was done because an average trend for samples with such high variance in diversity would not be meaningful. Bins were not used in the analysis of these data, and only serve to visually summarize rarefaction curves that overlap to such a high extent that without binning, individual curves for samples would be impossible to visually distinguish.

