



Figure 4 - figure supplement 3. Measuring synchronized dynamics in the same ASV across many hosts. The cartoon in panel (A) shows the sample selection procedure. We selected pairs of samples from different hosts collected within 24 hours of each other, producing 20,000 “same-day” pairs (e.g., purple and mustard-colored pairs on days 2, 3, 6, and 9). We subset these pairs to one same-day pair per host pair, producing 1,540 same-day pairs from these thinned host series and extracted the correlated ASV abundance from these pairs. Synchrony for a given taxon is estimated as the correlation of the centered log-ratio abundance of that taxon across Series 1 and 2. Panel (B) shows the correlation between log-ratio abundance estimates in paired host samples for the most synchronous taxon, ASV #21 (*Clostridiaceae* 1; $r = 0.480$). Panel (C) shows the time-aligned model-estimated centered log-ratio abundances of ASV #23 in five well-sampled hosts that each lived in a different baboon social group (hosts from top to bottom are F09, F31, F35, F27, F20). Panel (D) shows the distribution of observed synchrony estimates for all 125 ASVs (light blue) compared to synchrony estimates from a permuted/null distribution (gray). 118 of 125 ASVs had significantly higher synchrony than expected ($FDR \leq 0.05$; permutation scheme).