**Figure S1: Venn diagram of phylotype sharing among host populations.** Shown are the presence absence patterns of OTUs across host populations. All counts reflect the presence/absence of OTUs in the original, unrarefied OTU table.

**Figure S2: Phylogeny of great ape gut microbiota.** Shown is a parsimony reconstruction of the relationships among great ape gut bacterial communities based on the log abundances of bacterial phylotypes (methods described in Ochman et al. 2010). Analysis was performed in PAUP\* 4.0 using default parameters and 100 bootstrap replicates. All nodes supported by fewer than 95 of the replicate trees were collapsed into polytomies.

**Figure S3: Principal coordinates plots of the distances among gut microbiota recovered from all samples.** Shown are the first two principal coordinates for the pairwise Euclidean, Pearson and weighted UniFrac distances among samples. Samples are colored to correspond with **Figure 1**. In these plots, the microbiota of sympatric *Pan* and *Gorilla* are closer on average than the microbiota of allopatric *Pan* and *Gorilla,* and the microbiota of congenerics are on average more similar than those of heterogenerics (all p-values < 0.05).

**Figure S4. Taxonomic classifications of the most abundant bacterial phylotypes shared by sympatric chimpanzees and gorillas.** Pie charts show the relative frequencies of the bacterial phylotypes shared by sympatric chimpanzees and gorillas classified at the level of order. Each slice represents the relative abundance of a bacterial order as indicated by the key.

**Figure S5: Rarefaction curves for ape fecal samples.** Rarefaction analyses were performed in QIIME v1.5.0 using default parameters. Plots were generated with make\_rarefaction\_plots.py. Note that the sampling depth applied for each sample appears sufficient to recover the prominent bacterial phylotypes present in each community.