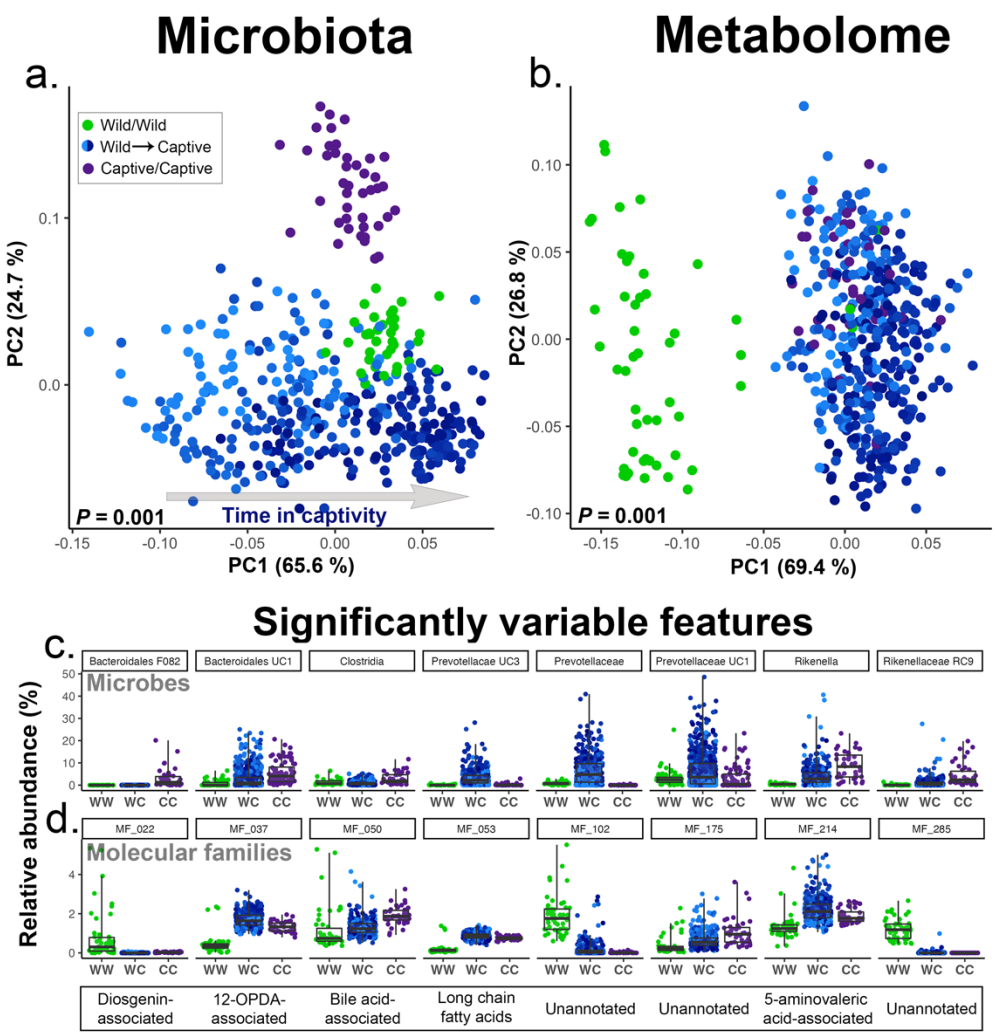

Figure 1. The microbiome differs across rhino populations. Differences in beta-diversity displayed by Robust Aitchison PCA using DEICODE for a) microbiota (16S rRNA sequencing) and b) metabolome (untargeted RP-LC-MS/MS). Significantly variable features [c) bacterial ASVs and d) molecular families] were identified by calculating similarity percentages, and features that contributed to > 2 % of variability between populations were tested for differences in relative abundance by ANOVA.

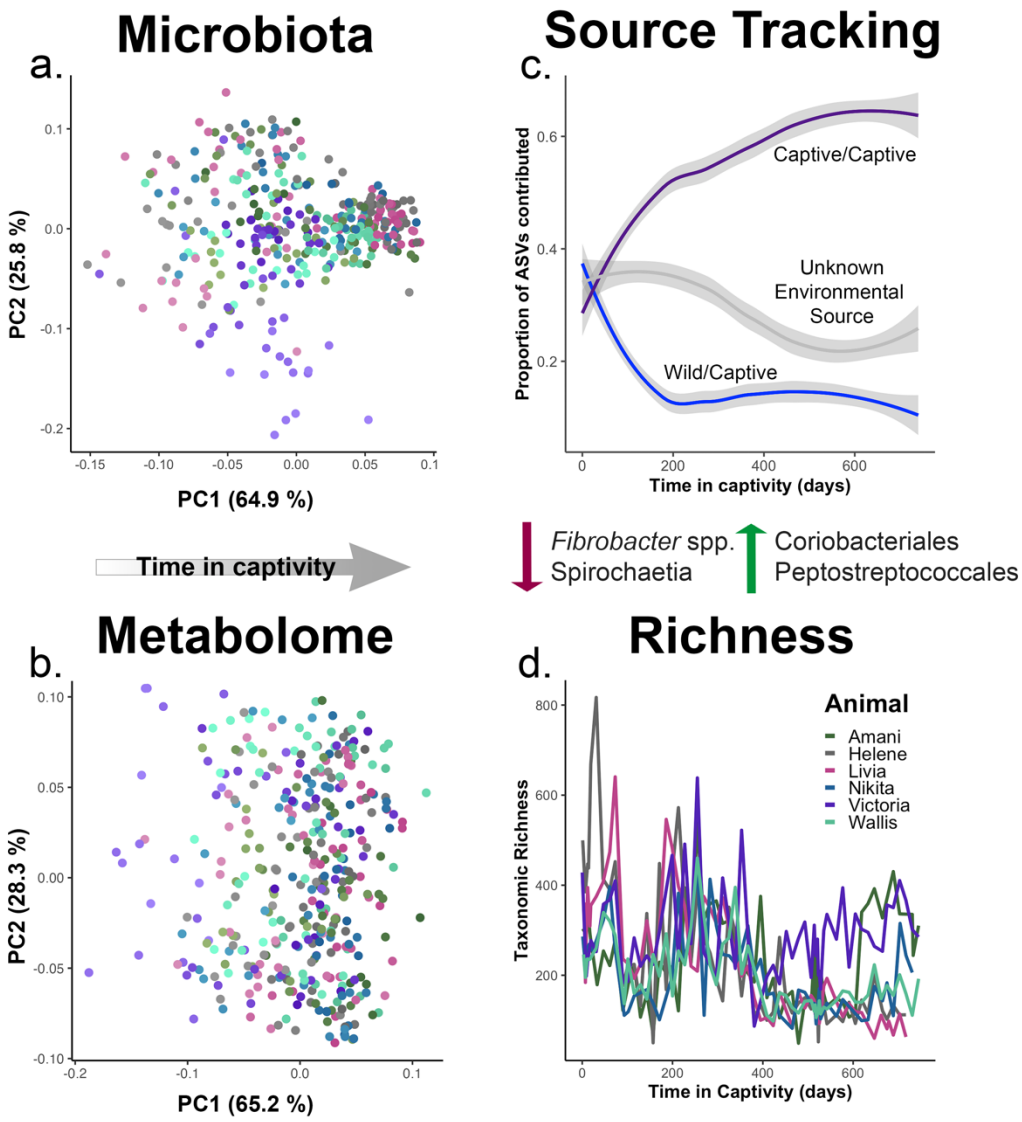

Figure 2. Adaptation to captivity alters the rhino microbiome. Differences in beta-diversity displayed by Robust Aitchison PCA using DEICODE for a) microbiota (16S rRNA sequencing) and b) metabolome (untargeted RP-LC-MS/MS). Time in captivity is associated with c) increased replacement of microbiota by captive/captive rhinos as observed by SourceTracker and d) corresponding loss of richness by 'breakaway' analyses.

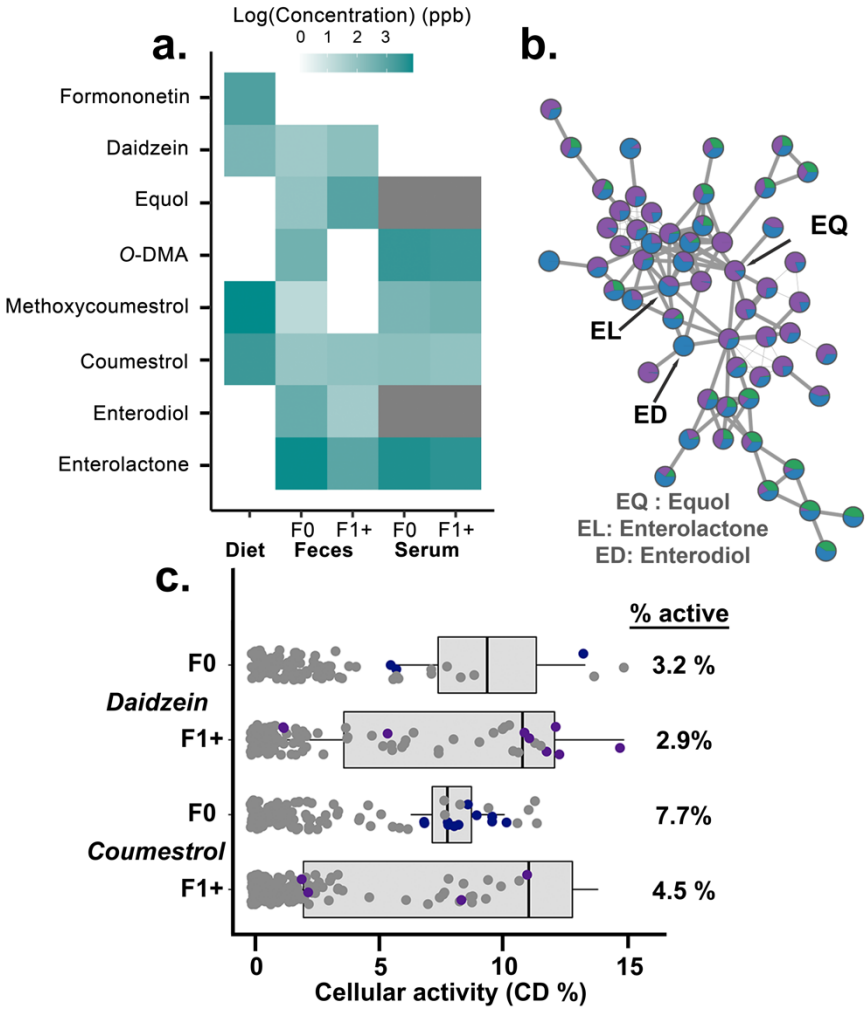

Figure 3. Phytoestrogens and their microbial activity in southern white rhinoceros. a) Log-transformed mean concentrations of phytoestrogens and their microbial metabolites are observed in both wild-born (F0) and captive-born (F1+) white rhinoceros diets, feces, and serum by liquid chromatography--tandem mass spectrometry (LC-MS/MS). Chromatography was insufficient for serum quantification of equol and enterodiol, therefore not determined here, as indicated by gray coloring. O-DMA: o-desmethylangolensin; ppb: parts per billion. b) Visualization of molecular family containing dietary phytoestrogens across rhino populations by GNPS feature-based molecular networking. c) Microbial utilization of daidzein and coumestrol has been observed by both F0 and F1+ by Raman microspectroscopy measuring cellular activity [percent deuterium incorporation (CD %)] following heavy water incubations; colored data points (blue/purple) indicate active cells as determined by CD% deviations of cellular activity of no amendment incubation.