

Benedict et al. (Supplementary material)

Supplementary Figure 1. (A) Neither sleep condition nor fecal collection day (time effect) were found to be significant drivers for beta diversity using weighted abundances (baseline vs day 2; or day 2 samples for Sleep vs PSD). (B) Hierarchical clustering of samples across participant, BMI, cage timepoints and conditions (partial sleep deprivation, PSD, or normal sleep, NS) revealed clustering primarily according to participant. d0, day 0 (baseline sample); d2, day 2. Subjects have been arbitrarily numbered.

Fig 1A

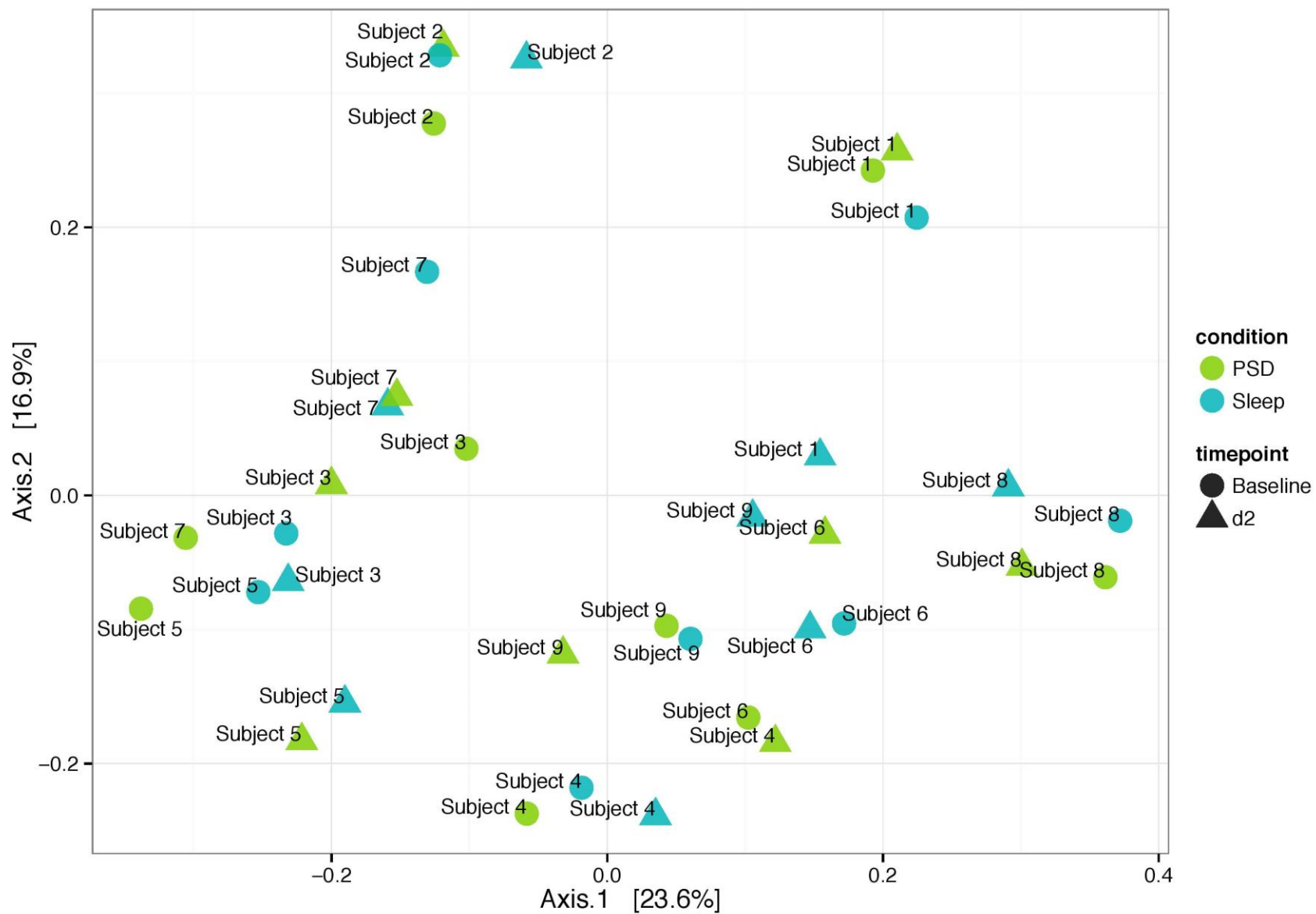
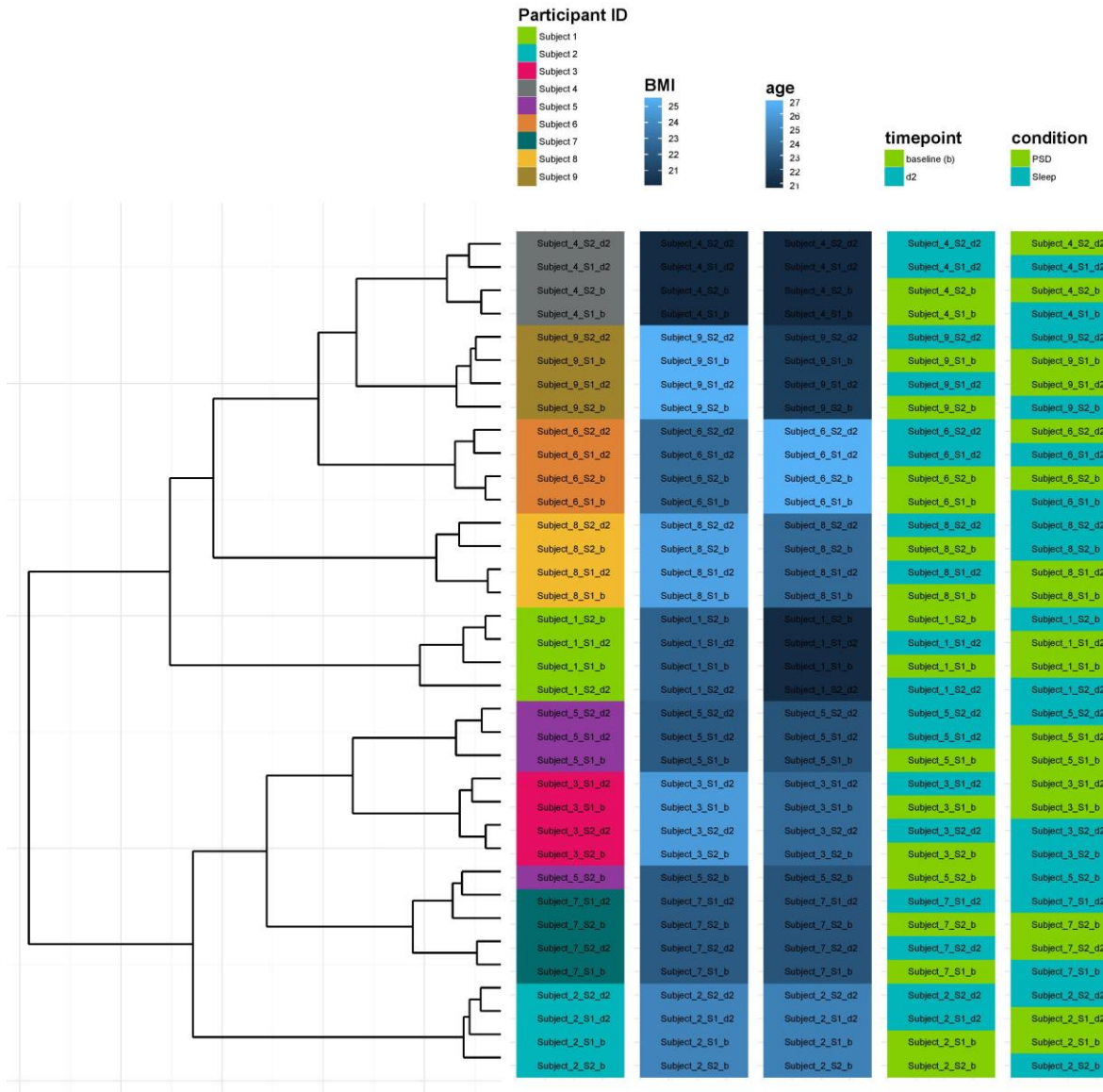


Fig 1B



Supplementary Figure 2. Bacterial composition at the (A) phylum and (B) family taxa level after two nights of partial sleep deprivation (PSD) or normal sleep (“Sleep”).

Fig 2A

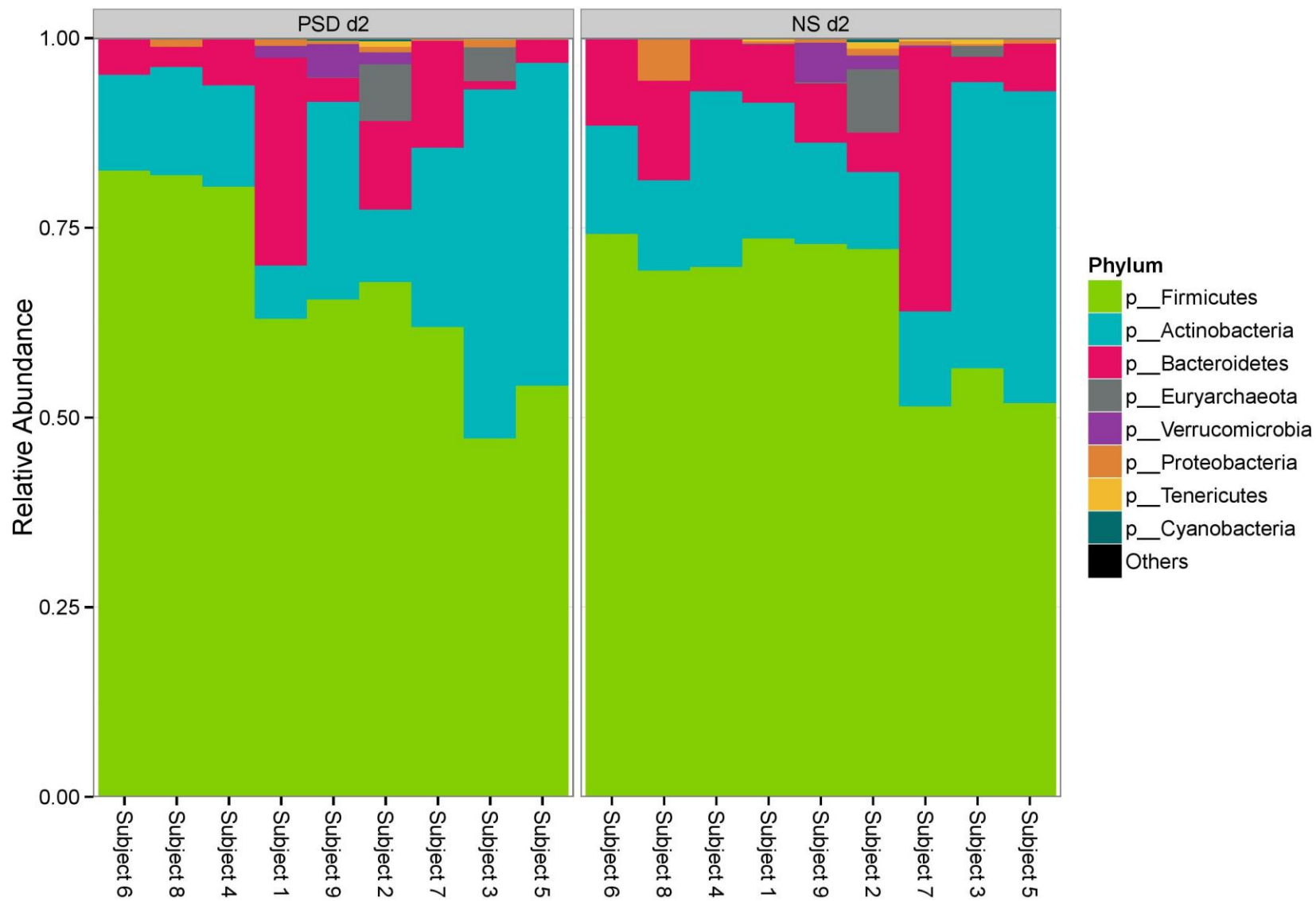
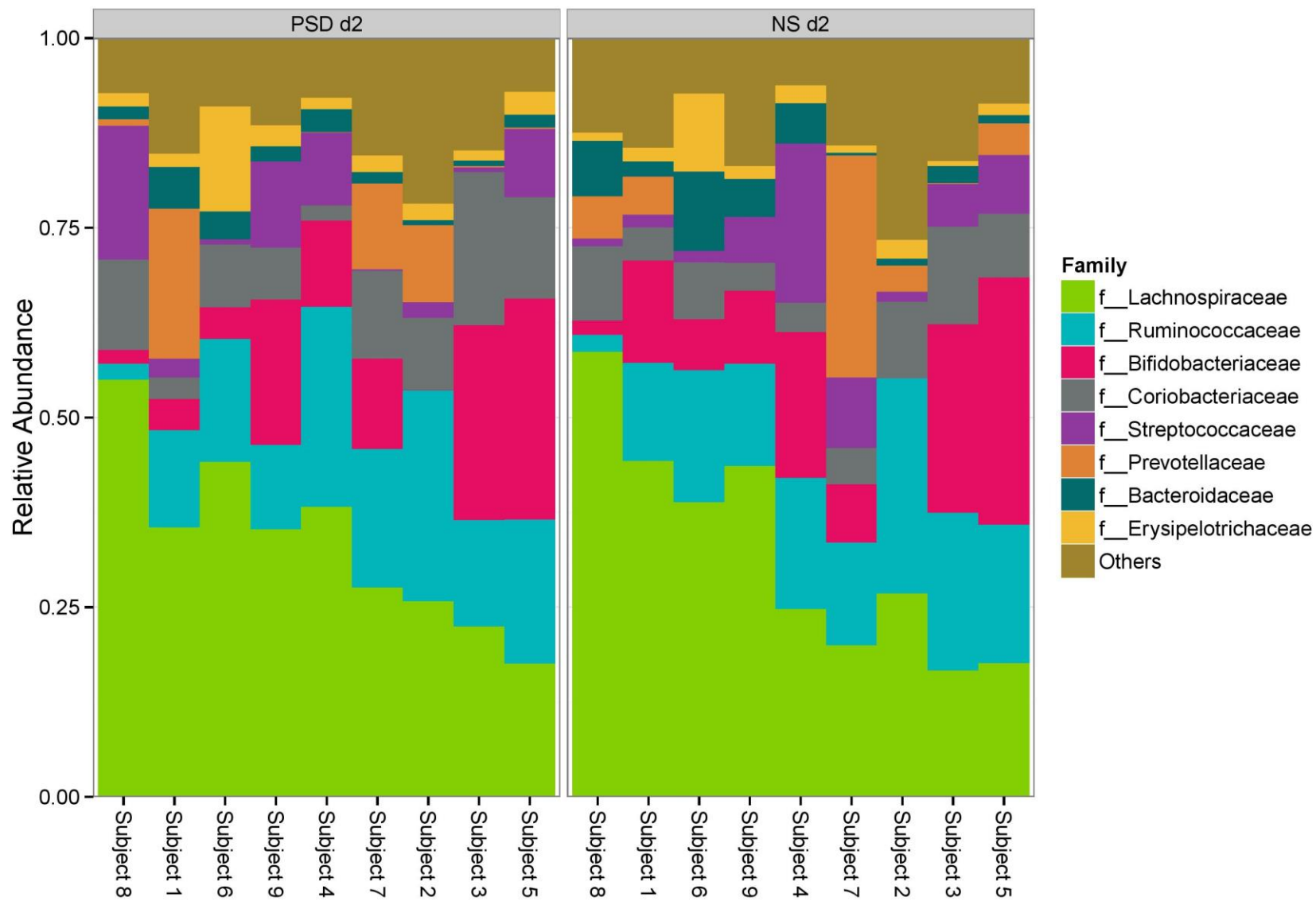


Fig 2B



Supplementary Table 1. Number of categories observed at each taxonomic rank following sequencing of the feces samples obtained after normal sleep and partial sleep deprivation.

Rank	Number of Types
Kingdom	2
Phylum	14
Class	27
Order	45
Family	136
Genus	398
Species	546

Supplementary Table 2. Alpha diversity measures according to timepoint and condition, using both observed and Shannon's method. Tested with Kruskal-Wallis rank sum test with Dunn's post-hoc test, followed by Bonferroni correction for multiple comparisons.

Formula	Value	Chi-square	P value
<i>~ timepoint</i>	<i>Observed</i>	1.766	0.18
<i>~ condition</i>	<i>Observed</i>	0.324	0.57
<i>~ timepoint</i>	<i>Shannon</i>	0.677	0.41
<i>~ condition</i>	<i>Shannon</i>	0.009	0.92