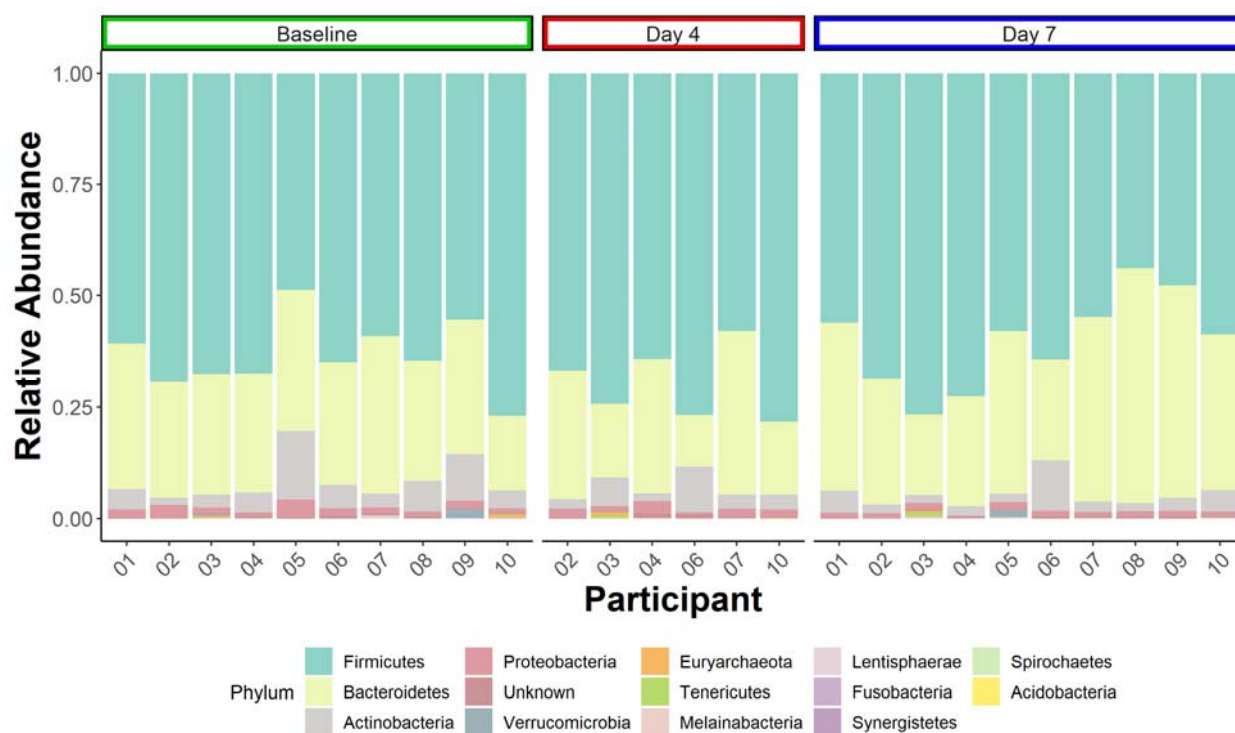
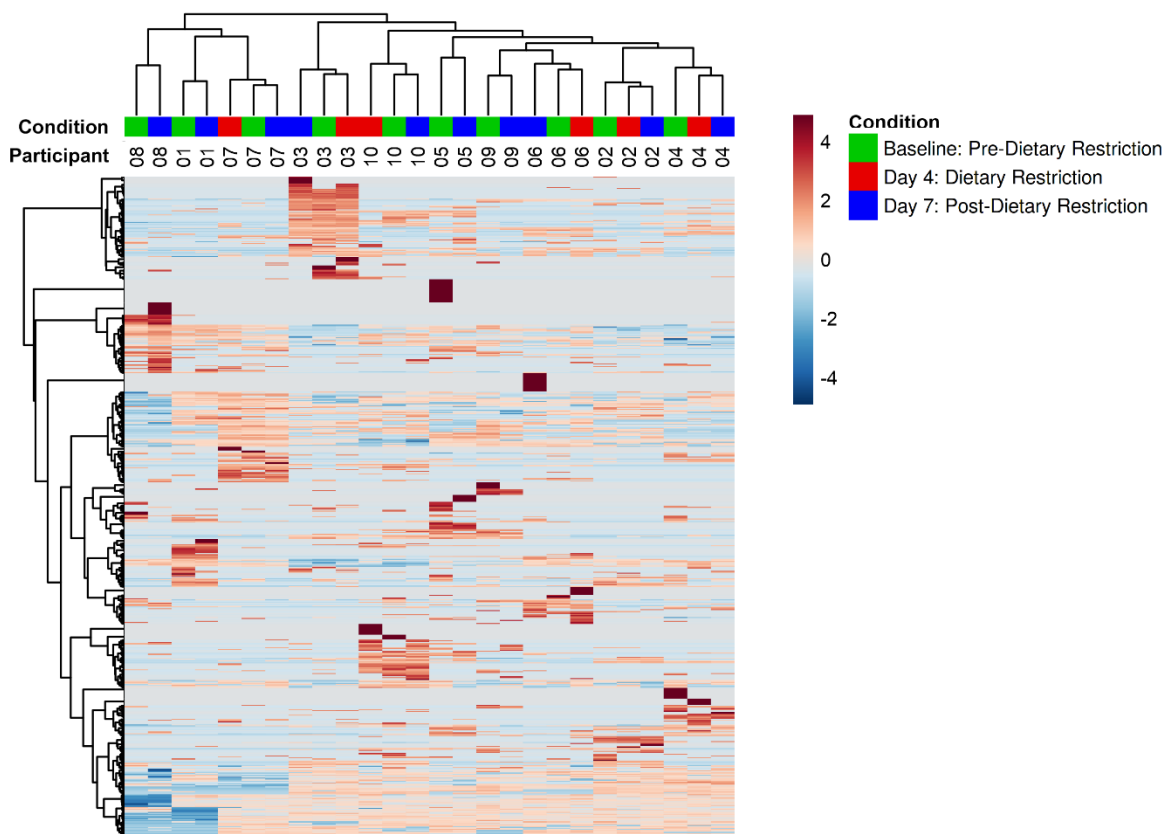


Supplemental Figures/Tables



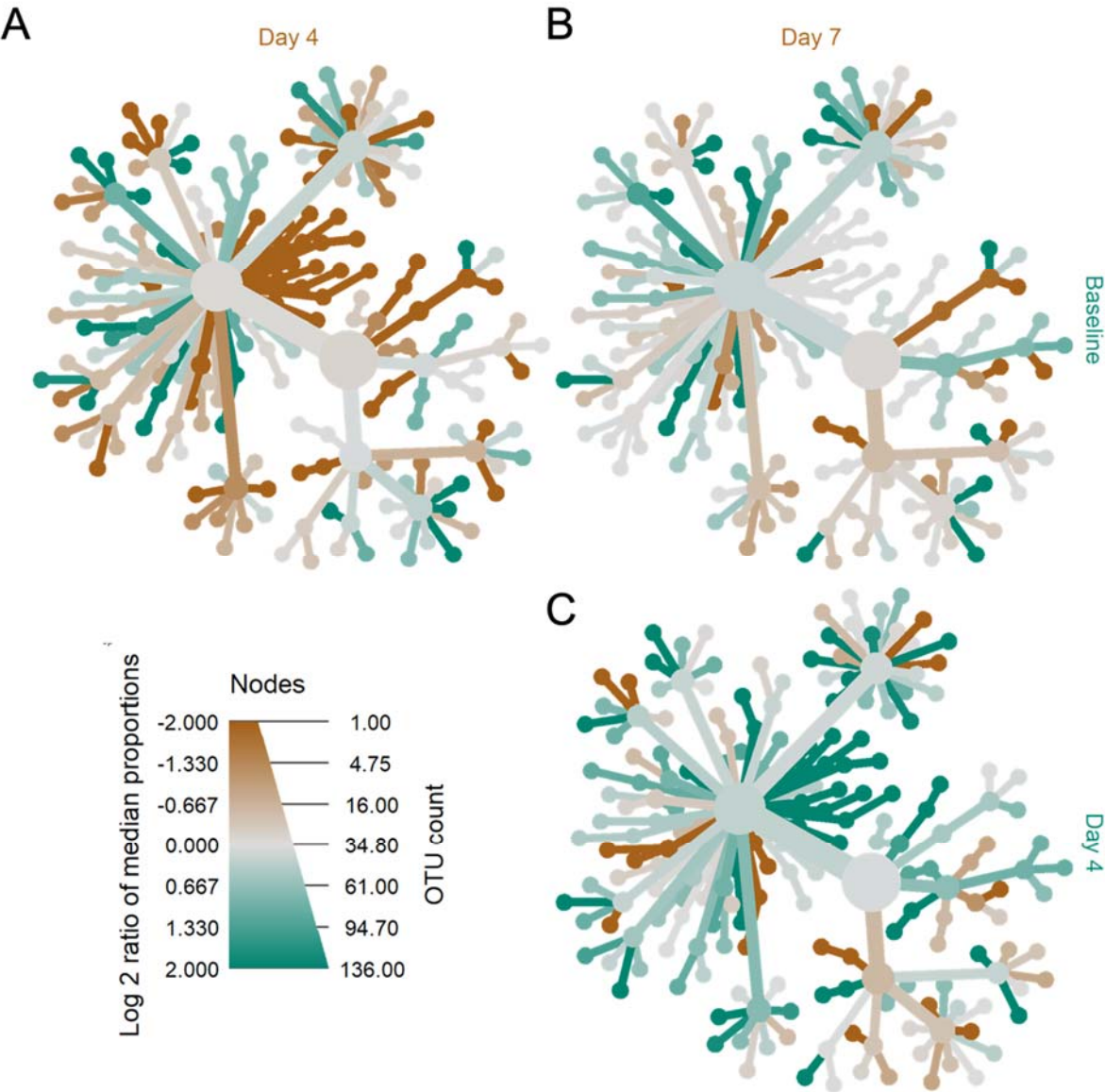
Supplemental Figure S1. Phylum-level Diversity. The relative abundance of each phylum is depicted for each participant at each time-point.



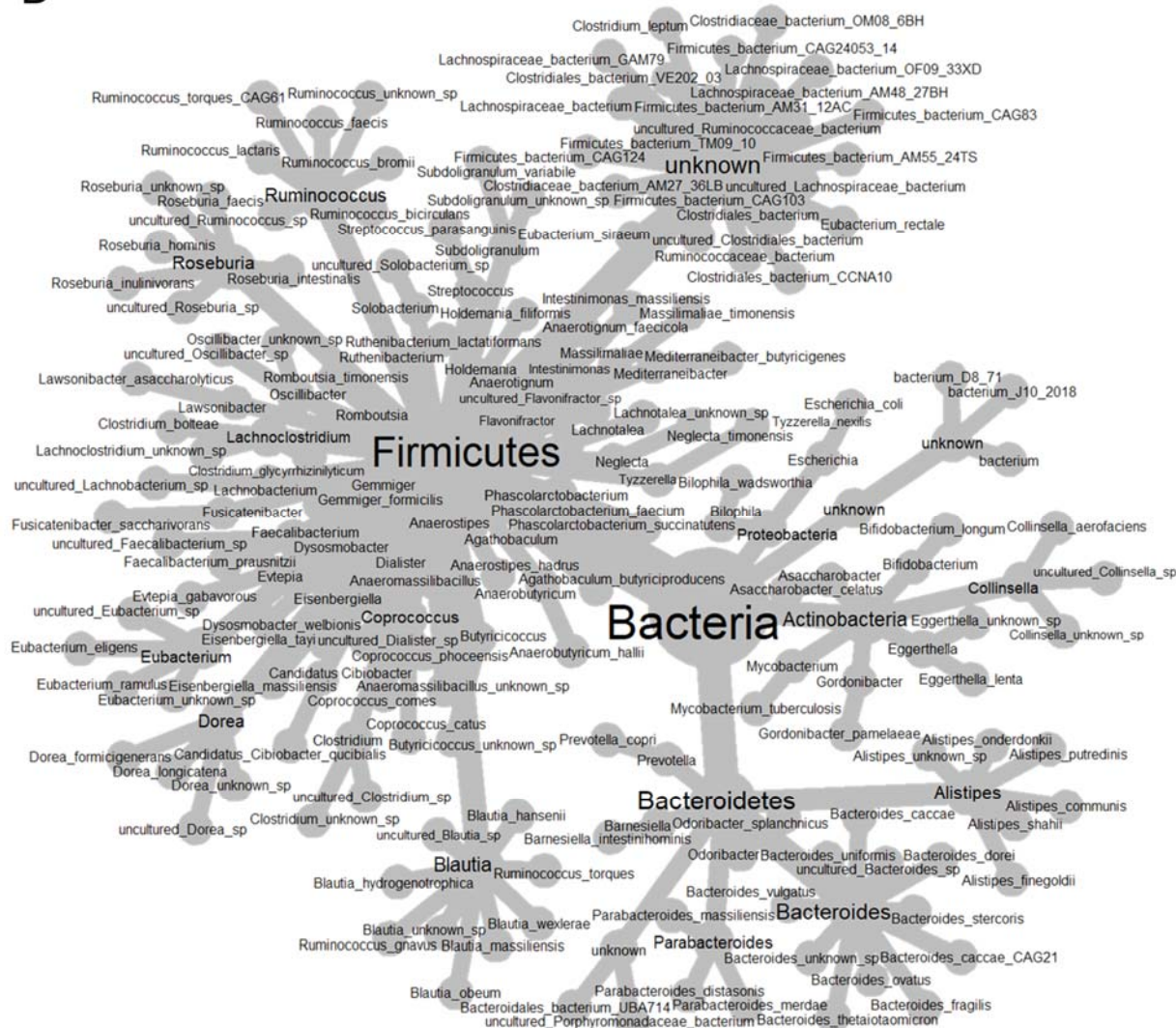
Supplemental Figure S2. Hierarchical clustering of unfiltered species. Species abundance patterns group by patient rather than condition.

Supplemental Table S1. Species PIME prevalence filtering output. Random forests were built at sequential prevalence intervals to determine the ideal cut off value. Out-of-bin (OOB) error rate of 0% was achieved at a 70% prevalence cut off. 74,291,605 reads corresponding to 136 species were present above this filtering threshold.

| Prevalence Interval (%) | OOB Error Rate (%) | OTUs (N) | Sequences (N) |
|-------------------------|--------------------|----------|---------------|
| 5 | 96.15 | 681 | 91,410,253 |
| 10 | 92.31 | 530 | 90,013,248 |
| 15 | 96.15 | 530 | 90,013,248 |
| 20 | 92.31 | 354 | 88,450,002 |
| 25 | 84.62 | 354 | 88,450,002 |
| 30 | 80.77 | 313 | 86,738,175 |
| 35 | 53.85 | 268 | 86,252,647 |
| 40 | 30.77 | 241 | 83,549,022 |
| 45 | 46.15 | 241 | 83,549,022 |
| 50 | 7.69 | 191 | 80,761,545 |
| 55 | 3.85 | 191 | 80,761,545 |
| 60 | 3.85 | 176 | 78,332,889 |
| 65 | 7.69 | 176 | 78,332,889 |
| 70 | 0 | 136 | 74,291,605 |
| 75 | 3.85 | 136 | 74,291,605 |
| 80 | 0 | 128 | 68,893,931 |
| 85 | 0 | 104 | 67,269,799 |
| 90 | 0 | 92 | 59,055,438 |
| 95 | 0 | 92 | 59,055,438 |



D

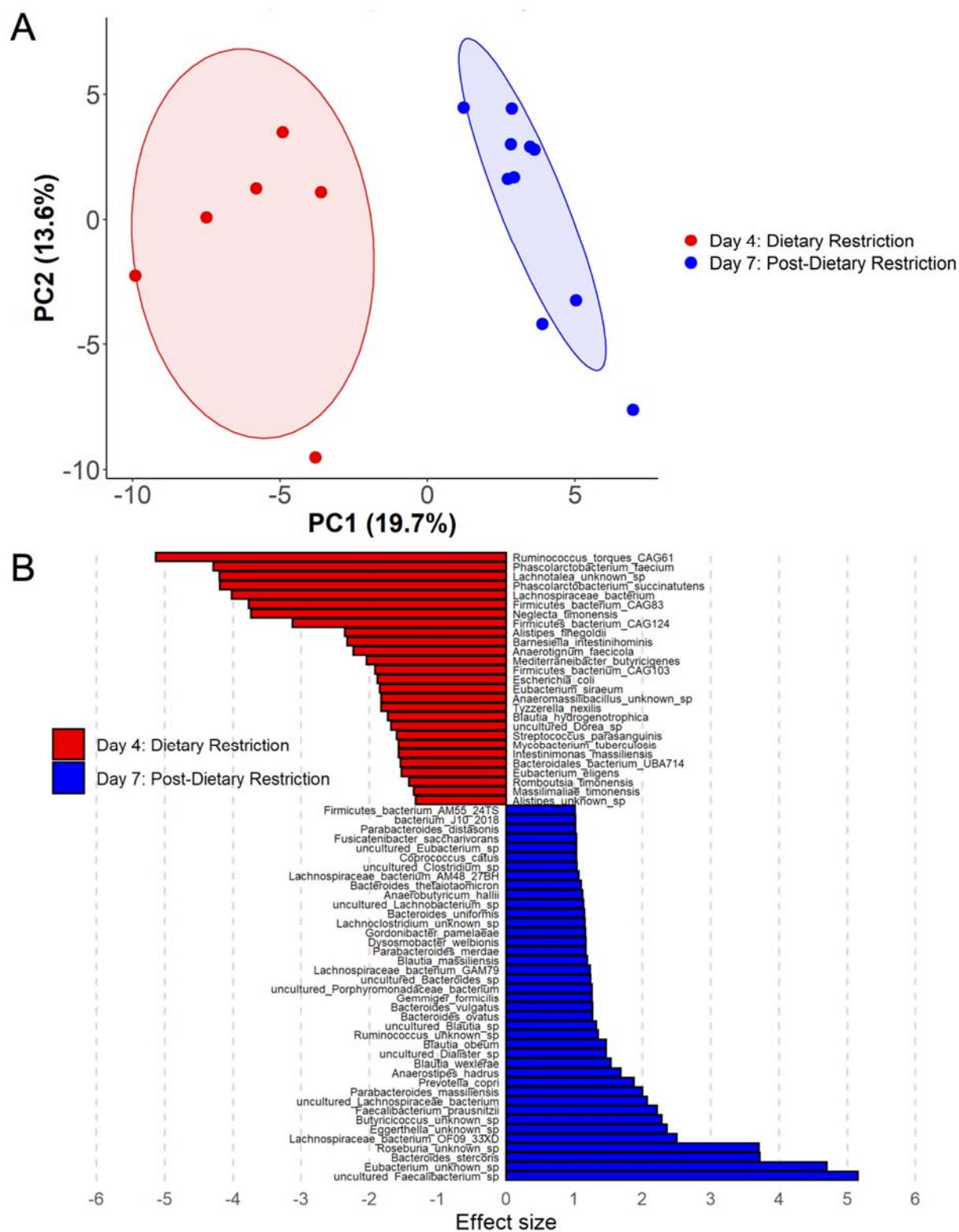


Supplemental Figure S3. Heat tree comparing condition variation at all taxonomy levels. Pairwise comparisons between the three conditions (A-C). Size of each node represents the number of species contained within that group. The color of each node shows the favored condition. Comparisons were performed using Wilcoxon rank-sum test for median read proportion of paired conditions. Heat tree taxa legend (D). Kingdom, phylum, genus, and species taxonomy levels were included.

Supplemental Table S2. Significantly different species between Baseline and Day-4 conditions (FDR $p < 0.05$).

| Kingdom | Phylum | Genus | Species | Effect Size | FDR p-value |
|----------|----------------|------------------------|--|-------------|-------------|
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_stercoris | -4.92 | <0.001 |
| Bacteria | Firmicutes | Faecalibacterium | uncultured_Faecalibacterium_sp | -4.73 | <0.001 |
| Bacteria | Bacteroidetes | Parabacteroides | Parabacteroides_massiliensis | -4.65 | <0.001 |
| Bacteria | Firmicutes | Roseburia | Roseburia_unknown_sp | -3.98 | <0.001 |
| Bacteria | unknown | unknown | bacterium_D8_71 | -3.26 | <0.001 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_dorei | -2.81 | <0.001 |
| Bacteria | Firmicutes | Eubacterium | Eubacterium_unknown_sp | -2.66 | <0.001 |
| Bacteria | Firmicutes | Candidatus Cibiobacter | Candidatus_Cibiobacter_quci bialis | -2.50 | 0.002 |
| Bacteria | Firmicutes | Butyricicoccus | Butyricicoccus_unknown_sp | -2.43 | 0.002 |
| Bacteria | Firmicutes | unknown | Lachnospiraceae_bacterium_GAM79 | -2.14 | 0.001 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_fragilis | -2.12 | 0.002 |
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_bicirculans | -2.03 | 0.002 |
| Bacteria | Firmicutes | Faecalibacterium | Faecalibacterium_prausnitzii | -1.58 | 0.004 |
| Bacteria | Firmicutes | Anaerostipes | Anaerostipes_hadrus | -1.57 | 0.003 |
| Bacteria | Firmicutes | Subdoligranulum | Subdoligranulum_unknown_sp | -1.42 | 0.037 |
| Bacteria | unknown | unknown | bacterium_J10_2018 | -1.41 | 0.012 |
| Bacteria | Firmicutes | Roseburia | Roseburia_intestinalis | -1.40 | 0.010 |
| Bacteria | Firmicutes | Dialister | uncultured_Dialister_sp | -1.39 | 0.005 |
| Bacteria | Firmicutes | unknown | uncultured_Lachnospiraceae_bacterium | -1.34 | 0.005 |
| Bacteria | Bacteroidetes | Bacteroides | uncultured_Bacteroides_sp | -1.32 | 0.011 |
| Bacteria | Firmicutes | Anaerobutyricum | Anaerobutyricum_hallii | -1.24 | 0.025 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_ovatus | -1.20 | 0.028 |
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_unknown_sp | -1.17 | 0.015 |
| Bacteria | Firmicutes | Blautia | Blautia_wexlerae | -1.12 | 0.016 |
| Bacteria | Firmicutes | Blautia | uncultured_Blautia_sp | -1.12 | 0.025 |
| Bacteria | Firmicutes | Eubacterium | uncultured_Eubacterium_sp | -1.09 | 0.040 |
| Bacteria | Firmicutes | unknown | uncultured_Ruminococcaceae_bacterium | -1.08 | 0.034 |
| Bacteria | Firmicutes | Dysosmobacter | Dysosmobacter_welbionis | -1.07 | 0.013 |
| Bacteria | Firmicutes | Gemmiger | Gemmiger_formicilis | -1.05 | 0.024 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_vulgatus | -1.02 | 0.017 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_thetaiotaomicron | -1.00 | 0.030 |
| Bacteria | Firmicutes | Clostridium | uncultured_Clostridium_sp | -0.96 | 0.031 |
| Bacteria | Firmicutes | unknown | Clostridiales_bacterium_VE20_2_03 | -0.96 | 0.015 |
| Bacteria | Firmicutes | Fusicatenibacter | Fusicatenibacter_saccharivora ns | -0.87 | 0.040 |
| Bacteria | Bacteroidetes | unknown | uncultured_Porphyrimonada ceae_bacterium | -0.86 | 0.047 |
| Bacteria | Firmicutes | Blautia | Blautia_obeum | -0.84 | 0.032 |
| Bacteria | Actinobacteria | Mycobacterium | Mycobacterium_tuberculosis | 1.46 | 0.043 |
| Bacteria | Firmicutes | Massilimaliae | Massilimaliae_timonensis | 1.59 | 0.030 |
| Bacteria | Firmicutes | Intestinimonas | Intestinimonas_massiliensis | 1.73 | 0.045 |
| Bacteria | Firmicutes | Dorea | uncultured_Dorea_sp | 1.77 | 0.034 |

| | | | | | |
|----------|----------------|-----------------------|-------------------------------------|------|--------|
| Bacteria | Proteobacteria | Escherichia | Escherichia_coli | 1.81 | 0.030 |
| Bacteria | Firmicutes | Mediterraneibacter | Mediterraneibacter_butyricigenes | 1.81 | 0.032 |
| Bacteria | Firmicutes | Blautia | Blautia_hydrogenotrophica | 1.81 | 0.032 |
| Bacteria | Firmicutes | Lachnoclostridium | Clostridium_glycyrrhizinilyticum | 1.84 | 0.022 |
| Bacteria | Firmicutes | Flavonifractor | uncultured_Flavonifractor_sp | 1.85 | 0.025 |
| Bacteria | Firmicutes | Tyzzzerella | Tyzzzerella_nexilis | 1.87 | 0.028 |
| Bacteria | Firmicutes | Holdemania | Holdemania_filiformis | 1.95 | 0.031 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_AM31_12AC | 1.95 | 0.032 |
| Bacteria | Firmicutes | unknown | Eubacterium_siraeum | 1.97 | 0.035 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_CAG103 | 2.05 | 0.031 |
| Bacteria | unknown | unknown | bacterium | 2.08 | 0.026 |
| Bacteria | Bacteroidetes | Barnesiella | Barnesiella_intestinihominis | 2.21 | 0.025 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_finegoldii | 2.23 | 0.026 |
| Bacteria | Actinobacteria | Collinsella | Collinsella_unknown_sp | 2.35 | 0.021 |
| Bacteria | Firmicutes | Anaerotignum | Anaerotignum_faecicola | 2.42 | 0.024 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_onderdonkii | 3.05 | <0.001 |
| Bacteria | Firmicutes | Neglecta | Neglecta_timonensis | 3.93 | <0.001 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_CAG83 | 4.09 | <0.001 |
| Bacteria | Firmicutes | Phascolarctobacterium | Phascolarctobacterium_succinatutens | 4.21 | <0.001 |
| Bacteria | Firmicutes | Lachnospiraea | Lachnospiraea_unknown_sp | 4.23 | <0.001 |
| Bacteria | Firmicutes | Coproccoccus | Coproccoccus_comes | 4.28 | <0.001 |
| Bacteria | Firmicutes | Phascolarctobacterium | Phascolarctobacterium_faecium | 4.72 | <0.001 |
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_torques_CAG61 | 5.13 | <0.001 |

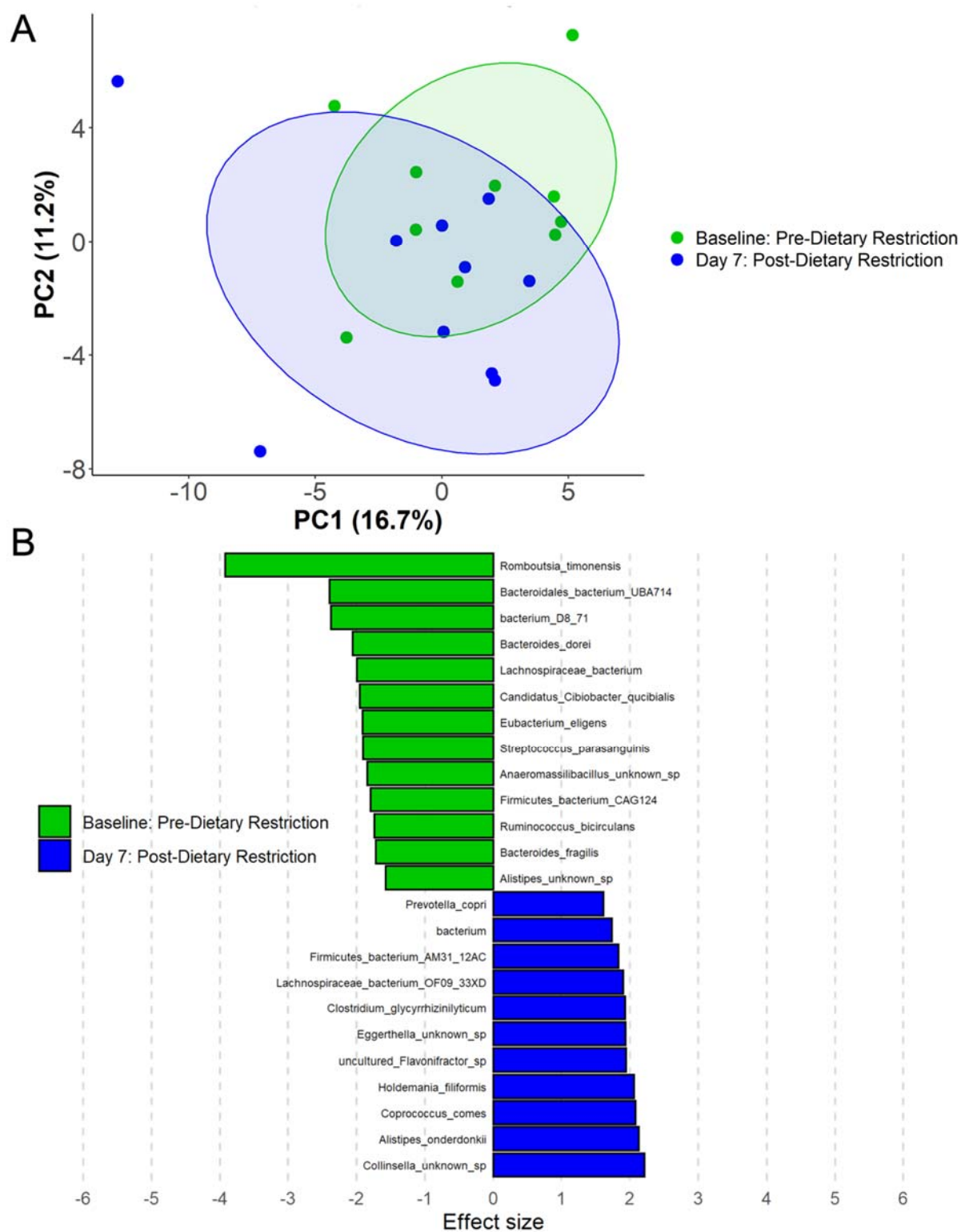


Supplemental Figure S4. Day-4 v. Day-7. Principal component analysis of species present between the two conditions (A). Effect size graph of significantly different species (FDR $p < 0.05$, effect size > 1) (B).

Supplemental Table S3. Significantly different species between Day-4 and Day-7 conditions (FDR $p < 0.05$).

| Kingdom | Phylum | Genus | Species | Effect Size | FDR p-value |
|----------|----------------|-----------------------|---|-------------|-------------|
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_torques_CAG6 1 | -5.13 | <0.001 |
| Bacteria | Firmicutes | Phascolarctobacterium | Phascolarctobacterium_faeci m | -4.29 | <0.001 |
| Bacteria | Firmicutes | Lachnотalea | Lachnотalea_unknown_sp | -4.20 | <0.001 |
| Bacteria | Firmicutes | Phascolarctobacterium | Phascolarctobacterium_succin atutens | -4.19 | <0.001 |
| Bacteria | Firmicutes | unknown | Lachnospiraceae_bacterium | -4.02 | <0.001 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_CAG83 | -3.77 | <0.001 |
| Bacteria | Firmicutes | Neglecta | Neglecta_timonensis | -3.74 | <0.001 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_CAG12 4 | -3.13 | <0.001 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_finegoldii | -2.36 | 0.032 |
| Bacteria | Bacteroidetes | Barnesiella | Barnesiella_intestinihominis | -2.32 | 0.024 |
| Bacteria | Firmicutes | Anaerotignum | Anaerotignum_faecicola | -2.24 | 0.029 |
| Bacteria | Firmicutes | Mediterraneibacter | Mediterraneibacter_butyrice nes | -2.04 | 0.038 |
| Bacteria | Firmicutes | unknown | Firmicutes_bacterium_CAG10 3 | -1.92 | 0.032 |
| Bacteria | Proteobacteria | Escherichia | Escherichia_coli | -1.88 | 0.029 |
| Bacteria | Firmicutes | unknown | Eubacterium_siraeum | -1.85 | 0.032 |
| Bacteria | Firmicutes | Anaeromassilibacillus | Anaeromassilibacillus_unkno wn_sp | -1.83 | 0.035 |
| Bacteria | Firmicutes | Tyzzereella | Tyzzereella_nexilis | -1.83 | 0.027 |
| Bacteria | Firmicutes | Blautia | Blautia_hydrogenotrophica | -1.73 | 0.042 |
| Bacteria | Firmicutes | Dorea | uncultured_Dorea_sp | -1.68 | 0.036 |
| Bacteria | Firmicutes | Streptococcus | Streptococcus_parasanguinis | -1.60 | 0.041 |
| Bacteria | Actinobacteria | Mycobacterium | Mycobacterium_tuberculosis | -1.58 | 0.032 |
| Bacteria | Firmicutes | Intestinimonas | Intestinimonas_massiliensis | -1.57 | 0.044 |
| Bacteria | Bacteroidetes | unknown | Bacteroidales_bacterium_UBA 714 | -1.54 | 0.047 |
| Bacteria | Firmicutes | Eubacterium | Eubacterium_eligens | -1.53 | 0.034 |
| Bacteria | Firmicutes | Romboutsia | Romboutsia_timonensis | -1.42 | 0.044 |
| Bacteria | Firmicutes | Massimalia | Massimalia_timonensis | -1.35 | 0.037 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_unknown_sp | -1.32 | 0.048 |
| Bacteria | Actinobacteria | Eggerthella | Eggerthella_lenta | 0.72 | 0.046 |
| Bacteria | Firmicutes | Blautia | Blautia_unknown_sp | 0.89 | 0.043 |
| Bacteria | Firmicutes | unknown | Clostridiales_bacterium_VE20 2_03 | 0.98 | 0.022 |
| Bacteria | unknown | unknown | bacterium_J10_2018 | 1.01 | 0.019 |
| Bacteria | Bacteroidetes | Parabacteroides | Parabacteroides_distasonis | 1.01 | 0.026 |
| Bacteria | Firmicutes | Fusicatenibacter | Fusicatenibacter_saccharivora ns | 1.03 | 0.020 |
| Bacteria | Firmicutes | Eubacterium | uncultured_Eubacterium_sp | 1.03 | 0.029 |
| Bacteria | Firmicutes | Coprococcus | Coprococcus_catus | 1.03 | 0.023 |
| Bacteria | Firmicutes | Clostridium | uncultured_Clostridium_sp | 1.04 | 0.017 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_thetaiotaomicron | 1.10 | 0.013 |
| Bacteria | Firmicutes | Anaerobutyricum | Anaerobutyricum_hallii | 1.12 | 0.020 |

| | | | | | |
|----------|----------------|------------------|--|------|--------|
| Bacteria | Firmicutes | Lachnobacterium | uncultured_Lachnobacterium_sp | 1.14 | 0.013 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_uniformis | 1.15 | 0.018 |
| Bacteria | Firmicutes | Dysosmobacter | Dysosmobacter_welbionis | 1.17 | 0.011 |
| Bacteria | Firmicutes | Blautia | Blautia_massiliensis | 1.19 | 0.015 |
| Bacteria | Bacteroidetes | Bacteroides | uncultured_Bacteroides_sp | 1.24 | 0.010 |
| Bacteria | Bacteroidetes | unknown | uncultured_Porphyromonada_ceae_bacterium | 1.26 | 0.011 |
| Bacteria | Firmicutes | Gemmiger | Gemmiger_formicilis | 1.26 | 0.009 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_vulgatus | 1.26 | 0.011 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_ovatus | 1.27 | 0.010 |
| Bacteria | Firmicutes | Blautia | uncultured_Blautia_sp | 1.32 | 0.009 |
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_unknown_sp | 1.35 | 0.008 |
| Bacteria | Firmicutes | Blautia | Blautia_obeum | 1.47 | 0.008 |
| Bacteria | Firmicutes | Dialister | uncultured_Dialister_sp | 1.47 | 0.005 |
| Bacteria | Firmicutes | Blautia | Blautia_wexlerae | 1.53 | 0.004 |
| Bacteria | Firmicutes | Anaerostipes | Anaerostipes_hadrus | 1.68 | 0.001 |
| Bacteria | Bacteroidetes | Prevotella | Prevotella_copri | 1.88 | 0.002 |
| Bacteria | Bacteroidetes | Parabacteroides | Parabacteroides_massiliensis | 2.00 | 0.002 |
| Bacteria | Firmicutes | unknown | uncultured_Lachnospiraceae_bacterium | 2.07 | <0.001 |
| Bacteria | Firmicutes | Faecalibacterium | Faecalibacterium_prausnitzii | 2.21 | 0.001 |
| Bacteria | Firmicutes | Butyricicoccus | Butyricicoccus_unknown_sp | 2.28 | 0.001 |
| Bacteria | Actinobacteria | Eggerthella | Eggerthella_unknown_sp | 2.36 | 0.001 |
| Bacteria | Firmicutes | unknown | Lachnospiraceae_bacterium_OF09_33XD | 2.50 | 0.002 |
| Bacteria | Firmicutes | Roseburia | Roseburia_unknown_sp | 3.71 | <0.001 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_stercoris | 3.72 | <0.001 |
| Bacteria | Firmicutes | Eubacterium | Eubacterium_unknown_sp | 4.70 | <0.001 |
| Bacteria | Firmicutes | Faecalibacterium | uncultured_Faecalibacterium_sp | 5.16 | <0.001 |



Supplemental Figure S5. Baseline v. Day-7. Principal component analysis of species present between the two conditions (A). Effect size graph of significantly different species (FDR $p < 0.05$, effect size > 1) (B).

Supplemental Table S4. Significantly different species between Baseline and Day-7 conditions (FDR $p < 0.05$).

| Kingdom | Phylum | Genus | Species | Effect Size | FDR p-value |
|----------|----------------|------------------------|--------------------------------|-------------|-------------|
| Bacteria | Firmicutes | Romboutsia | Romboutsia_timonensis | -3.92 | <0.001 |
| | | | Bacteroidales_bacterium_UBA | | |
| Bacteria | Bacteroidetes | unknown | 714 | -2.39 | 0.002 |
| Bacteria | unknown | unknown | bacterium_D8_71 | -2.38 | <0.001 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_dorei | -2.05 | 0.002 |
| Bacteria | Firmicutes | unknown | Lachnospiraceae_bacterium | -1.99 | 0.001 |
| | | | Candidatus_Cibiobacter_quci | | |
| Bacteria | Firmicutes | Candidatus Cibiobacter | bialis | -1.95 | 0.003 |
| Bacteria | Firmicutes | Eubacterium | Eubacterium_eligens | -1.91 | 0.004 |
| Bacteria | Firmicutes | Streptococcus | Streptococcus_parasanguinis | -1.91 | 0.005 |
| | | | Anaeromassilibacillus_unkno | | |
| Bacteria | Firmicutes | Anaeromassilibacillus | wn_sp | -1.85 | 0.004 |
| | | | Firmicutes_bacterium_CAG12 | | |
| Bacteria | Firmicutes | unknown | 4 | -1.79 | 0.005 |
| Bacteria | Firmicutes | Ruminococcus | Ruminococcus_bicirculans | -1.74 | 0.008 |
| Bacteria | Bacteroidetes | Bacteroides | Bacteroides_fragilis | -1.72 | 0.005 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_unknown_sp | -1.57 | 0.008 |
| Bacteria | Bacteroidetes | Prevotella | Prevotella_copri | 1.61 | 0.004 |
| Bacteria | unknown | unknown | bacterium | 1.73 | 0.004 |
| | | | Firmicutes_bacterium_AM31_ | | |
| Bacteria | Firmicutes | unknown | 12AC | 1.83 | 0.004 |
| | | | Lachnospiraceae_bacterium_ | | |
| Bacteria | Firmicutes | unknown | OF09_33XD | 1.90 | 0.001 |
| | | | Clostridium_glycyrrhizinilytic | | |
| Bacteria | Firmicutes | Lachnoclostridium | um | 1.93 | 0.002 |
| Bacteria | Actinobacteria | Eggerthella | Eggerthella_unknown_sp | 1.94 | 0.002 |
| Bacteria | Firmicutes | Flavonifractor | uncultured_Flavonifractor_sp | 1.94 | 0.001 |
| Bacteria | Firmicutes | Holdemania | Holdemania_filiformis | 2.06 | 0.002 |
| Bacteria | Firmicutes | Coprococcus | Coprococcus_comes | 2.08 | 0.002 |
| Bacteria | Bacteroidetes | Alistipes | Alistipes_onderdonkii | 2.13 | 0.002 |
| Bacteria | Actinobacteria | Collinsella | Collinsella_unknown_sp | 2.21 | 0.001 |