

*Supplementary Note: Noncompliant participants.*

Ninety-two percent (143 out of 155) of sequenced microbiome samples were from participants compliant with the prune treatment. Alpha and beta diversity, as well as differential taxa, were compared among all samples including noncompliant participants post-intervention (58 Control, 58 50g prune, 39 100g prune).

*Demographics.* For the 155 participants whose fecal microbiomes were sequenced, the average age was 62.3 years (range: 55-75) at baseline, and 98% (n=152) were Caucasian. Participants were mostly healthy or overweight (78 healthy, 52 overweight, 25 obese), with an average BMI of 25.6 kg/m<sup>2</sup> (range: 18.5-39.2).

*Alpha Diversity.* Post intervention, Pielou's Evenness was significant (p=0.049), and Shannon trended significant (p=0.077) between groups. The 50g prune group had slightly lower alpha diversity than the control and 100g prune groups (Pielou's Evenness, significant, q<0.098). These values represent slightly less significance than among compliant individuals only.

*Beta Diversity.* As in compliant individuals only, differences in the microbiomes of control, 50g prune, and 100g prune groups were observed in all four beta diversity metrics tested (Bray-Curtis, weighted Unifrac, significant, p<0.03; Jaccard, unweighted Unifrac, trend, p<0.07). PermDISP was not significant for any metric (p>0.31), so these differences are due to true differences in the means of groups. Bray-Curtis detected significant differences between control and the 50g prune group (p=0.036), as well as between control and the 100g prune group (p=0.048). The difference between 50g and 100g prunes was a trend (q=0.069). For weighted Unifrac, all three comparisons trended significant (q=0.076). Jaccard found trends comparing the 100g prune group to the other two groups (q=0.0975). On the whole, these results indicate slightly less significance than among compliant individuals only.

*Differential Taxa.* As before, no taxa were significant by ANCOM. However, LEfSe identified 52 taxa as differentially abundant at  $LDA > 2$ , slightly less than among compliant samples only (75). The same taxa were identified as highly differentially abundant (Lachnospiraceae,  $LDA = 4.5$ ; *Blautia*, 4.4; *Anaerostipes*, 4.2; Oscillospirales, 3.9).

*Phenolics.* Post-intervention, hippuric acid was the only metabolite to be differentially excreted in urine among the 155 participants (Kruskal-Wallis,  $p = 0.001$ ). Hippuric acid was significantly increased in the 50g and 100g prune groups compared to control ( $p < 0.01$ ). These results indicate less significance than among compliant individuals only.

Table S1. Phenolic composition of supplied prunes in year 1 and year 3 of the study. STD is the standard deviation. DW is the dry weight of the prunes.

| <b>Phenolic acids and flavonoids</b> |         |      |         |       |
|--------------------------------------|---------|------|---------|-------|
|                                      | Year 1  |      | Year 3  |       |
| mg/g DW                              | Average | STD  | Average | STD   |
| Ferulic acid                         | 1.44    | 0.05 | 2.42    | 0.04  |
| Caffeic acid                         | 8.08    | 0.96 | 9.27    | 0.24  |
| p coumaric acid                      | 5.4     | 0.05 | 8.77    | 0.48  |
| protocatechuic acid                  | 3.21    | 0.11 | 1.63    | 0.026 |
| quercetin                            | 0.01    | 0    | 0.05    | 0.01  |
| quercetin-3-glucoside                | 0.16    | 0.03 | 0.26    | 0.01  |

| <b>Chlorogenic acid derivatives</b> |         |      |         |      |
|-------------------------------------|---------|------|---------|------|
|                                     | Year 1  |      | Year 3  |      |
| mg/g DW                             | Average | STD  | Average | STD  |
| 3-Caffeoylquinic acid               | 59.9    | 3.7  | 64.2    | 5.1  |
| 5-Caffeoylquinic acid               | 4.81    | 1.2  | 5.03    | 0.53 |
| 4-Caffeoylquinic acid               | 68.3    | 16.5 | 66.4    | 3.3  |
| 3-Feruleoylquinic acid              | 5.1     | 0.32 | 5.31    | 0.08 |
| 4-Feruleoylquinic acid              | 3.88    | 1    | 4.48    | 0.49 |
| 5-Feruleoylquinic acid              | 3.53    | 0.48 | 3.35    | 0.23 |

Table S2. Differential taxa among compliant participants post-intervention by prune treatment. Taxa presented are LDA>2. ‘Group’ represents the treatment group in which specific taxa was most abundant for that comparison.

| id                                                                                                                                | LEFSe: Overall |      |          | LEFSe: Control vs. 50g |      | LEFSe: Control vs. 100g |      | LEFSe: 50g Prune vs. 100g |      |
|-----------------------------------------------------------------------------------------------------------------------------------|----------------|------|----------|------------------------|------|-------------------------|------|---------------------------|------|
|                                                                                                                                   | Group          | LDA  | p        | Group                  | LDA  | Group                   | LDA  | Group                     | LDA  |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales                                                                            | Control        | 4.31 | 1.21E-02 | Control                | 4.34 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae                                                         | Control        | 3.99 | 1.16E-03 | Control                | 3.98 |                         |      | 100g Prune                | 3.77 |
| d_Bacteria.p_Firmicutes.c_Bacilli                                                                                                 | Control        | 3.94 | 1.28E-03 |                        |      | Control                 | 3.96 | 50g Prune                 | 3.88 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Peptostreptococcales_Tissierellales                                                        | Control        | 3.86 | 1.13E-02 | Control                | 3.88 |                         |      | 100g Prune                | 3.24 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Peptostreptococcaceae                                | Control        | 3.83 | 2.10E-02 | Control                | 3.85 |                         |      | 100g Prune                | 3.17 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_UCG-002                                               | Control        | 3.67 | 2.00E-02 | Control                | 3.65 |                         |      | 100g Prune                | 3.58 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Christensenellales                                                                         | Control        | 3.64 | 4.31E-02 |                        |      |                         |      | 100g Prune                | 3.18 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Christensenellales.f_Christensenellaceae                                                   | Control        | 3.64 | 4.31E-02 |                        |      |                         |      | 100g Prune                | 3.18 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_UCG-002;_                                             | Control        | 3.60 | 2.61E-02 | Control                | 3.58 |                         |      | 100g Prune                | 3.41 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Peptostreptococcaceae.g_Romboutsia                   | Control        | 3.56 | 4.90E-02 | Control                | 3.56 |                         |      | 100g Prune                | 2.99 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Peptostreptococcaceae.g_Romboutsia;_                 | Control        | 3.56 | 4.90E-02 | Control                | 3.56 |                         |      | 100g Prune                | 2.99 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales                                                                              | Control        | 3.55 | 1.07E-02 | Control                | 3.54 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae                                                             | Control        | 3.55 | 1.07E-02 | Control                | 3.54 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae.g_Clostridium_sensu_stricto_1                               | Control        | 3.55 | 1.07E-02 | Control                | 3.54 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae.g_Clostridium_sensu_stricto_1;_                             | Control        | 3.49 | 5.89E-03 | Control                | 3.46 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Incertae_Sedis;_                                       | Control        | 3.39 | 2.25E-02 |                        |      | Control                 | 3.38 | 50g Prune                 | 2.92 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_NK4A214_group                                         | Control        | 3.26 | 9.81E-03 | Control                | 3.21 |                         |      | 100g Prune                | 2.92 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Erysipelotrichales                                                                            | Control        | 3.25 | 1.52E-03 | Control                | 3.24 | Control                 | 3.19 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_UCG-005                                               | Control        | 3.23 | 9.55E-03 | Control                | 3.24 |                         |      | 100g Prune                | 2.91 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Erysipelotrichales.f_Erysipelotrichaceae                                                      | Control        | 3.23 | 1.18E-02 | Control                | 3.23 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Turicibacter                                       | Control        | 3.23 | 2.08E-02 | Control                | 3.22 | Control                 | 3.16 |                           |      |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Turicibacter;_                                     | Control        | 3.23 | 2.08E-02 | Control                | 3.22 | Control                 | 3.16 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_uncultured                                            | Control        | 3.03 | 4.87E-03 | Control                | 3.02 | Control                 | 3.00 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_[Ruminococcus]_torques_group;s_Ruminococcus_torques     | Control        | 2.90 | 1.57E-02 | Control                | 3.02 | Control                 | 2.79 |                           |      |
| d_Bacteria.p_Verrucomicrobiota.c_Verrucomicrobiae.o_Verrucomicrobiales                                                            | Control        | 2.80 | 3.20E-02 | Control                | 2.54 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Monoglobales.f_Monoglobaceae.g_Monoglobus;_                                                | Control        | 2.79 | 2.74E-02 |                        |      | Control                 | 2.69 |                           |      |
| d_Bacteria.p_Verrucomicrobiota.c_Verrucomicrobiae                                                                                 | Control        | 2.76 | 3.20E-02 | Control                | 2.75 |                         |      |                           |      |
| d_Bacteria.p_Verrucomicrobiota                                                                                                    | Control        | 2.73 | 3.20E-02 | Control                | 2.69 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Eisenbergiella                                          | Control        | 2.68 | 1.42E-02 | Control                | 2.54 | Control                 | 2.39 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Eisenbergiella;s_uncultured_organism                    | Control        | 2.66 | 8.33E-03 | Control                | 2.53 | Control                 | 2.41 |                           |      |
| d_Bacteria.p_Verrucomicrobiota.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Akkermansia                                              | Control        | 2.59 | 3.20E-02 | Control                | 2.73 |                         |      |                           |      |
| d_Bacteria.p_Verrucomicrobiota.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Akkermansia                                              | Control        | 2.58 | 3.20E-02 | Control                | 2.63 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_UCG-005;s_gut_metagenome                              | Control        | 2.53 | 4.46E-02 | Control                | 2.60 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_uncultured                                                               | Control        | 2.51 | 2.07E-02 | Control                | 2.74 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_uncultured                                                               | Control        | 2.50 | 2.07E-02 | Control                | 2.72 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Incertae_Sedis;s_uncultured_bacterium                  | Control        | 2.40 | 3.63E-02 |                        |      | Control                 | 2.35 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_UBA1819                                                | Control        | 2.34 | 2.86E-02 | Control                | 2.33 | Control                 | 2.37 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_UBA1819;s_uncultured_organism                          | Control        | 2.34 | 2.86E-02 | Control                | 2.33 | Control                 | 2.37 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillospiraceae.g_NK4A214_group;s_uncultured_rumen                      | Control        | 2.32 | 3.19E-02 | Control                | 2.29 |                         |      | 100g Prune                | 2.17 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae                                                           | 50g Prune      | 4.57 | 5.71E-03 | 50g Prune              | 4.58 |                         |      | 50g Prune                 | 4.46 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales                                                                             | 50g Prune      | 4.57 | 5.52E-03 | 50g Prune              | 4.58 |                         |      | 50g Prune                 | 4.46 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Blautia                                                 | 50g Prune      | 4.38 | 7.49E-03 | 50g Prune              | 4.33 |                         |      | 50g Prune                 | 4.37 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Blautia;_                                               | 50g Prune      | 4.36 | 7.82E-03 | 50g Prune              | 4.34 |                         |      | 50g Prune                 | 4.36 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales                                                                               | 50g Prune      | 3.93 | 2.77E-03 |                        |      | Control                 | 3.86 | 50g Prune                 | 3.90 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus                                            | 50g Prune      | 3.91 | 2.36E-03 |                        |      | Control                 | 3.85 | 50g Prune                 | 3.88 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus;_                                          | 50g Prune      | 3.91 | 2.45E-03 |                        |      | Control                 | 3.85 | 50g Prune                 | 3.88 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae                                                            | 50g Prune      | 3.91 | 4.16E-03 |                        |      | Control                 | 3.85 | 50g Prune                 | 3.88 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_[Eubacterium]_hallii_group                              | 50g Prune      | 3.68 | 4.34E-02 | 50g Prune              | 3.66 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_[Eubacterium]_hallii_group;_                            | 50g Prune      | 3.68 | 4.34E-02 | 50g Prune              | 3.66 |                         |      |                           |      |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.g_Granulicatella;_                                        | 50g Prune      | 3.00 | 2.25E-02 |                        |      |                         |      | 50g Prune                 | 2.49 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Faecalibacterium;s_metagenome                          | 50g Prune      | 2.90 | 8.73E-03 | 50g Prune              | 2.83 | 100g Prune              | 2.68 |                           |      |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae                                                           | 50g Prune      | 2.87 | 2.25E-02 |                        |      |                         |      | 50g Prune                 | 2.49 |
| d_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carnobacteriaceae.g_Granulicatella                                          | 50g Prune      | 2.76 | 2.25E-02 |                        |      |                         |      | 50g Prune                 | 2.60 |
| d_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales                                                                    | 50g Prune      | 2.68 | 4.09E-02 |                        |      | Control                 | 3.10 | 50g Prune                 | 2.17 |
| d_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Actinomycetaceae.g_Actinomycetes                                 | 50g Prune      | 2.67 | 4.09E-02 |                        |      | Control                 | 3.12 | 50g Prune                 | 2.30 |
| d_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Actinomycetaceae                                                 | 50g Prune      | 2.48 | 4.09E-02 |                        |      | Control                 | 3.19 | 50g Prune                 | 2.33 |
| d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Burkholderiales.f_Sutterellaceae.g_Parauterella;s_uncultured_organism         | 50g Prune      | 2.39 | 3.66E-02 | 50g Prune              | 2.31 | 100g Prune              | 2.32 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Lachnospiraceae.g_[Clostridium]_glycyrhizini;_          | 50g Prune      | 2.11 | 1.75E-02 |                        |      |                         |      | 50g Prune                 | 2.26 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Anaerostipes                                            | 100g Prune     | 4.27 | 1.04E-04 | 50g Prune              | 4.10 | 100g Prune              | 4.30 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Anaerostipes;_                                          | 100g Prune     | 4.27 | 1.15E-04 | 50g Prune              | 4.10 | 100g Prune              | 4.30 |                           |      |
| d_Bacteria.p_Actinobacteria.c_Coribacteriales.f_Eggerthellaceae                                                                   | 100g Prune     | 3.66 | 3.82E-03 | 50g Prune              | 3.33 | 100g Prune              | 3.64 |                           |      |
| d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales                                                             | 100g Prune     | 3.58 | 3.30E-02 | 50g Prune              | 3.16 | 100g Prune              | 3.47 |                           |      |
| d_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae                                        | 100g Prune     | 3.58 | 3.30E-02 | 50g Prune              | 3.16 | 100g Prune              | 3.47 |                           |      |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Tannerellaceae.g_Parabacteroides_merdae                                 | 100g Prune     | 3.48 | 5.80E-03 |                        |      |                         |      | 100g Prune                | 3.43 |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Tannerellaceae.g_Parabacteroides                                        | 100g Prune     | 3.46 | 9.42E-03 | Control                | 3.25 |                         |      | 100g Prune                | 3.41 |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Tannerellaceae.g_Parabacteroides                                        | 100g Prune     | 3.46 | 9.42E-03 | Control                | 3.25 |                         |      | 100g Prune                | 3.41 |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides;s_Bacteroides_ovatus                       | 100g Prune     | 3.22 | 2.64E-03 |                        |      | 100g Prune              | 3.31 | 100g Prune                | 2.91 |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Alistipes;s_Alistipes_shahii                            | 100g Prune     | 3.05 | 1.74E-02 |                        |      | 100g Prune              | 2.92 | 100g Prune                | 3.12 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Coproccoccus;_unidentified                              | 100g Prune     | 2.98 | 3.02E-02 | Control                | 2.78 |                         |      | 100g Prune                | 2.90 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Lachnospira;s_uncultured_bacterium                      | 100g Prune     | 2.87 | 1.08E-02 |                        |      | 100g Prune              | 2.84 |                           |      |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Moryella                                                | 100g Prune     | 2.56 | 2.07E-02 |                        |      |                         |      | 100g Prune                | 2.19 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Moryella;s_human_gut                                    | 100g Prune     | 2.53 | 2.07E-02 |                        |      |                         |      | 100g Prune                | 2.12 |
| d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Barnesiellaceae.g_Coprobacter                                           | 100g Prune     | 2.44 | 1.02E-02 |                        |      | 100g Prune              | 2.43 | 100g Prune                | 2.42 |
| d_Bacteria.p_Desulfobacterota.c_Desulfovibrionia.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Desulfovibrio;s_Desulfovibrio_piger | 100g Prune     | 2.37 | 1.25E-02 |                        |      |                         |      | 100g Prune                | 2.47 |
| d_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Ruminococcus;s_gut_metagenome                          | 100g Prune     | 2.24 | 1.20E-02 |                        |      |                         |      | 100g Prune                | 2.37 |

Figure S1. CONSORT flow diagram for this study. The number of subjects that participated at each step are depicted. Reasons for dropout or exclusion from analysis are summarized.

Figure S2. Alpha Rarefaction. Each curve represents one sample. This plot diagrams the number of species retained as a function of sequencing depth. Choosing a depth where most samples have plateaued will maximize the number of features retained and ensure diversity metrics reflect the actual diversity. A sequencing depth of 11,940 reads was chosen, which maximizes retained features minimizing excluded samples.

Figure S3. Significant correlations between log counts of taxa and phenolics using data both pre- and post-intervention. Data are for compliant and noncompliant subjects who had detectable metabolite. (A) 3-Hydroxyhippuric acid vs. *Oscillospiraceae* UCG-005 (Bonferroni-corrected  $p=0.02$ , Spearman's  $r=-0.33$ ), (B) 3-hydroxyhippuric acid vs. *Hydrogenoanaerobacterium* ( $p=0.08$ ,  $r=-0.31$ ), (C) Total urinary phenolics vs. *Blautia* metagenome ( $p=0.03$ ,  $r=-0.24$ ), (D) Total urinary phenolics vs. uncultured *Lachnospiraceae* ( $p=0.05$ ,  $r=0.24$ ). Blue lines are a linear model and a shaded 95% confidence interval. Note that for plots (A) and (B), an outlier with 800  $\mu\text{M}$  3-hydroxyhippuric acid and 0 counts of both taxa was removed from the figure to improve readability.

Figure S4. Correlation between *Lachnospiraceae* UCG-001 and (A) plasma IL-1B (Bonferroni-corrected  $p=0.002$ , Spearman's  $r=-0.29$ ) or (B) plasma IL-6 (Bonferroni-corrected  $p=0.09$ , Spearman's  $r=-0.25$ ). The blue line is a linear model and shaded indicates 95% confidence interval.  $n=308$ .