

Table S2. The effects of prenatal MD supplemented diet on colonic mucosa and feces associated bacterial taxa.

MD-C Mucosa-Feces	Mucosa	Feces	
Phyla	%	%	Paired T test
Bacteroidetes	8.80	33.91	0.000012
Tenericutes	29.84	1.17	0.0026
Cyanobacteria	0.02	0	0.0216
Genera	%	%	Paired T test
<i>Pseudobutyrvibrio</i>	0.07	0.12	0.0001
<i>Parabacteroides</i>	7.88	27.97	0.0039
<i>Butyrvibrio</i>	0.15	0.49	0.0041
<i>Psb</i>	0.07	0.22	0.0112
<i>Lachnospira</i>	0.01	0.18	0.0126
<i>Brevibacillus</i>	13.64	0.29	0.0179
<i>Allobaculum</i>	17.78	0.34	0.018
<i>Caloramator</i>	0.03	0.15	0.0192
<i>Granulicatella</i>	9.80	0.15	0.0202
<i>Anaerostipes</i>	1.48	3.25	0.0218
<i>P</i>	1.57	0.06	0.0222
<i>Prevotella</i>	0.78	5.52	0.0223
<i>Blautia</i>	3.92	21.61	0.0225
<i>Dorea</i>	0.06	0.01	0.0231
<i>Enterococcus</i>	0.07	0	0.0252
<i>Pontibacter</i>	0.06	0.19	0.0269
<i>Alkaliphilus</i>	0.03	0.28	0.0287
<i>Tannerella</i>	0.03	0.19	0.0293
<i>Roseburia</i>	2.02	4.43	0.0318
<i>Clostridium</i>	13.92	6.01	0.0329
<i>Oscillospira</i>	1.24	3.95	0.0342
<i>Shimazuella</i>	0.03	0.01	0.0457
Species	%	%	Paired T test
<i>Pseudobutyrvibrio ruminis</i>	0.07	0.12	0.0001
<i>Parabacteroides distasonis</i>	7.88	27.97	0.0039
<i>Clostridium orbiscindens</i>	0.26	0.72	0.0046
<i>Butyrvibrio hungatei</i>	0.05	0.35	0.0061
<i>Clostridium methylpentosum</i>	0.06	0.22	0.01
<i>Psb</i>	0.07	0.22	0.0112
<i>Blautia ruminococcus obeum</i>	0.13	0.32	0.0122
<i>Lachnospira pectinoschiza</i>	0.01	0.18	0.0126
<i>Brevibacillus laterosporus</i>	13.64	0.29	0.0179
<i>Allobaculum stercoricanis</i>	17.70	0.33	0.018
<i>Clostridium cocleatum</i>	10.37	0.40	0.0188
<i>Caloramator (species unknown)</i>	0.03	0.15	0.0192
<i>Granulicatella adiacens</i>	9.75	0.15	0.0202
<i>Clostridium perfringens</i>	0.28	0.01	0.0208
<i>Anaerostipes caccae</i>	1.48	3.25	0.0218
<i>P</i>	1.57	0.06	0.0222

Species continued	%	%	Paired T test
<i>Dorea formicigenerans</i>	0.06	0.01	0.0231
<i>Blautia producta</i>	3.79	21.28	0.0238
<i>Clostridium celerecrescens</i>	0.43	1.06	0.0251
<i>Enterococcus faecalis</i>	0.07	0	0.0252
<i>Prevotella copri</i>	0.20	1.03	0.0264
<i>Prevotella multiformis</i>	0.11	0.30	0.0264
<i>Pontibacter korlensis</i>	0.06	0.19	0.0269
<i>Granulicatella elegans</i>	0.04	0.00	0.0275
<i>Tannerella forsythia</i>	0.03	0.19	0.0293
<i>Alkaliphilus transvaalensis</i>	0.02	0.28	0.0302
<i>Prevotella falsenii</i>	0.26	1.86	0.0307
<i>Oscillospira guilliermondii</i>	1.24	3.95	0.0342
<i>Roseburia eubacterium rectale</i>	0.60	1.41	0.0351
<i>Allobaculum sp id4</i>	0.08	0.02	0.0386
<i>Roseburia faecis</i>	1.43	3.02	0.0387
<i>Shimazuella (species unknown)</i>	0.03	0.01	0.0457
<i>Prevotella intermedia</i>	0.11	1.12	0.0486

Significant bacterial abundance differences at the phyla, genera, and species level between the mucosal and fecal samples of the MD-C Group (MD-C: MD *in utero* and control diet in lactation). Paired T test comparisons between the two groups (see Materials and Methods). A total of 22 genera and 33 species were significantly different between mucosa and feces in the prenatally MD supplemented group.