

Supplementary Table I. Significant quantitative differences in microbial taxa abundance analyzed by partial 16S rRNA gene sequencing of fecal bacteria (94% sequence similarity) in cesarean and vaginal delivered NOD mice at weaning.

Phylum	Class	Order	Family	Genus	P value* (per 1000 OTU tables)	Bonferroni_ corrected P value [†] for 161 OTUs	FDR corrected P value [‡] for 161 OTUs	mean (%) Vaginal	mean (%) C-section
Bacteroidetes	Bacteroidia	Bacteroidales	-	-	0.003	0.402	0.134	0.010	0.219
Bacteroidetes	Bacteroidia	Bacteroidales	-	-	0.011	1.417	0.129	0.012	0.084
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	0.010	1.259	0.126	0.009	0.099
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	0.003	0.315	0.315	1.221	6.766
Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	-	0.008	0.991	0.124	2.049	0.458
Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	-	0.014	1.765	0.136	0.313	0.844
Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	-	0.032	4.010	0.201	0.202	0.025
Firmicutes	Clostridia	-	-	-	0.018	2.245	0.140	0.364	0.099
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	-	0.004	0.472	0.094	1.071	0.256
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.003	0.417	0.104	0.000	0.131
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.004	0.511	0.085	0.323	3.721
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.006	0.772	0.110	0.012	0.318
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.009	1.165	0.129	0.002	0.268
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.013	1.694	0.141	0.118	0.484
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.016	2.025	0.135	0.005	0.593
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.019	2.409	0.142	0.001	0.426
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.021	2.619	0.146	0.045	0.314
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.015	1.832	0.131	0.007	0.647
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.003	0.328	0.164	2.554	0.631
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	0.045	5.607	0.267	0.371	0.089

*ANOVA analysis verifies whether the relative abundance of given OTU (94% sequence similarity) is different between C-section and vaginal delivered NOD mice. *P*-value was calculated based on 1000 subsampled OTU tables rarefied to the identical number of reads (2000 per sample). [†]*P* value after correction for multiple tests with Bonferroni correction. [‡]*P* value after correction with False Discovery Rate (FDR).

Supplementary Table II. Significant qualitative differences in microbial taxa analyzed by partial 16S rRNA gene sequencing of fecal bacteria in cesarean and vaginal delivered NOD mice at weaning.

OTU (97%)

Phylum	Class	Order	Family	Genus	g_P value* per 1000 OTU tables	Bonferroni corrected P value** for 158 OTUs	FDR corrected P value*** for 158 OTUs	OTU pos. C-section†	OTU pos. Vaginal†	OTU neg. C-section‡	OTU neg. Vaginal‡
Bacteroidetes	Bacteroidia	Bacteroidales	-		0.042	6.659	0.666	[9, 5.5]	[2, 5.5]	[3, 6.5]	[10, 6.5]
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	0.003	0.447	0.224	[8, 4.0]	[0, 4.0]	[4, 8.0]	[12, 8.0]
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	0.005	0.834	0.139	[7, 3.5]	[0, 3.5]	[5, 8.5]	[12, 8.5]
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	0.043	6.698	0.609	[9, 5.0]	[1, 5.0]	[3, 7.0]	[11, 7.0]
Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	-	0.045	7.049	0.587	[4, 7.5]	[11, 7.5]	[8, 4.5]	[1, 4.5]
Firmicutes	Clostridia	Clostridiales	-	-	0.000	0.029	0.029	[0, 5.5]	[11, 5.5]	[12, 6.5]	[1, 6.5]
Firmicutes	Clostridia	Clostridiales	-	-	0.005	0.802	0.160	[0, 3.5]	[7, 3.5]	[12, 8.5]	[5, 8.5]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.004	0.690	0.173	[7, 3.5]	[0, 3.5]	[5, 8.5]	[12, 8.5]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.003	0.495	0.165	[8, 4.0]	[0, 4.0]	[4, 8.0]	[12, 8.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.018	2.903	0.415	[6, 3.0]	[0, 3.0]	[6, 9.0]	[12, 9.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.038	5.937	0.660	[3, 7.0]	[11, 7.0]	[9, 5.0]	[1, 5.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.019	2.952	0.369	[10, 5.0]	[0, 5.0]	[2, 7.0]	[12, 7.0]

OTU (94%)

Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	-	0.043	5.144	0.643	[5, 8.0]	[11, 8.0]	[7, 4.0]	[1, 4.0]
Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	-	0.016	1.890	0.315	[10, 6.0]	[2, 6.0]	[2, 6.0]	[10, 6.0]
Firmicutes	Clostridia	Clostridiales	-	-	0.000	0.020	0.020	[0, 5.5]	[11, 5.5]	[12, 6.5]	[1, 6.5]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.002	0.263	0.131	[8, 4.0]	[0, 4.0]	[4, 8.0]	[12, 8.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.003	0.325	0.108	[8, 4.0]	[0, 4.0]	[4, 8.0]	[12, 8.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.008	1.008	0.252	[8, 4.0]	[0, 4.0]	[4, 8.0]	[12, 8.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.012	1.471	0.294	[9, 5.0]	[1, 5.0]	[3, 7.0]	[11, 7.0]
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	-	0.028	3.370	0.481	[11, 6.0]	[1, 6.0]	[1, 6.0]	[11, 6.0]
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.047	5.684	0.632	[8, 5.0]	[2, 5.0]	[4, 7.0]	[10, 7.0]

*G test of independence (g_test) based on 1000 subsampled OTU tables rarefied to the identical number of reads (2000 per sample) concludes whether species presence/absence is associated with delivery mode. **P value after correction for multiple tests with Bonferroni correction. ***P value after correction with False Discovery Rate (FDR). †represents a number of OTUs observed within a given group and a number of OTUs expected to be observed if the OTU was distributed randomly across samples from this group. ‡ represents a number of OTUs missing within a given group and a number of OTUs expected to be missed if the OTU was distributed randomly across samples from this group.