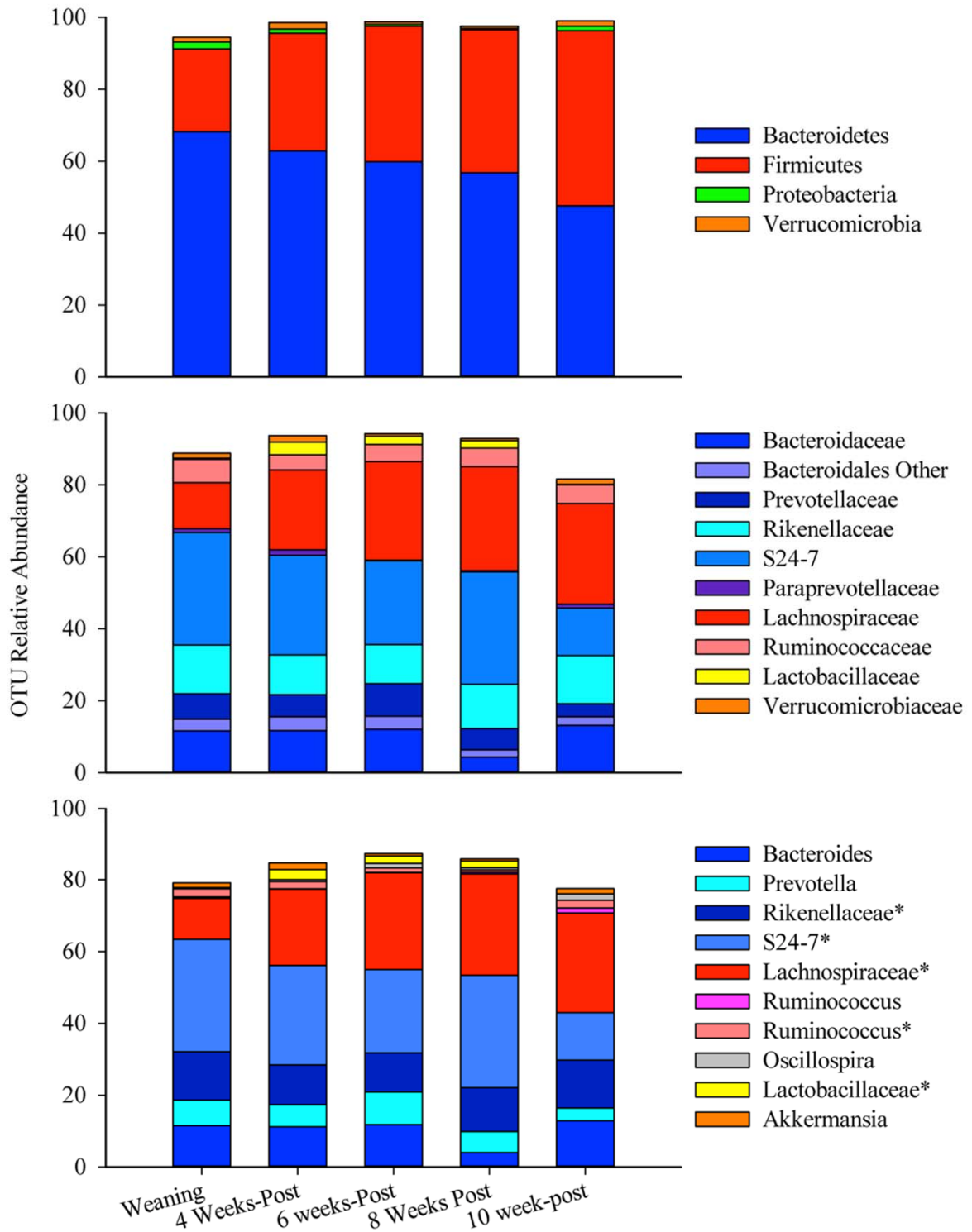


Supplementary Figure 1: Alpha diversity rarefaction plots sorted by sample period. A) Chao1, B) PD whole tree and C) Observed OTUs. Each line represents the alpha diversity at a sample period across the active season. Each point in the curve represents the mean value  $\pm$  the standard error. Symbols are: weaning (red), 4-weeks post (blue), 6-weeks post (green), 8-weeks post (yellow) and 10-weeks post (teal). Letters indicate a statistical difference among litters. Rarefaction plots were produced in QIIME 1.6.0

Supplemental  
Figure 2



Supplemental Figure 2: Relative abundance of the dominant taxa. Bar stacks are the mean abundance of a particular bacterial assignment at a given sample point. Values coincide with the number values listed in Supplementary Table 1. Taxa with abundances less than 1% were not included. \* represented unclassified families or genera.

Supplementary Table 1: The relative abundances of the dominant taxa.

Level	Taxonomy	Weaning (n=5)	4-Weeks Post (n=5)	6-Weeks Post (n=5)	8-Weeks Post (n=4)	10-Weeks Post (n=4)
	<i>Bacteroidetes</i>	68.21 ± 3.70	62.88 ± 10.30	59.88 ± 8.80	56.79 ± 13.70	47.59 ± 4.90
	<i>Firmicutes</i>	23.02 ± 5.09	32.74 ± 10.60	37.68 ± 9.20	39.78 ± 14.80	48.59 ± 5.40
	<i>Verrucomicrobia</i>	1.34 ± 0.57	1.84 ± 0.81	0.69 ± 0.37	0.61 ± 0.07	1.46 ± 0.97
	<i>Proteobacteria</i>	1.89 ± 0.57	1.12 ± 0.32	0.51 ± 0.30	0.38 ± 0.22	1.25 ± 0.09
Class	<i>Bacteroidia</i>	68.15 ± 3.70	62.84 ± 10.60	59.81 ± 8.40	56.74 ± 13.70	47.52 ± 5.00
	<i>Clostridia</i>	22.47 ± 3.60	29.09 ± 10.50	35.02 ± 8.80	37.48 ± 14.20	39.68 ± 8.00
	<i>Bacilli</i>	0.48 ± 0.29	3.57 ± 1.70	2.55 ± 0.57	2.23 ± 1.10	0.01 ± 0.01
	<i>Verrucomicrobiae</i>	1.34 ± 0.57	1.84 ± 0.81	0.69 ± 0.37	0.61 ± 0.07	1.46 ± 0.97
	<i>Alphaproteobacteria</i>	1.12 ± 0.53	0.83 ± 0.27	0.37 ± 0.08	0.14 ± 0.05	0.70 ± 0.28
Order	<i>Bacteroidales</i>	68.15 ± 3.70	62.84 ± 10.60	59.81 ± 8.40	56.74 ± 13.70	47.52 ± 5.00
	<i>Clostridia</i> <sup>§</sup>	1.72 ± 0.82	1.68 ± 0.56	1.81 ± 0.59	2.28 ± 1.20	5.25 ± 2.30
	<i>Clostridiales</i>	20.46 ± 5.09	27.14 ± 10.3	33.06 ± 9.10	34.93 ± 14.60	33.96 ± 6.50
	<i>Lactobacillales</i>	0.48 ± 0.29	3.57 ± 1.70	2.55 ± 0.57	2.23 ± 1.10	0.01 ± 0.01
	<i>Verrucomicrobiales</i>	1.34 ± 0.57	1.84 ± 0.81	0.69 ± 0.37	0.61 ± 0.07	1.46 ± 0.97
Family	<i>Bacteroidales</i> <sup>#</sup>	3.23 ± 0.78	3.87 ± 1.53	3.58 ± 0.81	2.03 ± 0.60	2.38 ± 0.29
	<i>Bacteroidaceae</i>	11.62 ± 3.30	11.67 ± 3.50	12.07 ± 6.50	4.32 ± 1.20	13.17 ± 3.80
	<i>Rikenellaceae</i>	13.58 ± 2.40	11.08 ± 1.80	10.92 ± 1.90	12.27 ± 4.10	13.40 ± 1.10
	<i>S24-7</i>	31.27 ± 5.50	27.68 ± 8.40	23.23 ± 6.90	31.31 ± 11.60	13.18 ± 4.60
	<i>Prevotellaceae</i>	7.08 ± 2.00	6.14 ± 2.30	9.07 ± 0.76	5.91 ± 2.20	3.59 ± 0.95
	<i>Lachnospiraceae</i>	12.77 ± 2.70	22.25 ± 9.10	27.43 ± 7.90	28.92 ± 13.10	28.01 ± 6.3
	<i>Ruminococcaceae</i>	6.51 ± 2.60	4.12 ± 1.20	4.67 ± 1.20	5.14 ± 1.40	5.14 ± 0.73

	<i>Lactobacillaceae</i>	0.32 ± 0.20	3.53 ± 0.00	2.37 ± 0.65	2.07 ± 0.97	0.18 ± 0.14
	<i>Verrucomicrobiaceae</i>	1.34 ± 0.57	1.84 ± 0.81	0.69 ± 0.37	0.61 ± 0.07	1.46 ± 0.97
Genus	<i>Bacteroides</i>	11.56 ± 3.30	11.23 ± 3.40	11.81 ± 6.40	3.98 ± 1.10	12.84 ± 3.90
	<i>Prevotella</i>	7.06 ± 2.00	6.13 ± 2.30	9.04 ± 0.80	5.90 ± 2.20	3.58 ± 1.10
	<i>S24-7*</i>	31.27 ± 5.50	27.68 ± 8.50	23.23 ± 6.90	31.31 ± 11.60	13.18 ± 0.94
	<i>Rikenellaceae*</i>	13.45 ± 2.40	11.04 ± 2.05	8.39 ± 1.40	6.21 ± 1.50	13.19 ± 4.50
	<i>Lactobacillaceae*</i>	0.31 ± 0.19	2.85 ± 1.50	2.04 ± 0.60	1.83 ± 0.90	0.01 ± 1.10
	<i>Lachnospiraceae*</i>	11.40 ± 2.10	21.30 ± 8.30	26.9 ± 7.70	28.2 ± 12.10	27.75 ± 6.90
	<i>Ruminococcus</i>	0.41 ± 0.10	0.07 ± 0.22	0.10 ± 0.05	0.05 ± 0.02	1.43 ± 0.23
	<i>Ruminococcaceae*</i>	2.3 ± 0.60	1.97 ± 0.23	1.22 ± 0.45	0.64 ± 0.22	2.13 ± 0.37
	<i>Oscillospira</i>	0.09 ± 0.05	0.5 ± 0.19	1.28 ± 0.50	0.60 ± 0.26	1.71 ± 0.38
	<i>Akkermansia</i>	1.34 ± 0.57	1.84 ± 0.81	0.69 ± 0.37	0.61 ± 0.07	1.46 ± 0.97

Values are the mean +/- the standard error. The values of this table coincide with Supplementary Figure 1.

\$ Represents unclassified orders

# Represents unclassified families

\* Represents unclassified genera.

Supplementary Table 2: The relative abundances of dominant taxa among litters.

	Taxonomy	11-05 (n=5)	11-12 (n=5)	11-19 (n=5)	11-13 (n=4)	11-21 (n=4)
Phylum	<i>Bacteroidetes</i>	35.27 ± 7.43	52.80 ± 6.58	66.82 ± 3.91	65.56 ± 7.33	74.21 ± 6.78
	<i>Firmicutes</i>	61.28 ± 7.51	44.20 ± 6.99	29.89 ± 5.02	26.75 ± 8.79	19.69 ± 6.76
	<i>Proteobacteria</i>	1.85 ± 0.89	0.85 ± 0.35	0.77 ± 0.01	1.25 ± 0.29	1.78 ± 0.97
	<i>Verrucomicrobia</i>	0.21 ± 0.57	0.87 ± 0.30	1.02 ± 0.82	0.75 ± 0.28	2.98 ± 1.36
Class	<i>Bacteroidia</i>	35.21 ± 7.42	52.71 ± 6.61	66.75 ± 3.18	65.48 ± 8.18	74.18 ± 6.79
	<i>Clostridia</i>	57.69 ± 6.73	43.54 ± 6.85	28.99 ± 2.88	15.14 ± 3.04	17.51 ± 7.27
	<i>Bacilli</i>	3.48 ± 0.29	0.59 ± 0.21	0.81 ± 0.45	3.79 ± 2.05	2.05 ± 1.00
	<i>Verrucomicrobiae</i>	1.85 ± 0.89	0.85 ± 0.35	0.77 ± 0.01	1.25 ± 0.29	1.78 ± 0.97
	<i>Alphaproteobacteria</i>	0.16 ± 0.09	0.47 ± 0.11	0.56 ± 0.23	0.24 ± 1.04	1.04 ± 0.65
Order	<i>Bacteroidales</i>	35.21 ± 7.42	52.71 ± 6.61	66.75 ± 3.18	65.48 ± 8.18	74.18 ± 6.79
	<i>Clostridia</i> <sup>§</sup>	1.60 ± 0.45	2.95 ± 2.21	2.66 ± 0.87	1.15 ± 0.63	3.15 ± 1.01
	<i>Clostridiales</i>	55.88 ± 6.59	40.20 ± 5.94	26.12 ± 3.56	13.14 ± 2.64	14.24 ± 6.65
	<i>Lactobacillales</i>	3.22 ± 0.79	0.45 ± 0.14	0.81 ± 0.45	3.79 ± 2.50	2.05 ± 1.00
	<i>Verrucomicrobiales</i>	1.85 ± 0.89	0.85 ± 0.35	0.77 ± 0.01	1.25 ± 0.29	1.78 ± 0.97
Family	<i>Bacteroidales</i> <sup>#</sup>	2.59 ± 1.09	2.49 ± 0.46	2.93 ± 0.32	5.01 ± 1.72	2.71 ± 0.82
	<i>Bacteroidaceae</i>	3.11 ± 0.73	9.32 ± 2.93	17.24 ± 3.17	20.31 ± 4.32	4.04 ± 1.58
	<i>Rikenellaceae</i>	6.53 ± 1.18	15.63 ± 1.82	15.42 ± 1.54	6.77 ± 1.92	14.43 ± 3.01
	<i>S24-7</i>	17.26 ± 4.81	15.79 ± 1.79	23.54 ± 3.60	22.18 ± 4.35	46.88 ± 9.11
	<i>Lachnospiraceae</i>	45.82 ± 8.70	32.00 ± 6.42	19.17 ± 3.15	10.17 ± 2.71	12.03 ± 5.49
	<i>Prevotellaceae</i>	4.99 ± 2.78	7.47 ± 1.84	6.52 ± 1.68	7.96 ± 2.23	5.54 ± 1.39
	<i>Ruminococcaceae</i>	8.69 ± 1.47	7.12 ± 0.58	5.83 ± 1.03	2.56 ± 1.16	1.63 ± 0.45

	<i>Lactobacillaceae</i>	3.14 ± 0.95	0.44 ± 0.14	0.72 ± 0.44	3.79 ± 2.50	2.04 ± 0.89
	<i>Verrucomicrobiaceae</i>	1.85 ± 0.89	0.85 ± 0.35	0.77 ± 0.01	1.25 ± 0.29	1.78 ± 0.97
Genus	<i>Bacteroides</i>	3.11 ± 0.65	9.04 ± 2.99	16.70 ± 3.23	20.14 ± 4.21	3.71 ± 1.76
	<i>Prevotella</i>	4.98 ± 2.48	7.46 ± 1.84	6.49 ± 1.67	7.93 ± 2.33	5.54 ± 1.55
	<i>S24-7*</i>	17.26 ± 4.81	15.79 ± 1.79	23.54 ± 3.60	22.18 ± 4.35	46.88 ± 9.11
	<i>Rikenellaceae*</i>	6.53 ± 1.18	15.63 ± 1.82	15.42 ± 1.54	6.77 ± 1.92	14.43 ± 3.01
	<i>Lactobacillaceae*</i>	2.64 ± 0.66	0.25 ± 0.15	0.69 ± 0.42	3.32 ± 2.17	1.70 ± 0.84
	<i>Lactobacillus</i>	0.43 ± 0.33	0.17 ± 0.11	0.02 ± 0.01	1.29 ± 1.70	0.30 ± 0.16
	<i>Lachnospiraceae*</i>	44.38 ± 7.93	30.54 ± 8.3	18.40 ± 7.7	9.99 ± 2.49	11.50 ± 2.62
	<i>Ruminococcus</i>	2.69 ± 0.56	1.97 ± 0.12	1.54 ± 0.49	0.42 ± 0.22	0.51 ± 0.31
	<i>Ruminococcaceae*</i>	4.20 ± 0.42	2.95 ± 0.23	1.95 ± 0.2	1.00 ± 0.49	0.38 ± 0.11
	<i>Akkermansia</i>	1.85 ± 0.89	0.85 ± 0.35	0.77 ± 0.01	1.25 ± 0.29	1.78 ± 0.97

Values are the mean +/- the standard error.

\$ Represents unclassified orders

# Represents unclassified families

\* Represents unclassified genera.