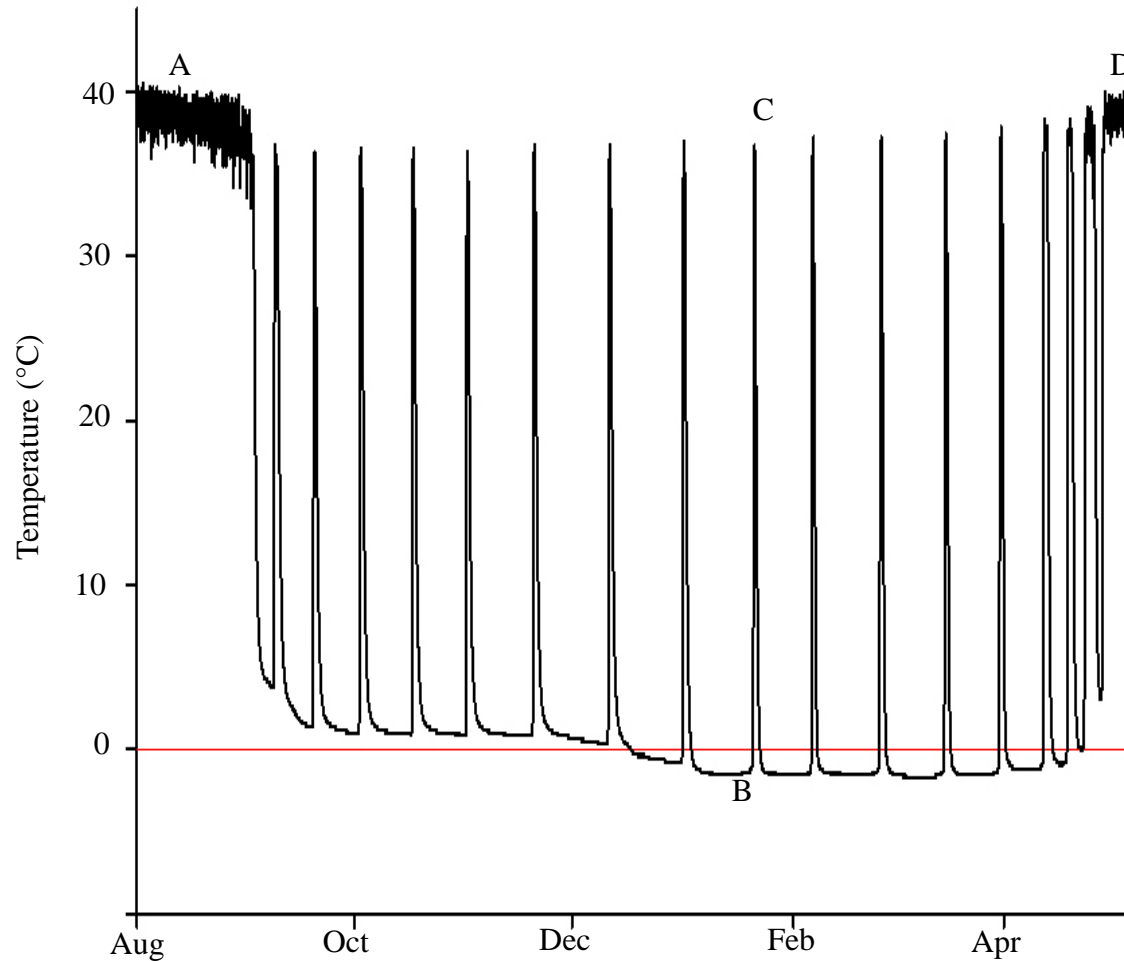
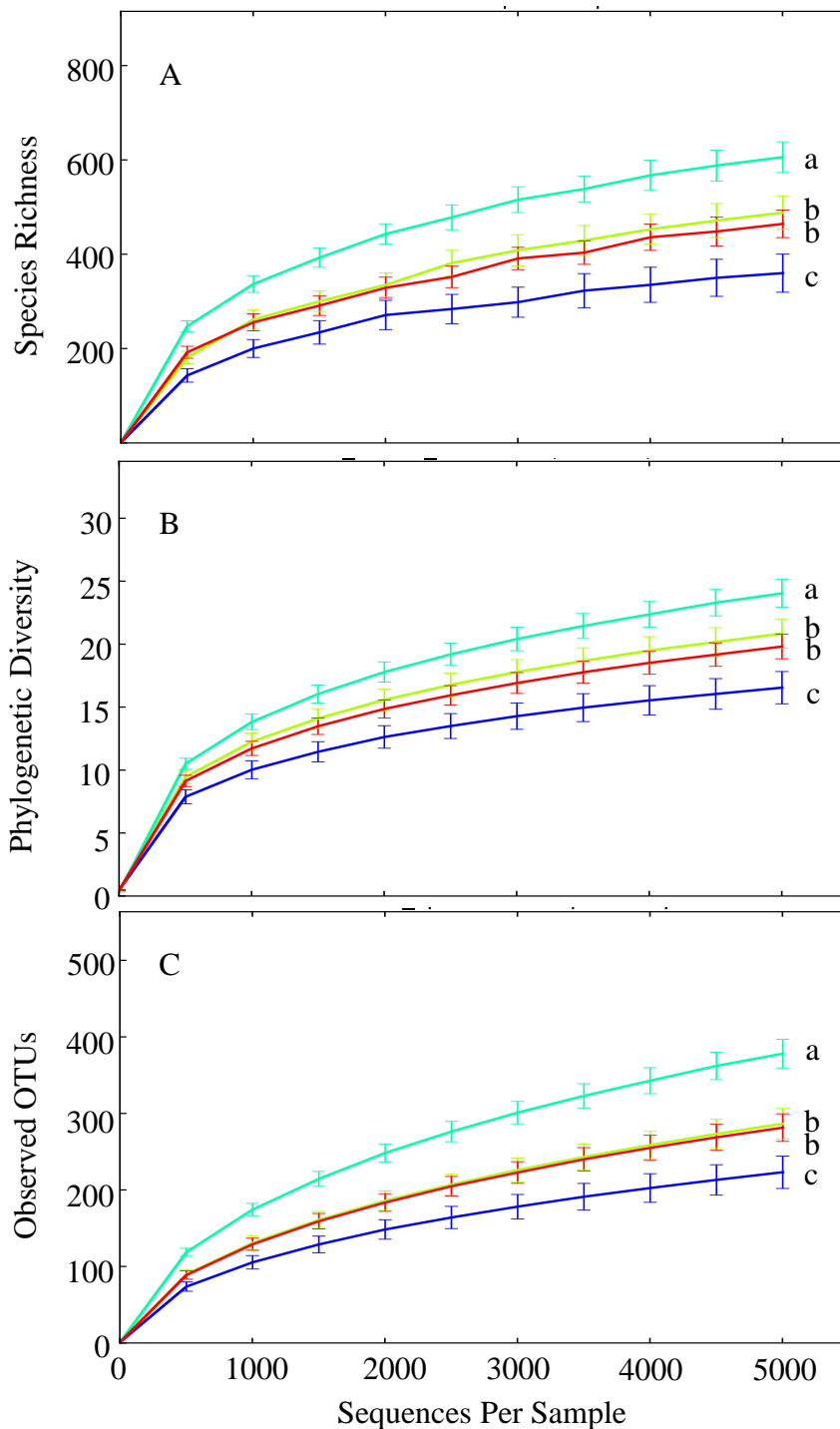


## Supplementary Figure 1

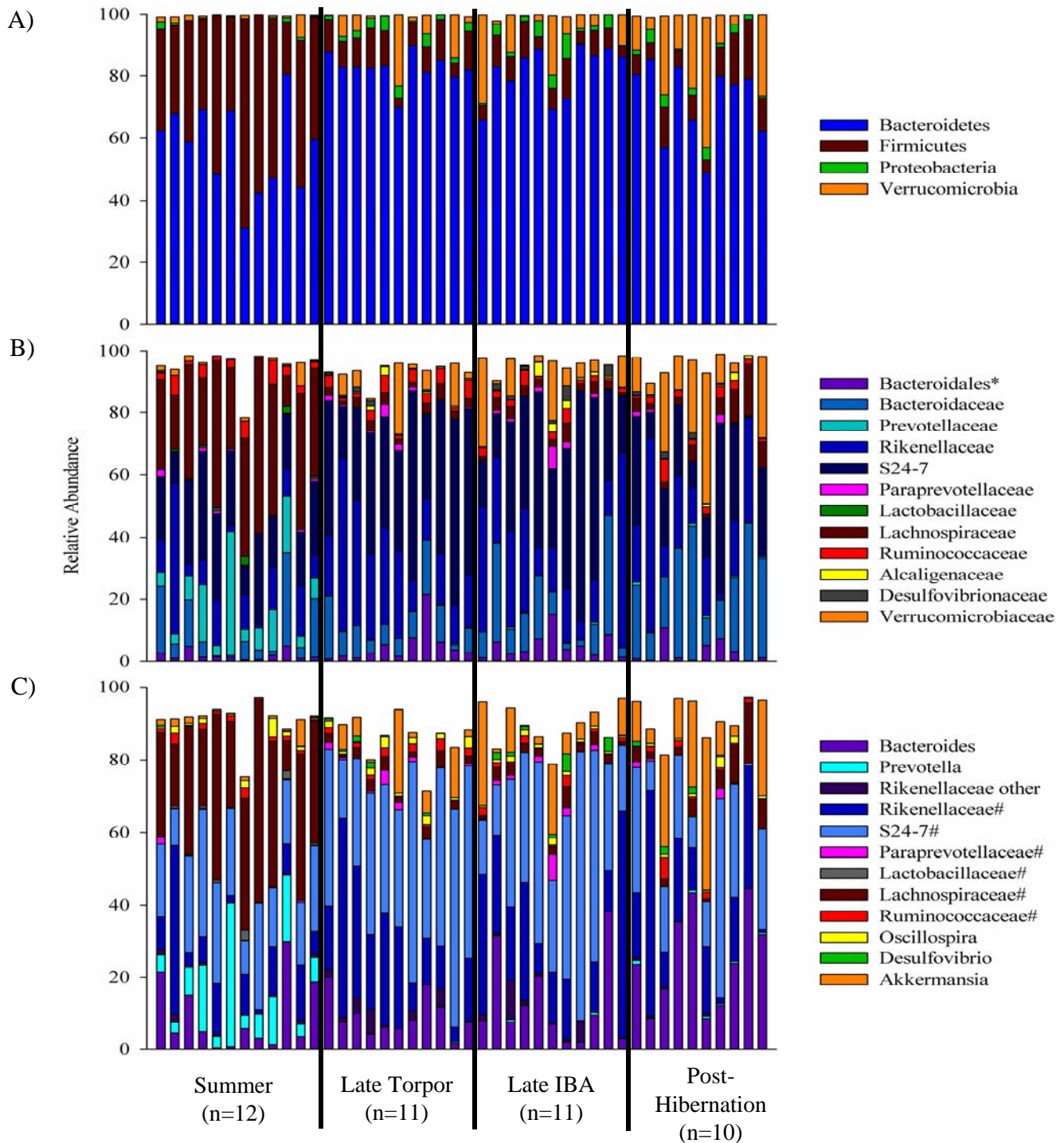


**Supplementary Figure 1.** Sample Design. Animals were sampled at four sample periods across hibernation. A) Summer, B) Late Torpor, C) Late IBA and D) Post-hibernation. The data are the body temperature trace of a female arctic ground squirrel from: **Williams CT, Goropashnaya AV, Buck CL, Fedorov VB, Kohl F, Lee TN, Barnes BM.** 2011. Hibernating above the permafrost: effects of ambient temperature and season on expression of metabolic genes in liver and brown adipose tissue of arctic ground squirrels. *J. Exp. Biol.* **214(8)**:1300-1306 (with permission from C.T. Williams).



**Supplementary Figure 2.** Rarefaction curves of cecal microbial communities. A) Chao1 metric, B) Observed species metric and C) PD whole metric. Each line represents a sample point and each point is the mean  $\pm$  the standard error. Significant differences are denoted by different letters. Symbols are: Summer (teal;  $n=12$ ), Late Torpor (green;  $n=11$ ), Late IBA (red;  $n=11$ ) and Post-Hibernation (blue;  $n=10$ ). Rarefaction plots were produced in QIIME 1.6.0.

Supplementary Figure 3



**Supplementary Figure 3.** The relative abundance of dominant taxa per sample period per animal. Unclassified family (\*) or genus (#) within a taxonomic group. Taxa with less than 1% relative abundance.

Supplementary Table 1: Rarefaction Analysis.

Sample Period	Samples Sequenced (N)	Average Sequences Passed Quality Check	Minimum Sequences After Quality Check	Observed Species (97%)*	PD Whole Tree*	Chao1*
Summer	12	13119 ± 703	10973	362 ± 19	24.03 ± 1.11	606 ± 32
Late Torpor	11	13846 ± 906	10486	286 ± 20	20.84 ± 1.17	488 ± 35
Late IBA	11	14399 ± 980	8757	281 ± 18	19.81 ± 0.97	464 ± 29
Post-Hibernation	10	13444 ± 1636	5858	223 ± 21	16.54 ± 1.28	360 ± 40

Values are the mean ± the standard error of the mean

\*Rarefaction values are based on a subsampling of 5001 sequences

Supplementary Table 2: The relative abundances of taxa that significantly differed among sample periods

Level	Taxonomy	Summer Active (n=12)	Late Torpor (n=11)	Late IBA (n=11)	Post-Hibernation (n=10)
Phylum	Bactroidetes	56.0 ± 4.1 <sup>a</sup>	82.4 ± 1.5 <sup>b</sup>	81.5 ± 2.6 <sup>b</sup>	72.9 ± 3.9 <sup>a</sup>
	Firmicutes	40.9 ± 4.1 <sup>a</sup>	9.20 ± 1.0 <sup>b</sup>	7.35 ± 0.1 <sup>b</sup>	9.86 ± 1.6 <sup>b</sup>
	Proteobacteria	0.63 ± 0.2 <sup>a</sup>	2.59 ± 1.0 <sup>b</sup>	2.88 ± 0.7 <sup>b</sup>	2.26 ± 0.5 <sup>b</sup>
	Verrucomicrobia	1.37 ± 0.6 <sup>a</sup>	5.43 ± 2.1 <sup>a</sup>	8.76 ± 2.9 <sup>b</sup>	15.6 ± 4.2 <sup>b</sup>
Class	Bacteroidia	56.7 ± 4.1 <sup>a</sup>	82.4 ± 1.5 <sup>b</sup>	81.0 ± 2.6 <sup>b</sup>	71.9 ± 3.9 <sup>a</sup>
	Clostridia	37.6 ± 3.6 <sup>a</sup>	7.46 ± 0.8 <sup>b</sup>	6.00 ± 0.8 <sup>b</sup>	8.9 ± 1.5 <sup>b</sup>
	Bacilli	0.98 ± 0.3 <sup>a</sup>	0.06 ± 0.02 <sup>b</sup>	0.03 ± 0.01 <sup>b</sup>	0.01 ± 0.01 <sup>b</sup>
	Betaproteobacteria	0.04 ± 0.01 <sup>a</sup>	0.73 ± 0.23 <sup>b</sup>	1.35 ± 0.45 <sup>b</sup>	0.65 ± 0.23 <sup>b</sup>
	Deltaproteobacteria	0.11 ± 0.05 <sup>a</sup>	0.53 ± 0.19 <sup>a</sup>	1.42 ± 0.5 <sup>b</sup>	0.62 ± 0.26 <sup>a</sup>
	Erysipelotrichi	0.03 ± 0.01 <sup>a</sup>	0.12 ± 0.03 <sup>b</sup>	0.28 ± 0.08 <sup>b</sup>	0.11 ± 0.01 <sup>a</sup>
	Verrucomicrobiae	1.37 ± 0.6 <sup>a</sup>	5.41 ± 2.1 <sup>a</sup>	8.76 ± 2.9 <sup>b</sup>	15.6 ± 4.2 <sup>b</sup>
Order	Bacteroidales	56.7 ± 4.1 <sup>a</sup>	82.4 ± 1.5 <sup>b</sup>	81.5 ± 2.6 <sup>b</sup>	71.9 ± 3.9 <sup>a</sup>
	Clostridiales	38.2 ± 4.4 <sup>a</sup>	7.1 ± 0.9 <sup>b</sup>	5.6 ± 0.77 <sup>b</sup>	9.1 ± 2.3 <sup>b</sup>
	Lactrobacillales	0.95 ± 0.3 <sup>a</sup>	0.05 ± 0.01 <sup>b</sup>	0.02 ± 0.01 <sup>b</sup>	0.0 ± 0.0 <sup>b</sup>
	Burkholderiales	0.03 ± 0.01 <sup>a</sup>	0.73 ± 0.23 <sup>b</sup>	1.23 ± 0.45 <sup>b</sup>	0.22 ± 0.22 <sup>b</sup>
	Desulfovibrionales	0.11 ± 0.05 <sup>a</sup>	0.52 ± 0.19 <sup>a</sup>	1.3 ± 0.5 <sup>b</sup>	0.63 ± 0.26 <sup>a</sup>
	Erysipelotrichales	0.03 ± 0.01 <sup>a</sup>	0.12 ± 0.03 <sup>b</sup>	0.24 ± 0.08 <sup>a</sup>	0.11 ± 0.06 <sup>b</sup>

	Verrucomicrobiales	$1.37 \pm 0.6^a$	$5.41 \pm 2.2^a$	$8.76 \pm 2.9^b$	$15.6 \pm 4.2^b$
Family	Bacteroidaceae	$9.11 \pm 2.8^a$	$9.21 \pm 1.7^a$	$12.9 \pm 3.7^a$	$24.9 \pm 4.2^b$
	Bacteroidales*	$1.93 \pm 0.43^a$	$5.03 \pm 1.8^b$	$5.13 \pm 1.2^b$	$3.02 \pm 1.13^a$
	Prevotellaceae	$10.8 \pm 3.1^a$	$0.15 \pm 0.05^b$	$0.24 \pm 0.08^b$	$0.46 \pm 0.12^b$
	Rikenellaceae	$12.2 \pm 3.6^a$	$24.8 \pm 4.2^b$	$24.2 \pm 5.1^a$	$19.9 \pm 5.7^a$
	S24-7	$21.38 \pm 2.2^a$	$40.58 \pm 4.3^b$	$36.40 \pm 5.8^b$	$21.95 \pm 5.7^a$
	Lachnospiraceae	$33.6 \pm 3.8^a$	$2.87 \pm 0.37^b$	$2.96 \pm 0.43^b$	$5.72 \pm 1.6^b$
	Lactobacillaceae	$0.73 \pm 0.3^a$	$0.00 \pm 0.0^b$	$0.00 \pm 0.0^b$	$0.00 \pm 0.0^b$
	Clostridiales*	$0.13 \pm 0.05^a$	$0.00 \pm 0.0^b$	$0.01 \pm 0.01^b$	$0.02 \pm 0.01^b$
	Clostridiaceae	$0.05 \pm 0.3^a$	$0.00 \pm 0.0^b$	$0.15 \pm 0.04^c$	$0.06 \pm 0.02^a$
	Burkholderiaceae	$0.04 \pm 0.01^a$	$0.55 \pm 0.17^b$	$0.95 \pm 0.34^b$	$0.60 \pm 0.19^b$
	Alcaligenaceae	$0.03 \pm 0.01^a$	$0.7 \pm 0.23^b$	$1.22 \pm 0.44$	$0.64 \pm 0.22^b$
	Odoribacteraceae	$0.06 \pm 0.02^a$	$0.85 \pm 0.2^b$	$0.71 \pm 0.21^b$	$0.78 \pm 0.40^b$
	Desulfovibrionaceae	$0.11 \pm 0.05^a$	$0.01 \pm 0.1^a$	$1.3 \pm 0.5^b$	$0.63 \pm 0.26^a$
	Verrucomicrobiaceae	$1.37 \pm 0.6^a$	$5.41 \pm 2.2^a$	$8.76 \pm 2.9^b$	$15.6 \pm 4.2^b$
Genus	Bacteroides	$9.11 \pm 2.8^a$	$9.21 \pm 1.7^a$	$12.9 \pm 3.7^a$	$24.9 \pm 4.2^b$
	Prevotella	$10.8 \pm 3.1^a$	$0.14 \pm 0.05^b$	$0.24 \pm 0.08^b$	$0.46 \pm 0.11^b$
	Rikenellaceae <sup>#</sup>	$11.5 \pm 3.45^a$	$22.1 \pm 4.4^b$	$22.3 \pm 5.2^b$	$19.7 \pm 5.7^a$
	S24-7 <sup>#</sup>	$21.38 \pm 2.2^a$	$40.58 \pm 4.3^b$	$36.40 \pm 5.8^b$	$21.95 \pm 5.7^a$
	Odoribacter	$0.06 \pm 0.02^a$	$0.85 \pm 0.12^b$	$0.72 \pm 0.22^b$	$0.78 \pm 0.4^a$
	Lachnospiraceae <sup>#</sup>	$30.0 \pm 4.0^a$	$1.60 \pm 0.25^b$	$1.63 \pm 0.23^b$	$4.26 \pm 1.5^b$
	Lactobacillaceae <sup>#</sup>	$0.71 \pm 0.25^a$	$0.03 \pm 0.02^b$	$0.00 \pm 0.0^b$	$0.00 \pm 0.0^b$

Roseburia	2.43 ± 0.78 <sup>a</sup>	0.03 ± 0.01 <sup>b</sup>	0.10 ± 0.04 <sup>b</sup>	0.03 ± 0.01 <sup>b</sup>
Ruminococcus	0.69 ± 0.12 <sup>a</sup>	0.11 ± 0.05 <sup>b</sup>	0.17 ± 0.01 <sup>b</sup>	0.13 ± 0.06 <sup>b</sup>
Clostridiaceae <sup>#</sup>	0.01 ± 0.00 <sup>a</sup>	0.18 ± 0.04 <sup>b,c</sup>	0.14 ± 0.04 <sup>b</sup>	4.26 ± 1.5 <sup>b</sup>
Blautia	0.41 ± 0.1 <sup>a</sup>	0.07 ± 0.22 <sup>b</sup>	0.1 ± 0.05 <sup>b</sup>	0.05 ± 0.02 <sup>b</sup>
Lachnospiraceae <sup>#</sup>	30.0 ± 4.0 <sup>a</sup>	1.60 ± 0.25 <sup>b</sup>	1.63 ± 0.23 <sup>b</sup>	0.06 ± 0.02 <sup>a</sup>
Clostridiaceae <sup>#</sup>	0.01 ± 0.00 <sup>a</sup>	0.18 ± 0.04 <sup>a,b</sup>	0.14 ± 0.04 <sup>b</sup>	0.00 ± 0.0 <sup>b</sup>
Coprococcus	0.58 ± 0.25 <sup>a</sup>	0.03 ± 0.13 <sup>b</sup>	0.06 ± 0.02 <sup>b</sup>	0.03 ± 0.02 <sup>b</sup>
Sutterella	0.04 ± 0.1 <sup>a</sup>	0.72 ± 0.22 <sup>b</sup>	1.22 ± 0.45 <sup>b</sup>	0.64 ± 0.22 <sup>b</sup>
Desulfovibrio	0.09 ± 0.05 <sup>a</sup>	0.5 ± 0.19 <sup>a</sup>	1.28 ± 0.5 <sup>b</sup>	0.60 ± 0.26 <sup>a</sup>
Akkermansia	1.37 ± 0.6 <sup>a</sup>	5.41 ± 2.2 <sup>a</sup>	8.76 ± 2.9 <sup>b</sup>	15.6 ± 4.2 <sup>b</sup>

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Values are the mean +/- the standard error of the mean.

Different letters indicate significant differences as determined by a Kruskal-Wallis Rank-Sum test

<sup>#</sup> = unclassified genus

<sup>\*</sup> = unclassified family