

## Supplementals

**Table S1.** Pen level Metadata of animals used to collect fecal composite samples. Sex listed without “Yearling” are calves.

Pen-level Fecal Composite Sample ID	Age/Sex
Nat-Win-B-25Oct16-M1	Yearling, Steers
Nat-Win-B-25Oct16-M2	Yearling, heifers
Con-Win-A-22Oct16-M4	Yearling, Steers
Nat-Win-C-31Jan17-M7	Steers
Con-Win-D-1Feb17-M9	Yearling, Steers
Con-Win-D-2Feb17-M10	Yearling, Heifers
Nat-Sum-B-28Jun17-M17	Yearling steers
Nat-Sum-B-28Jun17-M18	Yearling heifers
Nat-Win-B-1Mar17-MG2	Yearling, Heifers
Con-Win-A-1Mar17-MG3	Yearling, Not segregated
Con-Win-A-1Mar17-MG4	Yearling, Not segregated
Nat-Sum-B-26Apr17-MG5	Yearling, Steers
Nat-Sum-B-26Apr17-MG6	Yearling, Heifers
Con-Sum-A-26Apr17-MG7	Yearling, Heifers
Con-Sum-A-26Apr17-MG8	Yearling, Steers
Nat-Sum-C-10Apr18-MG9	Steers
Nat-Sum-C-10Apr18-MG10	Heifers
Con-Sum-D-10Apr18-MG11	Yearling, Not segregated
Con-Sum-D-10Apr18-MG12	Yearling, Not segregated
Nat-Win-B-13Mar18-MG13	Not segregated
Nat-Win-B-13Mar18-MG14	Not segregated
Con-Win-A-13Mar18-MG15	Yearling, Not segregated
Con-Win-A-13Mar18-MG16	Yearling, Not segregated
Nat-Sum-C-26Jun18-MG17	Steers
Nat-Sum-C-26Jun18-MG18	Heifers
Con-Sum-D-26Jun18-MG19	Yearling, Not segregated
Con-Sum-D-26Jun18-MG20	Yearling, Not segregated
Nat-Sum-B-25Jul18-MG21	Yearling, Steers
Nat-Sum-B-25Jul18-MG22	Yearling, Heifers
Con-Sum-A-25Jul18-MG23	Yearling, Not segregated
Con-Sum-A-25Jul18-MG24	Yearling, Not segregated
Nat-Sum-C-1Aug17-MG25	Heifers
Nat-Sum-C-1Aug17-MG26	Heifers
Con-Sum-D-1Aug17-MG27	Yearling, Heifers
Con-Sum-D-1Aug17-MG28	Yearling, Steers
Nat-Win-C-24Oct17-MG29	Heifers
Con-Win-D-24Oct17-MG31	Yearling, Steers
Con-Win-D-24Oct17-MG32	Yearling, Heifers
Nat-Win-C-29Jan18-MG33	Heifers
Nat-Win-C-29Jan18-MG34	Heifers
Con-Win-D-29Jan18-MG35	Yearling, Heifers
Con-Win-D-29Jan18-MG36	Yearling, Steers

Nat-Sum-B-05Sep17-MG41	Yearling, Steers
Nat-Sum-B-05Sep17-MG42	Yearling, Heifers
Con-Sum-A-05Sep17-MG43	Yearling, Steers
Con-Sum-A-05Sep17-MG44	Yearling, Heifers
Nat-Sum-B-29May18-MG45	Yearling, no data
Nat-Sum-B-29May18-MG46	Yearling, no data
Con-Sum-A-29May18-MG47	Yearling, Heifers
Con-Sum-A-29May18-MG48	Yearling, Steers
Con-Win-A-25Oct16-MG49	Yearling, Heifers
Nat-Win-C-31Jan17-MG50	Heifers
Nat-Win-B-11Dec17-MG53	Yearling, Steers
Nat-Win-B-11Dec17-MG54	Yearling, Heifers
Con-Win-A-11Dec17-MG55	Yearling, Steers
Con-Win-A-11Dec17-MG56	Yearling, Heifers
Nat-Win-C-29Mar17-MG57	Heifers
Nat-Win-C-29Mar17-MG58	Steers
Con-Win-D-29Mar17-MG59	Yearling, Heifers
Con-Win-D-29Mar17-MG60	Yearling, Steers

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**Table S2.** Most abundant archaeal and bacterial classes (>1%) and orders (top 20) of fecal and catch basin water samples with mean normalized abundance, interpreted significance of adjusted p-value ( $q > 0.05 = \text{ns}$ ;  $q < 0.05 = *$ ;  $q < 0.01 = **$ ;  $q < 0.001 = ***$ ;  $q < 0.0001 = ****$ ), and fold change for significant differences from natural (NAT) to conventional (CONV).

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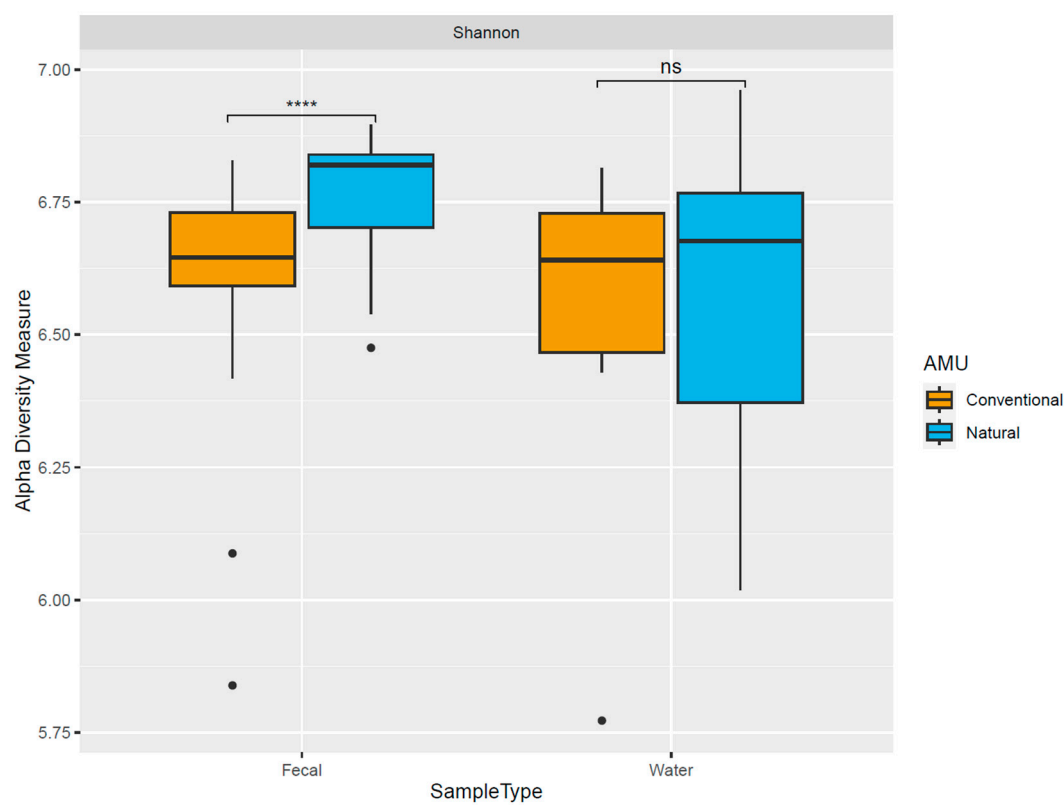
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Sample Type	Taxa Level	Taxon	CONV Mean Normalized Abundance	NAT Mean Normalized Abundance	Interpreted Significance	Fold Change
Fecal Composite	Class	Actinobacteria	0.055	0.066	**	1.09
		Alphaproteobacteria	0.041	0.045	ns	-
		Bacilli	0.078	0.091	*	1.06
		Bacteroidia	0.210	0.168	***	0.81
		Betaproteobacteria	0.031	0.033	ns	-
		Chlorobia	0.002	0.002	ns	-
		Clostridia	0.271	0.307	ns	-
		Coriobacteriia	0.012	0.014	ns	-
		Cytophagia	0.014	0.014	ns	-
		Deltaproteobacteria	0.016	0.017	ns	-
		Epsilonproteobacteria	0.012	0.009	****	0.97
		Flavobacteriia	0.039	0.038	*	0.93
		Gammaproteobacteria	0.096	0.091	*	0.91
		Methanobacteria	0.014	0.006	***	0.58
		Mollicutes	0.007	0.009	**	1.11
		Negativicutes	0.014	0.012	ns	-
		Spirochaetia	0.029	0.015	**	0.69
	Order	Alteromonadales	0.009	0.008	*	0.88
		Bacillales	0.051	0.059	*	1.05
		Bacteroidales	0.210	0.167	***	0.80
		Bifidobacteriales	0.006	0.011	***	1.33
		Burkholderiales	0.023	0.024	ns	-

		Campylobacterales	0.012	0.009	****	0.77
		Caulobacterales	-	-	-	-
		Chromatiales	-	-	-	-
		Clostridiales	0.266	0.301	ns	-
		Corynebacterales	0.012	0.013	ns	-
		Cytophagales	0.014	0.014	ns	-
		Desulfovibrionales	-	-	-	-
		Enterobacterales	0.026	0.024	*	0.90
		Erysipelotrichales	0.010	0.011	ns	-
		Flavobacteriales	0.040	0.039	*	0.92
		Lactobacillales	0.026	0.030	*	1.04
		Methanobacteriales	0.014	0.006	***	0.57
		Micrococcales	0.009	0.010	ns	-
		Nitrosomonadales	-	-	-	-
		Pseudomonadales	0.020	0.020	ns	-
		Rhizobiales	0.016	0.018	ns	-
		Rhodobacterales	-	-	-	-
		Rhodocyclales	-	-	-	-
		Sphingomonadales	-	-	-	-
		Spirochaetales	0.027	0.013	**	0.66
		Streptomycetales	0.009	0.010	ns	-
		Xanthomonadales	-	-	-	-
Catch Basin Water	Class	Actinobacteria	0.096	0.122	*	0.99
		Alphaproteobacteria	0.154	0.116	ns	-
		Bacilli	0.017	0.029	****	1.06
		Bacteroidia	0.019	0.041	****	1.01
		Betaproteobacteria	0.229	0.251	ns	-
		Clostridia	0.018	0.057	ns	-
		Cytophagia	0.009	0.015	ns	-
		Deltaproteobacteria	0.105	0.08	ns	-
		Epsilonproteobacteria	0.018	0.015	ns	-
		Flavobacteriia	0.030	0.041	****	1.13
		Gammaproteobacteria	0.249	0.161	ns	-
		Methanobacteria	0.000	0.002	****	1.18
	Order	Bacillales	0.012	0.02	ns	-
		Bacteroidales	0.018	0.04	ns	-
		Burkholderiales	0.174	0.202	ns	-
		Campylobacterales	0.019	0.015	ns	-
		Caulobacterales	0.017	0.01	ns	-
		Chromatiales	0.085	0.016	ns	-
		Clostridiales	0.017	0.055	ns	-
		Corynebacterales	0.018	0.022	ns	-
		Desulfovibrionales	0.086	0.062	ns	-
		Enterobacterales	0.019	0.018	ns	-
		Flavobacteriales	0.031	0.042	ns	-
		Micrococcales	0.022	0.025	ns	-
		Nitrosomonadales	0.011	0.02	ns	-
		Pseudomonadales	0.062	0.056	ns	-
		Rhizobiales	0.052	0.045	ns	-

		Rhodobacterales	0.047	0.031	ns	-
		Rhodocyclales	0.038	0.023	ns	-
		Sphingomonadales	0.021	0.015	ns	-
		Streptomycetales	0.023	0.026	ns	-
		Xanthomonadales	0.018	0.016	ns	-

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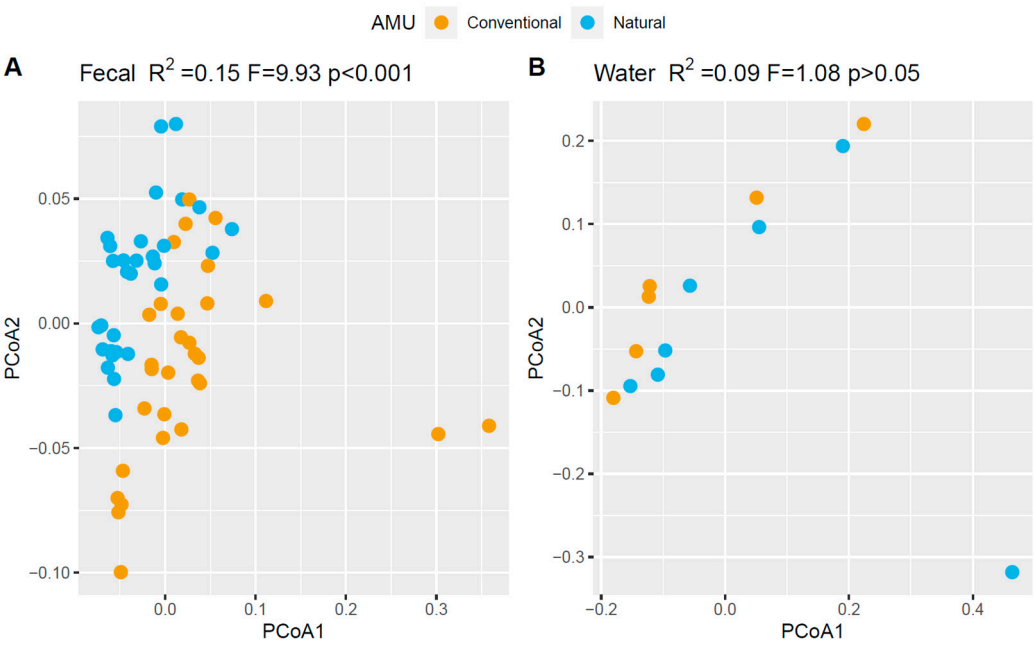


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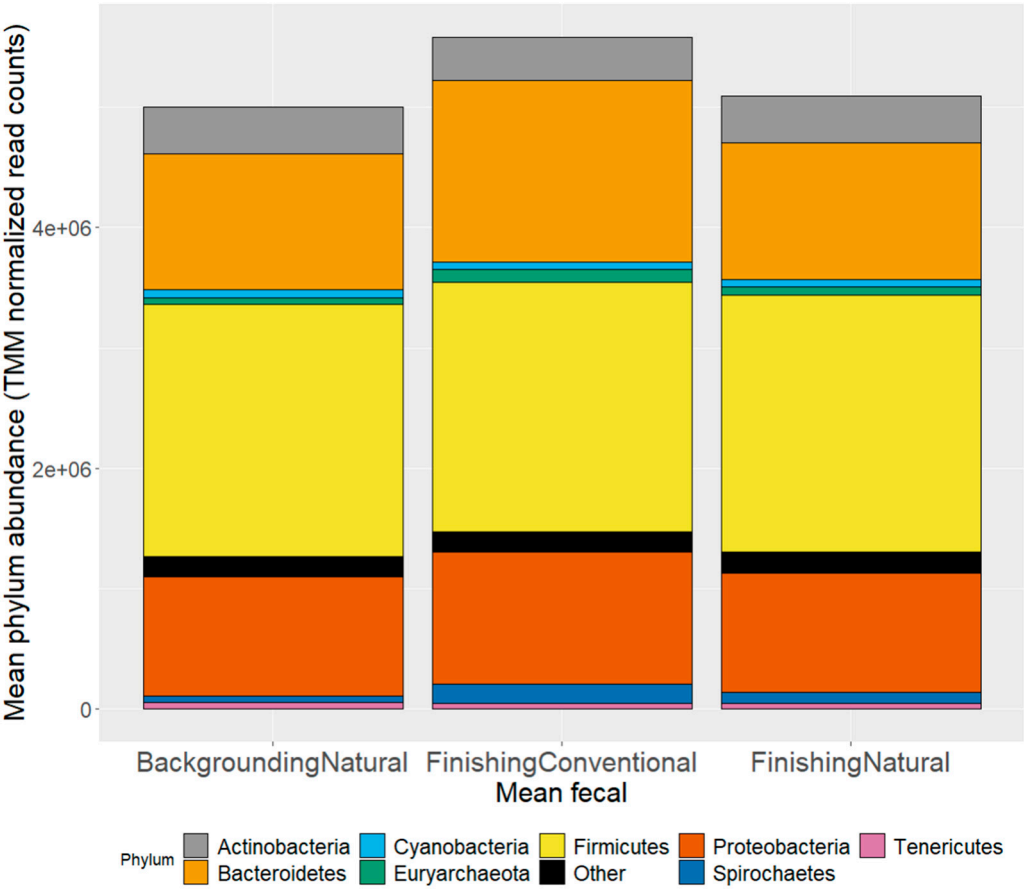
**Figure S1.** Boxplot of Shannon index comparisons between conventional and natural feedlots for fecal and catch basin water samples. (Wilcoxon signed rank test;  $p > 0.05$  = ns;  $p < 0.0001$  = \*\*\*\*)

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**Figure S2.** Principle component analyses (PCoA) of beta diversity differences using Bray-Curtis for fecal (A) and catch basin water (B) samples between conventional and natural feedlot types. (PER-MANOVA test)



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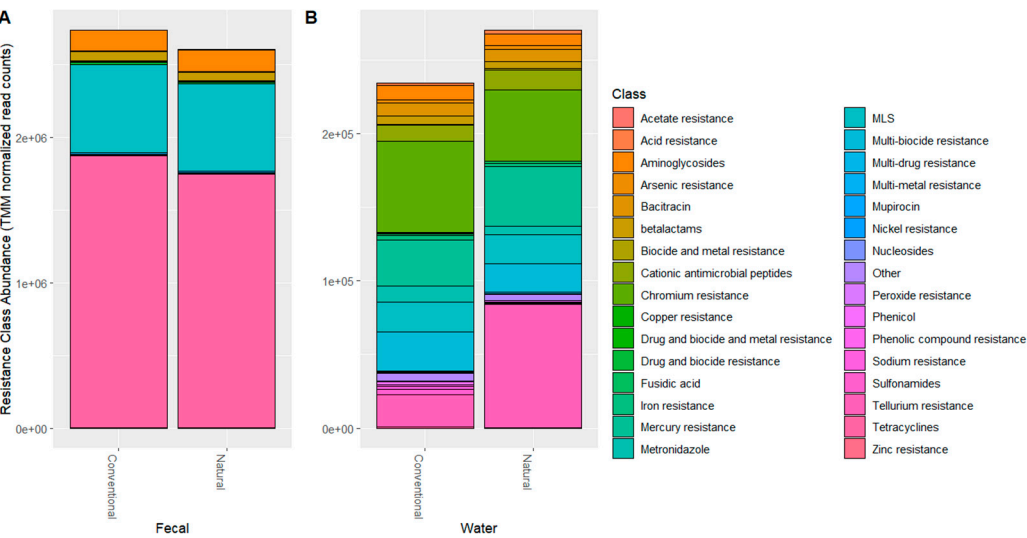
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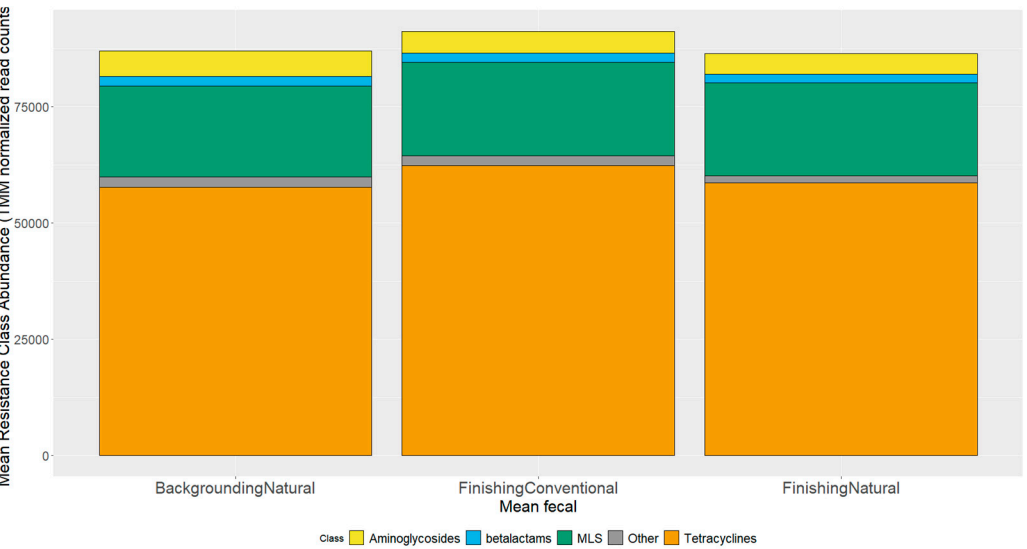
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**Figure S3.** Stacked bar plots comparing TMM (trimmed mean of m-values) normalized mean read counts per sample of prevalent phyla (>1%) across fecal sample diet (Backgrounding vs Finishing) and feedlot management practices (Conventional vs Natural).



**Figure S4.** Stacked bar plots of TMM (trimmed mean of m-values) normalized read counts per feedlot management practice for fecal (A) and catch basin water (B) antimicrobial resistance gene classes.



**Figure S5.** Stacked bar plots comparing TMM (trimmed mean of m-values) normalized mean read counts per sample of prevalent antimicrobial resistance gene classes (>1%) across fecal sample diet (Backgrounding vs Finishing) and feedlot management practices (Conventional vs Natural).