

**Supplemental Table 1. Differences in Fecal Metabolite between T<sub>0</sub> and T<sub>4</sub> in paired vs isolated group**

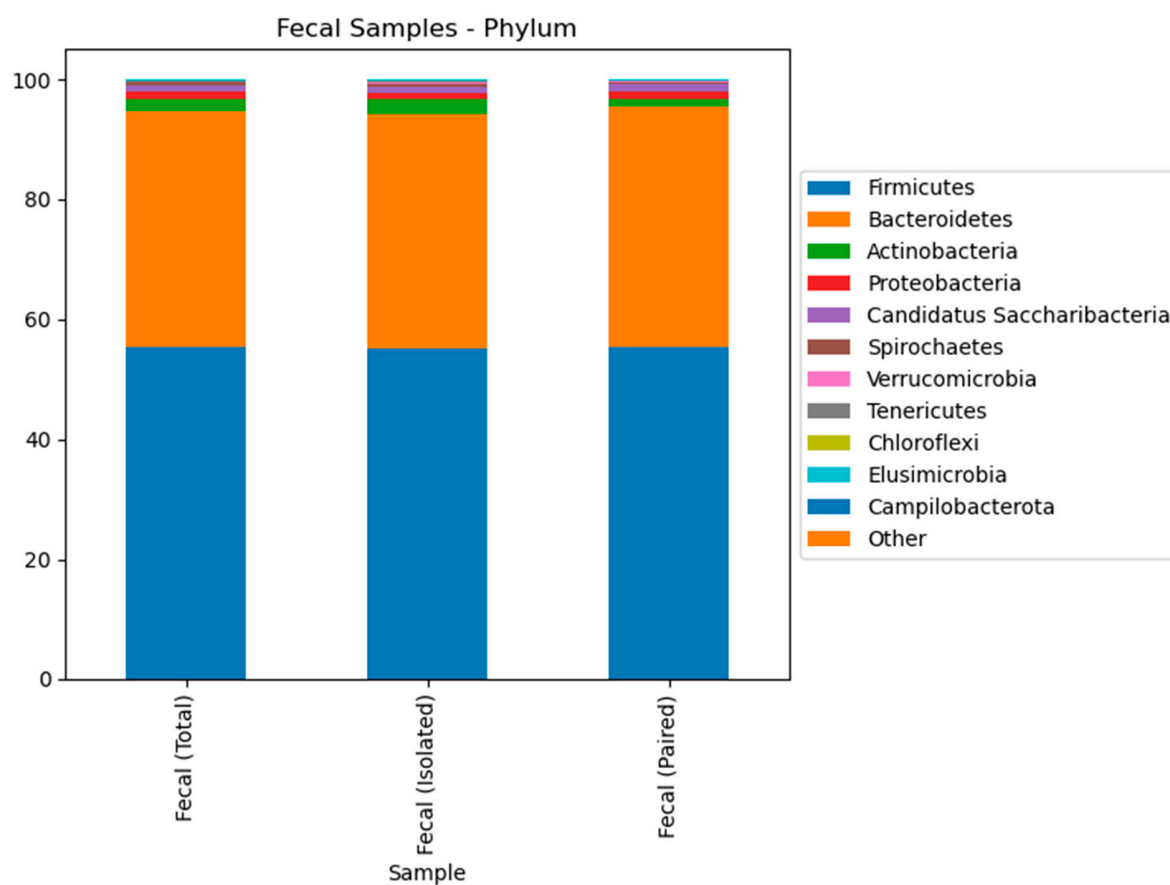
<u>Metabolite</u>	<u>Analysis</u>	<u>Results</u>	<u>Isolated</u>		<u>Paired</u>	
			<u>Mean</u>	<u>Std Dev</u>	<u>Mean</u>	<u>Std Dev</u>
<i>Tetradecanoic acid</i>	T-test	0.034	31.971	93.363	-69.175	72.403
<i>Xylose</i>	T-test	0.088	3076.129	4865.721	-1488.912	4702.852
<i>Glucose</i>	Mann-Whitney	0.072	1530.143	4105.073	-2350.075	5014.246
<i>Arabinose</i>	T-test	0.071	1167.15	1341.074	-582.569	1987.693
<i>O-phosphoethanolamine</i>	Mann-Whitney	0.094	5.843	15.684	-16.138	25.139
<i>Oxamic acid</i>	Mann-Whitney	0.072	2.693	8.938	-6.35	5.961
<i>N-acetylglucosamine</i>	T-test	0.096	-6.929	159.384	-168.588	185.343
<i>Adipic acid</i>	Mann-Whitney	0.094	-10.229	39.795	-101.675	113.563

**Supplemental Table 2. Differences in Fecal Metabolites at T<sub>4</sub>.**

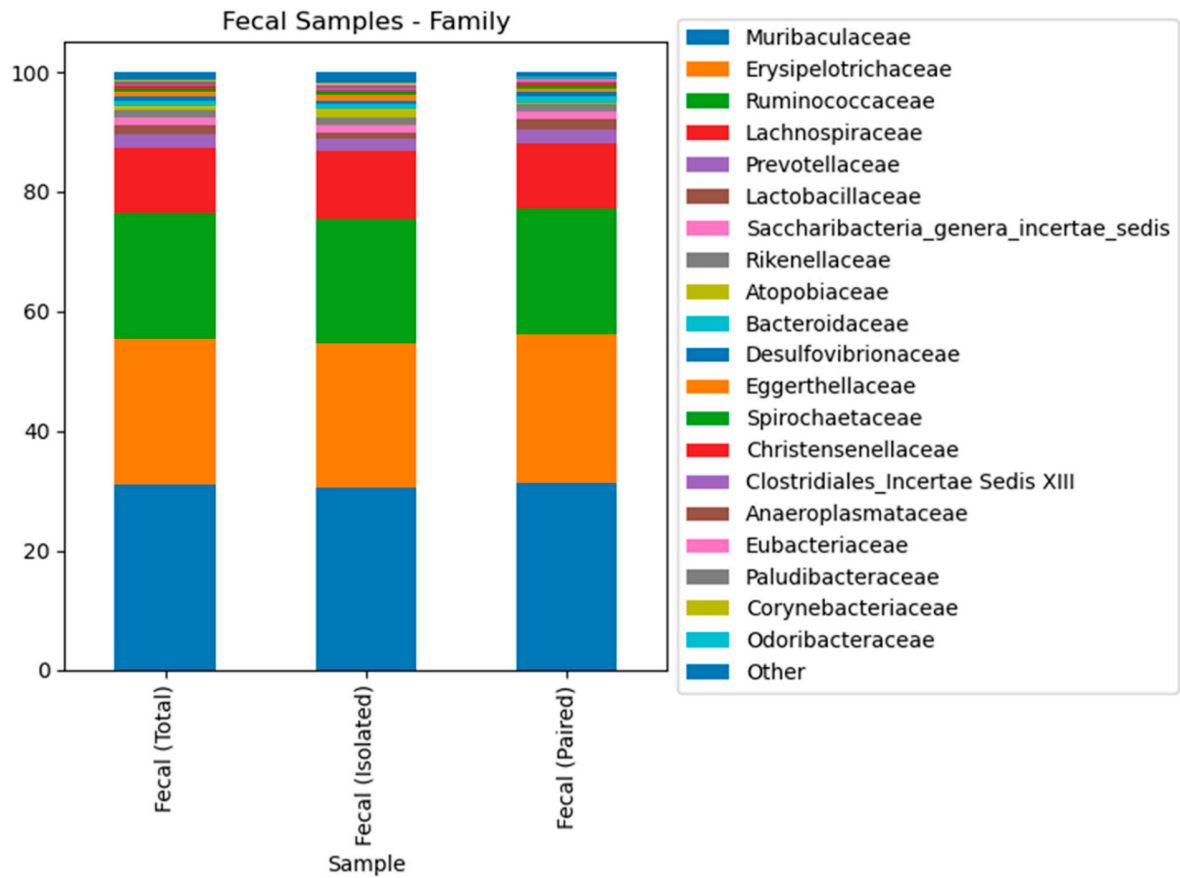
<u>Metabolites</u>	<u>Analysis</u>	<u>Results</u>	<u>Isolated</u>		<u>Paired</u>	
			<u>Mean</u>	<u>Std Dev</u>	<u>Mean</u>	<u>Std Dev</u>
<i>Succinic acid</i>	T-test	0.036	1053.656	432.8449	636.882	389.3606
<i>Tetradecanoic acid</i>	T-test	0.011	196.067	68.9565	109.173	66.6781
<i>Glucose</i>	Log10	0.097	7614.767	3822.3902	5272.345	4545.8686
<i>Arabinose</i>	Log10	0.088	3755.389	2600.9074	2163.568	1309.5832
<i>Galactose</i>	Log10	0.099	1444.178	812.4141	937.555	774.5478
<i>Hippuric acid</i>	Log10	0.064	418.278	572.0355	639.118	497.2158
<i>N-Acetyl glucosamine</i>	Mann-Whitney	0.08	236.722	101.5849	161.673	71.0349
<i>Oxalic acid</i>	T-test	0.091	43.411	19.4825	31.355	10.0978
<i>O-phosphoethanolamine</i>	T-test	0.082	36.933	10.0652	29.382	8.3091

**Supplemental Table 3. Differences in Serum Metabolites at T<sub>4</sub> in paired vs isolated group.**

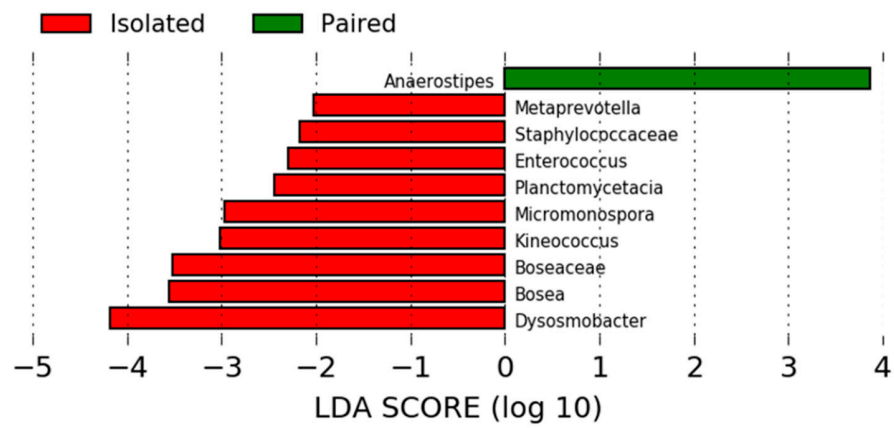
<u>Metabolite</u>	<u>Analysis</u>	<u>Results</u>	<u>Isolated</u>		<u>Paired</u>	
			<u>Mean</u>	<u>Std Dev</u>	<u>Mean</u>	<u>Std Dev</u>
<i>Hippuric acid</i>	T-test	0.04	12.5	6.8178	19.627	8.3211
<i>Lactic acid</i>	Log10	0.057	10865.845	3496.8387	13662.927	3435.1915
<i>Sorbitol</i>	T-test	0.053	60.624	22.7011	43.145	15.6869
<i>Glyoxylic acid</i>	Mann-Whitney	0.088	23.618	13.1432	12.836	9.7589



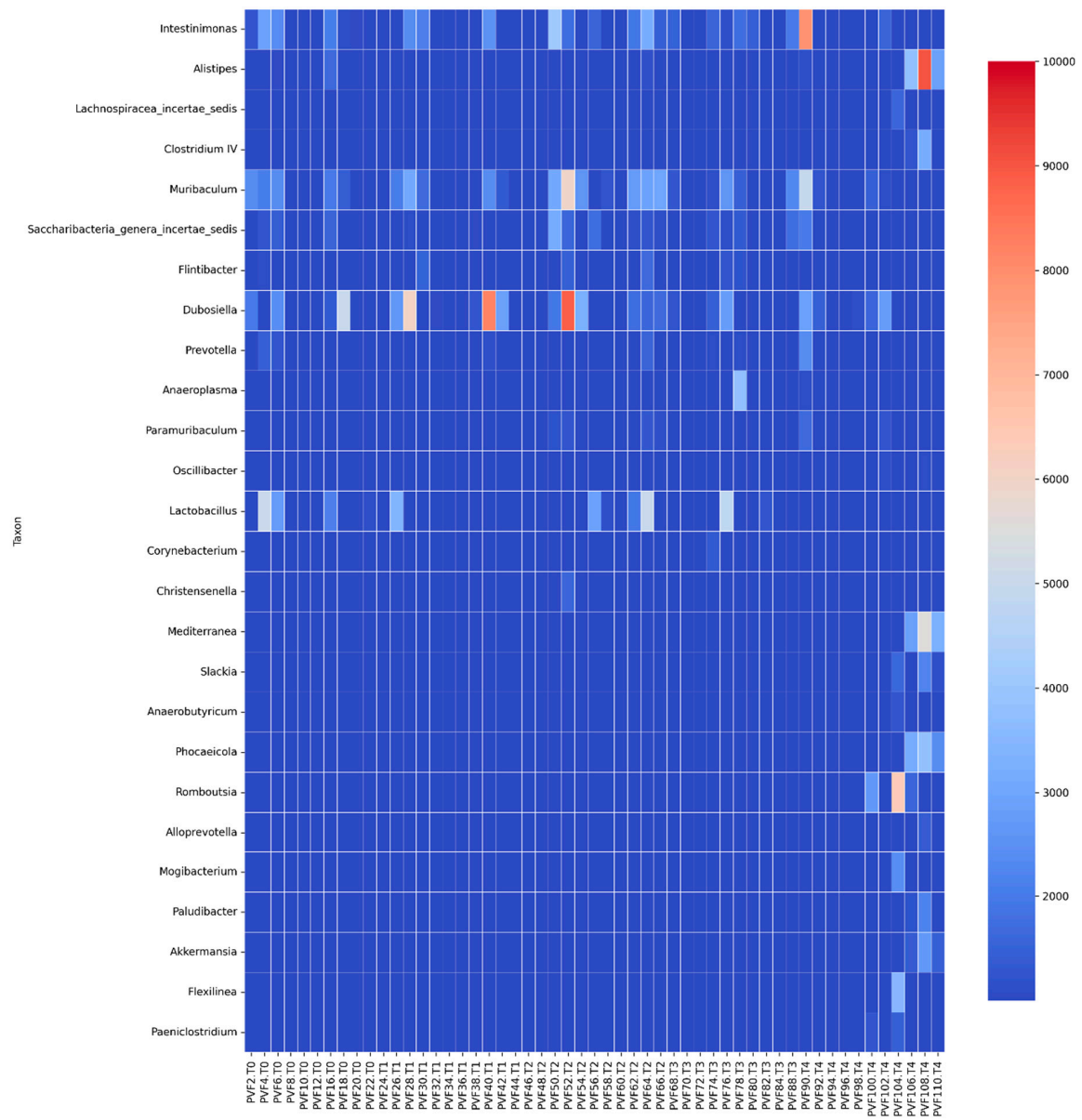
**Supplemental Figure S1.** Firmicutes (55.36%) and Bacteroidetes (39.44%) were the dominant phyla in pooled prairie vole fecal communities, followed by Actinobacteria (1.82%), Proteobacteria (1.24%), and Candidatus Saccharibacteria (1.1%). All other phyla comprised less than 1% of prairie vole fecal communities. Phyla contained in “Other” made up less than 0.01% of fecal communities.



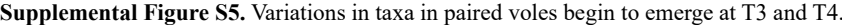
**Supplemental Figure S2.** Muribaculaceae (31.07%), Erysipelotrichaceae (24.44) and Ruminococcaceae (20.92%) were the dominant families in pooled prairie vole fecal communities, followed by Lachnospiraceae (11.02%), Prevotellaceae (2.14%), Lactobacillaceae (1.44%), Saccharibacteria genera incertae sedis (1.28%), and Rikenellaceae (1.24%). All other families comprised less than 1% of prairie vole fecal communities. Families contained in “Other” made up less than 0.1% of fecal communities.



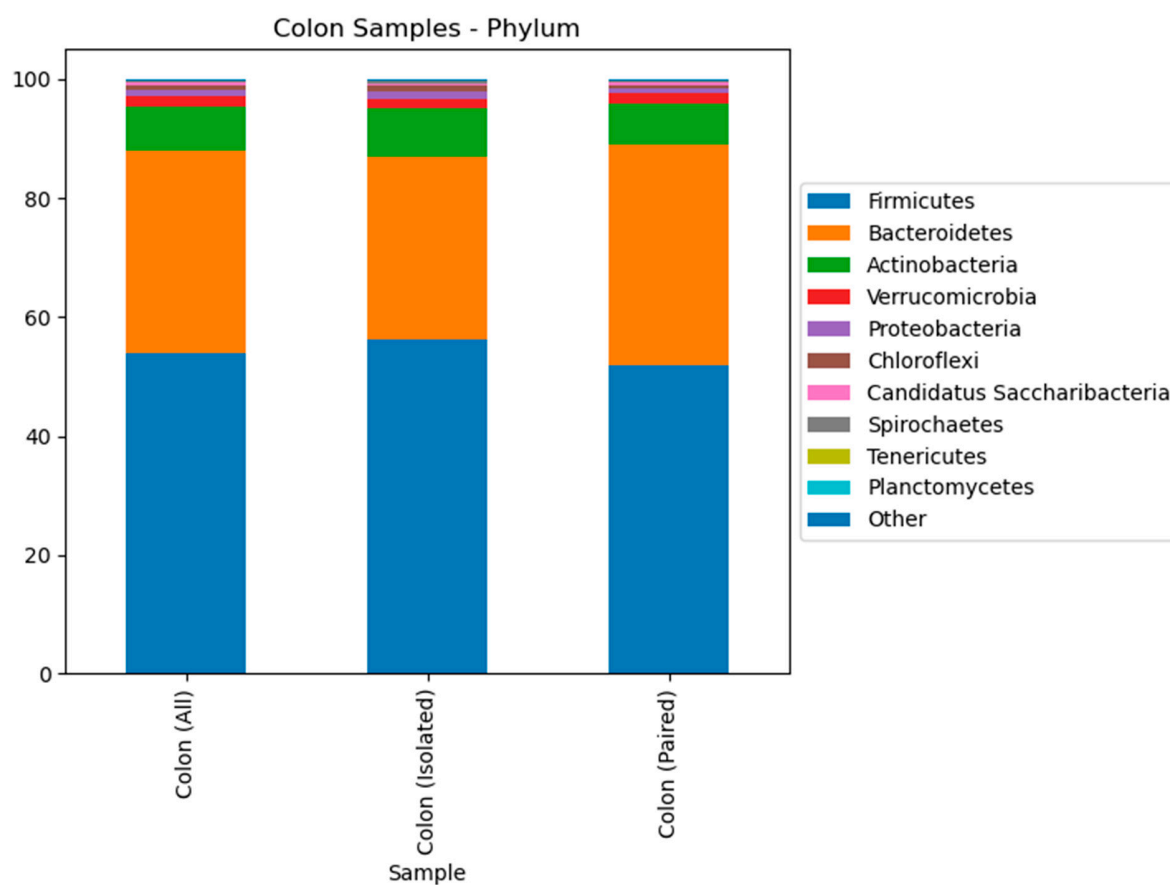
**Supplemental Figure S3.** LEfSe analyses revealed numerous differences in the fecal communities of paired (N = 55) and isolated prairie voles (N = 53). Paired voles had a greater proportional abundance of *Anaerostipes*. Isolated voles had a greater proportional abundance of nine taxa, most notably *Metaprevotella*, *Staphylococcaceae*, and *Enterococcus*.



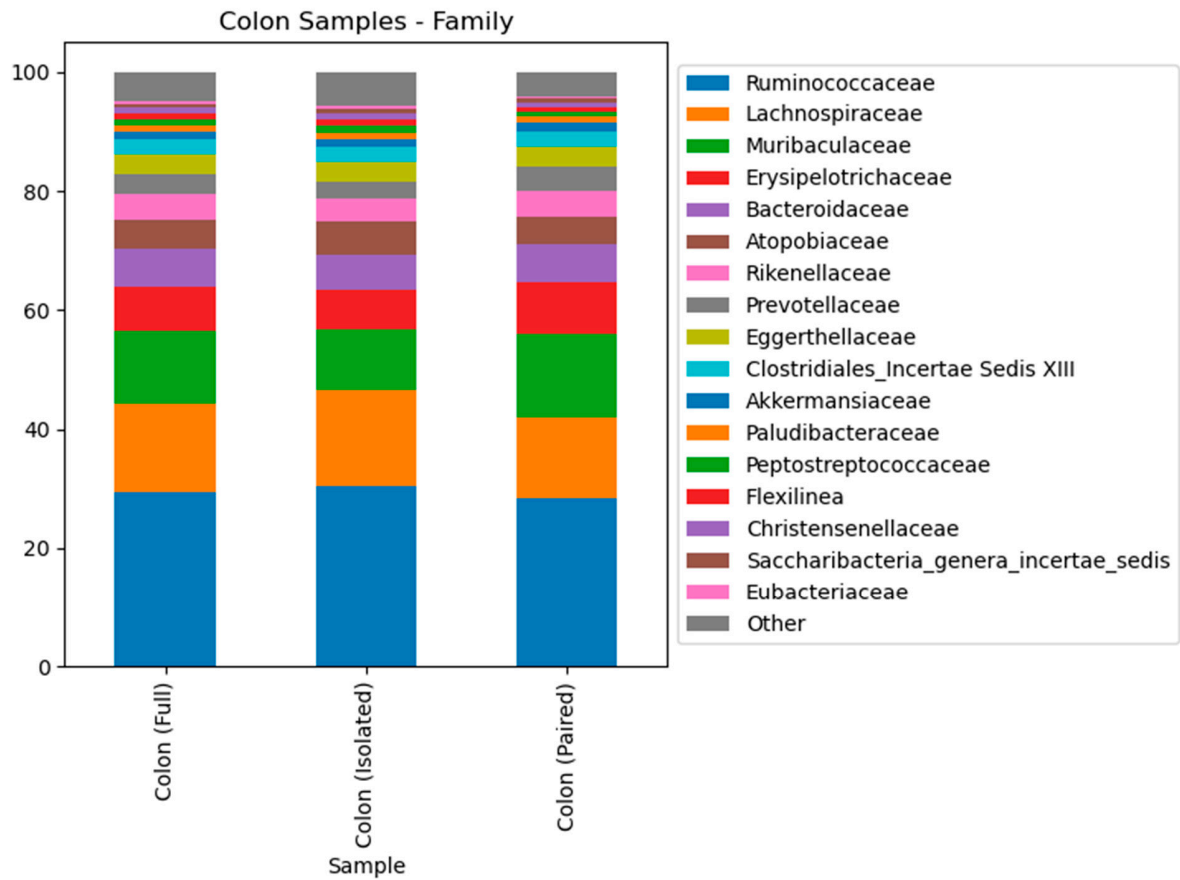
**Supplemental Figure S4.** Variations in taxa in isolated voles begin to emerge at T3 and T4.



**Supplemental Figure S5.** Variations in taxa in paired voles begin to emerge at T3 and T4.

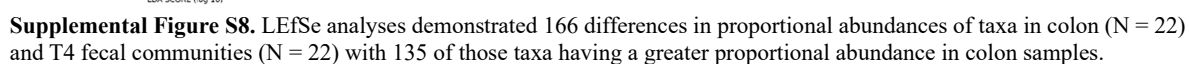


**Supplemental Figure S6.** Firmicutes (54.04%) and Bacteroidetes (33.895%) were the dominant phyla in pooled colon communities followed by Actinobacteria (7.496%), Verrucomicrobia (1.71%), and Proteobacteria (1.06%). All other phyla comprised less than 1% of prairie vole colon communities. Phyla contained in “Other” made up less than 0.05% of colon communities



**Supplemental Figure S7.** Ruminococcaceae (29.34%), Lachnospiraceae (14.95%), Muribaculaceae (12.19%) were the dominant families in pooled colon fecal samples followed by Erysipelotrichaceae (7.5%), Bacteroidaceae (6.24%), Atopobiaceae (5.07%), Rikenellaceae (4.16%), Prevotellaceae (3.46%), Eggerthellaceae (3.17%), Clostridiales\_Incertae Sedis XIII (2.62%), Akkermansiaceae (1.38%), Paludibacteraceae (1.05%), and Peptostreptococcaceae (1%). All other families comprised less than 1% of colon communities. Families contained in “Other” made up less than 0.1% of colon communities





**Supplemental Figure S8.** LEfSe analyses demonstrated 166 differences in proportional abundances of taxa in colon (N = 22) and T4 fecal communities (N = 22) with 135 of those taxa having a greater proportional abundance in colon samples.