

**Supplementary Table S3.** Mean relative abundances of bacterial genera in ruminal samples of cows when fed a concentrate formulated with cold-pressed rapeseed cake or a control concentrate

Genus	Treatment		SEM	P-value
	CTR	CPRC		
<i>Prevotella</i> <sup>1</sup>	37.1	47.6	4.46	0.1194
<i>Ruminococcus</i> <sup>4</sup>	1.89	1.45	0.142	0.0468
<i>Clostridium</i> <sup>1</sup>	0.31	0.21	0.040	0.0989
<i>Anaerovibrio</i> <sup>1</sup>	0.07	0.09	0.012	0.3404
<i>Succinivasticum</i> <sup>2</sup>	0.59	0.48	0.073	0.3102
<i>Pyramidobacter</i> <sup>2</sup>	-0.97	-1.16	0.067	0.0717
<i>Treponema</i> <sup>3</sup>	0.51	0.58	0.103	0.6045
<i>Desulfovibrio</i> <sup>1</sup>	0.10	0.08	0.012	0.3026
<i>Acetobacter</i> <sup>2</sup>	-0.95	-1.05	0.096	0.4855
<i>p-75-a5</i> <sup>2</sup>	-1.21	-1.43	0.054	0.0132
<i>Bulleidia</i> <sup>2</sup>	-1.28	-1.41	0.109	0.4216
<i>Mogibacterium</i> <sup>2</sup>	-0.82	-0.91	0.096	0.5429
<i>Shuttleworthia</i> <sup>2</sup>	-0.99	-1.28	0.095	0.0506
<i>Pseudobutyribacter</i> <sup>2</sup>	-0.75	-0.91	0.195	0.5877
<i>Lachnospira</i> <sup>2</sup>	-1.45	-1.47	0.195	0.9362
<i>Coprococcus</i> <sup>2</sup>	-0.42	-0.52	0.098	0.4953
<i>Butyrivibrio</i> <sup>1</sup>	5.9	4.8	0.98	0.4197
<i>Blautia</i> <sup>1</sup>	0.10	0.06	0.015	0.0459
<i>SHD231</i> <sup>2</sup>	-1.04	-1.09	0.104	0.7324
<i>YRC22</i> <sup>1</sup>	0.68	0.96	0.158	0.2319
<i>CF231</i> <sup>1</sup>	0.20	0.22	0.042	0.8229
<i>Bifidobacterium</i> <sup>2</sup>	-1.53	-2.06	0.373	0.3310
<i>Vadin CA11</i> <sup>2</sup>	-1.09	-0.81	0.161	0.2315
<i>Methanobrevibacter</i> <sup>2</sup>	0.02	0.09	0.083	0.5507
<i>Methanospaera</i> <sup>2</sup>	-1.21	-1.07	0.102	0.3411
<i>UG_Coriobacteriaceae</i> <sup>2</sup>	-0.65	-0.76	0.106	0.4999
<i>UG_Bacteroidales</i> <sup>1</sup>	4.4	4.0	0.54	0.5688
<i>UG_BS11</i> <sup>1</sup>	1.53	1.49	0.247	0.9092
<i>UG_RF16</i> <sup>1</sup>	0.04	0.05	0.012	0.7448
<i>UG_S247</i> <sup>1</sup>	1.45	1.33	0.293	0.7592
<i>UG_Ys2</i> <sup>1</sup>	0.11	0.12	0.031	0.9226
<i>UG_Paraprevotellaceae</i> <sup>1</sup>	0.13	0.12	0.024	0.6910
<i>UG_Clostridiales</i> <sup>2</sup>	0.94	0.71	0.056	0.0160
<i>UG_Christensenellaceae</i> <sup>2</sup>	-0.45	-0.64	0.057	0.0331
<i>UG_Clostridiaceae</i> <sup>2</sup>	-1.28	-1.29	0.091	0.9358
<i>UG_Lachnospiraceae</i> <sup>2</sup>	-0.91	-1.16	0.059	0.0110
<i>UG_Ruminococcaceae</i> <sup>4</sup>	0.14	0.19	0.015	0.0344
<i>UG_Veillonaceae</i> <sup>2</sup>	0.035	-0.003	0.0936	0.7783
<i>UG_Mogibacteriaceae</i> <sup>1</sup>	0.42	0.34	0.042	0.2259
<i>UG_Pirellulaceae</i> <sup>1</sup>	1.26	0.84	0.144	0.0553
<i>UG_Rickettsiales</i> <sup>2</sup>	-1.35	-1.57	0.104	0.1549
<i>UG_Succinivibrionaceae</i> <sup>2</sup>	-1.02	-0.76	0.127	0.1651
<i>UG_RF16</i> <sup>1</sup>	4.60	3.46	0.683	0.2553
<i>UG_RF39</i> <sup>2</sup>	-0.47	-0.67	0.061	0.0243
<i>UG_RFP12</i> <sup>2</sup>	-0.72	-0.86	0.077	0.2434
<i>UG_WCHB125</i> <sup>2</sup>	-0.90	-1.08	0.084	0.1565

CTR: Control; CPRC: cold-pressed rapeseed cake; <sup>1</sup>Untransformed data; <sup>2</sup>Log transformation; <sup>3</sup> square root transformation; <sup>4</sup>reciprocal transformation; SEM: standard error of the mean