

**Table S1: Breakdown of select genes and corresponding KEGG ID analyzed.**

KEGG IDs	Gene Name
K00929	Butyrate Kinase
K01034	Acetate CoA subunit A
K01035	Acetate CoA subunit B
K01908	Propionyl-CoA Synthetase
K01895	Acetyl-CoA Synthetase
K00932	Propionate Kinase
K19697	Propionate Kinase
K18372	Methyl Acetate Hydrolase
K00467	Lactate 2-Monooxygenase
K00156	Pyruvate Dehydrogenase
K00925	Acetate Kinase
K01512	Acylphosphatase
K01067	Acetyl-CoA Hydrolase
K18118	Succinyl-CoA:Acetate
K01026	Propionate CoA-Transferase
K01905	Acetate—CoA Ligase subunit A
K22224	Acetate—CoA Ligase subunit B
K01895	Acetyl-CoA Synthetase
K00128	Aldehyde Dehydrogenase
K14085	Aldehyde Dehydrogenase Family 7
K00149	Aldehyde Dehydrogenase Family 9
K00138	Aldehyde Dehydrogenase

**Table S2: Breakdown of Kruskal-Wallis tests using PICRUSt imputed relative abundance of select genes in SCFA pathways.**

KEGG IDs	Rank Sum	Statistic	P-value	BH
K00929	0.102		0.950	0.997
K01026	0.058		0.971	0.997
K00467	0.054		0.973	0.997
K01908	0.053		0.974	0.997
K01035	0.049		0.976	0.997
K01905	0.042		0.979	0.997
K00128	0.032		0.984	0.997
K01512	0.030		0.985	0.997
K00156	0.025		0.988	0.997
K00925	0.024		0.988	0.997
K01067	0.024		0.988	0.997
K01895	0.023		0.988	0.997
K01034	0.005		0.997	0.997

**Table S3: Breakdown of Kruskal-Wallis tests using counts per million from metagenomic sequencing of select genes in SCFA pathways.**

KEGG IDs	Rank Sum Statistic	P-value	BH
K00925	4.212	0.122	0.730
K00128	1.726	0.422	0.762
K01067	1.690	0.429	0.762
K01512	0.989	0.610	0.762
K00156	0.754	0.686	0.762
K00929	0.543	0.762	0.762