Relative Abundance Heatmap | Product
pval < 0.05 different between fiber_cat using MannWhitneyWilcoxon
Feature must be >50PPM in at least 20% of samples
Number of samples in heatmap = 94 | Number of features assessed = 2036
log2foldchange > 1 | log2foldchange > Inf
Positive l2fc means increased in Sufficient_intake

fiber_cat

	p	FDR p	geom_mean Log2FC
etylbacillosaminyl–diphospho–undecaprenol alpha–1%2C3–N–acetylgalactosaminyltransferase–pglA	0.002	1.000	1.1
Autoinducer 2 sensor kinase/phosphatase LuxQ–luxQ	0.002	1.000	1.1
Putative fimbrium tip subunit Fim1C–none	0.014	1.000	1.2
IS91 family transposase ISAzo26–none	0.039	1.000	1
Transcriptional regulatory protein NatR–natR	0.001	1.000	1.3
Transcriptional regulatory protein QseF–qseF	0.006	1.000	1.5
IPT/TIG domain–containing protein–none	0.030	1.000	1.1
Xyloglucan–specific endo–beta–1%2C4–glucanase BoGH5A–none	0.025	1.000	1.2
Type–1 restriction enzyme EcoKI specificity protein–hsdS	0.009	1.000	1.3
IS1380 family transposase IS613–none	0.010	1.000	1.9
–mannose–dependent alpha–(1–6)–phosphatidylinositol monomannoside mannosyltransferase–pimB	0.009	1.000	1.5
Metal–pseudopaline receptor CntO–cntO	0.029	1.000	–1
Phosphoribosylformylglycinamidine synthase subunit PurL–purL	0.044	1.000	–1.3
Glutamate synthase [NADPH] large chain–gltA	0.018	1.000	–1.6
ISAs1 family transposase ISBf9–none	0.035	1.000	1.1
Chitobiase–chb	0.004	1.000	1.9
ISL3 family transposase ISAcma23–none	0.027	1.000	1.6
UDP–N–acetylglucosamine 2–epimerase–mnaA	0.038	1.000	1.8

fiber_cat

Insufficient_intake
Sufficient_intake

Parts Per Million

0 PPM   4 PPM   10.9 PPM   20.9 PPM   44 PPM   61.75 PPM   82.6 PPM   123.2 PPM   7213 PPM