

Relative Abundance Heatmap | LKT
 pval < 0.05 different between Group using MannWhitneyWilcoxon
 Feature must be >250PPM in at least 15% of samples
 Taxonomy information must come from >70% contigs in at least 50% of samples
 Taxon genome completeness must be >10% in at least 5% of samples
 Number of samples in heatmap = 32 | Number of features assessed = 277
 log2foldchange > 1 | log2foldchange > Inf
 Positive l2fc means increased in ME/CFS



