Relative Abundance Heatmap I LKT padj fdr < 0.05 different between Diet using MannWhitneyWilcoxon Feature must be >250PPM in at least 15% of samples Taxonomy information must come from >25% contigs in at least 10% of samples Taxon genome completeness must be >10% in at least 5% of samples Number of samples in heatmap = 40 | Number of features assessed = 77 log2foldchange > 1.5 | log2foldchange > Inf Positive I2fc means increased in Fiber Rich



