

# Freeze-dried vs Frozen samples taxonomy composition

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## Introduction

In this study, we want to investigate if Freeze Dried samples give the same data as samples stored at -80 freezer prior library preparation. We ask if relative abundance differ between the two sample types.

## Methods

We took 20 replicate samples from our fecal samples stored in -80 and freeze dried them at the Kalahari Research Centre for 48 h. Freeze Dried samples were then transported and stored at room temperature until 16S library preparation of fecal samples and randomized on three sequencing plates together with their replicates. On all three plates, 4 negative controls were used to remove contaminant reads from samples before further analysis.

## Results

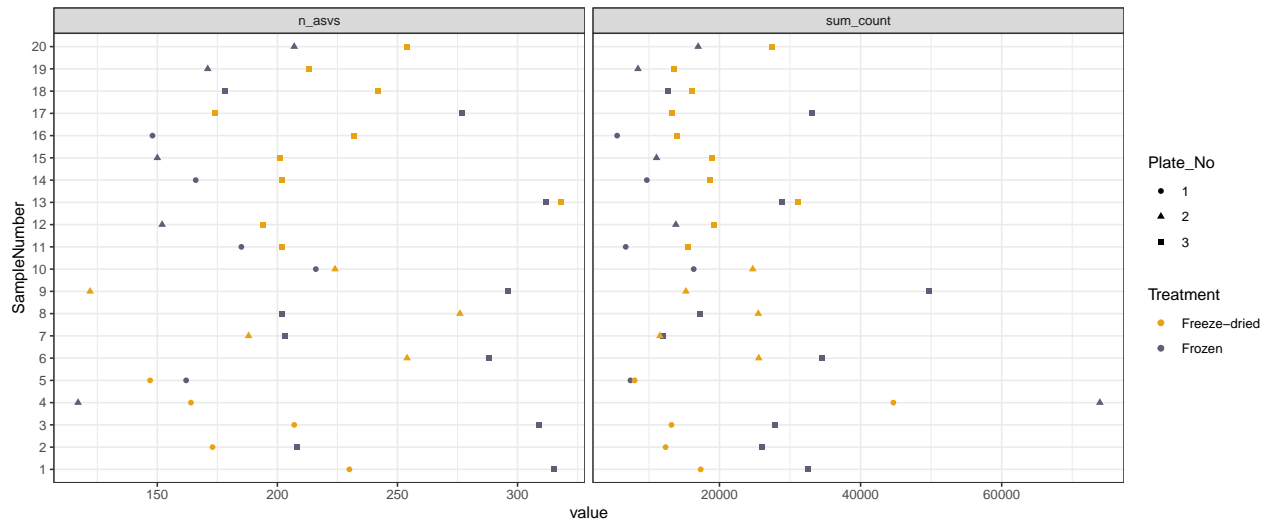


Figure 1: Sequencing depth and number of unique ASVs per sample. Colour by Sample Type.

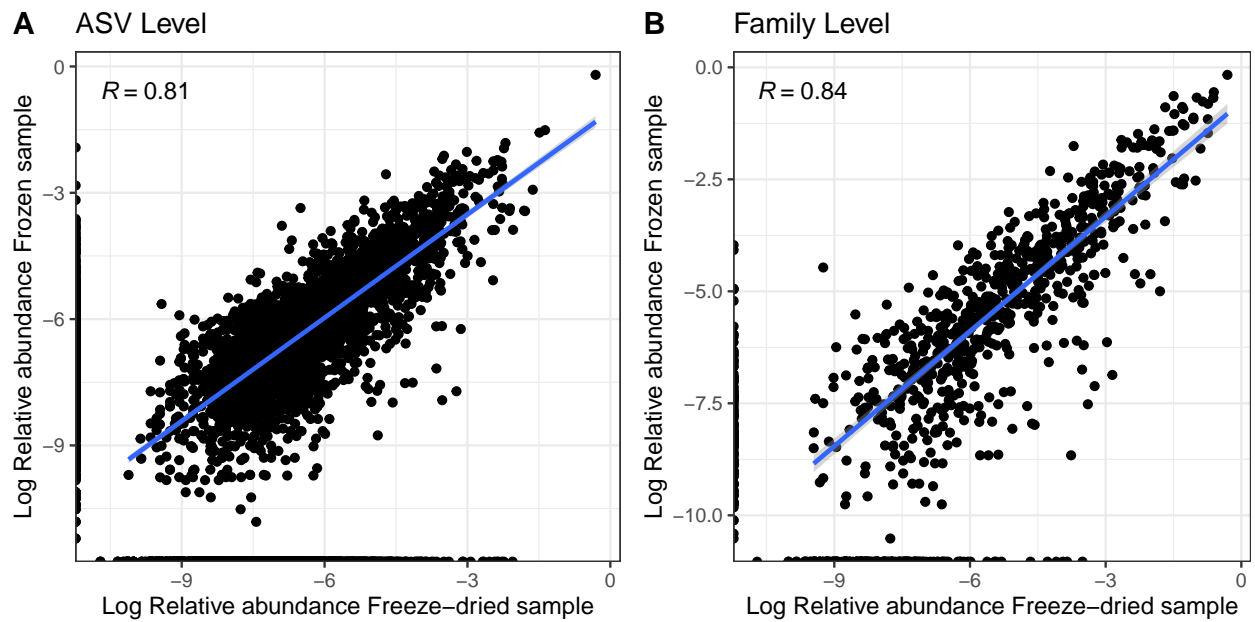


Figure 2: \*\* Correlation relative abundance within sample by sample storage method on n ASV (A) and Family (B) level.\*\*

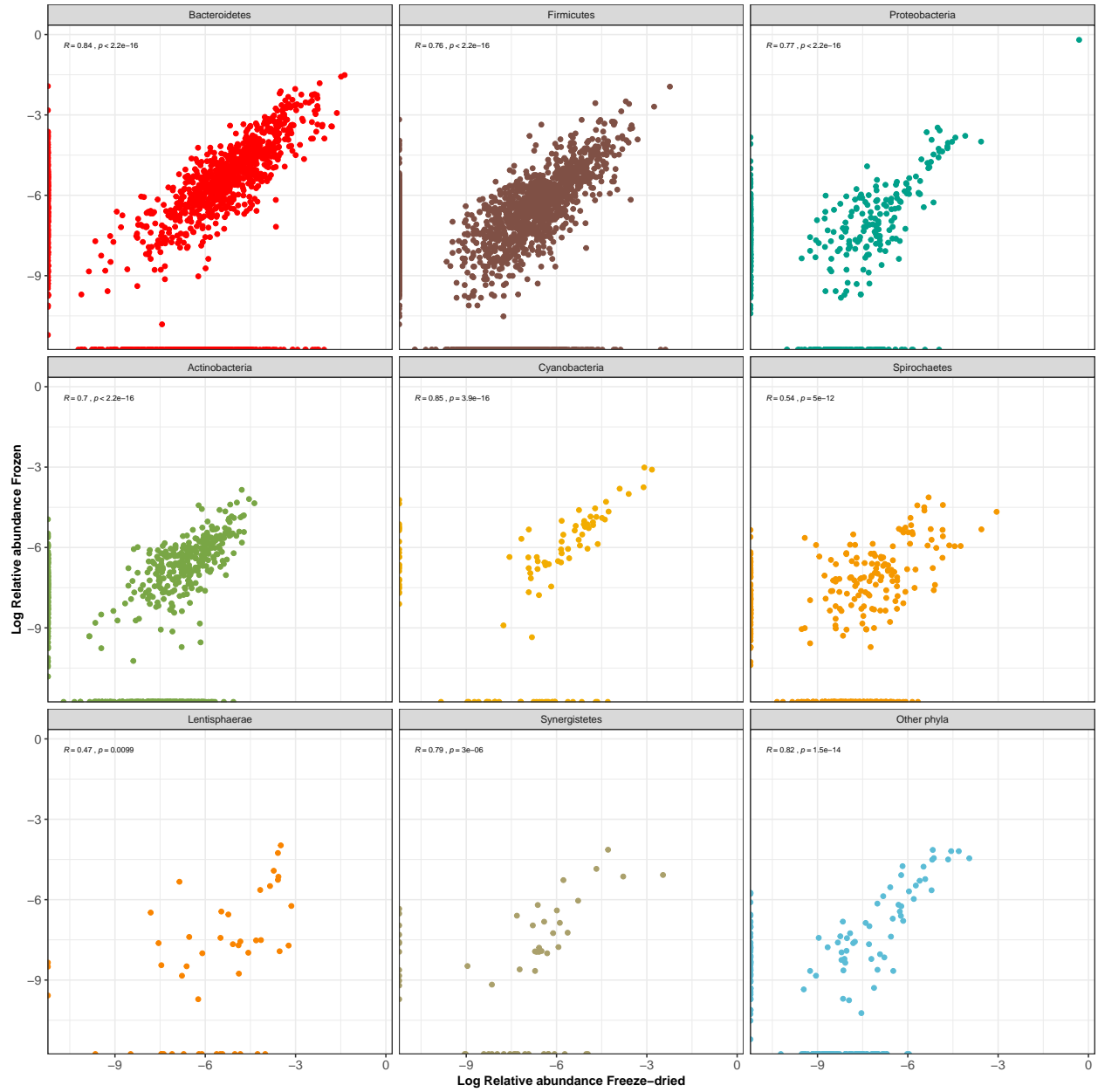


Figure 3: **Correlation relative abundance within sample by sample treatment on n ASV level.** Facet by phylum, colour by top 10 phyla.

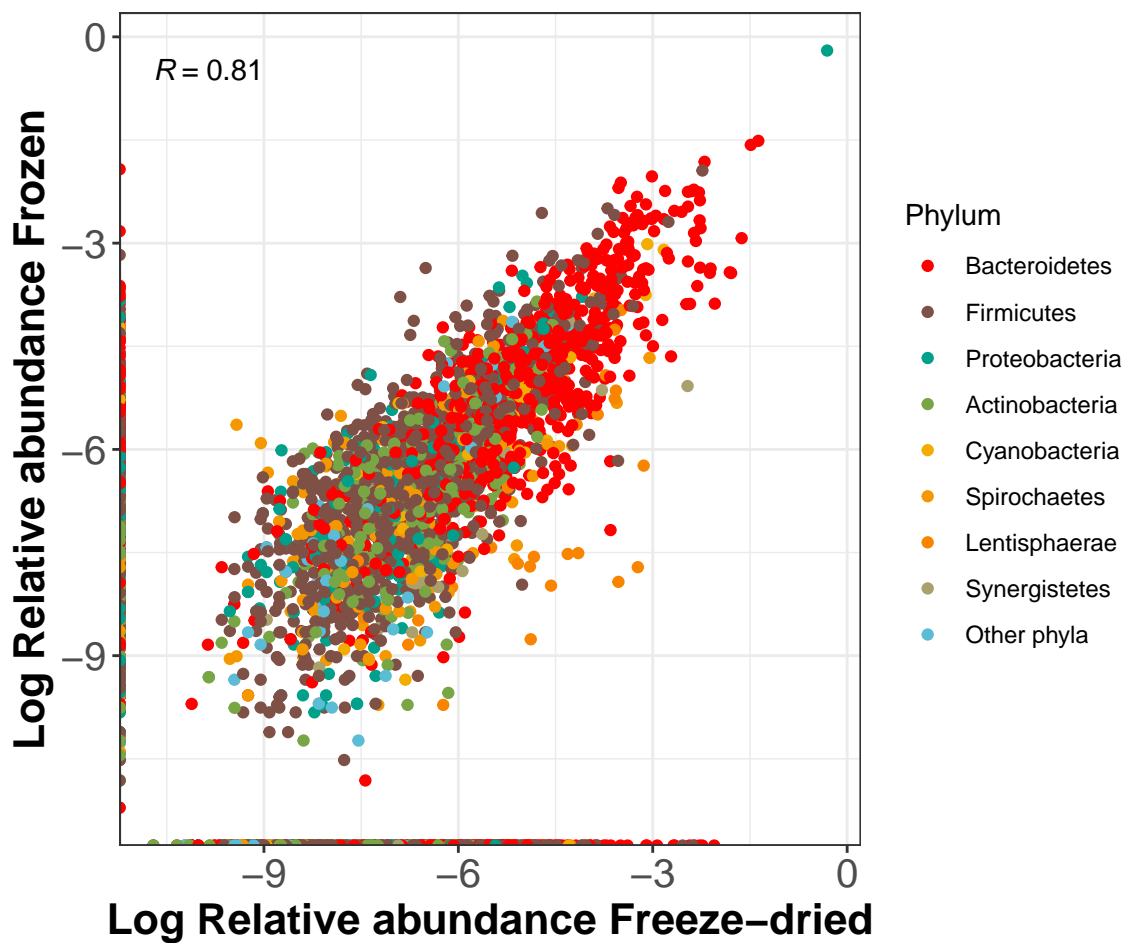


Figure 4: Correlation relative abundance within sample by sample treatment on n ASV level colour by top 10 phyla.

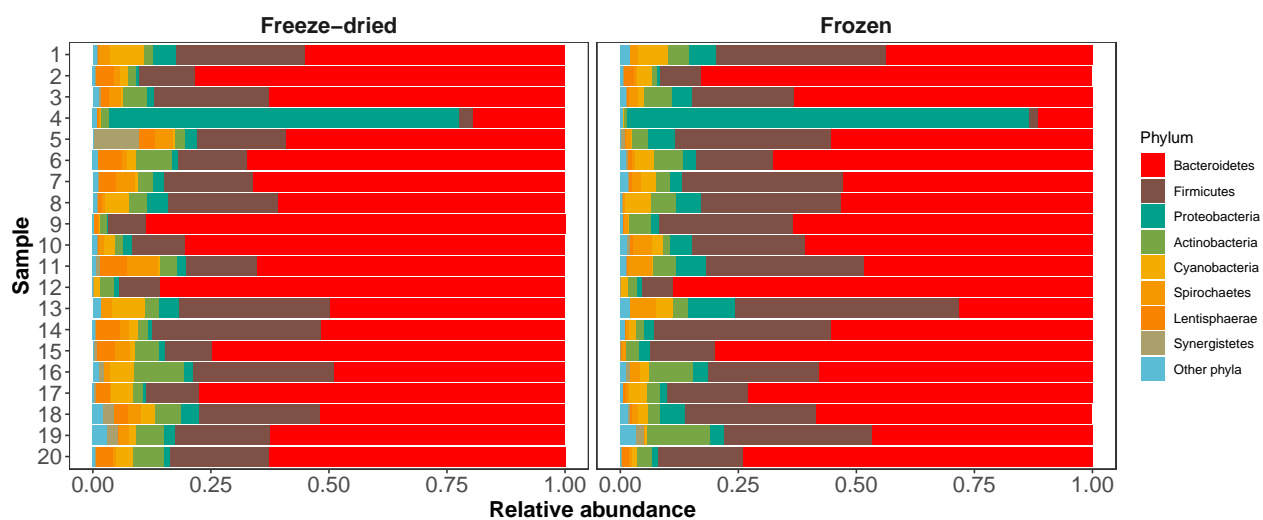


Figure 5: Stacked bar taxaplot per sample top 8 relab phylum. Sample 4 has very high relab of Proteobacteria.

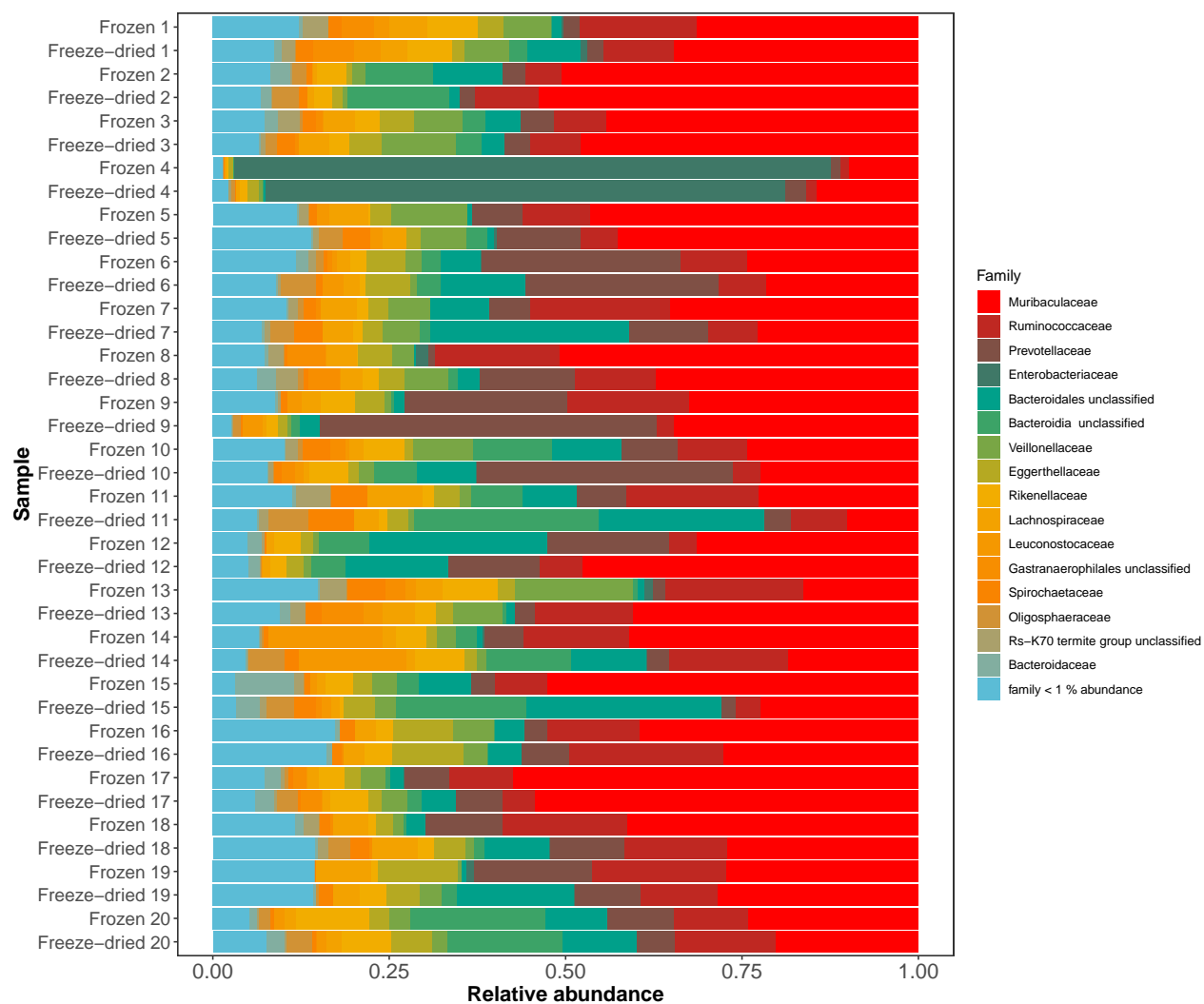


Figure 6: Stacked bar taxaplot per sample families with mean relab > 1 %.

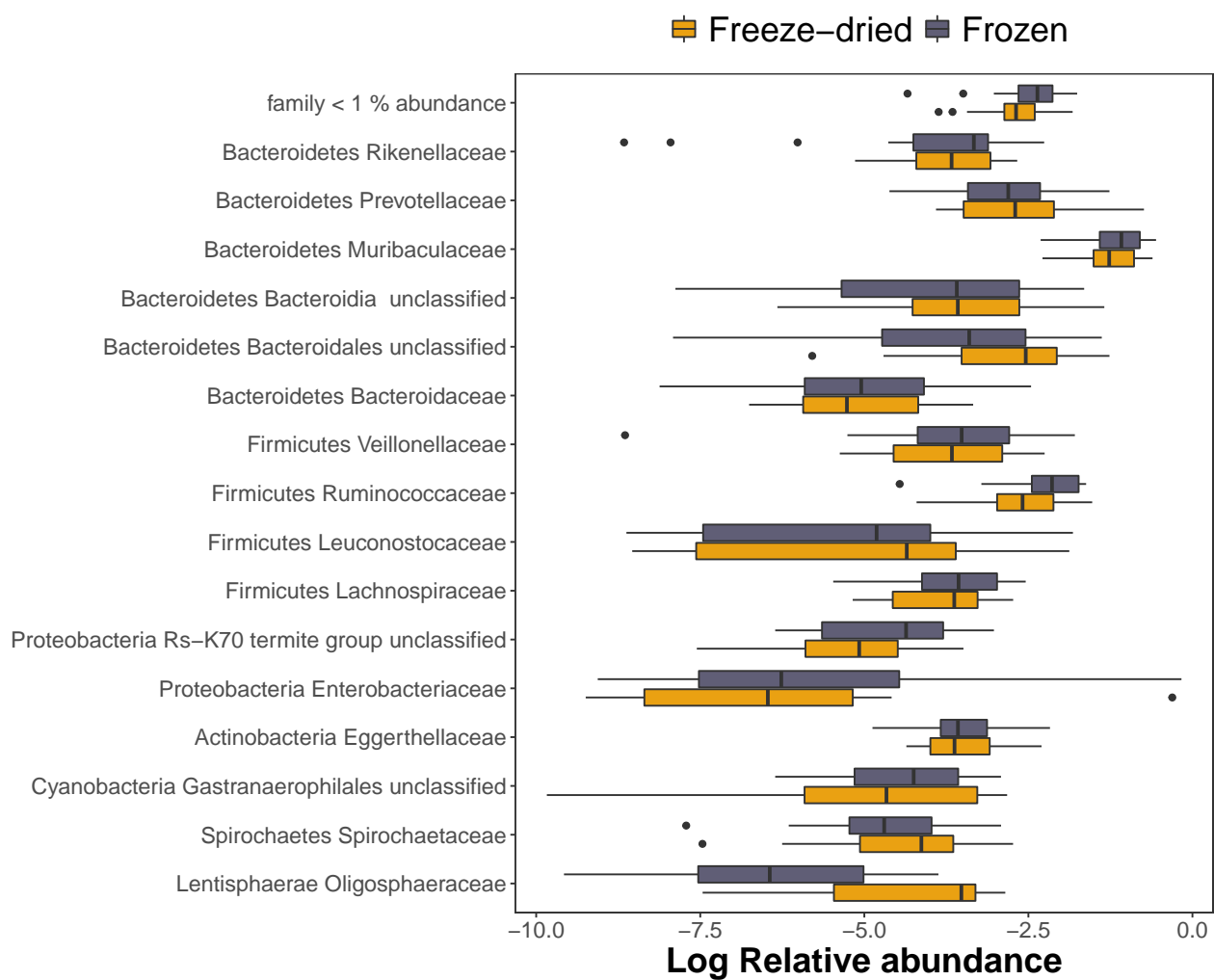


Figure 7: **Box plot taxaplot** per sample families with mean relab > 1 %.

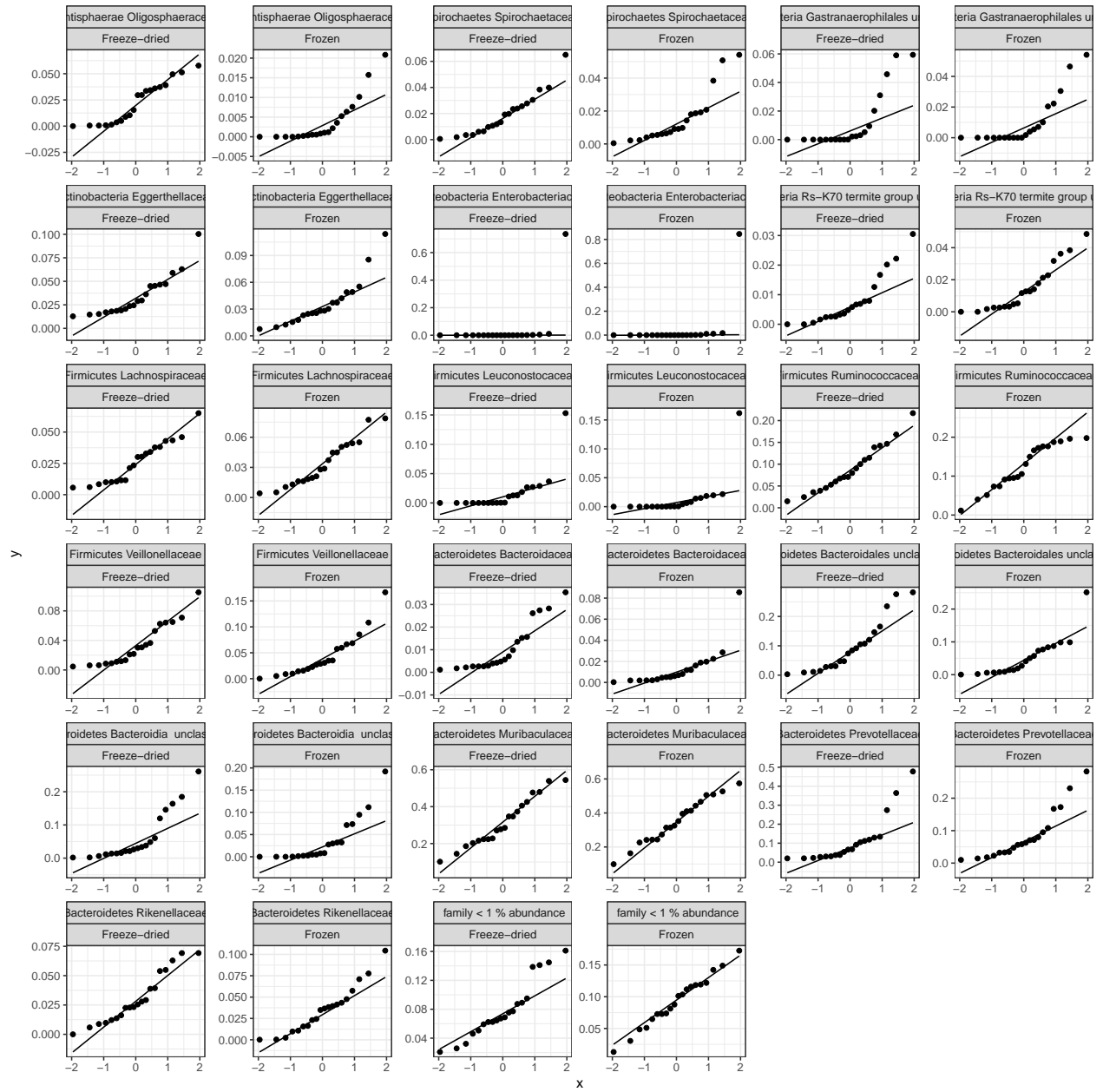


Figure 8: qqplot family level relab.