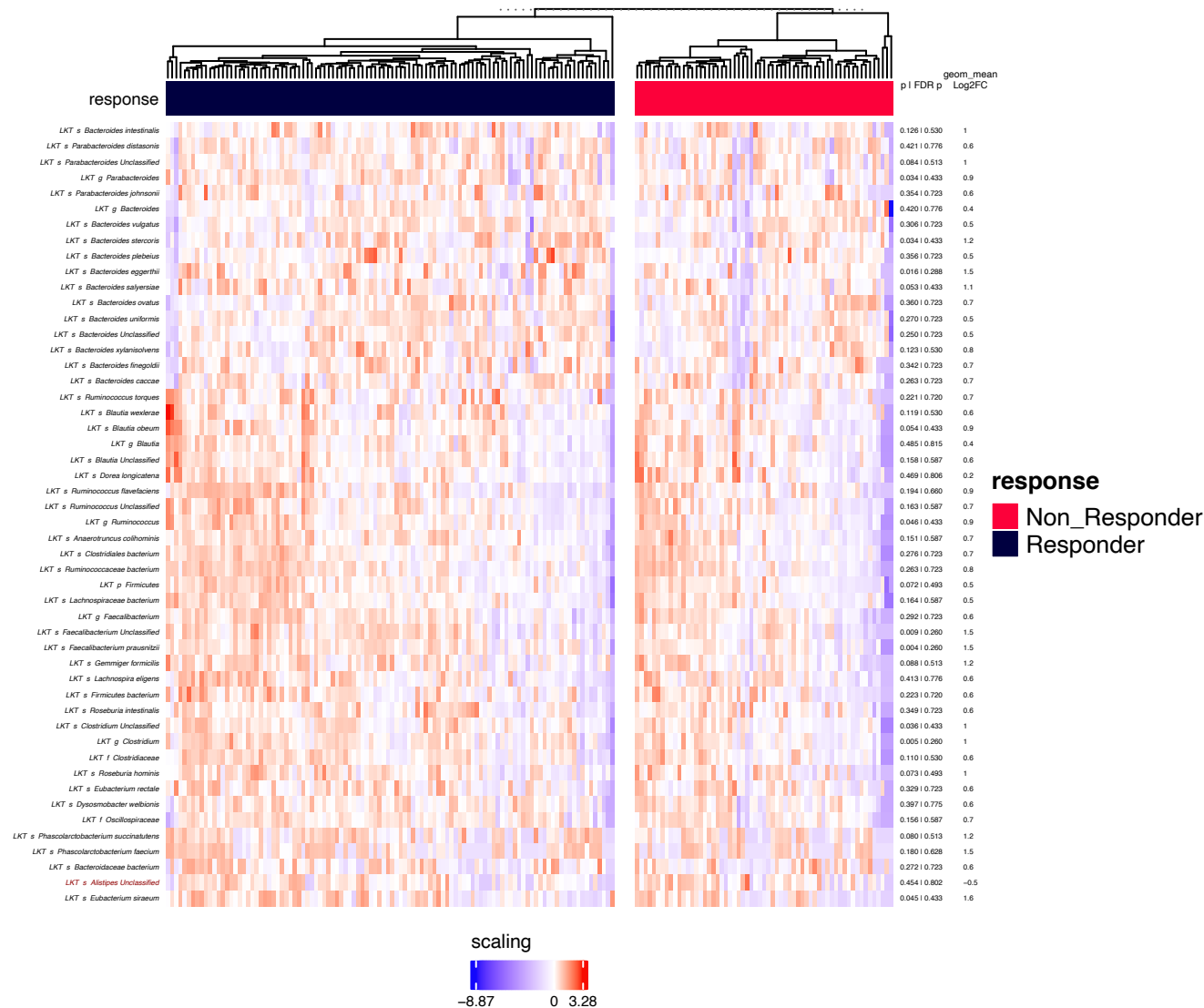
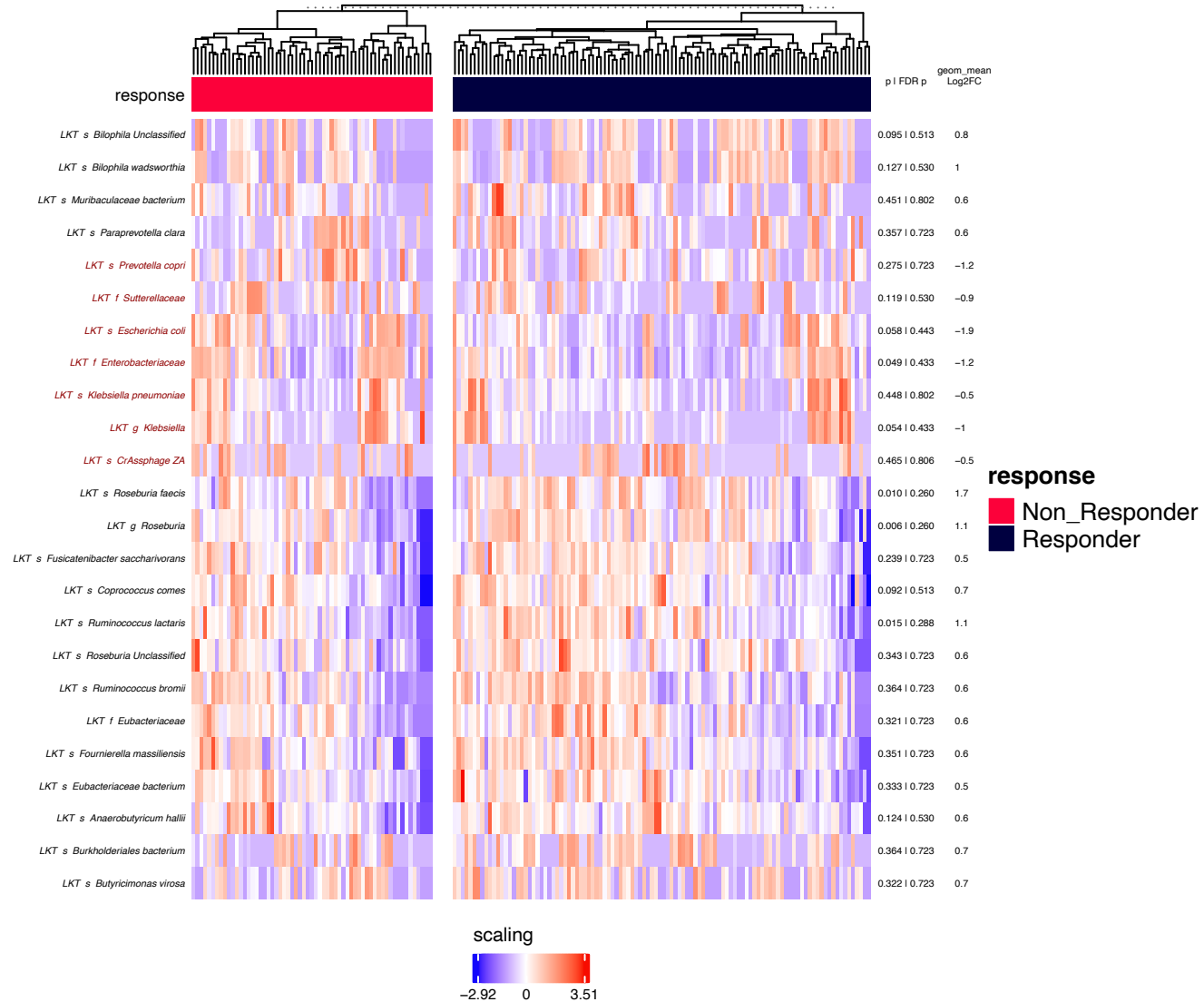


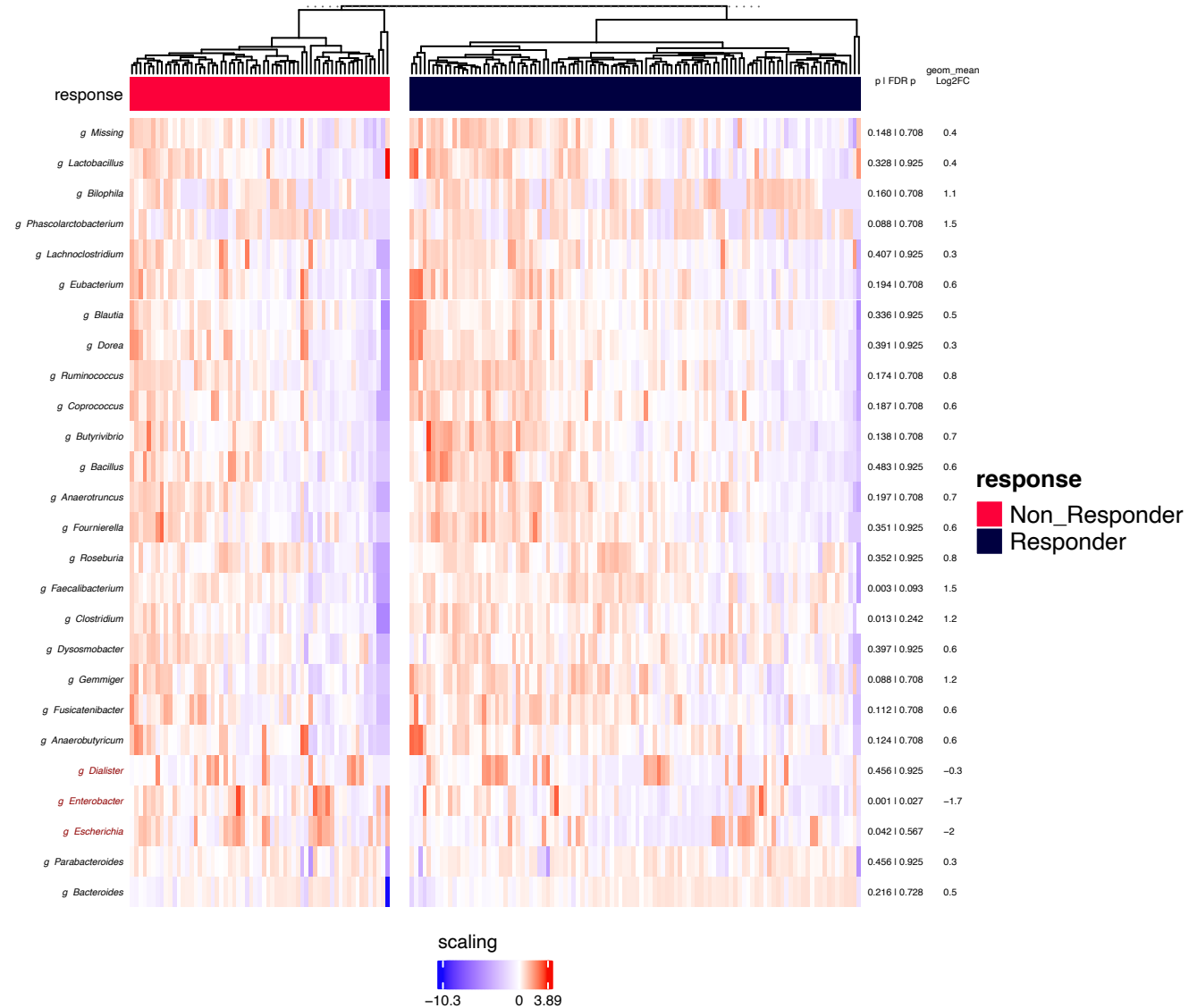
Relative Abundance Heatmap | LKT
 pval < 0.5 different between response using MannWhitneyWilcoxon
 Feature must be >250PPM in at least 15% of samples
 Taxonomy information must come from >25% contigs in at least 10% of samples
 Taxon genome completeness must be >10% in at least 5% of samples
 Number of samples in heatmap = 167 | Number of features assessed = 129
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder
 Heatmap 1/2



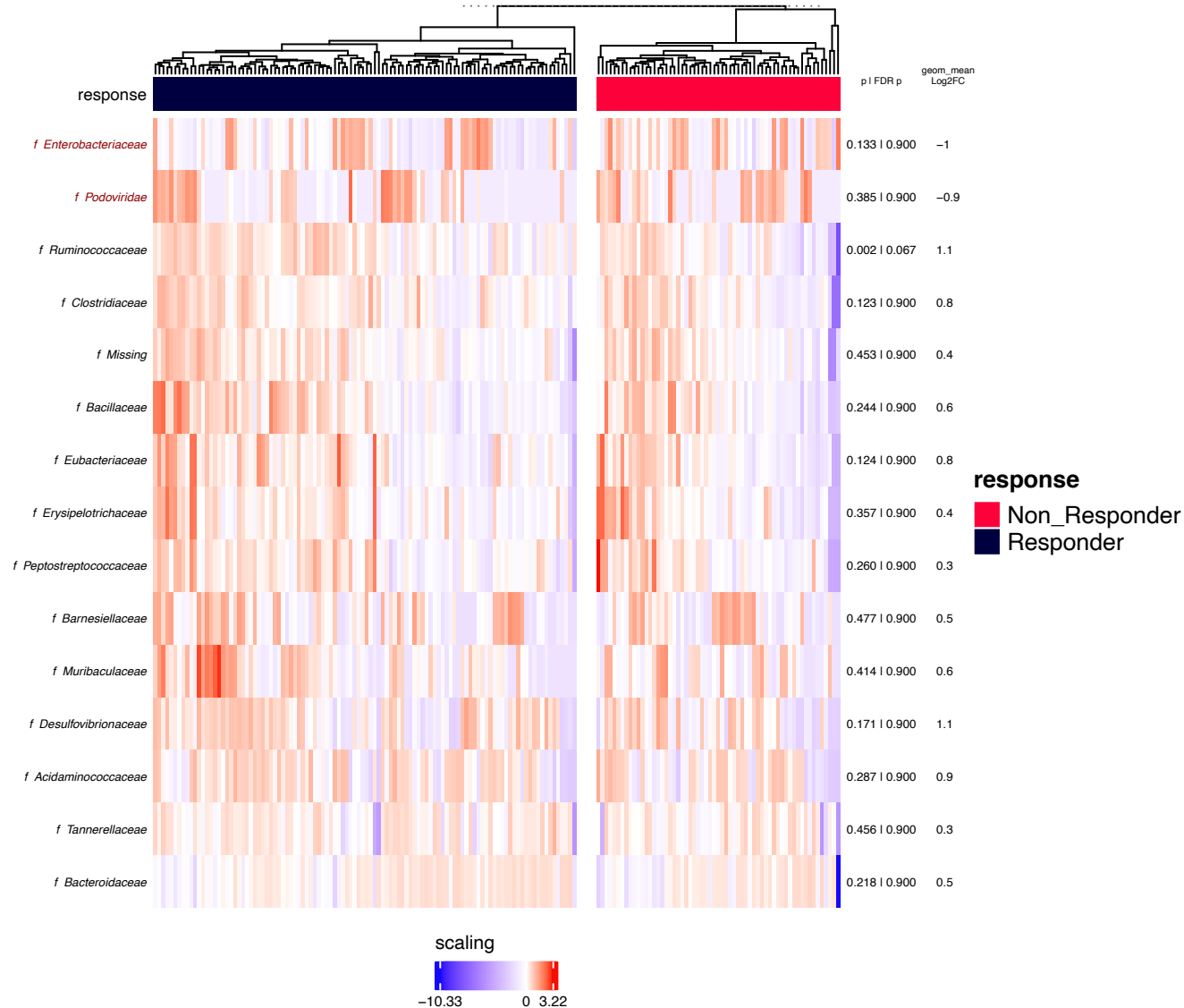
Relative Abundance Heatmap | LKT
 pval < 0.5 different between response using MannWhitneyWilcoxon
 Feature must be >250PPM in at least 15% of samples
 Taxonomy information must come from >25% contigs in at least 10% of samples
 Taxon genome completeness must be >10% in at least 5% of samples
 Number of samples in heatmap = 167 | Number of features assessed = 129
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder
 Heatmap 2/2



Relative Abundance Heatmap | Genus
 pval < 0.5 different between response 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 = 167 | Number of features assessed = 54
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Relative Abundance Heatmap | Family
 pval < 0.5 different between response 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 = 167 | Number of features assessed = 29
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Relative Abundance Heatmap | Class

pval < 0.5 different between response using MannWhitneyWilcoxon

Feature must be >250PPM in at least 15% of samples

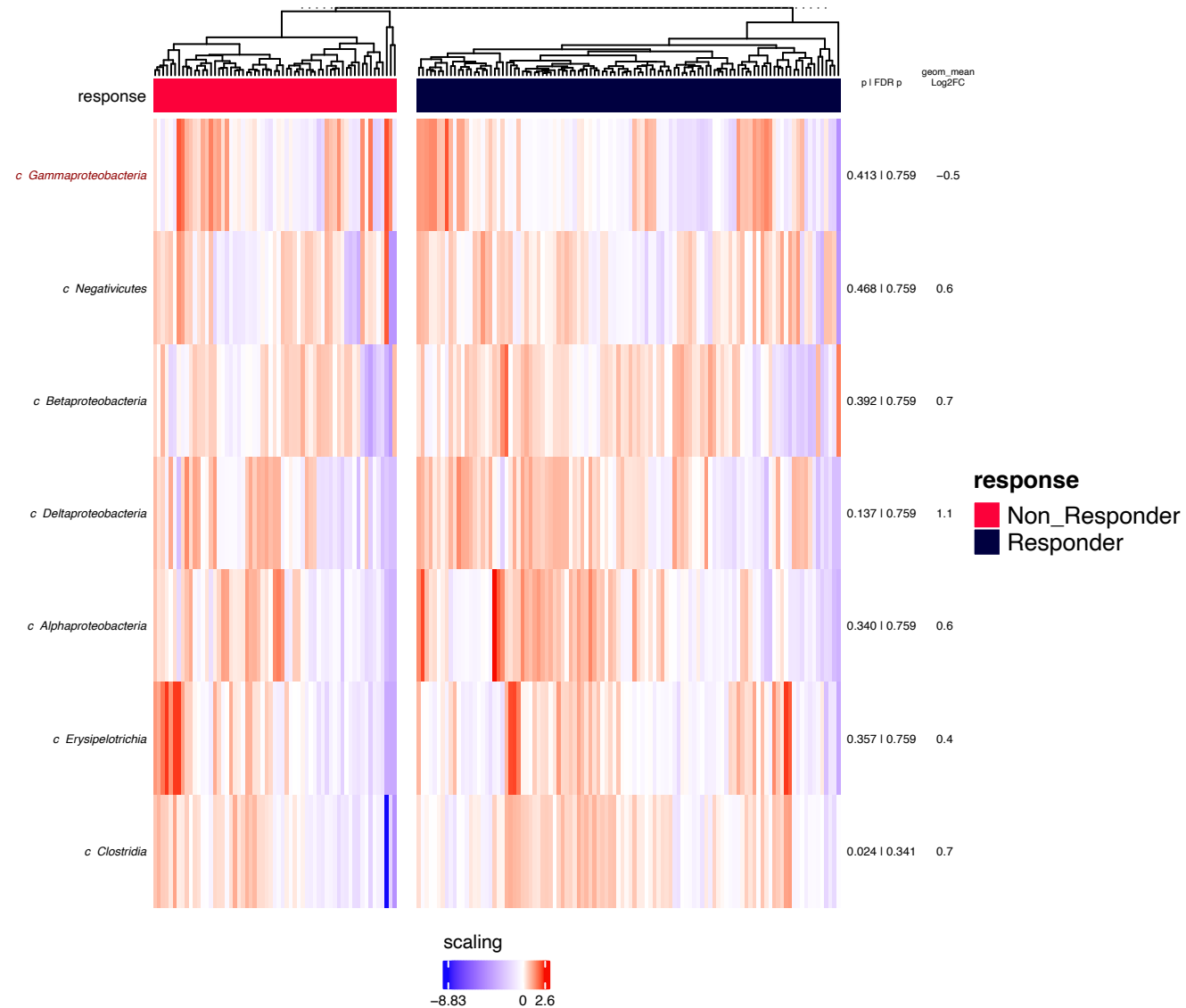
Taxonomy information must come from >25% contigs in at least 10% of samples

Taxon genome completeness must be >10% in at least 5% of samples

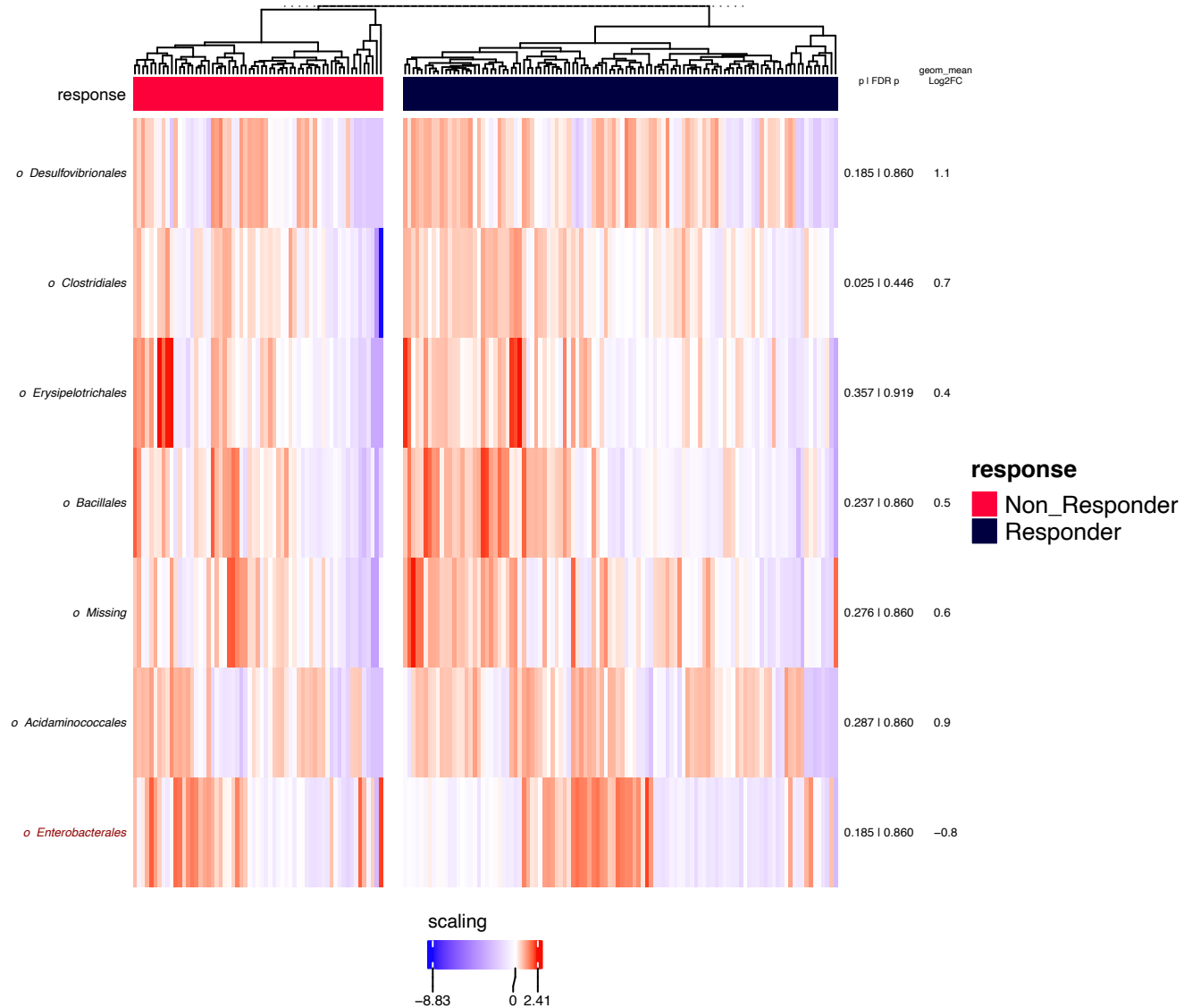
Number of samples in heatmap = 167 | Number of features assessed = 14

log2foldchange > 0.2 | log2foldchange > Inf

Positive l2fc means increased in Responder



Relative Abundance Heatmap | Order
 pval < 0.5 different between response 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 = 167 | Number of features assessed = 18
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Relative Abundance Heatmap | Phylum

pval < 0.5 different between response using MannWhitneyWilcoxon

Feature must be >250PPM in at least 15% of samples

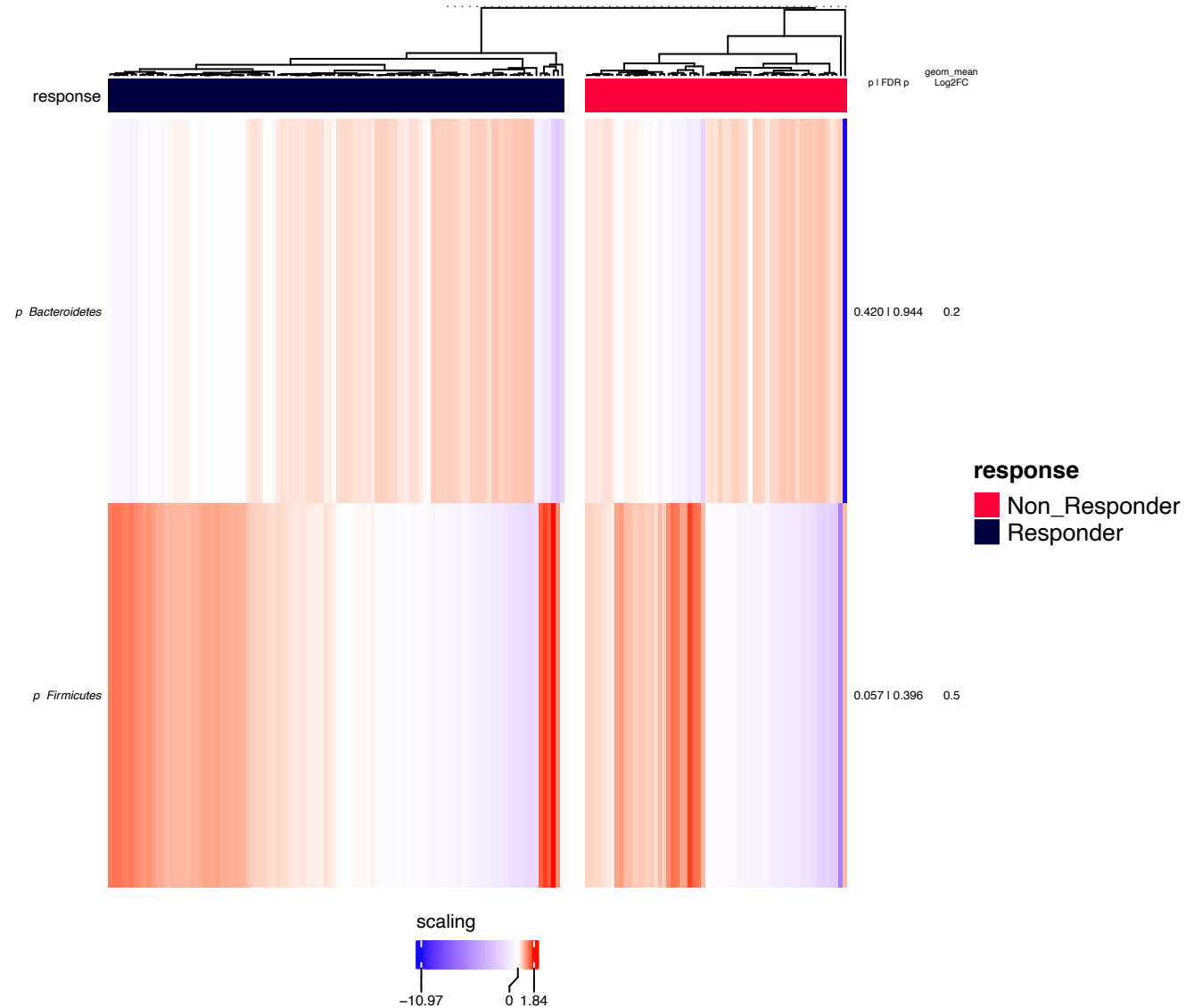
Taxonomy information must come from >25% contigs in at least 10% of samples

Taxon genome completeness must be >10% in at least 5% of samples

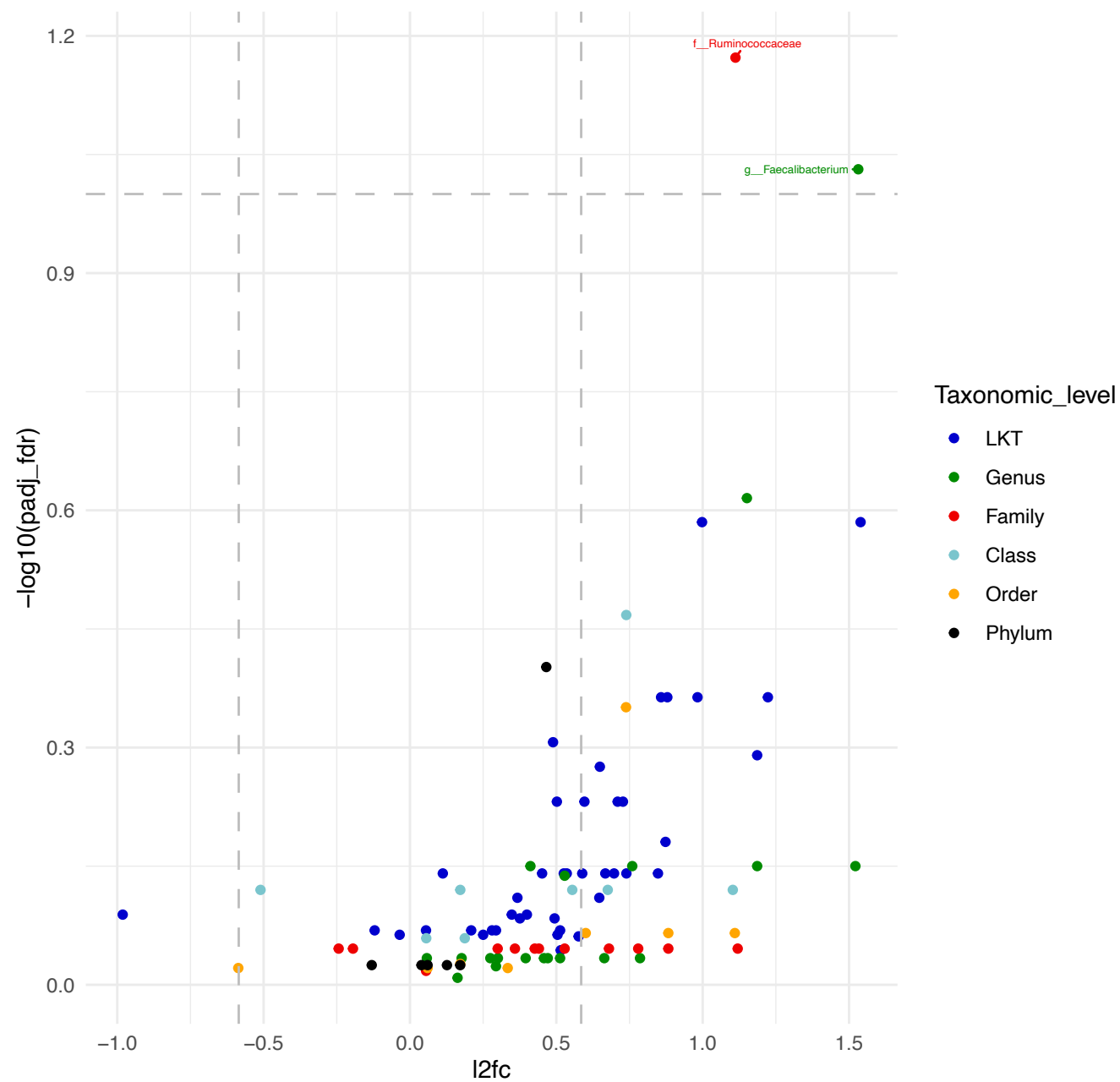
Number of samples in heatmap = 167 | Number of features assessed = 7

log2foldchange > 0.04 | log2foldchange > Inf

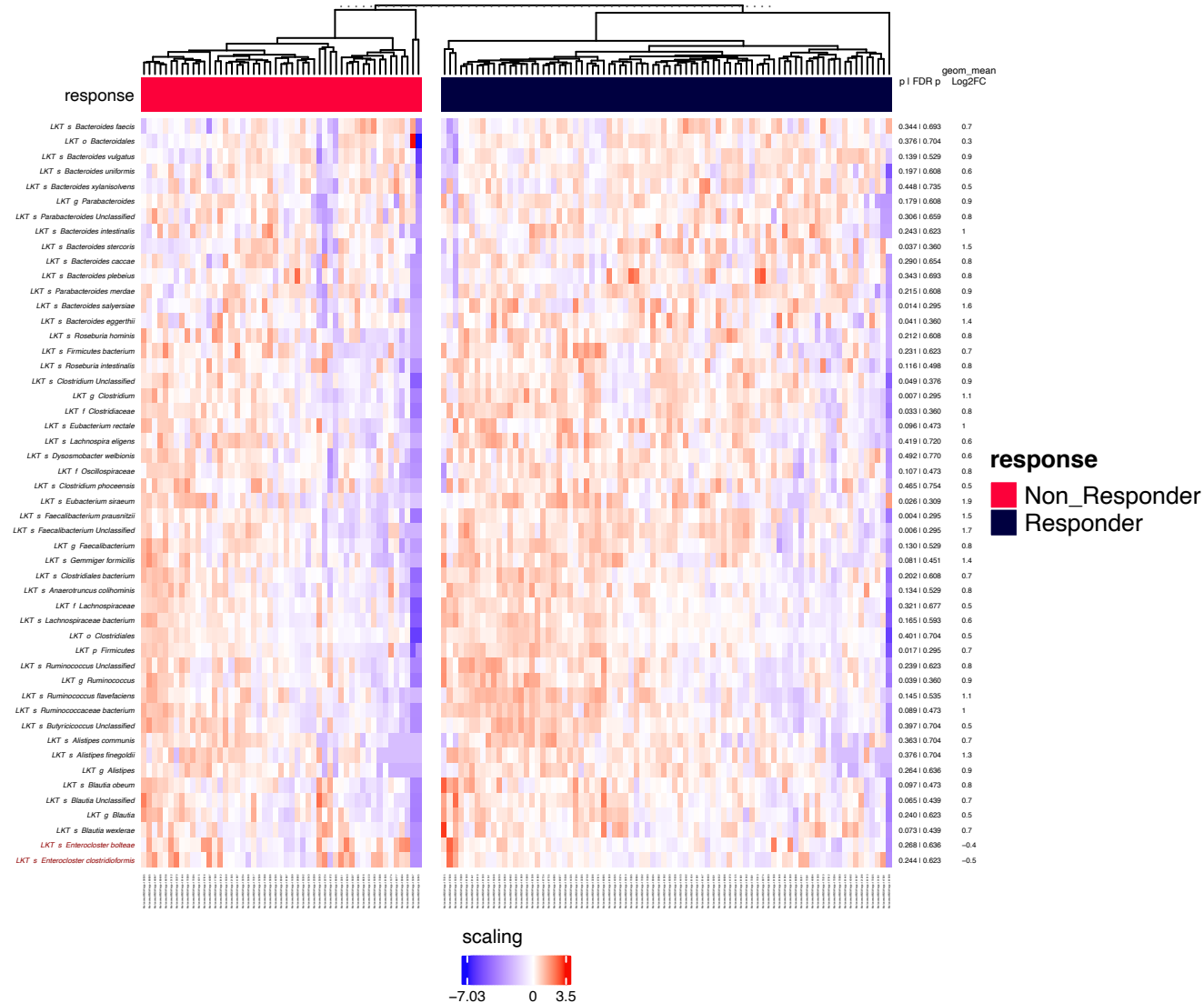
Positive l2fc means increased in Responder



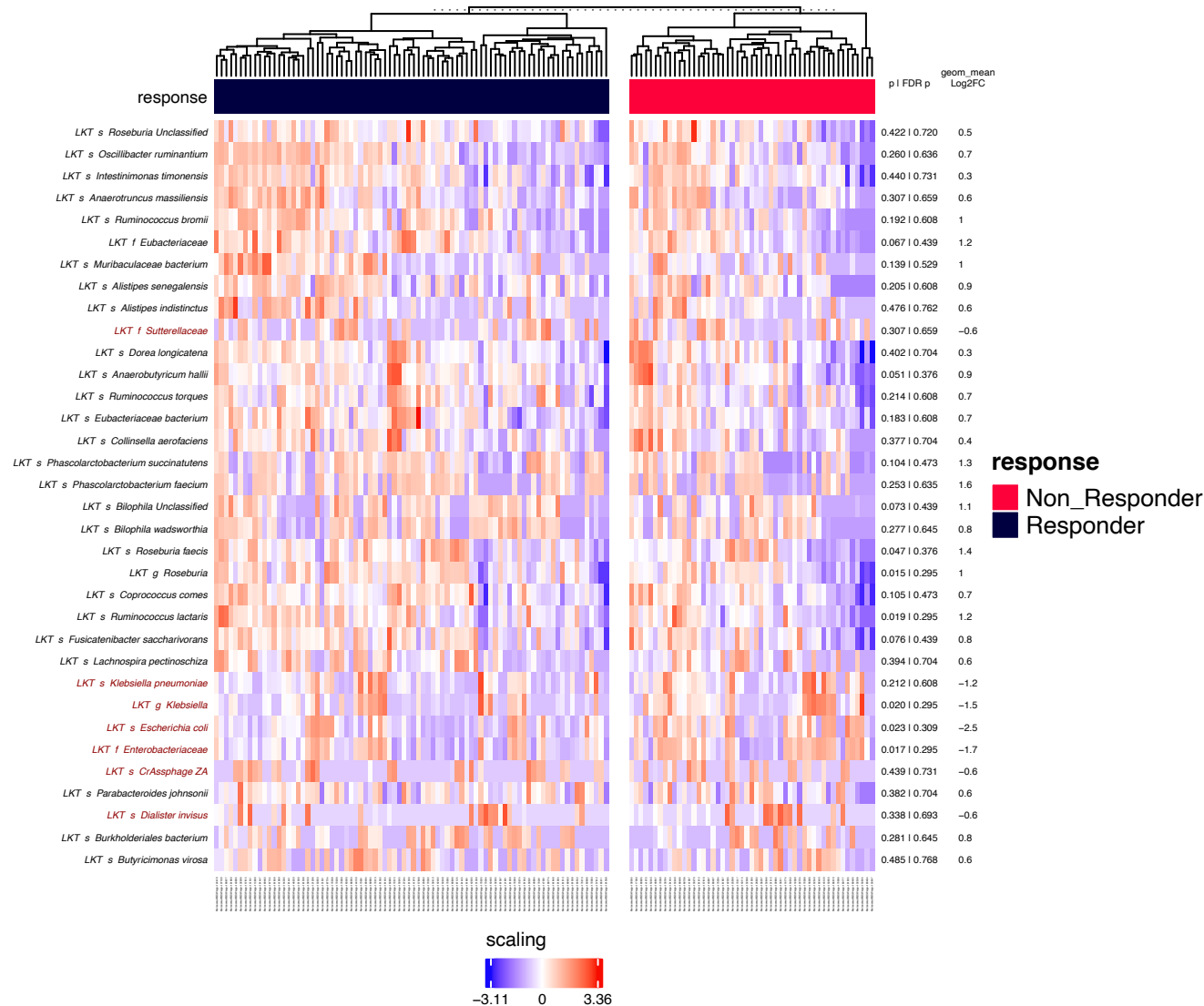
Samples_All Non_Responder=61 | Responder=106



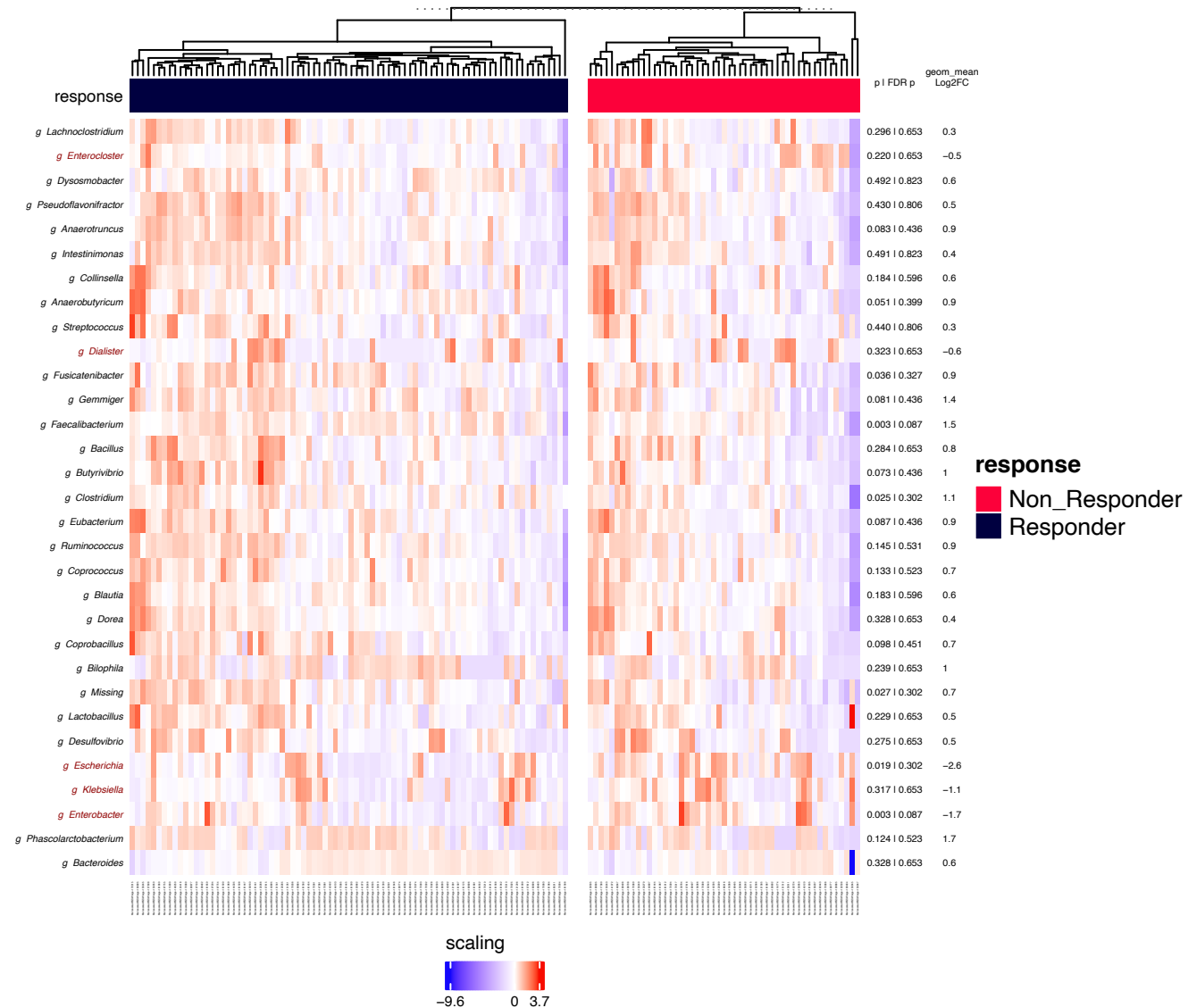
Relative Abundance Heatmap | LKT
 pval < 0.5 different between response using MannWhitneyWilcoxon
 Feature must be >250PPM in at least 15% of samples
 Taxonomy information must come from >25% contigs in at least 10% of samples
 Taxon genome completeness must be >10% in at least 5% of samples
 Number of samples in heatmap = 133 | Number of features assessed = 133
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder
 Heatmap 1/2



Relative Abundance Heatmap | LKT
pval < 0.5 different between response 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 = 133 | Number of features assessed = 133
log2foldchange > 0.2 | log2foldchange > Inf
Positive l2fc means increased in Responder
Heatmap 2/2



Relative Abundance Heatmap | Genus
 pval < 0.5 different between response 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 = 133 | Number of features assessed = 55
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Relative Abundance Heatmap | Family

pval < 0.5 different between response using MannWhitneyWilcoxon

Feature must be >250PPM in at least 15% of samples

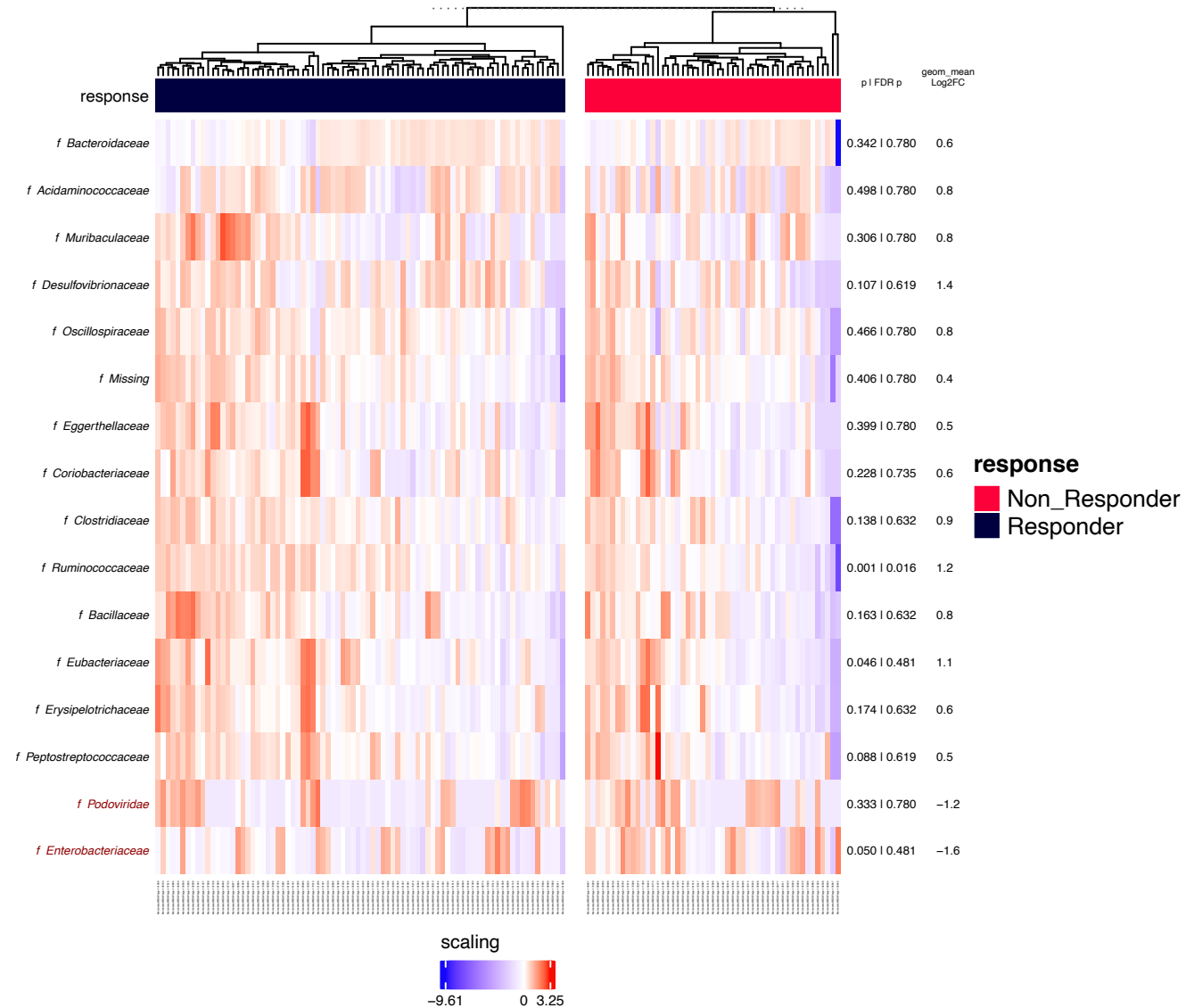
Taxonomy information must come from >25% contigs in at least 10% of samples

Taxon genome completeness must be >10% in at least 5% of samples

Number of samples in heatmap = 133 | Number of features assessed = 29

log2foldchange > 0.2 | log2foldchange > Inf

Positive l2fc means increased in Responder



Relative Abundance Heatmap | Class

pval < 0.5 different between response using MannWhitneyWilcoxon

Feature must be >250PPM in at least 15% of samples

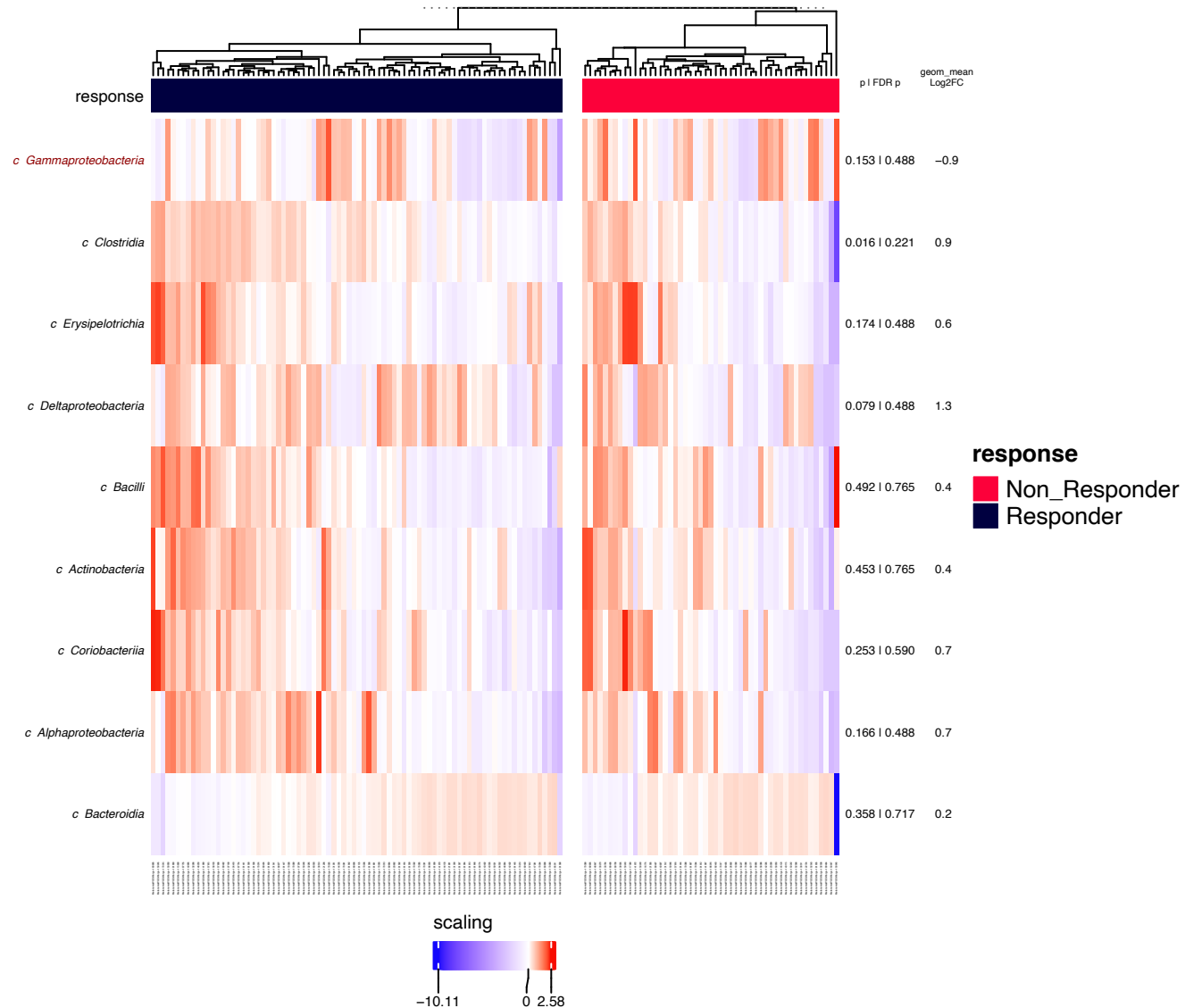
Taxonomy information must come from >25% contigs in at least 10% of samples

Taxon genome completeness must be >10% in at least 5% of samples

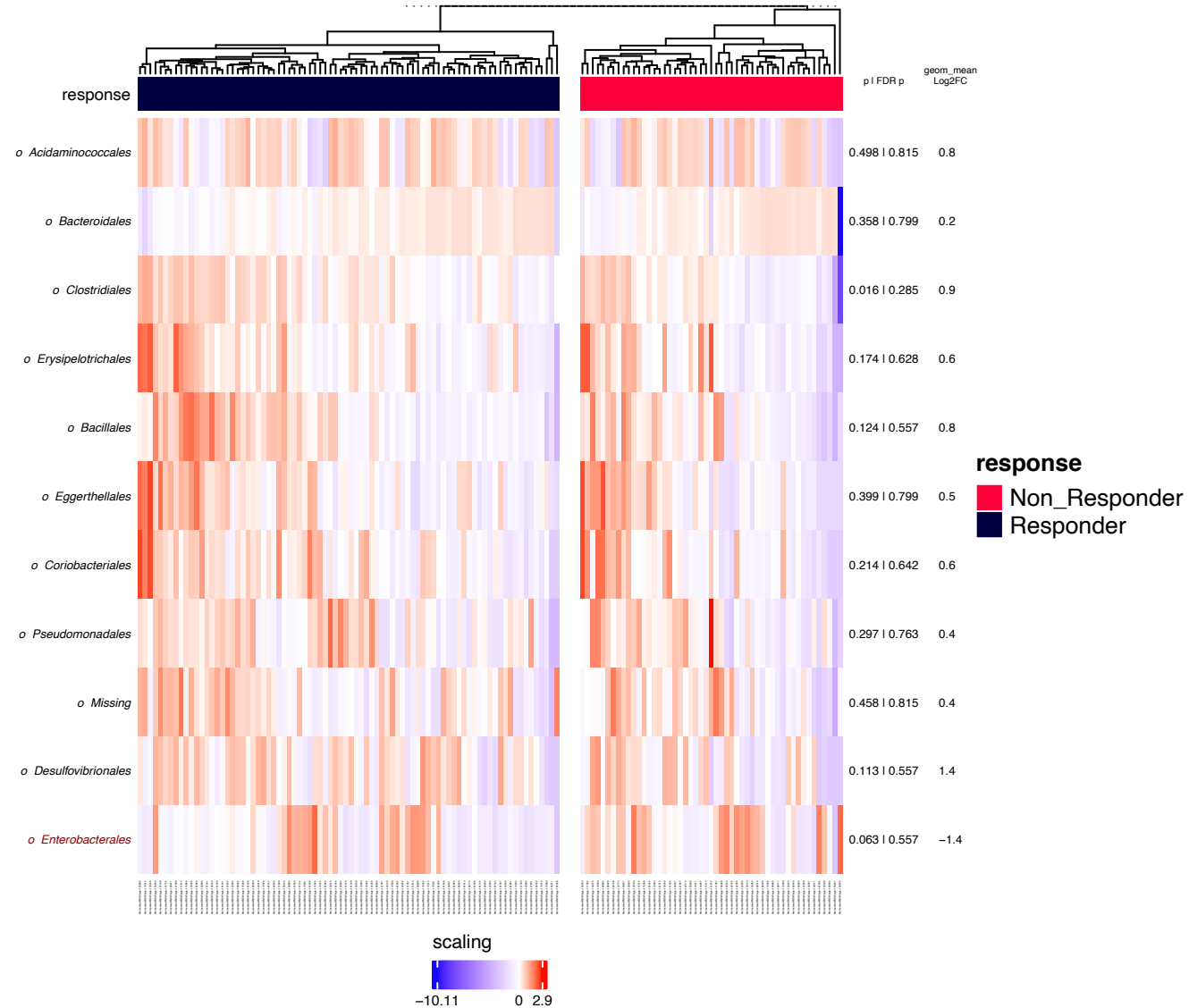
Number of samples in heatmap = 133 | Number of features assessed = 14

log2foldchange > 0.2 | log2foldchange > Inf

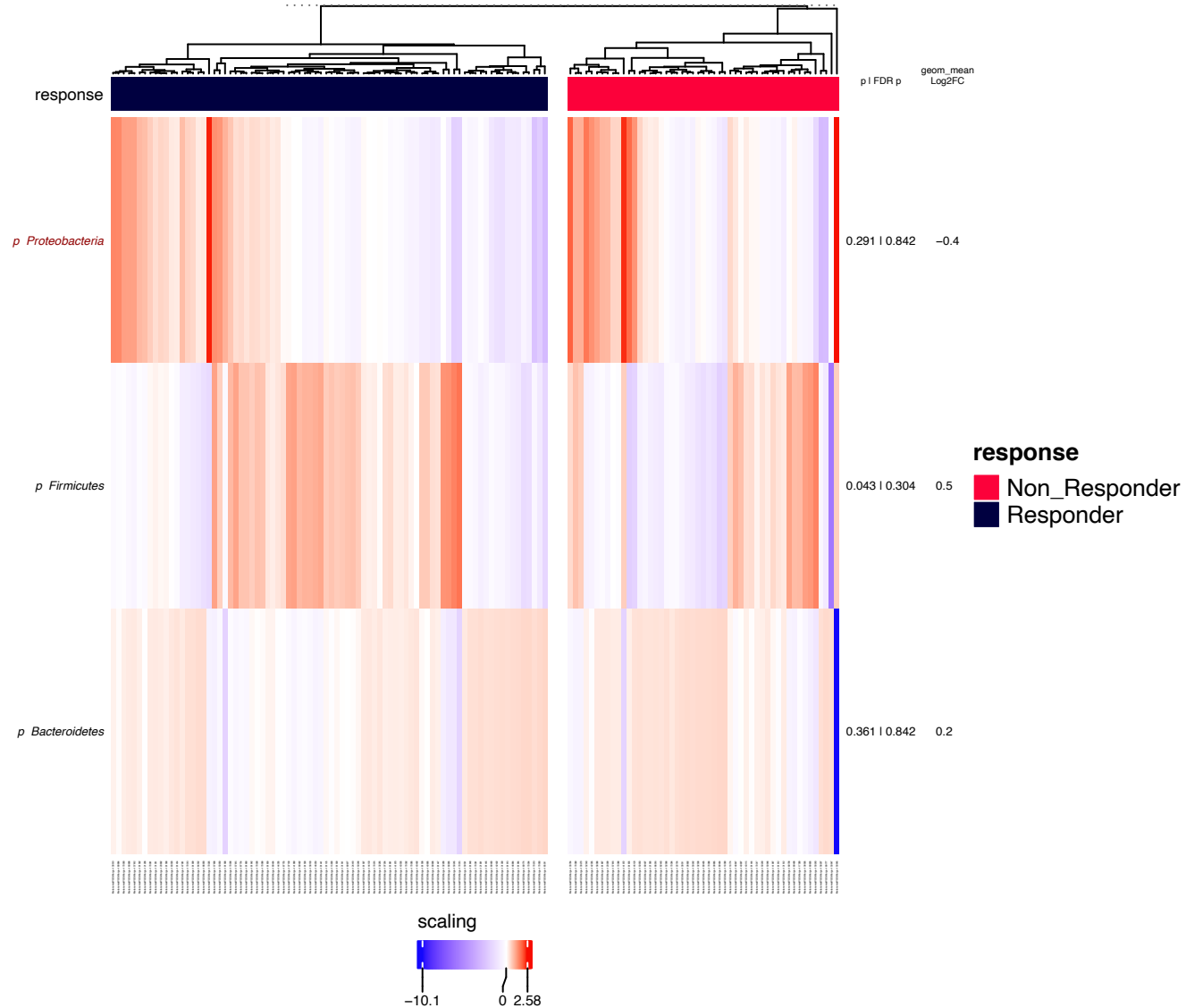
Positive l2fc means increased in Responder



Relative Abundance Heatmap | Order
 pval < 0.5 different between response 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 = 133 | Number of features assessed = 18
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Relative Abundance Heatmap | Phylum
 pval < 0.5 different between response 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 = 133 | Number of features assessed = 7
 log2foldchange > 0.2 | log2foldchange > Inf
 Positive l2fc means increased in Responder



Samples_antiPD1 Non_Responder=51 | Responder=82

