k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__Clostridium perfringens

Correlation with all samples

Relative abundance (%)

Cq value
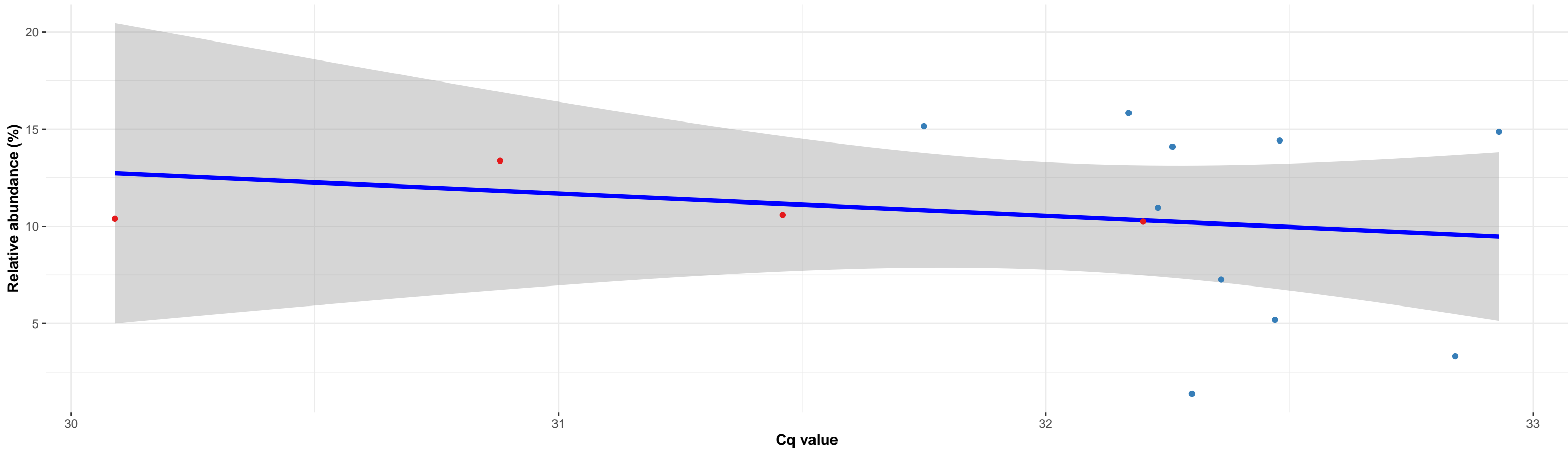
Correlation within: PCR−blank
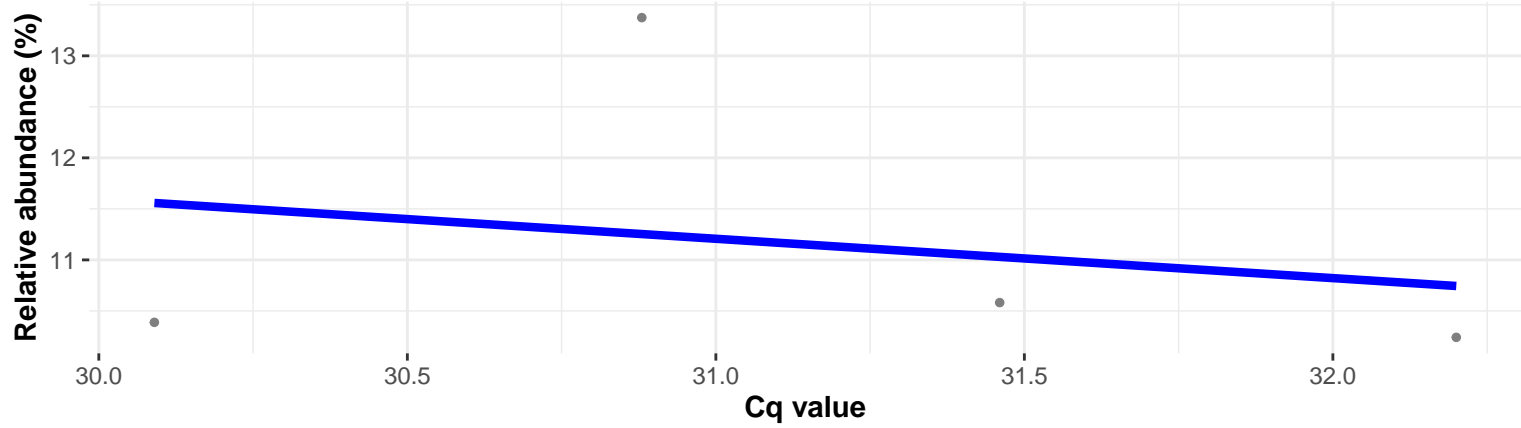
Relative abundance (%)

Cq value

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Undibacterium; NA

Correlation with all samples

$\log_e(S) = 6.306$, $p = 0.483$, $\hat{\rho}_{Spearman} = -0.204$, $CI_{95\%}$ [−0.673, 0.381], $n_{pairs} = 14$

SampleType ● REF−PIM ● REF−DIM
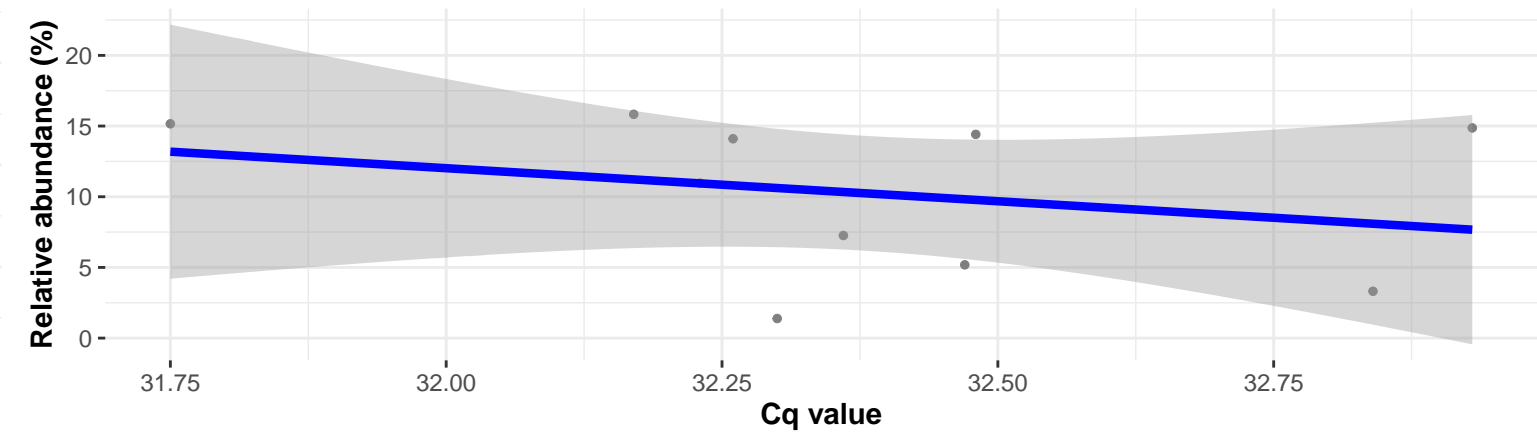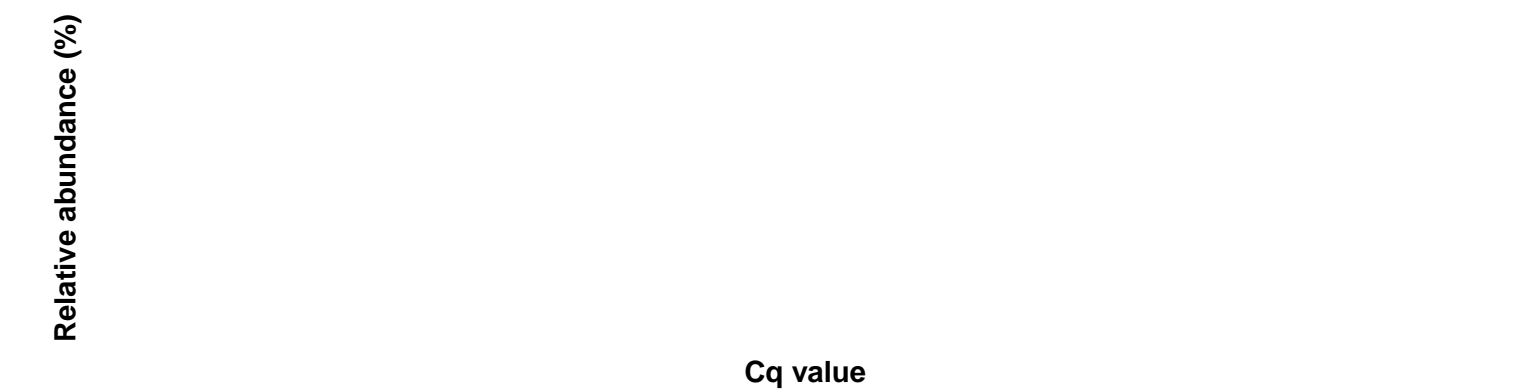
Correlation within: REF−DIM

$\log_e(S) = 5.421$, $p = 0.293$, $\hat{\rho}_{Spearman} = -0.370$, $CI_{95\%}$ [−0.818, 0.358], $n_{pairs} = 10$
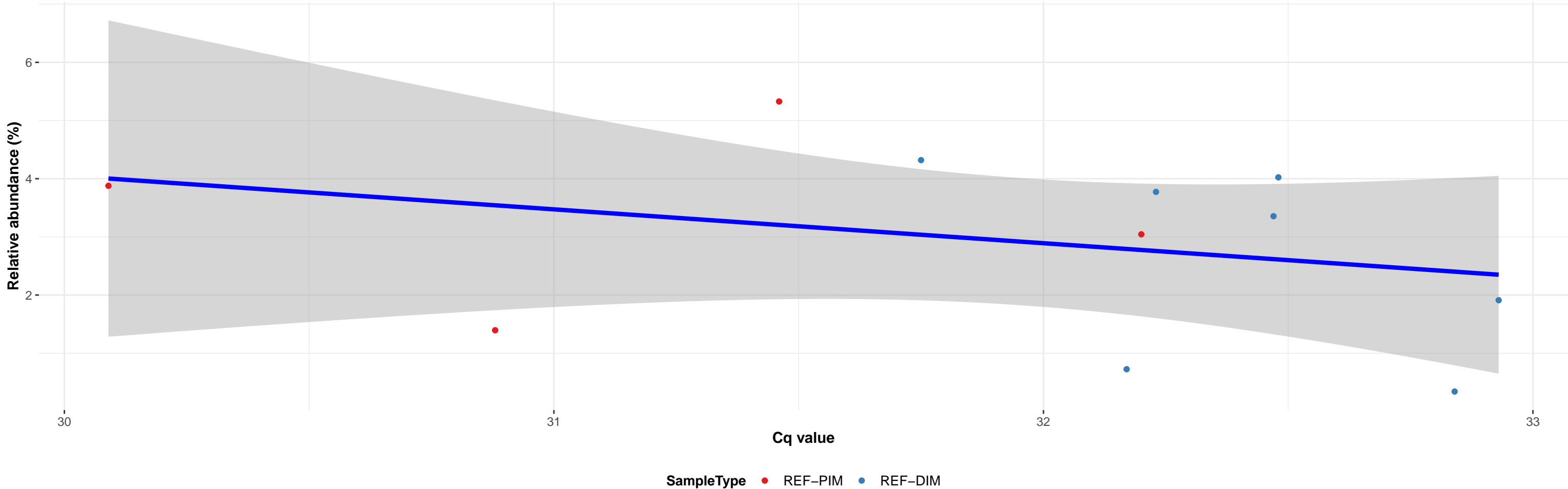
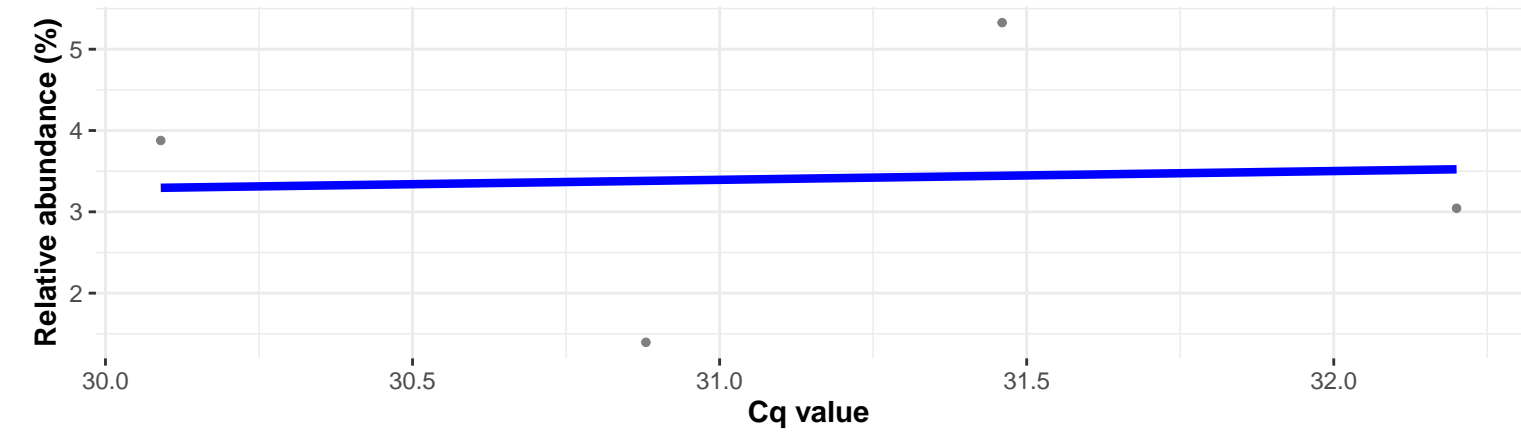**Correlation within: REF−PIM**

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; NA; NA; NA

Correlation with all samples

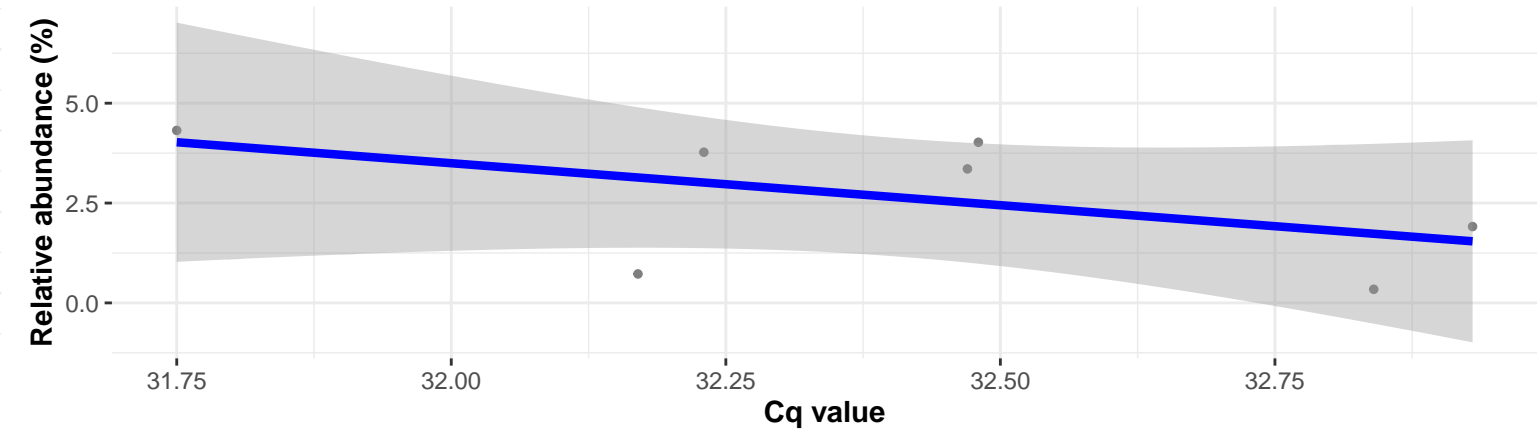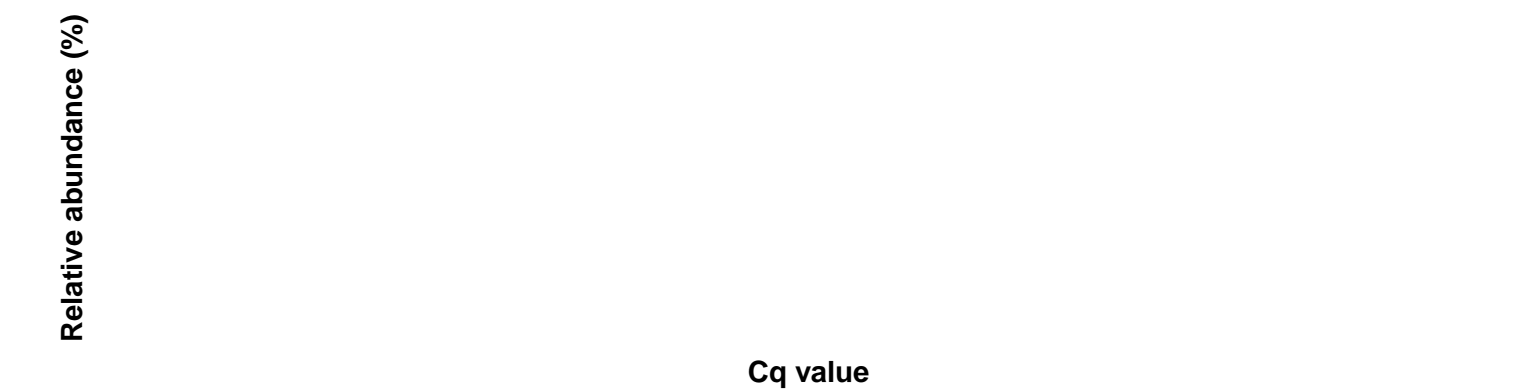$\log_e(S) = 5.684$, $p = 0.312$, $\hat{\rho}_{Spearman} = -0.336$, $CI_{95\%}$ [−0.787, 0.348], $n_{pairs} = 11$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM
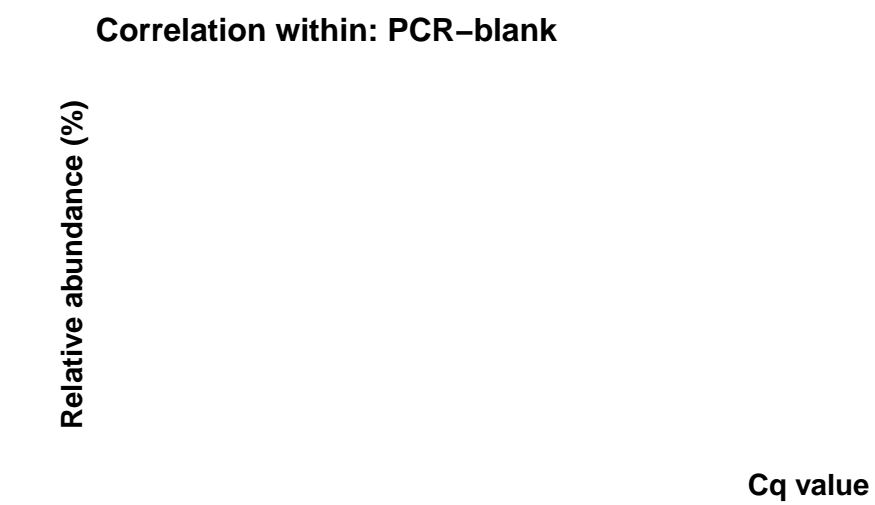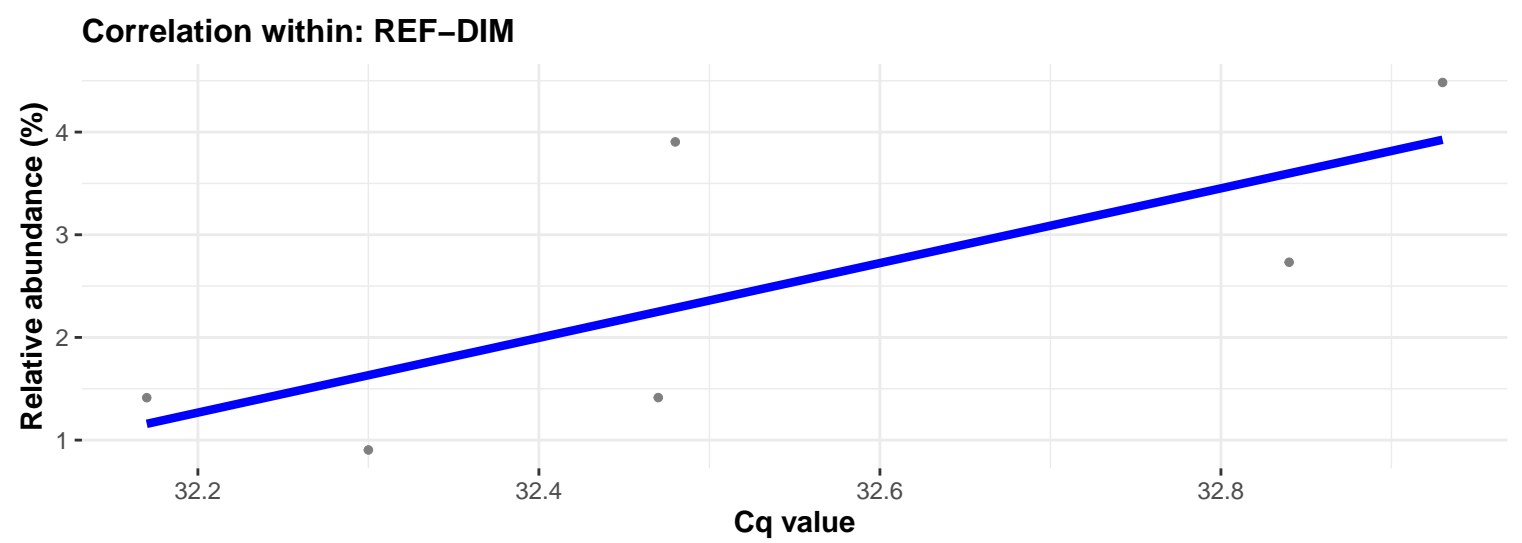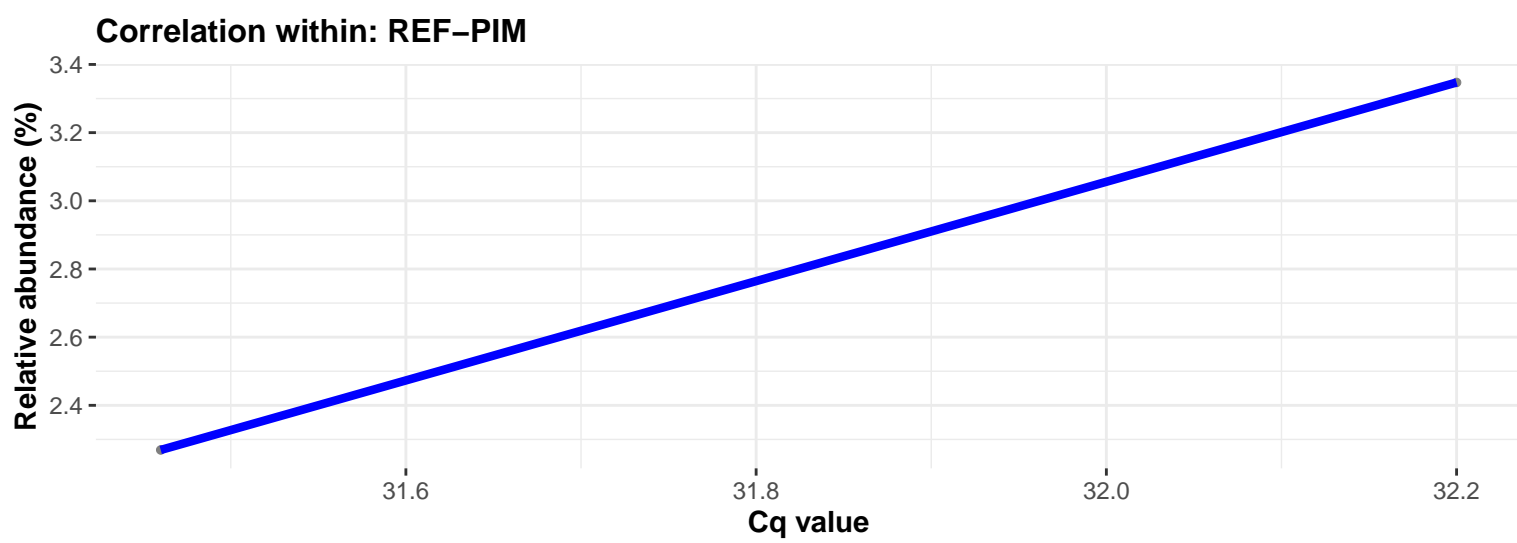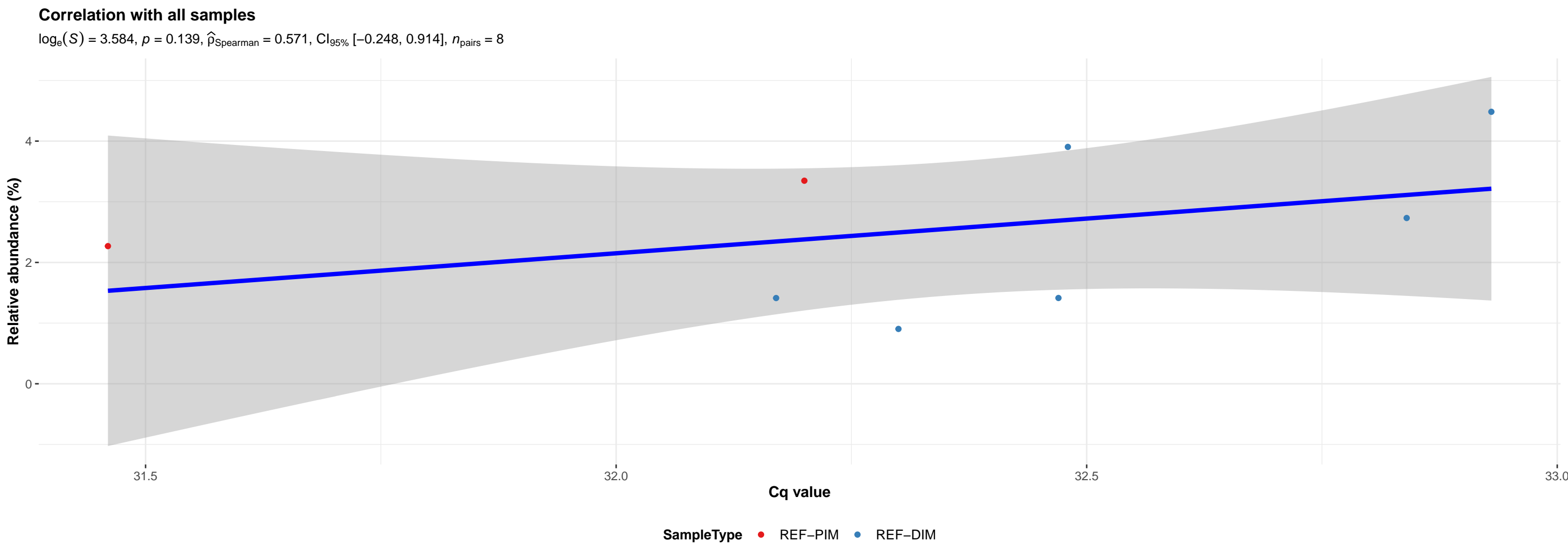
$\log_e(S) = 4.407$, $p = 0.294$, $\hat{\rho}_{Spearman} = -0.464$, $CI_{95\%}$ [−0.907, 0.467], $n_{pairs} = 7$

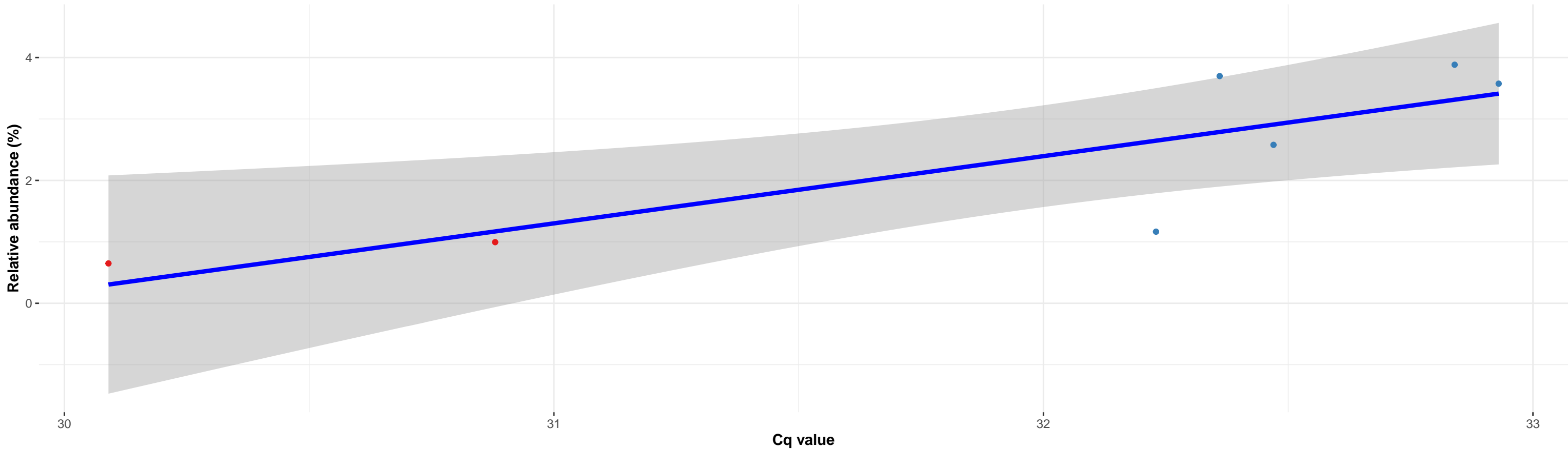**Correlation within: PCR−blank**

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium aurimucosum ATCC 700975
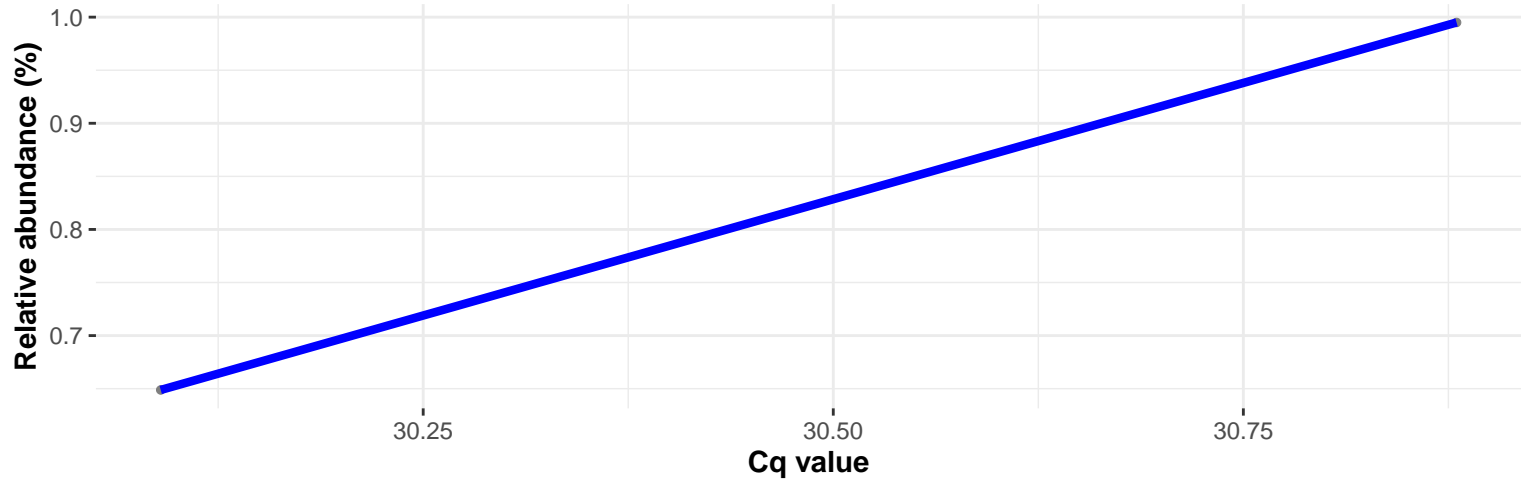
Correlation with all samples

$\log_e(S) = 3.584$, $p = 0.139$, $\hat{\rho}_{Spearman} = 0.571$, $CI_{95\%}$ [−0.248, 0.914], $n_{pairs} = 8$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni
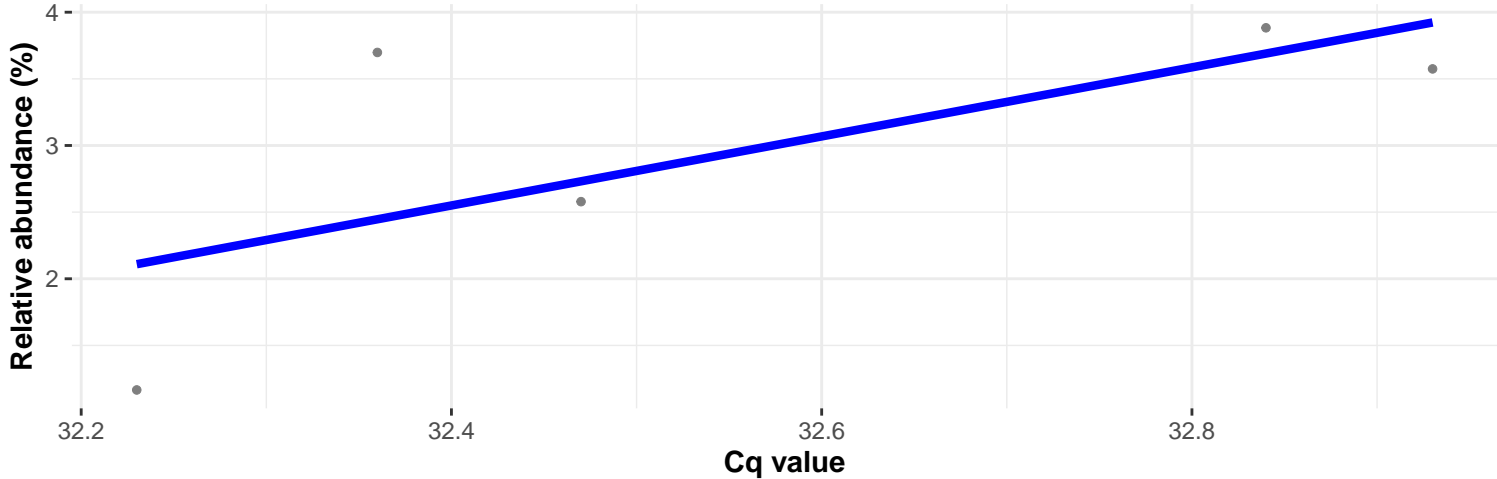
Correlation with all samples

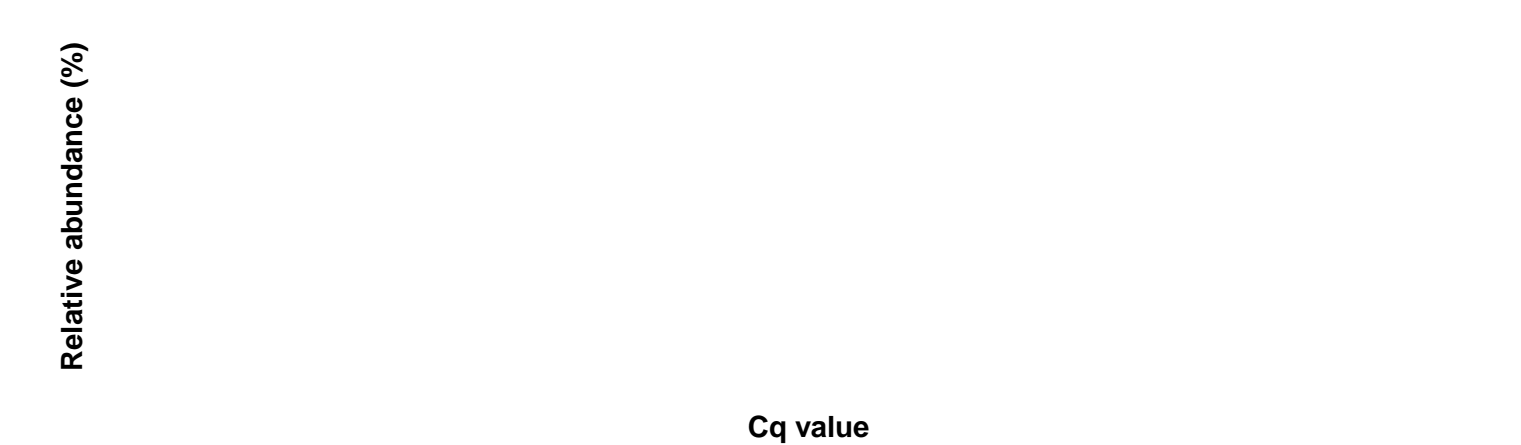$\log_e(S) = 2.303$, $p = 0.023$, $\hat{\rho}_{Spearman} = 0.821$, $CI_{95\%}$ [0.151, 0.974], $n_{pairs} = 7$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

Correlation within: PCR−blank

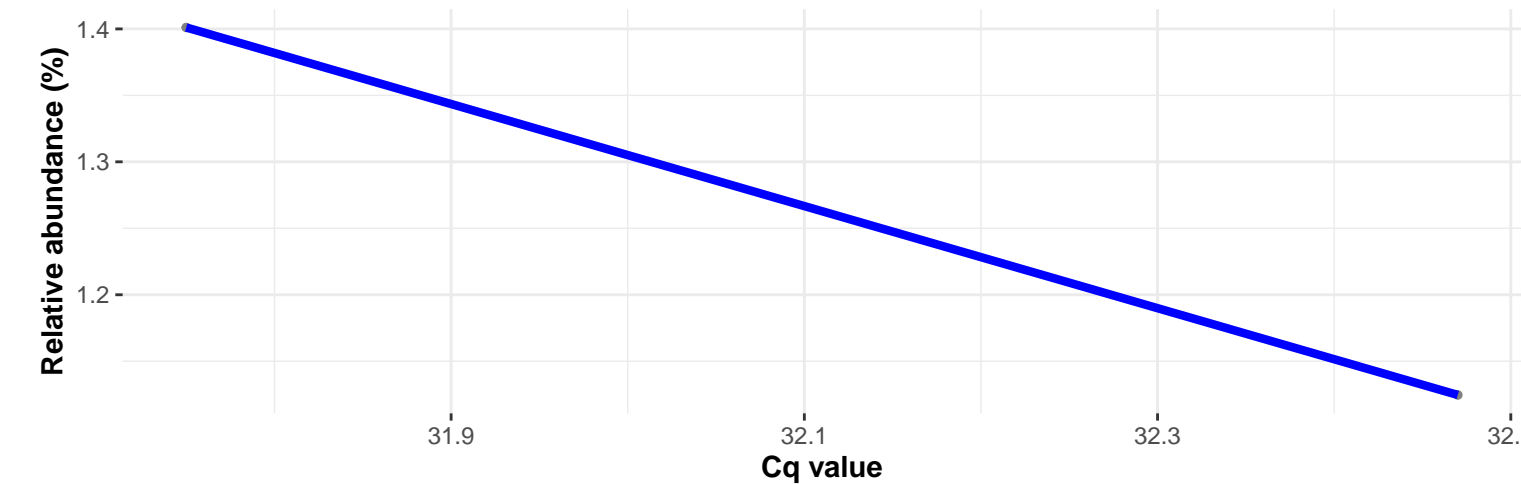**k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa**

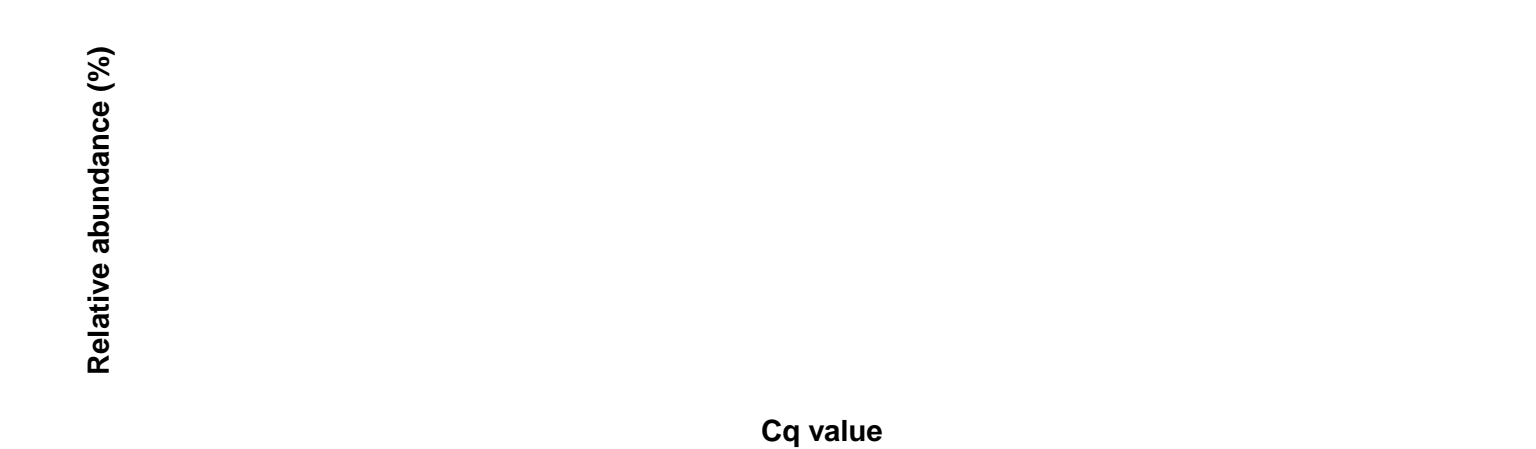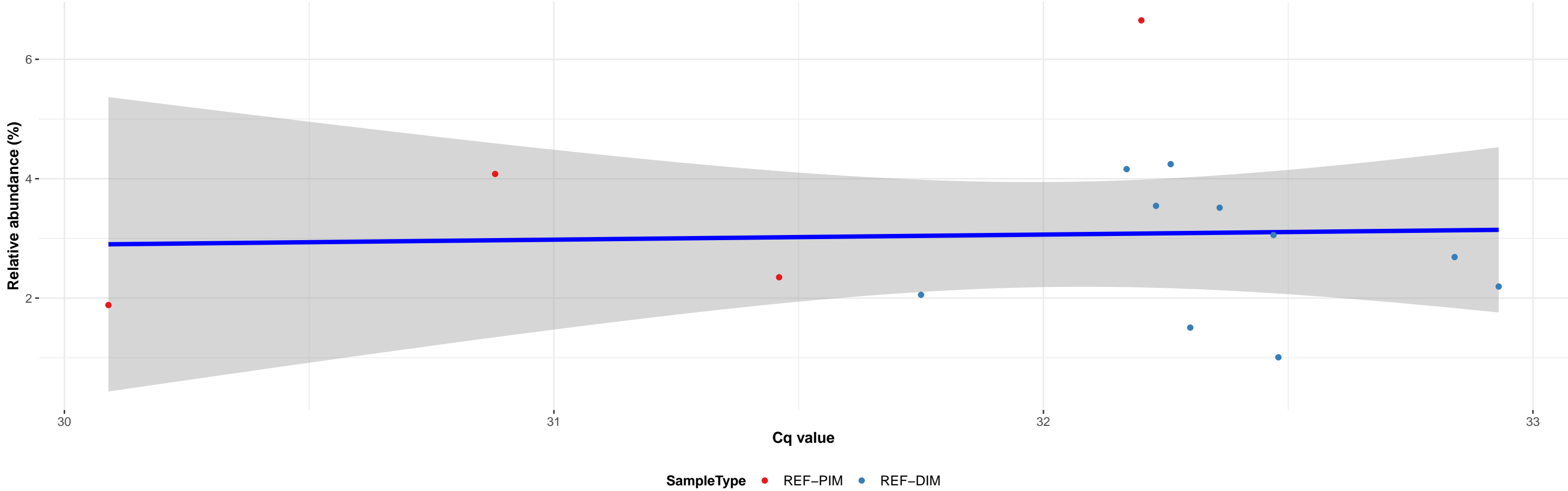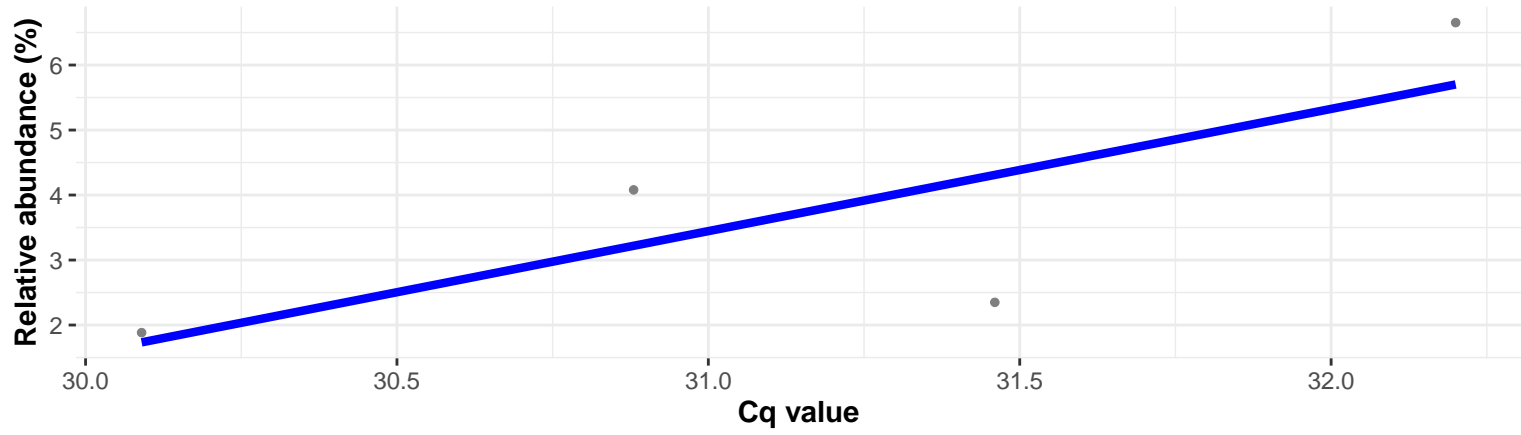# k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 6.288$, $p = 0.533$, $\hat{\rho}_{Spearman} = -0.182$, $CI_{95\%}$ [−0.660, 0.400], $n_{pairs} = 14$

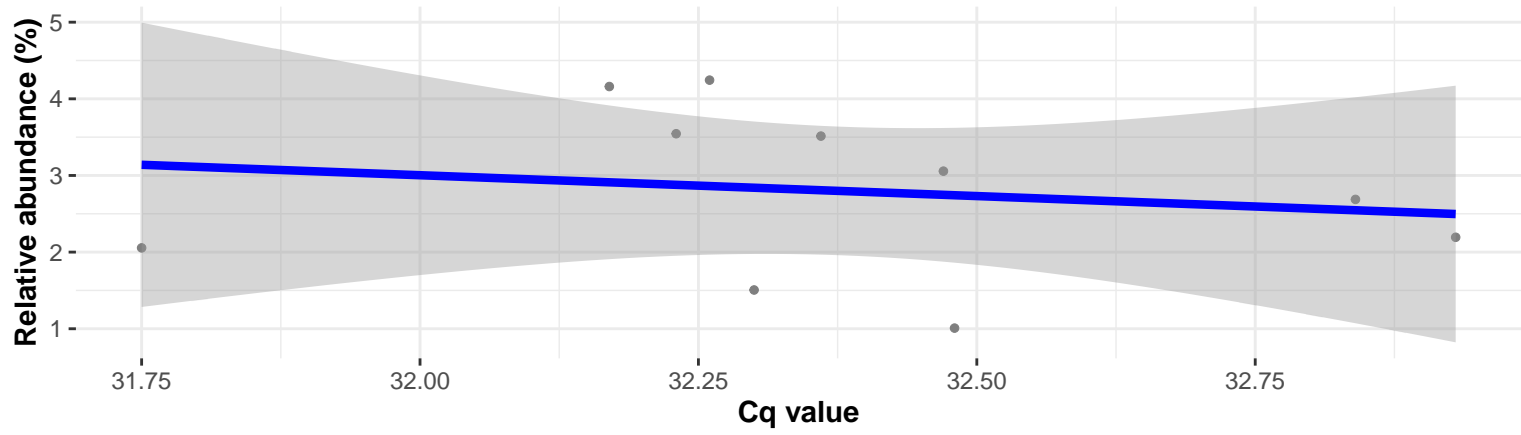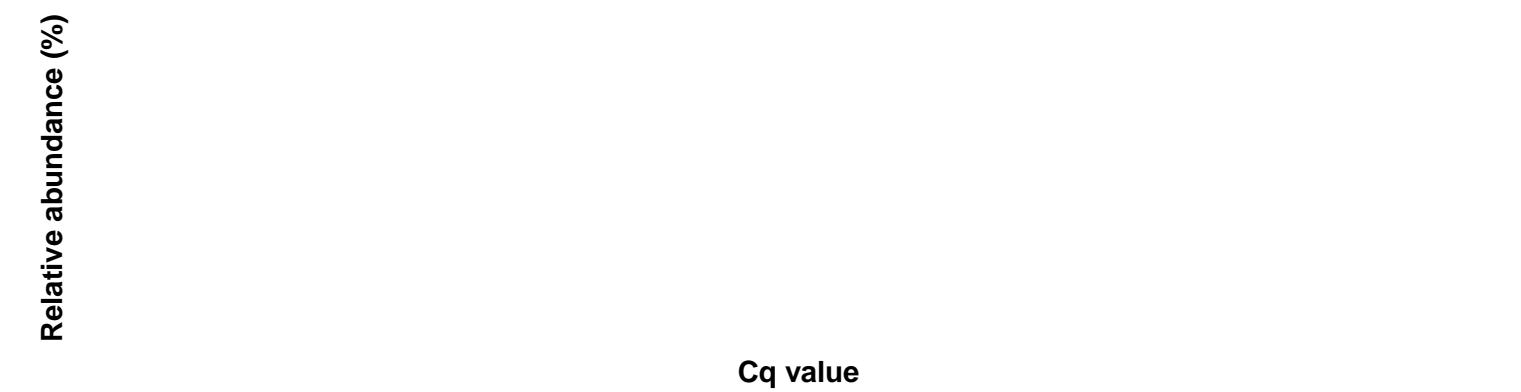SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−DIM

$\log_e(S) = 5.421$, $p = 0.293$, $\hat{\rho}_{Spearman} = -0.370$, $CI_{95\%}$ [−0.818, 0.358], $n_{pairs} = 10$
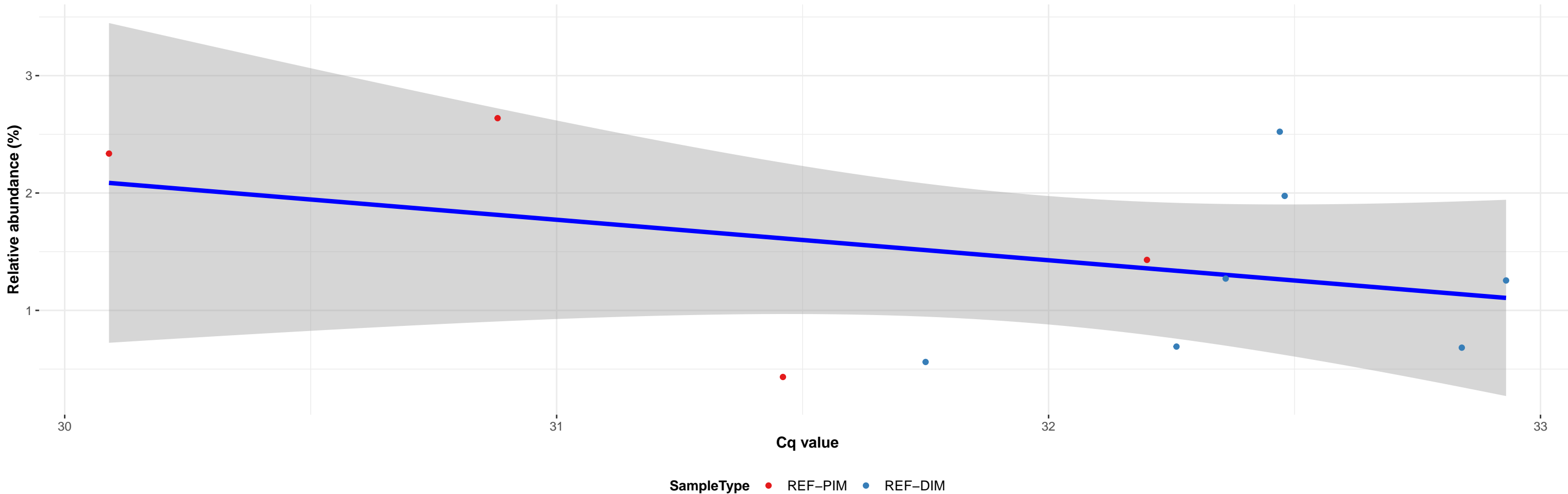
Correlation within: REF−PIM

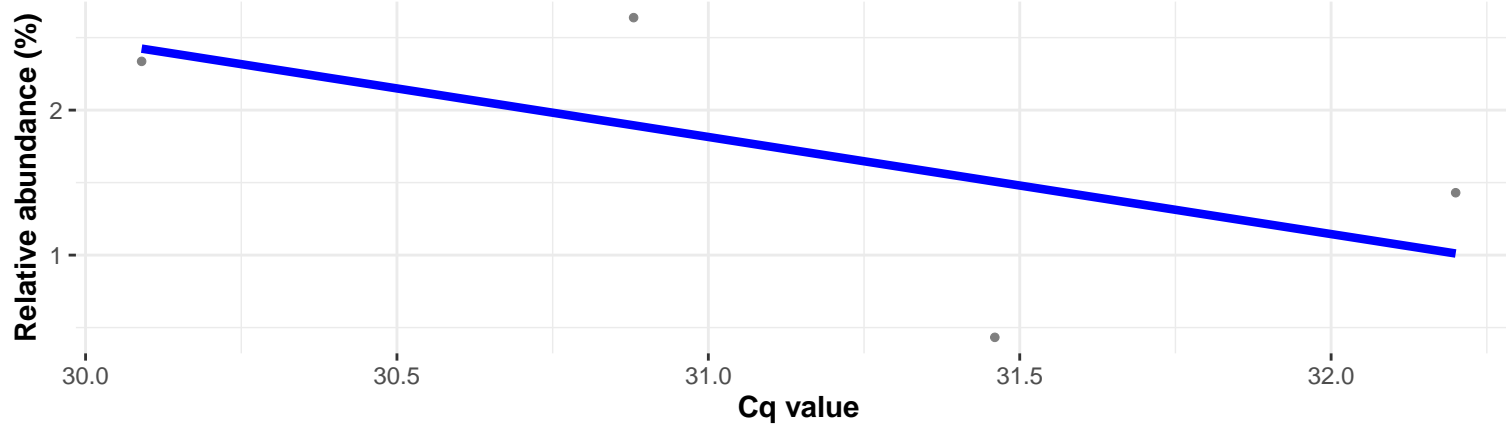**Correlation within: PCR−blank**

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

Correlation with all samples

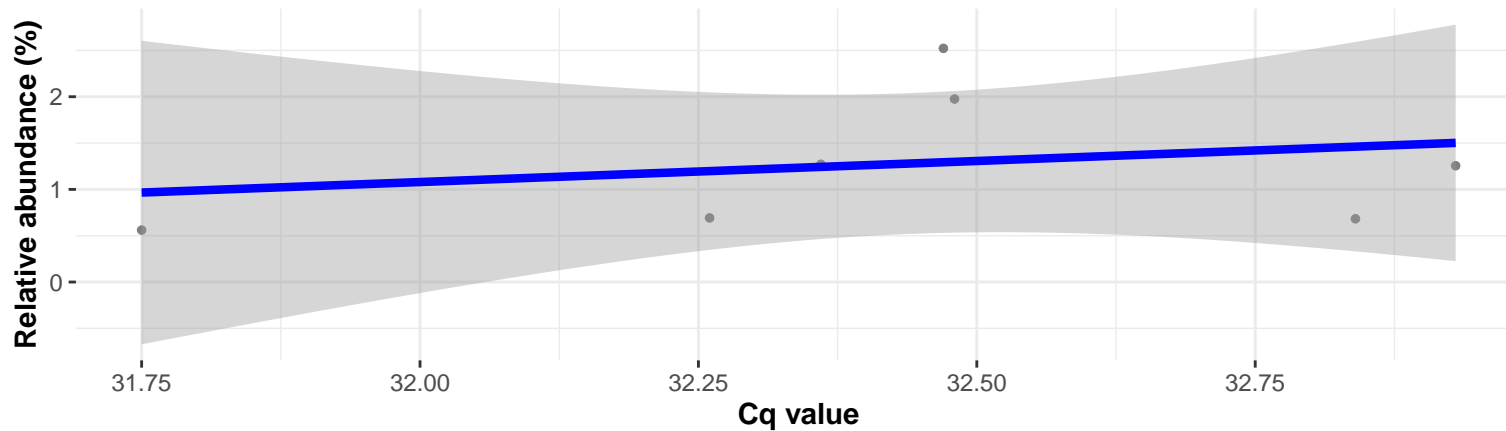$\log_e(S) = 5.529$, $p = 0.670$, $\widehat{\rho}_{Spearman} = -0.145$, $CI_{95\%}$ [−0.696, 0.513], $n_{pairs} = 11$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−DIM

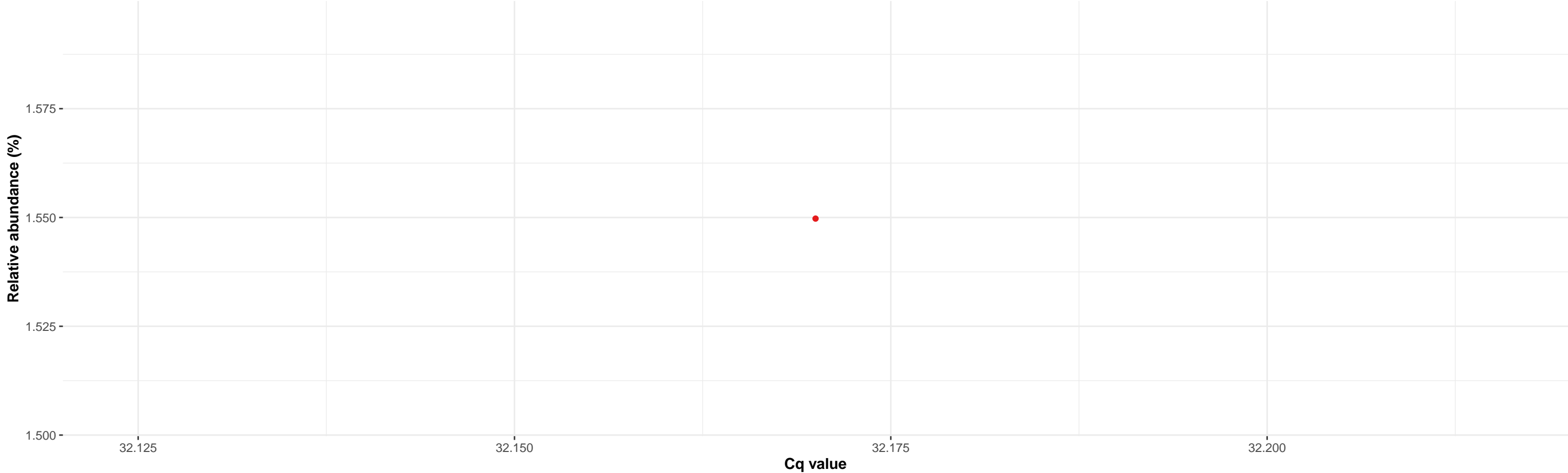$\log_e(S) = 3.689$, $p = 0.535$, $\widehat{\rho}_{Spearman} = 0.286$, $CI_{95\%}$ [−0.614, 0.862], $n_{pairs} = 7$

Correlation within: REF−PIM

Correlation within: PCR−blank

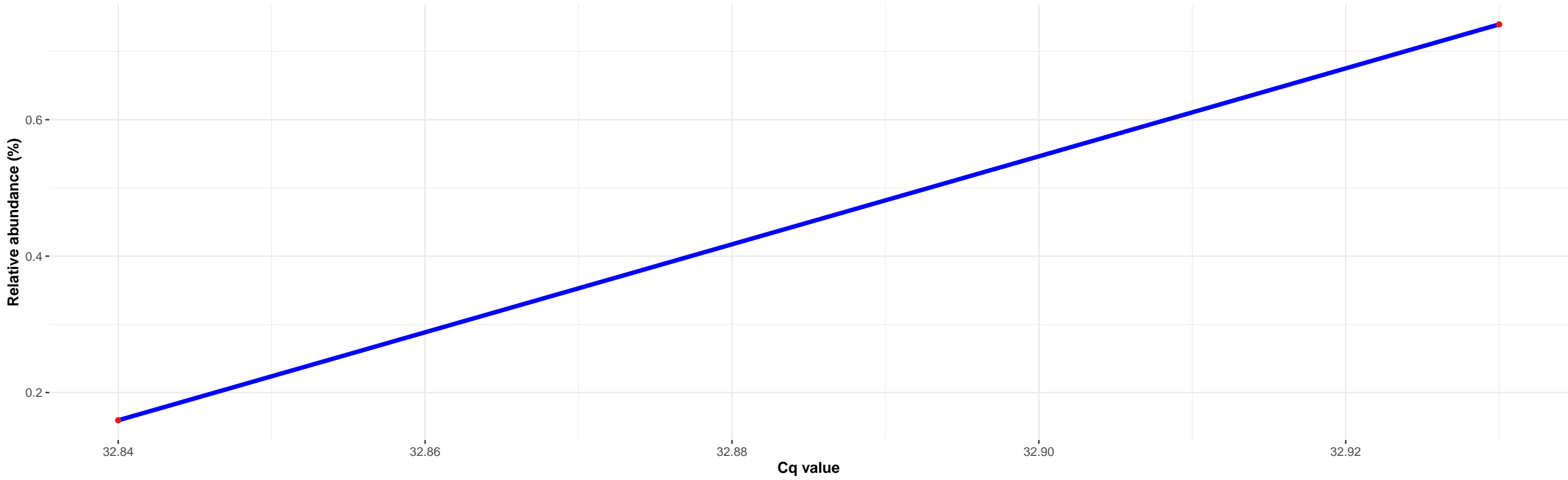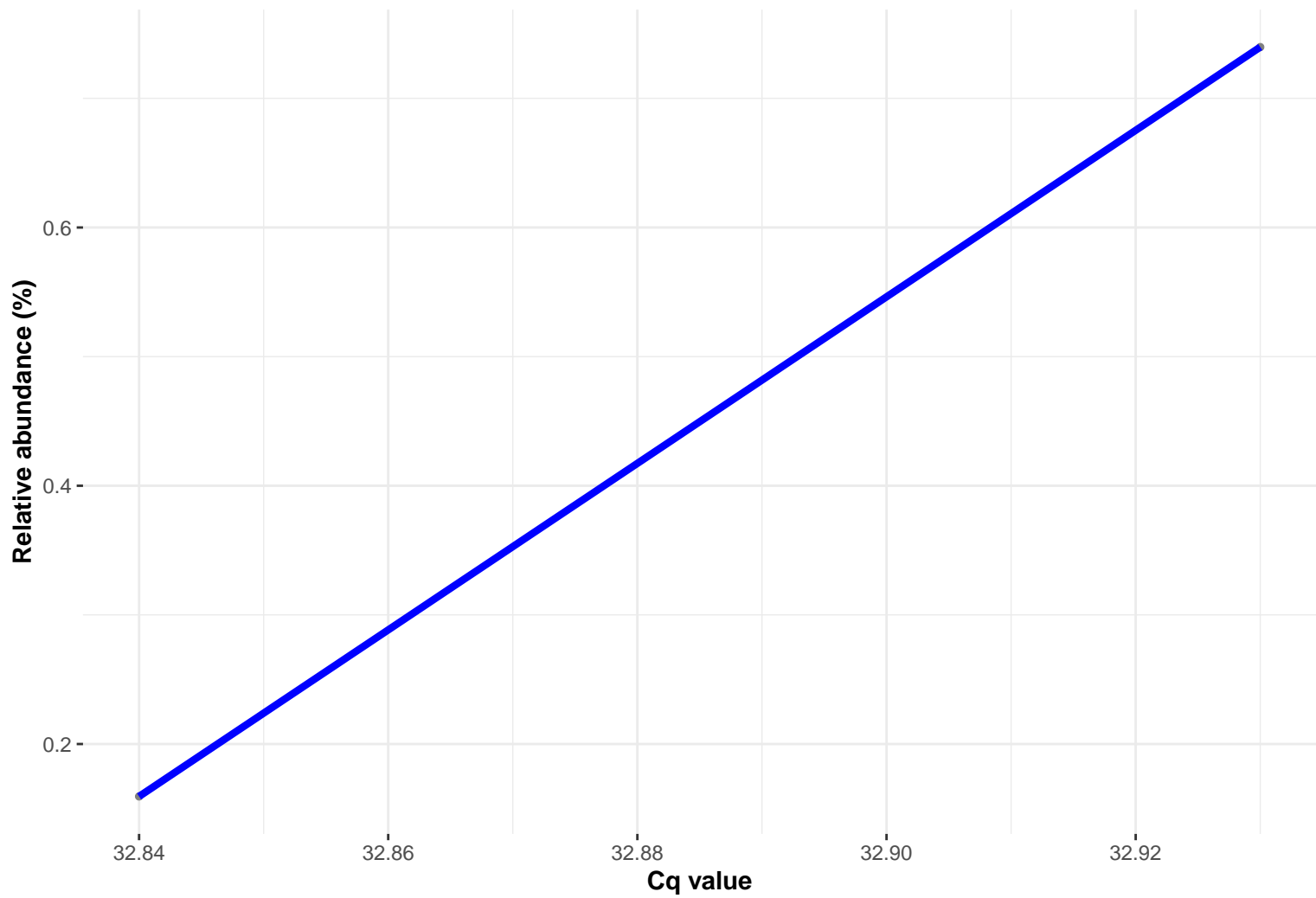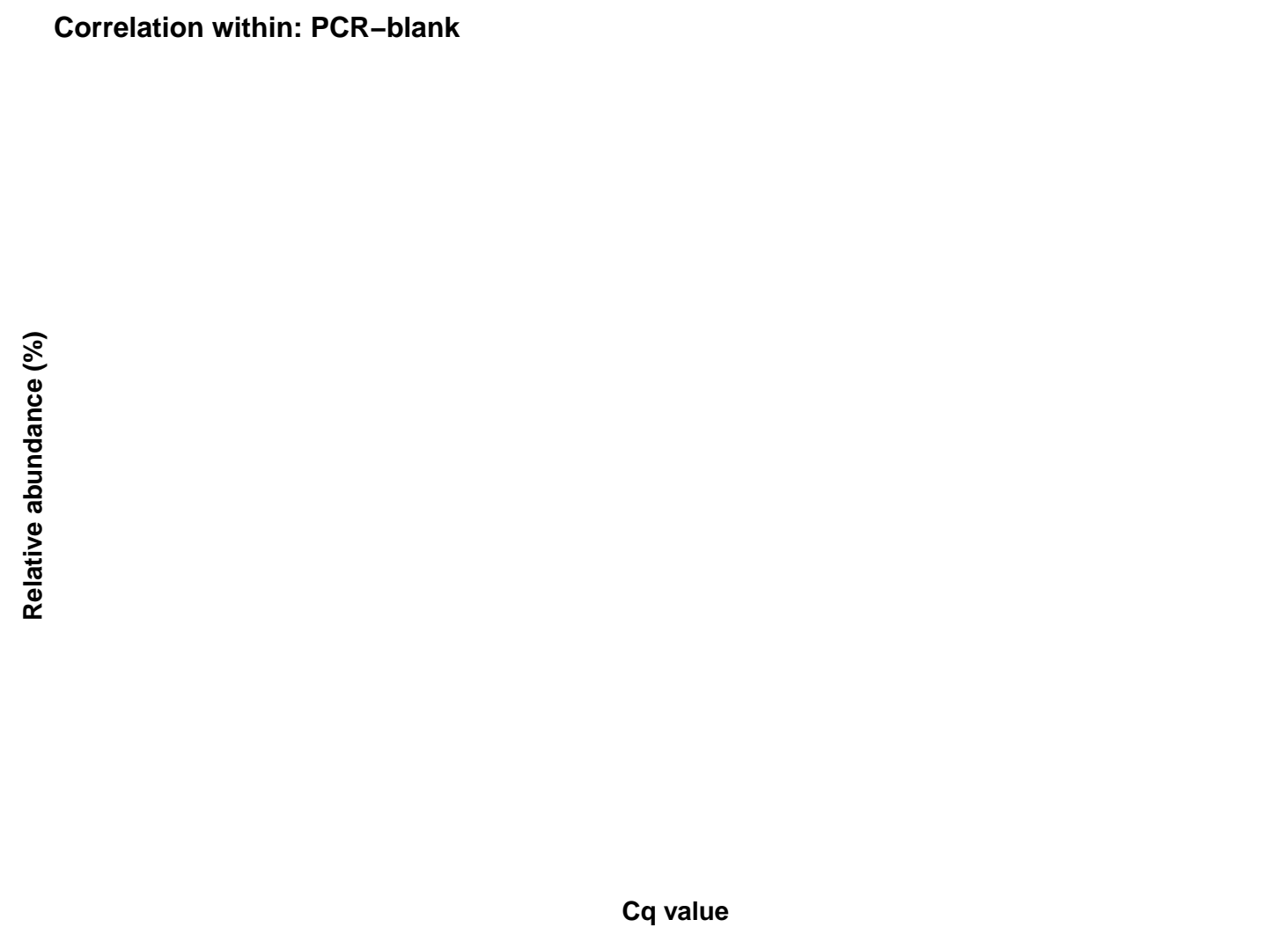# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Lysinibacillus; s__uncultured bacterium
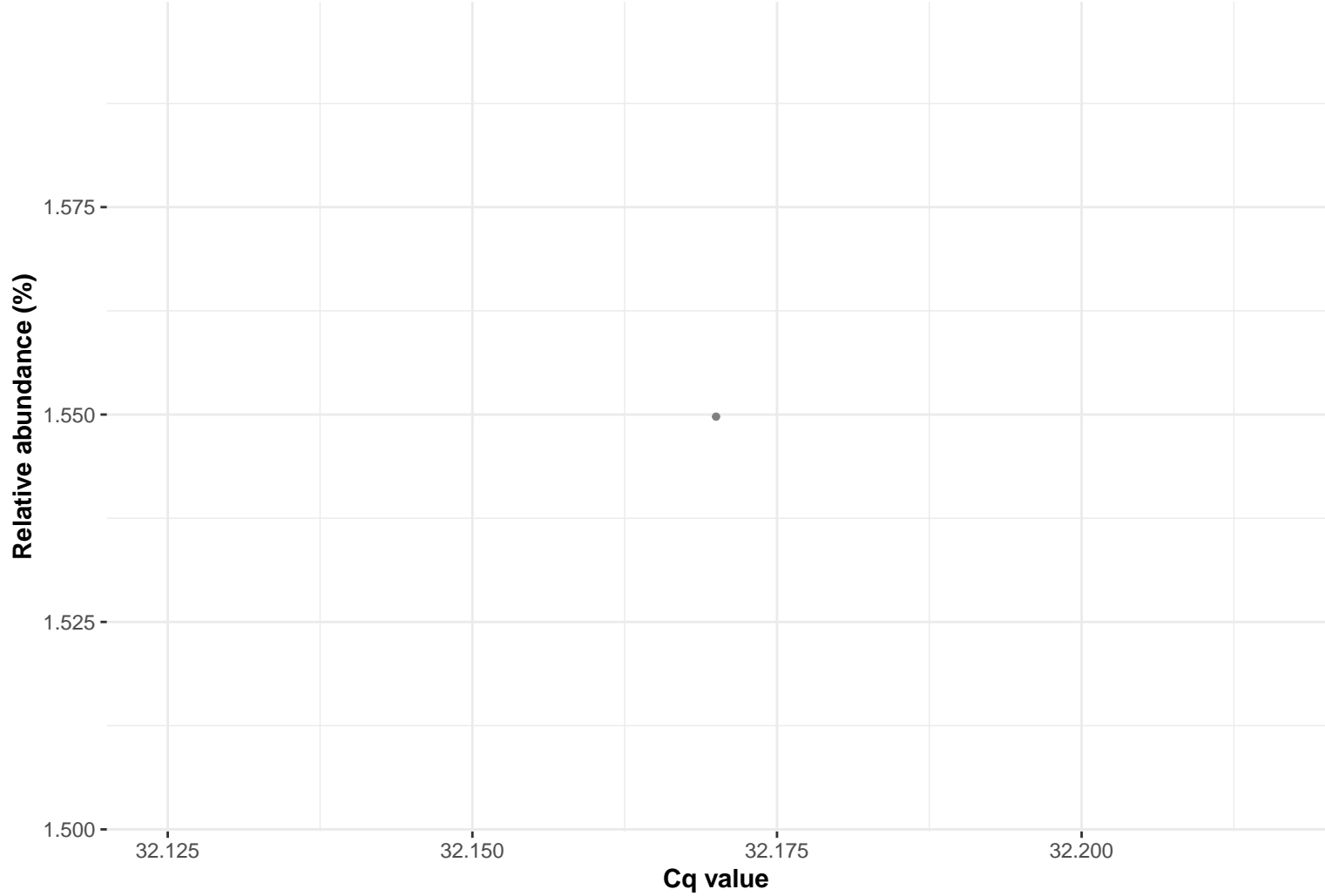
k__Bacteria; p__Cyanobacteria; c__Melainabacteria; o__Obscuribacterales; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa
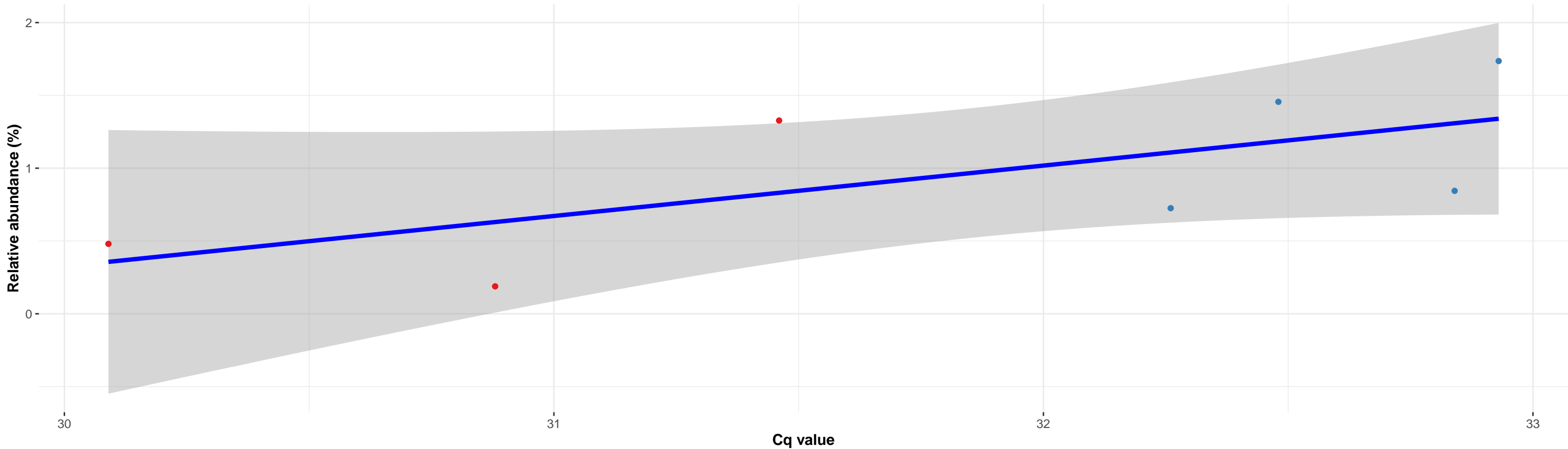
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; NA; NA
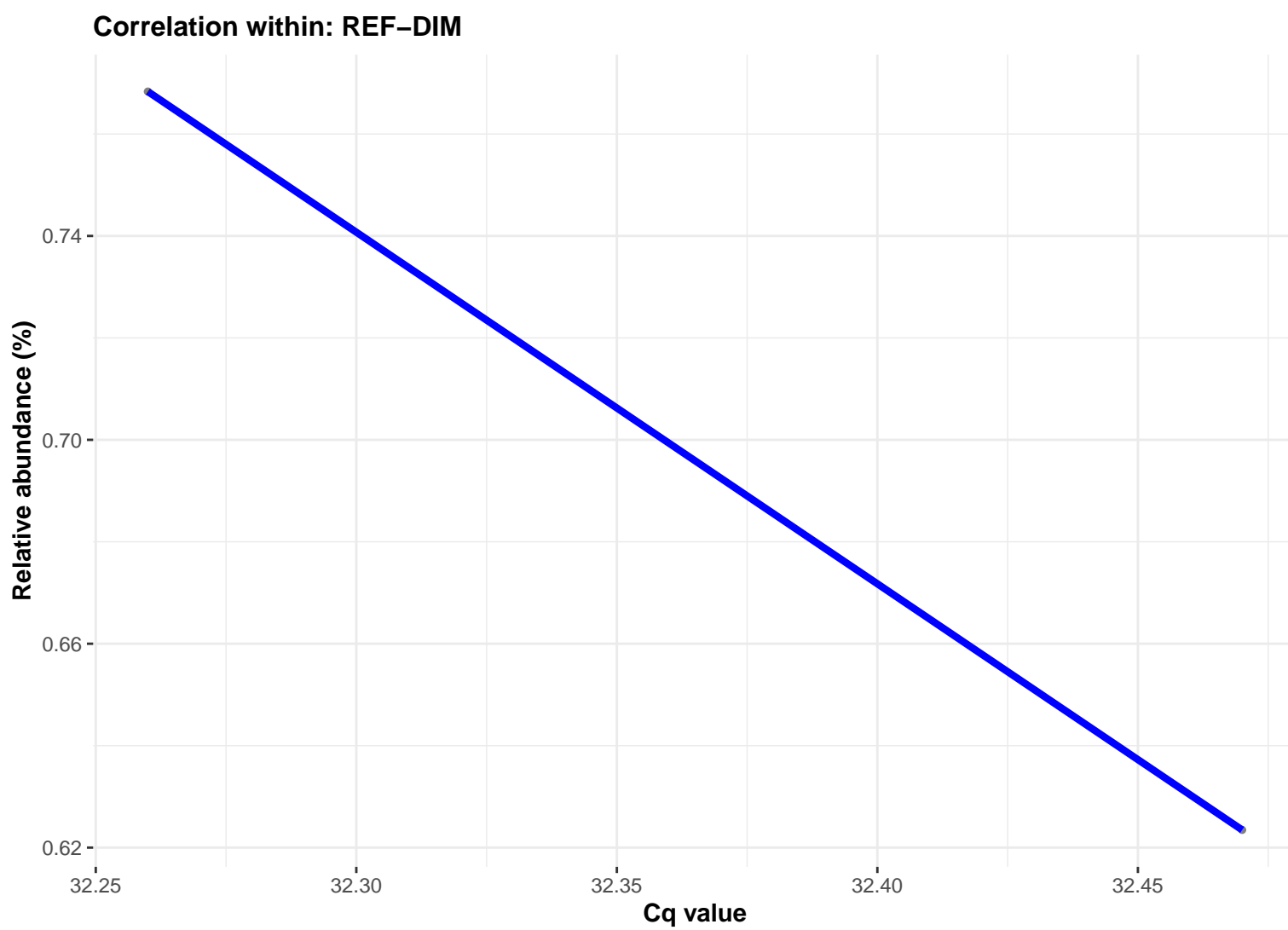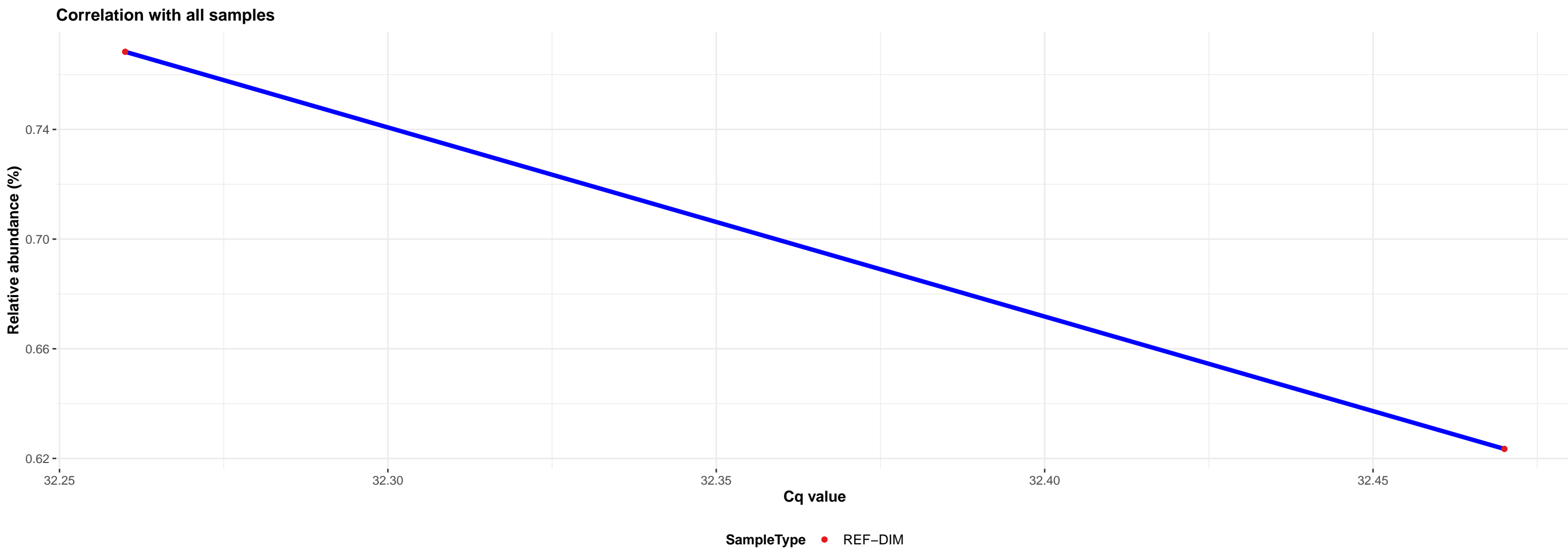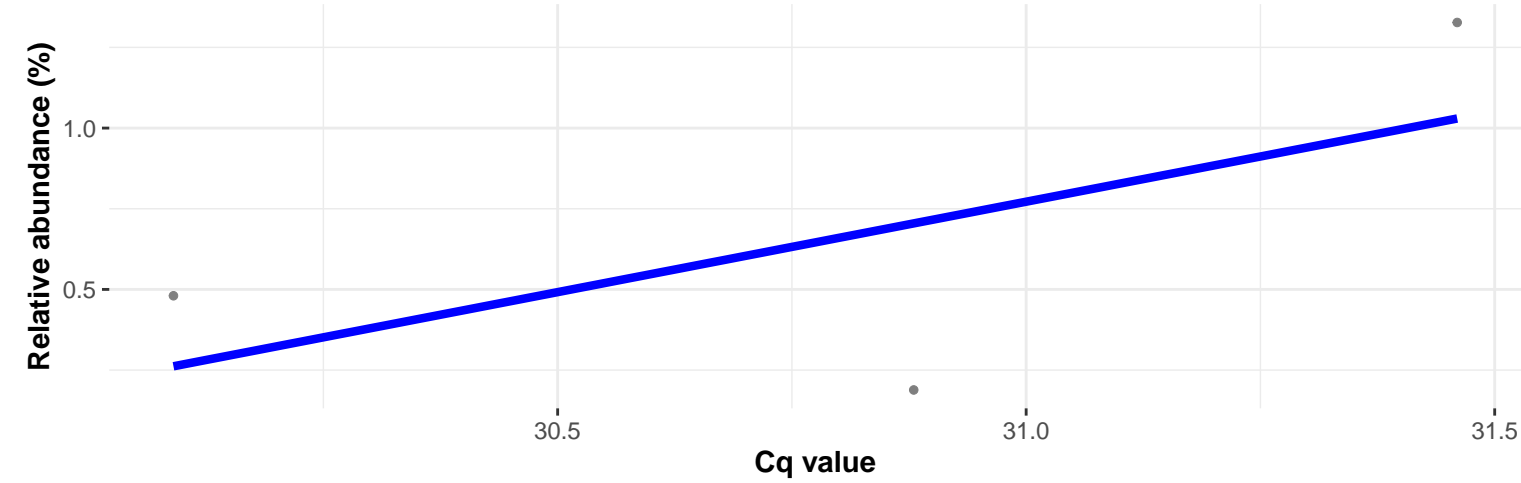
k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium
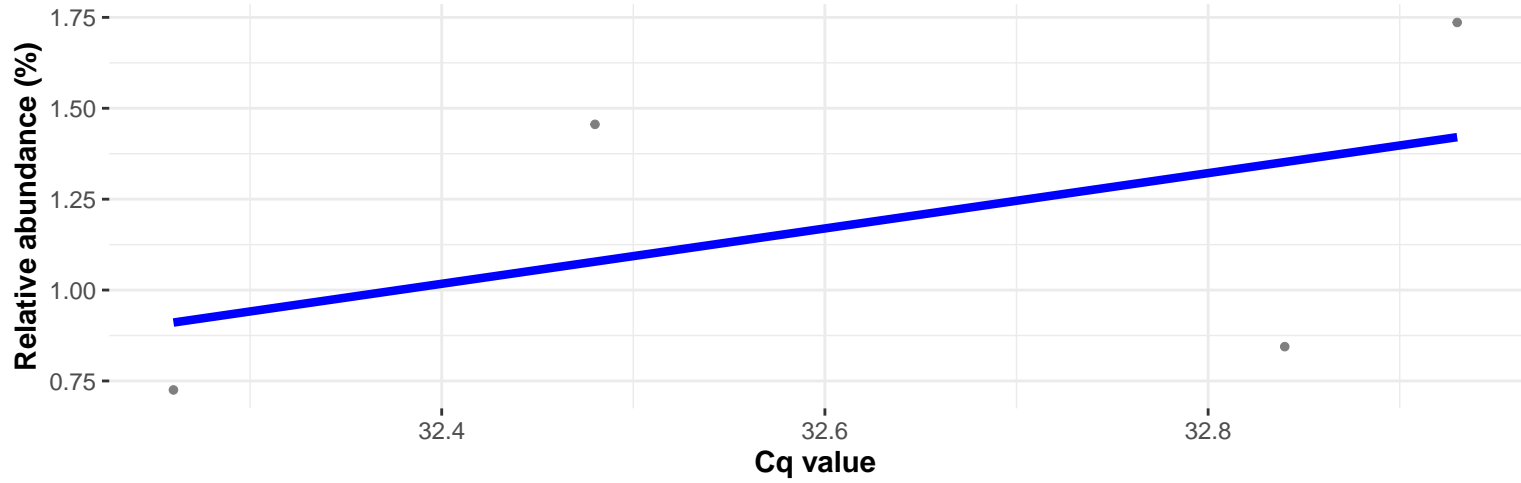
Correlation with all samples

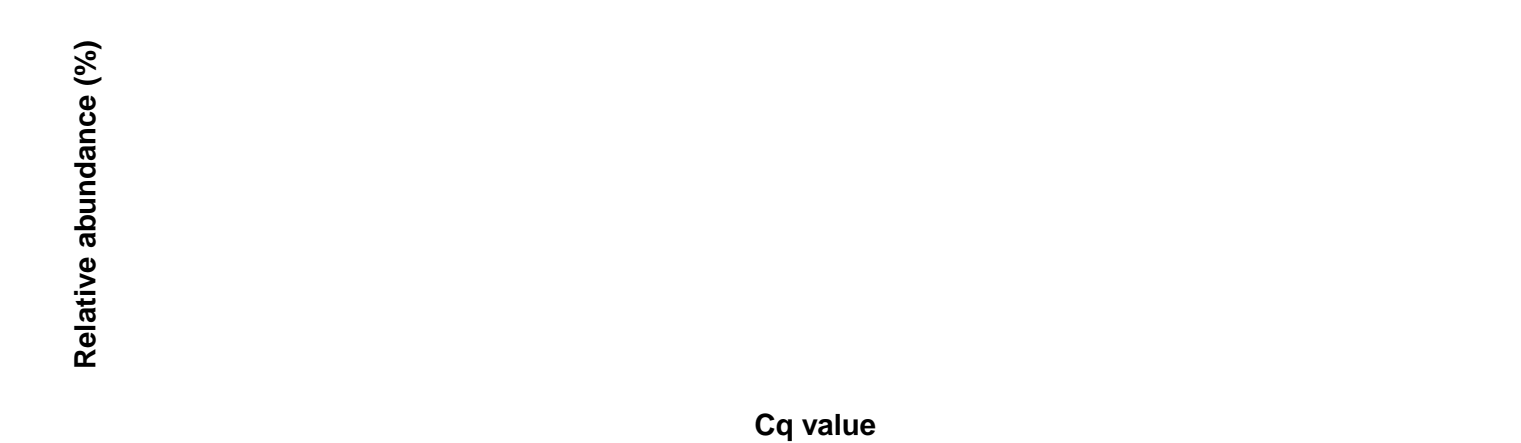$\log_e(S) = 2.485$, $p = 0.036$, $\hat{\rho}_{Spearman} = 0.786$, $CI_{95\%}$ [0.051, 0.969], $n_{pairs} = 7$
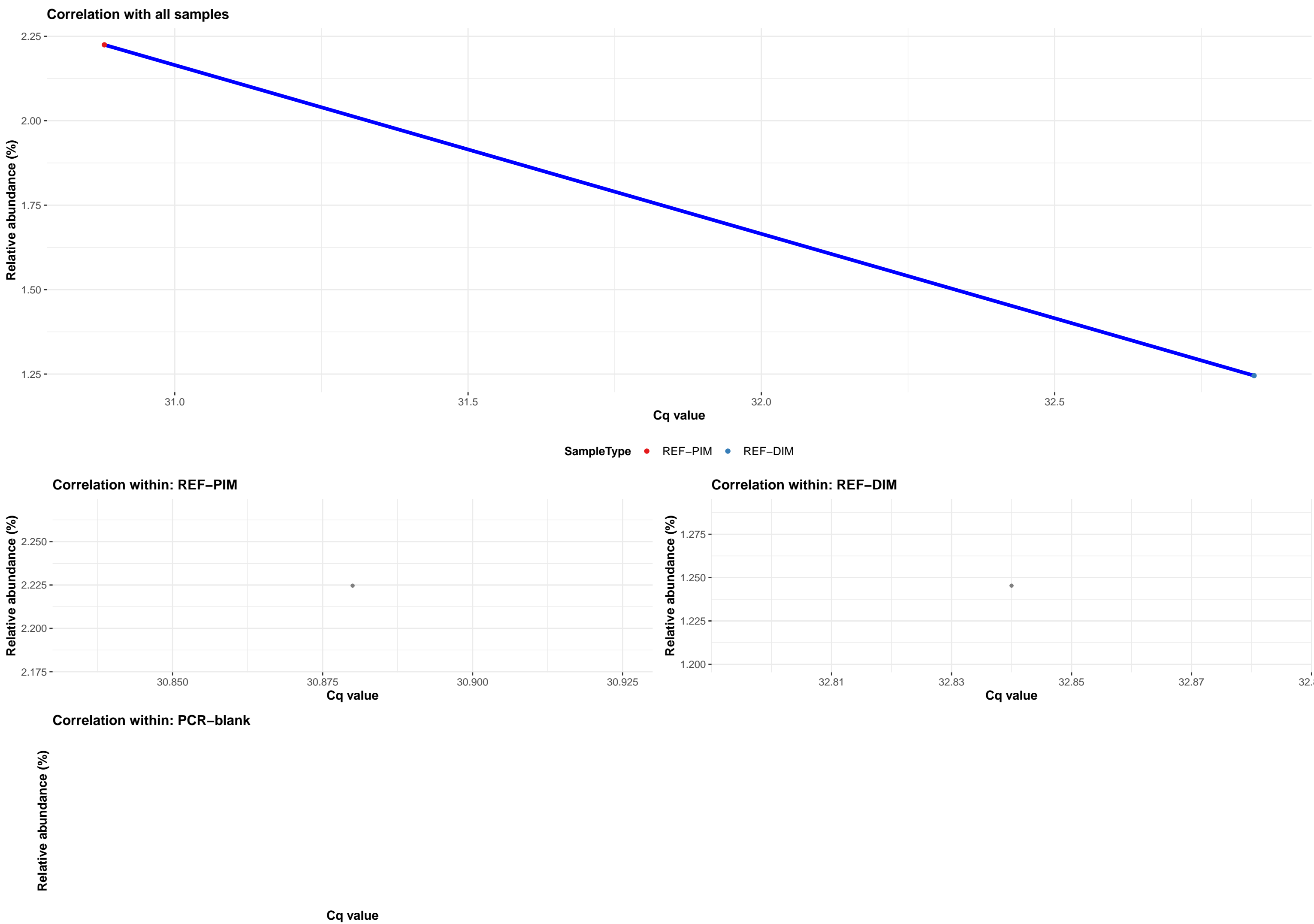

SampleType ● REF−PIM ● REF−DIM

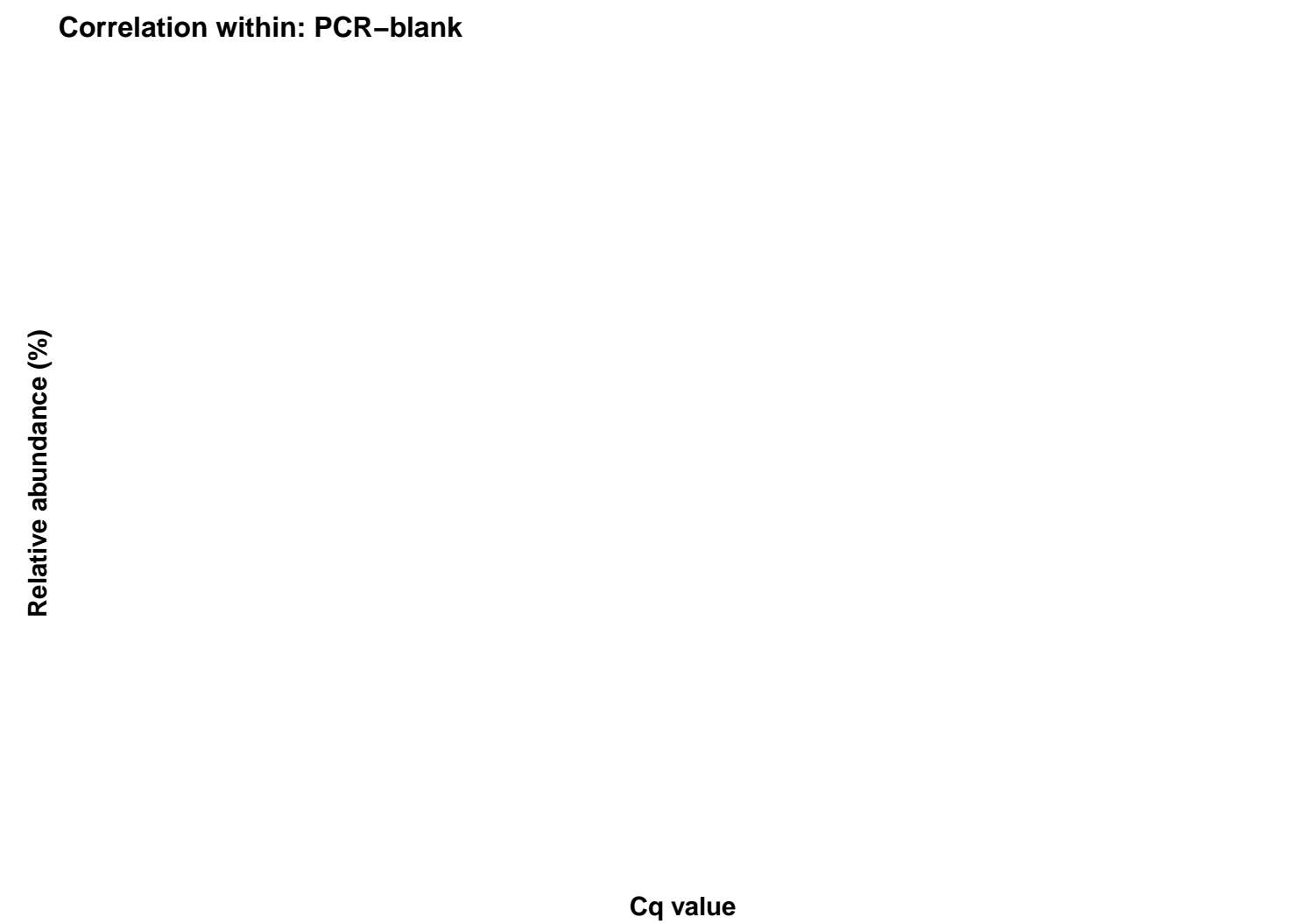**Correlation within: REF−PIM**

Correlation within: REF−DIM

Correlation within: PCR−blank

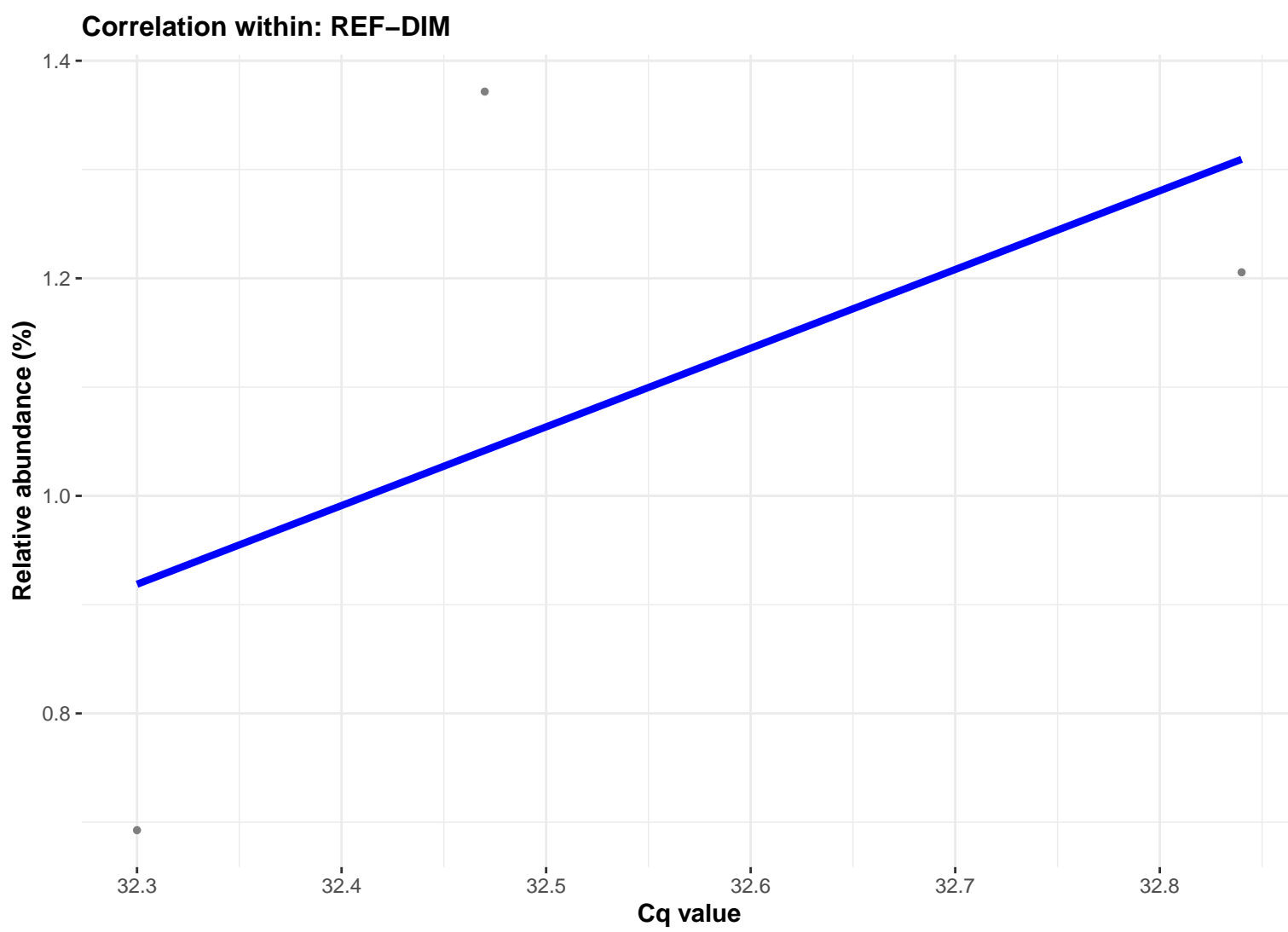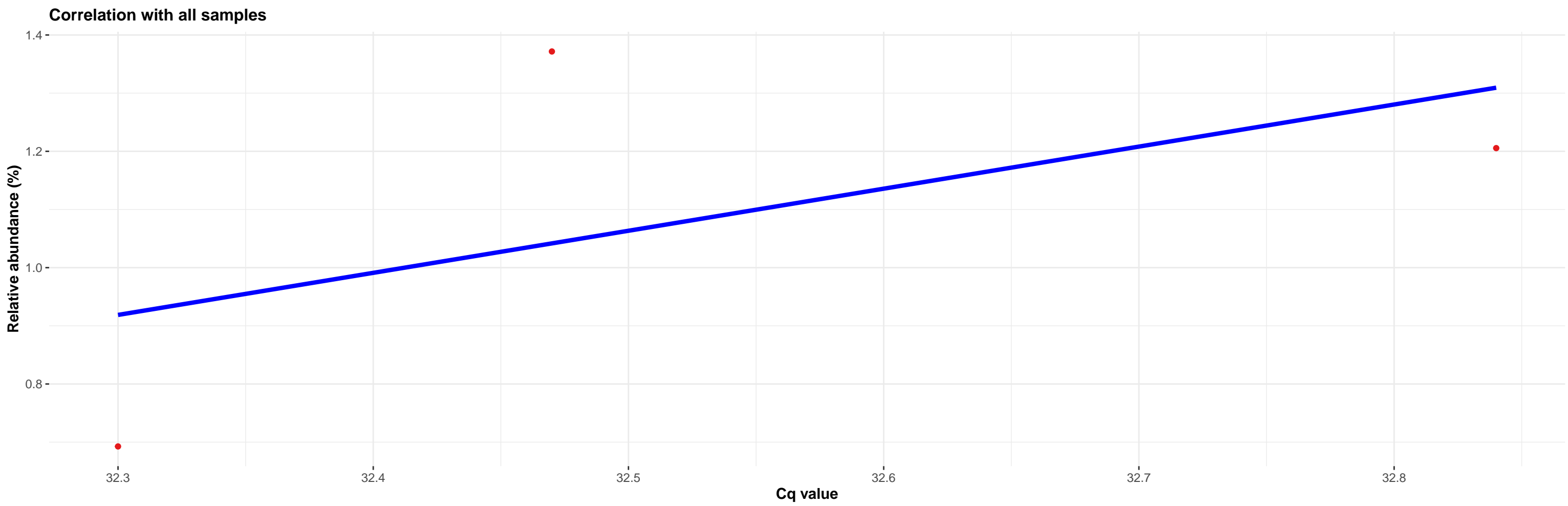**k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa**
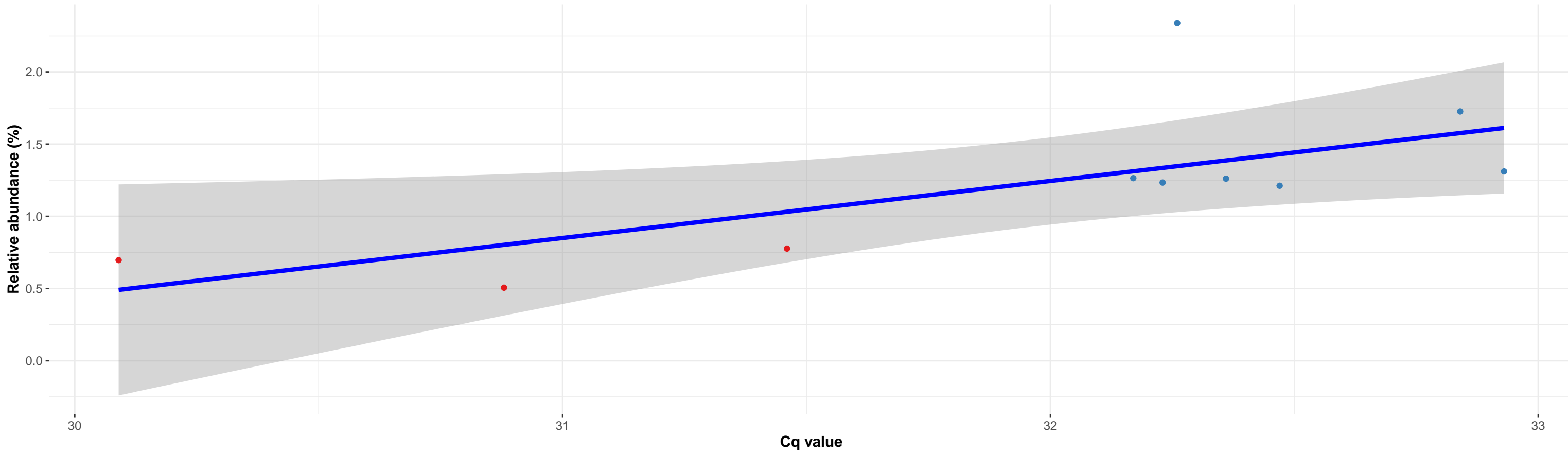
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA
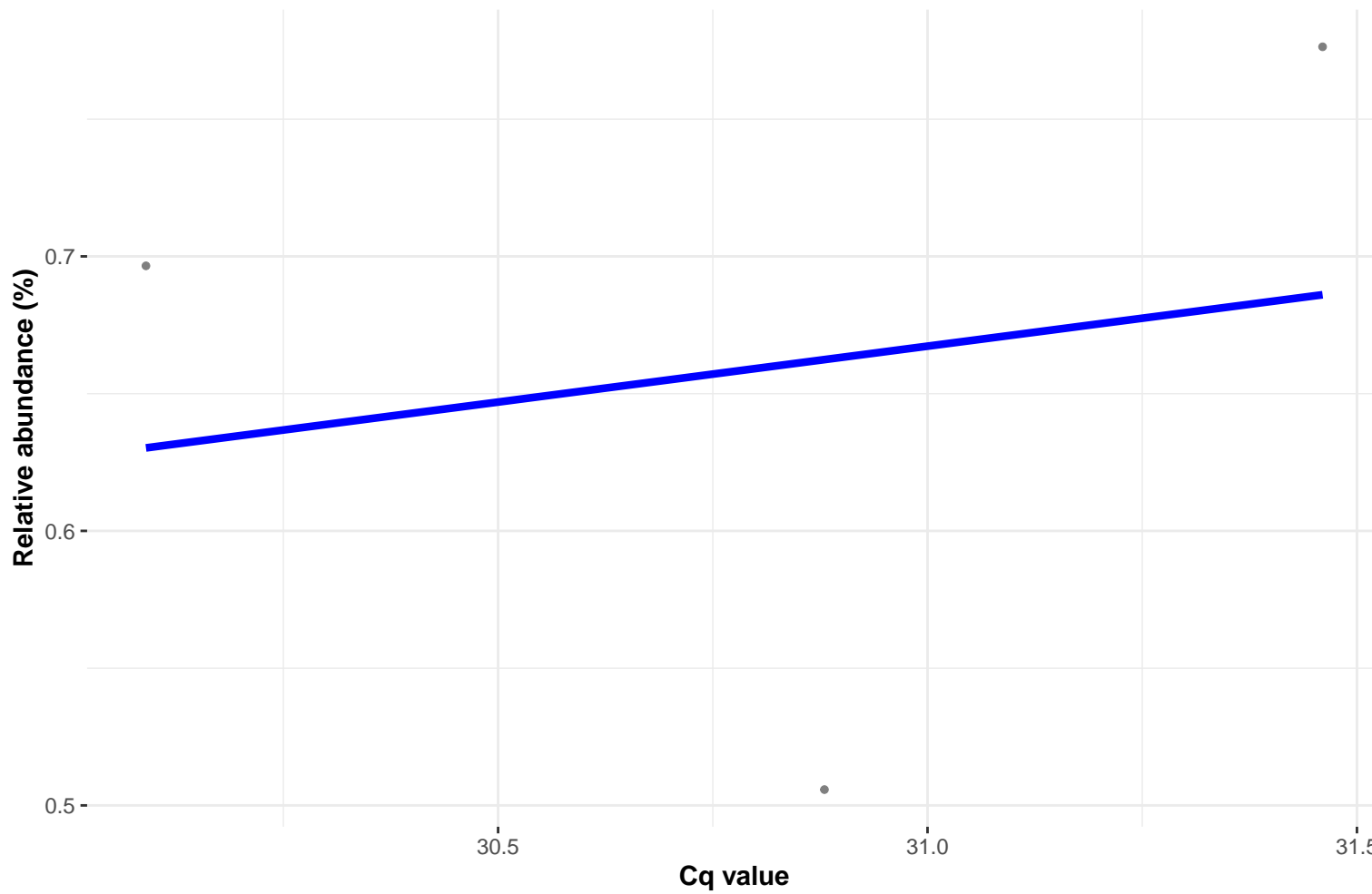
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa

Correlation with all samples

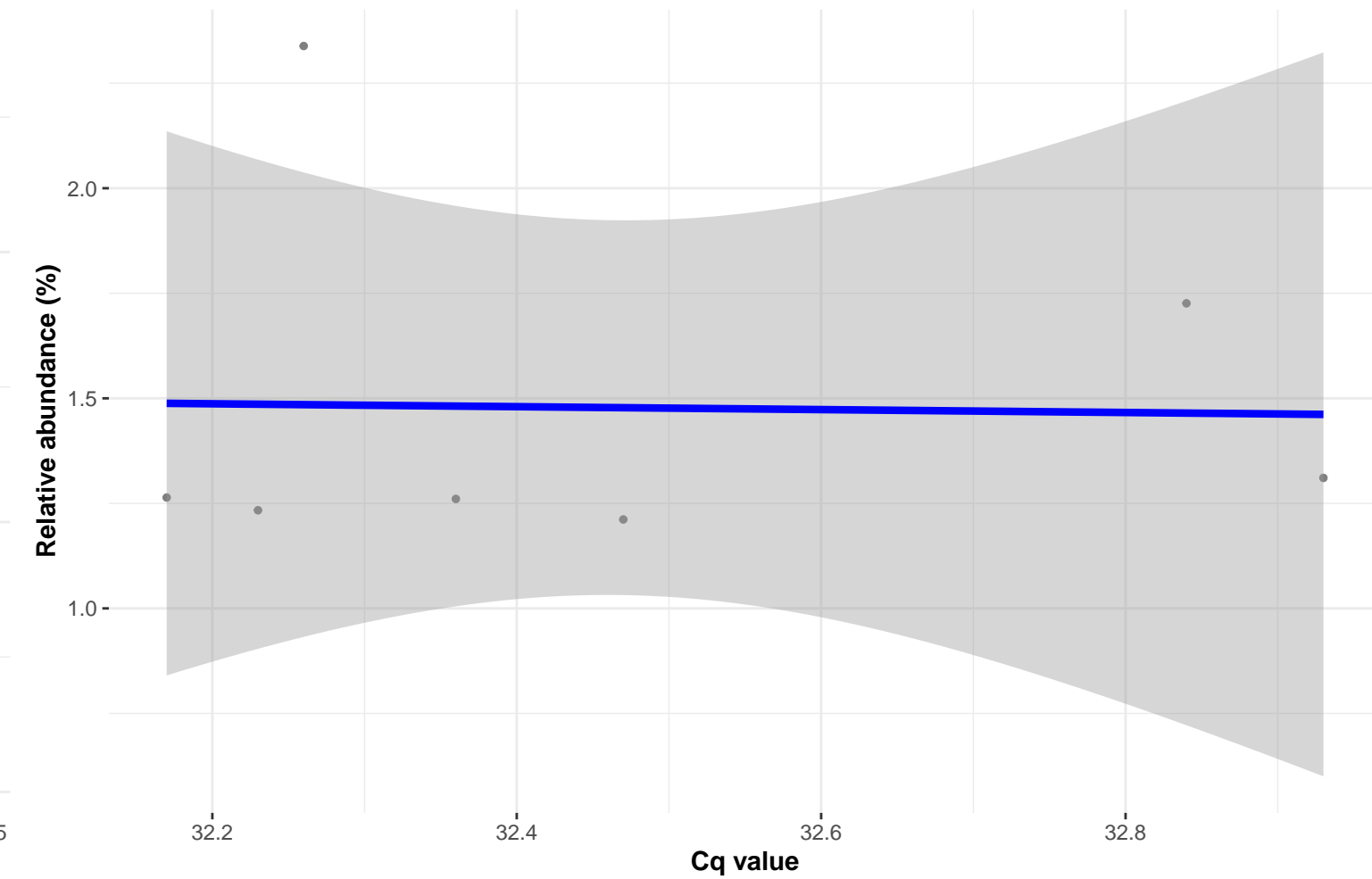$\log_e(S) = 3.871$, $p = 0.022$, $\hat{\rho}_{Spearman} = 0.709$, $CI_{95\%}$ [0.122, 0.929], $n_{pairs} = 10$

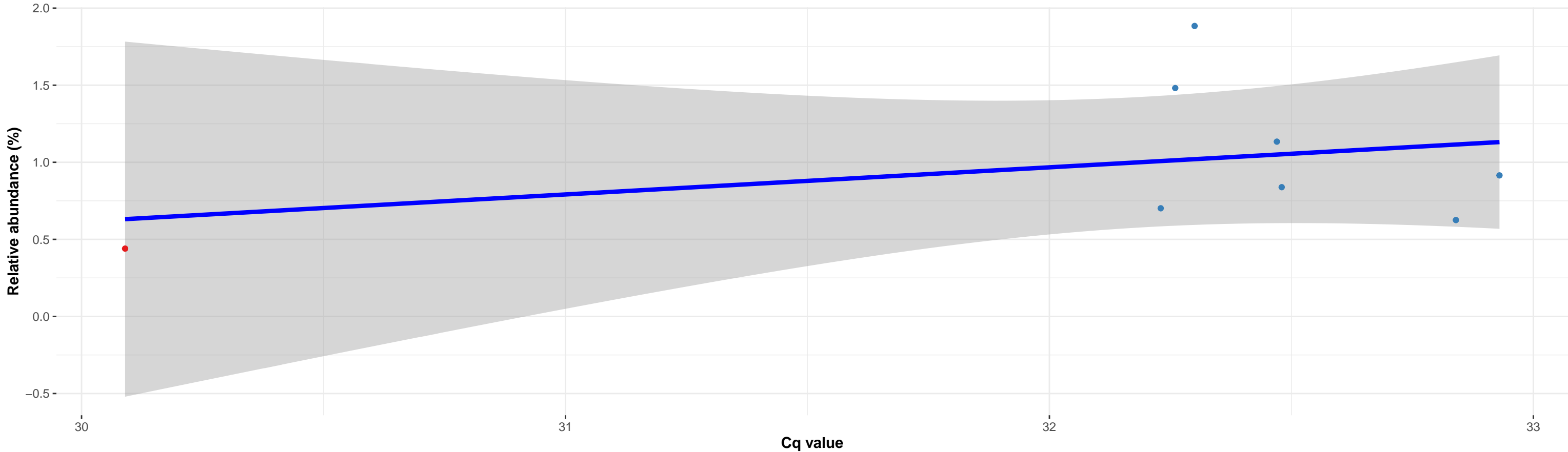SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

$\log_e(S) = 3.829$, $p = 0.702$, $\hat{\rho}_{Spearman} = 0.179$, $CI_{95\%}$ [−0.680, 0.830], $n_{pairs} = 7$
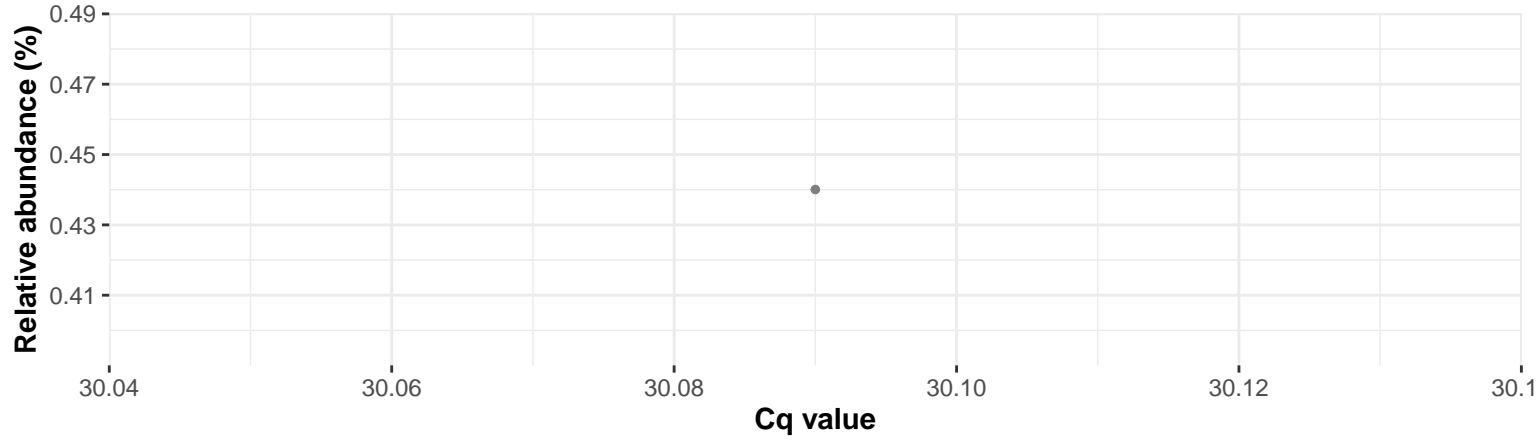
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; NA; NA

Correlation with all samples

$\log_e(S) = 4.277$, $p = 0.736$, $\hat{\rho}_{Spearman} = 0.143$, $CI_{95\%}$ [−0.640, 0.780], $n_{pairs} = 8$

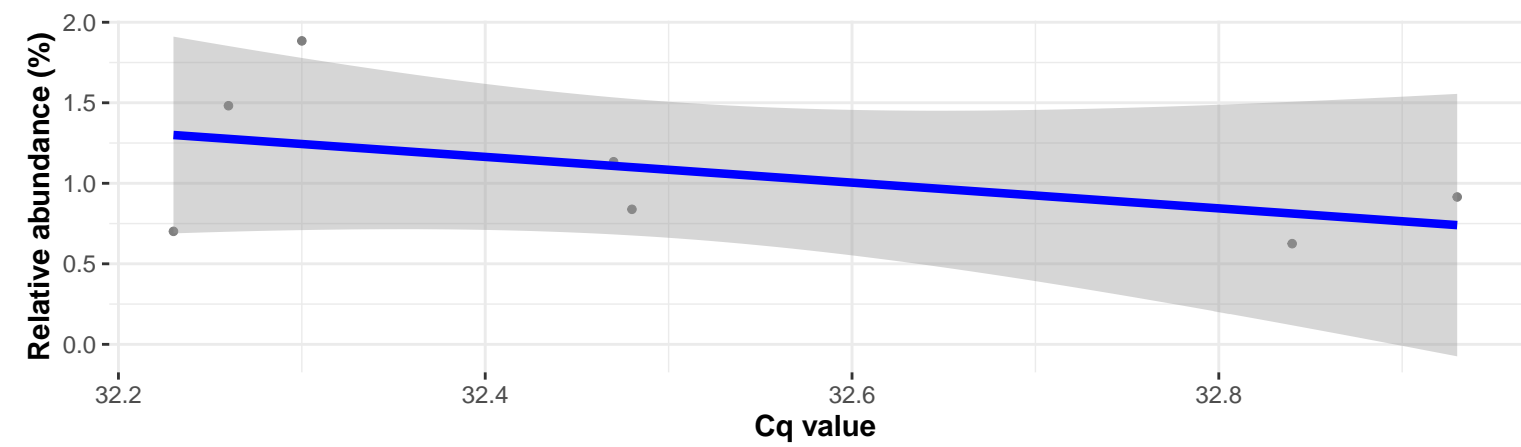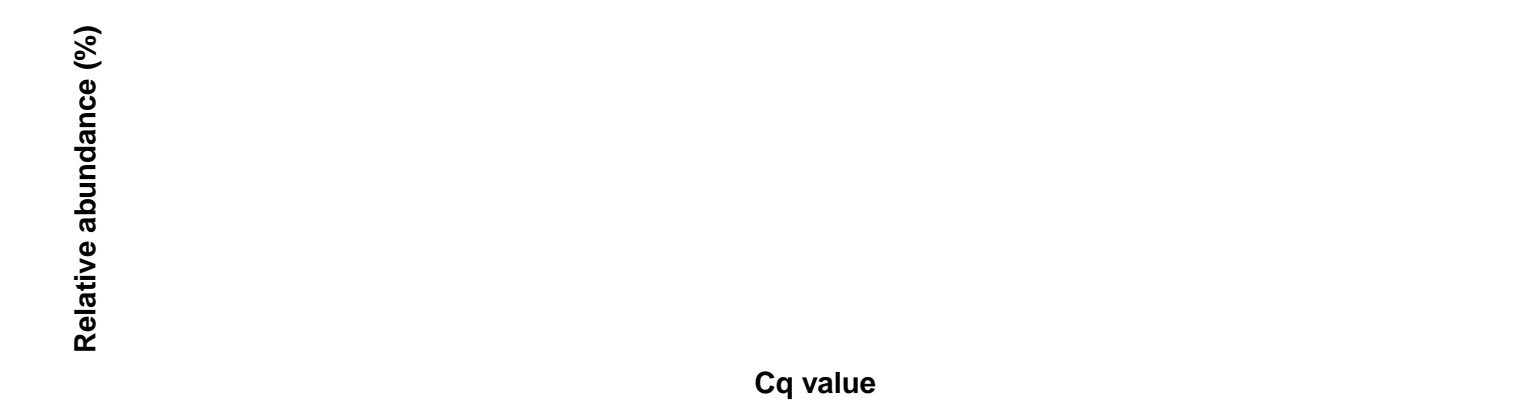**SampleType** ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

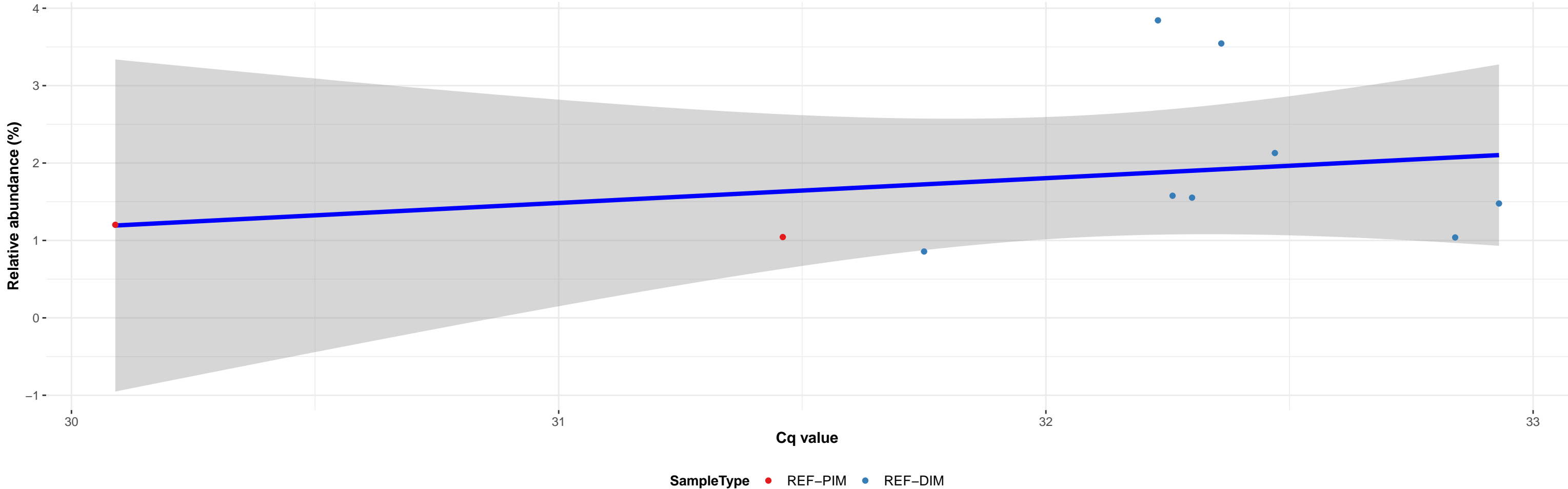$\log_e(S) = 4.277$, $p = 0.535$, $\hat{\rho}_{Spearman} = -0.286$, $CI_{95\%}$ [−0.862, 0.614], $n_{pairs} = 7$
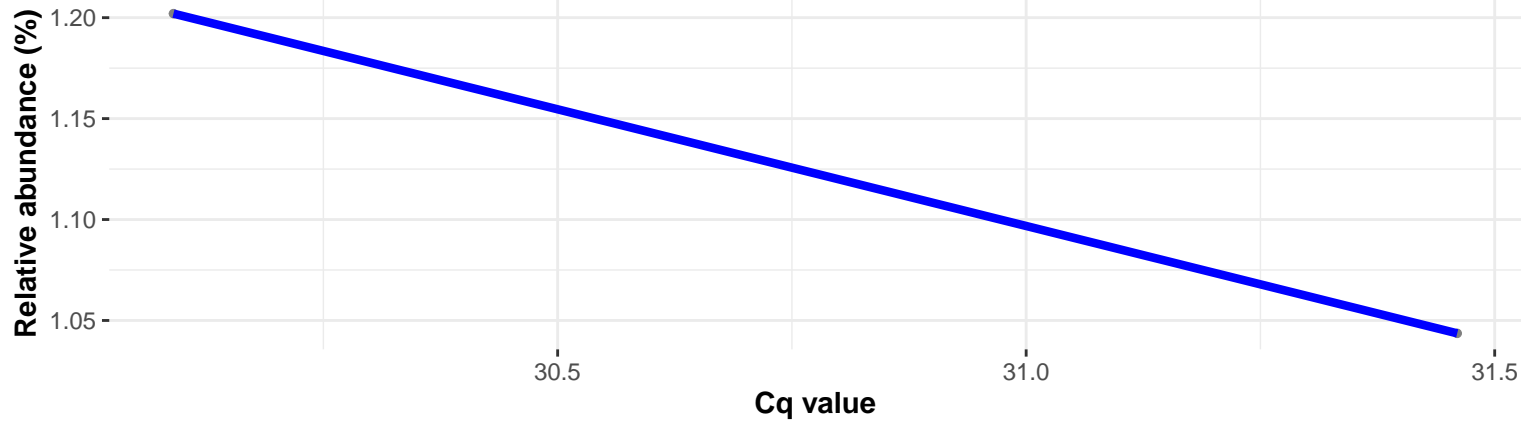
Correlation within: PCR−blank

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; NA

Correlation with all samples

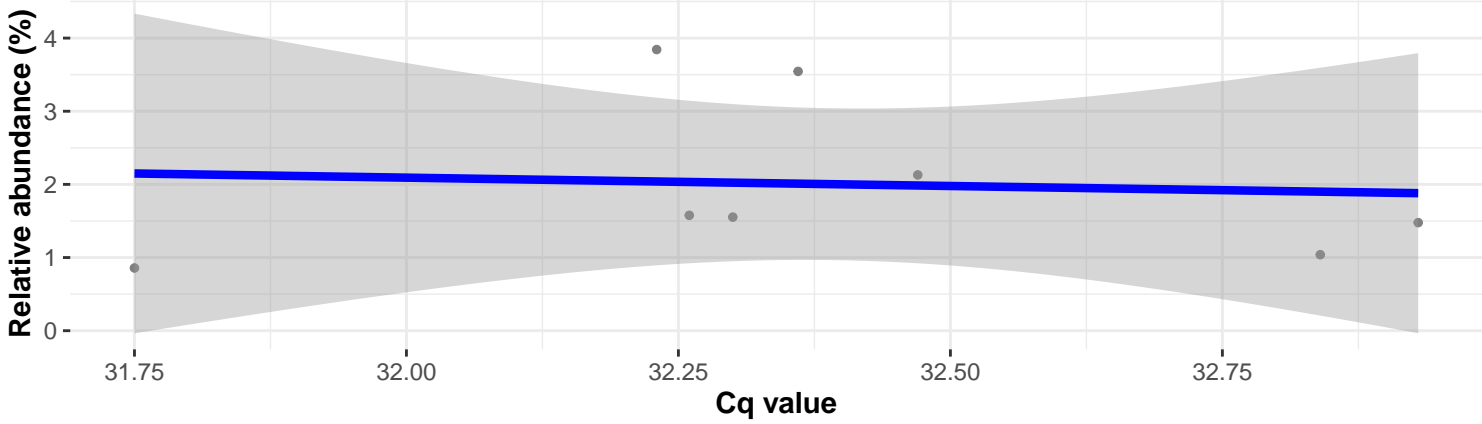$\log_e(S) = 4.883$, $p = 0.580$, $\hat{\rho}_{Spearman} = 0.200$, $CI_{95\%}$ [−0.508, 0.747], $n_{pairs} = 10$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

$\log_e(S) = 4.543$, $p = 0.779$, $\hat{\rho}_{Spearman} = -0.119$, $CI_{95\%}$ [−0.771, 0.654], $n_{pairs} = 8$

Correlation within: PCR−blank
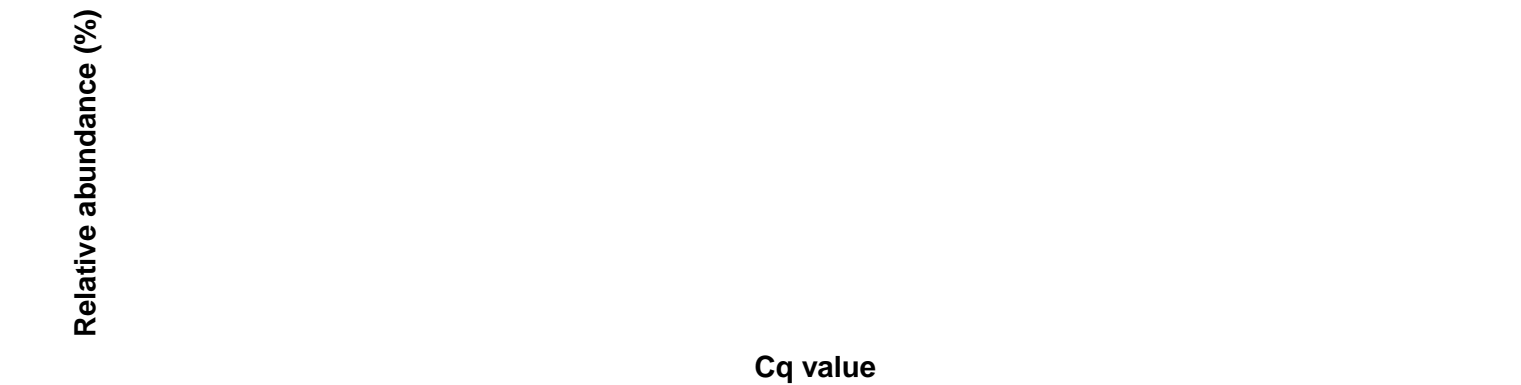
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Beutenbergiaceae; NA; NA
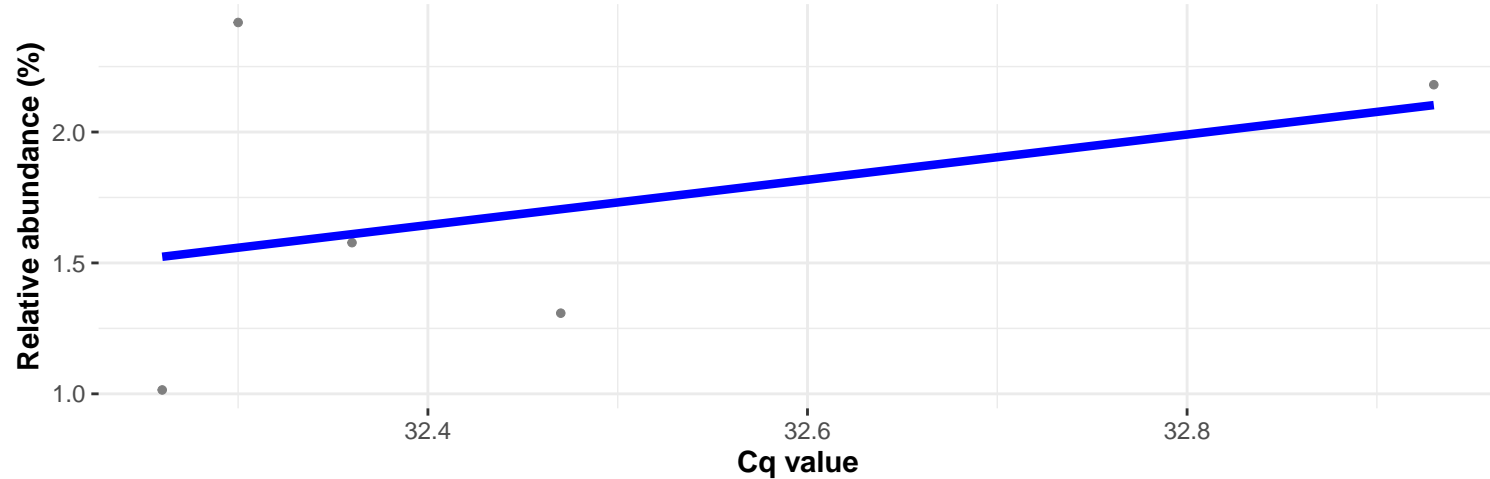

Correlation with all samples

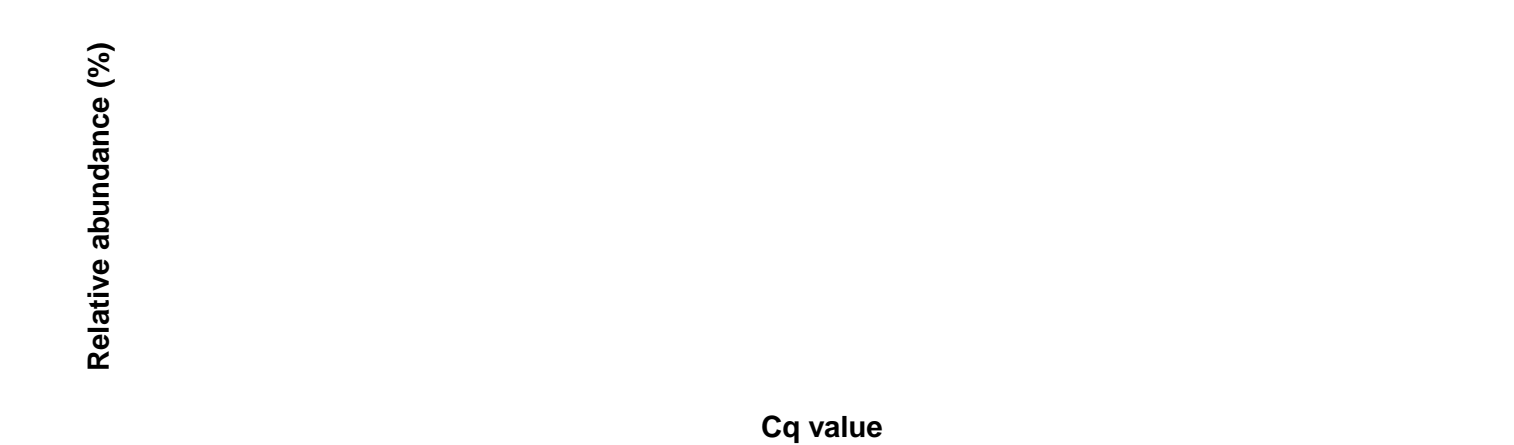$\log_e(S) = 2.639$, $p = 0.208$, $\hat{\rho}_{Spearman} = 0.600$, $CI_{95\%}$ [−0.440, 0.953], $n_{pairs} = 6$
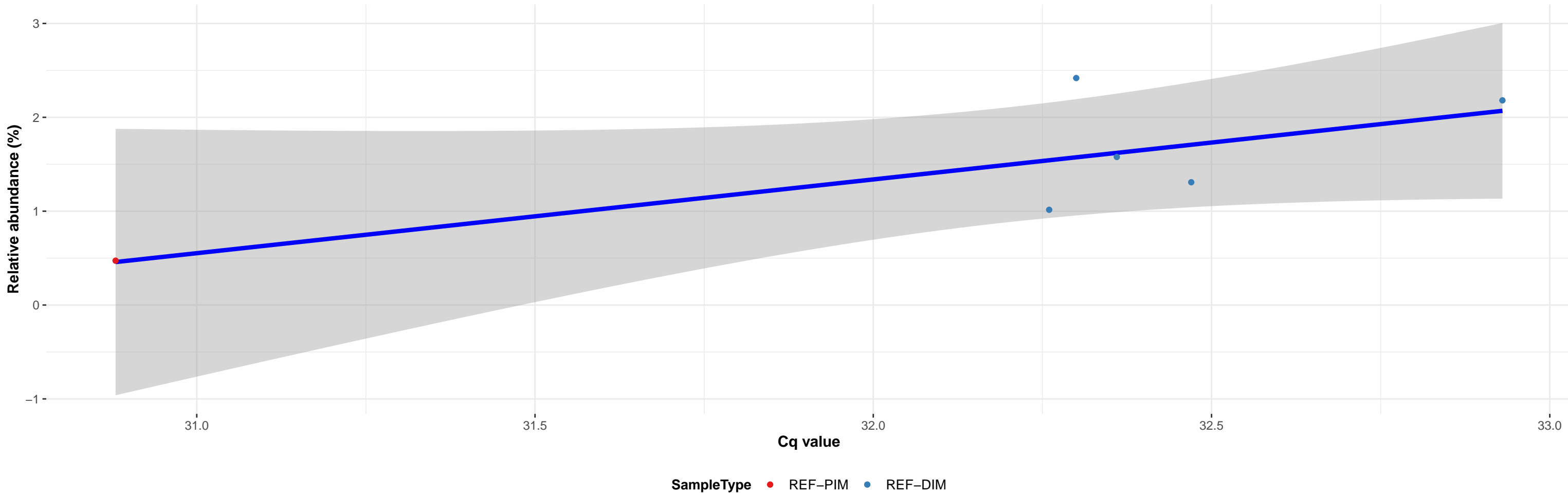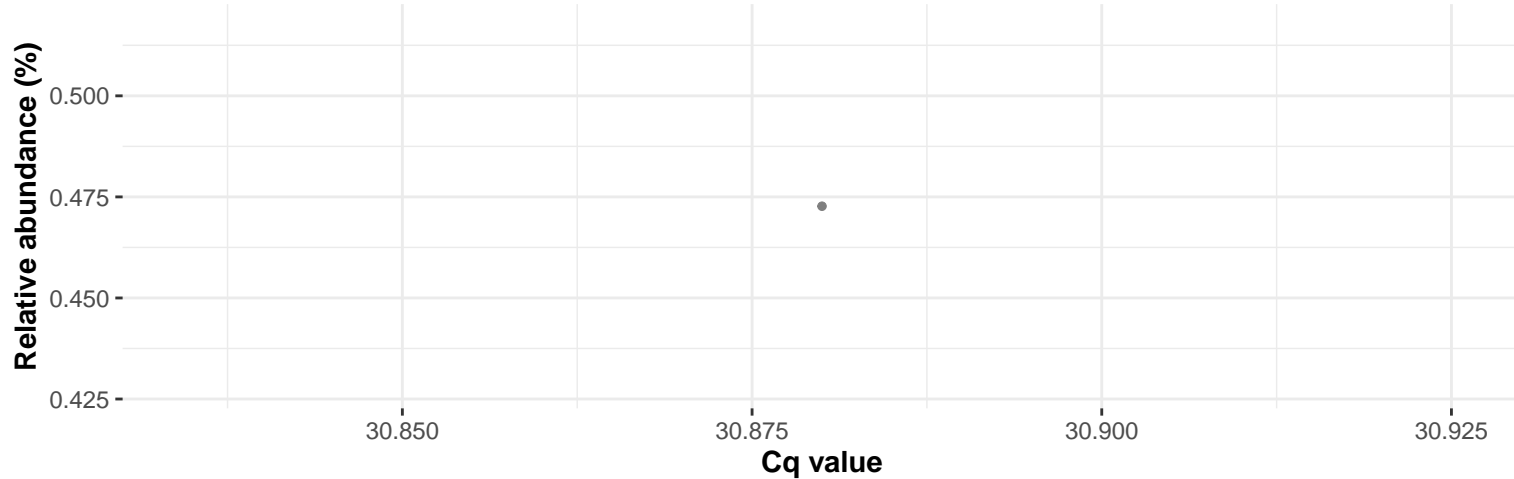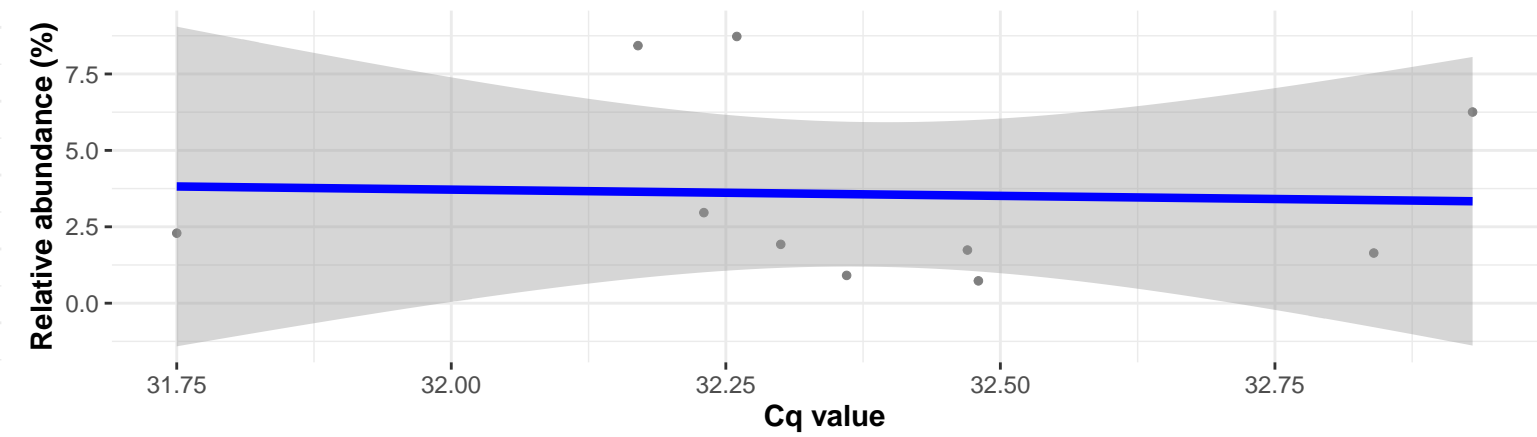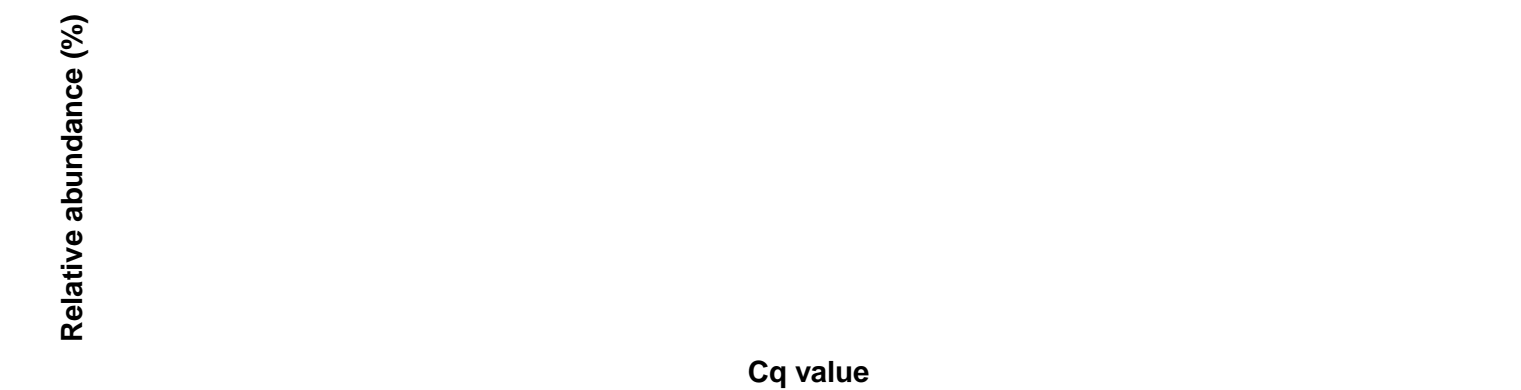
SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Sphingobacteriales; f__env.OPS 17; g__uncultured bacterium; s__uncultured bacterium

Correlation with all samples

Relative abundance (%)

Cq value

Correlation within: PCR−blank

Relative abundance (%)

Cq value

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Curvibacter; NA

Correlation with all samples

$\log_e(S) = 6.127$, $p = 0.982$, $\hat{\rho}_{Spearman} = -0.007$, $CI_{95\%}$ [-0.548, 0.538], $n_{pairs} = 14$

SampleType ● REF−PIM ● REF−DIM
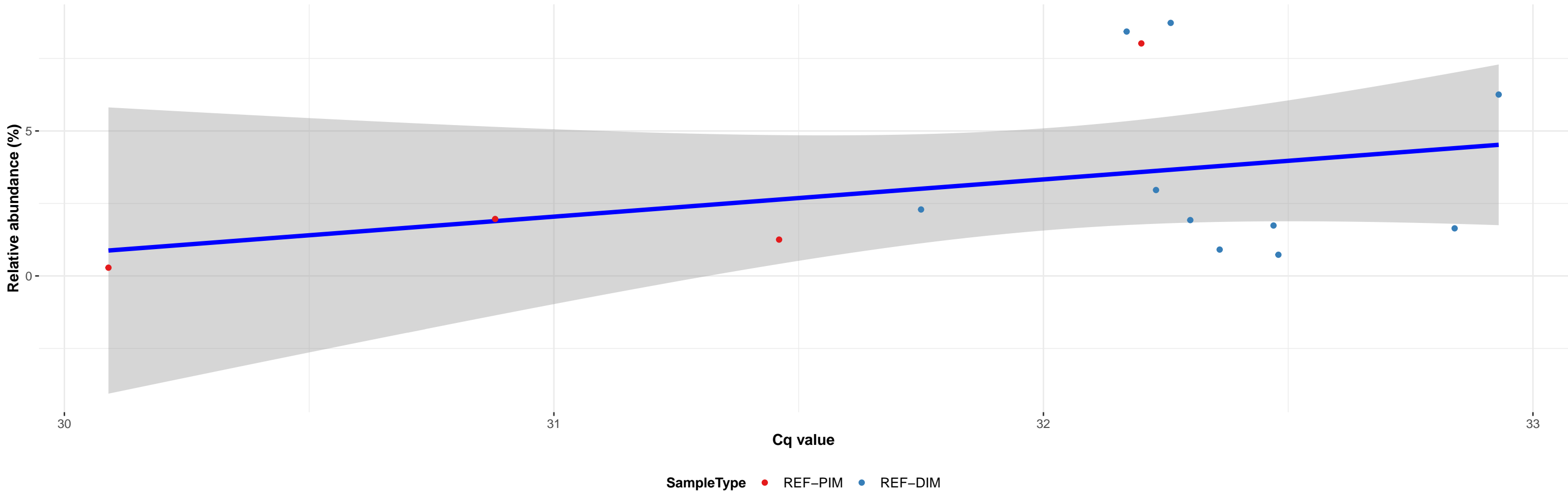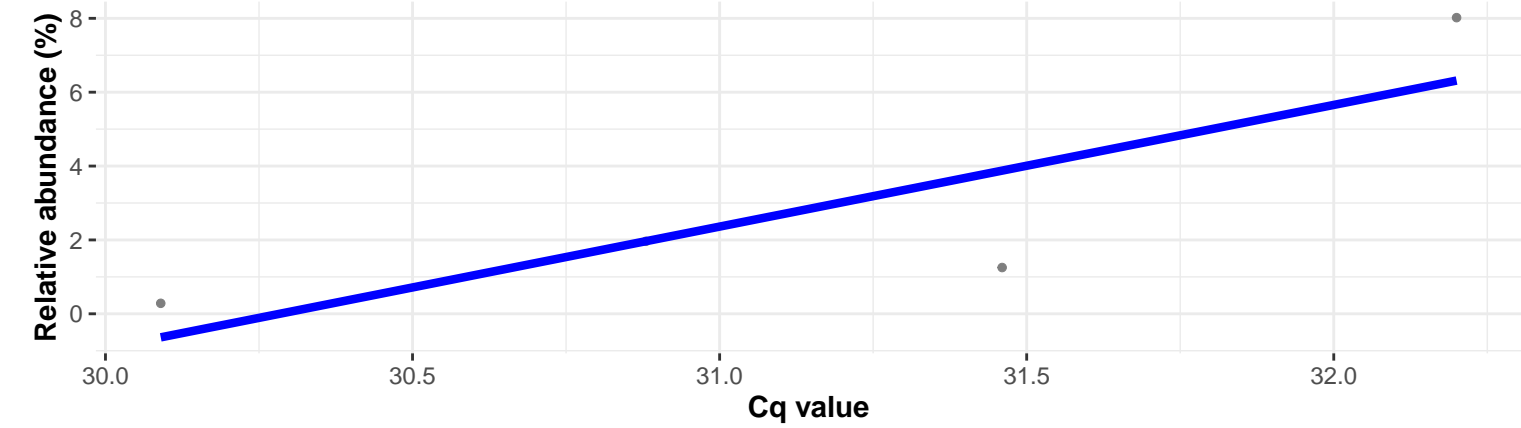
Correlation within: REF−DIM

$\log_e(S) = 5.481$, $p = 0.187$, $\hat{\rho}_{Spearman} = -0.455$, $CI_{95\%}$ [-0.849, 0.266], $n_{pairs} = 10$

Correlation within: REF−PIM

Correlation within: PCR−blank

**k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA**

Correlation with all samples

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM
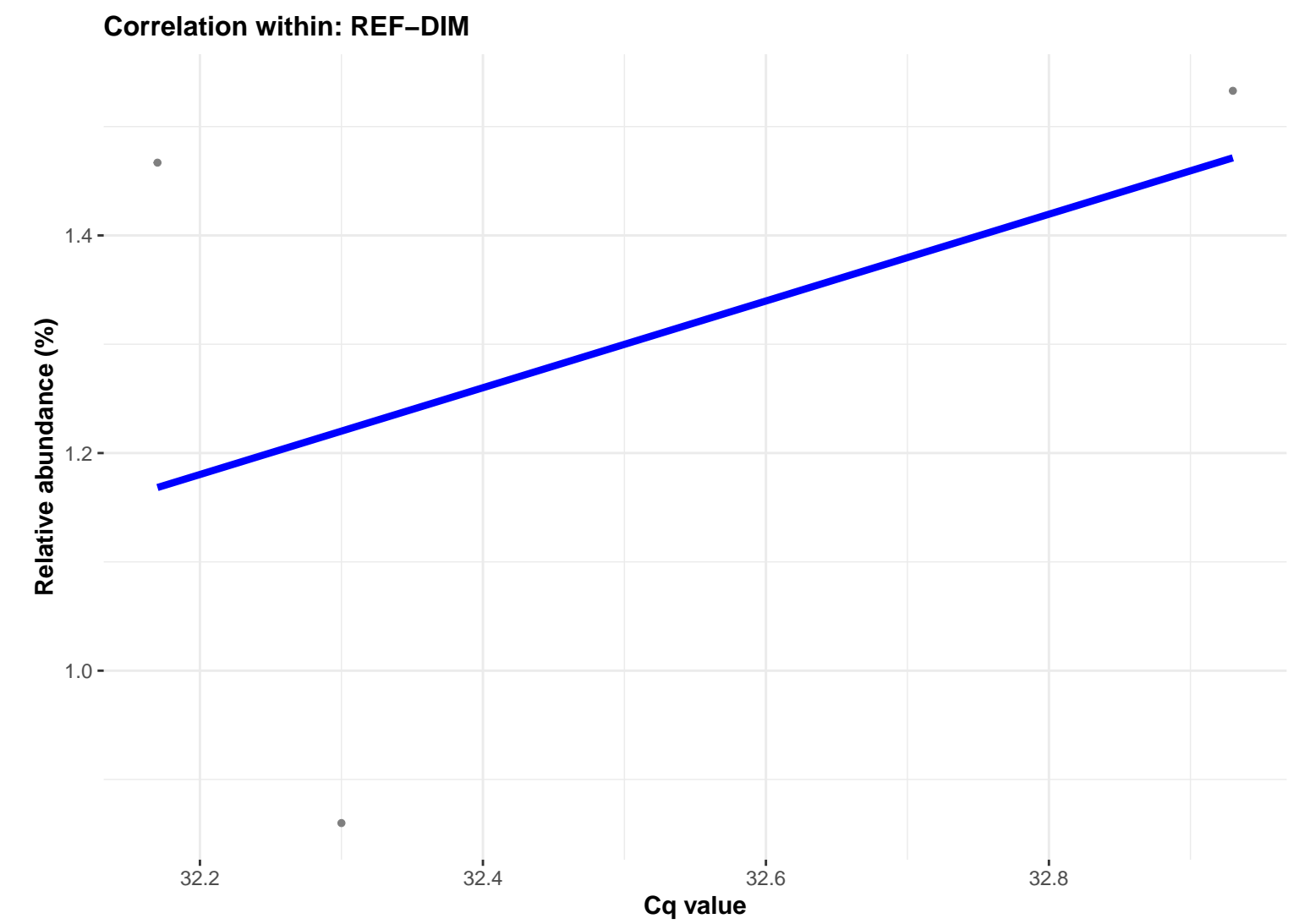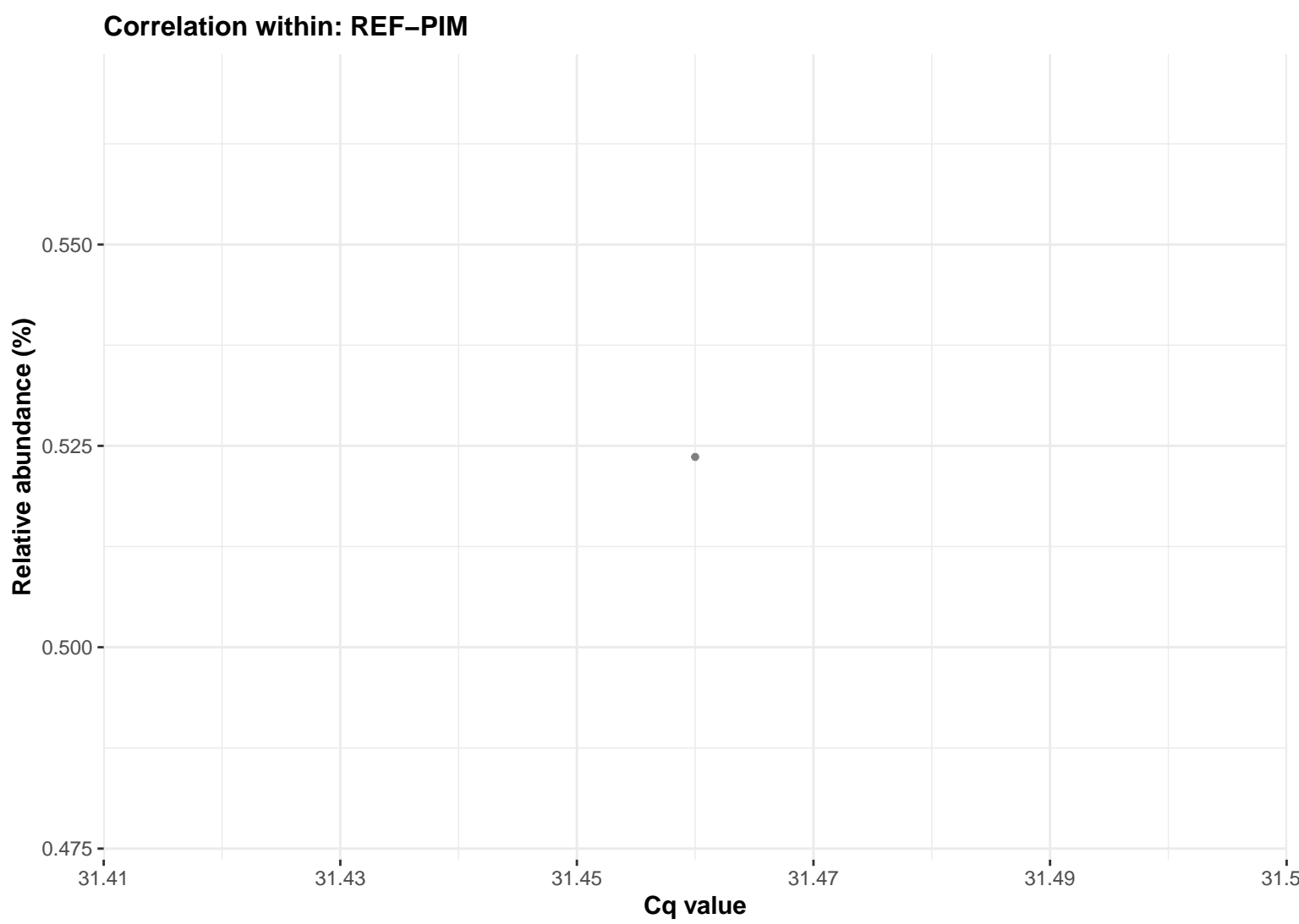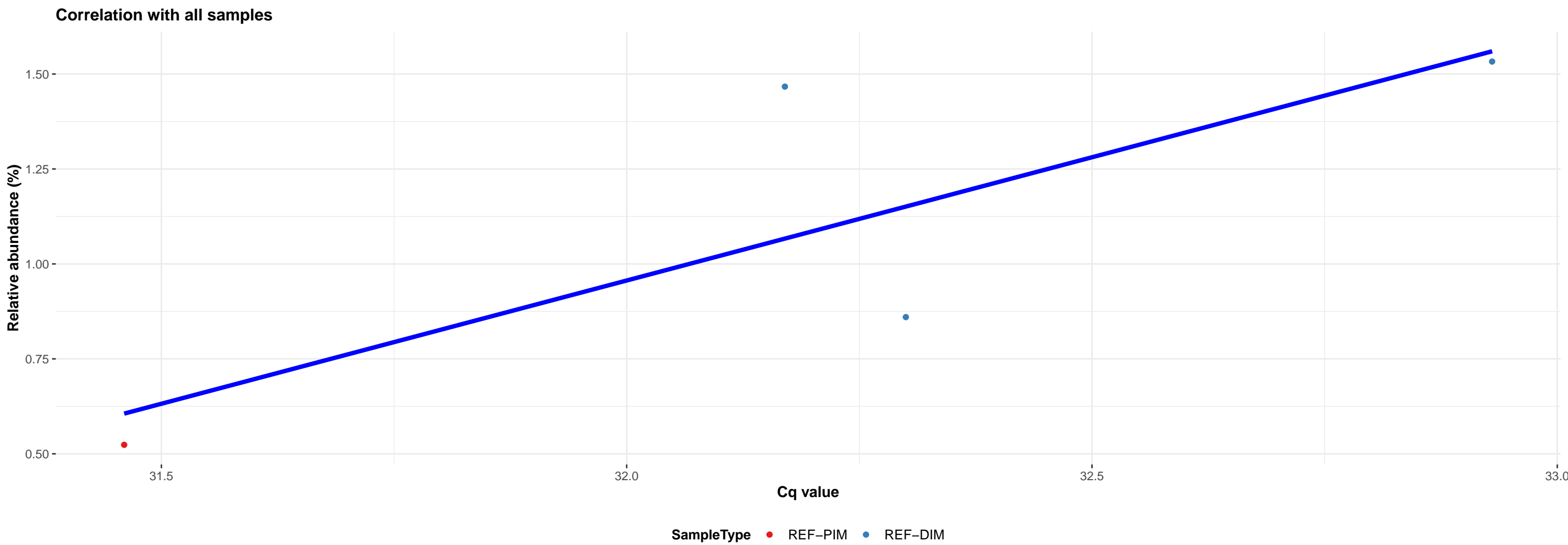
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA
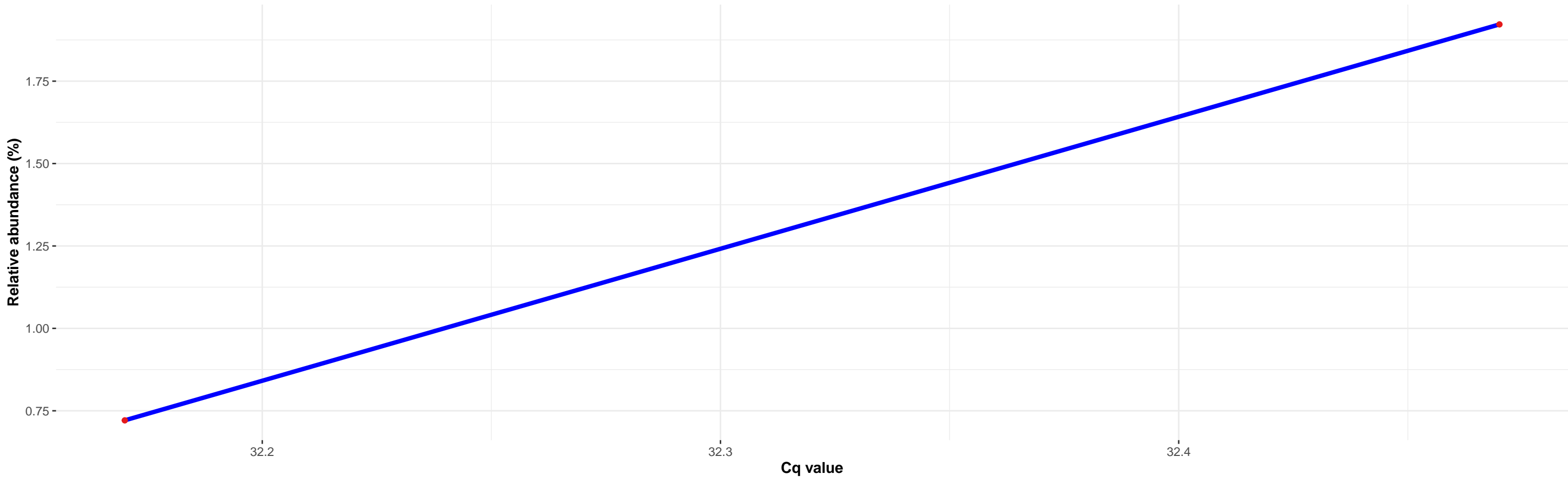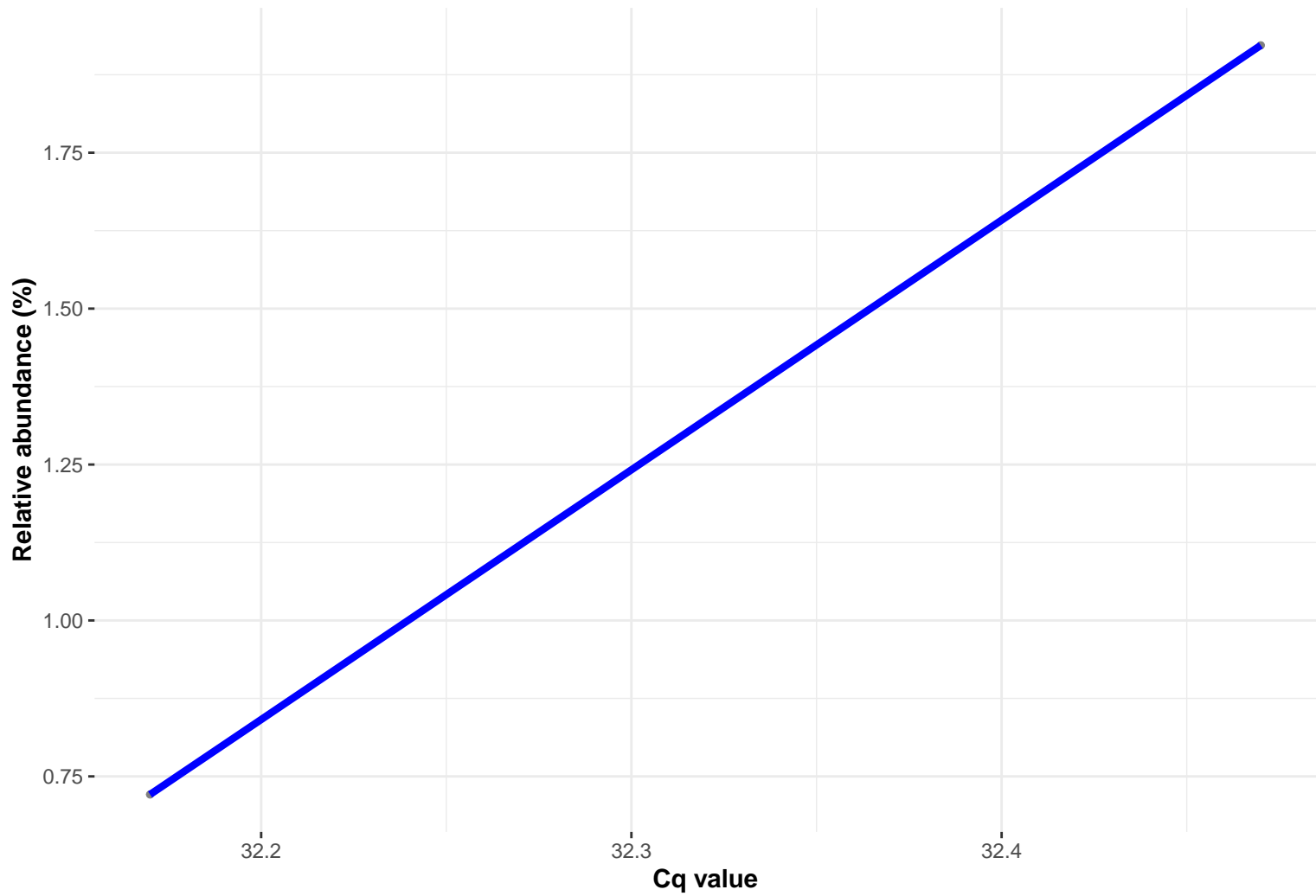
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa
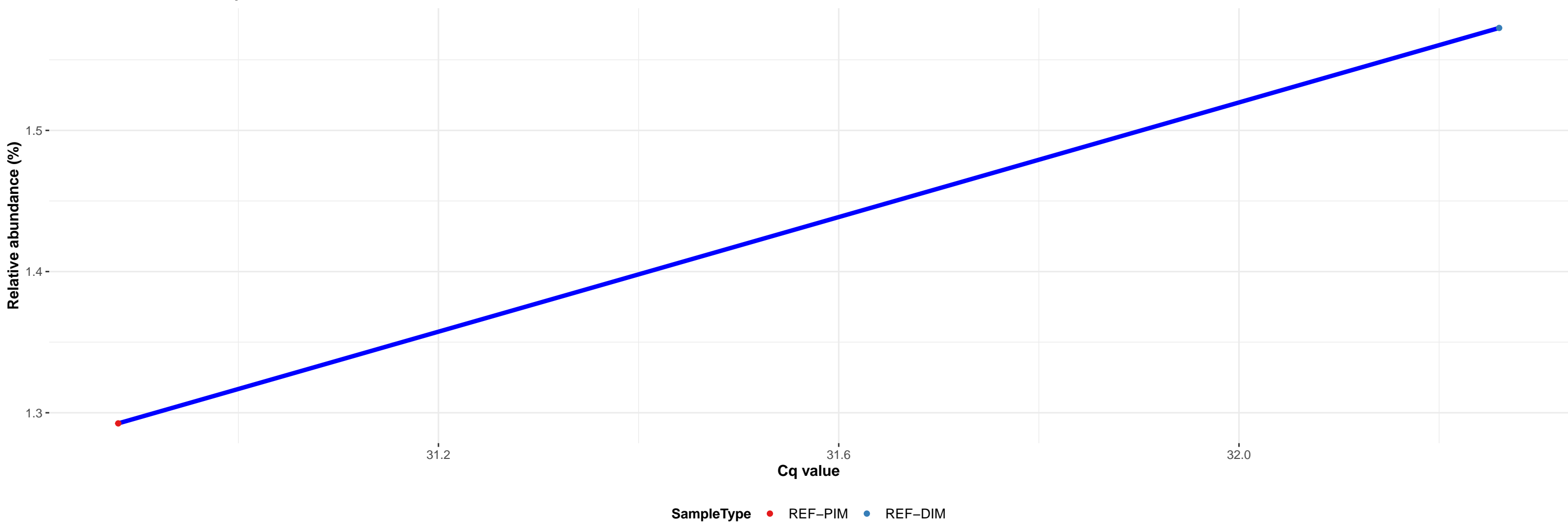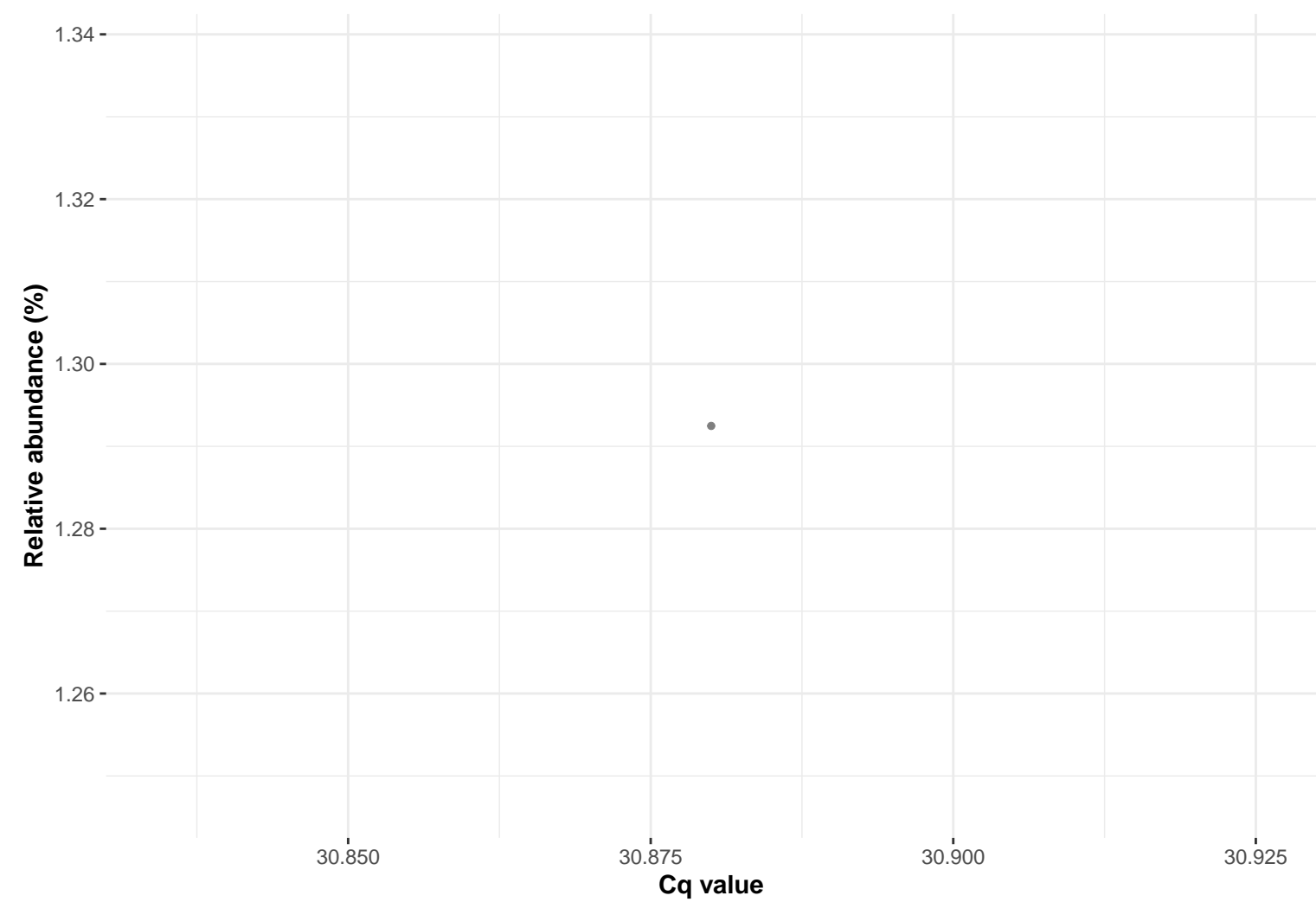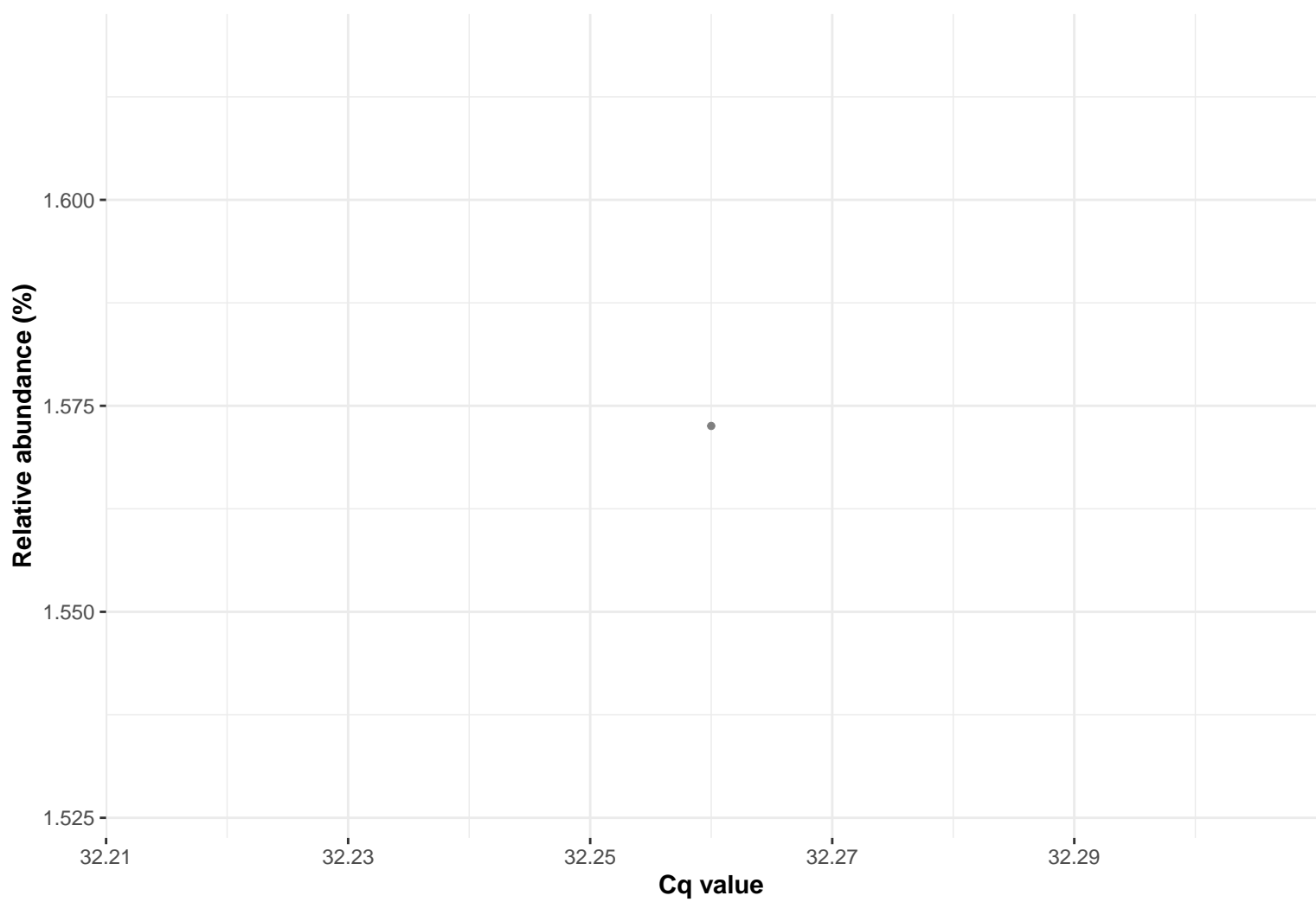
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; s__uncultured Ralstonia sp.

Correlation with all samples

$\log_e(S) = 6.040$, $p = 0.616$, $\widehat{\rho}_{Spearman} = -0.154$, $CI_{95\%}$ [−0.660, 0.449], $n_{pairs} = 13$

SampleType ● REF−PIM ● REF−DIM
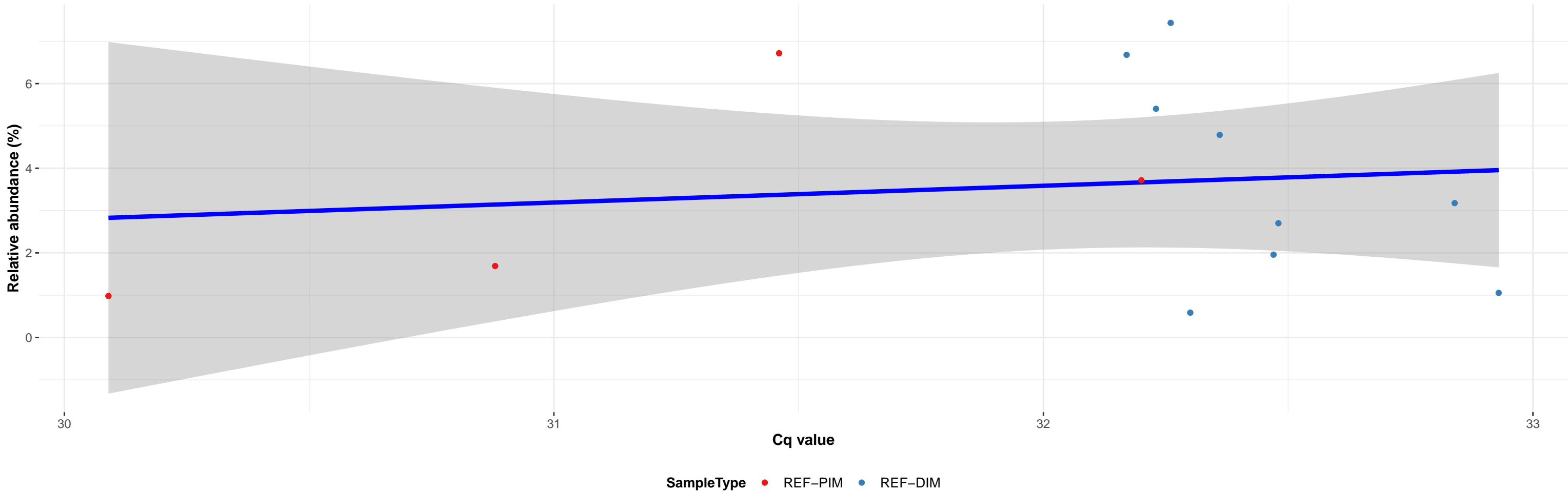
Correlation within: REF−PIM
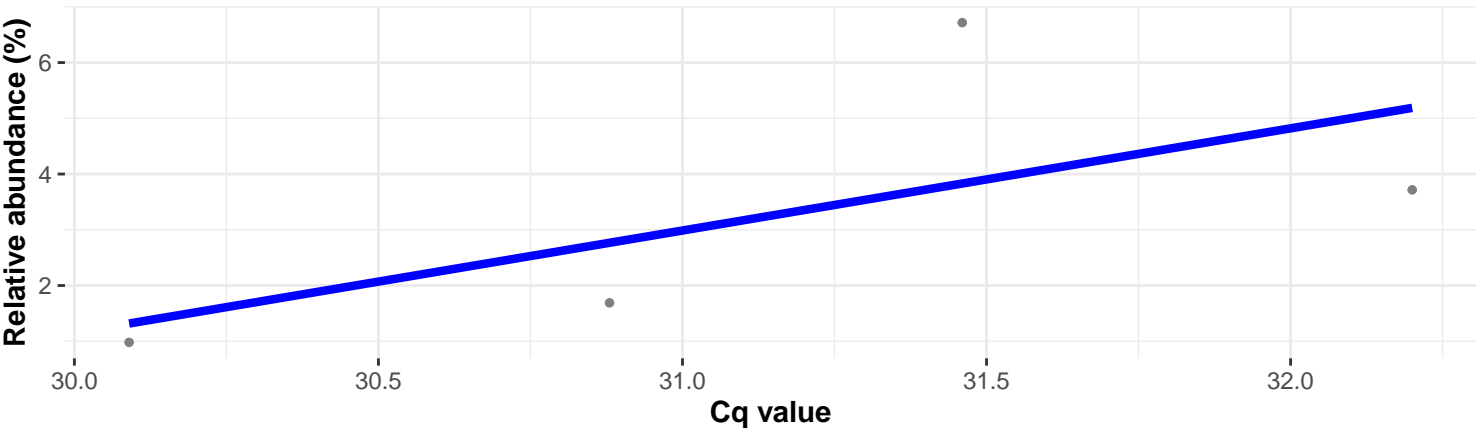
Correlation within: REF−DIM

$\log_e(S) = 5.278$, $p = 0.067$, $\widehat{\rho}_{Spearman} = -0.633$, $CI_{95\%}$ [−0.917, 0.077], $n_{pairs} = 9$
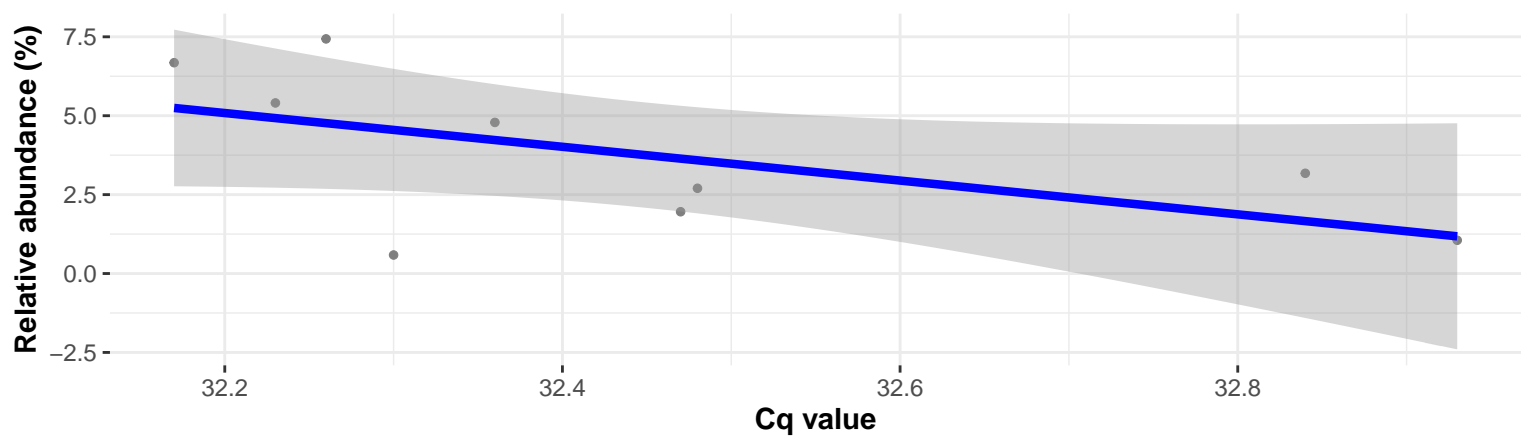
Correlation within: PCR−blank
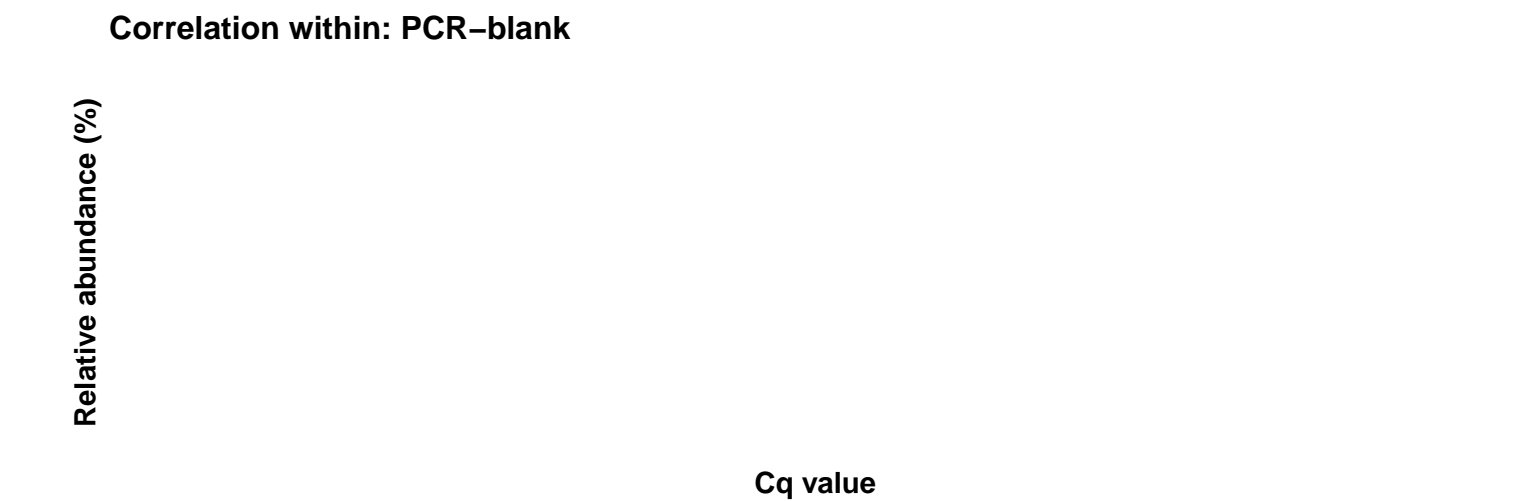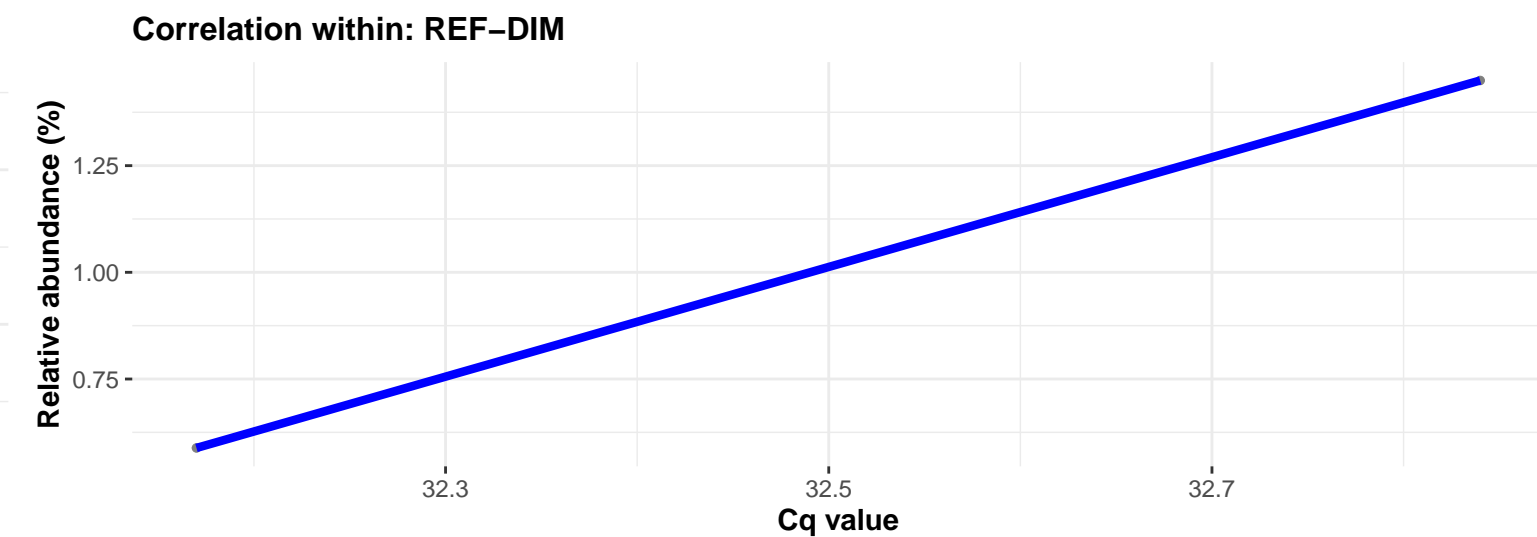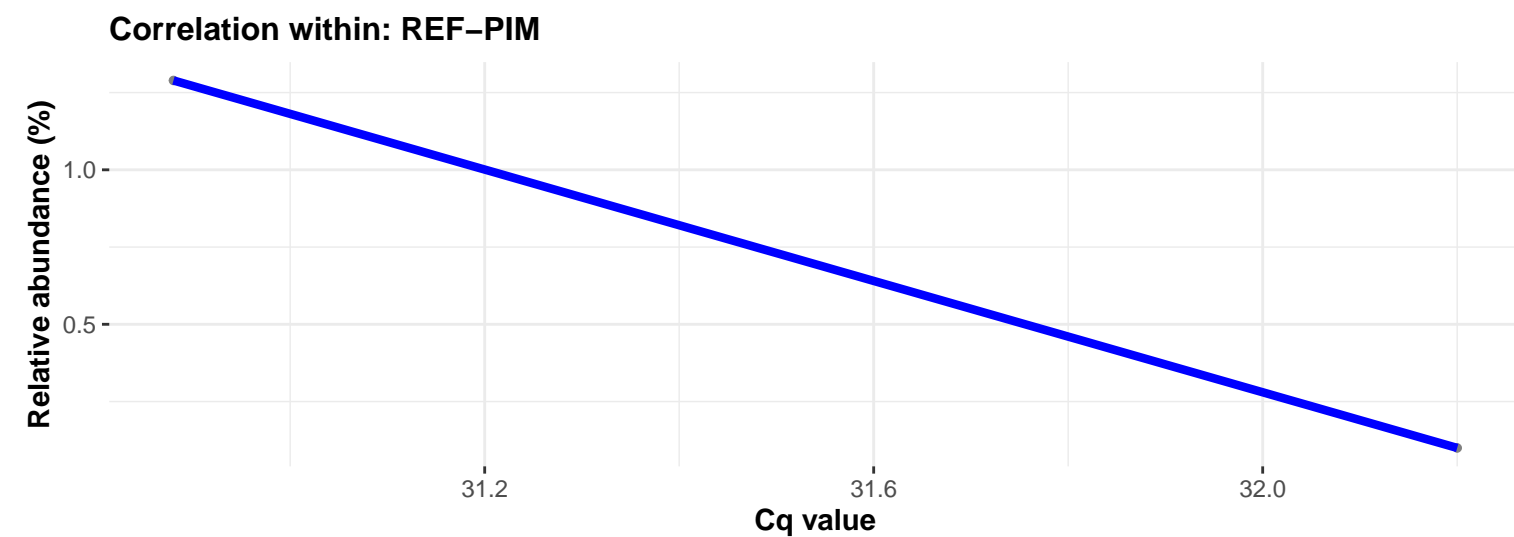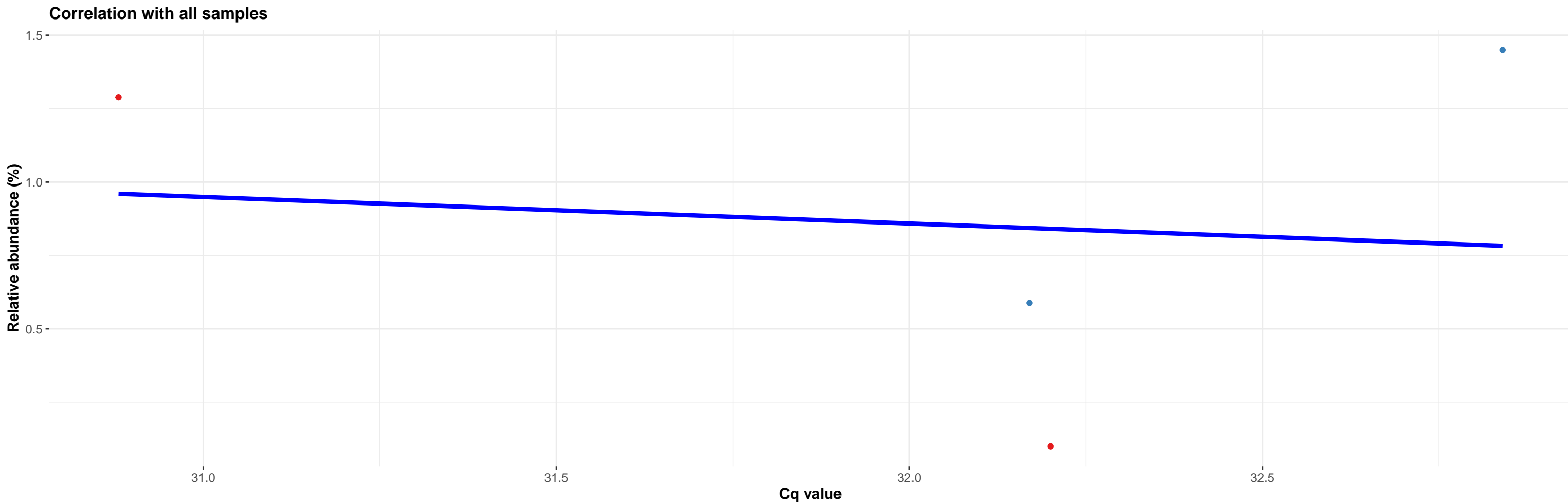
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Chitinophagales; f__Chitinophagaceae; NA; NA

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA
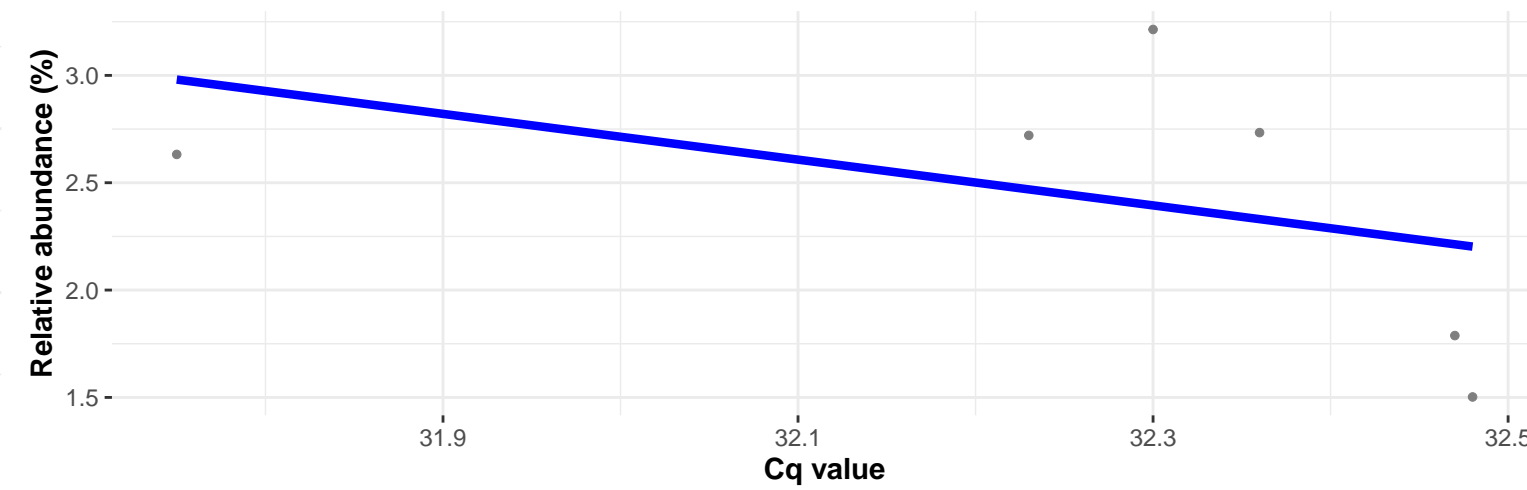
Correlation with all samples

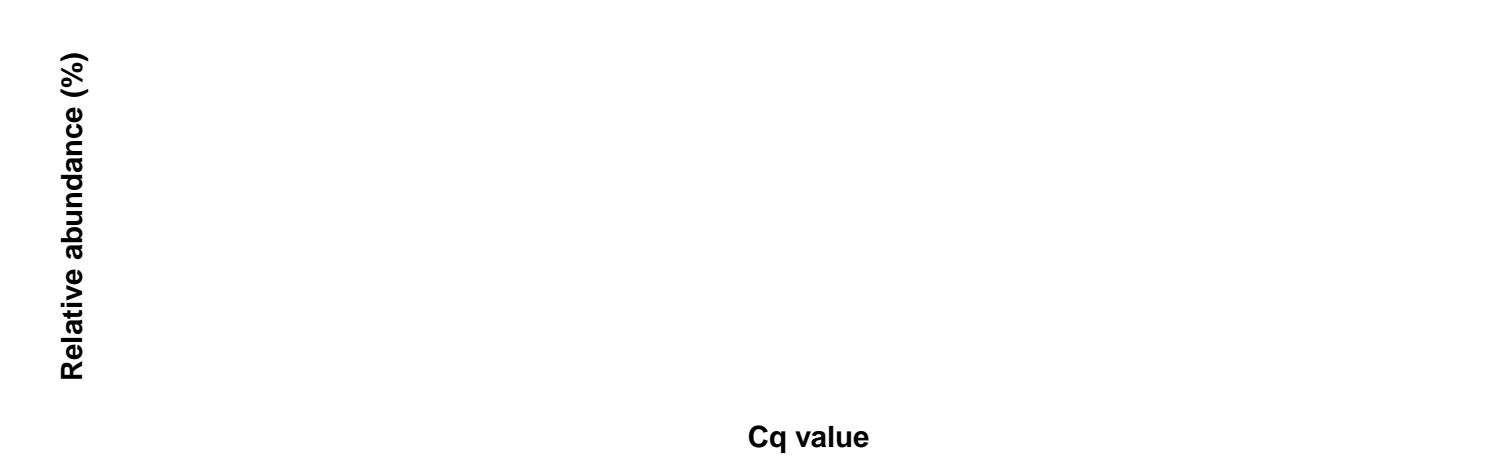$\log_e(S) = 4.357$, $p = 0.117$, $\hat{\rho}_{Spearman} = 0.527$, $CI_{95\%}$ [−0.175, 0.874], $n_{pairs} = 10$
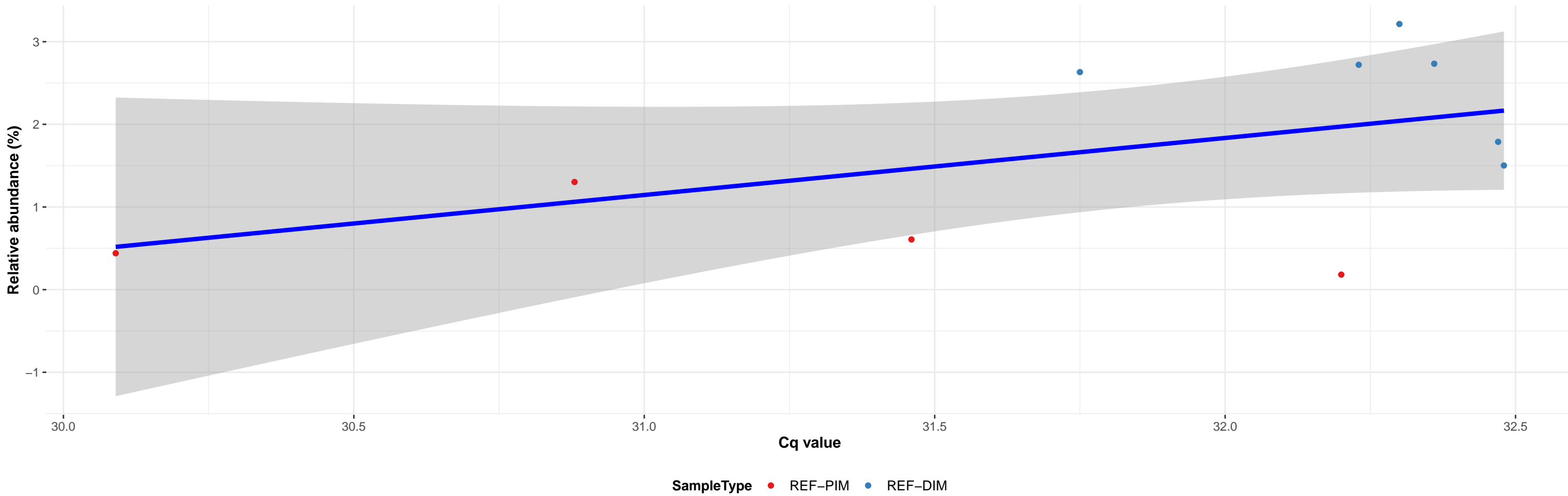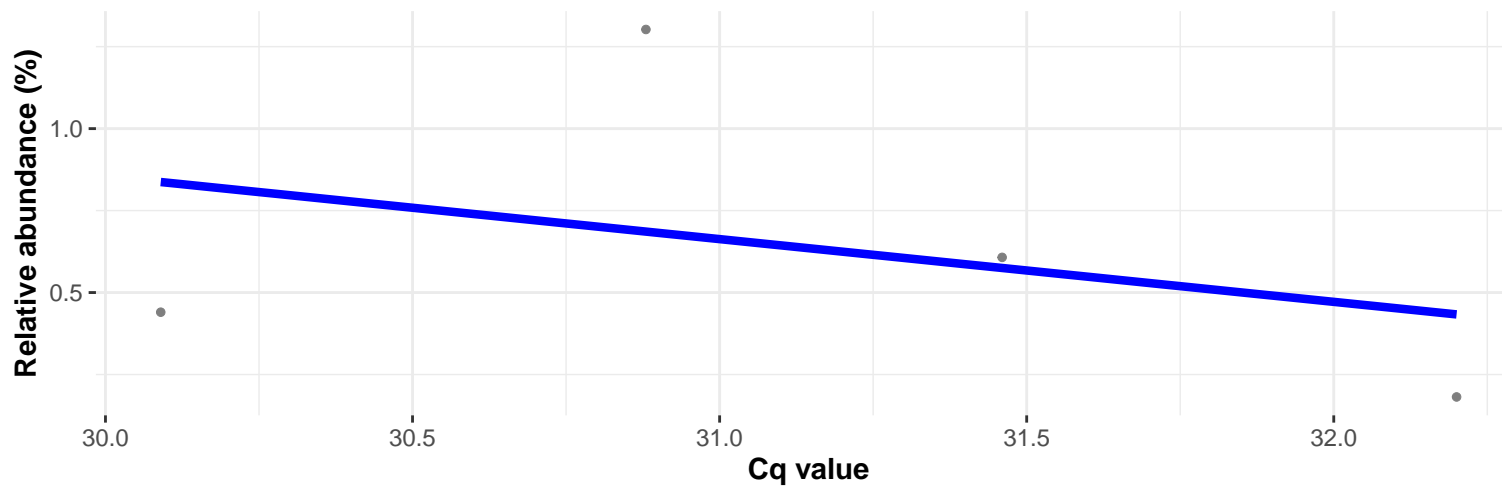
SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Chitinophagales; f__Chitinophagaceae; g__Sediminibacterium; NA

Correlation with all samples

$\log_e(S) = 5.775$, $p = 0.311$, $\hat{\rho}_{Spearman} = 0.292$, $CI_{95\%}$ [−0.298, 0.721], $n_{pairs} = 14$

SampleType ● REF−PIM ● REF−DIM
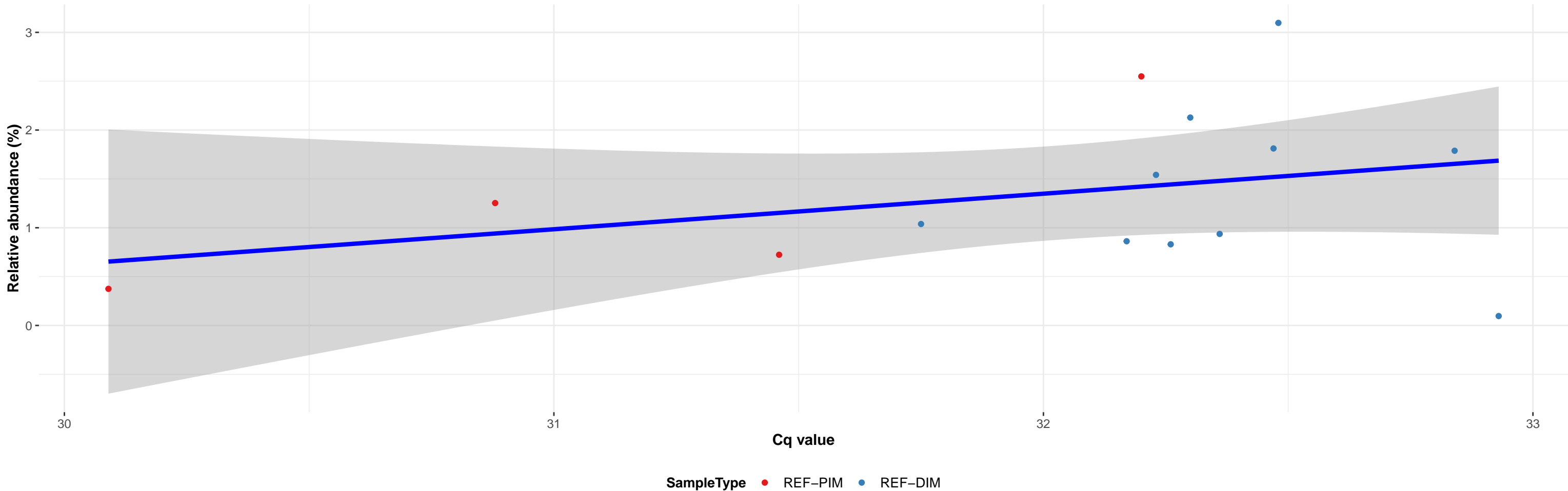
Correlation within: REF−PIM
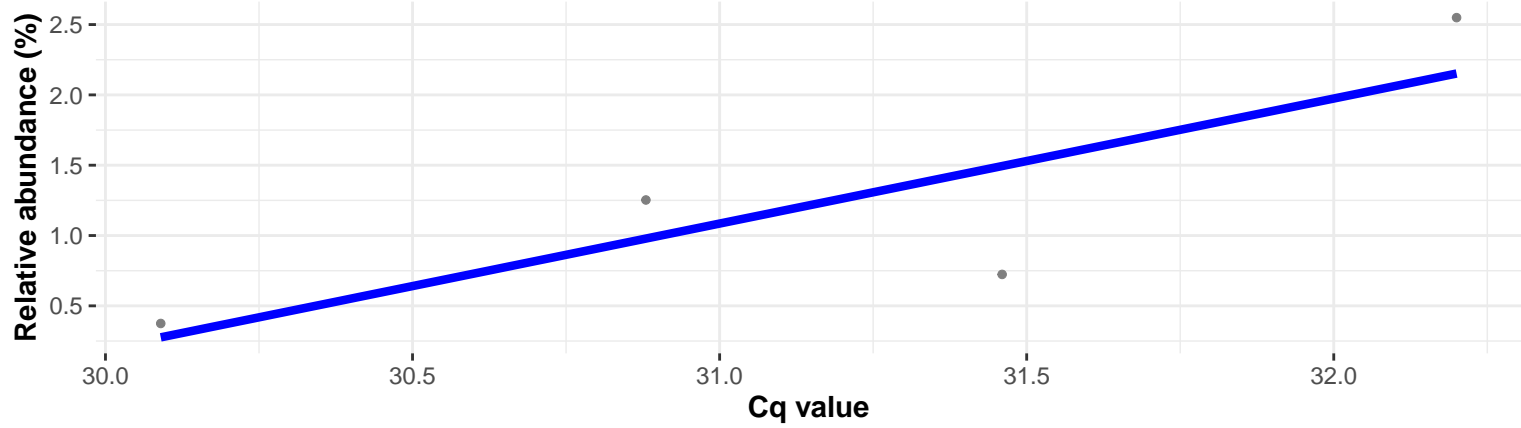
Correlation within: REF−DIM

$\log_e(S) = 4.942$, $p = 0.676$, $\hat{\rho}_{Spearman} = 0.152$, $CI_{95\%}$ [−0.544, 0.724], $n_{pairs} = 10$
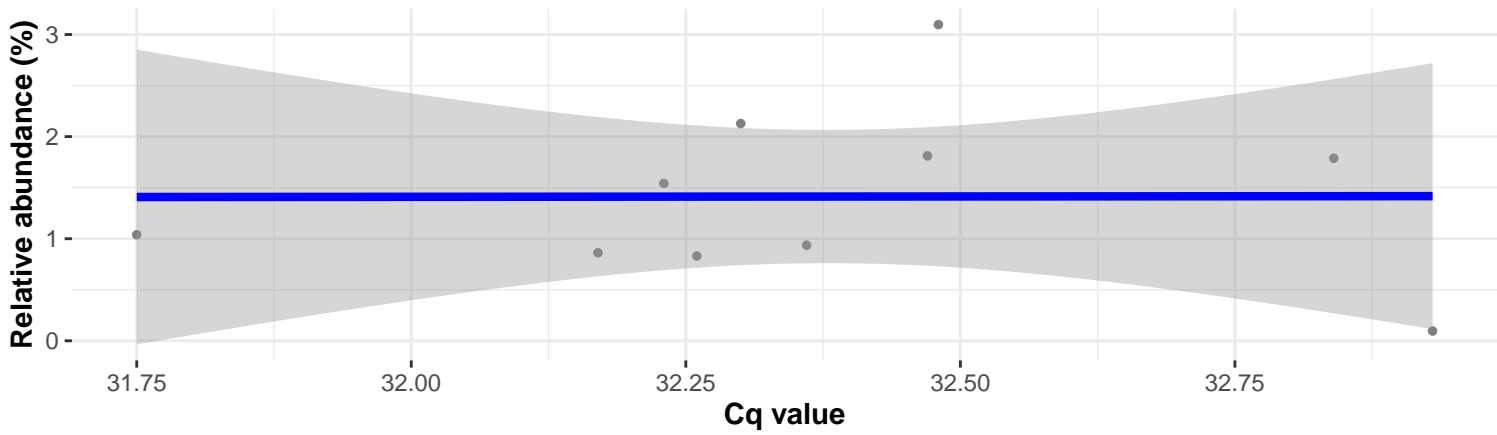
Correlation within: PCR−blank

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

$\log_e(S) = 1.792$, $p = 0.188$, $\hat{\rho}_{Spearman} = 0.700$, $CI_{95\%}$ [−0.508, 0.980], $n_{pairs} = 5$
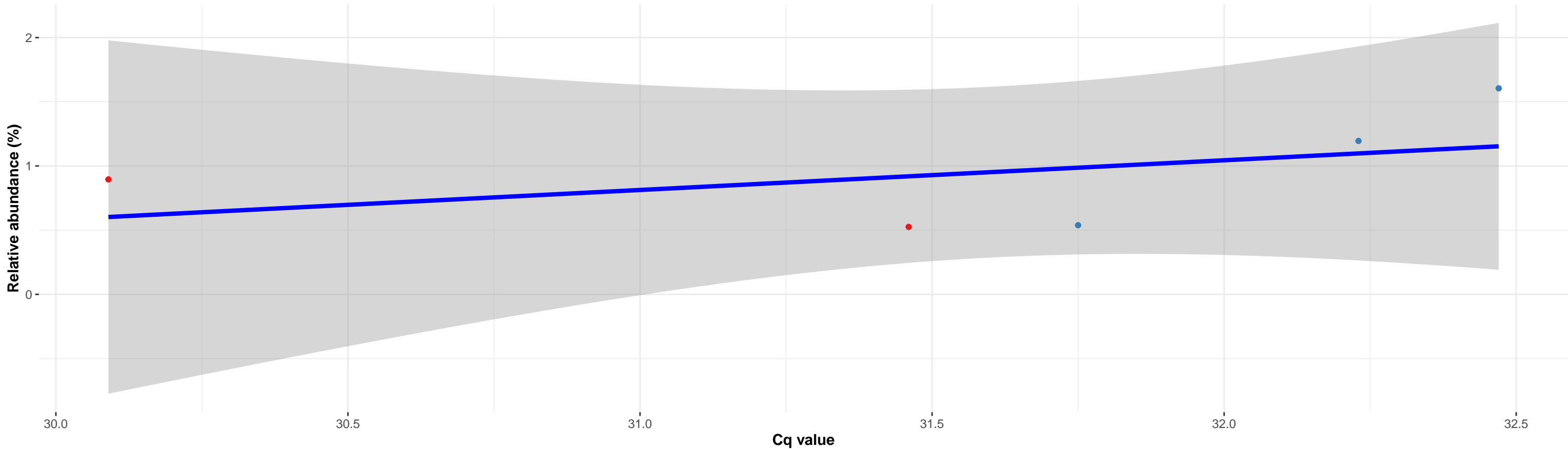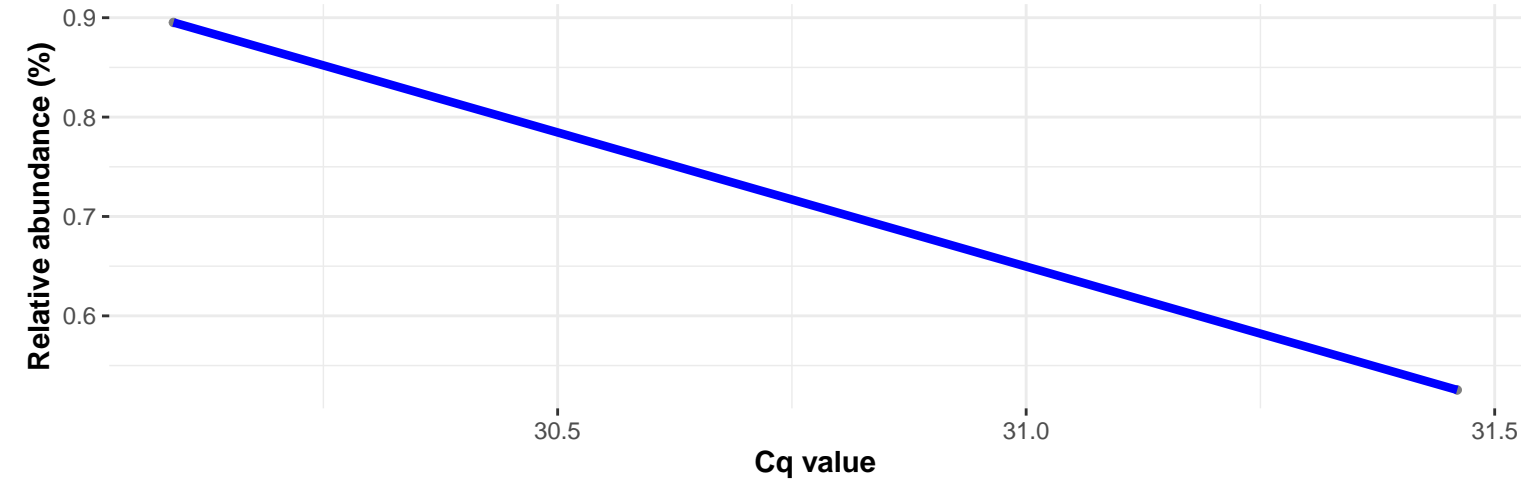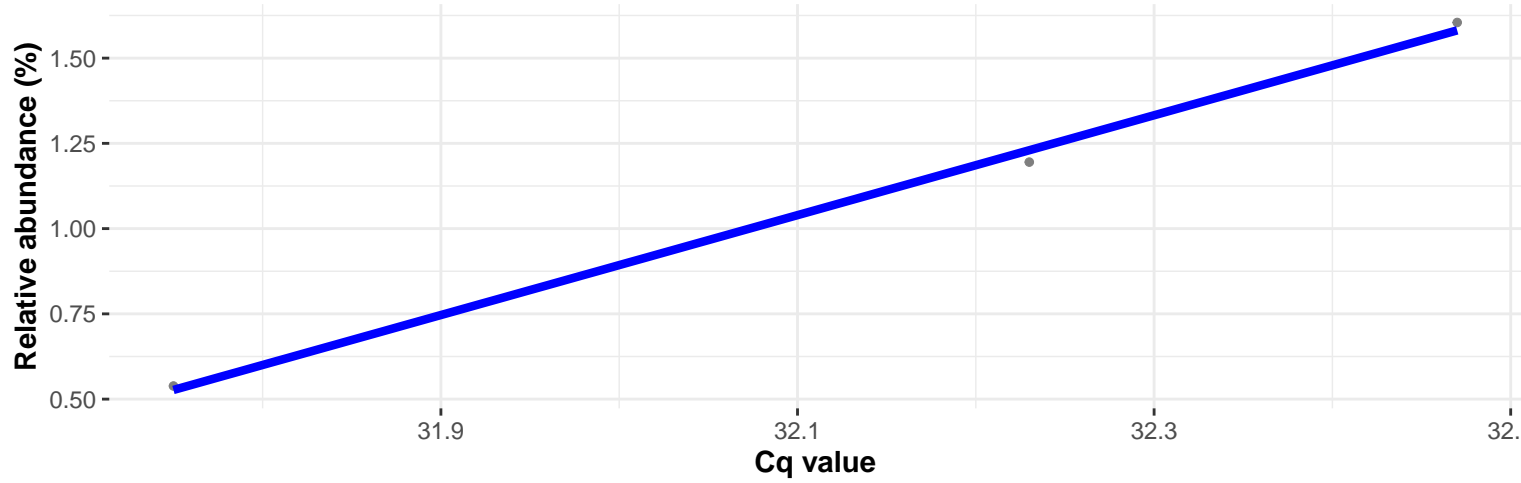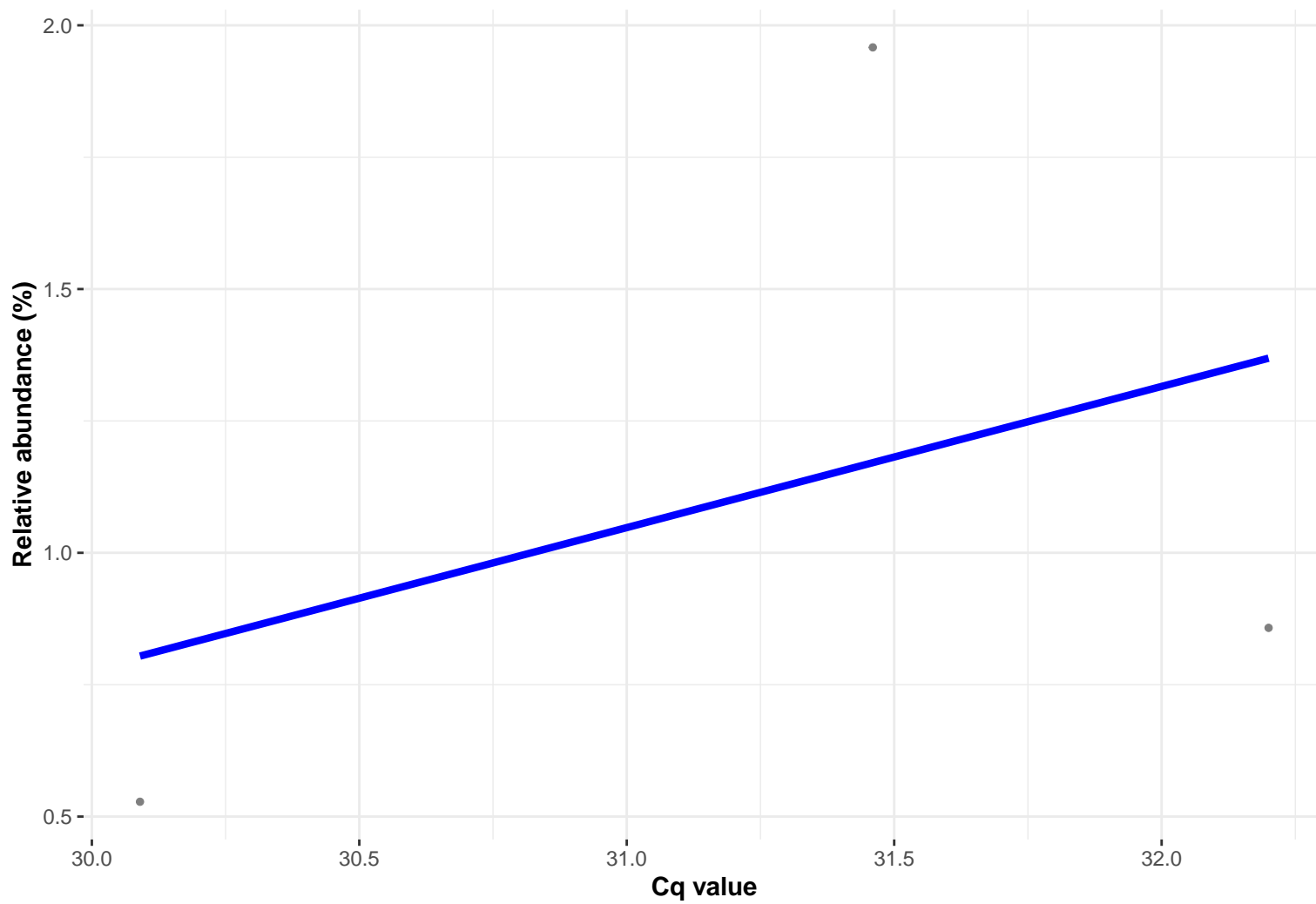
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; NA; NA

Correlation with all samples

$\log_e(S) = 4.500$, $p = 0.516$, $\hat{\rho}_{Spearman} = 0.250$, $CI_{95\%}$ [−0.514, 0.793], $n_{pairs} = 9$
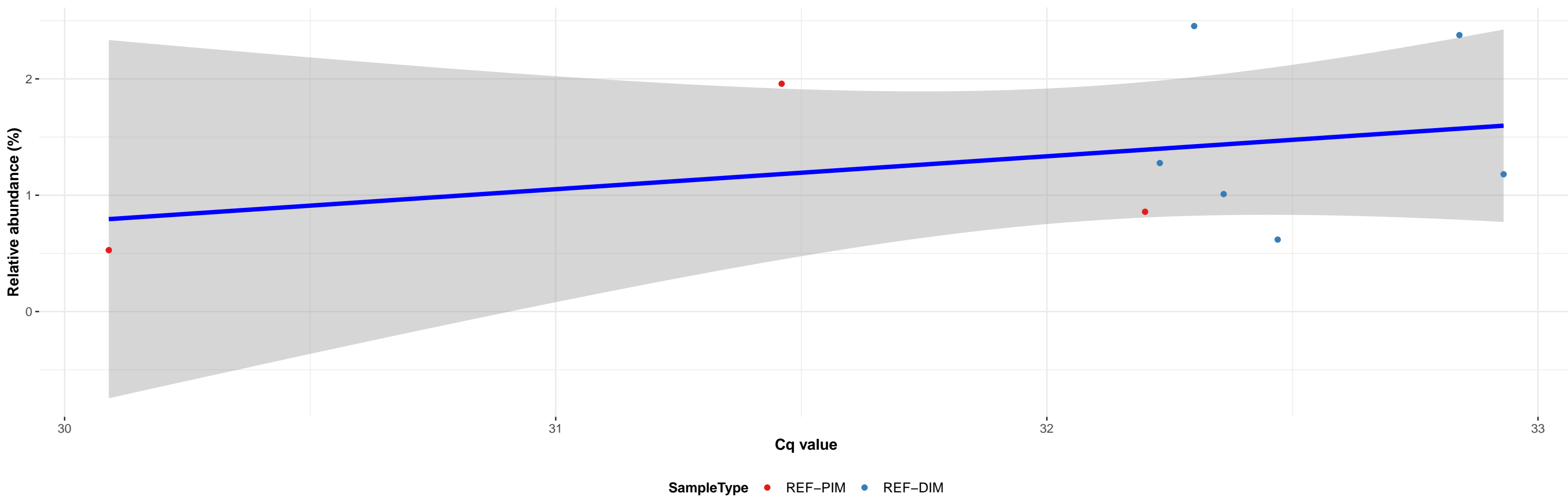
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; Ambiguous_taxa; Ambiguous_taxa

Correlation with all samples

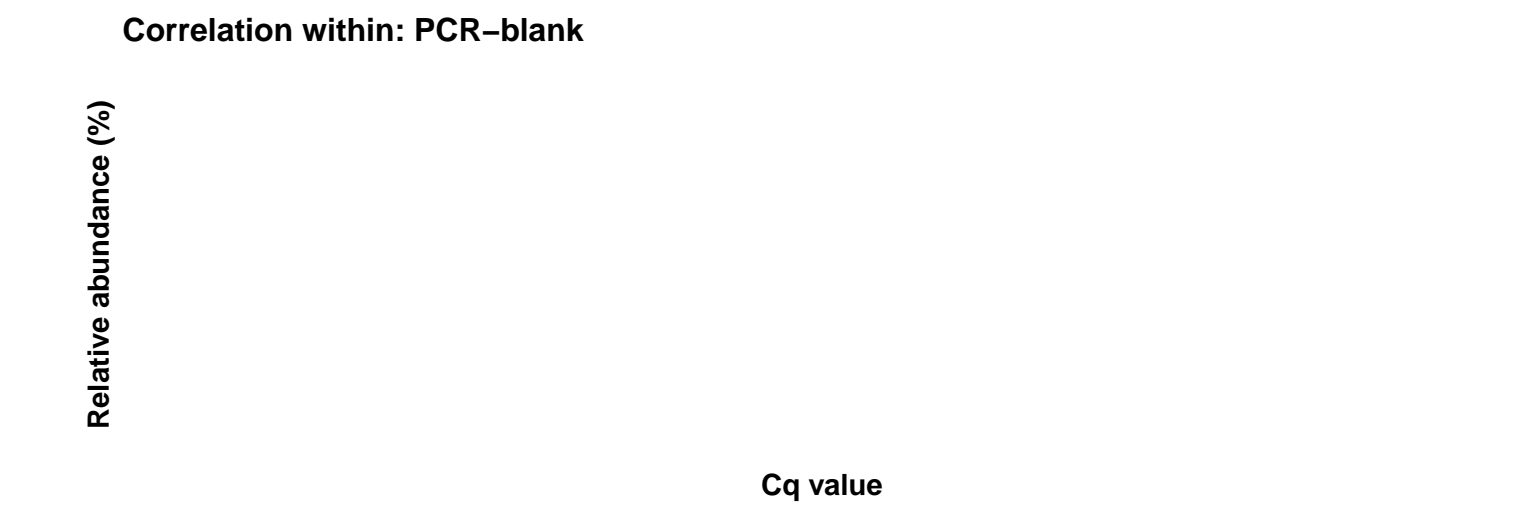SampleType ● REF−PIM ● REF−DIM
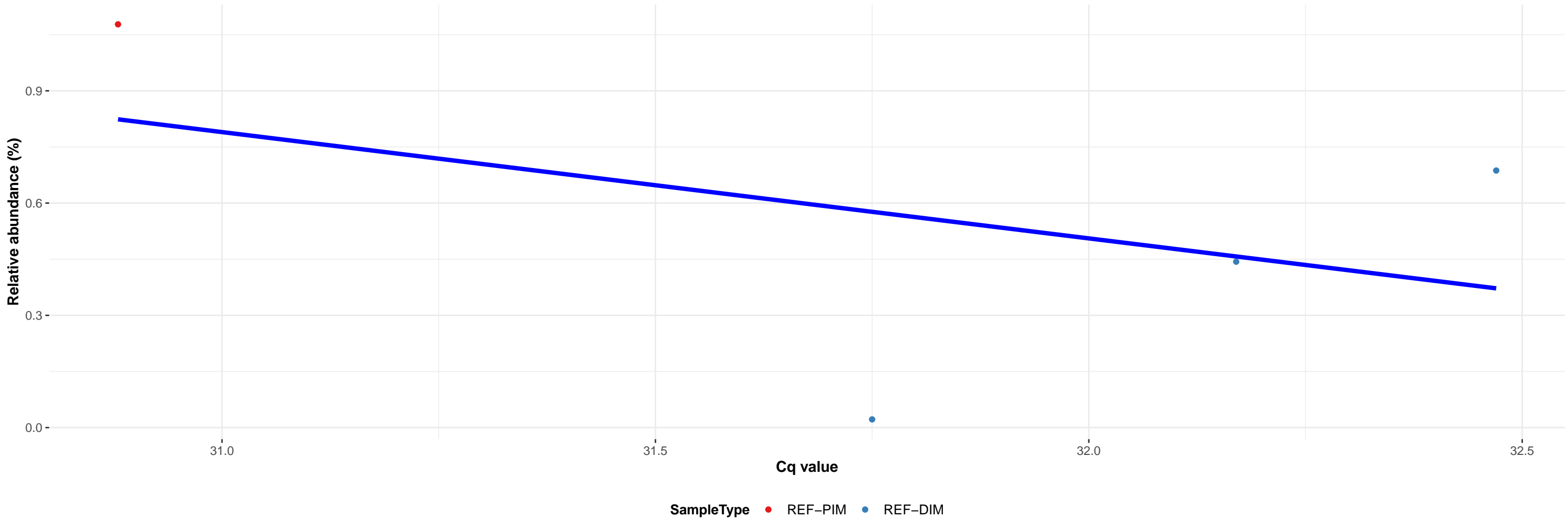
Correlation within: REF−PIM
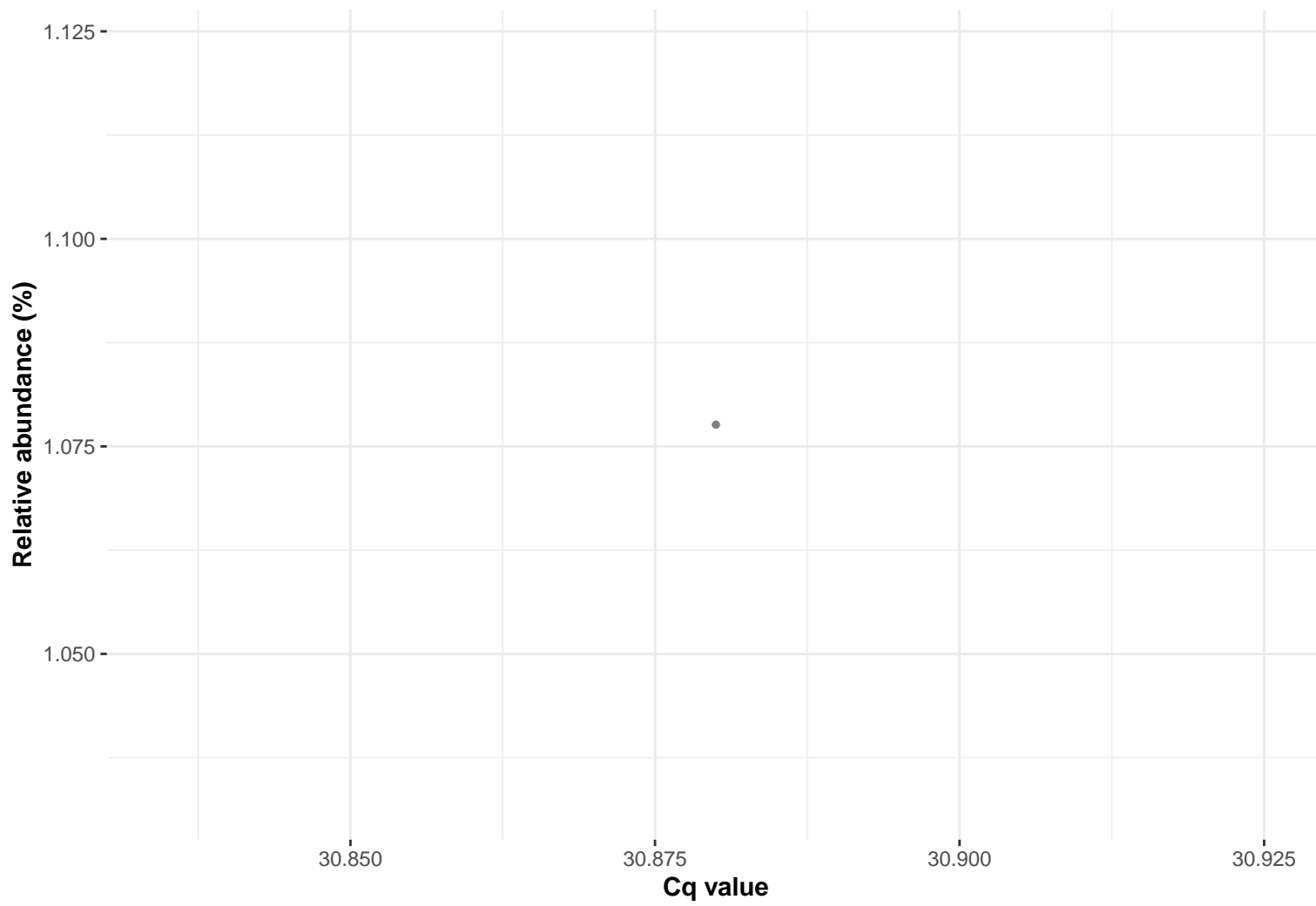
Correlation within: REF−DIM
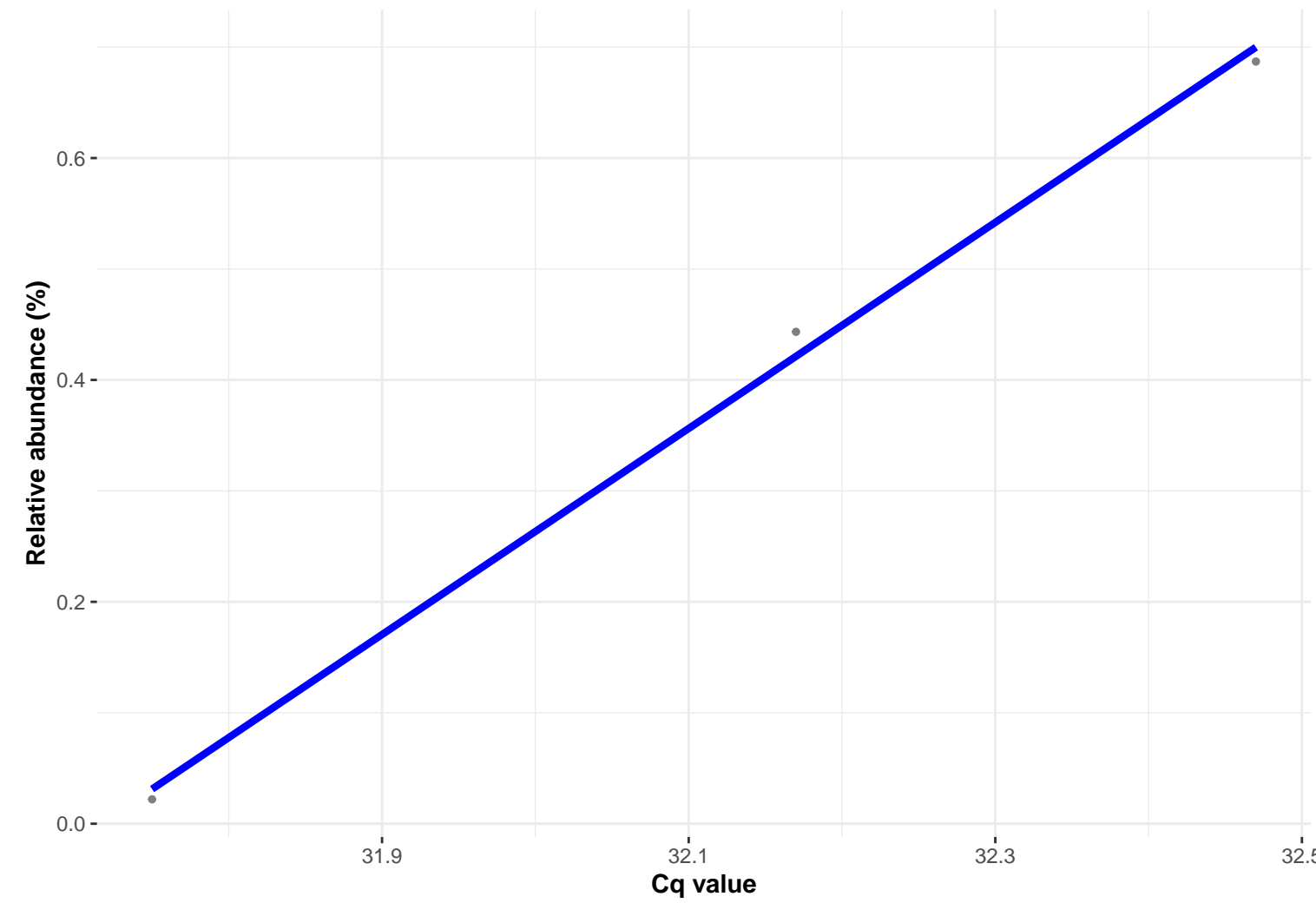
k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium

Correlation with all samples

$\log_e(S) = 3.584$, $p = 0.432$, $\hat{\rho}_{Spearman} = 0.357$, $CI_{95\%}$ [−0.562, 0.882], $n_{pairs} = 7$
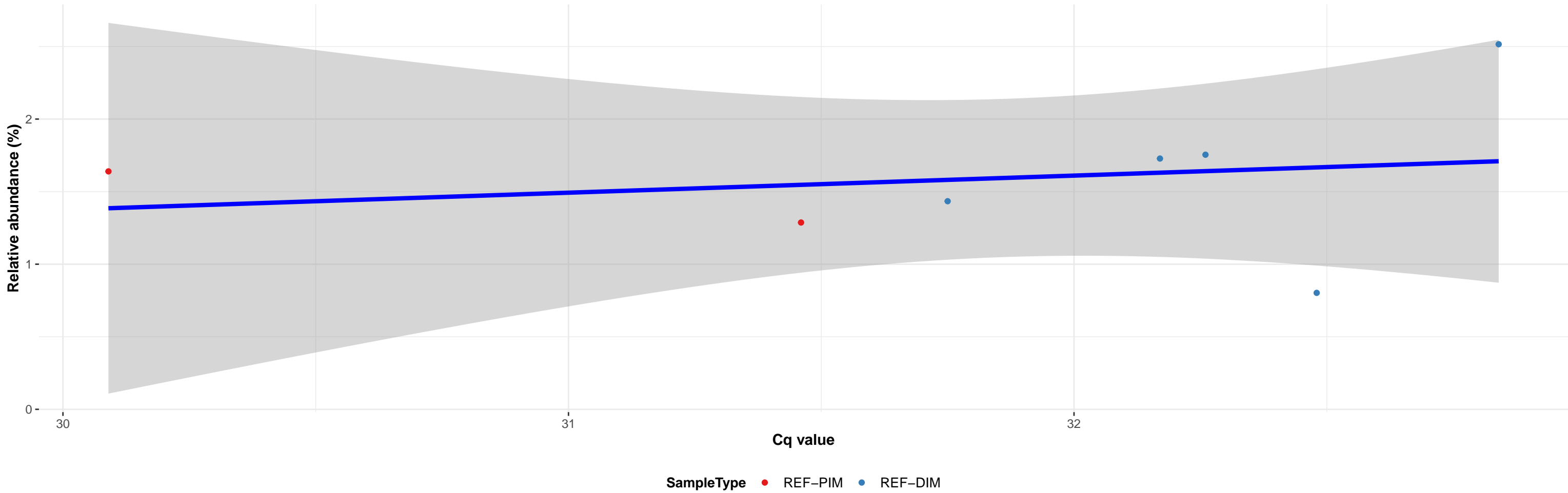
SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM
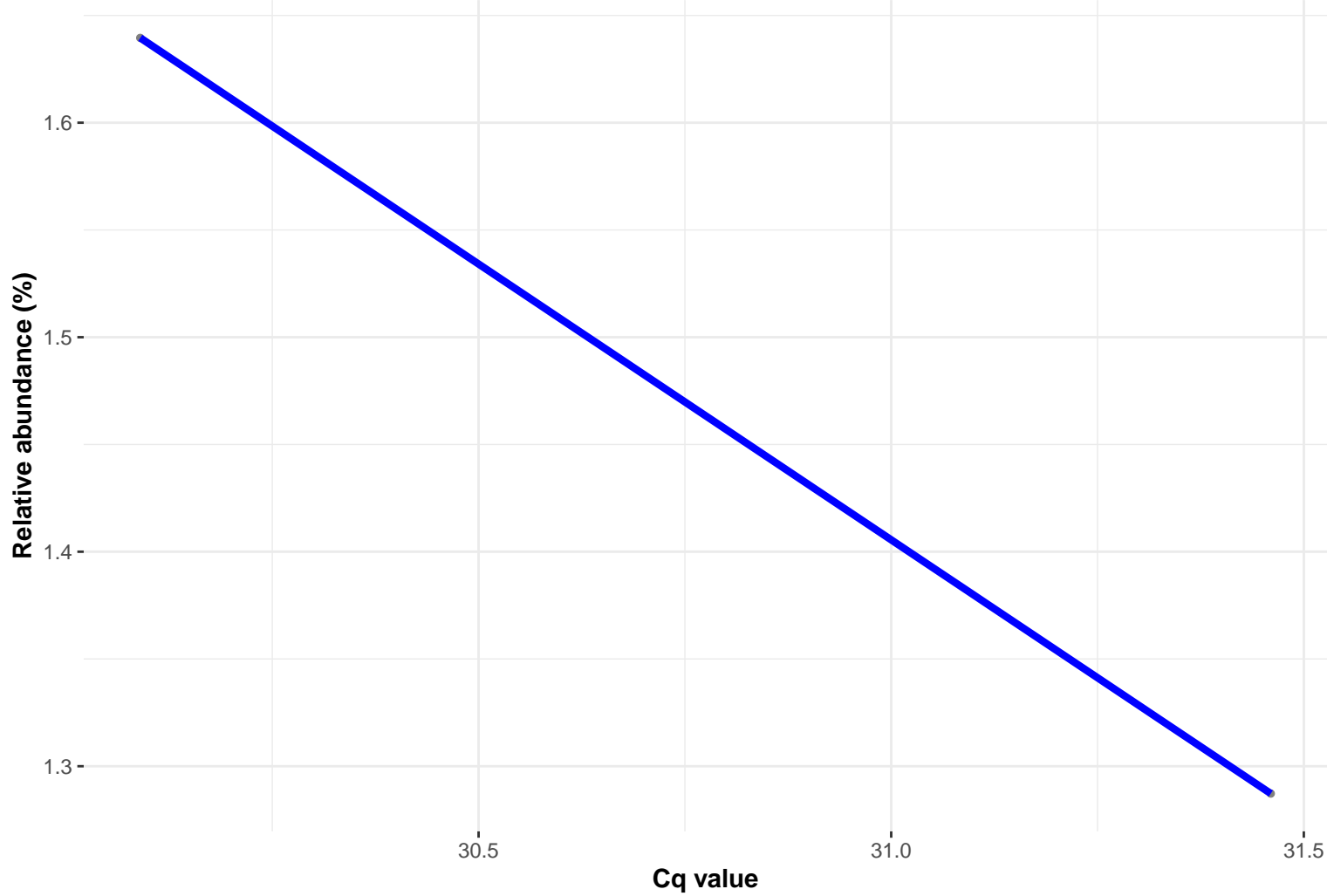
Correlation within: REF−DIM
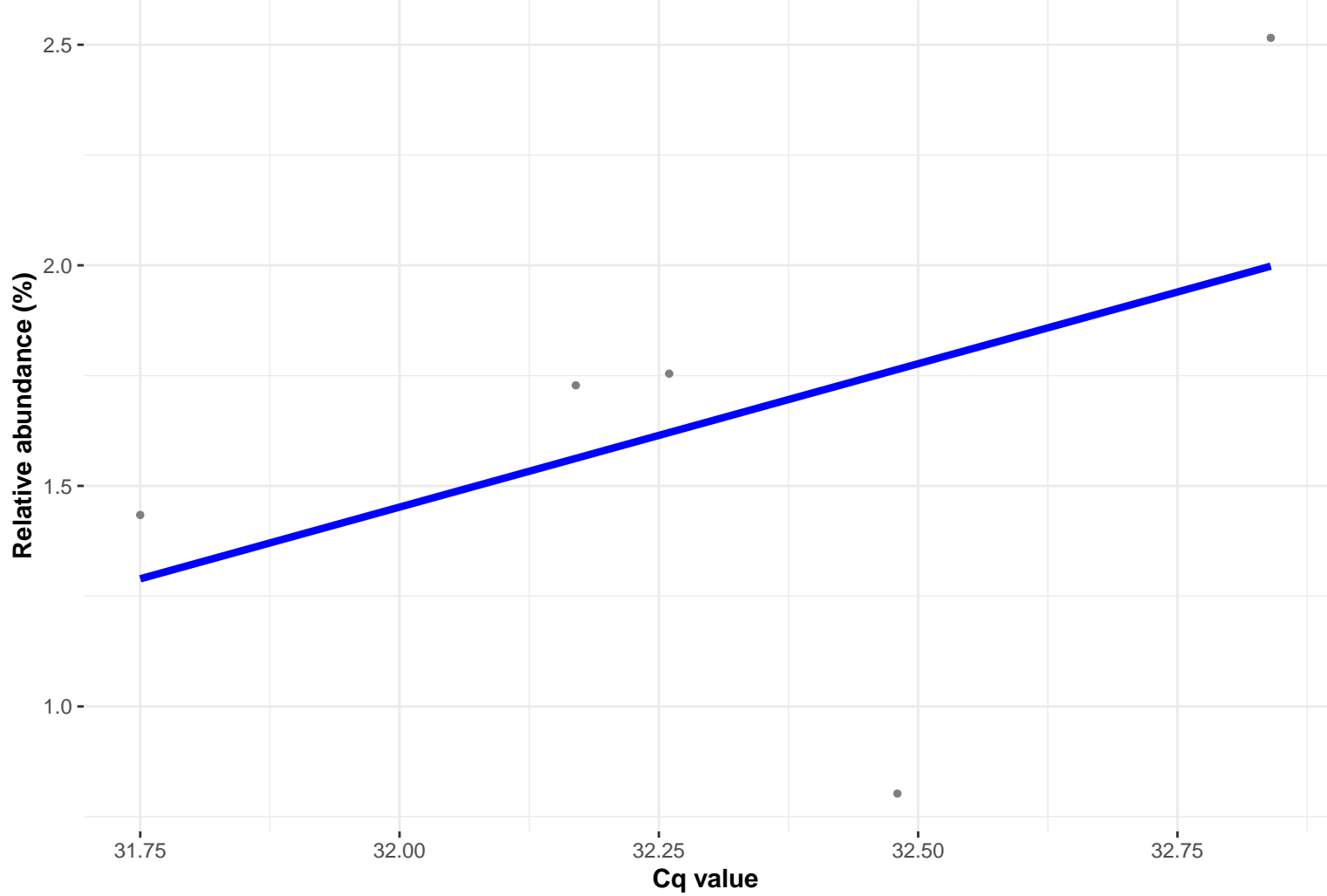
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; NA; NA

Correlation with all samples

$\log_e(S) = 5.903$, $p = 0.379$, $\hat{p}_{Spearman} = -0.280$, $CI_{95\%}$ [−0.744, 0.367], $n_{pairs} = 12$

SampleType ● REF−PIM ● REF−DIM
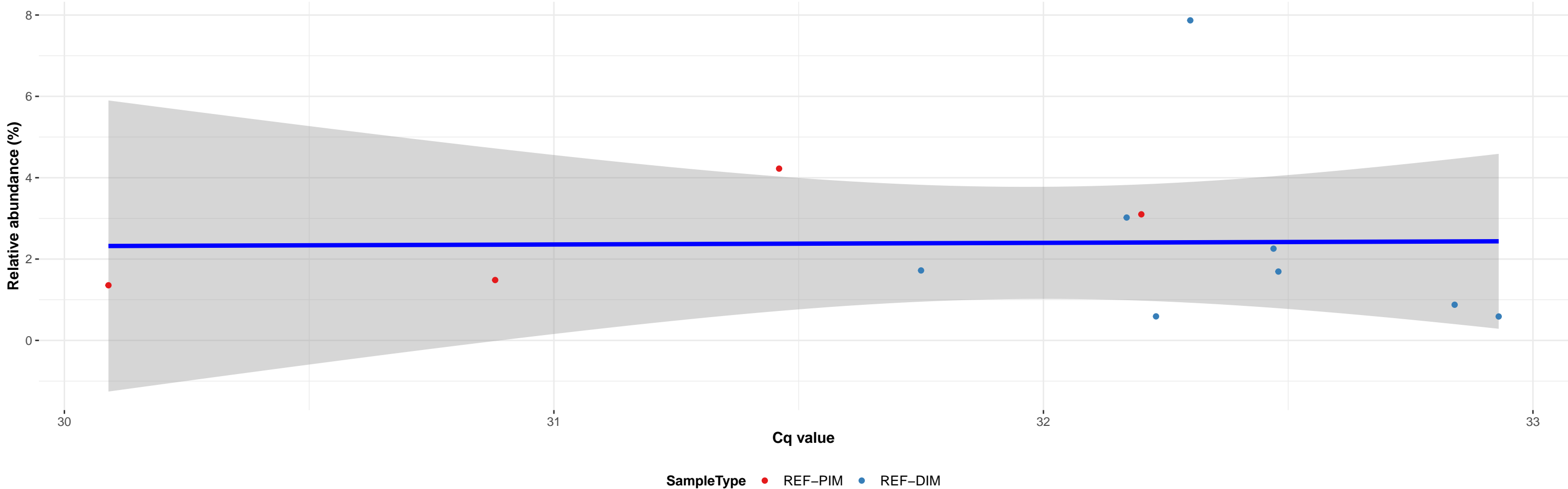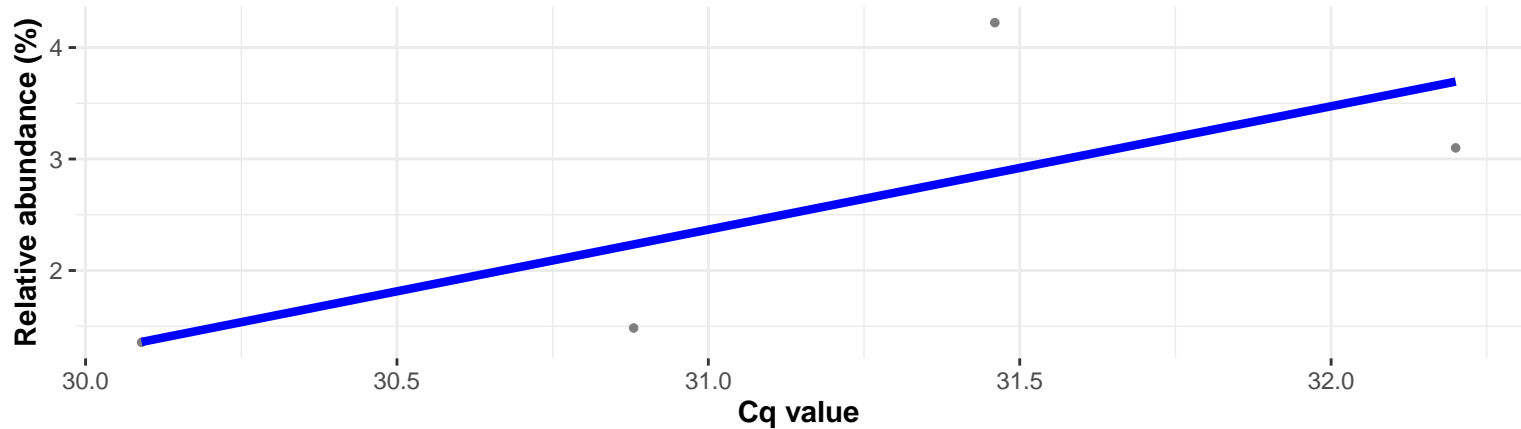
Correlation within: REF−DIM

$\log_e(S) = 4.852$, $p = 0.183$, $\hat{p}_{Spearman} = -0.524$, $CI_{95\%}$ [−0.902, 0.310], $n_{pairs} = 8$
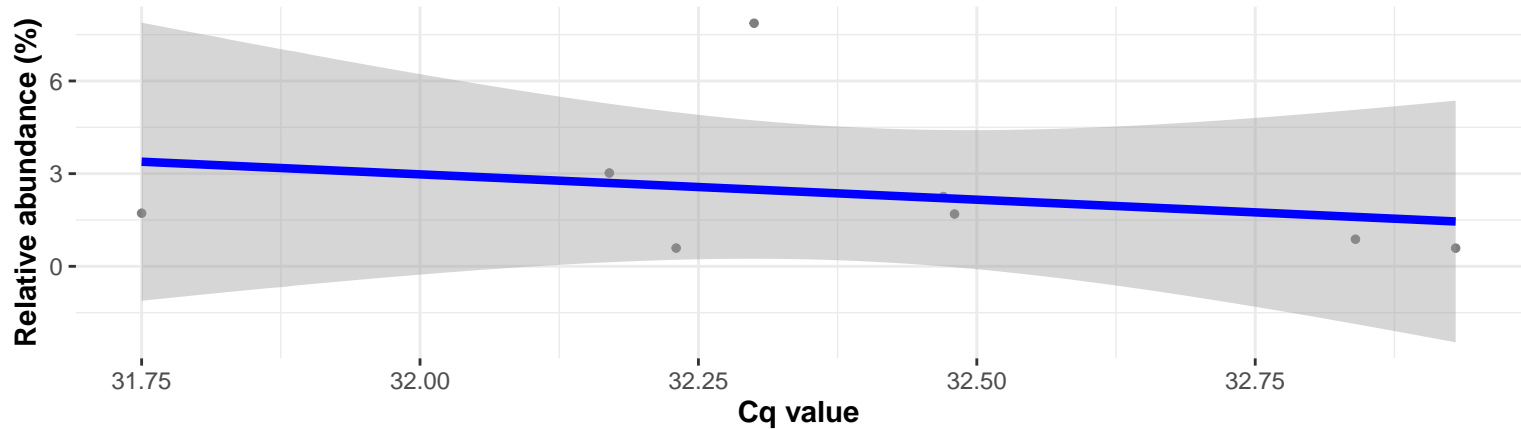
Correlation within: REF−PIM

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus sciuri
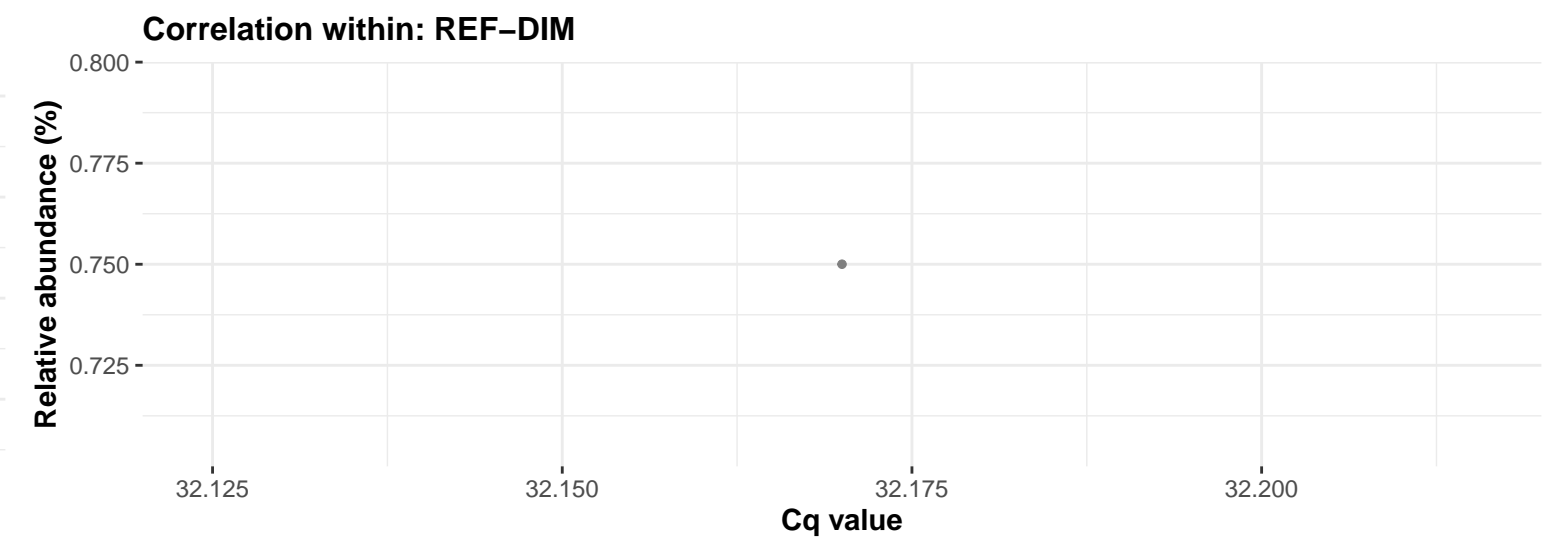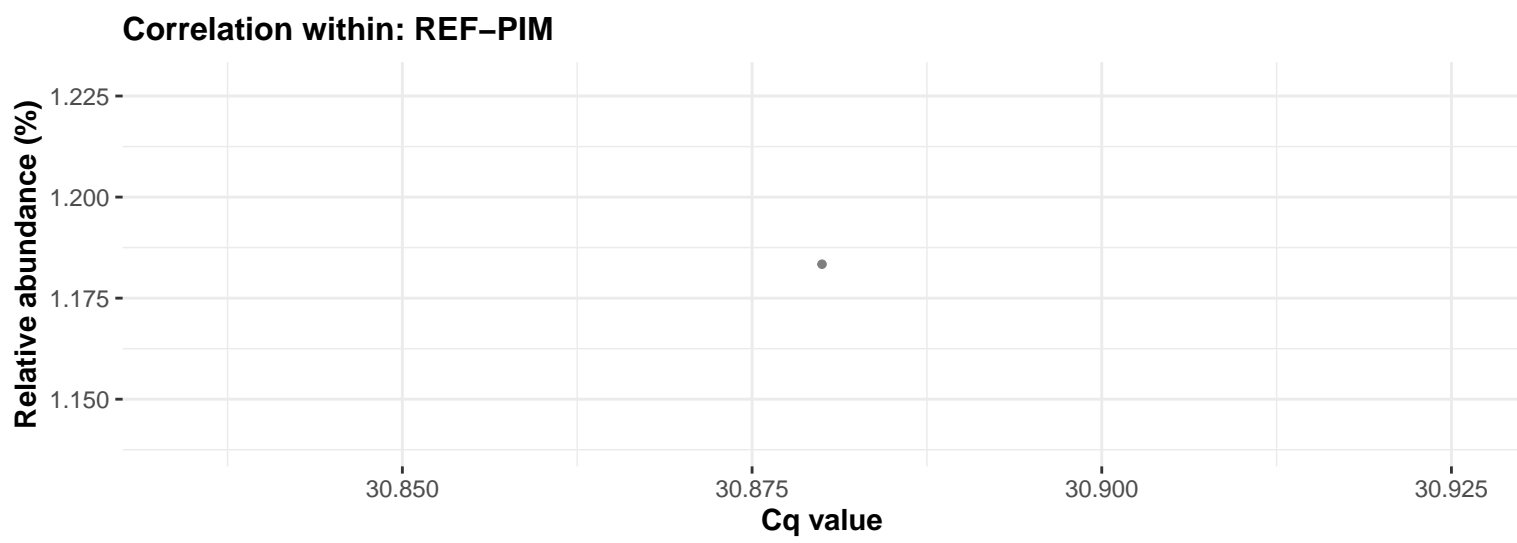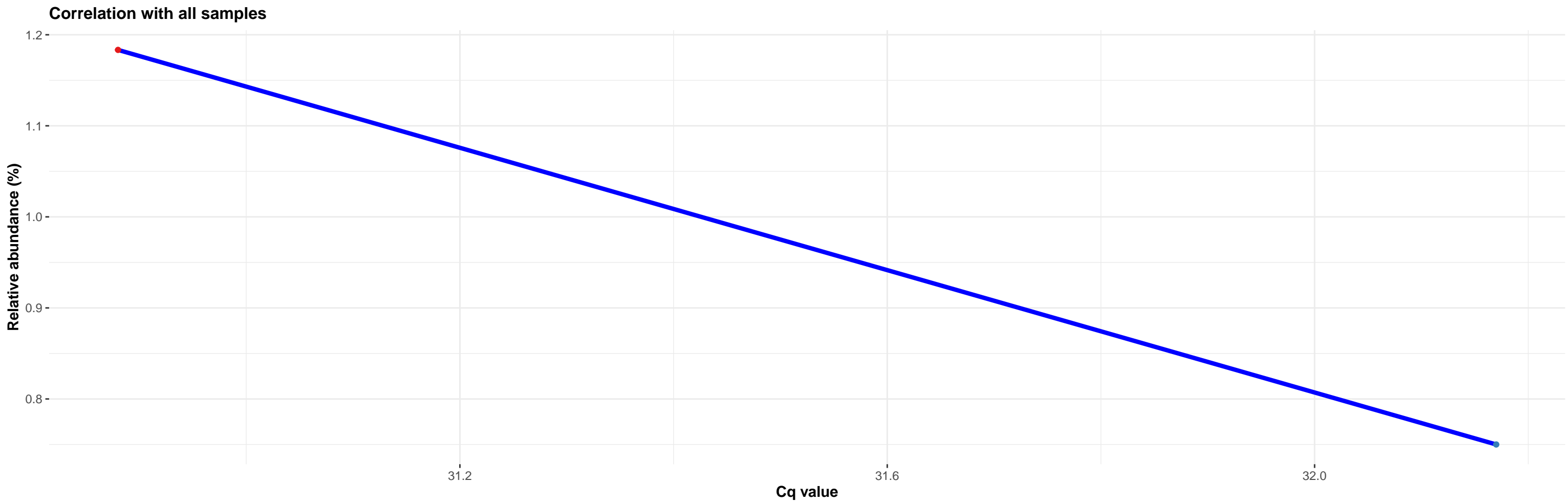
# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

Correlation with all samples
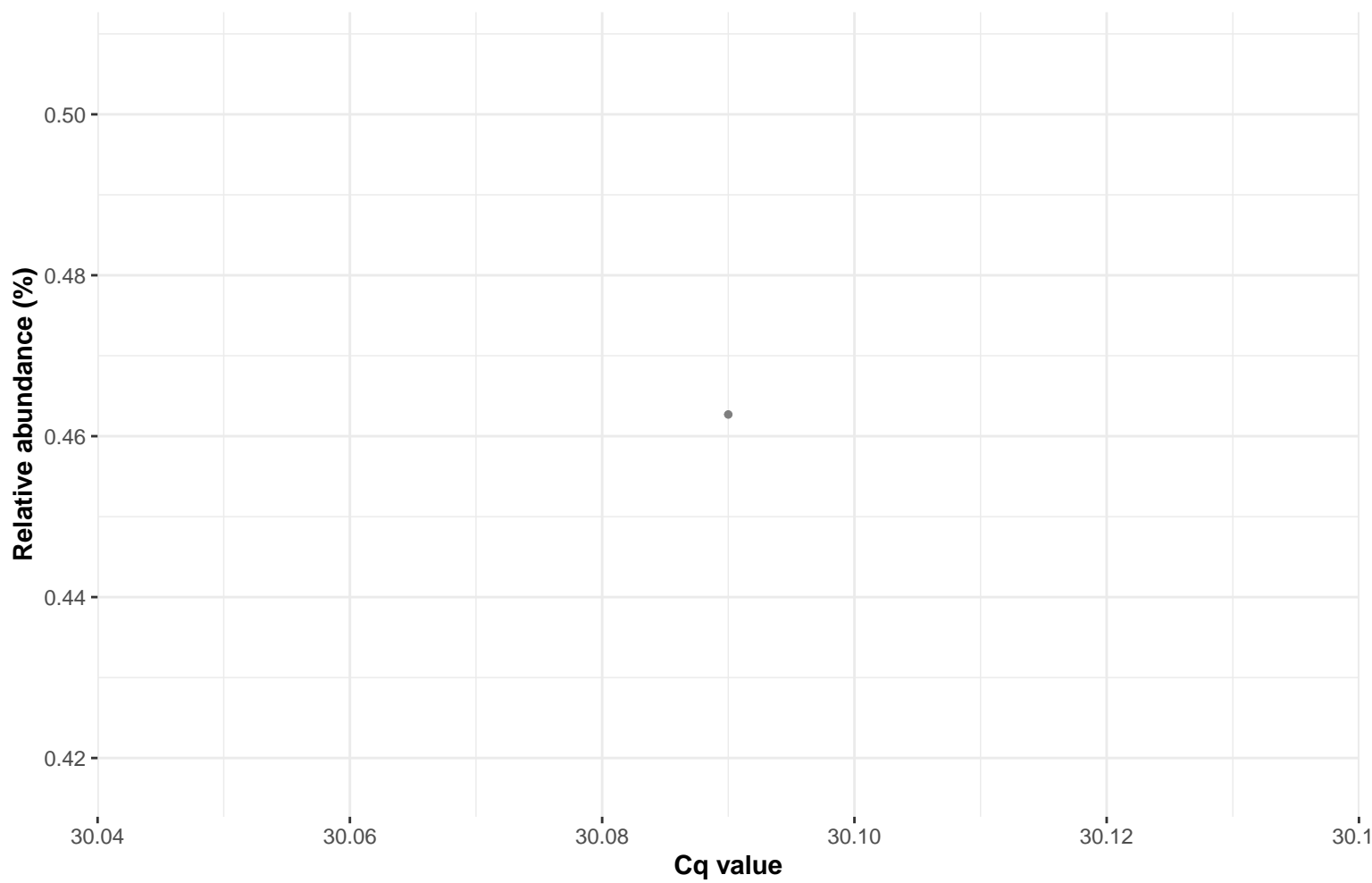

SampleType ● REF−DIM
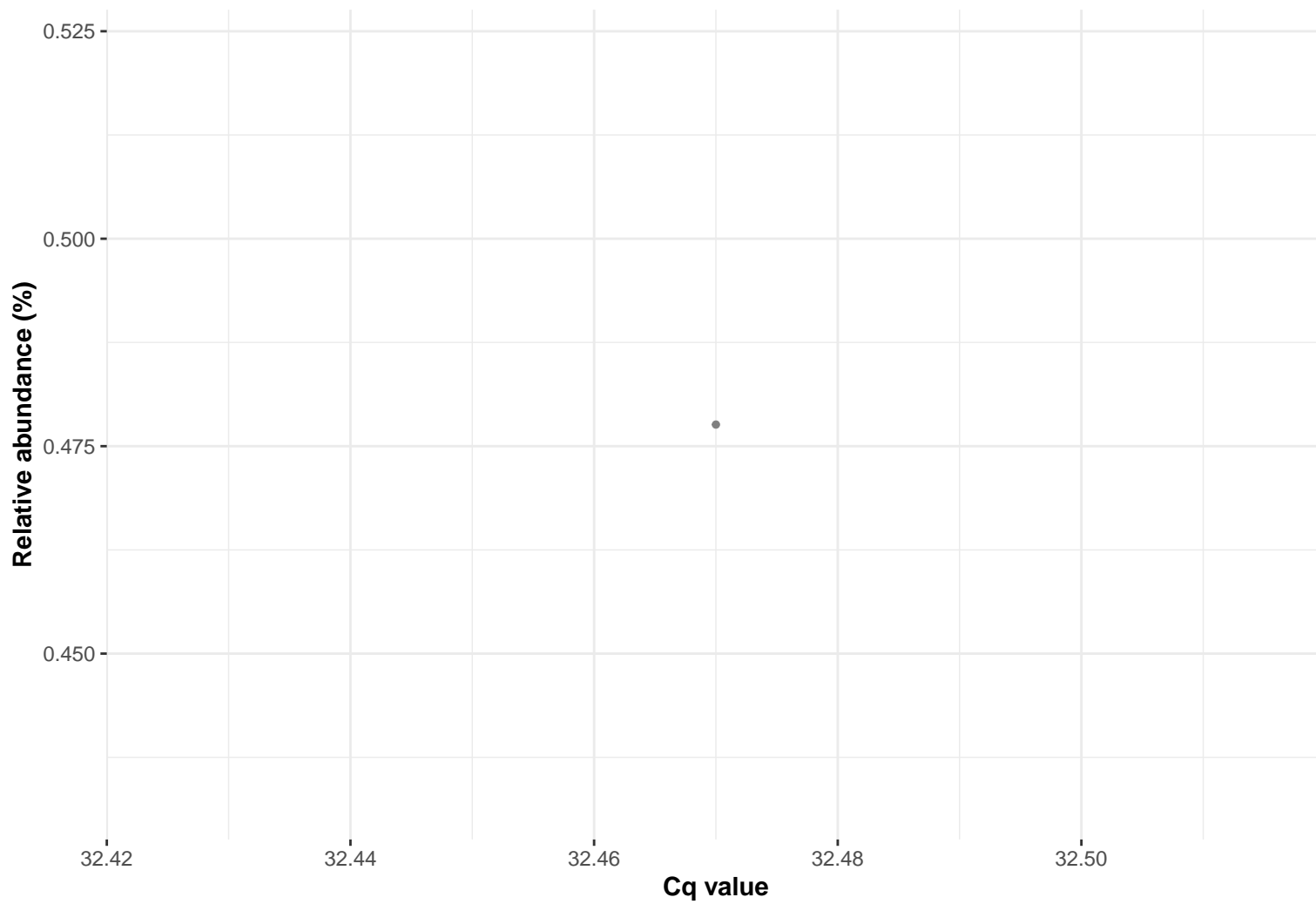
Correlation within: REF−DIM

Correlation within: PCR−blank
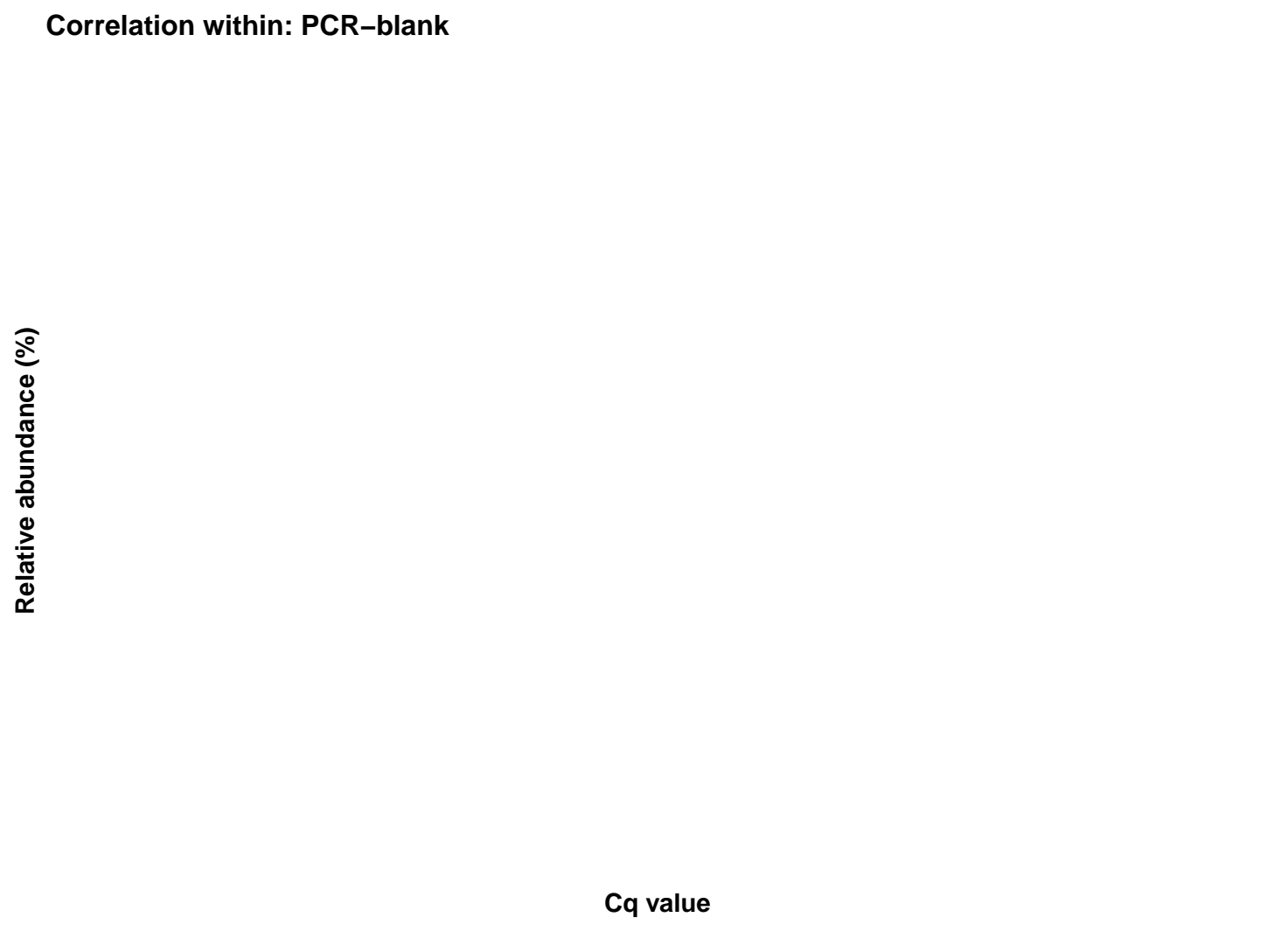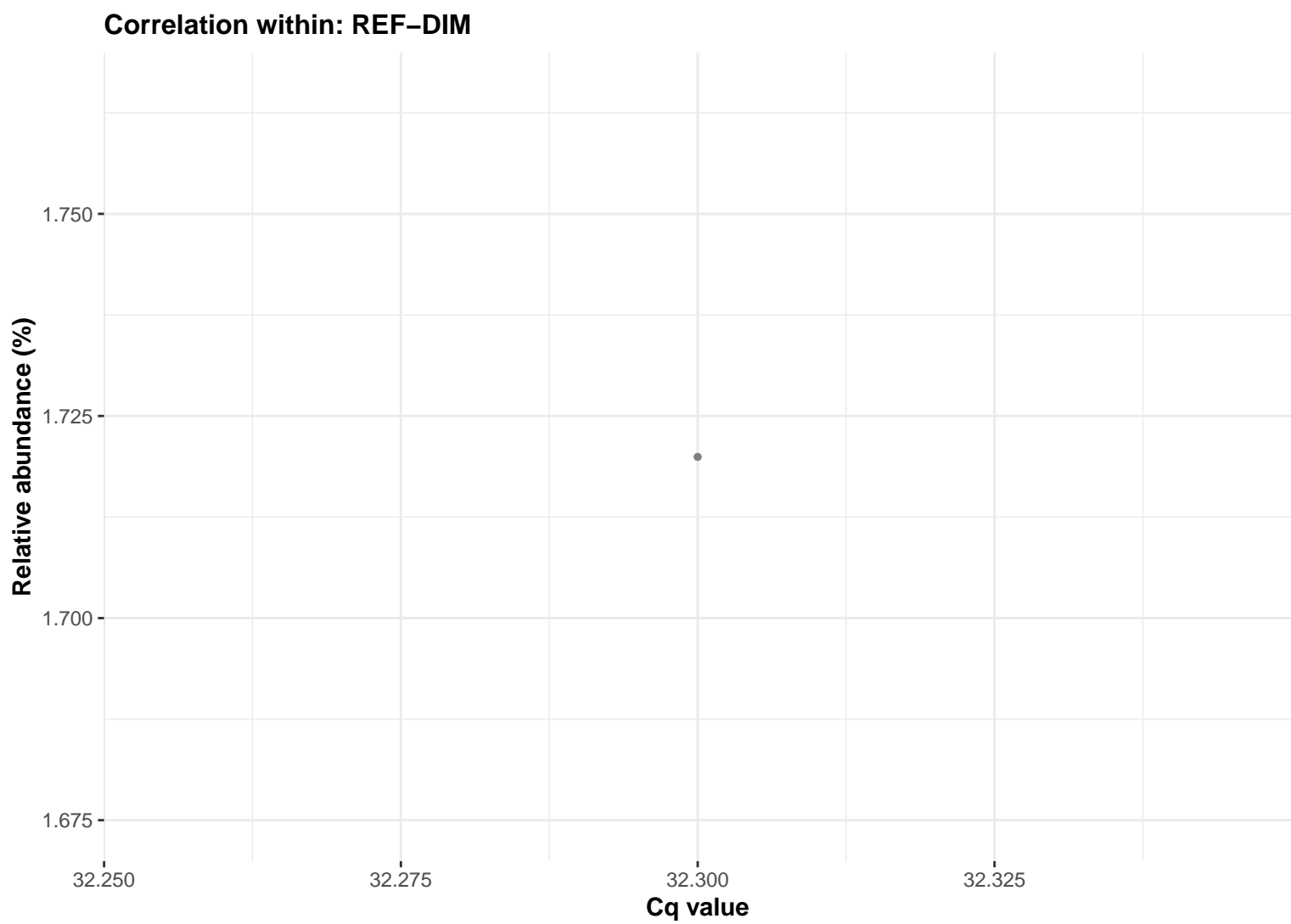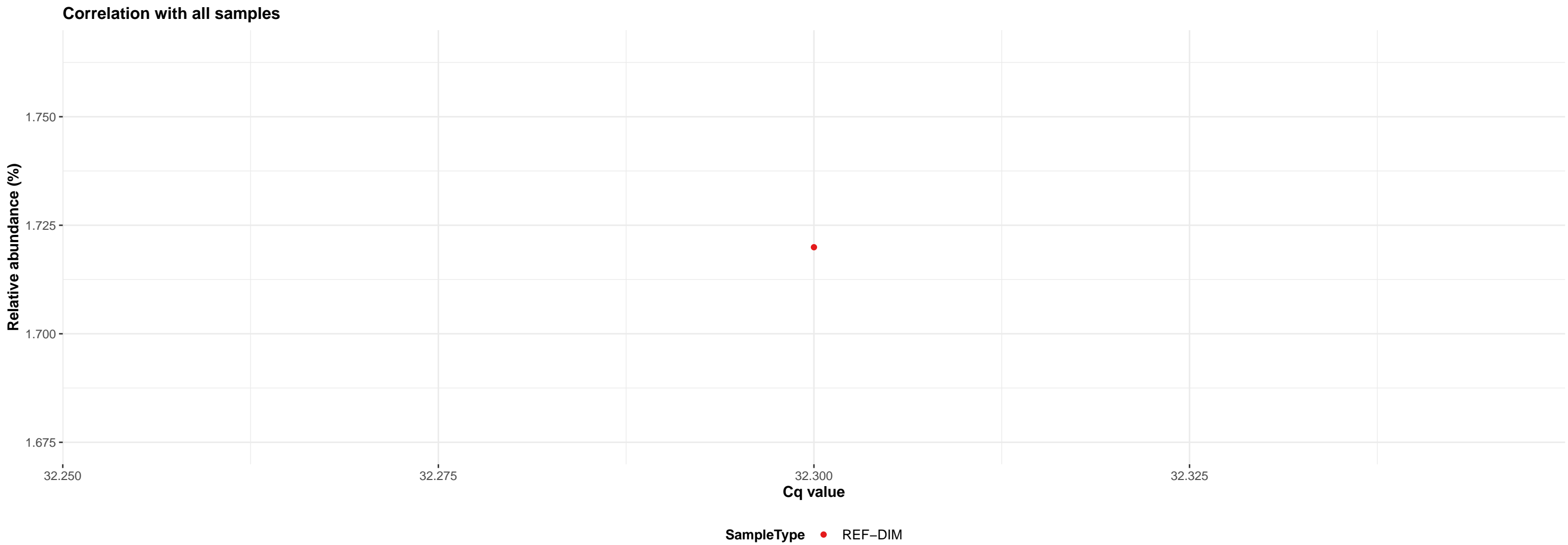
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Lysinibacillus; NA

Correlation with all samples

$\log_e(S) = 4.159$, $p = 0.570$, $\hat{\rho}_{Spearman} = 0.238$, $CI_{95\%}$ [−0.578, 0.816], $n_{pairs} = 8$

SampleType ● REF−PIM ● REF−DIM
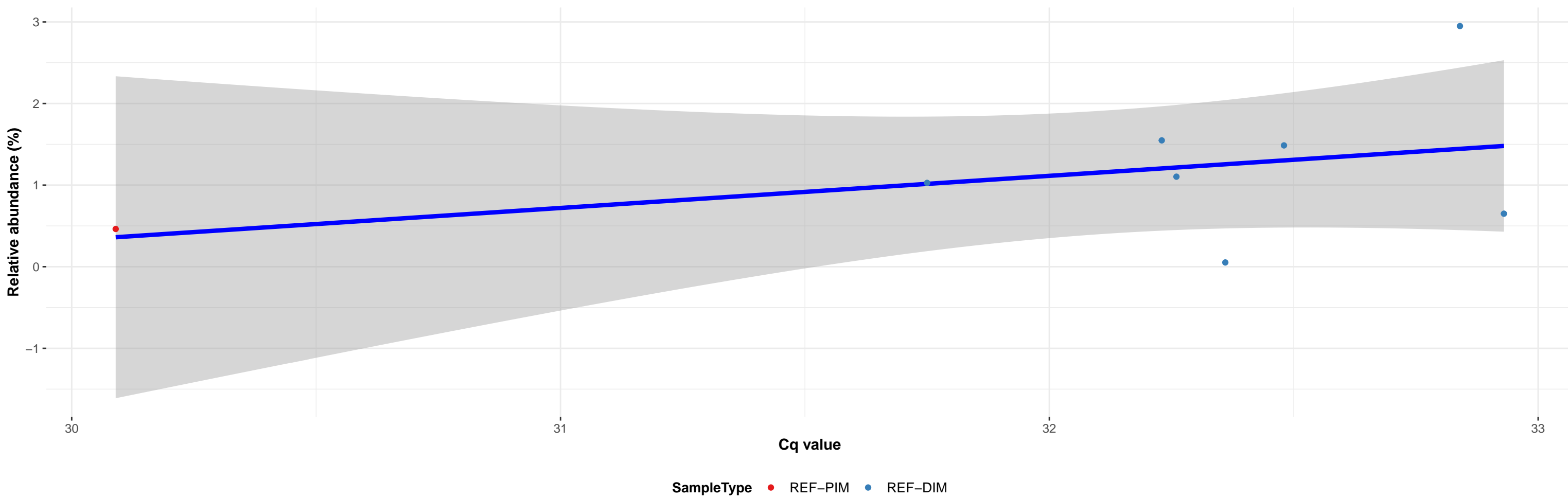
Correlation within: REF−PIM

Correlation within: REF−DIM

$\log_e(S) = 4.025$, $p = 1.000$, $\hat{\rho}_{Spearman} = 0.000$, $CI_{95\%}$ [−0.765, 0.765], $n_{pairs} = 7$
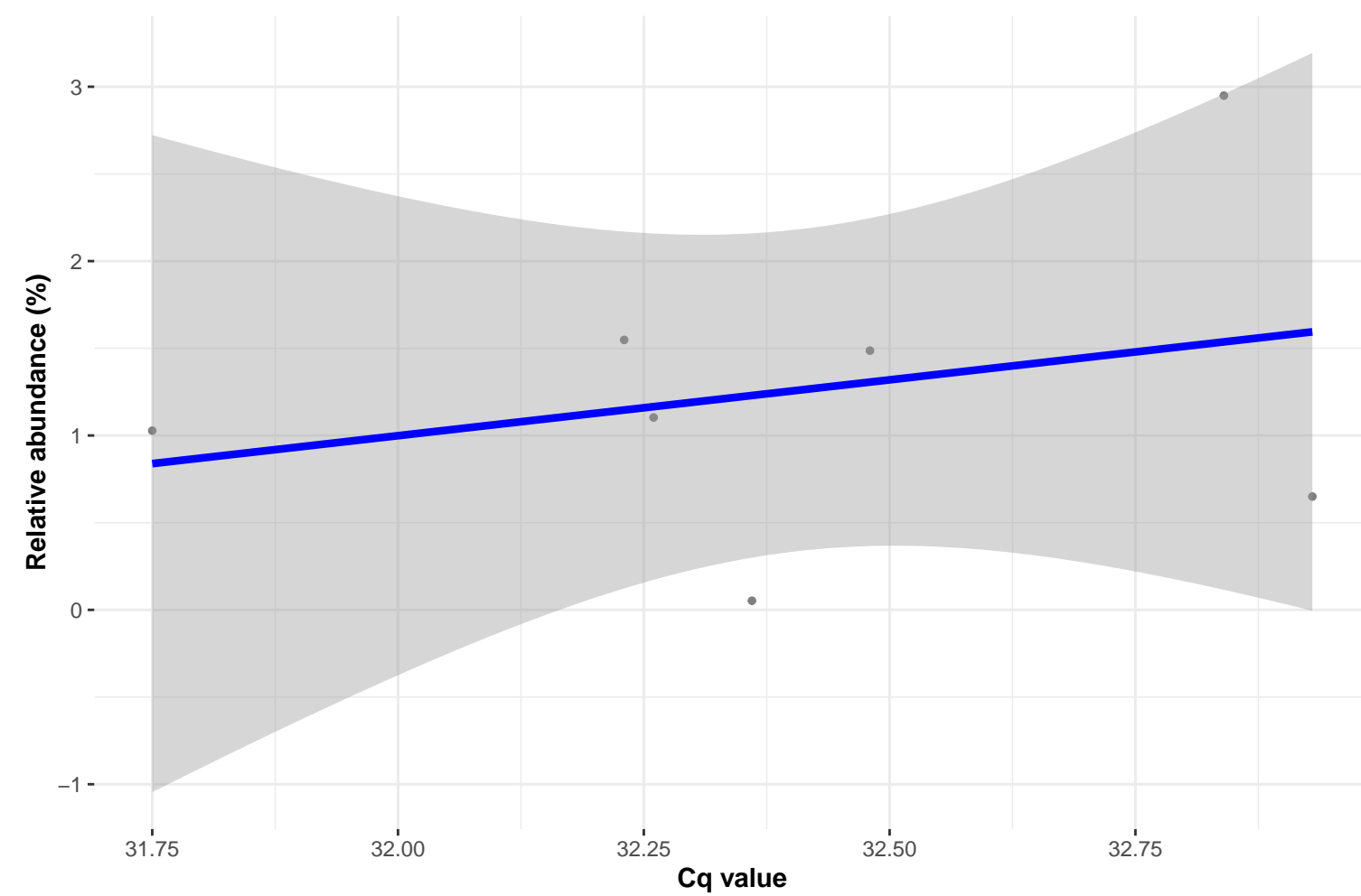
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

$\log_e(S) = 4.477$, $p = 0.180$, $\hat{\rho}_{Spearman} = -0.571$, $CI_{95\%}$ [−0.930, 0.345], $n_{pairs} = 7$
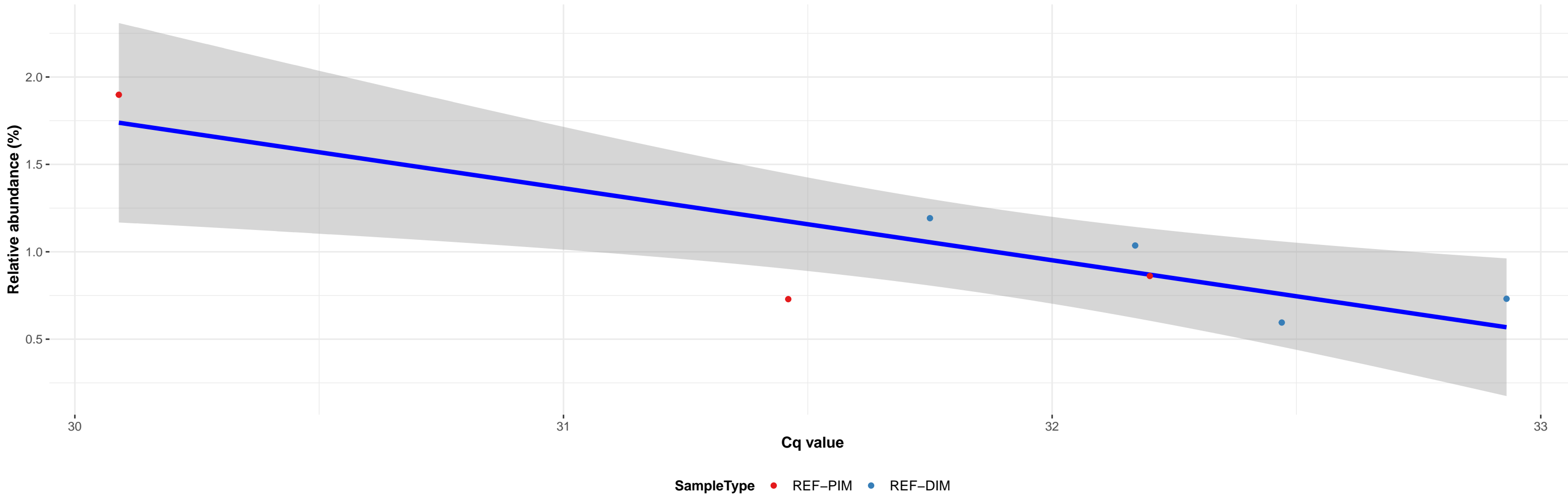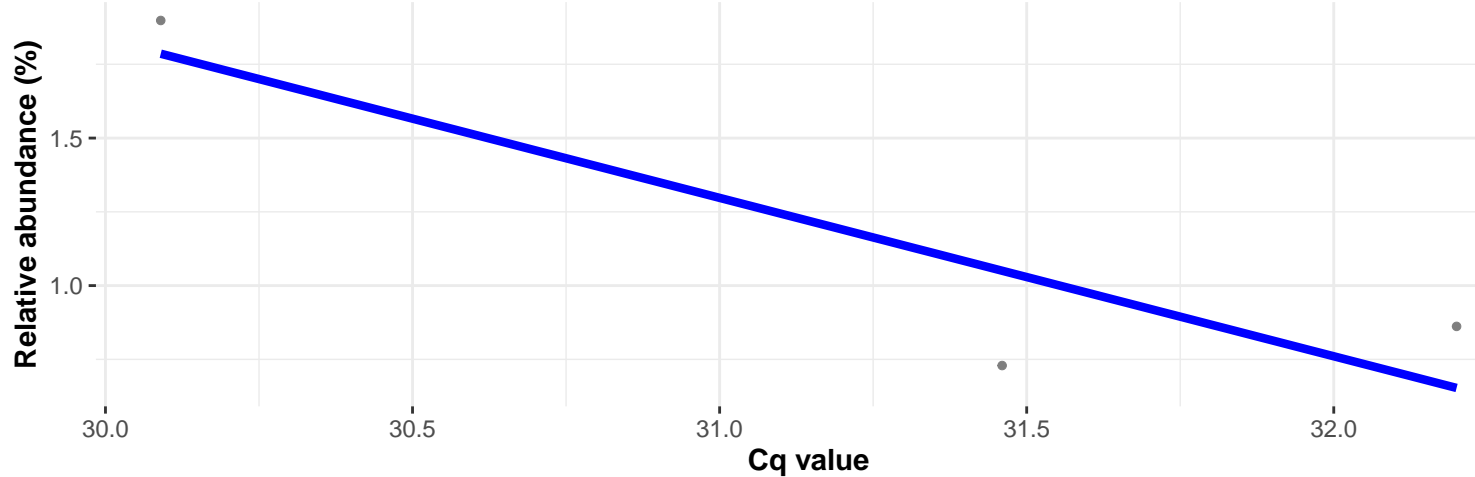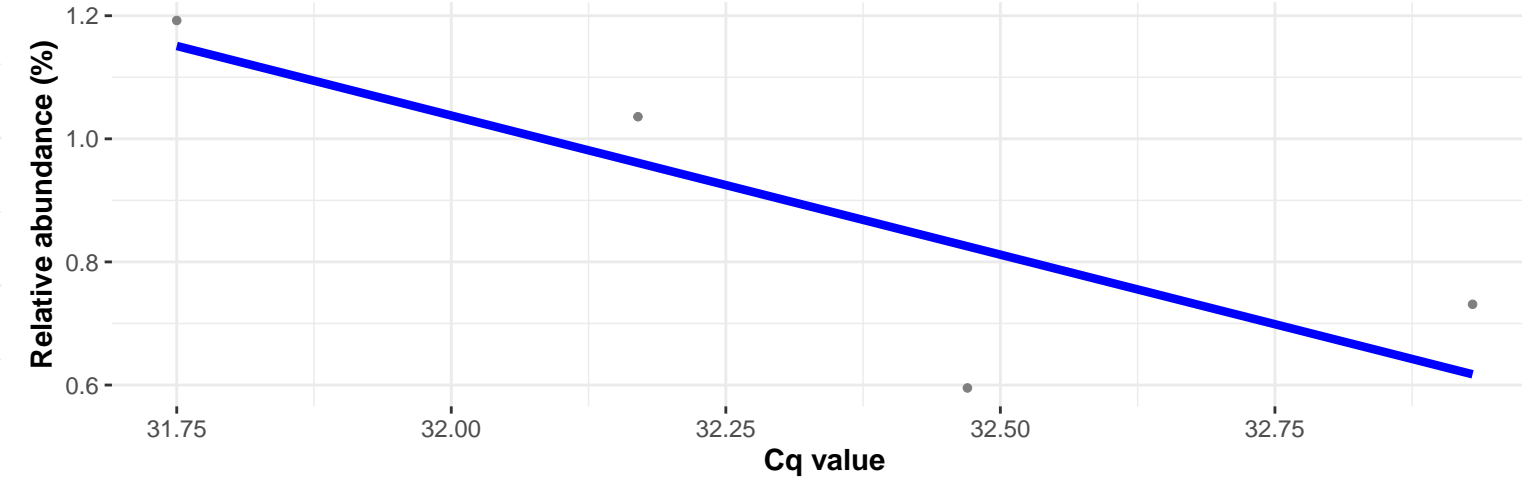
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus cecorum
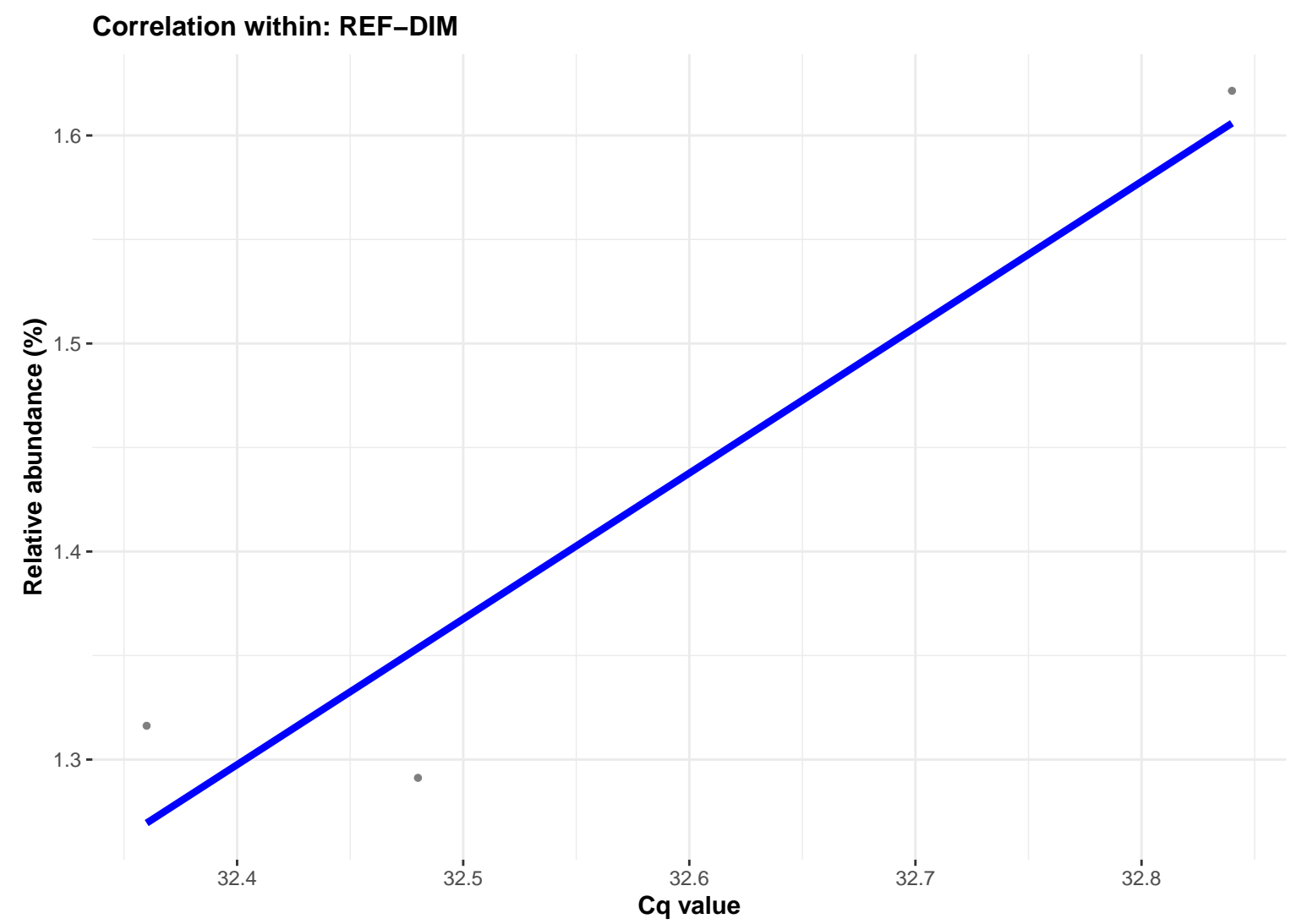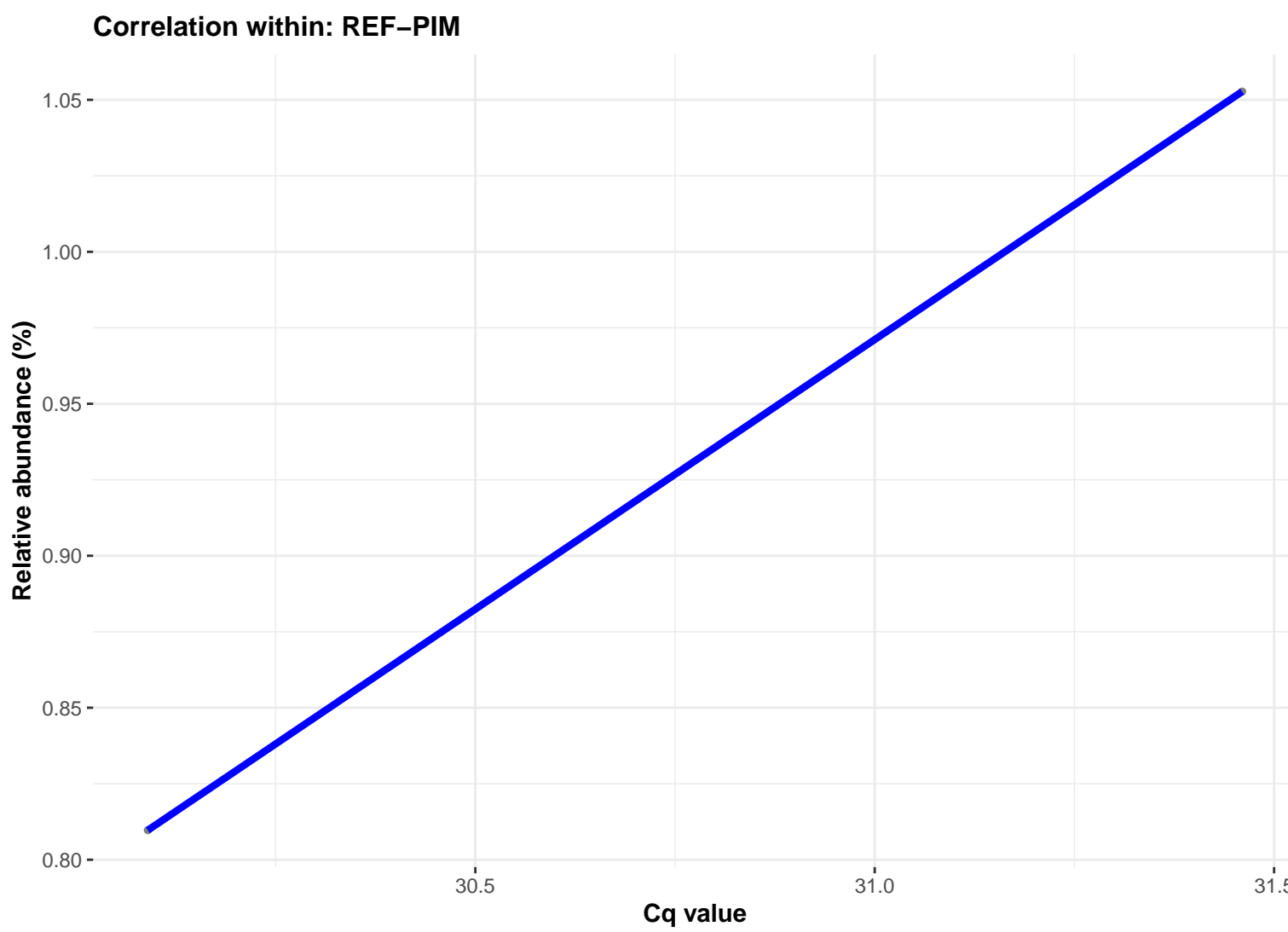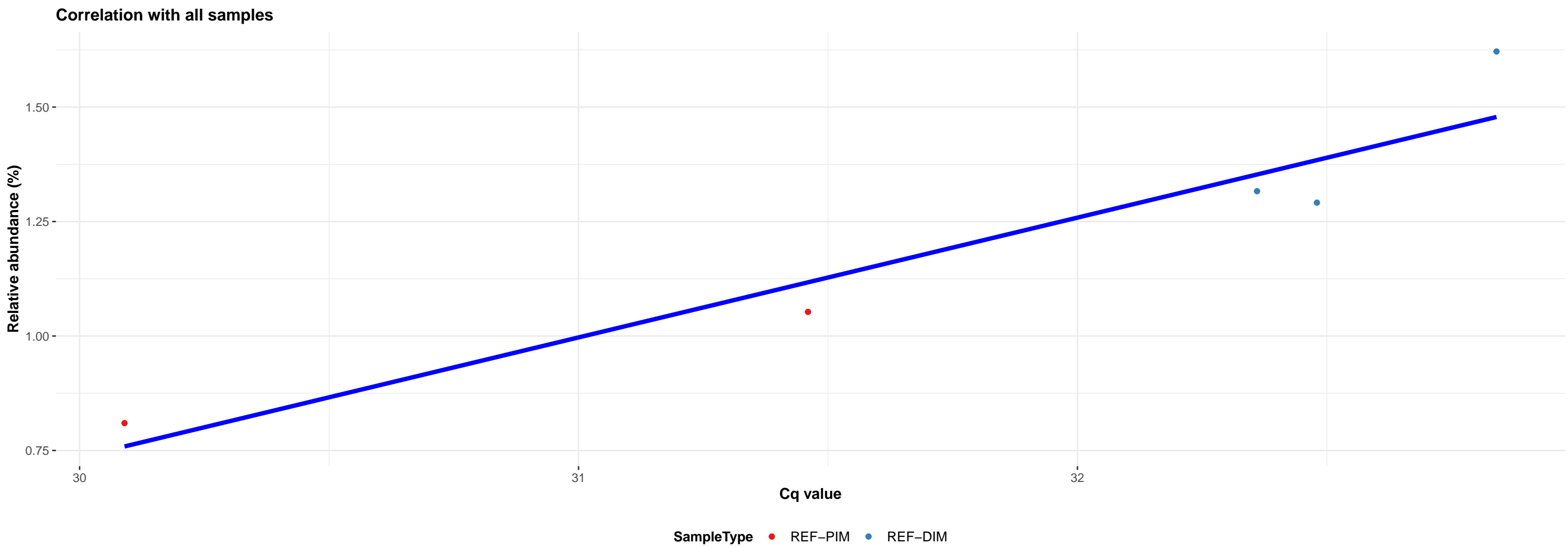
Correlation with all samples

SampleType ● REF−PIM
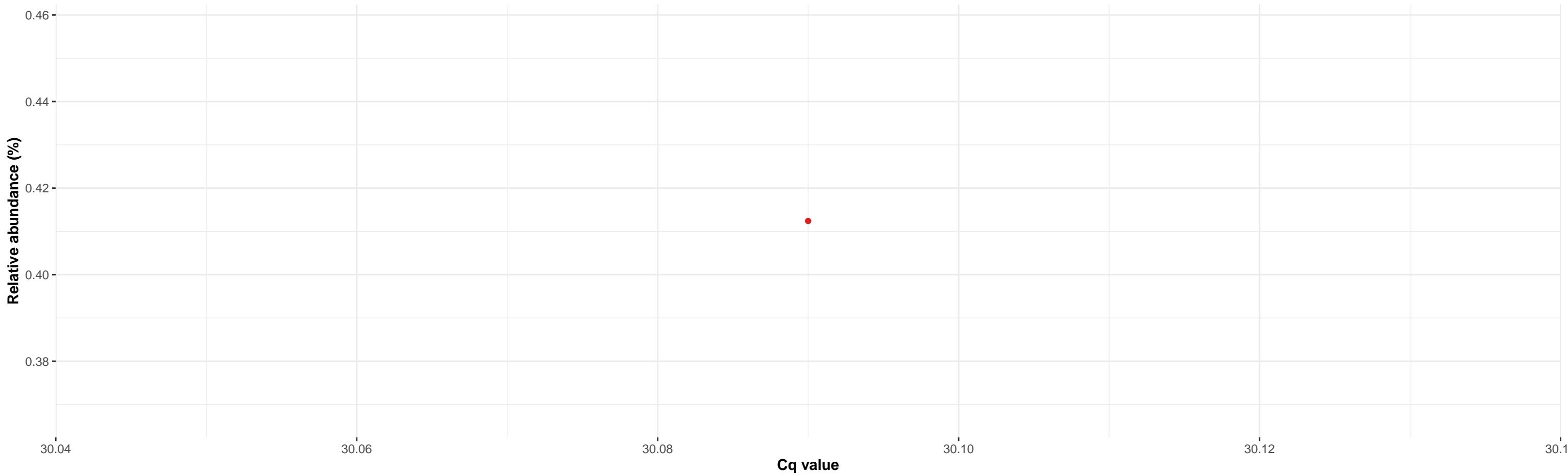
Correlation within: REF−PIM
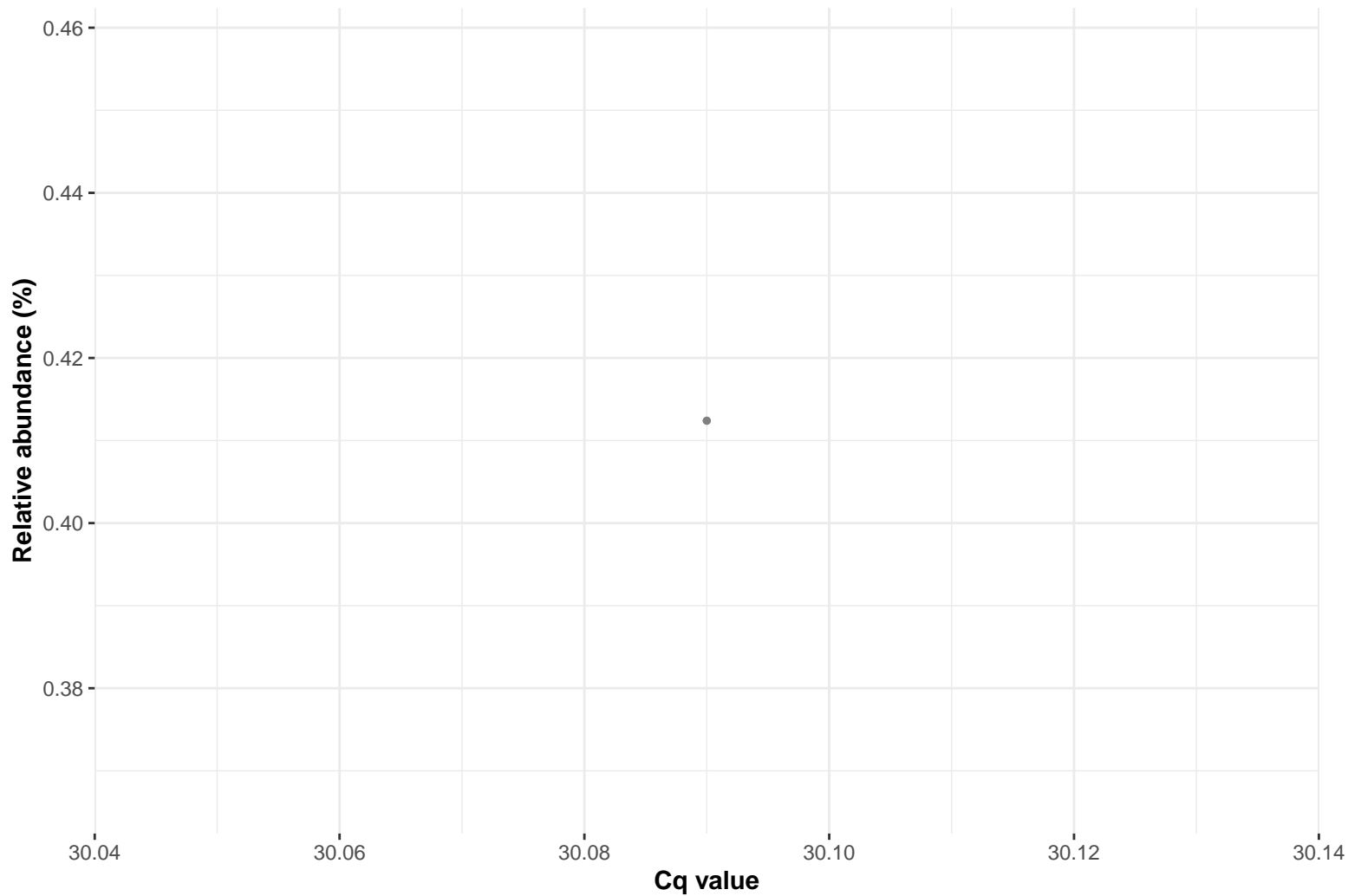
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecium

Correlation with all samples

Relative abundance (%)

Cq value

Correlation within: PCR−blank

Relative abundance (%)

Cq value

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__uncultured Virgibacillus sp.

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__TRA3-20; NA; NA
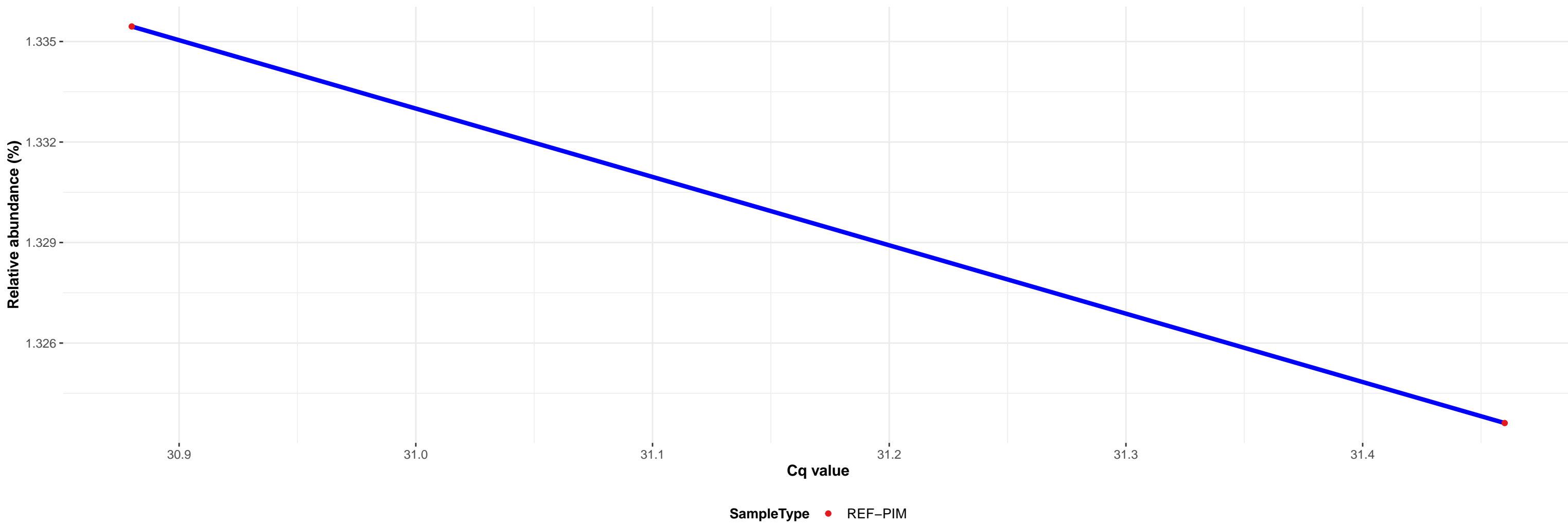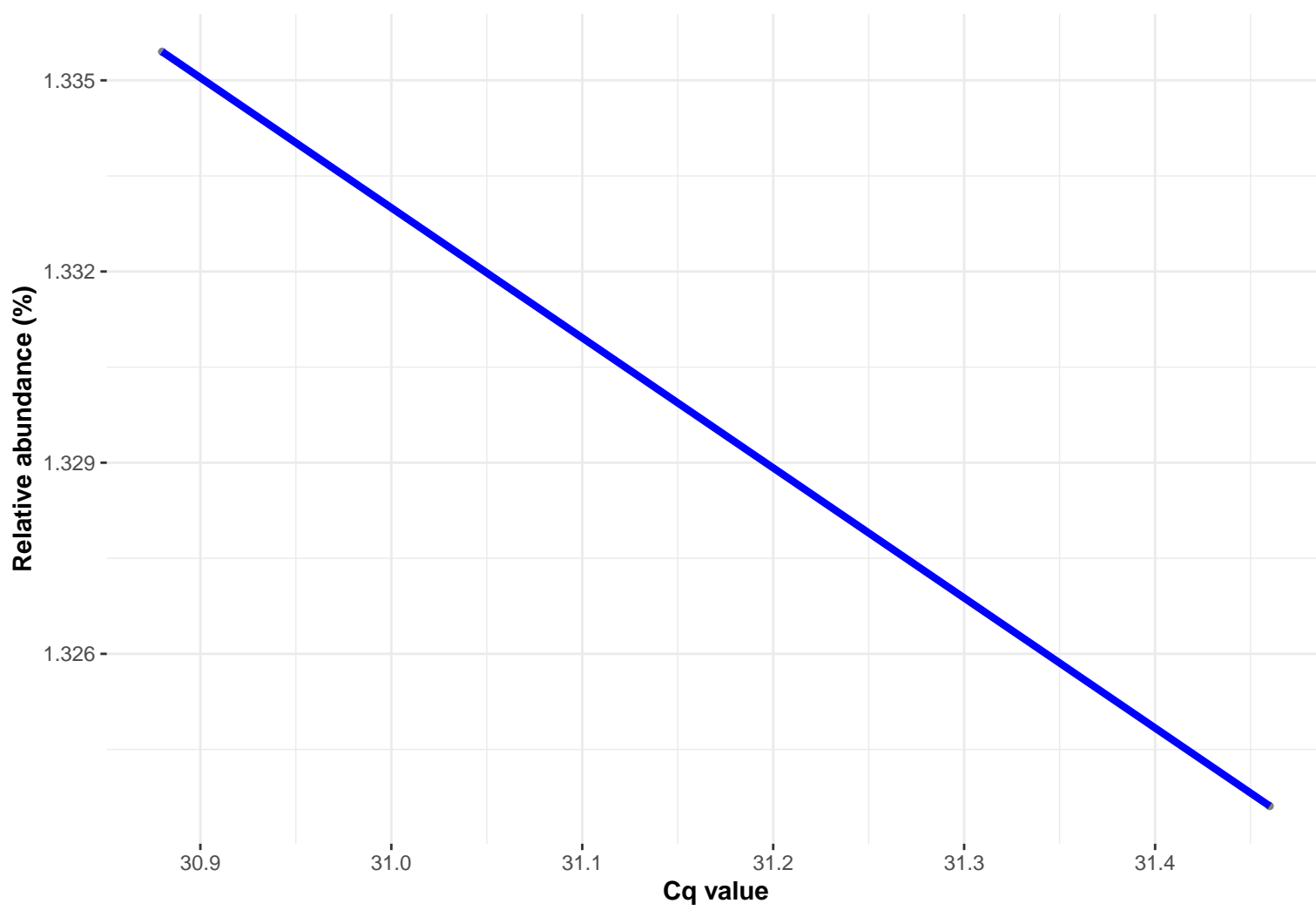
k__Bacteria; p__Cyanobacteria; c__Melainabacteria; o__Obscuribacterales; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa

Correlation with all samples
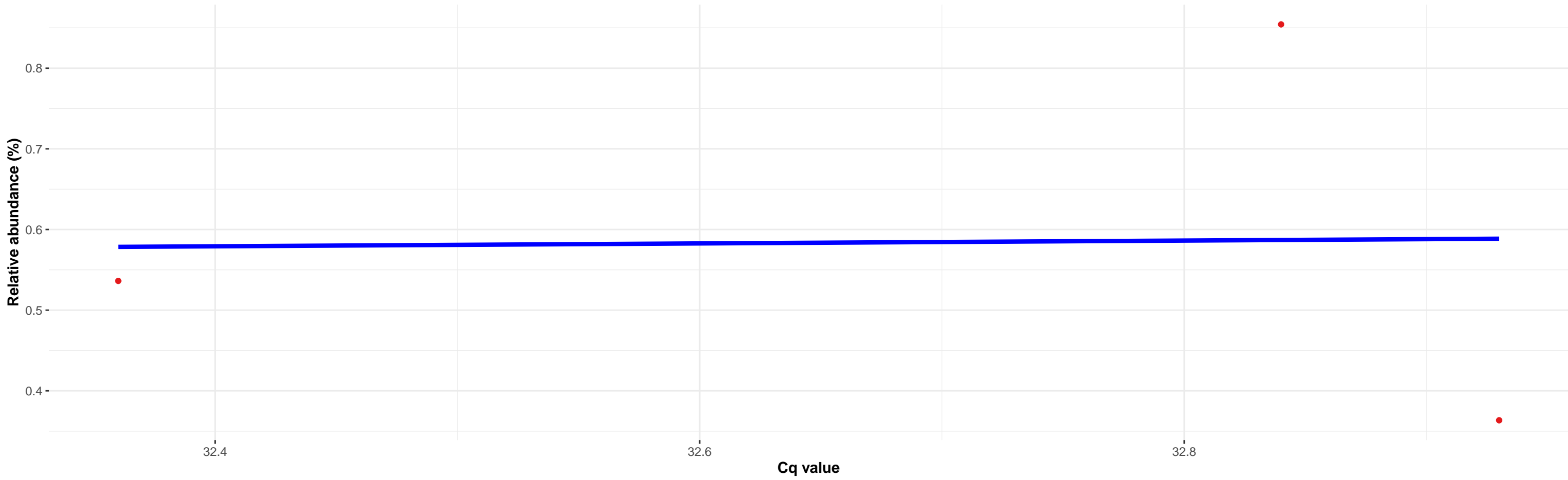
SampleType ● REF−DIM

Correlation within: REF−DIM
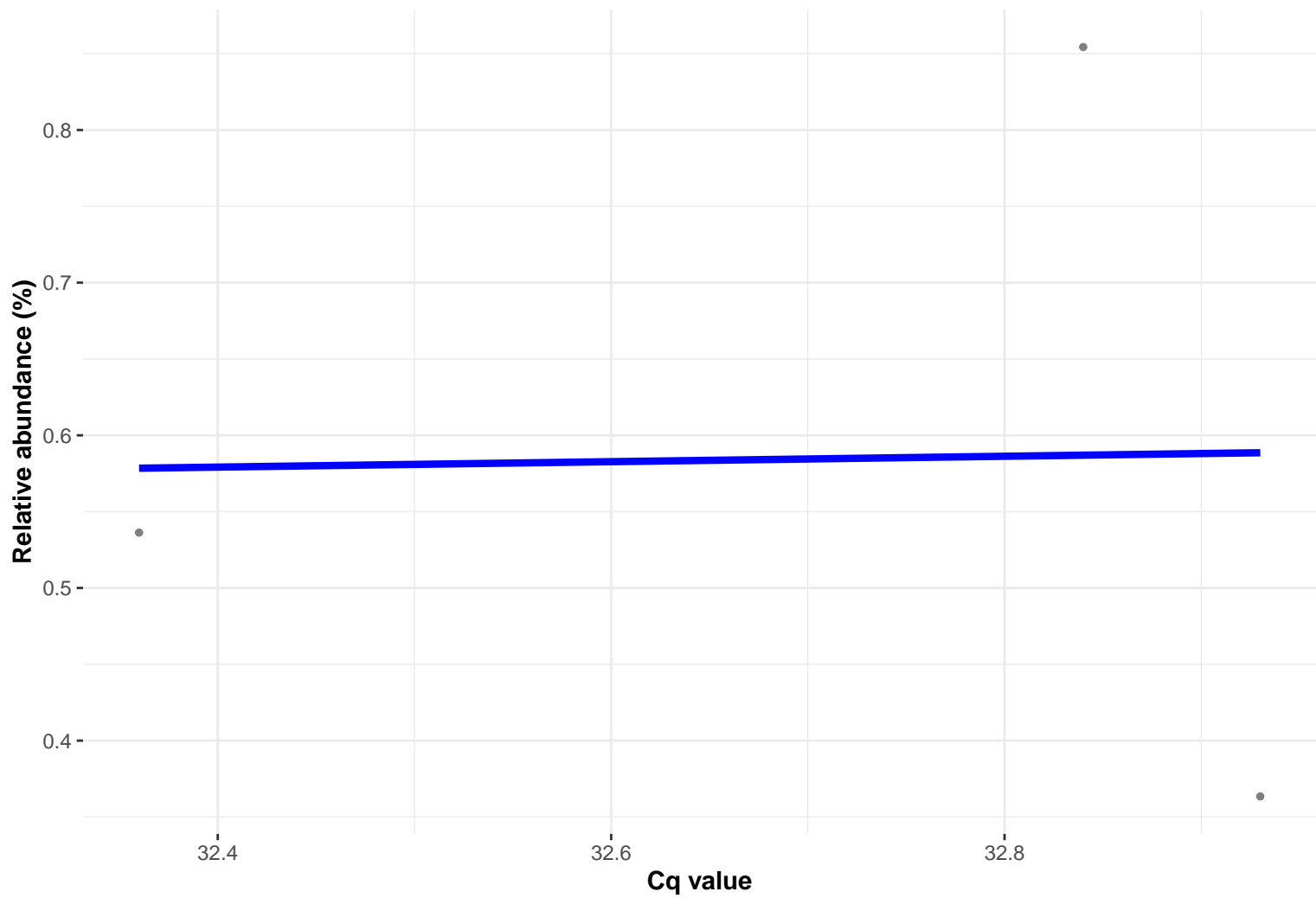
Correlation within: PCR−blank

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Diplorickettsiales; f__Diplorickettsiaceae; g__Rickettsiella; s__Proasellus assaforensis

Correlation with all samples

SampleType ● REF−DIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Microbacterium; Ambiguous_taxa

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; NA

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; NA

Correlation with all samples

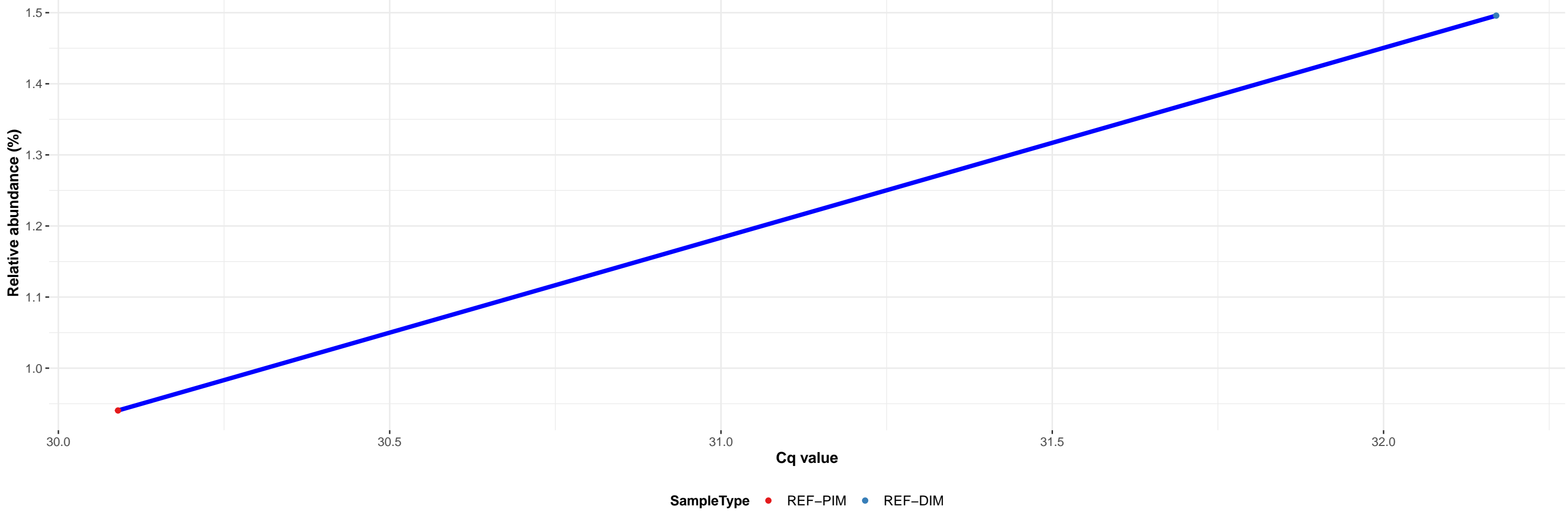SampleType ● REF−PIM ● REF−DIM

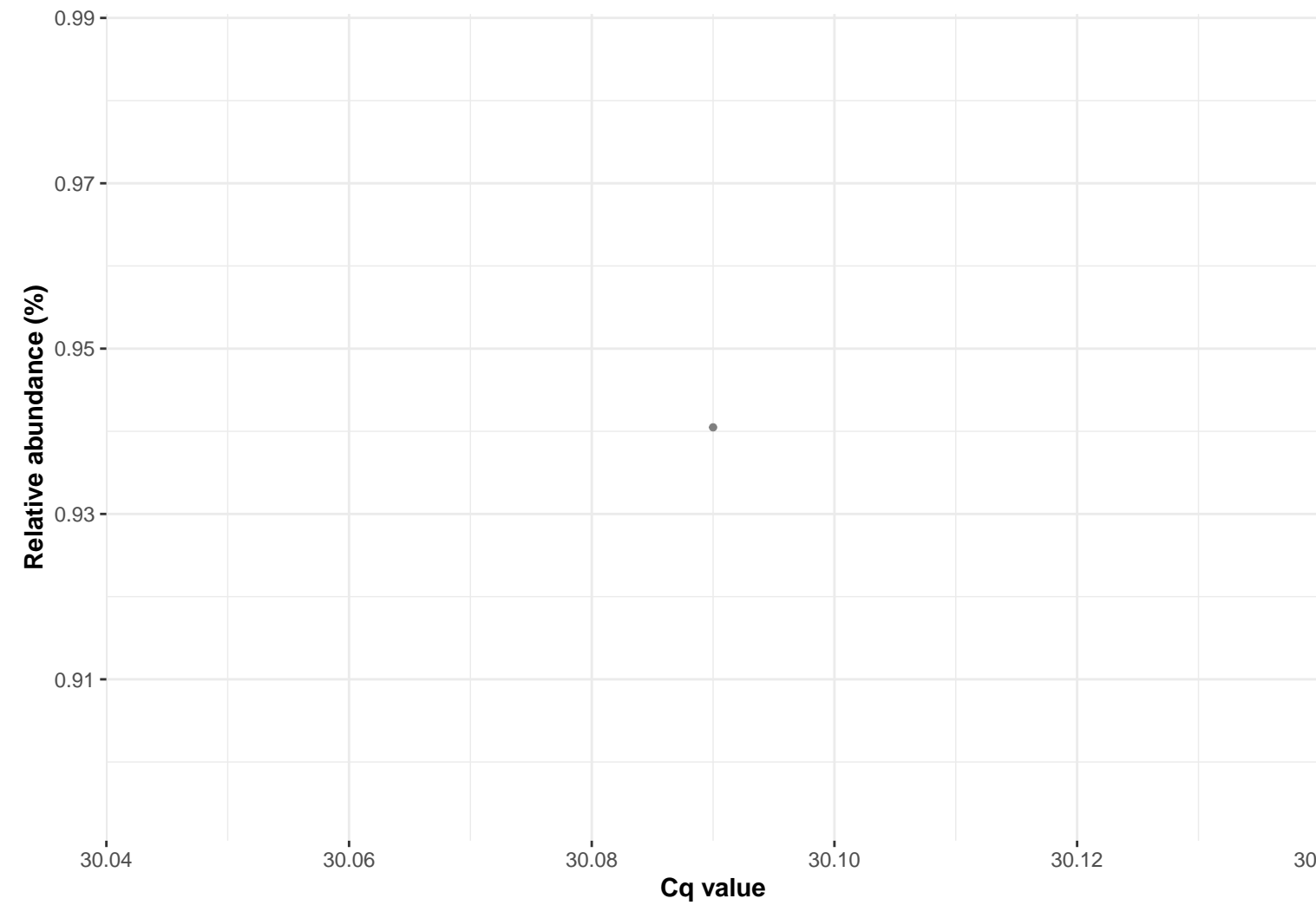**Correlation within: REF−PIM**

Correlation within: REF−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

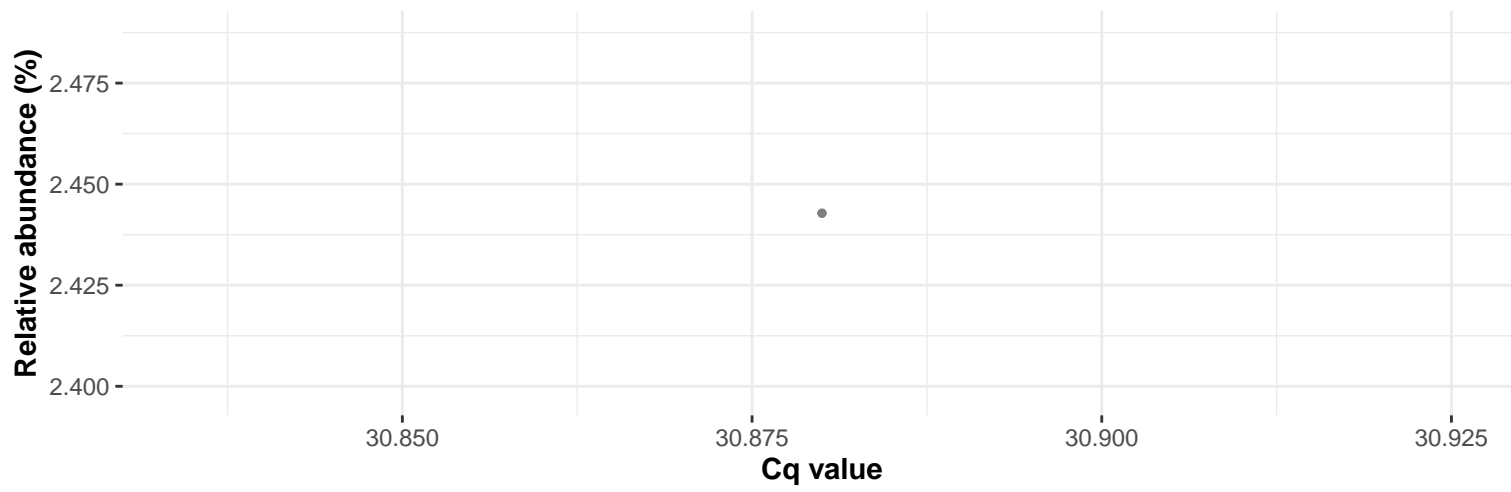# k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium xerosis

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa
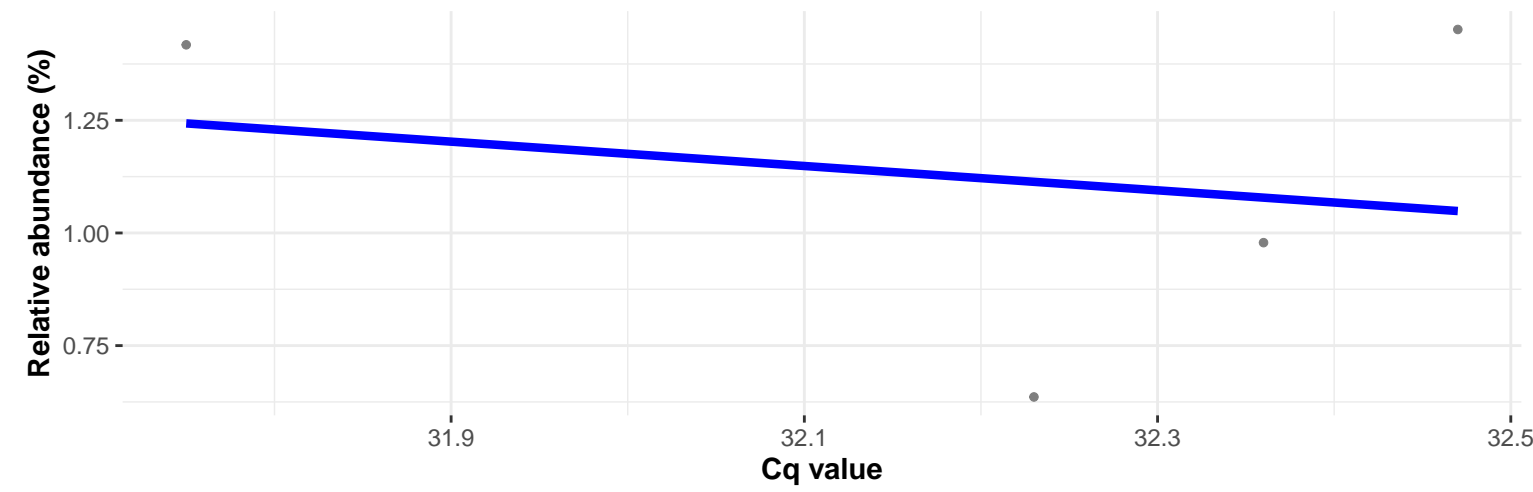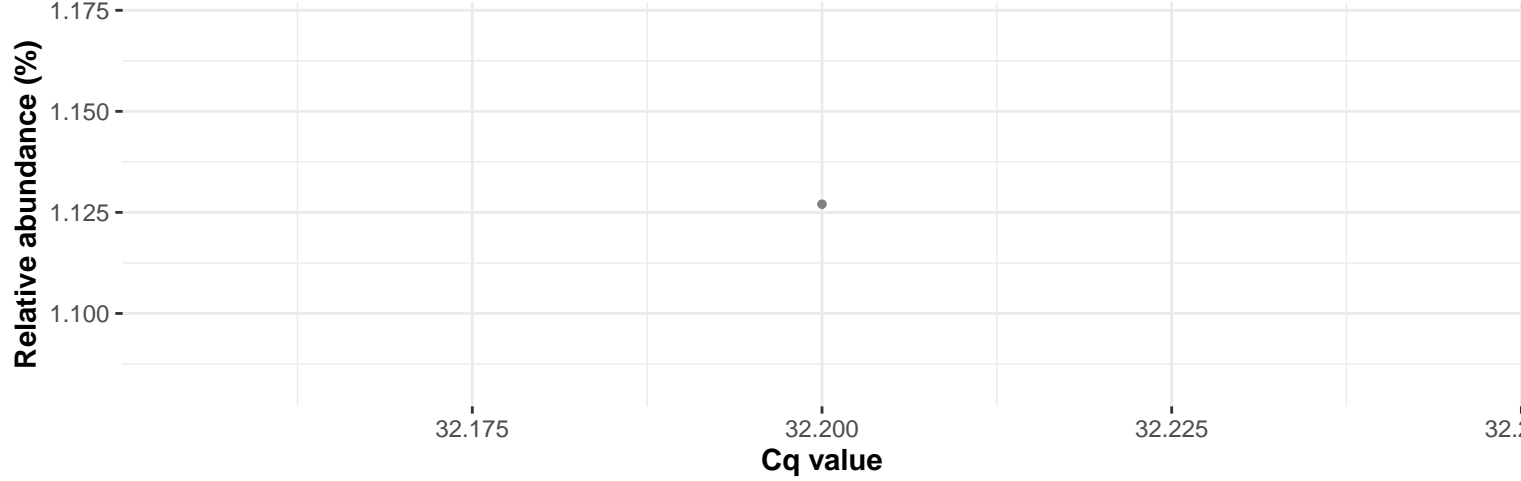
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Pseudorhodobacter; NA
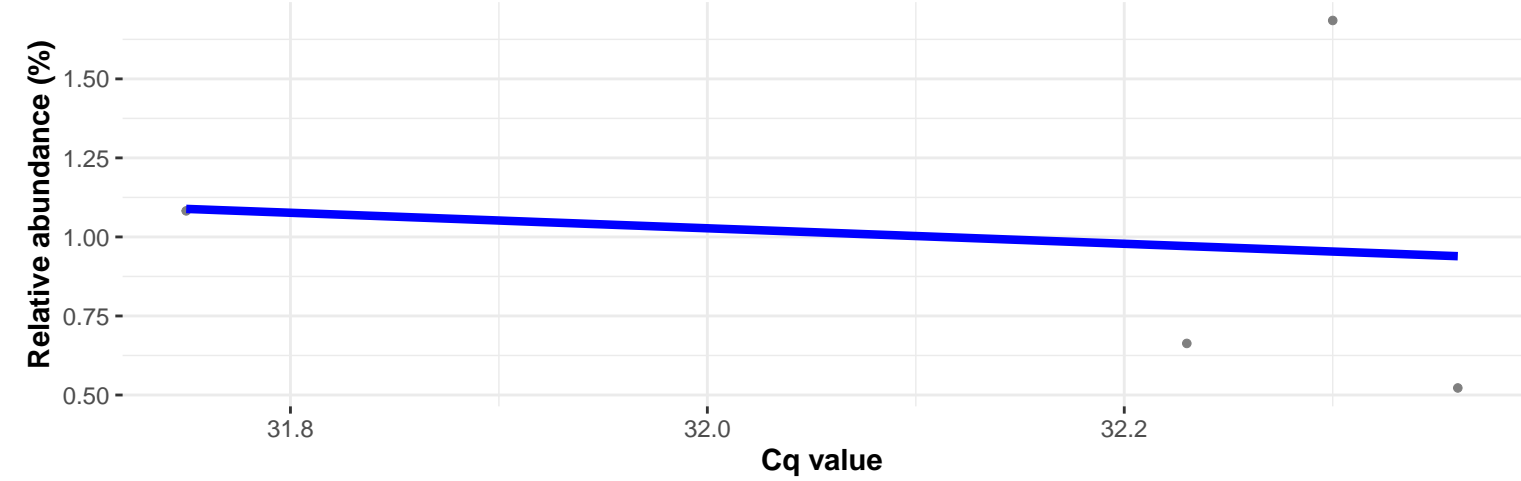
Correlation with all samples
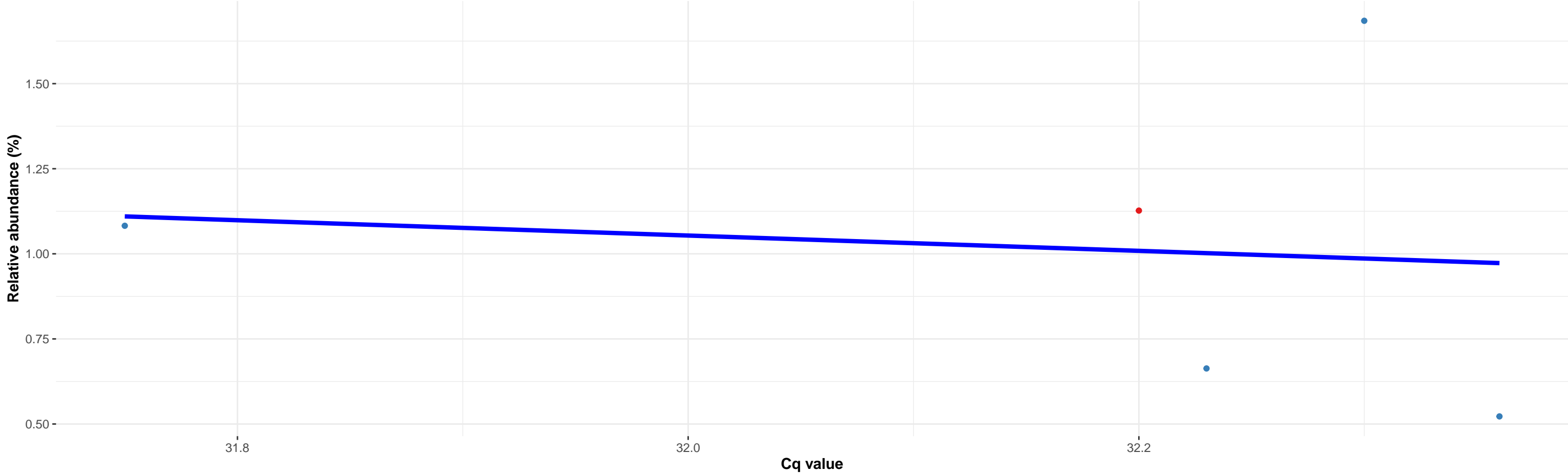
SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM
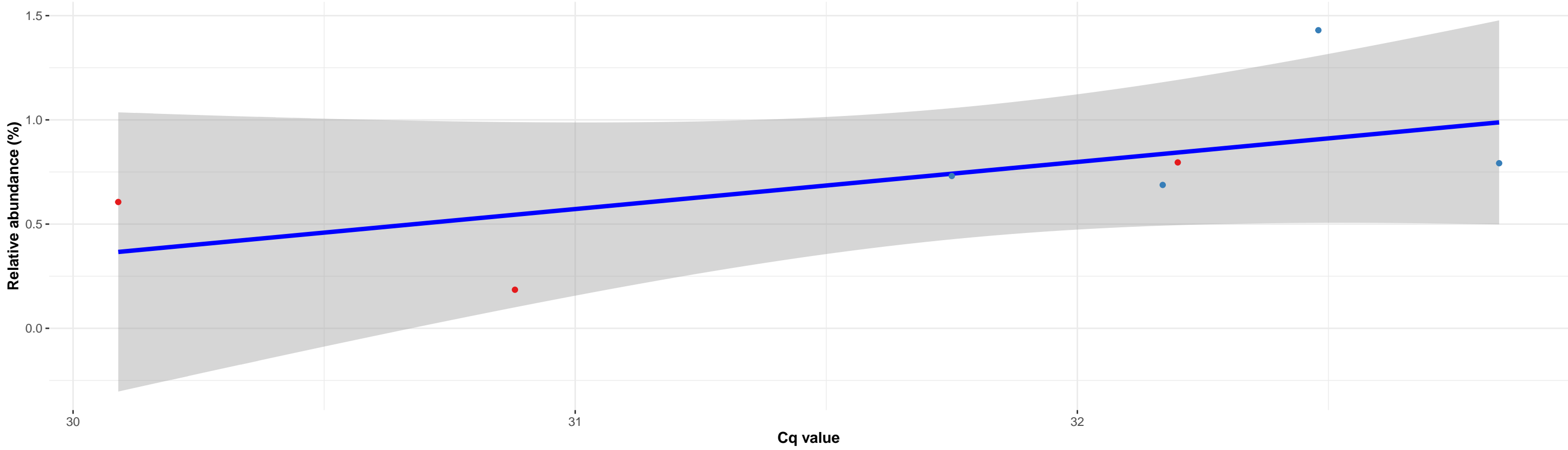

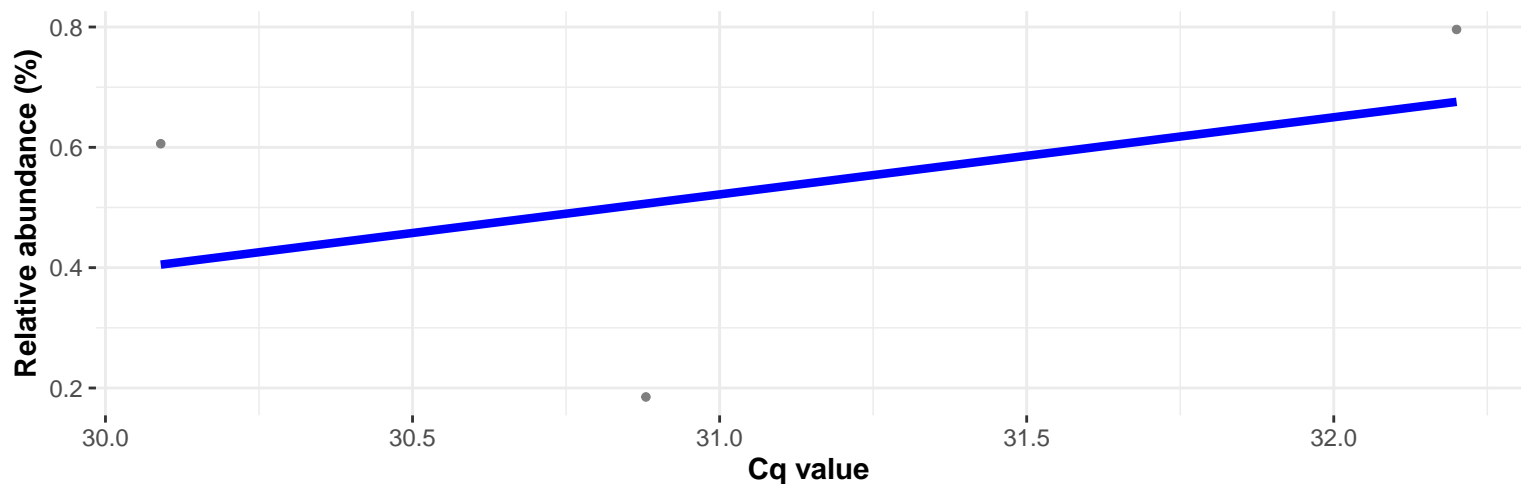**Correlation within: REF−DIM**

Correlation within: PCR−blank

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Afipia; Ambiguous_taxa
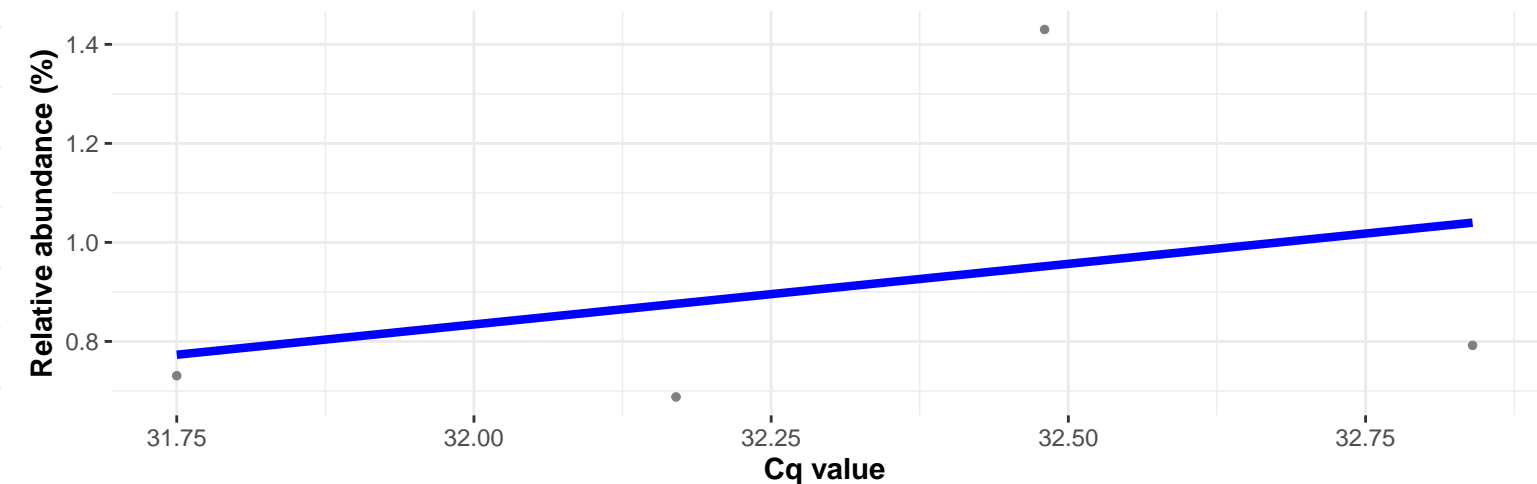
Correlation with all samples

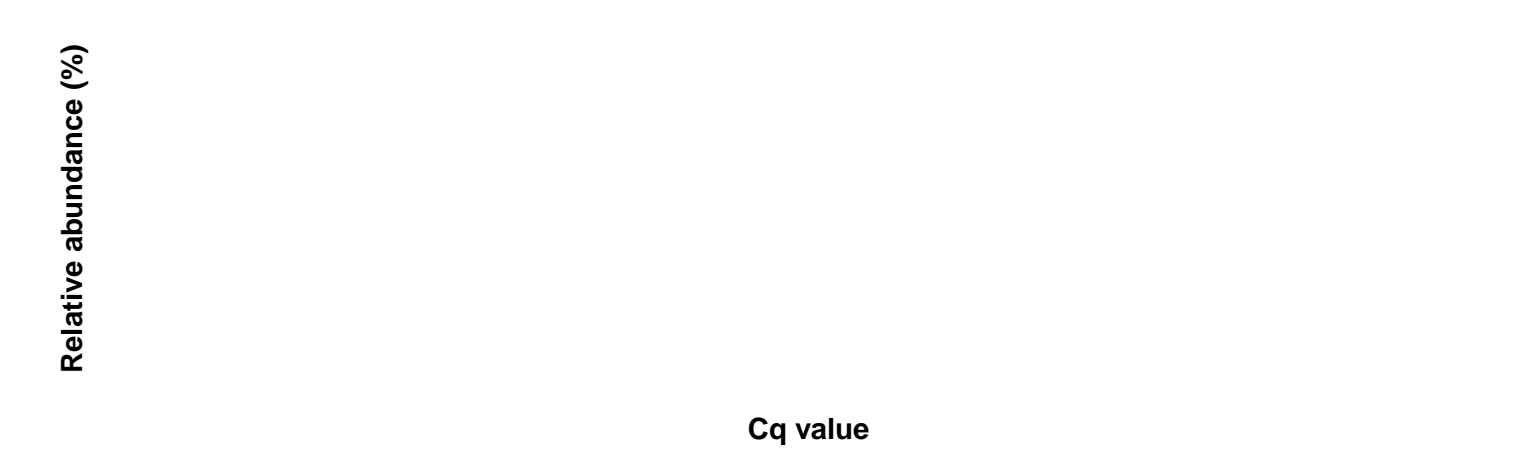$\log_e(S) = 2.303$, $p = 0.023$, $\hat{\rho}_{Spearman} = 0.821$, $CI_{95\%}$ [0.151, 0.974], $n_{pairs} = 7$

SampleType ● REF−PIM ● REF−DIM

Correlation within: REF−PIM

Correlation within: REF−DIM

Correlation within: PCR−blank

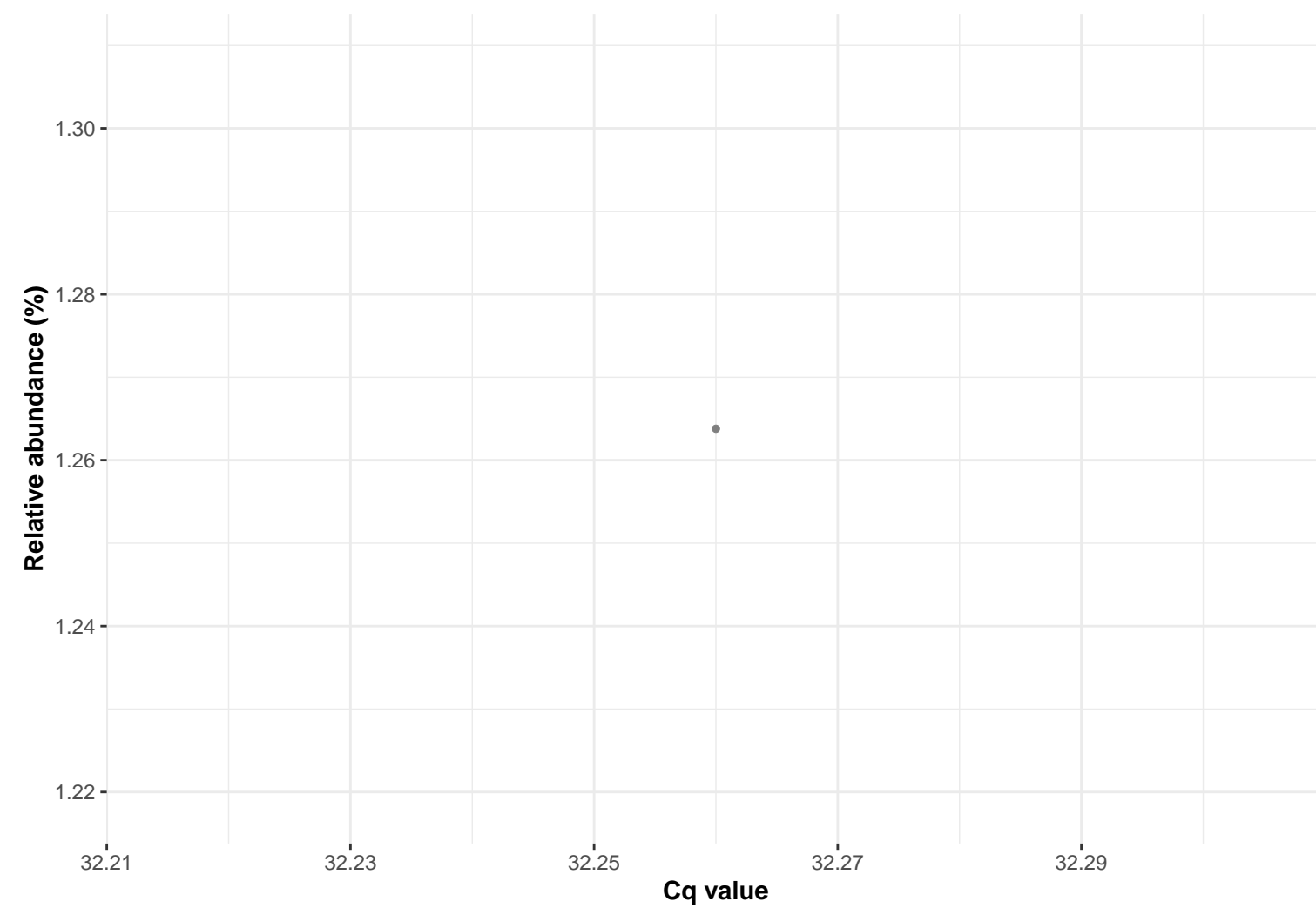# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Macrococcus; Ambiguous_taxa
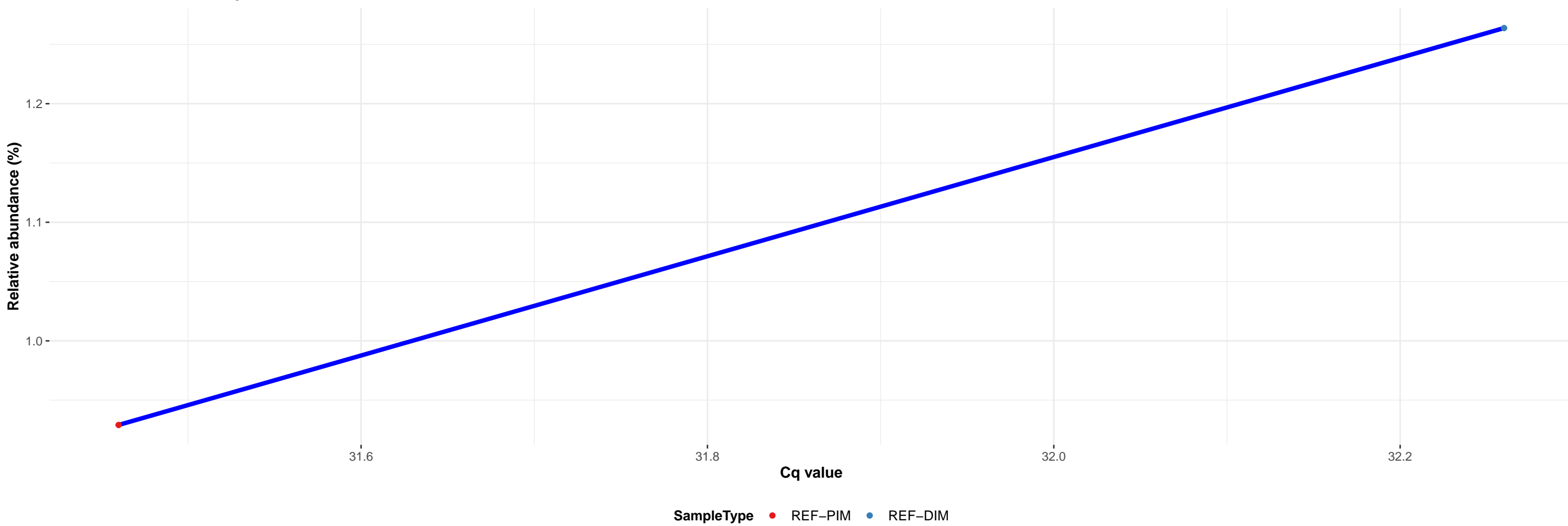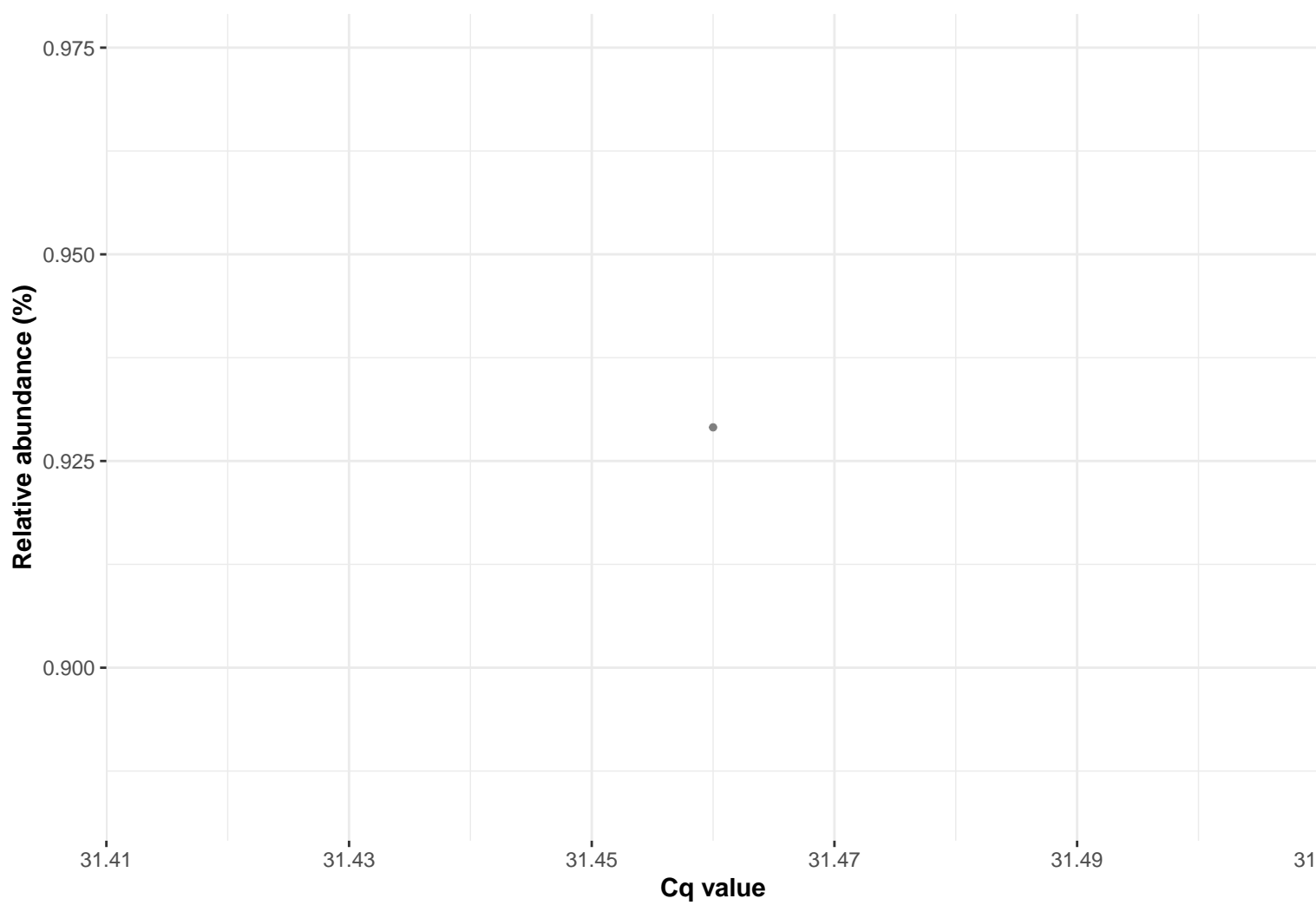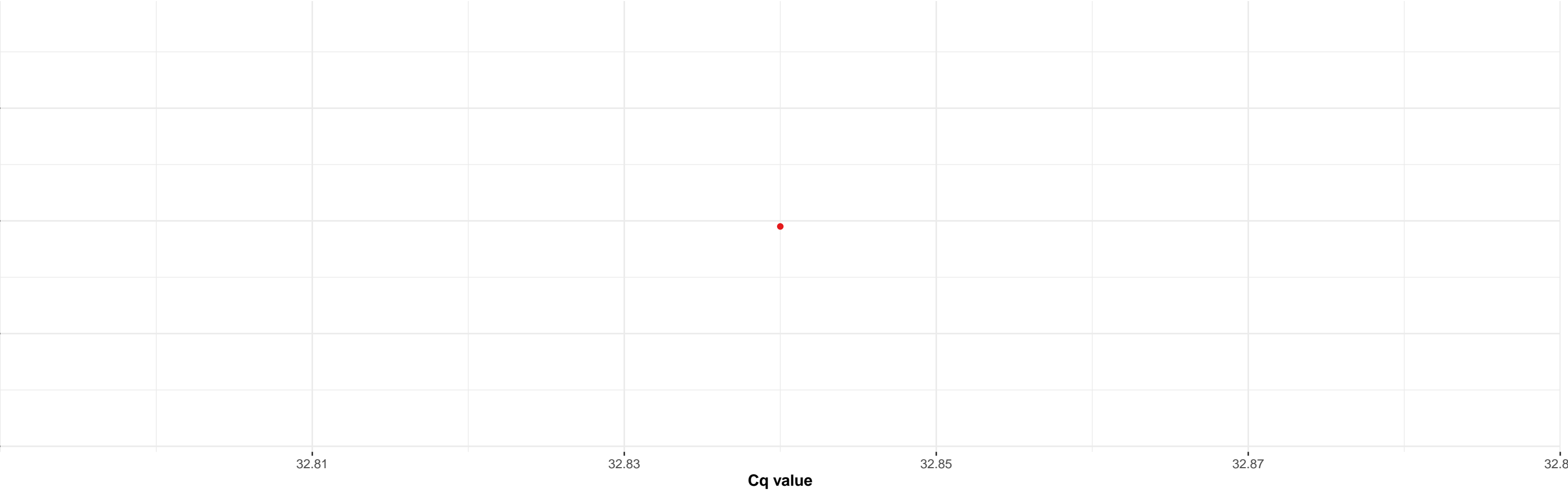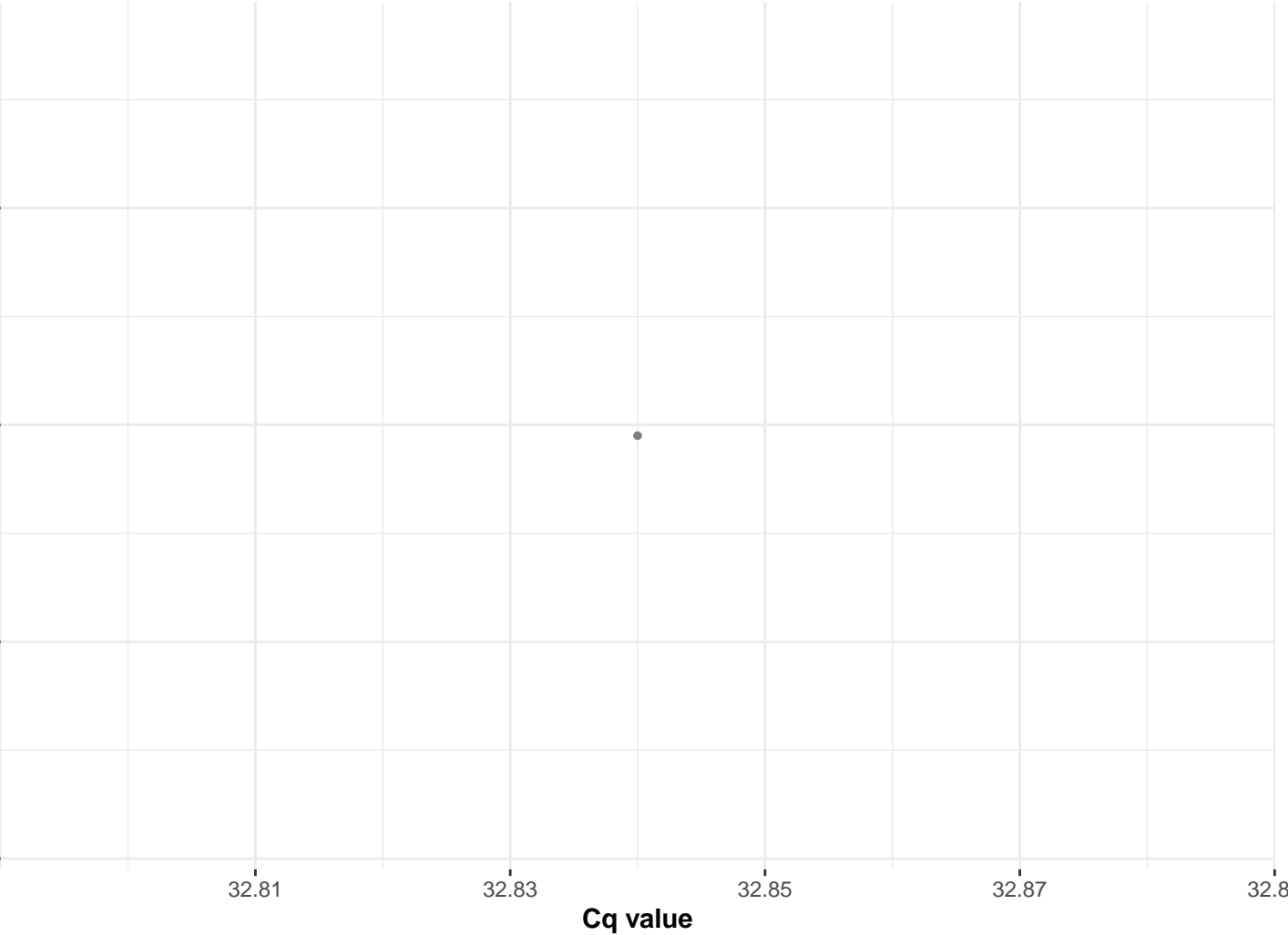
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

Correlation with all samples

SampleType ● REF−DIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples

Relative abundance (%)
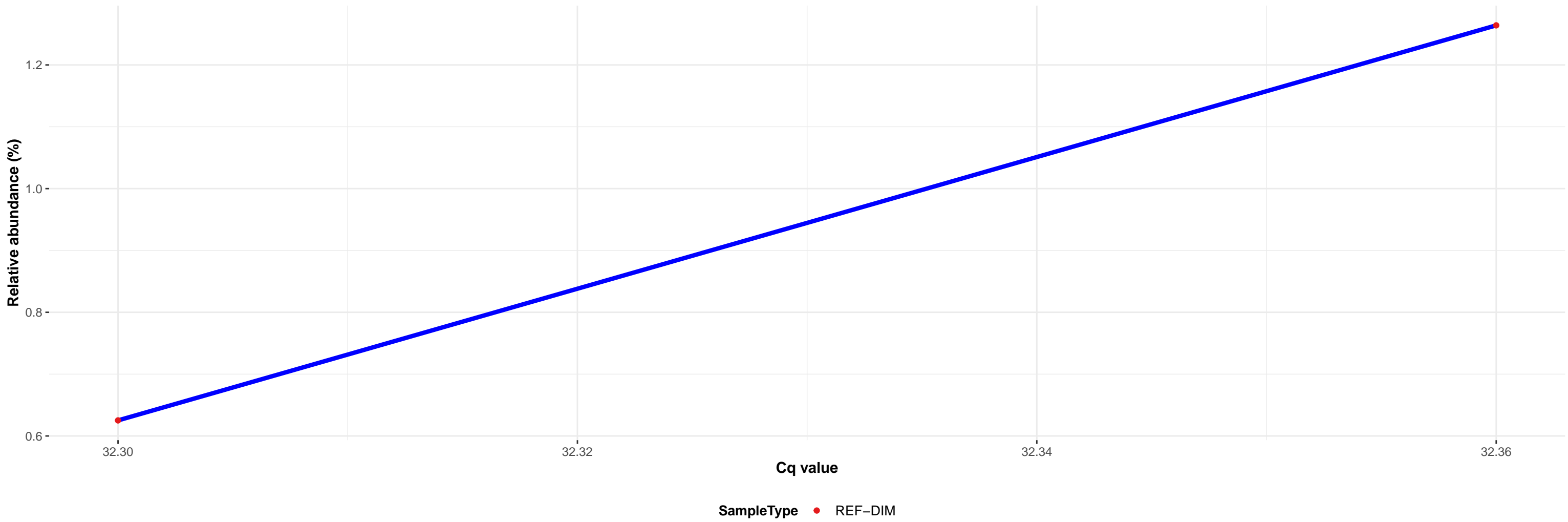
Cq value
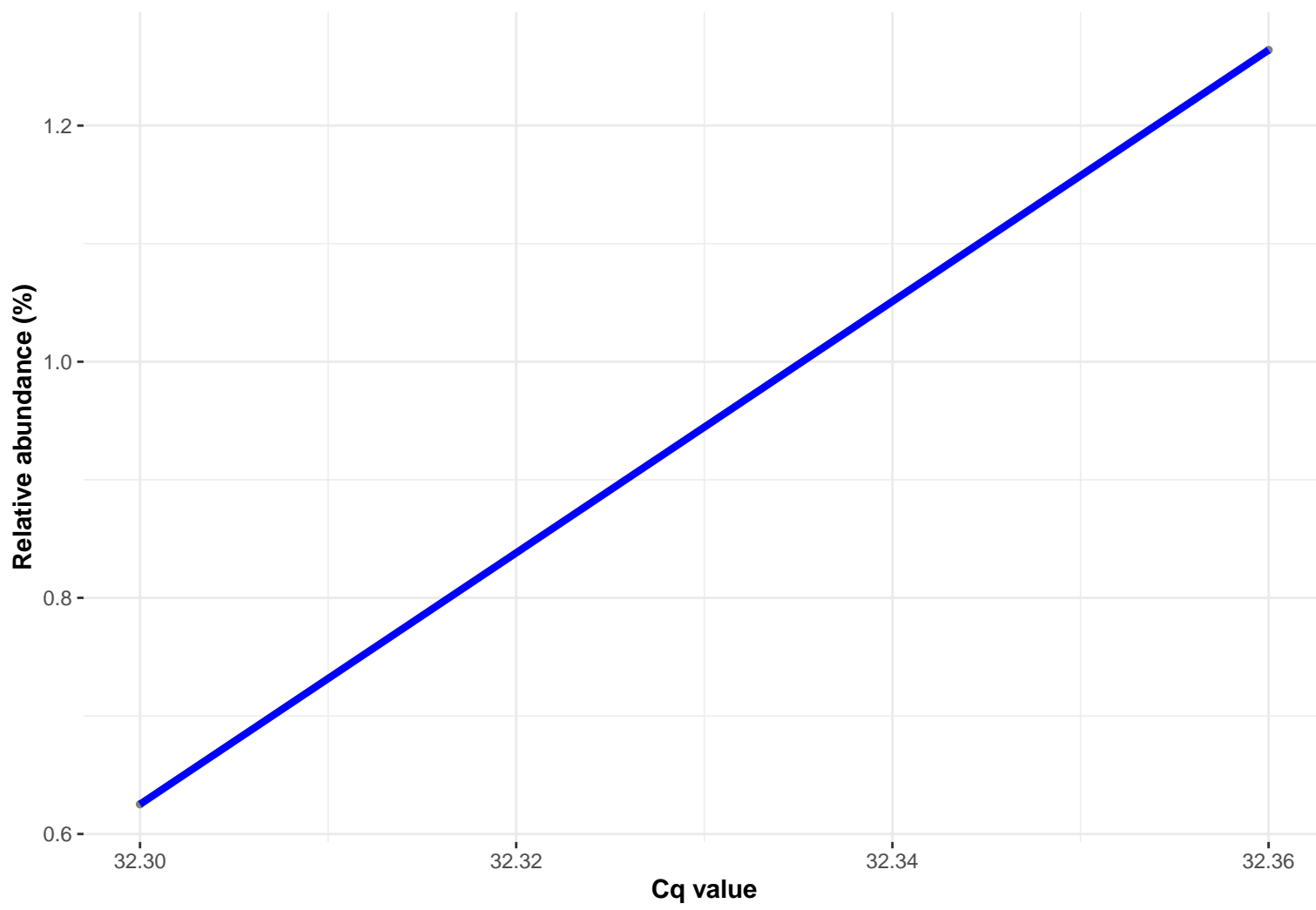
Correlation within: PCR−blank

Relative abundance (%)

Cq value

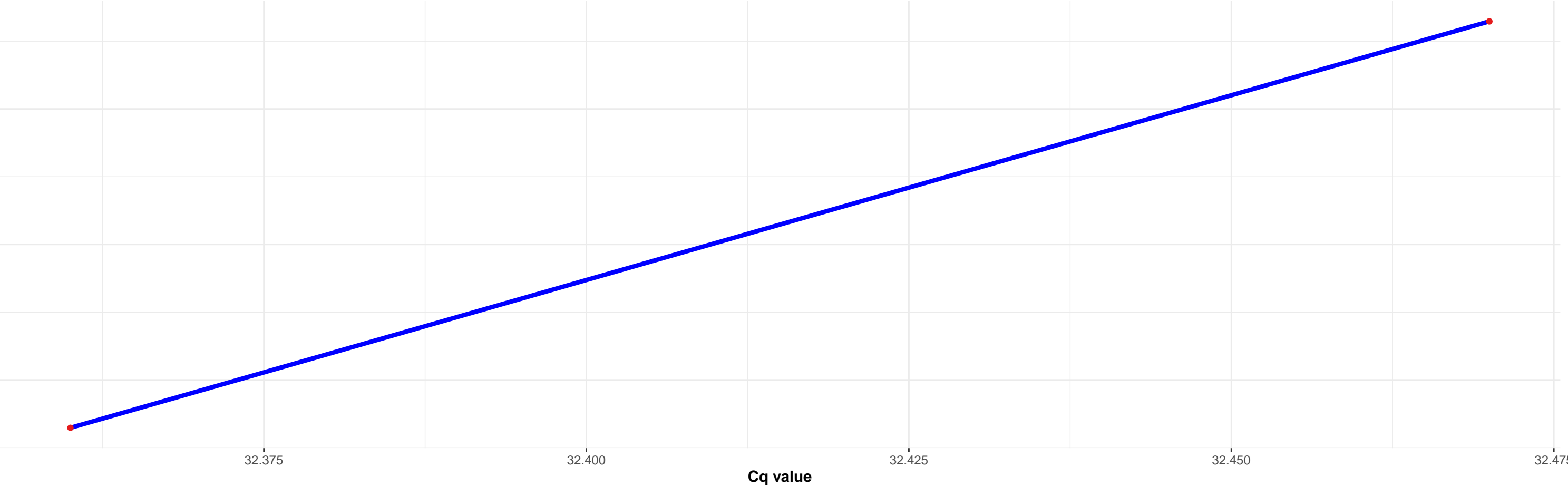# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa

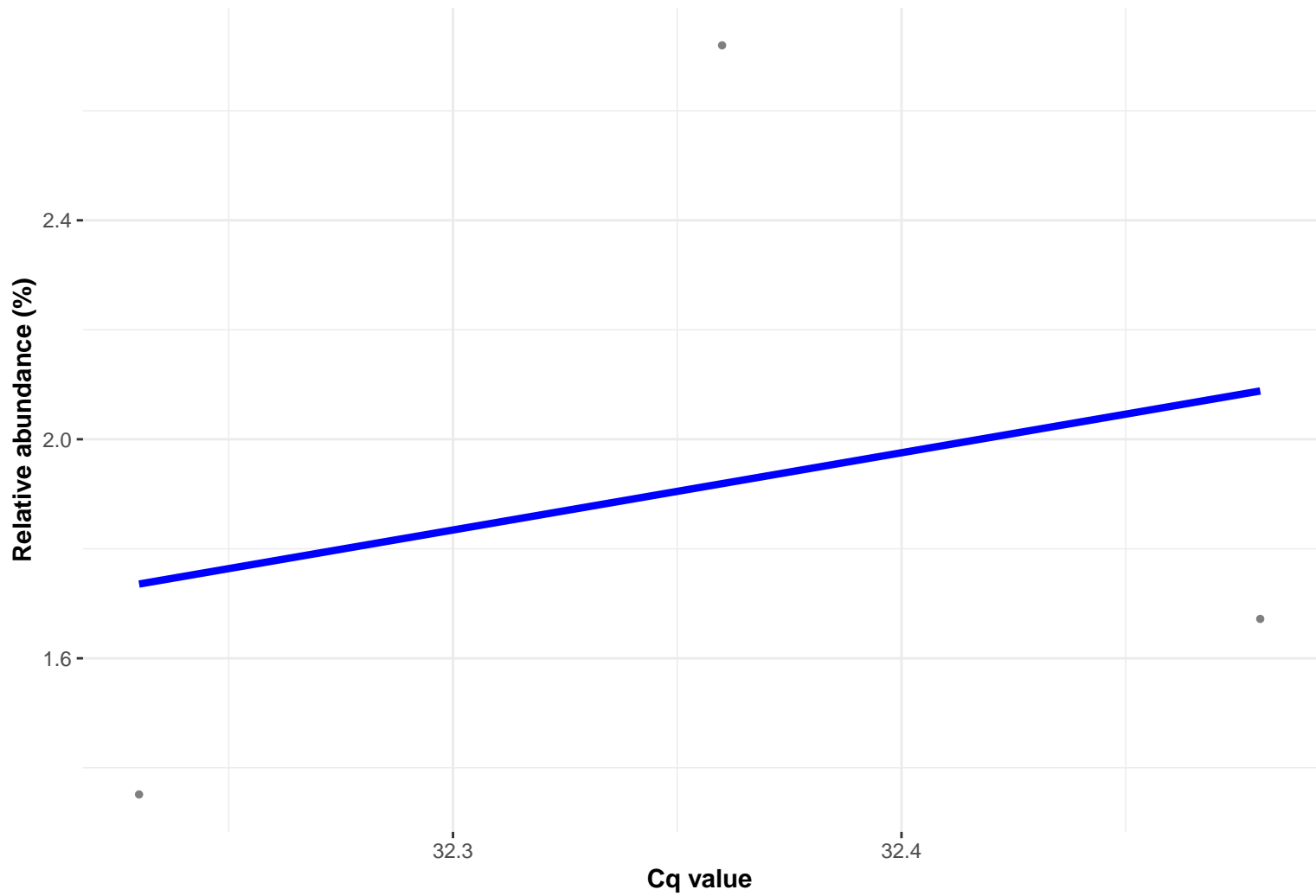# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Chitinophagales; f__Chitinophagaceae; g__Sediminibacterium; s__uncultured bacterium
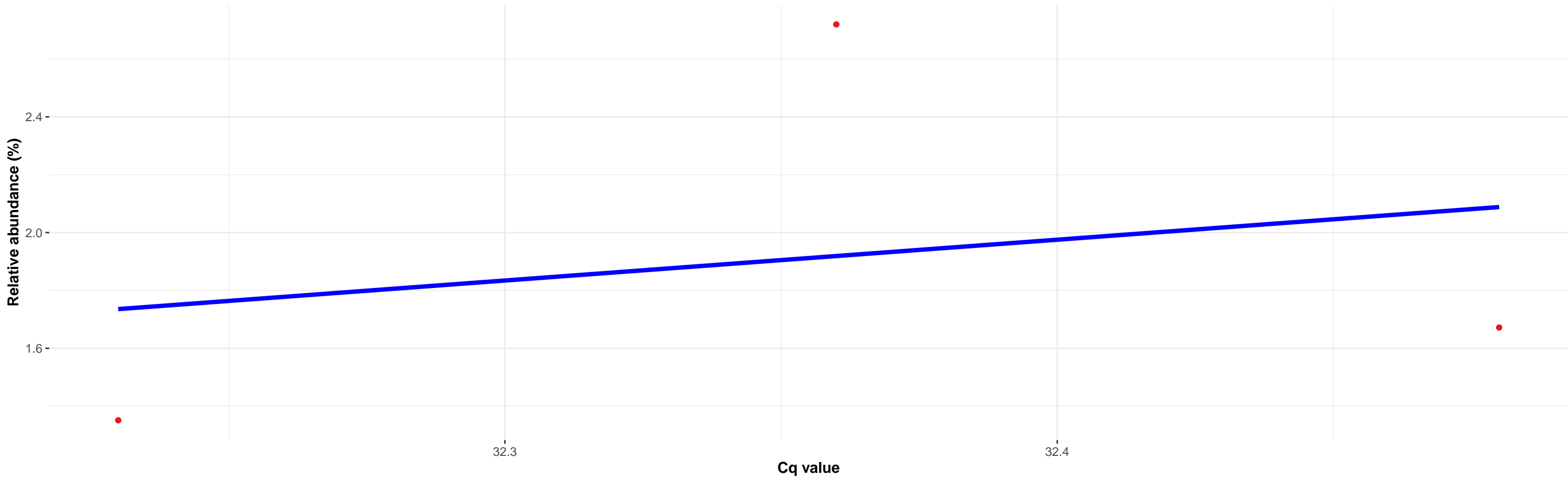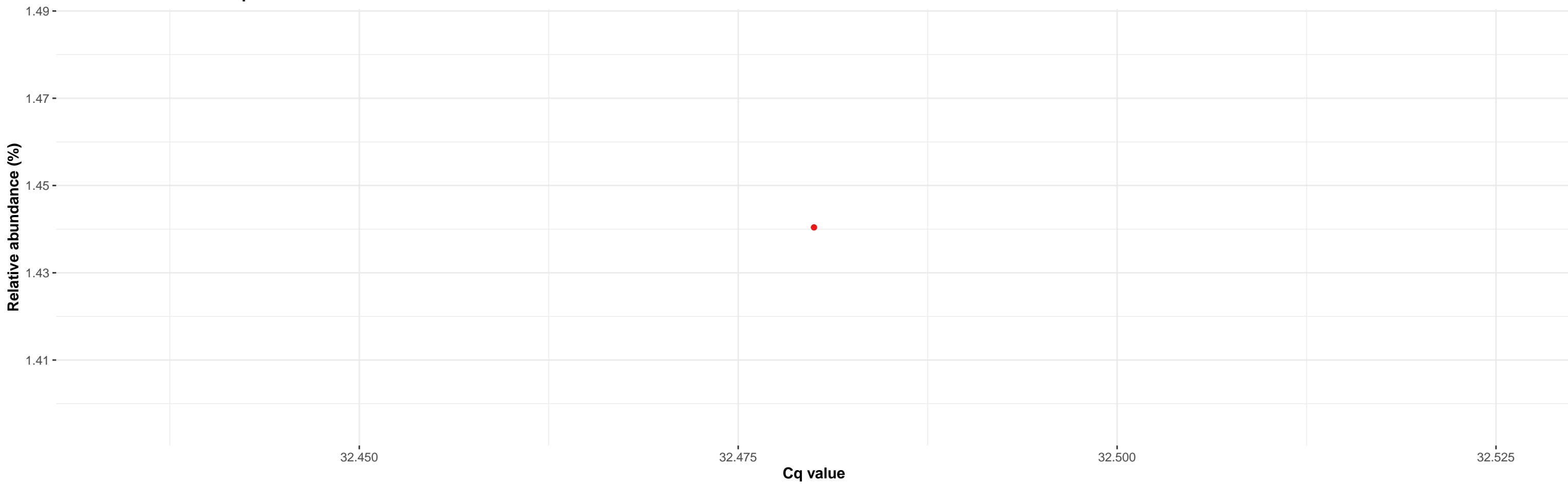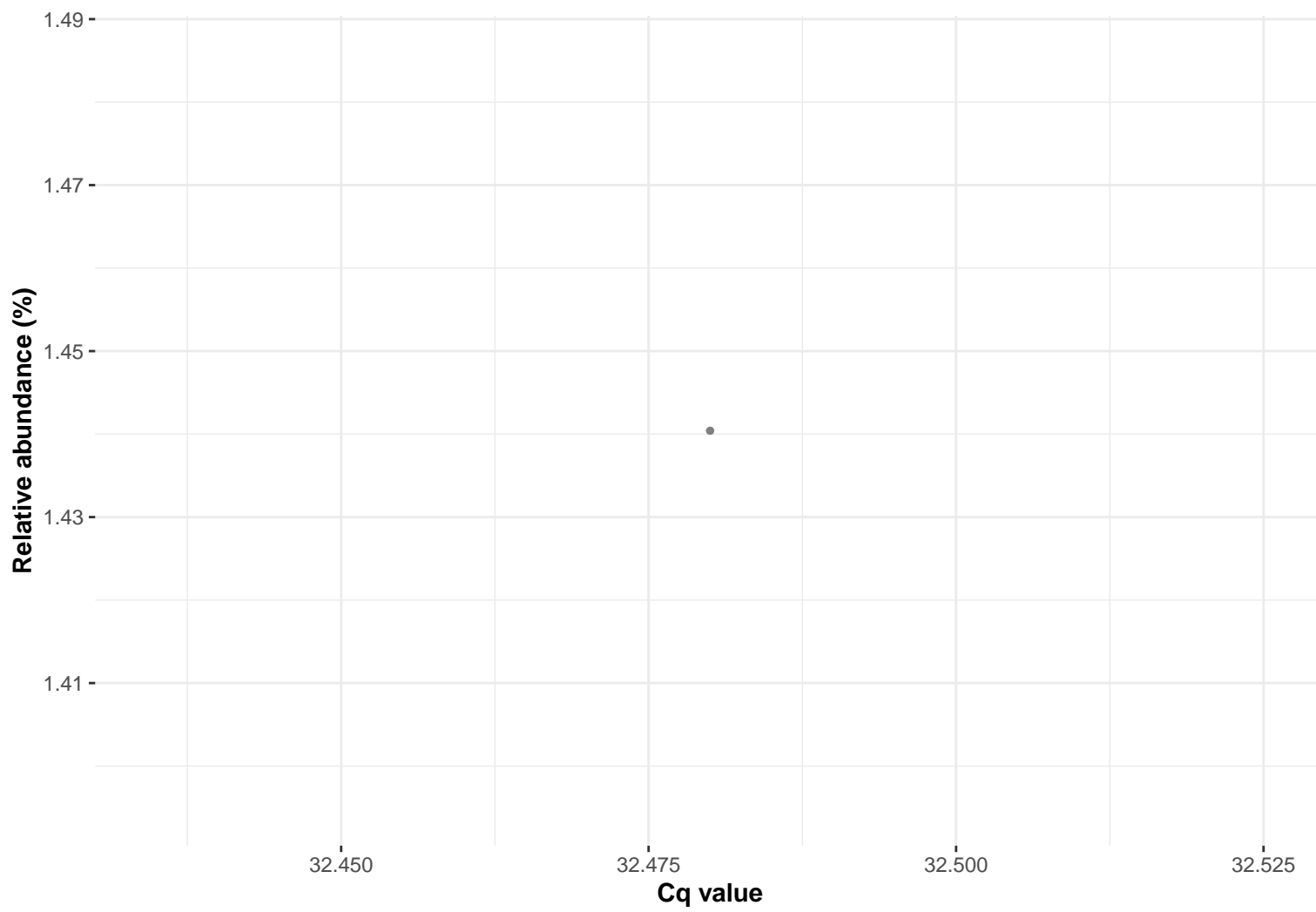
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium xerosis

Correlation with all samples

SampleType ● REF−DIM

Correlation within: REF−DIM

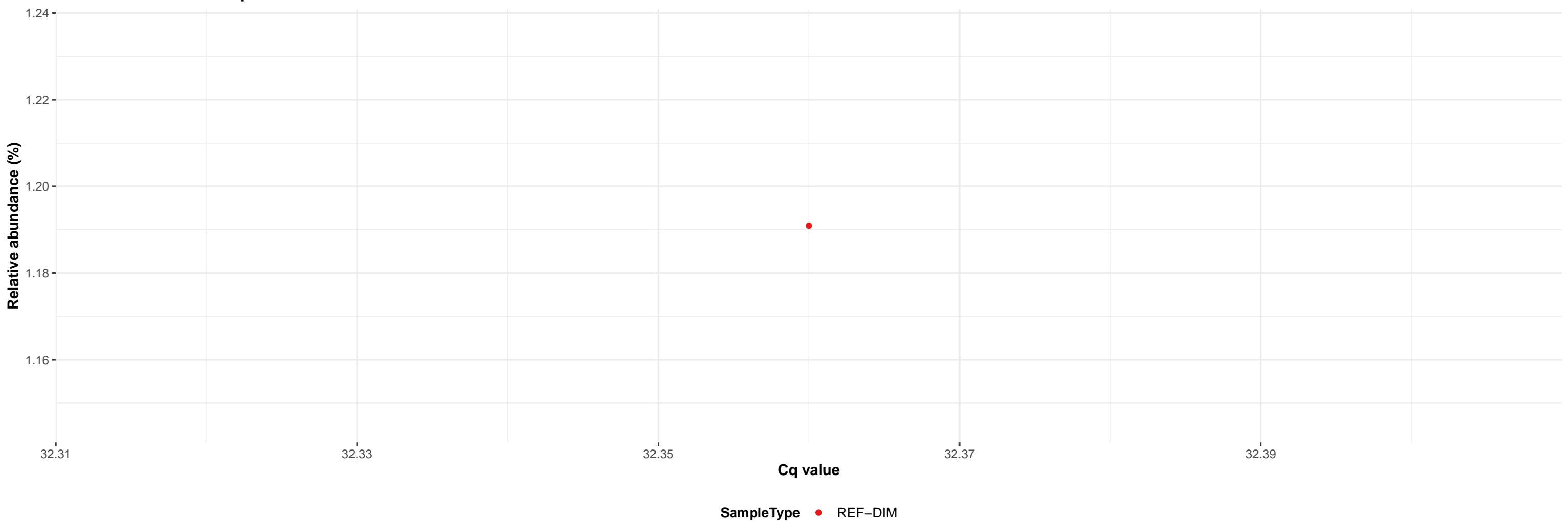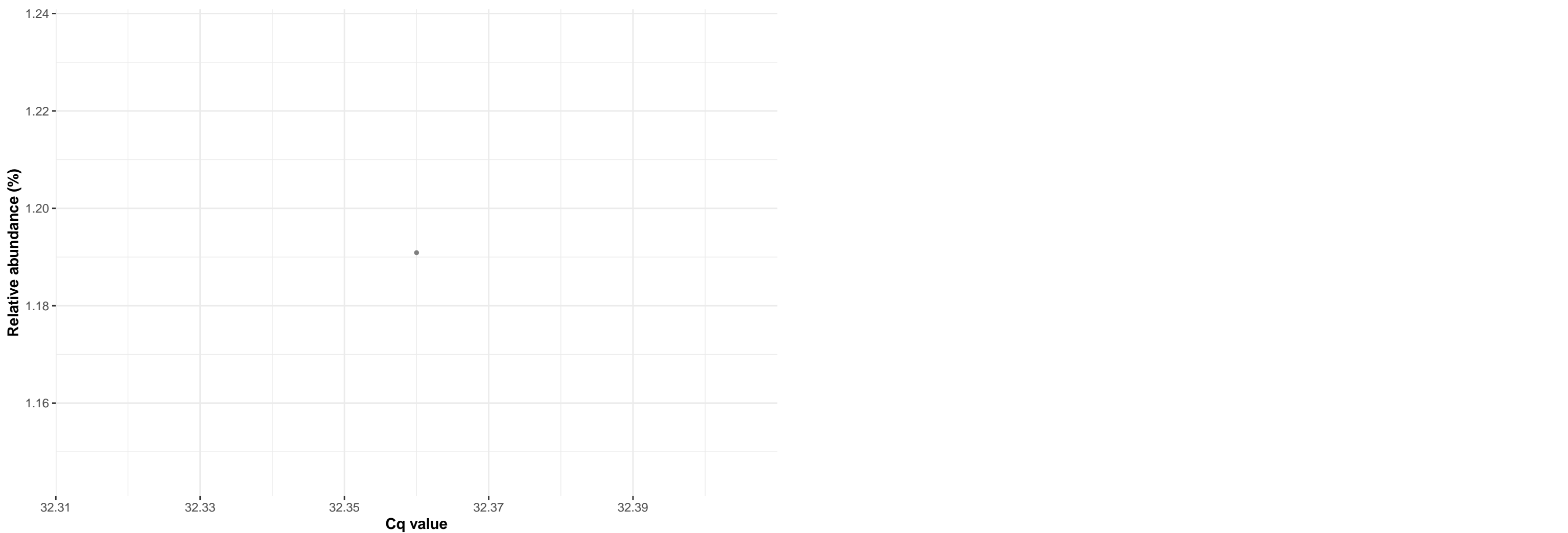**Correlation within: PCR−blank**

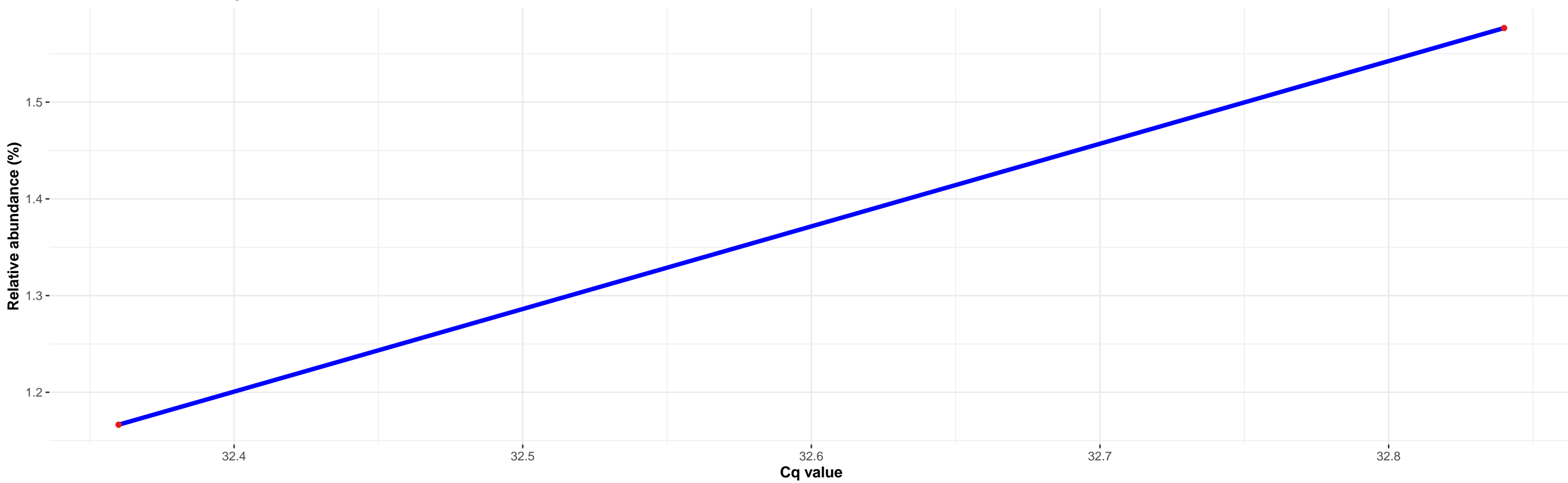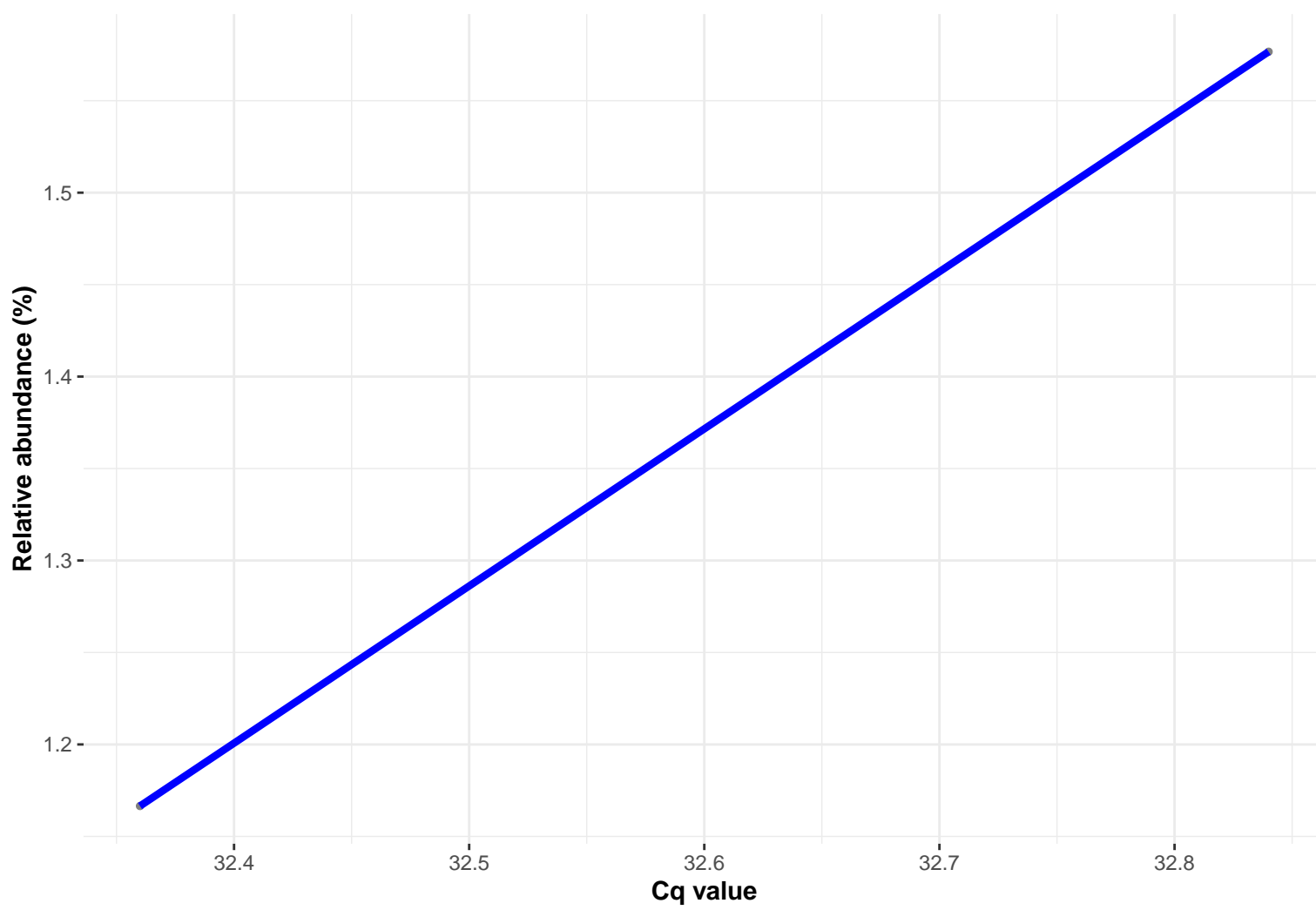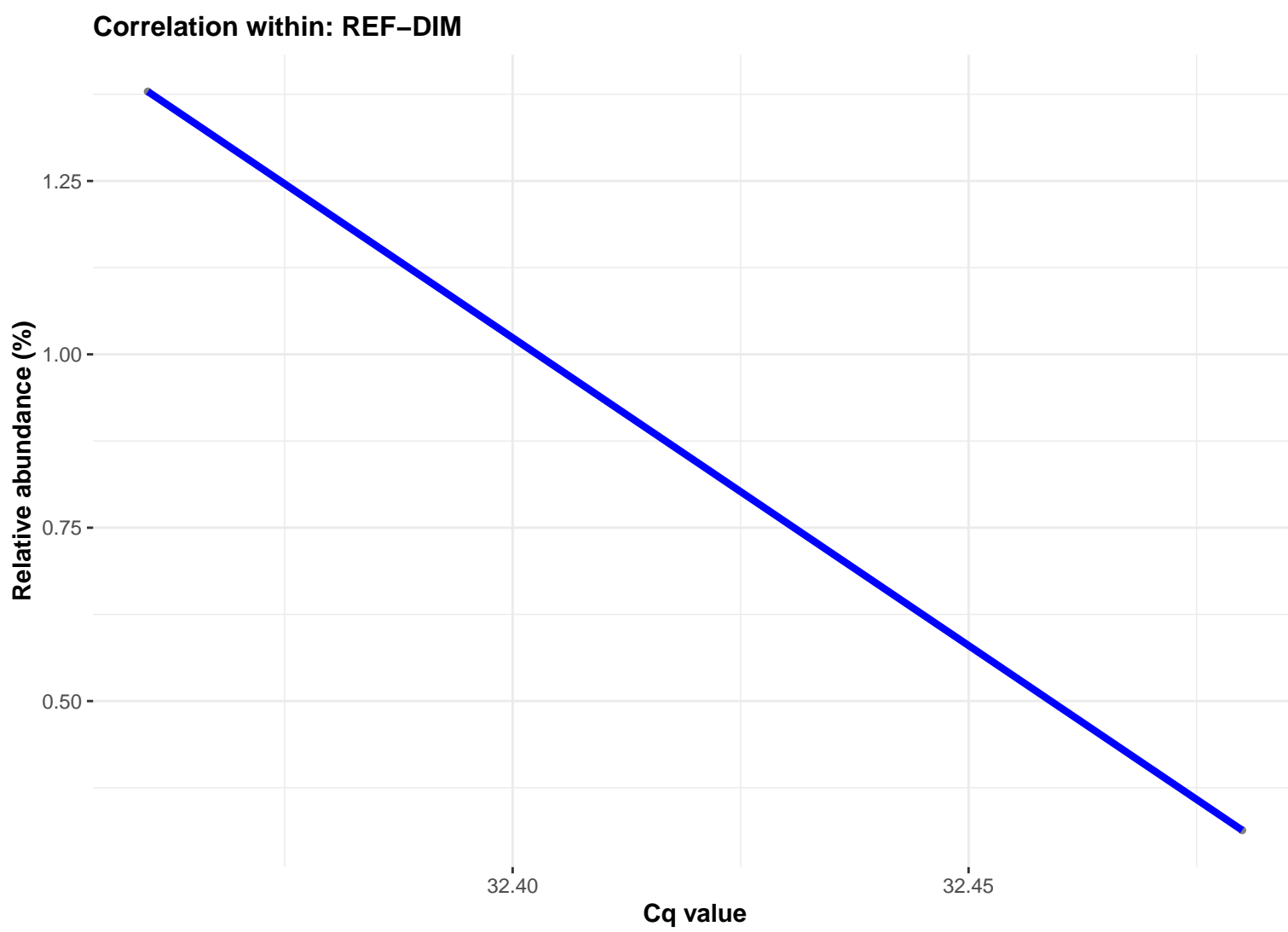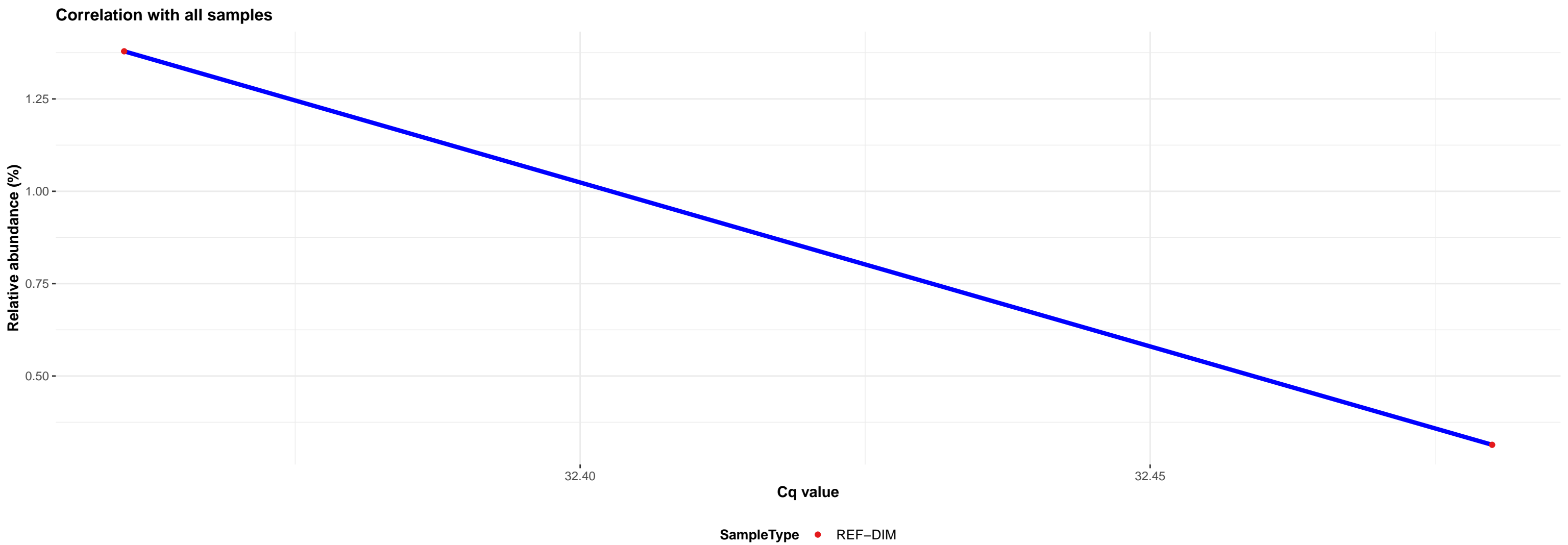# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Gracilibacillus; Ambiguous_taxa

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni
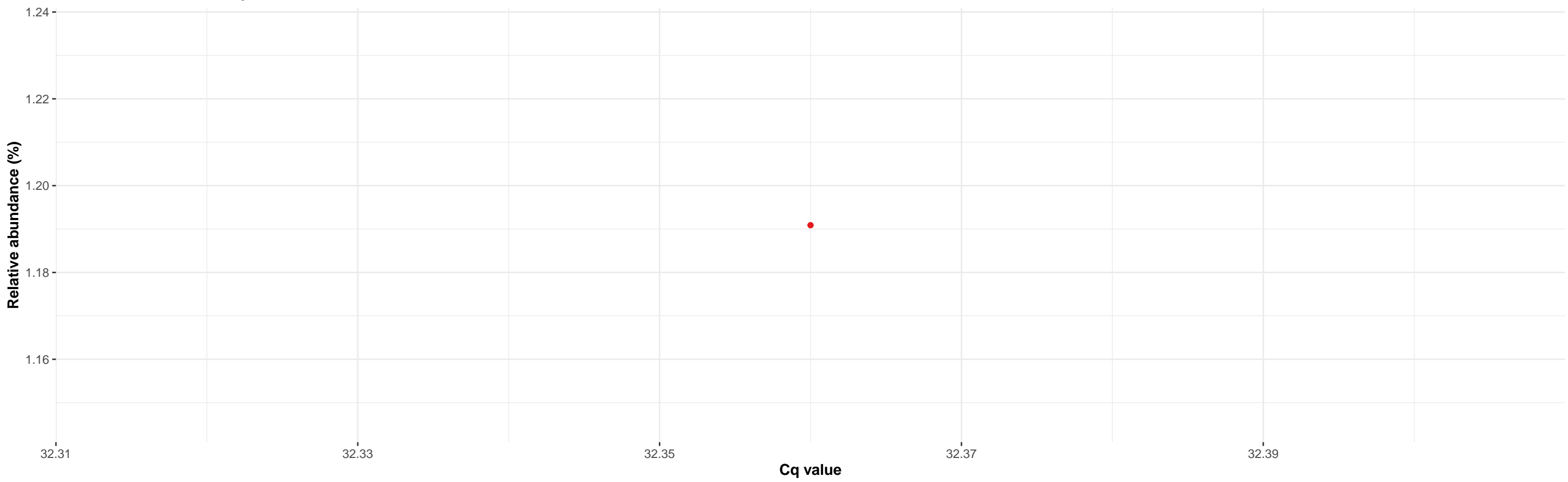
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Savagea; Ambiguous_taxa
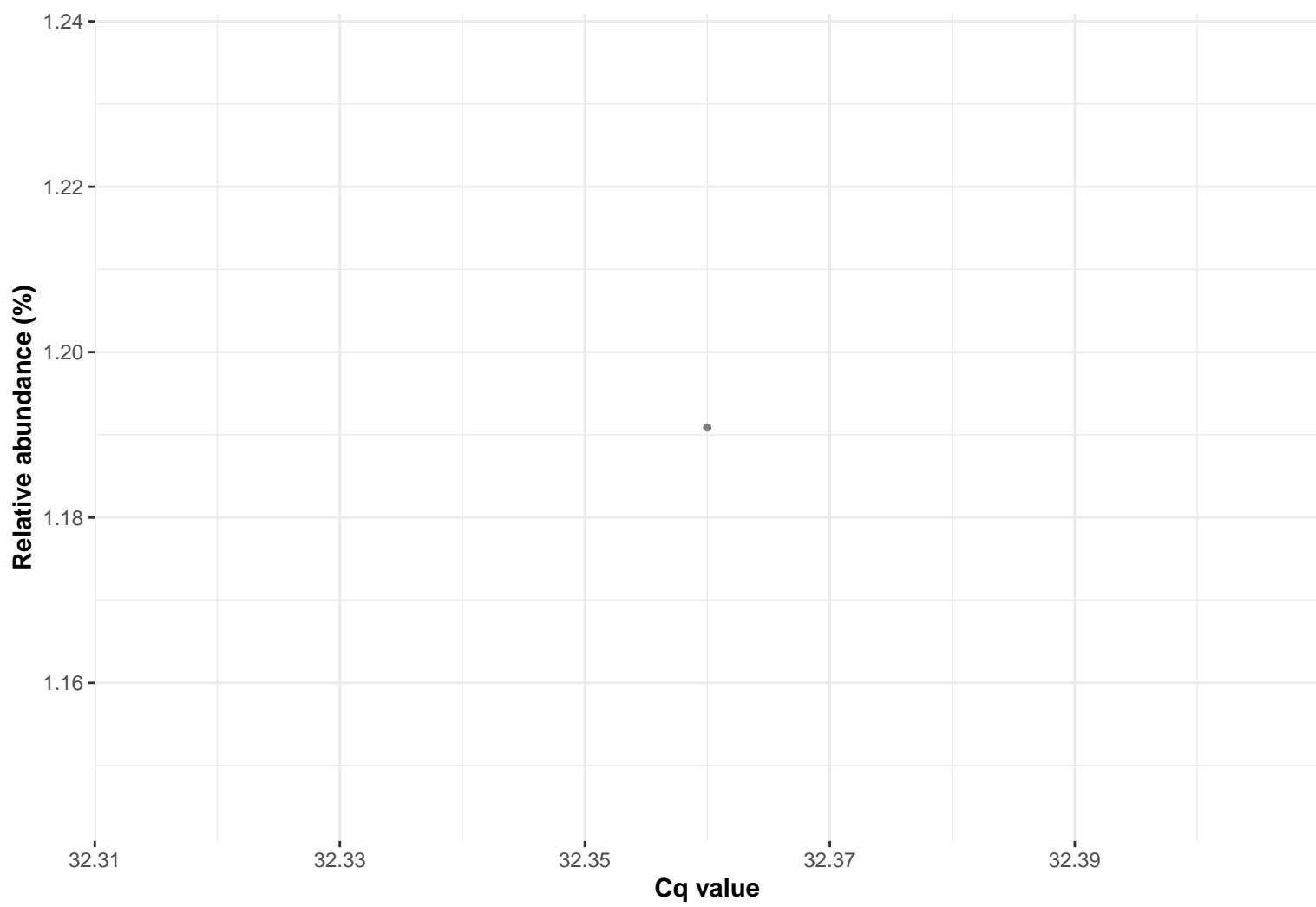
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Microbacterium; Ambiguous_taxa
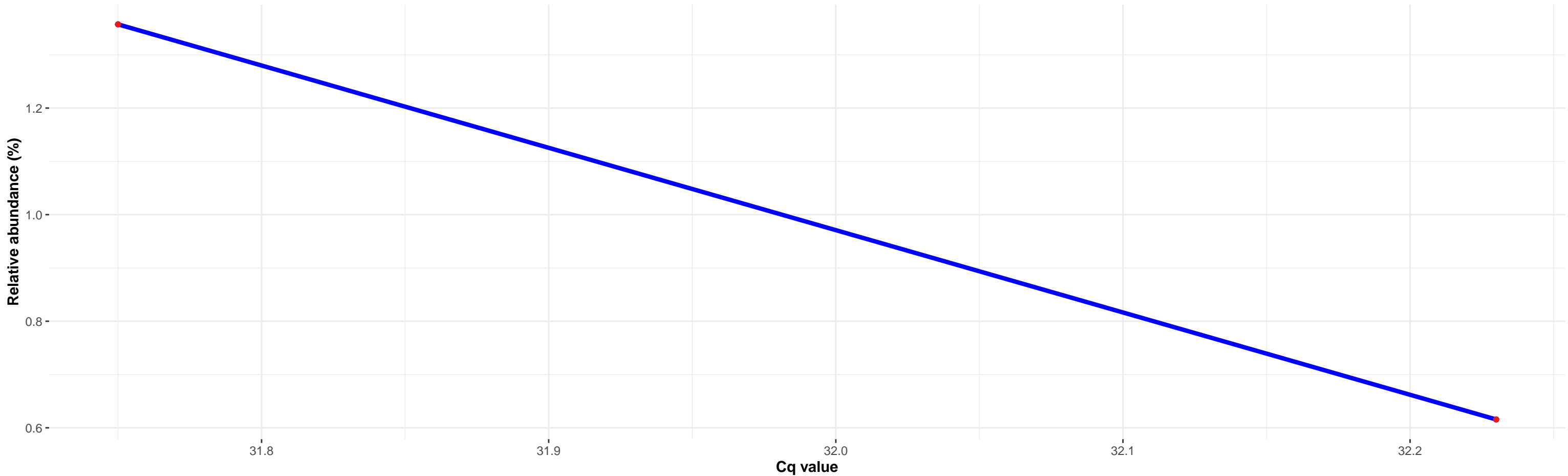
Correlation with all samples

Correlation within: REF−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus cecorum
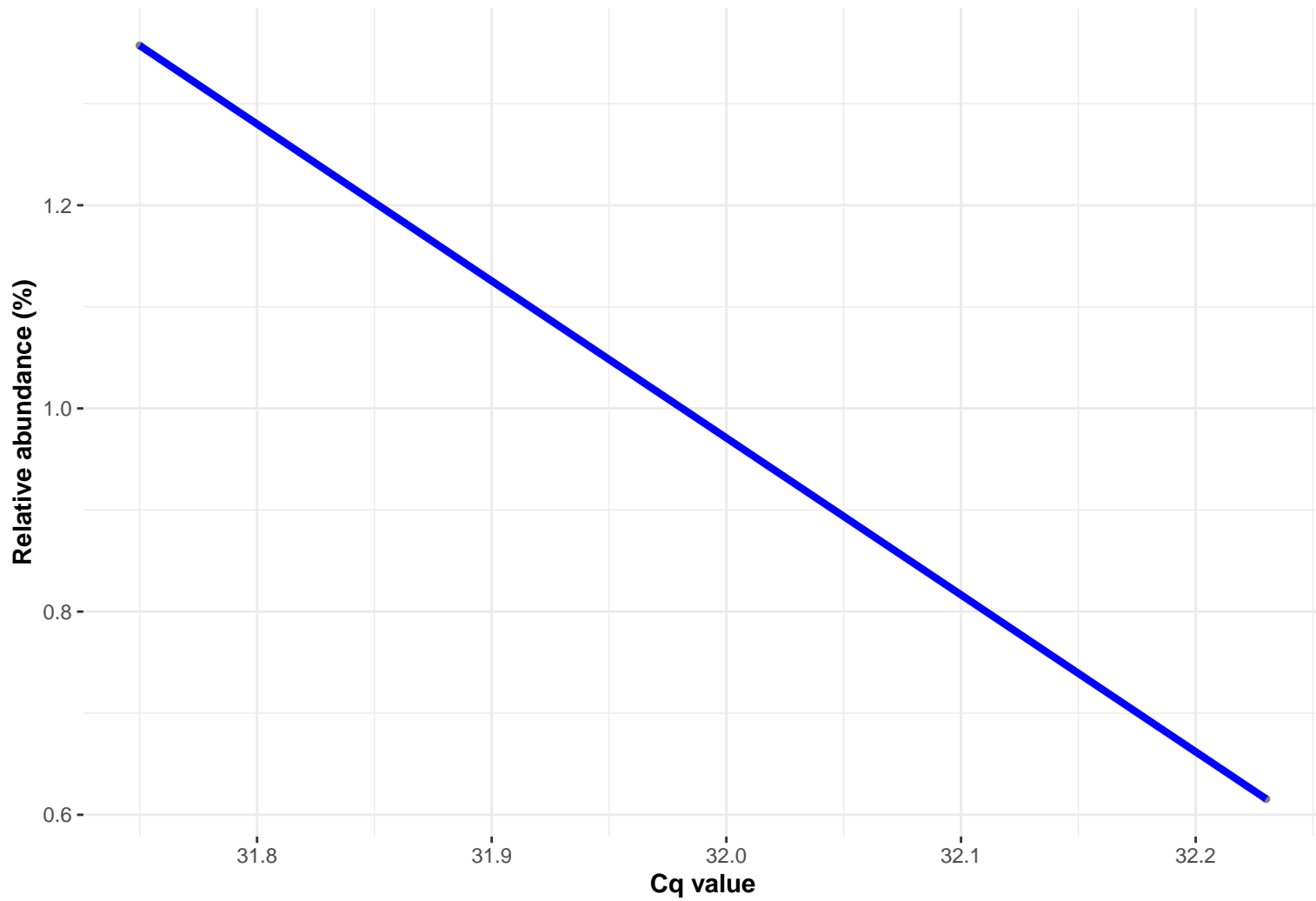
Correlation with all samples
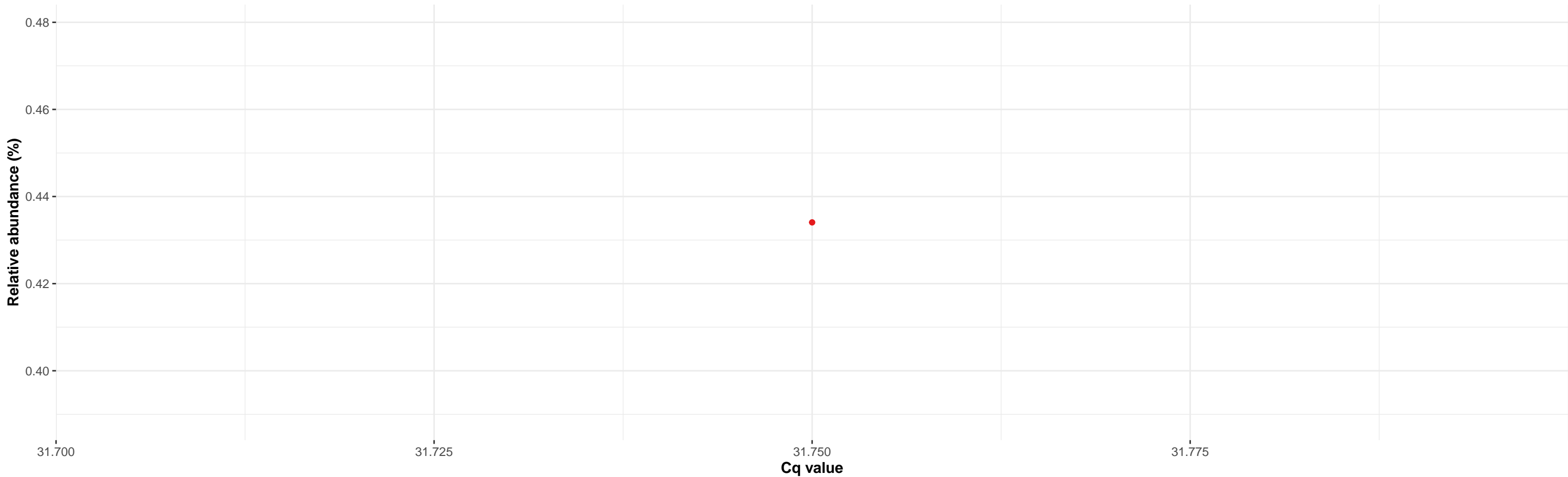
SampleType ● REF−DIM

Correlation within: REF−DIM
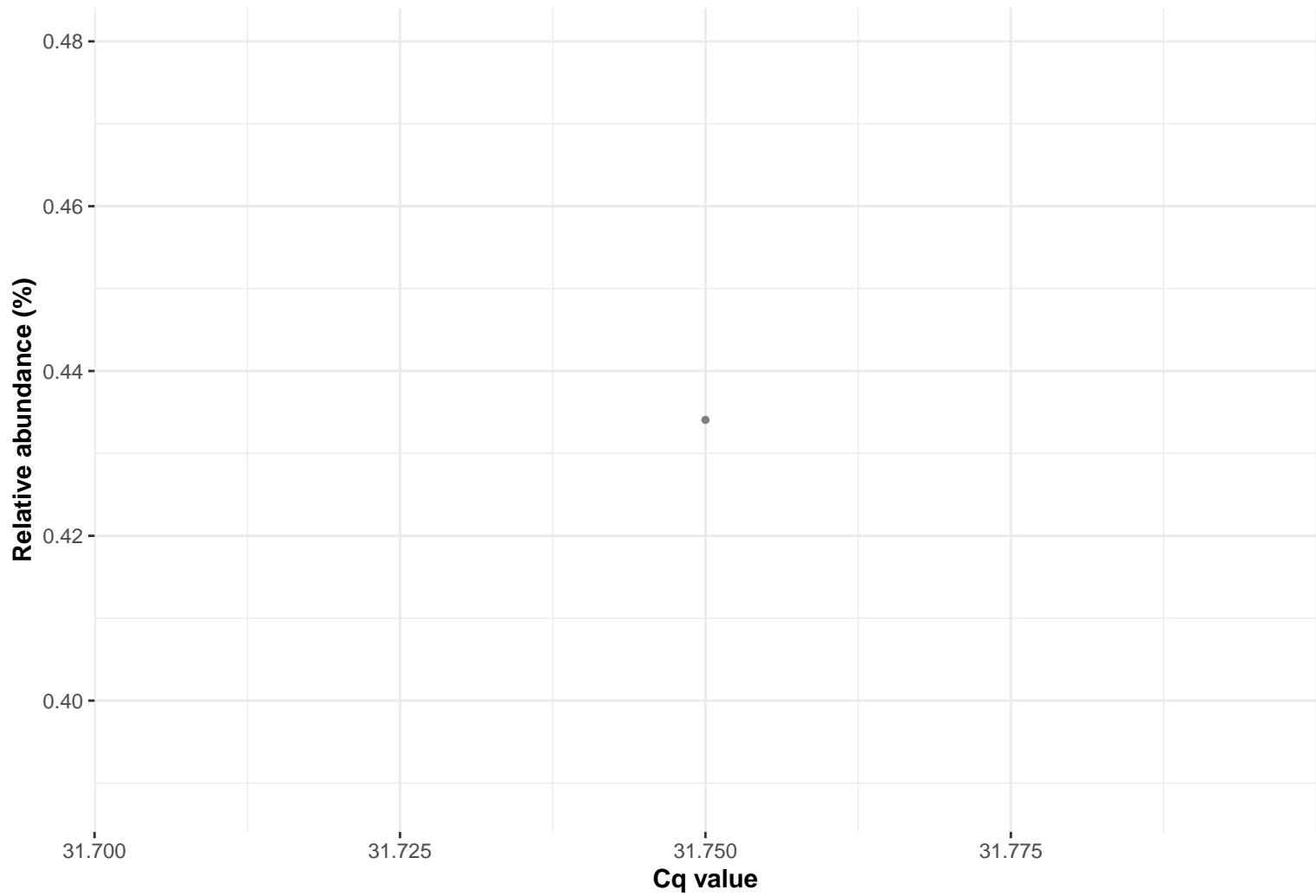
Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples

SampleType ● REF−DIM
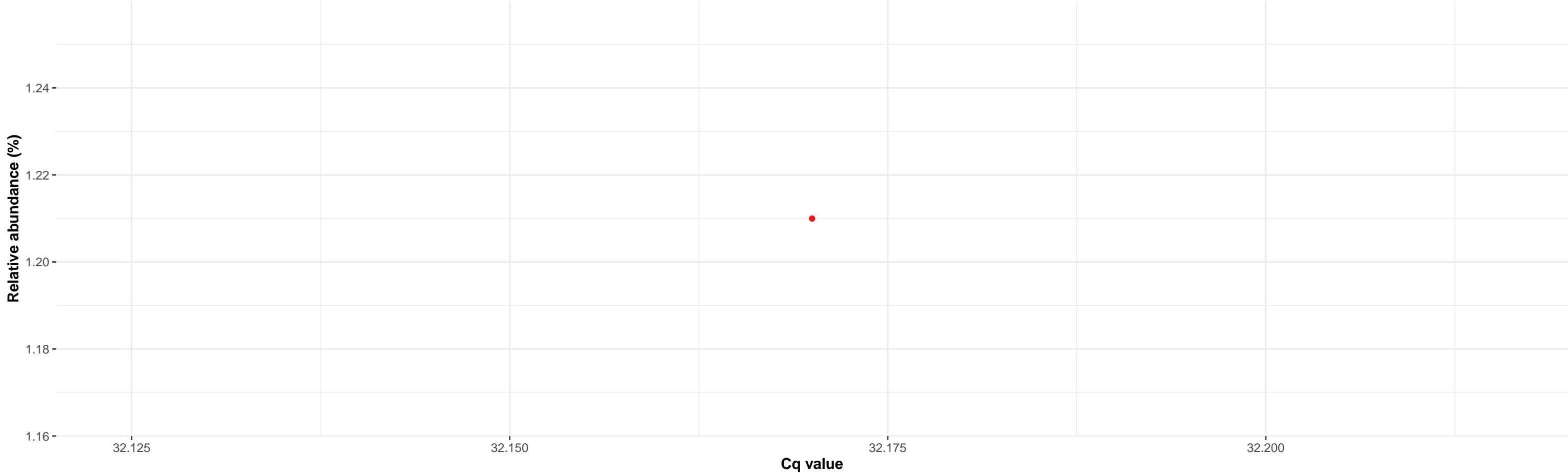
Correlation within: REF−DIM
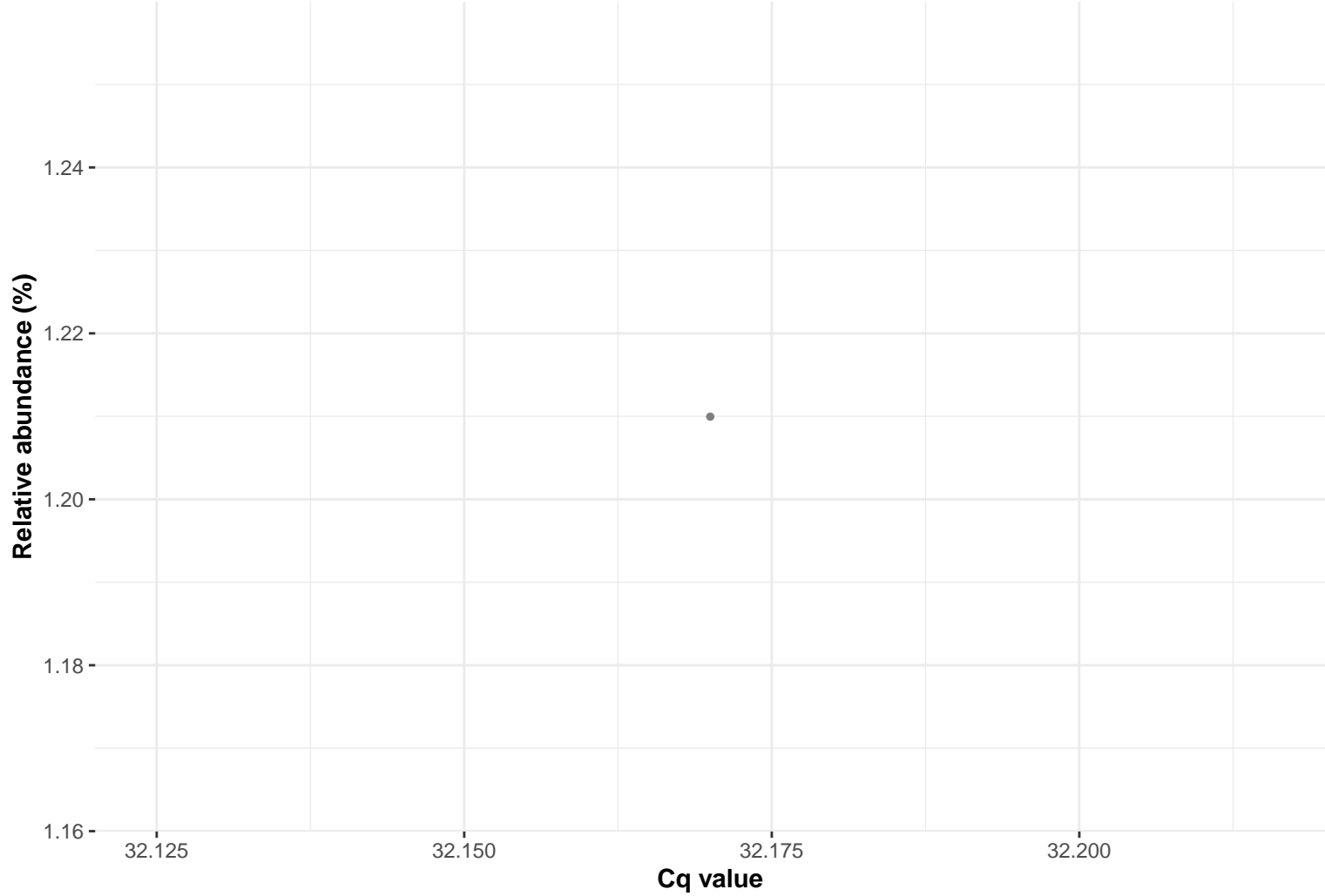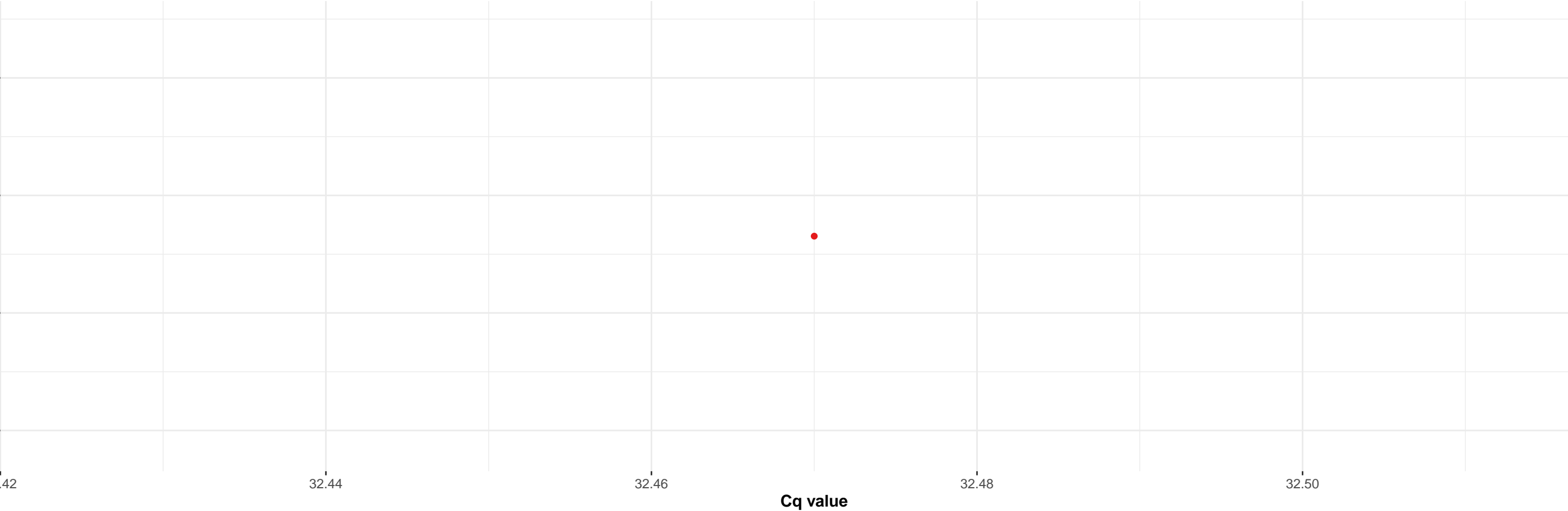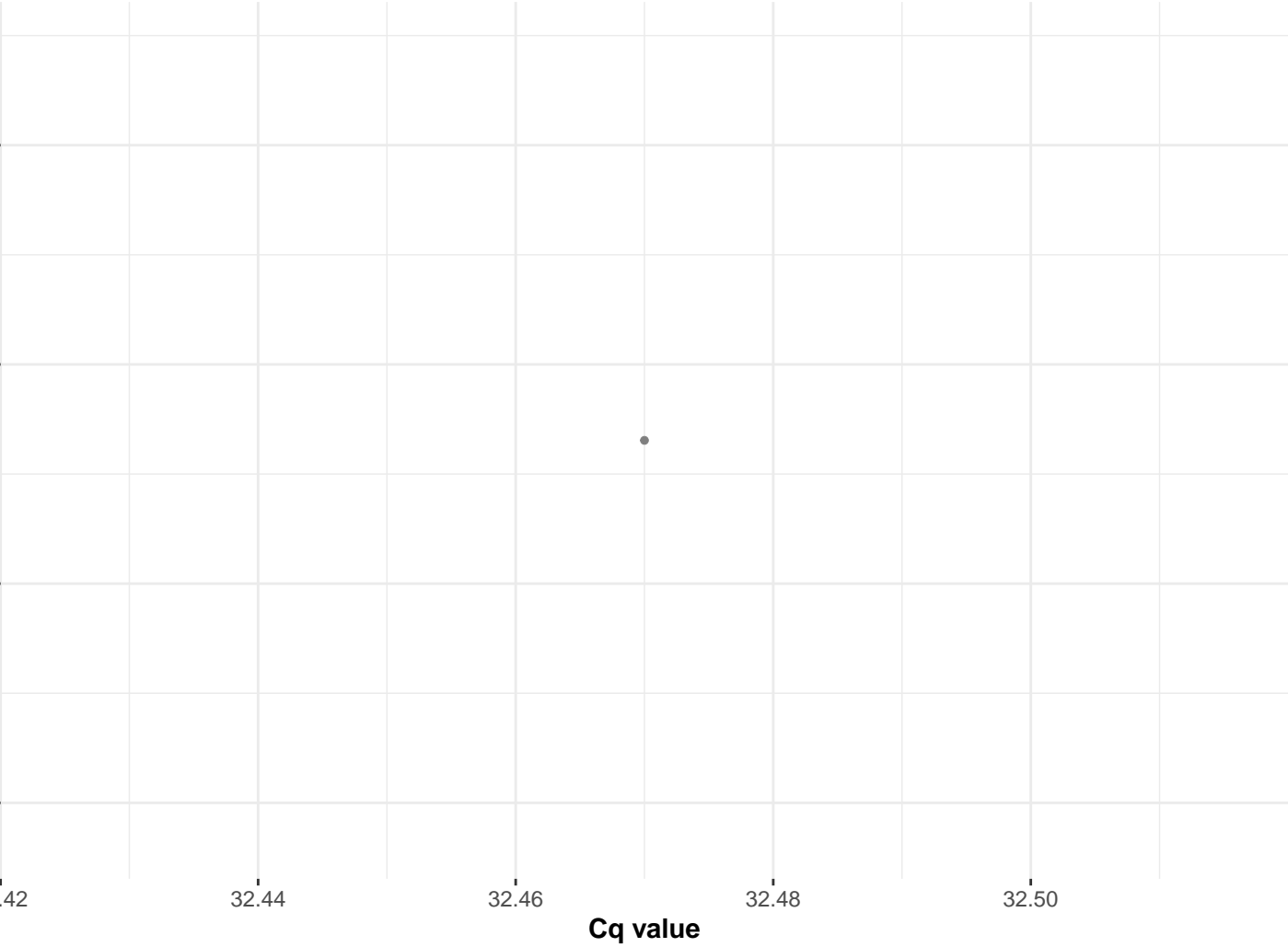
Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__uncultured bacterium

Correlation with all samples

SampleType ● REF−DIM

Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Nosocomiicoccus; s__uncultured bacterium

Correlation with all samples

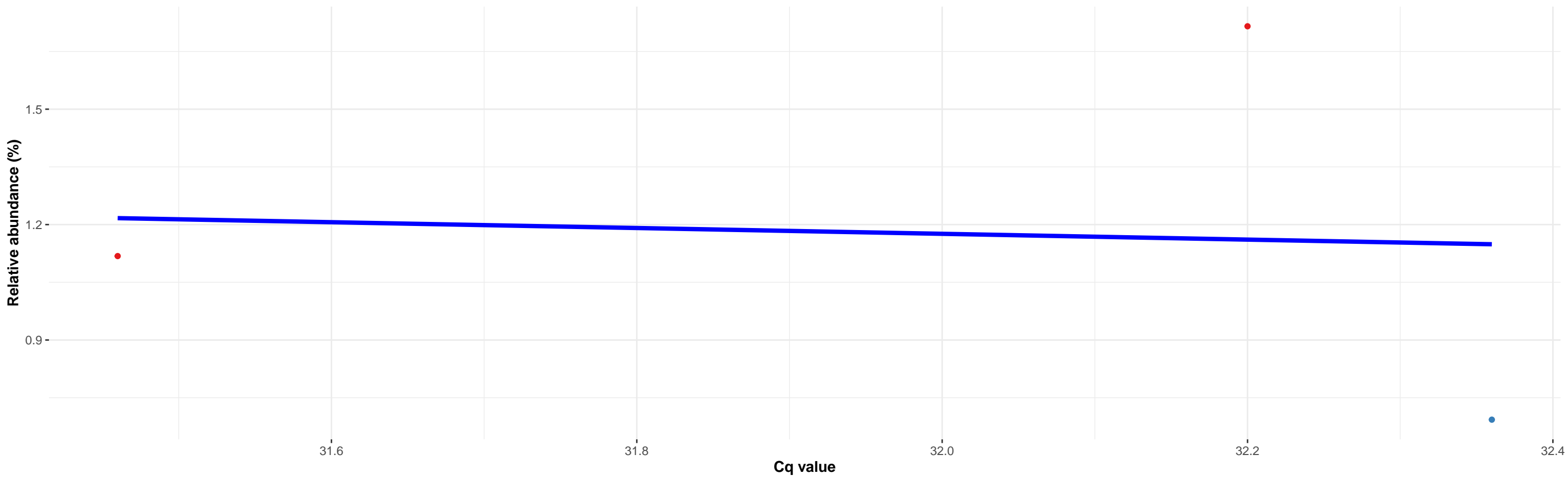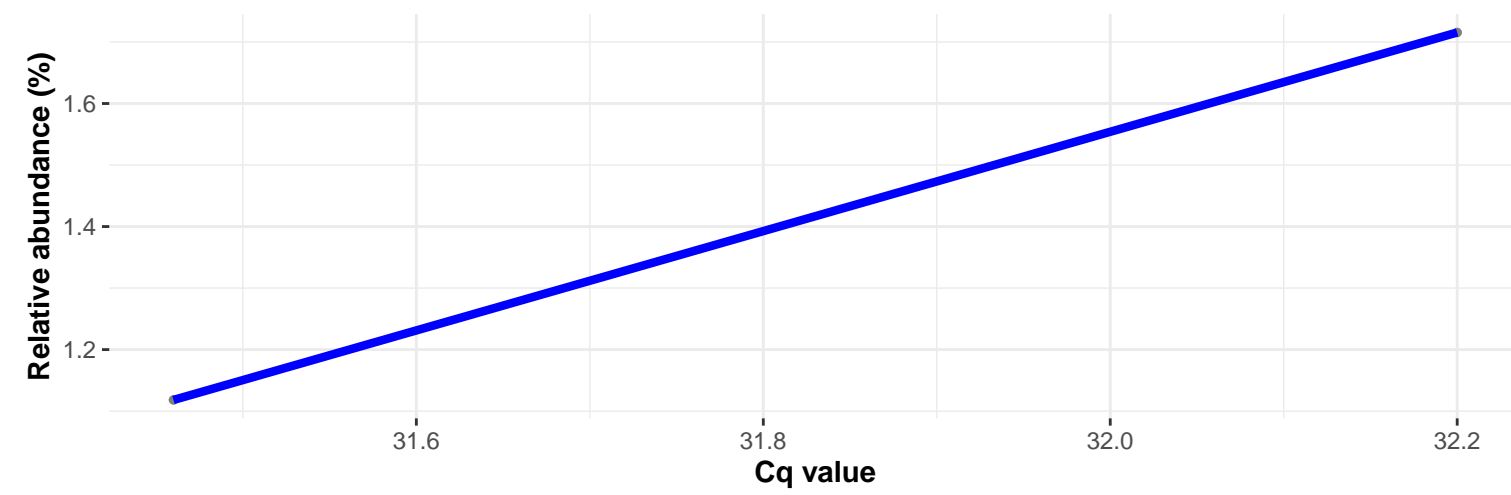Relative abundance (%)

Cq value

Correlation within: PCR−blank

Relative abundance (%)

Cq value

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa
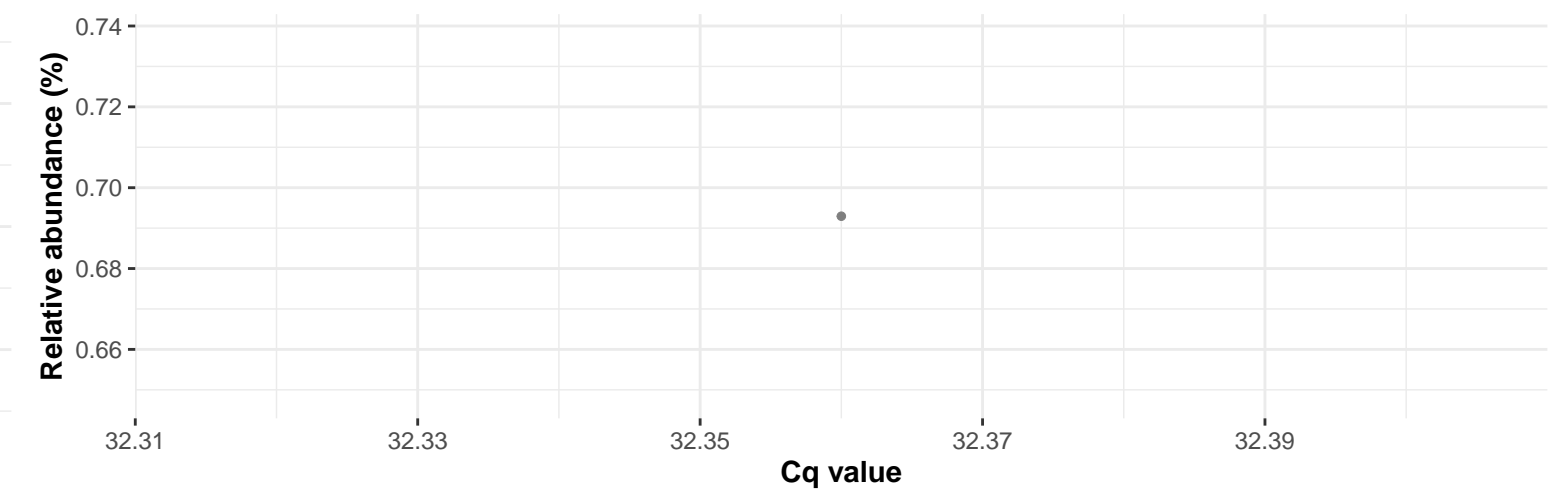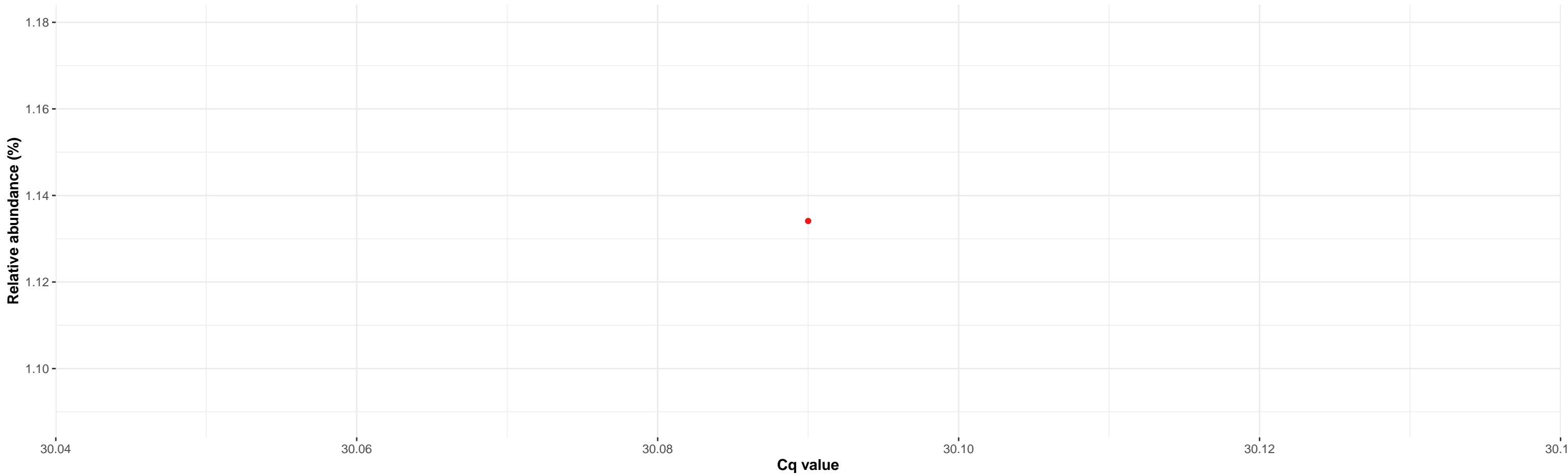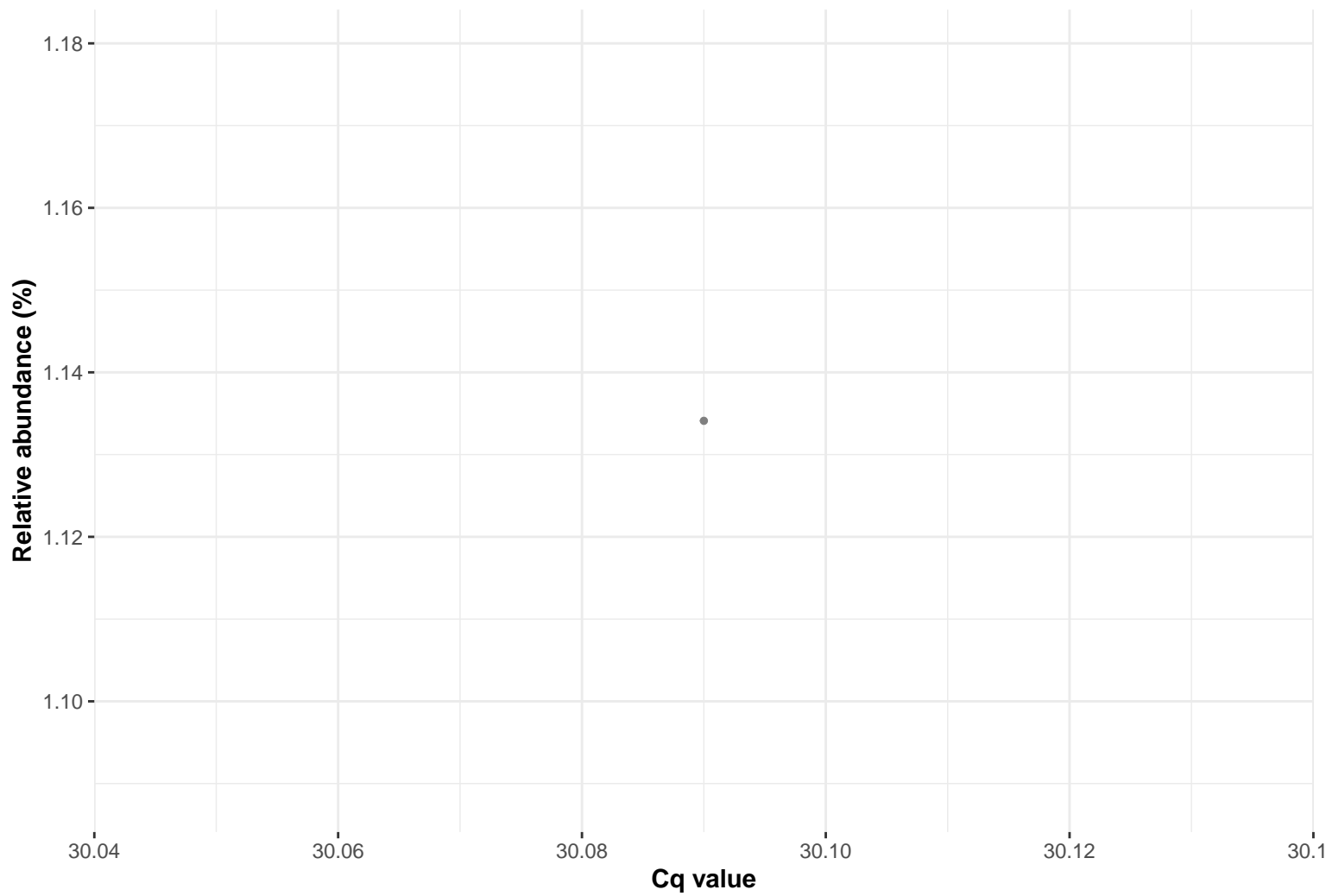
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Hydrogenophaga; NA
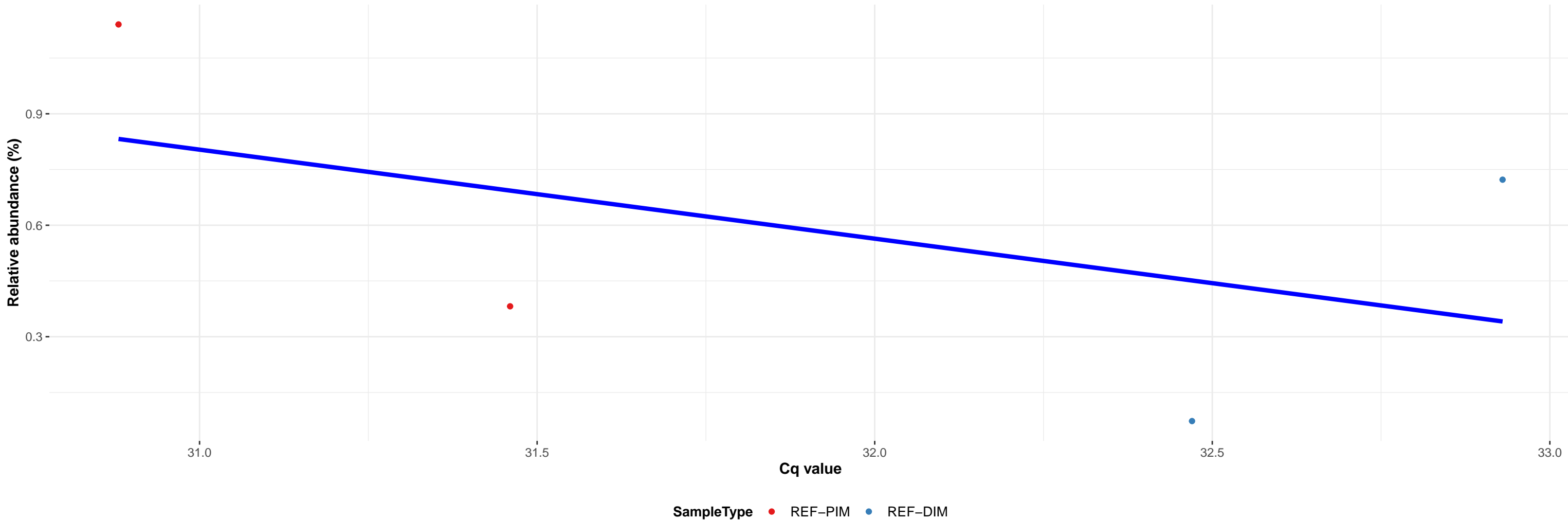
Correlation with all samples
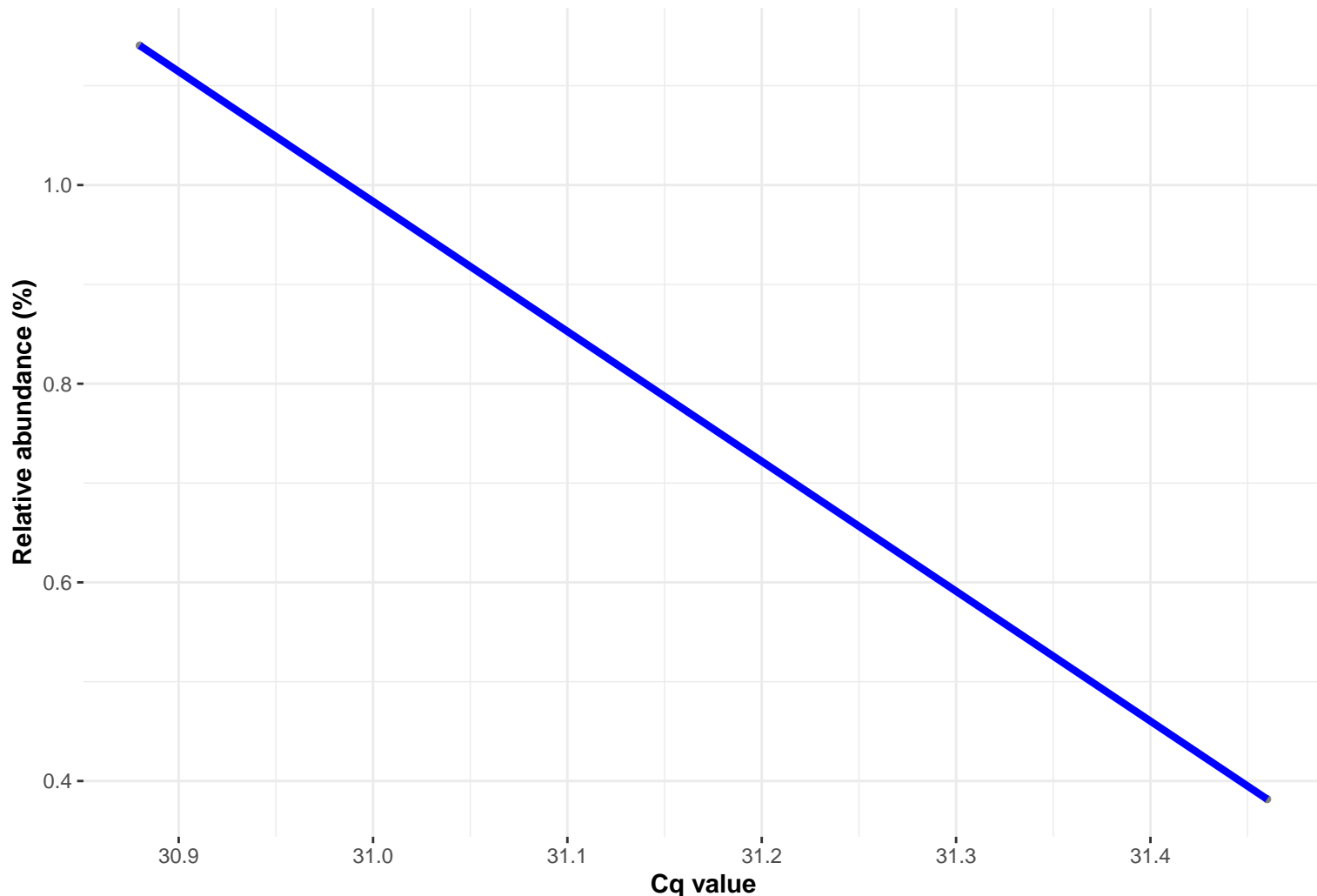

SampleType ● REF−PIM

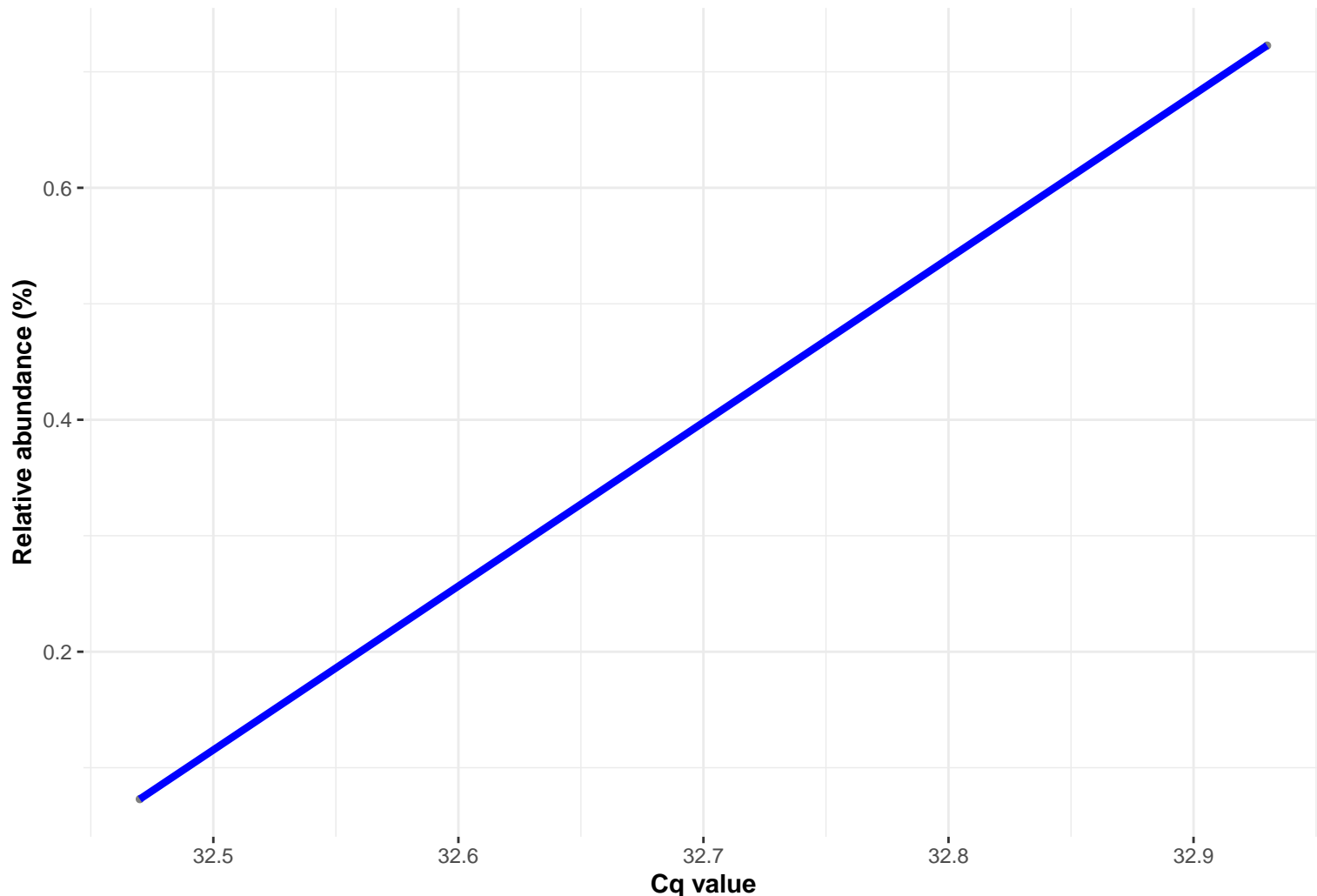**Correlation within: REF−PIM**

Correlation within: PCR−blank

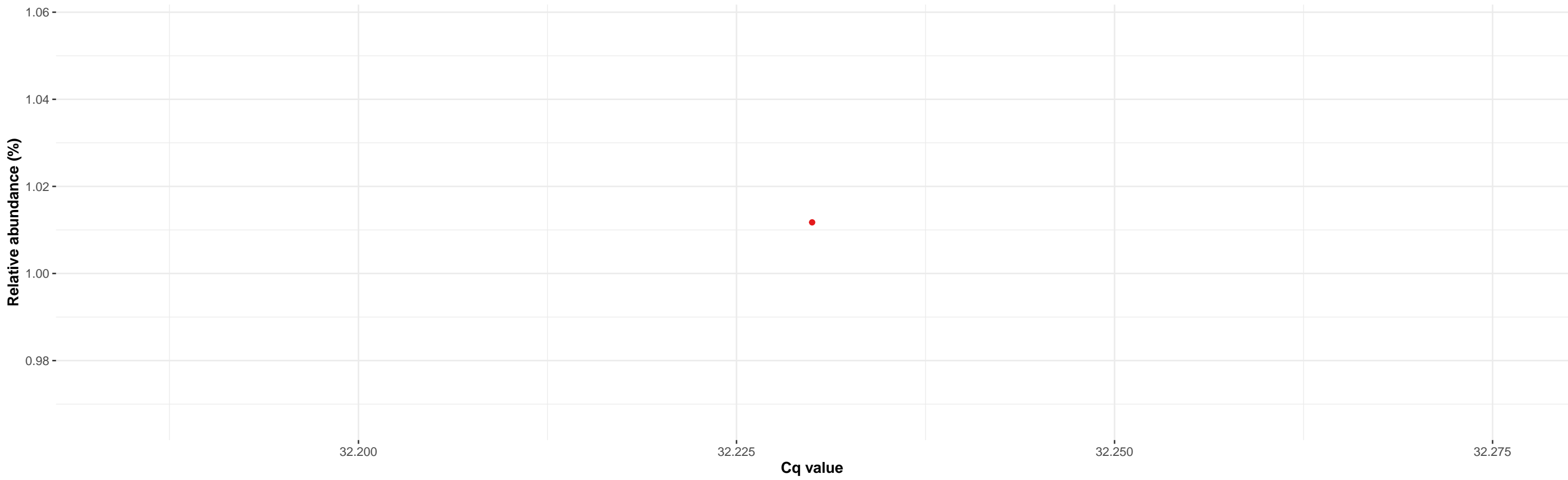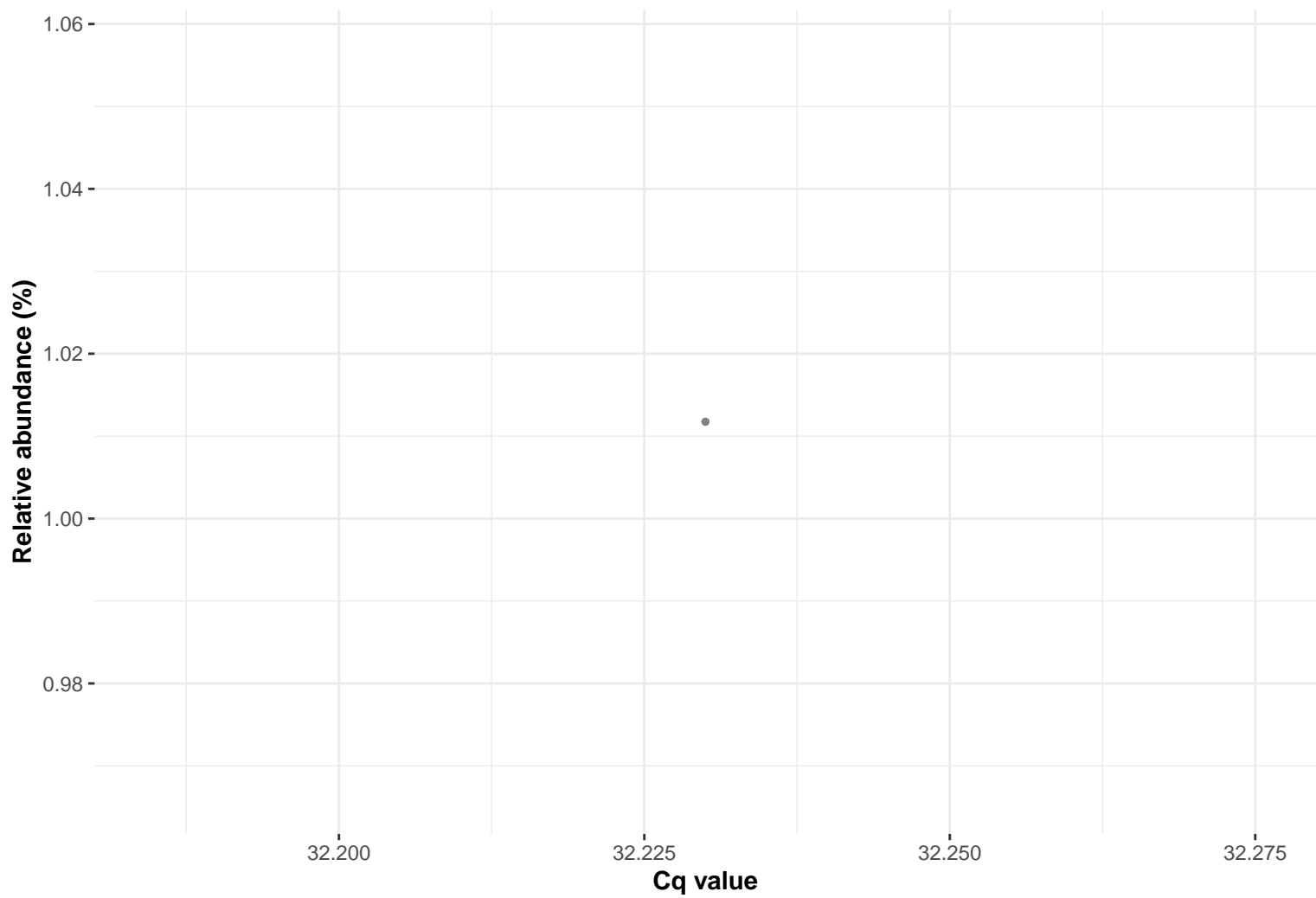**k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Kurthia; s__Kurthia sp. PAOGL173**

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples
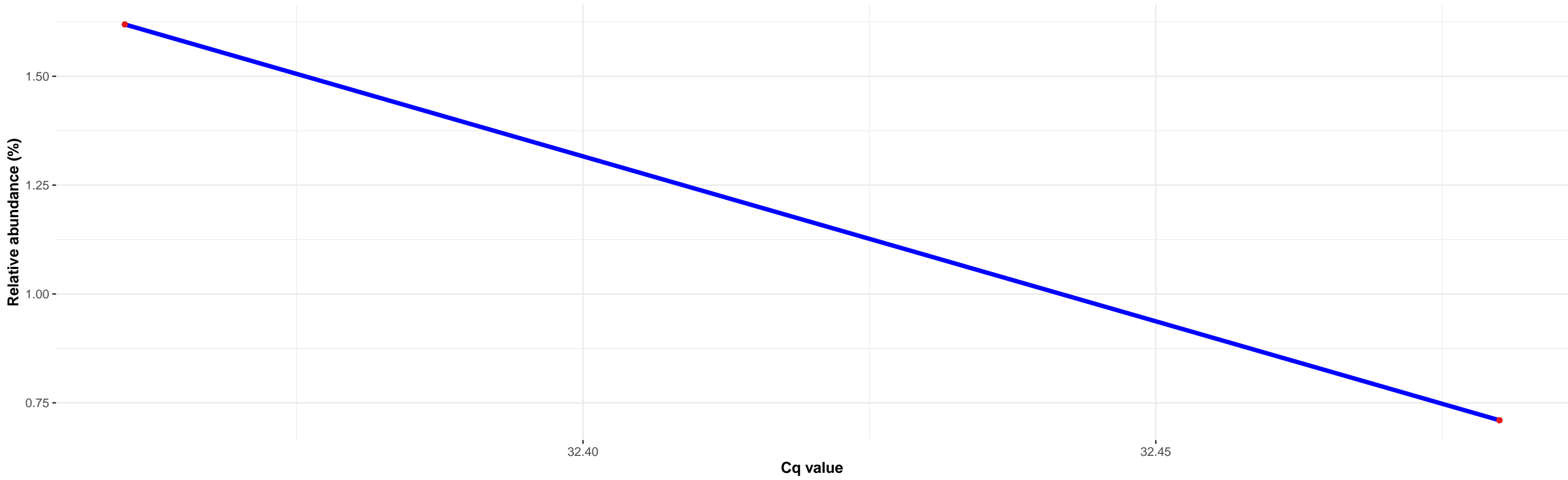

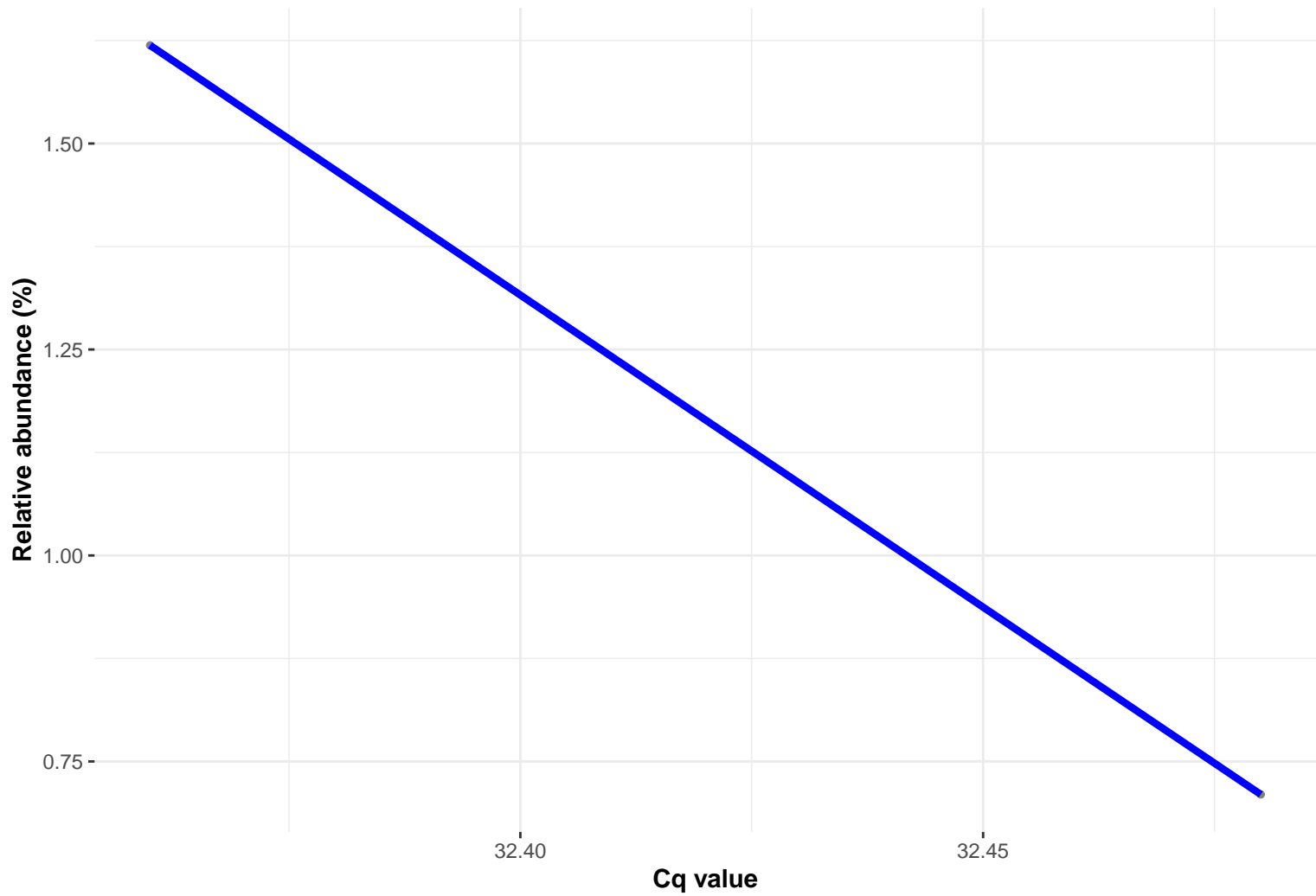**SampleType** ● REF–DIM

Correlation within: REF–DIM

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium
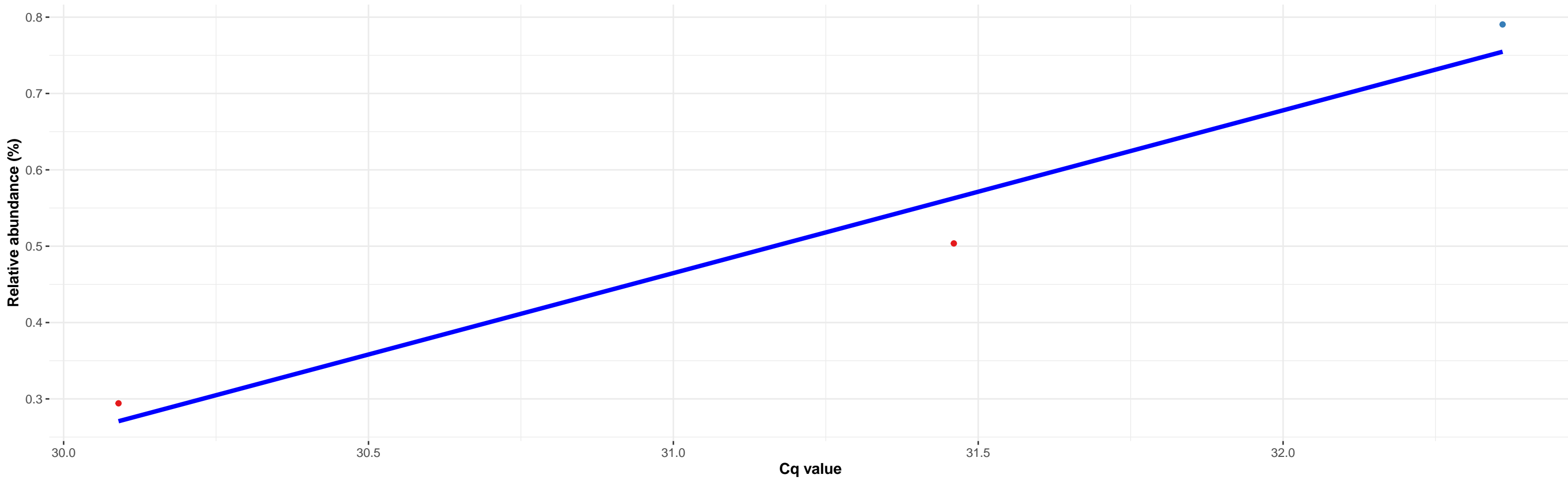
Correlation with all samples
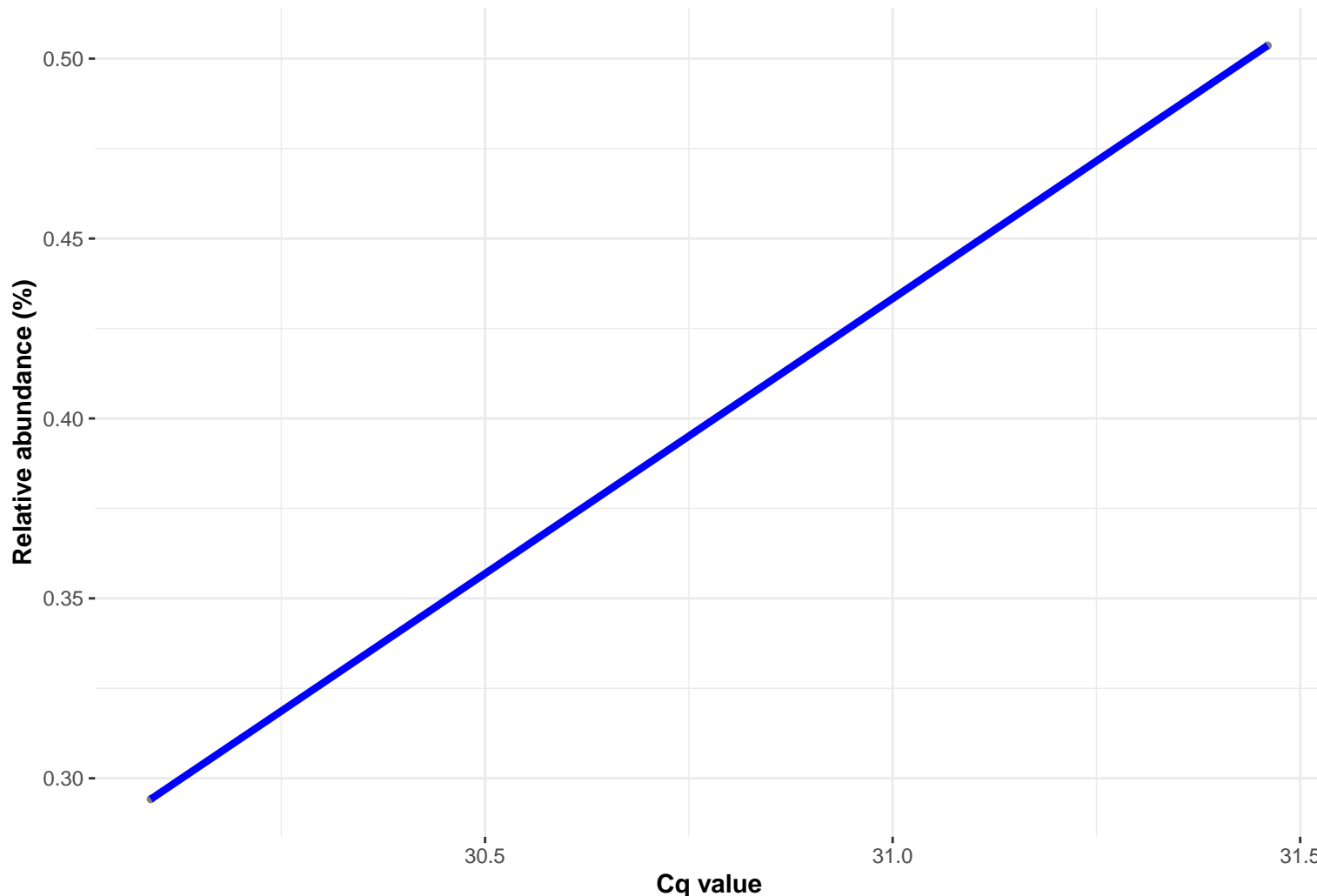

Correlation within: REF−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus helveticus
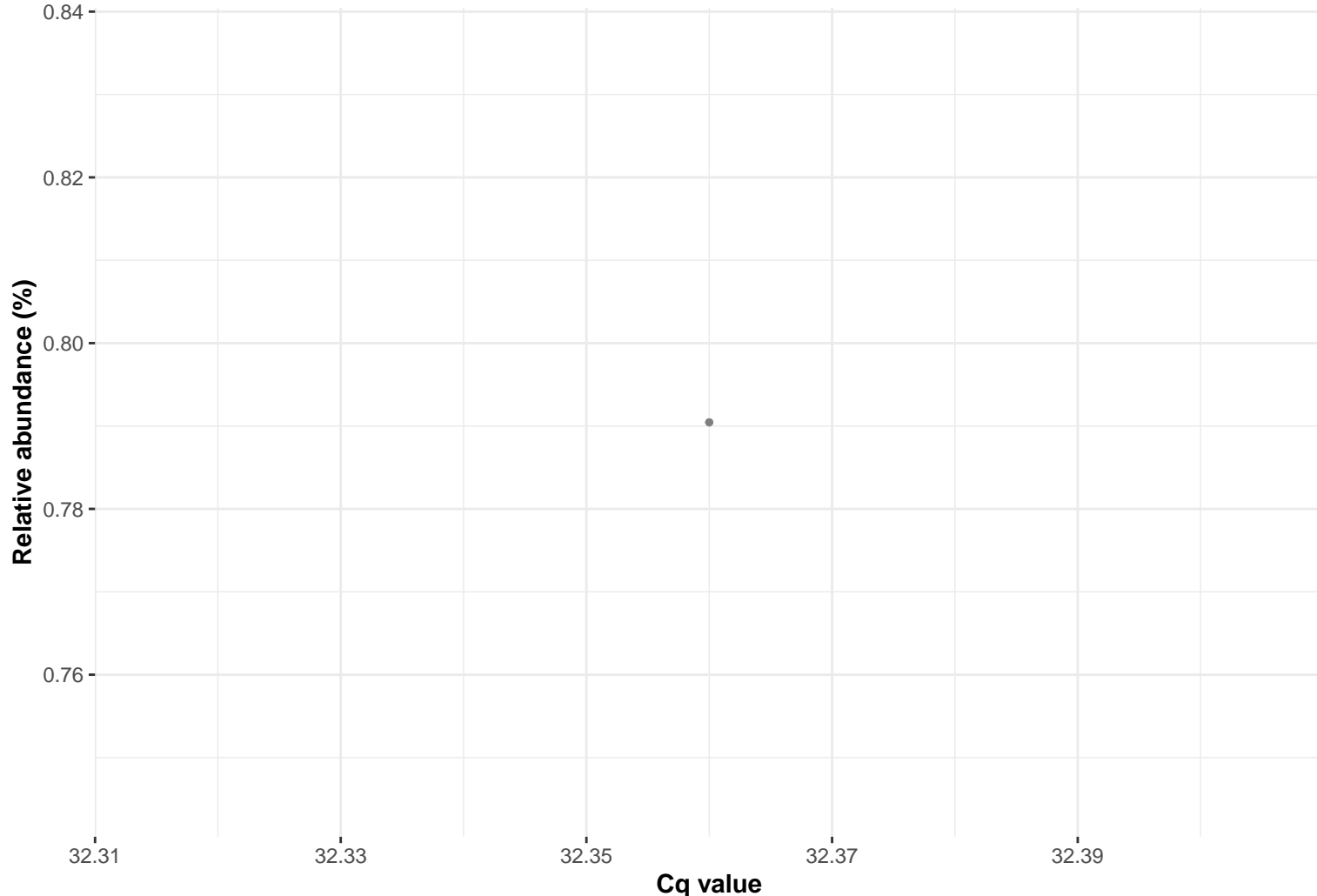
Correlation with all samples

SampleType ● REF−PIM ● REF−DIM
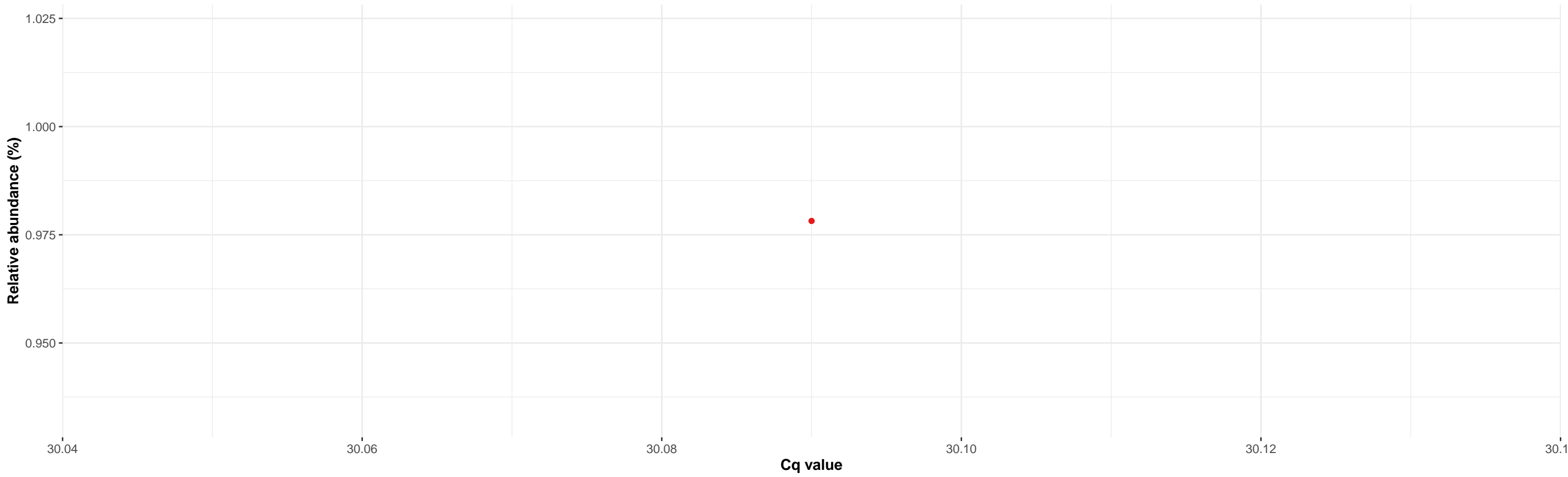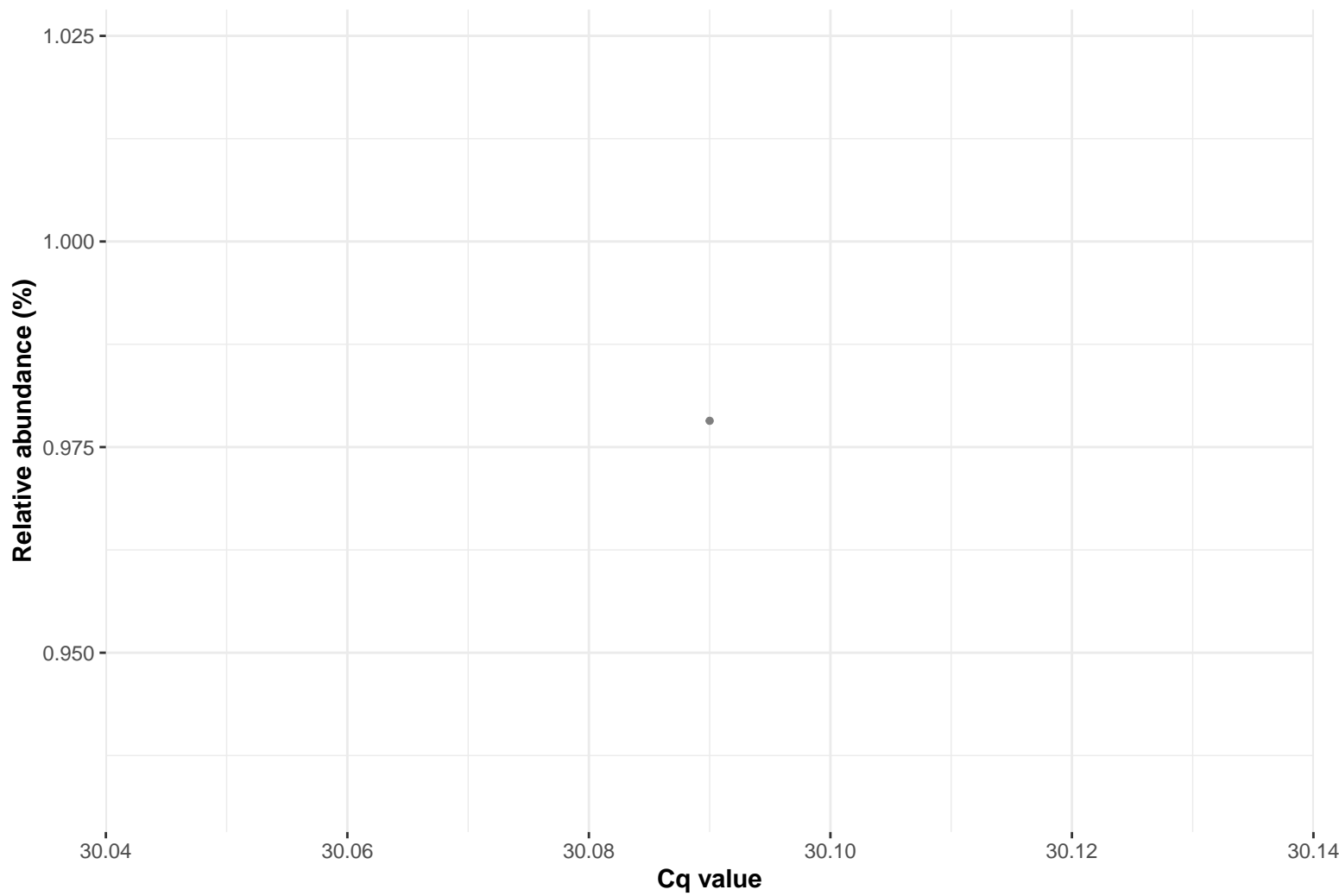
Correlation within: REF−PIM

Correlation within: REF−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; NA
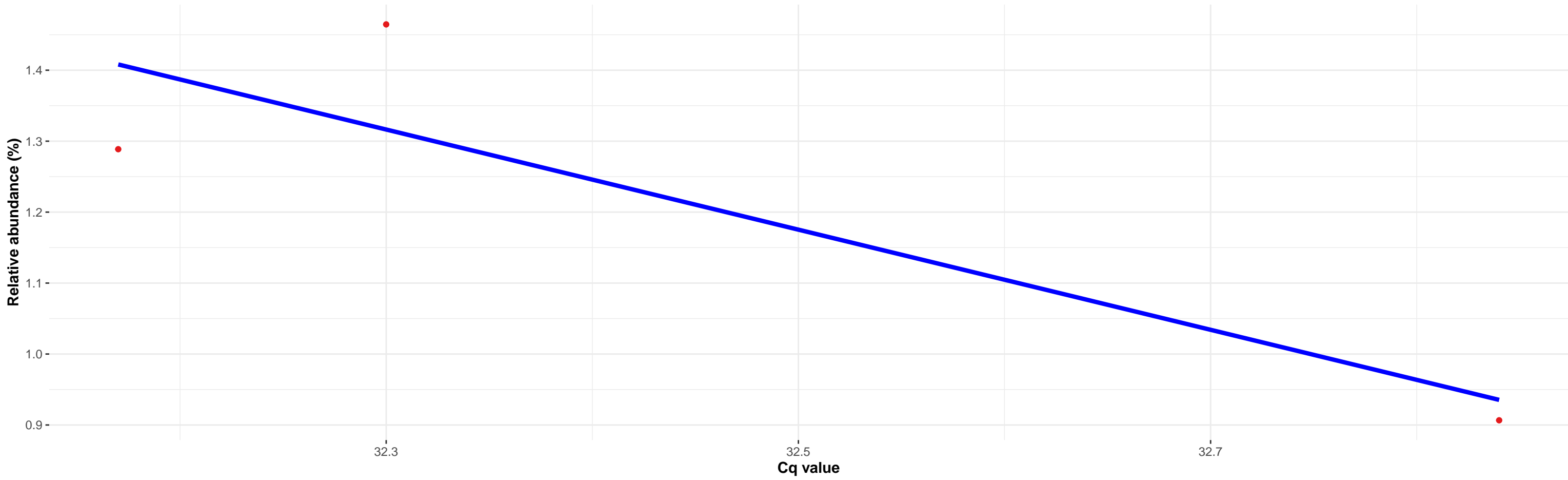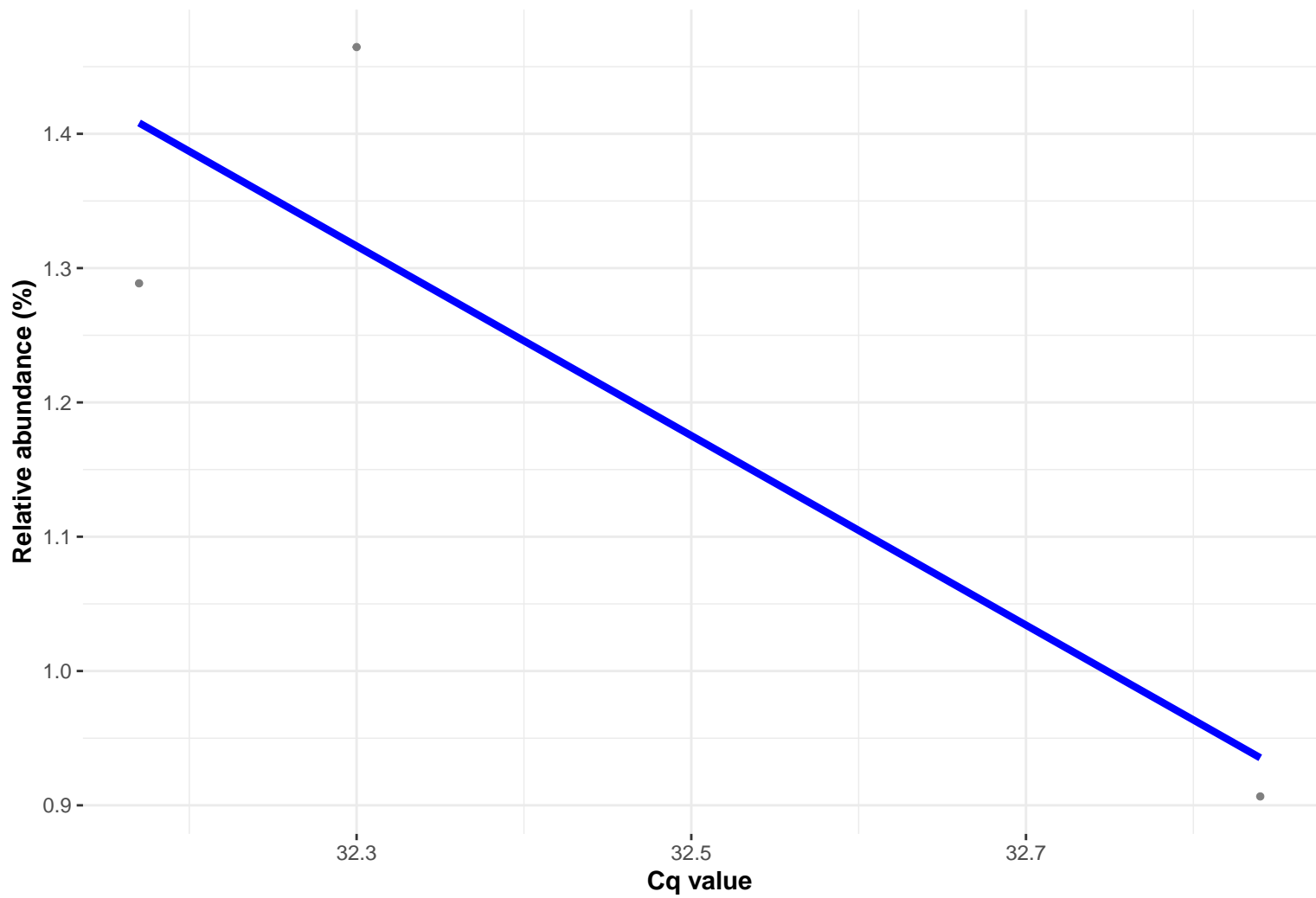
Correlation with all samples

SampleType ● REF−PIM

Correlation within: REF−PIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples
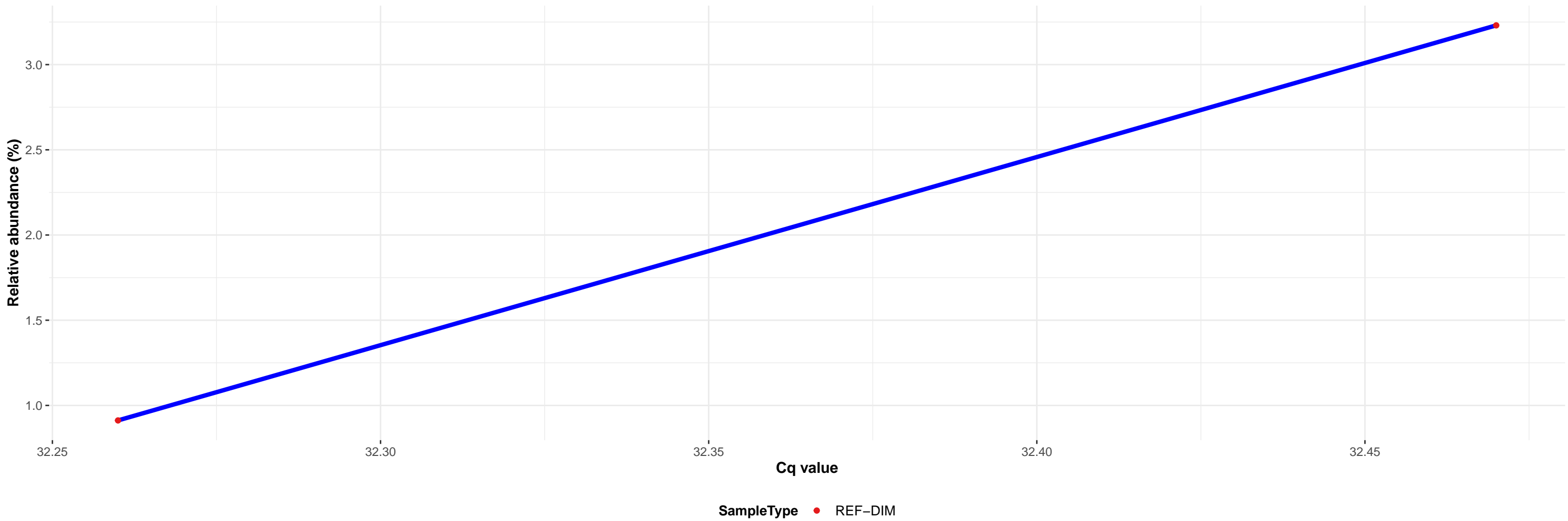
Correlation within: REF−DIM

Correlation within: PCR−blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. DJF_WC57

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples
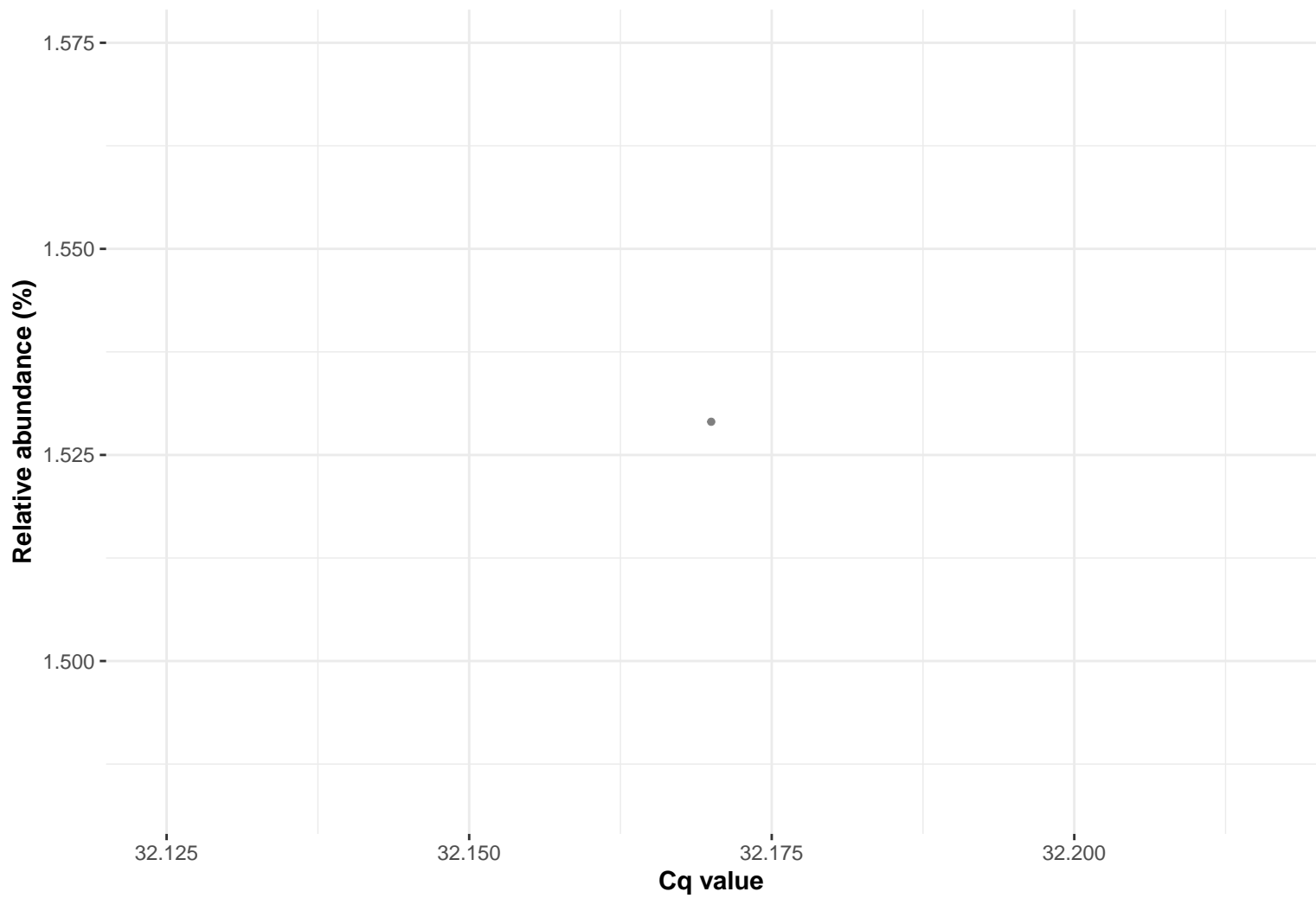
SampleType ● REF−DIM
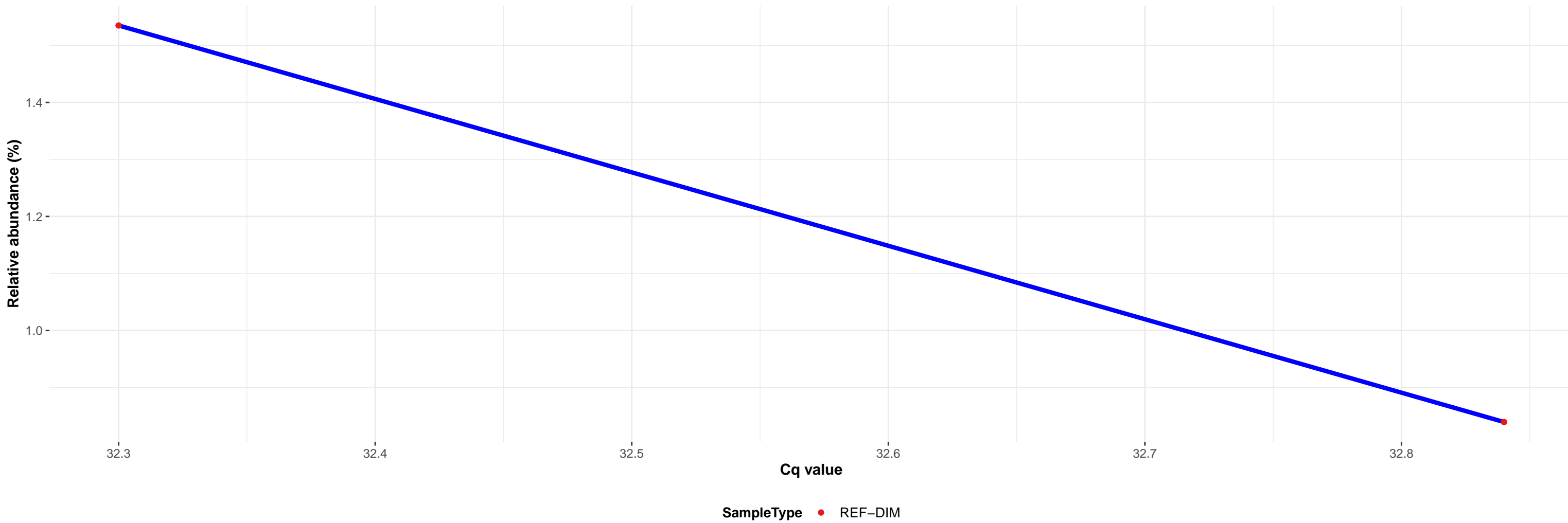
Correlation within: REF−DIM
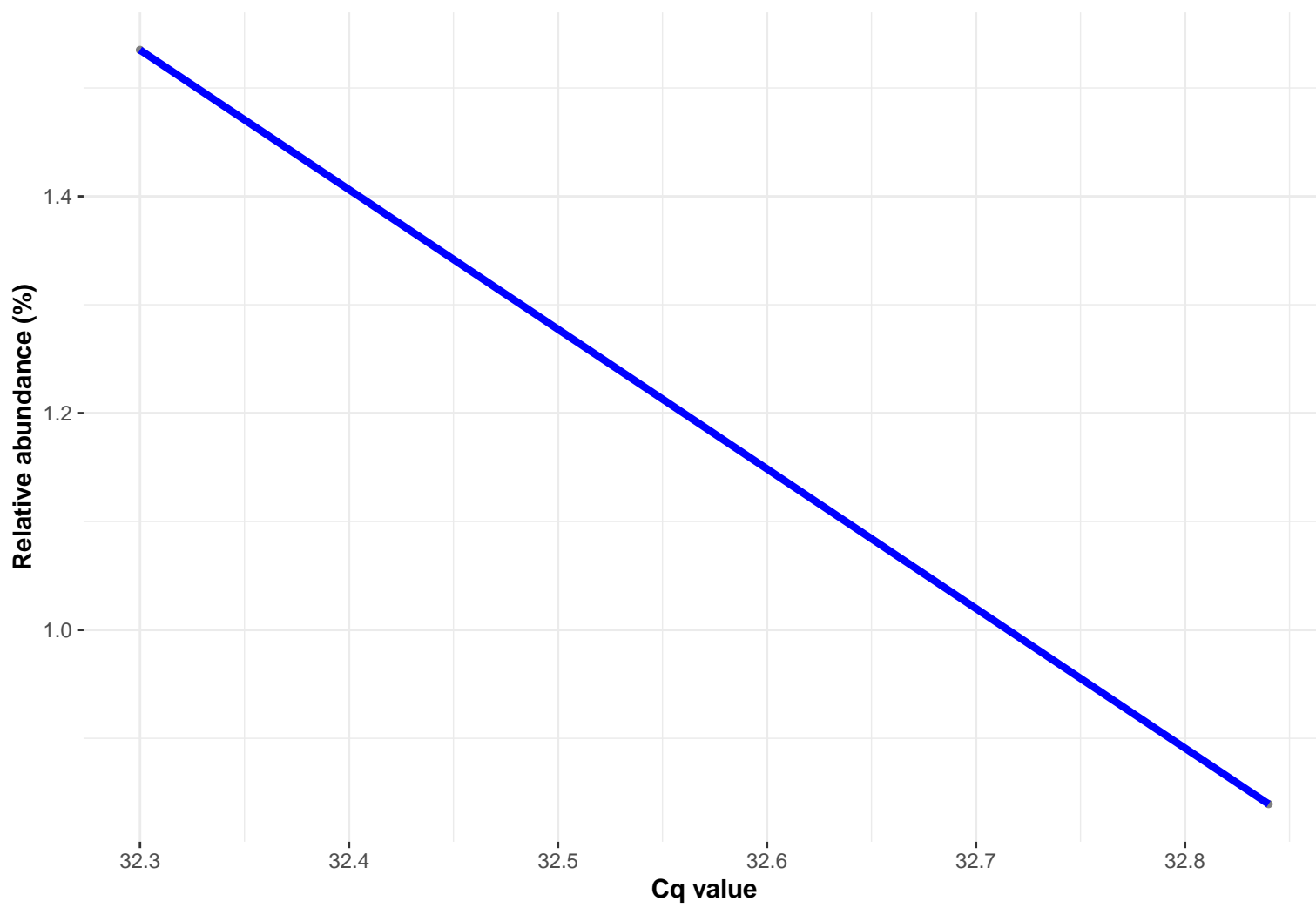
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; NA

Correlation with all samples

SampleType ● REF–DIM
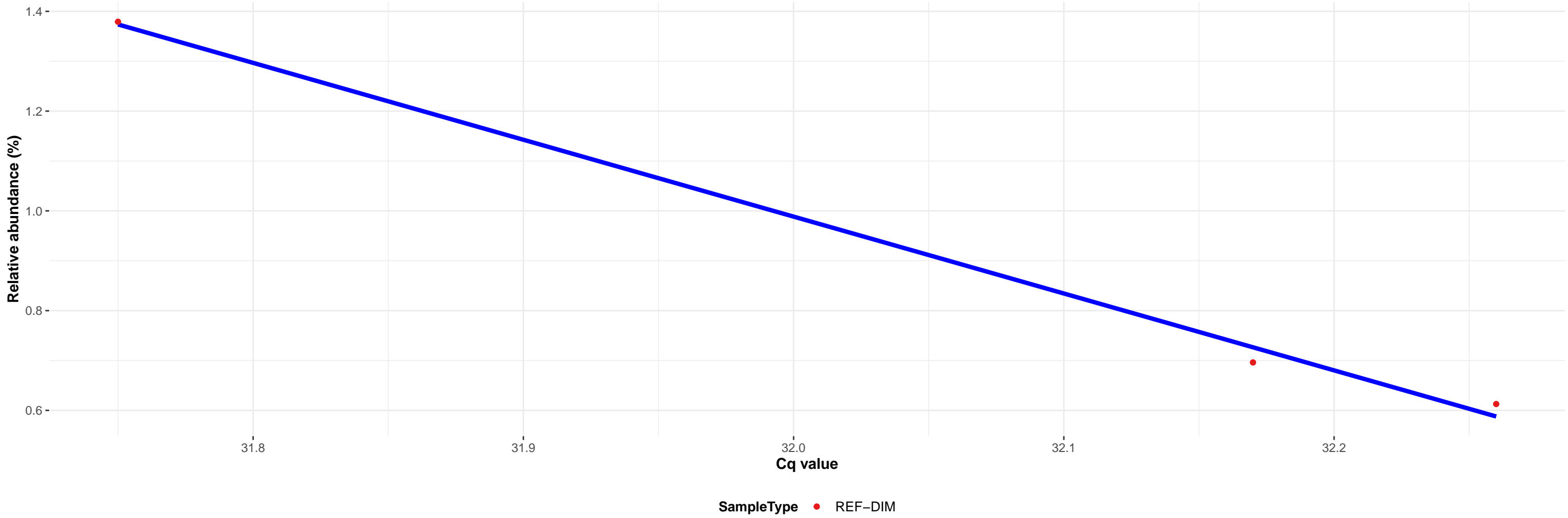
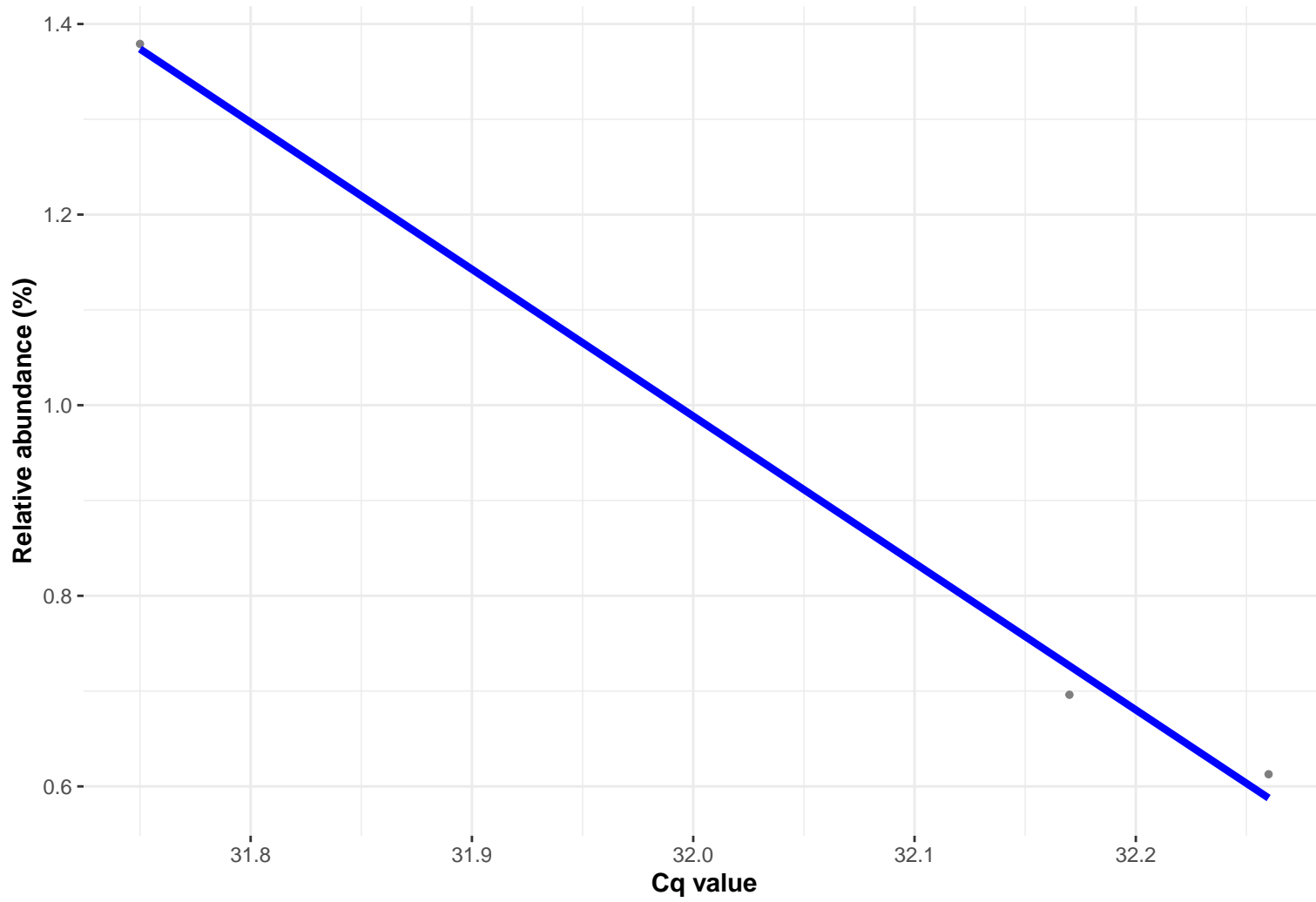**Correlation within: REF–DIM**

Correlation within: PCR–blank

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Kurthia; s__uncultured bacterium
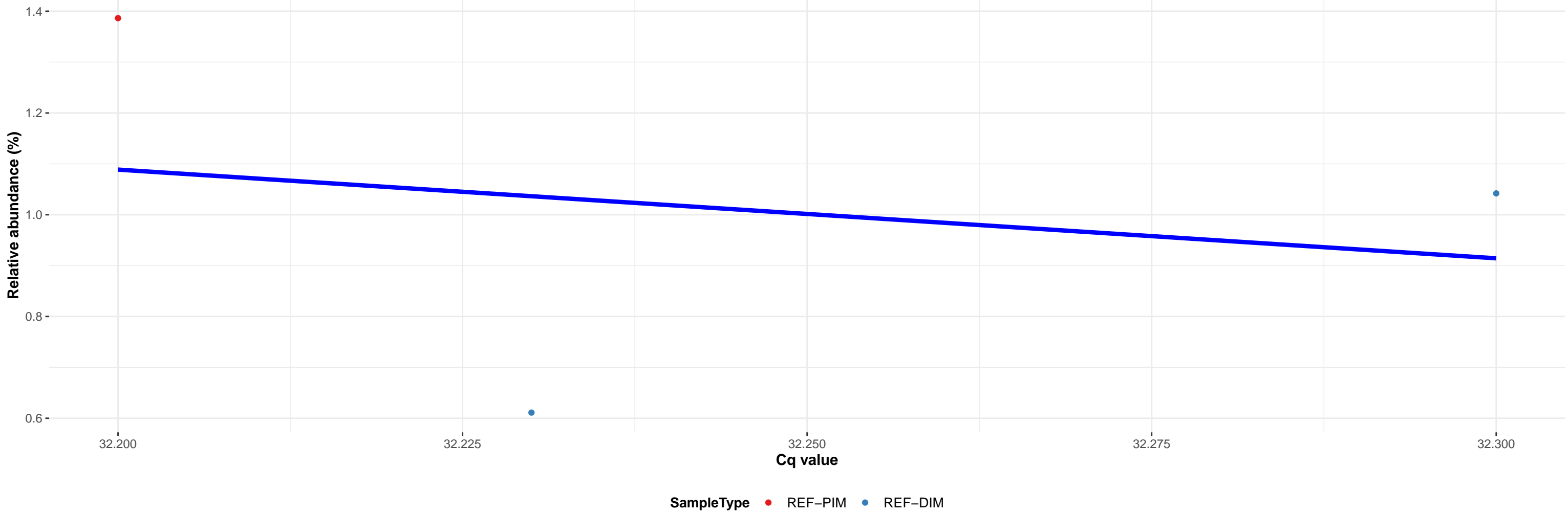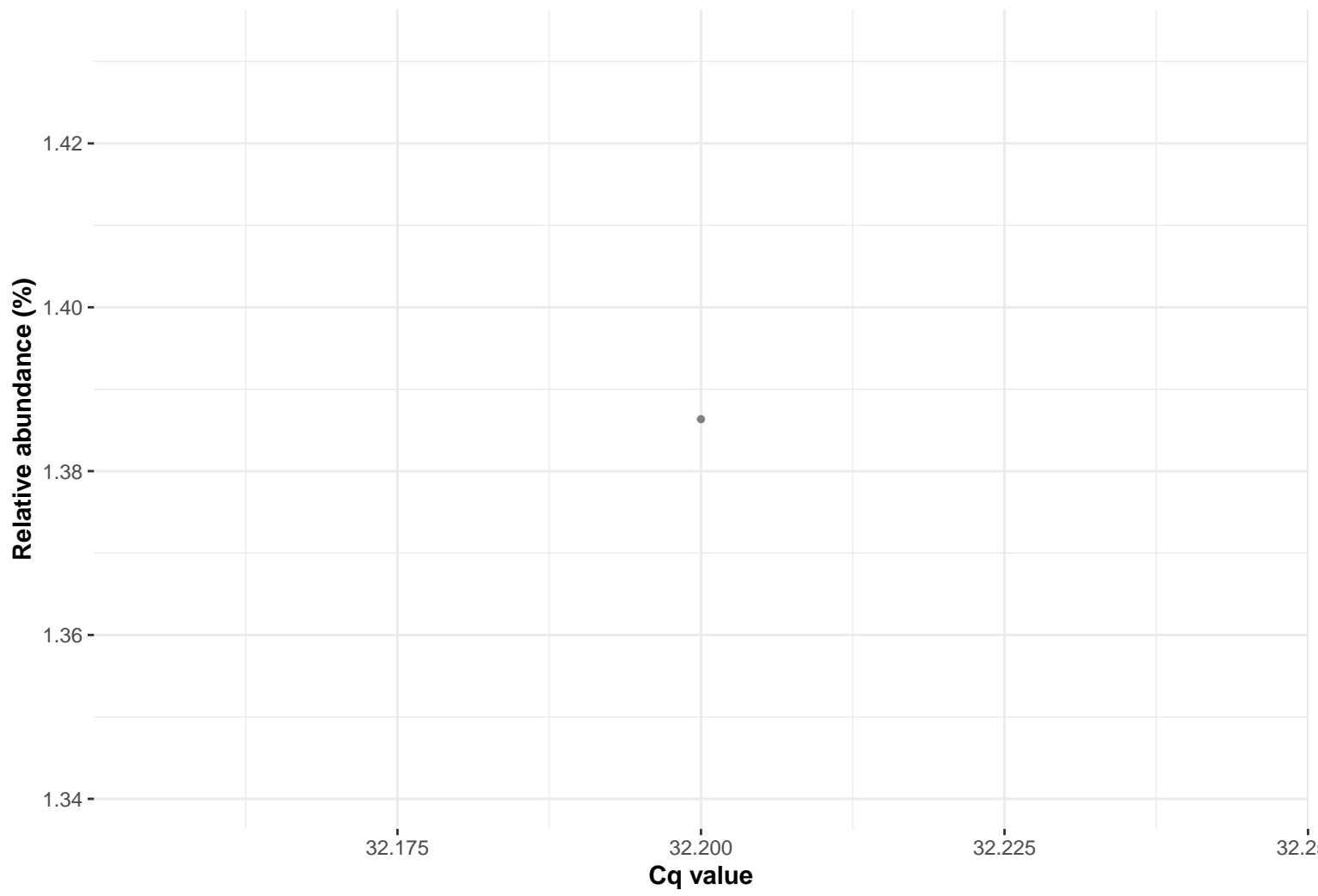
Correlation with all samples

SampleType ● REF−DIM

Correlation within: REF−DIM

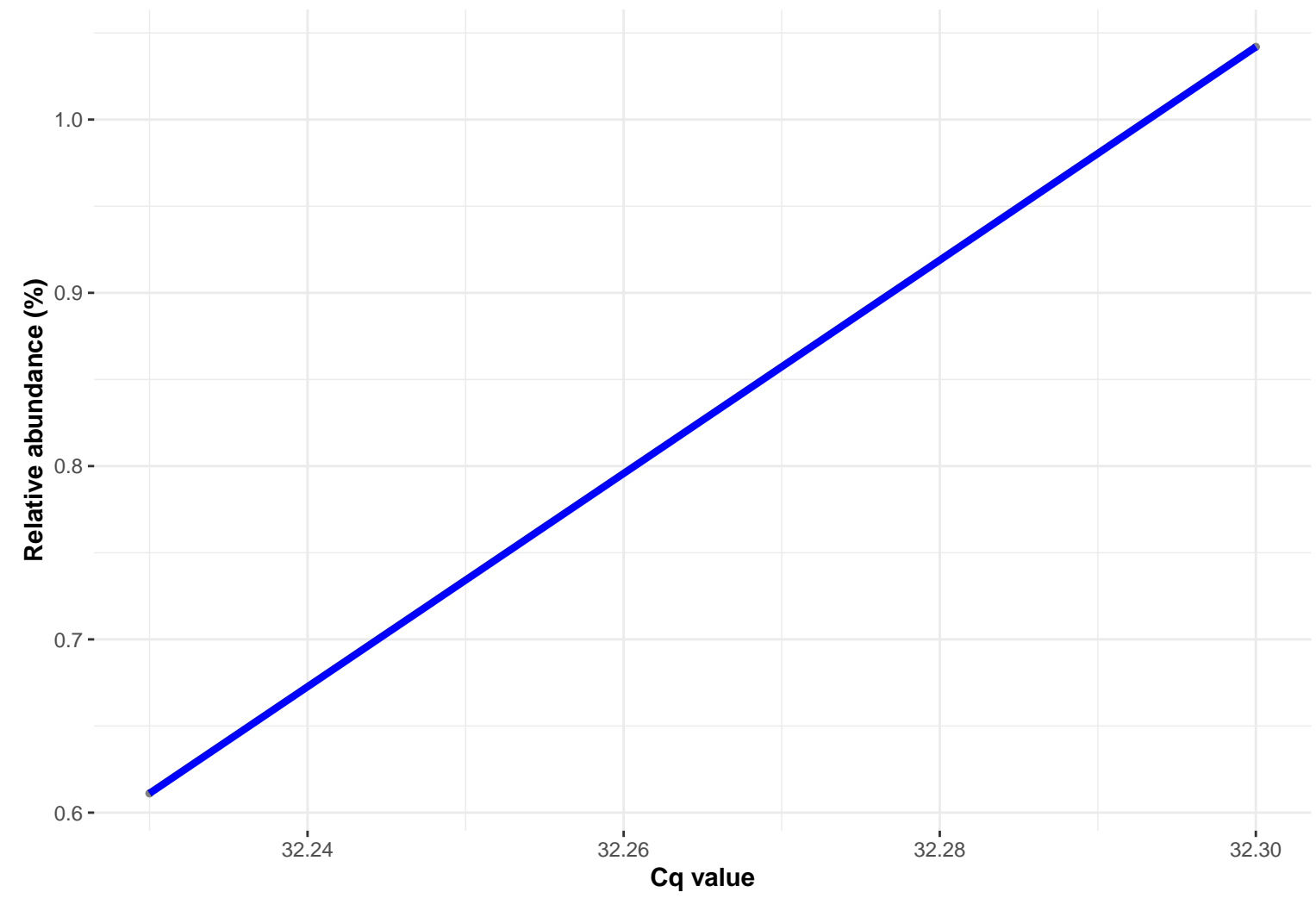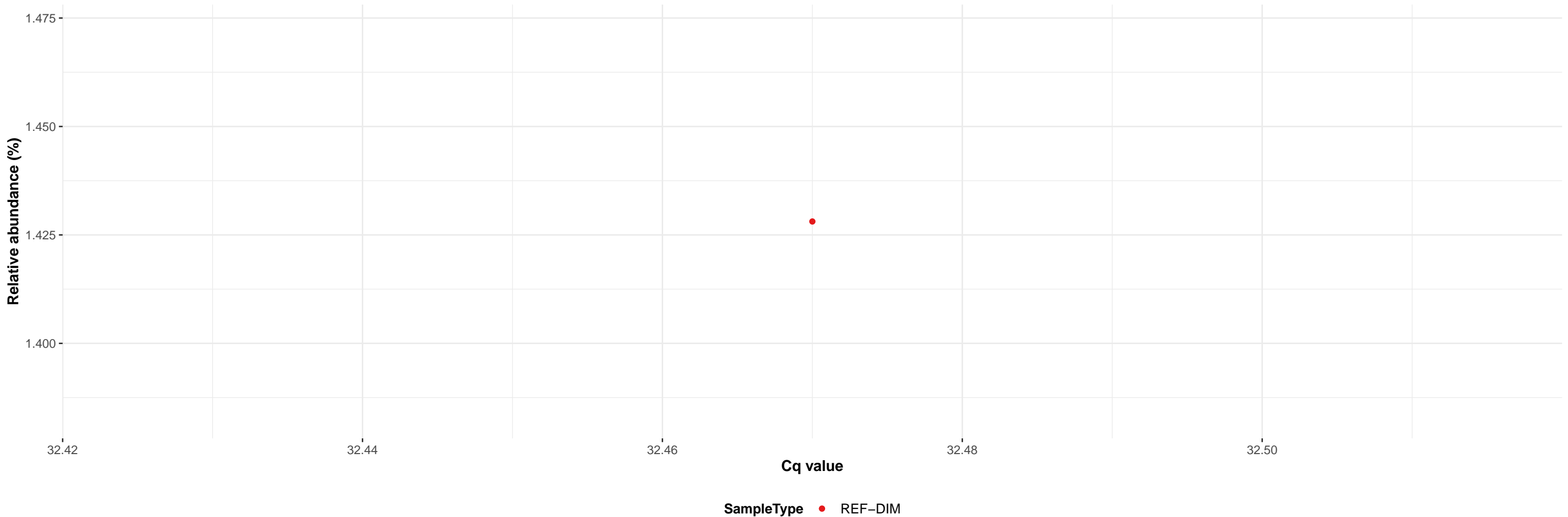k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; Ambiguous_taxa
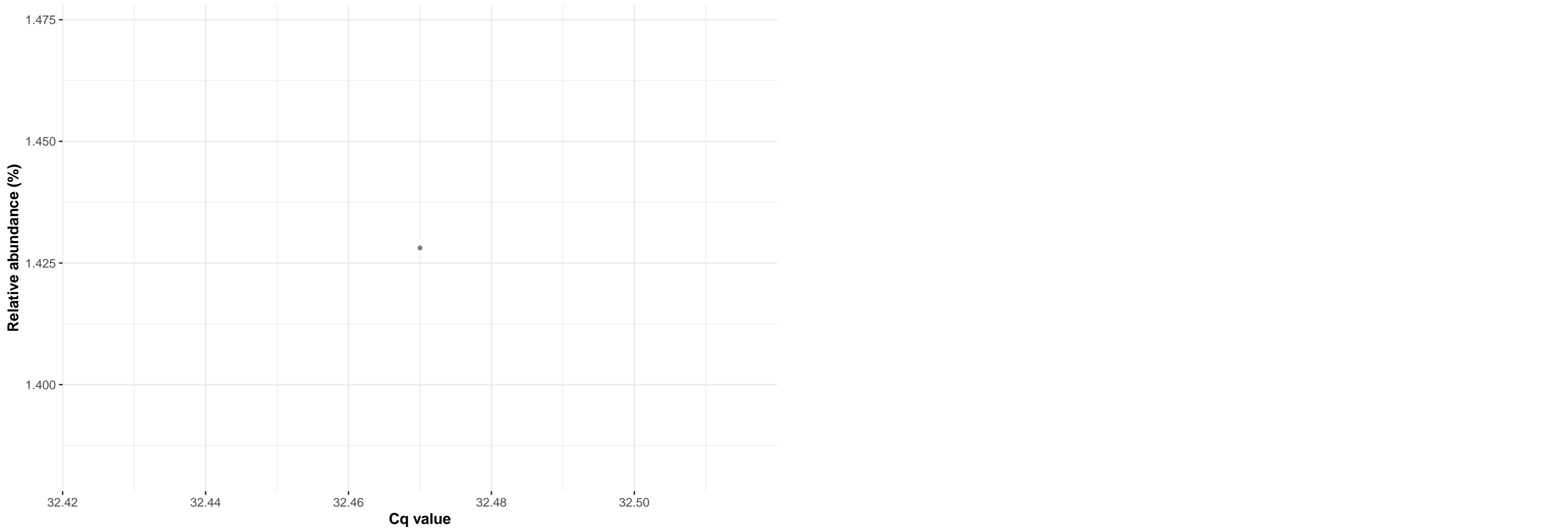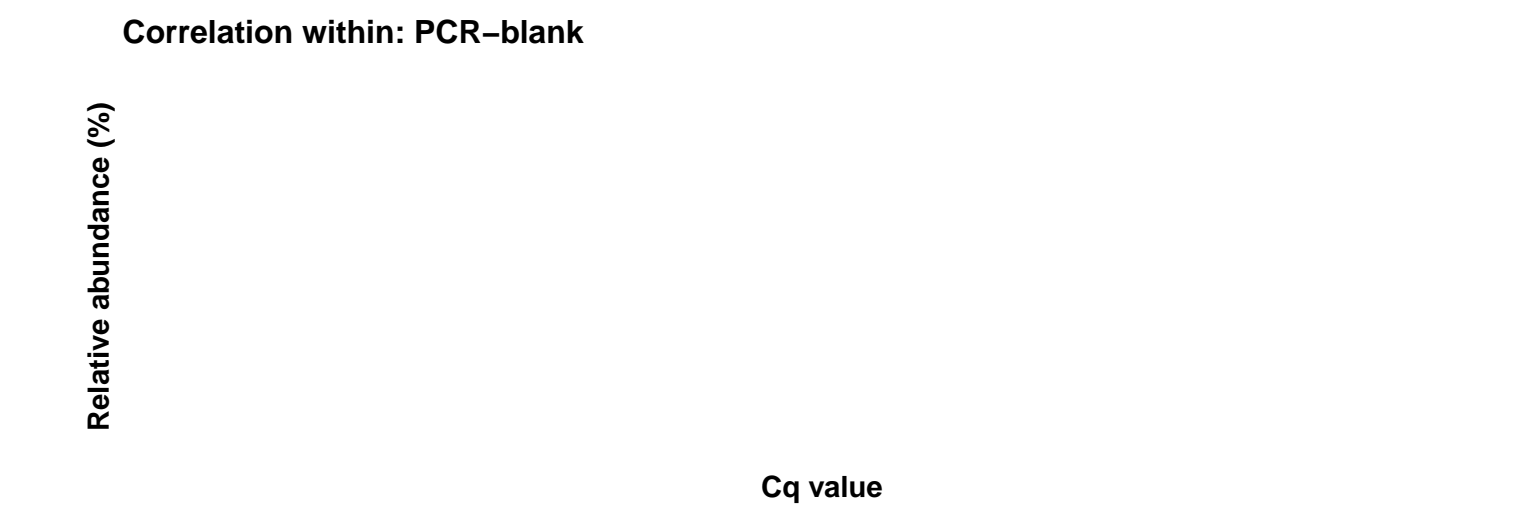
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

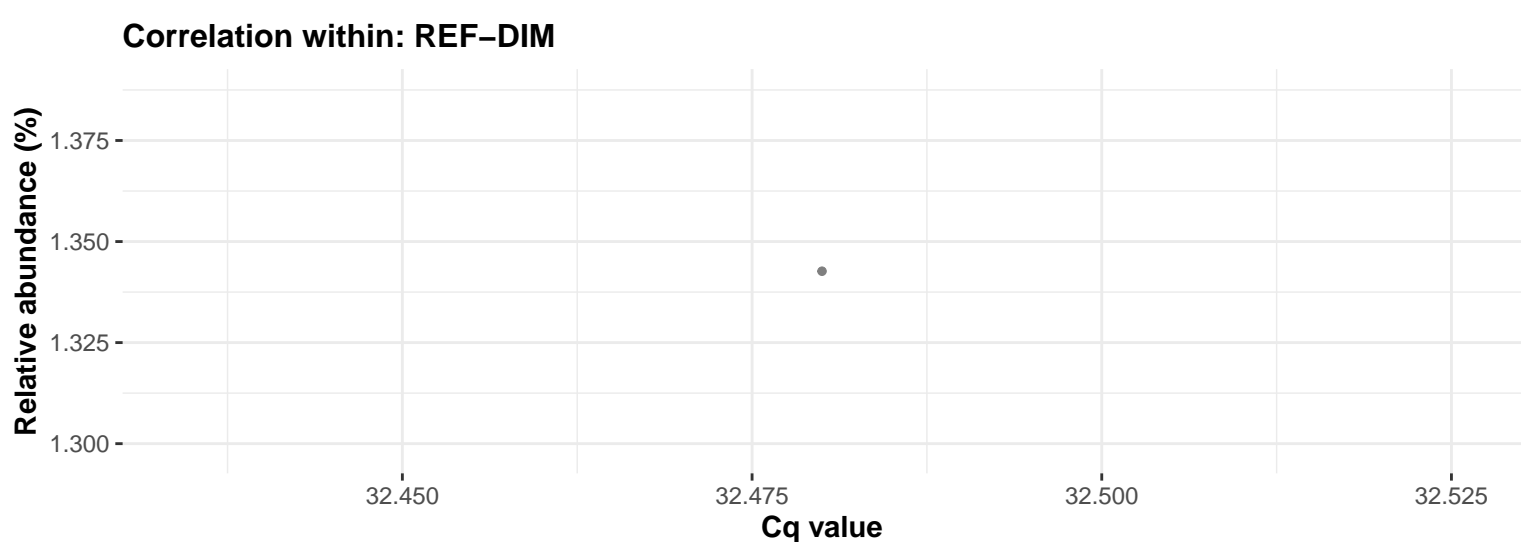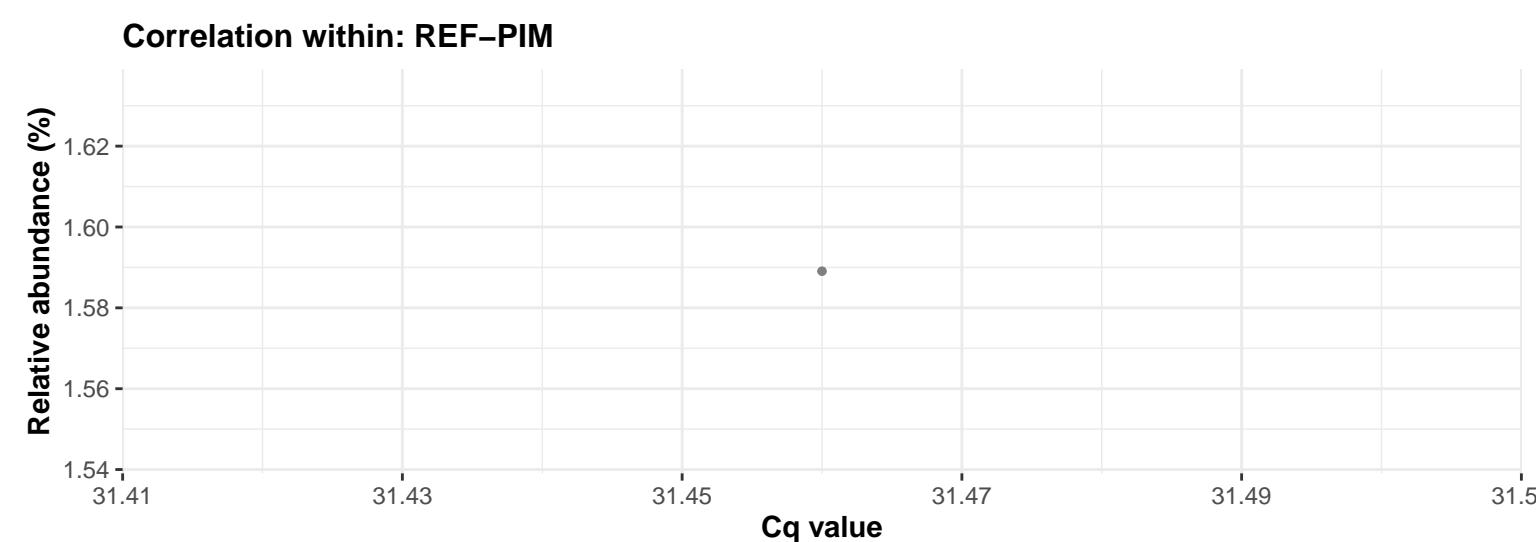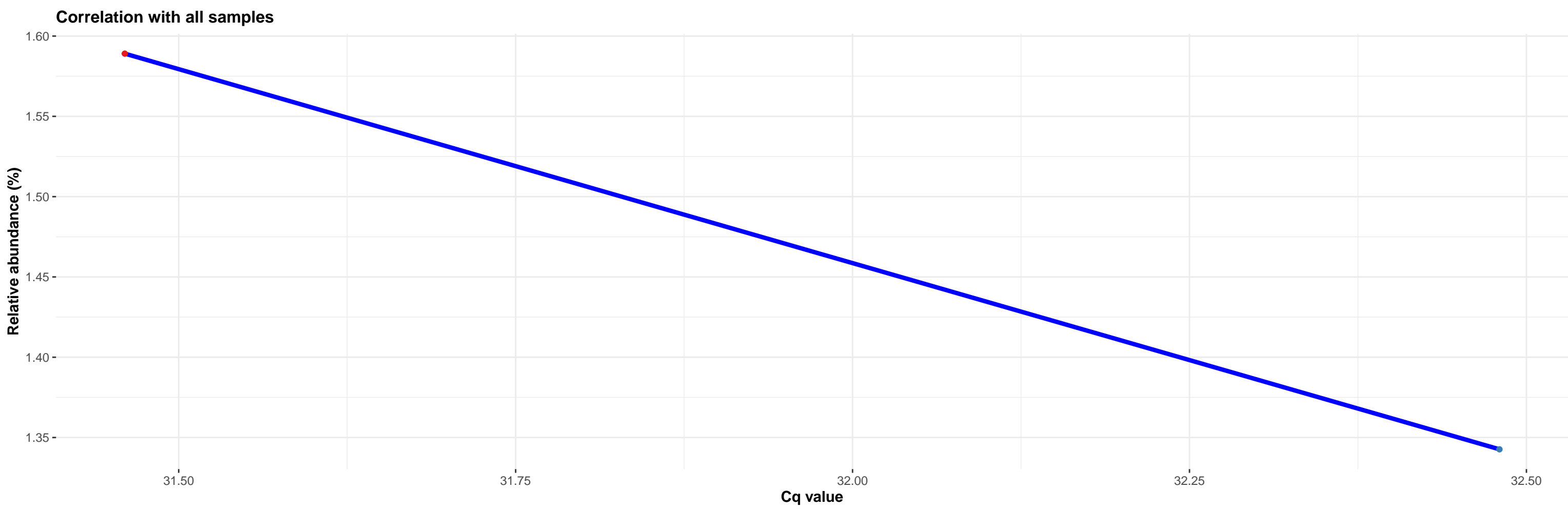# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; NA

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. LA−6
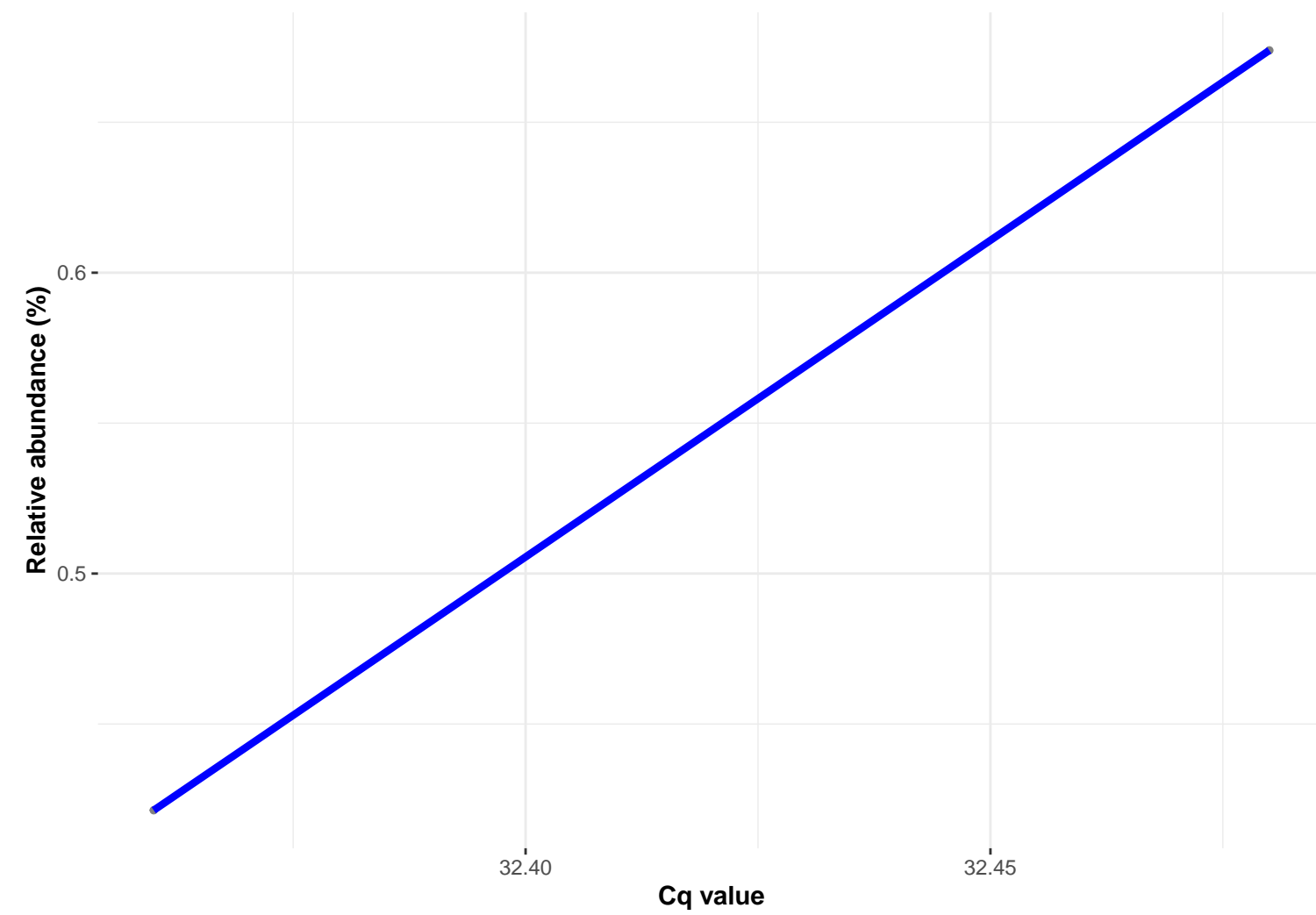
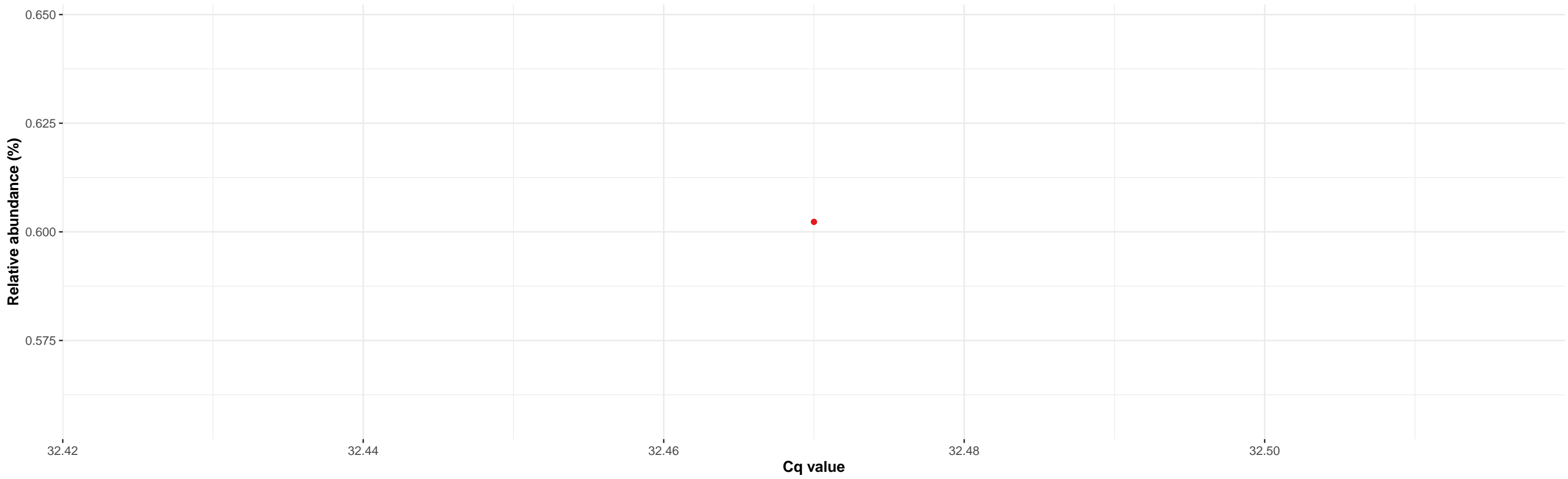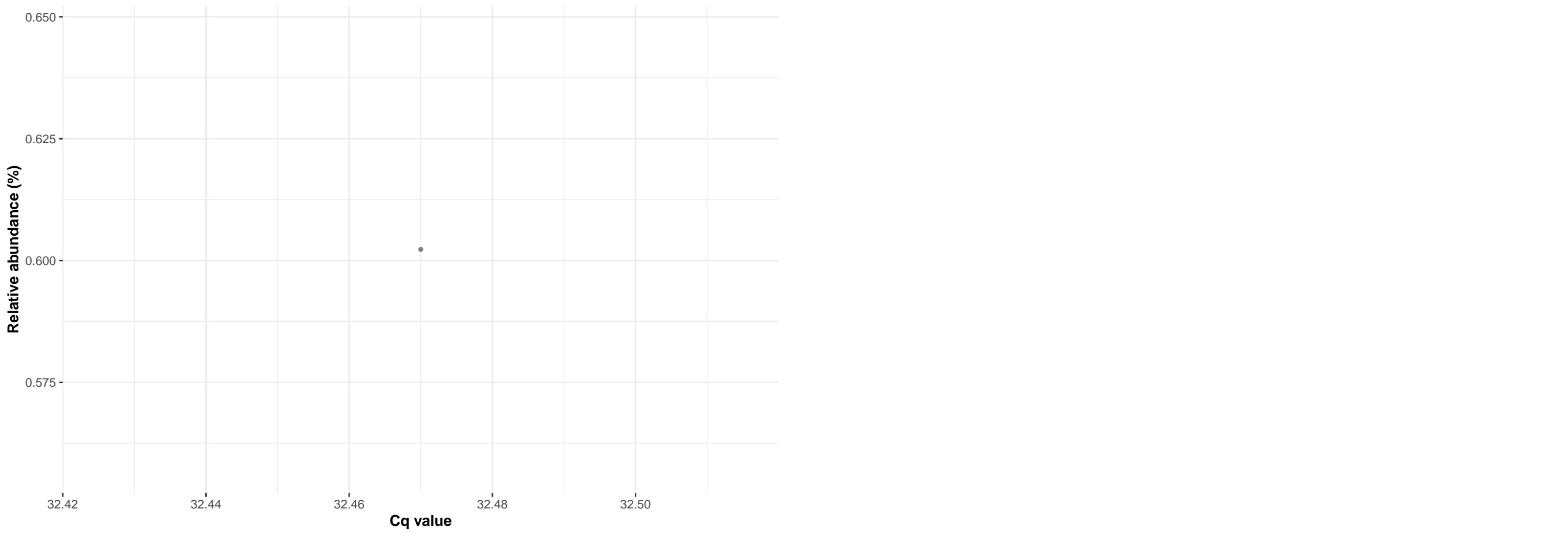# k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; NA

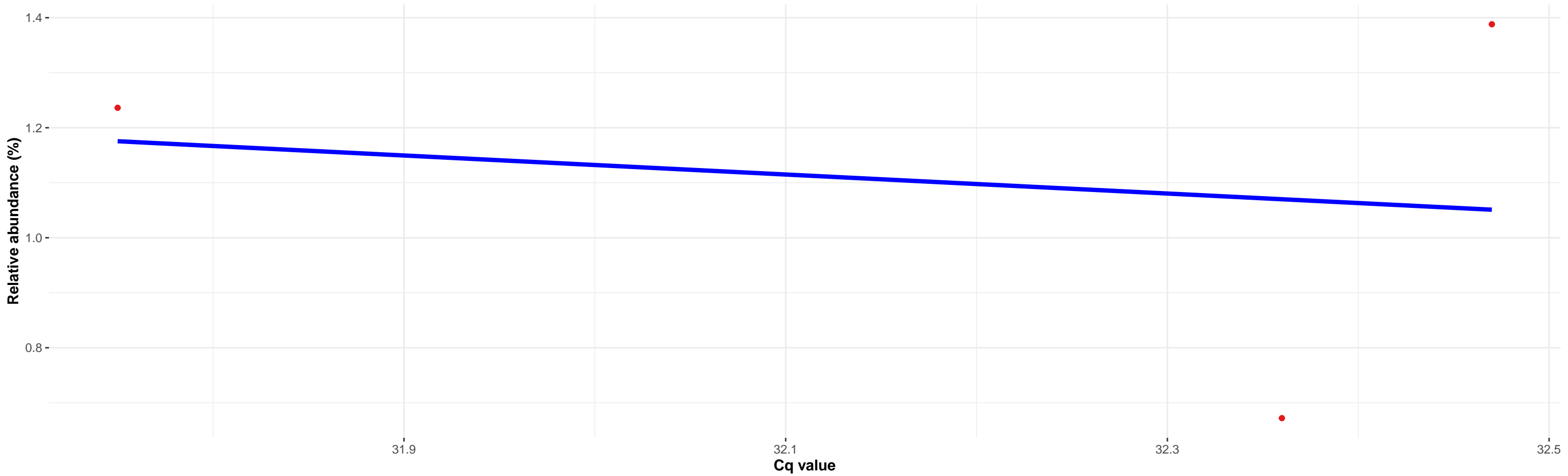**Correlation with all samples**

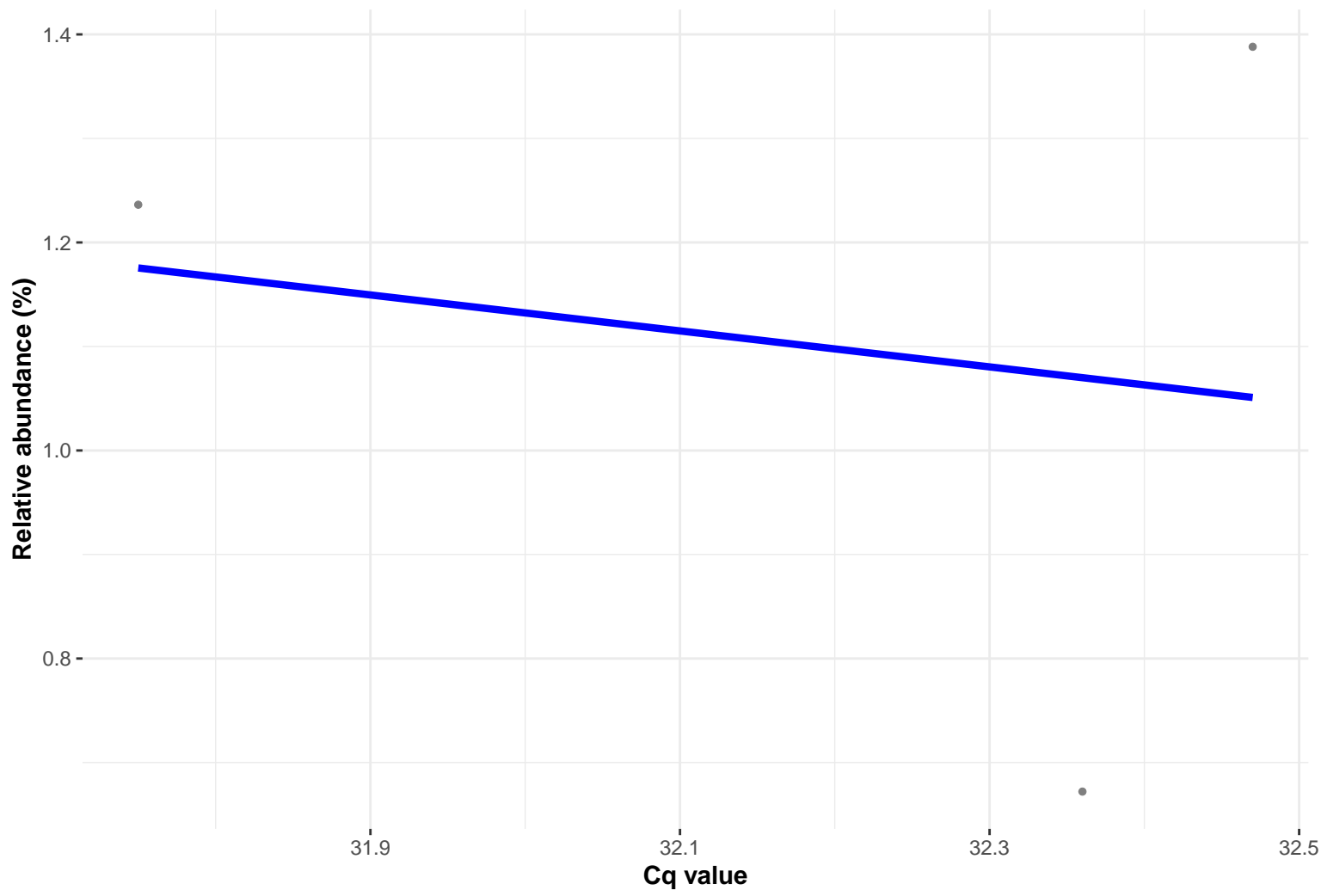**SampleType** ● REF−DIM

Correlation within: REF−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__uncultured Virgibacillus sp.