

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 (%)

Correlation within: PCR–blank

Cq value

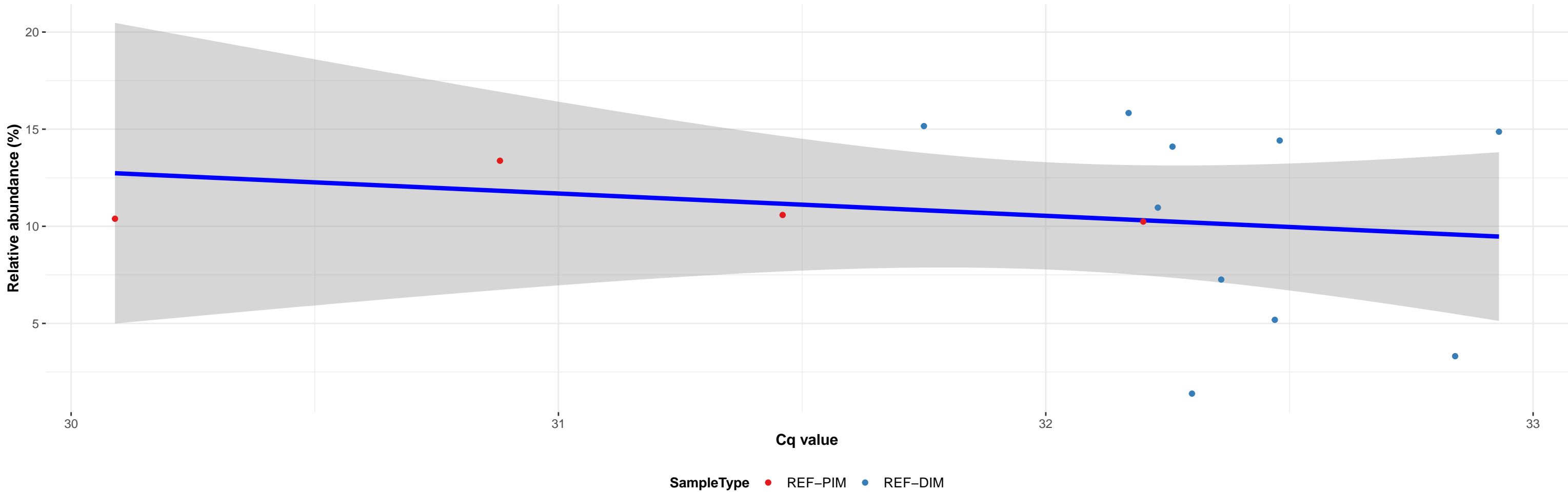
Relative abundance (%)

Cq value

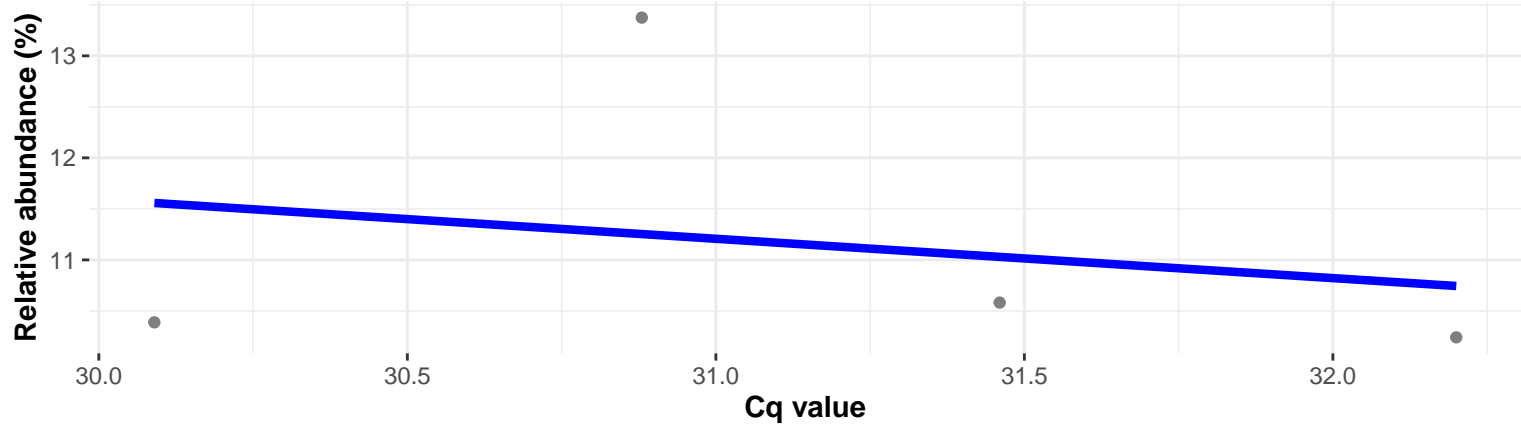
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Undibacterium; NA

Correlation with all samples

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

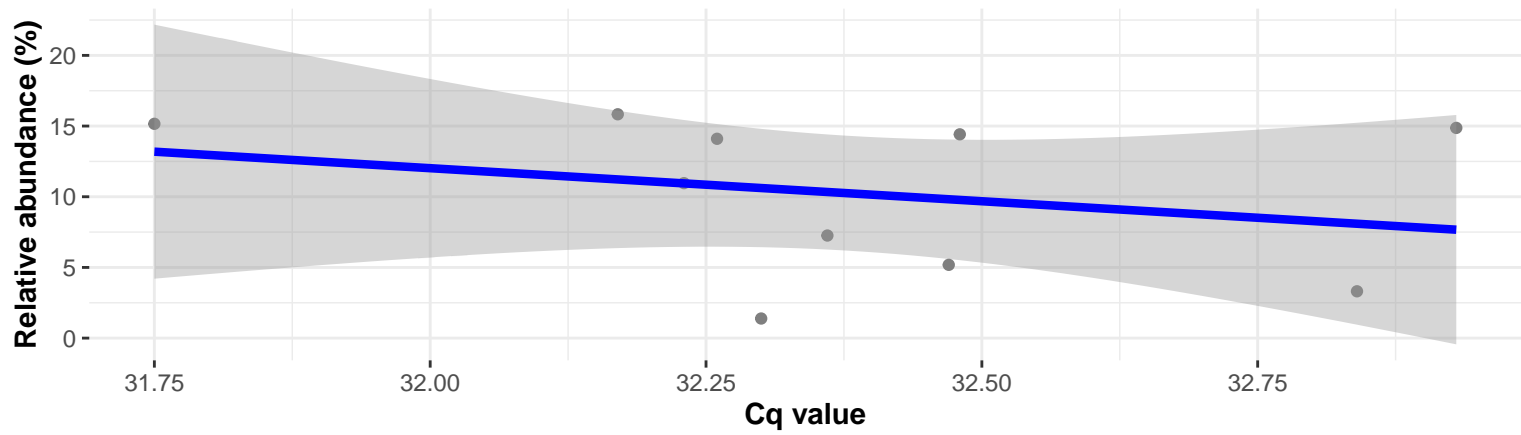


Correlation within: REF-PIM

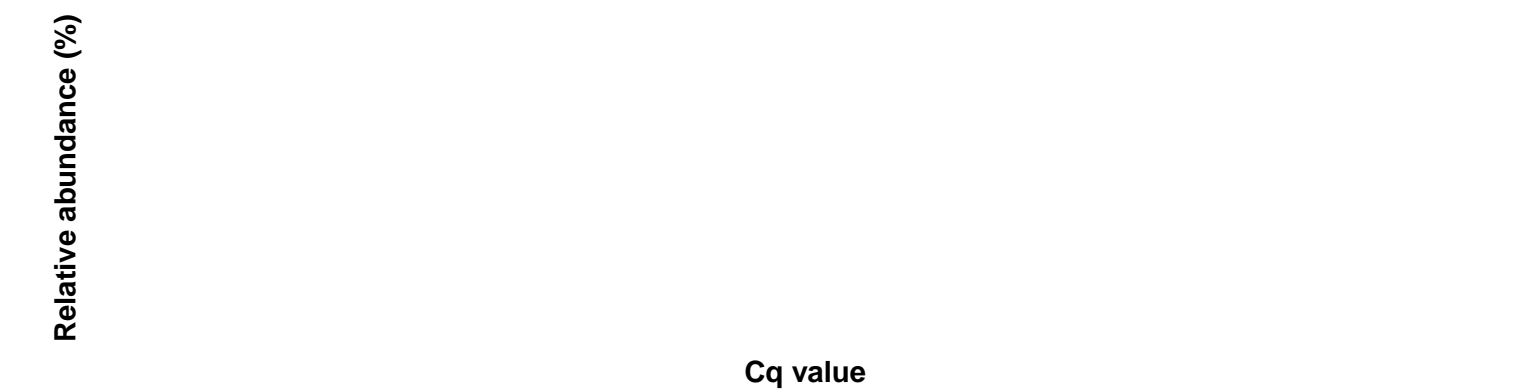


Correlation within: REF-DIM

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



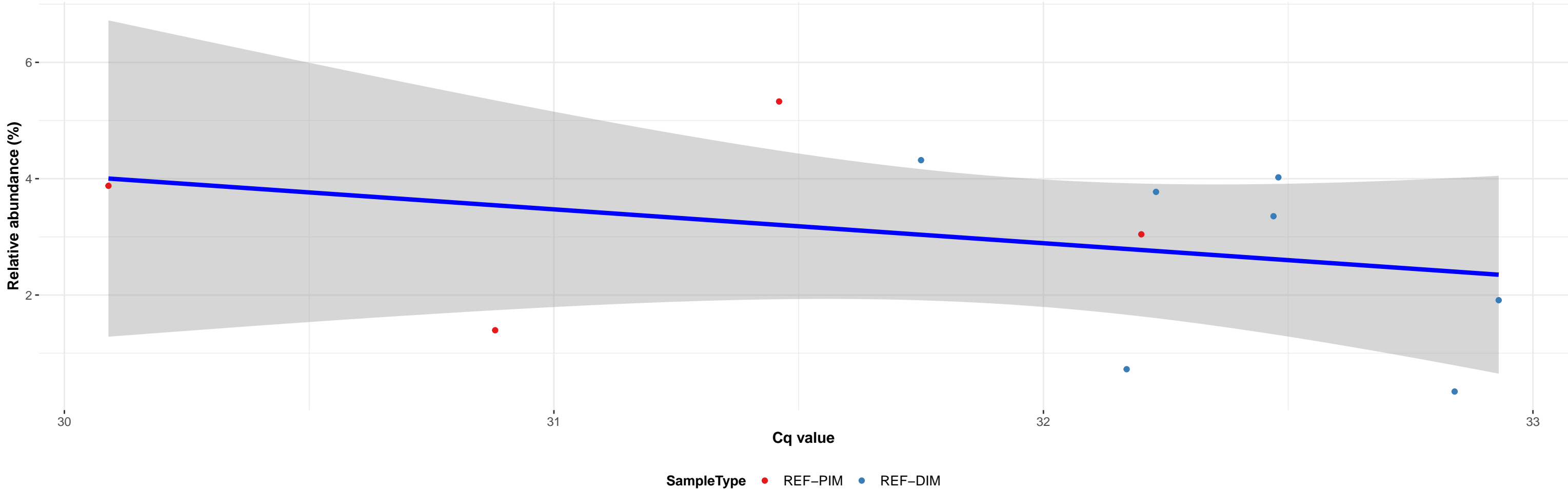
Correlation within: PCR-blank



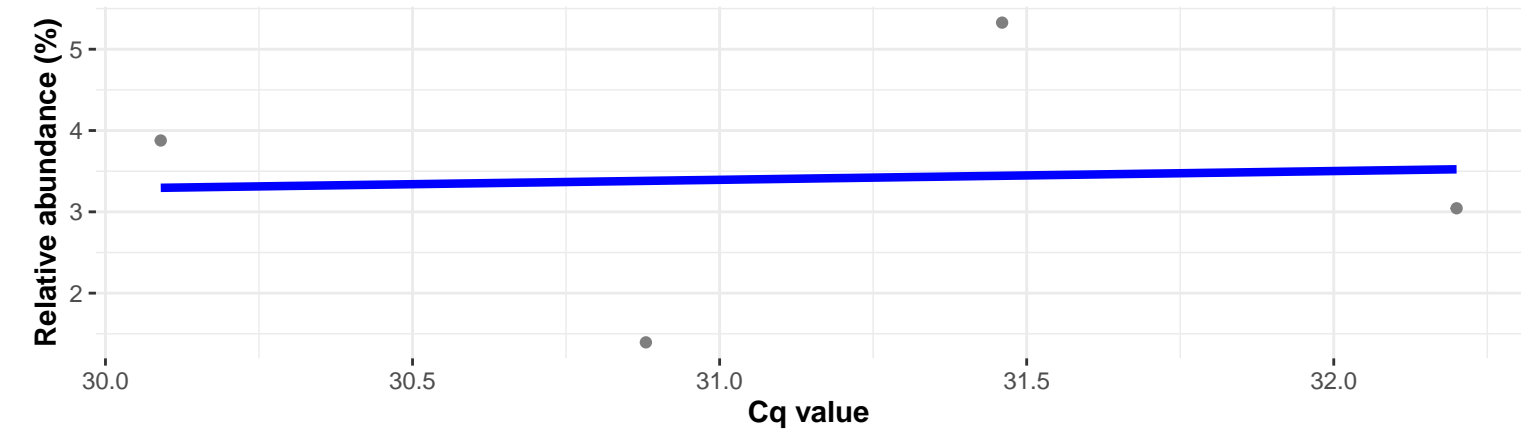
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; NA; NA; NA

Correlation with all samples

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

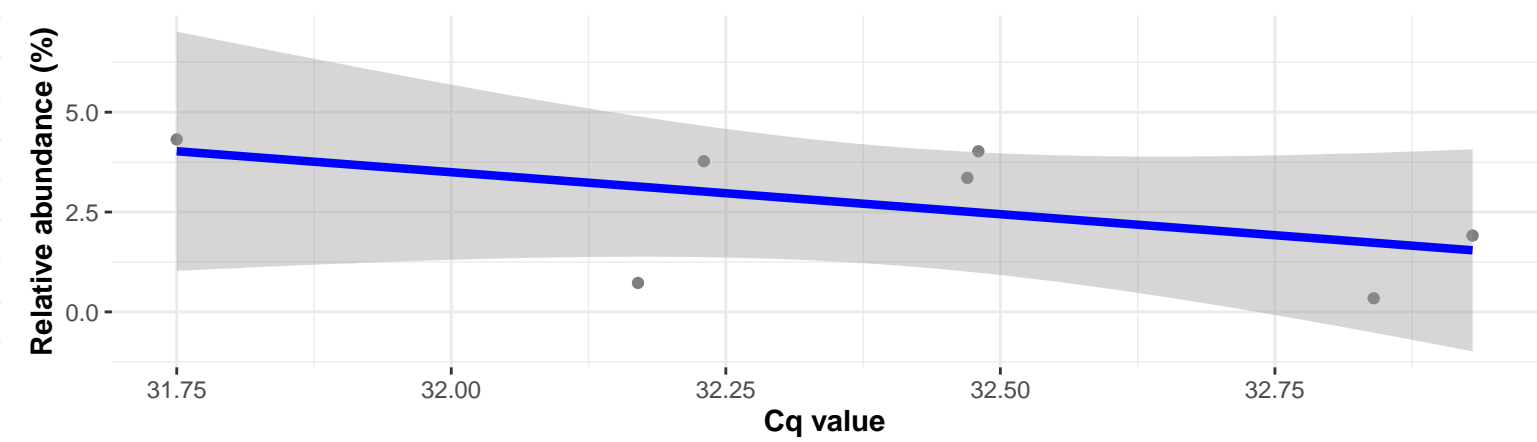


Correlation within: REF-PIM

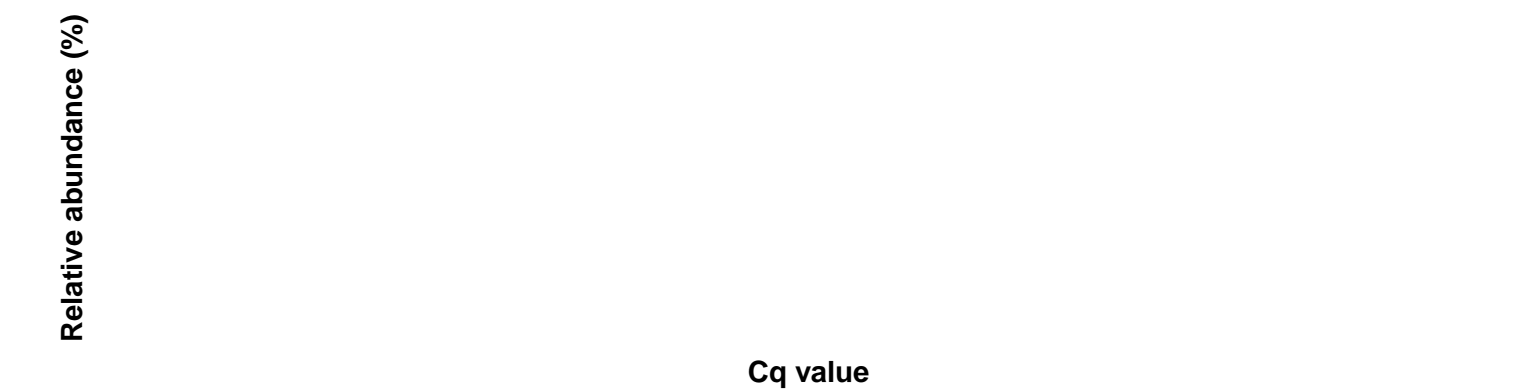


Correlation within: REF-DIM

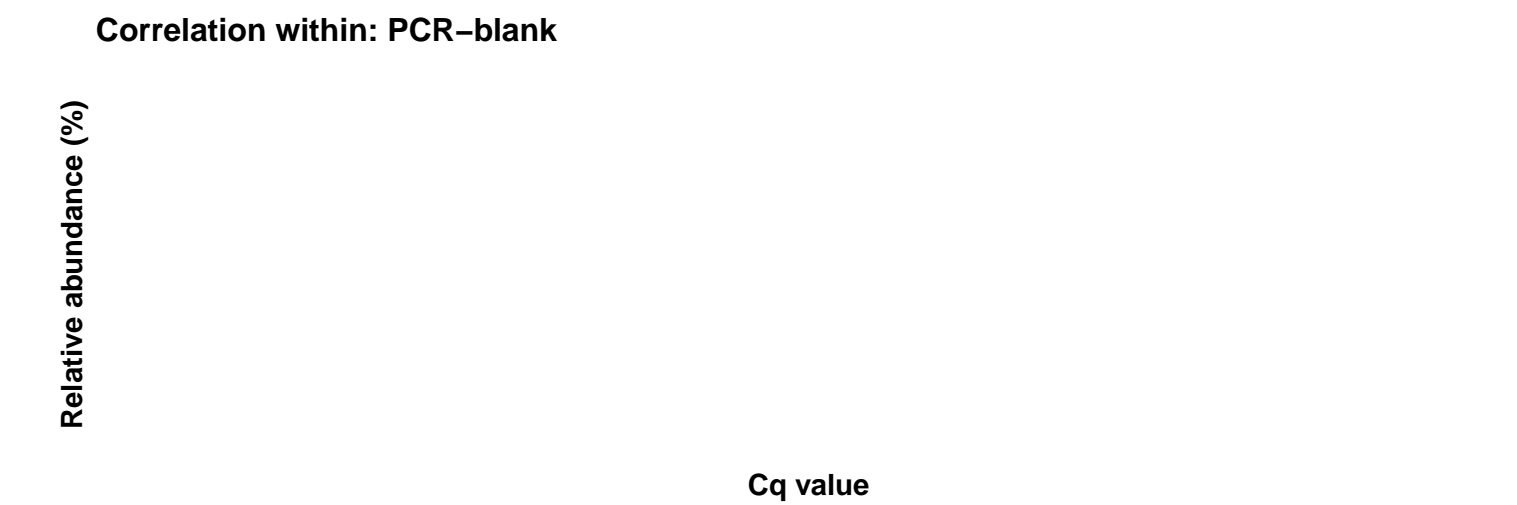
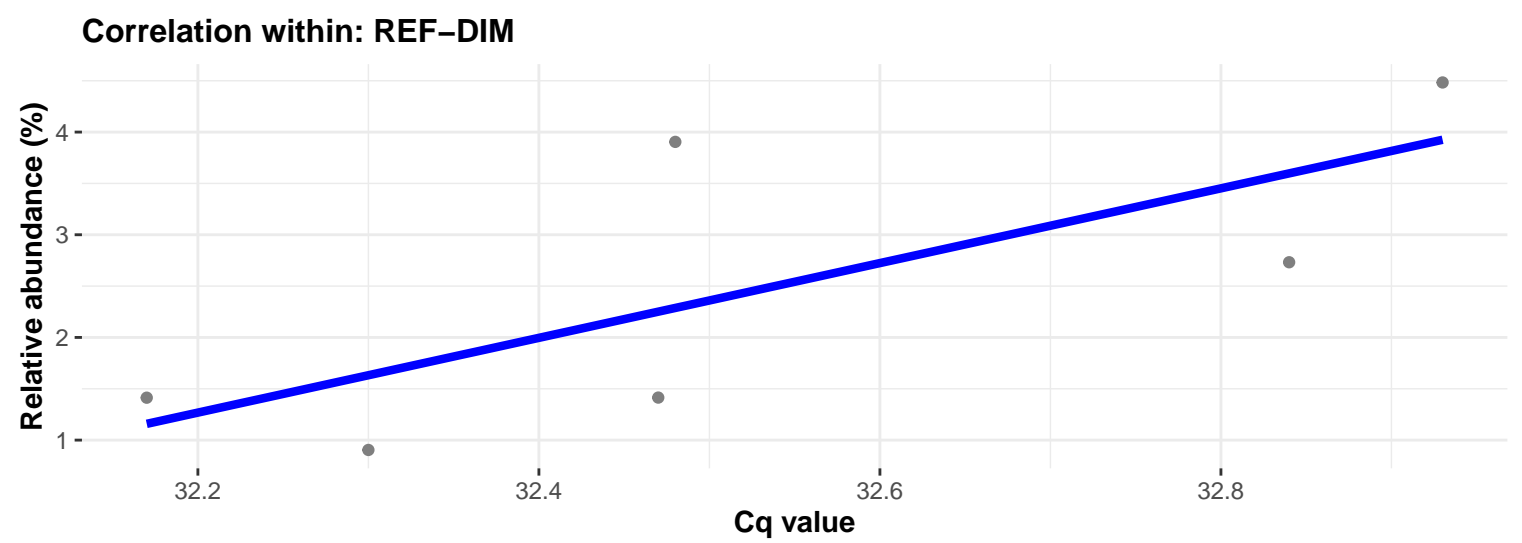
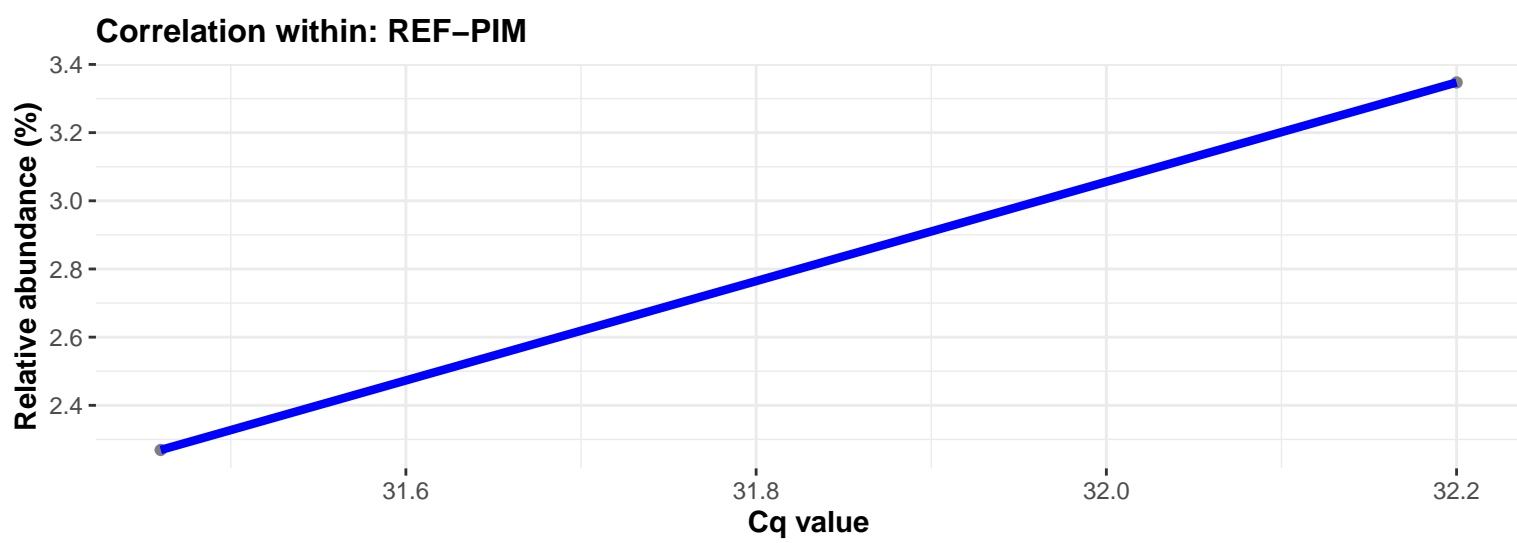
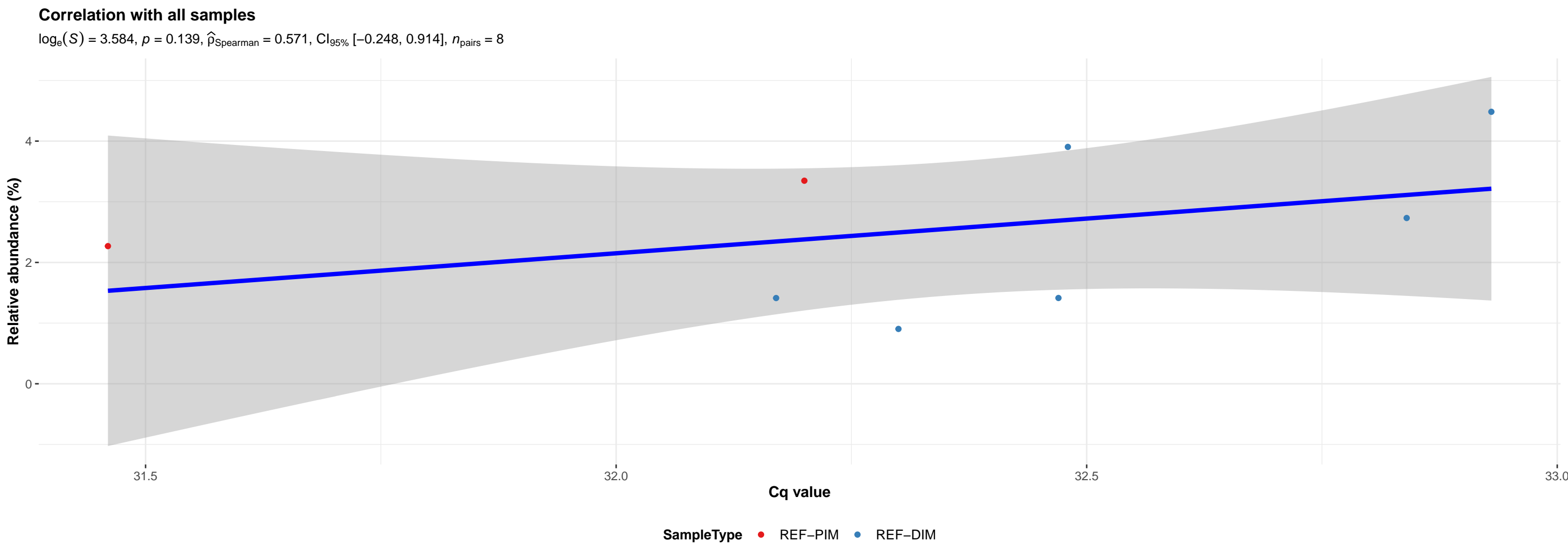
$\log_e(S) = 4.407$ ,  $p = 0.294$ ,  $\hat{\rho}_{\text{Spearman}} = -0.464$ ,  $CI_{95\%} [-0.907, 0.467]$ ,  $n_{\text{pairs}} = 7$



Correlation within: PCR-blank



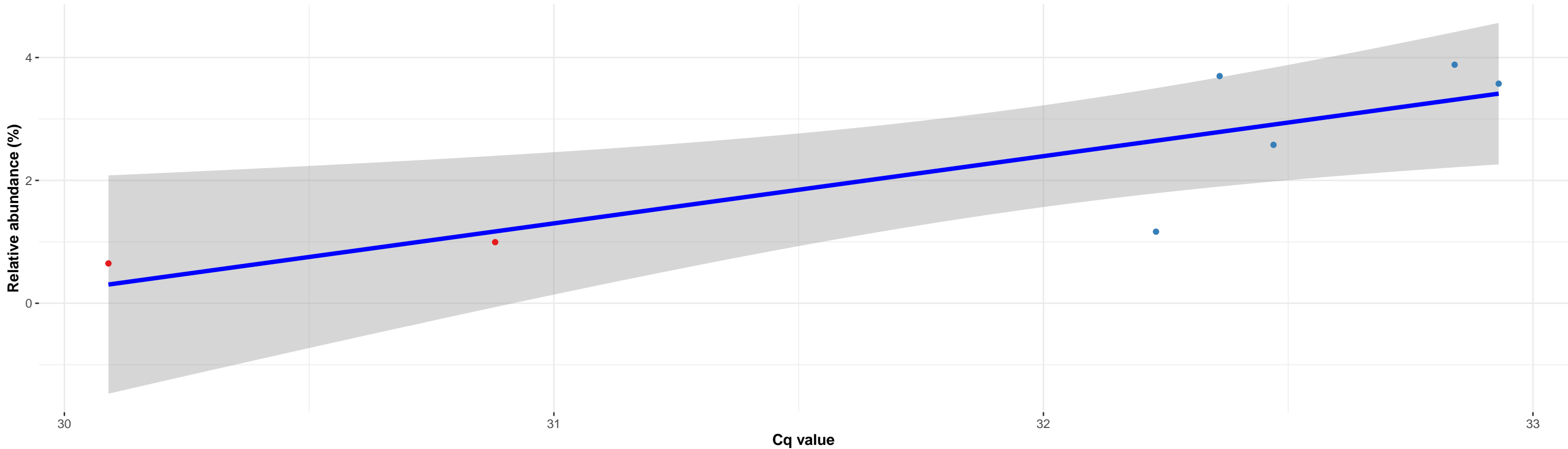
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; s\_\_Corynebacterium aurimucosum ATCC 700975



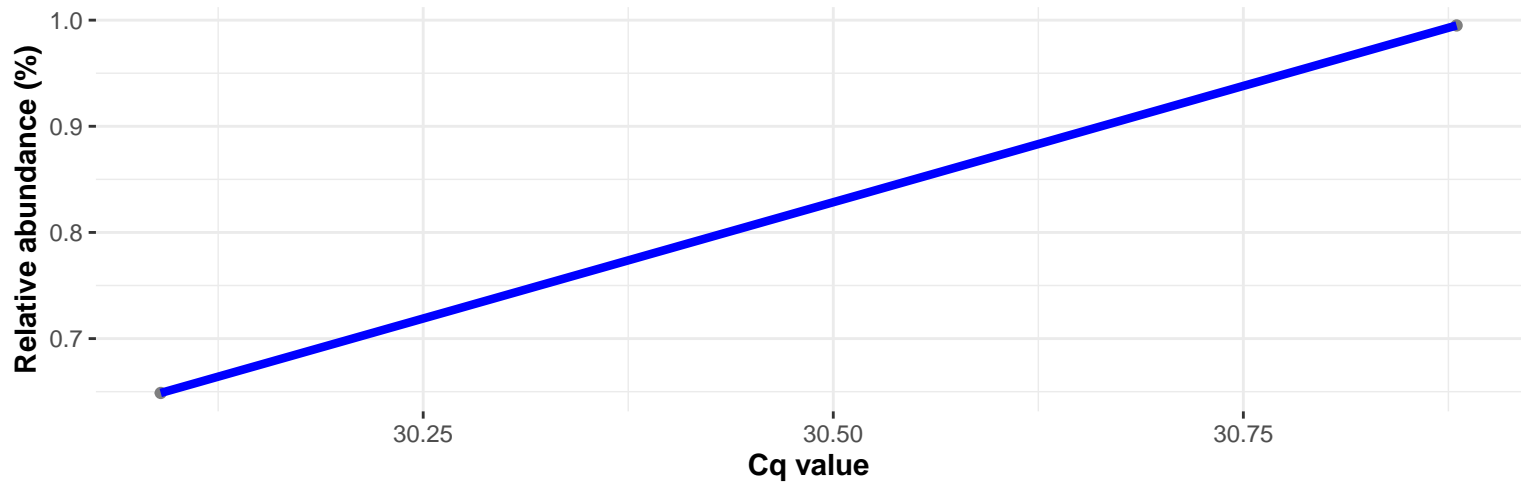
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; s\_\_Oceanobacillus caeni

Correlation with all samples

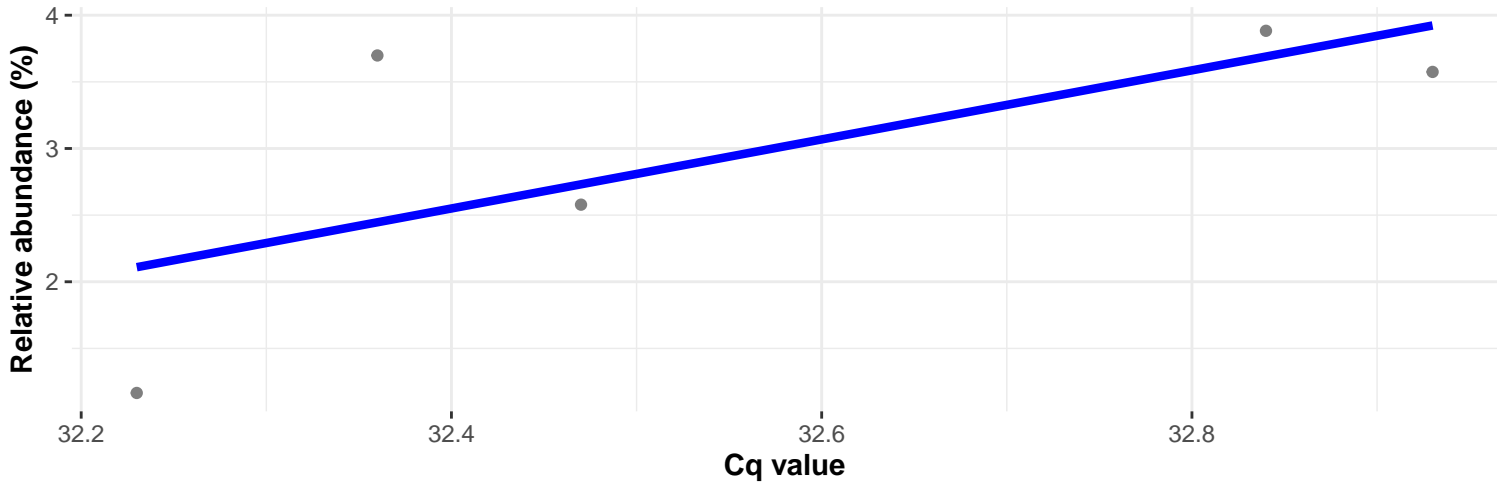
$\log_e(S) = 2.303$ ,  $p = 0.023$ ,  $\hat{\rho}_{\text{Spearman}} = 0.821$ ,  $CI_{95\%} [0.151, 0.974]$ ,  $n_{\text{pairs}} = 7$



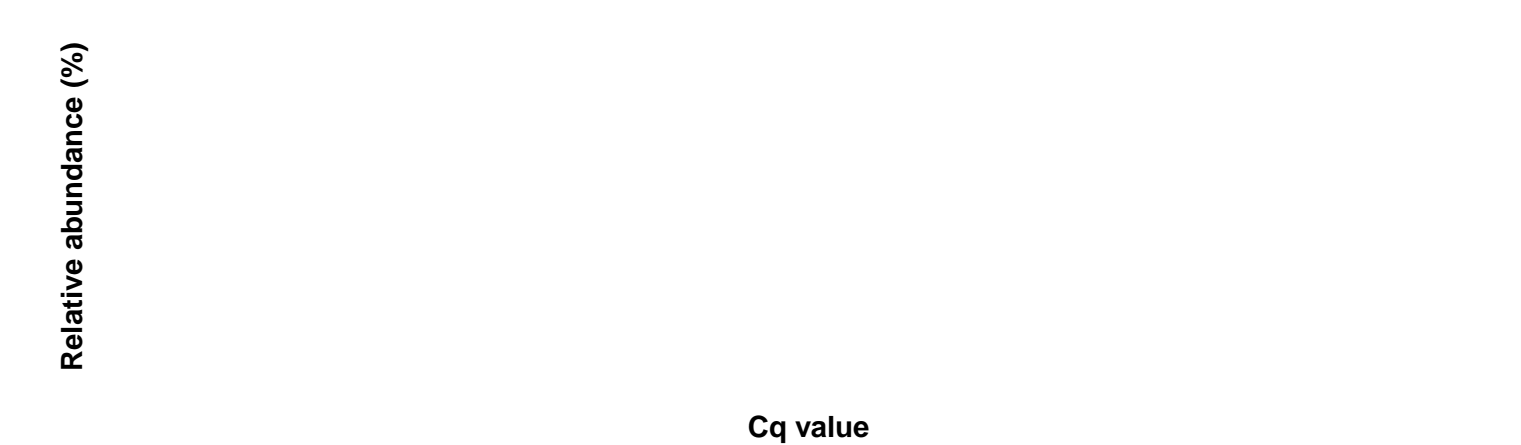
Correlation within: REF-PIM



Correlation within: REF-DIM

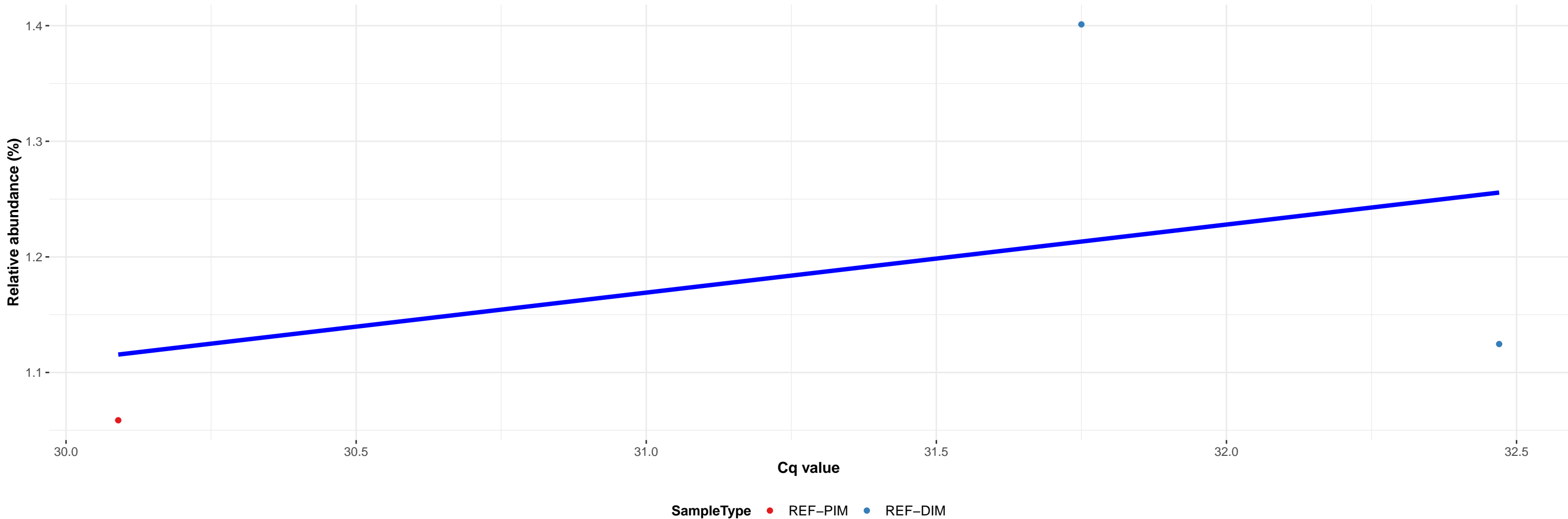


Correlation within: PCR-blank

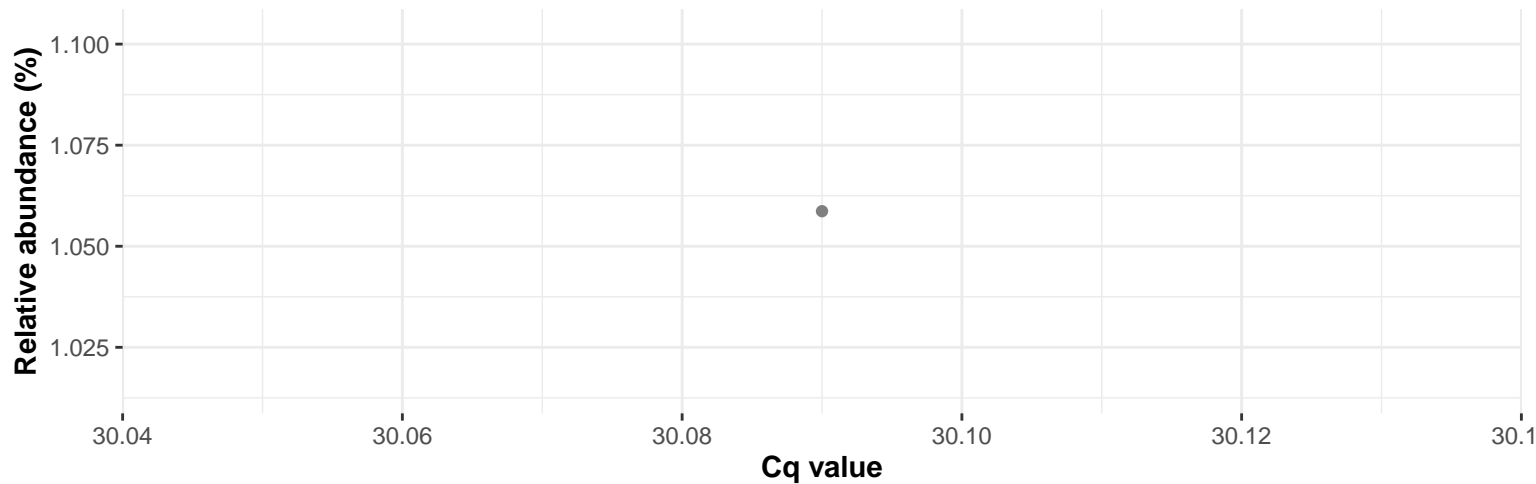


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Aerococcaceae; g\_\_Globicatella; Ambiguous\_taxa

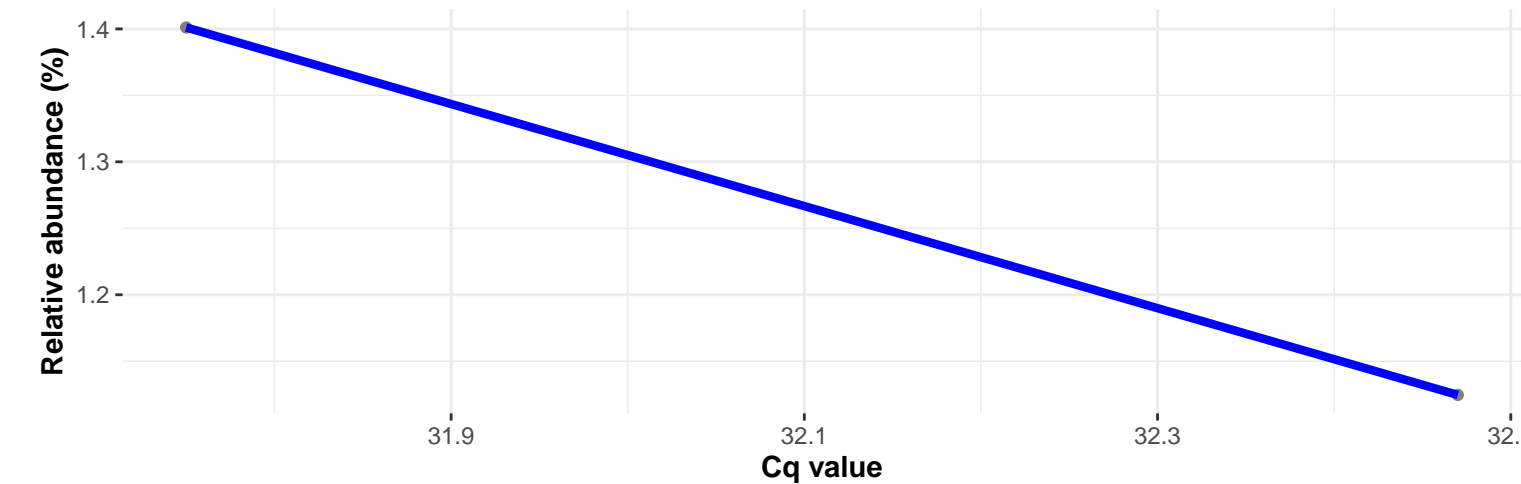
Correlation with all samples



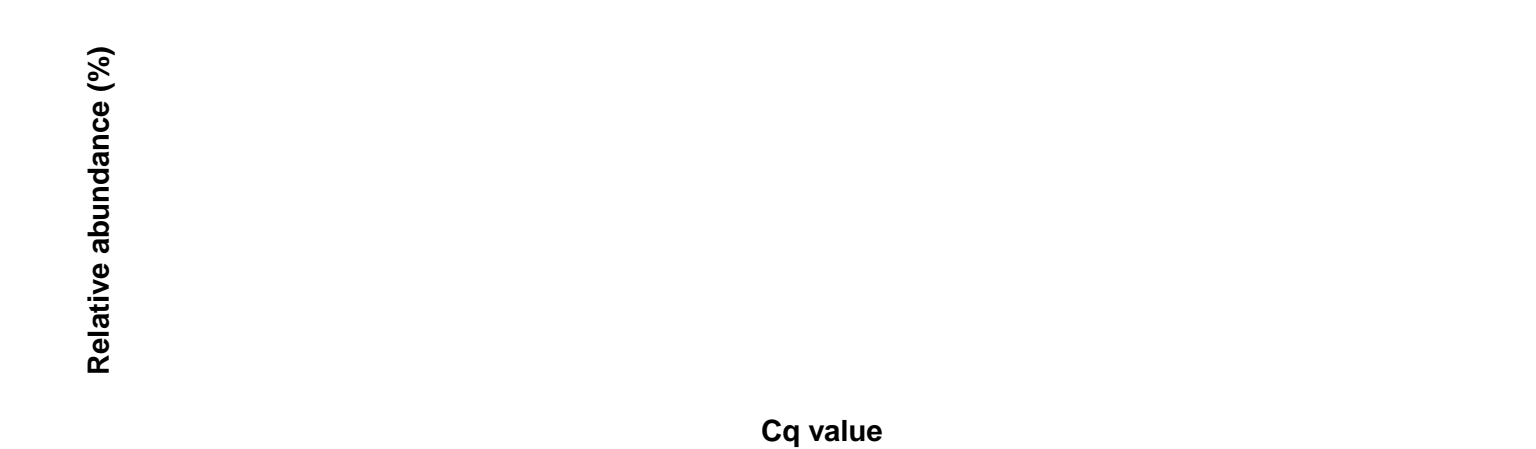
Correlation within: REF-PIM



Correlation within: REF-DIM



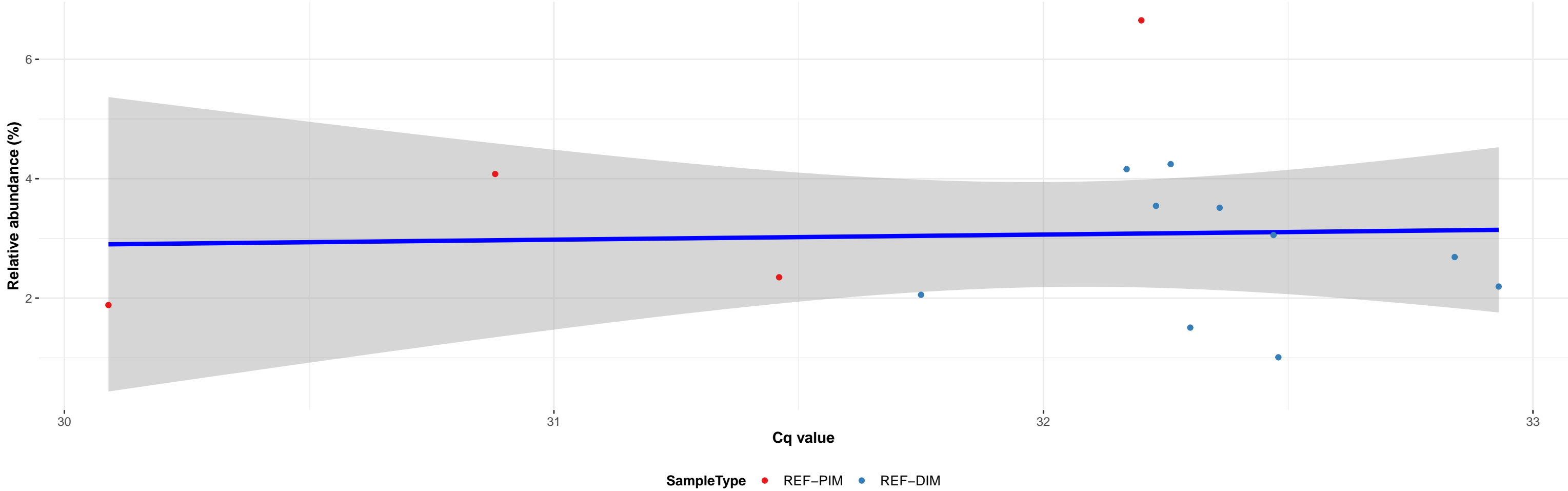
Correlation within: PCR-blank



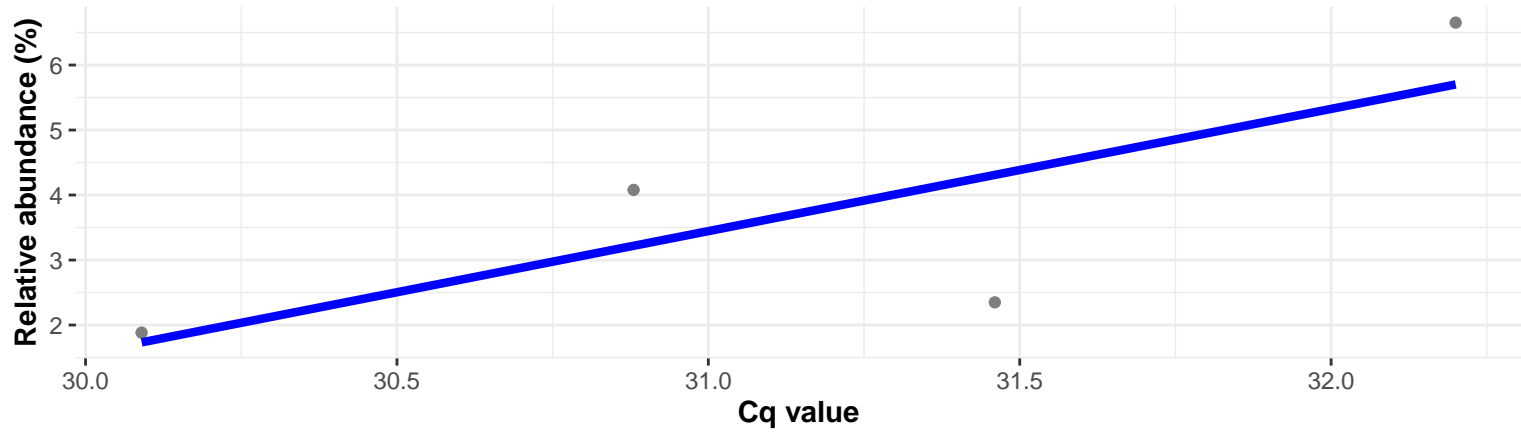
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

Correlation with all samples

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

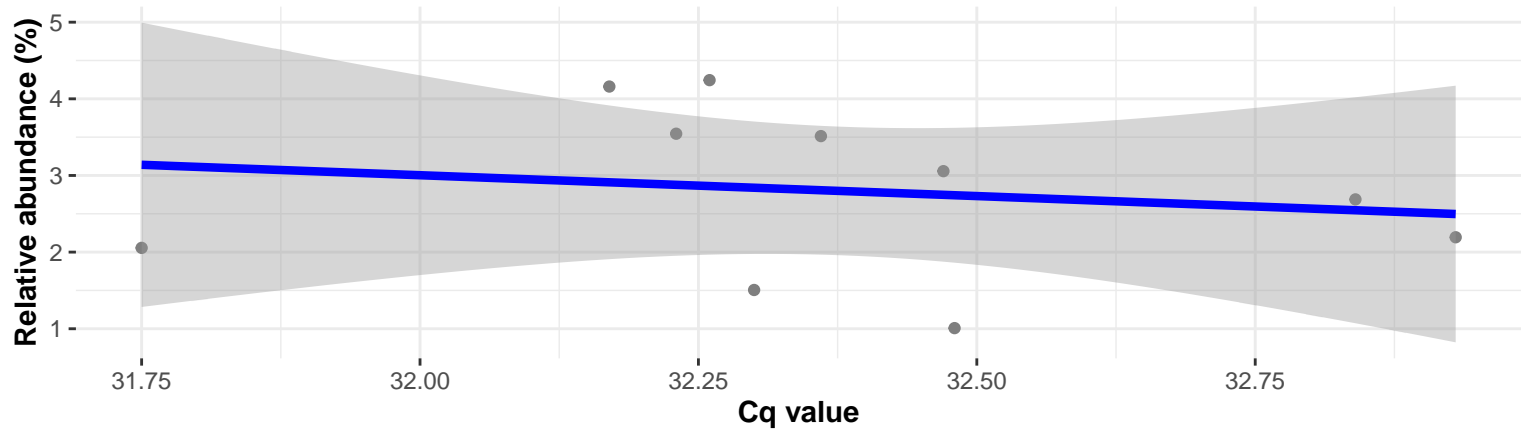


Correlation within: REF-PIM



Correlation within: REF-DIM

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



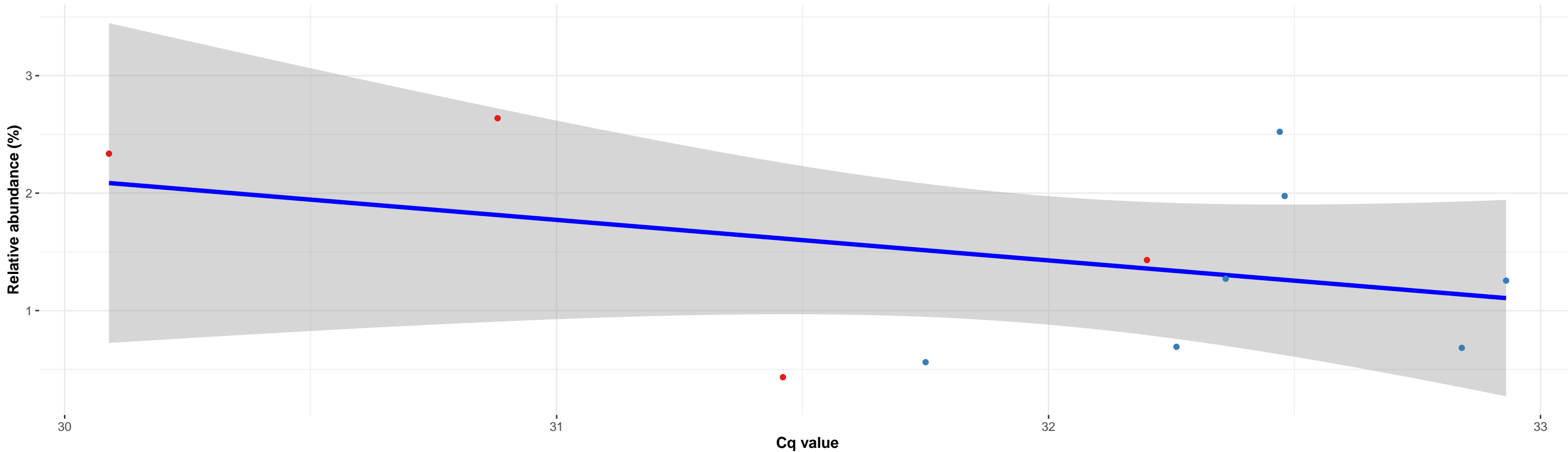
Correlation within: PCR-blank



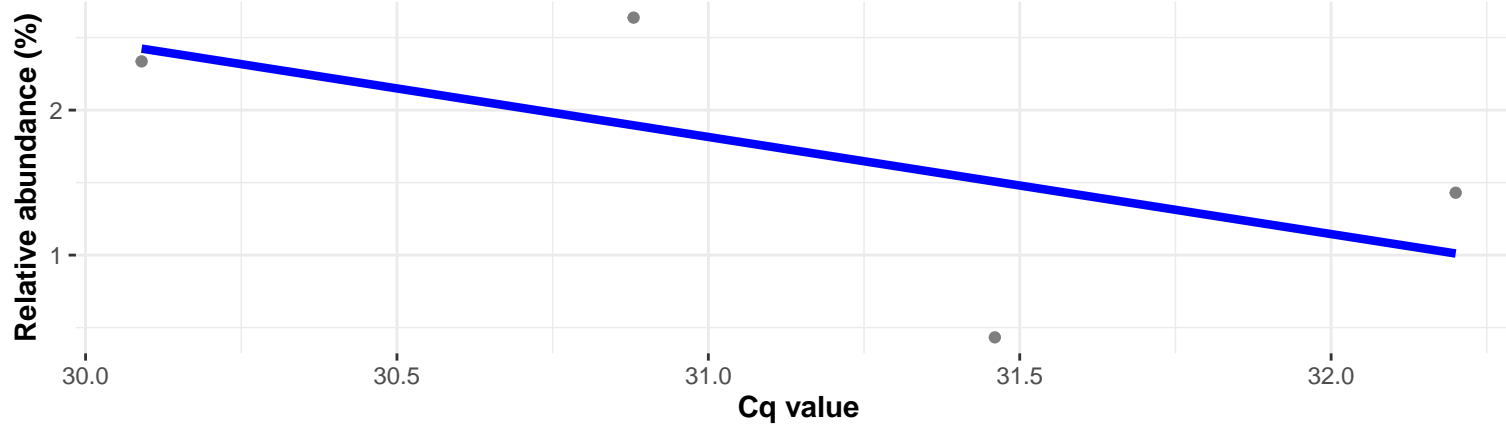
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; s\_\_Oceanobacillus caeni

Correlation with all samples

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

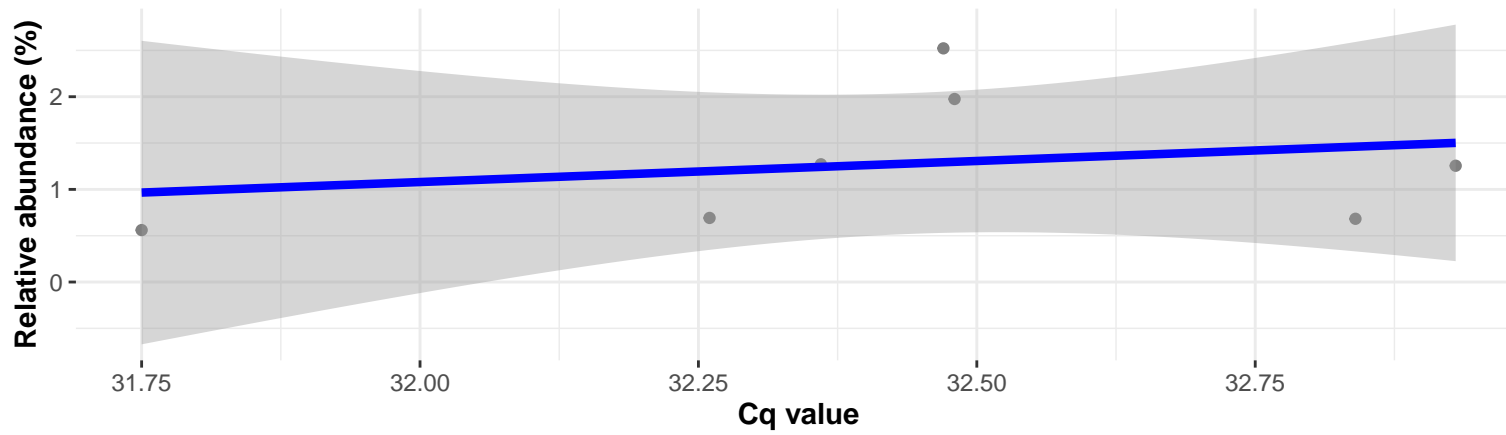


Correlation within: REF-PIM



Correlation within: REF-DIM

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



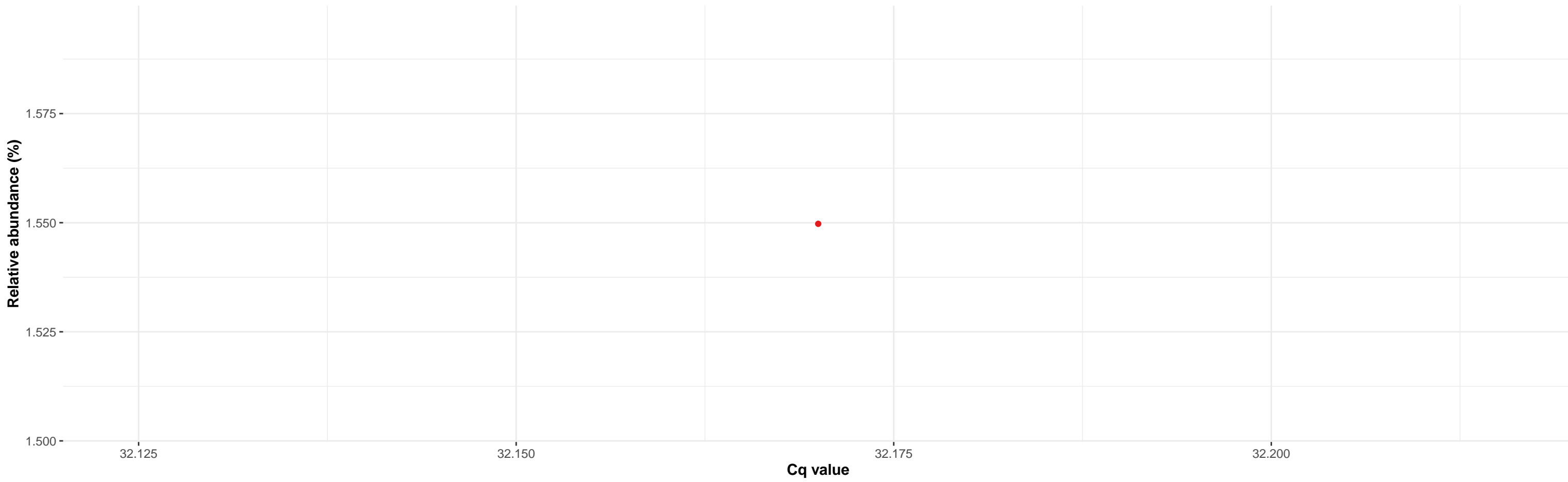
Correlation within: PCR-blank





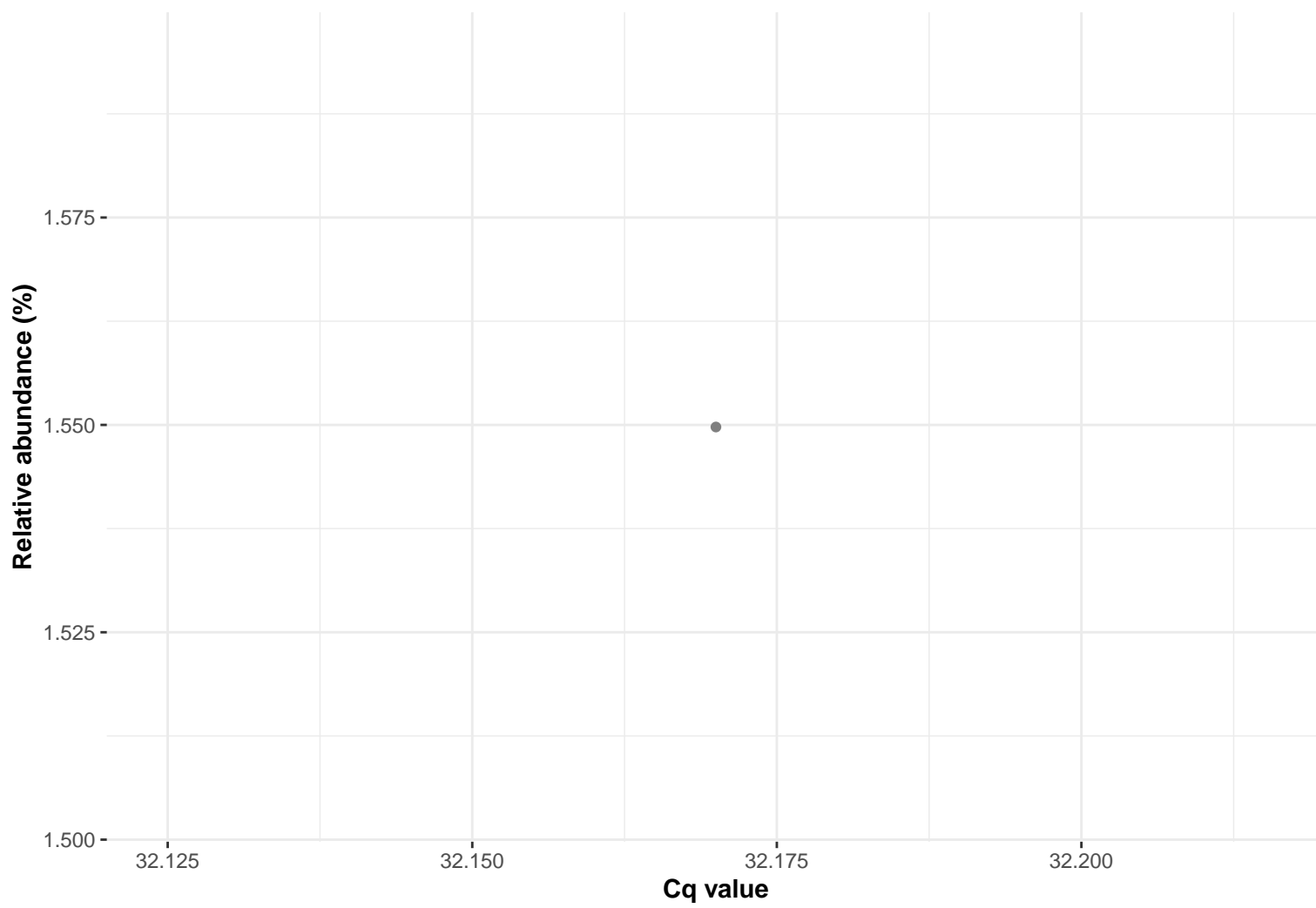
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Lysinibacillus; s\_\_uncultured bacterium

Correlation with all samples

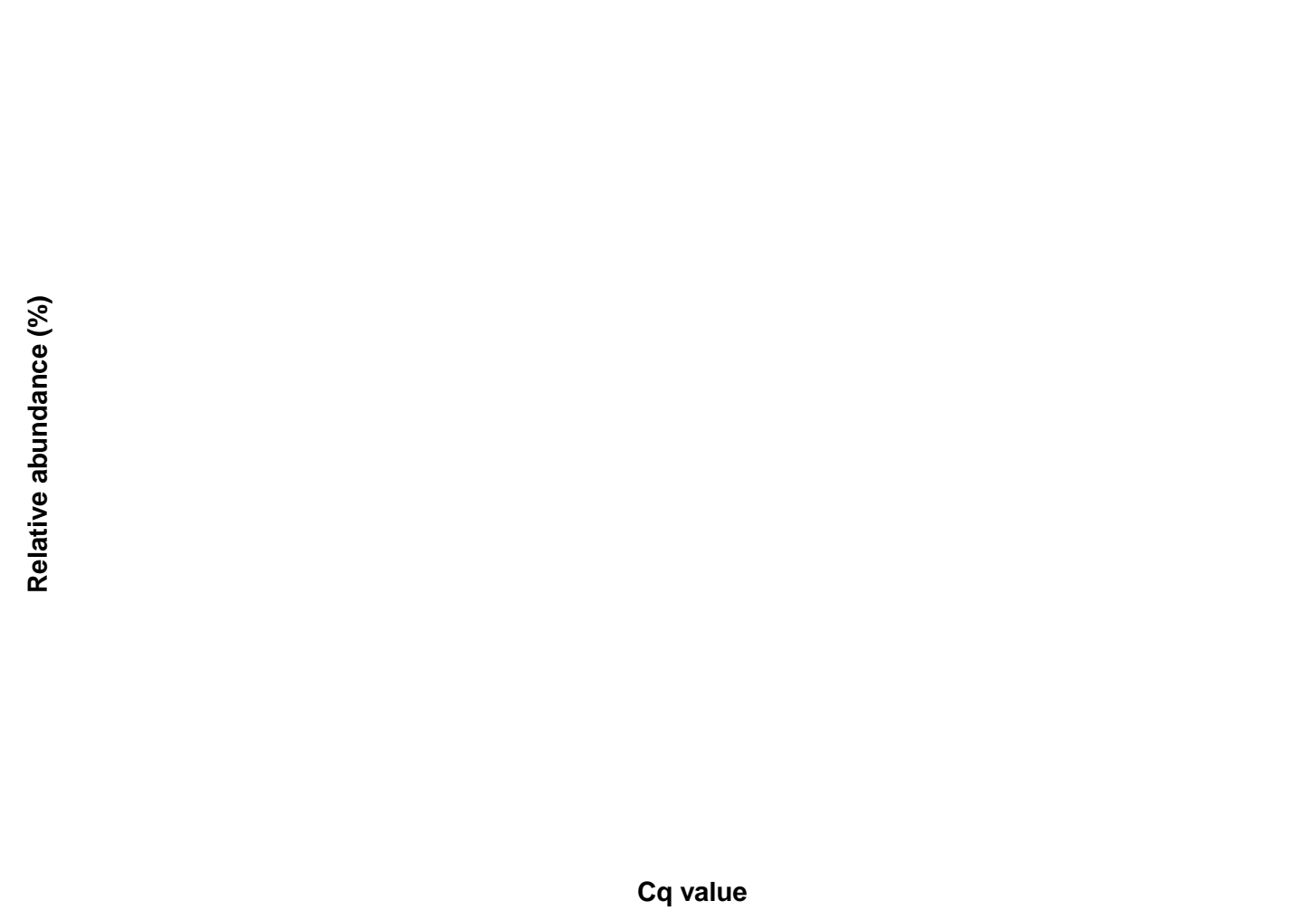


SampleType • REF-DIM

Correlation within: REF-DIM

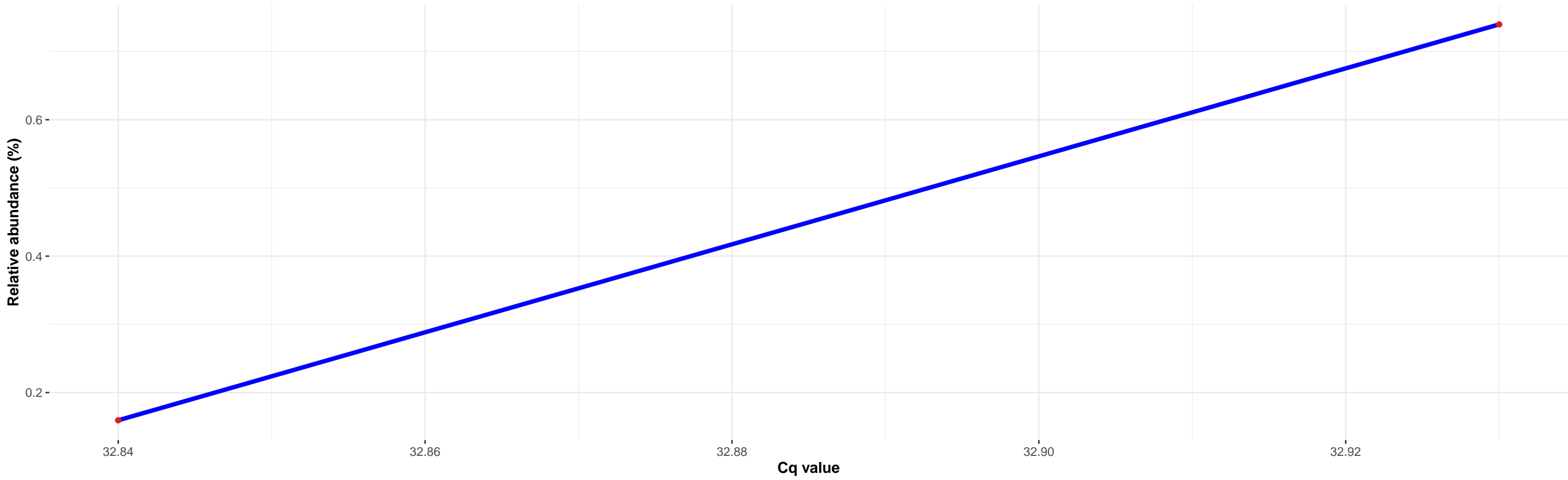


Correlation within: PCR-blank



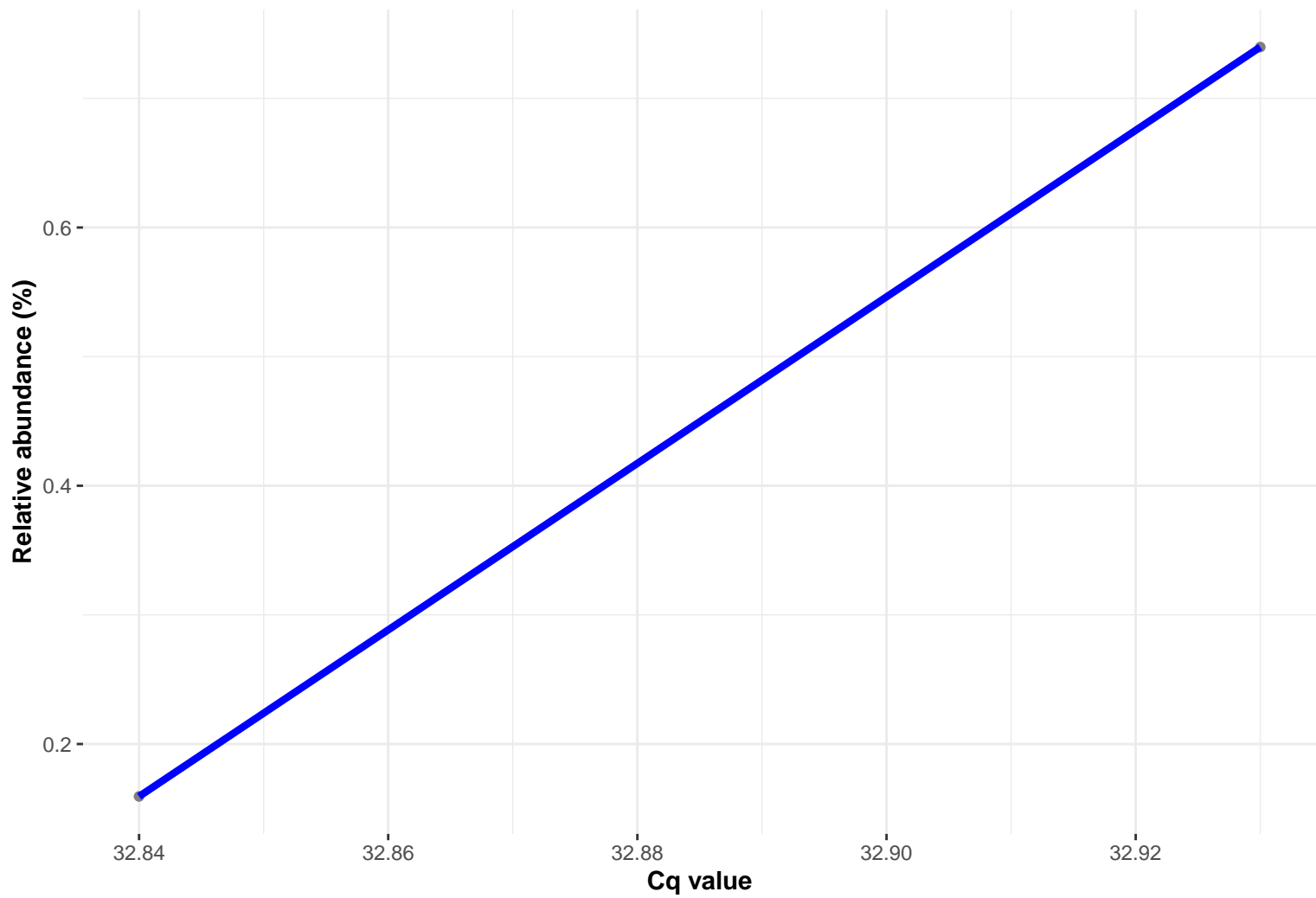
k\_\_Bacteria; p\_\_Cyanobacteria; c\_\_Melainabacteria; o\_\_Obscuribacterales; Ambiguous\_taxa; Ambiguous\_taxa; Ambiguous\_taxa

Correlation with all samples



SampleType • REF-DIM

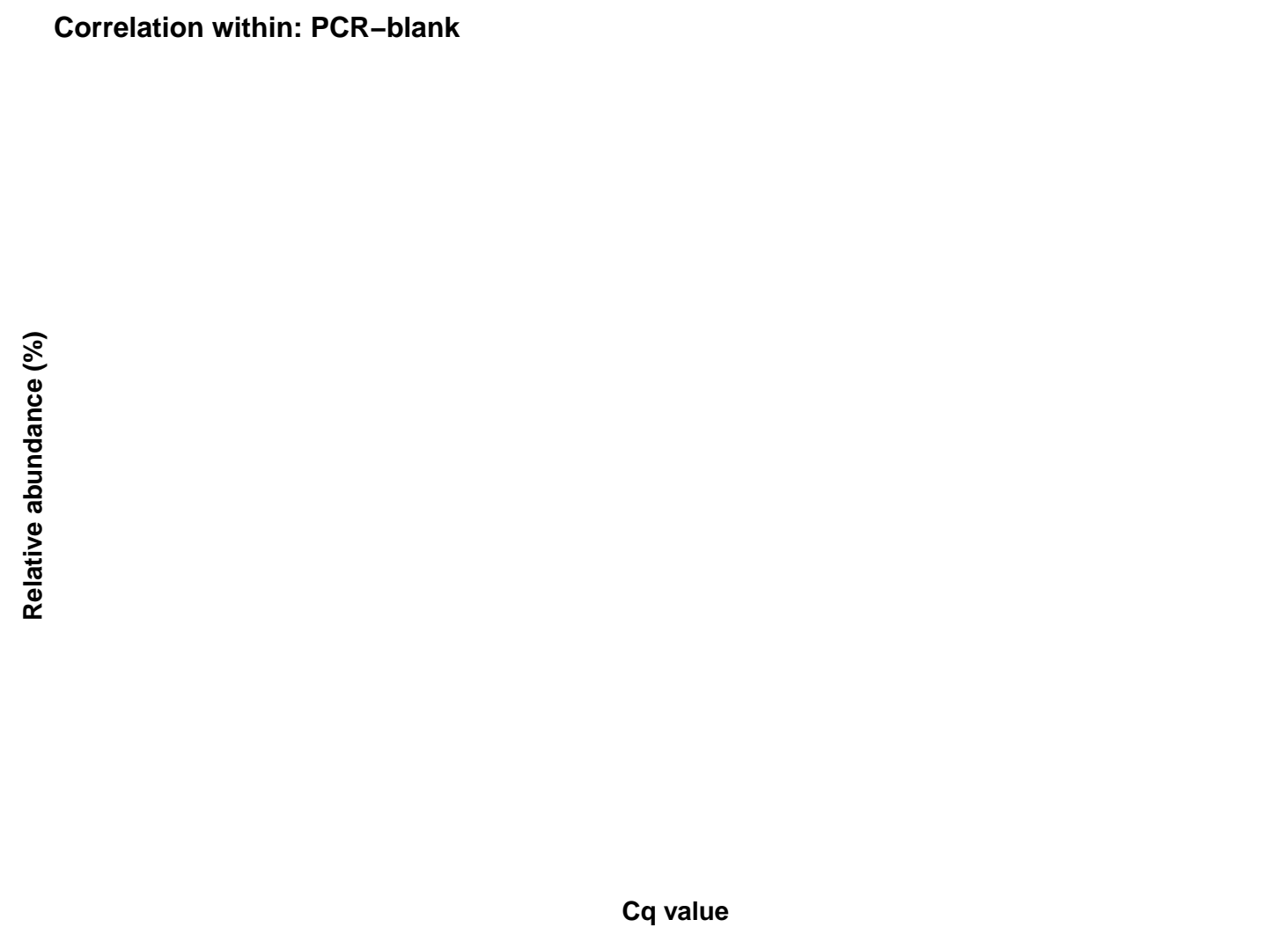
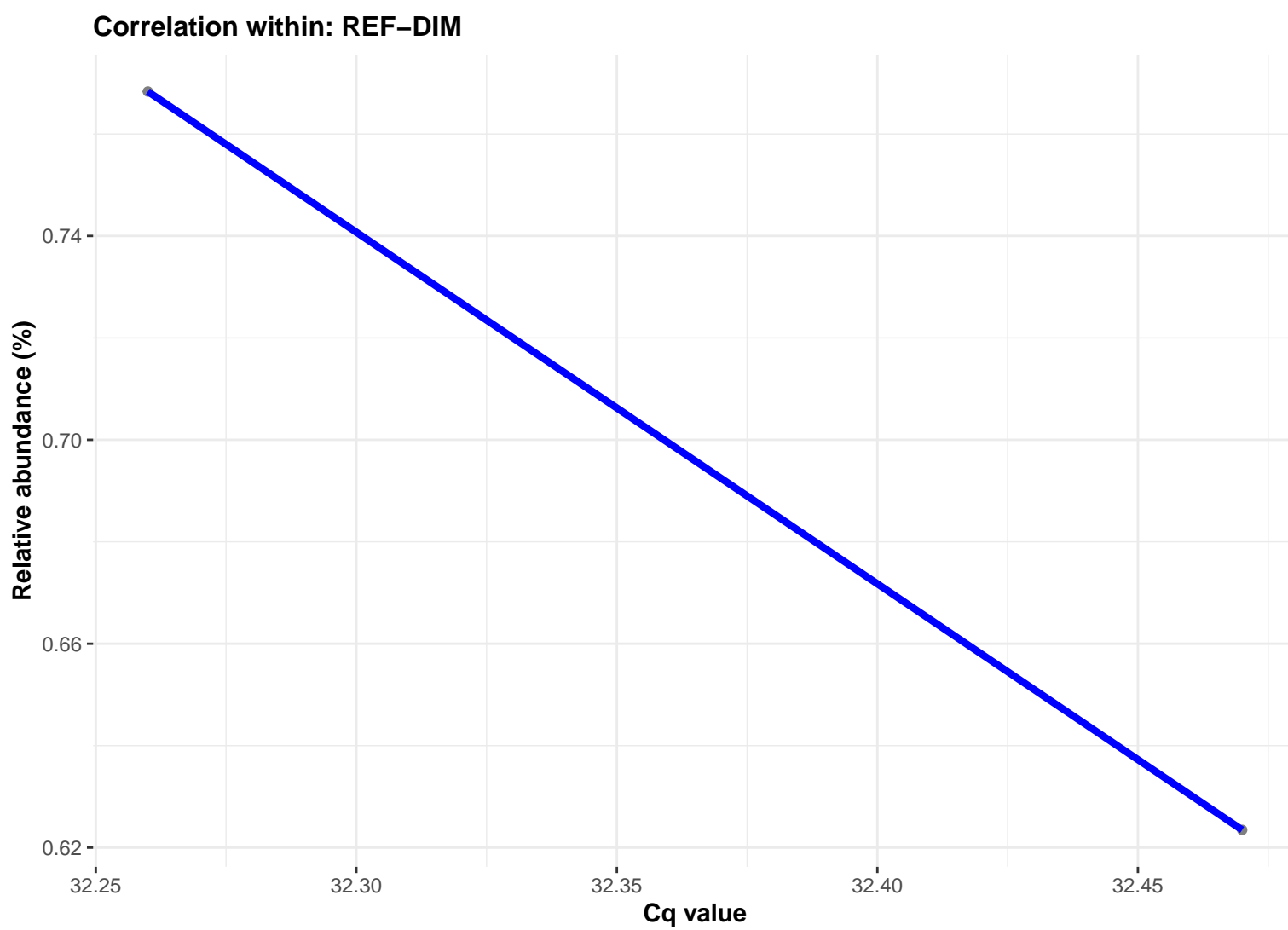
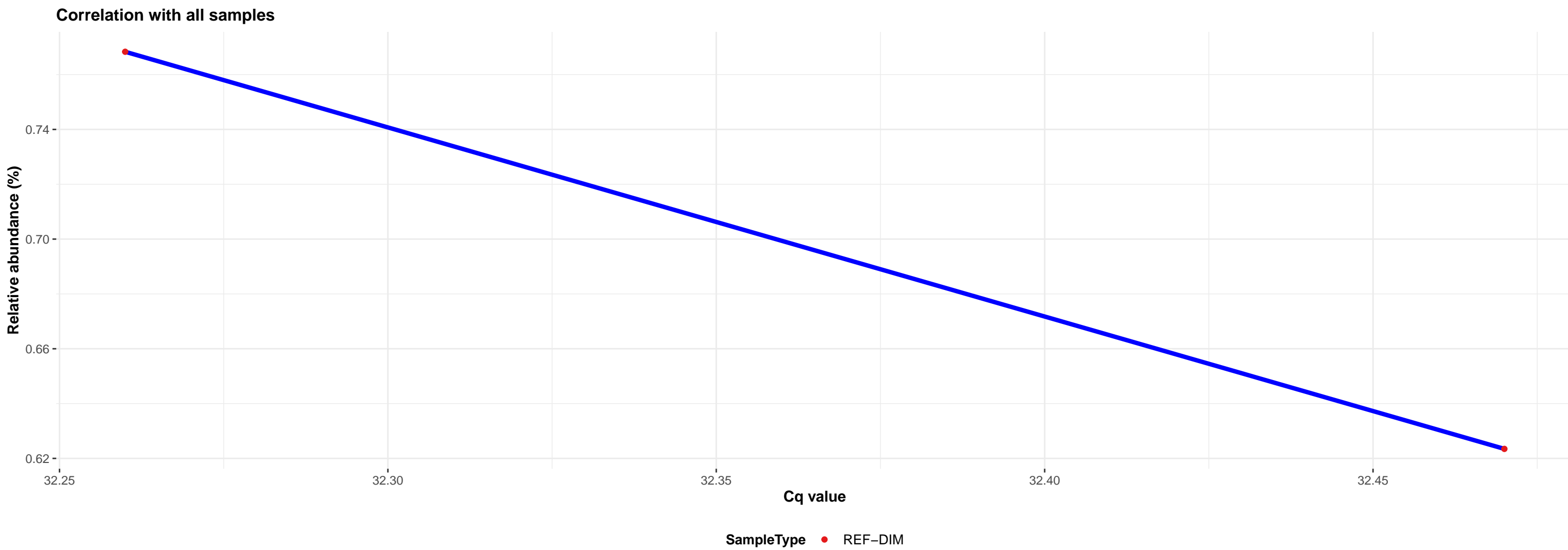
Correlation within: REF-DIM



Correlation within: PCR-blank



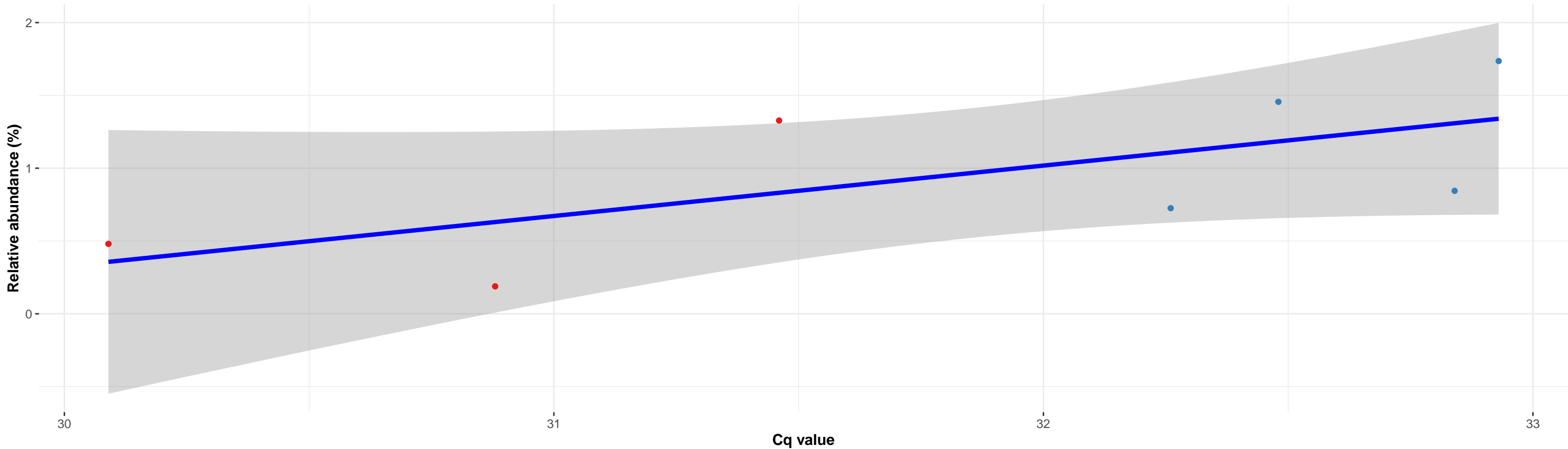
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; NA; NA



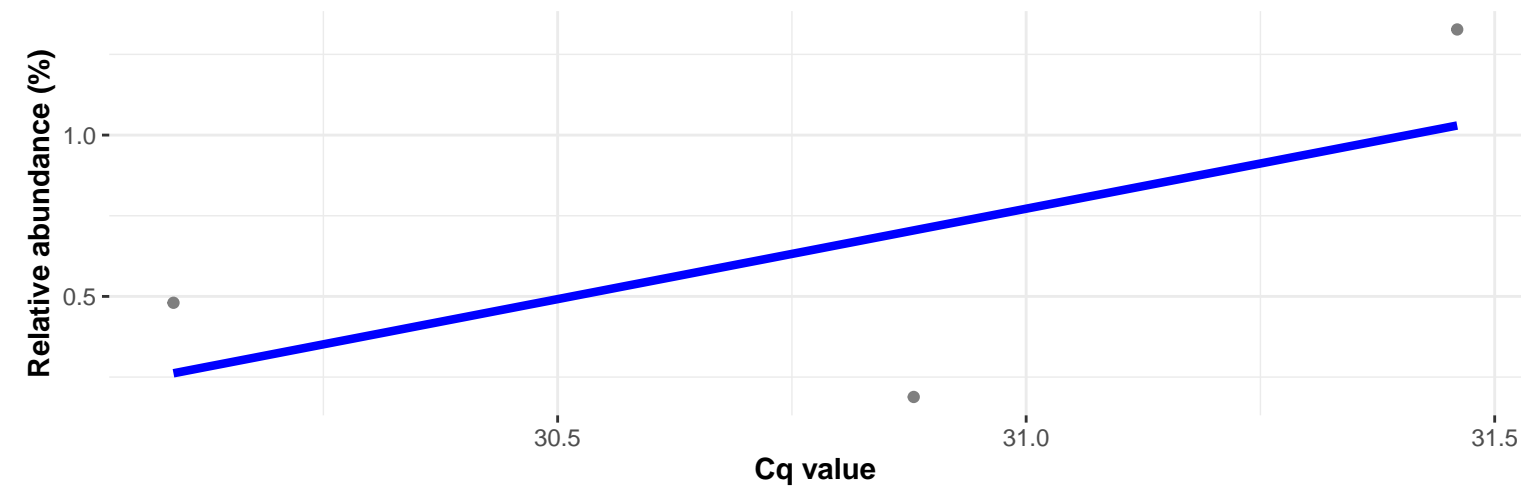
k\_\_Bacteria; p\_\_RsaHF231; c\_\_uncultured bacterium; o\_\_uncultured bacterium; f\_\_uncultured bacterium; g\_\_uncultured bacterium; s\_\_uncultured bacterium

Correlation with all samples

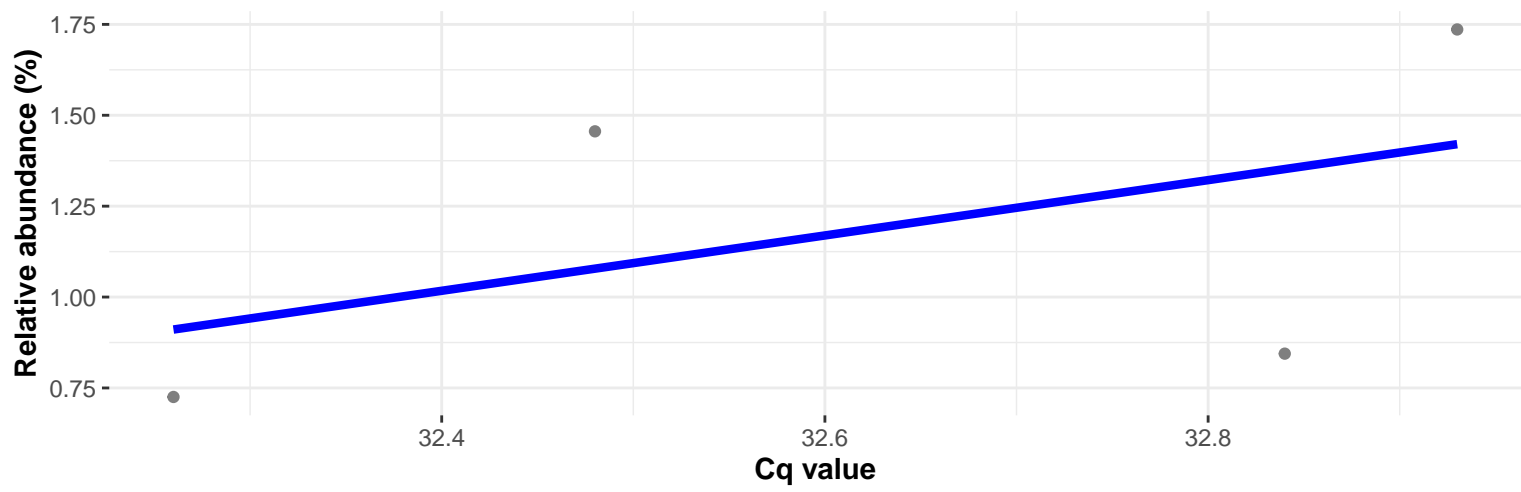
$\log_e(S) = 2.485$ ,  $p = 0.036$ ,  $\hat{\rho}_{\text{Spearman}} = 0.786$ ,  $CI_{95\%} [0.051, 0.969]$ ,  $n_{\text{pairs}} = 7$



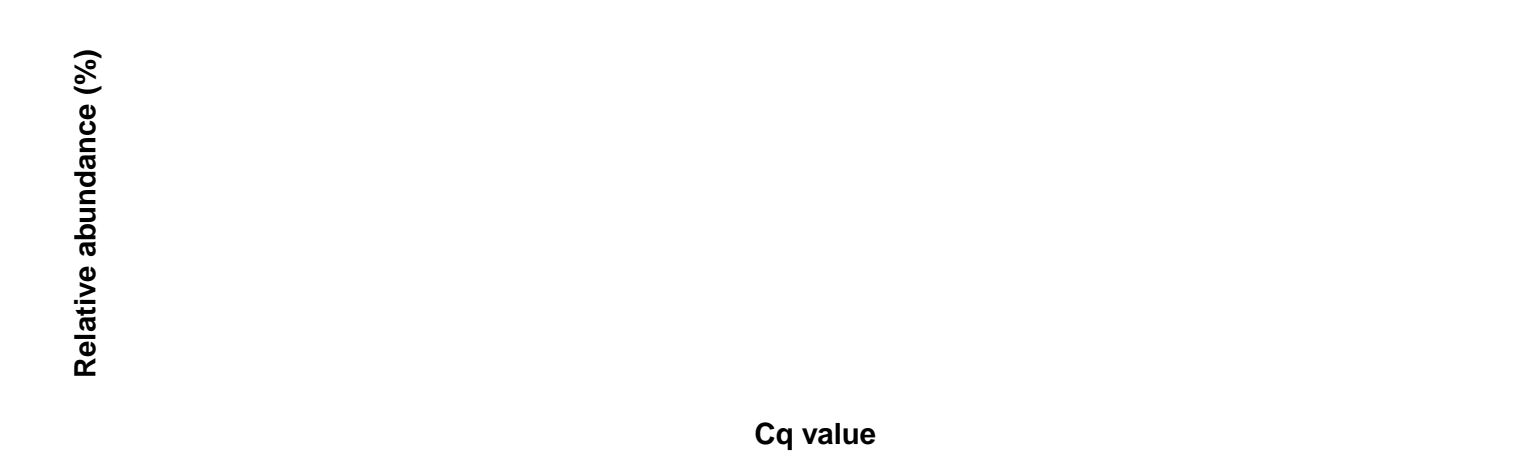
Correlation within: REF-PIM



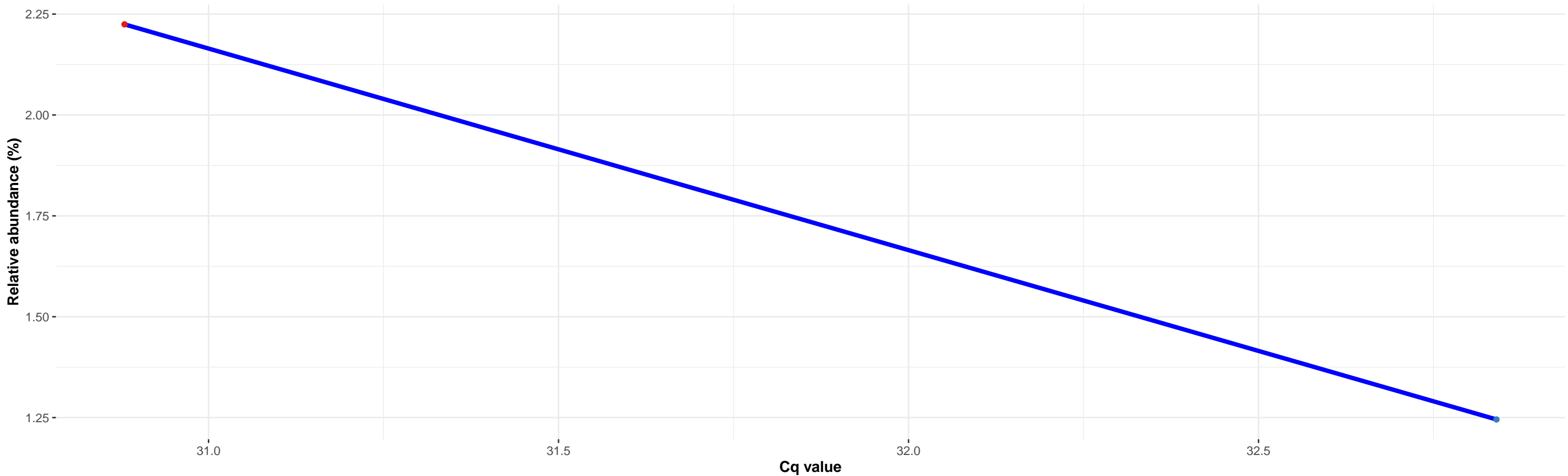
Correlation within: REF-DIM



Correlation within: PCR-blank

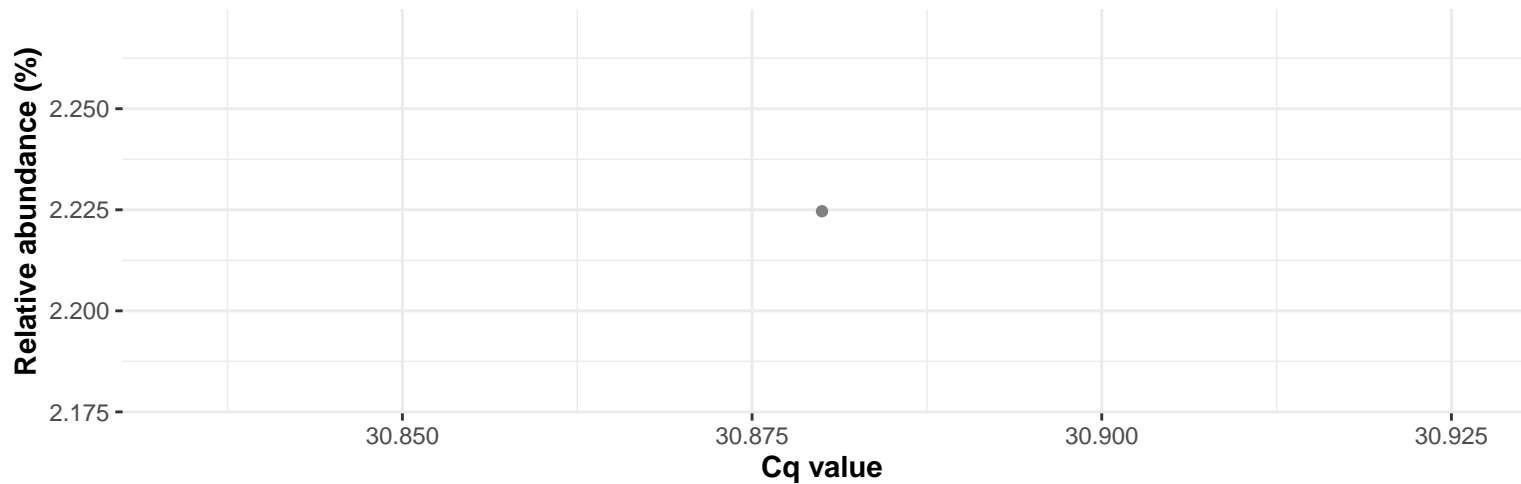


Correlation with all samples

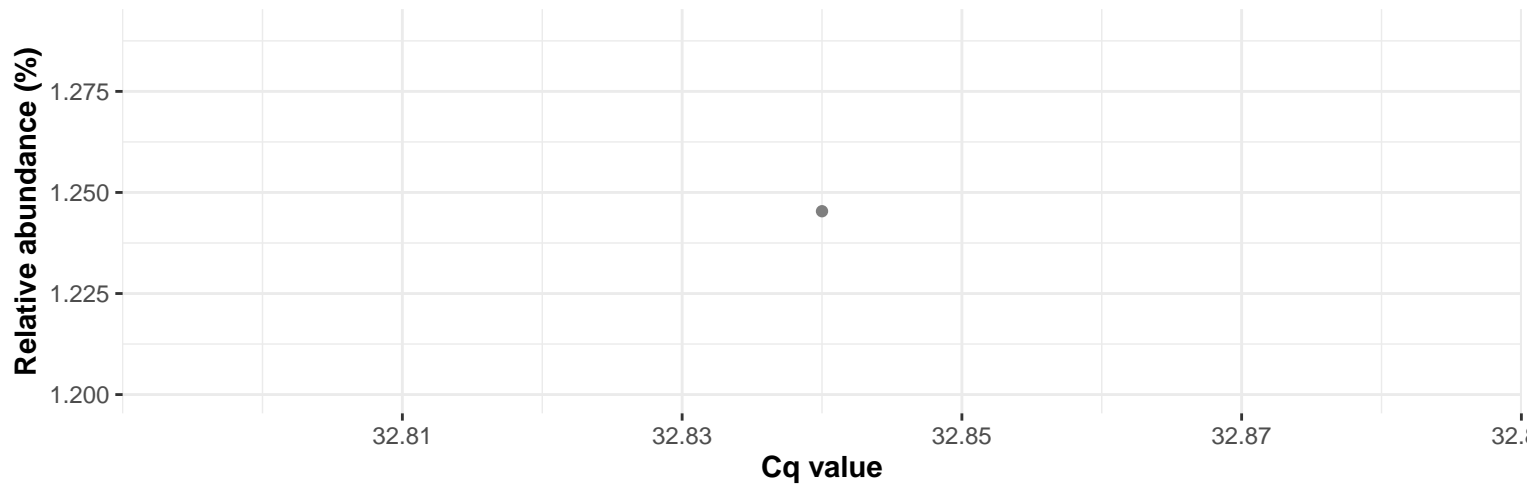


SampleType REF-PIM REF-DIM

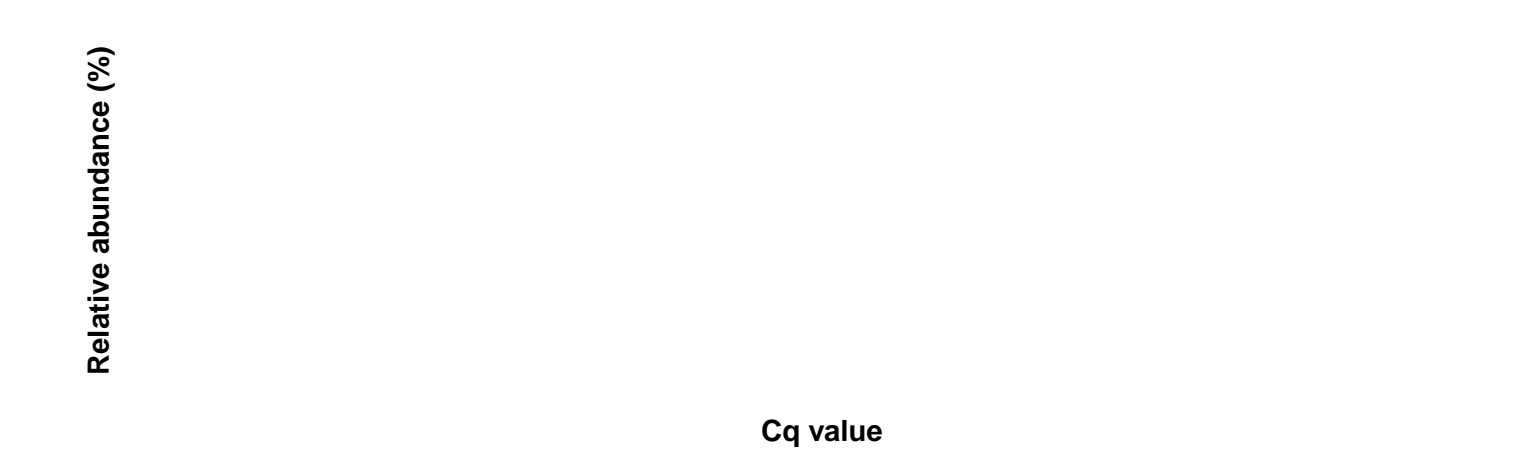
Correlation within: REF-PIM

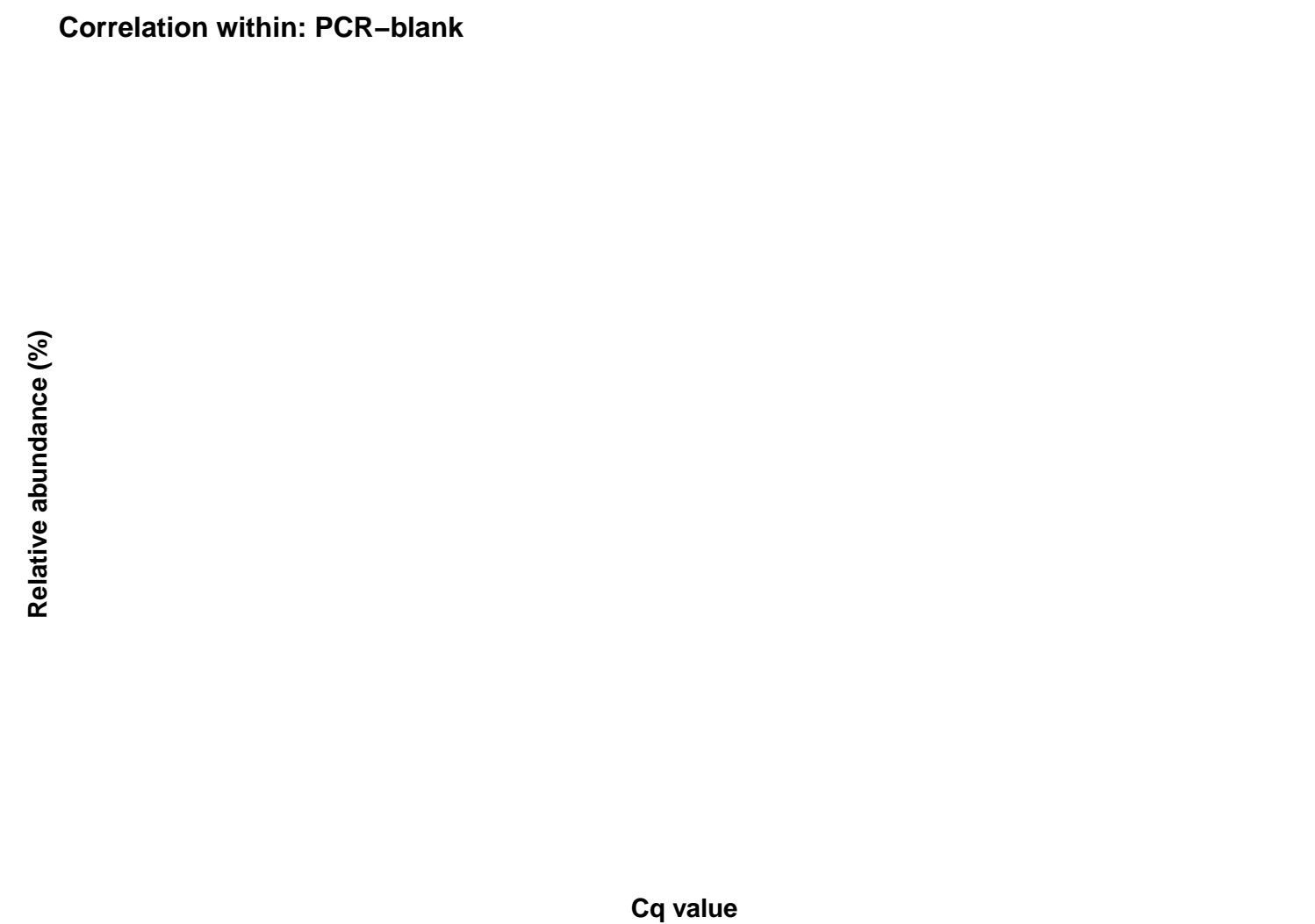
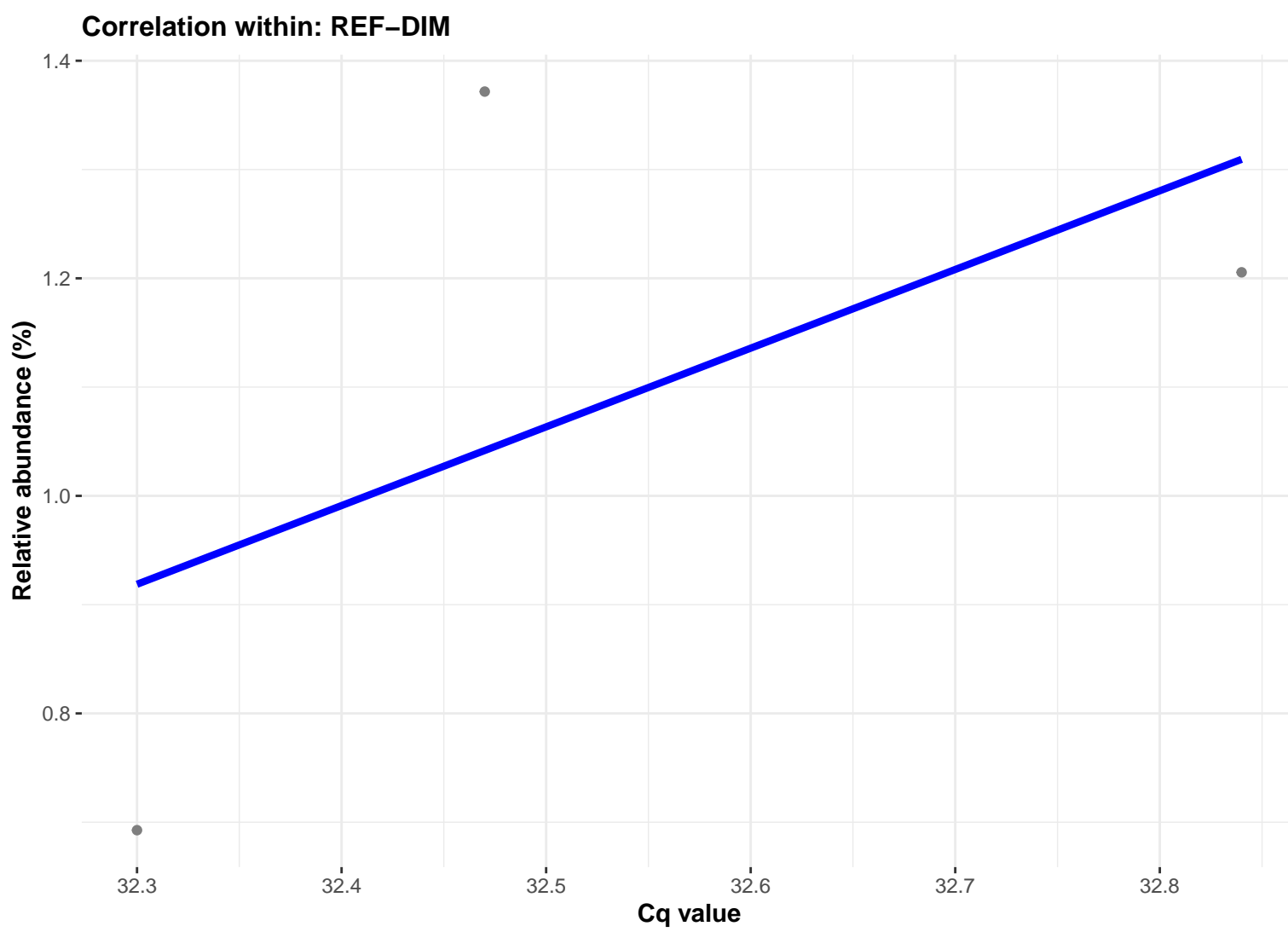
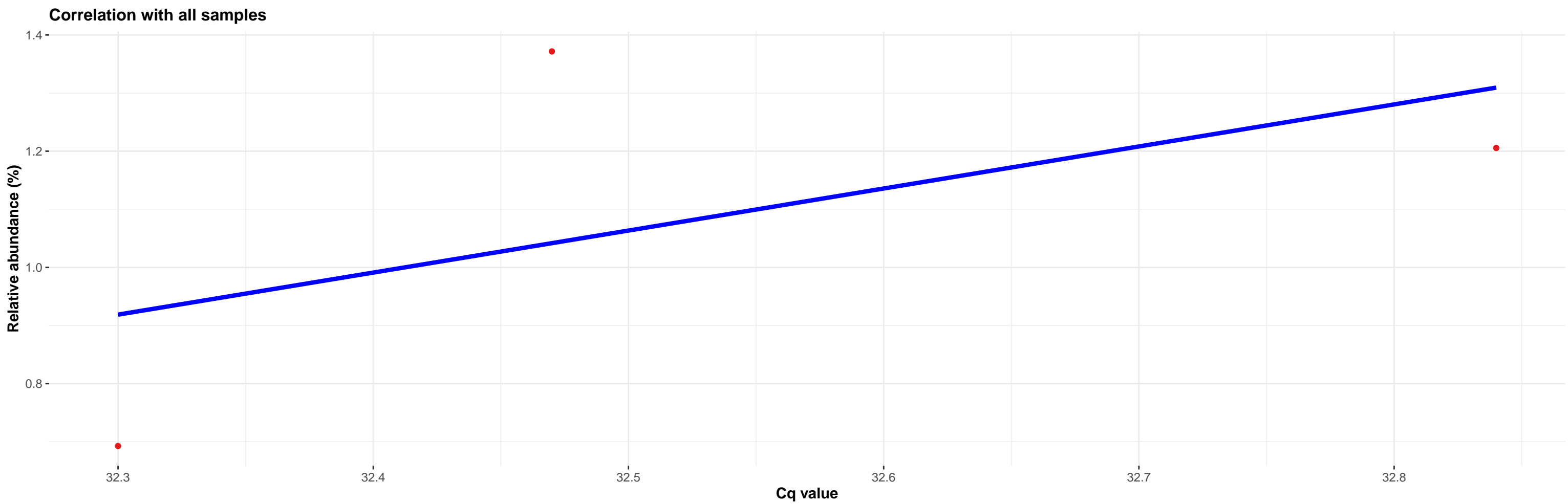


Correlation within: REF-DIM



Correlation within: PCR-blank

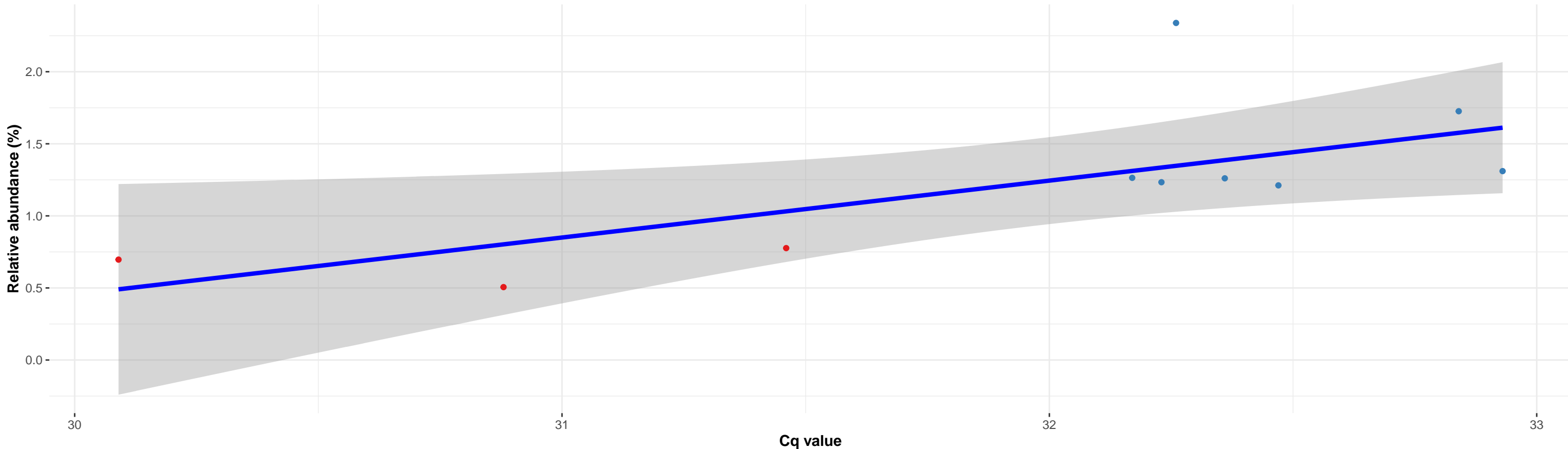




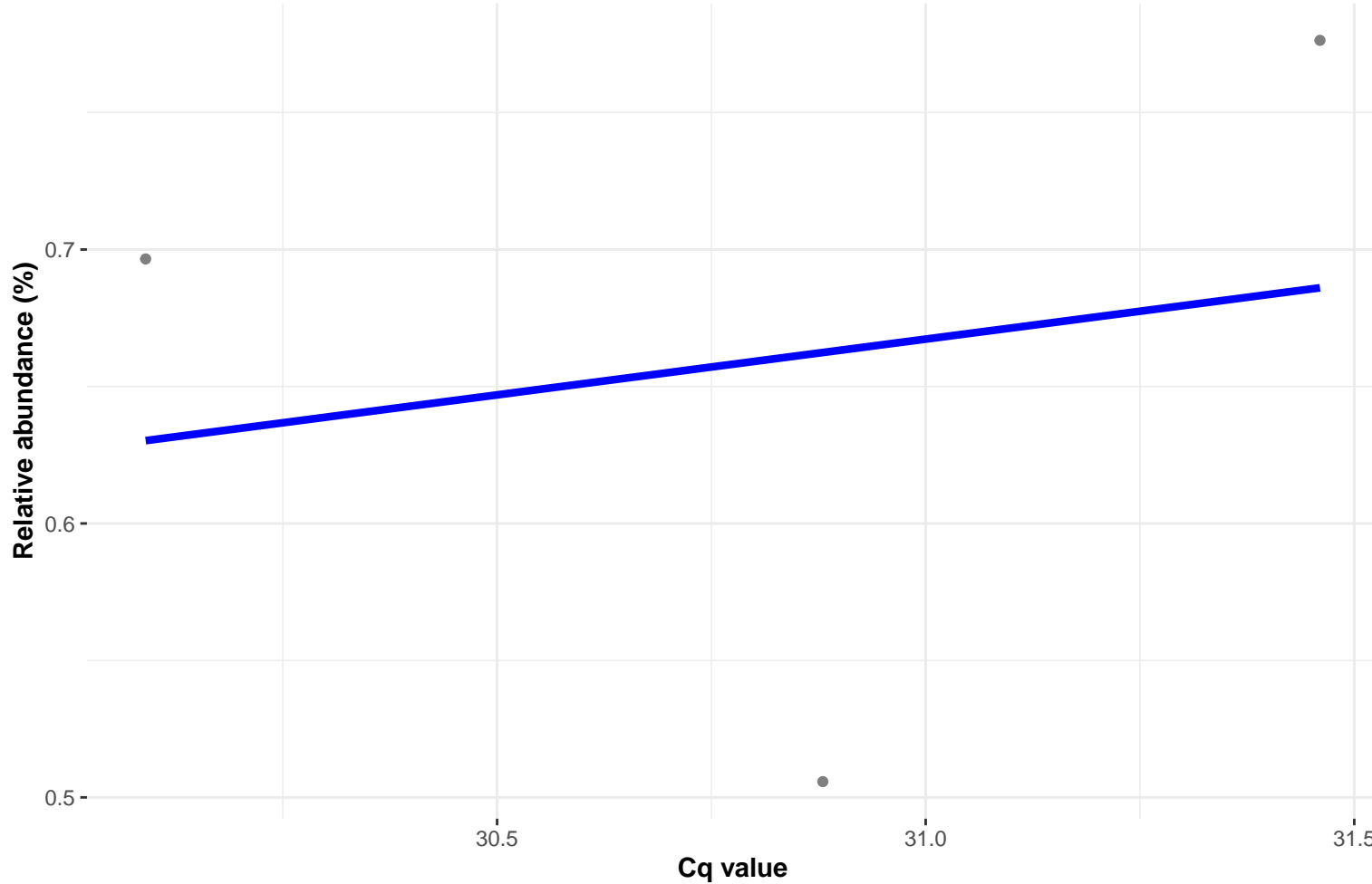
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; Ambiguous\_taxa

Correlation with all samples

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

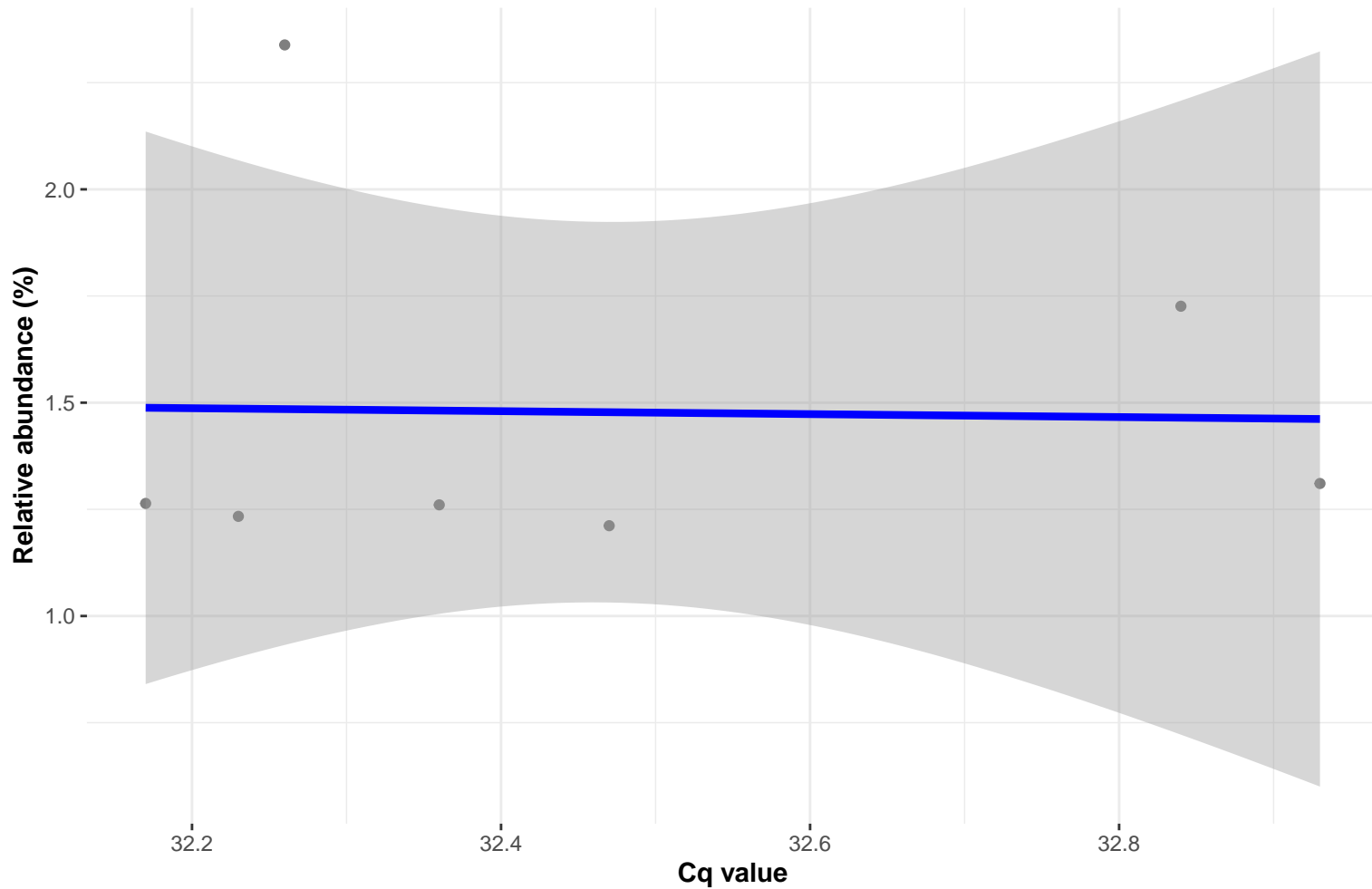


Correlation within: REF-PIM



Correlation within: REF-DIM

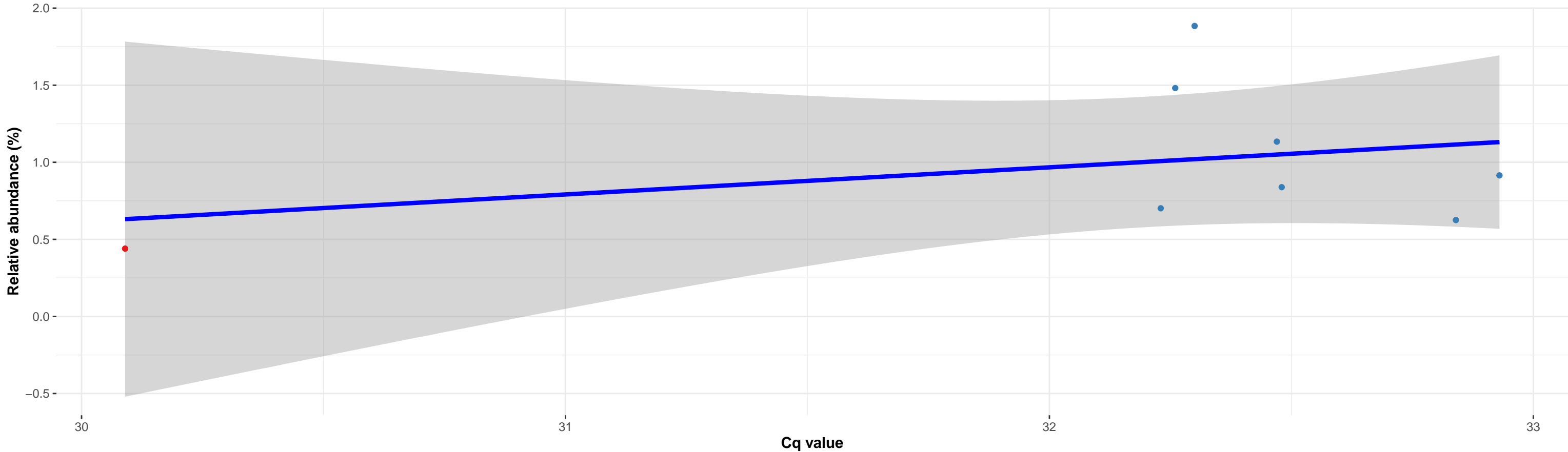
$\log_e(S) = 3.829$ ,  $p = 0.702$ ,  $\hat{\rho}_{\text{Spearman}} = 0.179$ ,  $CI_{95\%} [-0.680, 0.830]$ ,  $n_{\text{pairs}} = 7$



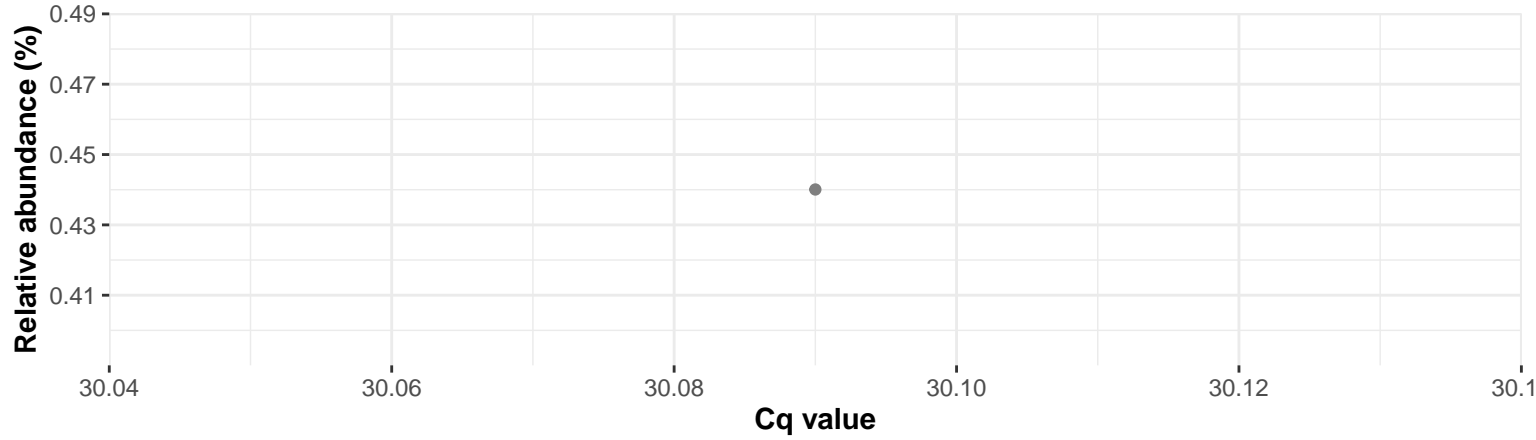
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; NA; NA

Correlation with all samples

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

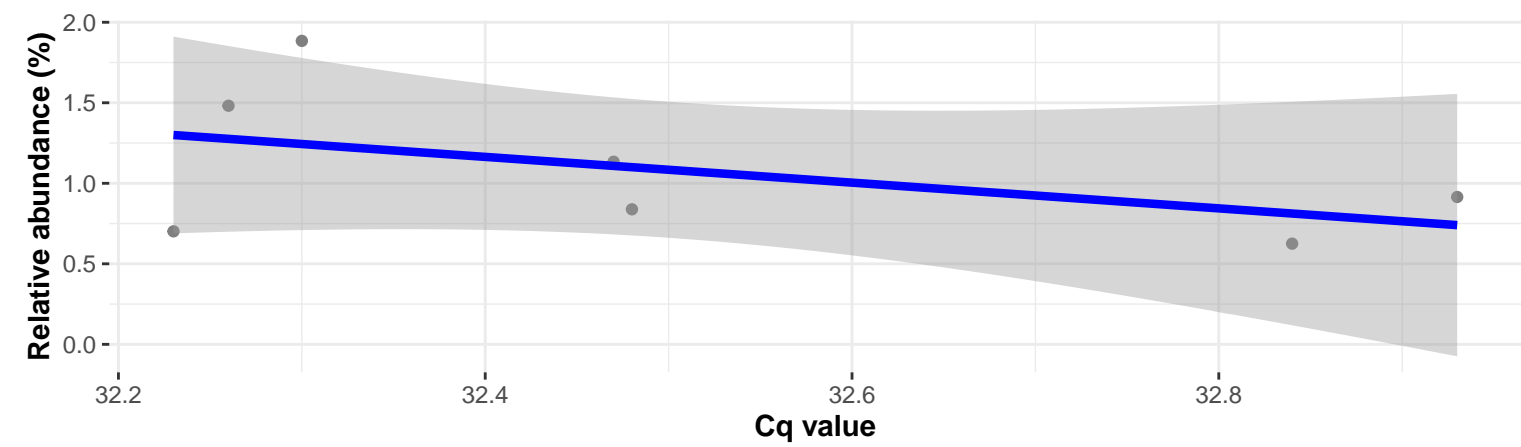


Correlation within: REF-PIM

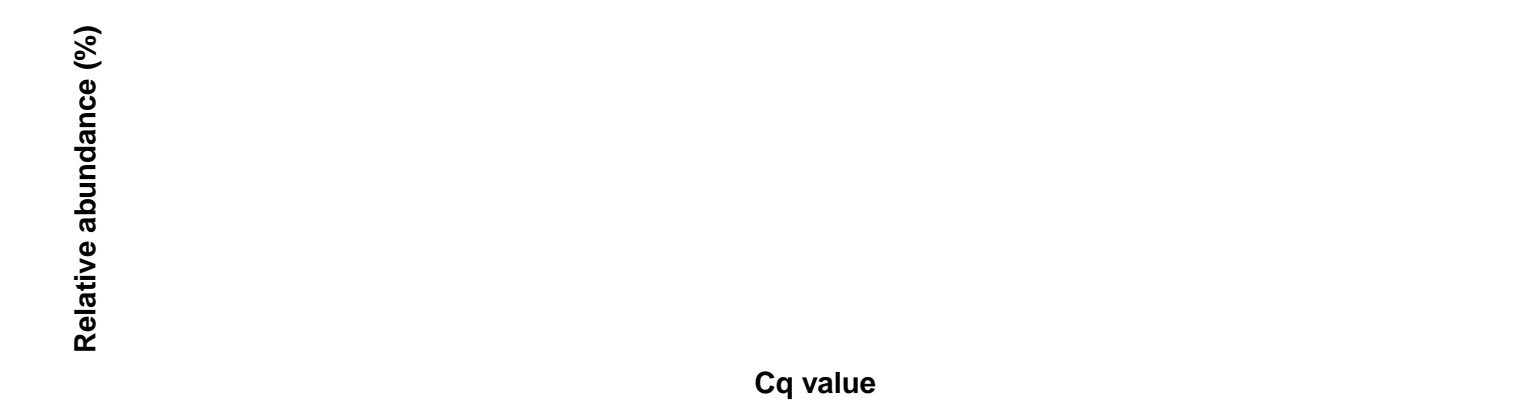


Correlation within: REF-DIM

$\log_e(S) = 4.277, p = 0.535, \hat{\rho}_{\text{Spearman}} = -0.286, \text{CI}_{95\%} [-0.862, 0.614], n_{\text{pairs}} = 7$



Correlation within: PCR-blank

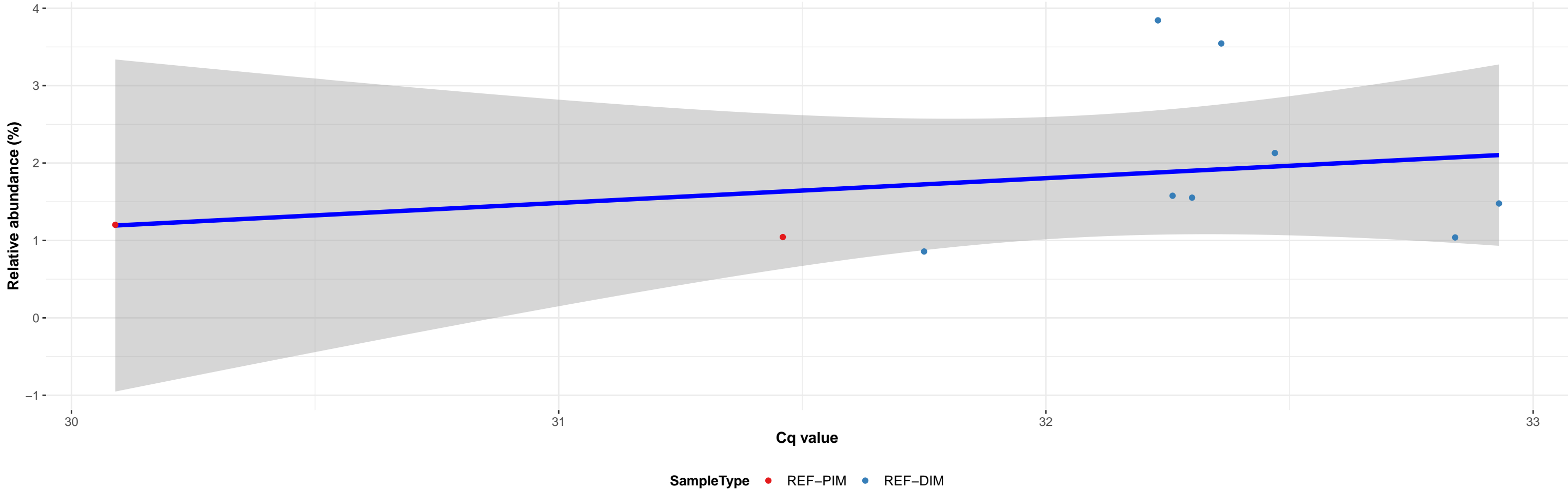




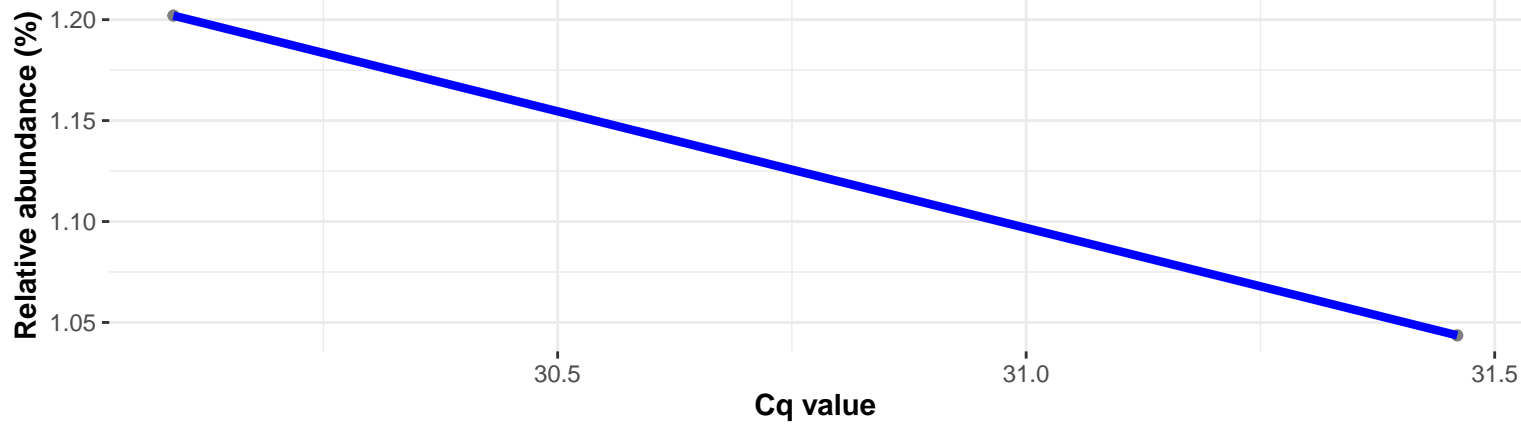
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Brevibacteriaceae; g\_\_Brevibacterium; NA

Correlation with all samples

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

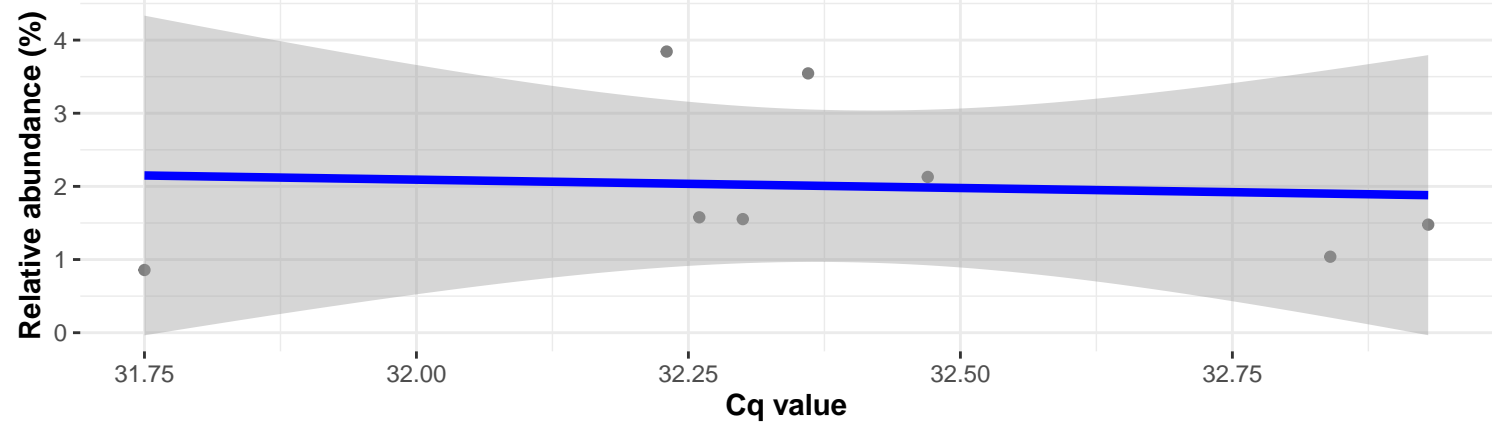


Correlation within: REF-PIM

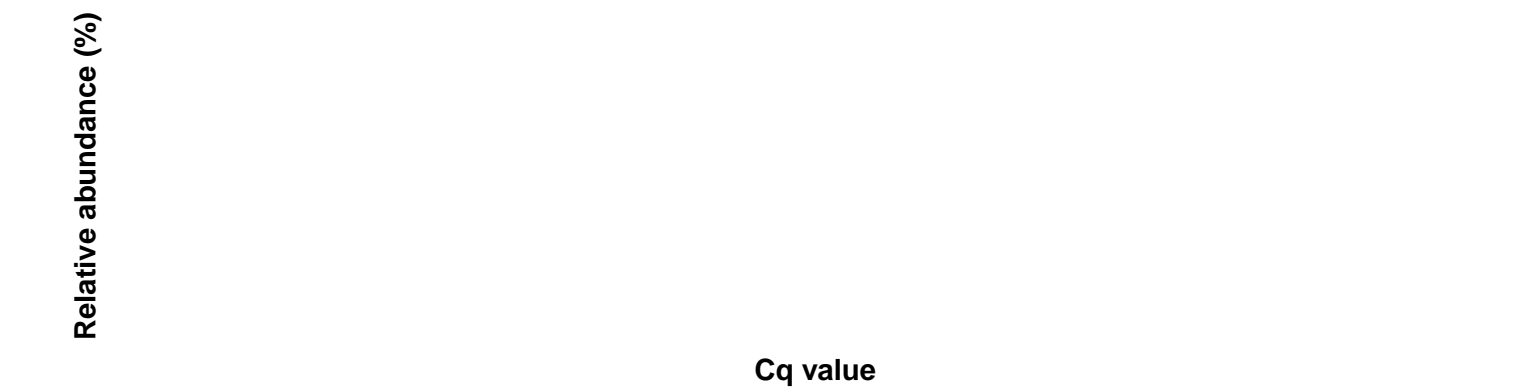


Correlation within: REF-DIM

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



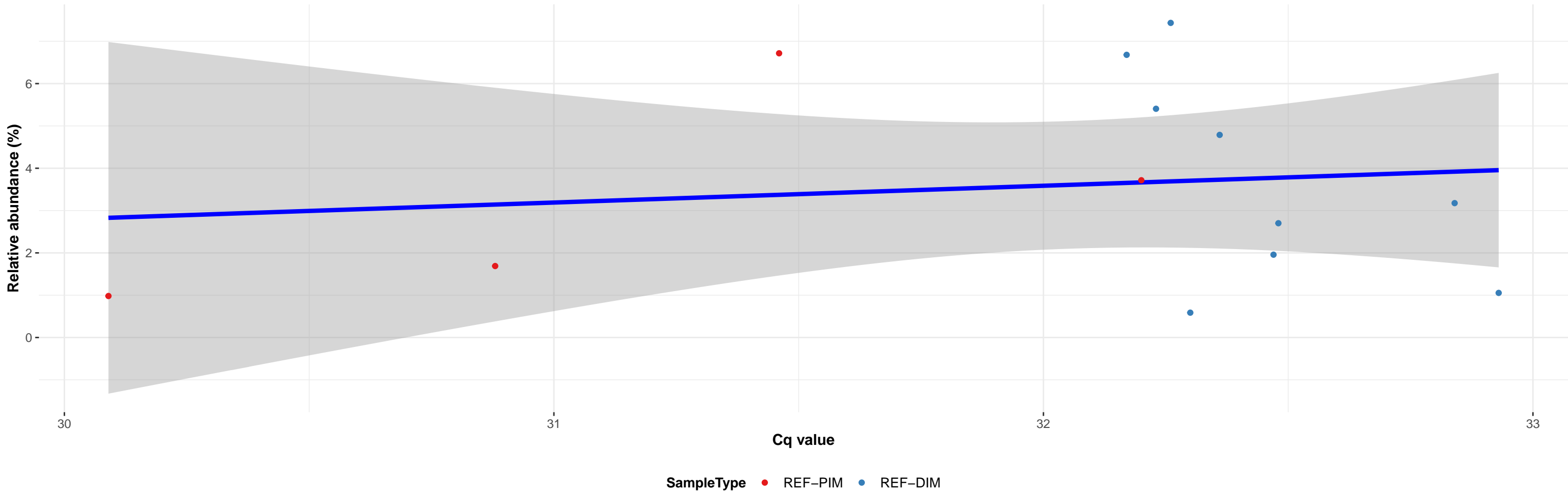
Correlation within: PCR-blank



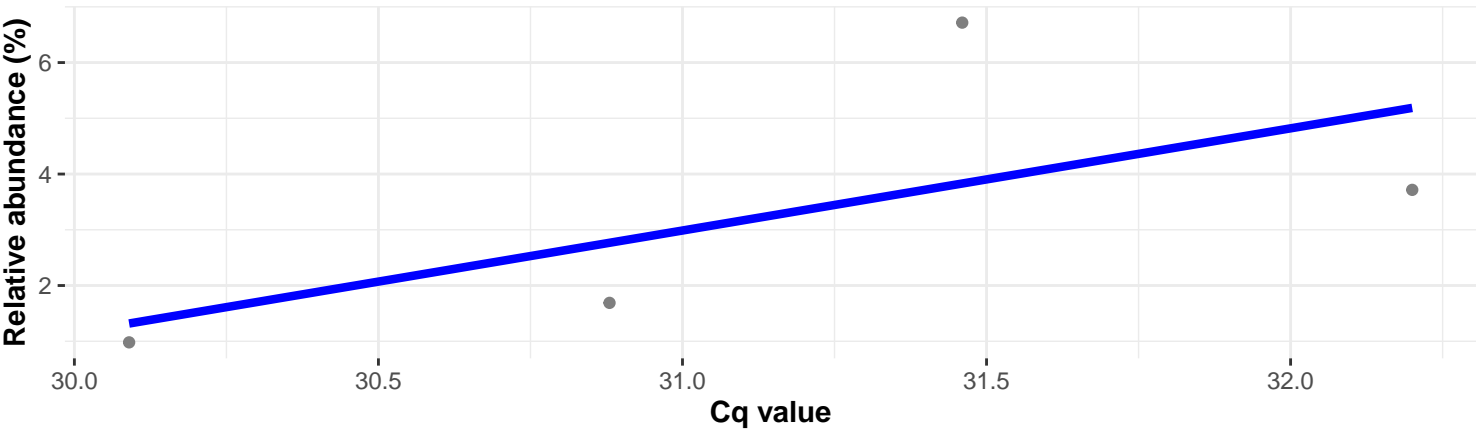
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Ralstonia; s\_\_uncultured Ralstonia sp.

Correlation with all samples

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

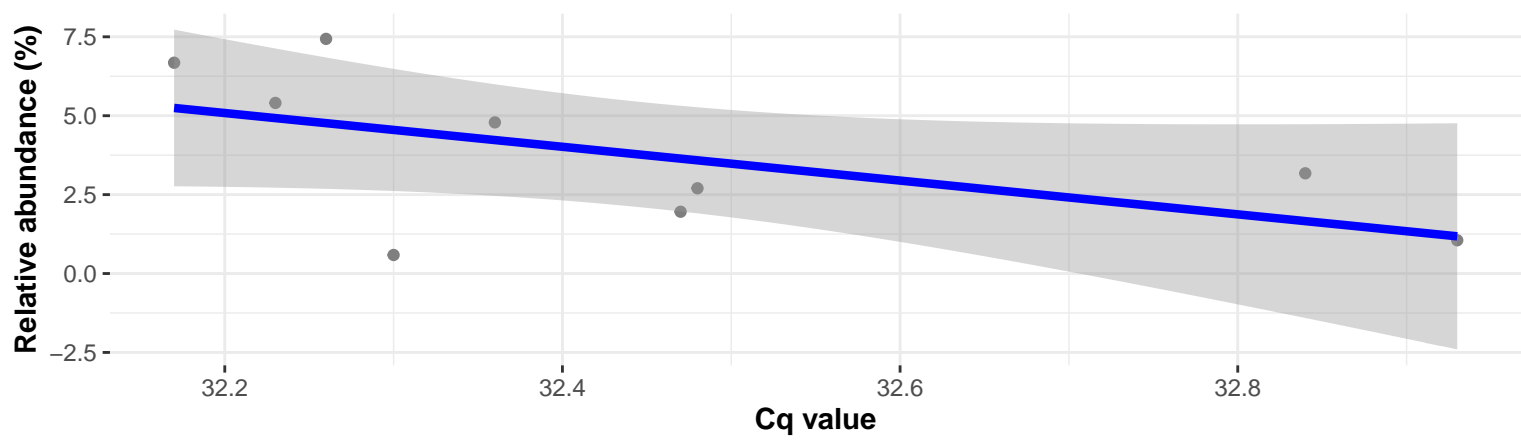


Correlation within: REF-PIM



Correlation within: REF-DIM

$\log_e(S) = 5.278$ ,  $p = 0.067$ ,  $\hat{\rho}_{\text{Spearman}} = -0.633$ ,  $CI_{95\%} [-0.917, 0.077]$ ,  $n_{\text{pairs}} = 9$



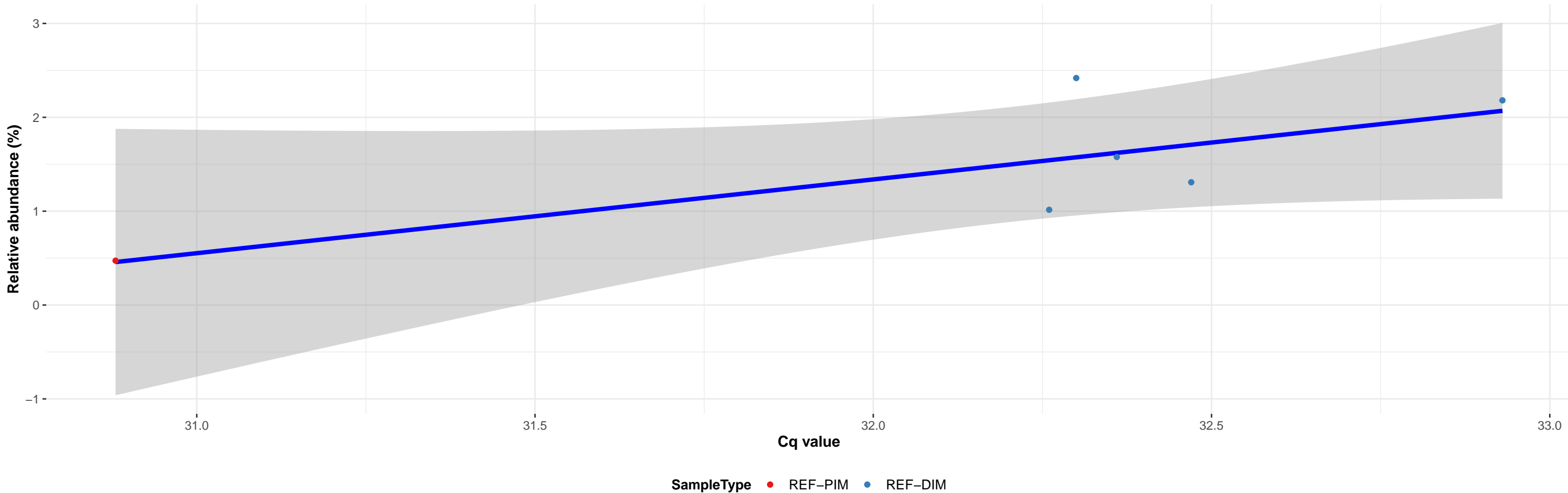
Correlation within: PCR-blank



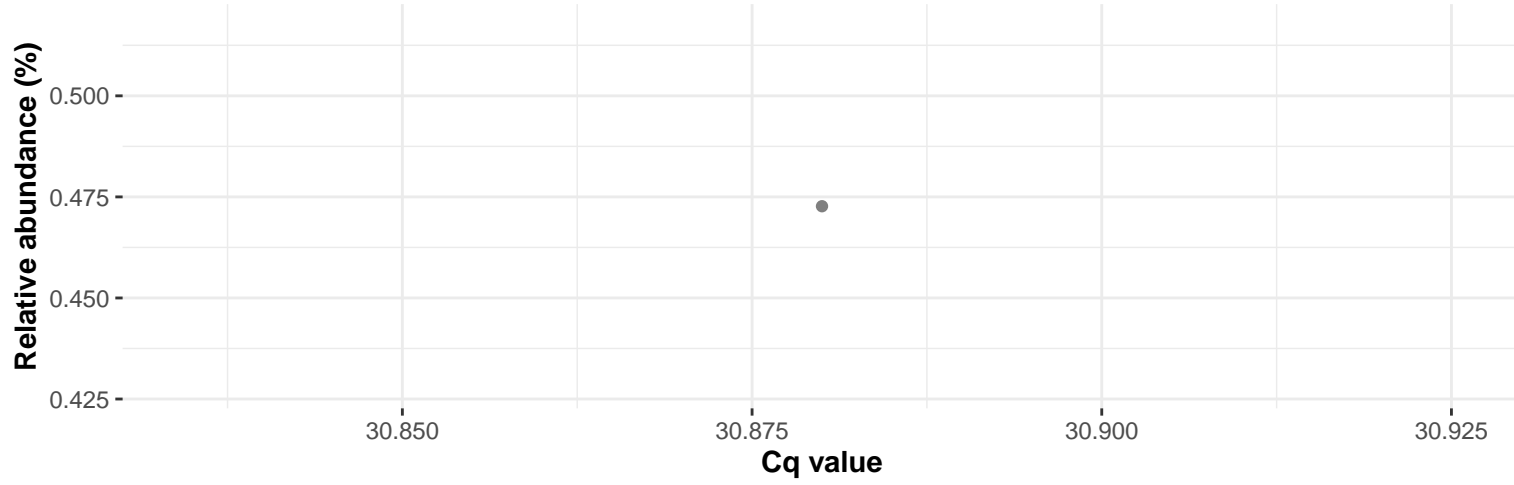
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Beutenbergiaceae; NA; NA

Correlation with all samples

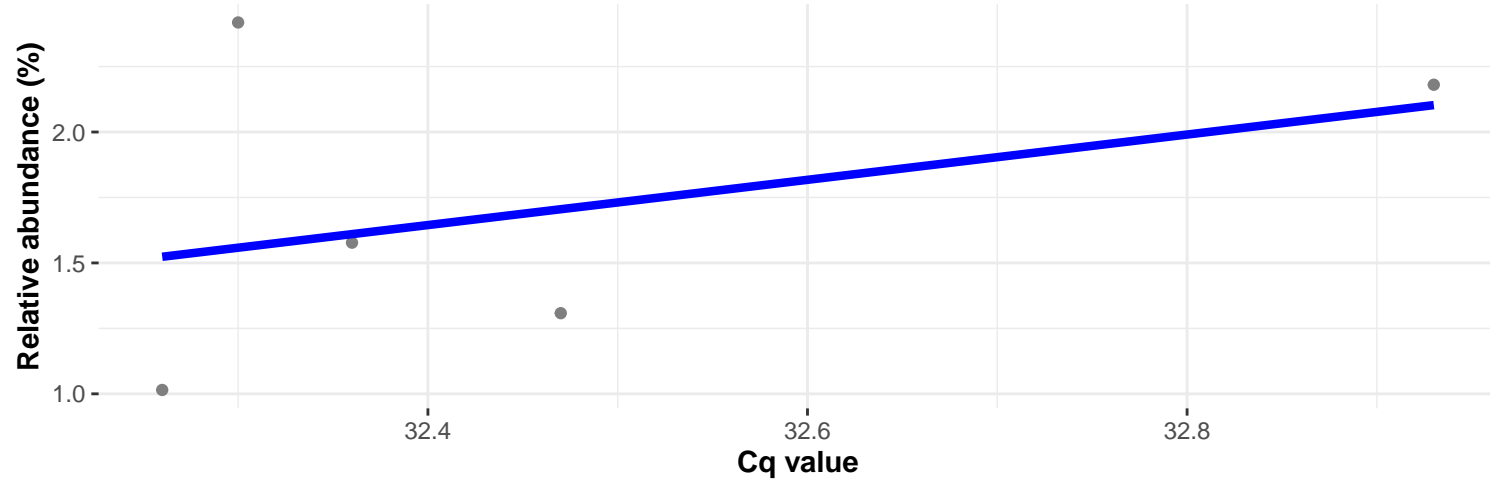
$\log_e(S) = 2.639$ ,  $p = 0.208$ ,  $\hat{\rho}_{\text{Spearman}} = 0.600$ ,  $CI_{95\%} [-0.440, 0.953]$ ,  $n_{\text{pairs}} = 6$



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 (%)

Correlation within: PCR–blank

Cq value

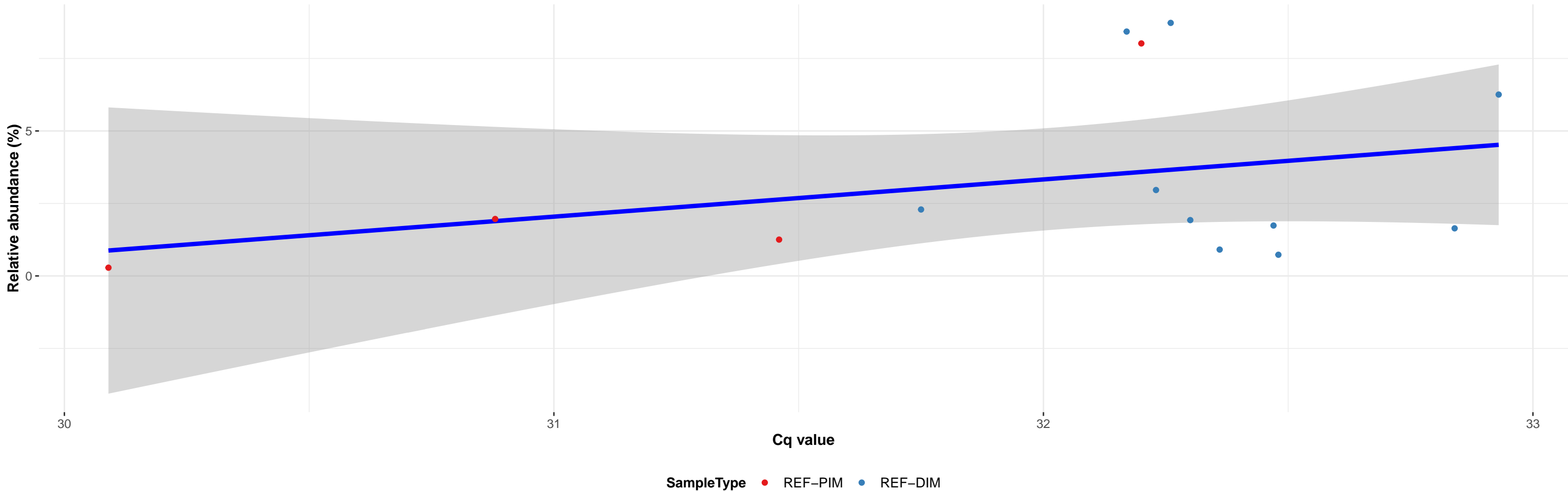
Relative abundance (%)

Cq value

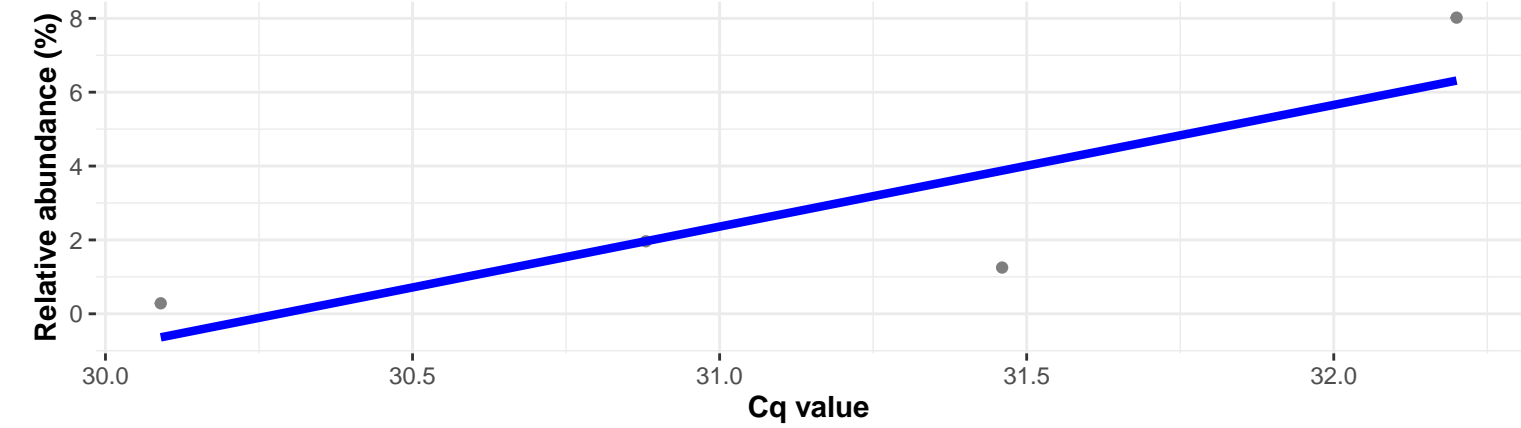
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Curvibacter; NA

Correlation with all samples

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

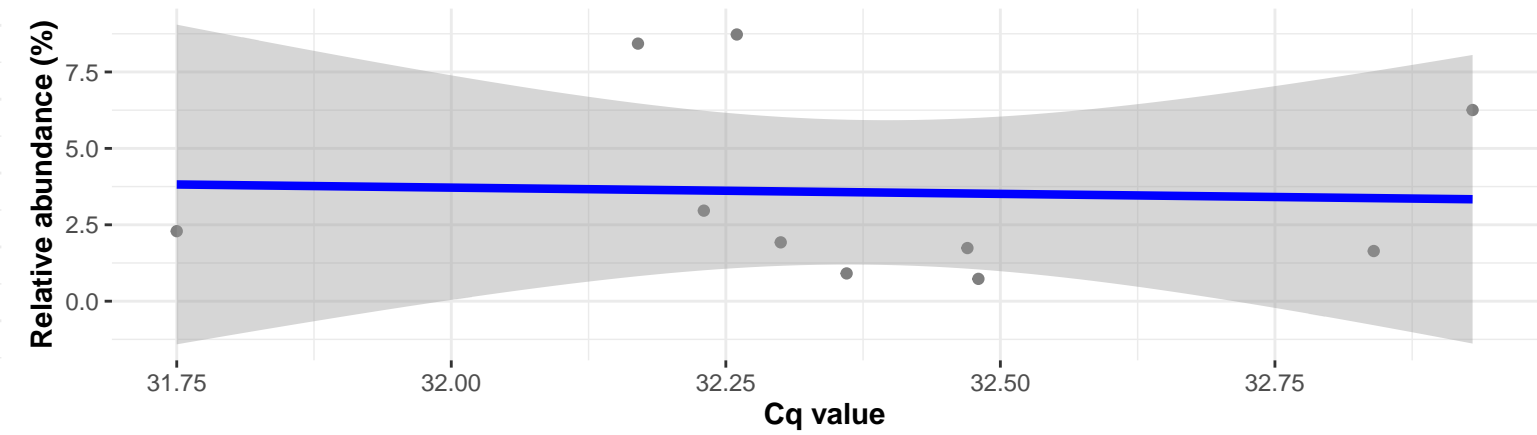


Correlation within: REF-PIM



Correlation within: REF-DIM

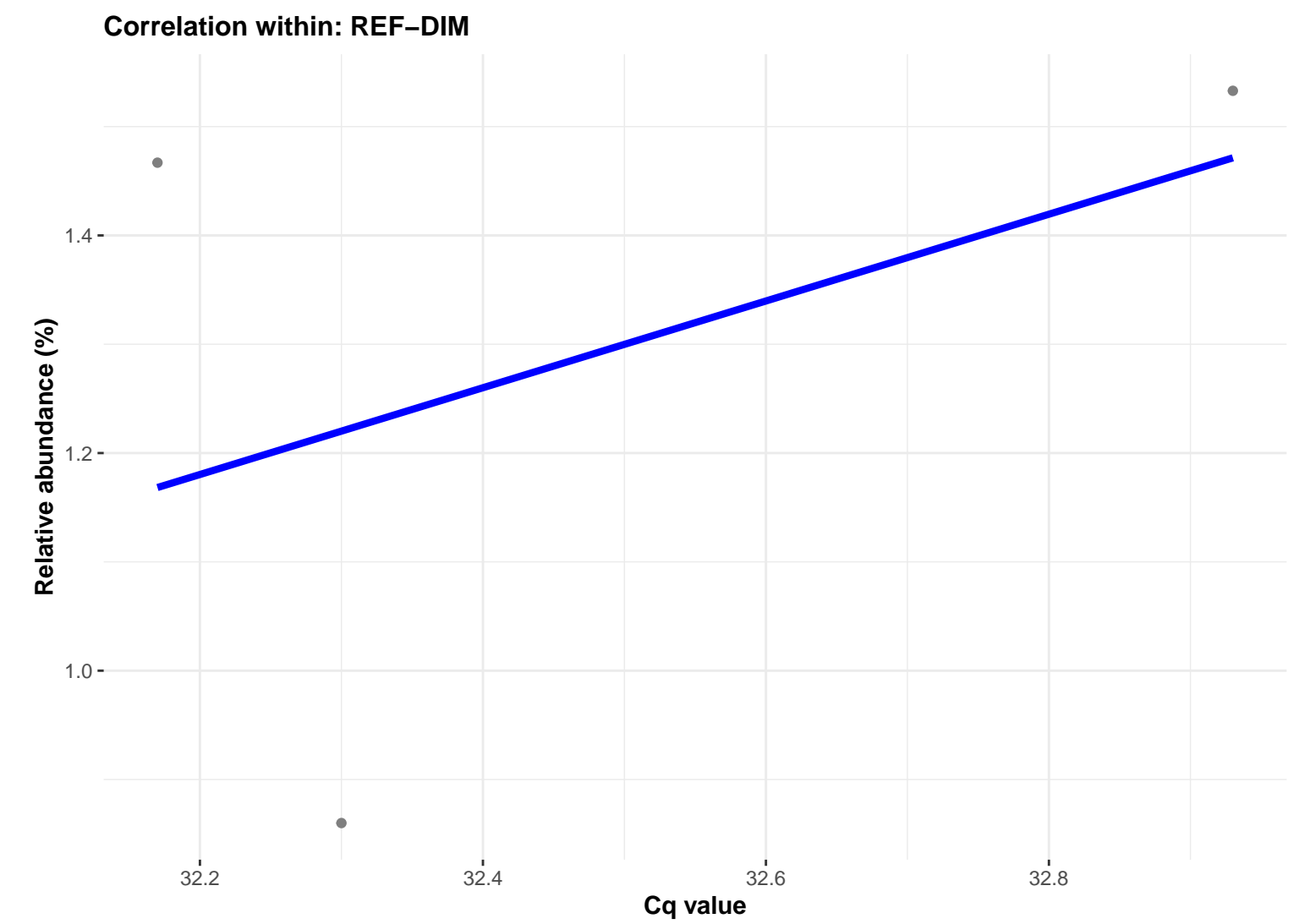
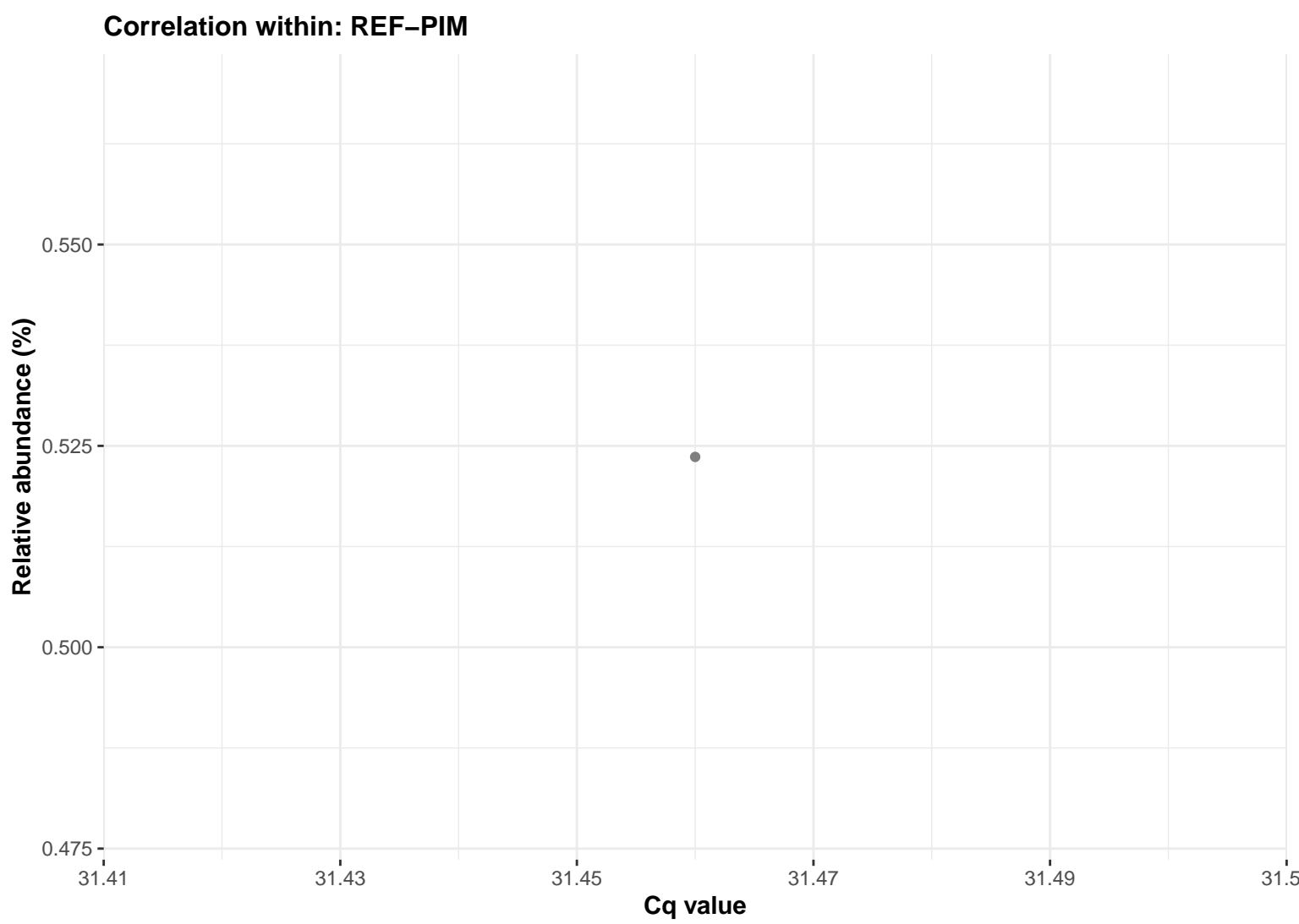
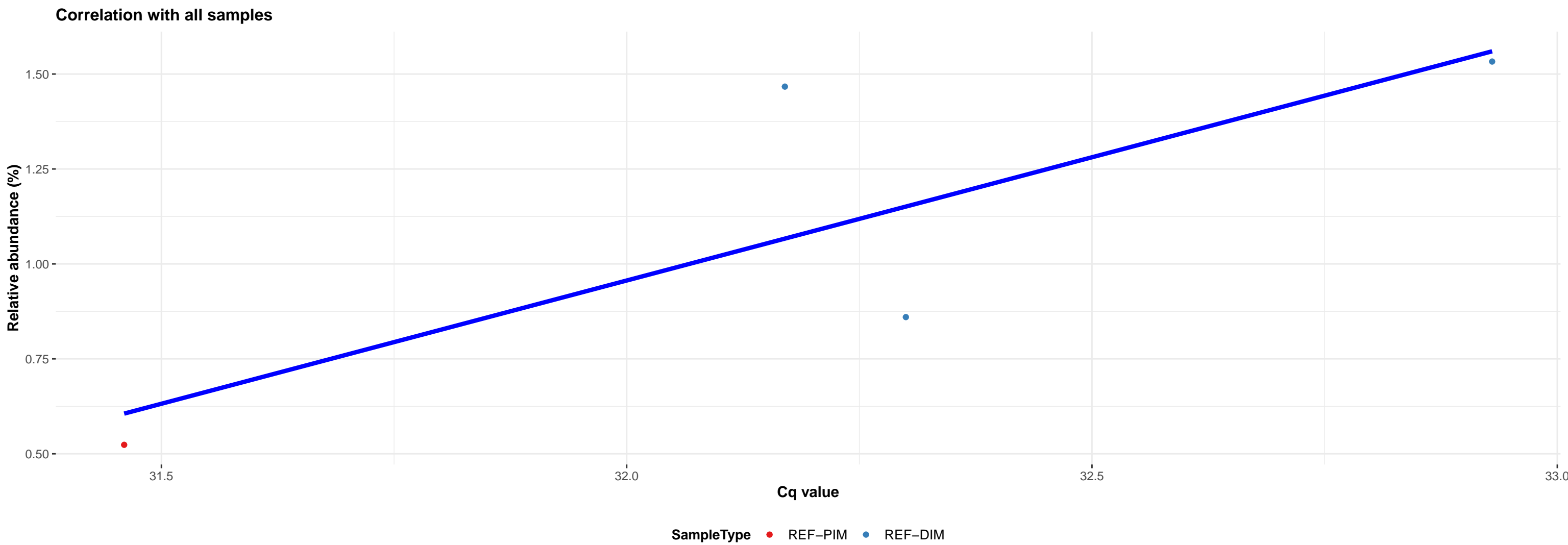
$\log_e(S) = 5.481$ ,  $p = 0.187$ ,  $\hat{\rho}_{\text{Spearman}} = -0.455$ ,  $CI_{95\%} [-0.849, 0.266]$ ,  $n_{\text{pairs}} = 10$



Correlation within: PCR-blank

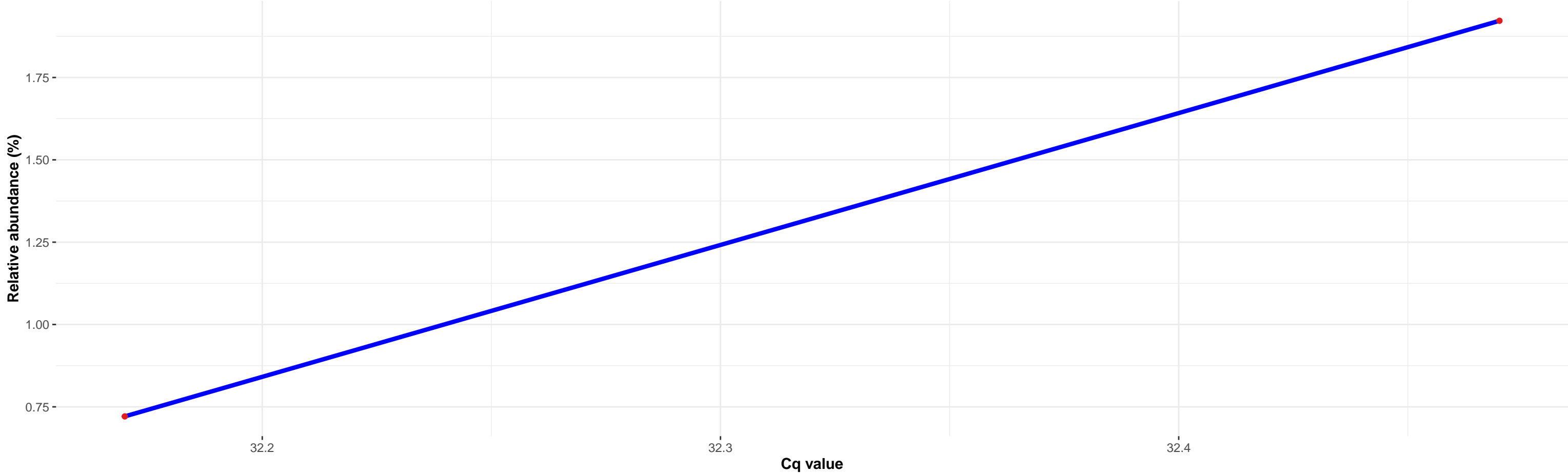


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; NA



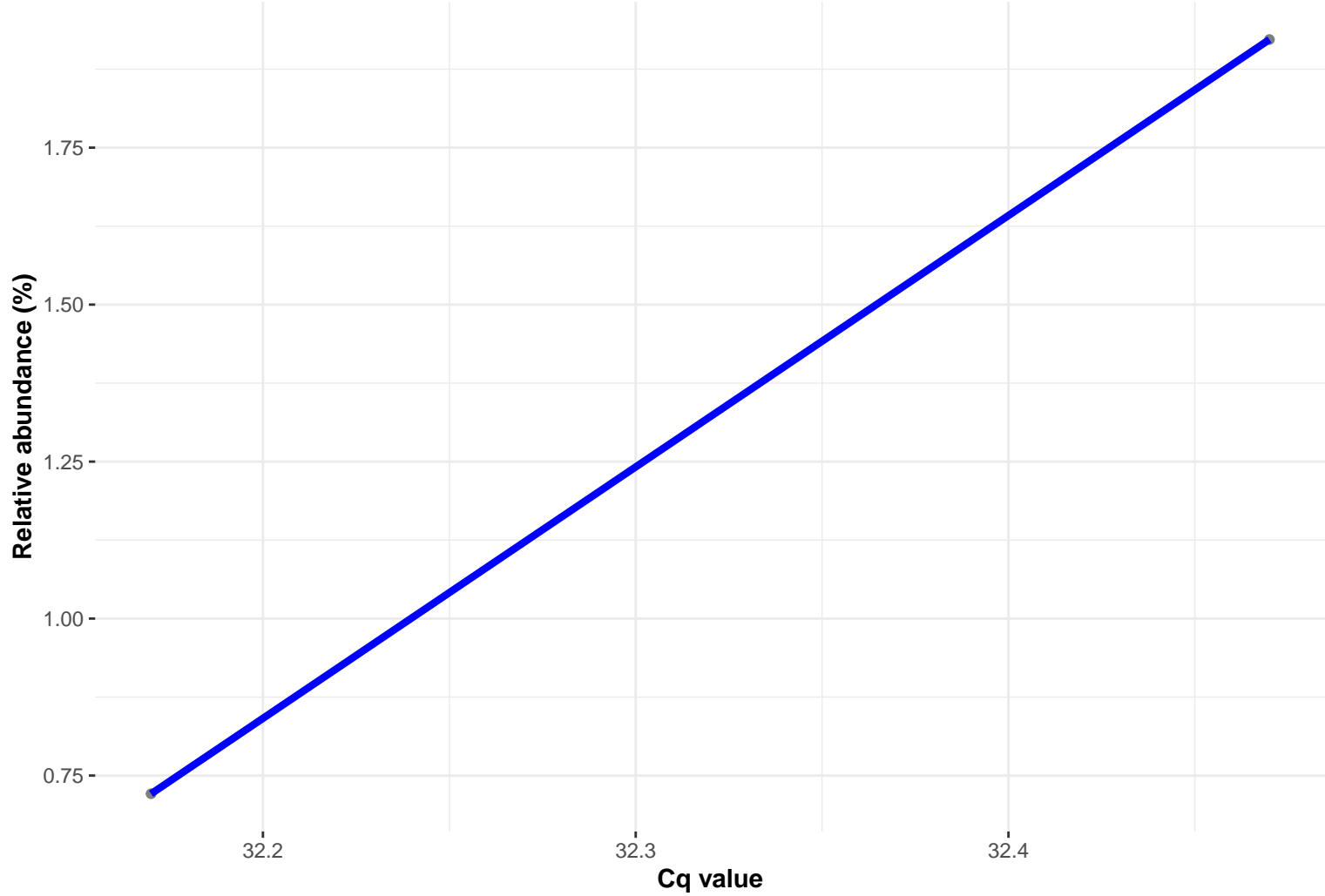
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Rhizobiales; f\_\_Xanthobacteraceae; g\_\_Bradyrhizobium; NA

Correlation with all samples



SampleType • REF-DIM

Correlation within: REF-DIM

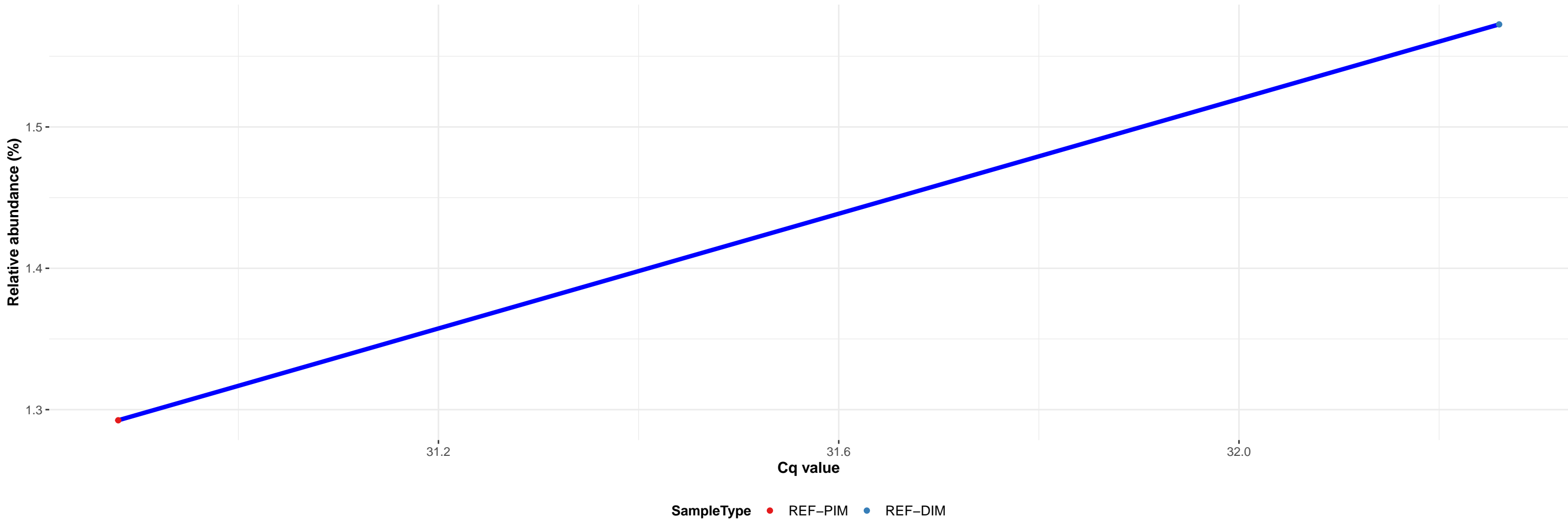


Correlation within: PCR-blank

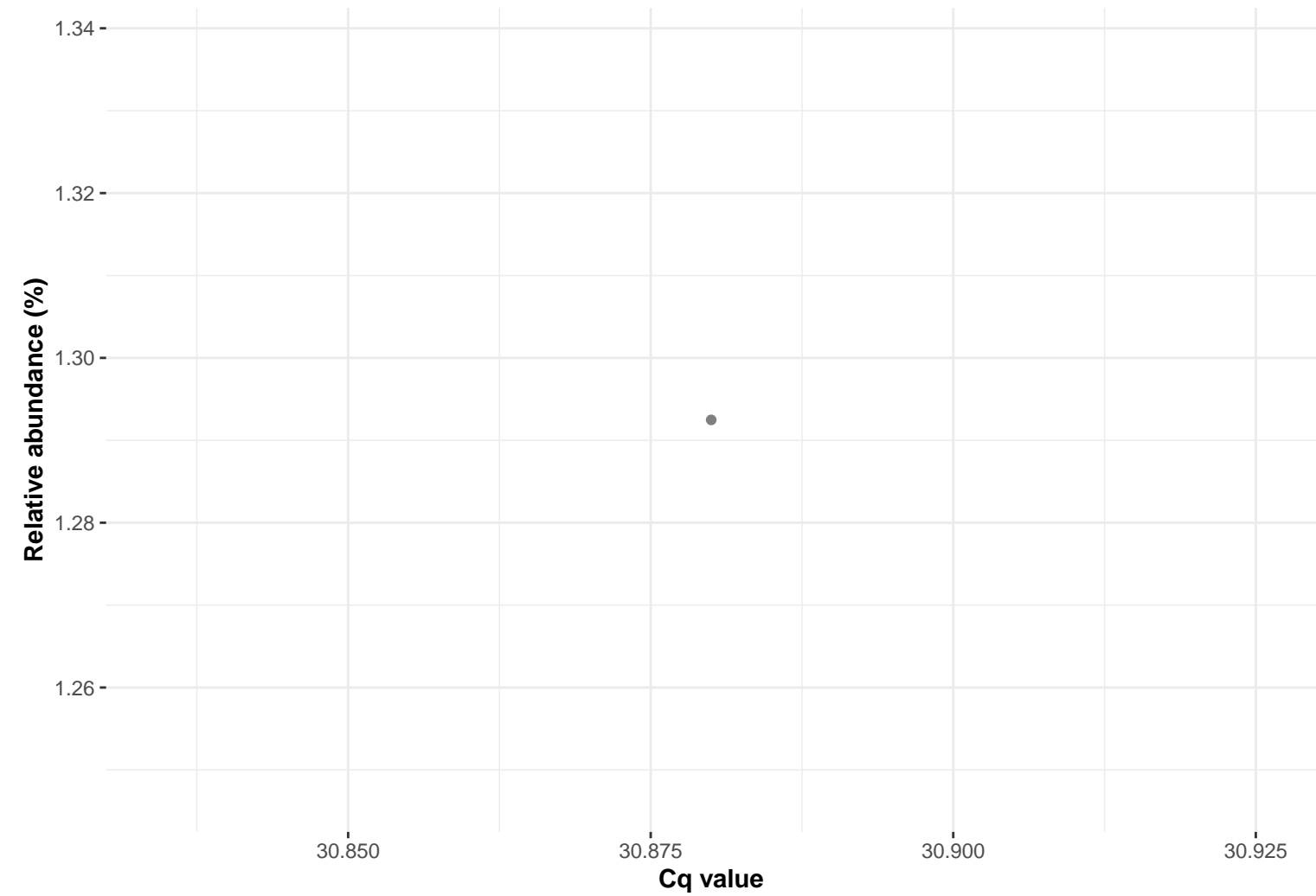


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Aerococcaceae; g\_\_Globicatella; Ambiguous\_taxa

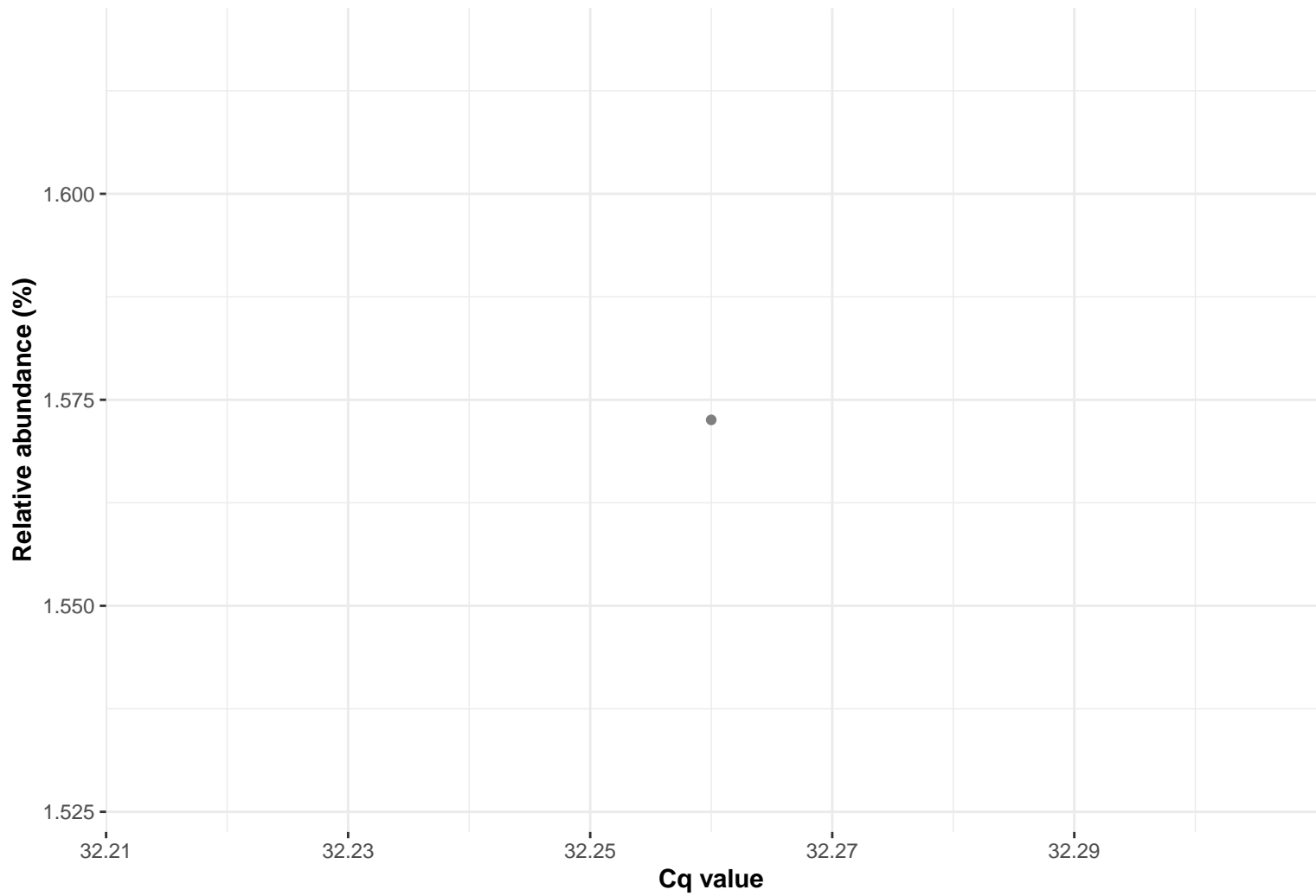
Correlation with all samples



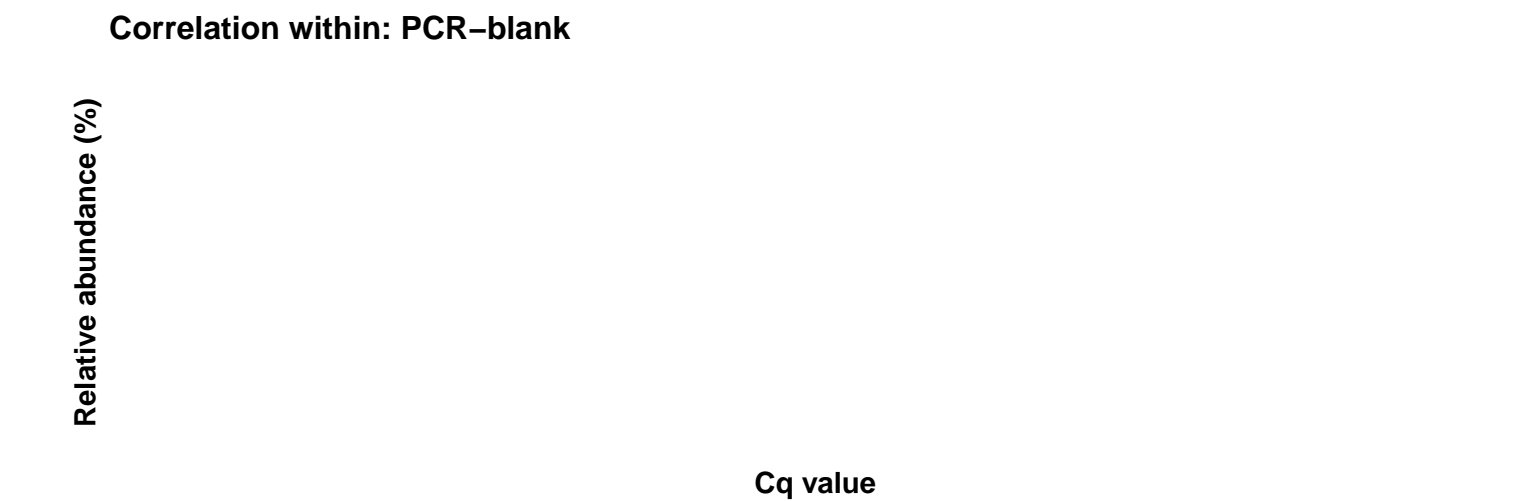
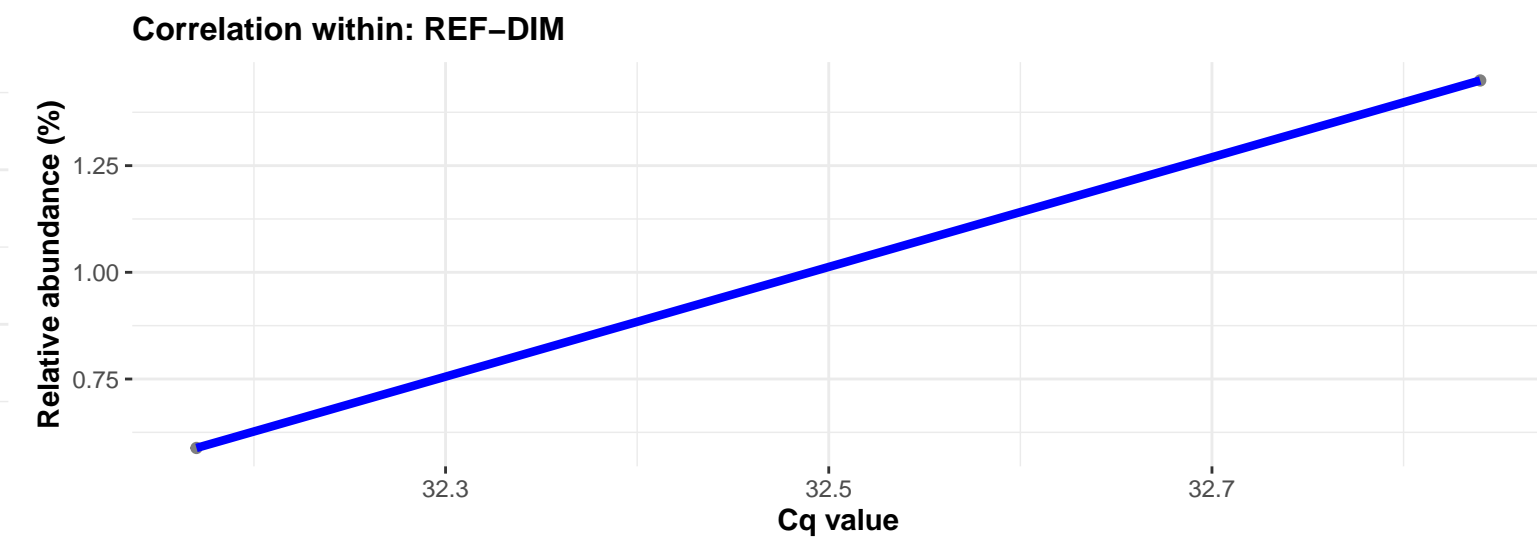
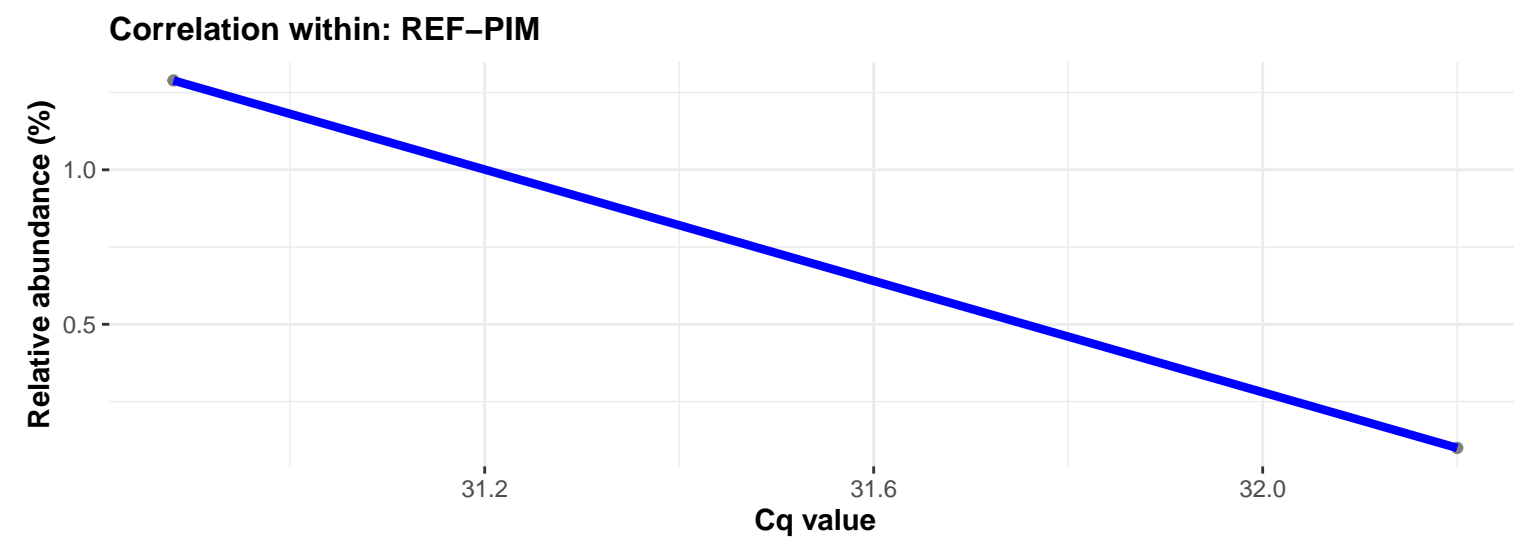
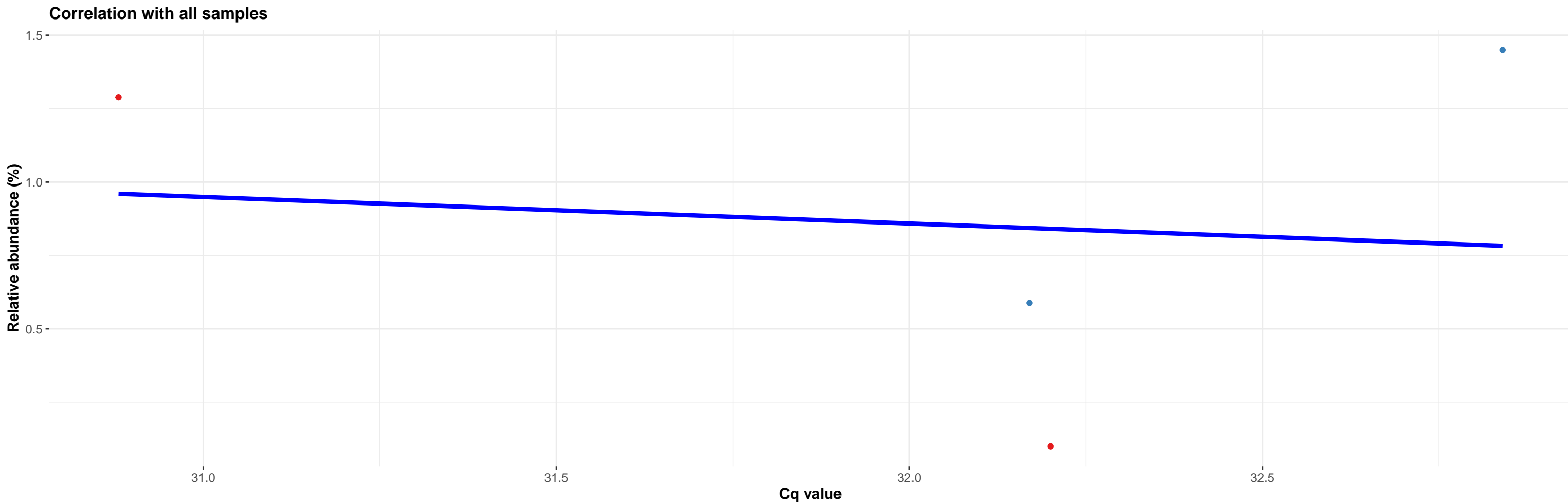
Correlation within: REF-PIM



Correlation within: REF-DIM



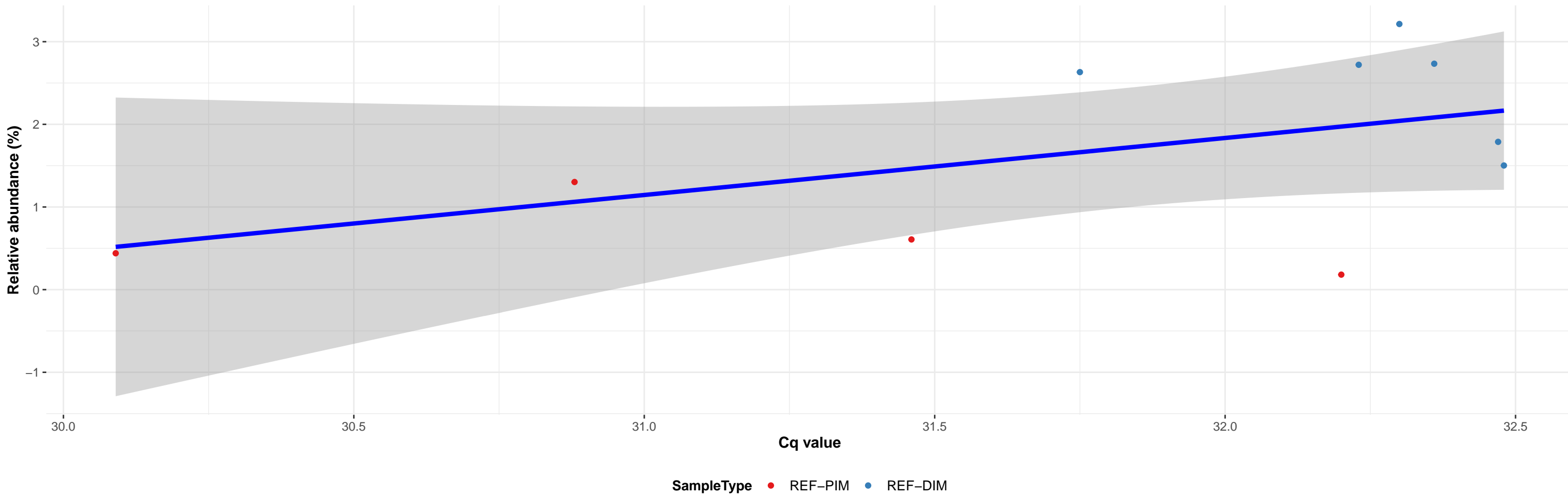




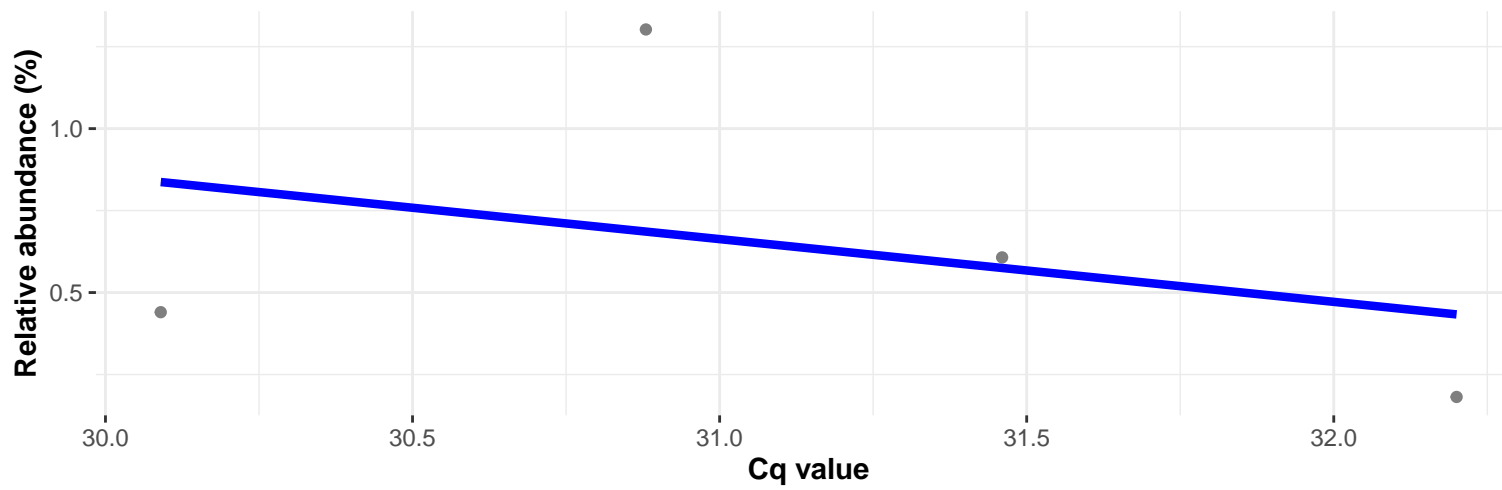
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Ralstonia; NA

### Correlation with all samples

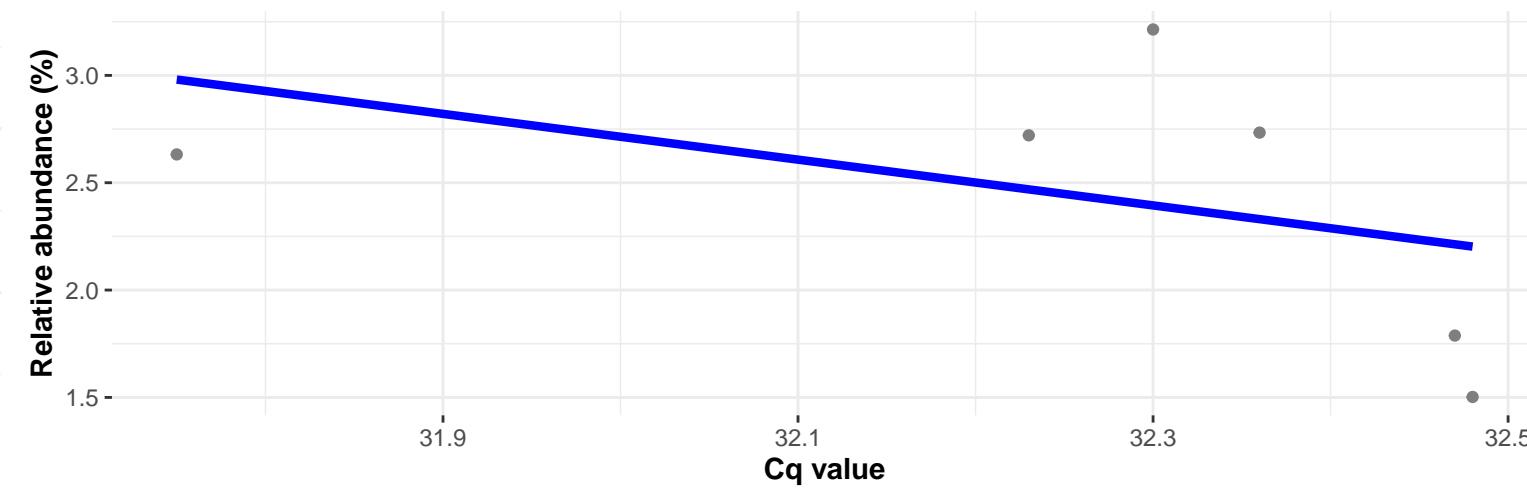
$\log_e(S) = 4.357$ ,  $p = 0.117$ ,  $\hat{\rho}_{\text{Spearman}} = 0.527$ ,  $CI_{95\%} [-0.175, 0.874]$ ,  $n_{\text{pairs}} = 10$



### Correlation within: REF-PIM



### Correlation within: REF-DIM



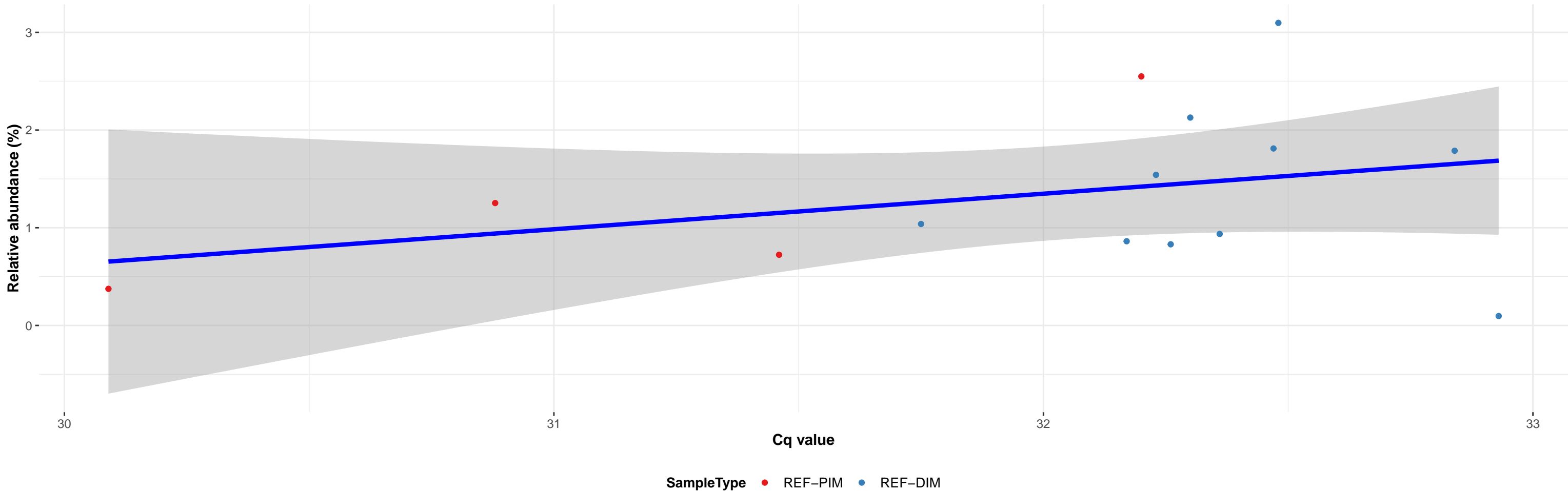
### Correlation within: PCR-blank



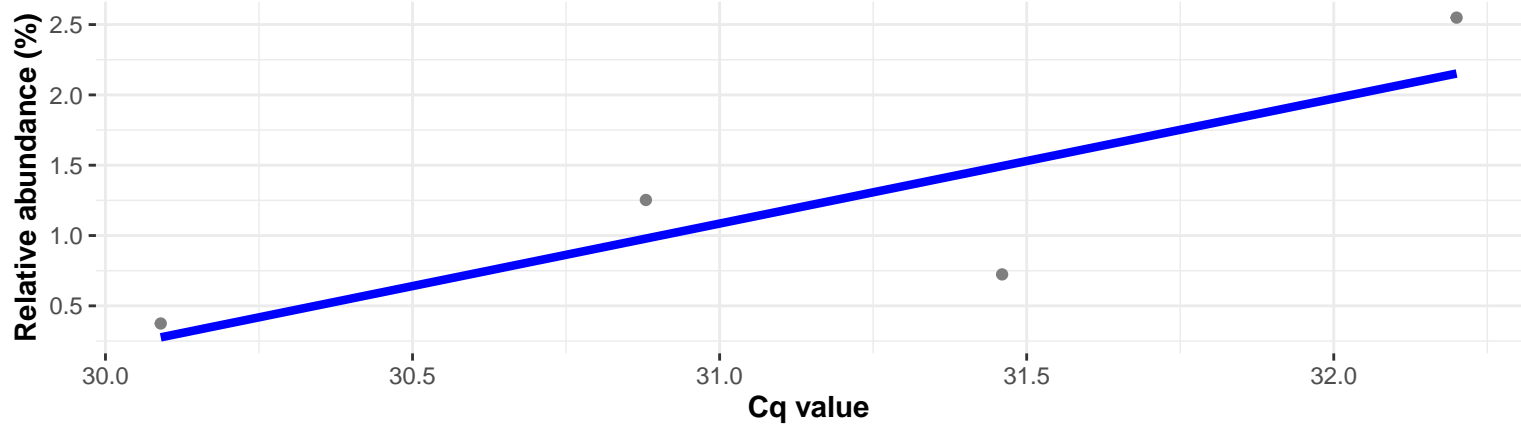
k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Chitinophagales; f\_\_Chitinophagaceae; g\_\_Sediminibacterium; NA

Correlation with all samples

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

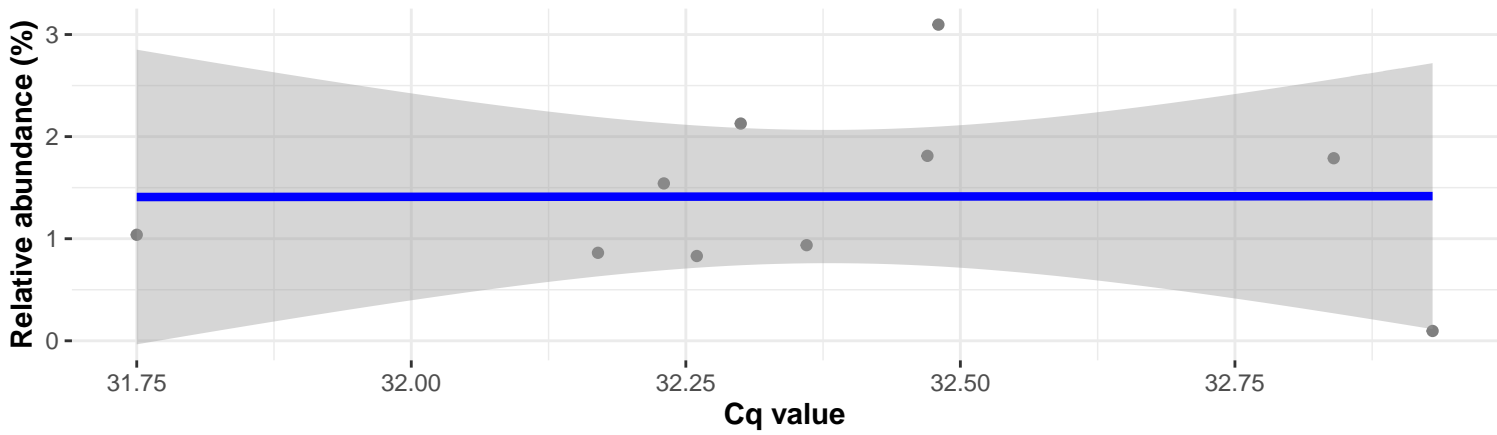


Correlation within: REF-PIM

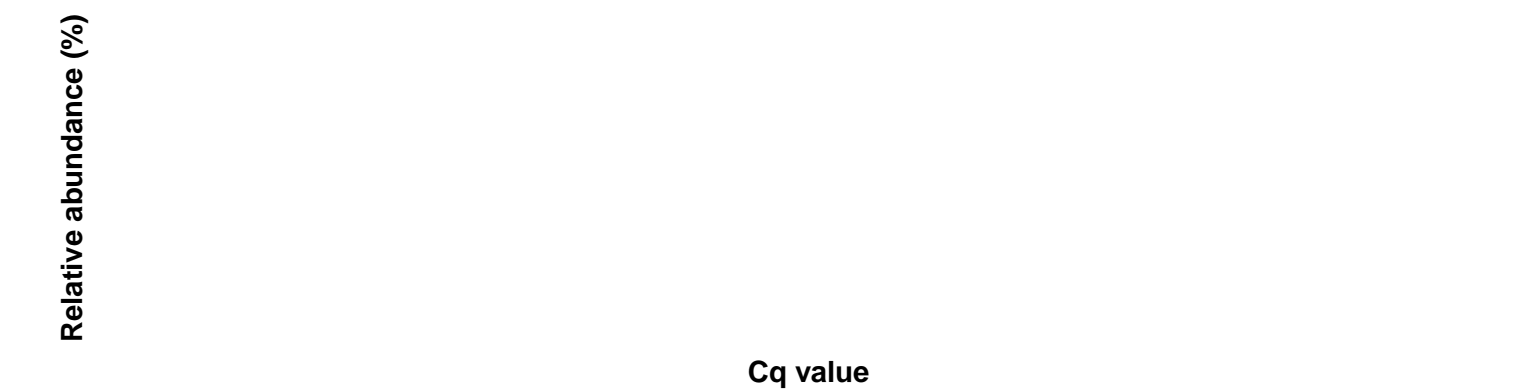


Correlation within: REF-DIM

$\log_e(S) = 4.942$ ,  $p = 0.676$ ,  $\hat{\rho}_{\text{Spearman}} = 0.152$ ,  $CI_{95\%} [-0.544, 0.724]$ ,  $n_{\text{pairs}} = 10$



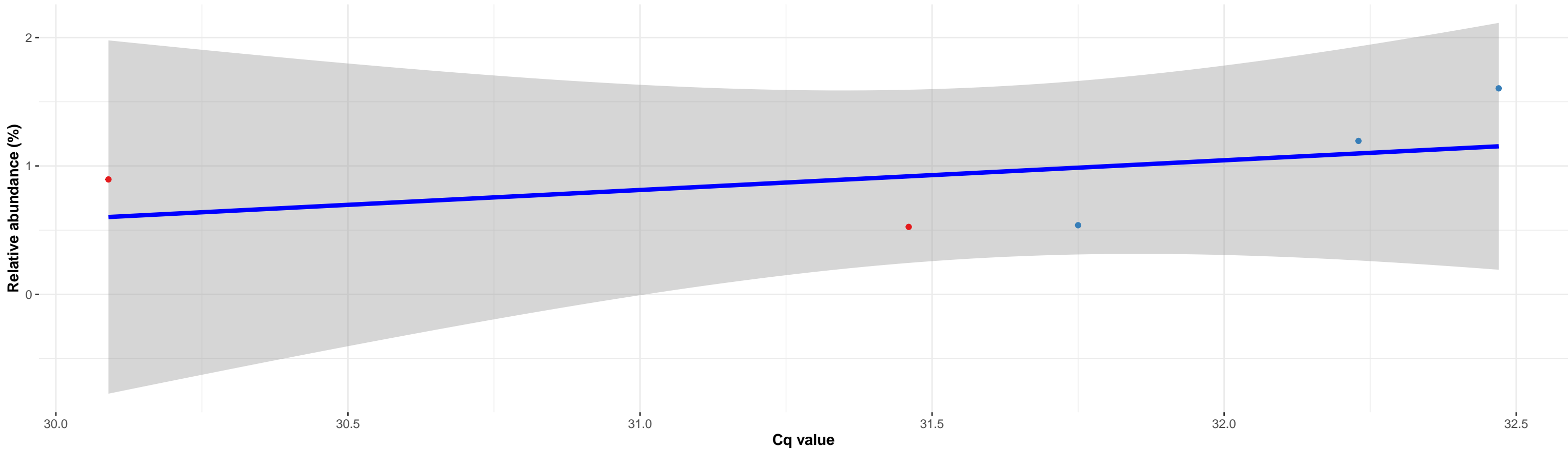
Correlation within: PCR-blank



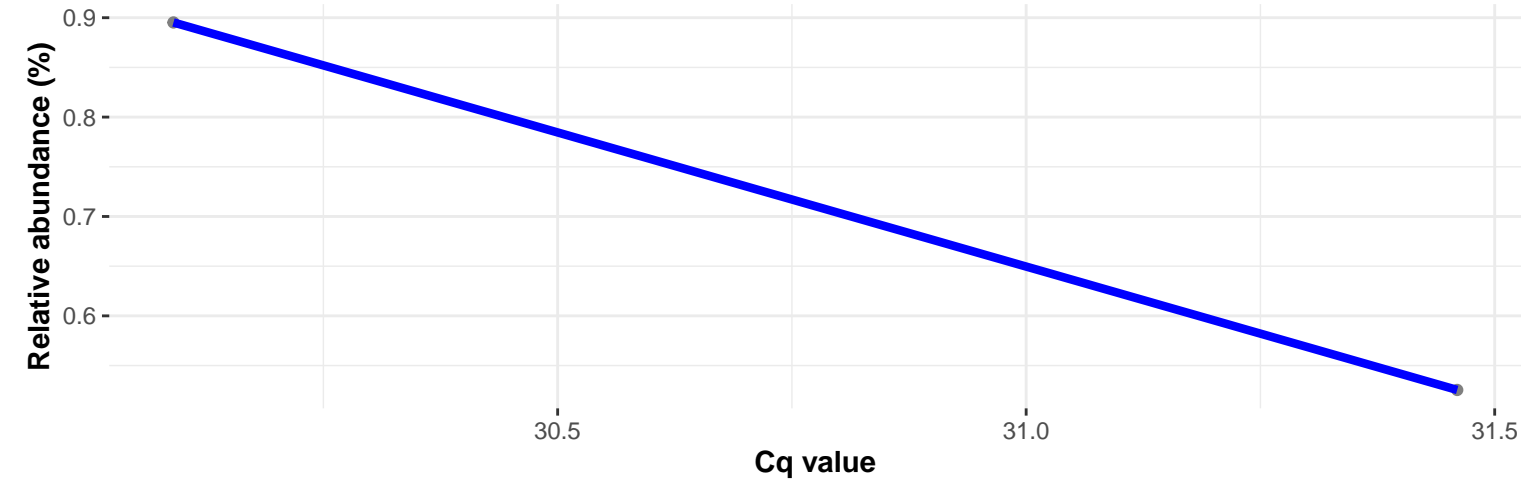
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

Correlation with all samples

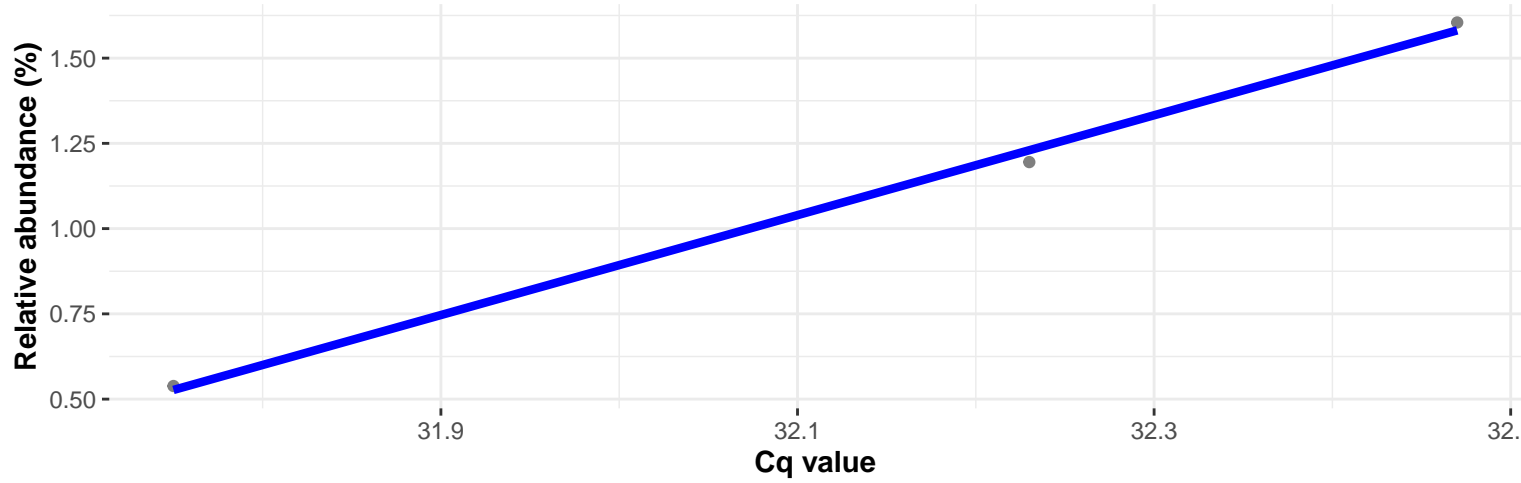
$\log_e(S) = 1.792$ ,  $p = 0.188$ ,  $\hat{\rho}_{\text{Spearman}} = 0.700$ ,  $CI_{95\%} [-0.508, 0.980]$ ,  $n_{\text{pairs}} = 5$



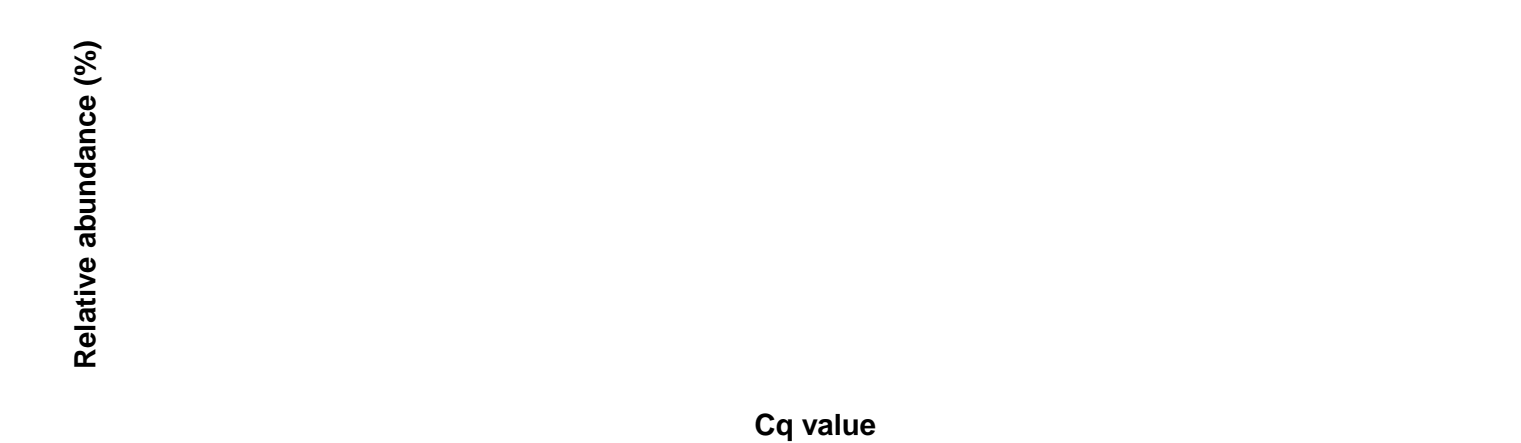
Correlation within: REF-PIM



Correlation within: REF-DIM



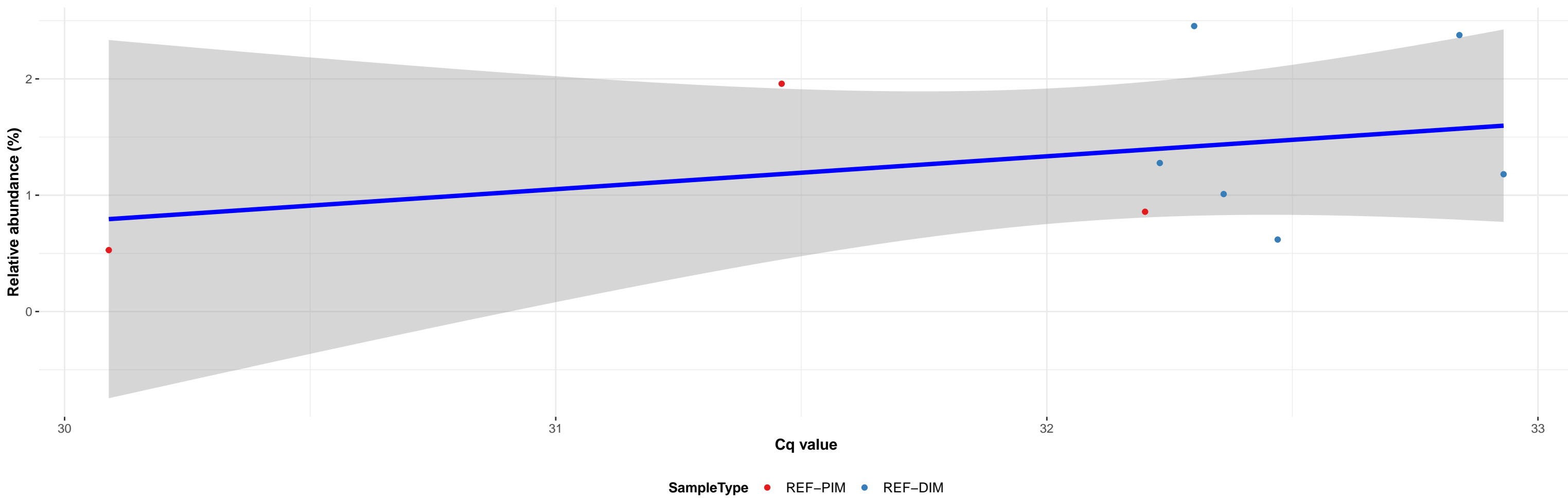
Correlation within: PCR-blank



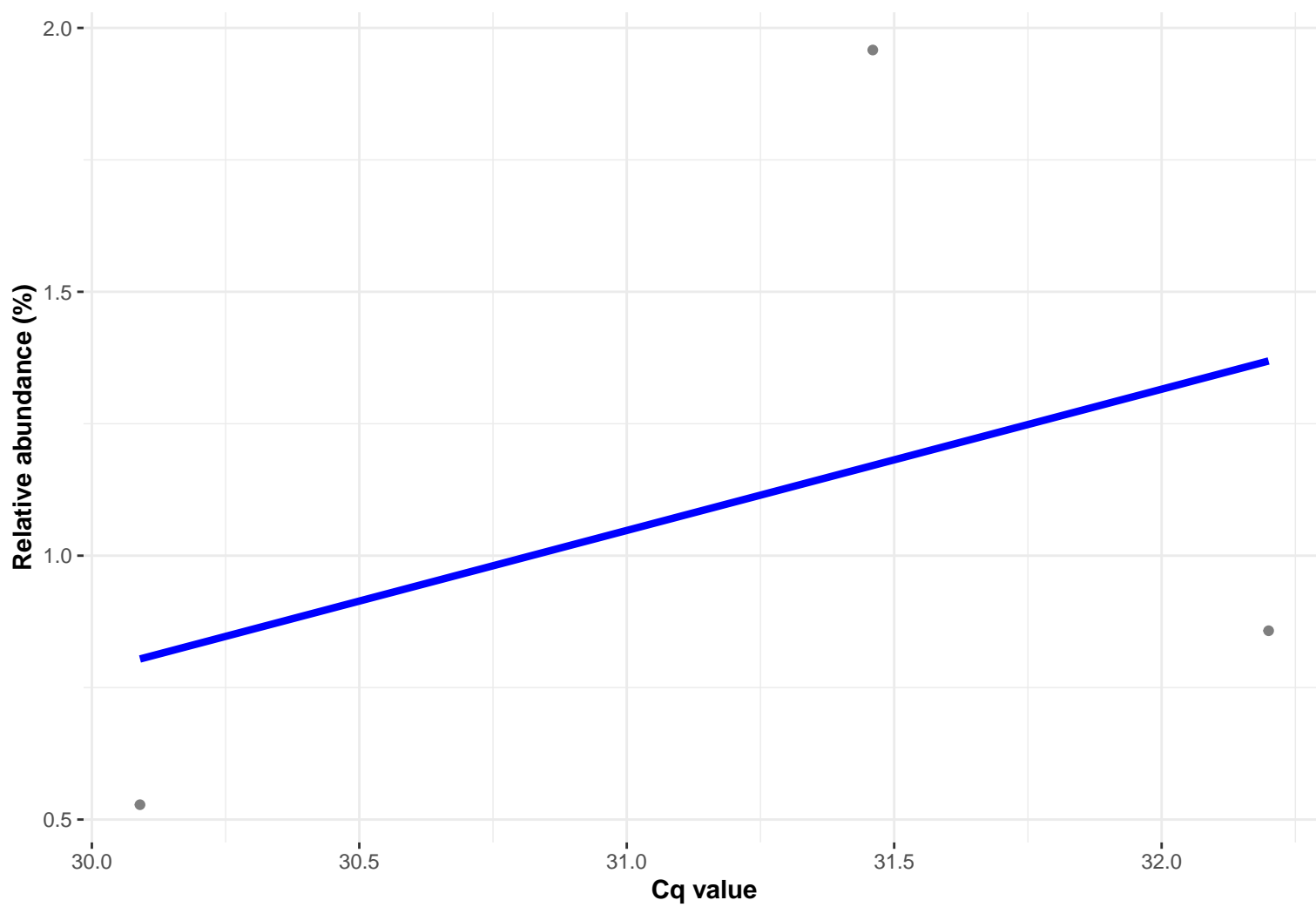
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; NA; NA

### Correlation with all samples

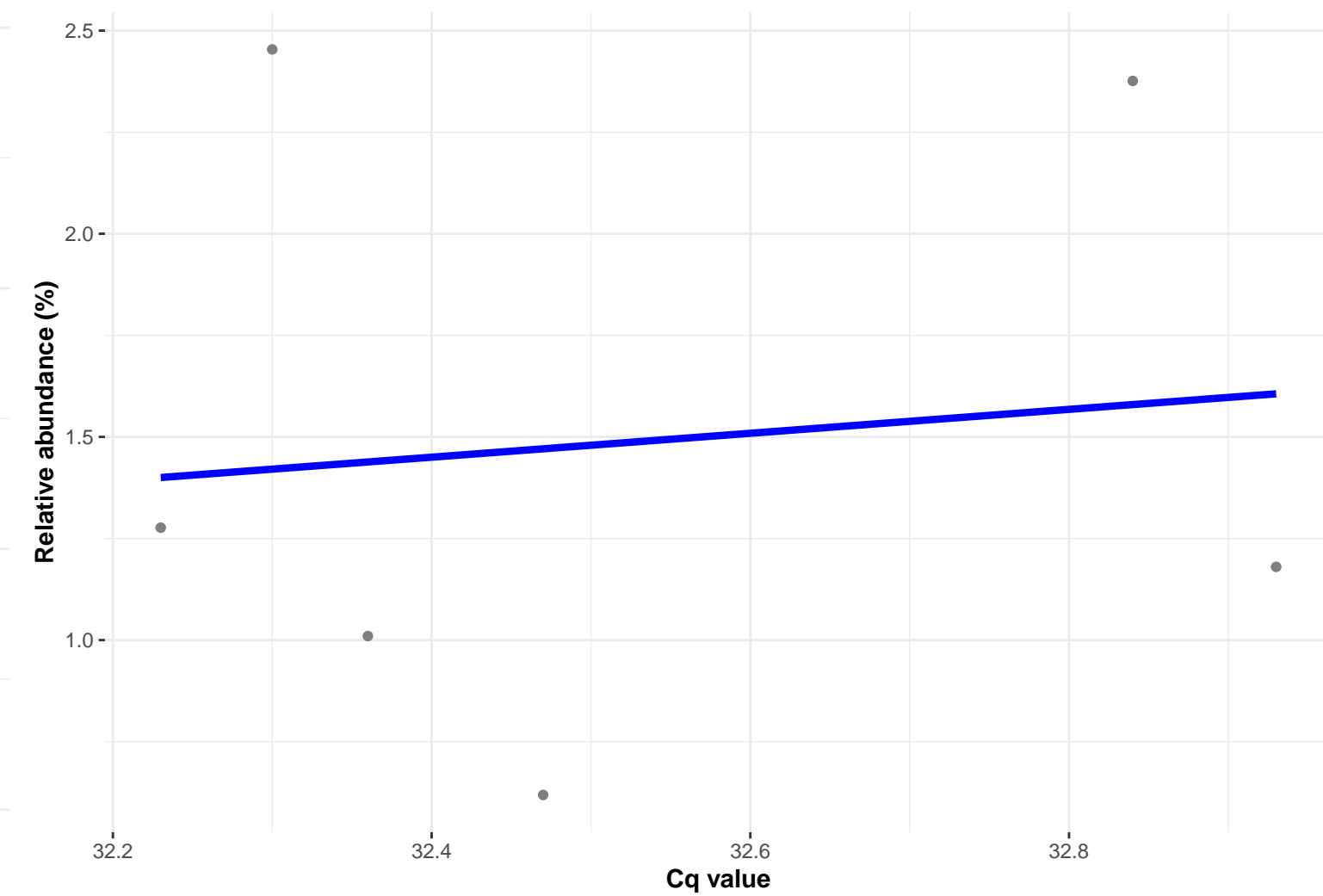
$\log_e(S) = 4.500$ ,  $p = 0.516$ ,  $\hat{\rho}_{\text{Spearman}} = 0.250$ ,  $CI_{95\%} [-0.514, 0.793]$ ,  $n_{\text{pairs}} = 9$



### Correlation within: REF-PIM

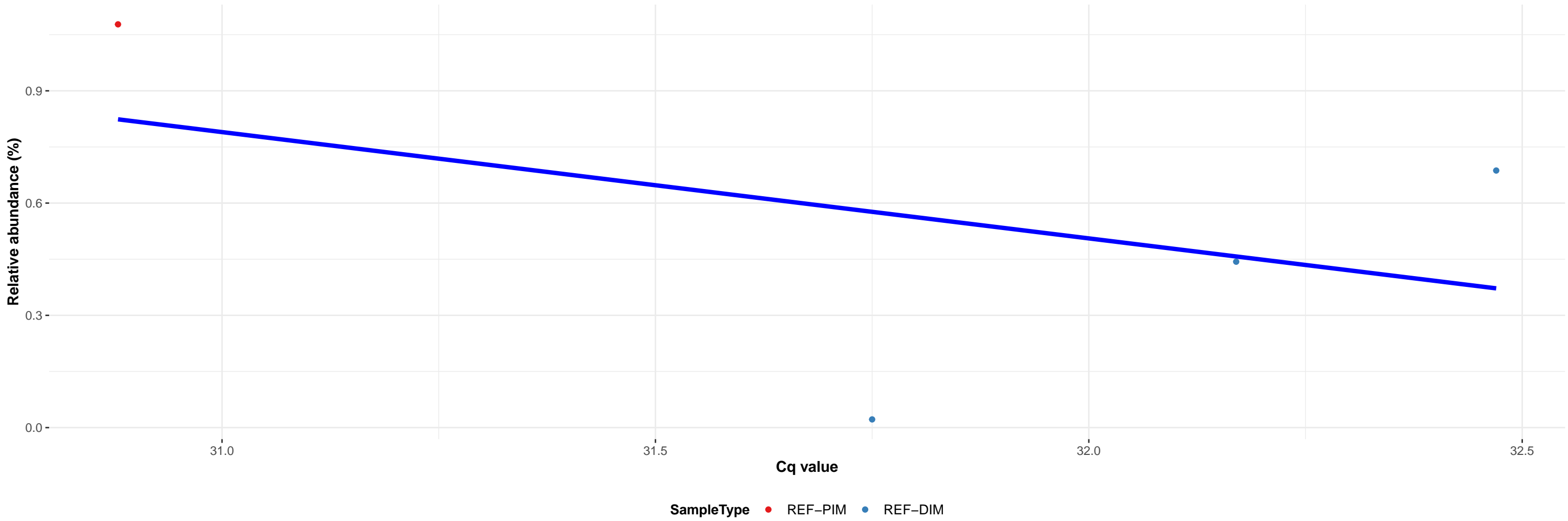


### Correlation within: REF-DIM

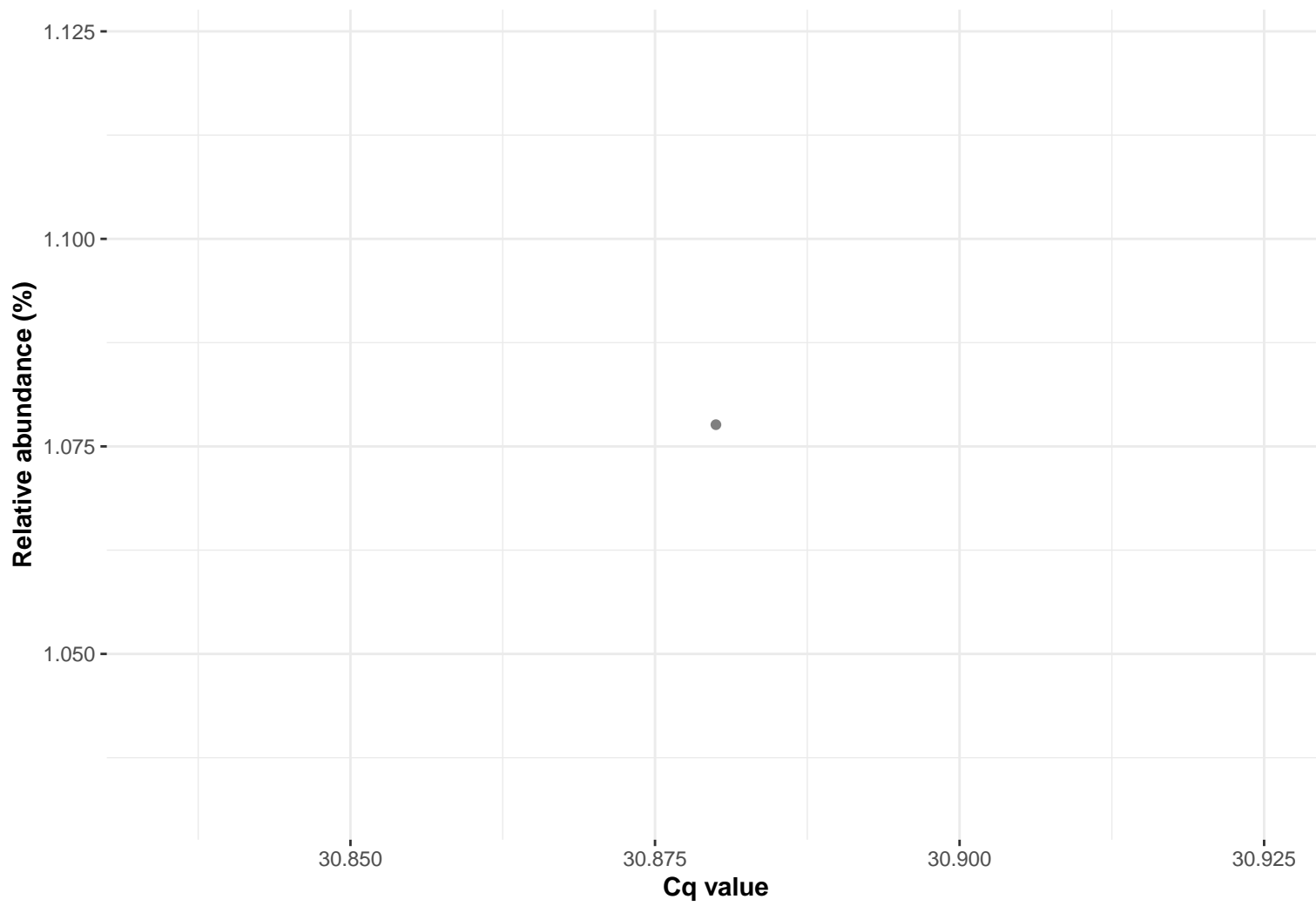


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; Ambiguous\_taxa; Ambiguous\_taxa

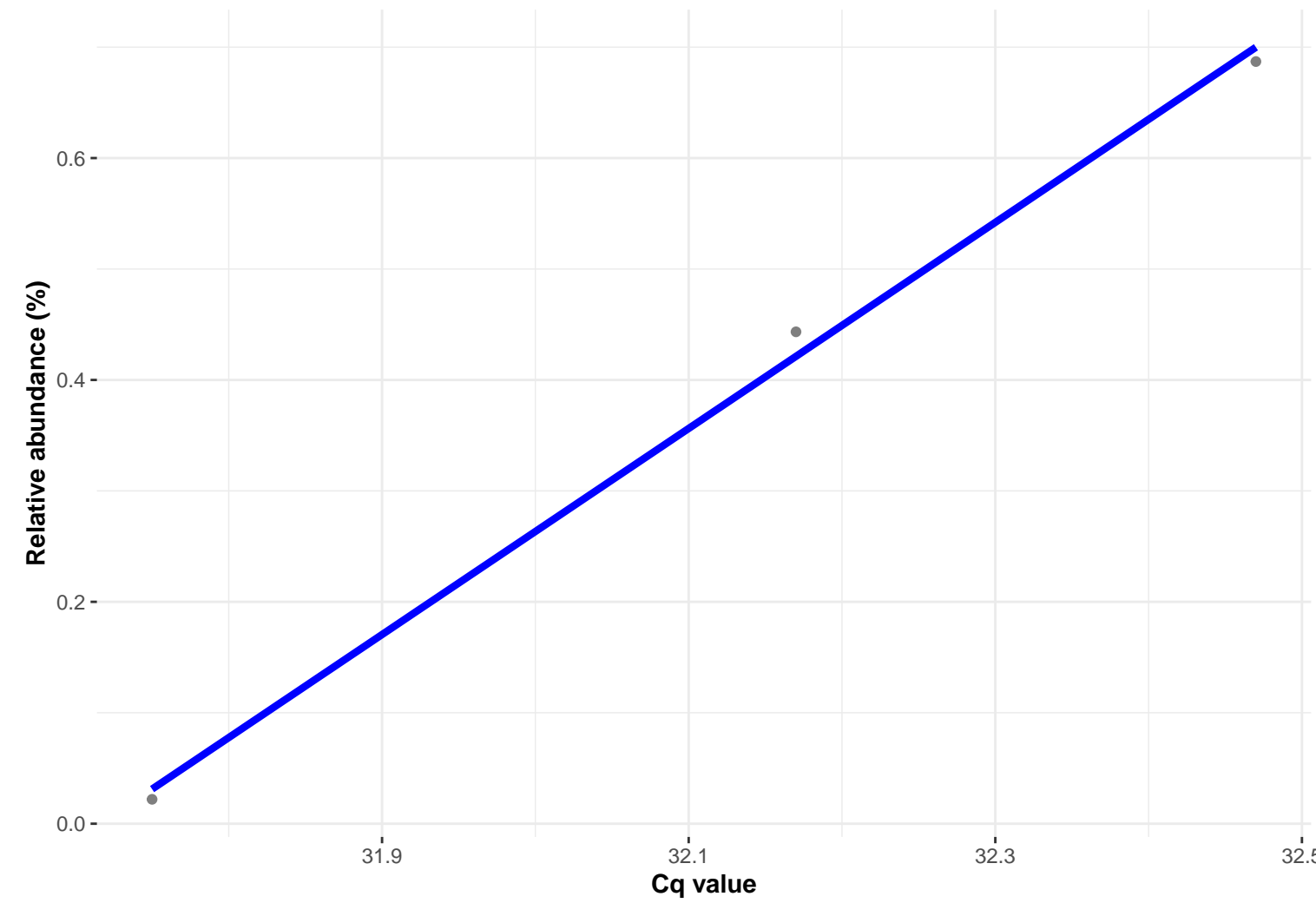
Correlation with all samples



Correlation within: REF-PIM



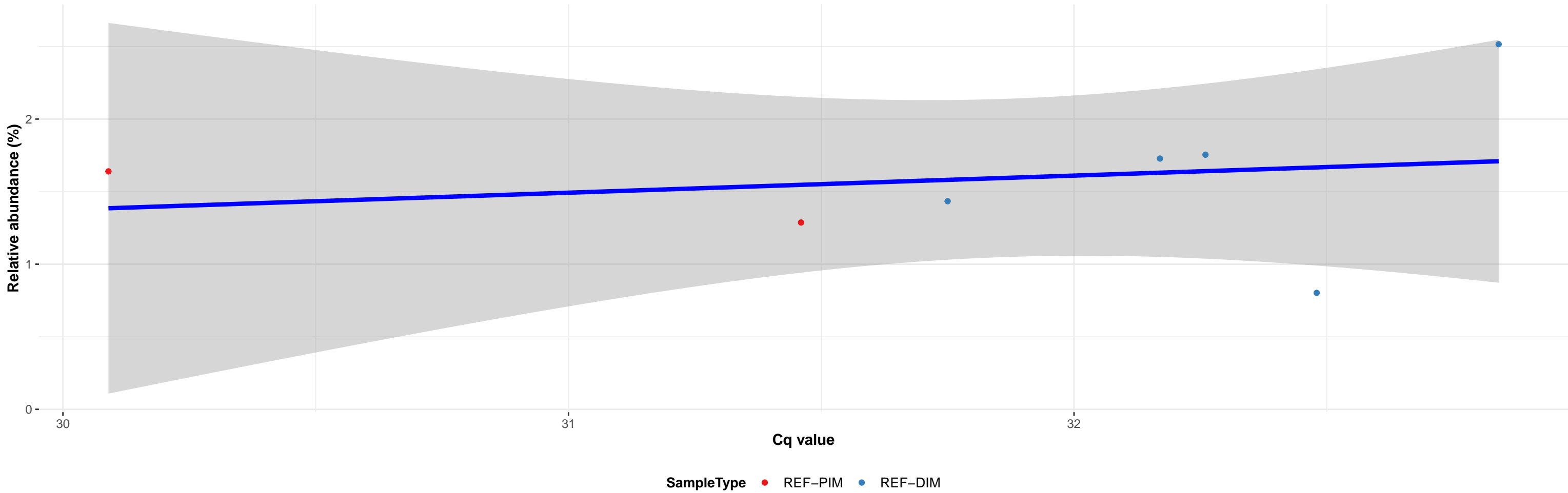
Correlation within: REF-DIM



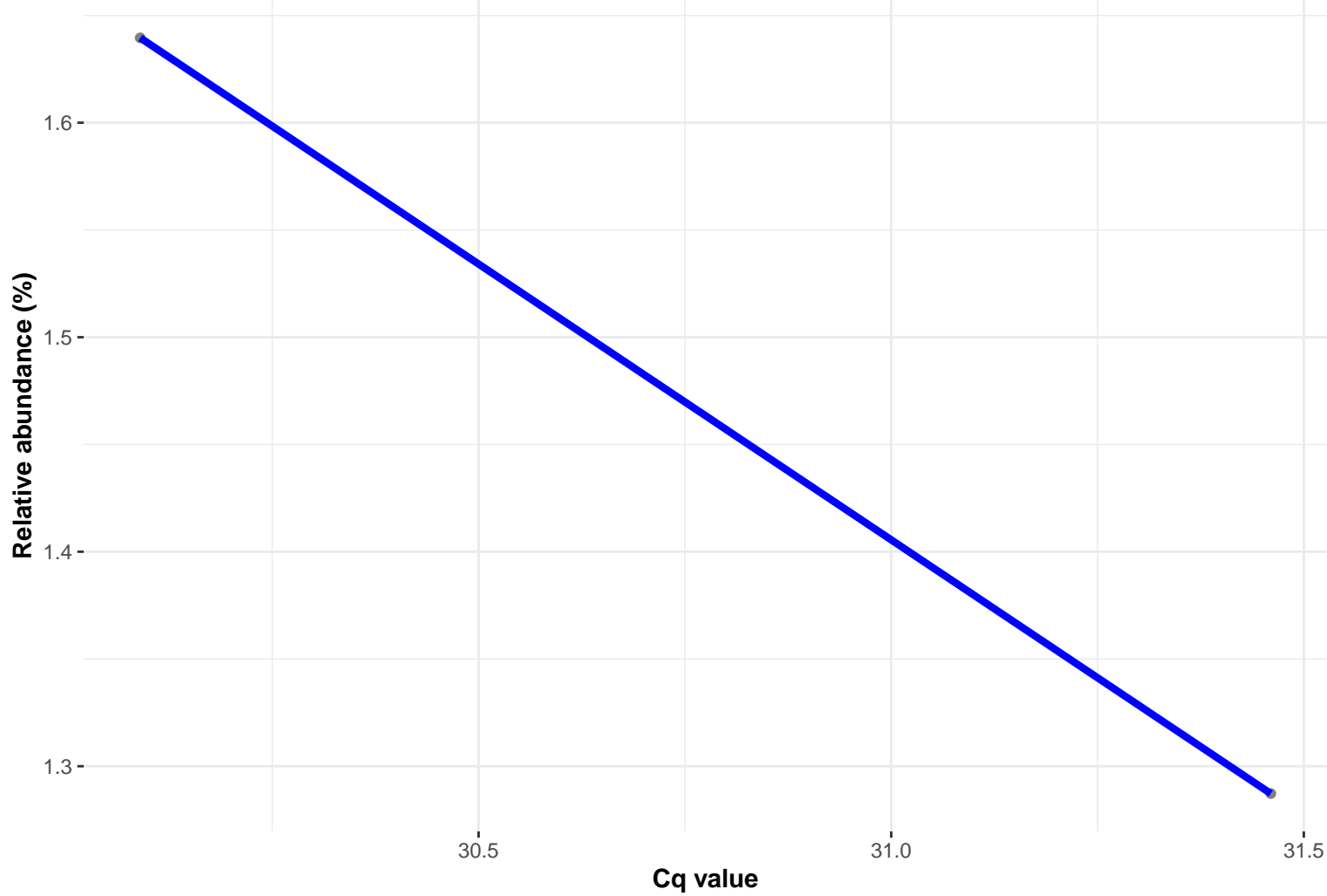
k\_\_Bacteria; p\_\_RsaHF231; c\_\_uncultured bacterium; o\_\_uncultured bacterium; f\_\_uncultured bacterium; g\_\_uncultured bacterium; s\_\_uncultured bacterium

Correlation with all samples

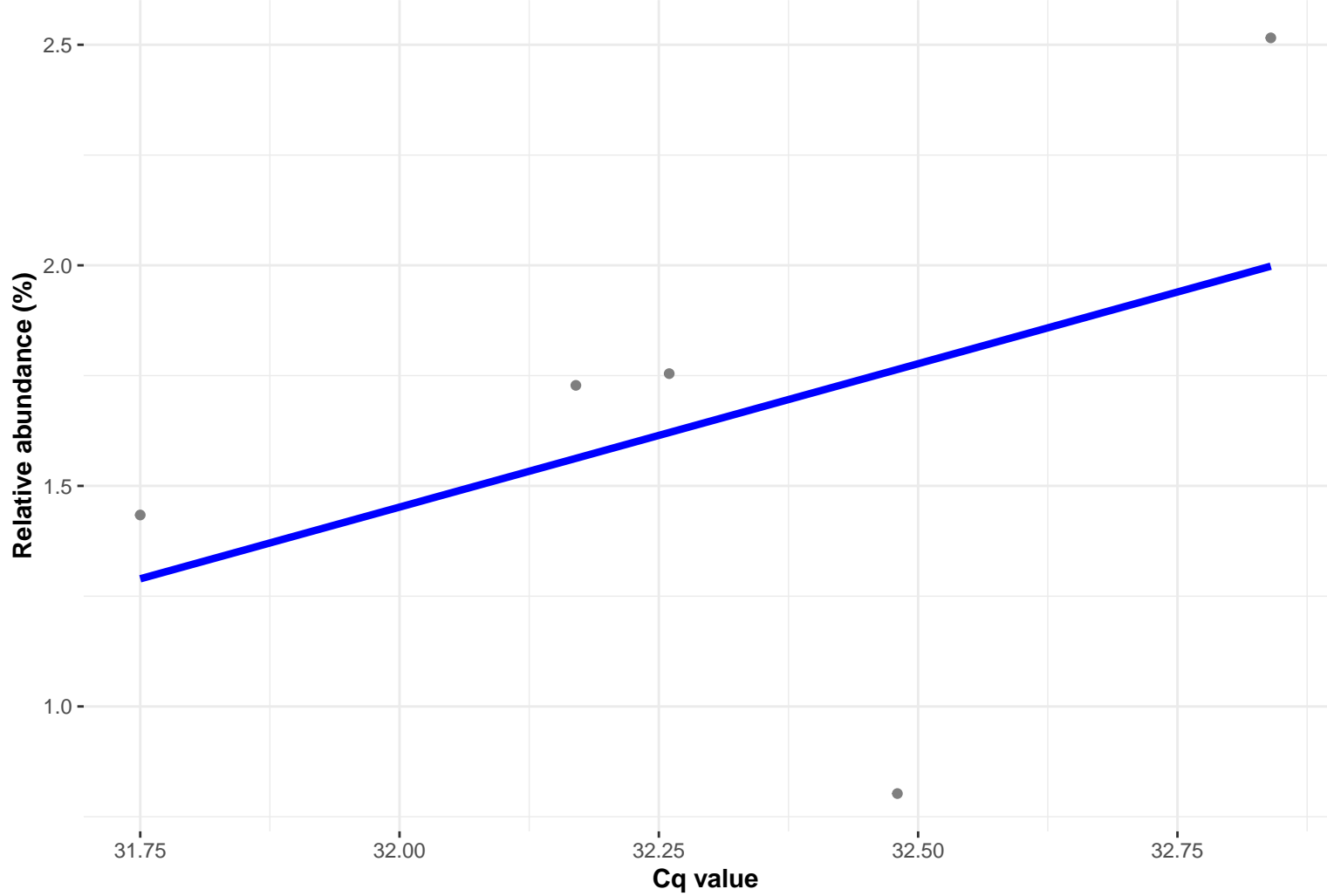
$\log_e(S) = 3.584$ ,  $p = 0.432$ ,  $\hat{\rho}_{\text{Spearman}} = 0.357$ ,  $CI_{95\%} [-0.562, 0.882]$ ,  $n_{\text{pairs}} = 7$



Correlation within: REF-PIM



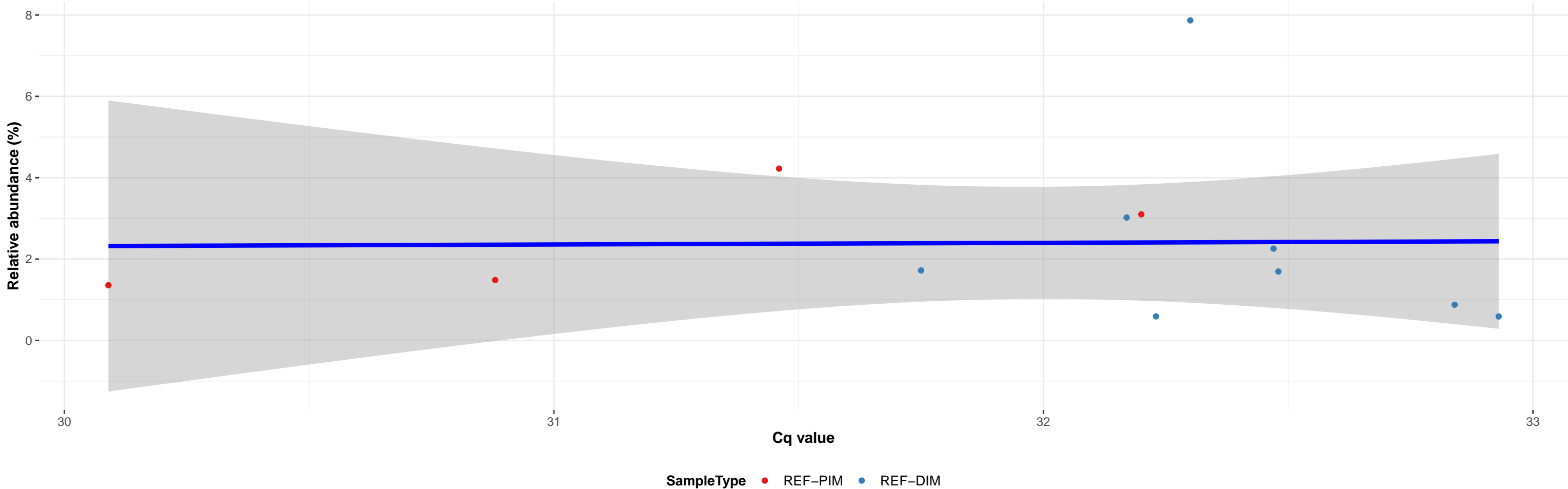
Correlation within: REF-DIM



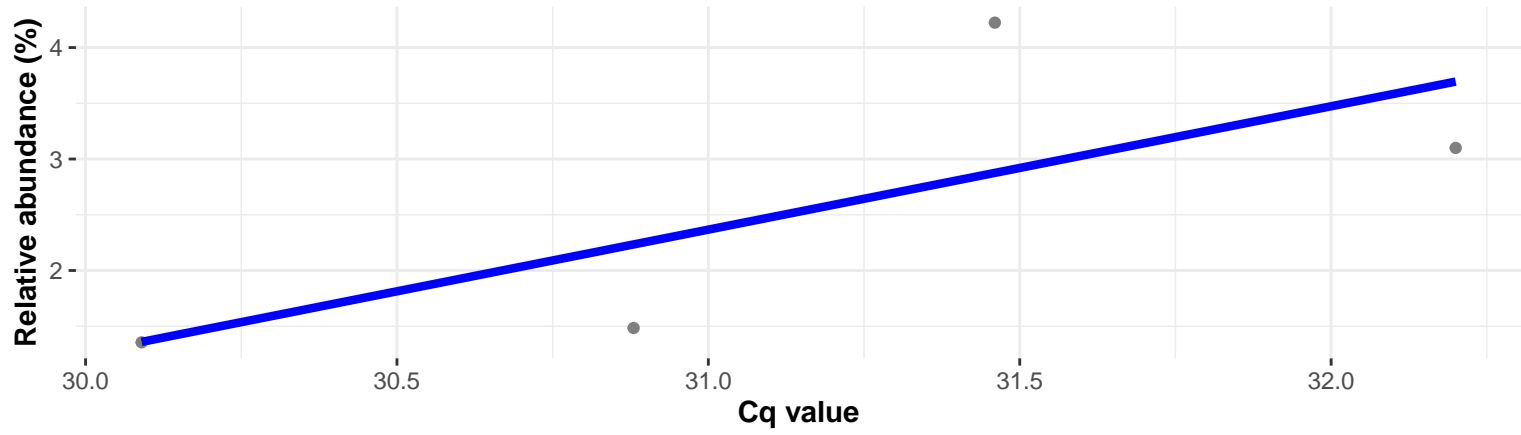
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Peptostreptococcaceae; NA; NA

Correlation with all samples

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

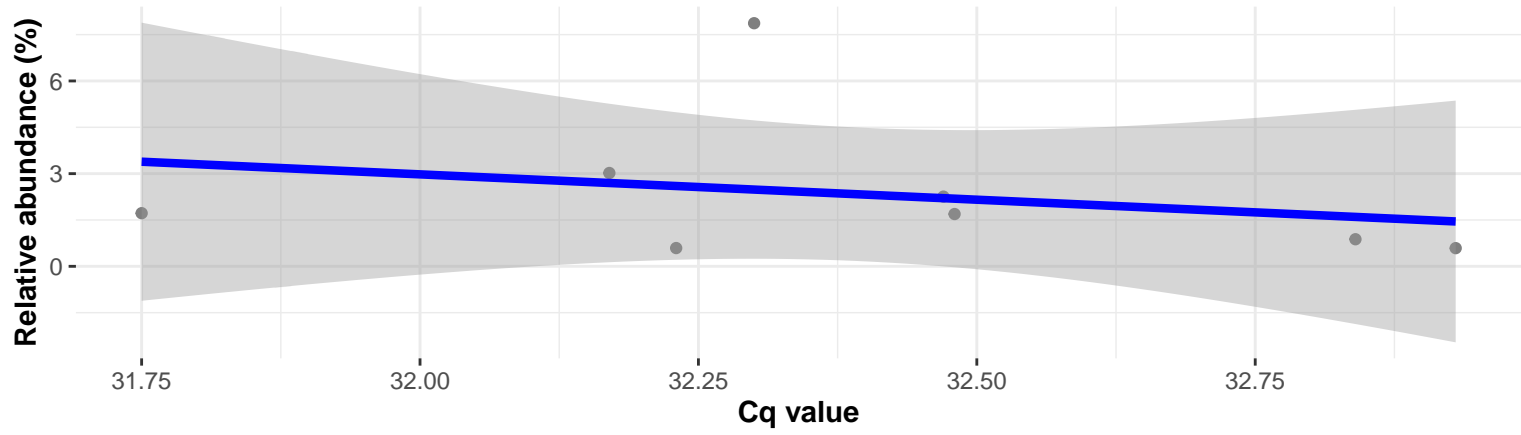


Correlation within: REF-PIM



Correlation within: REF-DIM

$\log_e(S) = 4.852$ ,  $p = 0.183$ ,  $\hat{\rho}_{\text{Spearman}} = -0.524$ ,  $CI_{95\%} [-0.902, 0.310]$ ,  $n_{\text{pairs}} = 8$

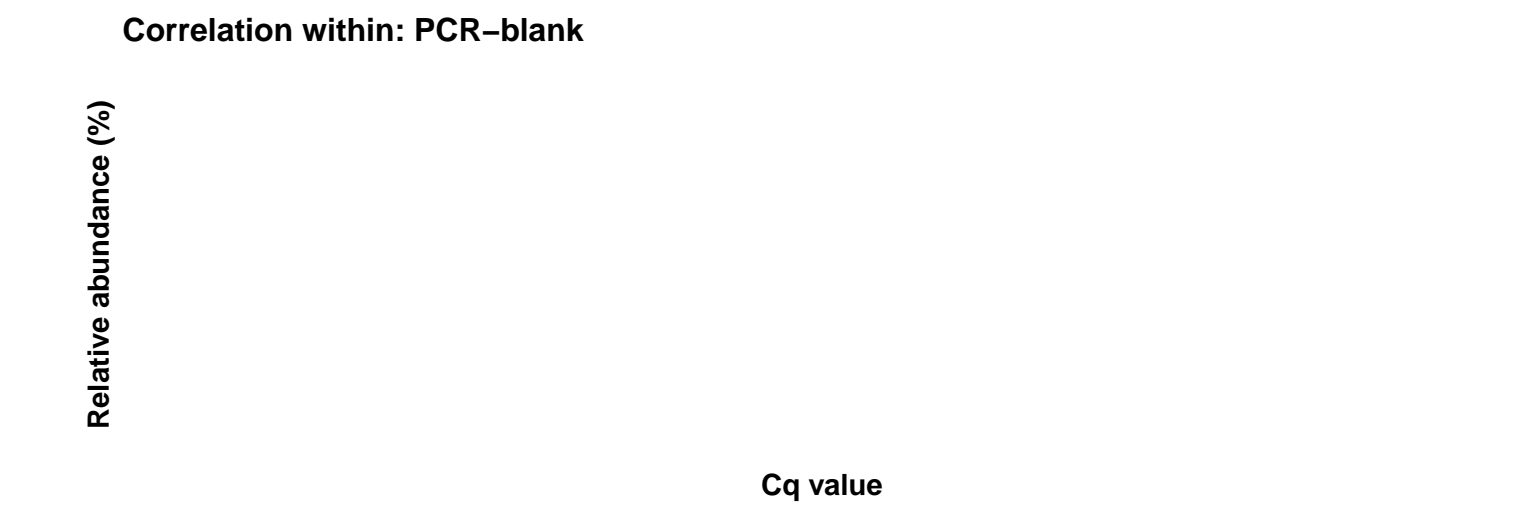
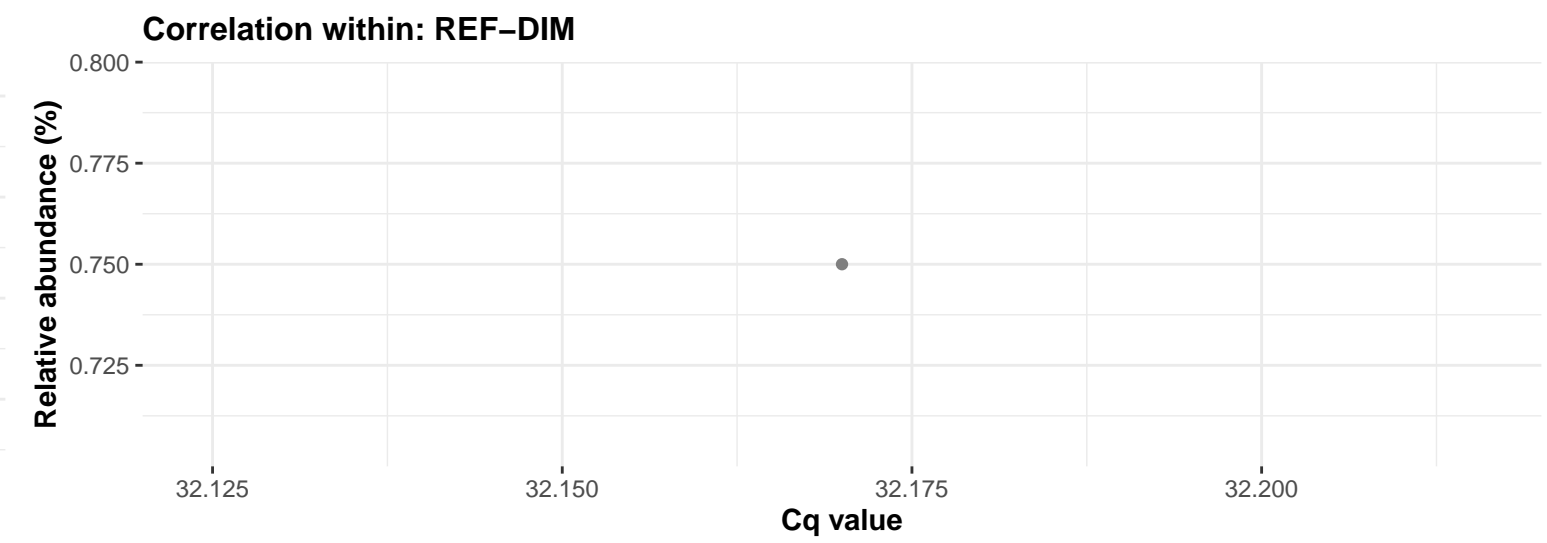
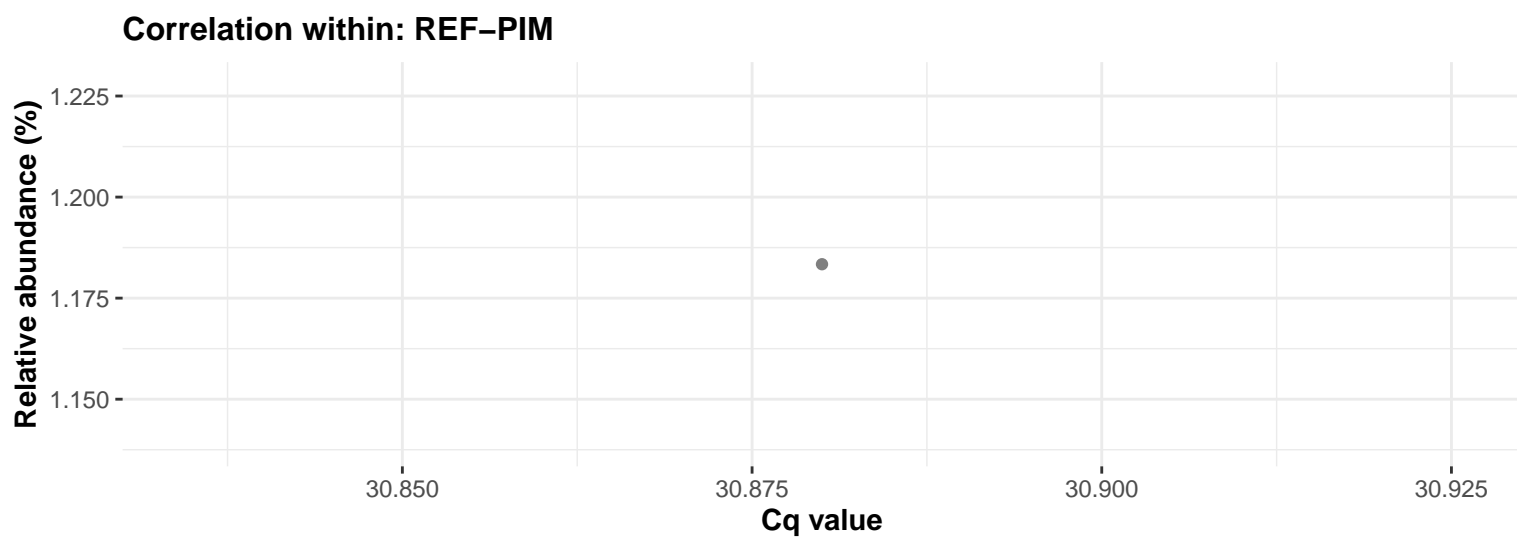
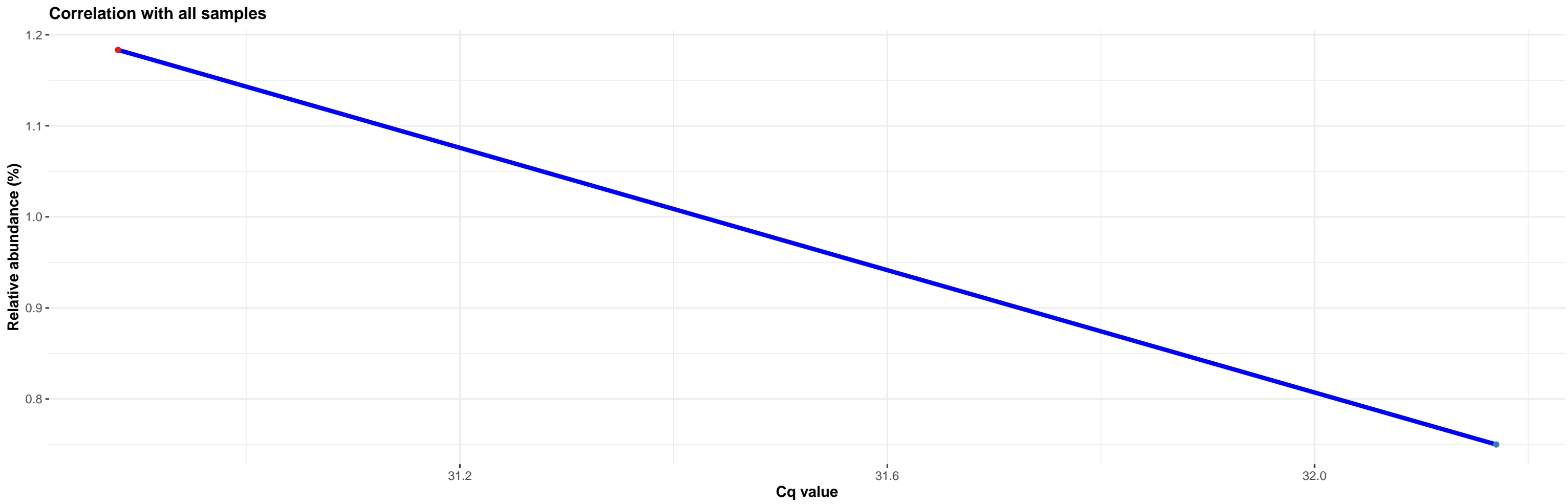


Correlation within: PCR-blank



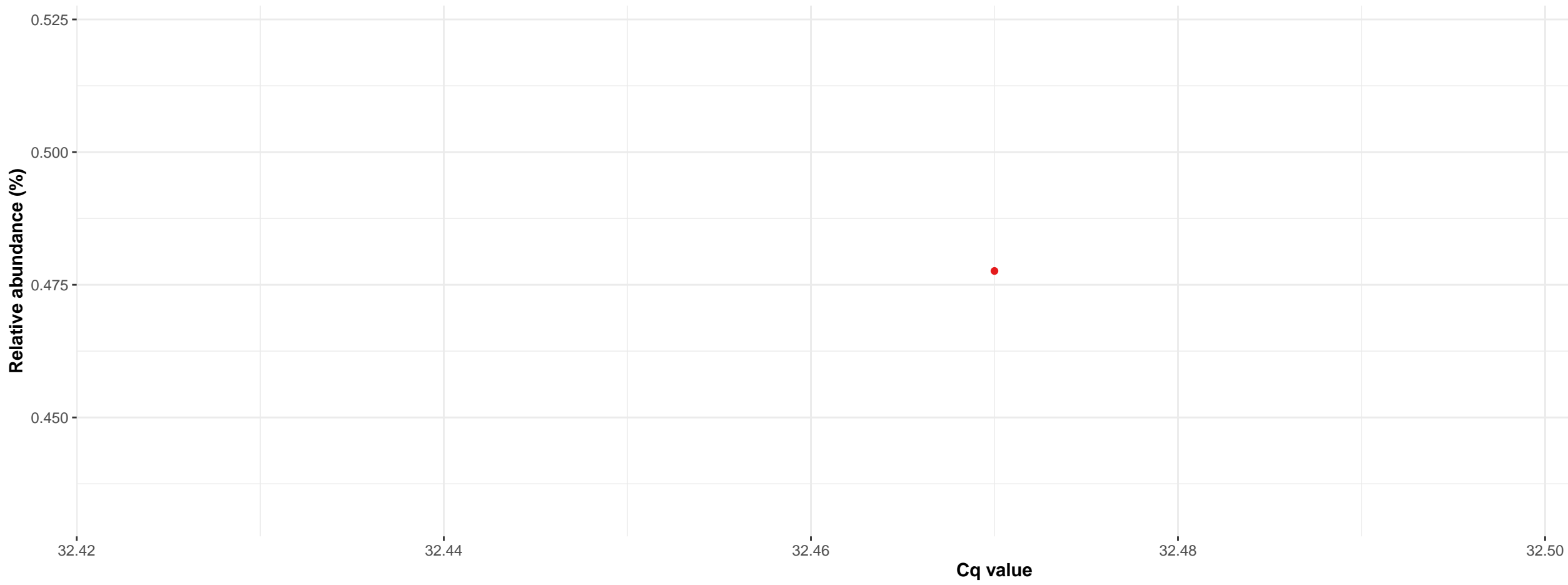


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Staphylococcus; s\_\_Staphylococcus sciuri



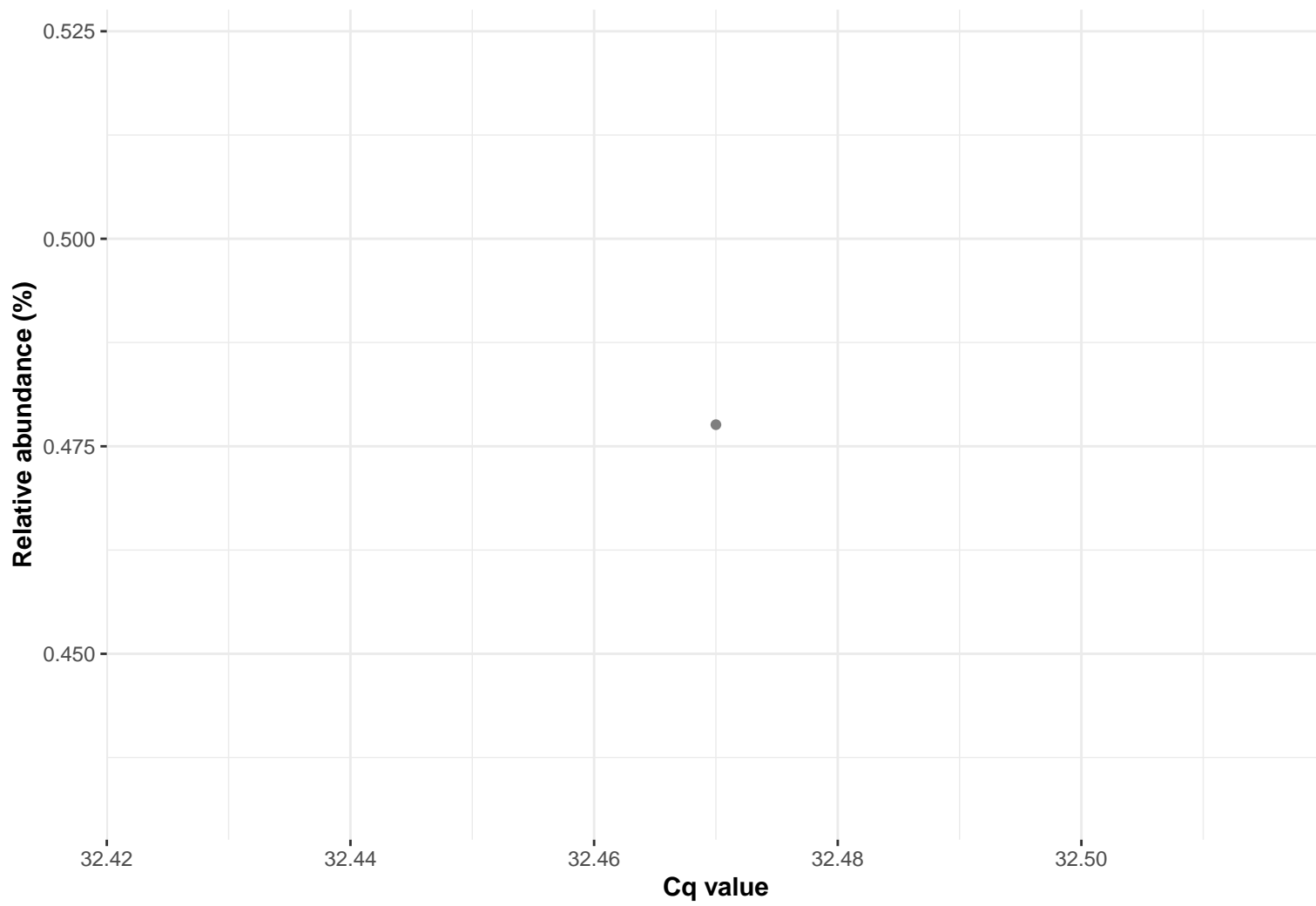
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

Correlation with all samples

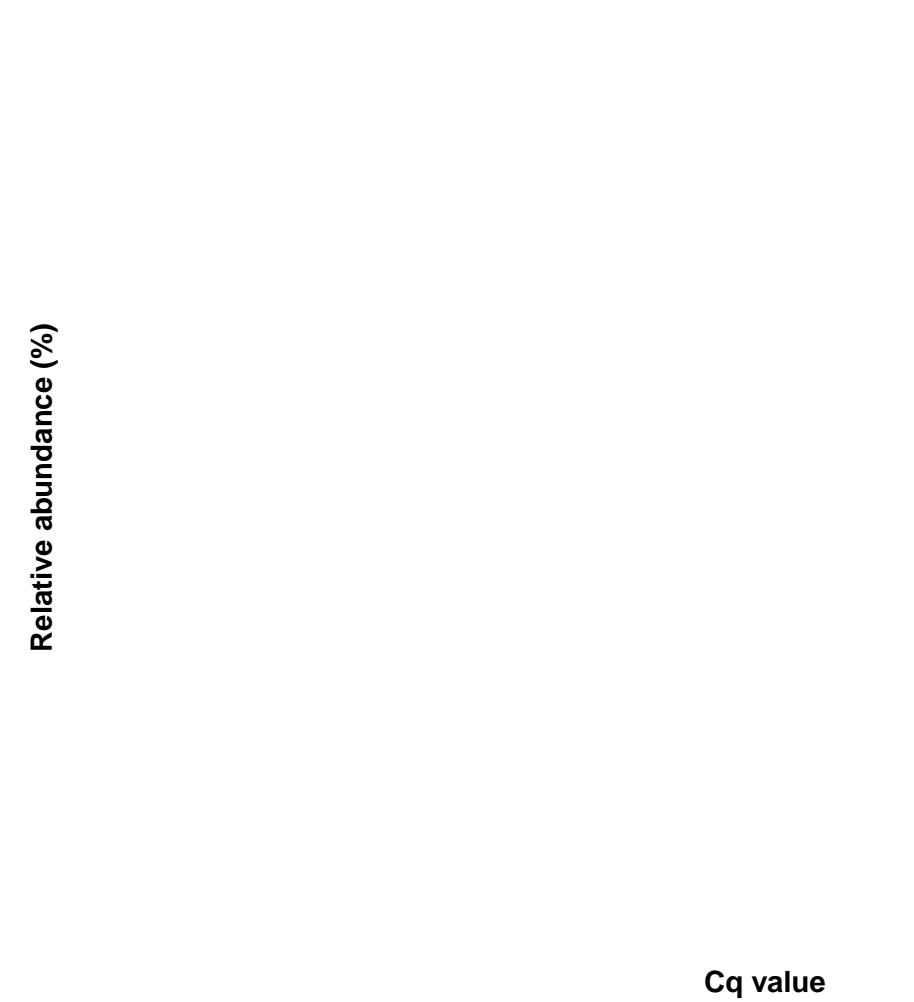


SampleType • REF-DIM

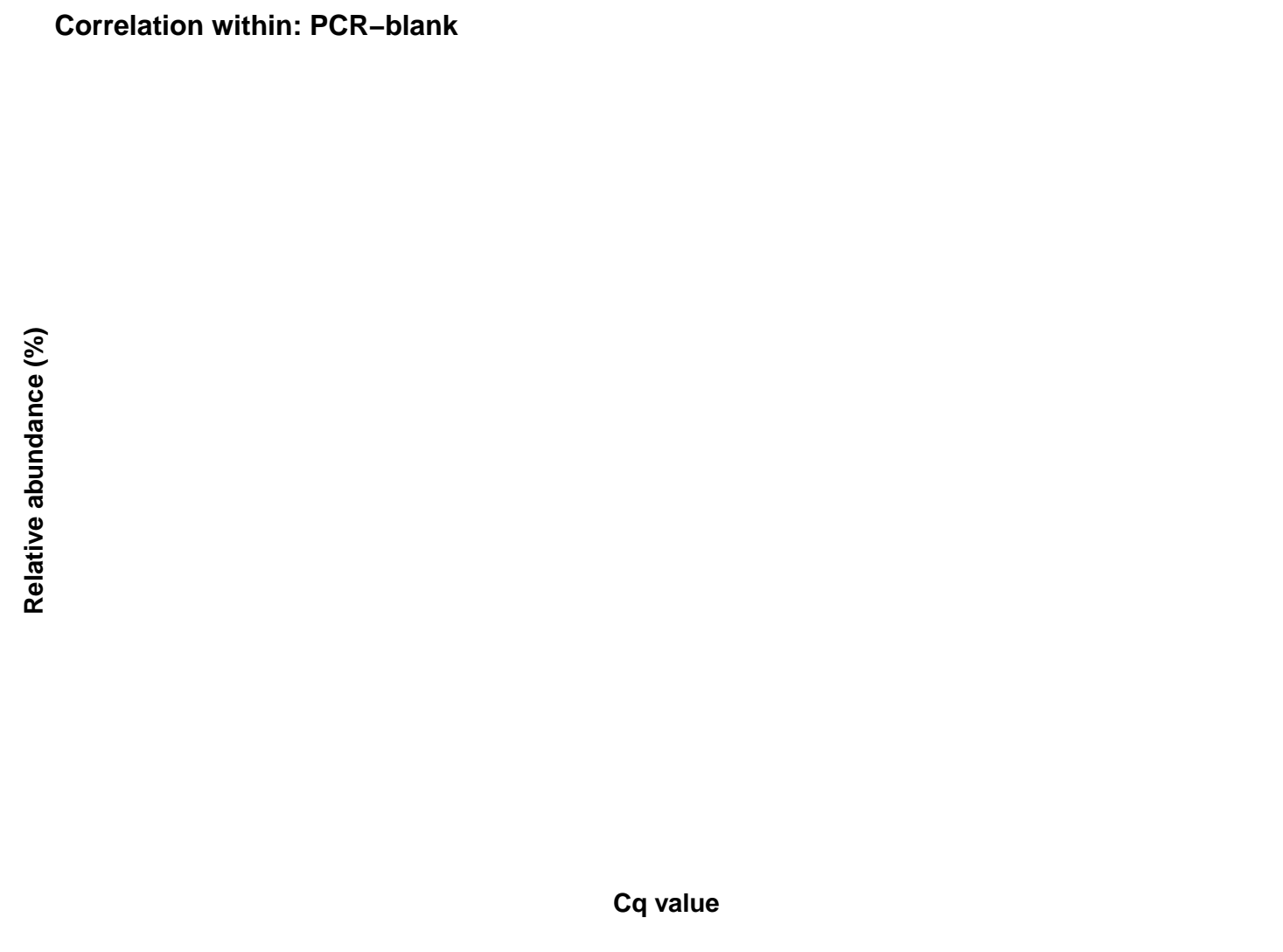
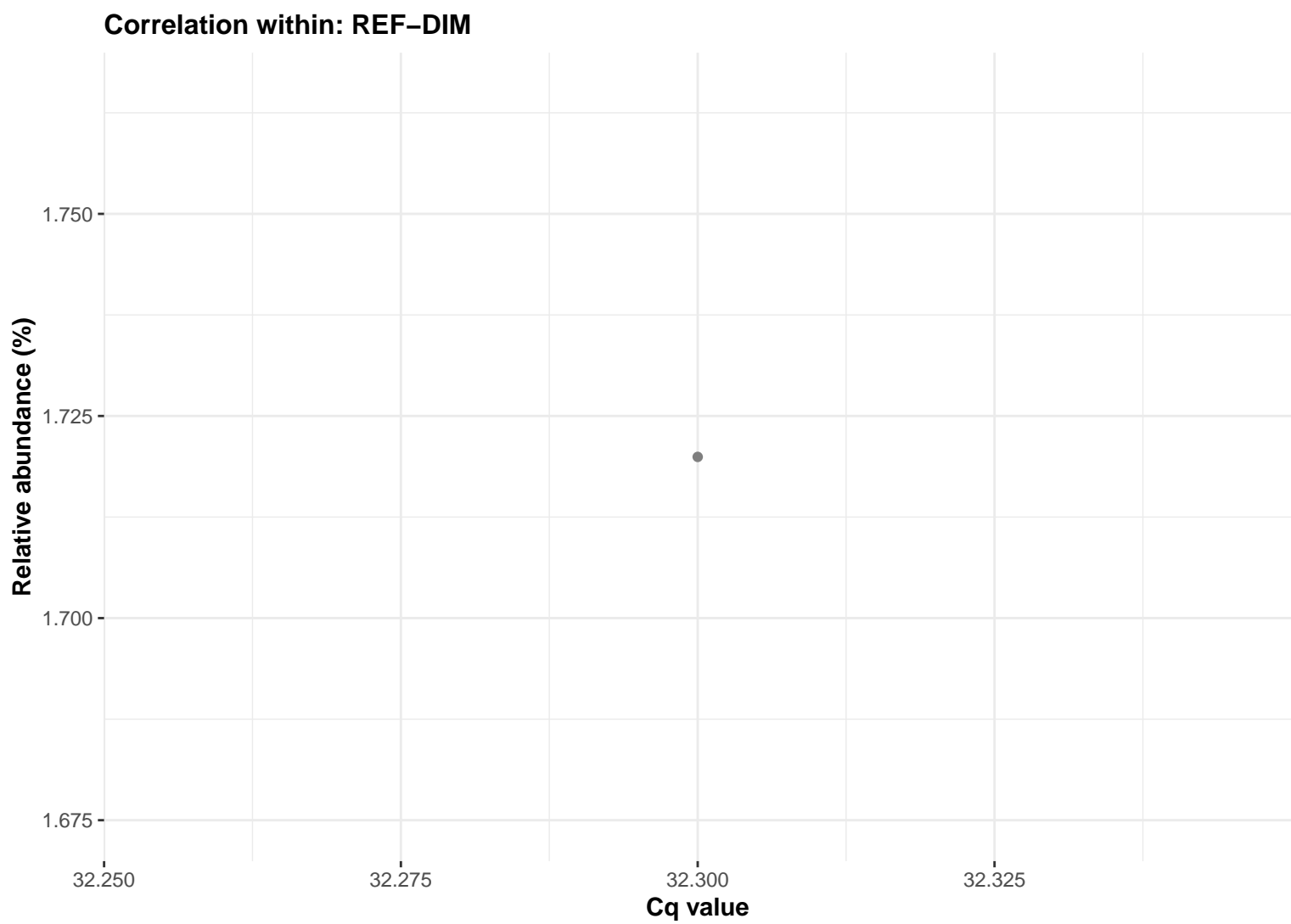
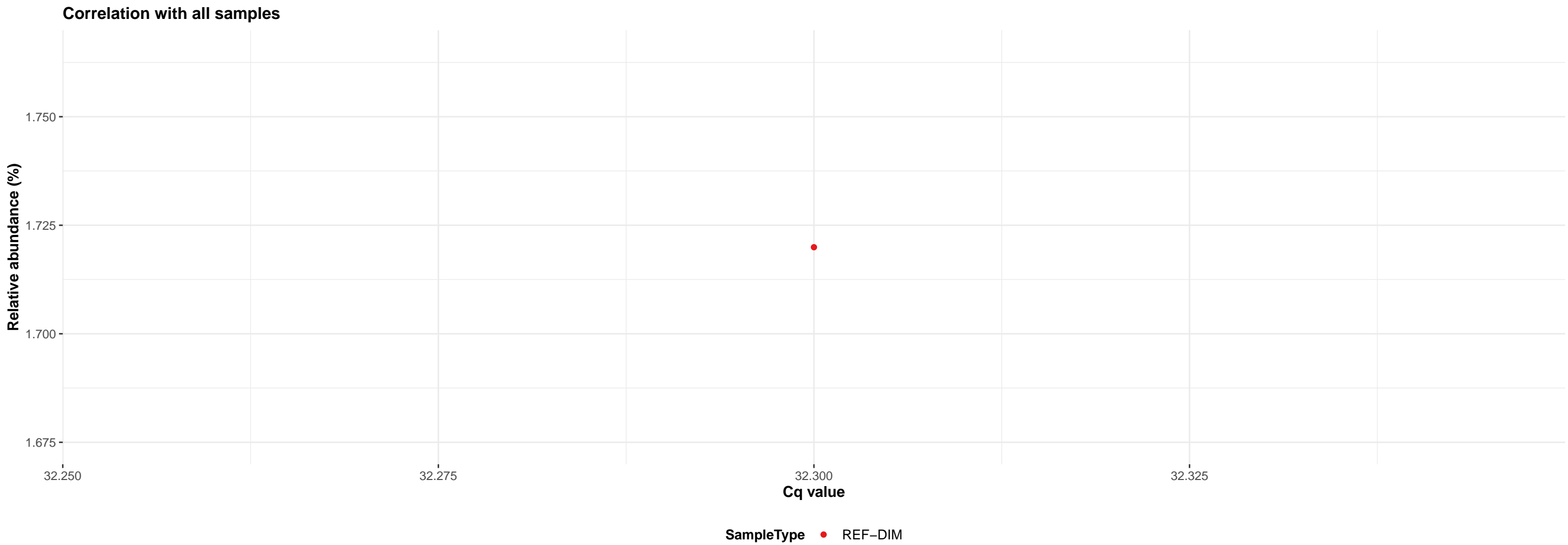
Correlation within: REF-DIM



Correlation within: PCR-blank



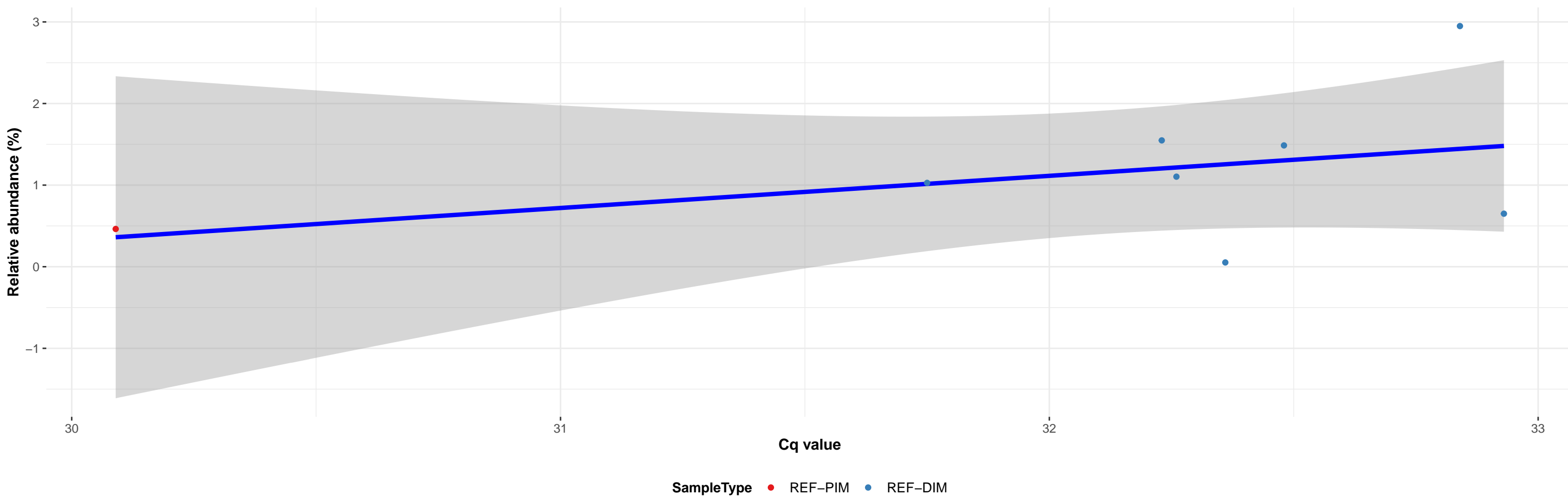
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae 1; g\_\_Clostridium sensu stricto 1; NA



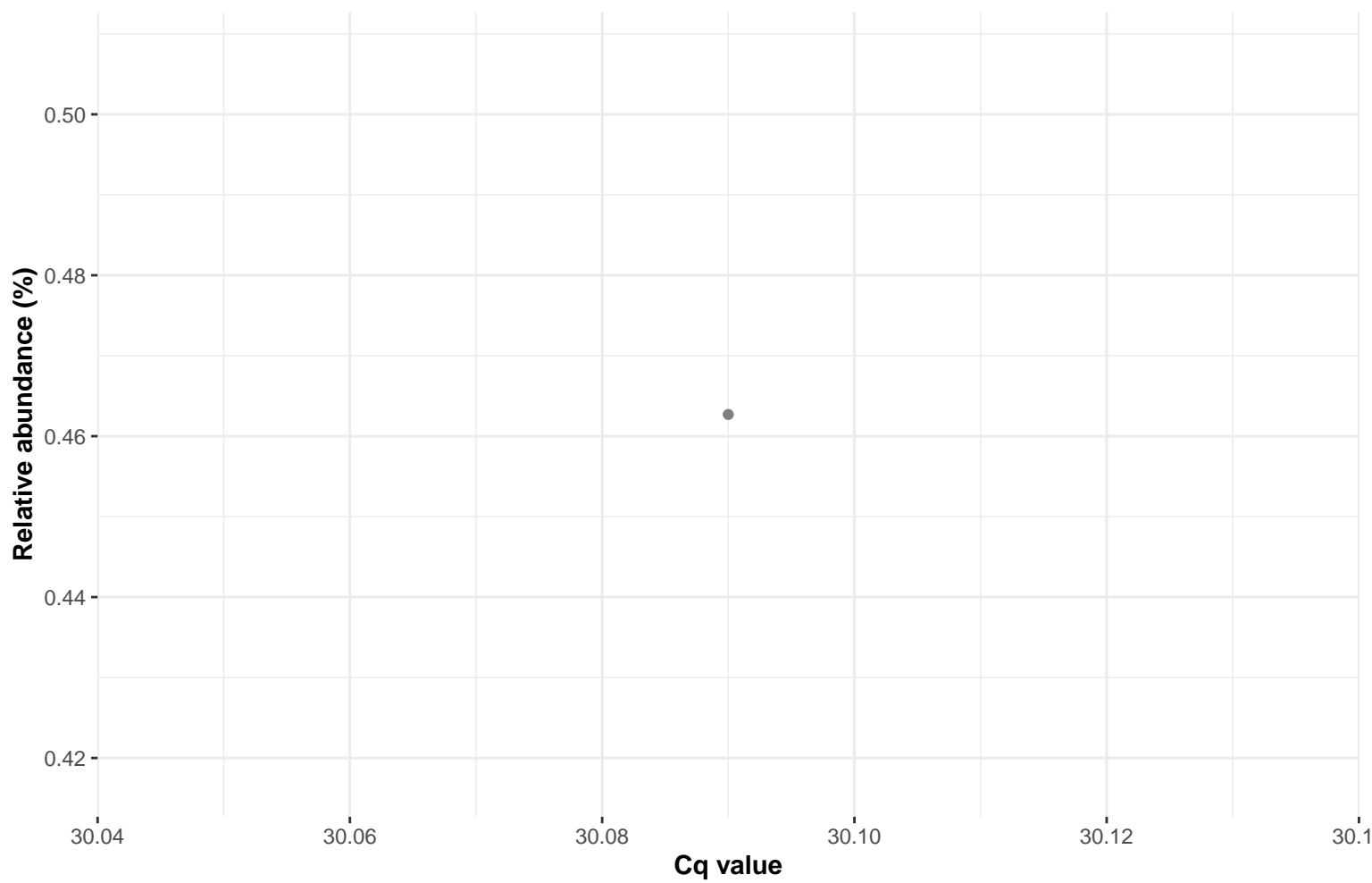
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Lysinibacillus; NA

### Correlation with all samples

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

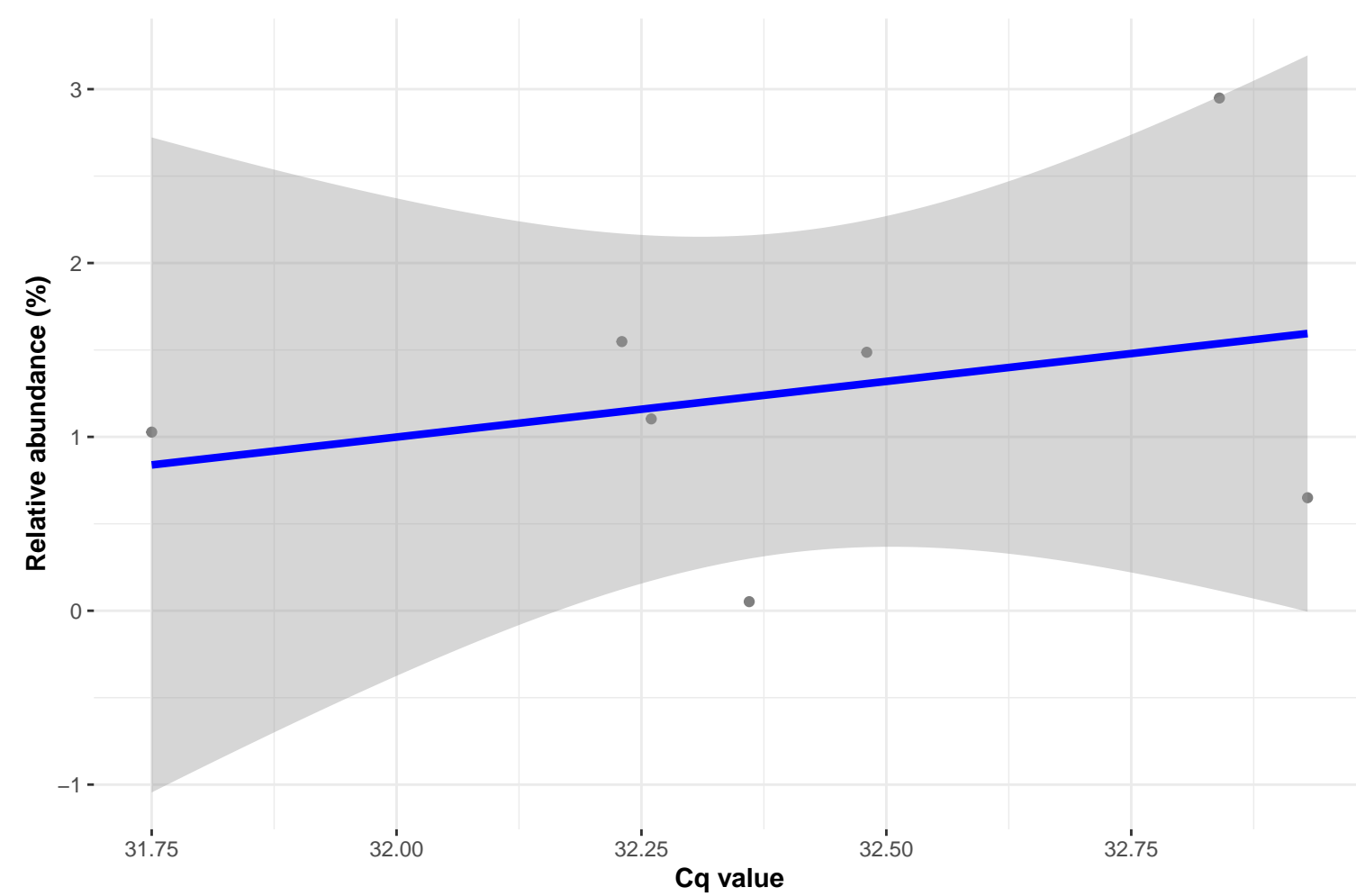


### Correlation within: REF-PIM



### Correlation within: REF-DIM

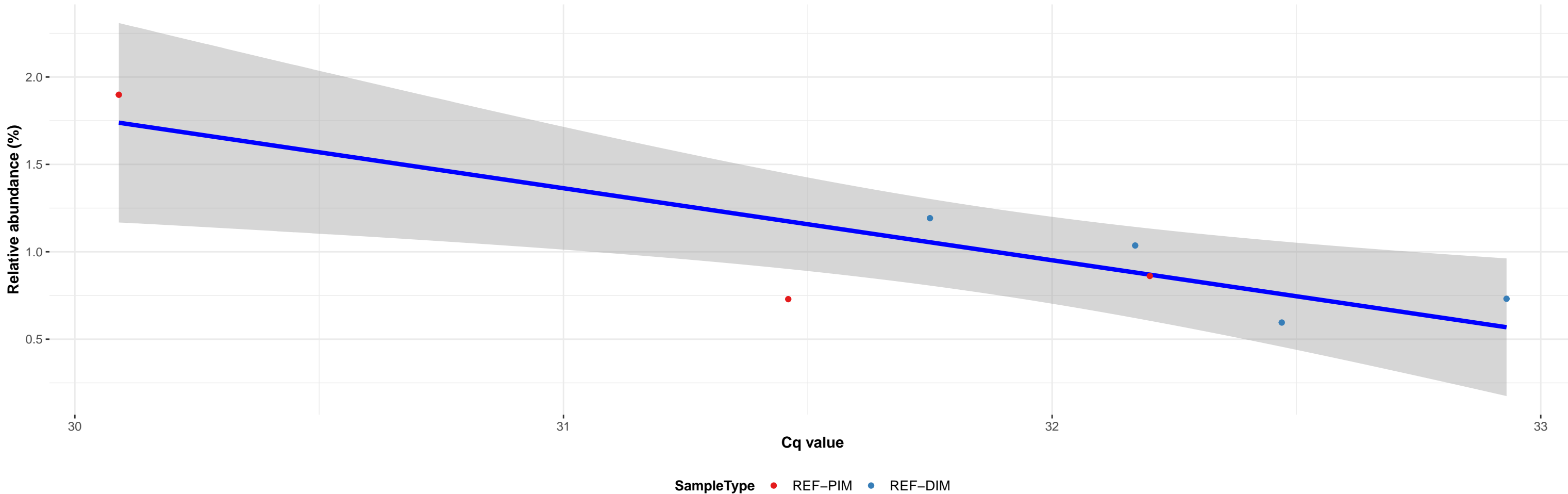
$\log_e(S) = 4.025$ ,  $p = 1.000$ ,  $\hat{\rho}_{\text{Spearman}} = 0.000$ ,  $CI_{95\%} [-0.765, 0.765]$ ,  $n_{\text{pairs}} = 7$



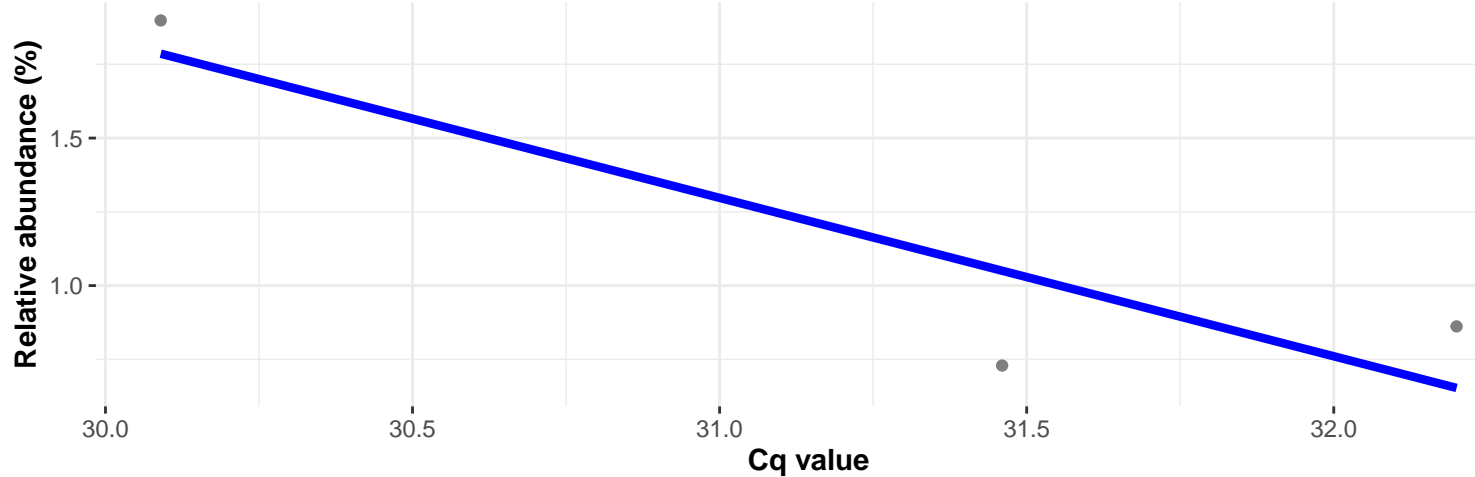
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

Correlation with all samples

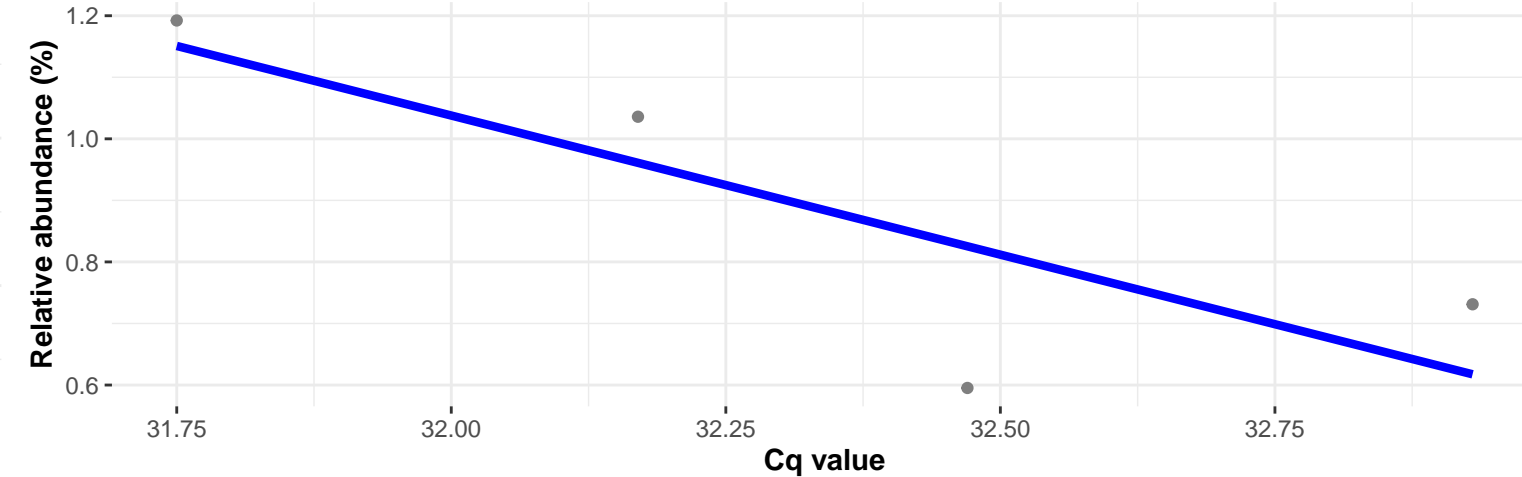
$\log_e(S) = 4.477$ ,  $p = 0.180$ ,  $\hat{\rho}_{\text{Spearman}} = -0.571$ ,  $CI_{95\%} [-0.930, 0.345]$ ,  $n_{\text{pairs}} = 7$



Correlation within: REF-PIM



Correlation within: REF-DIM

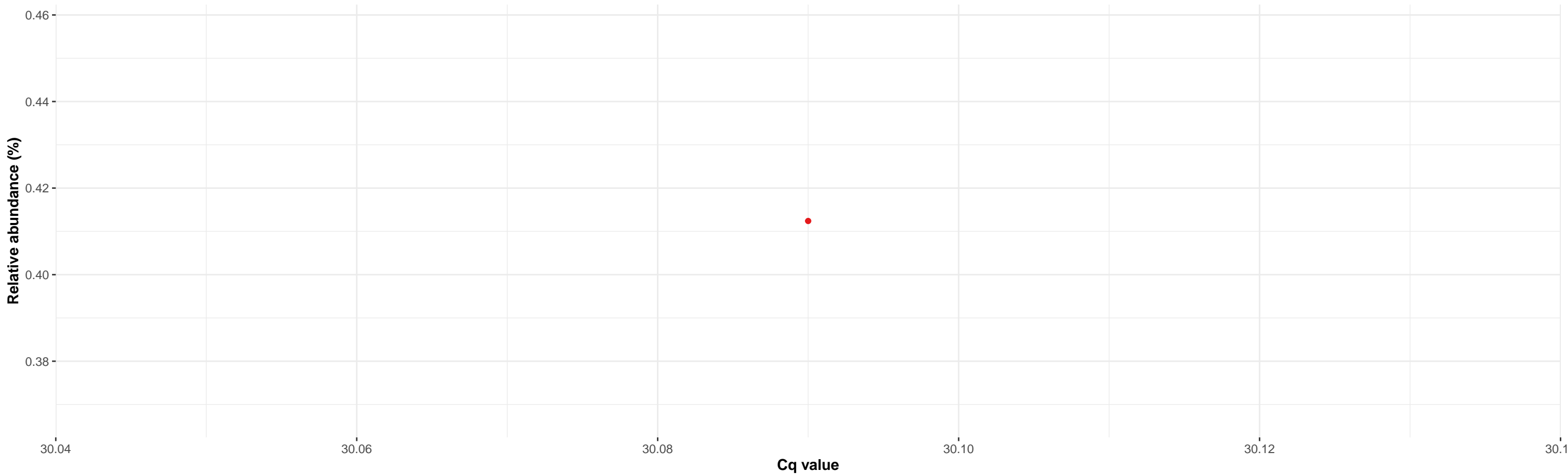


Correlation within: PCR-blank



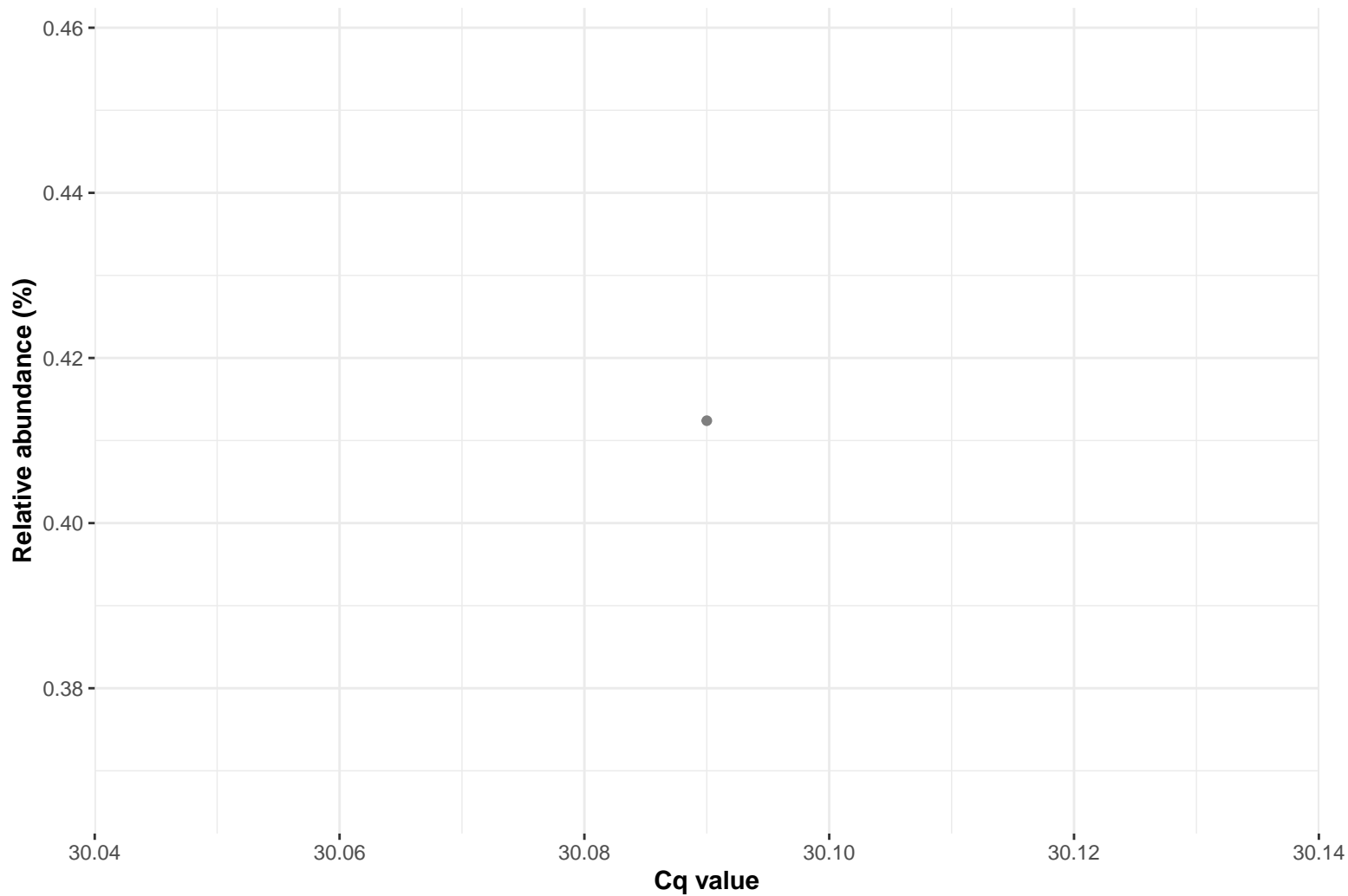
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus cecorum

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 (%)

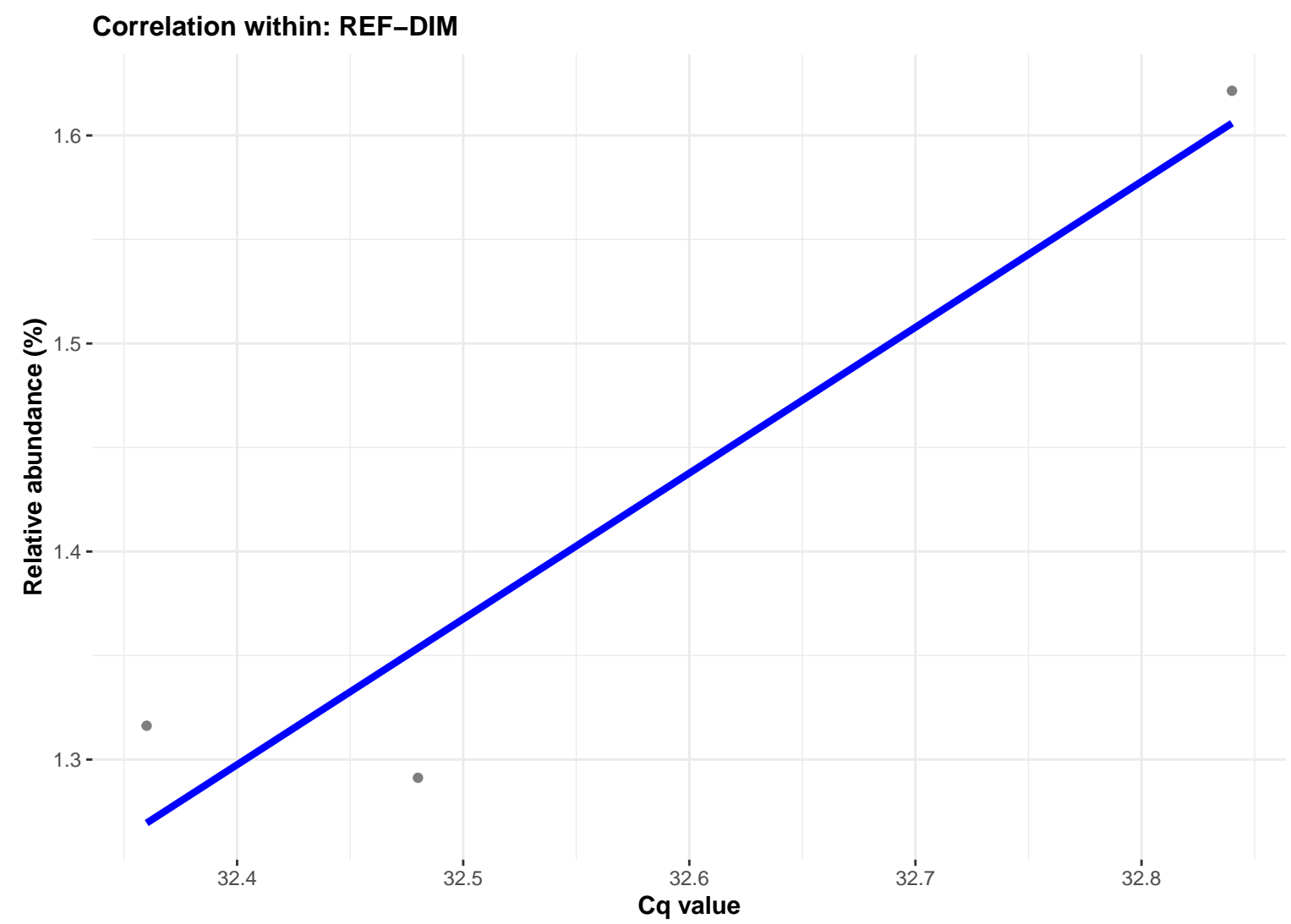
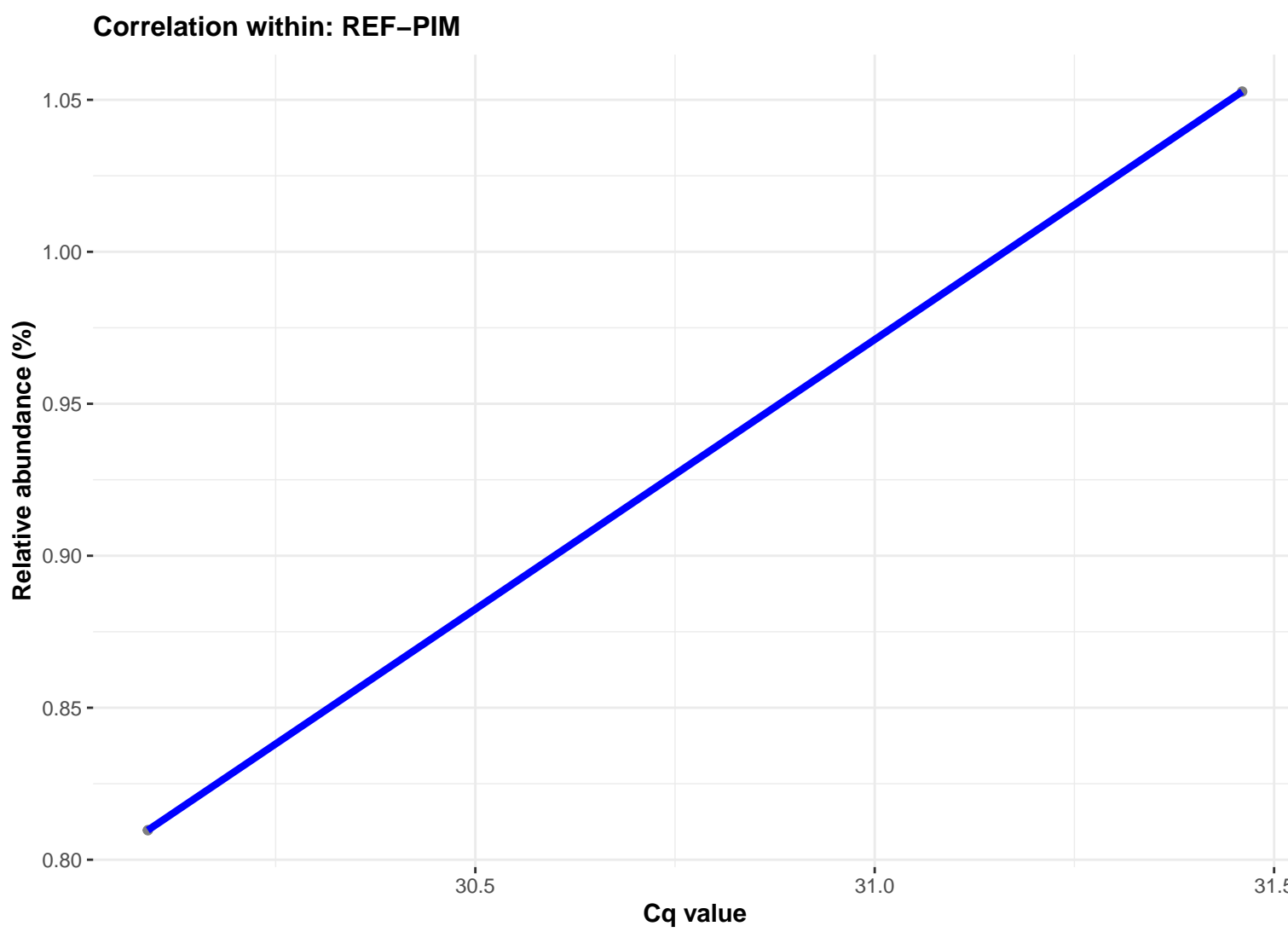
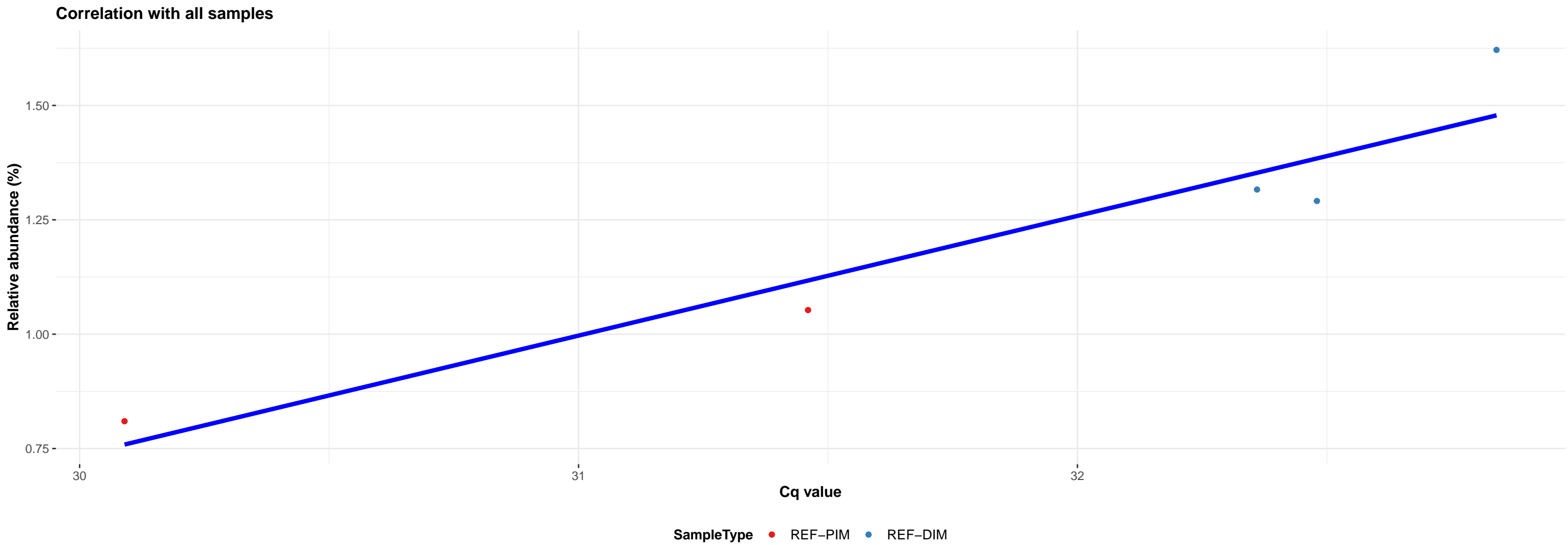
Correlation within: PCR–blank

Cq value

Relative abundance (%)

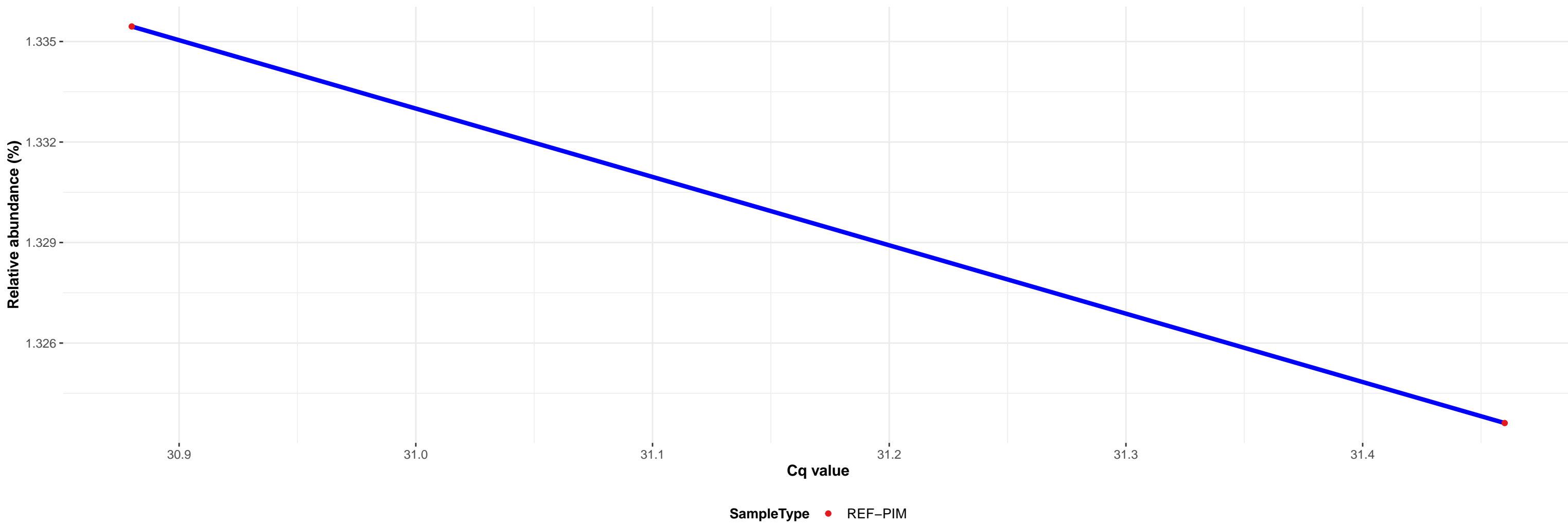
Cq value

k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; s\_\_uncultured Virgibacillus sp.

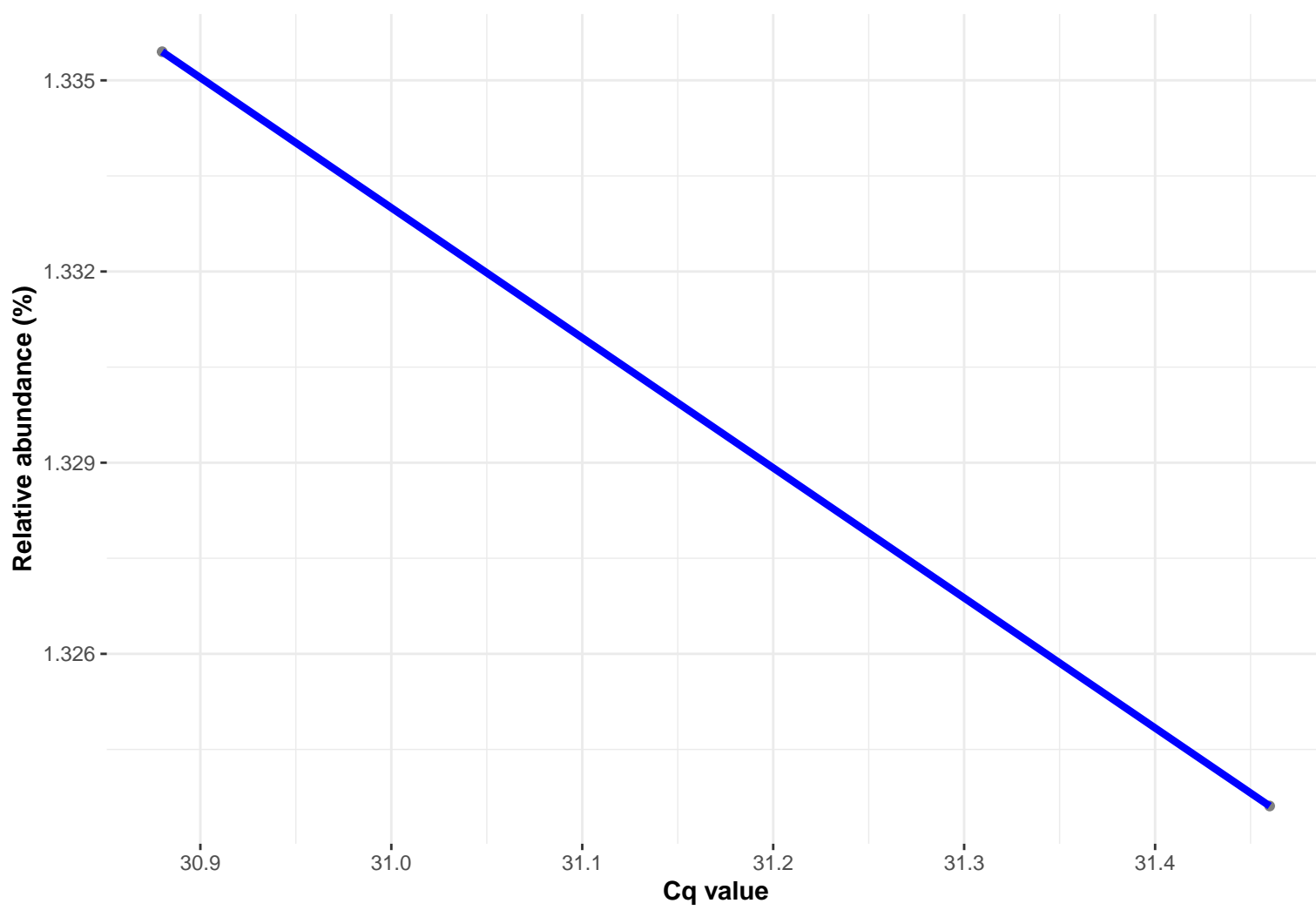




Correlation with all samples



Correlation within: REF-PIM

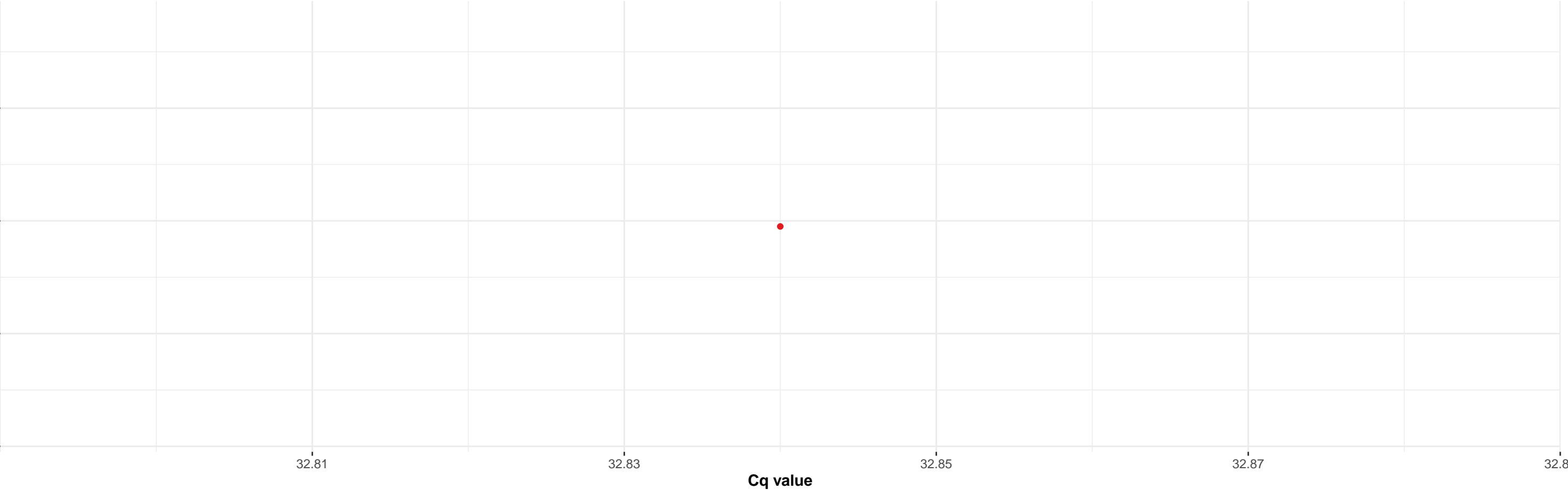


Correlation within: PCR-blank



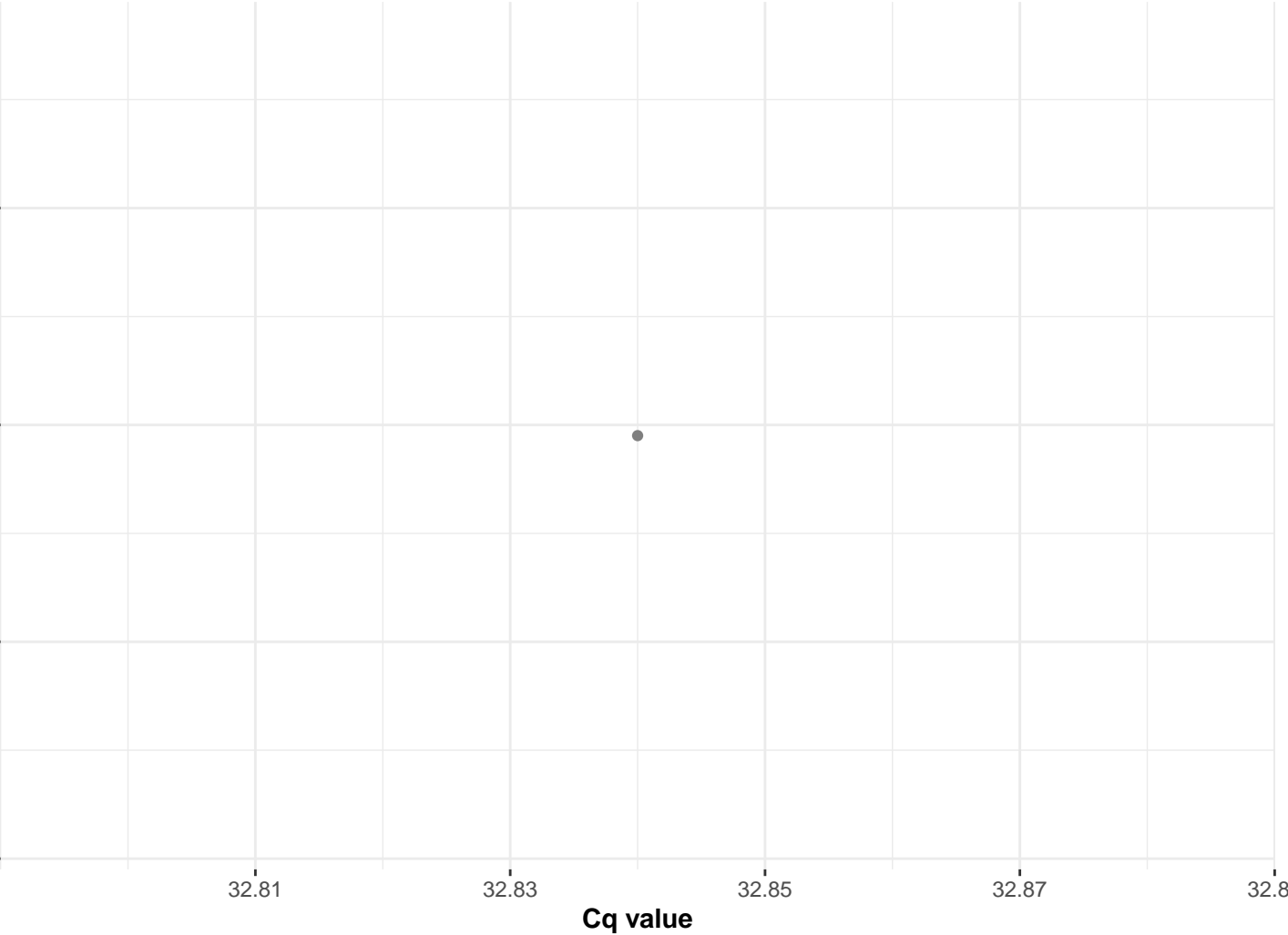
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Propionibacteriales; f\_\_Propionibacteriaceae; g\_\_Cutibacterium; NA

Correlation with all samples



SampleType REF-DIM

Correlation within: REF-DIM

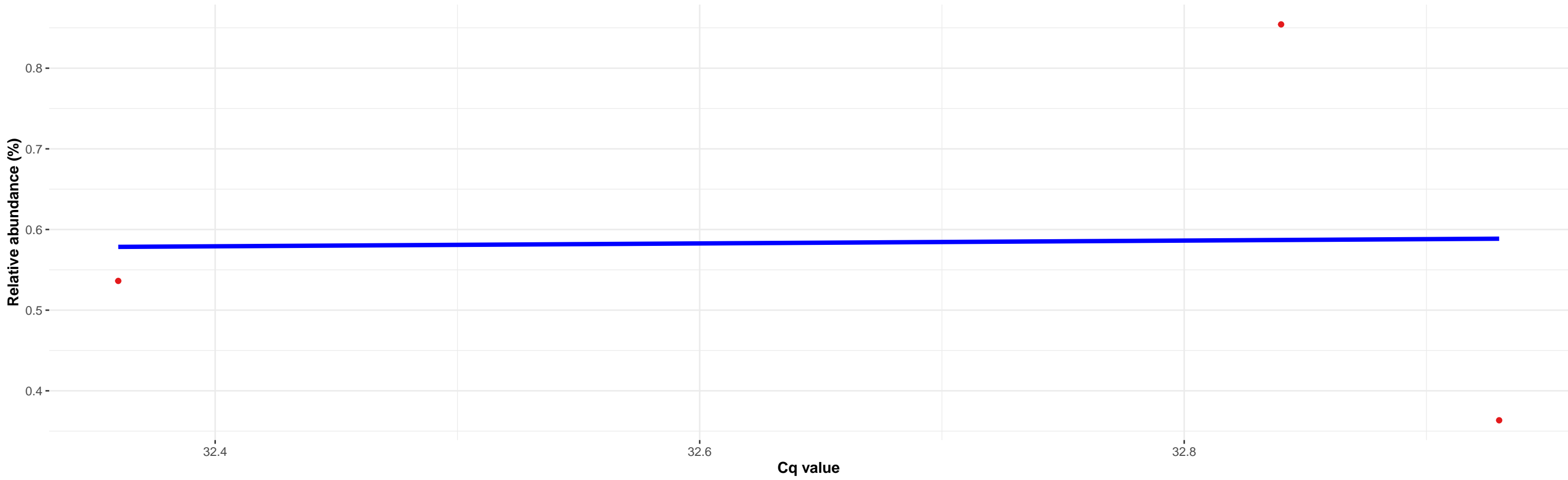


Correlation within: PCR-blank



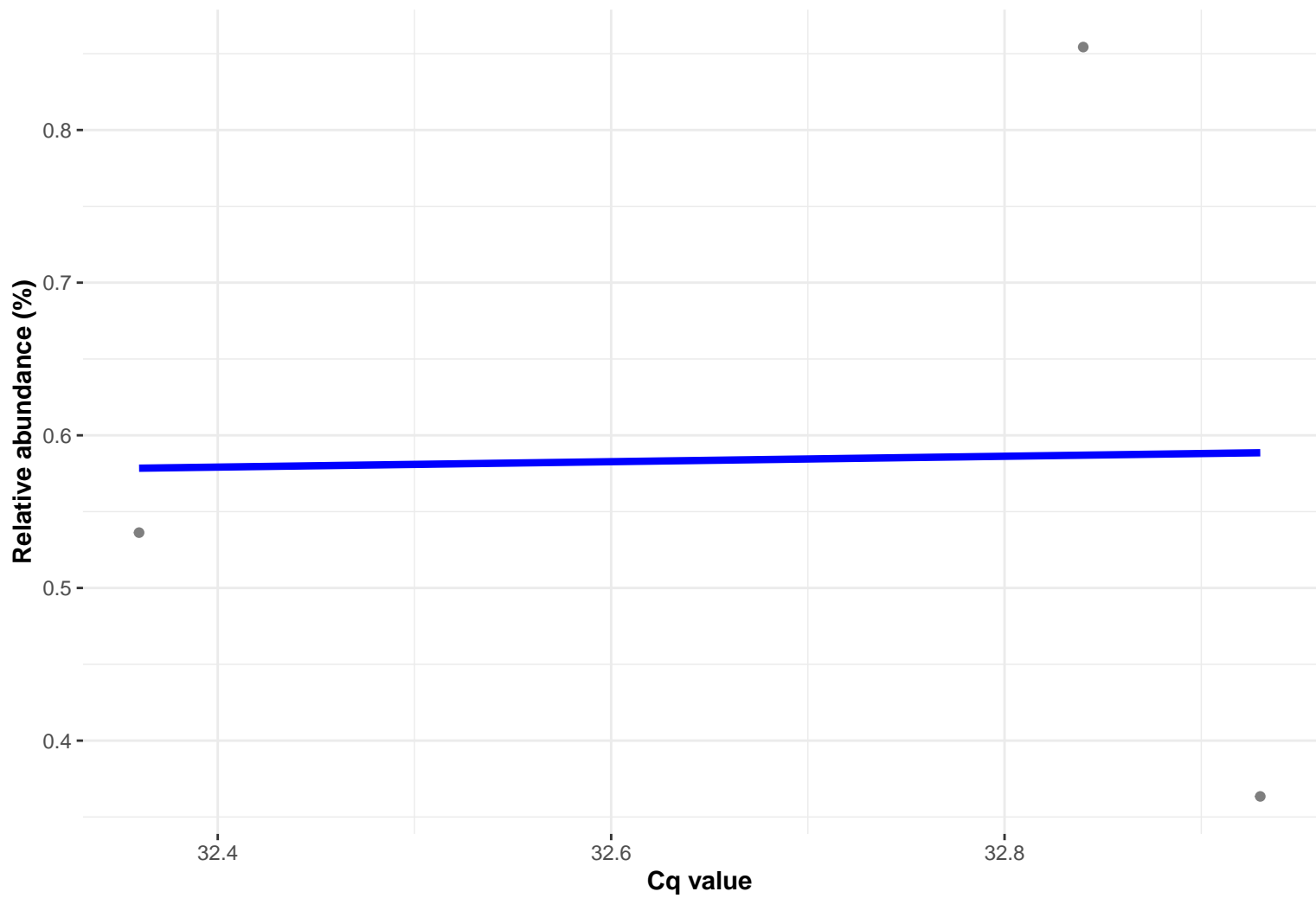
k\_\_Bacteria; p\_\_Cyanobacteria; c\_\_Melainabacteria; o\_\_Obscuribacterales; Ambiguous\_taxa; Ambiguous\_taxa; Ambiguous\_taxa

Correlation with all samples



SampleType • REF-DIM

Correlation within: REF-DIM

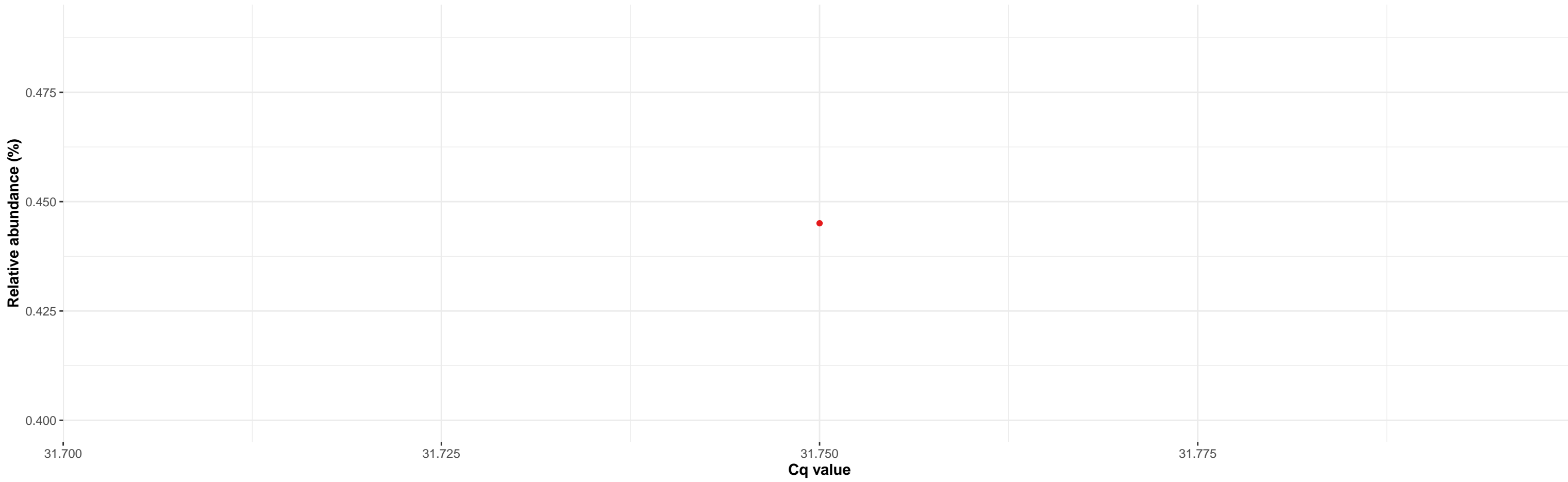


Correlation within: PCR-blank



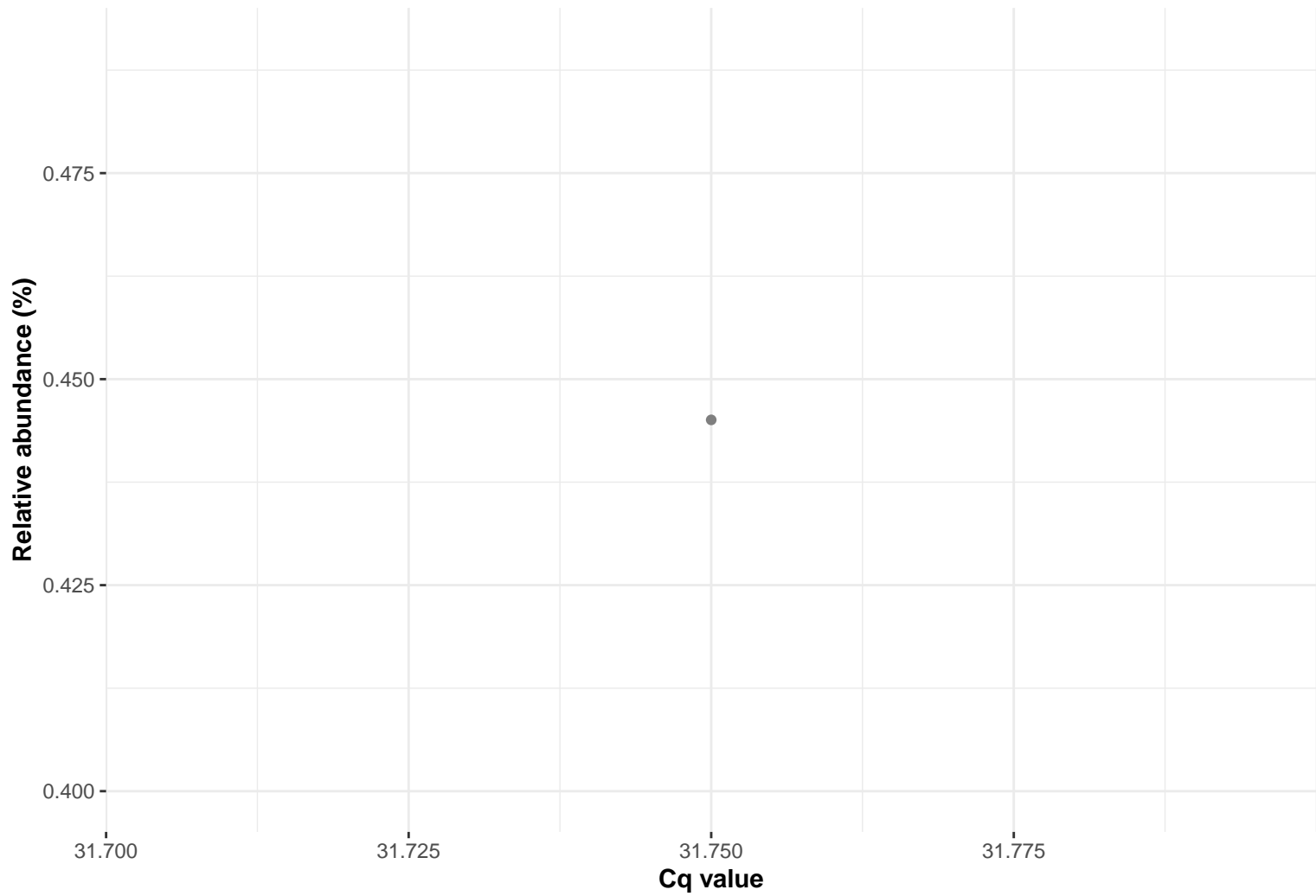
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Diplorickettsiales; f\_\_Diplorickettsiaceae; g\_\_Rickettsiella; s\_\_Proasellus assaforensis

Correlation with all samples



SampleType • REF-DIM

Correlation within: REF-DIM

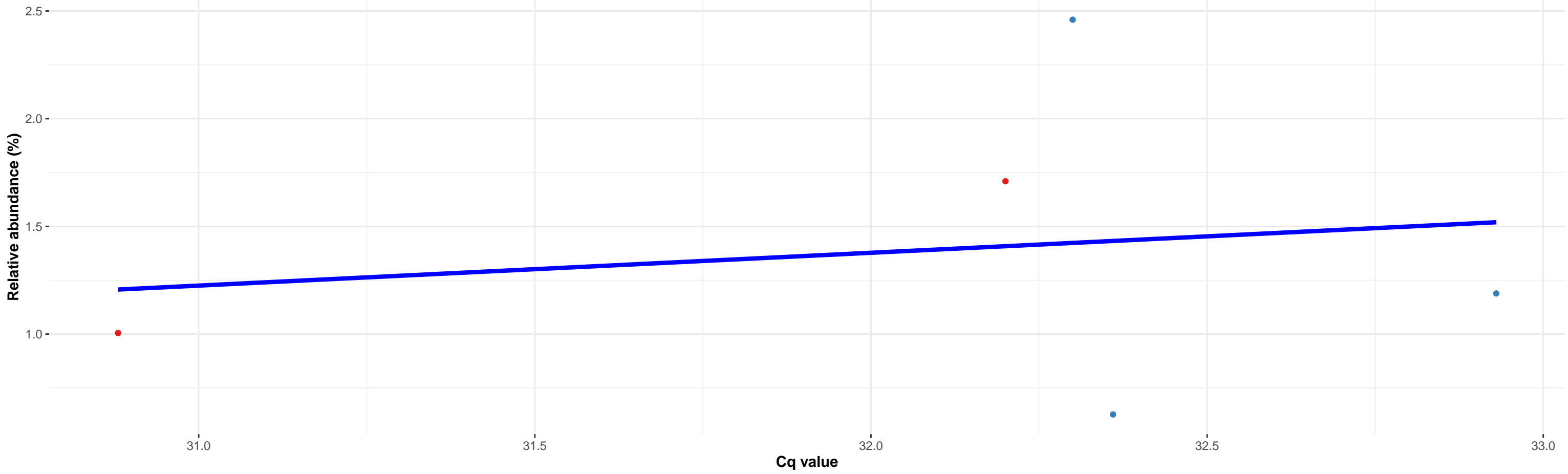


Correlation within: PCR-blank

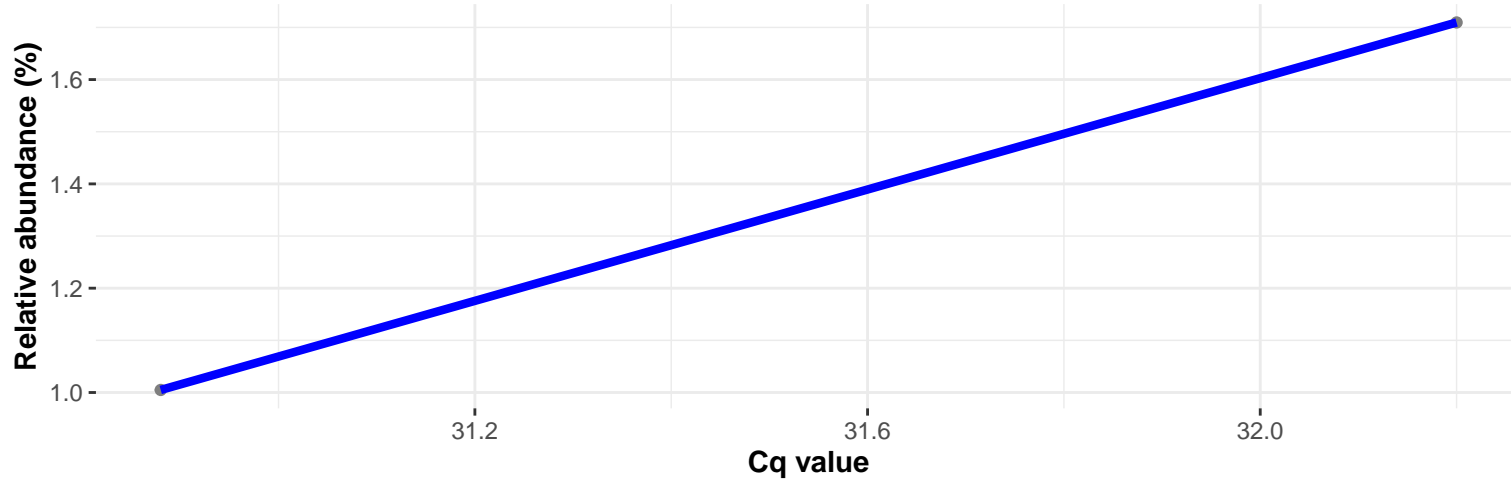


k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Microbacteriaceae; g\_\_Microbacterium; Ambiguous\_taxa

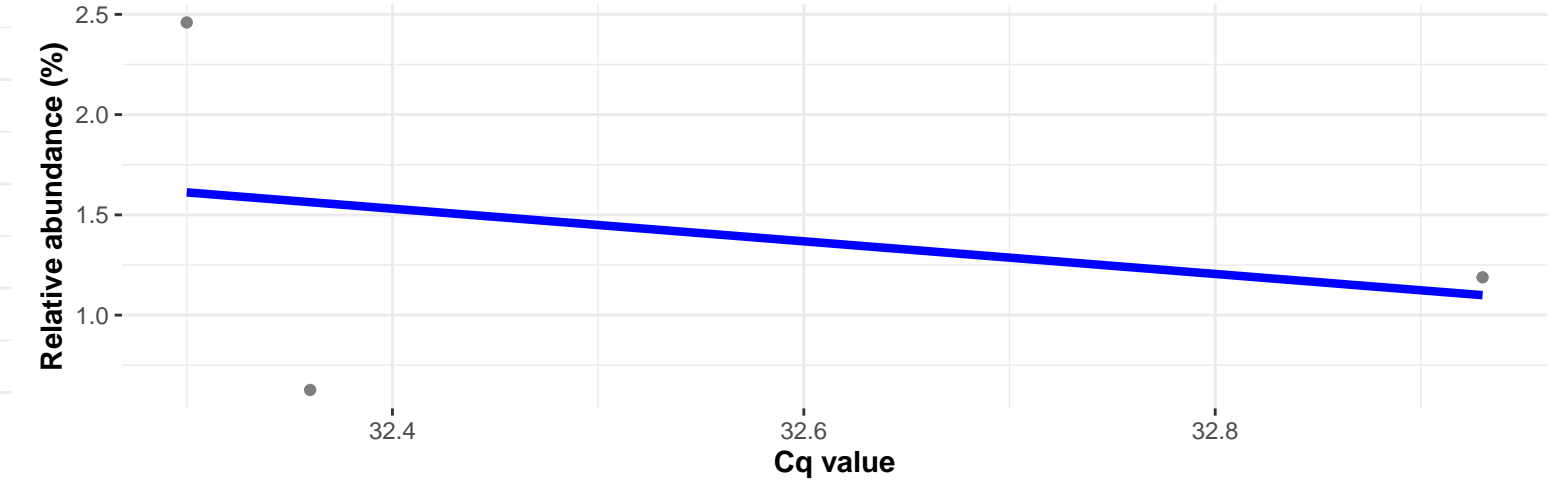
Correlation with all samples



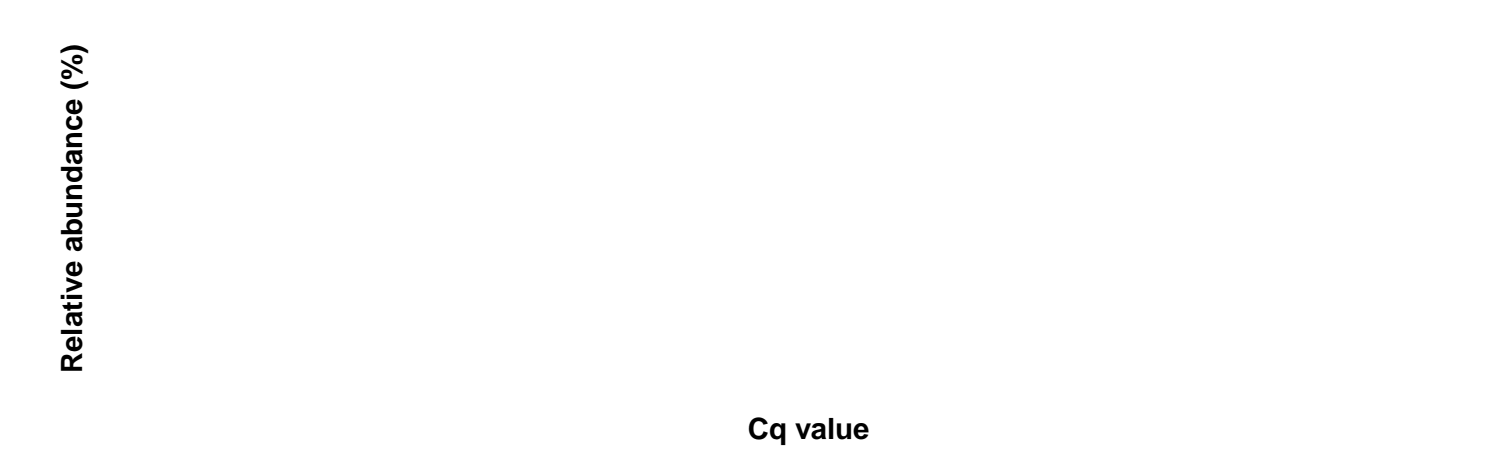
Correlation within: REF-PIM



Correlation within: REF-DIM

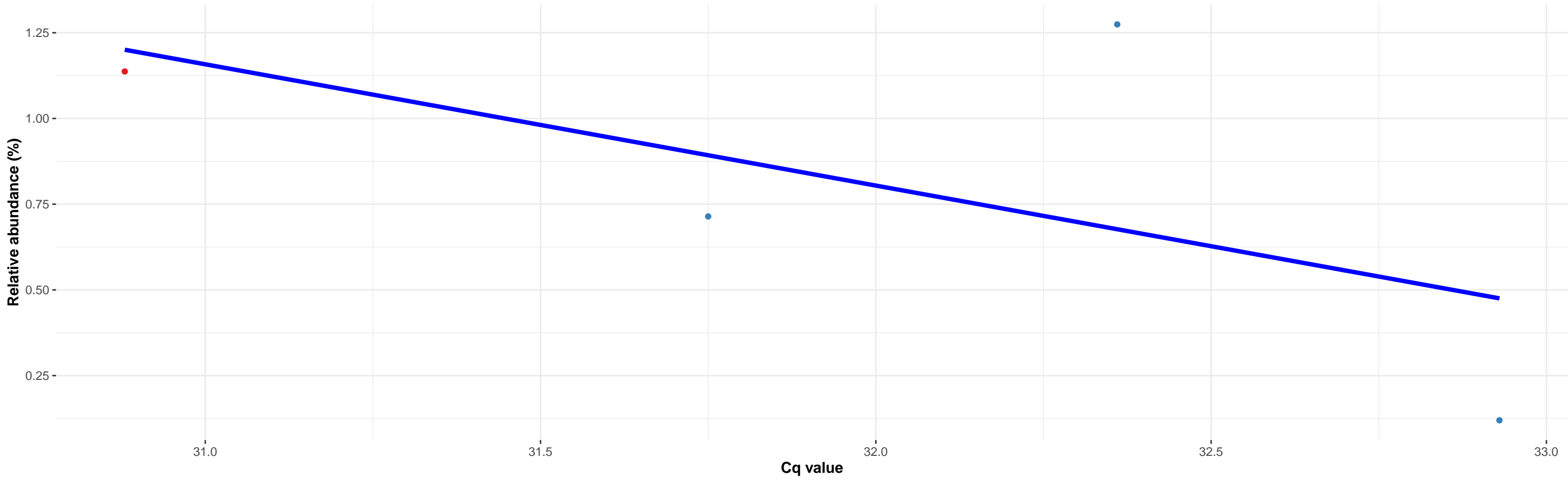


Correlation within: PCR-blank

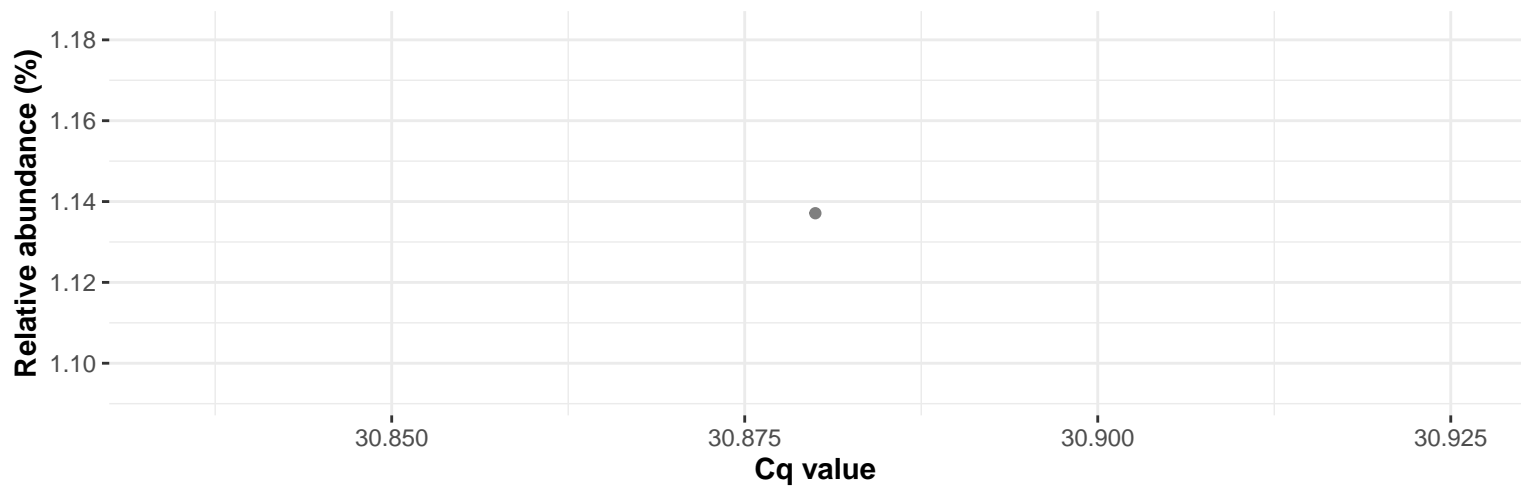


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; NA

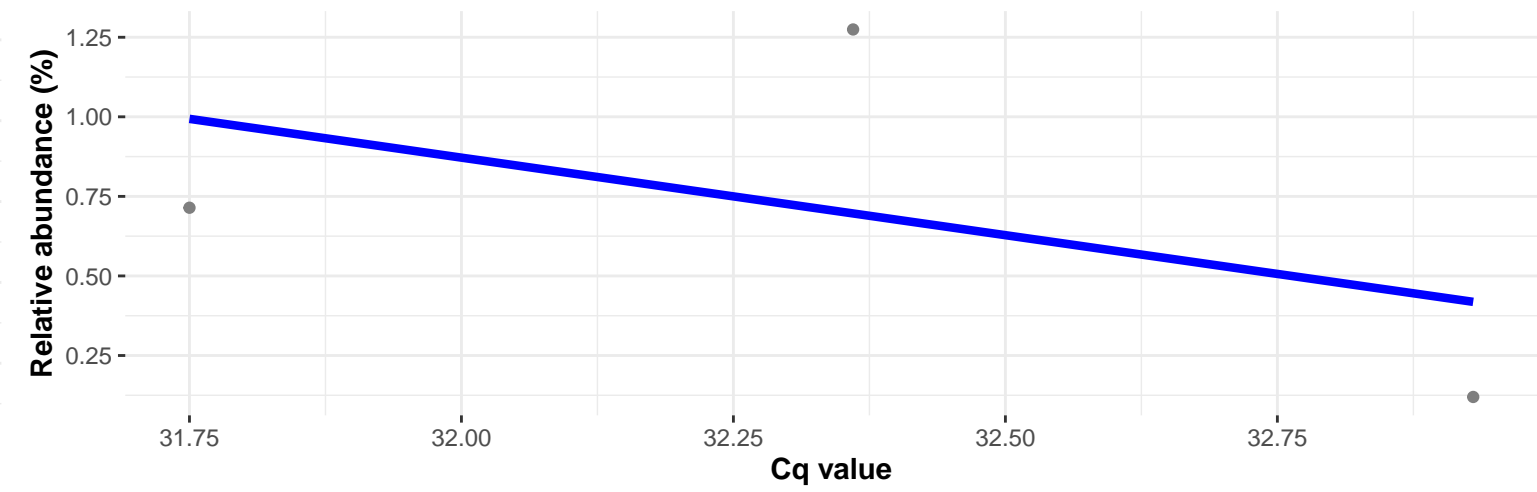
Correlation with all samples



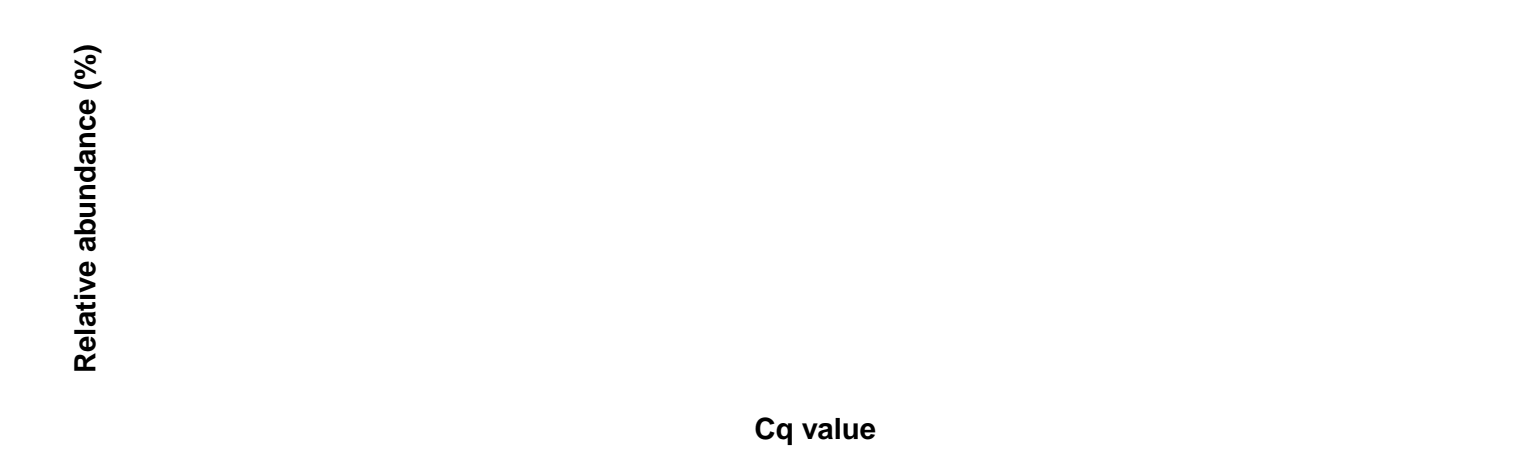
Correlation within: REF-PIM



Correlation within: REF-DIM

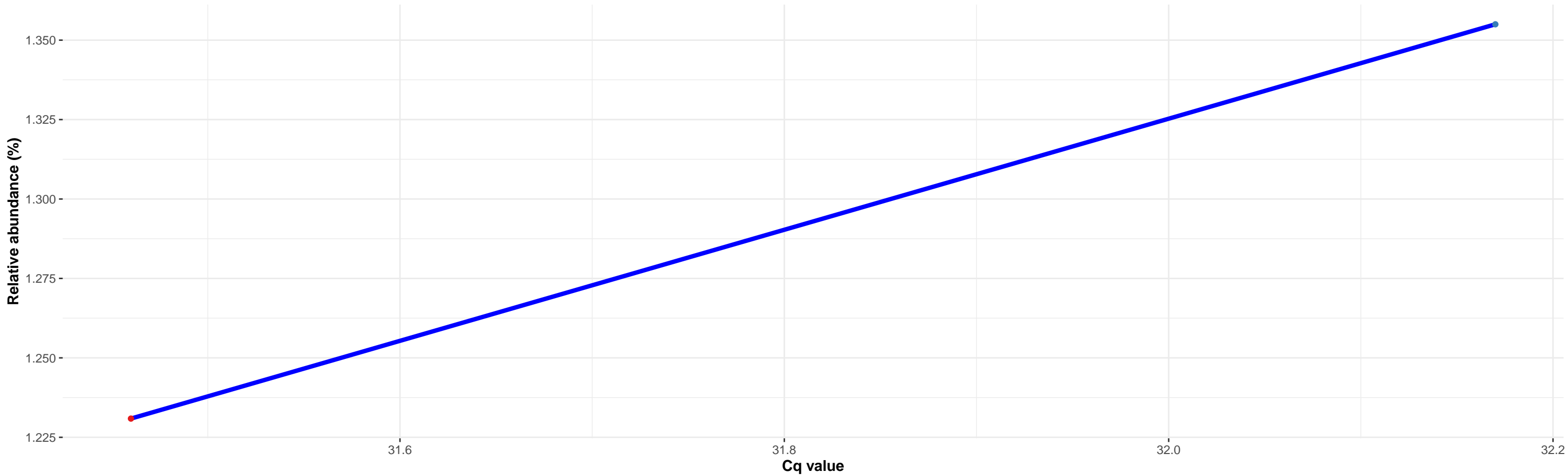


Correlation within: PCR-blank



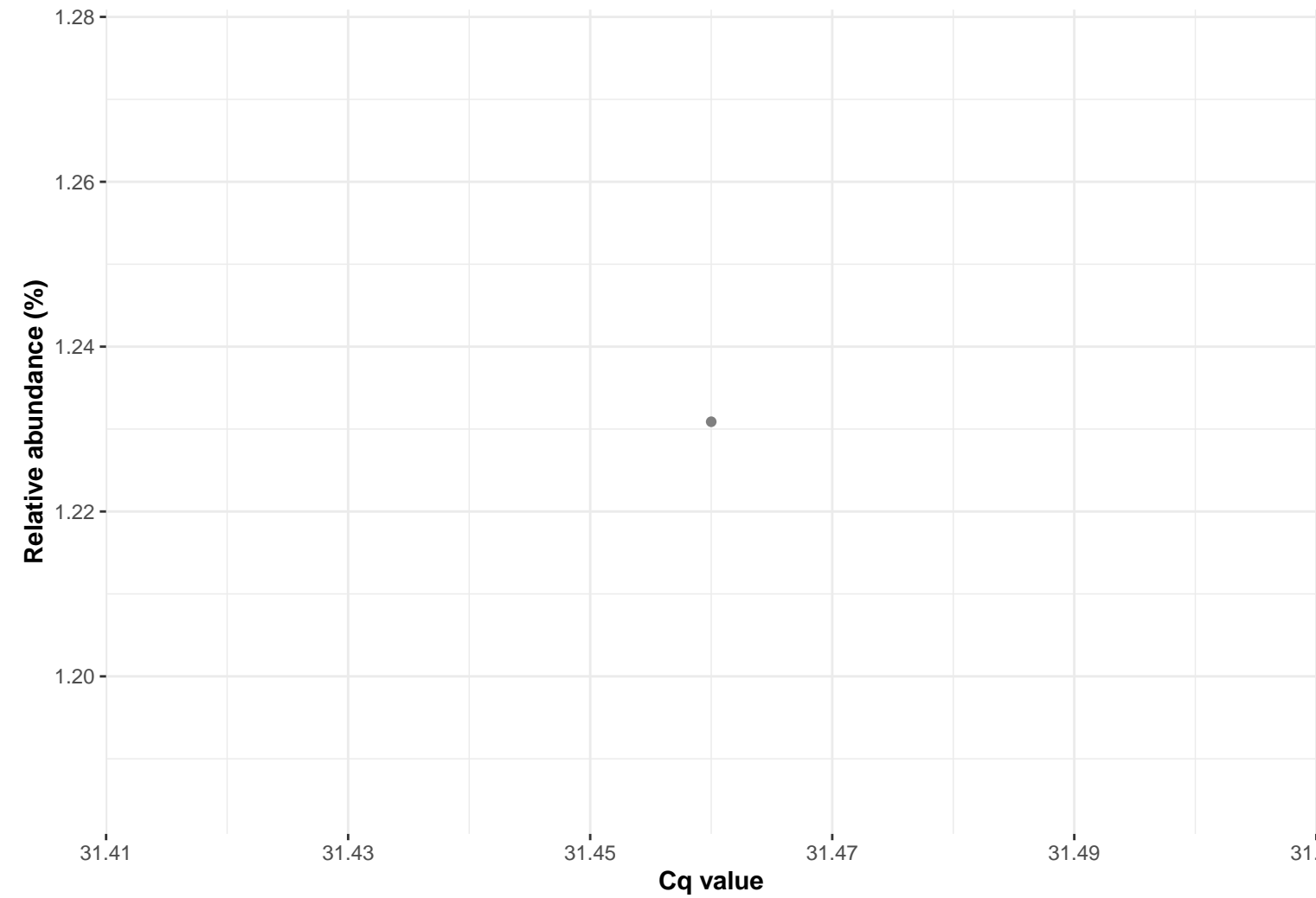
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; NA

Correlation with all samples

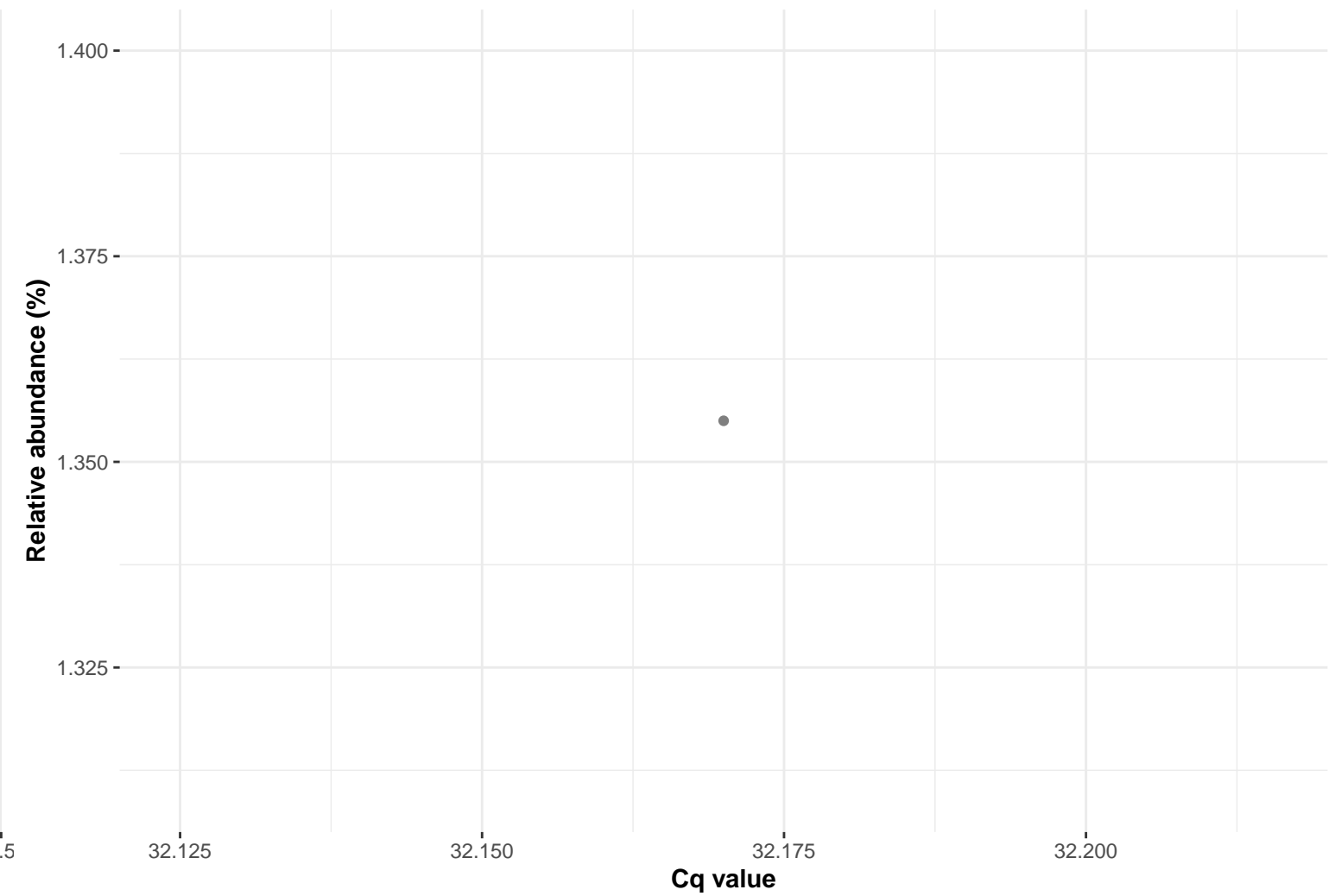


SampleType REF-PIM REF-DIM

Correlation within: REF-PIM

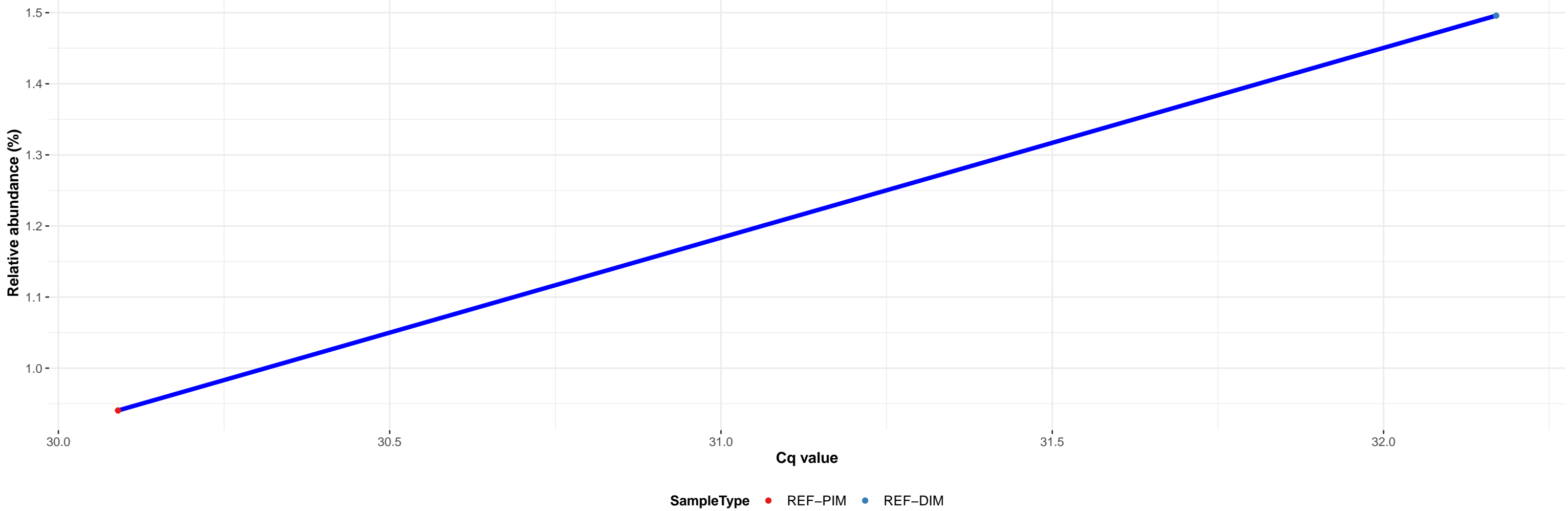


Correlation within: REF-DIM

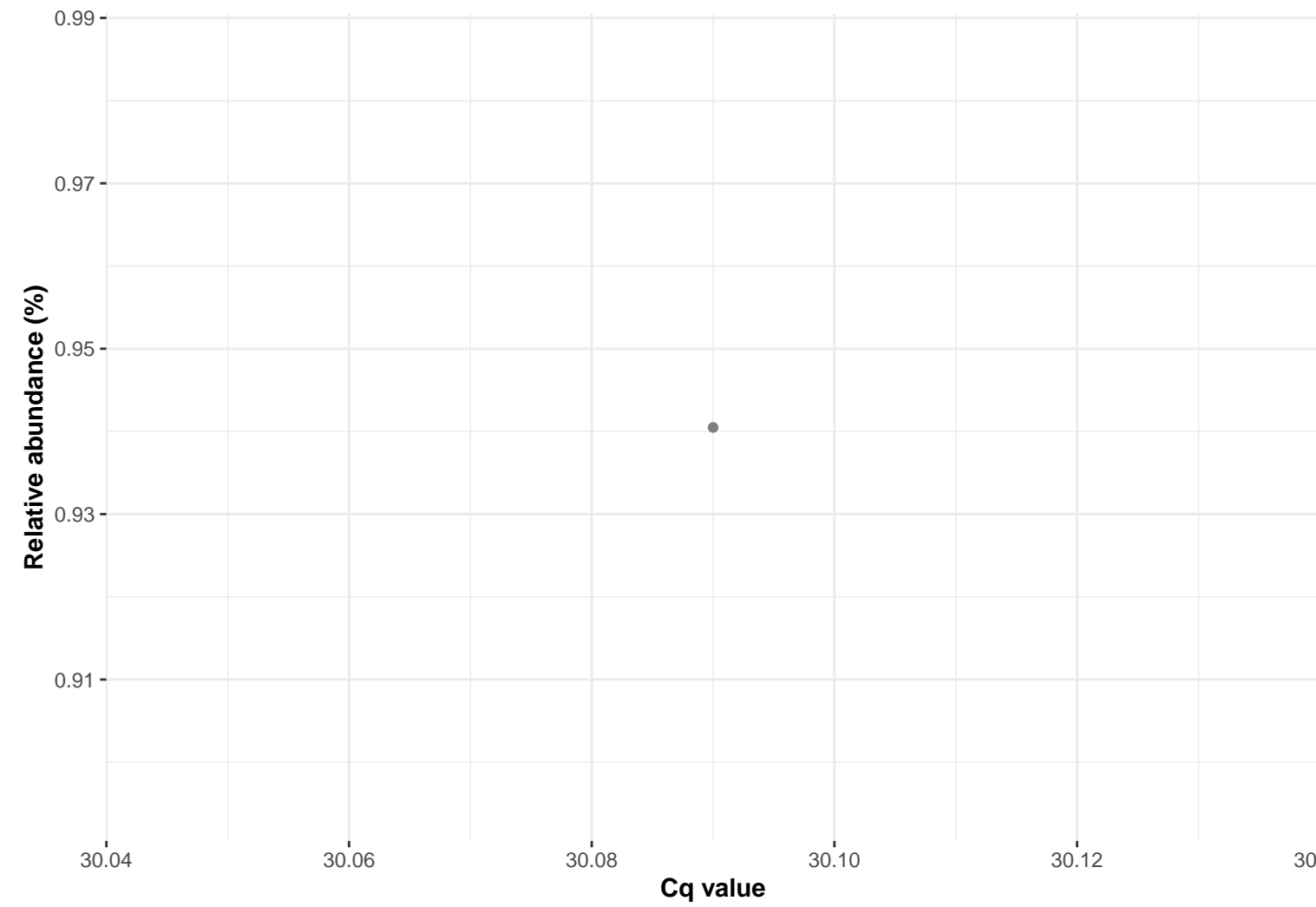


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

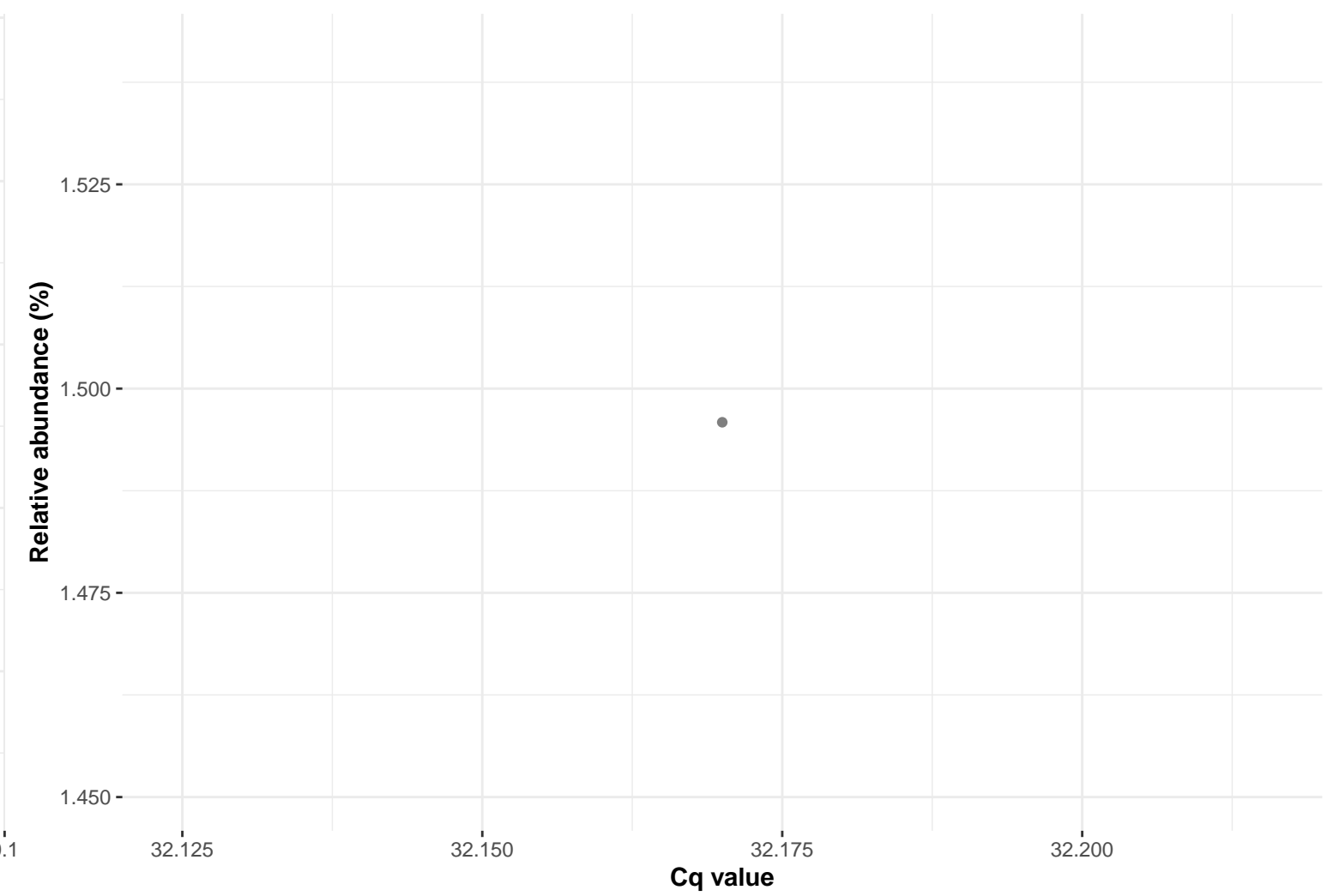
Correlation with all samples



Correlation within: REF-PIM



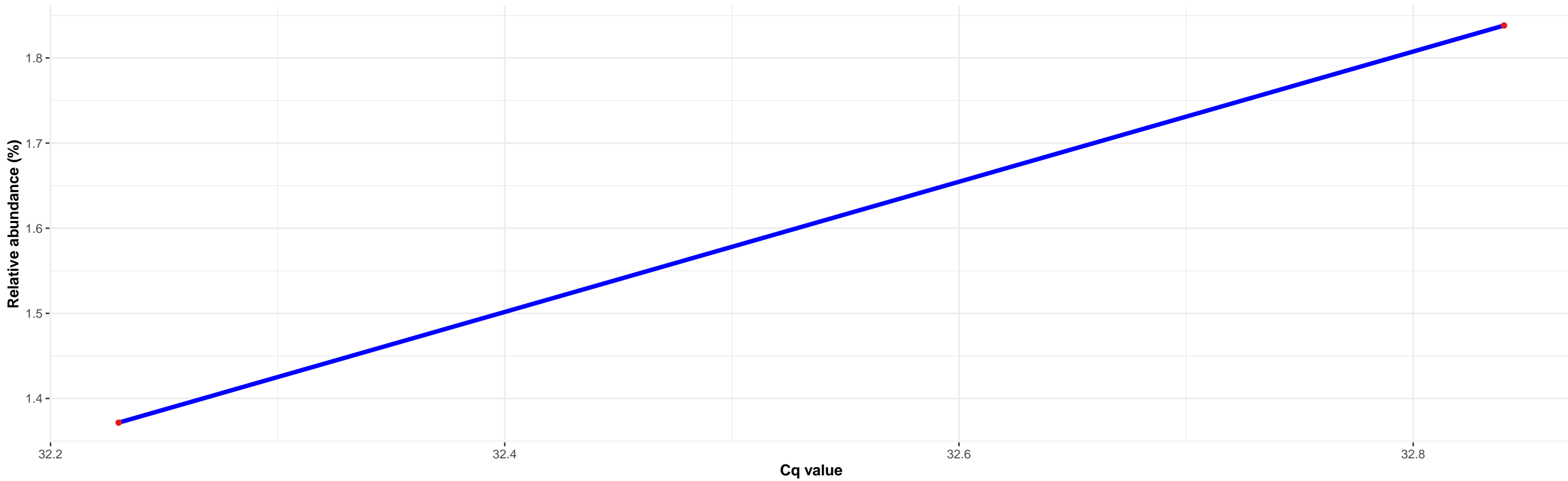
Correlation within: REF-DIM





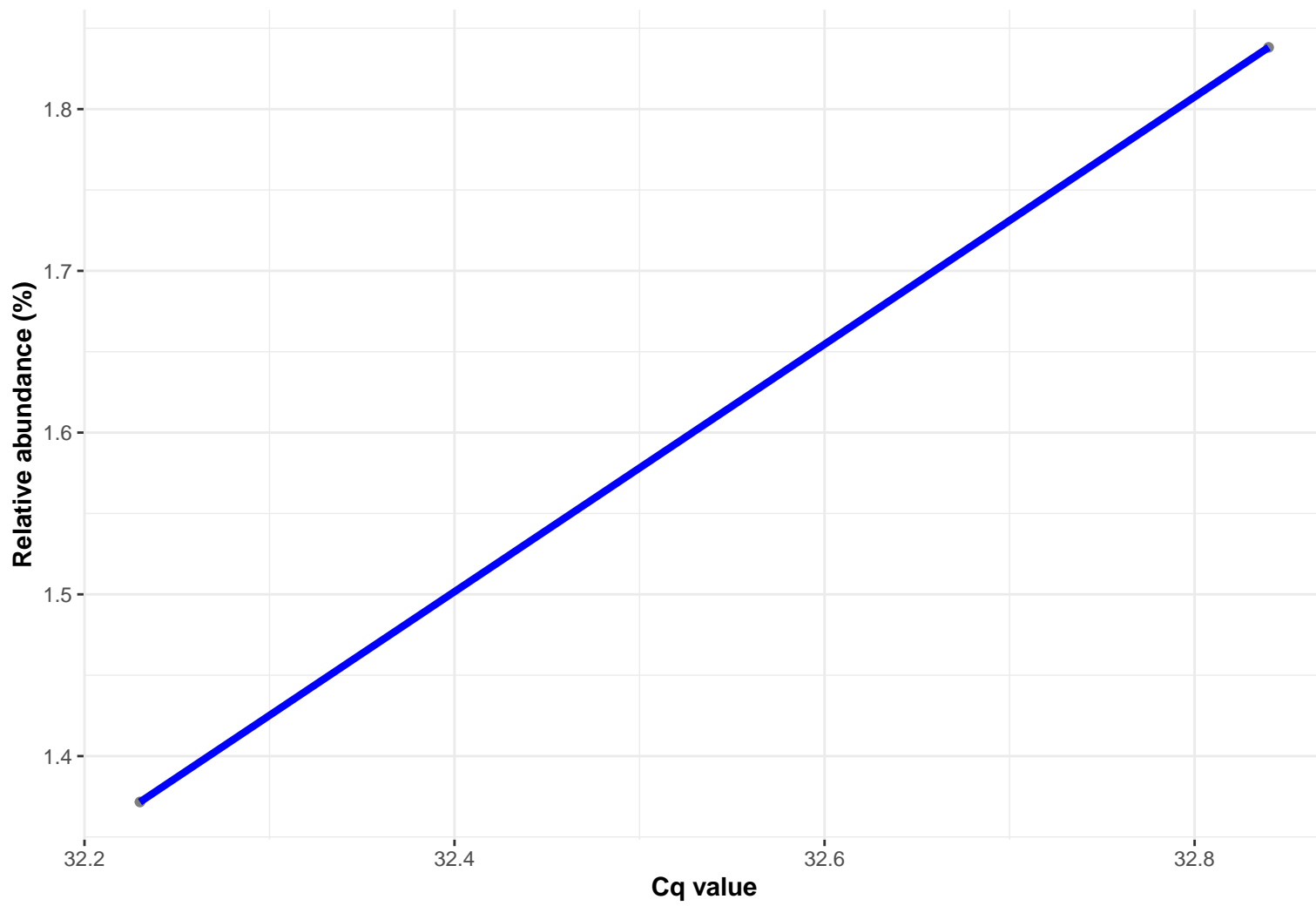
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; s\_\_Corynebacterium xerosis

Correlation with all samples



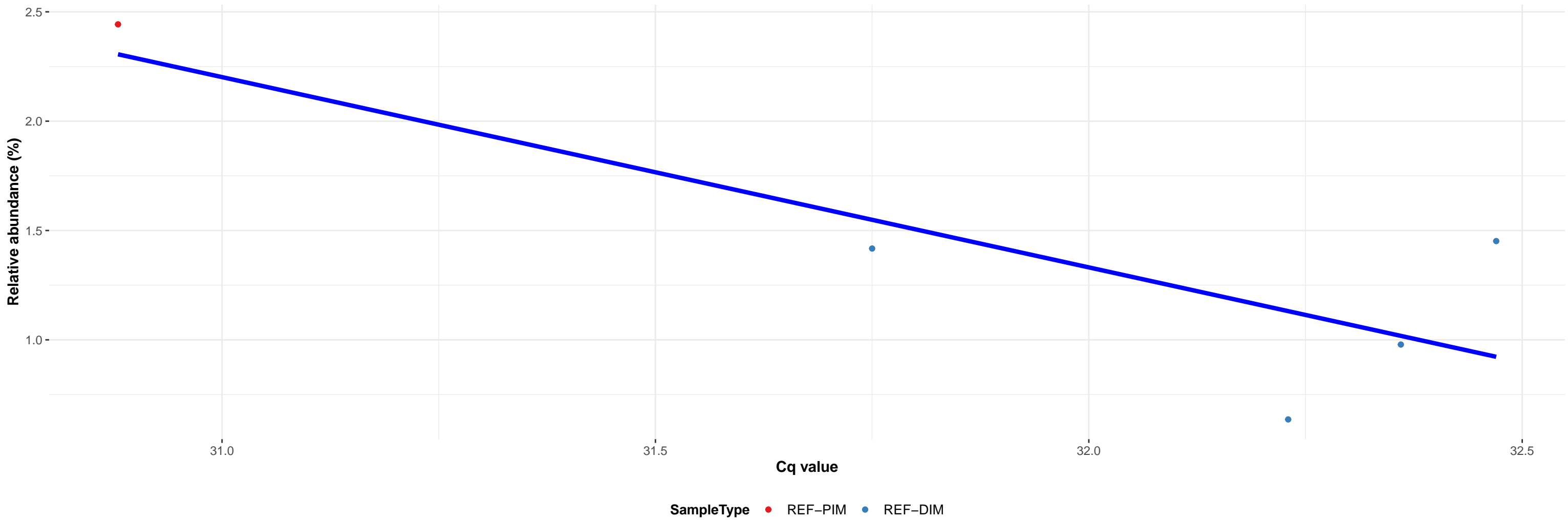
SampleType • REF-DIM

Correlation within: REF-DIM

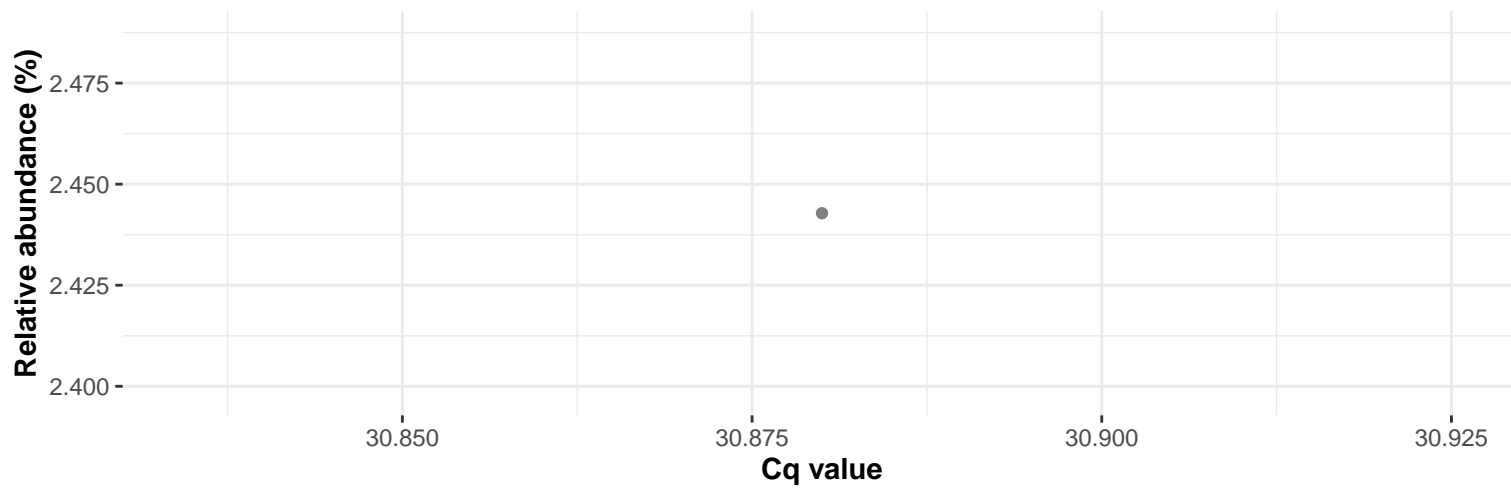


k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

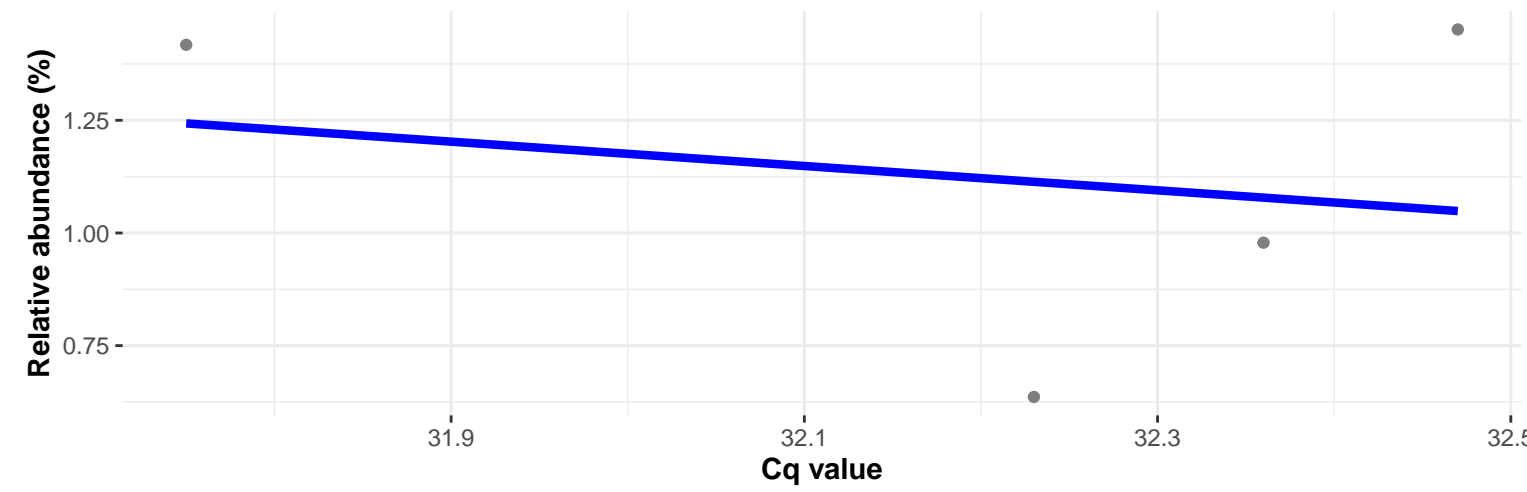
Correlation with all samples



Correlation within: REF-PIM



Correlation within: REF-DIM



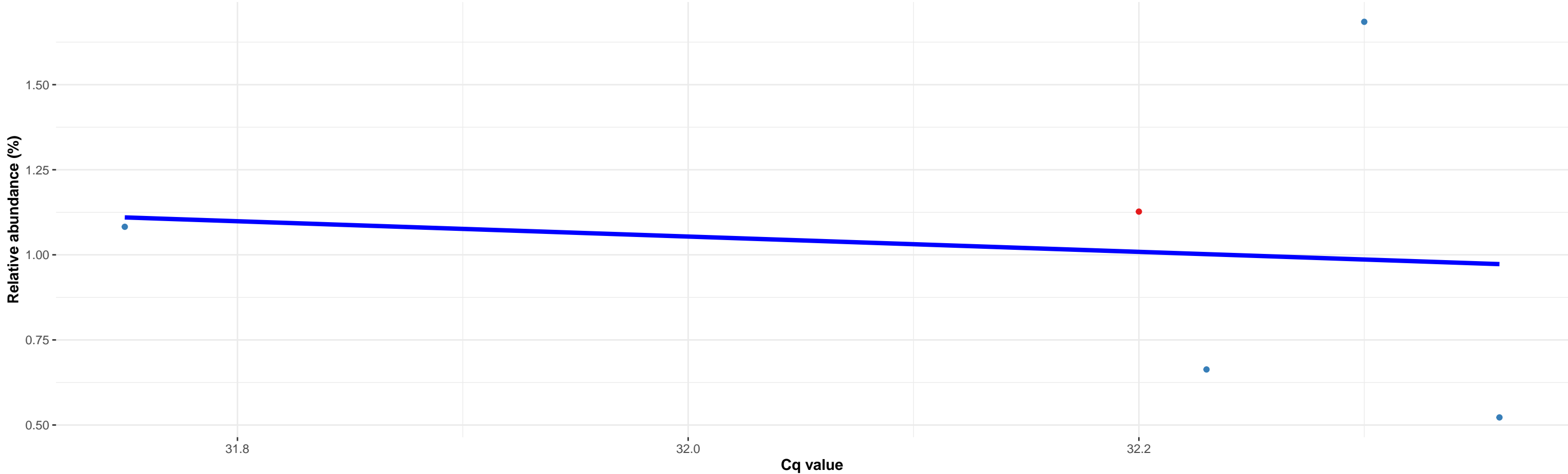
Correlation within: PCR-blank

Relative abundance (%)

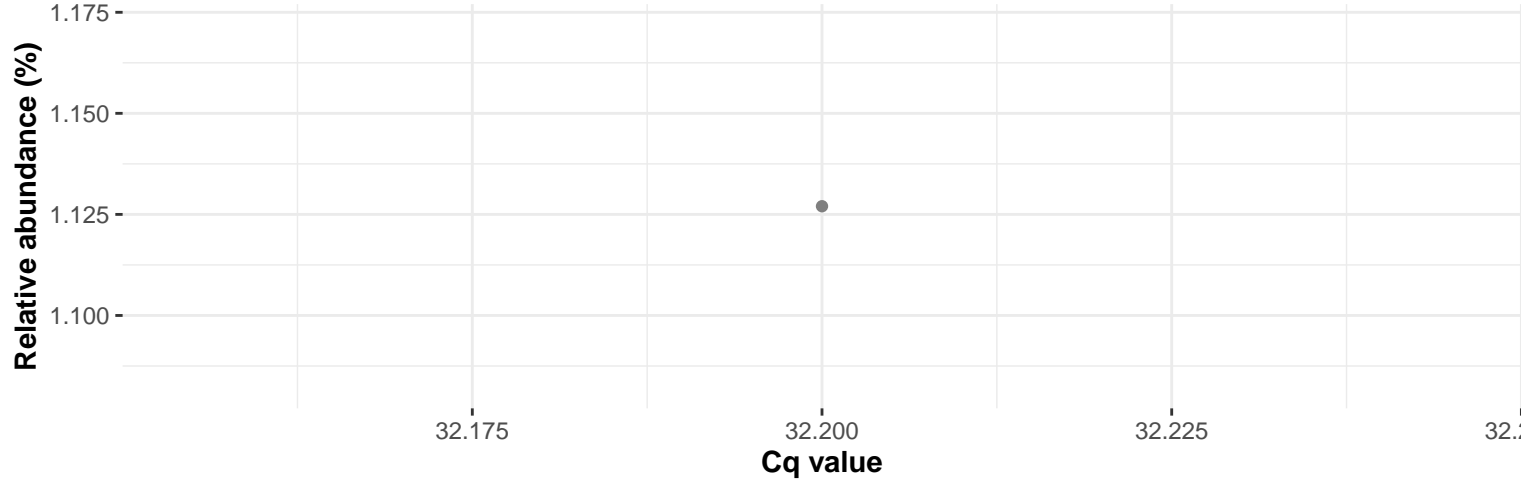
Cq value

k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Rhodobacterales; f\_\_Rhodobacteraceae; g\_\_Pseudorhodobacter; NA

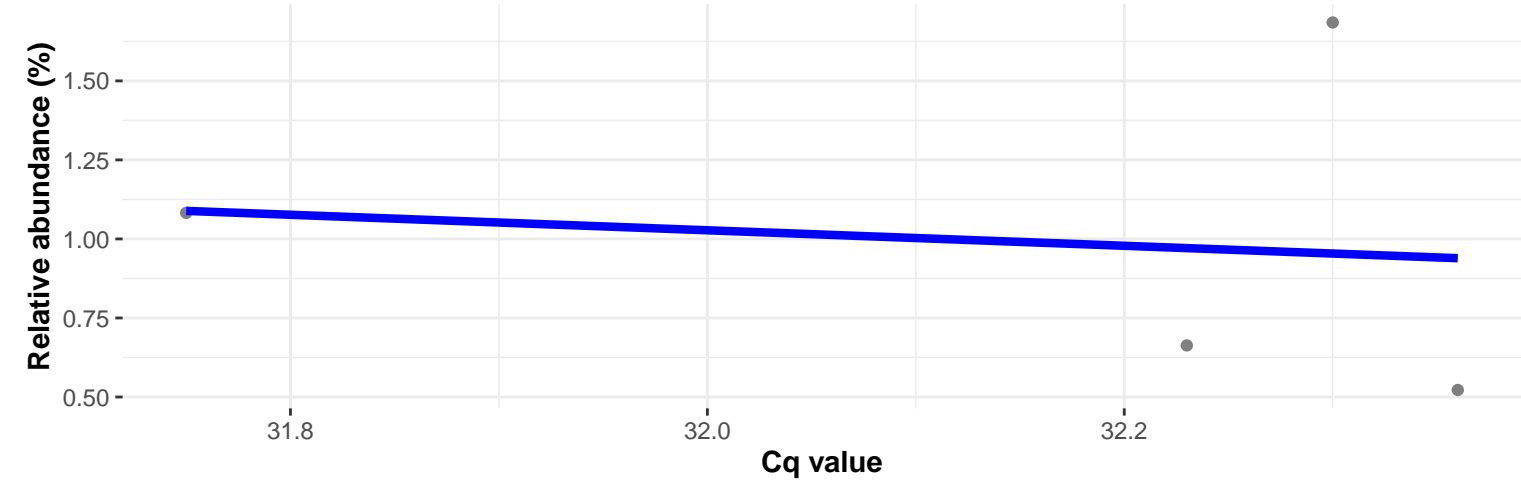
Correlation with all samples



Correlation within: REF-PIM



Correlation within: REF-DIM



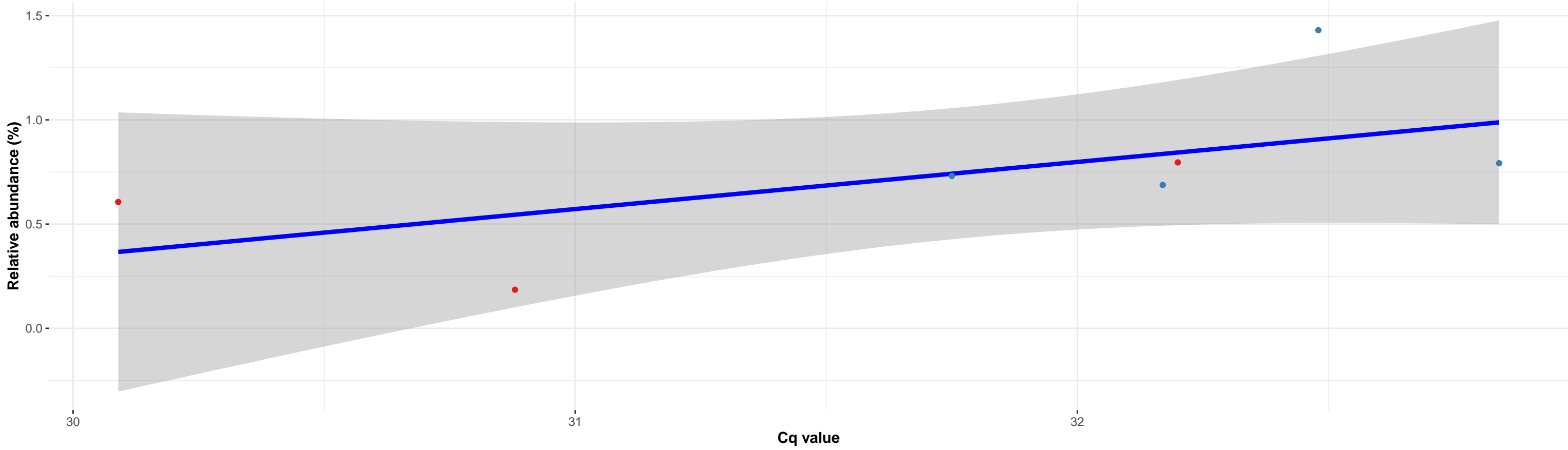
Correlation within: PCR-blank



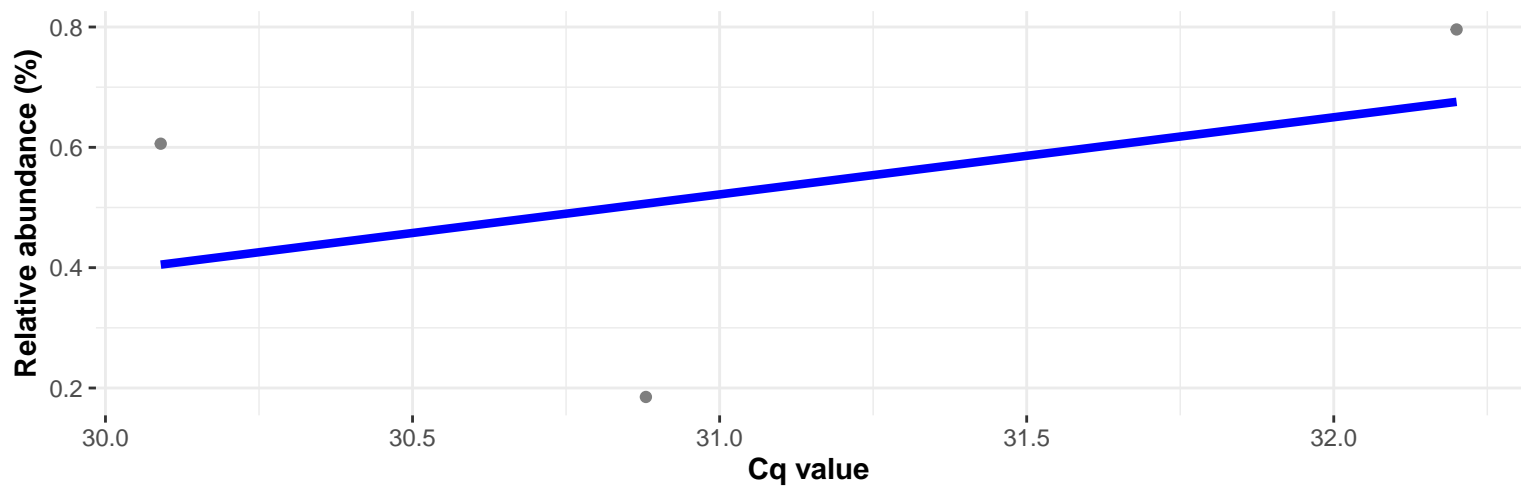
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Rhizobiales; f\_\_Xanthobacteraceae; g\_\_Afipia; Ambiguous\_taxa

Correlation with all samples

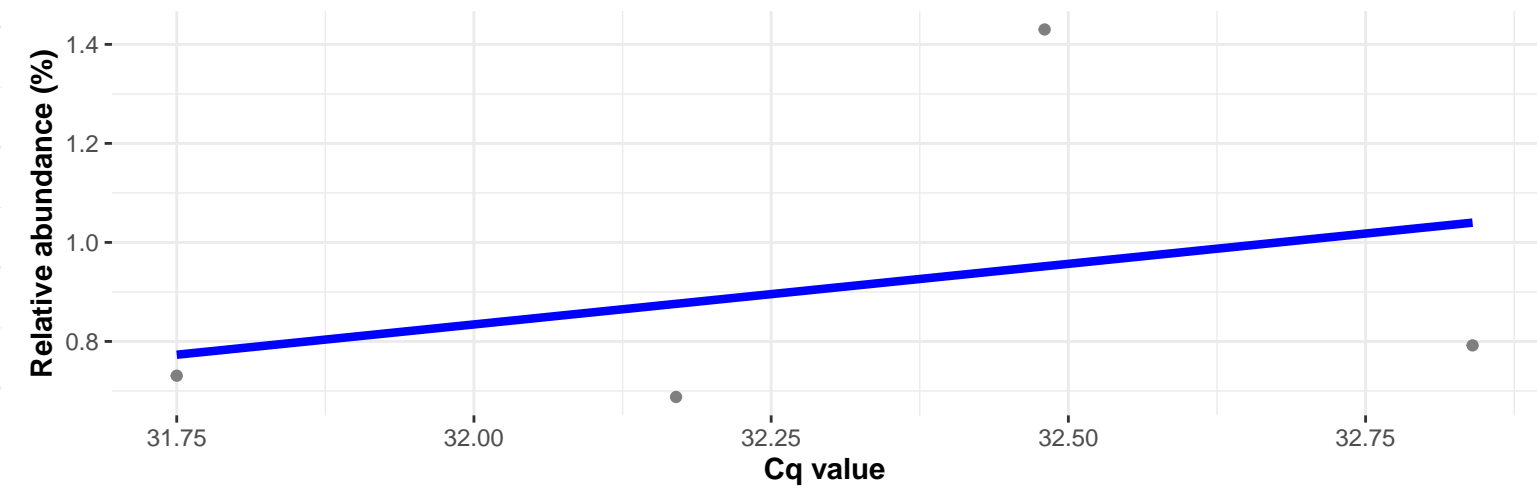
$\log_e(S) = 2.303$ ,  $p = 0.023$ ,  $\hat{\rho}_{\text{Spearman}} = 0.821$ ,  $CI_{95\%} [0.151, 0.974]$ ,  $n_{\text{pairs}} = 7$



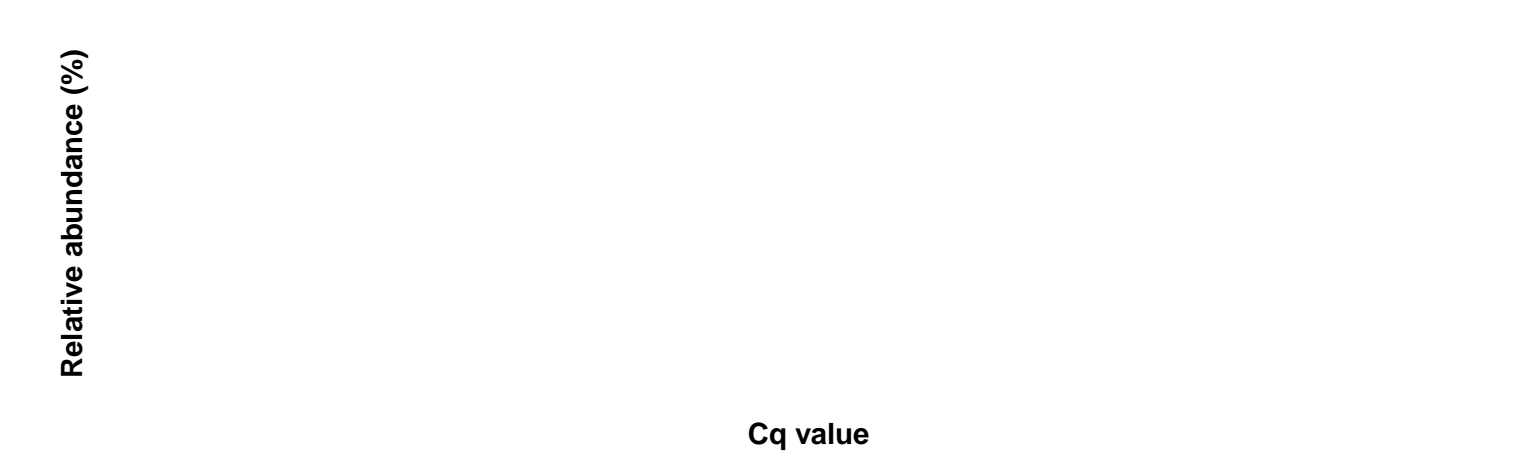
Correlation within: REF-PIM



Correlation within: REF-DIM

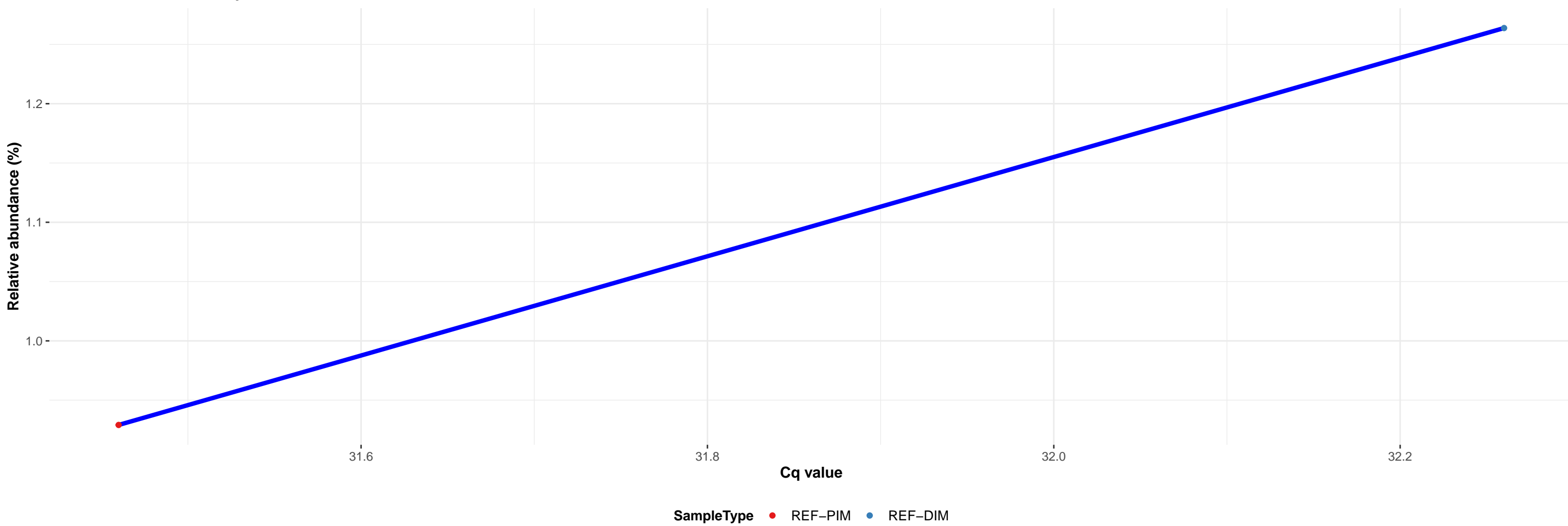


Correlation within: PCR-blank

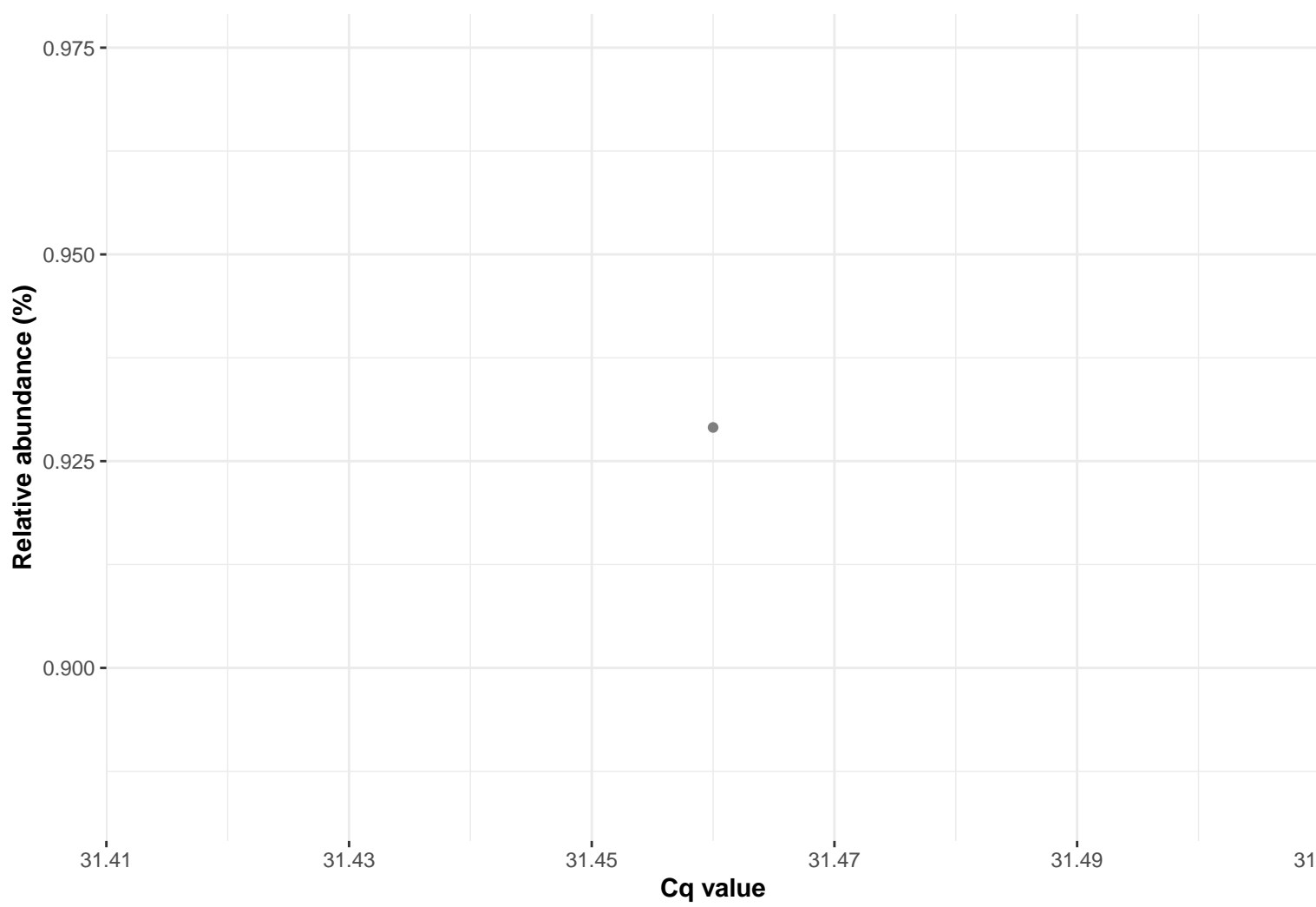


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Macrococcus; Ambiguous\_taxa

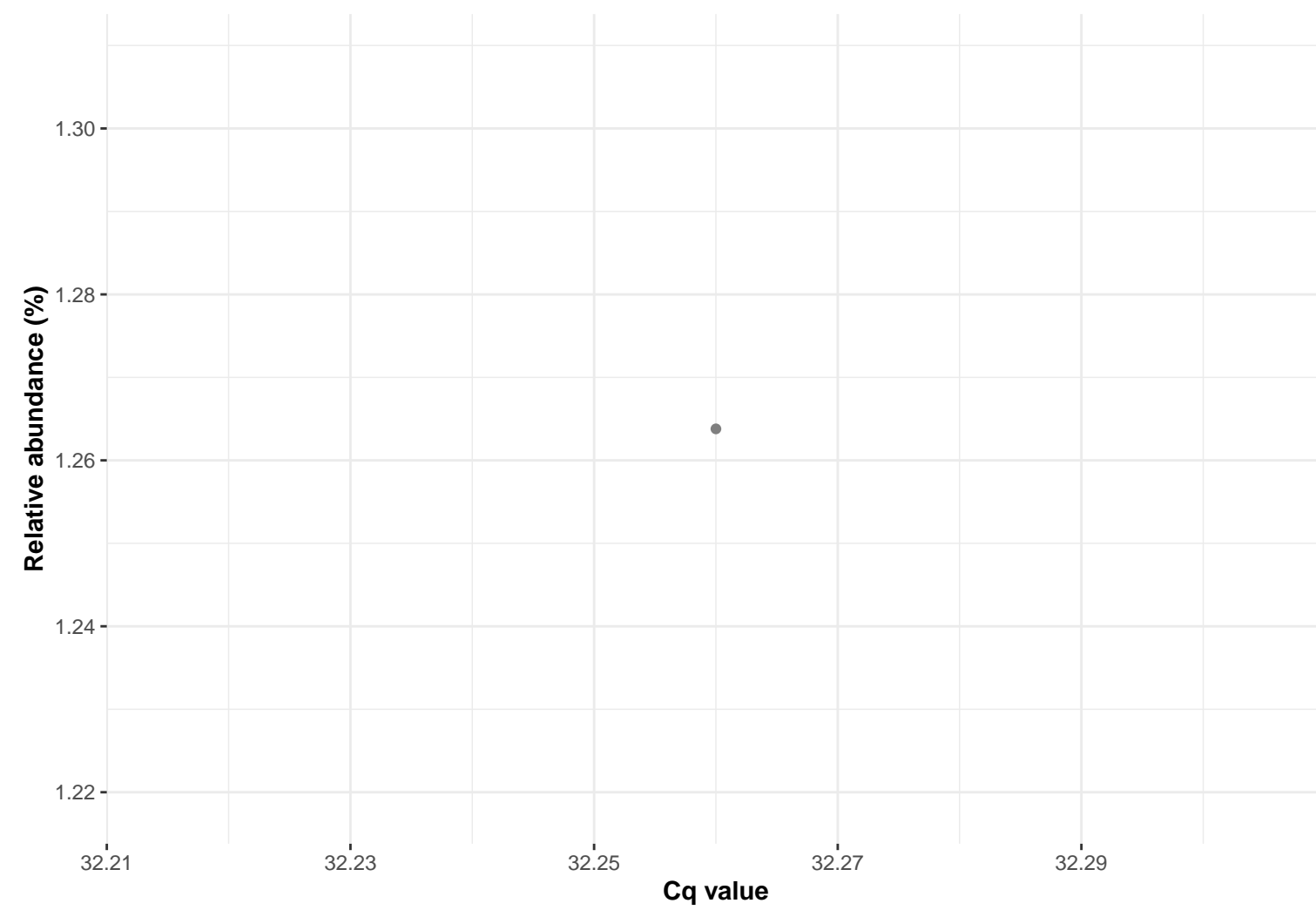
Correlation with all samples



Correlation within: REF-PIM



Correlation within: REF-DIM



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples

Relative abundance (%)

Correlation within: PCR-blank

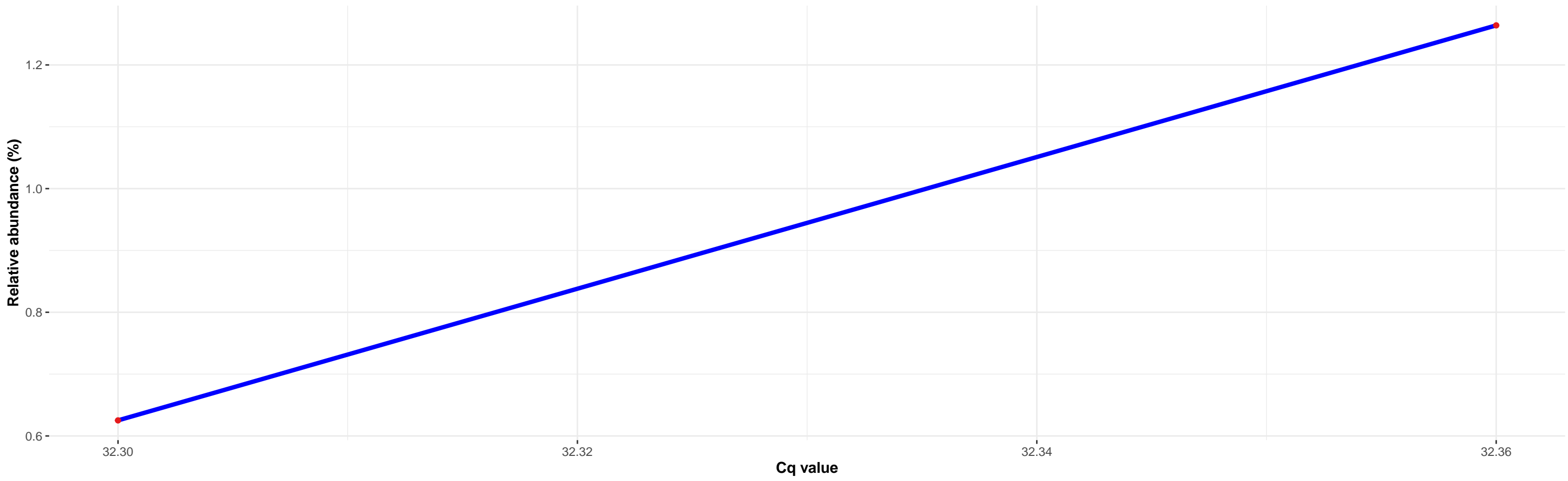
Cq value

Relative abundance (%)

Cq value

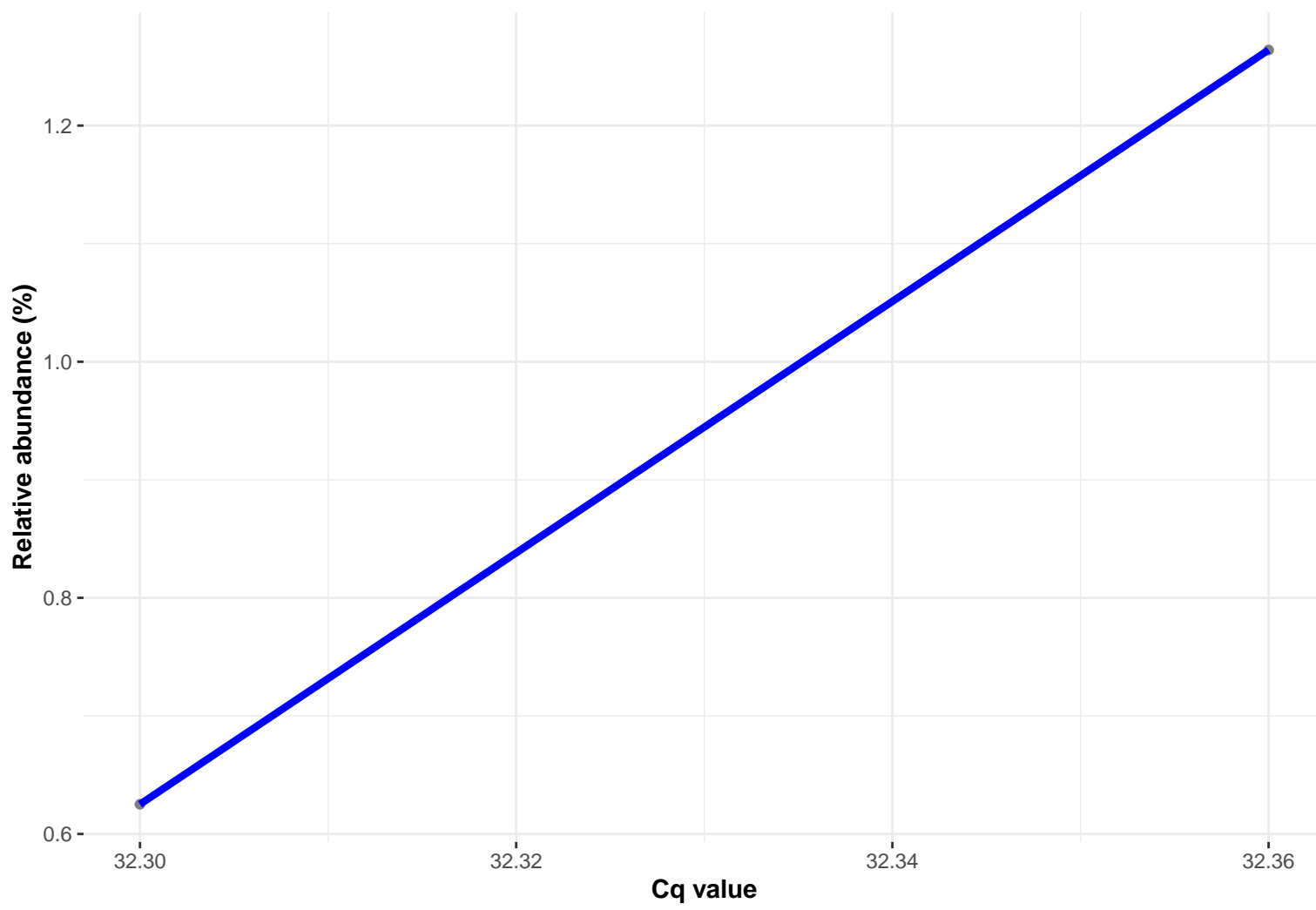
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; Ambiguous\_taxa

Correlation with all samples



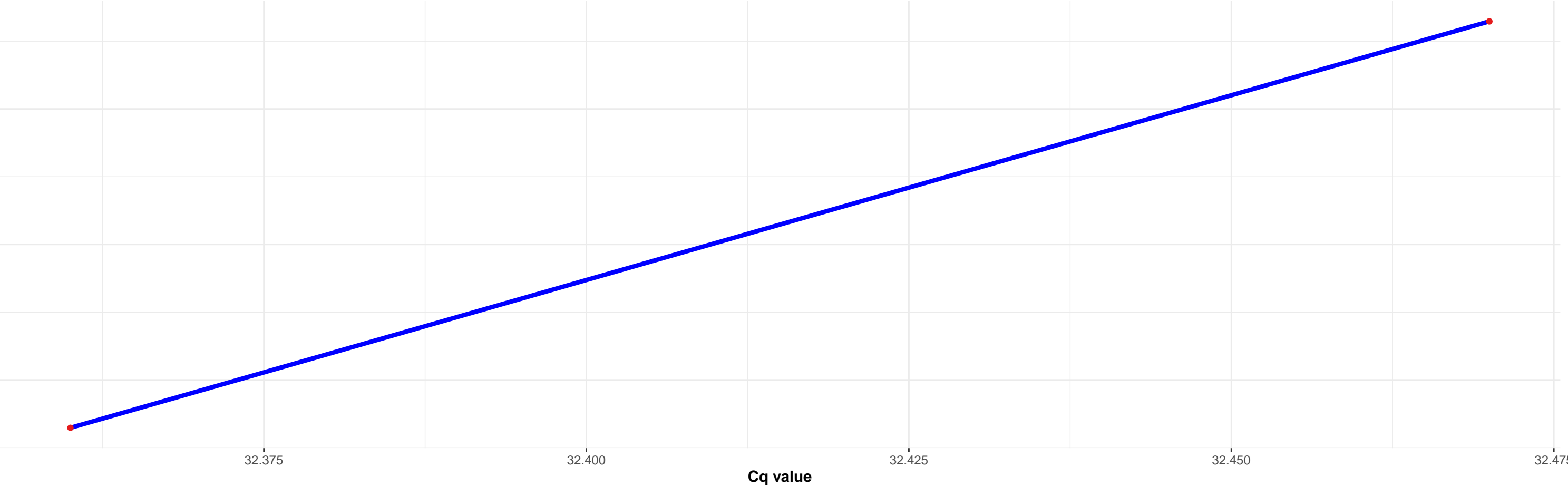
SampleType • REF-DIM

Correlation within: REF-DIM



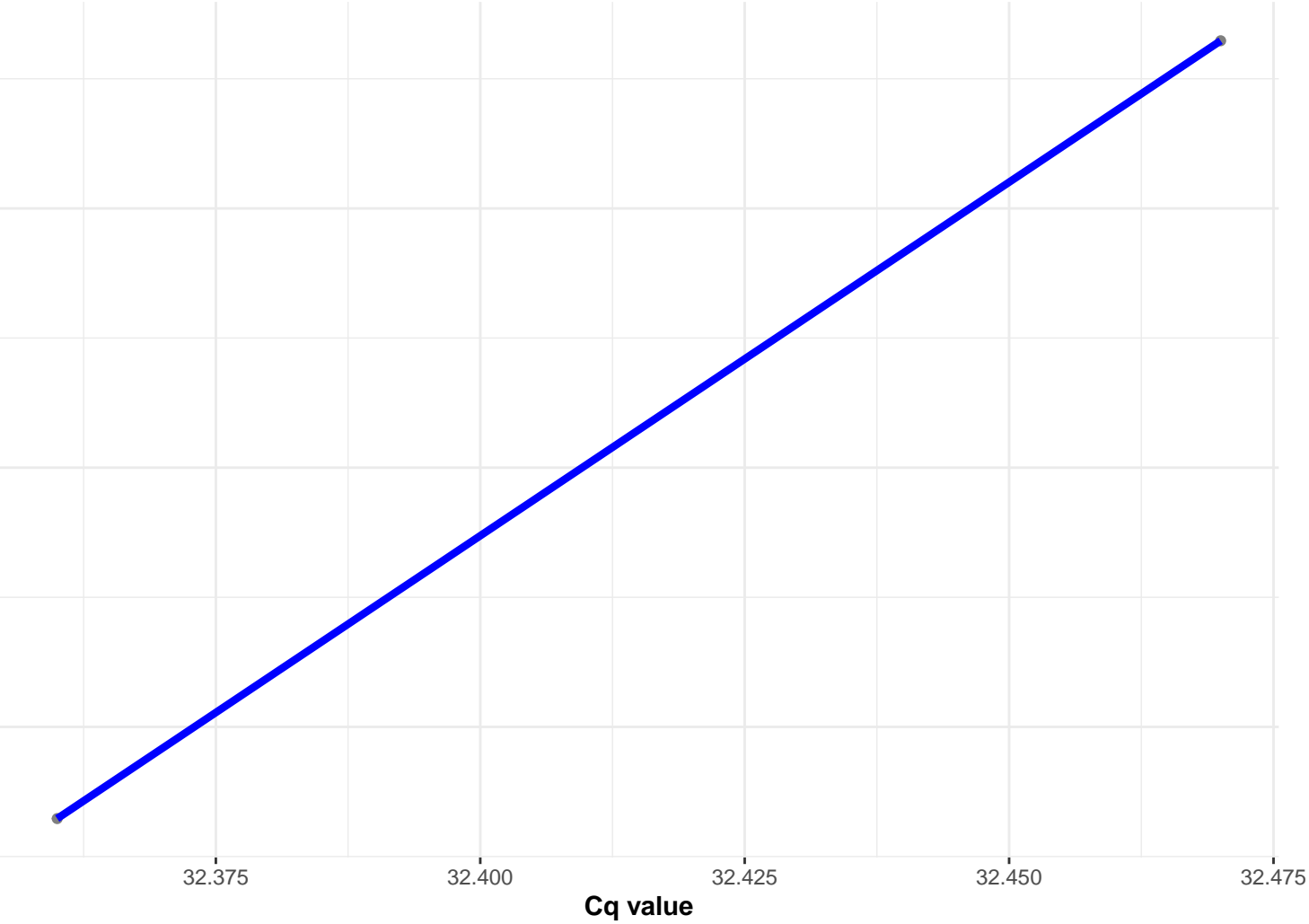
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples



SampleType • REF-DIM

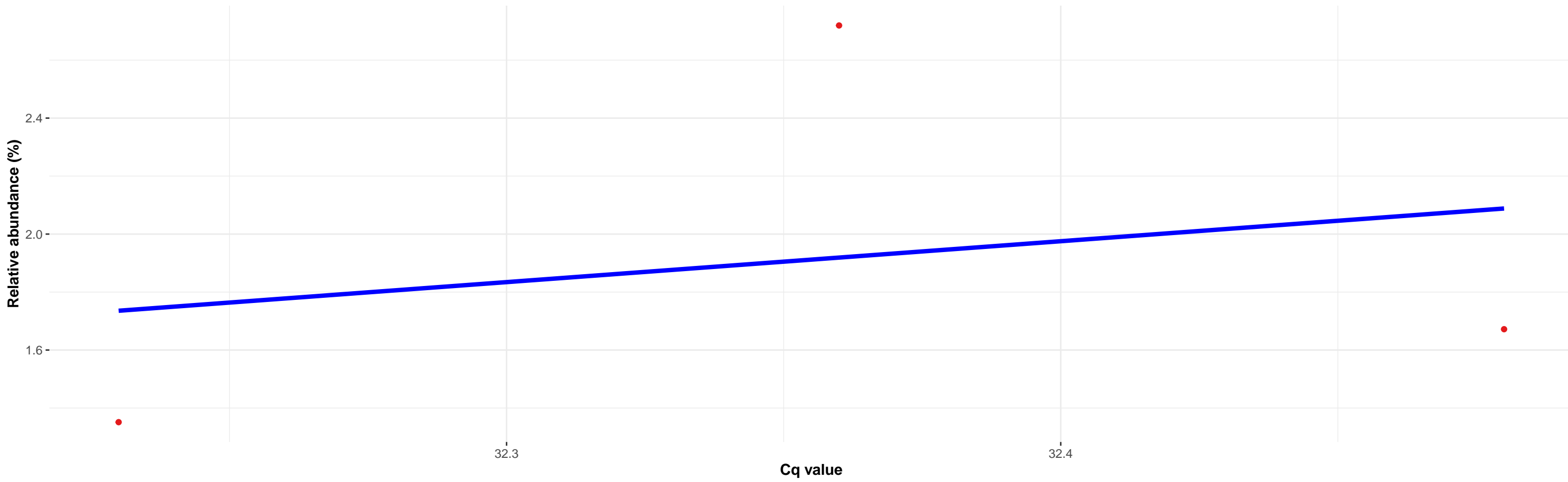
Correlation within: REF-DIM



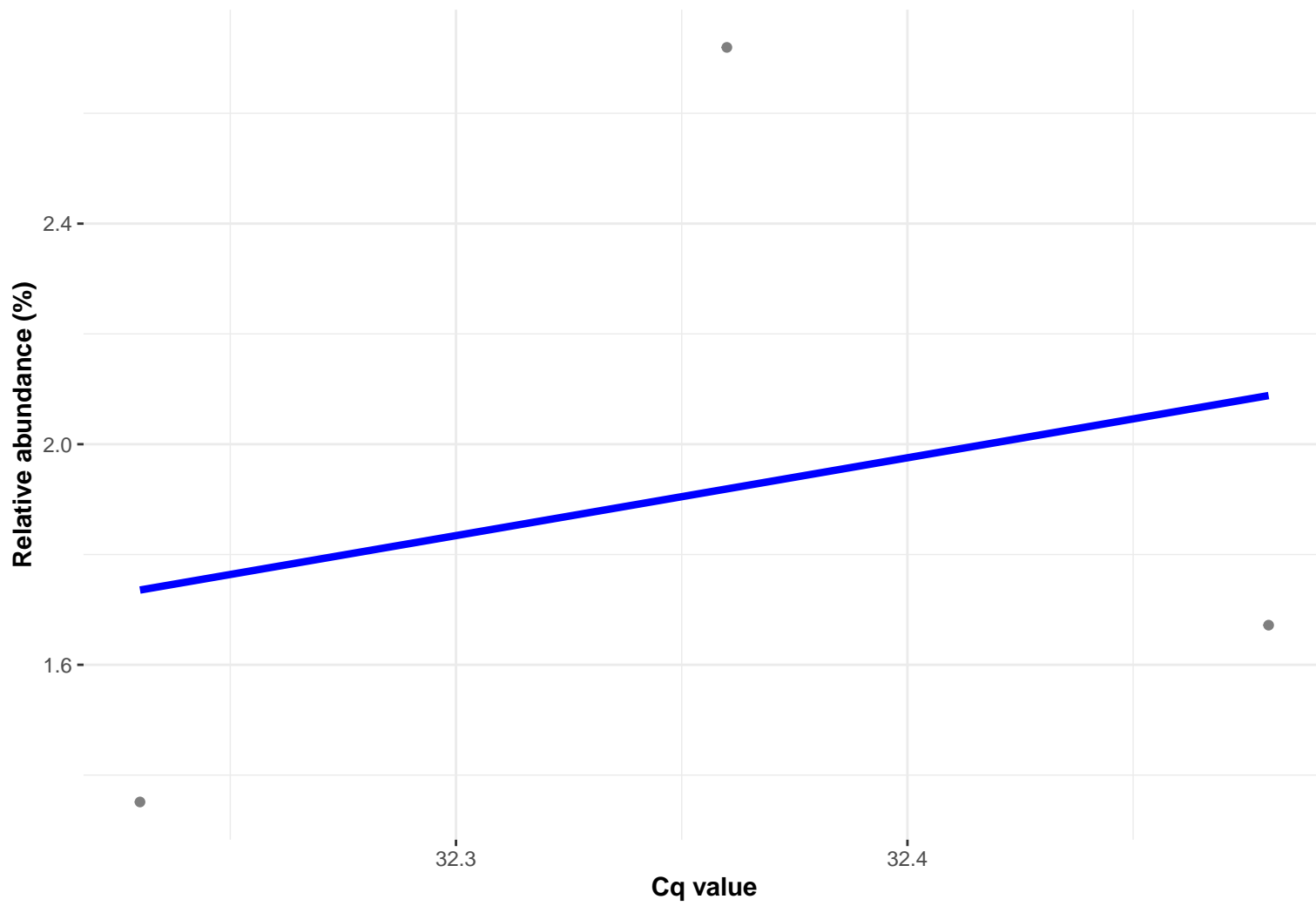


k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Chitinophagales; f\_\_Chitinophagaceae; g\_\_Sediminibacterium; s\_\_uncultured bacterium

Correlation with all samples



Correlation within: REF-DIM

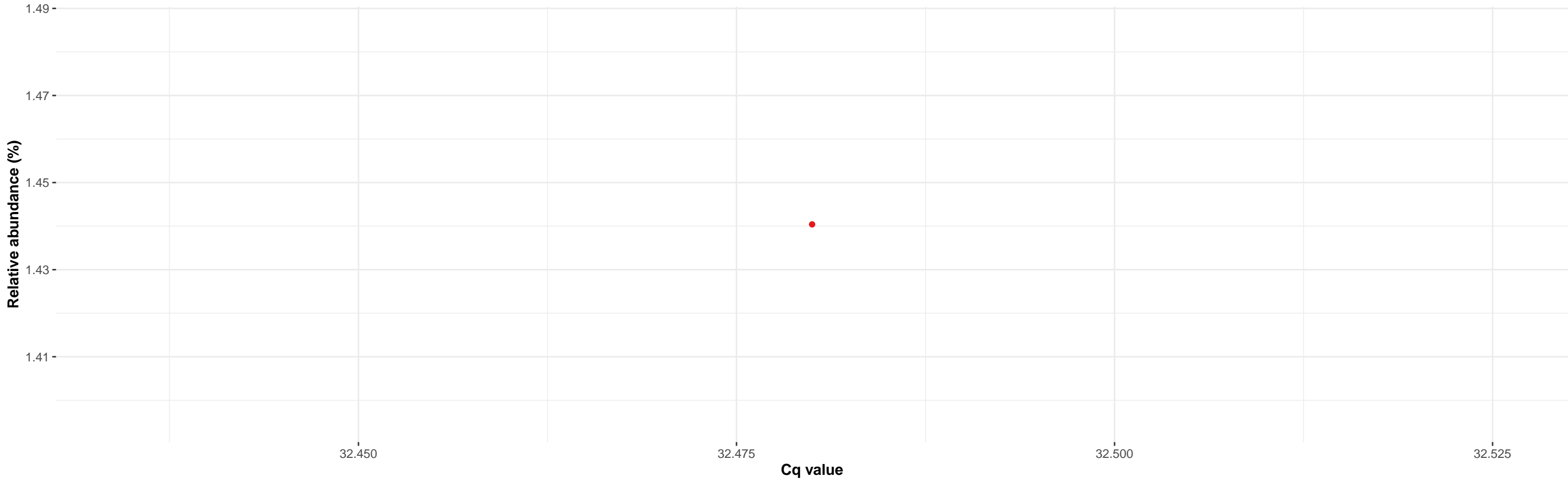


Correlation within: PCR-blank



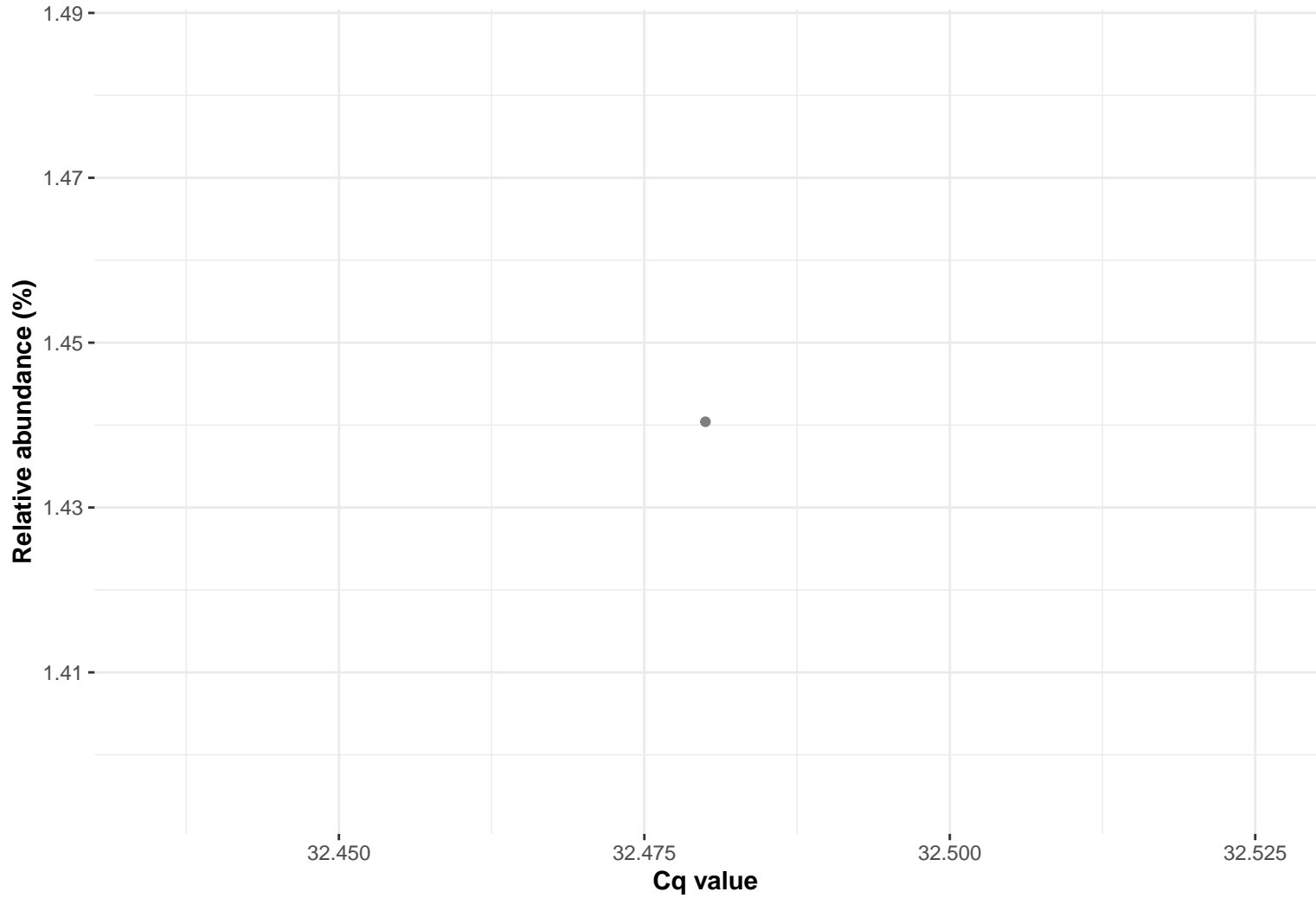
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; s\_\_Corynebacterium xerosis

Correlation with all samples



SampleType • REF-DIM

Correlation within: REF-DIM

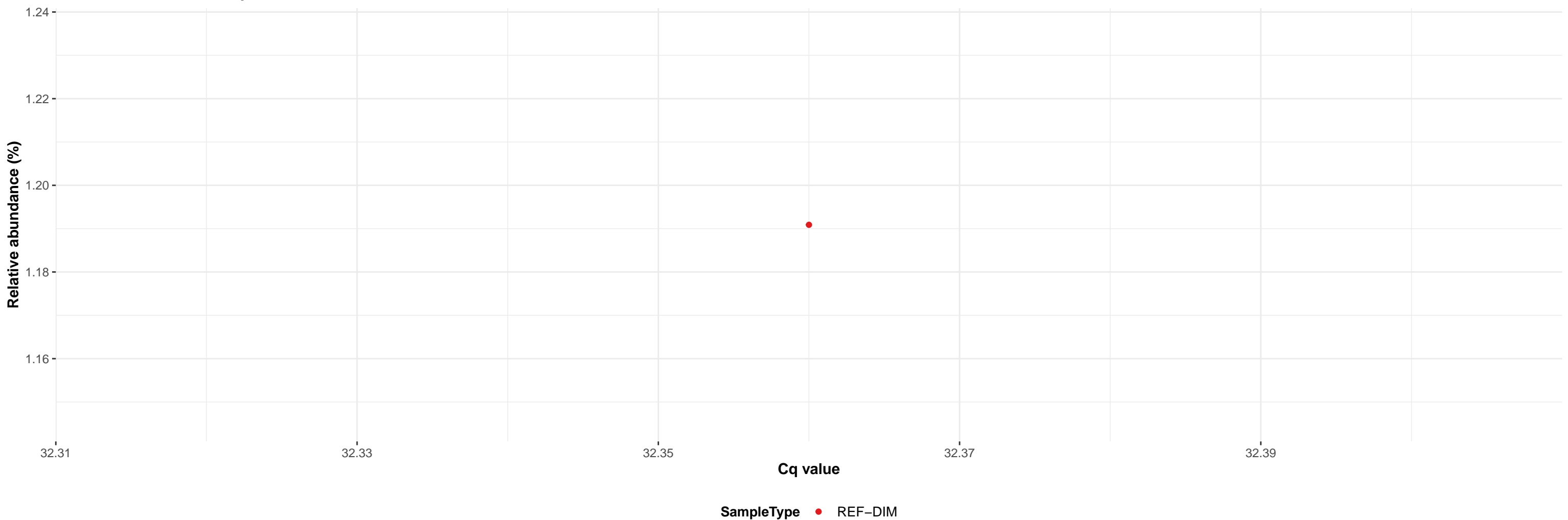


Correlation within: PCR-blank

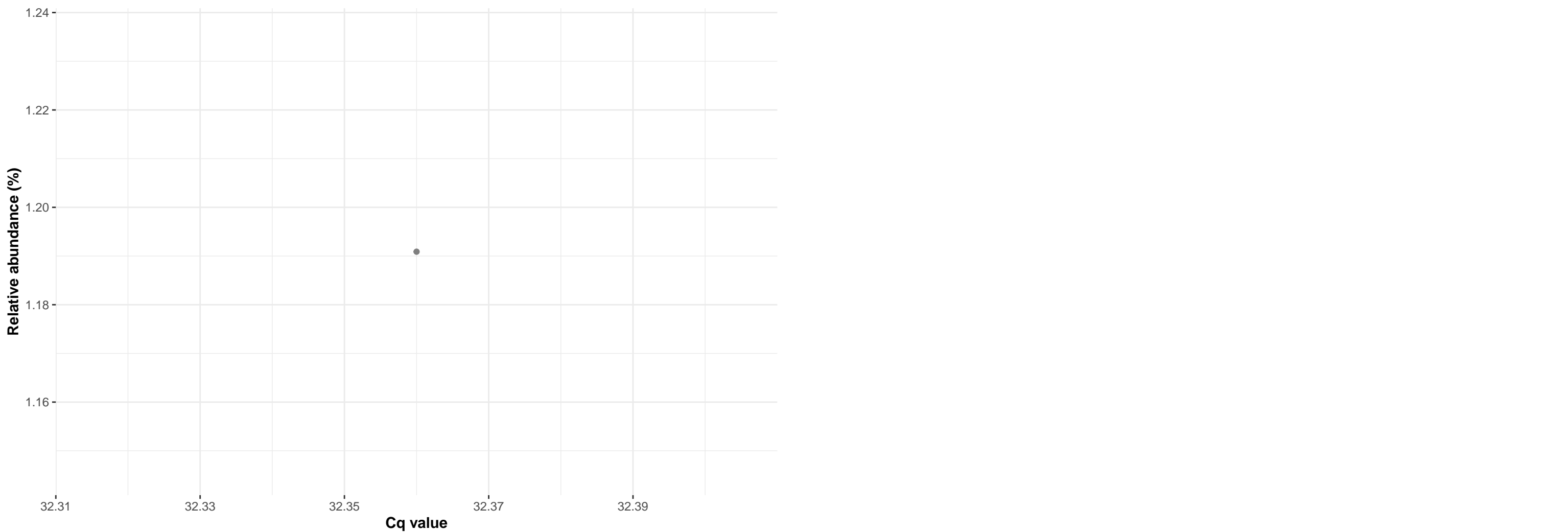


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Gracilibacillus; Ambiguous\_taxa

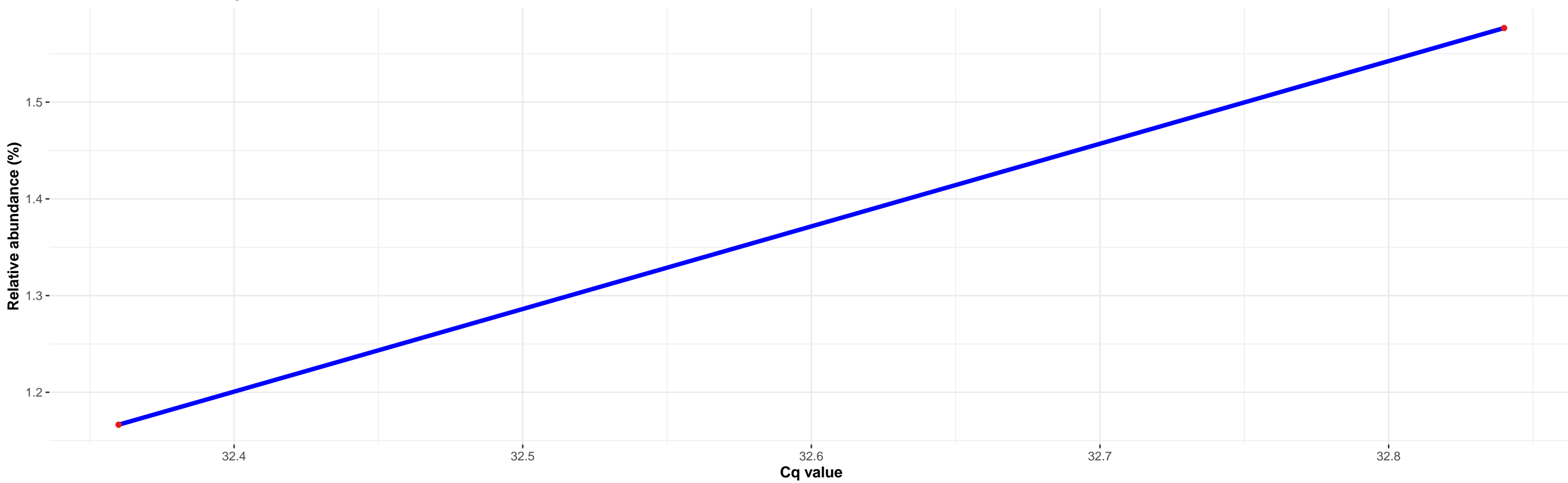
Correlation with all samples



Correlation within: REF-DIM

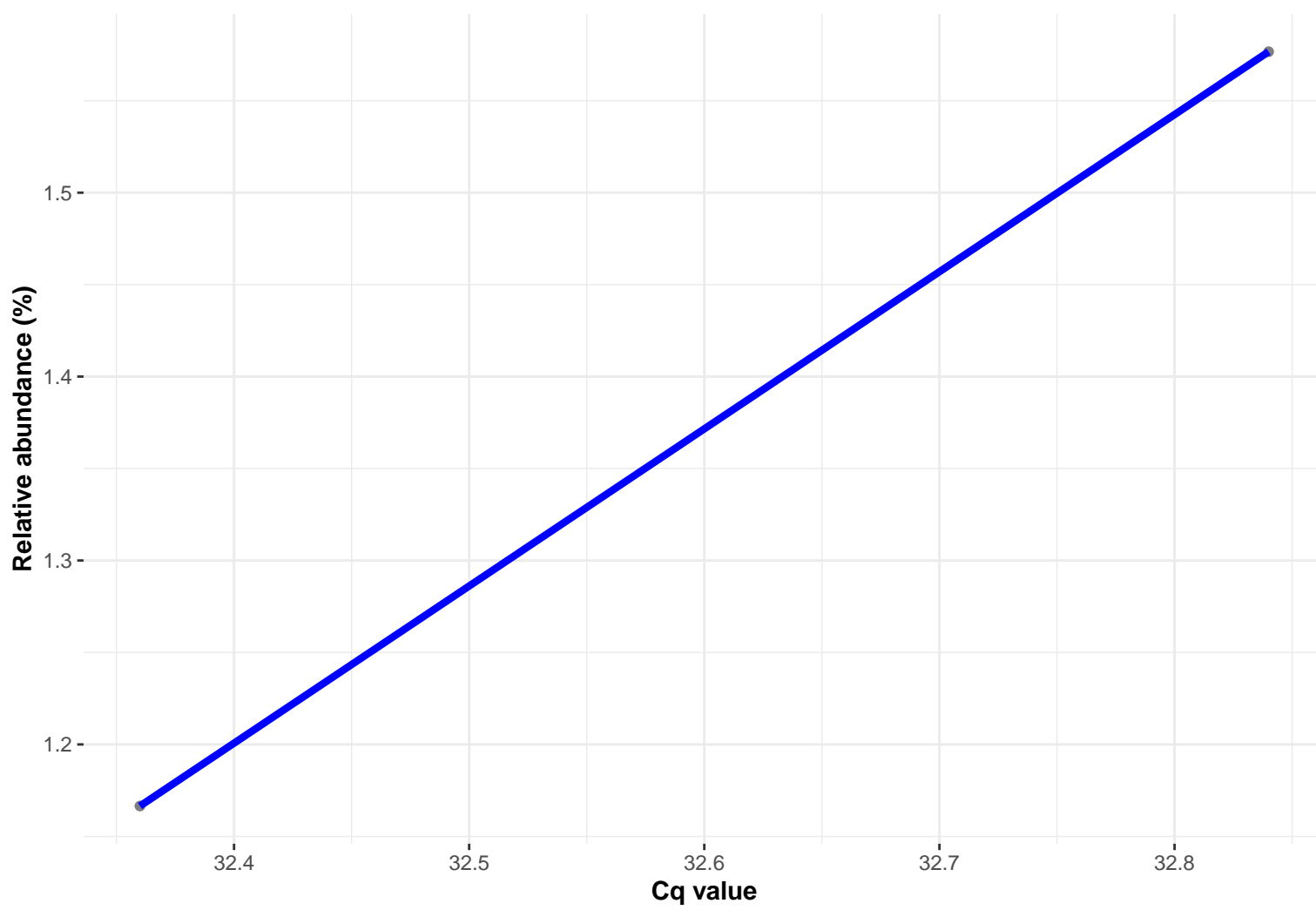


Correlation with all samples

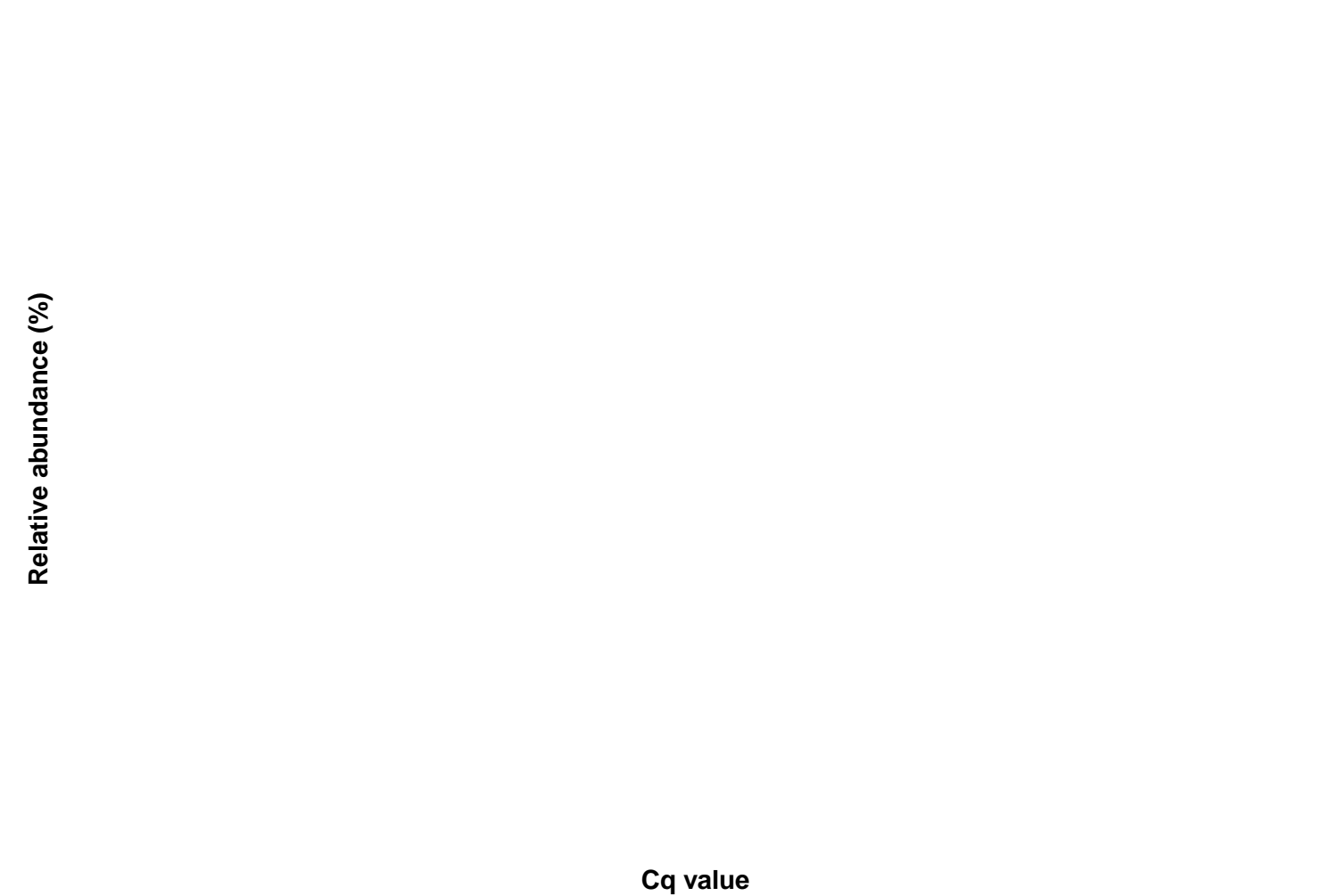


SampleType • REF-DIM

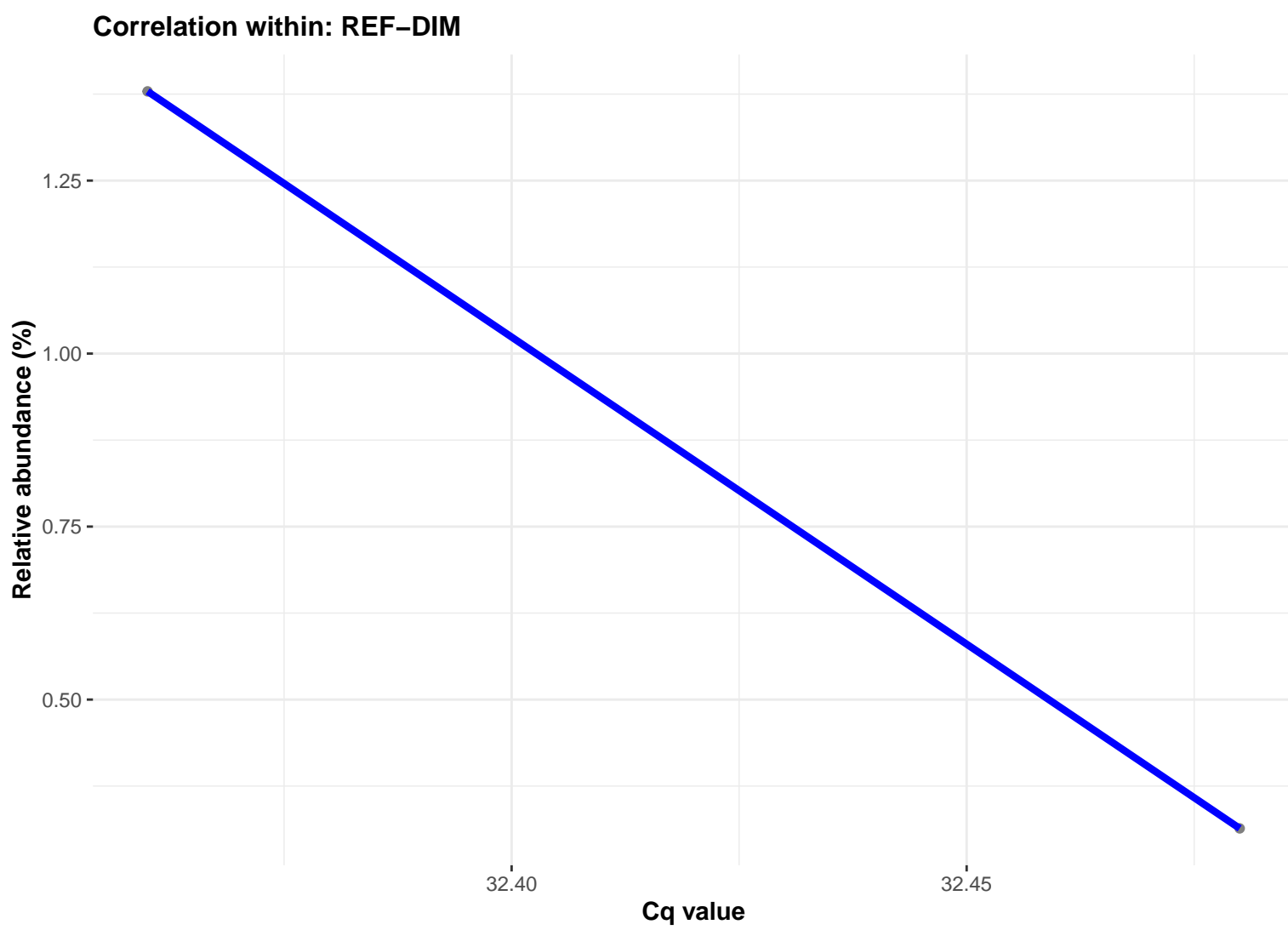
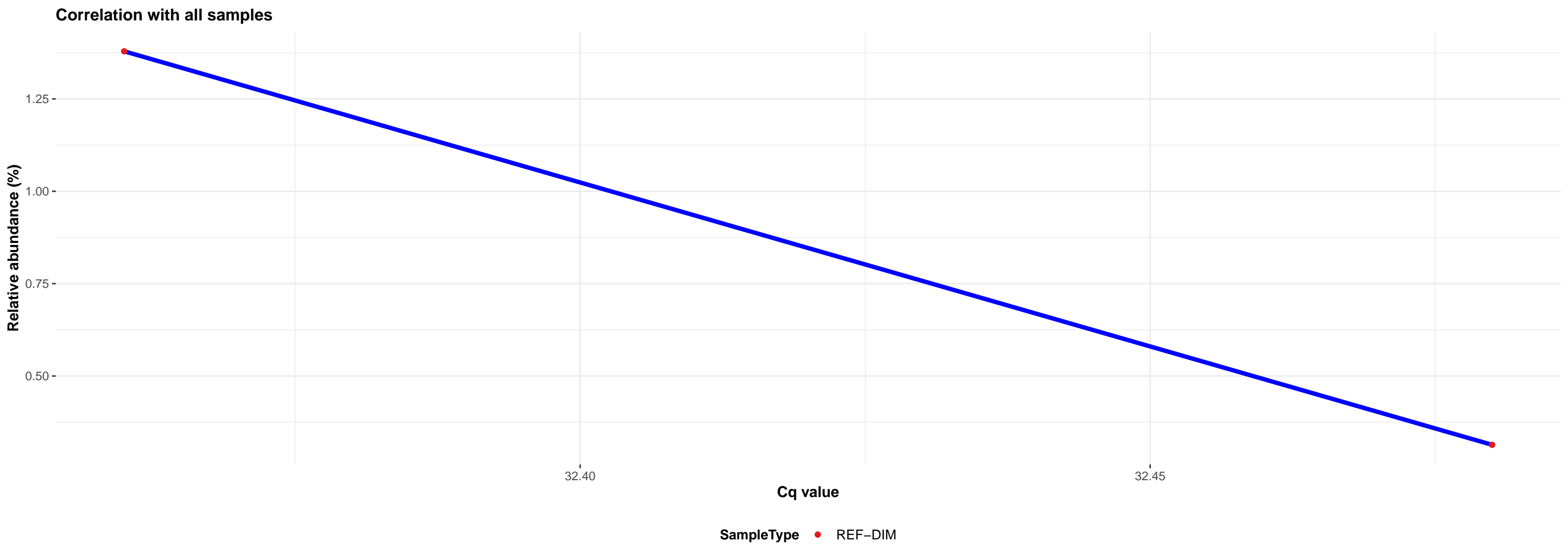
Correlation within: REF-DIM



Correlation within: PCR-blank

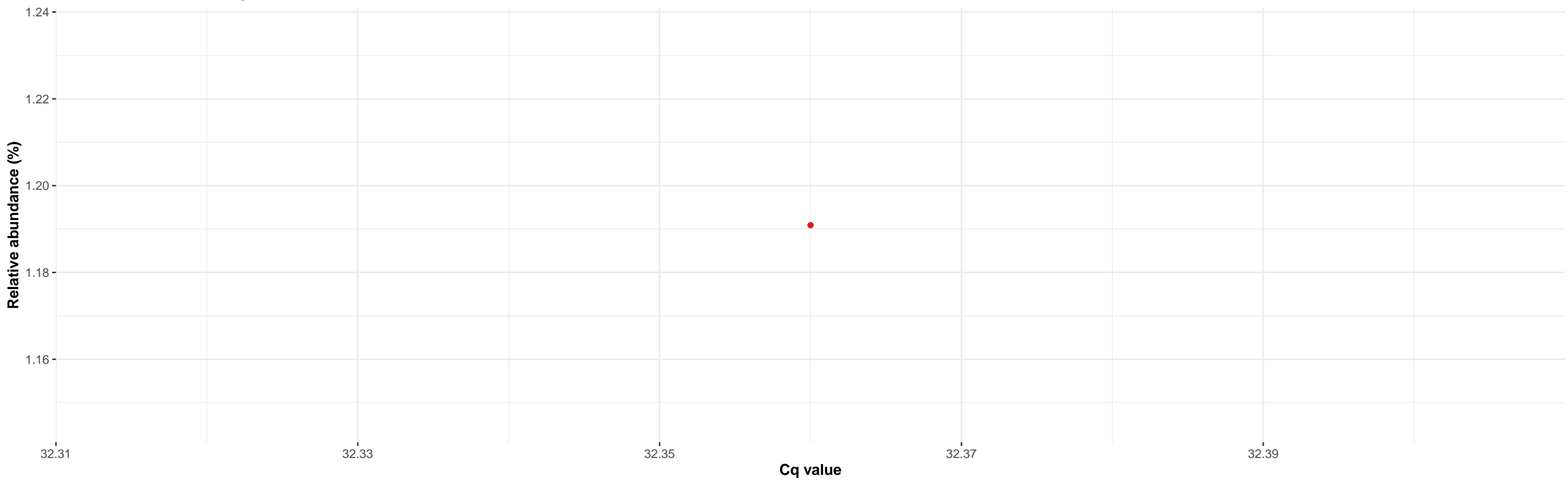


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Savagea; Ambiguous\_taxa



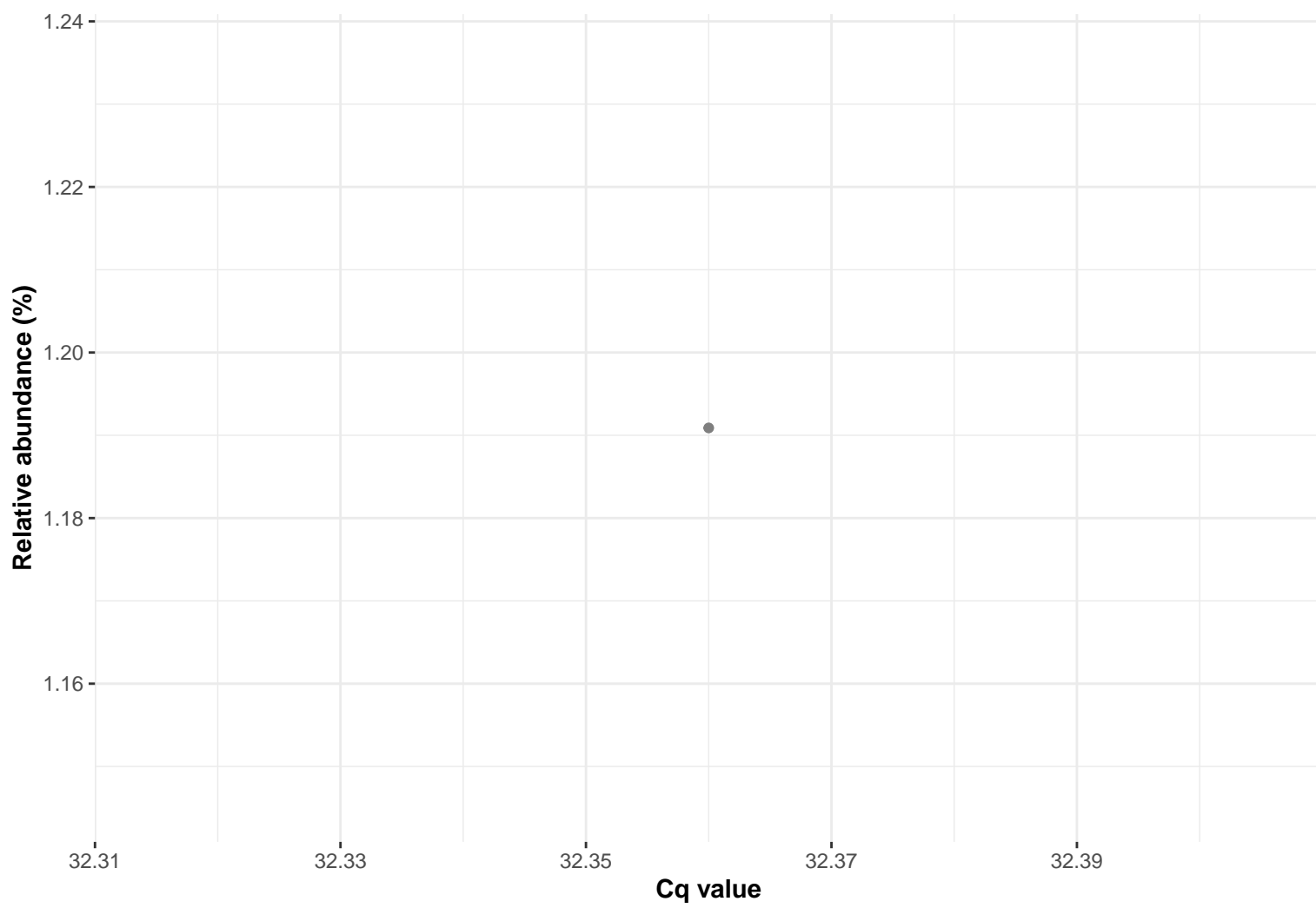
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Microbacteriaceae; g\_\_Microbacterium; Ambiguous\_taxa

Correlation with all samples



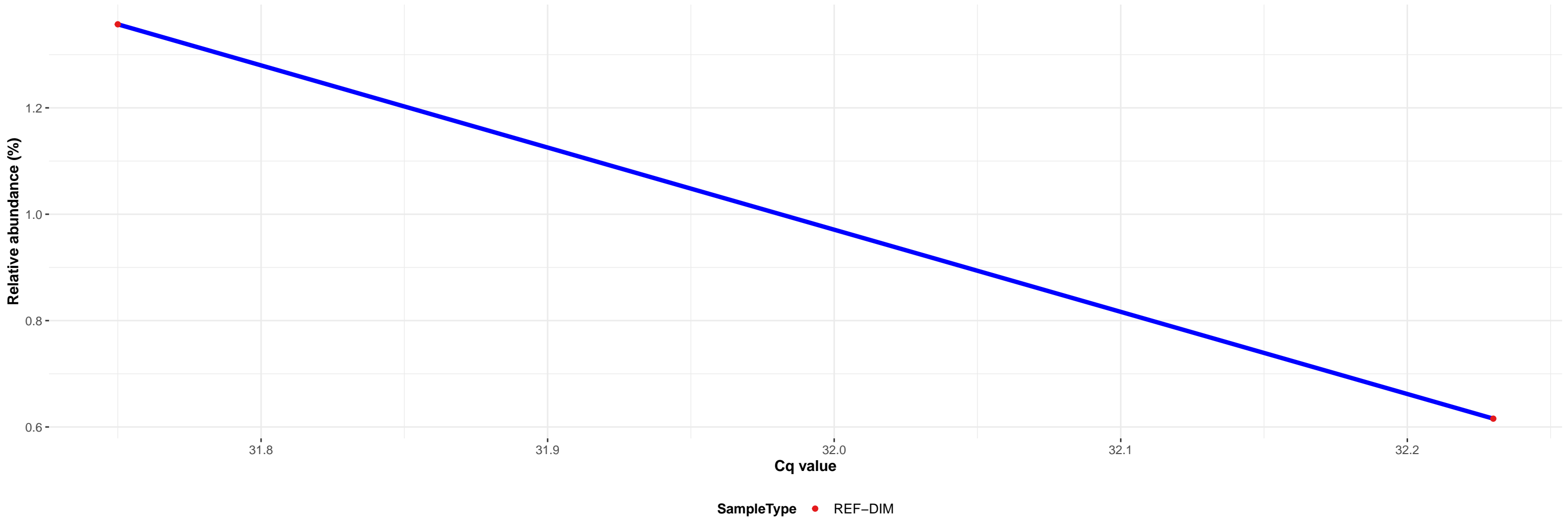
SampleType • REF-DIM

Correlation within: REF-DIM

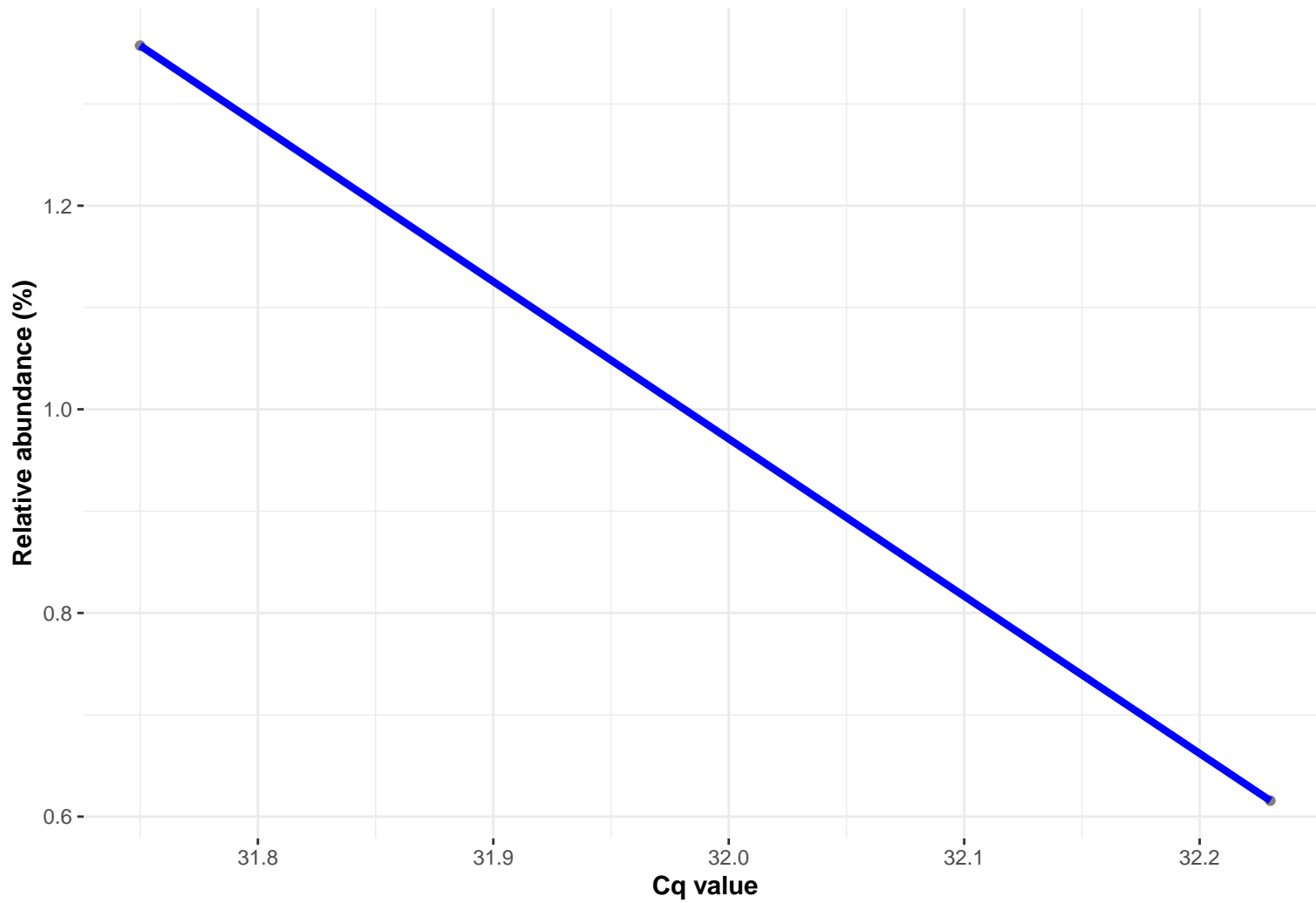


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus cecorum

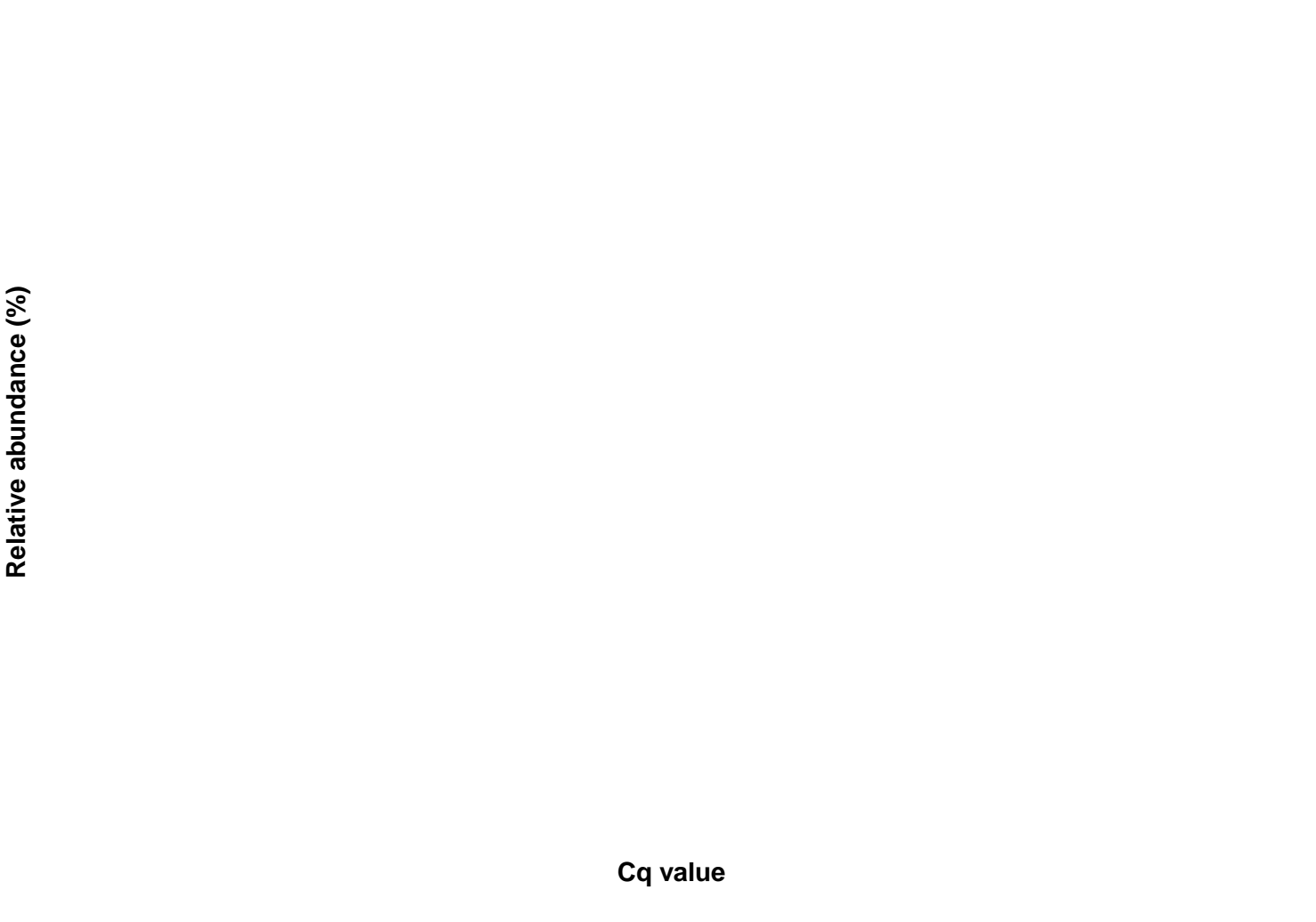
Correlation with all samples



Correlation within: REF-DIM



Correlation within: PCR-blank

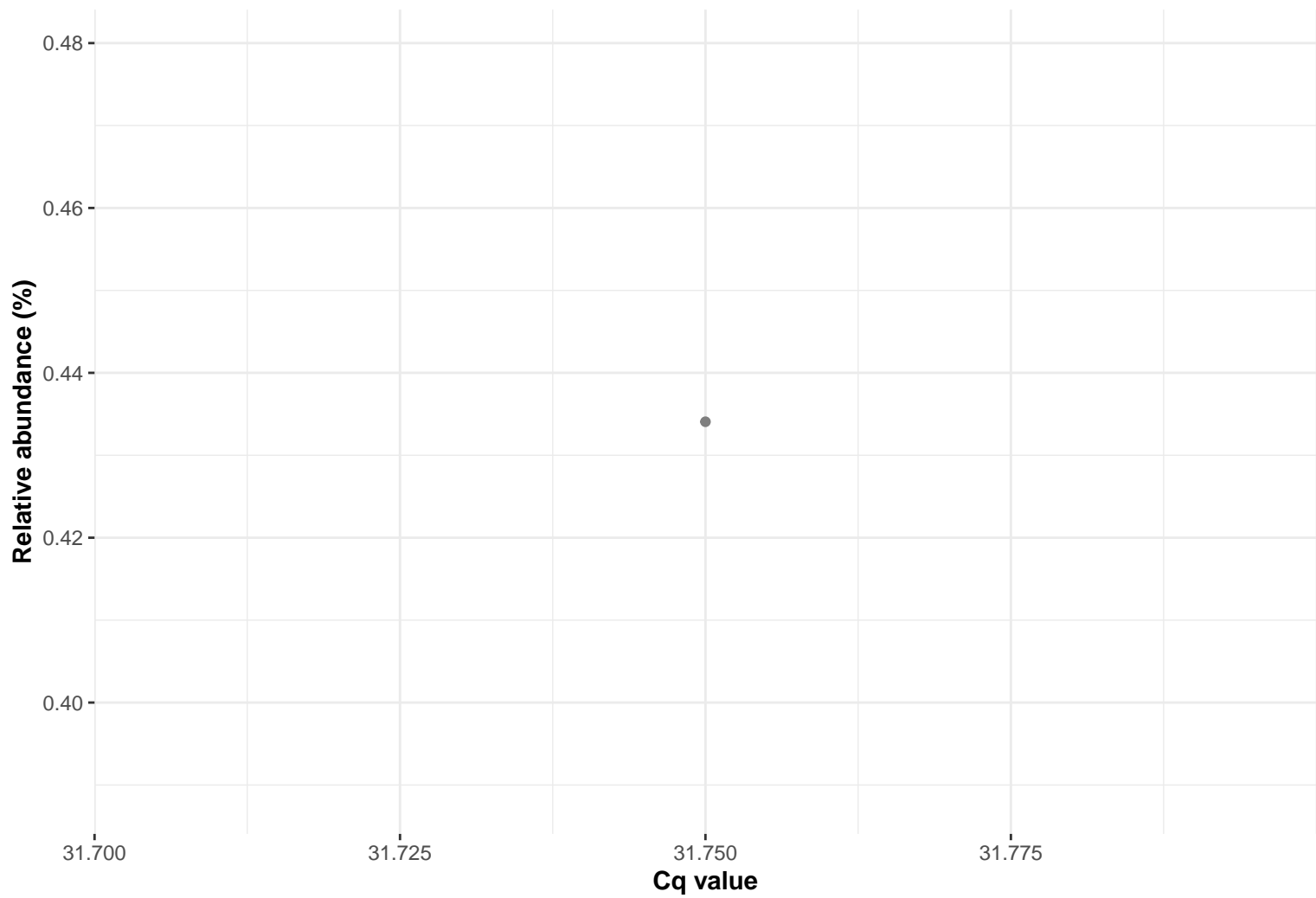


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples



Correlation within: REF-DIM



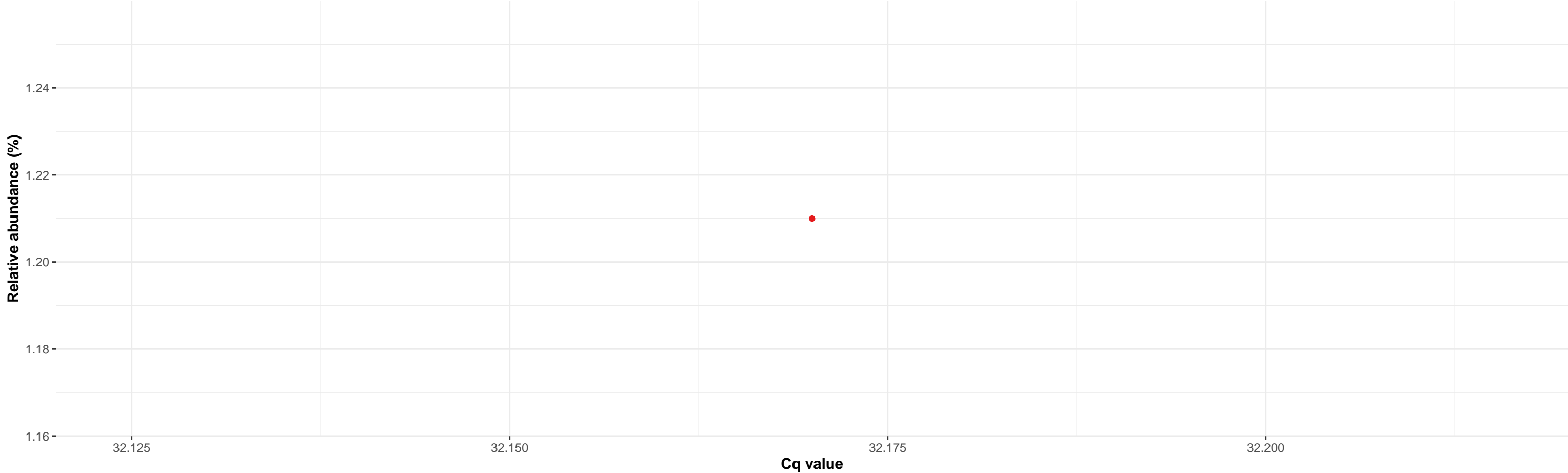
Correlation within: PCR-blank





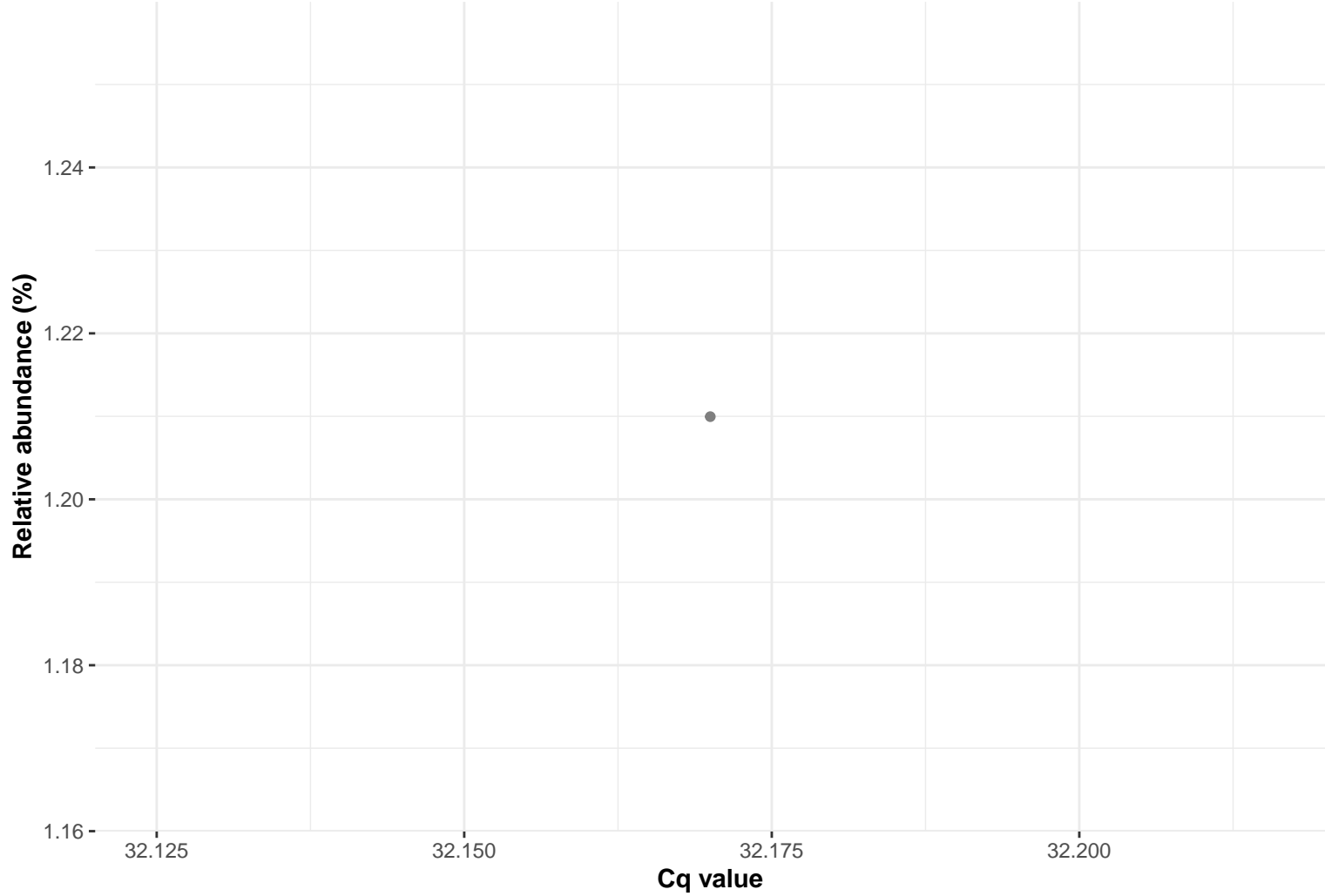
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; s\_\_uncultured bacterium

Correlation with all samples



SampleType • REF-DIM

Correlation within: REF-DIM

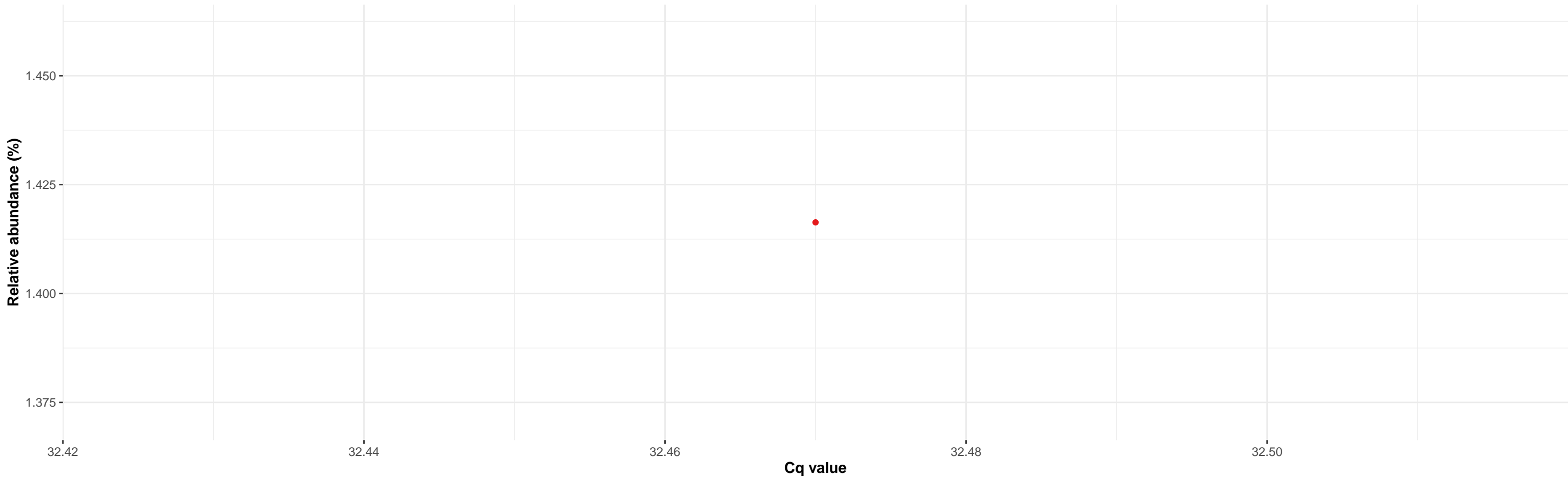


Correlation within: PCR-blank



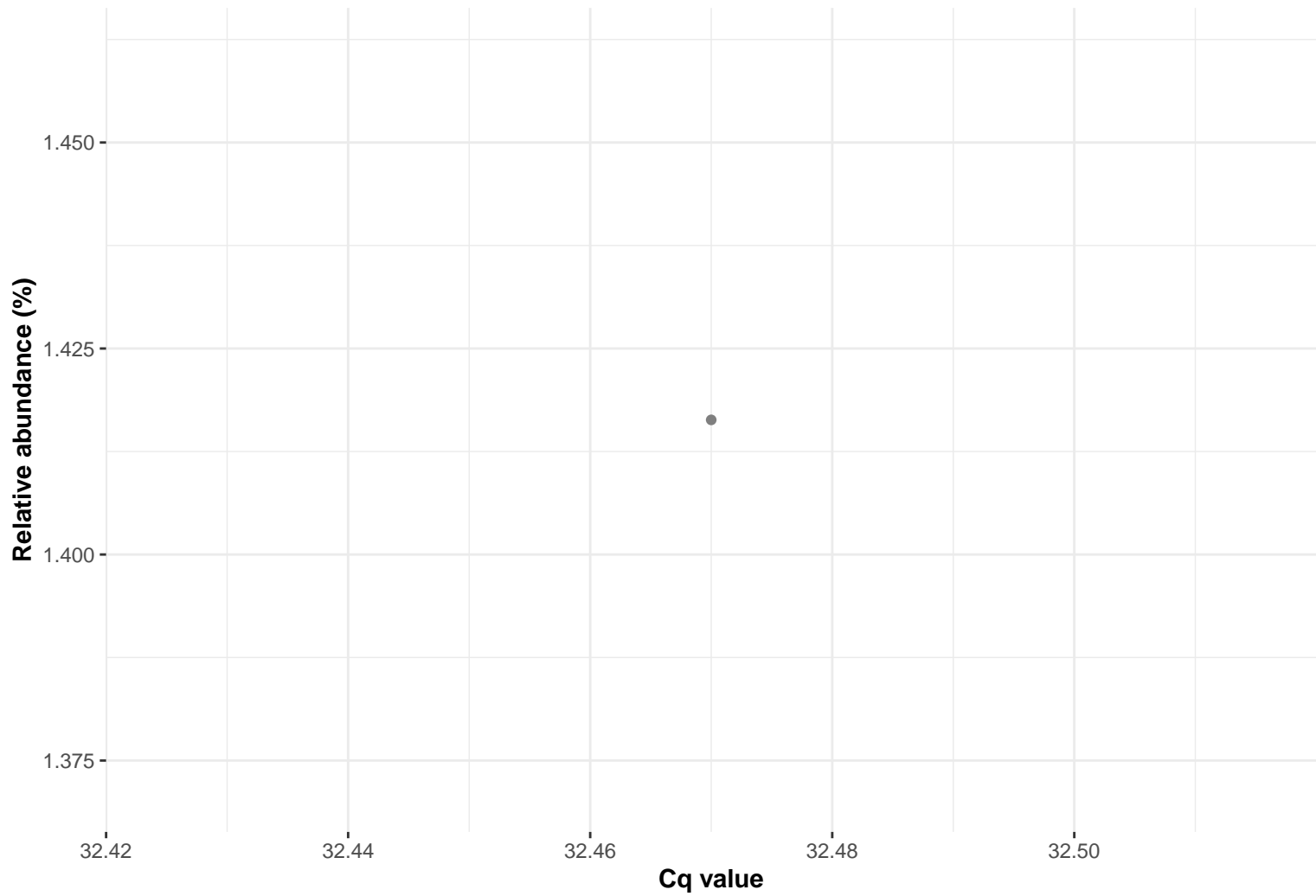
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples



SampleType    • REF-DIM

Correlation within: REF-DIM



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Nosocomiicoccus; s\_\_uncultured bacterium

Correlation with all samples

Relative abundance (%)

Correlation within: PCR–blank

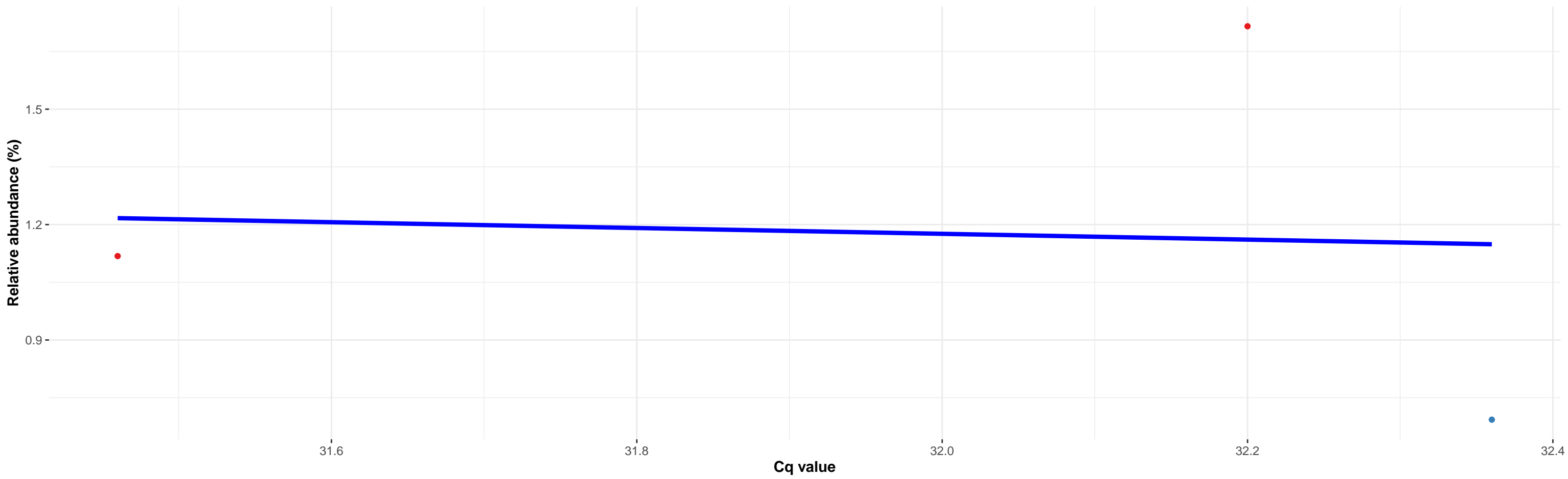
Cq value

Relative abundance (%)

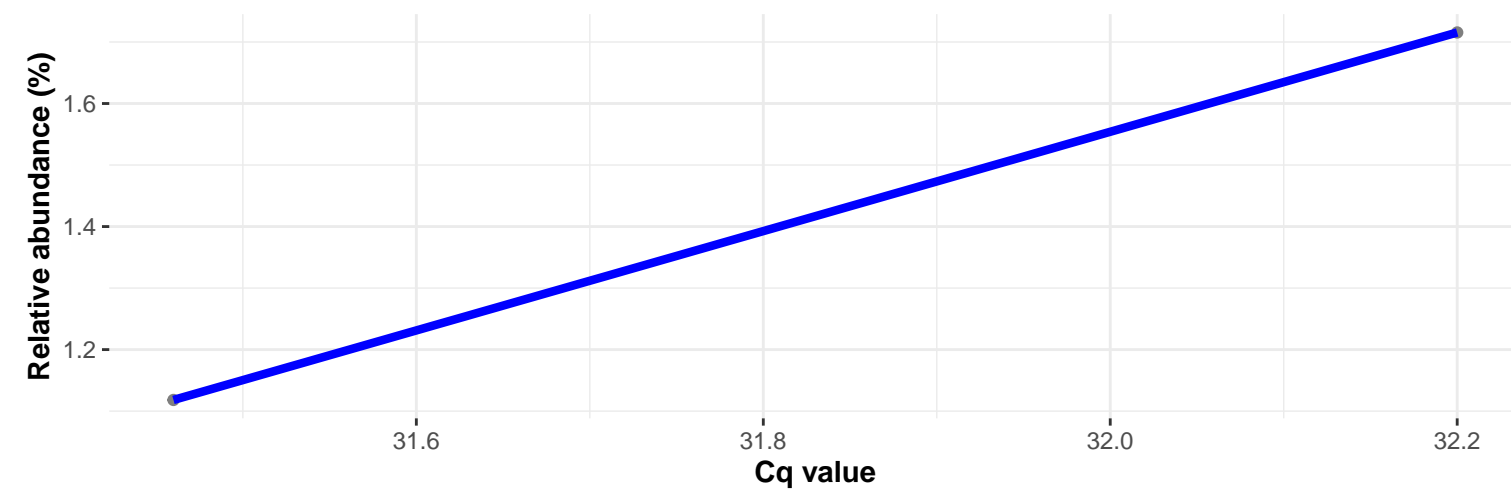
Cq value

k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

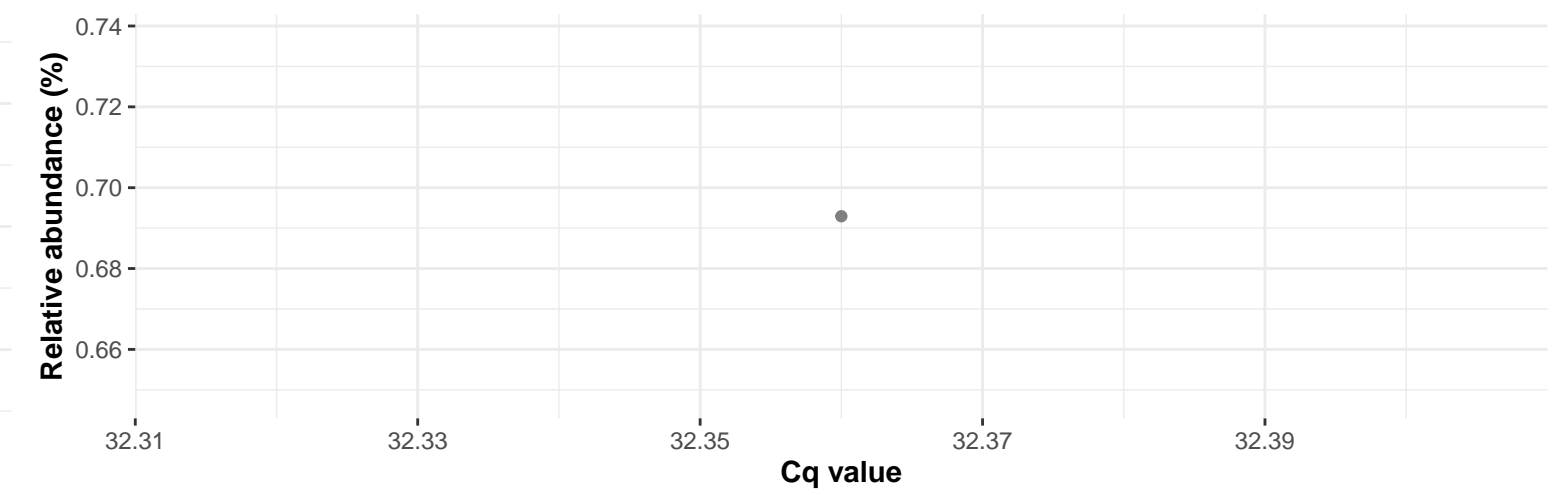
Correlation with all samples



Correlation within: REF-PIM



Correlation within: REF-DIM

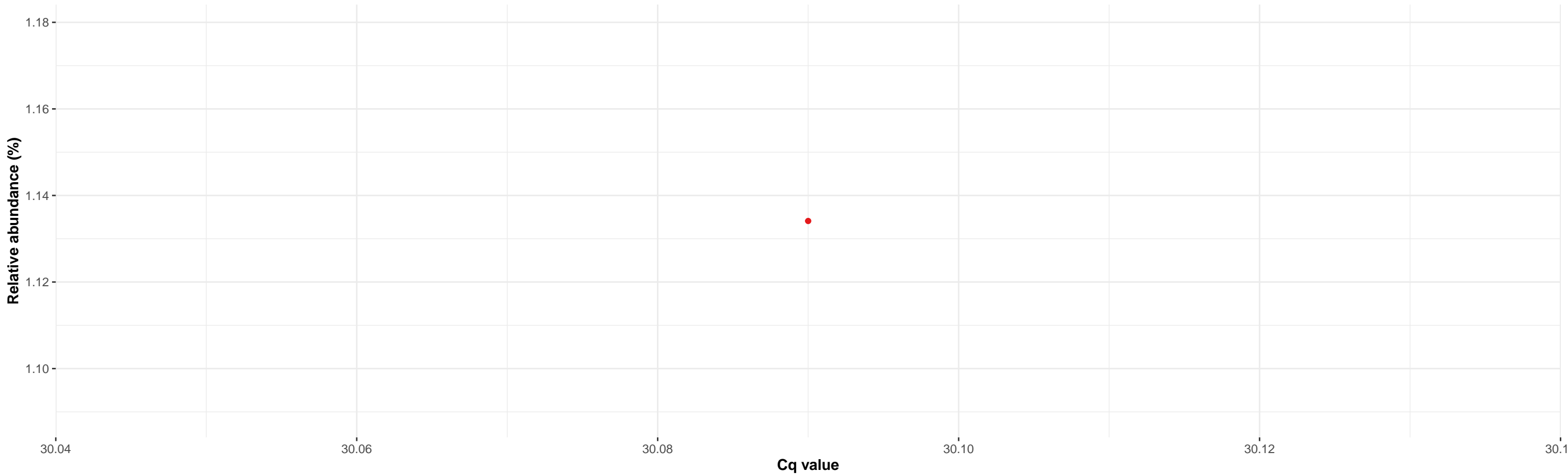


Correlation within: PCR-blank



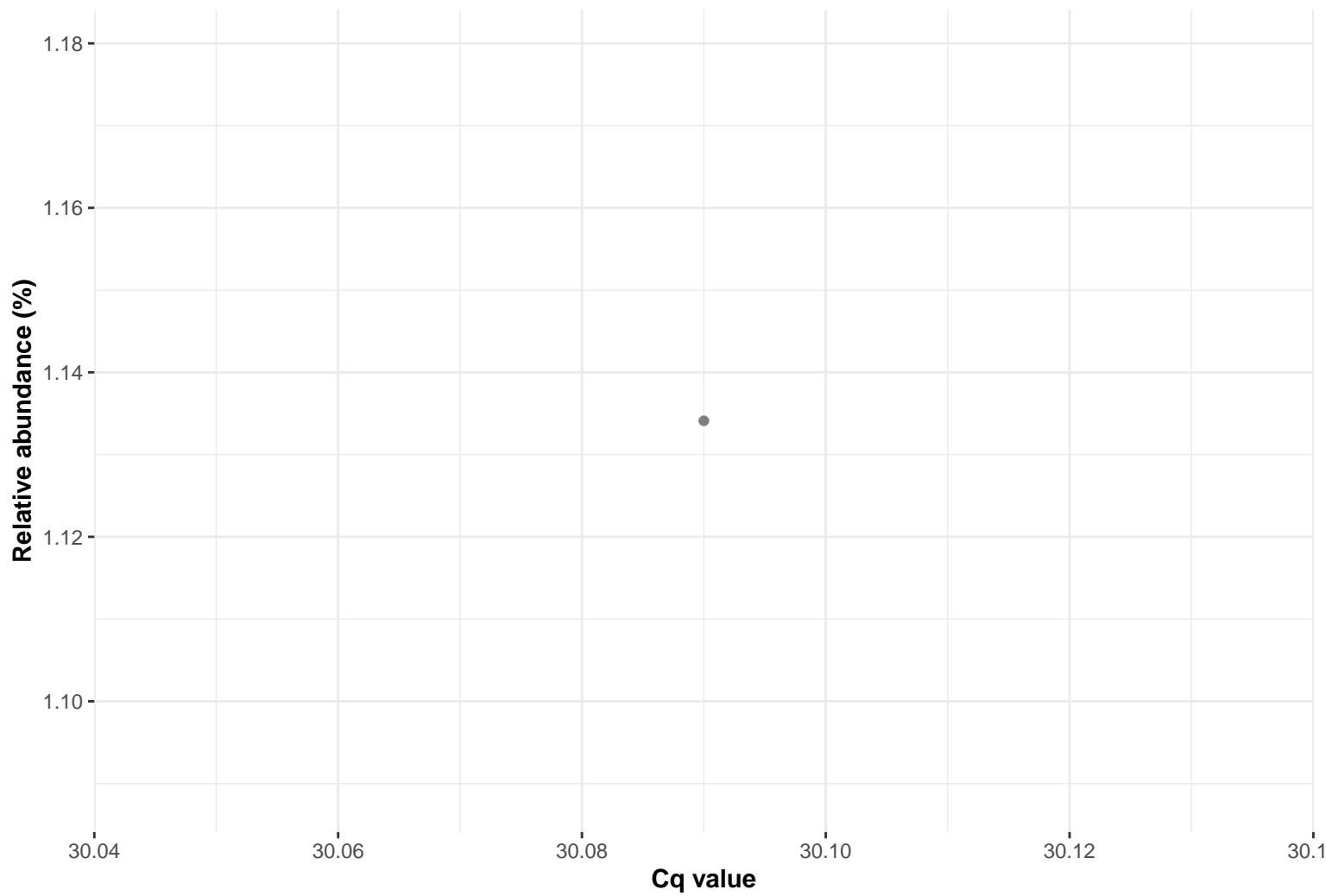
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Hydrogenophaga; NA

Correlation with all samples



SampleType • REF-PIM

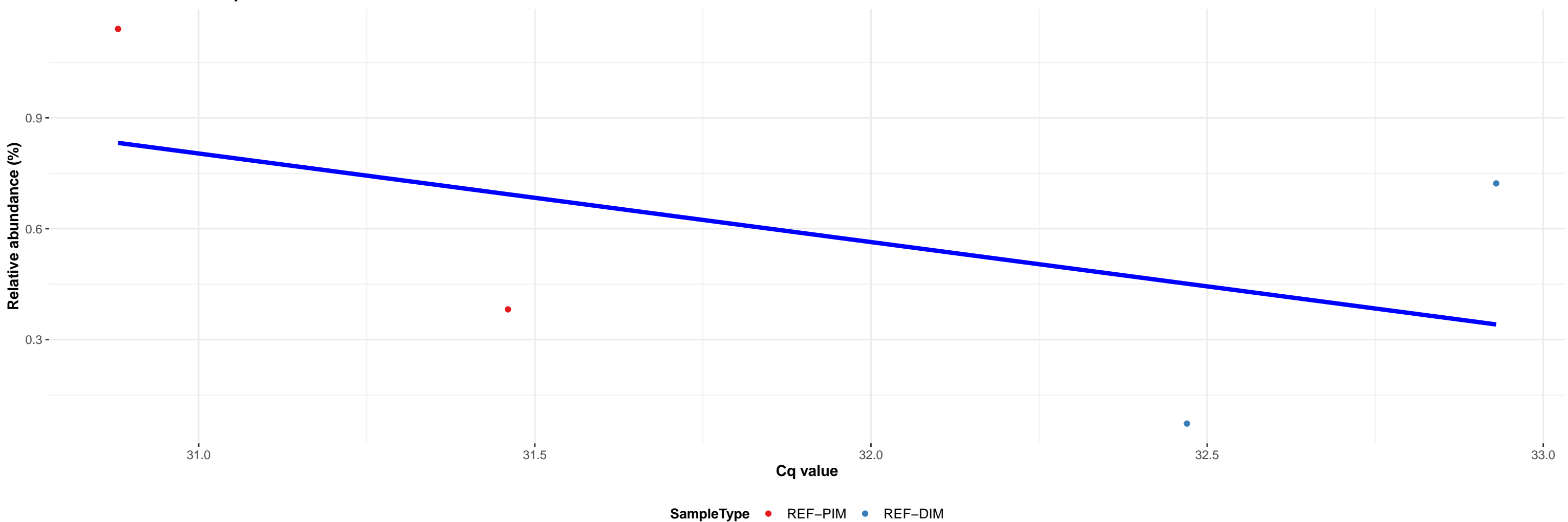
Correlation within: REF-PIM



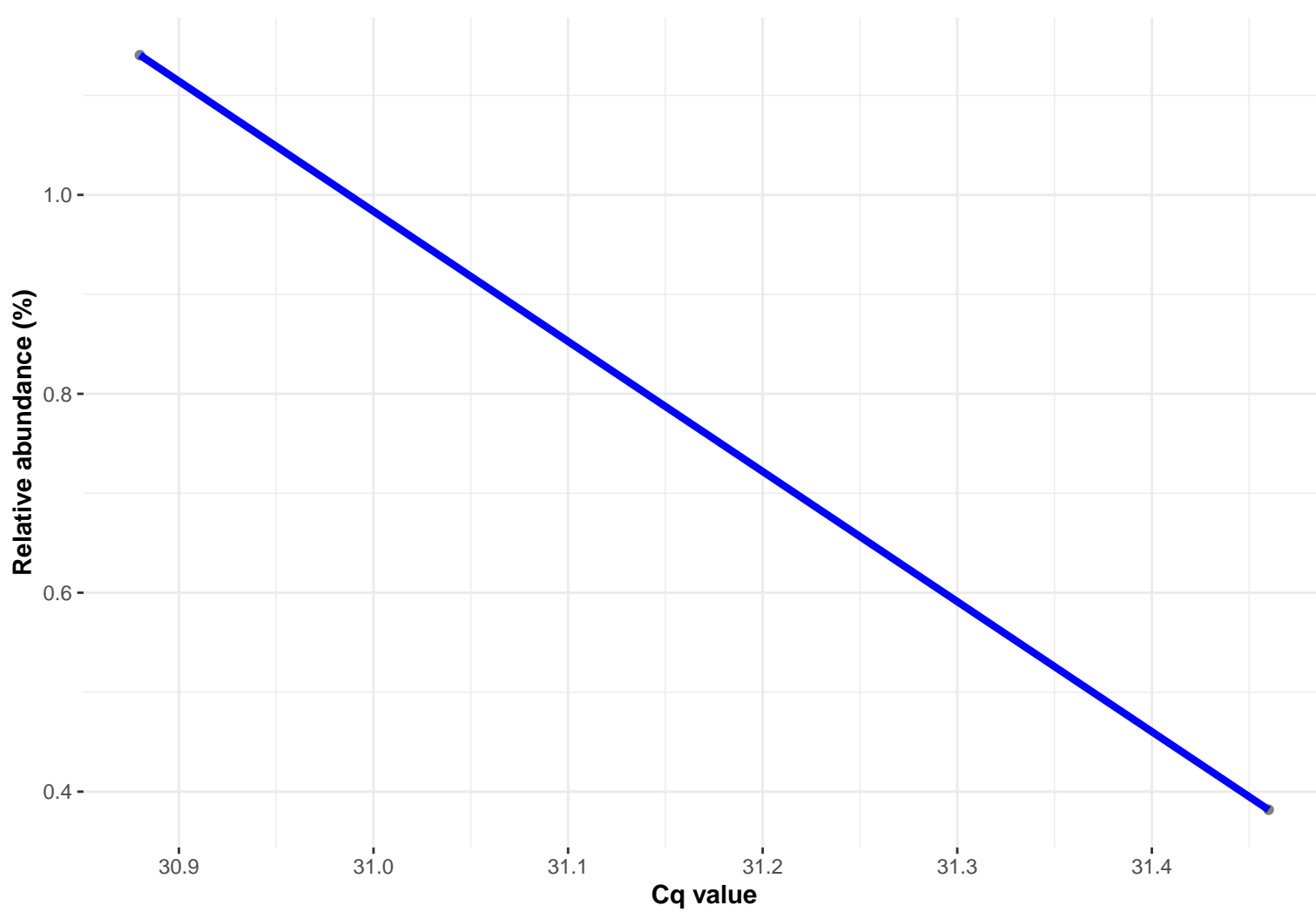
Correlation within: PCR-blank



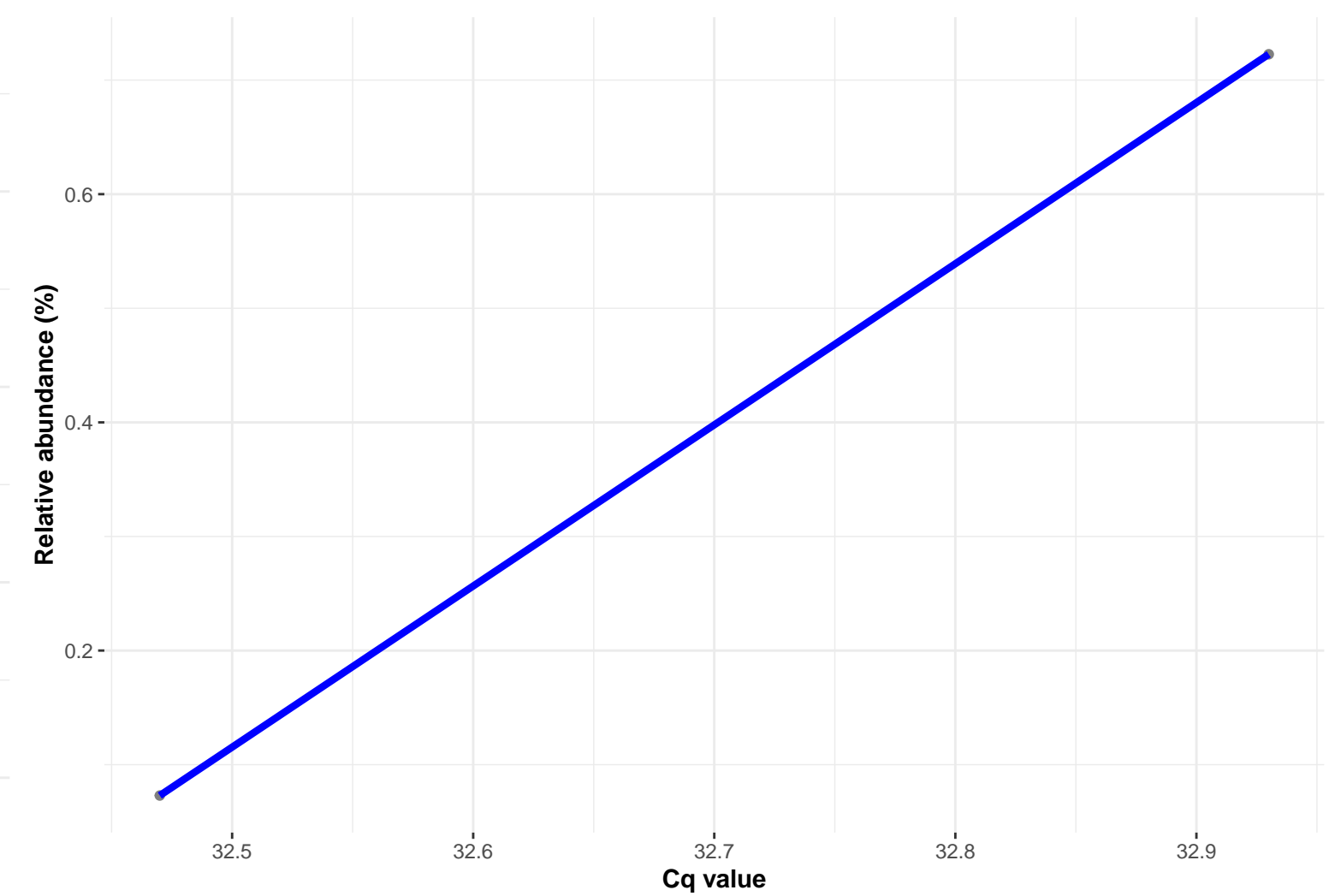
Correlation with all samples



Correlation within: REF-PIM

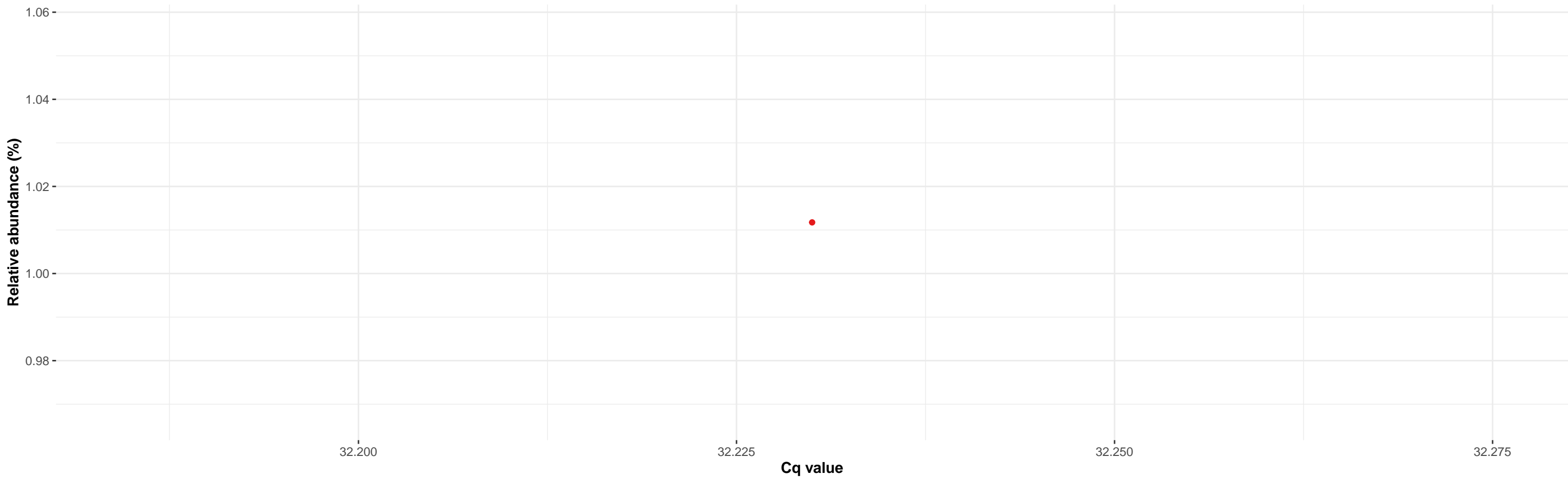


Correlation within: REF-DIM



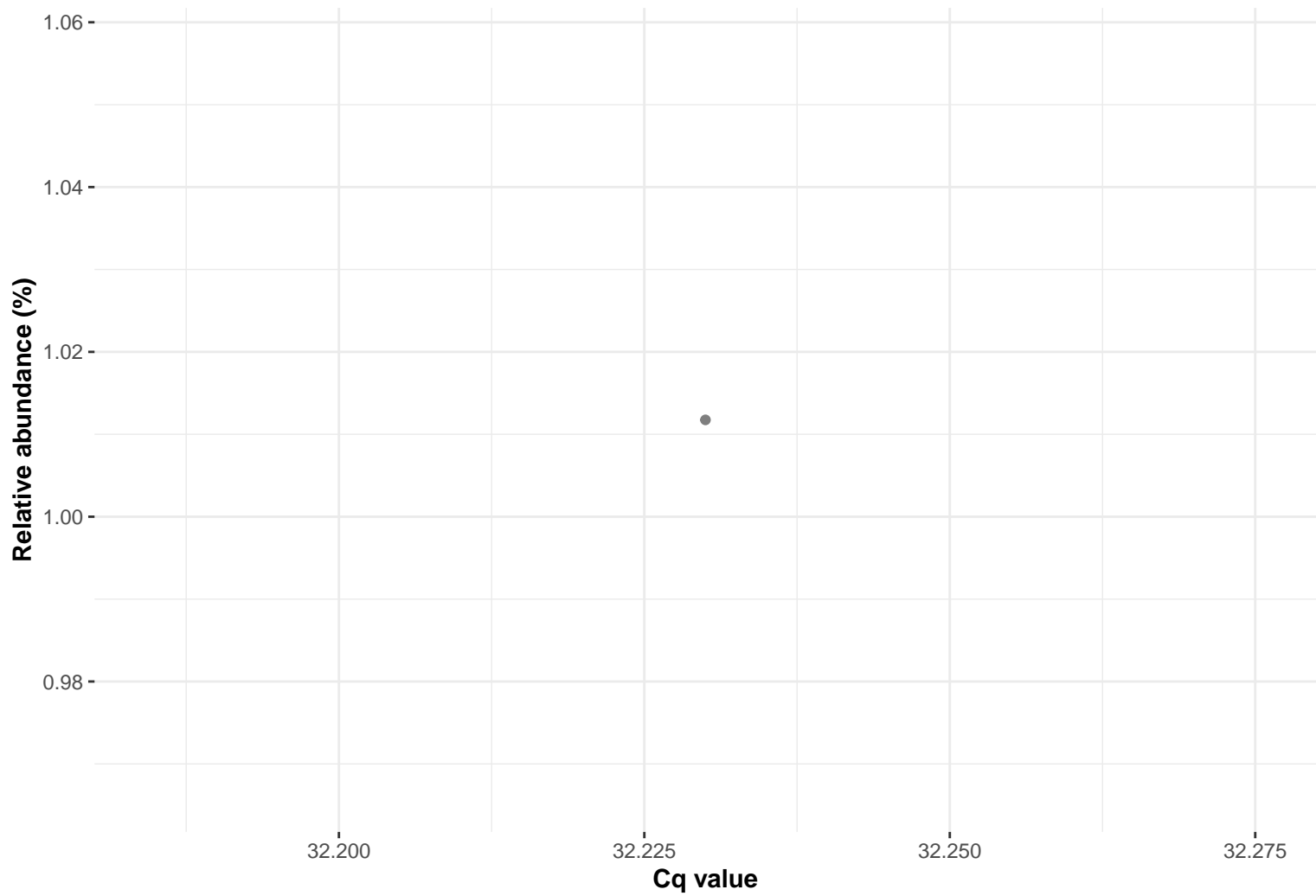
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples

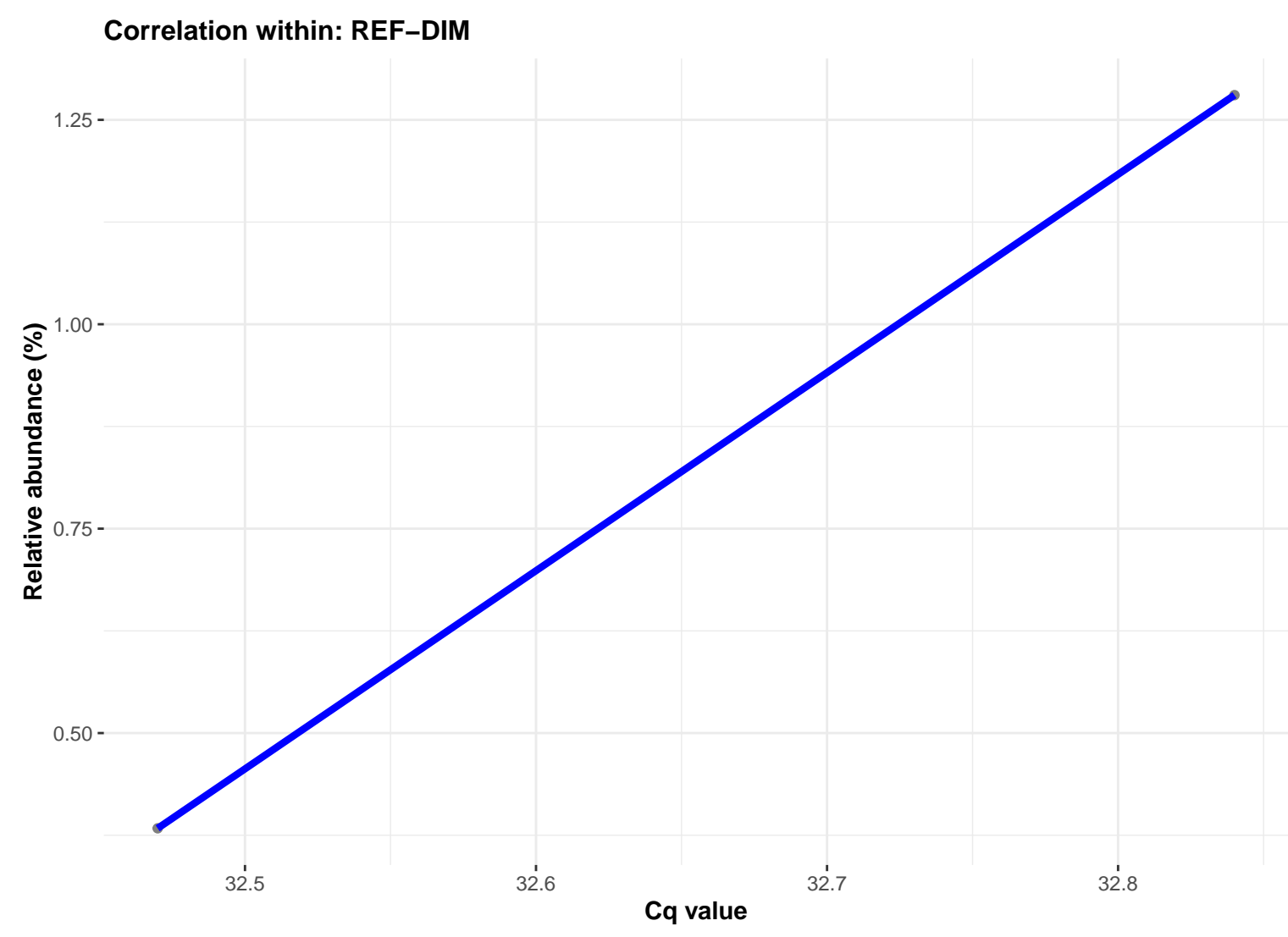
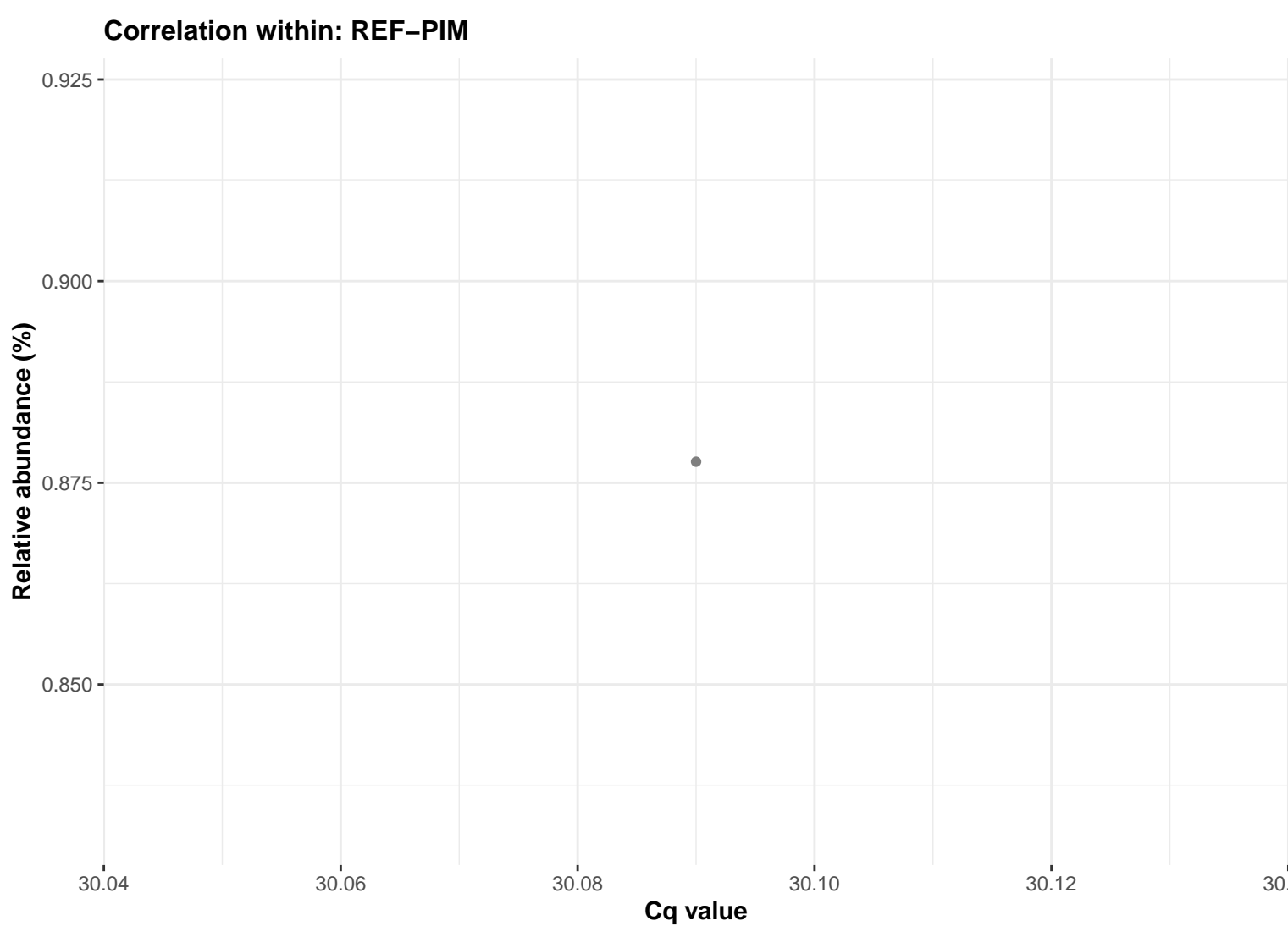
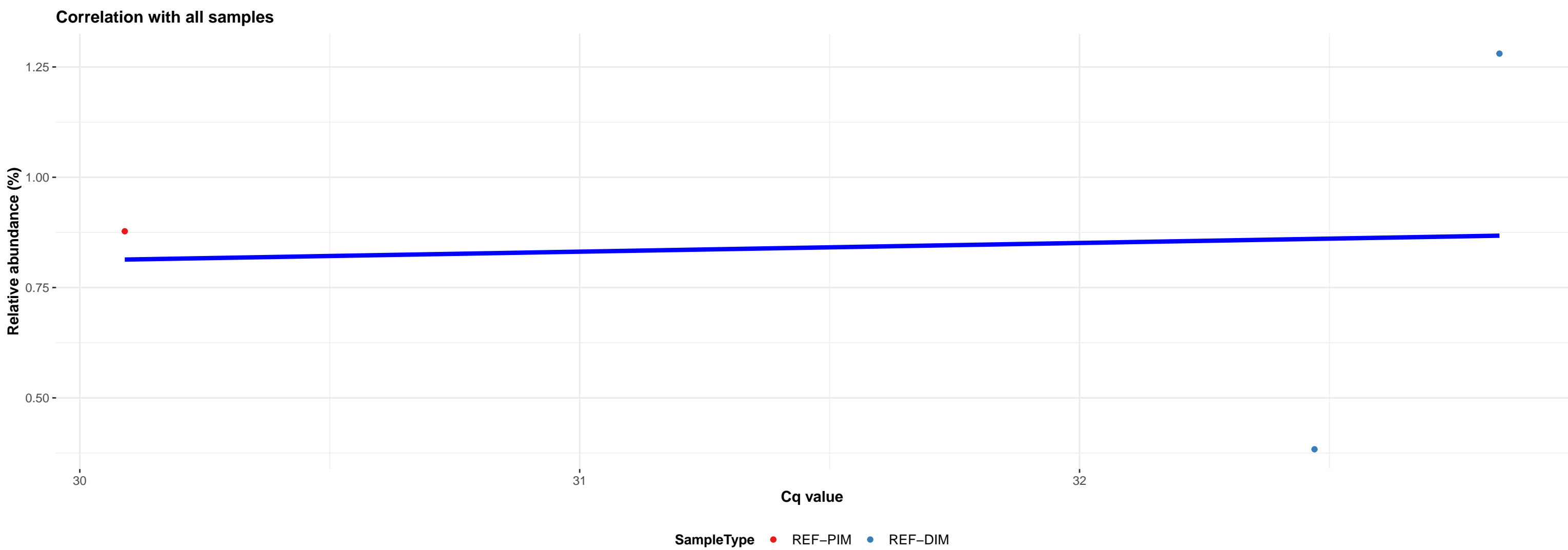


SampleType • REF-DIM

Correlation within: REF-DIM



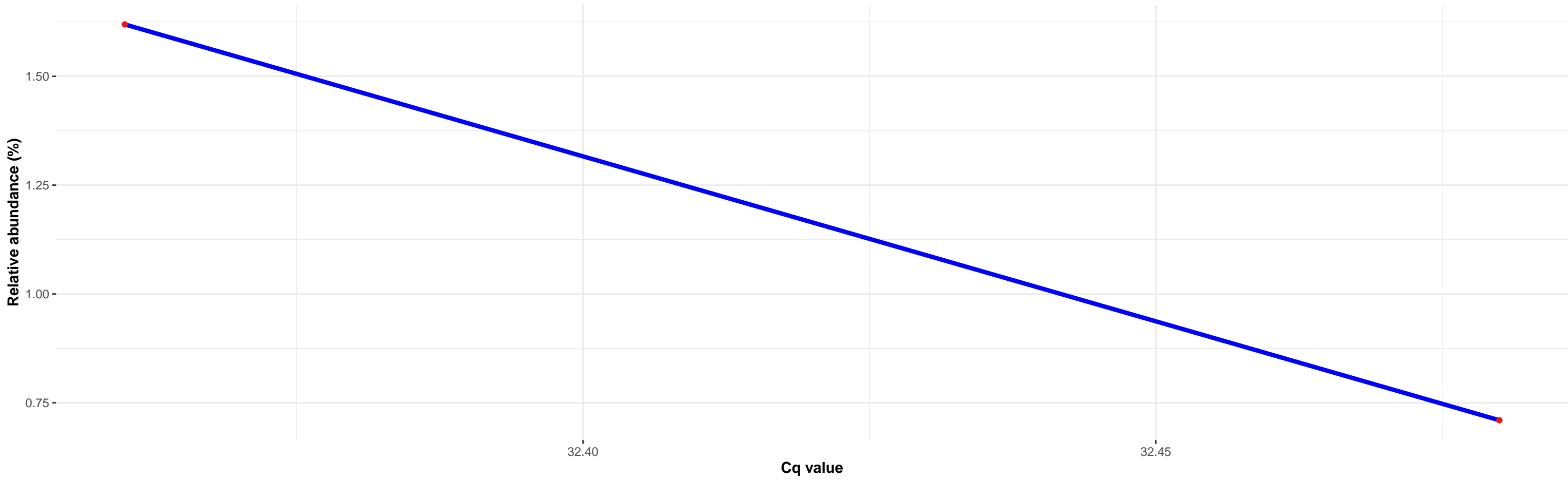
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Deltaproteobacteria; o\_\_Desulfuromonadales; f\_\_Desulfuromonadaceae; g\_\_Pelobacter; s\_\_uncultured bacterium





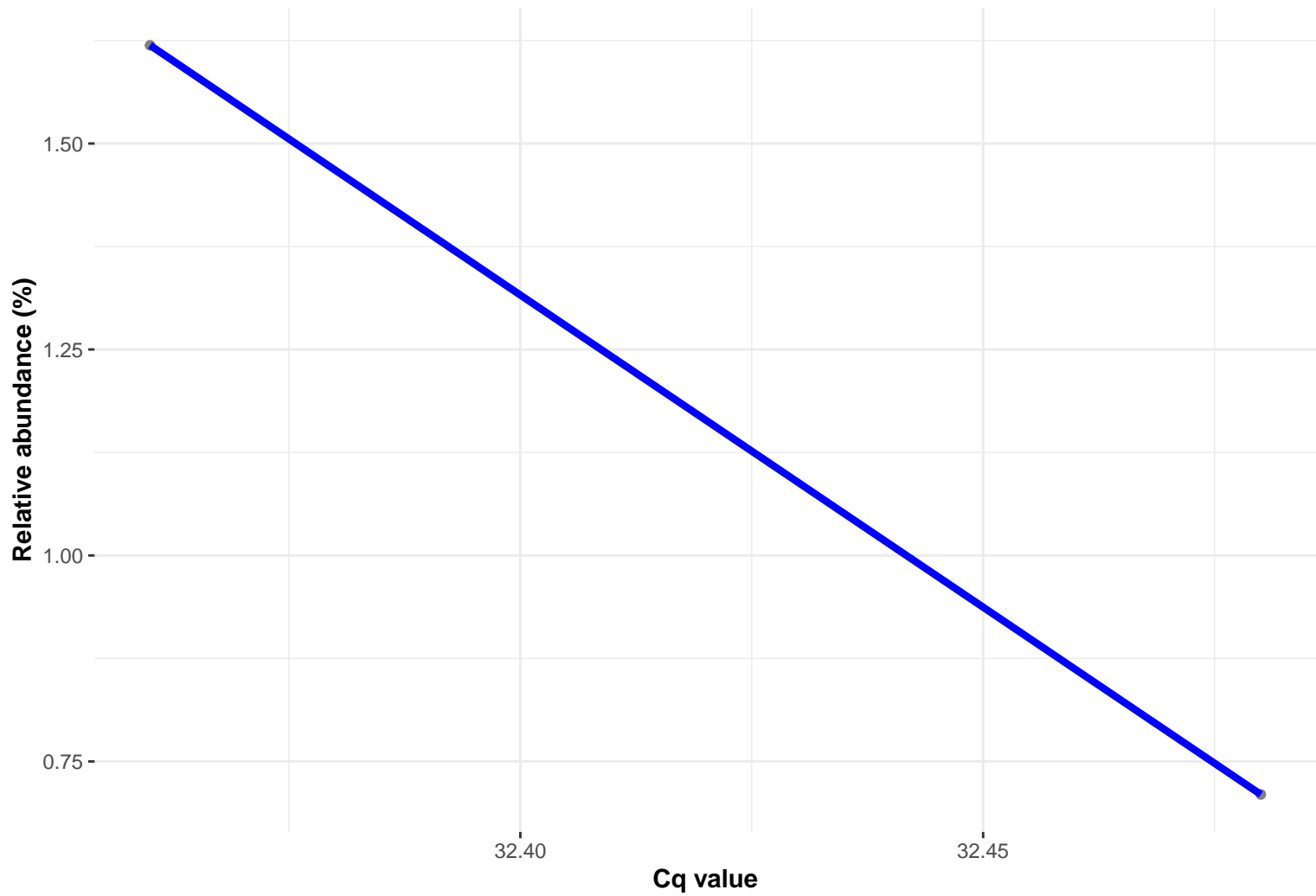
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

Correlation with all samples

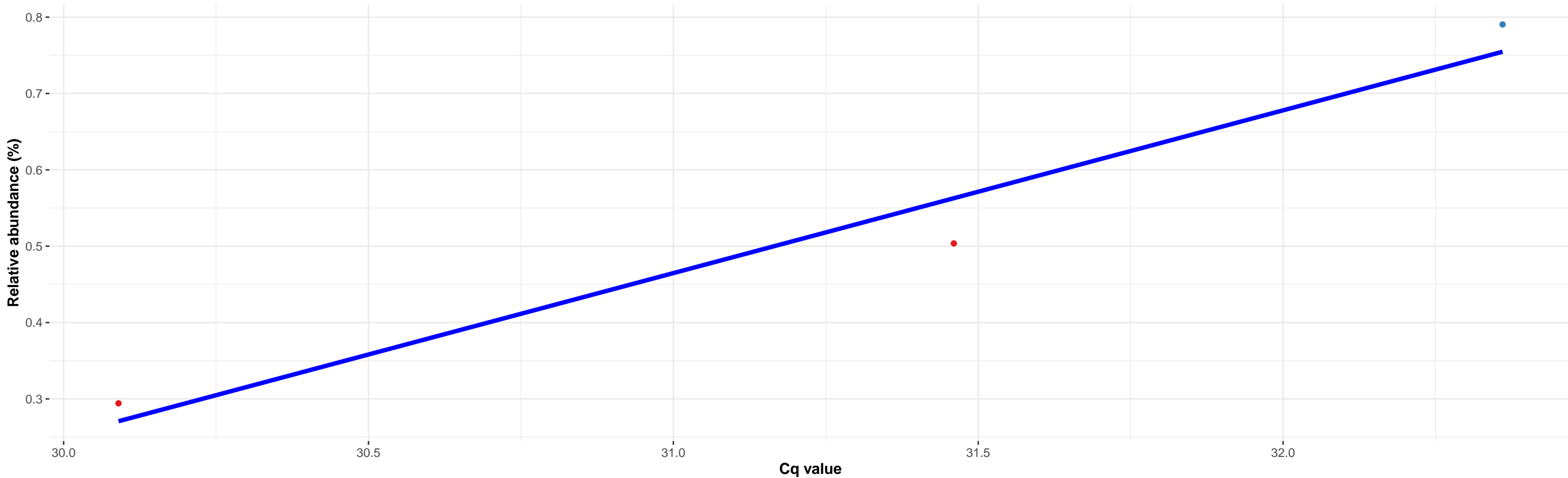


SampleType REF-DIM

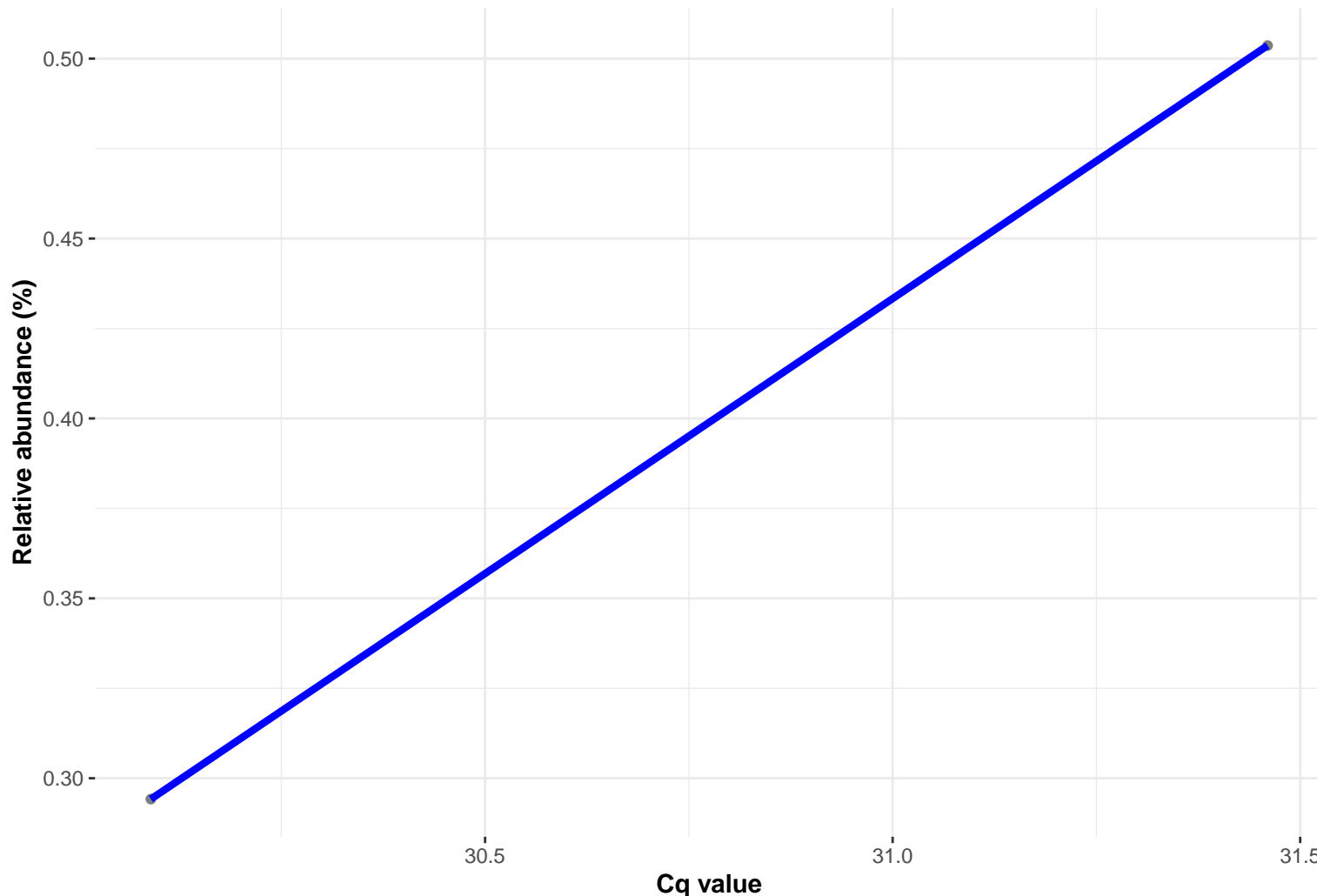
Correlation within: REF-DIM



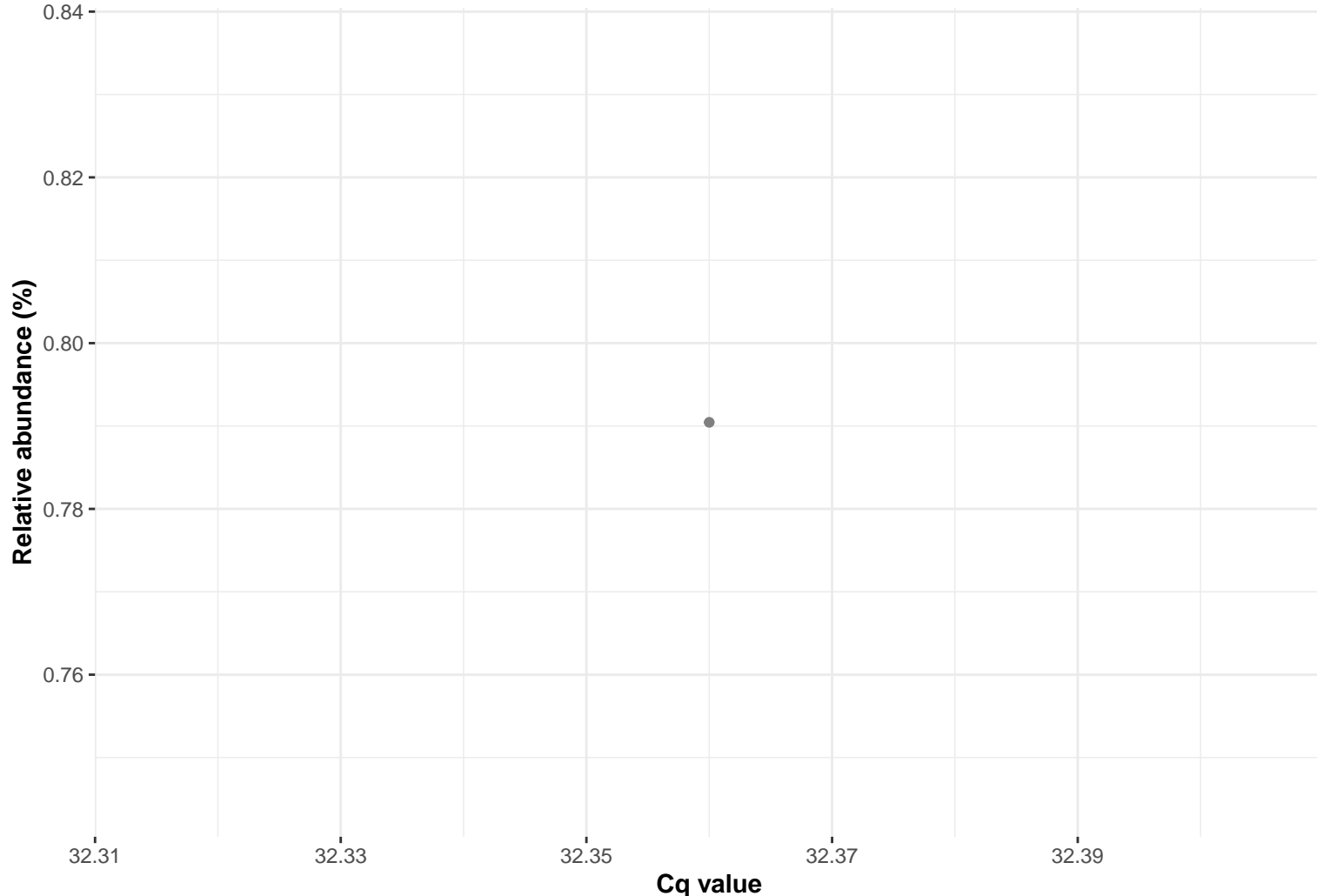
Correlation with all samples



Correlation within: REF-PIM

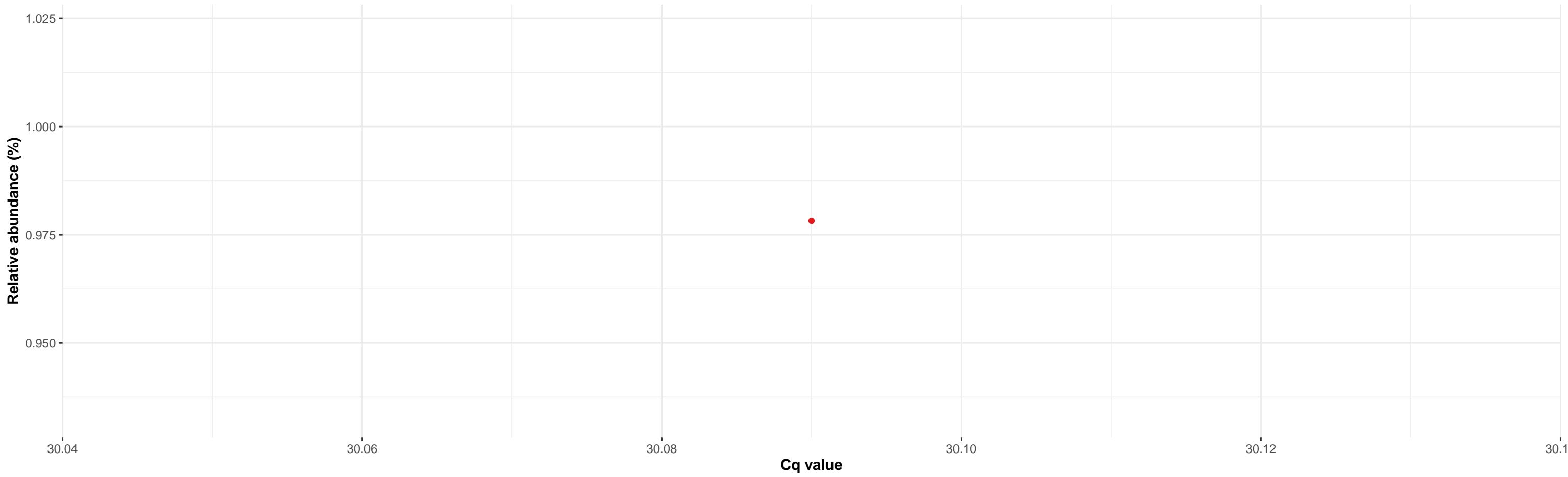


Correlation within: REF-DIM

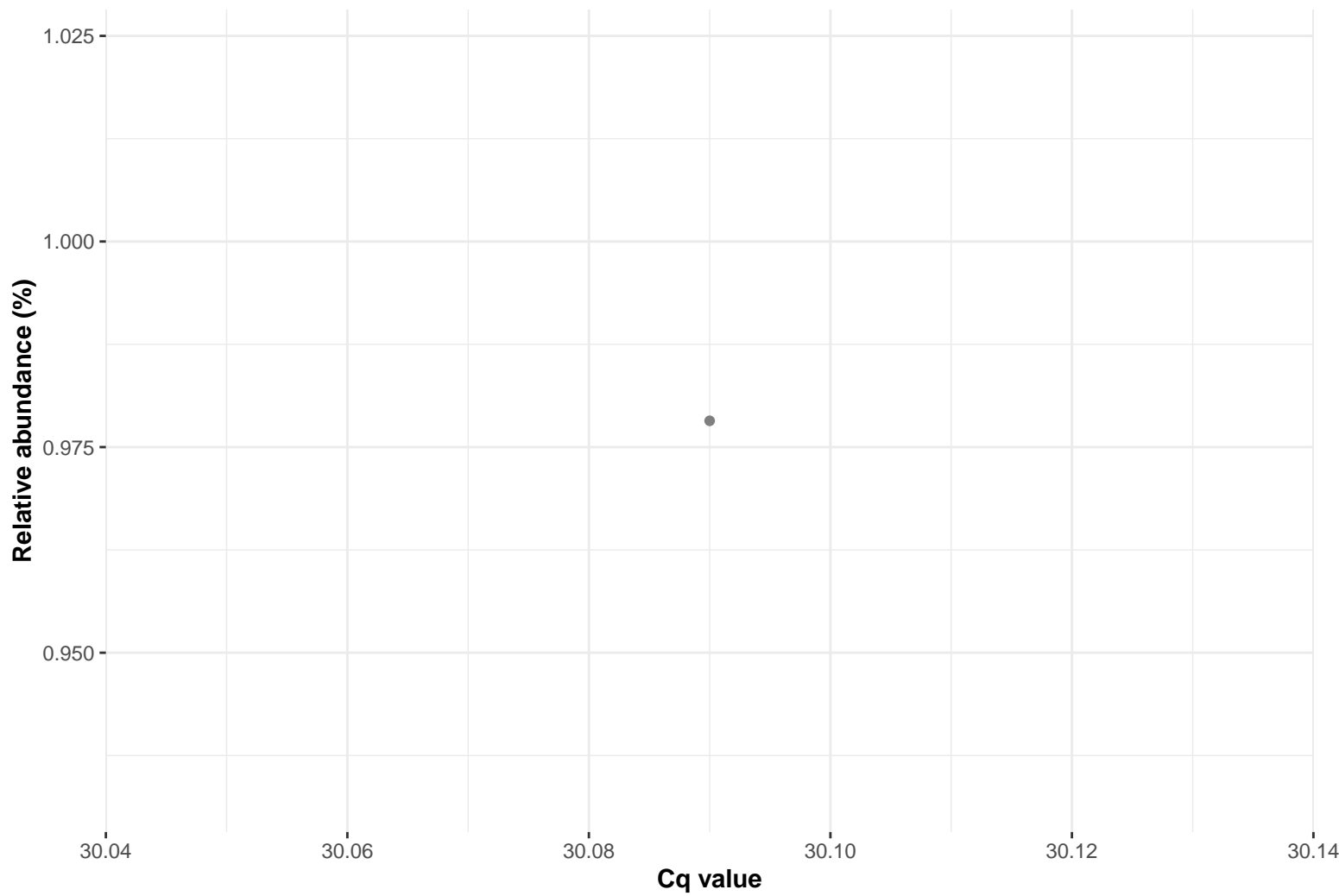


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; NA

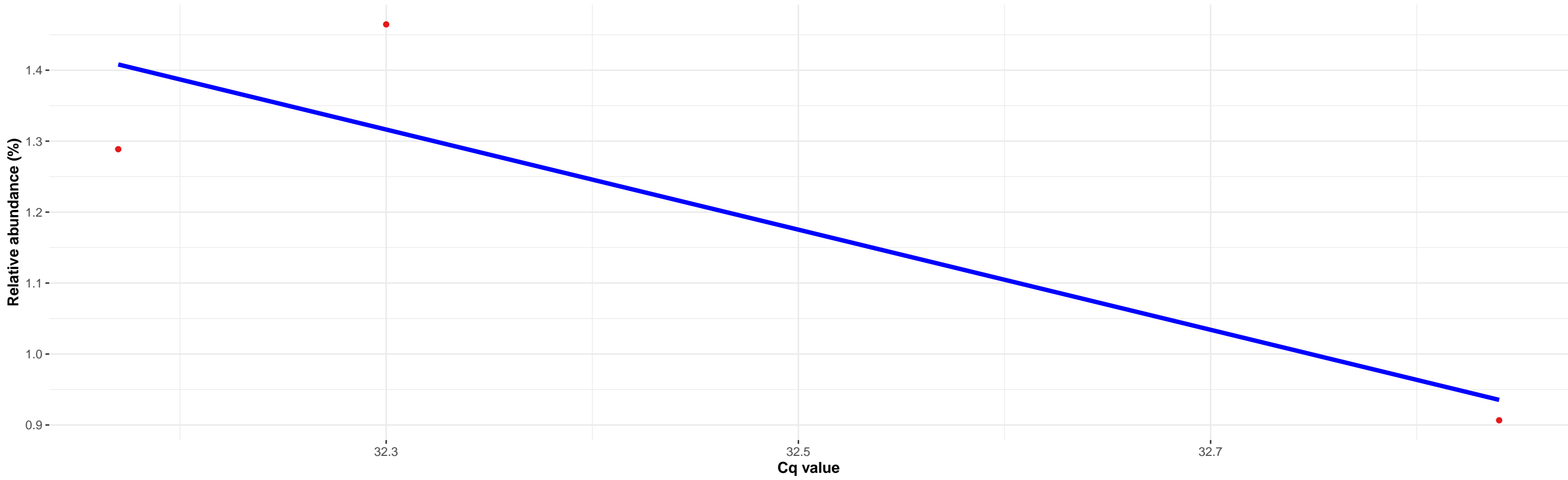
Correlation with all samples



Correlation within: REF-PIM

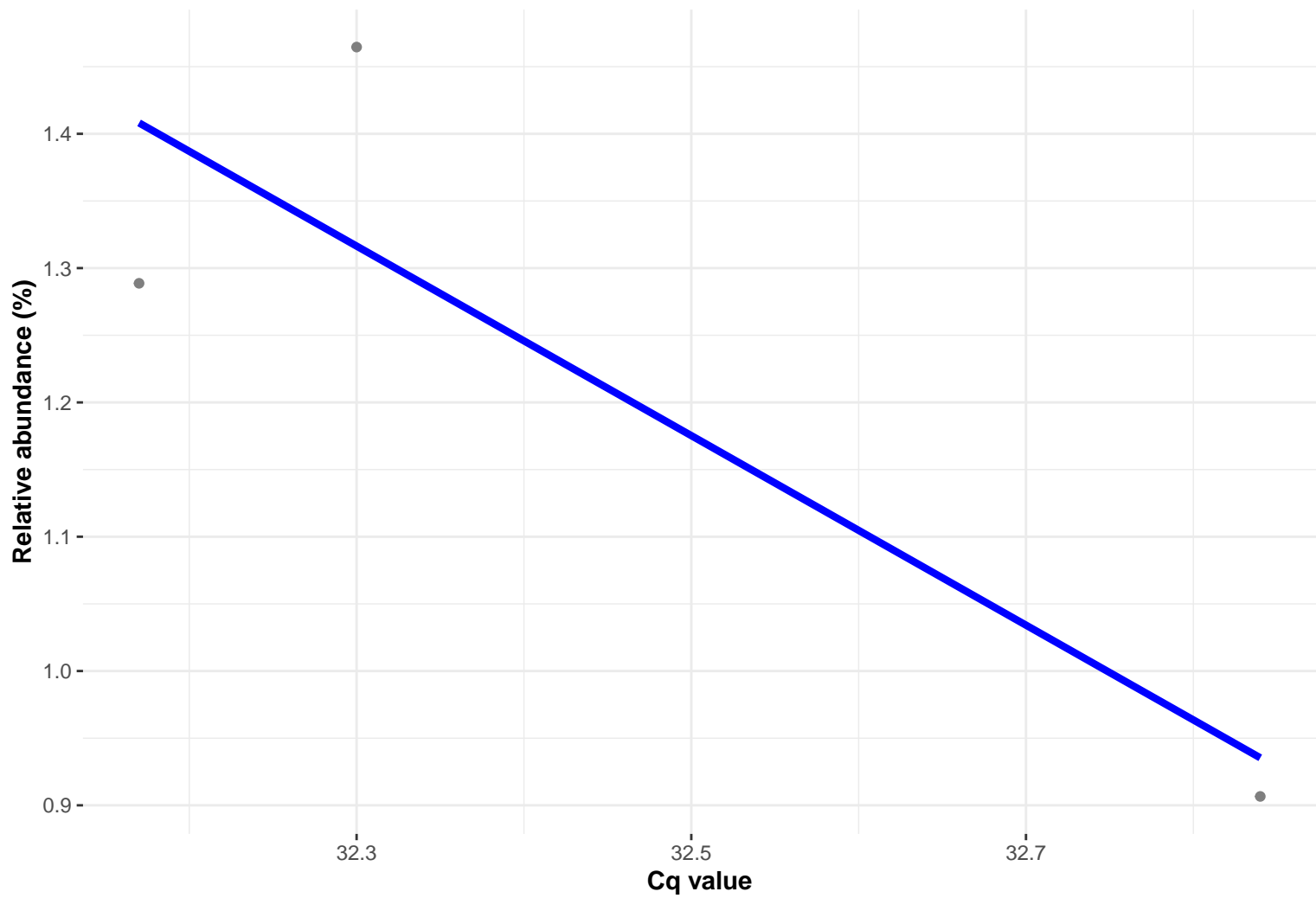


Correlation with all samples

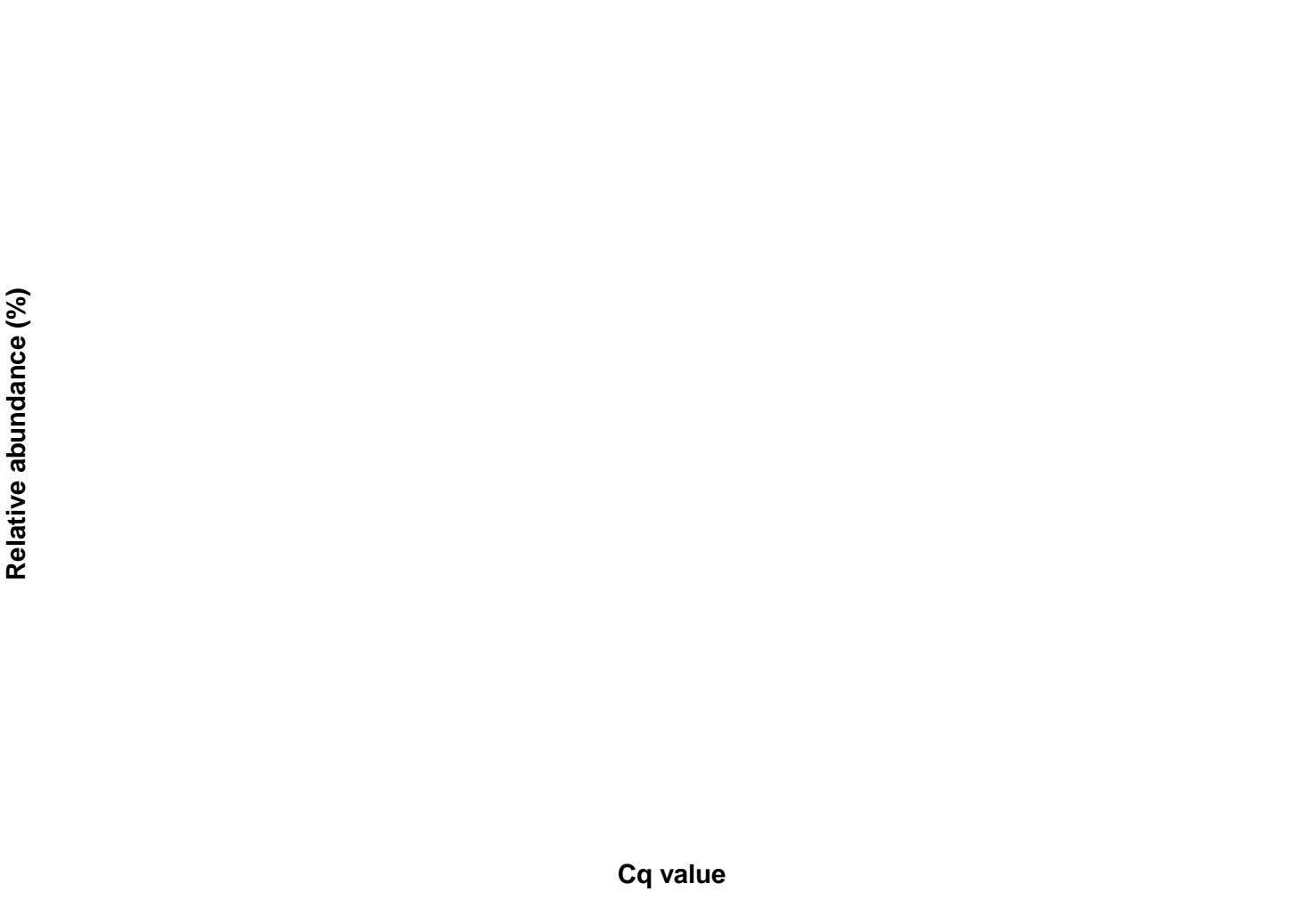


SampleType • REF-DIM

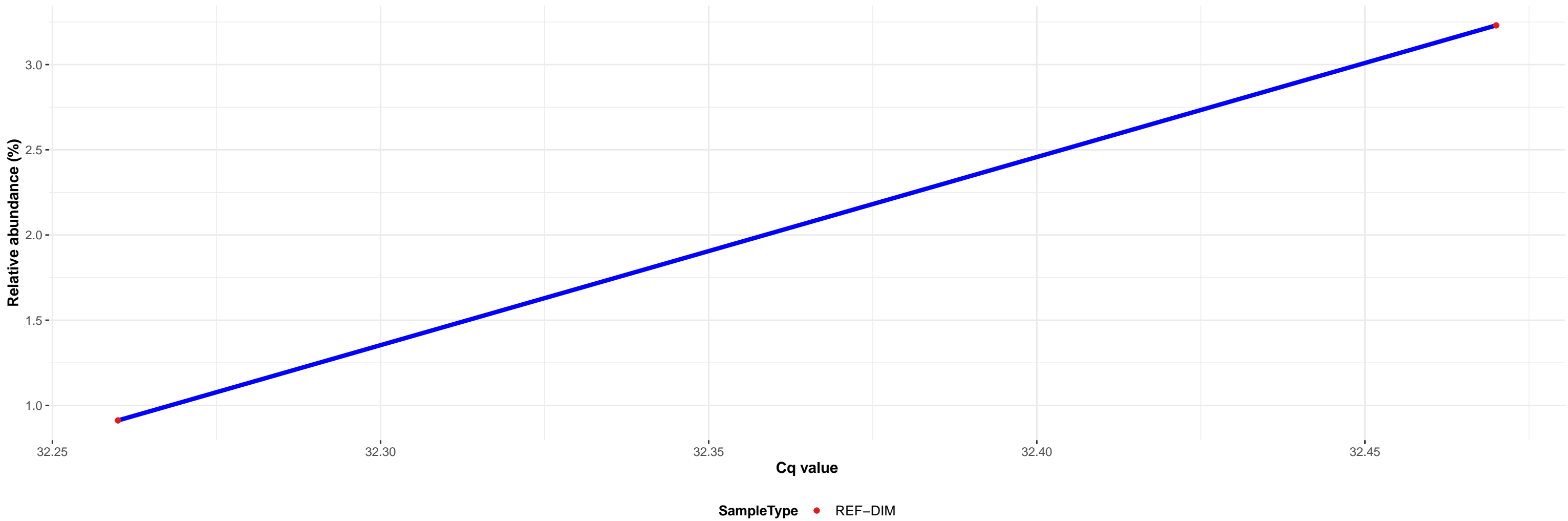
Correlation within: REF-DIM



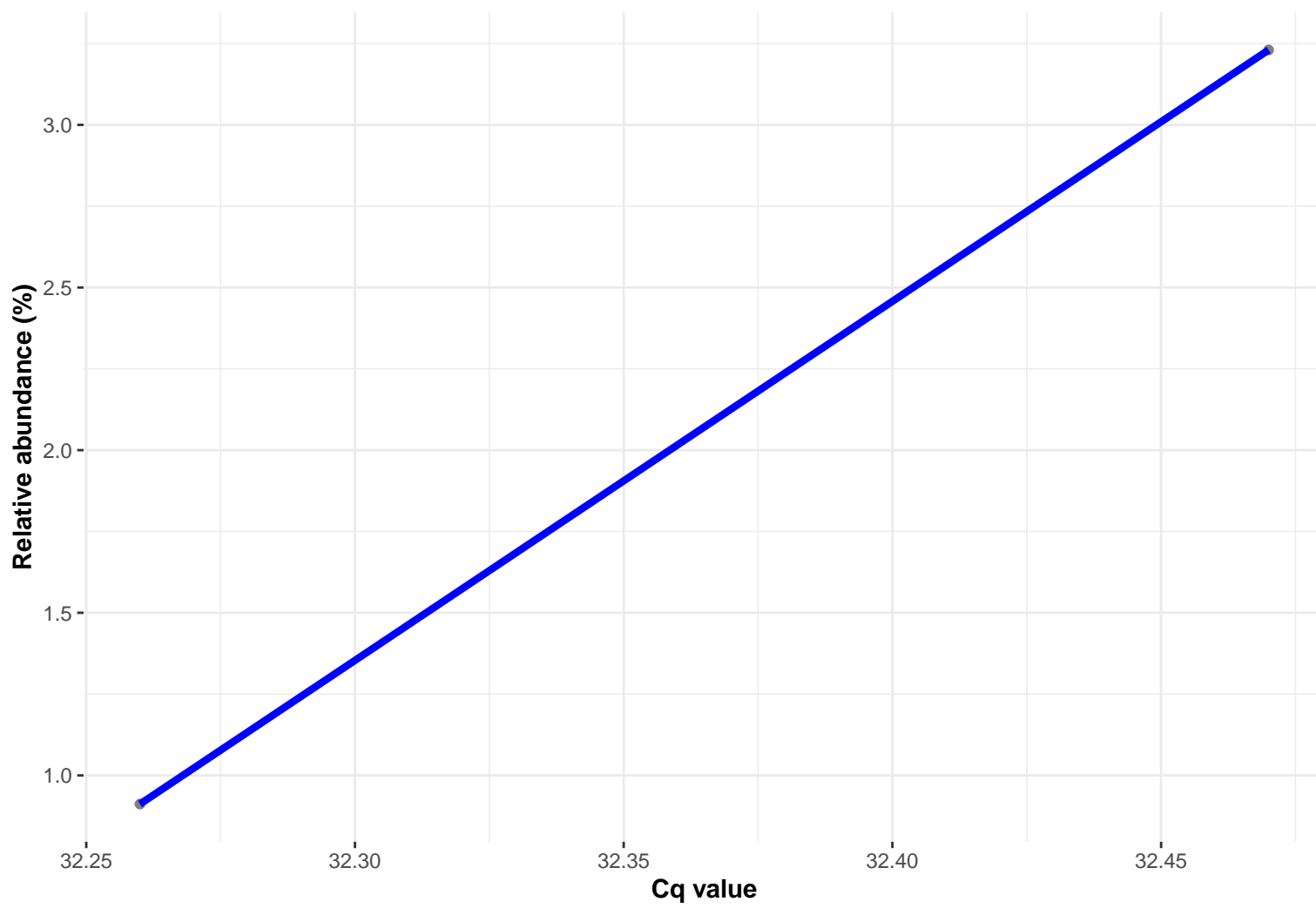
Correlation within: PCR-blank



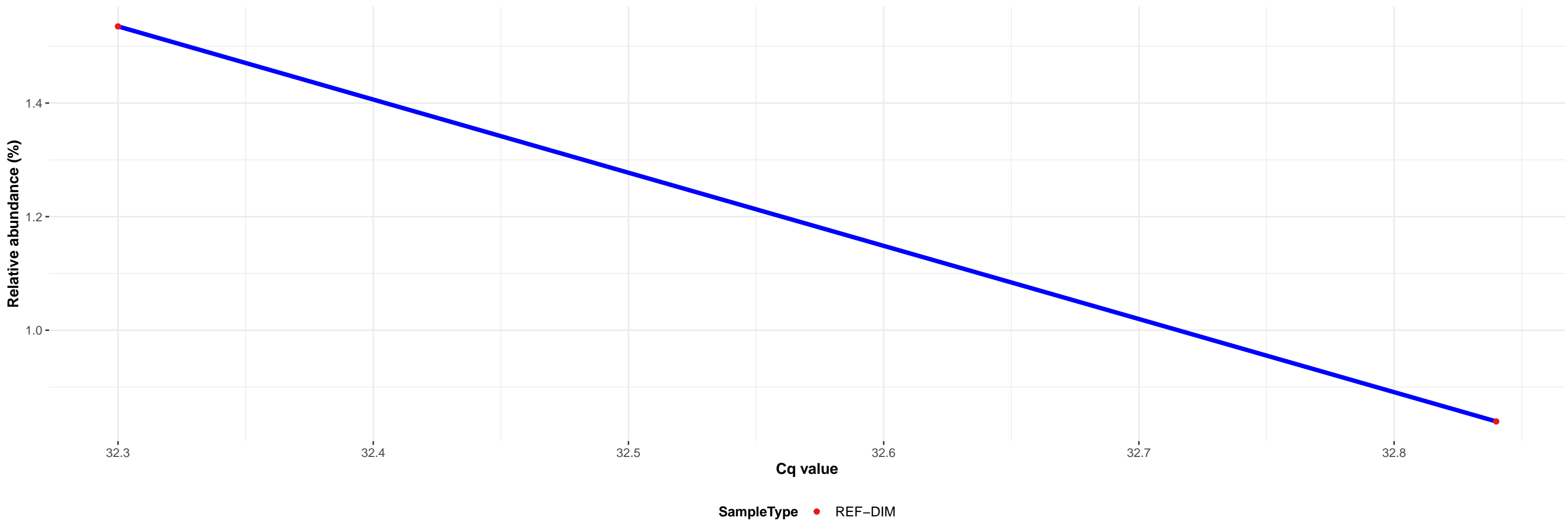
Correlation with all samples



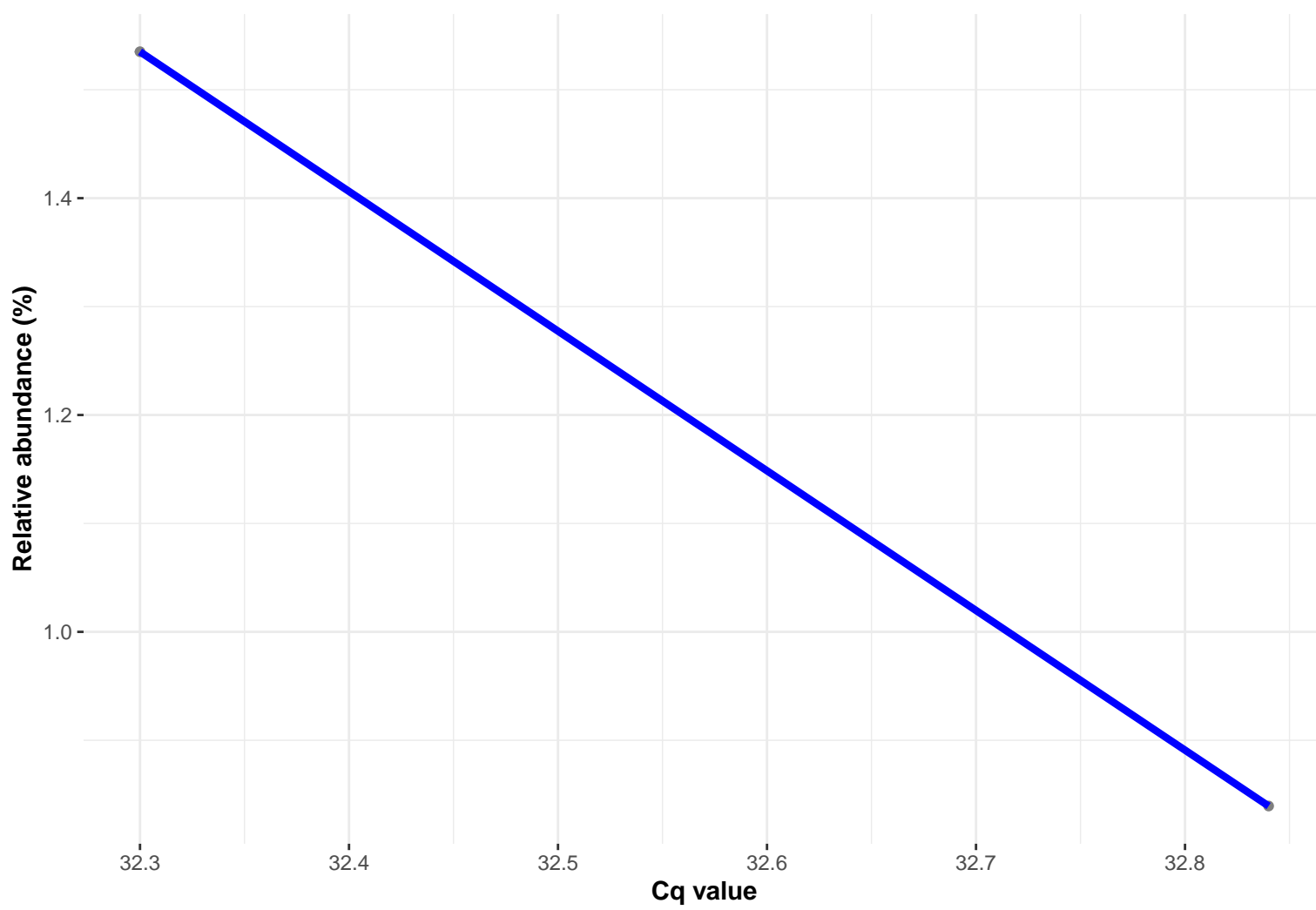
Correlation within: REF-DIM



Correlation with all samples

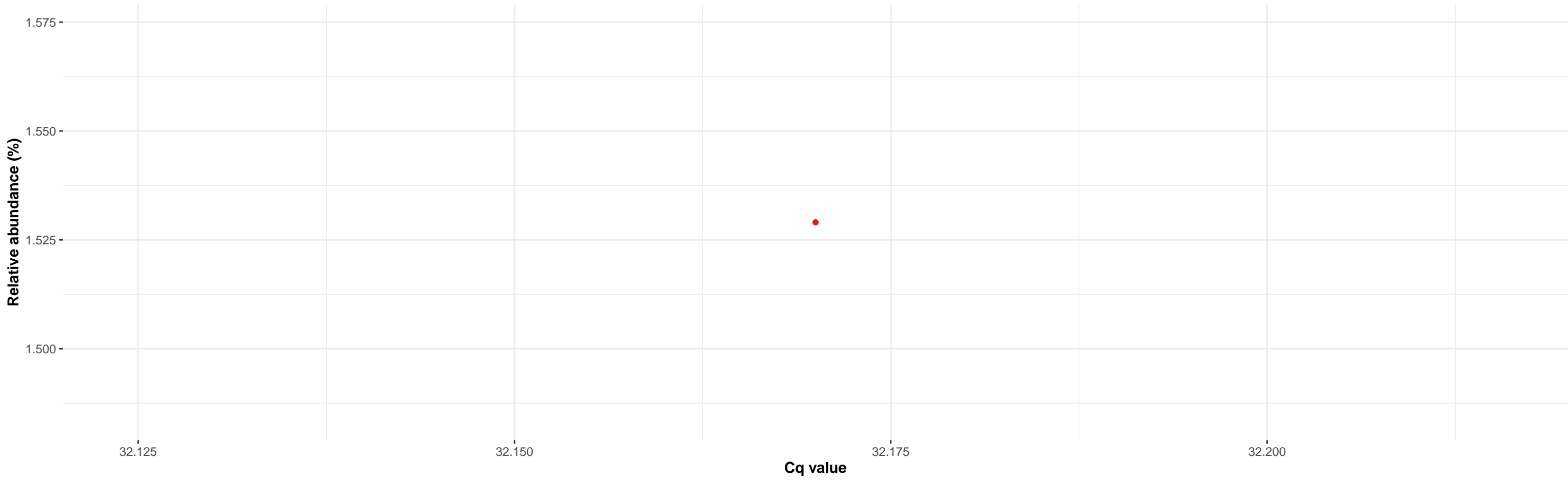


Correlation within: REF-DIM

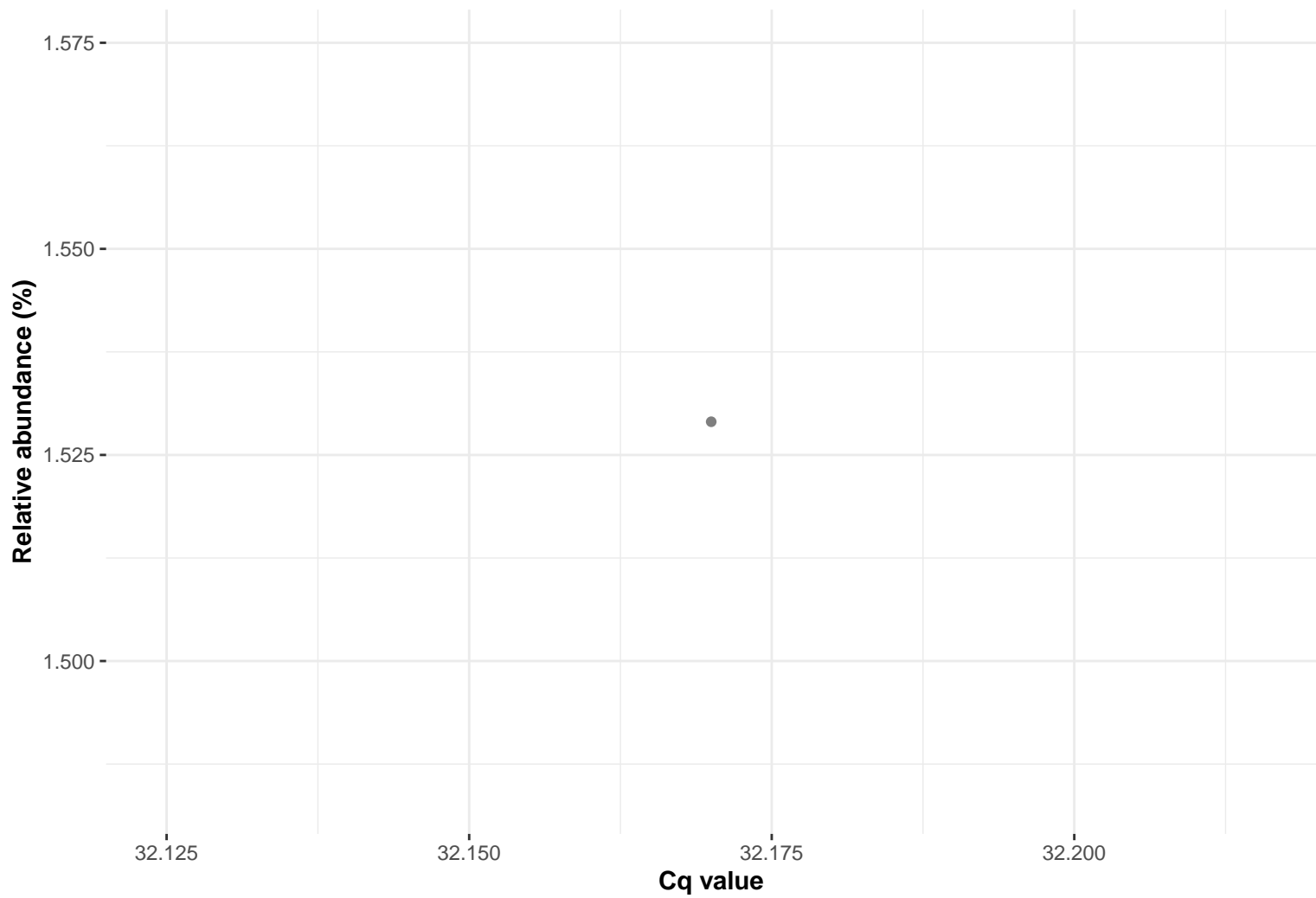


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingomonas; NA

Correlation with all samples



Correlation within: REF-DIM

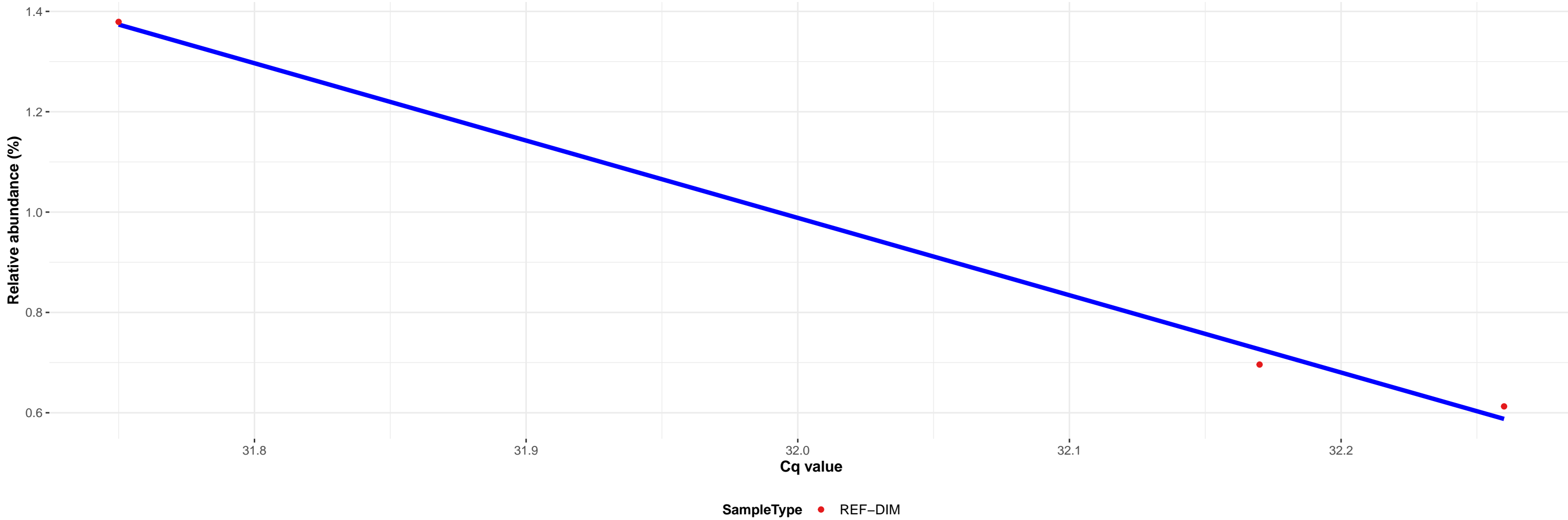


Correlation within: PCR-blank

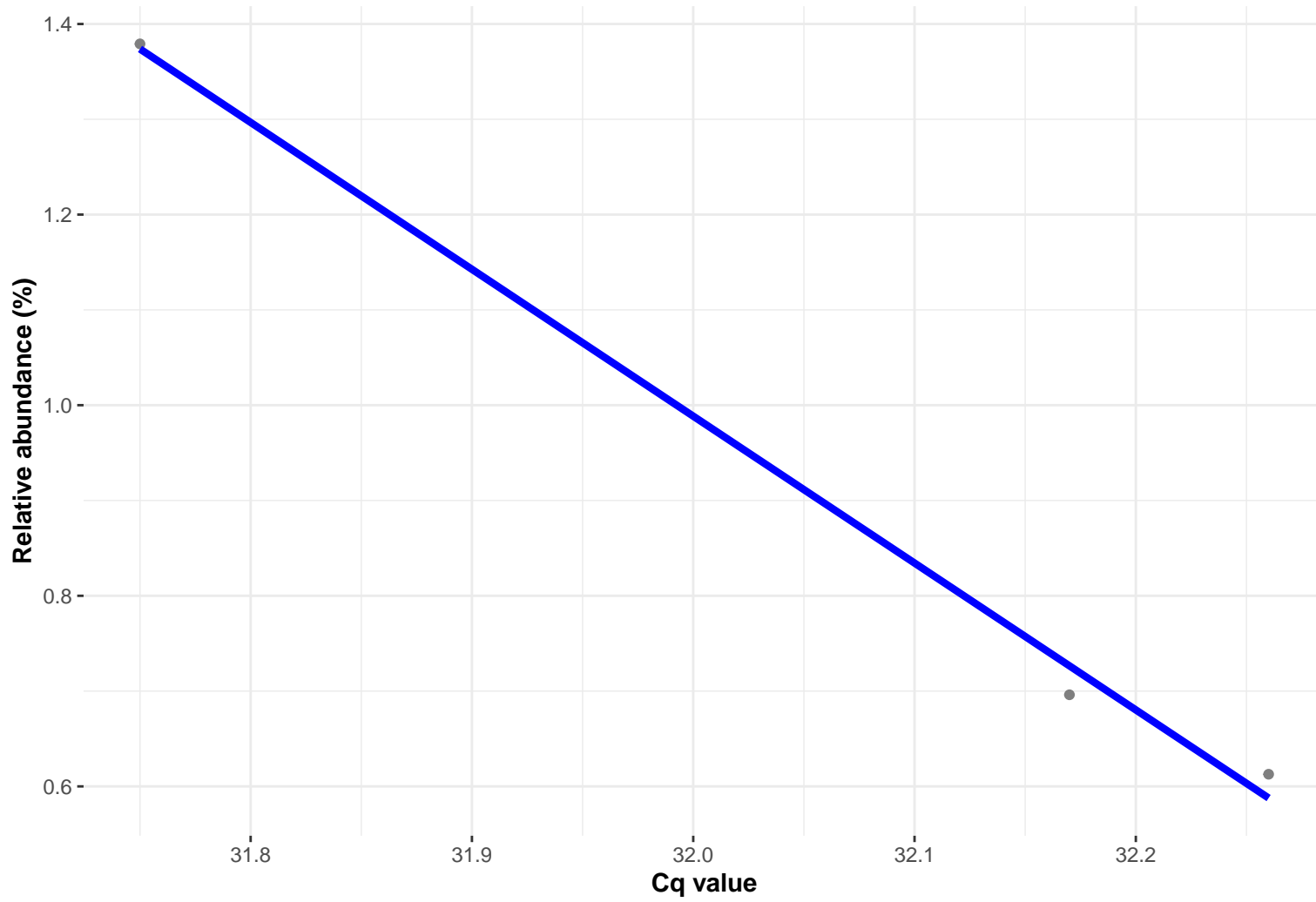


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Kurthia; s\_\_uncultured bacterium

Correlation with all samples



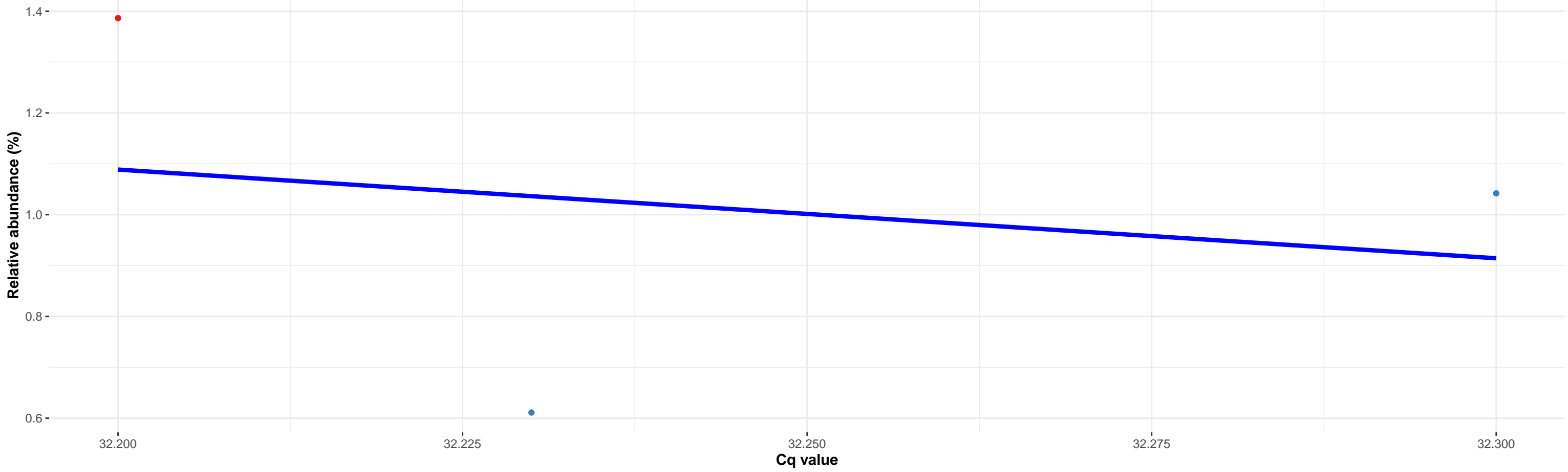
Correlation within: REF-DIM



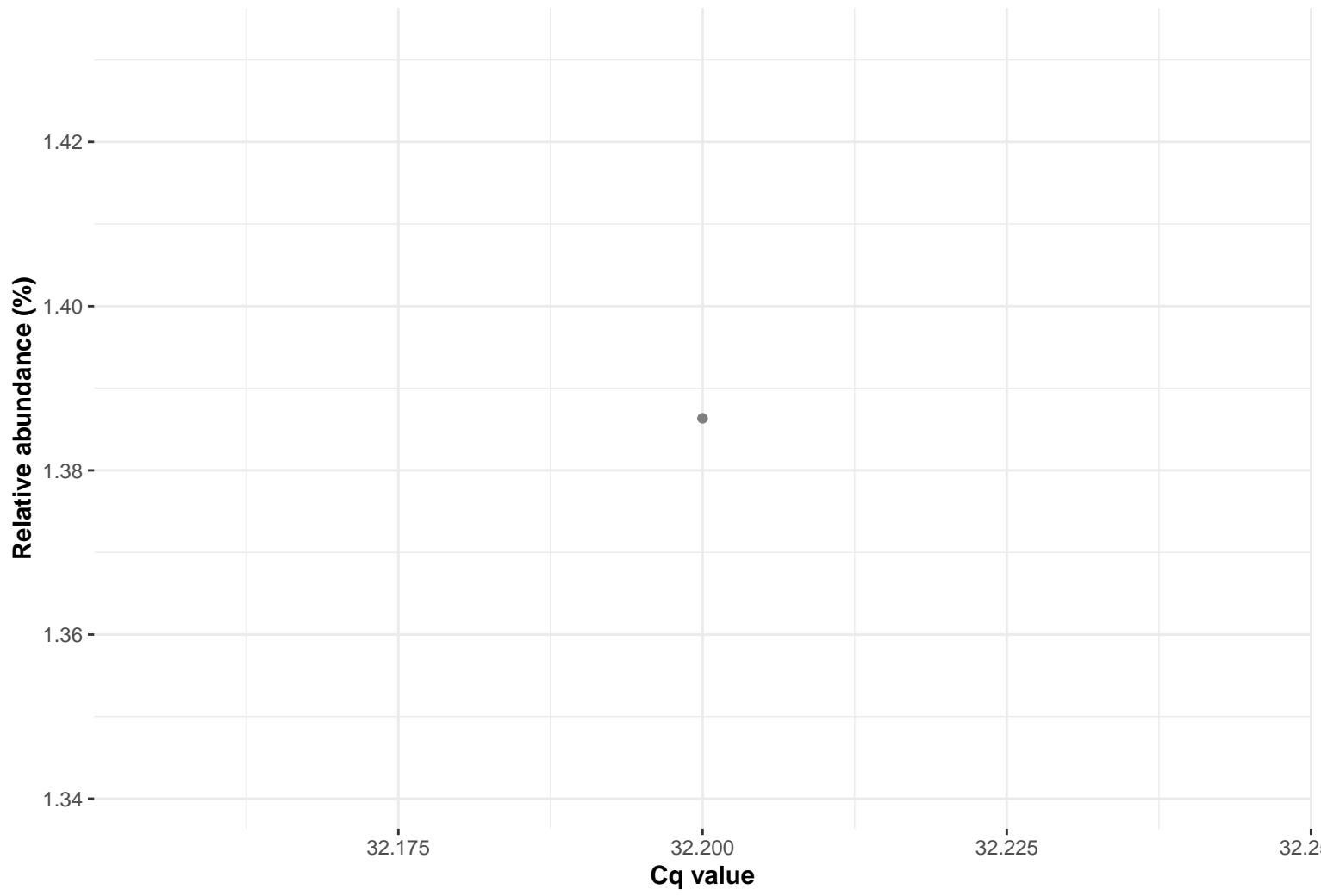


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus; Ambiguous\_taxa

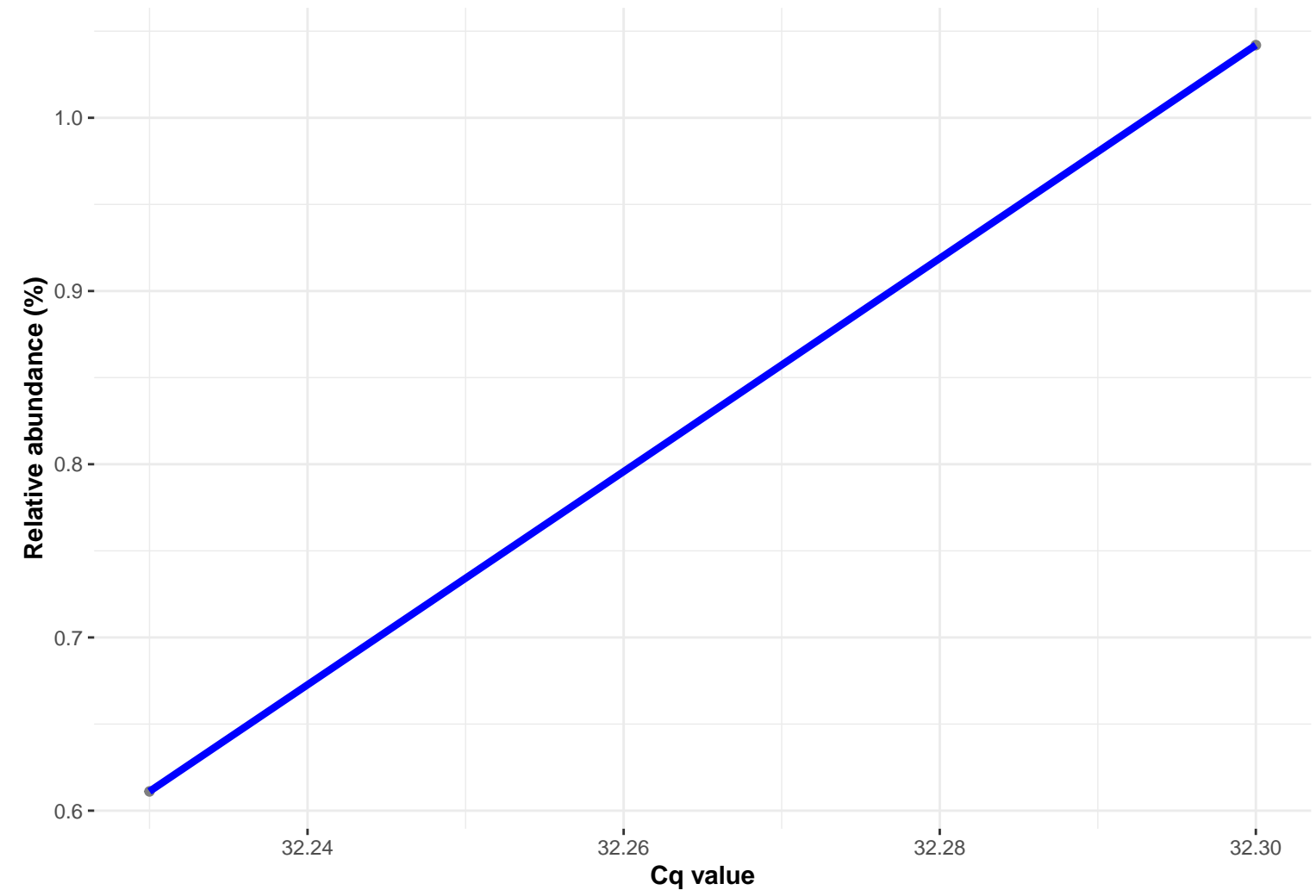
Correlation with all samples



Correlation within: REF-PIM

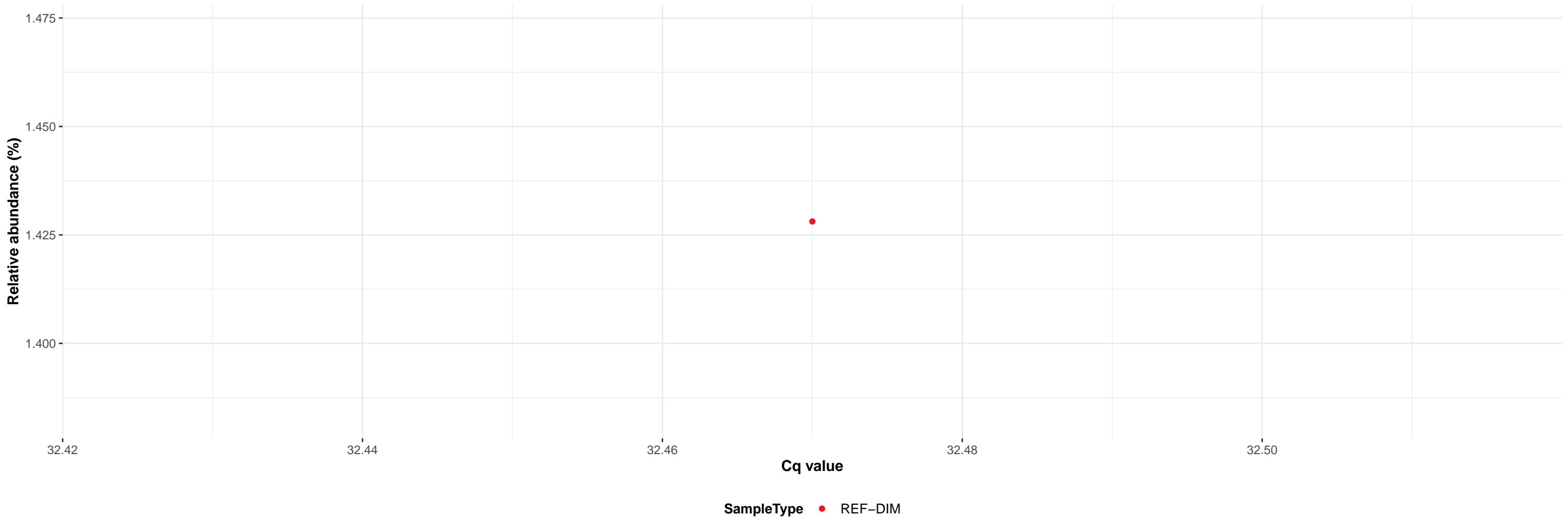


Correlation within: REF-DIM

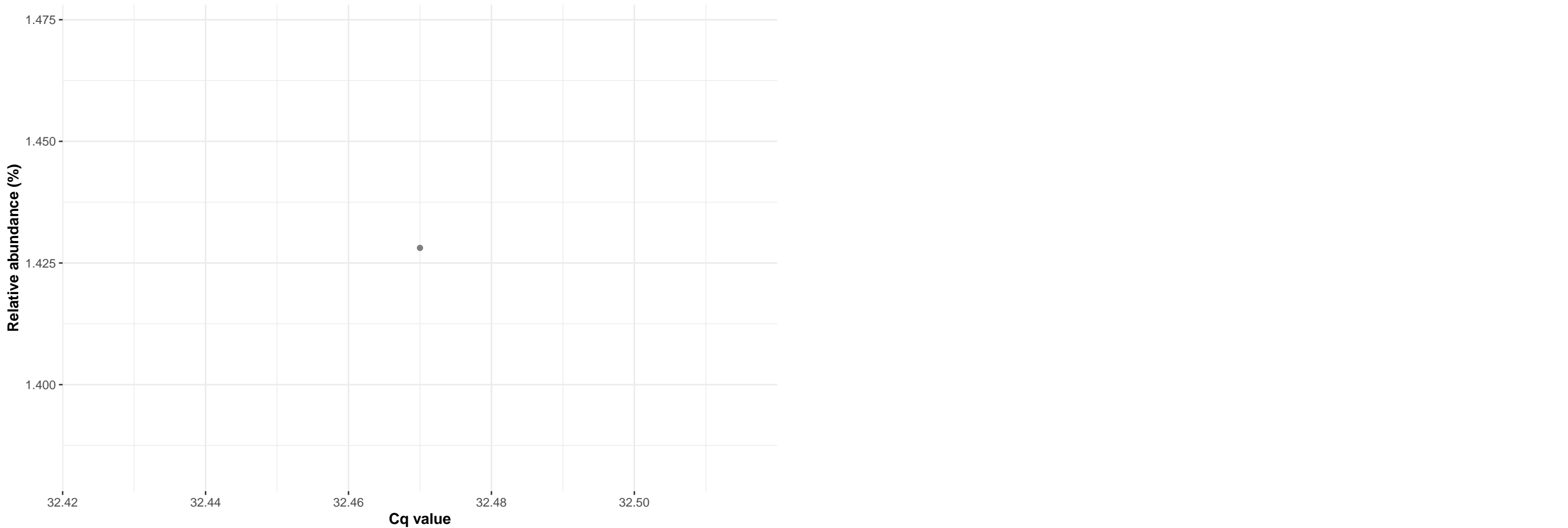


k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

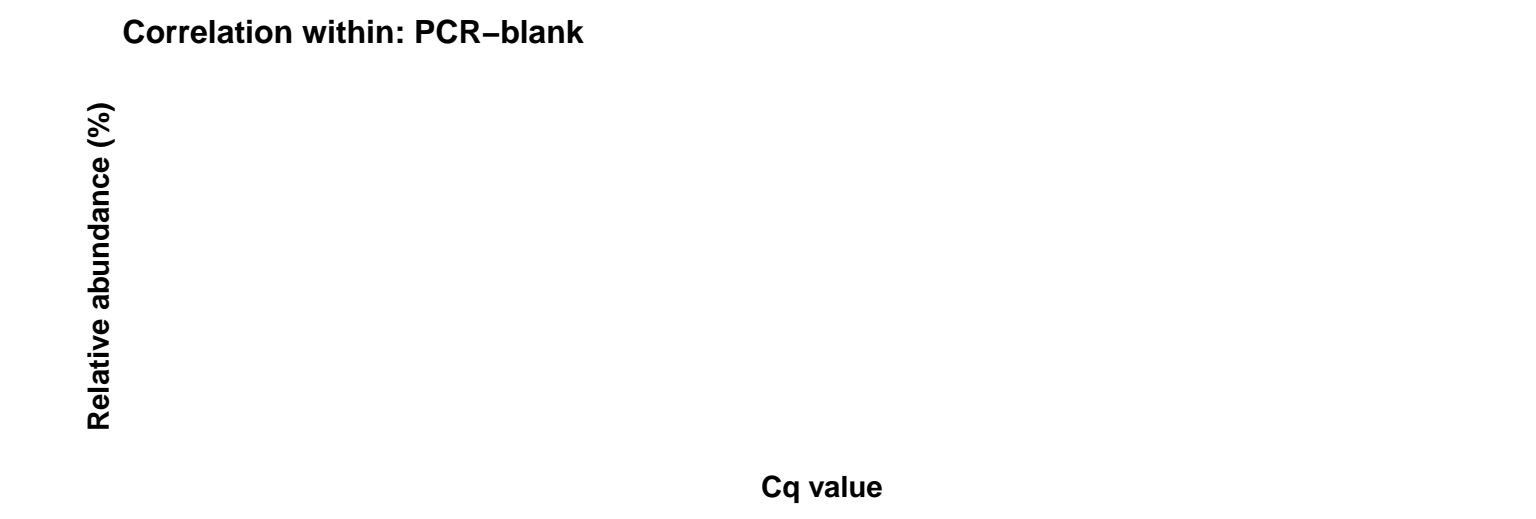
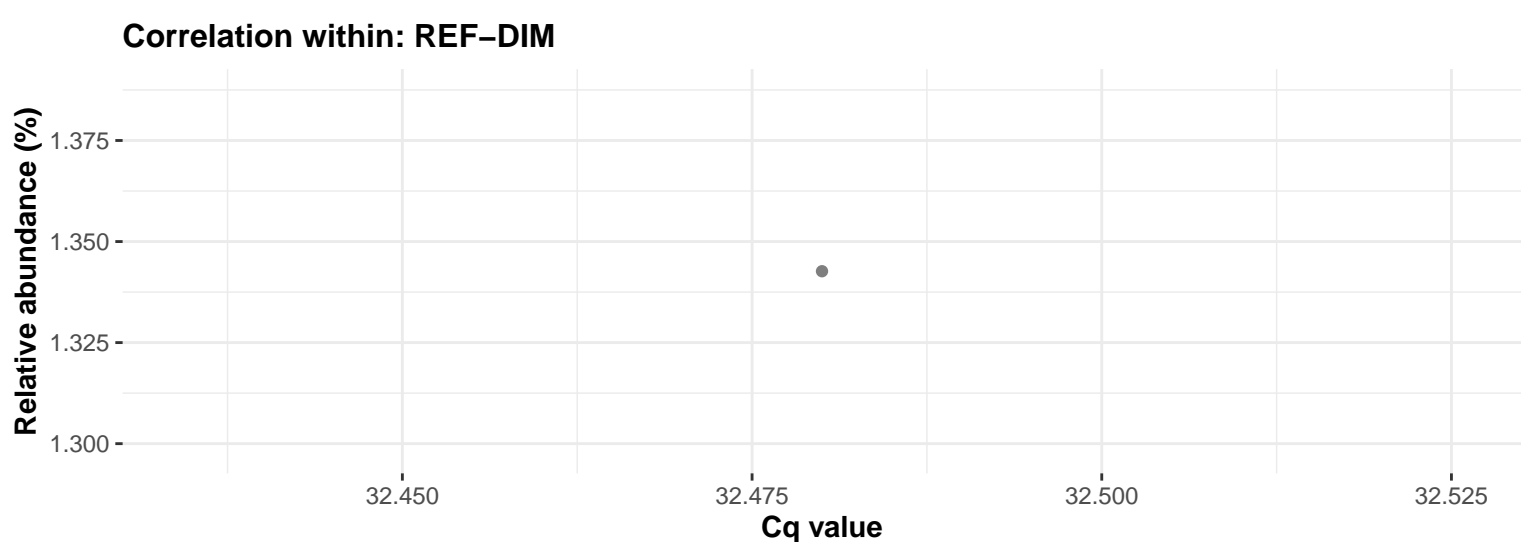
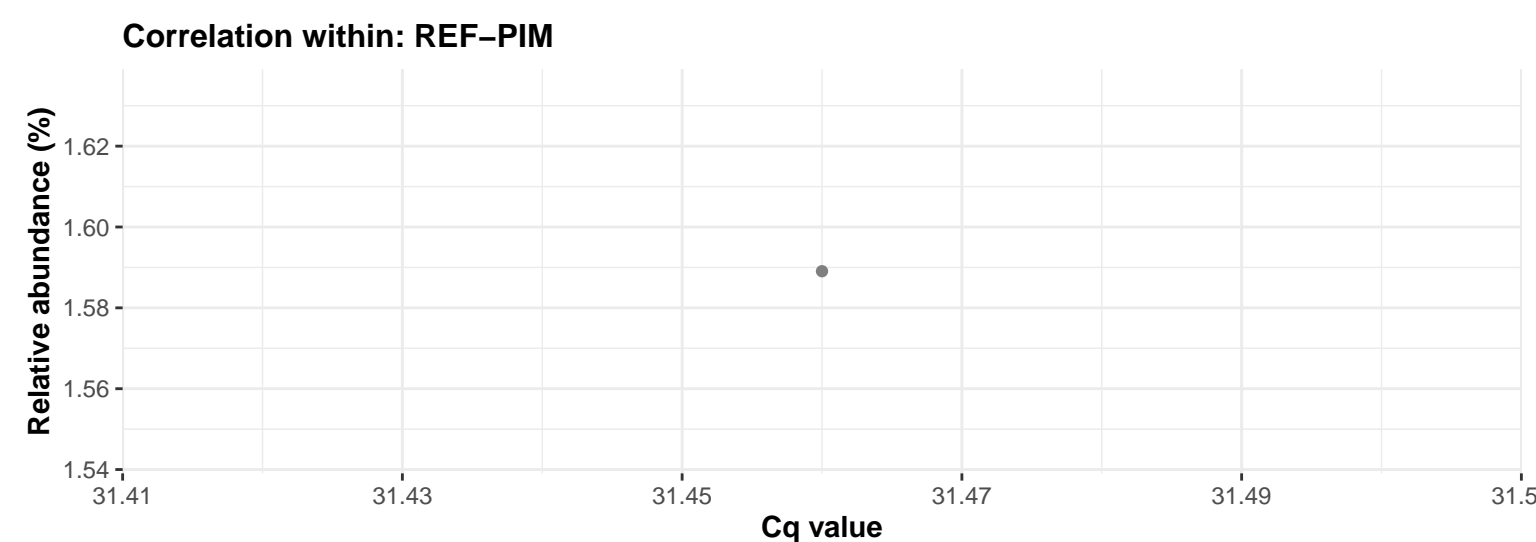
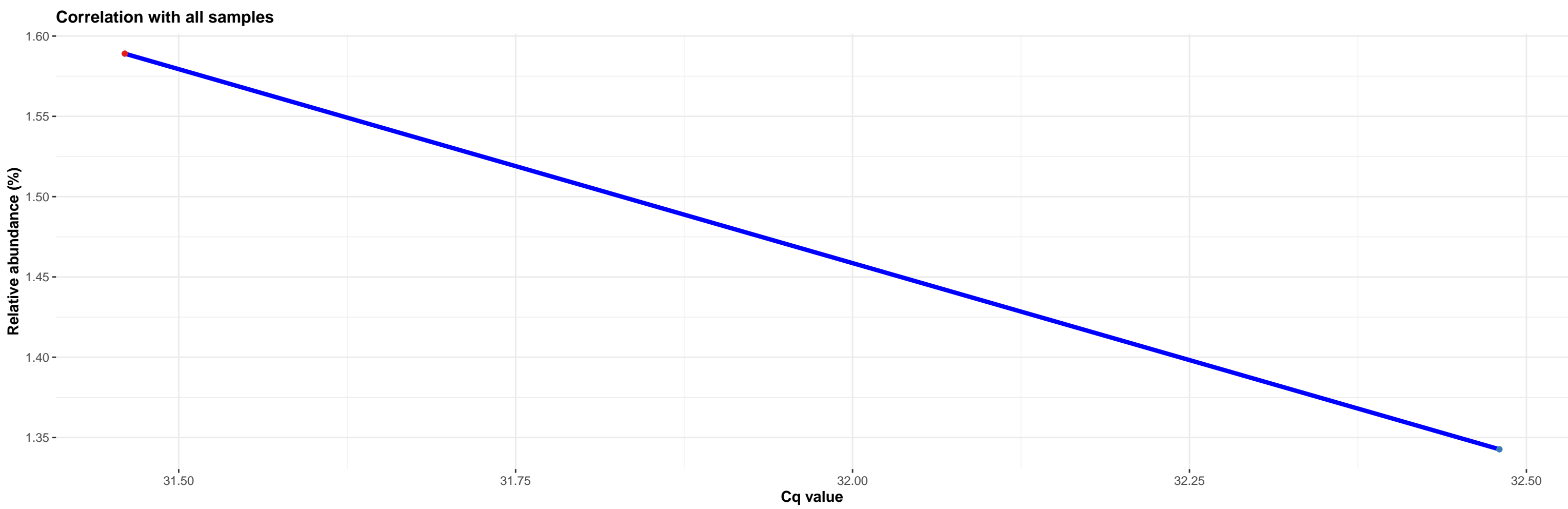
Correlation with all samples

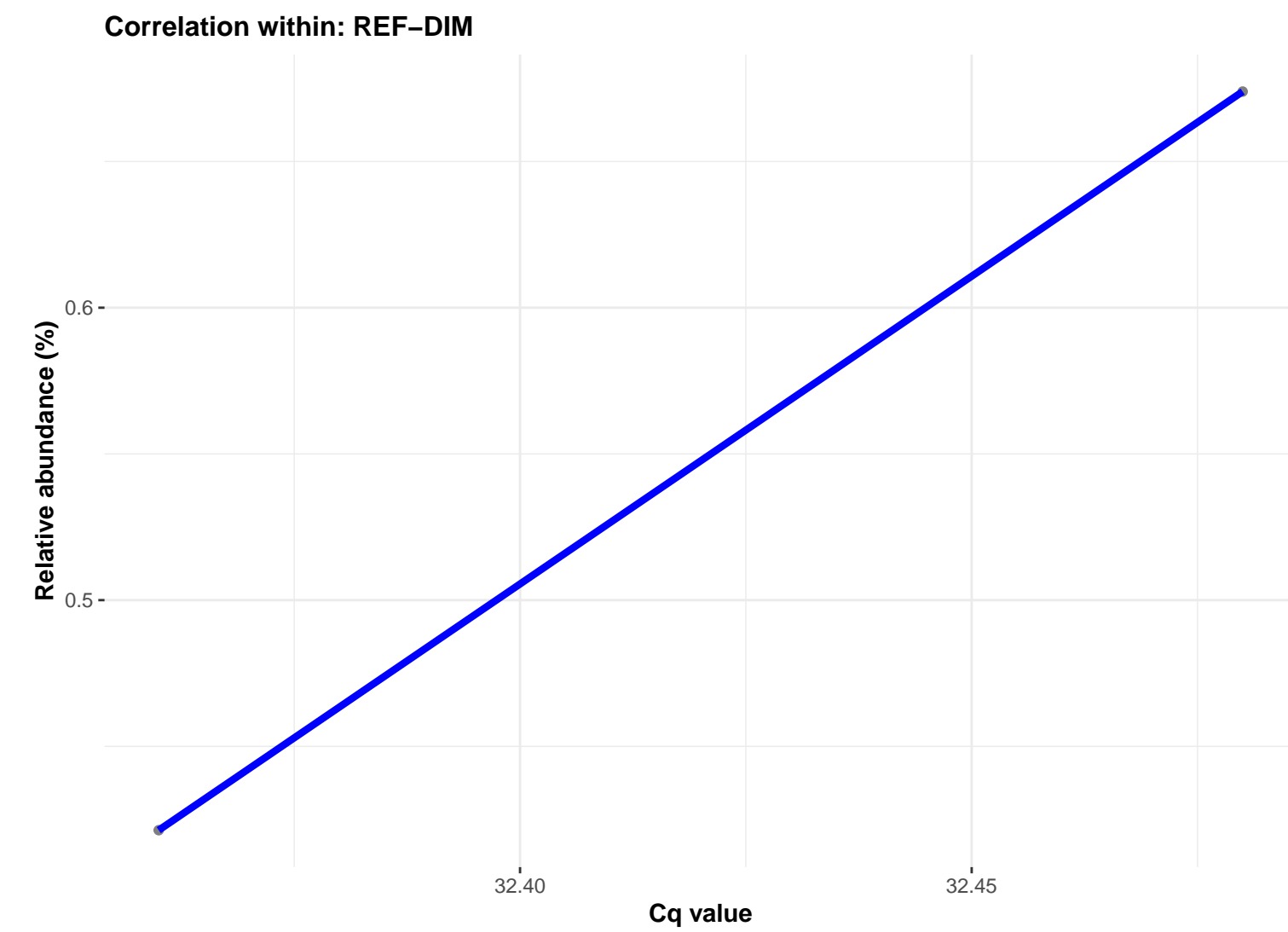
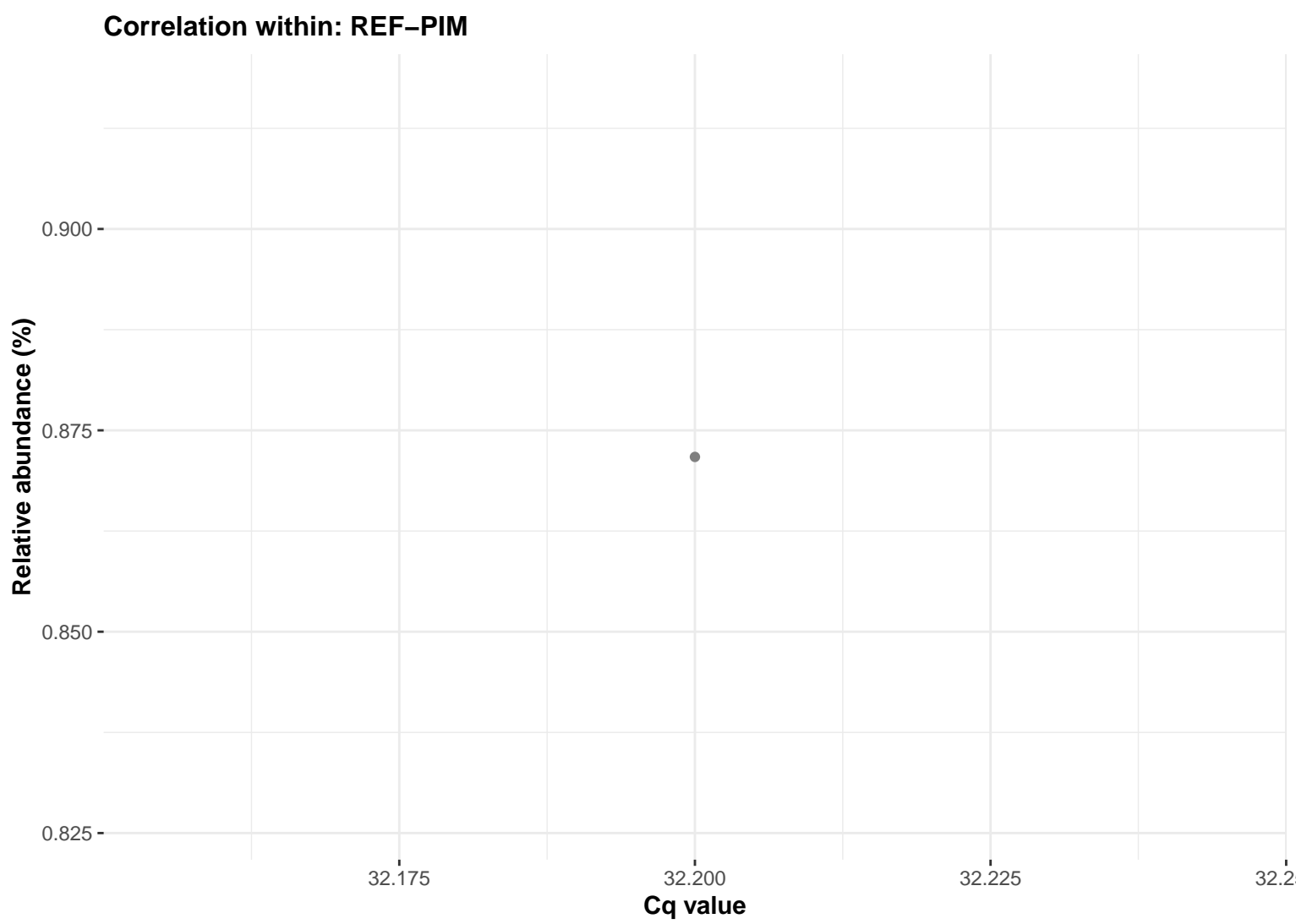
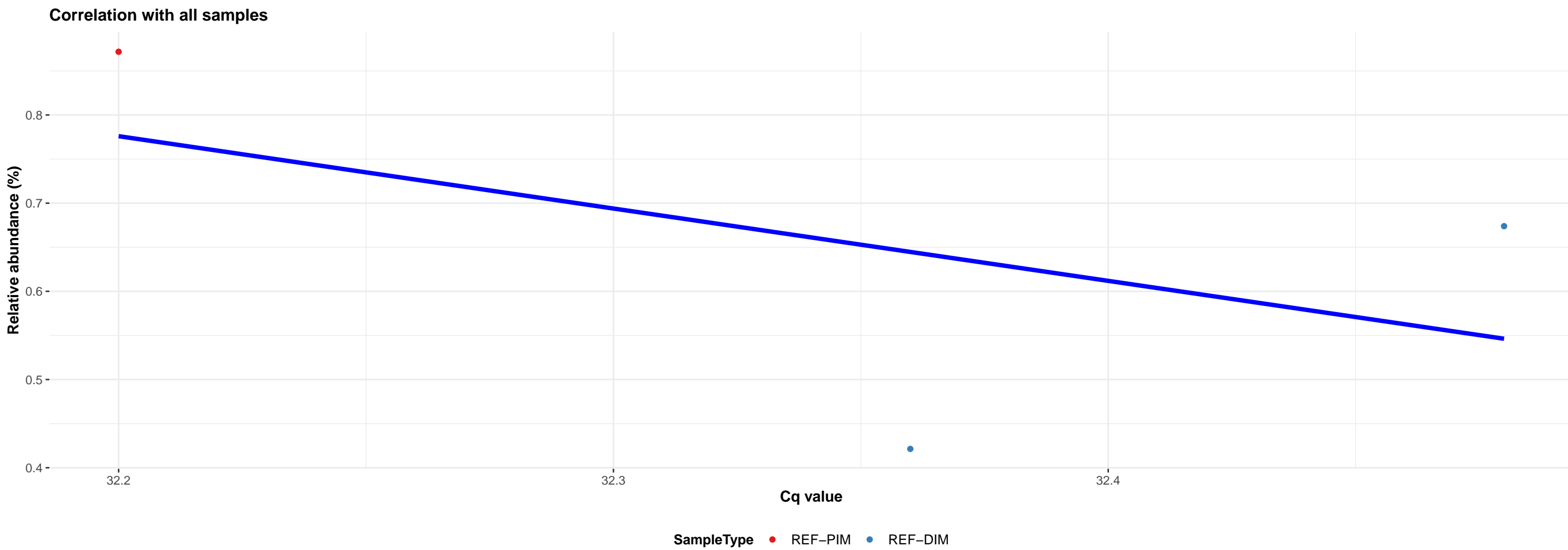


Correlation within: REF-DIM



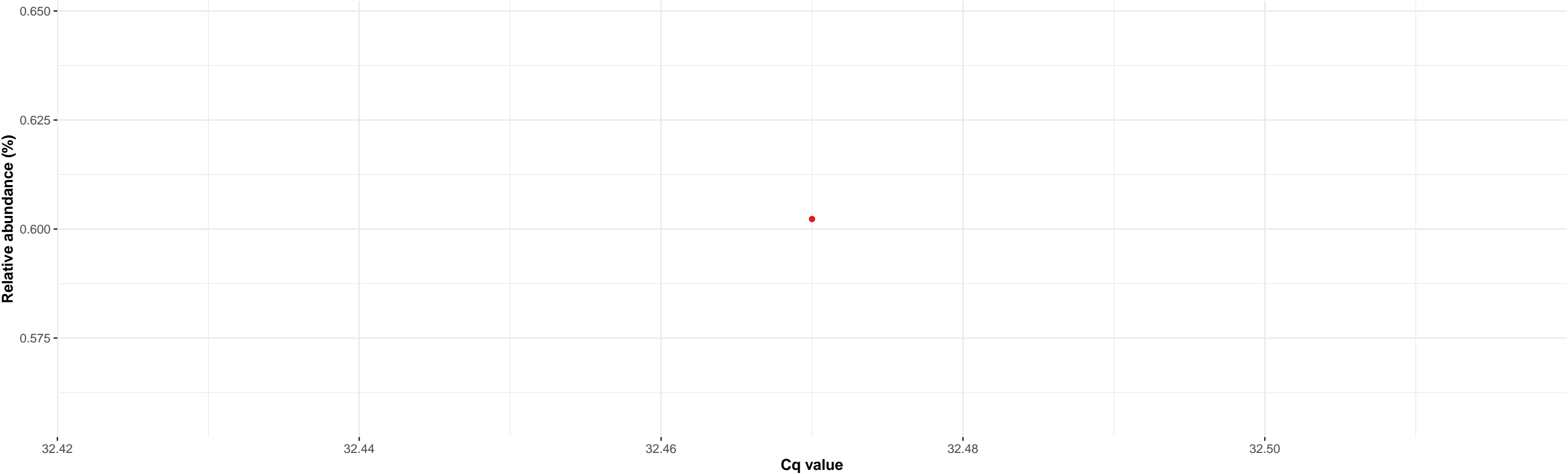
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; NA





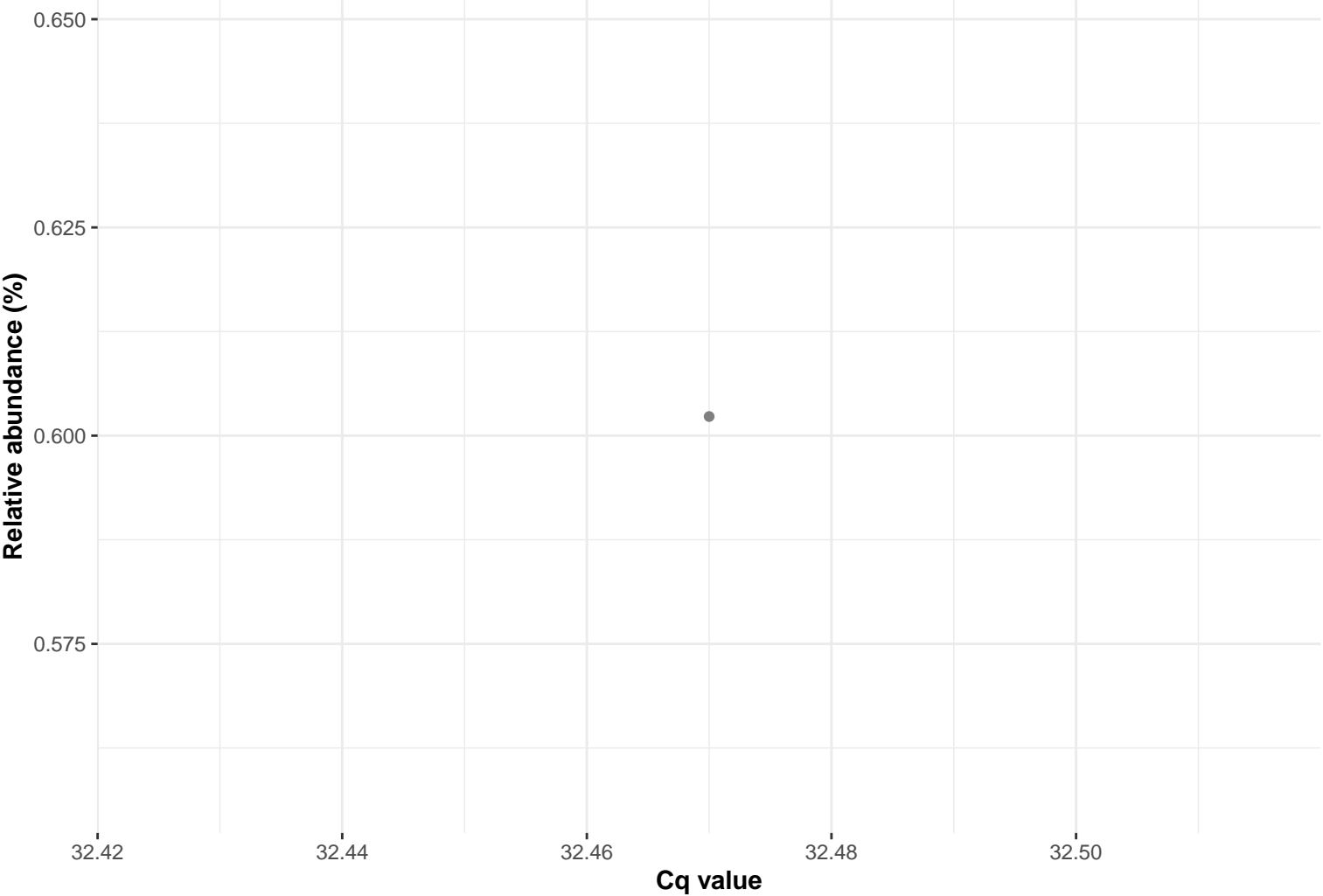
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Lactococcus; NA

Correlation with all samples



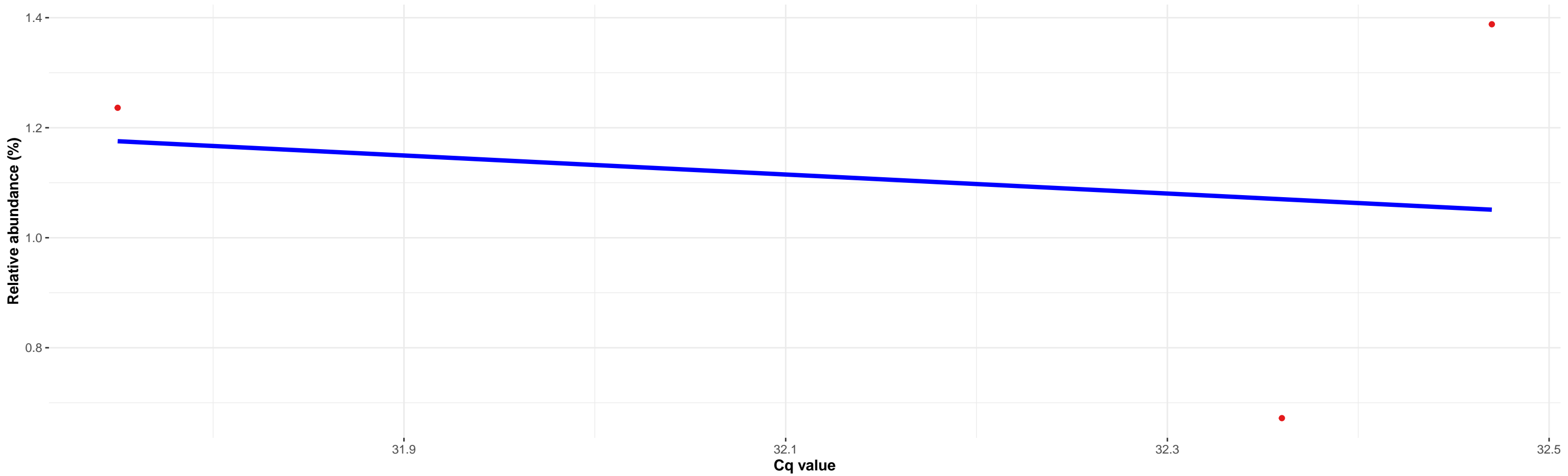
SampleType • REF-DIM

Correlation within: REF-DIM

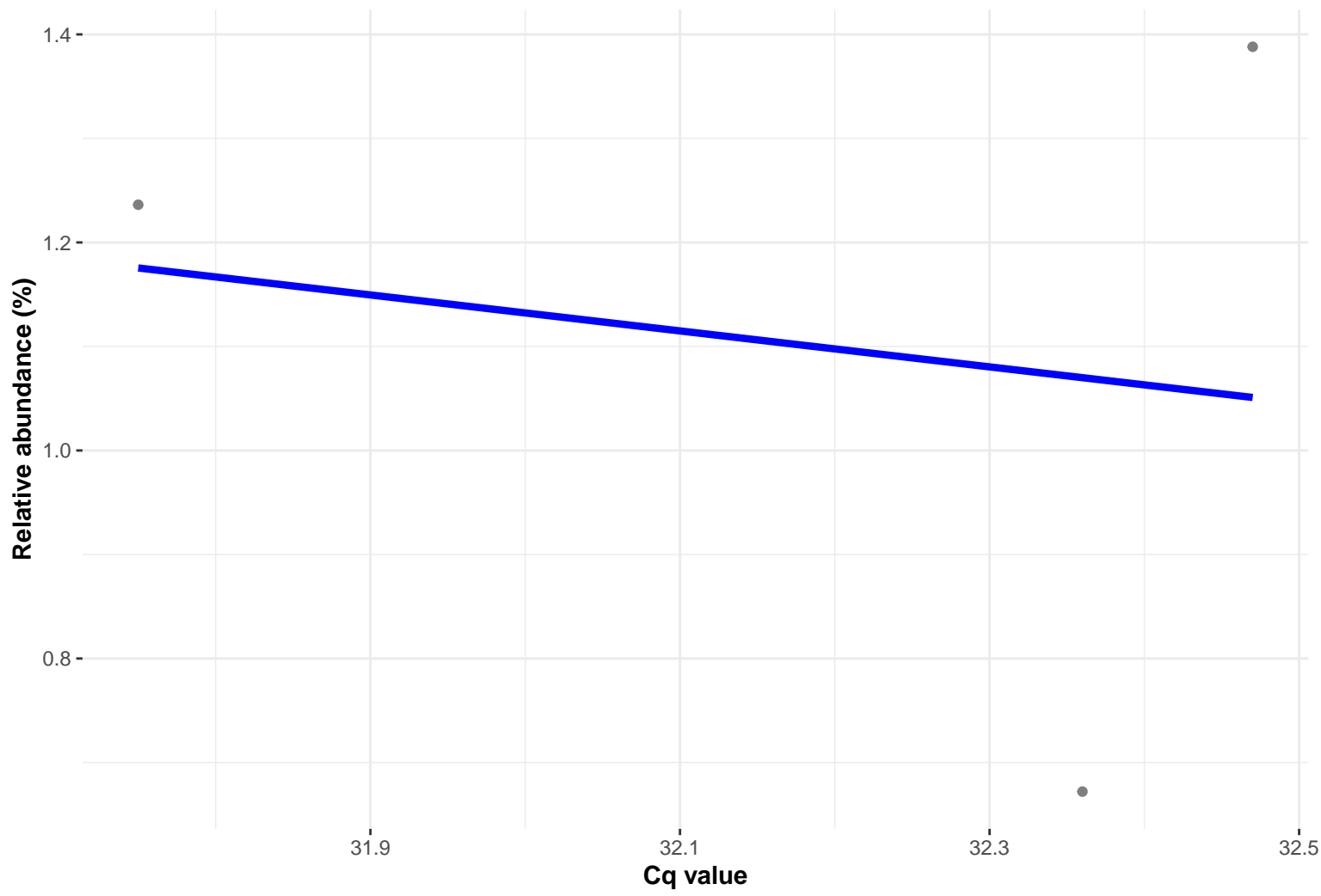


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; s\_\_uncultured Virgibacillus sp.

Correlation with all samples



Correlation within: REF-DIM



Correlation within: PCR-blank

