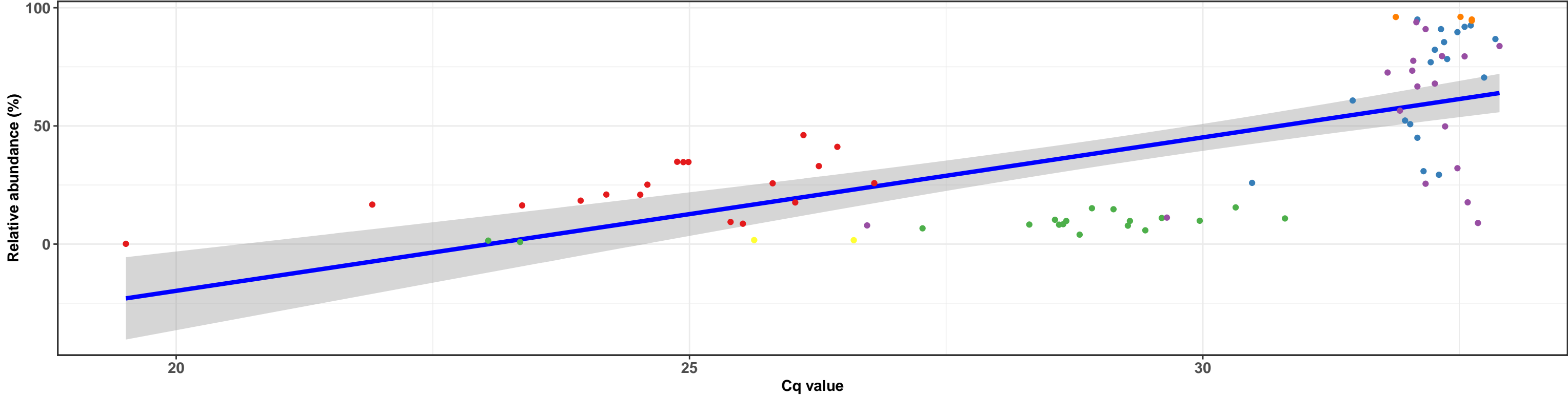


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

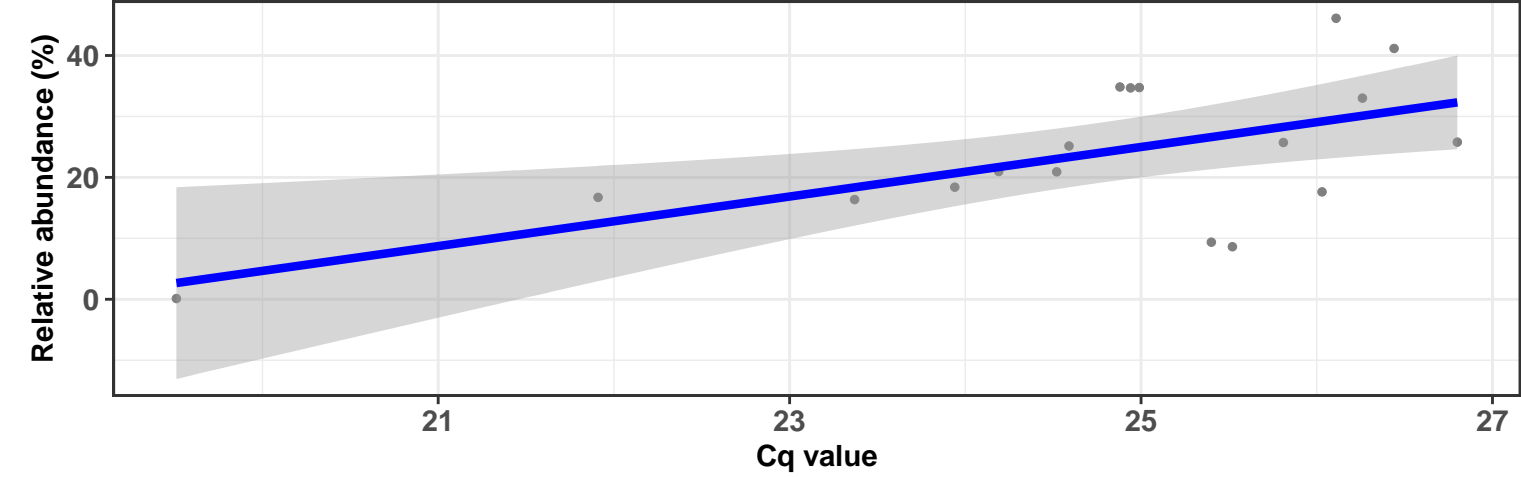
$\log_e(S) = 10.174$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.668$, $CI_{95\%} [0.536, 0.821]$, $n_{\text{pairs}} = 78$



SampleType ● REF-DID ● REF-DIM ● IM-DID ● IM-DIM ● Extraction-blank ● Mock

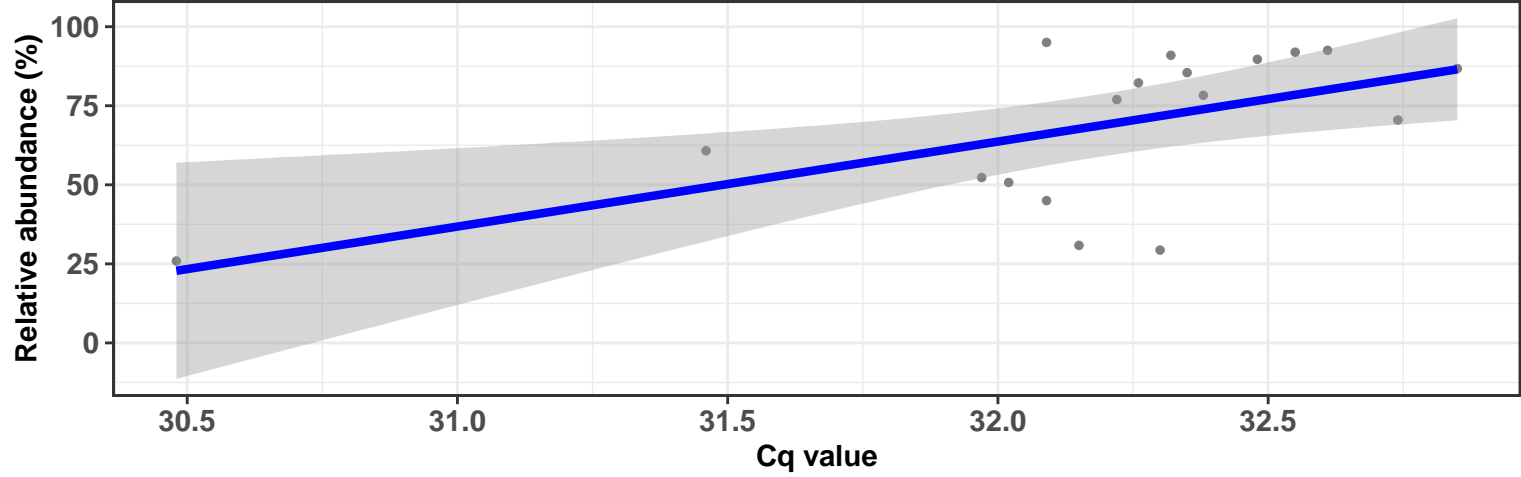
Correlation within: REF-DID

$\log_e(S) = 6.105$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = 0.538$, $CI_{95\%} [0.185, 0.936]$, $n_{\text{pairs}} = 18$



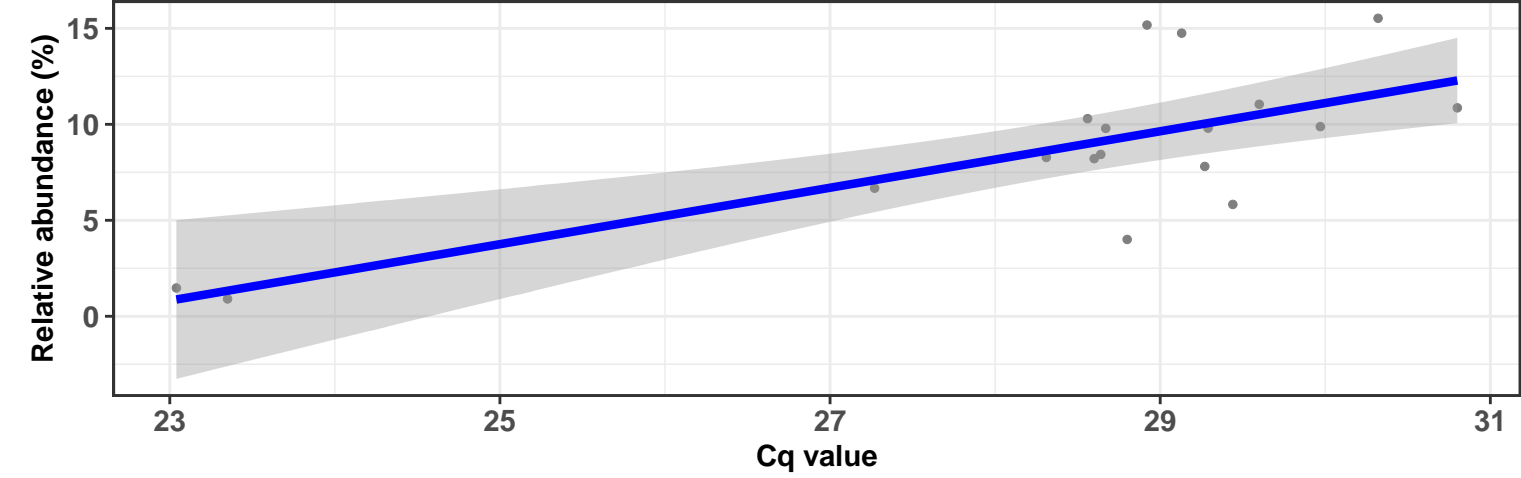
Correlation within: REF-DIM

$\log_e(S) = 6.020$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = 0.575$, $CI_{95\%} [0.232, 0.940]$, $n_{\text{pairs}} = 18$



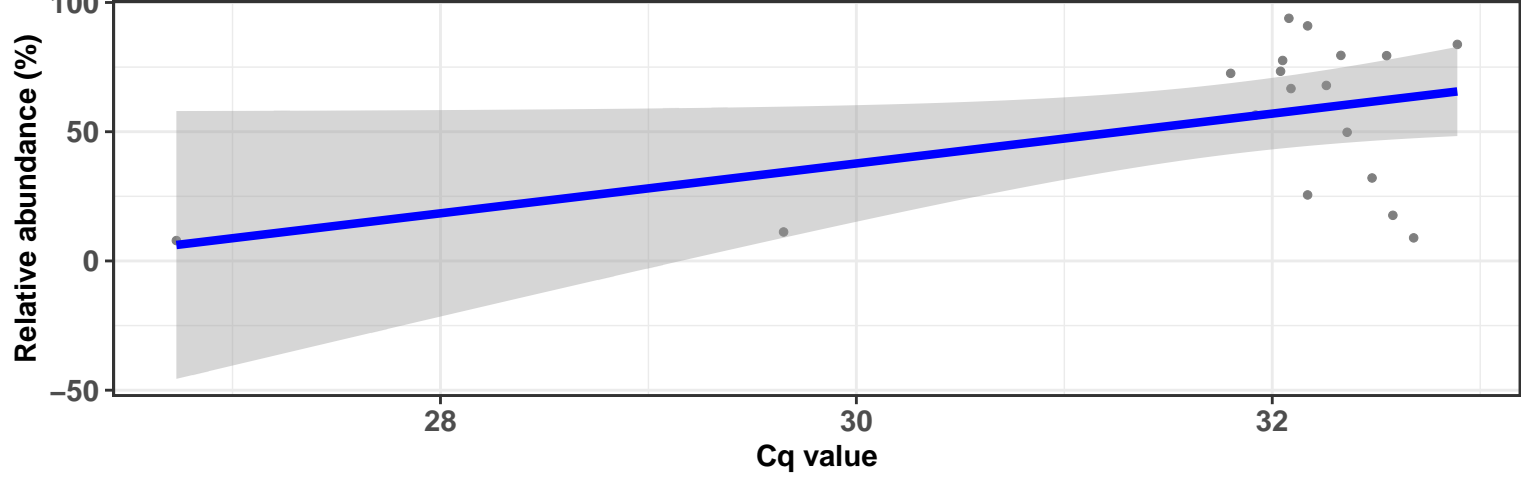
Correlation within: IM-DID

$\log_e(S) = 5.935$, $p = 0.007$, $\hat{\rho}_{\text{Spearman}} = 0.610$, $CI_{95\%} [0.252, 0.987]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

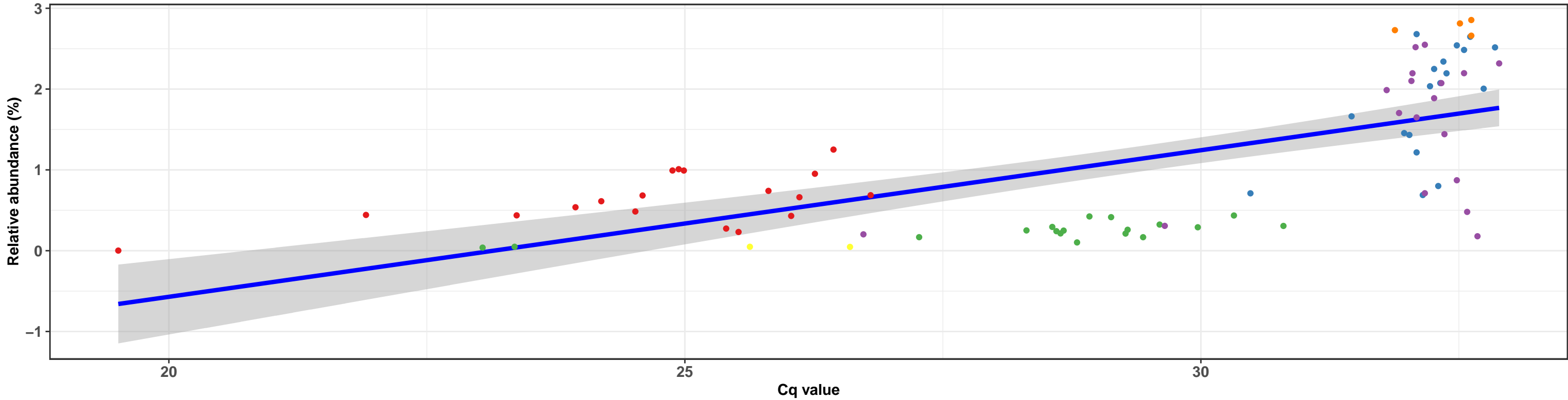
$\log_e(S) = 6.759$, $p = 0.663$, $\hat{\rho}_{\text{Spearman}} = 0.110$, $CI_{95\%} [-0.434, 0.694]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

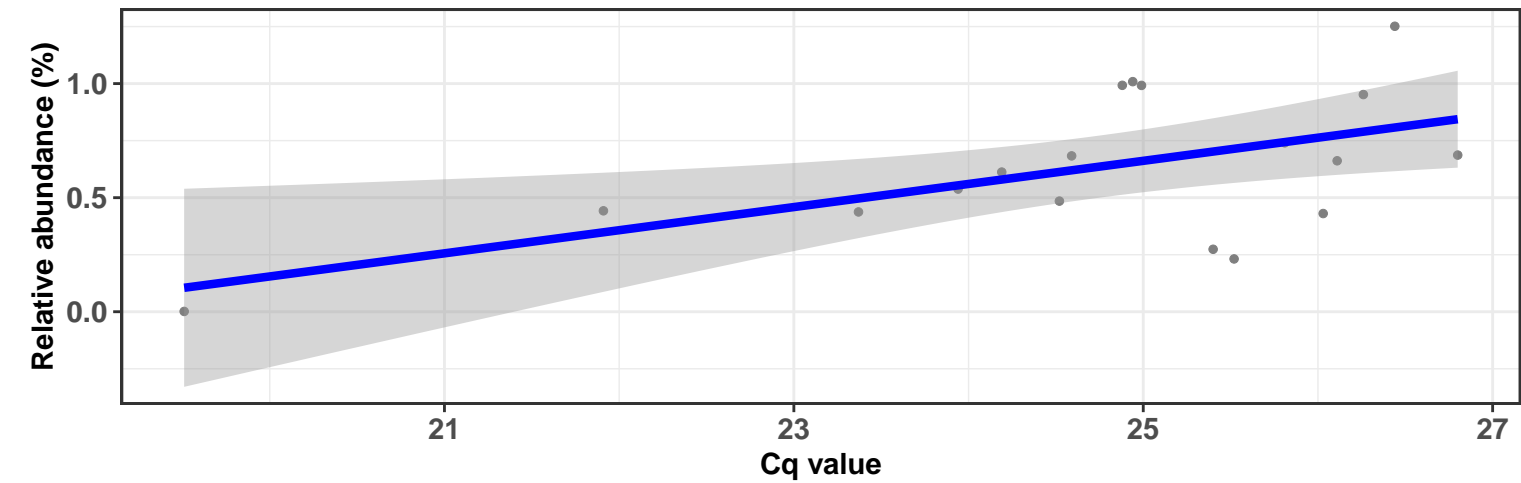
Correlation with all samples

$\log_e(S) = 10.184$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.665$, $\text{CI}_{95\%} [0.514, 0.848]$, $n_{\text{pairs}} = 78$



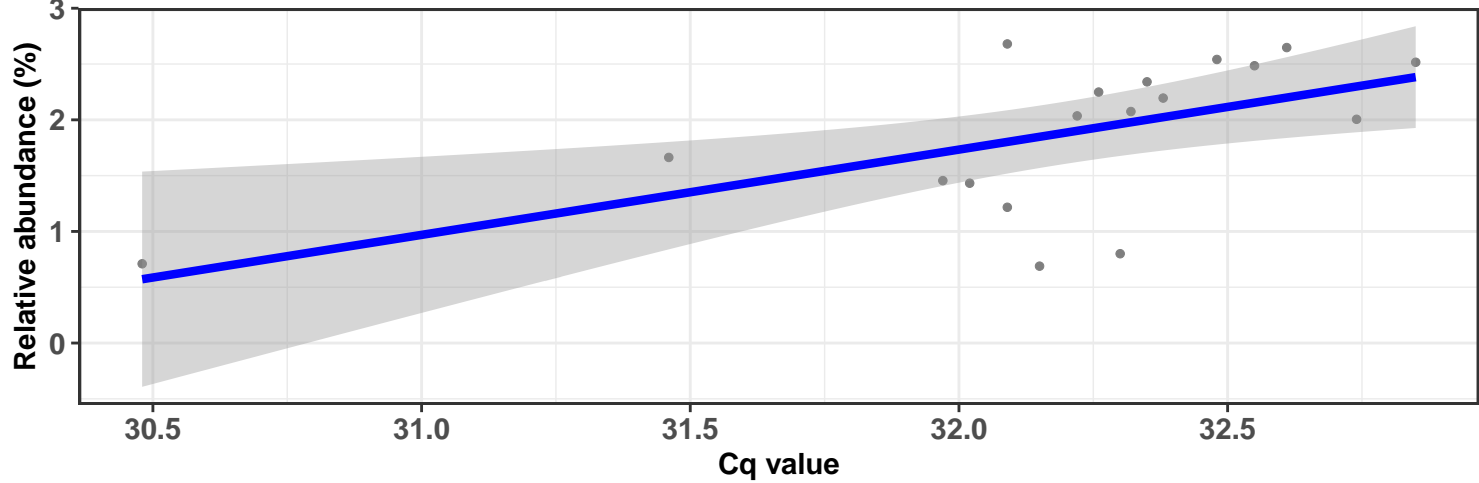
Correlation within: REF-DID

$\log_e(S) = 6.314$, $p = 0.075$, $\hat{\rho}_{\text{Spearman}} = 0.430$, $\text{CI}_{95\%} [0.054, 0.844]$, $n_{\text{pairs}} = 18$



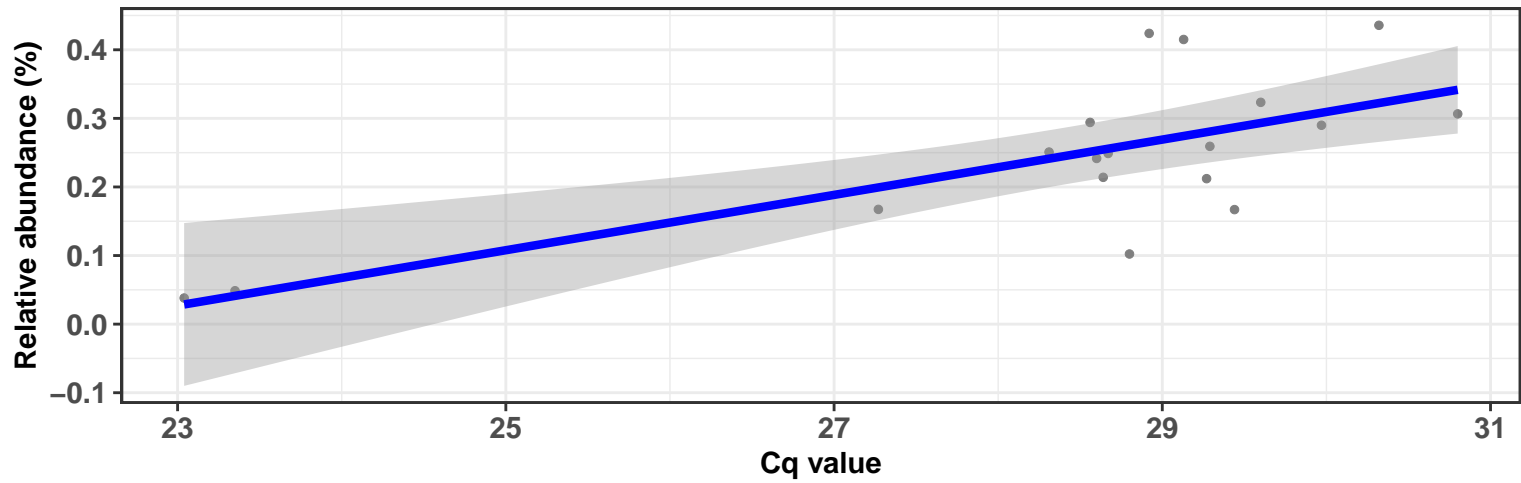
Correlation within: REF-DIM

$\log_e(S) = 5.971$, $p = 0.009$, $\hat{\rho}_{\text{Spearman}} = 0.596$, $\text{CI}_{95\%} [0.241, 0.972]$, $n_{\text{pairs}} = 18$



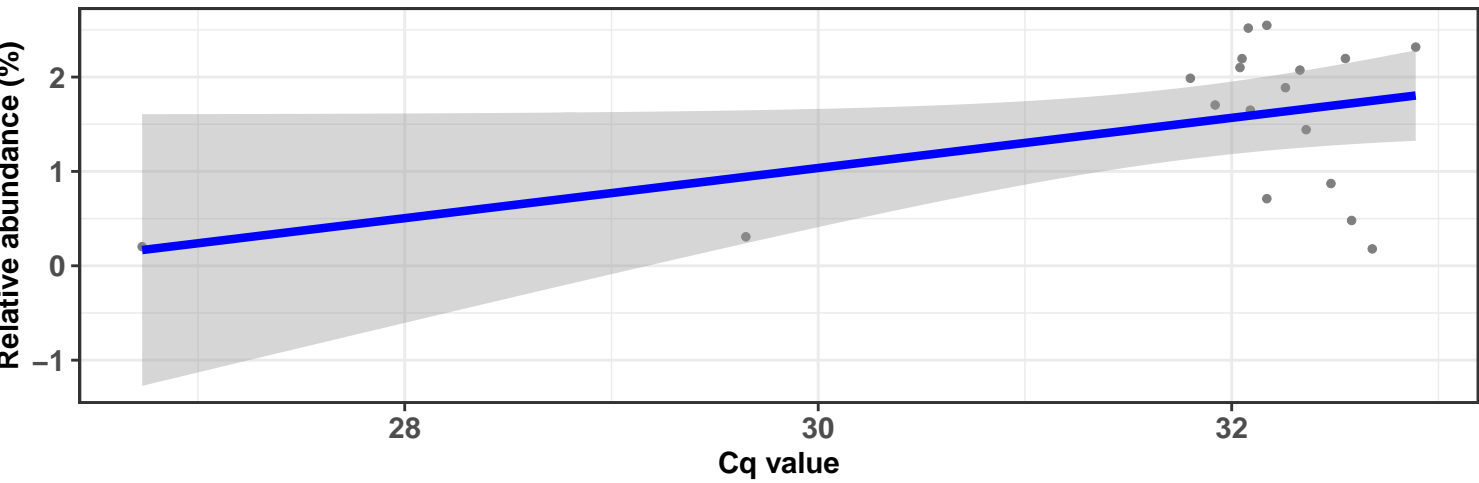
Correlation within: IM-DID

$\log_e(S) = 5.971$, $p = 0.009$, $\hat{\rho}_{\text{Spearman}} = 0.595$, $\text{CI}_{95\%} [0.268, 0.920]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

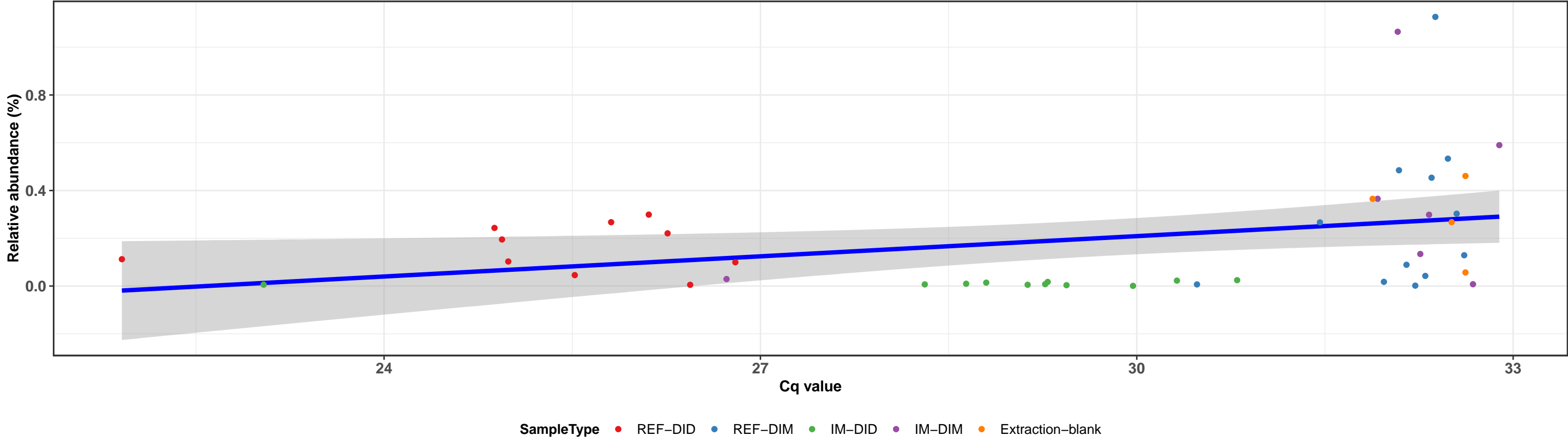
$\log_e(S) = 6.821$, $p = 0.832$, $\hat{\rho}_{\text{Spearman}} = 0.054$, $\text{CI}_{95\%} [-0.522, 0.657]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

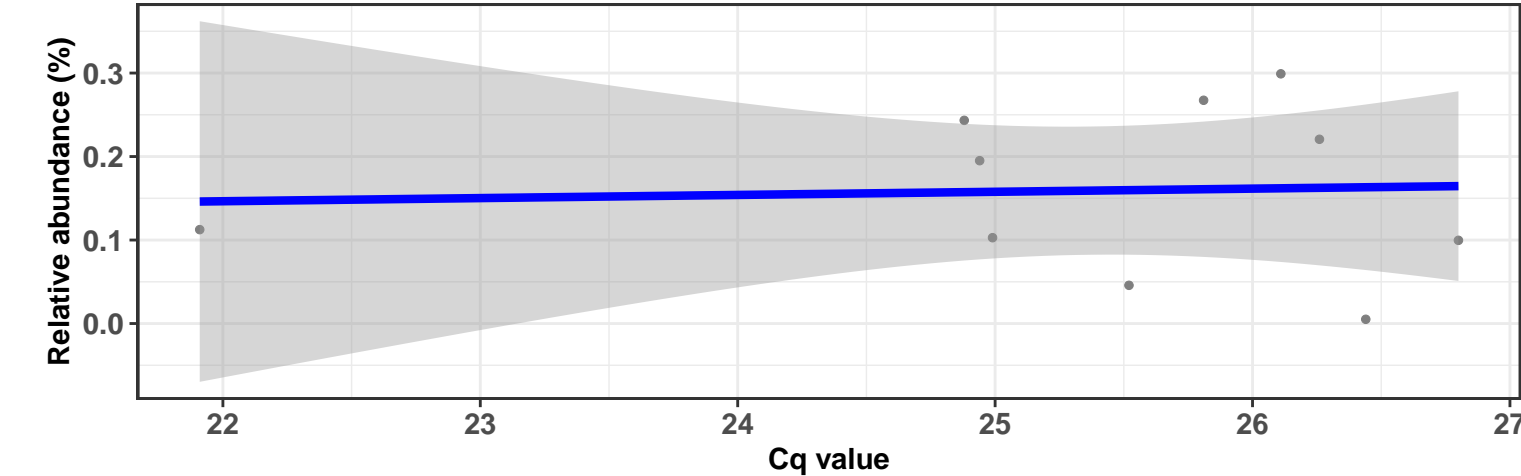
Correlation with all samples

$\log_e(S) = 9.123$, $p = 0.018$, $\hat{\rho}_{\text{Spearman}} = 0.354$, $\text{CI}_{95\%} [0.065, 0.646]$, $n_{\text{pairs}} = 44$



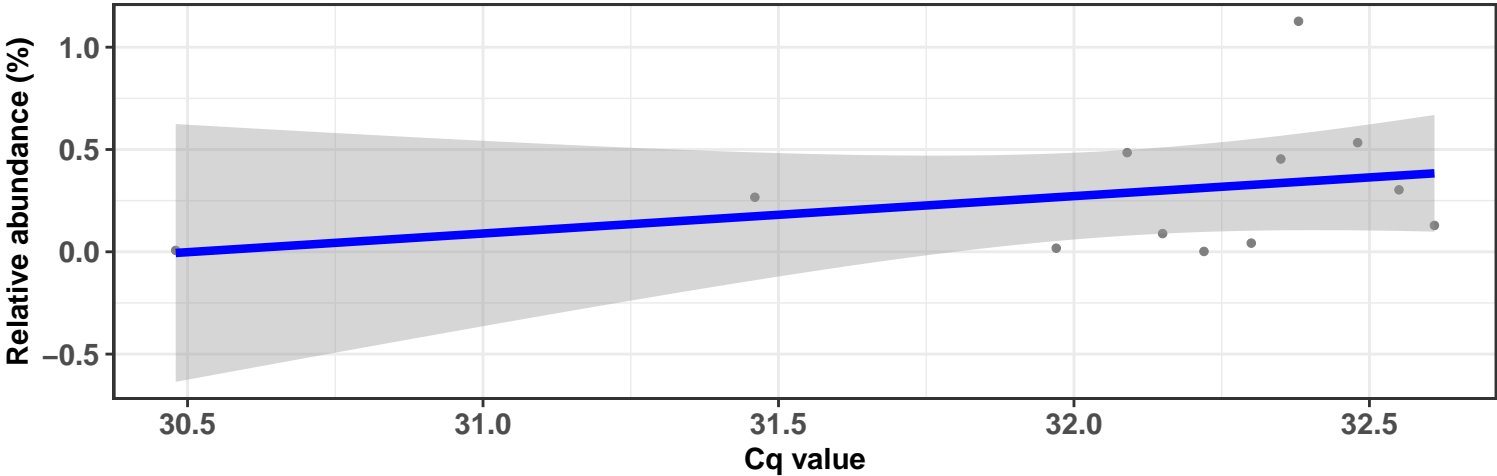
Correlation within: REF-DID

$\log_e(S) = 5.308$, $p = 0.533$, $\hat{\rho}_{\text{Spearman}} = -0.224$, $\text{CI}_{95\%} [-0.872, 0.455]$, $n_{\text{pairs}} = 10$



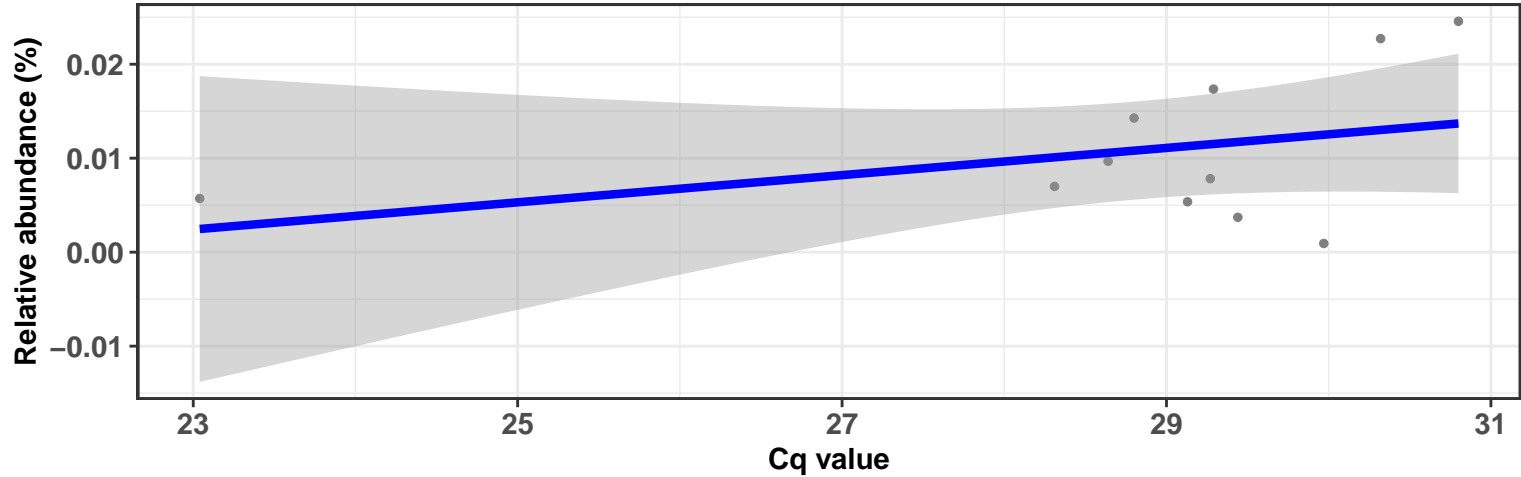
Correlation within: REF-DIM

$\log_e(S) = 5.024$, $p = 0.124$, $\hat{\rho}_{\text{Spearman}} = 0.469$, $\text{CI}_{95\%} [0.060, 0.955]$, $n_{\text{pairs}} = 12$



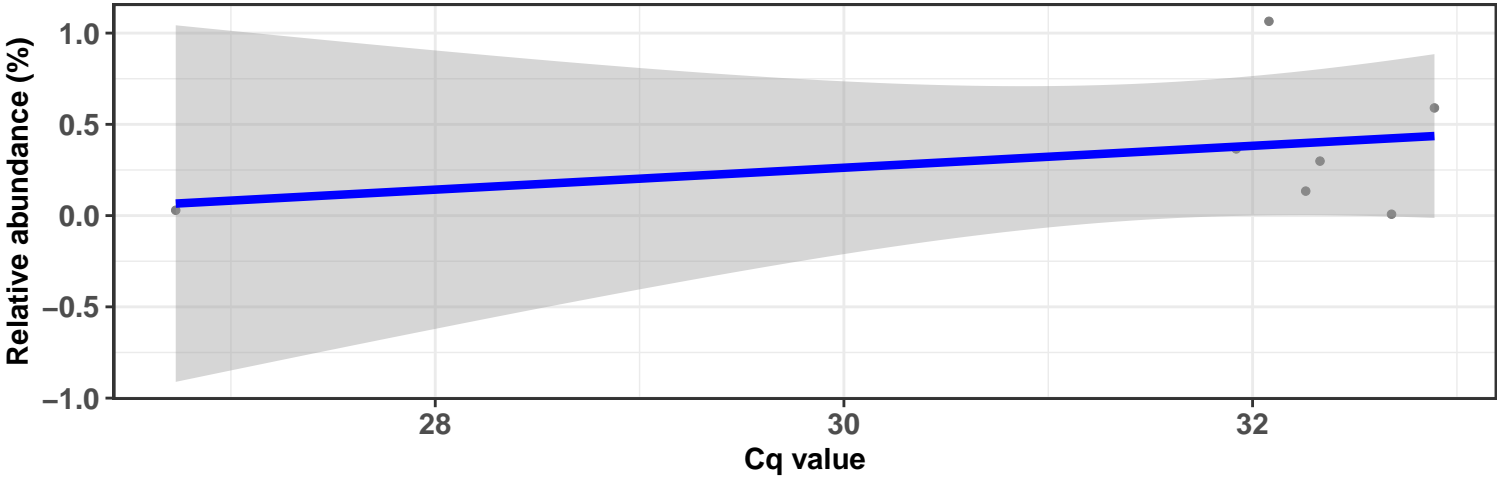
Correlation within: IM-DID

$\log_e(S) = 5.063$, $p = 0.401$, $\hat{\rho}_{\text{Spearman}} = 0.282$, $\text{CI}_{95\%} [-0.463, 1.011]$, $n_{\text{pairs}} = 11$



Correlation within: IM-DIM

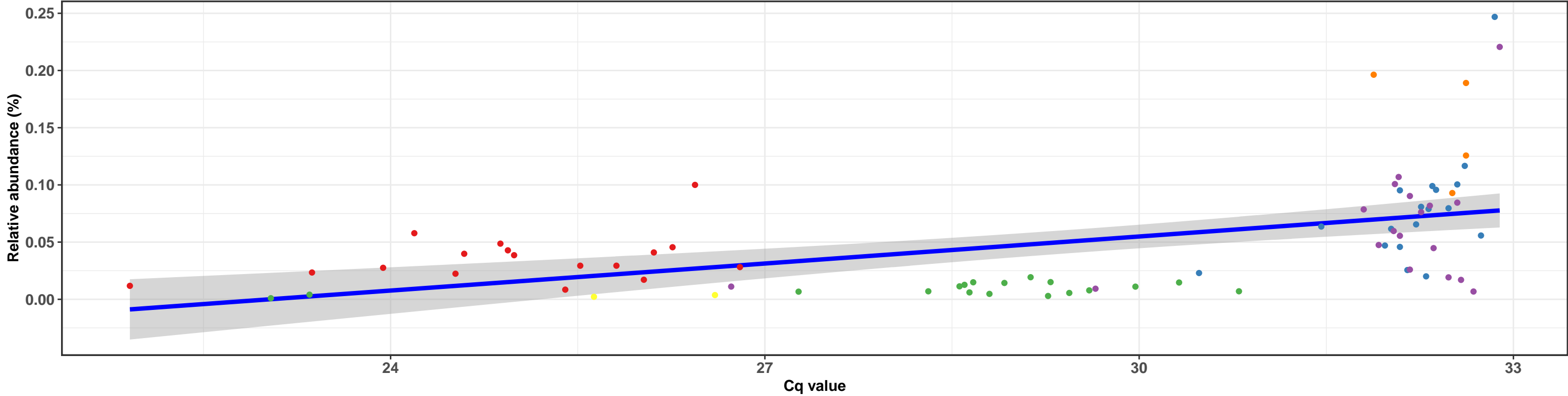
$\log_e(S) = 3.989$, $p = 0.939$, $\hat{\rho}_{\text{Spearman}} = 0.036$, $\text{CI}_{95\%} [-0.909, 0.892]$, $n_{\text{pairs}} = 7$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

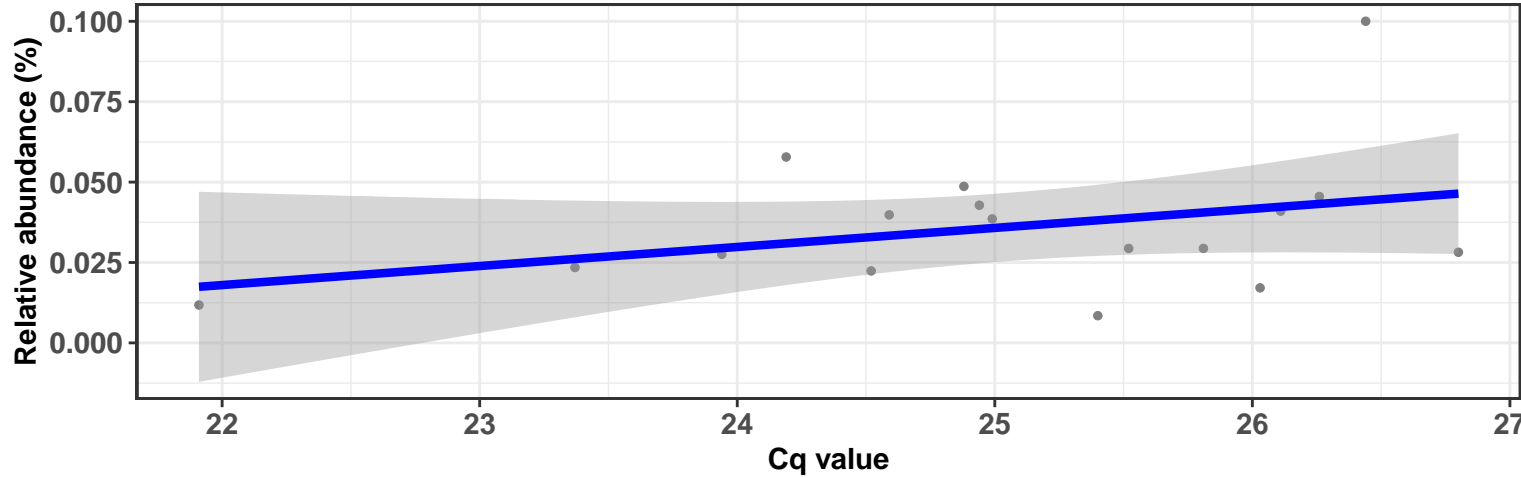
$\log_e(S) = 10.412$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.563$, $CI_{95\%} [0.412, 0.722]$, $n_{\text{pairs}} = 77$



SampleType REF-DID REF-DIM IM-DID IM-DIM Extraction-blank Mock

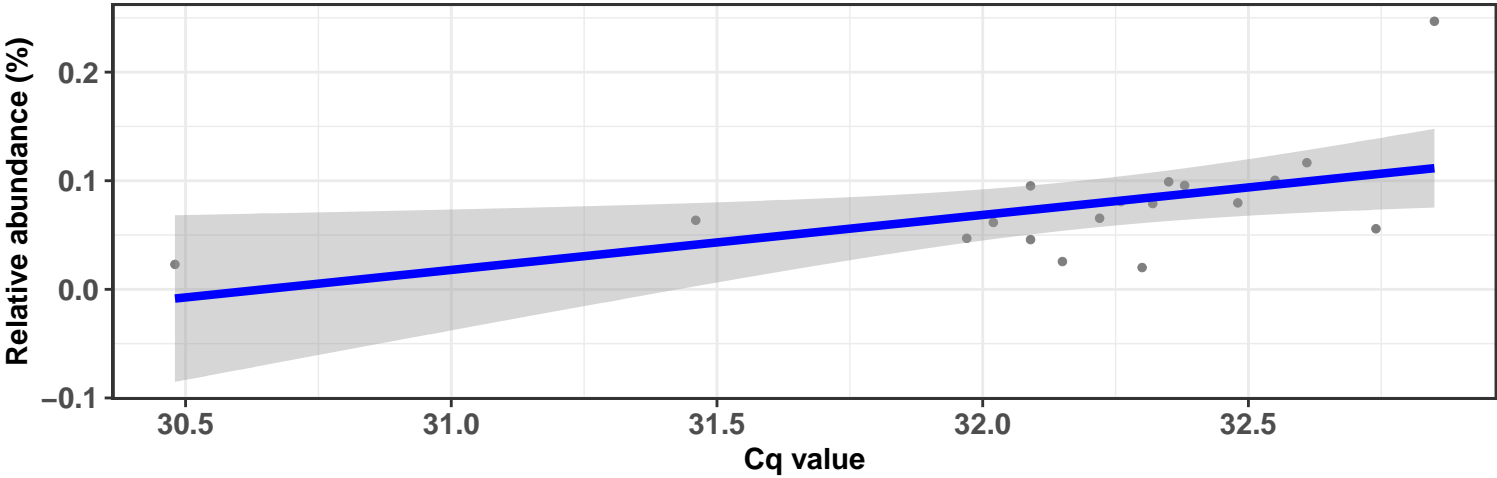
Correlation within: REF-DID

$\log_e(S) = 6.370$, $p = 0.269$, $\hat{\rho}_{\text{Spearman}} = 0.284$, $CI_{95\%} [-0.183, 0.798]$, $n_{\text{pairs}} = 17$



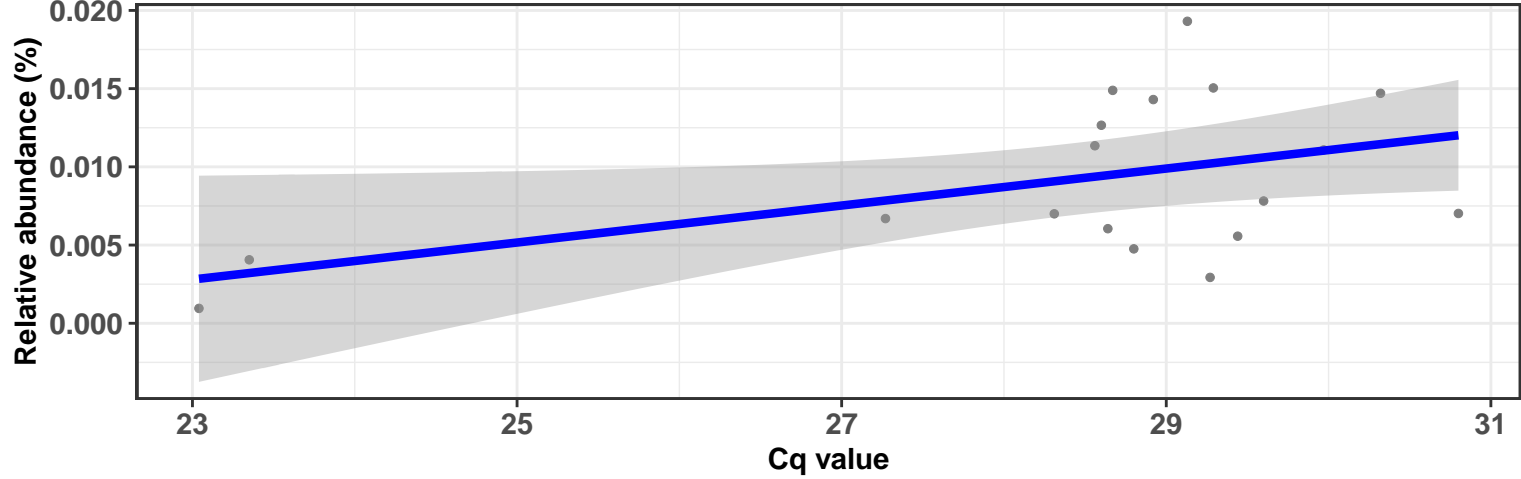
Correlation within: REF-DIM

$\log_e(S) = 5.882$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.630$, $CI_{95\%} [0.293, 0.921]$, $n_{\text{pairs}} = 18$



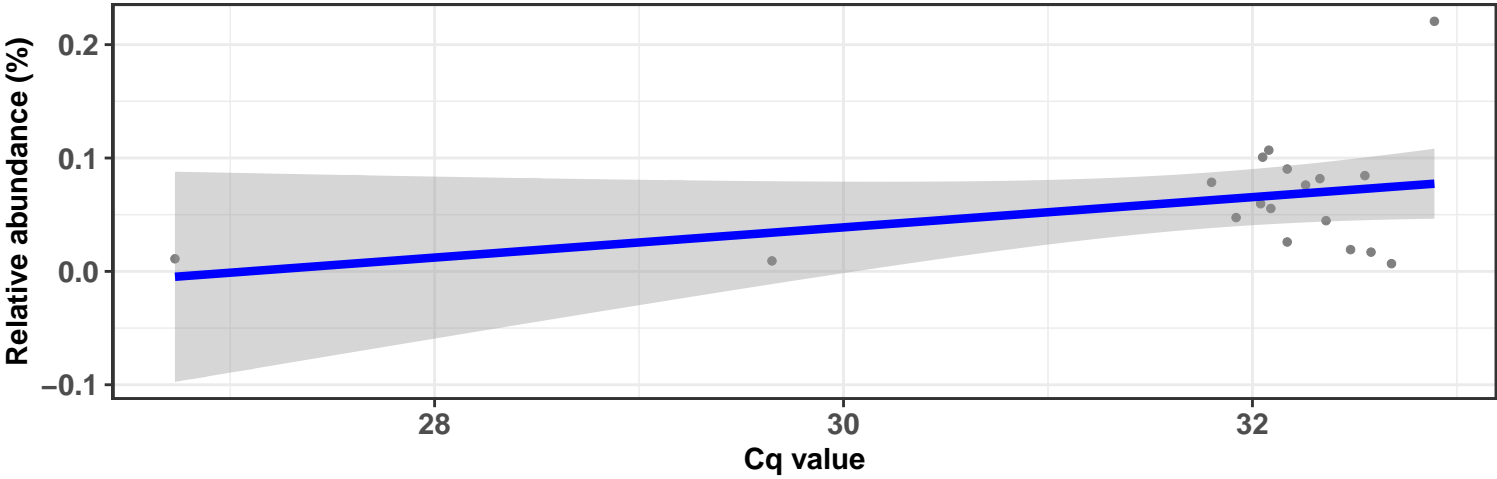
Correlation within: IM-DID

$\log_e(S) = 6.426$, $p = 0.140$, $\hat{\rho}_{\text{Spearman}} = 0.362$, $CI_{95\%} [-0.061, 0.743]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

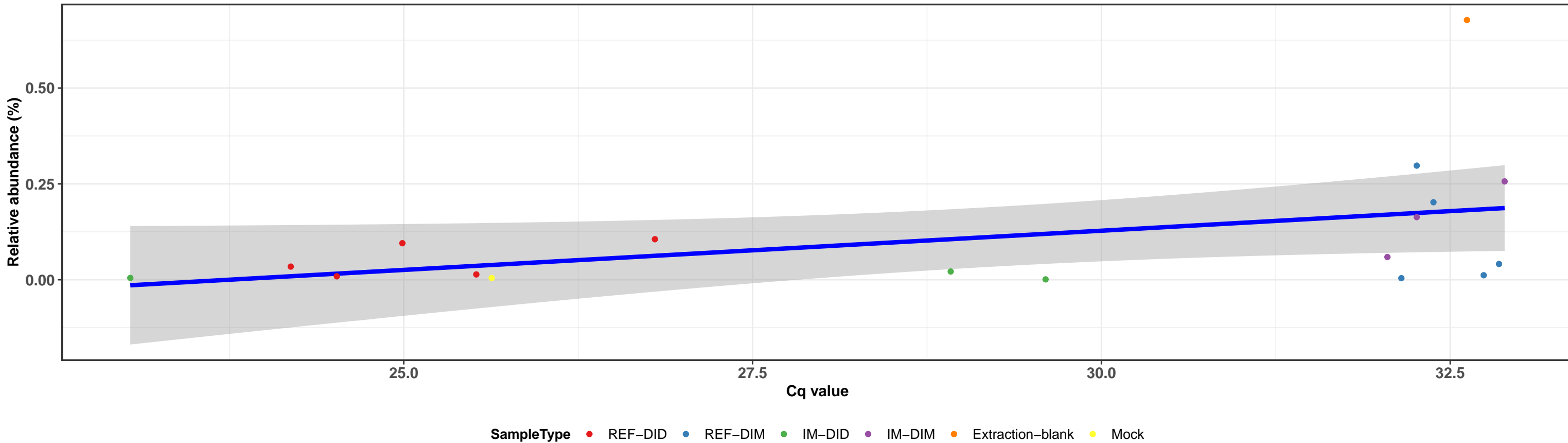
$\log_e(S) = 6.790$, $p = 0.745$, $\hat{\rho}_{\text{Spearman}} = 0.083$, $CI_{95\%} [-0.484, 0.715]$, $n_{\text{pairs}} = 18$



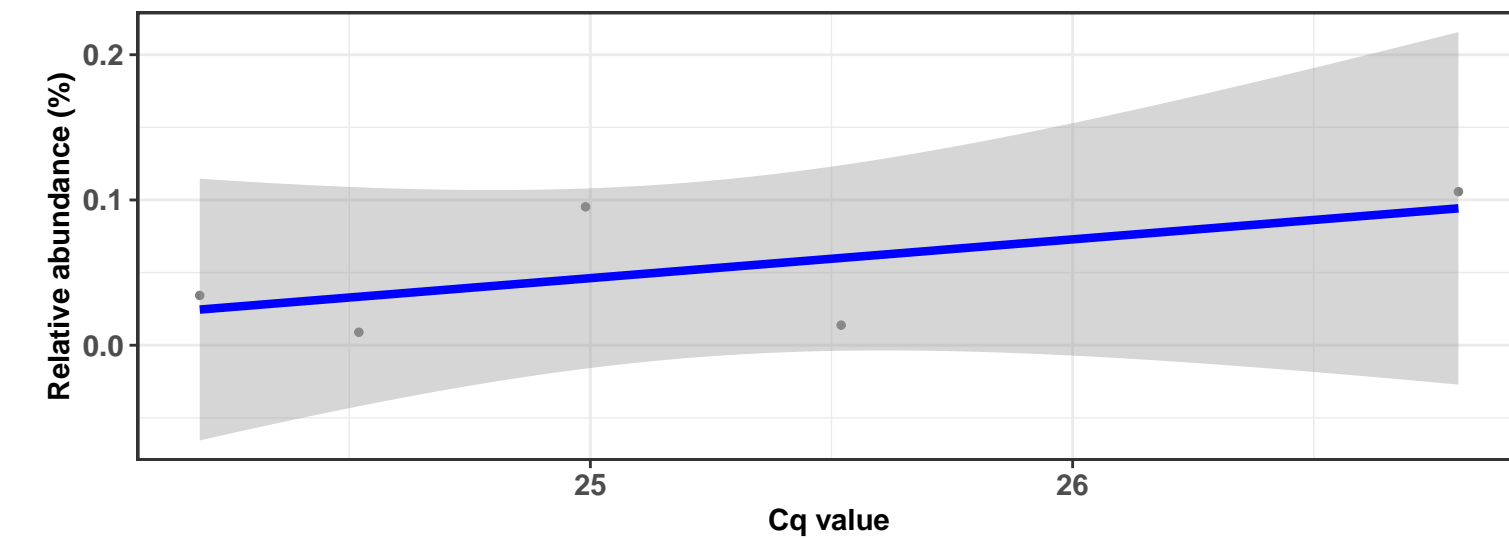
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Curtobacterium; Ambiguous_taxa

Correlation with all samples

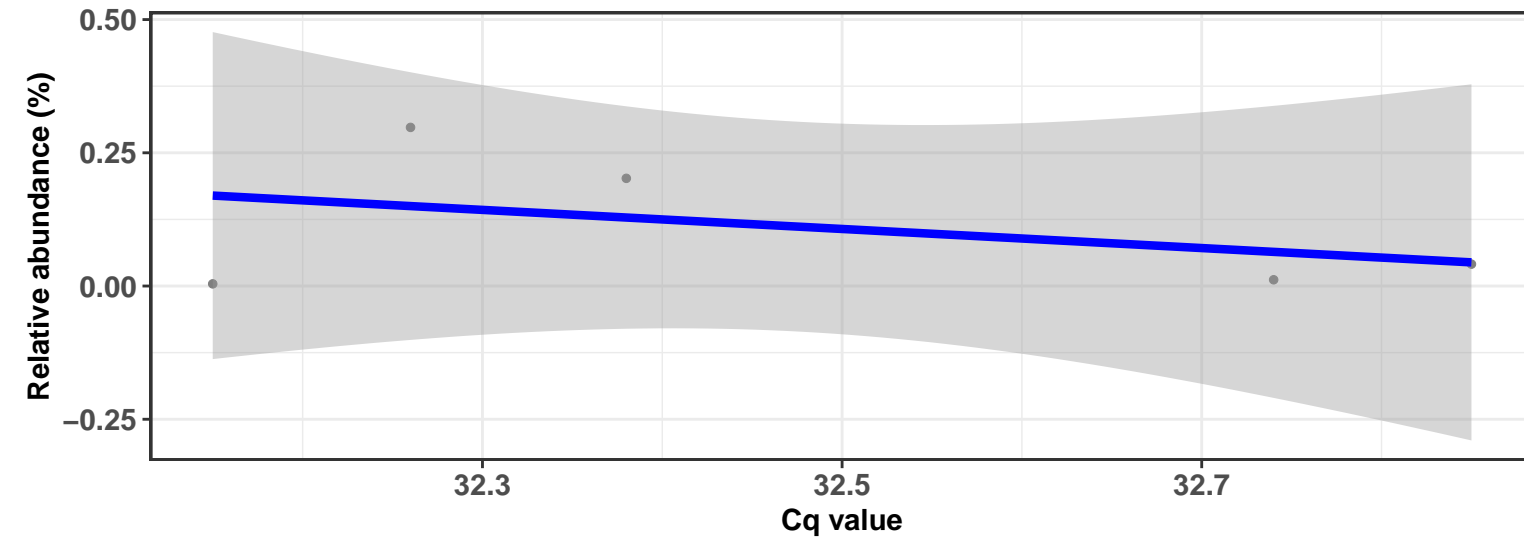
$\log_e(S) = 6.228$, $p = 0.045$, $\hat{\rho}_{\text{Spearman}} = 0.477$, $\text{CI}_{95\%} [0.167, 0.829]$, $n_{\text{pairs}} = 18$



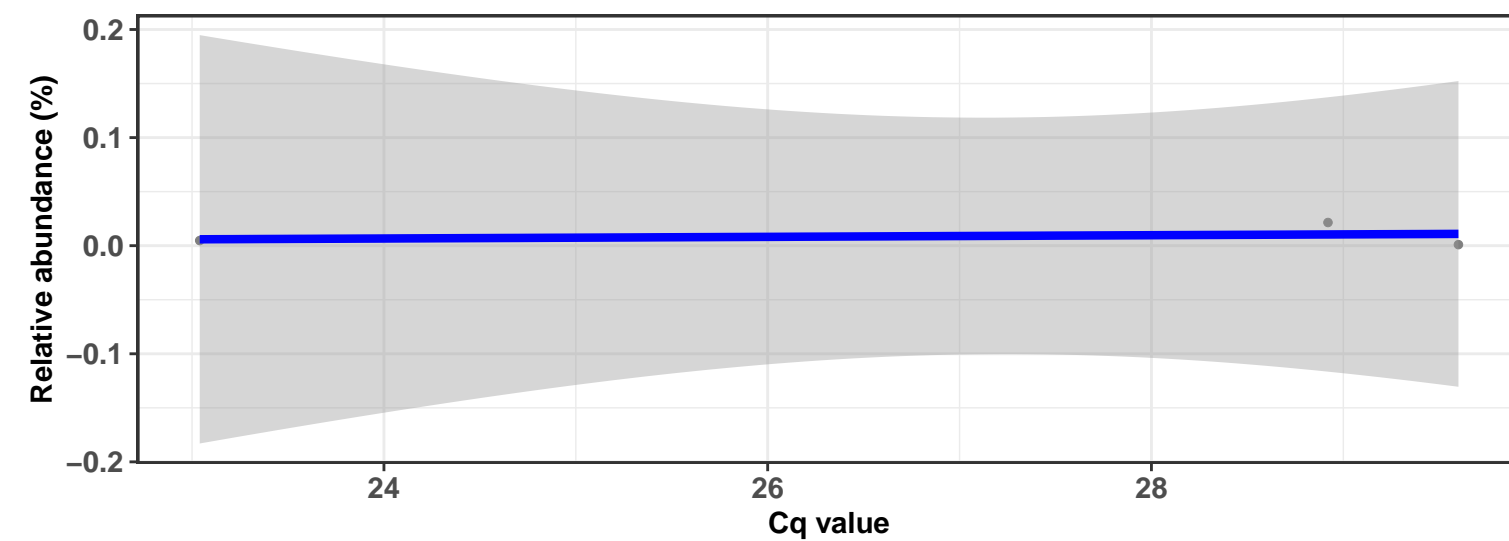
Correlation within: REF-DID



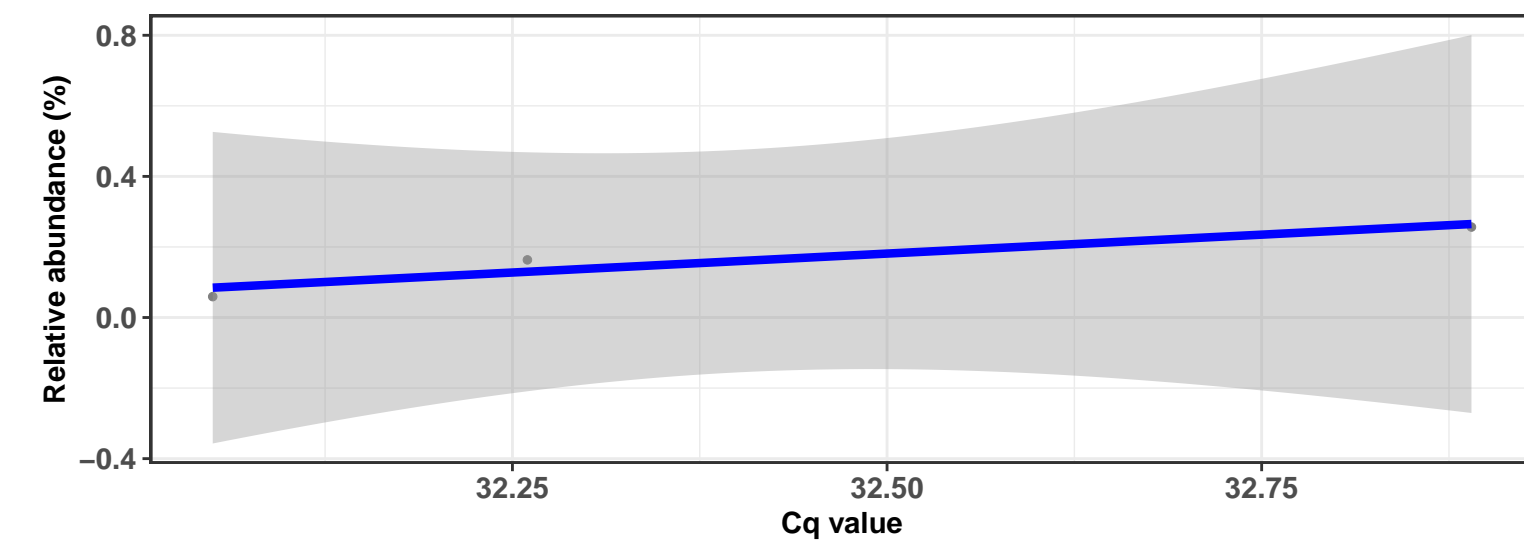
Correlation within: REF-DIM



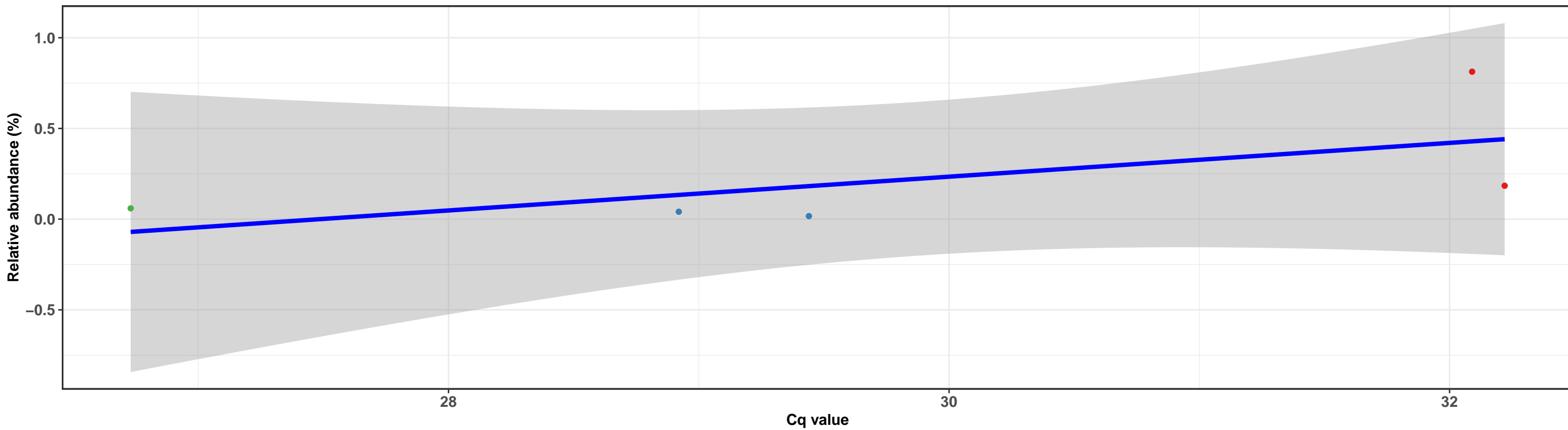
Correlation within: IM-DID



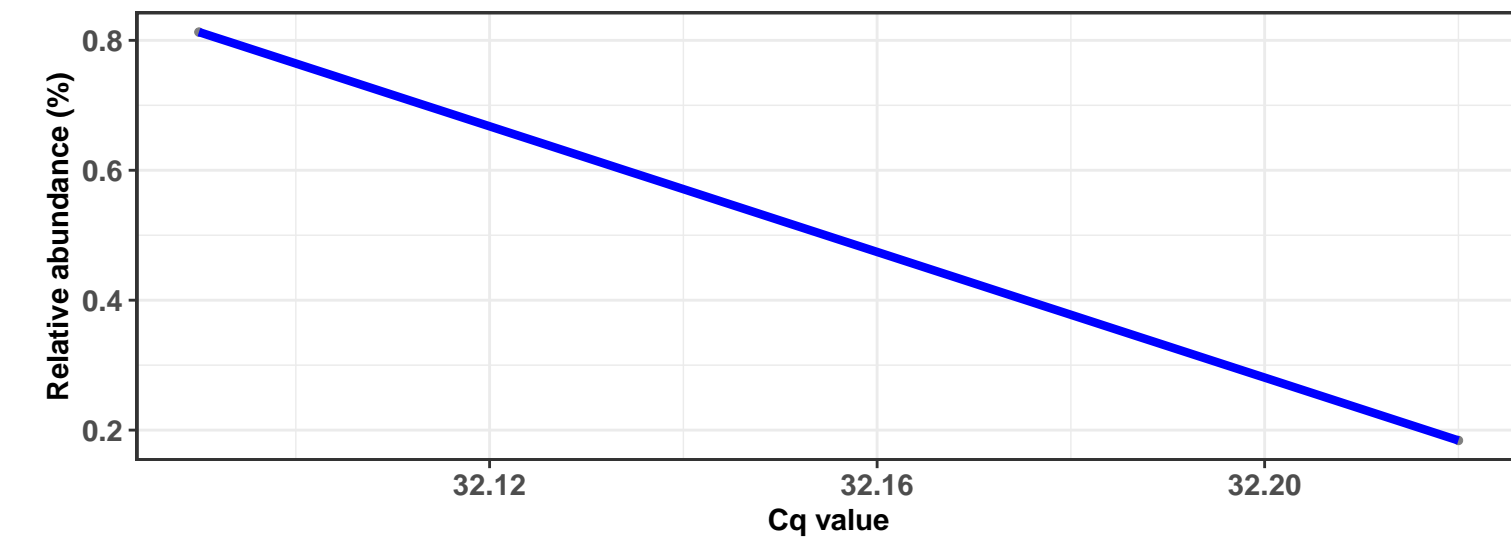
Correlation within: IM-DIM



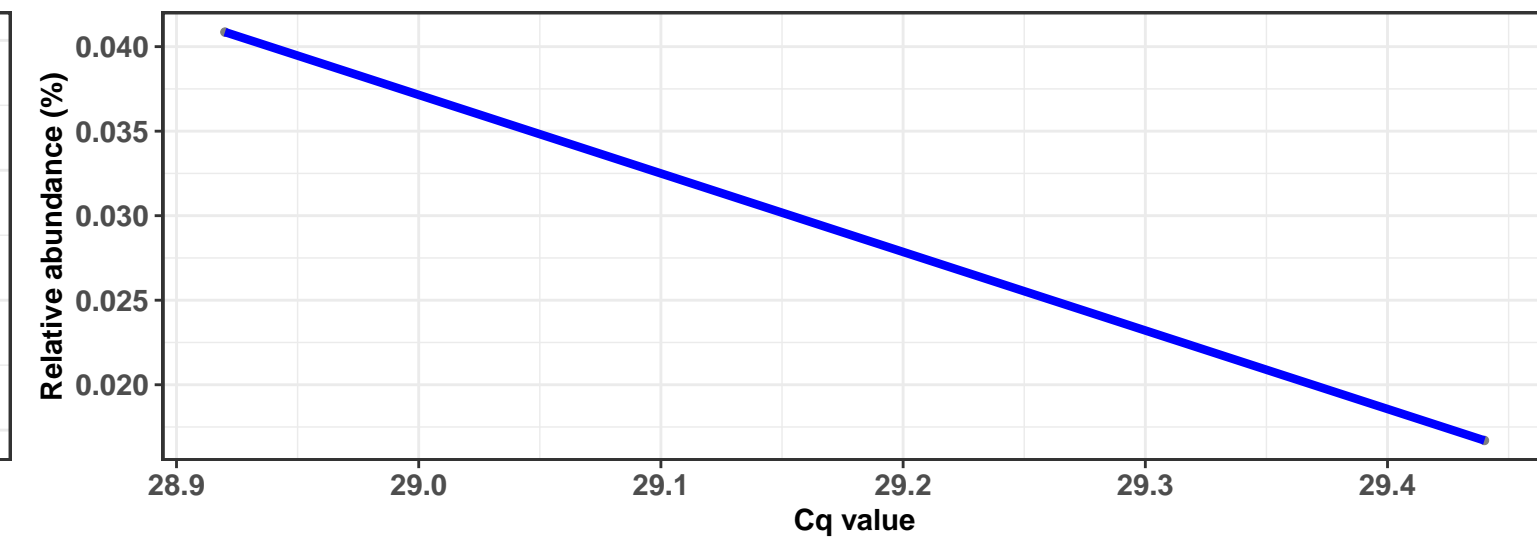
Correlation with all samples



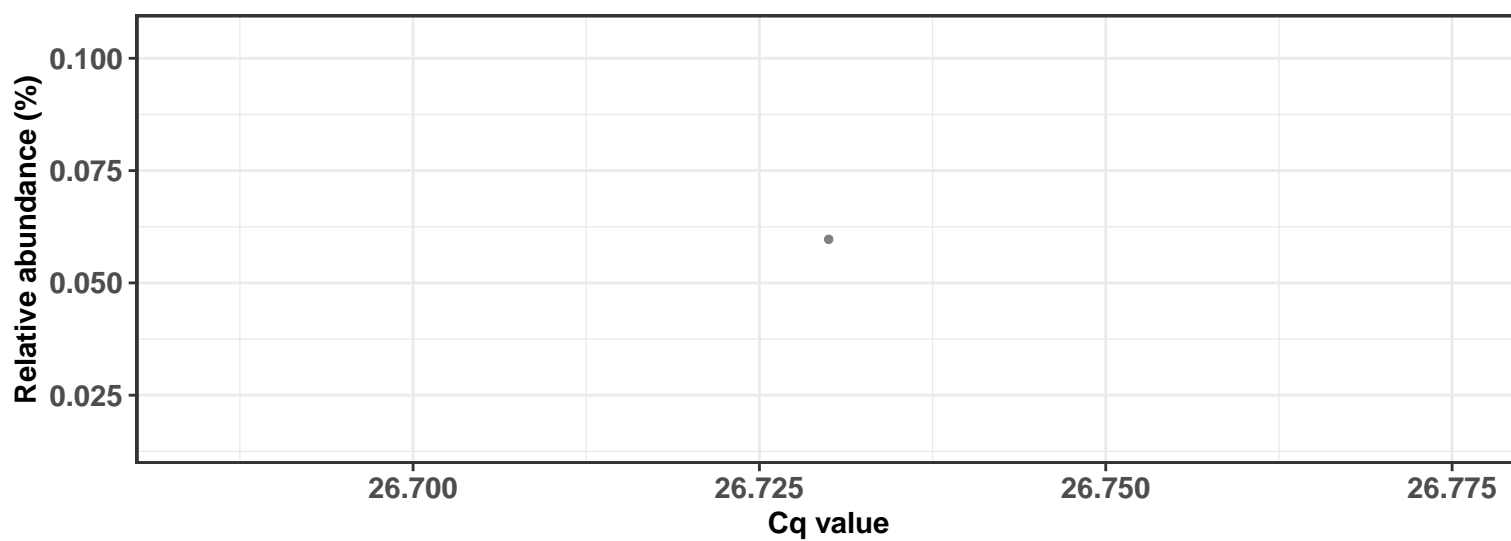
Correlation within: REF-DIM



Correlation within: IM-DID



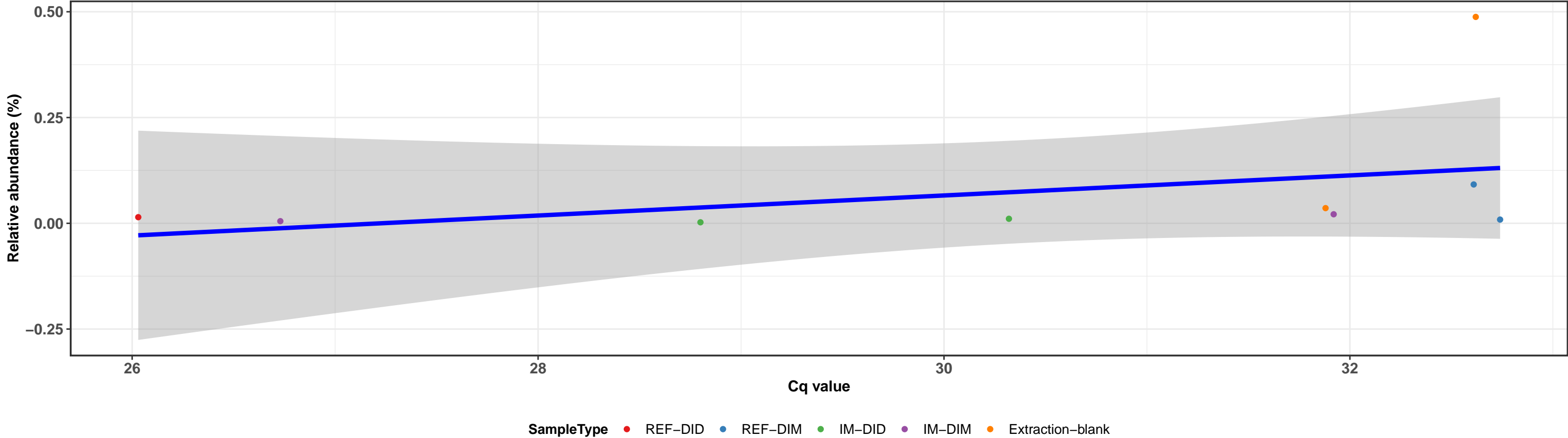
Correlation within: IM-DIM



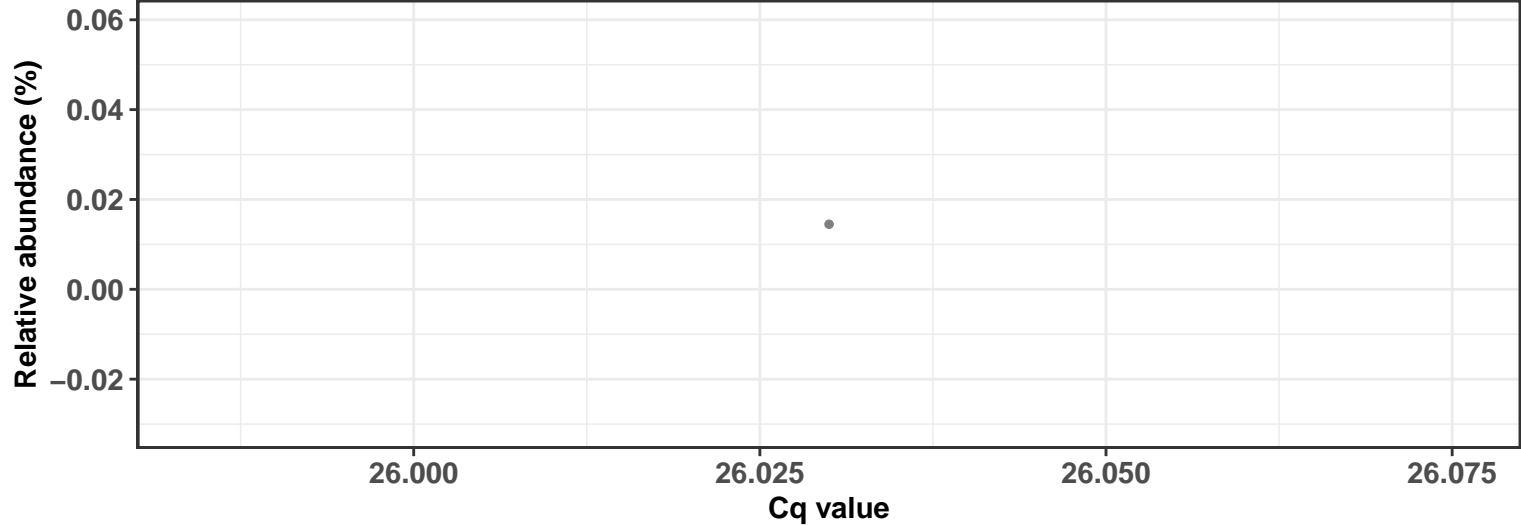
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Frankiales; f__Geodermatophilaceae; g__Modestobacter; Ambiguous_taxa

Correlation with all samples

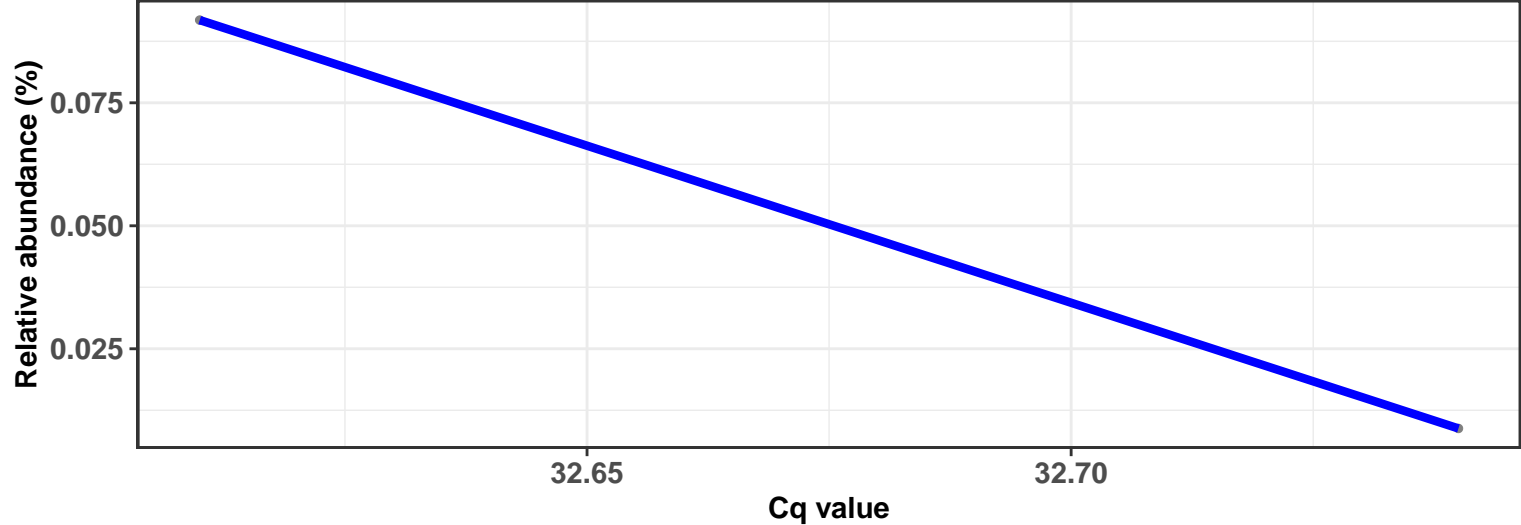
$\log_e(S) = 4.127$, $p = 0.187$, $\hat{\rho}_{\text{Spearman}} = 0.483$, $\text{CI}_{95\%} [-0.121, 1.177]$, $n_{\text{pairs}} = 9$



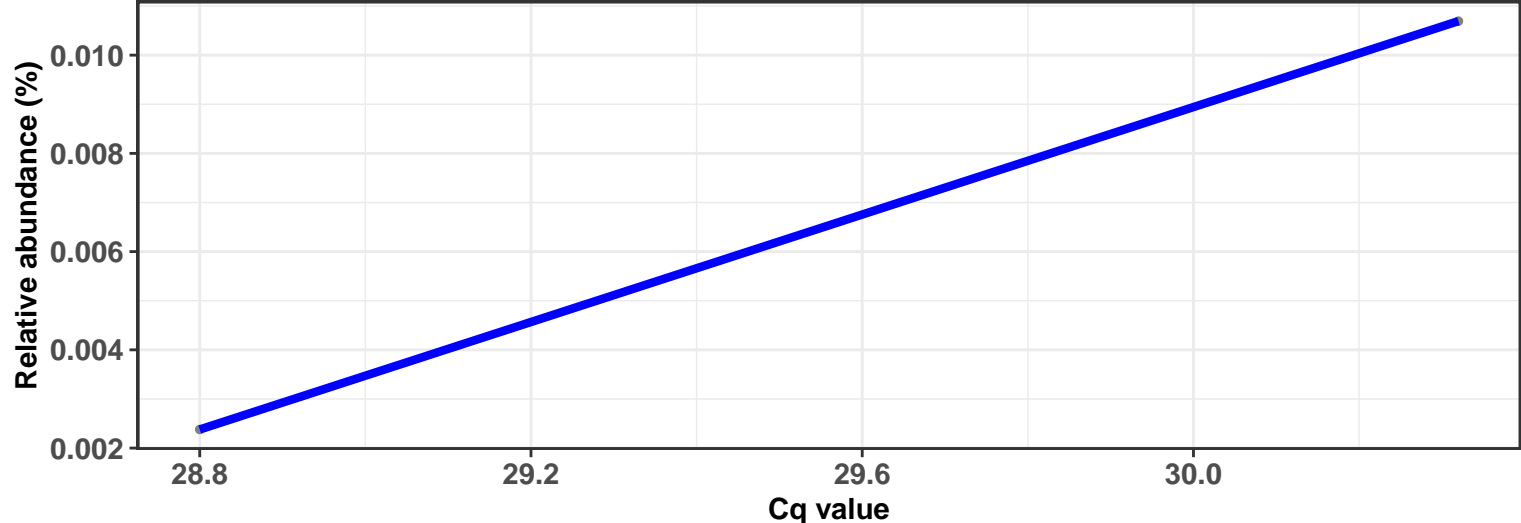
Correlation within: REF-DID



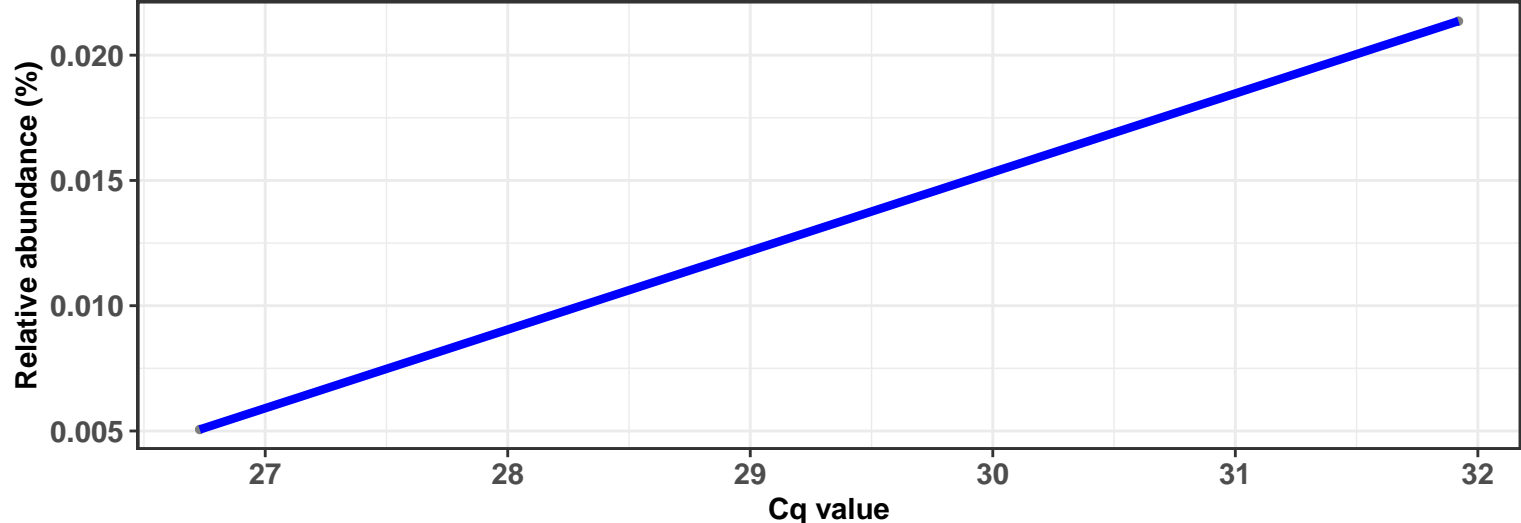
Correlation within: REF-DIM



Correlation within: IM-DID



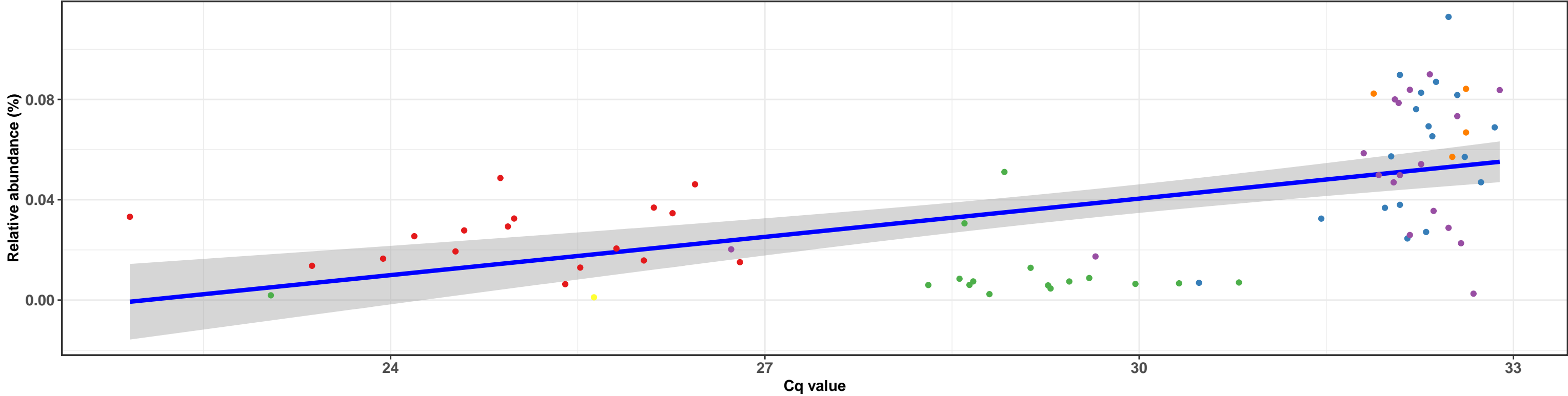
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

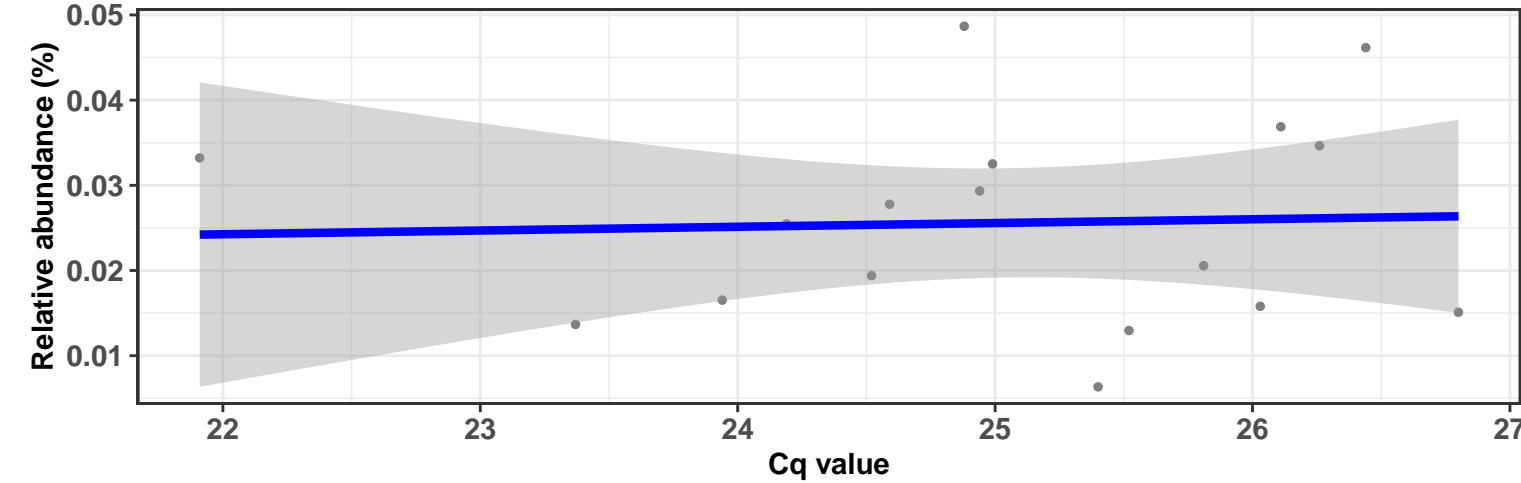
Correlation with all samples

$\log_e(S) = 10.265$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.575$, $\text{CI}_{95\%} [0.422, 0.756]$, $n_{\text{pairs}} = 74$



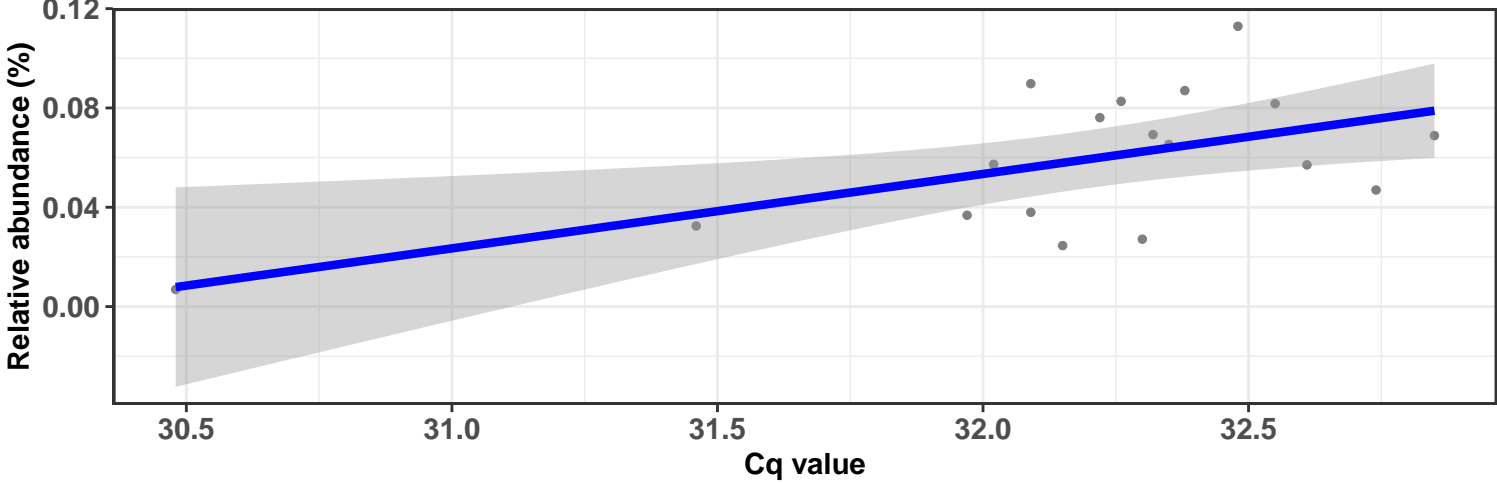
Correlation within: REF-DID

$\log_e(S) = 6.593$, $p = 0.687$, $\hat{\rho}_{\text{Spearman}} = 0.105$, $\text{CI}_{95\%} [-0.430, 0.618]$, $n_{\text{pairs}} = 17$



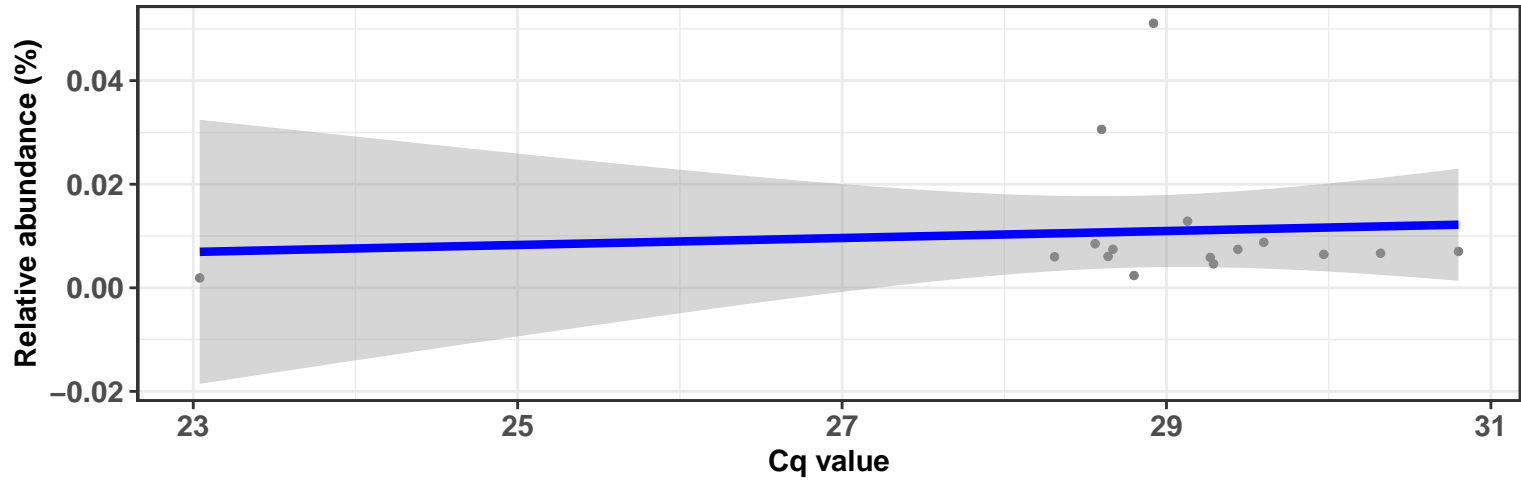
Correlation within: REF-DIM

$\log_e(S) = 6.300$, $p = 0.069$, $\hat{\rho}_{\text{Spearman}} = 0.438$, $\text{CI}_{95\%} [-0.007, 0.910]$, $n_{\text{pairs}} = 18$



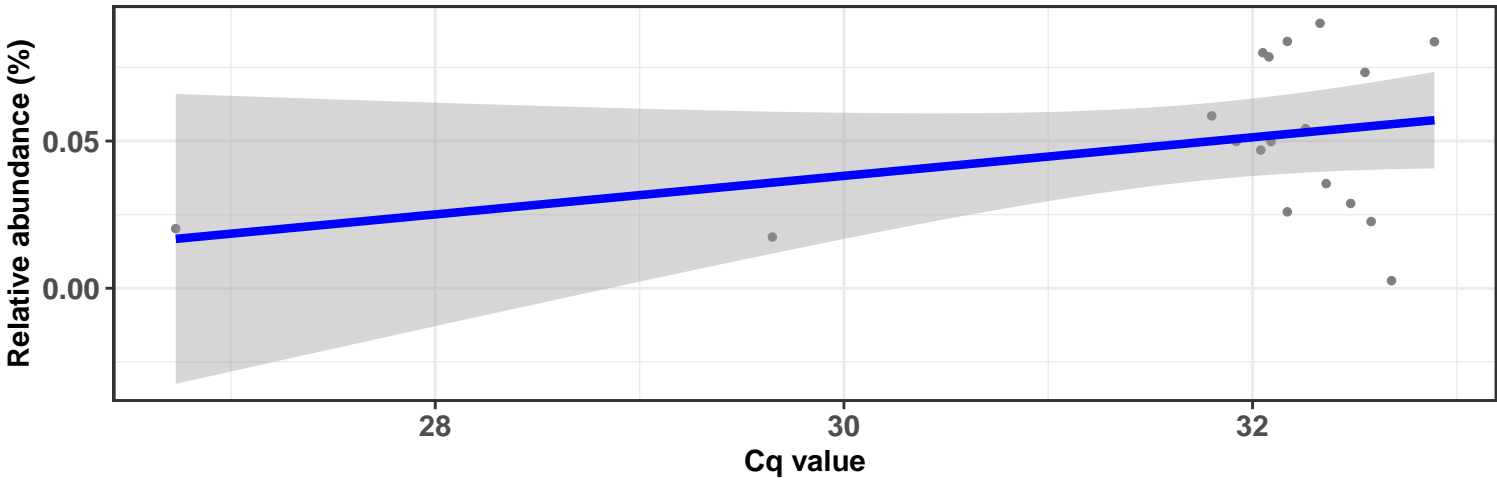
Correlation within: IM-DID

$\log_e(S) = 6.400$, $p = 0.672$, $\hat{\rho}_{\text{Spearman}} = 0.115$, $\text{CI}_{95\%} [-0.351, 0.606]$, $n_{\text{pairs}} = 16$



Correlation within: IM-DIM

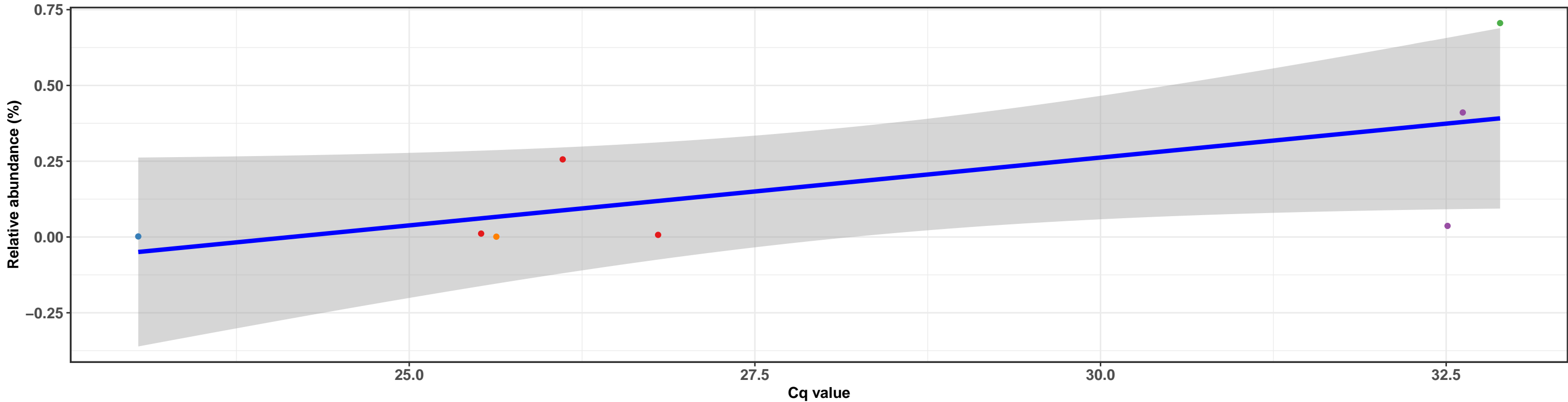
$\log_e(S) = 6.782$, $p = 0.723$, $\hat{\rho}_{\text{Spearman}} = 0.090$, $\text{CI}_{95\%} [-0.435, 0.600]$, $n_{\text{pairs}} = 18$



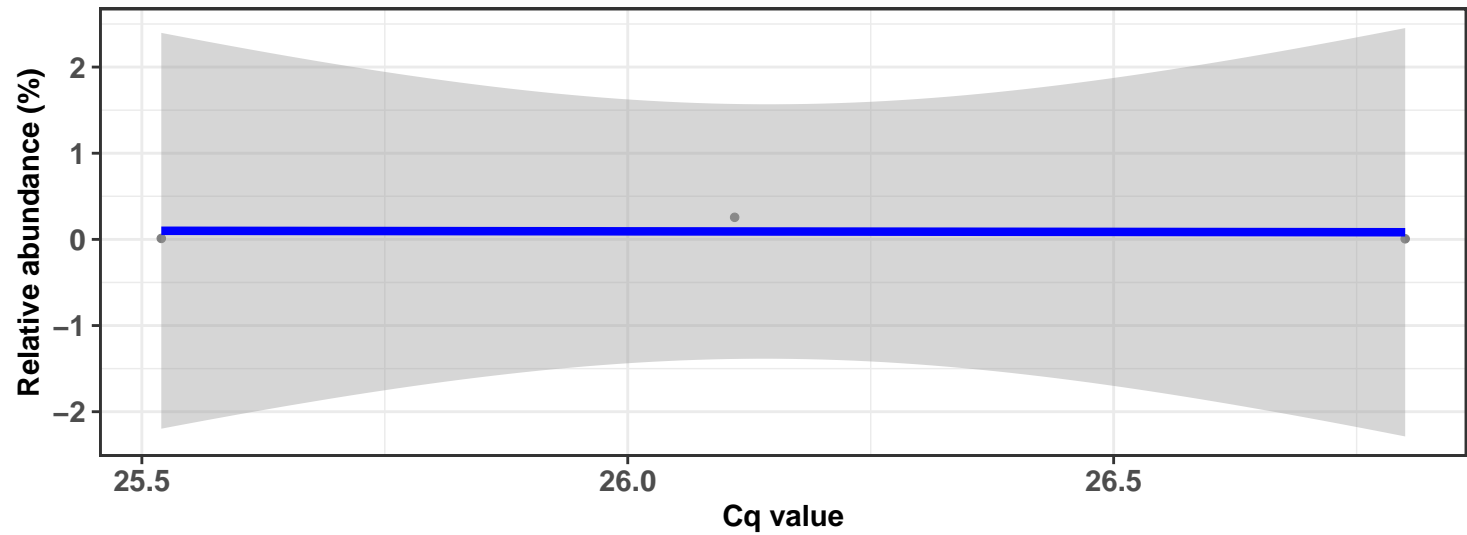
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium

Correlation with all samples

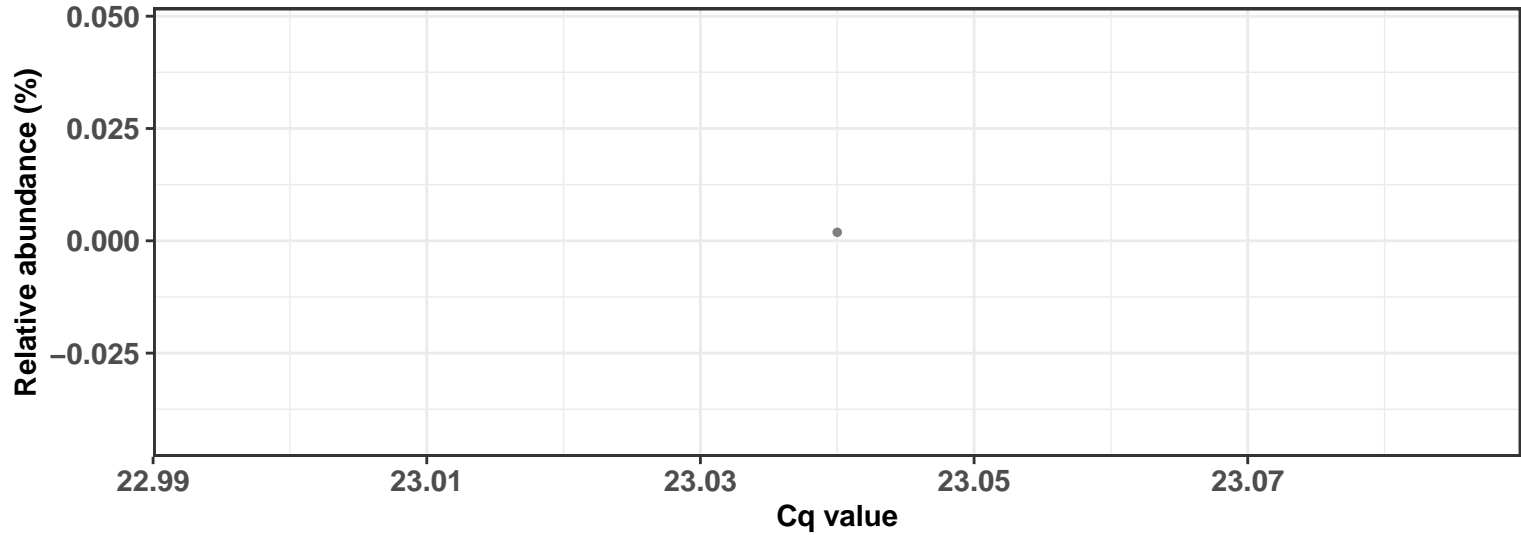
$\log_e(S) = 2.890$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = 0.786$, $\text{CI}_{95\%} [0.356, 1.339]$, $n_{\text{pairs}} = 8$



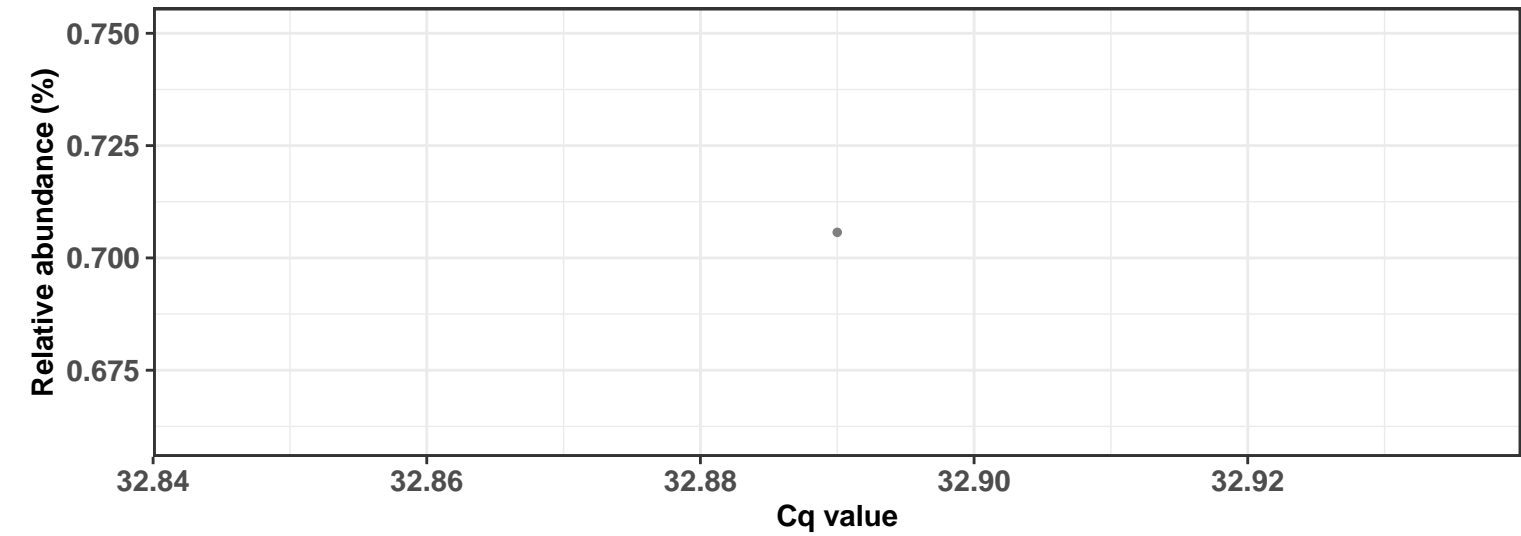
Correlation within: REF-DID



Correlation within: IM-DID



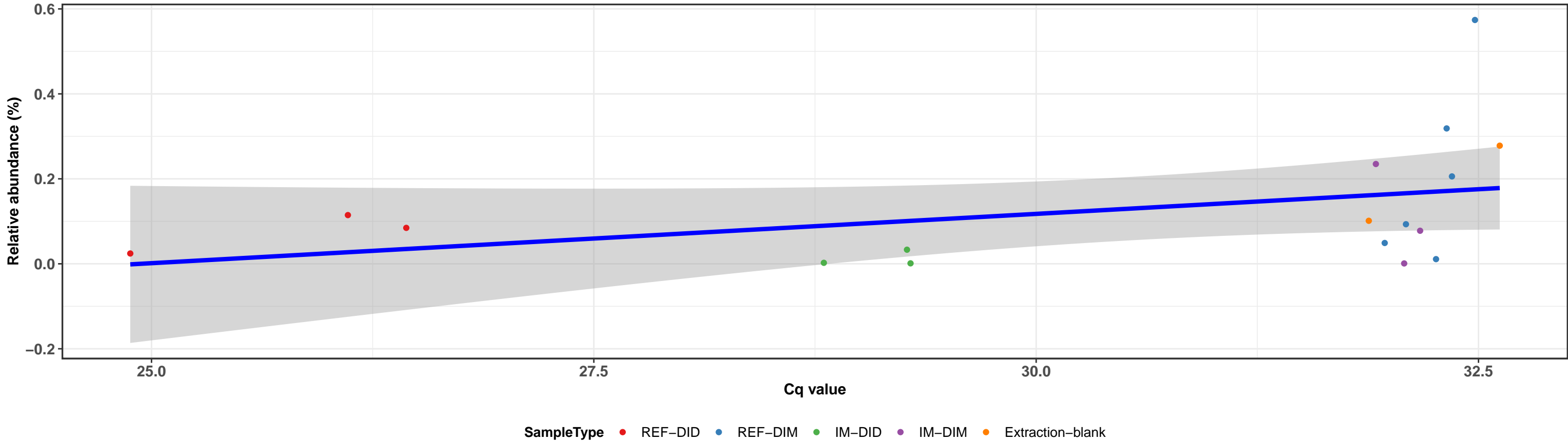
Correlation within: IM-DIM



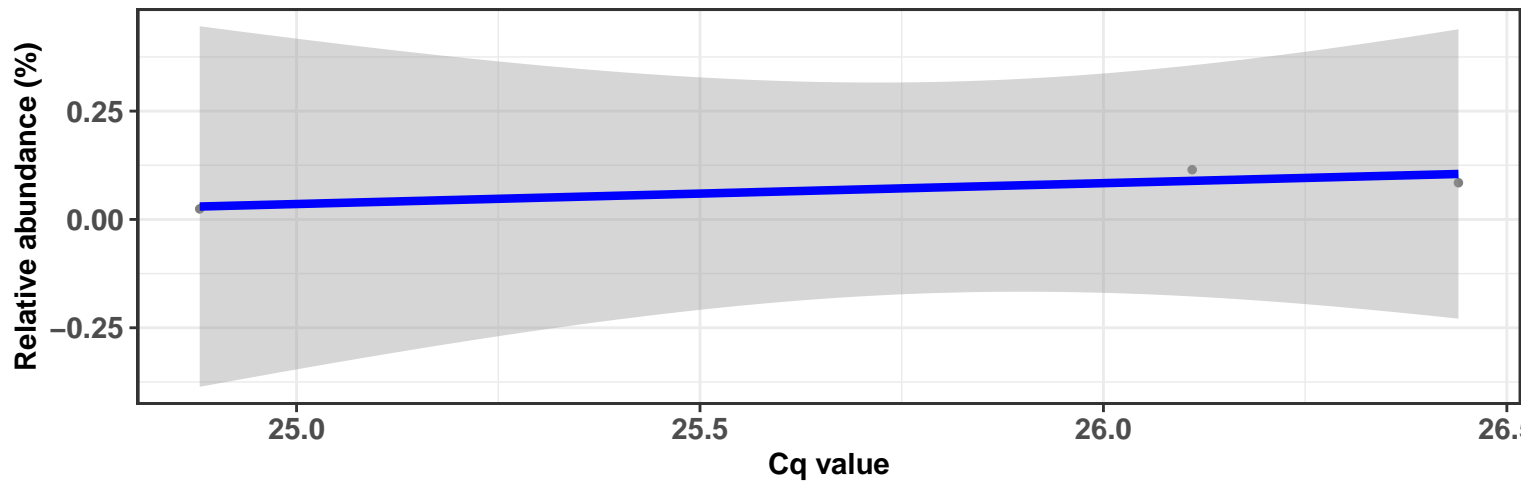
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 6.035$, $p = 0.047$, $\hat{\rho}_{\text{Spearman}} = 0.488$, $\text{CI}_{95\%} [0.093, 0.970]$, $n_{\text{pairs}} = 17$

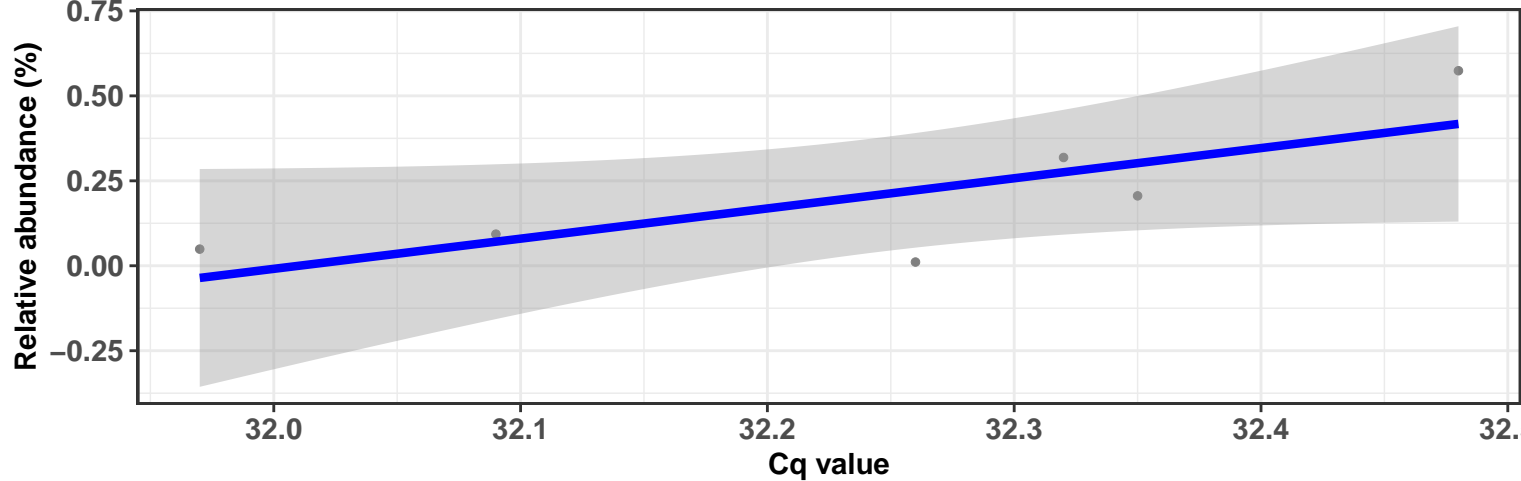


Correlation within: REF-DID

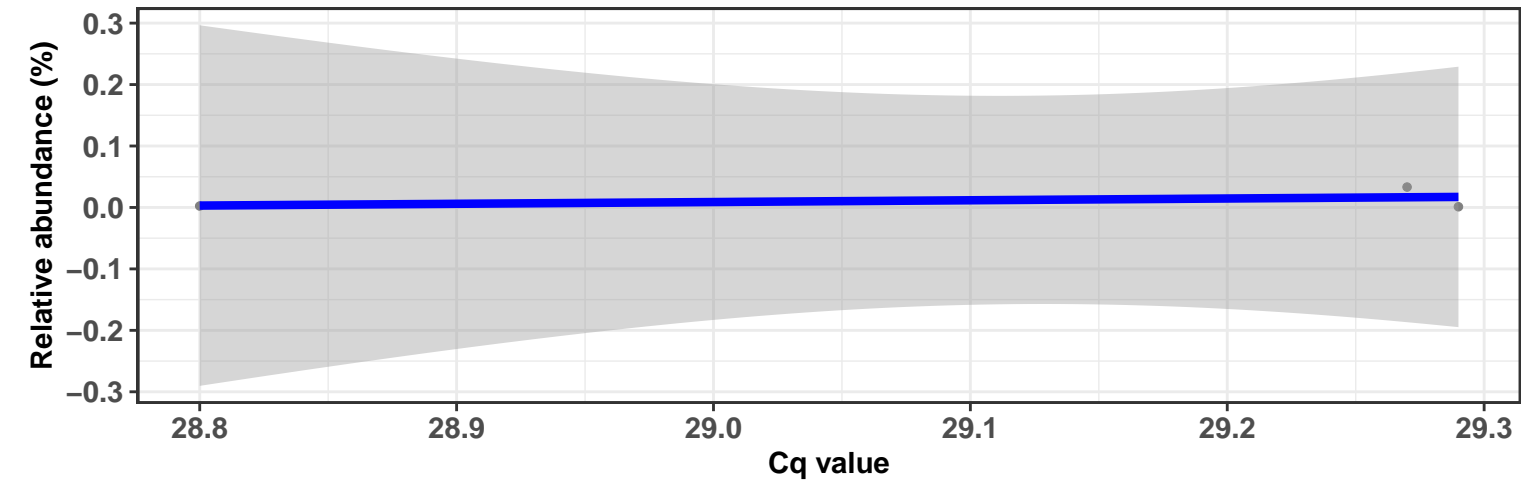


Correlation within: REF-DIM

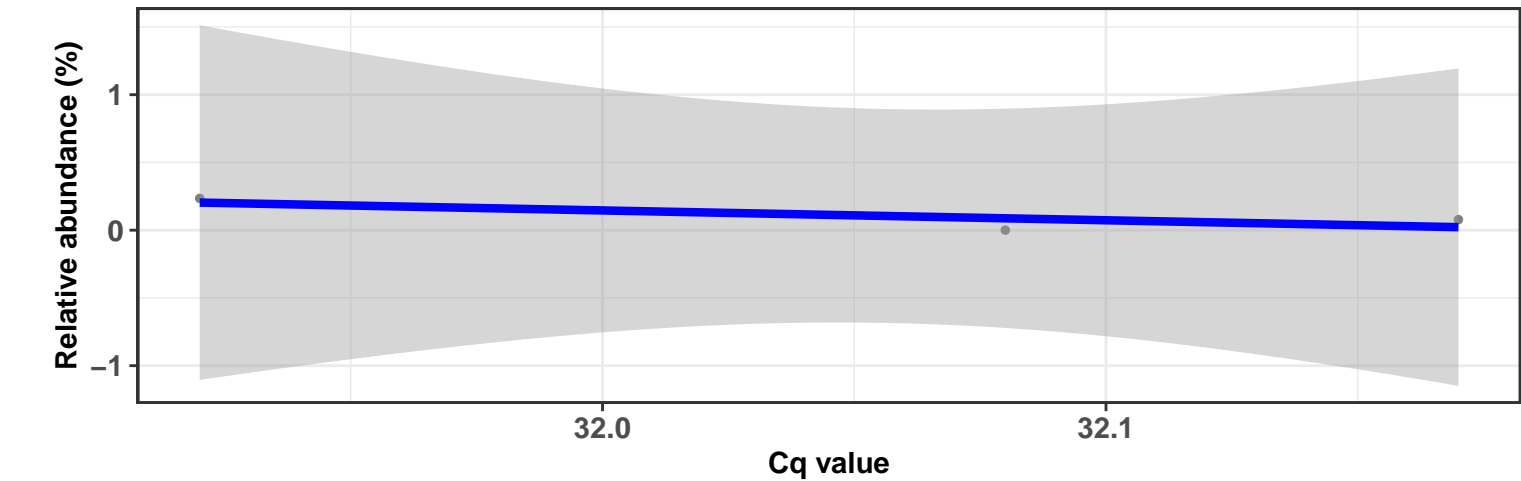
$\log_e(S) = 2.079$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = 0.771$, $\text{CI}_{95\%} [0.249, 1.366]$, $n_{\text{pairs}} = 6$



Correlation within: IM-DID



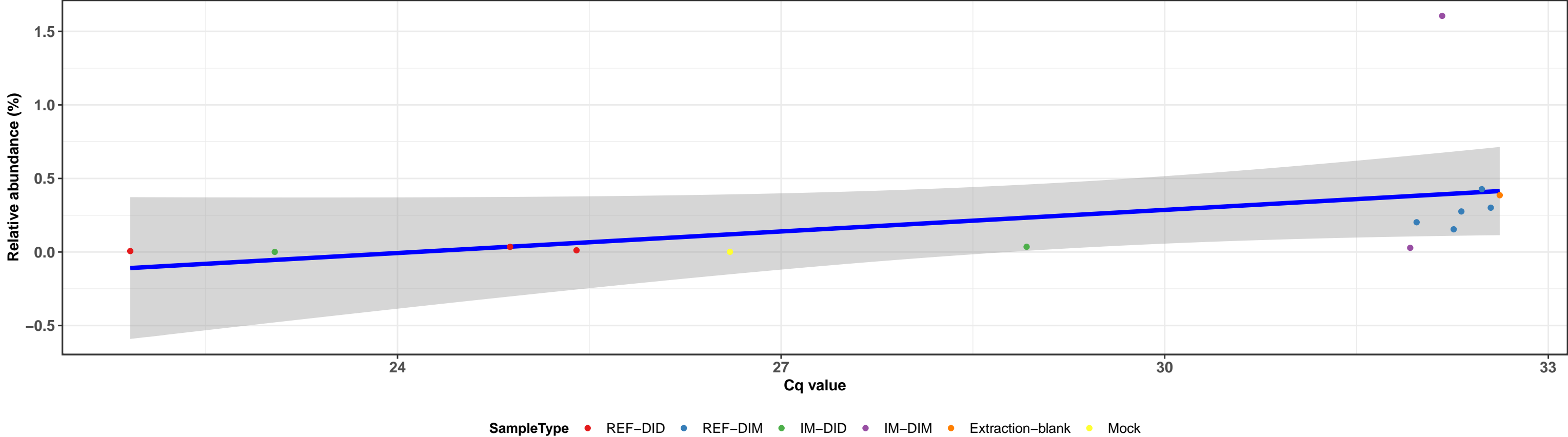
Correlation within: IM-DIM



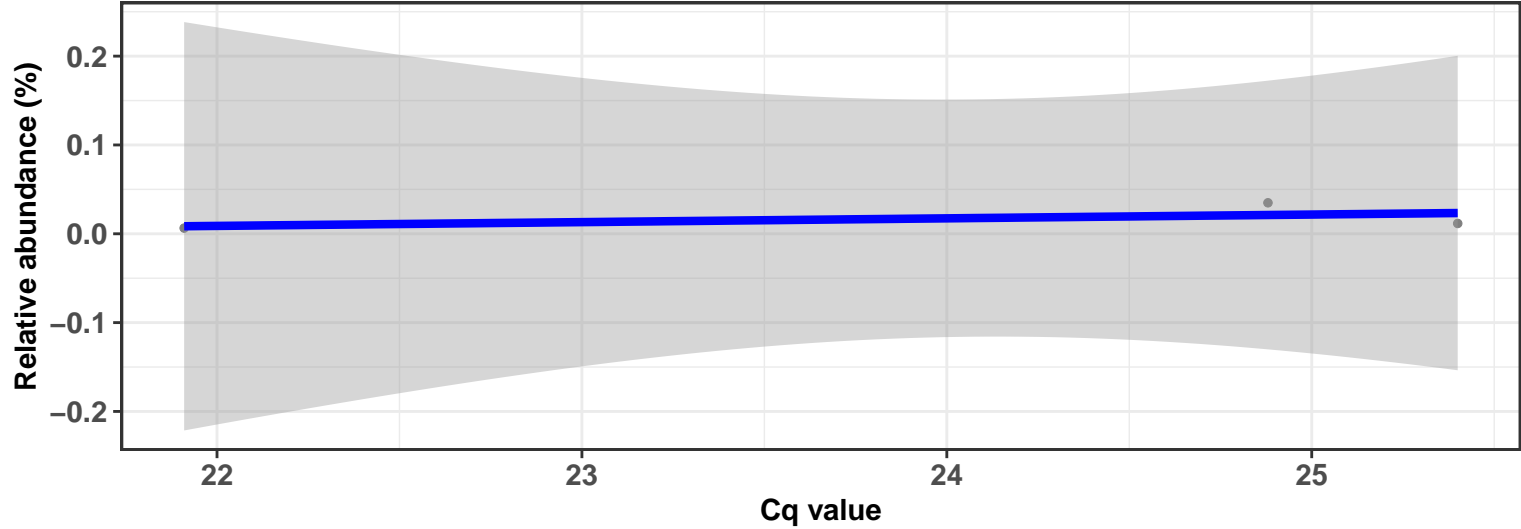
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; Ambiguous_taxa

Correlation with all samples

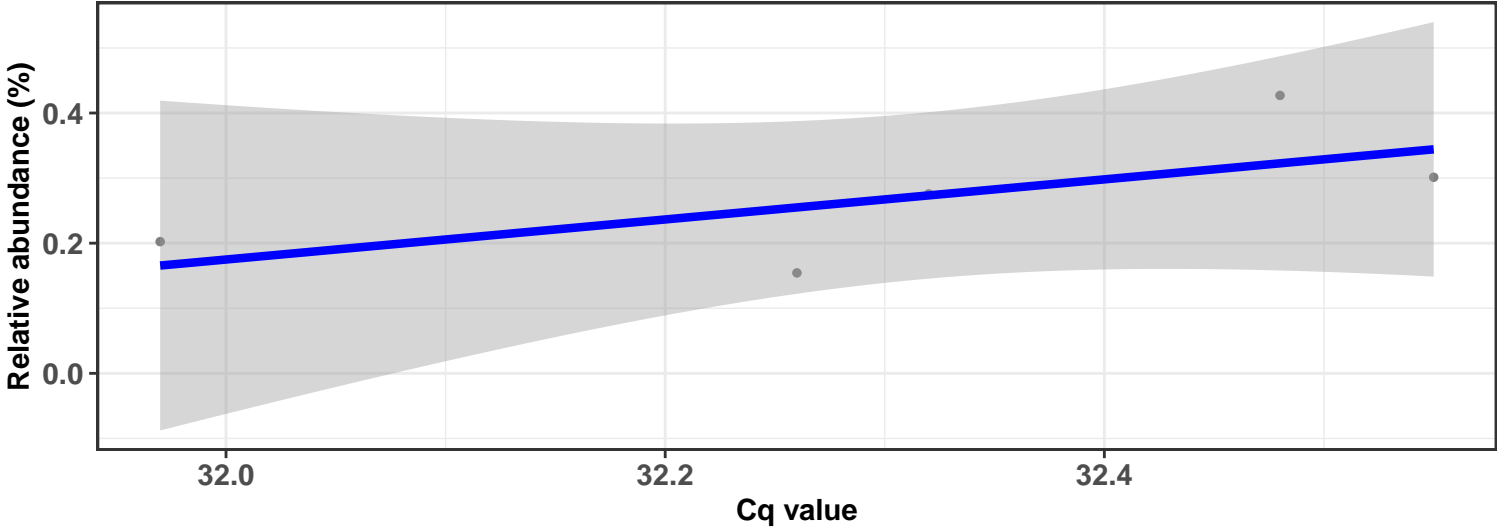
$\log_e(S) = 4.220$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.851$, $CI_{95\%} [0.677, 1.068]$, $n_{\text{pairs}} = 14$



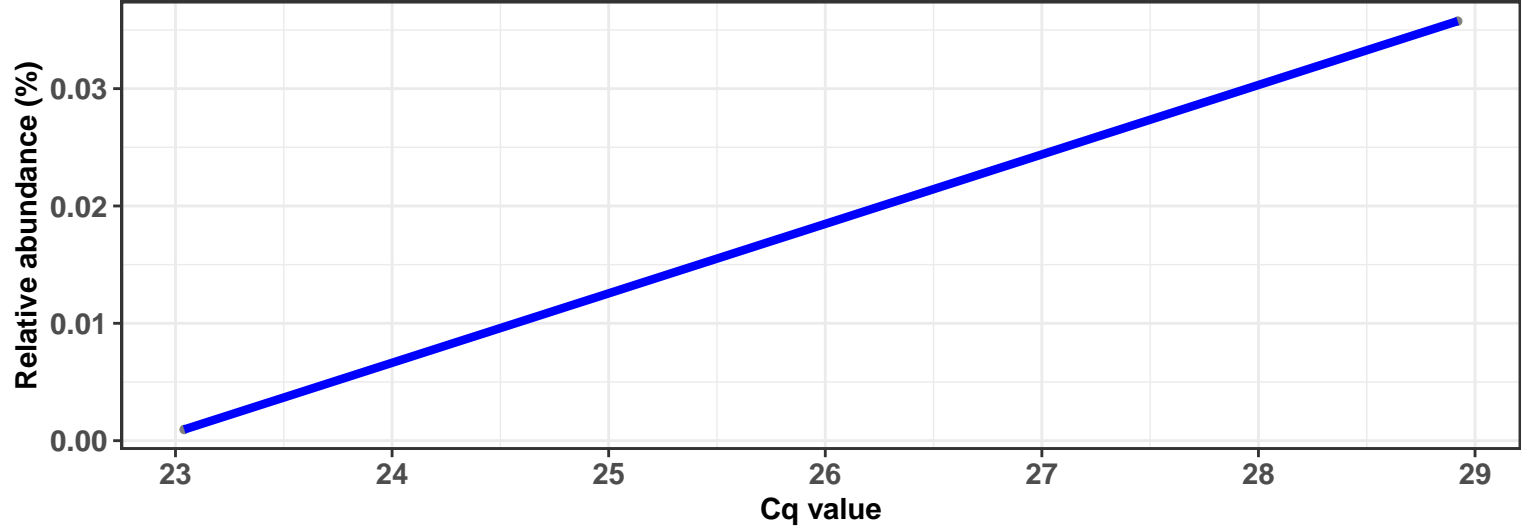
Correlation within: REF-DID



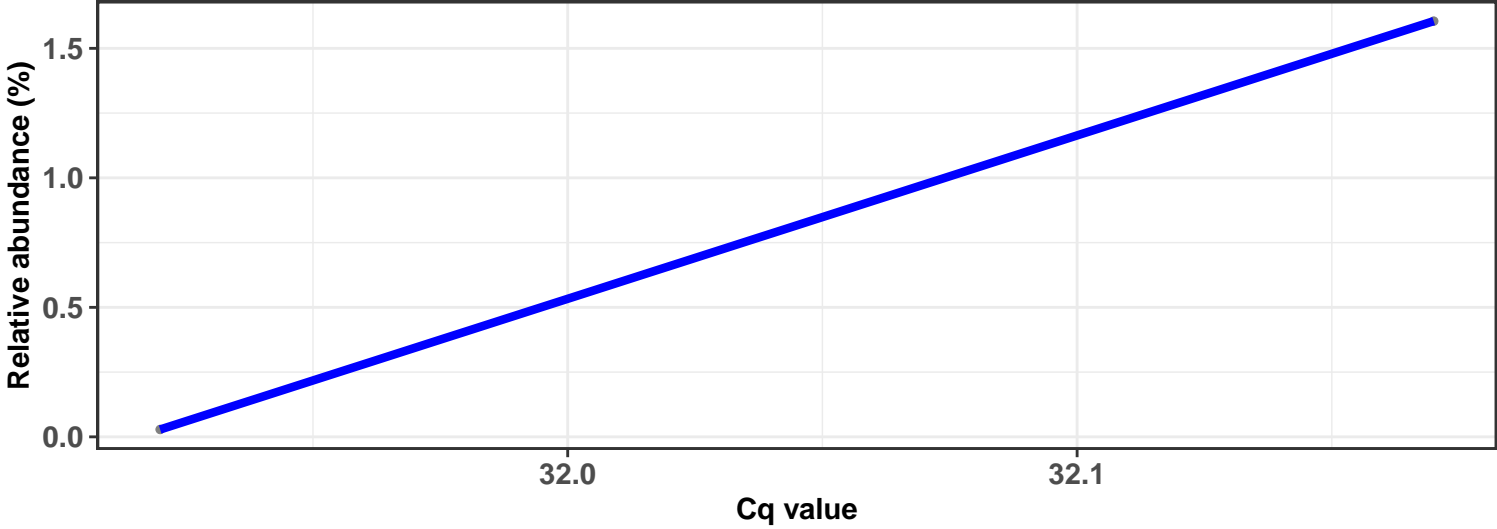
Correlation within: REF-DIM



Correlation within: IM-DID

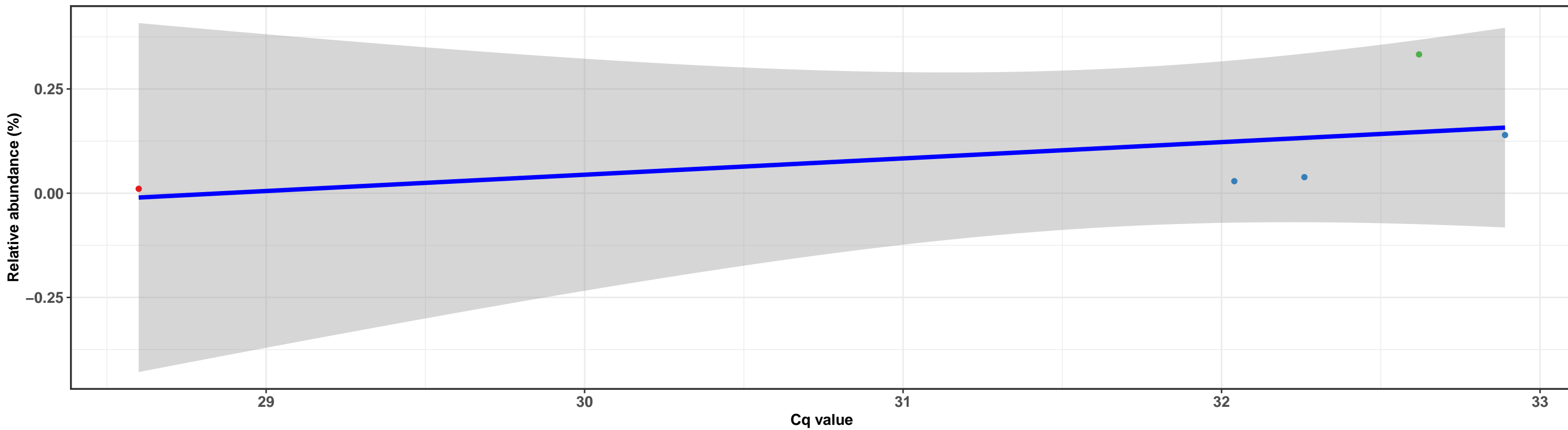


Correlation within: IM-DIM

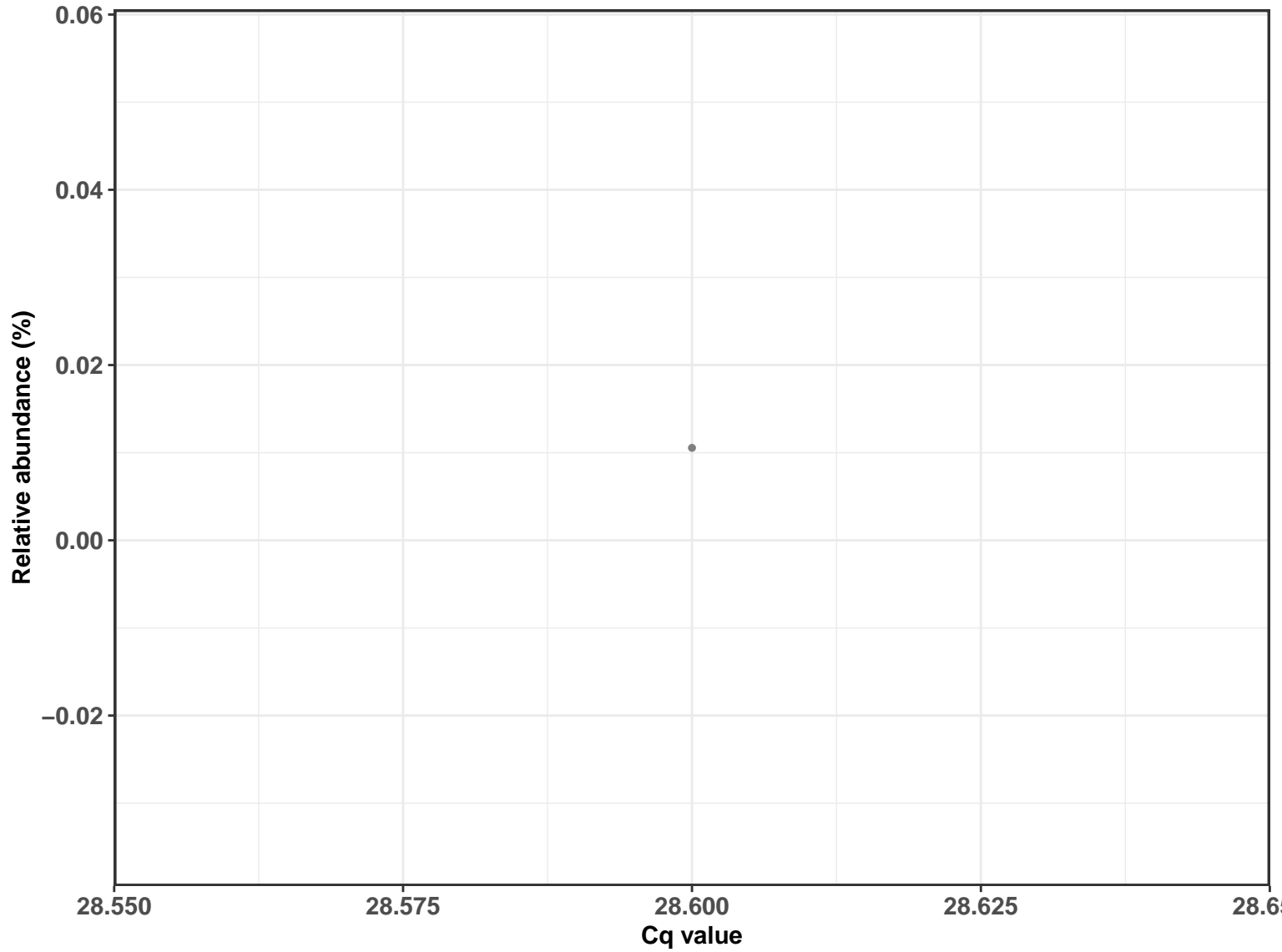


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium

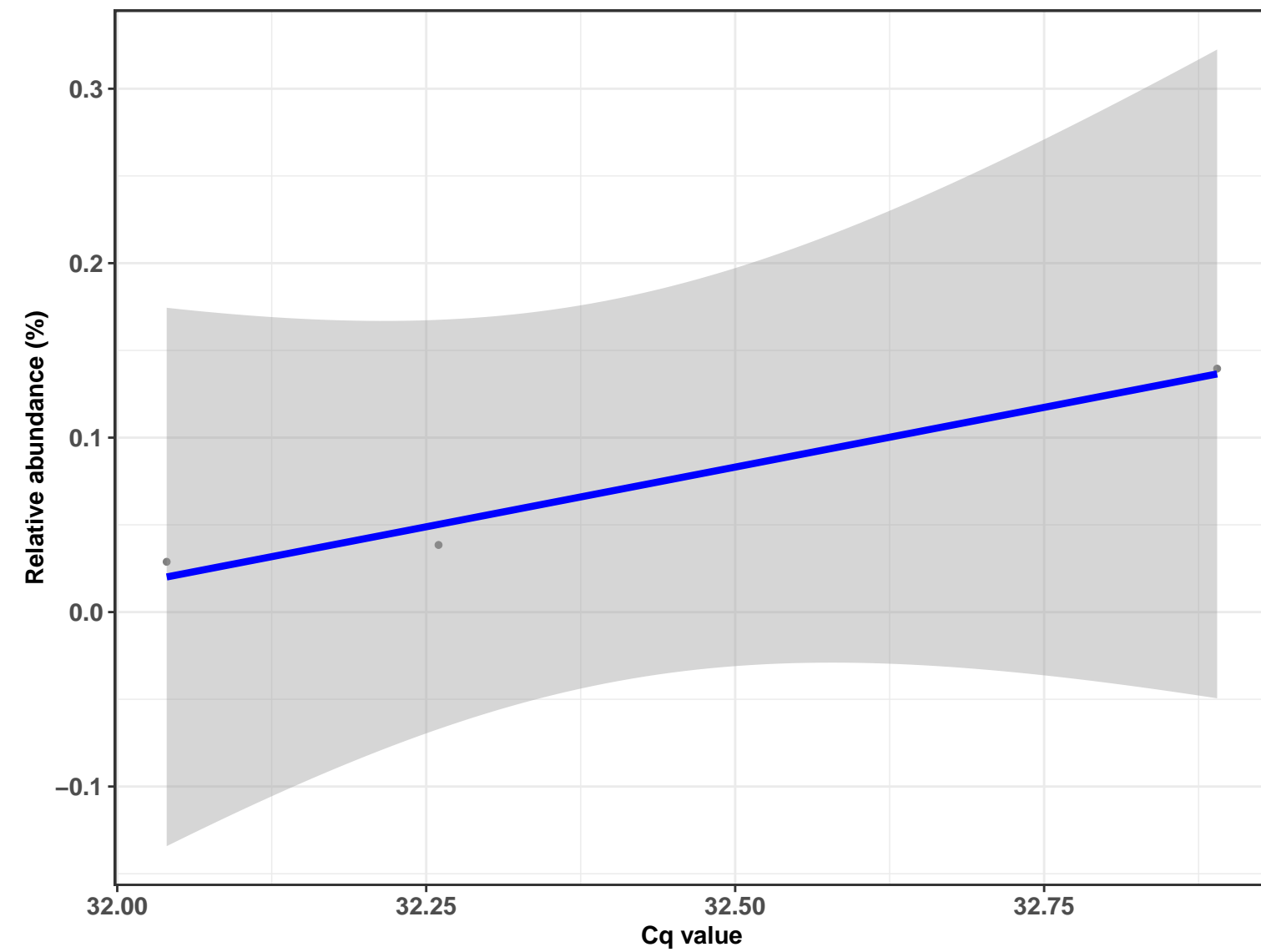
Correlation with all samples



Correlation within: IM-DID

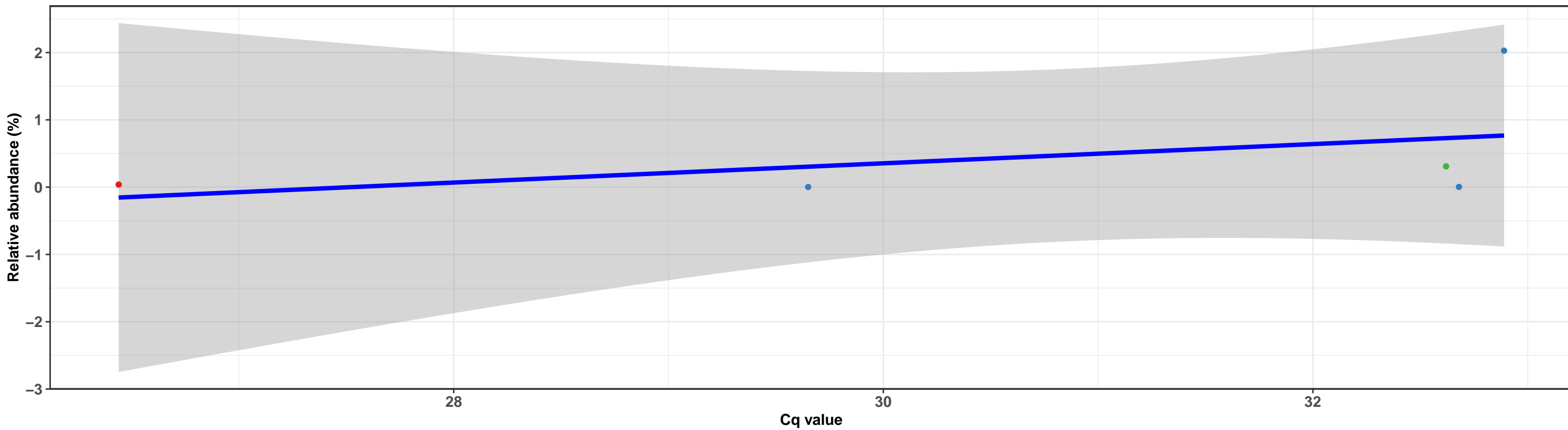


Correlation within: IM-DIM



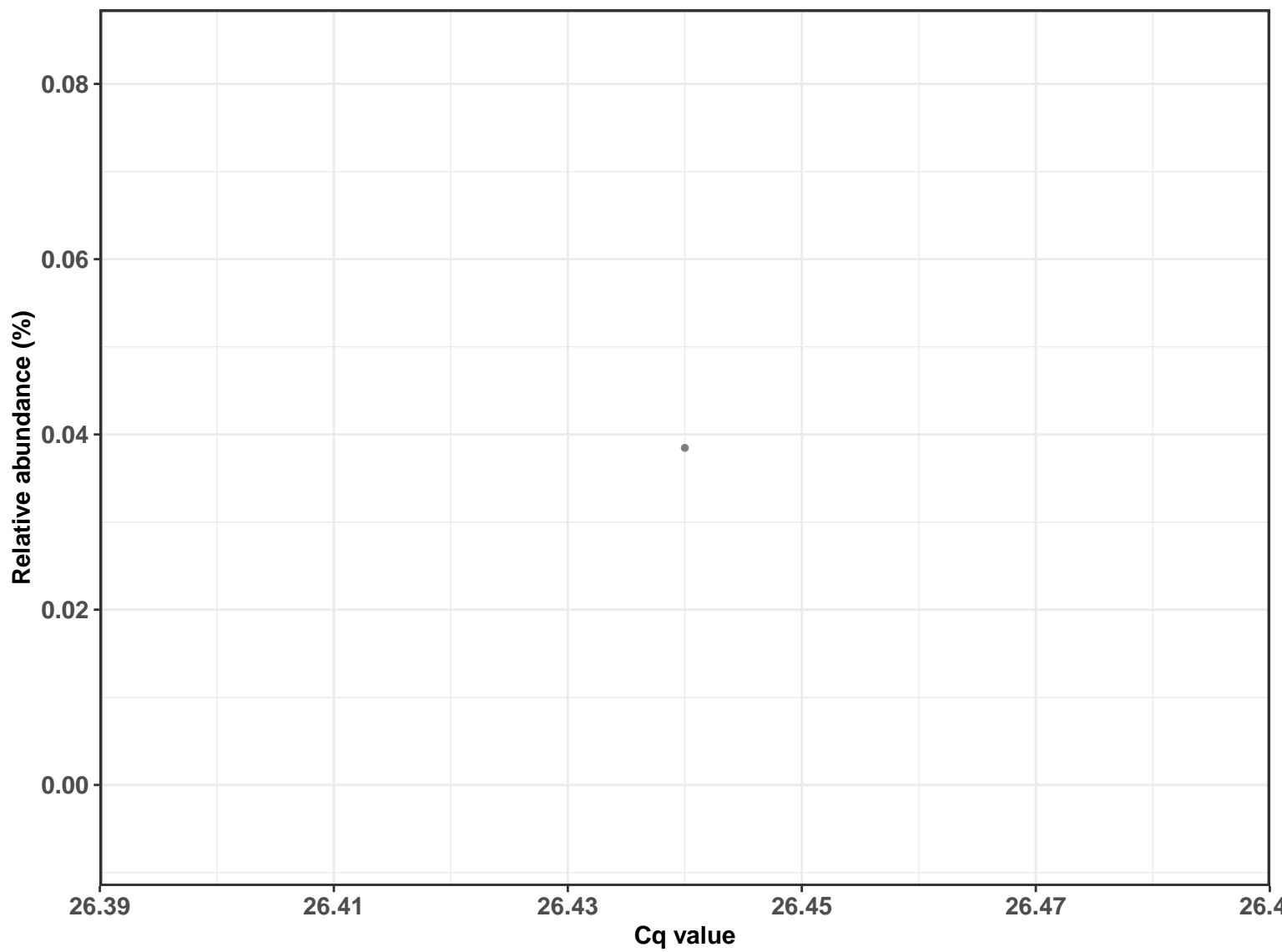
k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium

Correlation with all samples

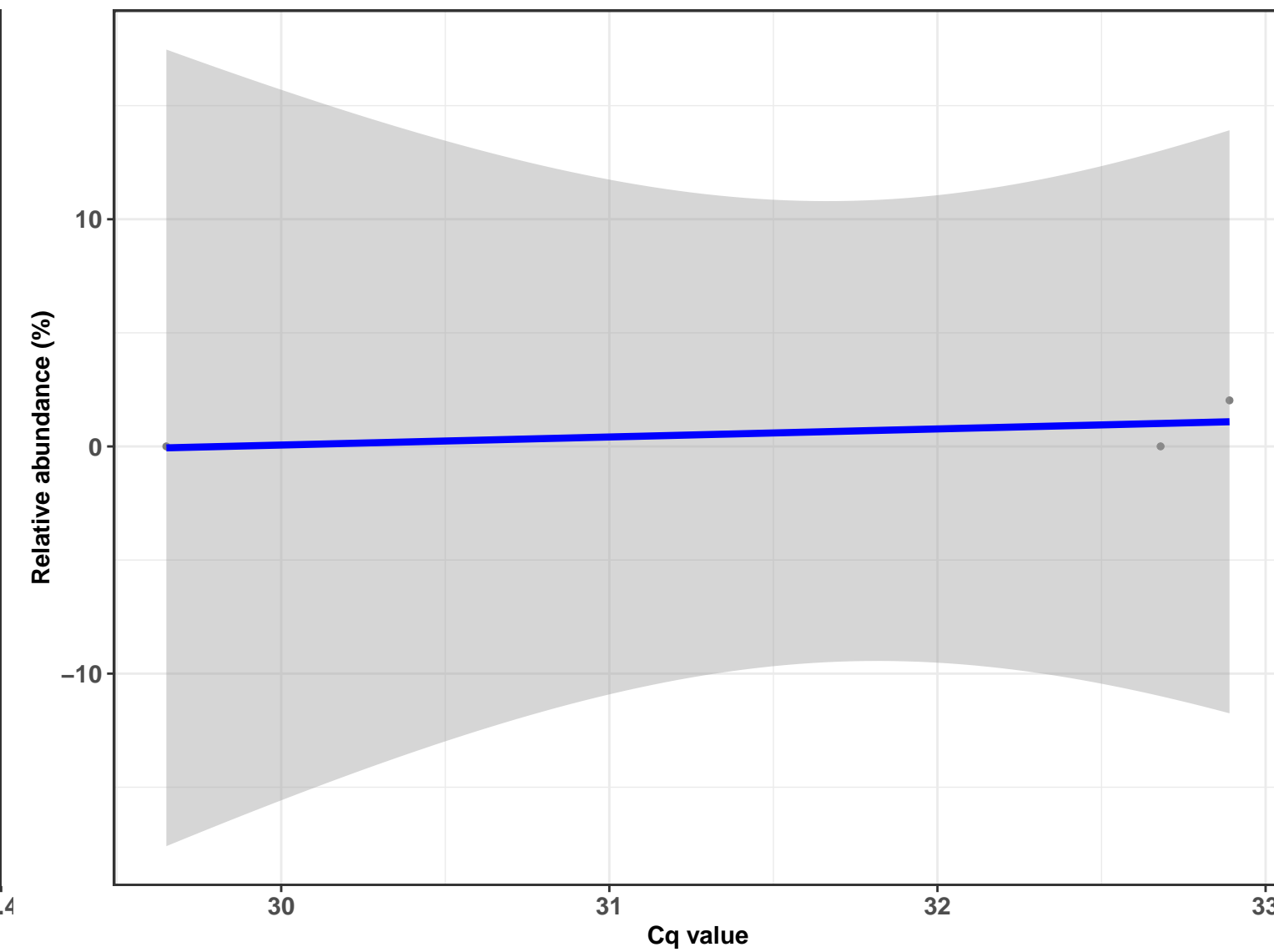


SampleType • REF-DID • IM-DIM • Extraction-blank

Correlation within: REF-DID

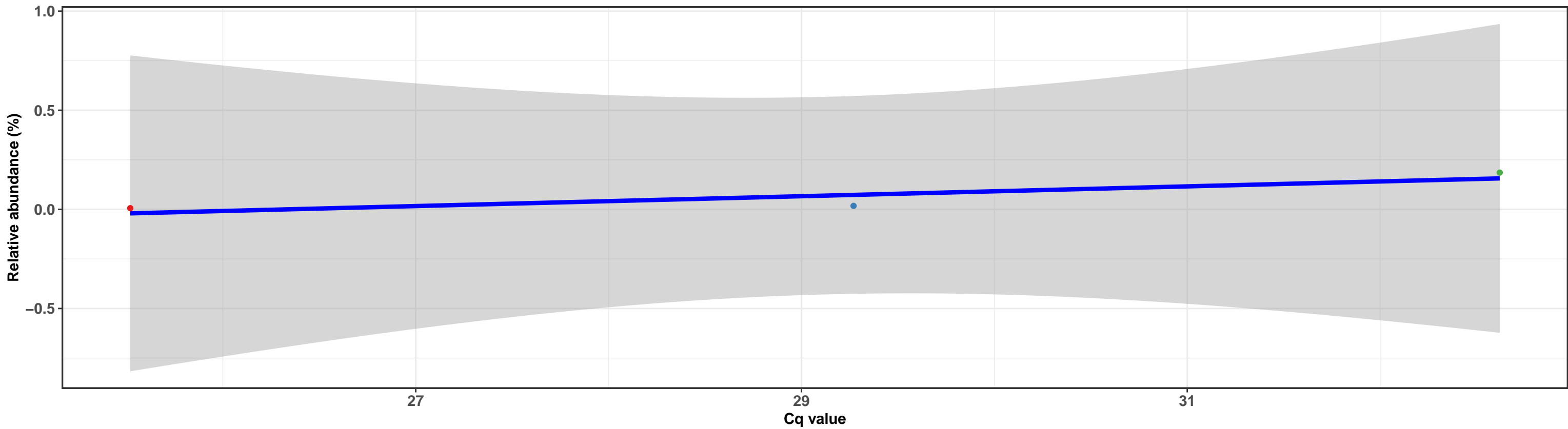


Correlation within: IM-DIM



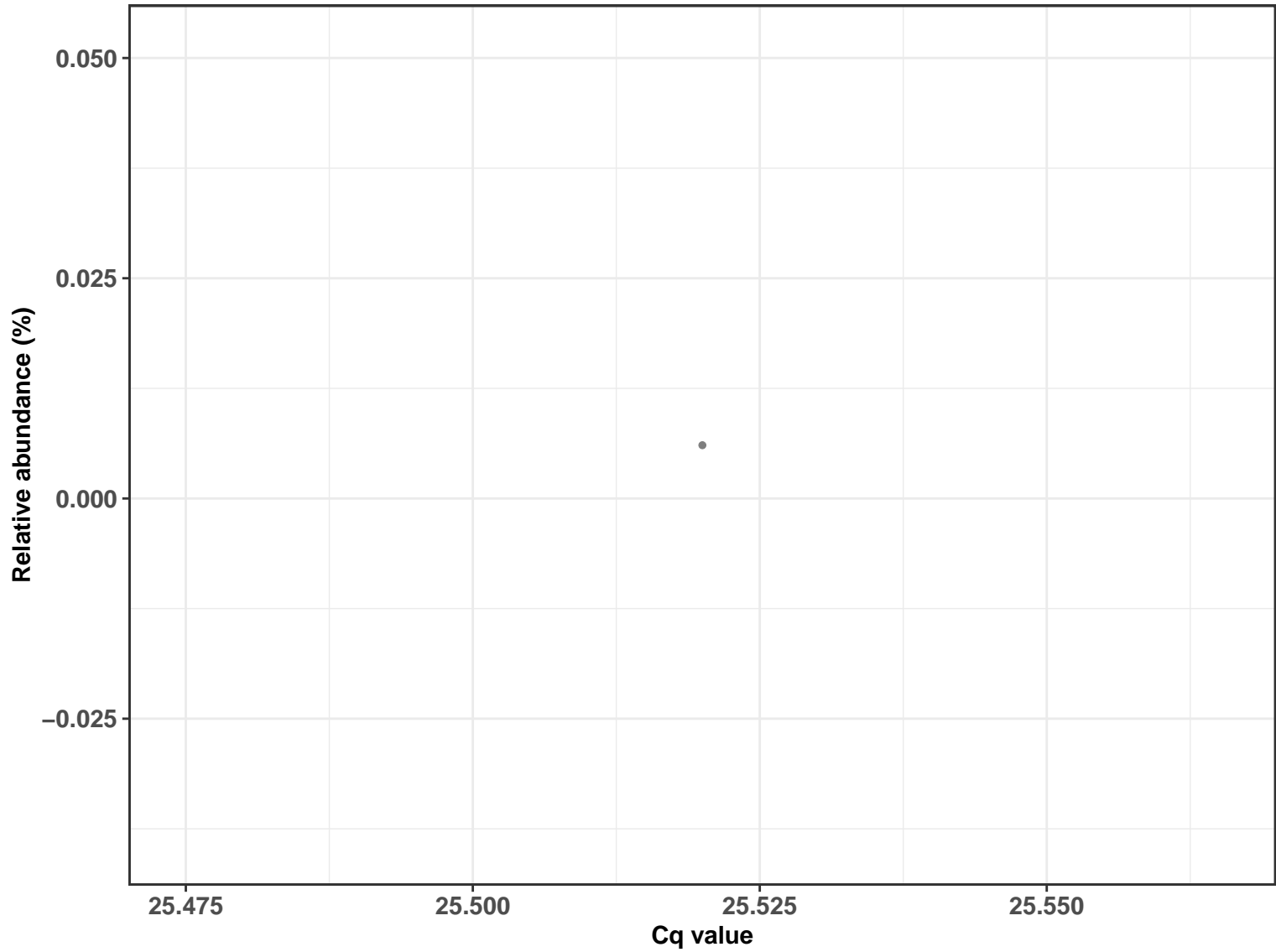
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Micrococcus; Ambiguous_taxa

Correlation with all samples

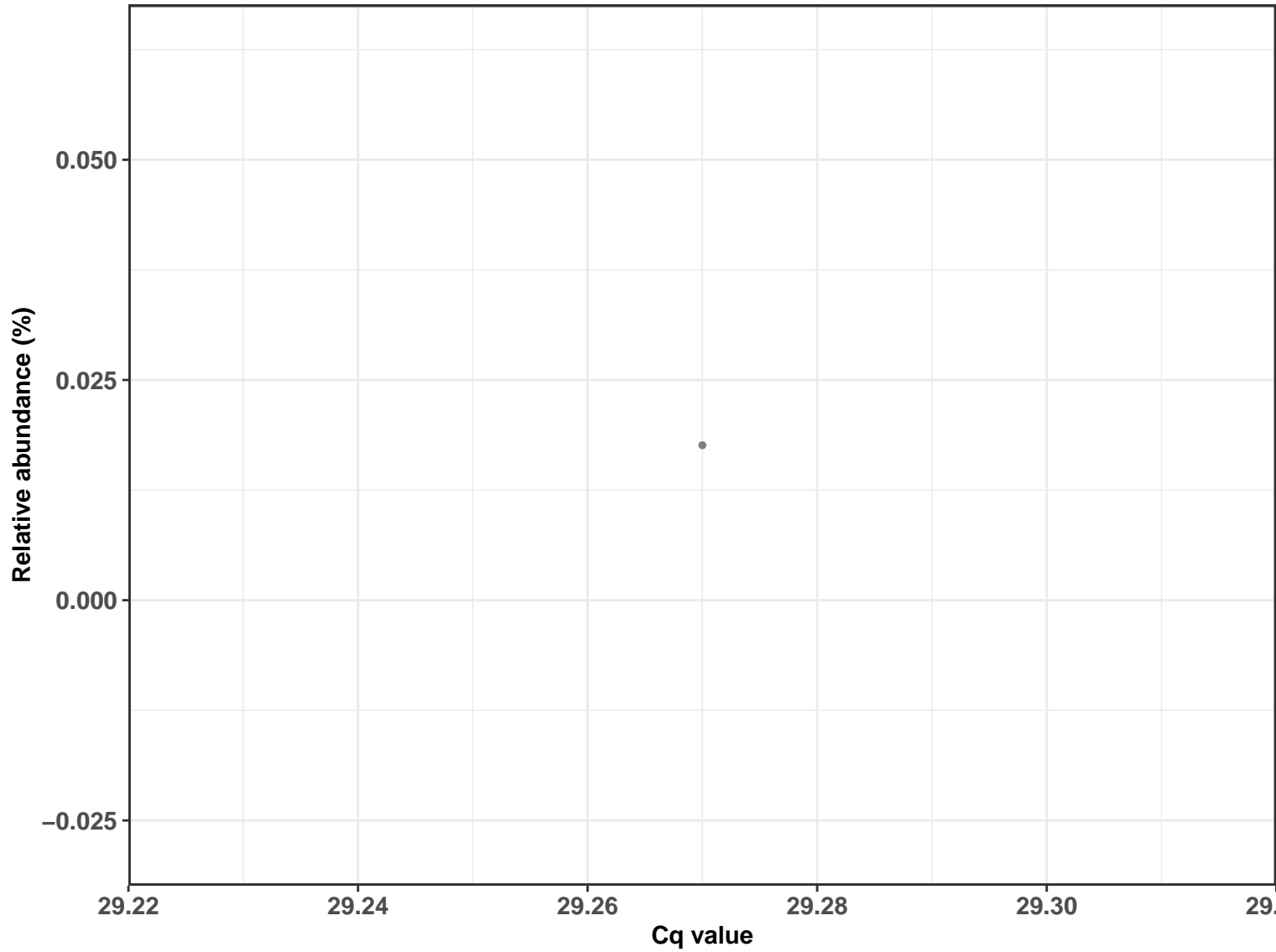


SampleType • REF-DID • IM-DID • Extraction-blank

Correlation within: REF-DID

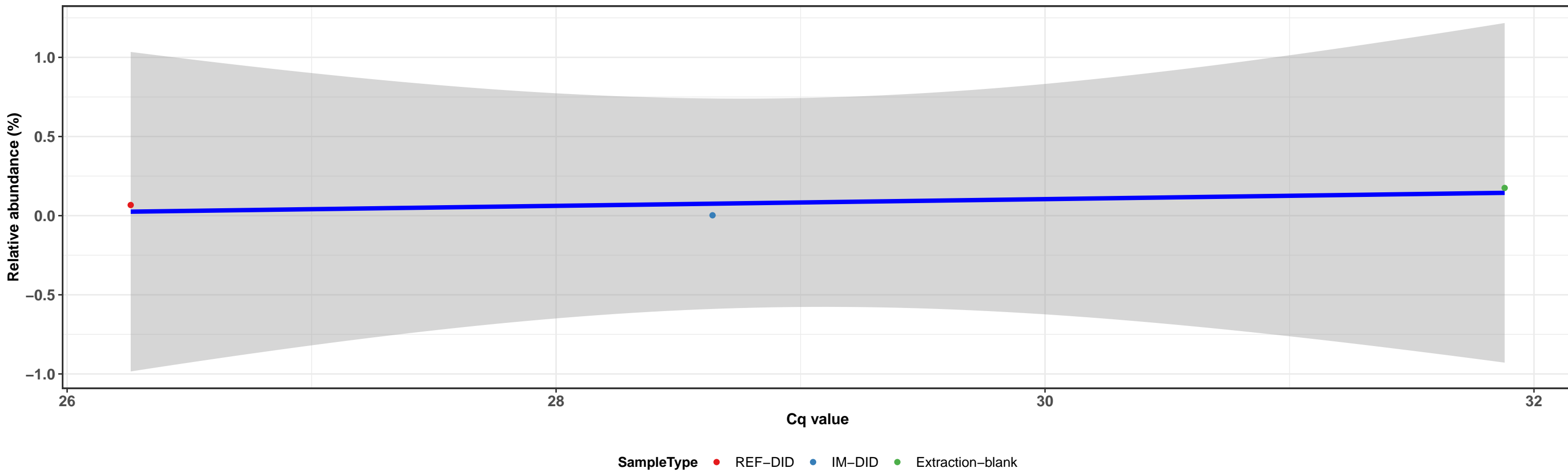


Correlation within: IM-DID

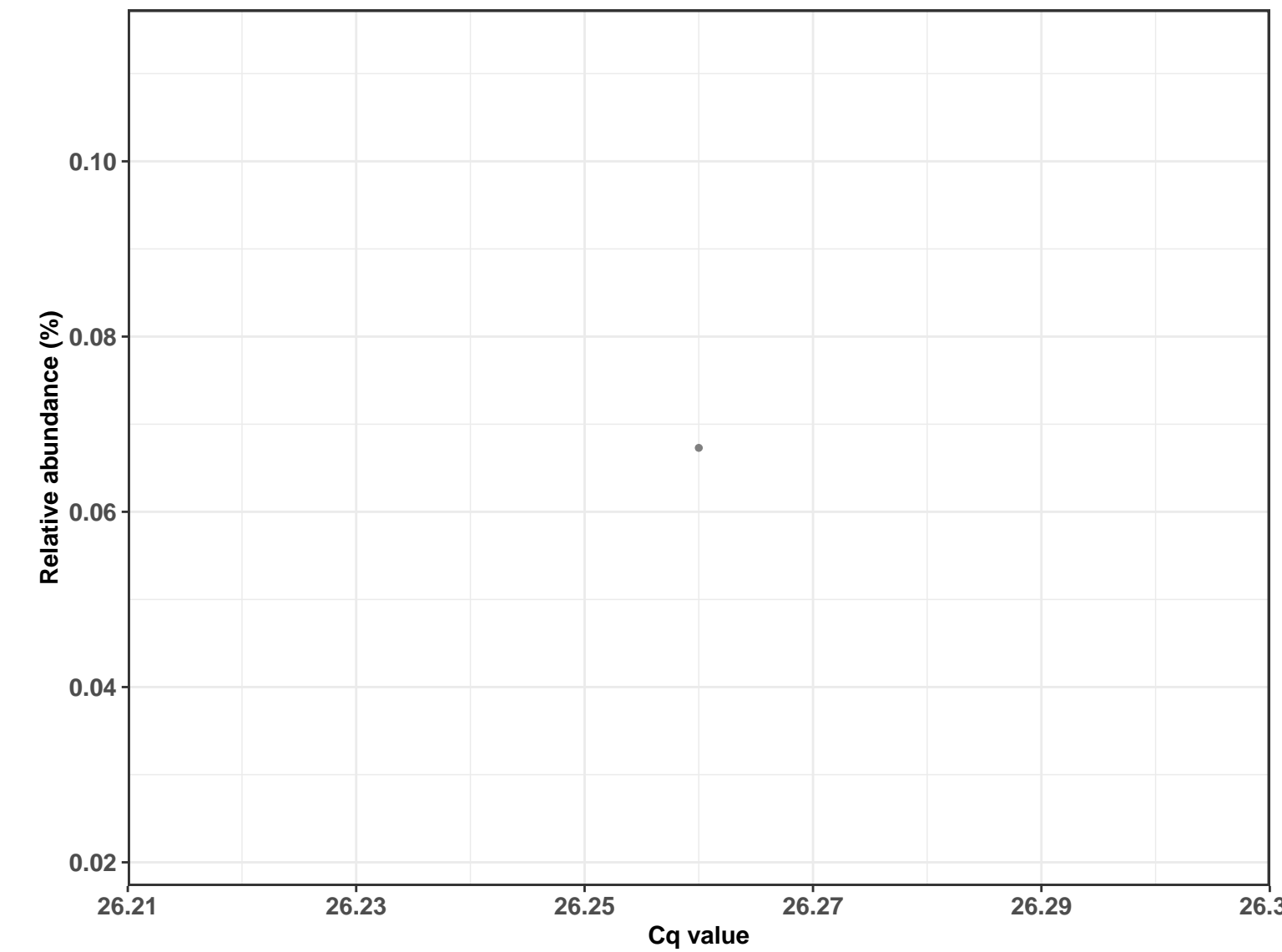


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium

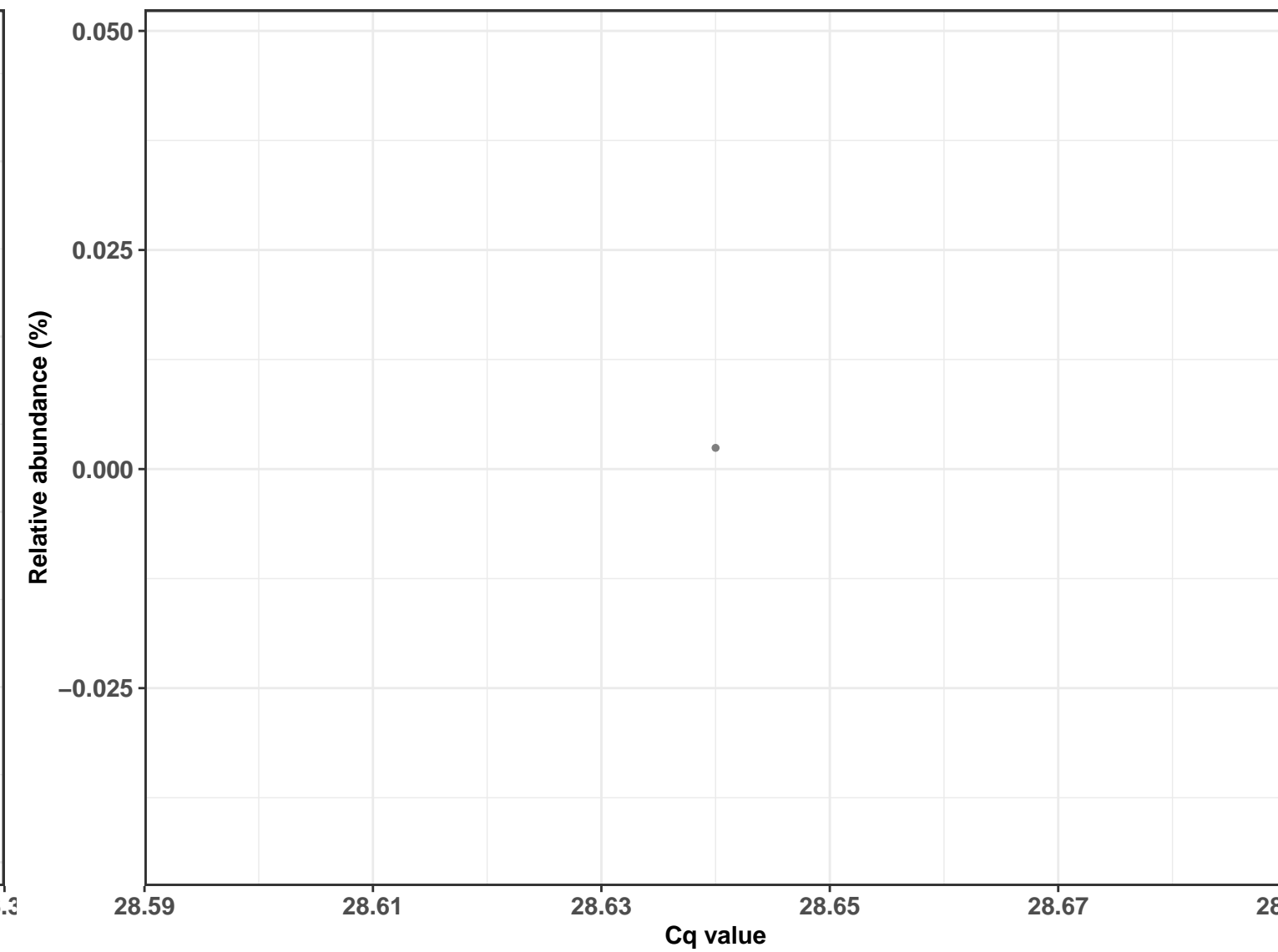
Correlation with all samples



Correlation within: REF-DID

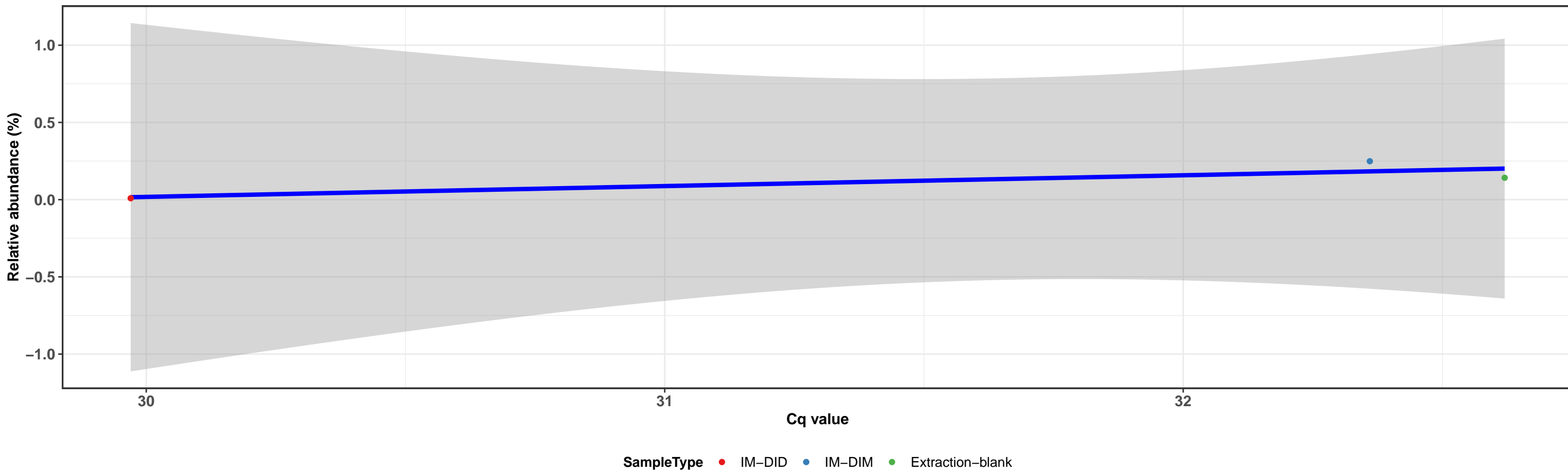


Correlation within: IM-DID

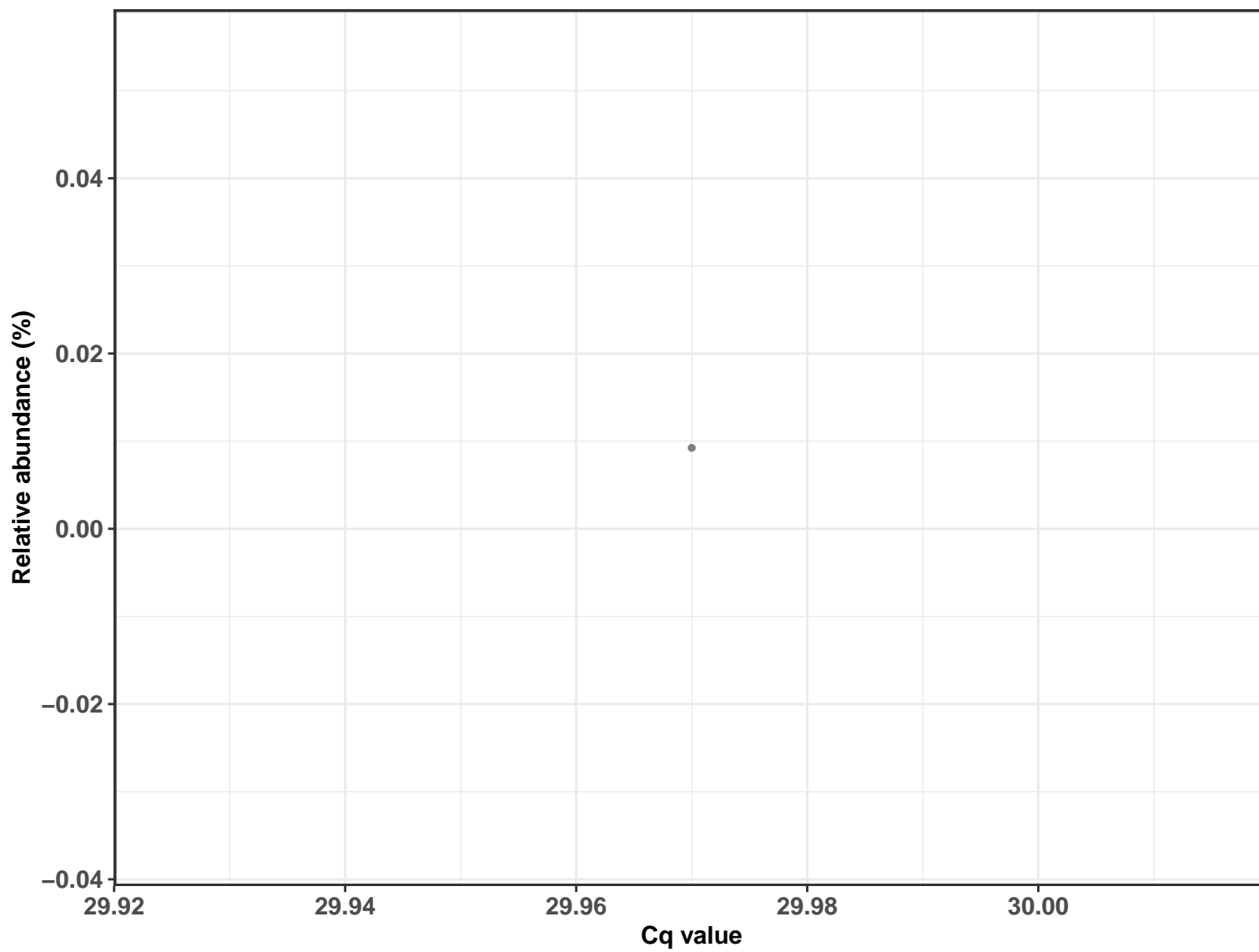


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; Ambiguous_taxa

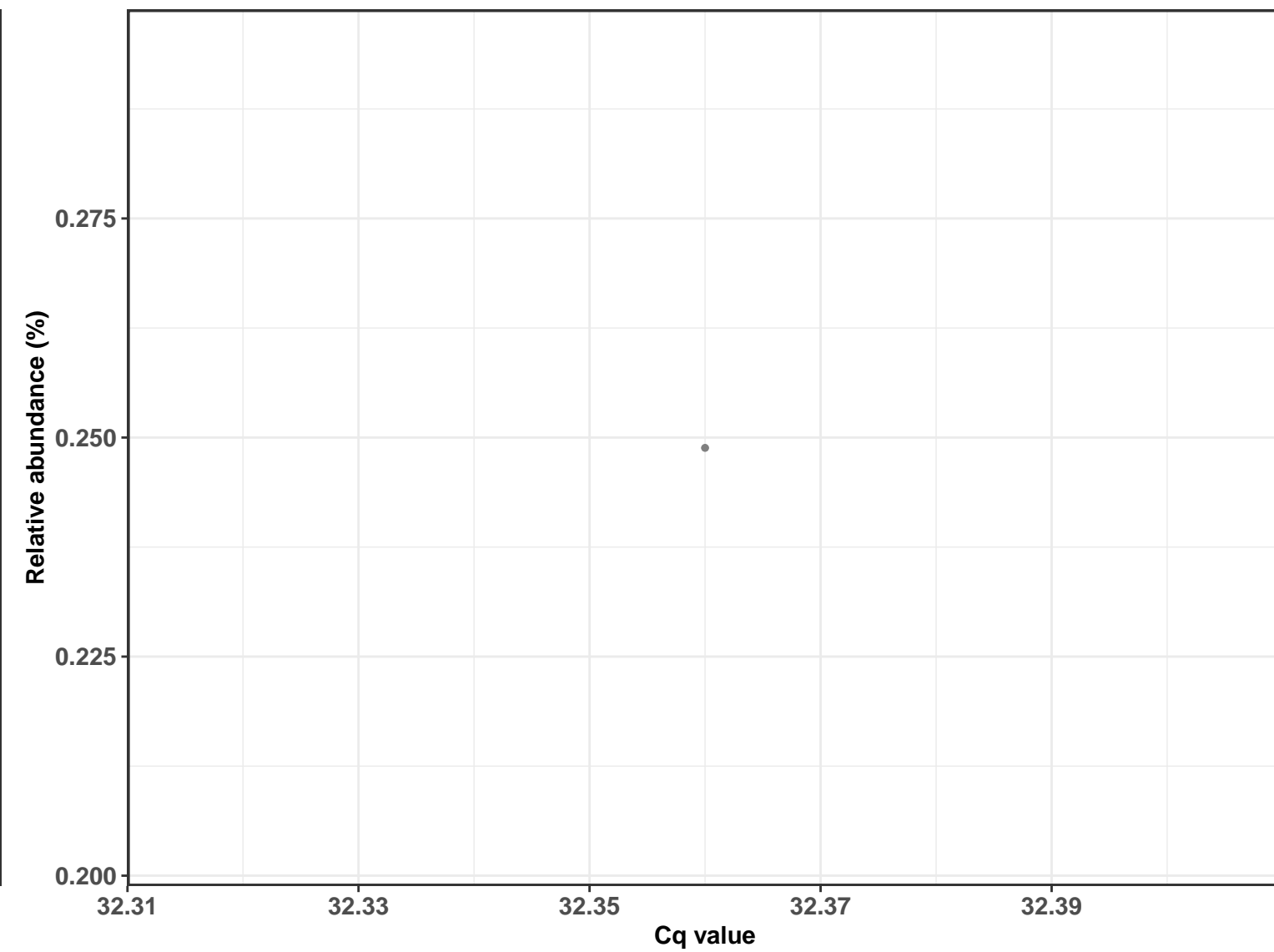
Correlation with all samples



Correlation within: IM-DID



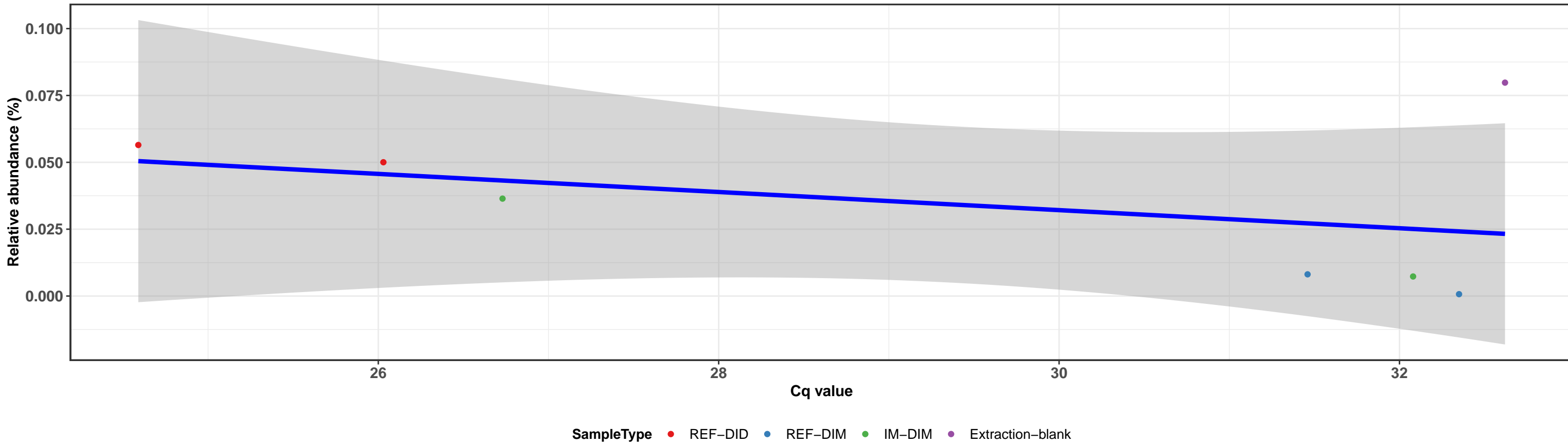
Correlation within: IM-DIM



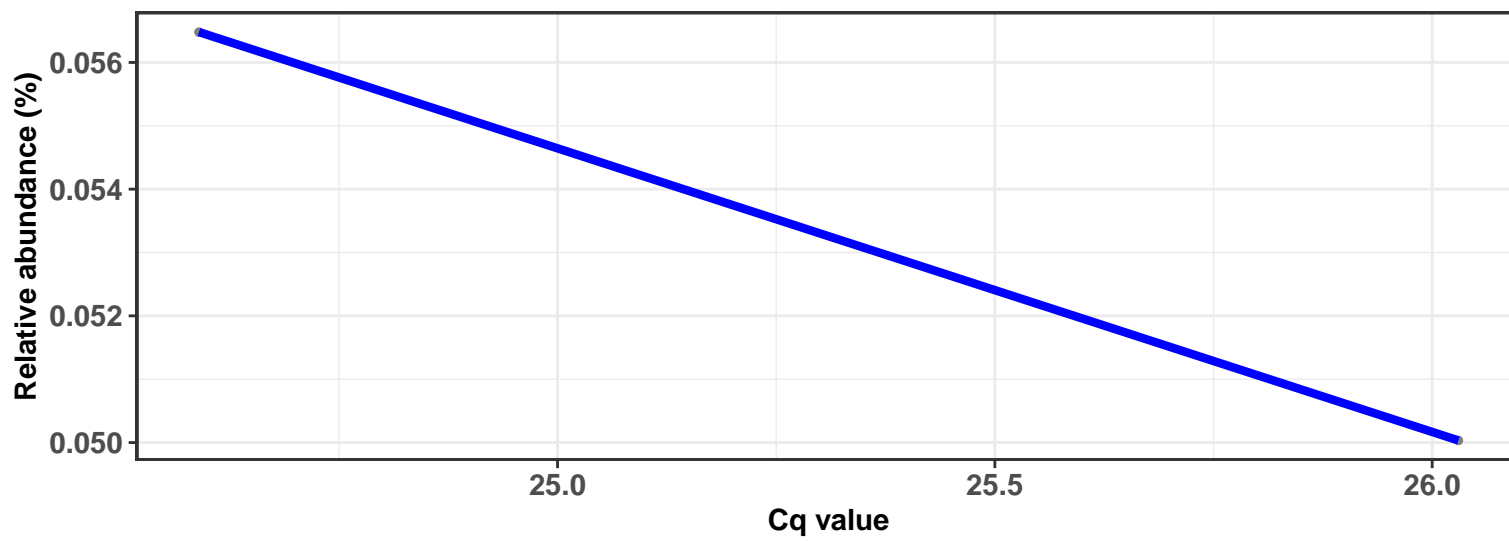
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; Ambiguous_taxa

Correlation with all samples

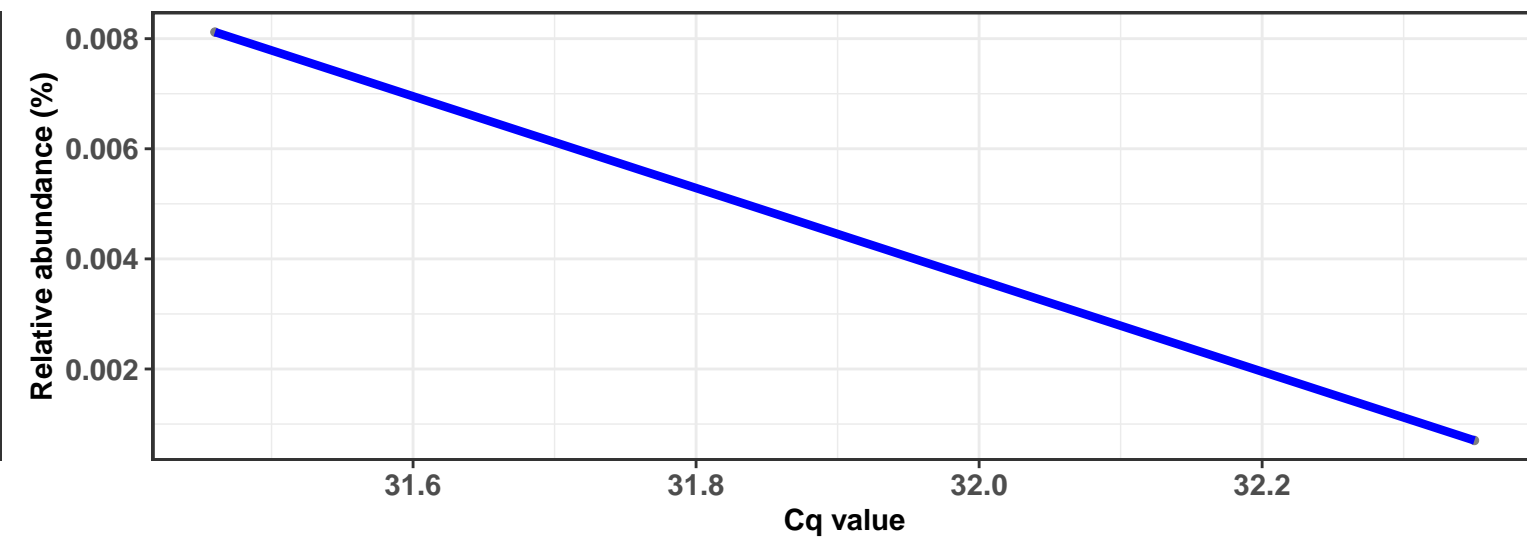
$\log_e(S) = 4.248$, $p = 0.589$, $\hat{\rho}_{\text{Spearman}} = -0.250$, $\text{CI}_{95\%} [-1.261, 0.907]$, $n_{\text{pairs}} = 7$



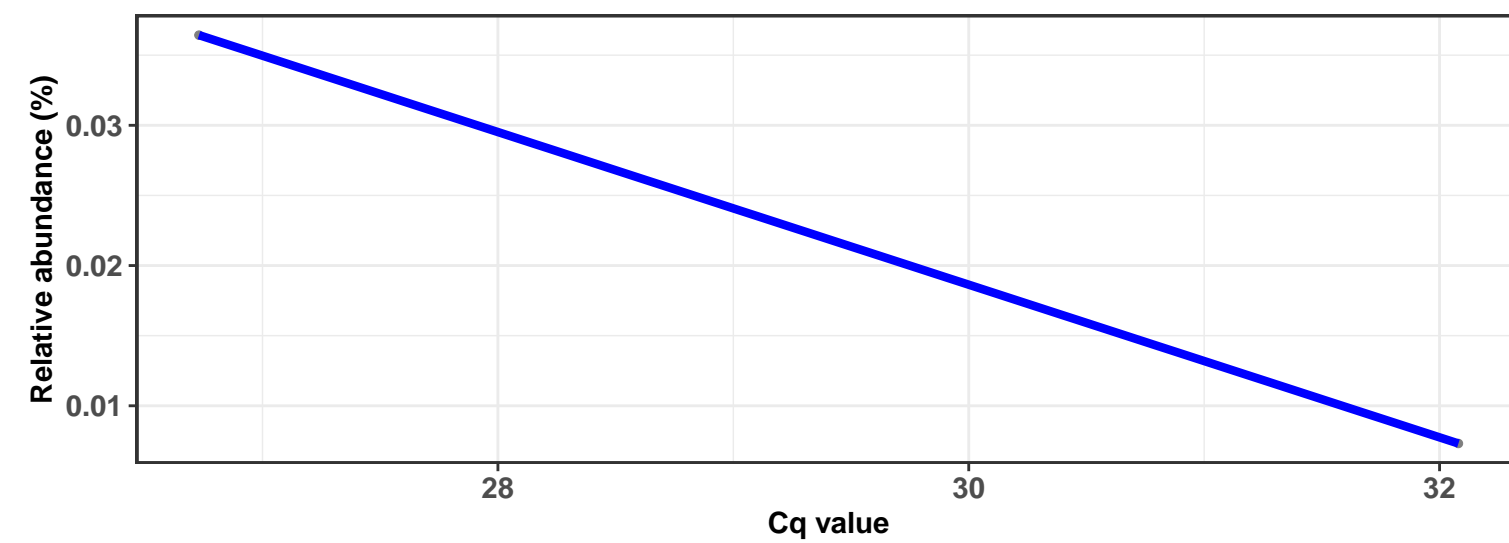
Correlation within: REF-DID



Correlation within: REF-DIM



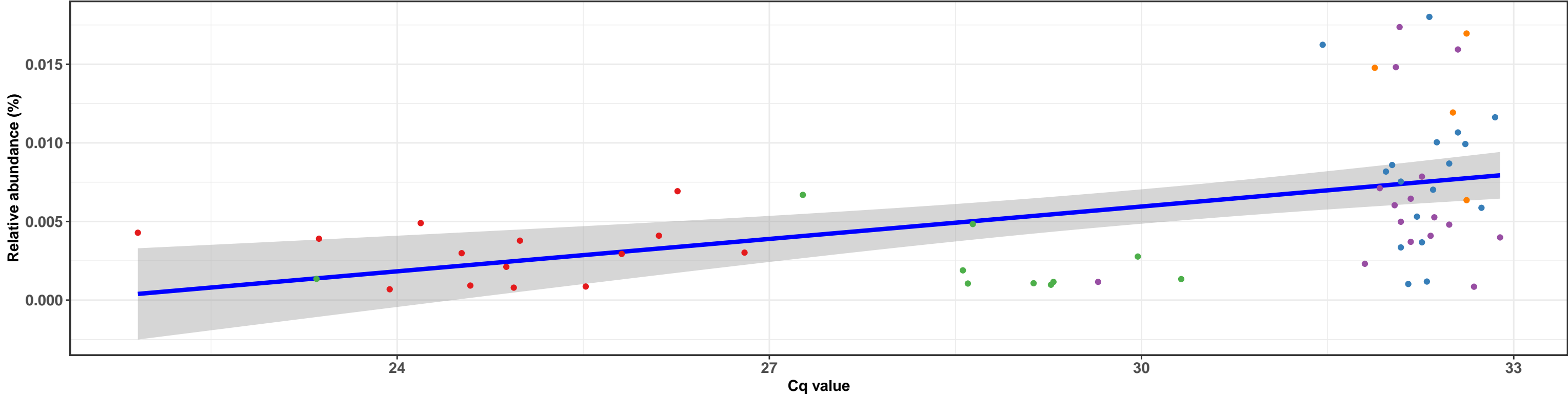
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

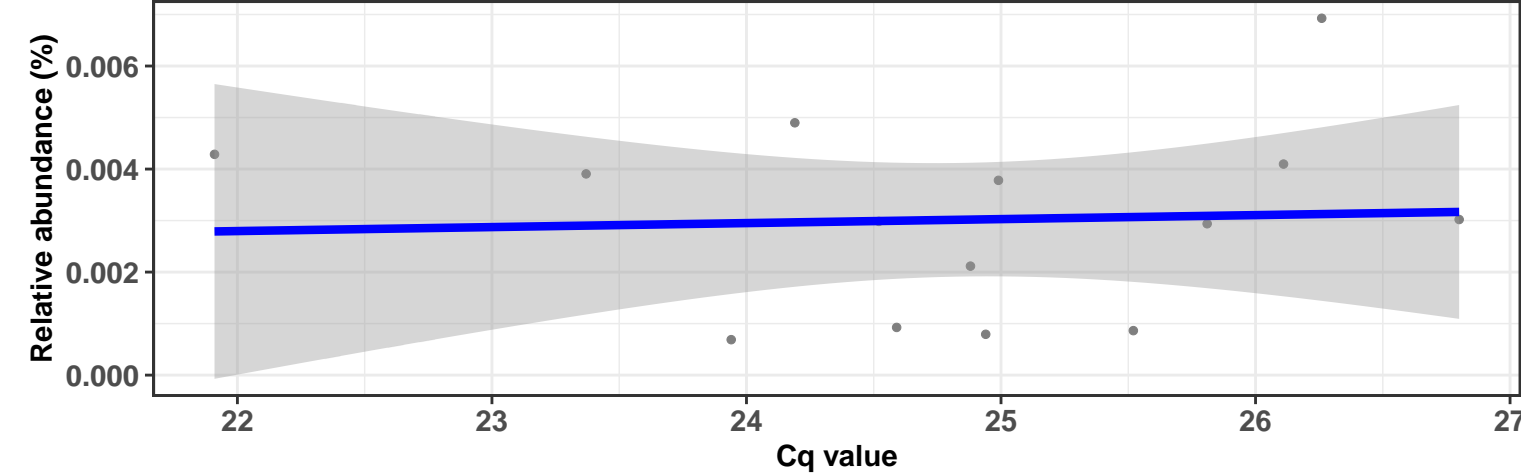
Correlation with all samples

$\log_e(S) = 9.840$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.504$, $\text{CI}_{95\%} [0.319, 0.675]$, $n_{\text{pairs}} = 61$



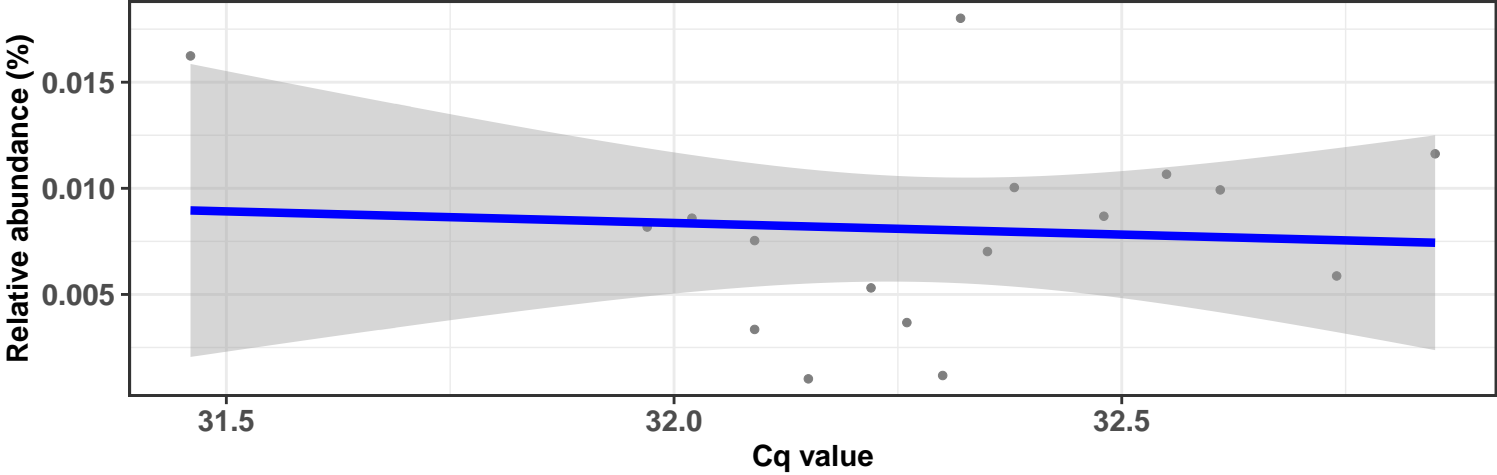
Correlation within: REF-DID

$\log_e(S) = 6.064$, $p = 0.852$, $\hat{\rho}_{\text{Spearman}} = 0.055$, $\text{CI}_{95\%} [-0.595, 0.722]$, $n_{\text{pairs}} = 14$



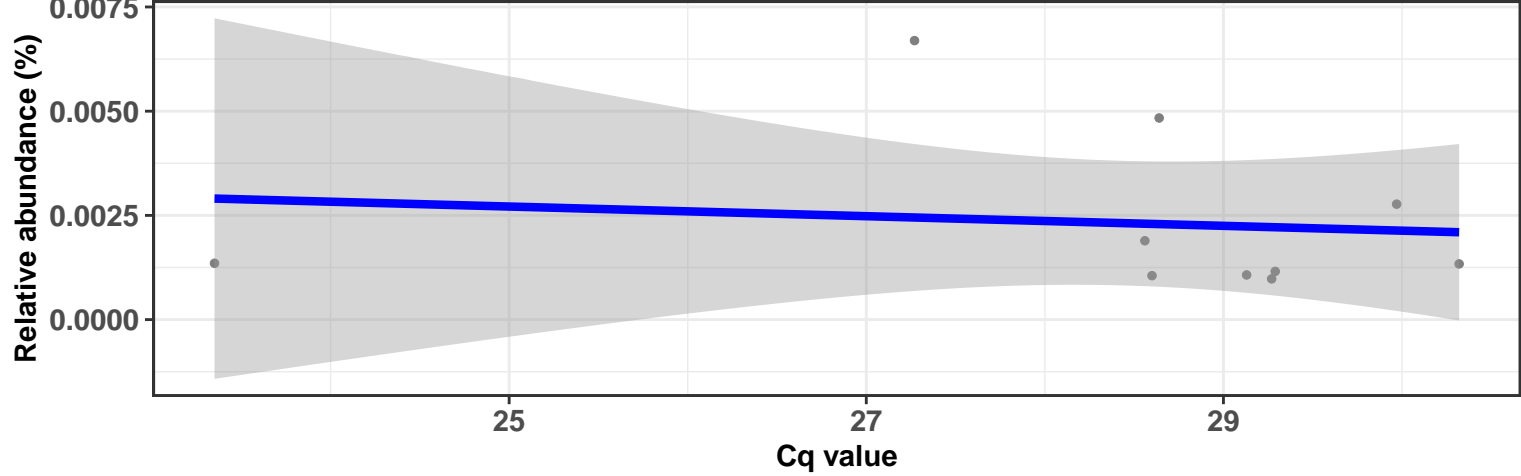
Correlation within: REF-DIM

$\log_e(S) = 6.421$, $p = 0.340$, $\hat{\rho}_{\text{Spearman}} = 0.246$, $\text{CI}_{95\%} [-0.166, 0.792]$, $n_{\text{pairs}} = 17$



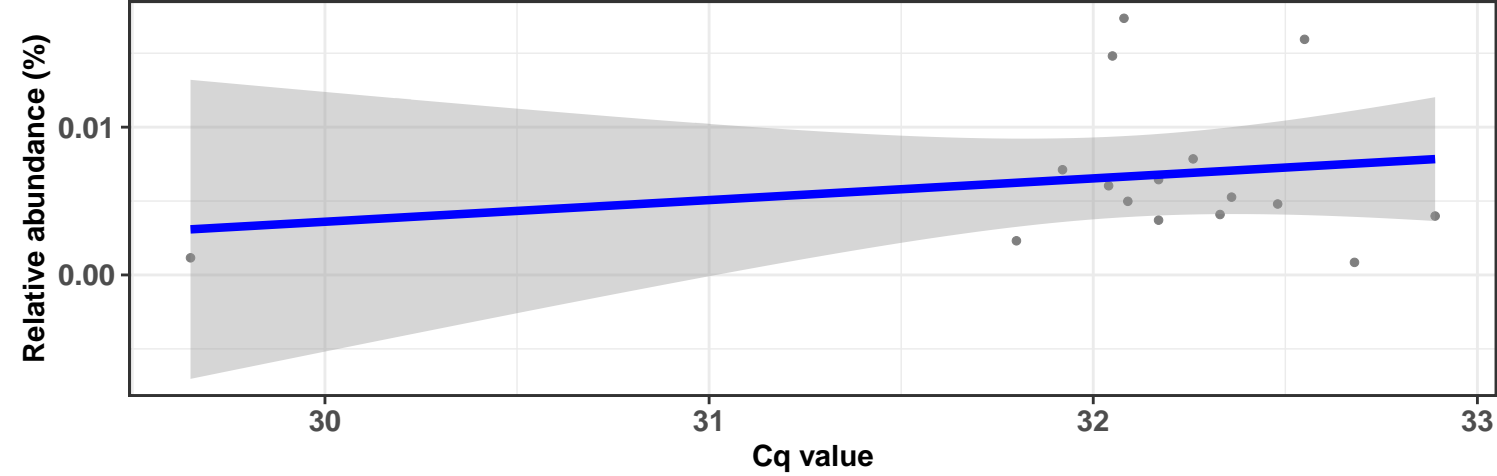
Correlation within: IM-DID

$\log_e(S) = 5.357$, $p = 0.425$, $\hat{\rho}_{\text{Spearman}} = -0.285$, $\text{CI}_{95\%} [-0.910, 0.300]$, $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

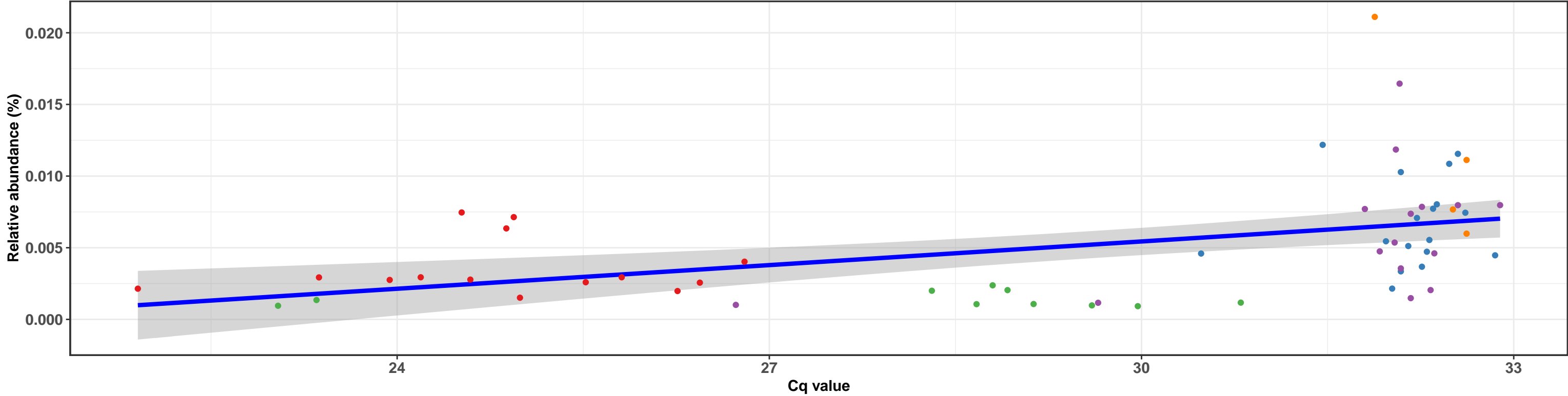
$\log_e(S) = 6.586$, $p = 0.807$, $\hat{\rho}_{\text{Spearman}} = -0.066$, $\text{CI}_{95\%} [-0.497, 0.596]$, $n_{\text{pairs}} = 16$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

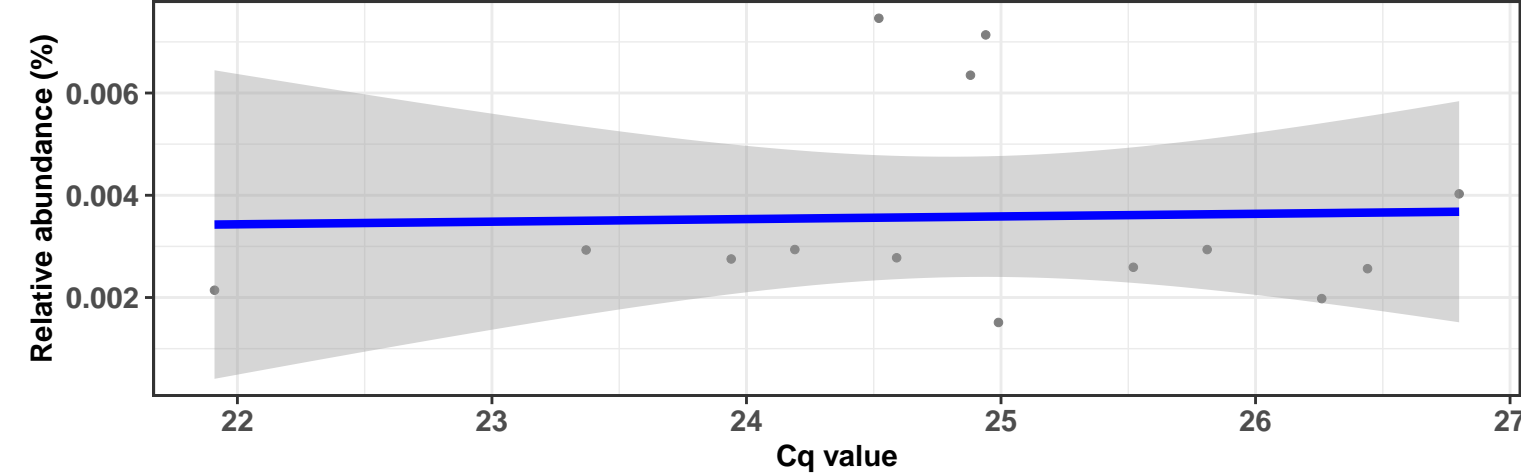
Correlation with all samples

$\log_e(S) = 9.676$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.557$, $\text{CI}_{95\%} [0.410, 0.709]$, $n_{\text{pairs}} = 60$



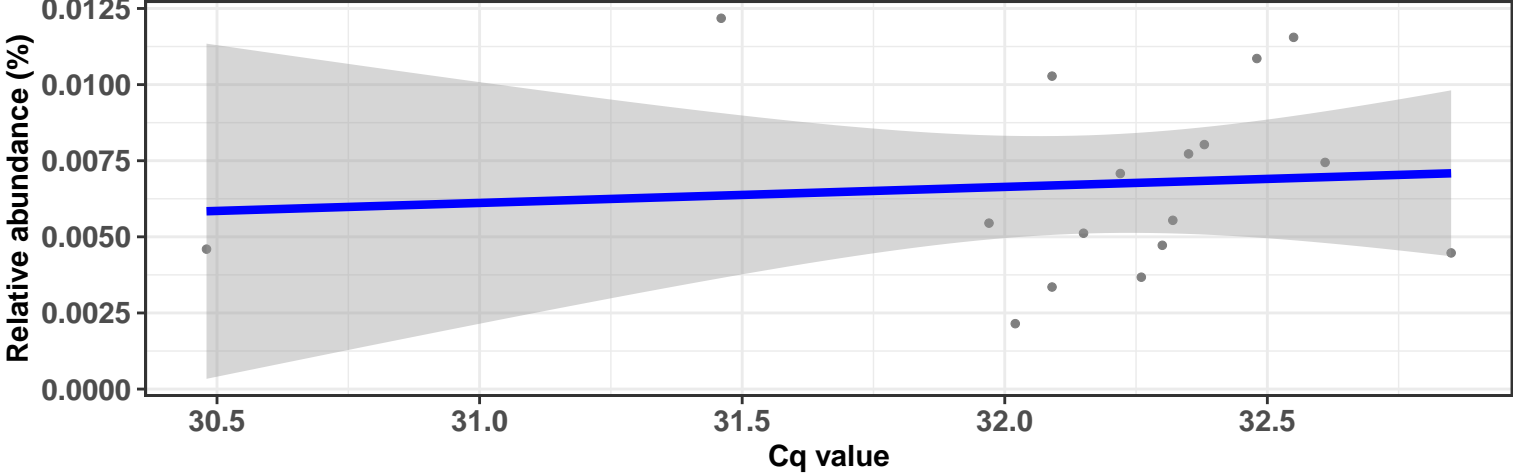
Correlation within: REF-DID

$\log_e(S) = 6.215$, $p = 0.737$, $\hat{\rho}_{\text{Spearman}} = -0.099$, $\text{CI}_{95\%} [-0.672, 0.470]$, $n_{\text{pairs}} = 14$



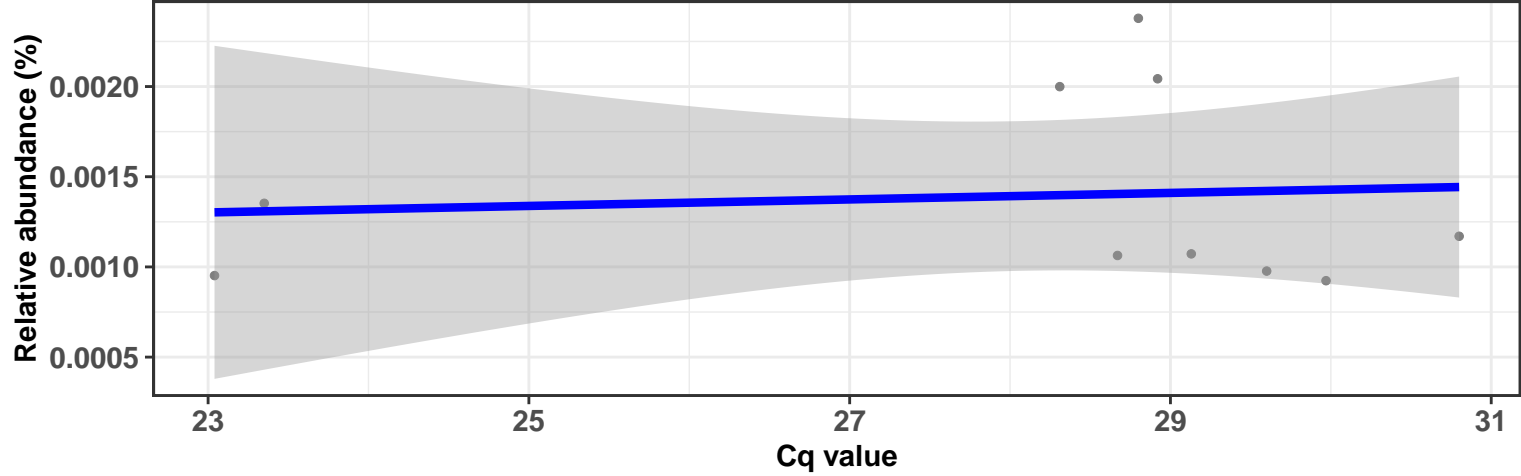
Correlation within: REF-DIM

$\log_e(S) = 6.423$, $p = 0.343$, $\hat{\rho}_{\text{Spearman}} = 0.245$, $\text{CI}_{95\%} [-0.328, 0.783]$, $n_{\text{pairs}} = 17$



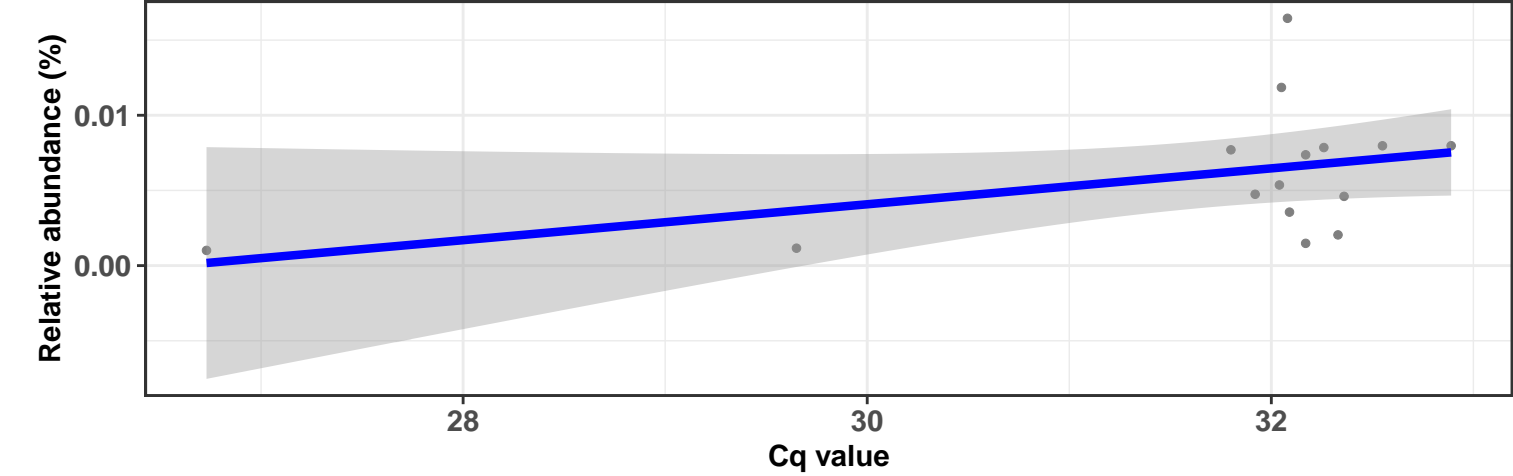
Correlation within: IM-DID

$\log_e(S) = 5.268$, $p = 0.627$, $\hat{\rho}_{\text{Spearman}} = -0.176$, $\text{CI}_{95\%} [-0.912, 0.466]$, $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

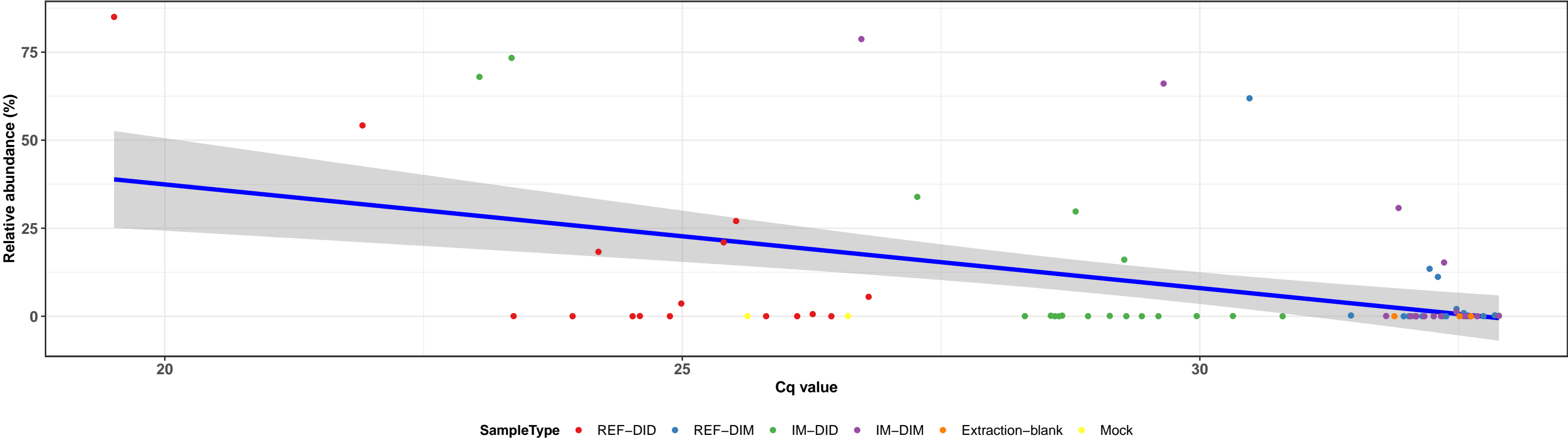
$\log_e(S) = 5.908$, $p = 0.210$, $\hat{\rho}_{\text{Spearman}} = 0.343$, $\text{CI}_{95\%} [-0.240, 0.843]$, $n_{\text{pairs}} = 15$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium

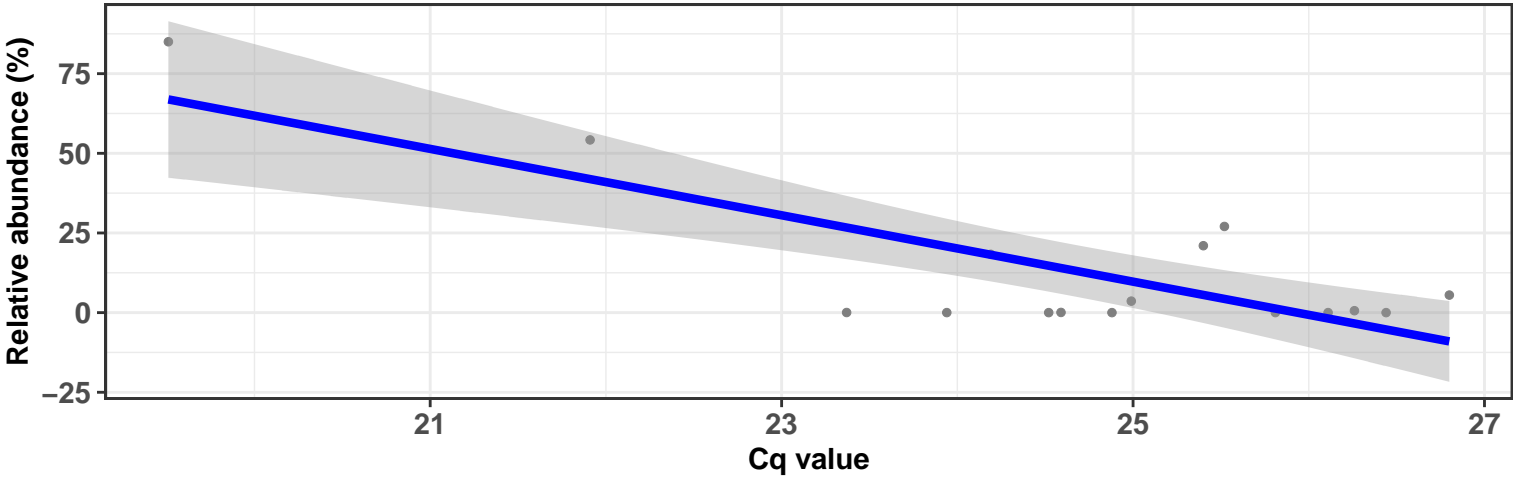
Correlation with all samples

$\log_e(S) = 11.335$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = -0.291$, $\text{CI}_{95\%} [-0.527, -0.095]$, $n_{\text{pairs}} = 73$



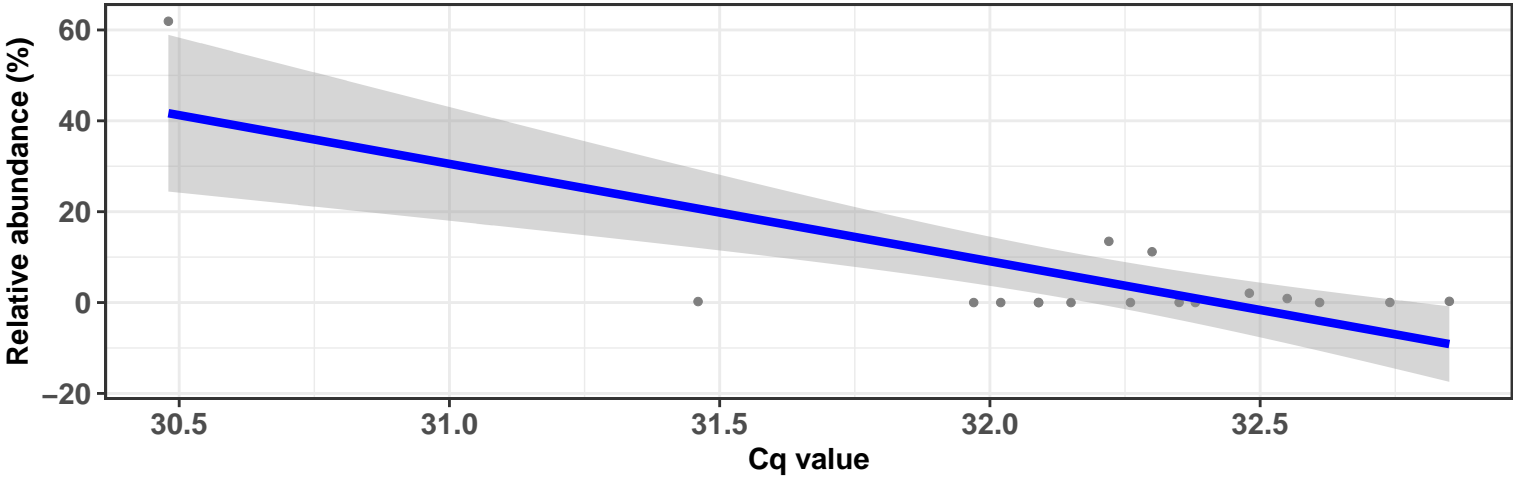
Correlation within: REF-DID

$\log_e(S) = 6.764$, $p = 0.305$, $\hat{\rho}_{\text{Spearman}} = -0.274$, $\text{CI}_{95\%} [-0.785, 0.195]$, $n_{\text{pairs}} = 16$



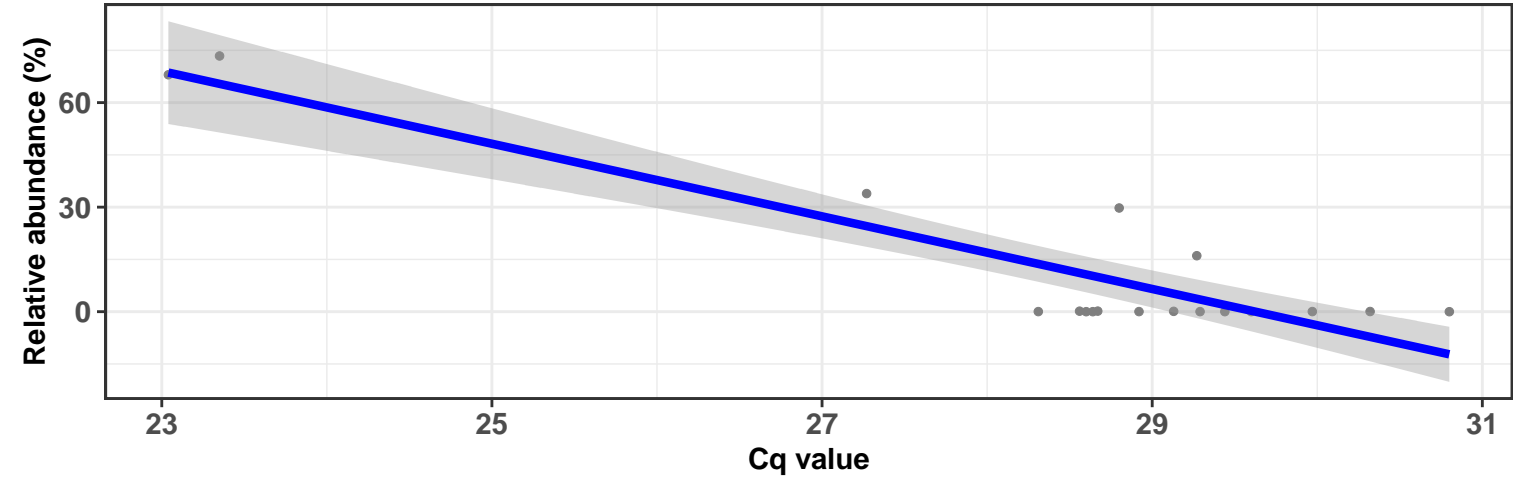
Correlation within: REF-DIM

$\log_e(S) = 6.525$, $p = 0.529$, $\hat{\rho}_{\text{Spearman}} = 0.164$, $\text{CI}_{95\%} [-0.384, 0.657]$, $n_{\text{pairs}} = 17$



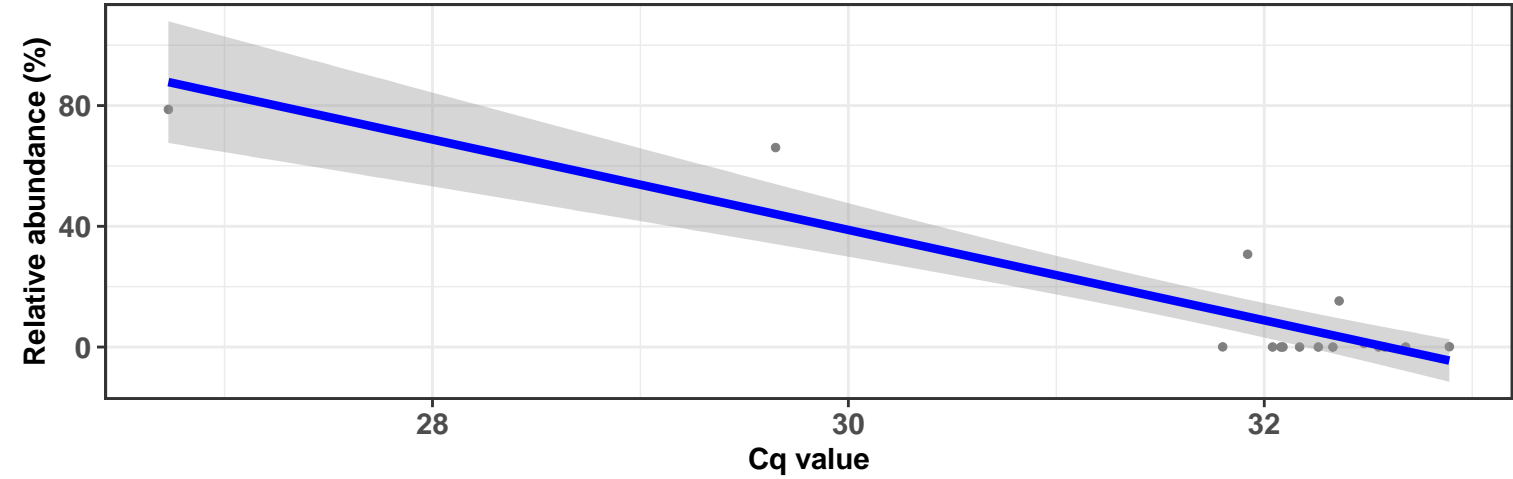
Correlation within: IM-DID

$\log_e(S) = 7.297$, $p = 0.026$, $\hat{\rho}_{\text{Spearman}} = -0.523$, $\text{CI}_{95\%} [-0.926, -0.166]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

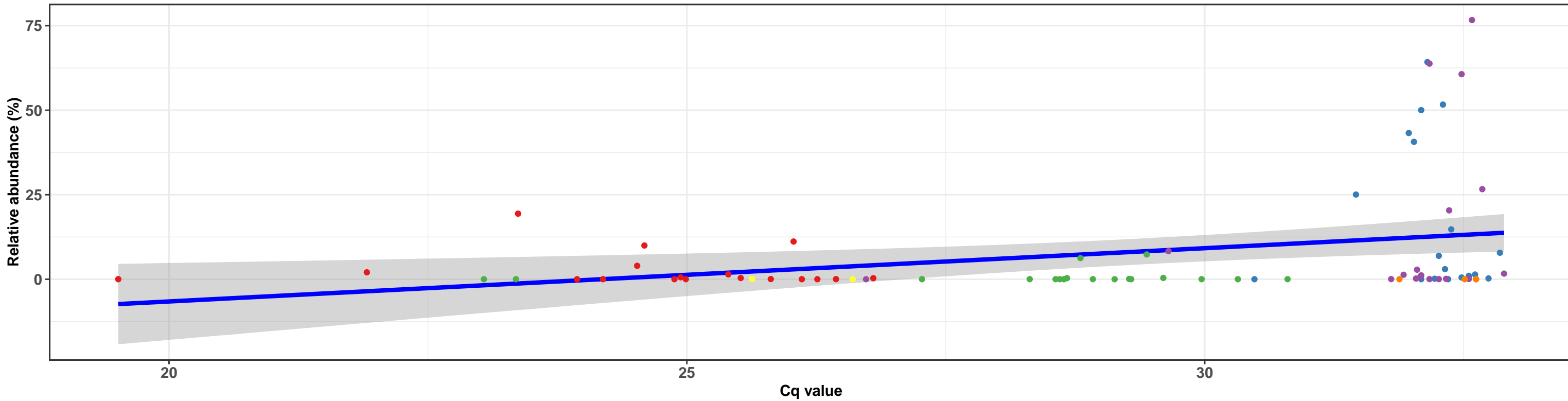
$\log_e(S) = 6.859$, $p = 0.125$, $\hat{\rho}_{\text{Spearman}} = -0.400$, $\text{CI}_{95\%} [-0.887, 0.105]$, $n_{\text{pairs}} = 16$



k__Bacteria; p__Spirochaetes; c__Spirochaetia; o__Brevinematales; f__Brevinemataceae; g__Brevinema; s__Brevinema andersonii

Correlation with all samples

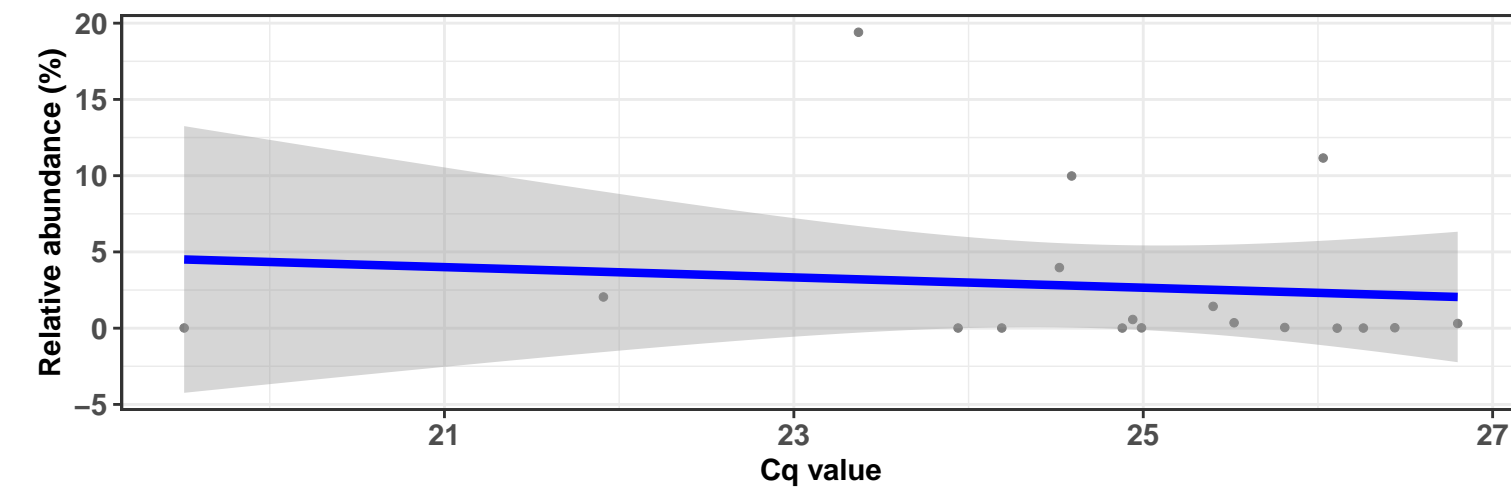
$\log_e(S) = 10.883$, $p = 0.004$, $\hat{\rho}_{\text{Spearman}} = 0.326$, $\text{CI}_{95\%} [0.122, 0.531]$, $n_{\text{pairs}} = 78$



SampleType REF-DID REF-DIM IM-DID IM-DIM Extraction-blank Mock

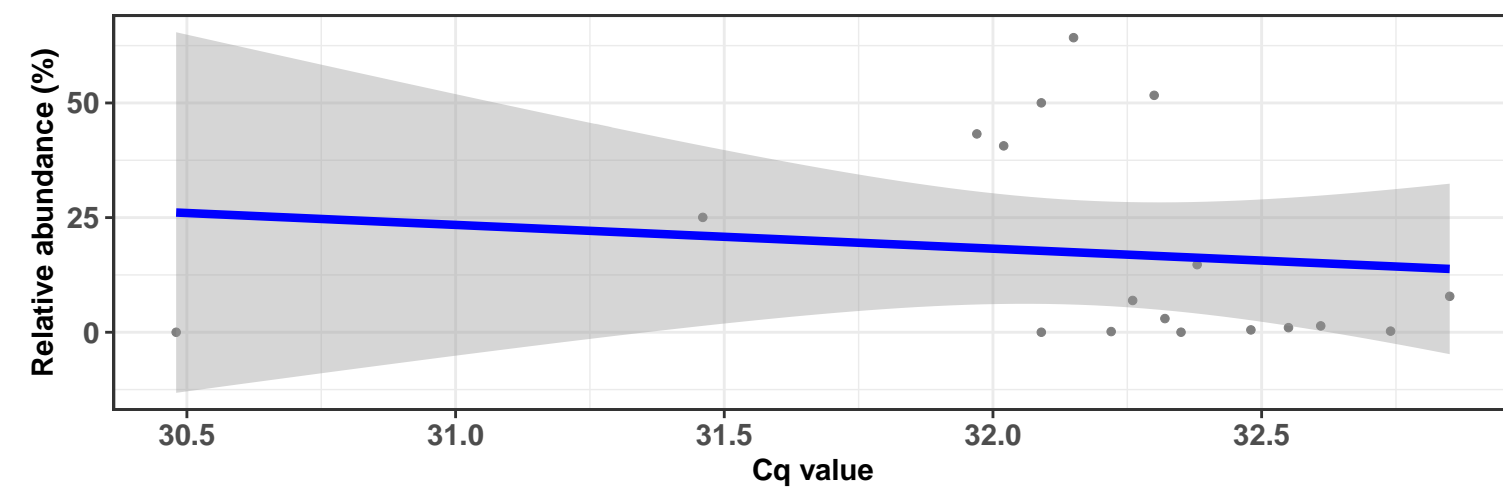
Correlation within: REF-DID

$\log_e(S) = 7.063$, $p = 0.414$, $\hat{\rho}_{\text{Spearman}} = -0.205$, $\text{CI}_{95\%} [-0.748, 0.250]$, $n_{\text{pairs}} = 18$



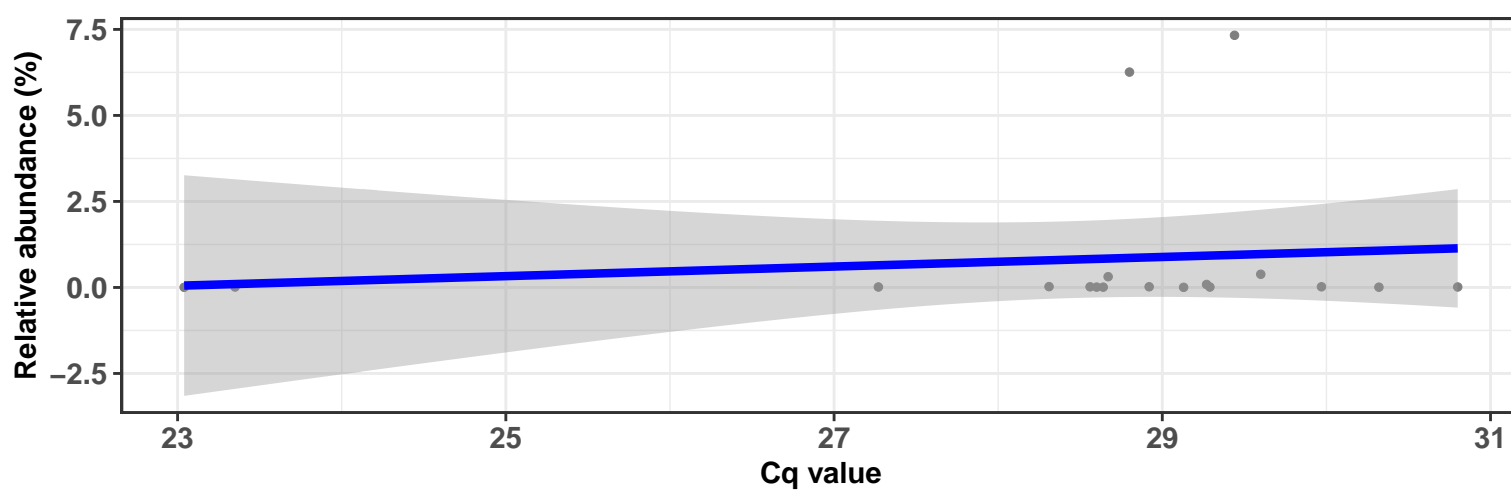
Correlation within: REF-DIM

$\log_e(S) = 7.044$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = -0.183$, $\text{CI}_{95\%} [-0.655, 0.308]$, $n_{\text{pairs}} = 18$



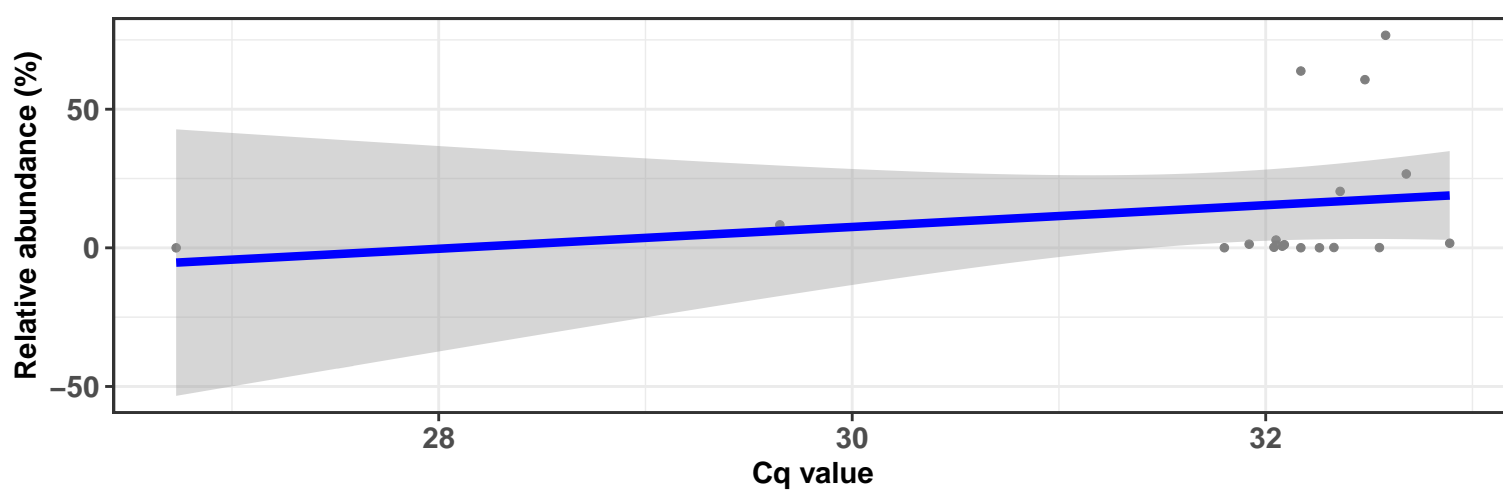
Correlation within: IM-DID

$\log_e(S) = 6.631$, $p = 0.385$, $\hat{\rho}_{\text{Spearman}} = 0.218$, $\text{CI}_{95\%} [-0.163, 0.671]$, $n_{\text{pairs}} = 18$



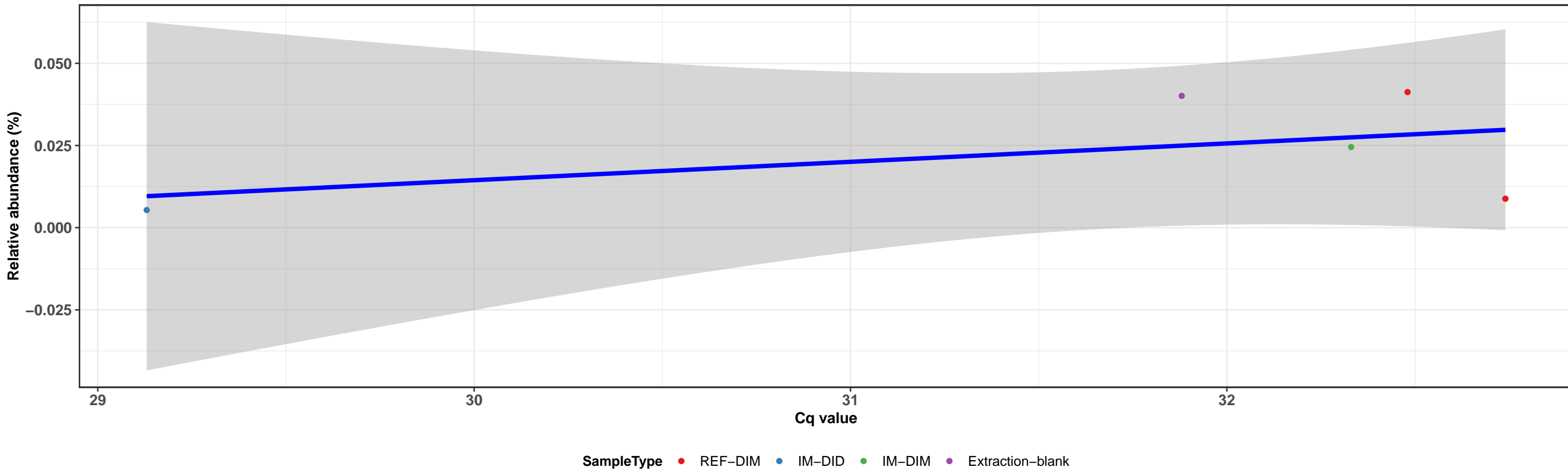
Correlation within: IM-DIM

$\log_e(S) = 6.359$, $p = 0.097$, $\hat{\rho}_{\text{Spearman}} = 0.404$, $\text{CI}_{95\%} [-0.017, 0.864]$, $n_{\text{pairs}} = 18$

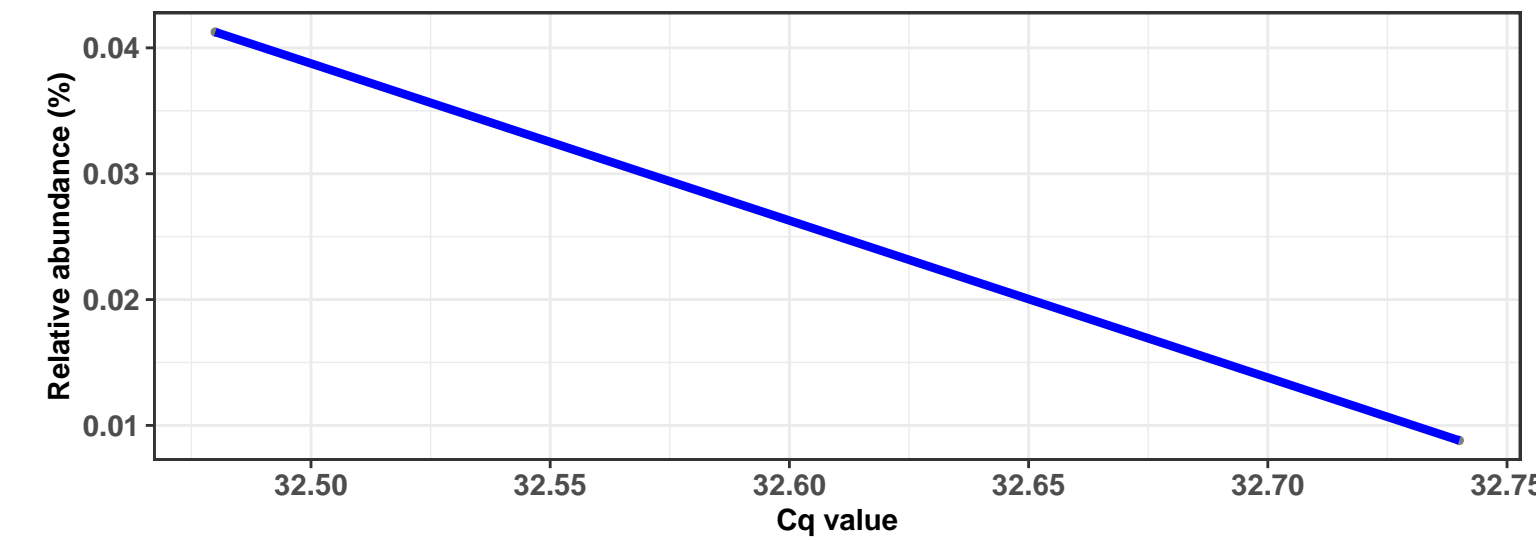


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Devosiaceae; g__Devosia; NA

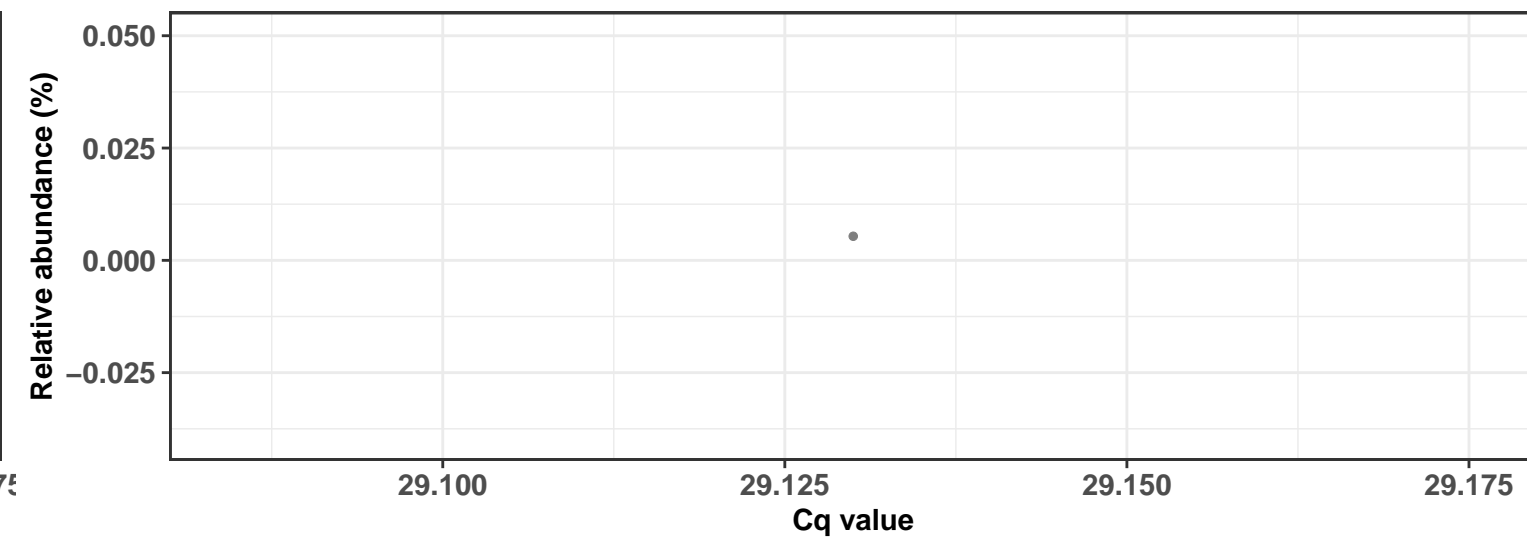
Correlation with all samples



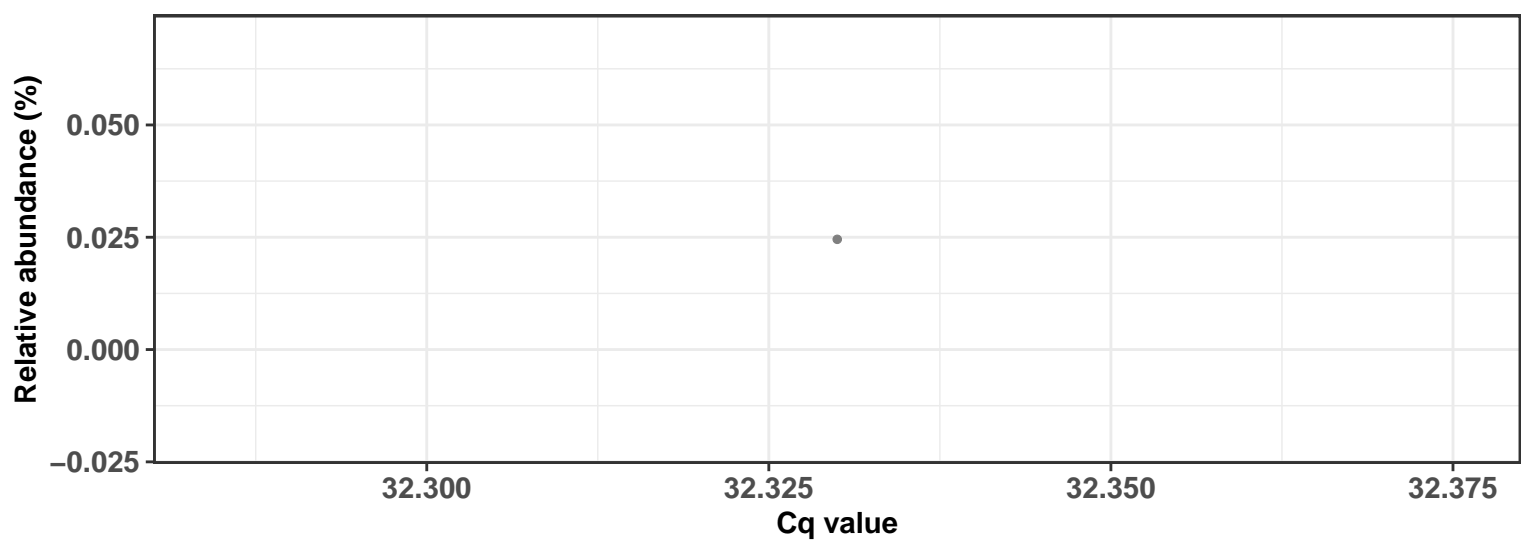
Correlation within: REF-DIM



Correlation within: IM-DID



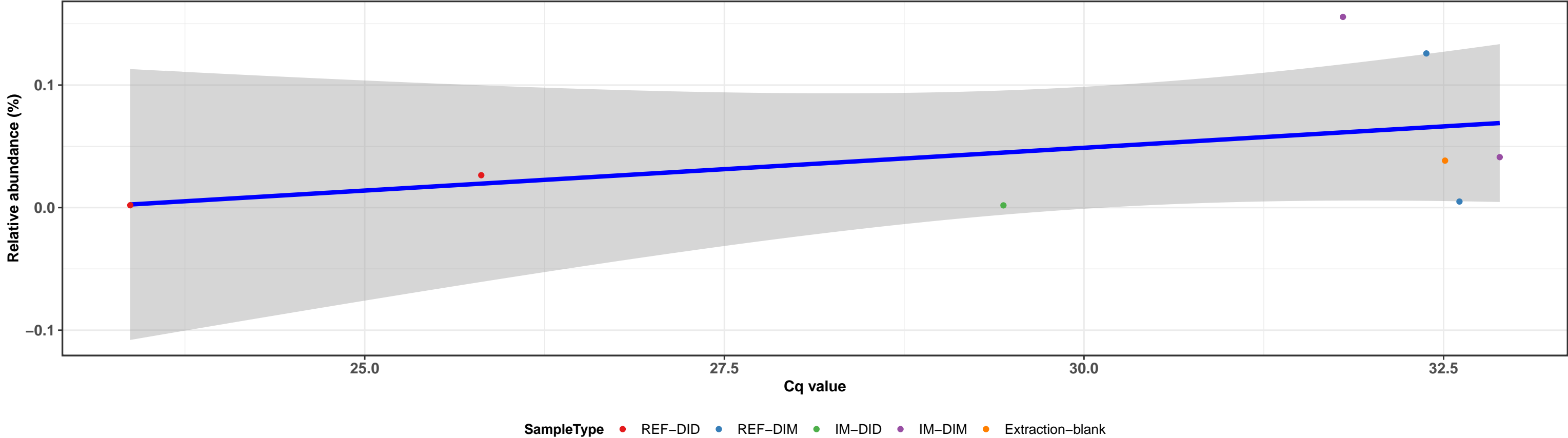
Correlation within: IM-DIM



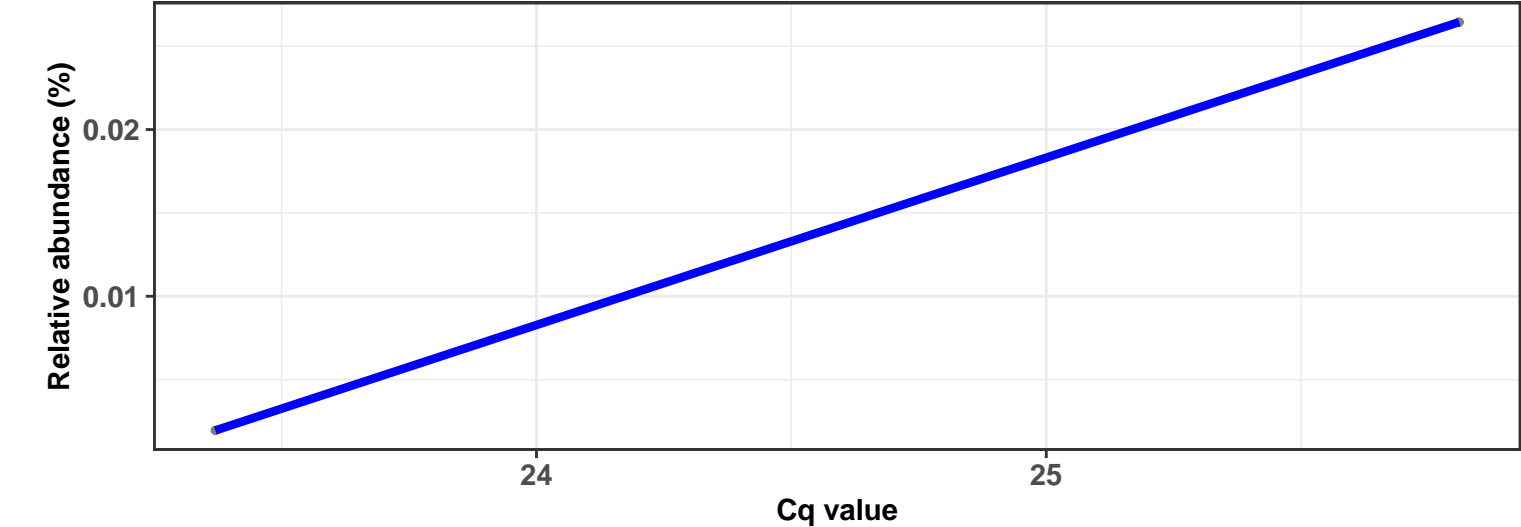
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__Sphingomonas aurantiaca

Correlation with all samples

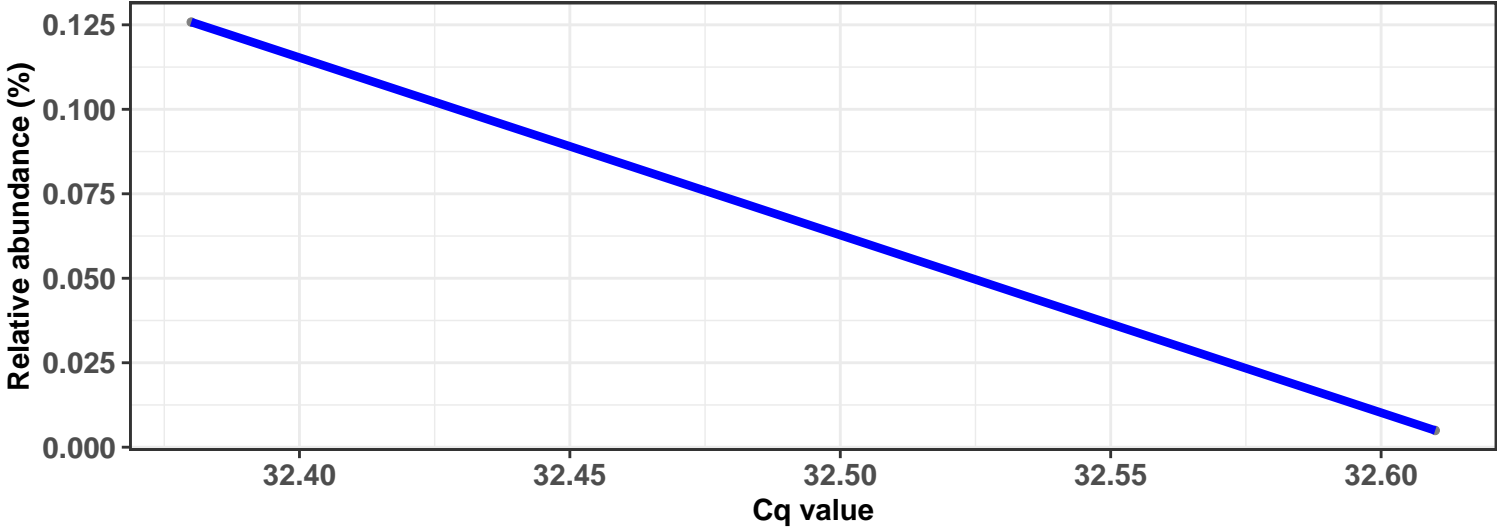
$\log_e(S) = 3.912$, $p = 0.320$, $\hat{\rho}_{\text{Spearman}} = 0.405$, $\text{CI}_{95\%} [-0.144, 0.995]$, $n_{\text{pairs}} = 8$



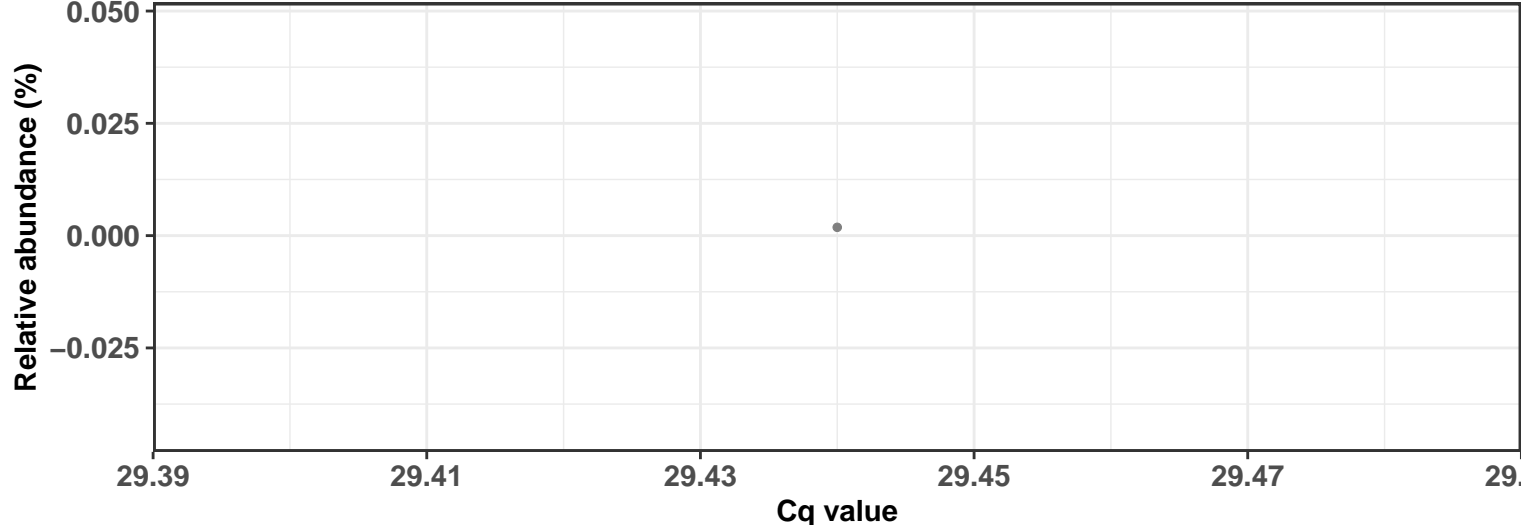
Correlation within: REF-DID



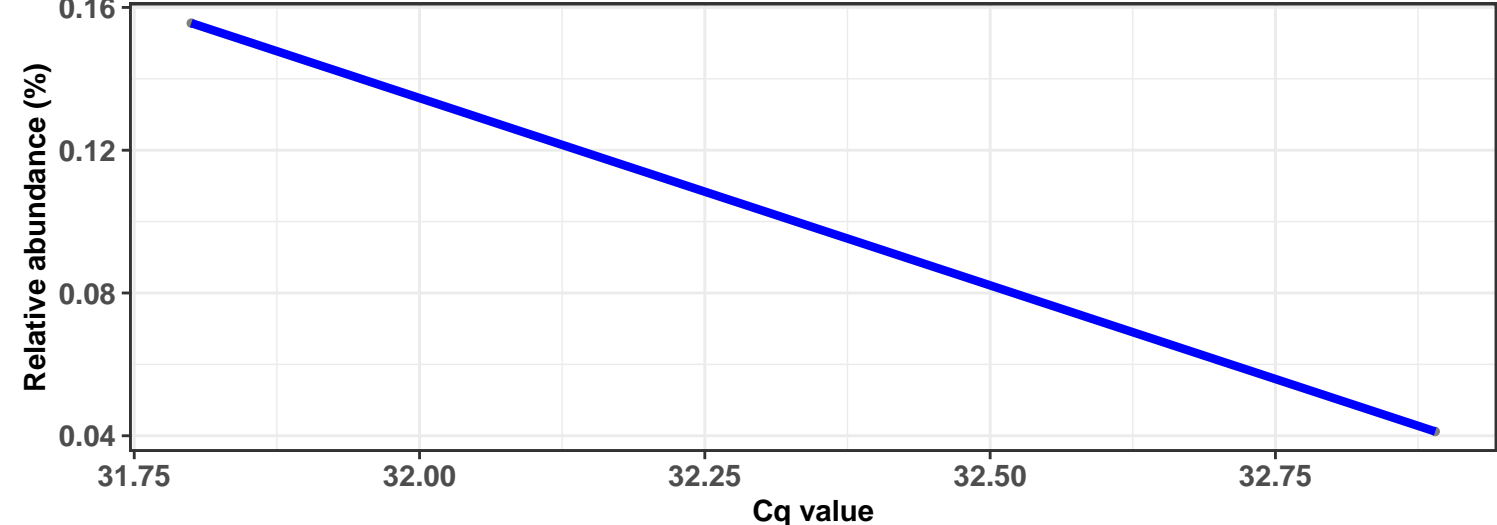
Correlation within: REF-DIM



Correlation within: IM-DID



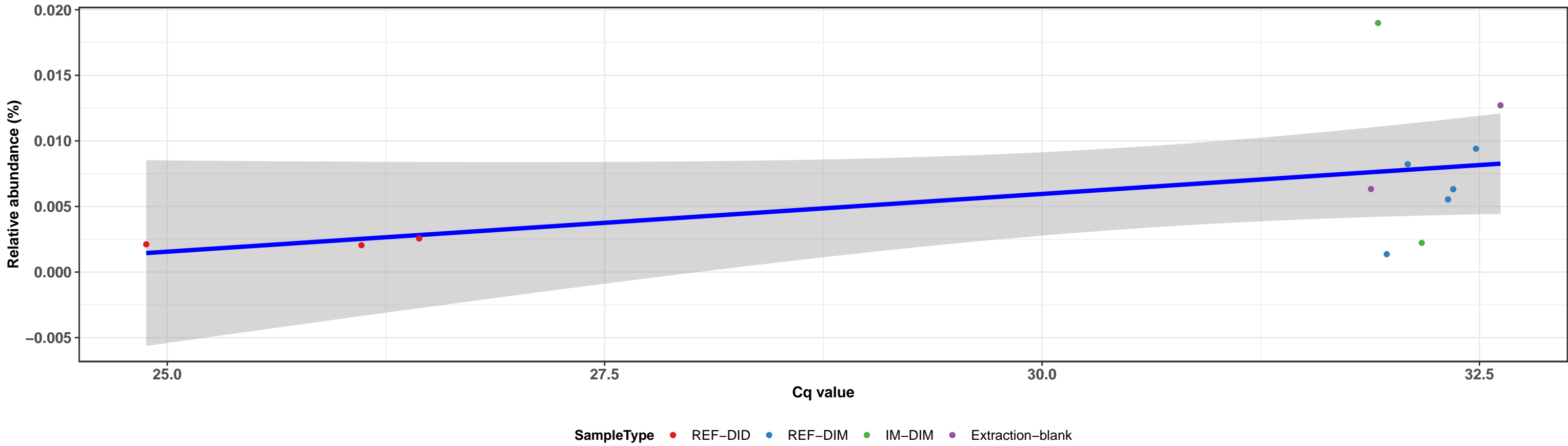
Correlation within: IM-DIM



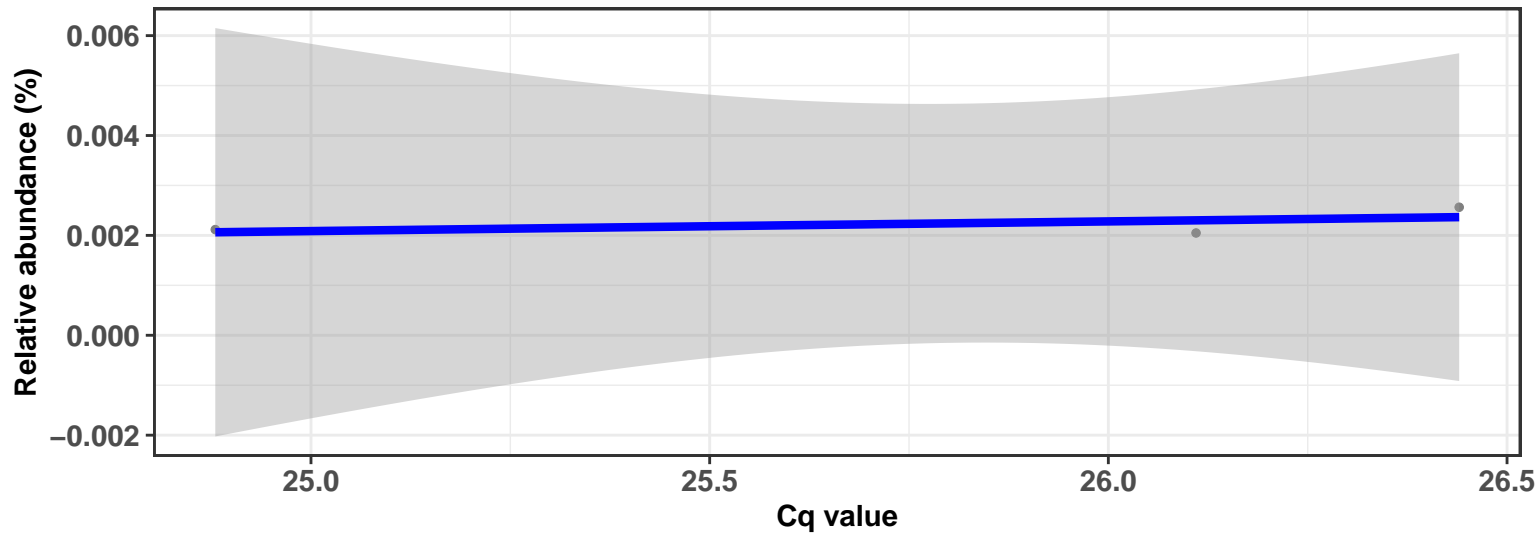
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; Ambiguous_taxa

Correlation with all samples

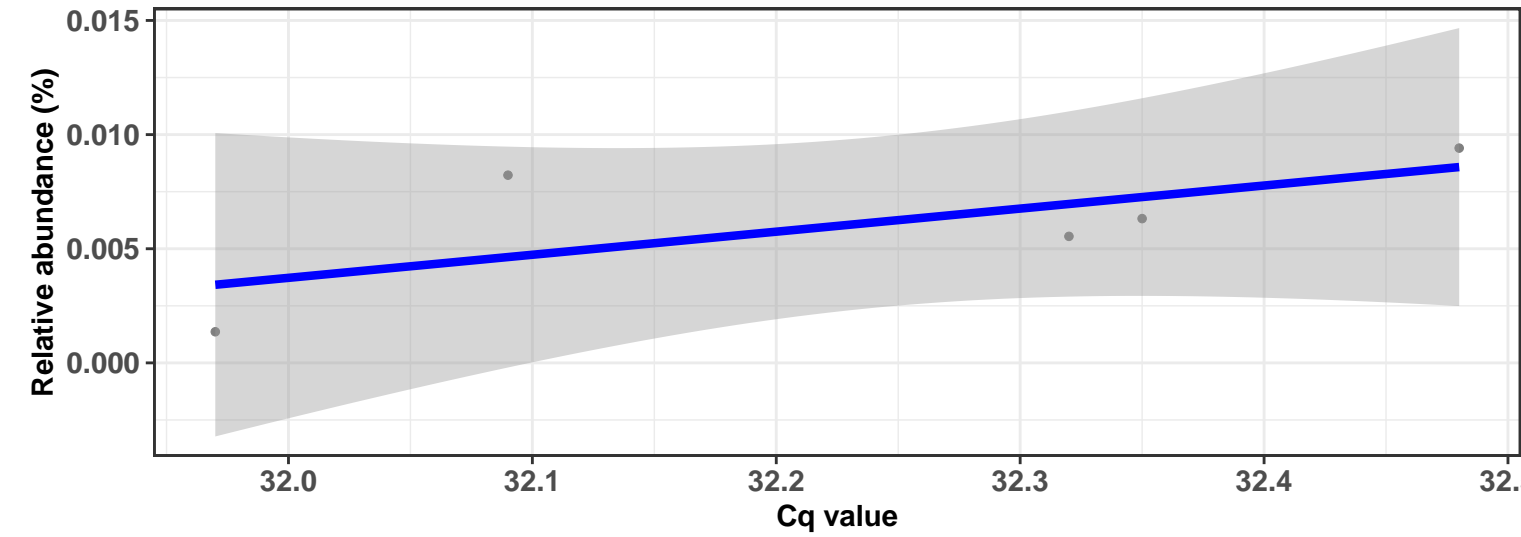
$\log_e(S) = 4.927$, $p = 0.085$, $\hat{\rho}_{\text{Spearman}} = 0.517$, $\text{CI}_{95\%} [-0.016, 1.078]$, $n_{\text{pairs}} = 12$



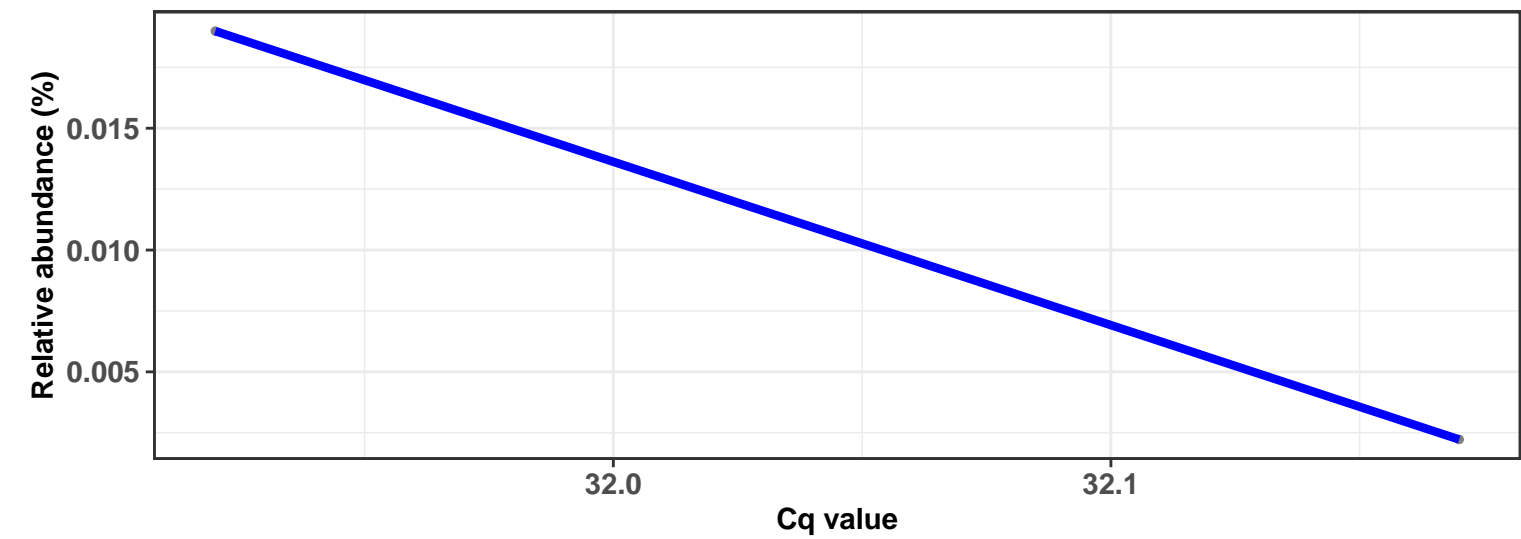
Correlation within: REF-DID



Correlation within: REF-DIM



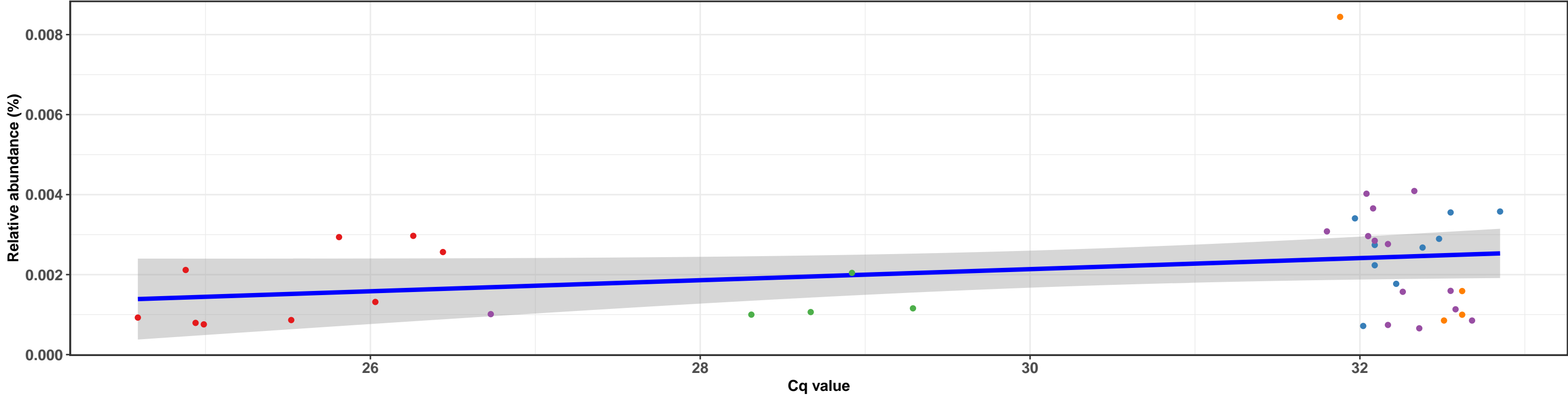
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

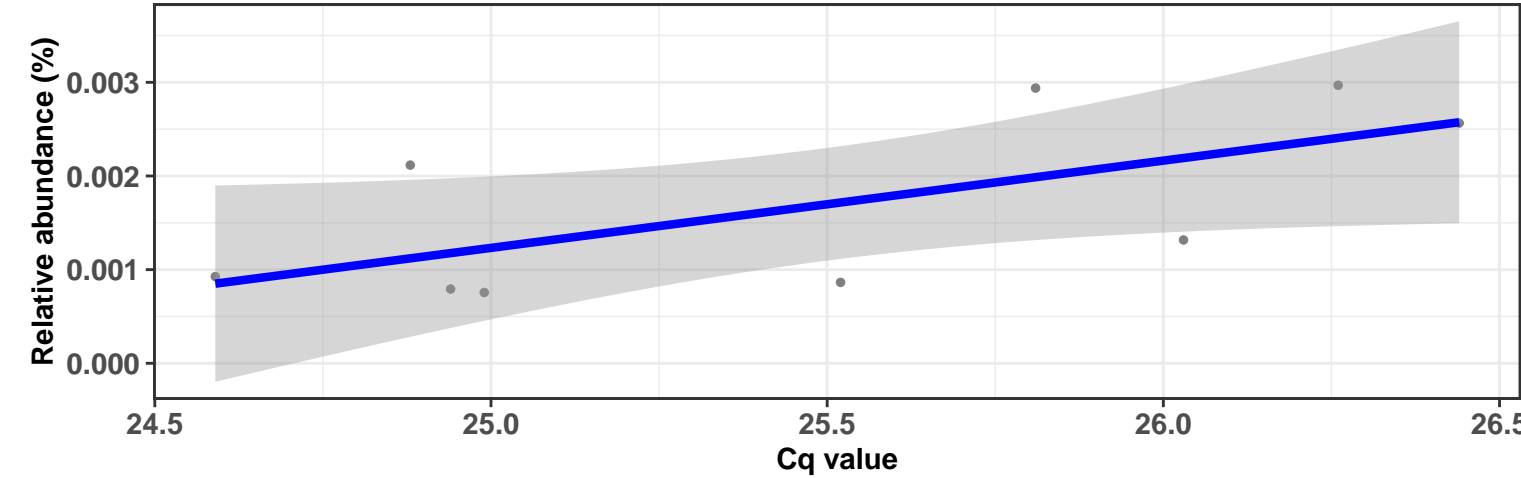
Correlation with all samples

$\log_e(S) = 9.162$, $p = 0.516$, $\hat{\rho}_{\text{Spearman}} = 0.106$, $\text{CI}_{95\%} [-0.210, 0.409]$, $n_{\text{pairs}} = 40$



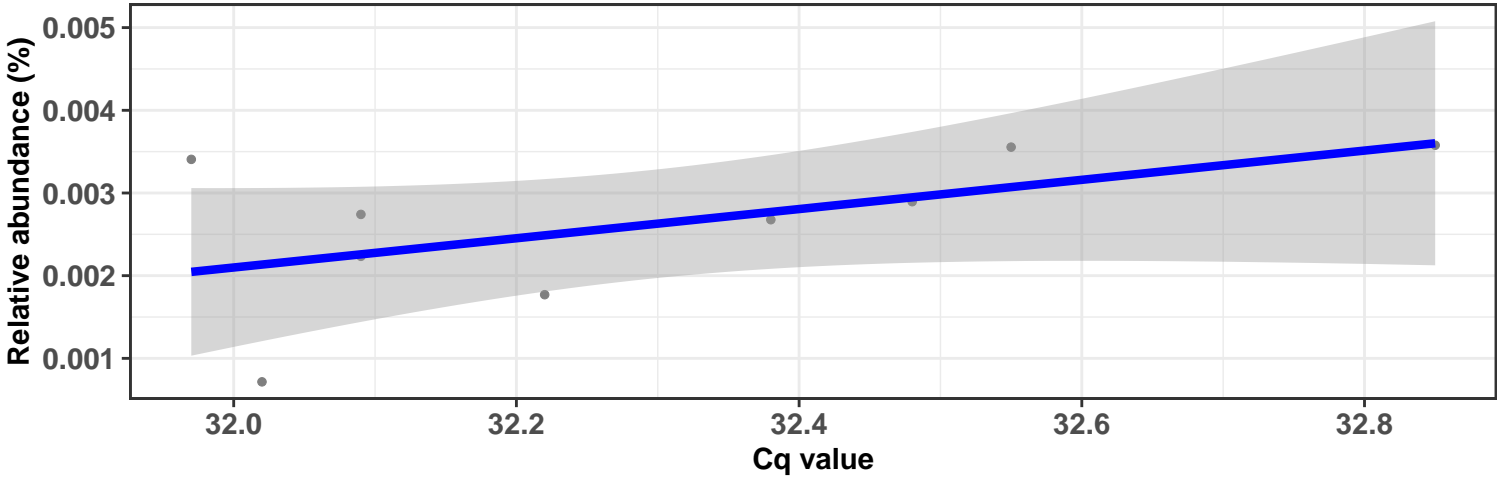
Correlation within: REF-DID

$\log_e(S) = 3.951$, $p = 0.112$, $\hat{\rho}_{\text{Spearman}} = 0.567$, $\text{CI}_{95\%} [0.191, 0.993]$, $n_{\text{pairs}} = 9$

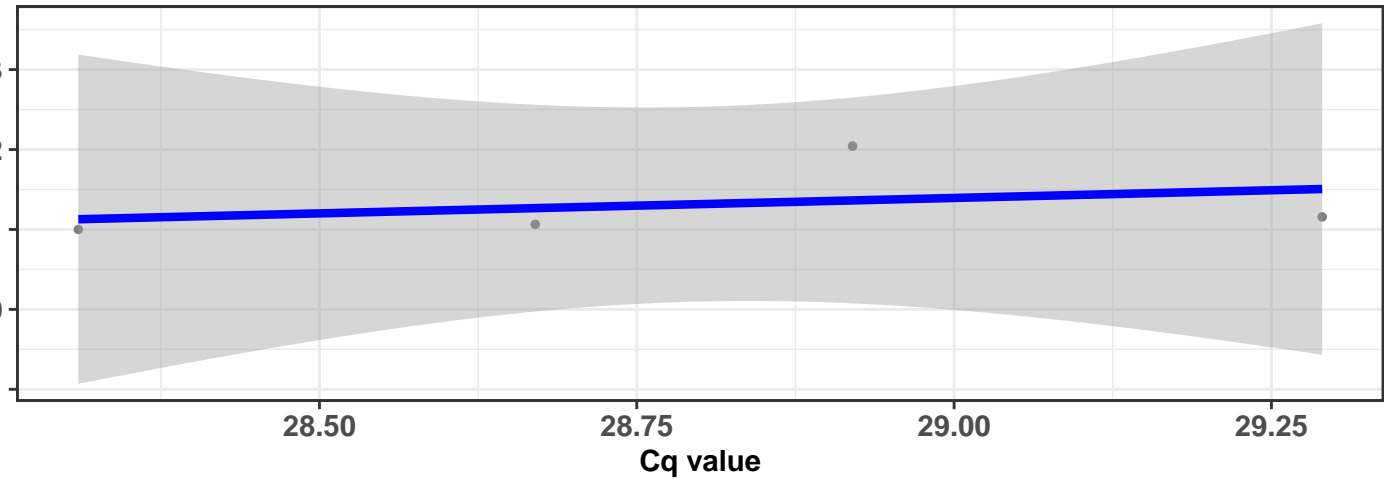


Correlation within: REF-DIM

$\log_e(S) = 3.984$, $p = 0.123$, $\hat{\rho}_{\text{Spearman}} = 0.552$, $\text{CI}_{95\%} [-0.121, 1.414]$, $n_{\text{pairs}} = 9$

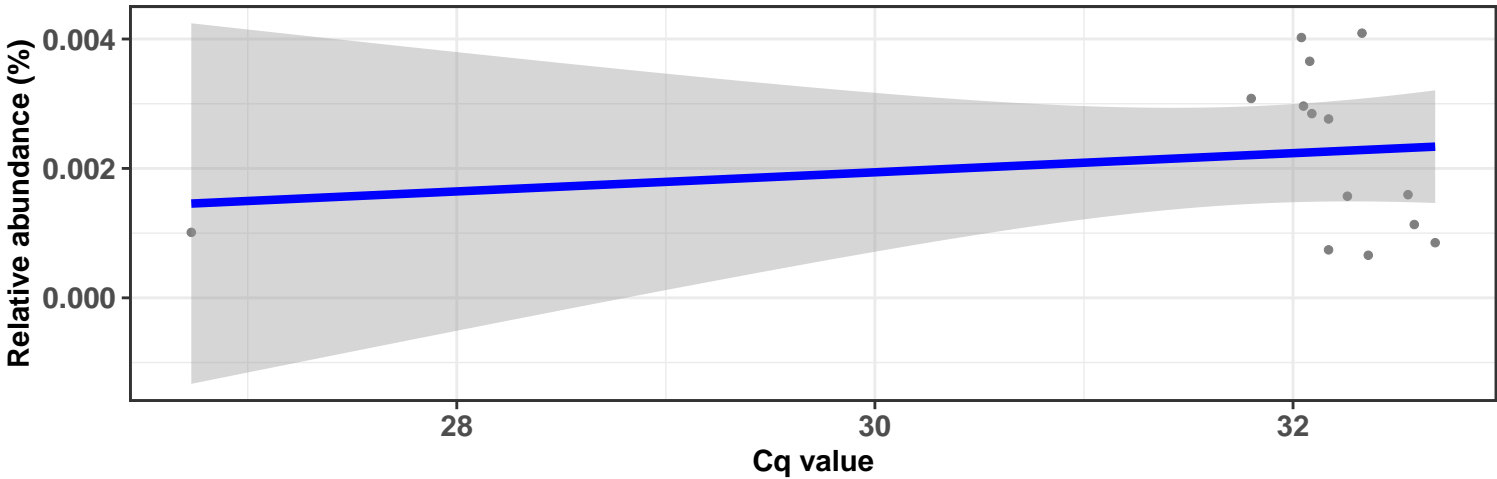


Correlation within: IM-DID



Correlation within: IM-DIM

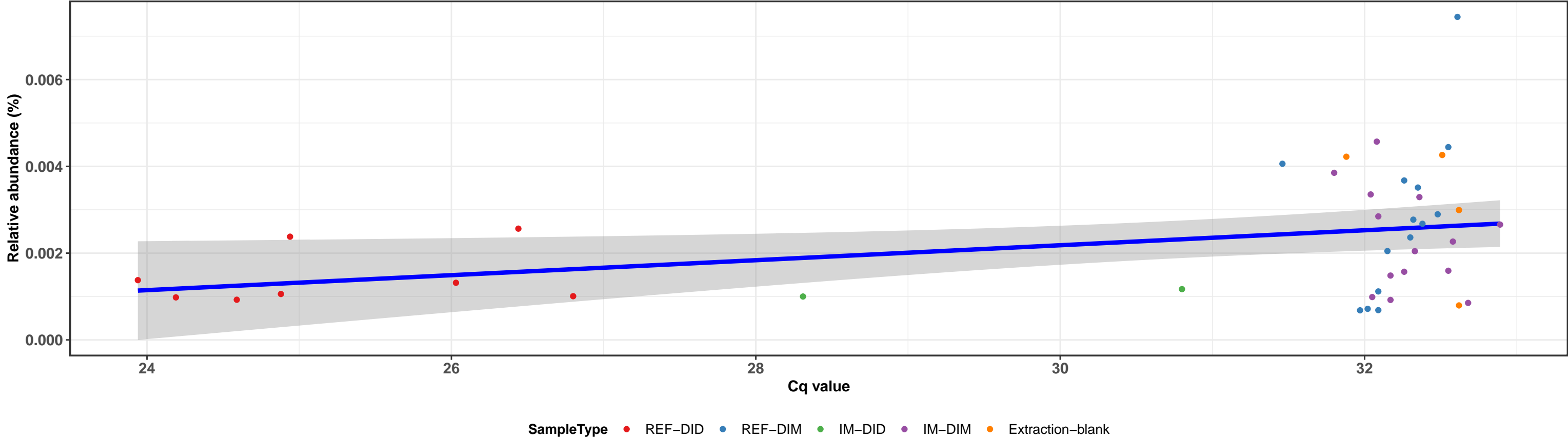
$\log_e(S) = 6.477$, $p = 0.126$, $\hat{\rho}_{\text{Spearman}} = -0.429$, $\text{CI}_{95\%} [-1.012, 0.032]$, $n_{\text{pairs}} = 14$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

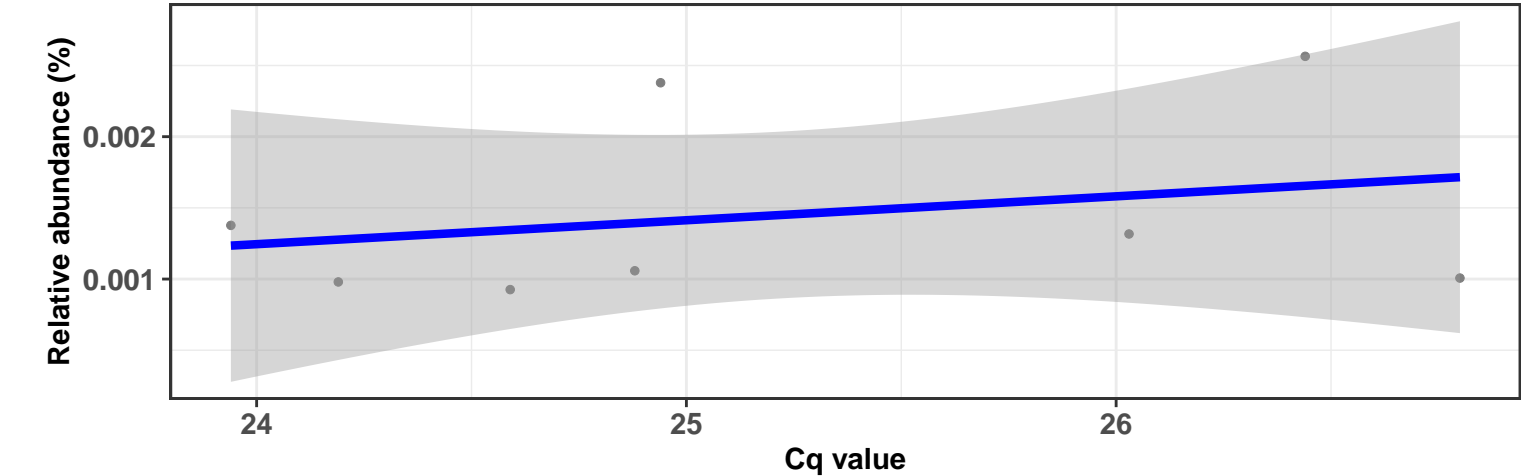
Correlation with all samples

$\log_e(S) = 9.077$, $p = 0.061$, $\hat{\rho}_{\text{Spearman}} = 0.291$, $\text{CI}_{95\%} [0.009, 0.620]$, $n_{\text{pairs}} = 42$



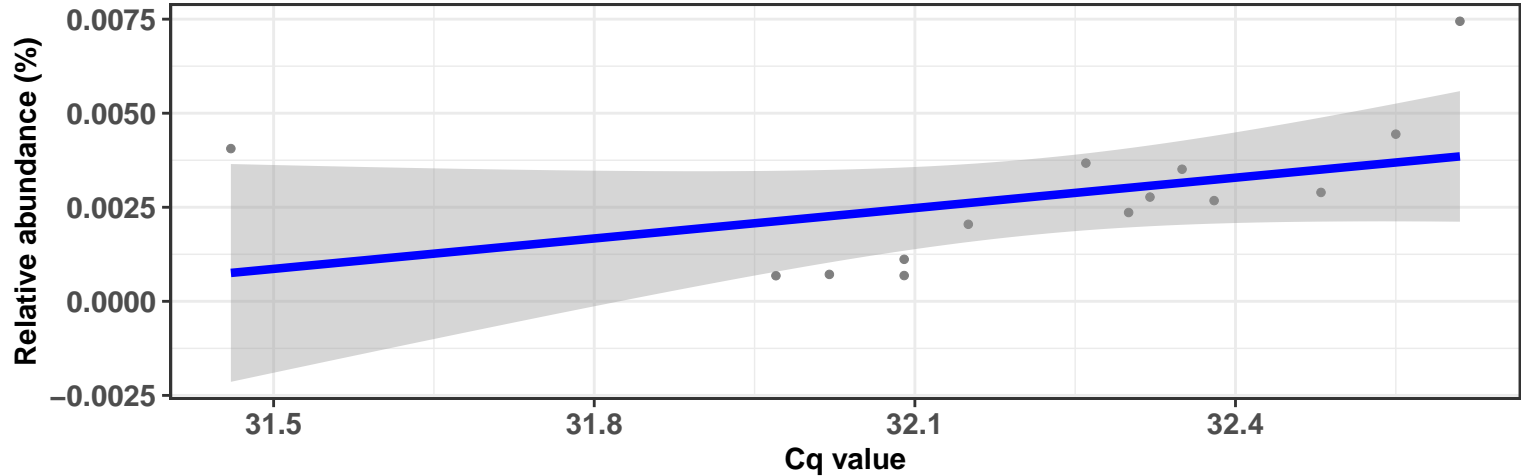
Correlation within: REF-DID

$\log_e(S) = 4.094$, $p = 0.493$, $\hat{\rho}_{\text{Spearman}} = 0.286$, $\text{CI}_{95\%} [-0.468, 1.016]$, $n_{\text{pairs}} = 8$

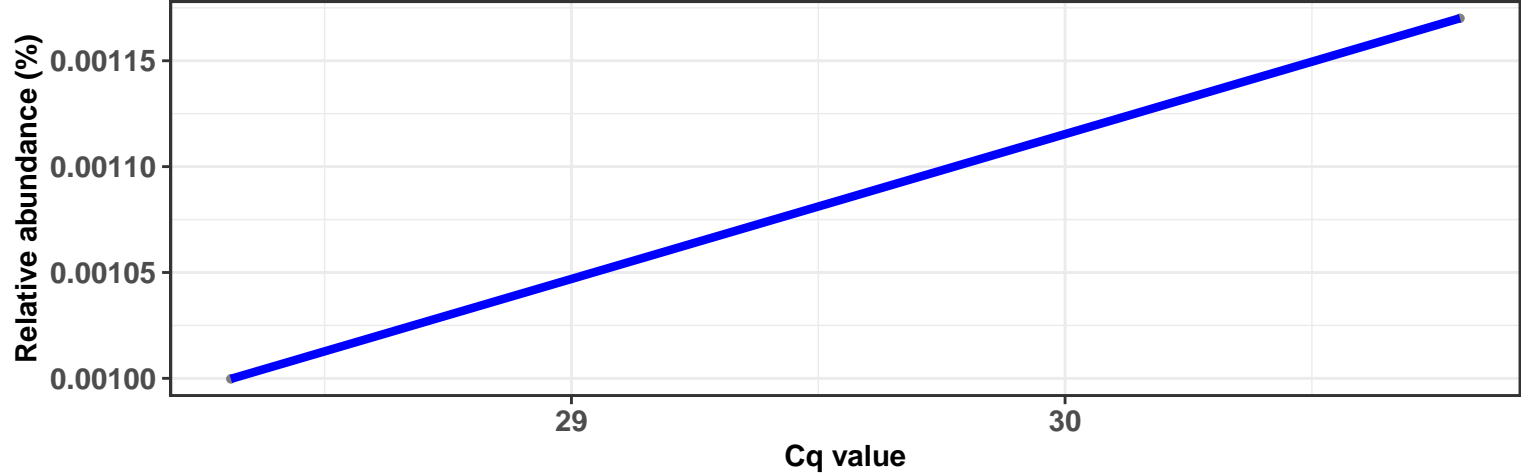


Correlation within: REF-DIM

$\log_e(S) = 5.169$, $p = 0.020$, $\hat{\rho}_{\text{Spearman}} = 0.614$, $\text{CI}_{95\%} [0.064, 1.281]$, $n_{\text{pairs}} = 14$

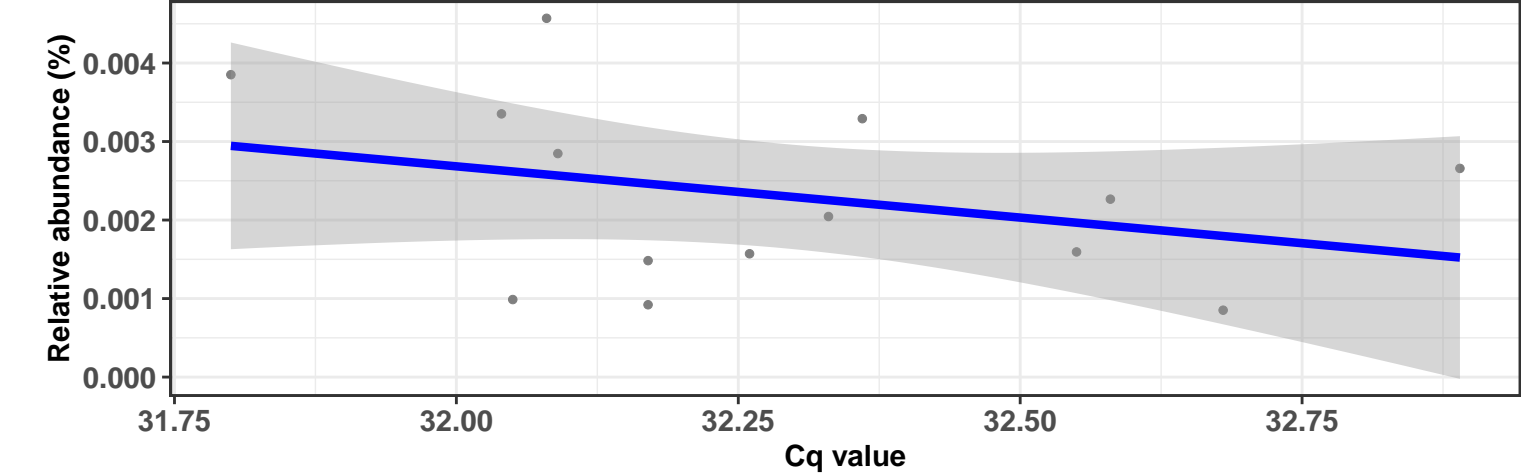


Correlation within: IM-DID



Correlation within: IM-DIM

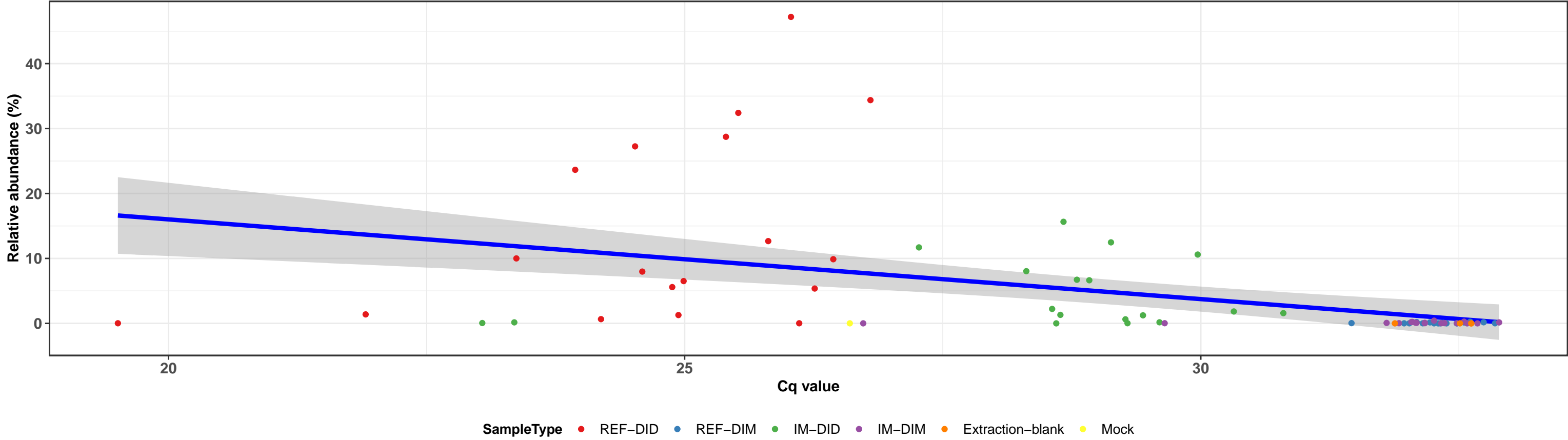
$\log_e(S) = 6.430$, $p = 0.202$, $\hat{\rho}_{\text{Spearman}} = -0.363$, $\text{CI}_{95\%} [-0.959, 0.123]$, $n_{\text{pairs}} = 14$



k__Bacteria; p__Tenericutes; c__Mollicutes; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma; s__uncultured bacterium

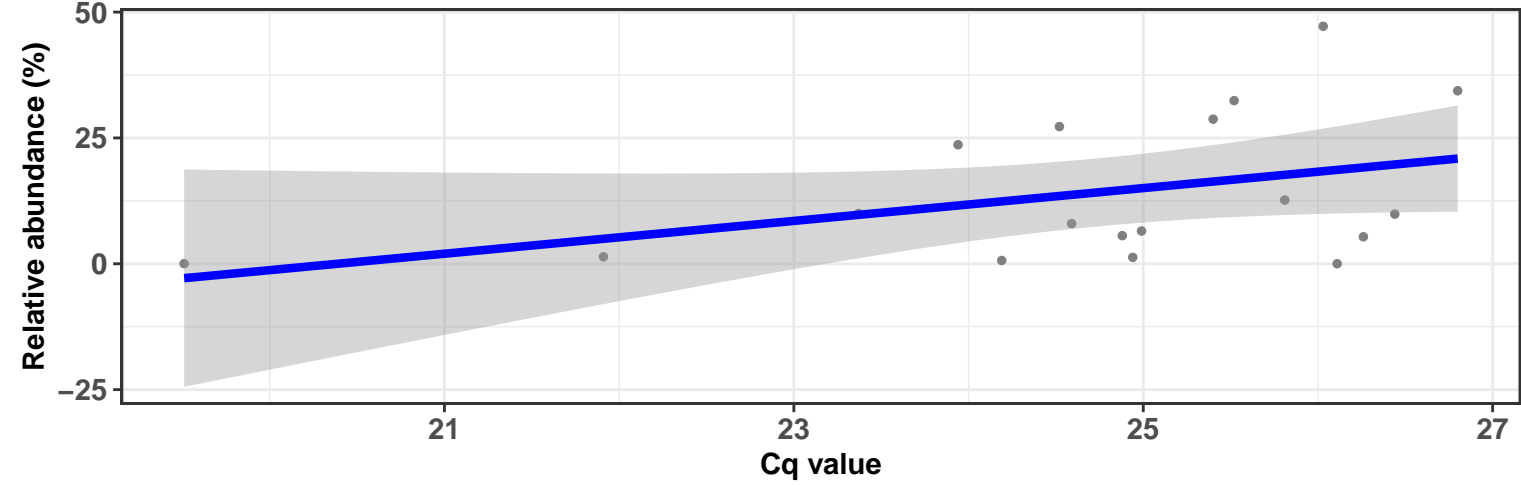
Correlation with all samples

$\log_e(S) = 11.658$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.581$, $\text{CI}_{95\%} [-0.722, -0.444]$, $n_{\text{pairs}} = 76$



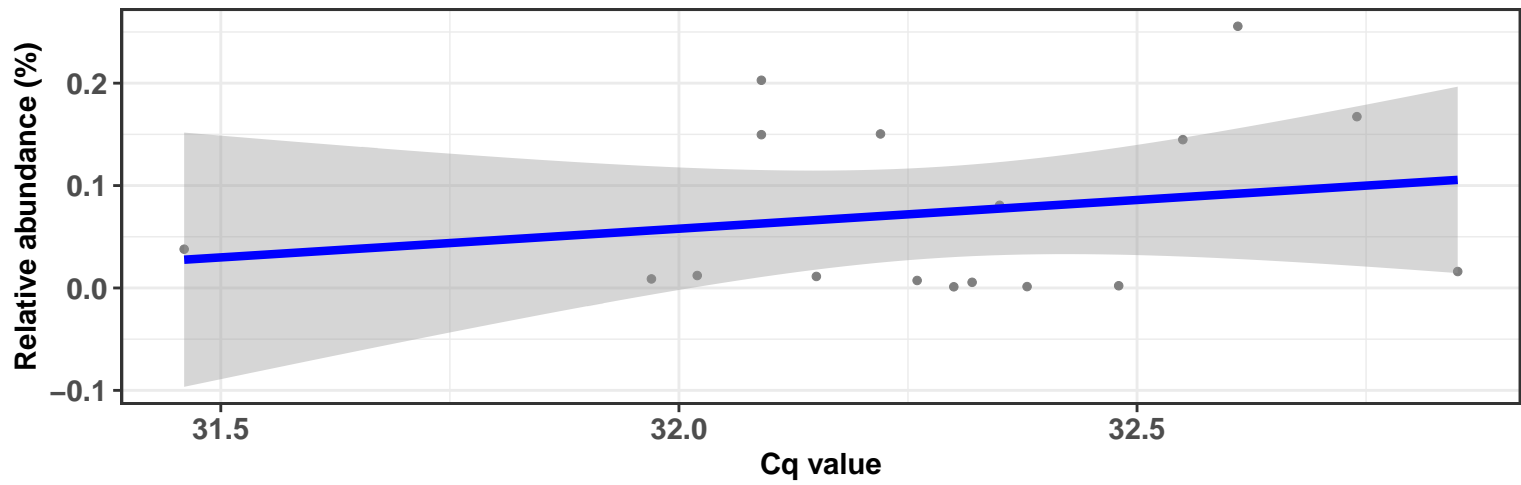
Correlation within: REF-DID

$\log_e(S) = 6.480$, $p = 0.185$, $\hat{\rho}_{\text{Spearman}} = 0.327$, $\text{CI}_{95\%} [-0.130, 0.850]$, $n_{\text{pairs}} = 18$



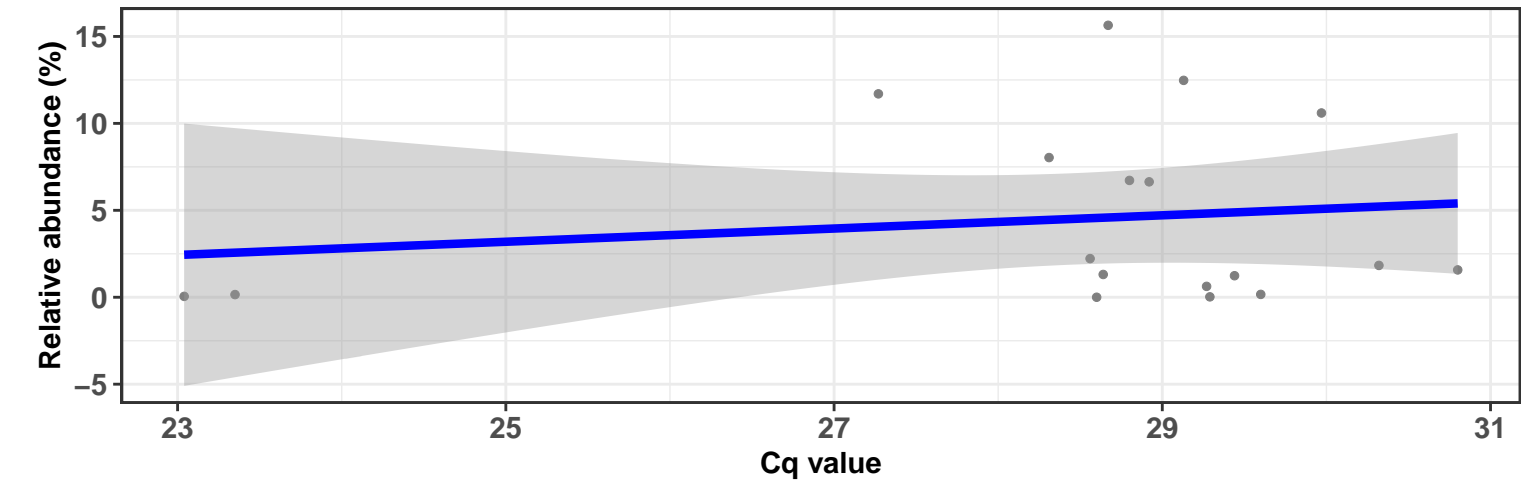
Correlation within: REF-DIM

$\log_e(S) = 6.632$, $p = 0.790$, $\hat{\rho}_{\text{Spearman}} = 0.070$, $\text{CI}_{95\%} [-0.474, 0.616]$, $n_{\text{pairs}} = 17$



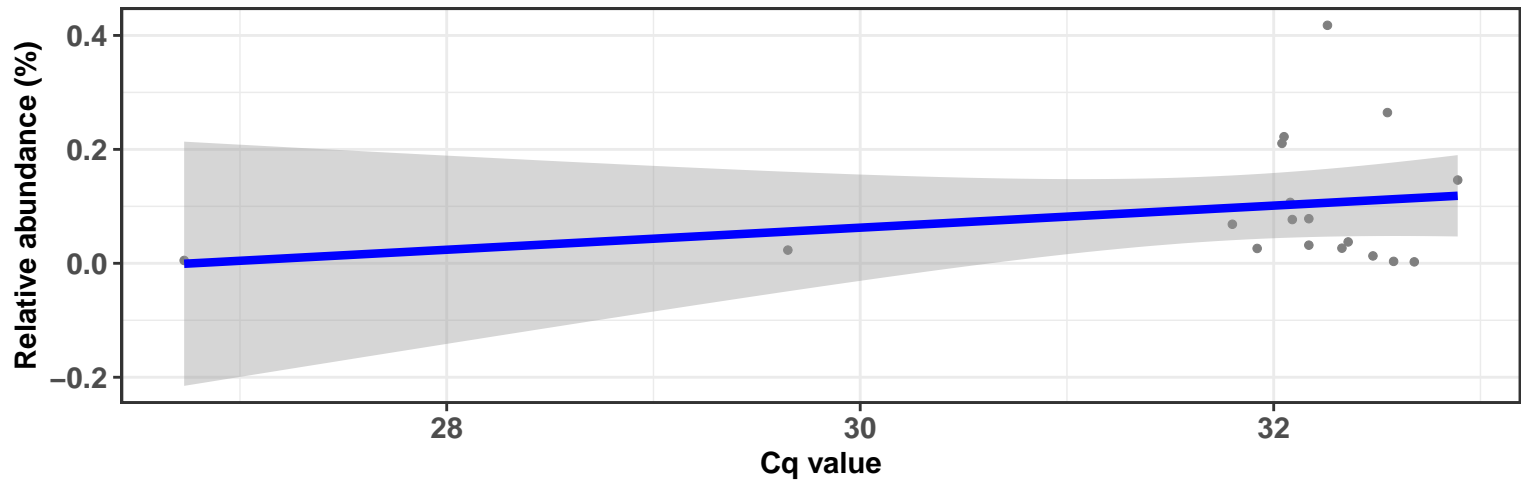
Correlation within: IM-DID

$\log_e(S) = 6.837$, $p = 0.880$, $\hat{\rho}_{\text{Spearman}} = 0.038$, $\text{CI}_{95\%} [-0.461, 0.615]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

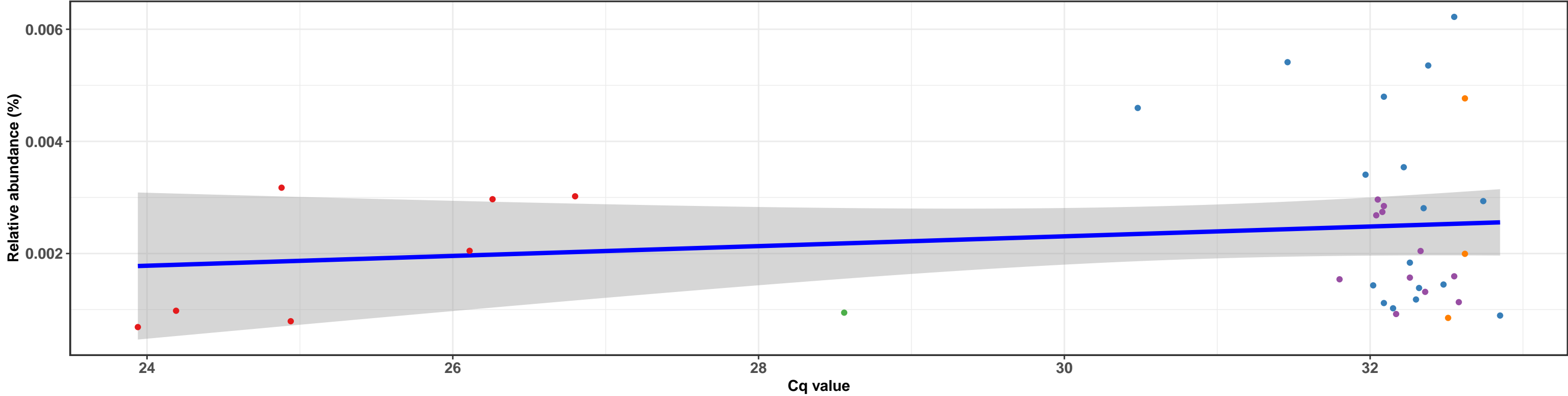
$\log_e(S) = 6.890$, $p = 0.958$, $\hat{\rho}_{\text{Spearman}} = -0.013$, $\text{CI}_{95\%} [-0.592, 0.536]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

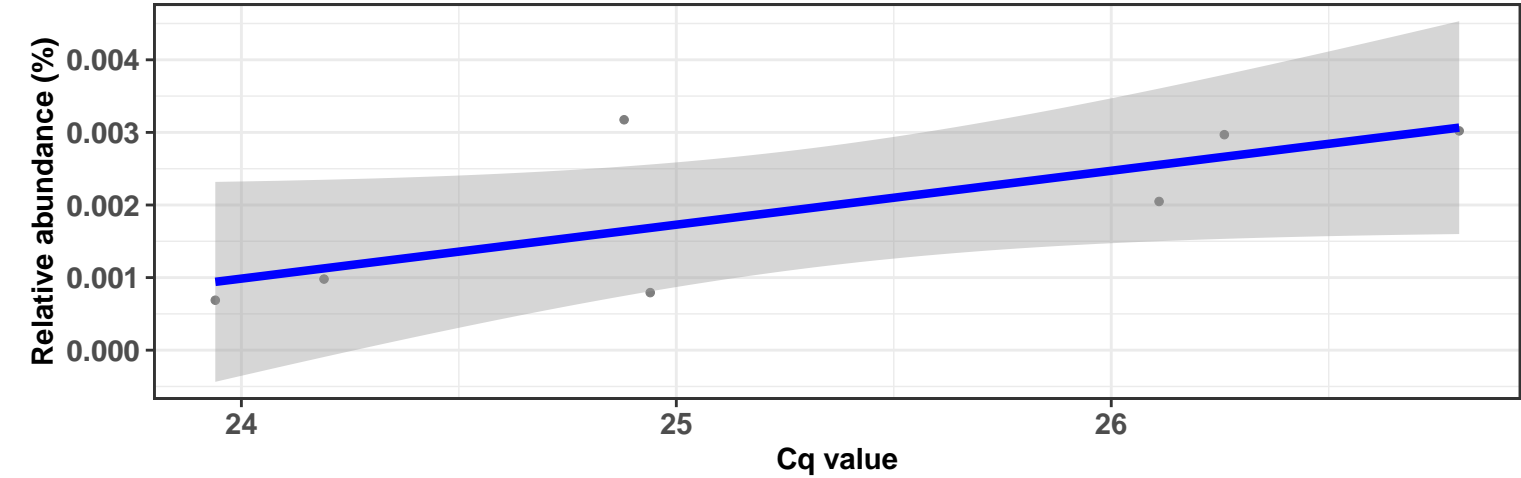
Correlation with all samples

$\log_e(S) = 9.183$, $p = 0.927$, $\hat{\rho}_{\text{Spearman}} = 0.015$, $\text{CI}_{95\%} [-0.292, 0.316]$, $n_{\text{pairs}} = 39$



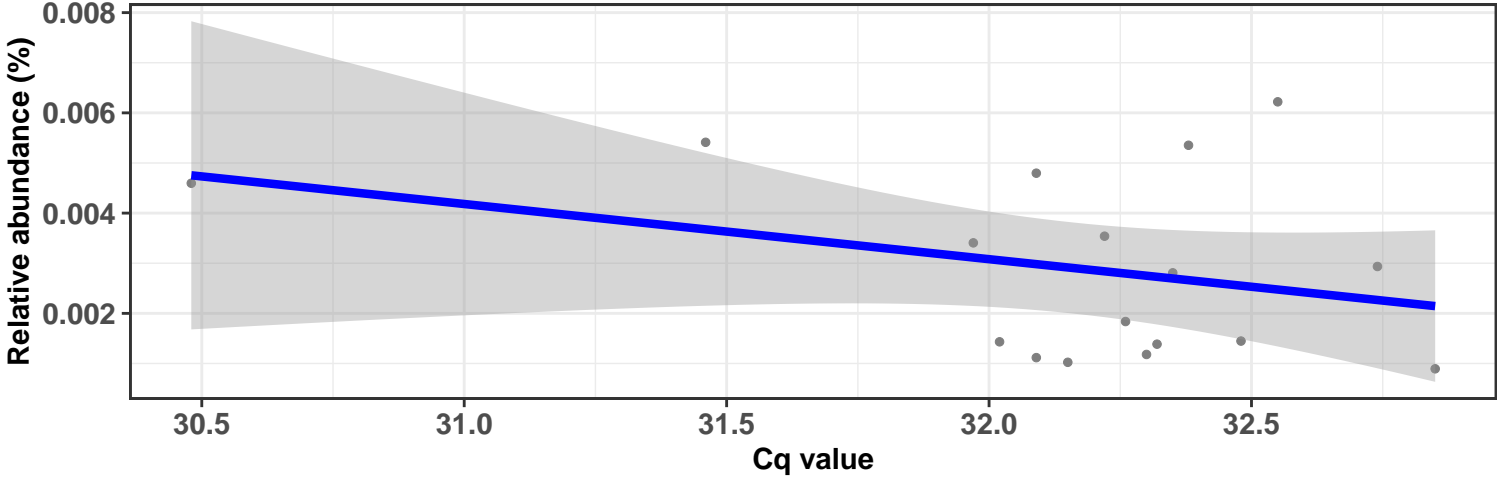
Correlation within: REF-DID

$\log_e(S) = 3.178$, $p = 0.180$, $\hat{\rho}_{\text{Spearman}} = 0.571$, $\text{CI}_{95\%} [-0.138, 1.292]$, $n_{\text{pairs}} = 7$

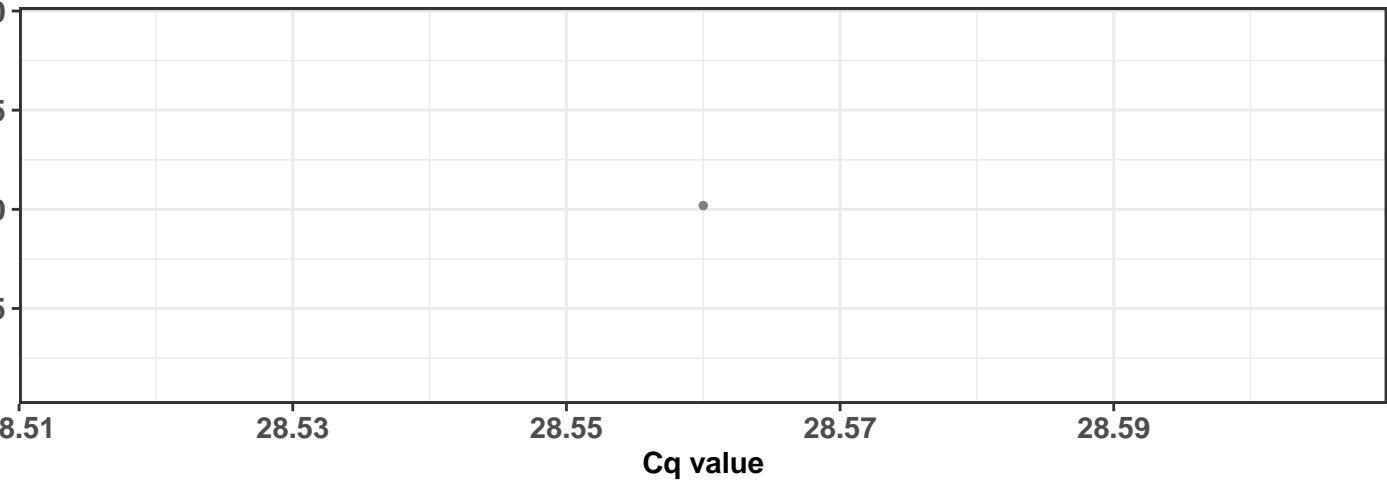


Correlation within: REF-DIM

$\log_e(S) = 6.866$, $p = 0.501$, $\hat{\rho}_{\text{Spearman}} = -0.175$, $\text{CI}_{95\%} [-0.769, 0.418]$, $n_{\text{pairs}} = 17$

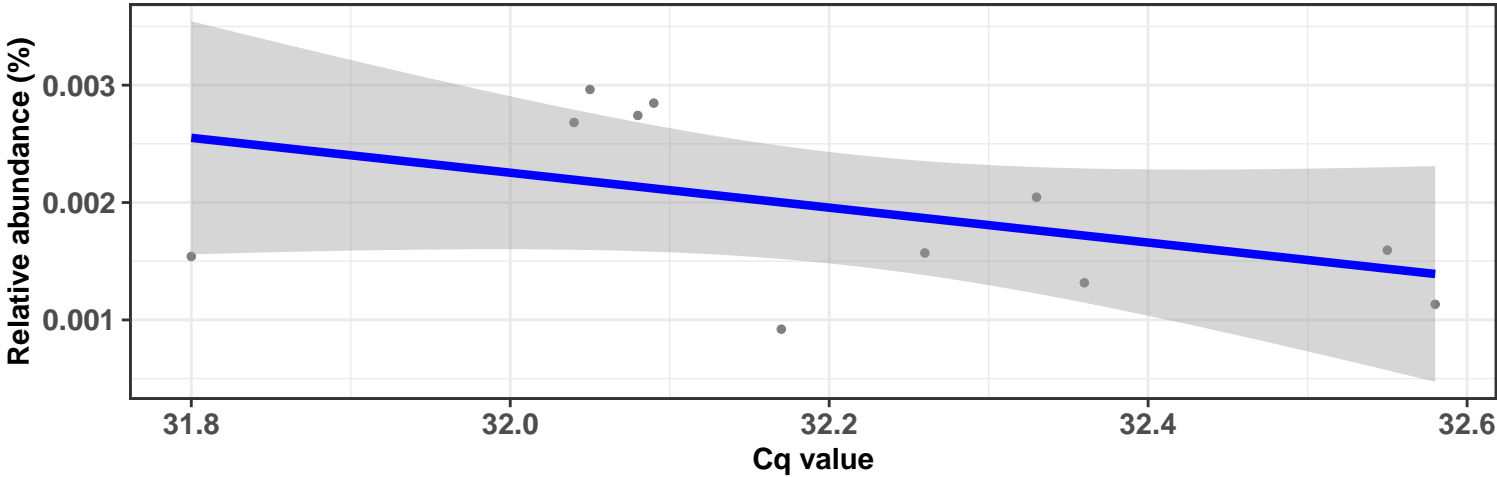


Correlation within: IM-DID



Correlation within: IM-DIM

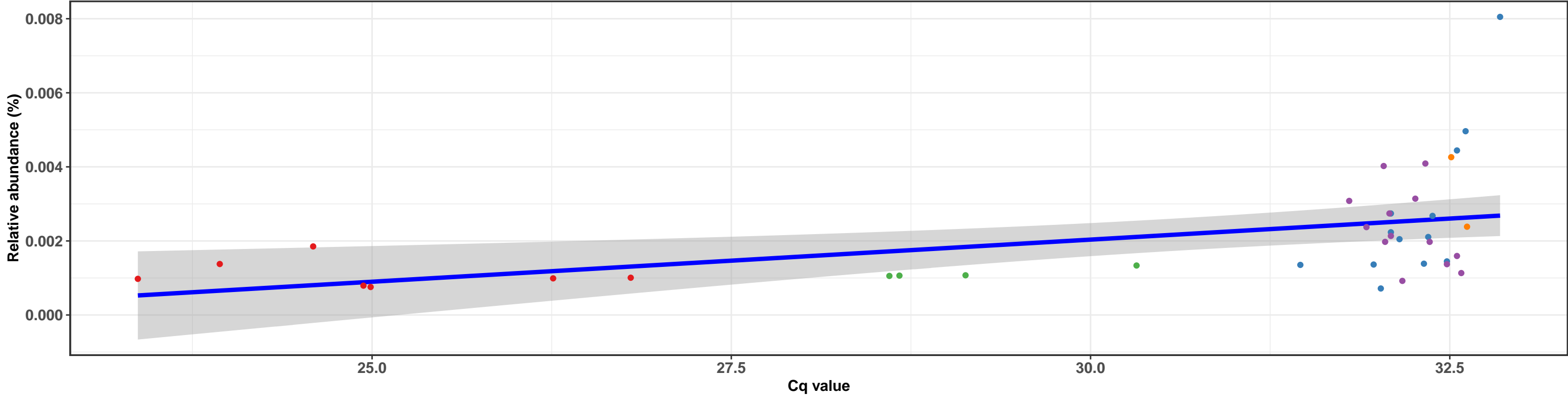
$\log_e(S) = 5.775$, $p = 0.151$, $\hat{\rho}_{\text{Spearman}} = -0.464$, $\text{CI}_{95\%} [-0.983, 0.030]$, $n_{\text{pairs}} = 11$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

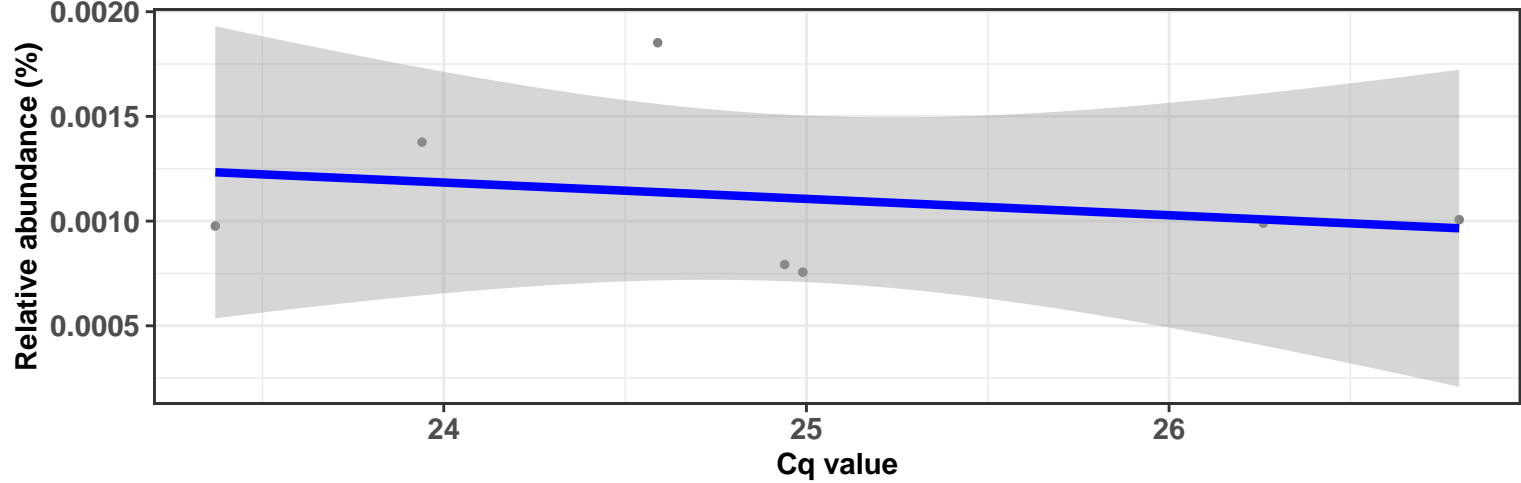
Correlation with all samples

$\log_e(S) = 8.286$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.598$, $\text{CI}_{95\%} [0.375, 0.857]$, $n_{\text{pairs}} = 39$



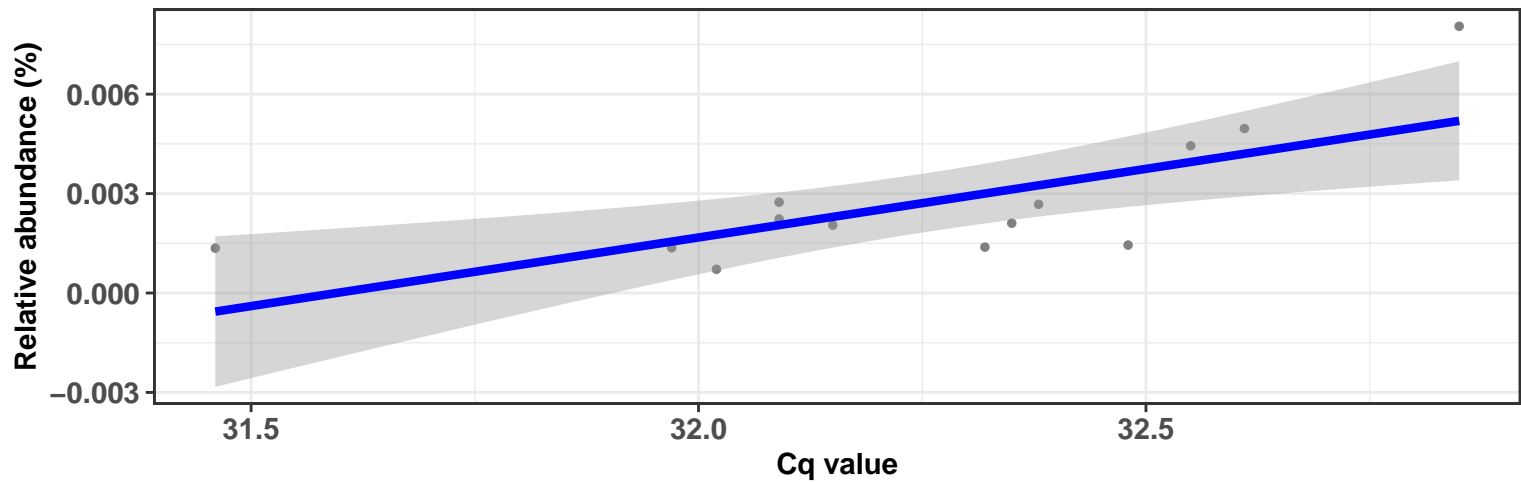
Correlation within: REF-DID

$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-1.139, 0.700]$, $n_{\text{pairs}} = 7$

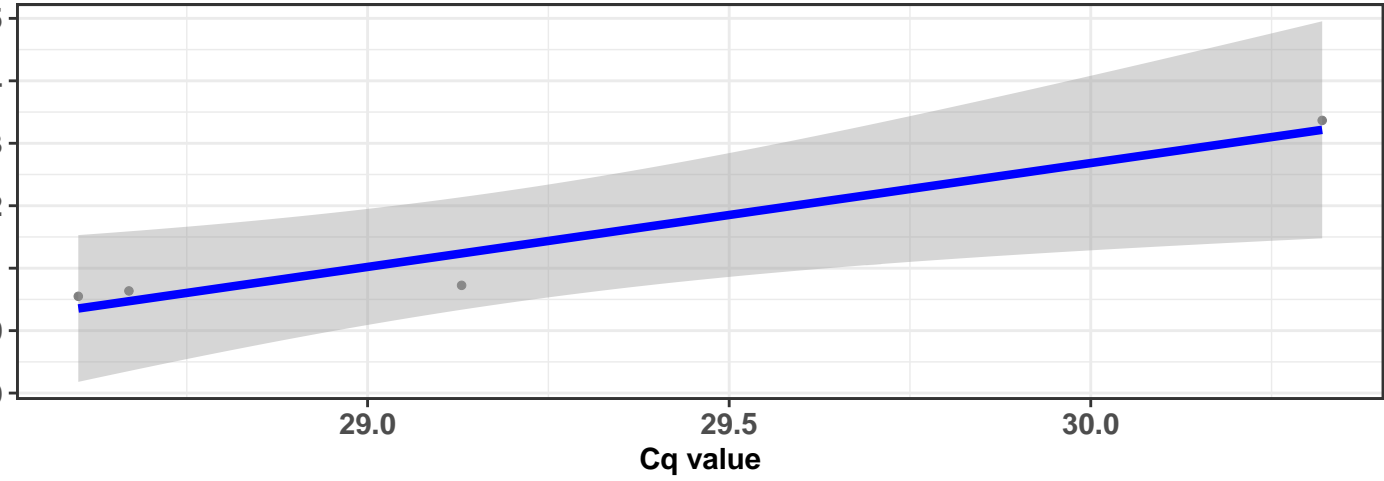


Correlation within: REF-DIM

$\log_e(S) = 4.426$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.770$, $\text{CI}_{95\%} [0.462, 1.026]$, $n_{\text{pairs}} = 13$

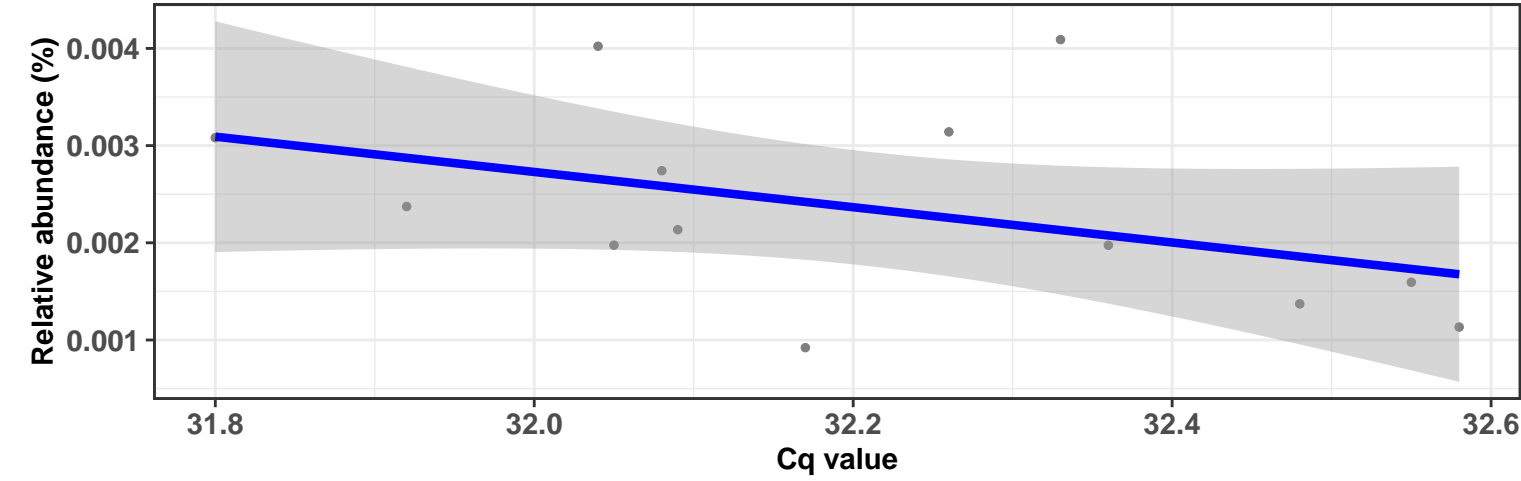


Correlation within: IM-DID



Correlation within: IM-DIM

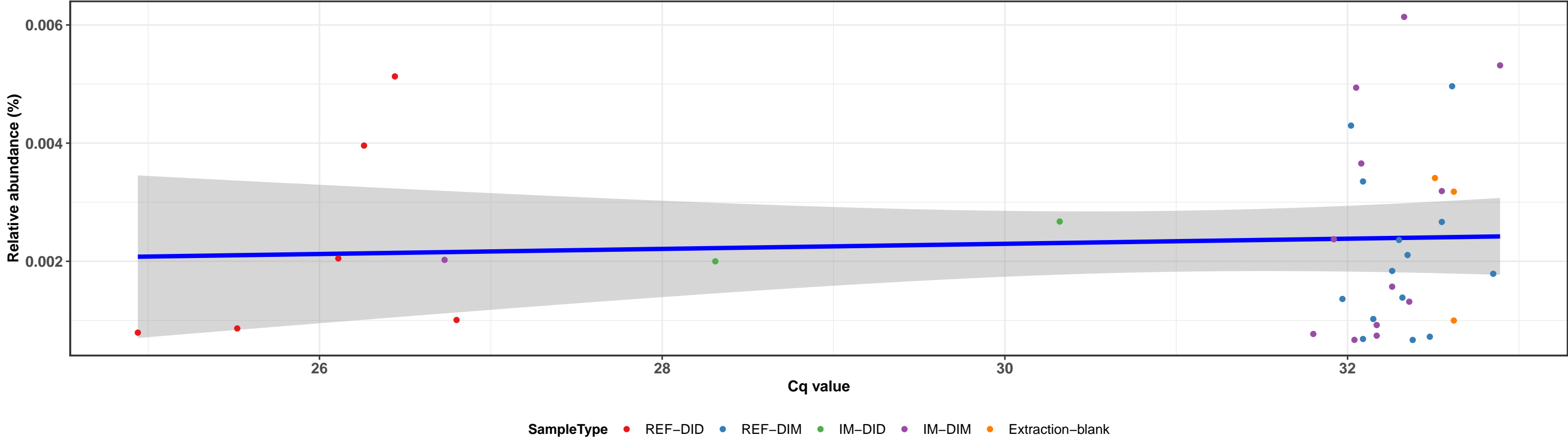
$\log_e(S) = 6.317$, $p = 0.067$, $\hat{\rho}_{\text{Spearman}} = -0.522$, $\text{CI}_{95\%} [-1.018, -0.111]$, $n_{\text{pairs}} = 13$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

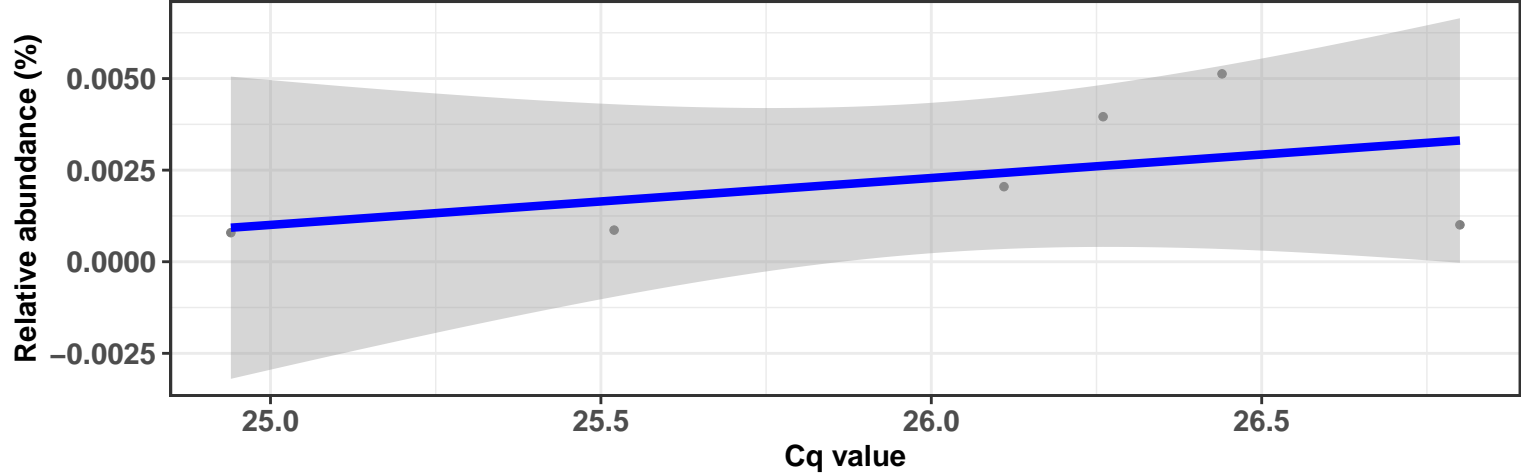
Correlation with all samples

$\log_e(S) = 8.996$, $p = 0.483$, $\hat{\rho}_{\text{Spearman}} = 0.117$, $\text{CI}_{95\%} [-0.236, 0.478]$, $n_{\text{pairs}} = 38$



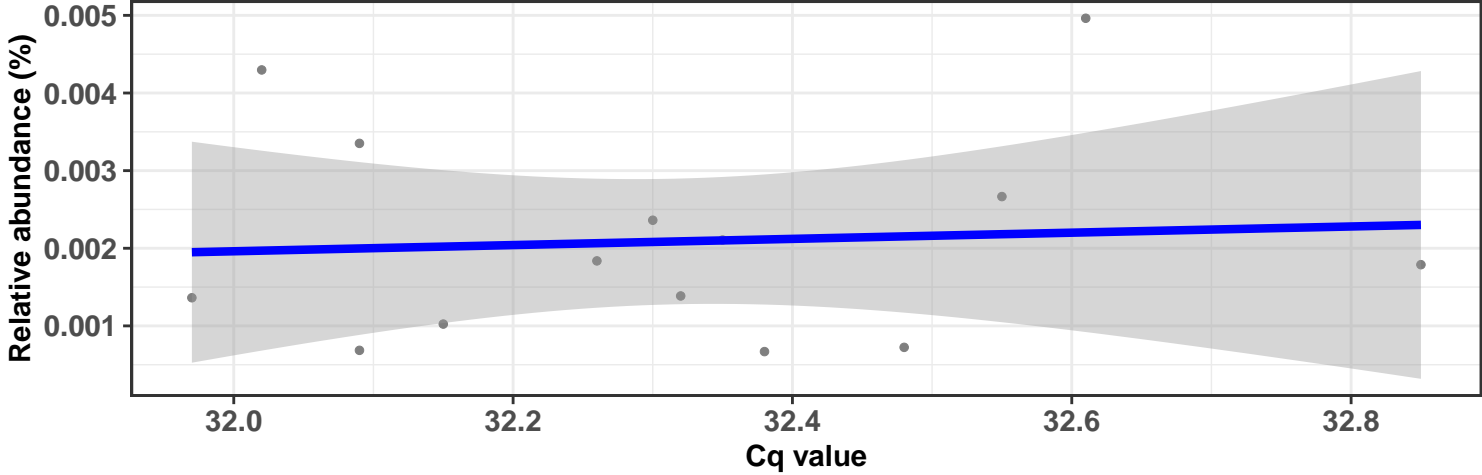
Correlation within: REF-DID

$\log_e(S) = 2.485$, $p = 0.156$, $\hat{\rho}_{\text{Spearman}} = 0.657$, $\text{CI}_{95\%} [-0.190, 1.560]$, $n_{\text{pairs}} = 6$

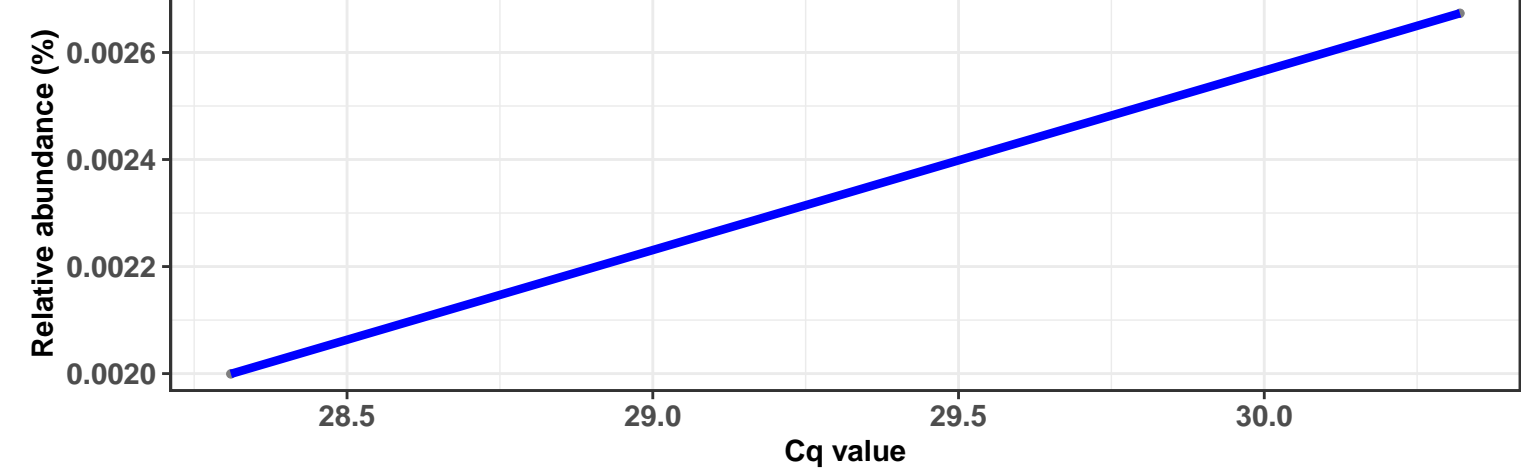


Correlation within: REF-DIM

$\log_e(S) = 6.054$, $p = 0.828$, $\hat{\rho}_{\text{Spearman}} = 0.064$, $\text{CI}_{95\%} [-0.526, 0.753]$, $n_{\text{pairs}} = 14$

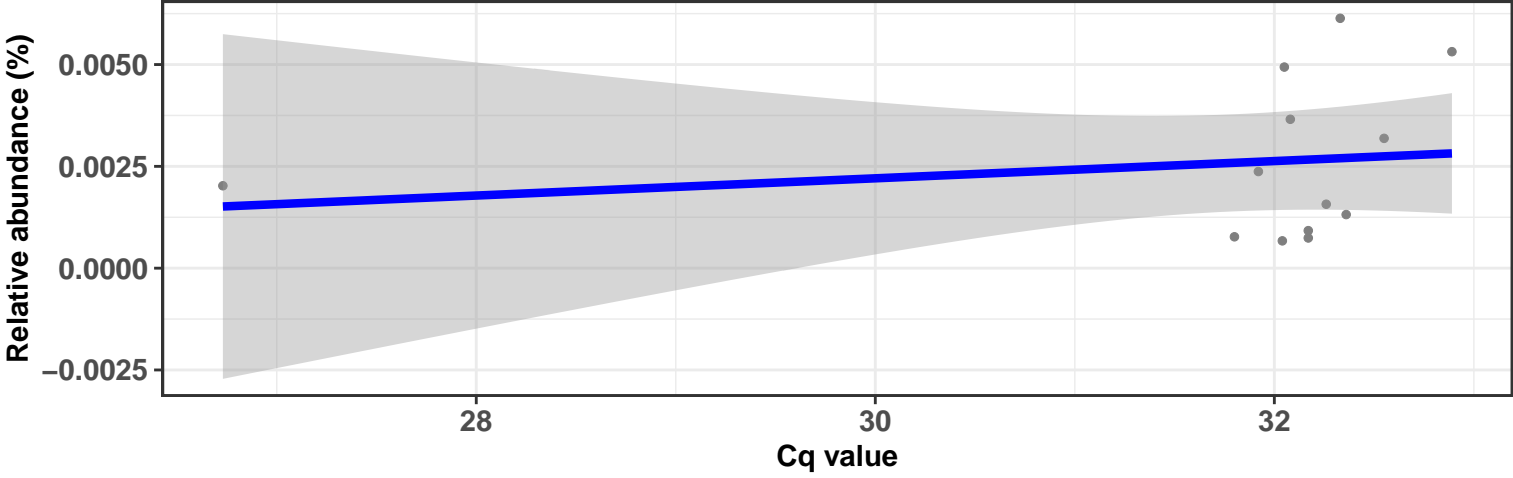


Correlation within: IM-DID



Correlation within: IM-DIM

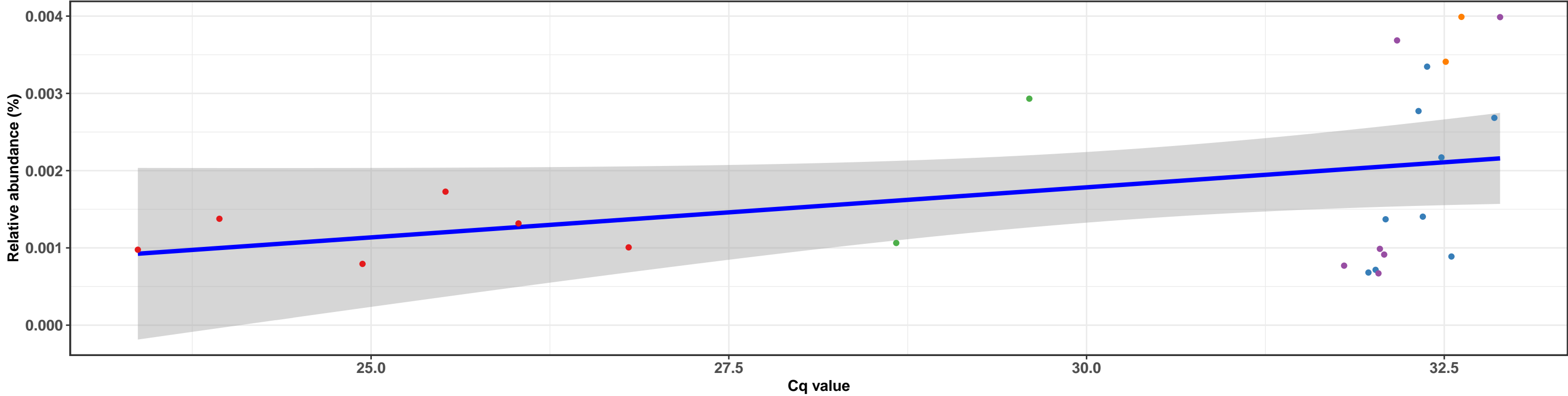
$\log_e(S) = 5.437$, $p = 0.215$, $\hat{\rho}_{\text{Spearman}} = 0.369$, $\text{CI}_{95\%} [-0.155, 0.838]$, $n_{\text{pairs}} = 13$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

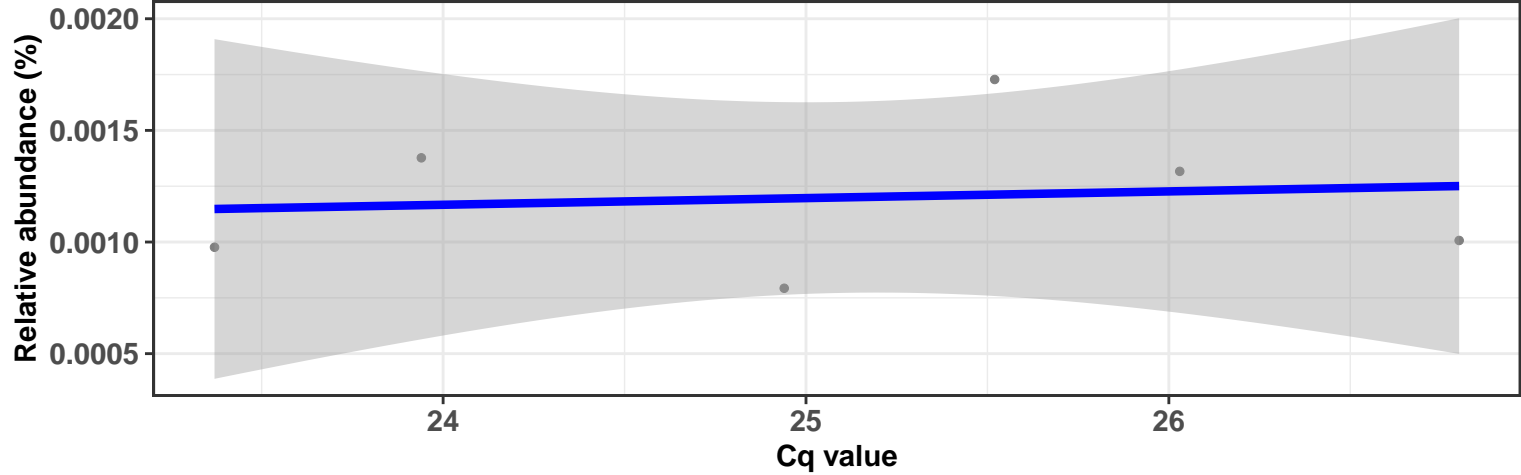
Correlation with all samples

$\log_e(S) = 7.156$, $p = 0.010$, $\hat{\rho}_{\text{Spearman}} = 0.507$, $\text{CI}_{95\%} [0.195, 0.849]$, $n_{\text{pairs}} = 25$



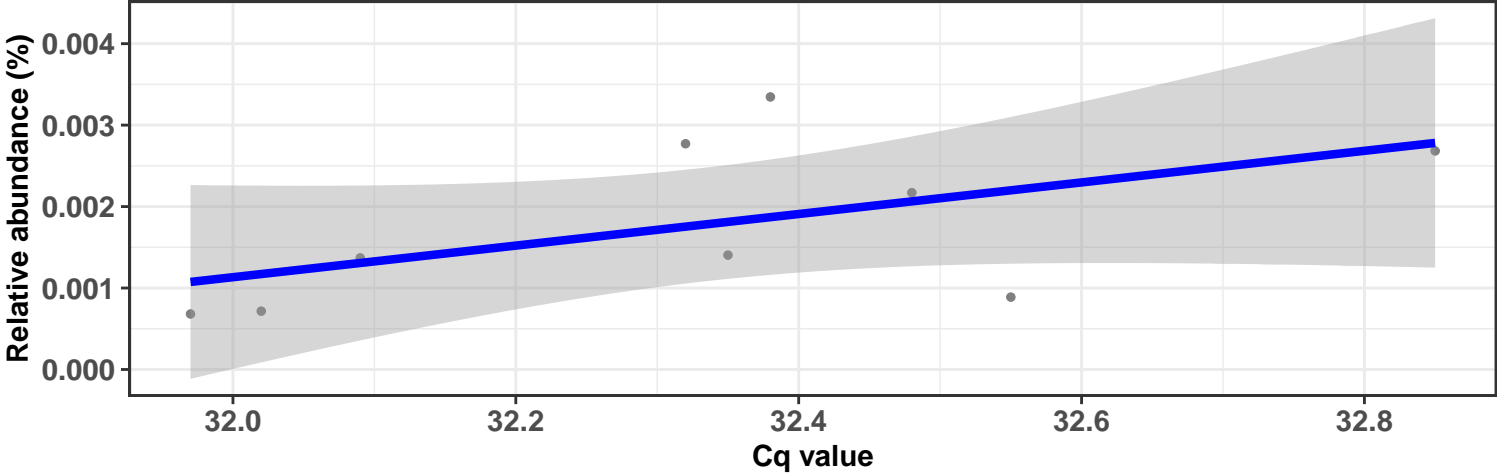
Correlation within: REF-DID

$\log_e(S) = 3.332$, $p = 0.704$, $\hat{\rho}_{\text{Spearman}} = 0.200$, $\text{CI}_{95\%} [-0.633, 1.183]$, $n_{\text{pairs}} = 6$

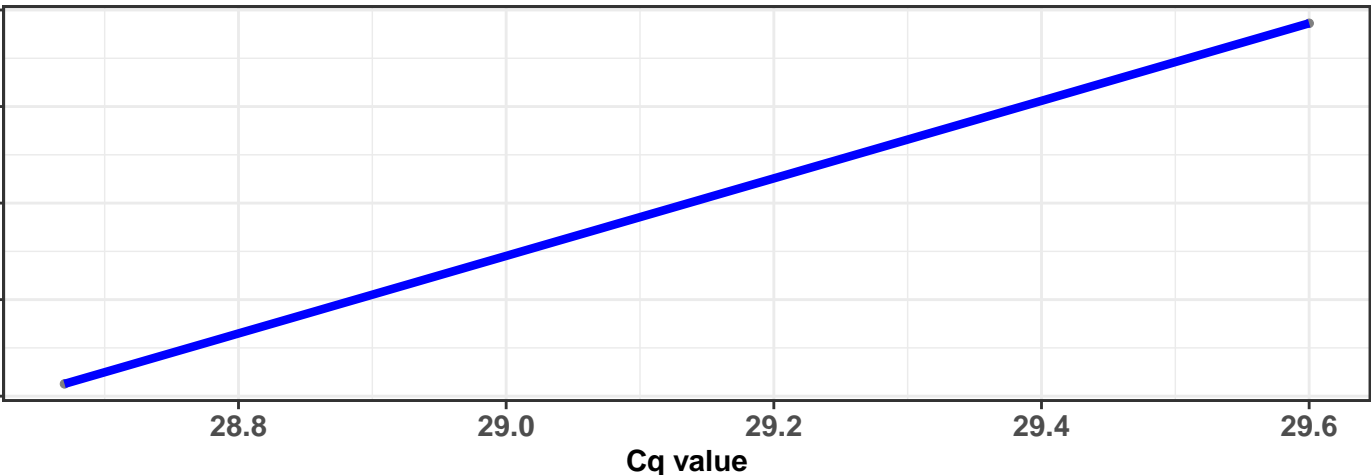


Correlation within: REF-DIM

$\log_e(S) = 4.025$, $p = 0.139$, $\hat{\rho}_{\text{Spearman}} = 0.533$, $\text{CI}_{95\%} [-0.150, 1.152]$, $n_{\text{pairs}} = 9$

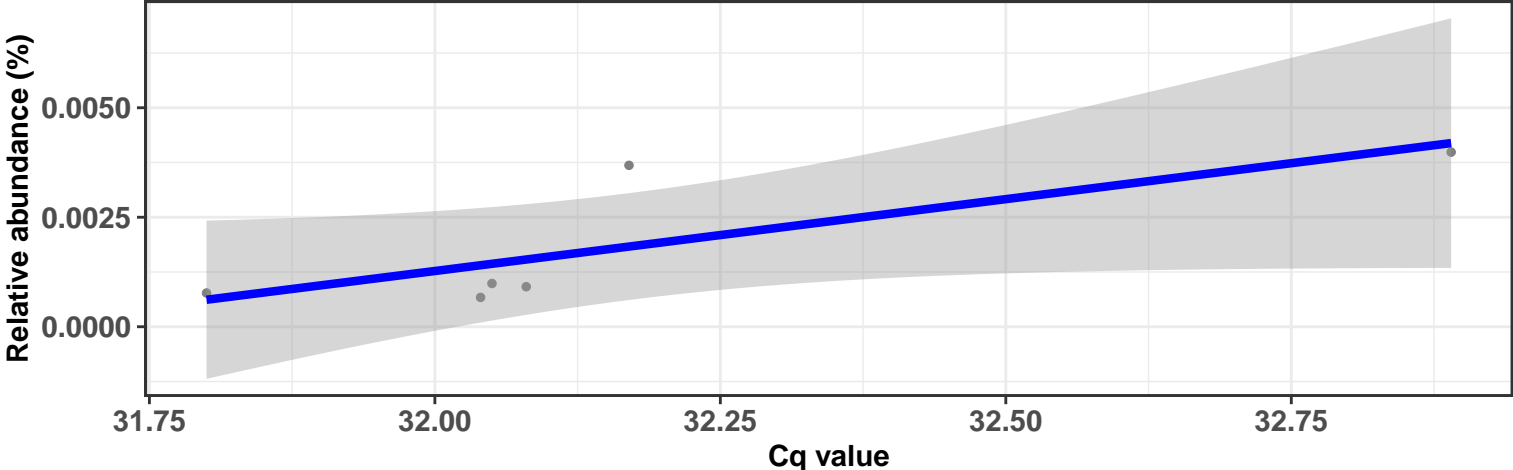


Correlation within: IM-DID



Correlation within: IM-DIM

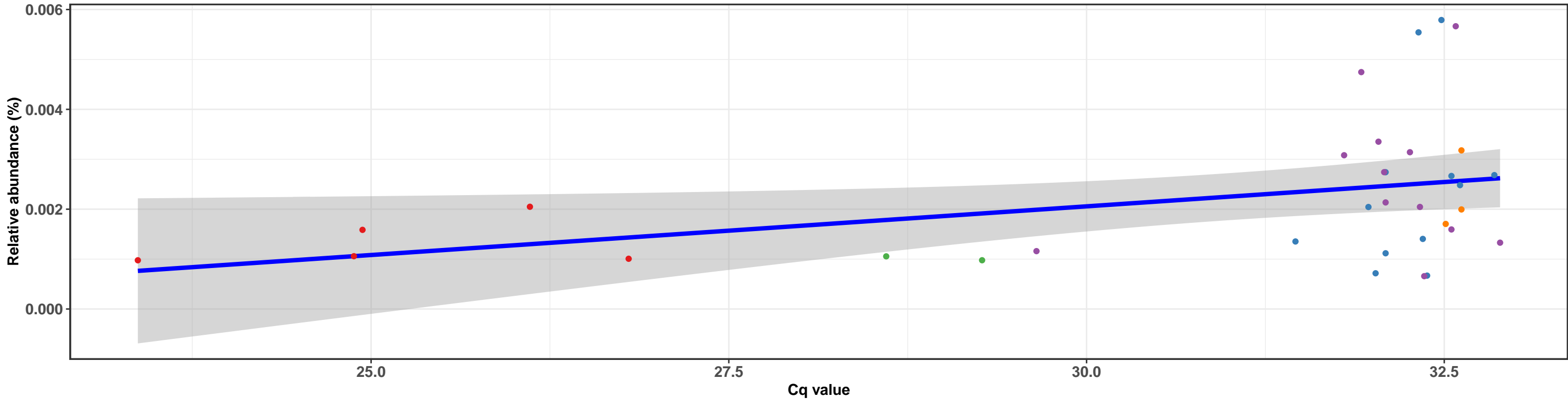
$\log_e(S) = 1.386$, $p = 0.019$, $\hat{\rho}_{\text{Spearman}} = 0.886$, $\text{CI}_{95\%} [0.484, 1.468]$, $n_{\text{pairs}} = 6$



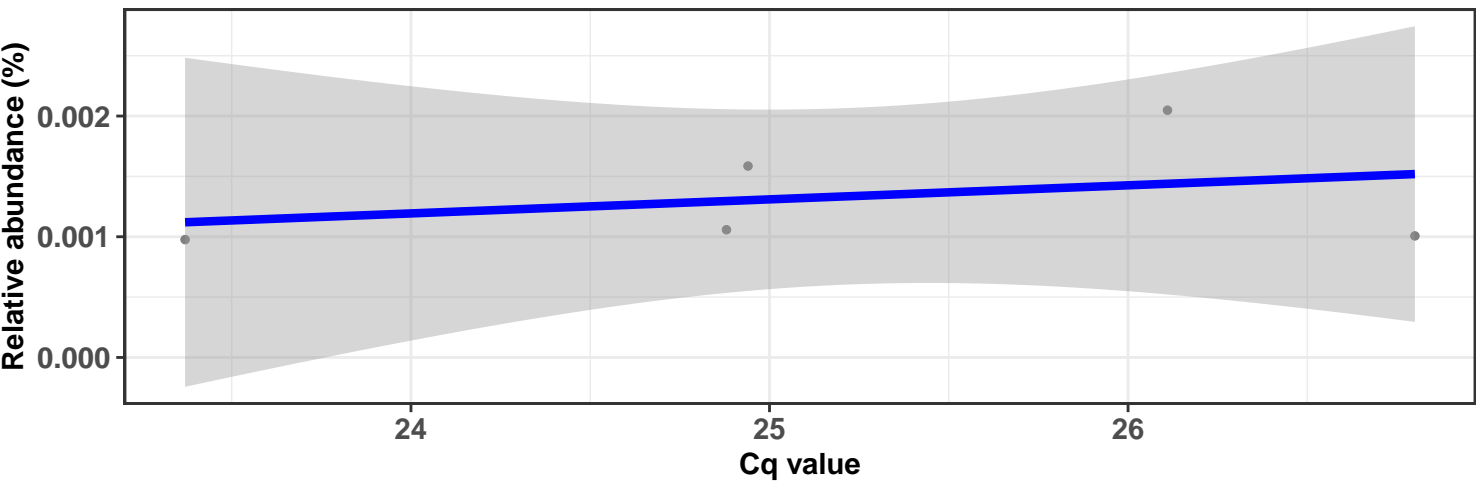
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 8.374$, $p = 0.050$, $\hat{\rho}_{\text{Spearman}} = 0.338$, $\text{CI}_{95\%} [0.038, 0.675]$, $n_{\text{pairs}} = 34$

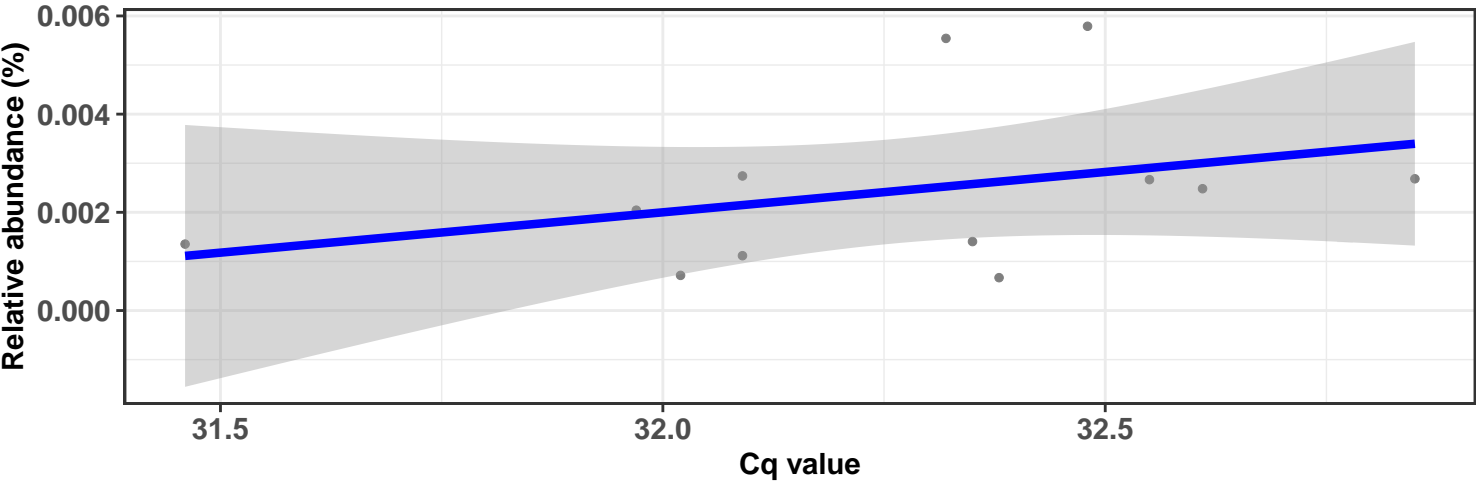


Correlation within: REF-DID

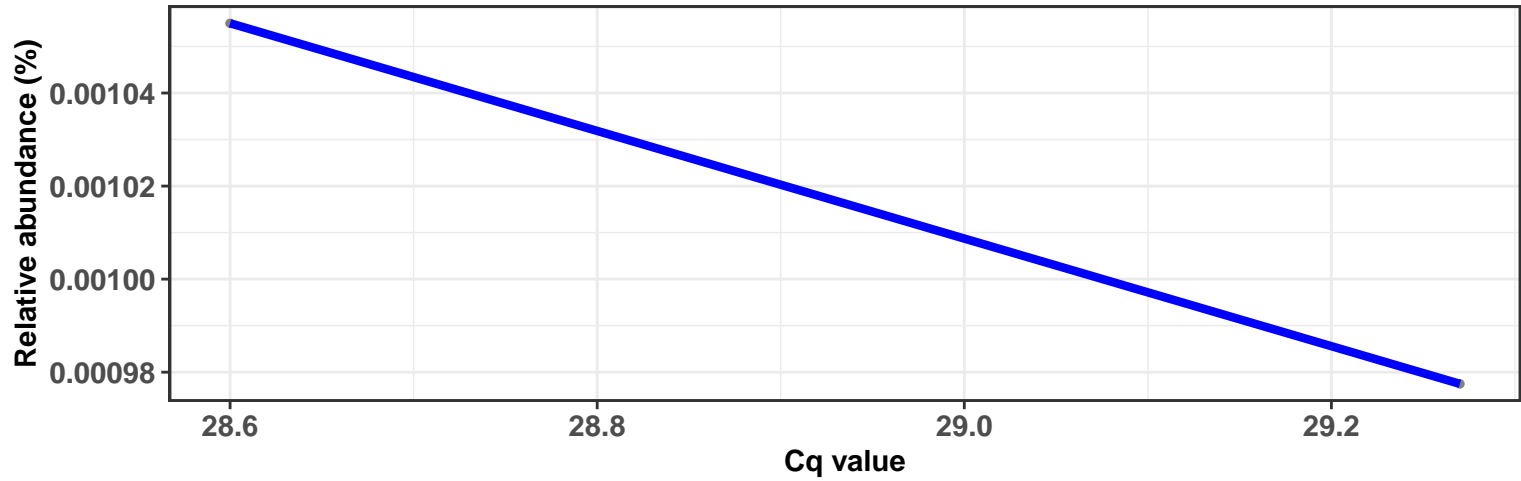


Correlation within: REF-DIM

$\log_e(S) = 5.164$, $p = 0.212$, $\hat{\rho}_{\text{Spearman}} = 0.389$, $\text{CI}_{95\%} [-0.040, 0.922]$, $n_{\text{pairs}} = 12$

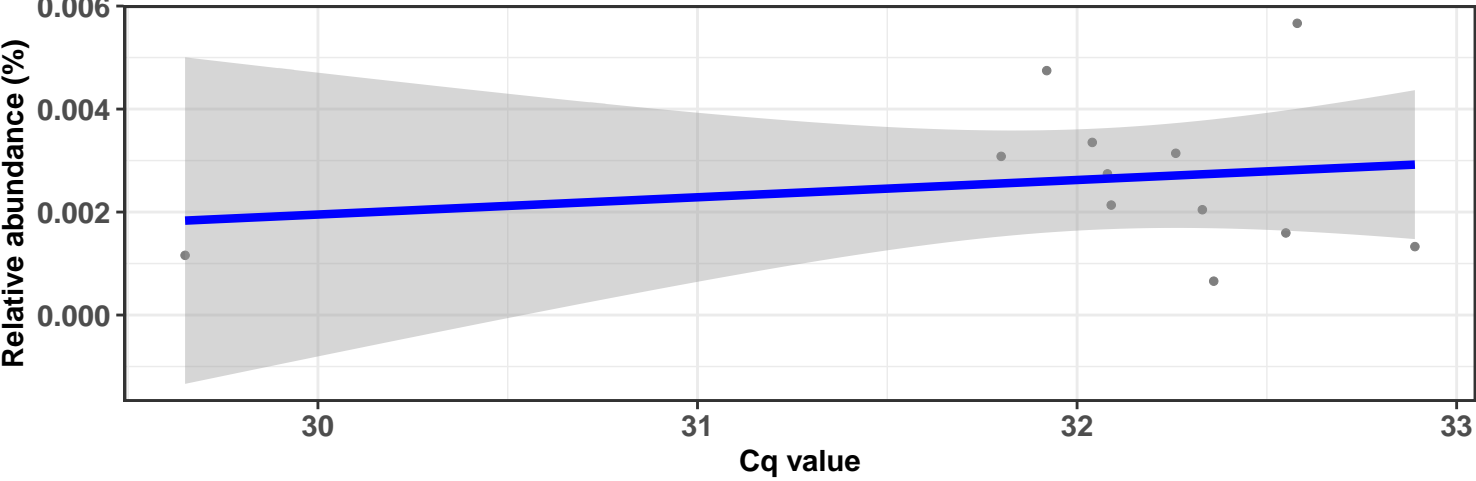


Correlation within: IM-DID



Correlation within: IM-DIM

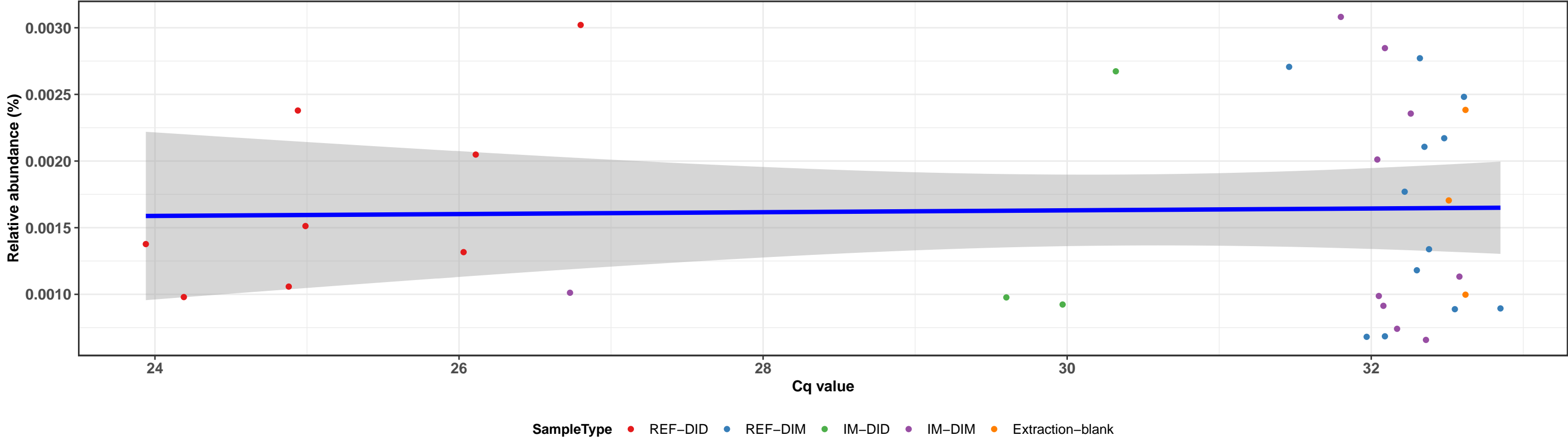
$\log_e(S) = 5.817$, $p = 0.587$, $\hat{\rho}_{\text{Spearman}} = -0.175$, $\text{CI}_{95\%} [-0.946, 0.468]$, $n_{\text{pairs}} = 12$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

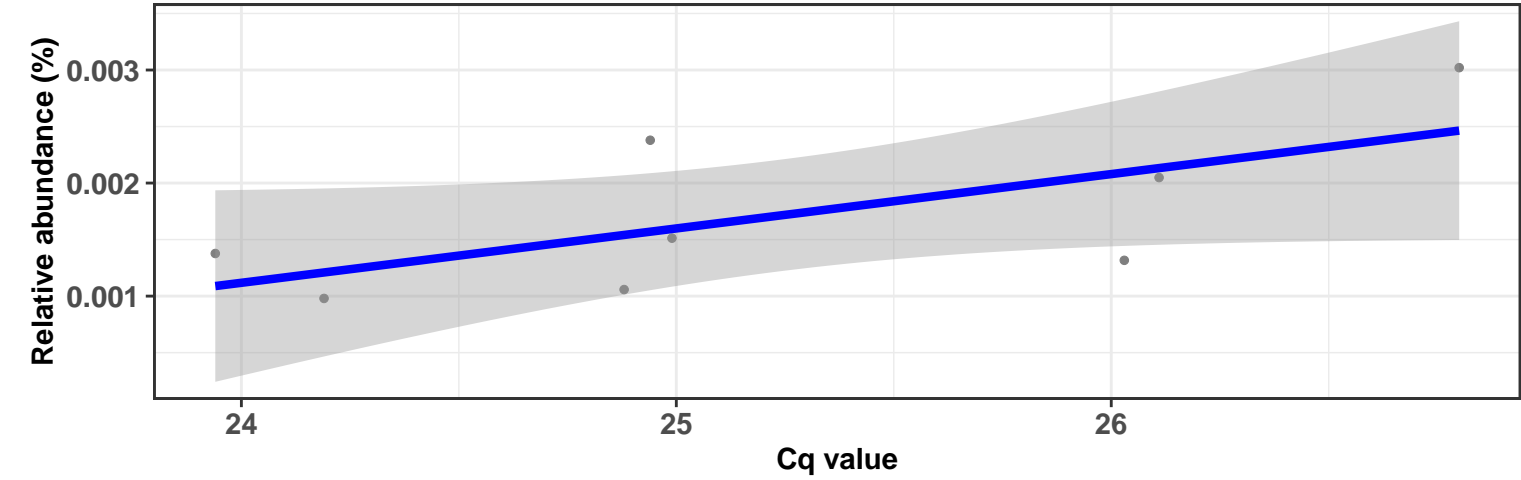
Correlation with all samples

$\log_e(S) = 9.013$, $p = 0.745$, $\hat{\rho}_{\text{Spearman}} = -0.056$, $\text{CI}_{95\%} [-0.345, 0.250]$, $n_{\text{pairs}} = 36$



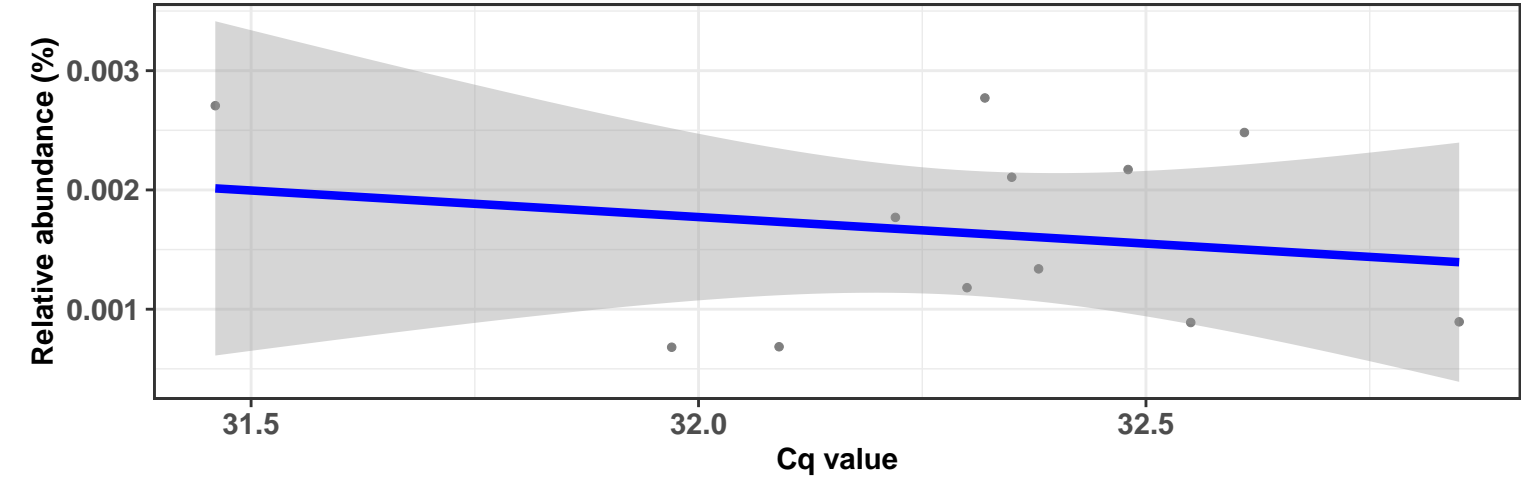
Correlation within: REF-DID

$\log_e(S) = 3.401$, $p = 0.086$, $\hat{\rho}_{\text{Spearman}} = 0.643$, $\text{CI}_{95\%} [0.158, 1.213]$, $n_{\text{pairs}} = 8$

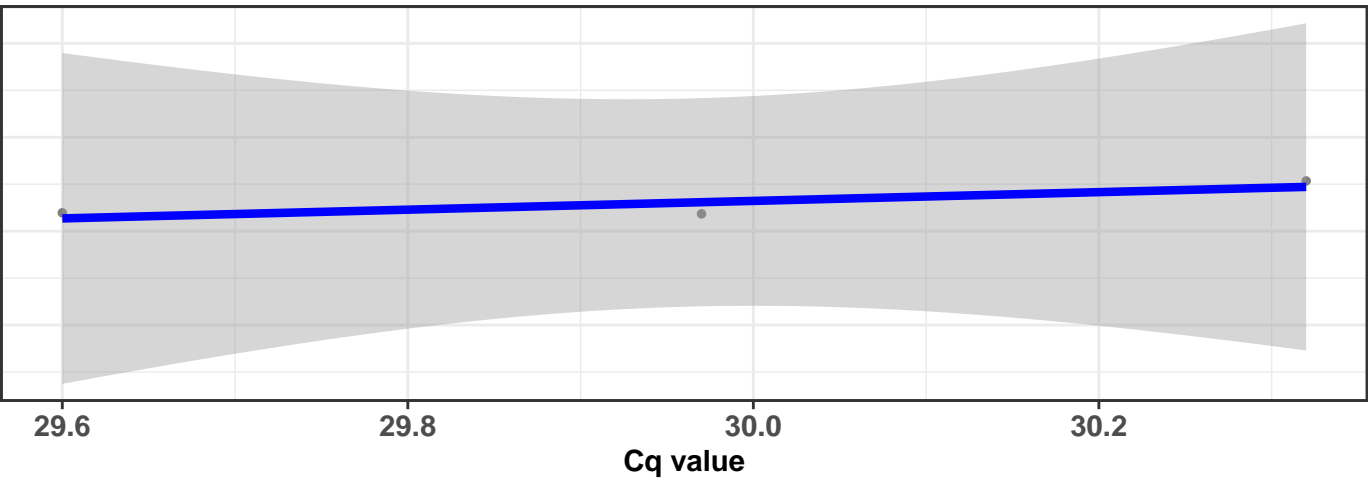


Correlation within: REF-DIM

$\log_e(S) = 5.583$, $p = 0.829$, $\hat{\rho}_{\text{Spearman}} = 0.070$, $\text{CI}_{95\%} [-0.653, 0.785]$, $n_{\text{pairs}} = 12$

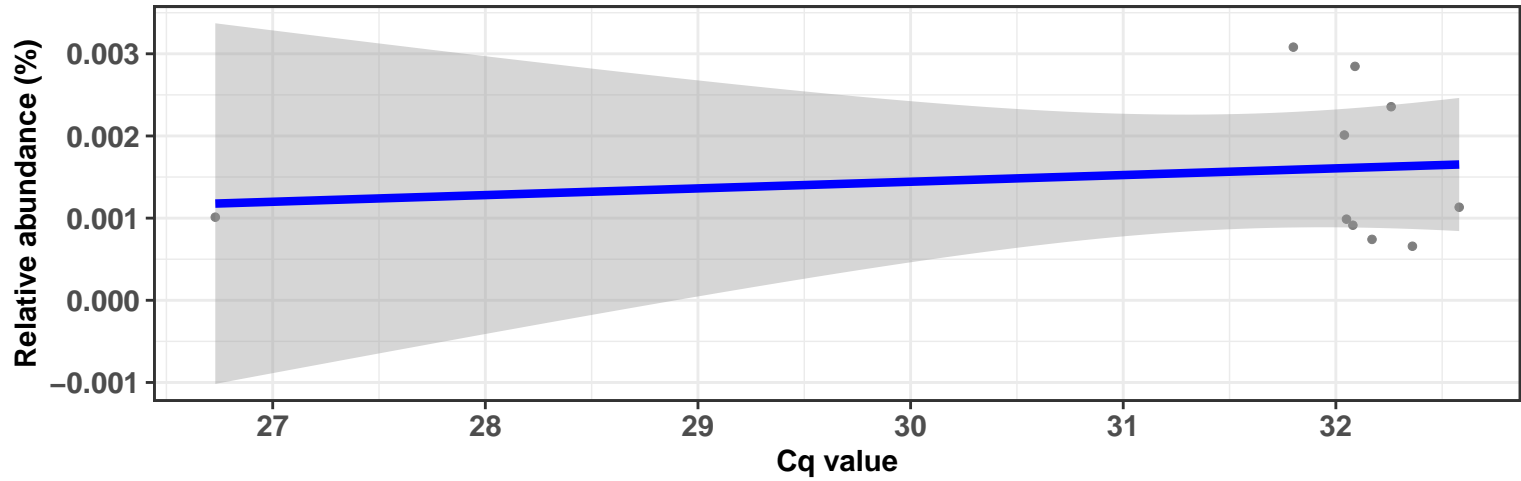


Correlation within: IM-DID



Correlation within: IM-DIM

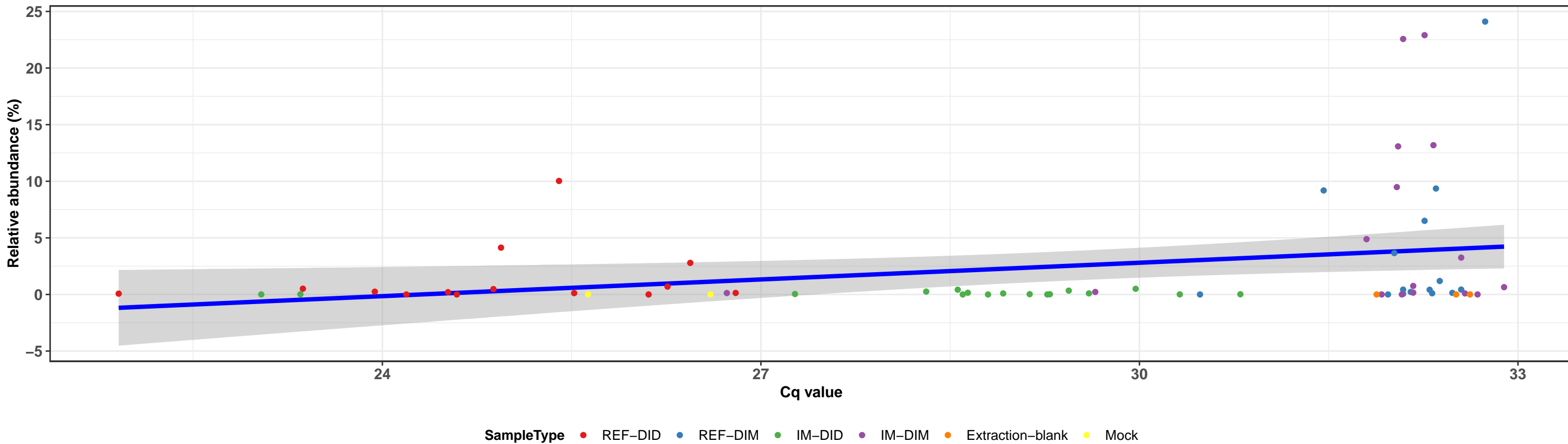
$\log_e(S) = 5.366$, $p = 0.405$, $\hat{\rho}_{\text{Spearman}} = -0.297$, $\text{CI}_{95\%} [-0.973, 0.307]$, $n_{\text{pairs}} = 10$



k__Bacteria; p__Spirochaetes; c__Spirochaetia; o__Spirochaetales; f__Spirochaetaceae; NA; NA

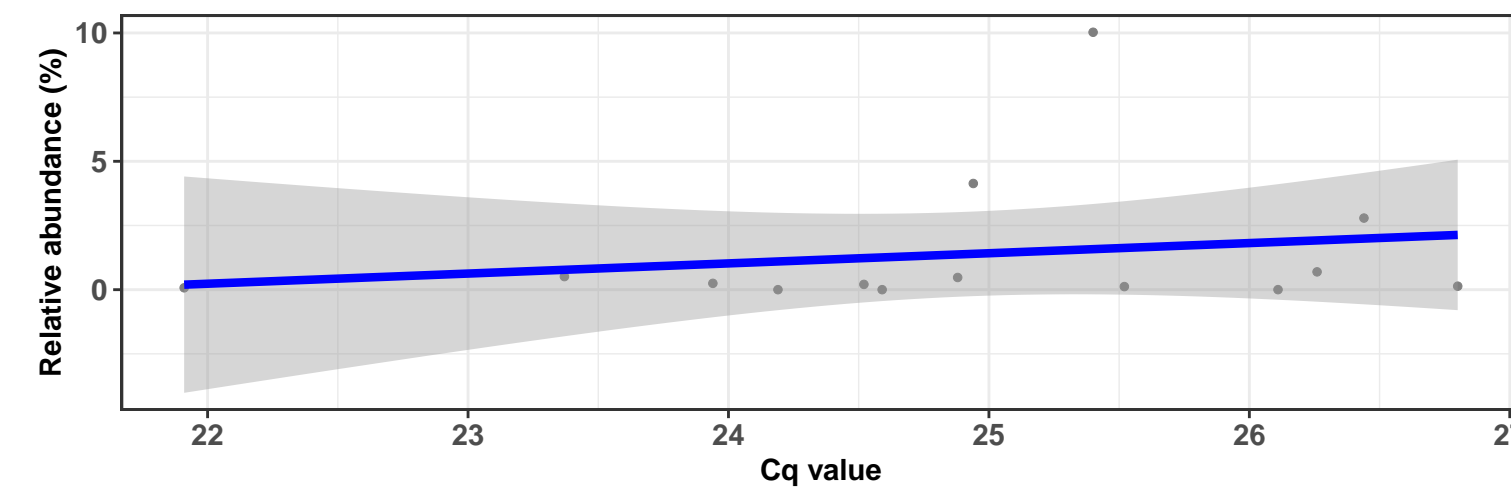
Correlation with all samples

$\log_e(S) = 10.544$, $p = 0.048$, $\hat{\rho}_{\text{Spearman}} = 0.243$, $\text{CI}_{95\%} [0.014, 0.490]$, $n_{\text{pairs}} = 67$



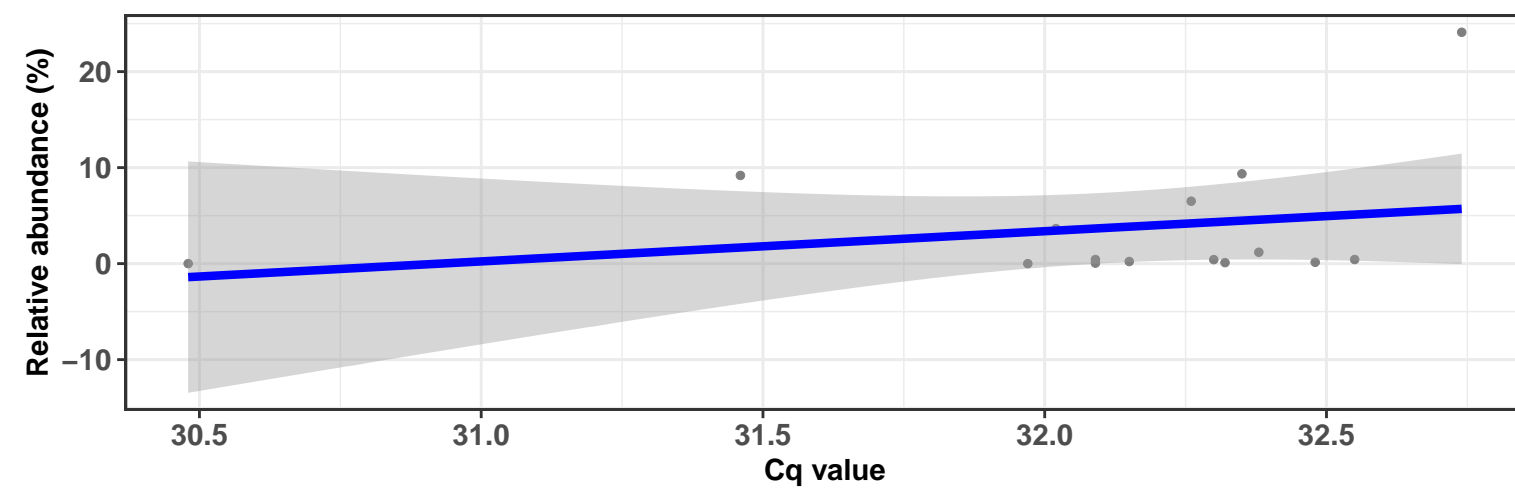
Correlation within: REF-DID

$\log_e(S) = 5.829$, $p = 0.383$, $\hat{\rho}_{\text{Spearman}} = 0.253$, $\text{CI}_{95\%} [-0.138, 0.727]$, $n_{\text{pairs}} = 14$



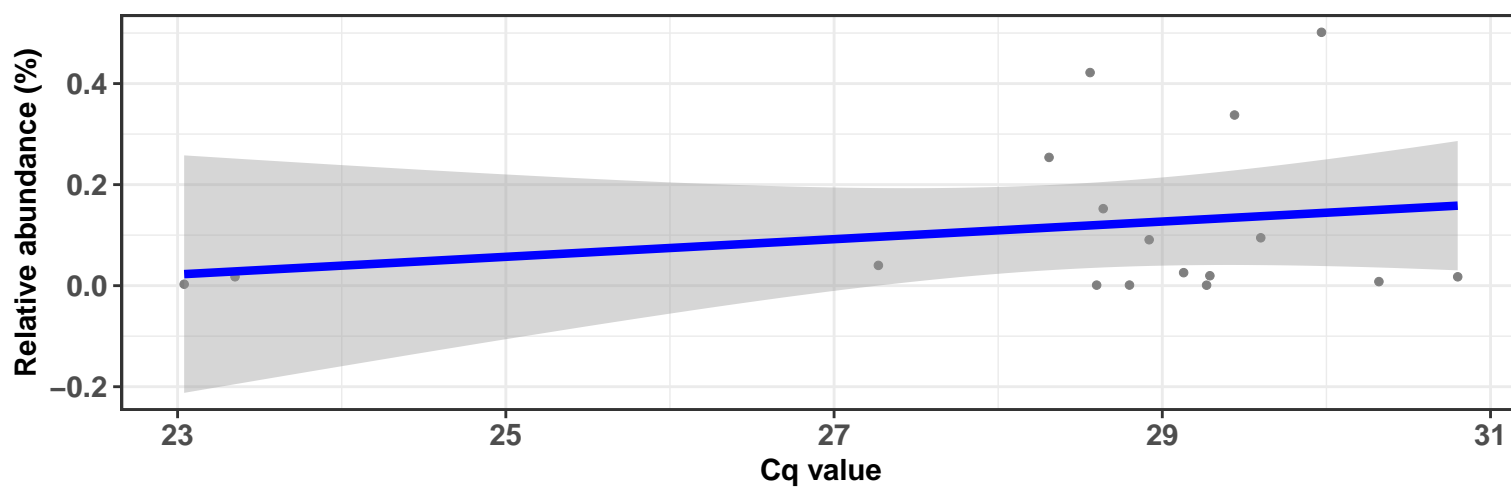
Correlation within: REF-DIM

$\log_e(S) = 5.849$, $p = 0.162$, $\hat{\rho}_{\text{Spearman}} = 0.381$, $\text{CI}_{95\%} [-0.098, 0.972]$, $n_{\text{pairs}} = 15$



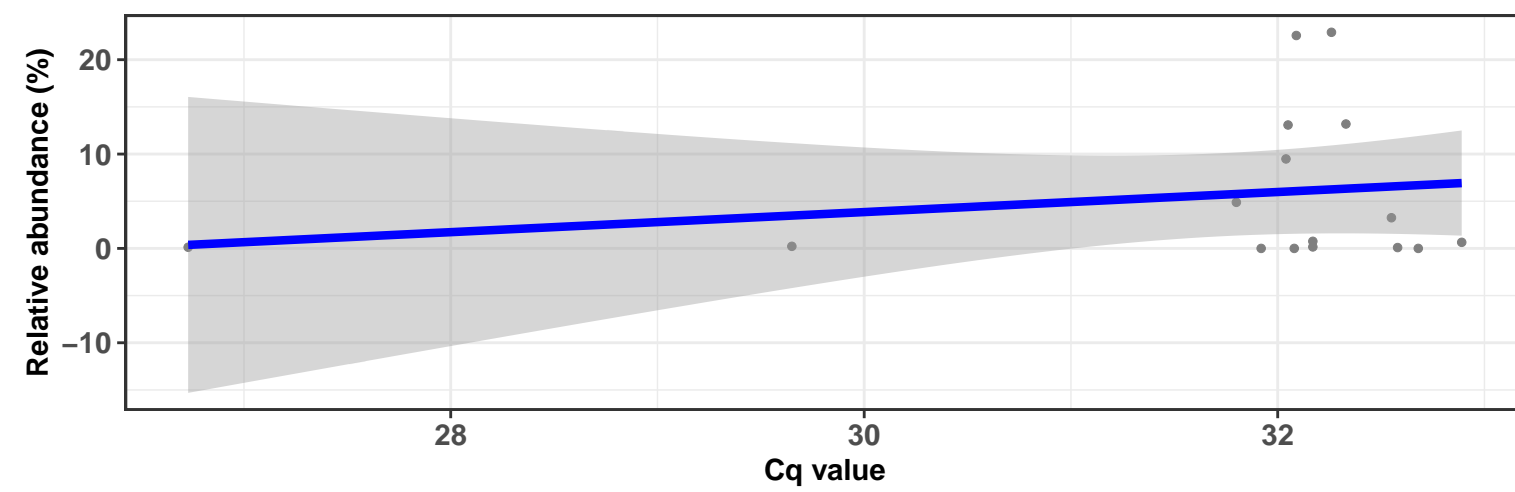
Correlation within: IM-DID

$\log_e(S) = 6.628$, $p = 0.779$, $\hat{\rho}_{\text{Spearman}} = 0.074$, $\text{CI}_{95\%} [-0.345, 0.549]$, $n_{\text{pairs}} = 17$



Correlation within: IM-DIM

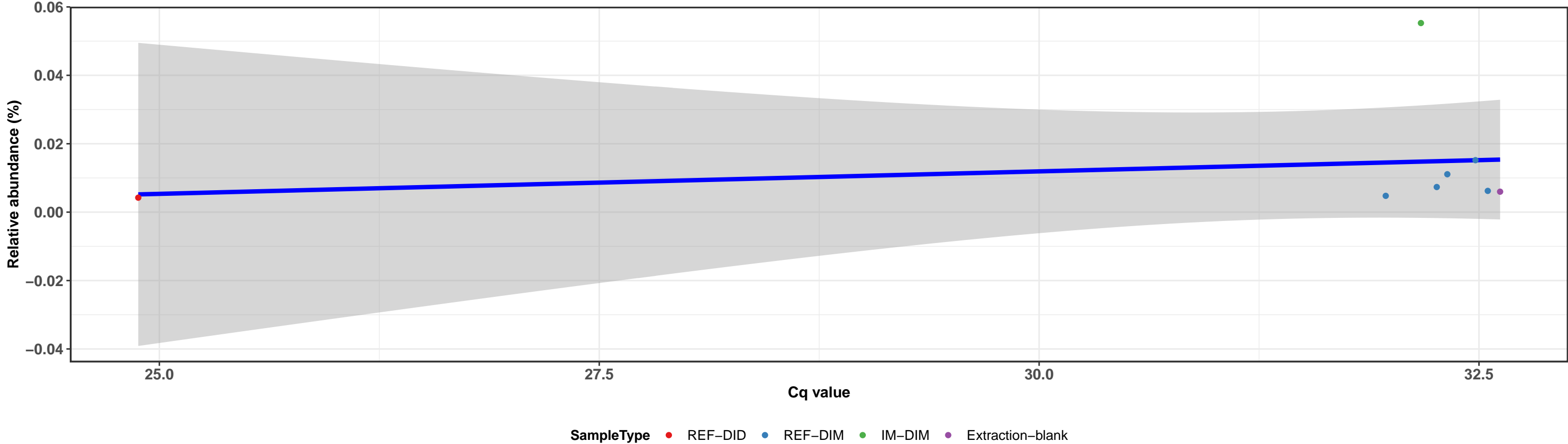
$\log_e(S) = 6.494$, $p = 0.918$, $\hat{\rho}_{\text{Spearman}} = 0.028$, $\text{CI}_{95\%} [-0.432, 0.514]$, $n_{\text{pairs}} = 16$



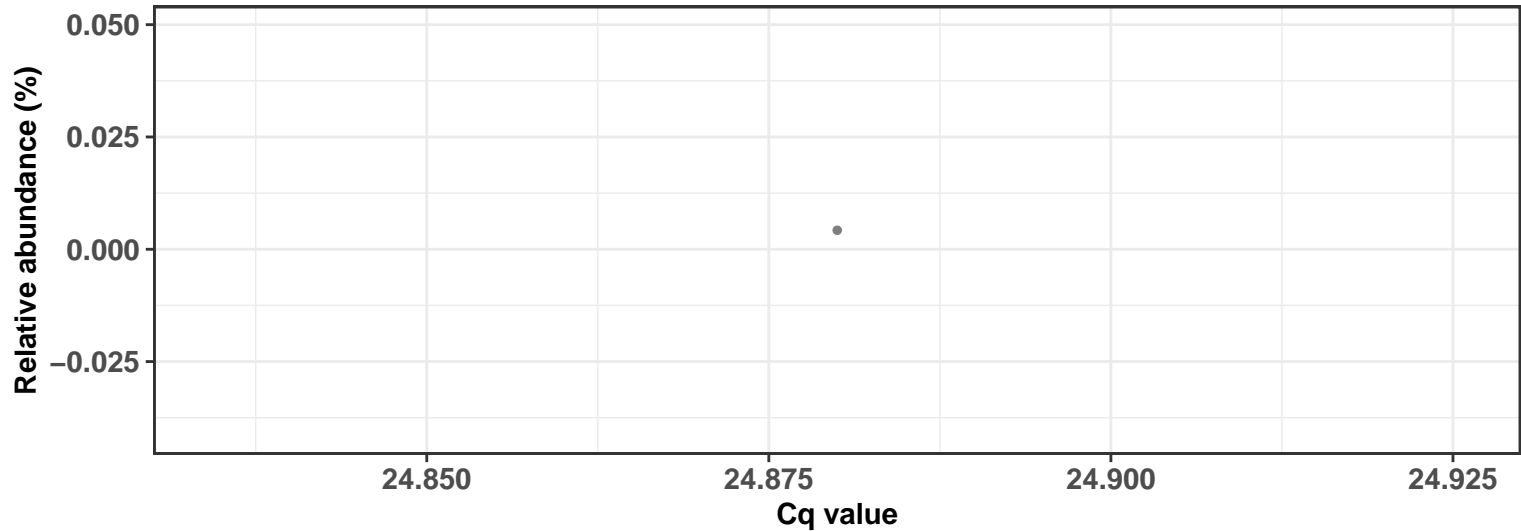
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; NA

Correlation with all samples

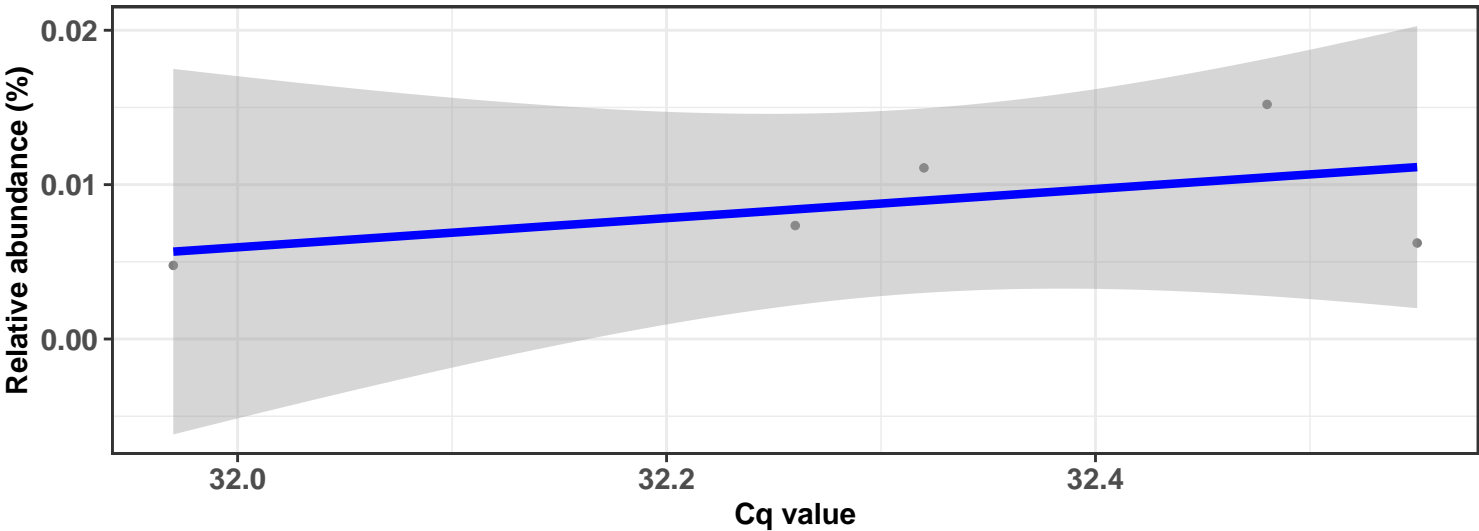
$\log_e(S) = 4.127$, $p = 0.531$, $\hat{\rho}_{\text{Spearman}} = 0.262$, $\text{CI}_{95\%} [-0.693, 1.490]$, $n_{\text{pairs}} = 8$



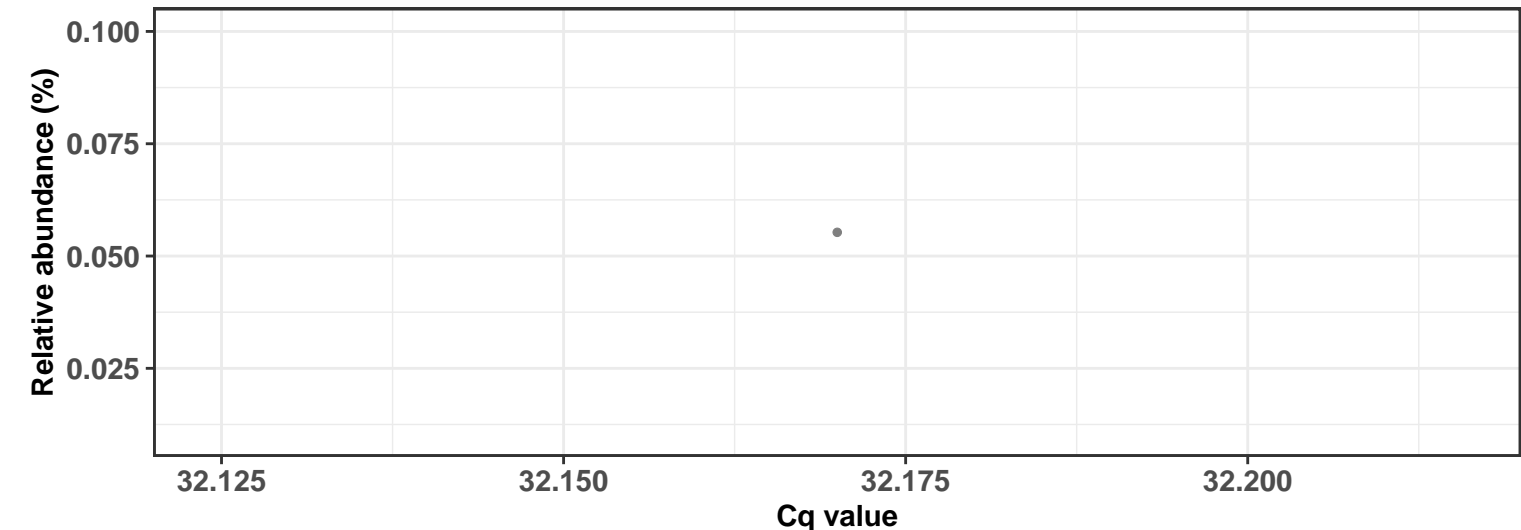
Correlation within: REF-DID



Correlation within: REF-DIM



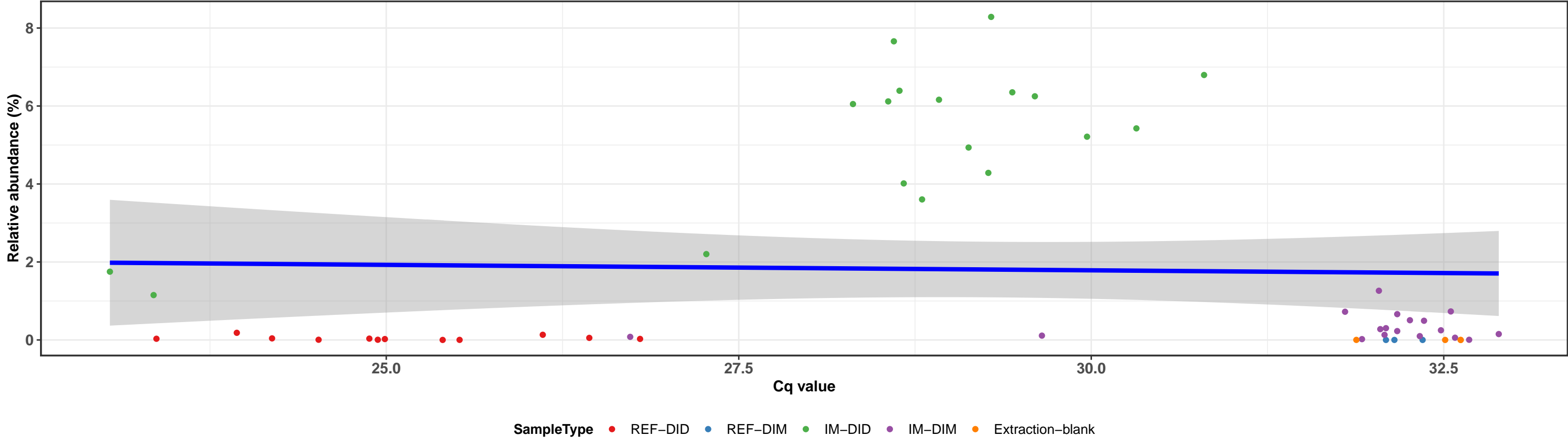
Correlation within: IM-DIM



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

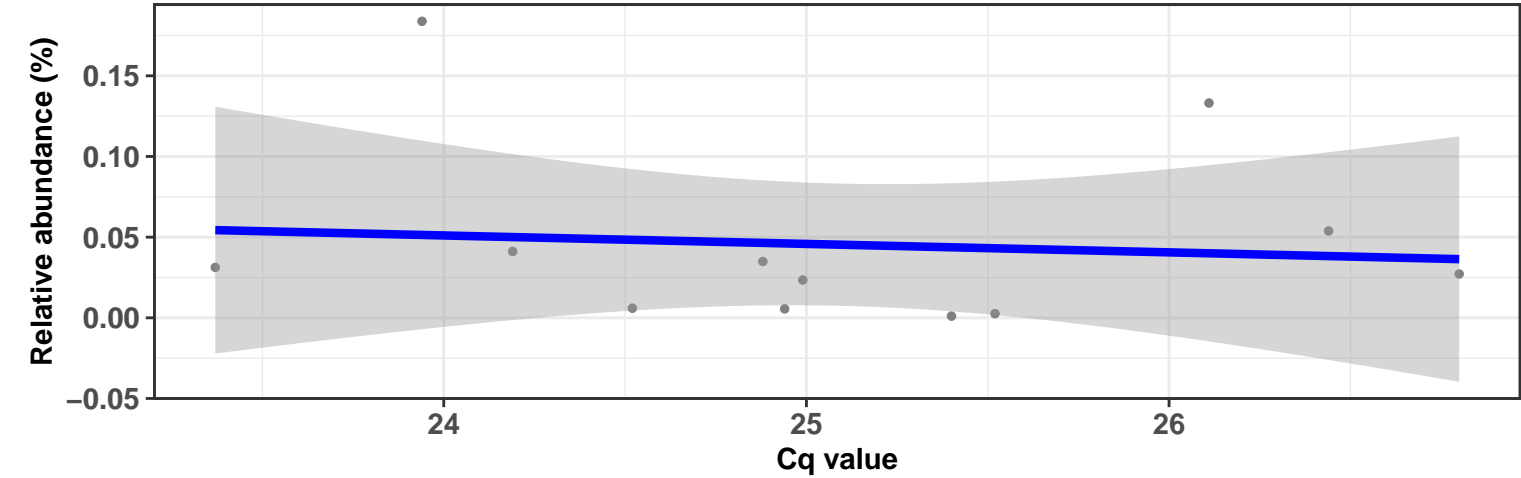
Correlation with all samples

$\log_e(S) = 10.372$, $p = 0.267$, $\hat{\rho}_{\text{Spearman}} = -0.152$, $\text{CI}_{95\%} [-0.405, 0.132]$, $n_{\text{pairs}} = 55$

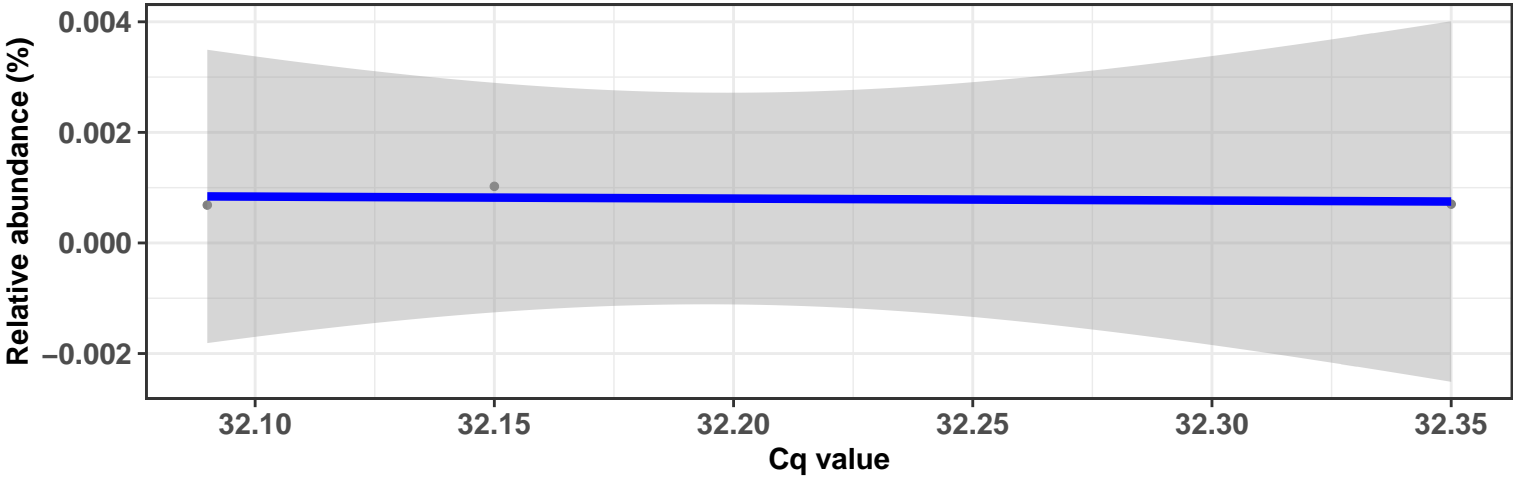


Correlation within: REF-DID

$\log_e(S) = 5.799$, $p = 0.633$, $\hat{\rho}_{\text{Spearman}} = -0.154$, $\text{CI}_{95\%} [-0.726, 0.409]$, $n_{\text{pairs}} = 12$

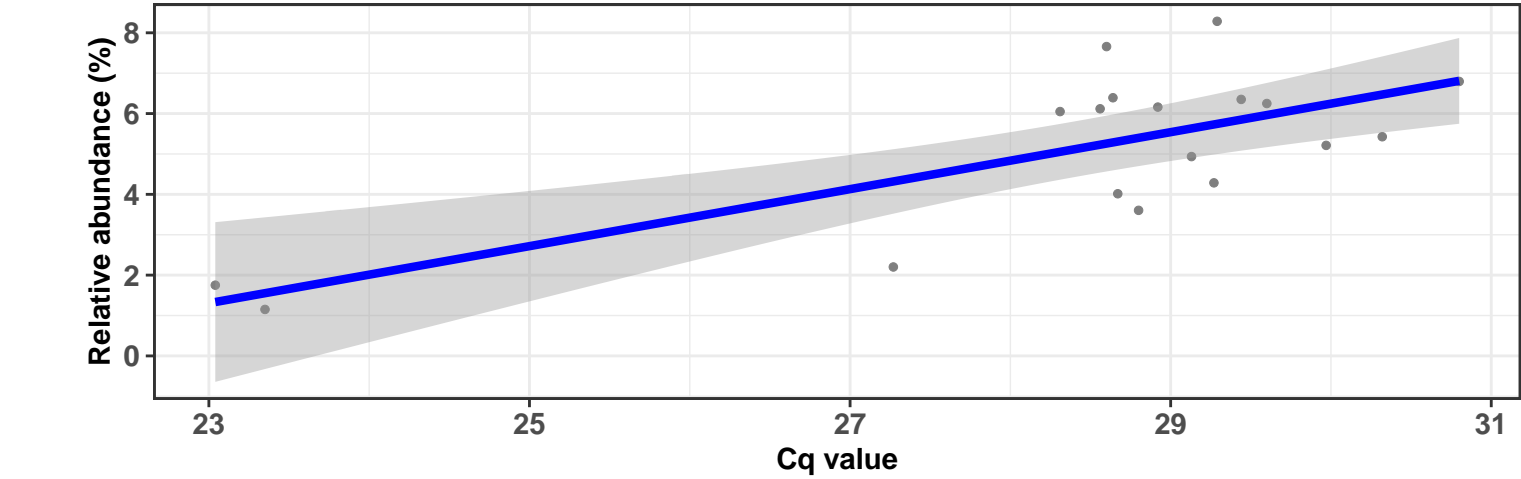


Correlation within: REF-DIM



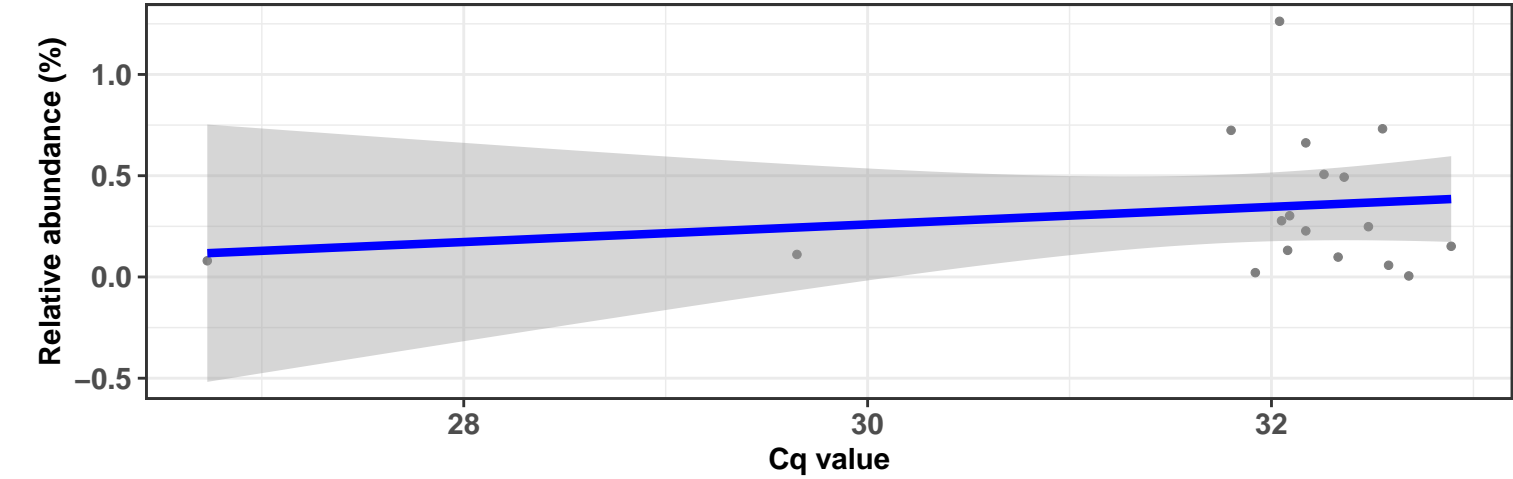
Correlation within: IM-DID

$\log_e(S) = 6.234$, $p = 0.047$, $\hat{\rho}_{\text{Spearman}} = 0.474$, $\text{CI}_{95\%} [0.041, 0.997]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

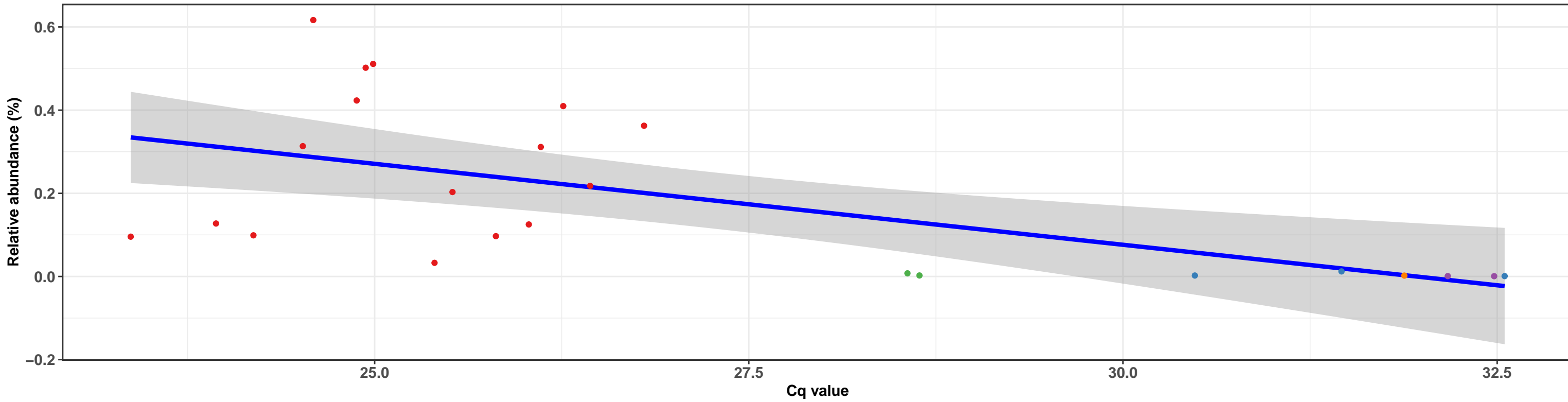
$\log_e(S) = 6.949$, $p = 0.766$, $\hat{\rho}_{\text{Spearman}} = -0.075$, $\text{CI}_{95\%} [-0.585, 0.493]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Family XI; g__Tepidimicrobium; s__Tepidimicrobium sp. GRC1

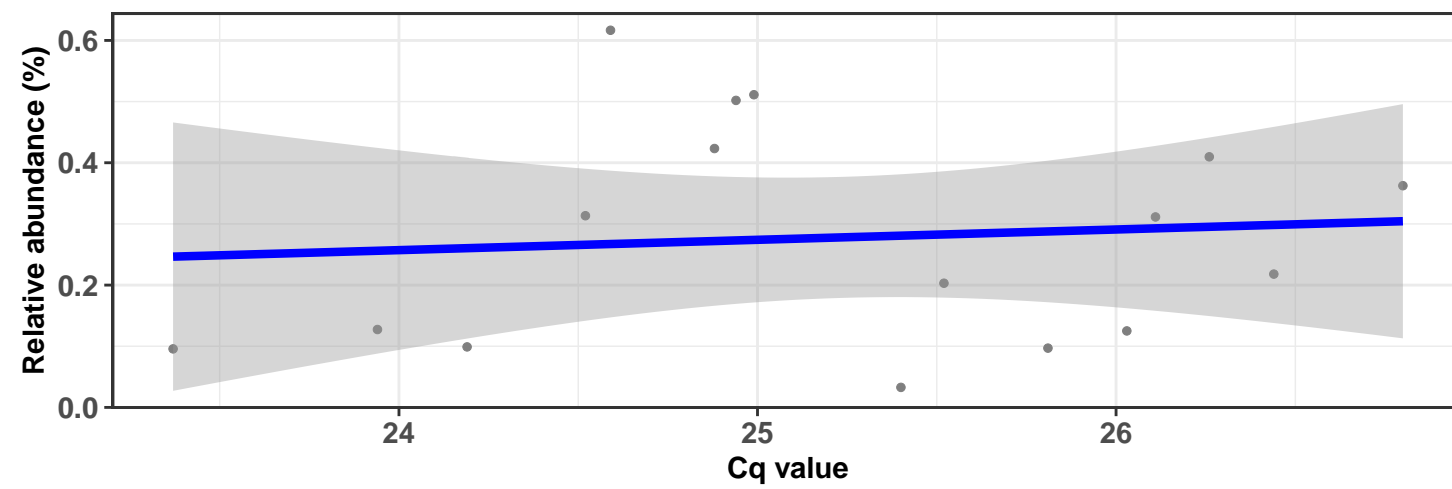
Correlation with all samples

$\log_e(S) = 8.250$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.664$, $\text{CI}_{95\%} [-0.979, -0.389]$, $n_{\text{pairs}} = 24$

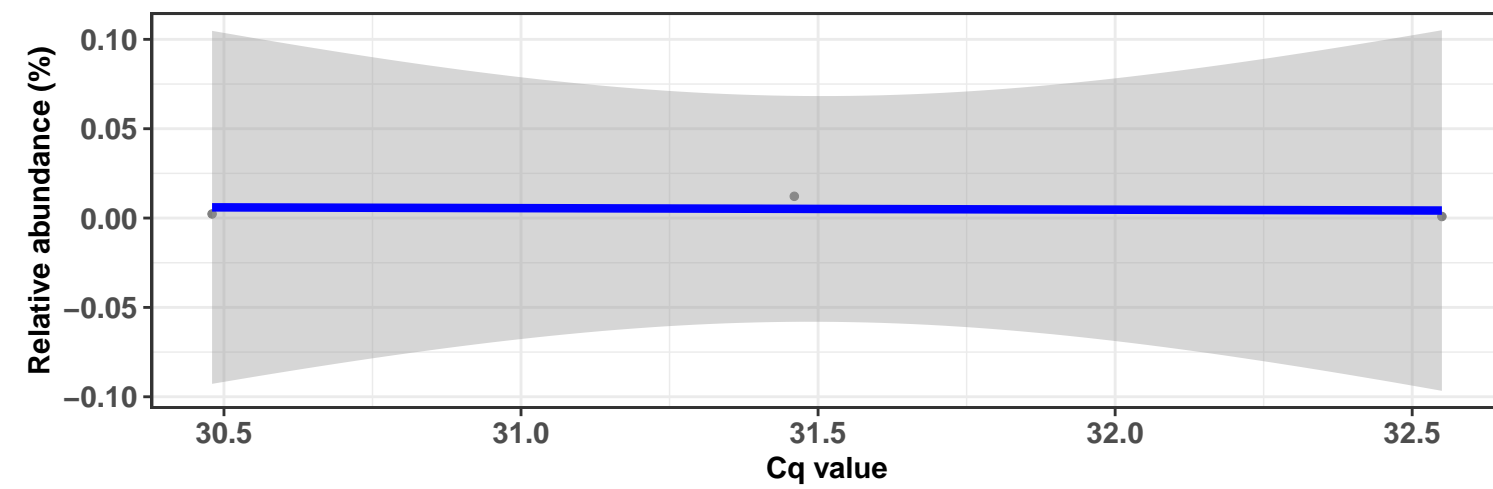


Correlation within: REF-DID

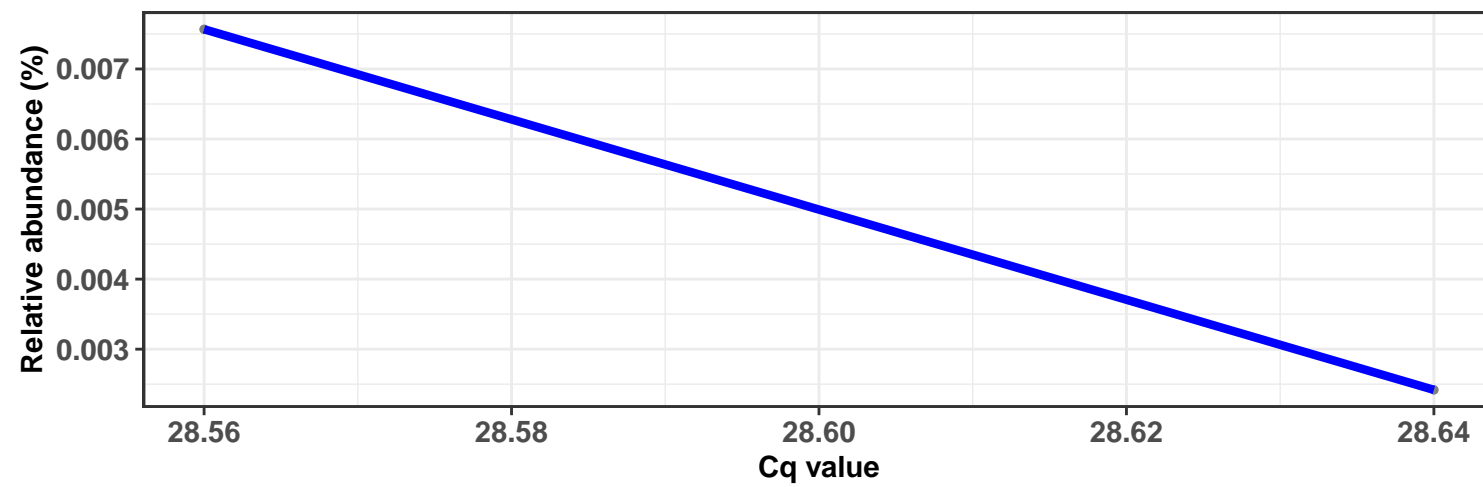
$\log_e(S) = 6.400$, $p = 0.672$, $\hat{\rho}_{\text{Spearman}} = 0.115$, $\text{CI}_{95\%} [-0.379, 0.562]$, $n_{\text{pairs}} = 16$



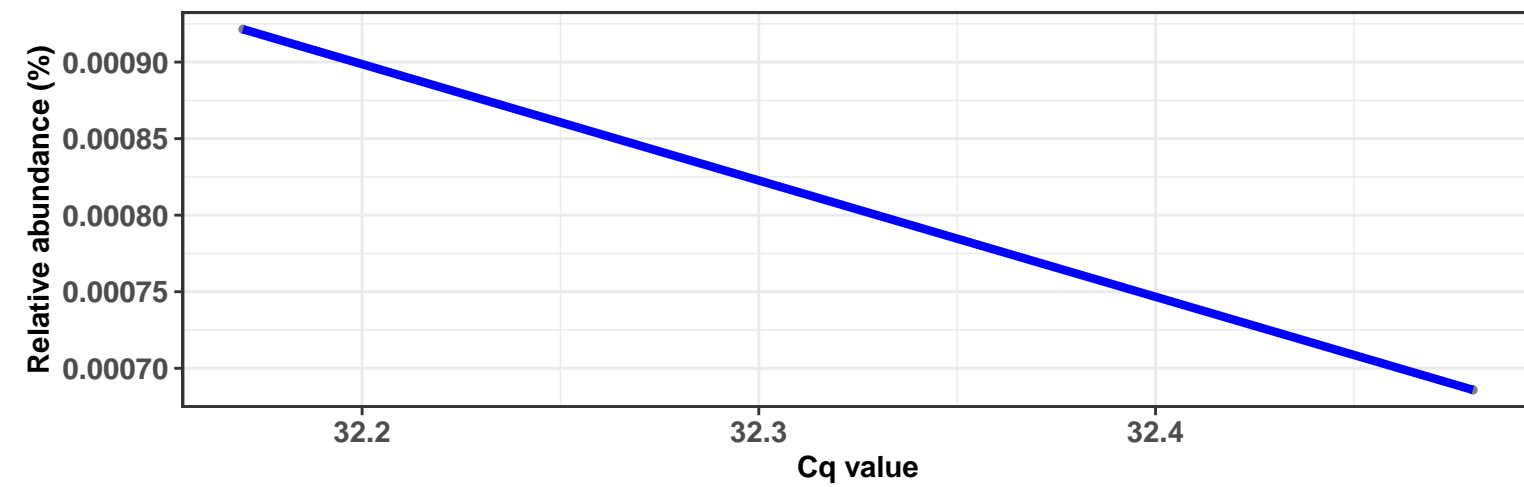
Correlation within: REF-DIM



Correlation within: IM-DID



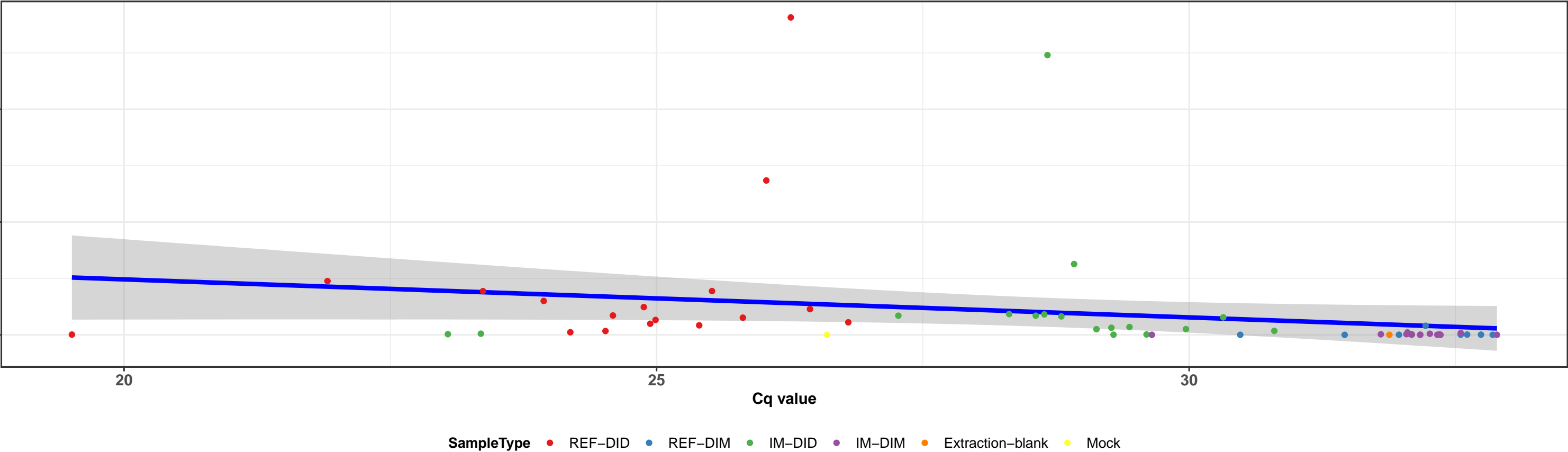
Correlation within: IM-DIM



k__Bacteria; p__Tenericutes; c__Mollicutes; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma; s__uncultured bacterium

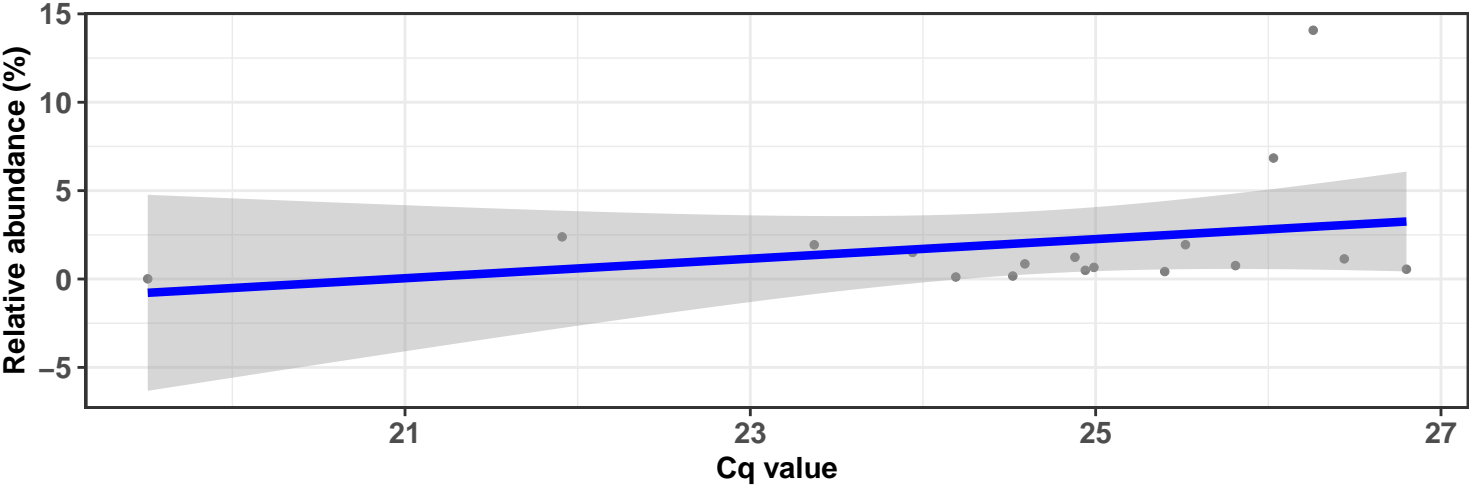
Correlation with all samples

$\log_e(S) = 10.967$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.609$, $\text{CI}_{95\%} [-0.768, -0.444]$, $n_{\text{pairs}} = 60$



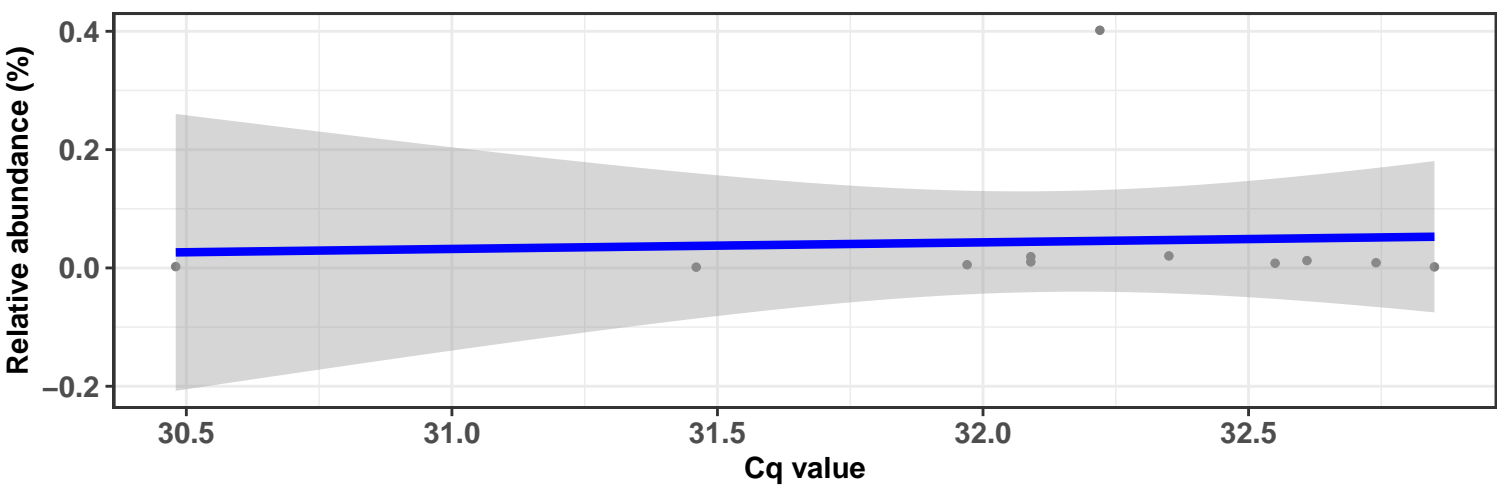
Correlation within: REF-DID

$\log_e(S) = 6.449$, $p = 0.384$, $\hat{\rho}_{\text{Spearman}} = 0.225$, $\text{CI}_{95\%} [-0.334, 0.801]$, $n_{\text{pairs}} = 17$



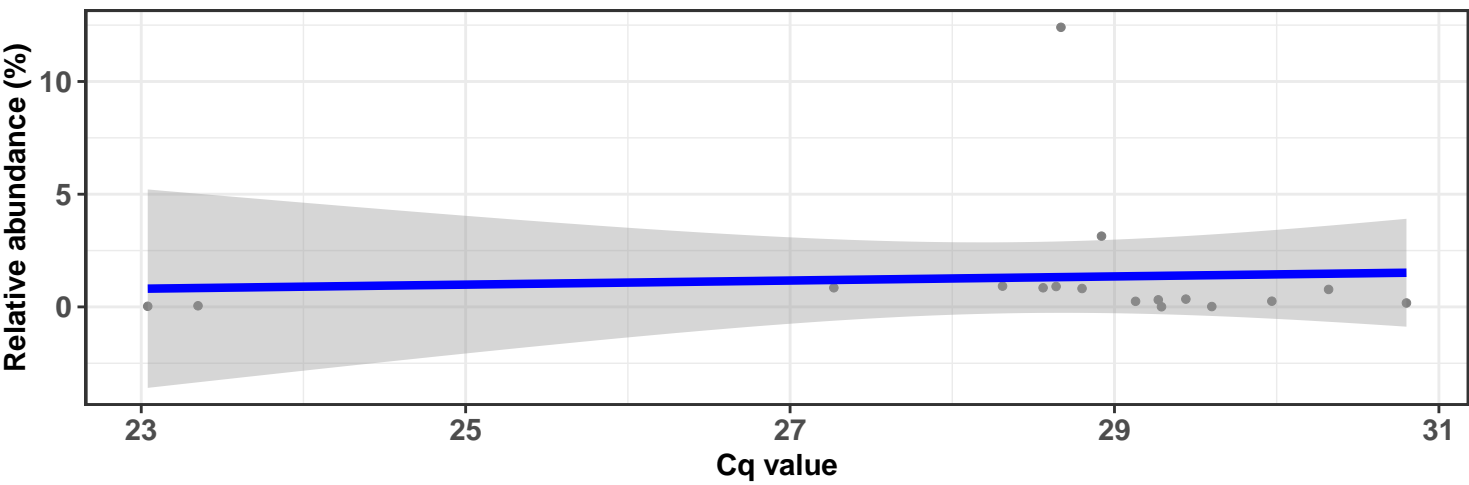
Correlation within: REF-DIM

$\log_e(S) = 5.158$, $p = 0.536$, $\hat{\rho}_{\text{Spearman}} = 0.210$, $\text{CI}_{95\%} [-0.518, 0.954]$, $n_{\text{pairs}} = 11$



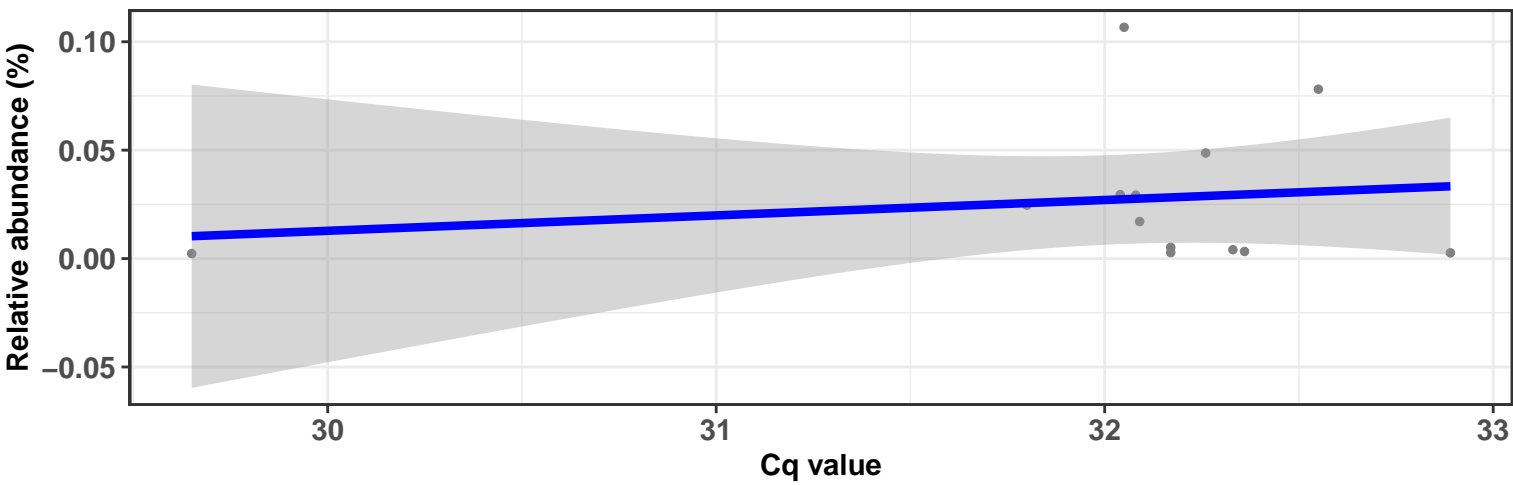
Correlation within: IM-DID

$\log_e(S) = 6.957$, $p = 0.264$, $\hat{\rho}_{\text{Spearman}} = -0.287$, $\text{CI}_{95\%} [-0.887, 0.282]$, $n_{\text{pairs}} = 17$



Correlation within: IM-DIM

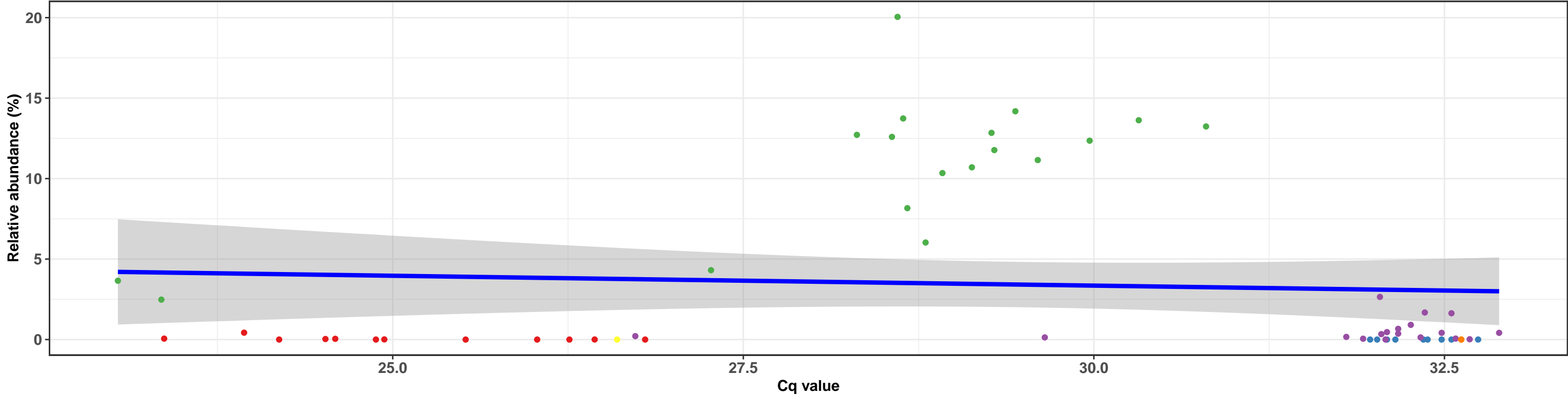
$\log_e(S) = 6.004$, $p = 0.714$, $\hat{\rho}_{\text{Spearman}} = -0.113$, $\text{CI}_{95\%} [-0.814, 0.639]$, $n_{\text{pairs}} = 13$



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

Correlation with all samples

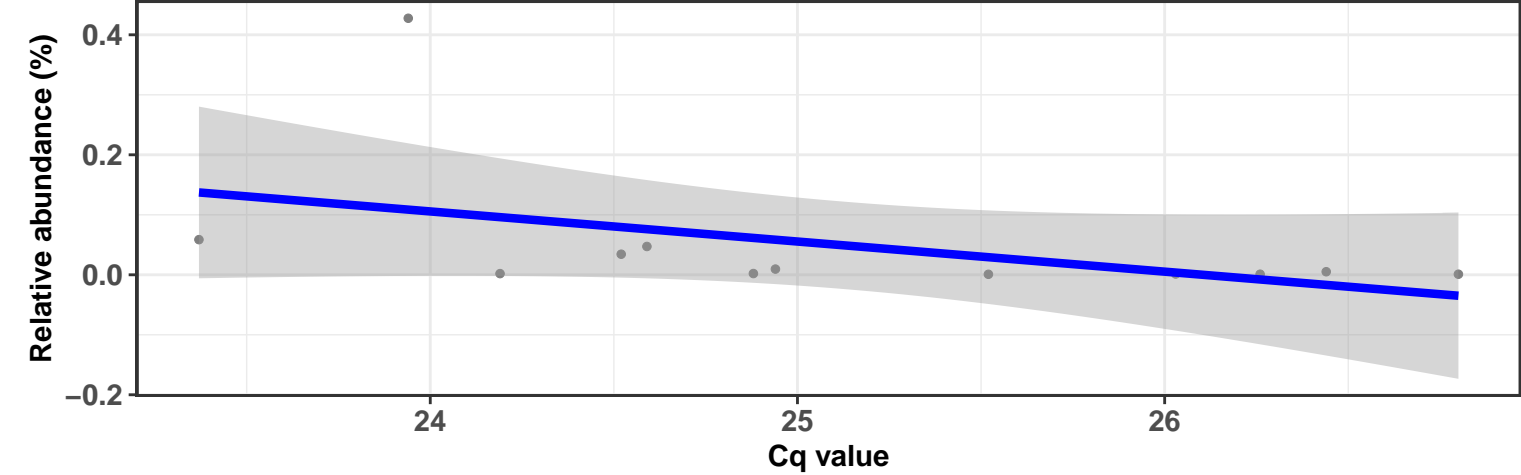
$\log_e(S) = 10.613$, $p = 0.324$, $\hat{\rho}_{\text{Spearman}} = -0.130$, $\text{CI}_{95\%} [-0.369, 0.128]$, $n_{\text{pairs}} = 60$



SampleType REF-DID REF-DIM IM-DID IM-DIM Extraction-blank Mock

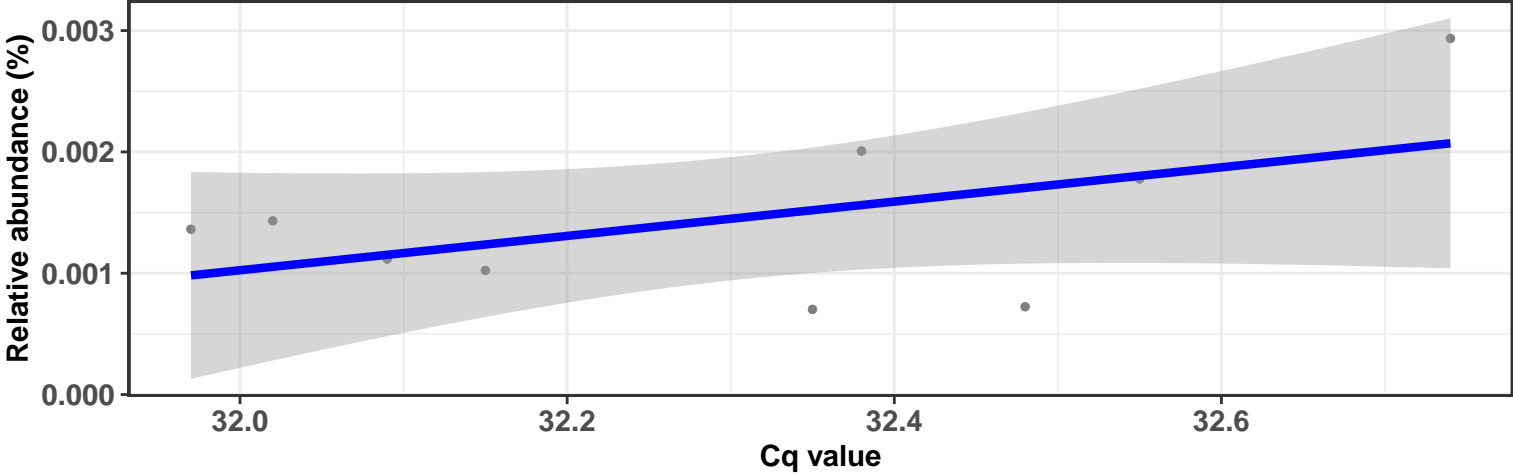
Correlation within: REF-DID

$\log_e(S) = 6.194$, $p = 0.009$, $\hat{\rho}_{\text{Spearman}} = -0.713$, $\text{CI}_{95\%} [-1.089, -0.434]$, $n_{\text{pairs}} = 12$



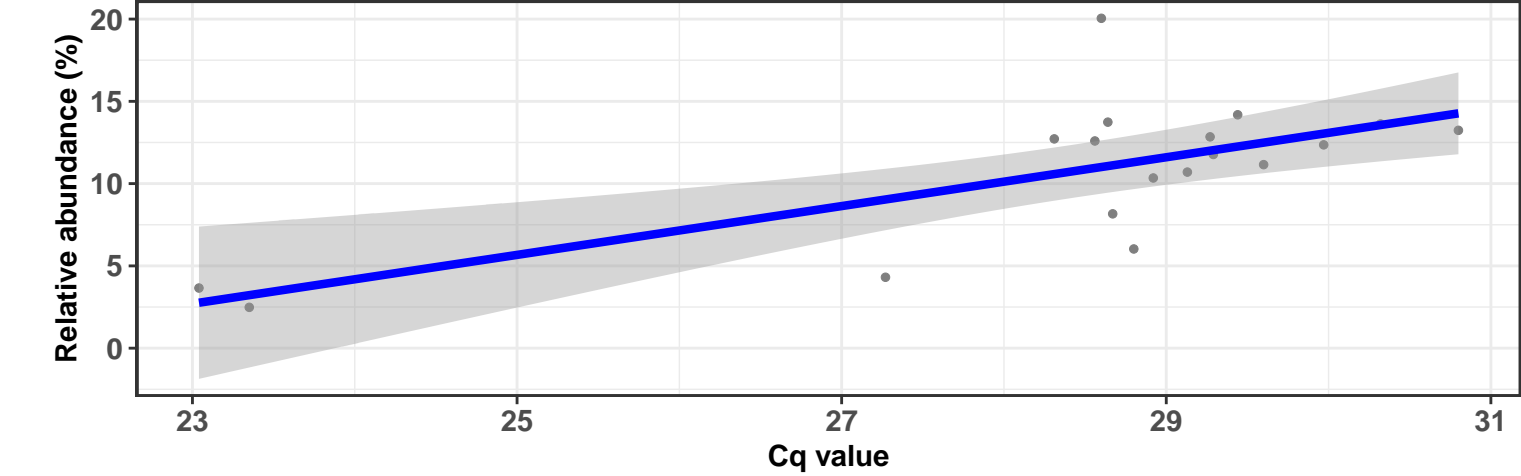
Correlation within: REF-DIM

$\log_e(S) = 4.382$, $p = 0.381$, $\hat{\rho}_{\text{Spearman}} = 0.333$, $\text{CI}_{95\%} [-0.523, 1.119]$, $n_{\text{pairs}} = 9$



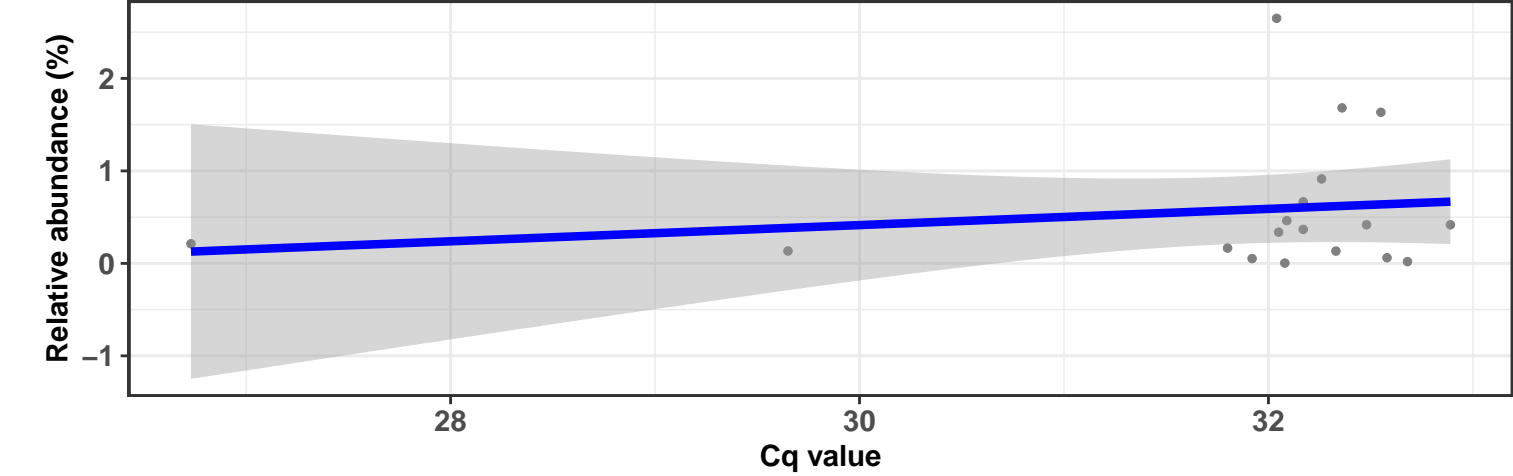
Correlation within: IM-DID

$\log_e(S) = 6.261$, $p = 0.055$, $\hat{\rho}_{\text{Spearman}} = 0.459$, $\text{CI}_{95\%} [0.057, 0.907]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

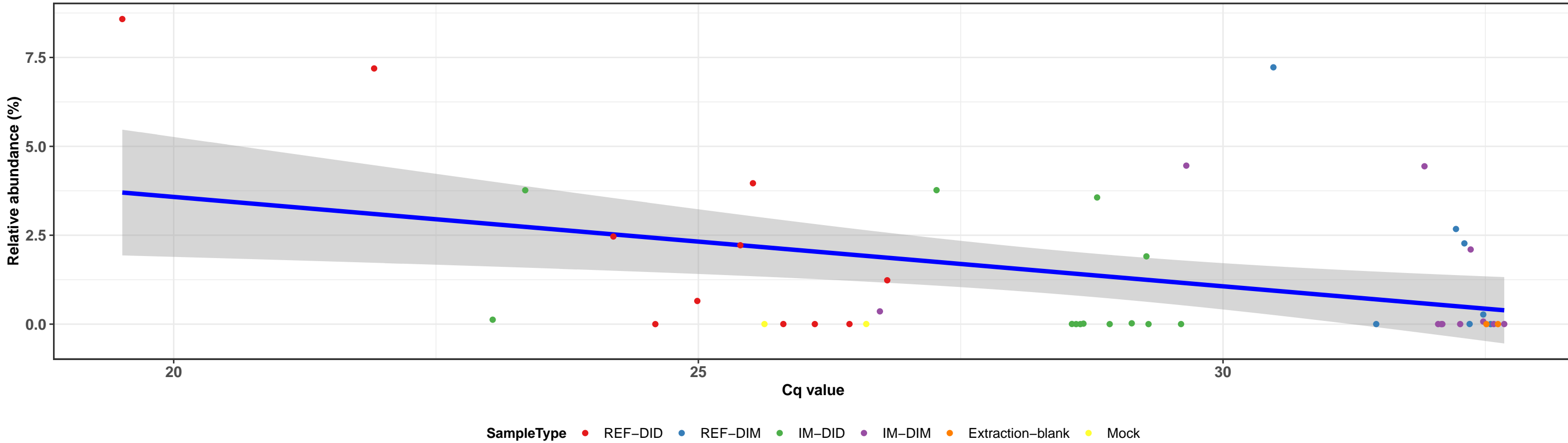
$\log_e(S) = 6.740$, $p = 0.616$, $\hat{\rho}_{\text{Spearman}} = 0.127$, $\text{CI}_{95\%} [-0.381, 0.646]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; Ambiguous_taxa

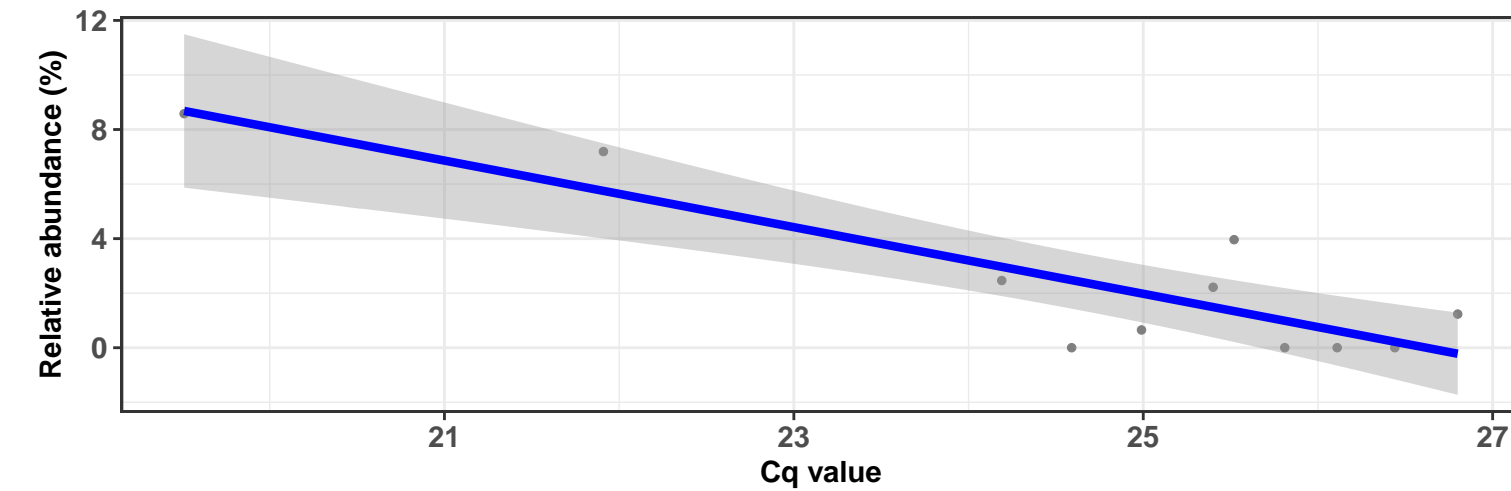
Correlation with all samples

$\log_e(S) = 9.993$, $p = 0.017$, $\hat{\rho}_{\text{Spearman}} = -0.349$, $\text{CI}_{95\%} [-0.586, -0.096]$, $n_{\text{pairs}} = 46$



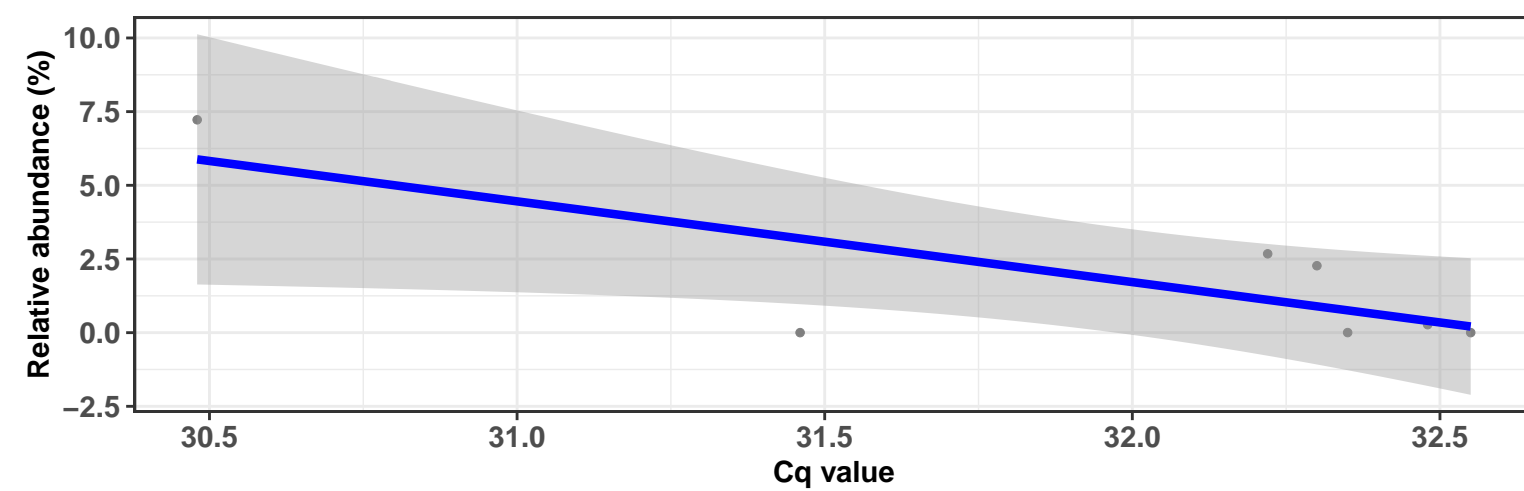
Correlation within: REF-DID

$\log_e(S) = 5.835$, $p = 0.077$, $\hat{\rho}_{\text{Spearman}} = -0.555$, $\text{CI}_{95\%} [-1.120, 0.006]$, $n_{\text{pairs}} = 11$



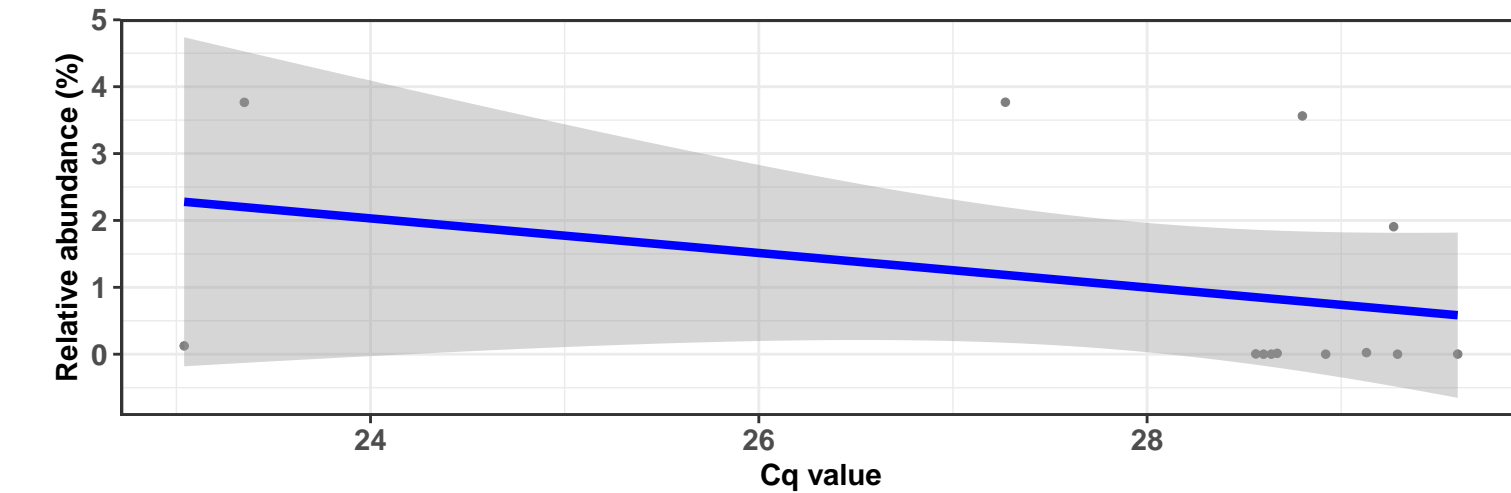
Correlation within: REF-DIM

$\log_e(S) = 4.500$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = -0.607$, $\text{CI}_{95\%} [-1.423, 0.204]$, $n_{\text{pairs}} = 7$



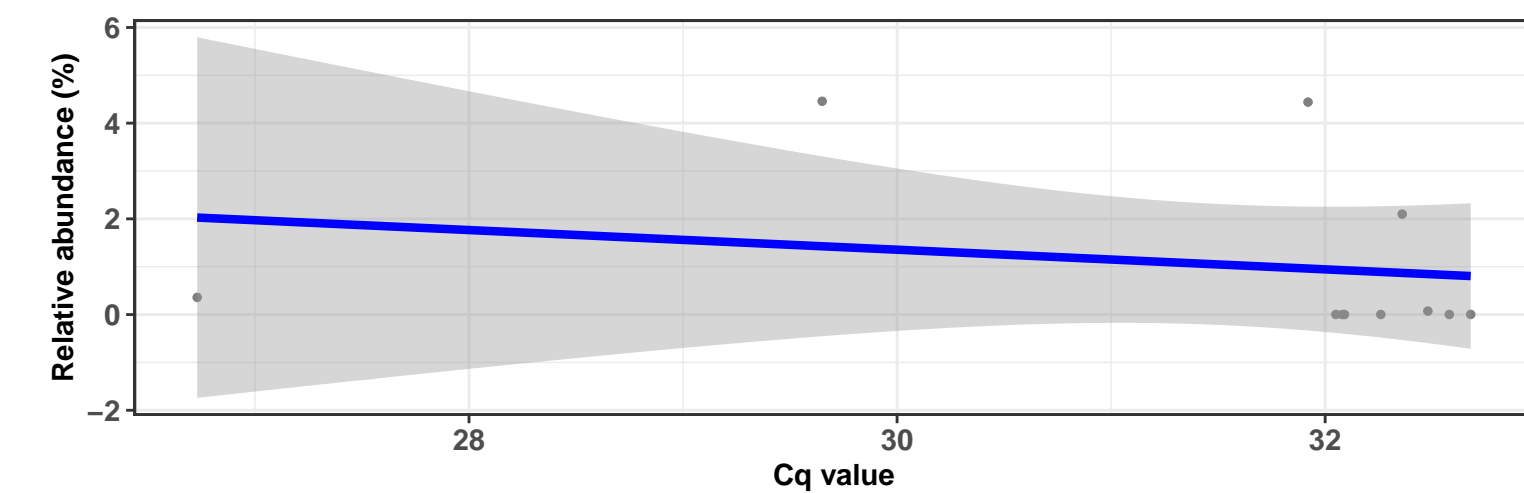
Correlation within: IM-DID

$\log_e(S) = 6.223$, $p = 0.194$, $\hat{\rho}_{\text{Spearman}} = -0.385$, $\text{CI}_{95\%} [-0.822, 0.079]$, $n_{\text{pairs}} = 13$



Correlation within: IM-DIM

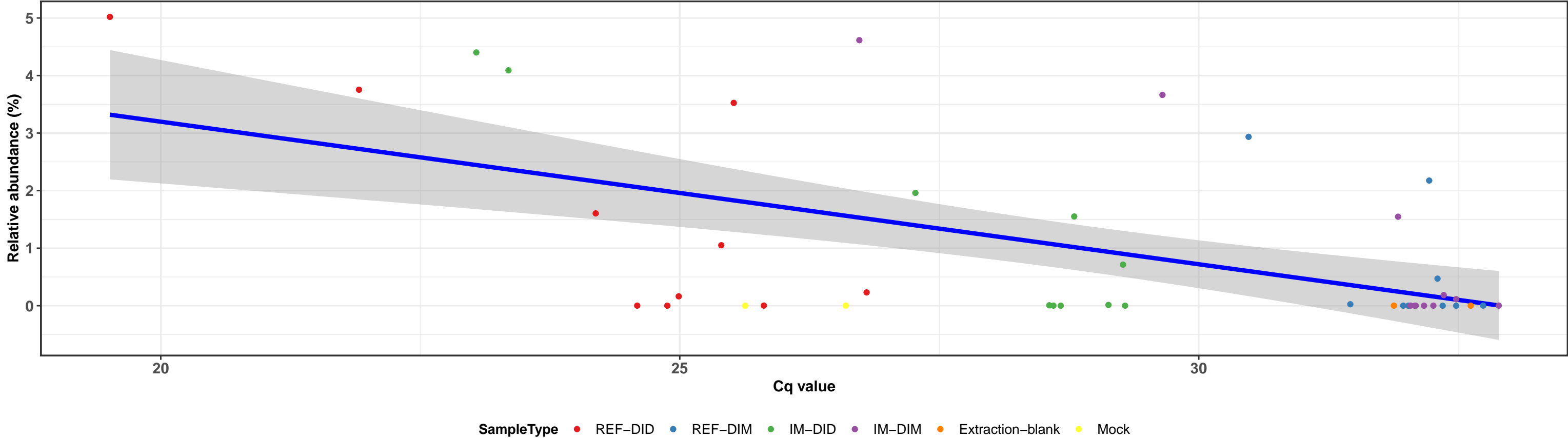
$\log_e(S) = 5.642$, $p = 0.401$, $\hat{\rho}_{\text{Spearman}} = -0.282$, $\text{CI}_{95\%} [-0.809, 0.281]$, $n_{\text{pairs}} = 11$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium

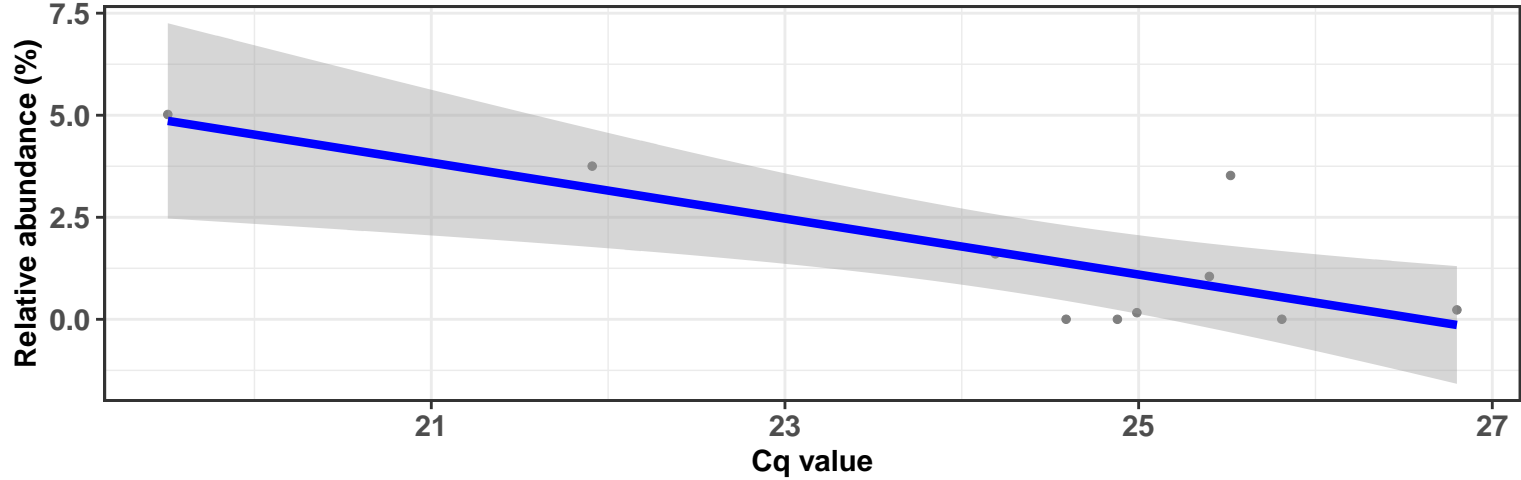
Correlation with all samples

$\log_e(S) = 9.945$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.469$, $\text{CI}_{95\%} [-0.737, -0.236]$, $n_{\text{pairs}} = 44$



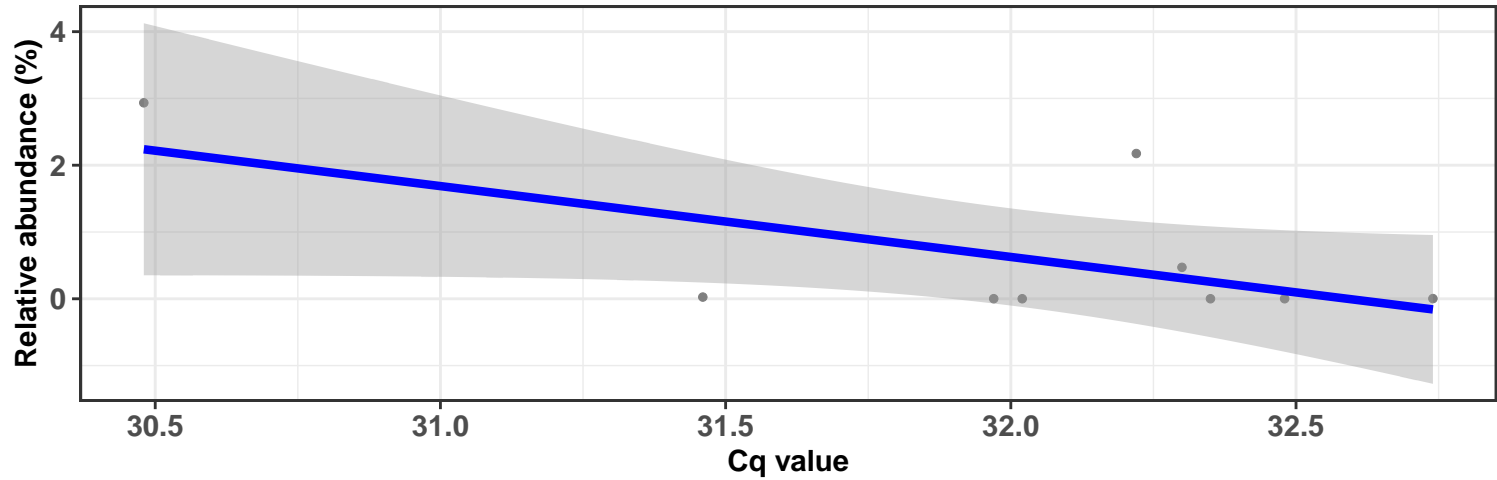
Correlation within: REF-DID

$\log_e(S) = 5.447$, $p = 0.244$, $\hat{\rho}_{\text{Spearman}} = -0.406$, $\text{CI}_{95\%} [-1.281, 0.332]$, $n_{\text{pairs}} = 10$



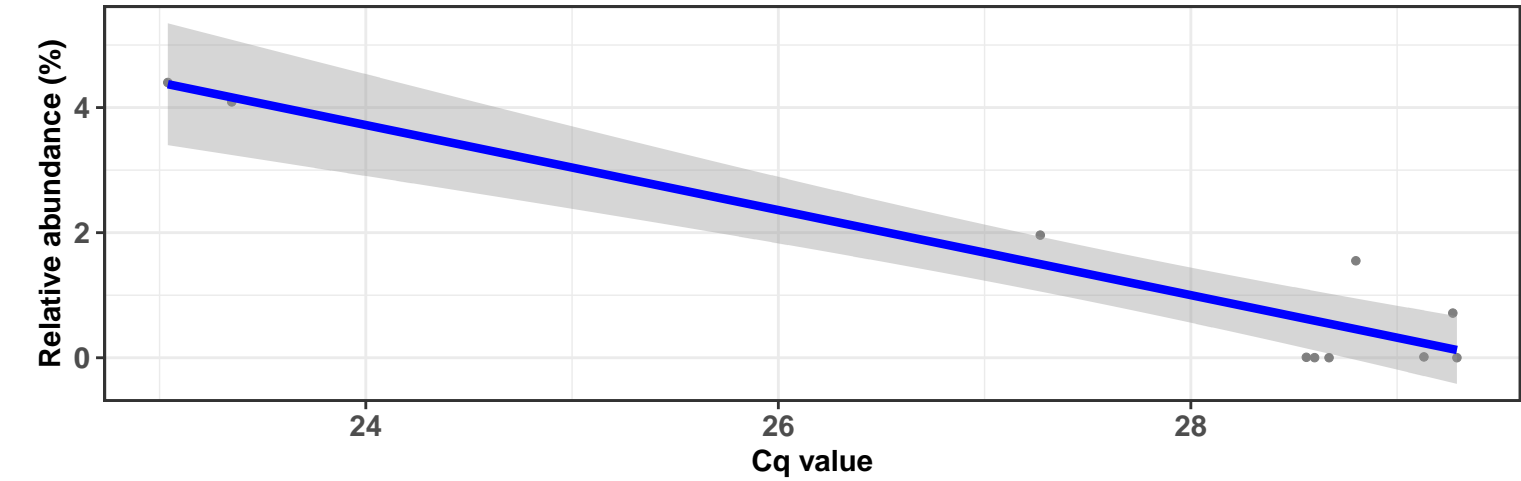
Correlation within: REF-DIM

$\log_e(S) = 5.147$, $p = 0.244$, $\hat{\rho}_{\text{Spearman}} = -0.433$, $\text{CI}_{95\%} [-1.088, 0.106]$, $n_{\text{pairs}} = 9$



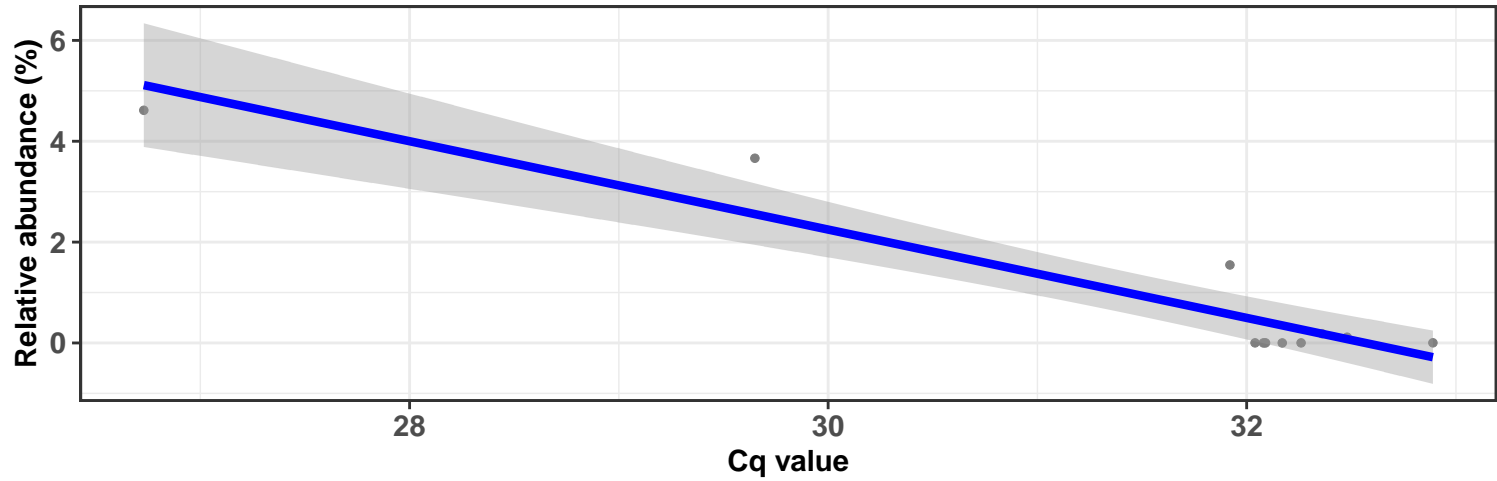
Correlation within: IM-DID

$\log_e(S) = 5.583$, $p = 0.060$, $\hat{\rho}_{\text{Spearman}} = -0.612$, $\text{CI}_{95\%} [-1.251, -0.094]$, $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

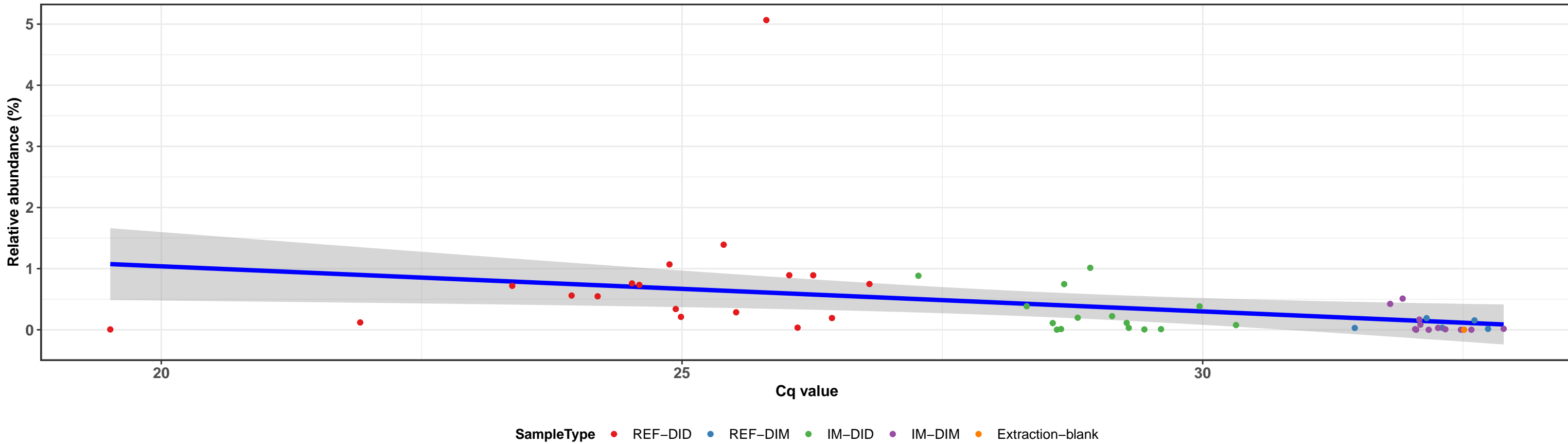
$\log_e(S) = 5.710$, $p = 0.259$, $\hat{\rho}_{\text{Spearman}} = -0.373$, $\text{CI}_{95\%} [-0.880, 0.311]$, $n_{\text{pairs}} = 11$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Photobacterium; NA

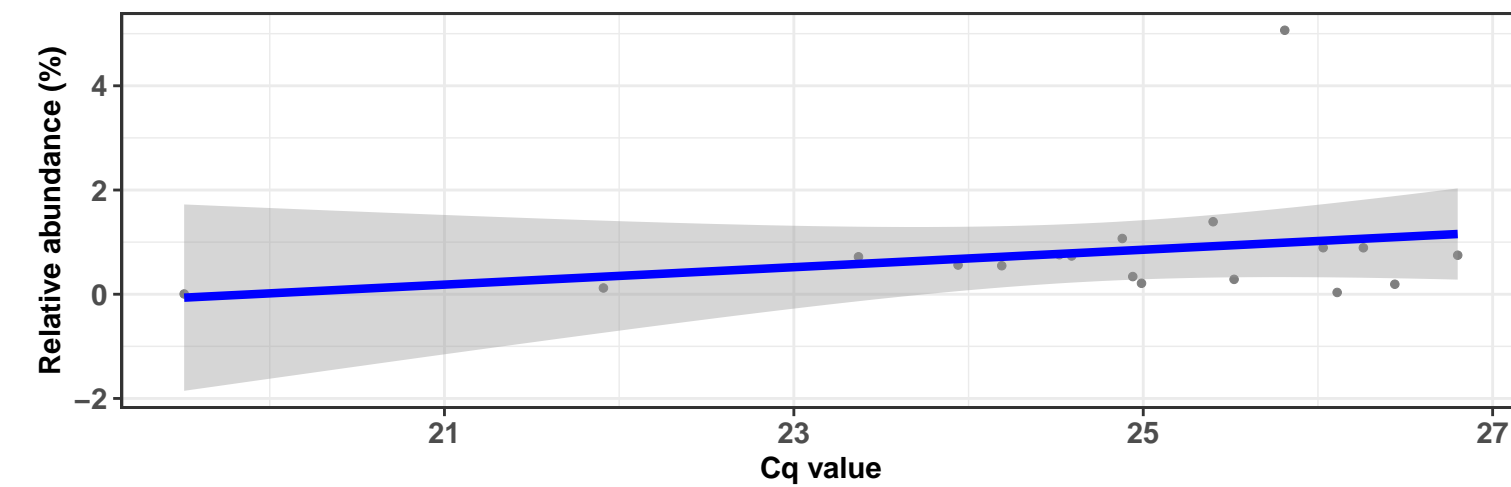
Correlation with all samples

$\log_e(S) = 10.474$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.600$, $\text{CI}_{95\%} [-0.776, -0.414]$, $n_{\text{pairs}} = 51$

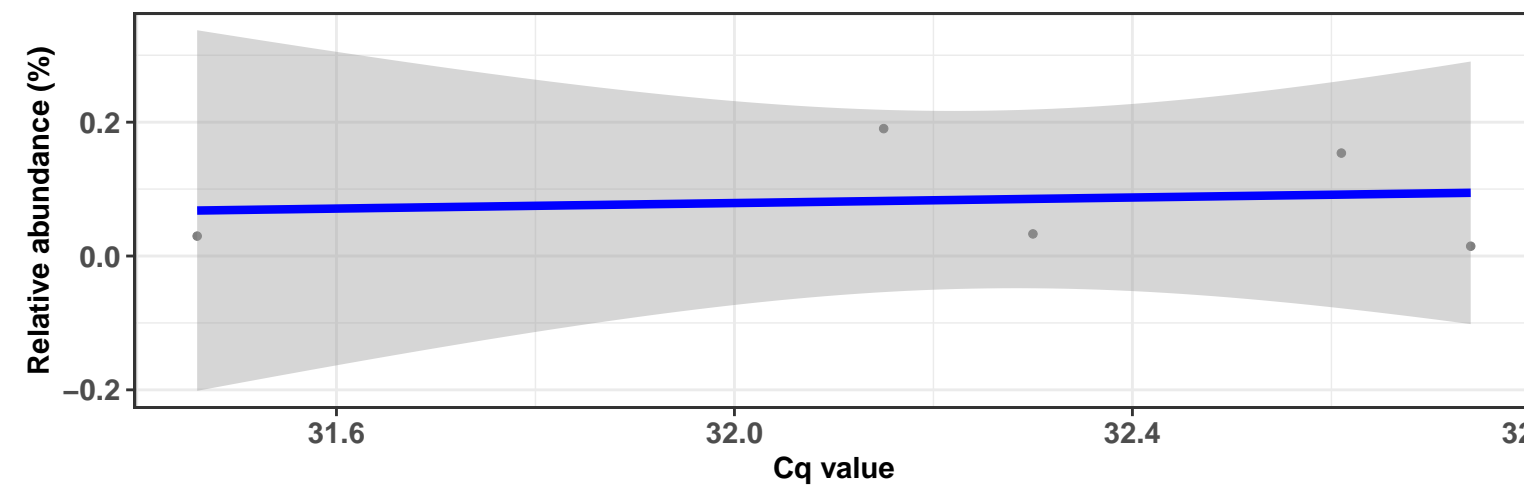


Correlation within: REF-DID

$\log_e(S) = 6.576$, $p = 0.299$, $\hat{\rho}_{\text{Spearman}} = 0.259$, $\text{CI}_{95\%} [-0.204, 0.729]$, $n_{\text{pairs}} = 18$

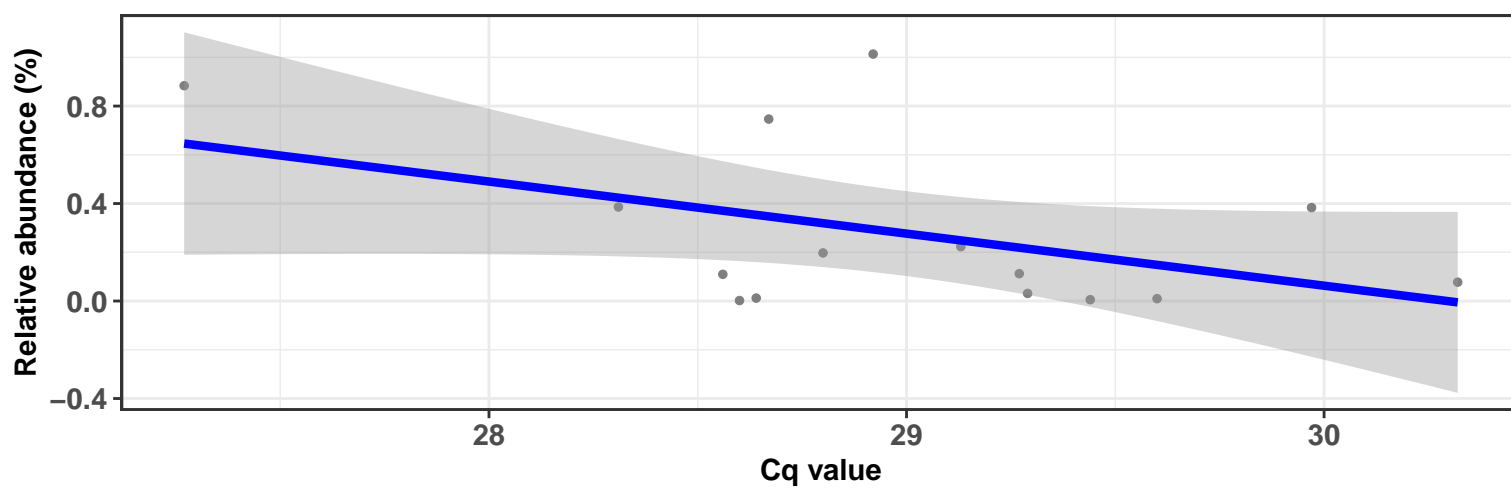


Correlation within: REF-DIM



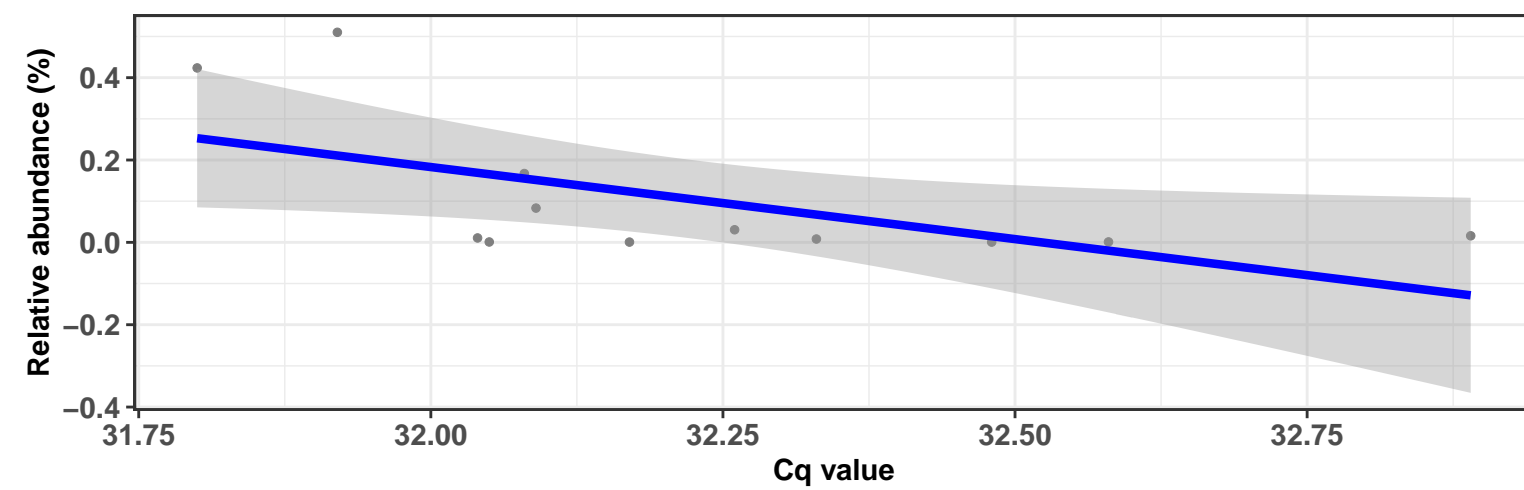
Correlation within: IM-DID

$\log_e(S) = 6.590$, $p = 0.277$, $\hat{\rho}_{\text{Spearman}} = -0.300$, $\text{CI}_{95\%} [-0.856, 0.198]$, $n_{\text{pairs}} = 15$



Correlation within: IM-DIM

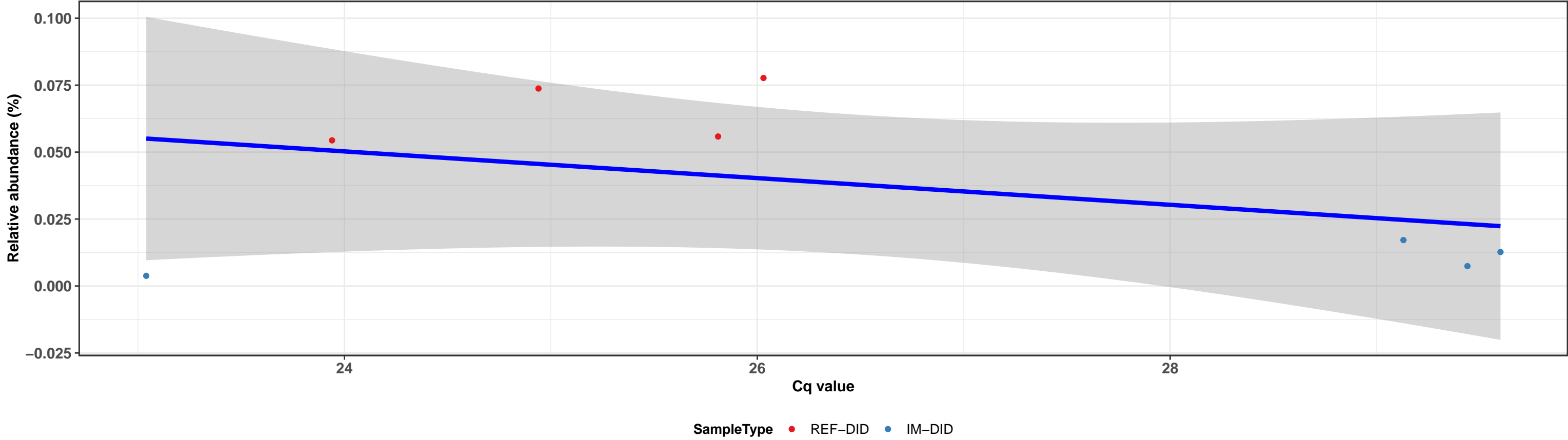
$\log_e(S) = 6.087$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = -0.538$, $\text{CI}_{95\%} [-1.075, -0.092]$, $n_{\text{pairs}} = 12$



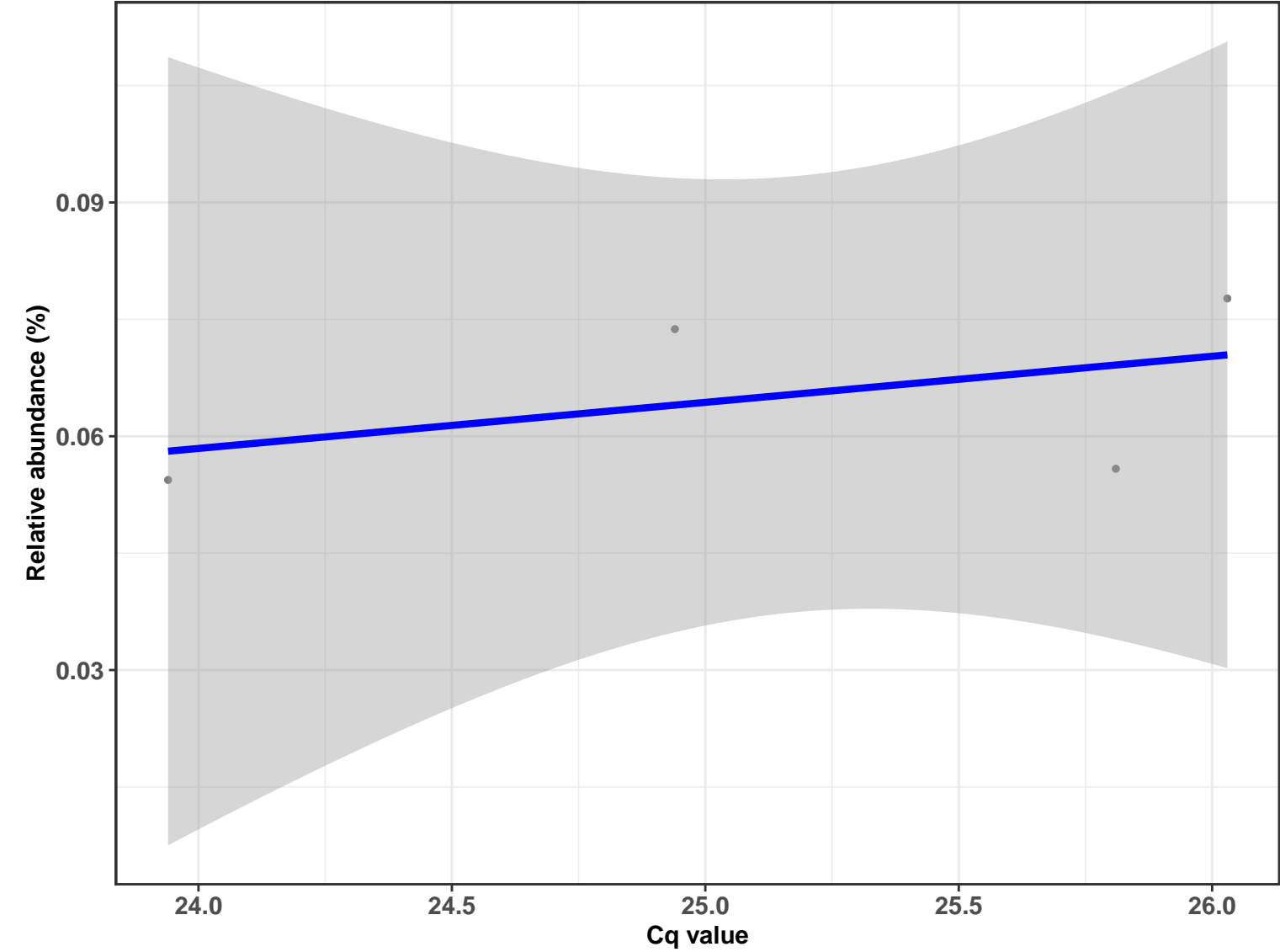
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples

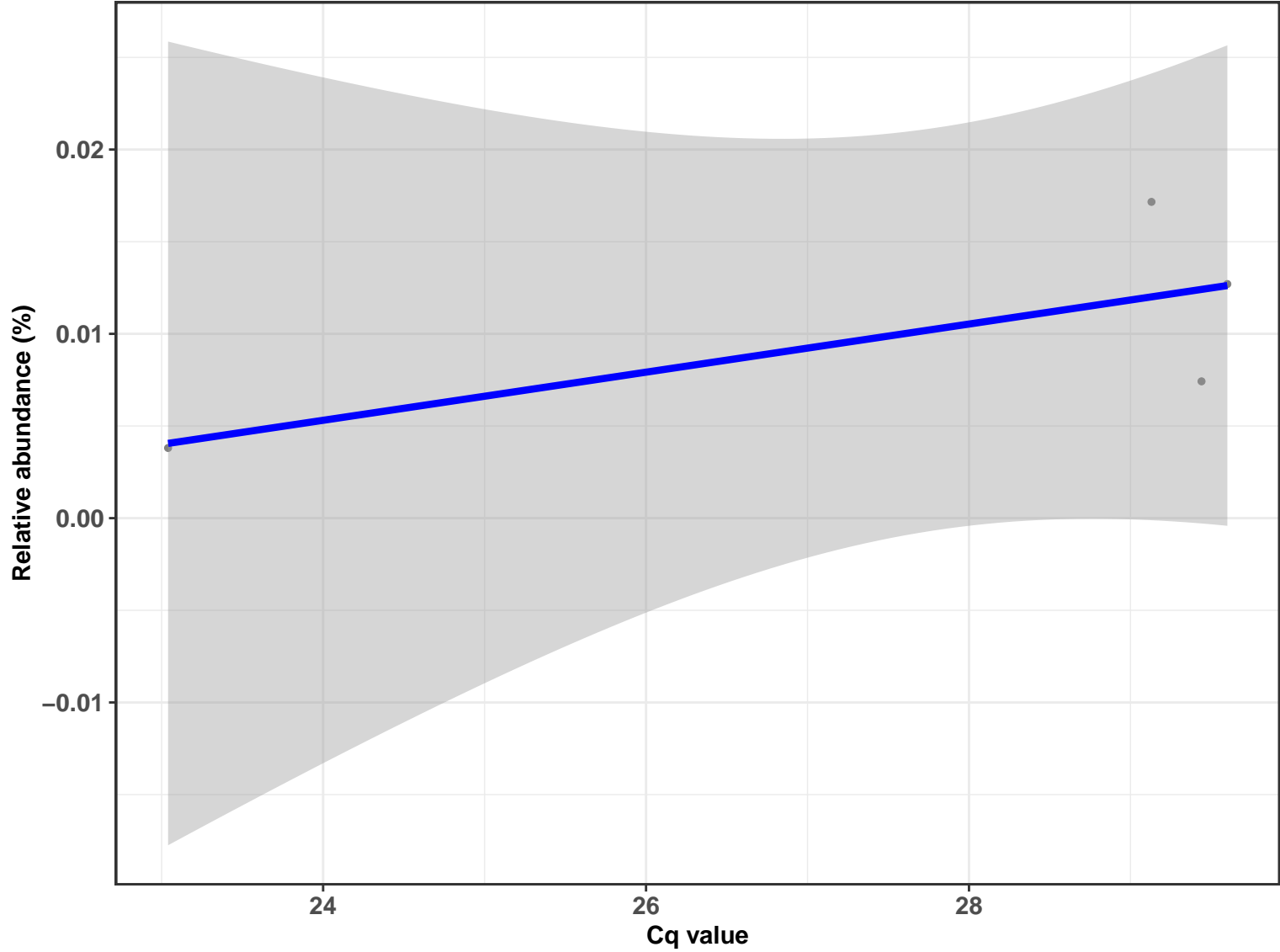
$\log_e(S) = 4.522$, $p = 0.823$, $\hat{\rho}_{\text{Spearman}} = -0.095$, $CI_{95\%} [-0.989, 0.913]$, $n_{\text{pairs}} = 8$



Correlation within: REF-DID



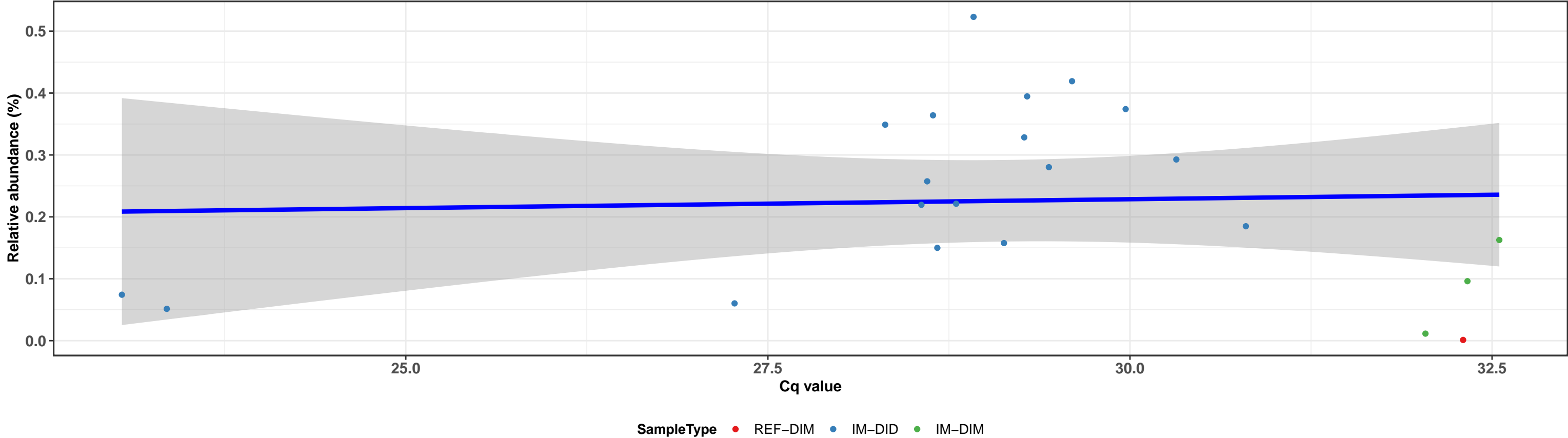
Correlation within: IM-DID



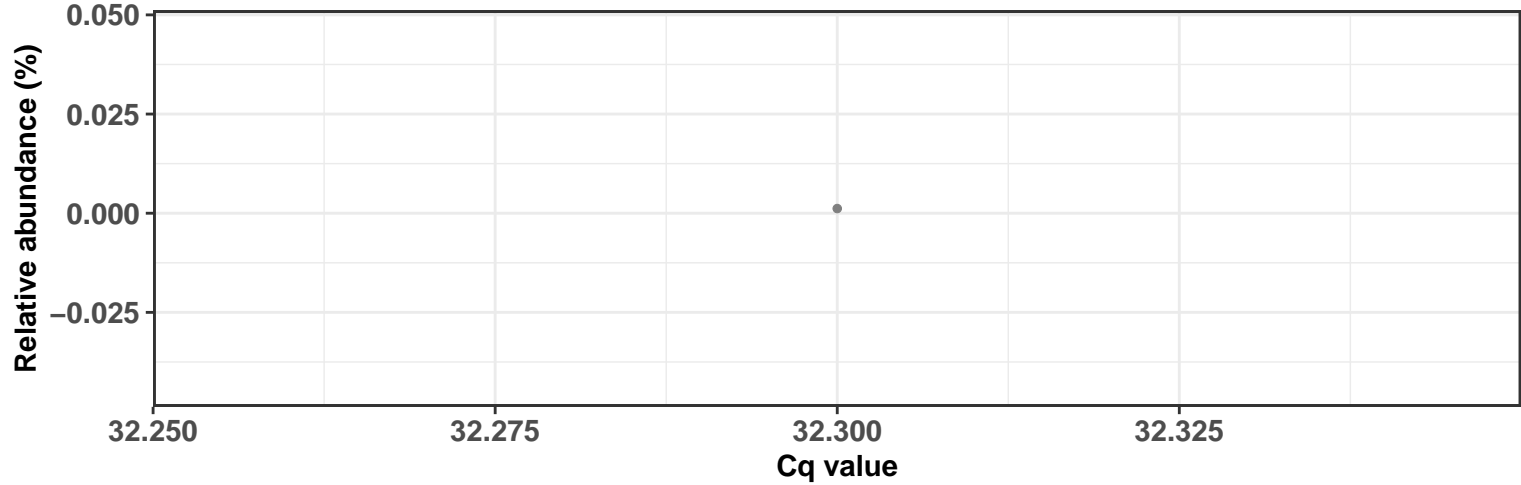
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; s__Brevibacterium album

Correlation with all samples

$\log_e(S) = 7.483$, $p = 0.986$, $\hat{\rho}_{\text{Spearman}} = -0.004$, $\text{CI}_{95\%} [-0.440, 0.492]$, $n_{\text{pairs}} = 22$

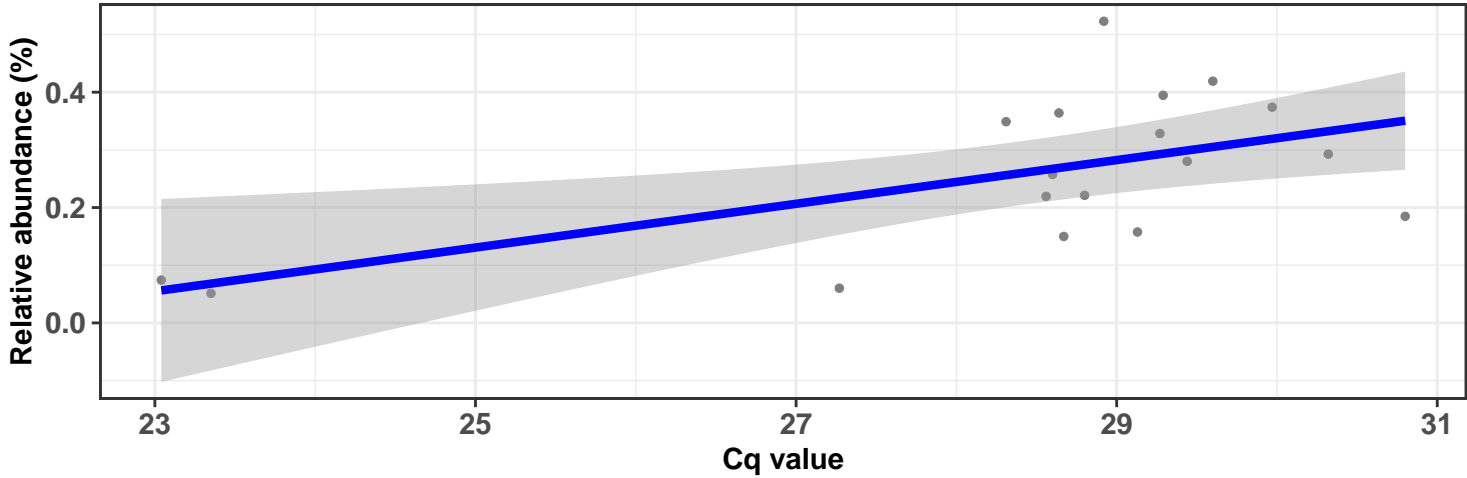


Correlation within: REF-DIM

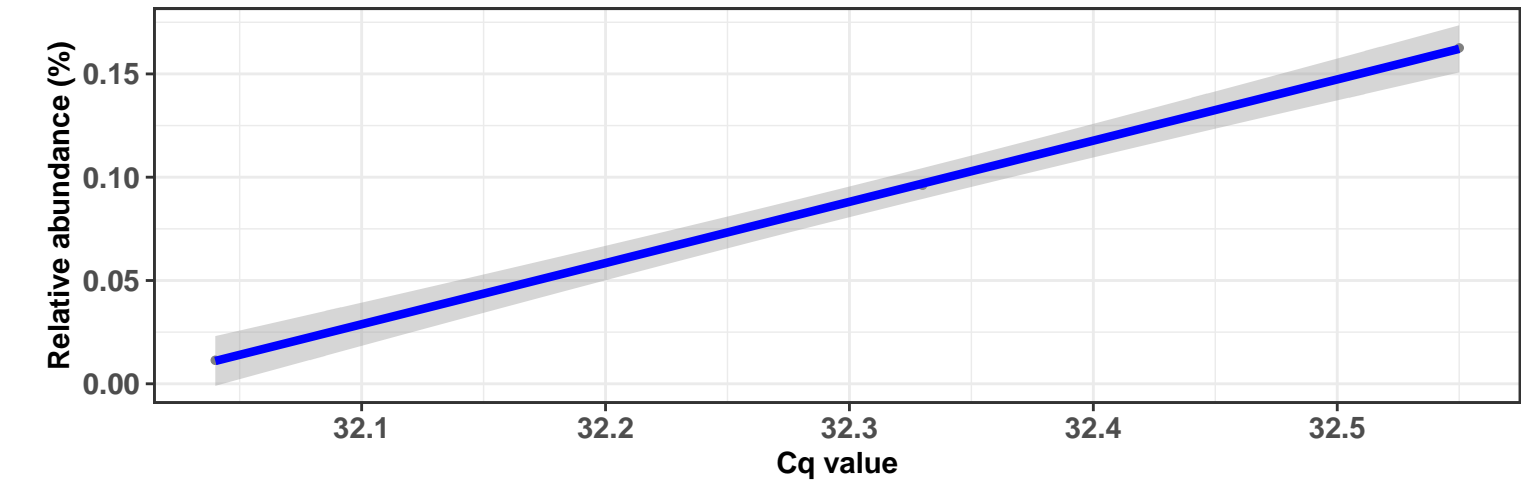


Correlation within: IM-DID

$\log_e(S) = 6.165$, $p = 0.031$, $\hat{\rho}_{\text{Spearman}} = 0.509$, $\text{CI}_{95\%} [0.101, 0.958]$, $n_{\text{pairs}} = 18$



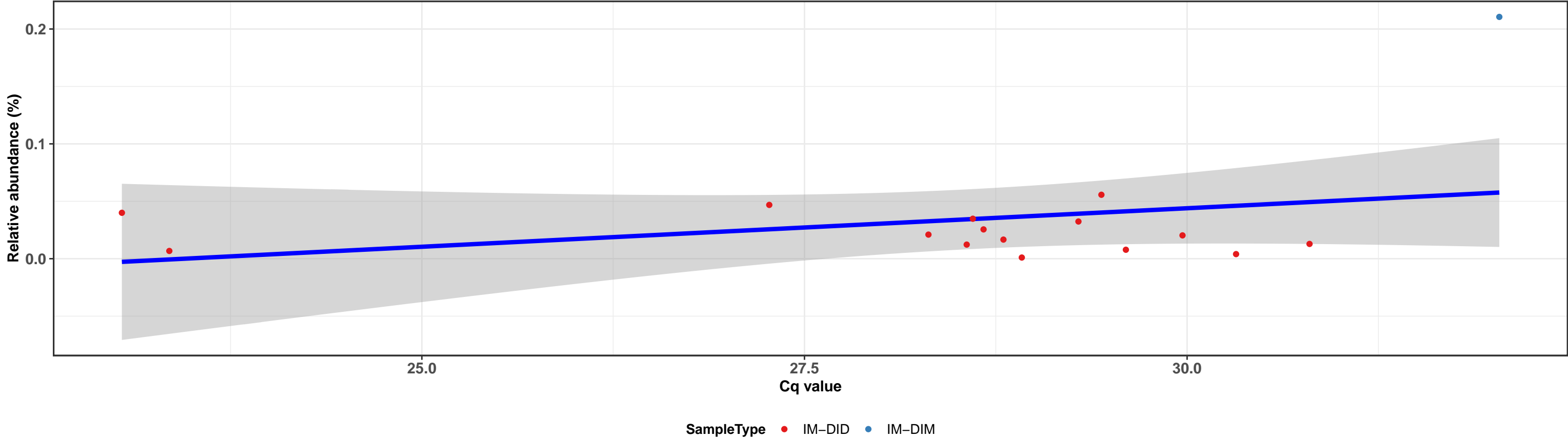
Correlation within: IM-DIM



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

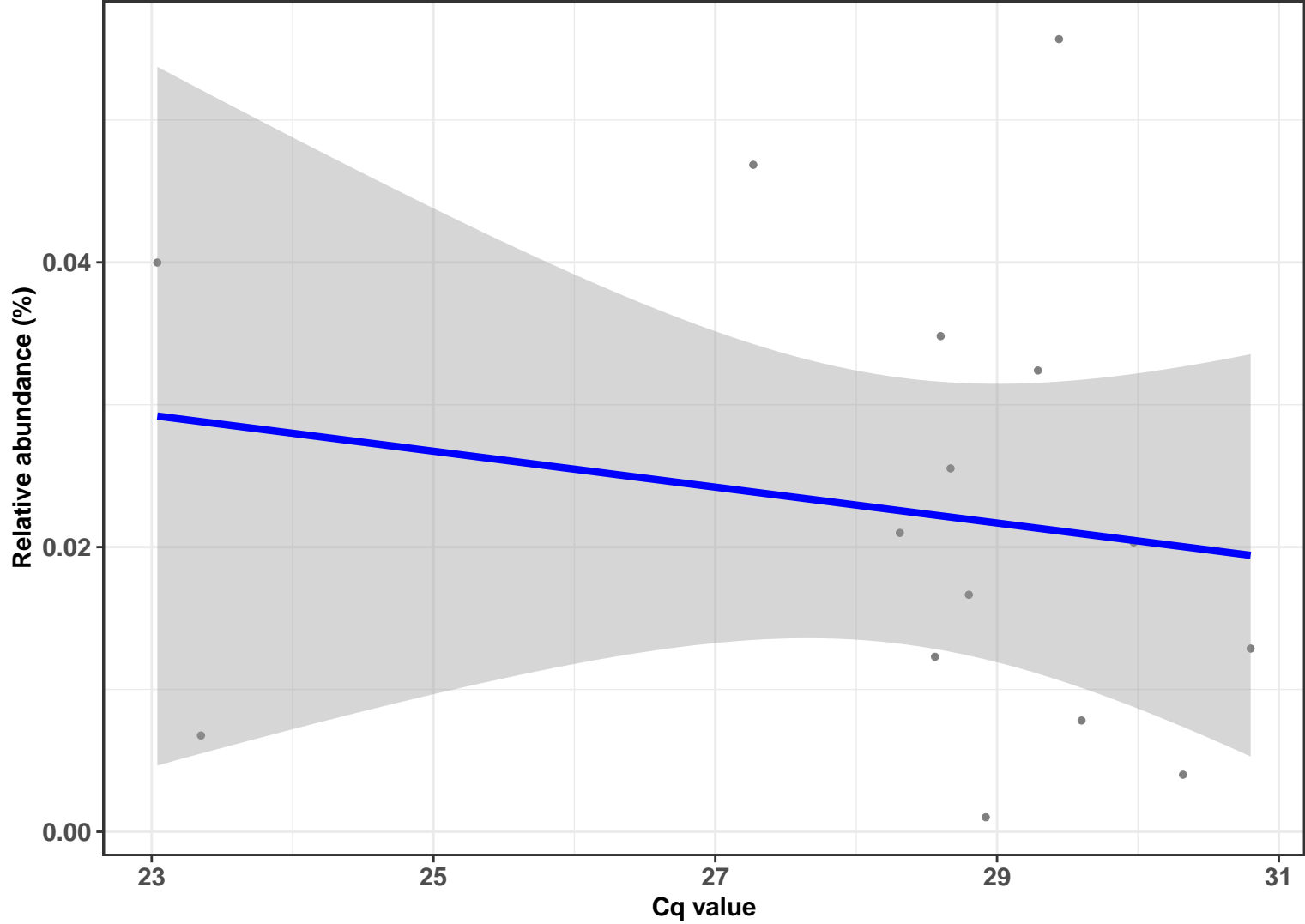
Correlation with all samples

$\log_e(S) = 6.596$, $p = 0.778$, $\hat{\rho}_{\text{Spearman}} = -0.076$, $\text{CI}_{95\%} [-0.662, 0.416]$, $n_{\text{pairs}} = 16$

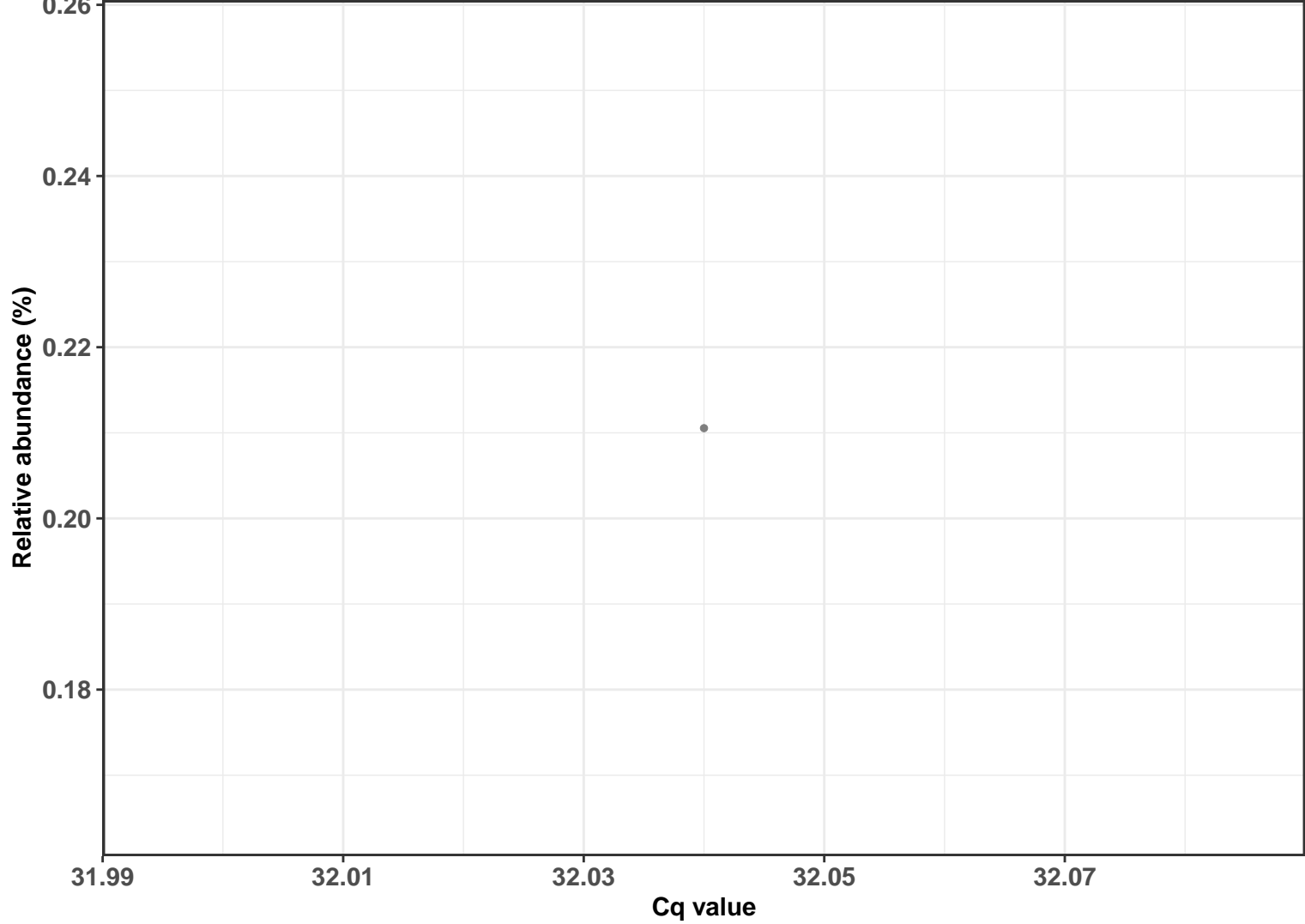


Correlation within: IM-DID

$\log_e(S) = 6.596$, $p = 0.265$, $\hat{\rho}_{\text{Spearman}} = -0.307$, $\text{CI}_{95\%} [-0.848, 0.152]$, $n_{\text{pairs}} = 15$

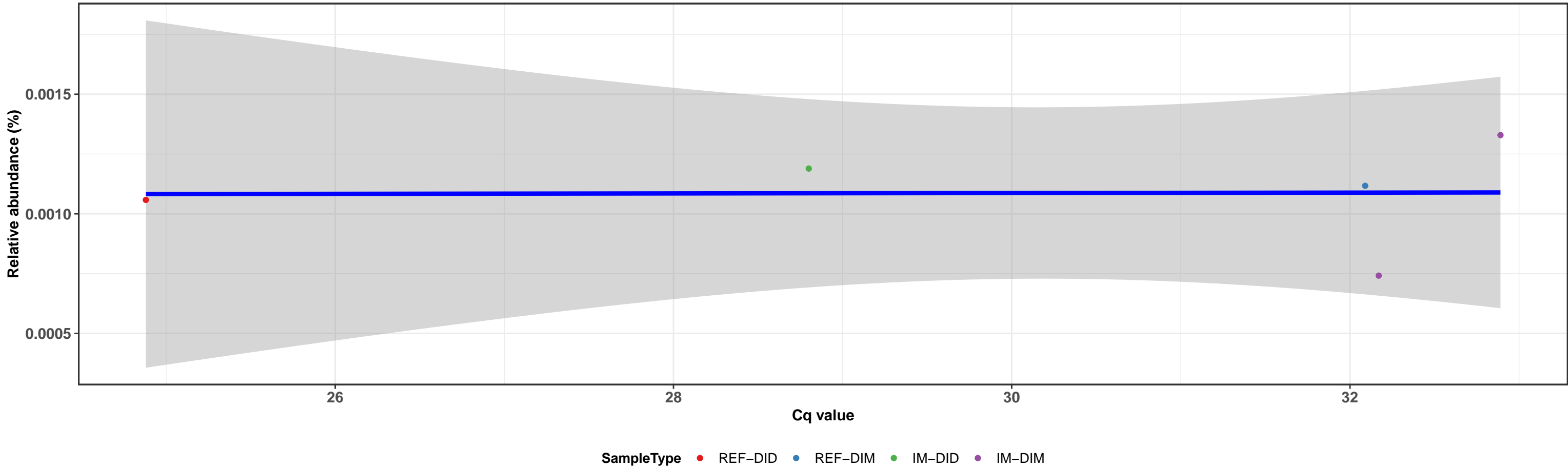


Correlation within: IM-DIM

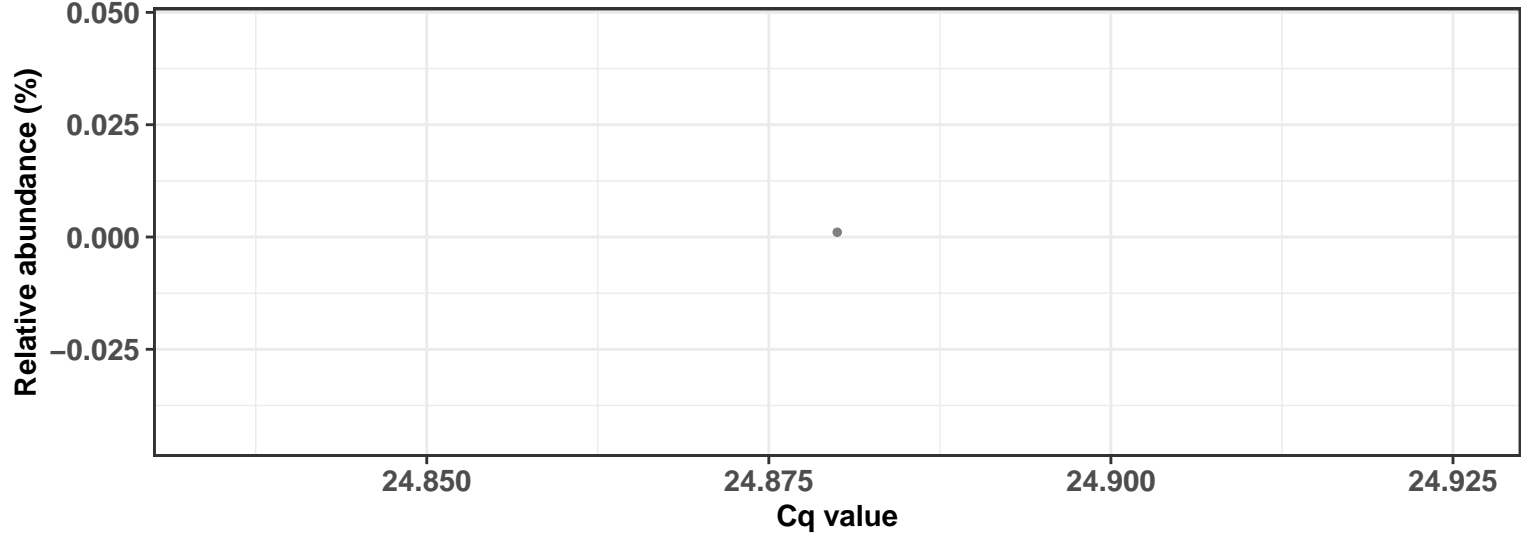


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__Marinobacter adhaerens

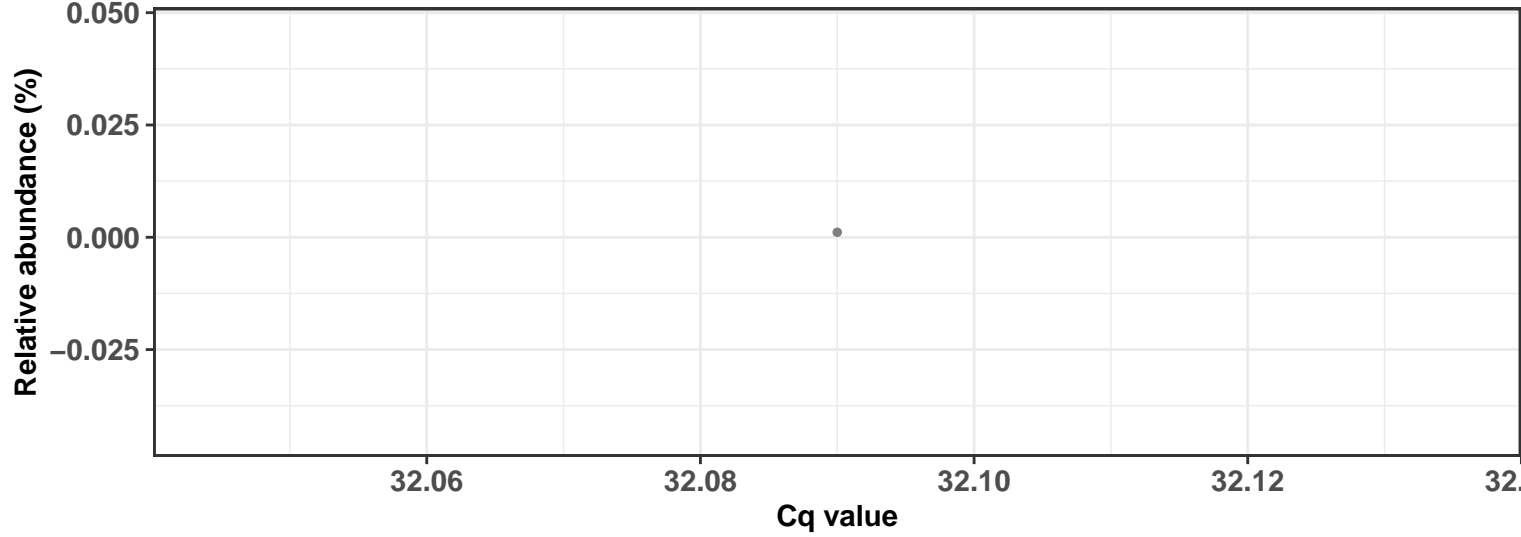
Correlation with all samples



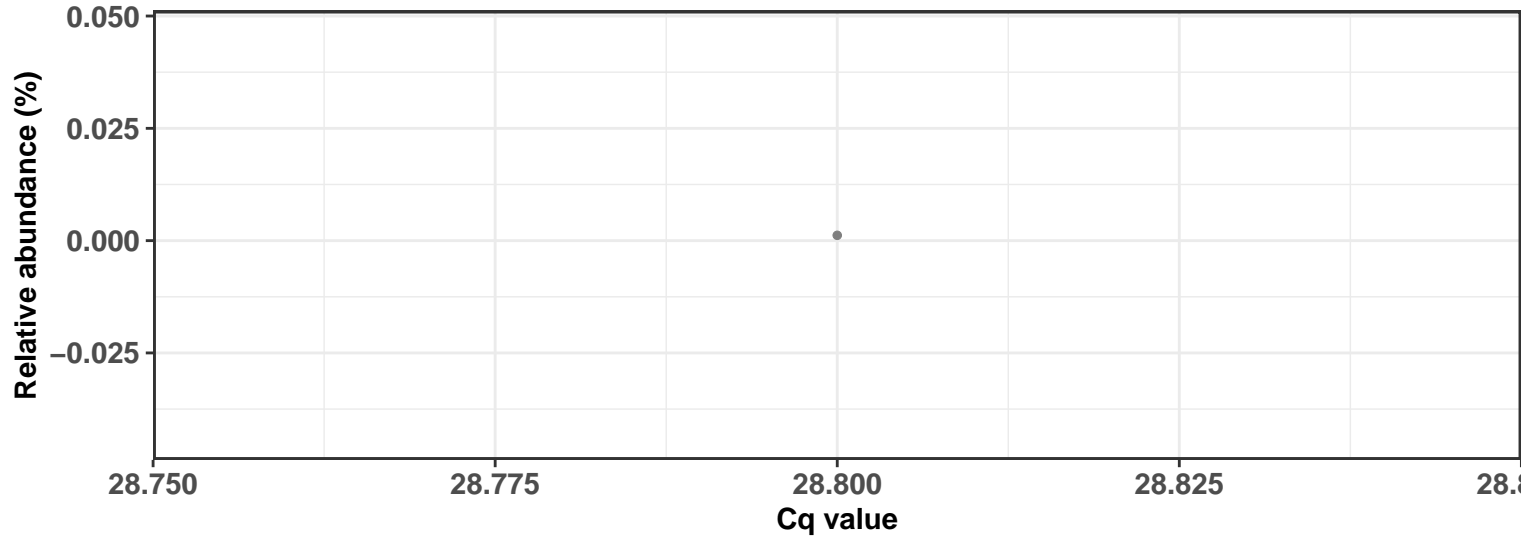
Correlation within: REF-DID



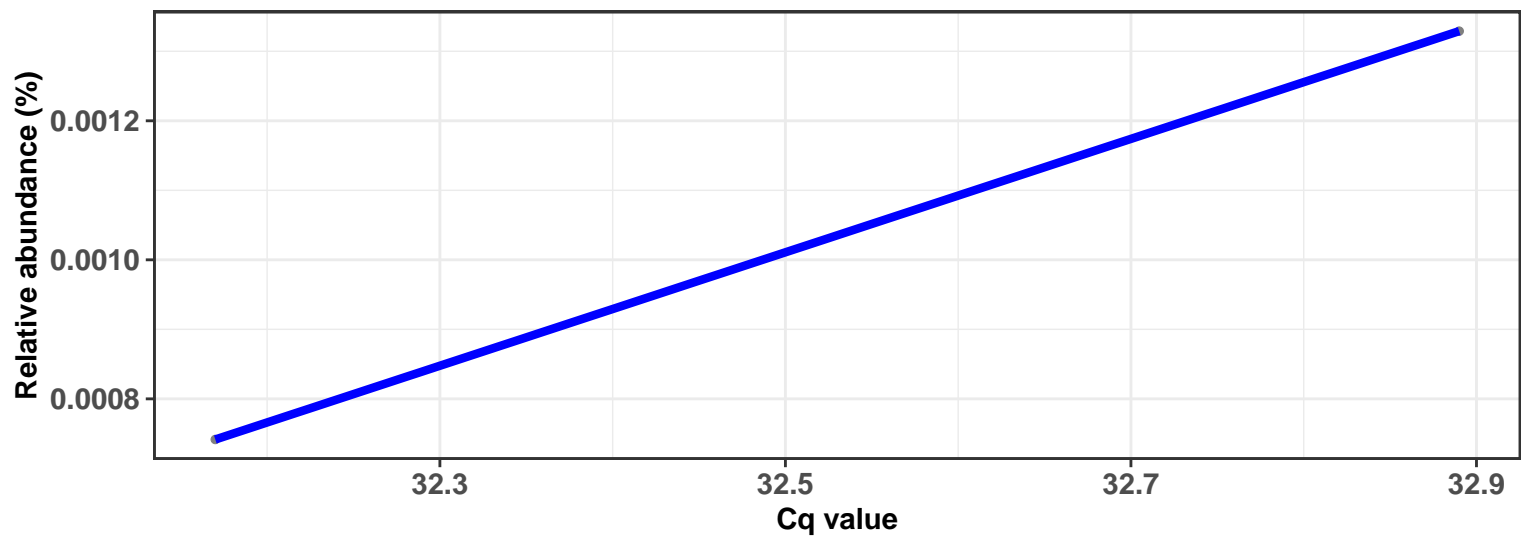
Correlation within: REF-DIM



Correlation within: IM-DID



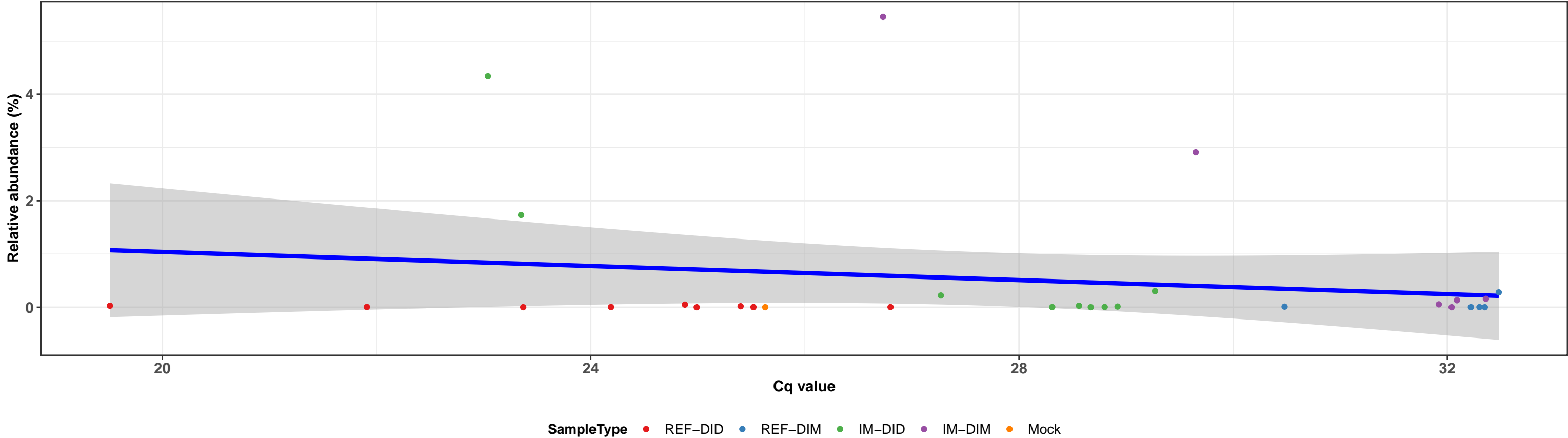
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium

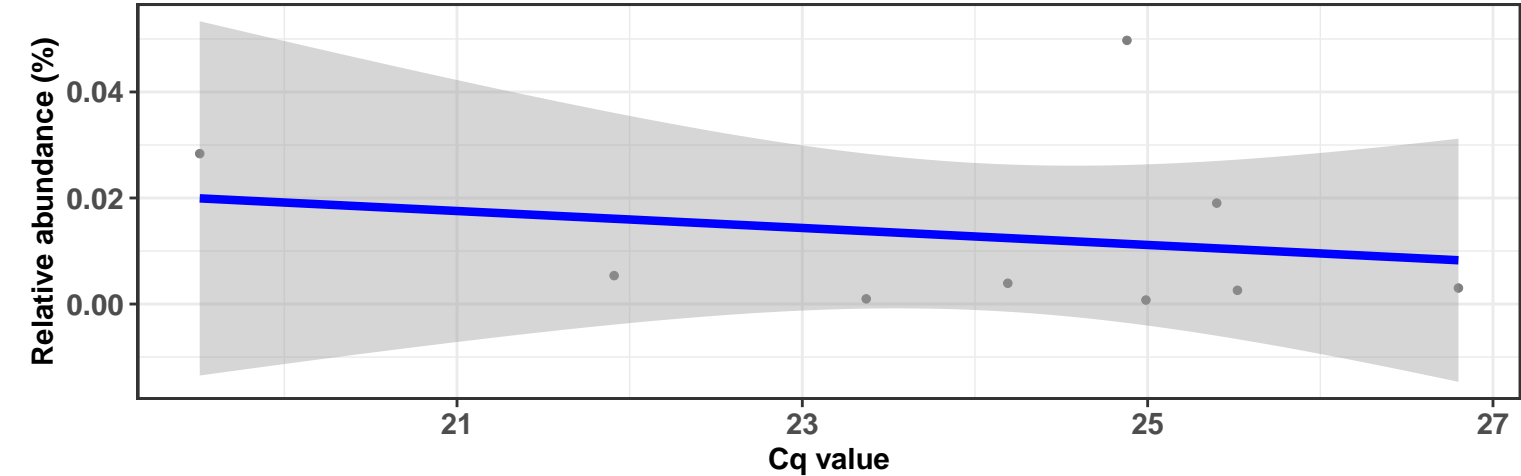
Correlation with all samples

$\log_e(S) = 8.469$, $p = 0.753$, $\hat{\rho}_{\text{Spearman}} = -0.060$, $\text{CI}_{95\%} [-0.404, 0.332]$, $n_{\text{pairs}} = 30$

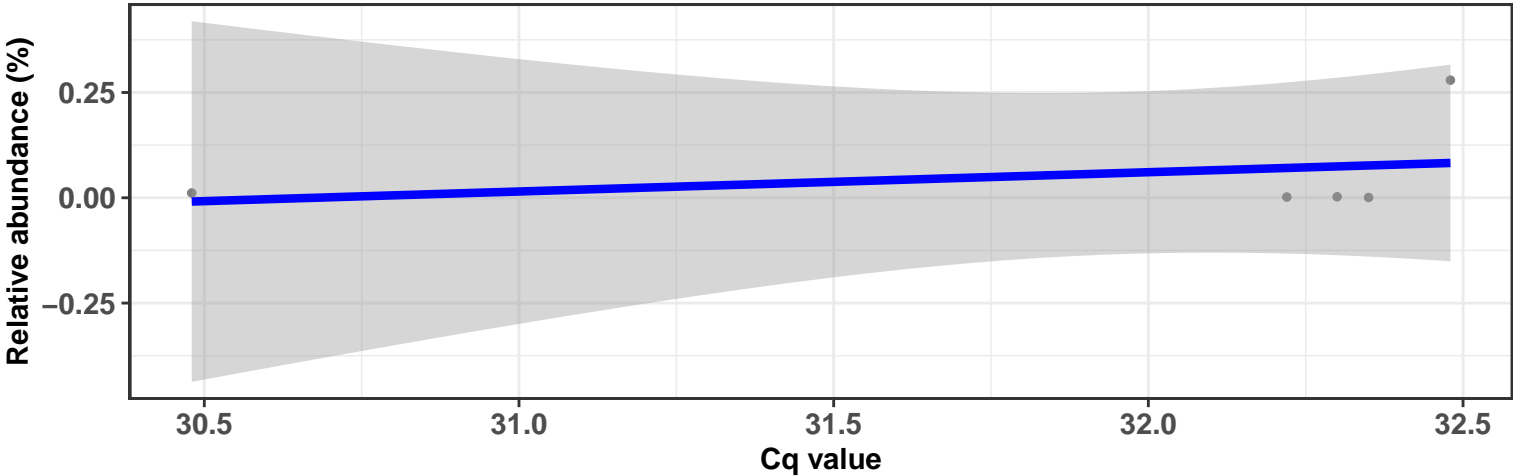


Correlation within: REF-DID

$\log_e(S) = 5.063$, $p = 0.406$, $\hat{\rho}_{\text{Spearman}} = -0.317$, $\text{CI}_{95\%} [-0.874, 0.229]$, $n_{\text{pairs}} = 9$

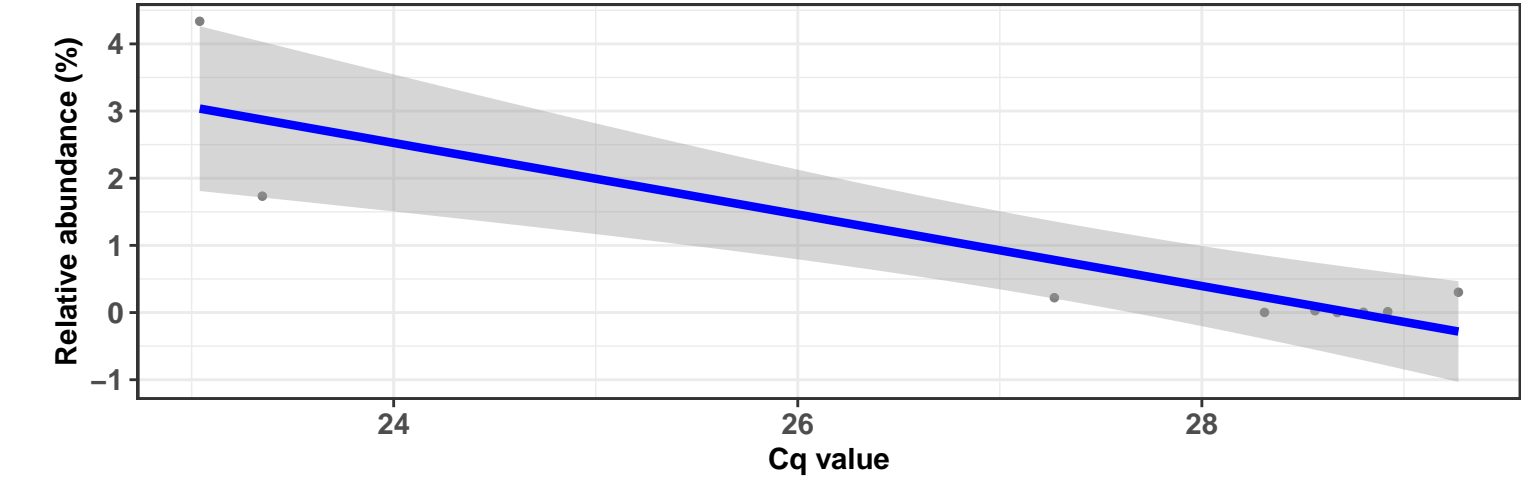


Correlation within: REF-DIM



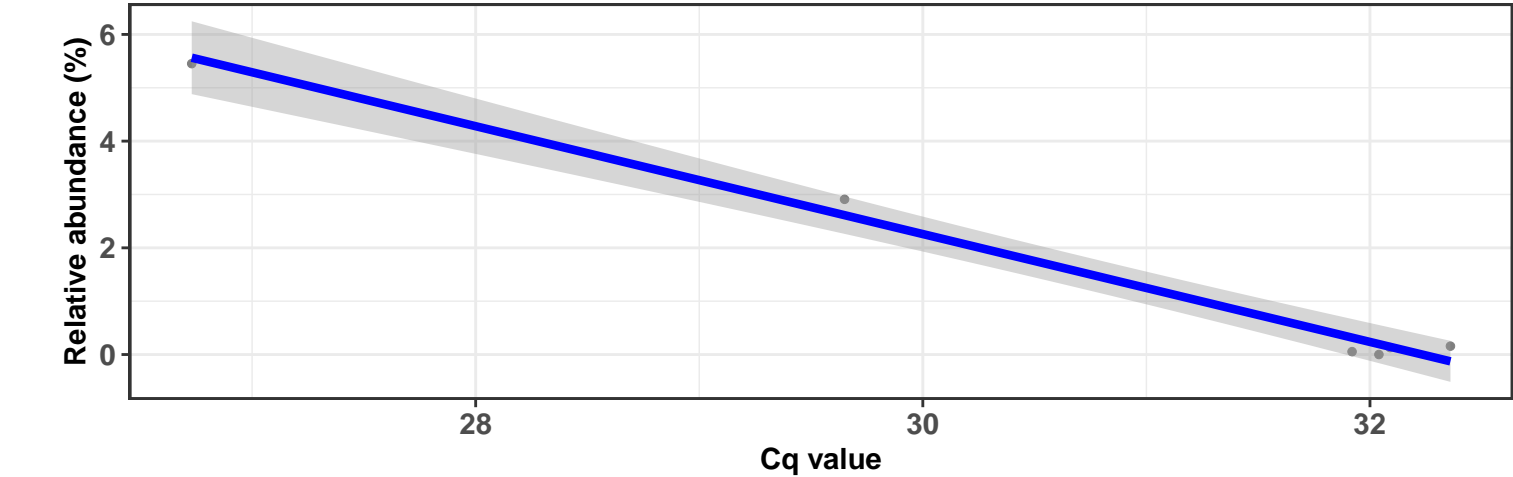
Correlation within: IM-DID

$\log_e(S) = 5.159$, $p = 0.224$, $\hat{\rho}_{\text{Spearman}} = -0.450$, $\text{CI}_{95\%} [-1.175, 0.273]$, $n_{\text{pairs}} = 9$



Correlation within: IM-DIM

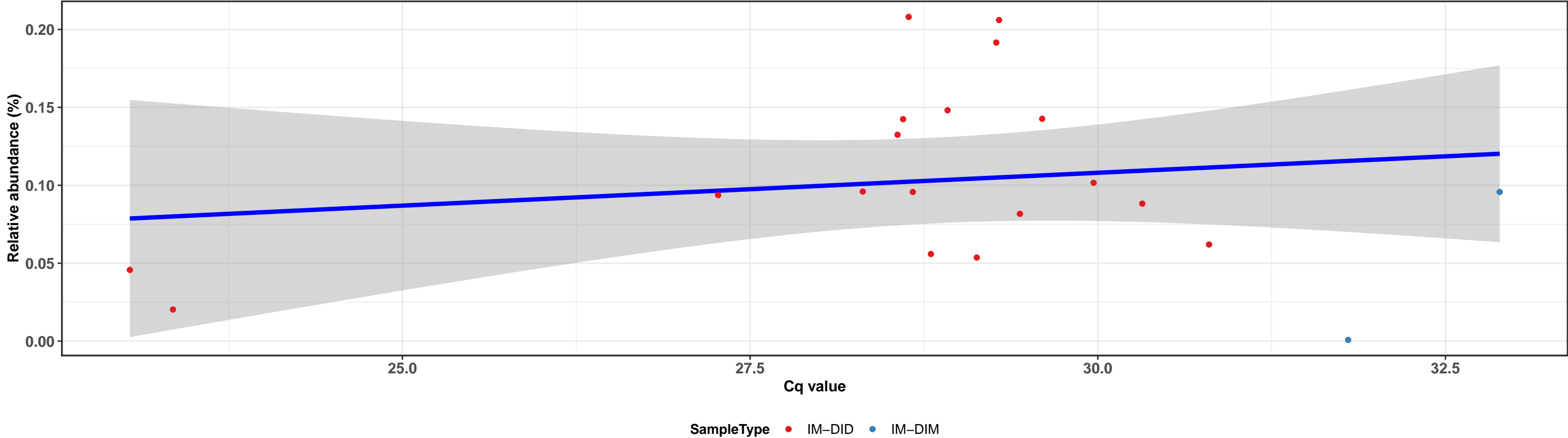
$\log_e(S) = 3.951$, $p = 0.329$, $\hat{\rho}_{\text{Spearman}} = -0.486$, $\text{CI}_{95\%} [-1.524, 0.375]$, $n_{\text{pairs}} = 6$



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

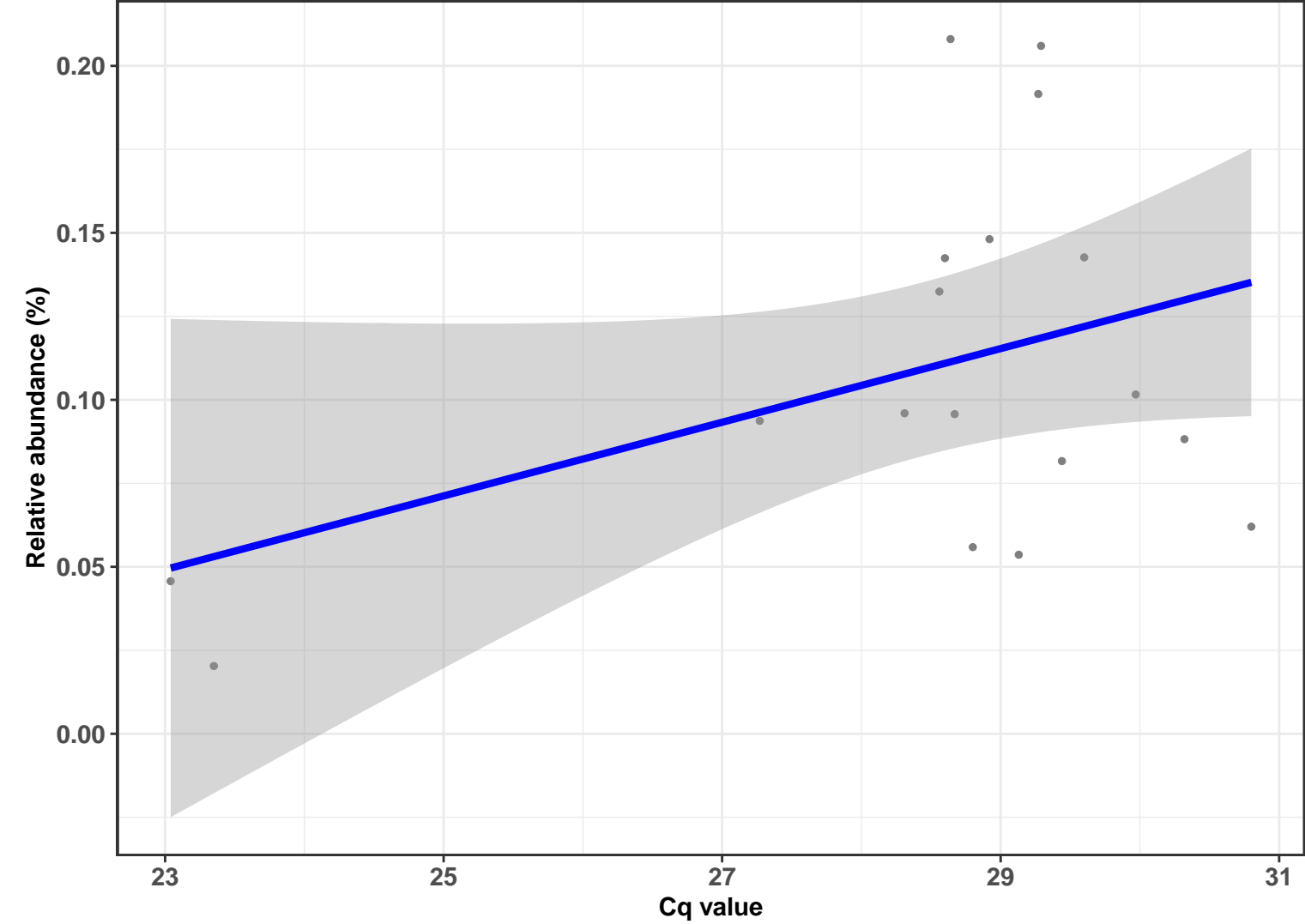
Correlation with all samples

$\log_e(S) = 7.199$, $p = 0.980$, $\hat{\rho}_{\text{Spearman}} = -0.006$, $\text{CI}_{95\%} [-0.531, 0.497]$, $n_{\text{pairs}} = 20$

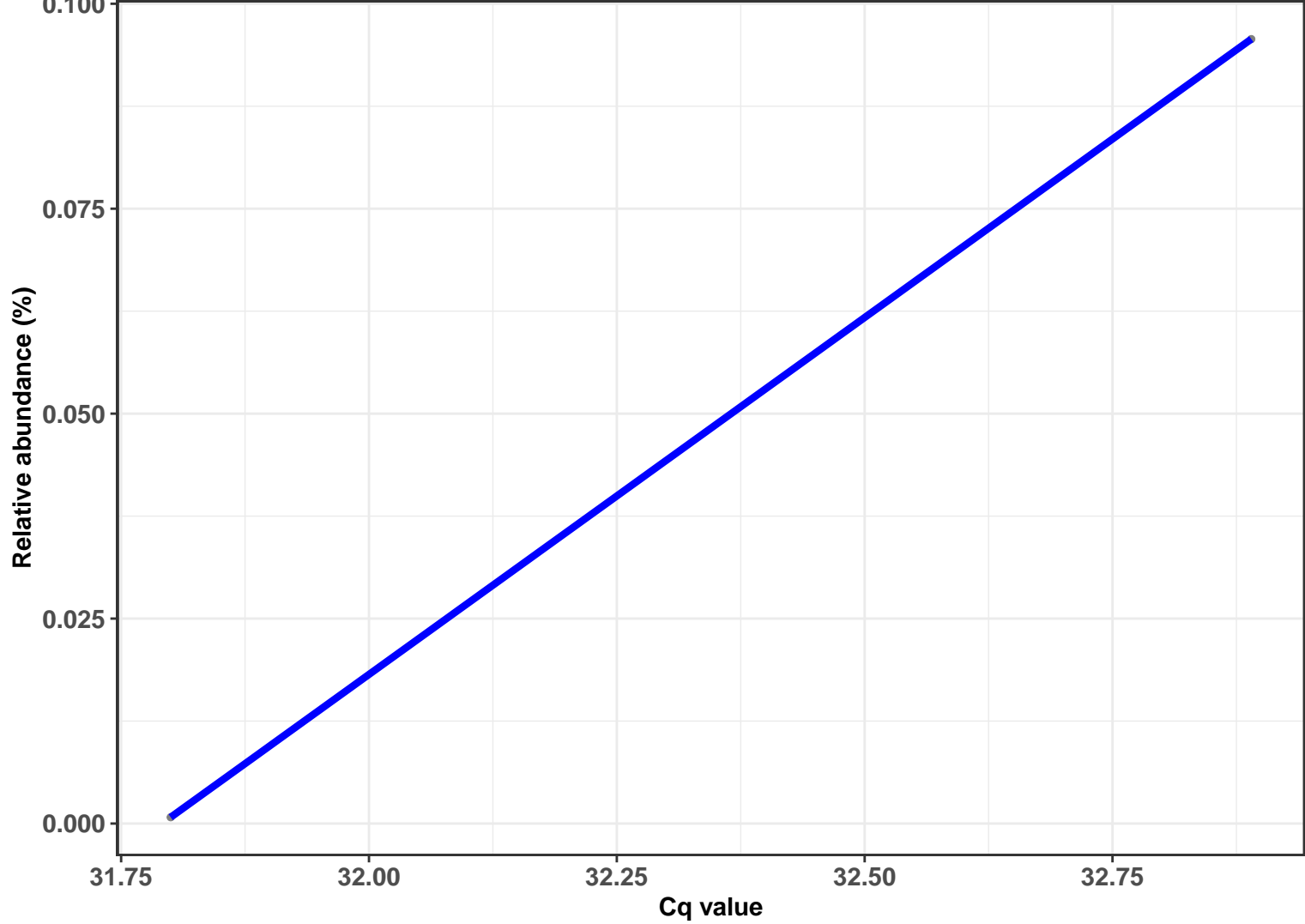


Correlation within: IM-DID

$\log_e(S) = 6.669$, $p = 0.458$, $\hat{\rho}_{\text{Spearman}} = 0.187$, $\text{CI}_{95\%} [-0.253, 0.699]$, $n_{\text{pairs}} = 18$



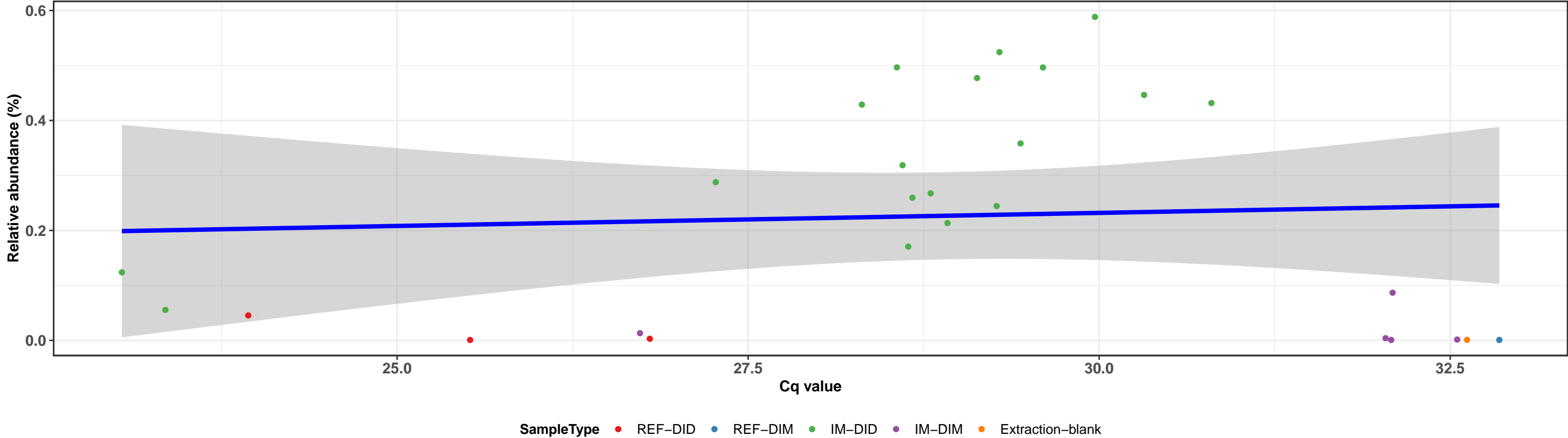
Correlation within: IM-DIM



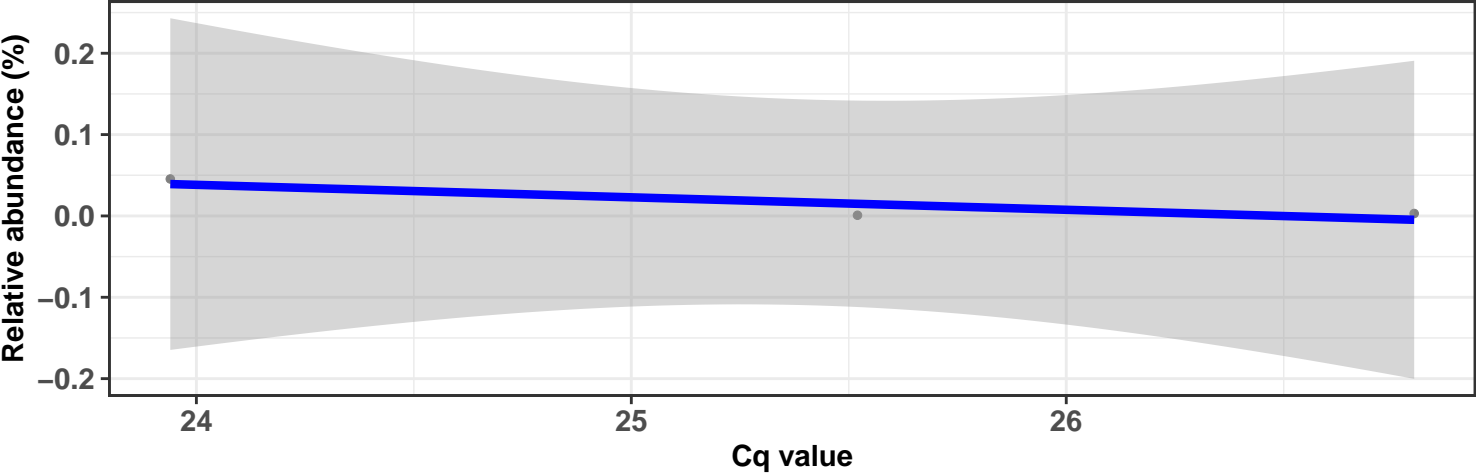
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa

Correlation with all samples

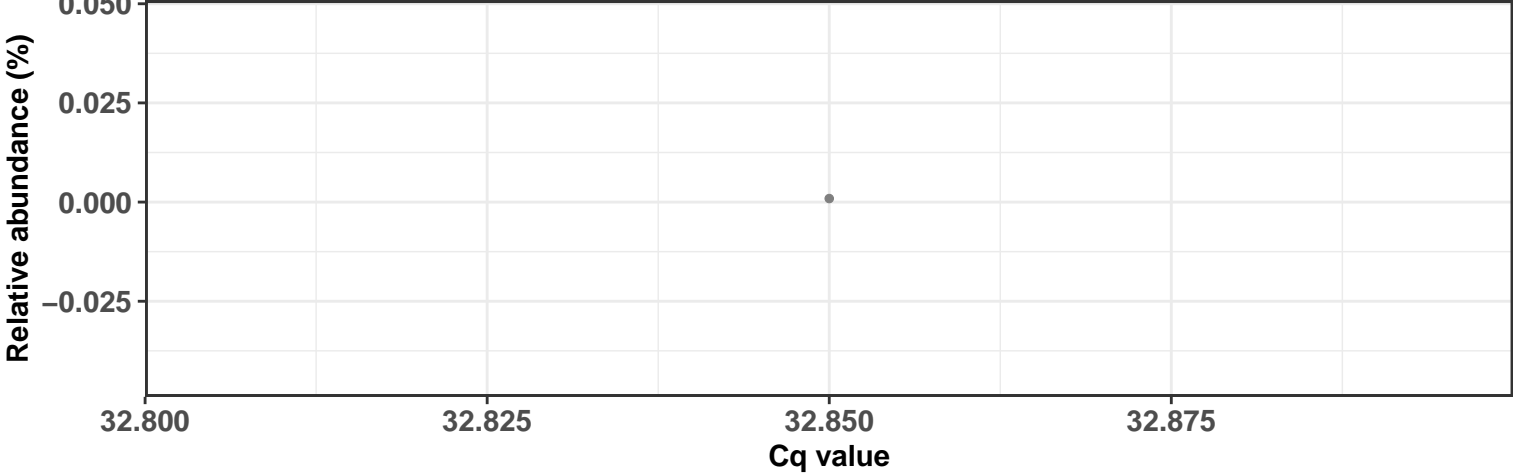
$\log_e(S) = 8.233$, $p = 0.879$, $\hat{\rho}_{\text{Spearman}} = -0.030$, $\text{CI}_{95\%} [-0.528, 0.433]$, $n_{\text{pairs}} = 28$



Correlation within: REF-DID

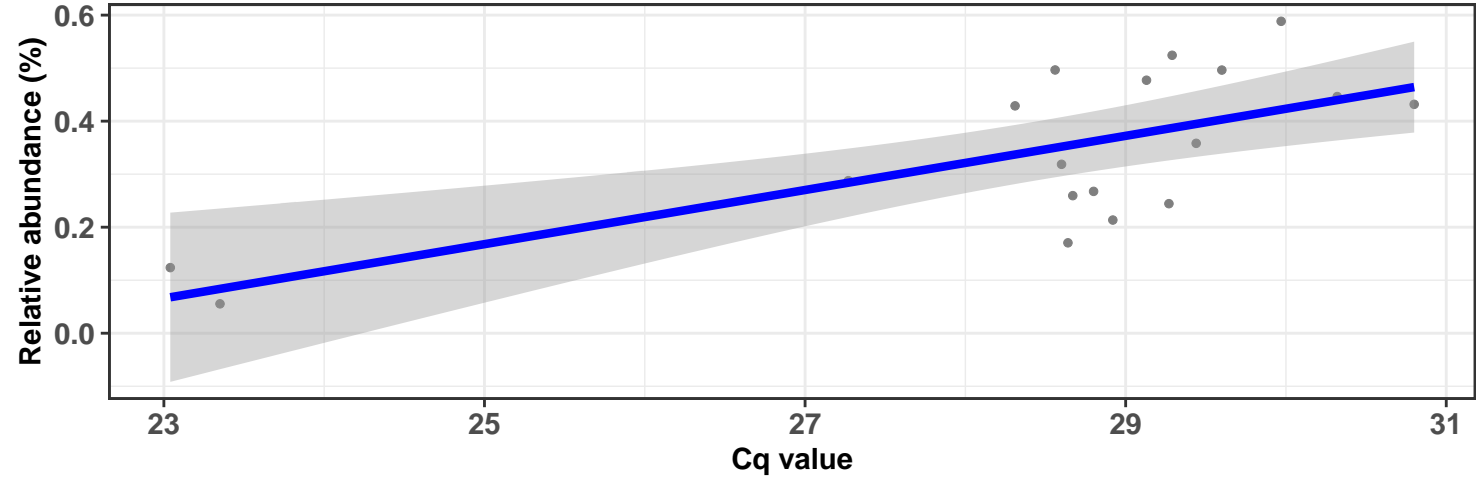


Correlation within: REF-DIM

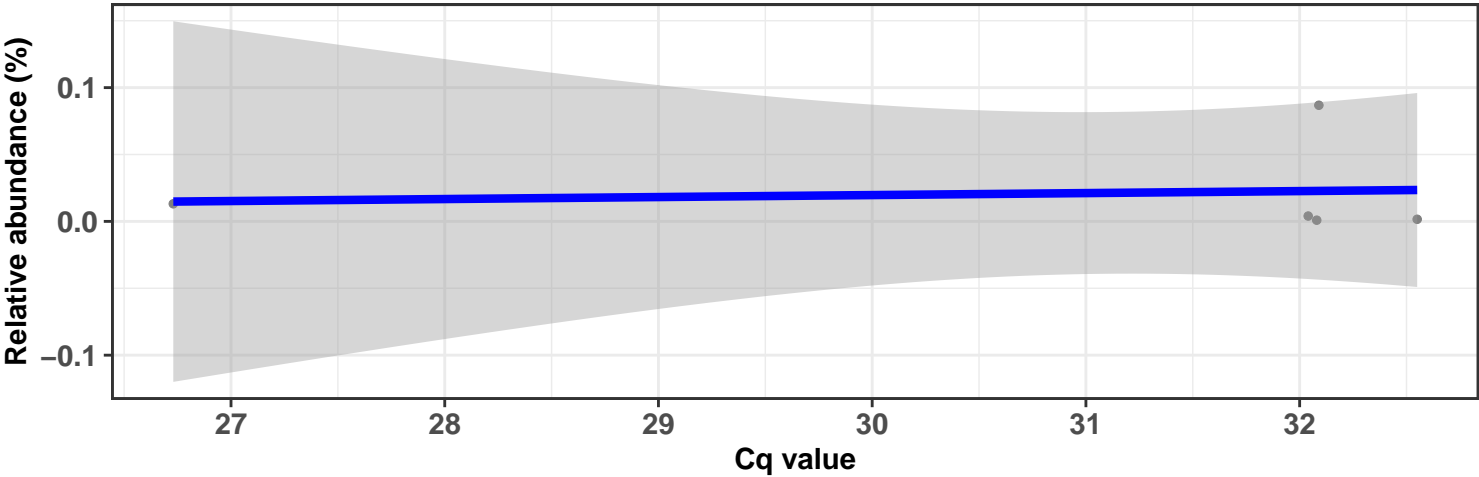


Correlation within: IM-DID

$\log_e(S) = 6.021$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = 0.575$, $\text{CI}_{95\%} [0.280, 0.961]$, $n_{\text{pairs}} = 18$



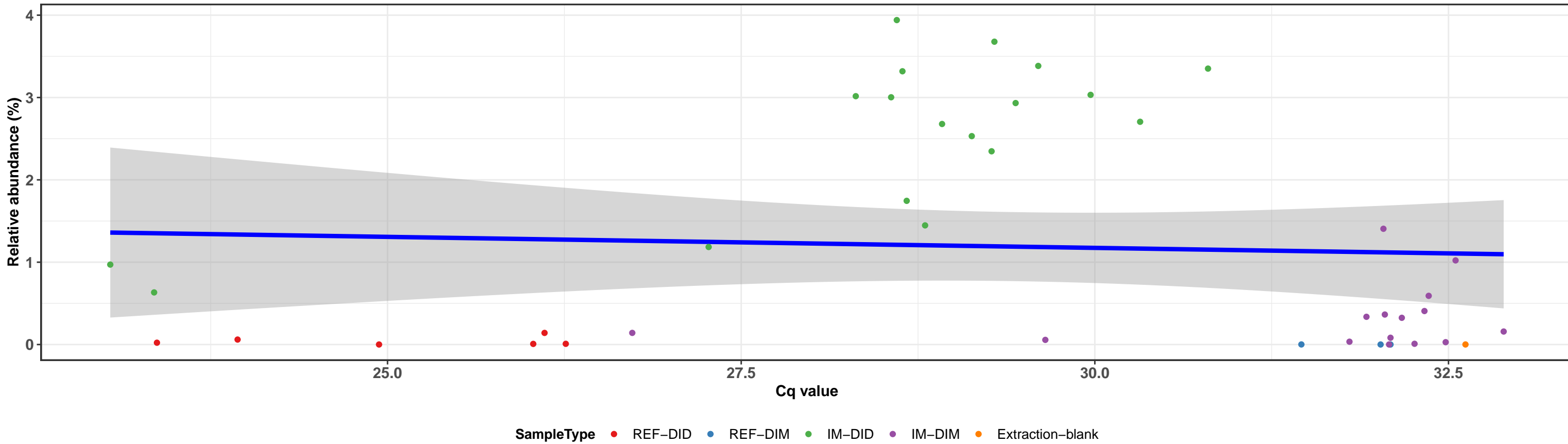
Correlation within: IM-DIM



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium aurimucosum ATCC 700975

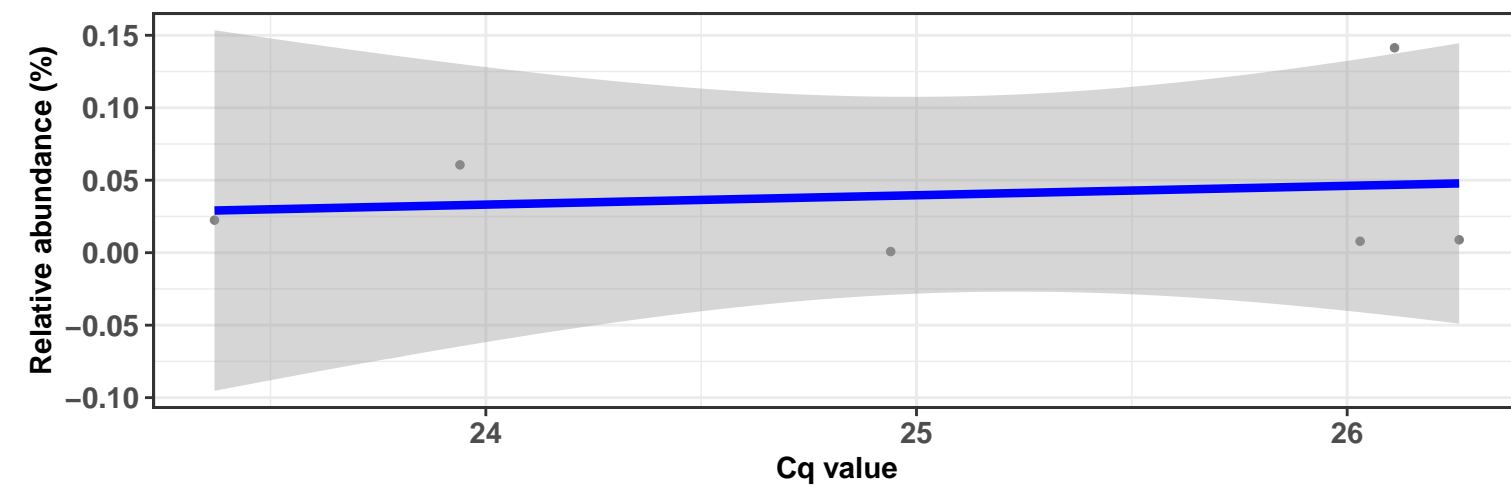
Correlation with all samples

$\log_e(S) = 9.662$, $p = 0.232$, $\hat{\rho}_{\text{Spearman}} = -0.186$, $\text{CI}_{95\%} [-0.524, 0.137]$, $n_{\text{pairs}} = 43$

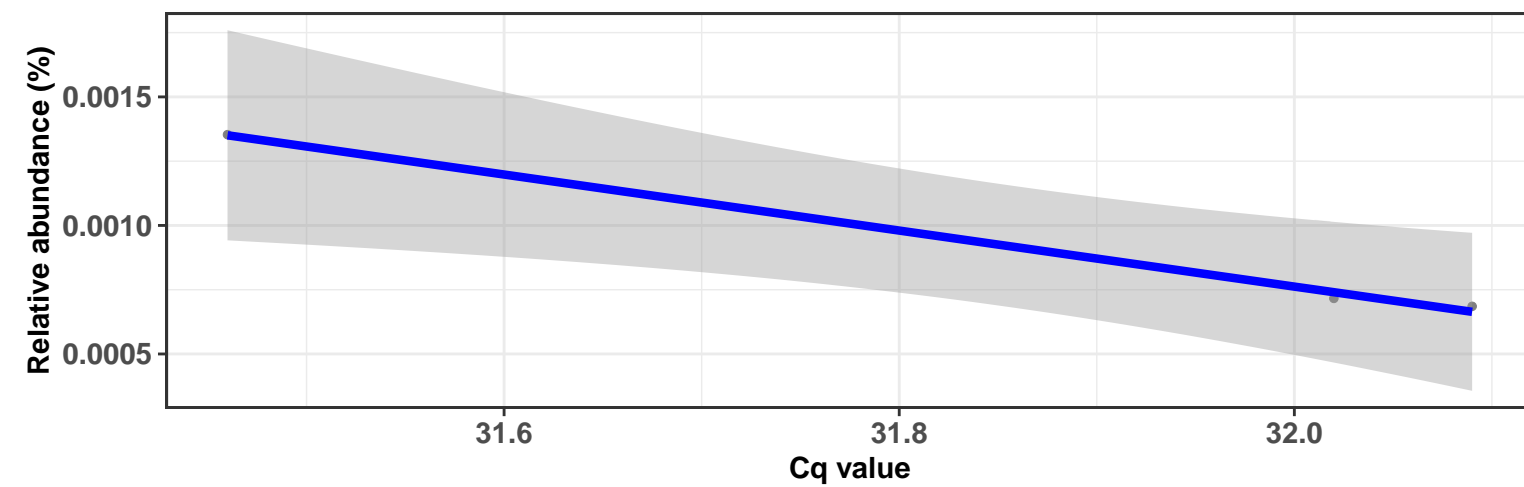


Correlation within: REF-DID

$\log_e(S) = 3.584$, $p = 0.957$, $\hat{\rho}_{\text{Spearman}} = -0.029$, $\text{CI}_{95\%} [-0.909, 0.909]$, $n_{\text{pairs}} = 6$

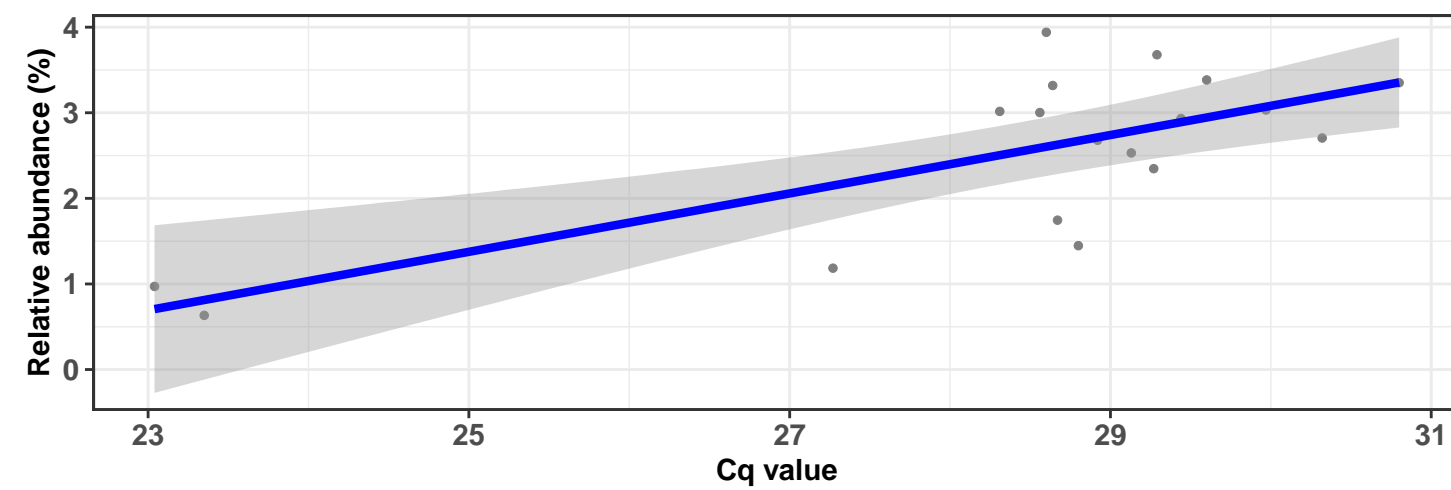


Correlation within: REF-DIM



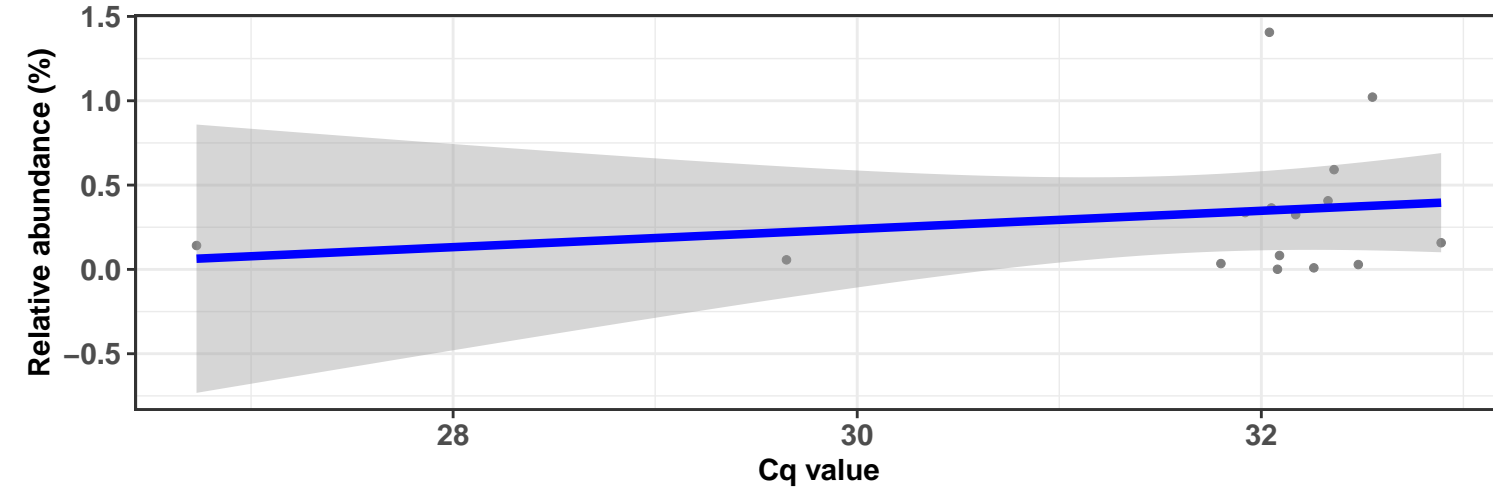
Correlation within: IM-DID

$\log_e(S) = 6.215$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.484$, $\text{CI}_{95\%} [0.141, 0.906]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

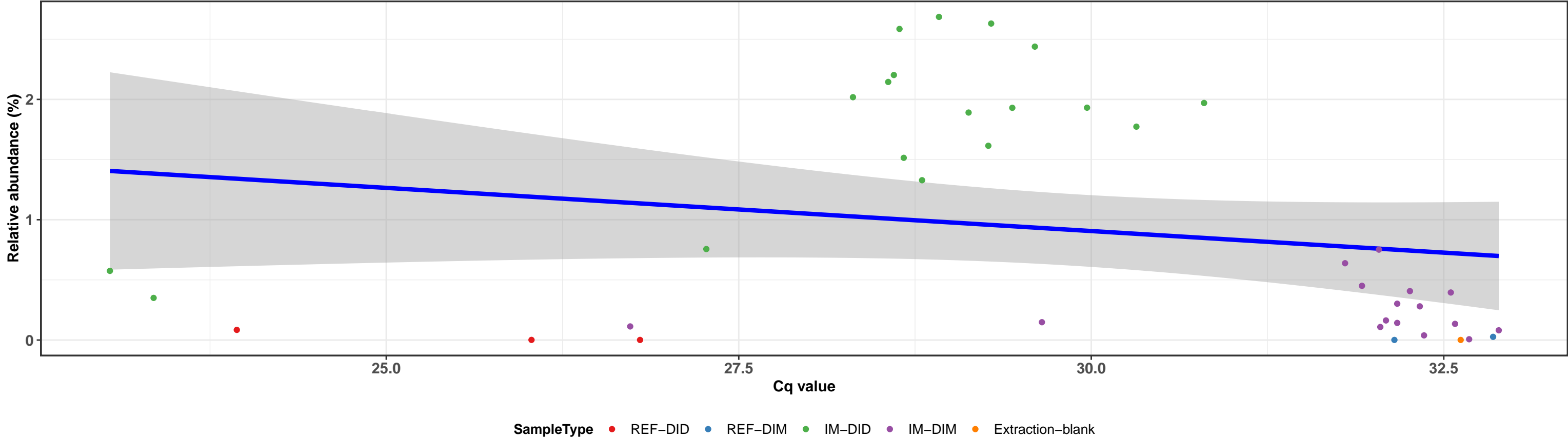
$\log_e(S) = 6.136$, $p = 0.533$, $\hat{\rho}_{\text{Spearman}} = 0.175$, $\text{CI}_{95\%} [-0.351, 0.679]$, $n_{\text{pairs}} = 15$



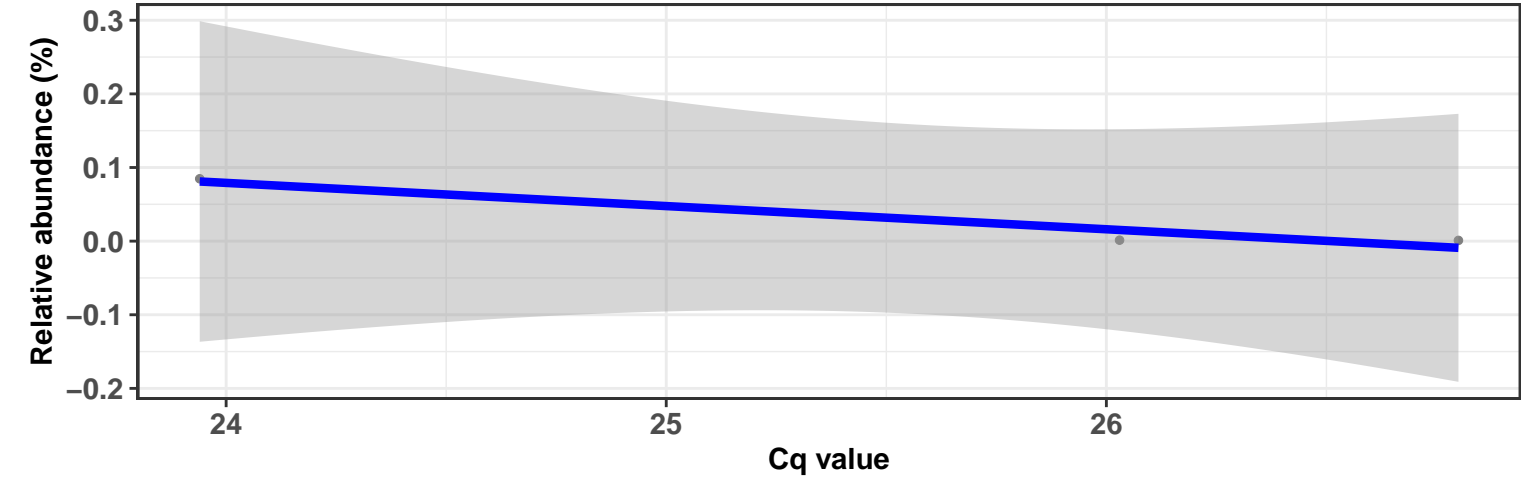
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

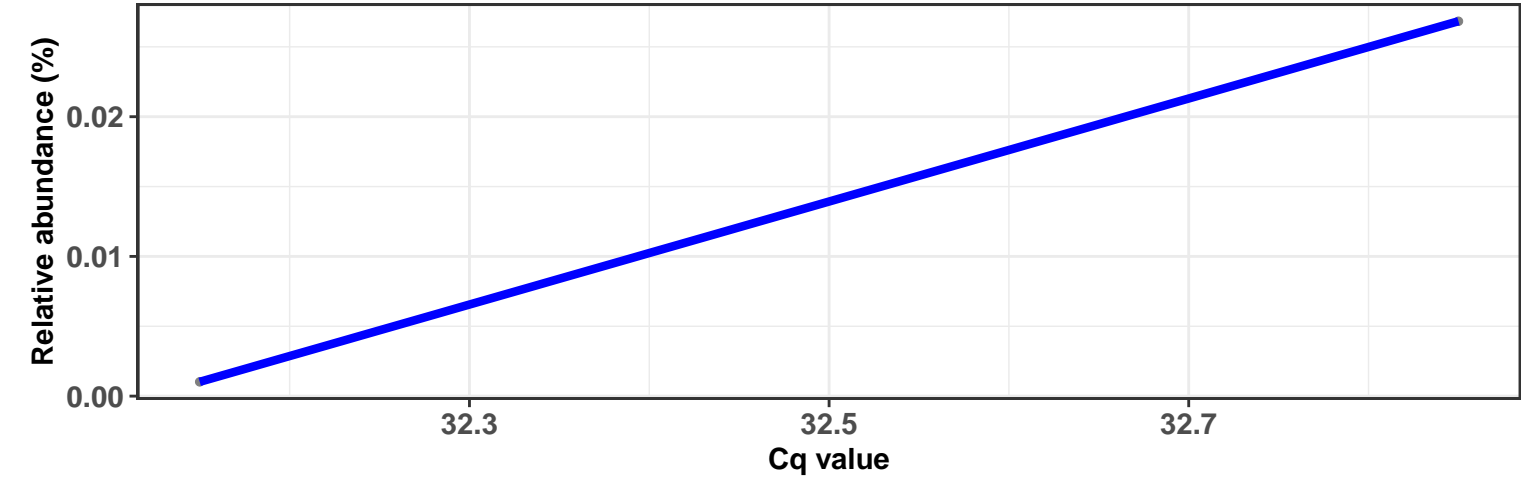
$\log_e(S) = 9.597$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = -0.381$, $\text{CI}_{95\%} [-0.727, -0.057]$, $n_{\text{pairs}} = 40$



Correlation within: REF-DID

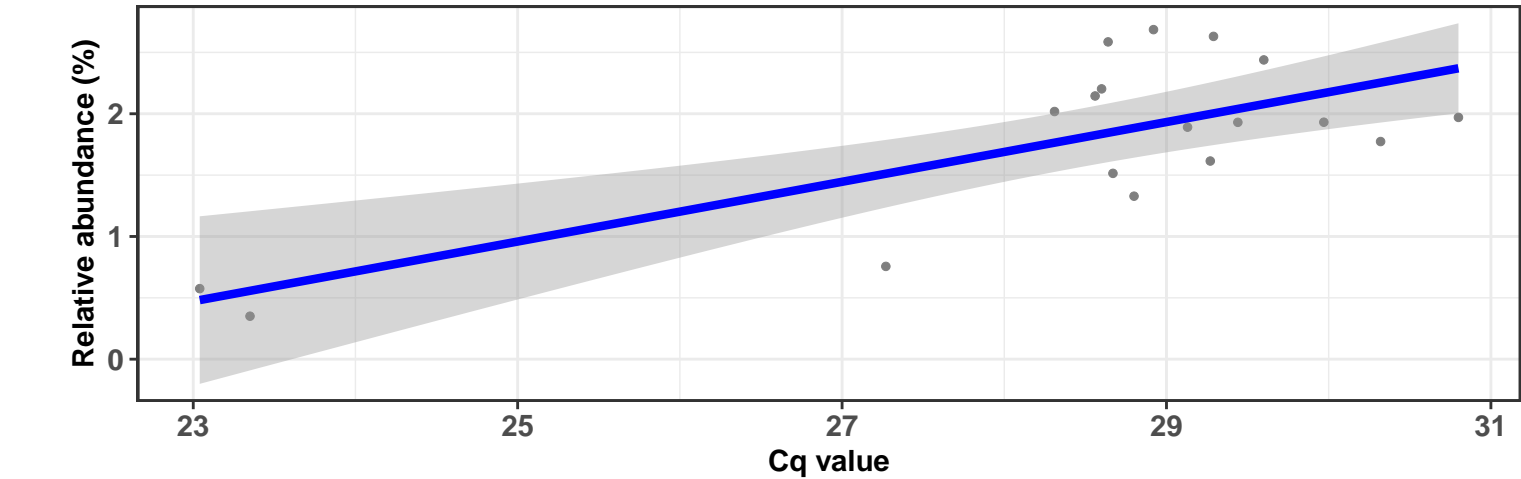


Correlation within: REF-DIM



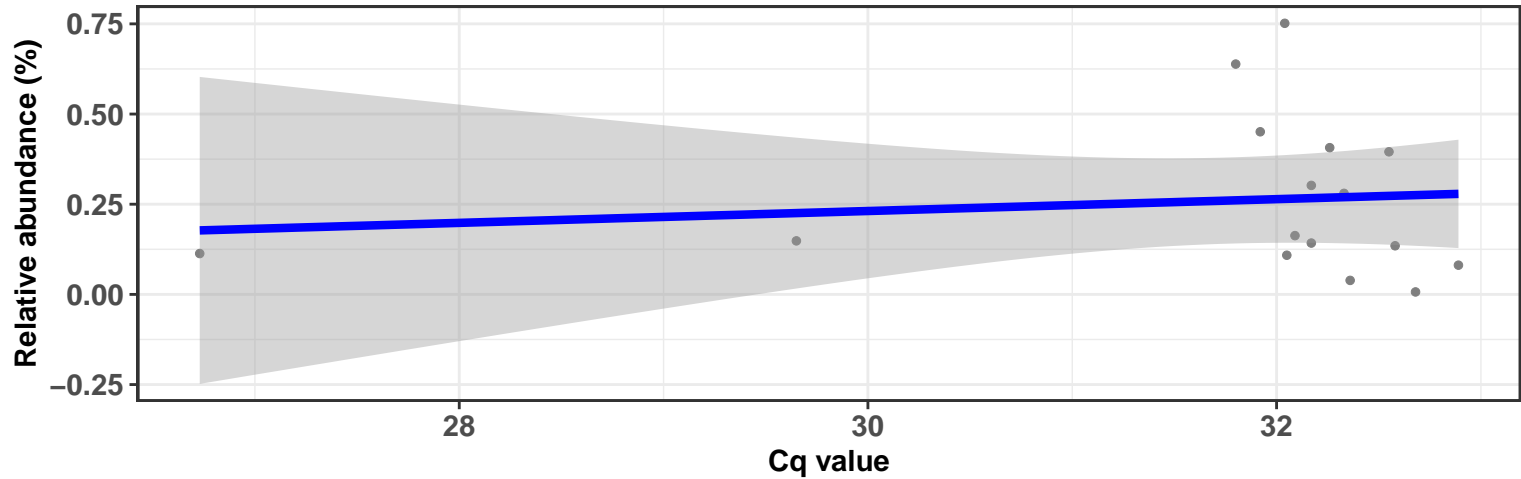
Correlation within: IM-DID

$\log_e(S) = 6.468$, $p = 0.174$, $\hat{\rho}_{\text{Spearman}} = 0.335$, $\text{CI}_{95\%} [-0.088, 0.804]$, $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

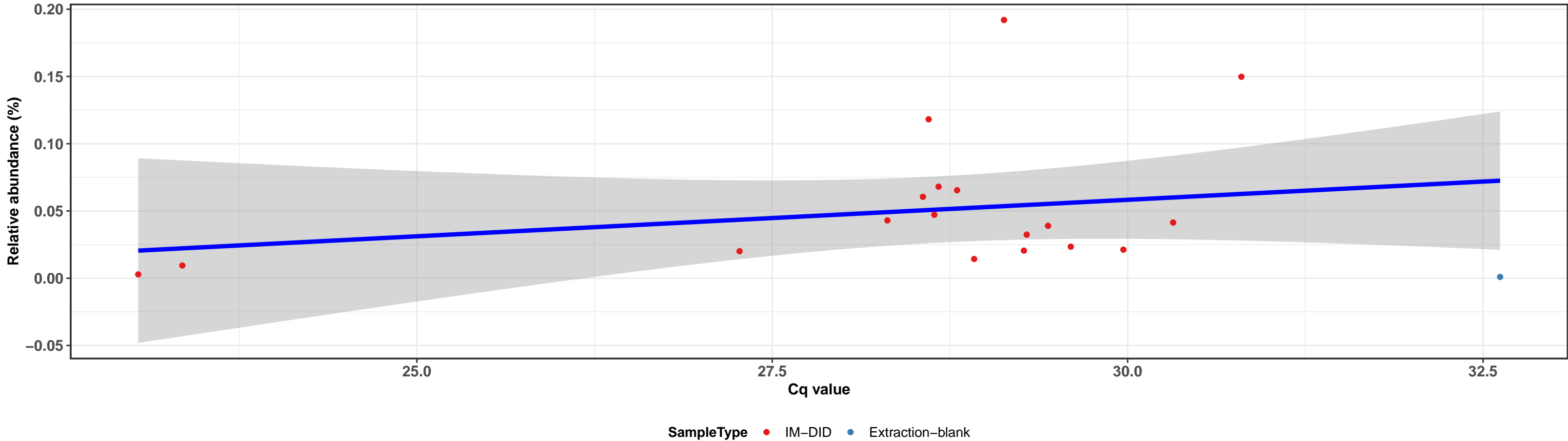
$\log_e(S) = 6.882$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = -0.433$, $\text{CI}_{95\%} [-0.964, 0.085]$, $n_{\text{pairs}} = 16$



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; Ambiguous_taxa

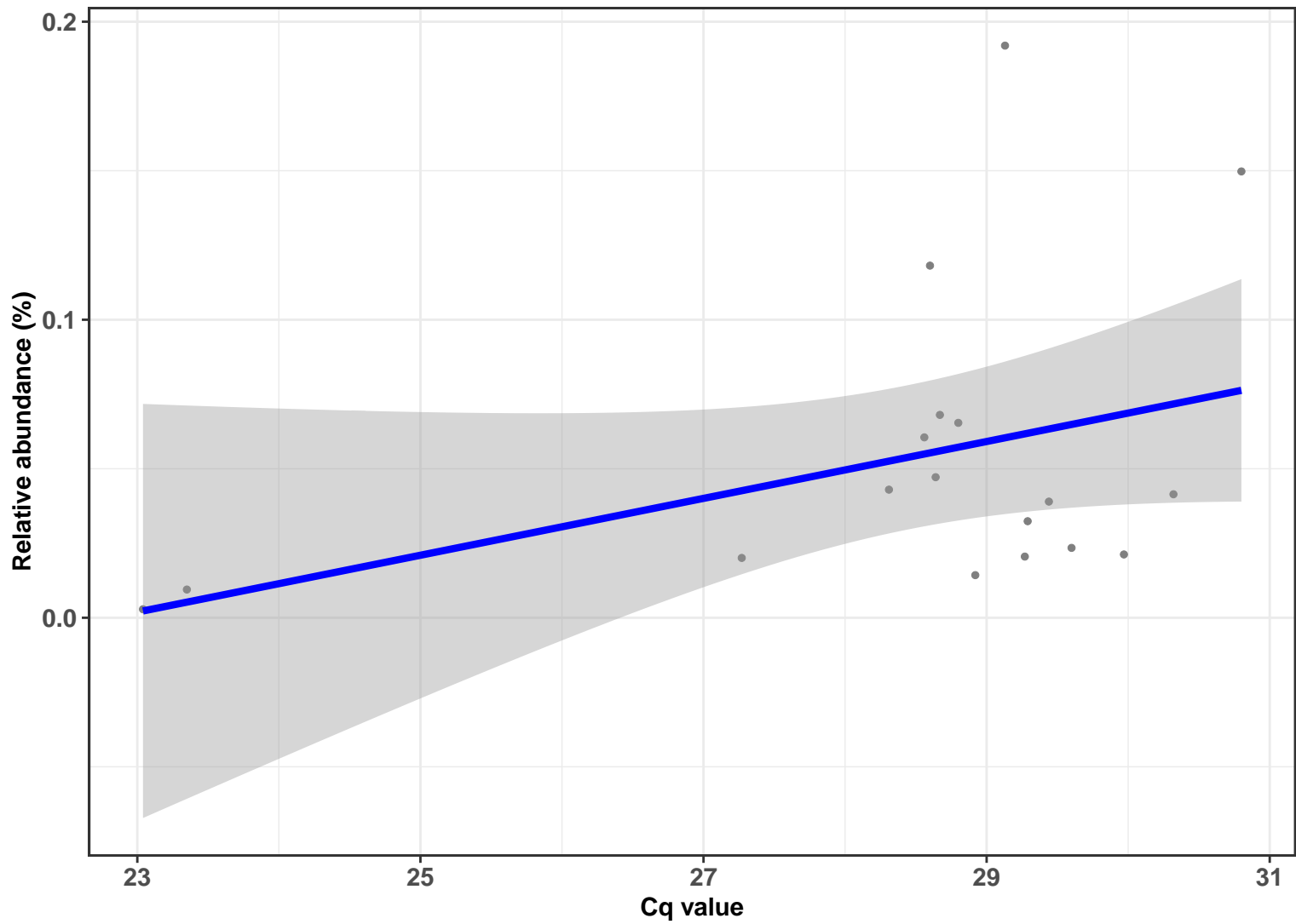
Correlation with all samples

$\log_e(S) = 6.972$, $p = 0.792$, $\hat{\rho}_{\text{Spearman}} = 0.065$, $\text{CI}_{95\%} [-0.458, 0.569]$, $n_{\text{pairs}} = 19$



Correlation within: IM-DID

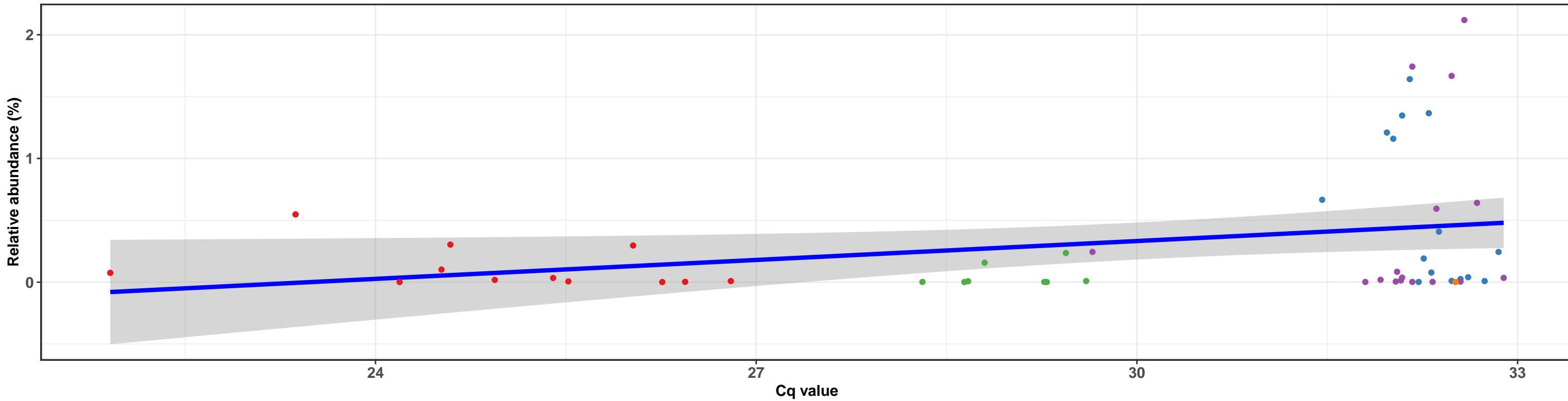
$\log_e(S) = 6.585$, $p = 0.311$, $\hat{\rho}_{\text{Spearman}} = 0.253$, $\text{CI}_{95\%} [-0.228, 0.786]$, $n_{\text{pairs}} = 18$



k__Bacteria; p__Spirochaetes; c__Spirochaetia; o__Brevinematales; f__Brevinemataceae; g__Brevinema; s__Brevinema andersonii

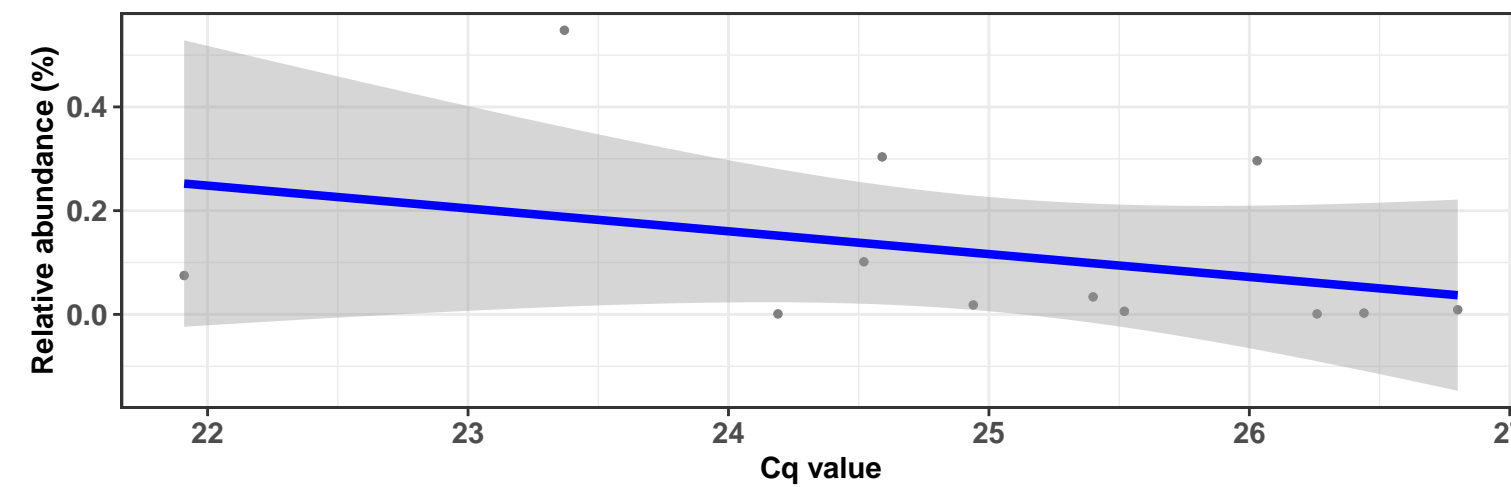
Correlation with all samples

$\log_e(S) = 9.818$, $p = 0.124$, $\hat{\rho}_{\text{Spearman}} = 0.216$, $\text{CI}_{95\%} [-0.024, 0.481]$, $n_{\text{pairs}} = 52$



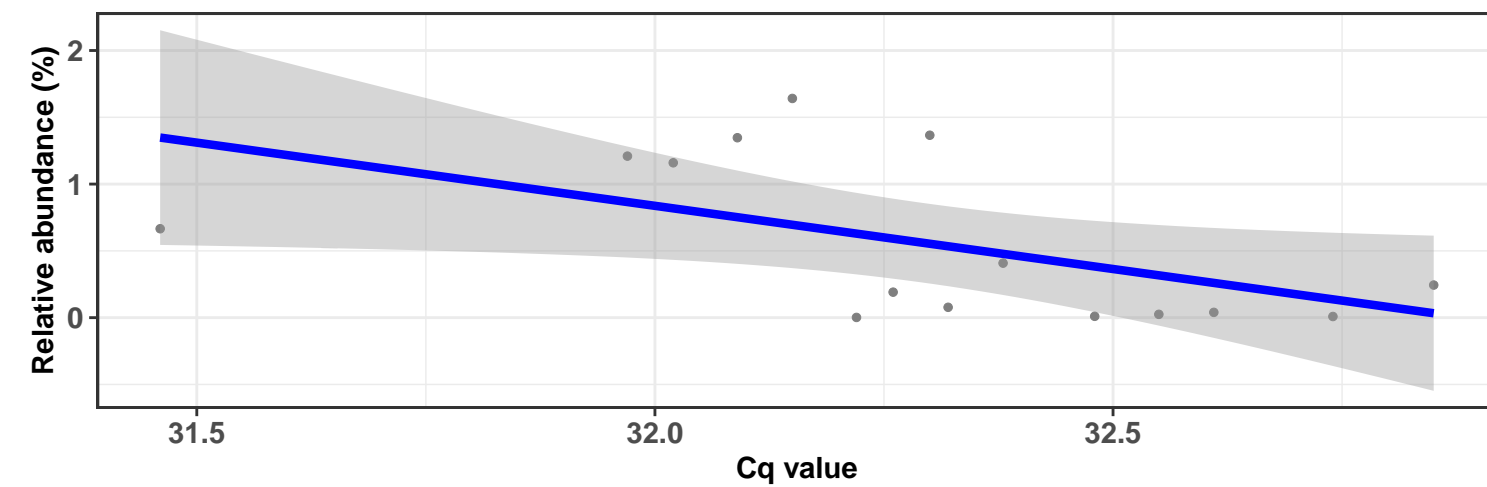
Correlation within: REF-DID

$\log_e(S) = 6.011$, $p = 0.167$, $\hat{\rho}_{\text{Spearman}} = -0.427$, $\text{CI}_{95\%} [-0.937, 0.043]$, $n_{\text{pairs}} = 12$



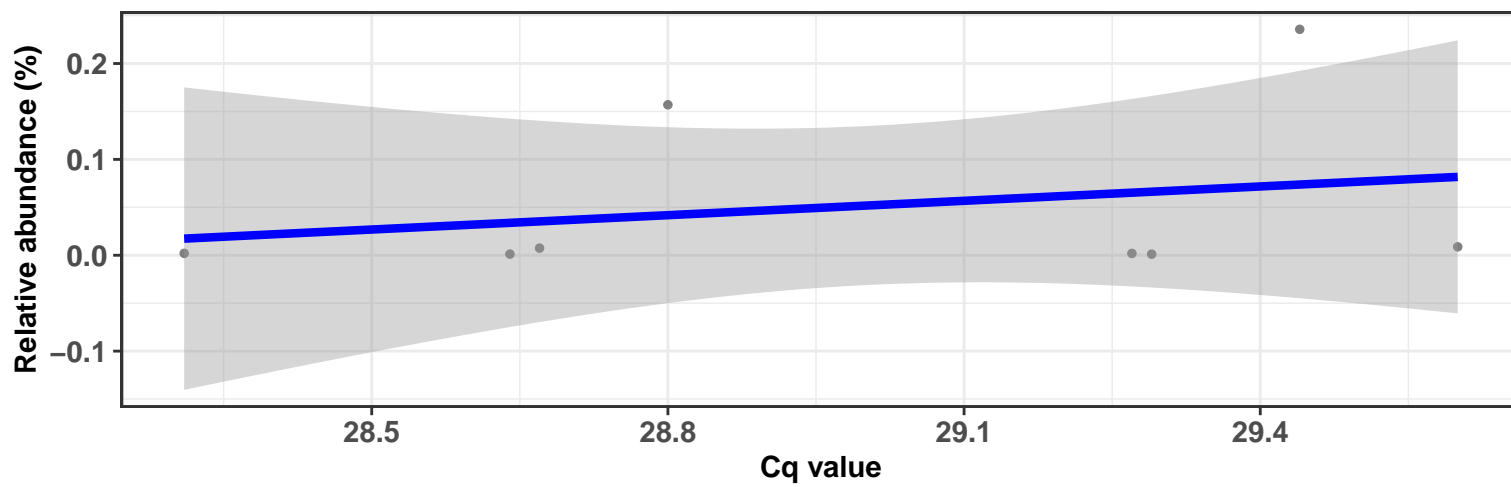
Correlation within: REF-DIM

$\log_e(S) = 6.782$, $p = 0.025$, $\hat{\rho}_{\text{Spearman}} = -0.575$, $\text{CI}_{95\%} [-0.919, -0.290]$, $n_{\text{pairs}} = 15$



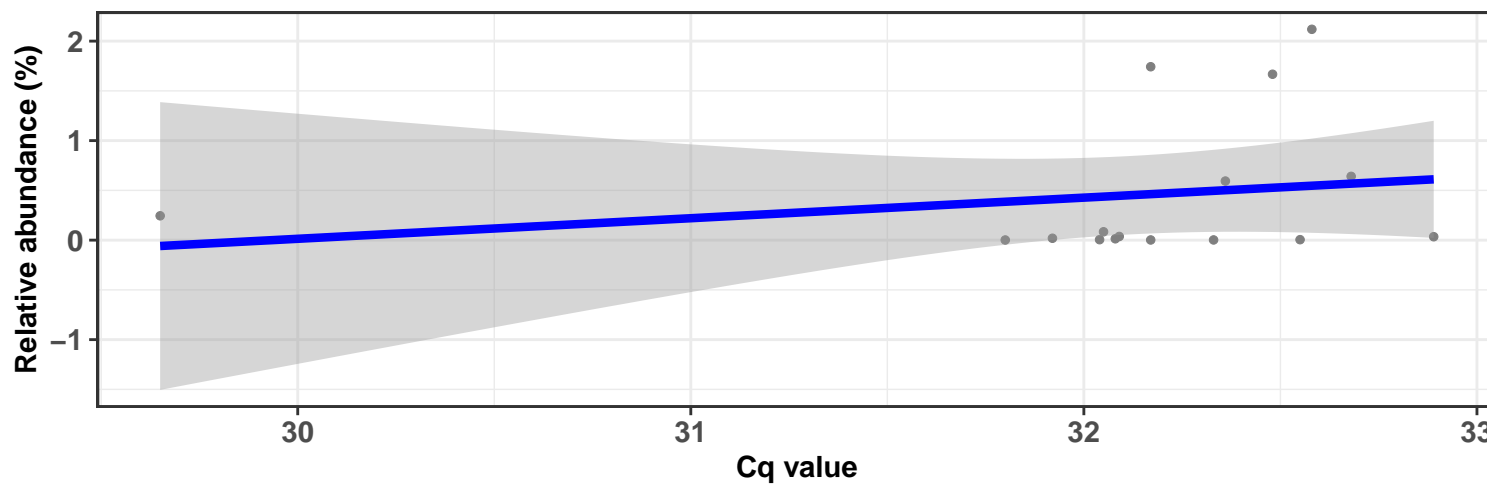
Correlation within: IM-DID

$\log_e(S) = 4.025$, $p = 0.420$, $\hat{\rho}_{\text{Spearman}} = 0.333$, $\text{CI}_{95\%} [-0.297, 1.091]$, $n_{\text{pairs}} = 8$



Correlation within: IM-DIM

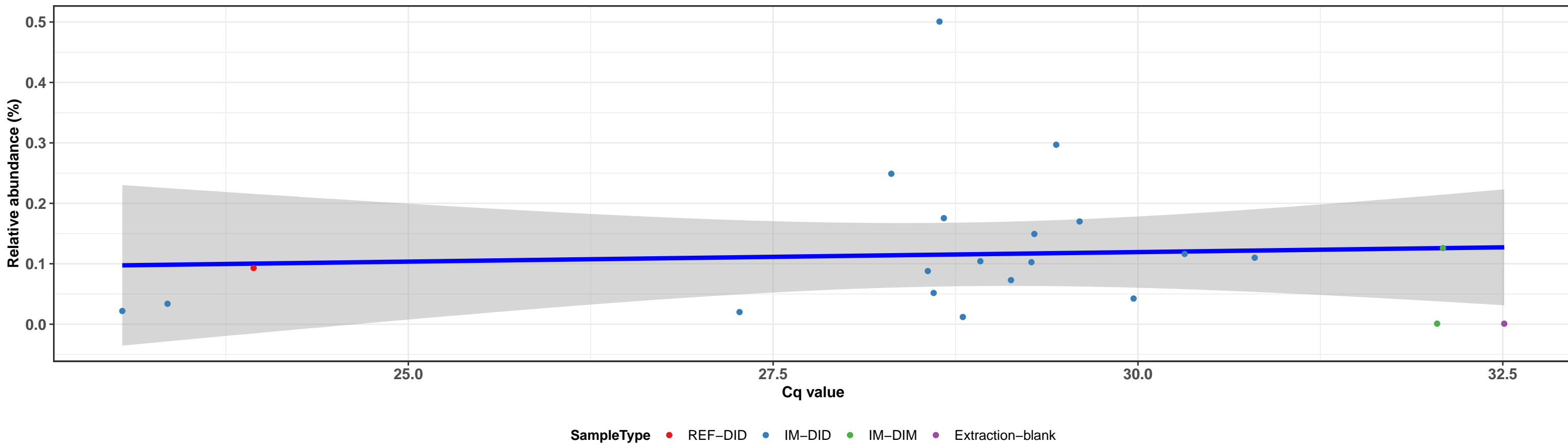
$\log_e(S) = 6.042$, $p = 0.145$, $\hat{\rho}_{\text{Spearman}} = 0.381$, $\text{CI}_{95\%} [-0.070, 0.852]$, $n_{\text{pairs}} = 16$



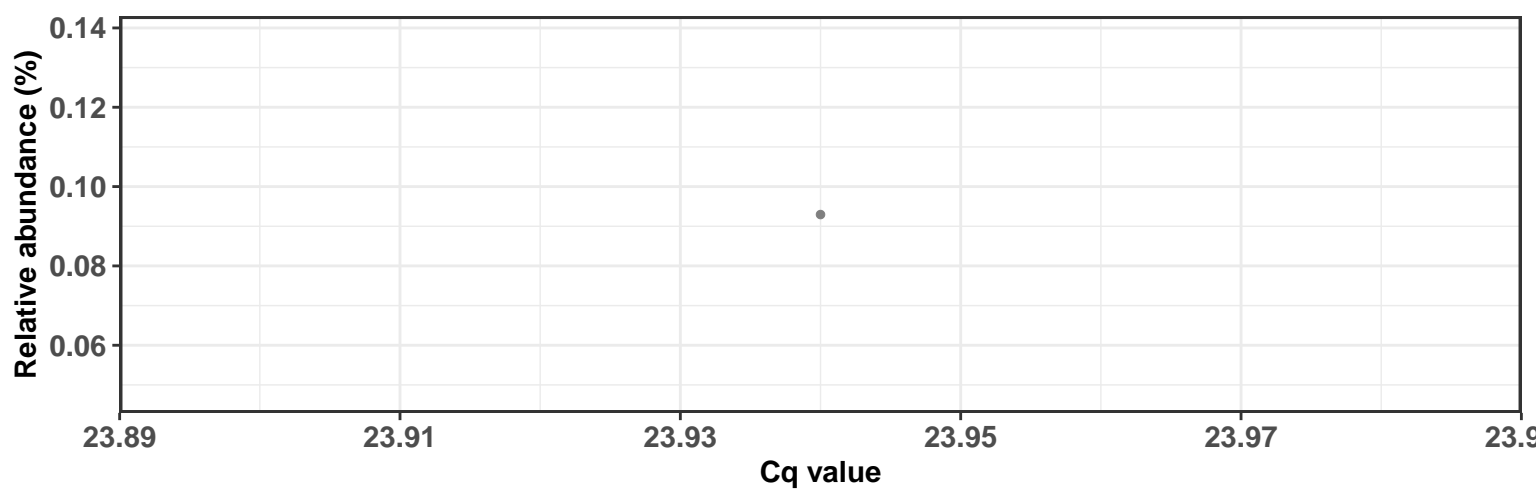
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__uncultured bacterium

Correlation with all samples

$\log_e(S) = 7.421$, $p = 0.801$, $\hat{\rho}_{\text{Spearman}} = 0.057$, $\text{CI}_{95\%} [-0.485, 0.596]$, $n_{\text{pairs}} = 22$

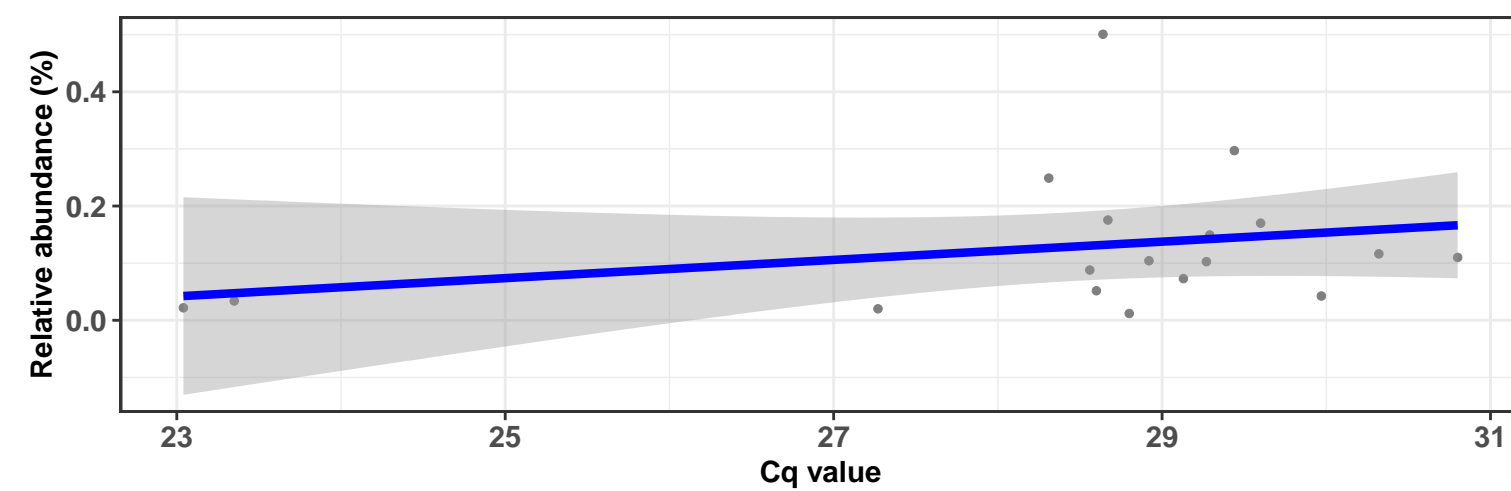


Correlation within: REF-DID

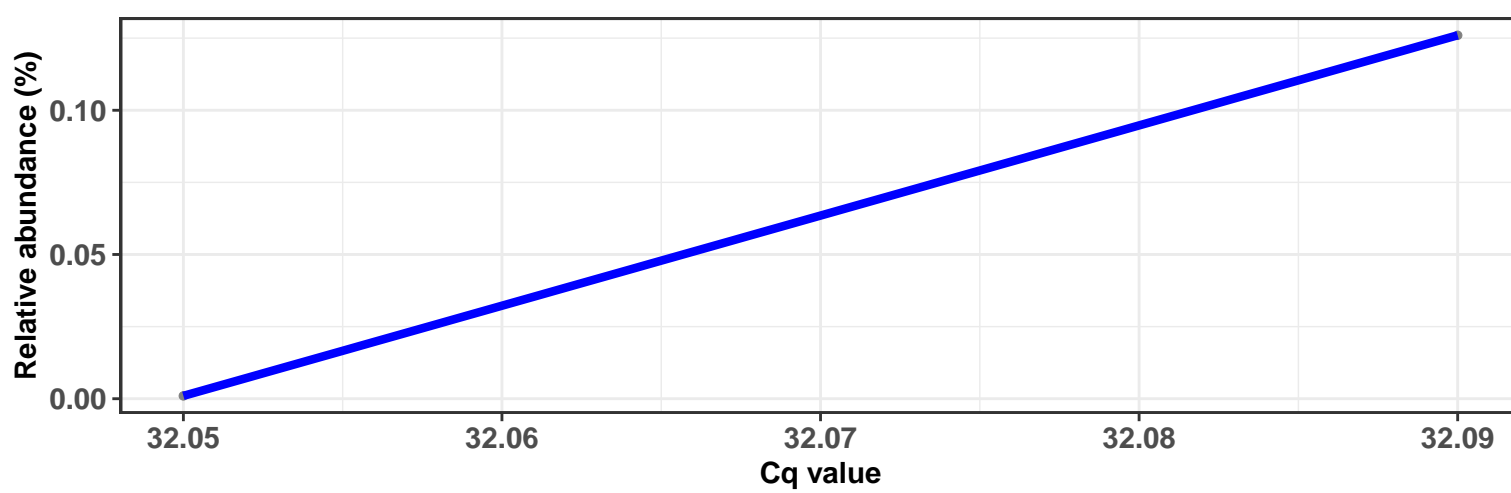


Correlation within: IM-DID

$\log_e(S) = 6.439$, $p = 0.150$, $\hat{\rho}_{\text{Spearman}} = 0.354$, $\text{CI}_{95\%} [-0.058, 0.852]$, $n_{\text{pairs}} = 18$



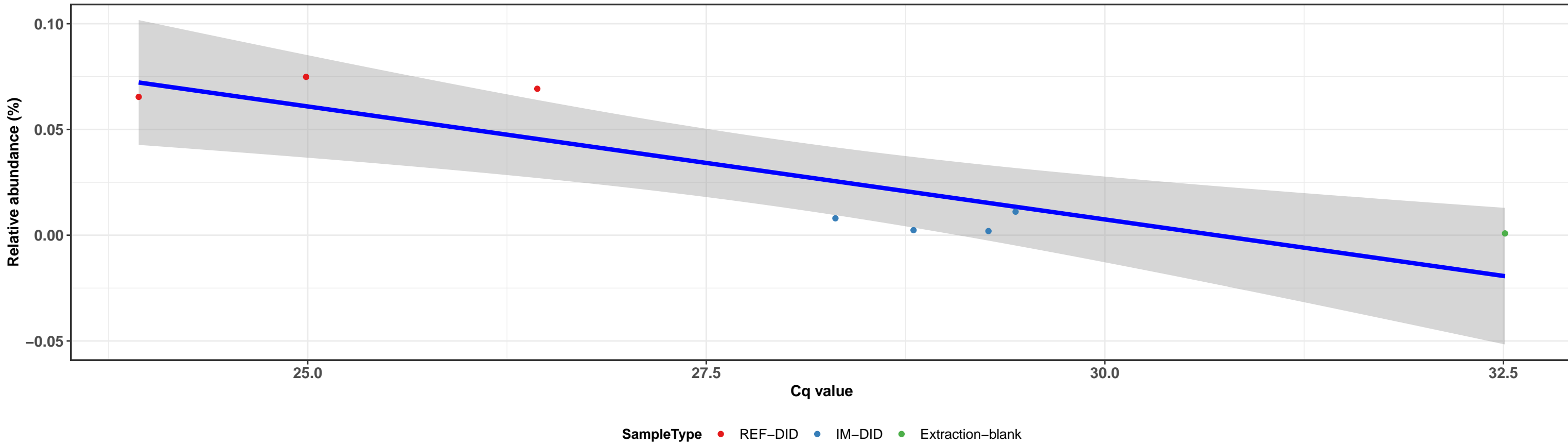
Correlation within: IM-DIM



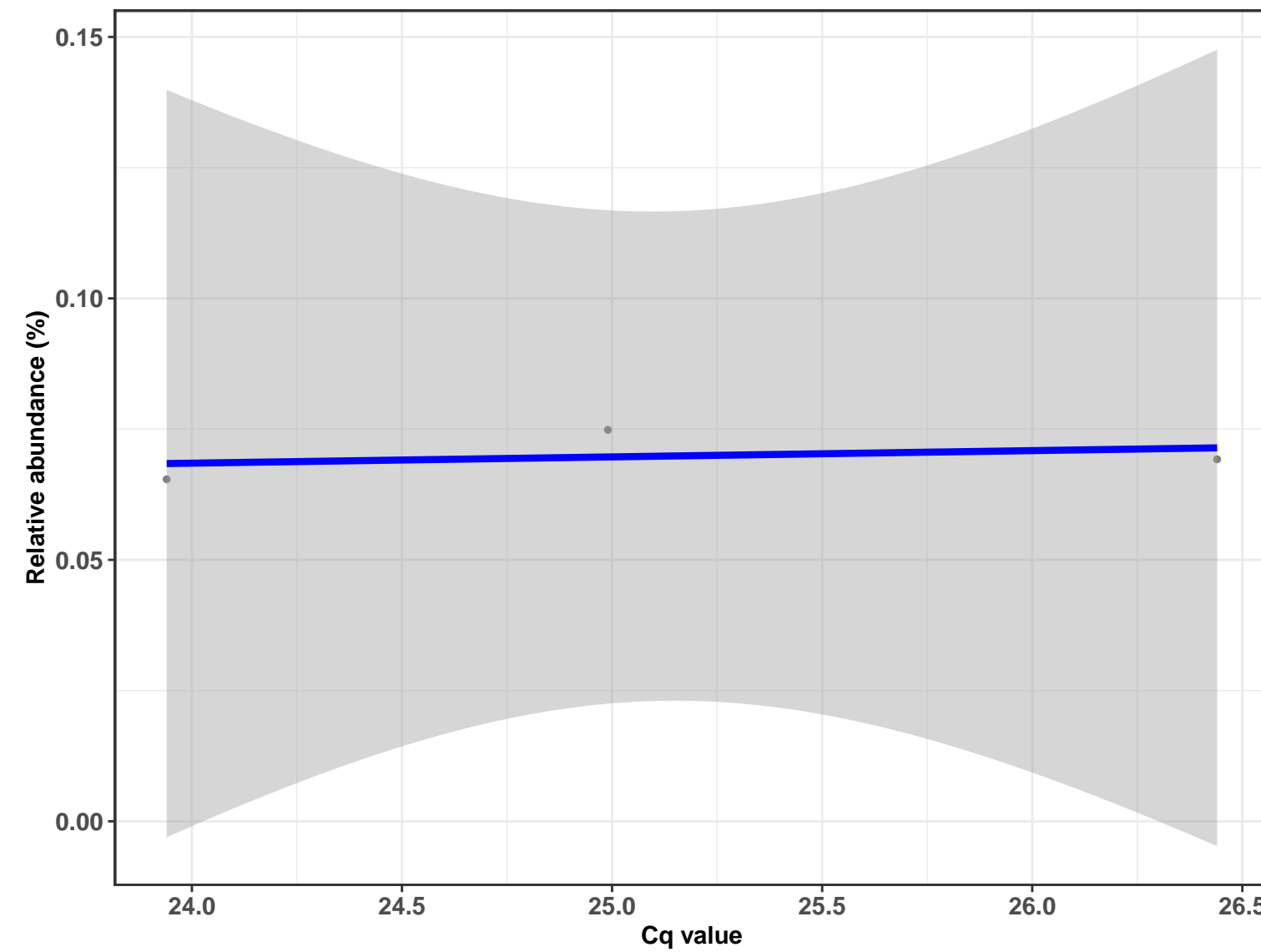
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; NA; NA

Correlation with all samples

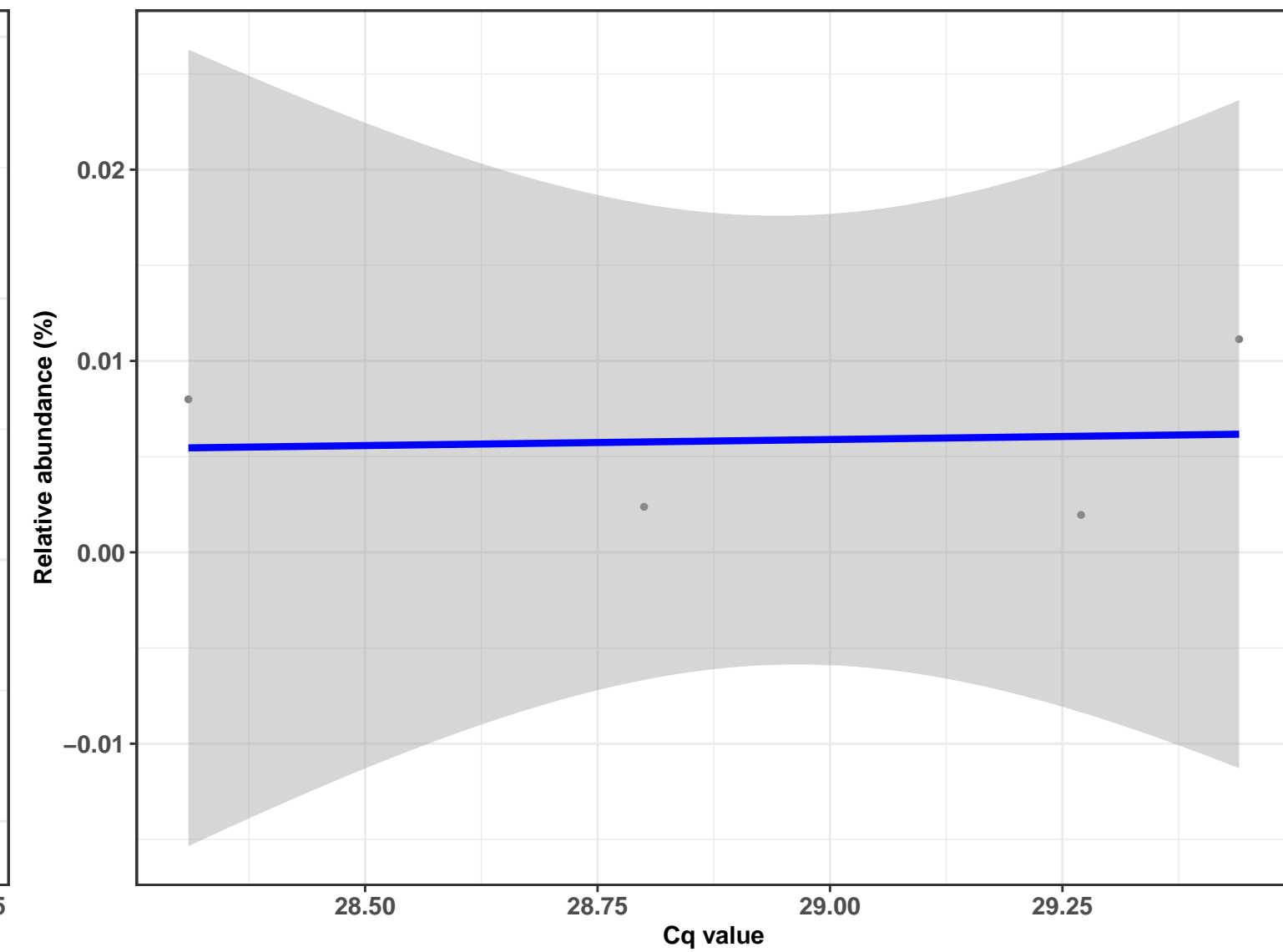
$\log_e(S) = 5.011$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = -0.786$, $\text{CI}_{95\%} [-1.285, -0.430]$, $n_{\text{pairs}} = 8$



Correlation within: REF-DID



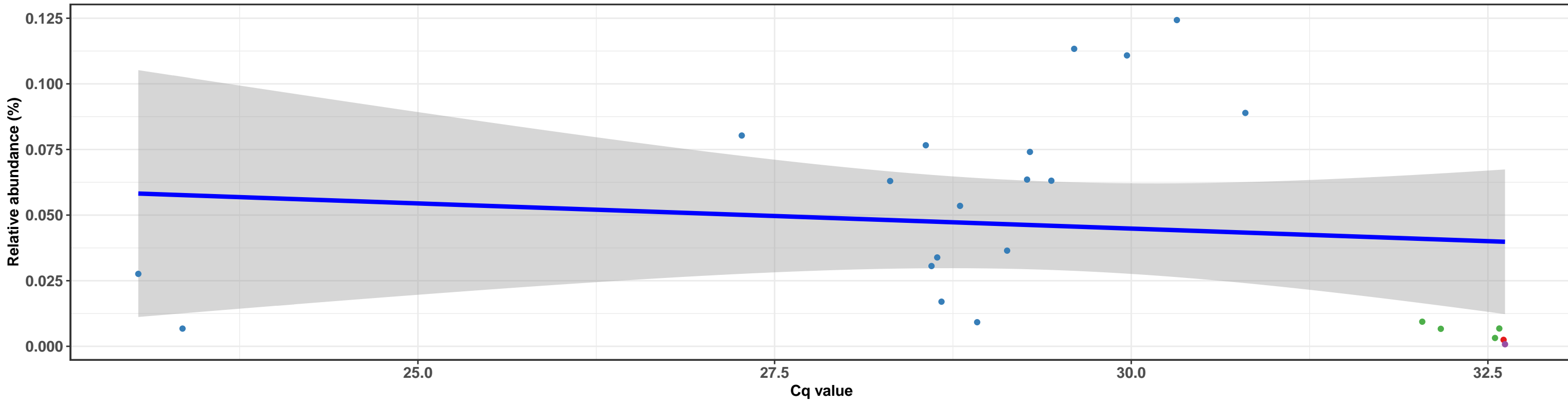
Correlation within: IM-DID



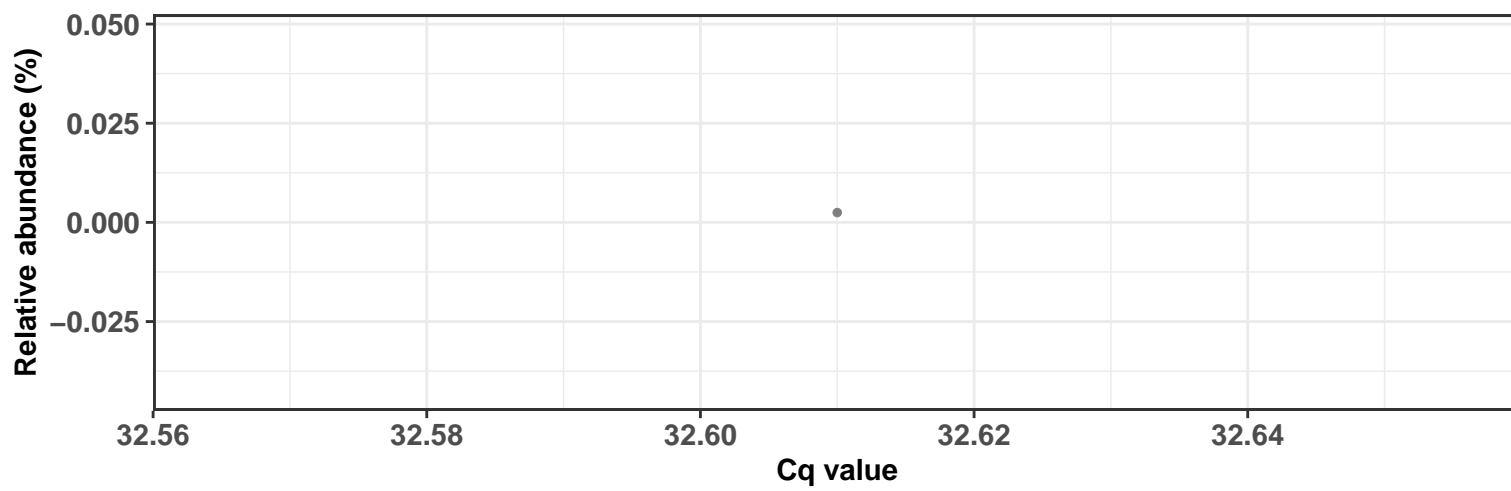
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 7.981$, $p = 0.200$, $\hat{\rho}_{\text{Spearman}} = -0.271$, $\text{CI}_{95\%} [-0.751, 0.254]$, $n_{\text{pairs}} = 24$

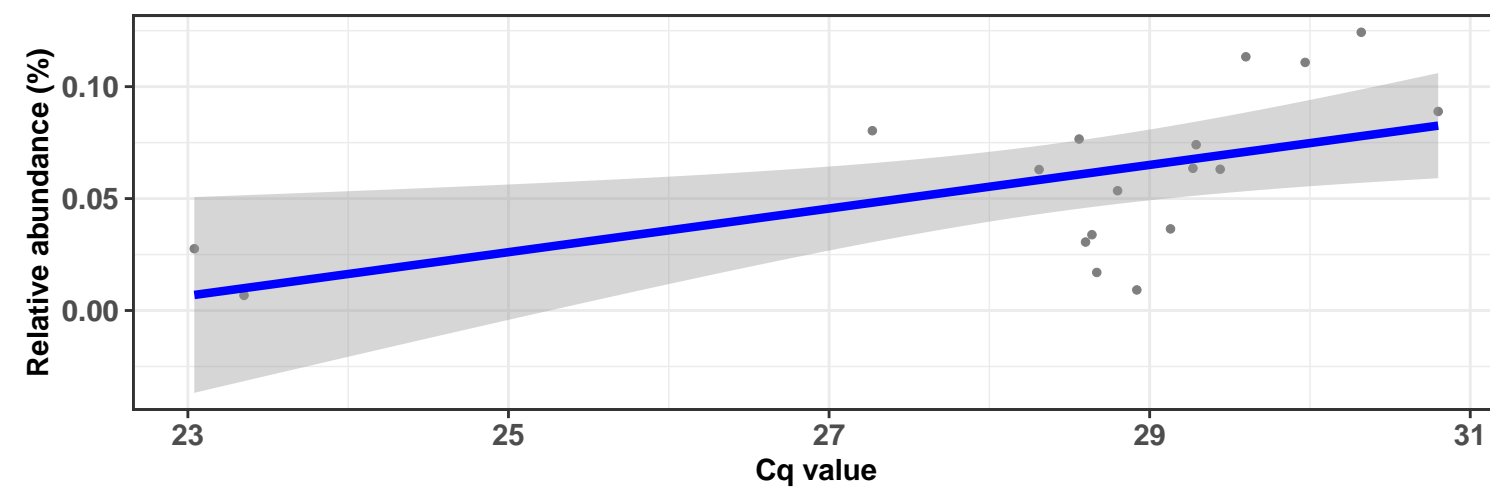


Correlation within: REF-DIM

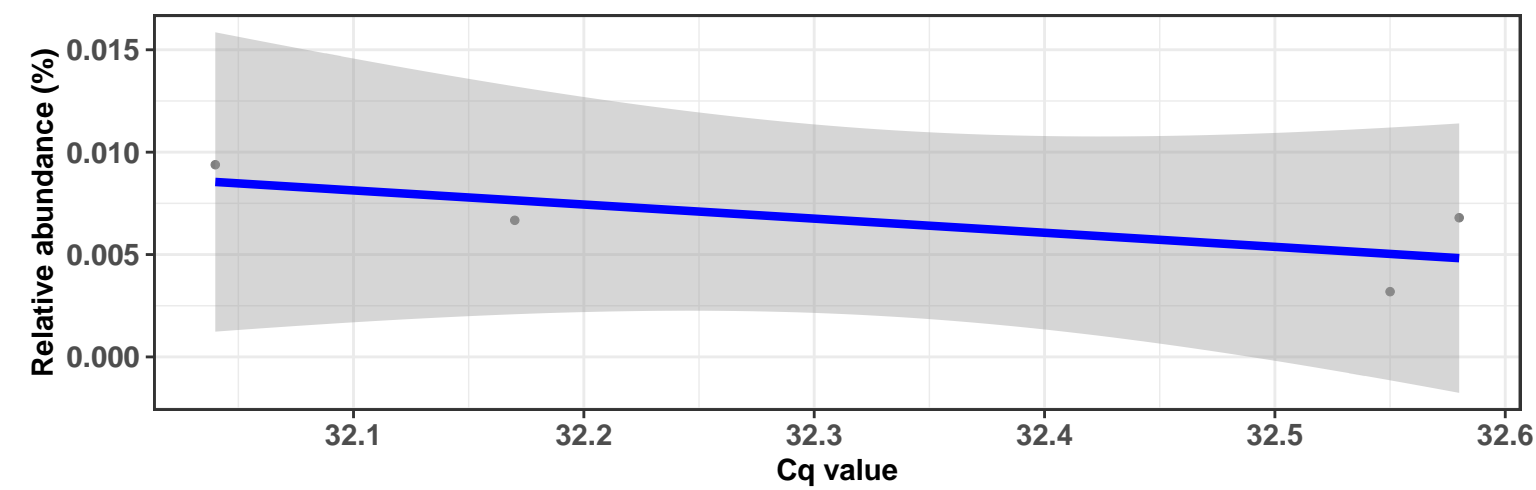


Correlation within: IM-DID

$\log_e(S) = 5.886$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.628$, $\text{CI}_{95\%} [0.208, 1.074]$, $n_{\text{pairs}} = 18$



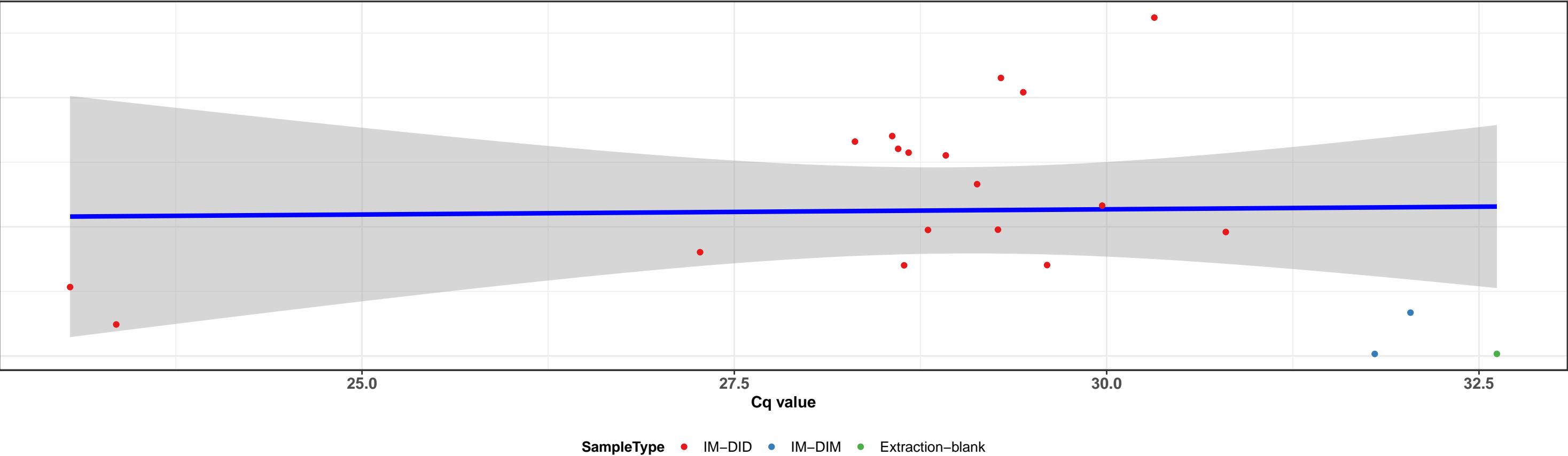
Correlation within: IM-DIM



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

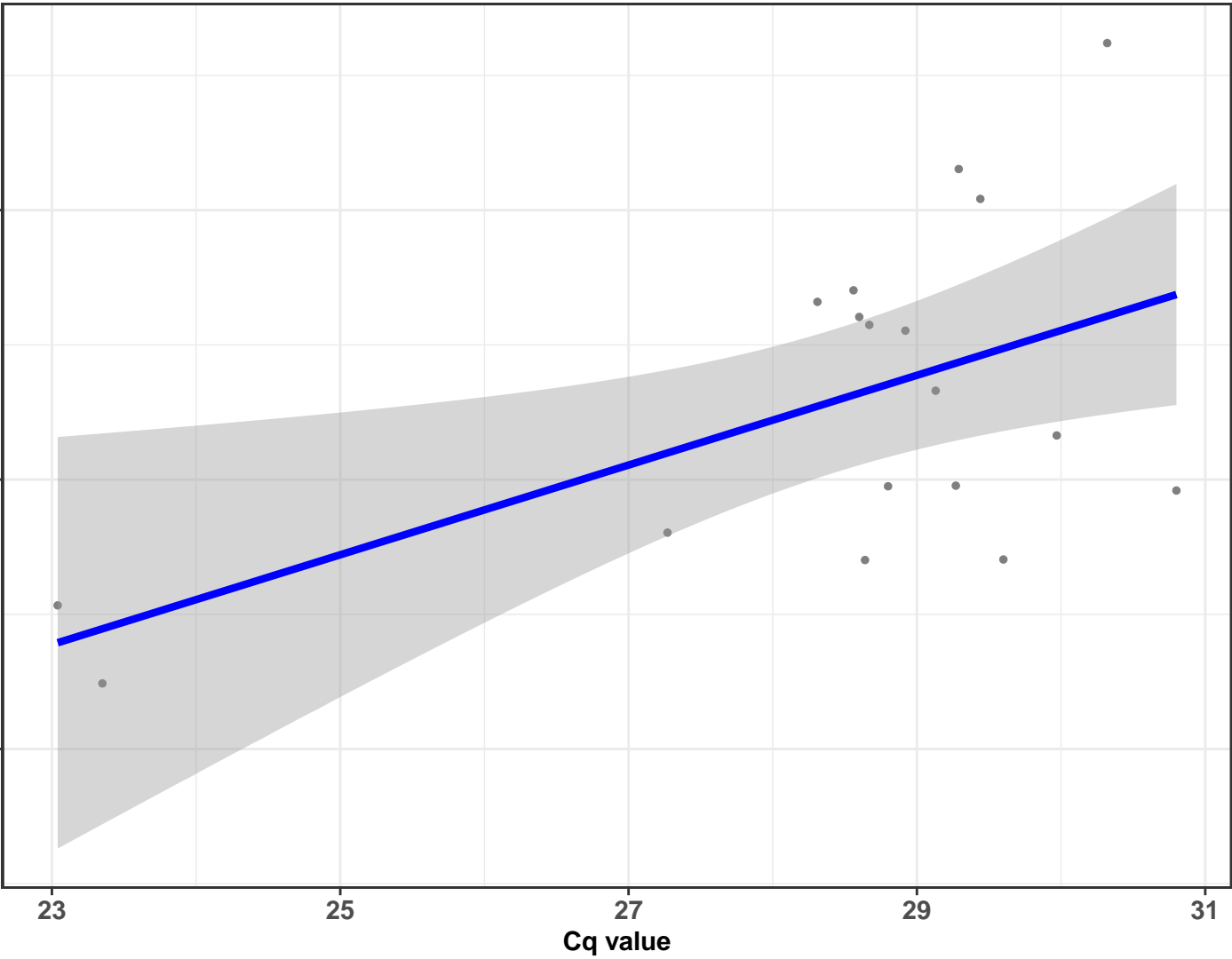
Correlation with all samples

$\log_e(S) = 7.464$, $p = 0.567$, $\hat{\rho}_{\text{Spearman}} = -0.132$, $\text{CI}_{95\%} [-0.688, 0.357]$, $n_{\text{pairs}} = 21$

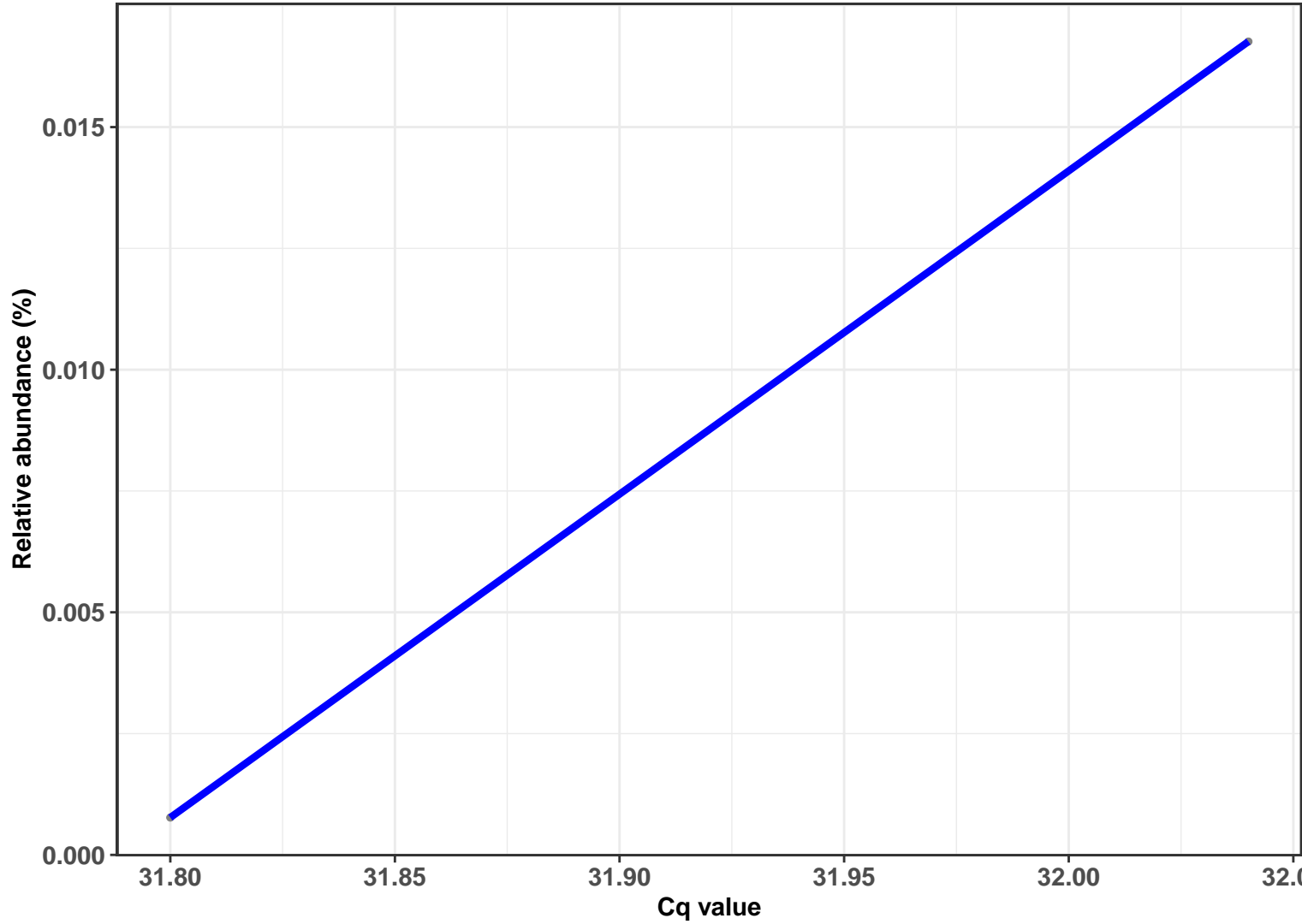


Correlation within: IM-DID

$\log_e(S) = 6.468$, $p = 0.174$, $\hat{\rho}_{\text{Spearman}} = 0.335$, $\text{CI}_{95\%} [-0.138, 0.836]$, $n_{\text{pairs}} = 18$



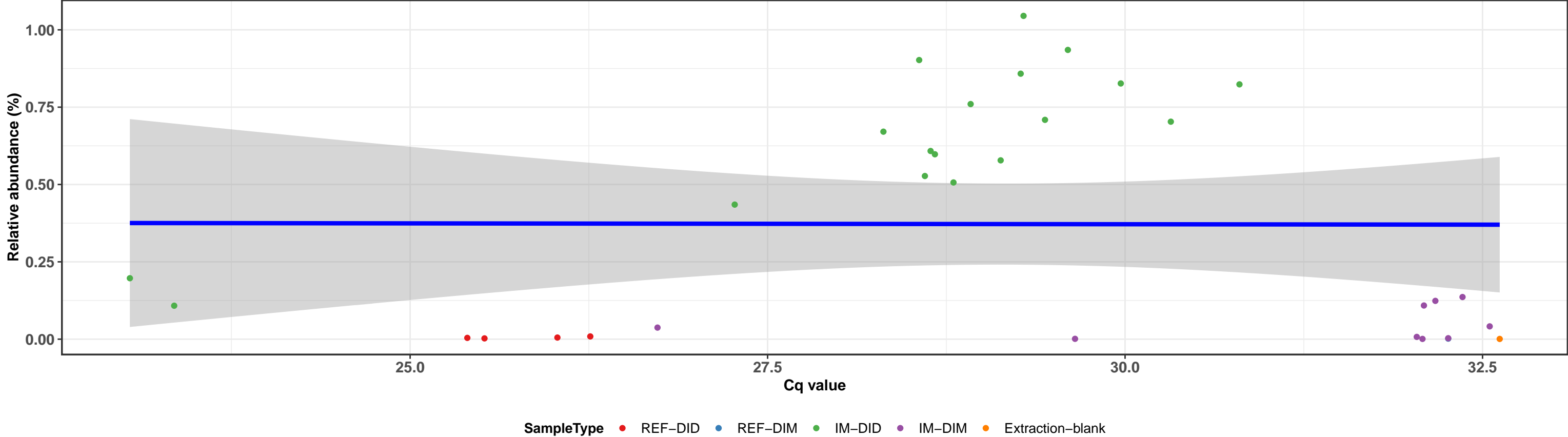
Correlation within: IM-DIM



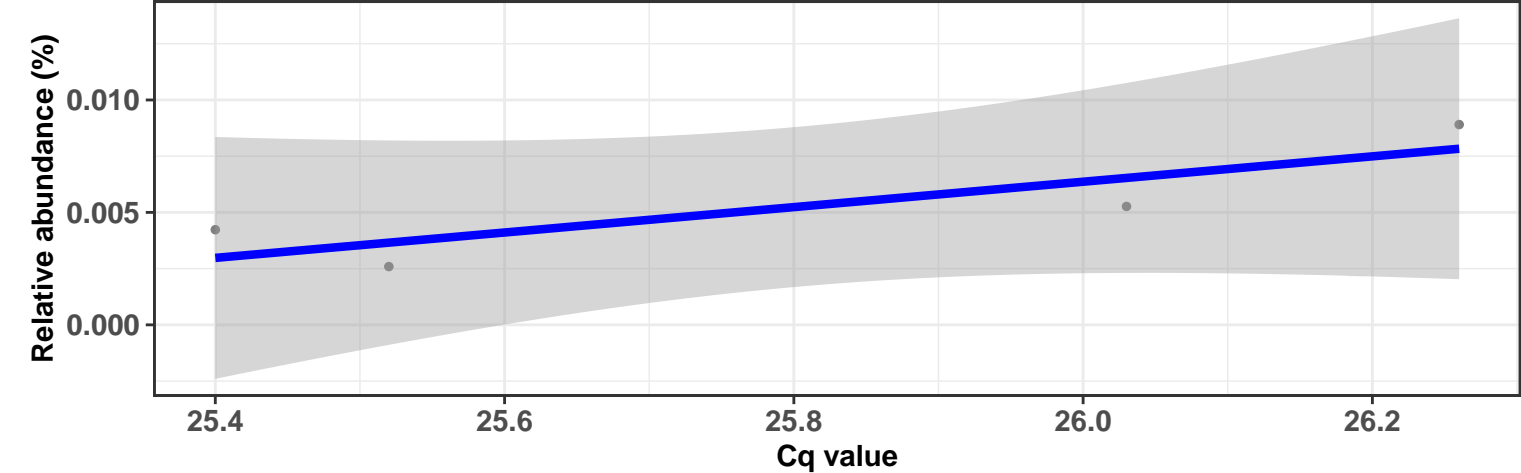
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

Correlation with all samples

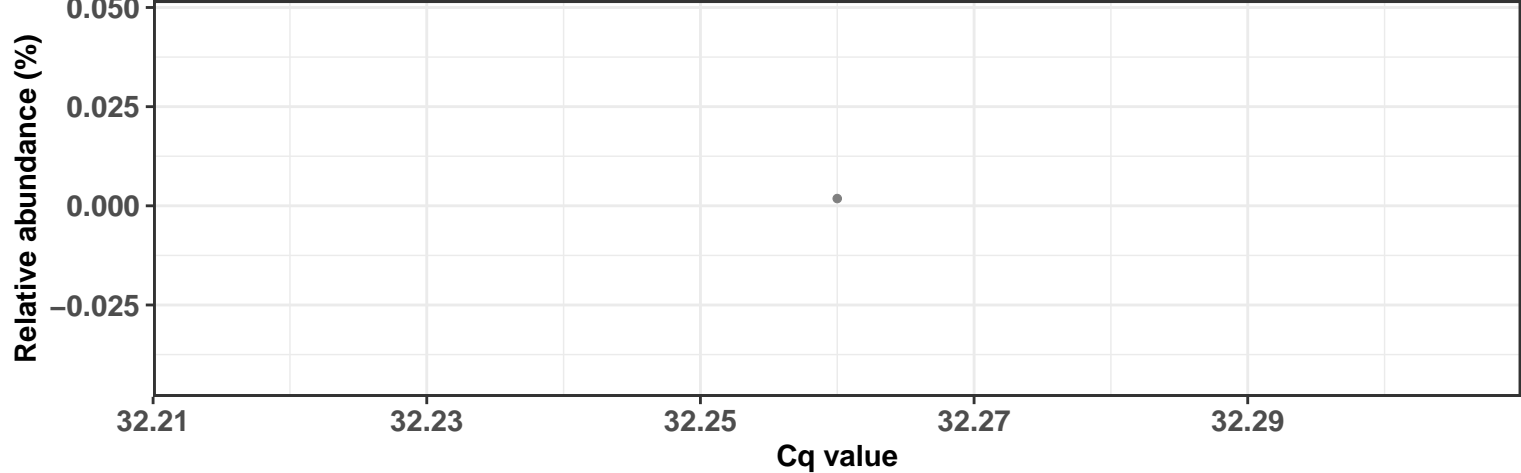
$\log_e(S) = 8.807$, $p = 0.519$, $\hat{\rho}_{\text{Spearman}} = -0.116$, $\text{CI}_{95\%} [-0.471, 0.250]$, $n_{\text{pairs}} = 33$



Correlation within: REF-DID

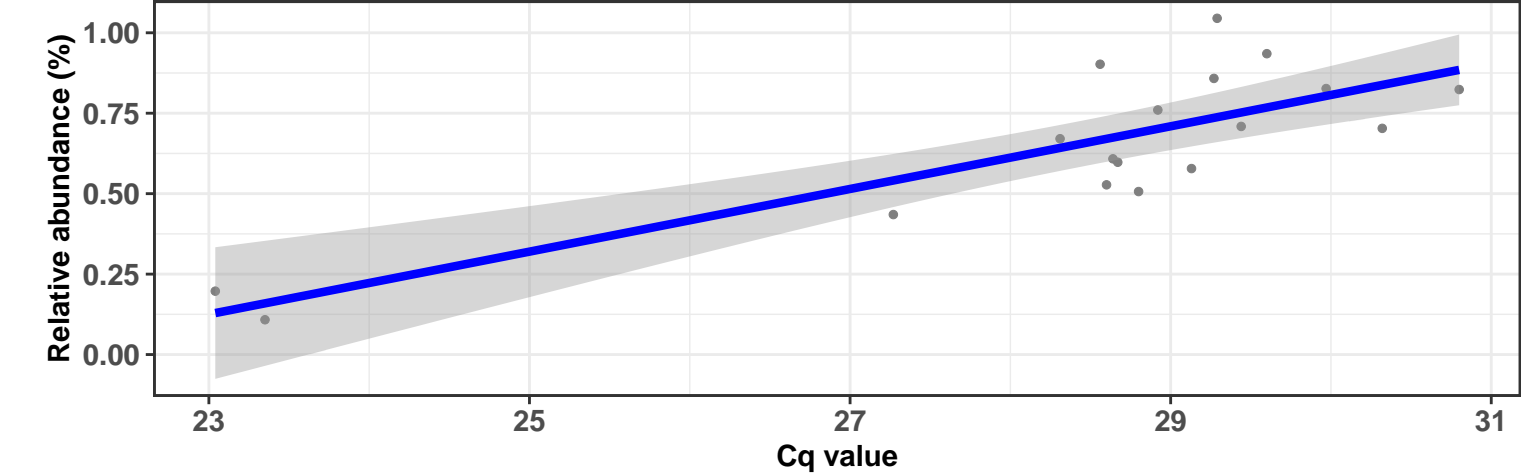


Correlation within: REF-DIM



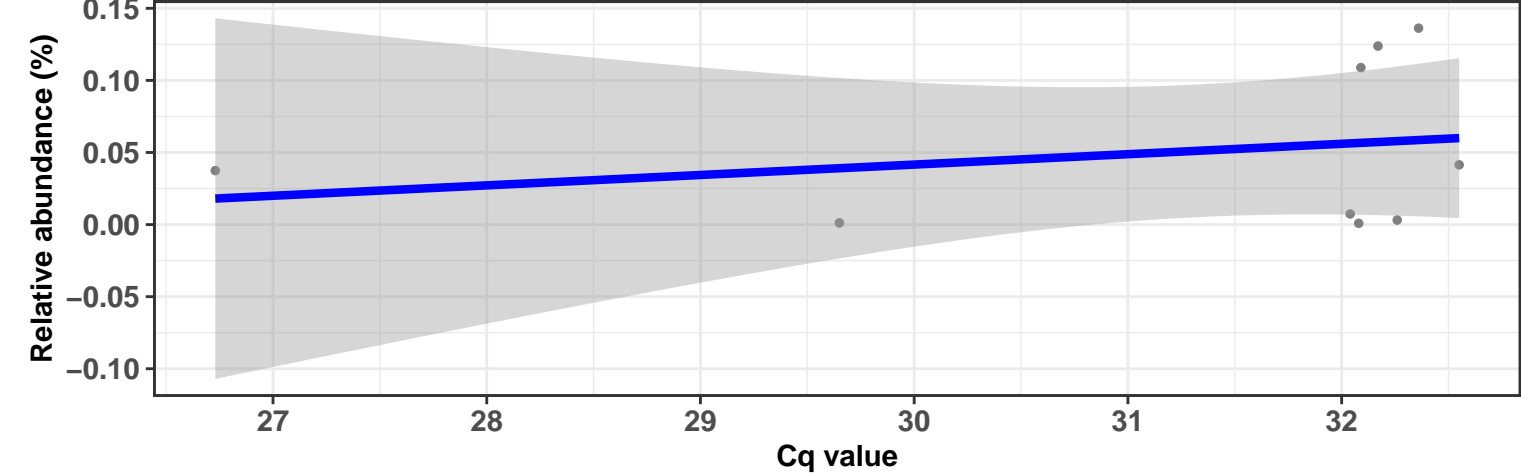
Correlation within: IM-DID

$\log_e(S) = 5.799$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.659$, $\text{CI}_{95\%} [0.388, 1.014]$, $n_{\text{pairs}} = 18$



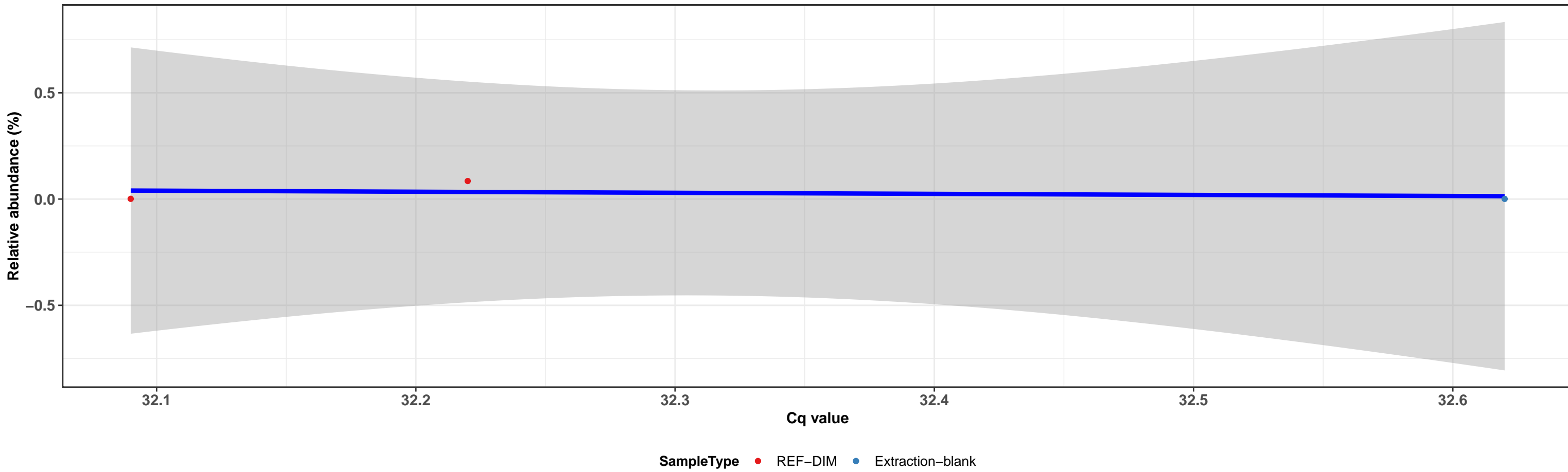
Correlation within: IM-DIM

$\log_e(S) = 4.094$, $p = 0.170$, $\hat{\rho}_{\text{Spearman}} = 0.500$, $\text{CI}_{95\%} [0.033, 0.967]$, $n_{\text{pairs}} = 9$

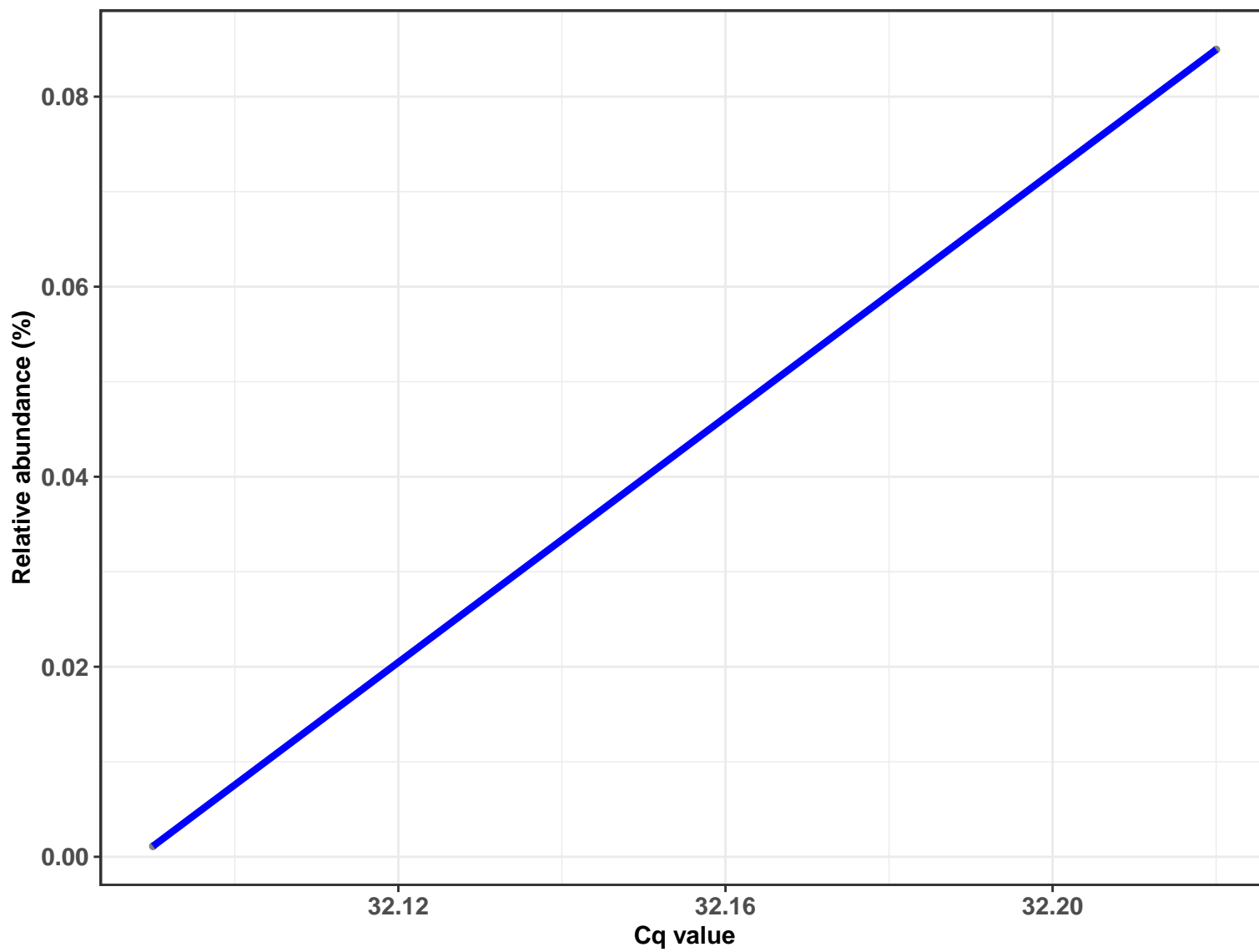


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

Correlation with all samples



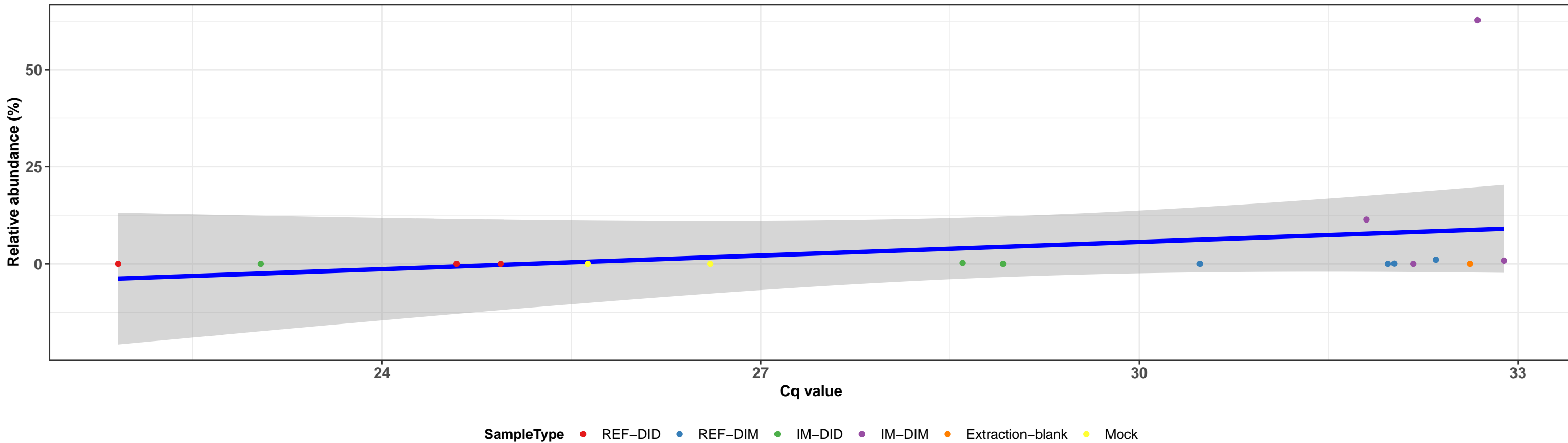
Correlation within: REF-DIM



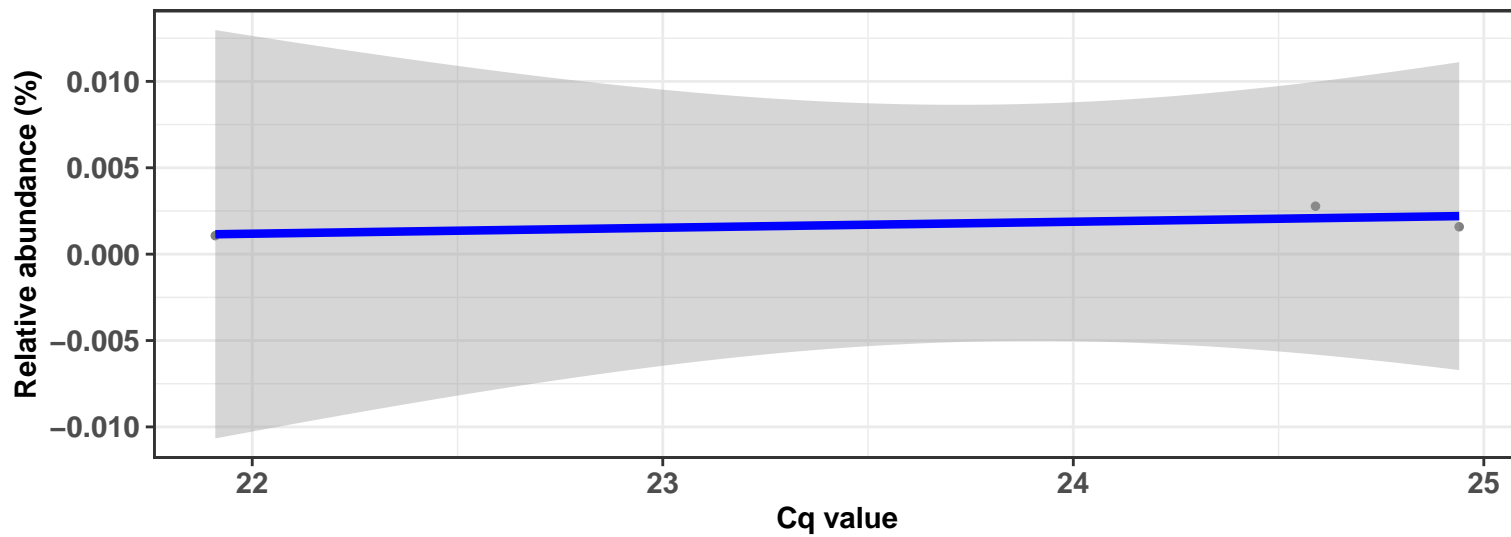
k__Bacteria; p__Tenericutes; c__Mollicutes; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma; s__uncultured Mycoplasma sp.

Correlation with all samples

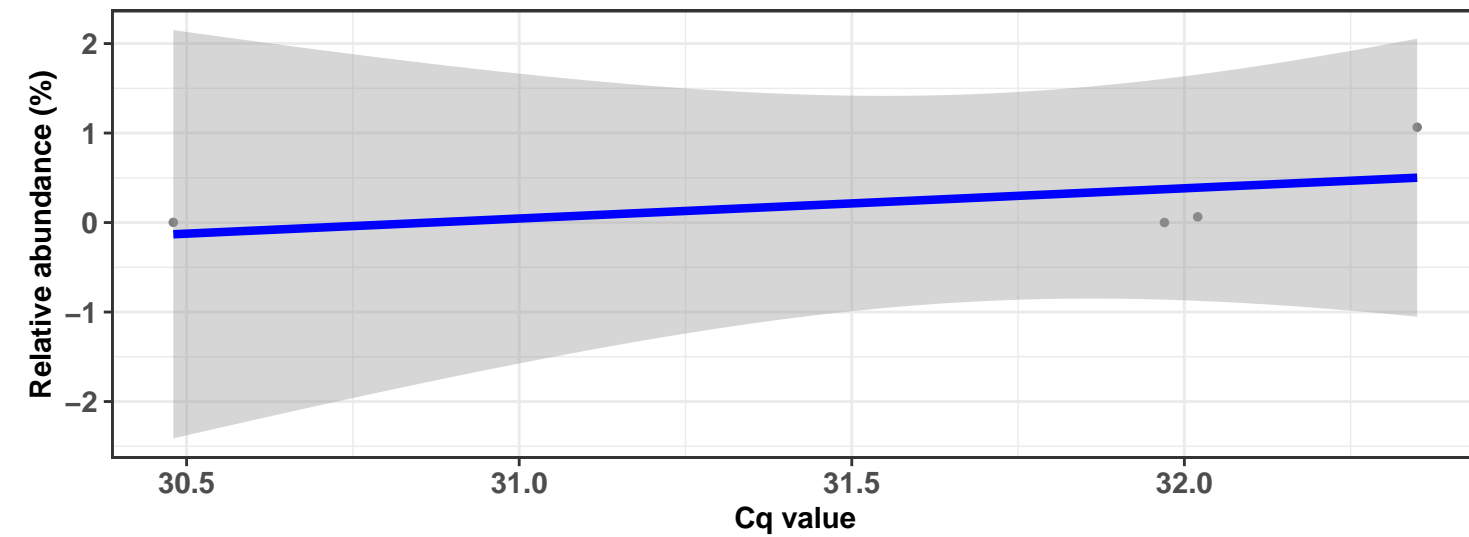
$\log_e(S) = 6.306$, $p = 0.198$, $\hat{\rho}_{\text{Spearman}} = 0.328$, $CI_{95\%} [-0.186, 0.841]$, $n_{\text{pairs}} = 17$



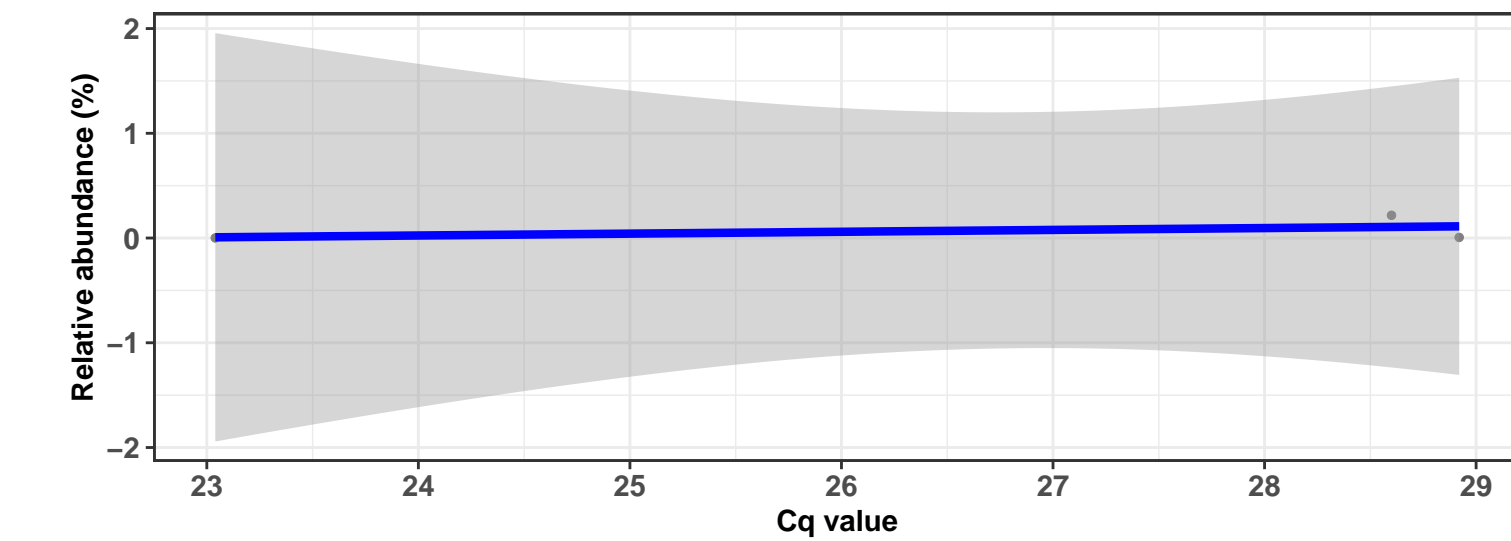
Correlation within: REF-DID



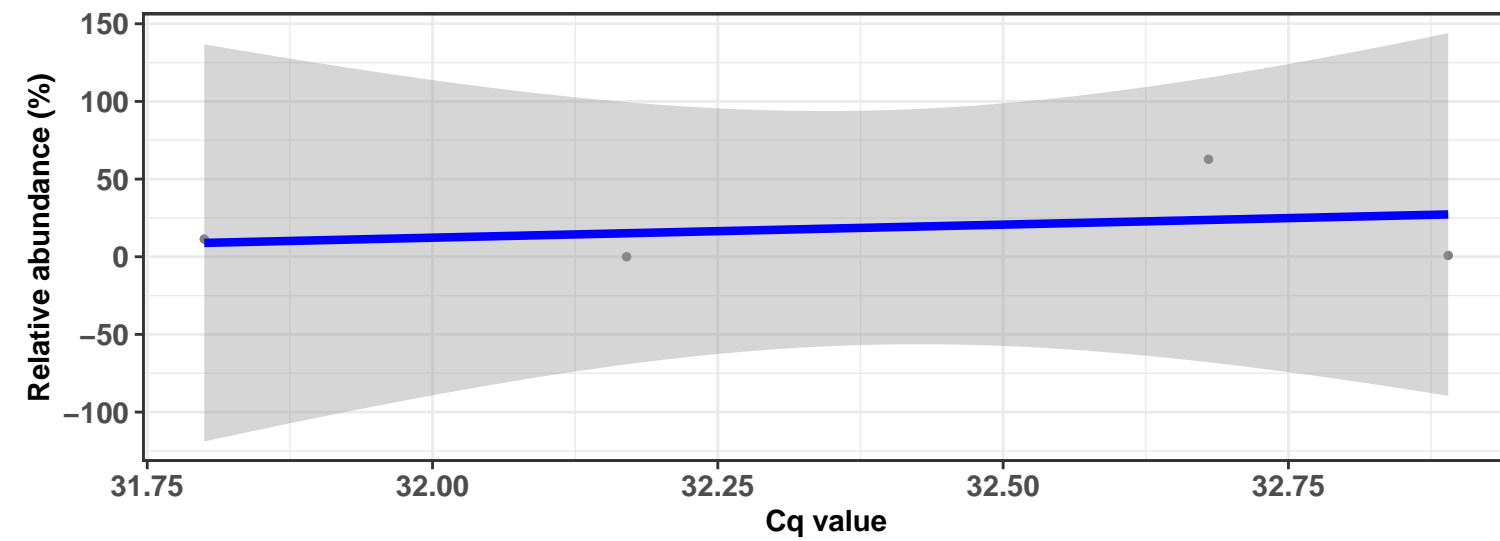
Correlation within: REF-DIM



Correlation within: IM-DID



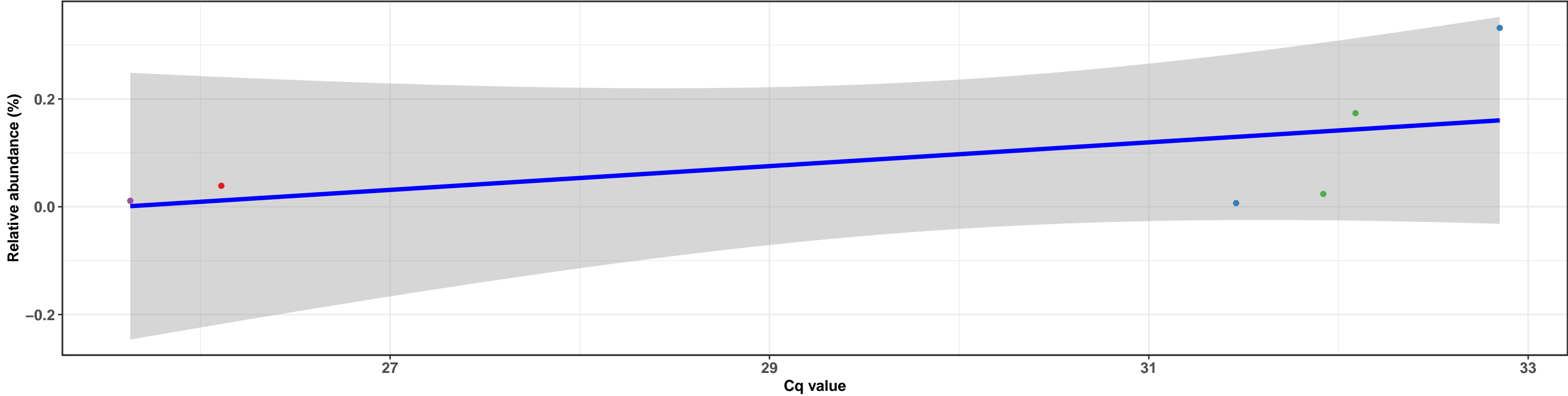
Correlation within: IM-DIM



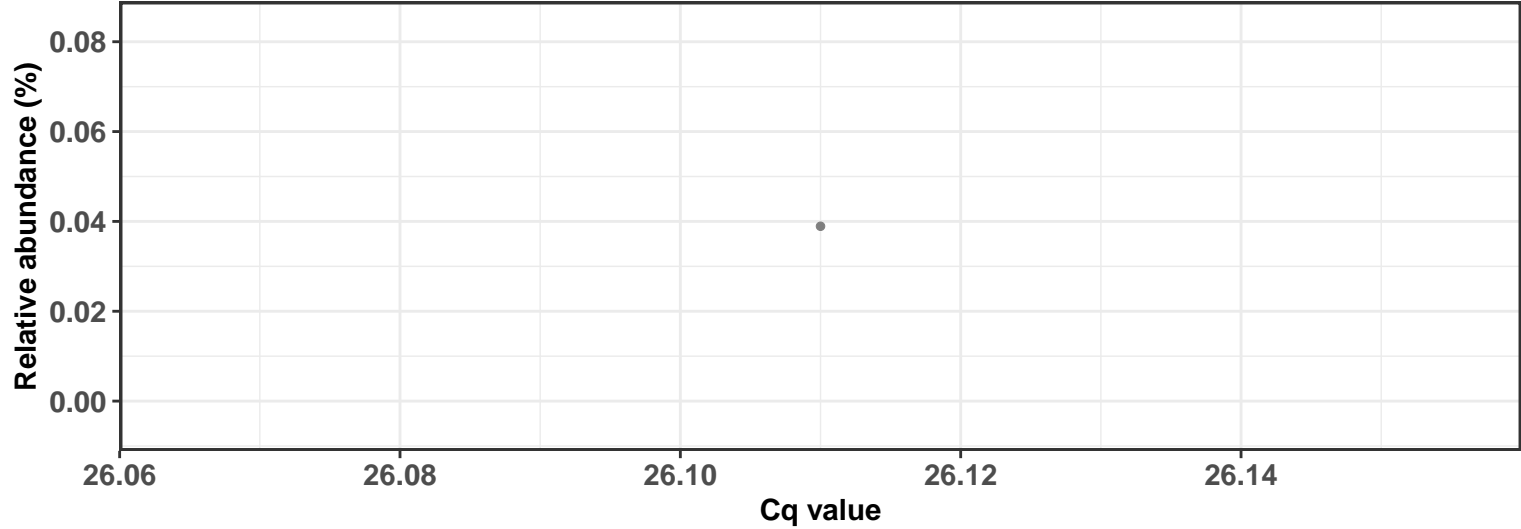
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; NA

Correlation with all samples

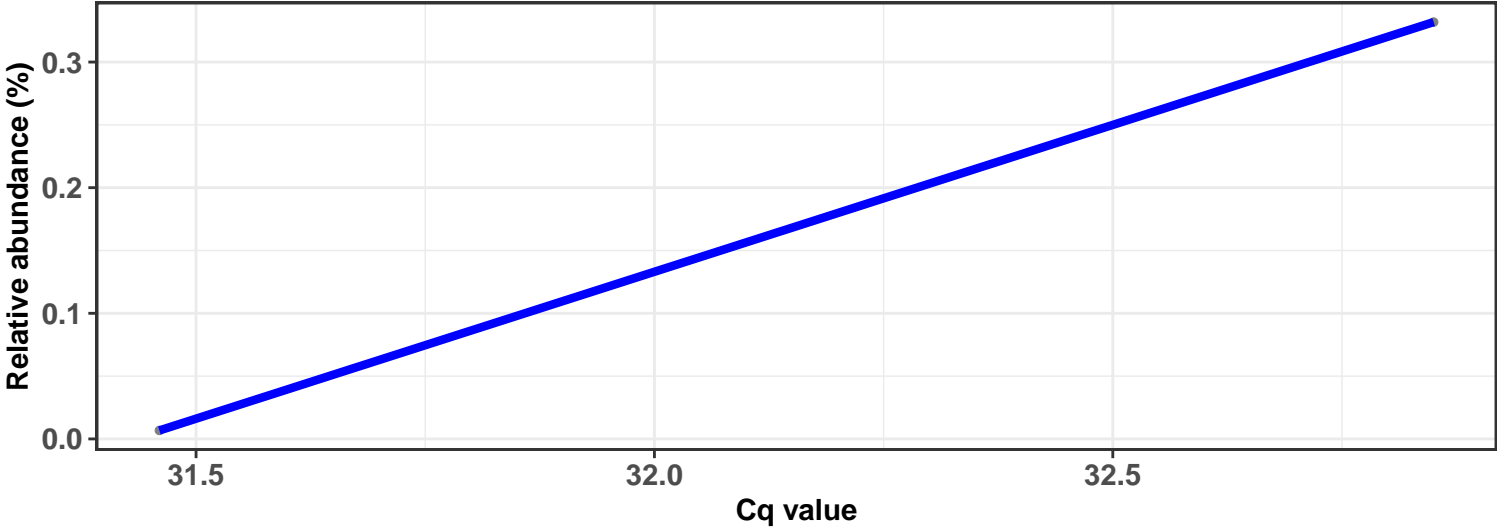
$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $\text{CI}_{95\%} [0.076, 1.423]$, $n_{\text{pairs}} = 6$



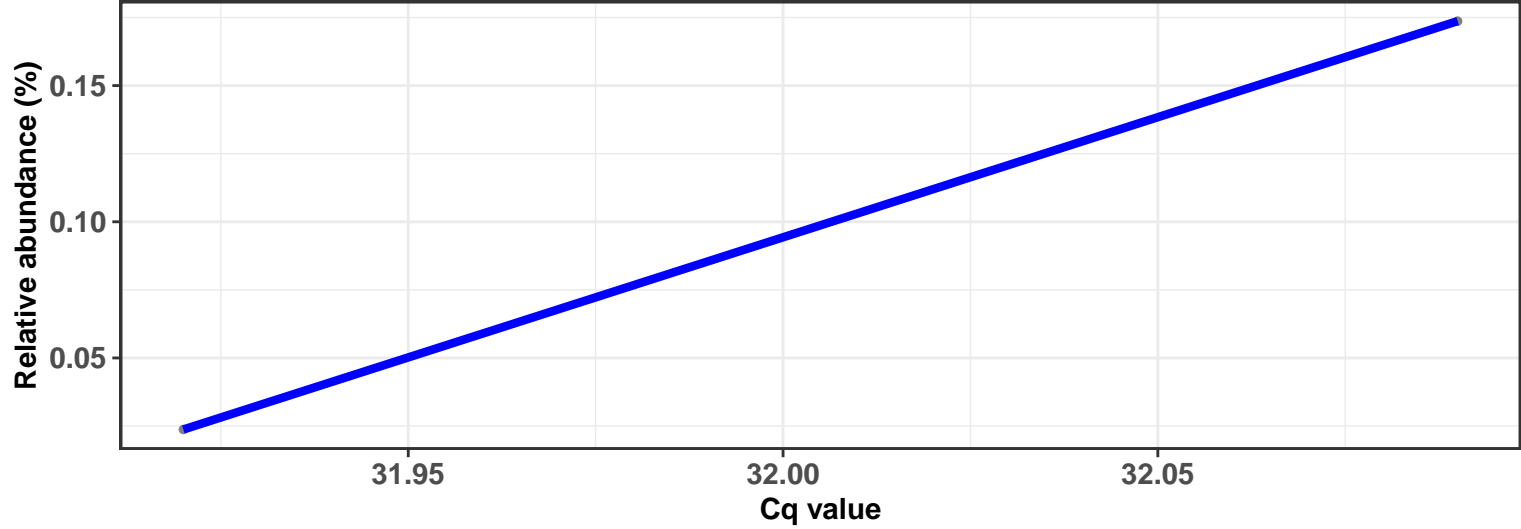
Correlation within: REF-DID



Correlation within: REF-DIM

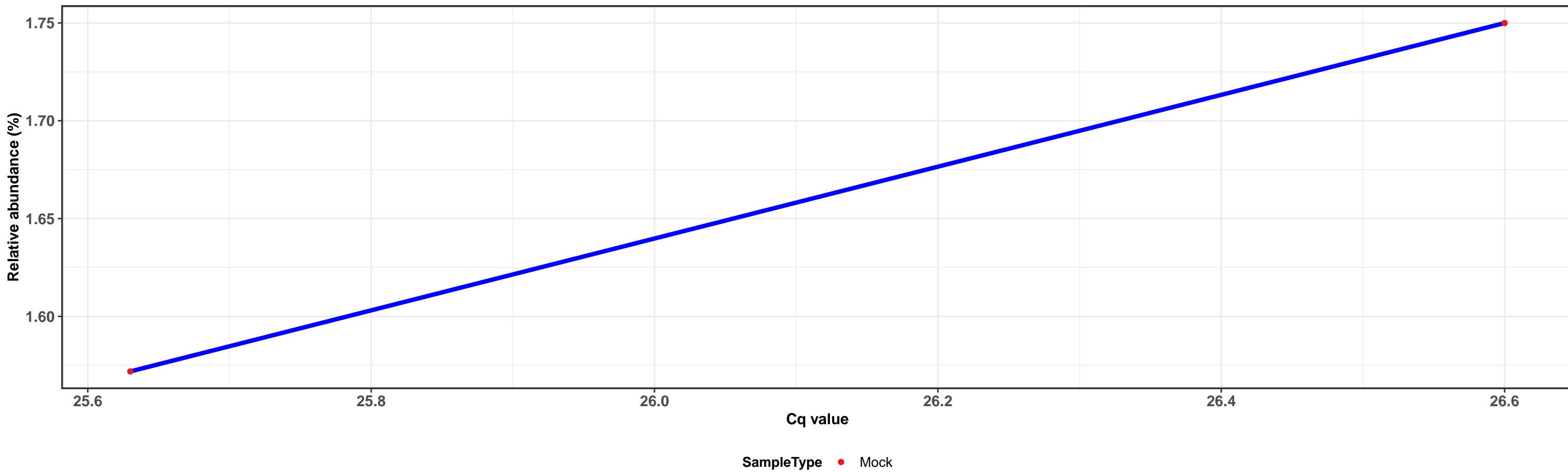


Correlation within: IM-DIM

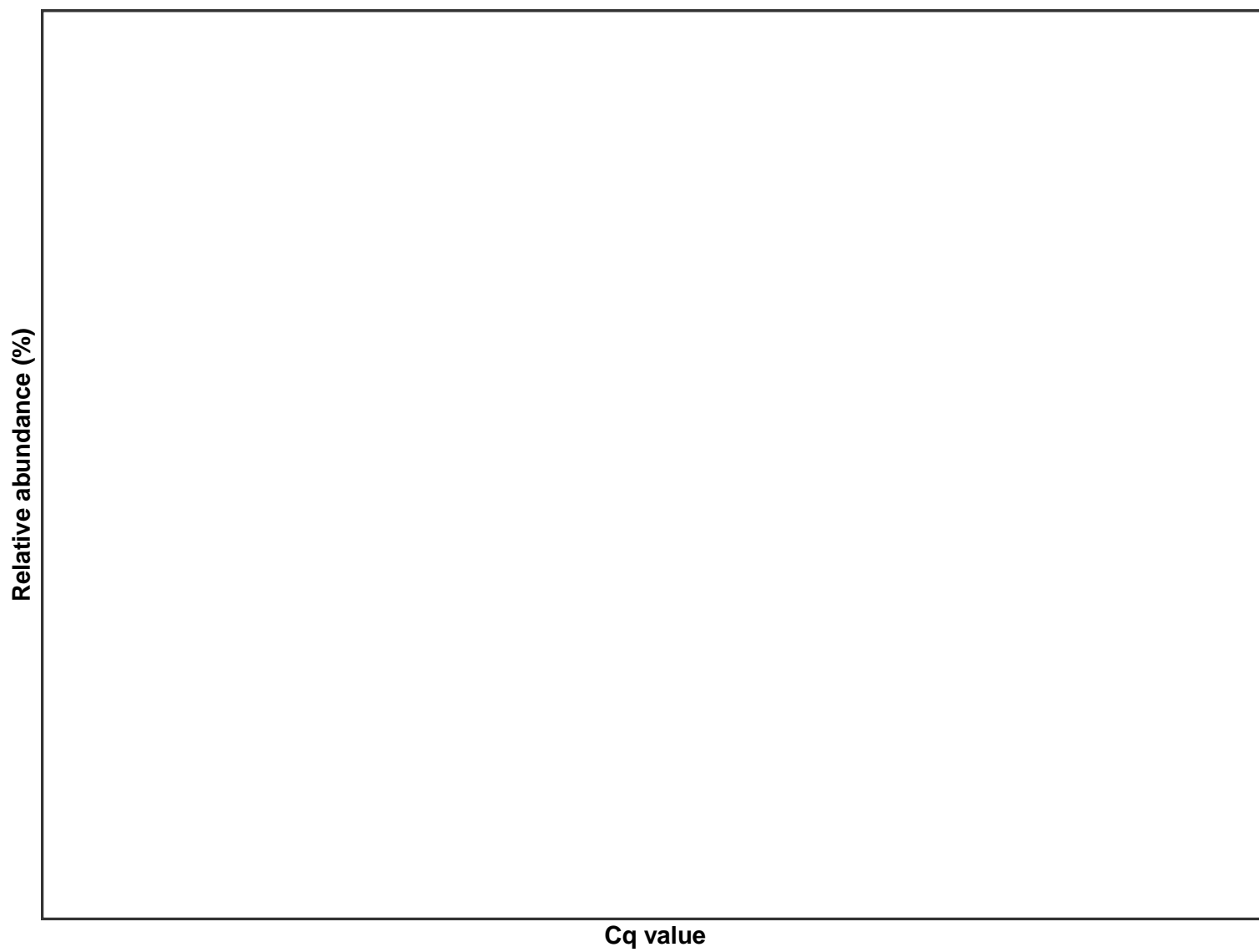


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus

Correlation with all samples



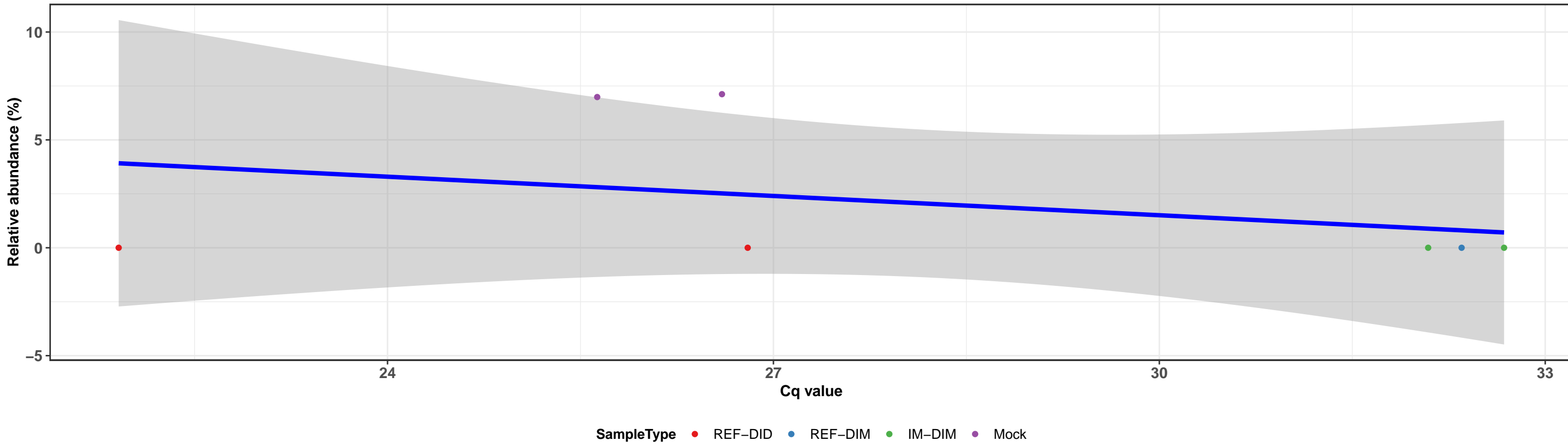
Correlation within:



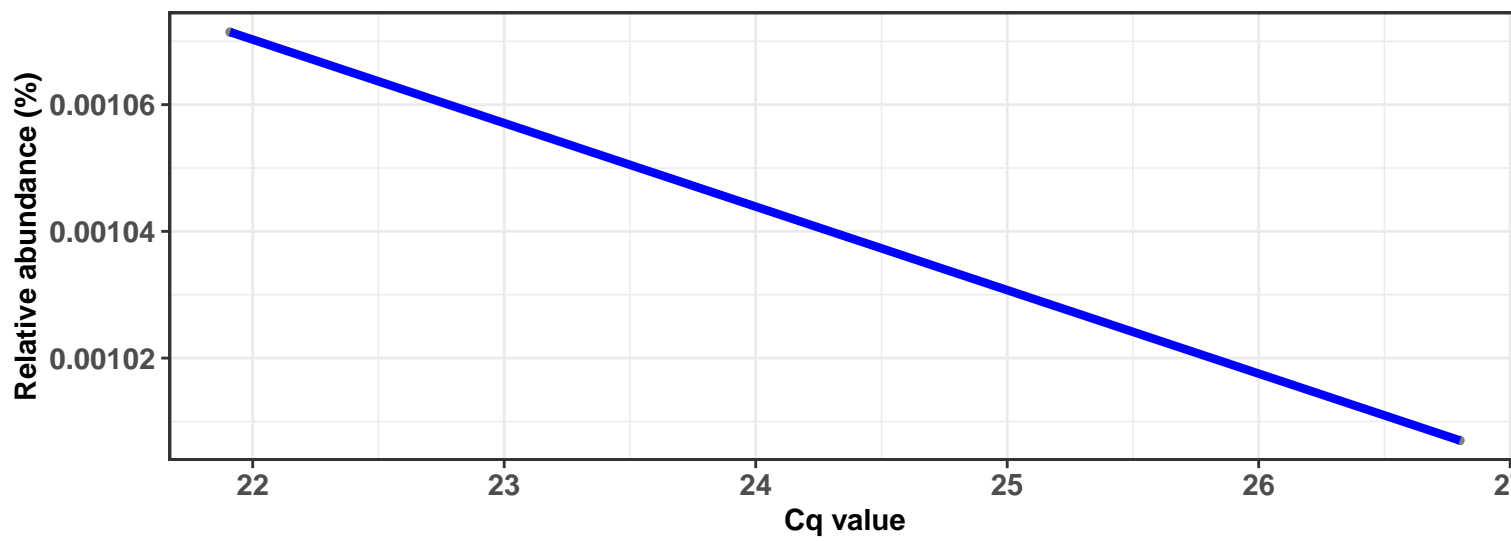
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia-Shigella; NA

Correlation with all samples

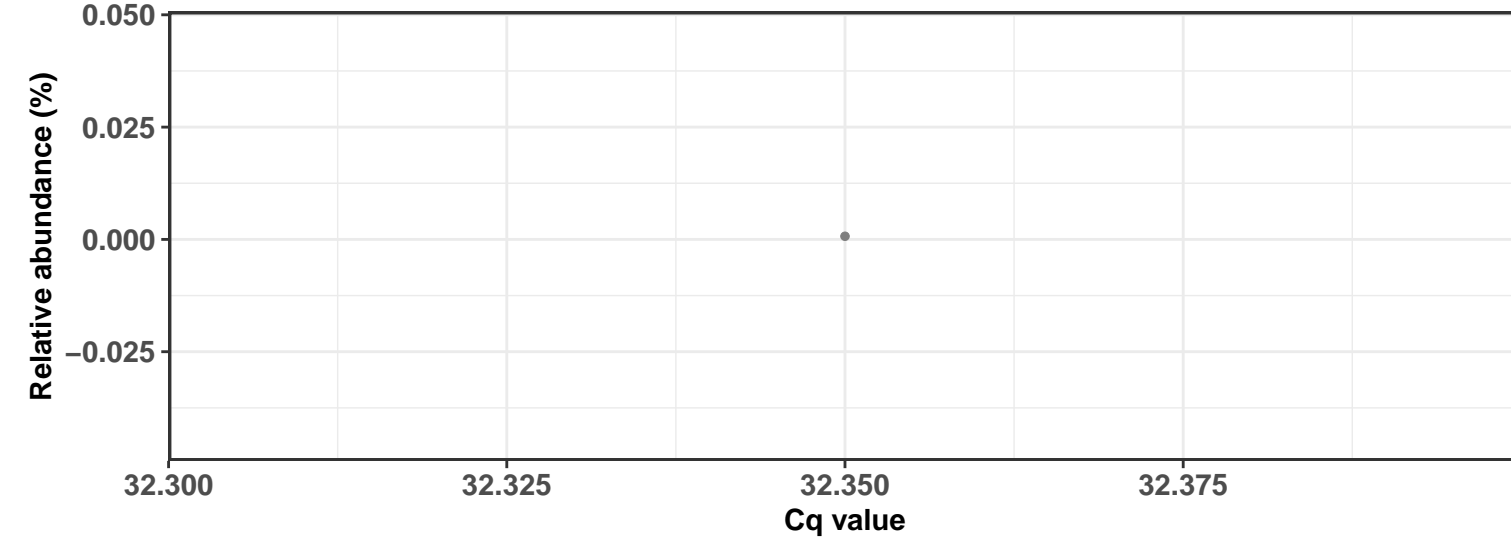
$\log_e(S) = 4.585$, $p = 0.052$, $\hat{\rho}_{\text{Spearman}} = -0.750$, $CI_{95\%} [-1.234, -0.404]$, $n_{\text{pairs}} = 7$



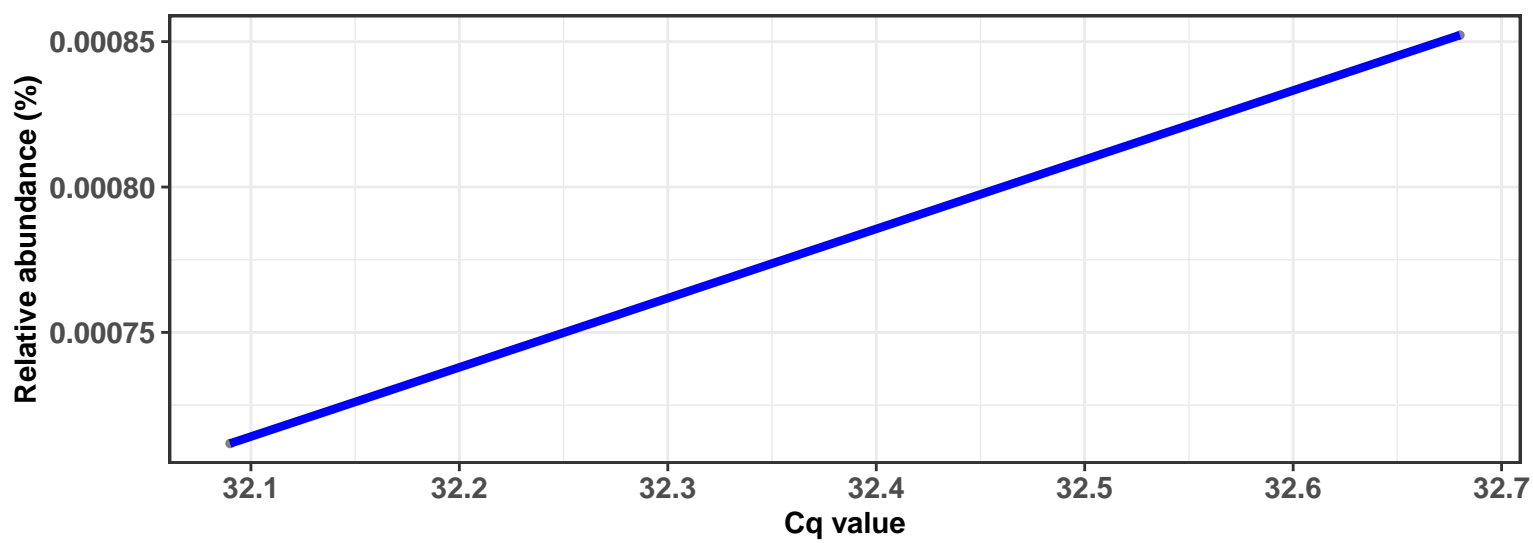
Correlation within: REF-DID



Correlation within: REF-DIM



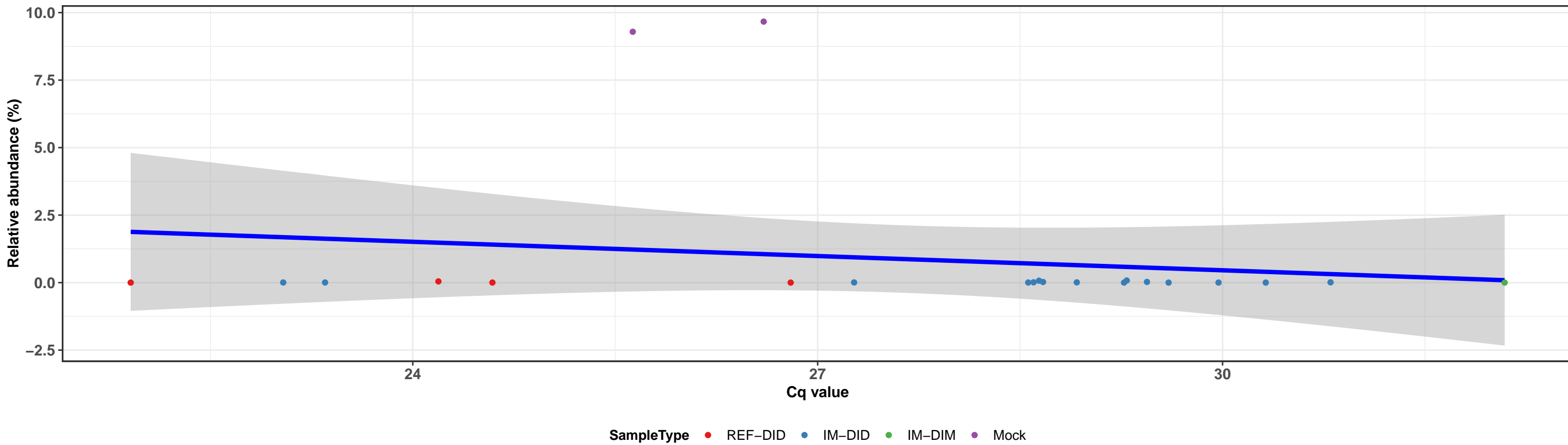
Correlation within: IM-DIM



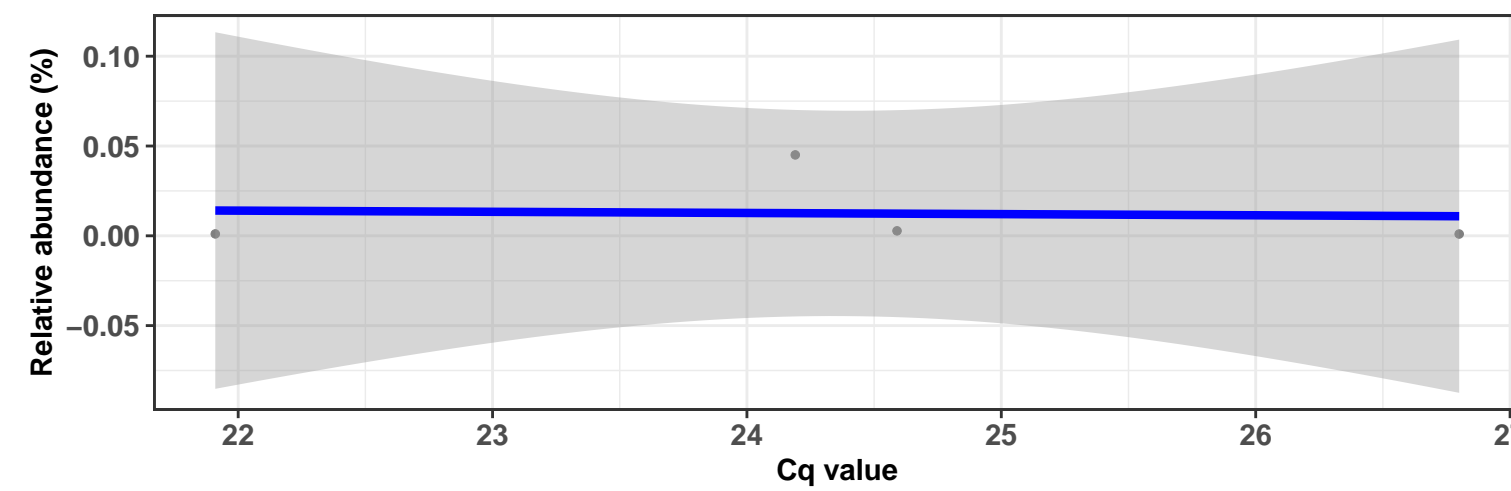
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia-Shigella; NA

Correlation with all samples

$\log_e(S) = 7.672$, $p = 0.342$, $\hat{\rho}_{\text{Spearman}} = -0.213$, $\text{CI}_{95\%} [-0.642, 0.235]$, $n_{\text{pairs}} = 22$

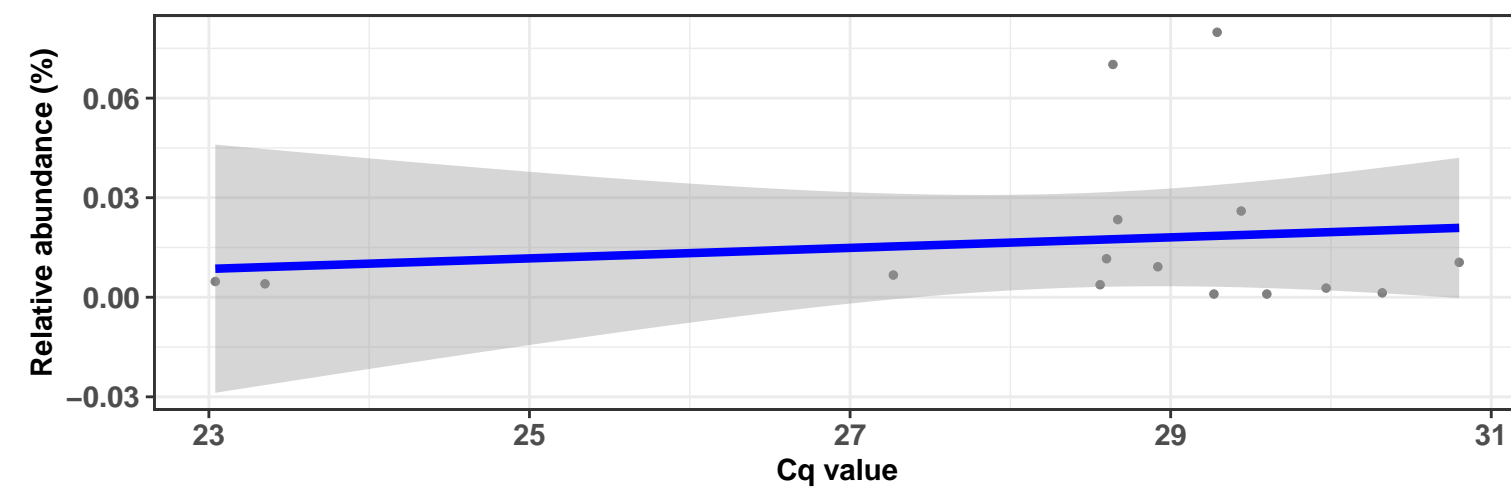


Correlation within: REF-DID

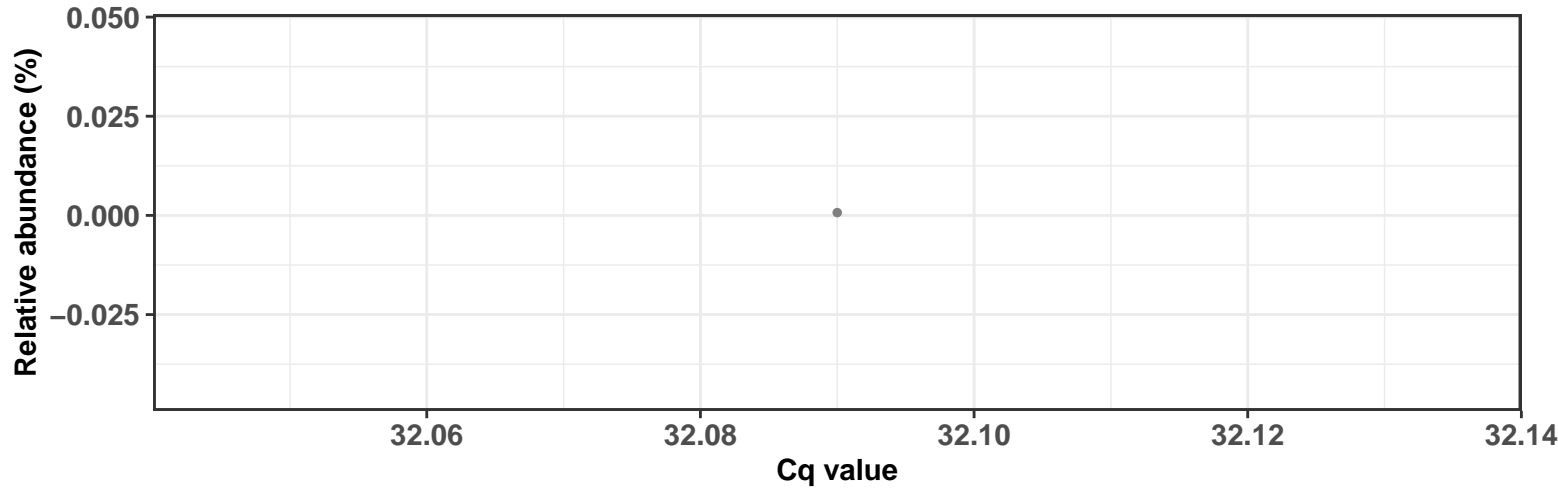


Correlation within: IM-DID

$\log_e(S) = 6.446$, $p = 0.657$, $\hat{\rho}_{\text{Spearman}} = -0.125$, $\text{CI}_{95\%} [-0.602, 0.414]$, $n_{\text{pairs}} = 15$



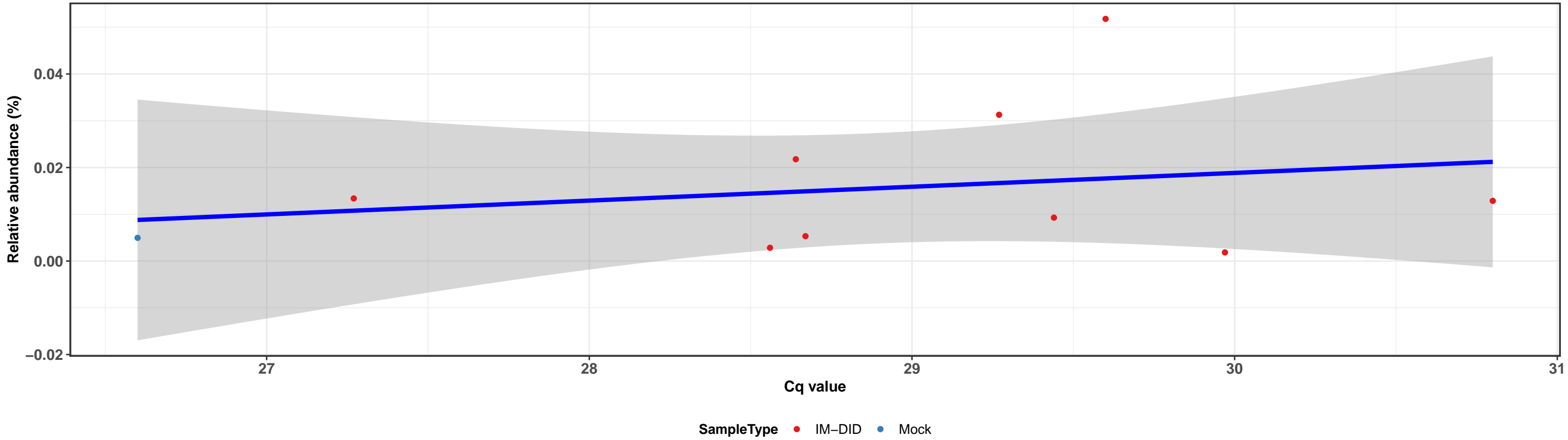
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia-Shigella; NA

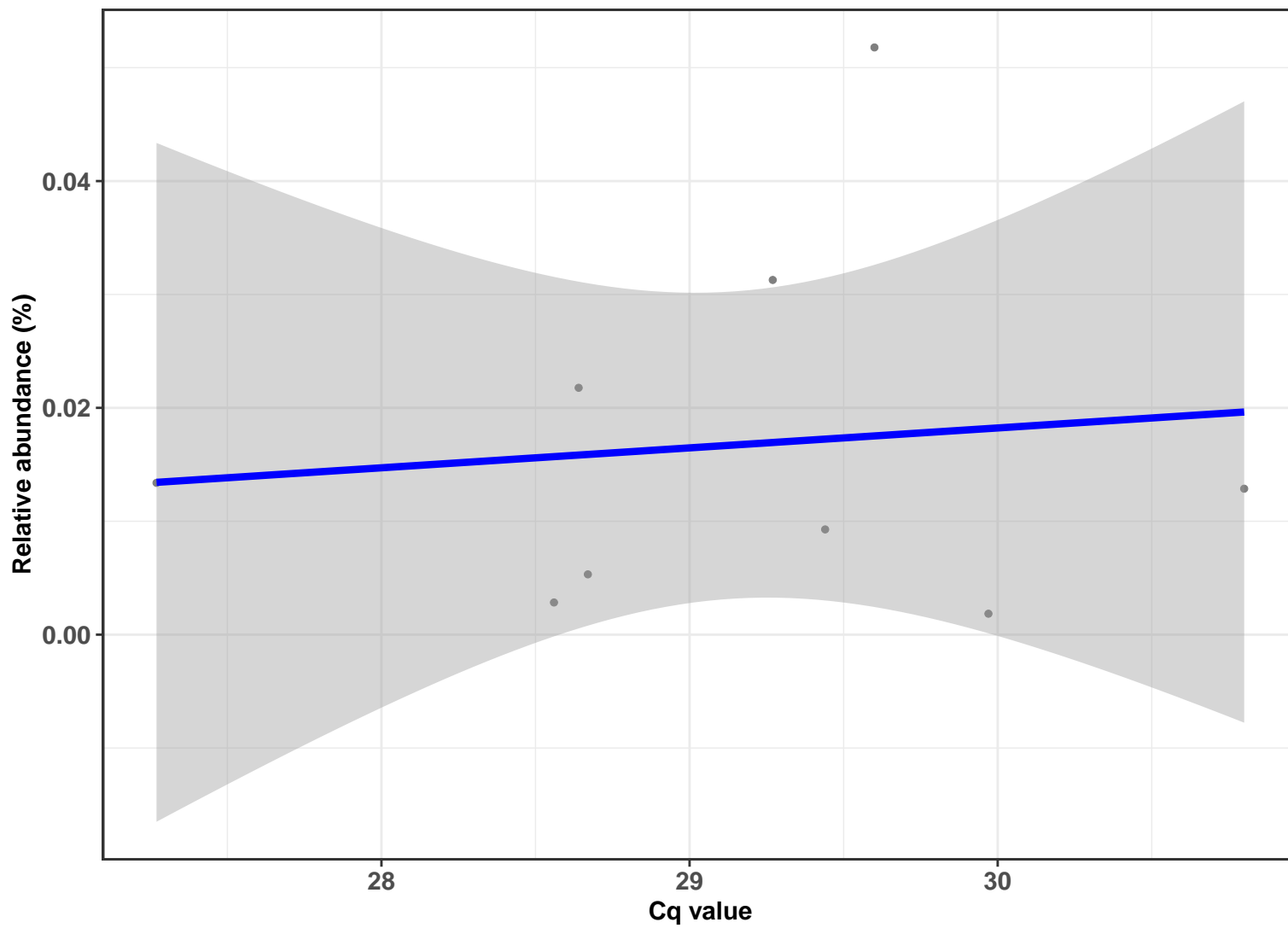
Correlation with all samples

$\log_e(S) = 4.970$, $p = 0.726$, $\hat{\rho}_{\text{Spearman}} = 0.127$, $\text{CI}_{95\%} [-0.589, 0.703]$, $n_{\text{pairs}} = 10$



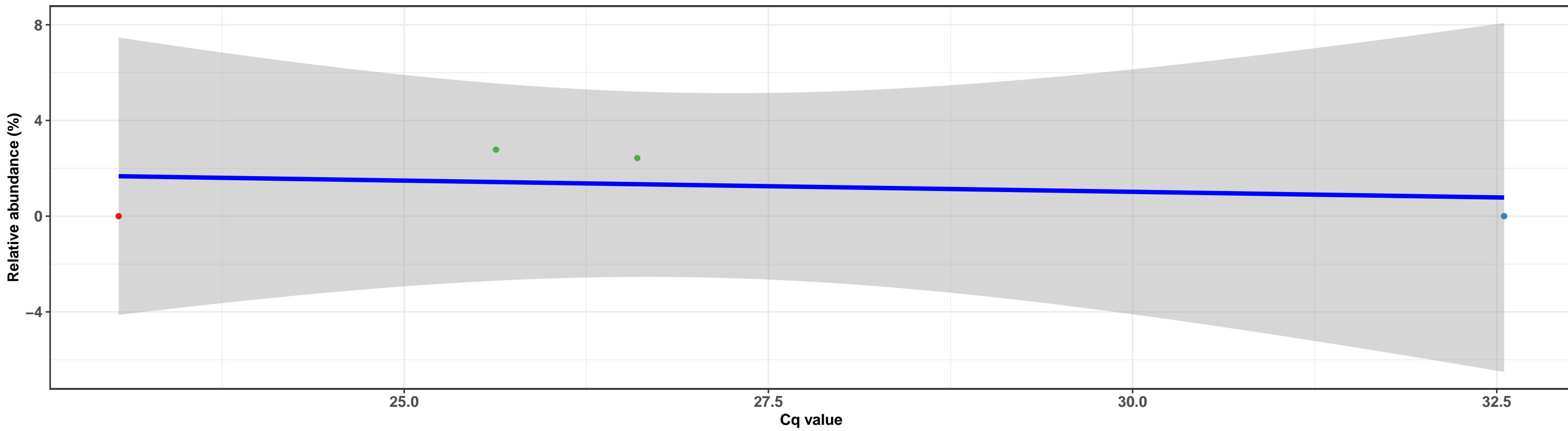
Correlation within: IM-DID

$\log_e(S) = 4.820$, $p = 0.932$, $\hat{\rho}_{\text{Spearman}} = -0.033$, $\text{CI}_{95\%} [-0.674, 0.606]$, $n_{\text{pairs}} = 9$



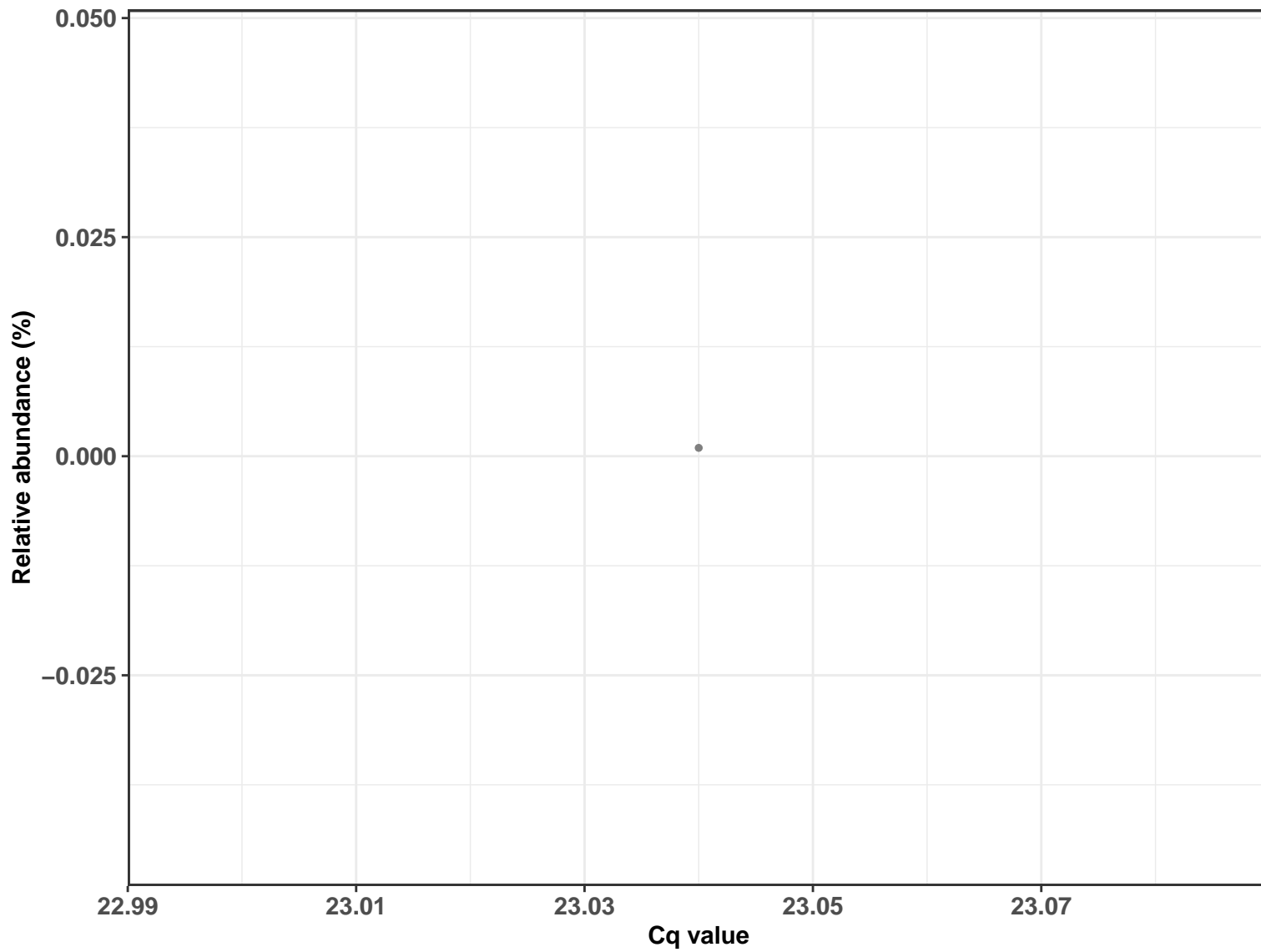
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Salmonella; NA

Correlation with all samples

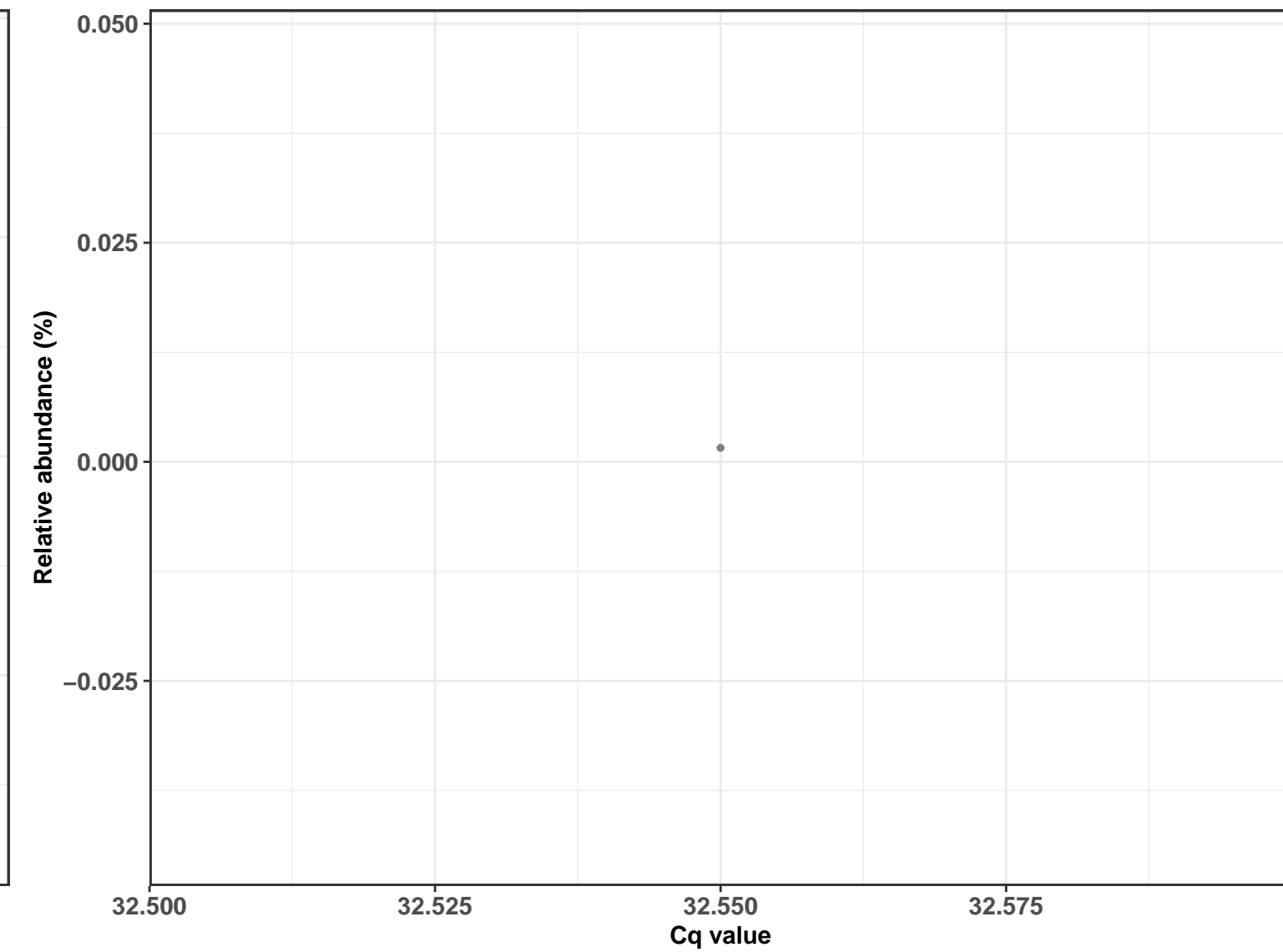


SampleType • IM-DID • IM-DIM • Mock

Correlation within: IM-DID



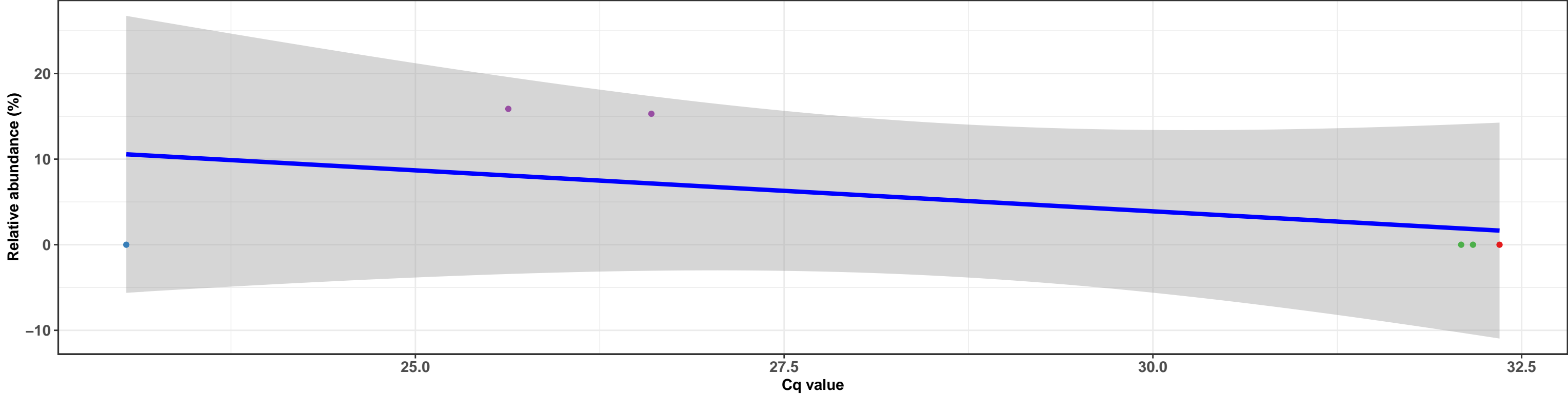
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Salmonella; NA

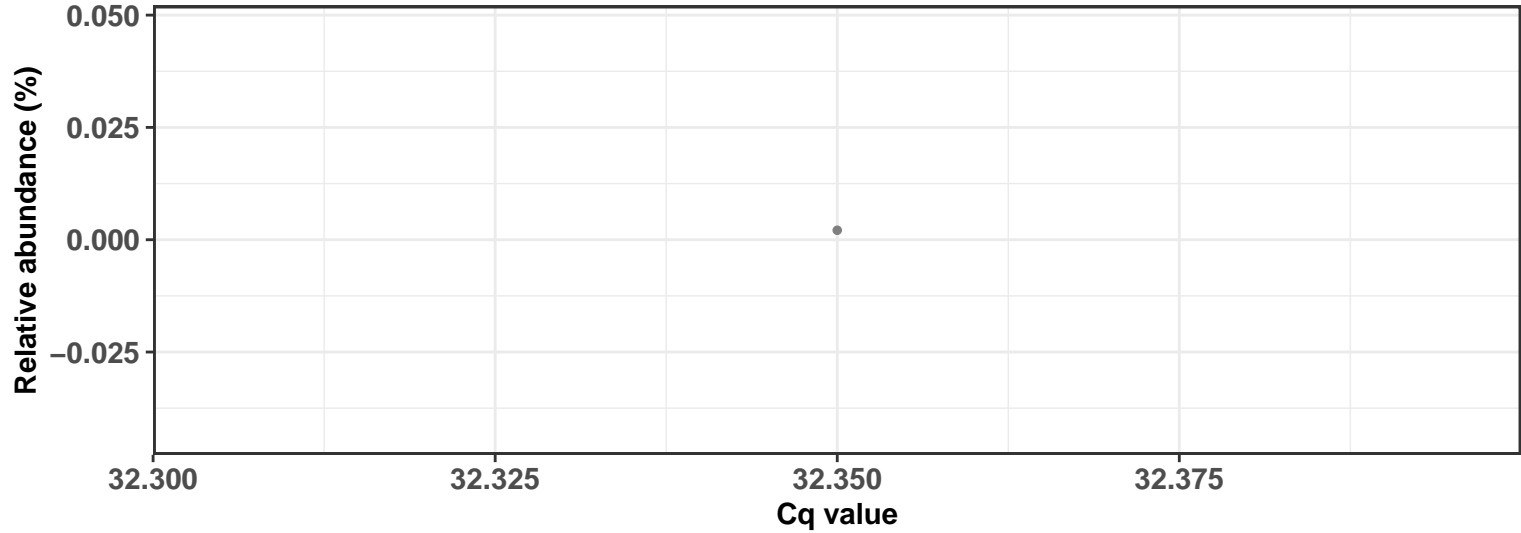
Correlation with all samples

$\log_e(S) = 3.738$, $\rho = 0.704$, $\hat{\rho}_{\text{Spearman}} = -0.200$, $\text{CI}_{95\%} [-1.113, 0.680]$, $n_{\text{pairs}} = 6$

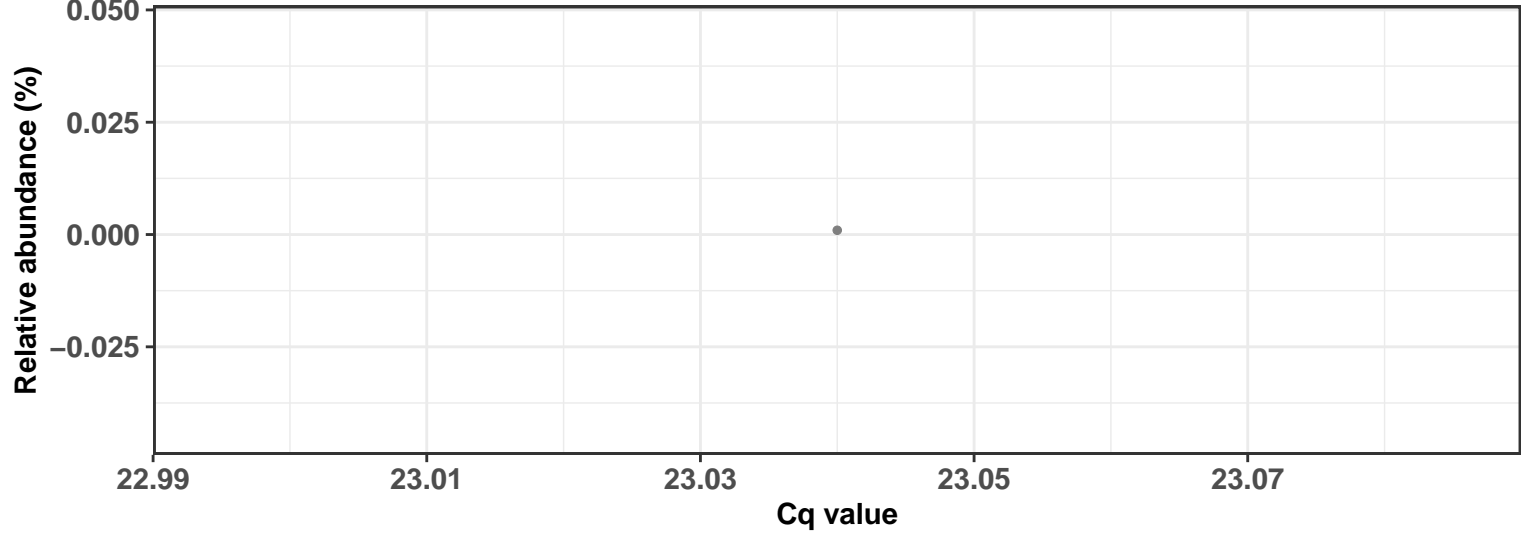


SampleType REF-DIM IM-DID IM-DIM Mock

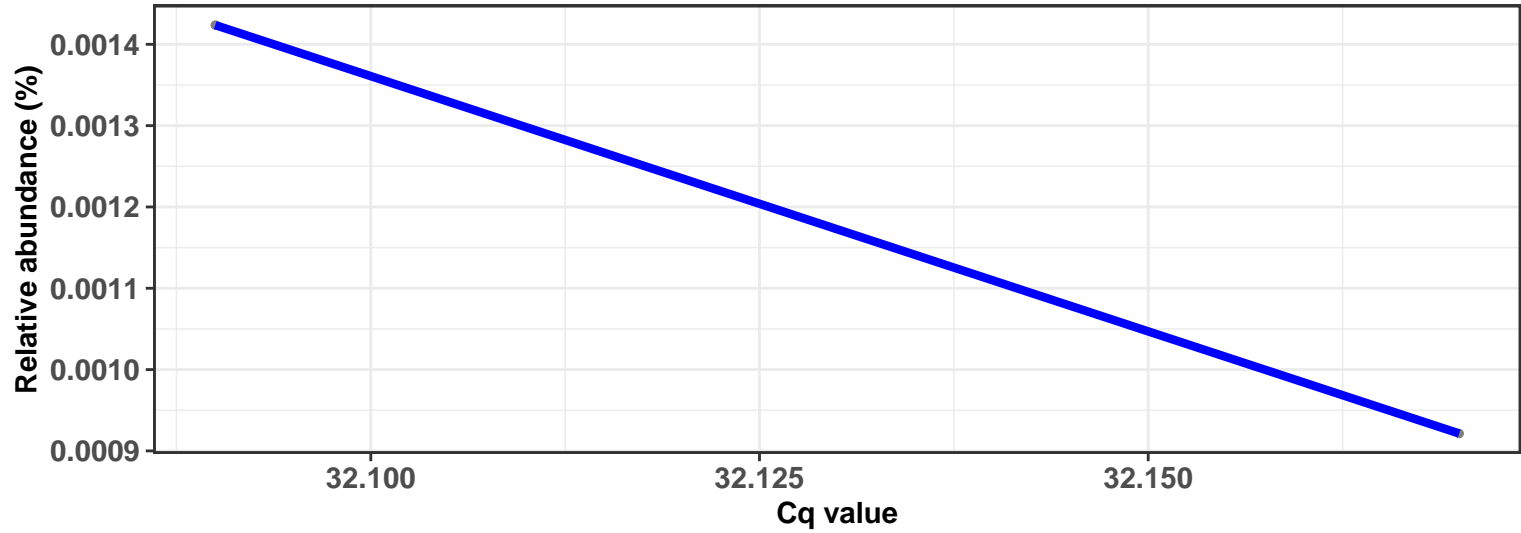
Correlation within: REF-DIM



Correlation within: IM-DID



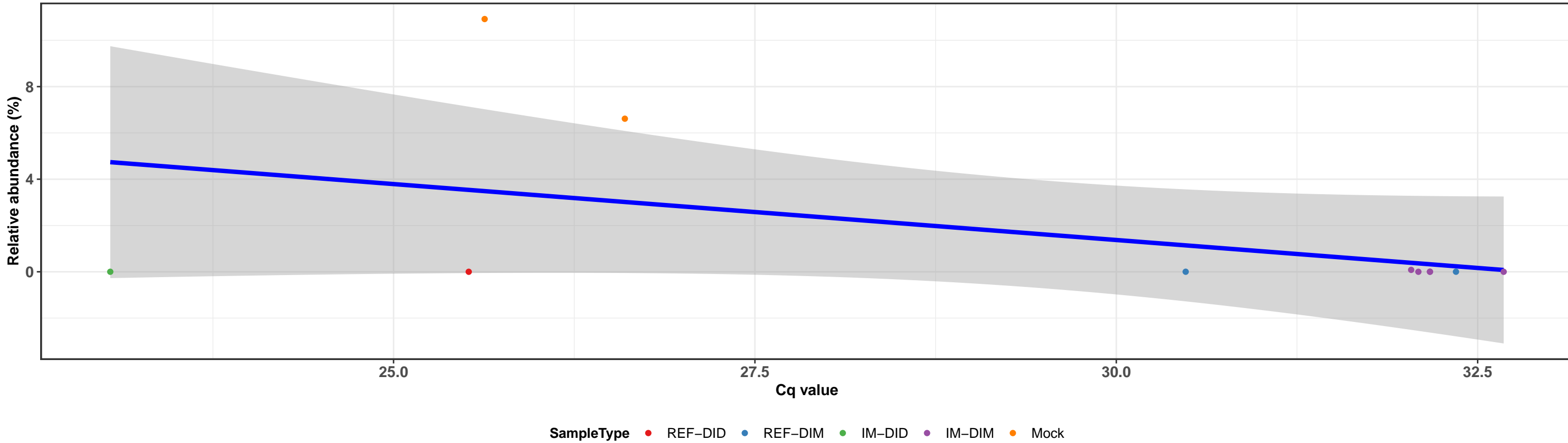
Correlation within: IM-DIM



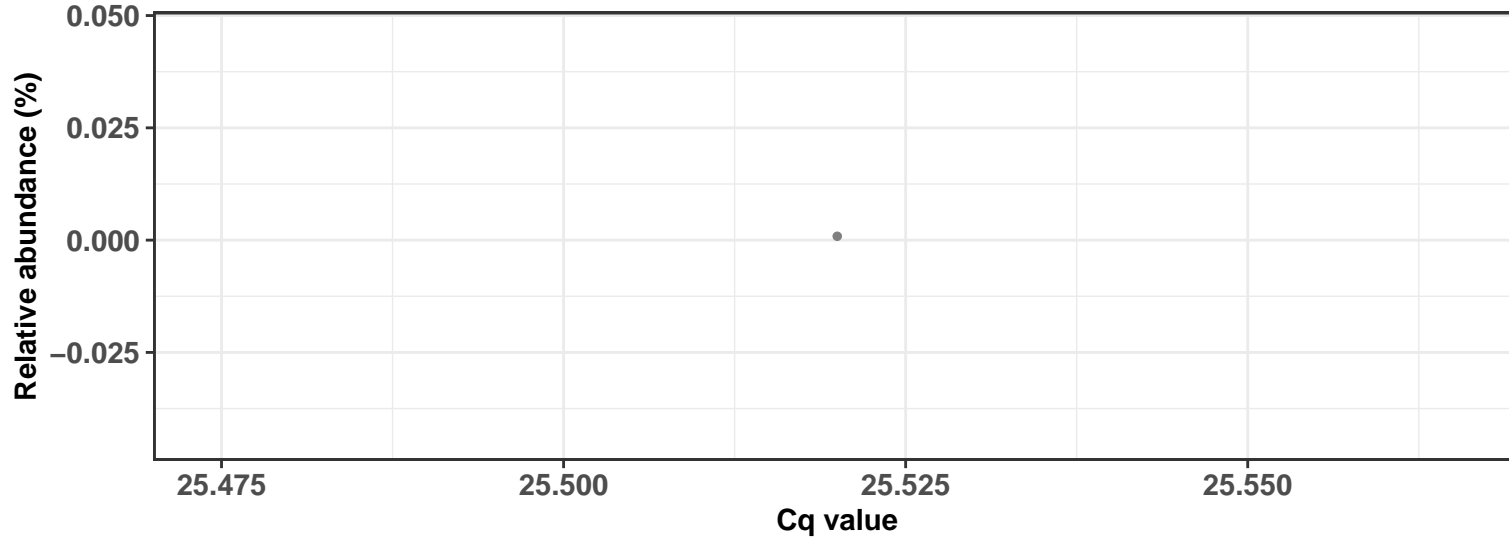
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

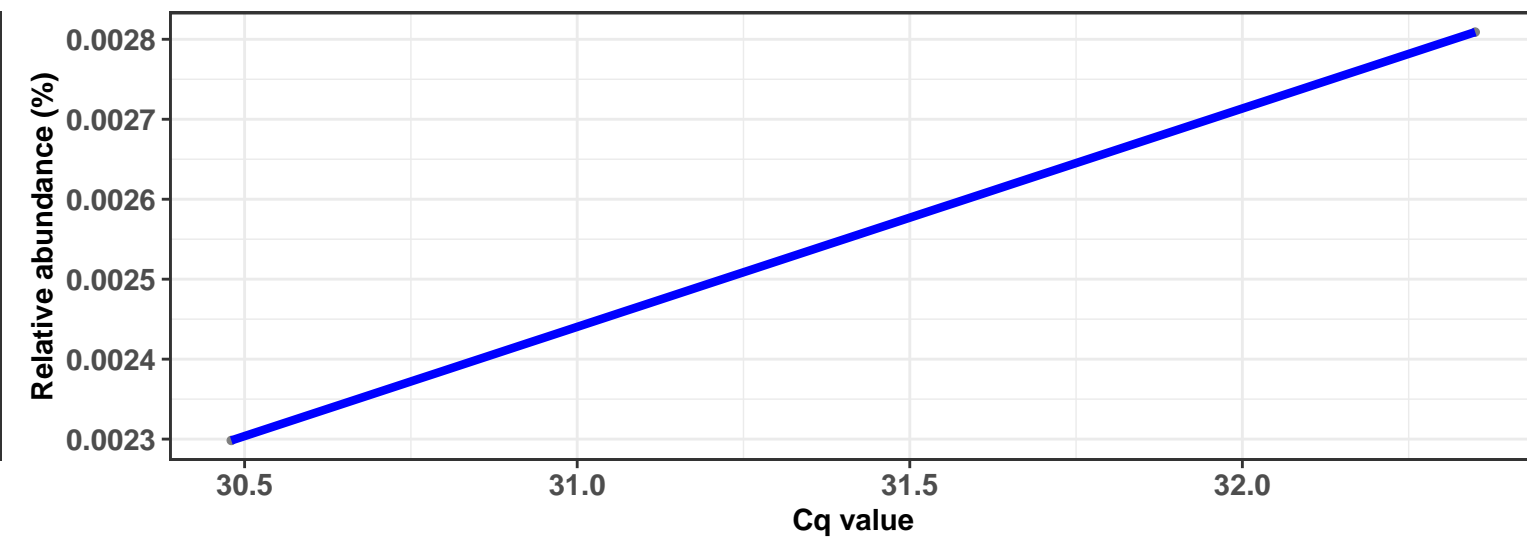
$\log_e(S) = 5.642$, $p = 0.400$, $\hat{\rho}_{\text{Spearman}} = -0.282$, $\text{CI}_{95\%} [-0.819, 0.277]$, $n_{\text{pairs}} = 11$



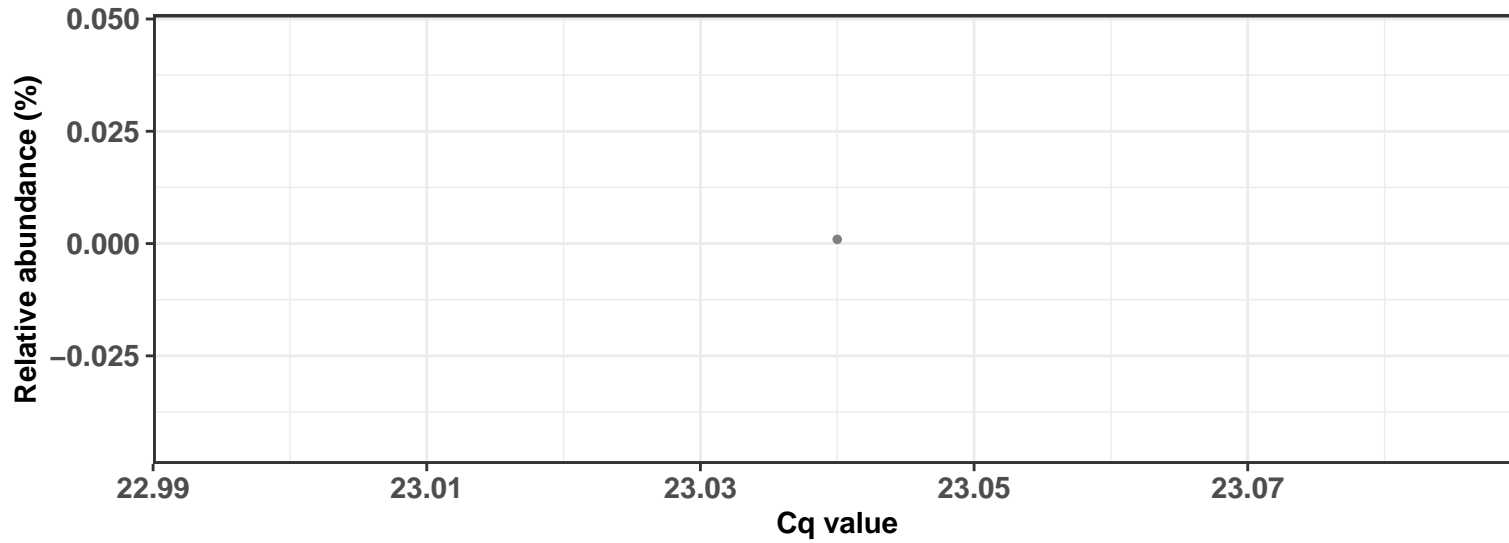
Correlation within: REF-DID



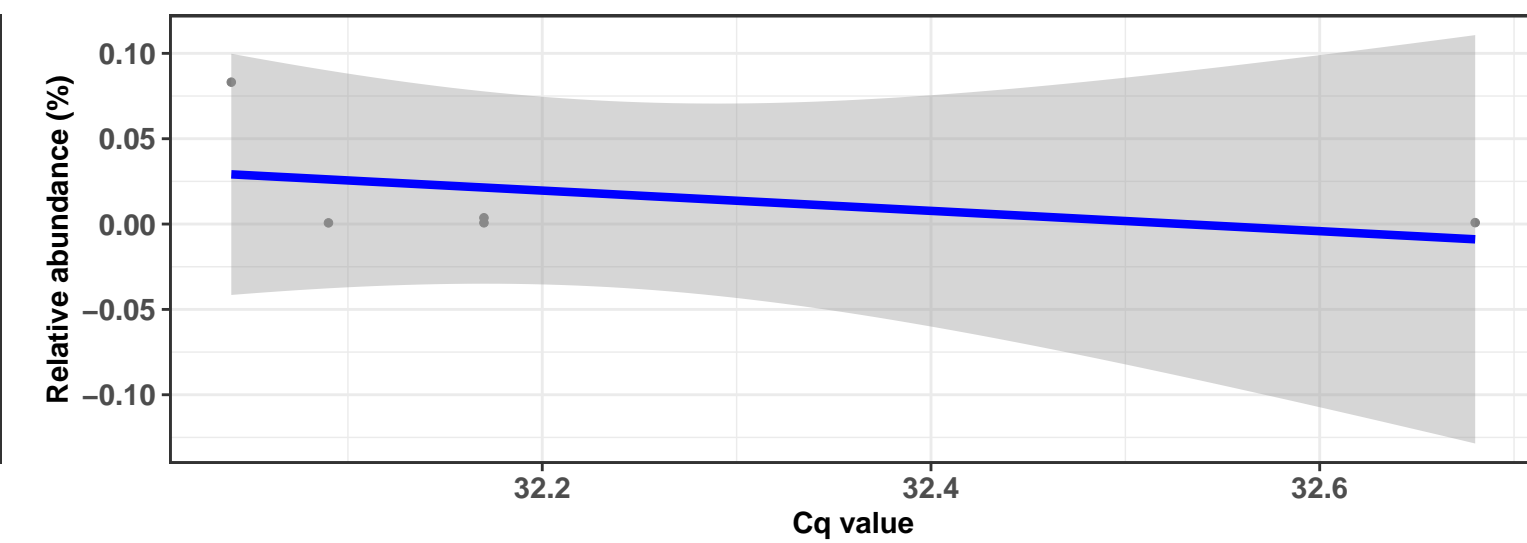
Correlation within: REF-DIM



Correlation within: IM-DID



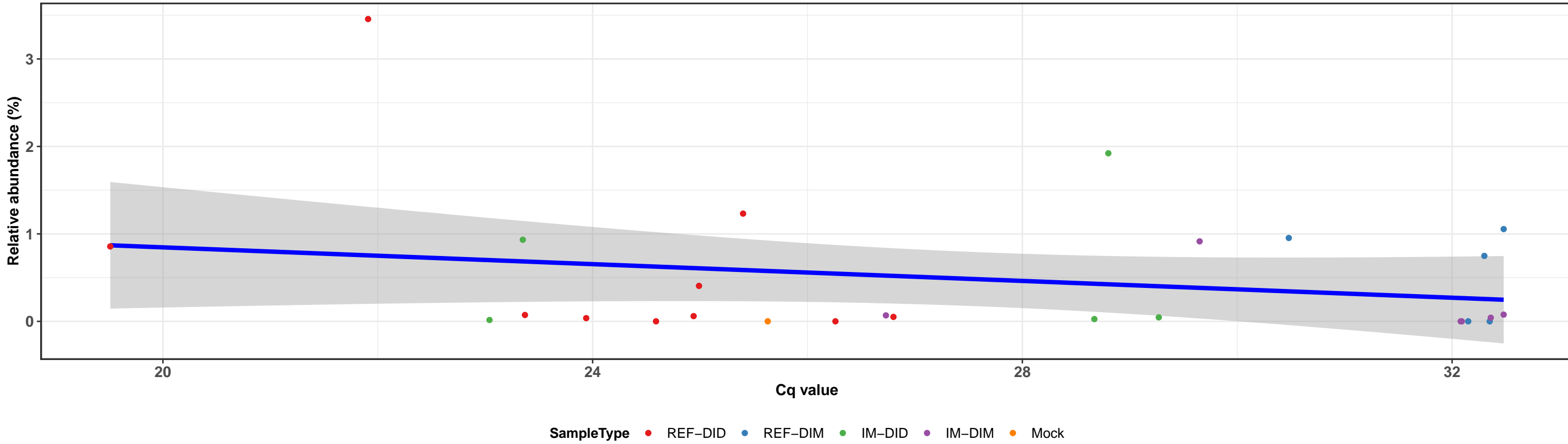
Correlation within: IM-DIM



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; Ambiguous_taxa

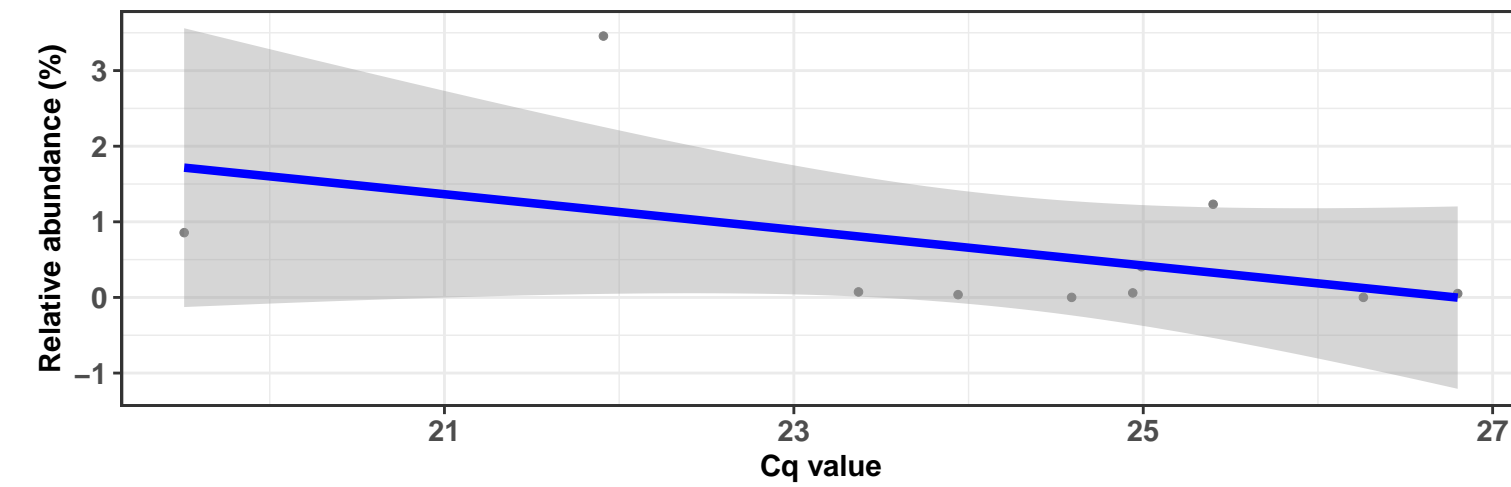
Correlation with all samples

$\log_e(S) = 8.249$, $p = 0.405$, $\hat{\rho}_{\text{Spearman}} = -0.167$, $\text{CI}_{95\%} [-0.571, 0.222]$, $n_{\text{pairs}} = 27$

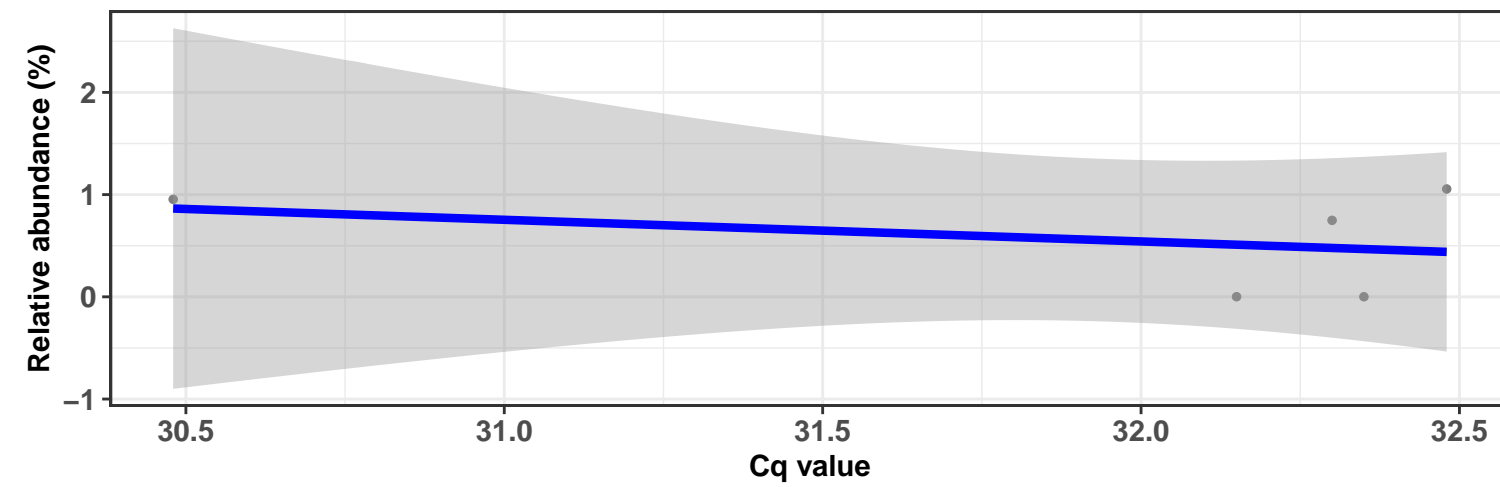


Correlation within: REF-DID

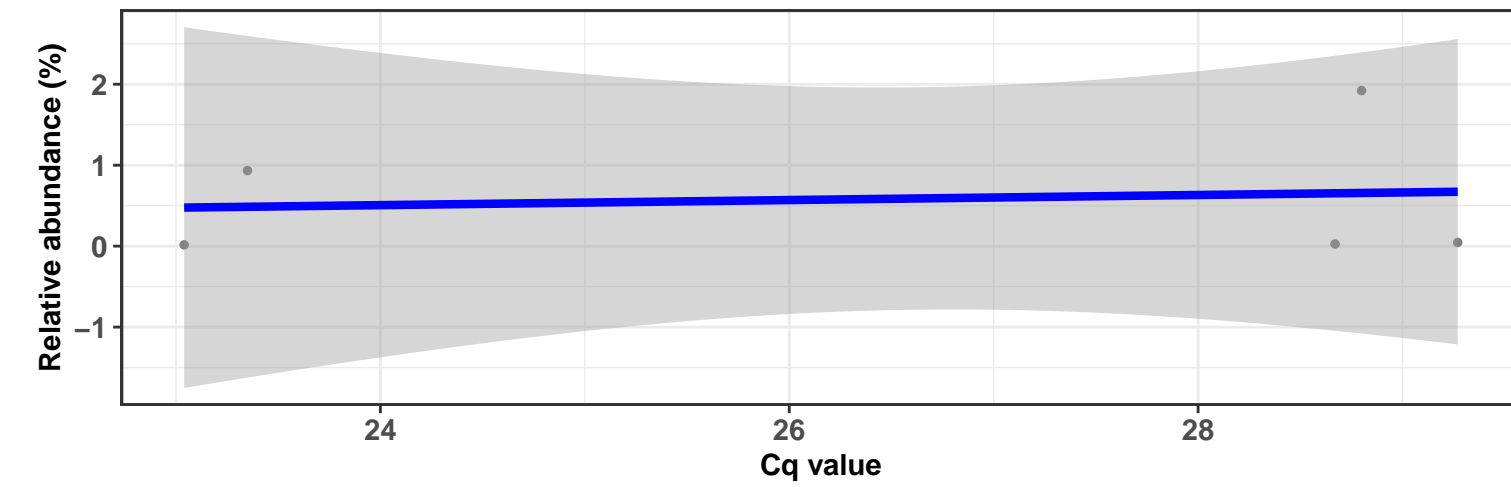
$\log_e(S) = 5.421$, $p = 0.293$, $\hat{\rho}_{\text{Spearman}} = -0.370$, $\text{CI}_{95\%} [-1.025, 0.220]$, $n_{\text{pairs}} = 10$



Correlation within: REF-DIM

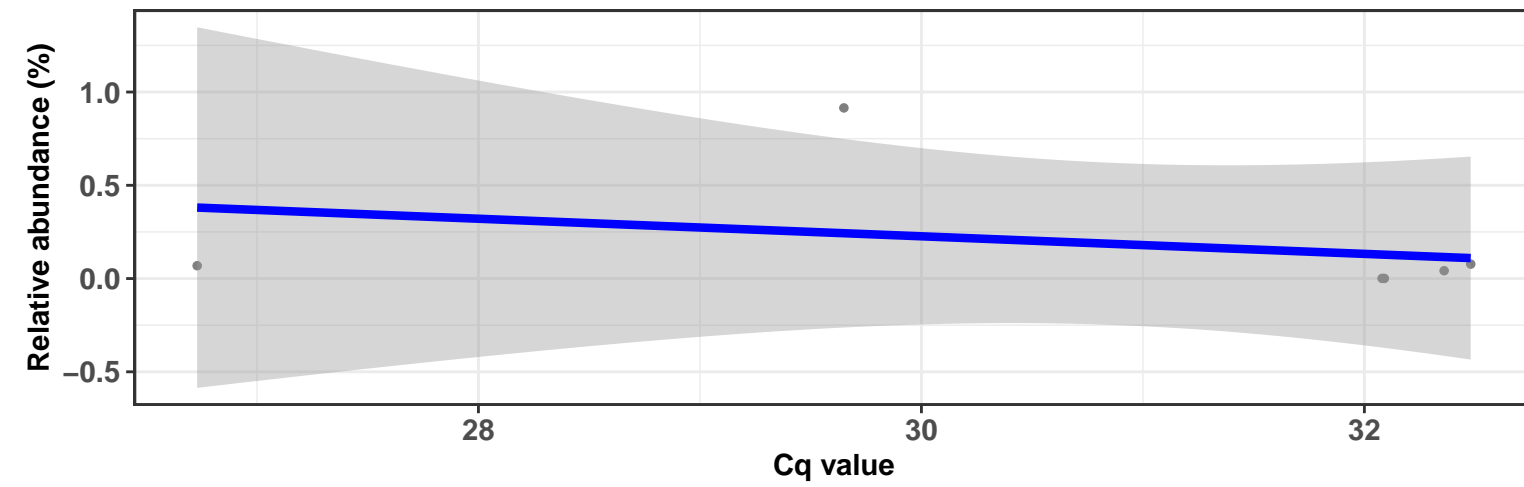


Correlation within: IM-DID



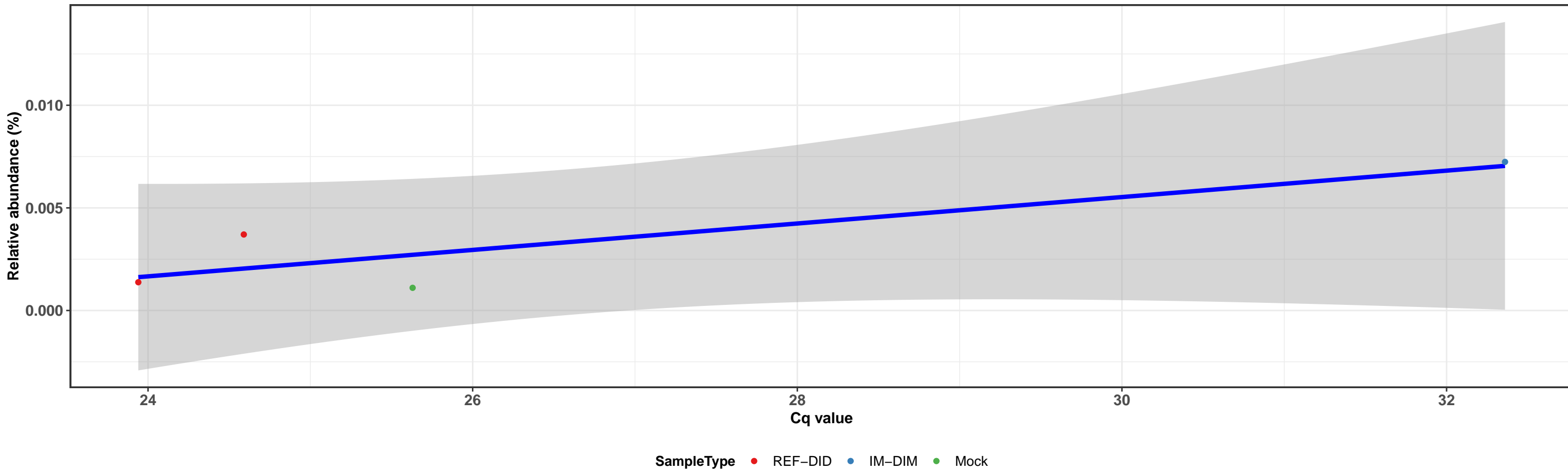
Correlation within: IM-DIM

$\log_e(S) = 3.689$, $p = 0.787$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-1.118, 0.881]$, $n_{\text{pairs}} = 6$

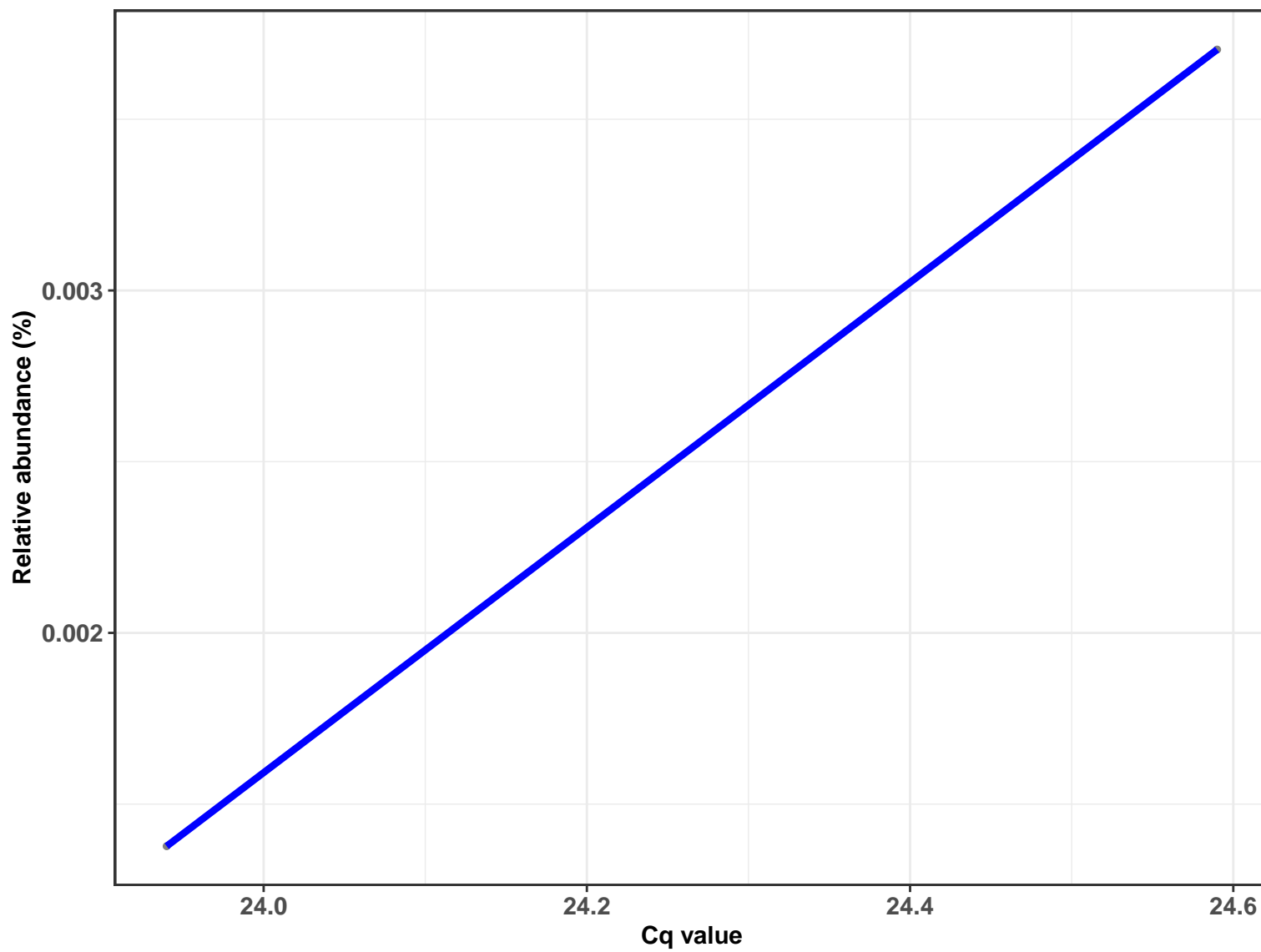


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Acidovorax; NA

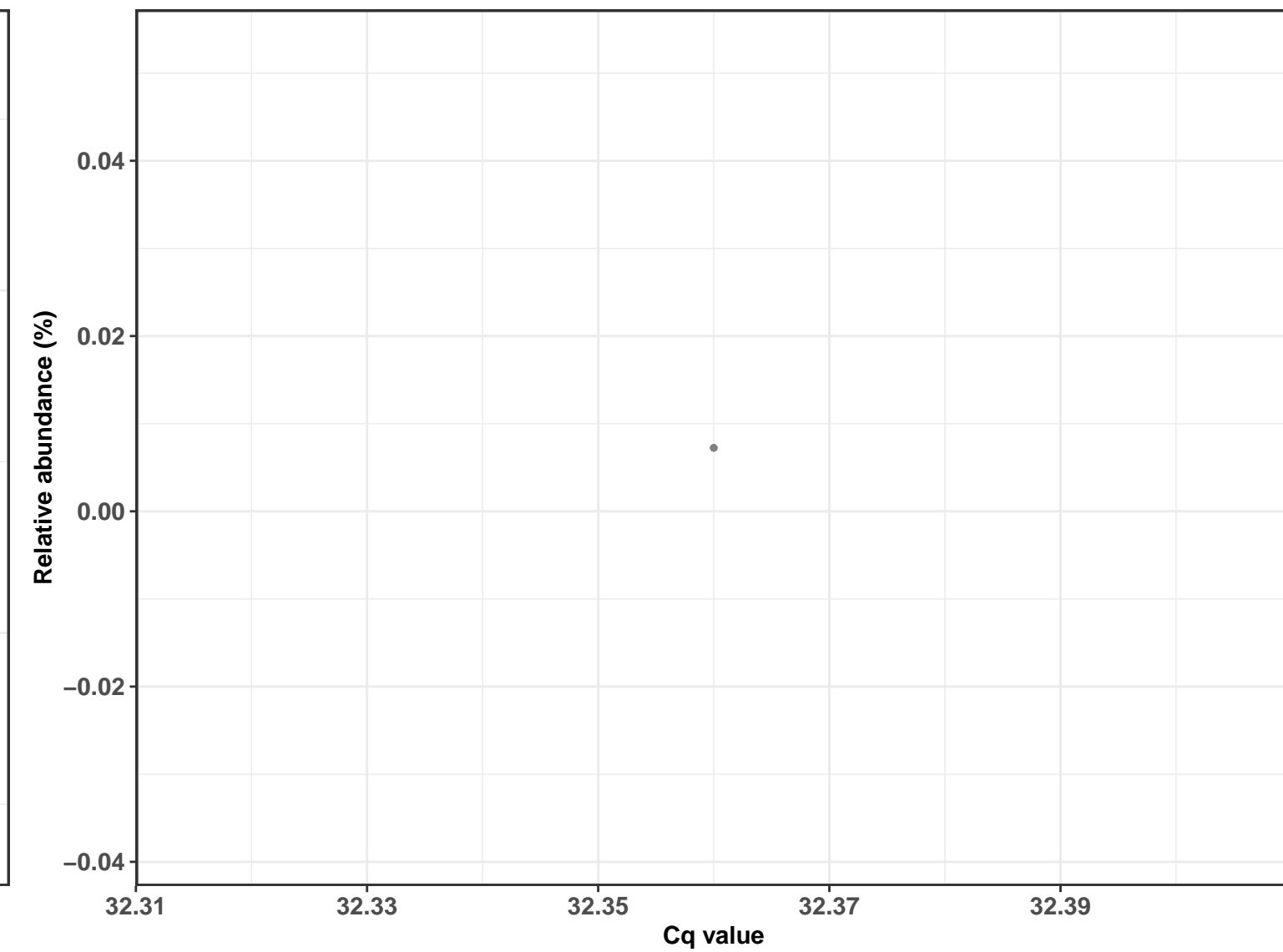
Correlation with all samples



Correlation within: REF-DID

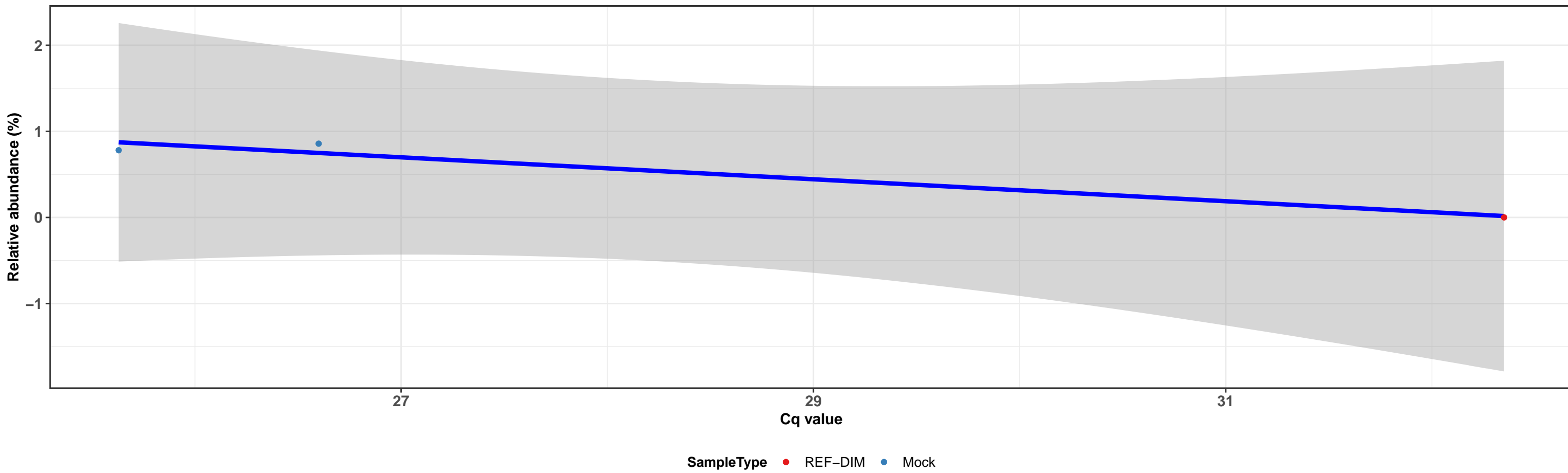


Correlation within: IM-DIM

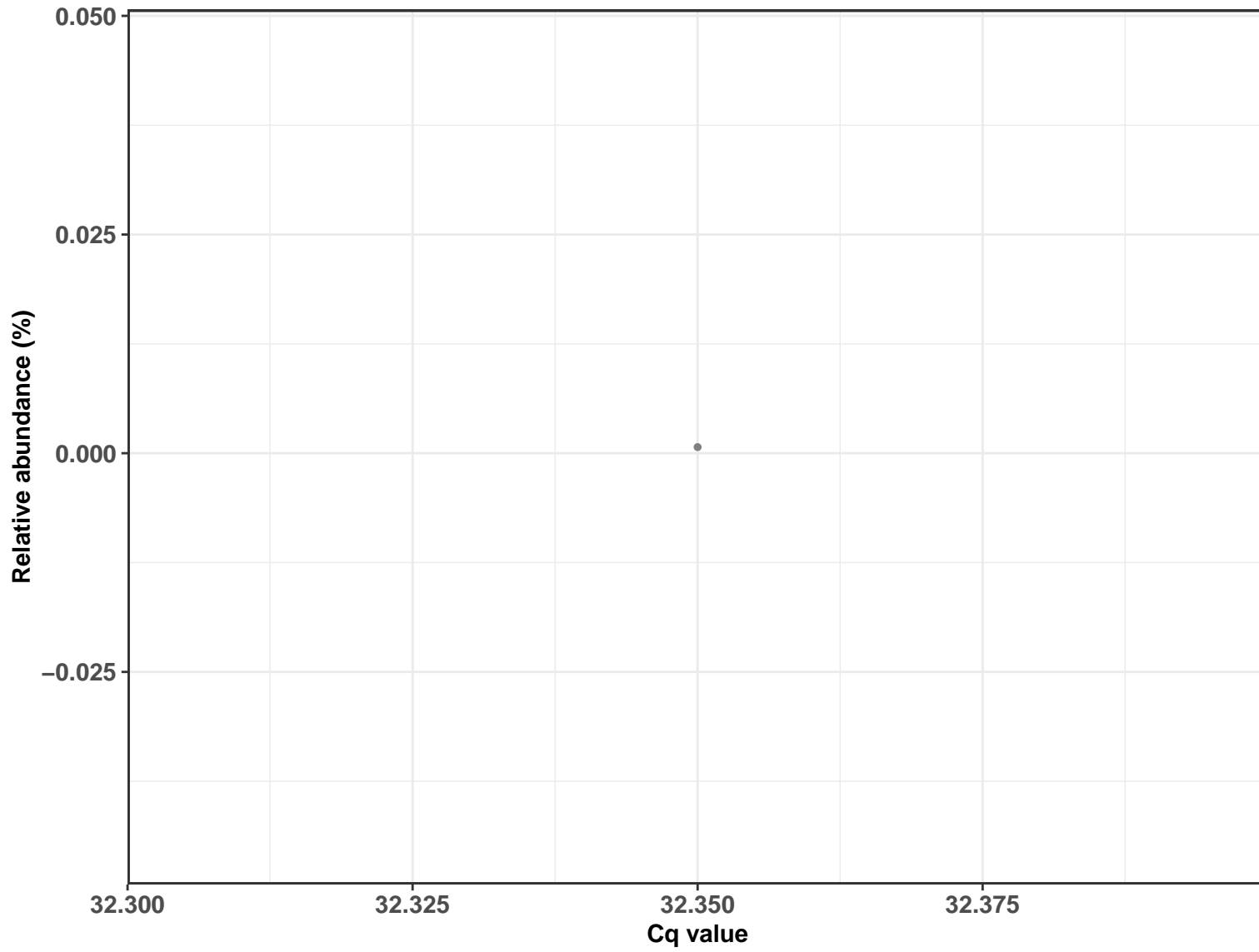


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes

Correlation with all samples

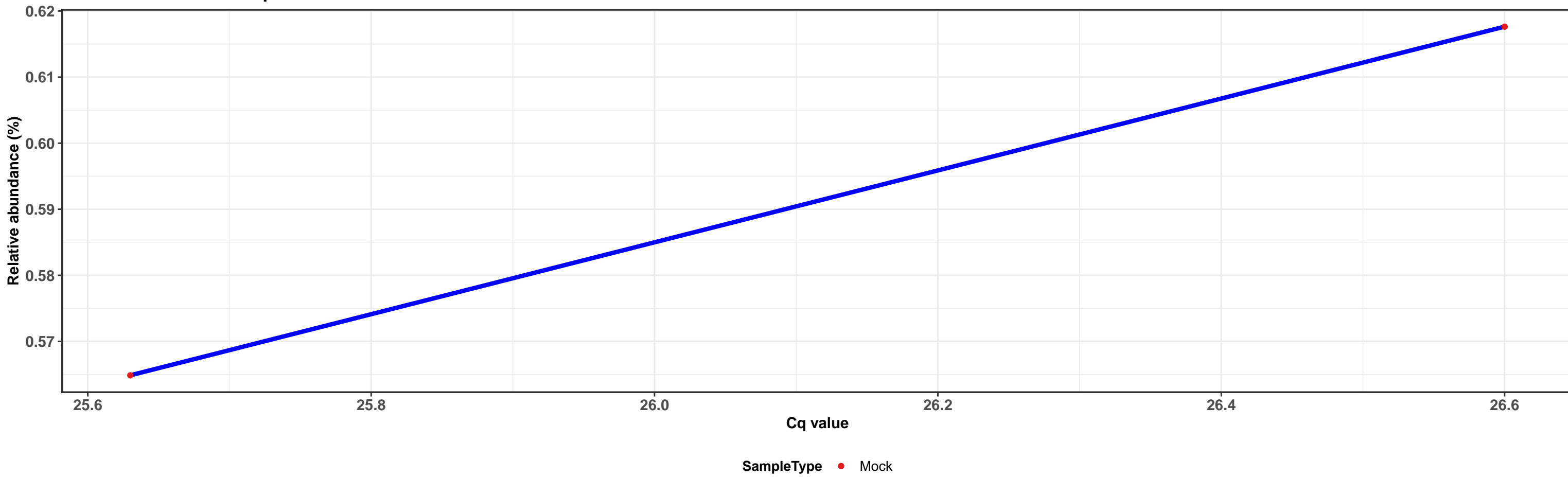


Correlation within: REF-DIM

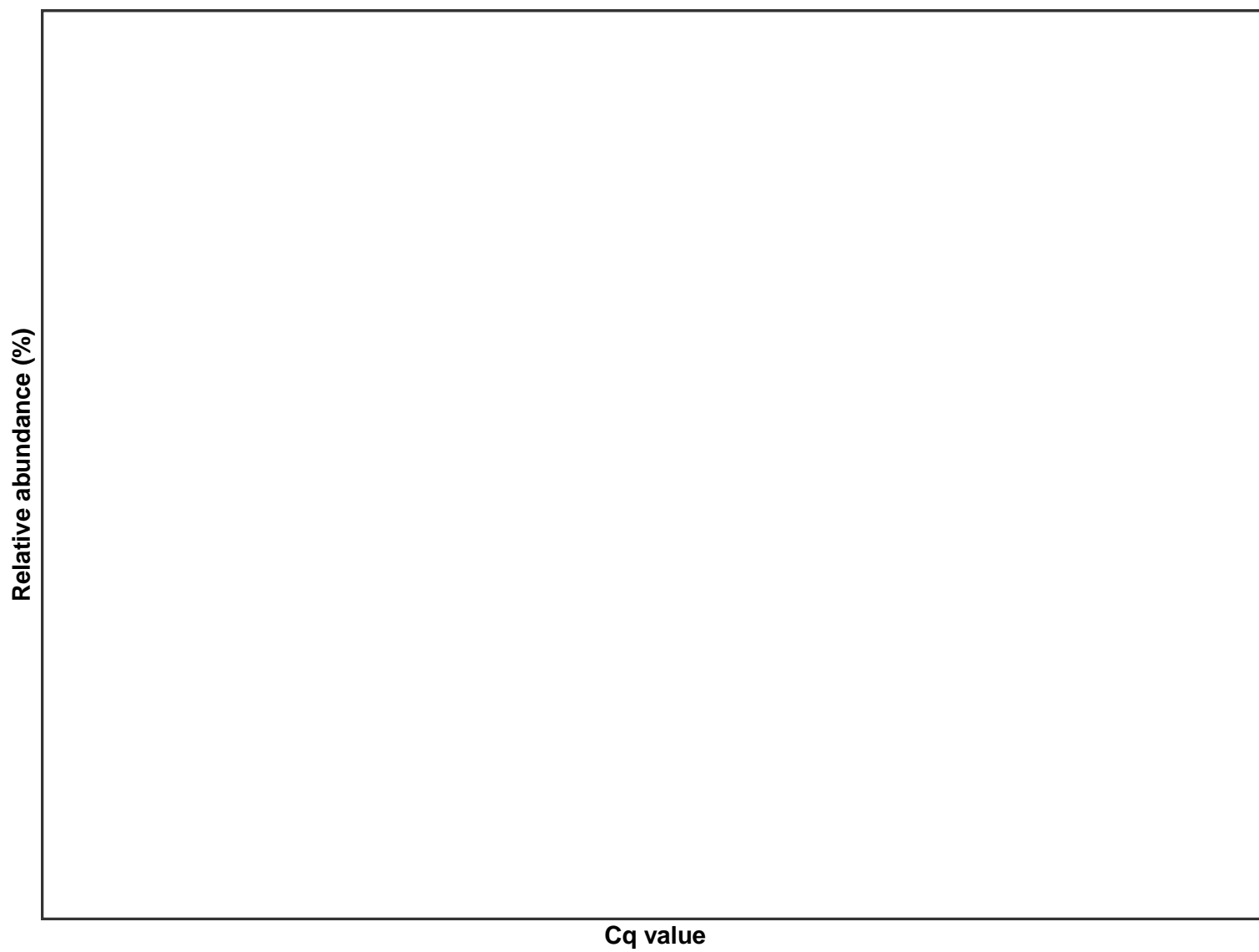


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes

Correlation with all samples

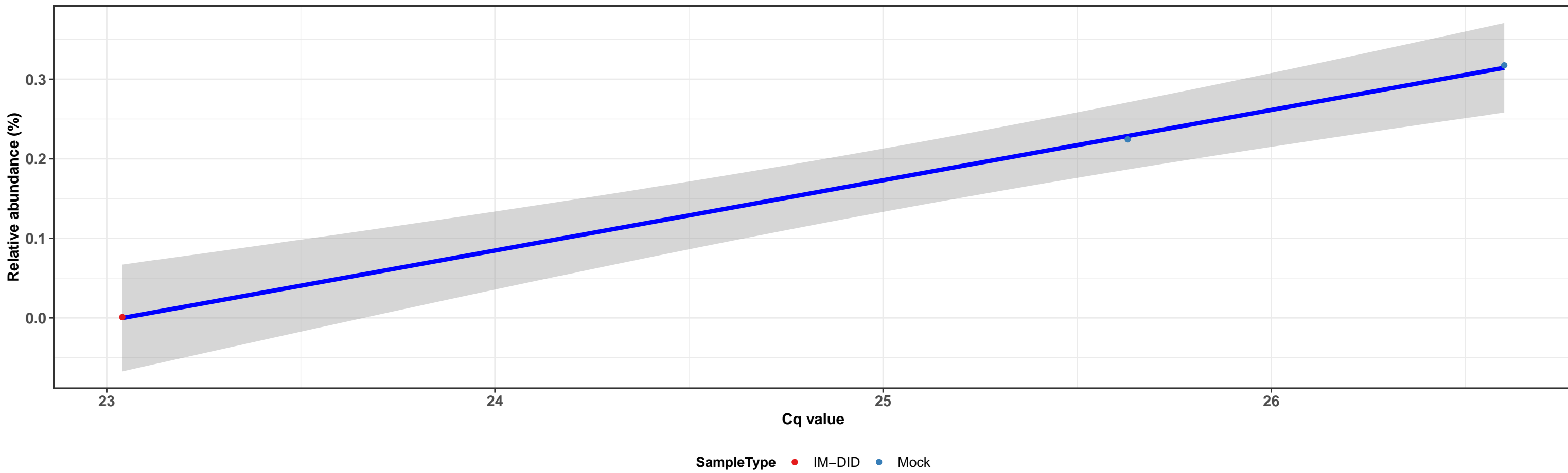


Correlation within:

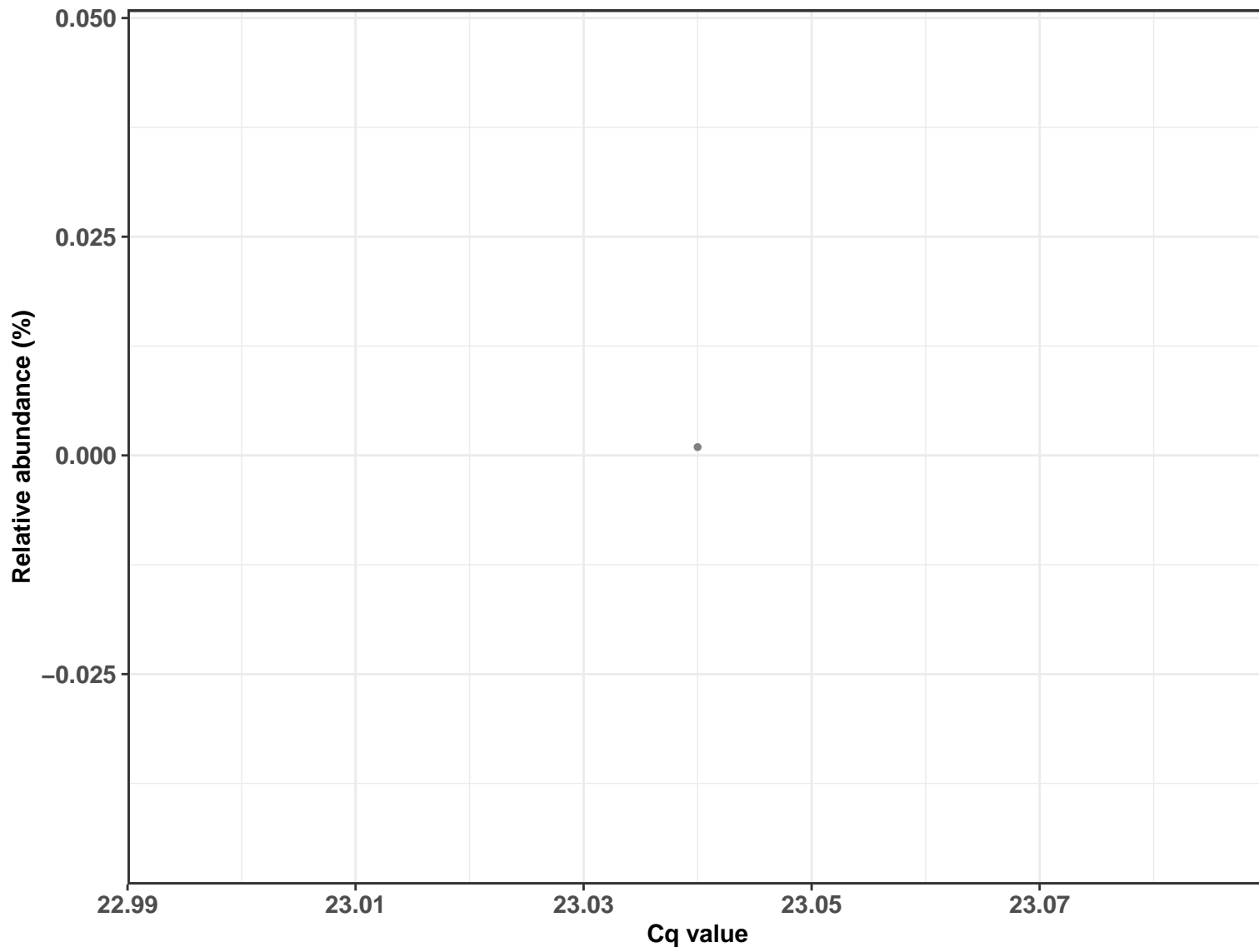


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes

Correlation with all samples



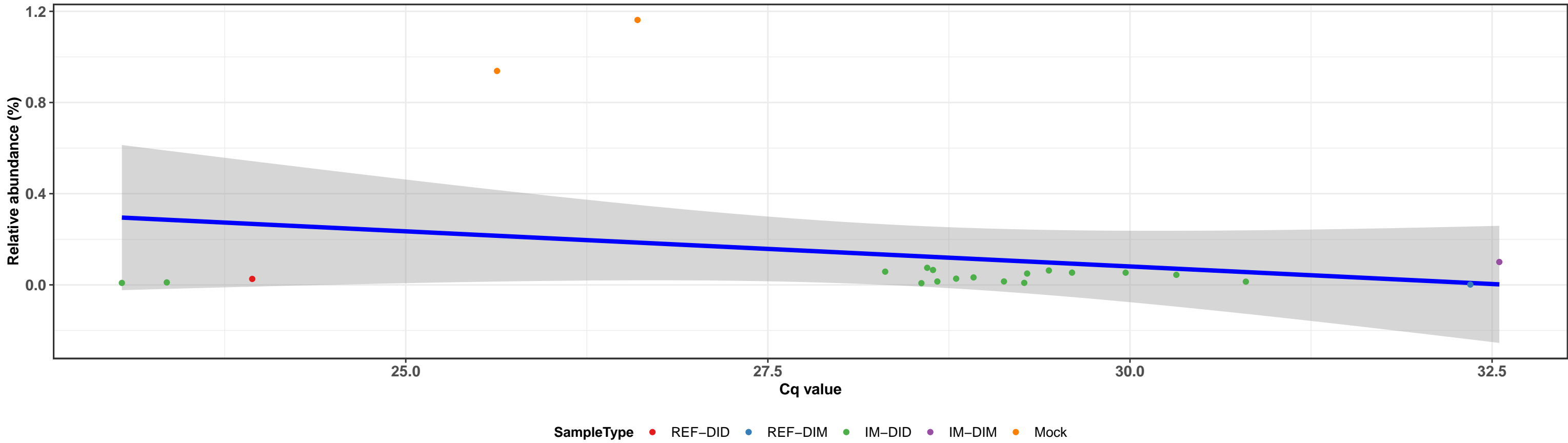
Correlation within: IM-DID



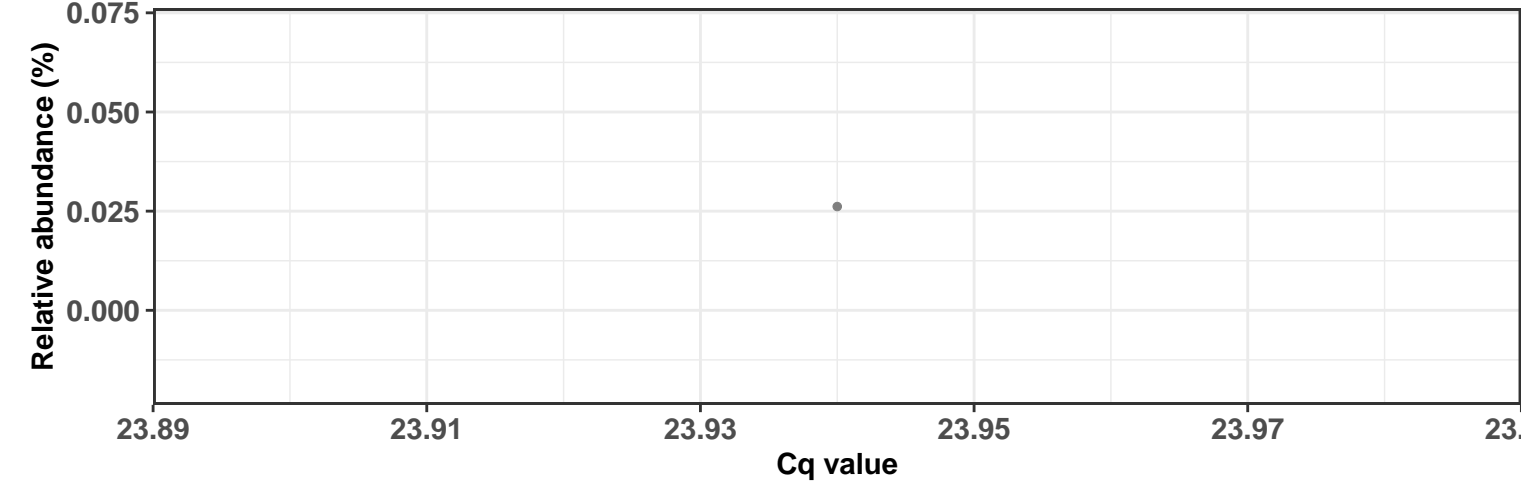
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecalis

Correlation with all samples

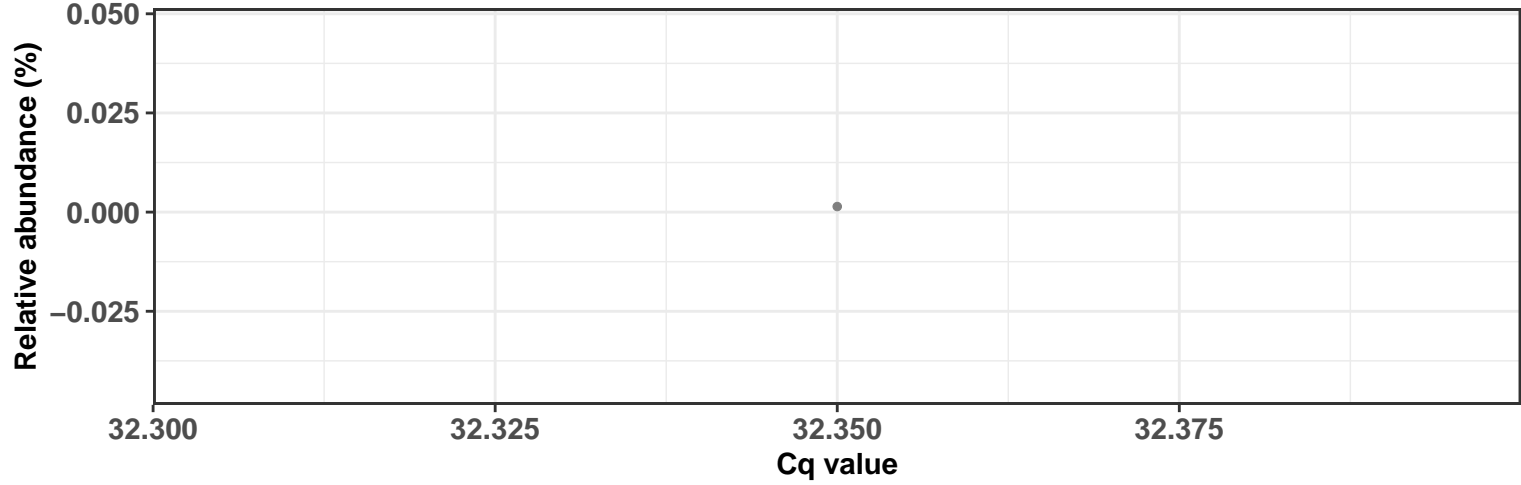
$\log_e(S) = 7.475$, $p = 0.986$, $\hat{\rho}_{\text{Spearman}} = 0.004$, $CI_{95\%} [-0.479, 0.531]$, $n_{\text{pairs}} = 22$



Correlation within: REF-DID

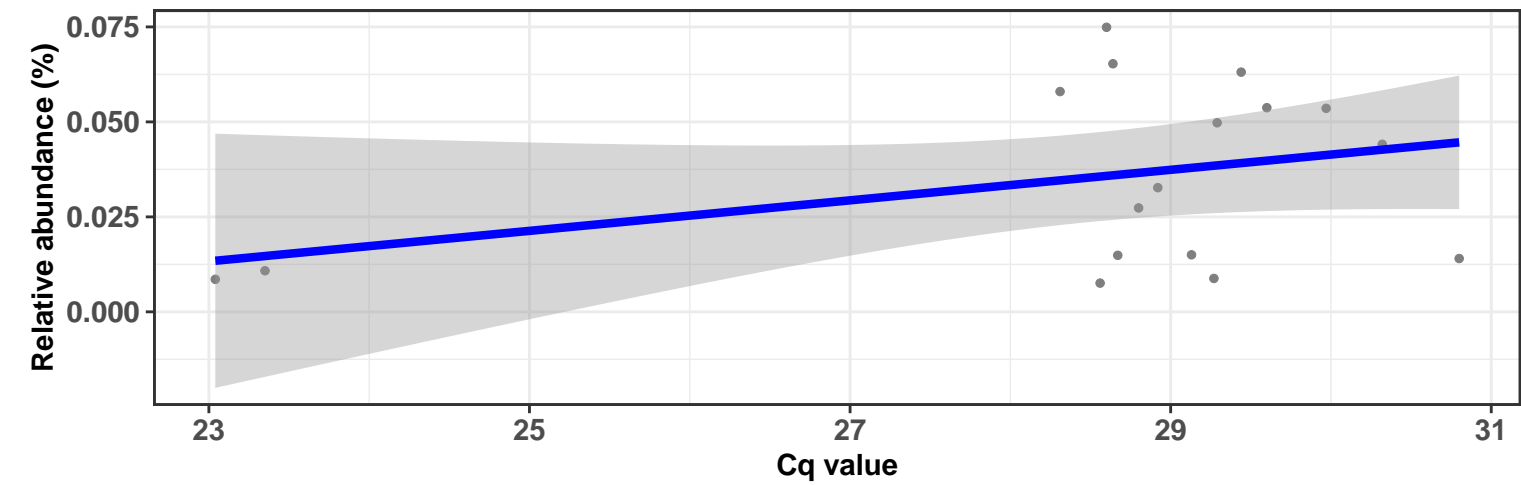


Correlation within: REF-DIM

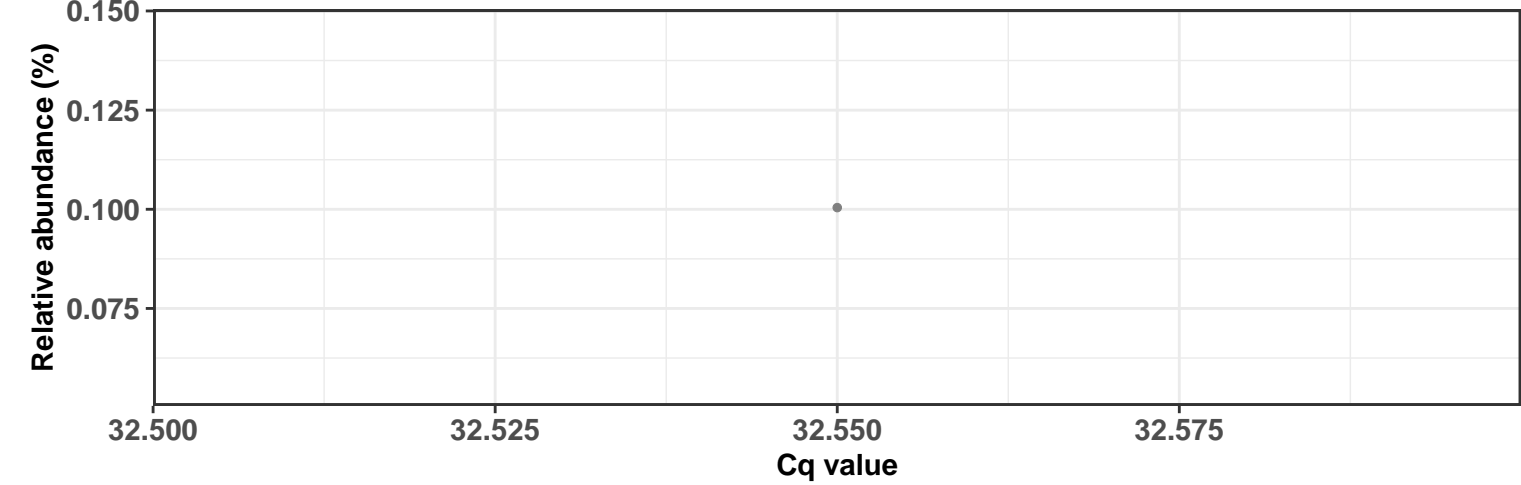


Correlation within: IM-DID

$\log_e(S) = 6.474$, $p = 0.428$, $\hat{\rho}_{\text{Spearman}} = 0.206$, $CI_{95\%} [-0.330, 0.802]$, $n_{\text{pairs}} = 17$

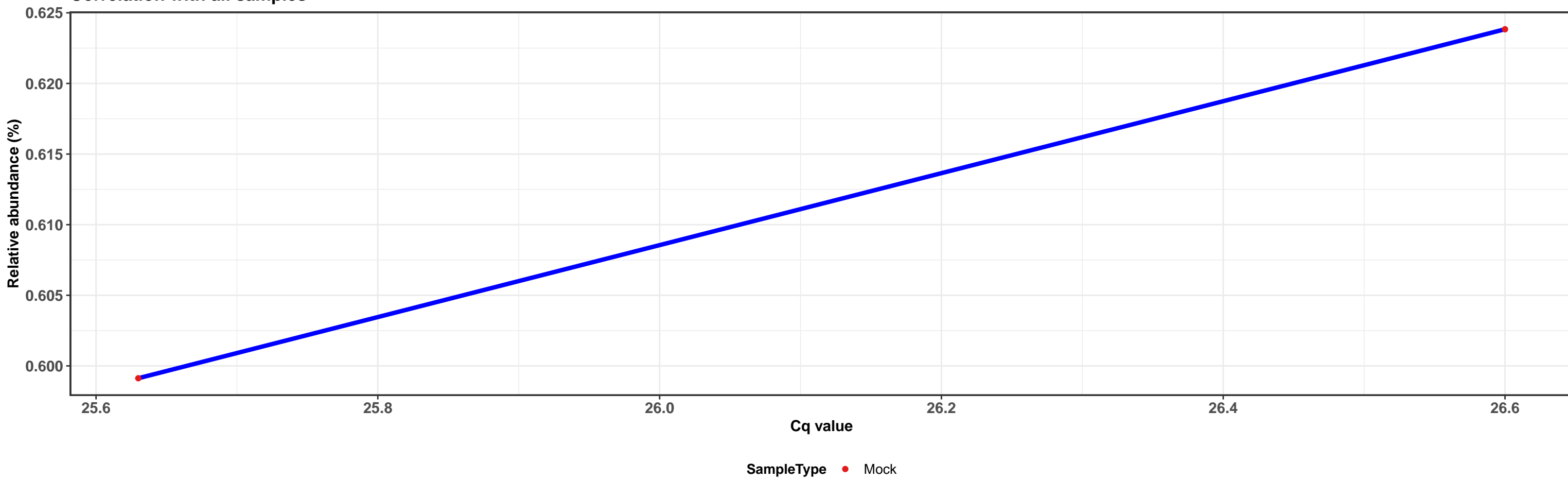


Correlation within: IM-DIM

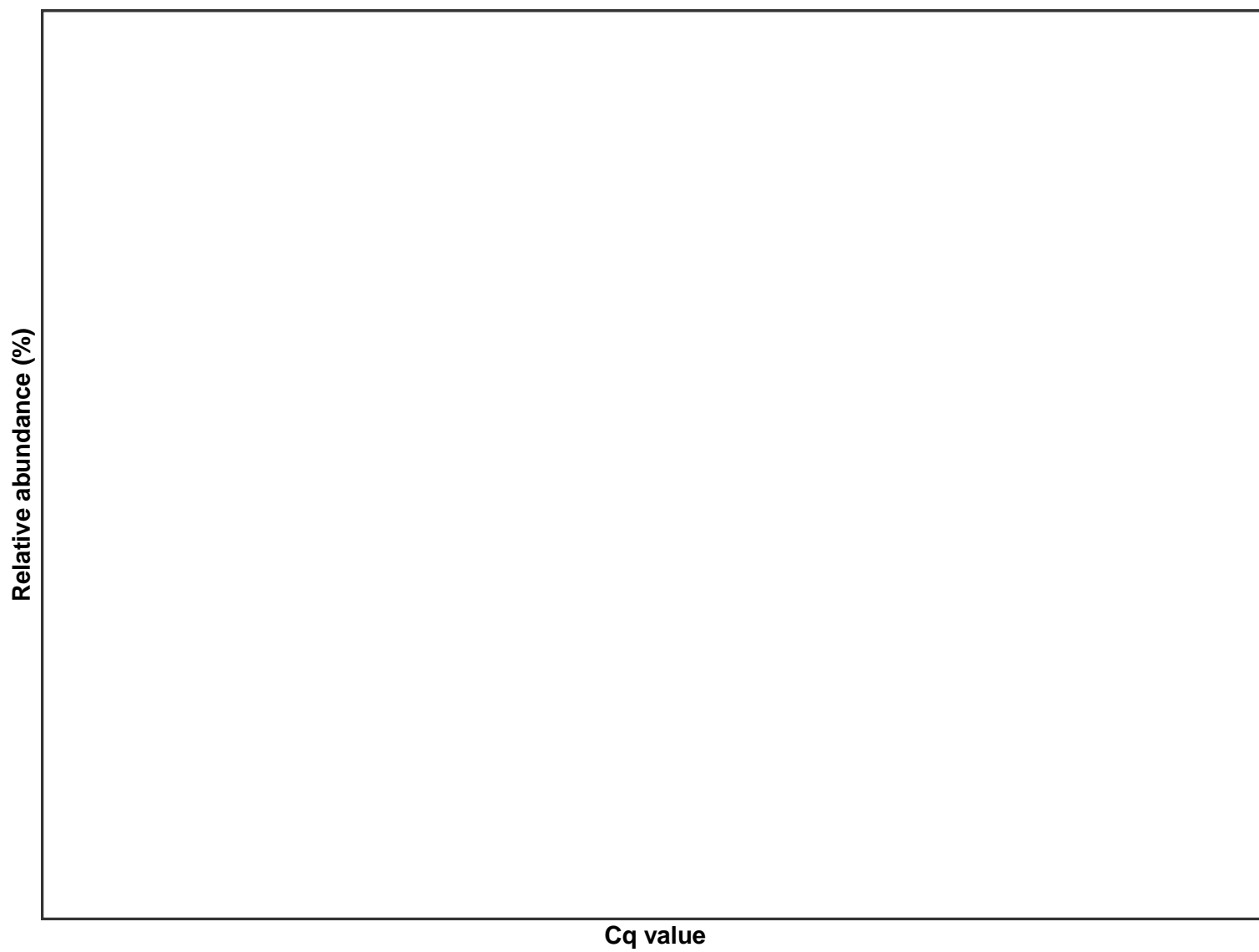


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecalis

Correlation with all samples

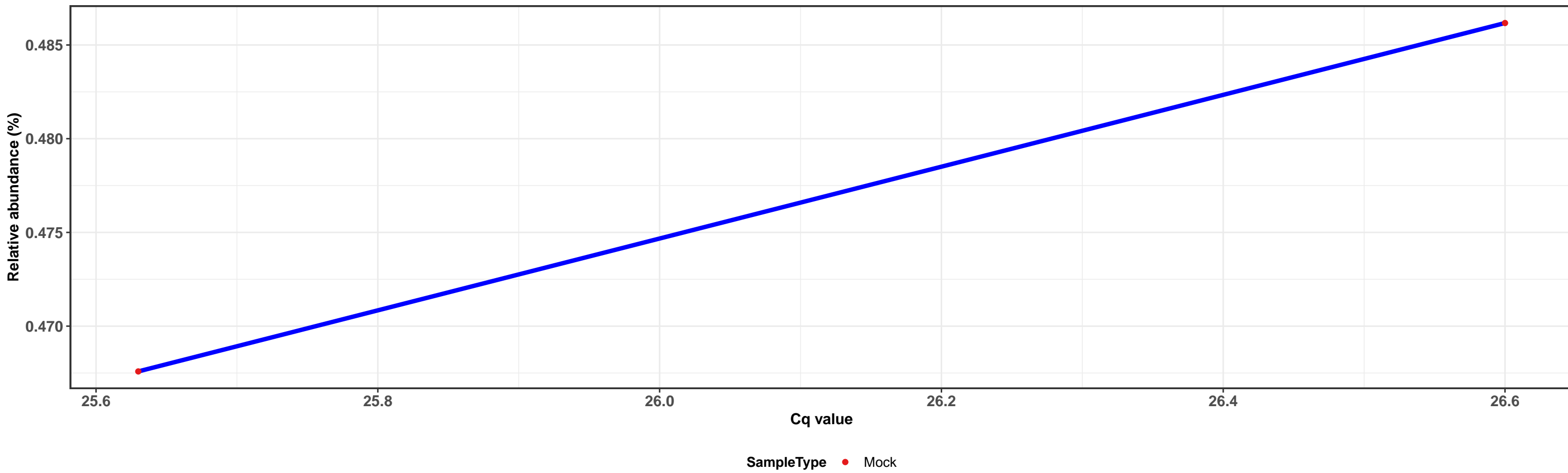


Correlation within:

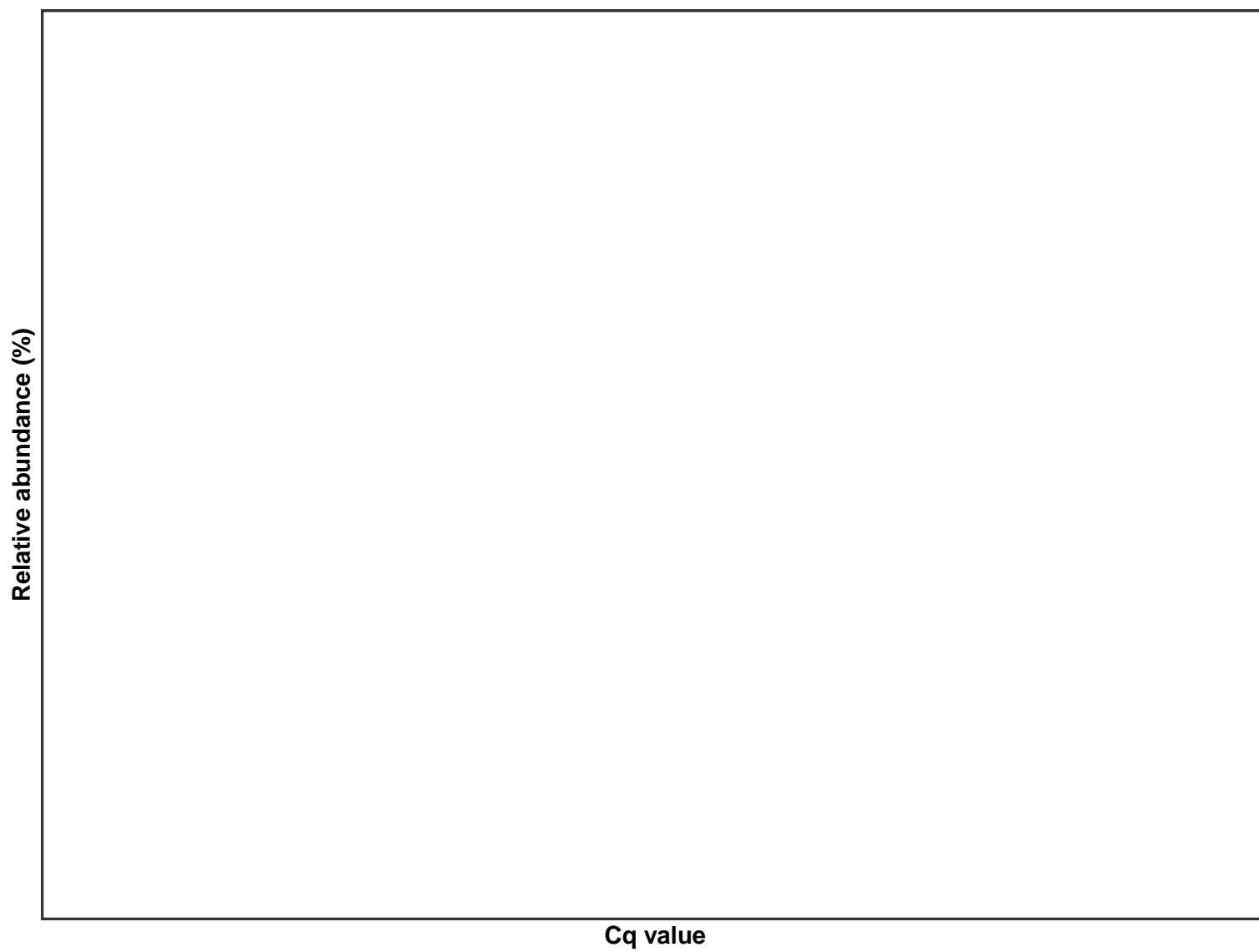


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecalis

Correlation with all samples



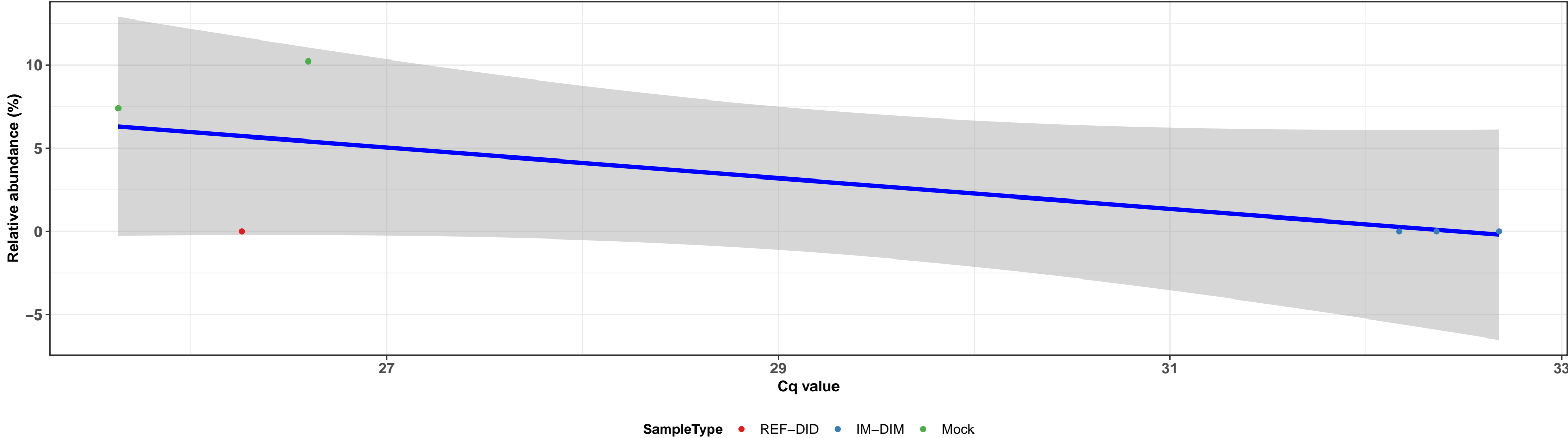
Correlation within:



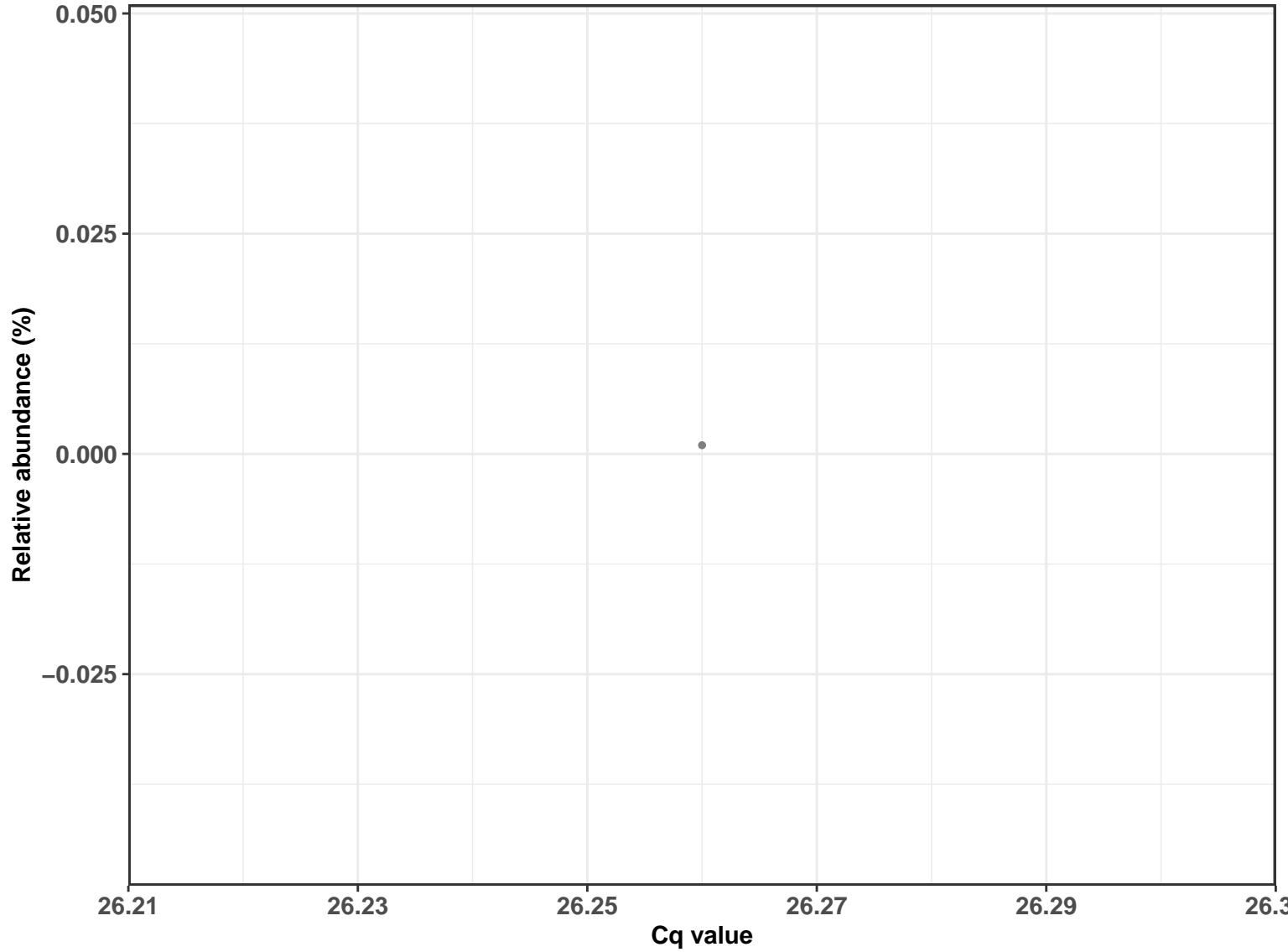
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples

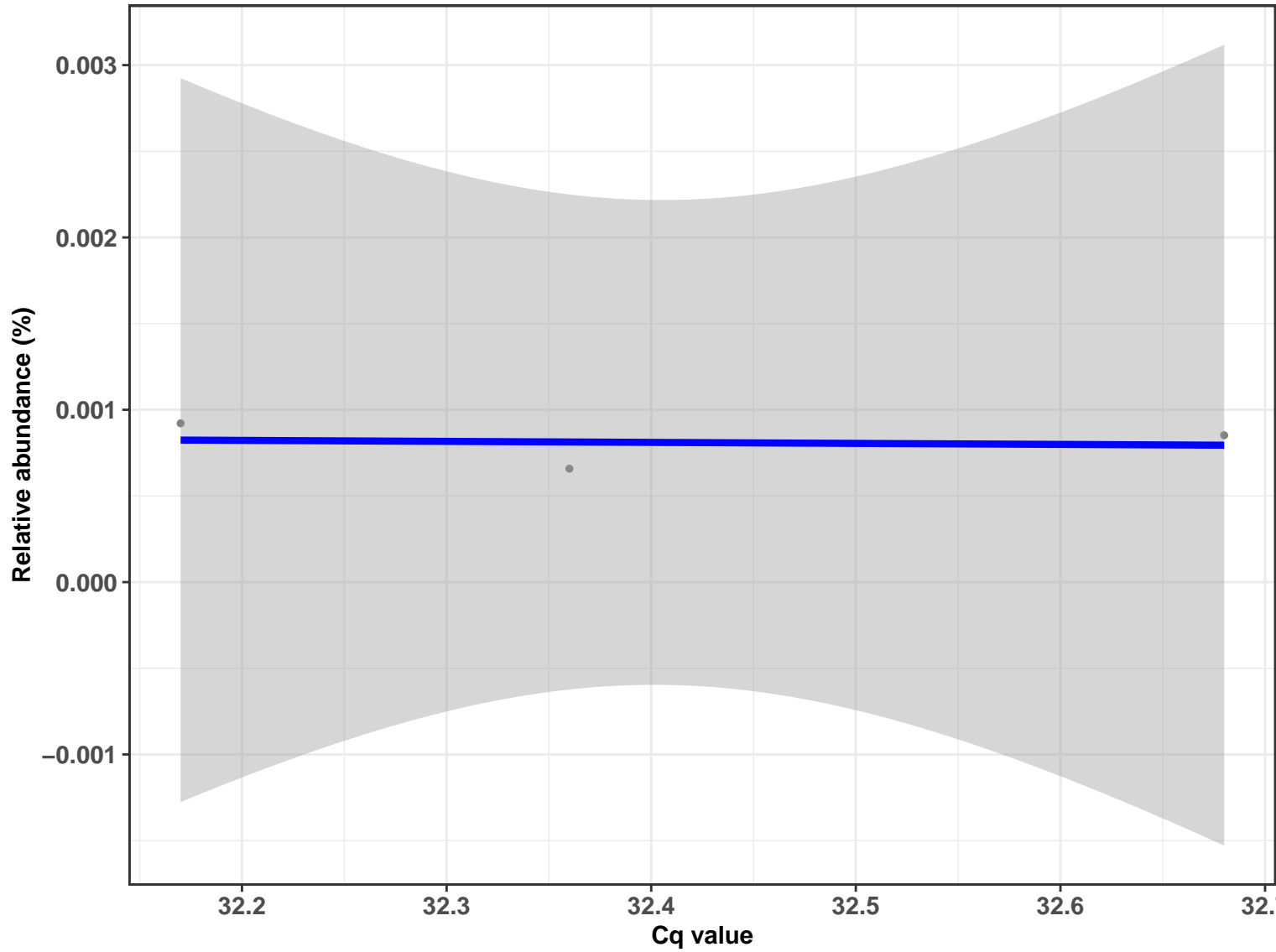
$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = -0.771$, $CI_{95\%} [-1.601, -0.192]$, $n_{\text{pairs}} = 6$



Correlation within: REF-DID

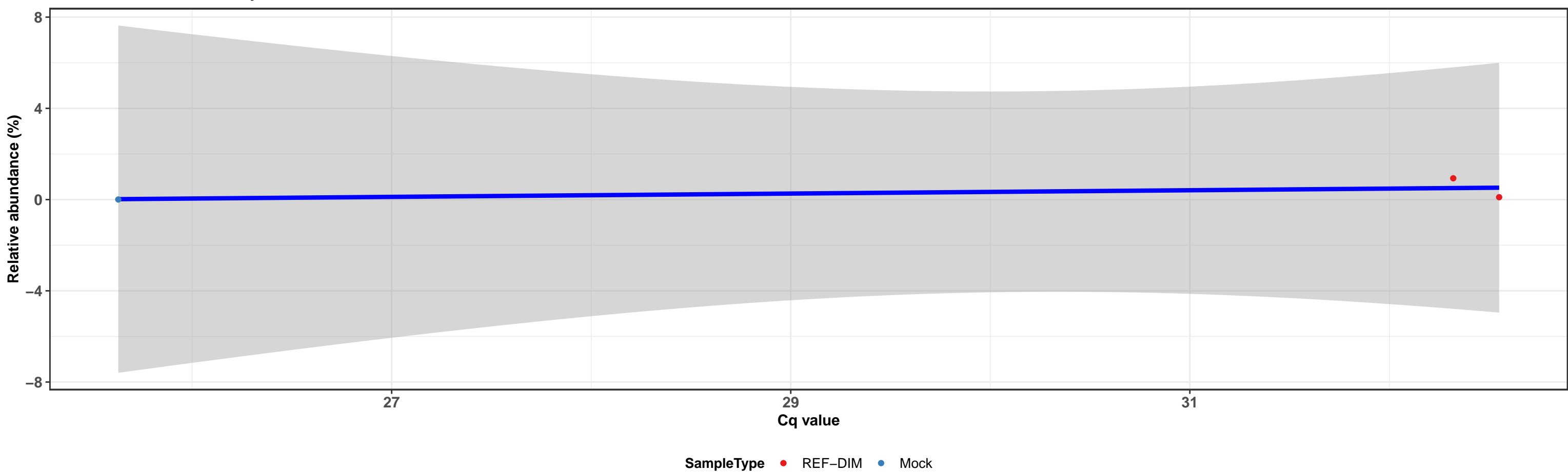


Correlation within: IM-DIM

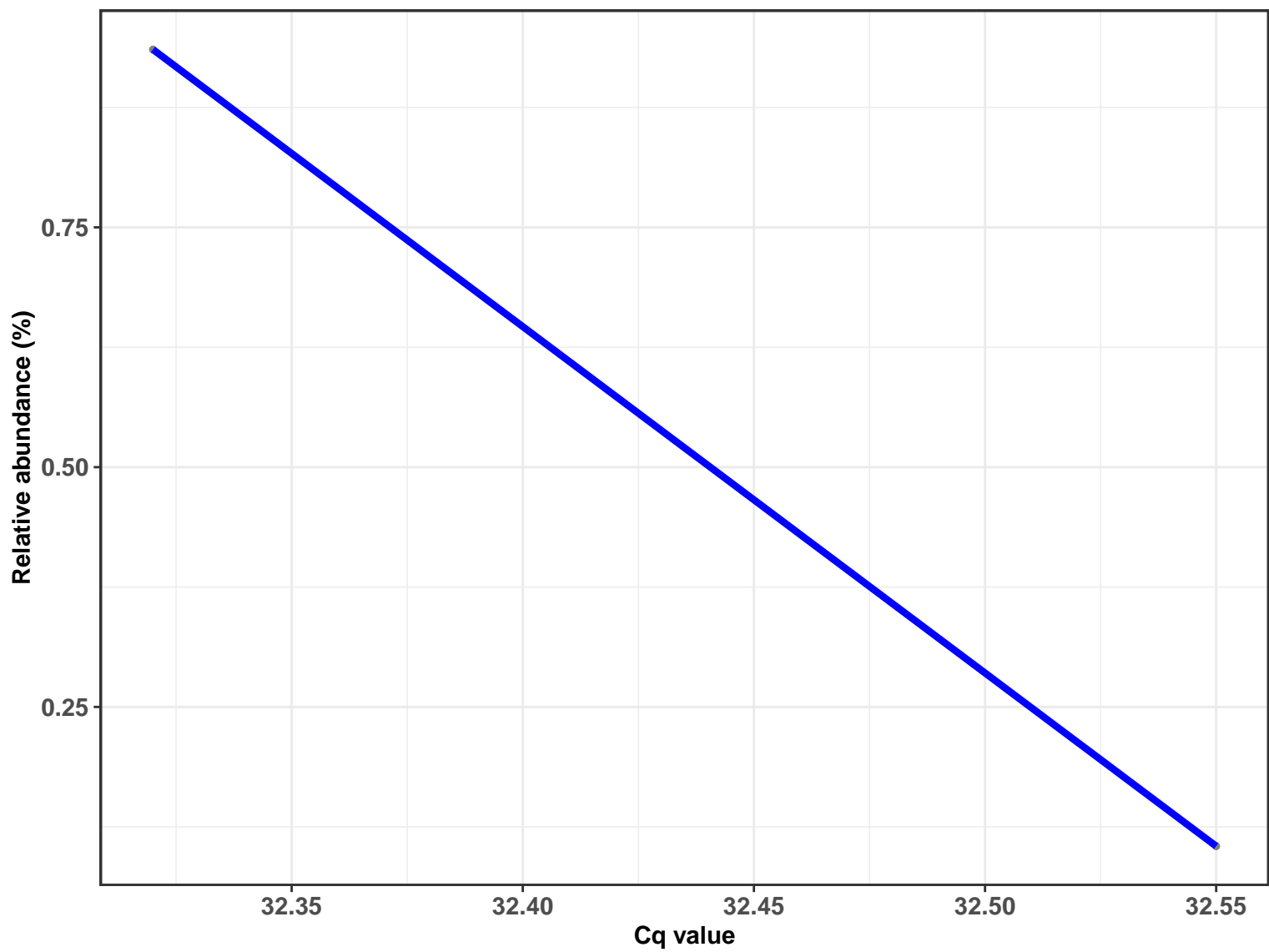


k__Bacteria; p__Cyanobacteria; c__Melainabacteria; o__Obscuribacterales; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa

Correlation with all samples

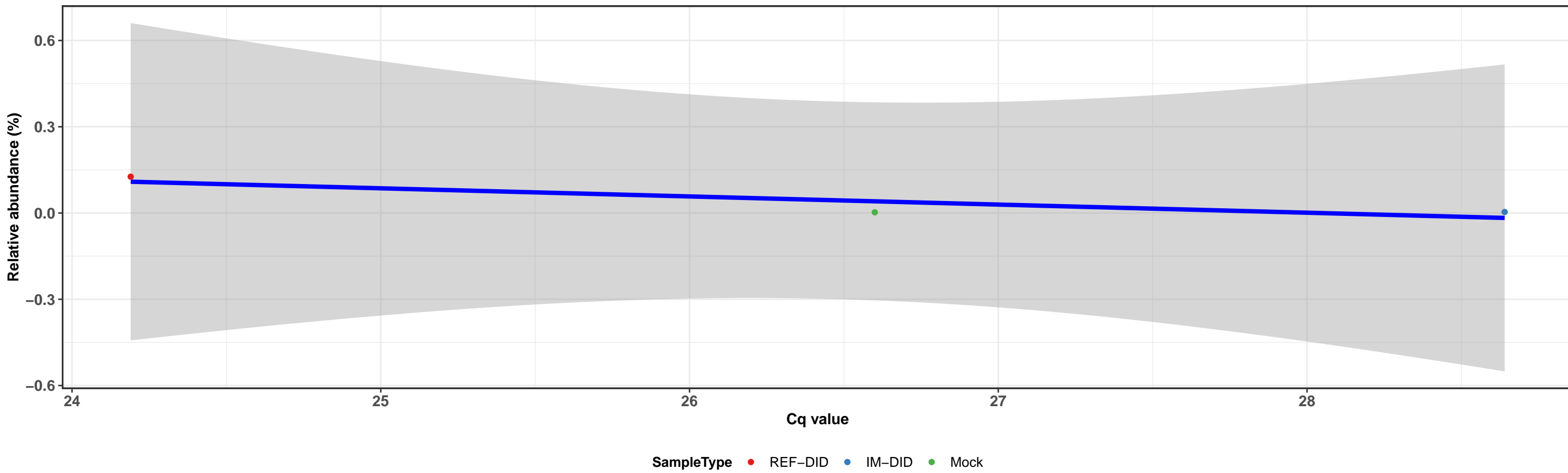


Correlation within: REF-DIM

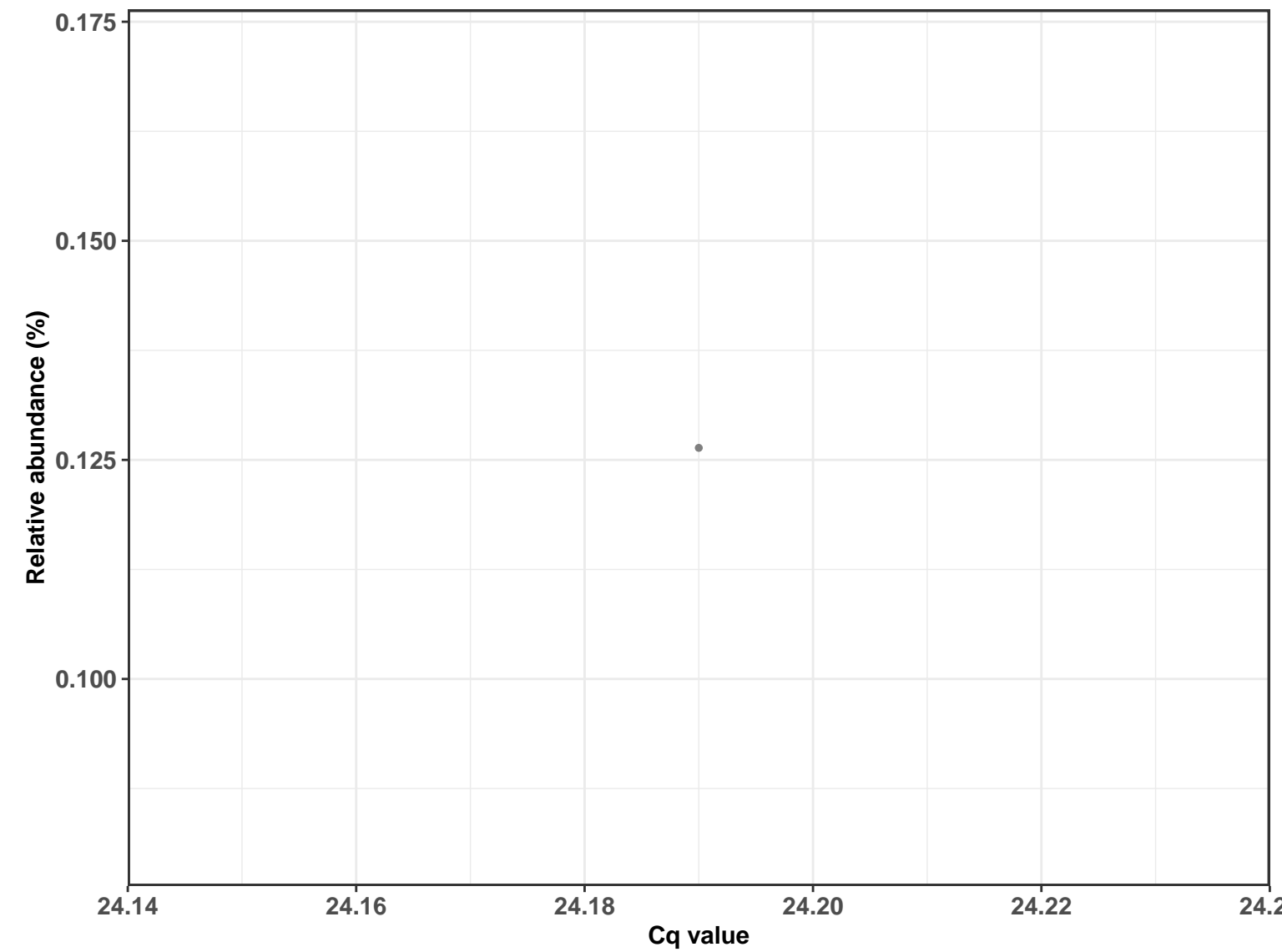


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

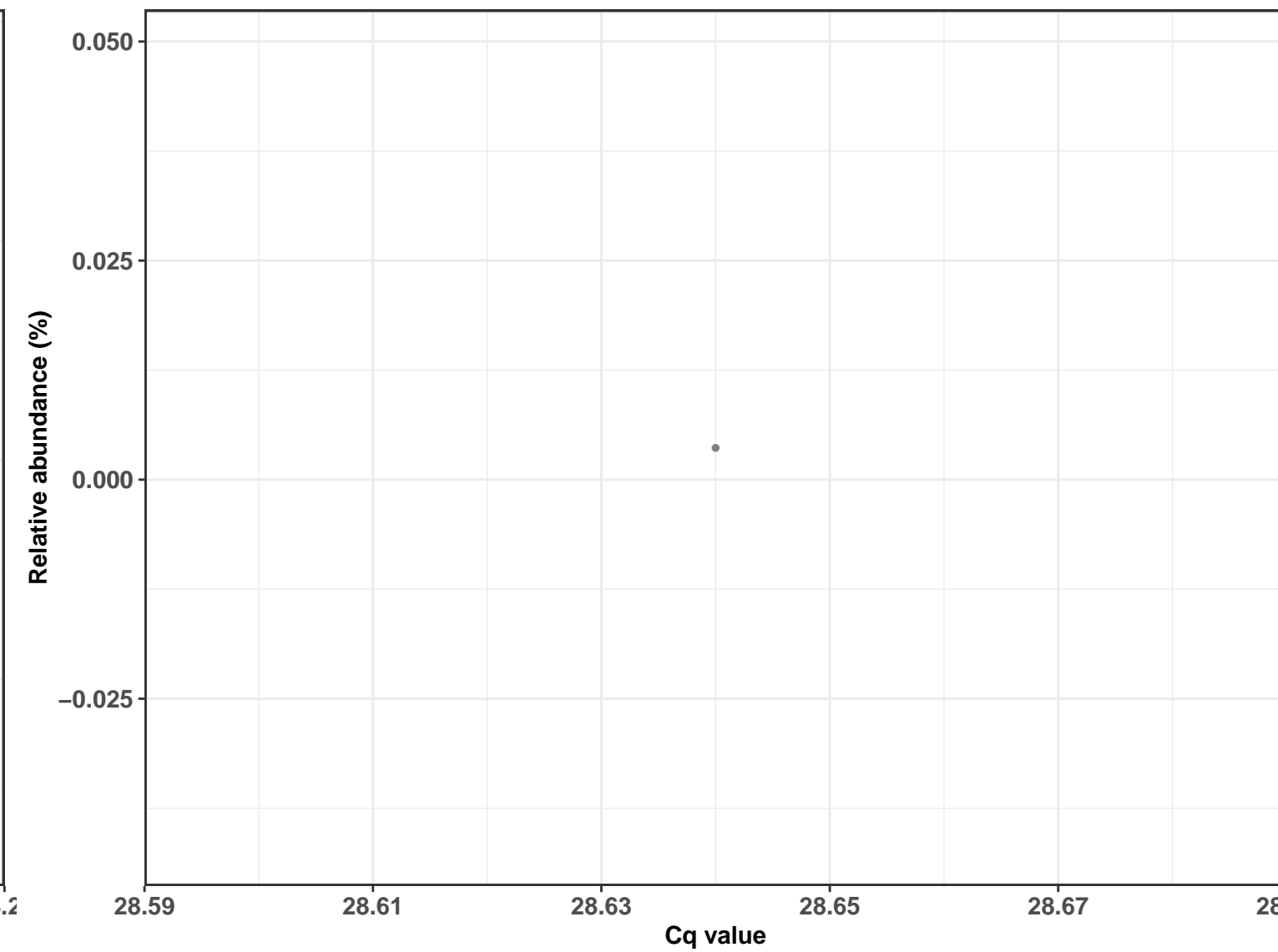
Correlation with all samples



Correlation within: REF-DID



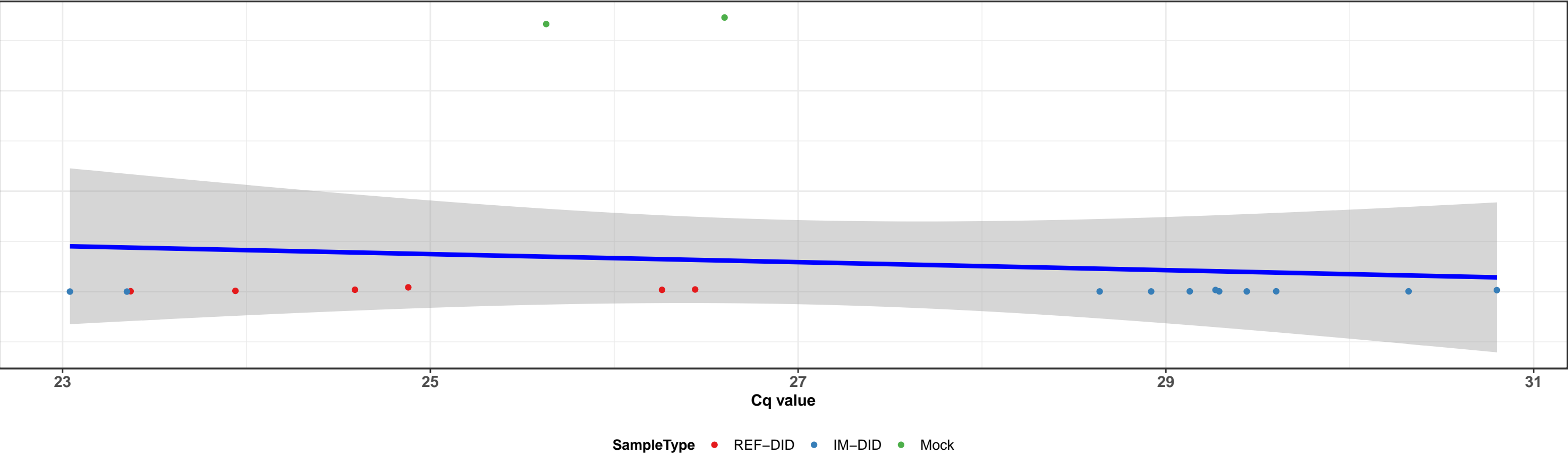
Correlation within: IM-DID



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

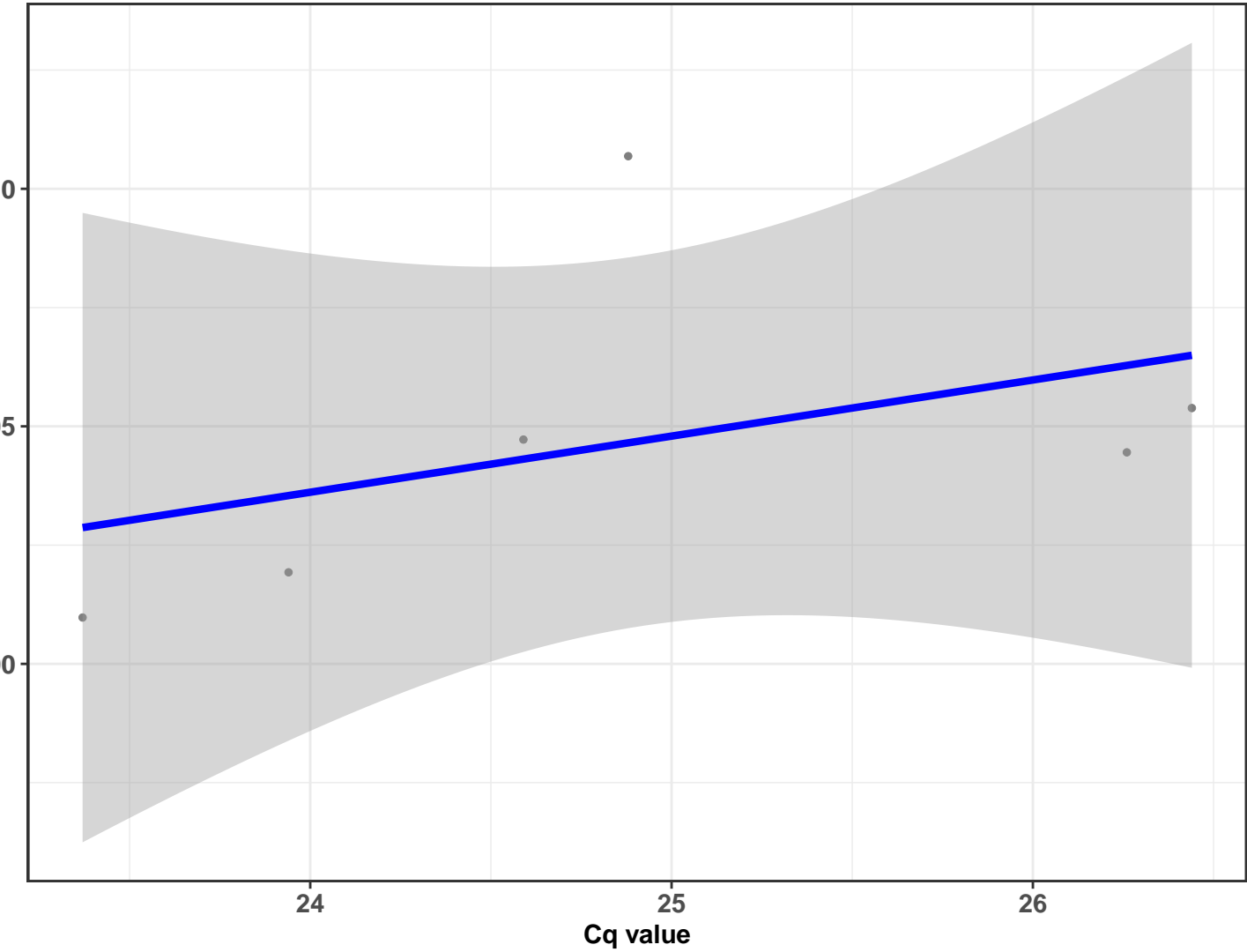
Correlation with all samples

$\log_e(S) = 7.080$, $p = 0.864$, $\hat{\rho}_{\text{Spearman}} = -0.042$, $\text{CI}_{95\%} [-0.547, 0.398]$, $n_{\text{pairs}} = 19$



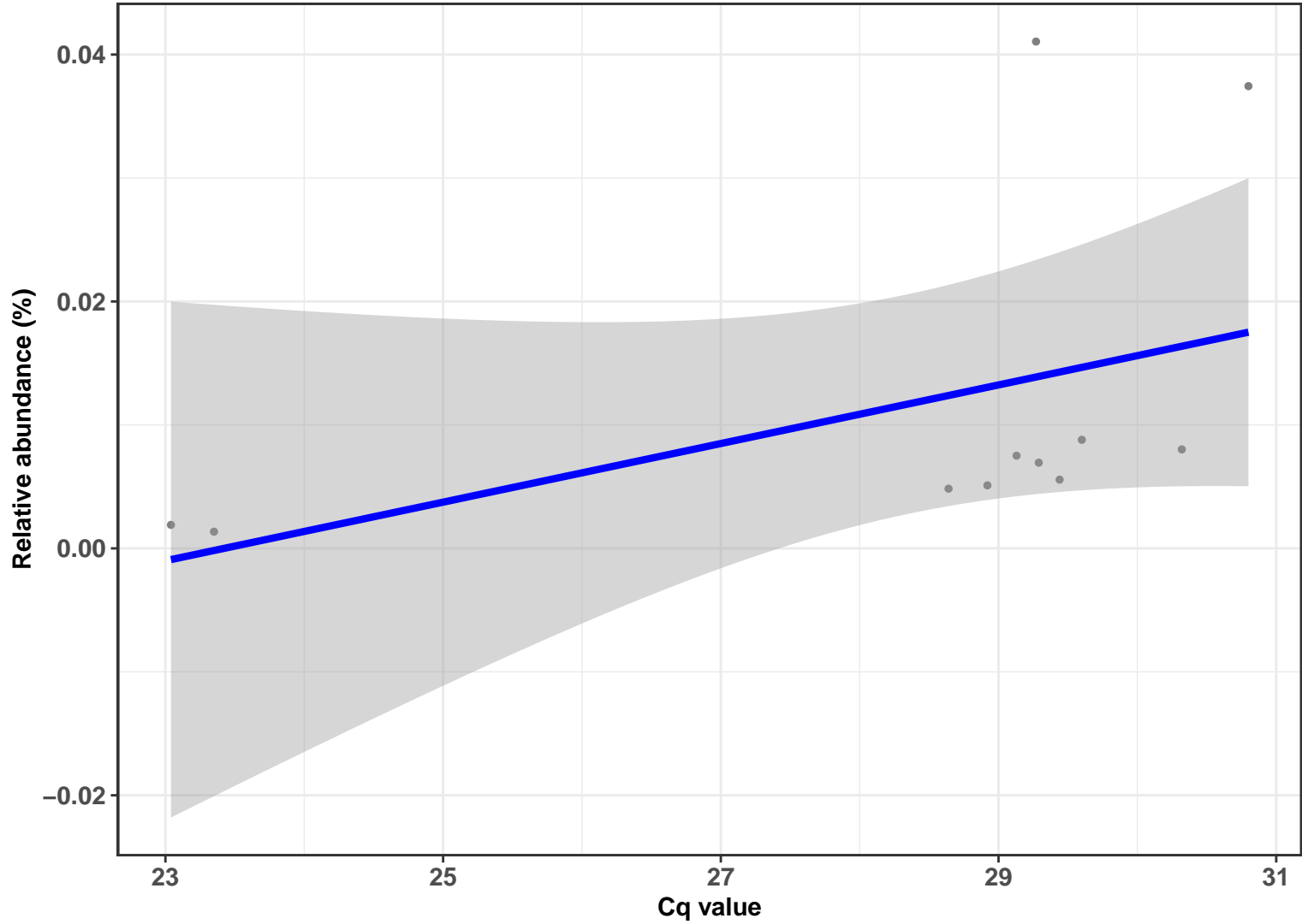
Correlation within: REF-DID

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $\text{CI}_{95\%} [0.100, 1.469]$, $n_{\text{pairs}} = 6$



Correlation within: IM-DID

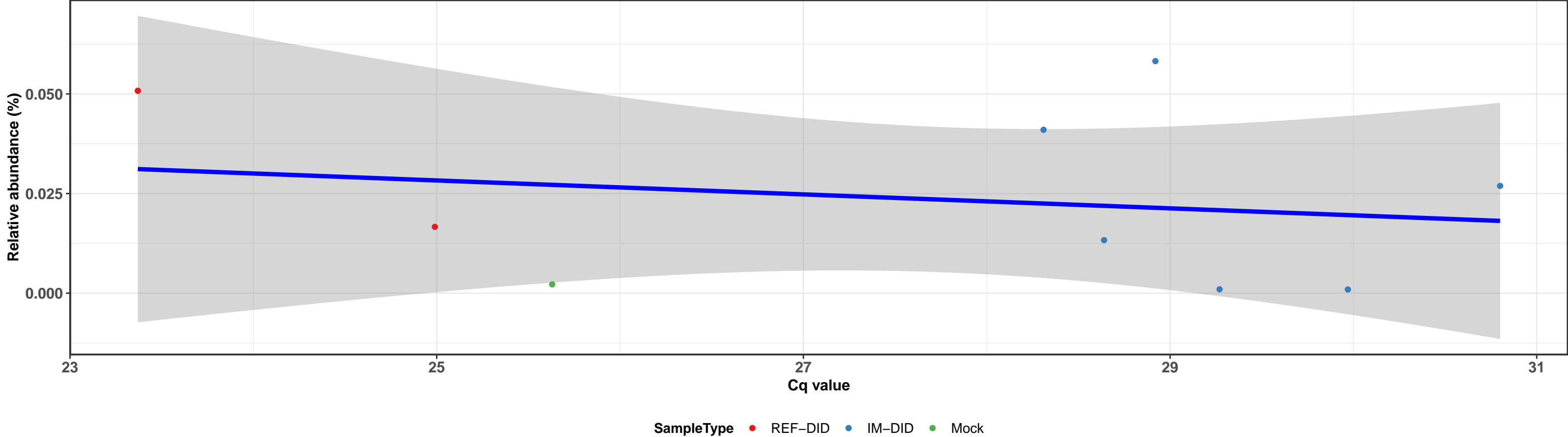
$\log_e(S) = 3.829$, $p = 0.004$, $\hat{\rho}_{\text{Spearman}} = 0.791$, $\text{CI}_{95\%} [0.402, 1.267]$, $n_{\text{pairs}} = 11$



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

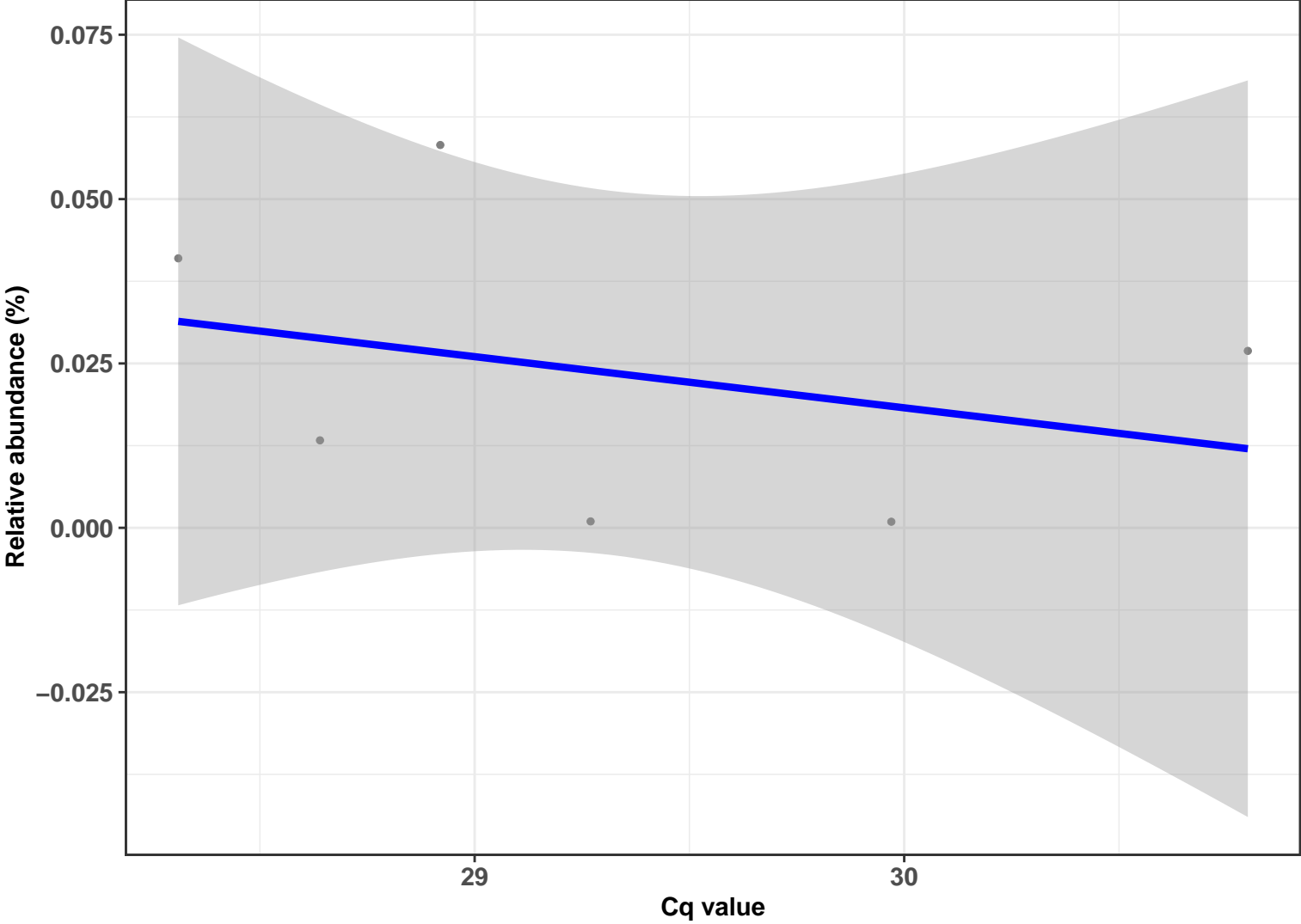
Correlation with all samples

$\log_e(S) = 5.075$, $p = 0.381$, $\hat{\rho}_{\text{Spearman}} = -0.333$, $\text{CI}_{95\%} [-1.129, 0.421]$, $n_{\text{pairs}} = 9$

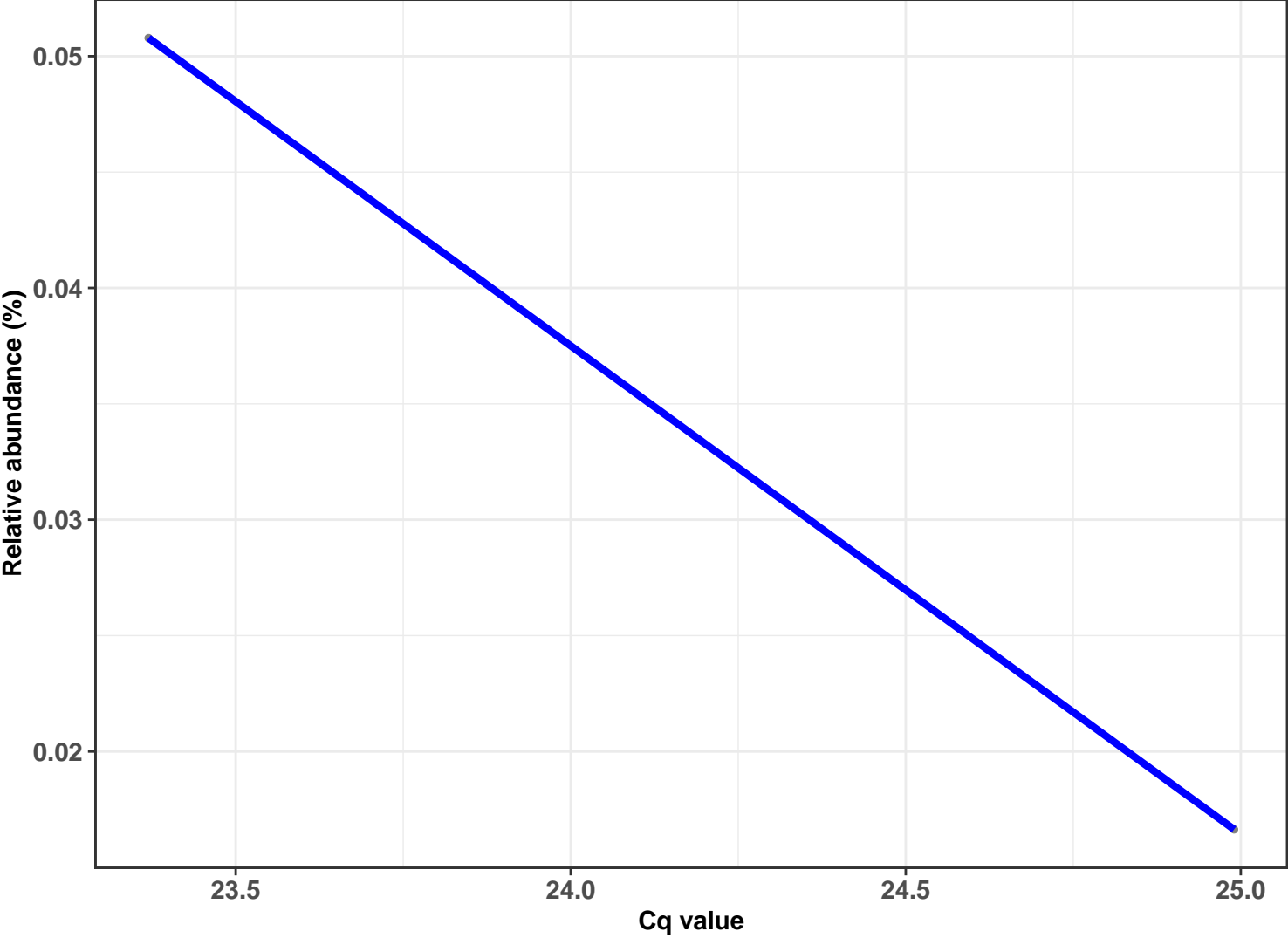


Correlation within: IM-DID

$\log_e(S) = 3.912$, $p = 0.397$, $\hat{\rho}_{\text{Spearman}} = -0.429$, $\text{CI}_{95\%} [-1.229, 0.401]$, $n_{\text{pairs}} = 6$

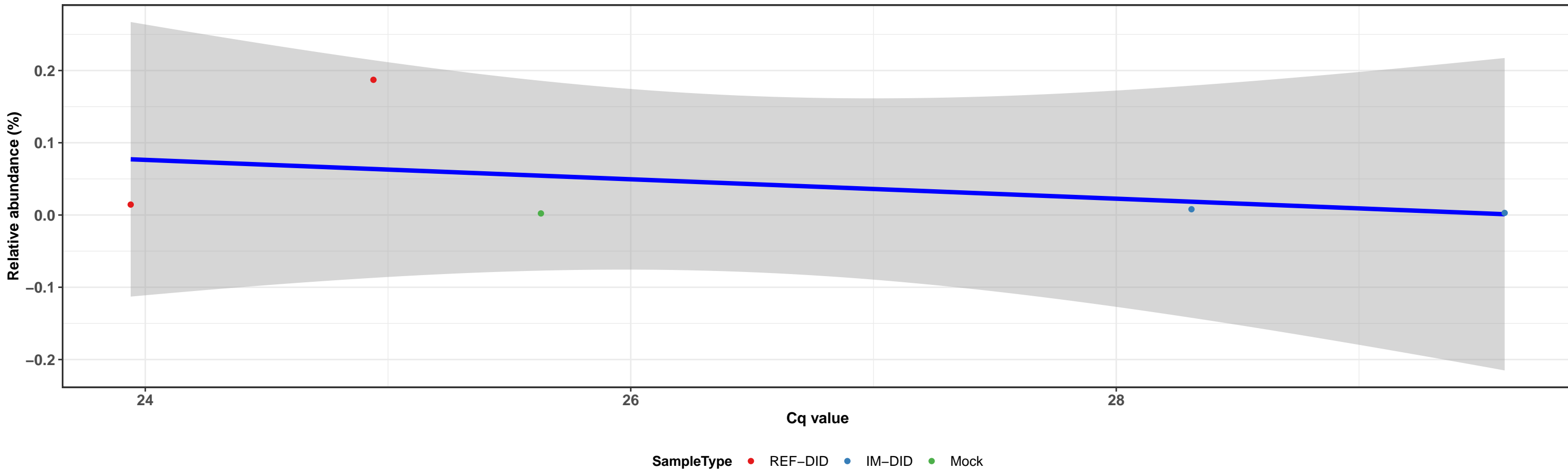


Correlation within: REF-DID

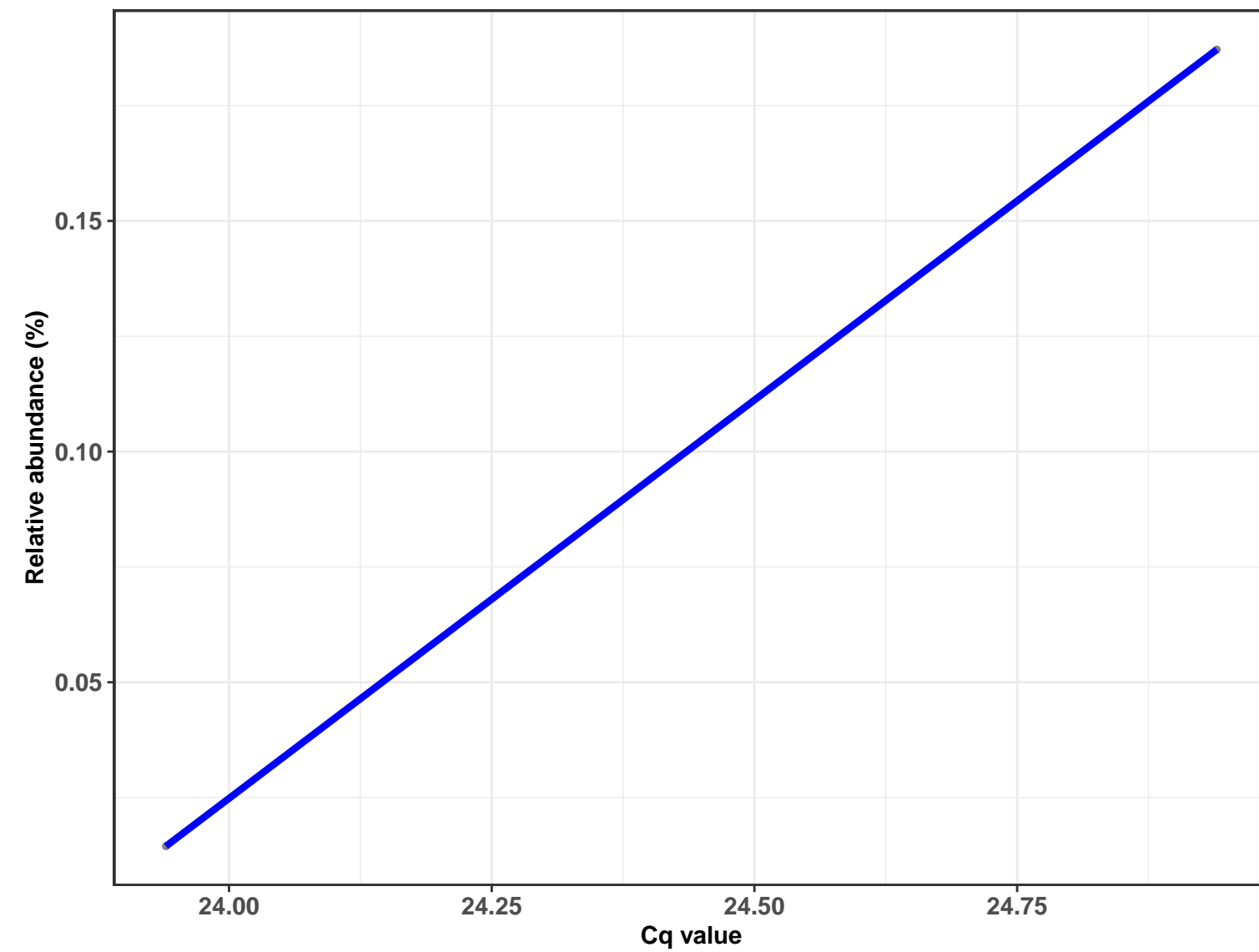


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

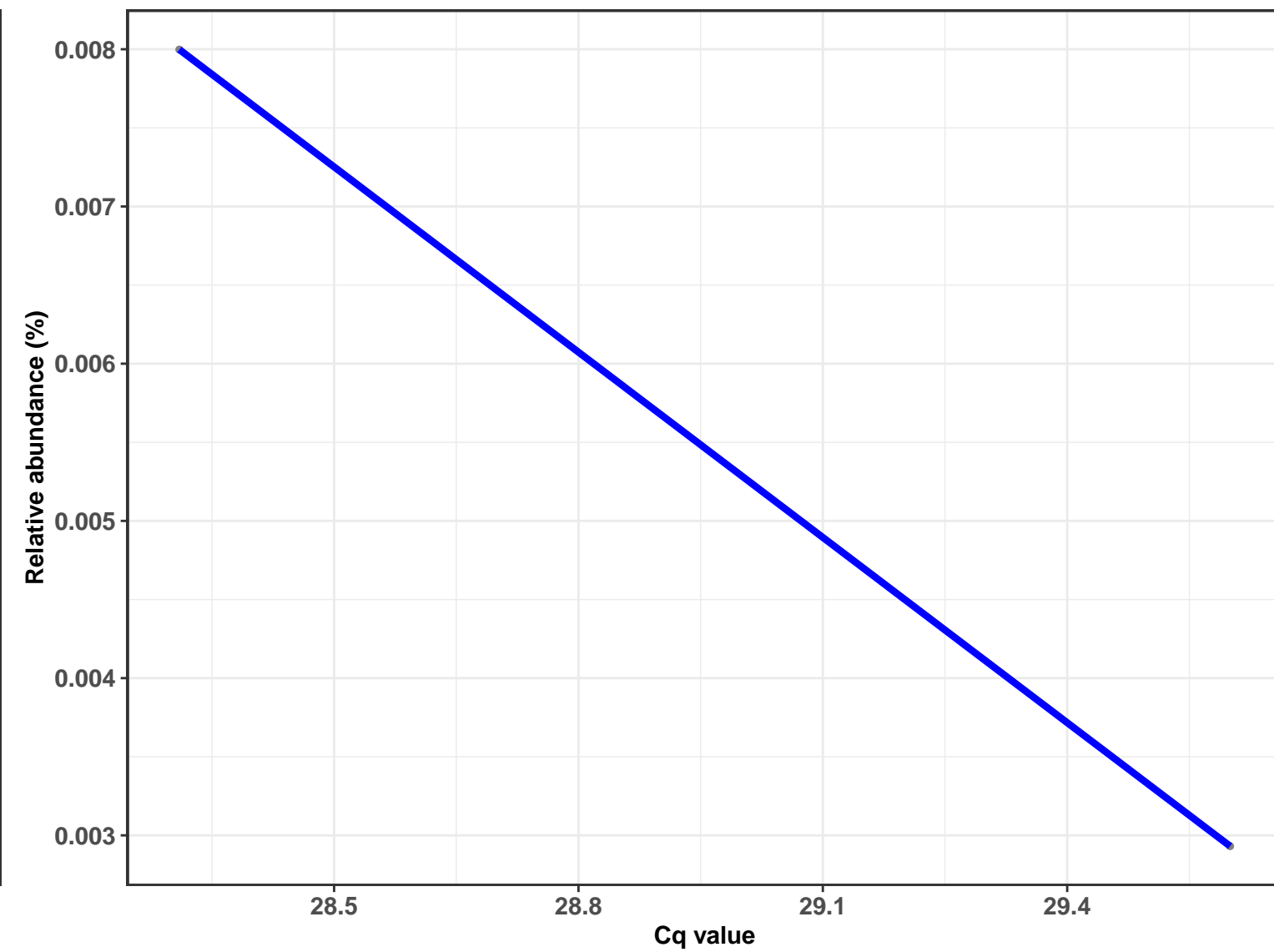
Correlation with all samples



Correlation within: REF-DID



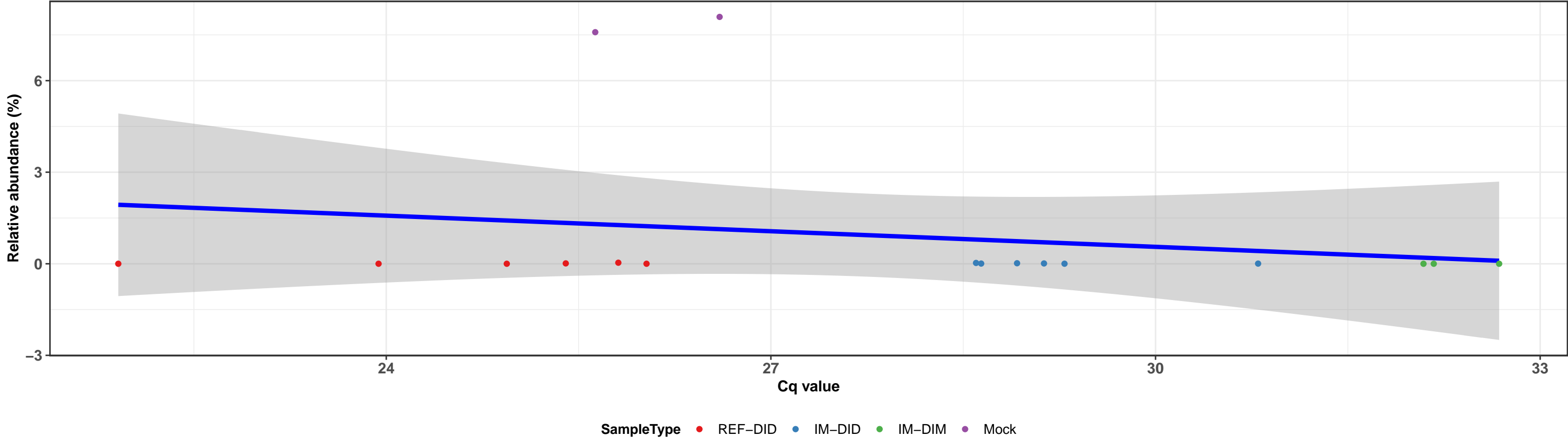
Correlation within: IM-DID



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

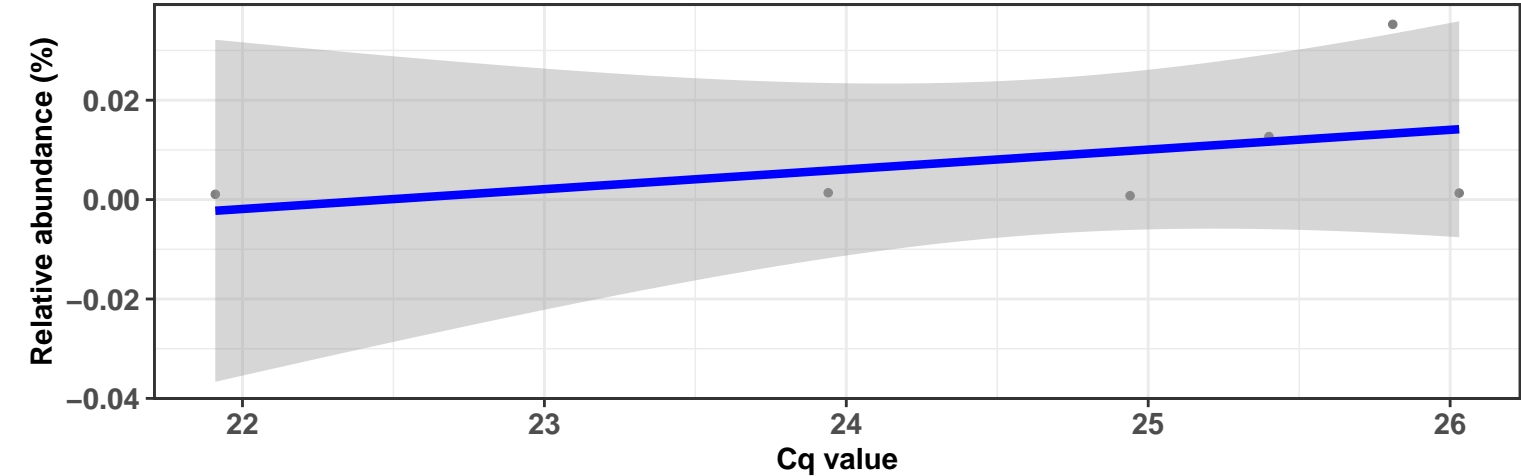
Correlation with all samples

$\log_e(S) = 6.914$, $p = 0.368$, $\hat{\rho}_{\text{Spearman}} = -0.233$, $\text{CI}_{95\%} [-0.874, 0.387]$, $n_{\text{pairs}} = 17$



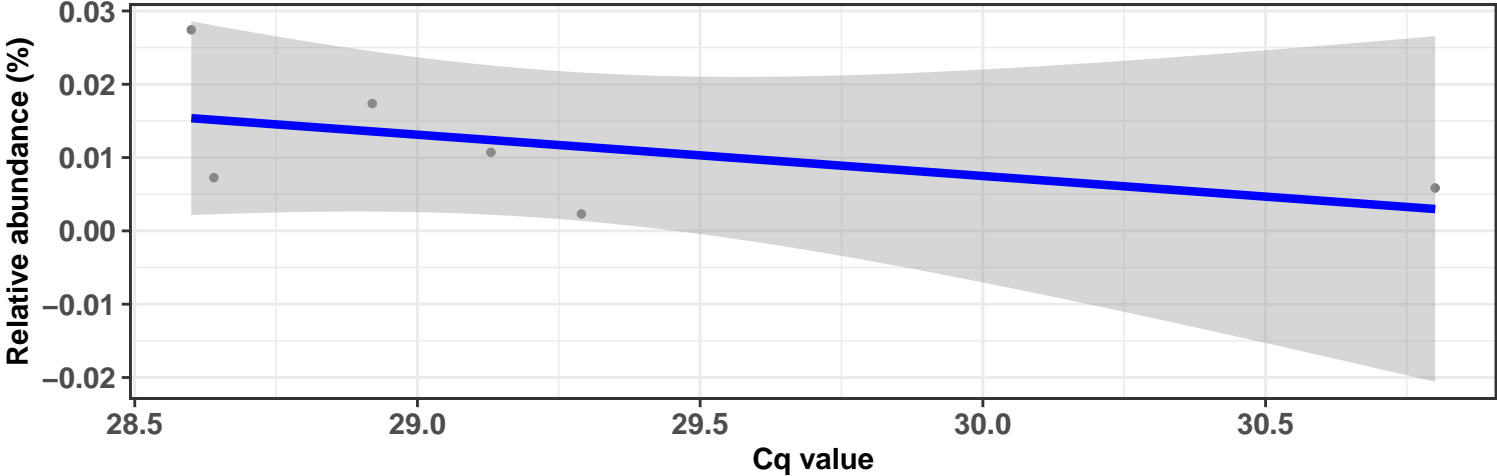
Correlation within: REF-DID

$\log_e(S) = 2.996$, $p = 0.397$, $\hat{\rho}_{\text{Spearman}} = 0.429$, $\text{CI}_{95\%} [-0.439, 1.347]$, $n_{\text{pairs}} = 6$

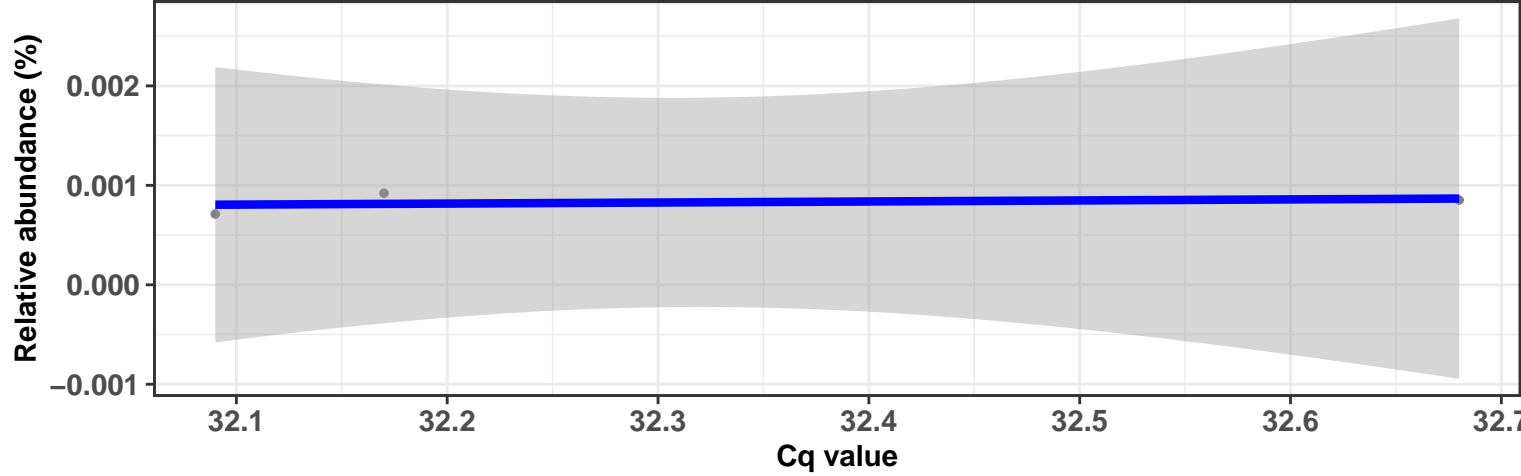


Correlation within: IM-DID

$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = -0.771$, $\text{CI}_{95\%} [-1.461, -0.219]$, $n_{\text{pairs}} = 6$



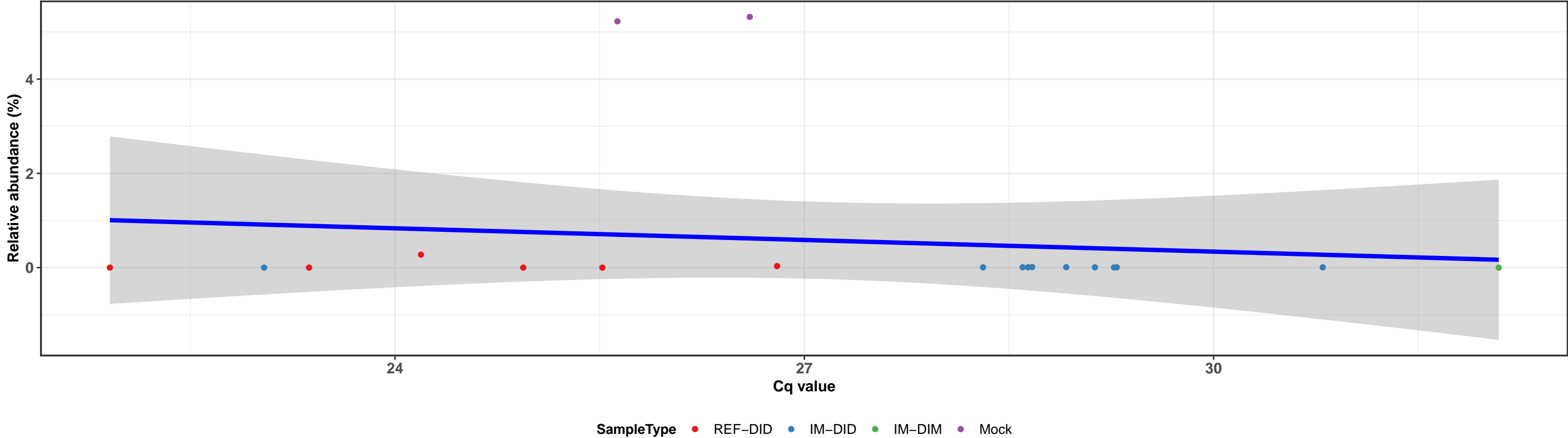
Correlation within: IM-DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

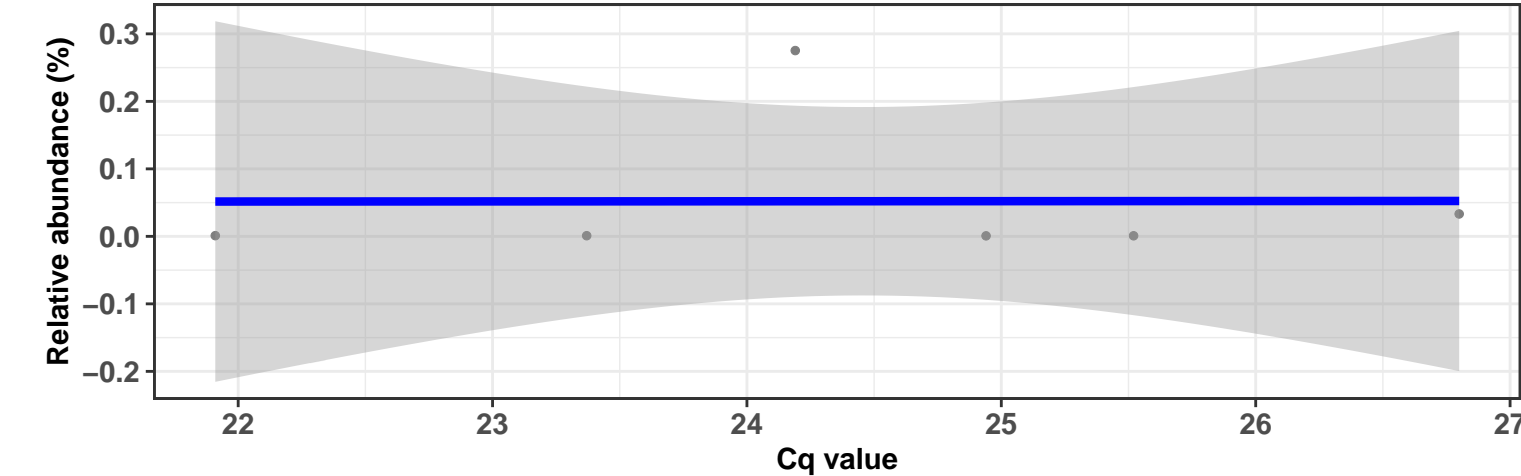
Correlation with all samples

$\log_e(S) = 6.968$, $p = 0.781$, $\hat{\rho}_{\text{Spearman}} = 0.068$, $CI_{95\%} [-0.454, 0.620]$, $n_{\text{pairs}} = 19$



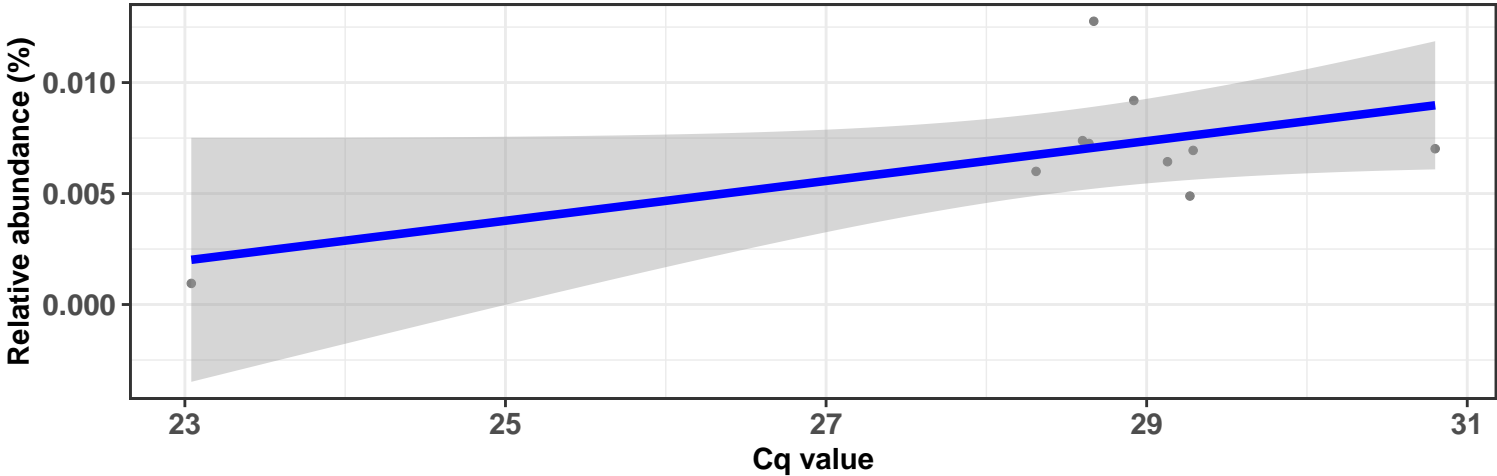
Correlation within: REF-DID

$\log_e(S) = 3.638$, $p = 0.872$, $\hat{\rho}_{\text{Spearman}} = -0.086$, $CI_{95\%} [-1.085, 0.888]$, $n_{\text{pairs}} = 6$

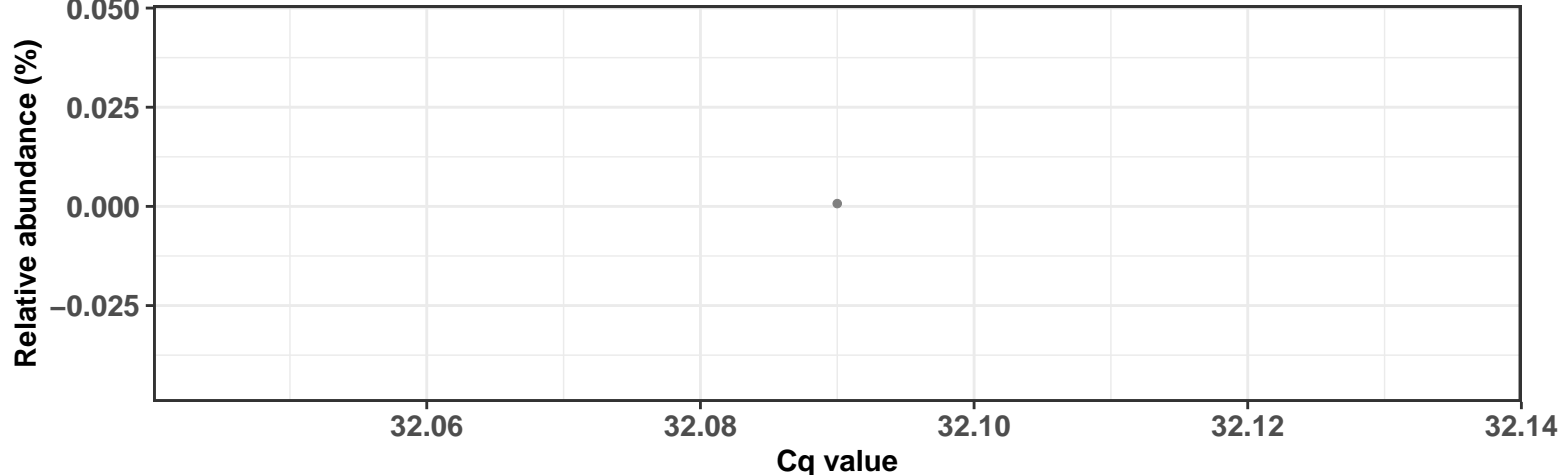


Correlation within: IM-DID

$\log_e(S) = 4.984$, $p = 0.751$, $\hat{\rho}_{\text{Spearman}} = 0.115$, $CI_{95\%} [-0.634, 0.797]$, $n_{\text{pairs}} = 10$



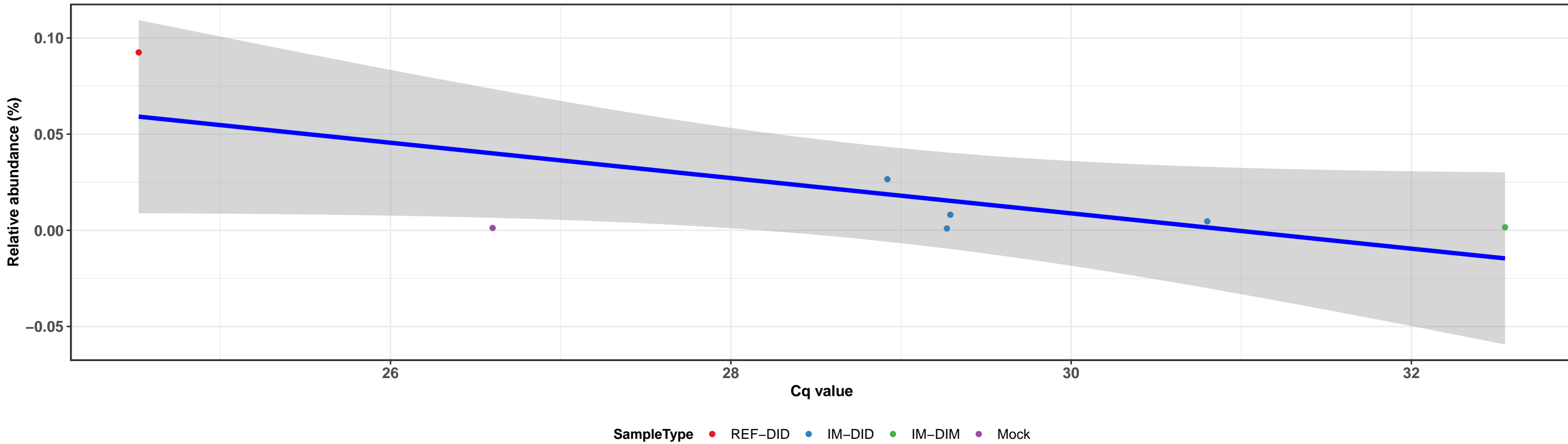
Correlation within: IM-DIM



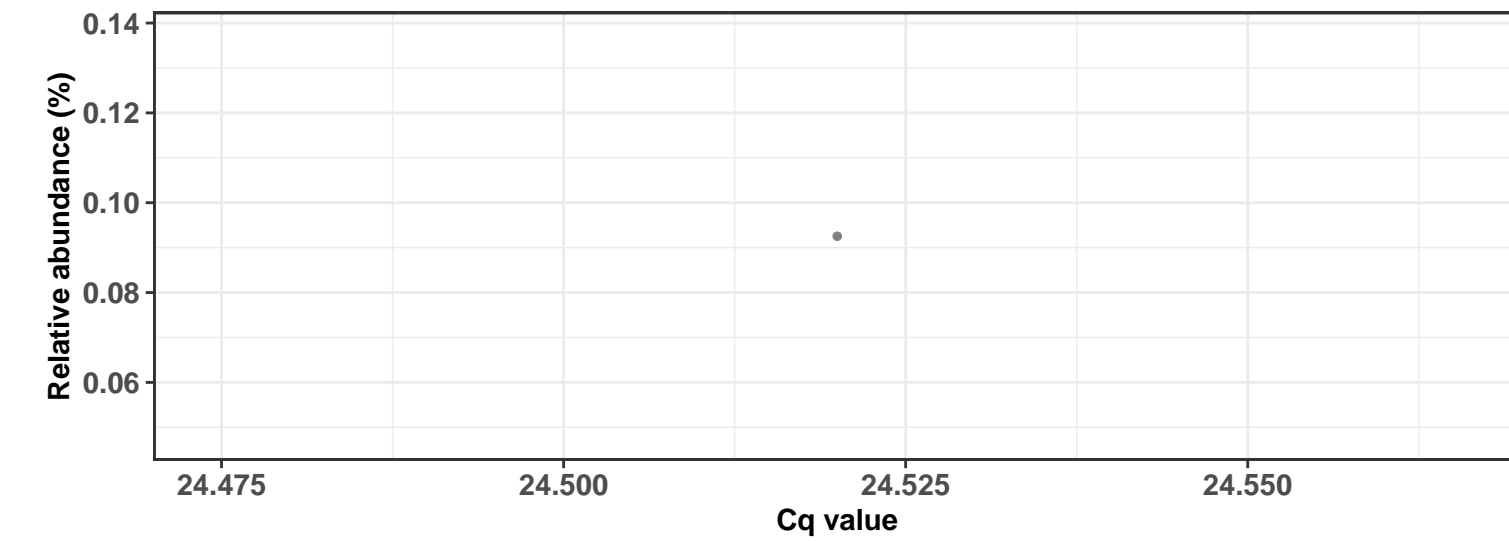
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

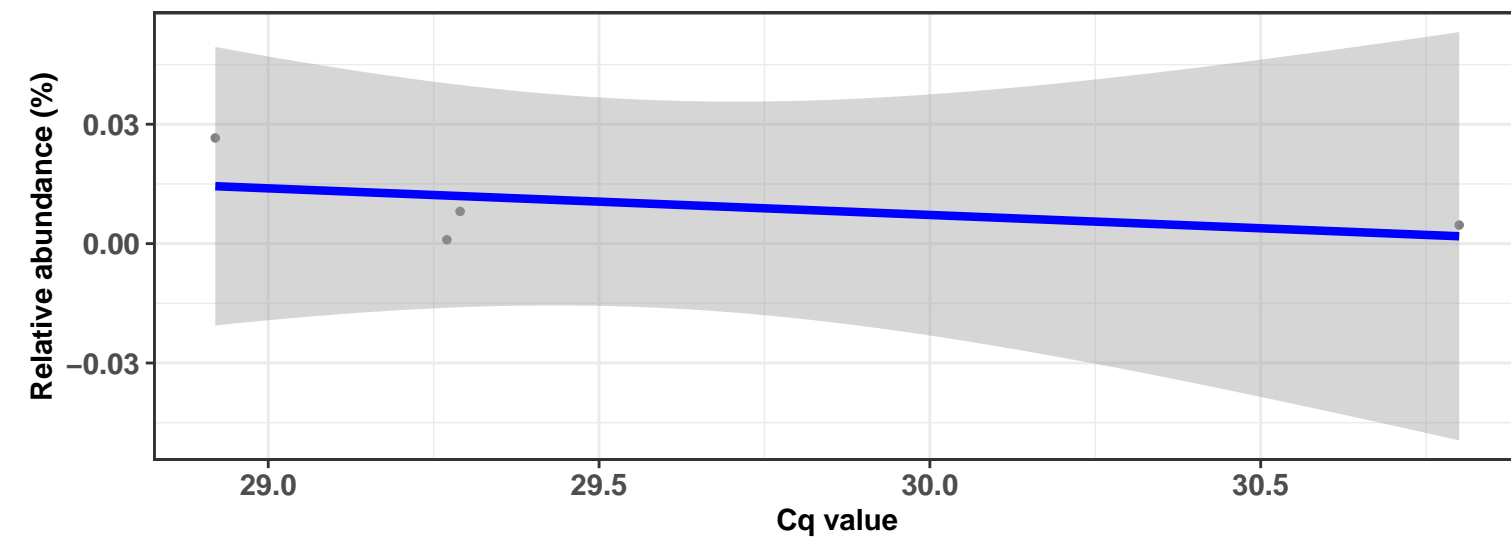
$\log_e(S) = 4.304$, $p = 0.482$, $\hat{\rho}_{\text{Spearman}} = -0.321$, $\text{CI}_{95\%} [-1.323, 0.593]$, $n_{\text{pairs}} = 7$



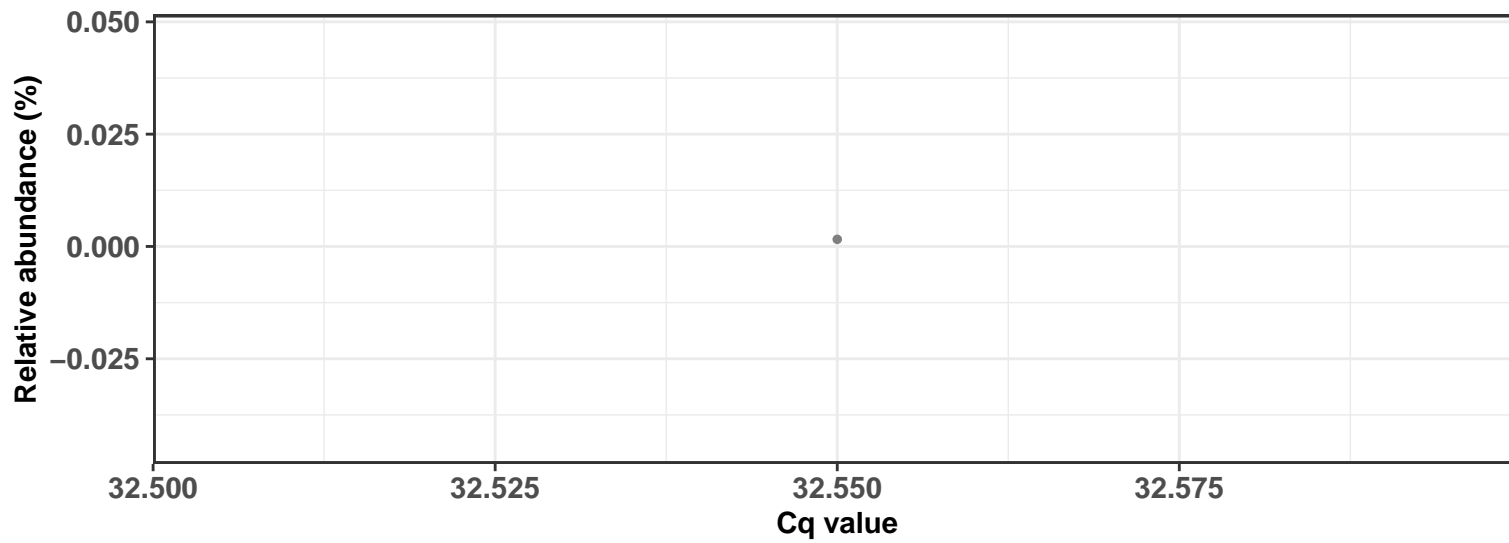
Correlation within: REF-DID



Correlation within: IM-DID

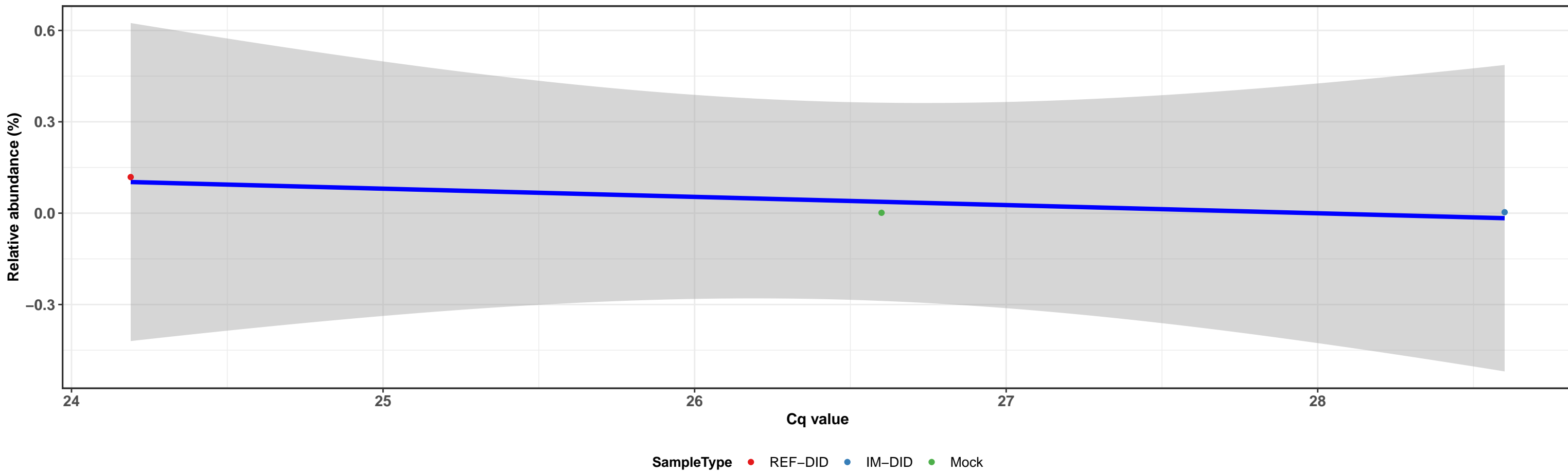


Correlation within: IM-DIM

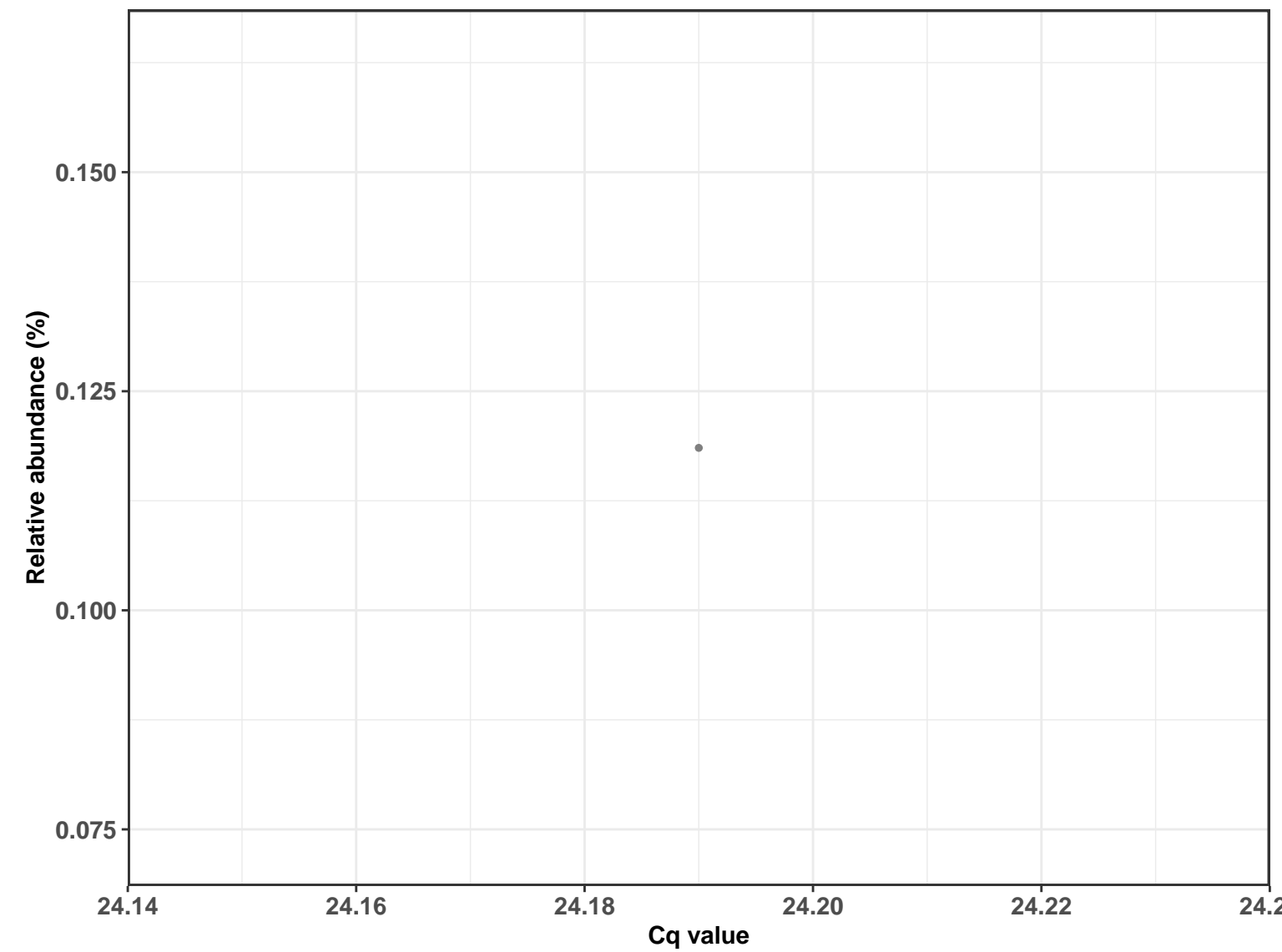


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

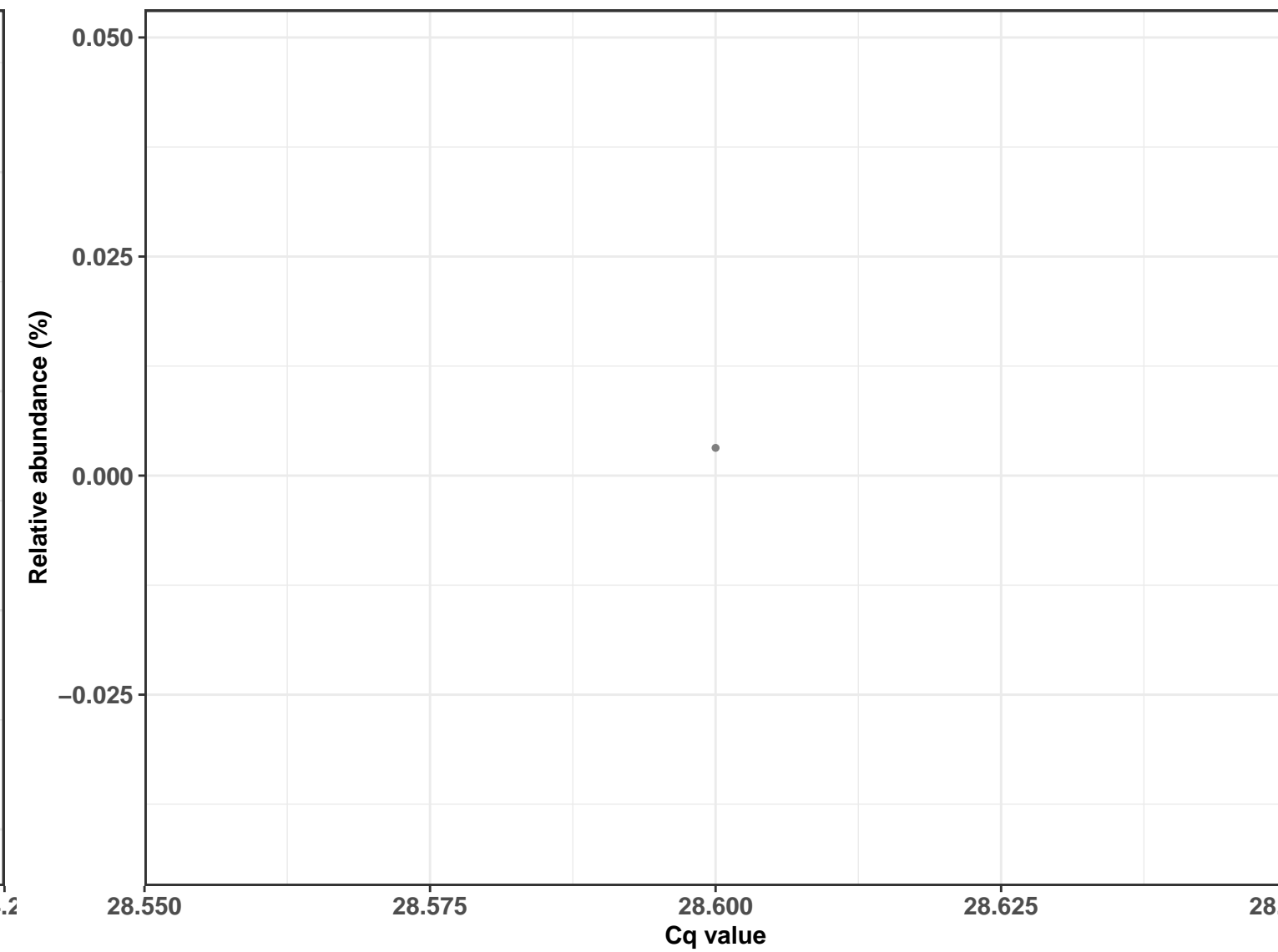
Correlation with all samples



Correlation within: REF-DID

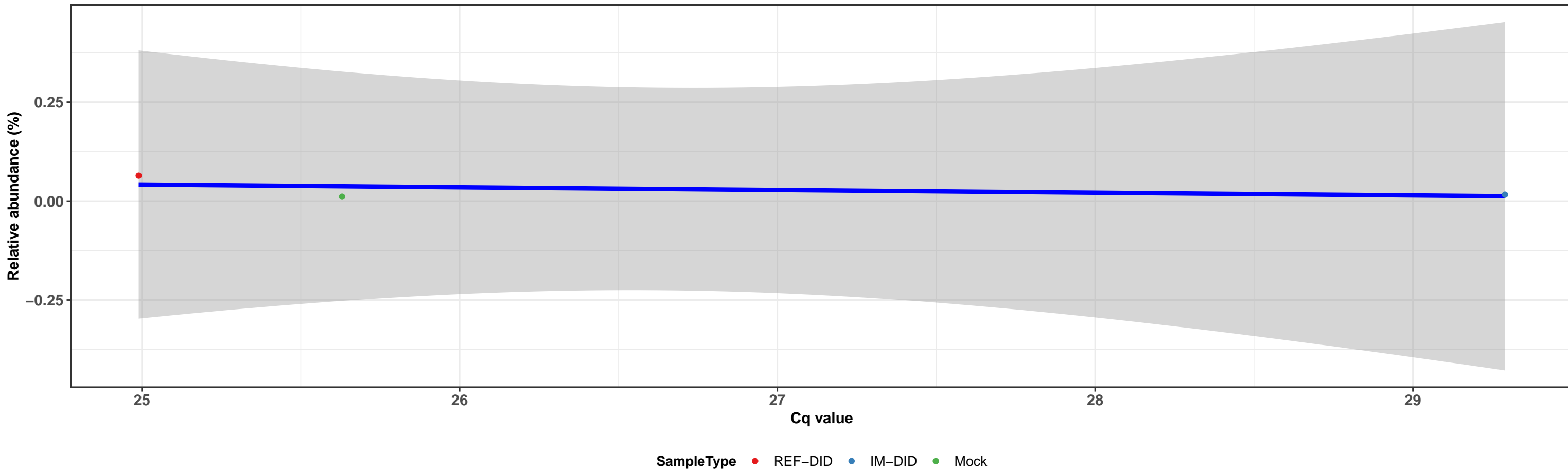


Correlation within: IM-DID

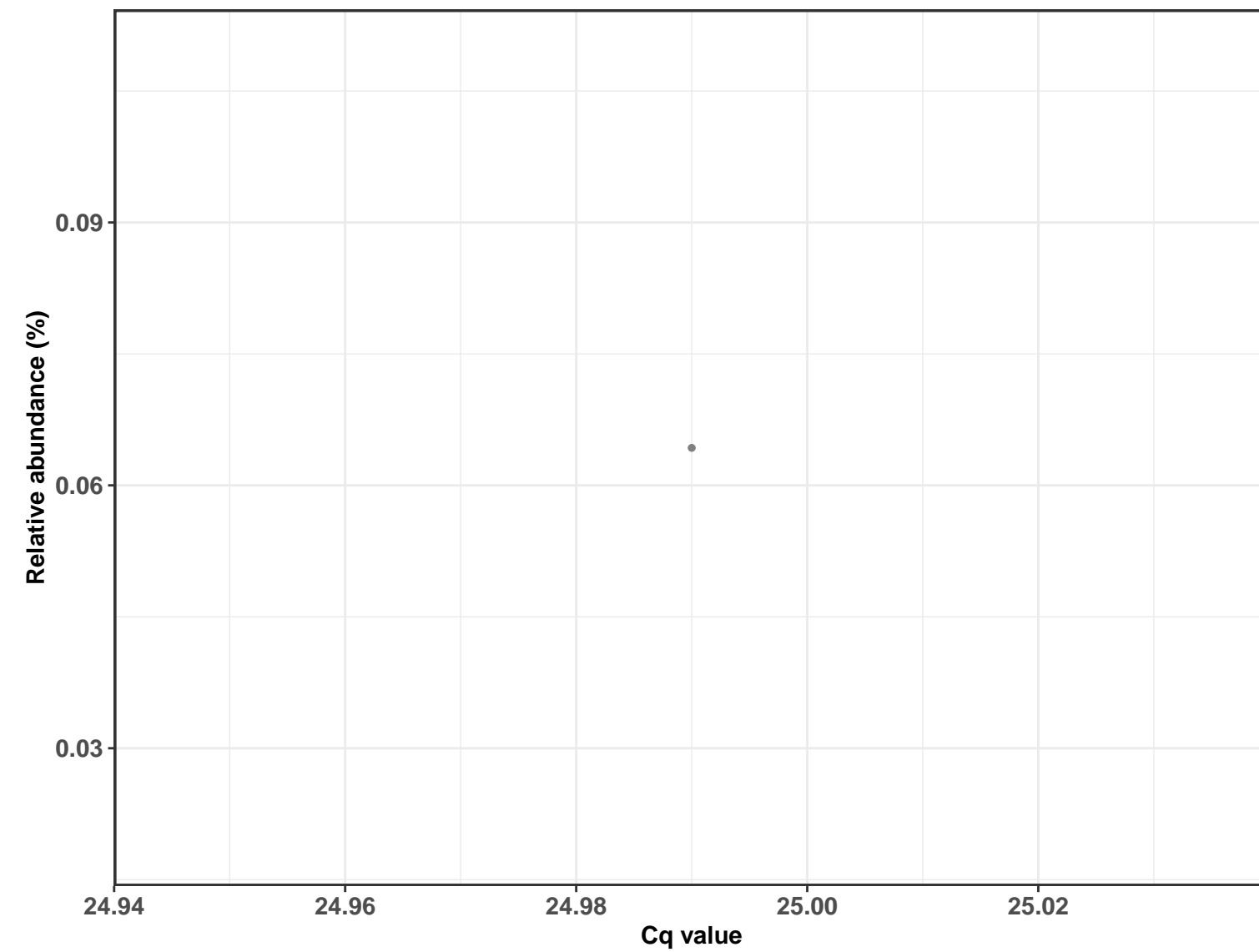


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

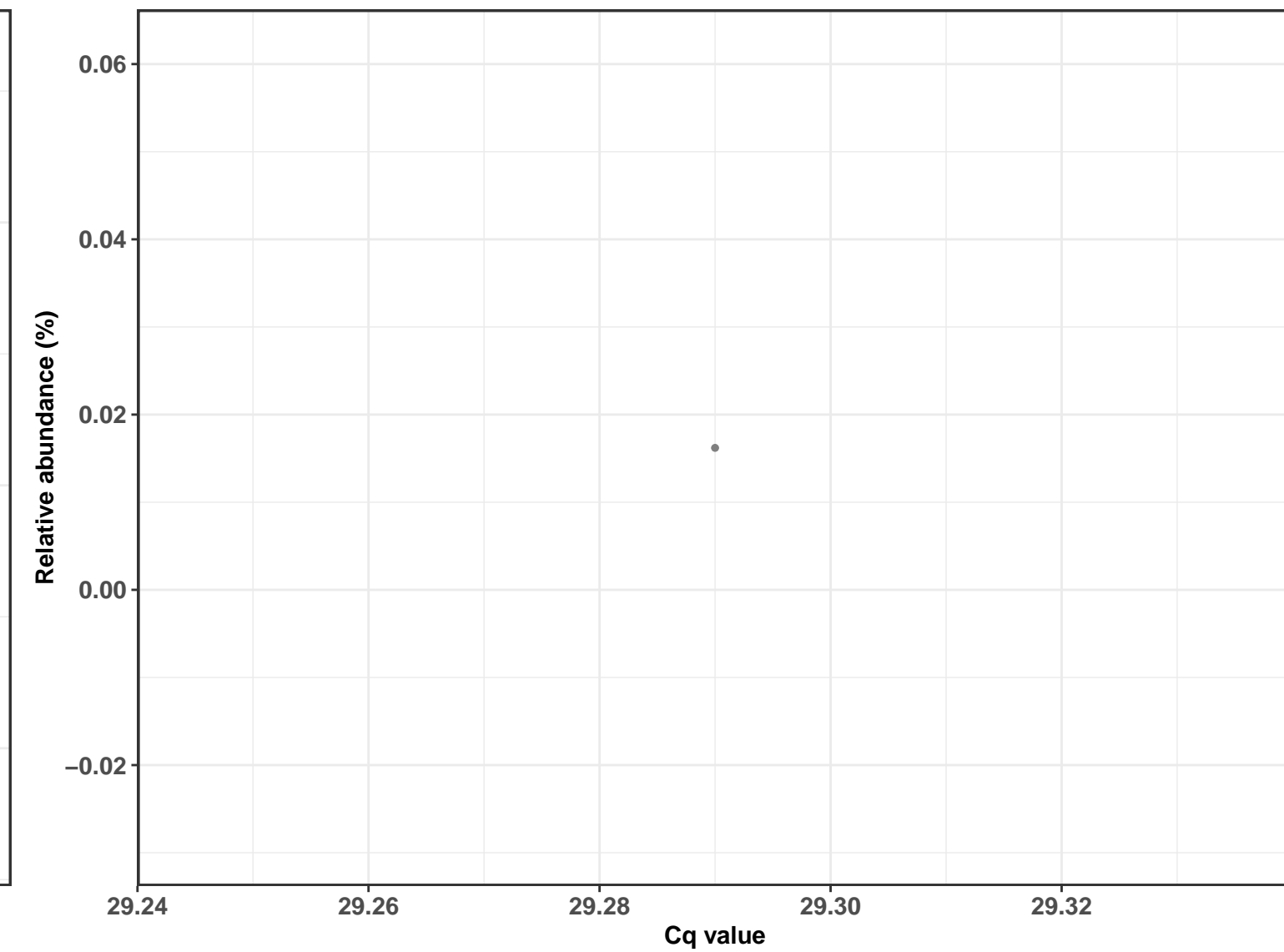
Correlation with all samples



Correlation within: REF-DID

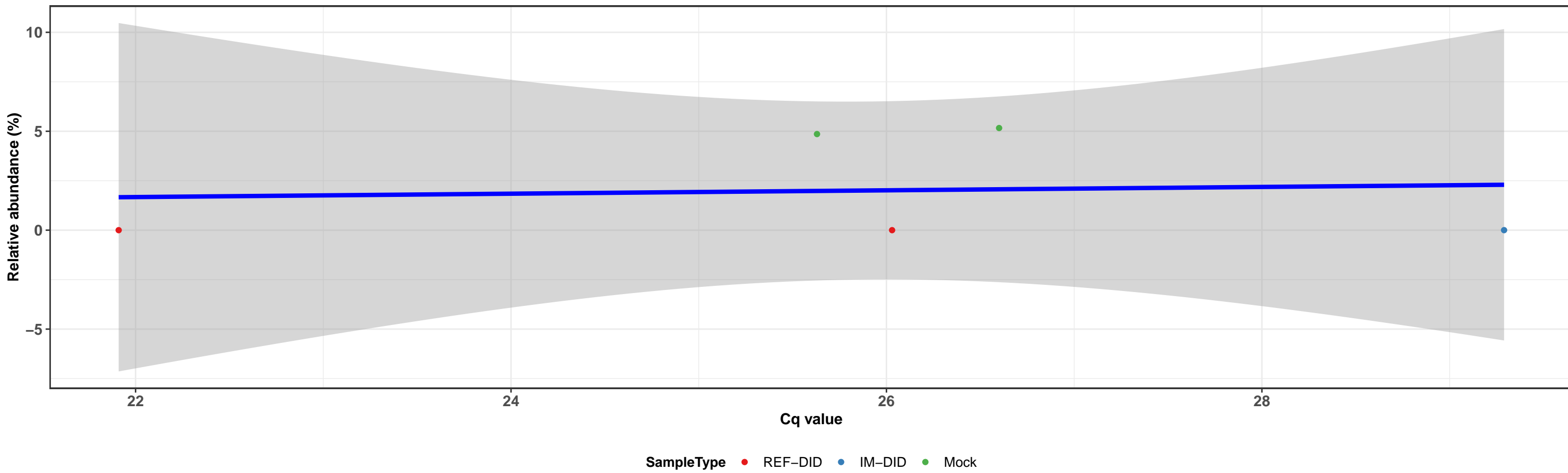


Correlation within: IM-DID

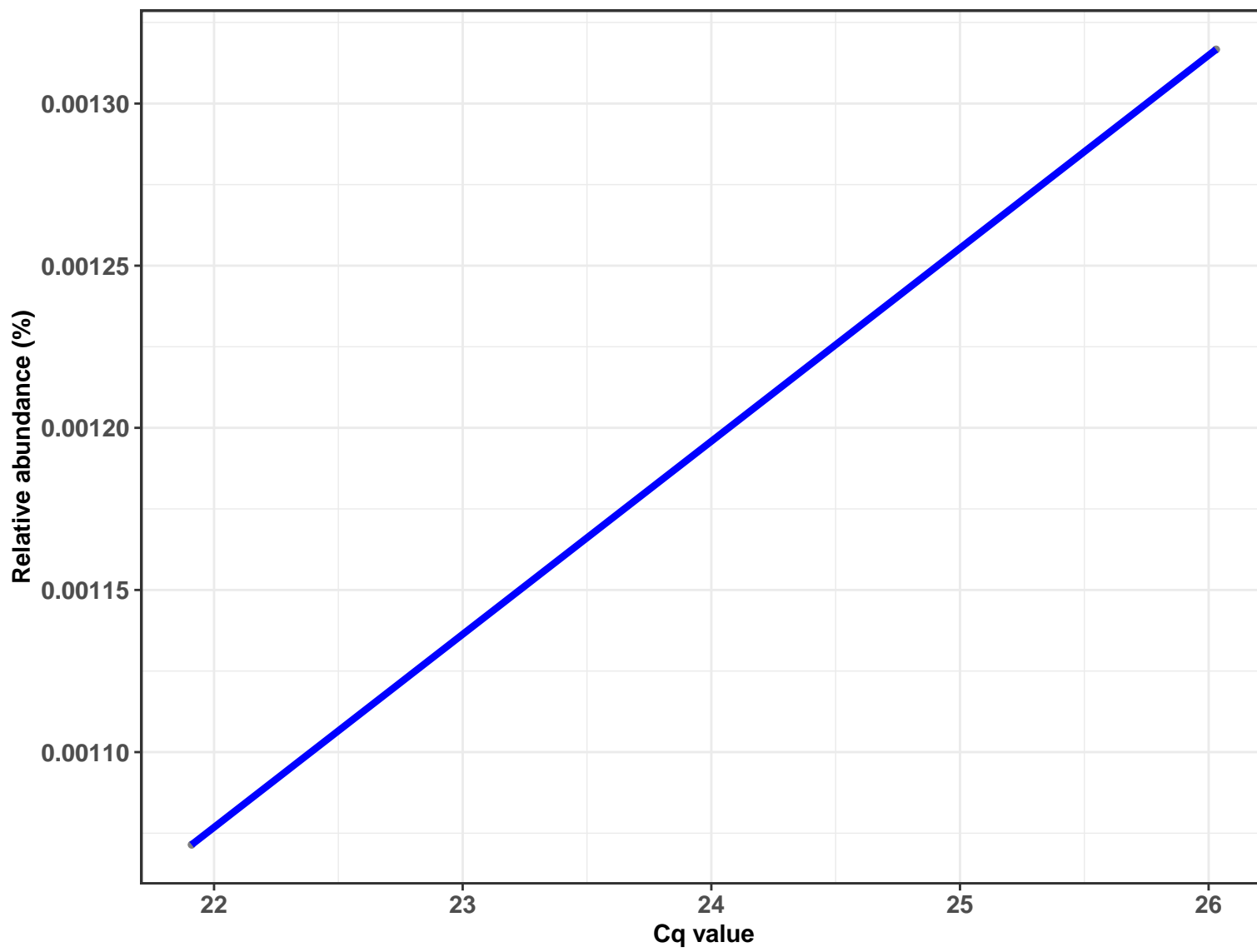


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

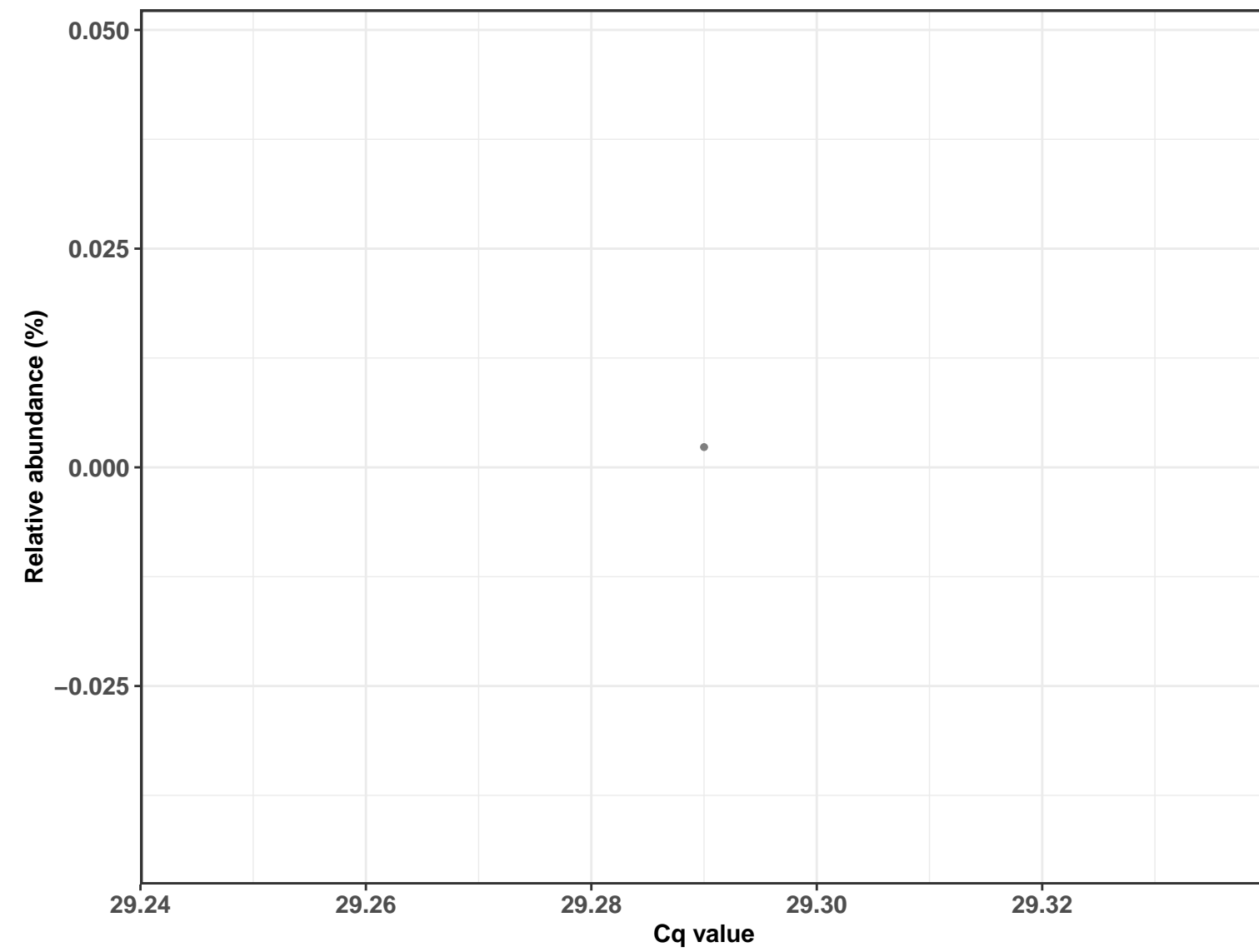
Correlation with all samples



Correlation within: REF-DID

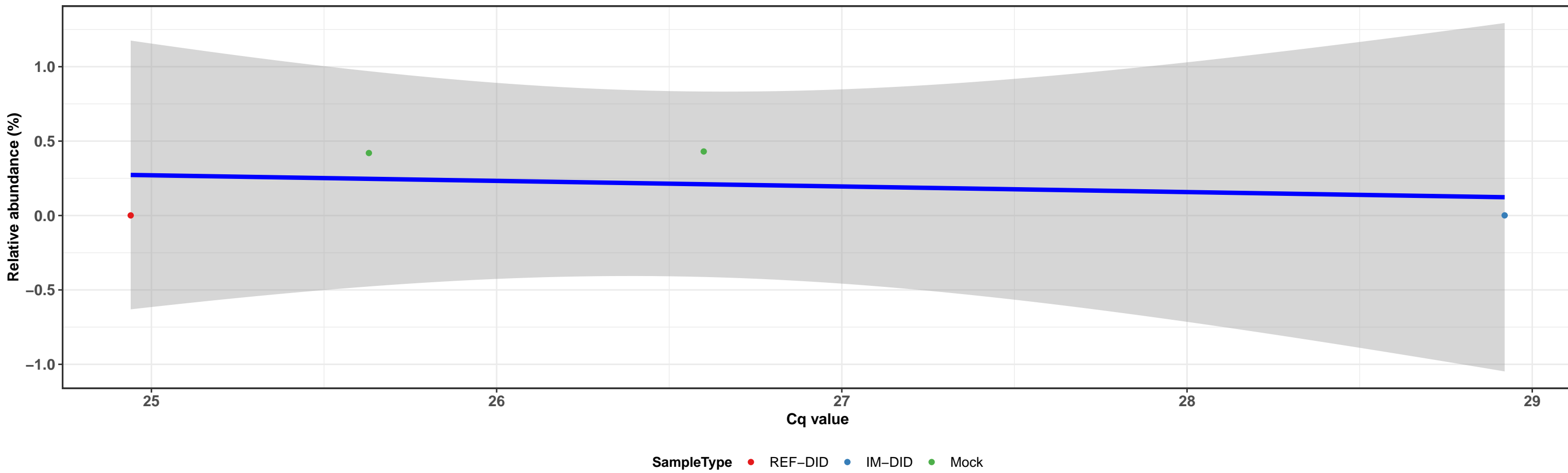


Correlation within: IM-DID

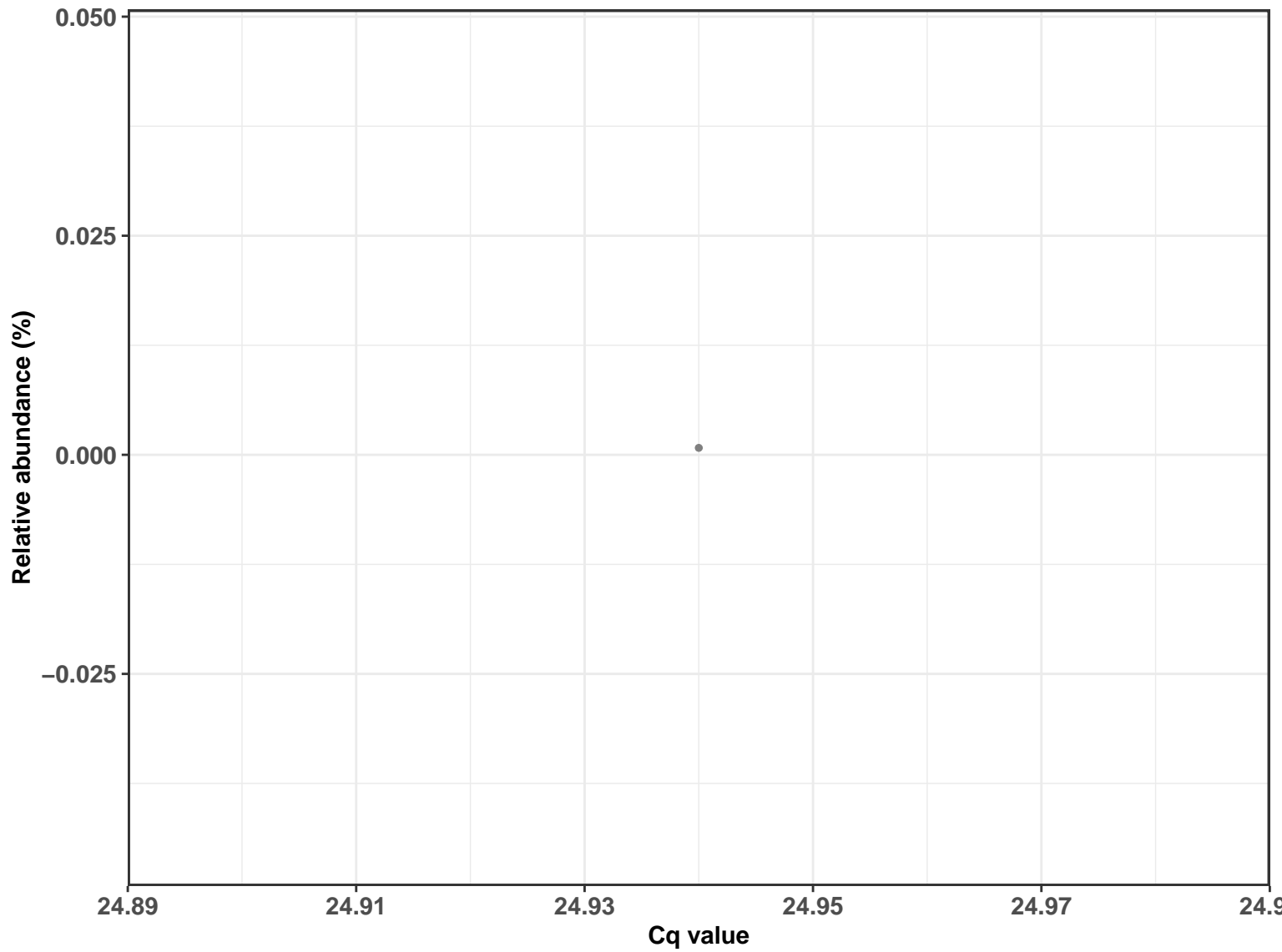


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

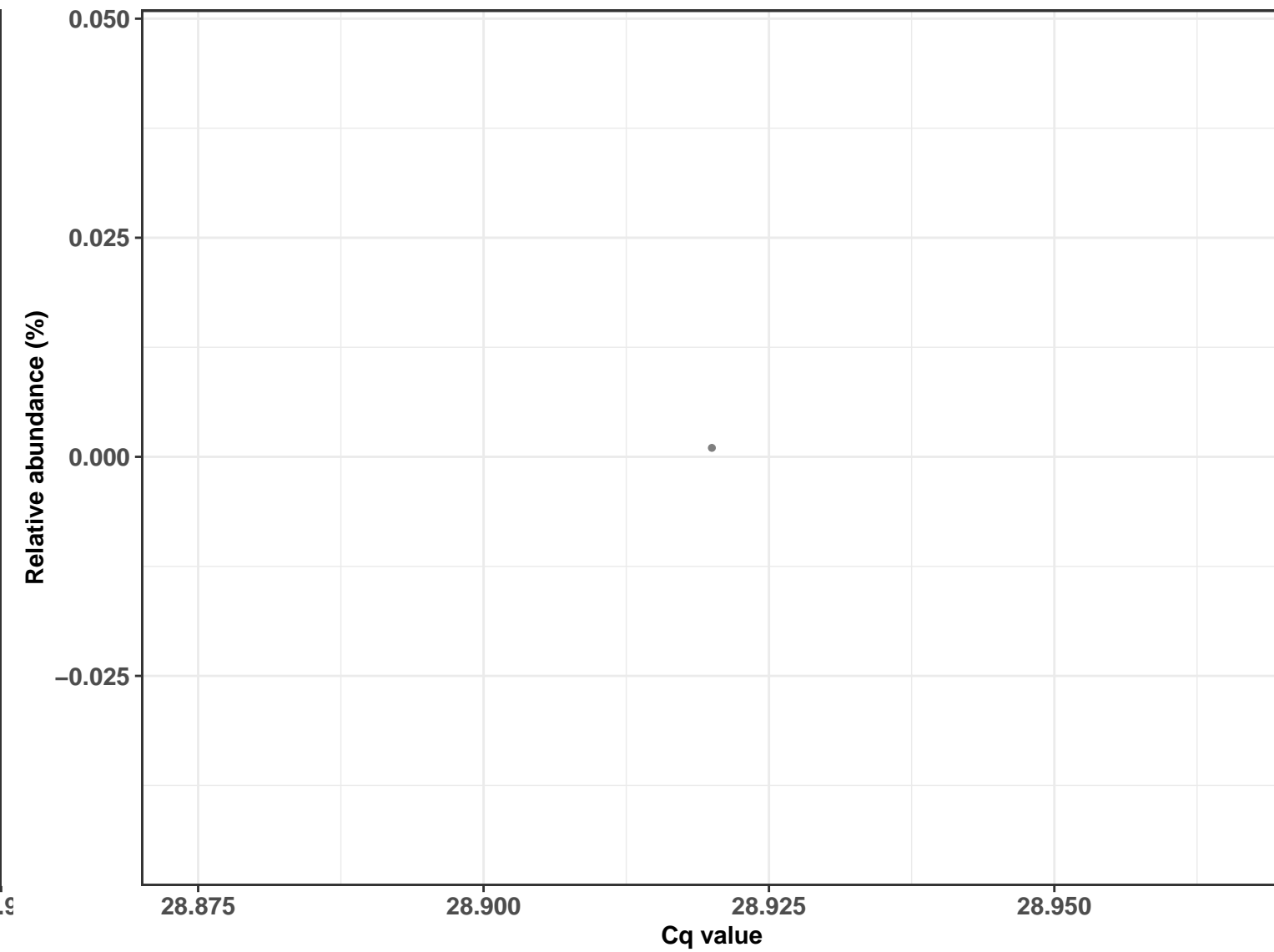
Correlation with all samples



Correlation within: REF-DID



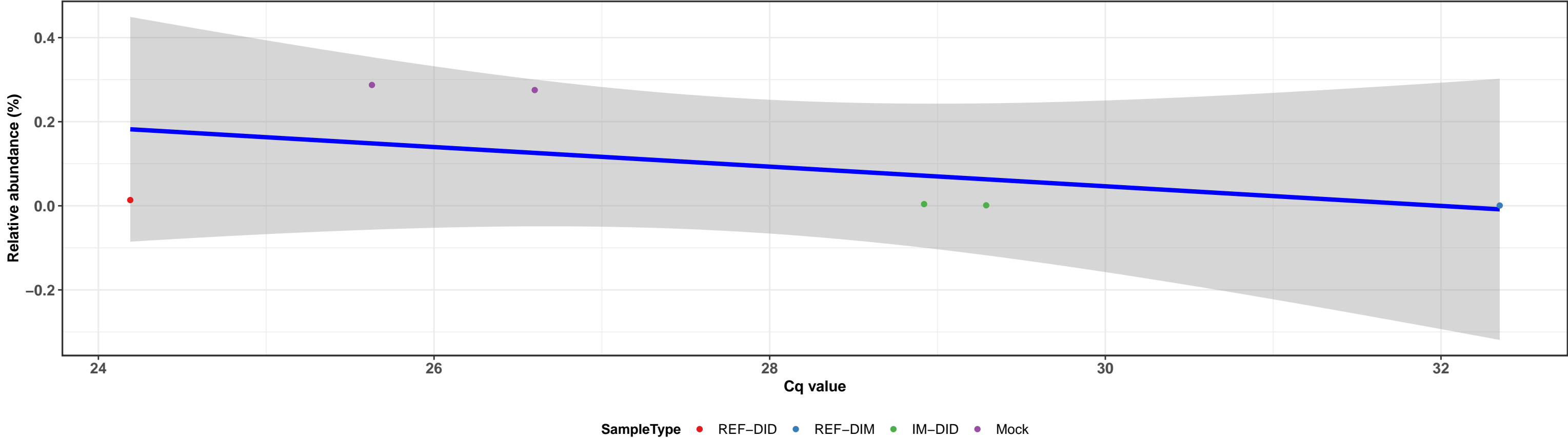
Correlation within: IM-DID



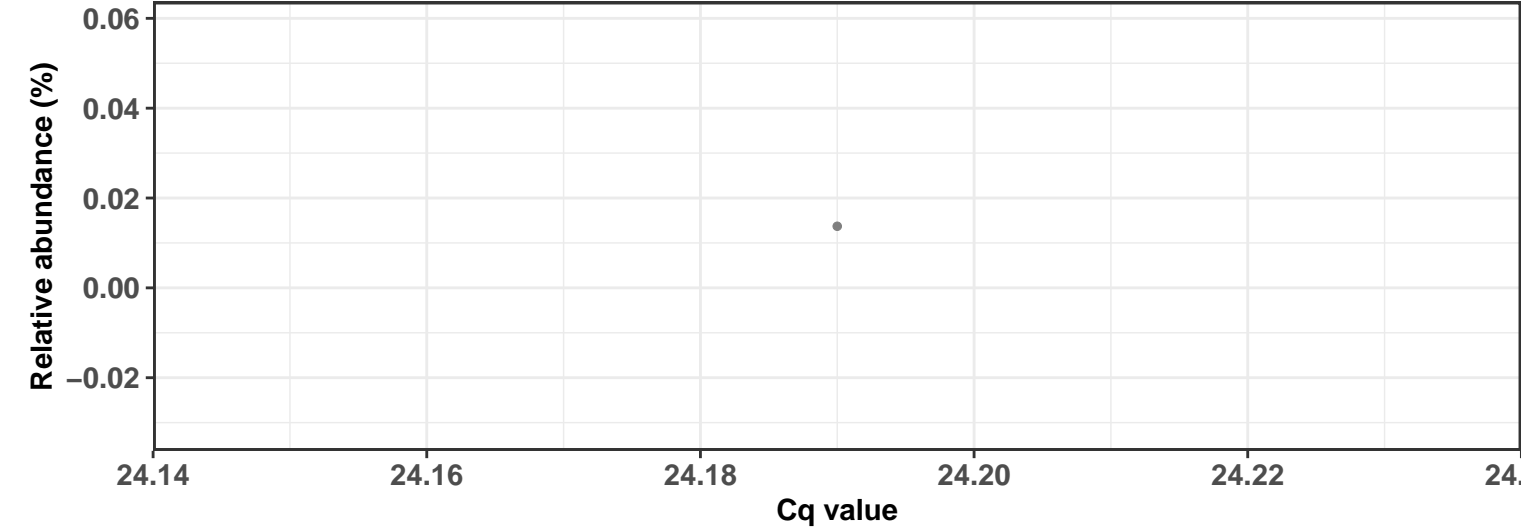
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

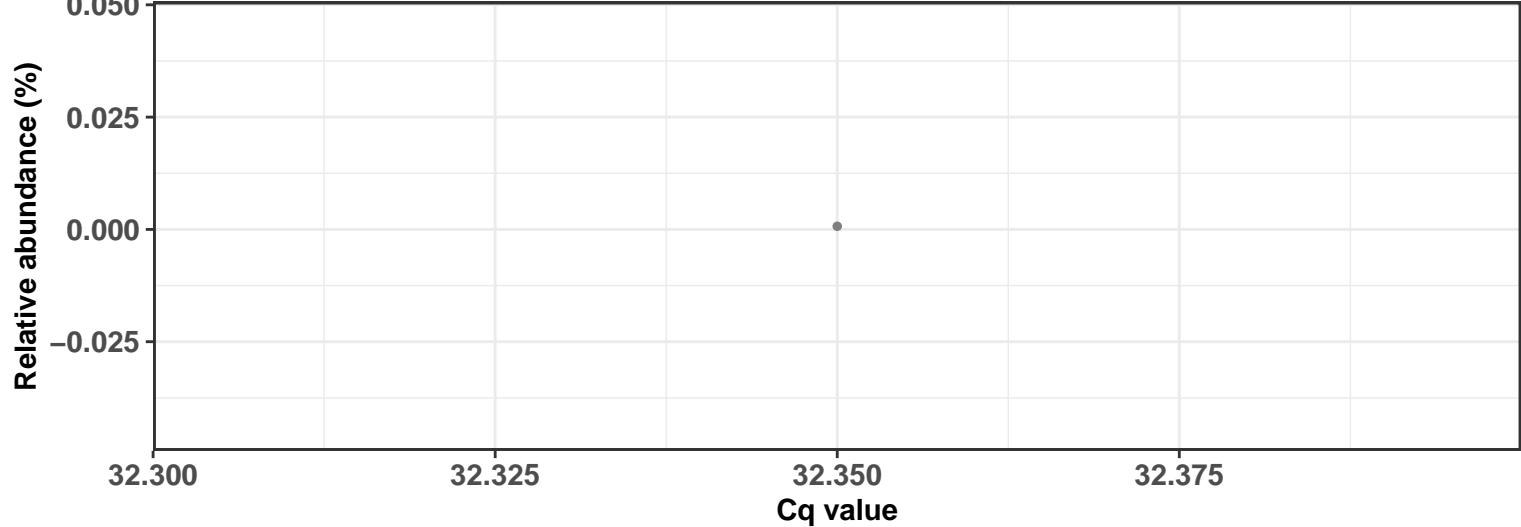
$\log_e(S) = 4.159$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = -0.829$, $\text{CI}_{95\%} [-1.523, -0.284]$, $n_{\text{pairs}} = 6$



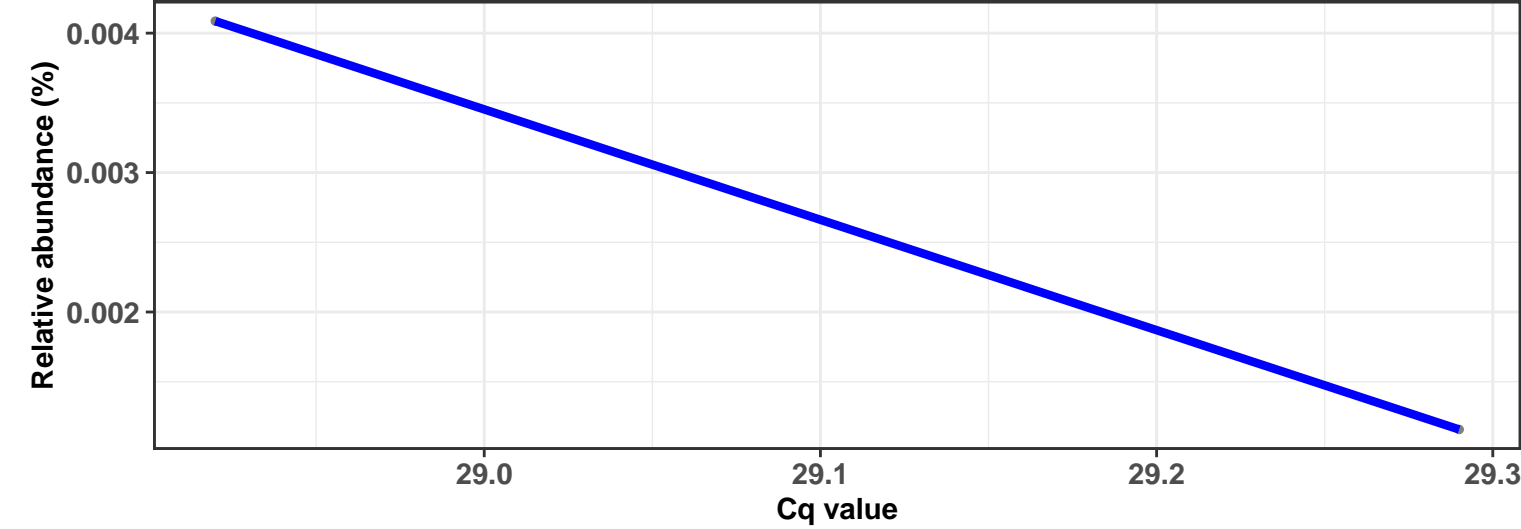
Correlation within: REF-DID



Correlation within: REF-DIM



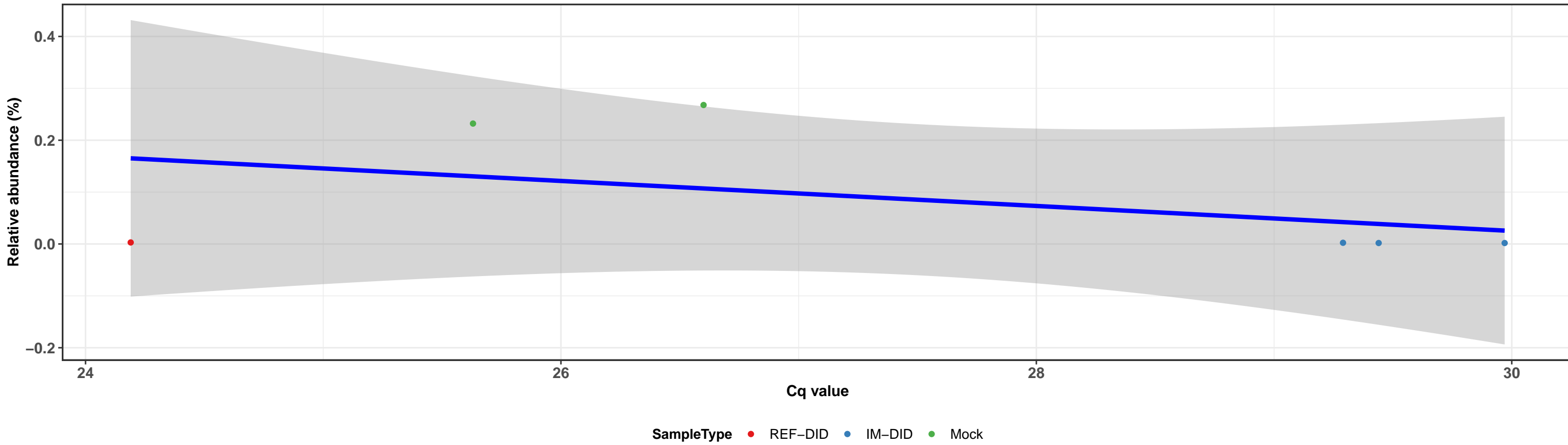
Correlation within: IM-DID



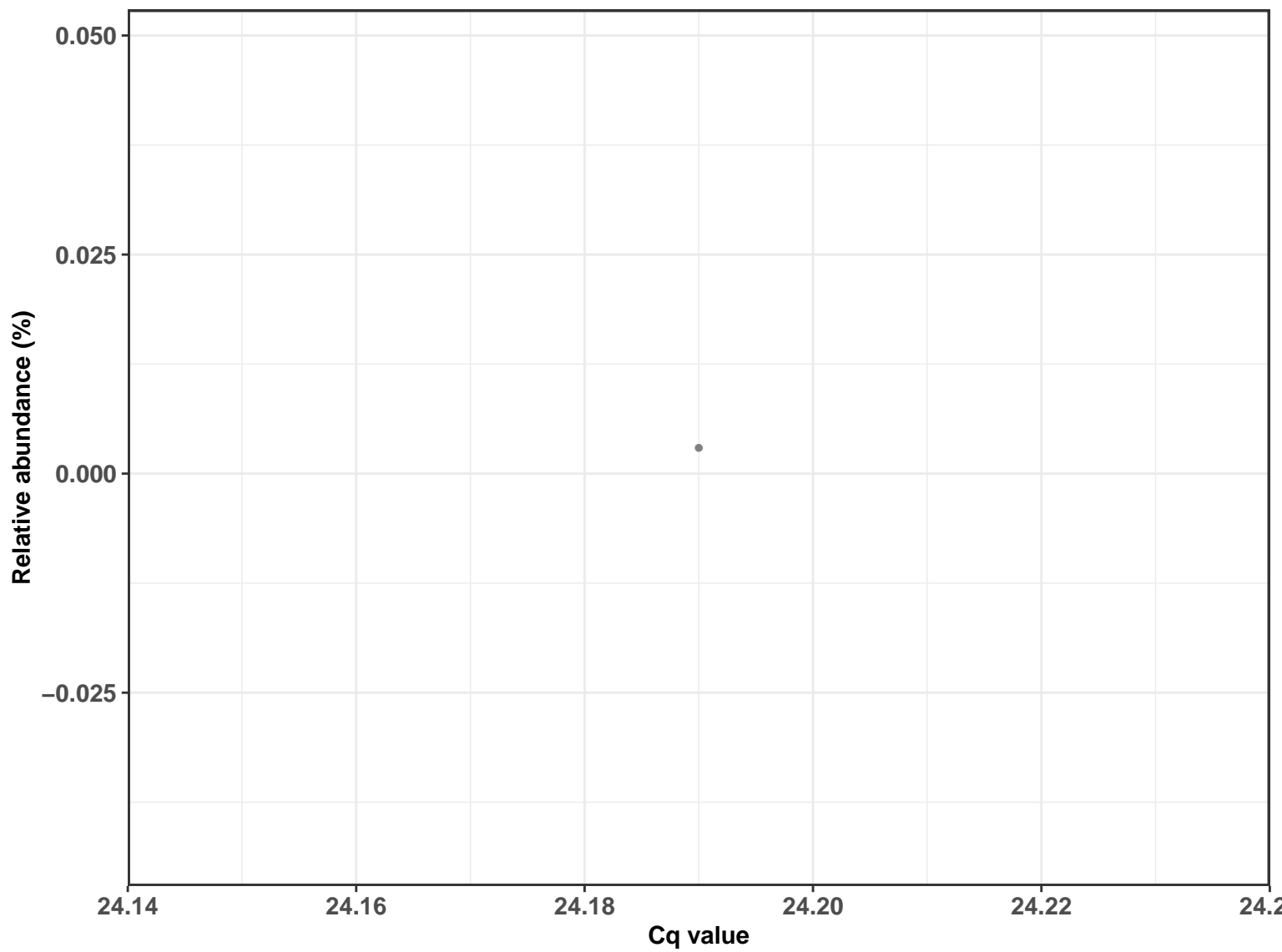
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

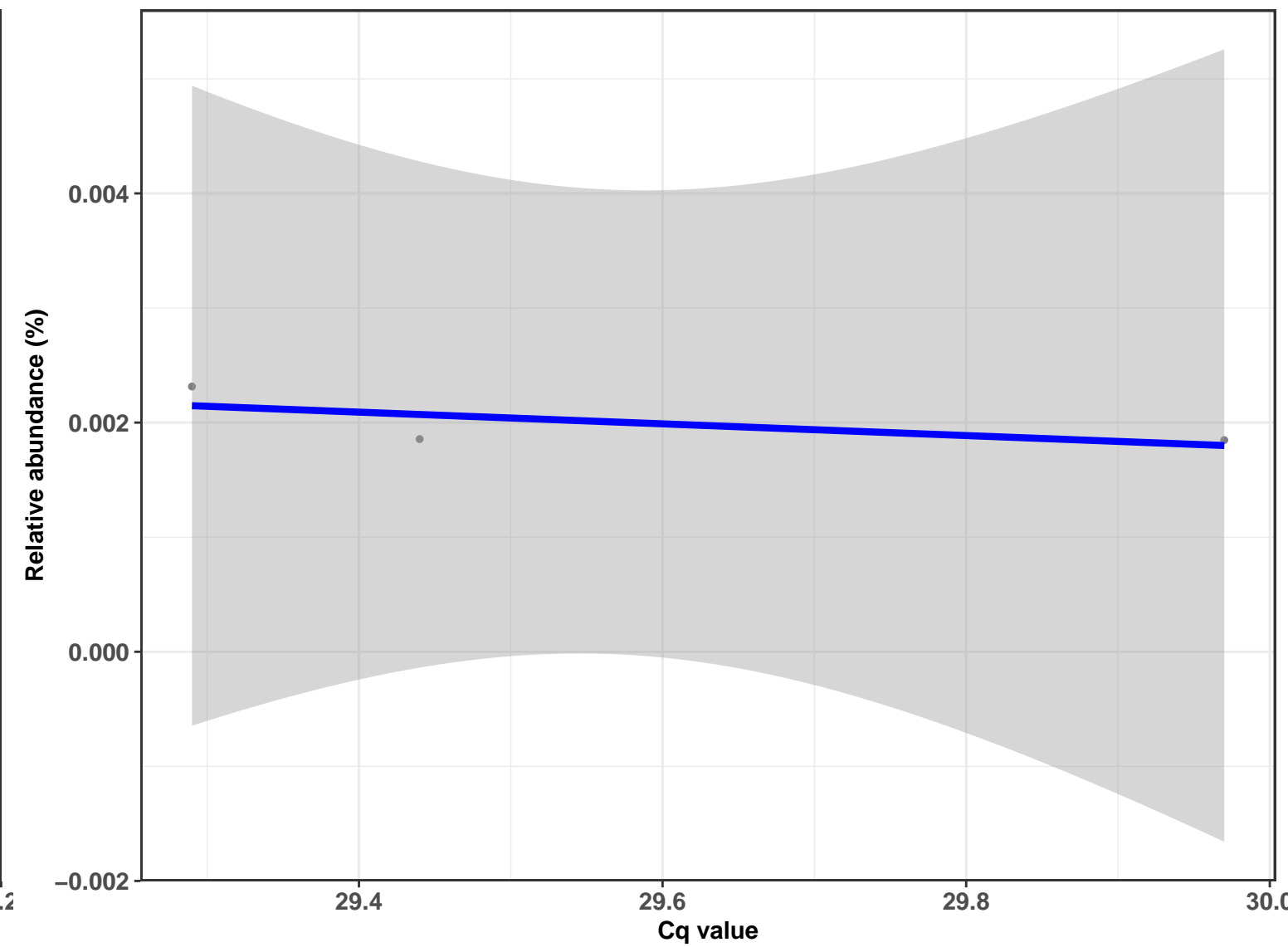
$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = -0.771$, $\text{CI}_{95\%} [-1.451, -0.196]$, $n_{\text{pairs}} = 6$



Correlation within: REF-DID



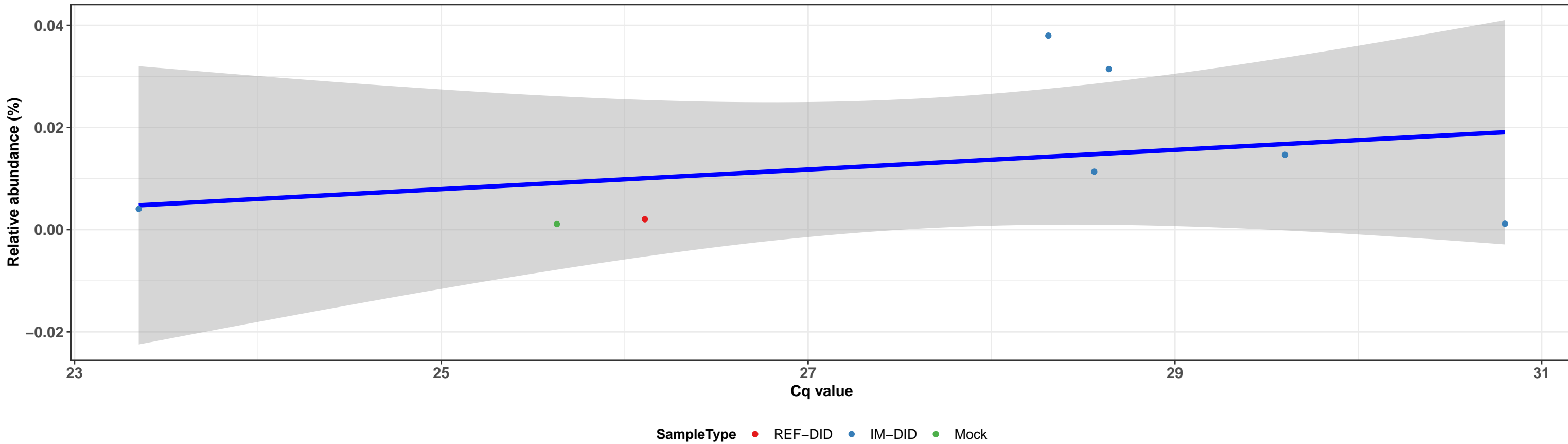
Correlation within: IM-DID



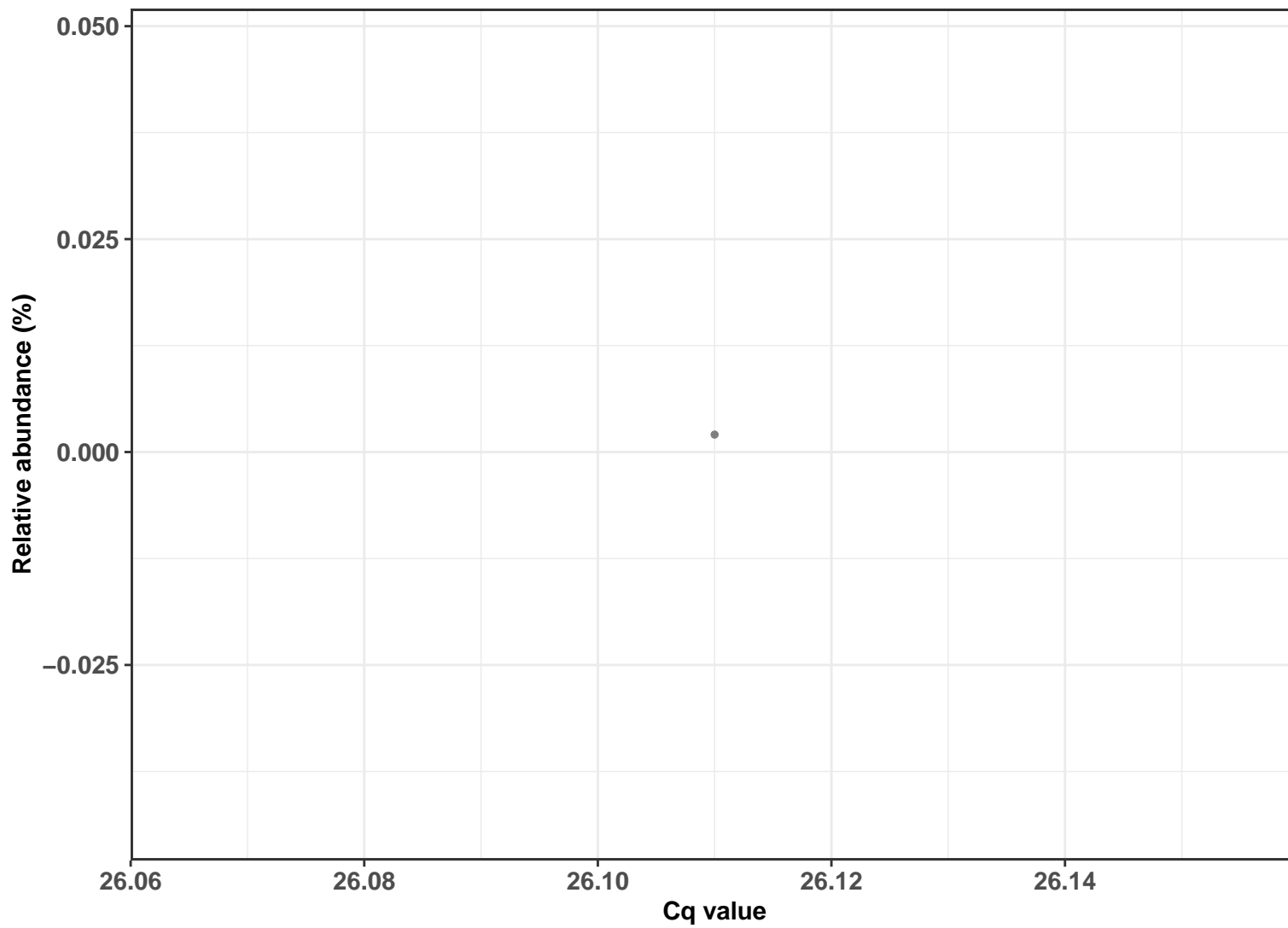
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

$\log_e(S) = 4.159$, $p = 0.570$, $\hat{\rho}_{\text{Spearman}} = 0.238$, $\text{CI}_{95\%} [-0.502, 1.102]$, $n_{\text{pairs}} = 8$

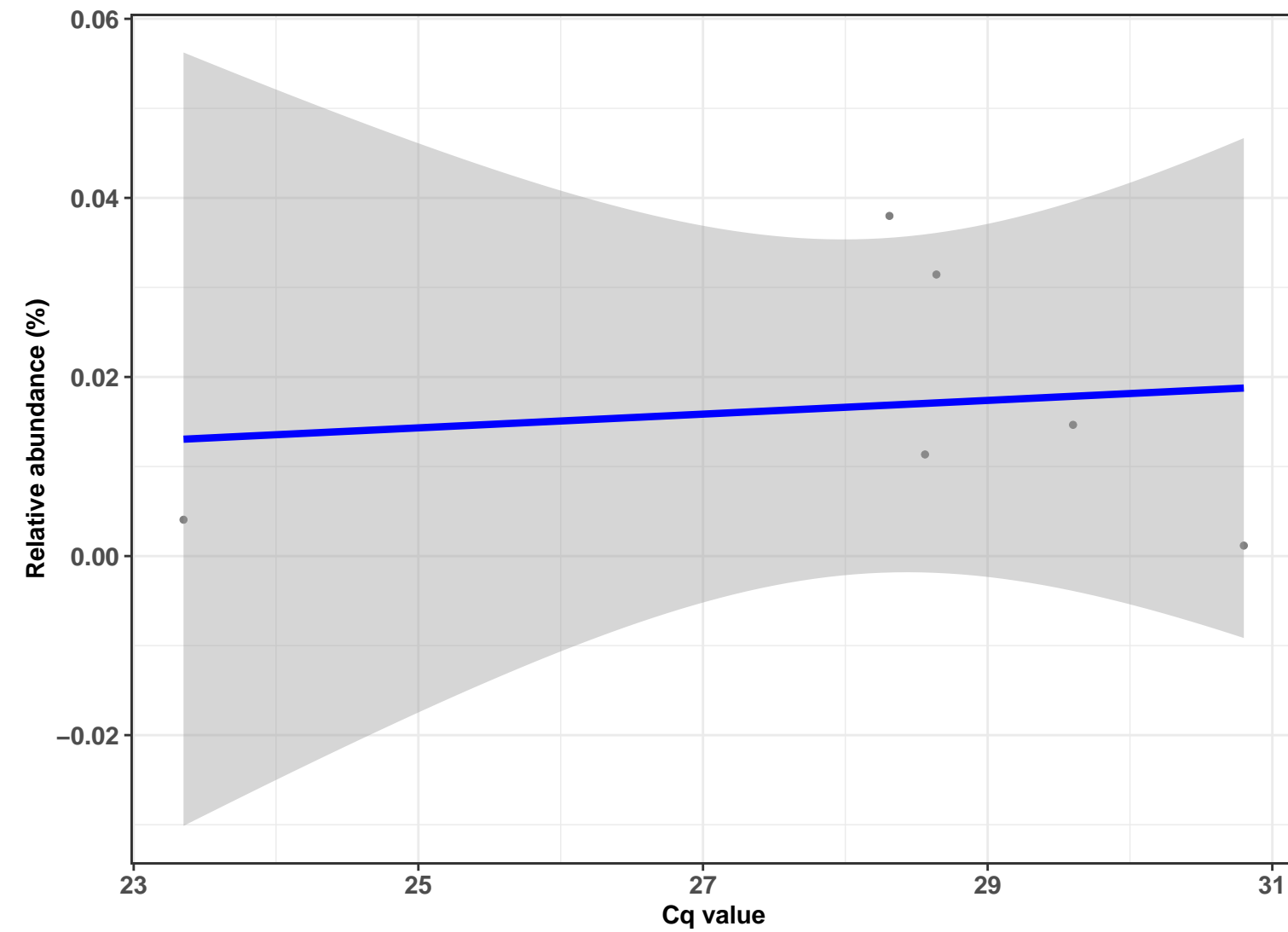


Correlation within: REF-DID



Correlation within: IM-DID

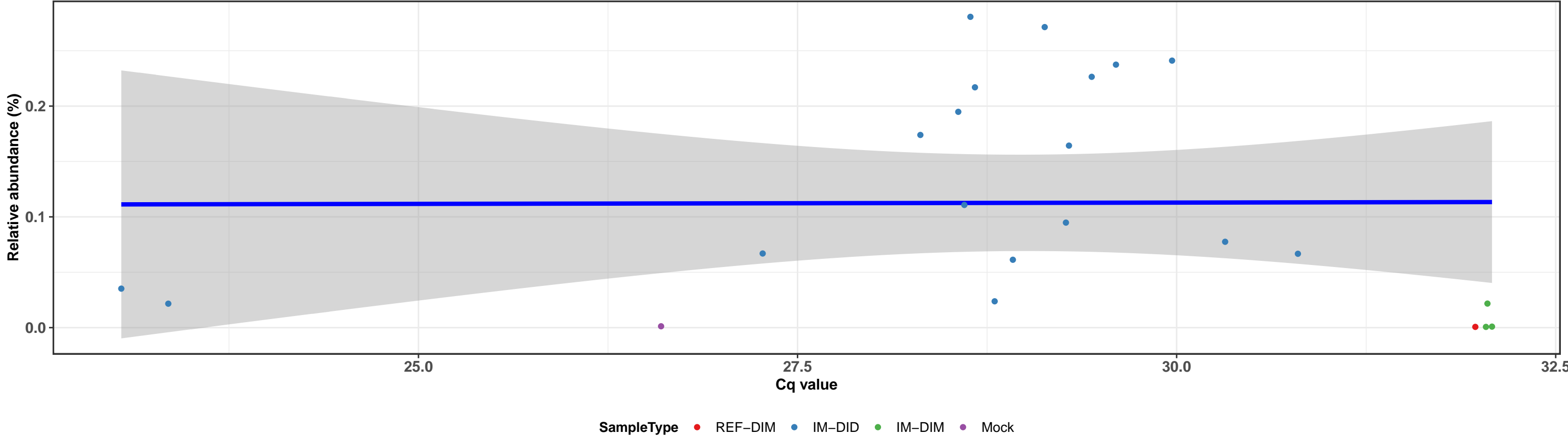
$\log_e(S) = 3.784$, $p = 0.623$, $\hat{\rho}_{\text{Spearman}} = -0.257$, $\text{CI}_{95\%} [-1.501, 0.857]$, $n_{\text{pairs}} = 6$



k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; NA

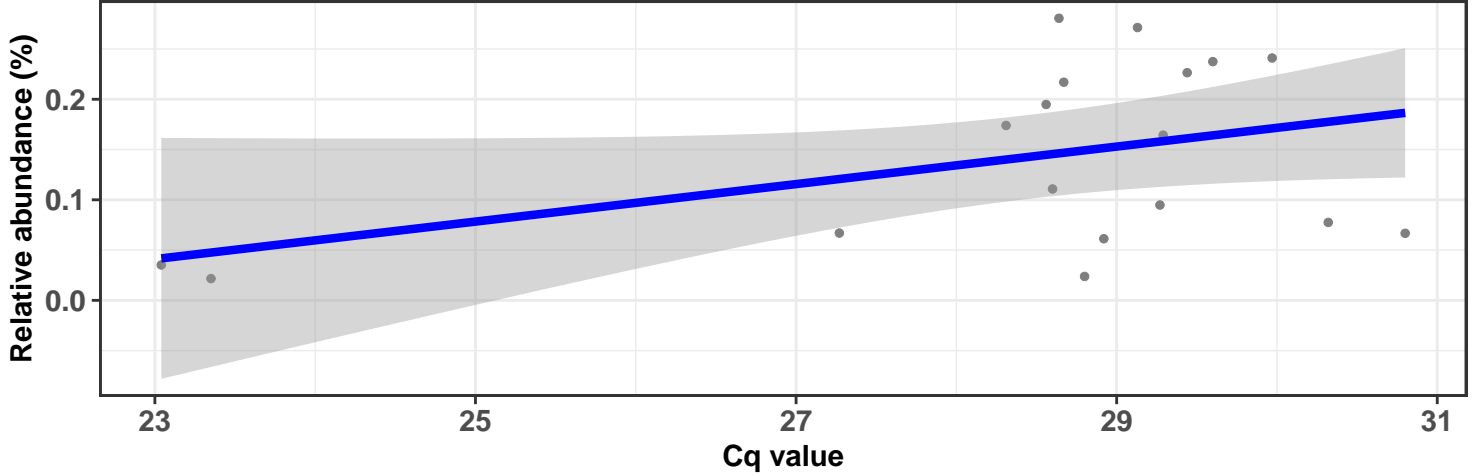
Correlation with all samples

$\log_e(S) = 7.768$, $p = 0.444$, $\hat{\rho}_{\text{Spearman}} = -0.168$, $\text{CI}_{95\%} [-0.641, 0.325]$, $n_{\text{pairs}} = 23$

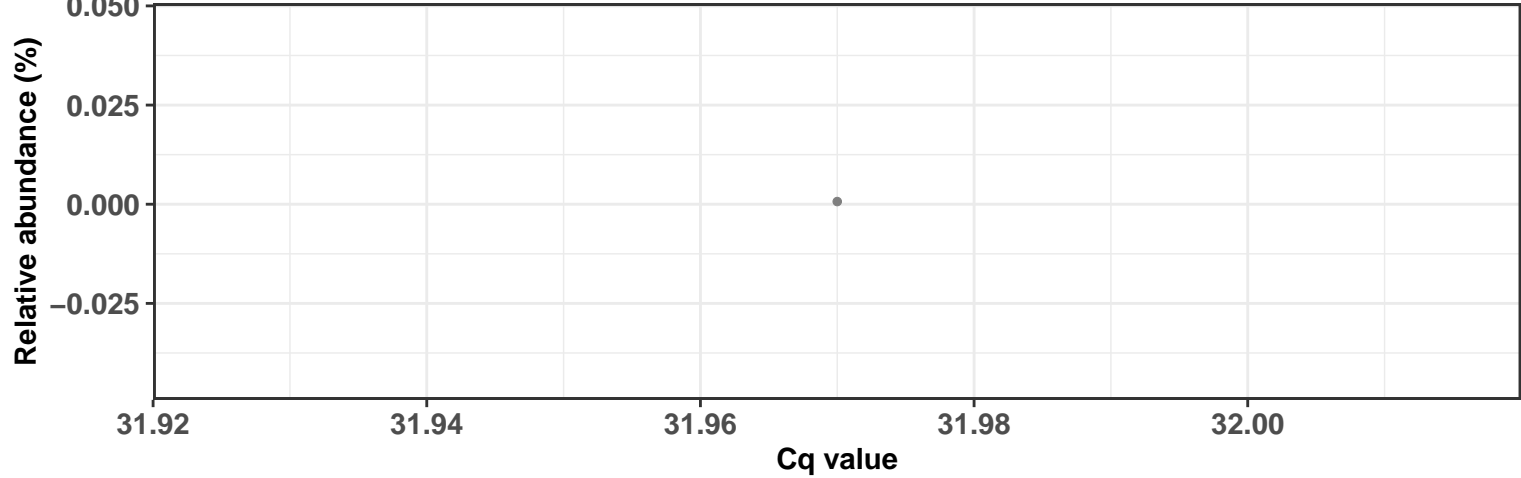


Correlation within: IM-DID

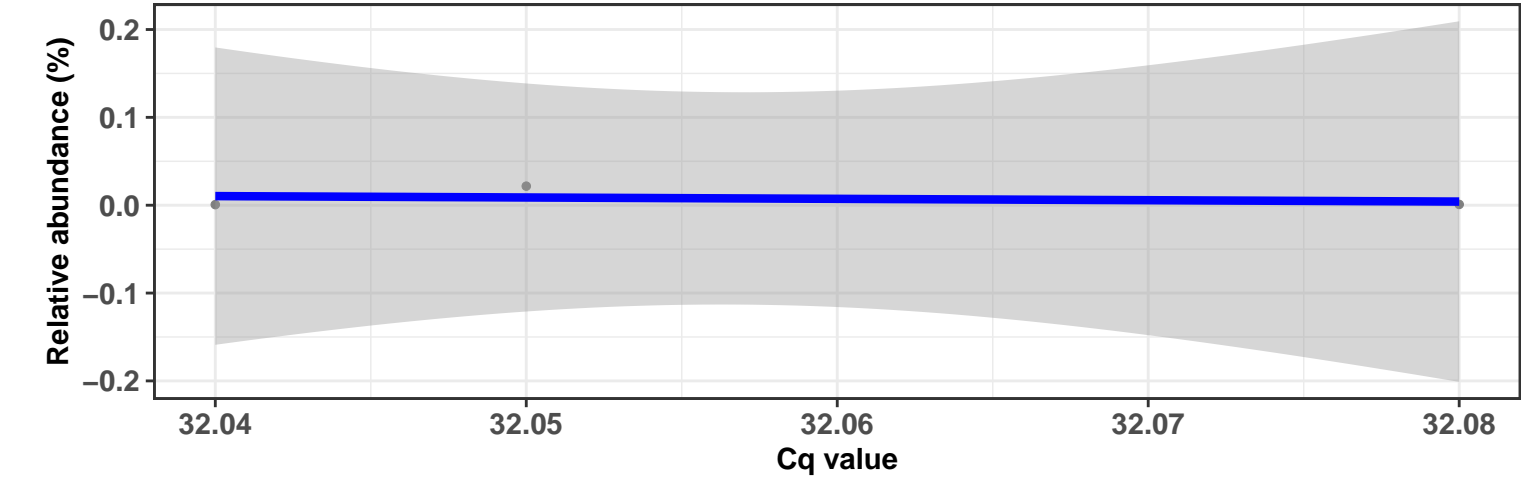
$\log_e(S) = 6.525$, $p = 0.233$, $\hat{\rho}_{\text{Spearman}} = 0.296$, $\text{CI}_{95\%} [-0.137, 0.767]$, $n_{\text{pairs}} = 18$



Correlation within: REF-DIM

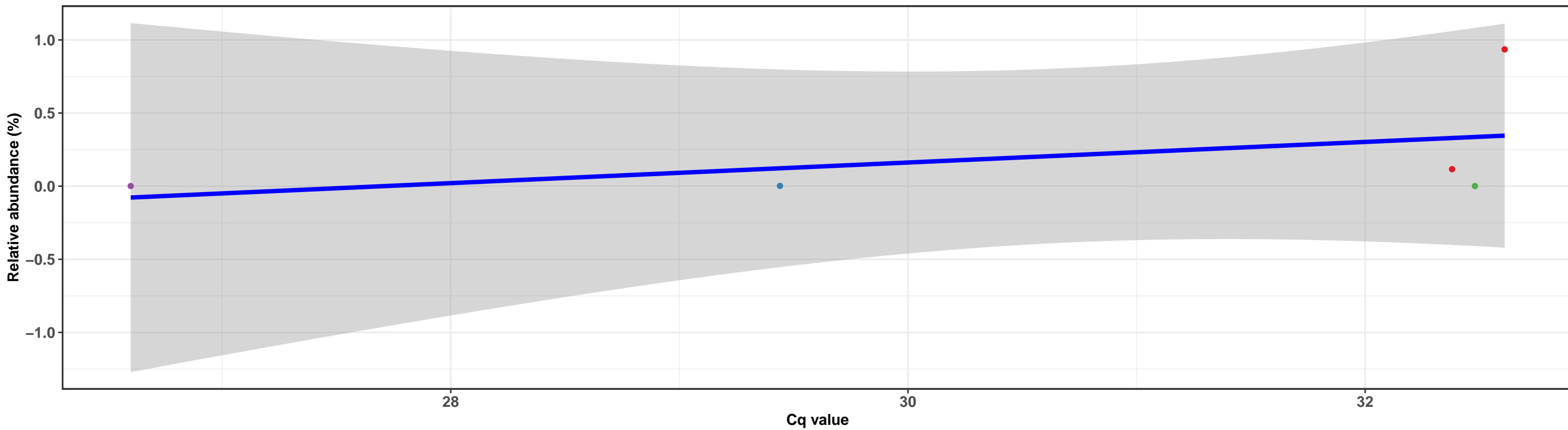


Correlation within: IM-DIM

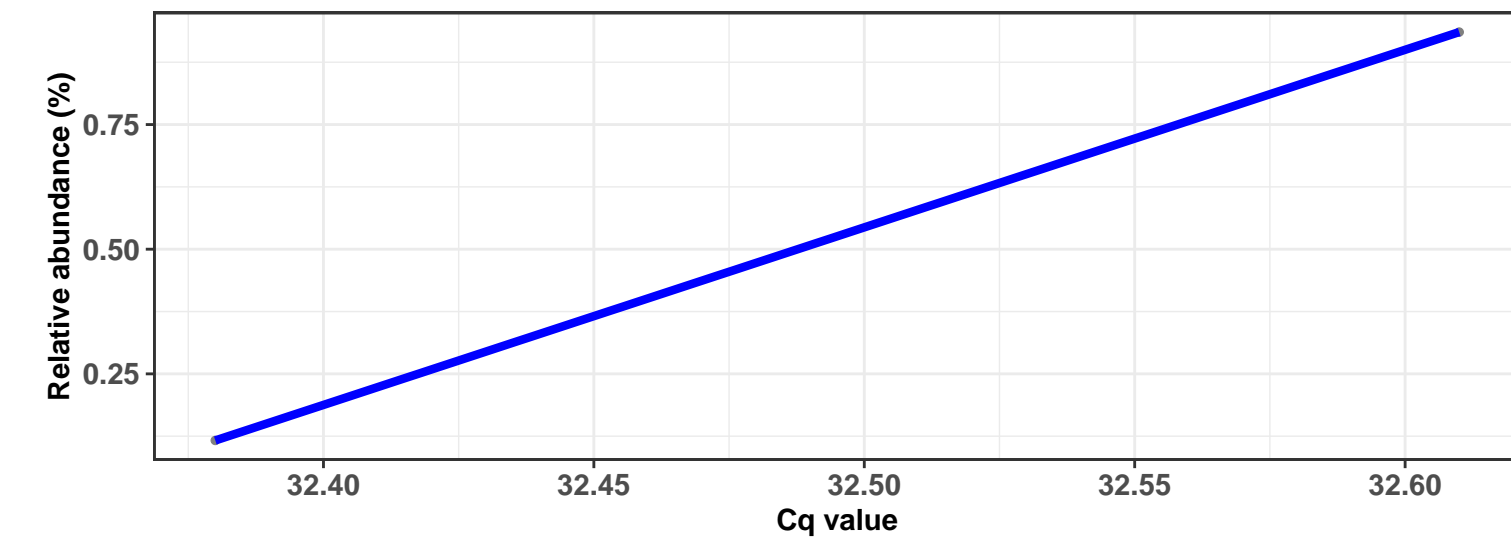


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium

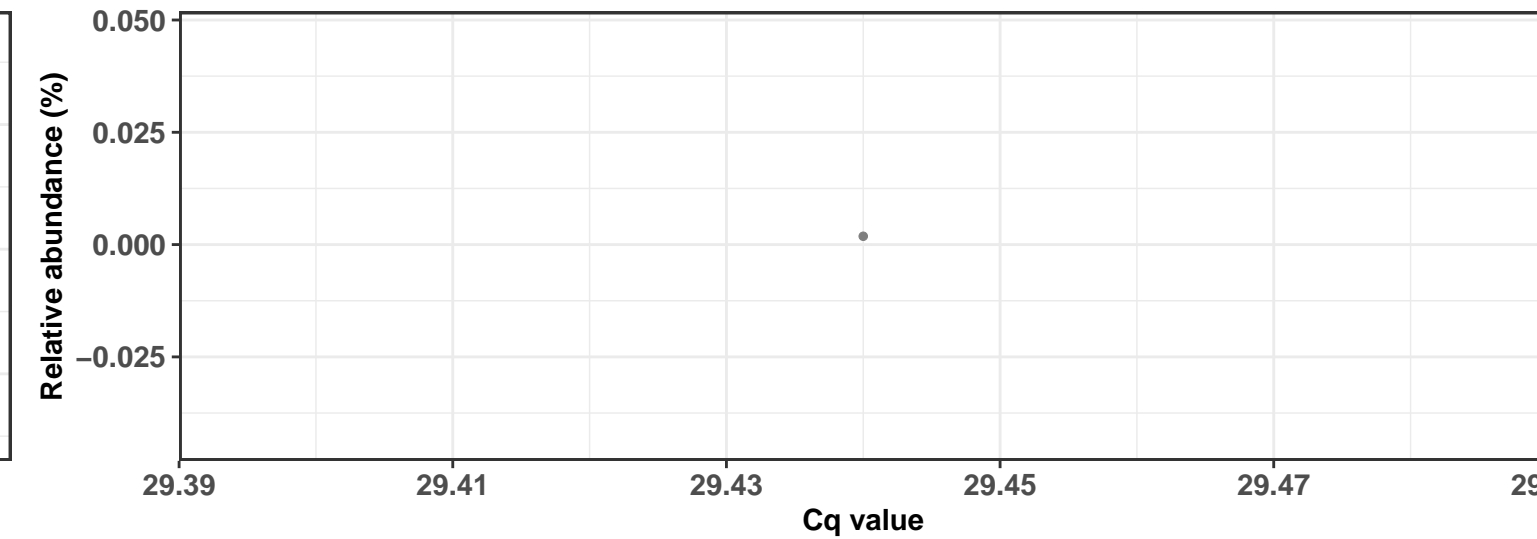
Correlation with all samples



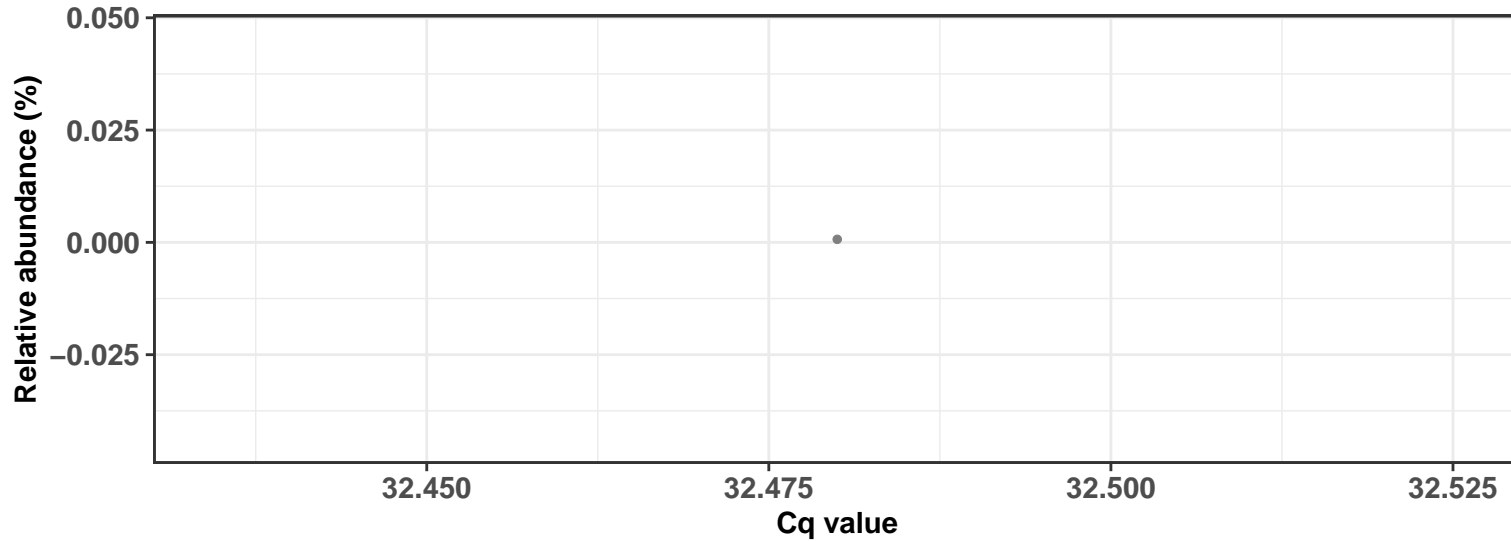
Correlation within: REF-DIM



Correlation within: IM-DID



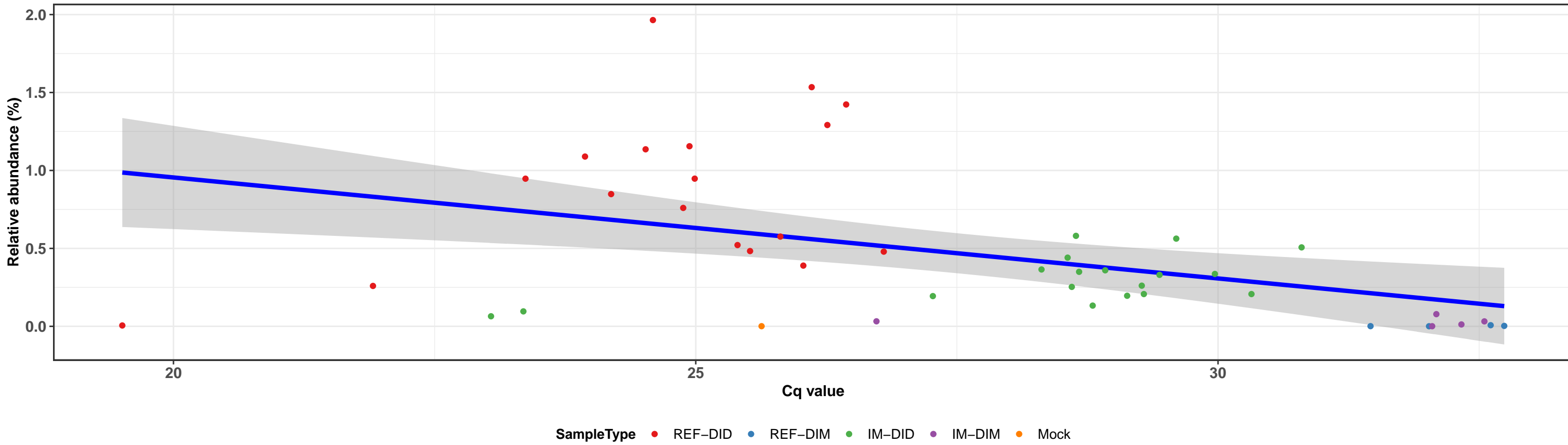
Correlation within: IM-DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Leuconostocaceae; g__Weissella; s__uncultured bacterium

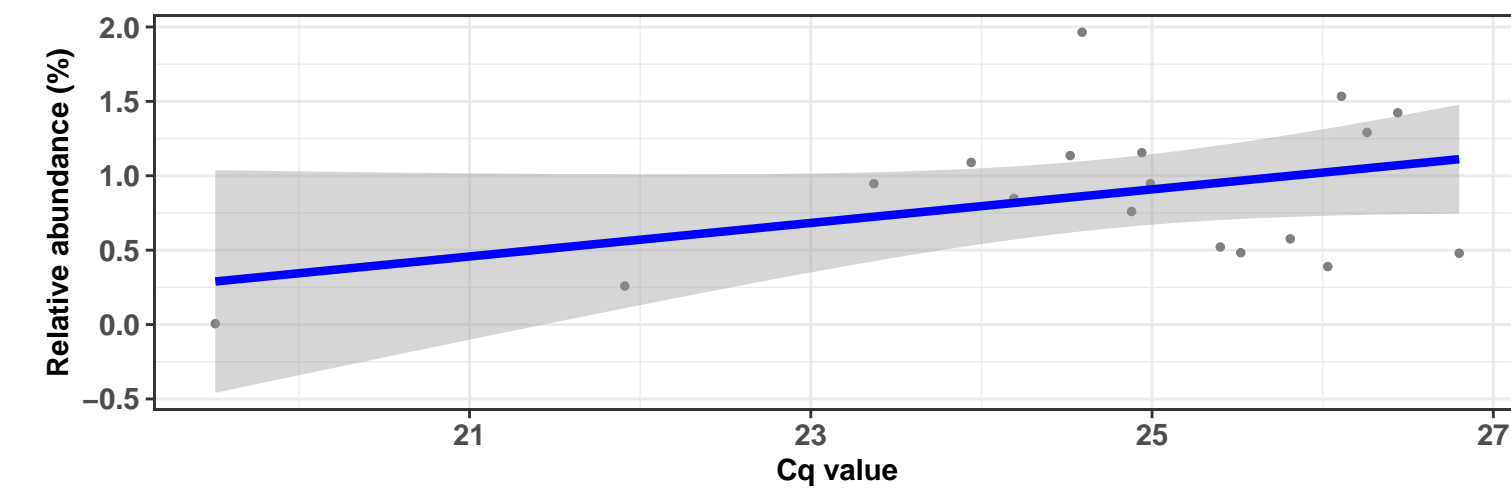
Correlation with all samples

$\log_e(S) = 10.095$, $p = < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.494$, $\text{CI}_{95\%} [-0.737, -0.251]$, $n_{\text{pairs}} = 46$

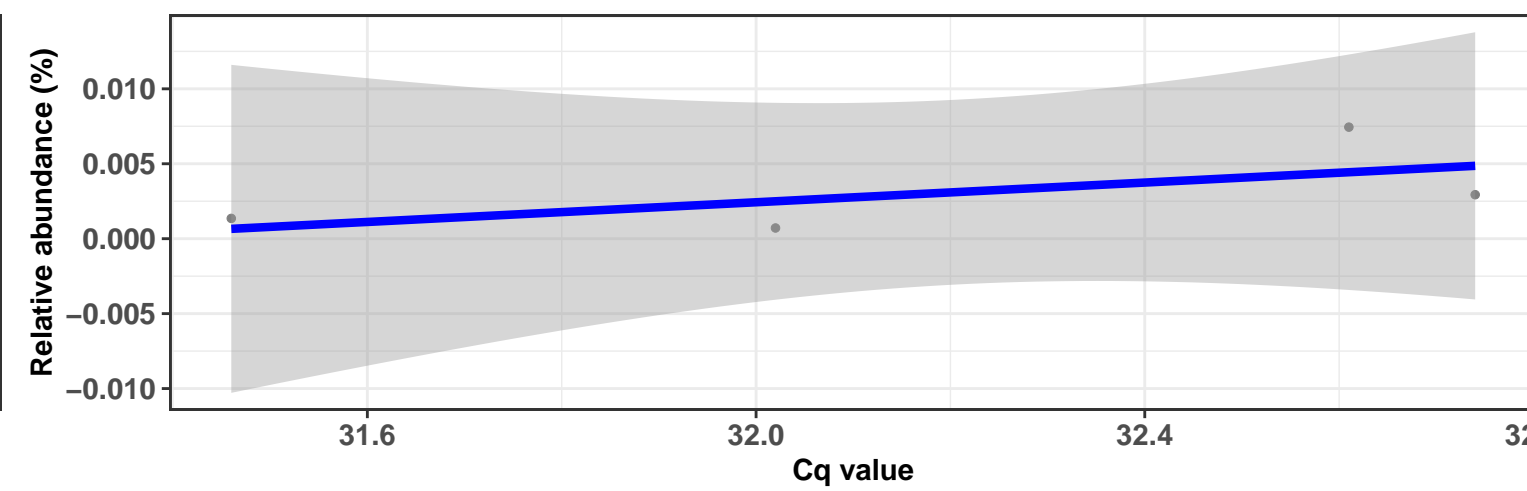


Correlation within: REF-DID

$\log_e(S) = 6.631$, $p = 0.385$, $\hat{\rho}_{\text{Spearman}} = 0.218$, $\text{CI}_{95\%} [-0.297, 0.670]$, $n_{\text{pairs}} = 18$

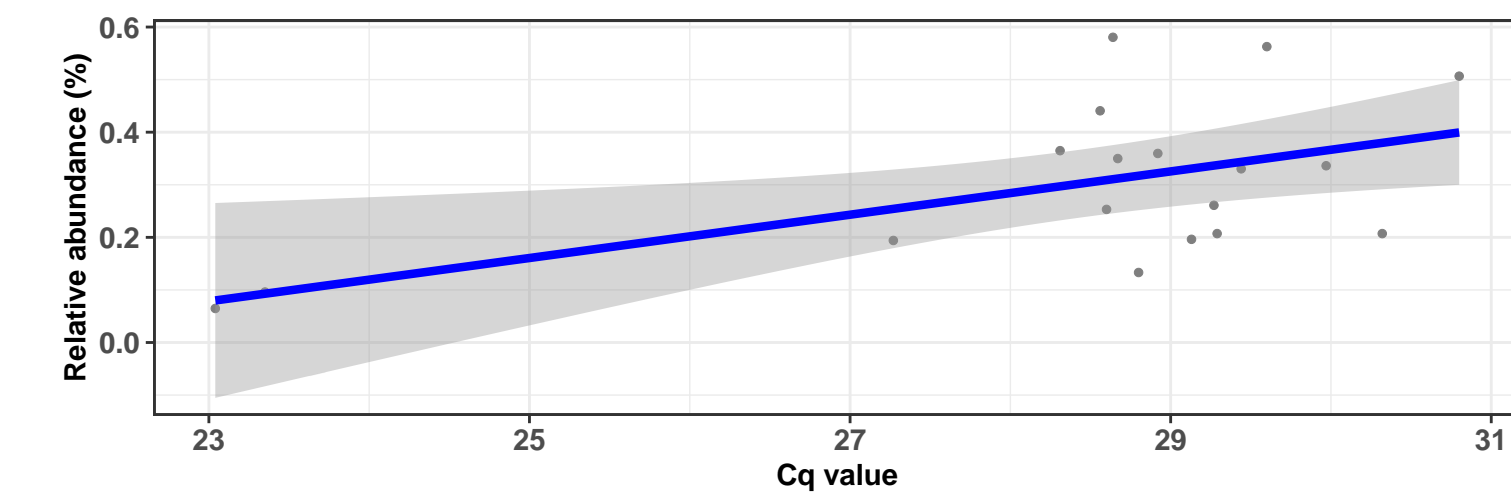


Correlation within: REF-DIM

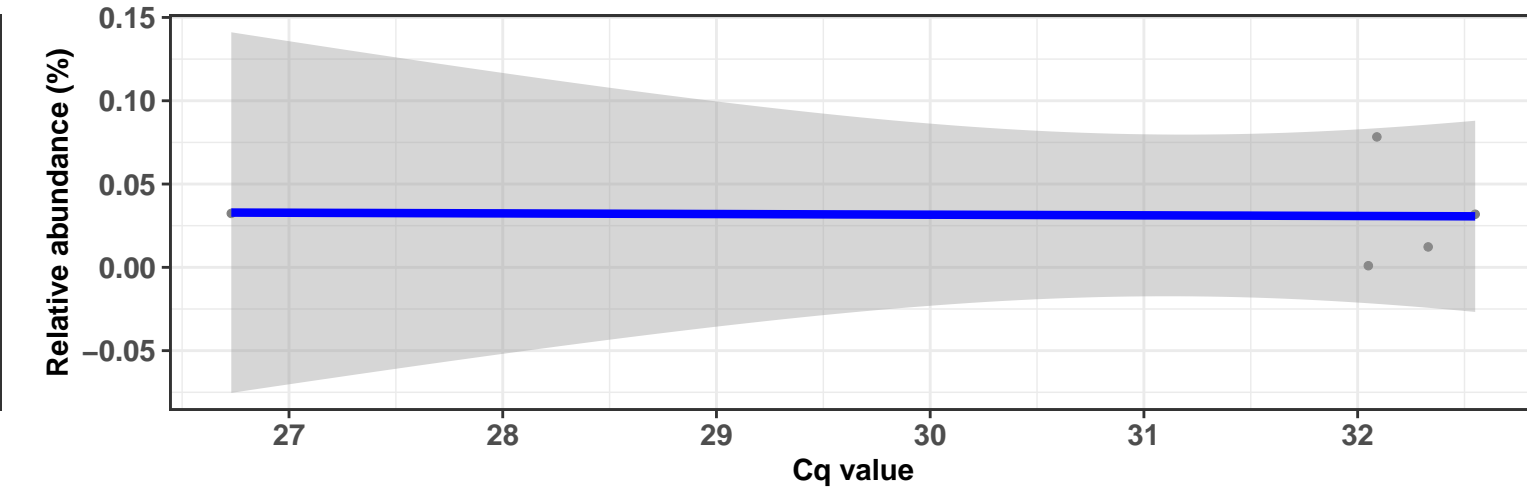


Correlation within: IM-DID

$\log_e(S) = 6.446$, $p = 0.155$, $\hat{\rho}_{\text{Spearman}} = 0.350$, $\text{CI}_{95\%} [-0.174, 0.844]$, $n_{\text{pairs}} = 18$

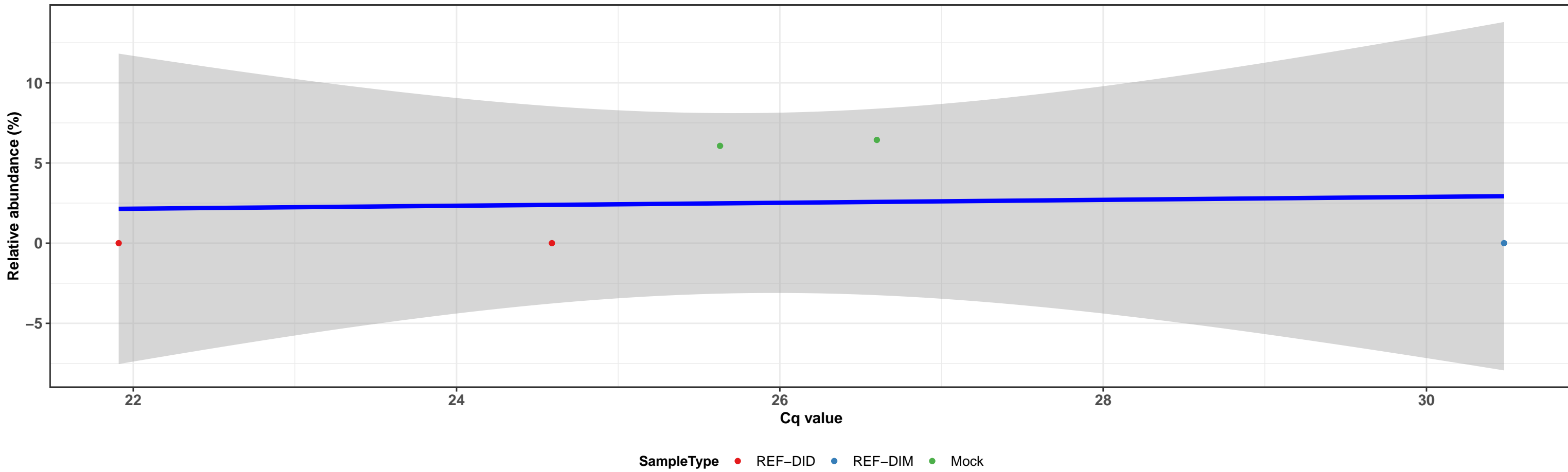


Correlation within: IM-DIM

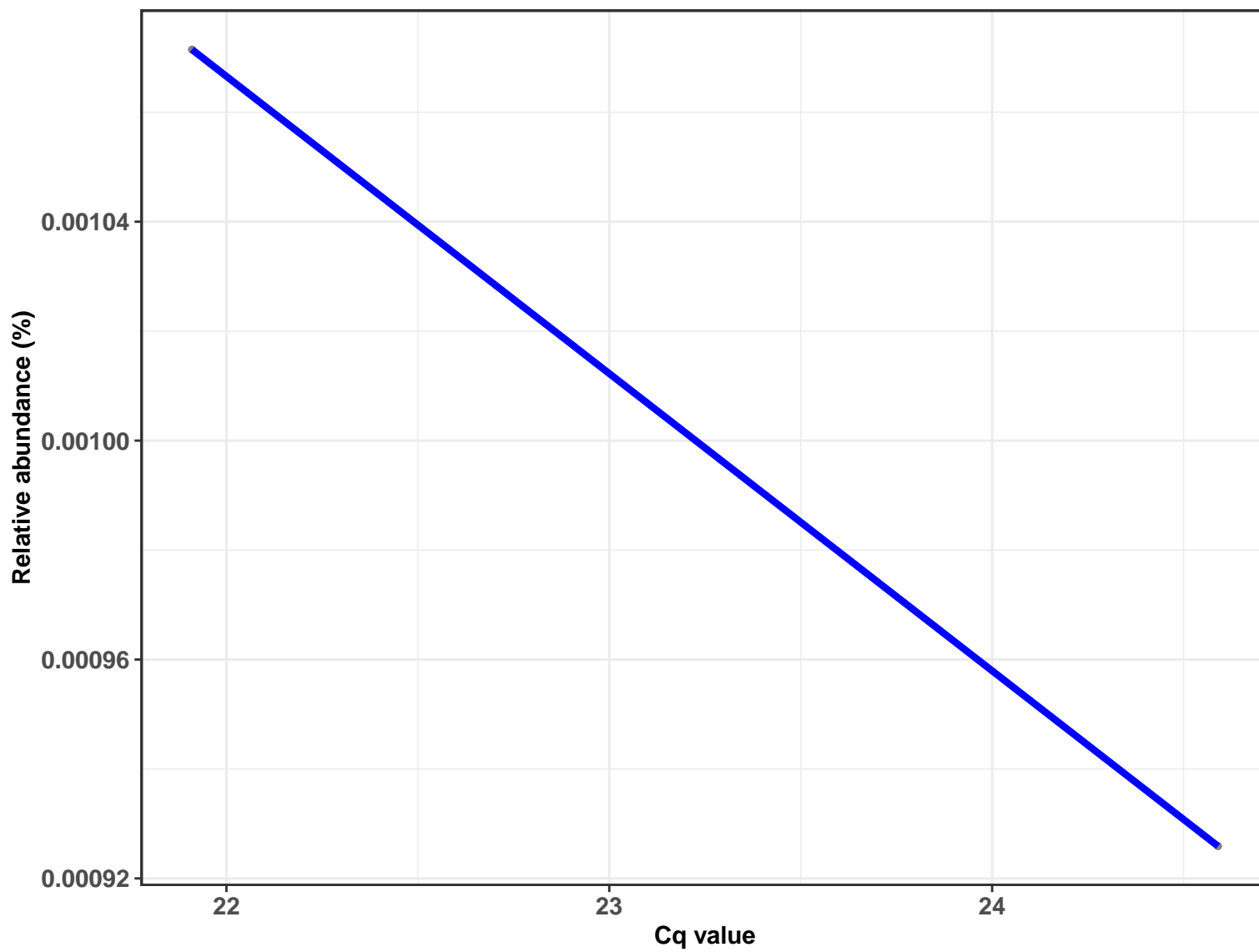


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus

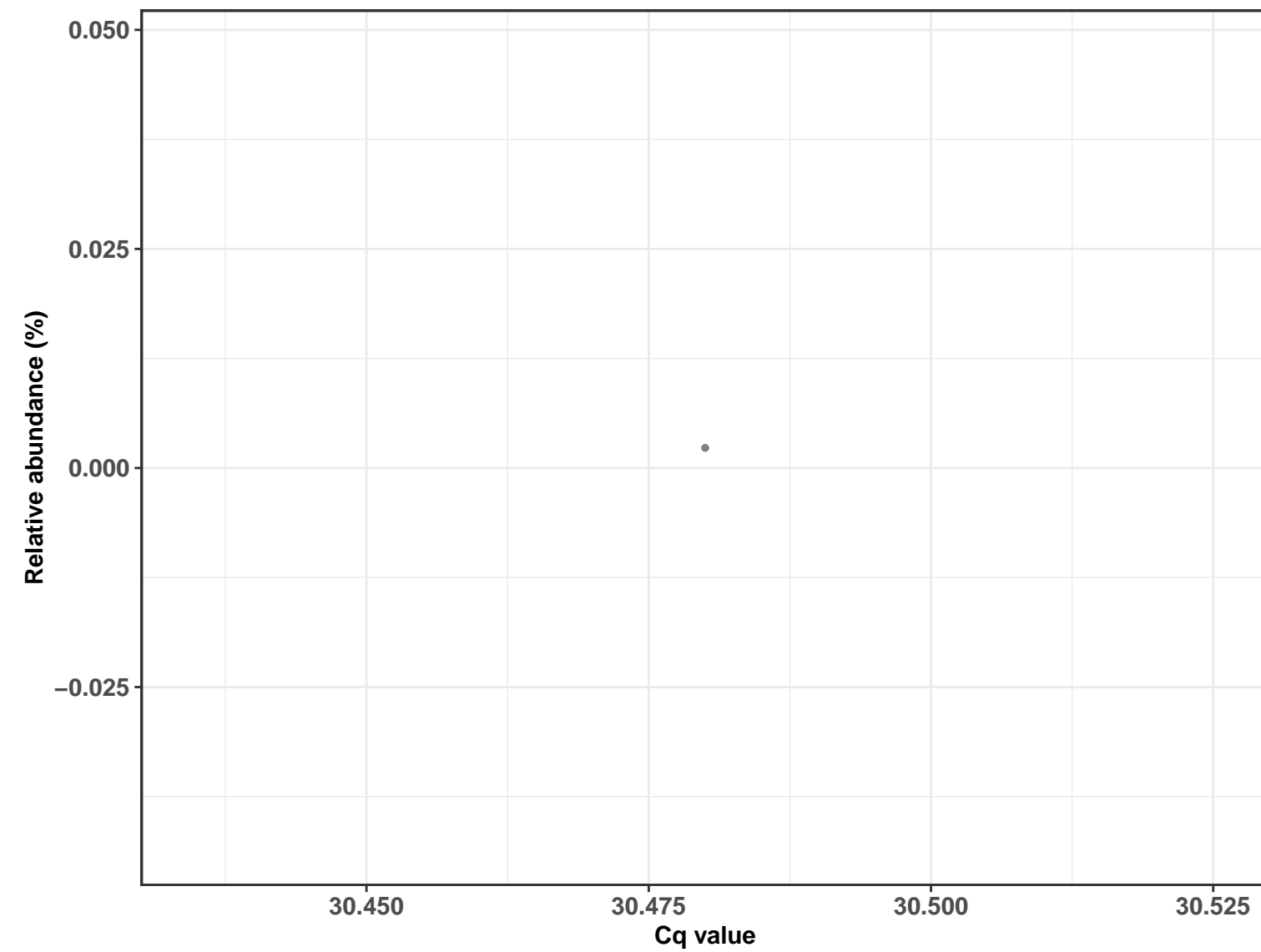
Correlation with all samples



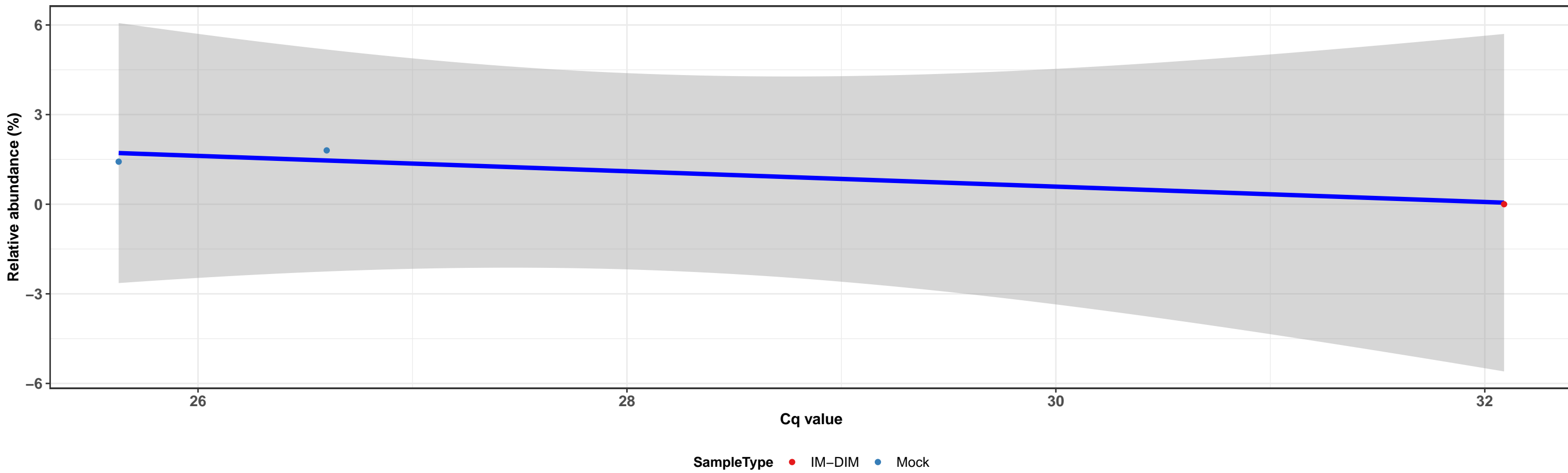
Correlation within: REF-DID



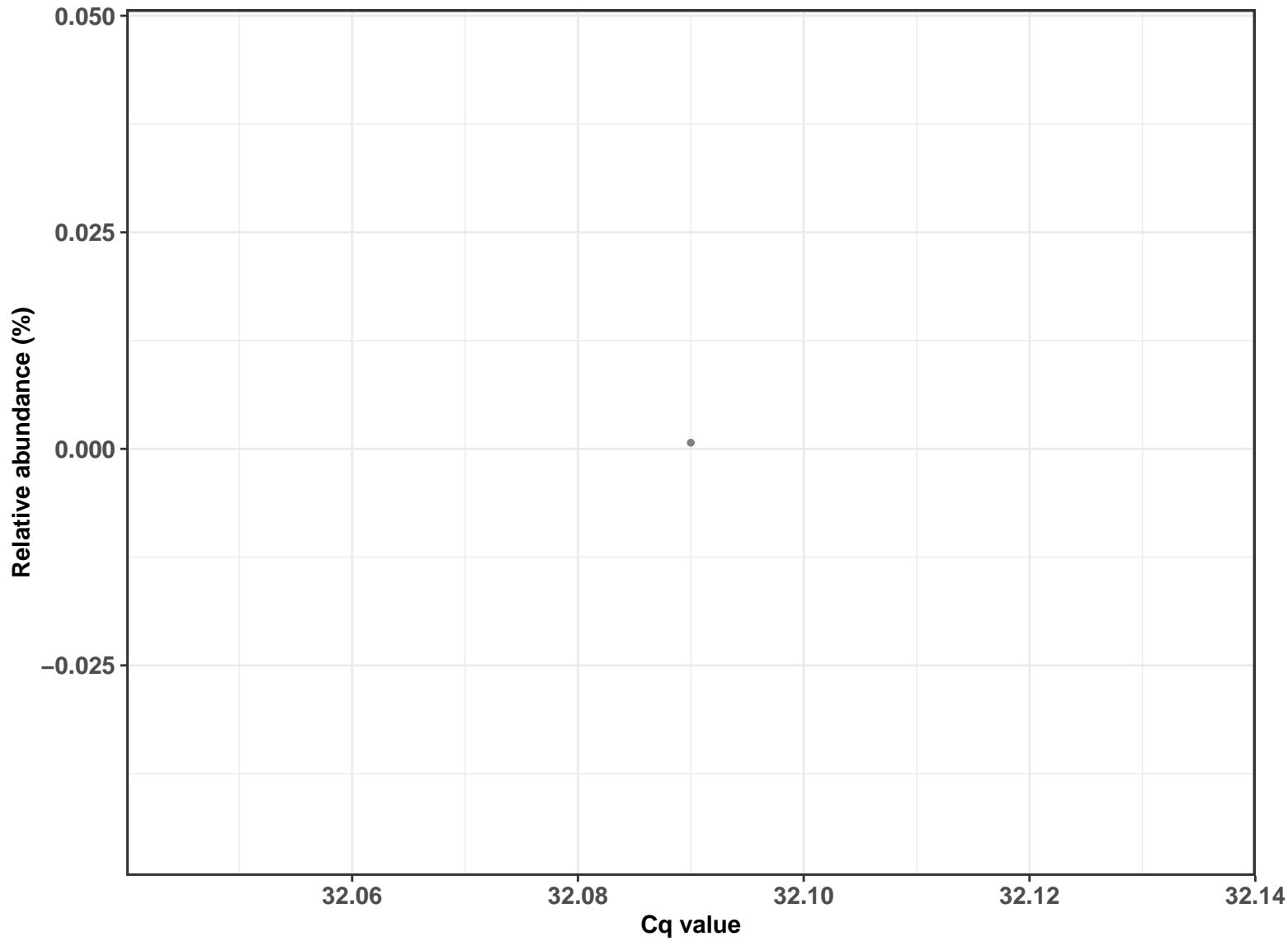
Correlation within: REF-DIM



Correlation with all samples

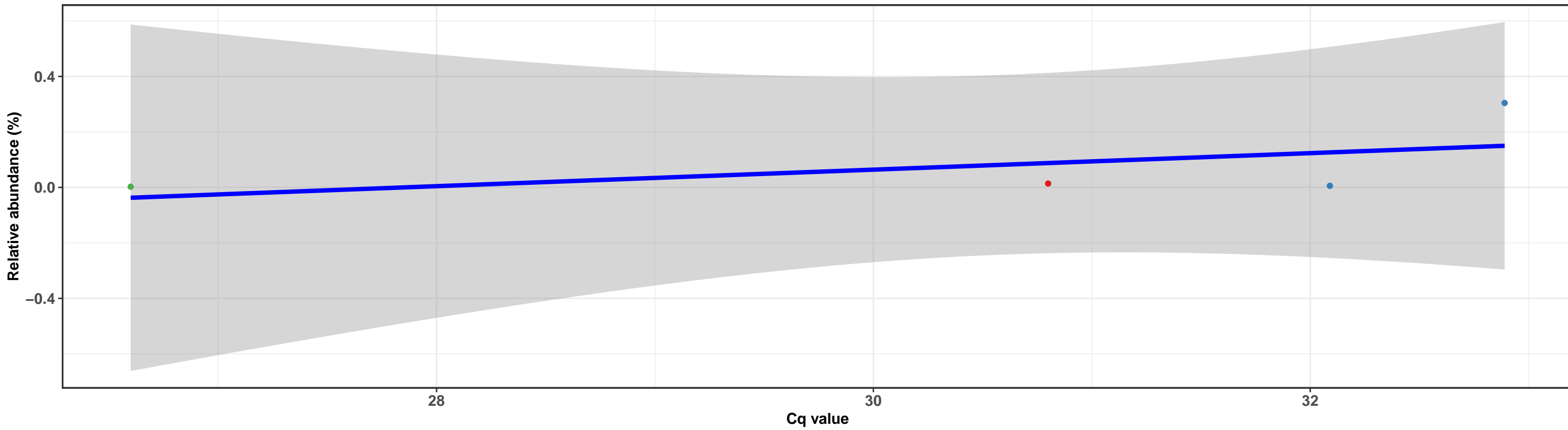


Correlation within: IM-DIM

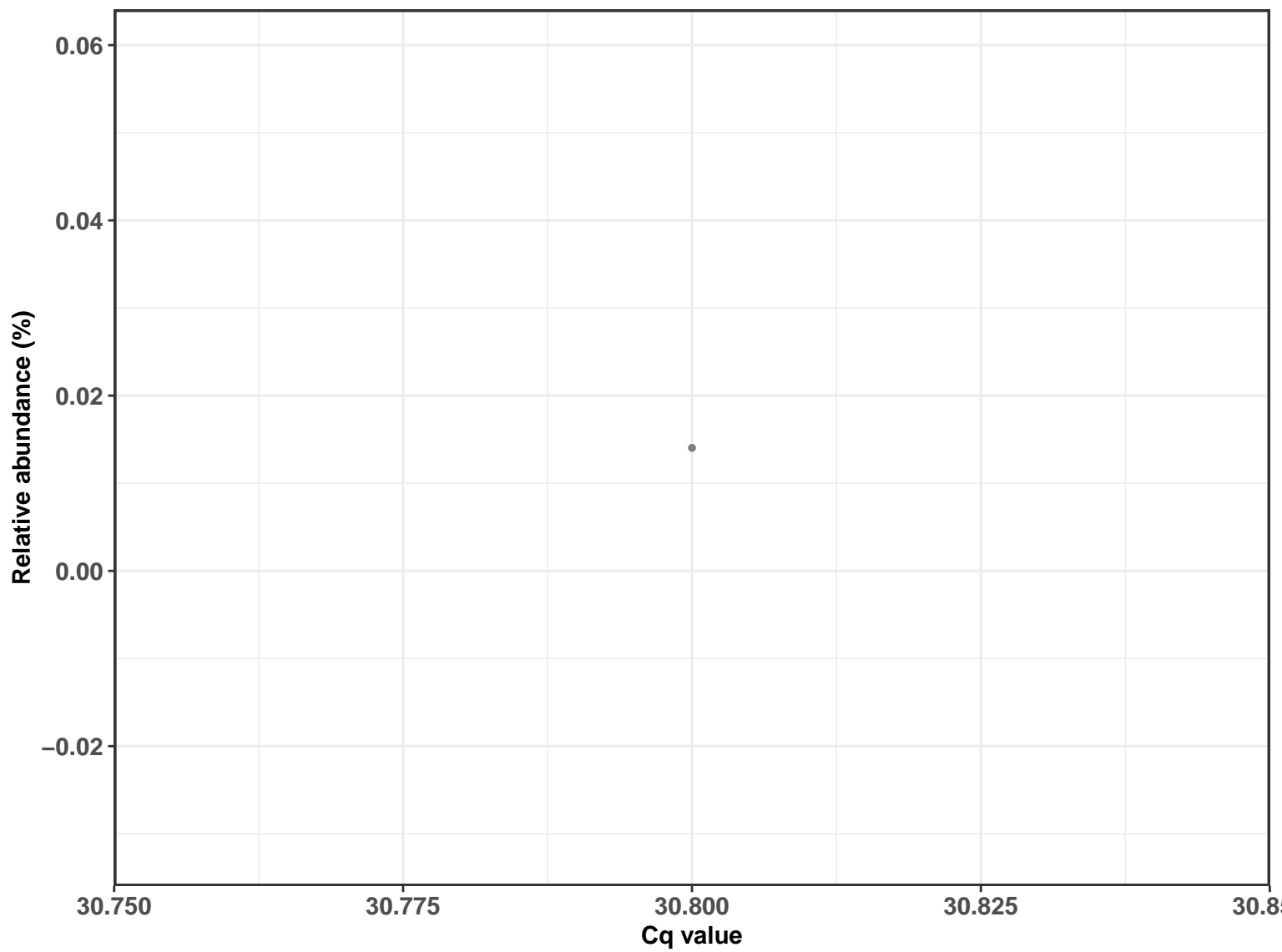


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Arthrobacter; Ambiguous_taxa

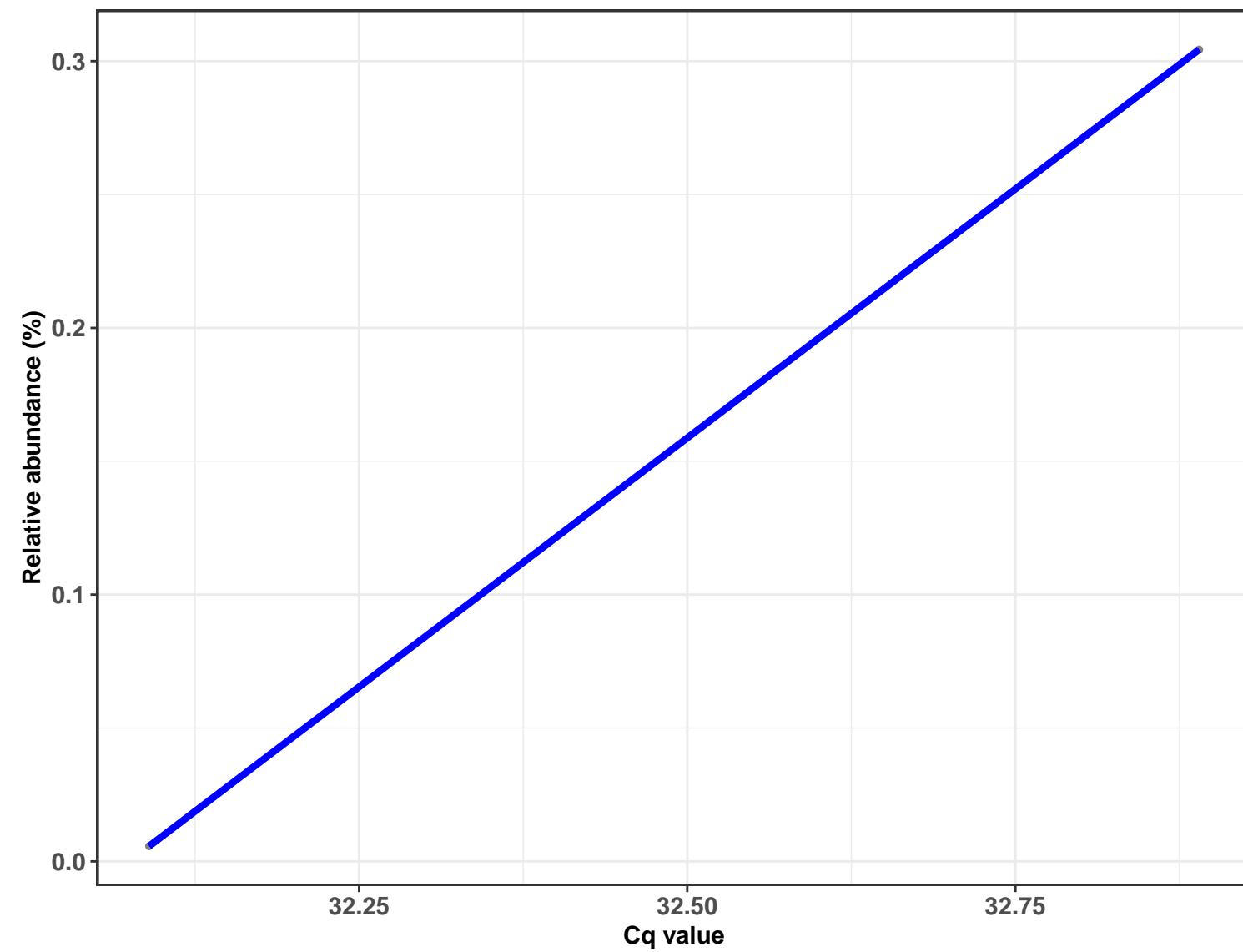
Correlation with all samples



Correlation within: IM-DID

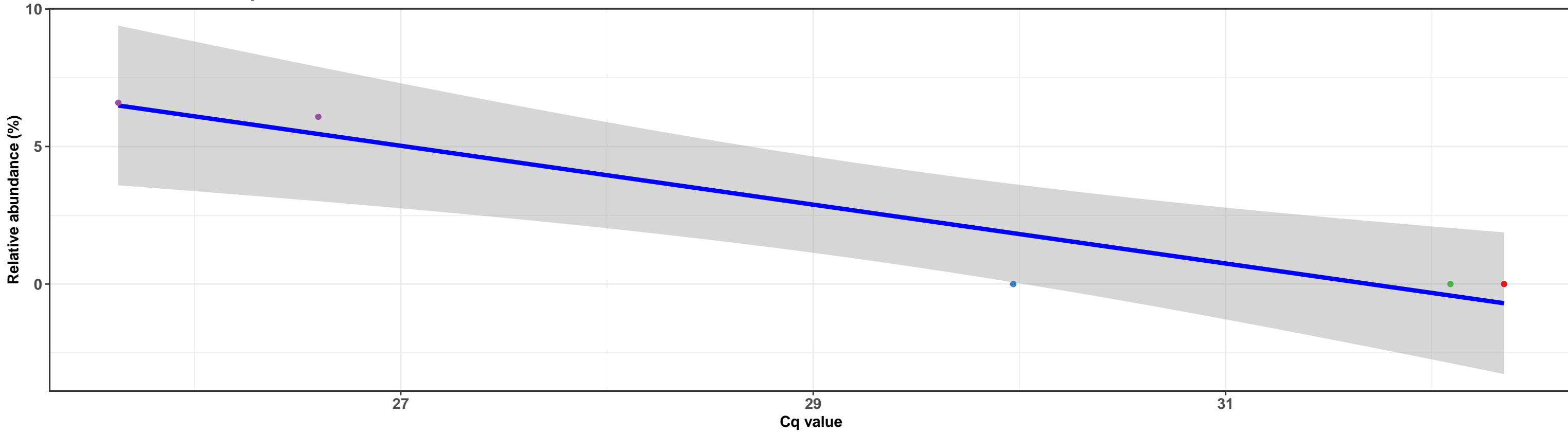


Correlation within: IM-DIM

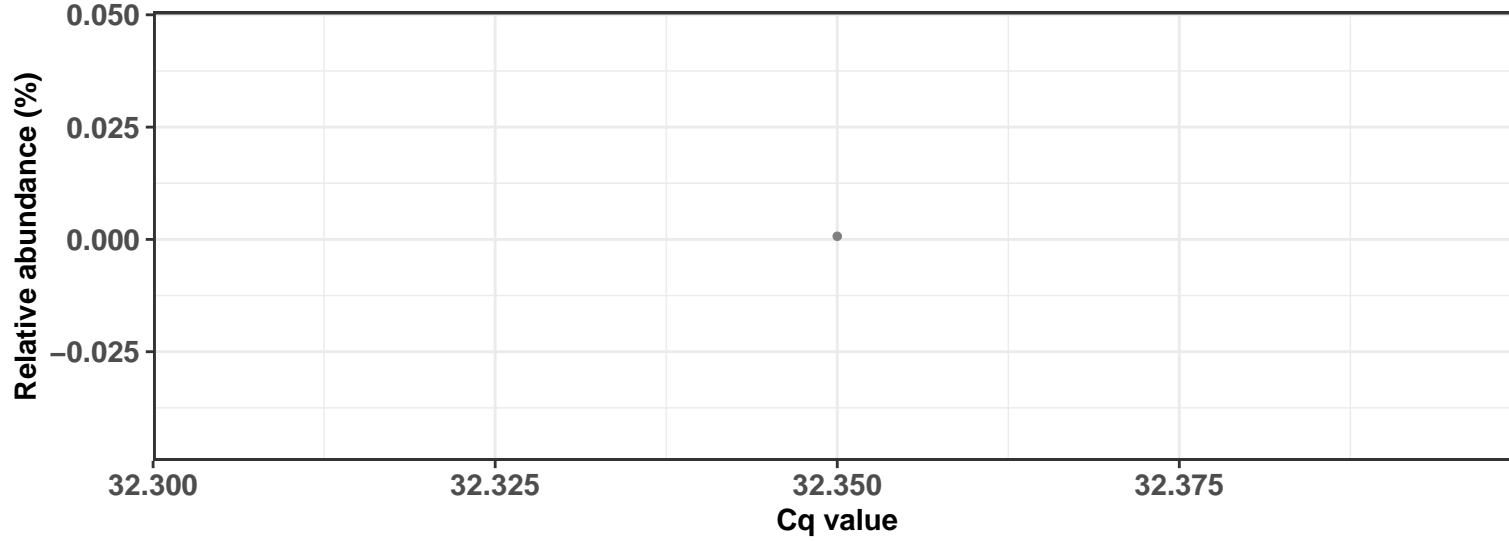


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

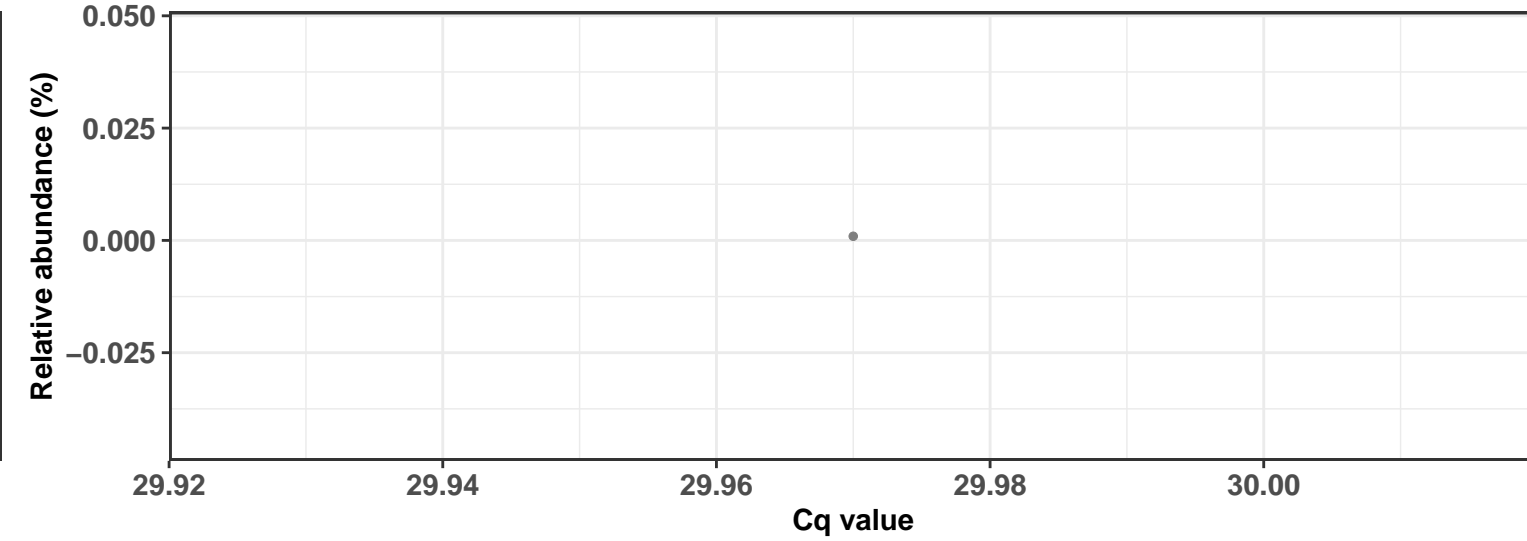
Correlation with all samples



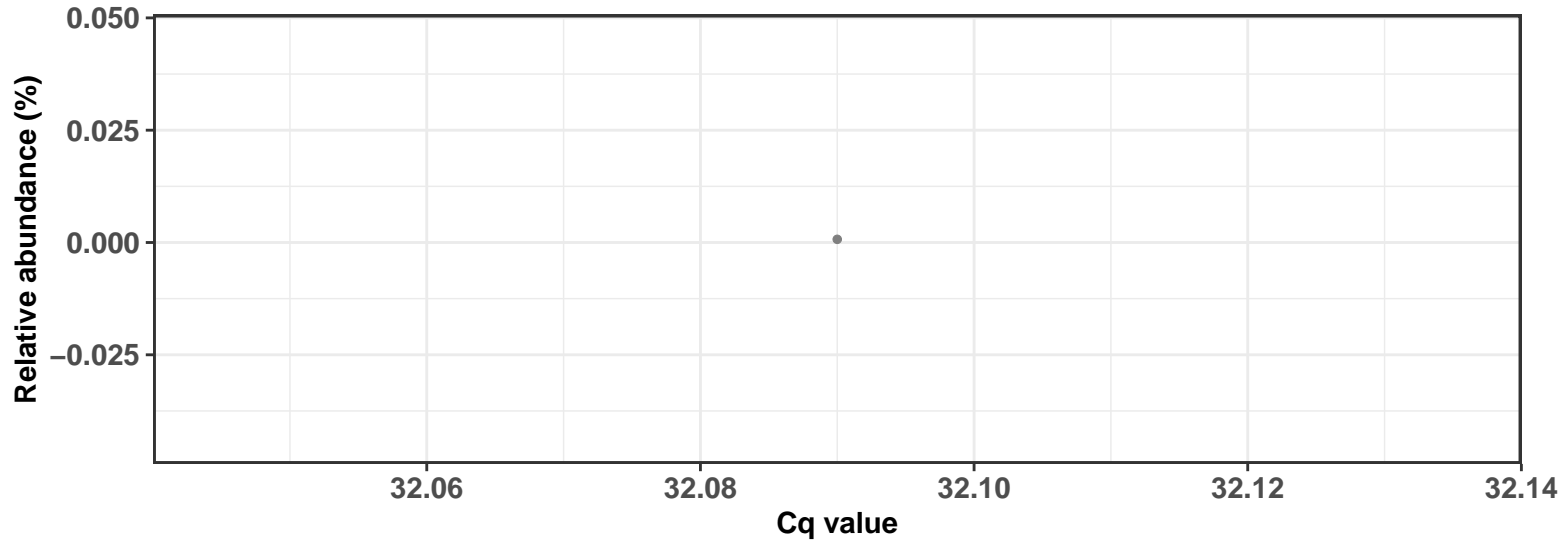
Correlation within: REF-DIM



Correlation within: IM-DID

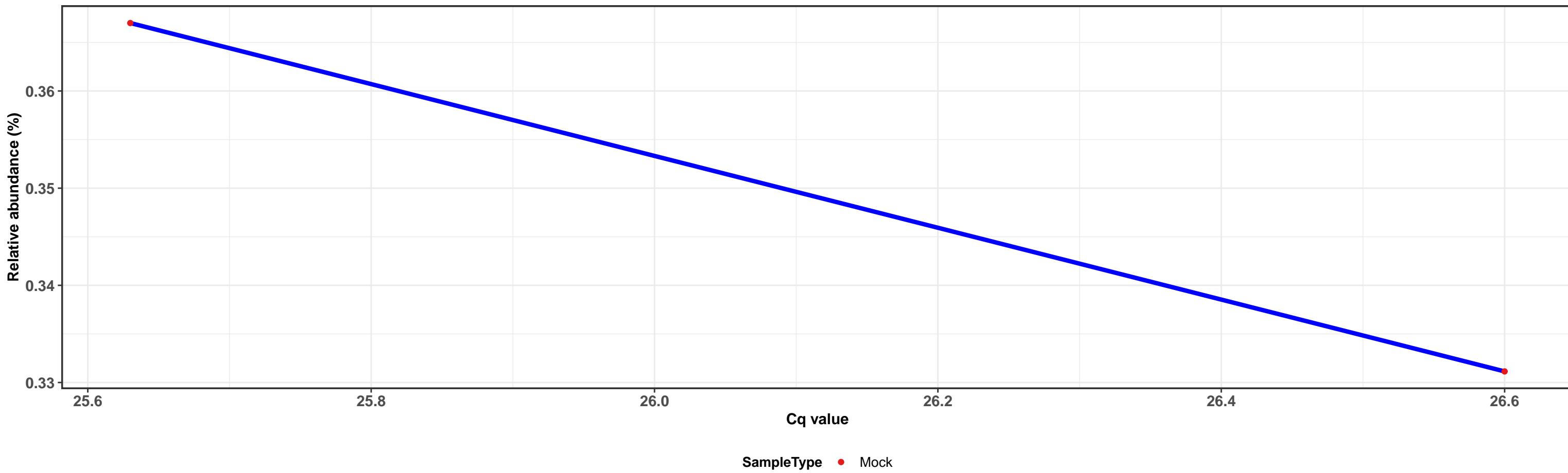


Correlation within: IM-DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples



Correlation within:

