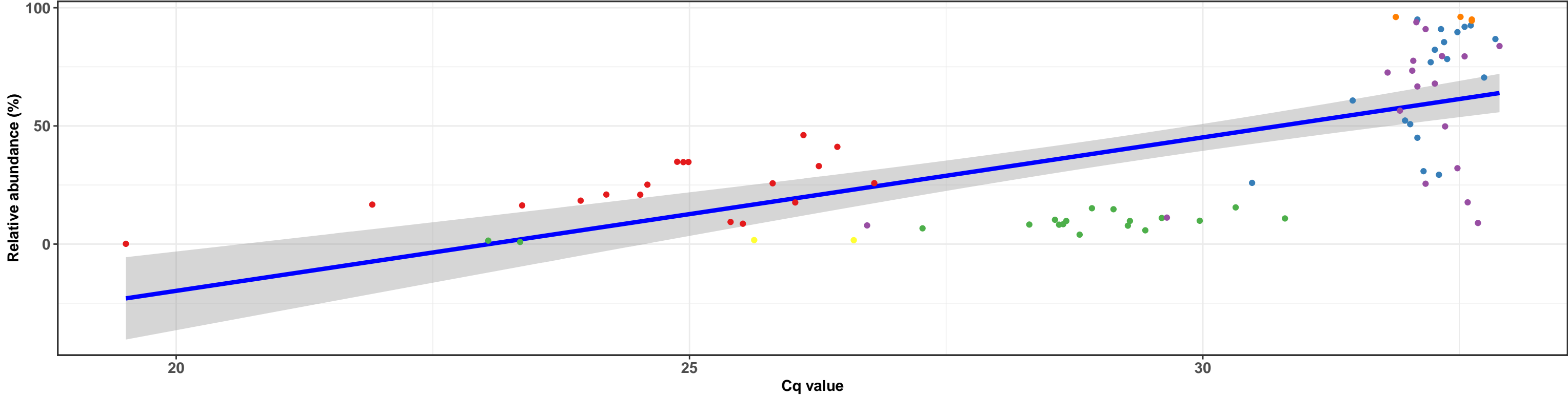# k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA
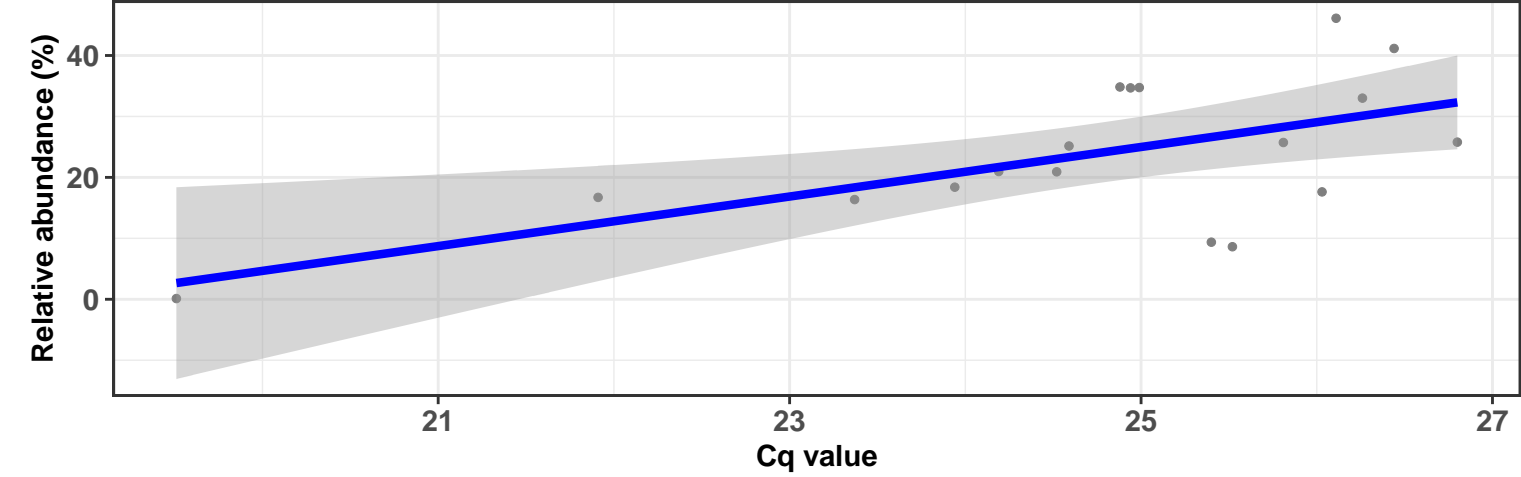
Correlation with all samples

$\log_e(S) = 10.174$, $p = < 0.001$, $\hat{\rho}_{Spearman} = 0.668$, $CI_{95\%}$ [0.544, 0.811], $n_{pairs} = 78$
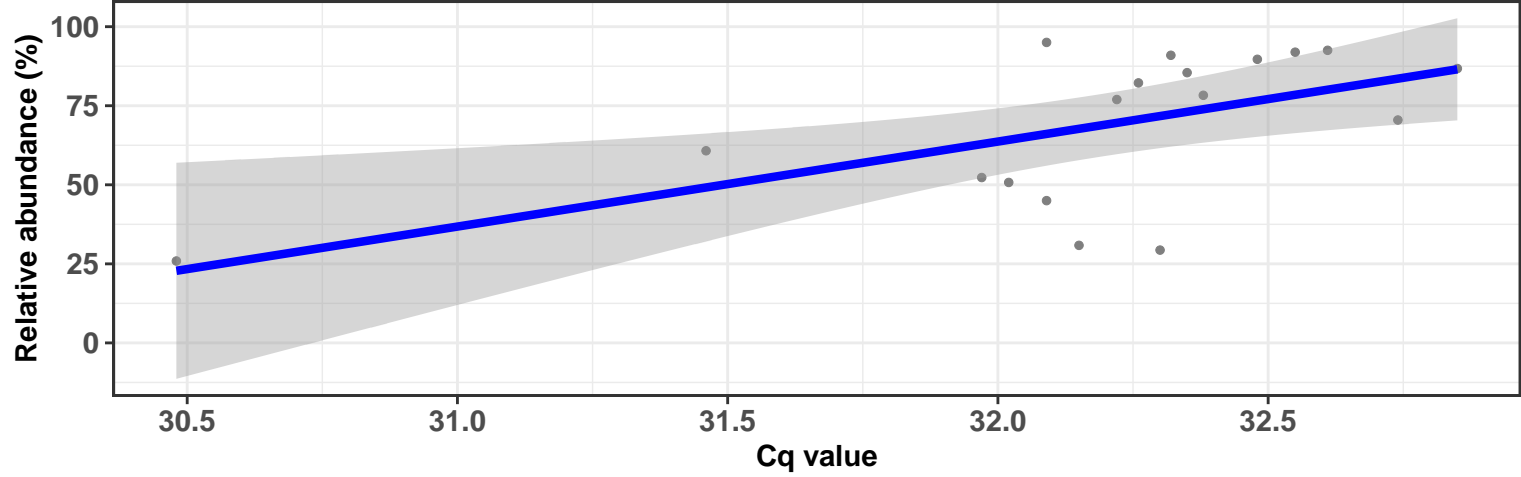

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock

Correlation within: REF−DIC

$\log_e(S) = 6.105$, $p = 0.021$, $\hat{\rho}_{Spearman} = 0.538$, $CI_{95\%}$ [0.172, 0.985], $n_{pairs} = 18$

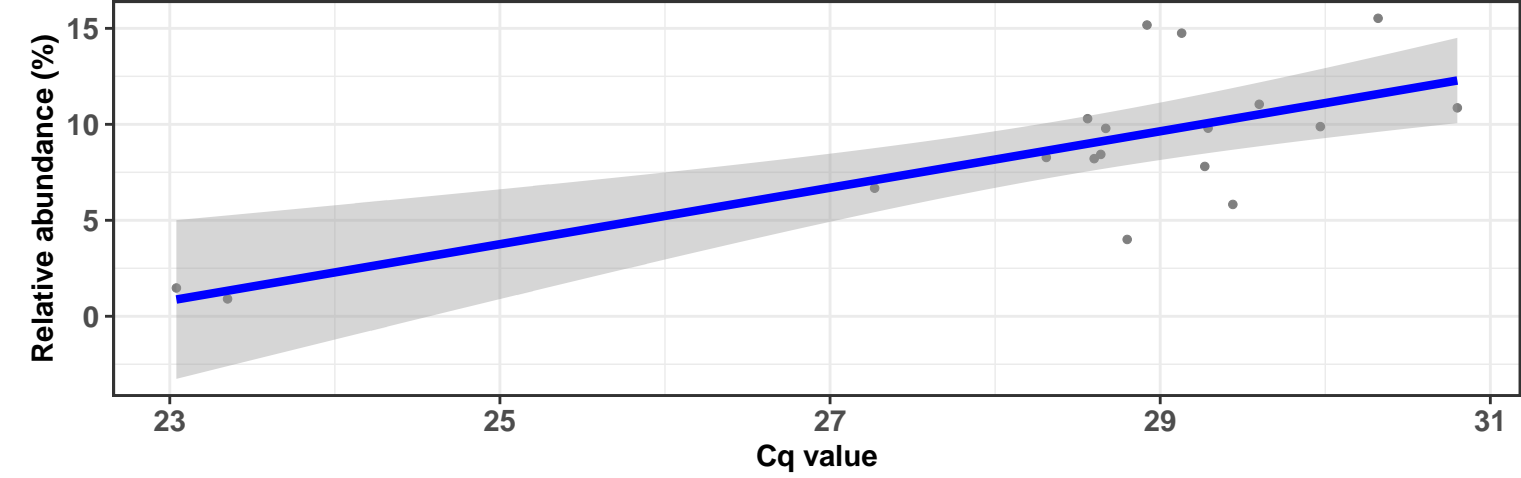**Correlation within: REF−DIM**

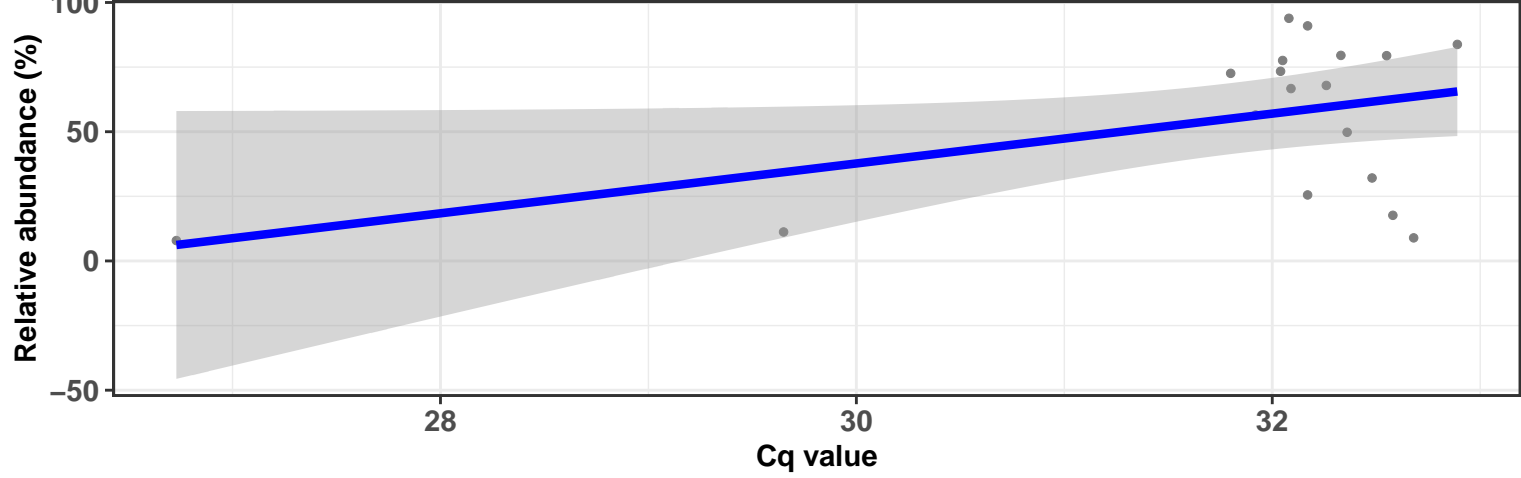$\log_e(S) = 6.020$, $p = 0.013$, $\hat{\rho}_{Spearman} = 0.575$, $CI_{95\%}$ [0.280, 0.951], $n_{pairs} = 18$

Correlation within: IM−DIC

$\log_e(S) = 5.935$, $p = 0.007$, $\hat{\rho}_{Spearman} = 0.610$, $CI_{95\%}$ [0.242, 1.008], $n_{pairs} = 18$
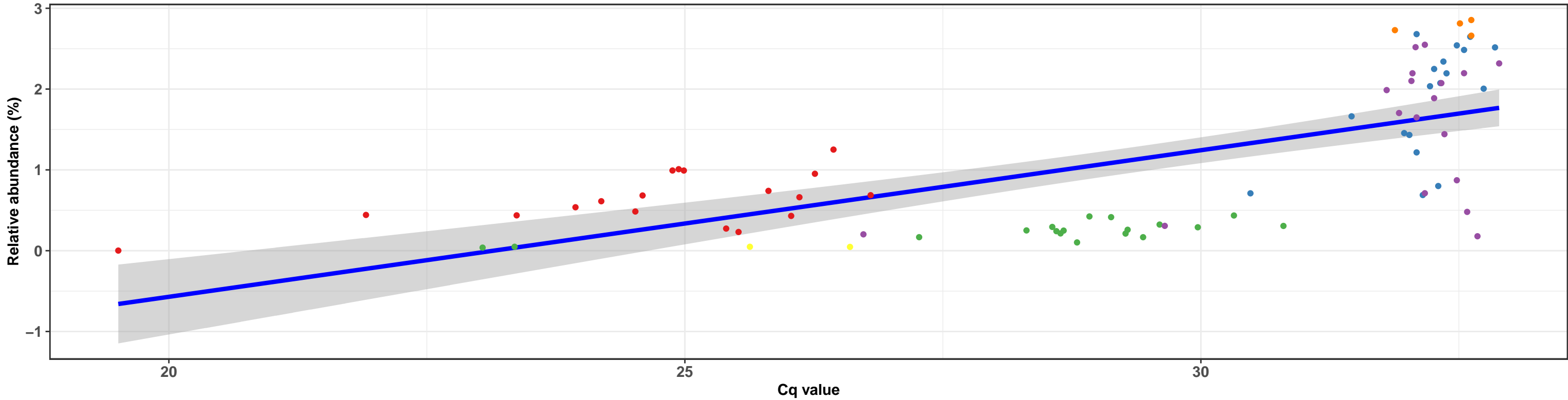
Correlation within: IM−DIM

$\log_e(S) = 6.759$, $p = 0.663$, $\hat{\rho}_{Spearman} = 0.110$, $CI_{95\%}$ [−0.418, 0.673], $n_{pairs} = 18$

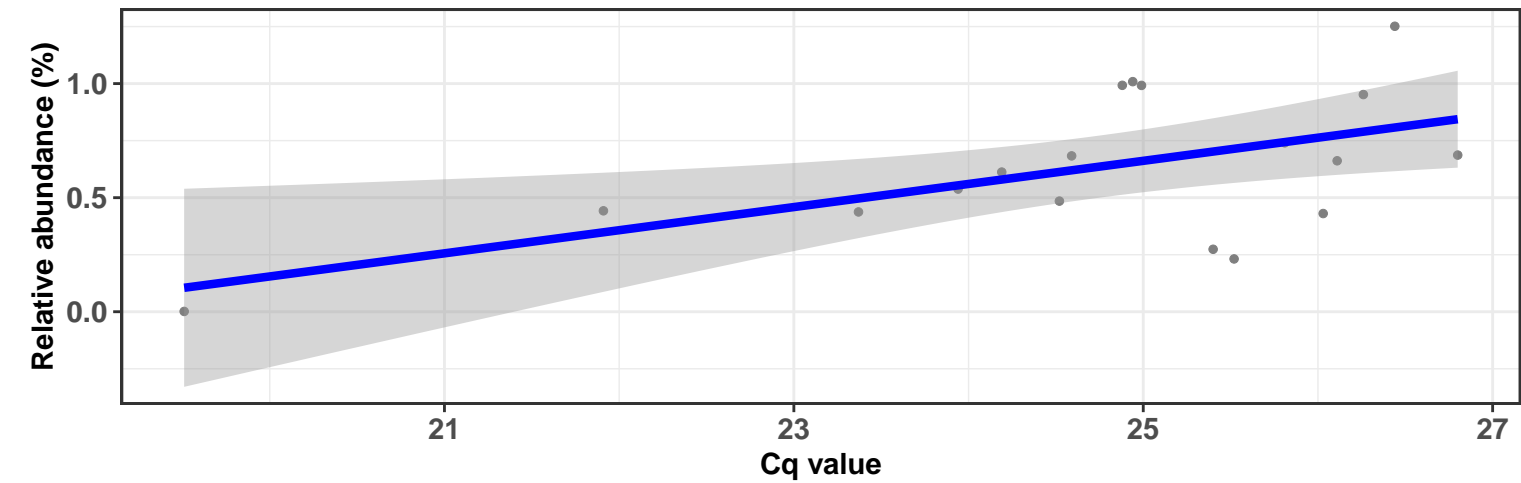# k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA
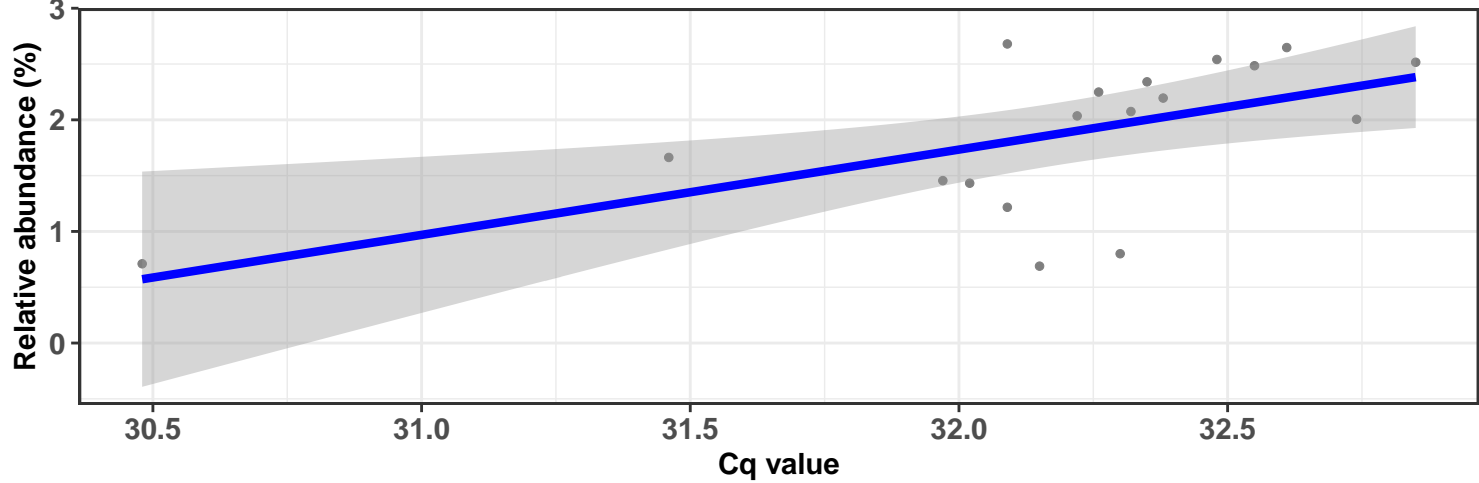
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

Correlation with all samples

$\log_e(S) = 9.123$, $p = 0.018$, $\hat{\rho}_{Spearman} = 0.354$, $CI_{95\%}$ [0.093, 0.692], $n_{pairs} = 44$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
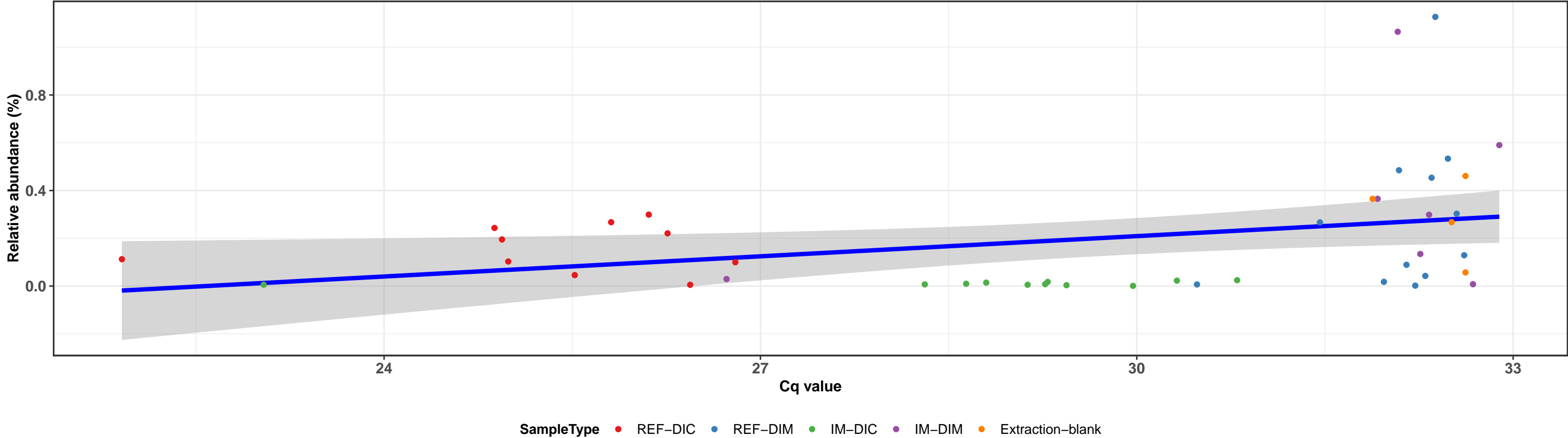
Correlation within: REF−DIC

$\log_e(S) = 5.308$, $p = 0.533$, $\hat{\rho}_{Spearman} = -0.224$, $CI_{95\%}$ [−0.932, 0.400], $n_{pairs} = 10$

Correlation within: REF−DIM

$\log_e(S) = 5.024$, $p = 0.124$, $\hat{\rho}_{Spearman} = 0.469$, $CI_{95\%}$ [0.017, 1.023], $n_{pairs} = 12$

Correlation within: IM−DIC

$\log_e(S) = 5.063$, $p = 0.401$, $\hat{\rho}_{Spearman} = 0.282$, $CI_{95\%}$ [−0.485, 1.157], $n_{pairs} = 11$
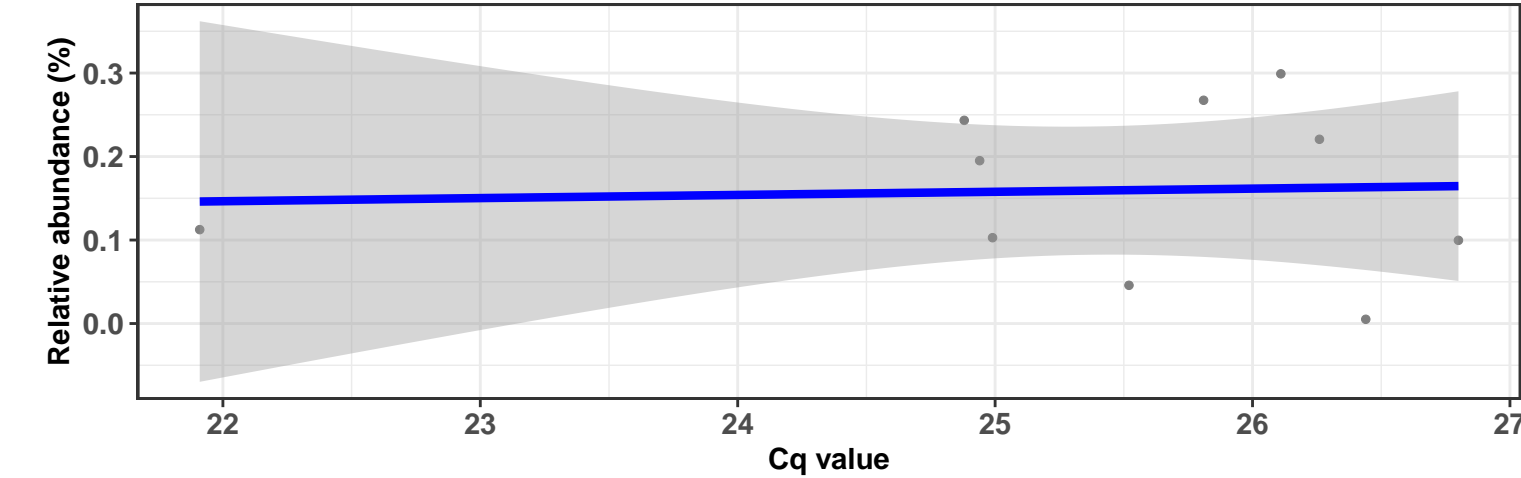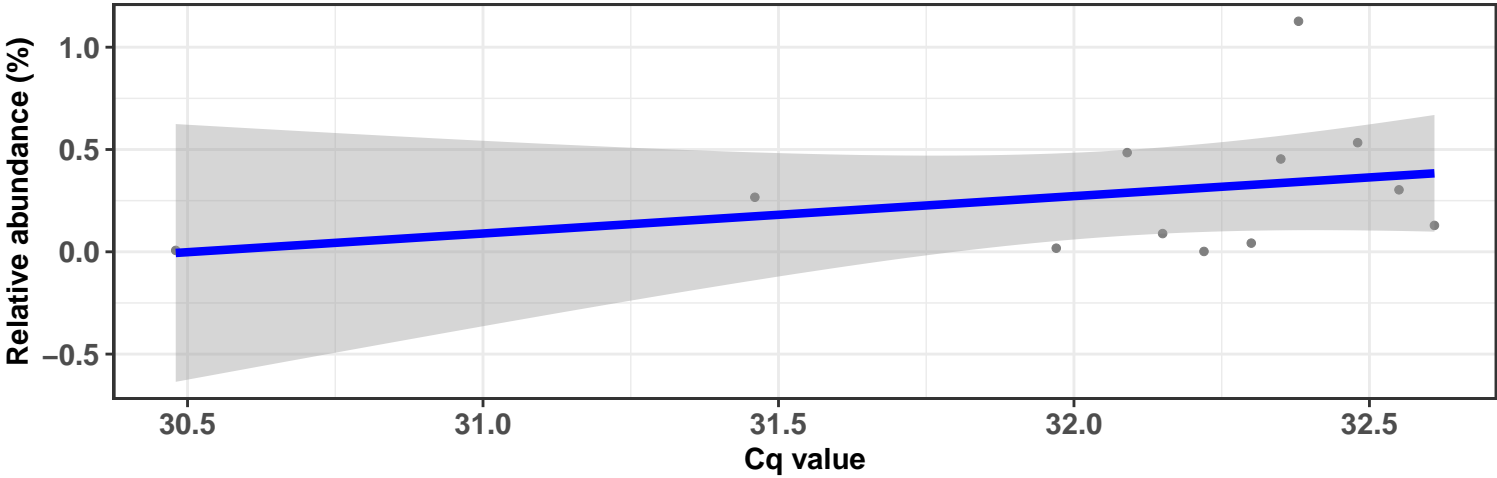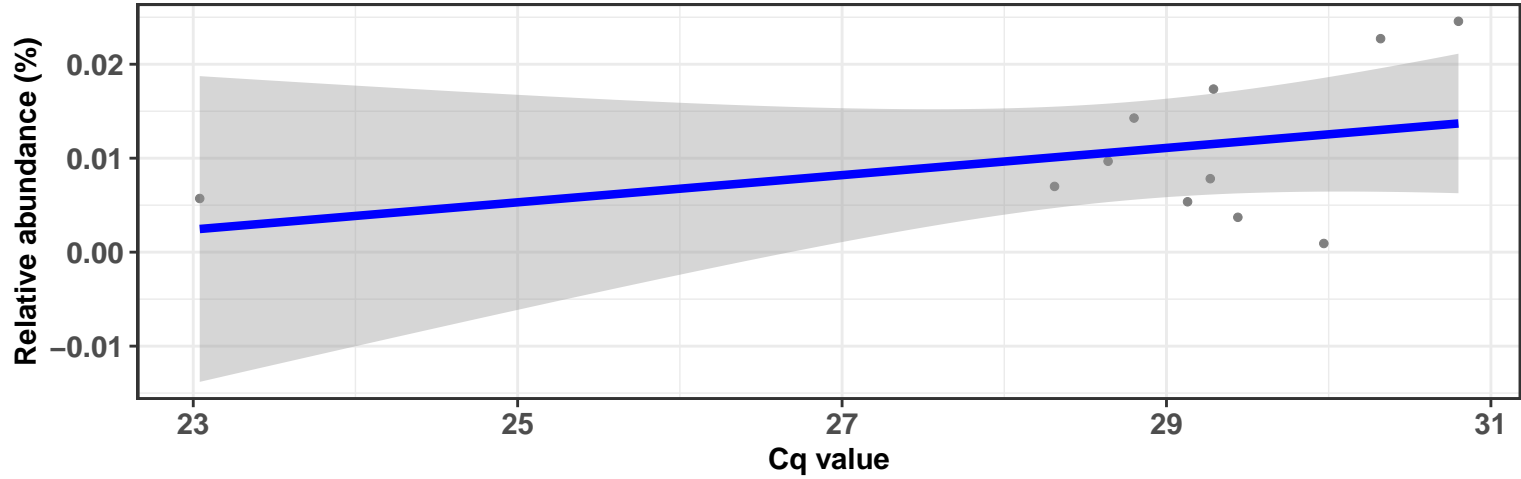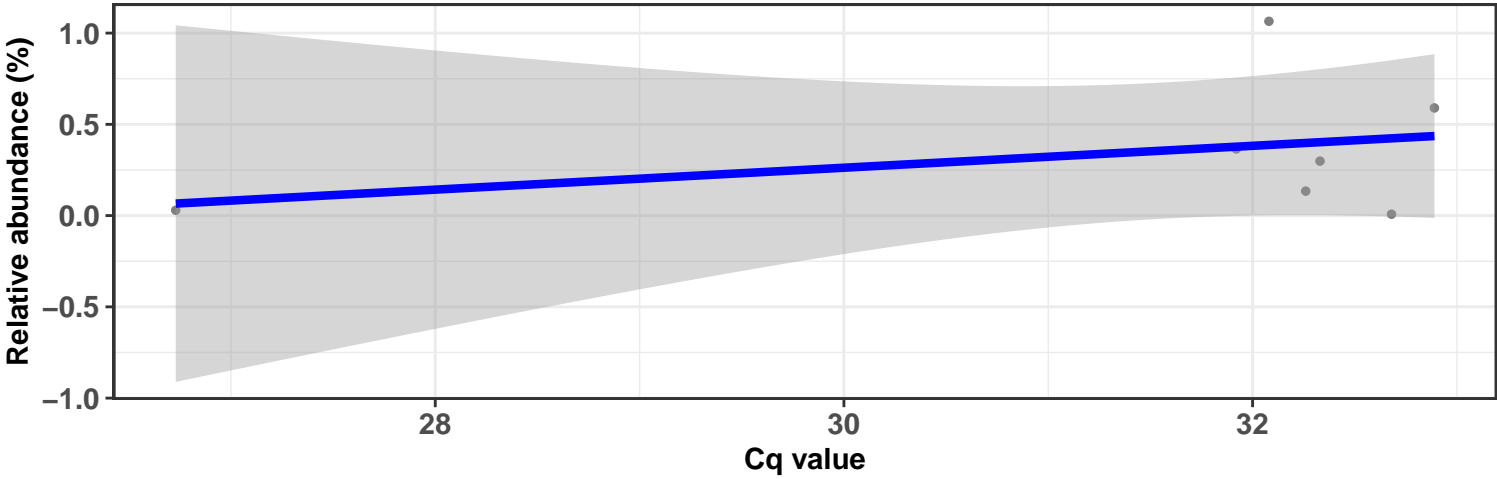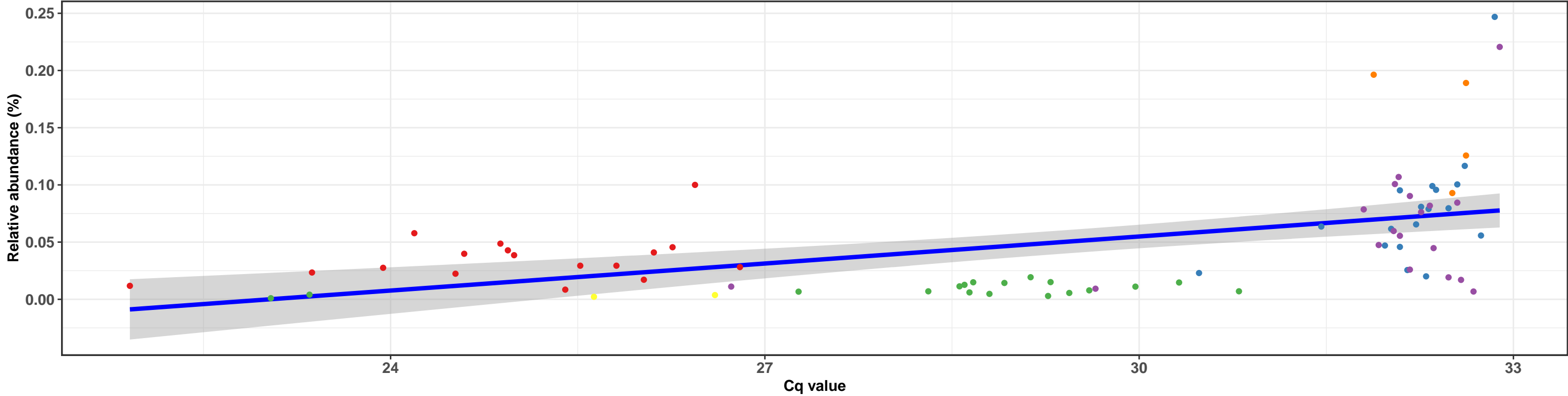
Correlation within: IM−DIM

$\log_e(S) = 3.989$, $p = 0.939$, $\hat{\rho}_{Spearman} = 0.036$, $CI_{95\%}$ [−0.850, 0.957], $n_{pairs} = 7$

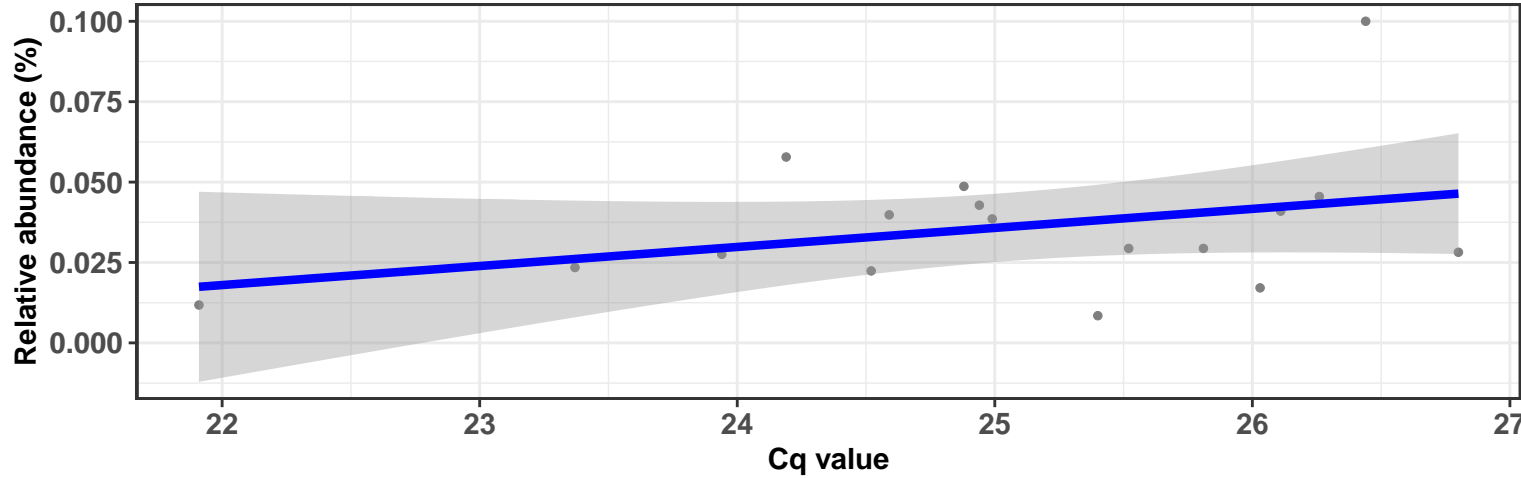k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

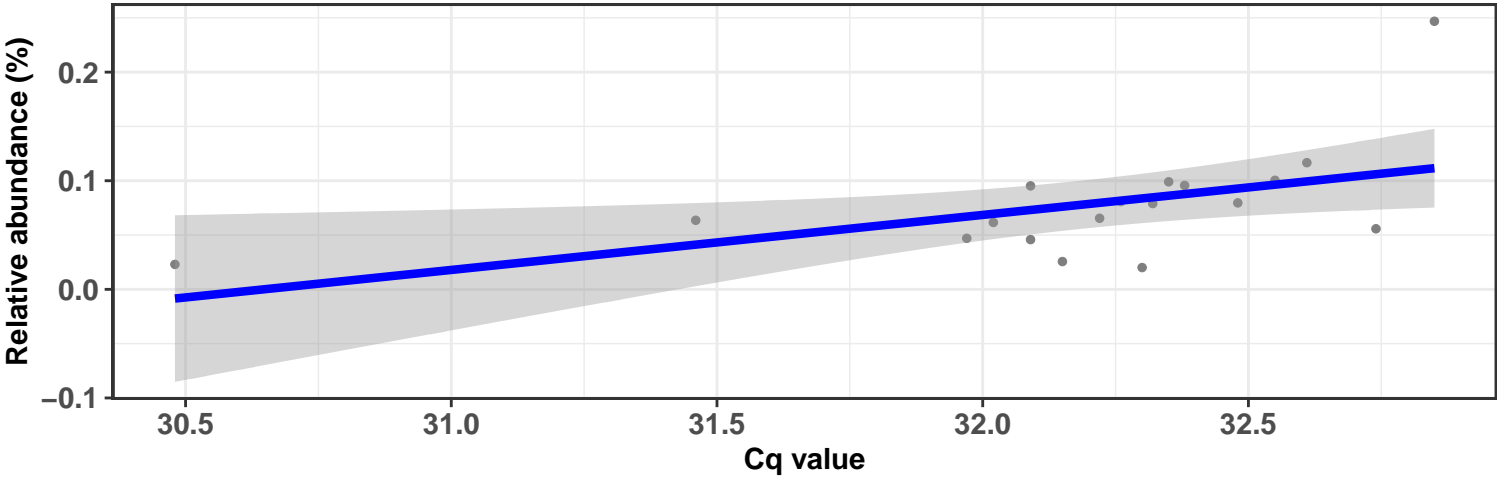$\log_e(S) = 10.412$, $p = < 0.001$, $\widehat{\rho}_{Spearman} = 0.563$, $CI_{95\%}$ [0.395, 0.753], $n_{pairs} = 77$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock

Correlation within: REF−DIC

$\log_e(S) = 6.370$, $p = 0.269$, $\widehat{\rho}_{Spearman} = 0.284$, $CI_{95\%}$ [−0.242, 0.923], $n_{pairs} = 17$

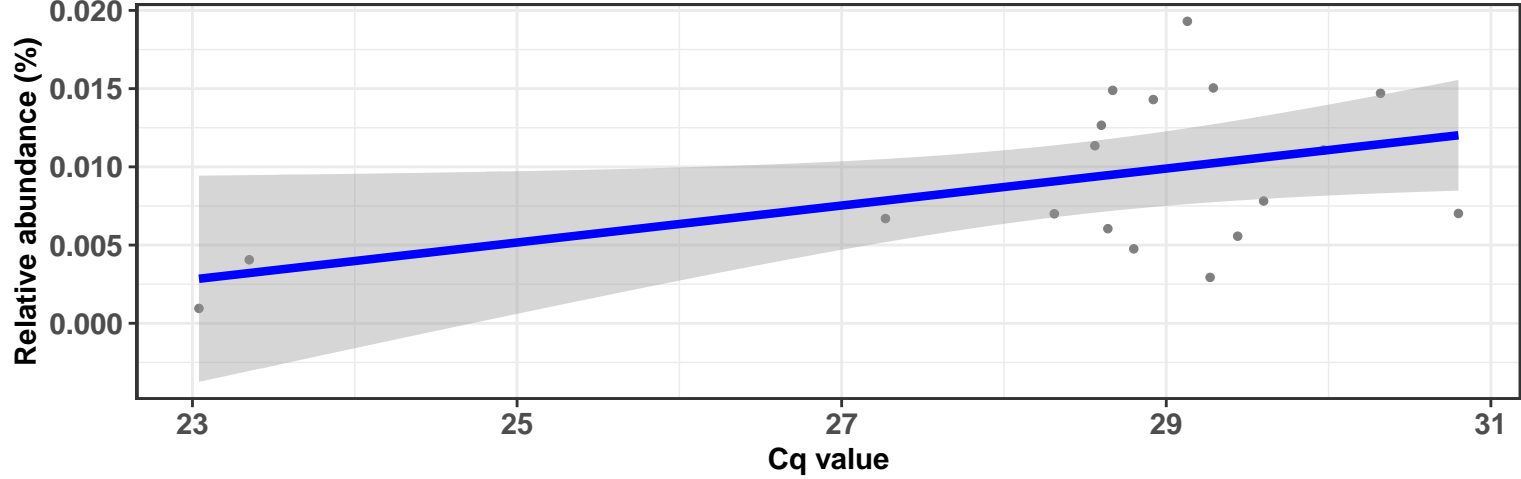**Correlation within: REF−DIM**

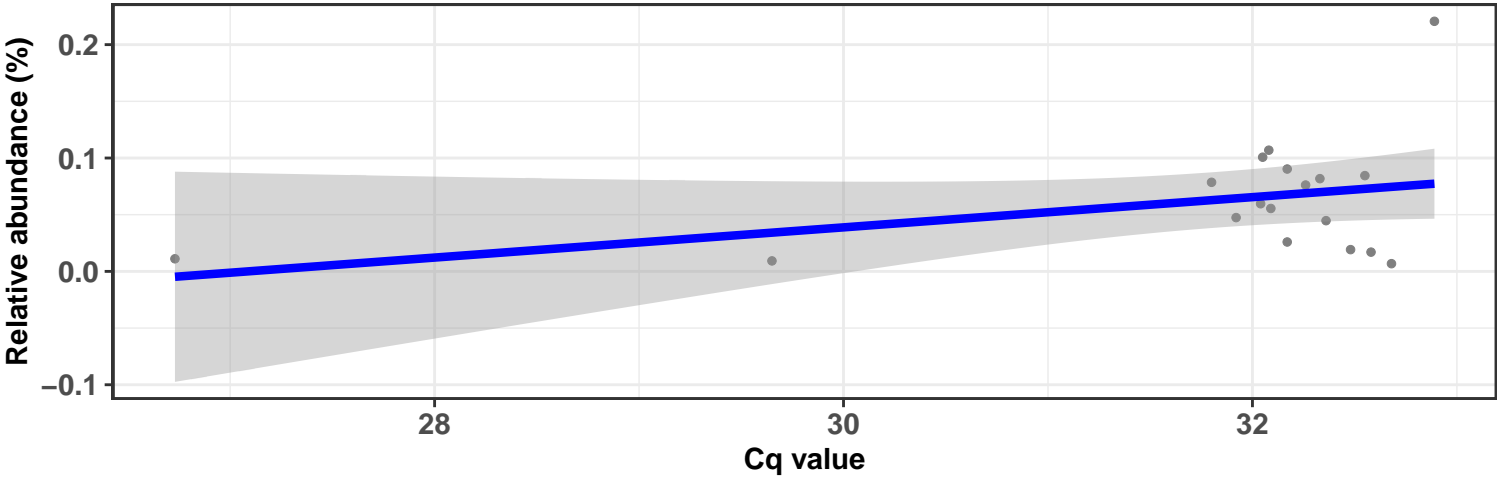$\log_e(S) = 5.882$, $p = 0.005$, $\widehat{\rho}_{Spearman} = 0.630$, $CI_{95\%}$ [0.293, 1.036], $n_{pairs} = 18$

Correlation within: IM−DIC

$\log_e(S) = 6.426$, $p = 0.140$, $\widehat{\rho}_{Spearman} = 0.362$, $CI_{95\%}$ [−0.034, 0.777], $n_{pairs} = 18$

Correlation within: IM−DIM

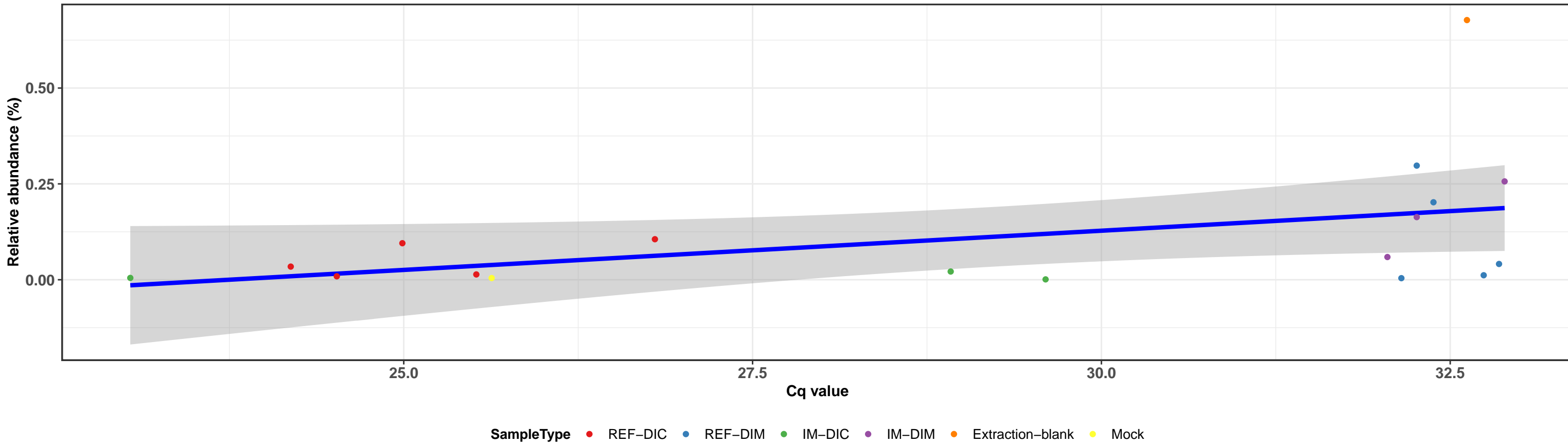$\log_e(S) = 6.790$, $p = 0.745$, $\widehat{\rho}_{Spearman} = 0.083$, $CI_{95\%}$ [−0.528, 0.706], $n_{pairs} = 18$
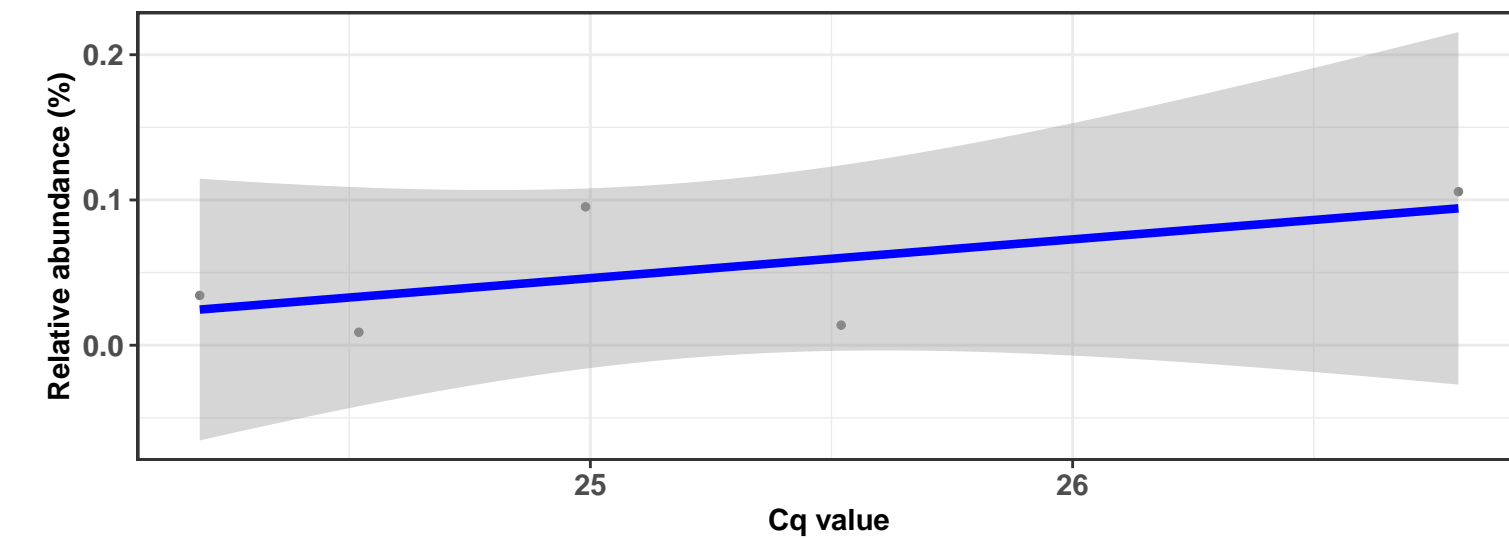
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Curtobacterium; Ambiguous_taxa
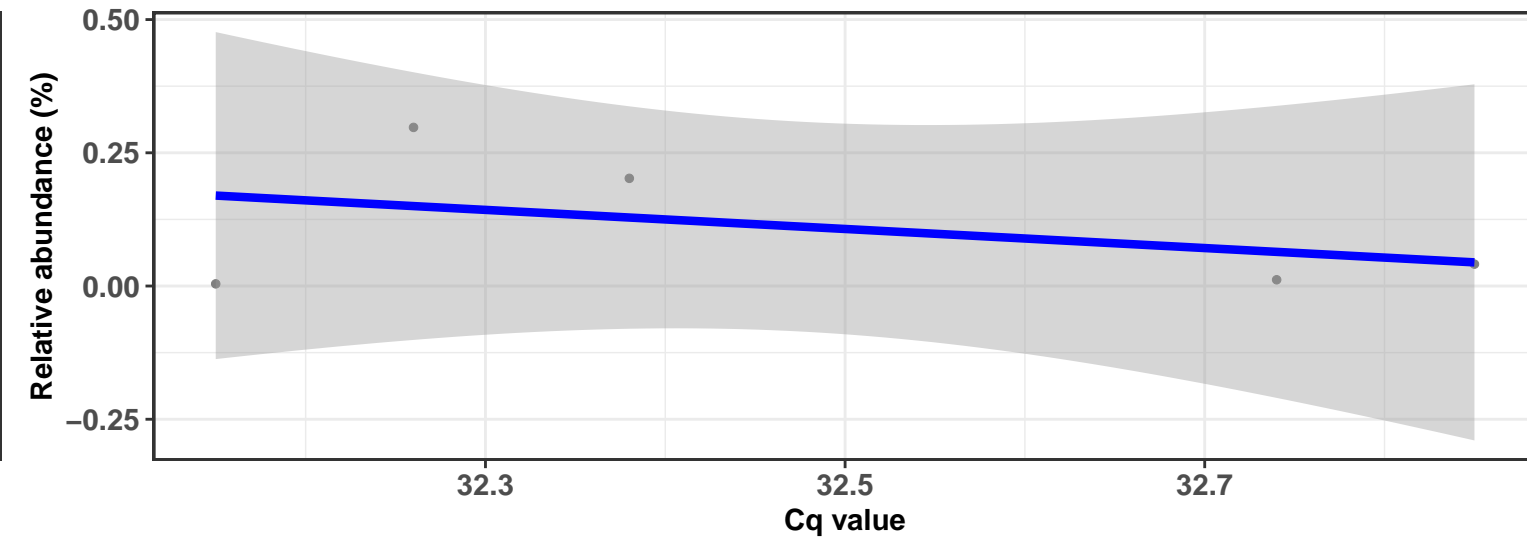
Correlation with all samples

$\log_e(S) = 6.228$, $p = 0.045$, $\hat{\rho}_{Spearman} = 0.477$, $CI_{95\%}$ [0.166, 0.859], $n_{pairs} = 18$

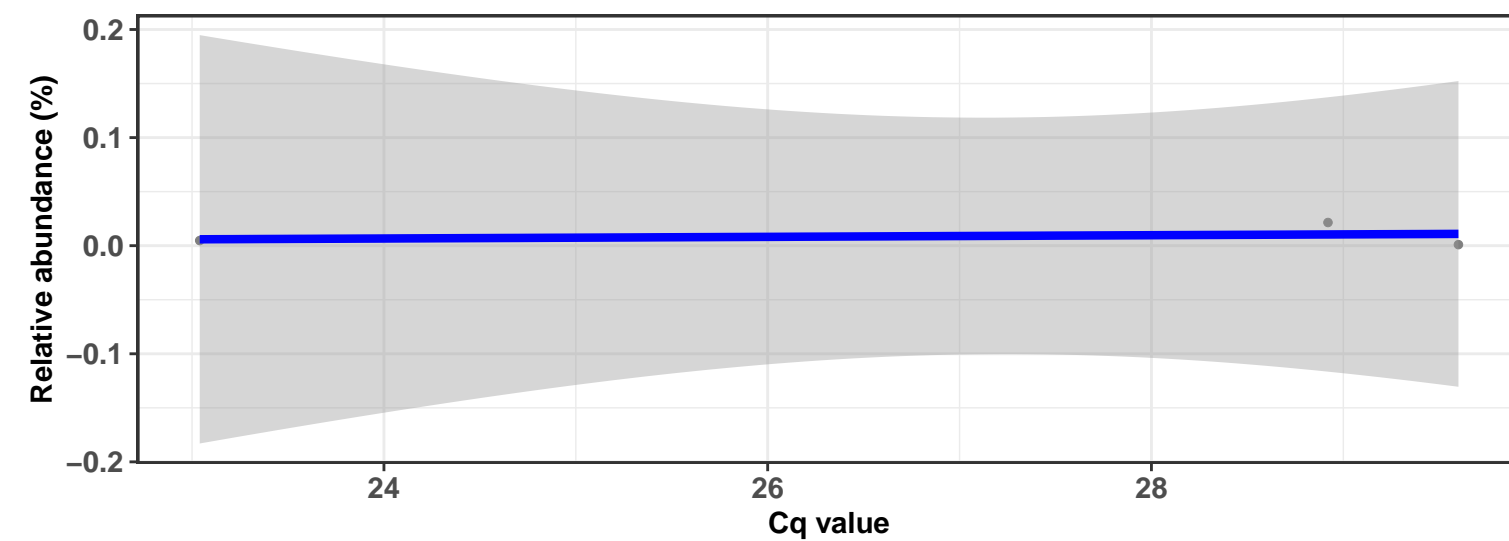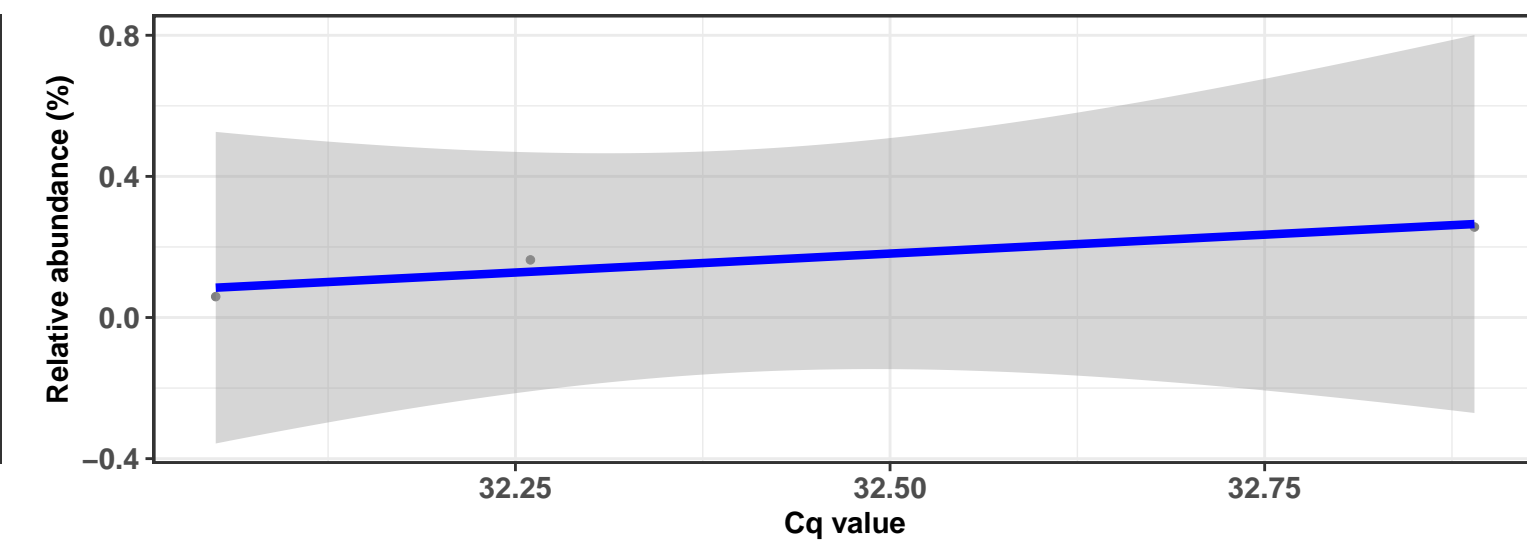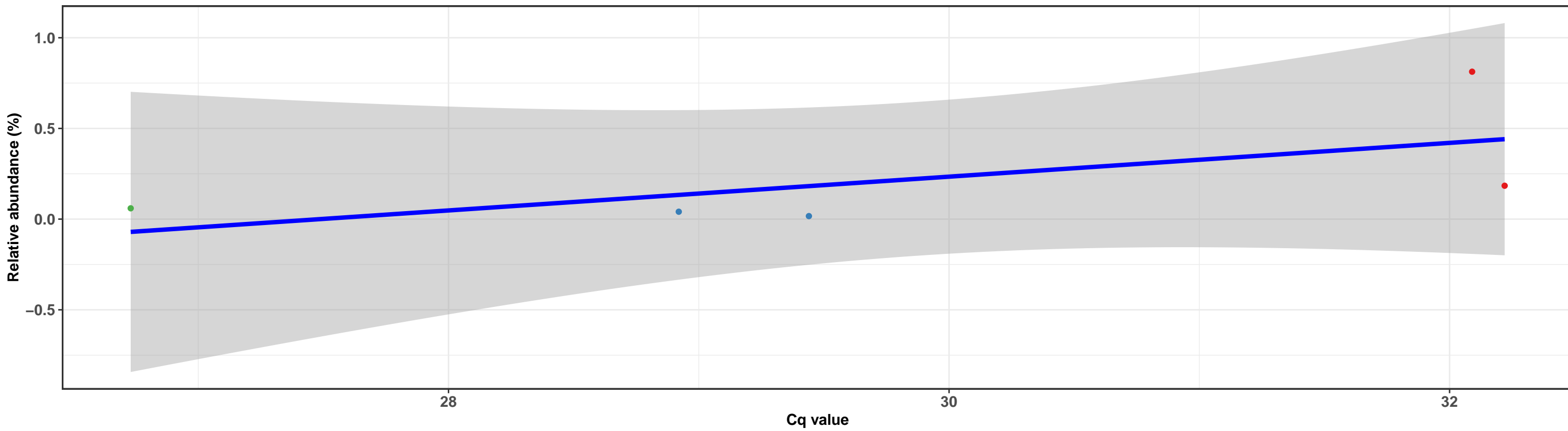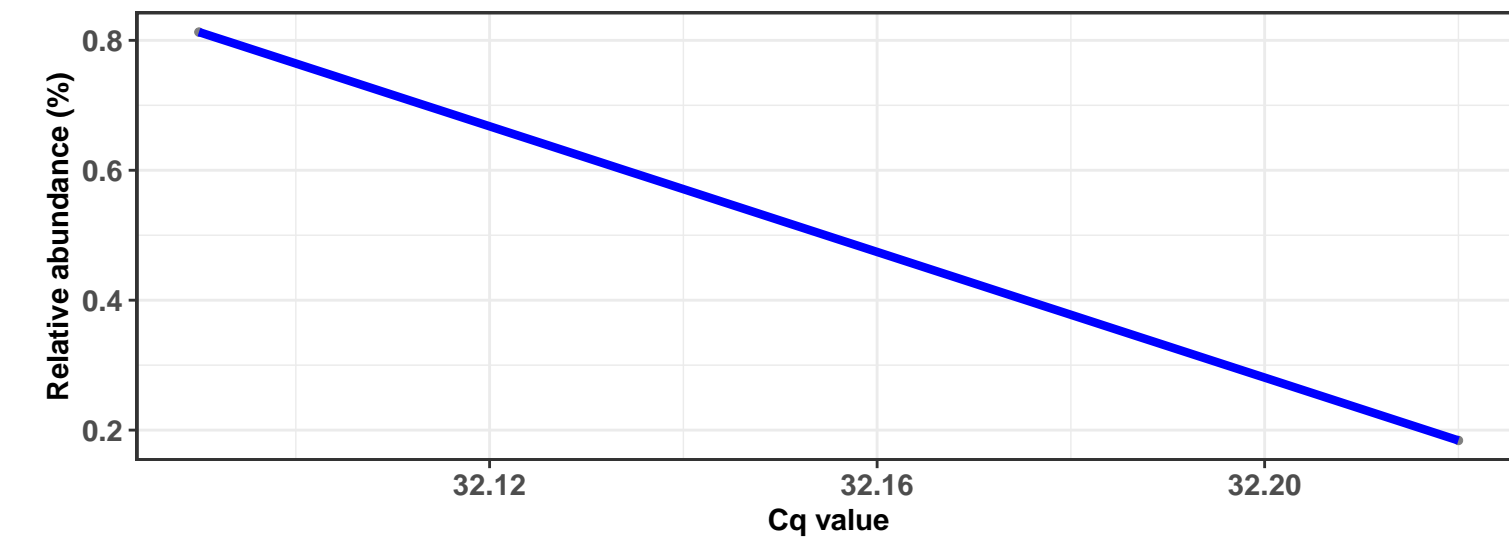# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Jeotgalicoccus; Ambiguous_taxa
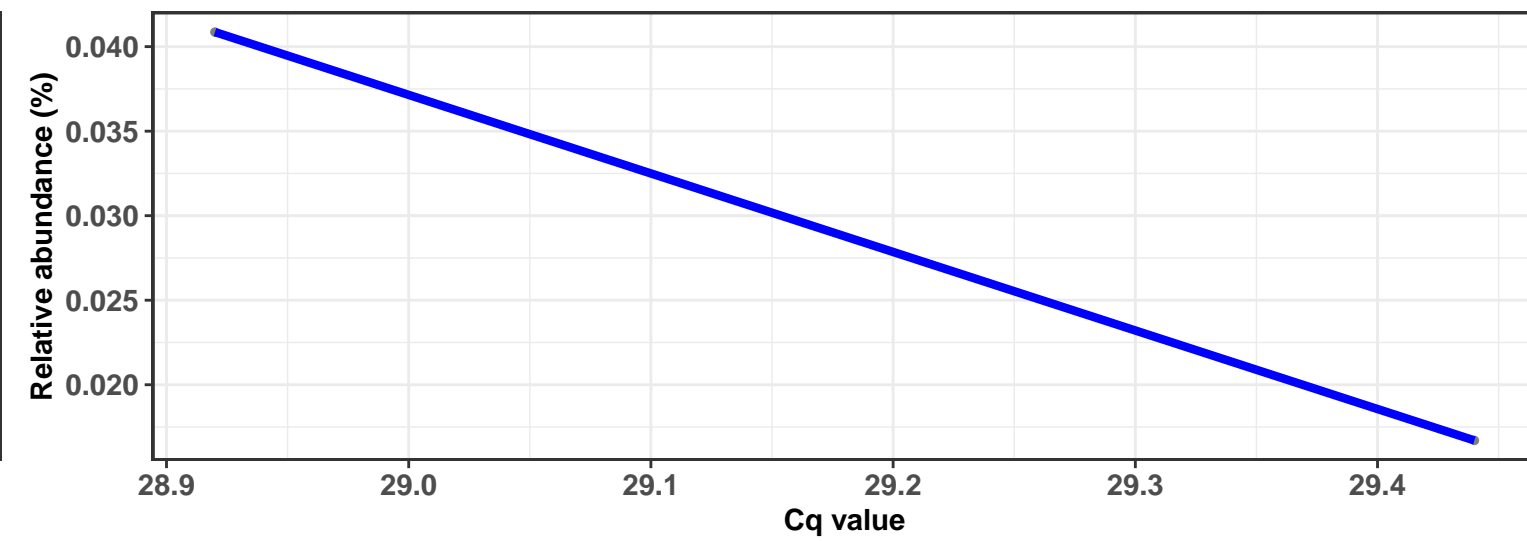
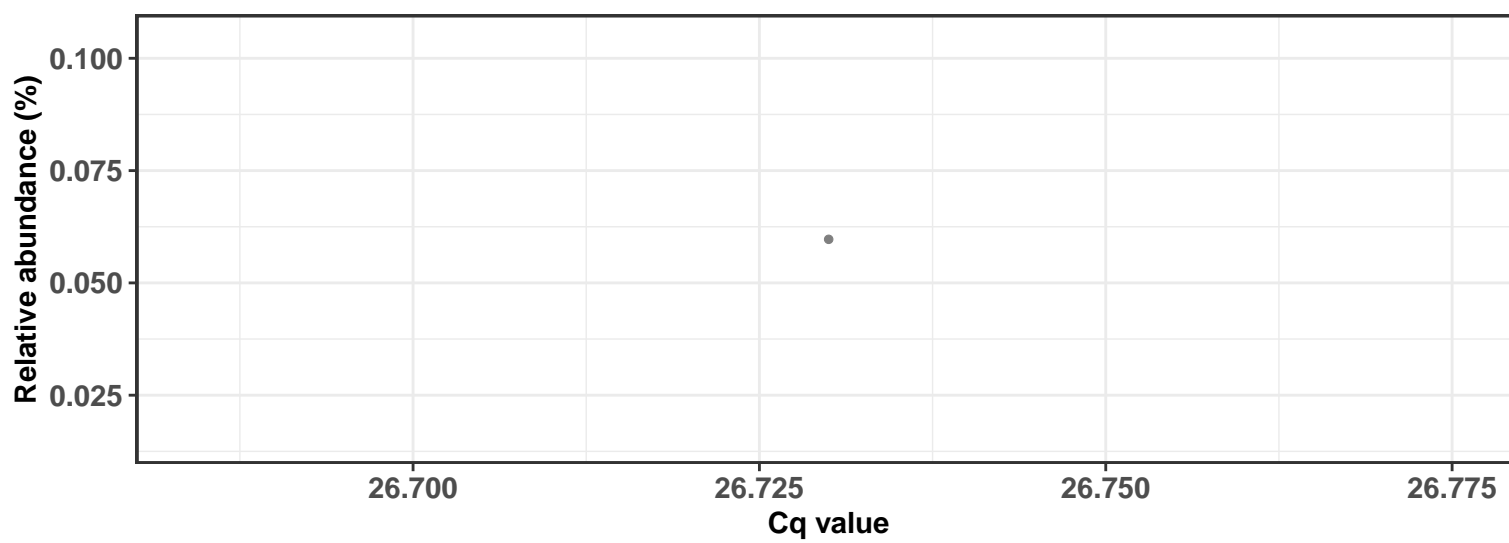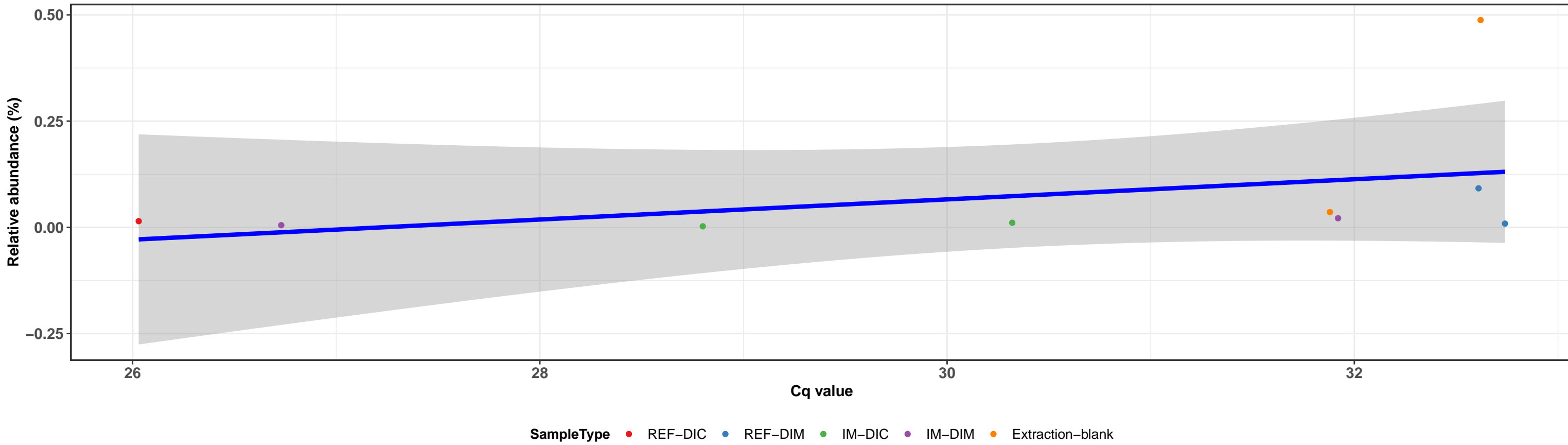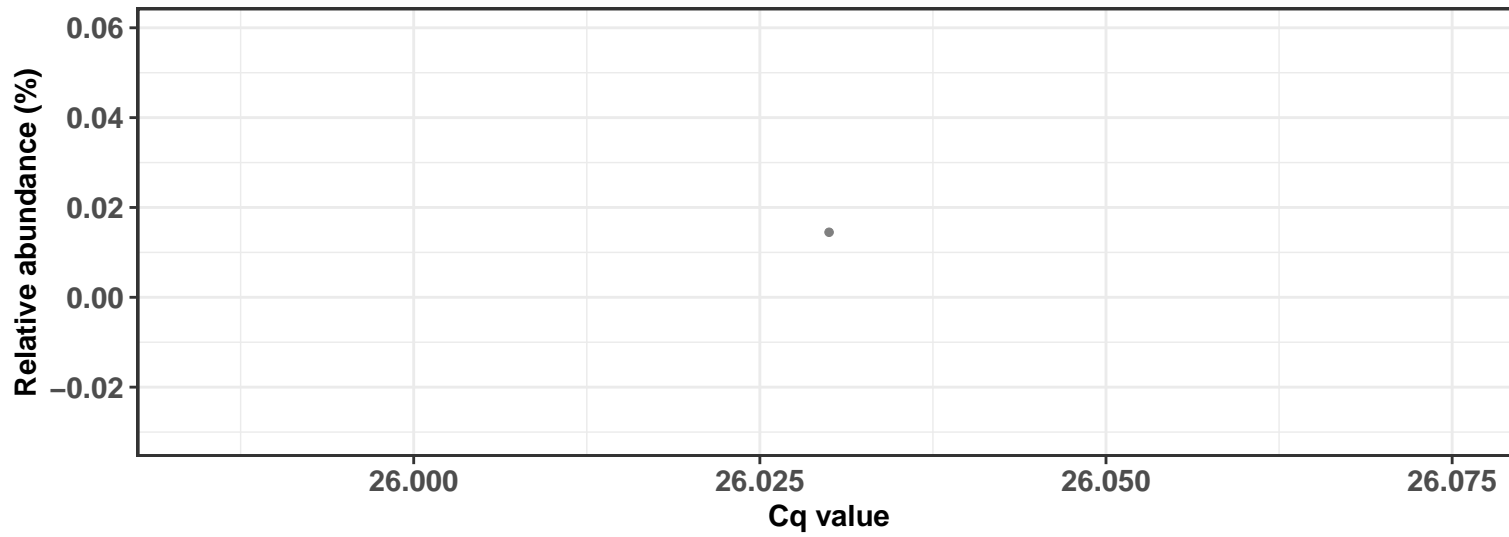# k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Frankiales; f__Geodermatophilaceae; g__Modestobacter; Ambiguous_taxa

Correlation with all samples
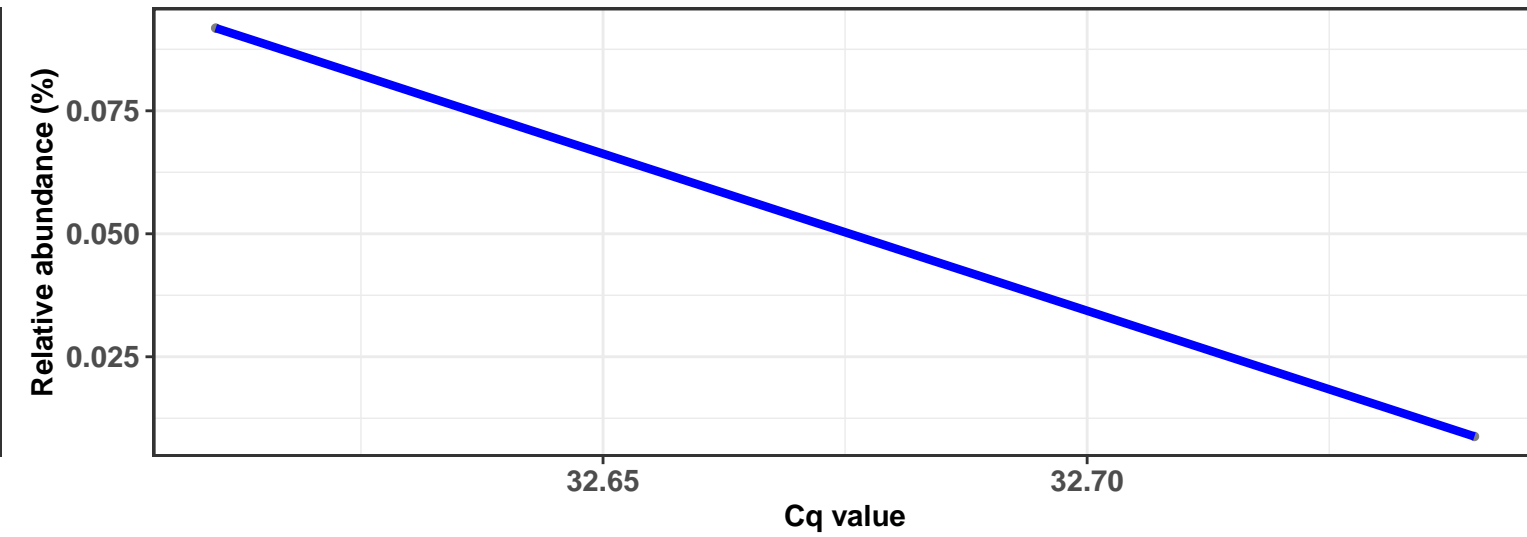
$\log_e(S) = 4.127$, $p = 0.187$, $\hat{\rho}_{Spearman} = 0.483$, $CI_{95\%}$ [−0.150, 1.260], $n_{pairs} = 9$

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

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

Correlation with all samples

$\log_e(S) = 2.890$, $p = 0.021$, $\hat{\rho}_{Spearman} = 0.786$, $CI_{95\%}$ [0.425, 1.193], $n_{pairs} = 8$
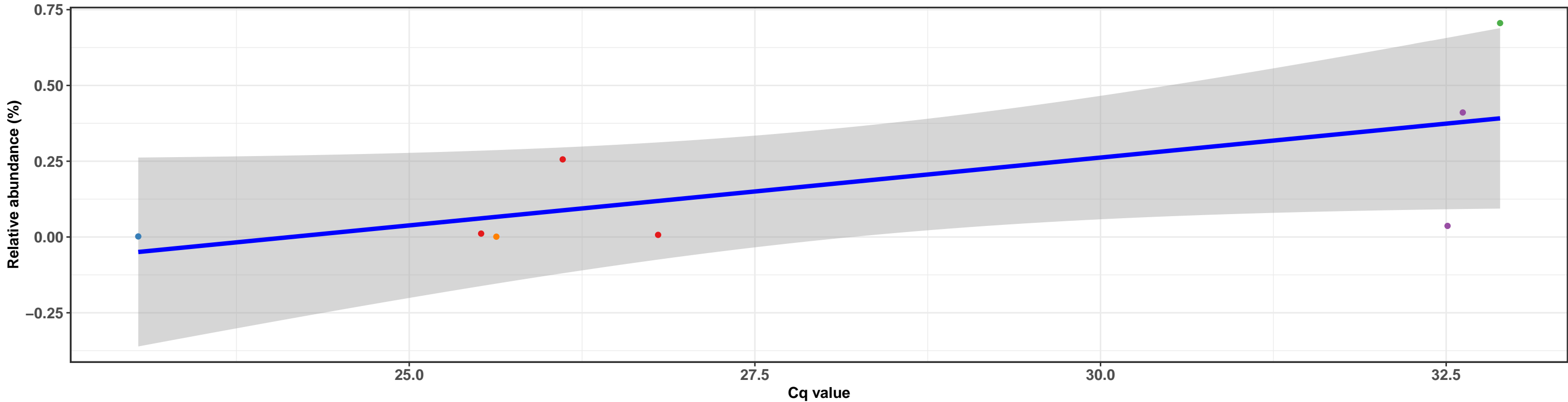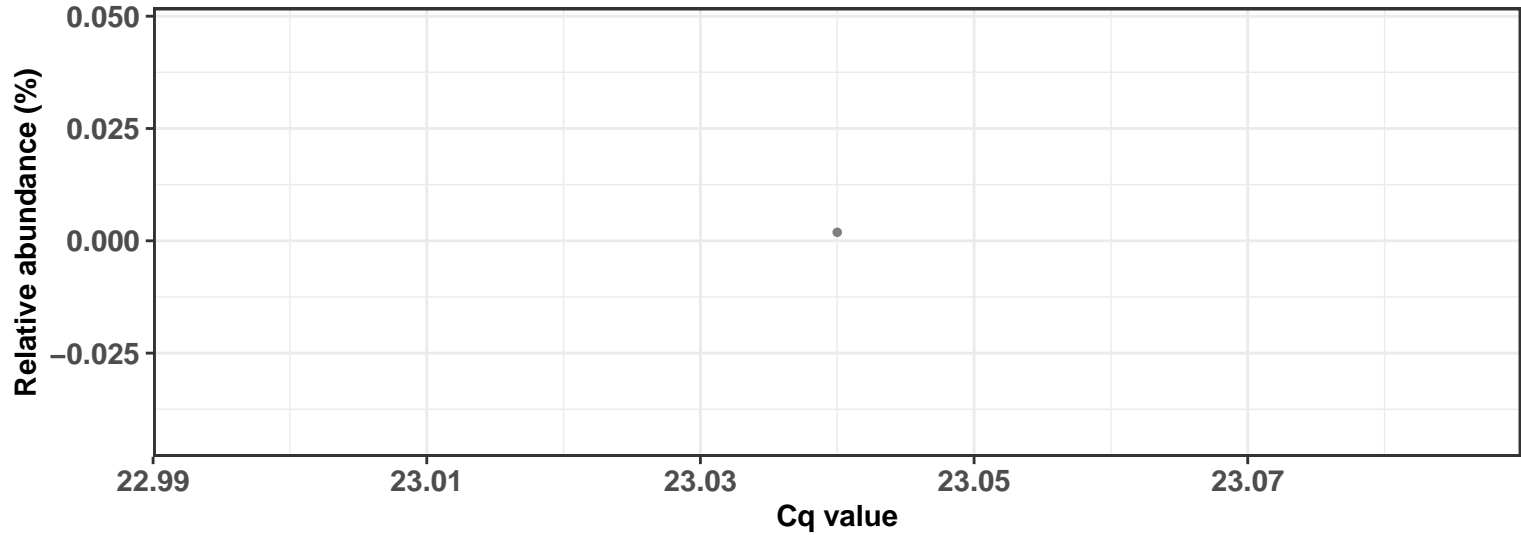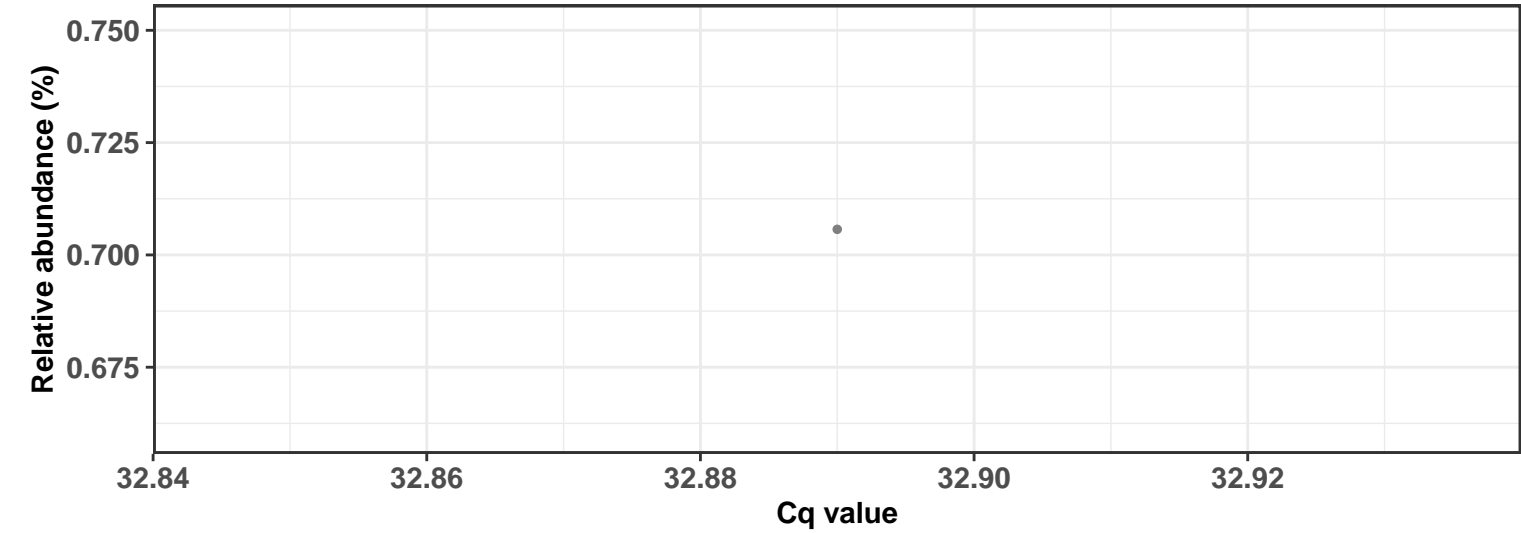
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 6.035$, $p = 0.047$, $\hat{\rho}_{Spearman} = 0.488$, $CI_{95\%}$ [0.052, 1.024], $n_{pairs} = 17$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
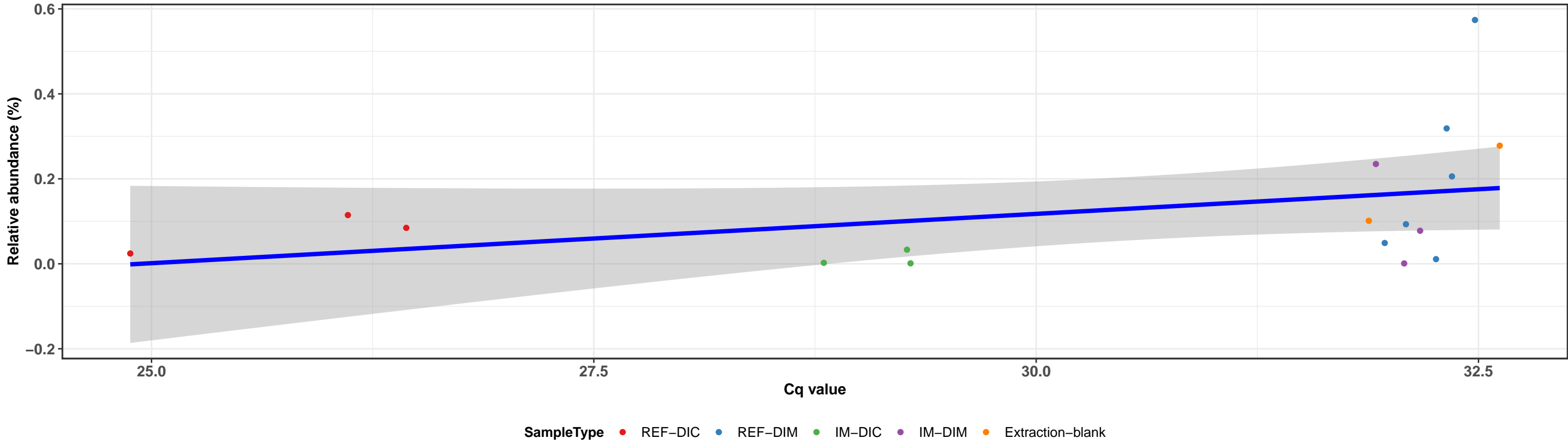
Correlation within: REF−DIC
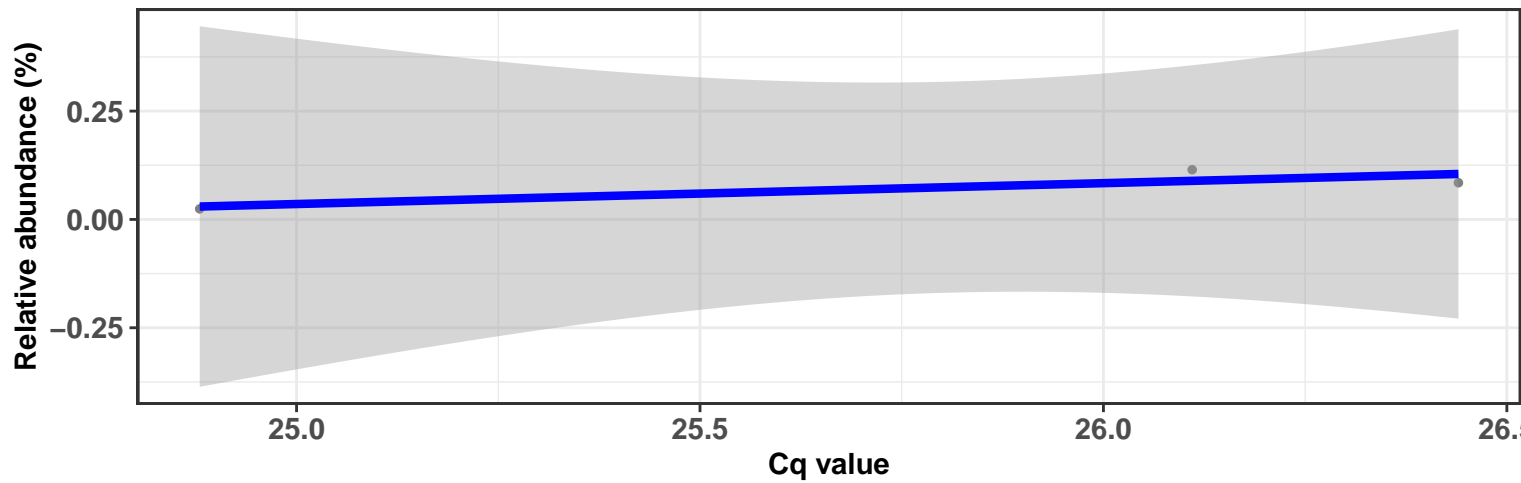
Correlation within: REF−DIM

$\log_e(S) = 2.079$, $p = 0.072$, $\hat{\rho}_{Spearman} = 0.771$, $CI_{95\%}$ [0.278, 1.252], $n_{pairs} = 6$
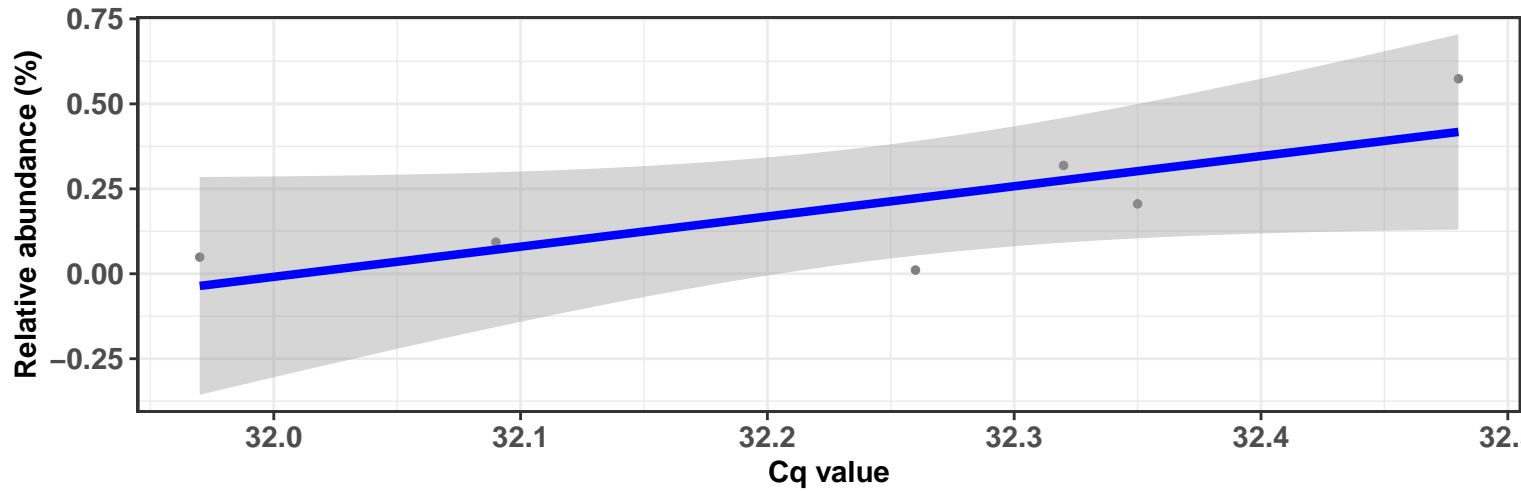
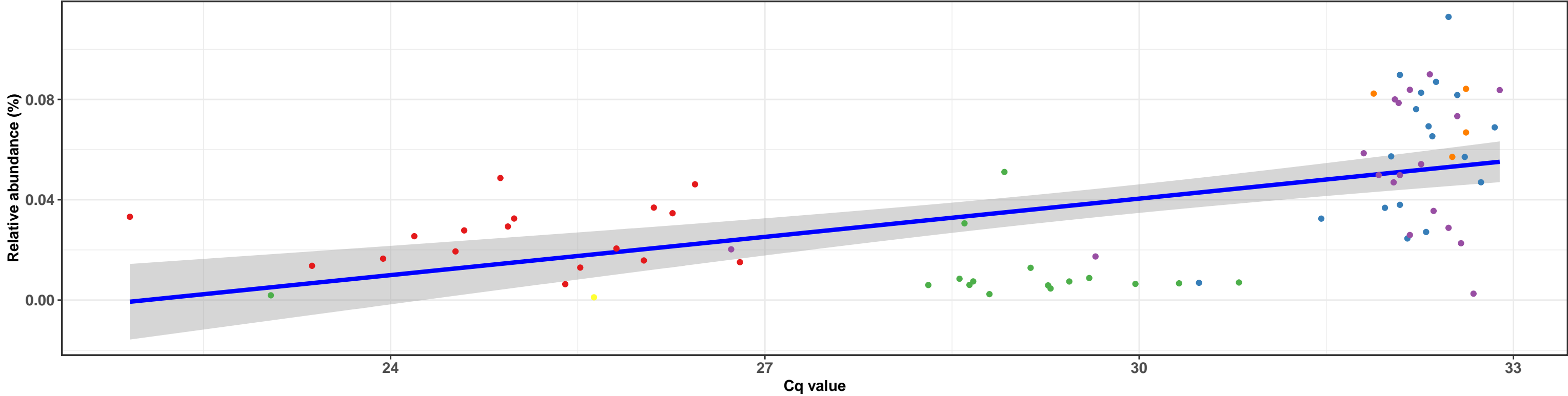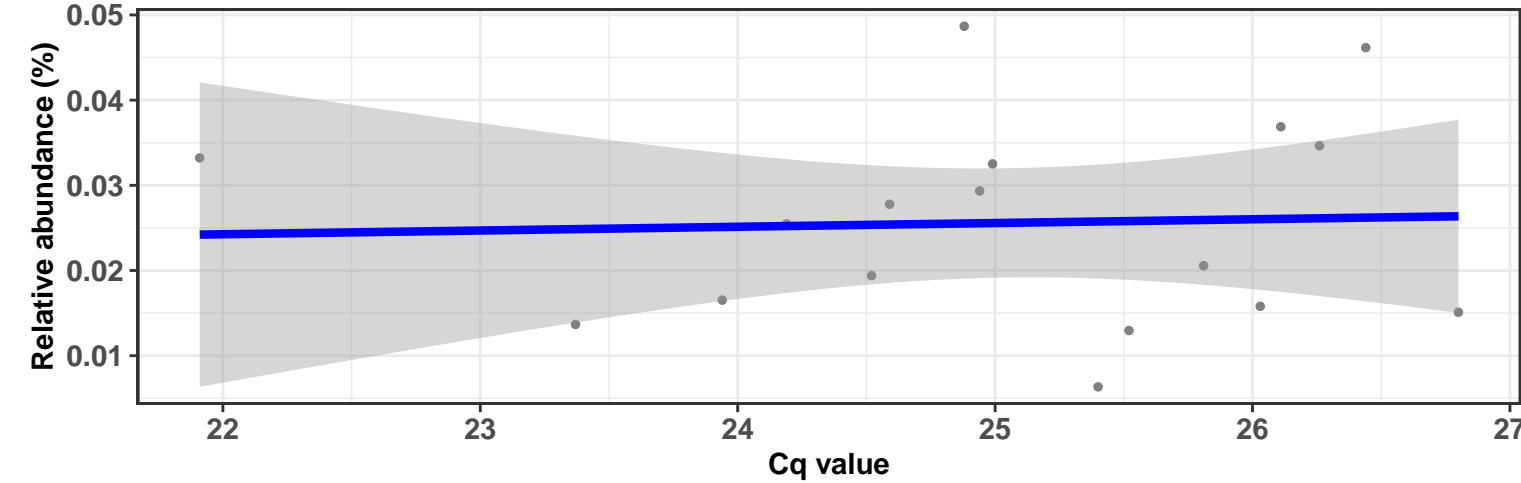**Correlation within: IM−DIC**
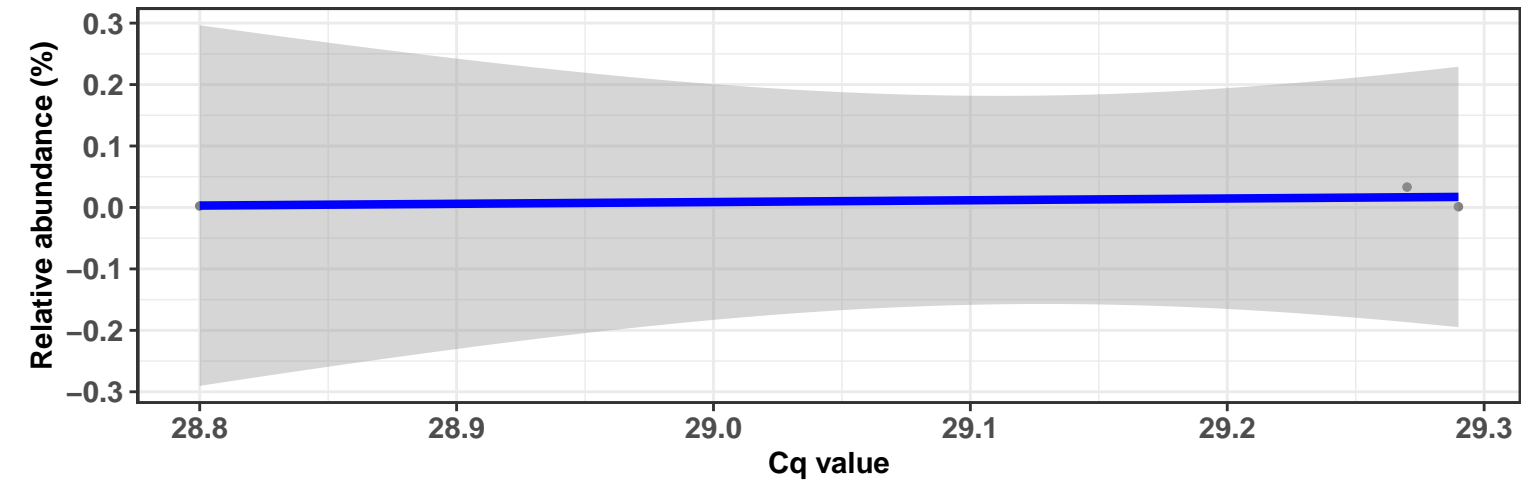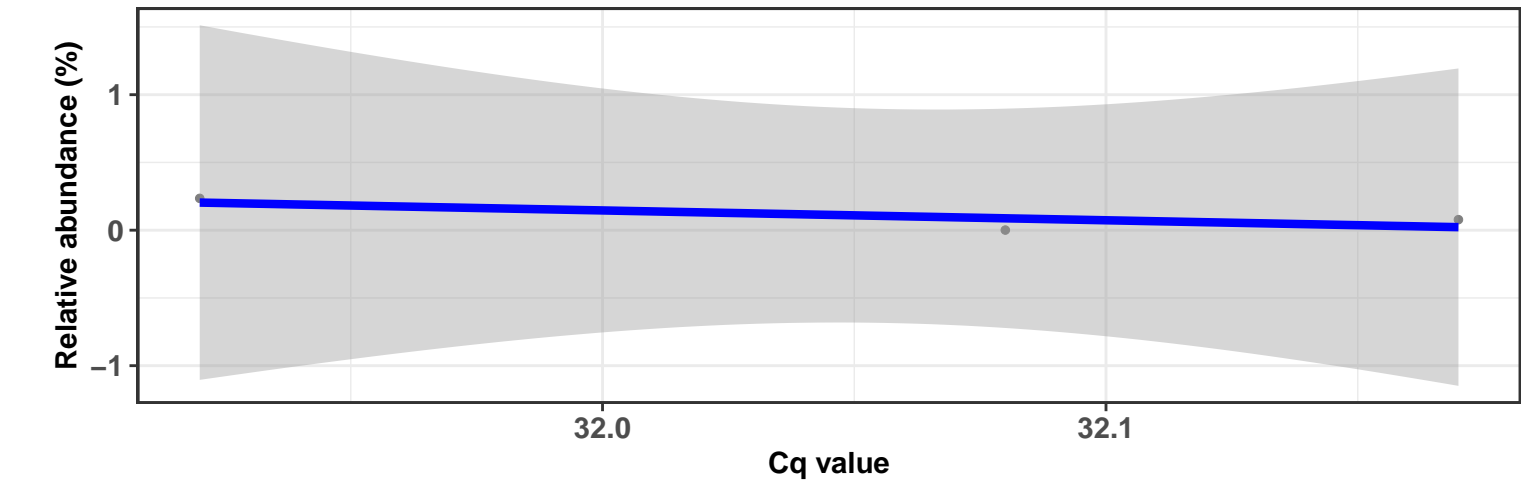
Correlation within: IM−DIM

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

Correlation with all samples

$\log_e(S) = 4.220$, $p = < 0.001$, $\widehat{\rho}_{Spearman} = 0.851$, $CI_{95\%}$ [0.687, 1.079], $n_{pairs} = 14$
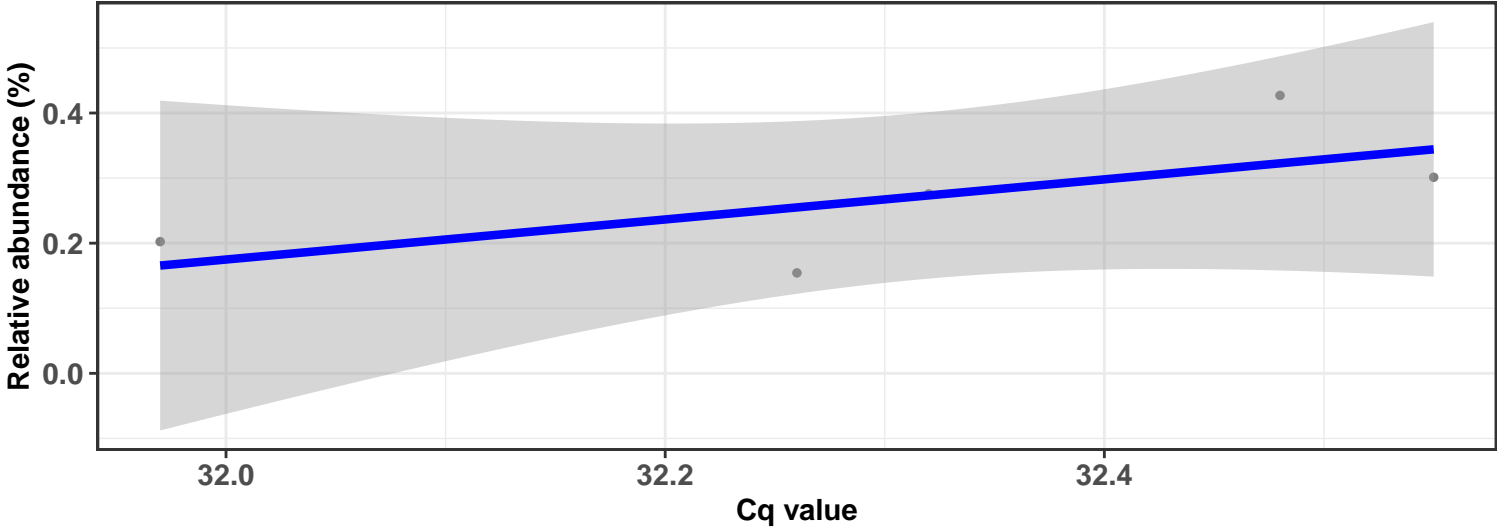
SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock

Correlation within: REF−DIC

Correlation within: REF−DIM
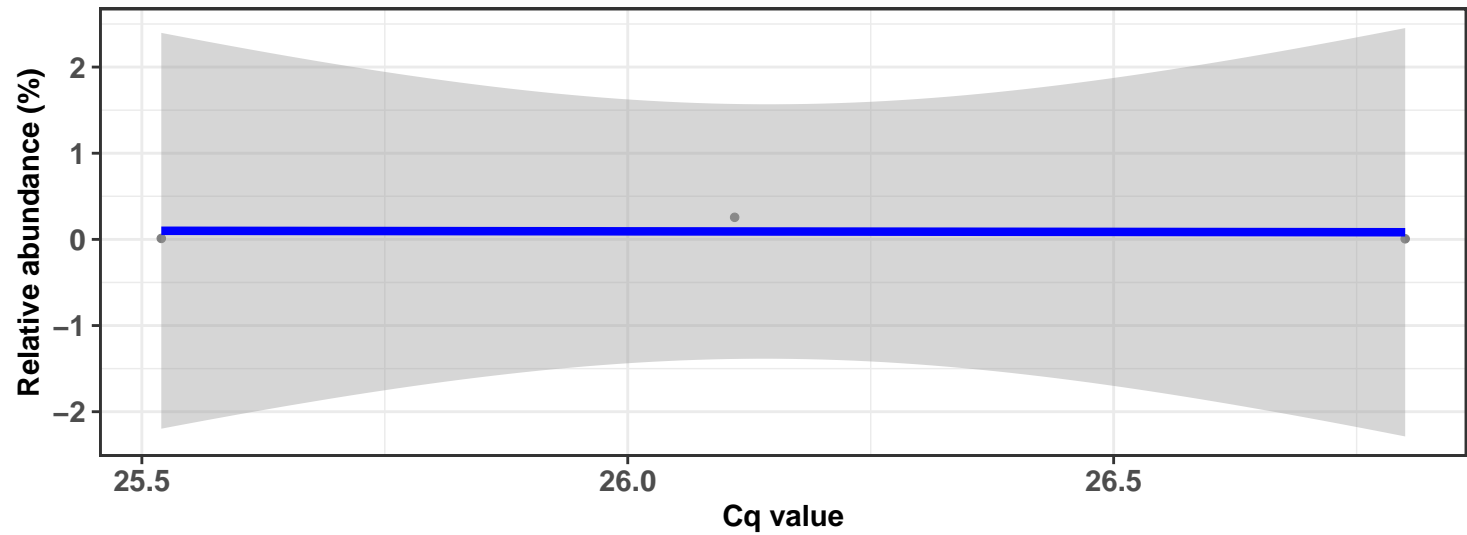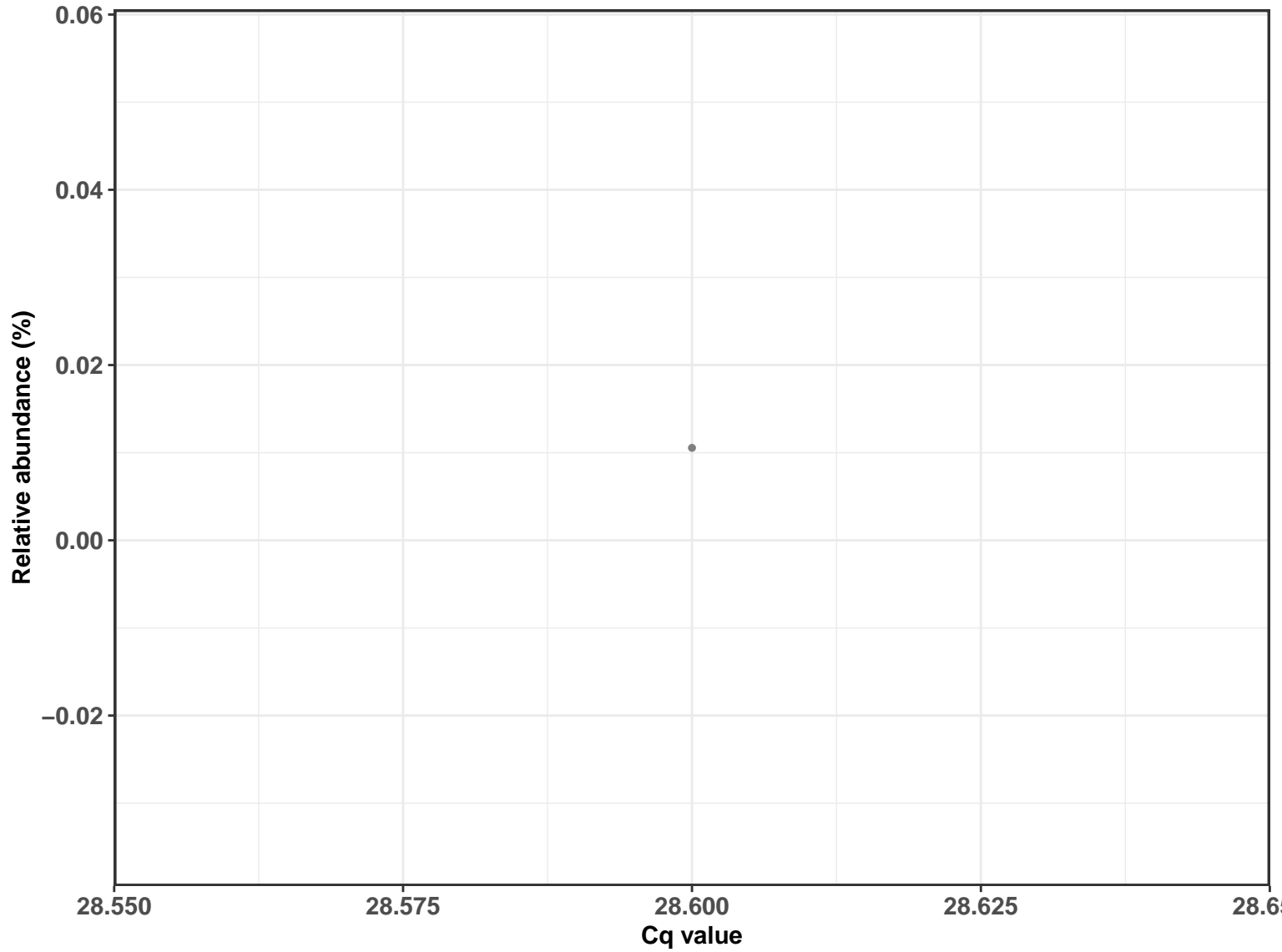
Correlation within: IM−DIC
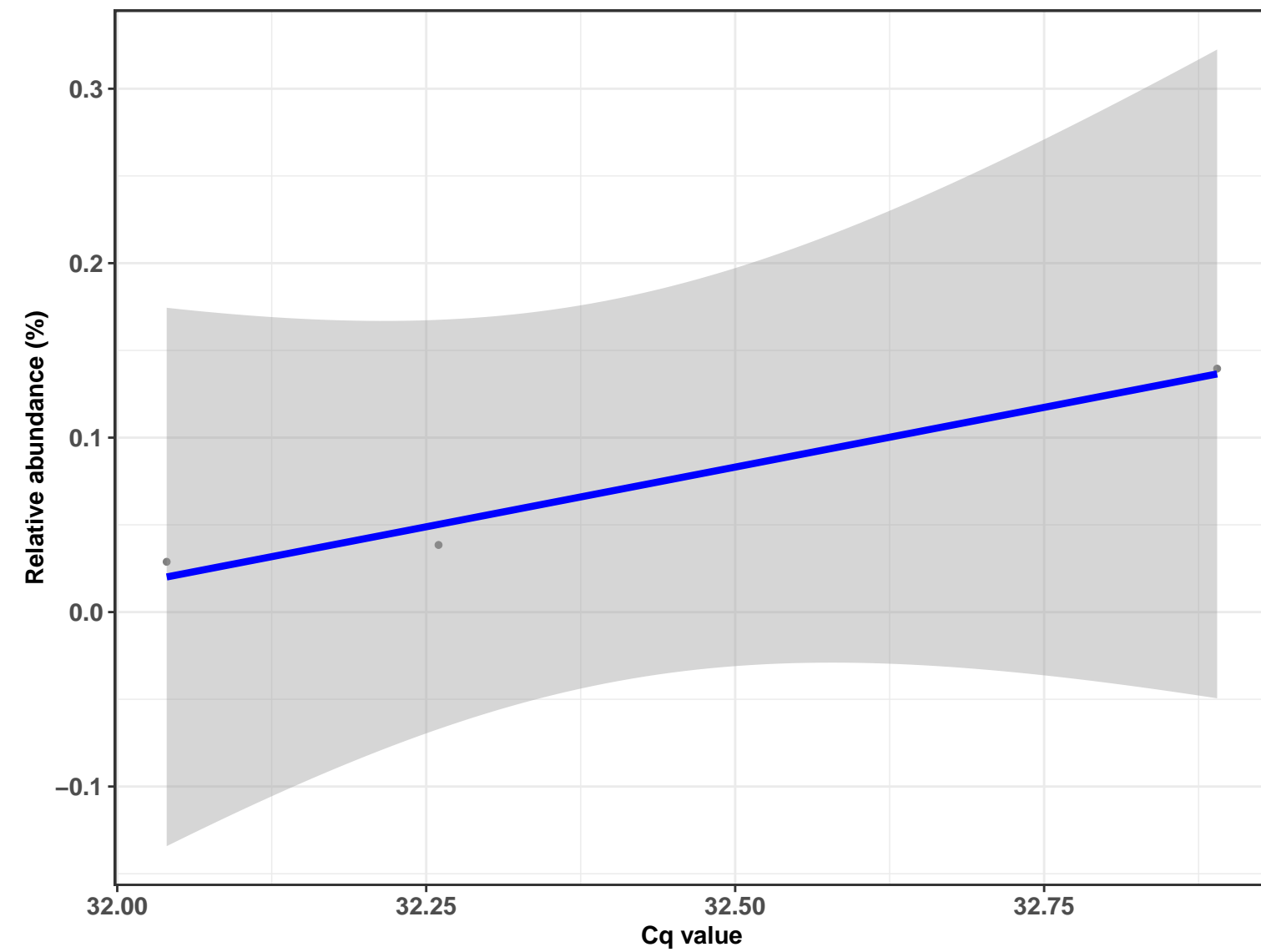
Correlation within: IM−DIM

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

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

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

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

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

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

Correlation with all samples

$\log_e(S) = 4.248$, $p = 0.589$, $\hat{\rho}_{Spearman} = -0.250$, $CI_{95\%}$ [−1.334, 0.787], $n_{pairs} = 7$
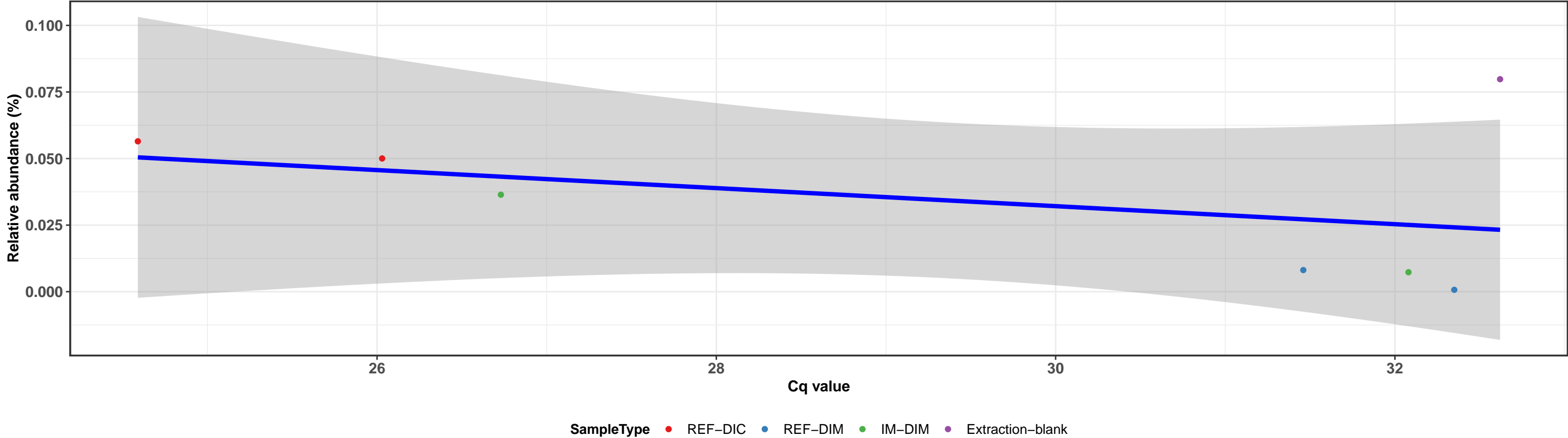
Correlation within: REF−DIC
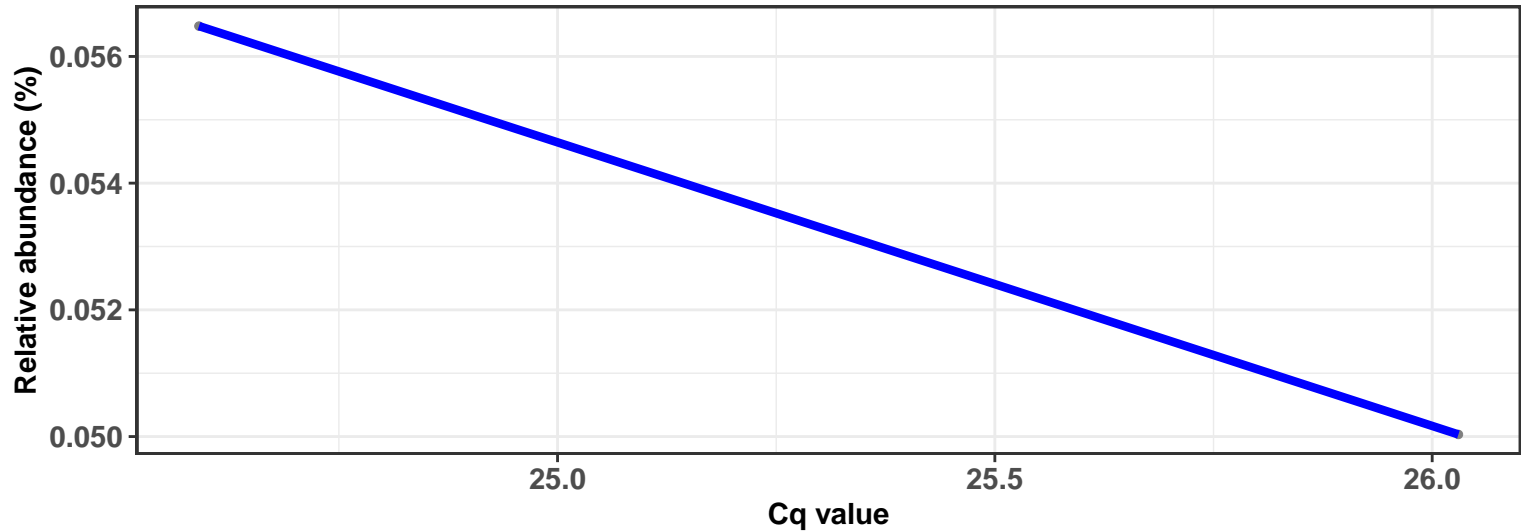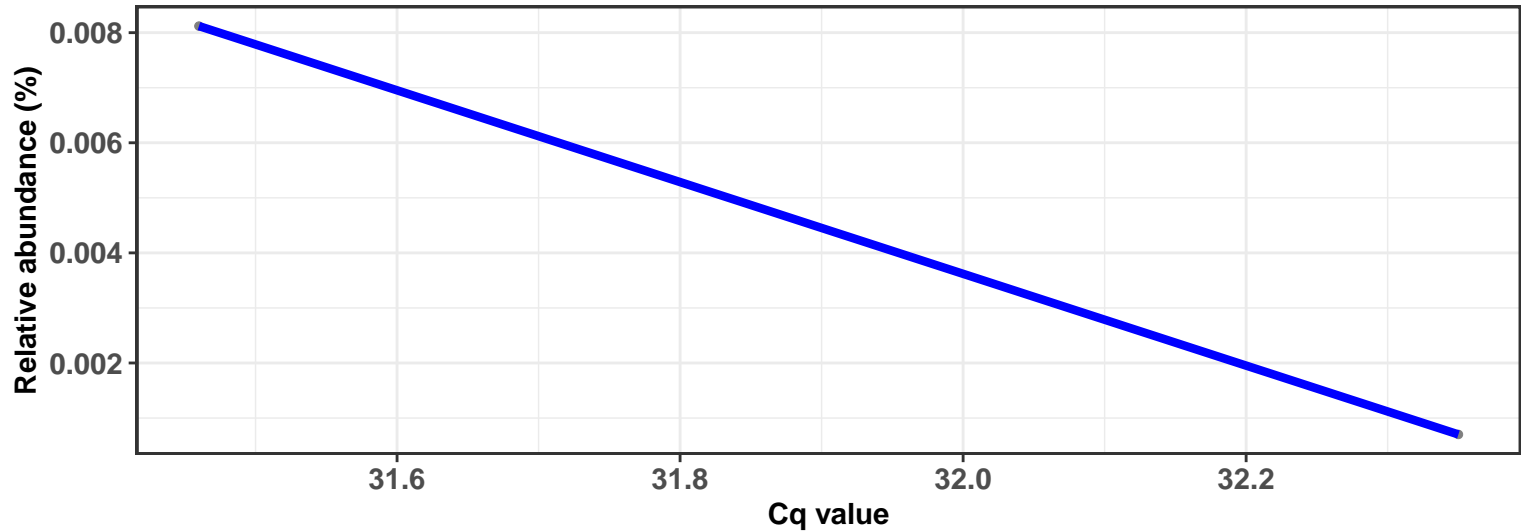
Correlation within: REF−DIM

Correlation within: IM−DIM
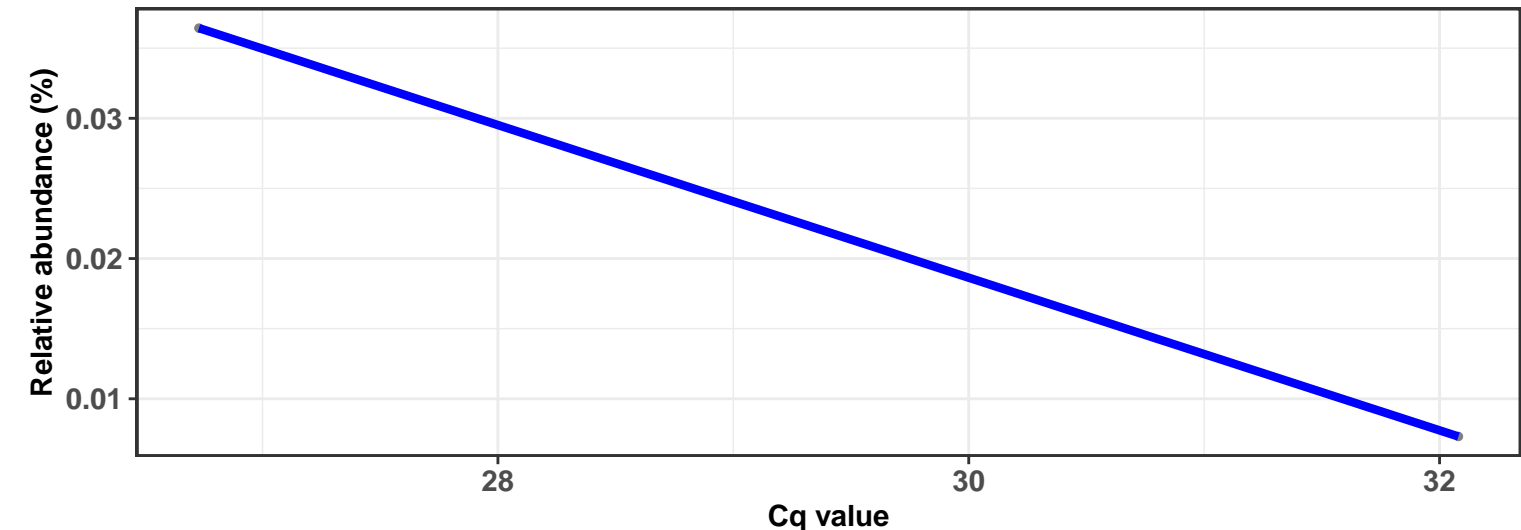
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.840$, $p = {}< 0.001$, $\hat{\rho}_{Spearman} = 0.504$, $CI_{95\%}$ [0.314, 0.741], $n_{pairs} = 61$

SampleType ● REF–DIC ● REF–DIM ● IM–DIC ● IM–DIM ● Extraction–blank
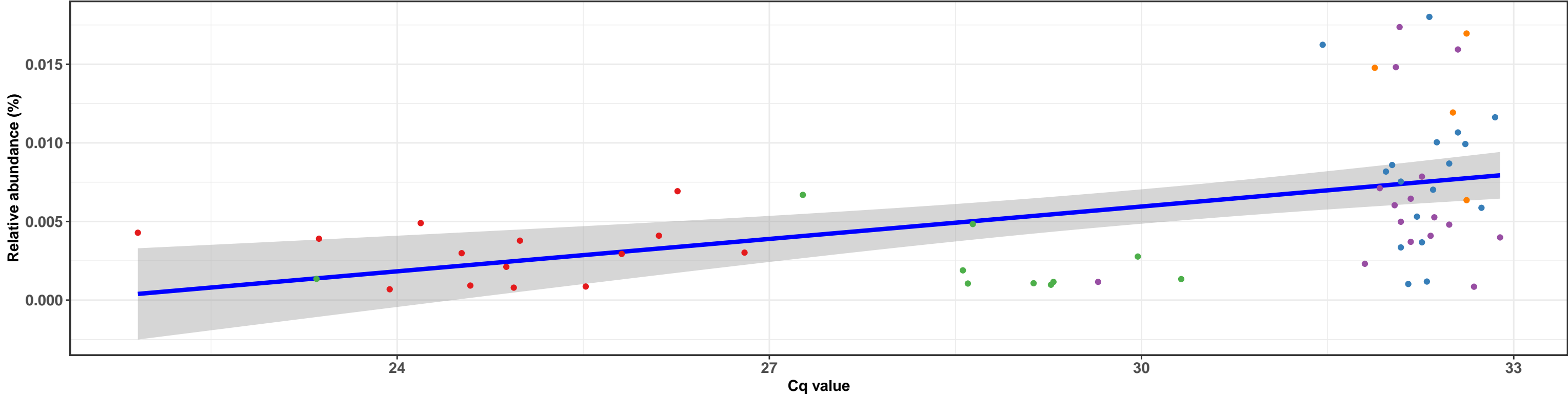
Correlation within: REF–DIC

$\log_e(S) = 6.064$, $p = 0.852$, $\hat{\rho}_{Spearman} = 0.055$, $CI_{95\%}$ [−0.544, 0.655], $n_{pairs} = 14$
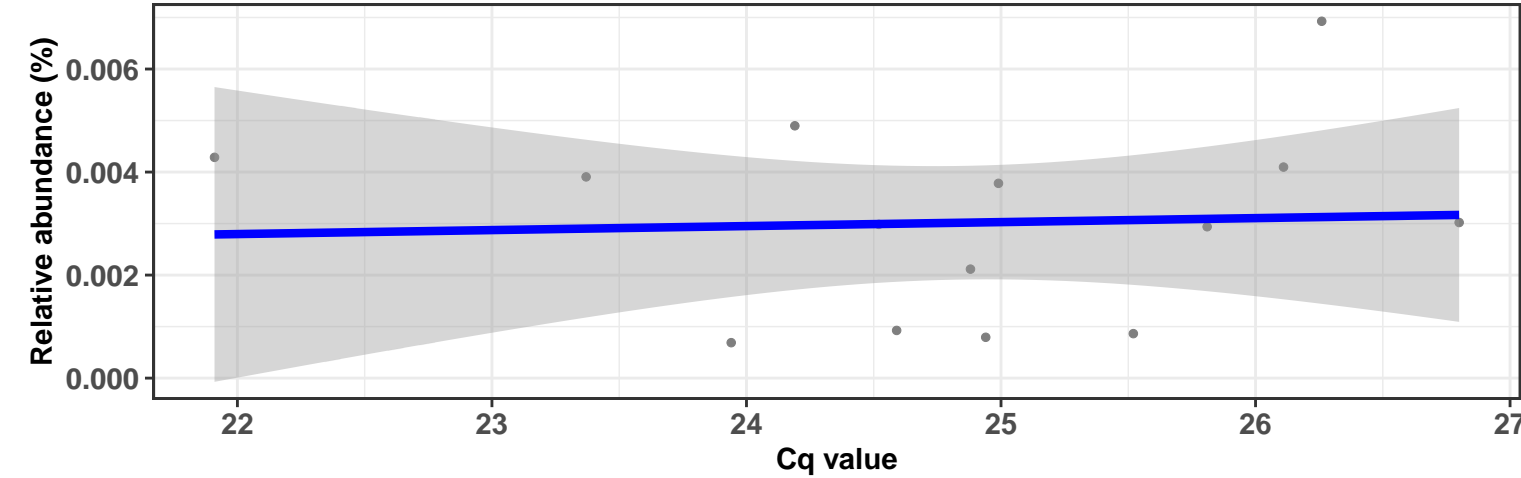
Correlation within: REF–DIM

$\log_e(S) = 6.421$, $p = 0.340$, $\hat{\rho}_{Spearman} = 0.246$, $CI_{95\%}$ [−0.297, 0.753], $n_{pairs} = 17$
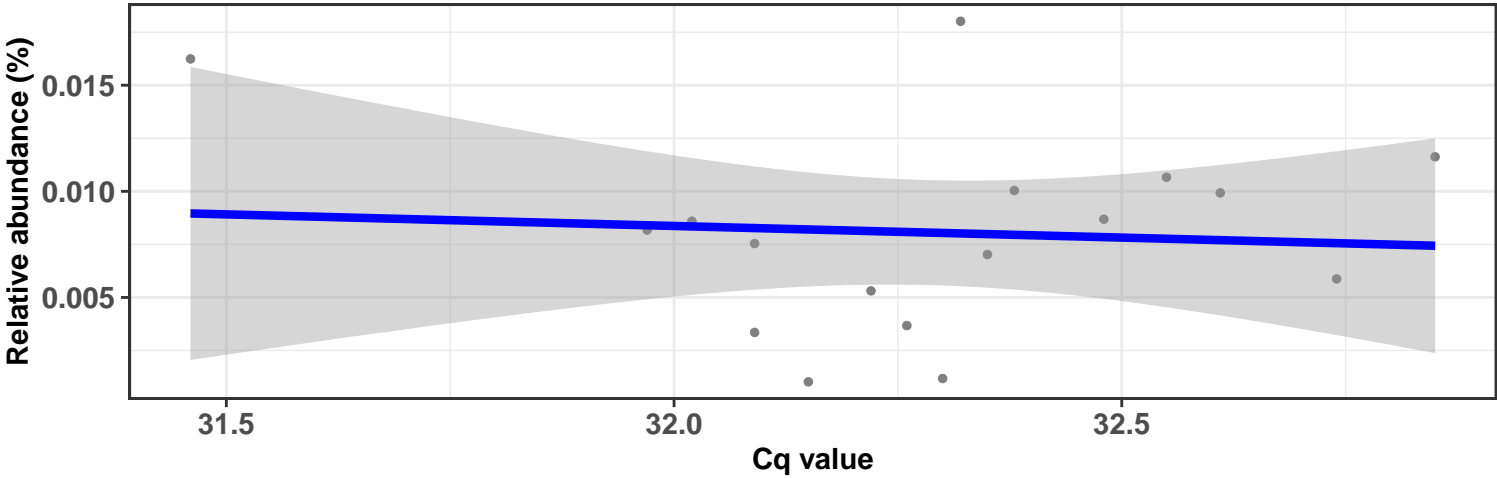
Correlation within: IM–DIC

$\log_e(S) = 5.357$, $p = 0.425$, $\hat{\rho}_{Spearman} = -0.285$, $CI_{95\%}$ [−0.970, 0.342], $n_{pairs} = 10$
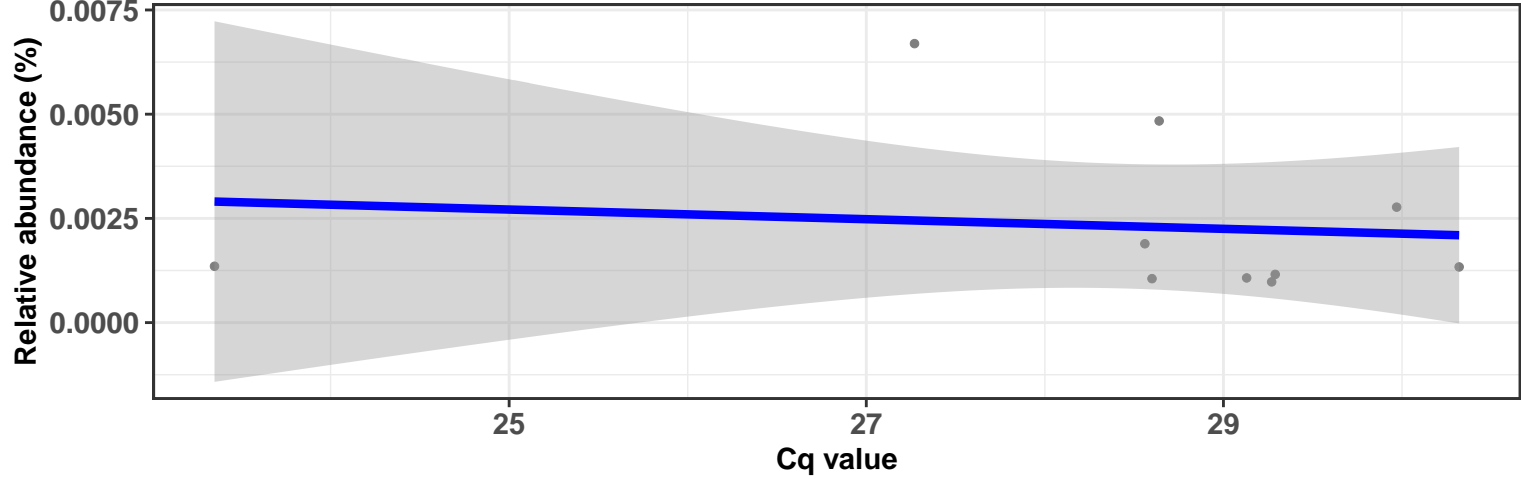
Correlation within: IM–DIM

$\log_e(S) = 6.586$, $p = 0.807$, $\hat{\rho}_{Spearman} = -0.066$, $CI_{95\%}$ [−0.623, 0.555], $n_{pairs} = 16$
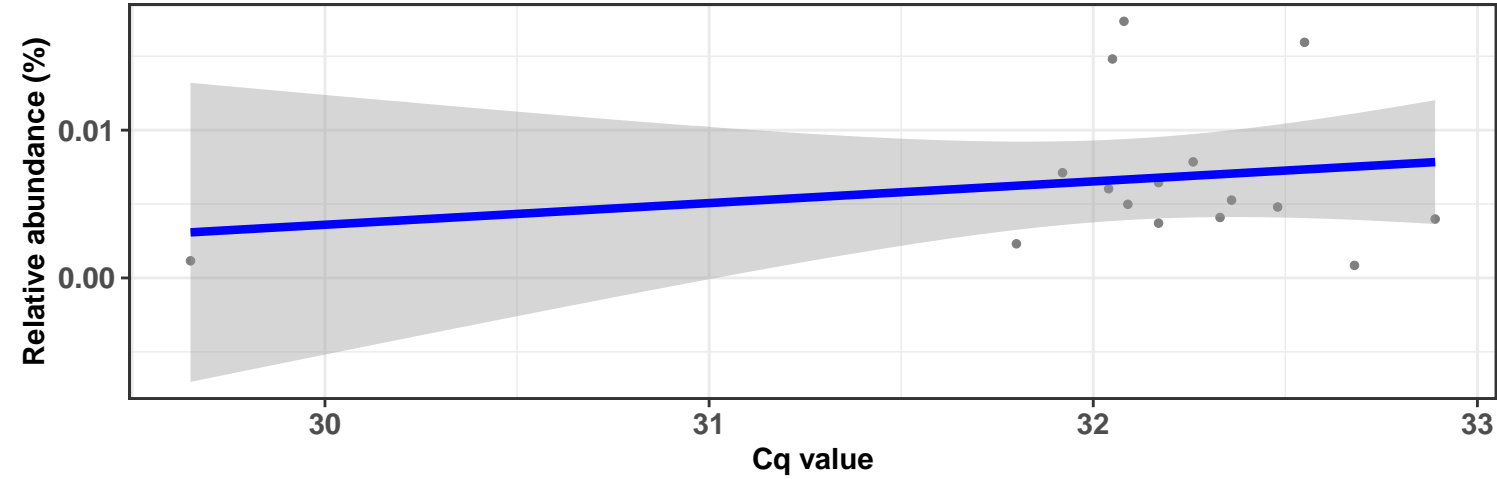
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.676$, $p = <0.001$, $\hat{\rho}_{Spearman} = 0.557$, $CI_{95\%}$ [0.433, 0.714], $n_{pairs} = 60$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
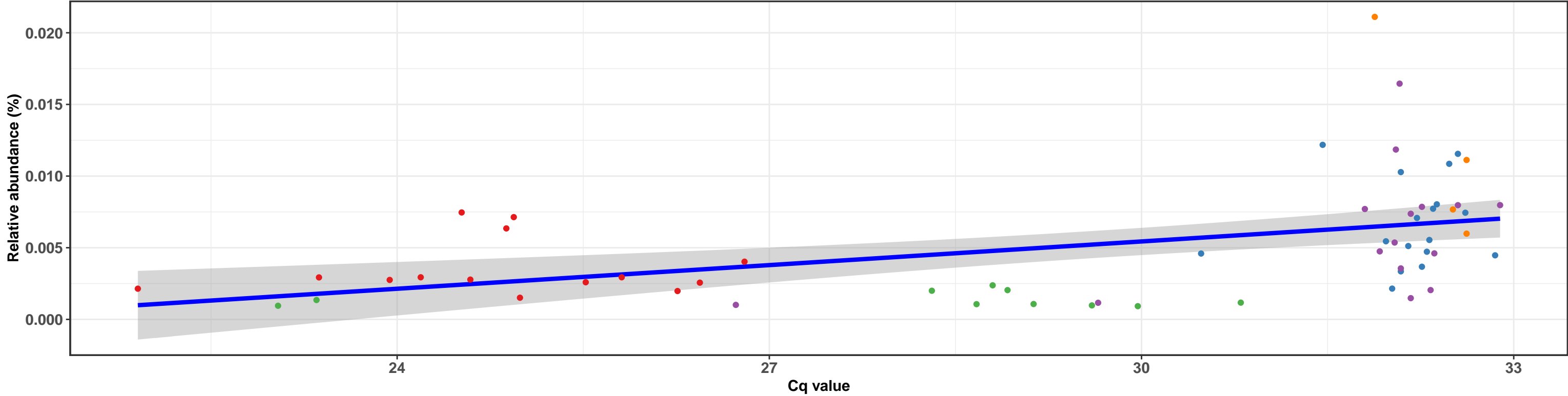
Correlation within: REF−DIC

$\log_e(S) = 6.215$, $p = 0.737$, $\hat{\rho}_{Spearman} = -0.099$, $CI_{95\%}$ [−0.705, 0.496], $n_{pairs} = 14$
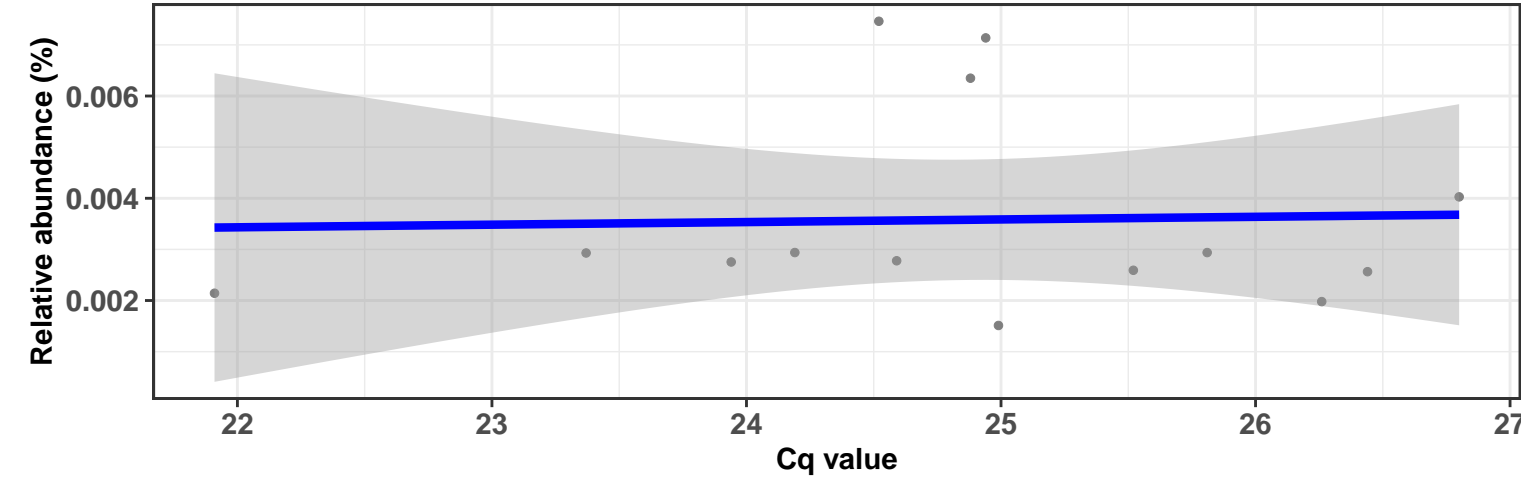
Correlation within: REF−DIM

$\log_e(S) = 6.423$, $p = 0.343$, $\hat{\rho}_{Spearman} = 0.245$, $CI_{95\%}$ [−0.292, 0.849], $n_{pairs} = 17$
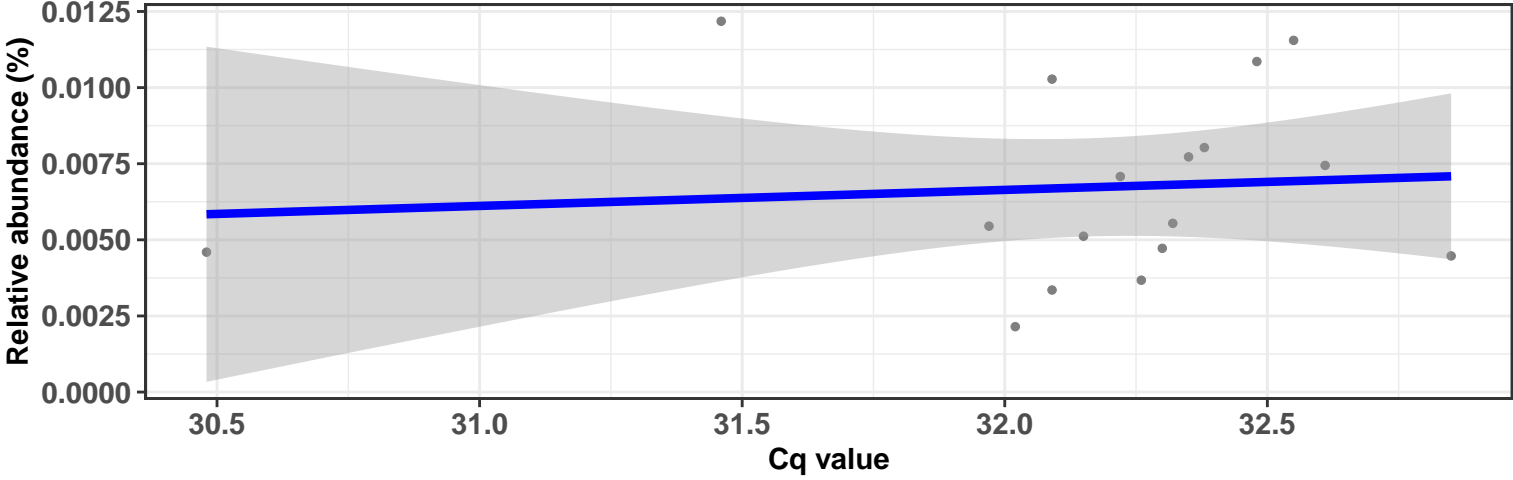
Correlation within: IM−DIC

$\log_e(S) = 5.268$, $p = 0.627$, $\hat{\rho}_{Spearman} = -0.176$, $CI_{95\%}$ [−0.908, 0.465], $n_{pairs} = 10$
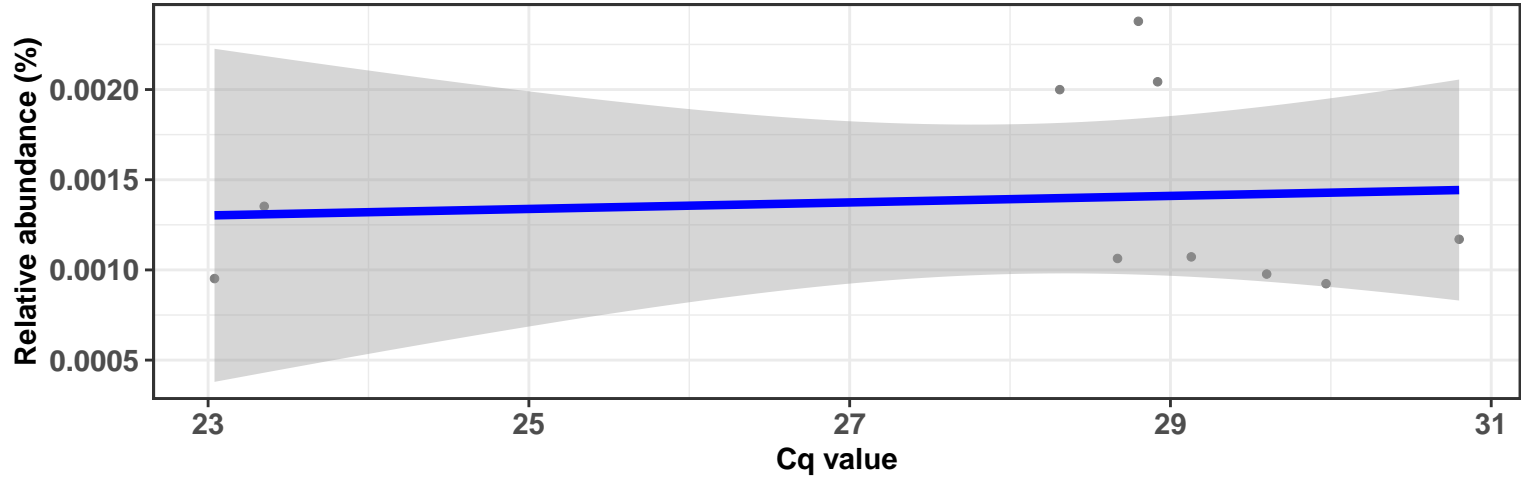
Correlation within: IM−DIM

$\log_e(S) = 5.908$, $p = 0.210$, $\hat{\rho}_{Spearman} = 0.343$, $CI_{95\%}$ [−0.216, 0.889], $n_{pairs} = 15$
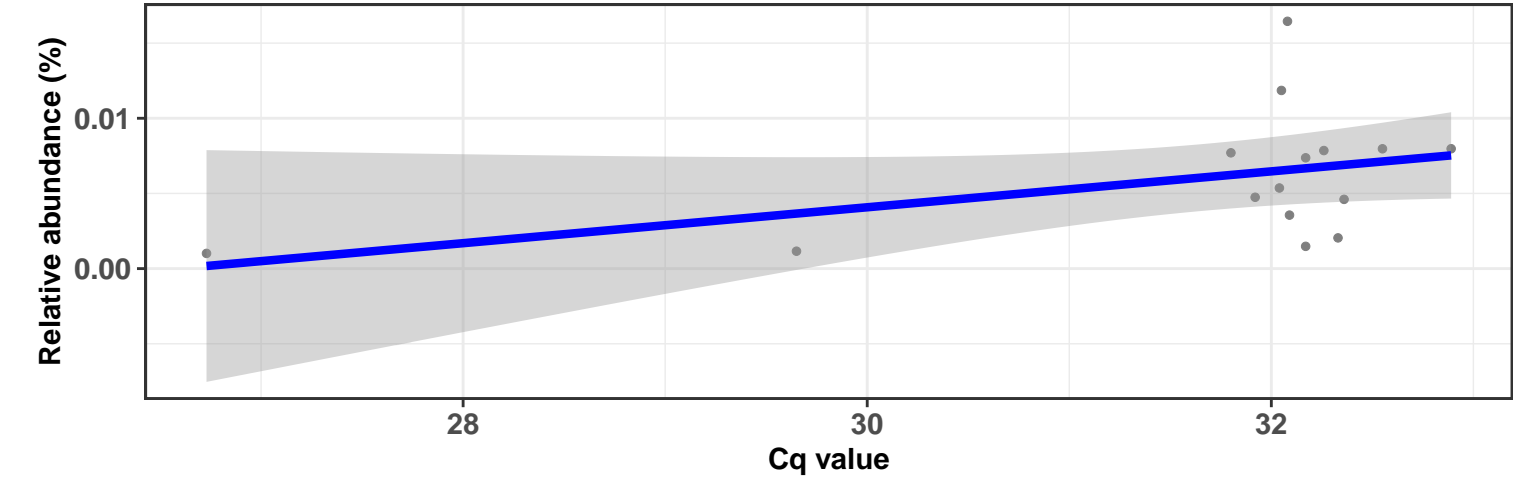
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium

Correlation with all samples

$\log_e(S) = 11.335$, $p = 0.013$, $\hat{\rho}_{Spearman} = -0.291$, $CI_{95\%}$ $[-0.538, -0.072]$, $n_{pairs} = 73$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock
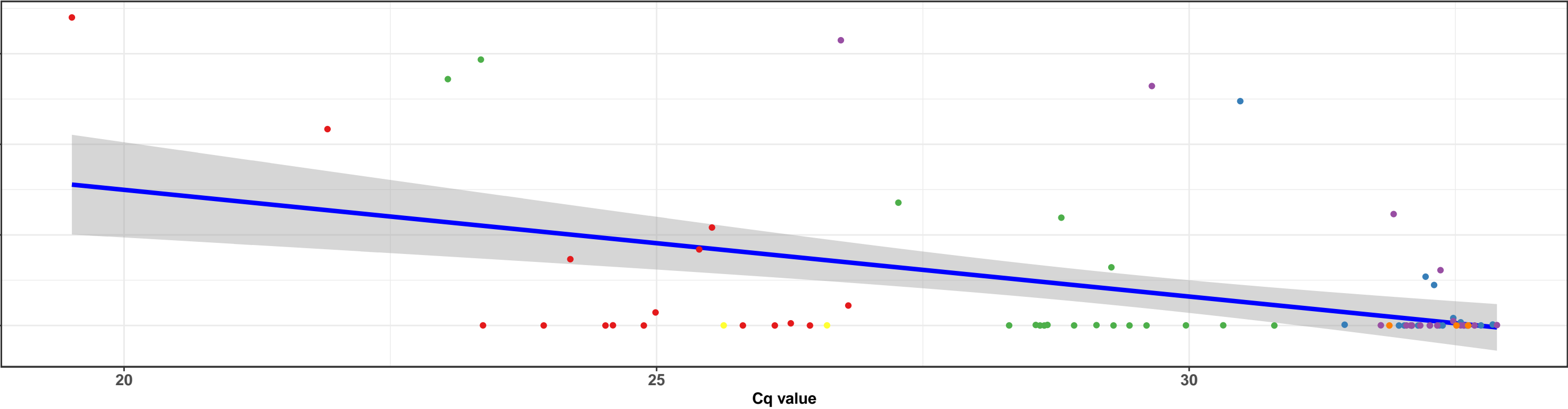
Correlation within: REF−DIC

$\log_e(S) = 6.764$, $p = 0.305$, $\hat{\rho}_{Spearman} = -0.274$, $CI_{95\%}$ $[-0.844, 0.248]$, $n_{pairs} = 16$
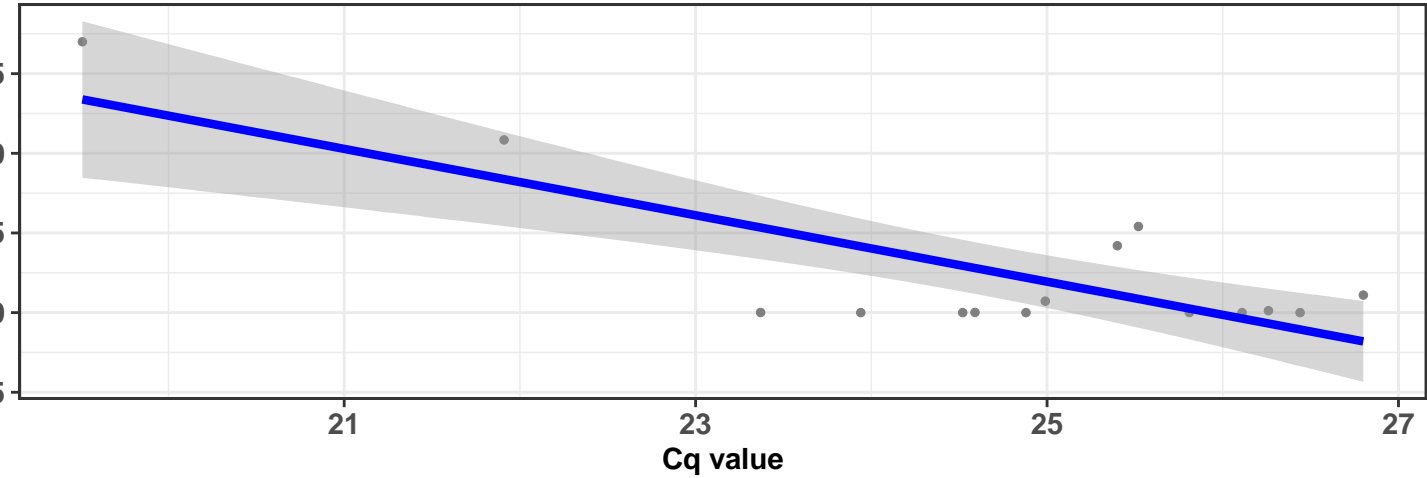
Correlation within: REF−DIM

$\log_e(S) = 6.525$, $p = 0.529$, $\hat{\rho}_{Spearman} = 0.164$, $CI_{95\%}$ $[-0.300, 0.623]$, $n_{pairs} = 17$
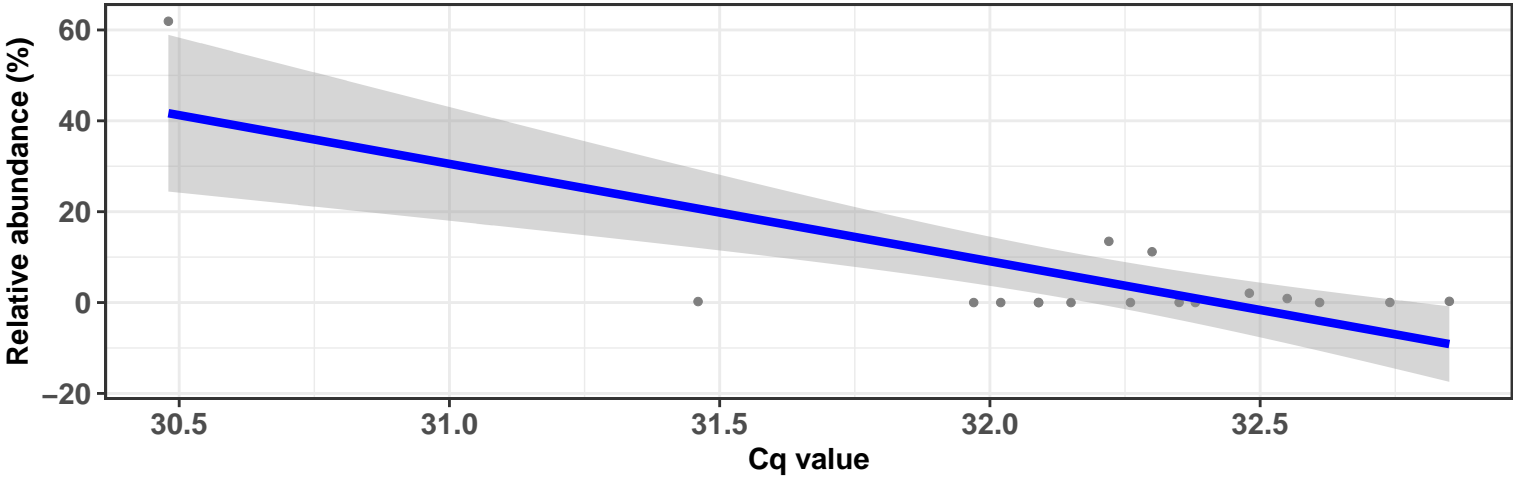
Correlation within: IM−DIC

$\log_e(S) = 7.297$, $p = 0.026$, $\hat{\rho}_{Spearman} = -0.523$, $CI_{95\%}$ $[-0.964, -0.128]$, $n_{pairs} = 18$
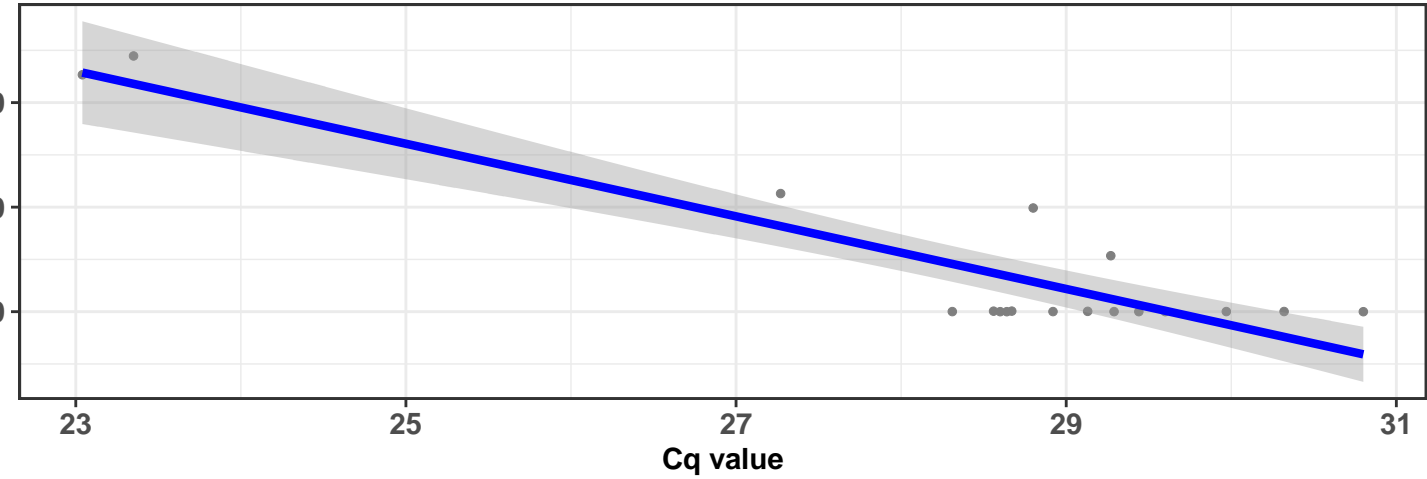
Correlation within: IM−DIM

$\log_e(S) = 6.859$, $p = 0.125$, $\hat{\rho}_{Spearman} = -0.400$, $CI_{95\%}$ $[-0.945, 0.099]$, $n_{pairs} = 16$
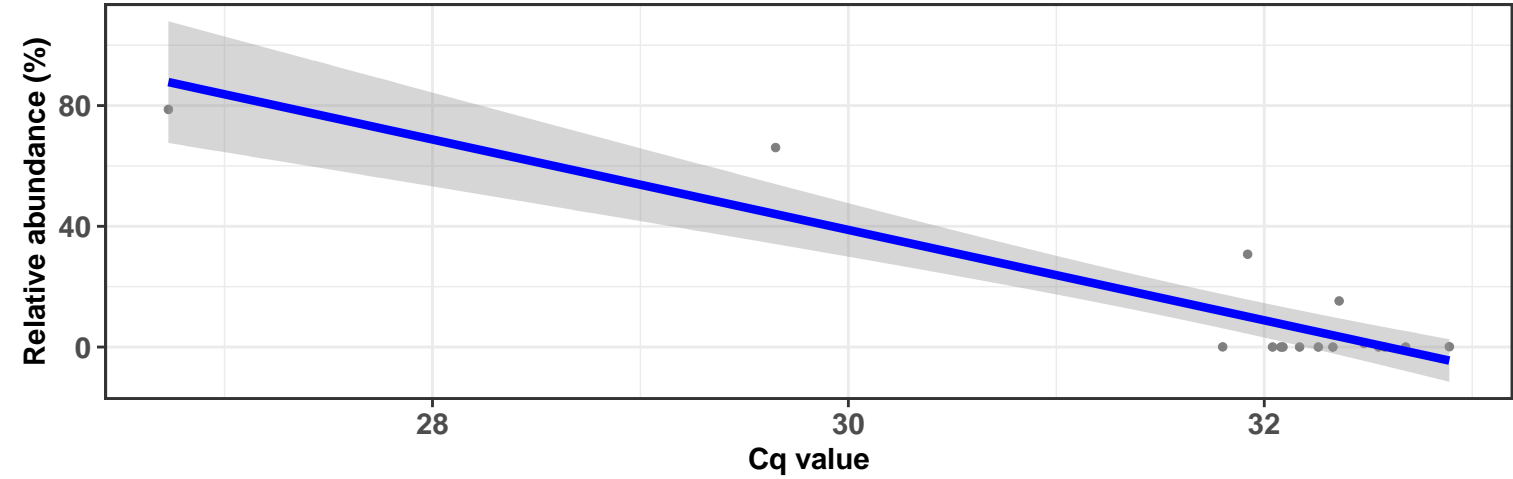
k__Bacteria; p__Spirochaetes; c__Spirochaetia; o__Brevinematales; f__Brevinemataceae; g__Brevinema; s__Brevinema andersonii

Correlation with all samples

$\log_e(S) = 10.883$, $p = 0.004$, $\hat{\rho}_{Spearman} = 0.326$, $CI_{95\%}$ [0.114, 0.554], $n_{pairs} = 78$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock
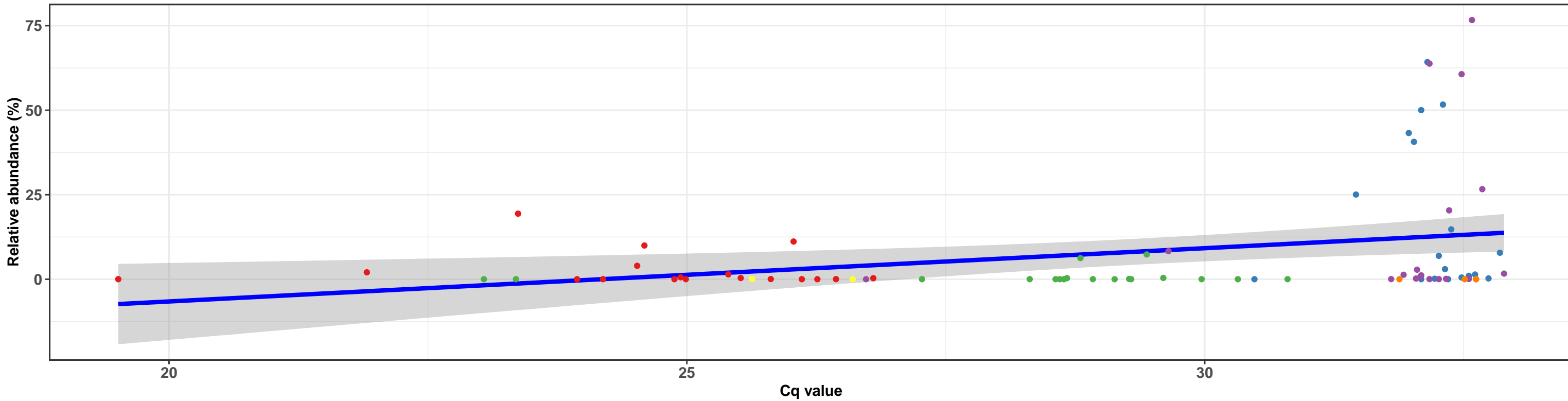
Correlation within: REF−DIC

$\log_e(S) = 7.063$, $p = 0.414$, $\hat{\rho}_{Spearman} = -0.205$, $CI_{95\%}$ [−0.751, 0.291], $n_{pairs} = 18$
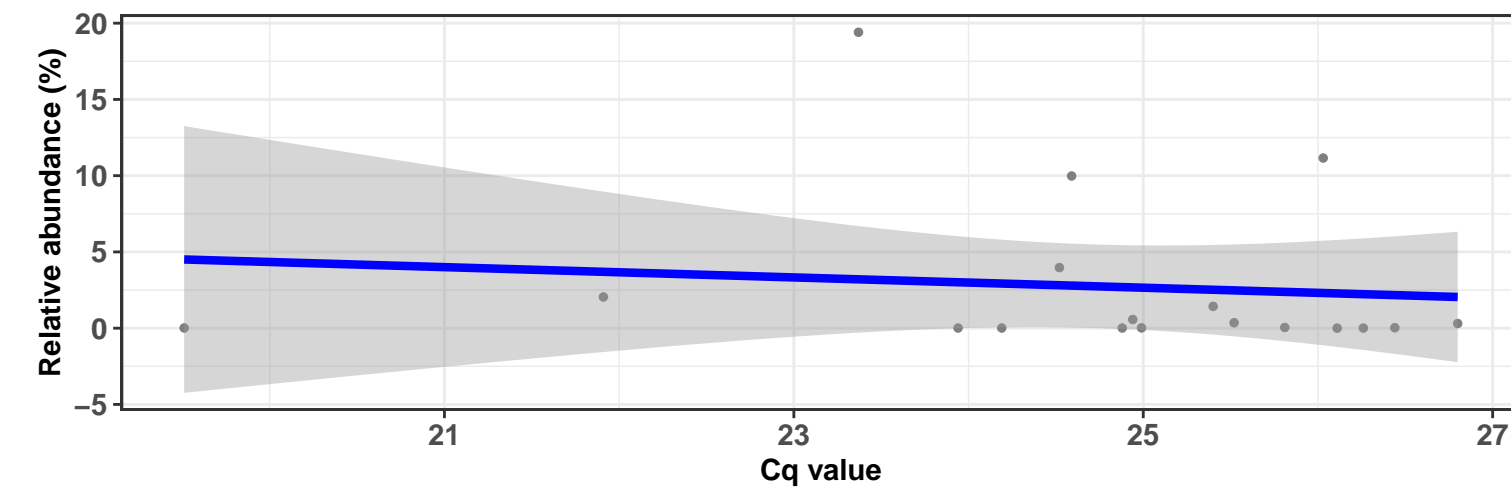
Correlation within: REF−DIM

$\log_e(S) = 7.044$, $p = 0.468$, $\hat{\rho}_{Spearman} = -0.183$, $CI_{95\%}$ [−0.747, 0.328], $n_{pairs} = 18$
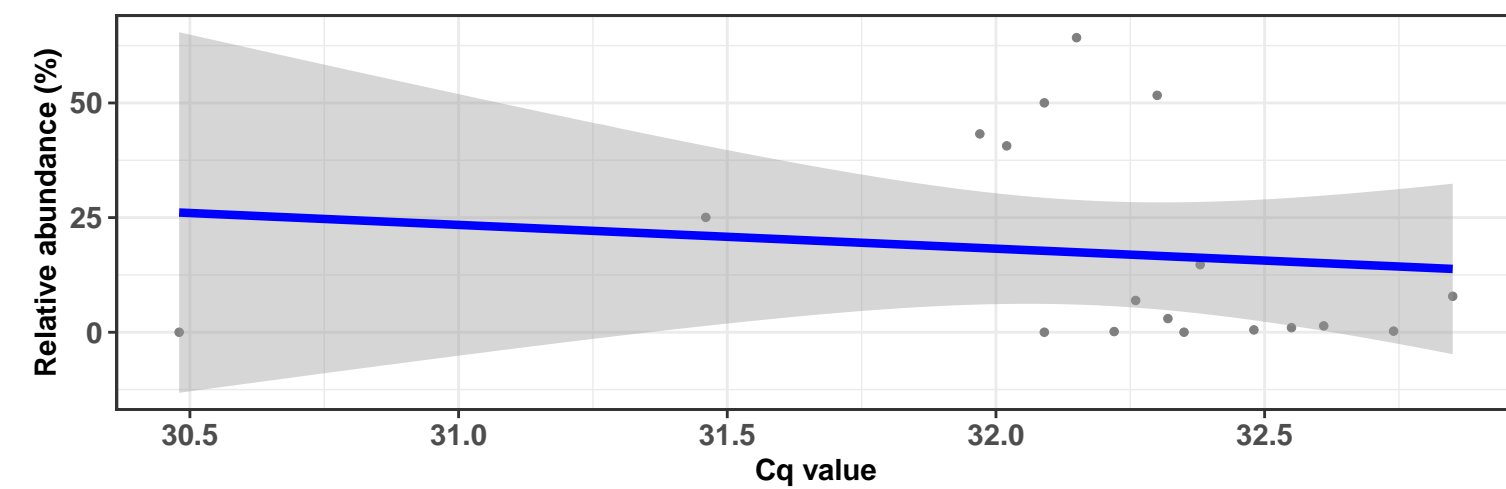
Correlation within: IM−DIC

$\log_e(S) = 6.631$, $p = 0.385$, $\hat{\rho}_{Spearman} = 0.218$, $CI_{95\%}$ [−0.219, 0.694], $n_{pairs} = 18$
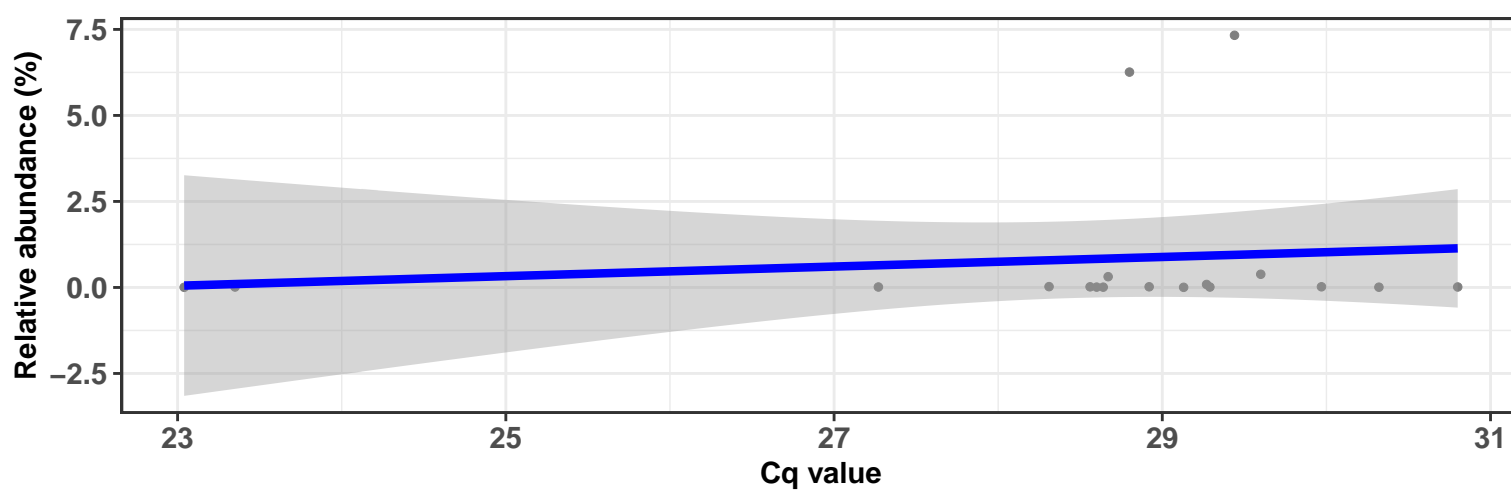
Correlation within: IM−DIM

$\log_e(S) = 6.359$, $p = 0.097$, $\hat{\rho}_{Spearman} = 0.404$, $CI_{95\%}$ [0.050, 0.826], $n_{pairs} = 18$
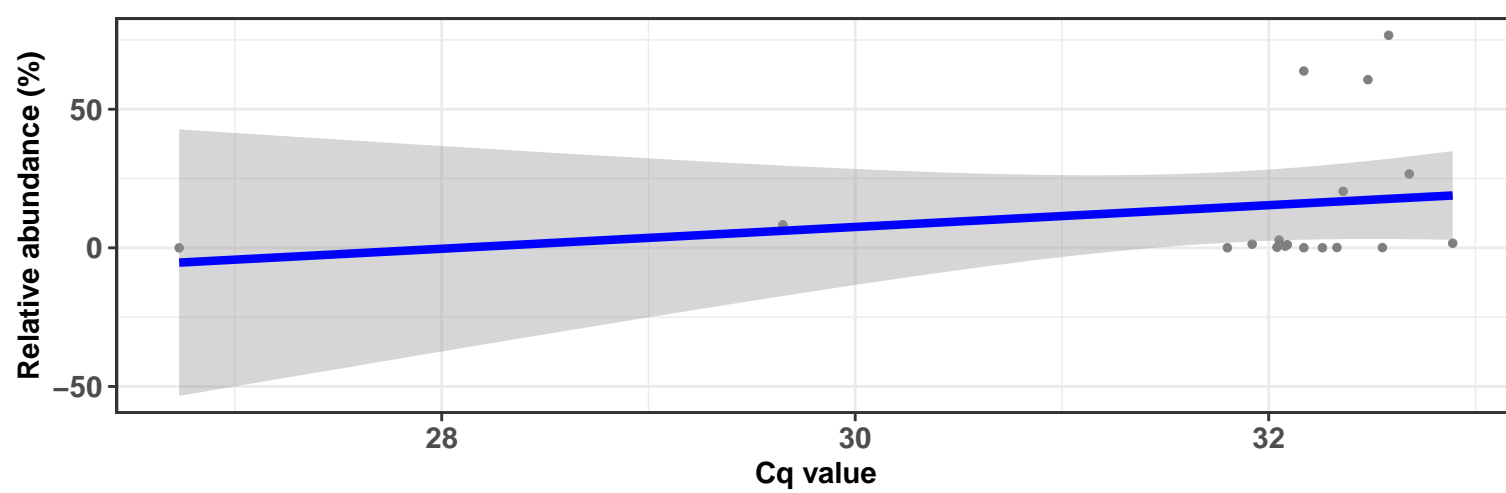
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Devosiaceae; g__Devosia; NA
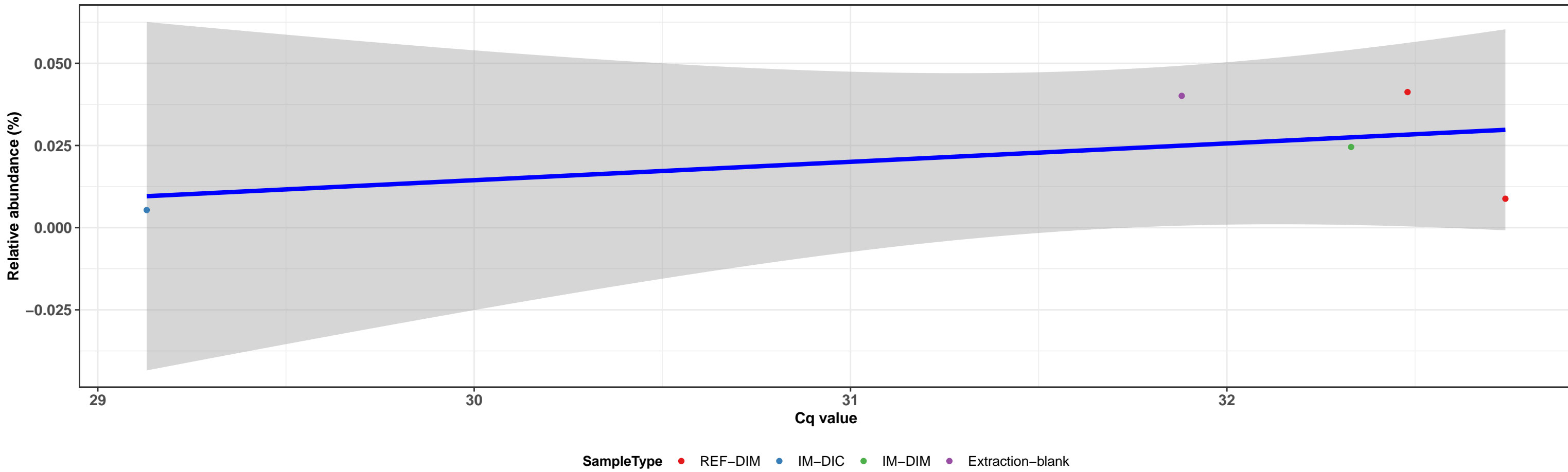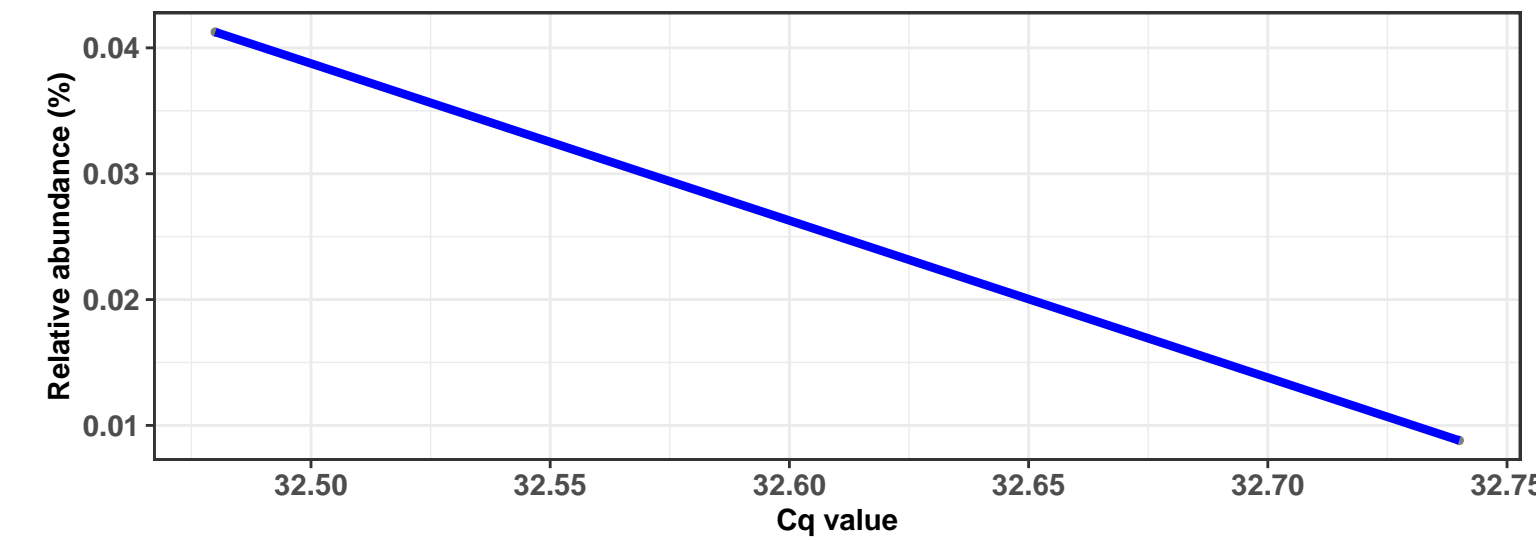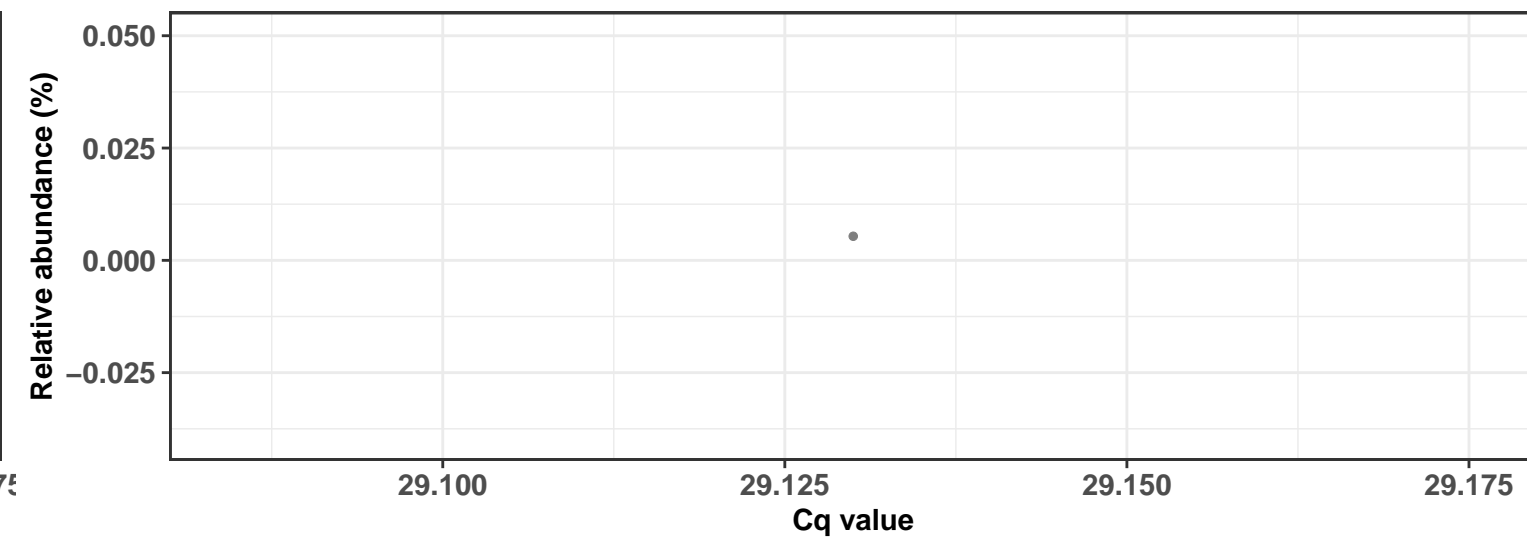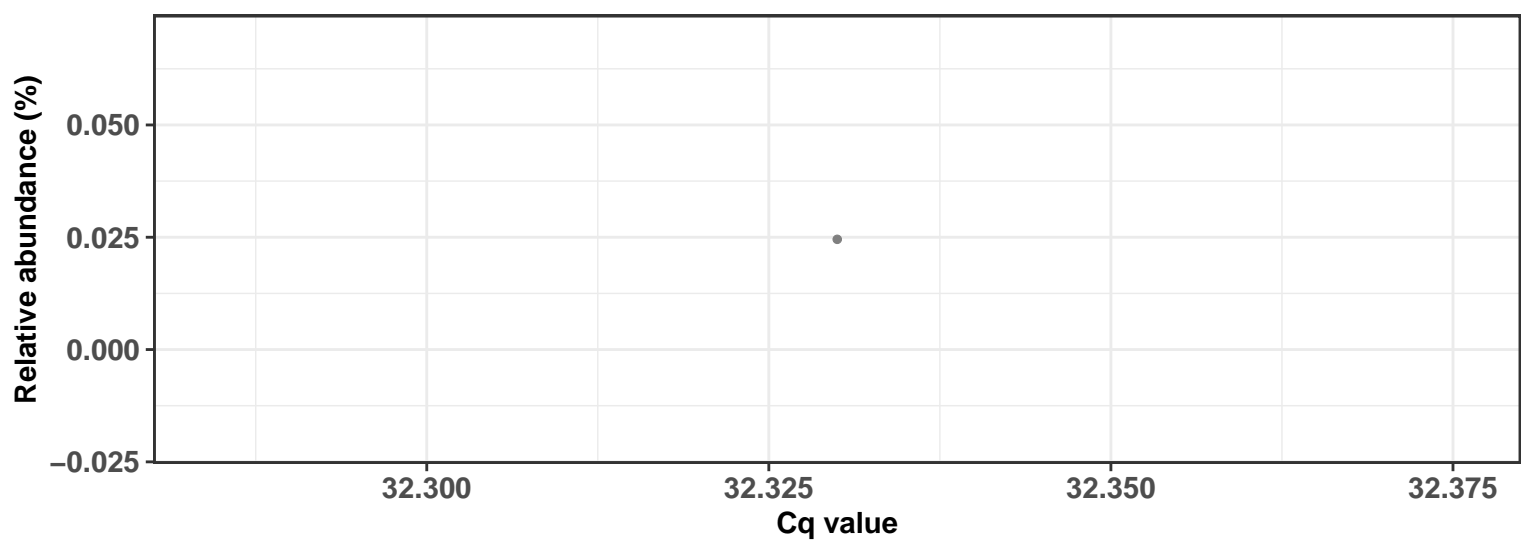
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__Sphingomonas aurantiaca

Correlation with all samples

$\log_e(S) = 3.912$, $p = 0.320$, $\hat{\rho}_{Spearman} = 0.405$, $CI_{95\%}$ [−0.198, 1.167], $n_{pairs} = 8$
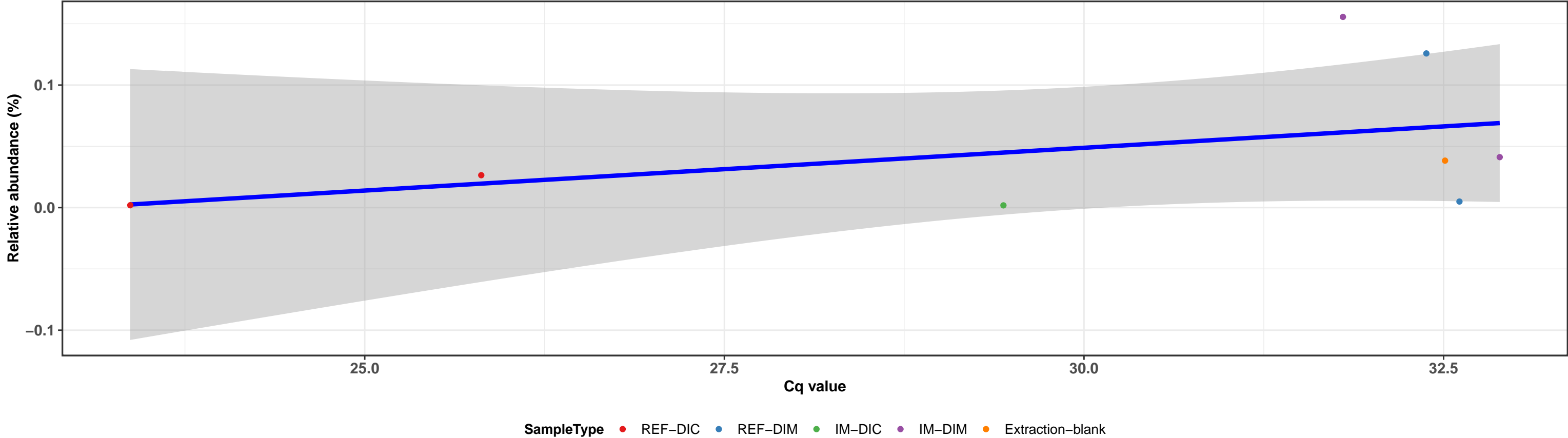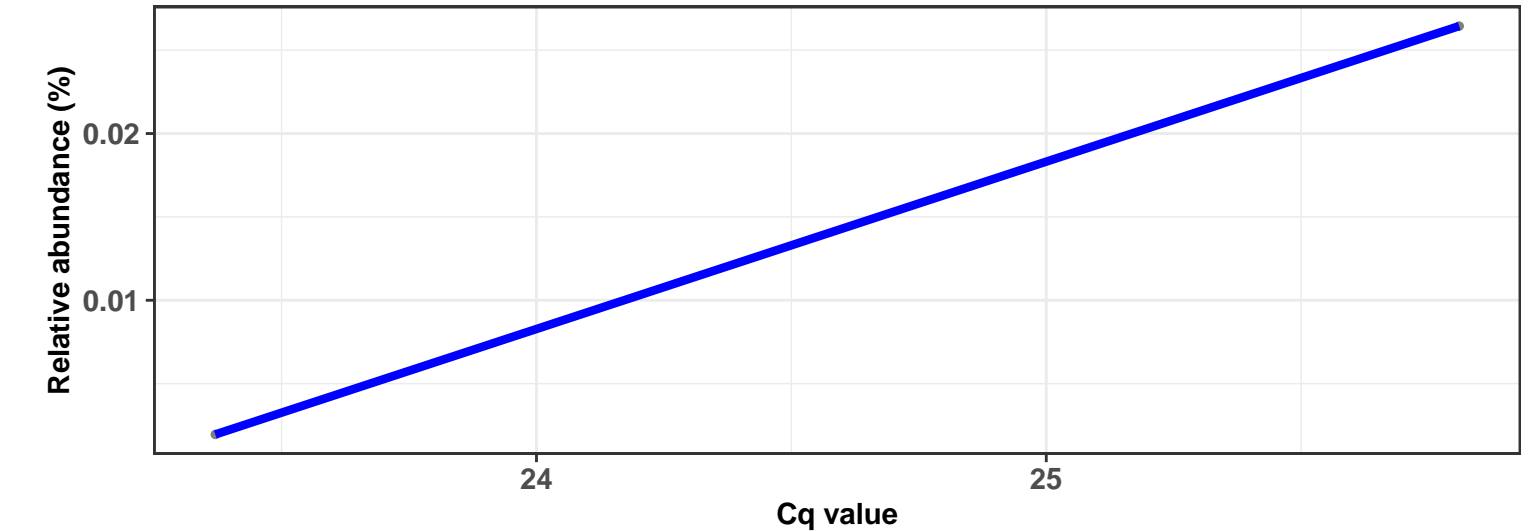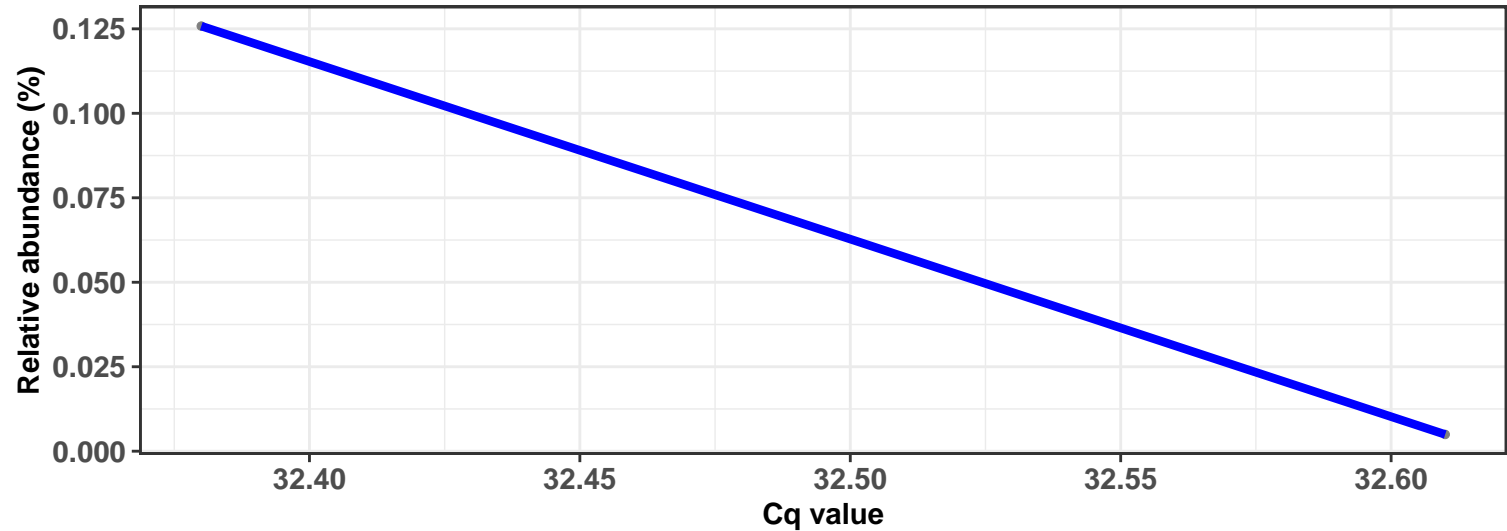
SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● IM−DIM   ● Extraction−blank
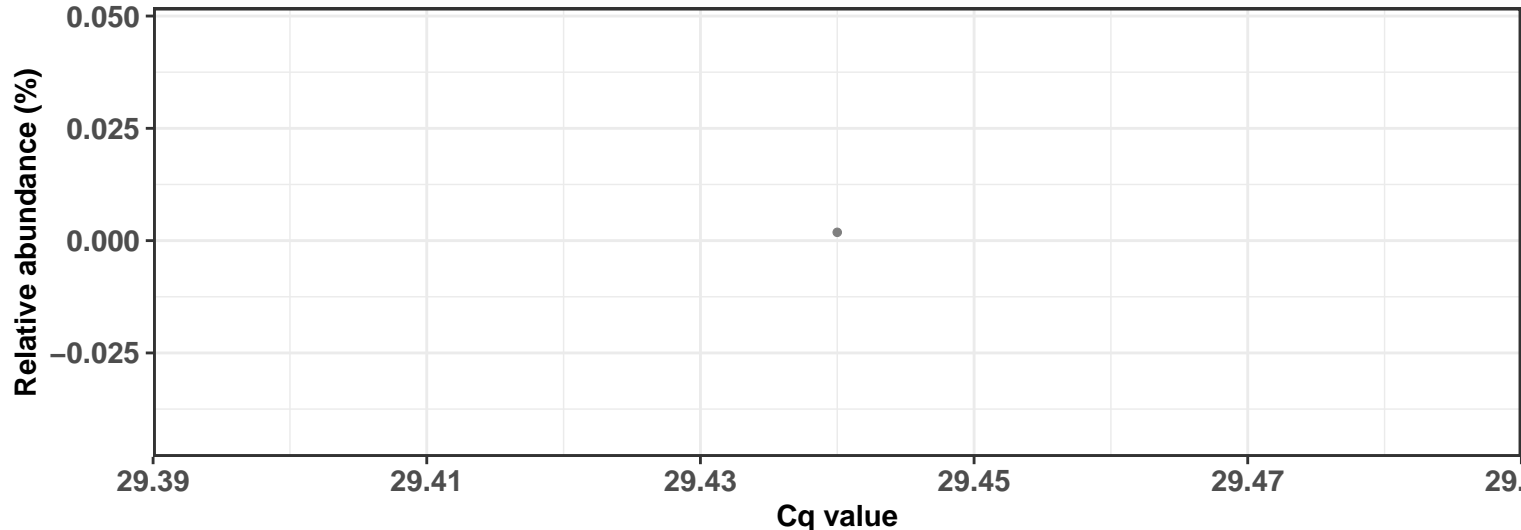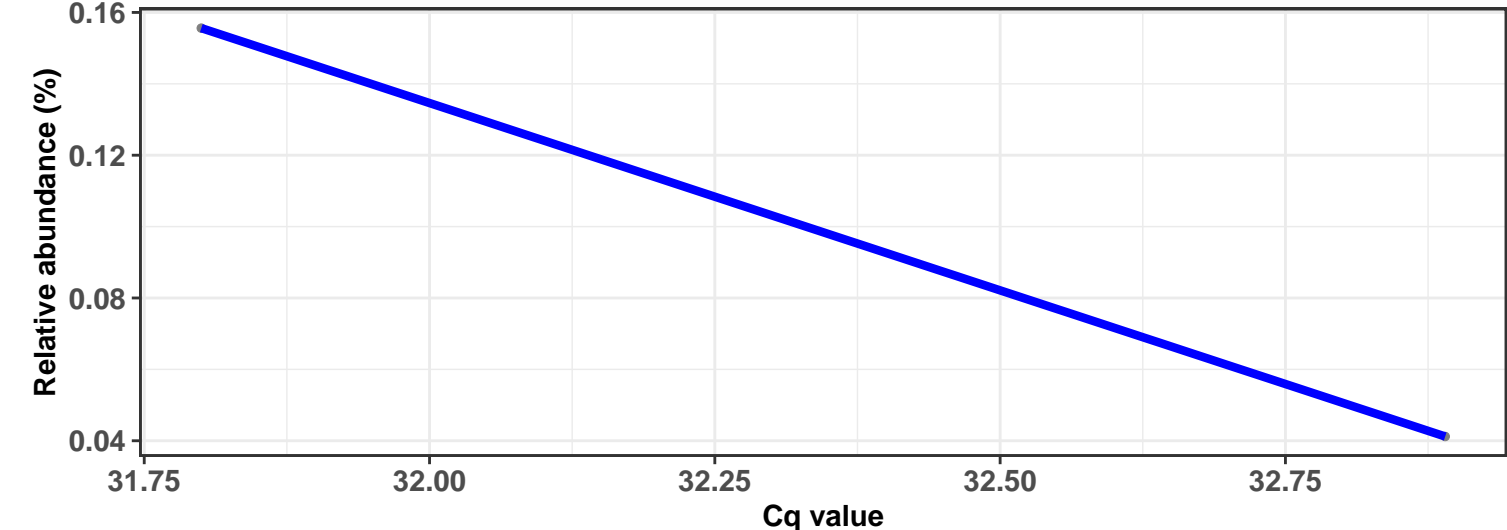
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 4.927$, $p = 0.085$, $\hat{p}_{\text{Spearman}} = 0.517$, $\text{CI}_{95\%}$ [0.081, 1.036], $n_{\text{pairs}} = 12$
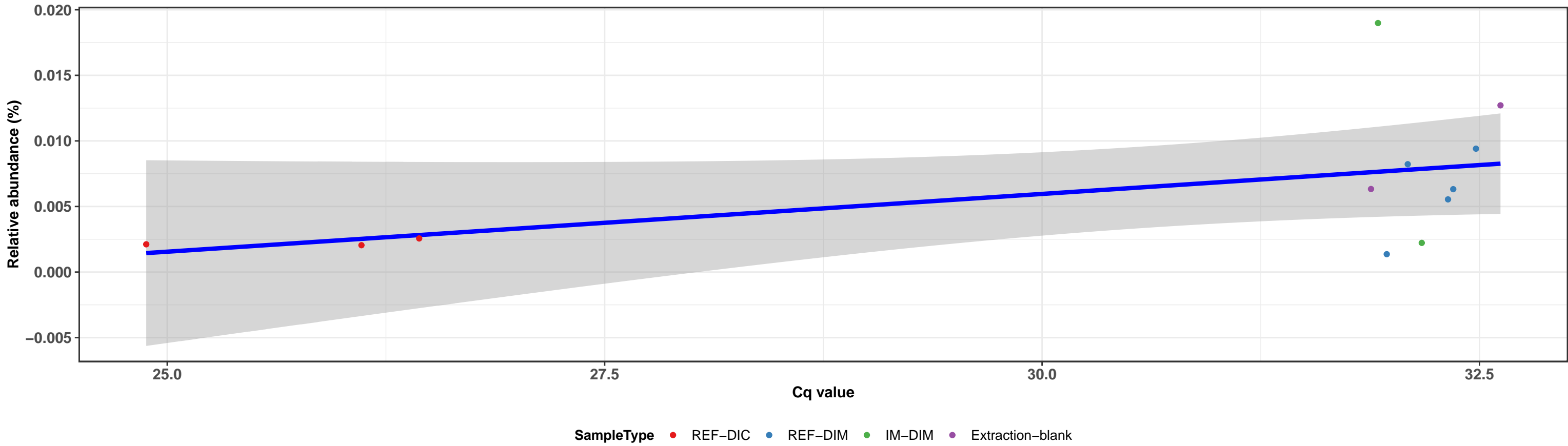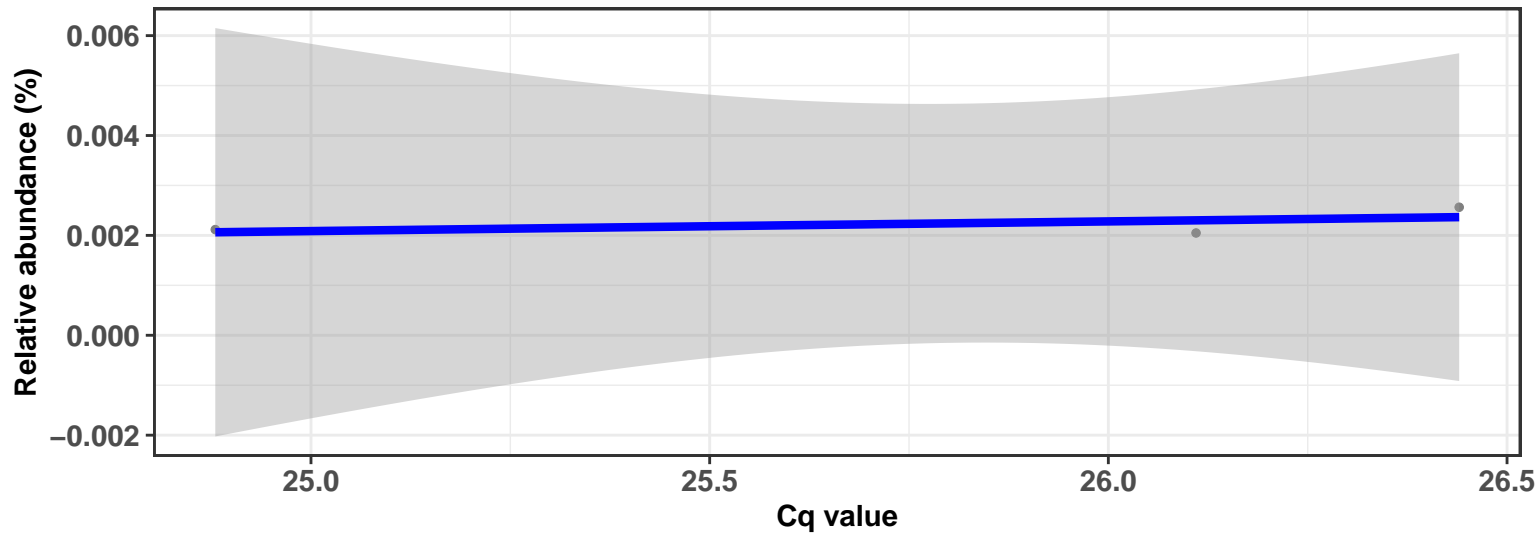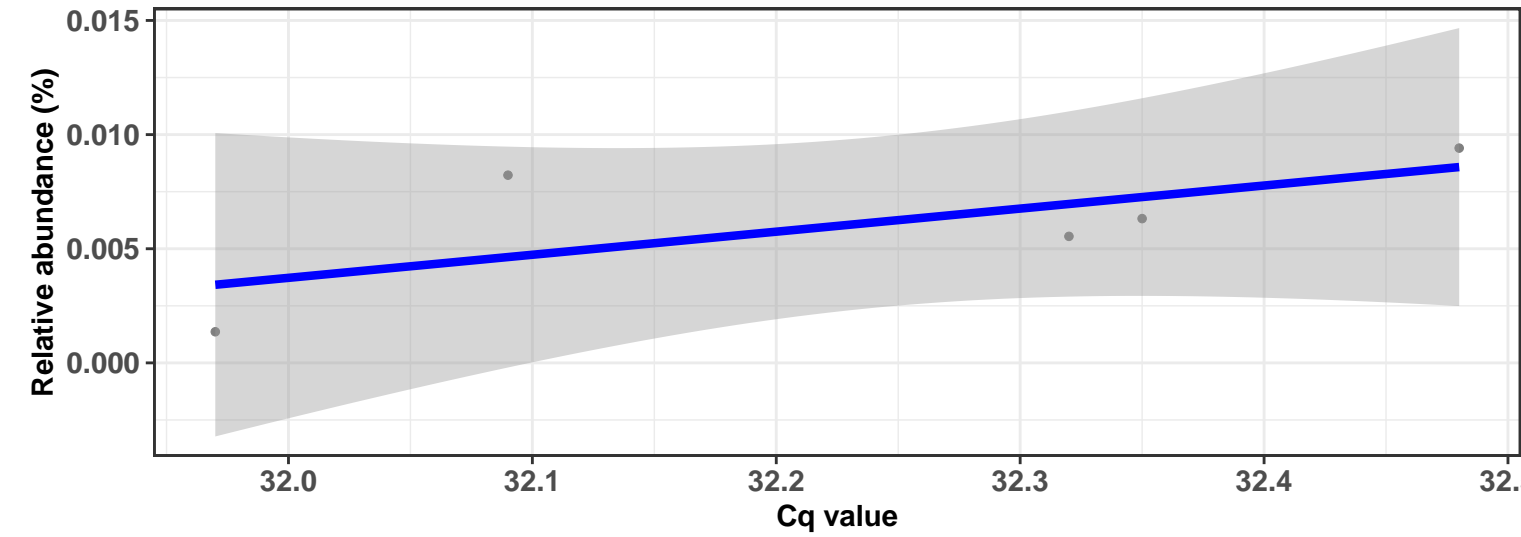

SampleType ● REF−DIC ● REF−DIM ● IM−DIM ● Extraction−blank
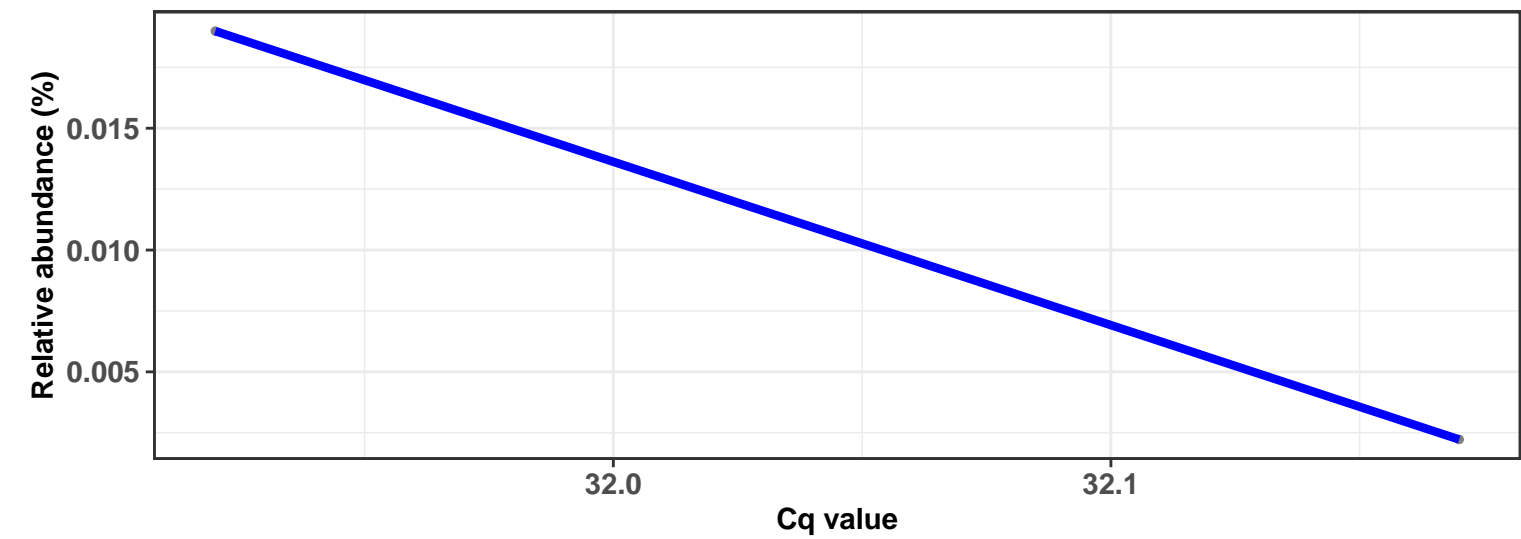
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.162$, $p = 0.516$, $\hat{\rho}_{Spearman} = 0.106$, $CI_{95\%}$ [−0.259, 0.392], $n_{pairs} = 40$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 3.951$, $p = 0.112$, $\hat{\rho}_{Spearman} = 0.567$, $CI_{95\%}$ [0.152, 1.039], $n_{pairs} = 9$
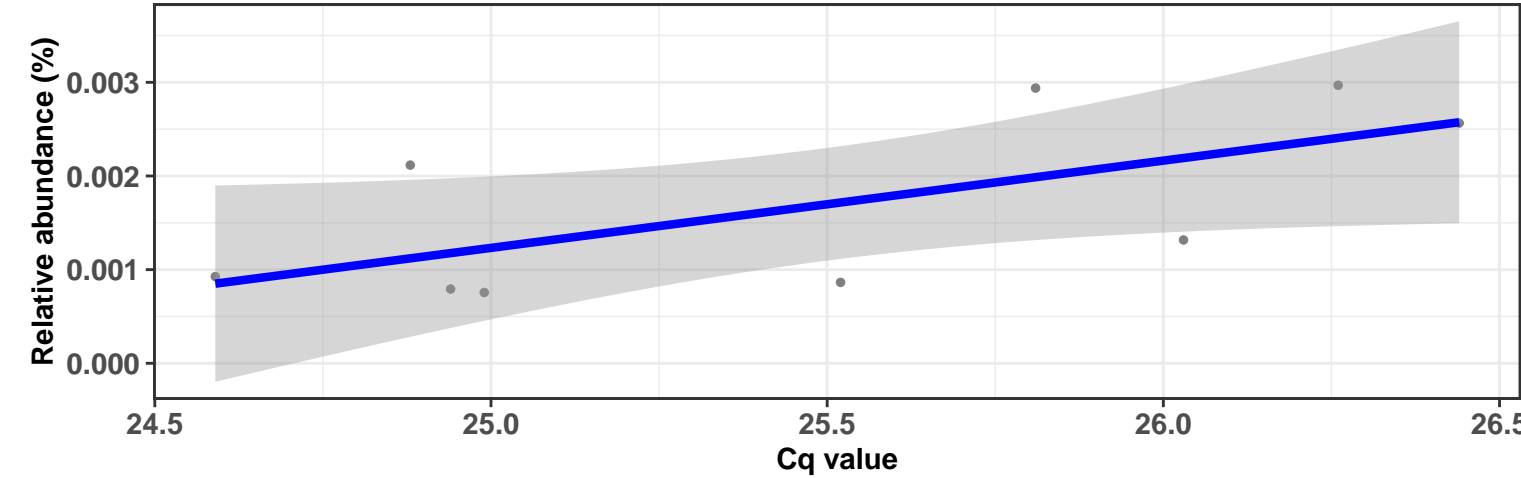
Correlation within: REF−DIM

$\log_e(S) = 3.984$, $p = 0.123$, $\hat{\rho}_{Spearman} = 0.552$, $CI_{95\%}$ [−0.217, 1.450], $n_{pairs} = 9$
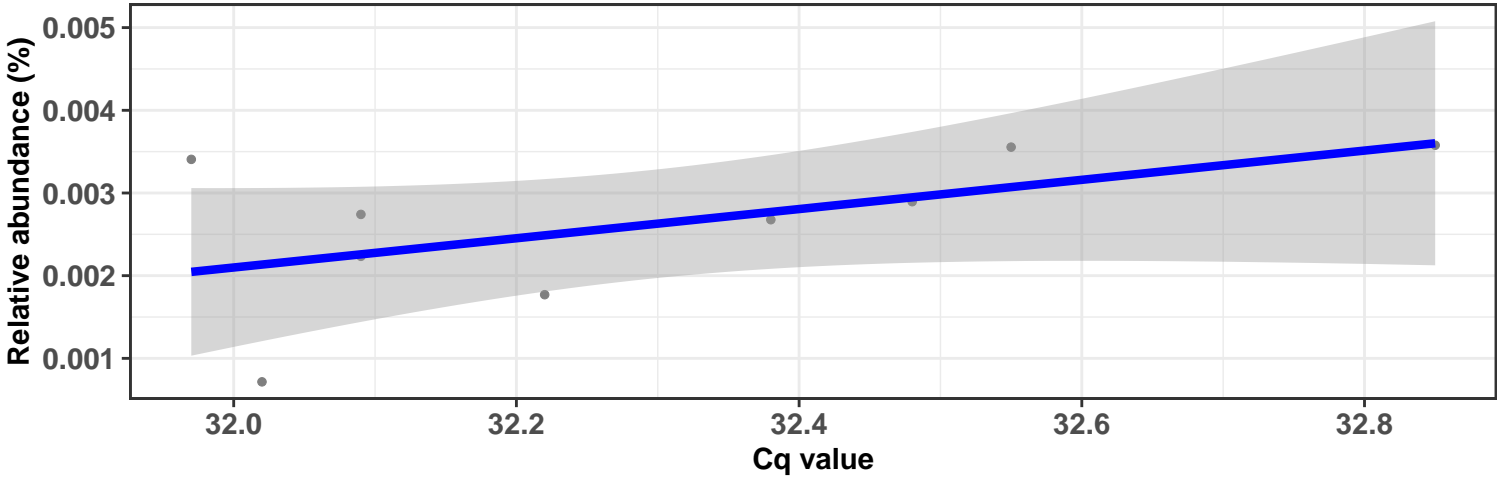
Correlation within: IM−DIC
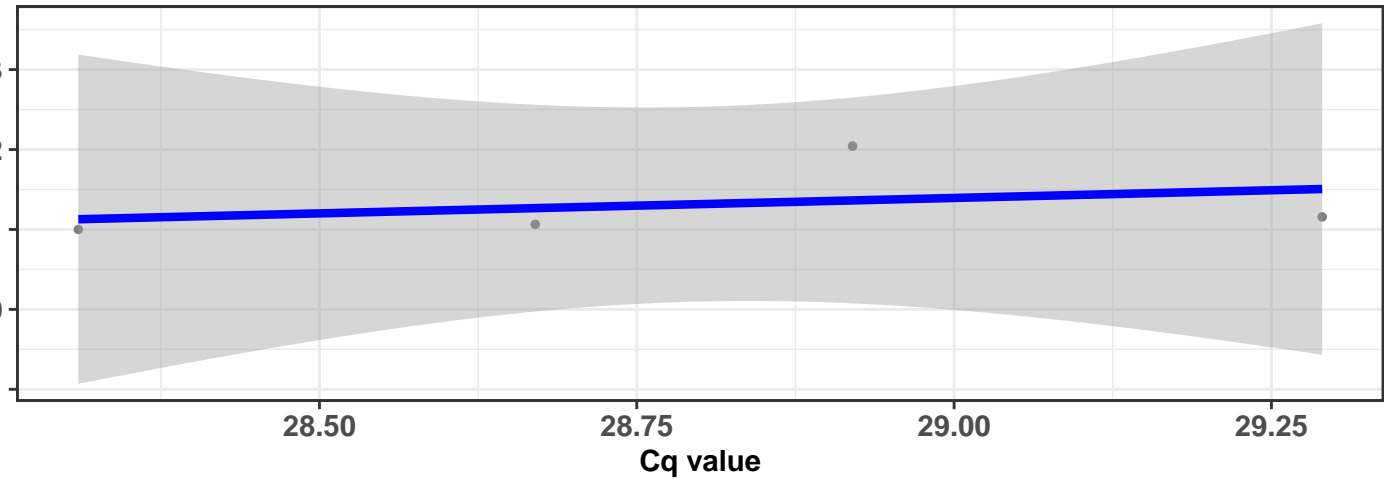
Correlation within: IM−DIM

$\log_e(S) = 6.477$, $p = 0.126$, $\hat{\rho}_{Spearman} = -0.429$, $CI_{95\%}$ [−0.870, 0.060], $n_{pairs} = 14$
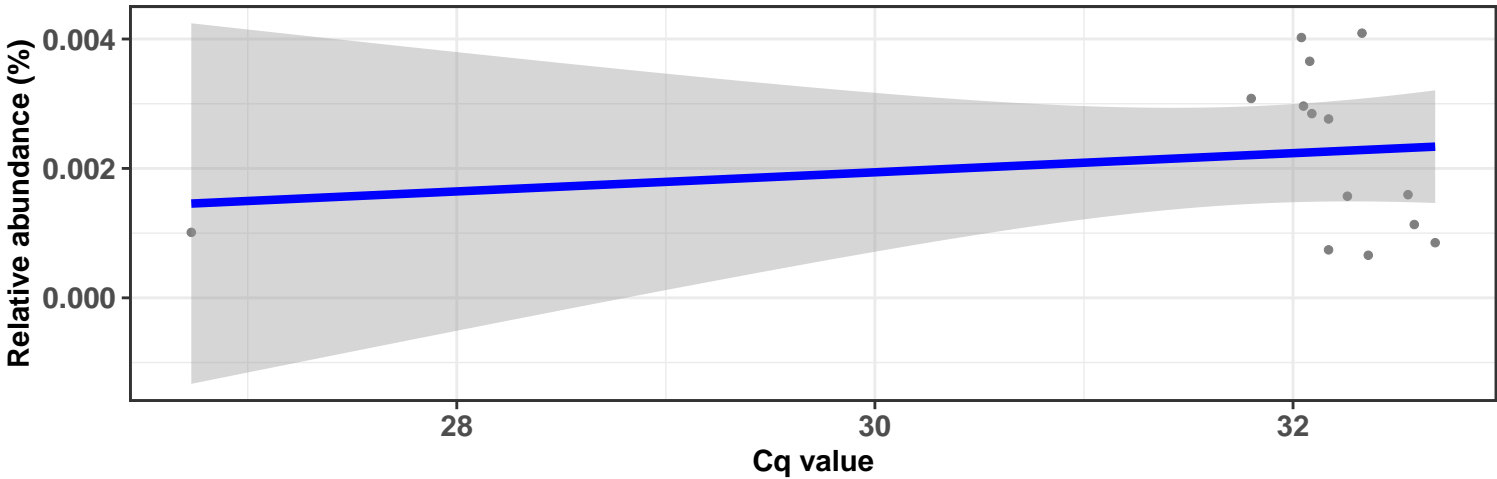
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.077$, $p = 0.061$, $\hat{\rho}_{Spearman} = 0.291$, $CI_{95\%}$ [0.052, 0.611], $n_{pairs} = 42$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
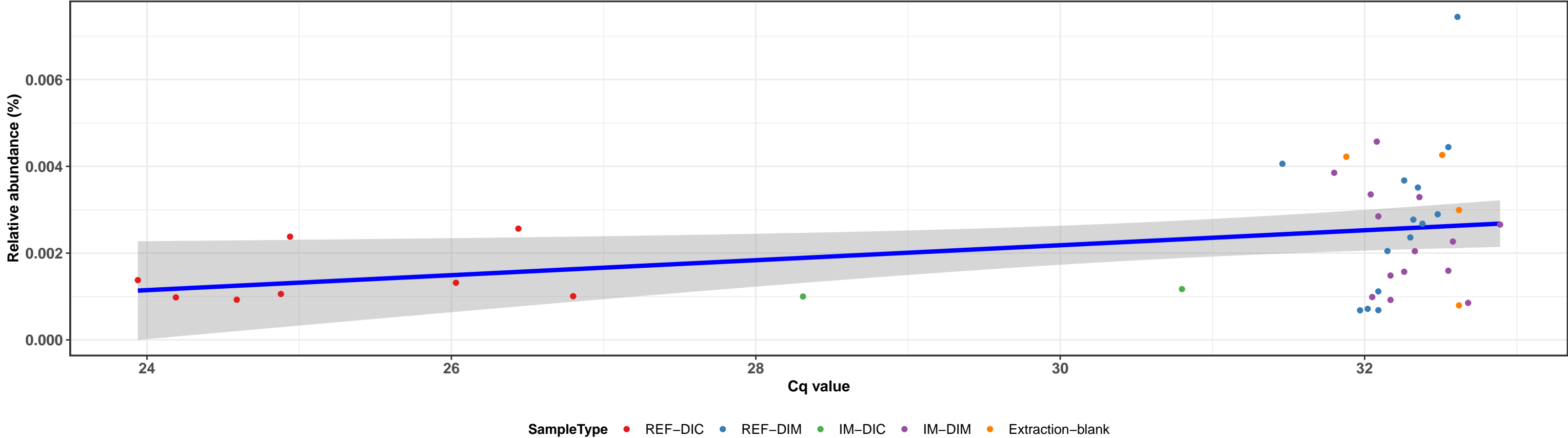
Correlation within: REF−DIC

$\log_e(S) = 4.094$, $p = 0.493$, $\hat{\rho}_{Spearman} = 0.286$, $CI_{95\%}$ [−0.420, 1.135], $n_{pairs} = 8$
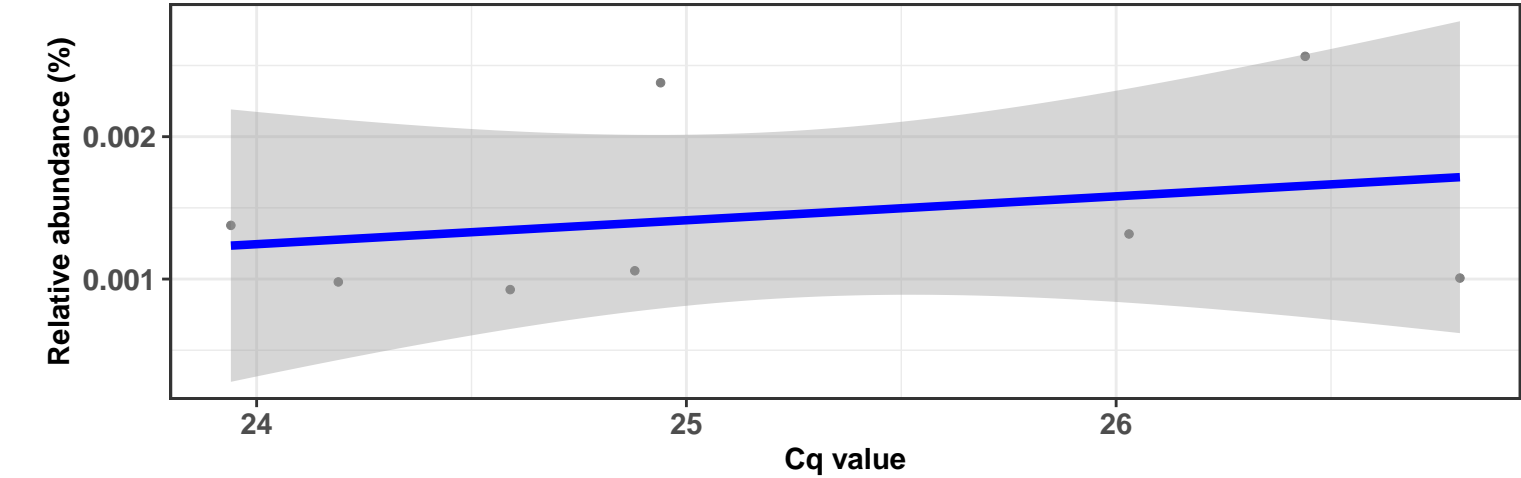
Correlation within: REF−DIM

$\log_e(S) = 5.169$, $p = 0.020$, $\hat{\rho}_{Spearman} = 0.614$, $CI_{95\%}$ [0.065, 1.151], $n_{pairs} = 14$

Correlation within: IM−DIC
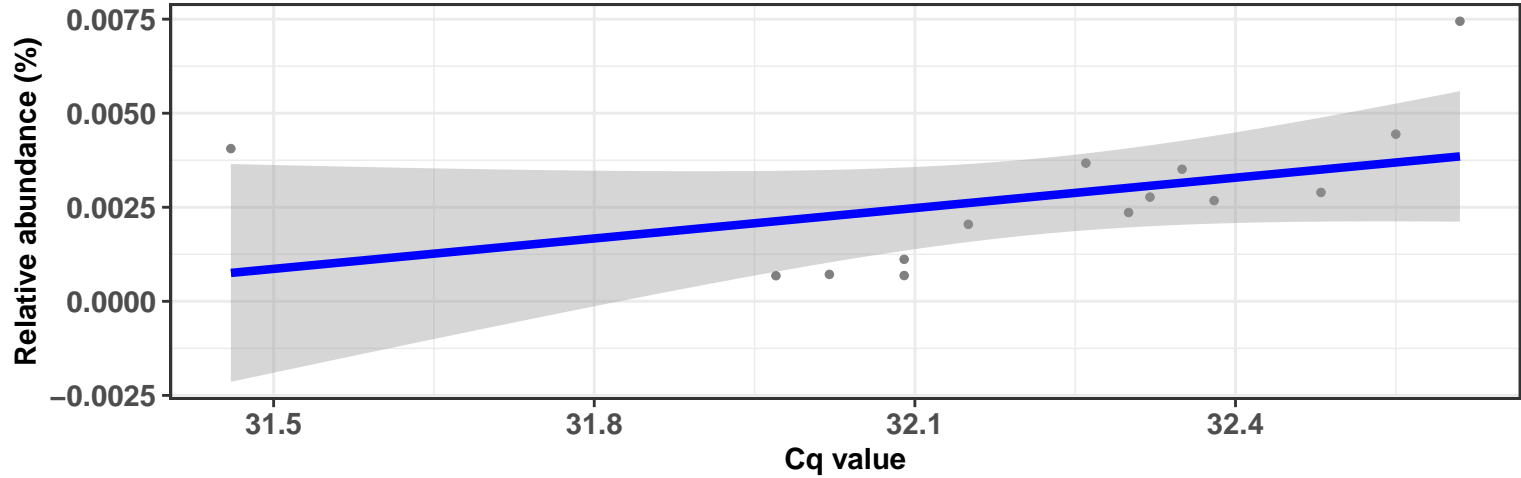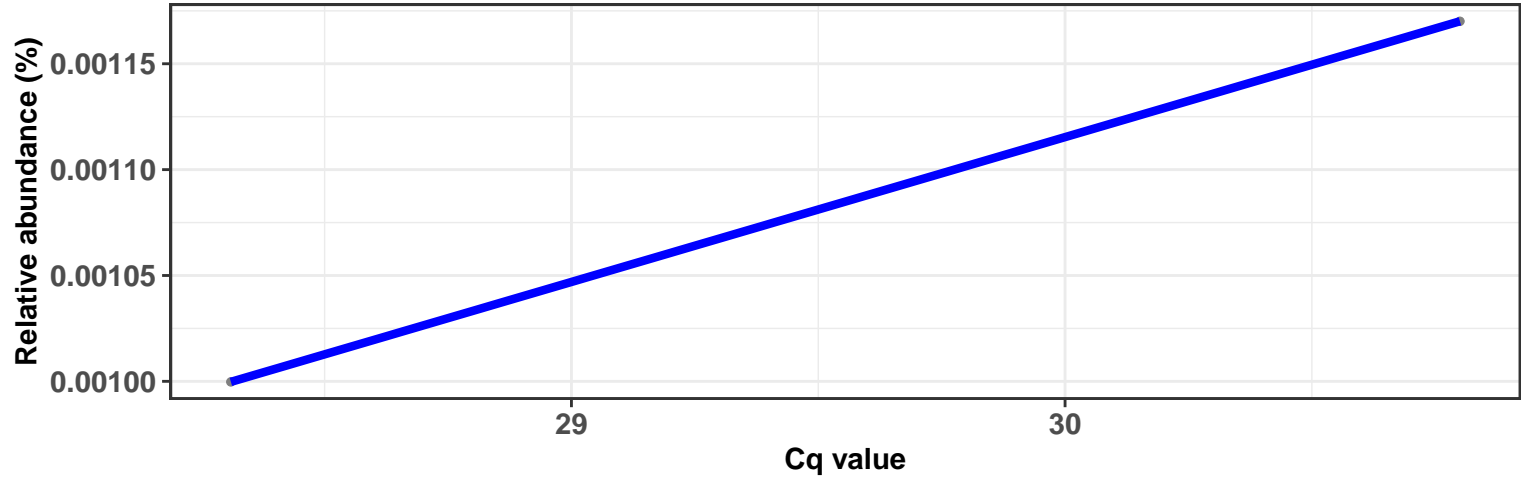
Correlation within: IM−DIM

$\log_e(S) = 6.430$, $p = 0.202$, $\hat{\rho}_{Spearman} = -0.363$, $CI_{95\%}$ [−0.913, 0.131], $n_{pairs} = 14$

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

Correlation with all samples

$\log_e(S) = 11.658$, $p = < 0.001$, $\hat{\rho}_{Spearman} = -0.581$, $CI_{95\%}$ [−0.724, −0.445], $n_{pairs} = 76$

SampleType: REF−DIC, REF−DIM, IM−DIC, IM−DIM, Extraction−blank, Mock
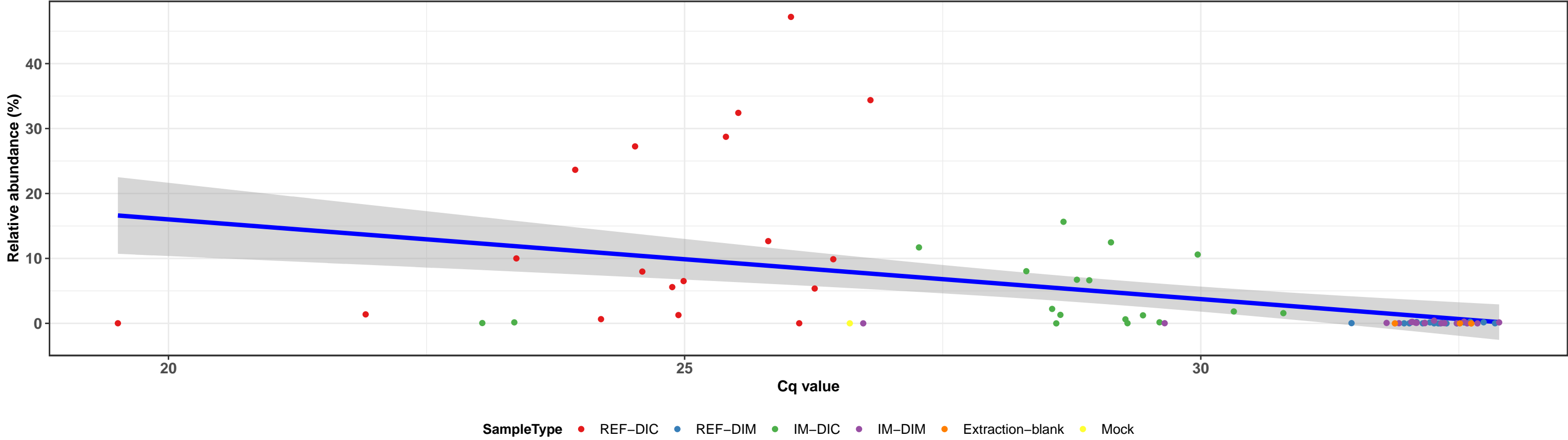
Correlation within: REF−DIC

$\log_e(S) = 6.480$, $p = 0.185$, $\hat{\rho}_{Spearman} = 0.327$, $CI_{95\%}$ [−0.146, 0.842], $n_{pairs} = 18$
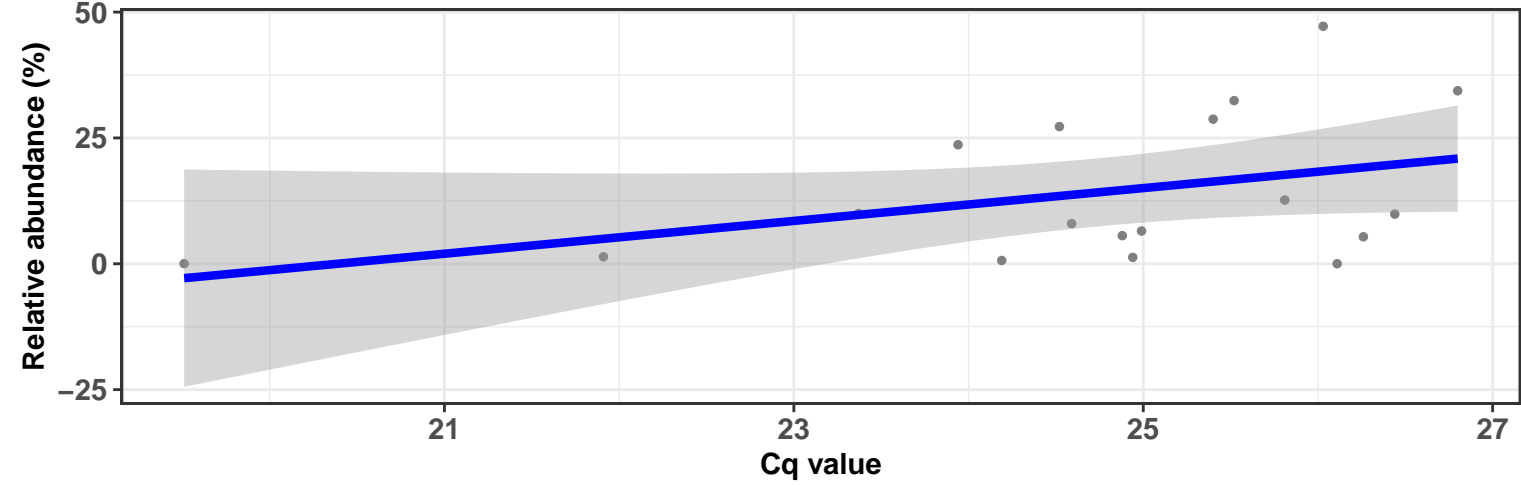
Correlation within: REF−DIM

$\log_e(S) = 6.632$, $p = 0.790$, $\hat{\rho}_{Spearman} = 0.070$, $CI_{95\%}$ [−0.393, 0.594], $n_{pairs} = 17$
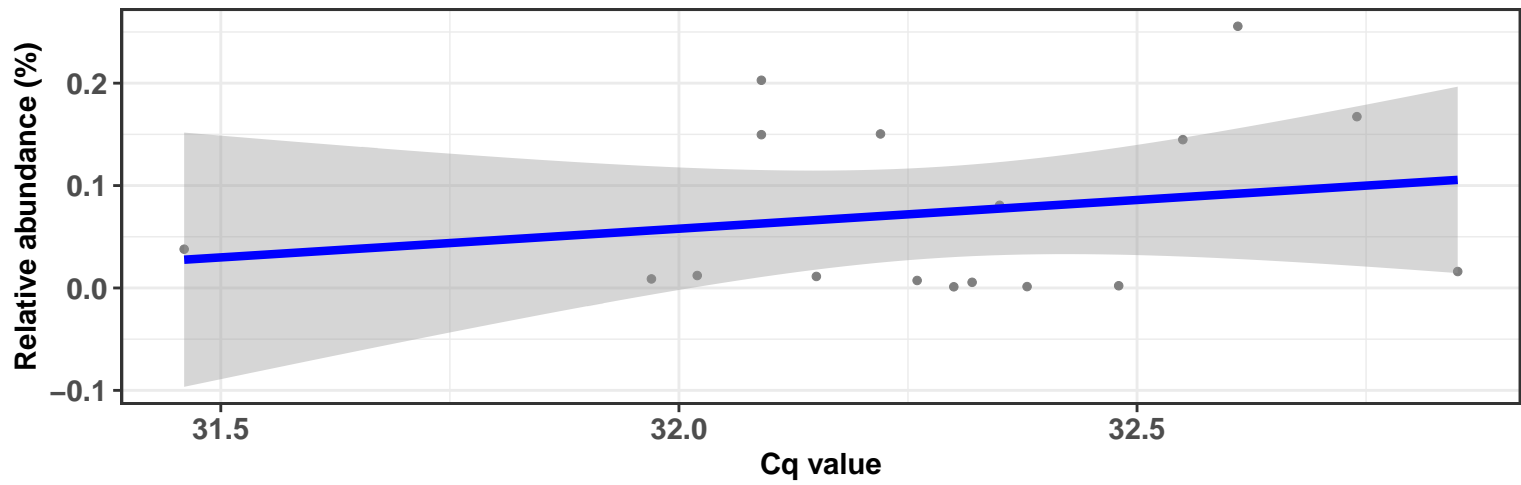
Correlation within: IM−DIC

$\log_e(S) = 6.837$, $p = 0.880$, $\hat{\rho}_{Spearman} = 0.038$, $CI_{95\%}$ [−0.426, 0.524], $n_{pairs} = 18$
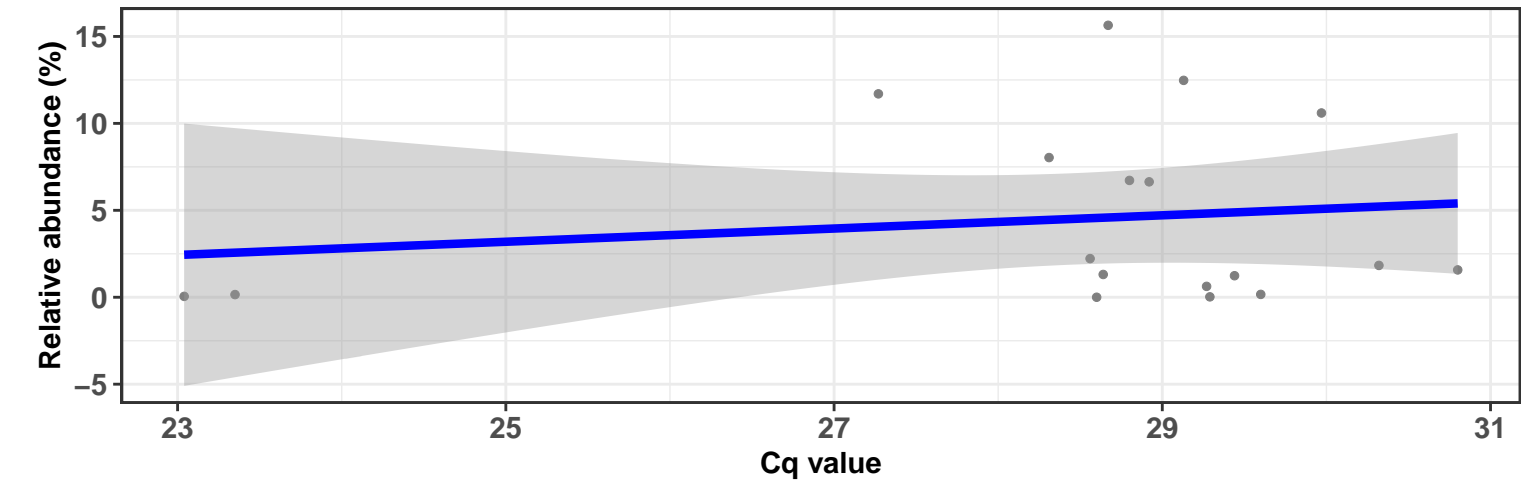
Correlation within: IM−DIM

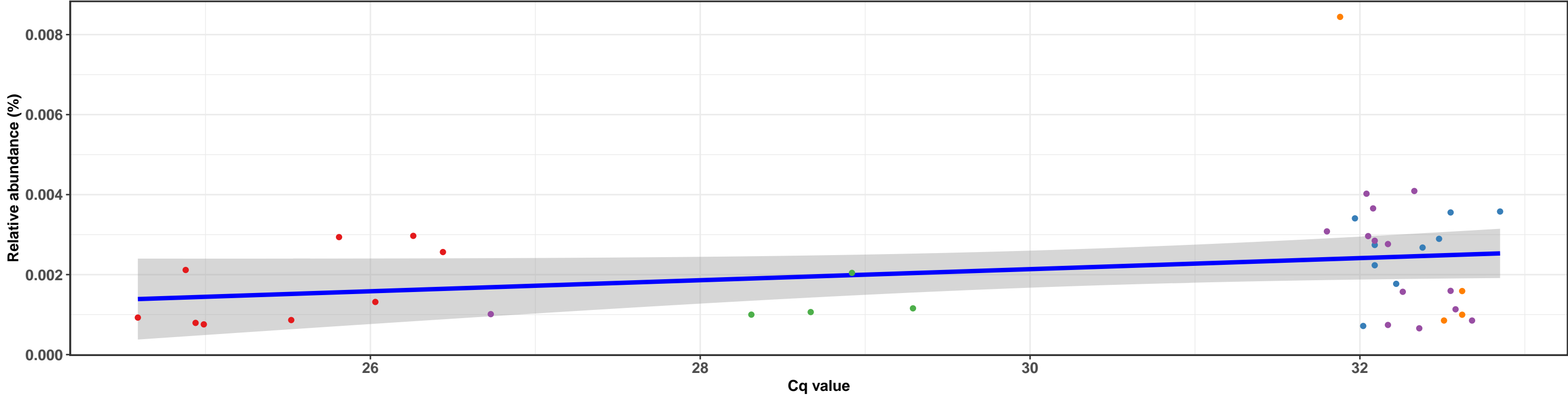$\log_e(S) = 6.890$, $p = 0.958$, $\hat{\rho}_{Spearman} = -0.013$, $CI_{95\%}$ [−0.441, 0.455], $n_{pairs} = 18$
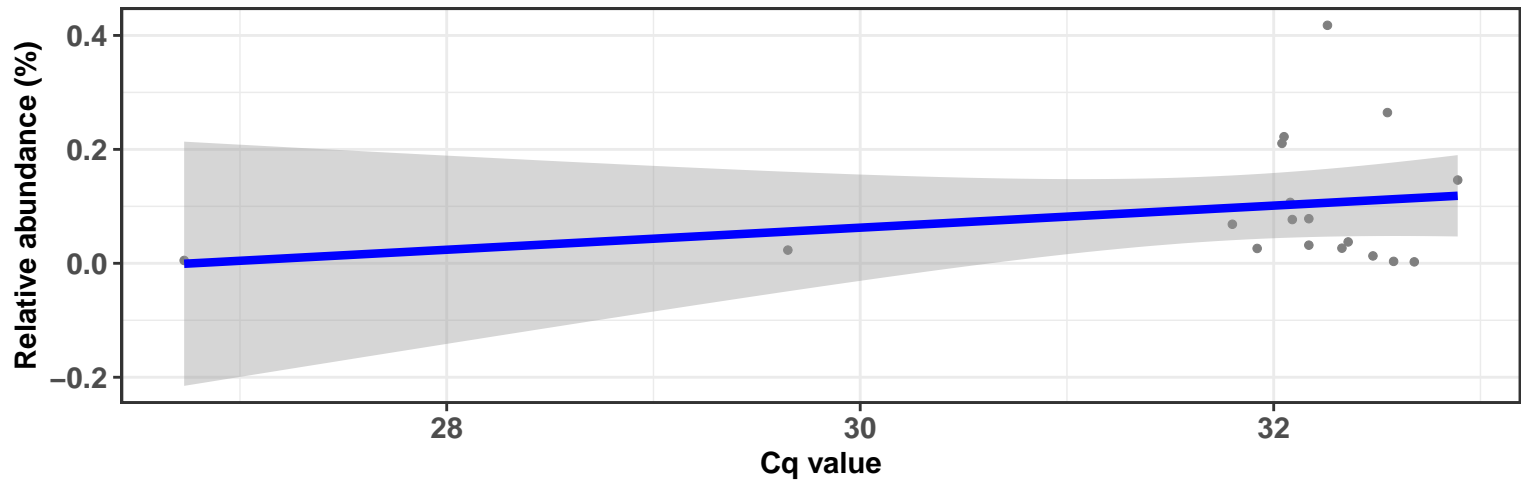
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.183$, $p = 0.927$, $\hat{\rho}_{Spearman} = 0.015$, $CI_{95\%}$ [−0.383, 0.388], $n_{pairs} = 39$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
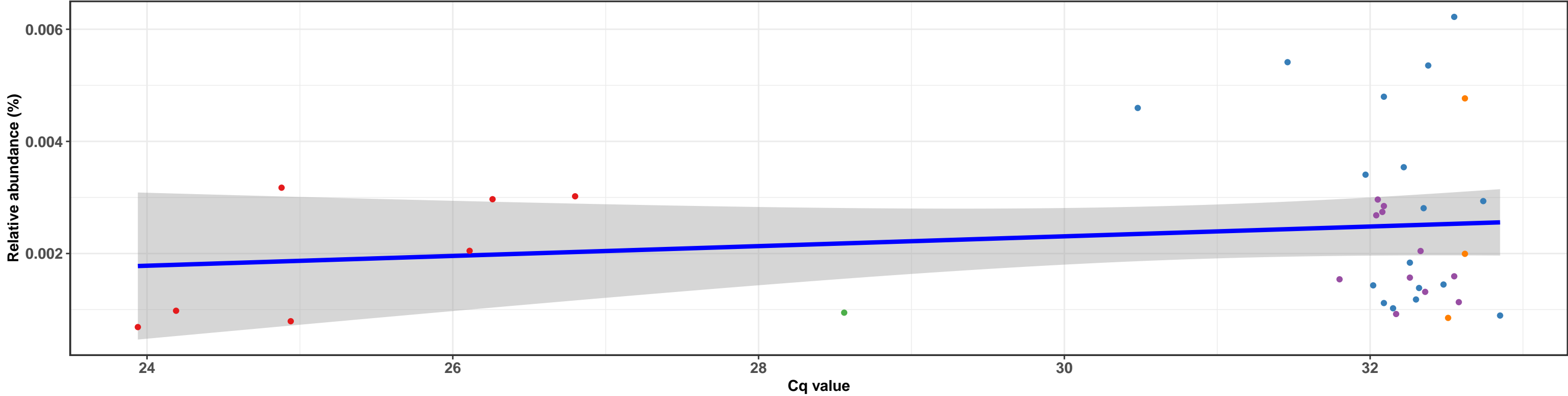
Correlation within: REF−DIC

$\log_e(S) = 3.178$, $p = 0.180$, $\hat{\rho}_{Spearman} = 0.571$, $CI_{95\%}$ [−0.276, 1.562], $n_{pairs} = 7$
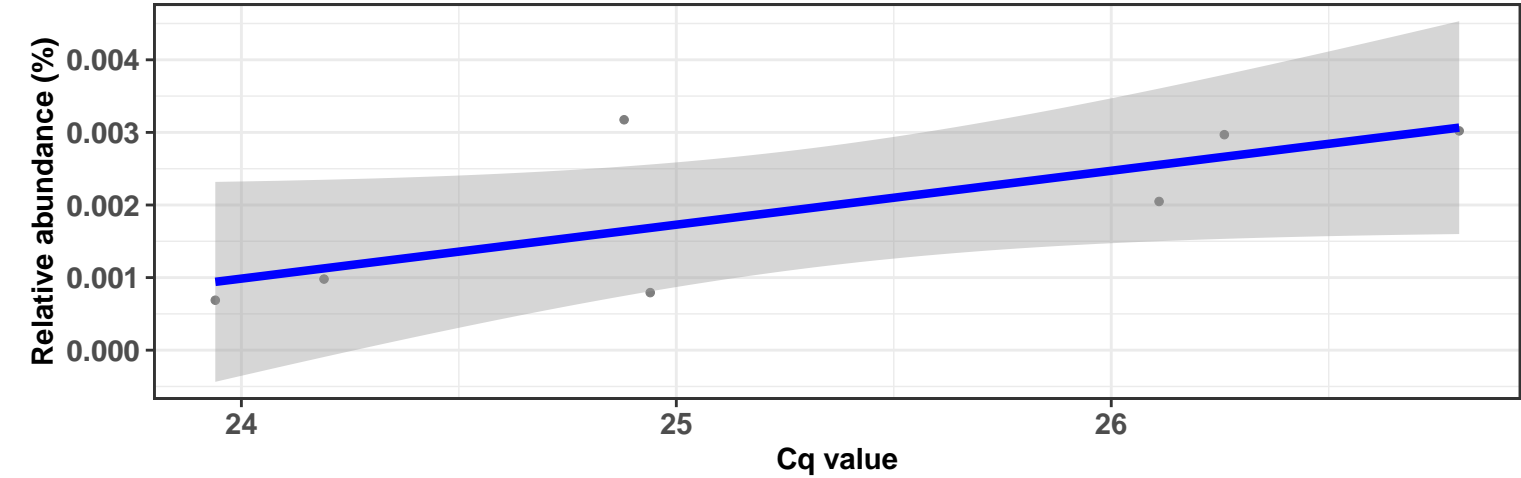
Correlation within: REF−DIM

$\log_e(S) = 6.866$, $p = 0.501$, $\hat{\rho}_{Spearman} = -0.175$, $CI_{95\%}$ [−0.704, 0.371], $n_{pairs} = 17$
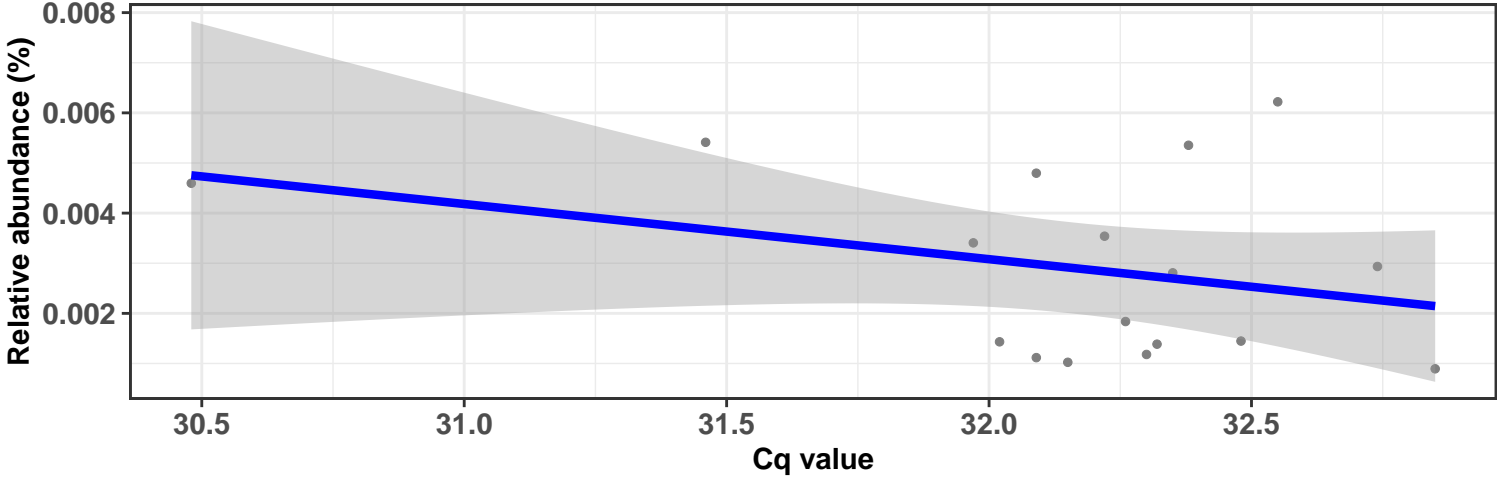
Correlation within: IM−DIC
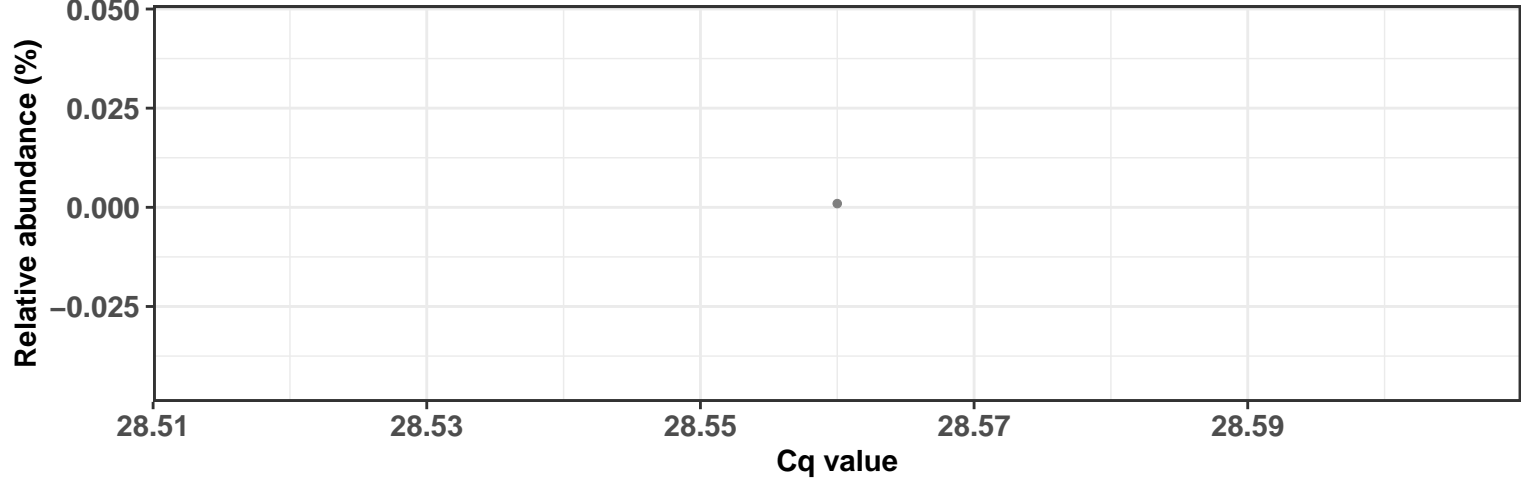
Correlation within: IM−DIM

$\log_e(S) = 5.775$, $p = 0.151$, $\hat{\rho}_{Spearman} = -0.464$, $CI_{95\%}$ [−0.982, 0.011], $n_{pairs} = 11$

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

Correlation with all samples

$\log_e(S) = 8.286$, $p = \, < 0.001$, $\hat{\rho}_{Spearman} = 0.598$, $CI_{95\%}$ [0.393, 0.834], $n_{pairs} = 39$

SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● IM−DIM   ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{Spearman} = -0.143$, $CI_{95\%}$ [−0.892, 0.617], $n_{pairs} = 7$

Correlation within: REF−DIM

$\log_e(S) = 4.426$, $p = 0.002$, $\hat{\rho}_{Spearman} = 0.770$, $CI_{95\%}$ [0.417, 1.199], $n_{pairs} = 13$

Correlation within: IM−DIC

Correlation within: IM−DIM

$\log_e(S) = 6.317$, $p = 0.067$, $\hat{\rho}_{Spearman} = -0.522$, $CI_{95\%}$ [−1.089, −0.058], $n_{pairs} = 13$

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

Correlation with all samples

$\log_e(S) = 8.996$, $p = 0.483$, $\hat{\rho}_{\text{Spearman}} = 0.117$, $\text{CI}_{95\%}$ [−0.210, 0.481], $n_{\text{pairs}} = 38$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 2.485$, $p = 0.156$, $\hat{\rho}_{\text{Spearman}} = 0.657$, $\text{CI}_{95\%}$ [−0.220, 1.678], $n_{\text{pairs}} = 6$

Correlation within: REF−DIM

$\log_e(S) = 6.054$, $p = 0.828$, $\hat{\rho}_{\text{Spearman}} = 0.064$, $\text{CI}_{95\%}$ [−0.581, 0.623], $n_{\text{pairs}} = 14$
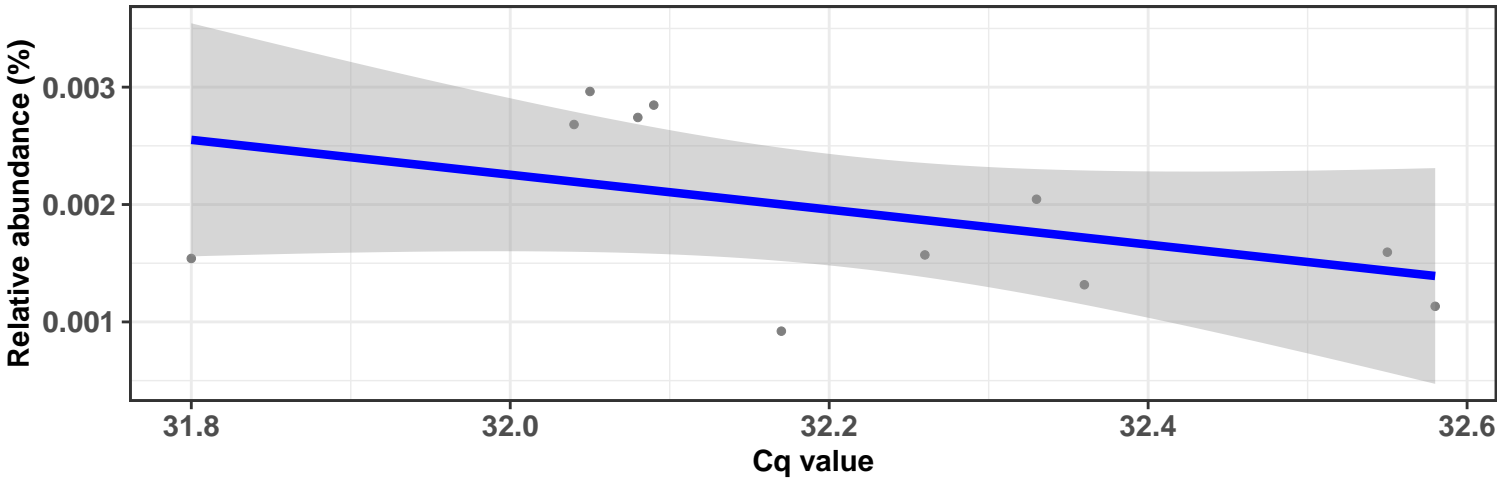

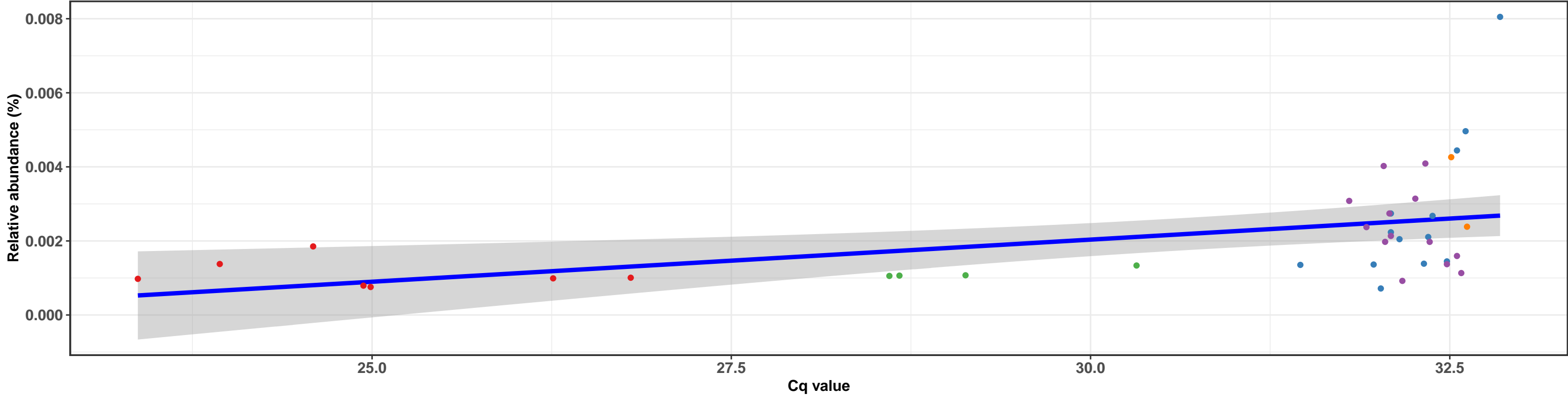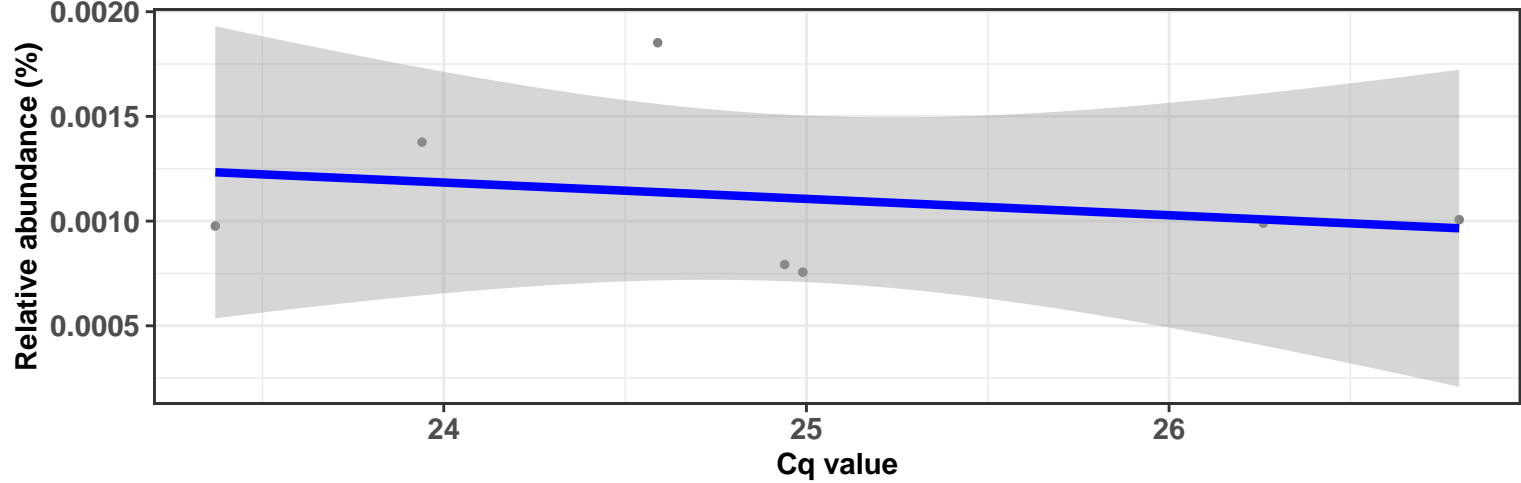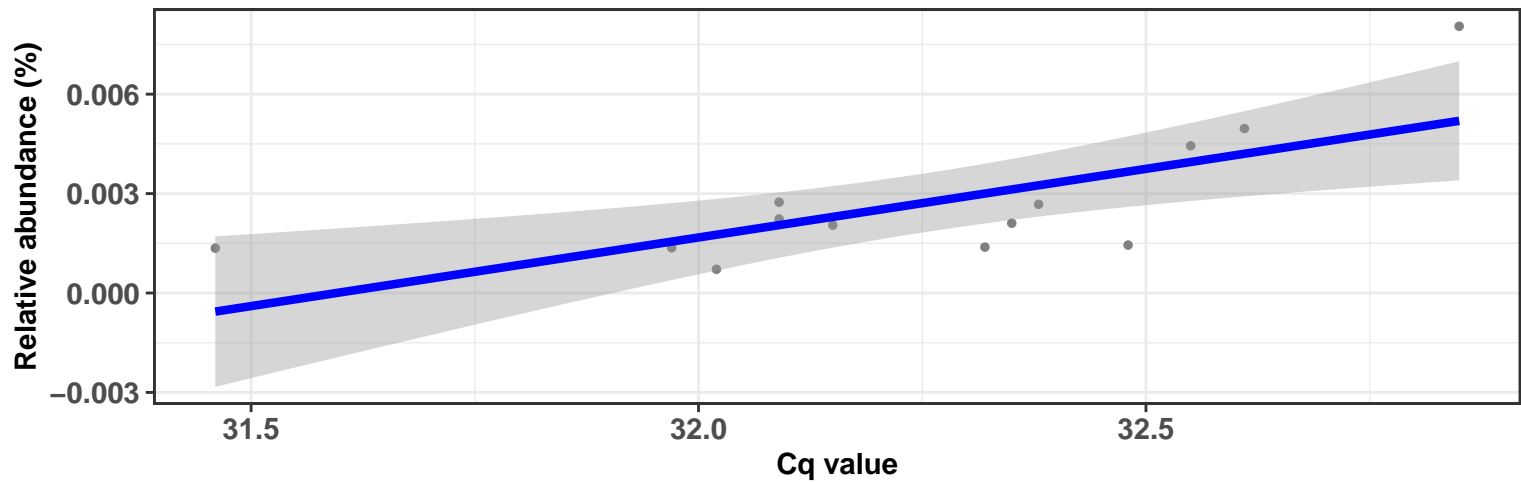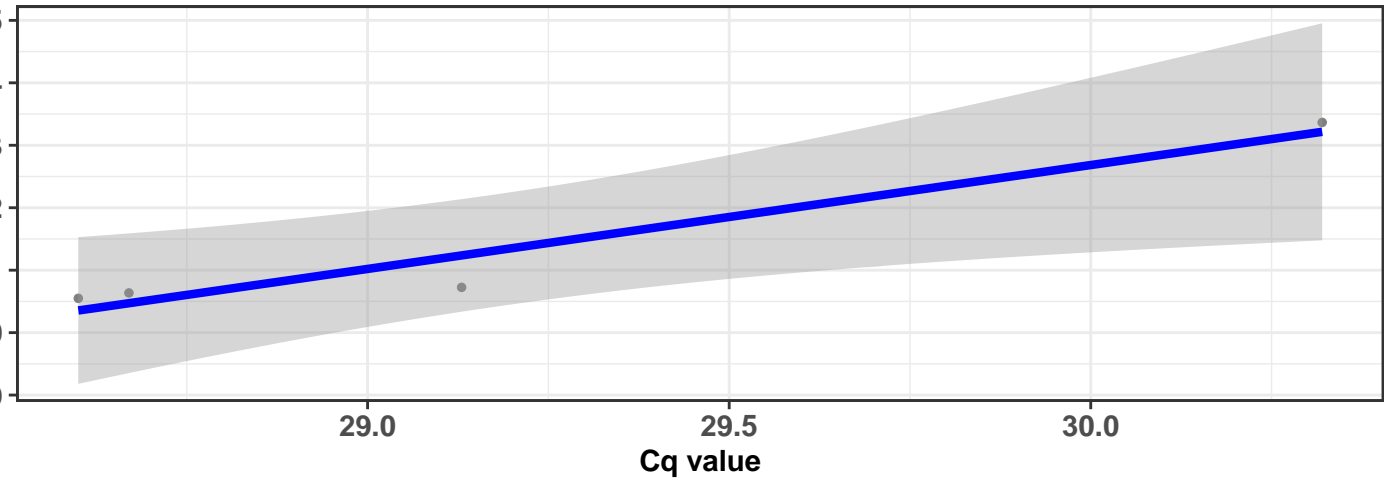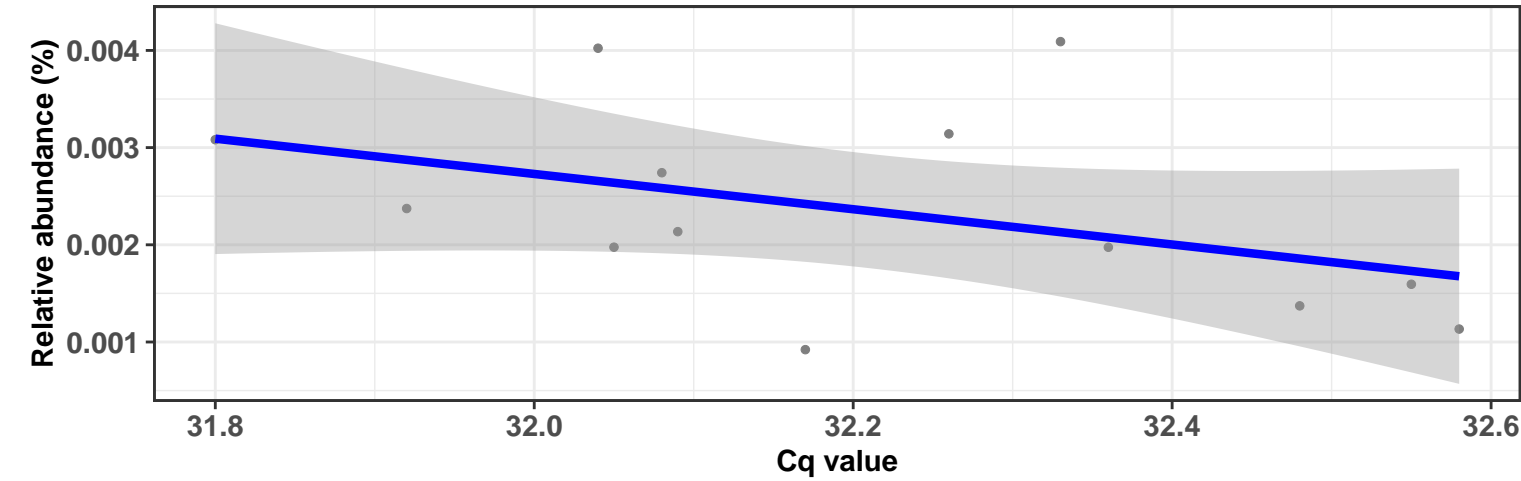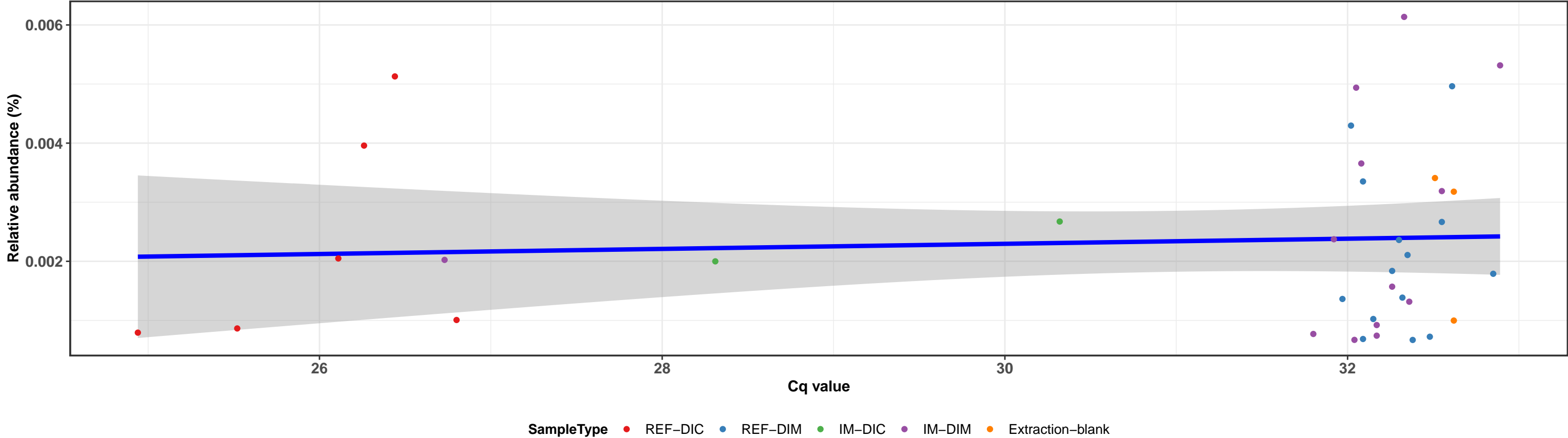**Correlation within: IM−DIC**

Correlation within: IM−DIM

$\log_e(S) = 5.437$, $p = 0.215$, $\hat{\rho}_{\text{Spearman}} = 0.369$, $\text{CI}_{95\%}$ [−0.112, 0.792], $n_{\text{pairs}} = 13$

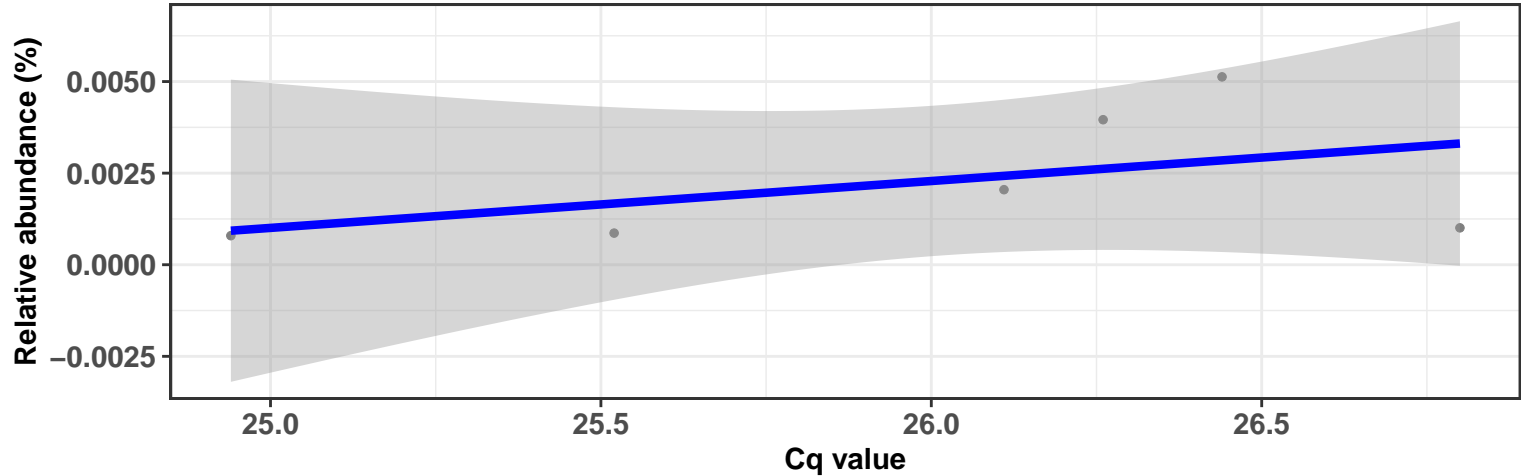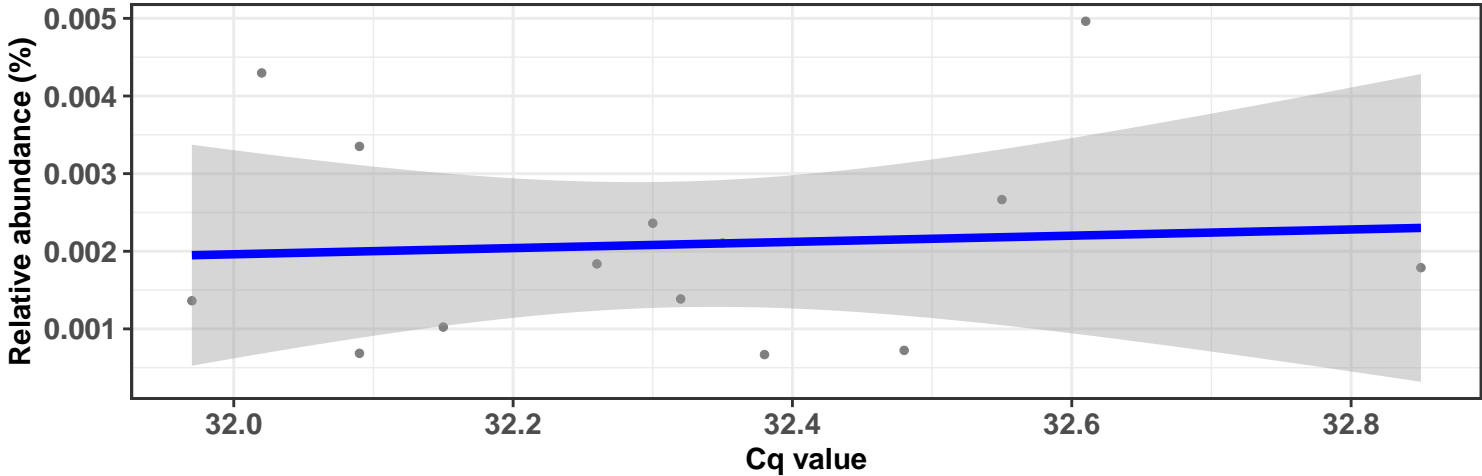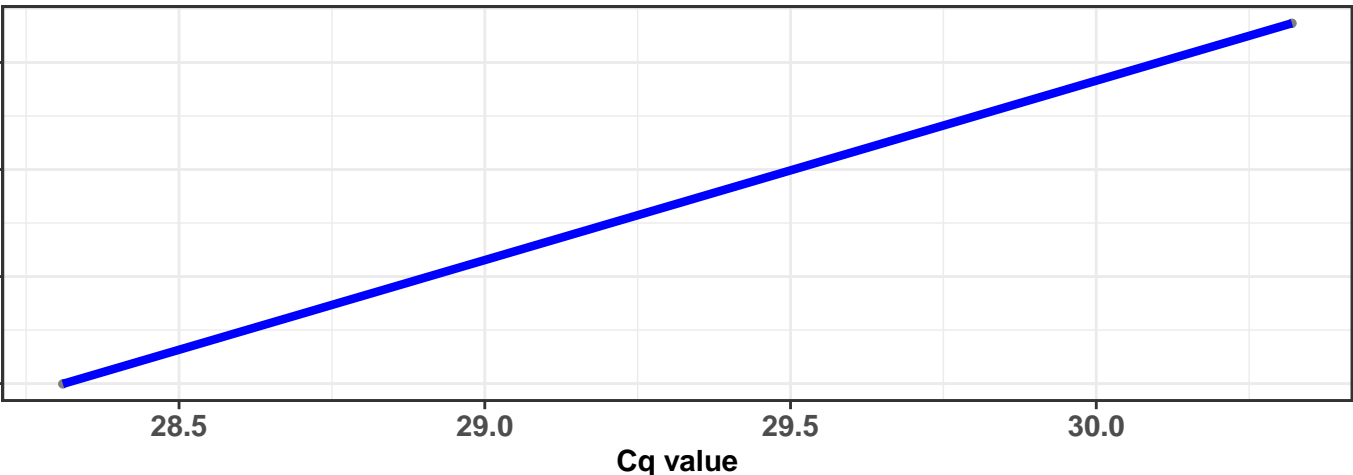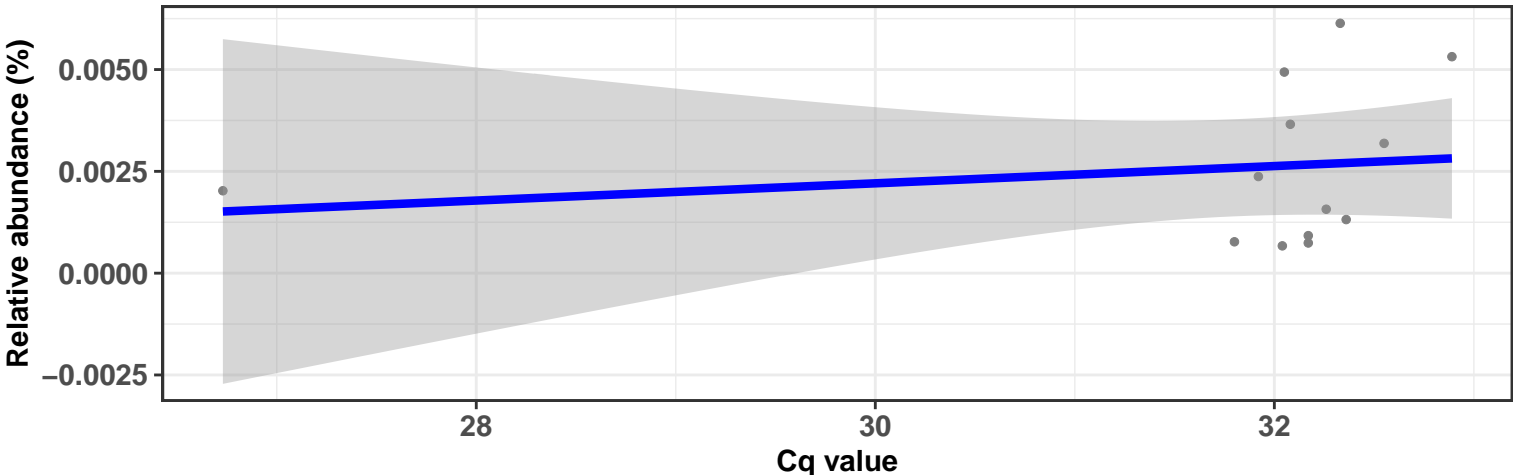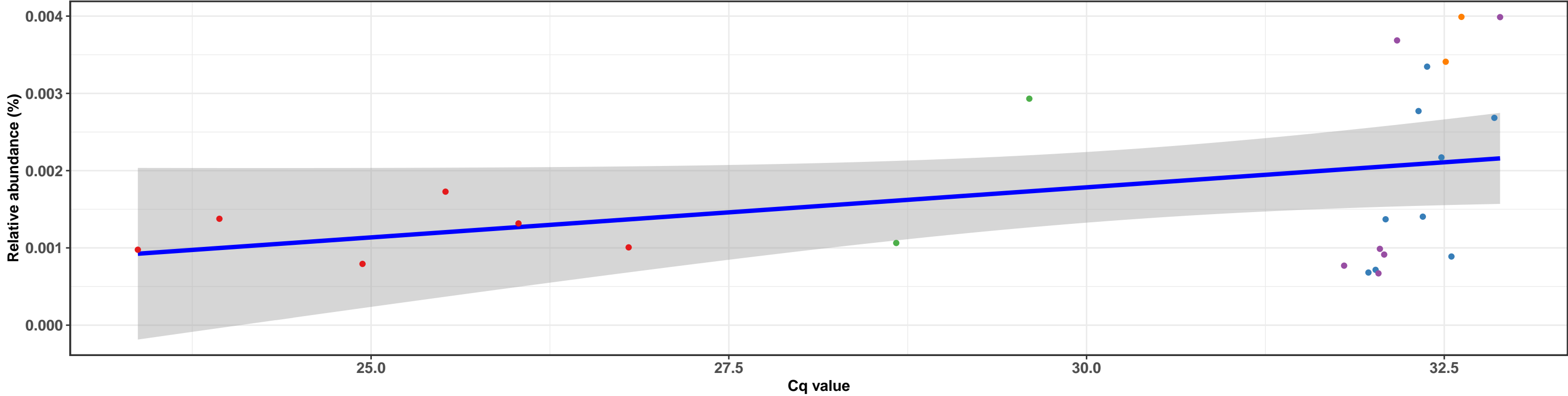# k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA
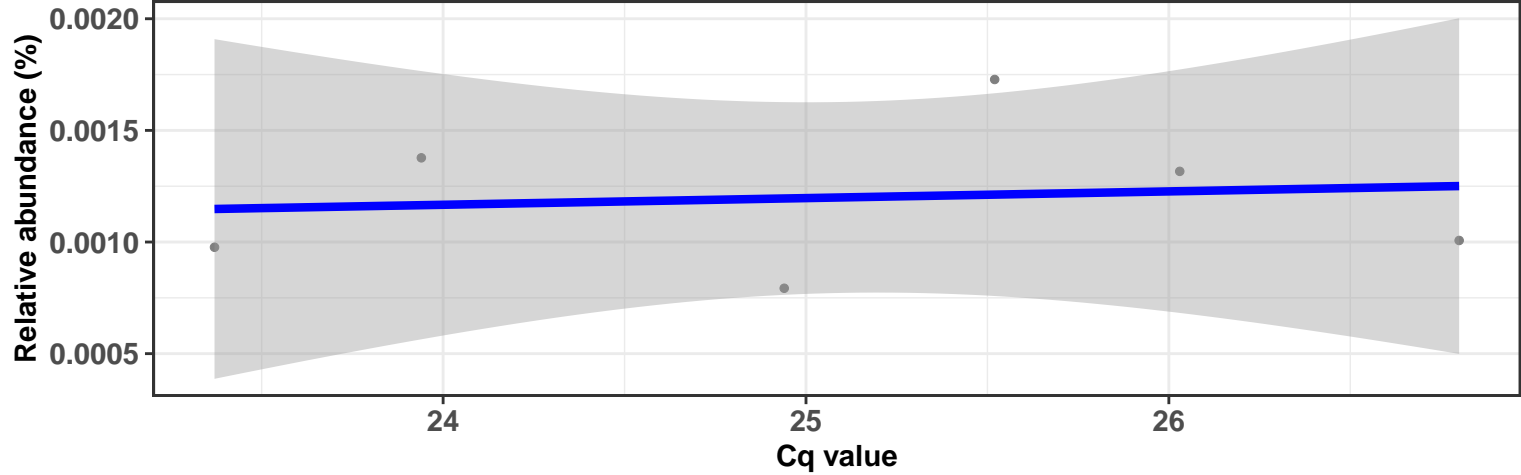
Correlation with all samples

$\log_e(S) = 7.156$, $p = 0.010$, $\hat{\rho}_{Spearman} = 0.507$, $CI_{95\%}$ [0.197, 0.888], $n_{pairs} = 25$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 3.332$, $p = 0.704$, $\hat{\rho}_{Spearman} = 0.200$, $CI_{95\%}$ [−0.585, 0.931], $n_{pairs} = 6$

Correlation within: REF−DIM

$\log_e(S) = 4.025$, $p = 0.139$, $\hat{\rho}_{Spearman} = 0.533$, $CI_{95\%}$ [−0.134, 1.158], $n_{pairs} = 9$
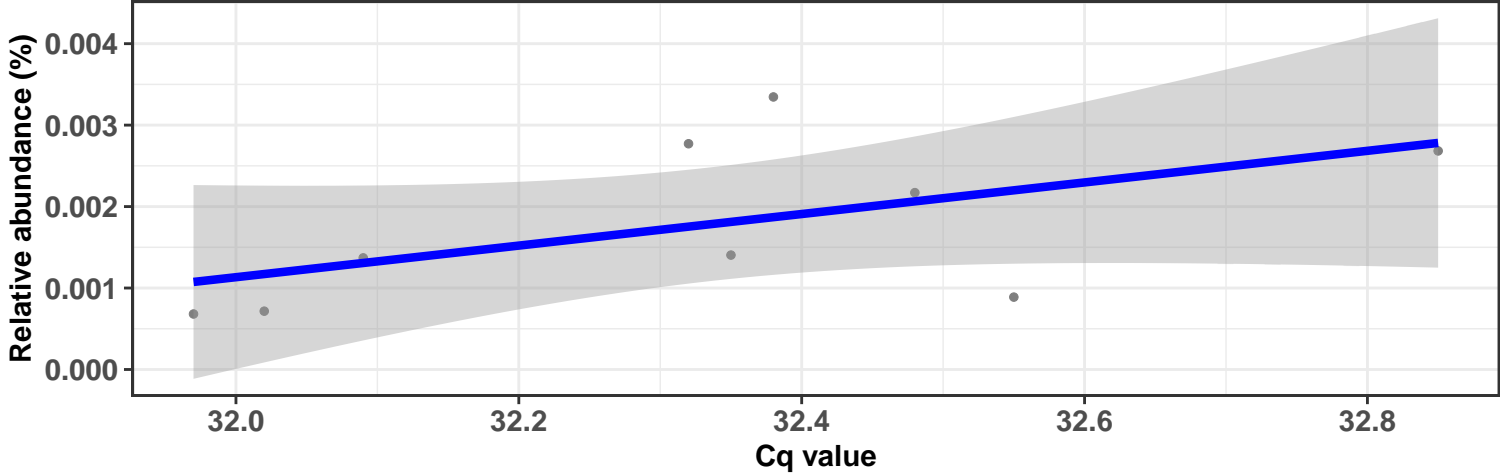
Correlation within: IM−DIC

Correlation within: IM−DIM

$\log_e(S) = 1.386$, $p = 0.019$, $\hat{\rho}_{Spearman} = 0.886$, $CI_{95\%}$ [0.406, 1.554], $n_{pairs} = 6$

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

Correlation with all samples

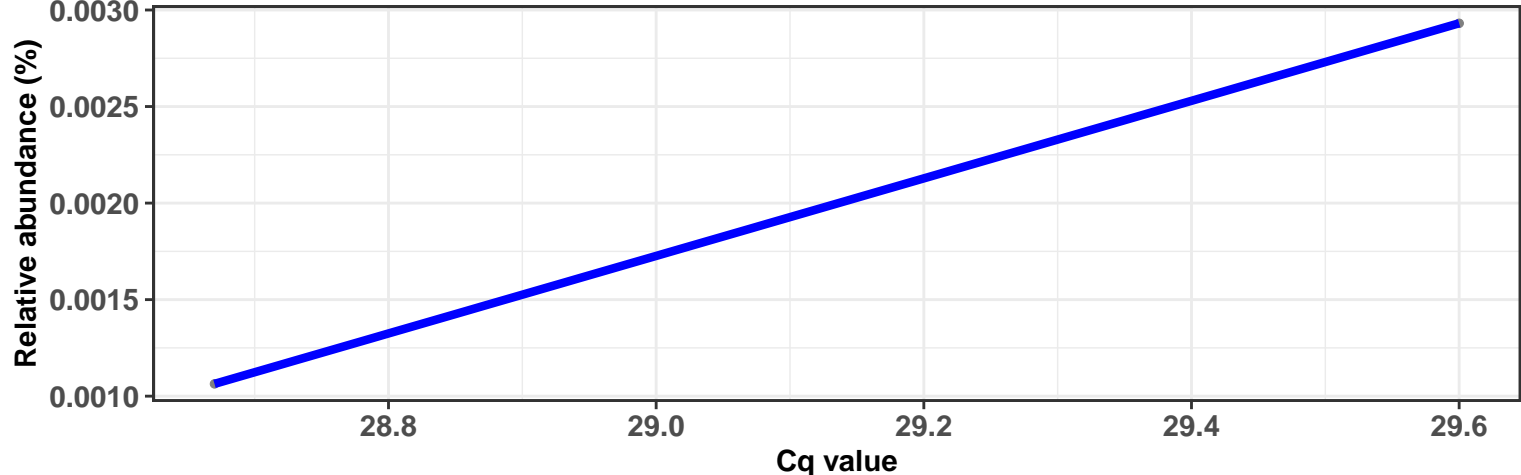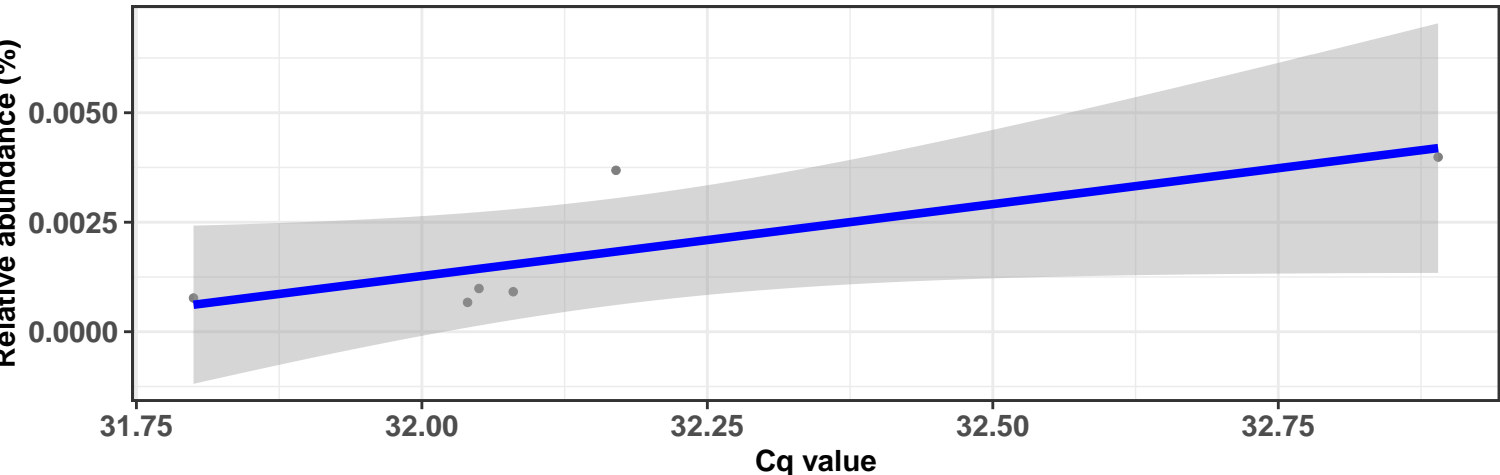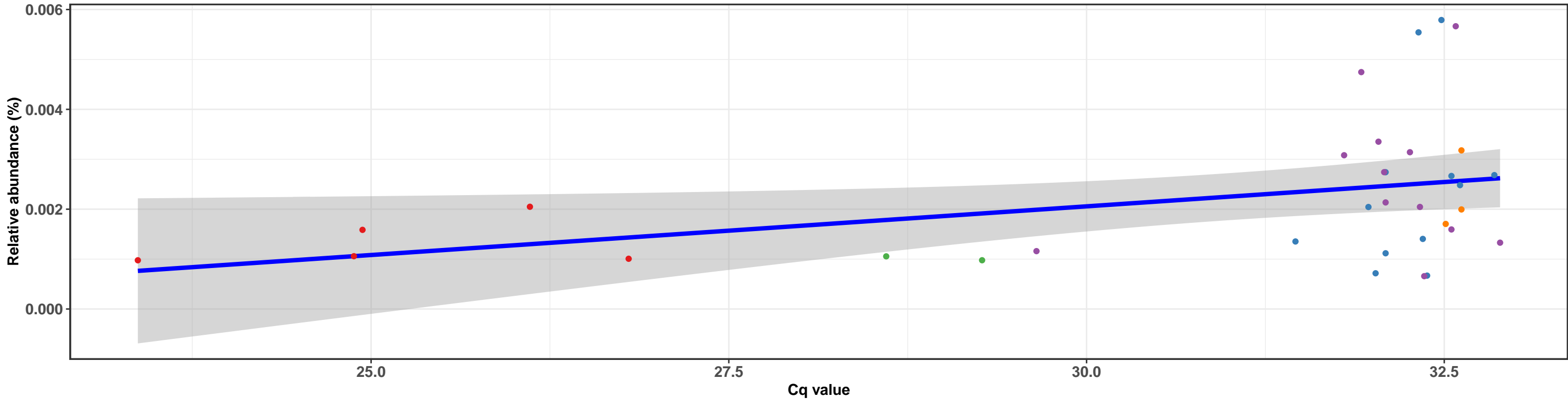$\log_e(S) = 8.374$, $p = 0.050$, $\hat{\rho}_{Spearman} = 0.338$, $CI_{95\%}$ [0.057, 0.607], $n_{pairs} = 34$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

Correlation within: REF−DIM

$\log_e(S) = 5.164$, $p = 0.212$, $\hat{\rho}_{Spearman} = 0.389$, $CI_{95\%}$ [−0.096, 0.867], $n_{pairs} = 12$

Correlation within: IM−DIC

Correlation within: IM−DIM

$\log_e(S) = 5.817$, $p = 0.587$, $\hat{\rho}_{Spearman} = -0.175$, $CI_{95\%}$ [−0.918, 0.550], $n_{pairs} = 12$

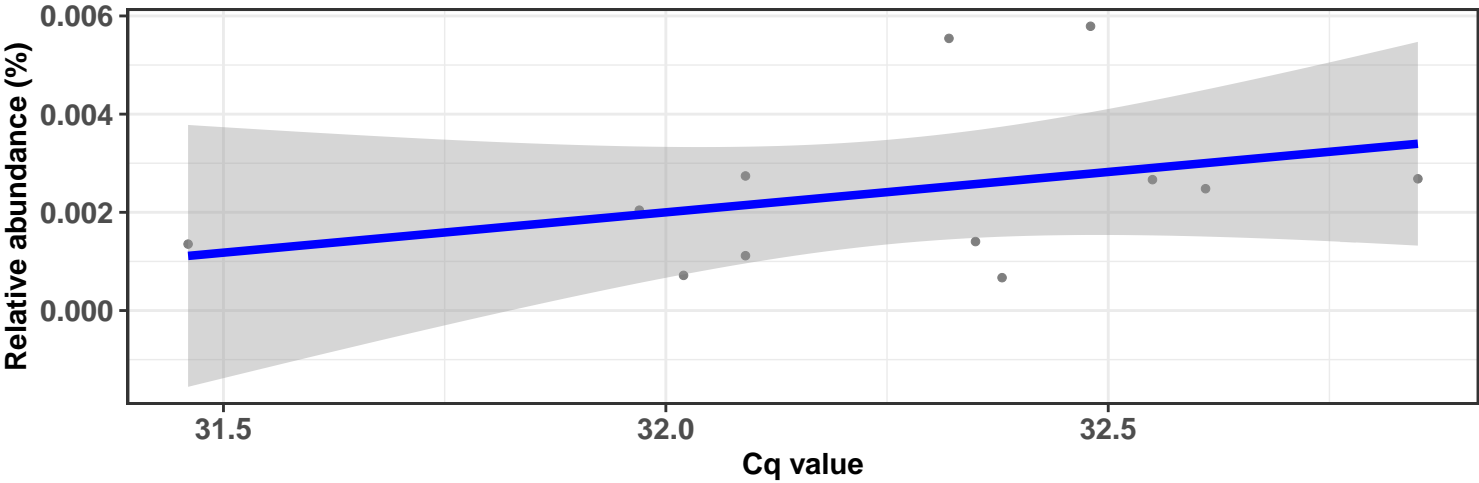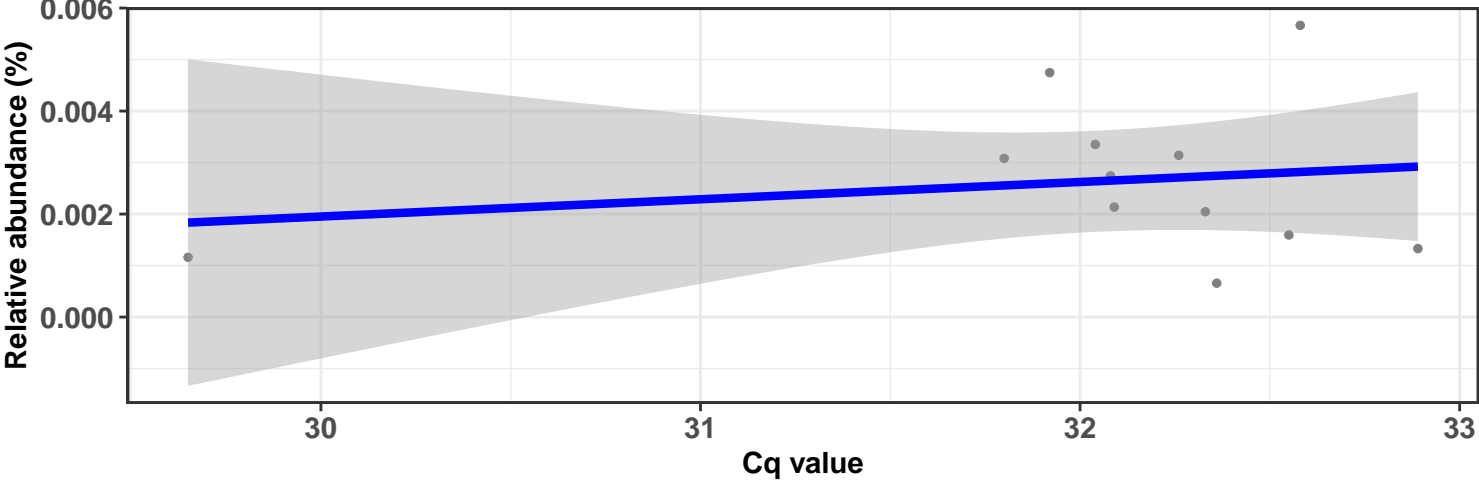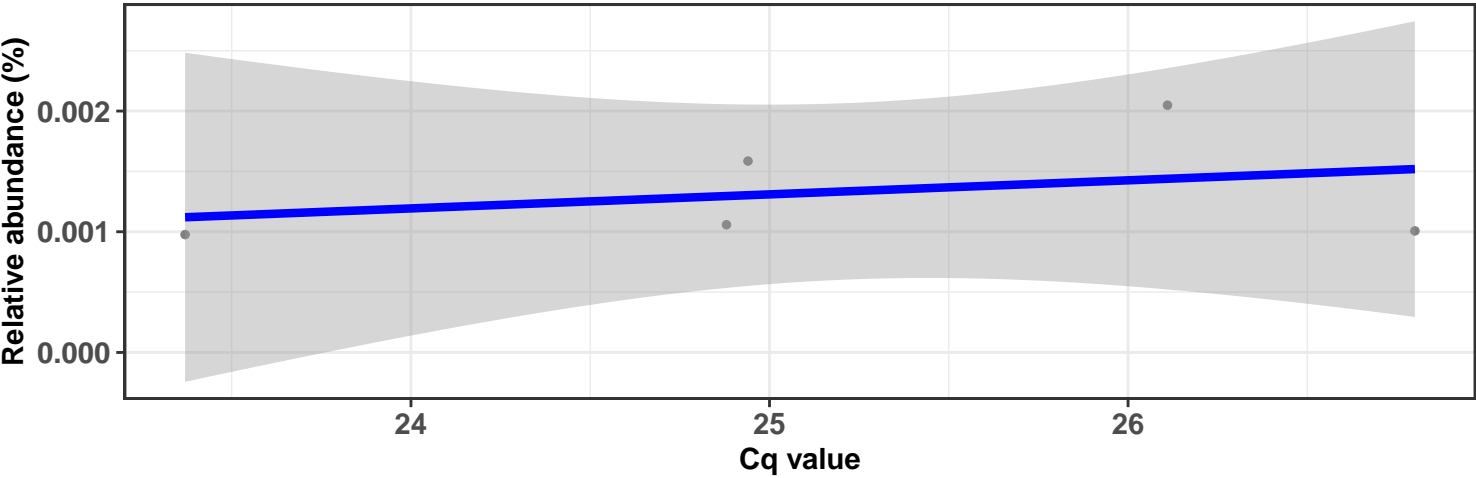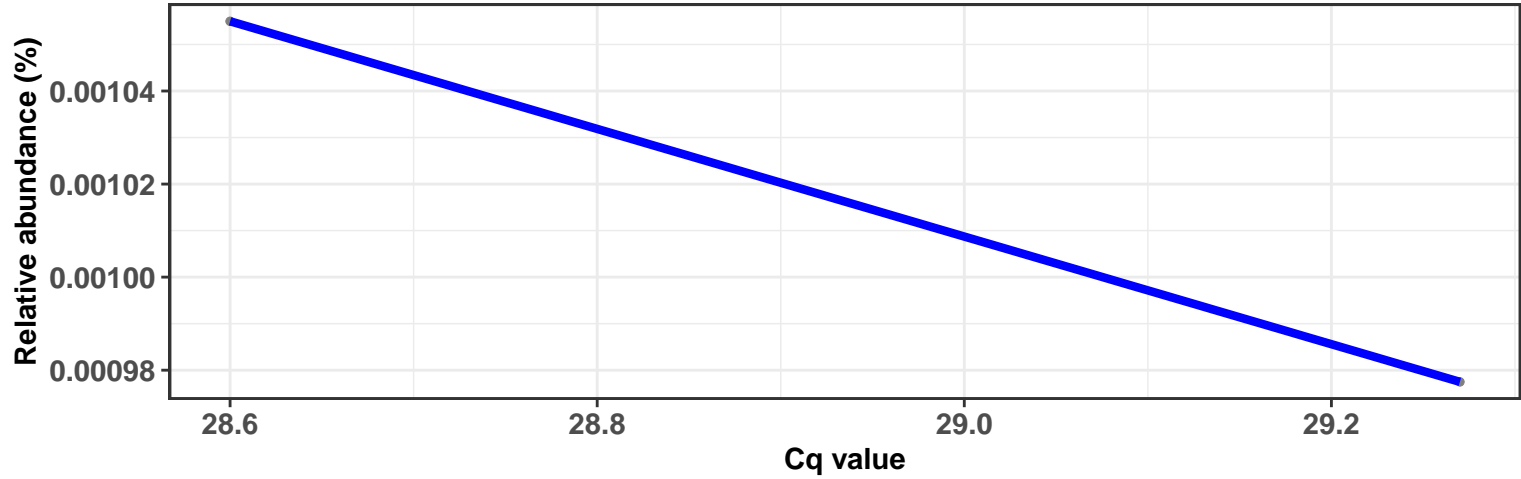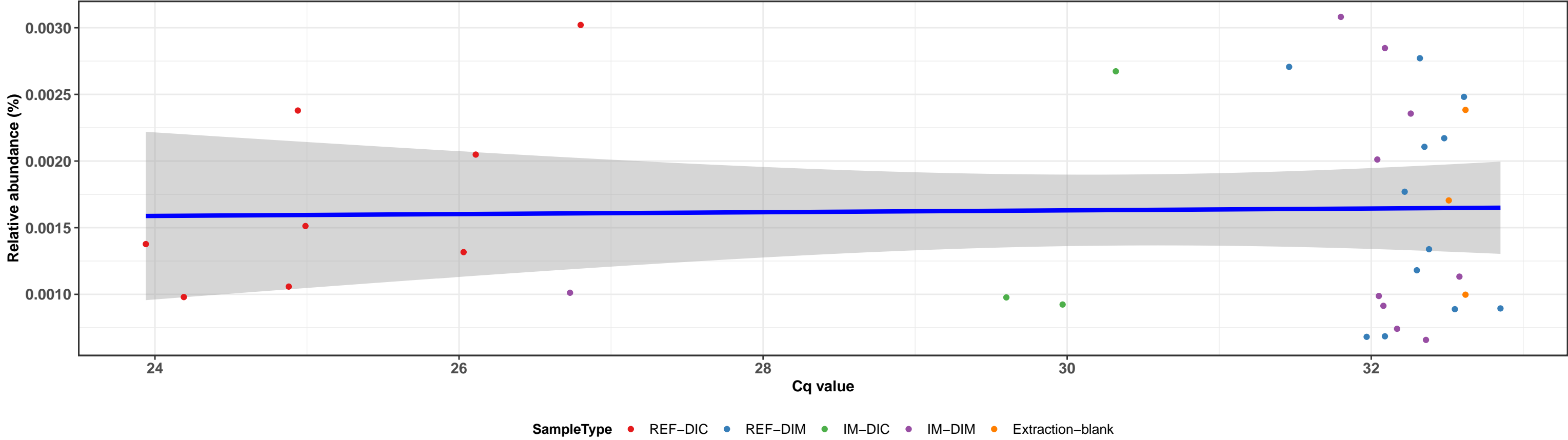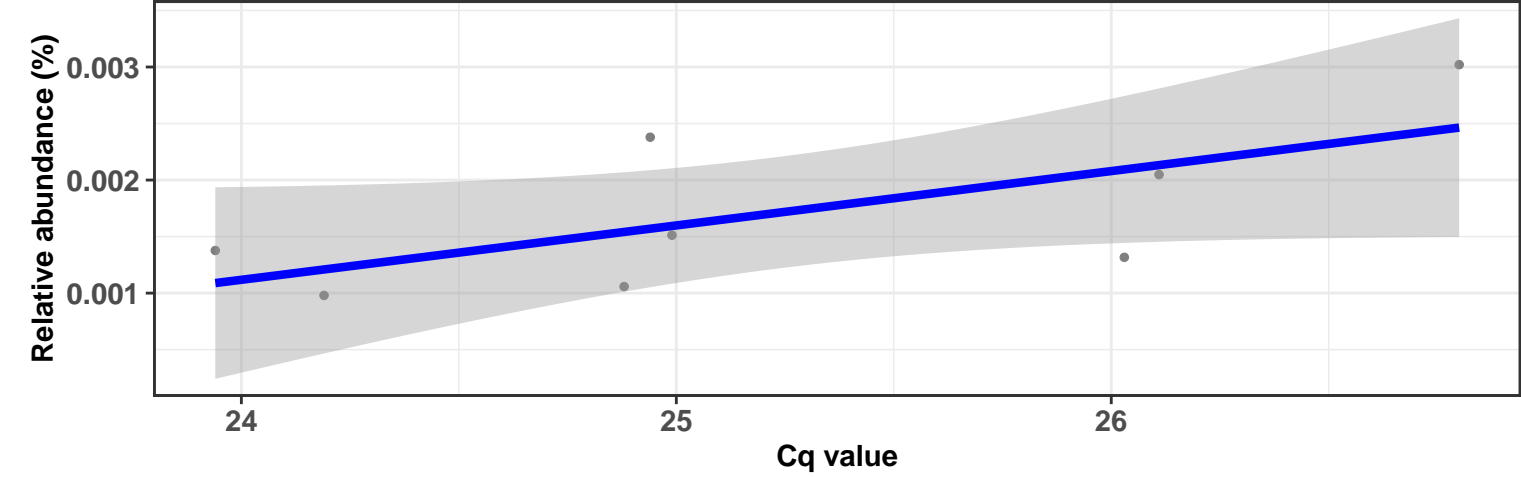# k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 9.013$, $p = 0.745$, $\hat{\rho}_{Spearman} = -0.056$, $CI_{95\%}$ [−0.383, 0.252], $n_{pairs} = 36$
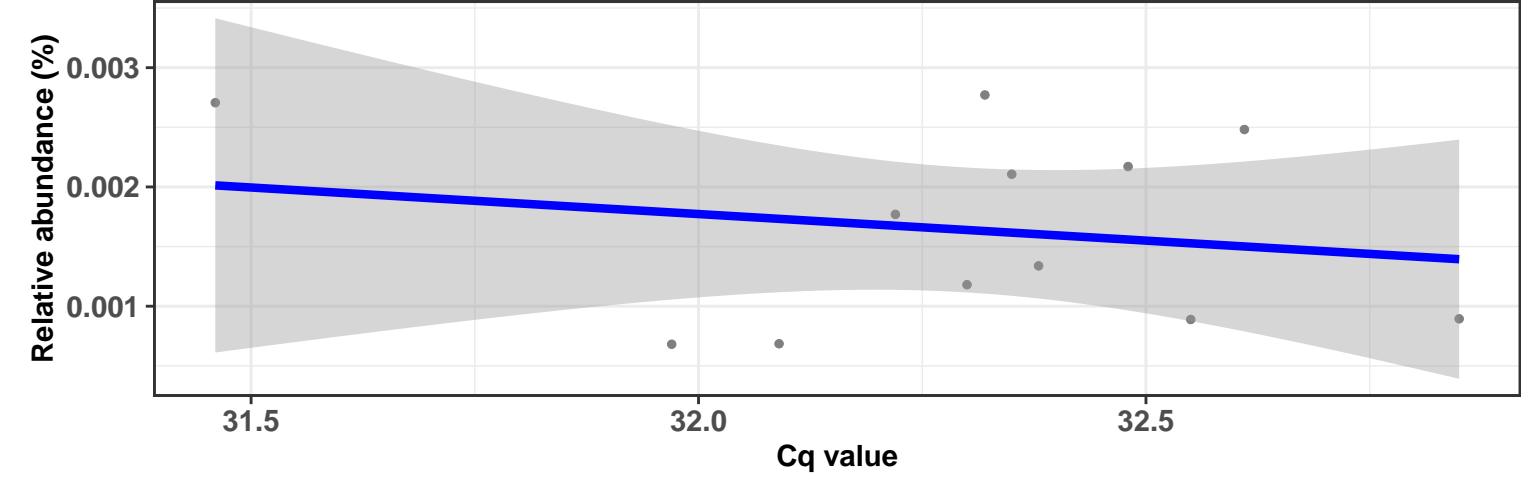

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 3.401$, $p = 0.086$, $\hat{\rho}_{Spearman} = 0.643$, $CI_{95\%}$ [0.102, 1.191], $n_{pairs} = 8$

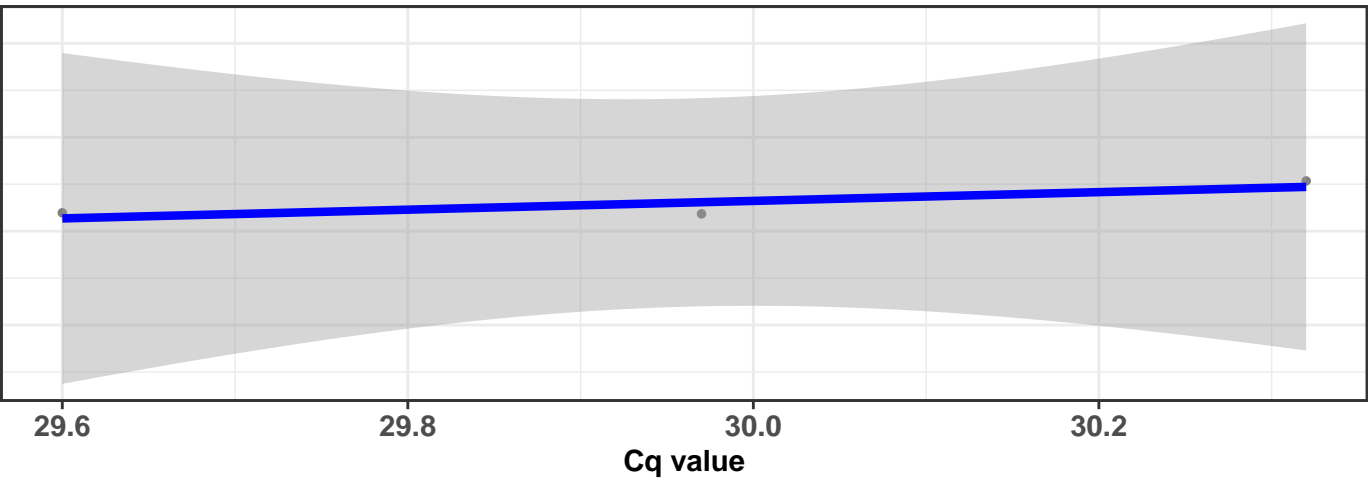**Correlation within: REF−DIM**

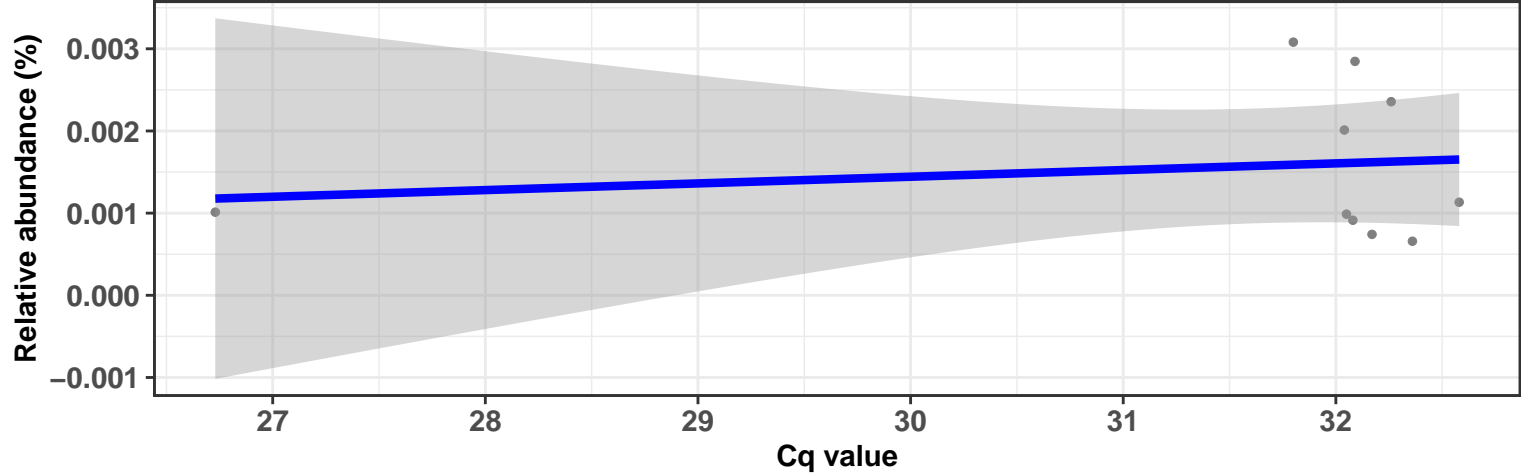$\log_e(S) = 5.583$, $p = 0.829$, $\hat{\rho}_{Spearman} = 0.070$, $CI_{95\%}$ [−0.620, 0.846], $n_{pairs} = 12$
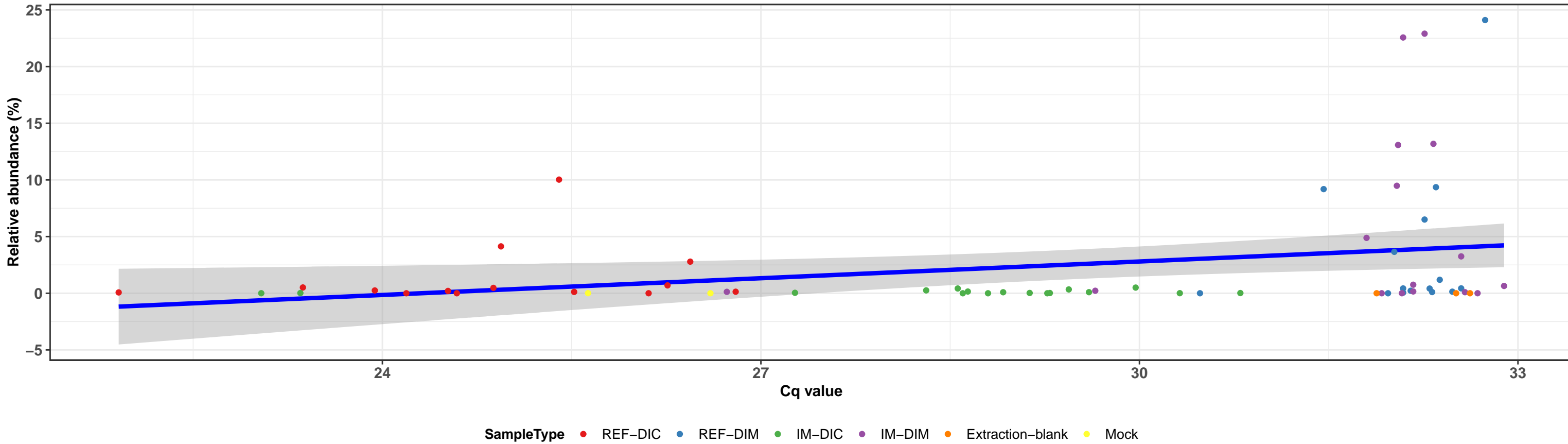

Correlation within: IM−DIC

Correlation within: IM−DIM

$\log_e(S) = 5.366$, $p = 0.405$, $\hat{\rho}_{Spearman} = -0.297$, $CI_{95\%}$ [−0.886, 0.230], $n_{pairs} = 10$

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

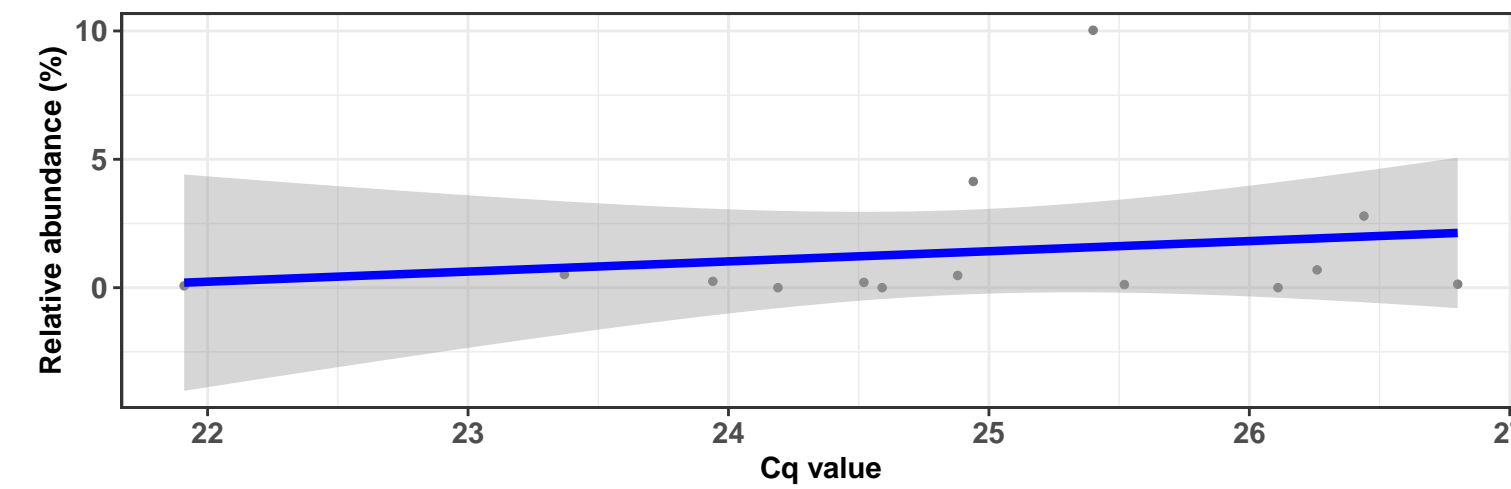**Correlation with all samples**

$\log_e(S) = 10.544$, $p = 0.048$, $\hat{\rho}_{Spearman} = 0.243$, $CI_{95\%}$ [0.004, 0.438], $n_{pairs} = 67$

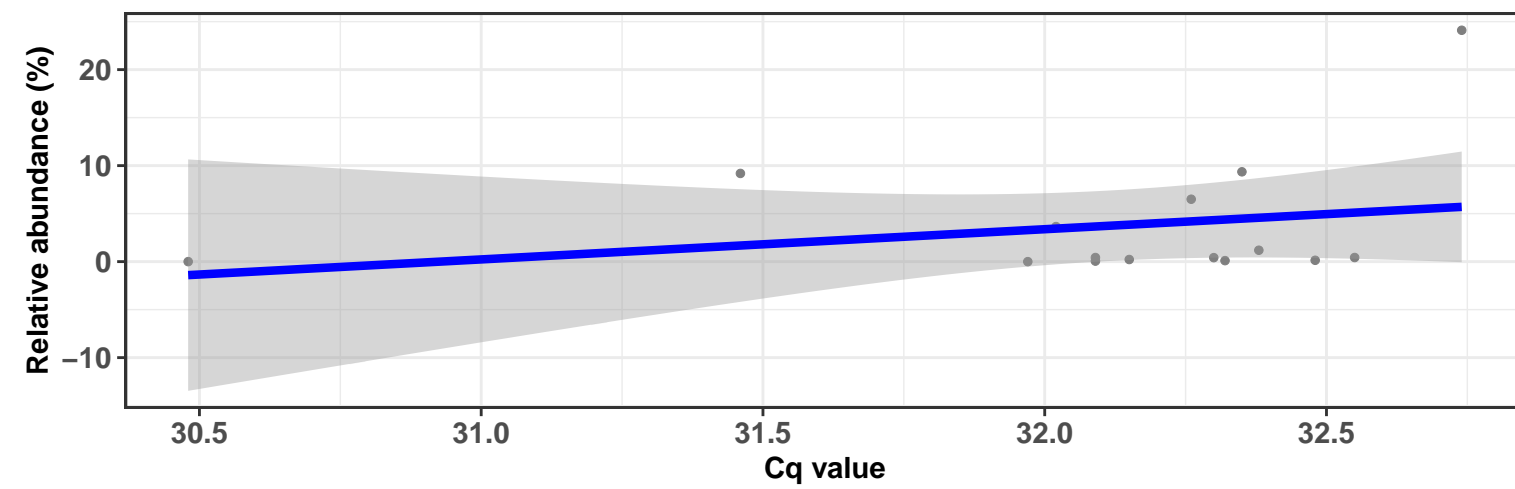SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock

Correlation within: REF−DIC

$\log_e(S) = 5.829$, $p = 0.383$, $\hat{\rho}_{Spearman} = 0.253$, $CI_{95\%}$ [−0.142, 0.739], $n_{pairs} = 14$

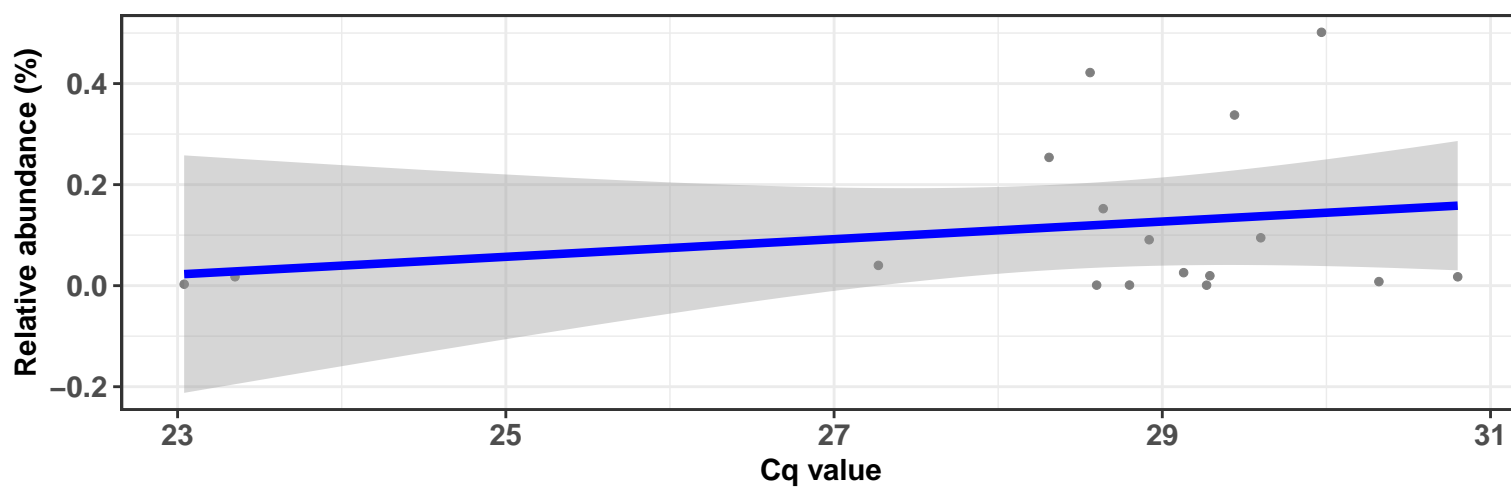**Correlation within: REF−DIM**

$\log_e(S) = 5.849$, $p = 0.162$, $\hat{\rho}_{Spearman} = 0.381$, $CI_{95\%}$ [−0.118, 0.880], $n_{pairs} = 15$

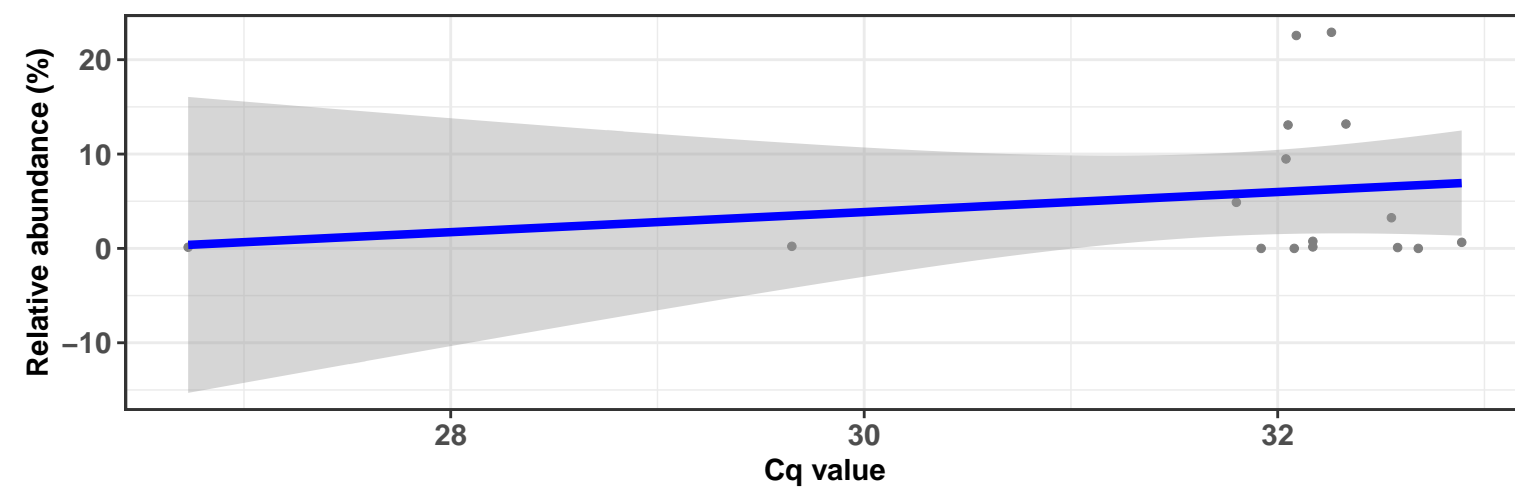**Correlation within: IM−DIC**

$\log_e(S) = 6.628$, $p = 0.779$, $\hat{\rho}_{Spearman} = 0.074$, $CI_{95\%}$ [−0.388, 0.539], $n_{pairs} = 17$
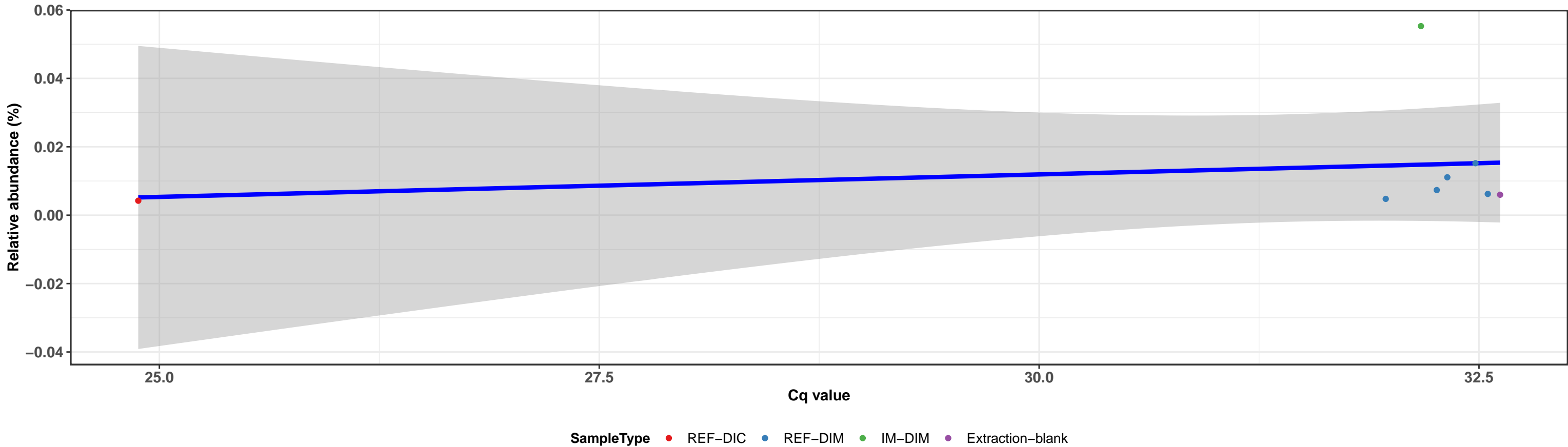
Correlation within: IM−DIM

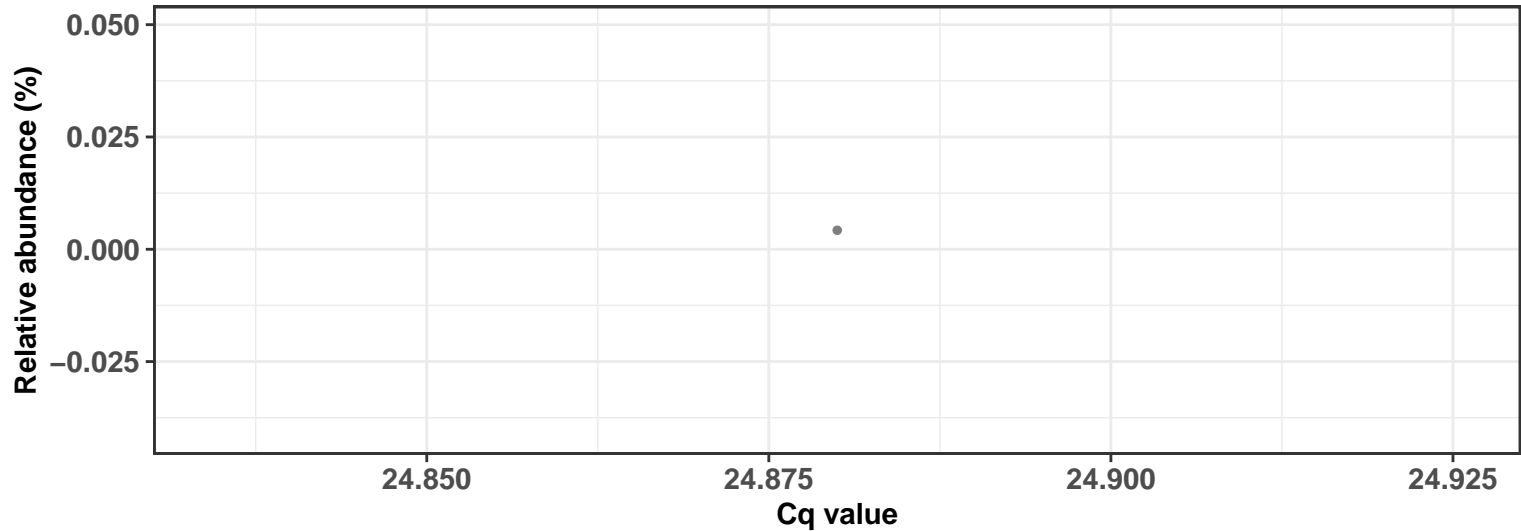$\log_e(S) = 6.494$, $p = 0.918$, $\hat{\rho}_{Spearman} = 0.028$, $CI_{95\%}$ [−0.439, 0.524], $n_{pairs} = 16$

k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Brevundimonas; NA
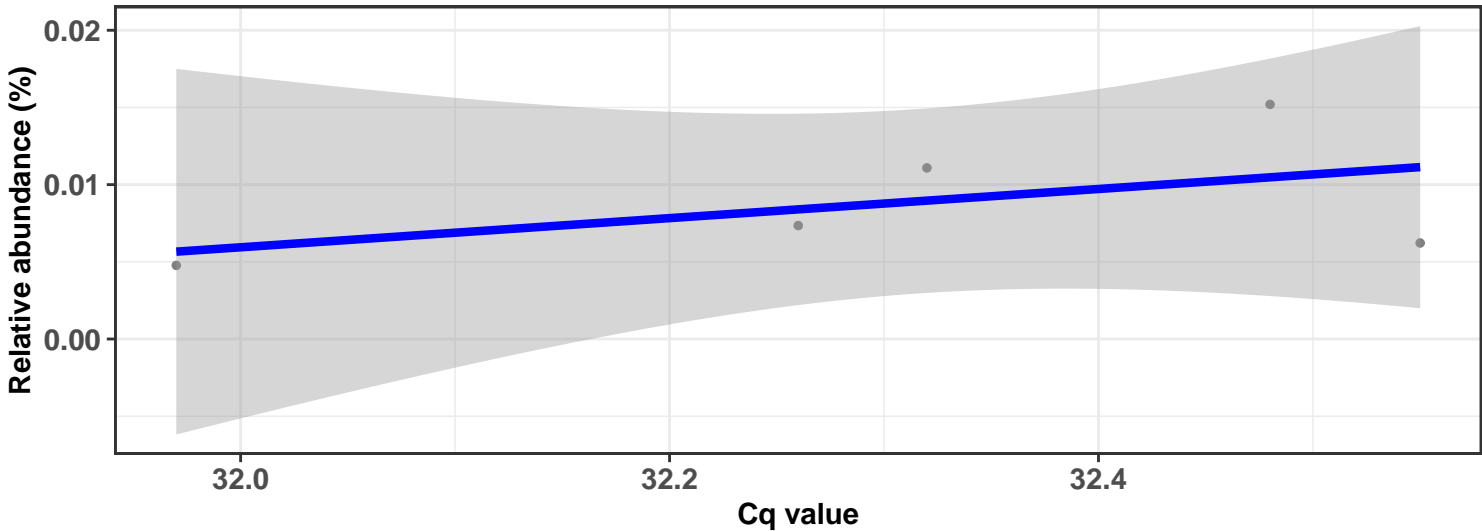
Correlation with all samples

$\log_e(S) = 4.127$, $p = 0.531$, $\hat{\rho}_{Spearman} = 0.262$, $CI_{95\%}$ [−0.627, 1.249], $n_{pairs} = 8$

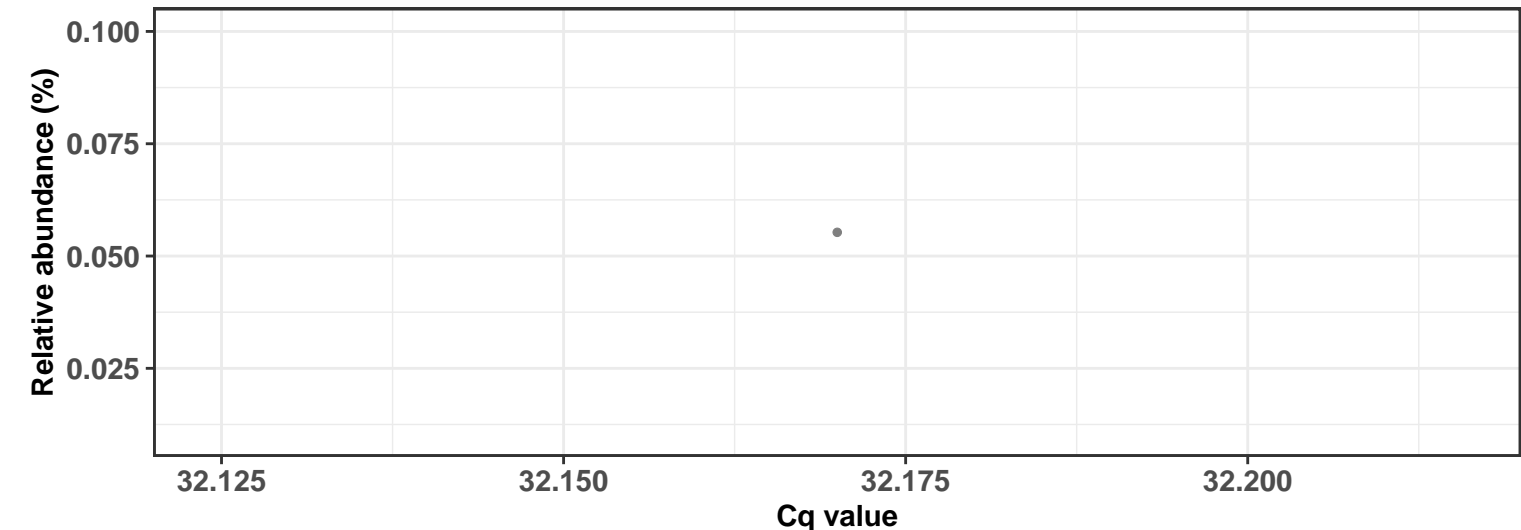SampleType ● REF−DIC ● REF−DIM ● IM−DIM ● Extraction−blank
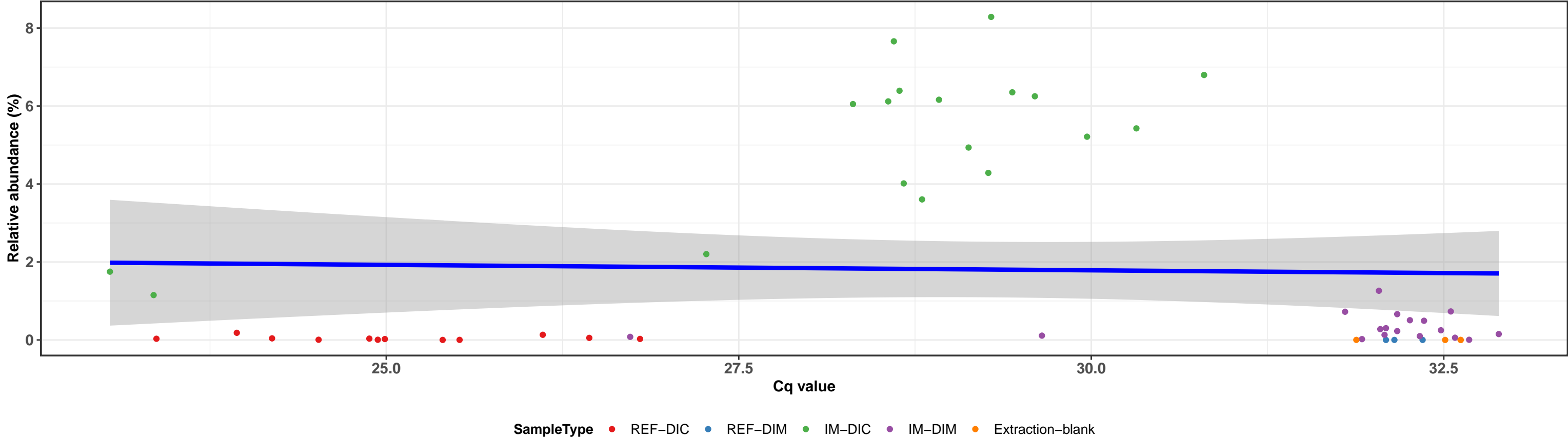
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

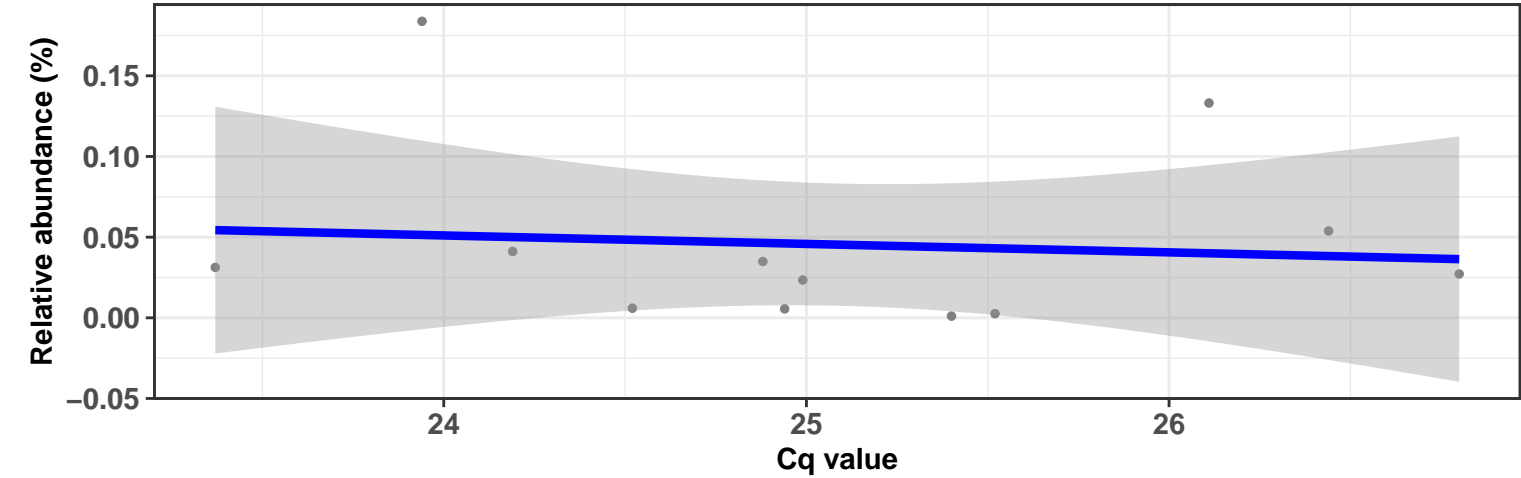**Correlation with all samples**

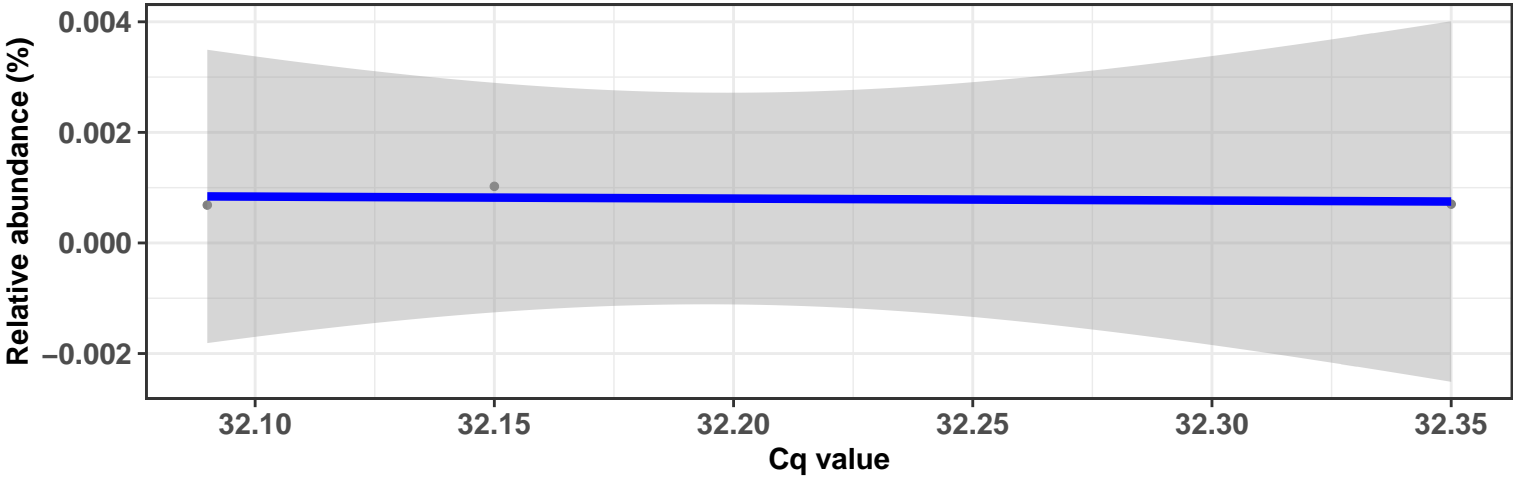$\log_e(S) = 10.372$, $p = 0.267$, $\hat{\rho}_{Spearman} = -0.152$, $CI_{95\%}$ [−0.420, 0.115], $n_{pairs} = 55$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

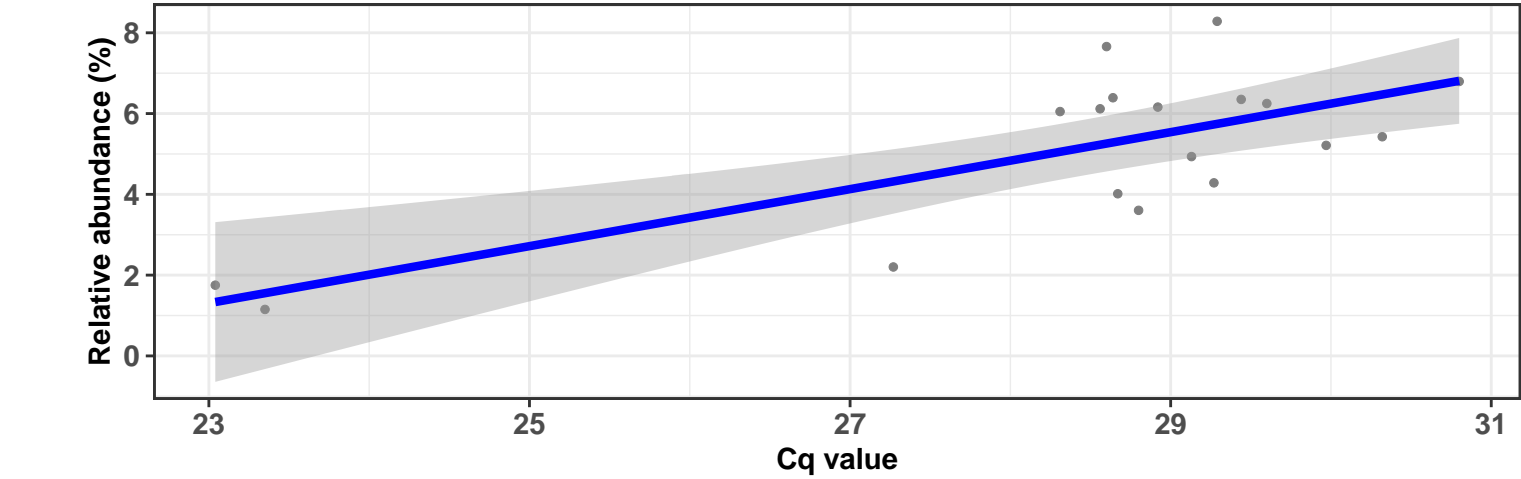$\log_e(S) = 5.799$, $p = 0.633$, $\hat{\rho}_{Spearman} = -0.154$, $CI_{95\%}$ [−0.805, 0.472], $n_{pairs} = 12$
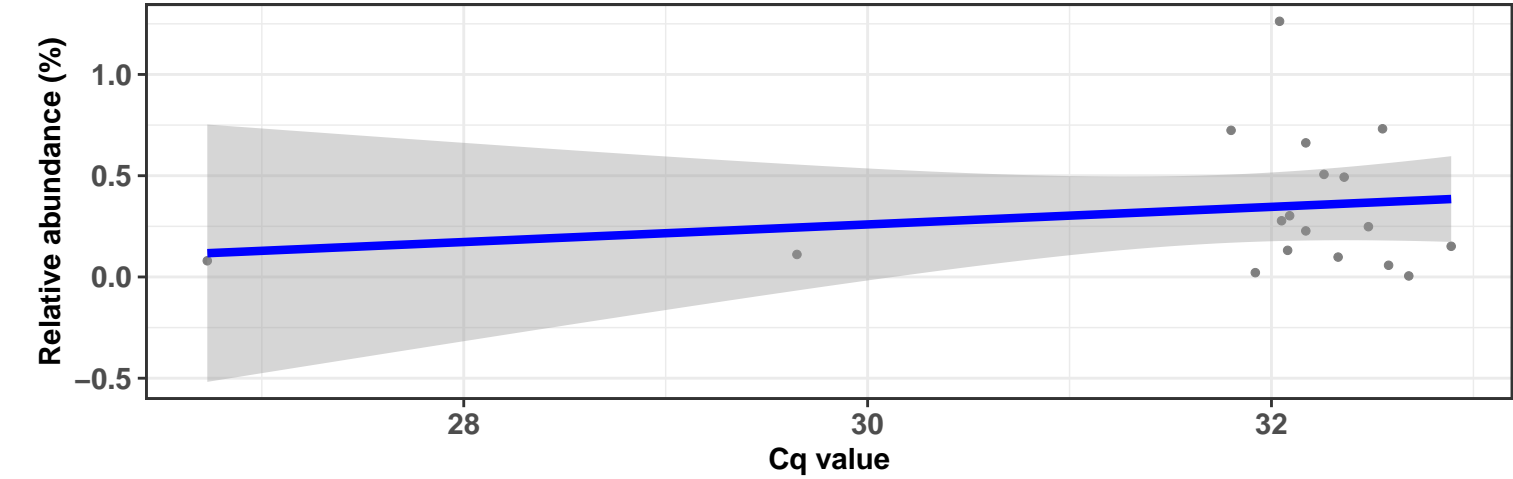
Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 6.234$, $p = 0.047$, $\hat{\rho}_{Spearman} = 0.474$, $CI_{95\%}$ [0.065, 0.883], $n_{pairs} = 18$

Correlation within: IM−DIM
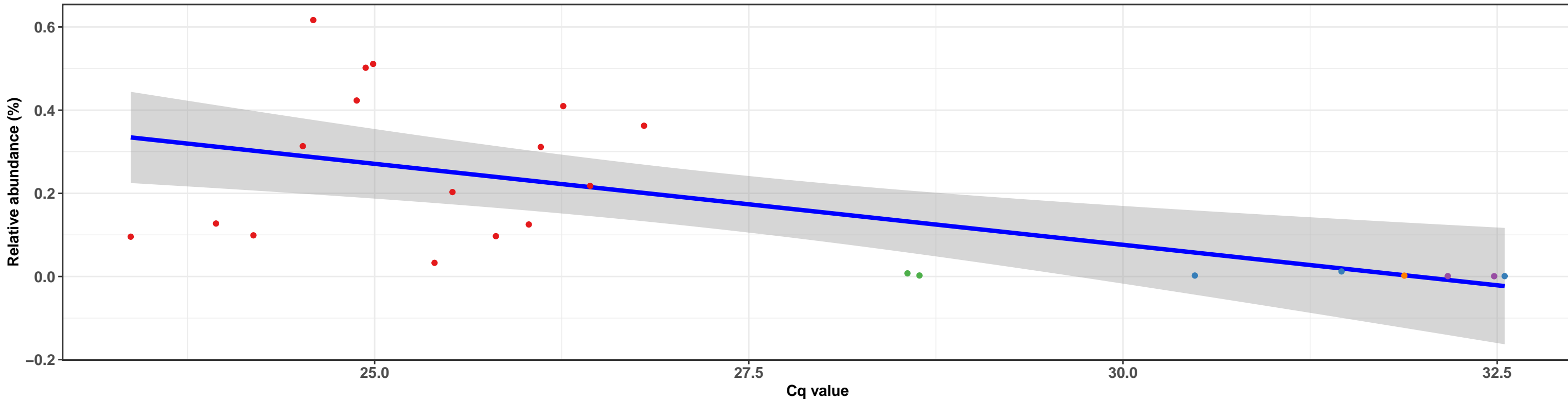
$\log_e(S) = 6.949$, $p = 0.766$, $\hat{\rho}_{Spearman} = -0.075$, $CI_{95\%}$ [−0.624, 0.403], $n_{pairs} = 18$

k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Family XI; g__Tepidimicrobium; s__Tepidimicrobium sp. GRC1
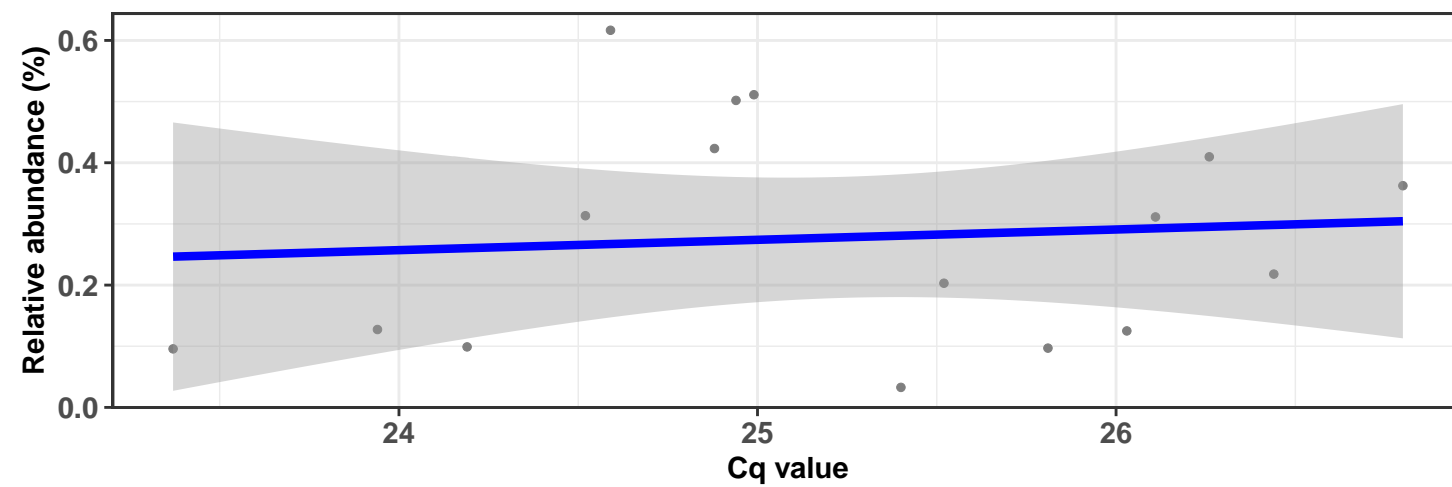
k__Bacteria; p__Tenericutes; c__Mollicutes; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma; s__uncultured bacterium

Correlation with all samples

$\log_e(S) = 10.967$, $p = \text{ } < 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.609$, $\text{CI}_{95\%}$ [−0.780, −0.451], $n_{\text{pairs}} = 60$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock
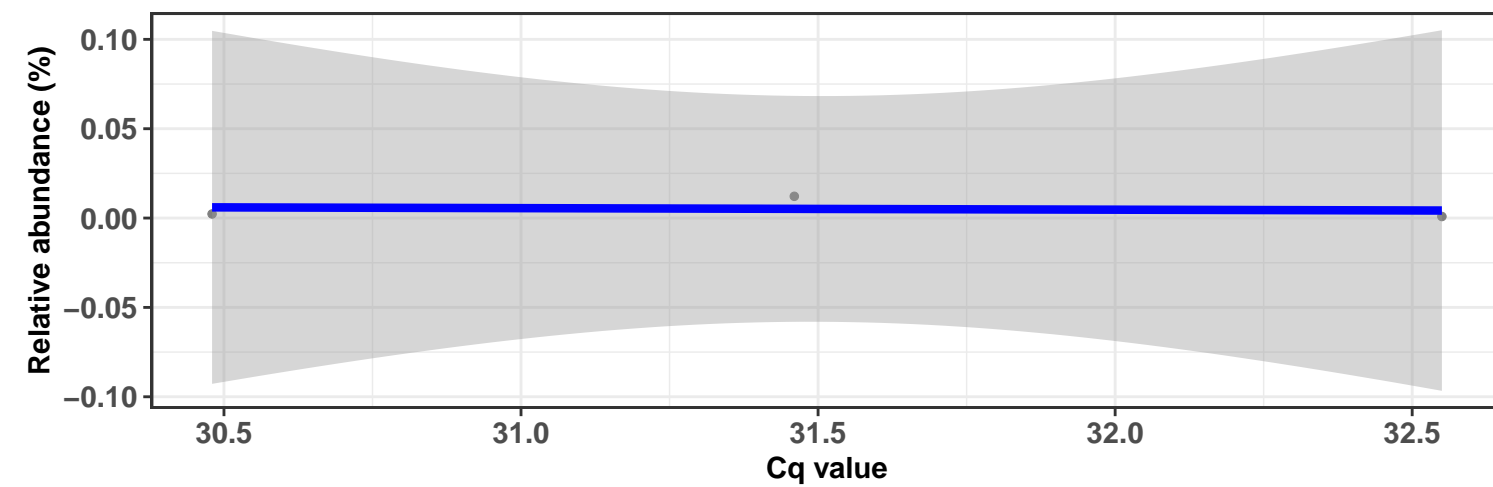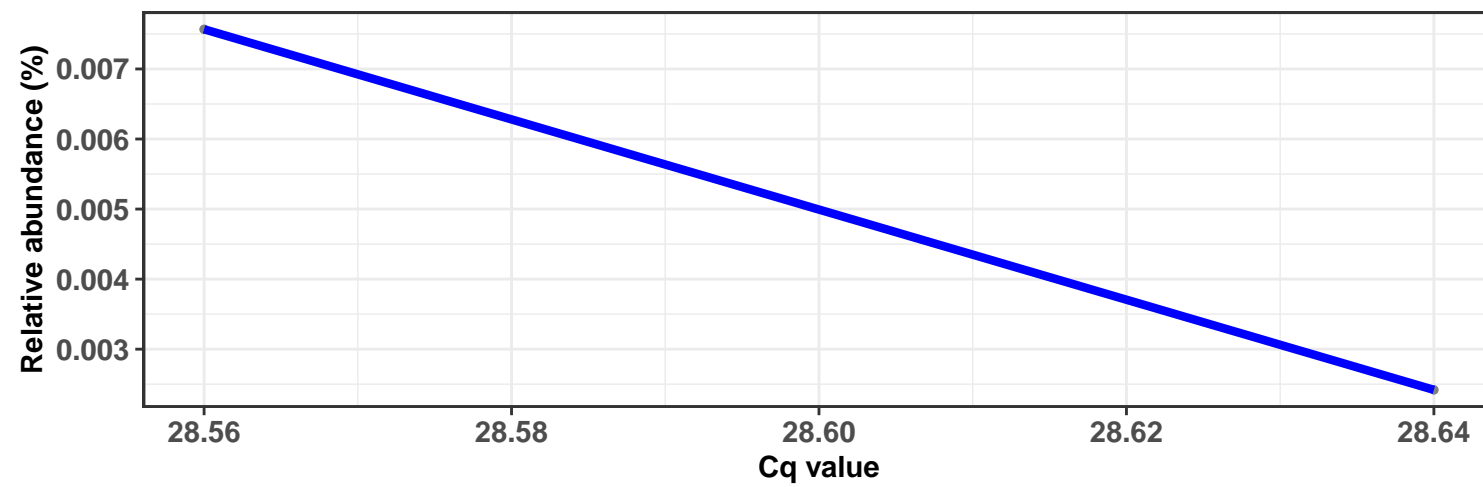
Correlation within: REF−DIC

$\log_e(S) = 6.449$, $p = 0.384$, $\hat{\rho}_{\text{Spearman}} = 0.225$, $\text{CI}_{95\%}$ [−0.249, 0.758], $n_{\text{pairs}} = 17$
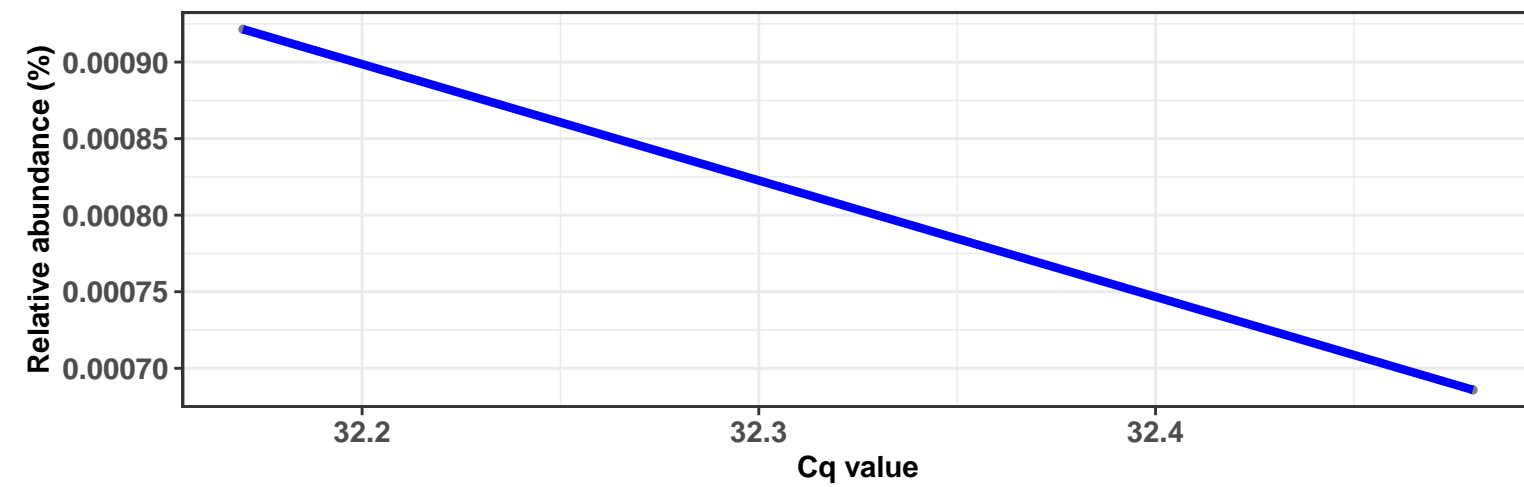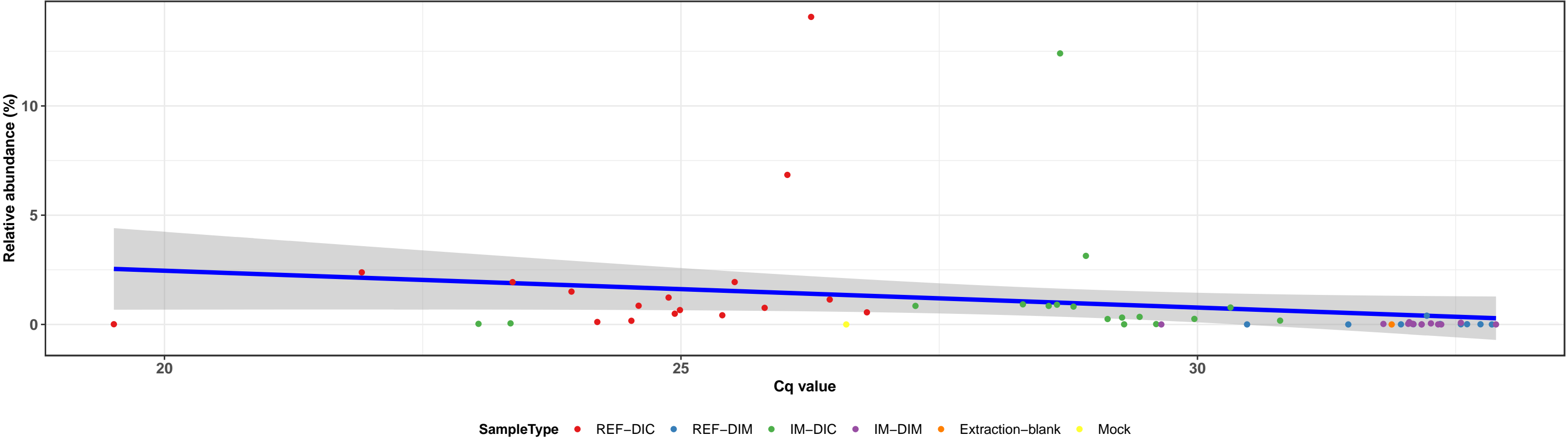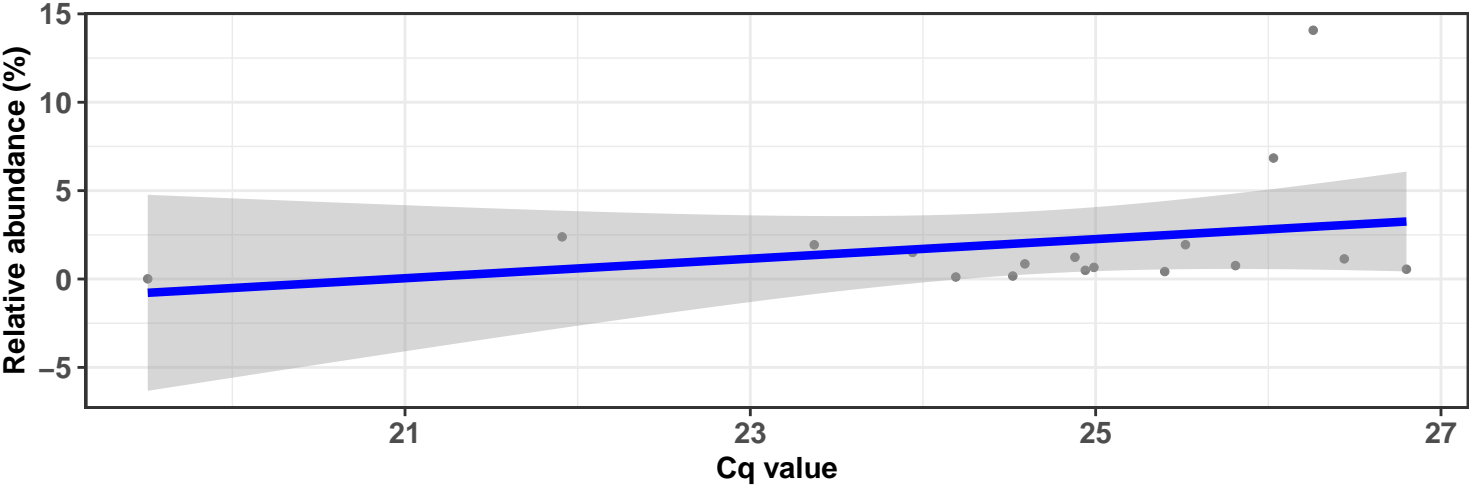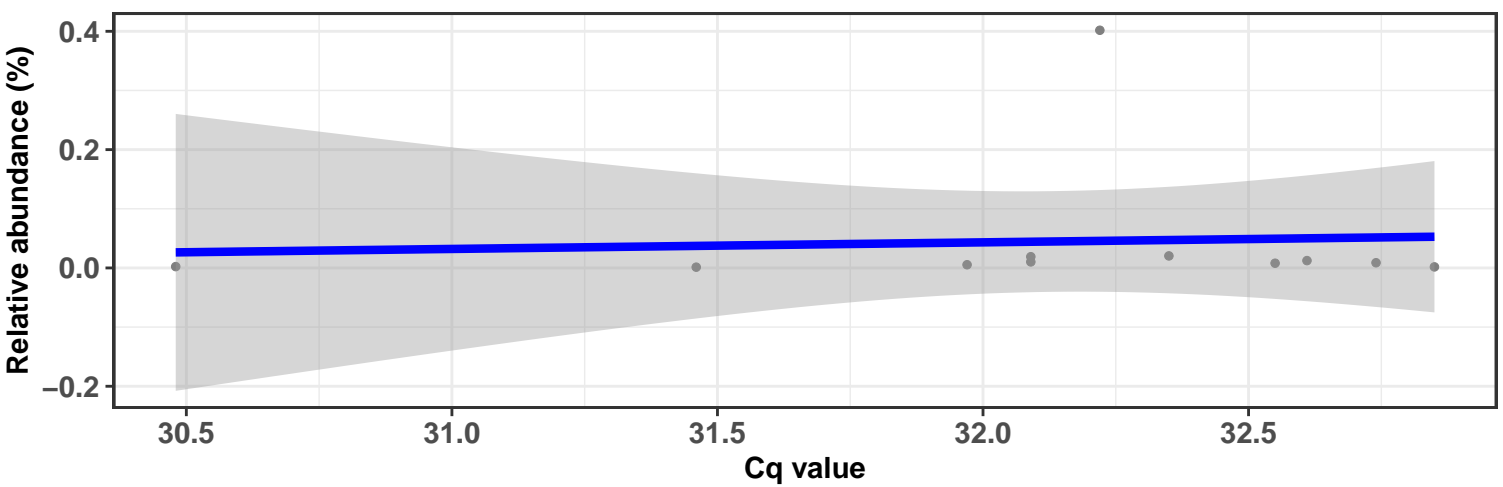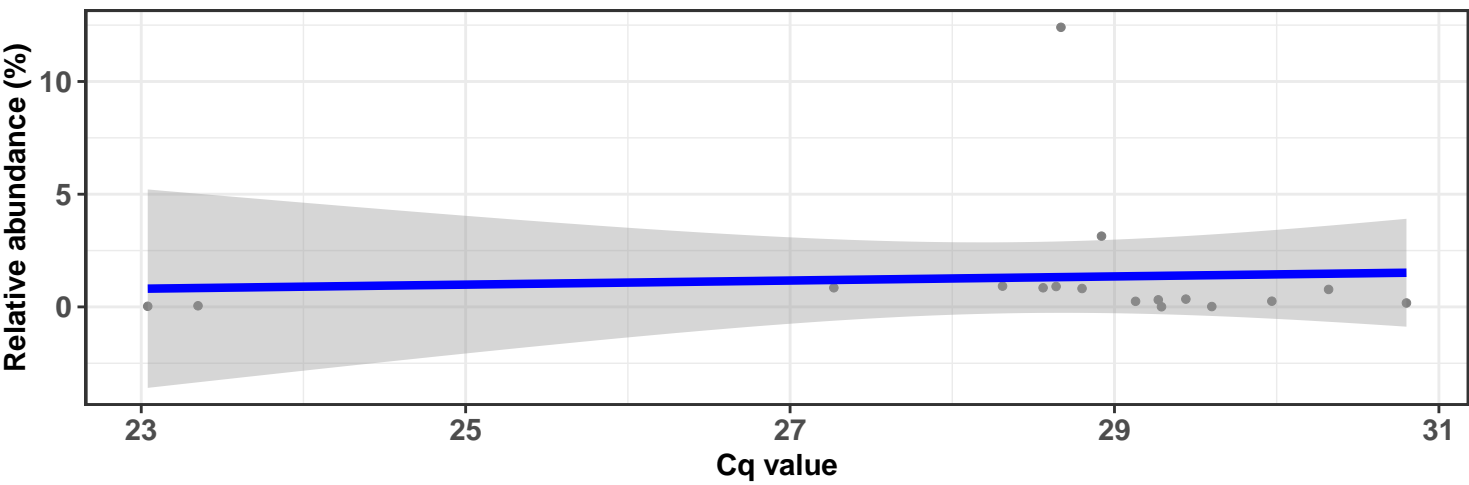
Correlation within: REF−DIM

$\log_e(S) = 5.158$, $p = 0.536$, $\hat{\rho}_{\text{Spearman}} = 0.210$, $\text{CI}_{95\%}$ [−0.462, 0.914], $n_{\text{pairs}} = 11$
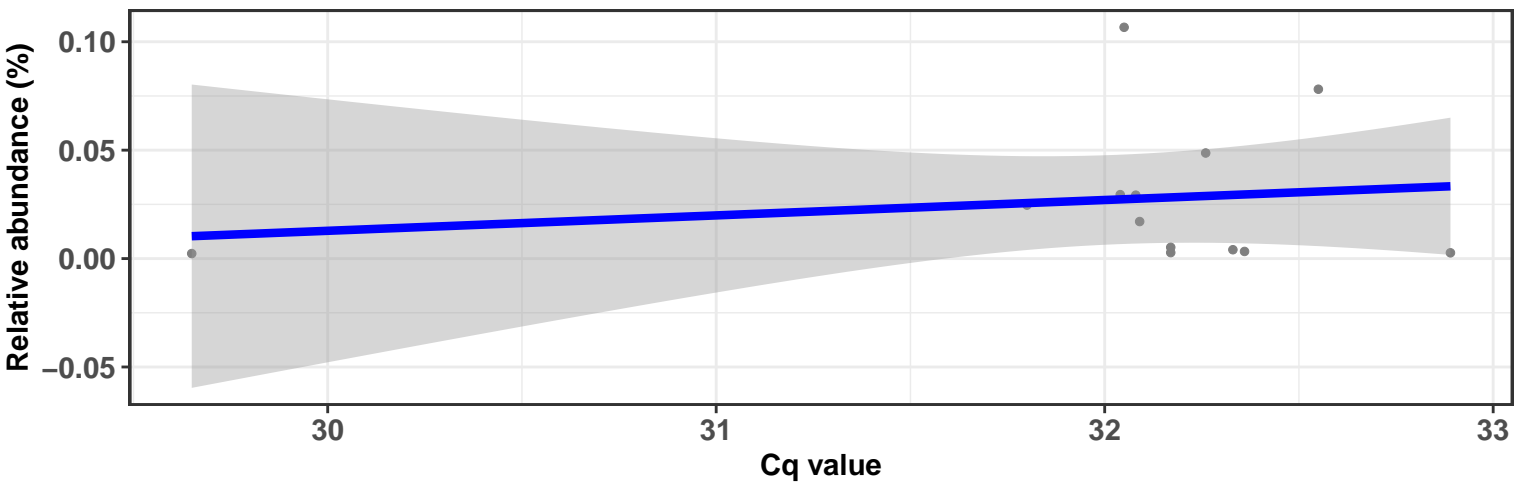
Correlation within: IM−DIC

$\log_e(S) = 6.957$, $p = 0.264$, $\hat{\rho}_{\text{Spearman}} = -0.287$, $\text{CI}_{95\%}$ [−0.790, 0.244], $n_{\text{pairs}} = 17$
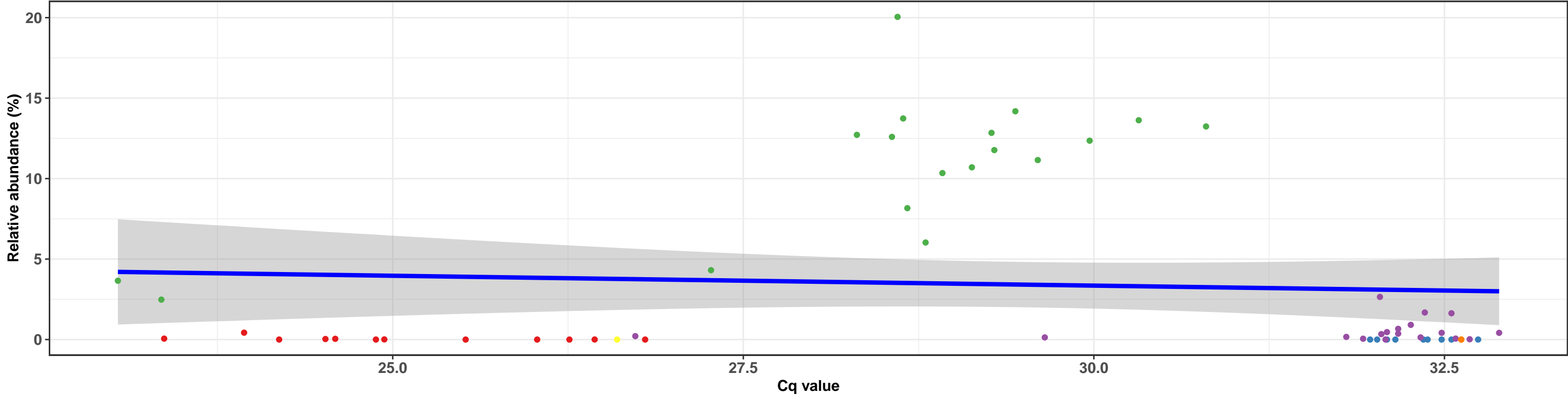
Correlation within: IM−DIM

$\log_e(S) = 6.004$, $p = 0.714$, $\hat{\rho}_{\text{Spearman}} = -0.113$, $\text{CI}_{95\%}$ [−0.817, 0.702], $n_{\text{pairs}} = 13$

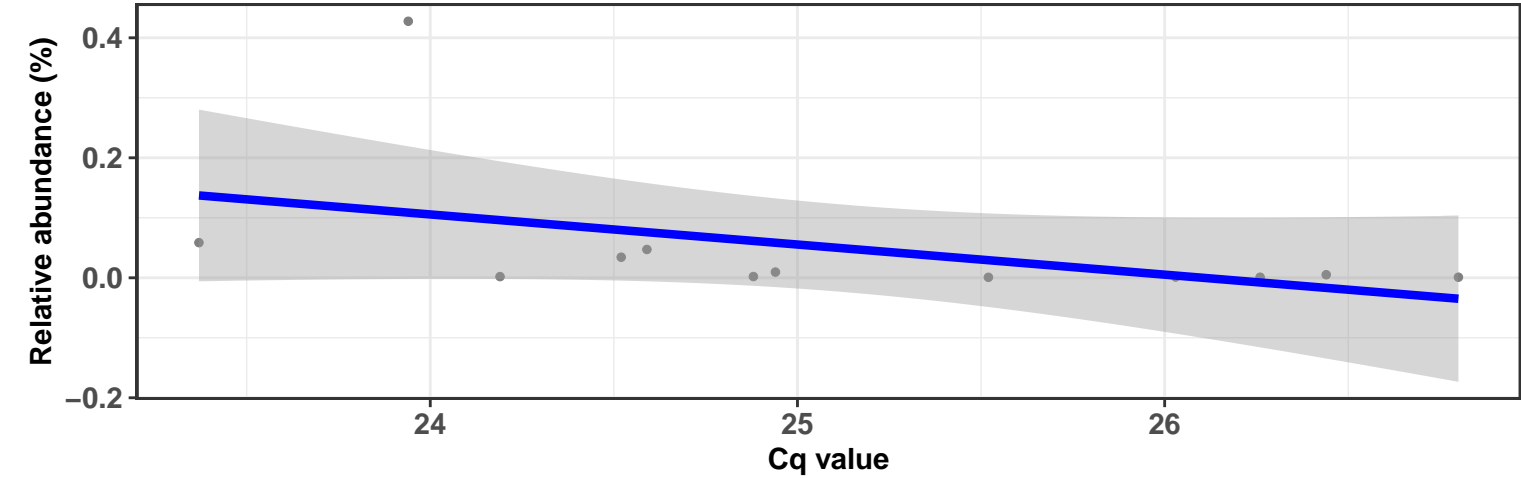# k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; NA; NA; NA

Correlation with all samples

$\log_e(S) = 10.613$, $p = 0.324$, $\hat{\rho}_{Spearman} = -0.130$, CI$_{95\%}$ [-0.400, 0.128], $n_{pairs} = 60$
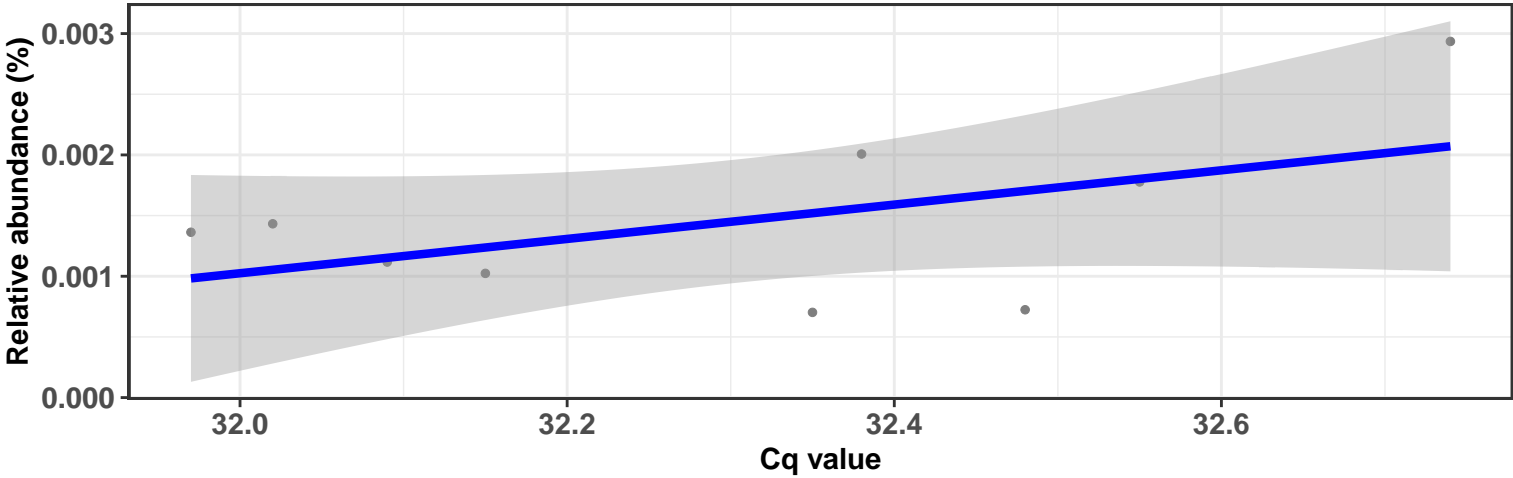

SampleType   ● REF–DIC   ● REF–DIM   ● IM–DIC   ● IM–DIM   ● Extraction–blank   ● Mock

Correlation within: REF–DIC

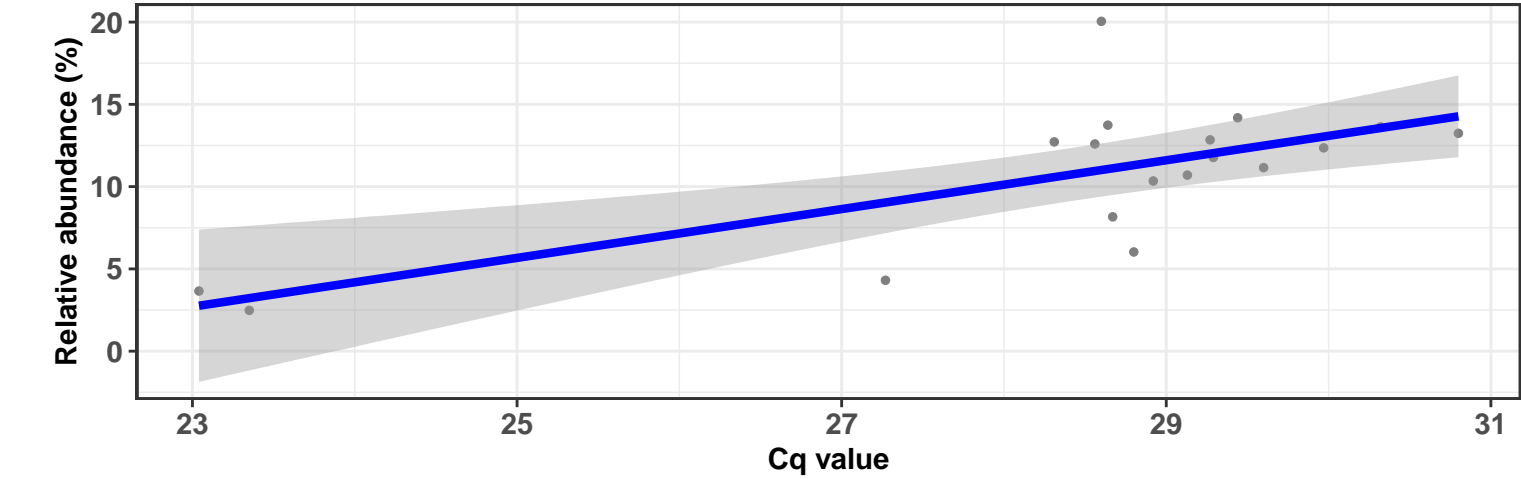$\log_e(S) = 6.194$, $p = 0.009$, $\hat{\rho}_{Spearman} = -0.713$, CI$_{95\%}$ [-1.113, -0.376], $n_{pairs} = 12$

Correlation within: REF–DIM

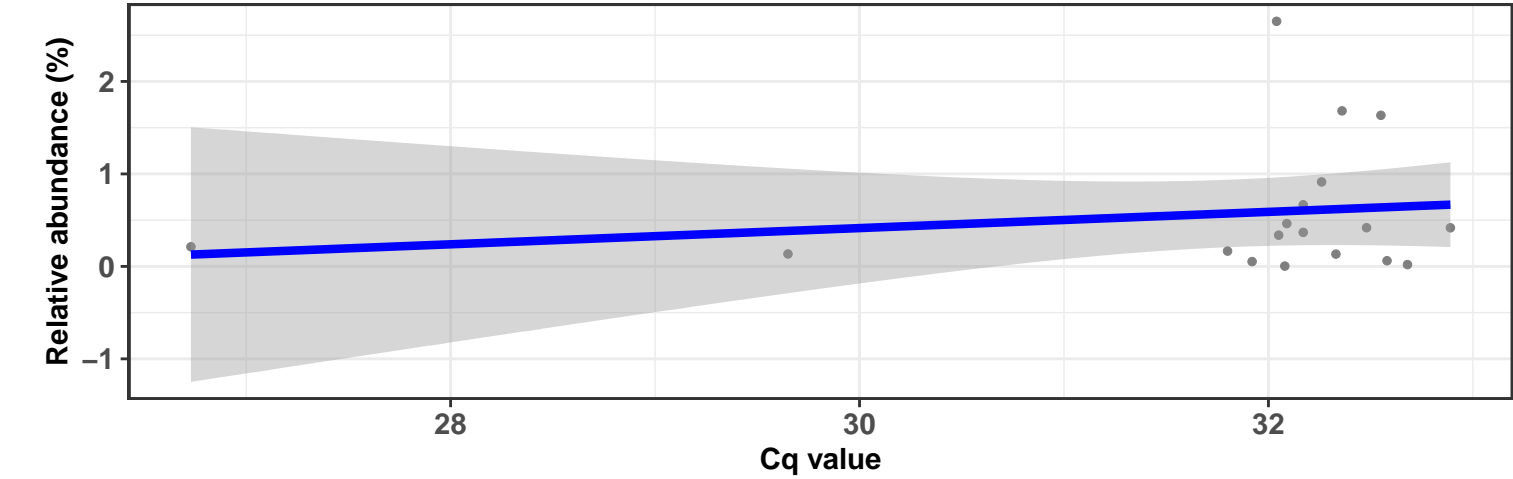$\log_e(S) = 4.382$, $p = 0.381$, $\hat{\rho}_{Spearman} = 0.333$, CI$_{95\%}$ [-0.313, 1.040], $n_{pairs} = 9$

Correlation within: IM–DIC

$\log_e(S) = 6.261$, $p = 0.055$, $\hat{\rho}_{Spearman} = 0.459$, CI$_{95\%}$ [0.005, 0.876], $n_{pairs} = 18$
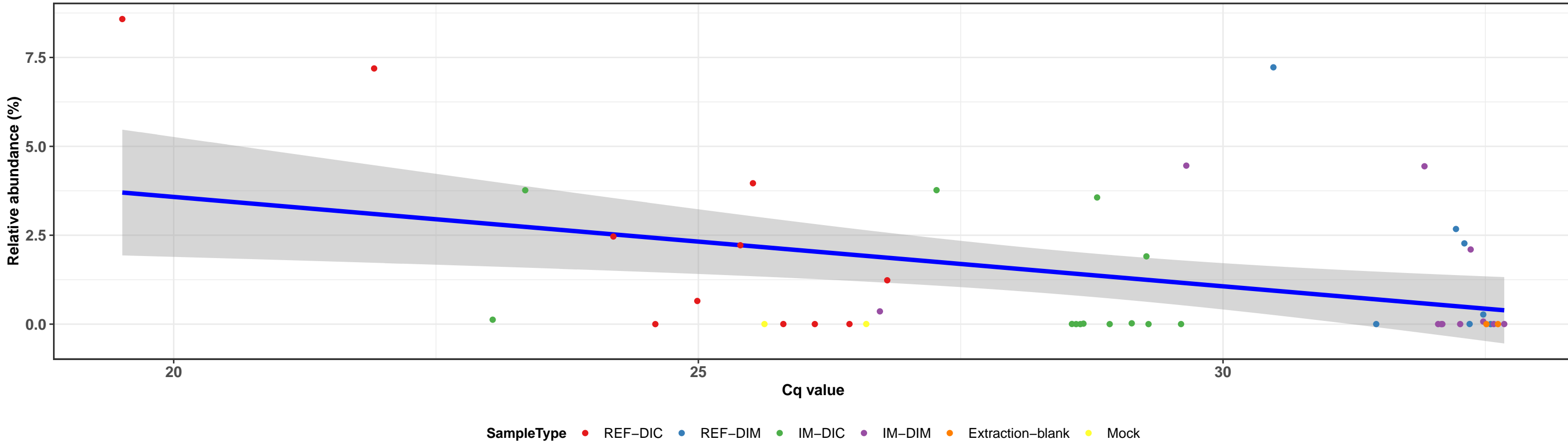

Correlation within: IM–DIM

$\log_e(S) = 6.740$, $p = 0.616$, $\hat{\rho}_{Spearman} = 0.127$, CI$_{95\%}$ [-0.303, 0.520], $n_{pairs} = 18$

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; Ambiguous_taxa
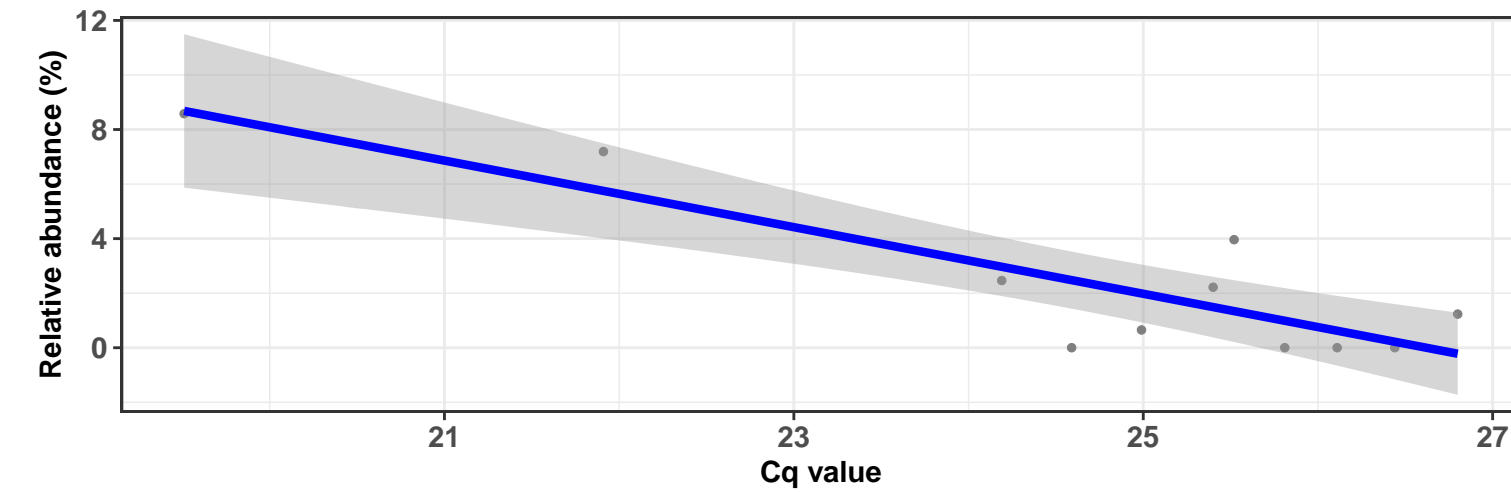
Correlation with all samples

$\log_e(S) = 9.993$, $p = 0.017$, $\hat{\rho}_{Spearman} = -0.349$, $CI_{95\%}$ [−0.592, −0.116], $n_{pairs} = 46$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock

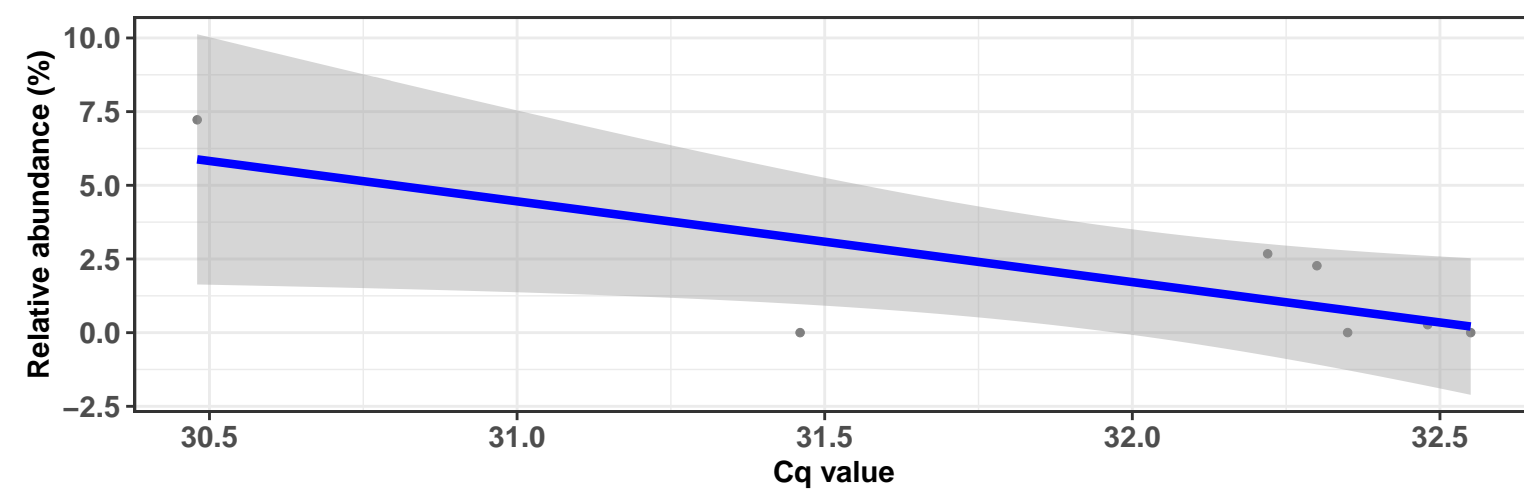**Correlation within: REF−DIC**

$\log_e(S) = 5.835$, $p = 0.077$, $\hat{\rho}_{Spearman} = -0.555$, $CI_{95\%}$ [−1.241, 0.032], $n_{pairs} = 11$

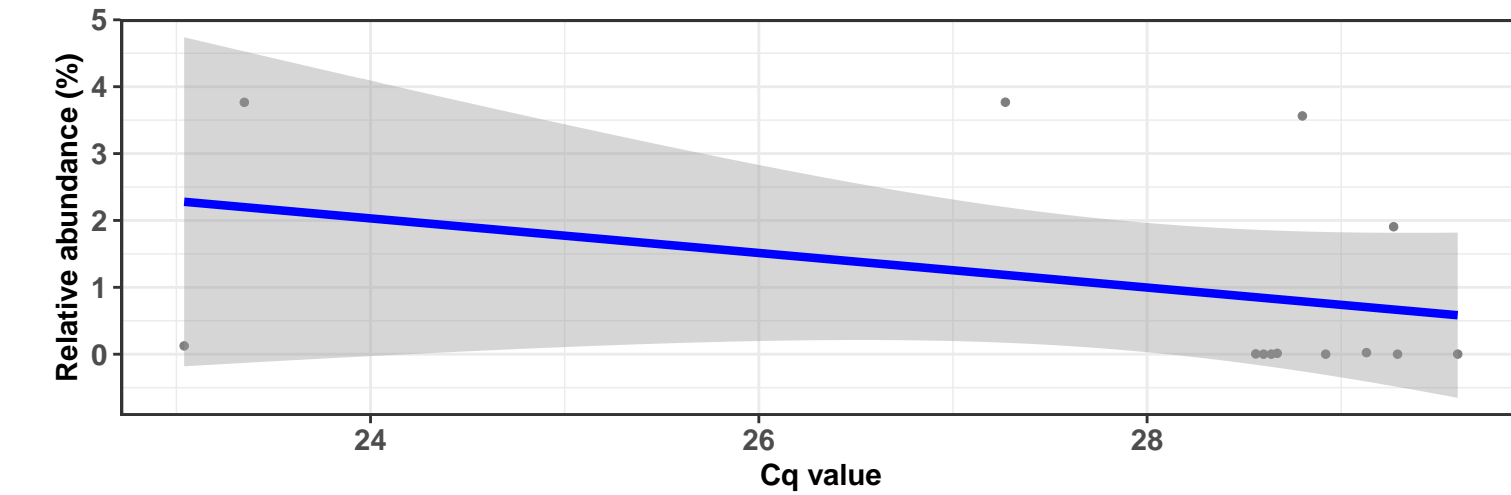**Correlation within: REF−DIM**

$\log_e(S) = 4.500$, $p = 0.148$, $\hat{\rho}_{Spearman} = -0.607$, $CI_{95\%}$ [−1.400, 0.117], $n_{pairs} = 7$

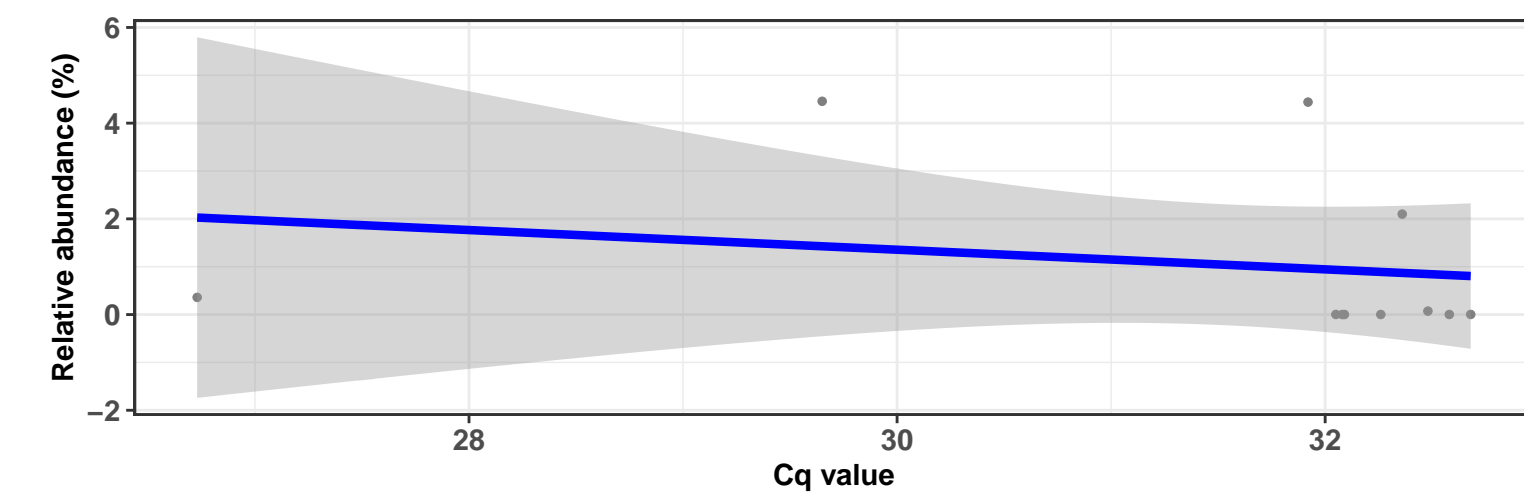**Correlation within: IM−DIC**

$\log_e(S) = 6.223$, $p = 0.194$, $\hat{\rho}_{Spearman} = -0.385$, $CI_{95\%}$ [−0.886, 0.060], $n_{pairs} = 13$

Correlation within: IM−DIM

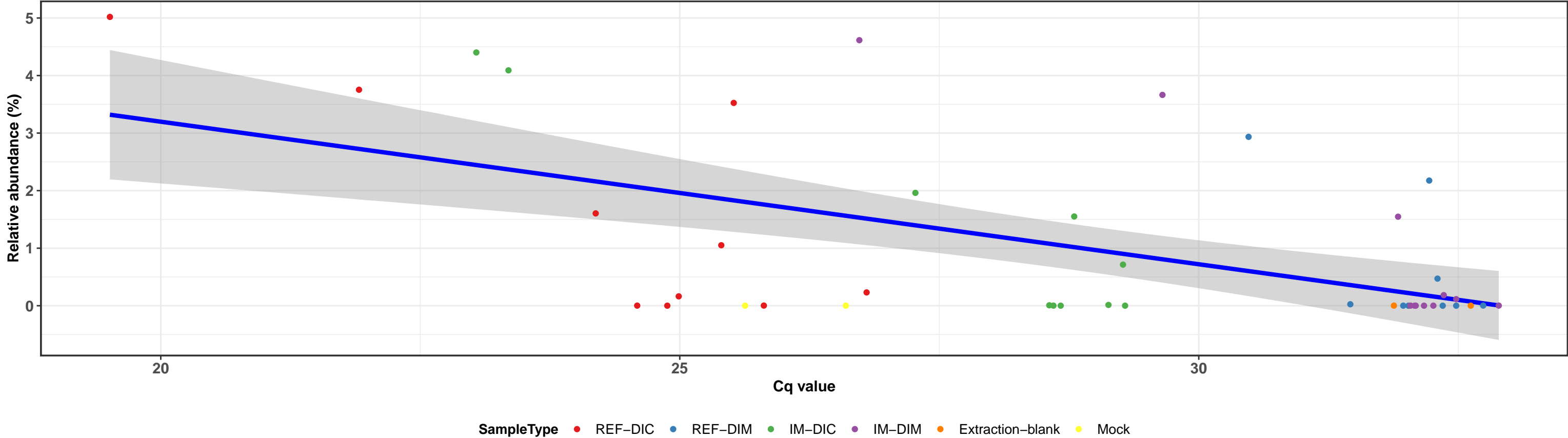$\log_e(S) = 5.642$, $p = 0.401$, $\hat{\rho}_{Spearman} = -0.282$, $CI_{95\%}$ [−0.818, 0.241], $n_{pairs} = 11$

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium
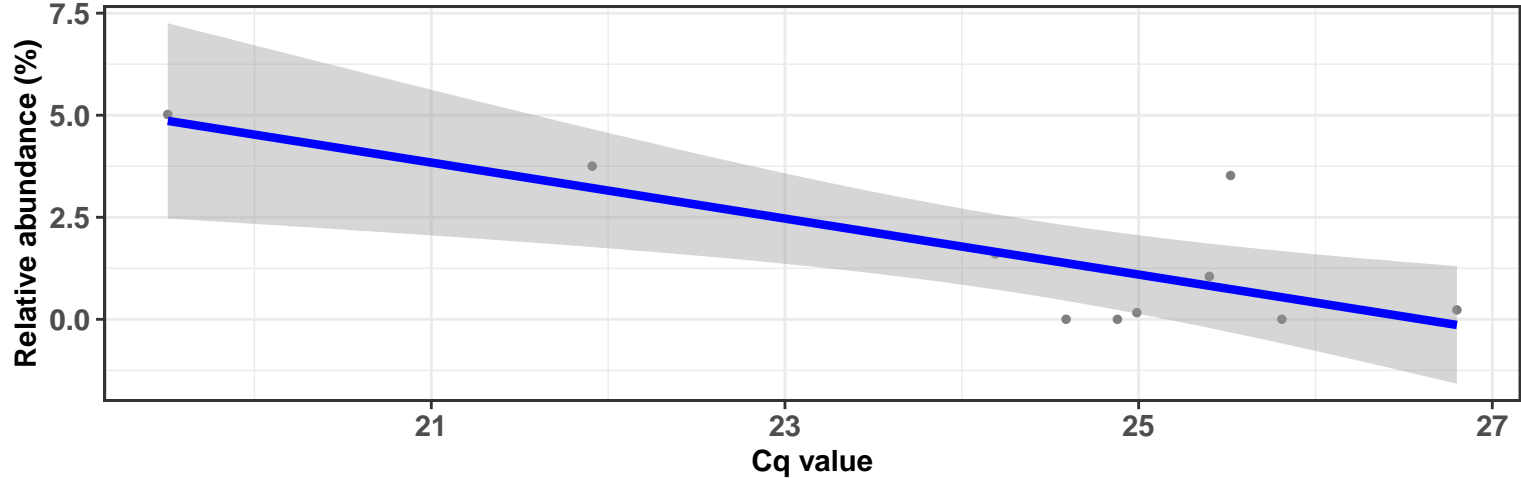
Correlation with all samples

$\log_e(S) = 9.945$, $p = 0.001$, $\hat{\rho}_{Spearman} = -0.469$, $CI_{95\%}$ [-0.762, -0.183], $n_{pairs} = 44$

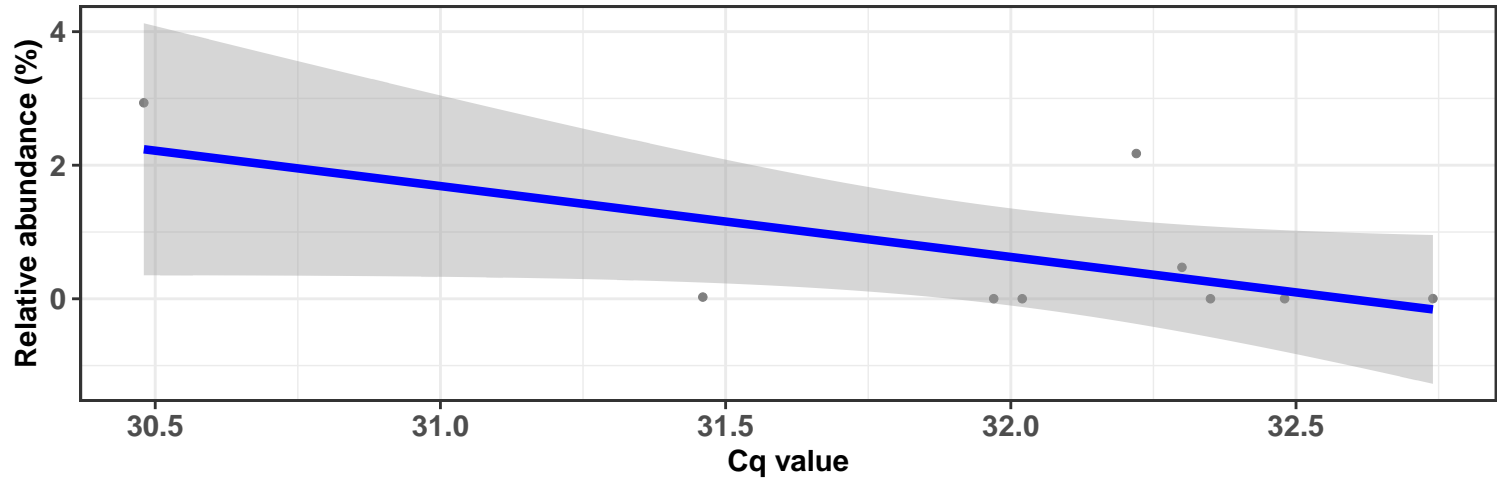SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● IM−DIM   ● Extraction−blank   ● Mock

Correlation within: REF−DIC

$\log_e(S) = 5.447$, $p = 0.244$, $\hat{\rho}_{Spearman} = -0.406$, $CI_{95\%}$ [-1.146, 0.194], $n_{pairs} = 10$

Correlation within: REF−DIM

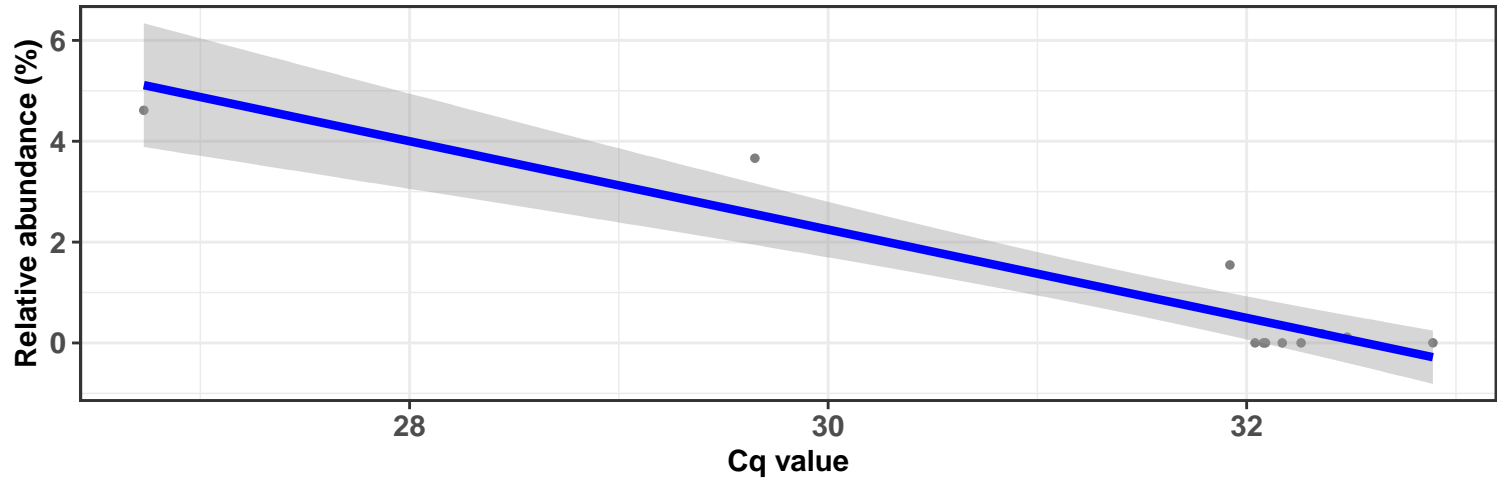$\log_e(S) = 5.147$, $p = 0.244$, $\hat{\rho}_{Spearman} = -0.433$, $CI_{95\%}$ [-1.056, 0.126], $n_{pairs} = 9$

Correlation within: IM−DIC

$\log_e(S) = 5.583$, $p = 0.060$, $\hat{\rho}_{Spearman} = -0.612$, $CI_{95\%}$ [-1.121, -0.106], $n_{pairs} = 10$
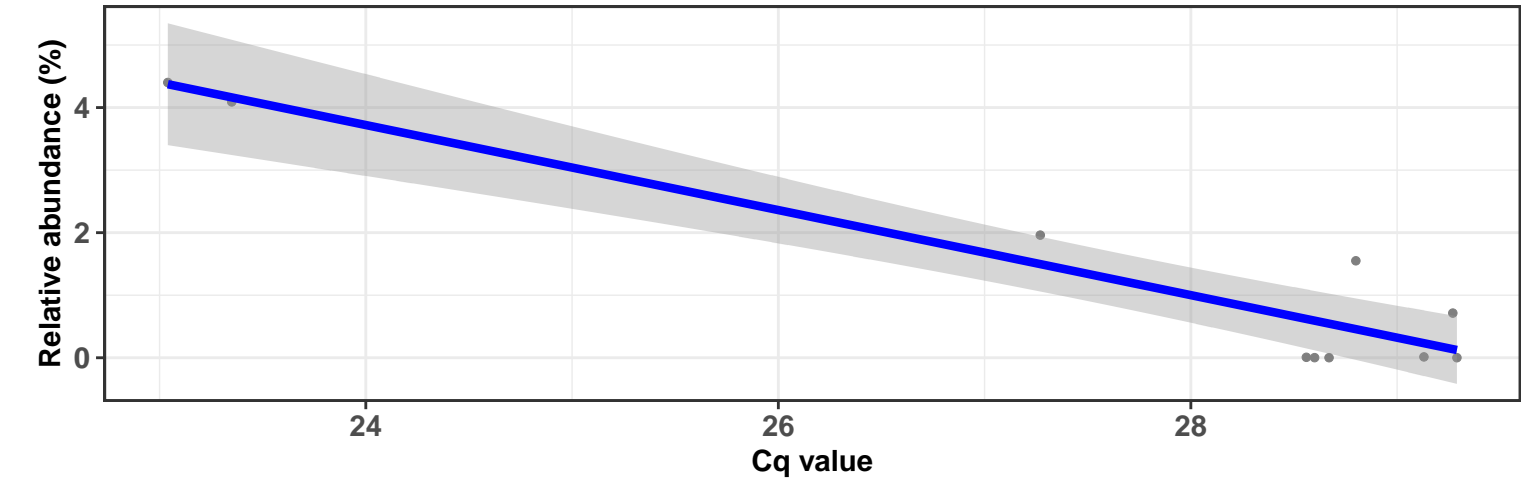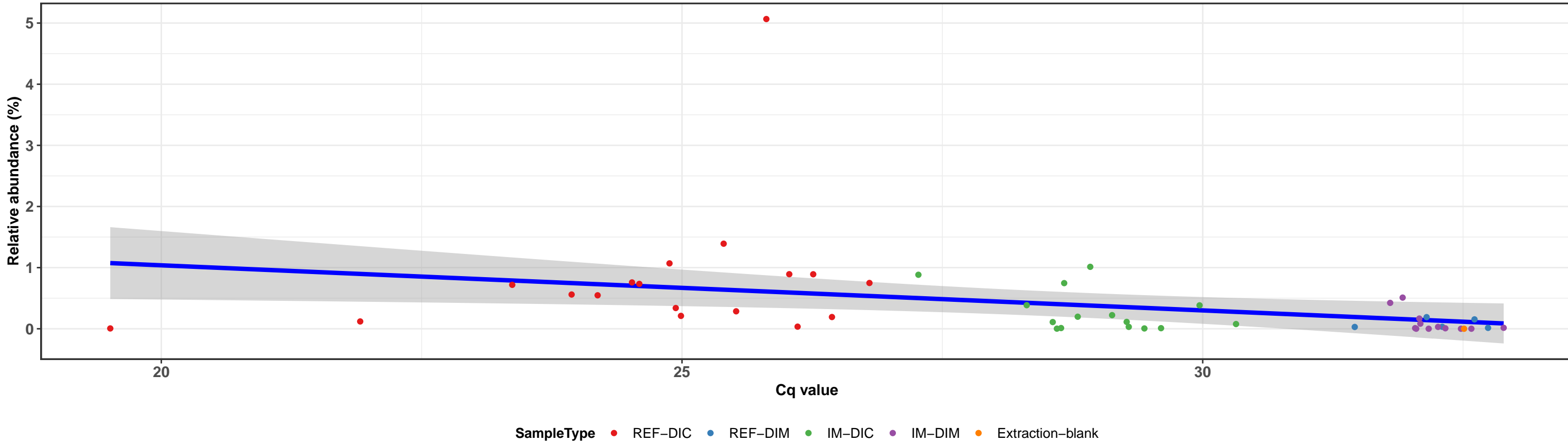

Correlation within: IM−DIM

$\log_e(S) = 5.710$, $p = 0.259$, $\hat{\rho}_{Spearman} = -0.373$, $CI_{95\%}$ [-1.066, 0.304], $n_{pairs} = 11$

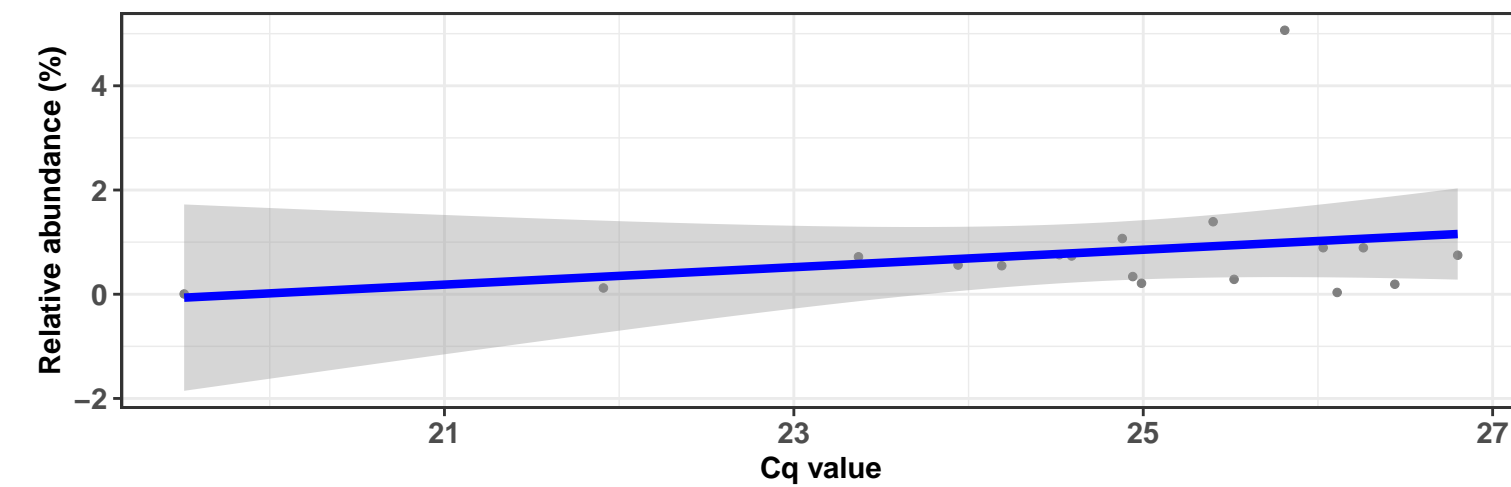# k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Photobacterium; NA

Correlation with all samples

$\log_e(S) = 10.474$, $p = < 0.001$, $\hat{\rho}_{Spearman} = -0.600$, $CI_{95\%}$ [−0.779, −0.420], $n_{pairs} = 51$

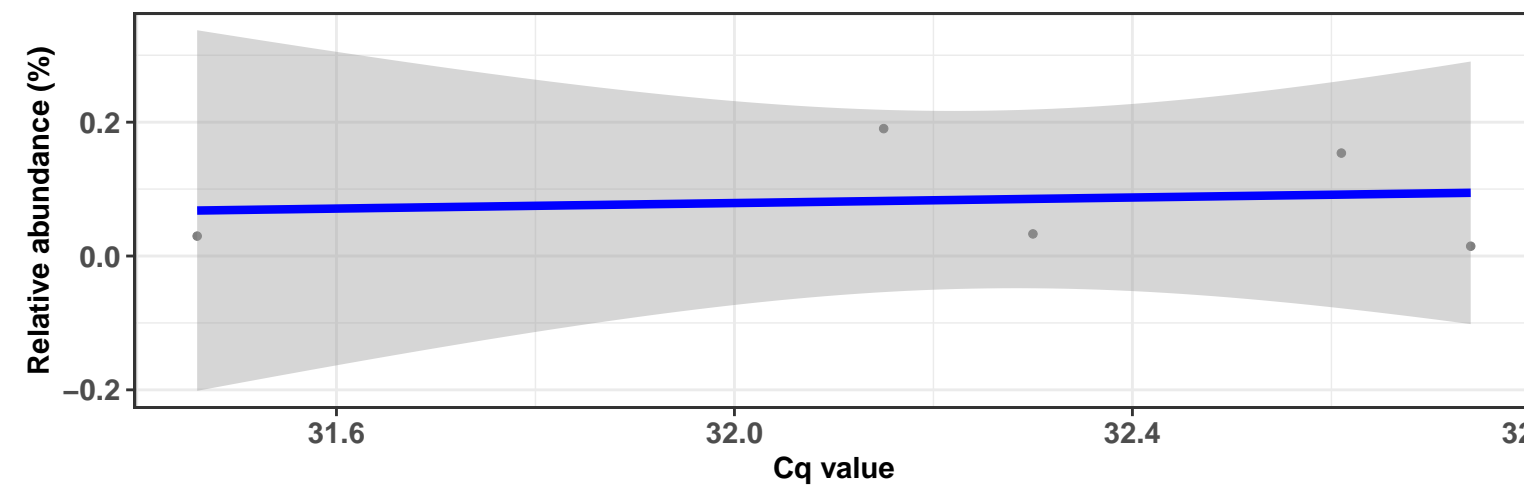SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 6.576$, $p = 0.299$, $\hat{\rho}_{Spearman} = 0.259$, $CI_{95\%}$ [−0.228, 0.728], $n_{pairs} = 18$

Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 6.590$, $p = 0.277$, $\hat{\rho}_{Spearman} = -0.300$, $CI_{95\%}$ [−0.824, 0.199], $n_{pairs} = 15$
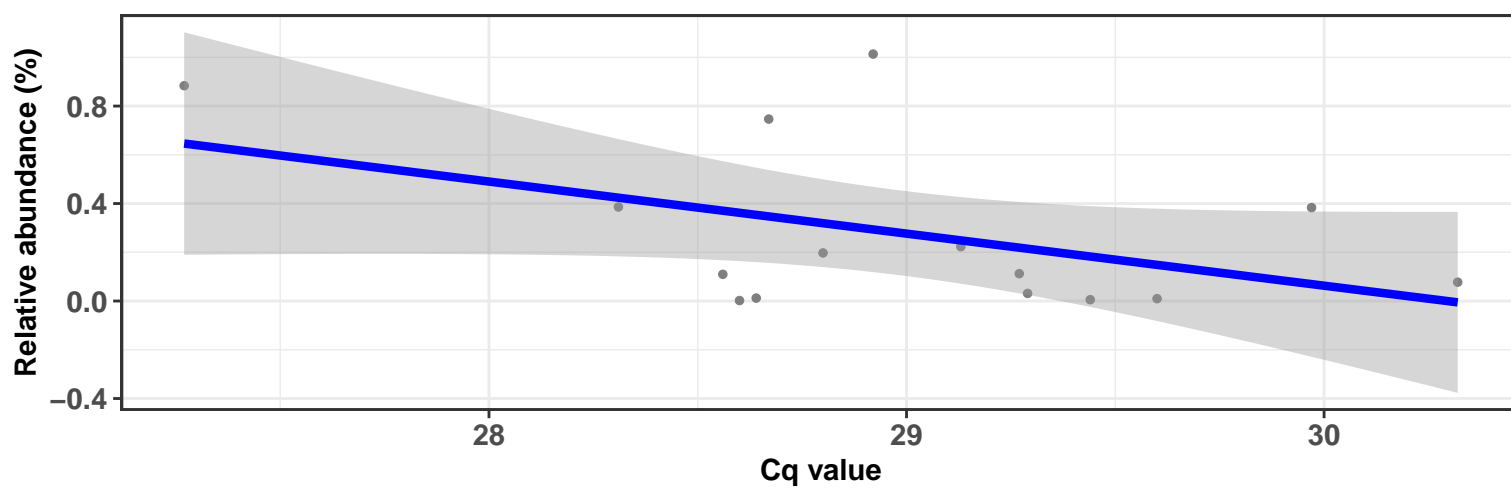
Correlation within: IM−DIM

$\log_e(S) = 6.087$, $p = 0.071$, $\hat{\rho}_{Spearman} = -0.538$, $CI_{95\%}$ [−1.030, −0.161], $n_{pairs} = 12$
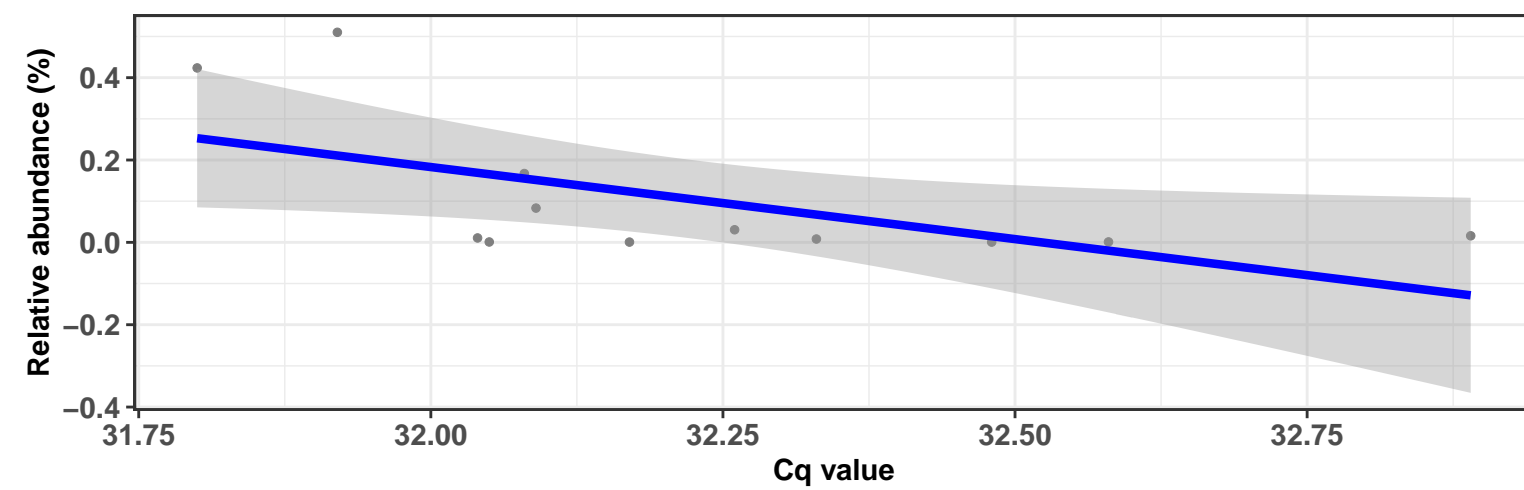
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA
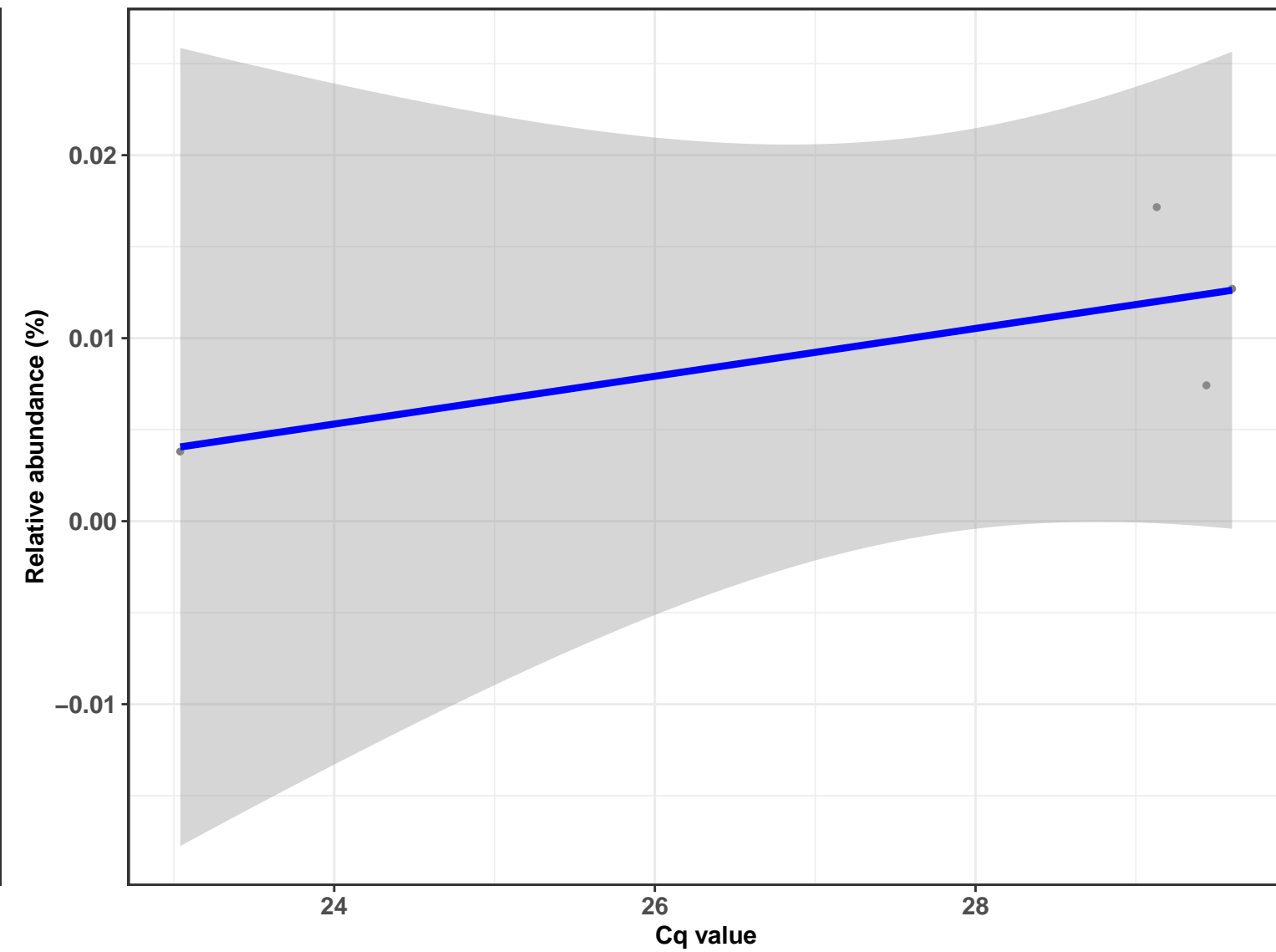

Correlation with all samples

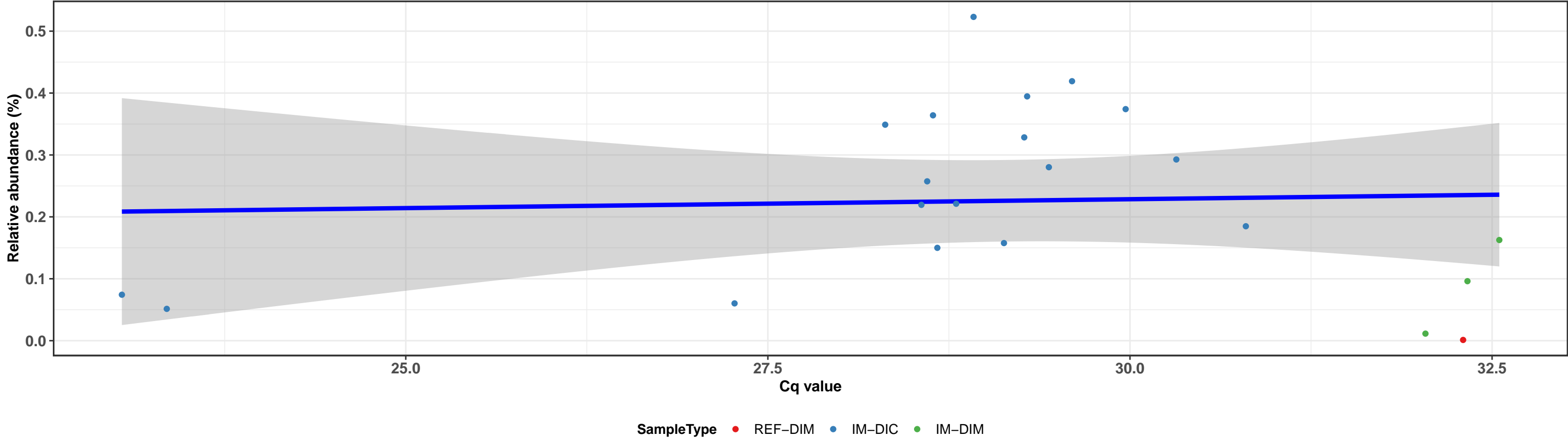$\log_e(S) = 4.522$, $p = 0.823$, $\hat{\rho}_{\text{Spearman}} = -0.095$, $CI_{95\%}$ [−1.033, 0.821], $n_{\text{pairs}} = 8$
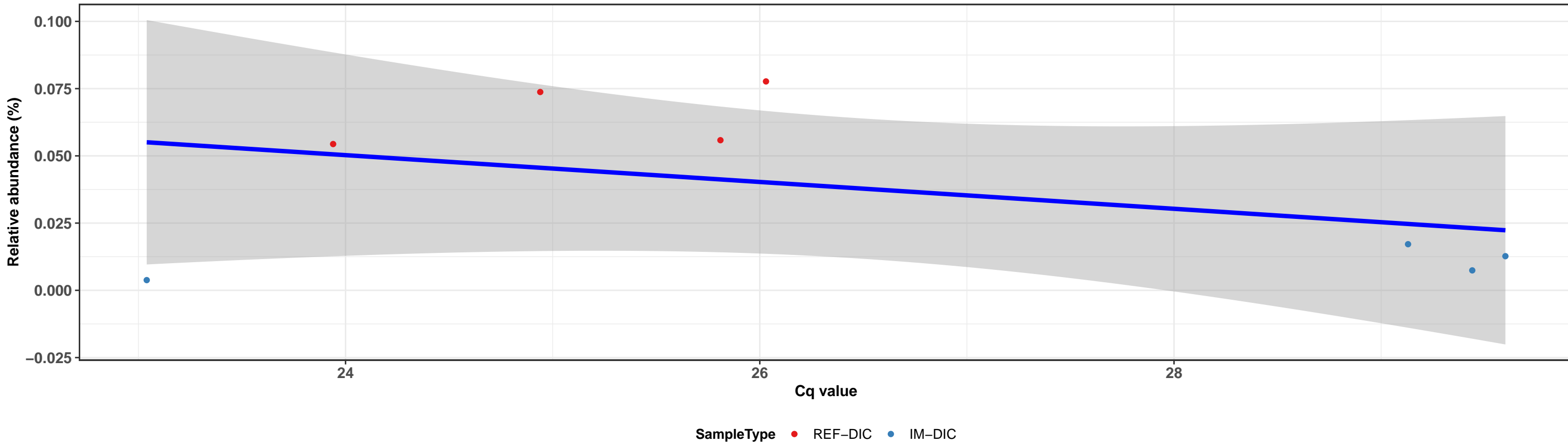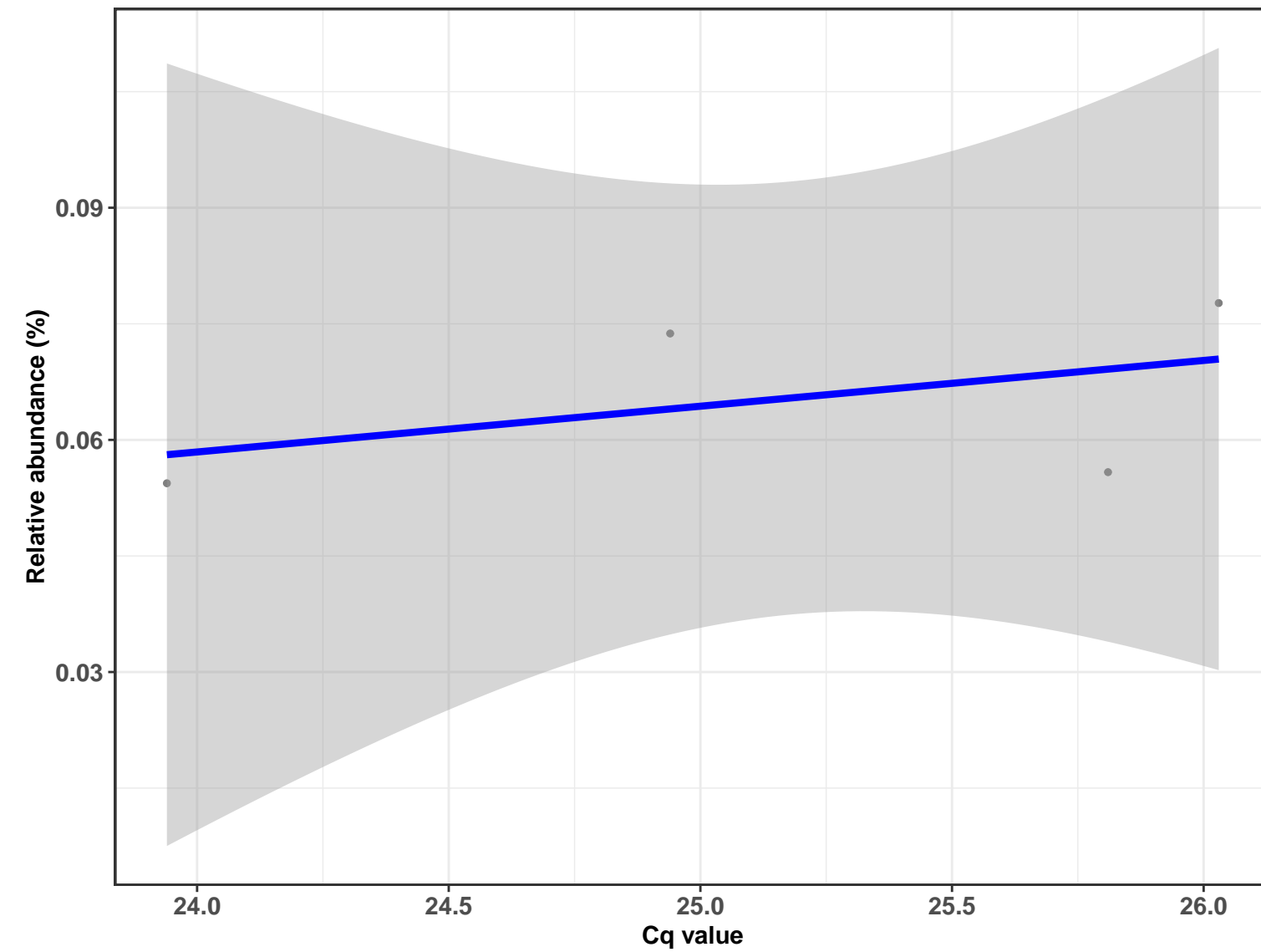
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; s__Brevibacterium album
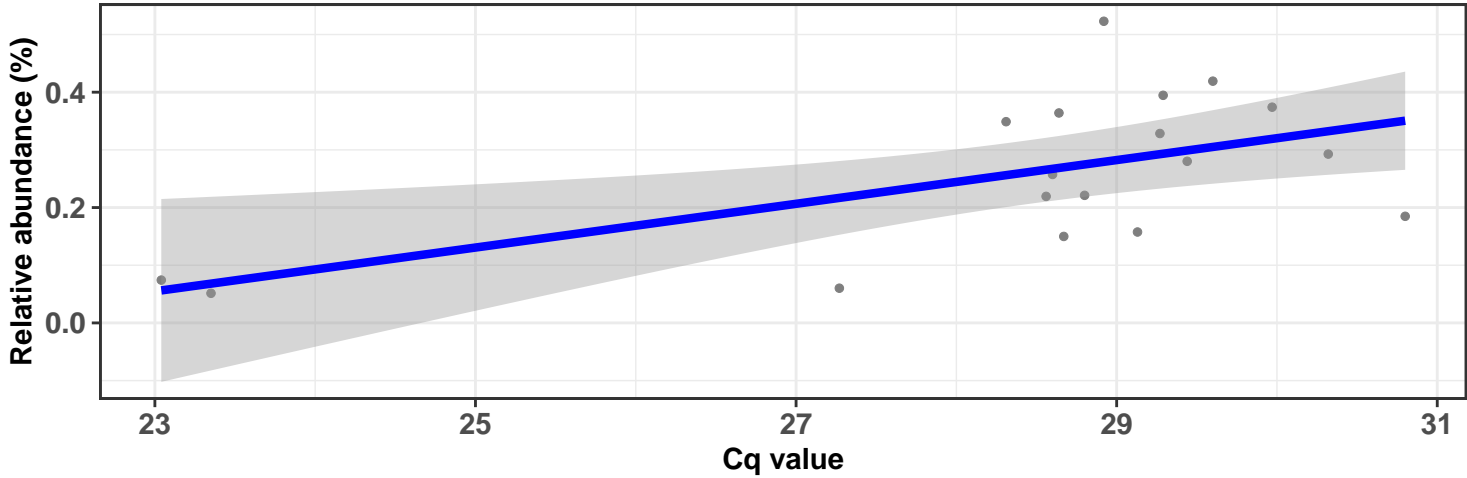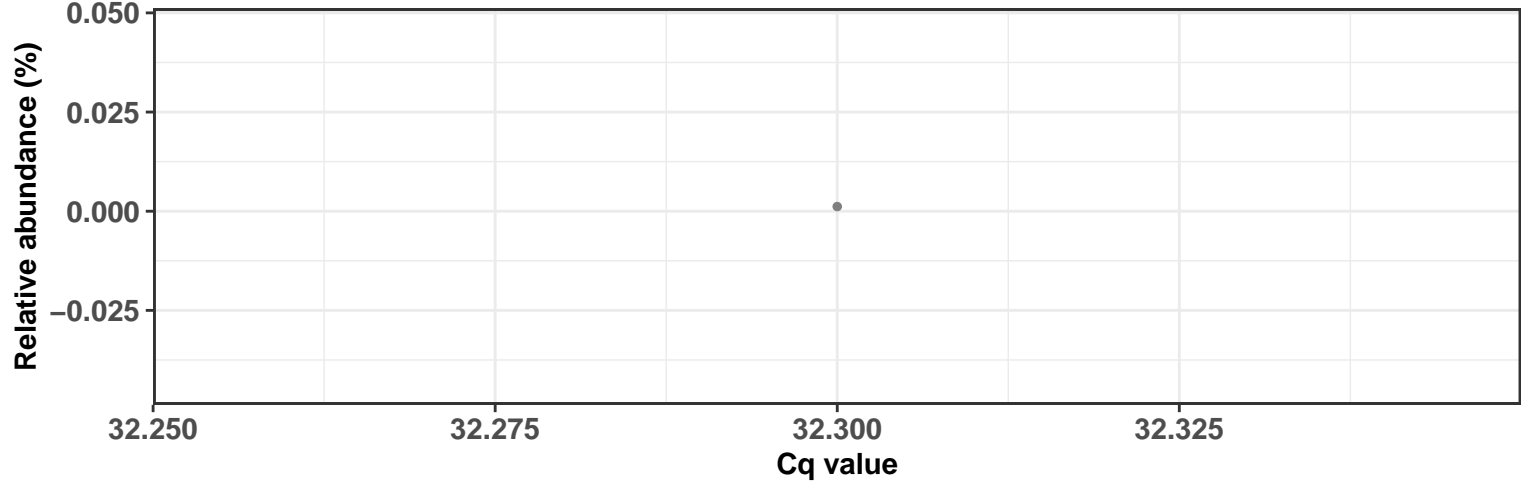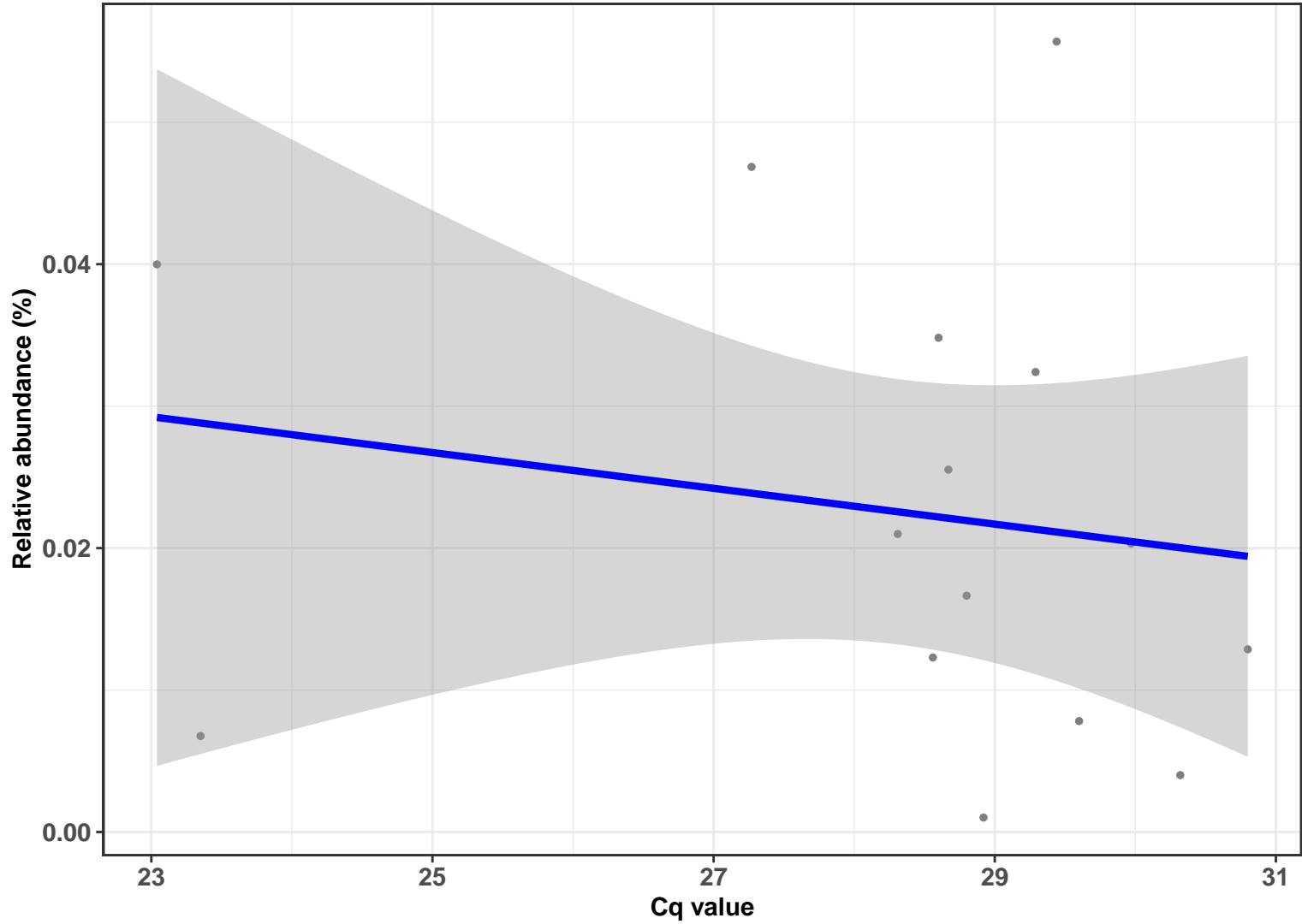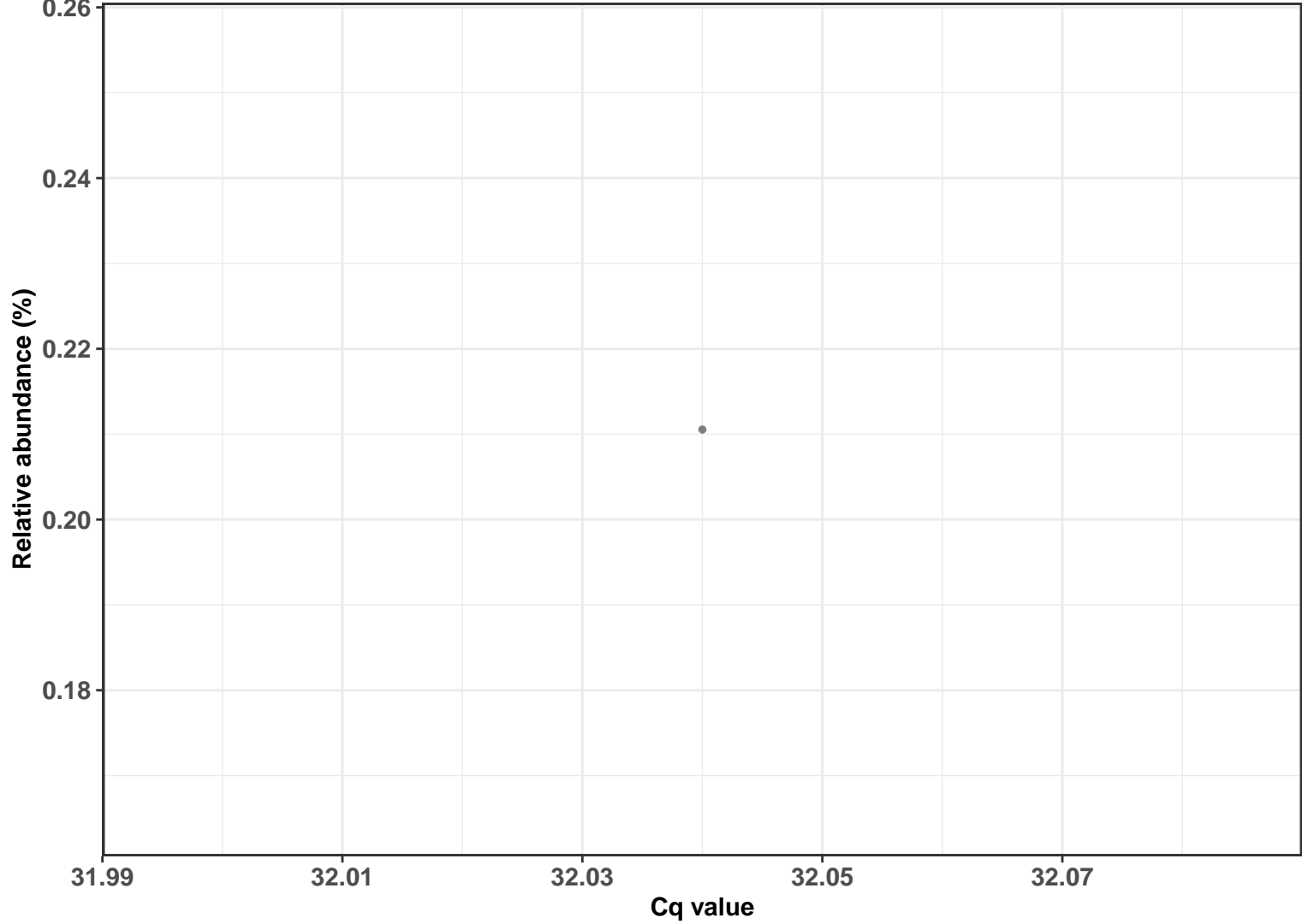
Correlation with all samples

$\log_e(S) = 7.483$, $p = 0.986$, $\hat{\rho}_{Spearman} = -0.004$, $CI_{95\%}$ [−0.469, 0.515], $n_{pairs} = 22$

SampleType ● REF−DIM ● IM−DIC ● IM−DIM

Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 6.165$, $p = 0.031$, $\hat{\rho}_{Spearman} = 0.509$, $CI_{95\%}$ [0.130, 0.874], $n_{pairs} = 18$

Correlation within: IM−DIM
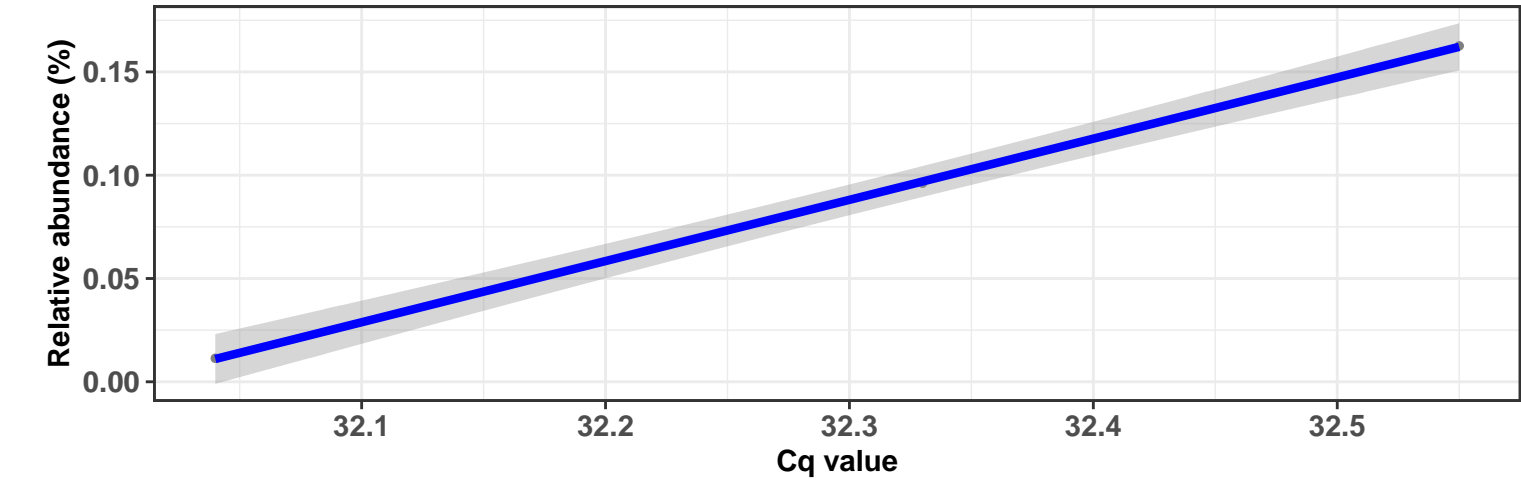
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

$\log_e(S) = 6.596$, $p = 0.778$, $\hat{\rho}_{Spearman} = -0.076$, $CI_{95\%}$ [−0.595, 0.528], $n_{pairs} = 16$
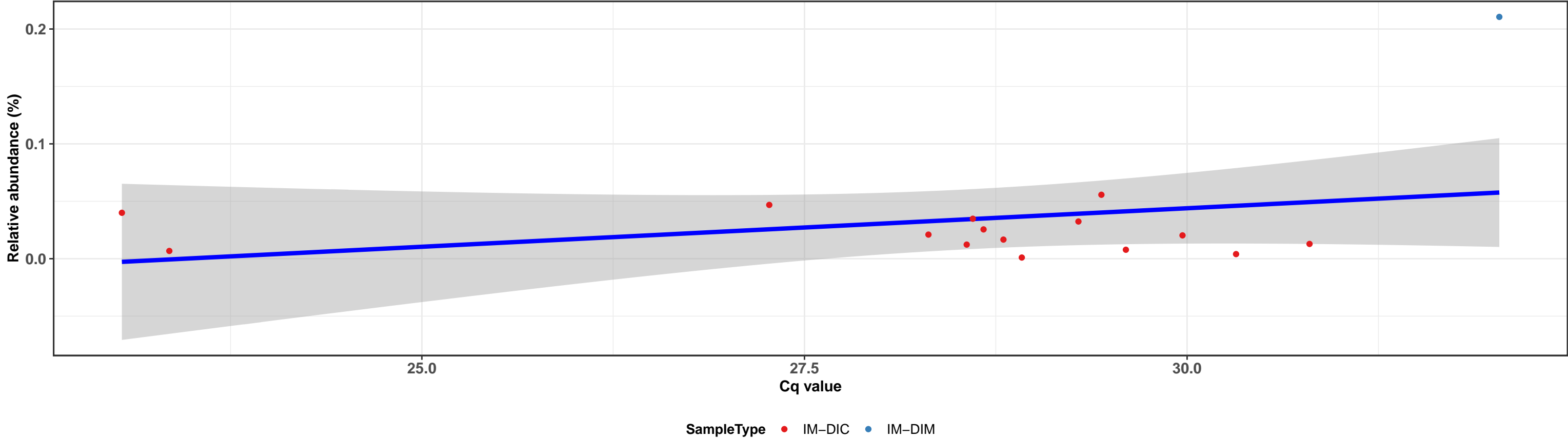
Correlation within: IM−DIC

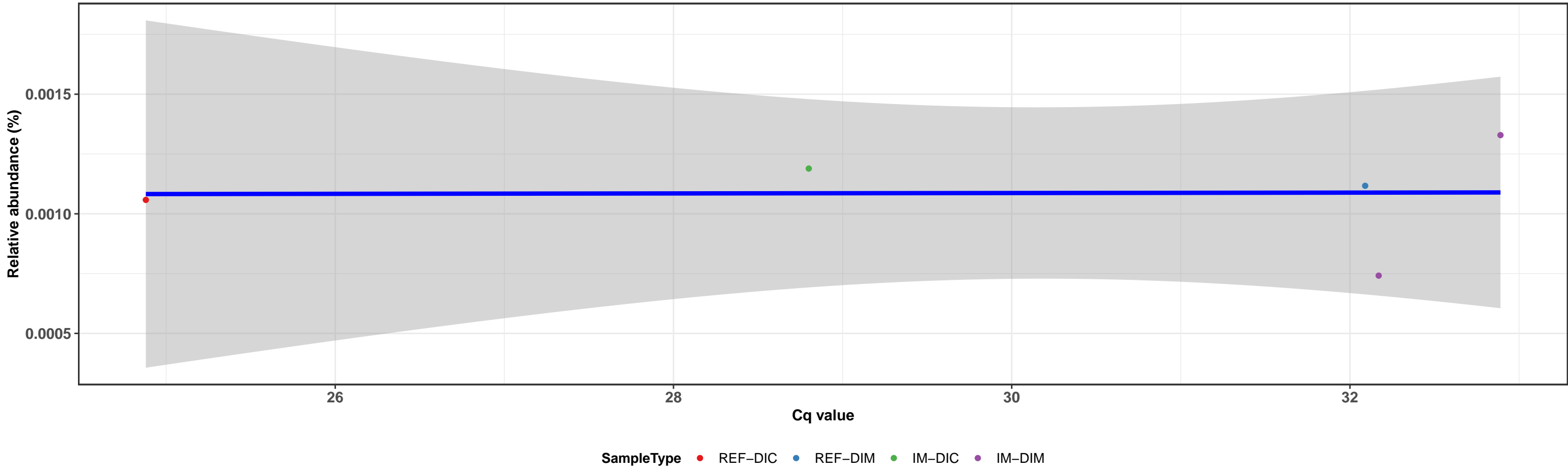$\log_e(S) = 6.596$, $p = 0.265$, $\hat{\rho}_{Spearman} = -0.307$, $CI_{95\%}$ [−0.879, 0.216], $n_{pairs} = 15$

Correlation within: IM−DIM

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Marinobacteraceae; g__Marinobacter; s__Marinobacter adhaerens
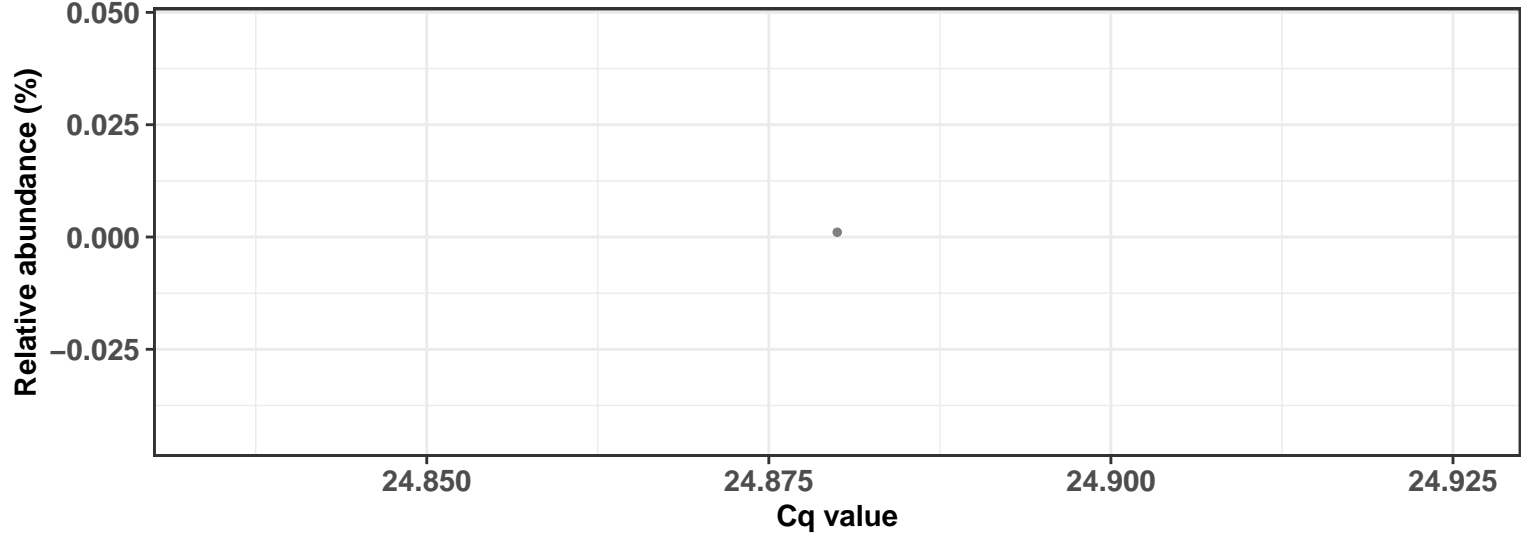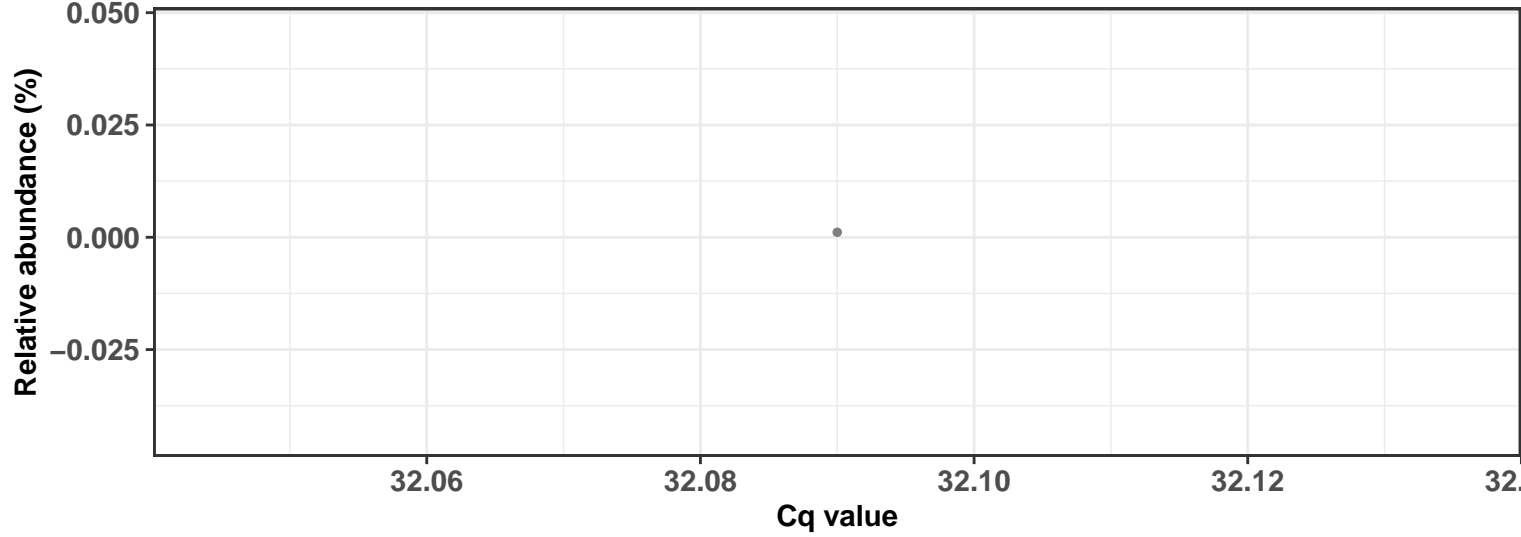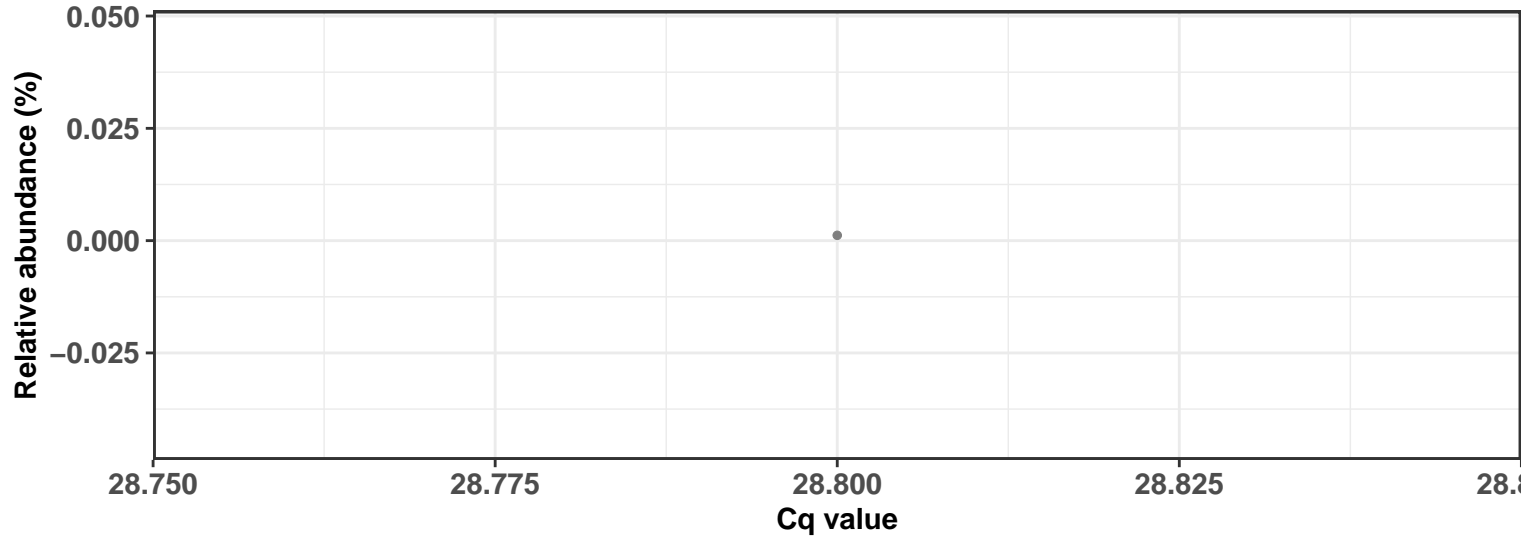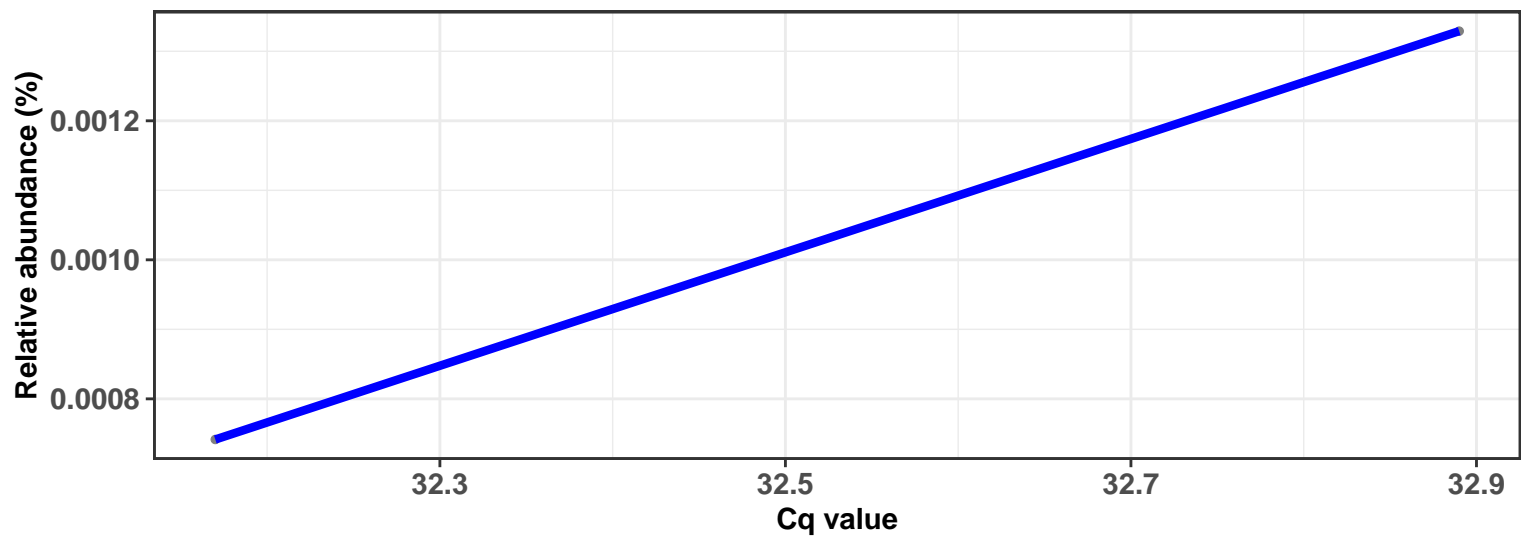
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; s__uncultured bacterium

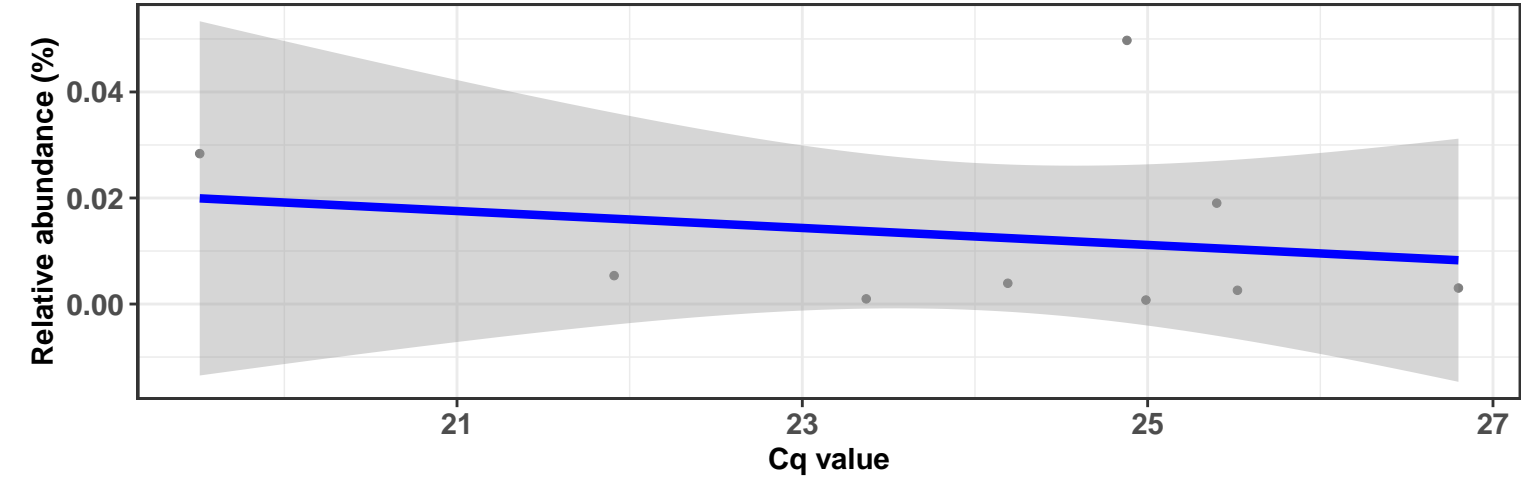**Correlation with all samples**

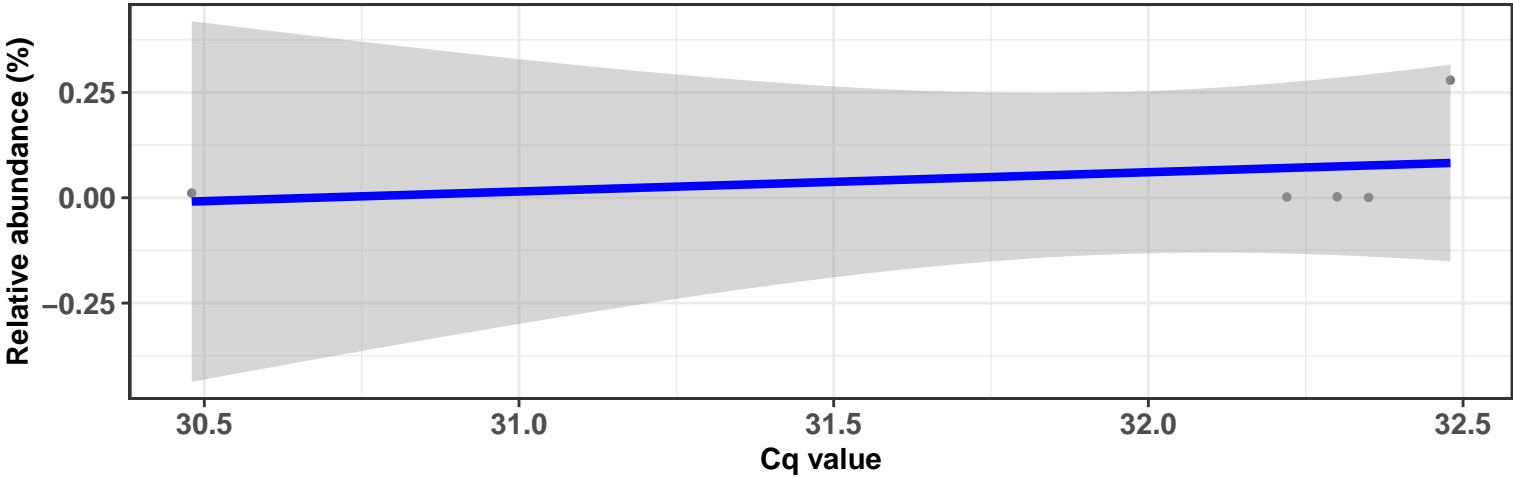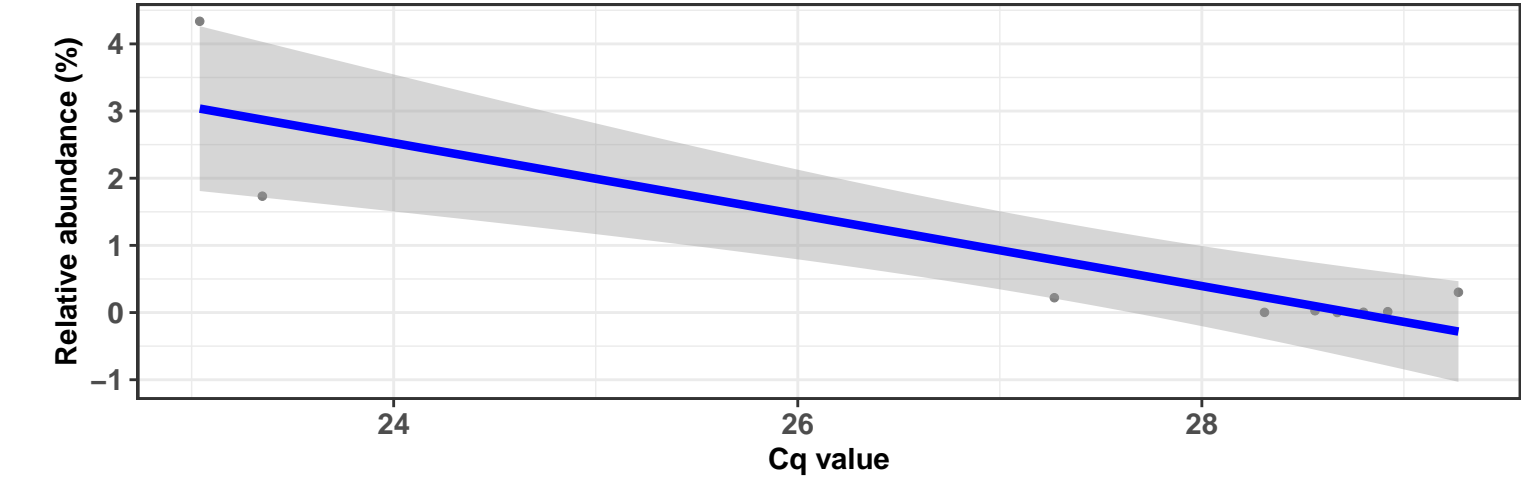$\log_e(S) = 8.469$, $p = 0.753$, $\hat{\rho}_{Spearman} = -0.060$, $CI_{95\%}$ $[-0.404, 0.327]$, $n_{pairs} = 30$

SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● IM−DIM   ● Mock
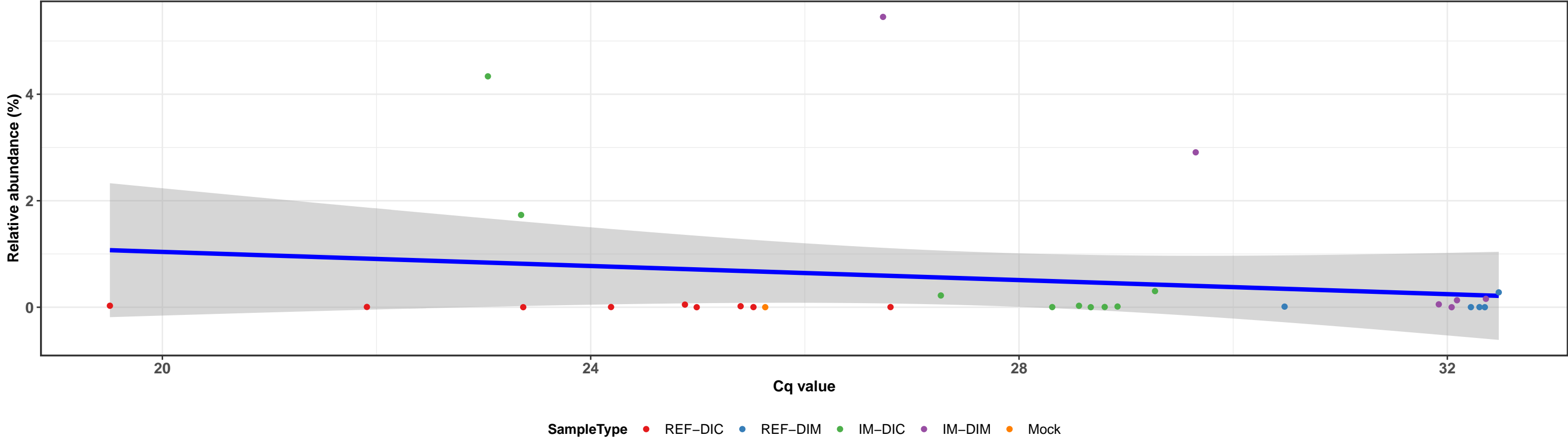
Correlation within: REF−DIC

$\log_e(S) = 5.063$, $p = 0.406$, $\hat{\rho}_{Spearman} = -0.317$, $CI_{95\%}$ $[-0.936, 0.264]$, $n_{pairs} = 9$

Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 5.159$, $p = 0.224$, $\hat{\rho}_{Spearman} = -0.450$, $CI_{95\%}$ $[-1.339, 0.340]$, $n_{pairs} = 9$

Correlation within: IM−DIM

$\log_e(S) = 3.951$, $p = 0.329$, $\hat{\rho}_{Spearman} = -0.486$, $CI_{95\%}$ $[-1.650, 0.488]$, $n_{pairs} = 6$
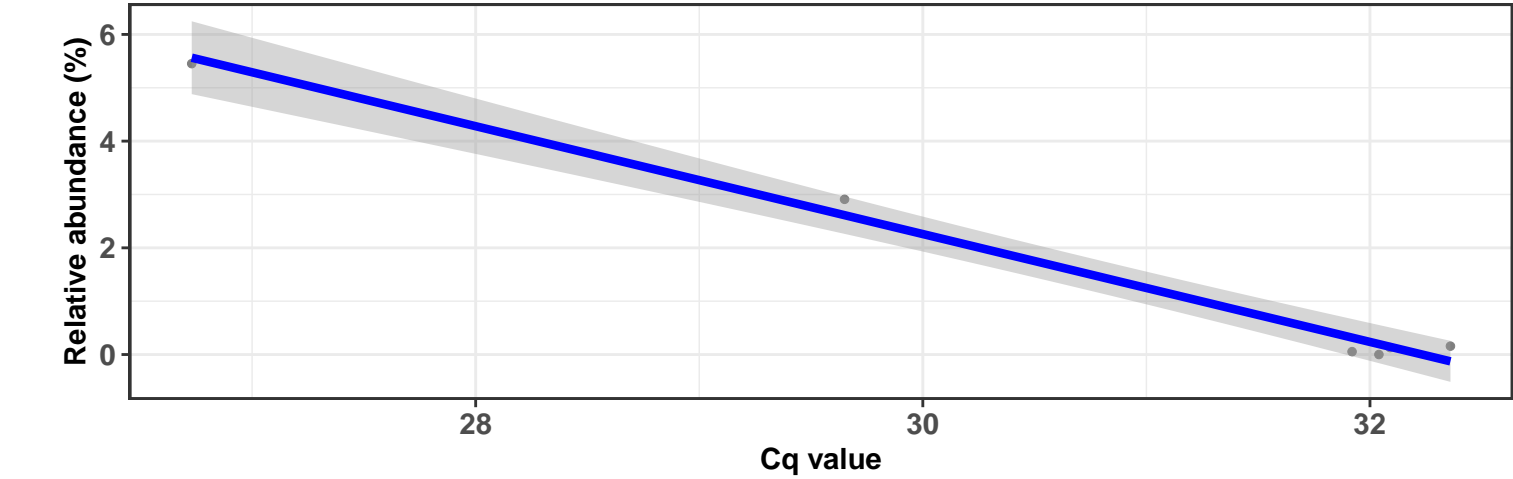
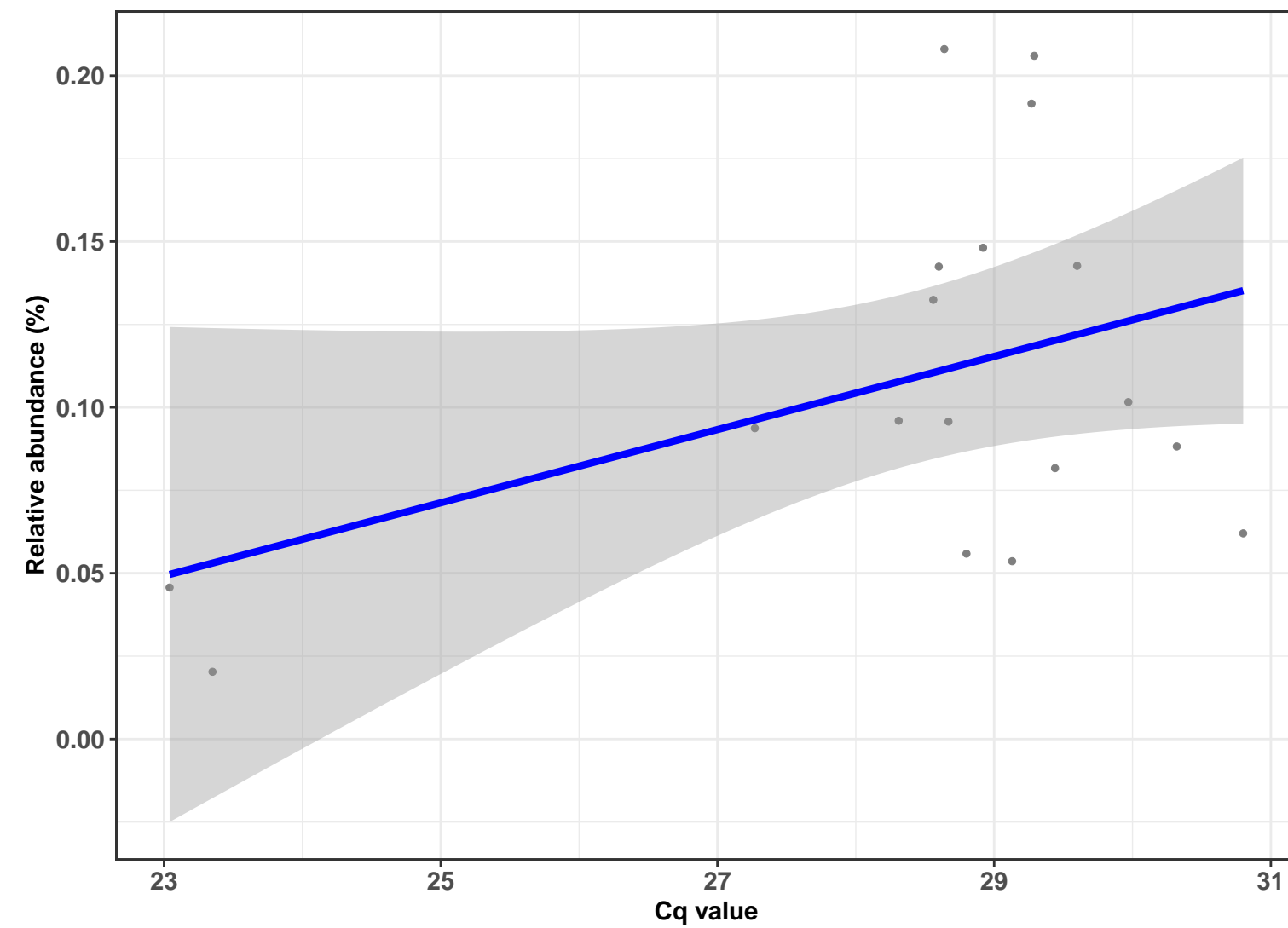**k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; NA**

Correlation with all samples

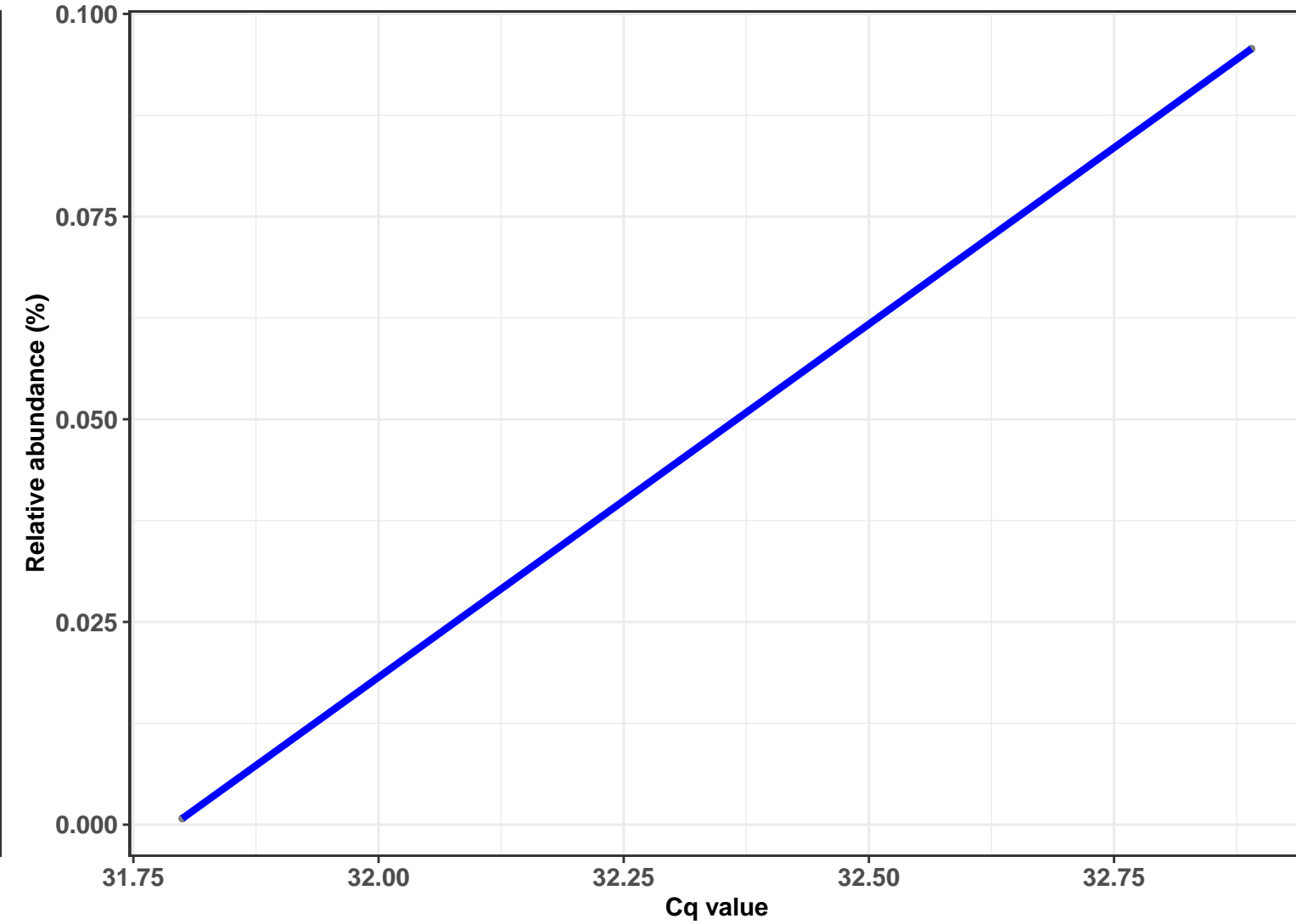$\log_e(S) = 7.199$, $p = 0.980$, $\hat{\rho}_{Spearman} = -0.006$, $CI_{95\%}$ [−0.548, 0.425], $n_{pairs} = 20$

SampleType ● IM−DIC ● IM−DIM
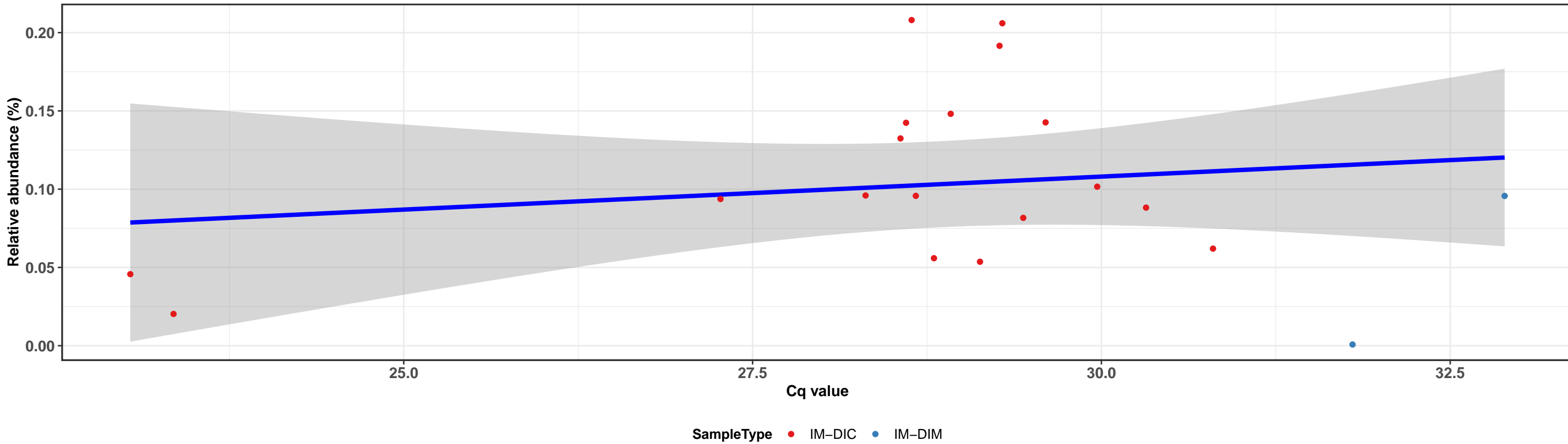
Correlation within: IM−DIC

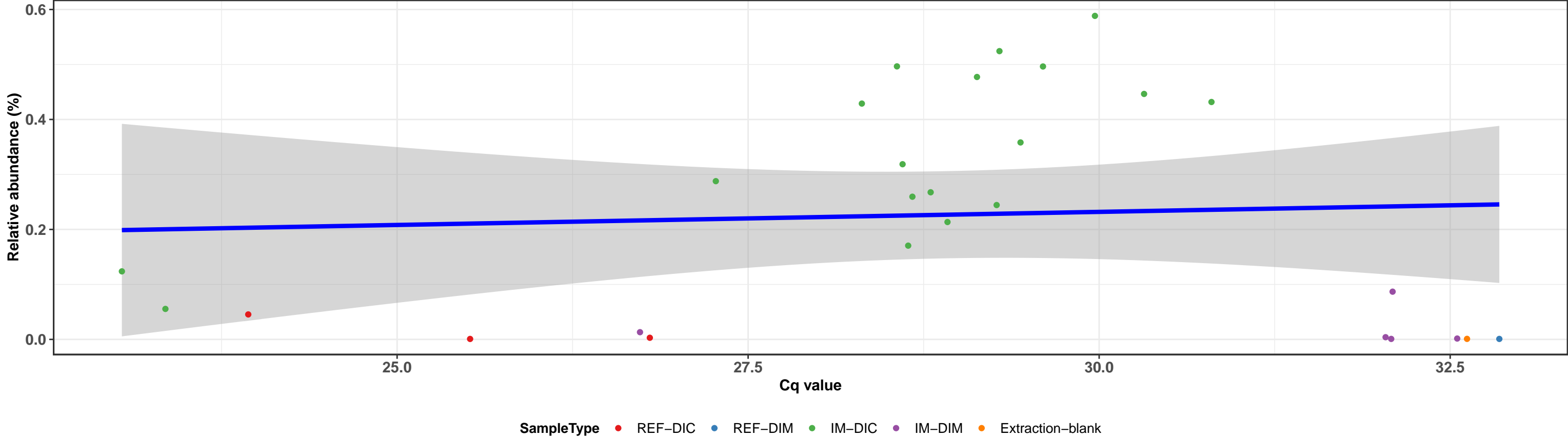$\log_e(S) = 6.669$, $p = 0.458$, $\hat{\rho}_{Spearman} = 0.187$, $CI_{95\%}$ [−0.316, 0.803], $n_{pairs} = 18$

Correlation within: IM−DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa
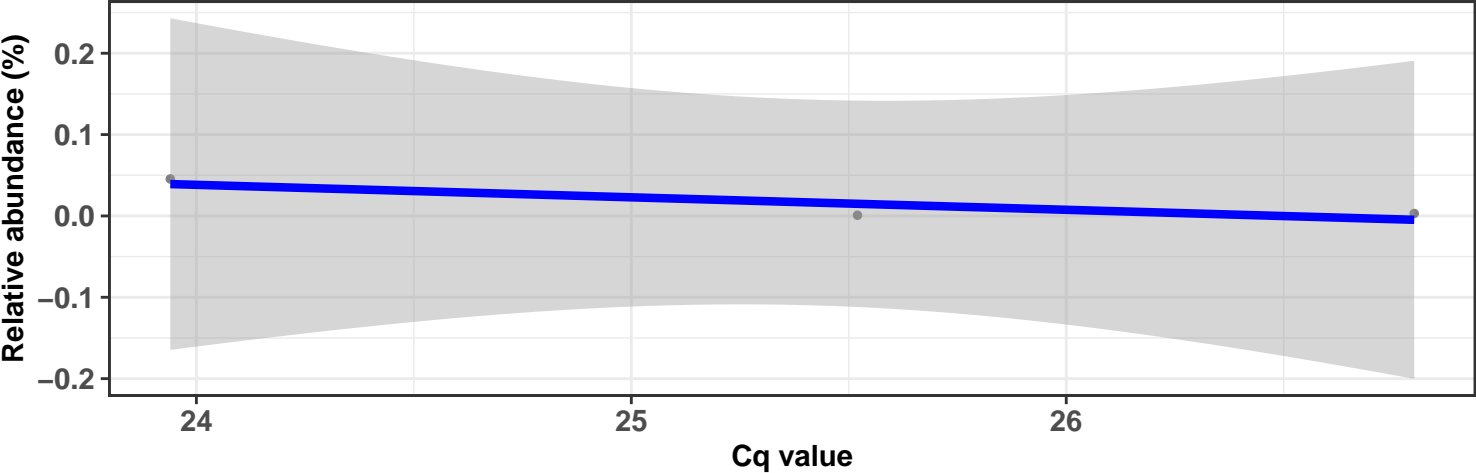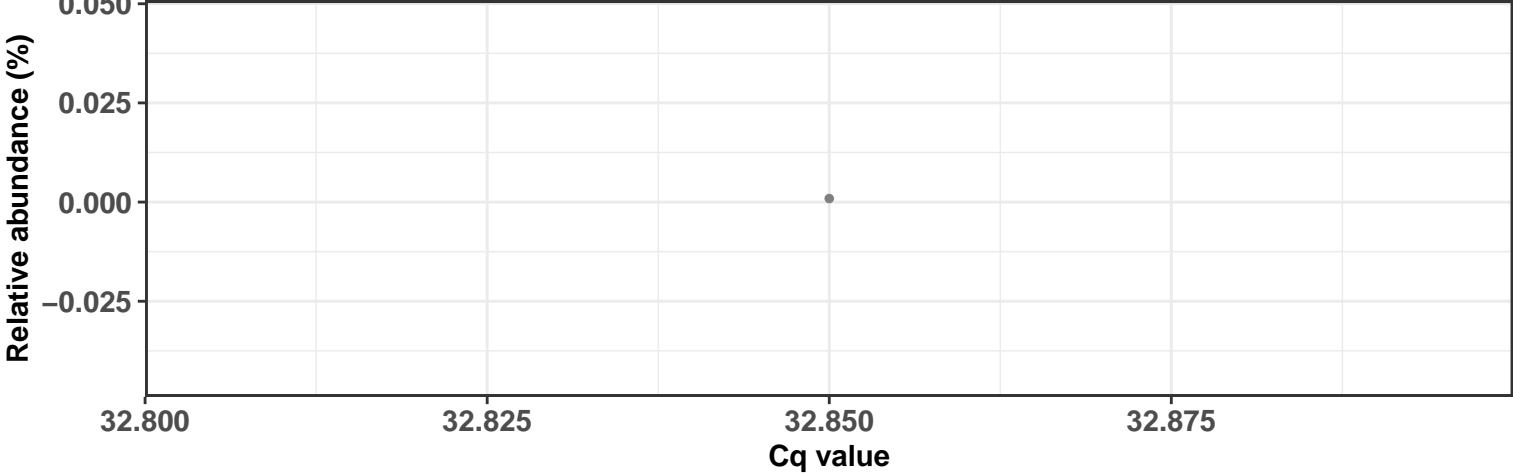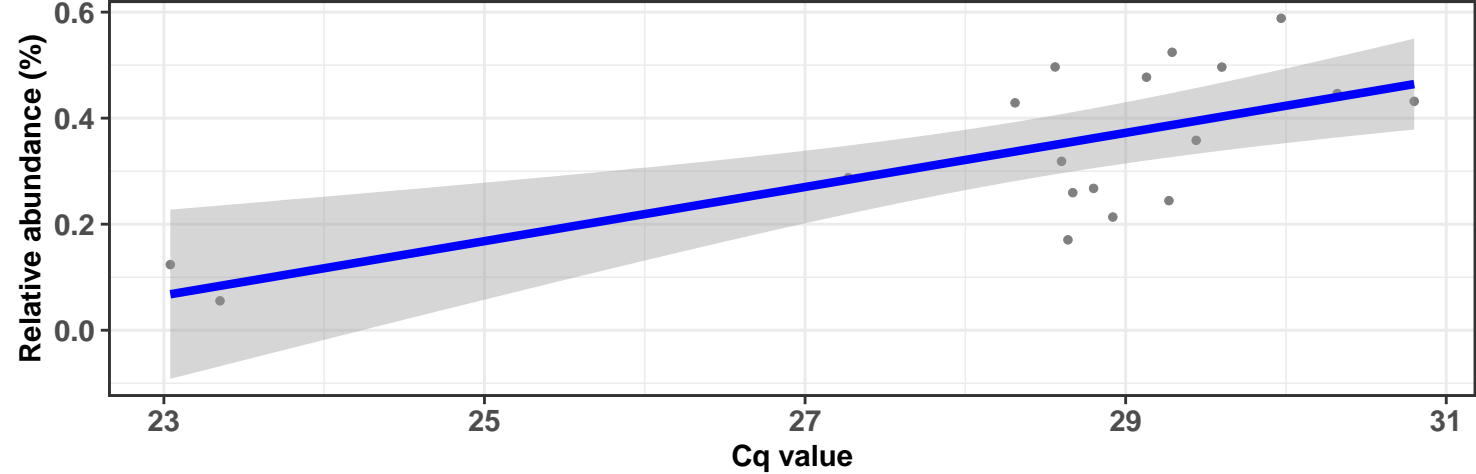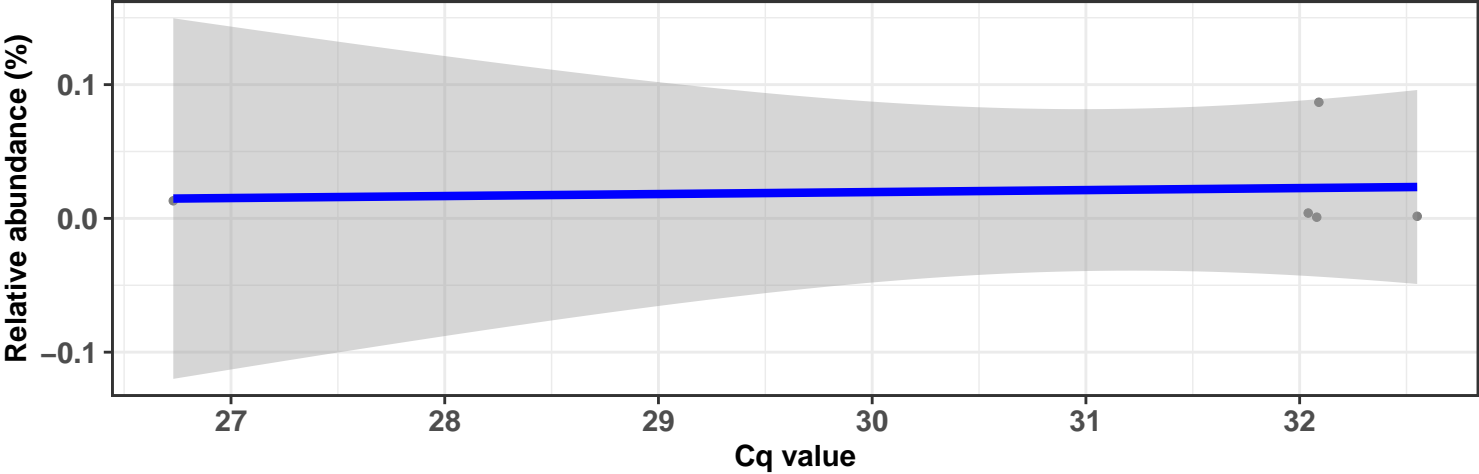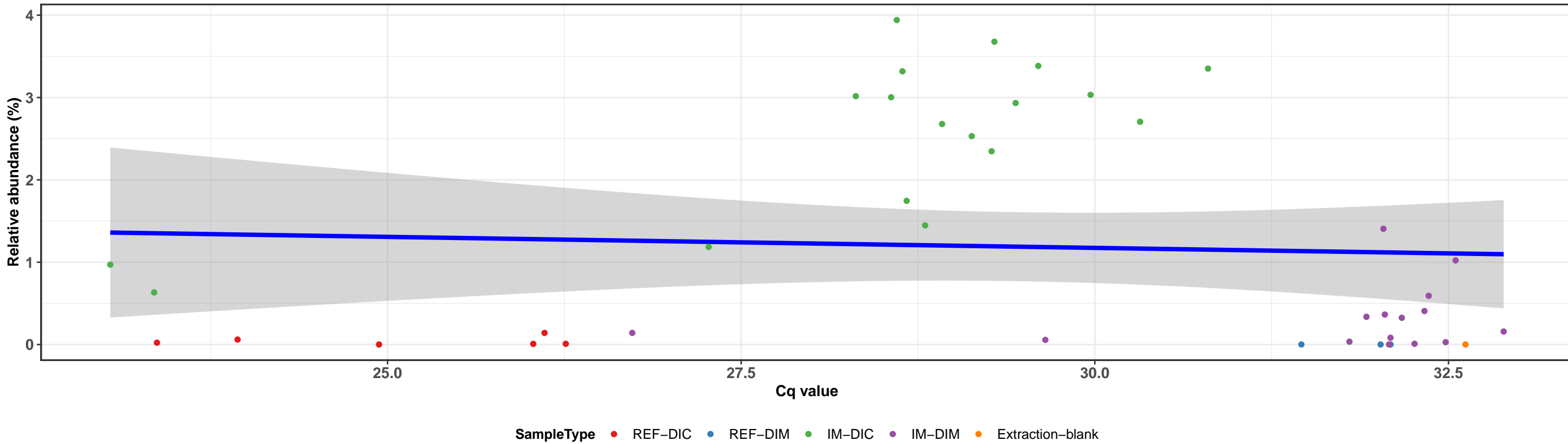
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium aurimucosum ATCC 700975
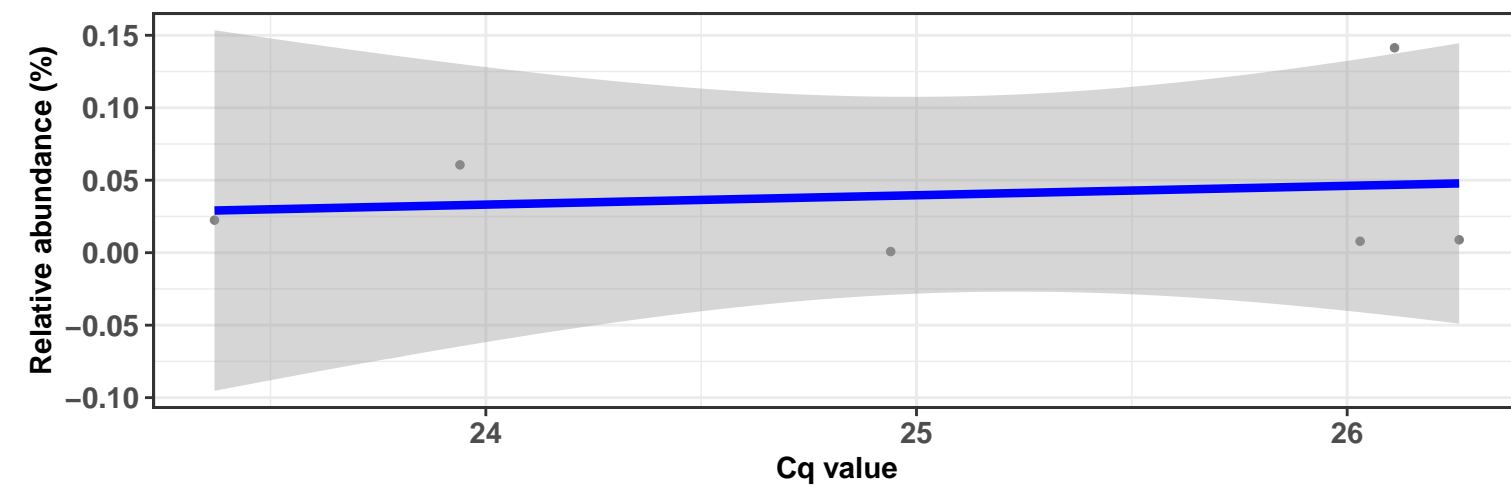

Correlation with all samples

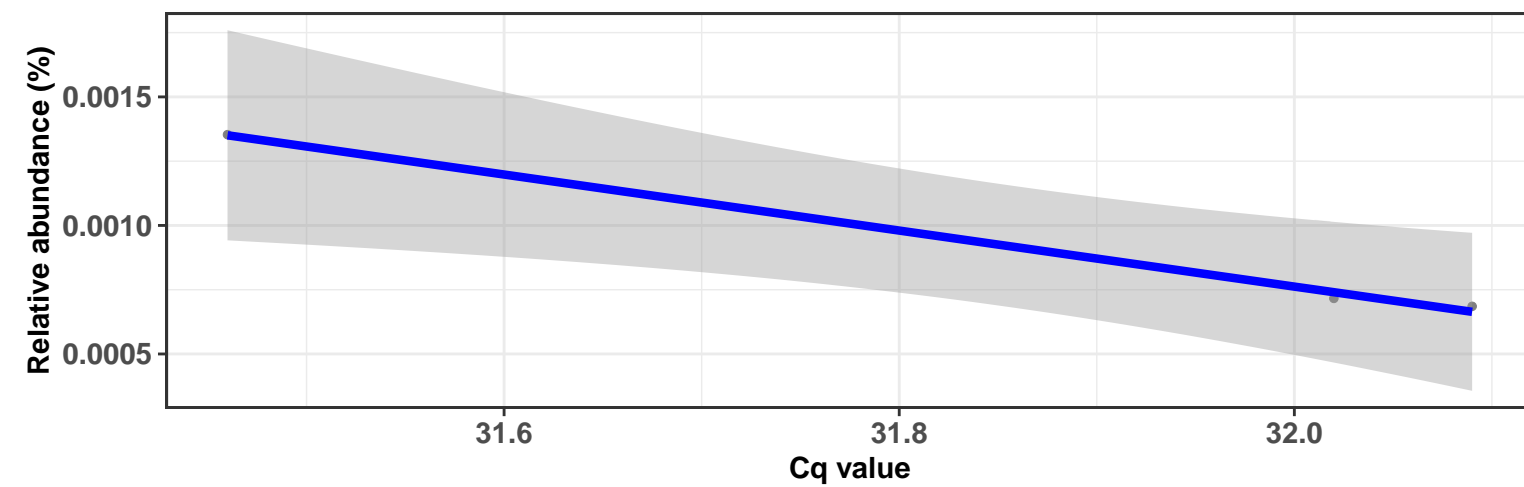$\log_e(S) = 9.662$, $p = 0.232$, $\hat{\rho}_{Spearman} = -0.186$, $CI_{95\%}$ $[-0.490, 0.093]$, $n_{pairs} = 43$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

$\log_e(S) = 3.584$, $p = 0.957$, $\hat{\rho}_{Spearman} = -0.029$, $CI_{95\%}$ $[-0.943, 0.937]$, $n_{pairs} = 6$
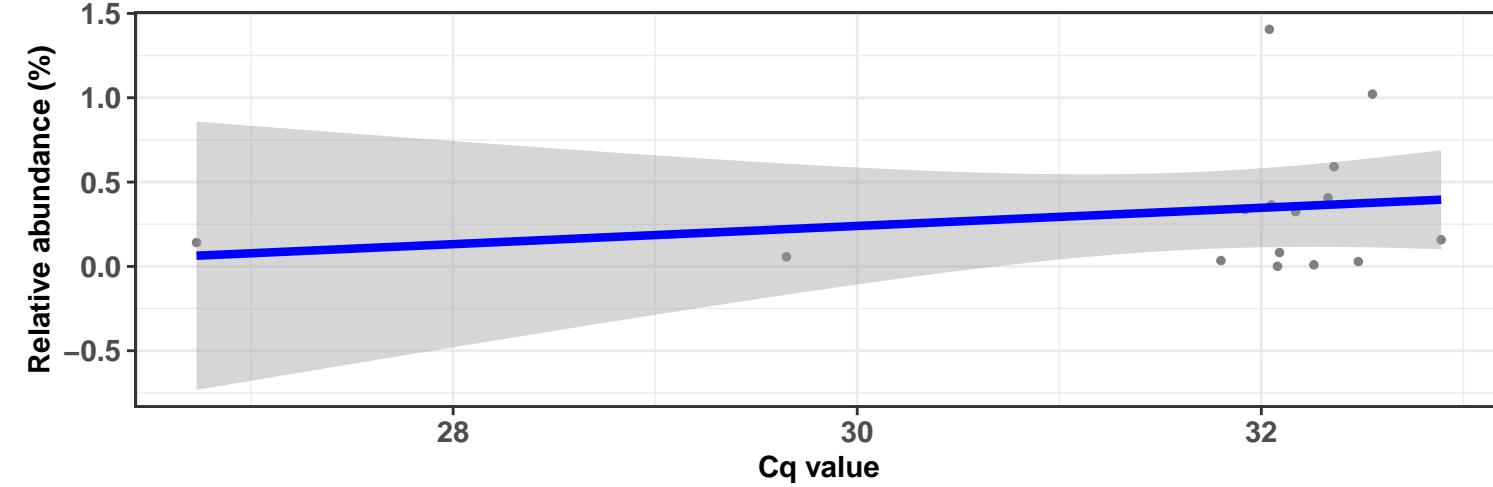
Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 6.215$, $p = 0.042$, $\hat{\rho}_{Spearman} = 0.484$, $CI_{95\%}$ $[0.032, 0.942]$, $n_{pairs} = 18$
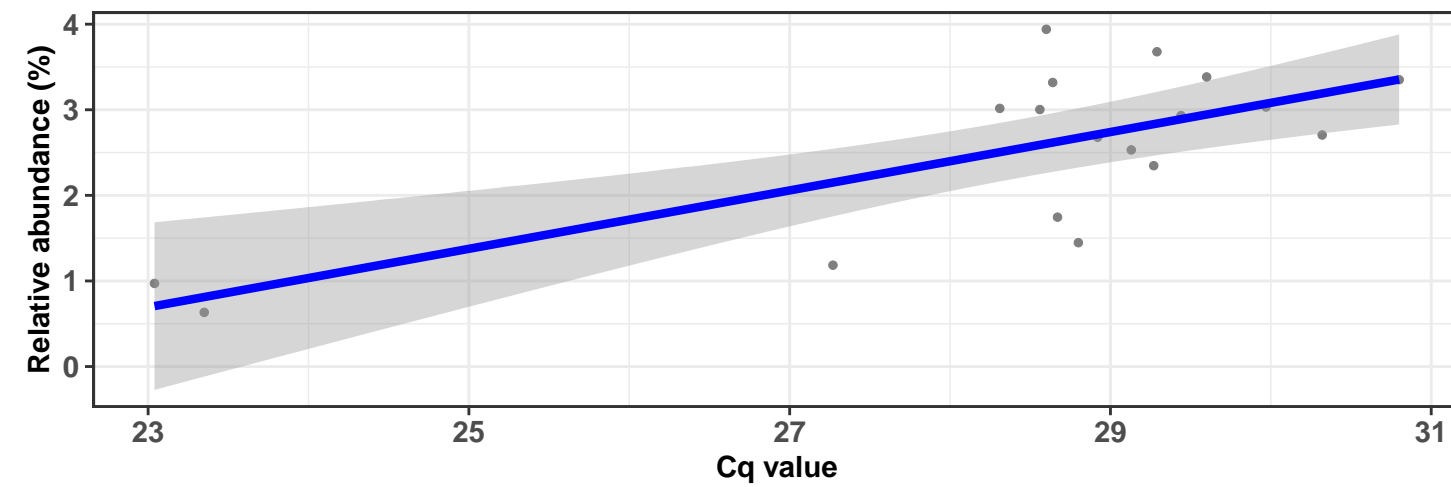
Correlation within: IM−DIM
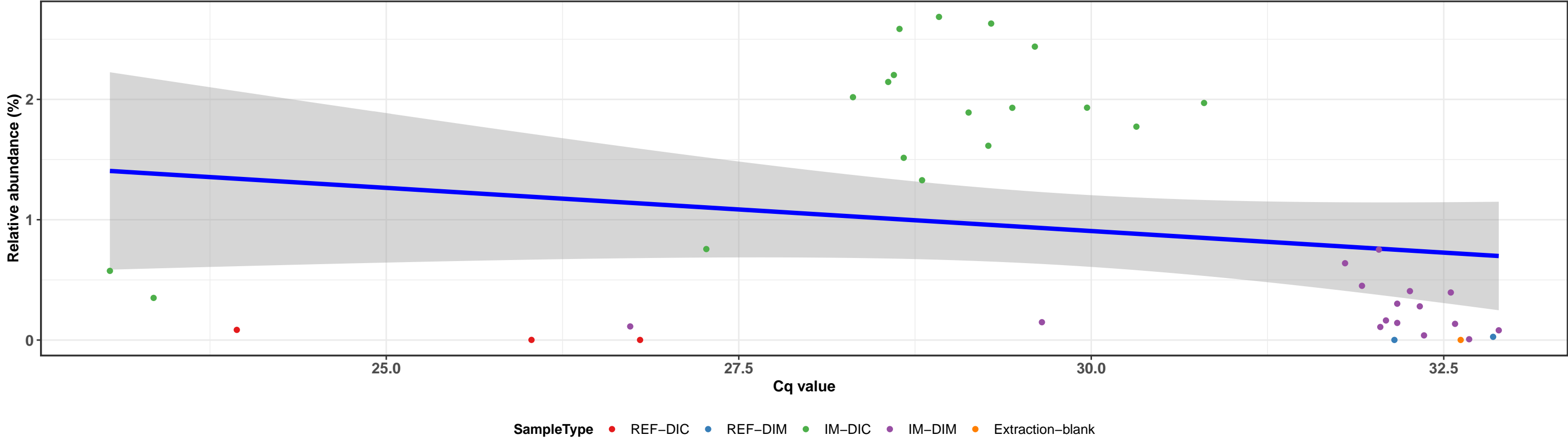
$\log_e(S) = 6.136$, $p = 0.533$, $\hat{\rho}_{Spearman} = 0.175$, $CI_{95\%}$ $[-0.333, 0.714]$, $n_{pairs} = 15$
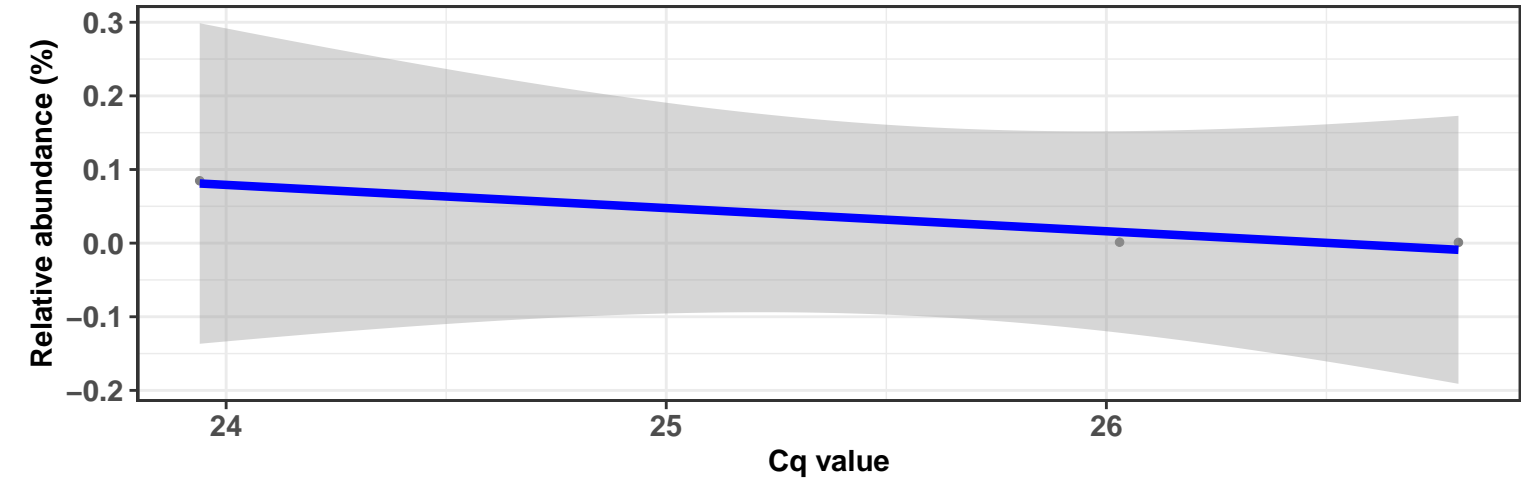
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium
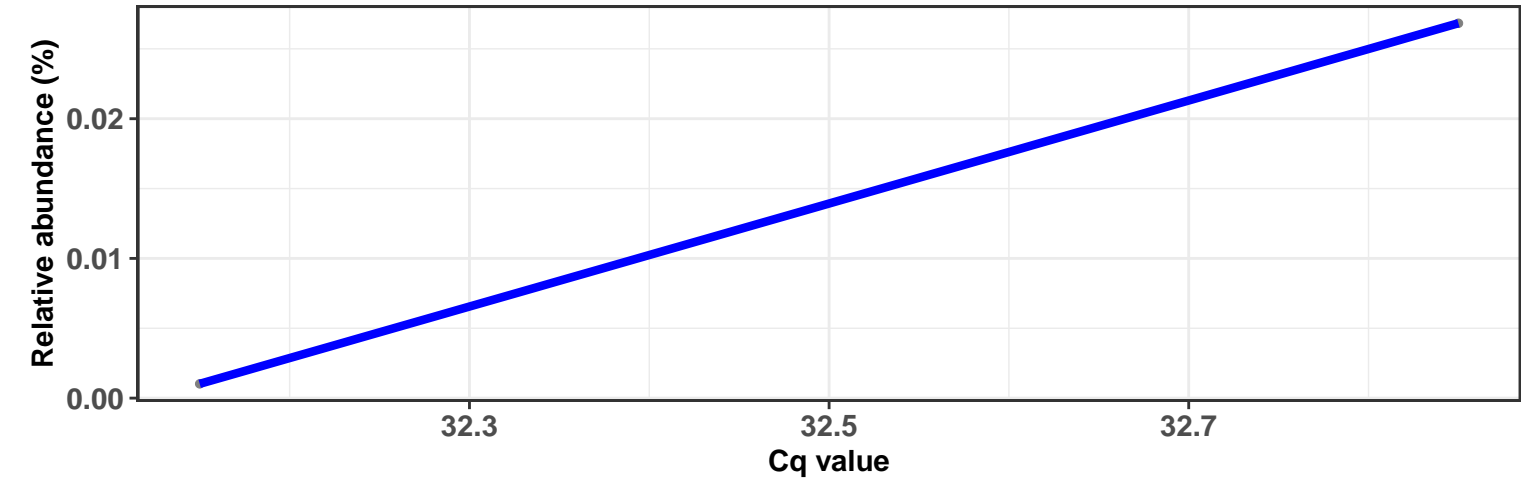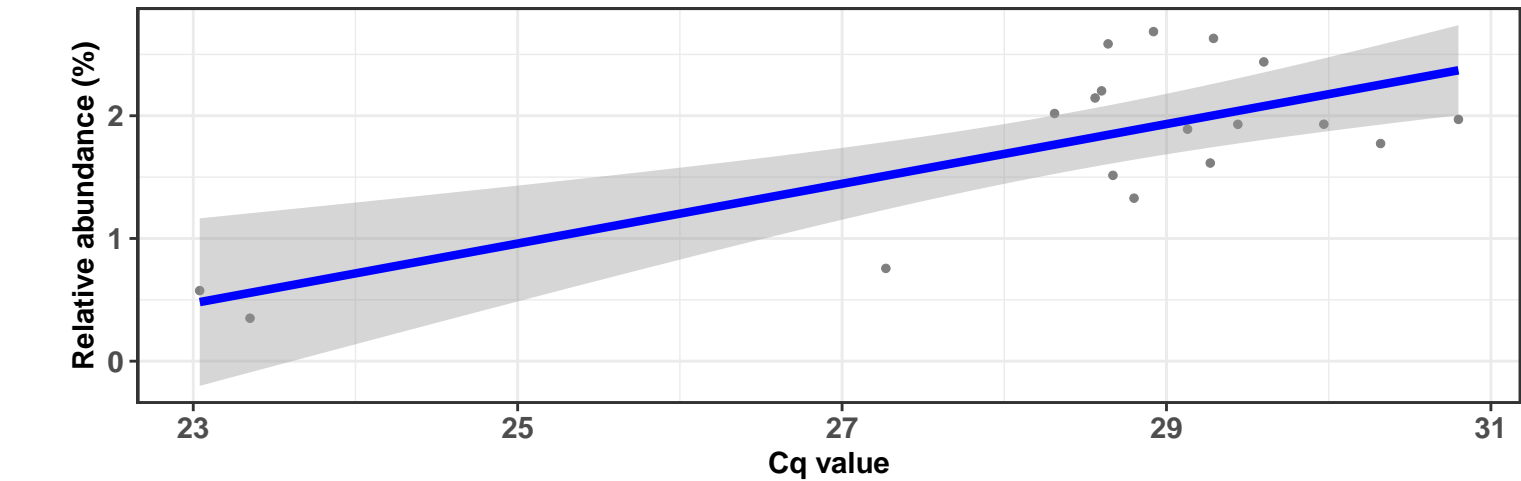
Correlation with all samples

$\log_e(S) = 9.597$, $p = 0.015$, $\hat{\rho}_{Spearman} = -0.381$, $CI_{95\%}$ [−0.770, −0.037], $n_{pairs} = 40$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank

Correlation within: REF−DIC

Correlation within: REF−DIM

Correlation within: IM−DIC

$\log_e(S) = 6.468$, $p = 0.174$, $\hat{\rho}_{Spearman} = 0.335$, $CI_{95\%}$ [−0.184, 0.906], $n_{pairs} = 18$

Correlation within: IM−DIM

$\log_e(S) = 6.882$, $p = 0.094$, $\hat{\rho}_{Spearman} = -0.433$, $CI_{95\%}$ [−0.823, −0.013], $n_{pairs} = 16$
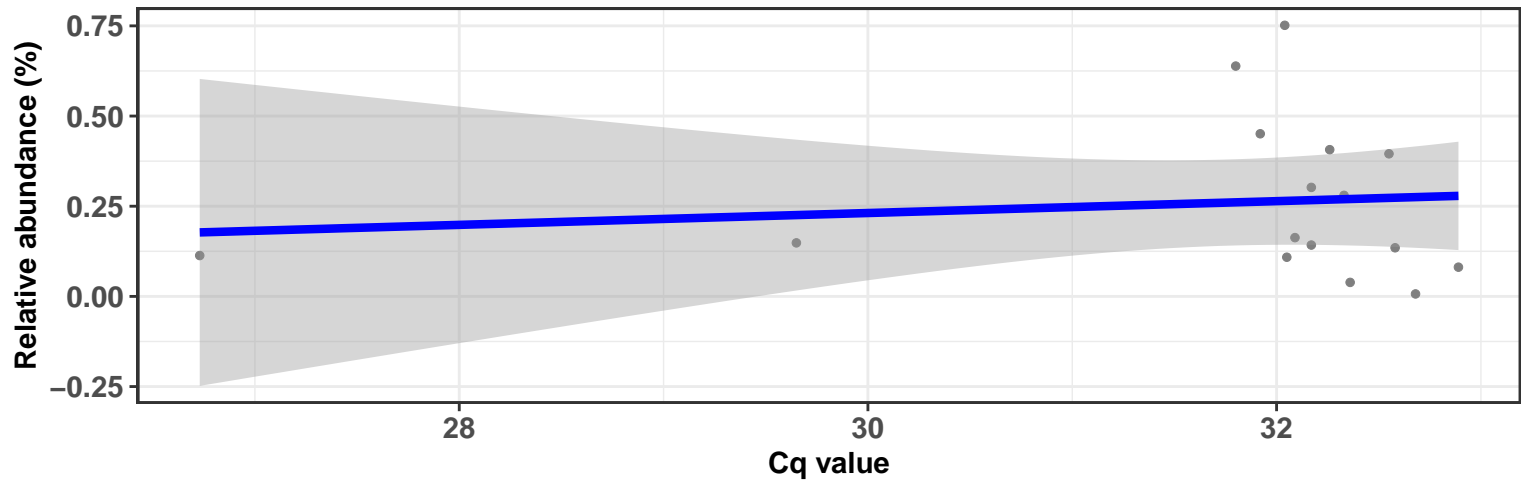
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; Ambiguous_taxa

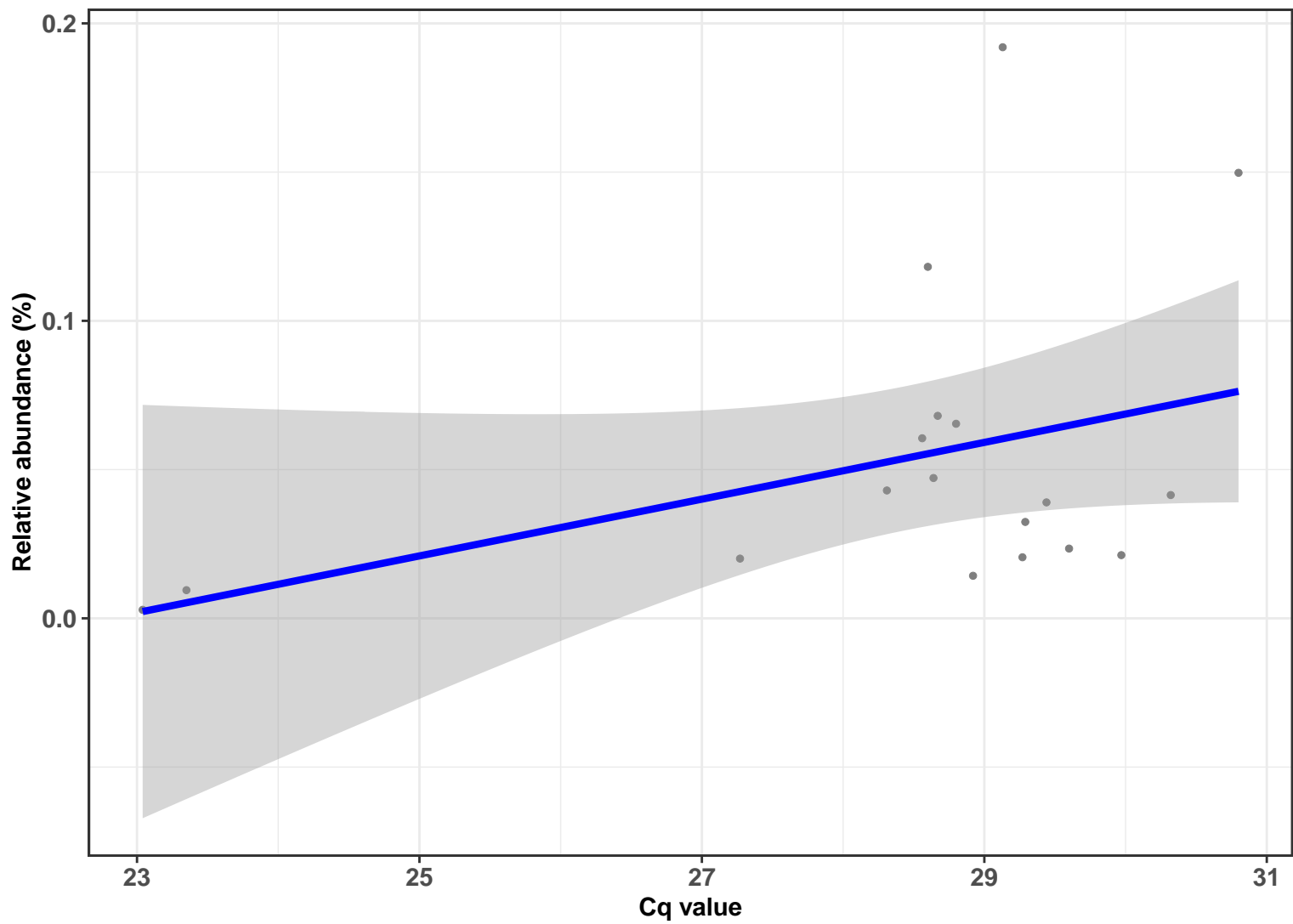**Correlation with all samples**

$\log_e(S) = 6.972$, $p = 0.792$, $\hat{\rho}_{Spearman} = 0.065$, $CI_{95\%}$ [−0.550, 0.644], $n_{pairs} = 19$

SampleType • IM−DIC • Extraction−blank
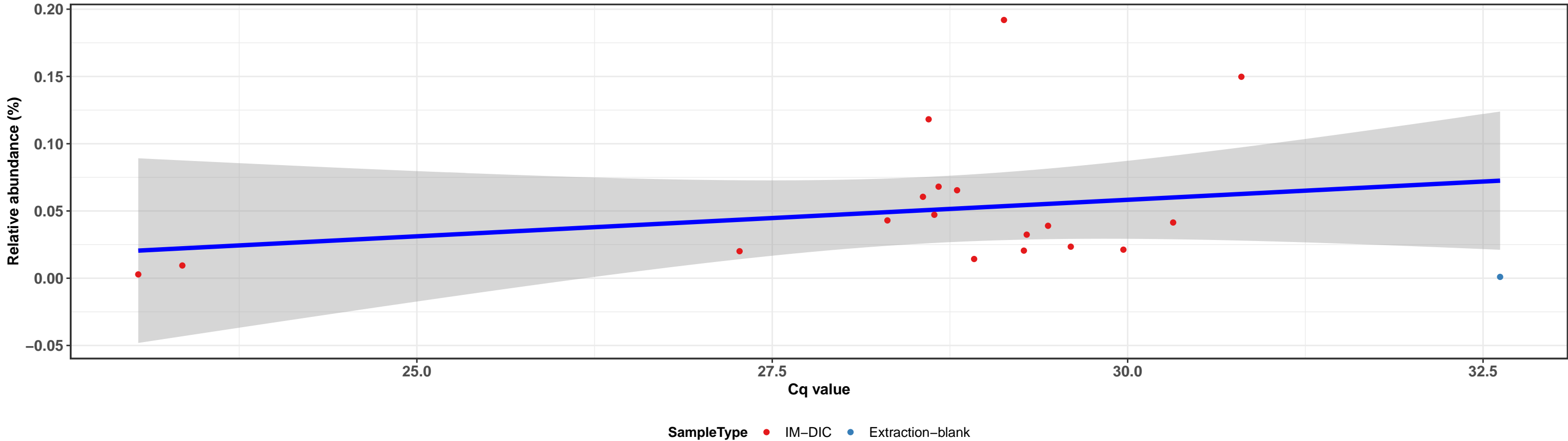
Correlation within: IM−DIC

$\log_e(S) = 6.585$, $p = 0.311$, $\hat{\rho}_{Spearman} = 0.253$, $CI_{95\%}$ [−0.267, 0.801], $n_{pairs} = 18$

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

Correlation with all samples

$\log_e(S) = 9.818$, $p = 0.124$, $\hat{\rho}_{Spearman} = 0.216$, $CI_{95\%}$ [−0.006, 0.502], $n_{pairs} = 52$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
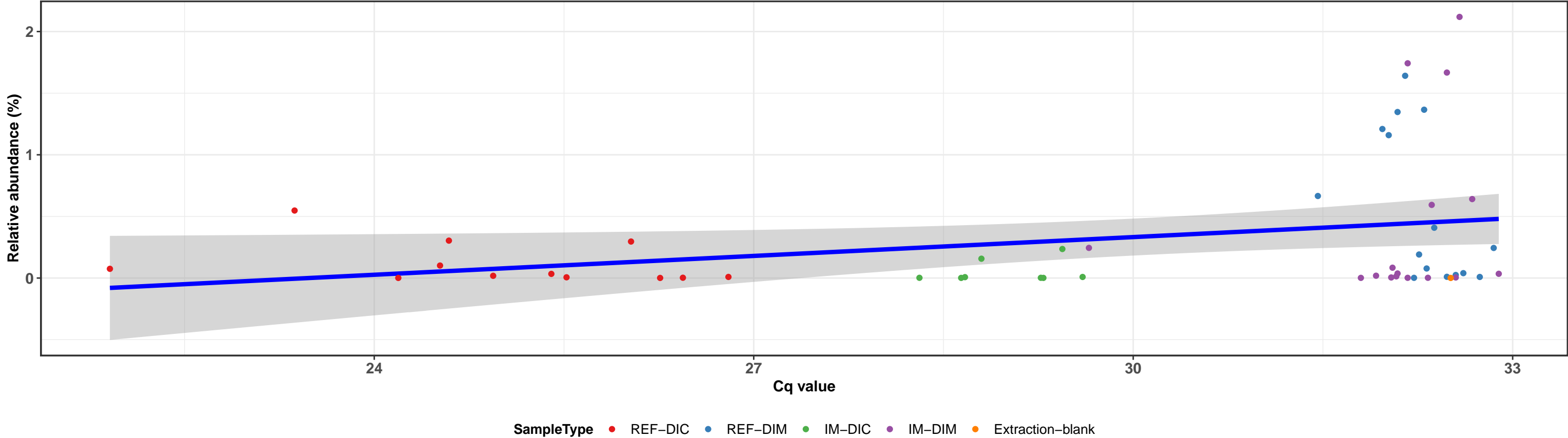
Correlation within: REF−DIC

$\log_e(S) = 6.011$, $p = 0.167$, $\hat{\rho}_{Spearman} = -0.427$, $CI_{95\%}$ [−1.038, 0.118], $n_{pairs} = 12$
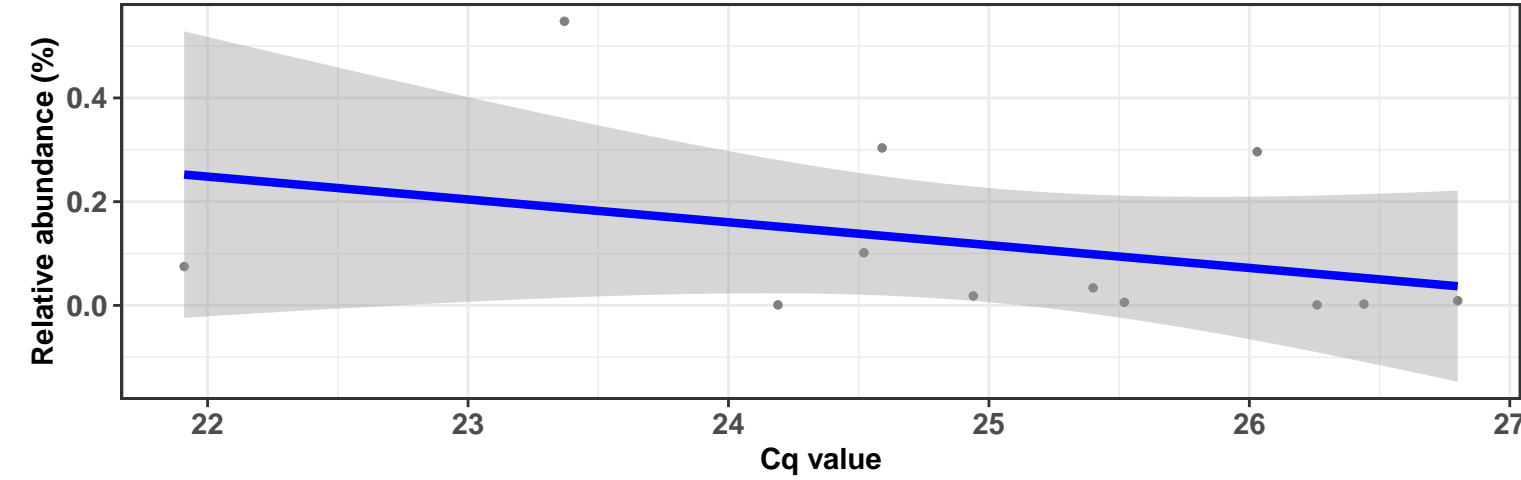
Correlation within: REF−DIM

$\log_e(S) = 6.782$, $p = 0.025$, $\hat{\rho}_{Spearman} = -0.575$, $CI_{95\%}$ [−0.922, −0.243], $n_{pairs} = 15$
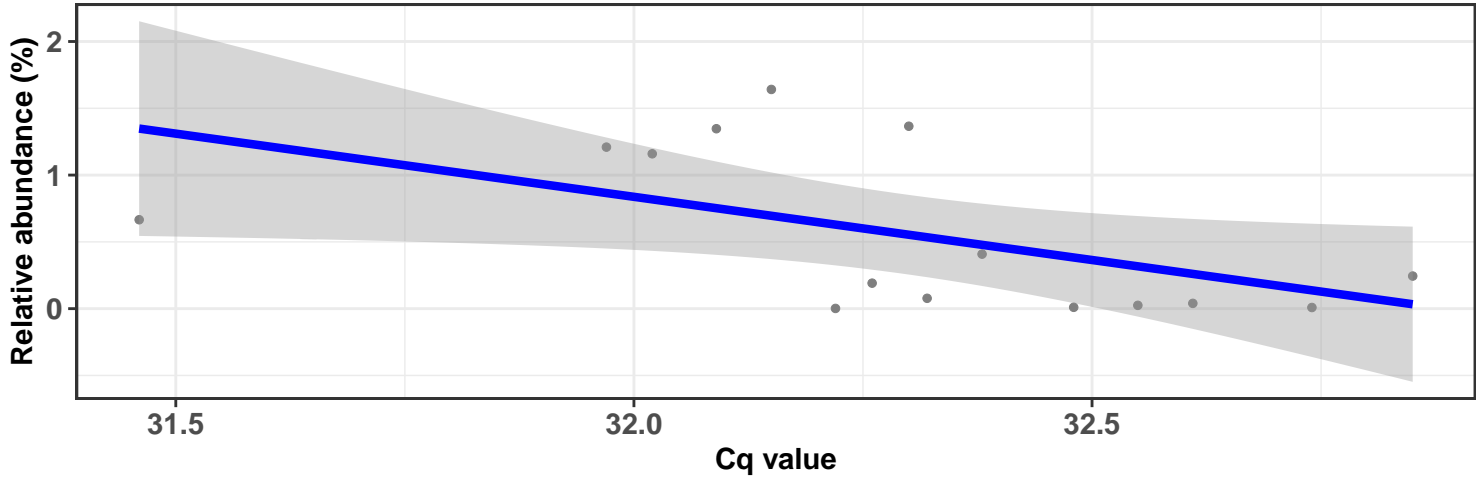
Correlation within: IM−DIC

$\log_e(S) = 4.025$, $p = 0.420$, $\hat{\rho}_{Spearman} = 0.333$, $CI_{95\%}$ [−0.383, 1.184], $n_{pairs} = 8$
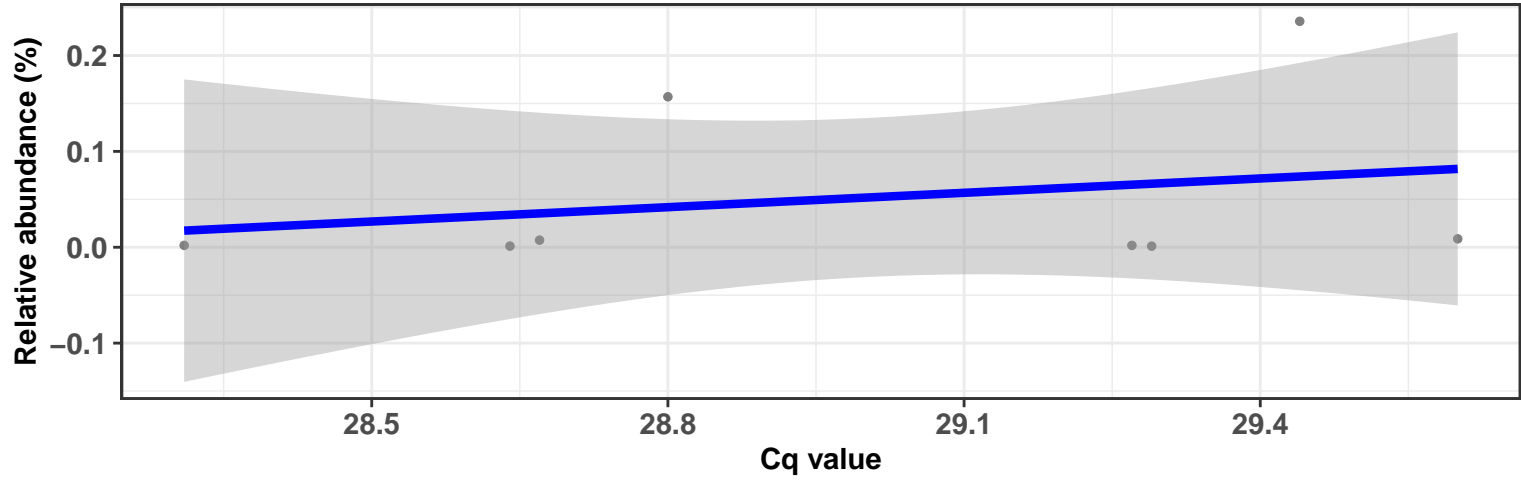
Correlation within: IM−DIM

$\log_e(S) = 6.042$, $p = 0.145$, $\hat{\rho}_{Spearman} = 0.381$, $CI_{95\%}$ [−0.065, 0.799], $n_{pairs} = 16$
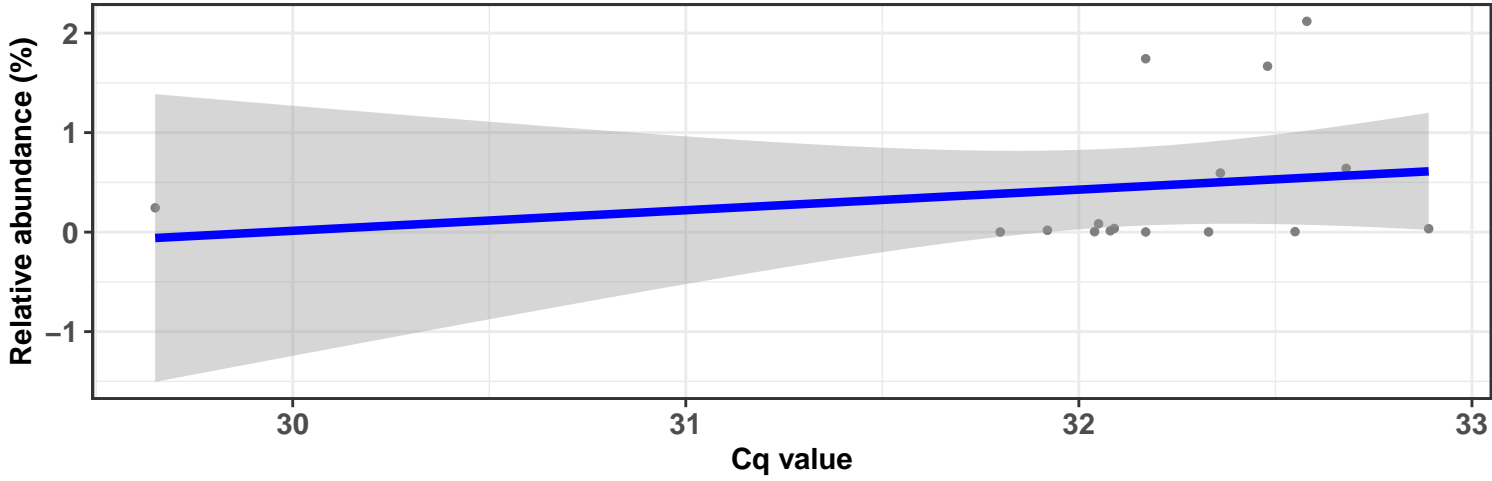
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__uncultured bacterium

Correlation with all samples

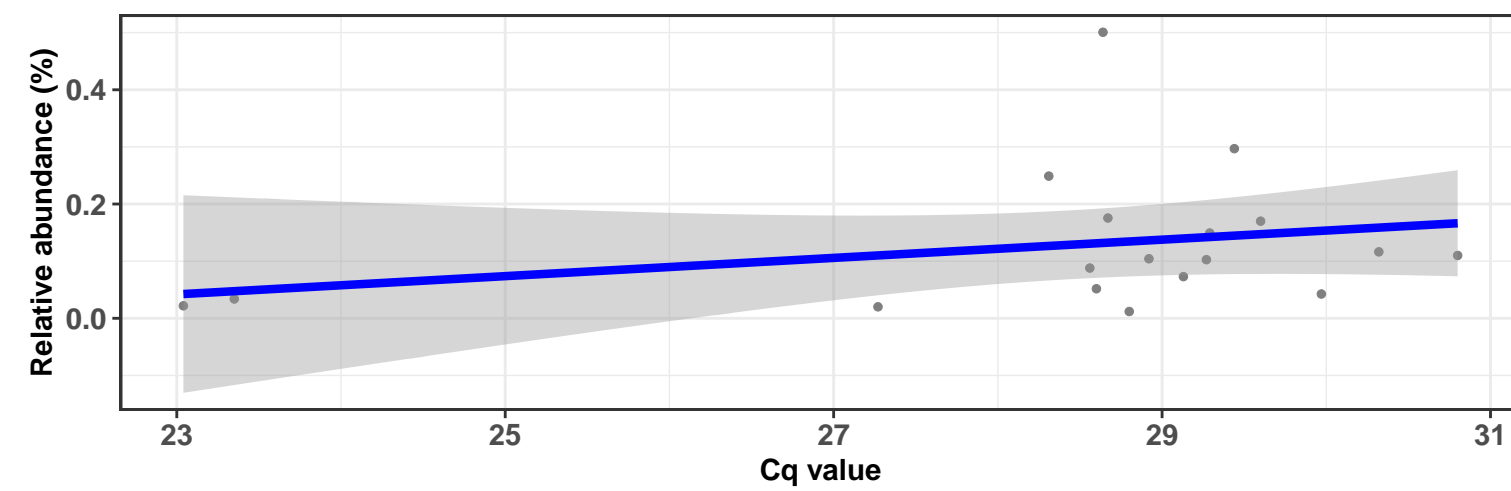$\log_e(S) = 7.421$, $p = 0.801$, $\hat{\rho}_{Spearman} = 0.057$, $CI_{95\%}$ [−0.472, 0.630], $n_{pairs} = 22$

SampleType ● REF−DIC ● IM−DIC ● IM−DIM ● Extraction−blank
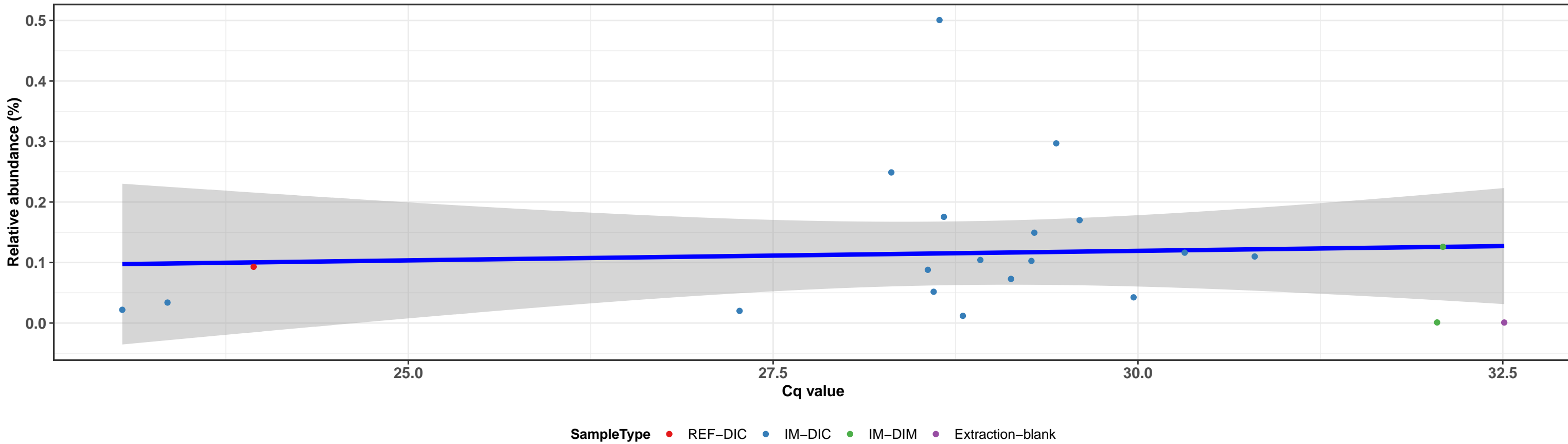
Correlation within: REF−DIC
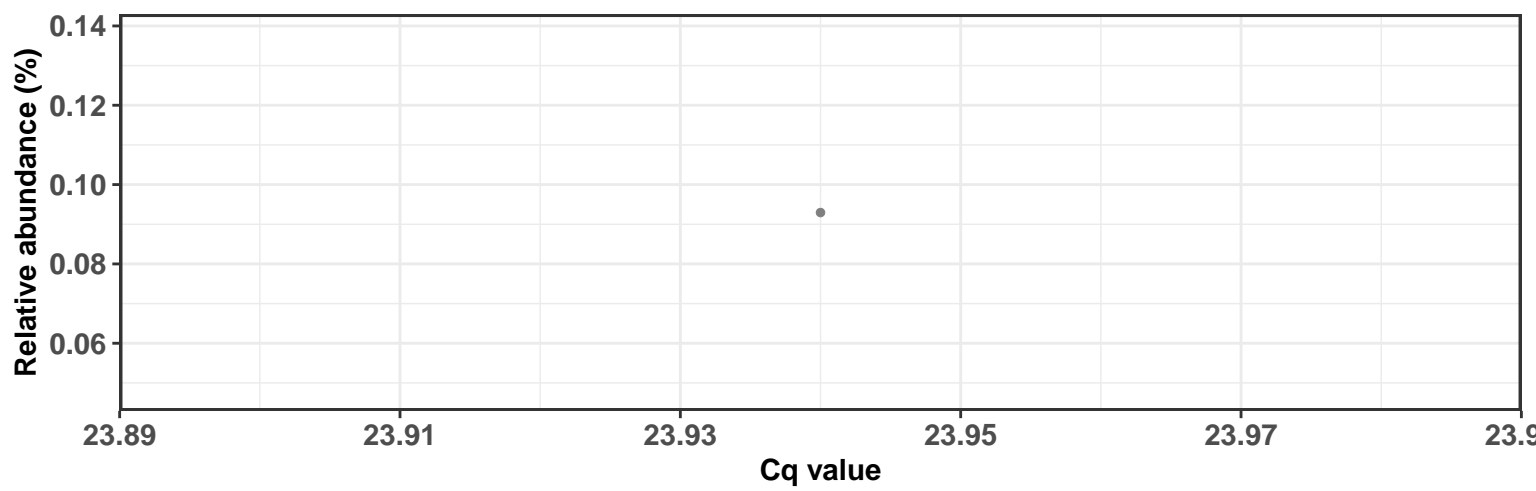
Correlation within: IM−DIC

$\log_e(S) = 6.439$, $p = 0.150$, $\hat{\rho}_{Spearman} = 0.354$, $CI_{95\%}$ [−0.110, 0.839], $n_{pairs} = 18$

Correlation within: IM−DIM
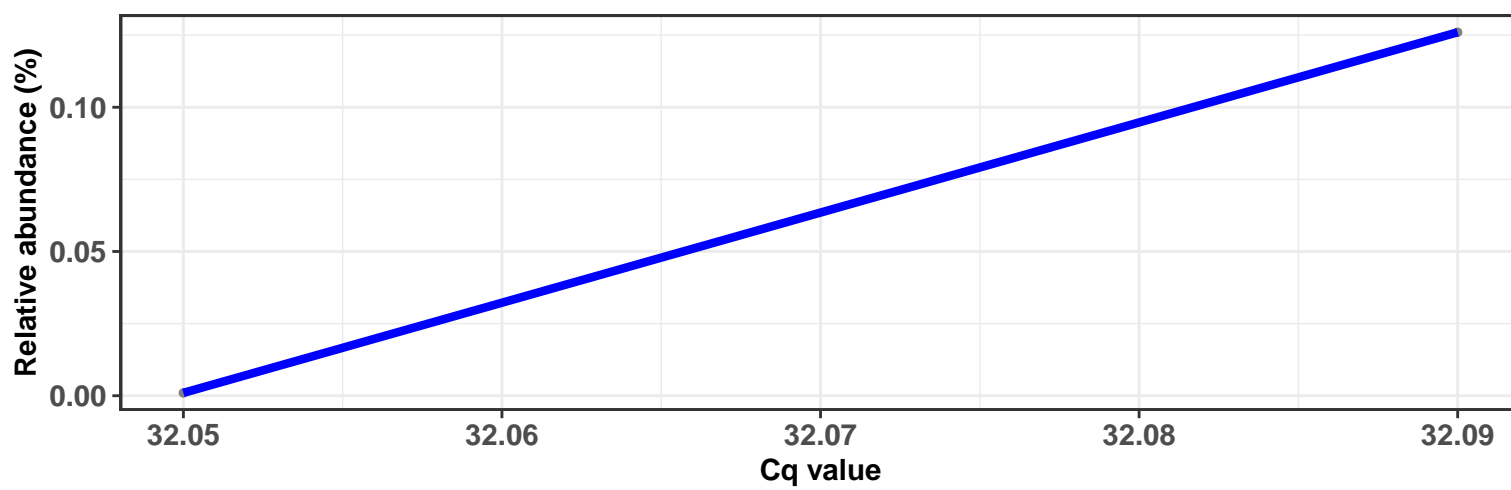
k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; NA; NA

Correlation with all samples

$\log_e(S) = 5.011$, $p = 0.021$, $\hat{\rho}_{Spearman} = -0.786$, $CI_{95\%}$ [-1.354, -0.331], $n_{pairs} = 8$
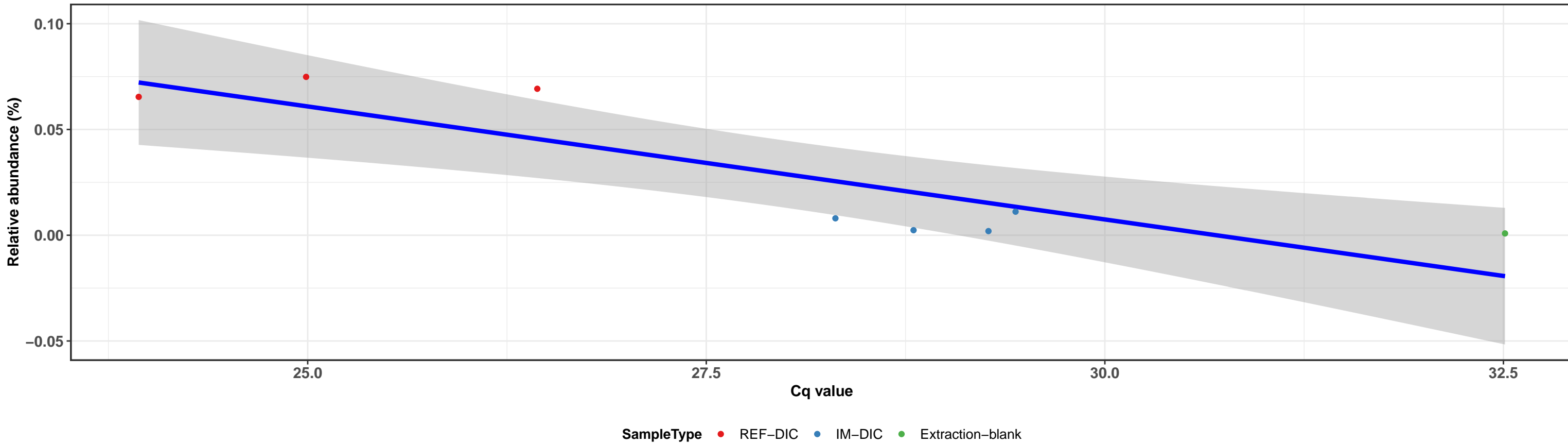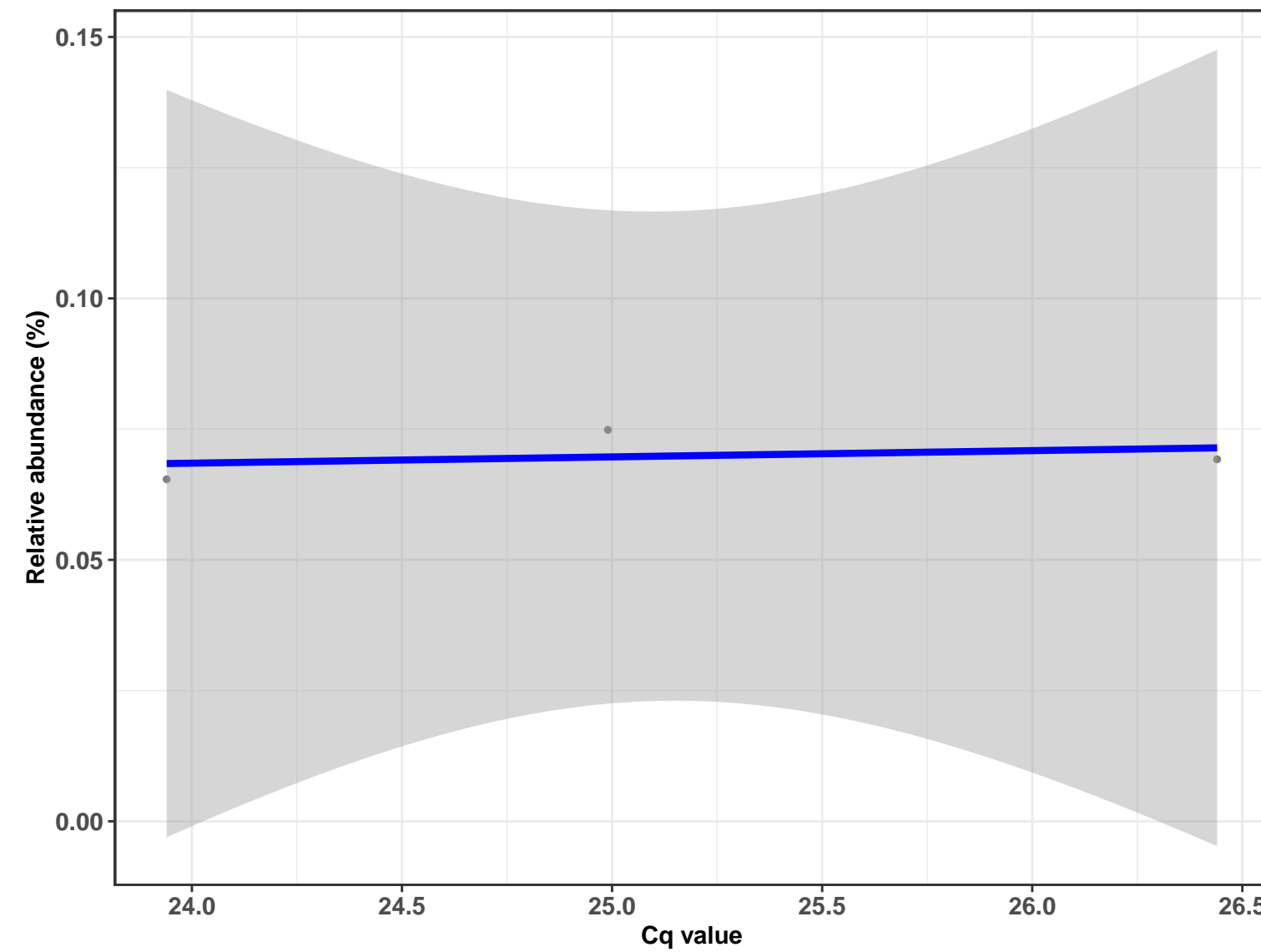
SampleType ● REF−DIC ● IM−DIC ● Extraction−blank
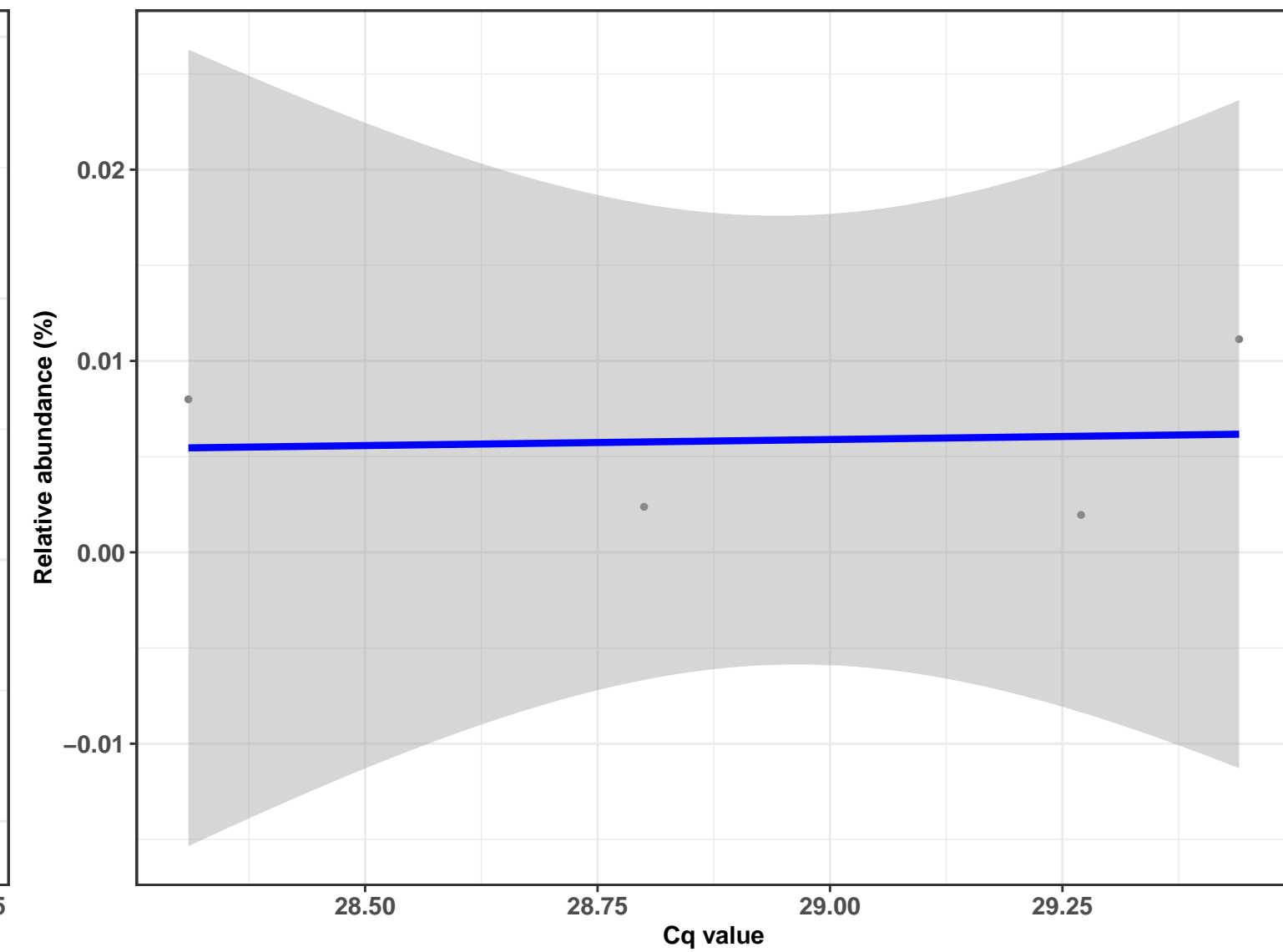
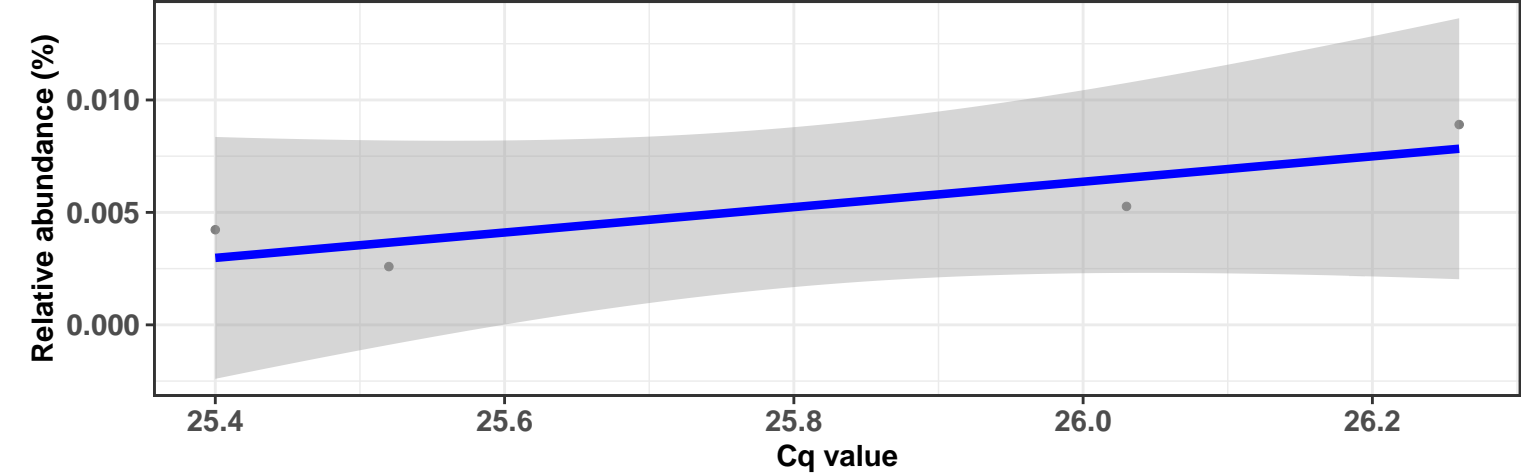# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa
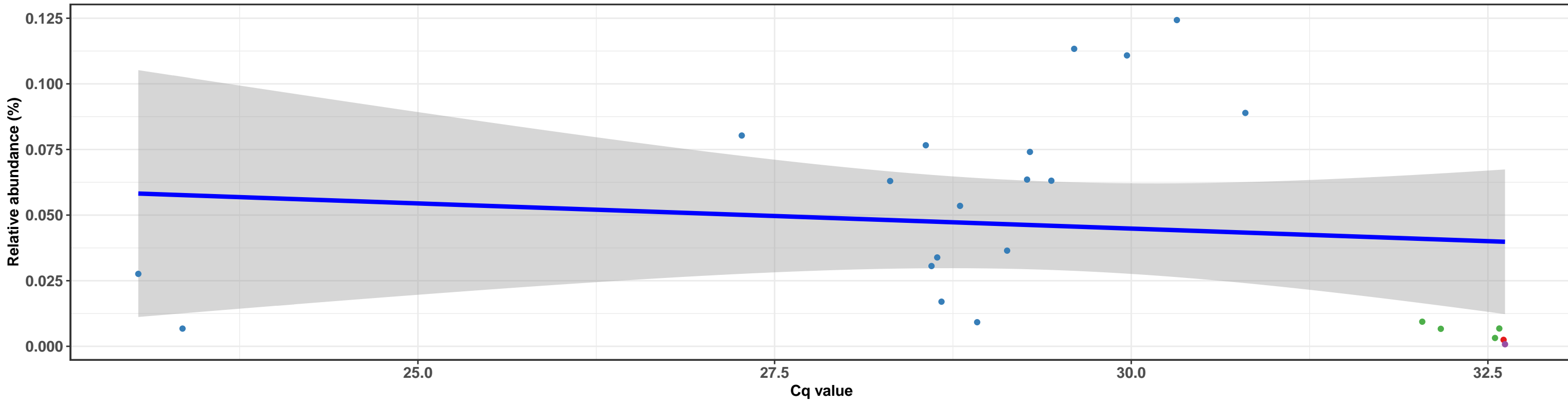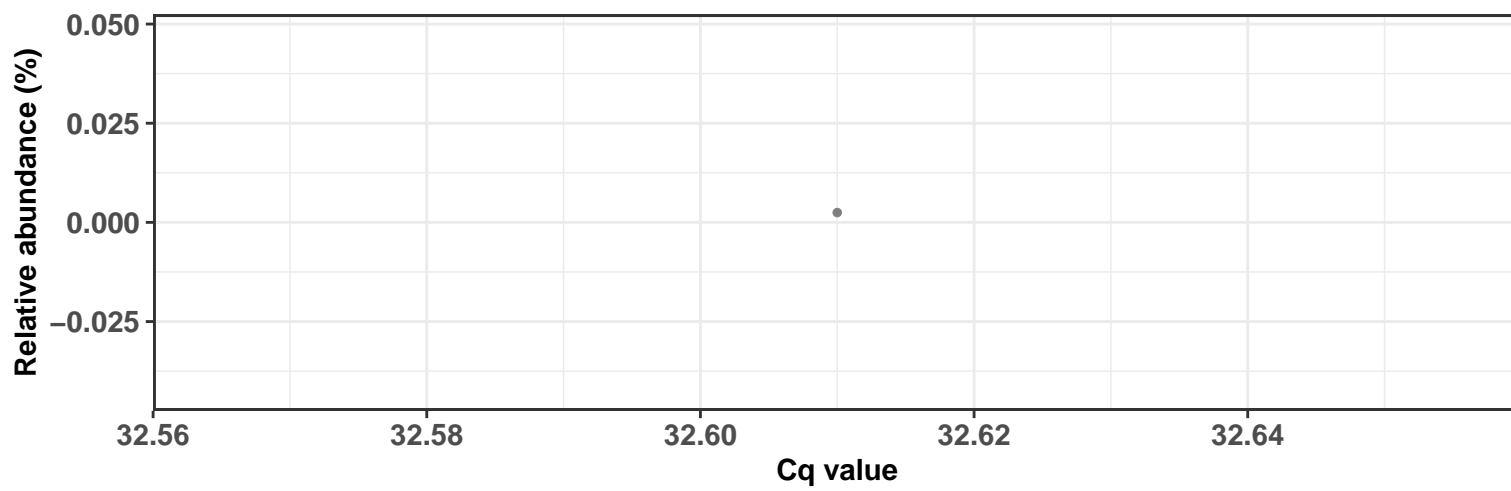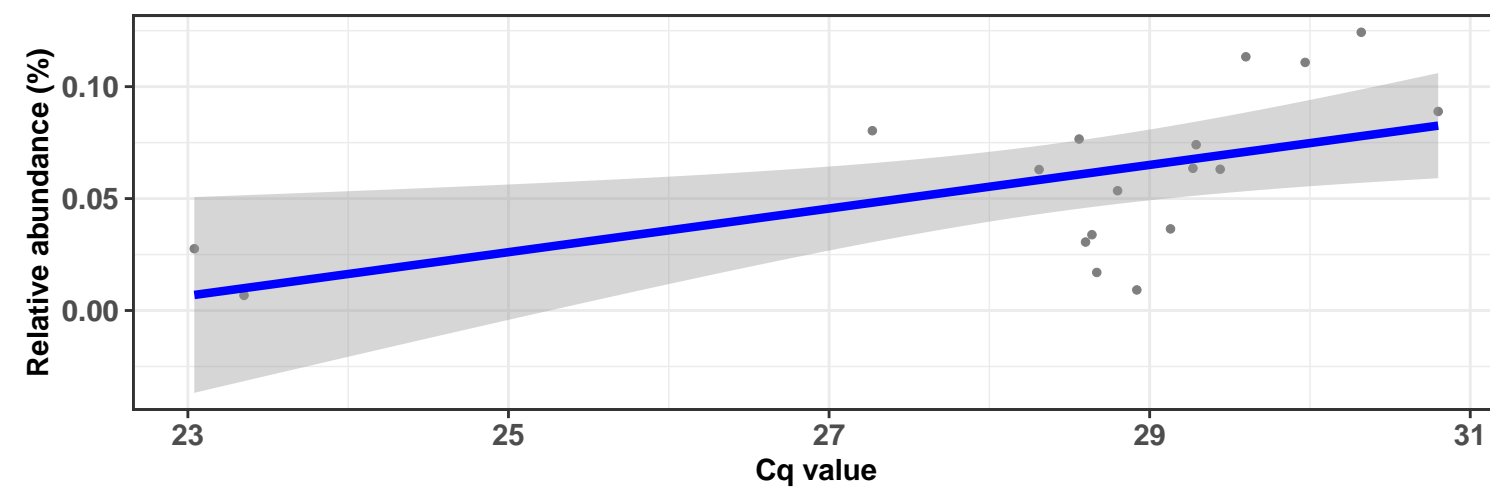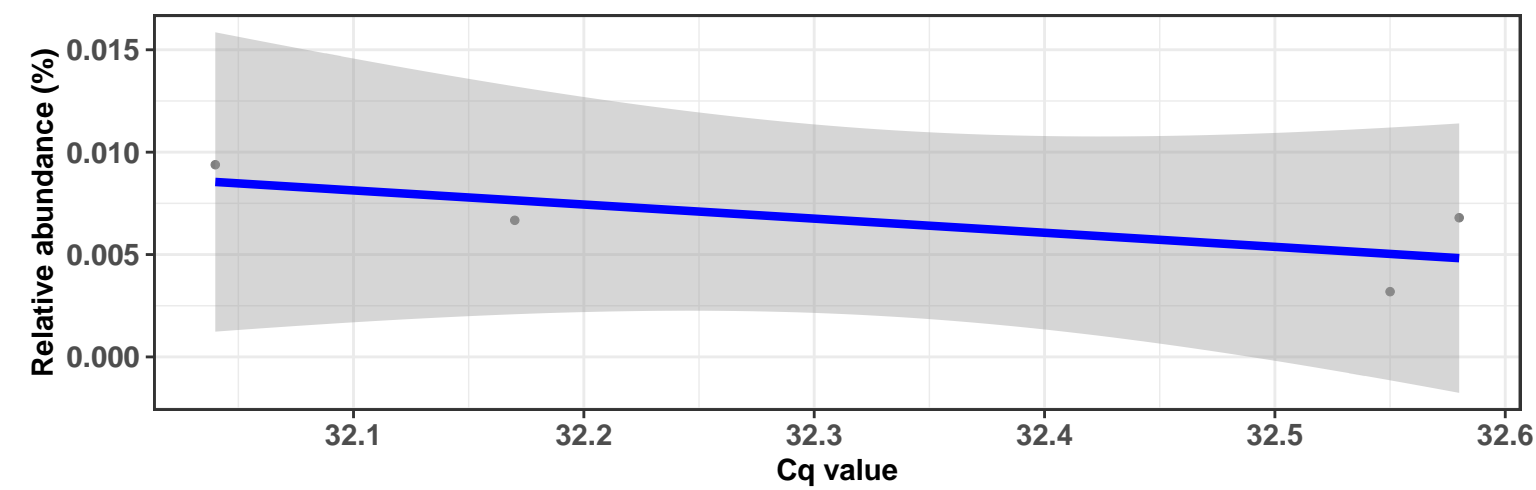
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Gracilibacillus; Ambiguous_taxa
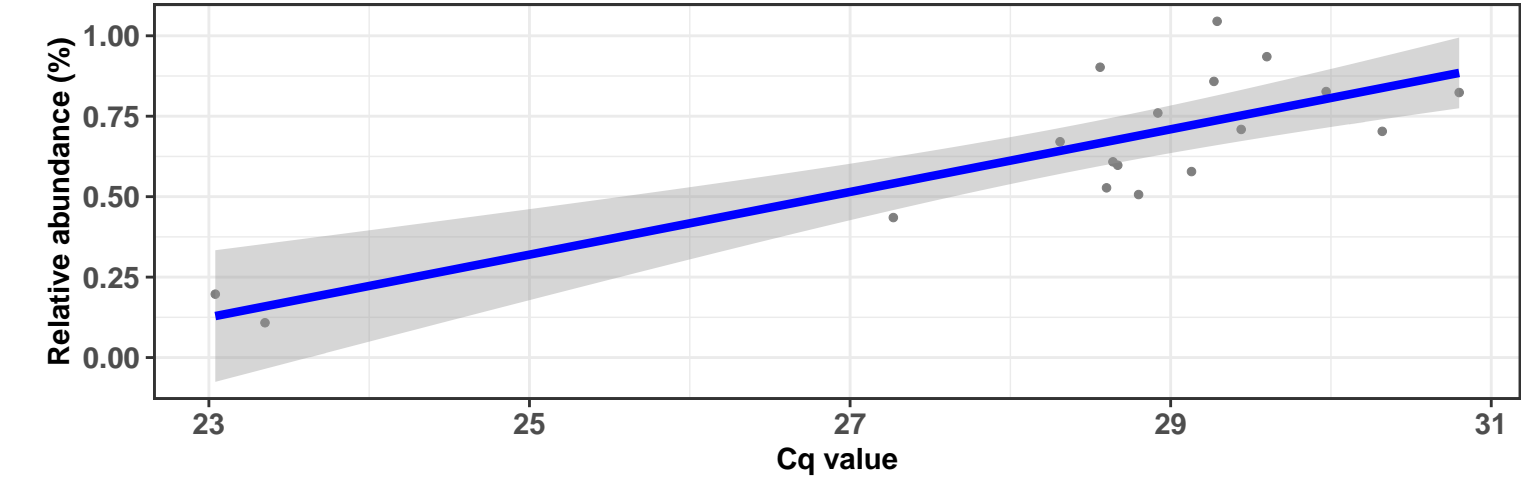
Correlation with all samples

$\log_e(S) = 7.464$, $p = 0.567$, $\widehat{\rho}_{Spearman} = -0.132$, $CI_{95\%}$ [−0.716, 0.425], $n_{pairs} = 21$

SampleType • IM−DIC • IM−DIM • Extraction−blank
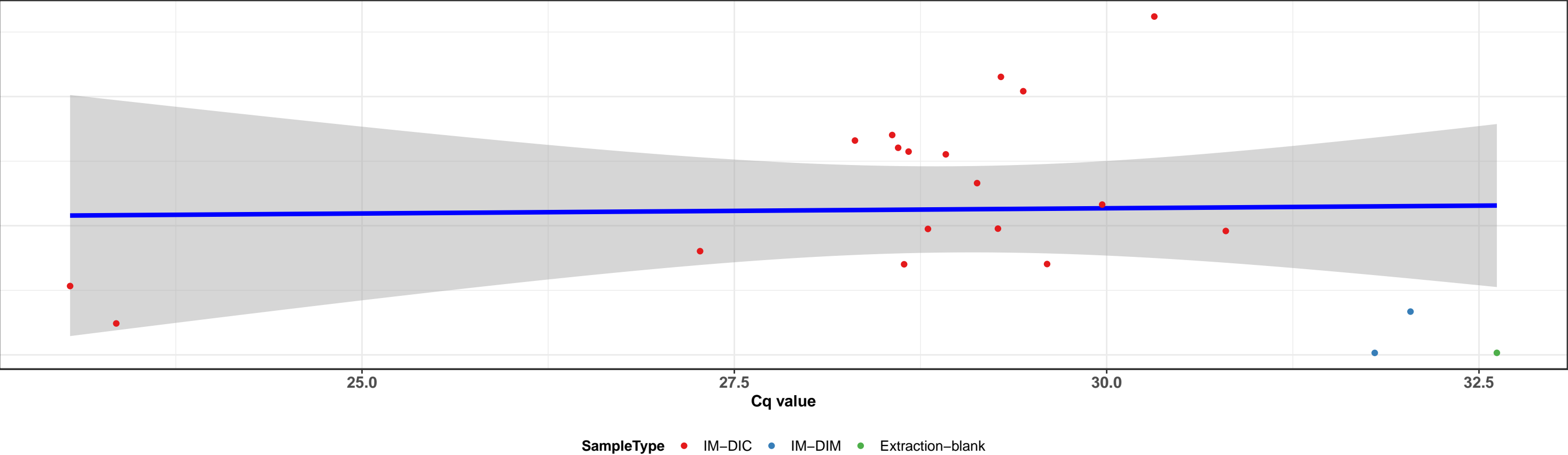
Correlation within: IM−DIC

$\log_e(S) = 6.468$, $p = 0.174$, $\widehat{\rho}_{Spearman} = 0.335$, $CI_{95\%}$ [−0.164, 0.880], $n_{pairs} = 18$
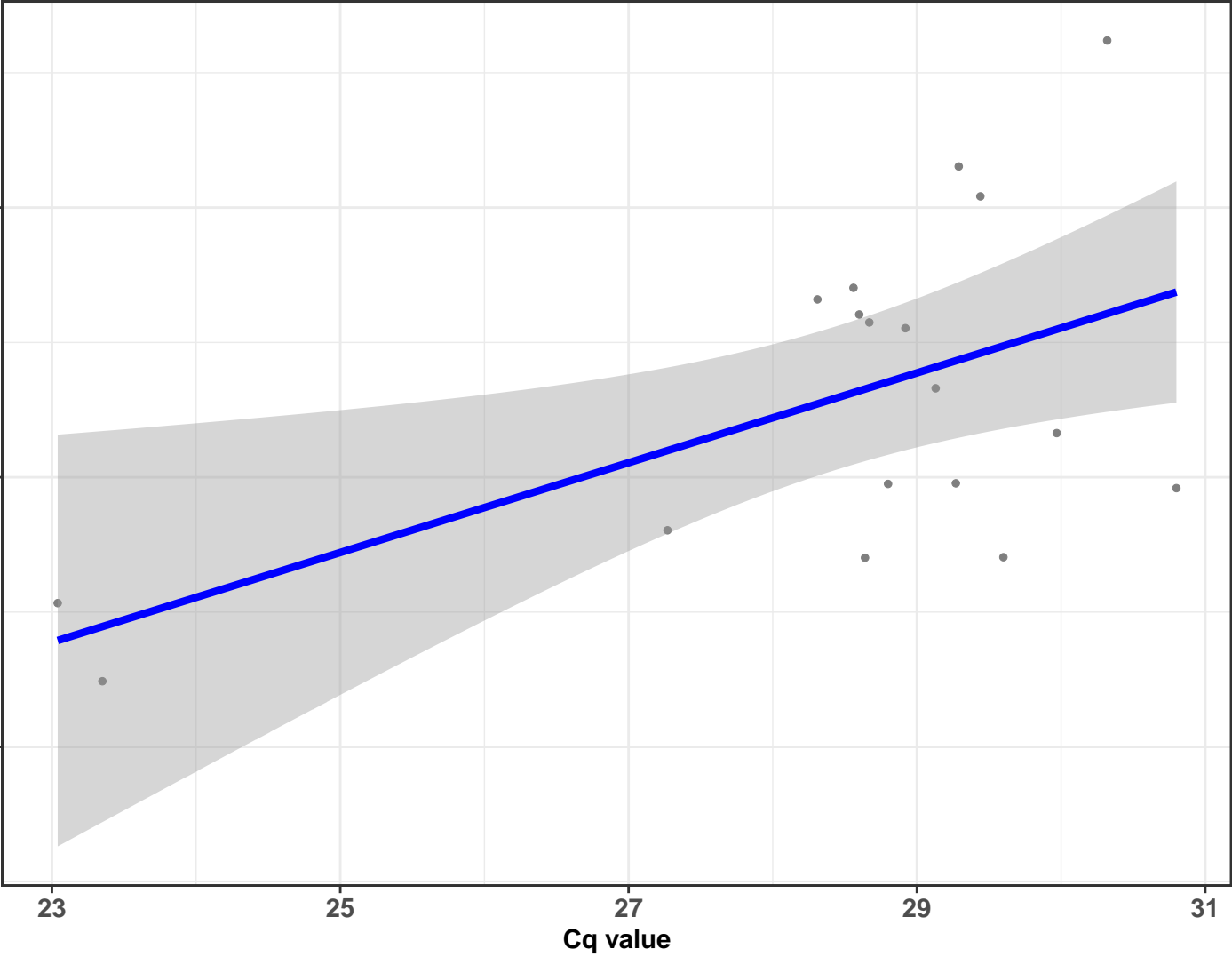
Correlation within: IM−DIM
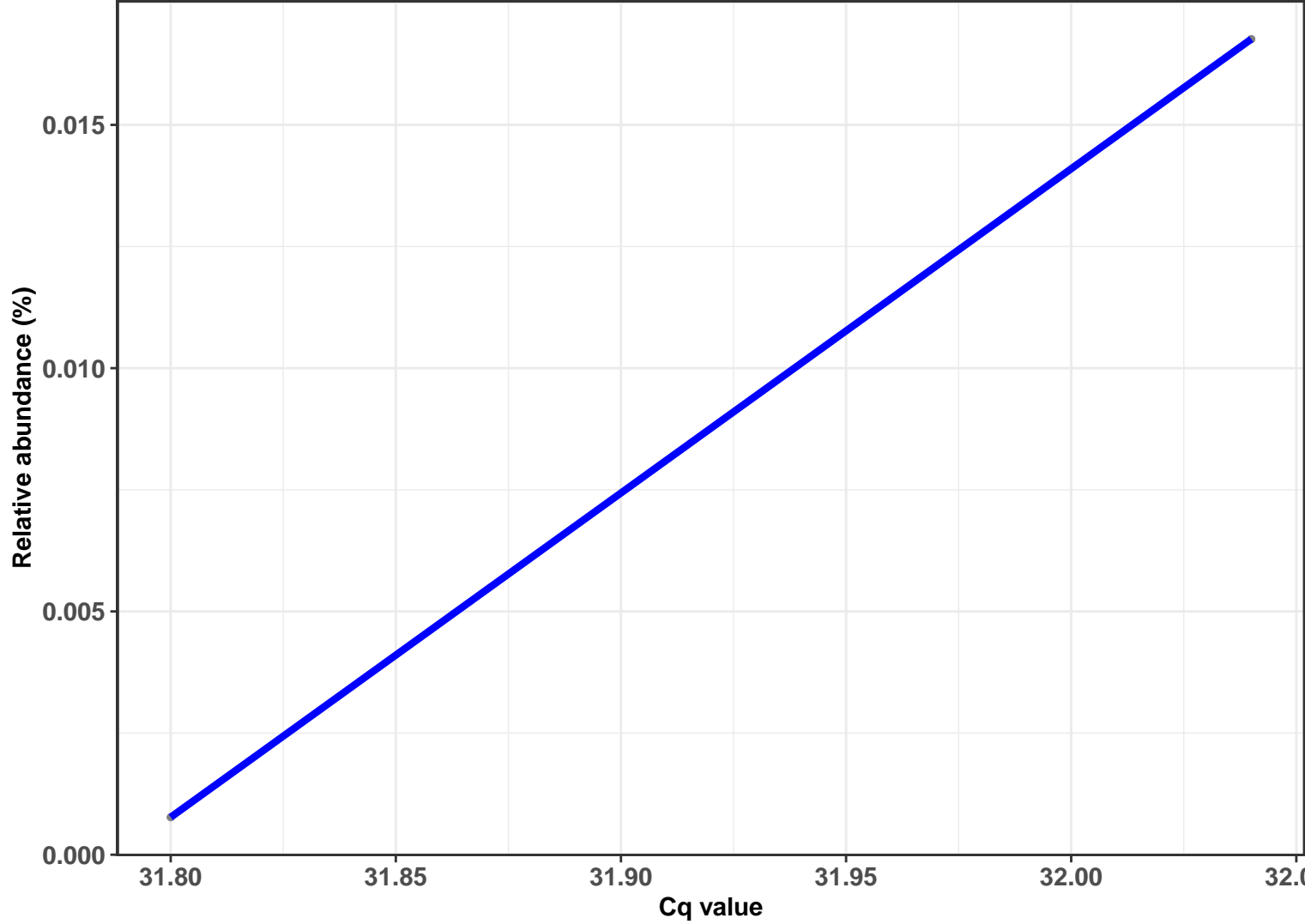
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

Correlation with all samples

$\log_e(S) = 8.807$, $p = 0.519$, $\hat{\rho}_{Spearman} = -0.116$, $CI_{95\%}$ [−0.468, 0.290], $n_{pairs} = 33$

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank
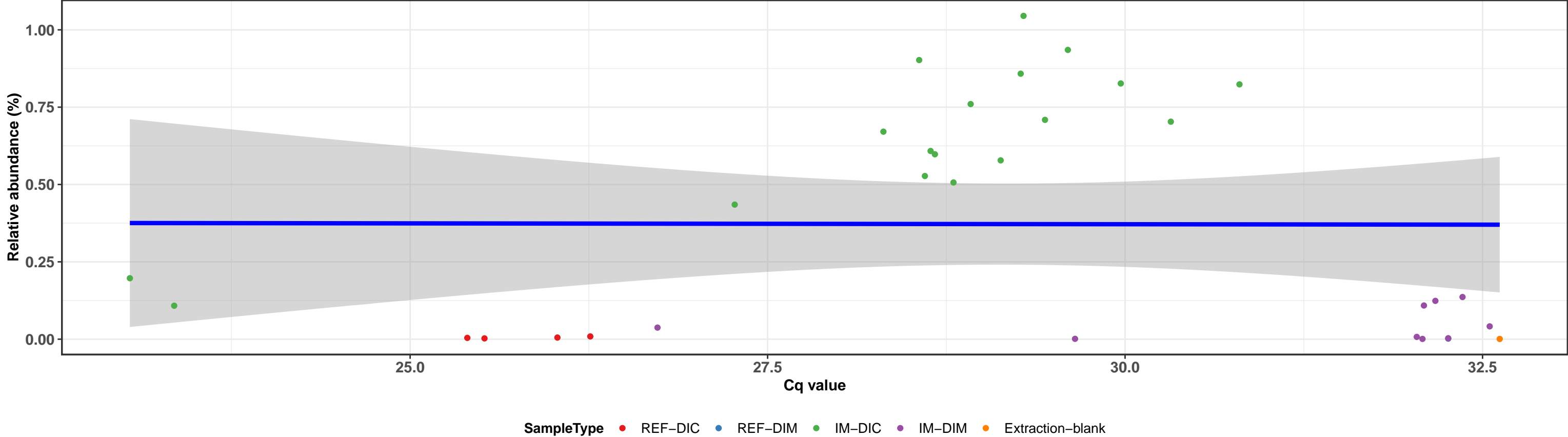
Correlation within: REF−DIC

Correlation within: REF−DIM
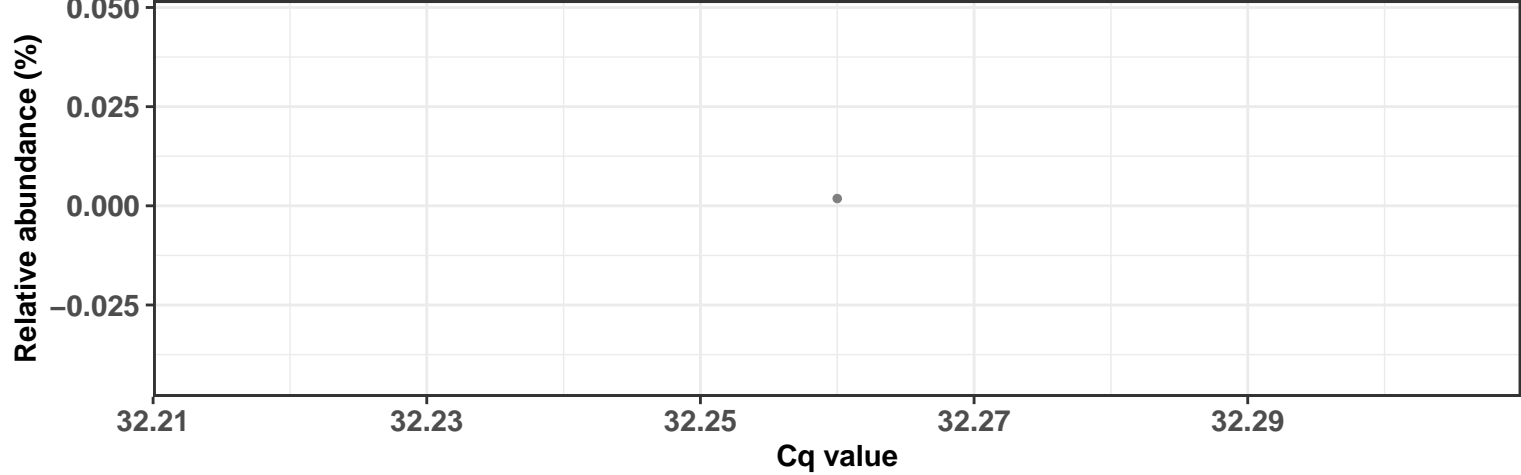
Correlation within: IM−DIC

$\log_e(S) = 5.799$, $p = 0.003$, $\hat{\rho}_{Spearman} = 0.659$, $CI_{95\%}$ [0.380, 1.018], $n_{pairs} = 18$

Correlation within: IM−DIM

$\log_e(S) = 4.094$, $p = 0.170$, $\hat{\rho}_{Spearman} = 0.500$, $CI_{95\%}$ [0.055, 1.091], $n_{pairs} = 9$
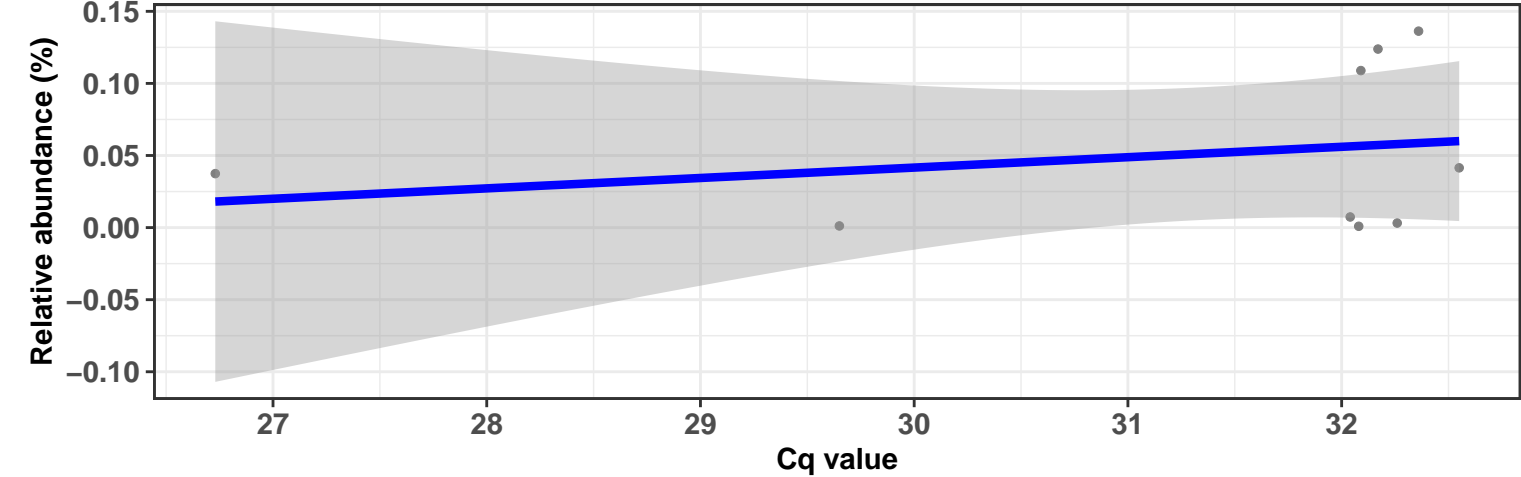
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA
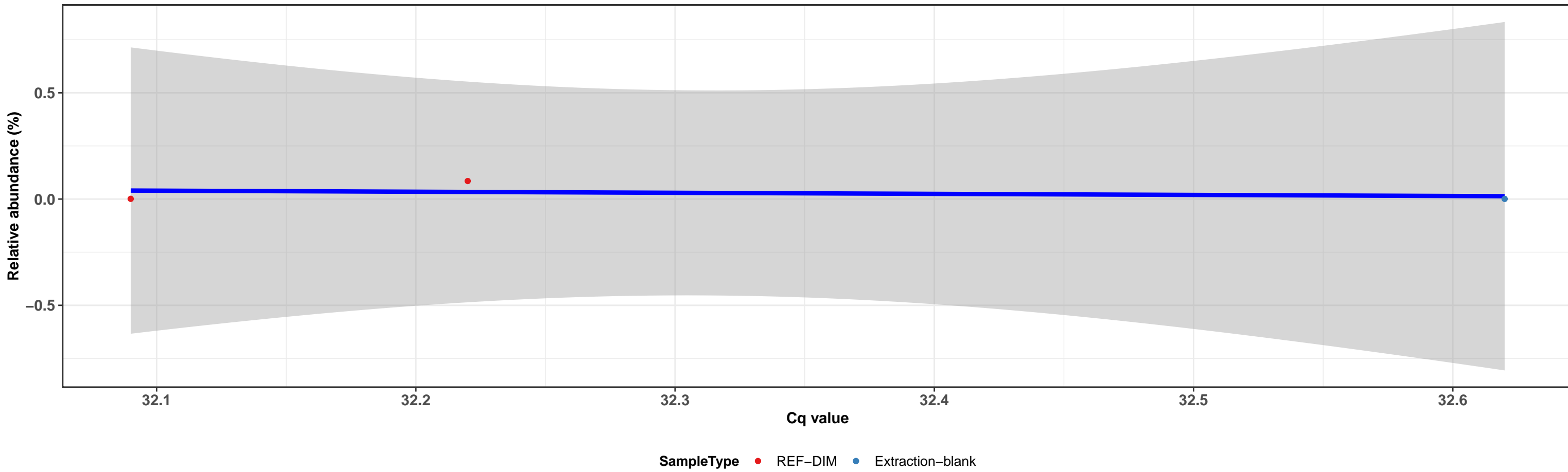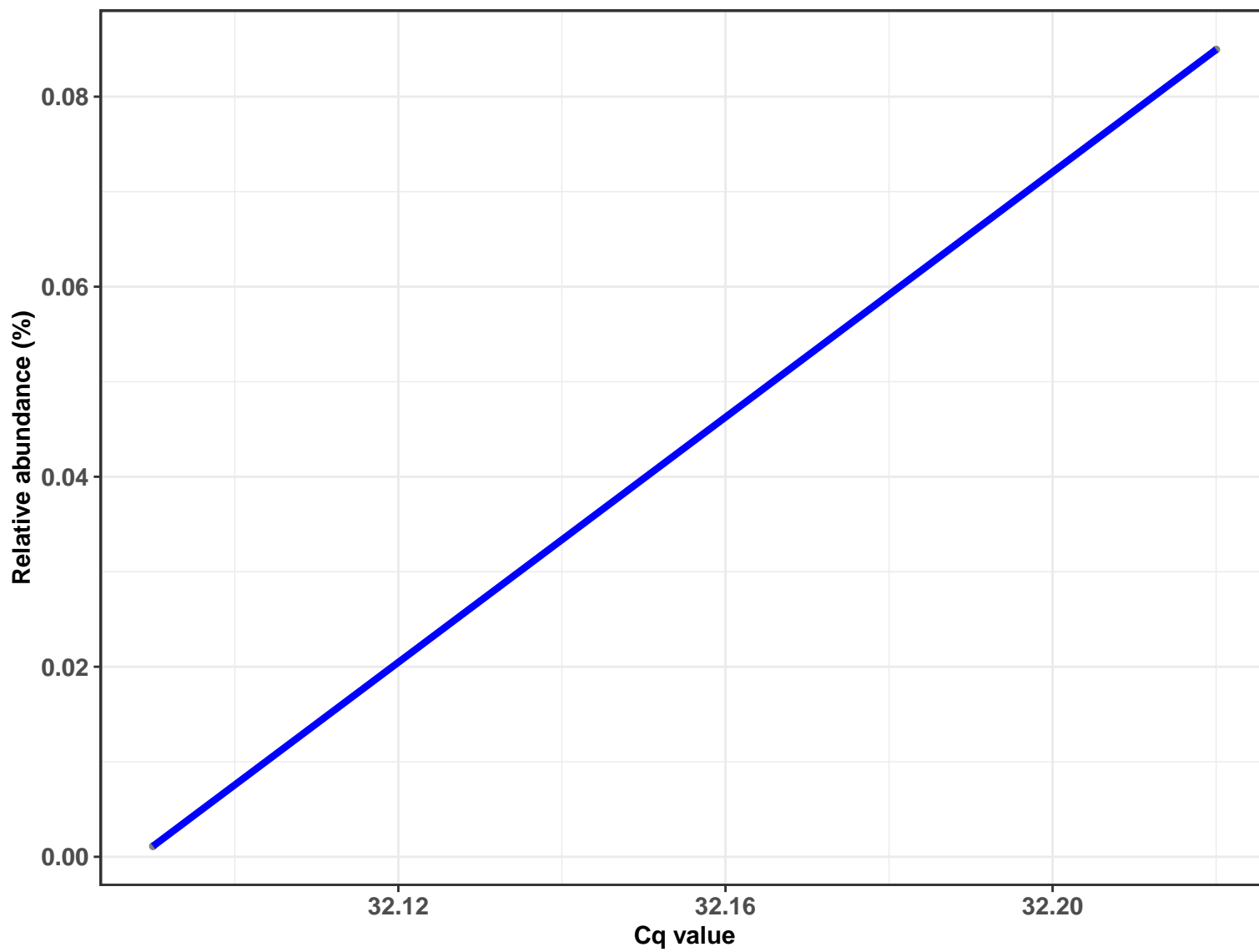
k__Bacteria; p__Tenericutes; c__Mollicutes; o__Mycoplasmatales; f__Mycoplasmataceae; g__Mycoplasma; s__uncultured Mycoplasma sp.
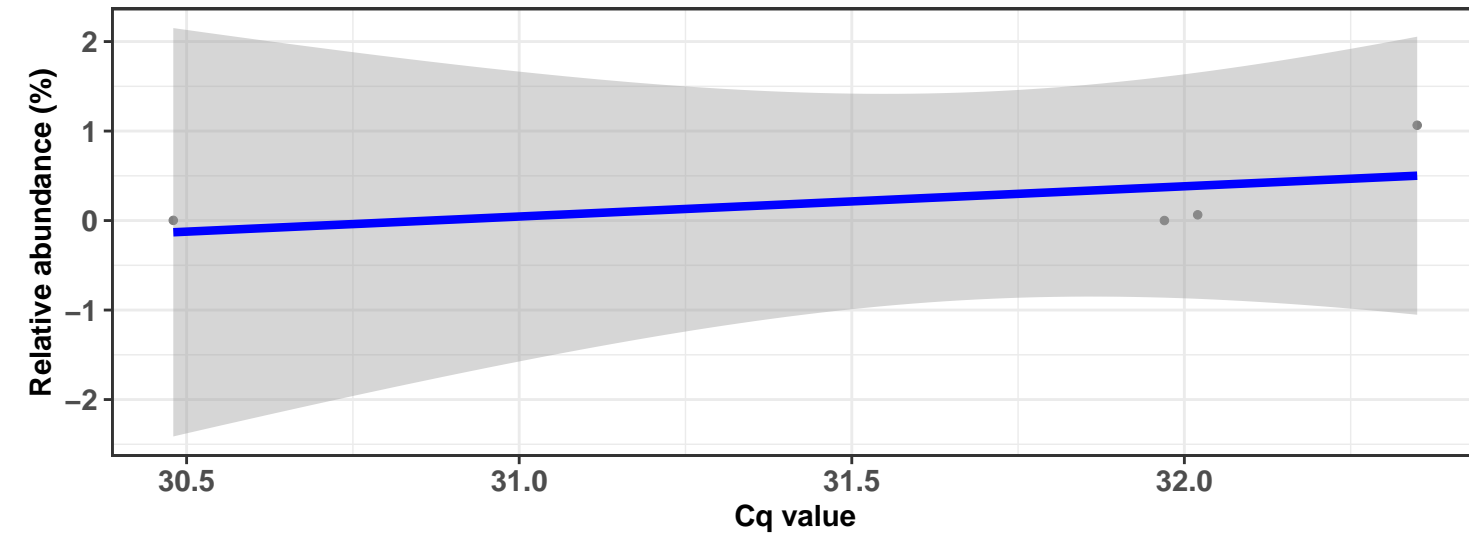

Correlation with all samples

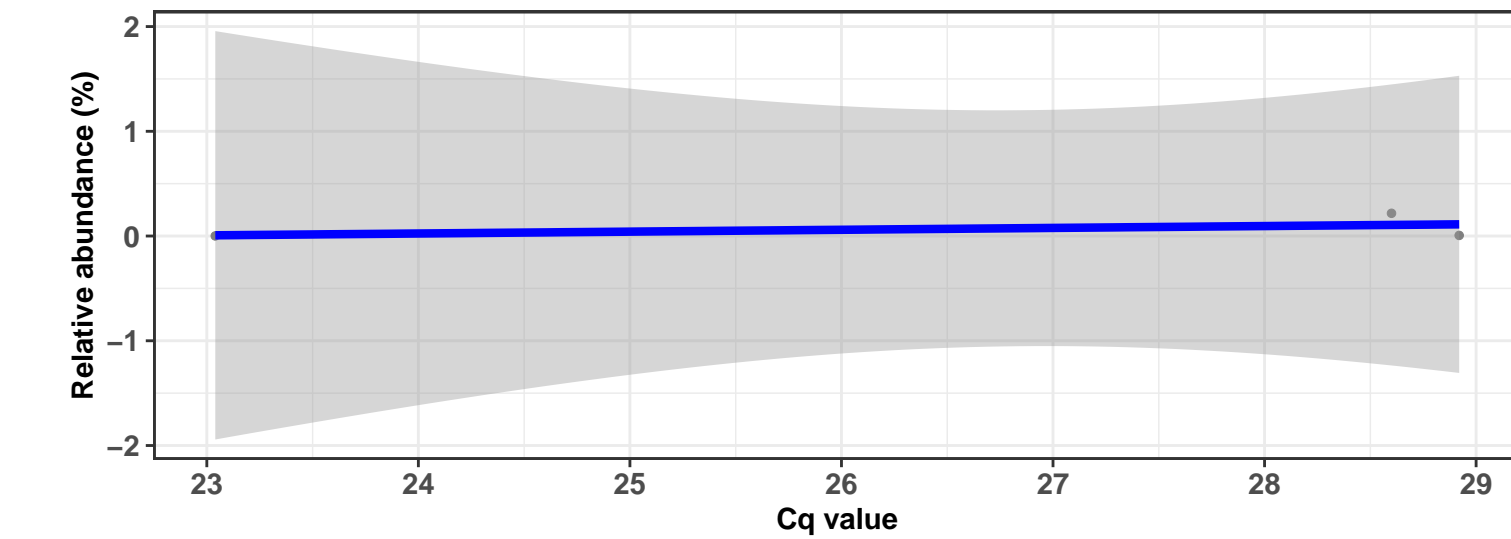$\log_e(S) = 6.306$, $p = 0.198$, $\hat{\rho}_{Spearman} = 0.328$, $CI_{95\%}$ [−0.214, 0.808], $n_{pairs} = 17$
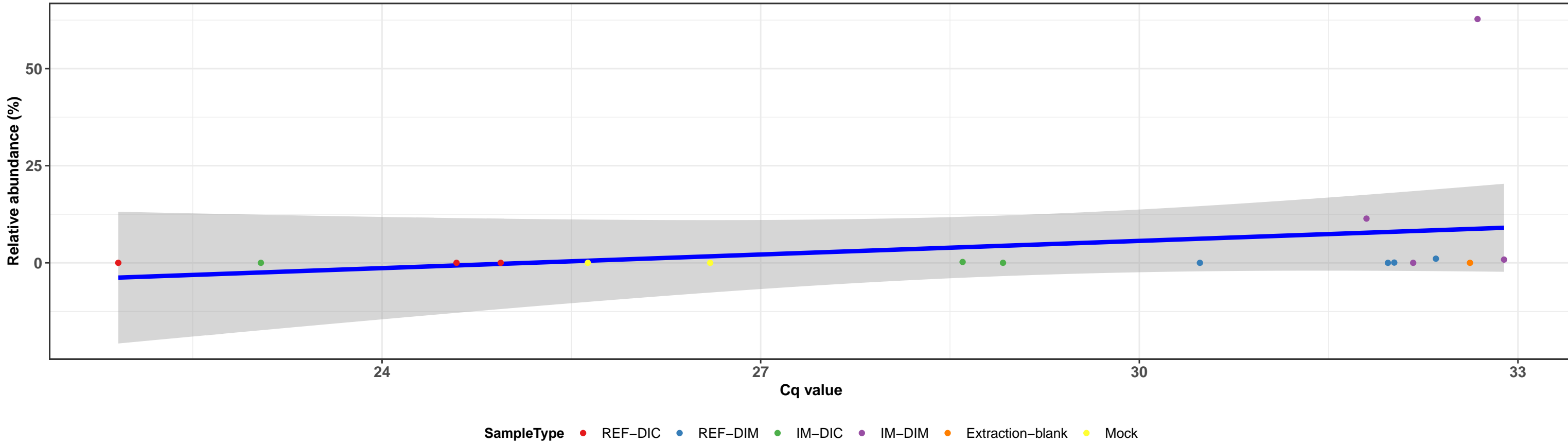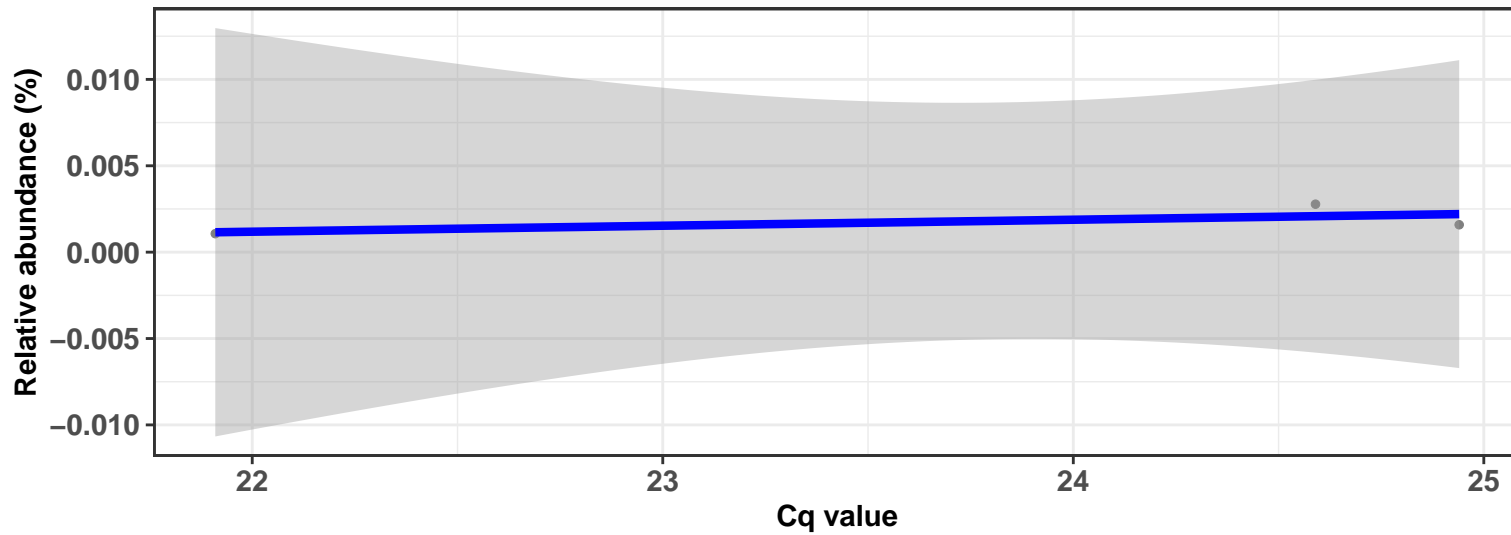
SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Extraction−blank ● Mock
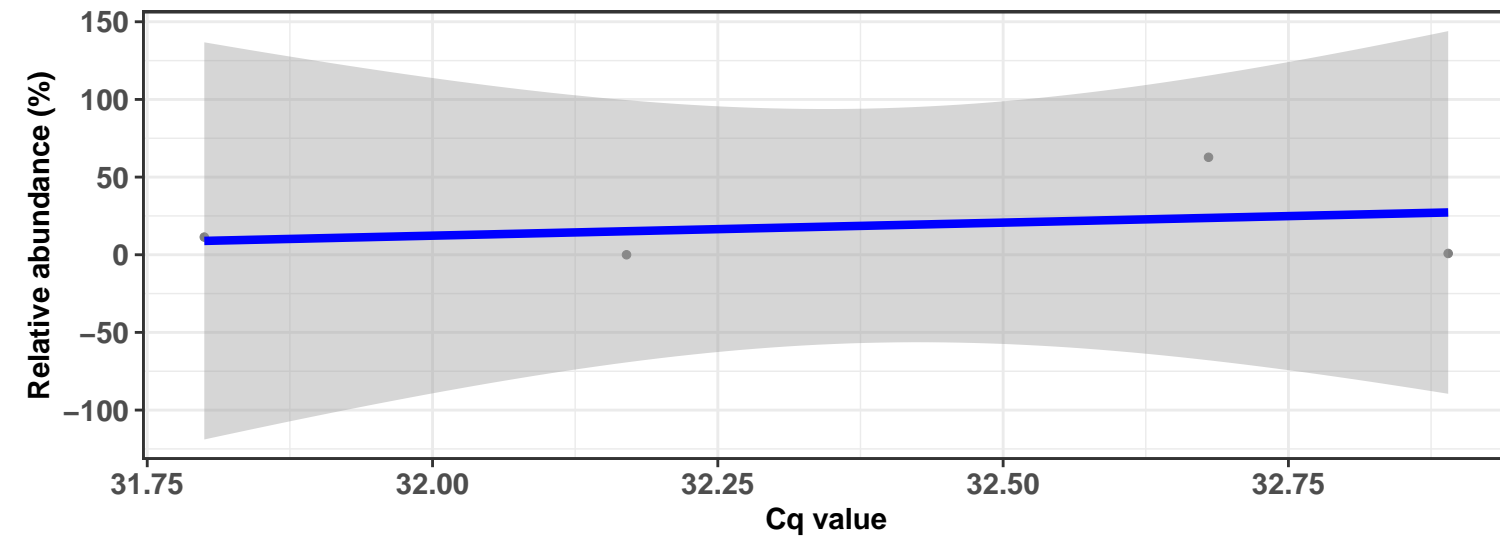
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; NA

Correlation with all samples

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{Spearman} = 0.714$, $CI_{95\%}$ [0.071, 1.467], $n_{pairs} = 6$
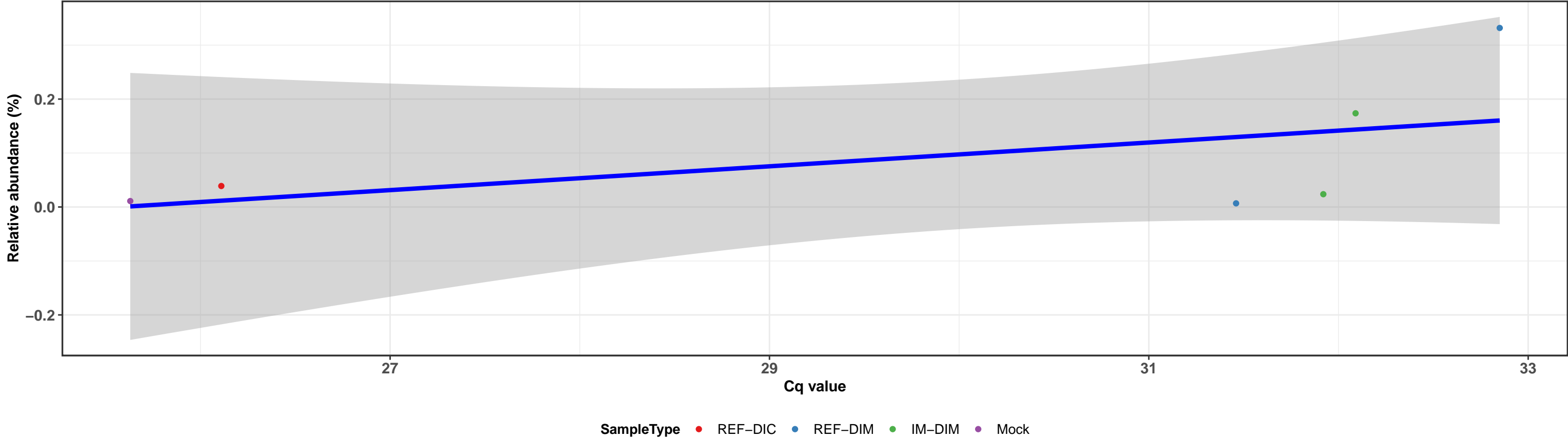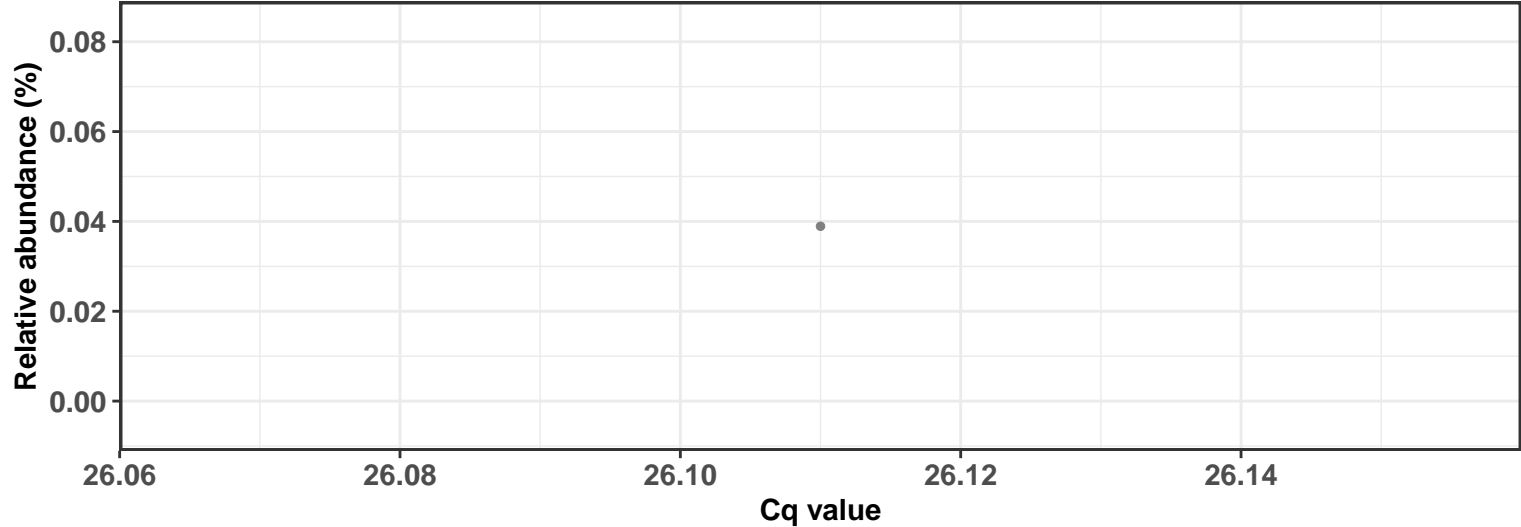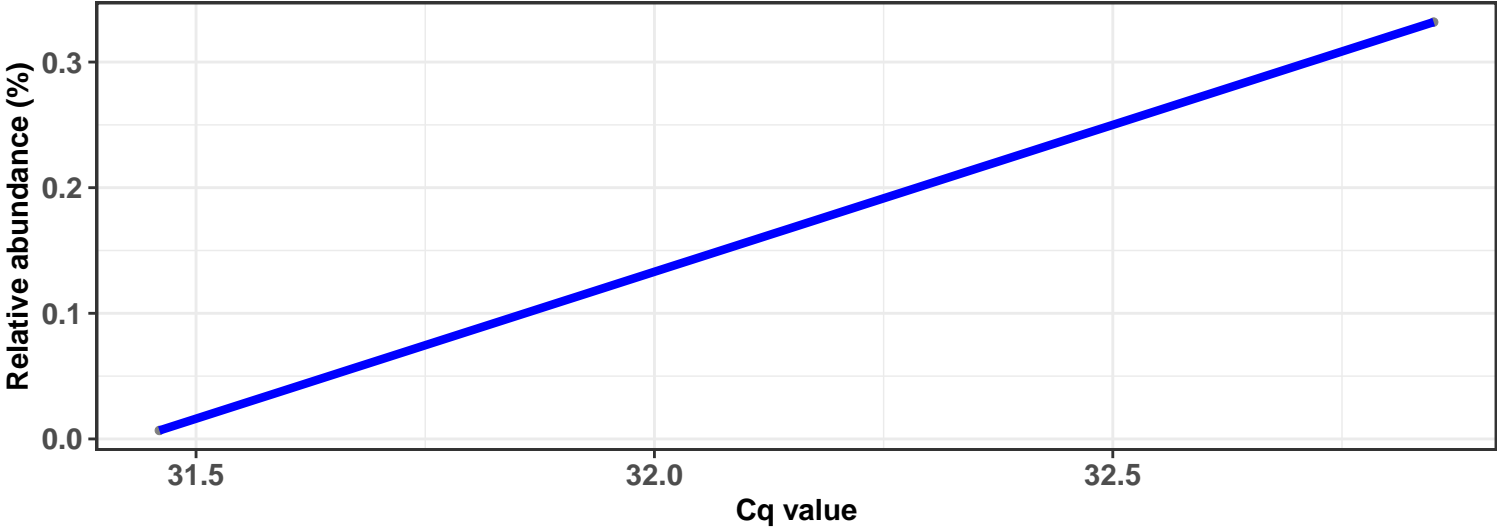
SampleType ● REF–DIC ● REF–DIM ● IM–DIM ● Mock

Correlation within: REF–DIC

Correlation within: REF–DIM

Correlation within: IM–DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus
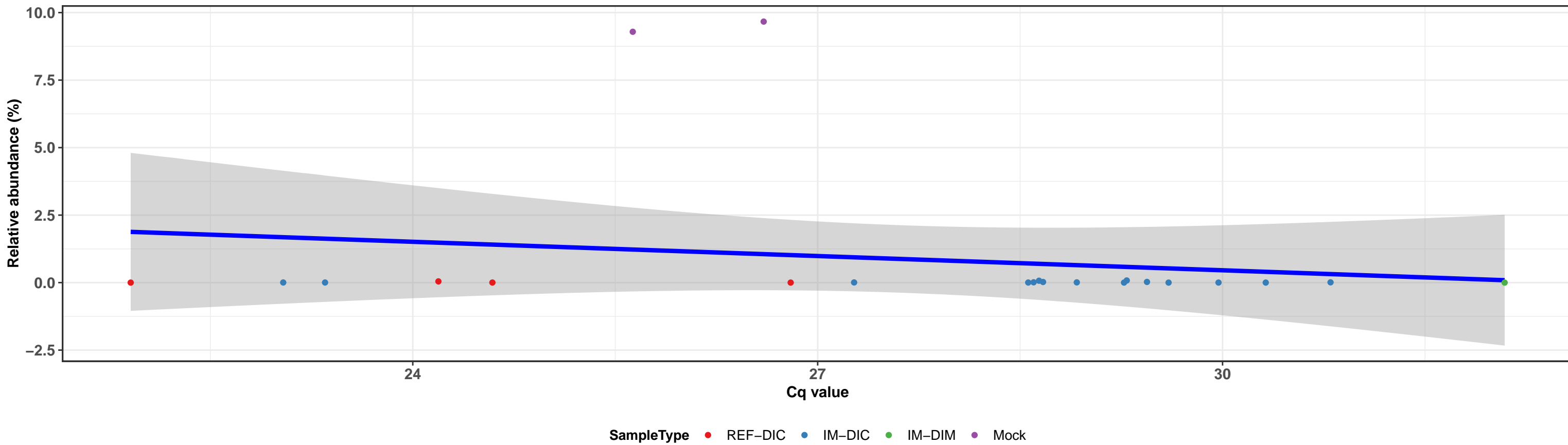
Correlation with all samples

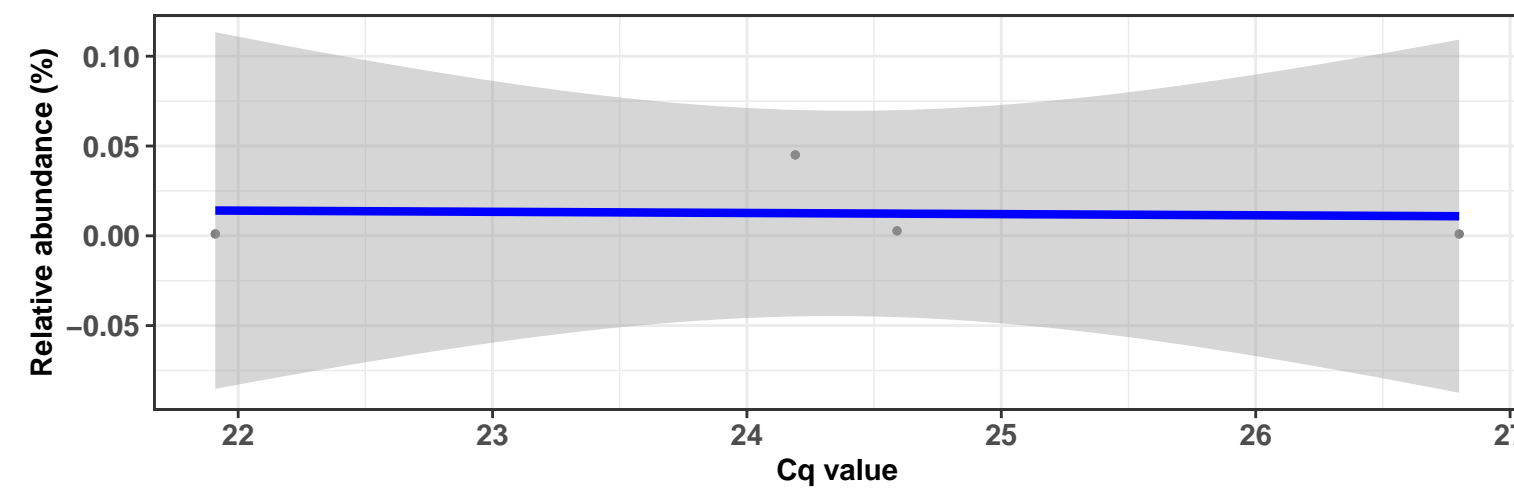SampleType • Mock
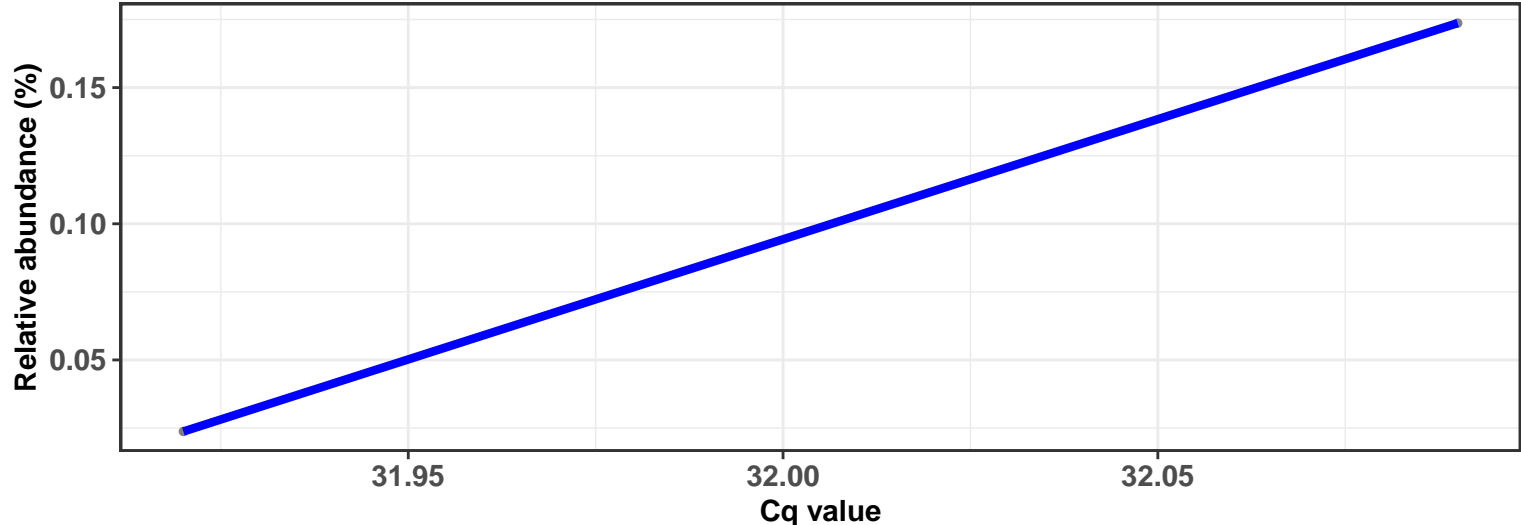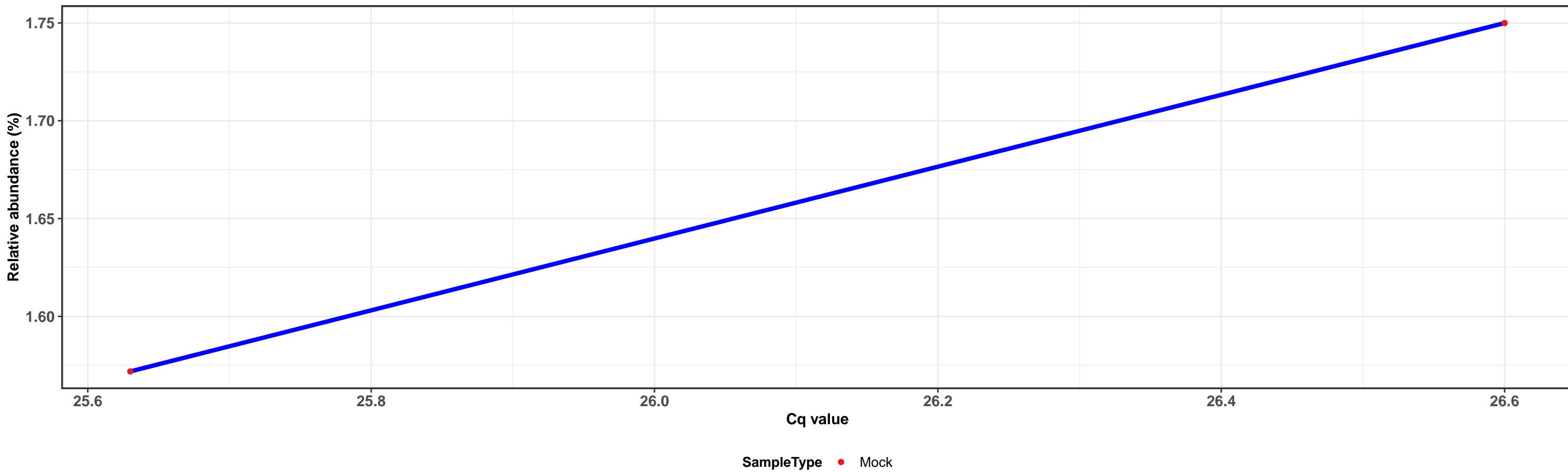
Correlation within:
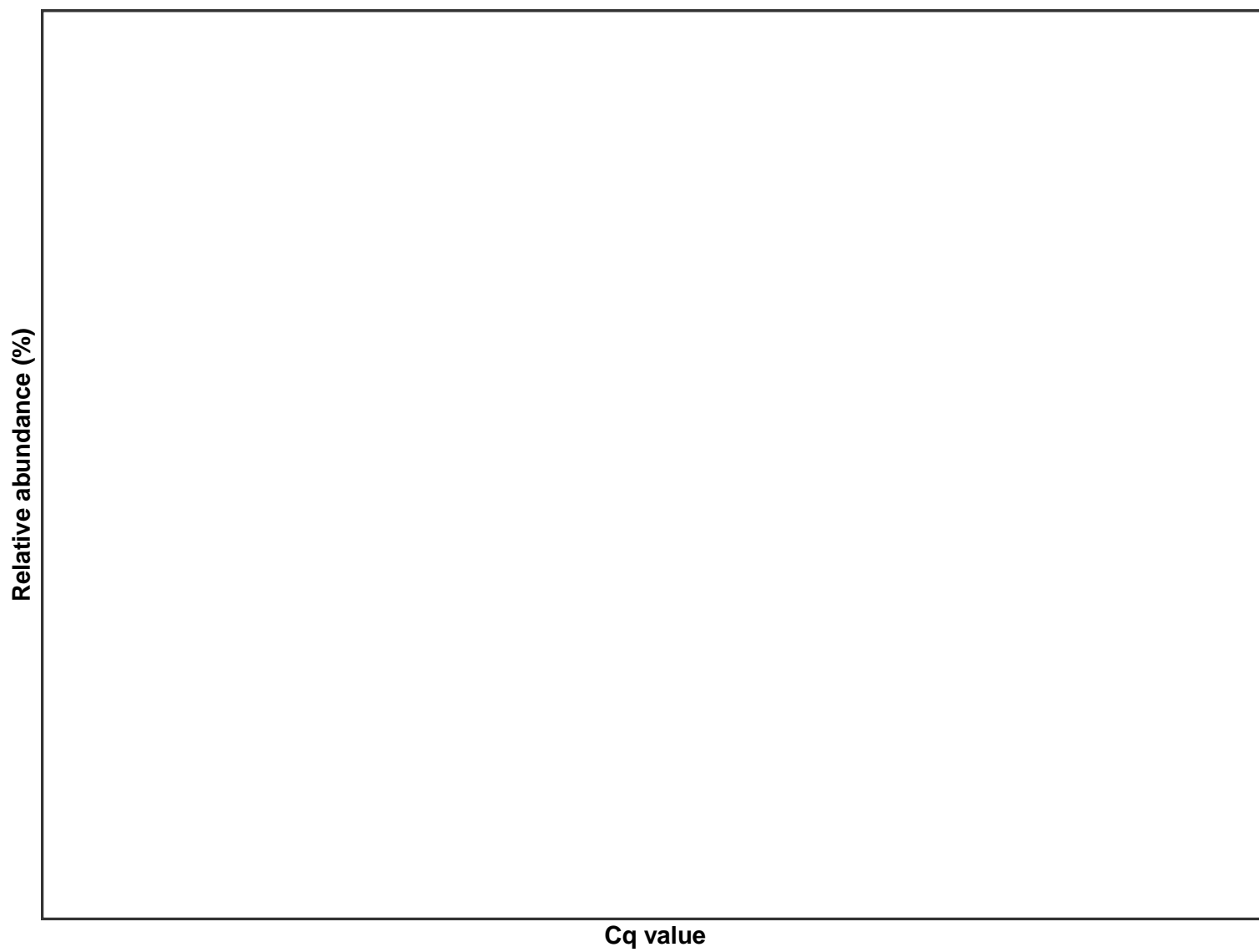
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia−Shigella; NA

Correlation with all samples

$\log_e(S) = 4.585$, $p = 0.052$, $\hat{\rho}_{Spearman} = -0.750$, $CI_{95\%}$ [−1.204, −0.438], $n_{pairs} = 7$
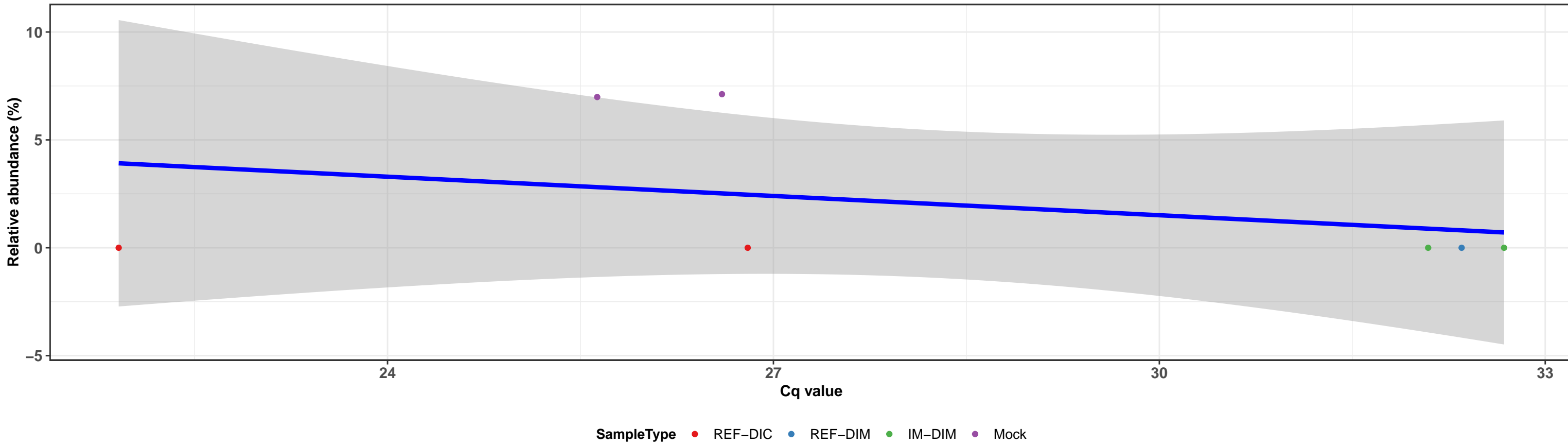
Correlation within: REF−DIC
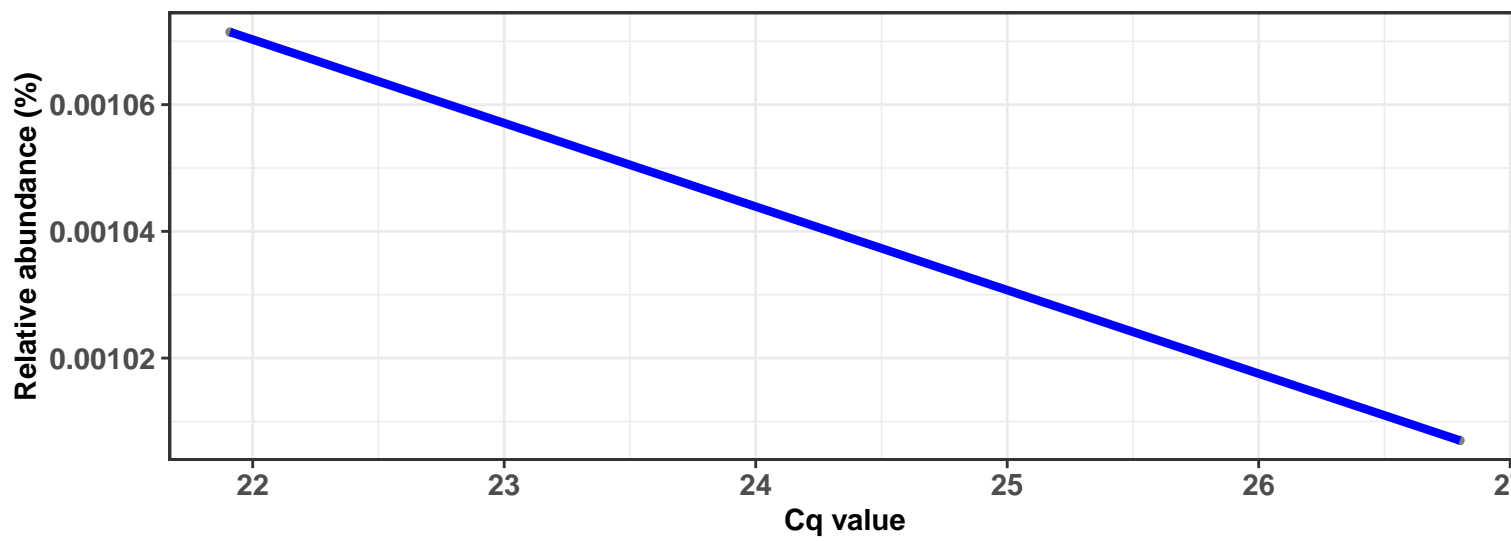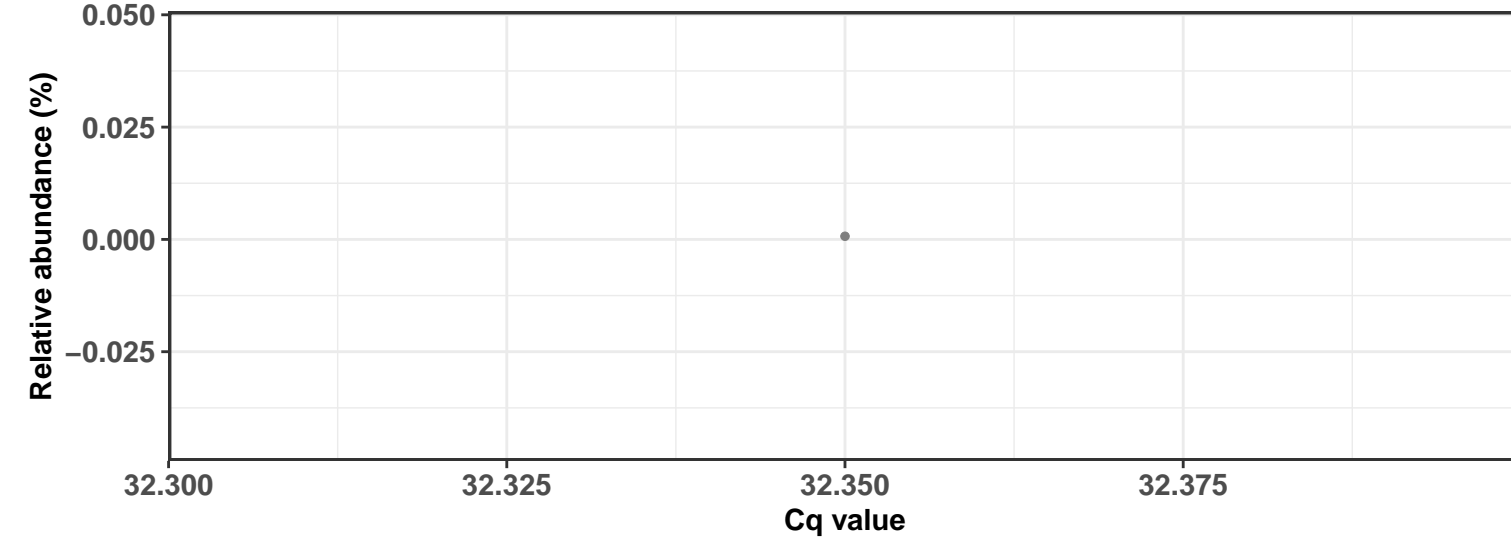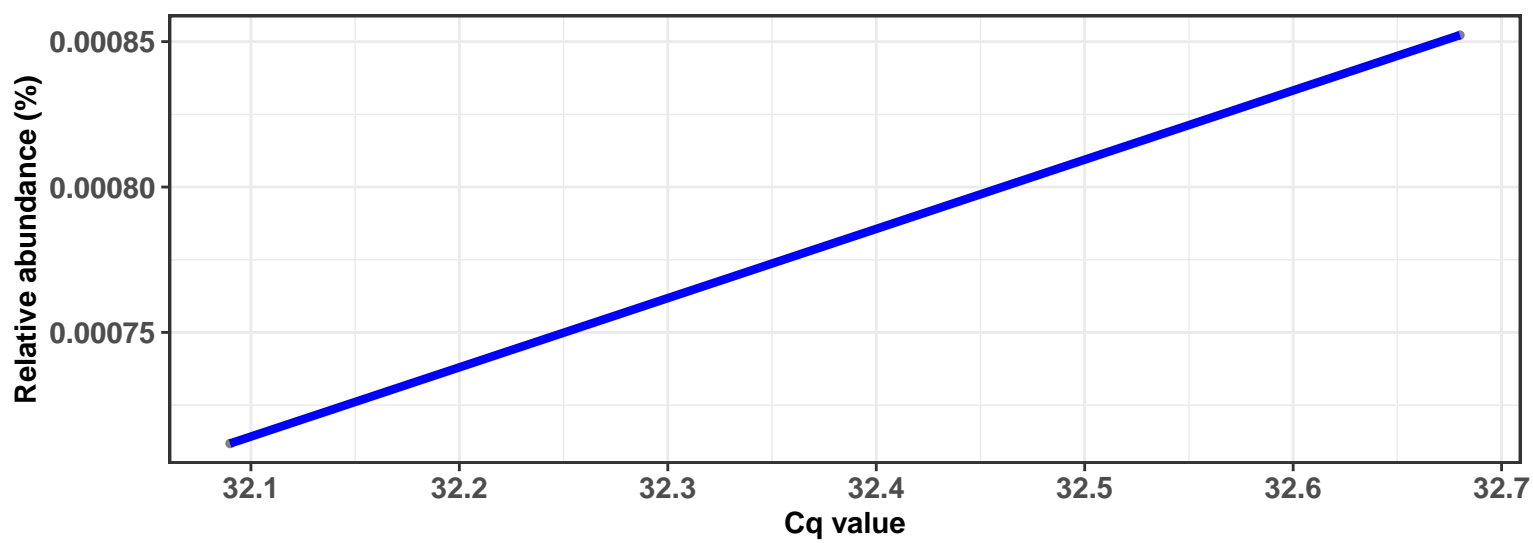
Correlation within: REF−DIM
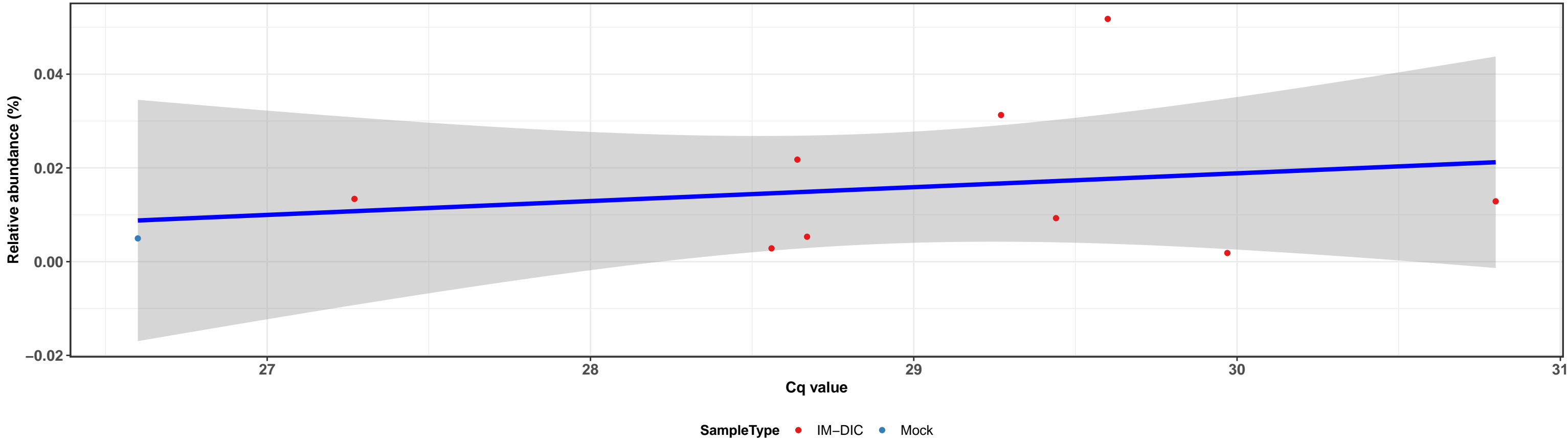
Correlation within: IM−DIM

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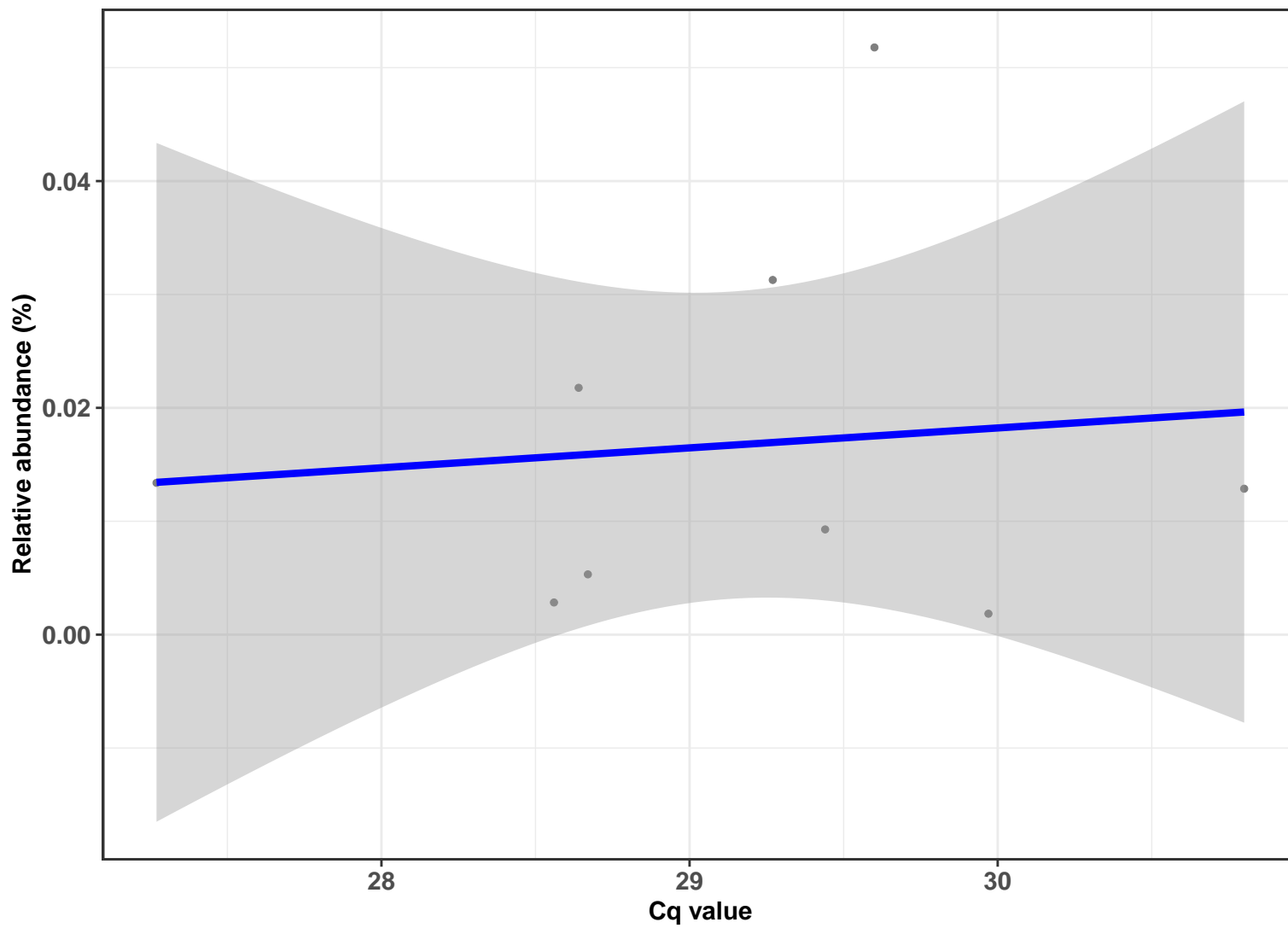

Correlation with all samples

$\log_e(S) = 7.672$, $p = 0.342$, $\hat{\rho}_{Spearman} = -0.213$, $CI_{95\%}$ [−0.620, 0.224], $n_{pairs} = 22$

SampleType ● REF−DIC ● IM−DIC ● IM−DIM ● Mock

Correlation within: REF−DIC

Correlation within: IM−DIC

$\log_e(S) = 6.446$, $p = 0.657$, $\hat{\rho}_{Spearman} = -0.125$, $CI_{95\%}$ [−0.632, 0.331], $n_{pairs} = 15$
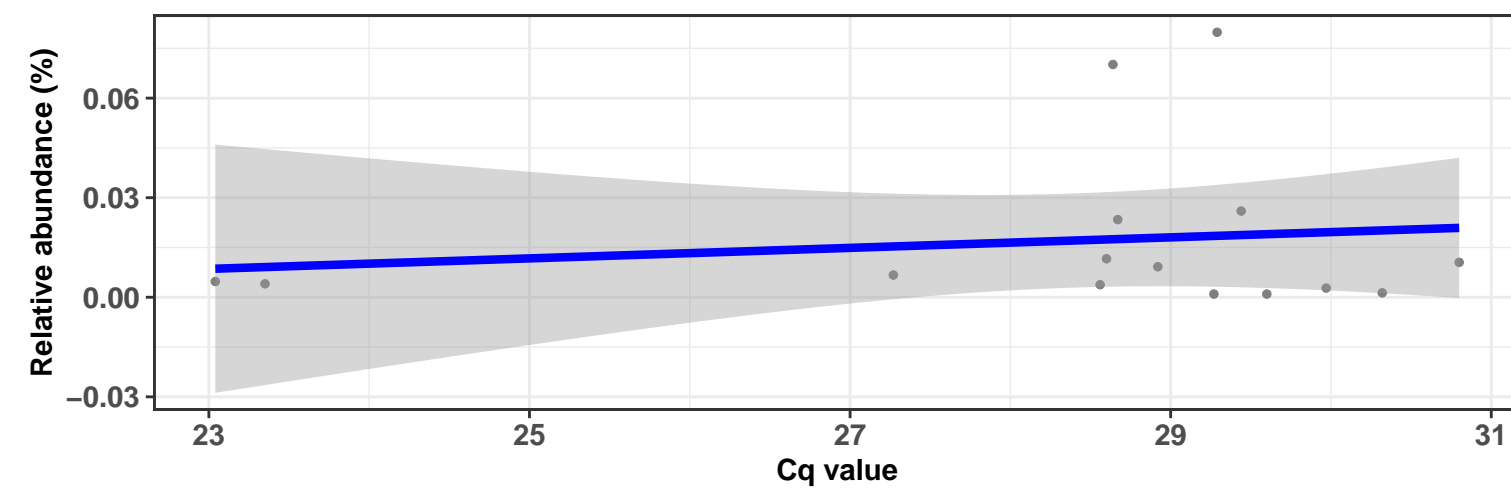
Correlation within: IM−DIM
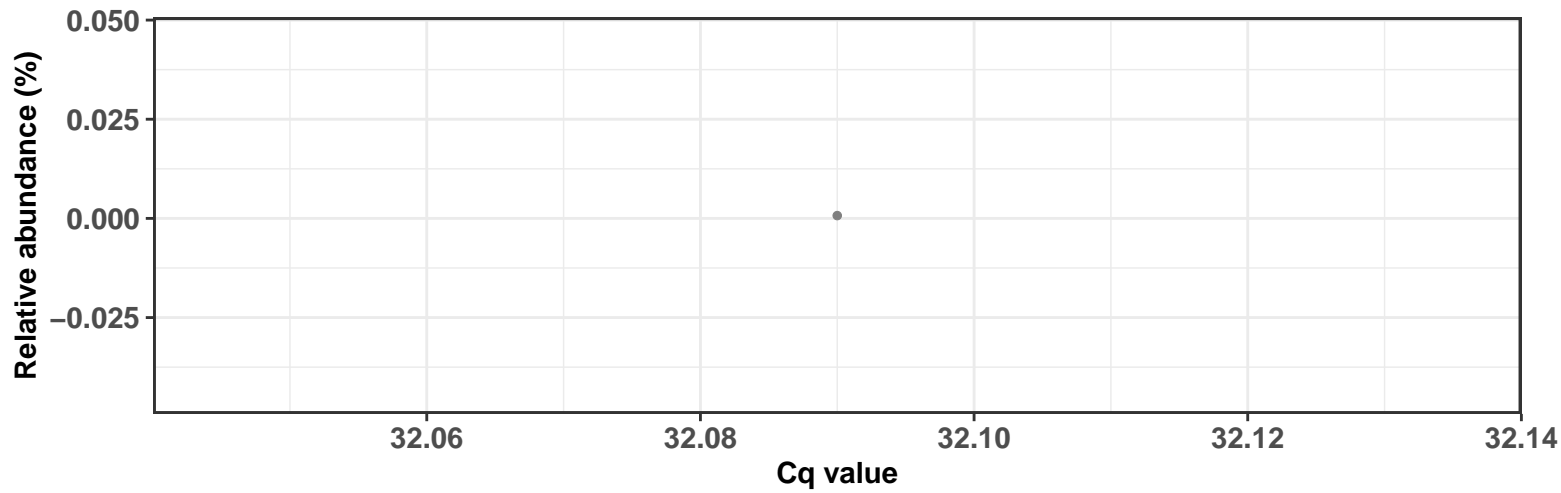
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia−Shigella; NA

Correlation with all samples

$\log_e(S) = 4.970$, $p = 0.726$, $\hat{\rho}_{Spearman} = 0.127$, $CI_{95\%}$ [−0.576, 0.789], $n_{pairs} = 10$

SampleType ● IM−DIC ● Mock

Correlation within: IM−DIC

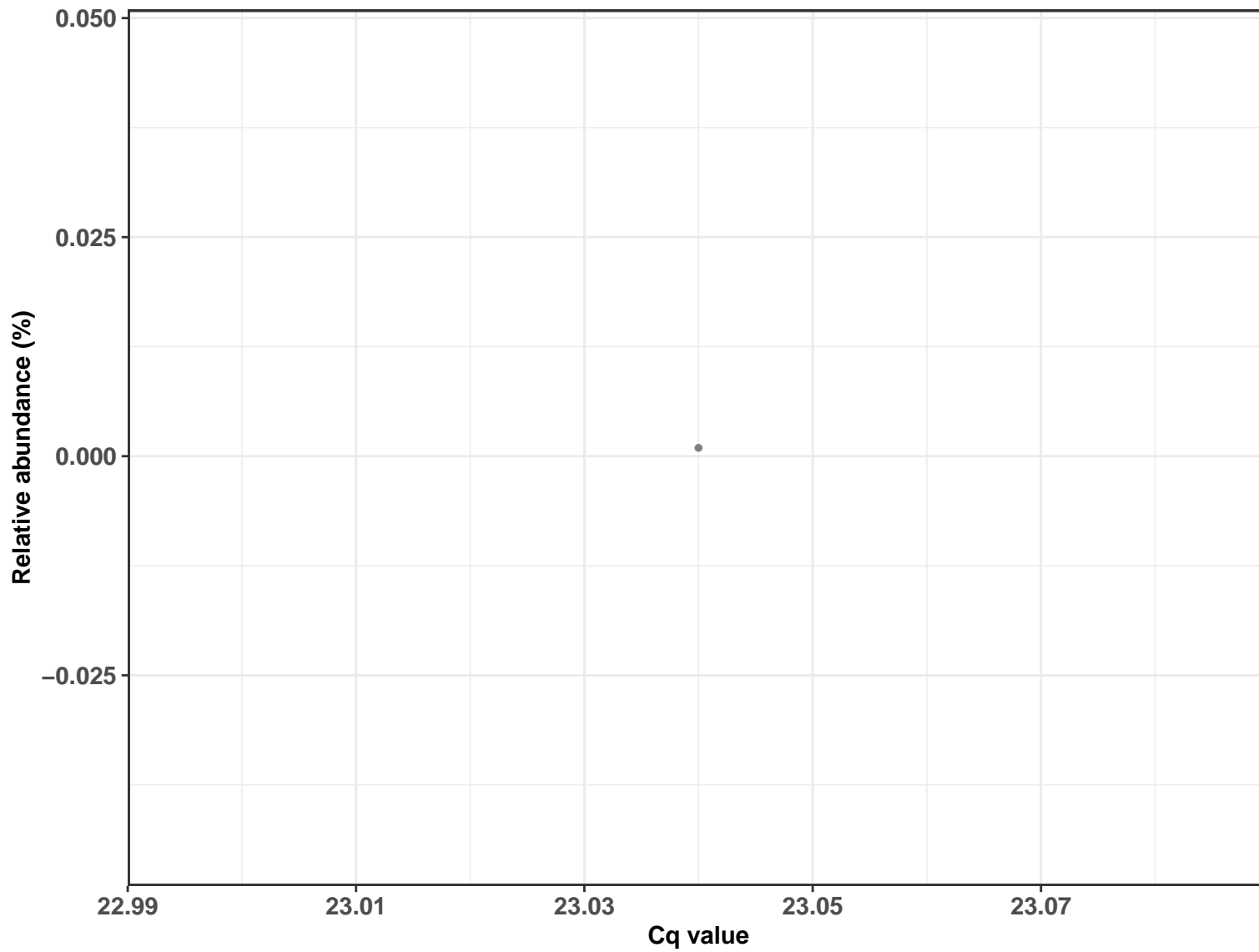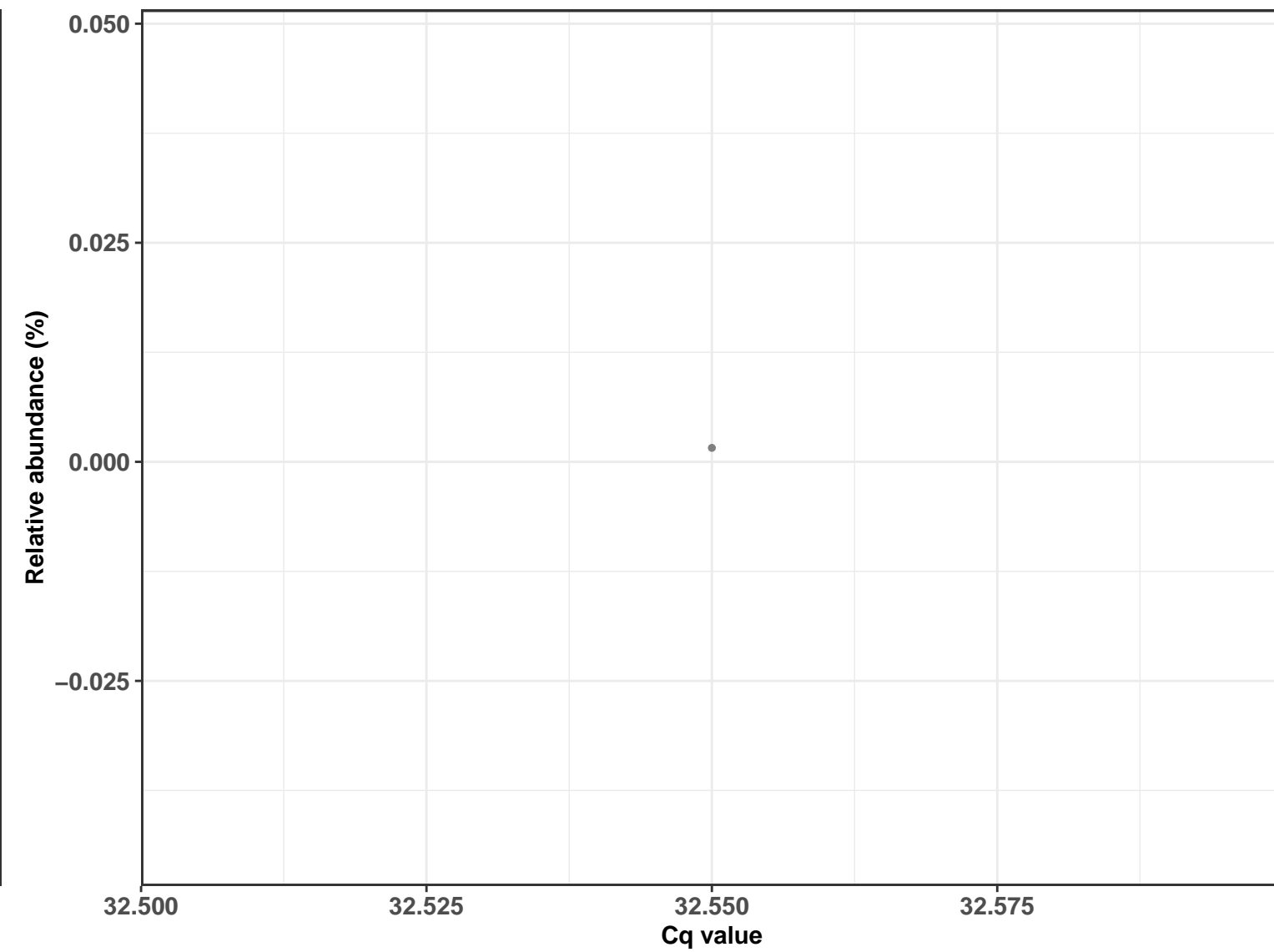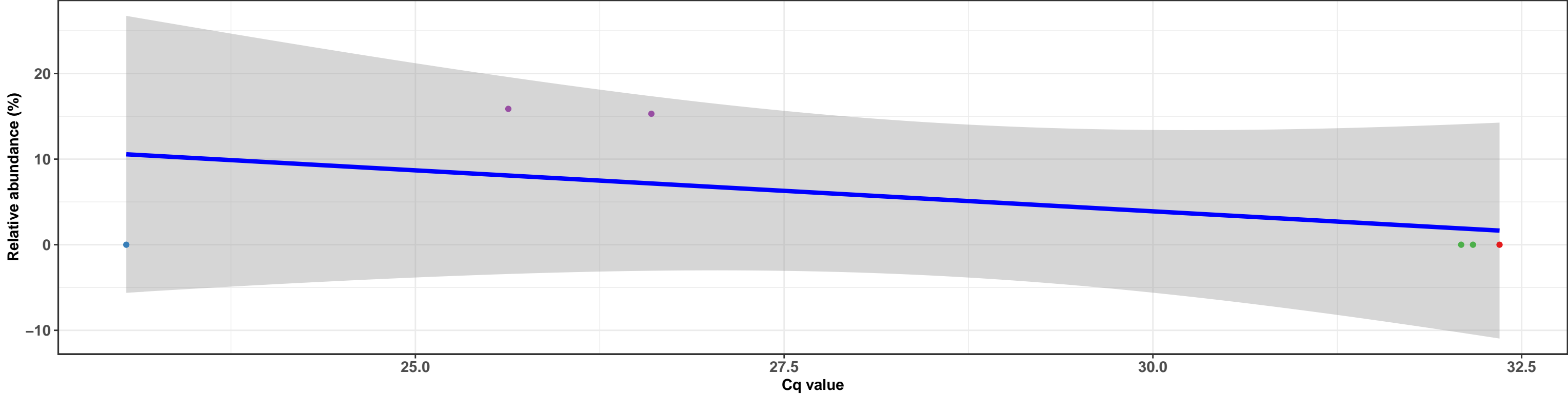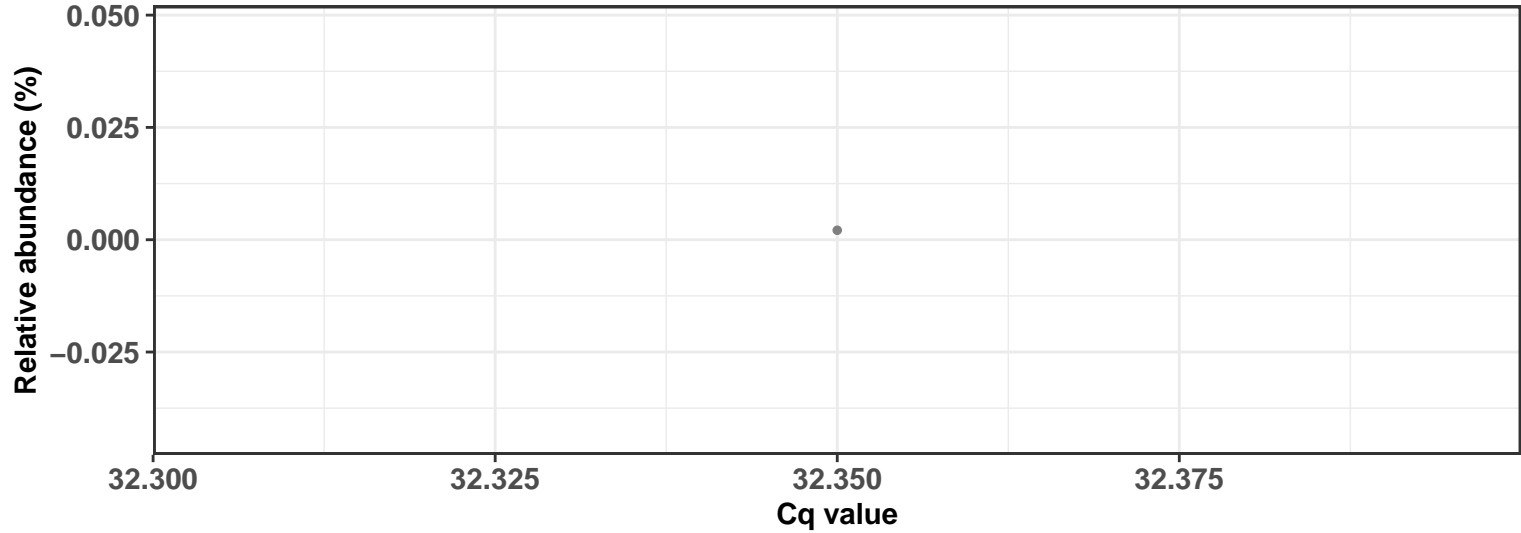$\log_e(S) = 4.820$, $p = 0.932$, $\hat{\rho}_{Spearman} = -0.033$, $CI_{95\%}$ [−0.752, 0.657], $n_{pairs} = 9$

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

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

Correlation with all samples

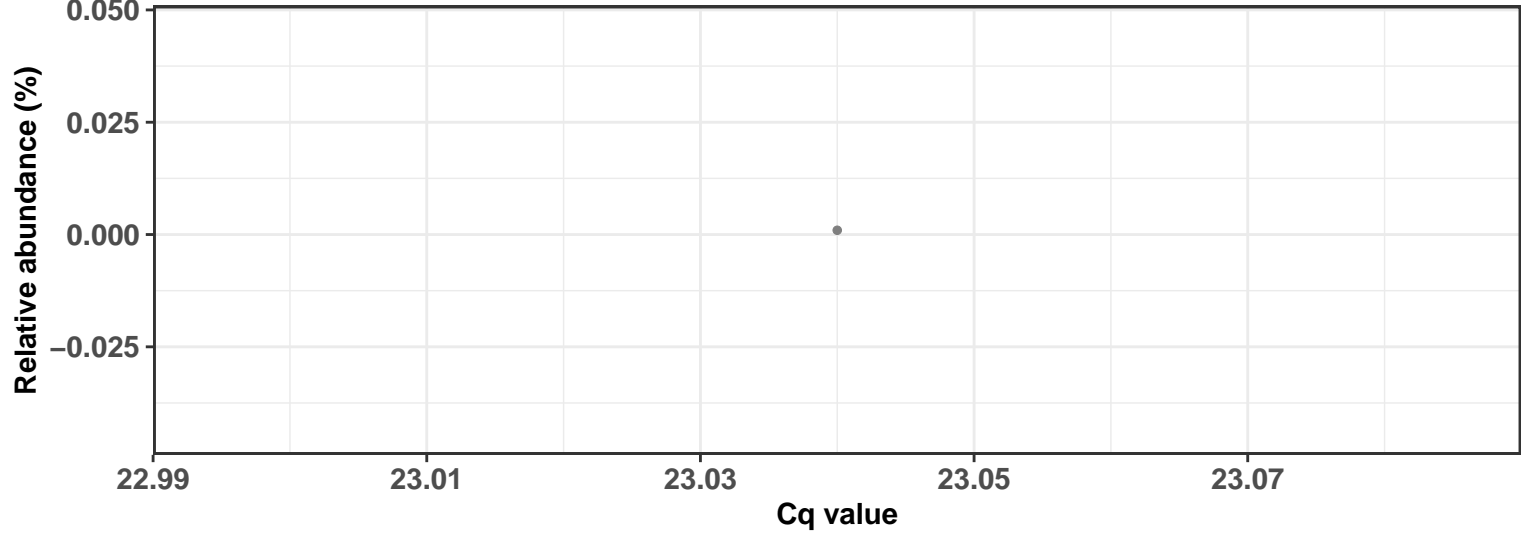$\log_e(S) = 3.738$, $p = 0.704$, $\hat{\rho}_{Spearman} = -0.200$, $CI_{95\%}$ [−1.160, 0.881], $n_{pairs} = 6$
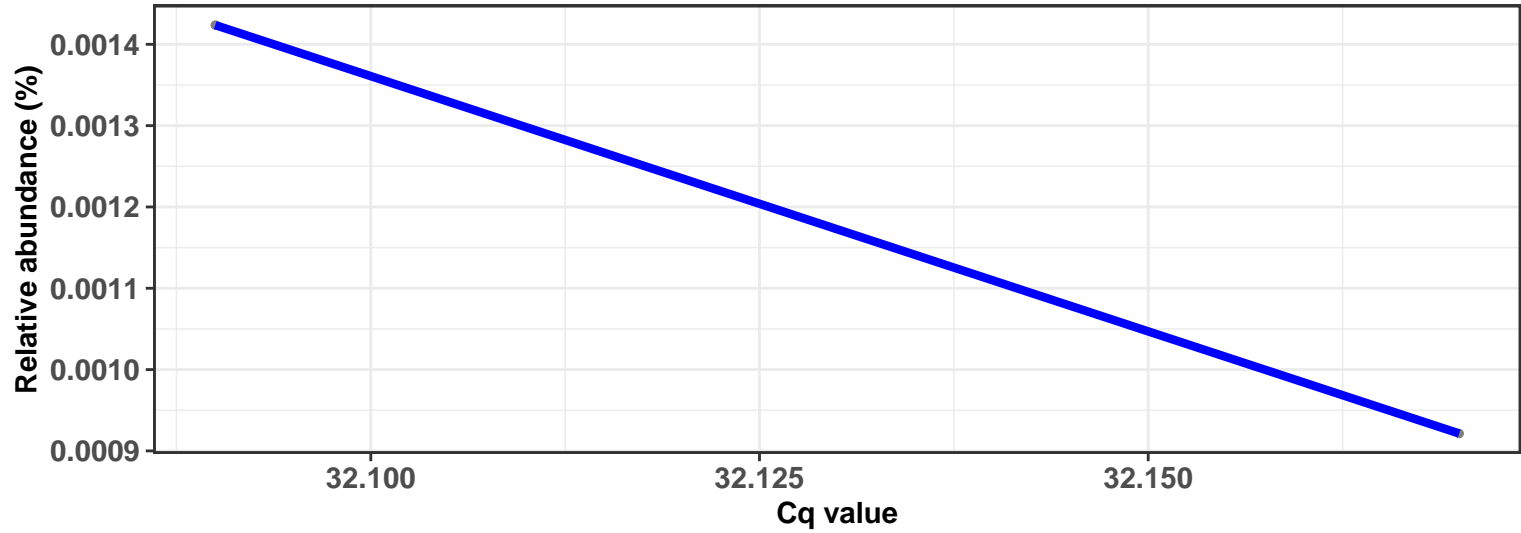
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

Correlation with all samples

$\log_e(S) = 5.642$, $p = 0.400$, $\hat{\rho}_{Spearman} = -0.282$, $CI_{95\%}$ [-0.791, 0.202], $n_{pairs} = 11$
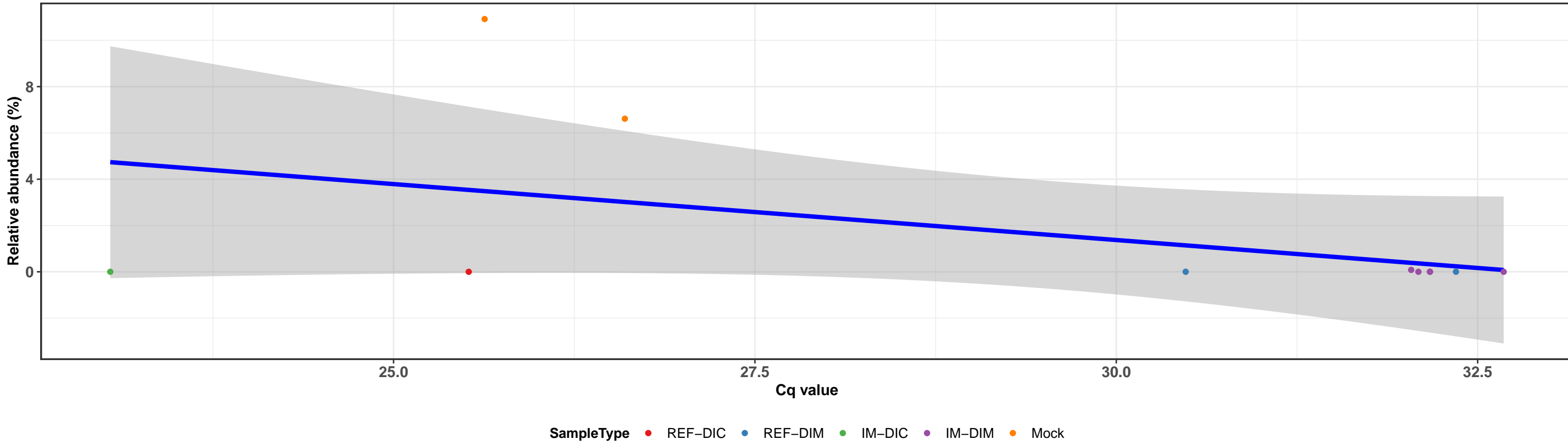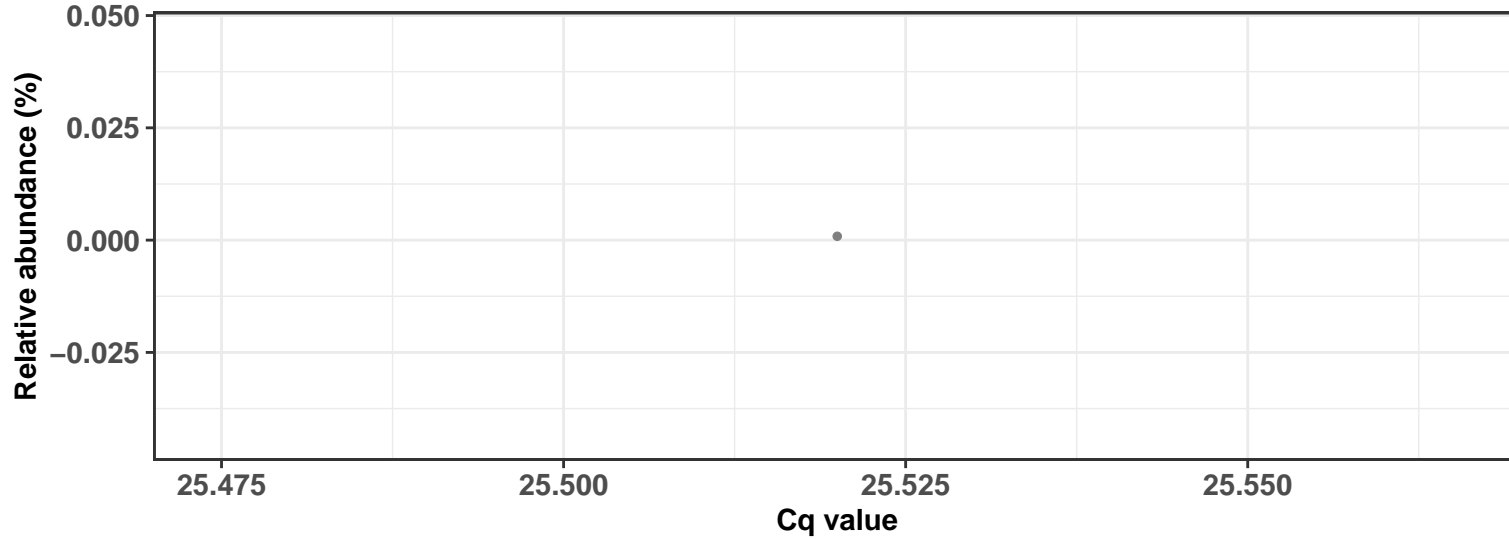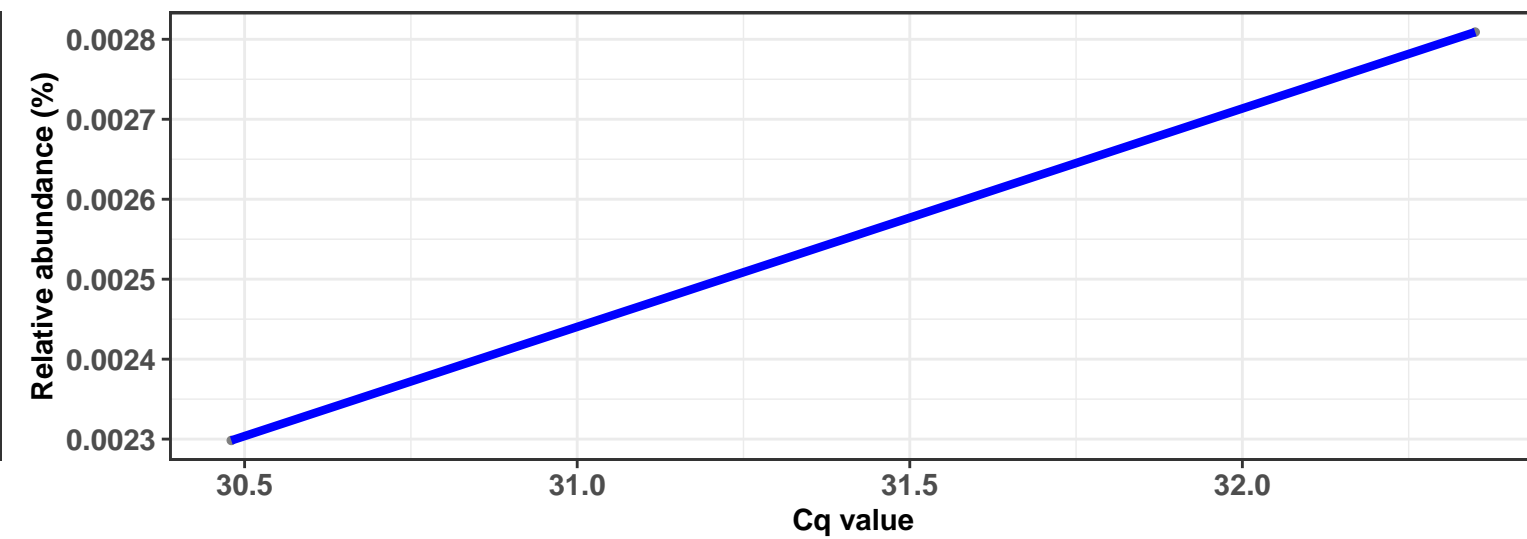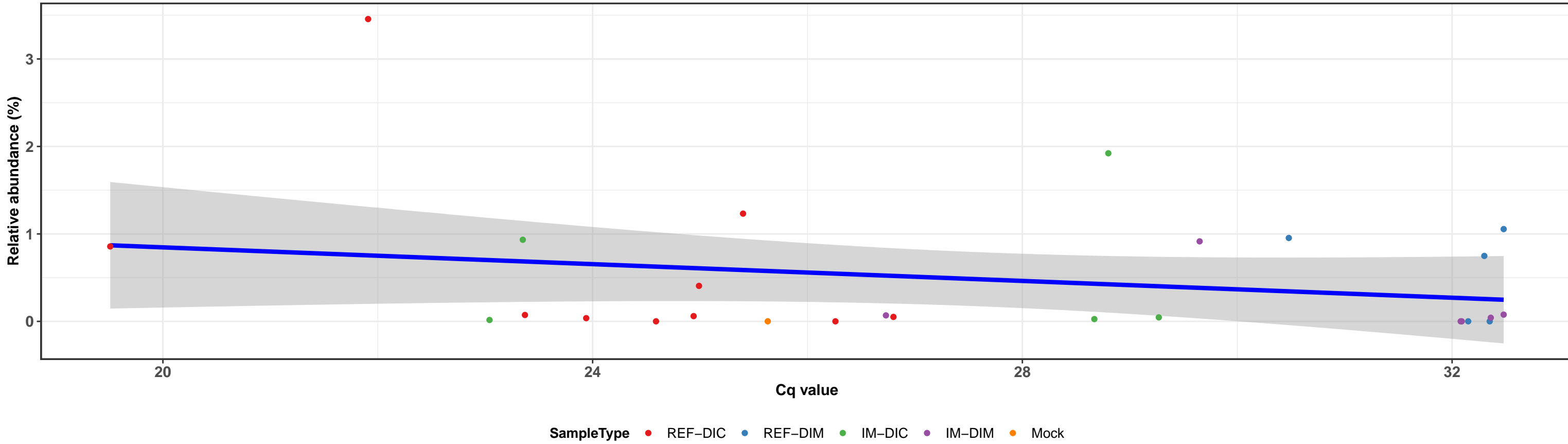

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Mock
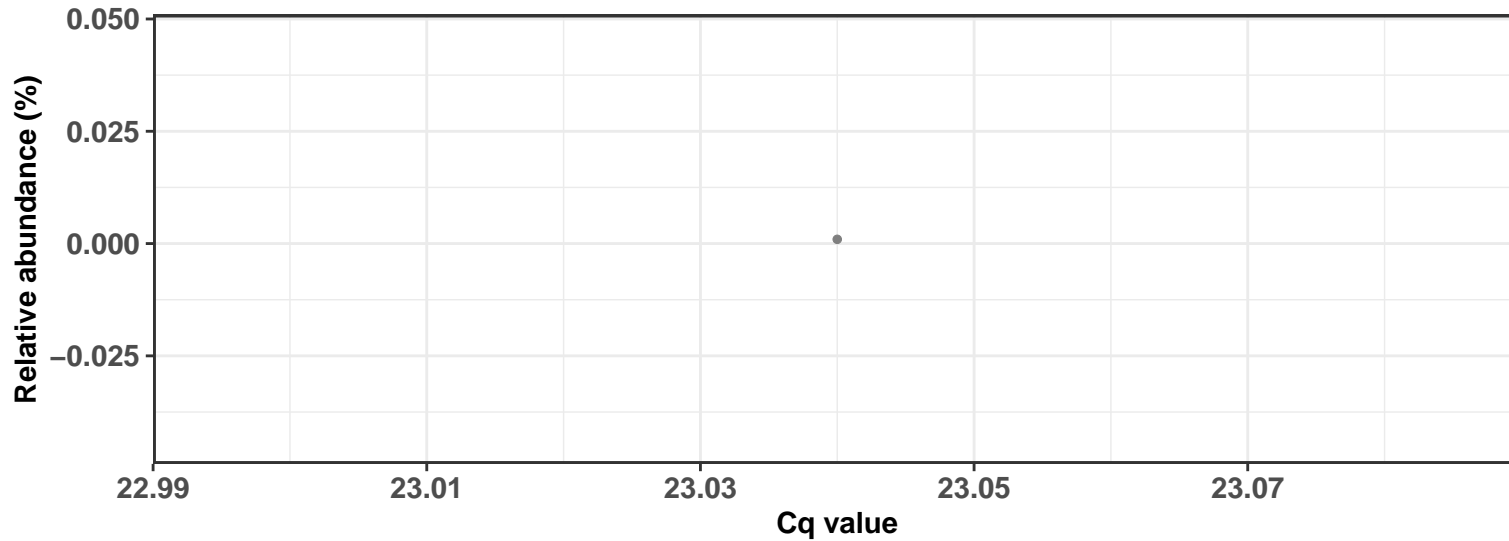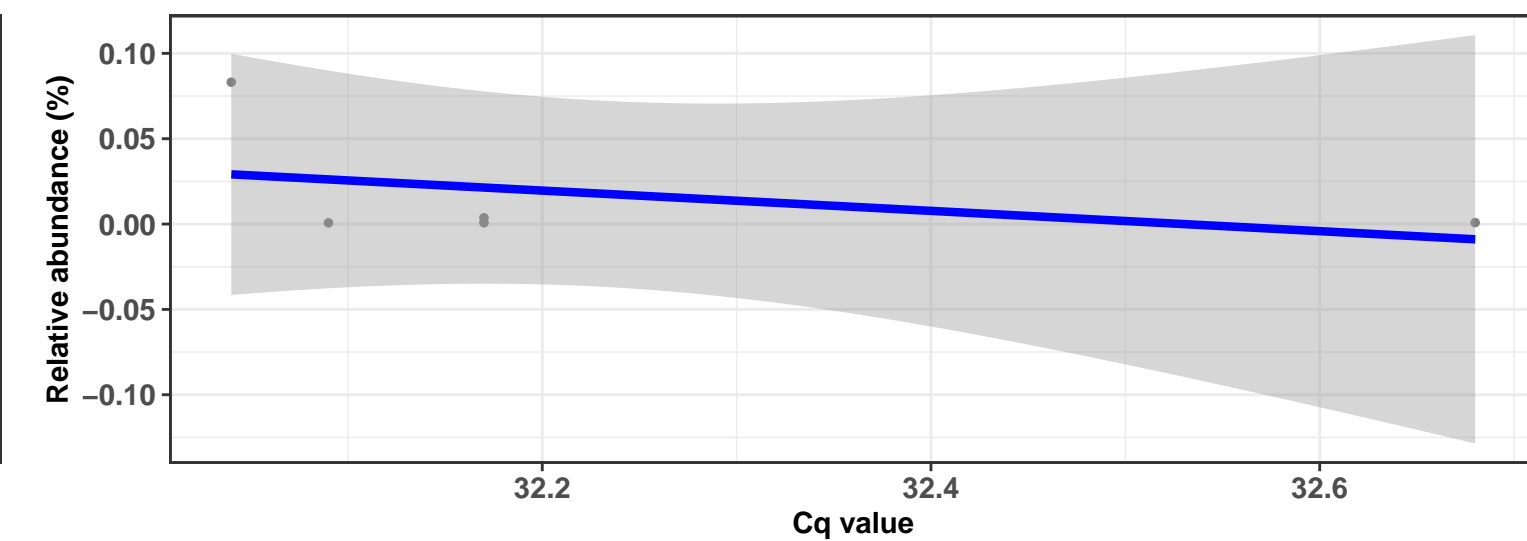
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Vibrionales; f__Vibrionaceae; g__Aliivibrio; Ambiguous_taxa
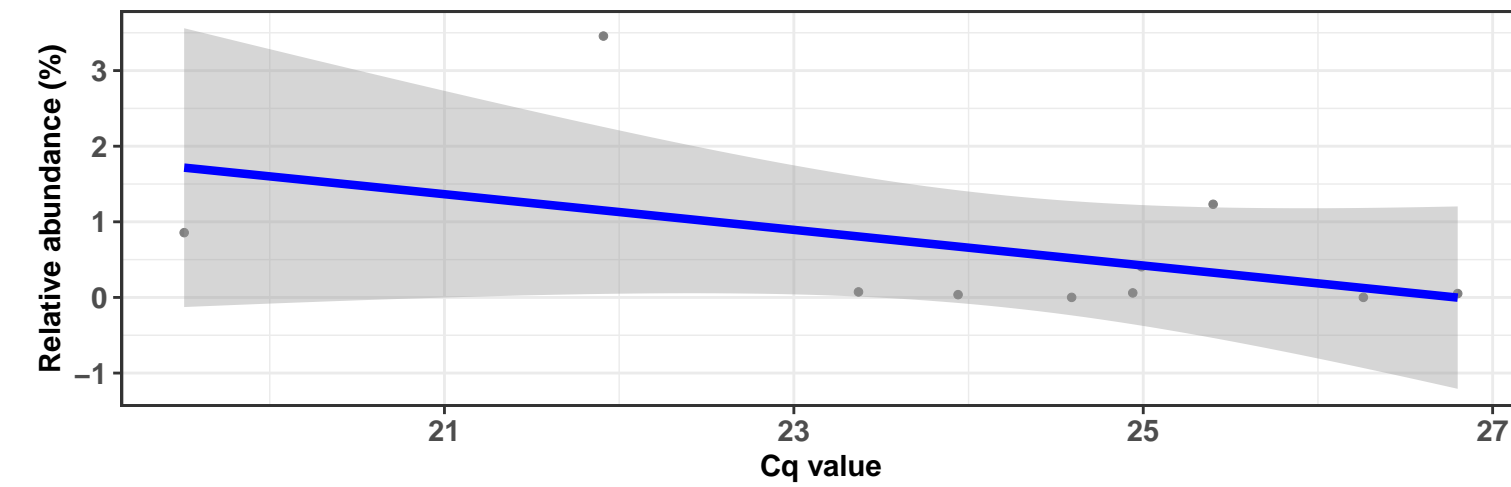
Correlation with all samples

$\log_e(S) = 8.249$, $p = 0.405$, $\hat{\rho}_{Spearman} = -0.167$, $CI_{95\%}$ $[-0.545, 0.224]$, $n_{pairs} = 27$

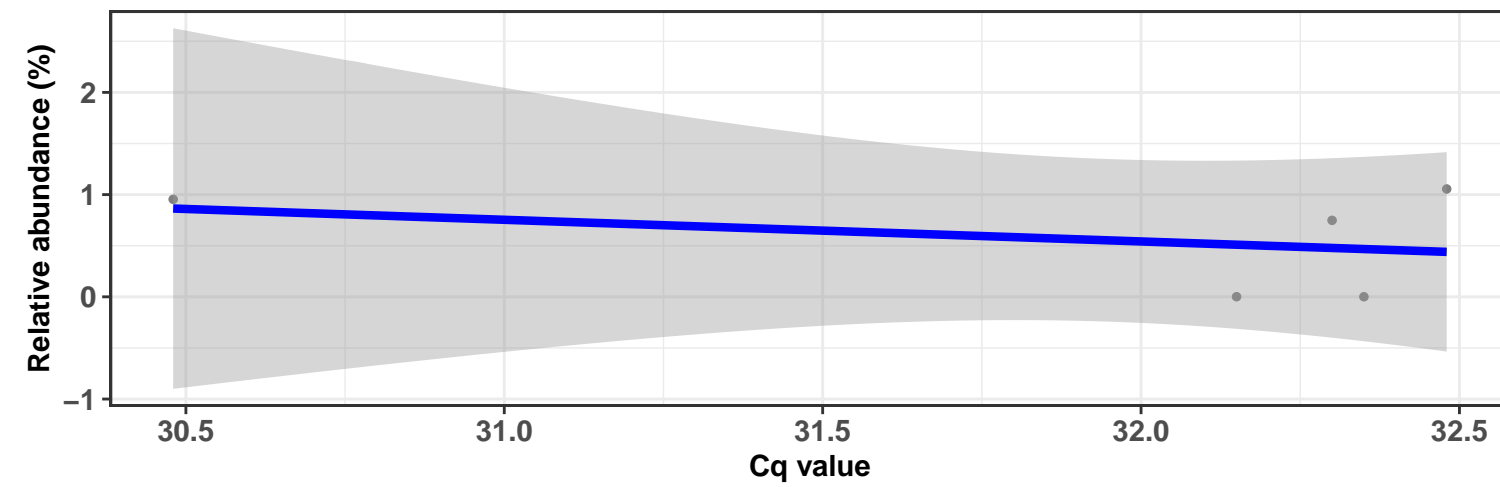SampleType ● REF–DIC ● REF–DIM ● IM–DIC ● IM–DIM ● Mock

Correlation within: REF–DIC

$\log_e(S) = 5.421$, $p = 0.293$, $\hat{\rho}_{Spearman} = -0.370$, $CI_{95\%}$ $[-1.069, 0.195]$, $n_{pairs} = 10$

Correlation within: REF–DIM

Correlation within: IM–DIC
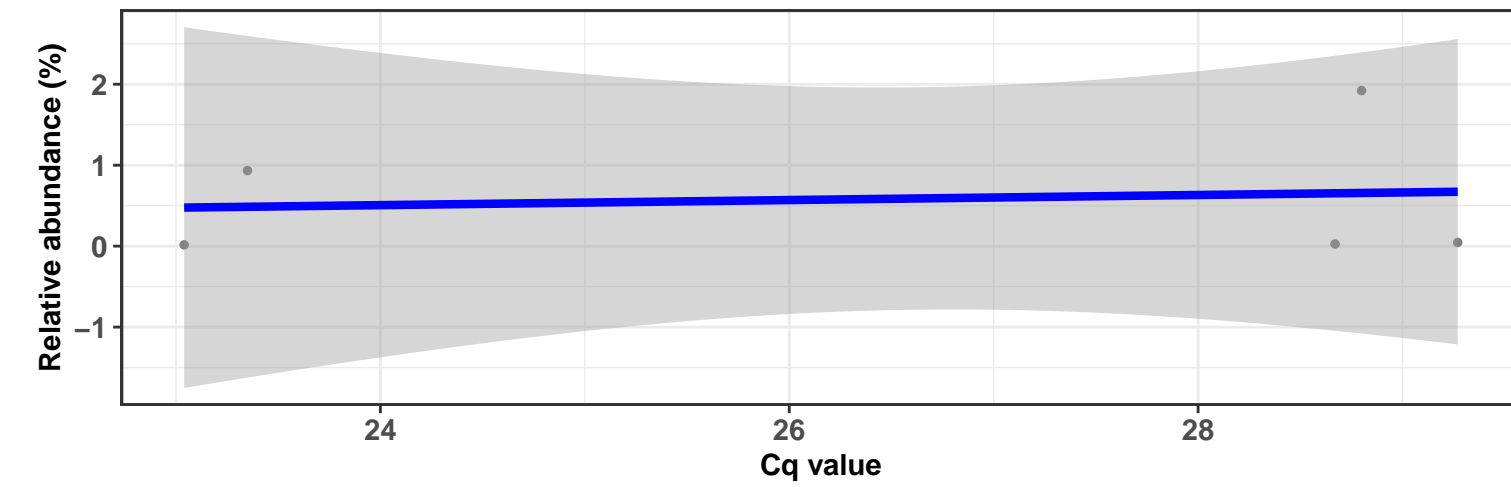
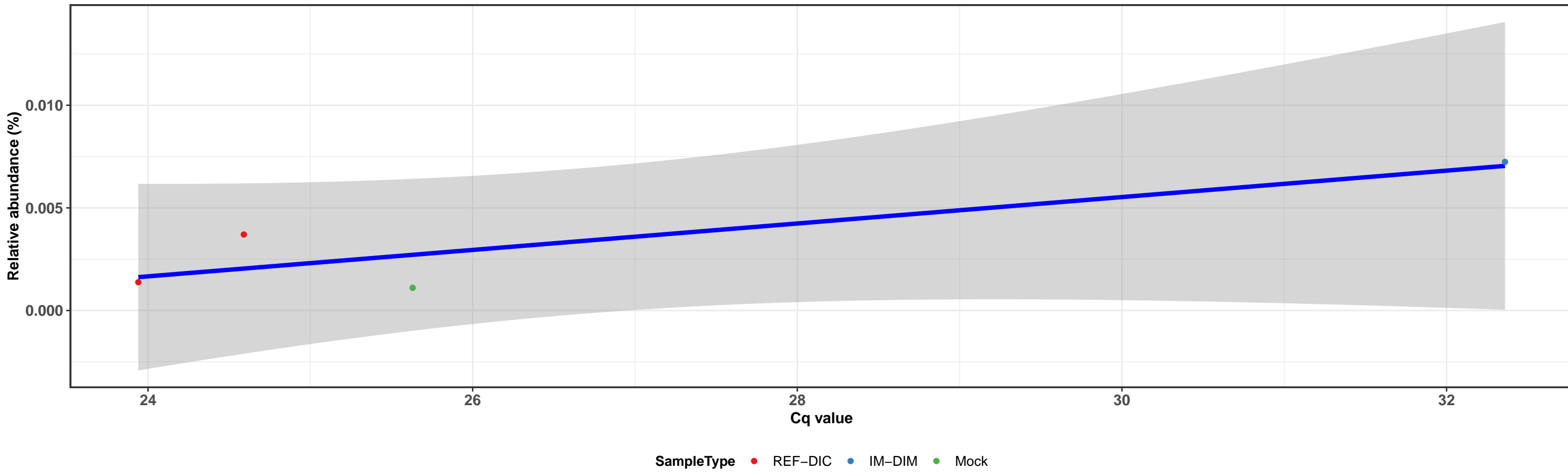**Correlation within: IM–DIM**

$\log_e(S) = 3.689$, $p = 0.787$, $\hat{\rho}_{Spearman} = -0.143$, $CI_{95\%}$ $[-1.233, 0.800]$, $n_{pairs} = 6$
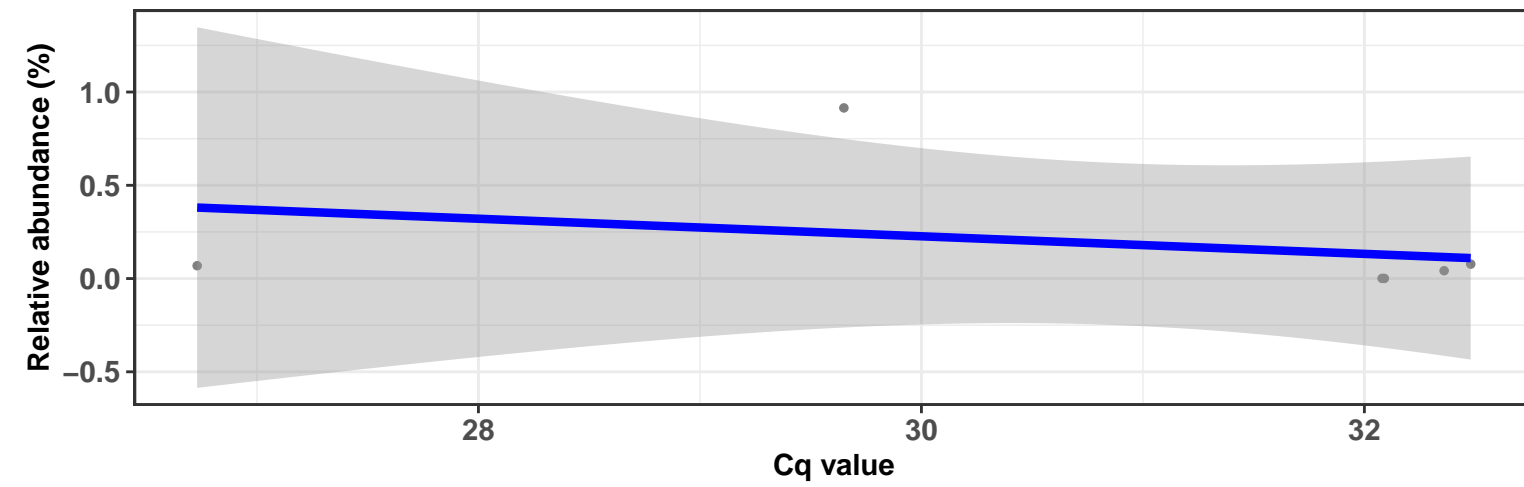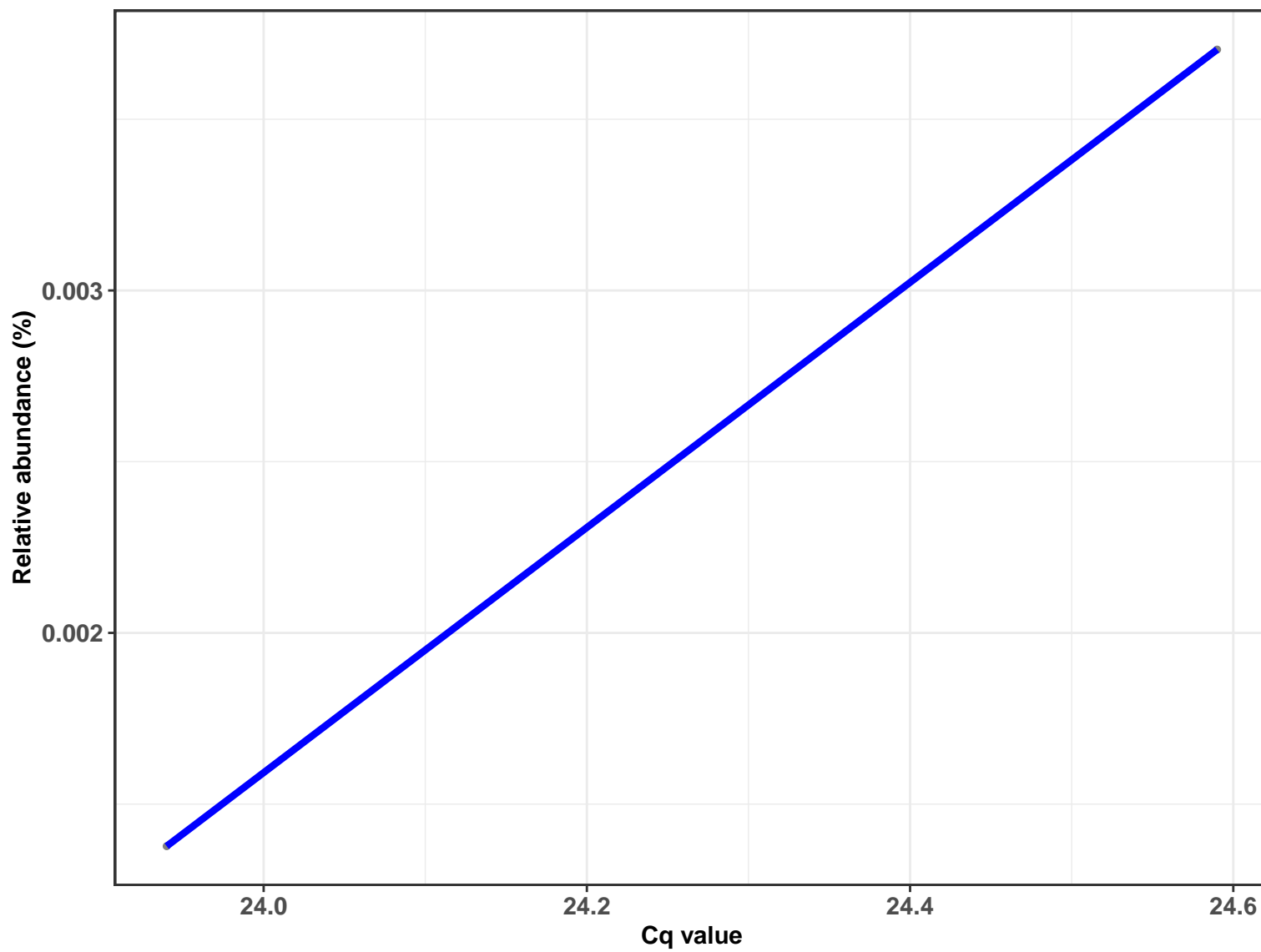
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Acidovorax; NA

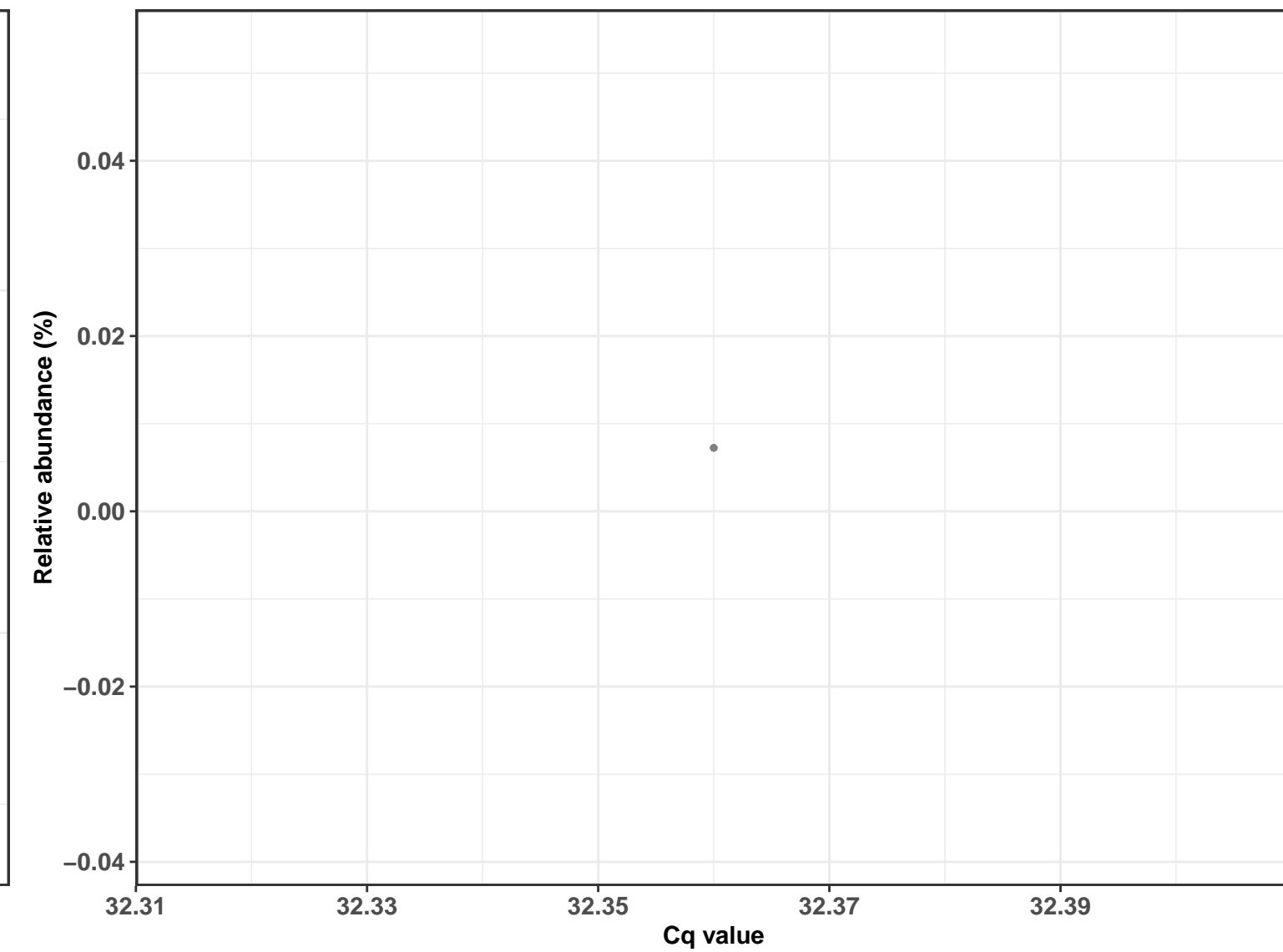Correlation with all samples

SampleType ● REF−DIC ● IM−DIM ● Mock

Correlation within: REF−DIC
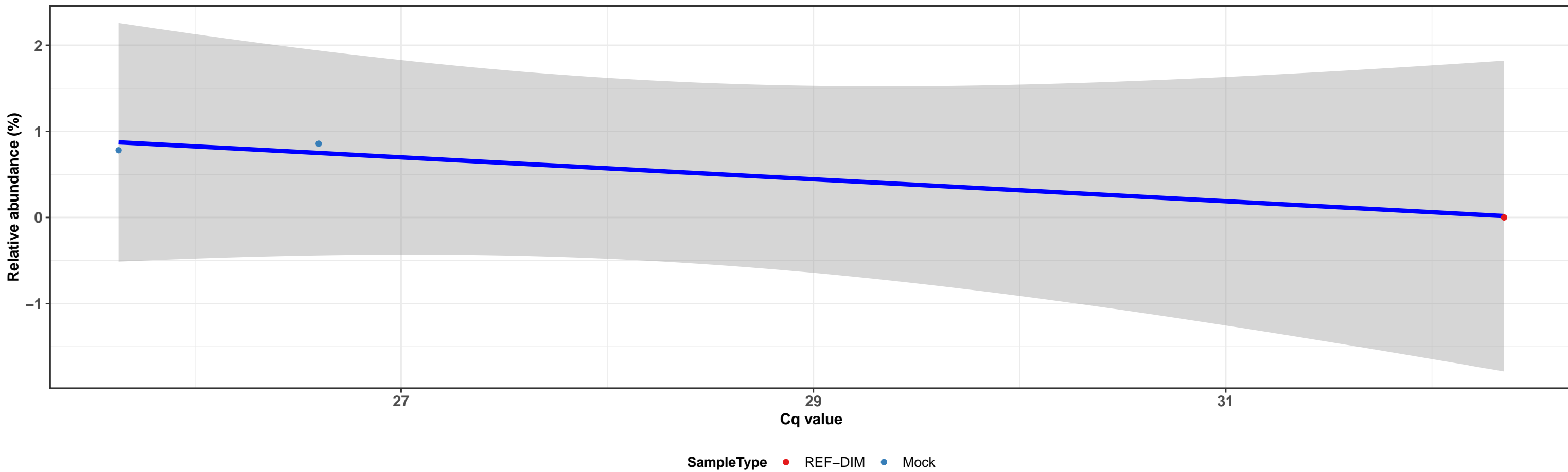
Correlation within: IM−DIM

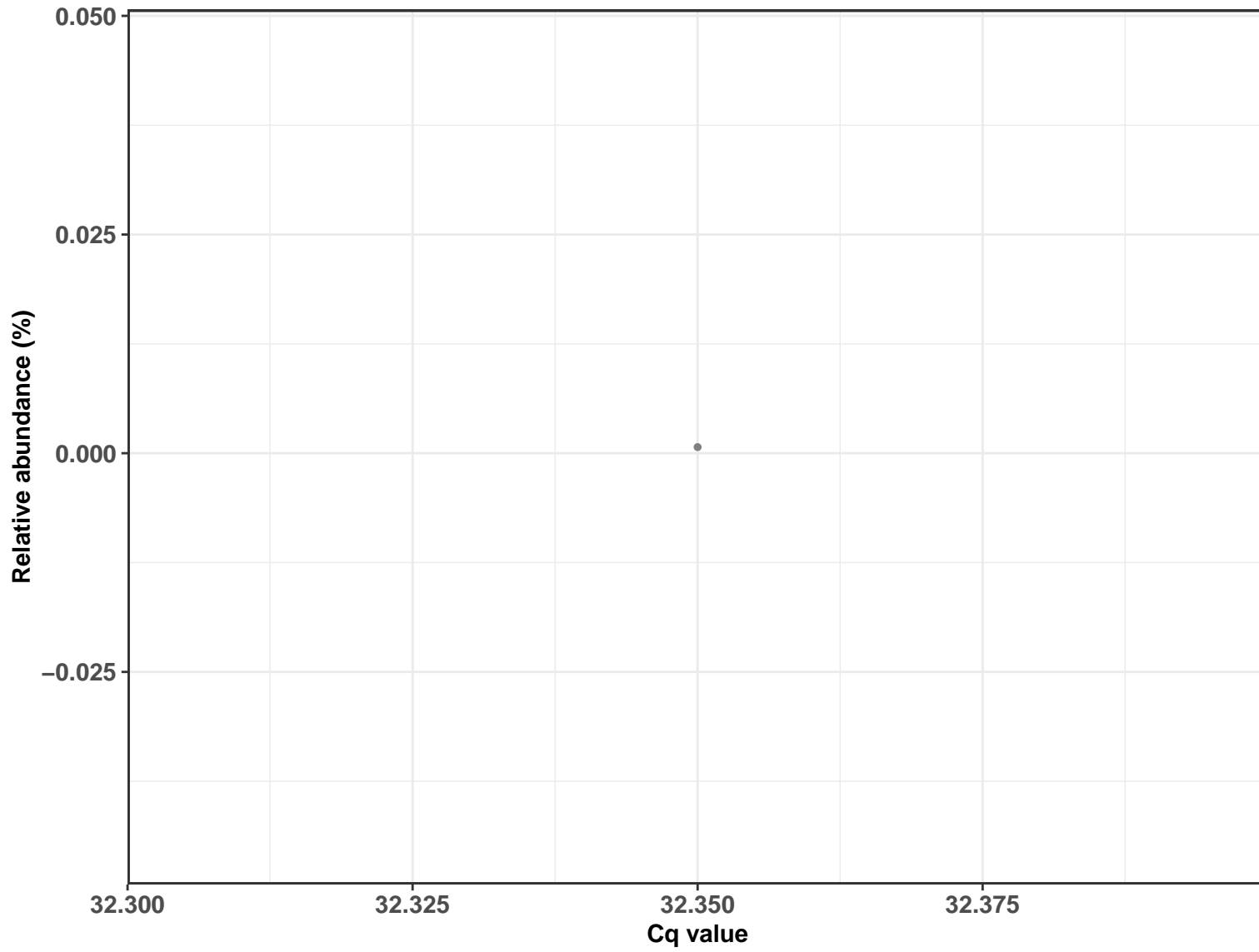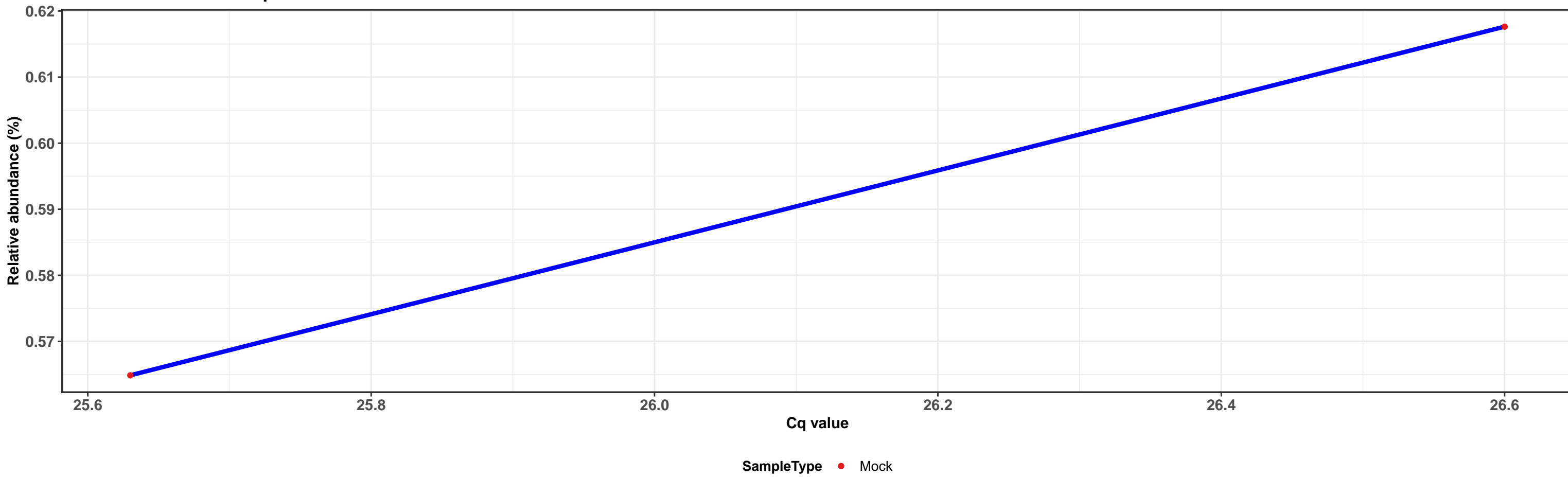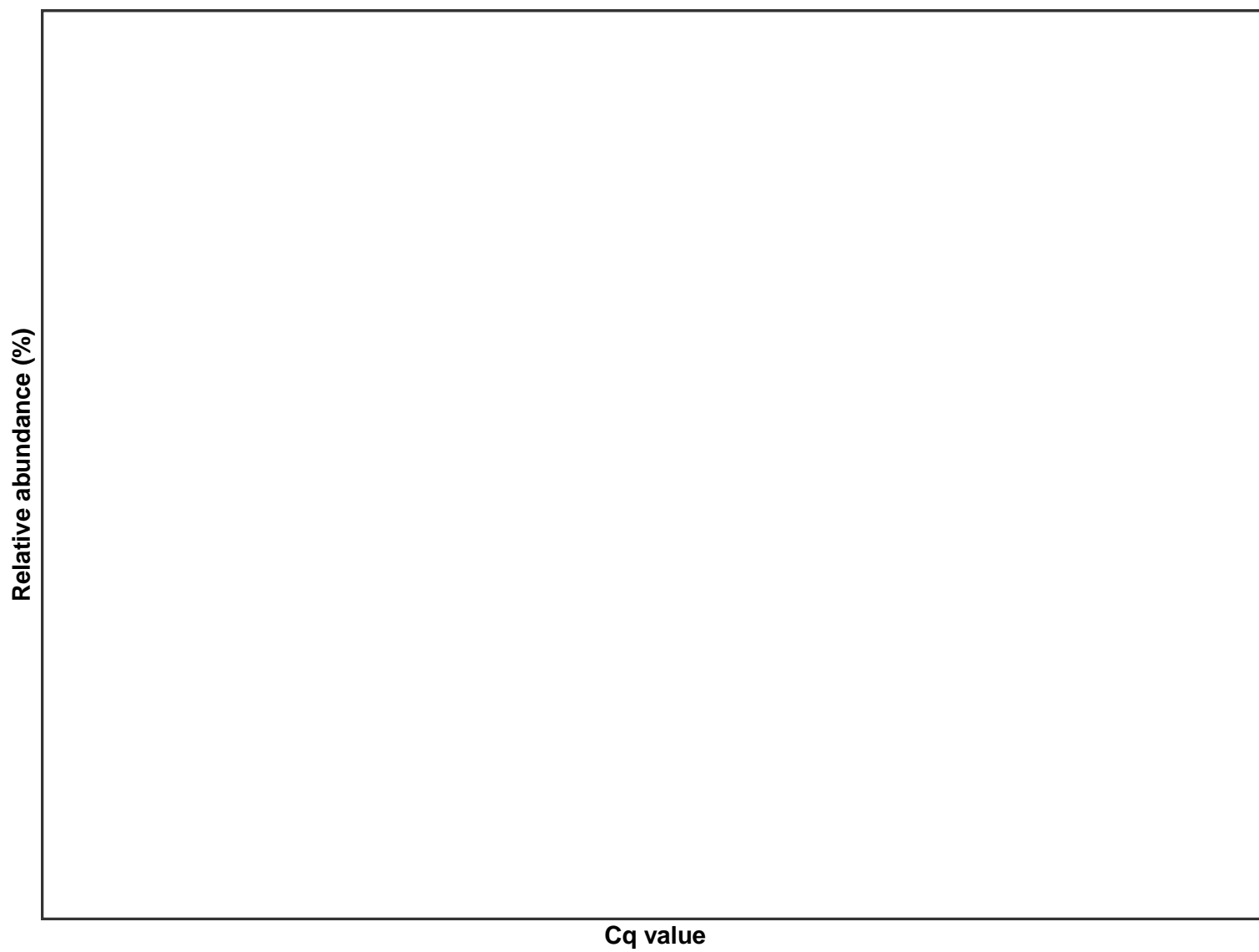# k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes
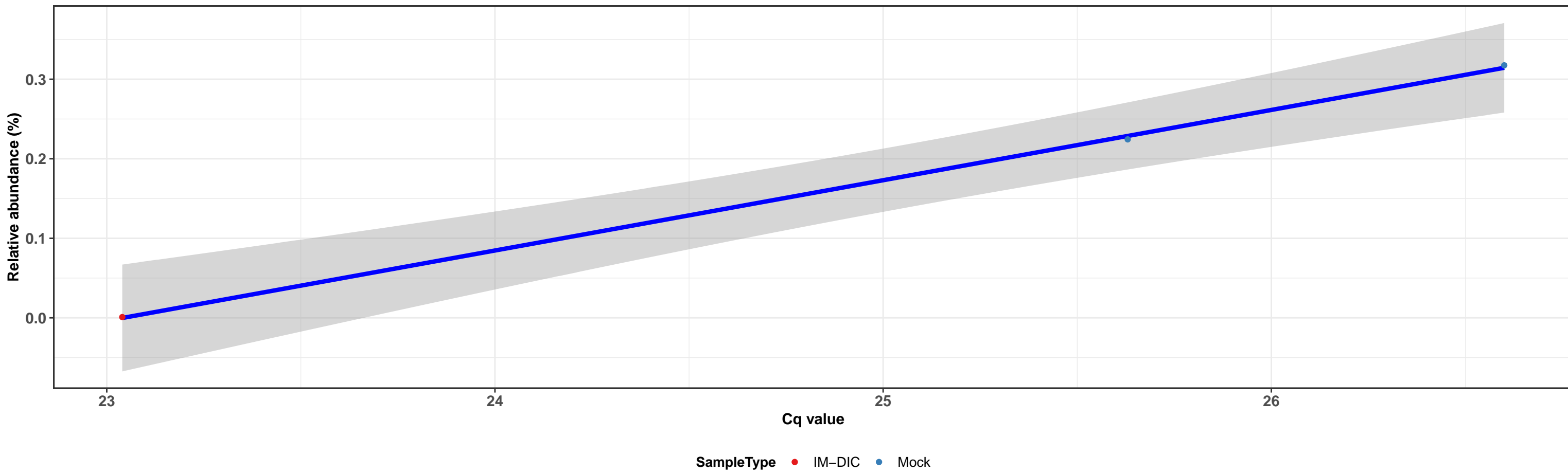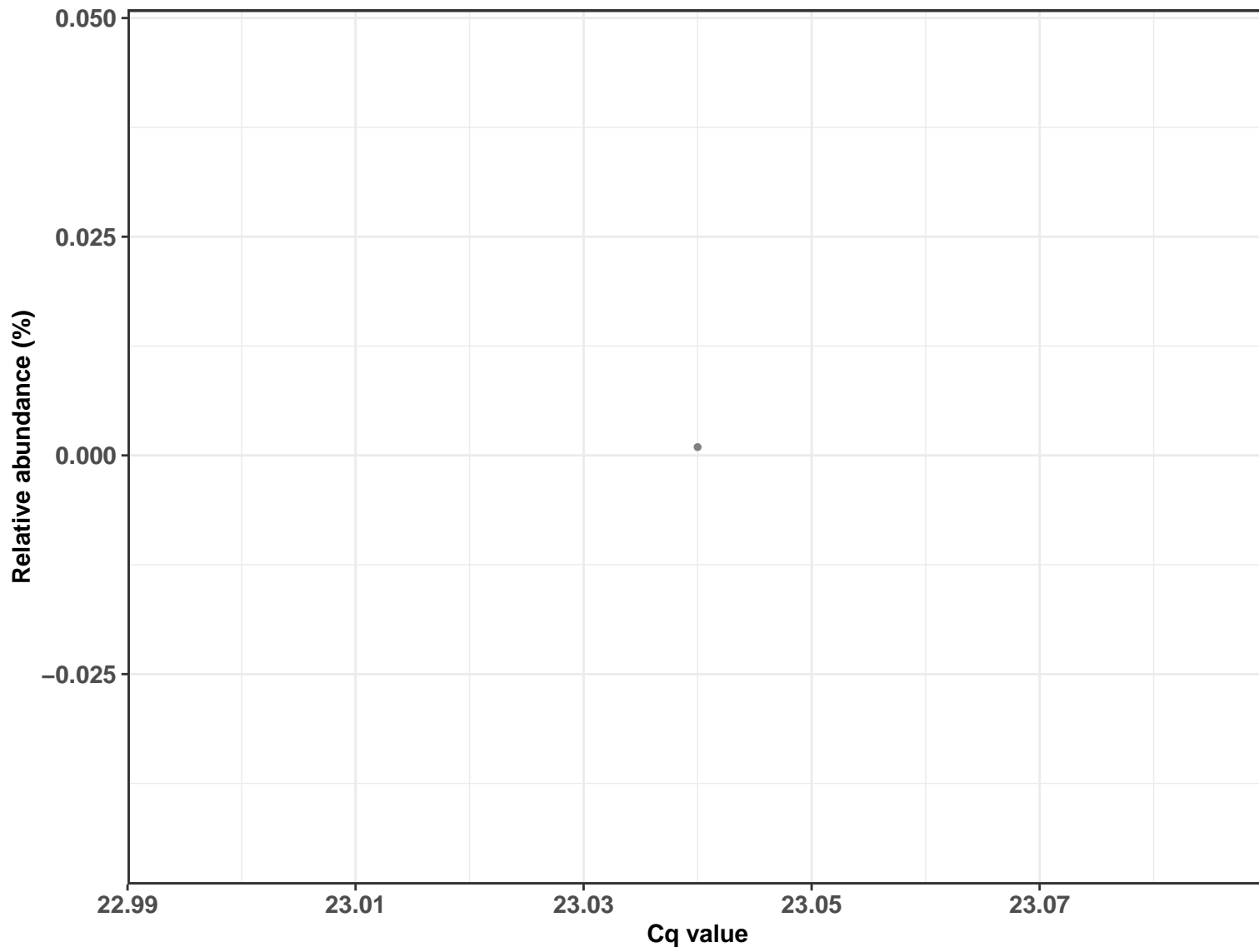
Correlation with all samples

SampleType • Mock

Correlation within:

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Listeriaceae; g__Listeria; s__Listeria monocytogenes
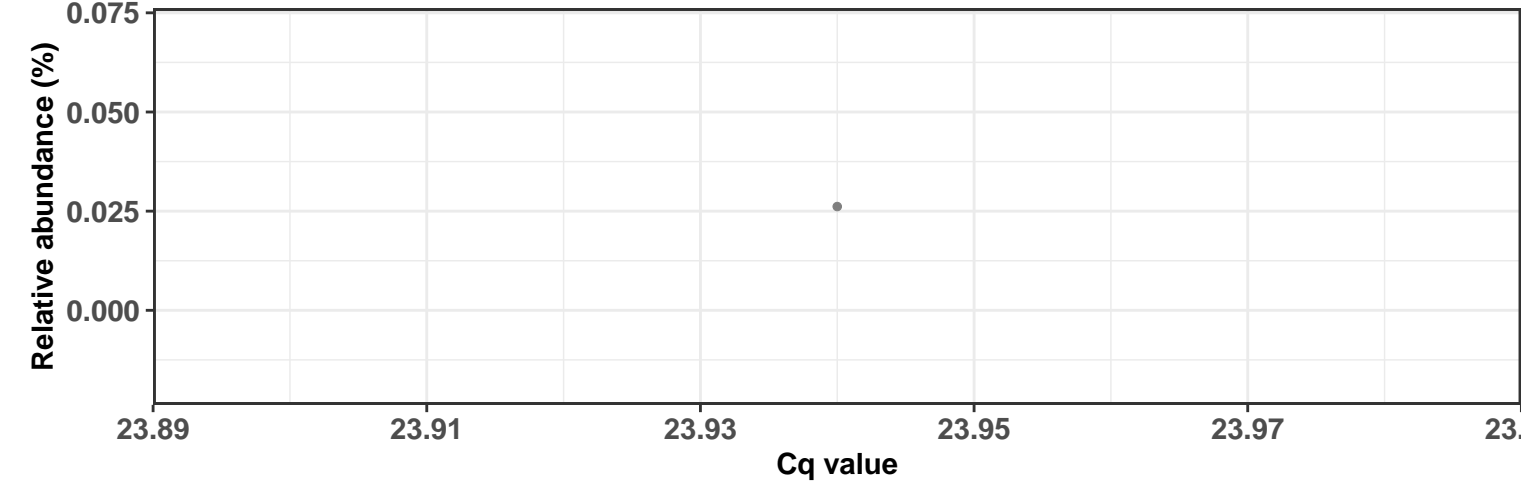
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecalis
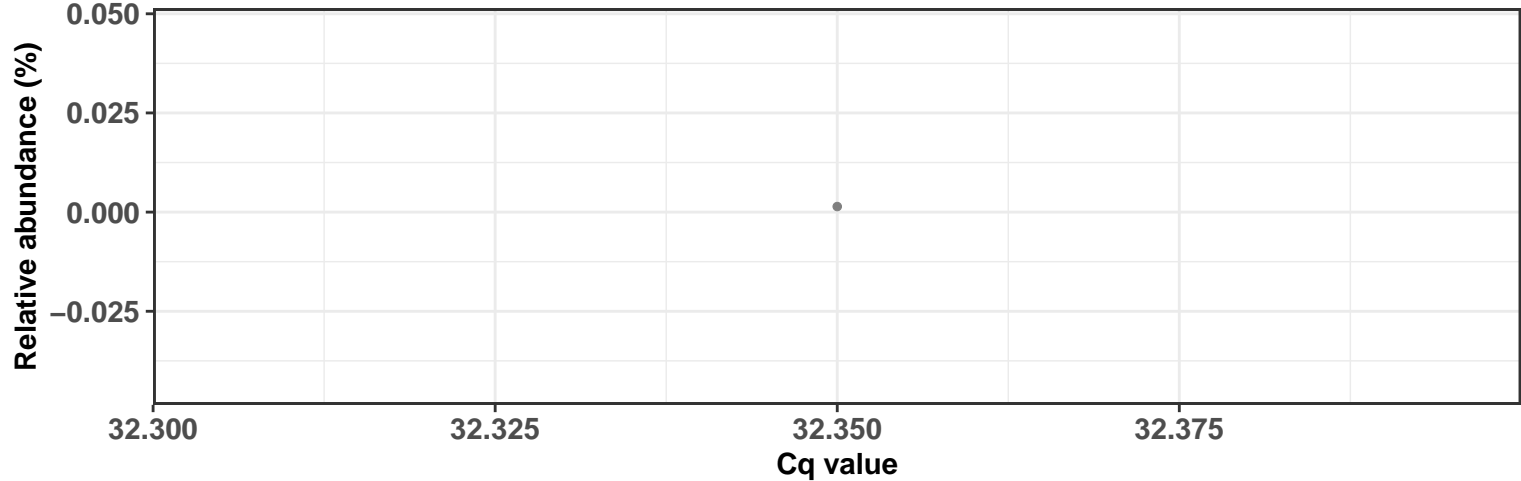
Correlation with all samples

$\log_e(S) = 7.475$, $p = 0.986$, $\hat{\rho}_{Spearman} = 0.004$, $CI_{95\%}$ [−0.540, 0.501], $n_{pairs} = 22$

SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● IM−DIM   ● Mock
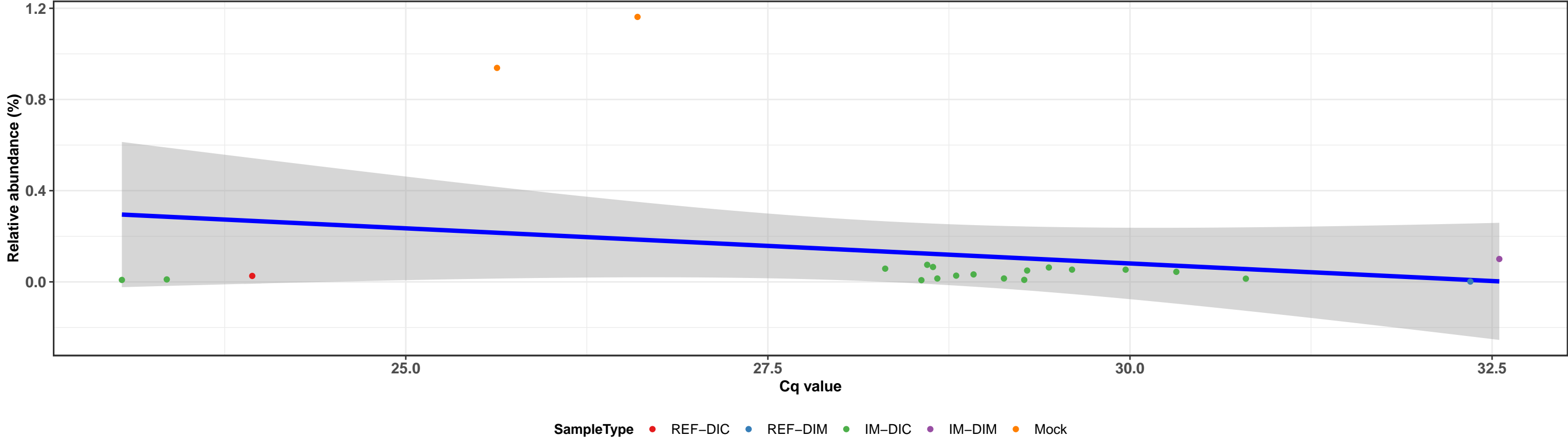
Correlation within: REF−DIC

Correlation within: REF−DIM

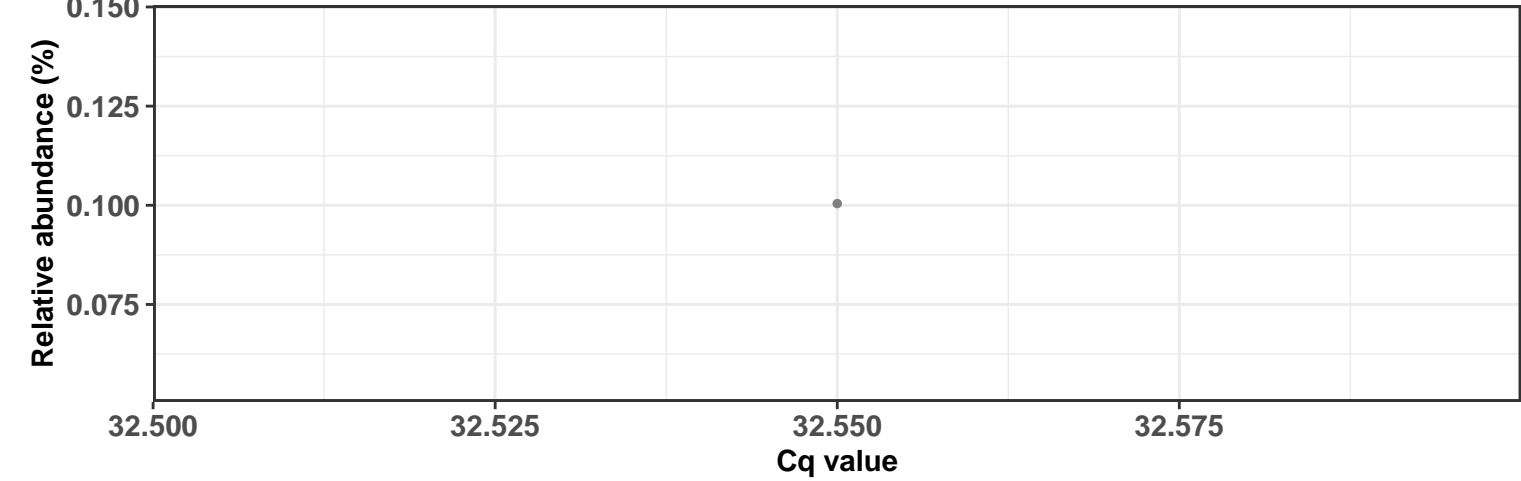**Correlation within: IM−DIC**

$\log_e(S) = 6.474$, $p = 0.428$, $\hat{\rho}_{Spearman} = 0.206$, $CI_{95\%}$ [−0.337, 0.799], $n_{pairs} = 17$
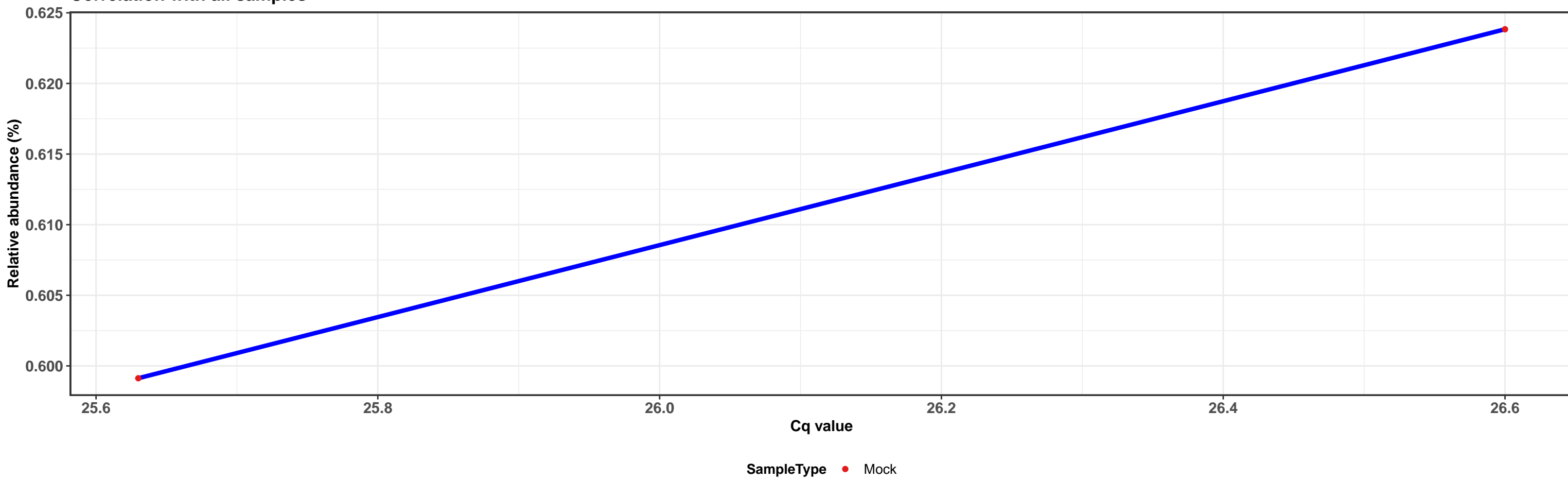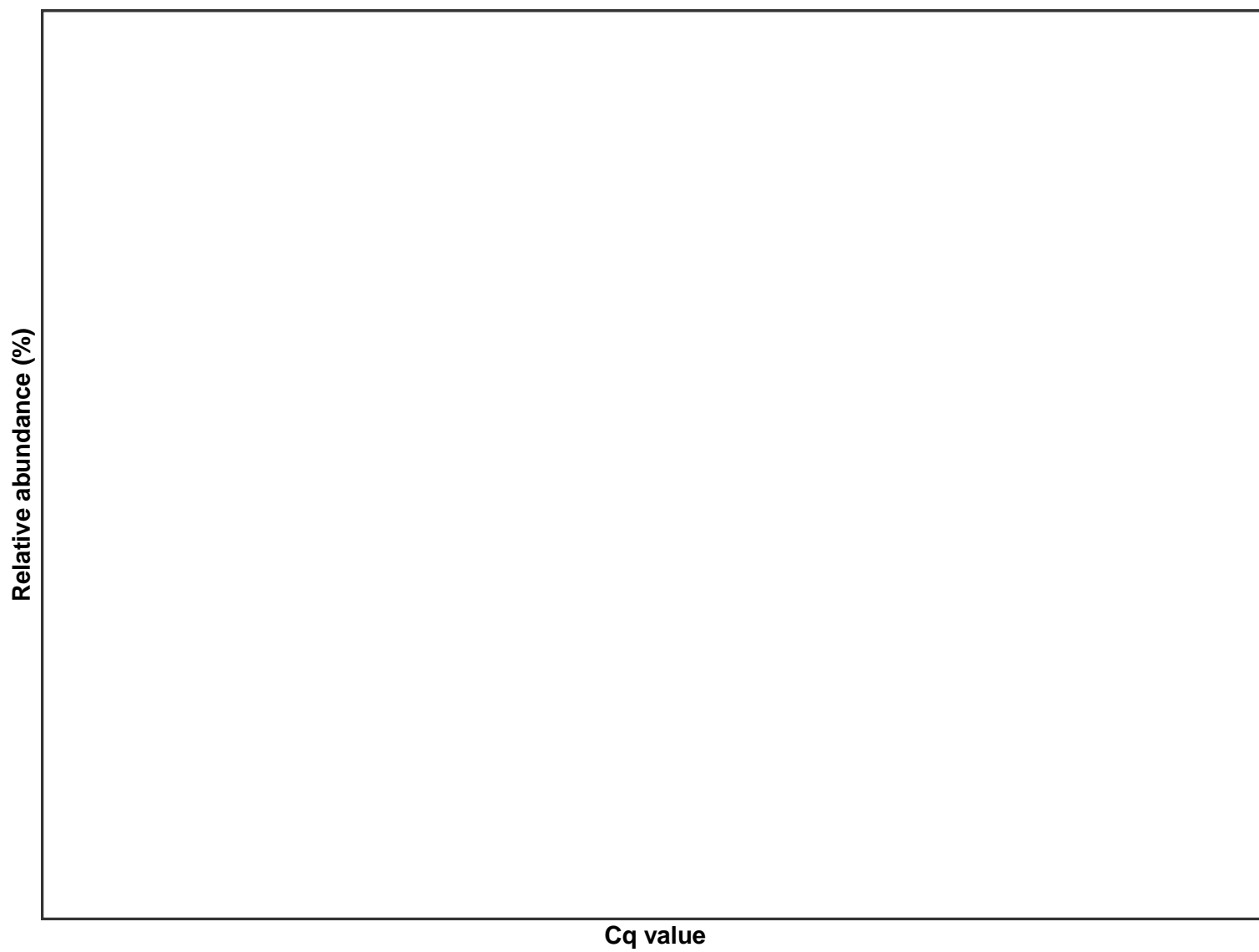
Correlation within: IM−DIM

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

k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecalis
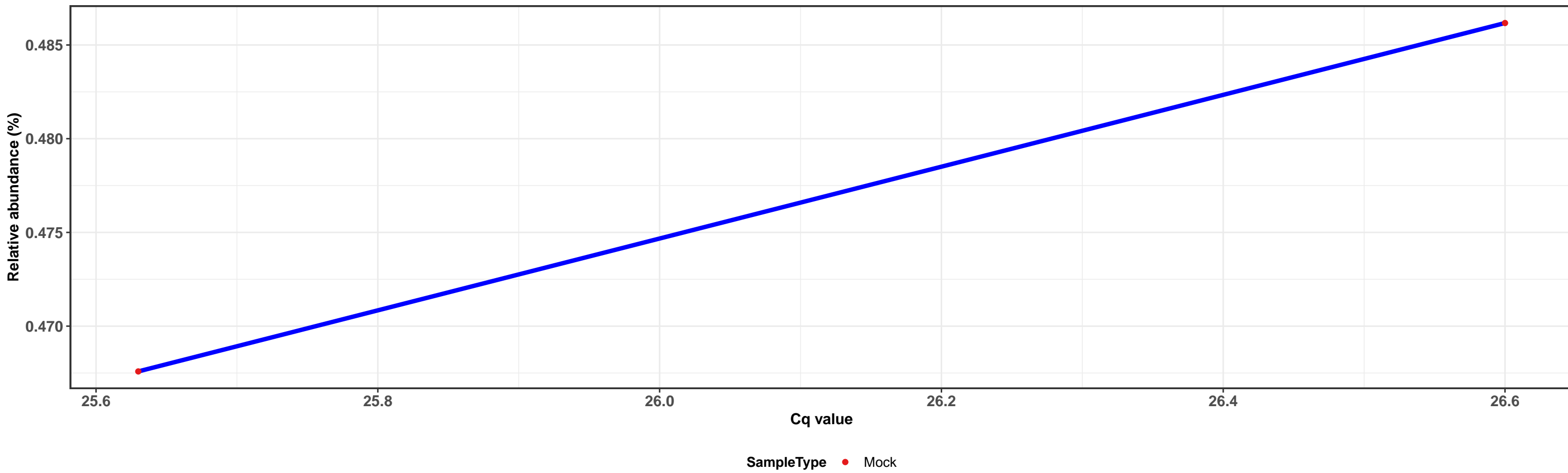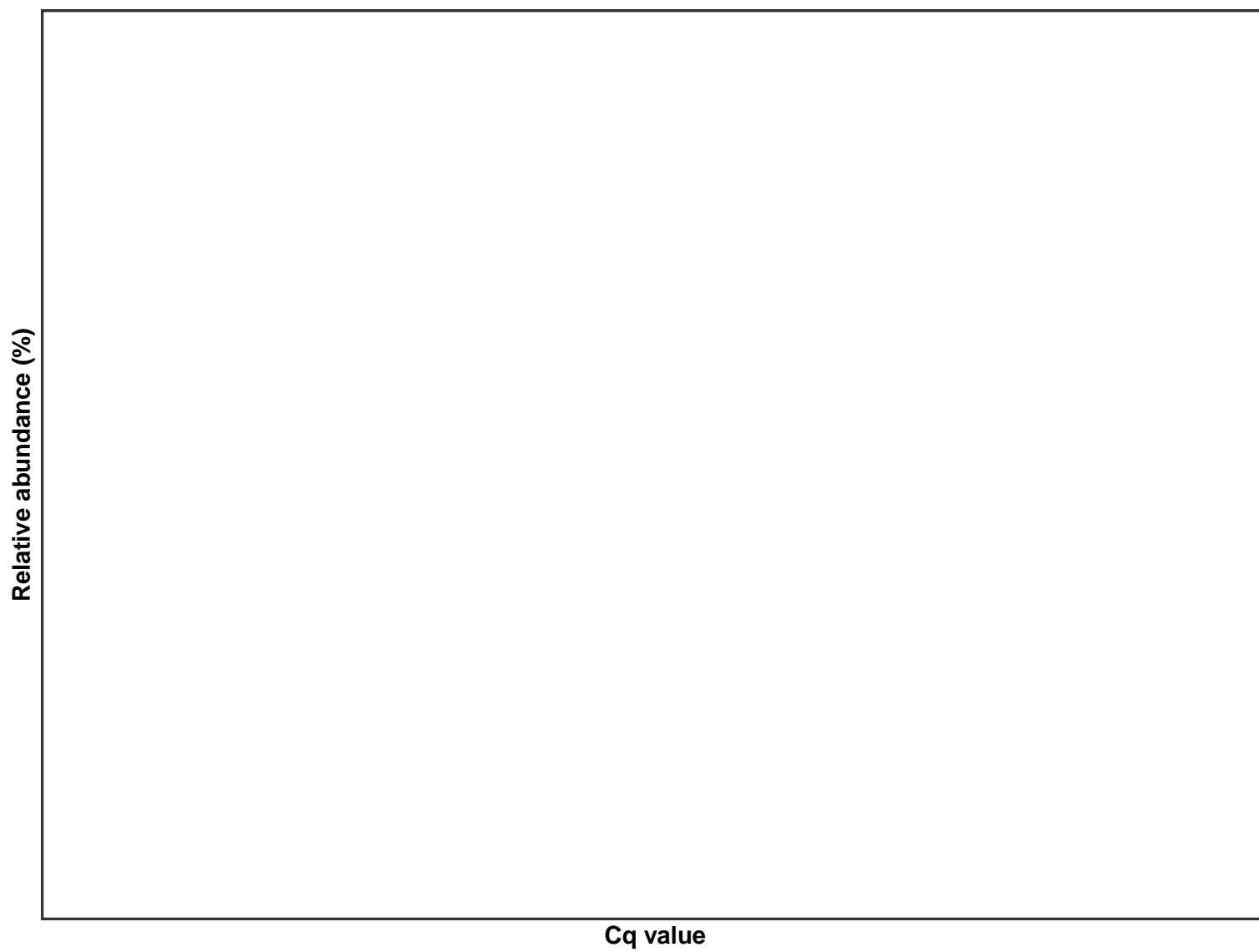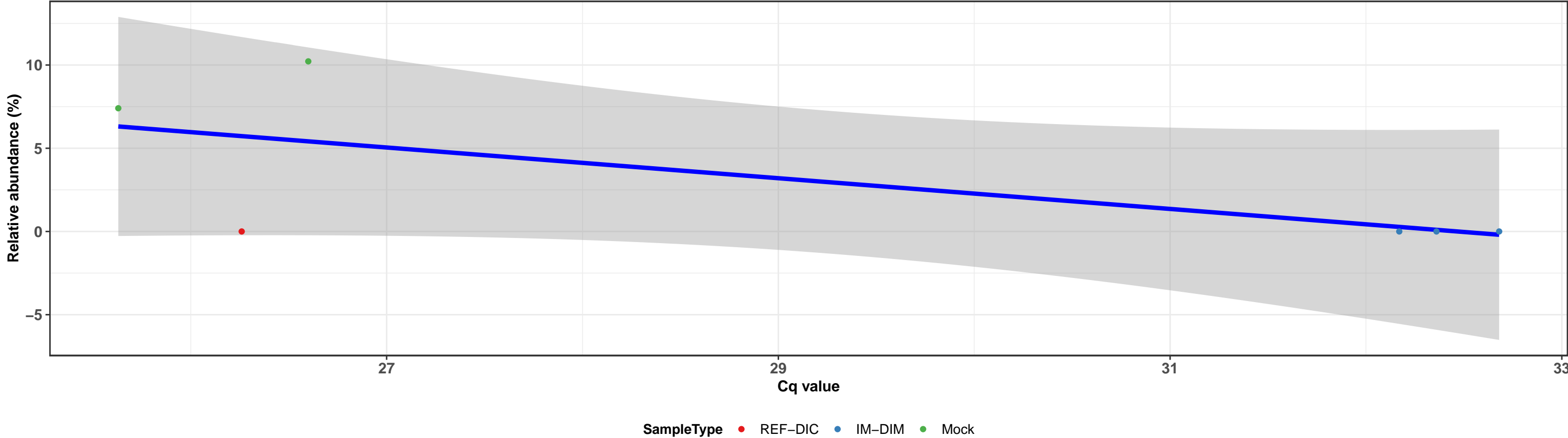
Correlation with all samples

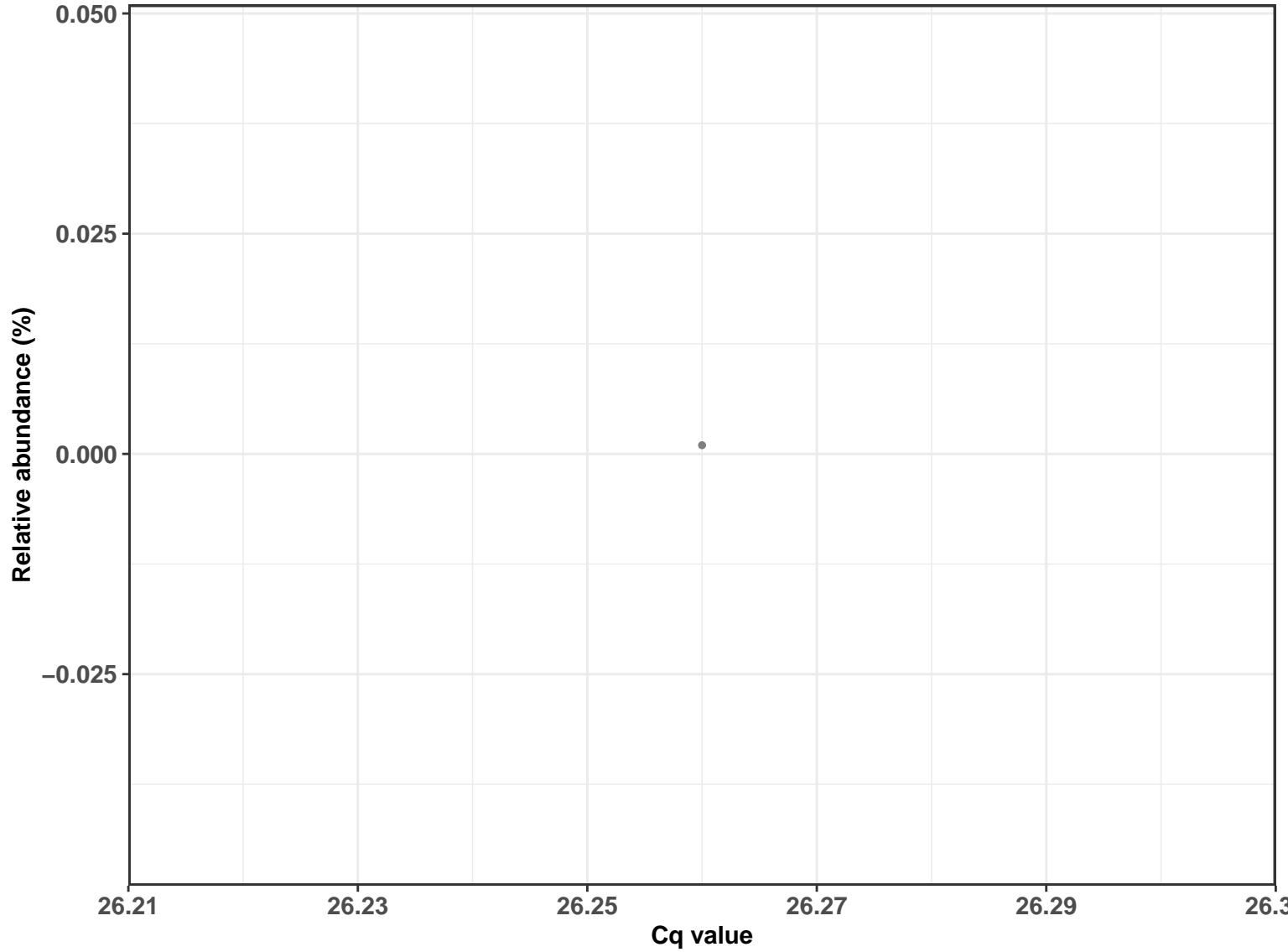SampleType ● Mock

Correlation within:

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA
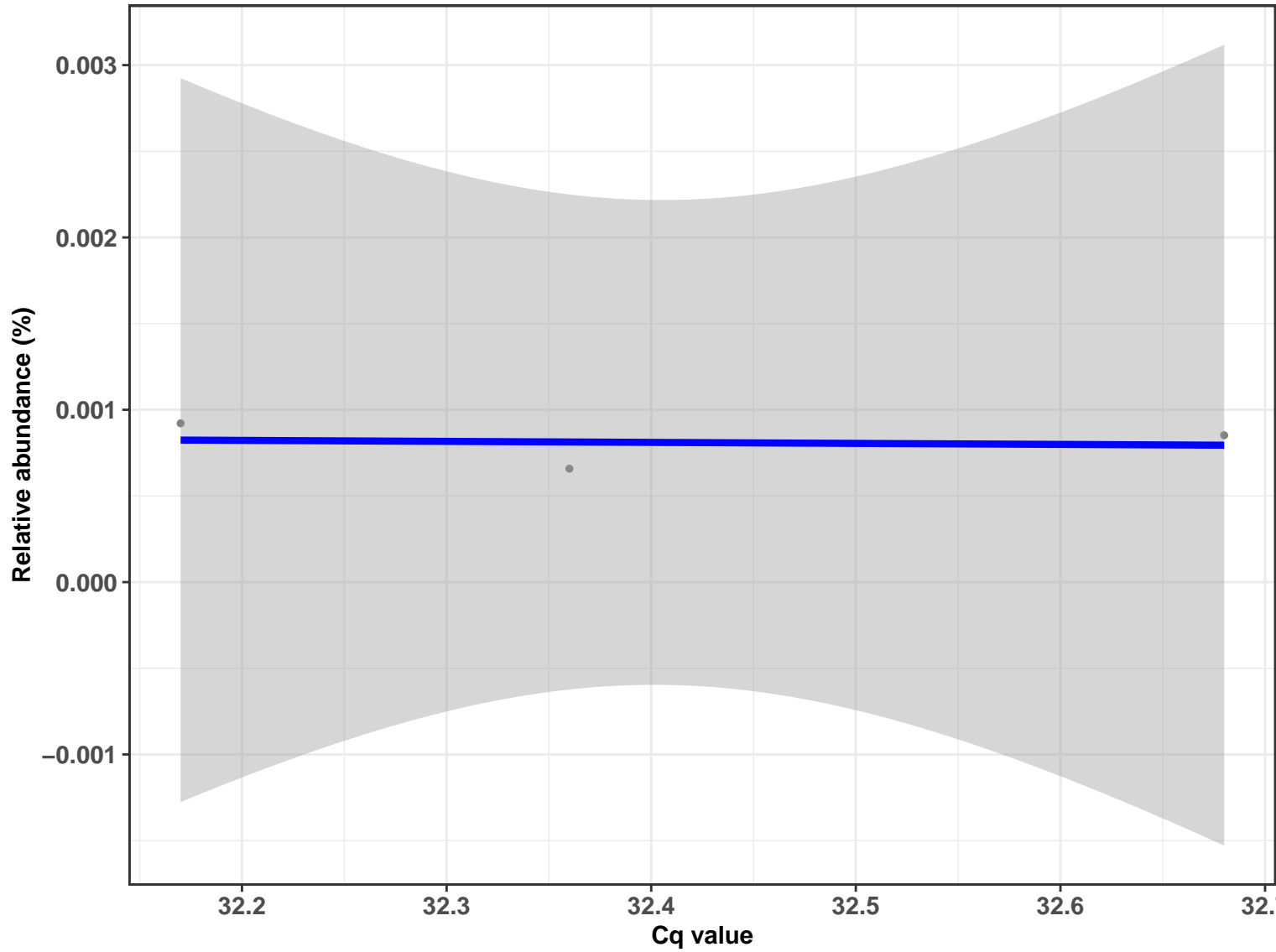
Correlation with all samples

$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{Spearman} = -0.771$, $CI_{95\%}$ [−1.325, −0.371], $n_{pairs} = 6$
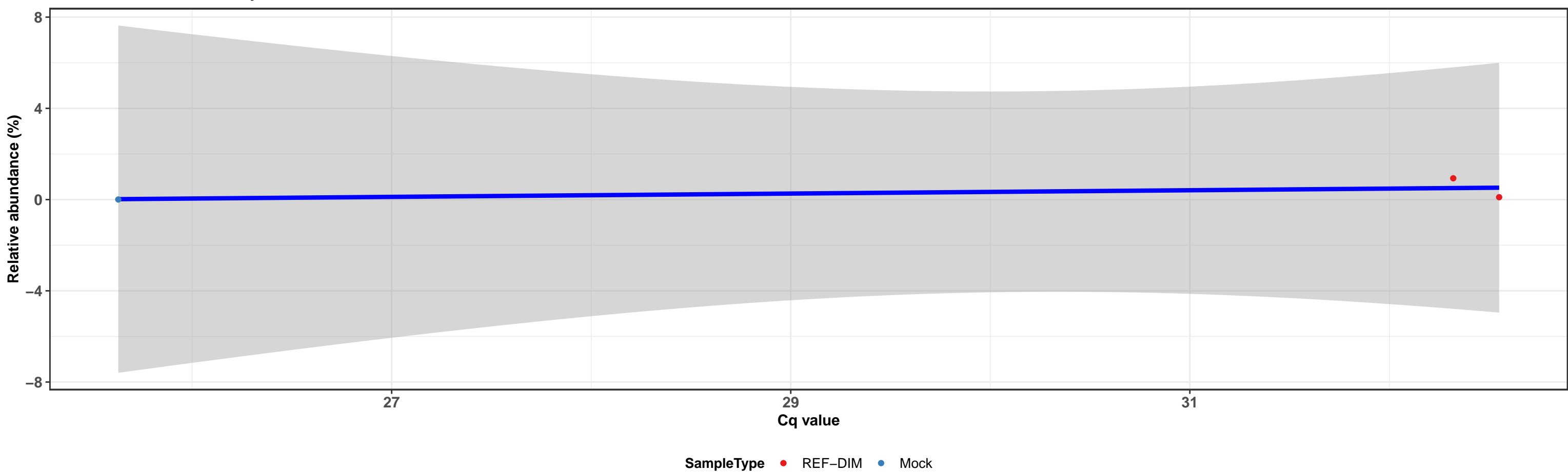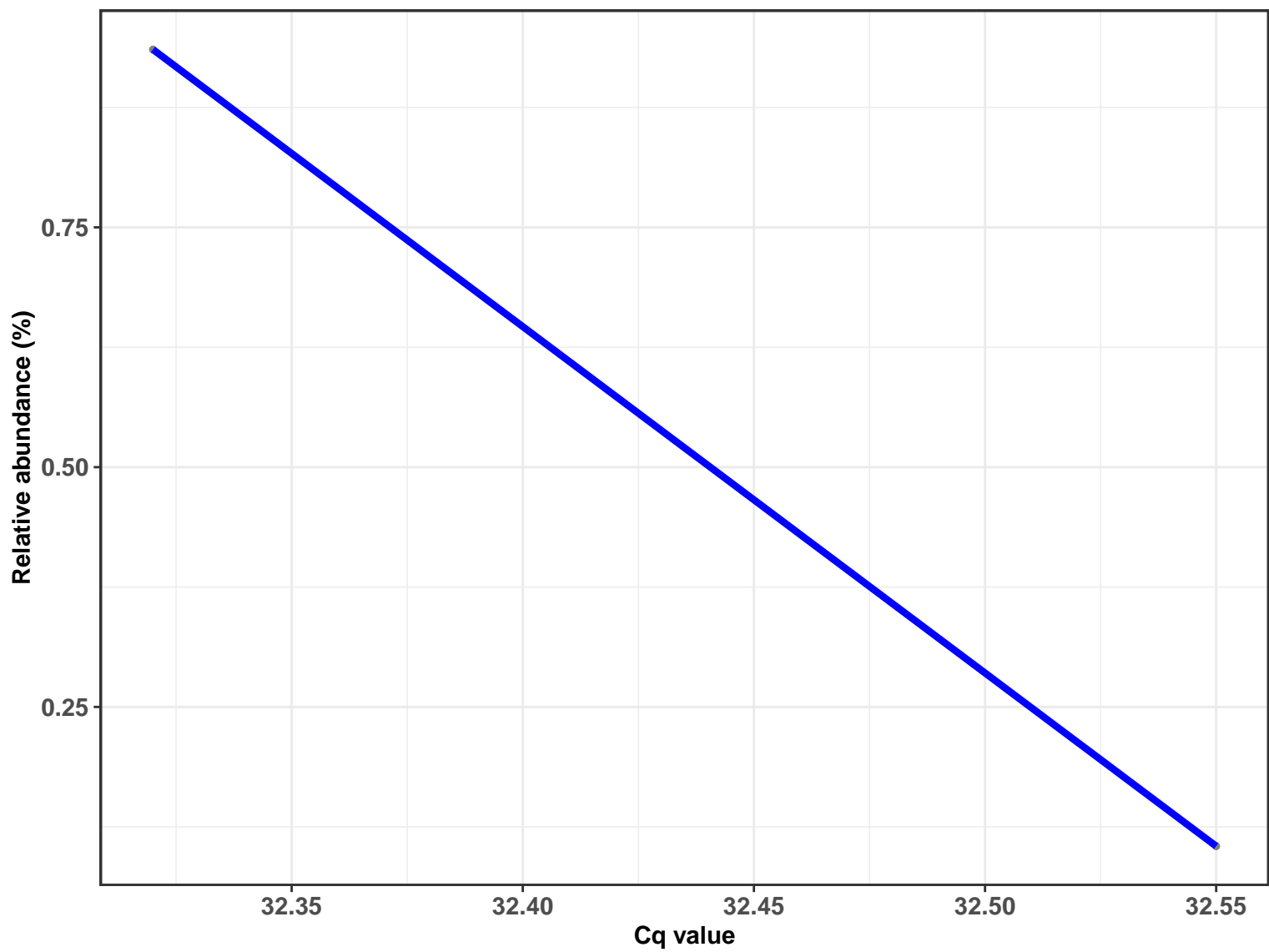
k__Bacteria; p__Cyanobacteria; c__Melainabacteria; o__Obscuribacterales; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa
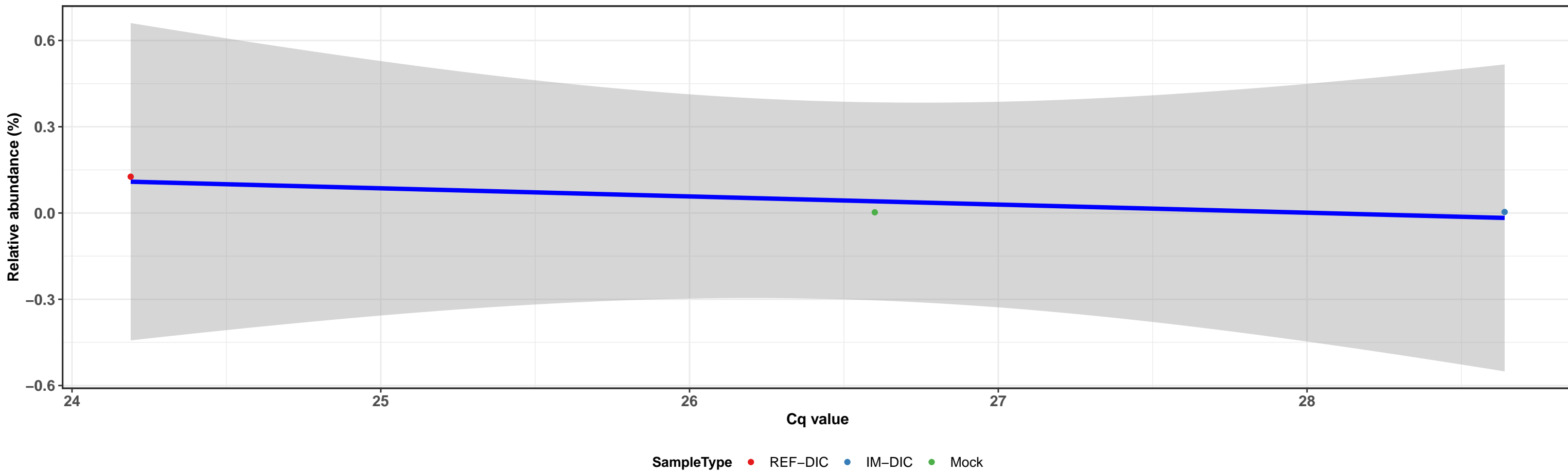
Correlation with all samples

SampleType ● REF−DIM ● Mock

Correlation within: REF−DIM

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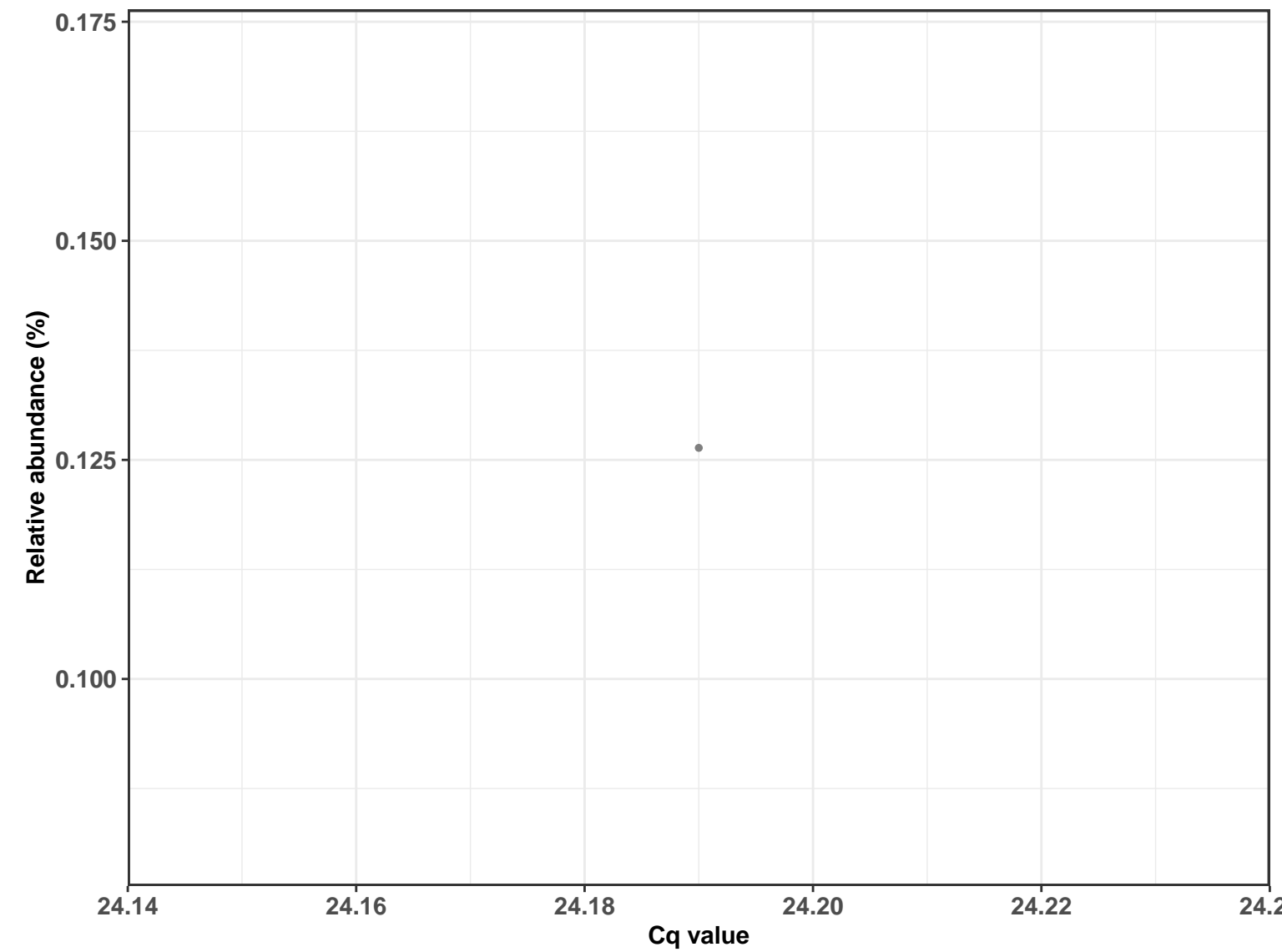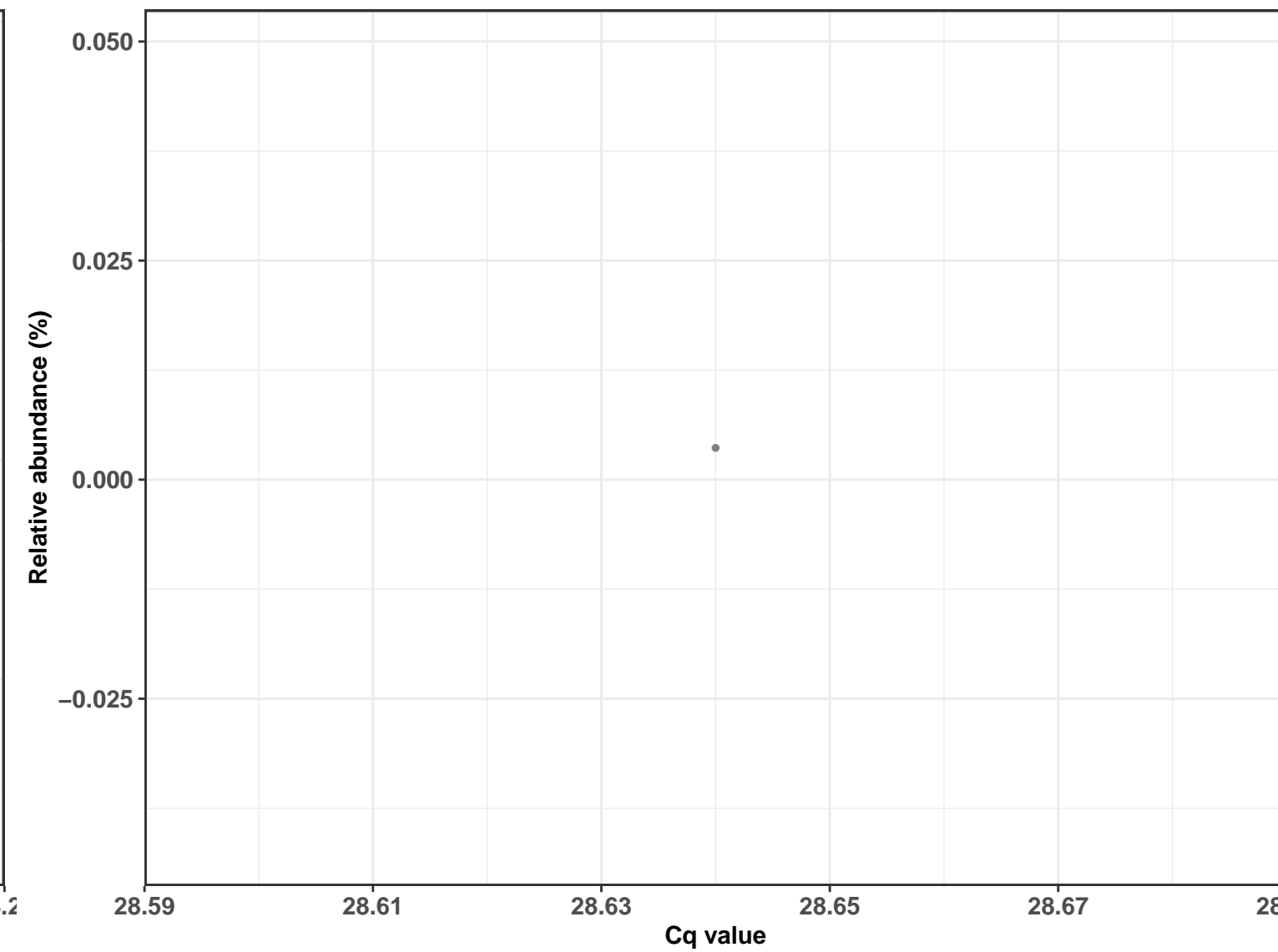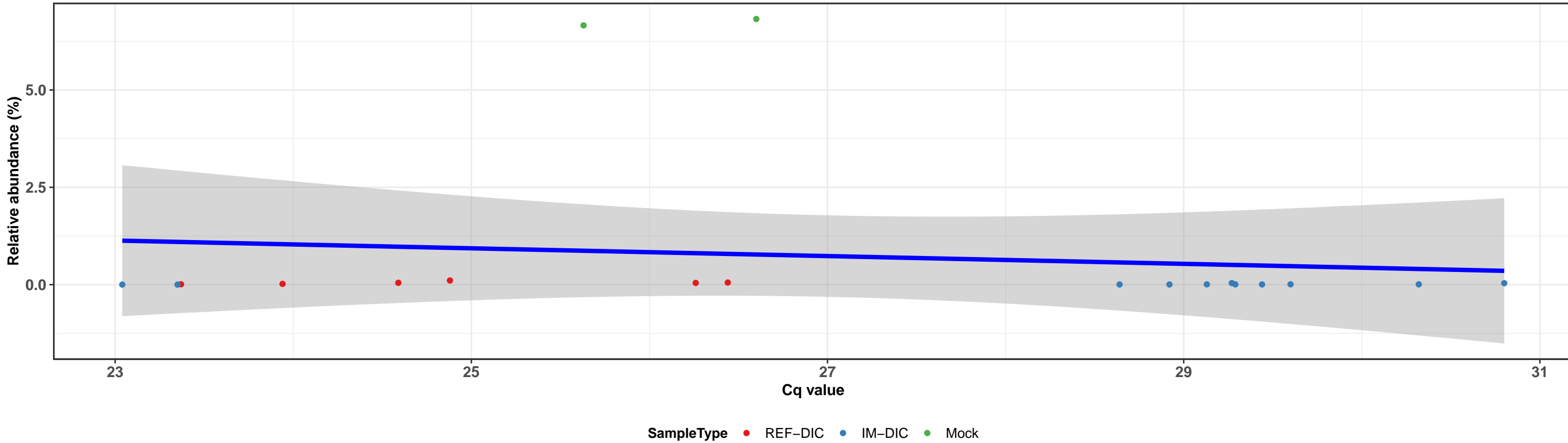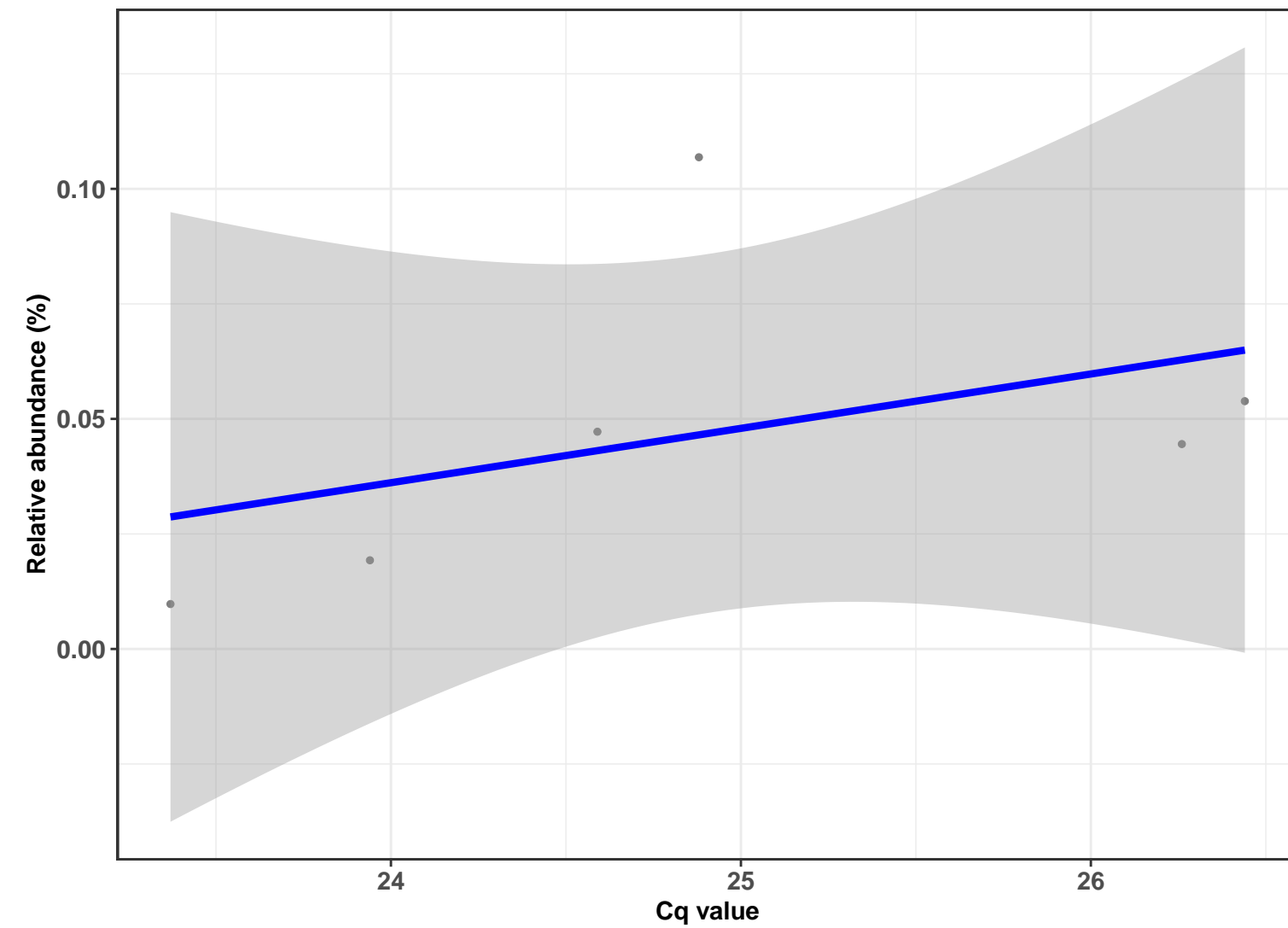
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

$\log_e(S) = 7.080$, $p = 0.864$, $\hat{\rho}_{Spearman} = -0.042$, $CI_{95\%}$ [−0.602, 0.464], $n_{pairs} = 19$

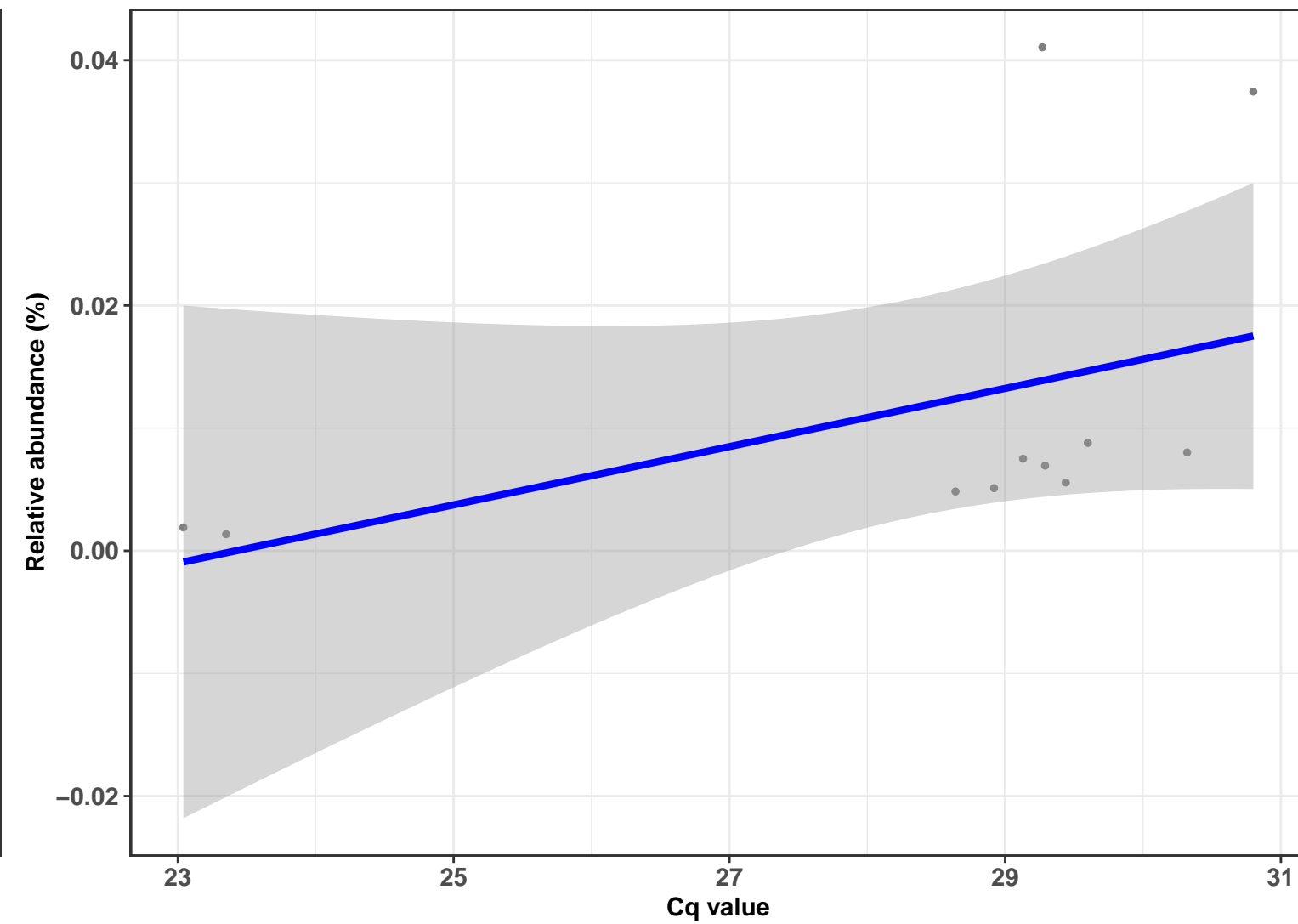SampleType ● REF−DIC ● IM−DIC ● Mock

Correlation within: REF−DIC

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{Spearman} = 0.714$, $CI_{95\%}$ [−0.029, 1.627], $n_{pairs} = 6$

Correlation within: IM−DIC
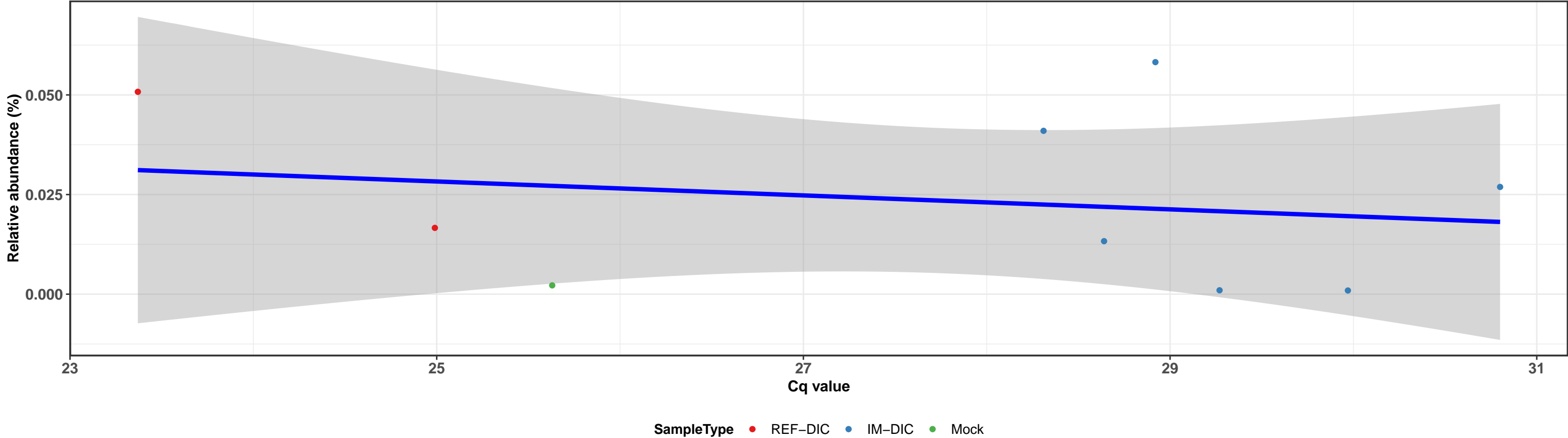
$\log_e(S) = 3.829$, $p = 0.004$, $\hat{\rho}_{Spearman} = 0.791$, $CI_{95\%}$ [0.446, 1.171], $n_{pairs} = 11$

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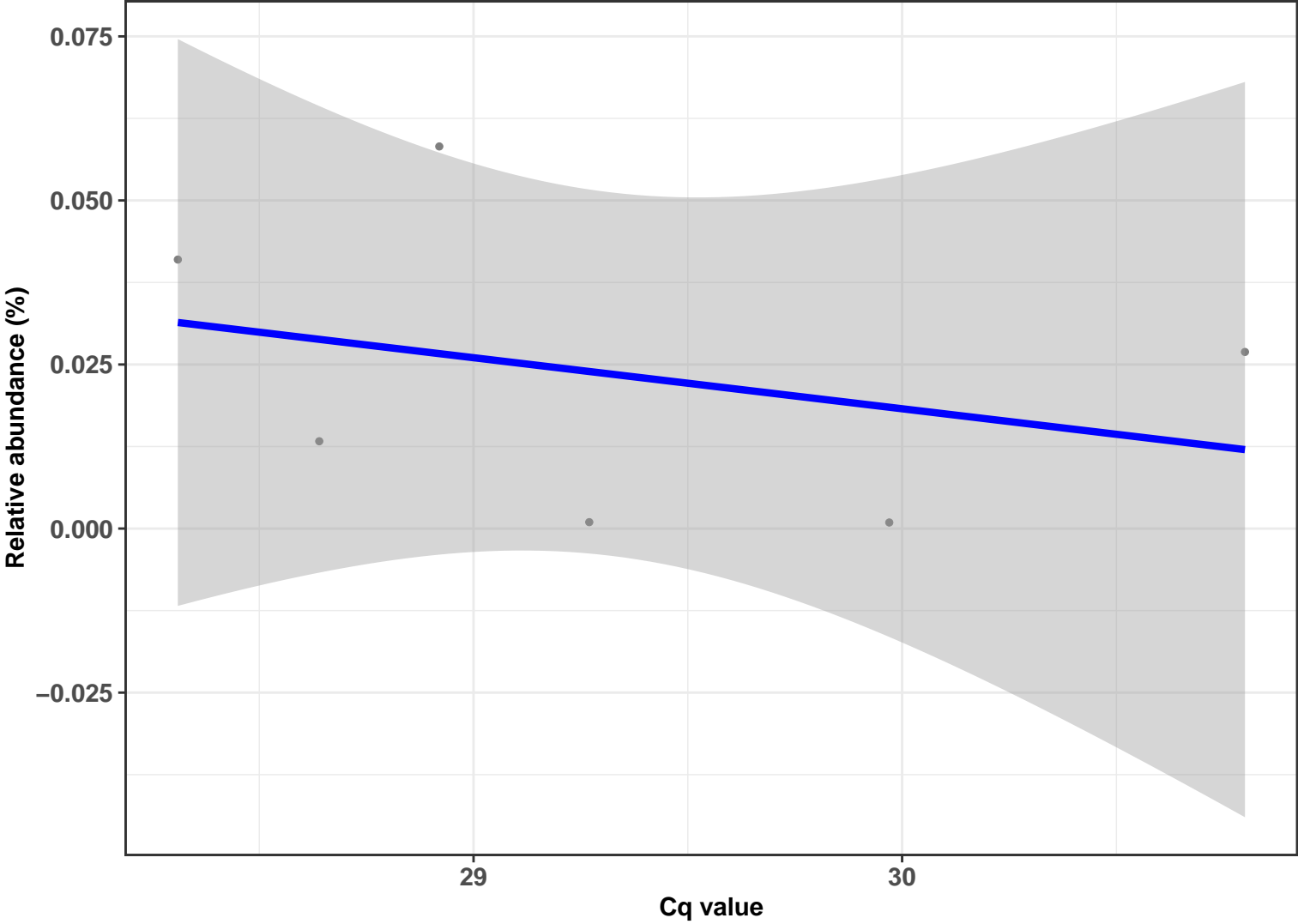
Correlation with all samples

$\log_e(S) = 5.075$, $p = 0.381$, $\hat{\rho}_{Spearman} = -0.333$, $CI_{95\%}$ [−1.087, 0.385], $n_{pairs} = 9$

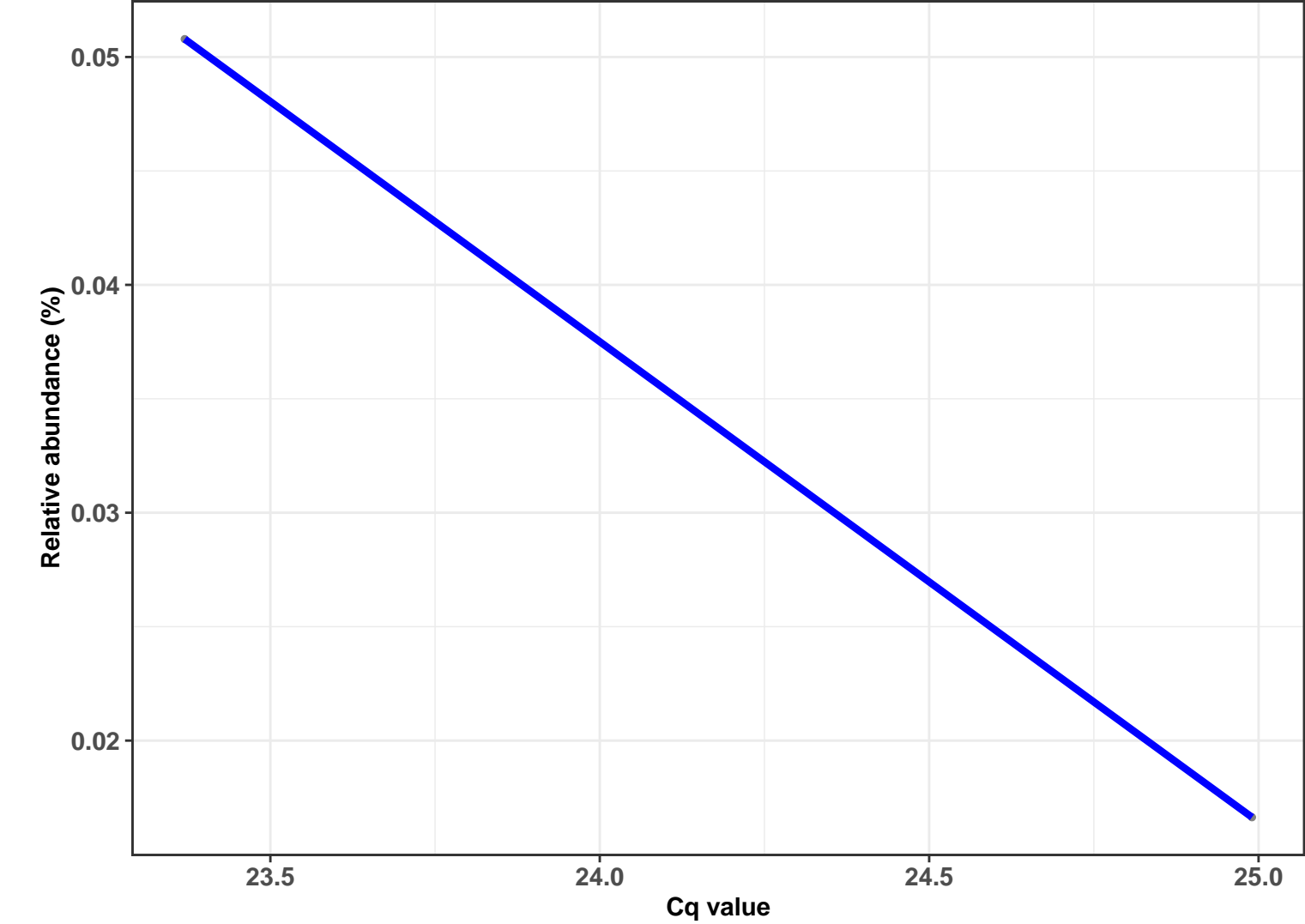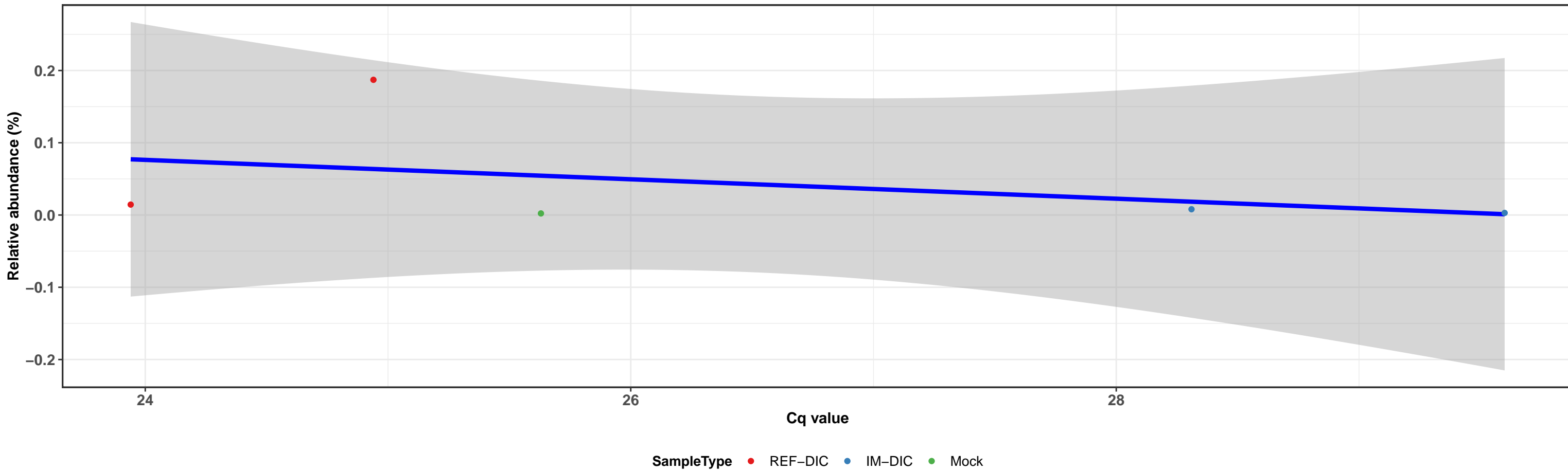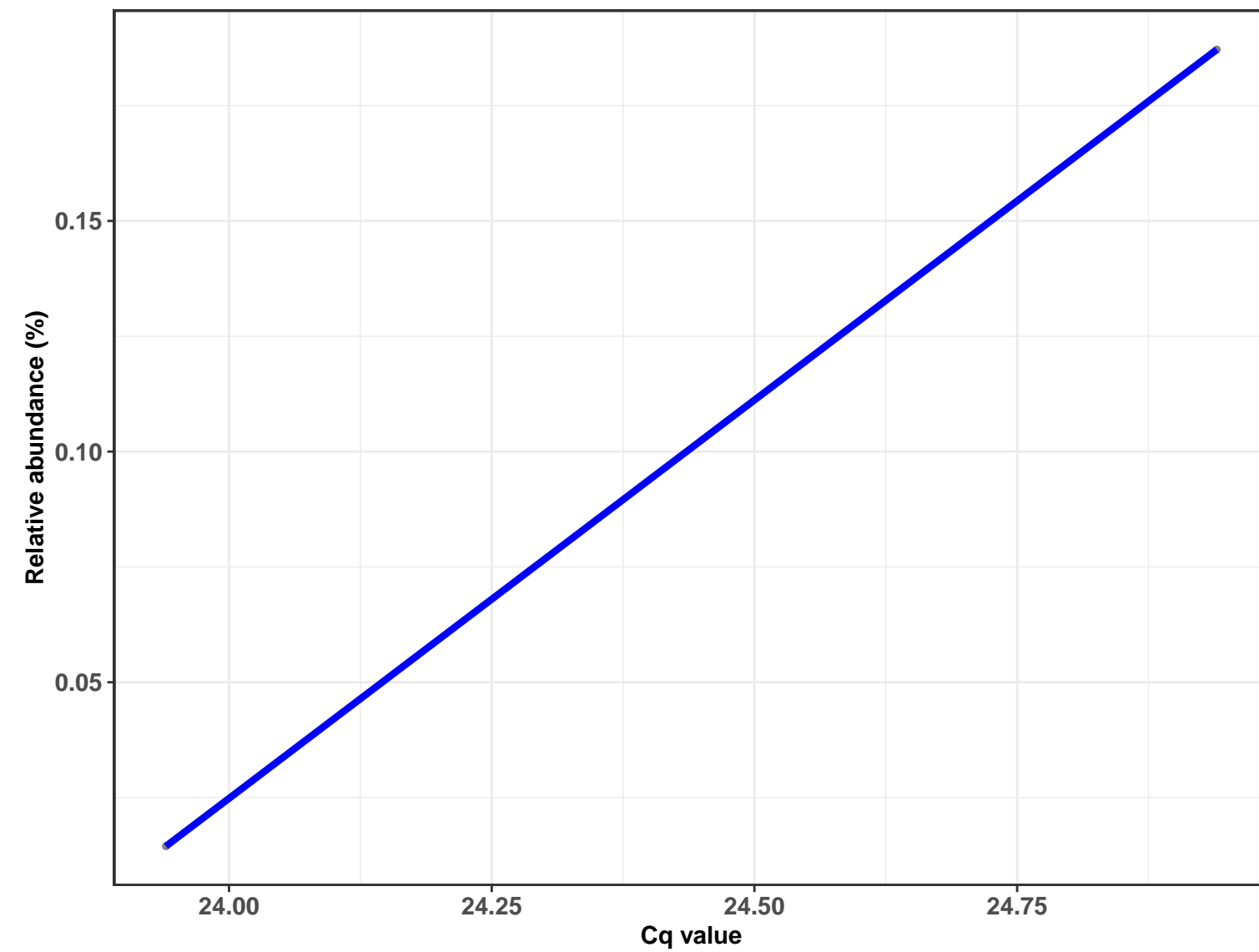SampleType ● REF−DIC ● IM−DIC ● Mock

Correlation within: REF−DIC

Correlation within: IM−DIC

$\log_e(S) = 3.912$, $p = 0.397$, $\hat{\rho}_{Spearman} = -0.429$, $CI_{95\%}$ [−1.186, 0.275], $n_{pairs} = 6$

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

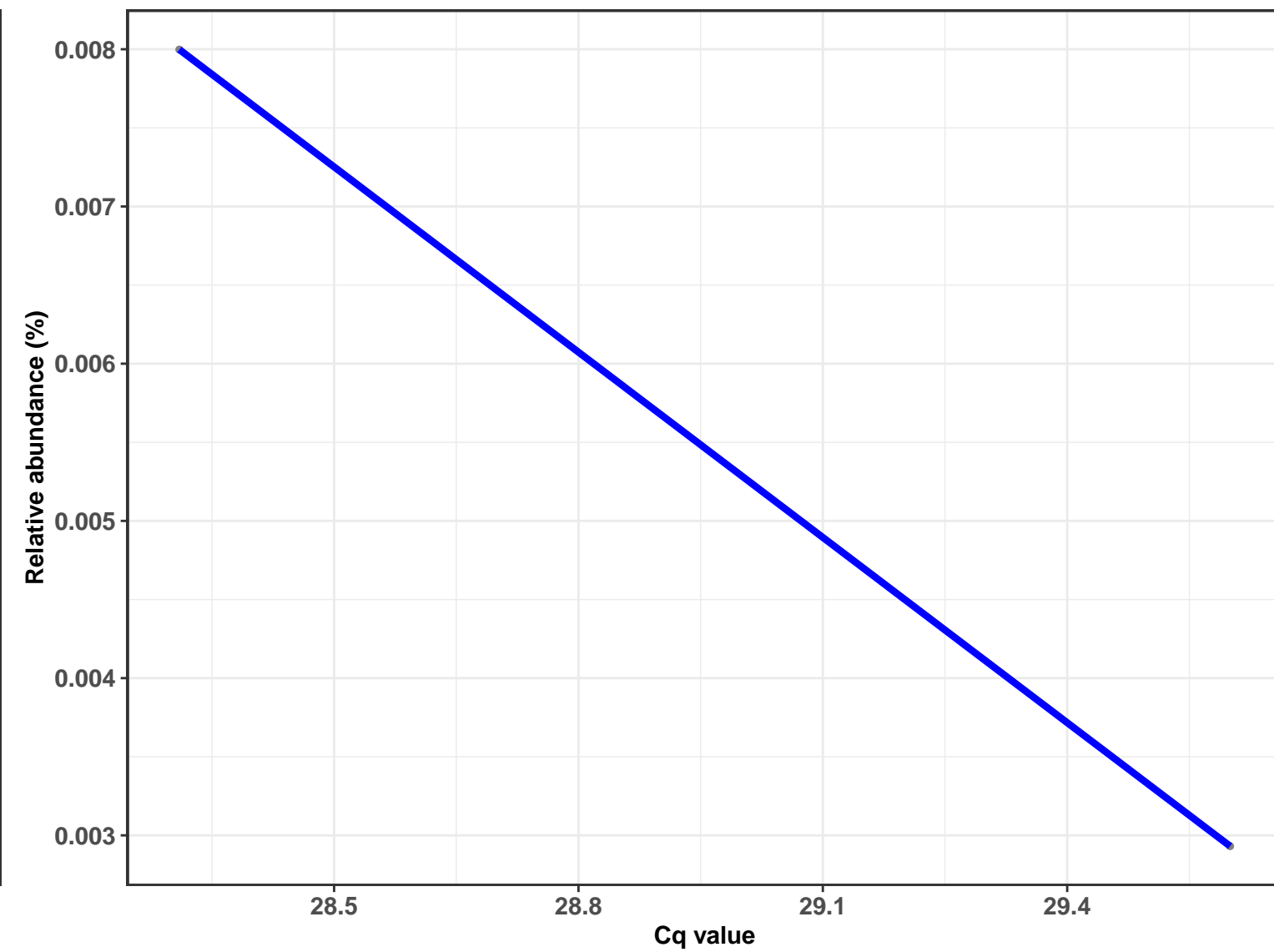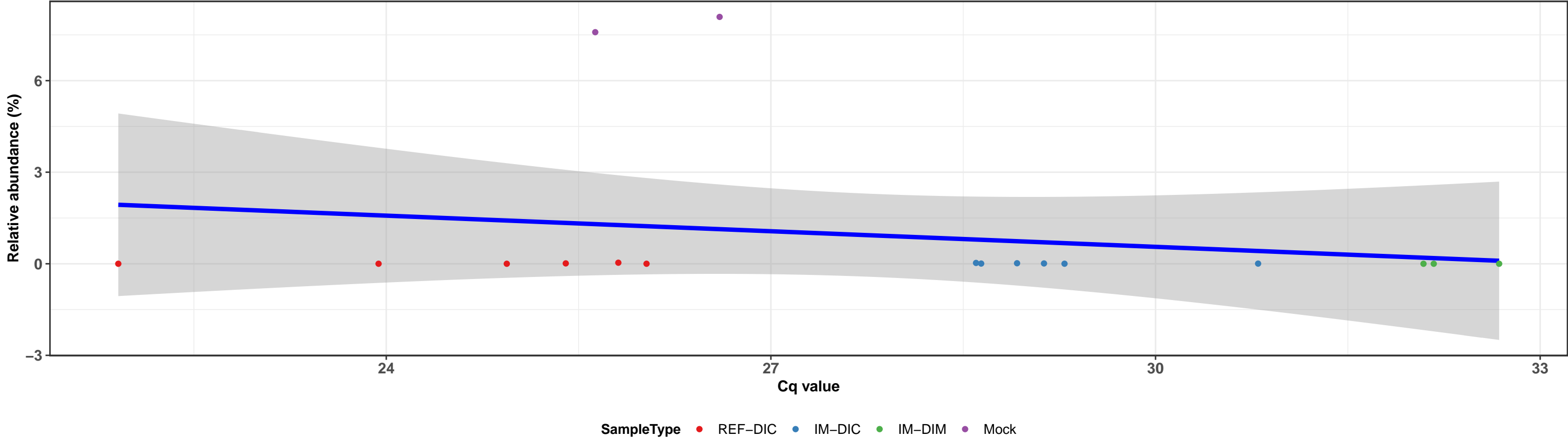**k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum**
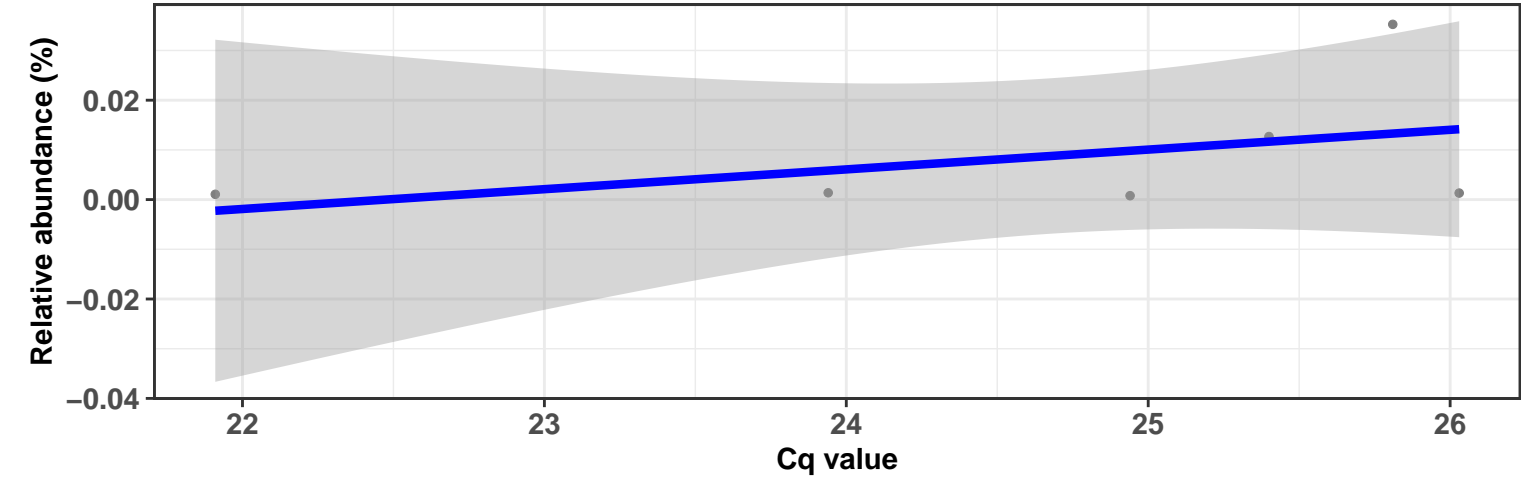

Correlation with all samples

$\log_e(S) = 6.914$, $p = 0.368$, $\hat{\rho}_{Spearman} = -0.233$, $CI_{95\%}$ [−0.868, 0.274], $n_{pairs} = 17$

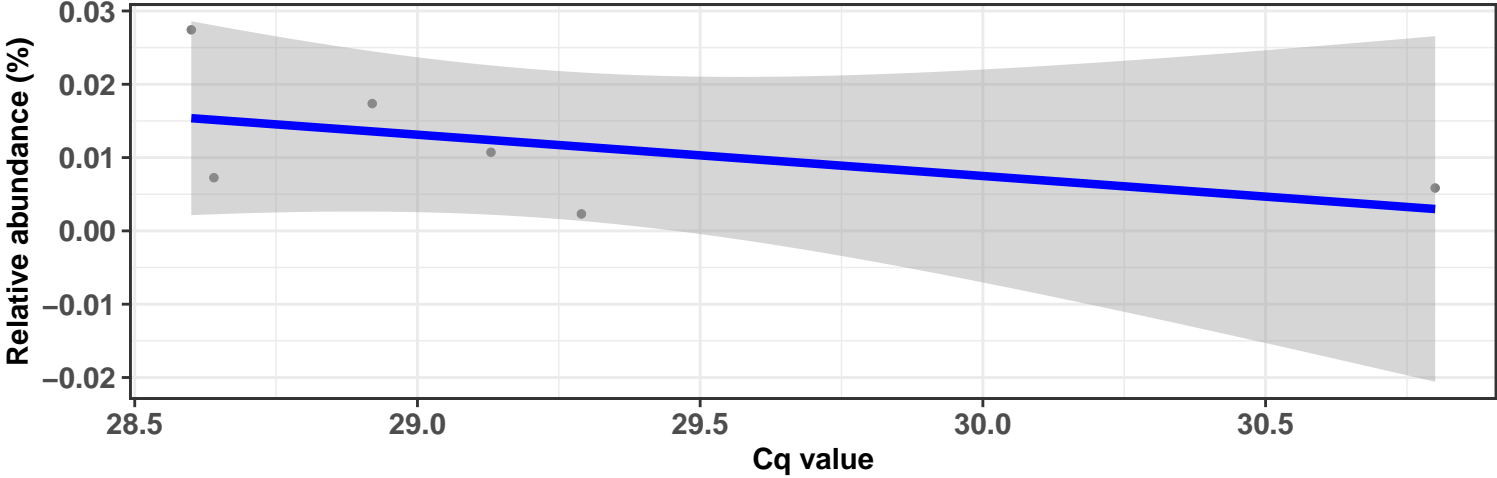SampleType: REF−DIC, IM−DIC, IM−DIM, Mock

Correlation within: REF−DIC

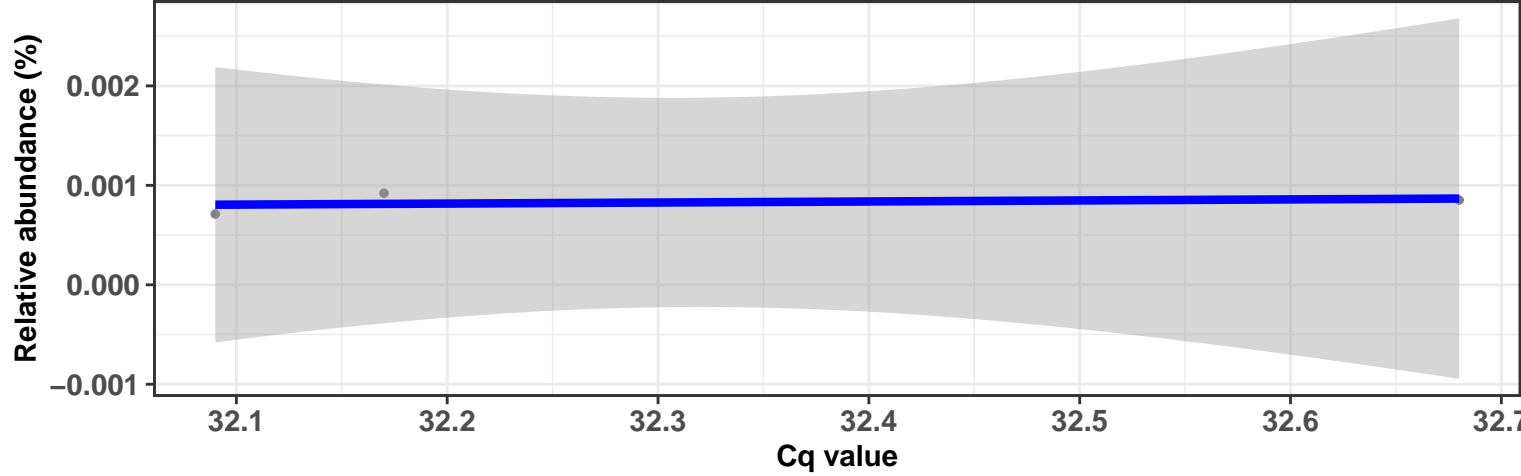$\log_e(S) = 2.996$, $p = 0.397$, $\hat{\rho}_{Spearman} = 0.429$, $CI_{95\%}$ [−0.280, 1.314], $n_{pairs} = 6$

Correlation within: IM−DIC

$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{Spearman} = -0.771$, $CI_{95\%}$ [−1.329, −0.278], $n_{pairs} = 6$
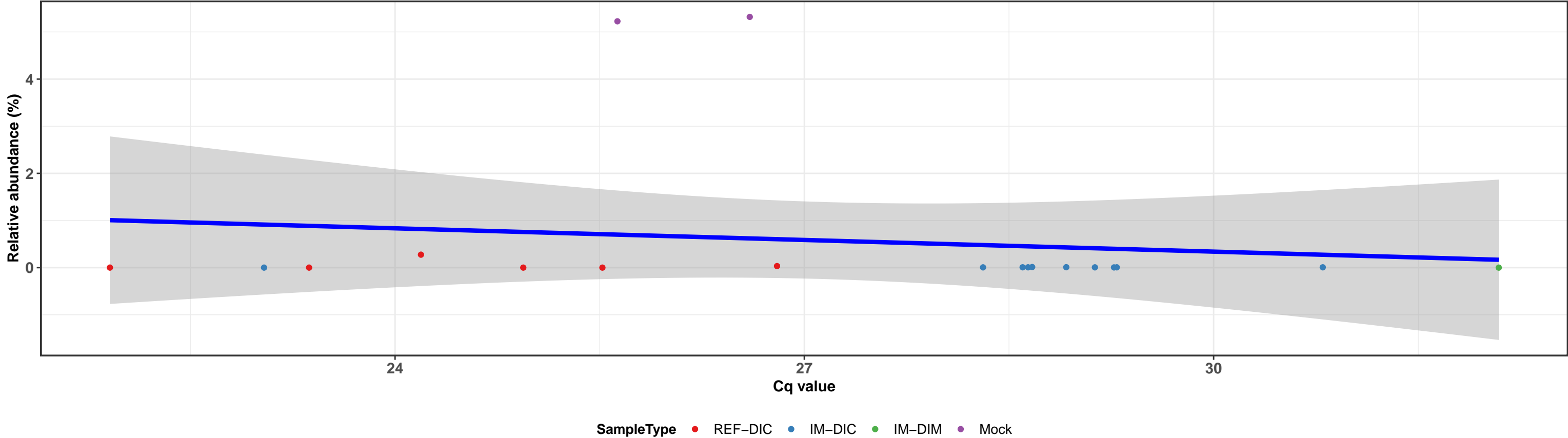
Correlation within: IM−DIM

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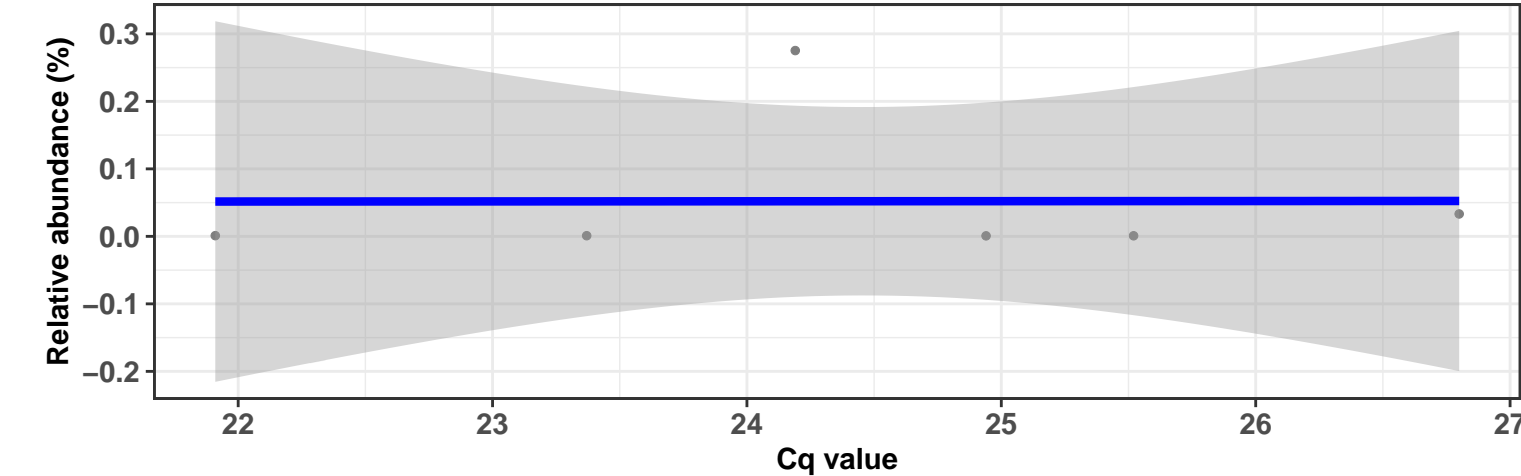
Correlation with all samples

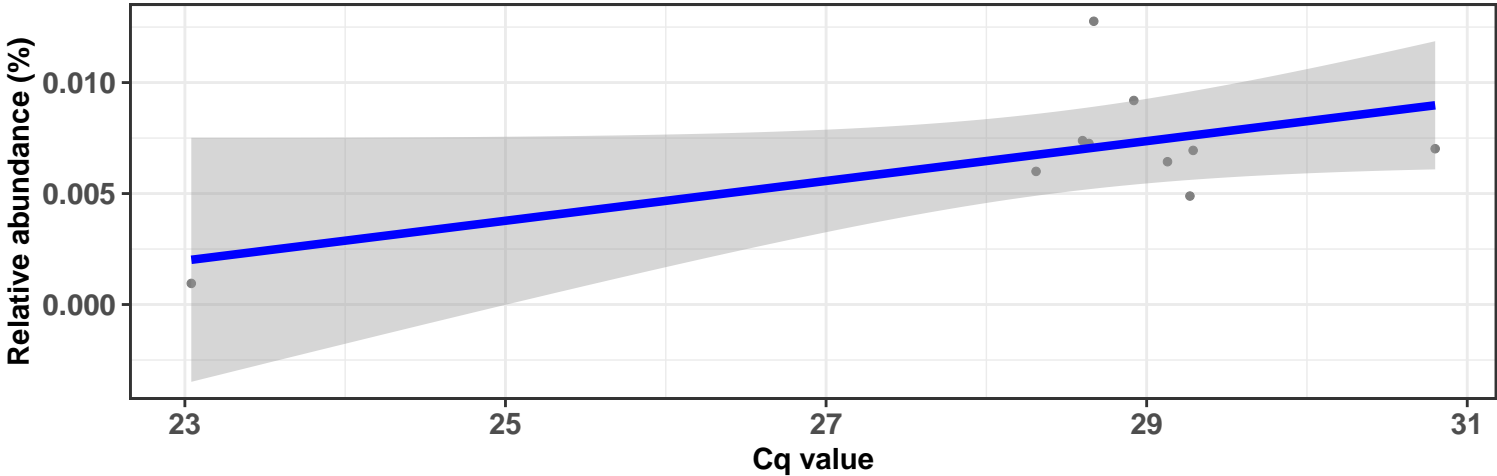$\log_e(S) = 6.968$, $p = 0.781$, $\hat{\rho}_{Spearman} = 0.068$, $CI_{95\%}$ [−0.455, 0.647], $n_{pairs} = 19$

SampleType ● REF−DIC ● IM−DIC ● IM−DIM ● Mock

Correlation within: REF−DIC

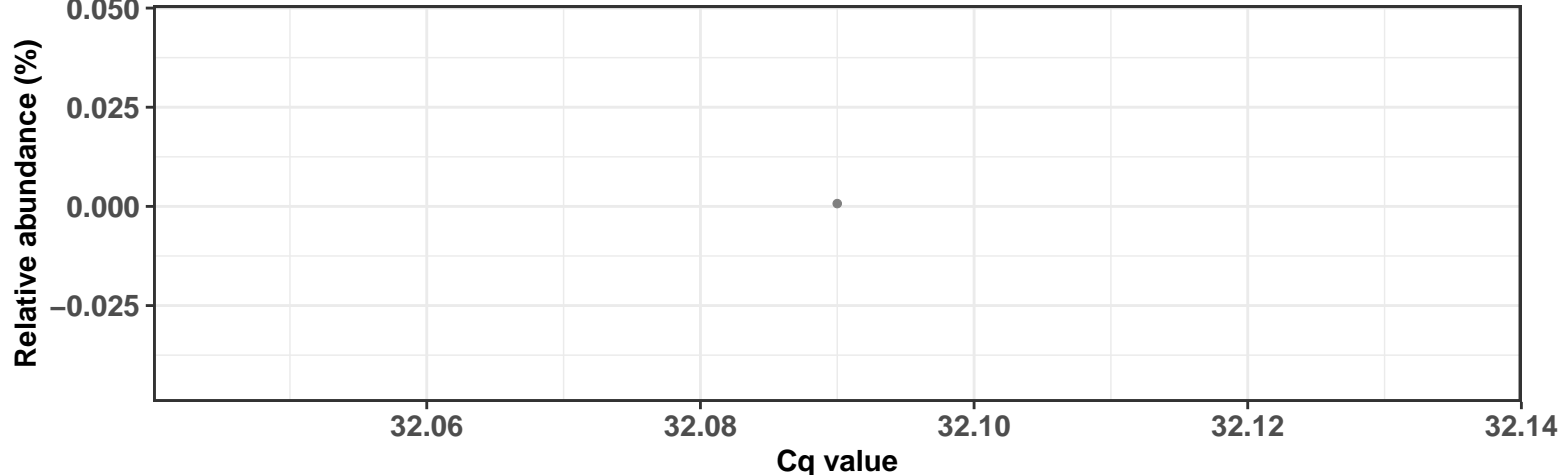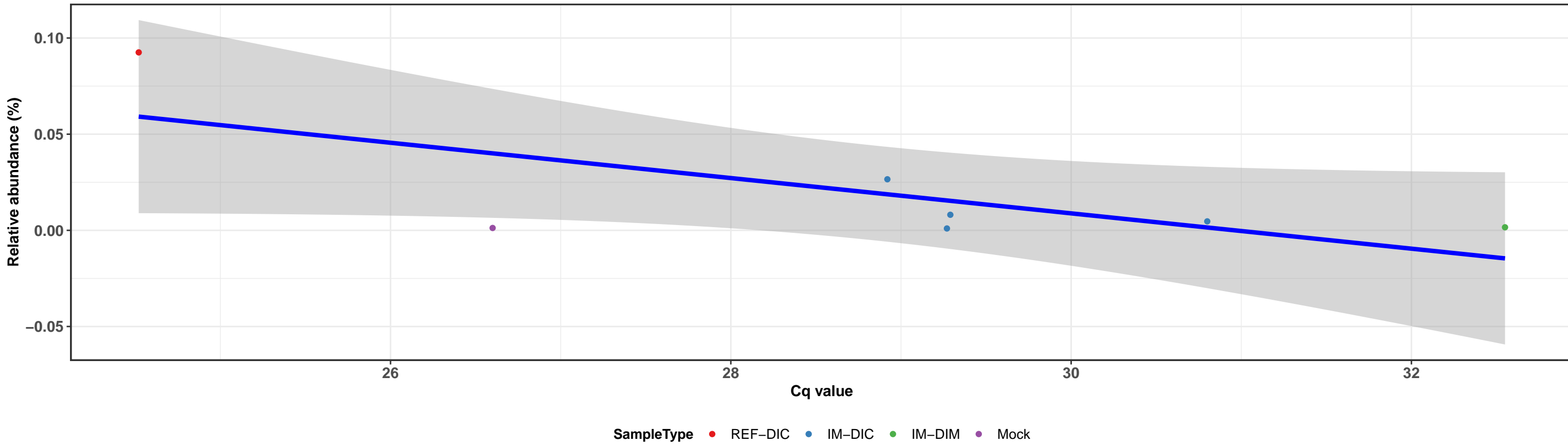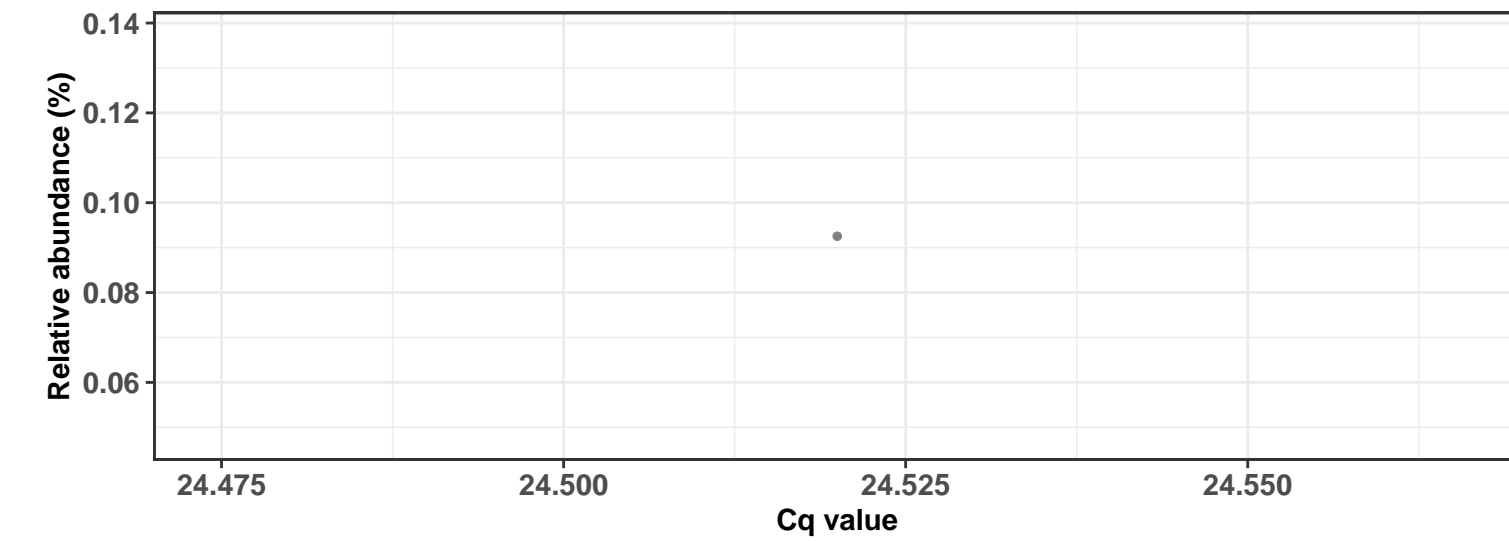$\log_e(S) = 3.638$, $p = 0.872$, $\hat{\rho}_{Spearman} = -0.086$, $CI_{95\%}$ [−0.937, 0.866], $n_{pairs} = 6$

Correlation within: IM−DIC

$\log_e(S) = 4.984$, $p = 0.751$, $\hat{\rho}_{Spearman} = 0.115$, $CI_{95\%}$ [−0.652, 0.832], $n_{pairs} = 10$

Correlation within: IM−DIM

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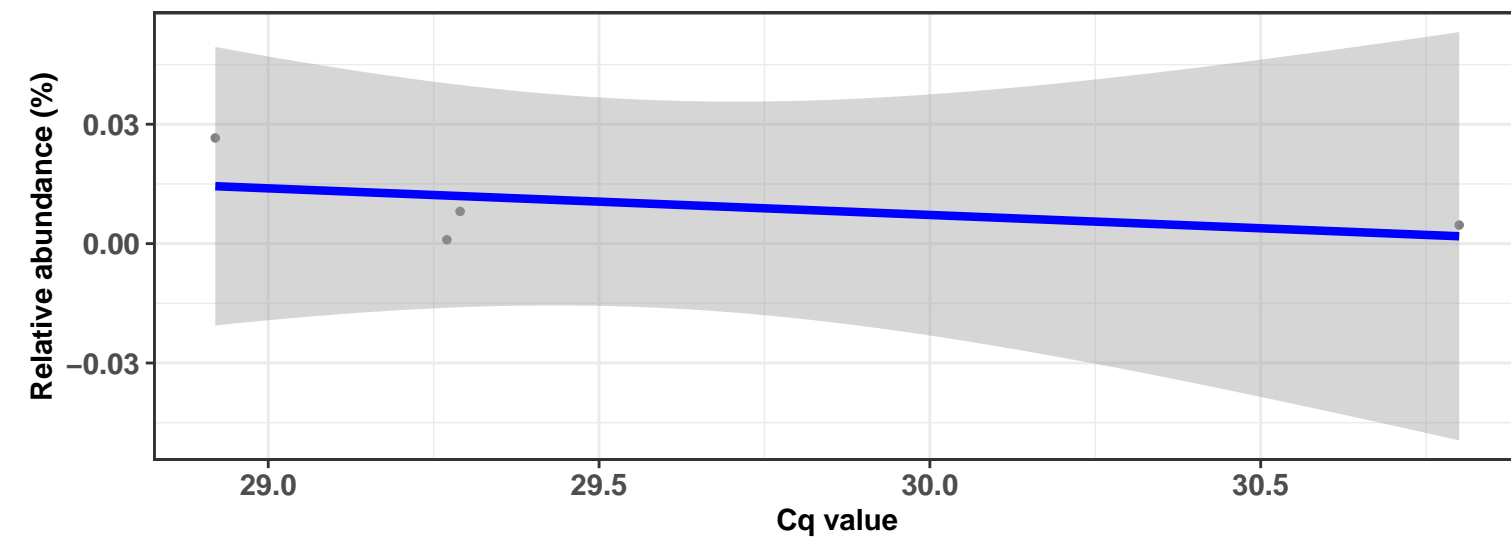
Correlation with all samples

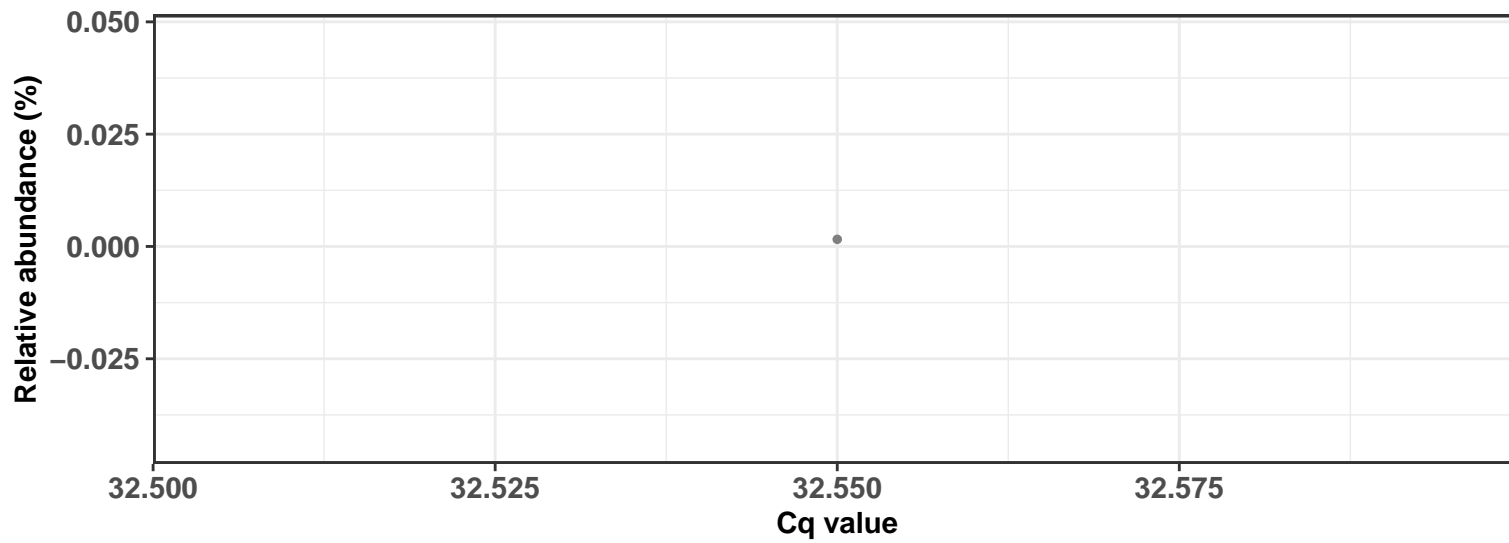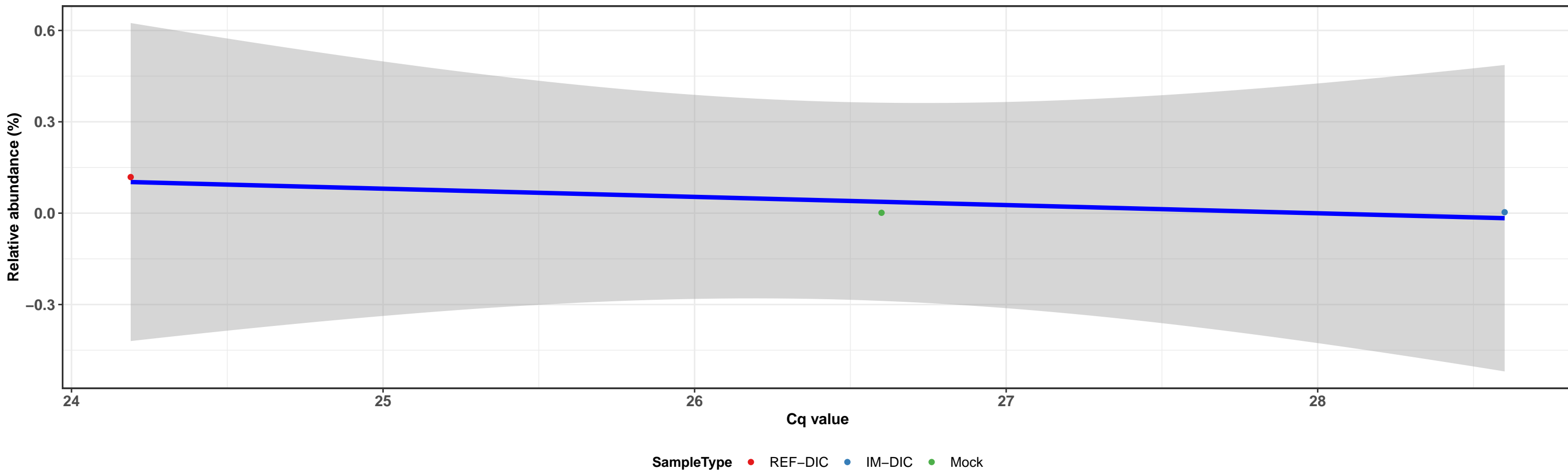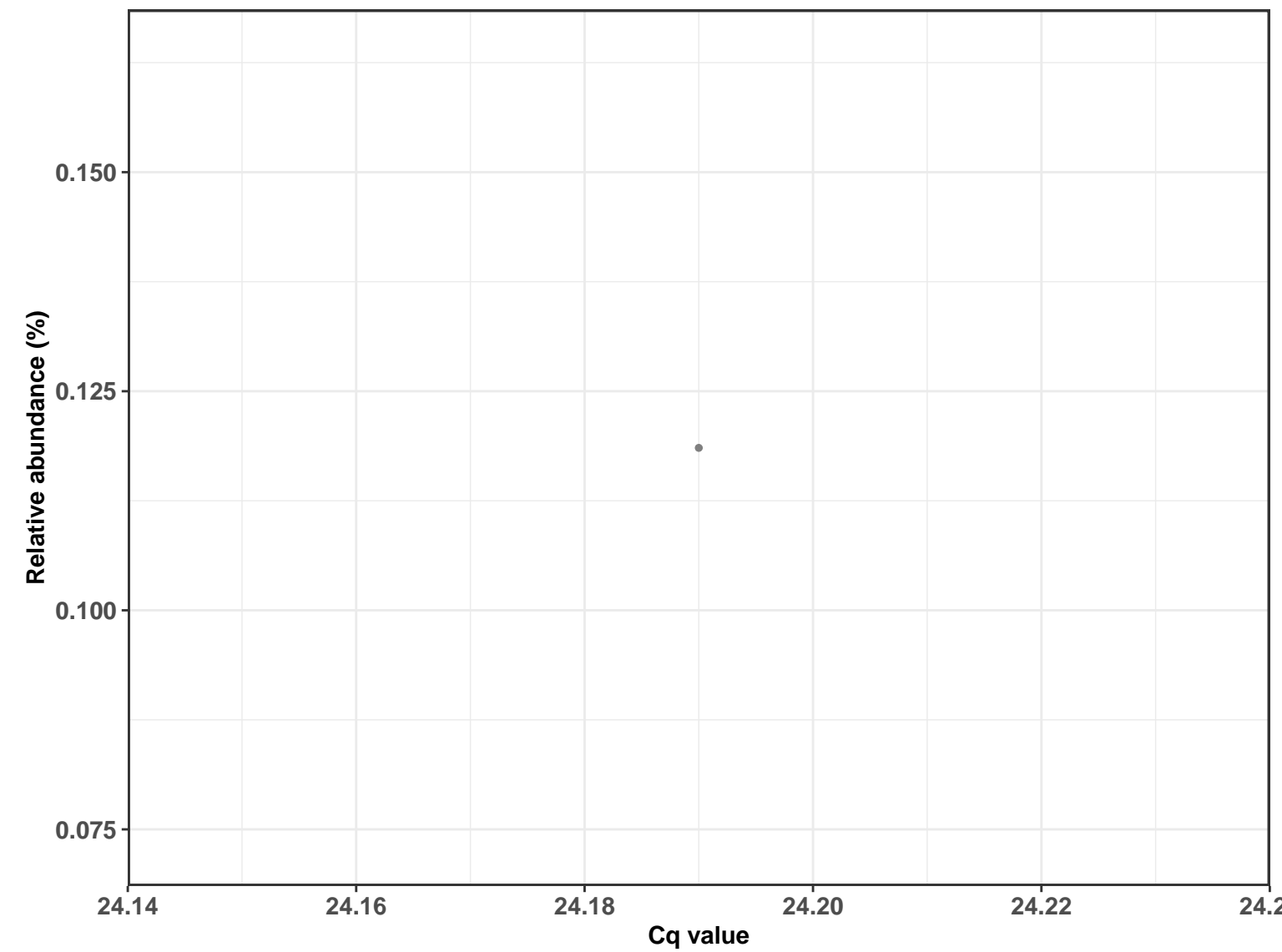$\log_e(S) = 4.304$, $p = 0.482$, $\hat{\rho}_{Spearman} = -0.321$, $CI_{95\%}$ [−1.255, 0.536], $n_{pairs} = 7$

SampleType ● REF−DIC ● IM−DIC ● IM−DIM ● Mock

Correlation within: REF−DIC

Correlation within: IM−DIC

Correlation within: IM−DIM

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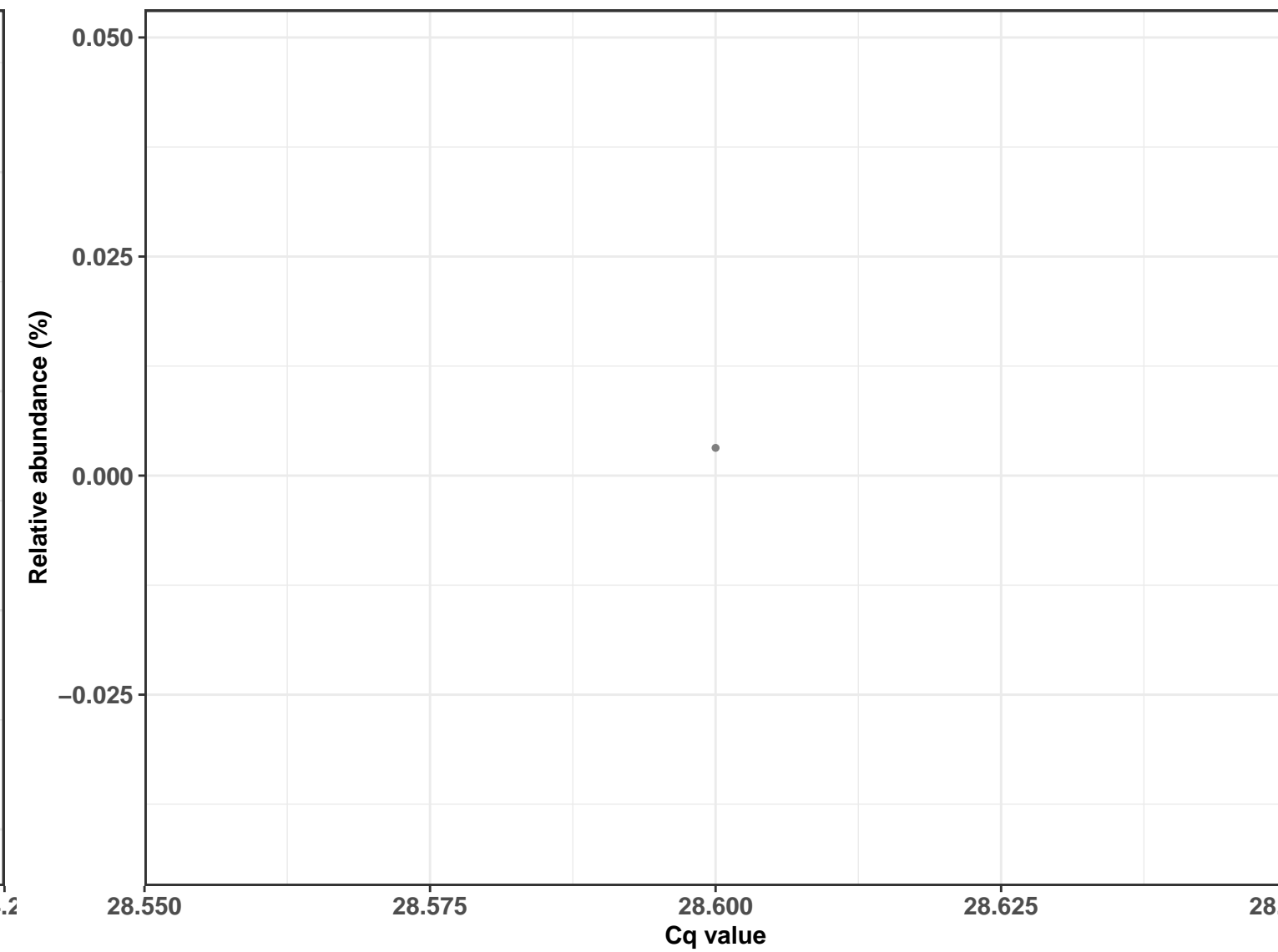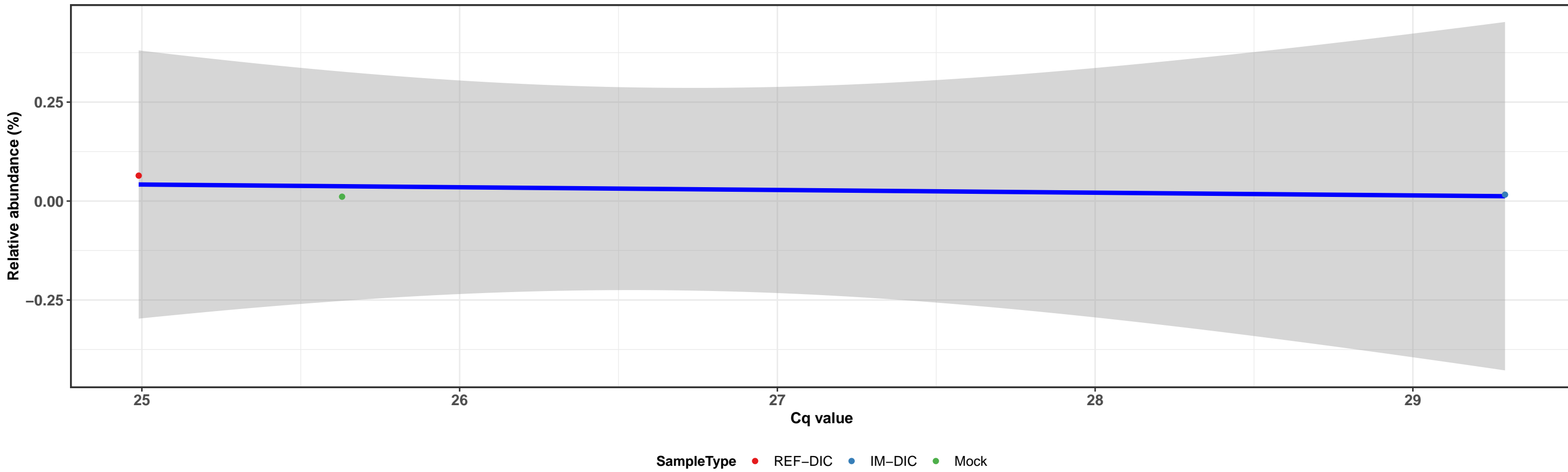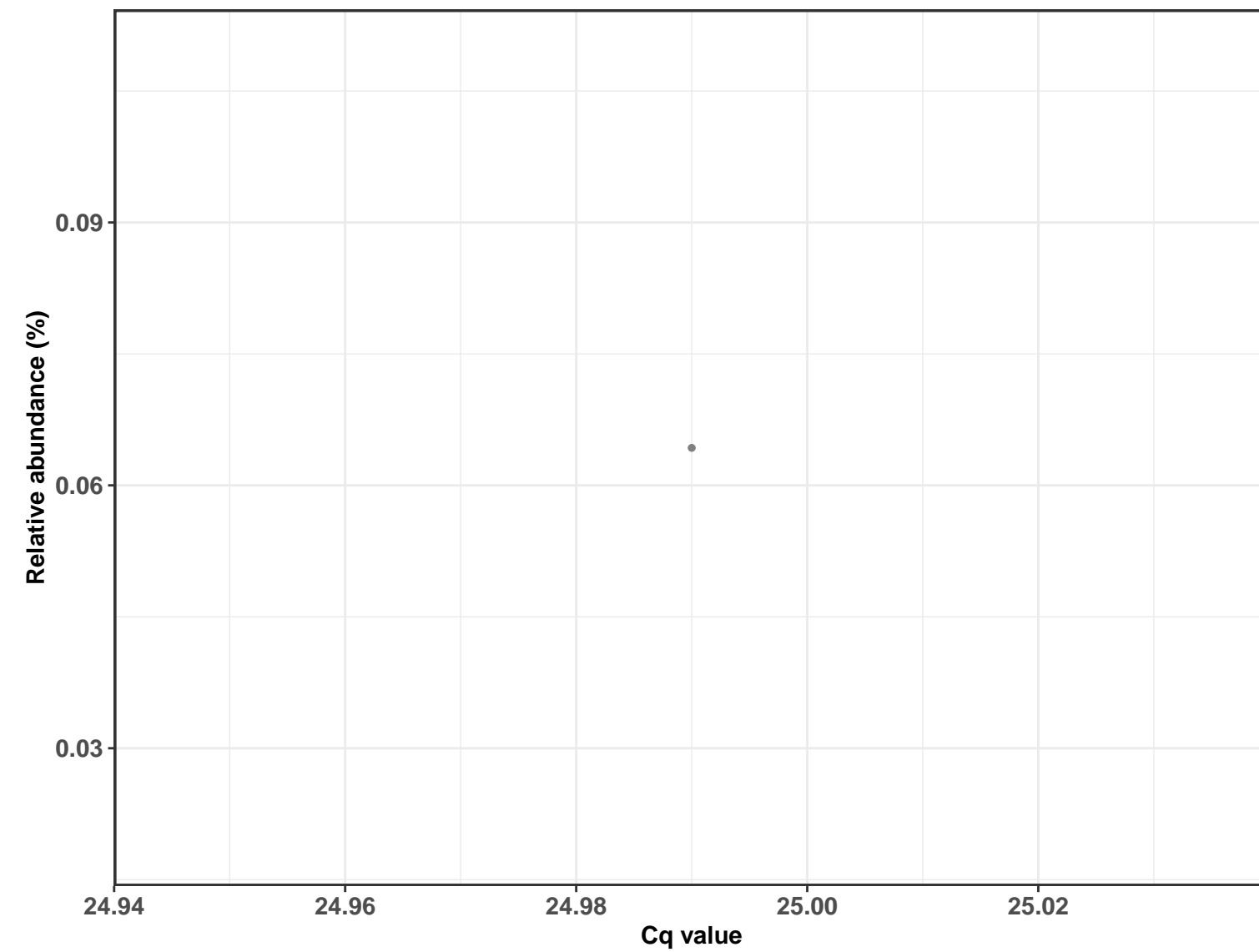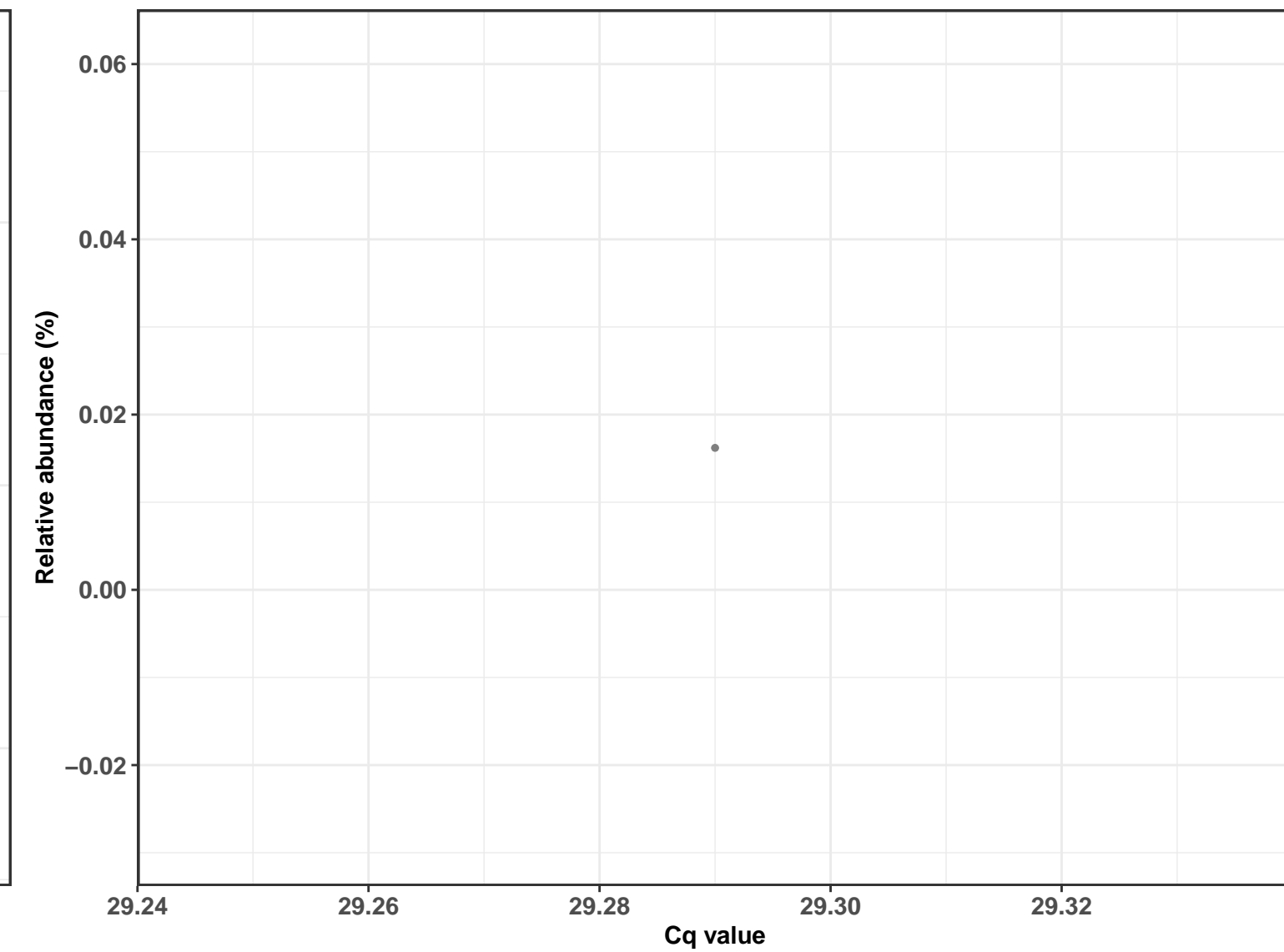
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples

SampleType ● REF−DIC ● IM−DIC ● Mock
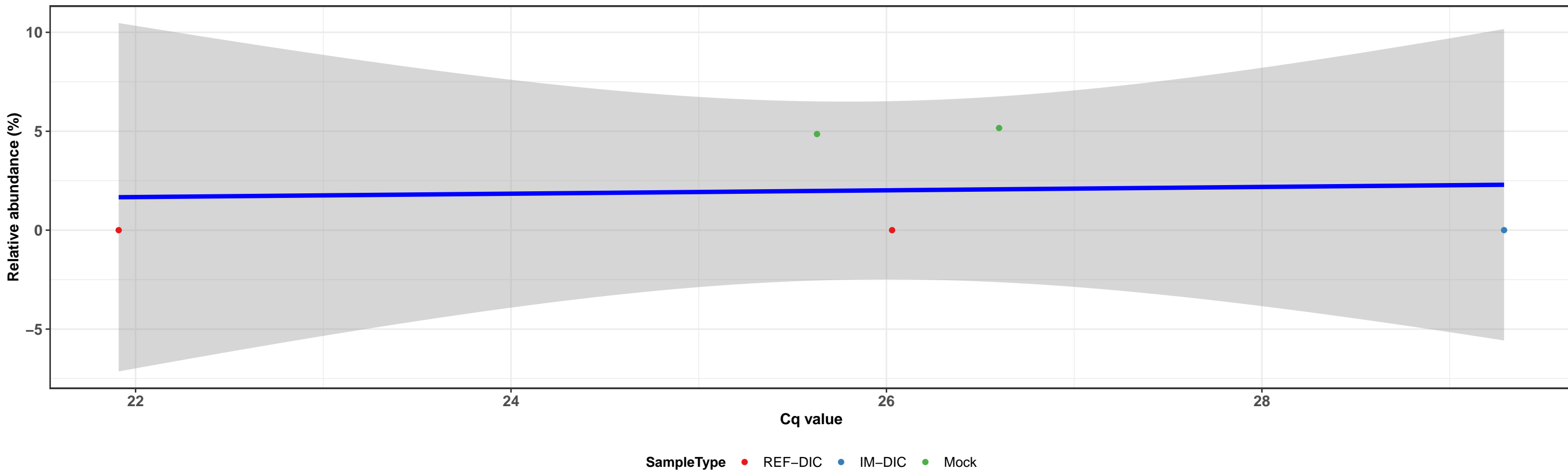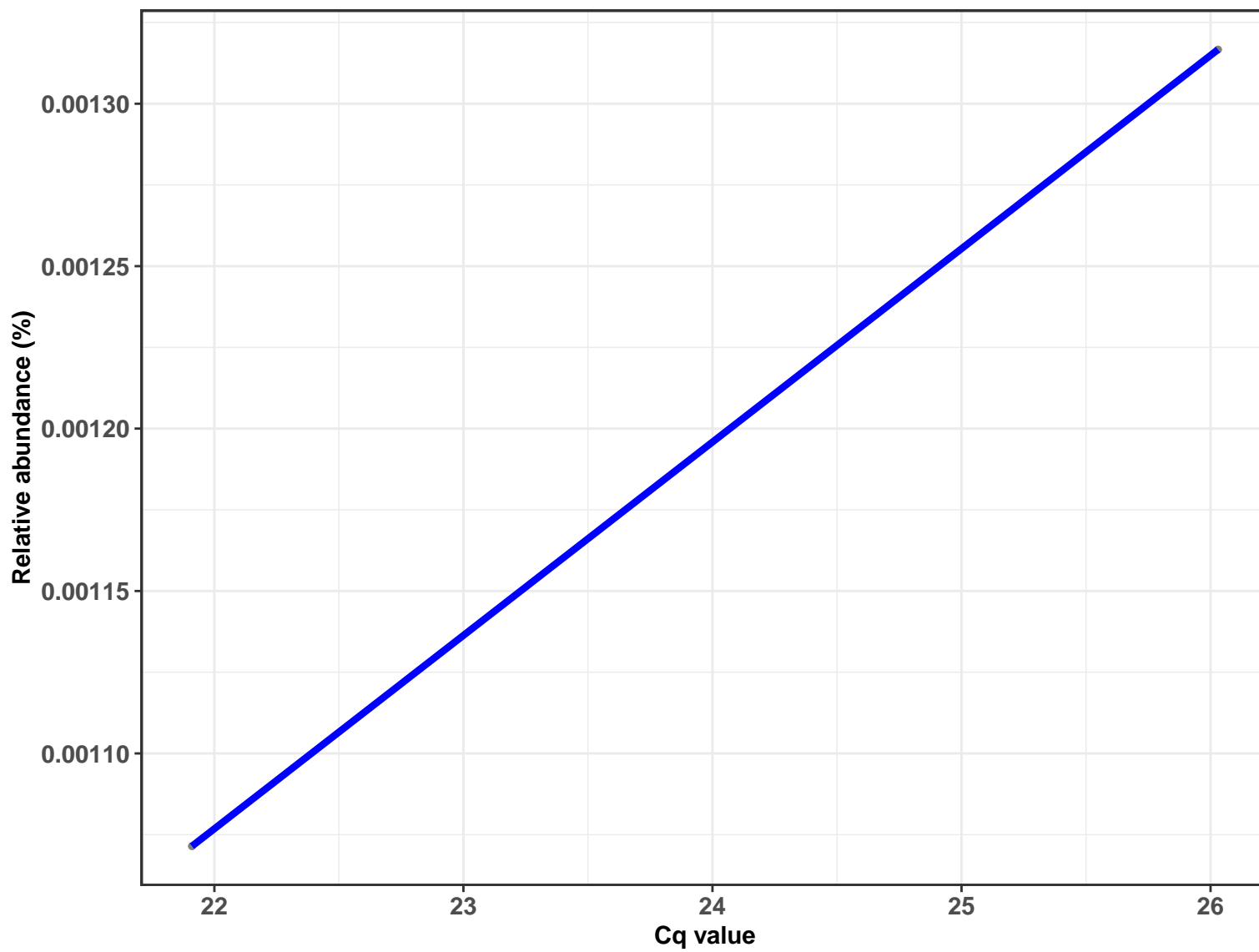
Correlation within: REF−DIC

Correlation within: IM−DIC

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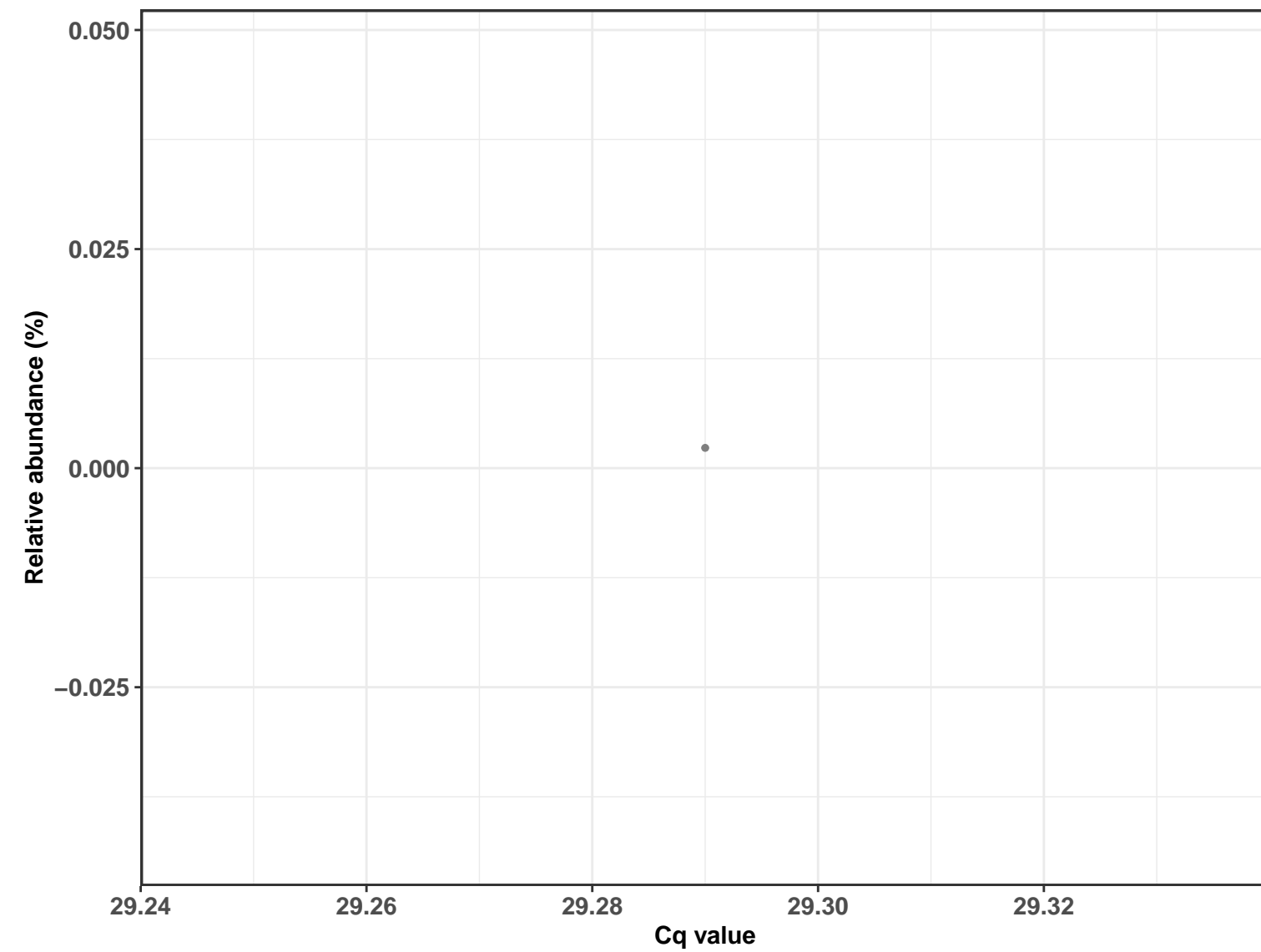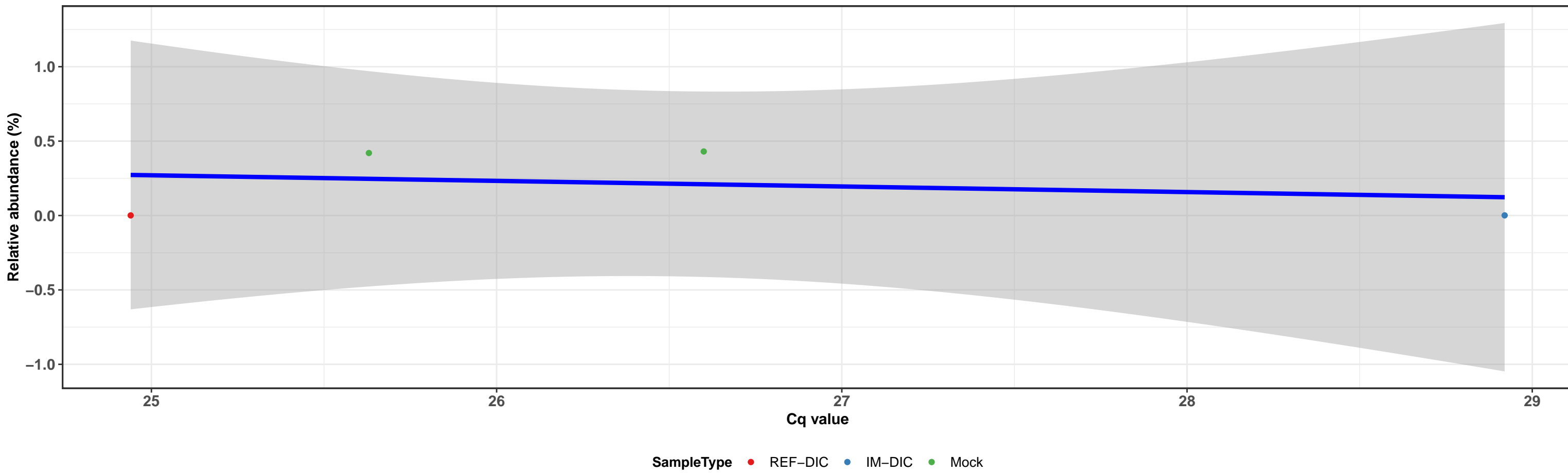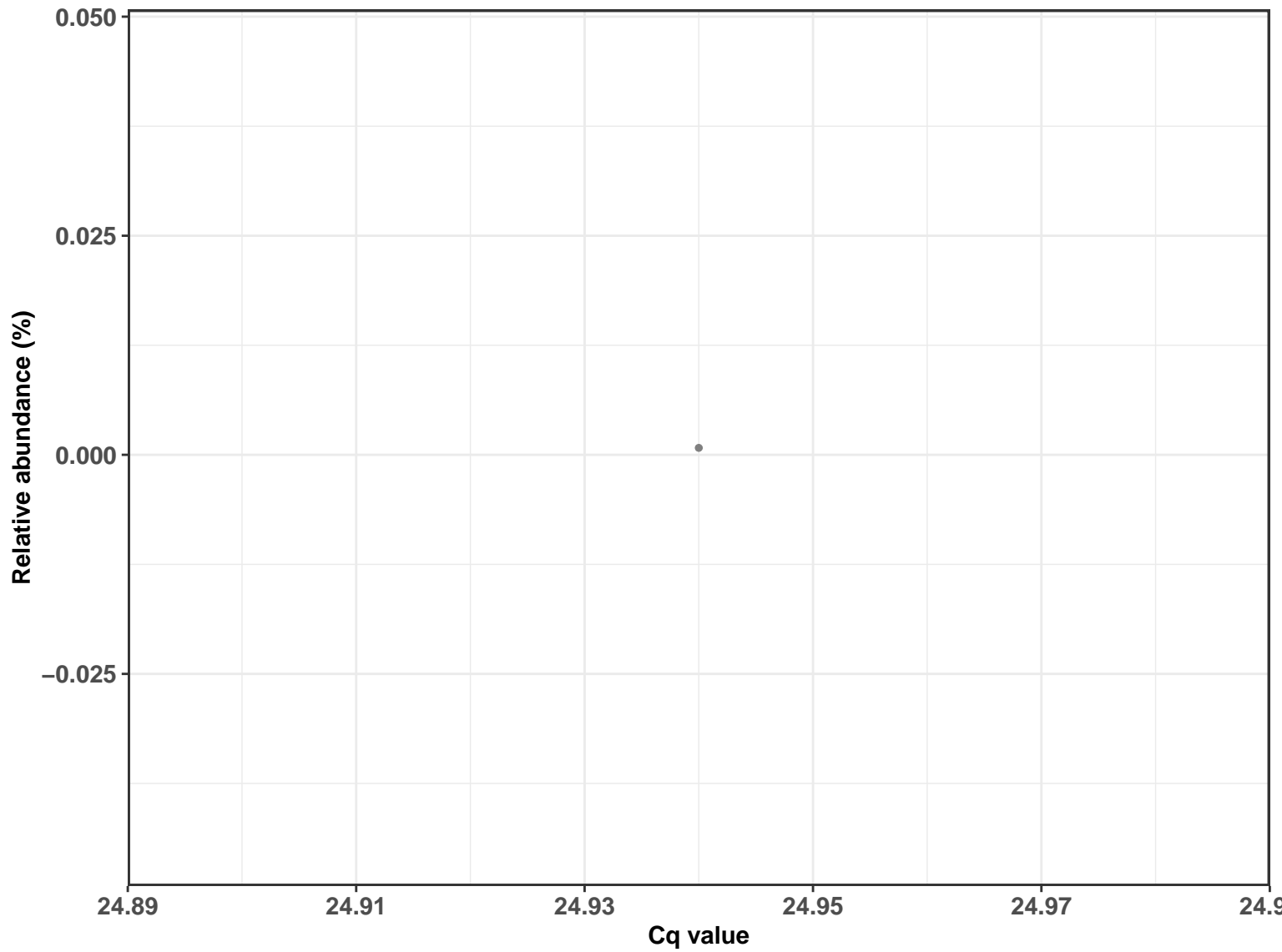

Correlation with all samples

SampleType ● REF−DIC ● IM−DIC ● Mock

Correlation within: REF−DIC

Correlation within: IM−DIC

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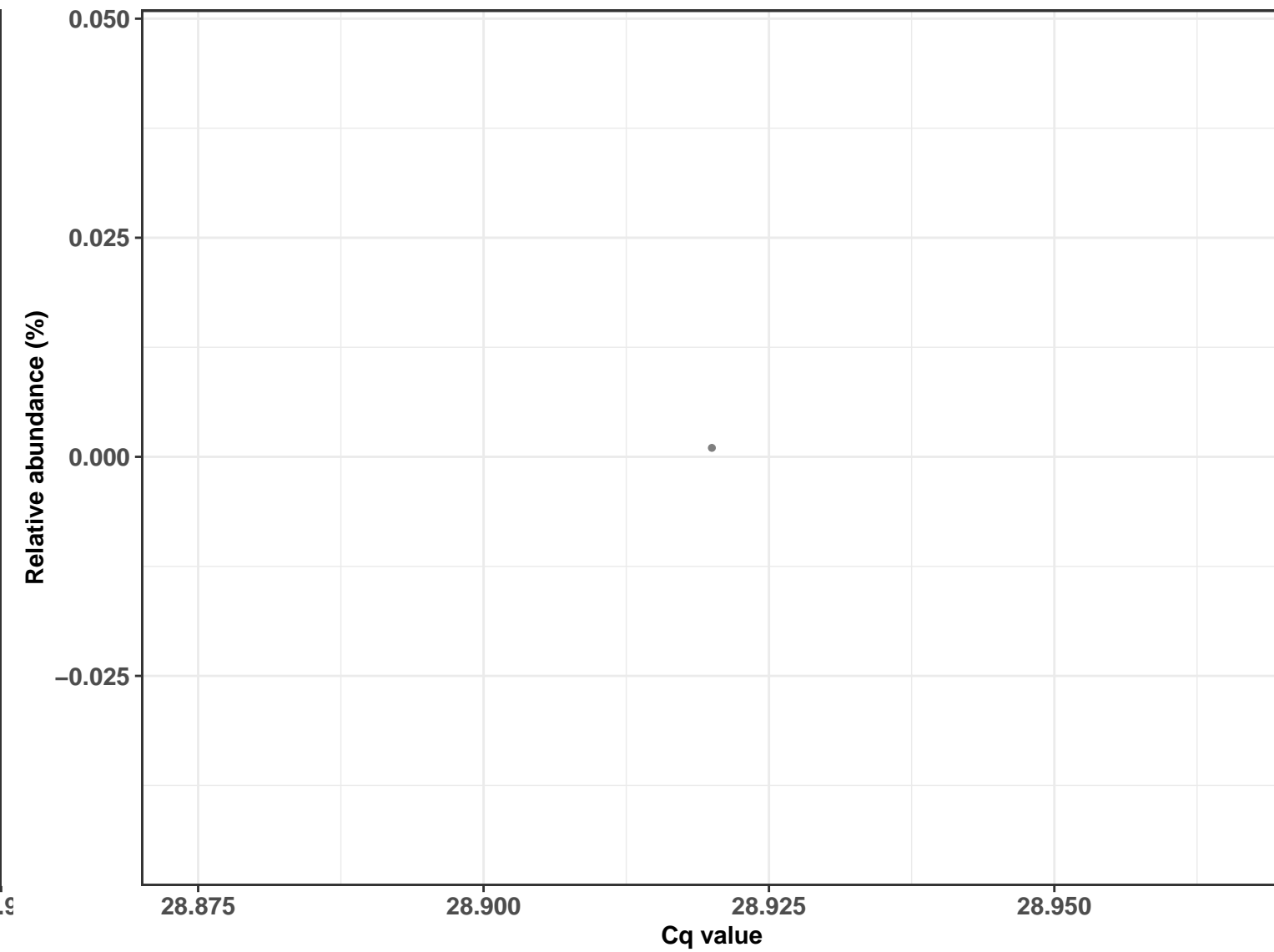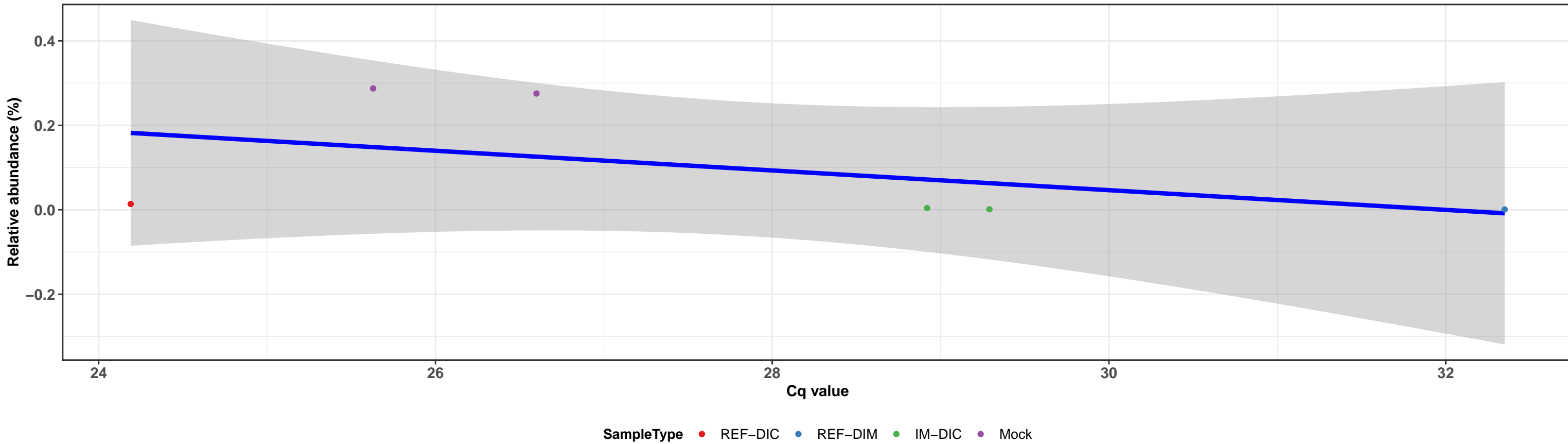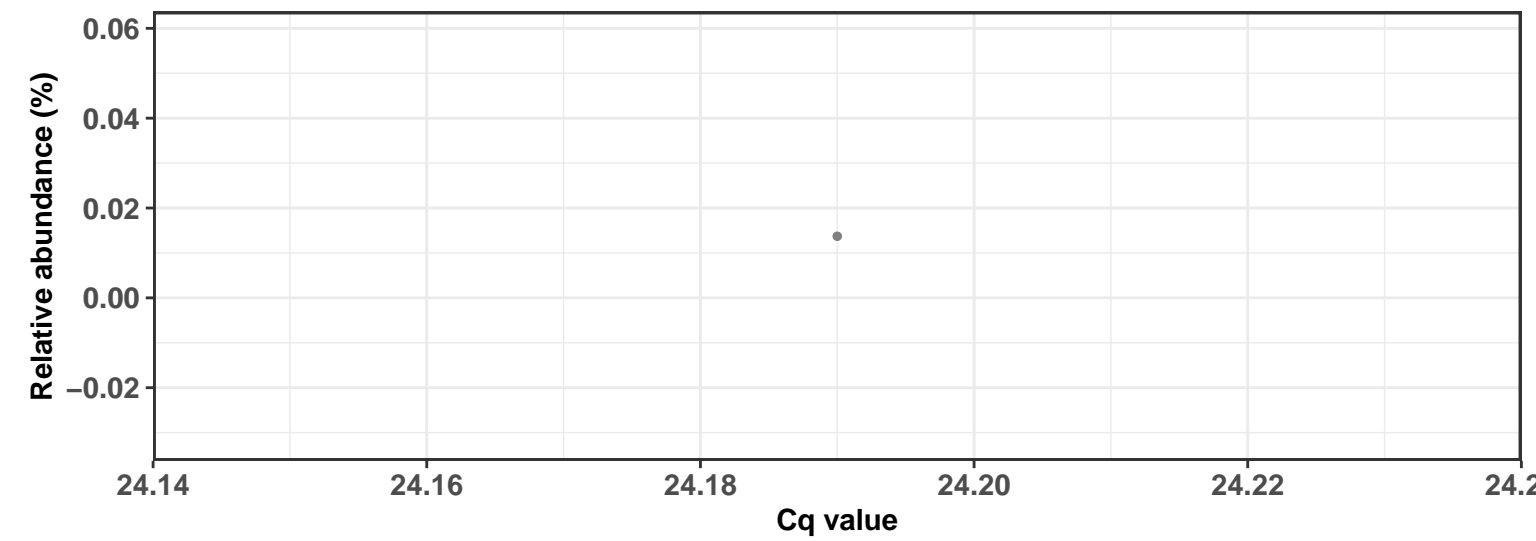
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum
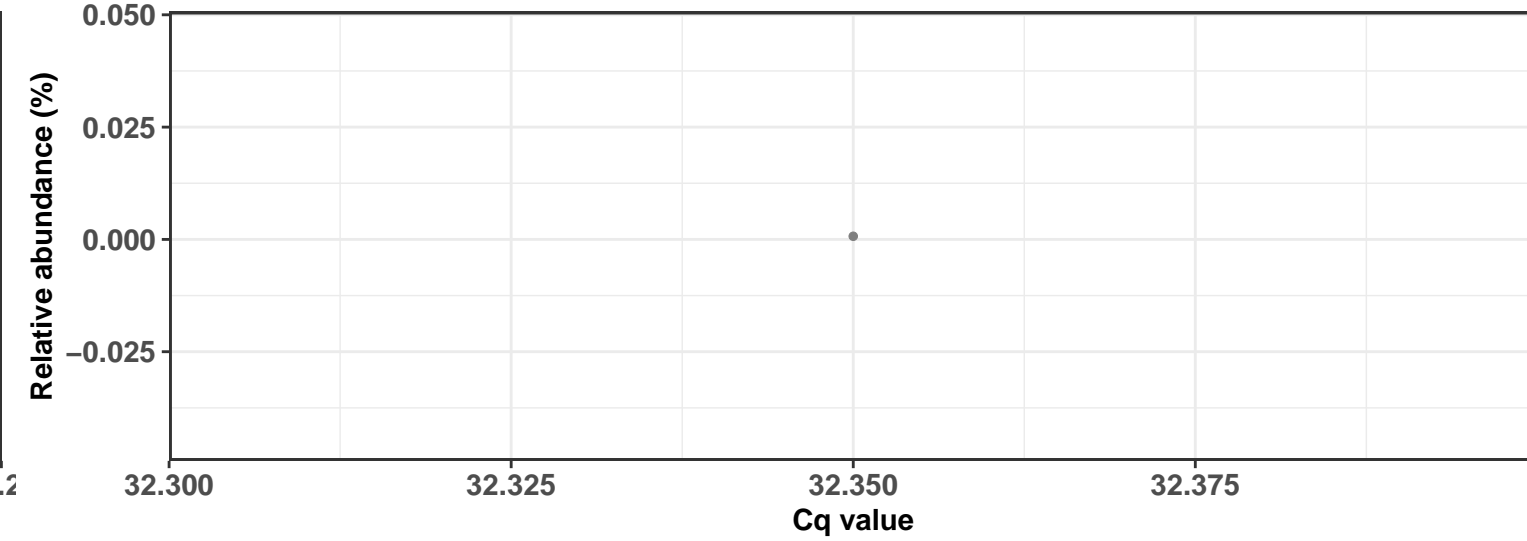
Correlation with all samples

$\log_e(S) = 4.159$, $p = 0.042$, $\hat{\rho}_{Spearman} = -0.829$, $CI_{95\%}$ [−1.550, −0.229], $n_{pairs} = 6$

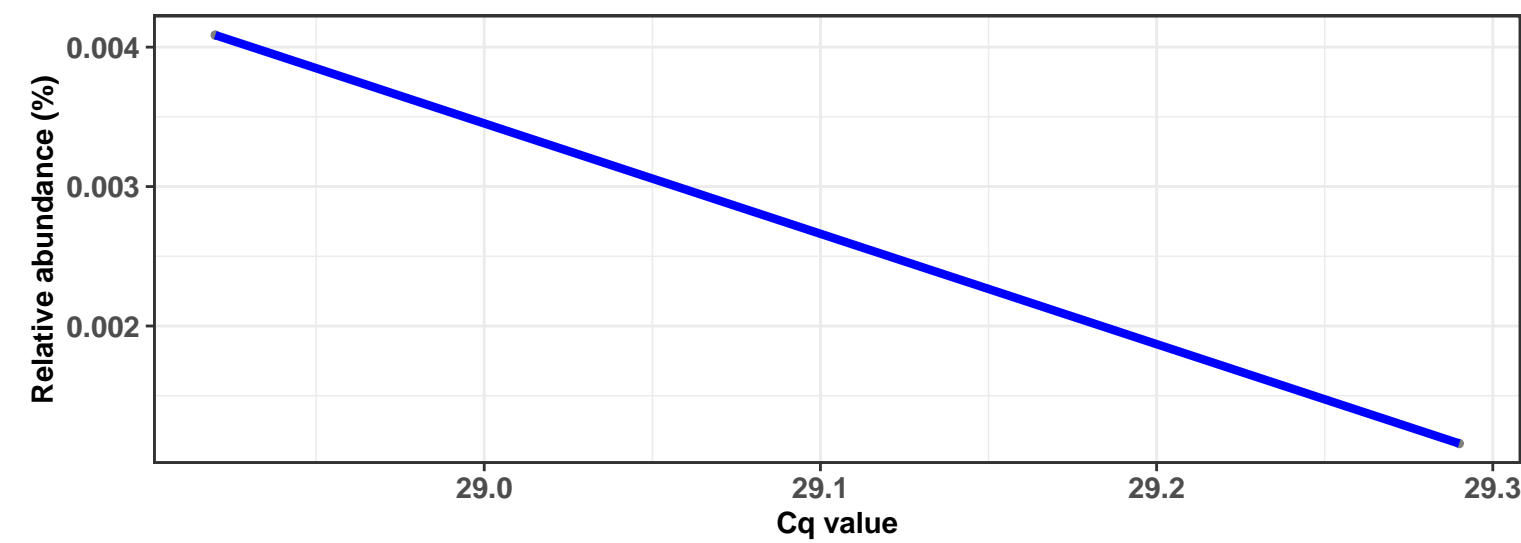SampleType   ● REF−DIC   ● REF−DIM   ● IM−DIC   ● Mock

Correlation within: REF−DIC

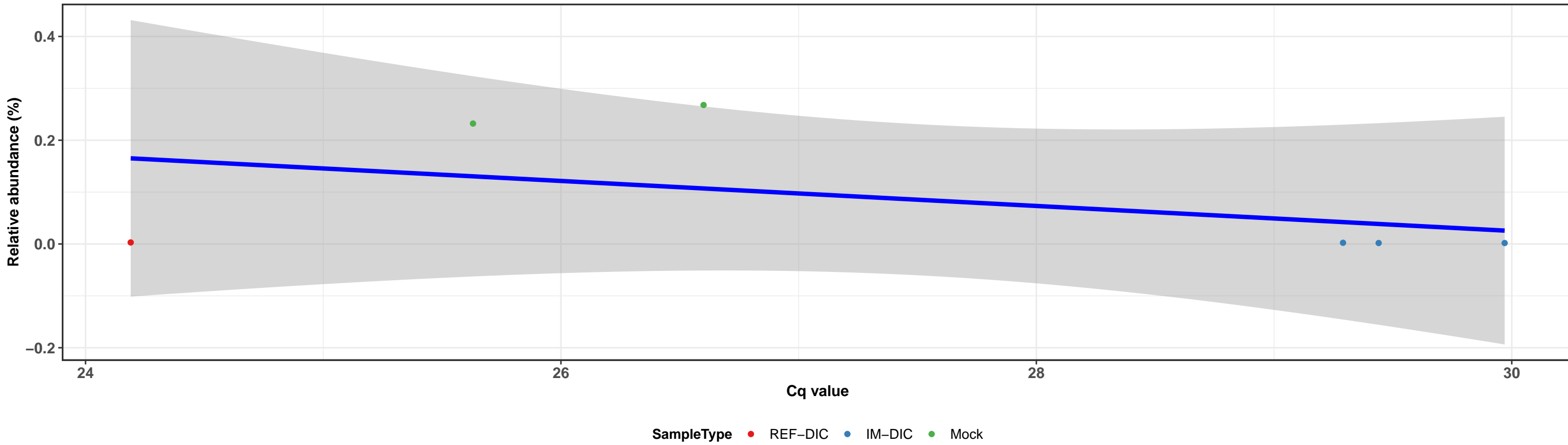**Correlation within: REF−DIM**

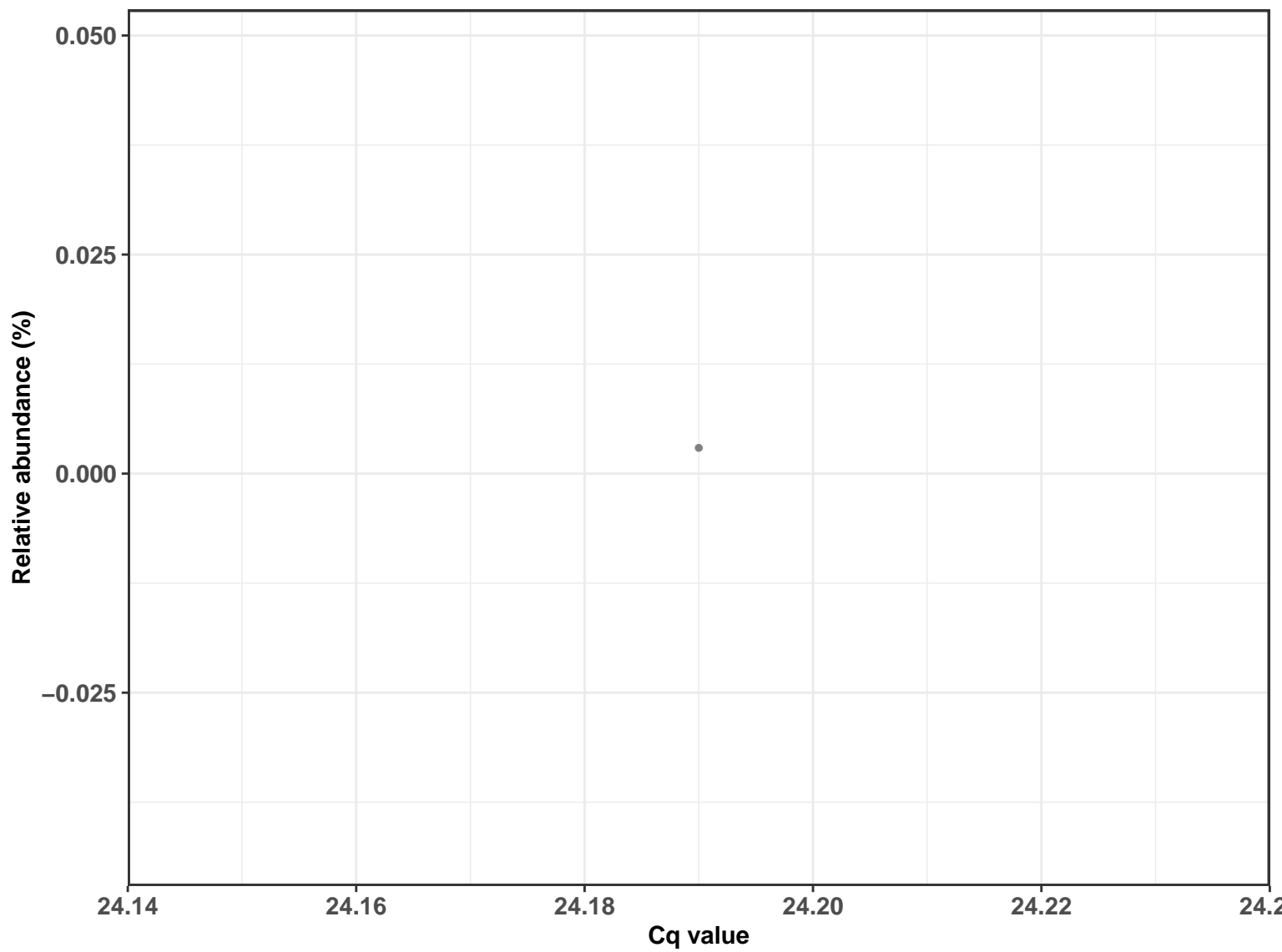**Correlation within: IM−DIC**

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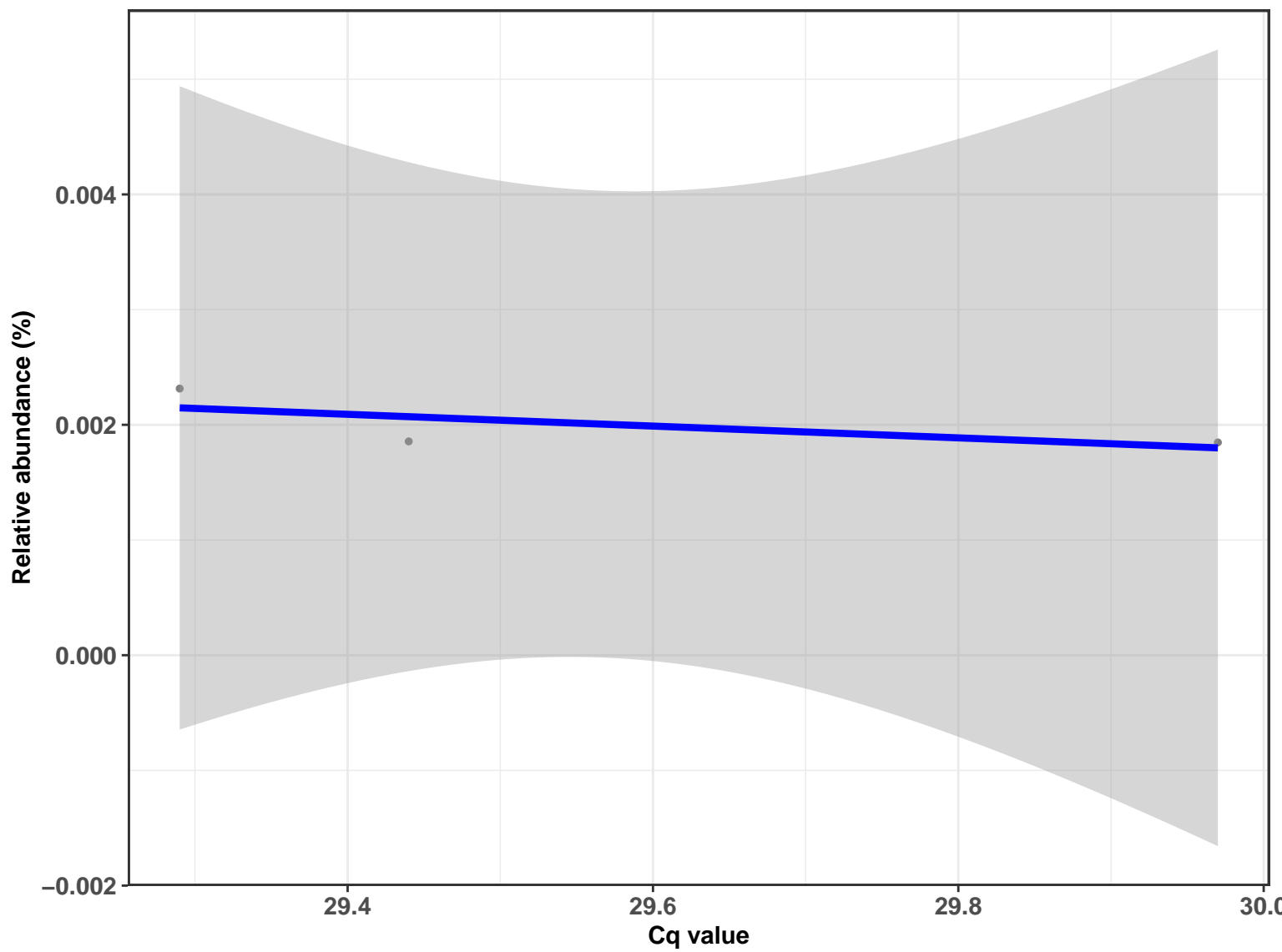
Correlation with all samples

$\log_e(S) = 4.127$, $p = 0.072$, $\hat{\rho}_{Spearman} = -0.771$, $CI_{95\%}$ [−1.887, 0.096], $n_{pairs} = 6$

SampleType ● REF−DIC ● IM−DIC ● Mock

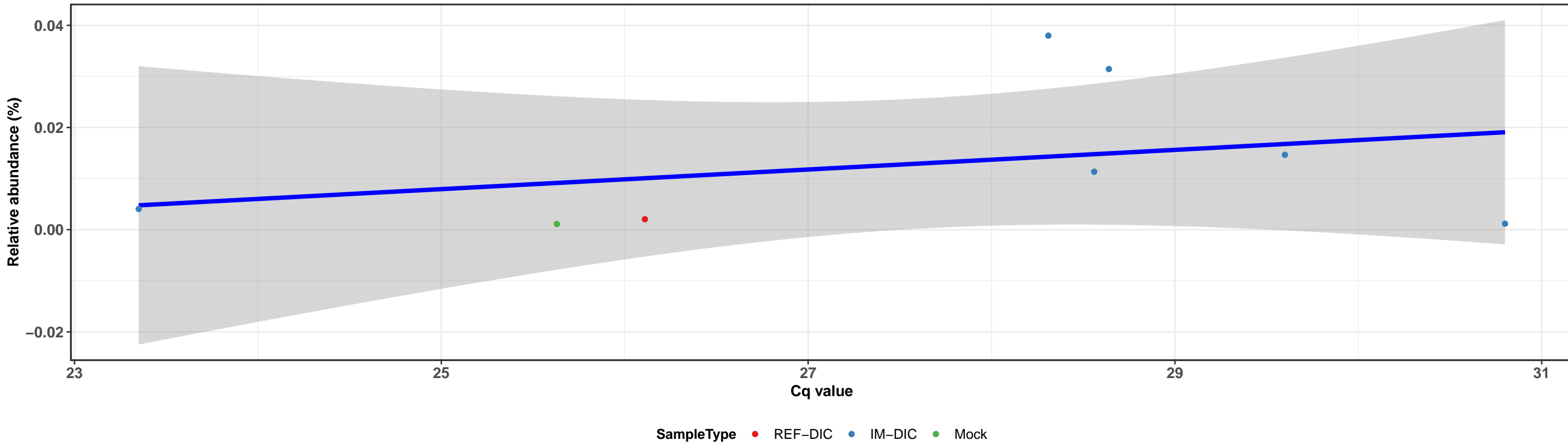**Correlation within: REF−DIC**

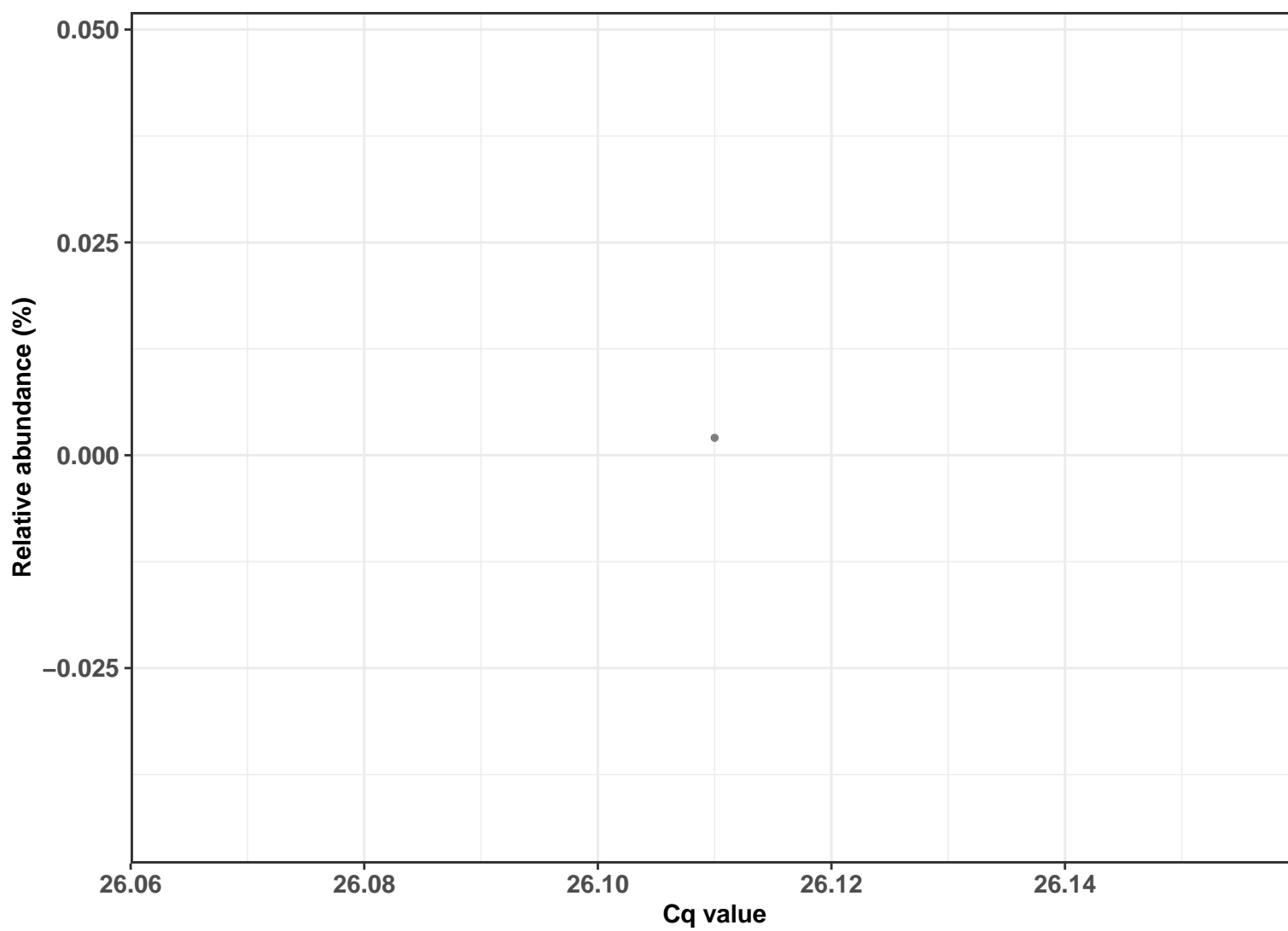**Correlation within: IM−DIC**

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

Correlation with all samples

$\log_e(S) = 4.159$, $p = 0.570$, $\widehat{\rho}_{Spearman} = 0.238$, $CI_{95\%}$ [−0.539, 1.003], $n_{pairs} = 8$
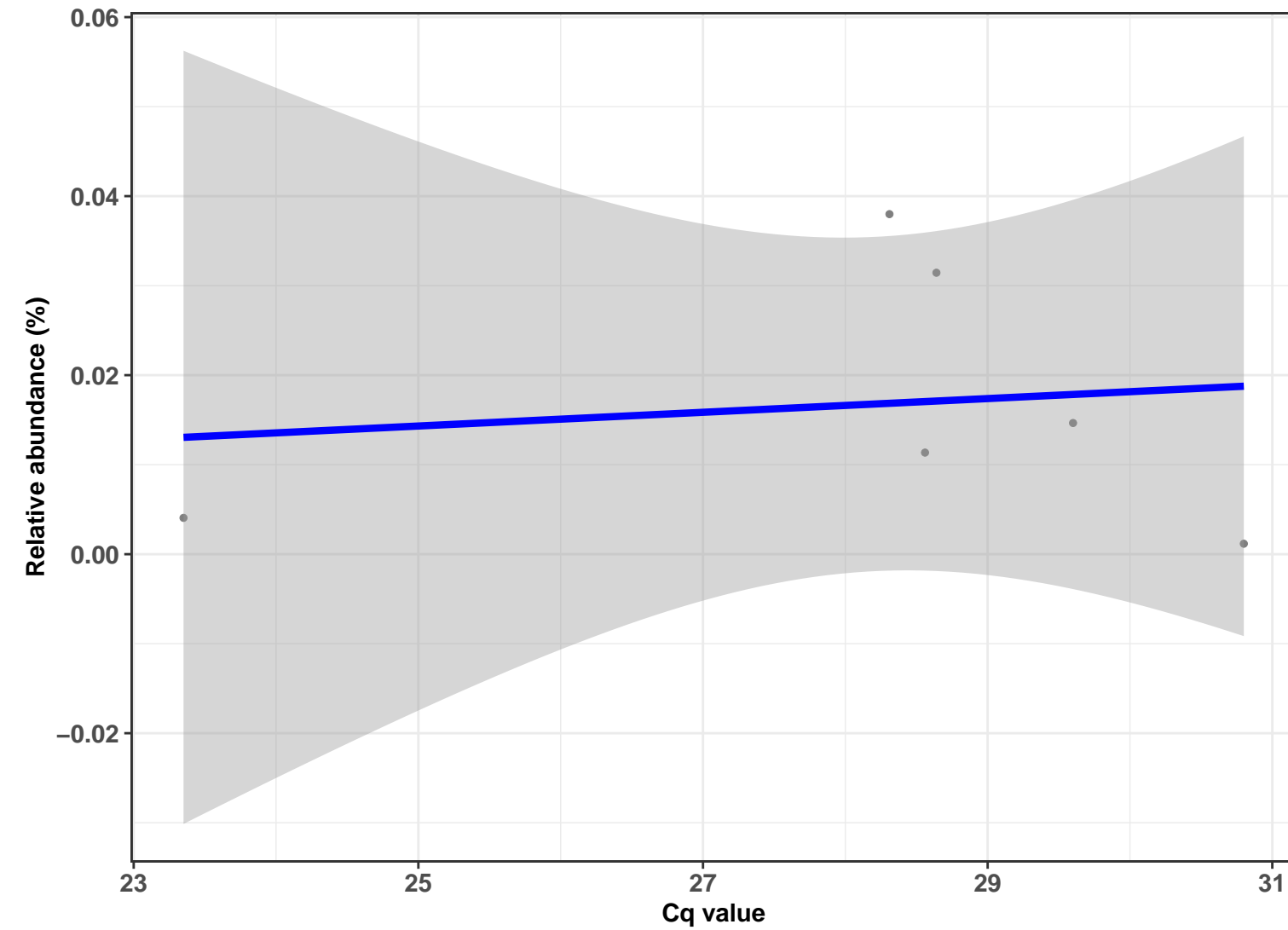

SampleType   ● REF−DIC   ● IM−DIC   ● Mock
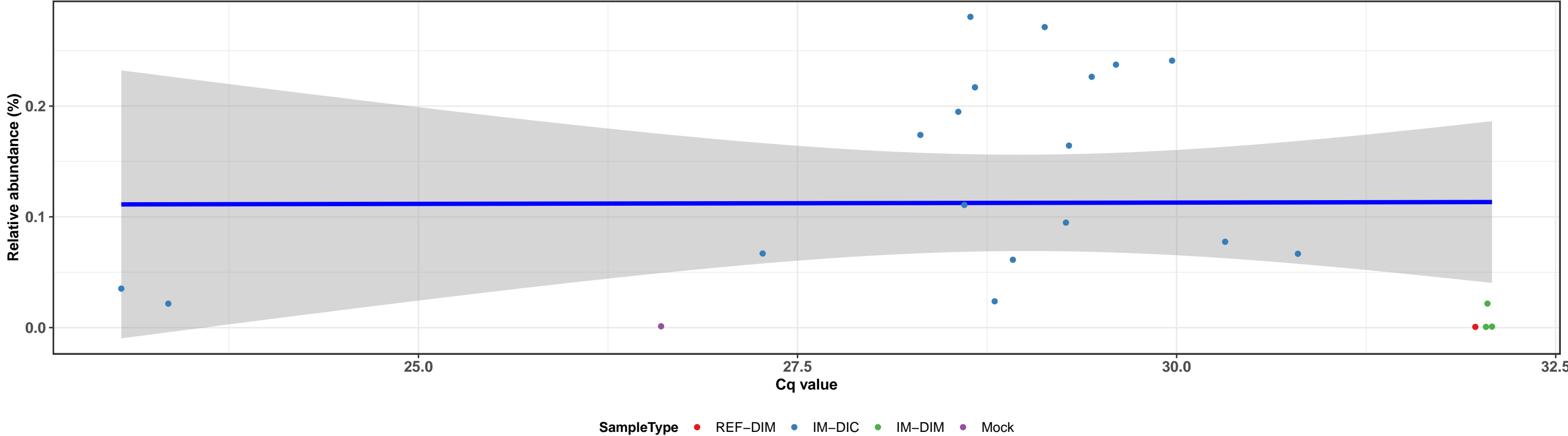
Correlation within: REF−DIC

Correlation within: IM−DIC

$\log_e(S) = 3.784$, $p = 0.623$, $\widehat{\rho}_{Spearman} = -0.257$, $CI_{95\%}$ [−1.290, 0.867], $n_{pairs} = 6$

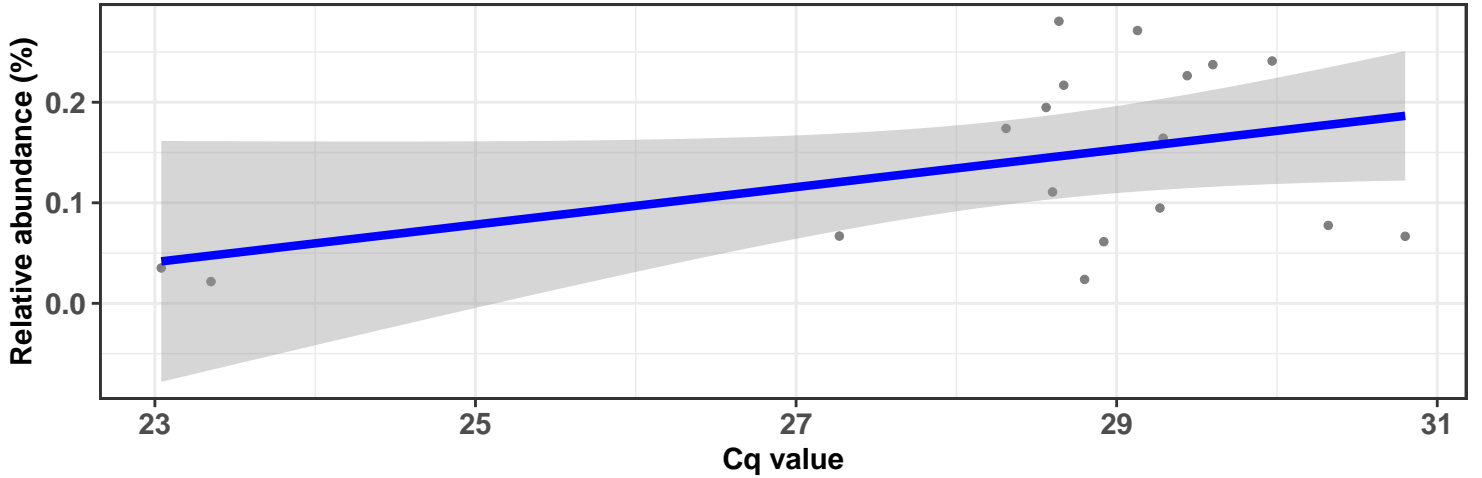# k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; NA

Correlation with all samples

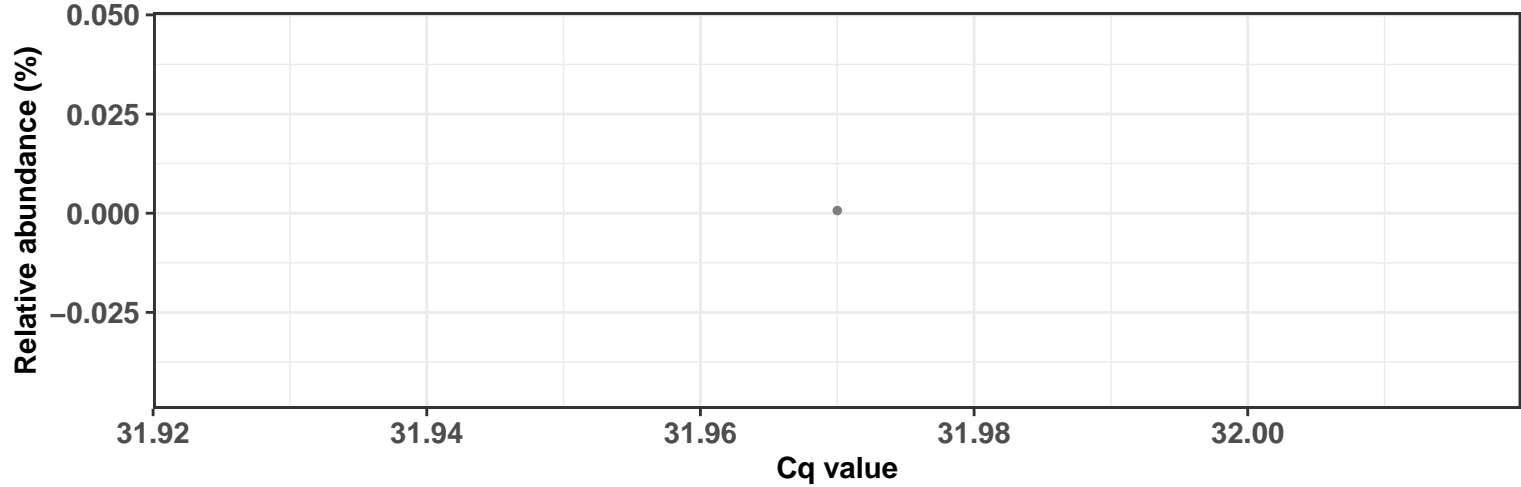$\log_e(S) = 7.768$, $p = 0.444$, $\widehat{\rho}_{Spearman} = -0.168$, $CI_{95\%}$ [−0.604, 0.287], $n_{pairs} = 23$

SampleType ● REF−DIM ● IM−DIC ● IM−DIM ● Mock

Correlation within: REF−DIM

Correlation within: IM−DIC
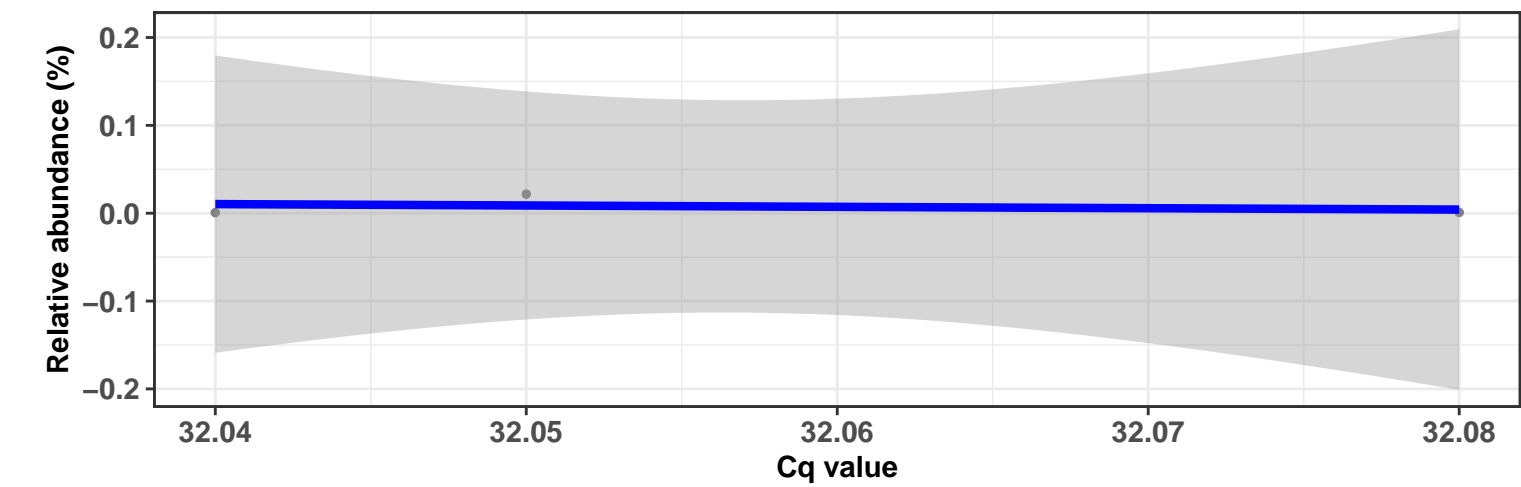
$\log_e(S) = 6.525$, $p = 0.233$, $\widehat{\rho}_{Spearman} = 0.296$, $CI_{95\%}$ [−0.221, 0.800], $n_{pairs} = 18$
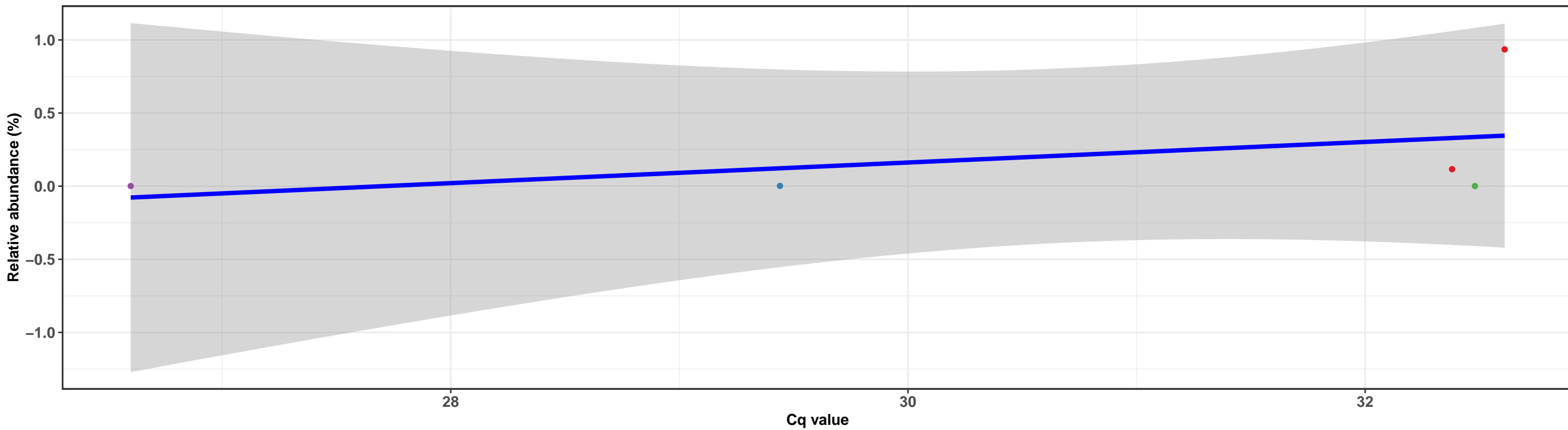
Correlation within: IM−DIM

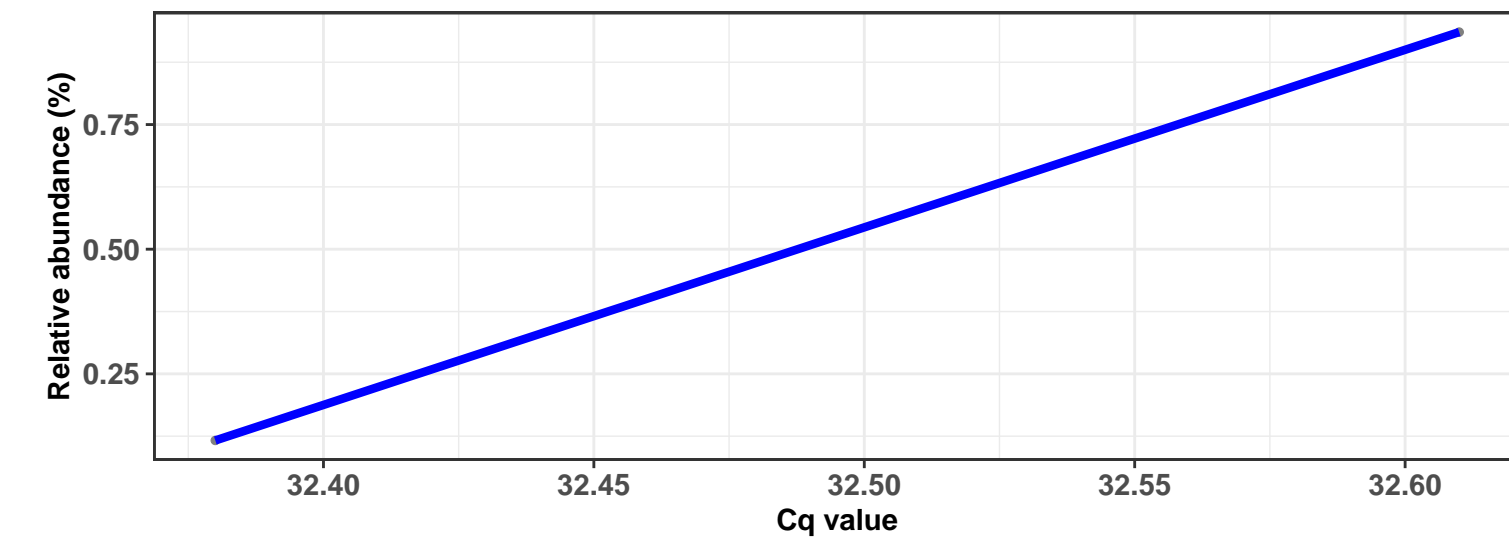**k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Cytophagales; f__Hymenobacteraceae; g__Hymenobacter; s__uncultured bacterium**
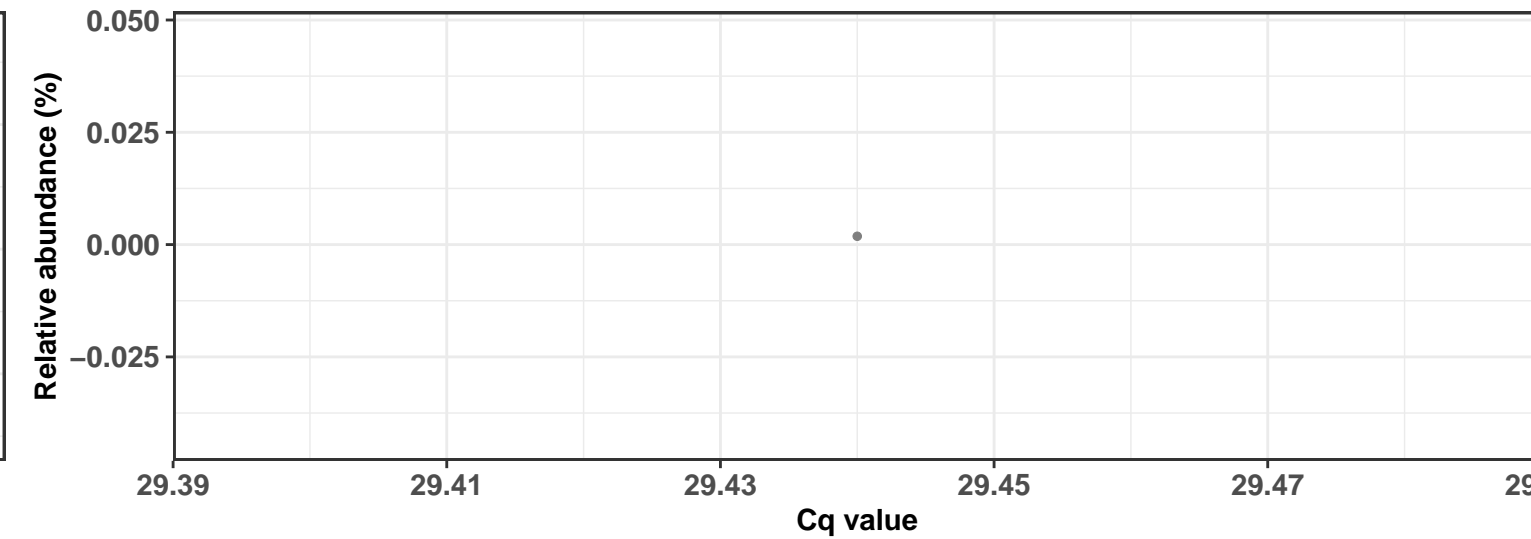
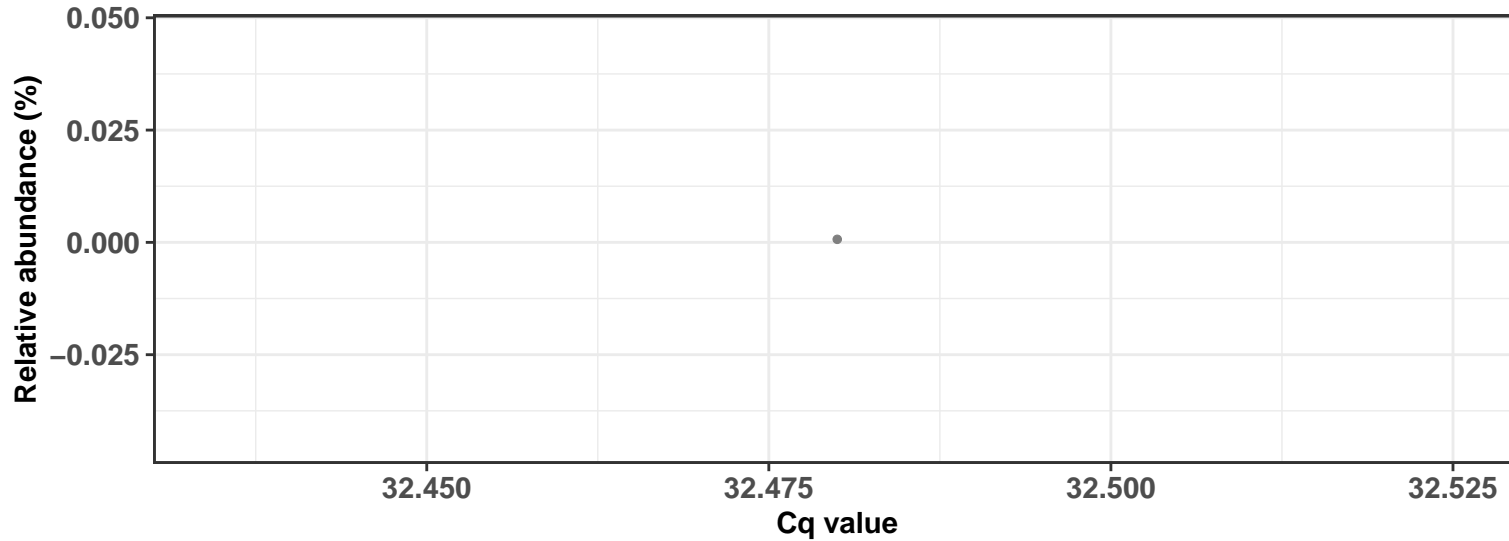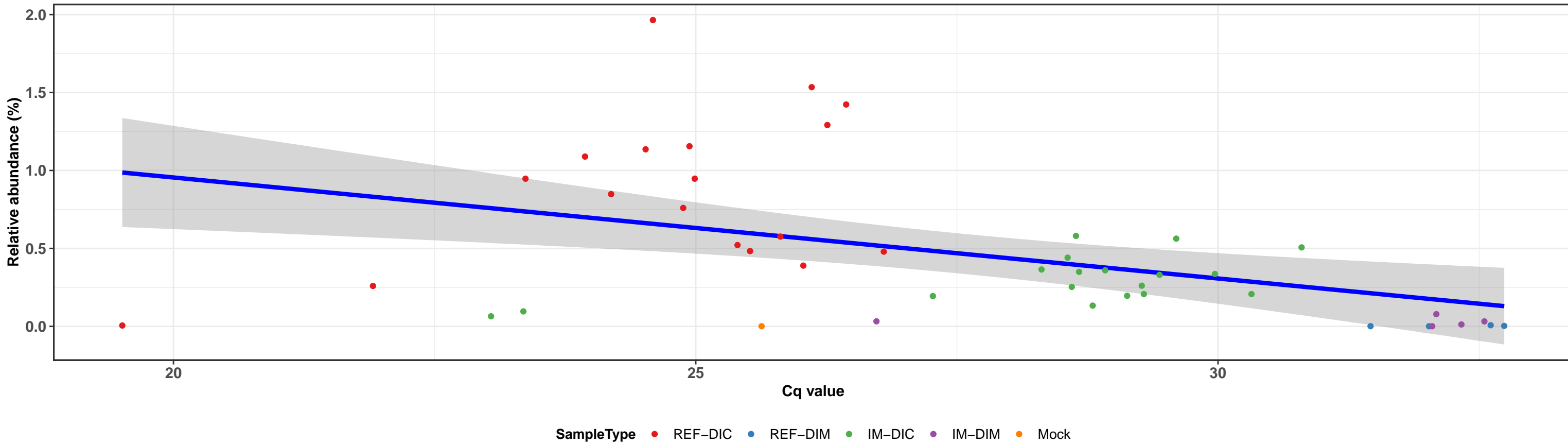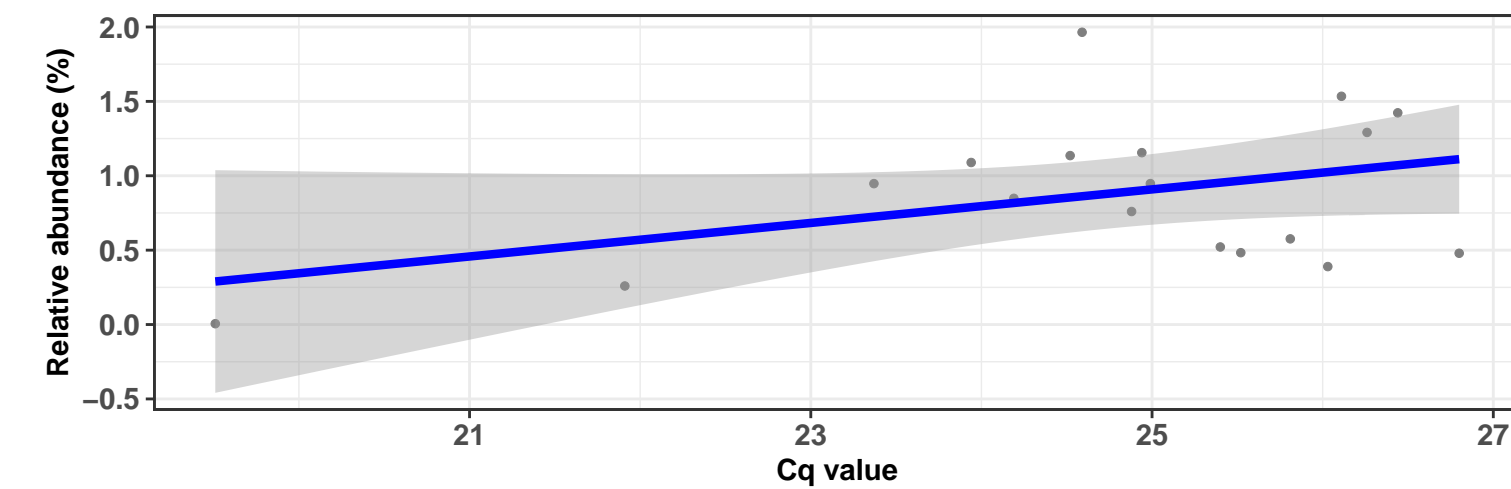**k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Leuconostocaceae; g__Weissella; s__uncultured bacterium**

Correlation with all samples

$\log_e(S) = 10.095$, p = < 0.001, $\hat{\rho}_{Spearman} = -0.494$, $CI_{95\%}$ [−0.815, −0.177], n_{pairs} = 46
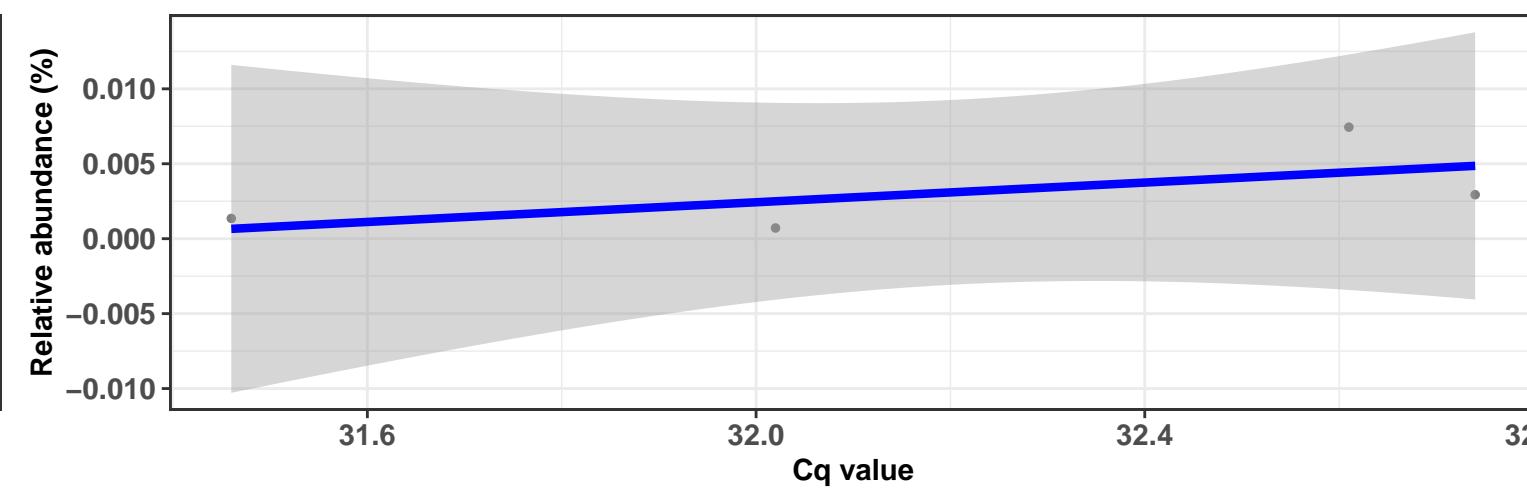

SampleType ● REF−DIC ● REF−DIM ● IM−DIC ● IM−DIM ● Mock

Correlation within: REF−DIC

$\log_e(S) = 6.631$, p = 0.385, $\hat{\rho}_{Spearman} = 0.218$, $CI_{95\%}$ [−0.392, 0.819], n_{pairs} = 18
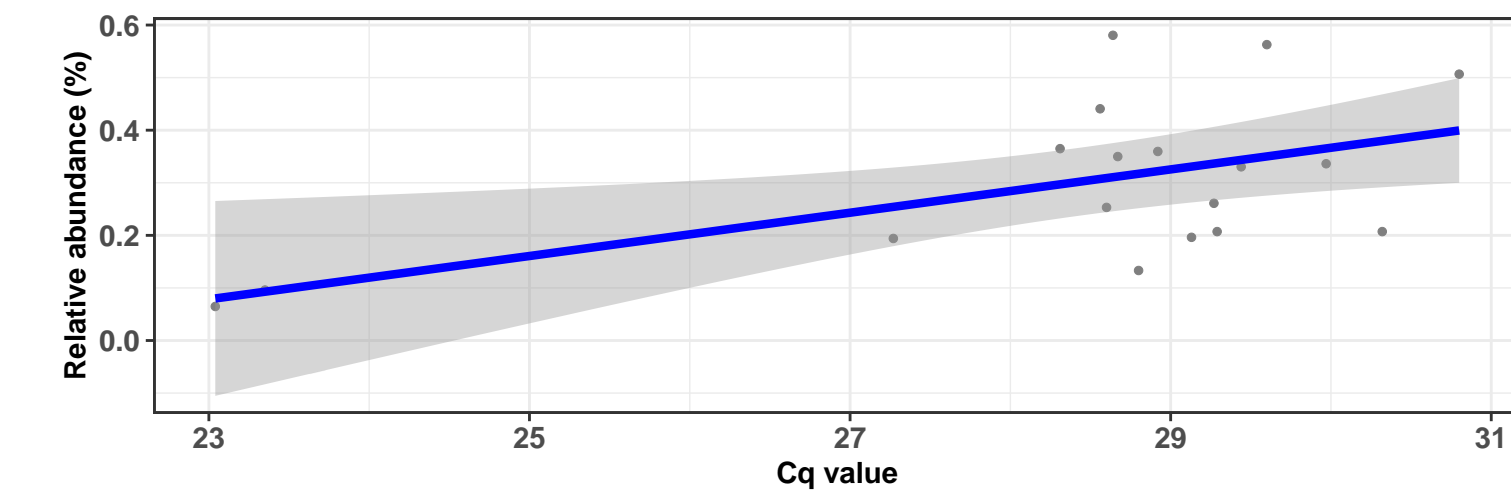

Correlation within: REF−DIM

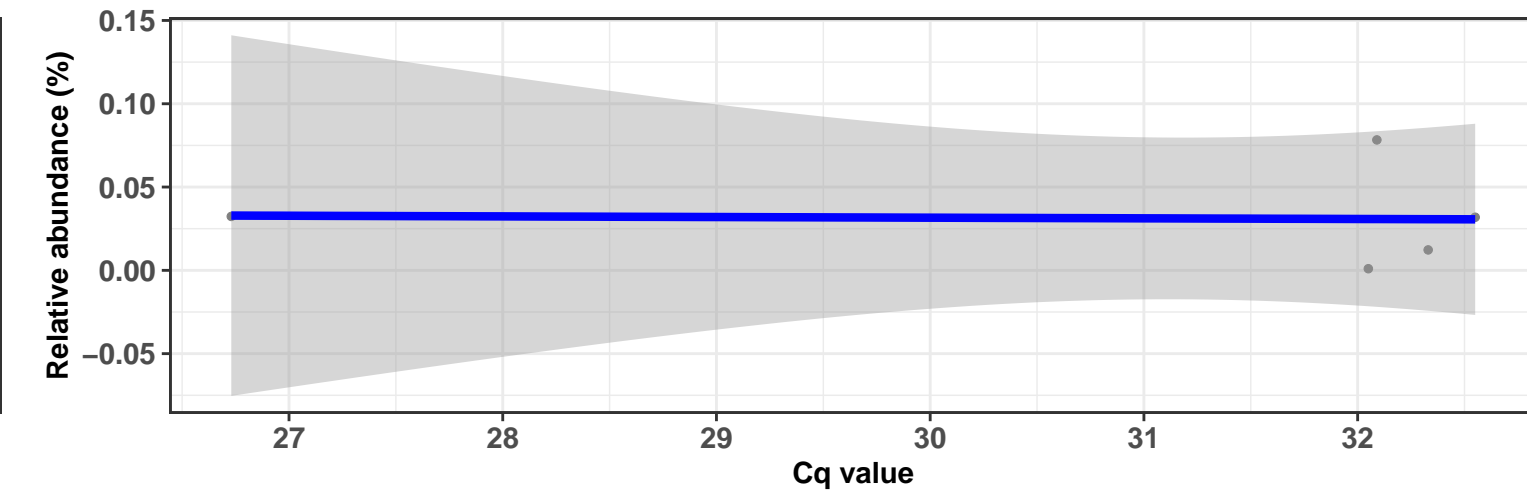**Correlation within: IM−DIC**

$\log_e(S) = 6.446$, p = 0.155, $\hat{\rho}_{Spearman} = 0.350$, $CI_{95\%}$ [−0.112, 0.858], n_{pairs} = 18
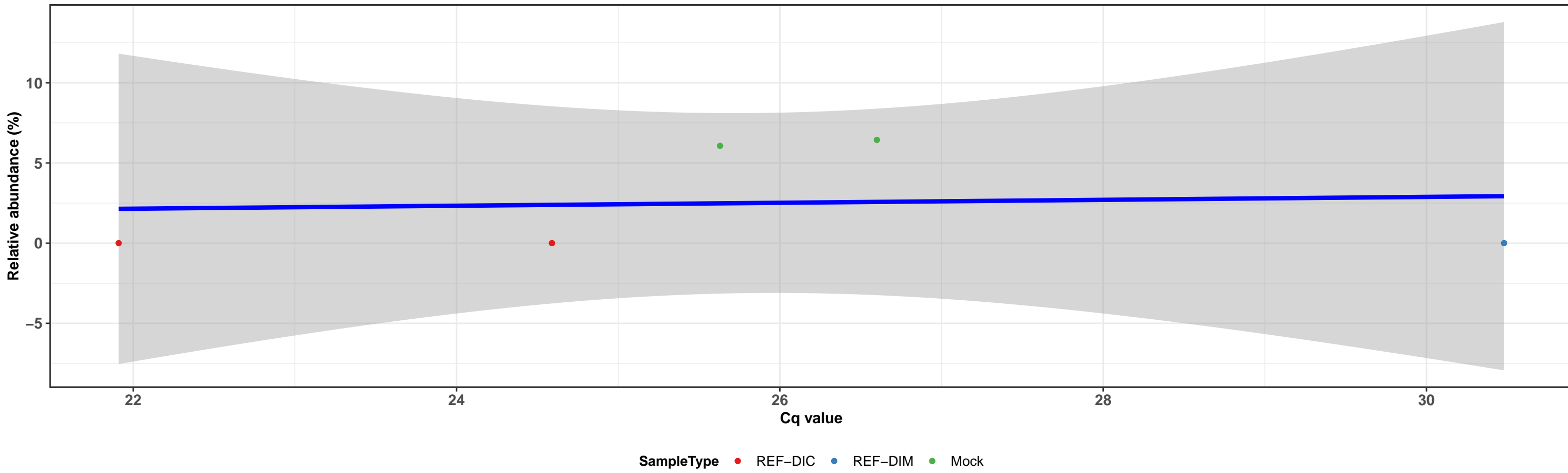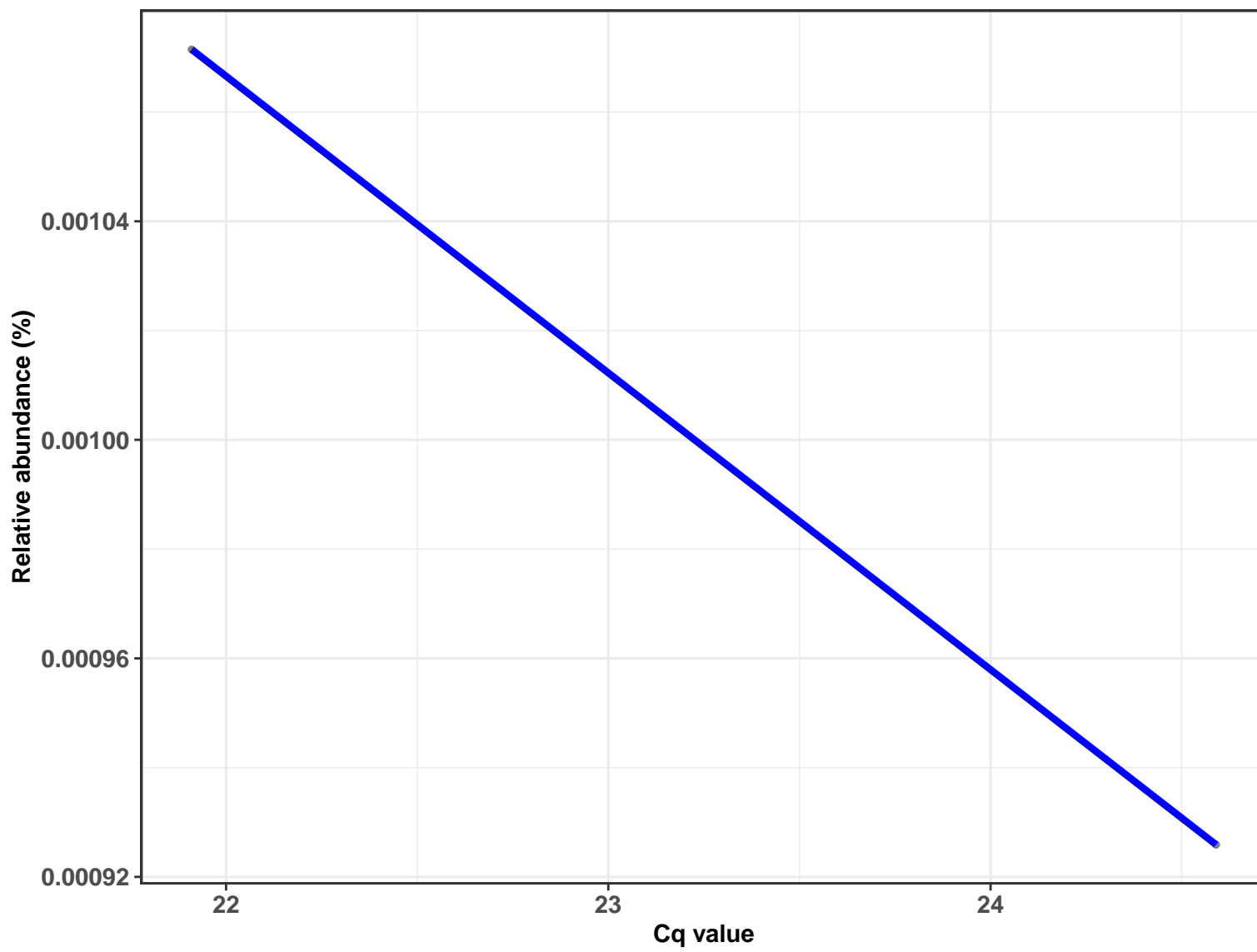

Correlation within: IM−DIM

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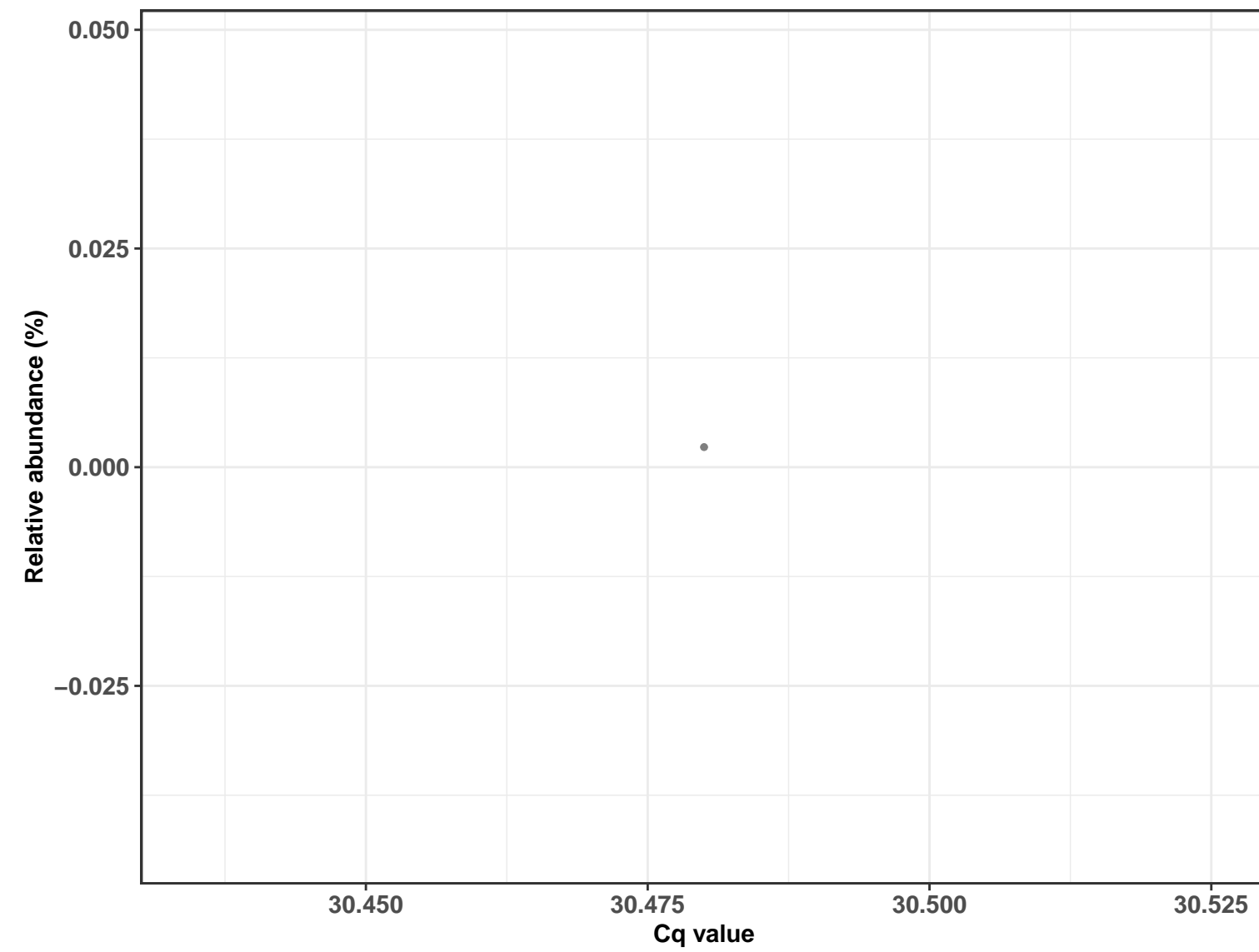

Correlation with all samples

Correlation within: REF-DIC

Correlation within: REF-DIM

k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus
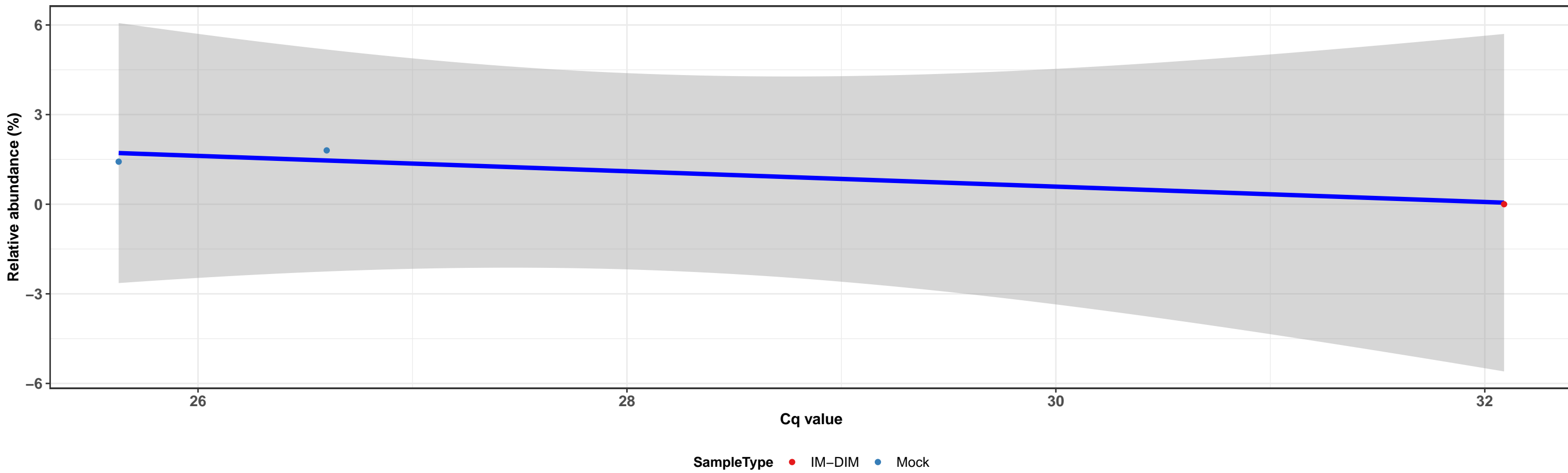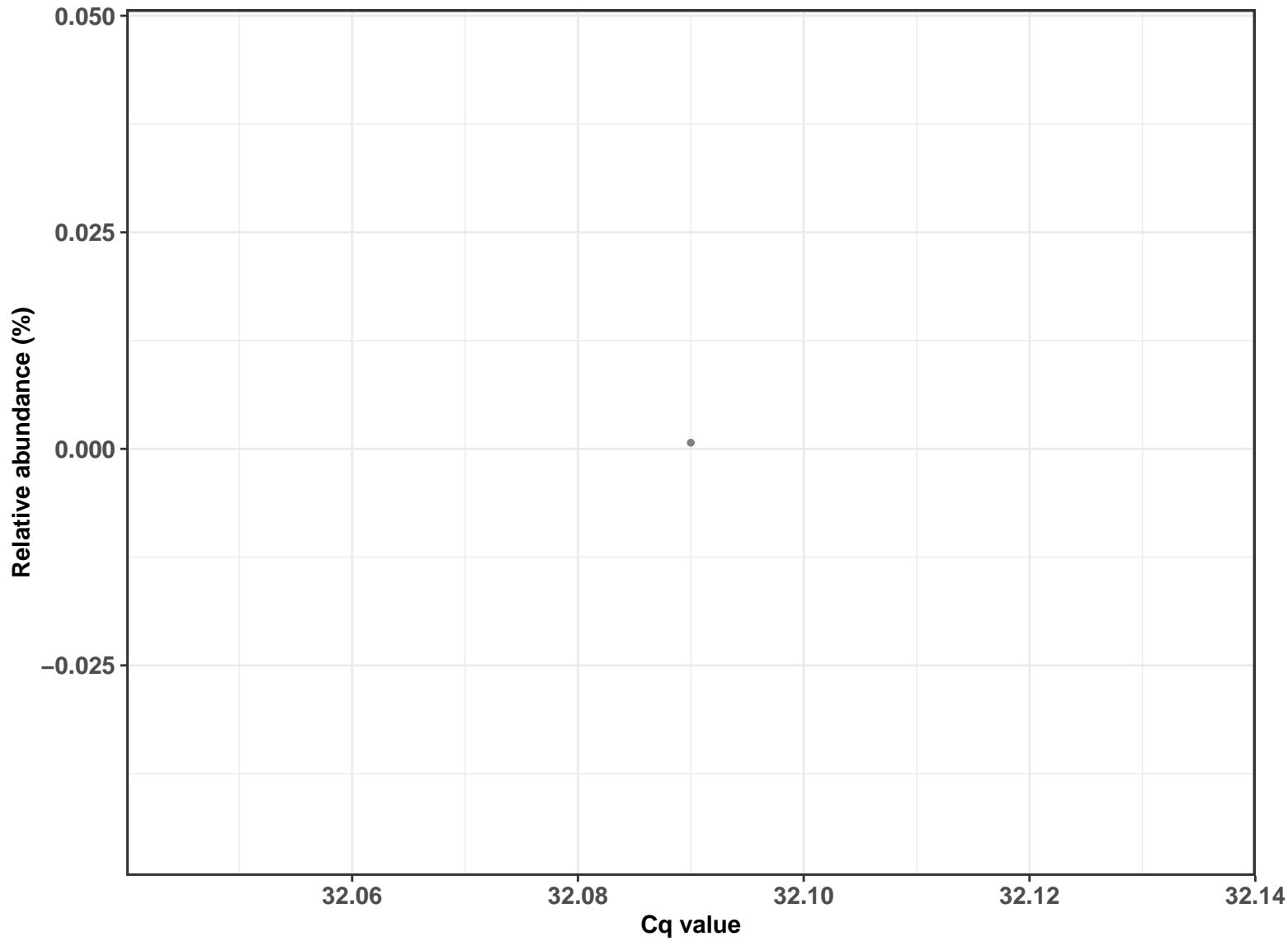
Correlation with all samples
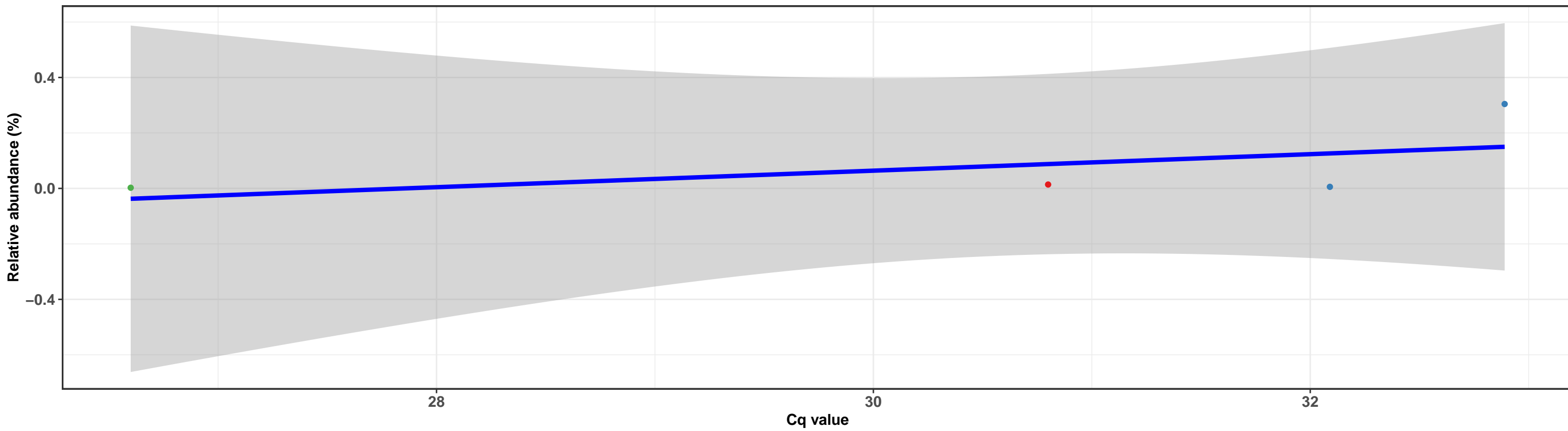

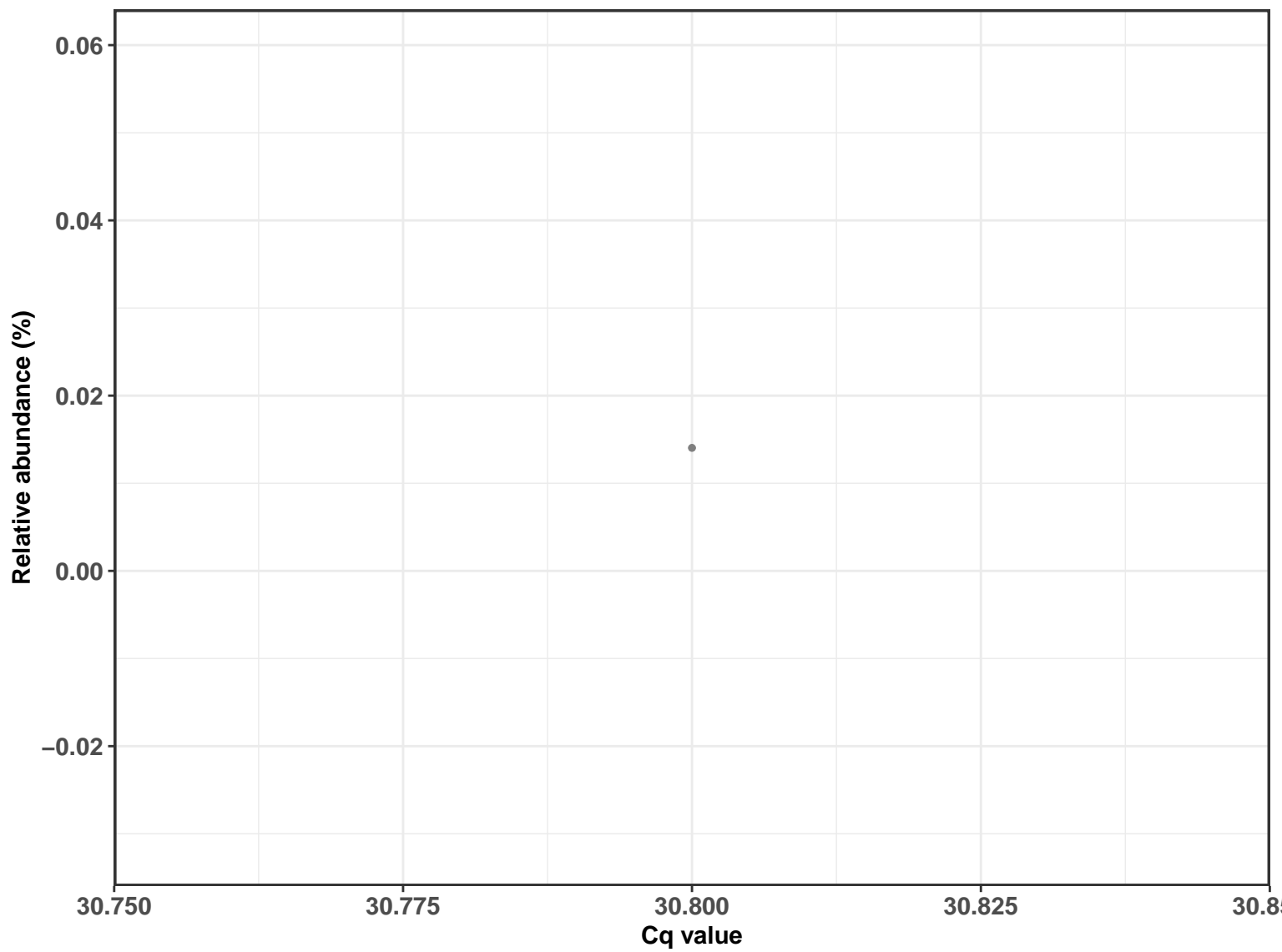**SampleType** ● IM−DIM ● Mock

Correlation within: IM−DIM

k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Arthrobacter; Ambiguous_taxa
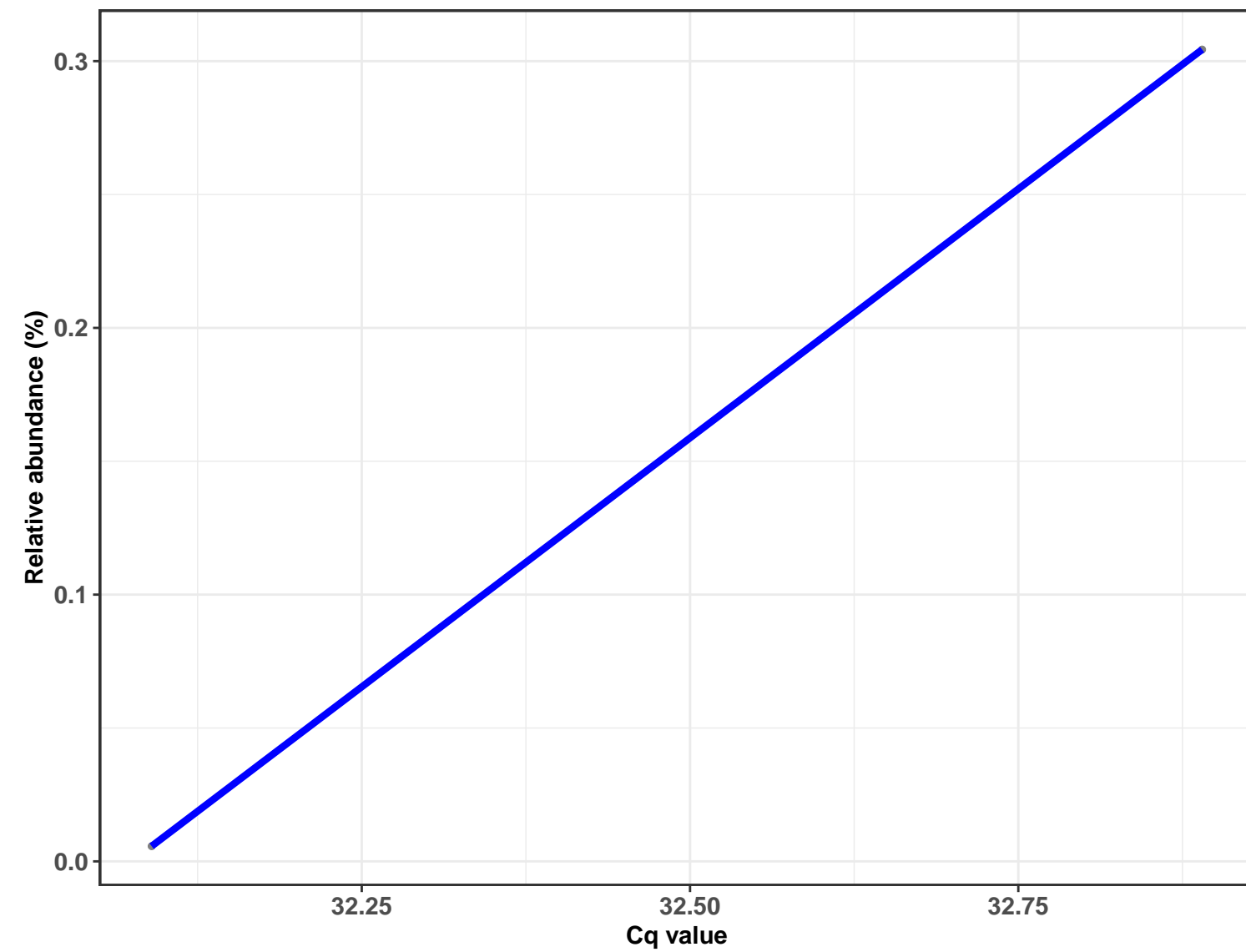
Correlation with all samples
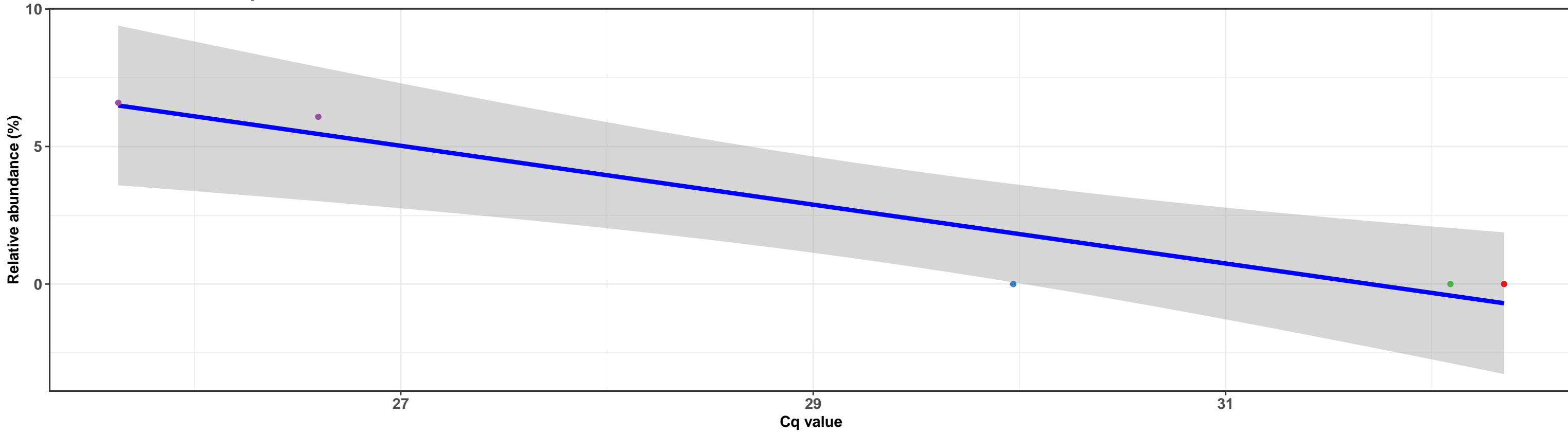

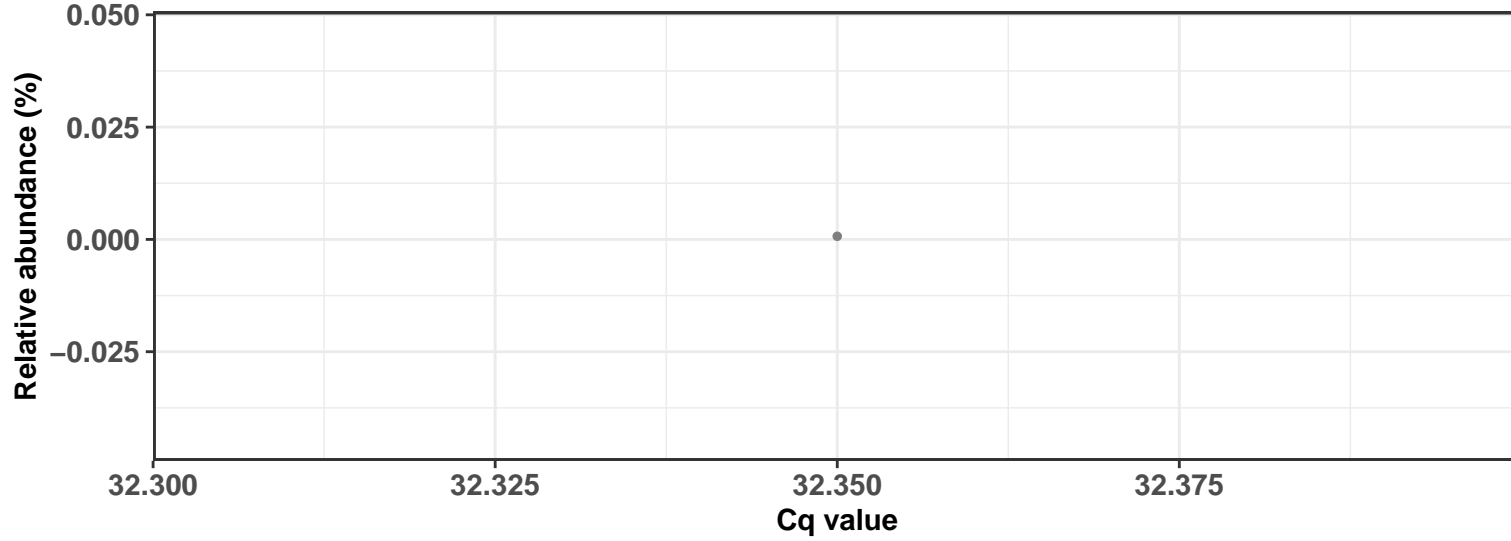SampleType ● IM–DIC ● IM–DIM ● Mock
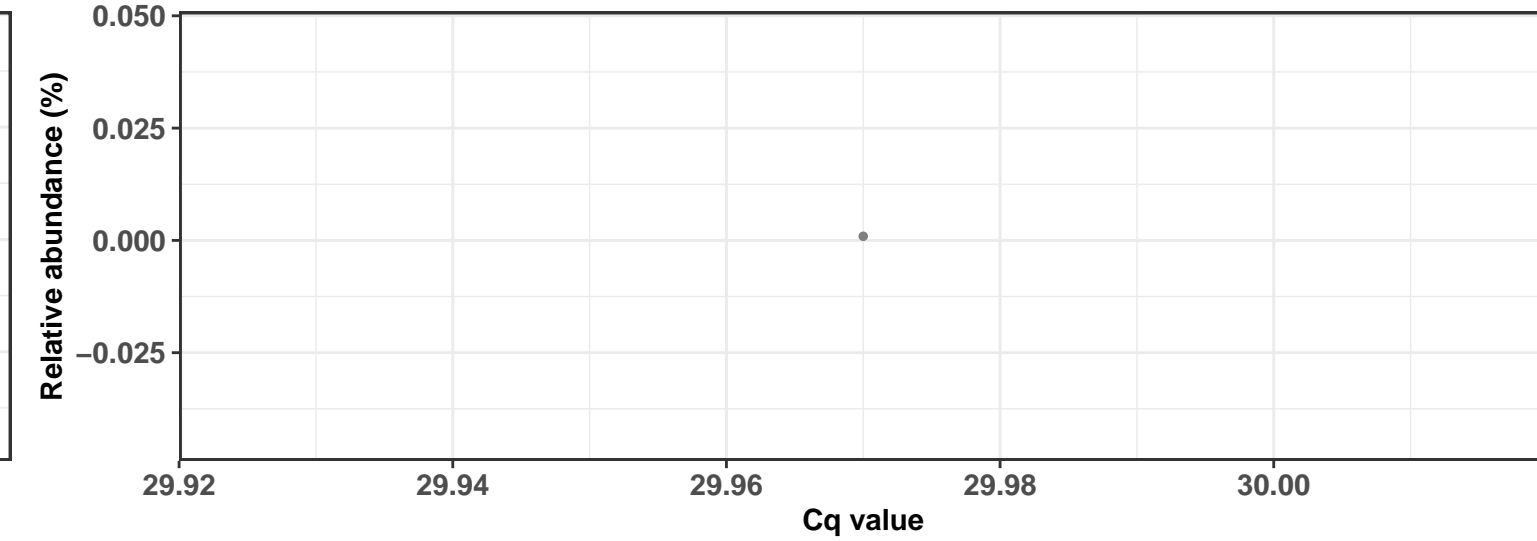
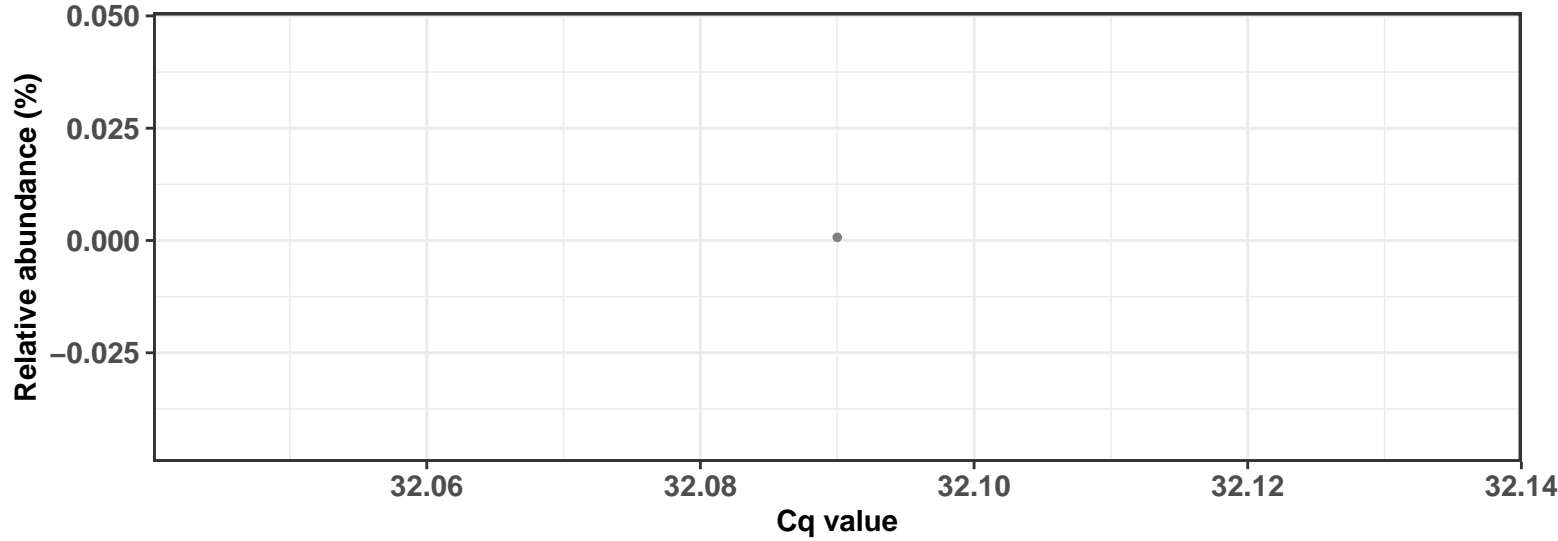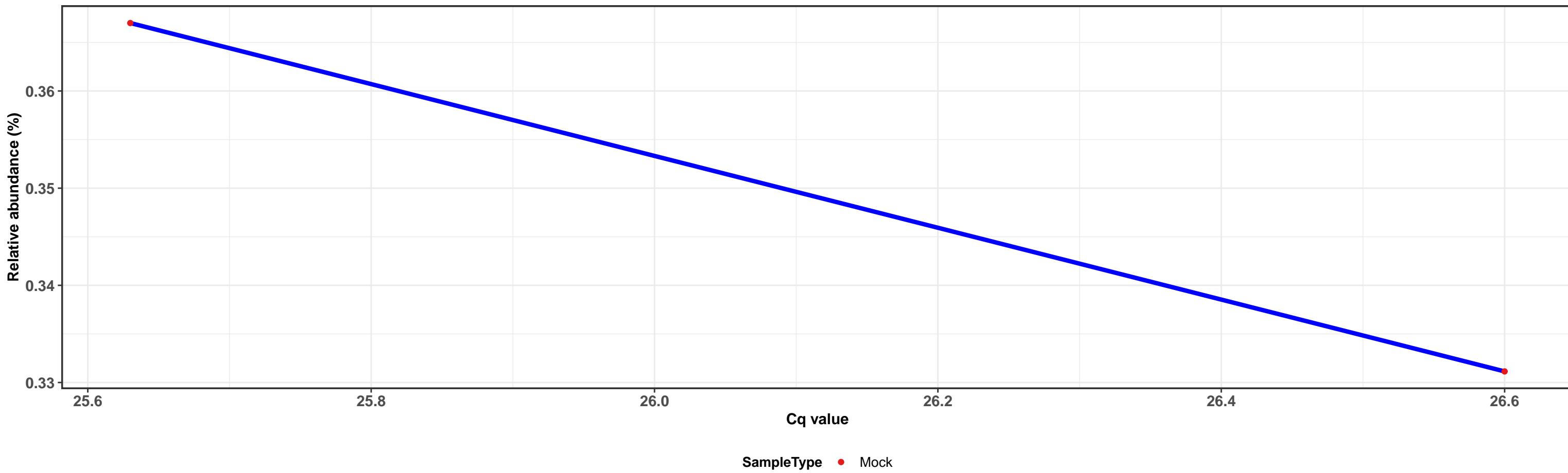**Correlation within: IM–DIC**

Correlation within: IM–DIM

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

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

Correlation with all samples

SampleType ● Mock

Correlation within: