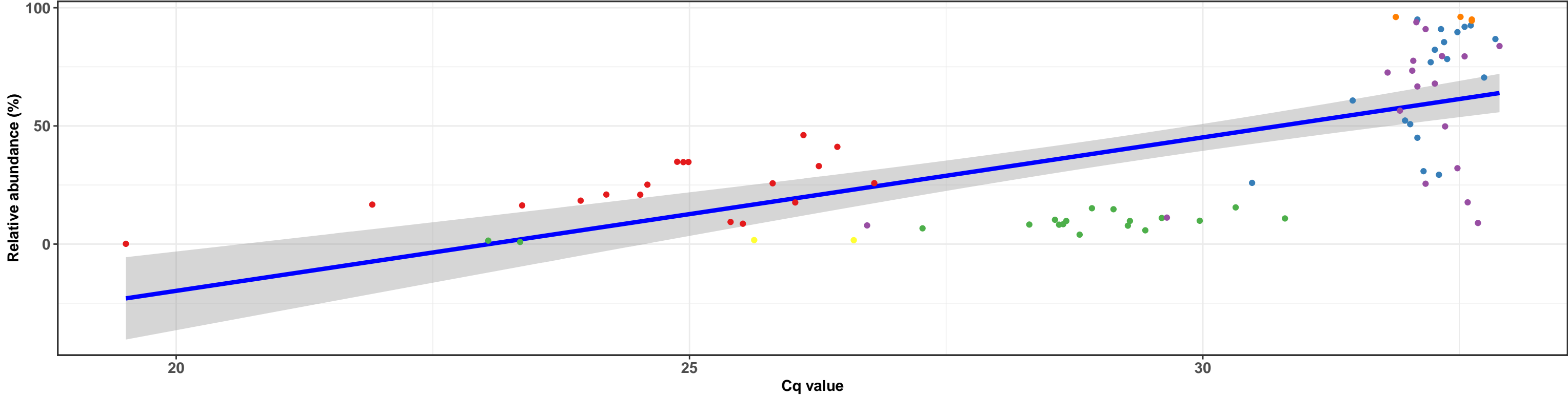


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

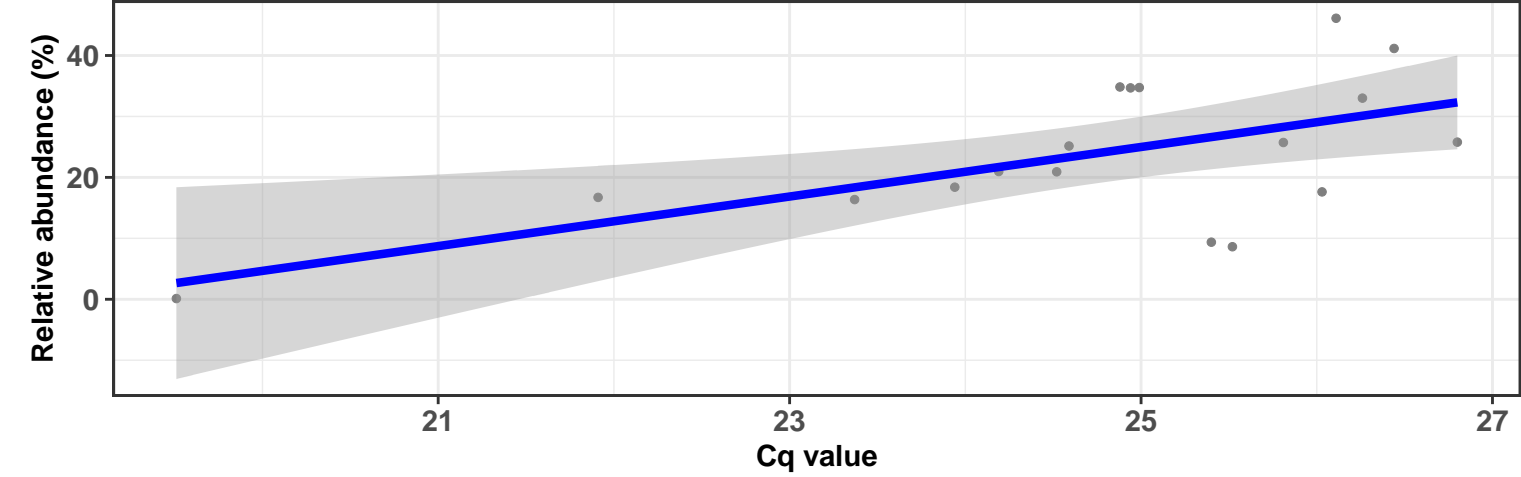
Correlation with all samples

$\log_e(S) = 10.174$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.668$ ,  $CI_{95\%} [0.536, 0.813]$ ,  $n_{\text{pairs}} = 78$



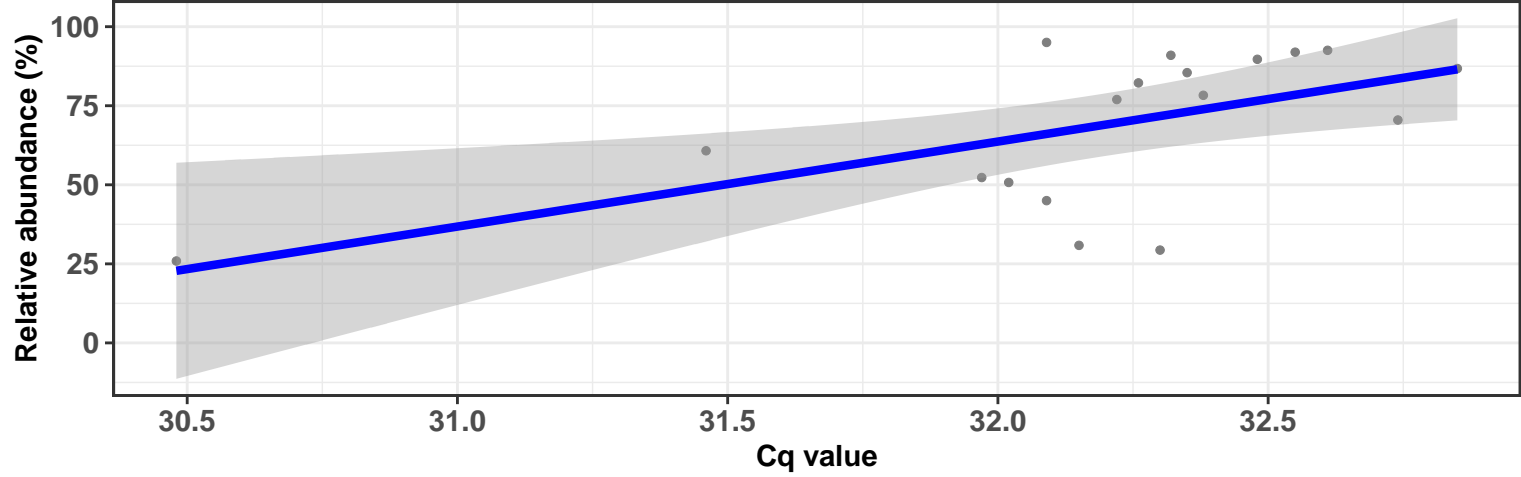
Correlation within: REF-DIC

$\log_e(S) = 6.105$ ,  $p = 0.021$ ,  $\hat{\rho}_{\text{Spearman}} = 0.538$ ,  $CI_{95\%} [0.161, 0.981]$ ,  $n_{\text{pairs}} = 18$



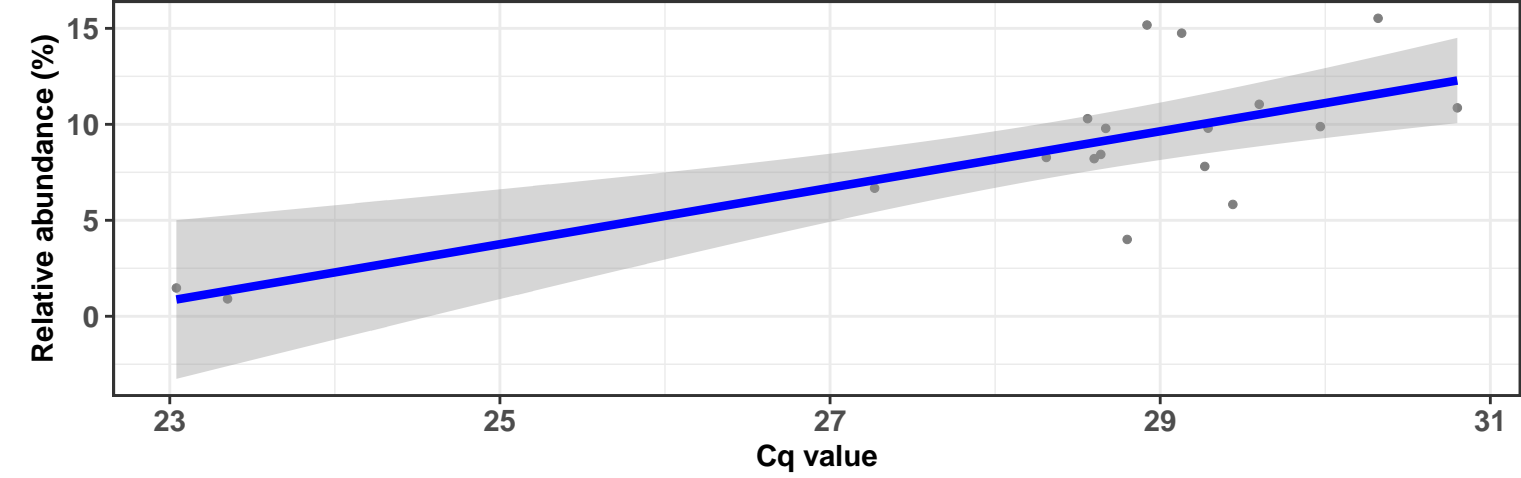
Correlation within: REF-DIM

$\log_e(S) = 6.020$ ,  $p = 0.013$ ,  $\hat{\rho}_{\text{Spearman}} = 0.575$ ,  $CI_{95\%} [0.211, 0.950]$ ,  $n_{\text{pairs}} = 18$



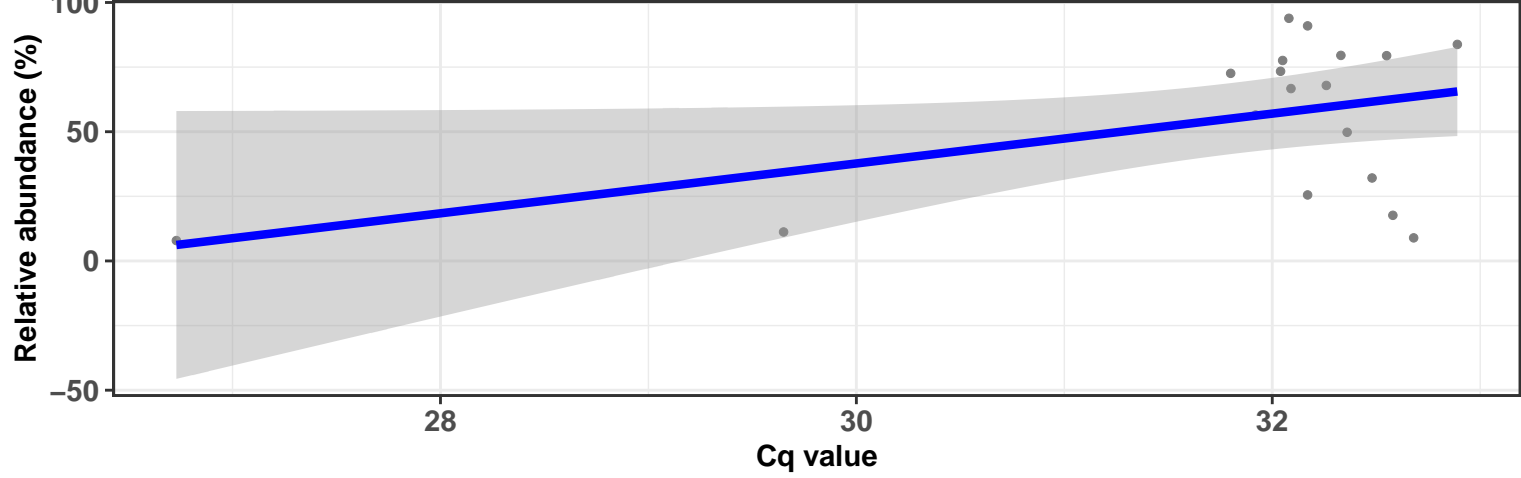
Correlation within: IM-DIC

$\log_e(S) = 5.935$ ,  $p = 0.007$ ,  $\hat{\rho}_{\text{Spearman}} = 0.610$ ,  $CI_{95\%} [0.284, 0.956]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

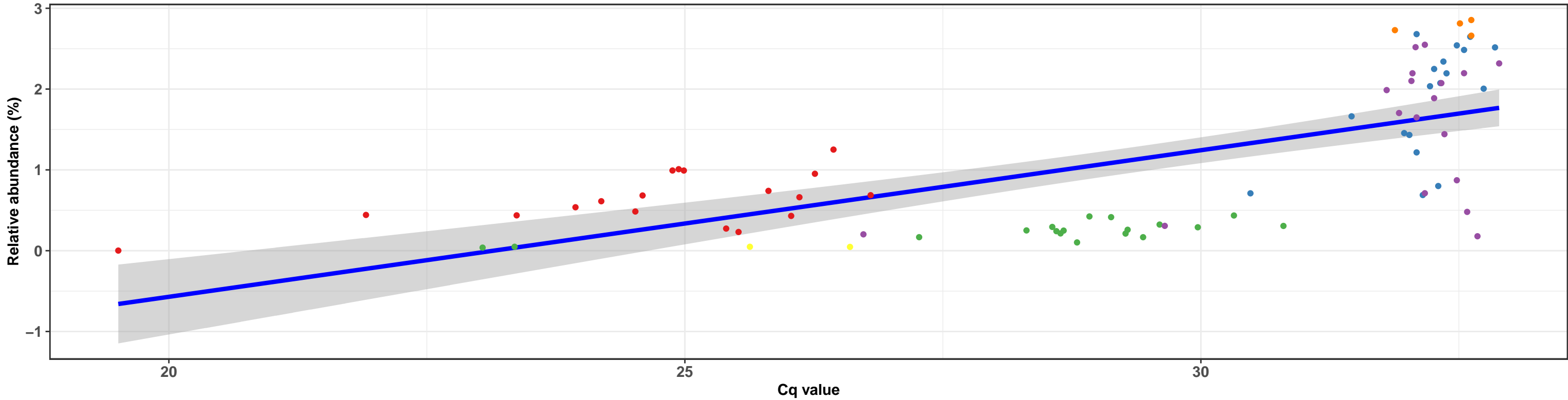
$\log_e(S) = 6.759$ ,  $p = 0.663$ ,  $\hat{\rho}_{\text{Spearman}} = 0.110$ ,  $CI_{95\%} [-0.472, 0.652]$ ,  $n_{\text{pairs}} = 18$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

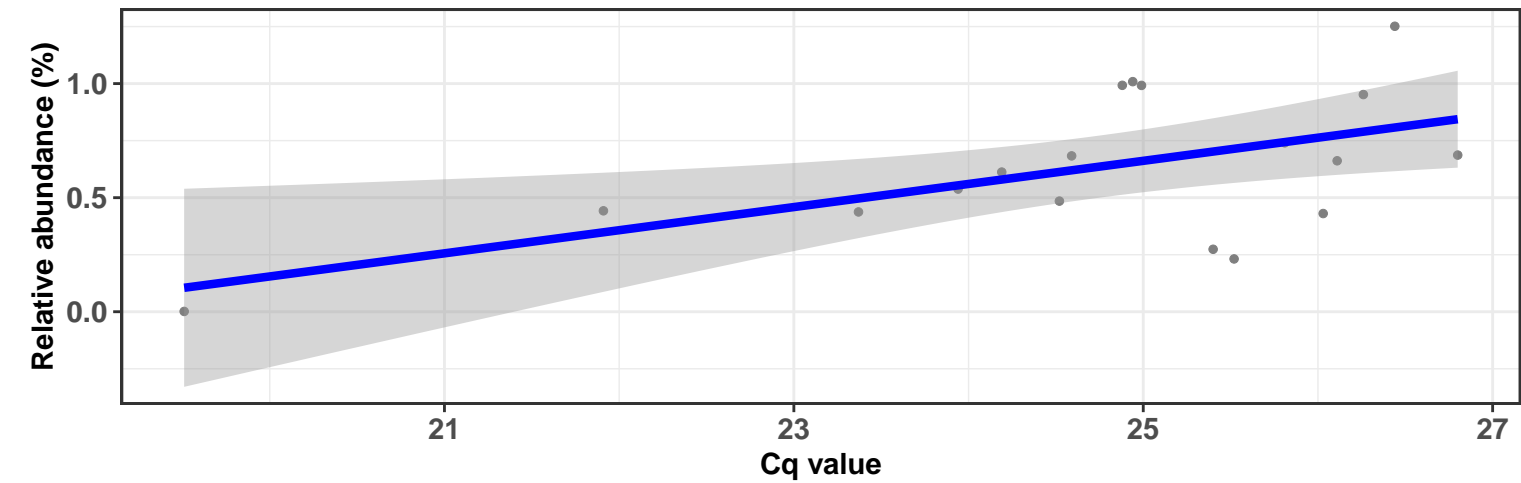
Correlation with all samples

$\log_e(S) = 10.184$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.665$ ,  $\text{CI}_{95\%} [0.517, 0.816]$ ,  $n_{\text{pairs}} = 78$



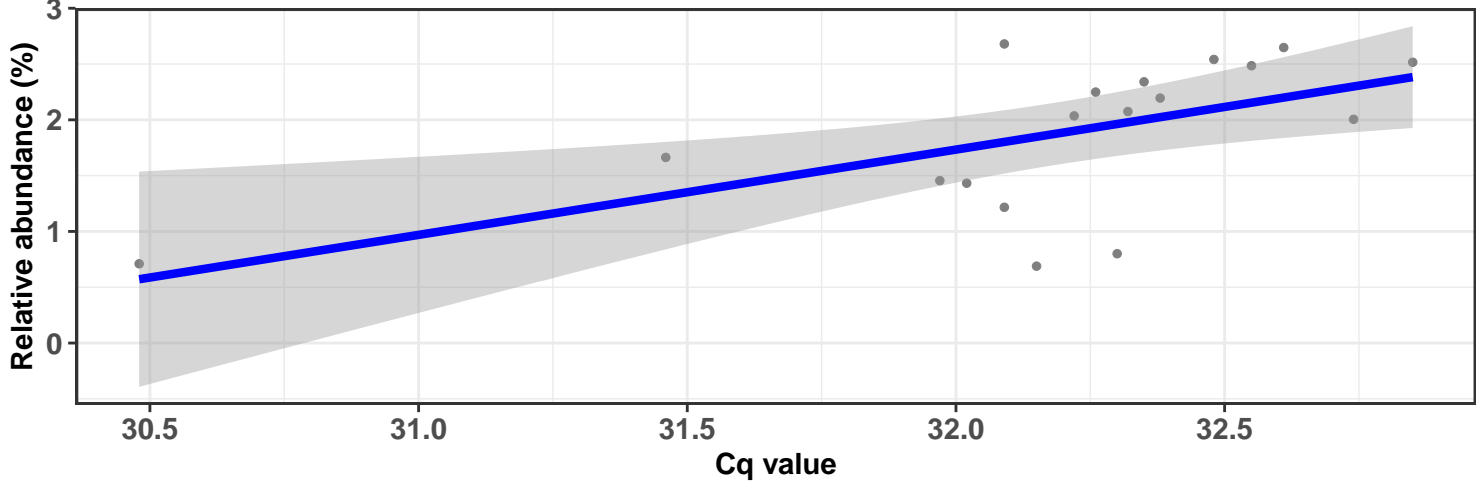
Correlation within: REF-DIC

$\log_e(S) = 6.314$ ,  $p = 0.075$ ,  $\hat{\rho}_{\text{Spearman}} = 0.430$ ,  $\text{CI}_{95\%} [0.012, 0.834]$ ,  $n_{\text{pairs}} = 18$



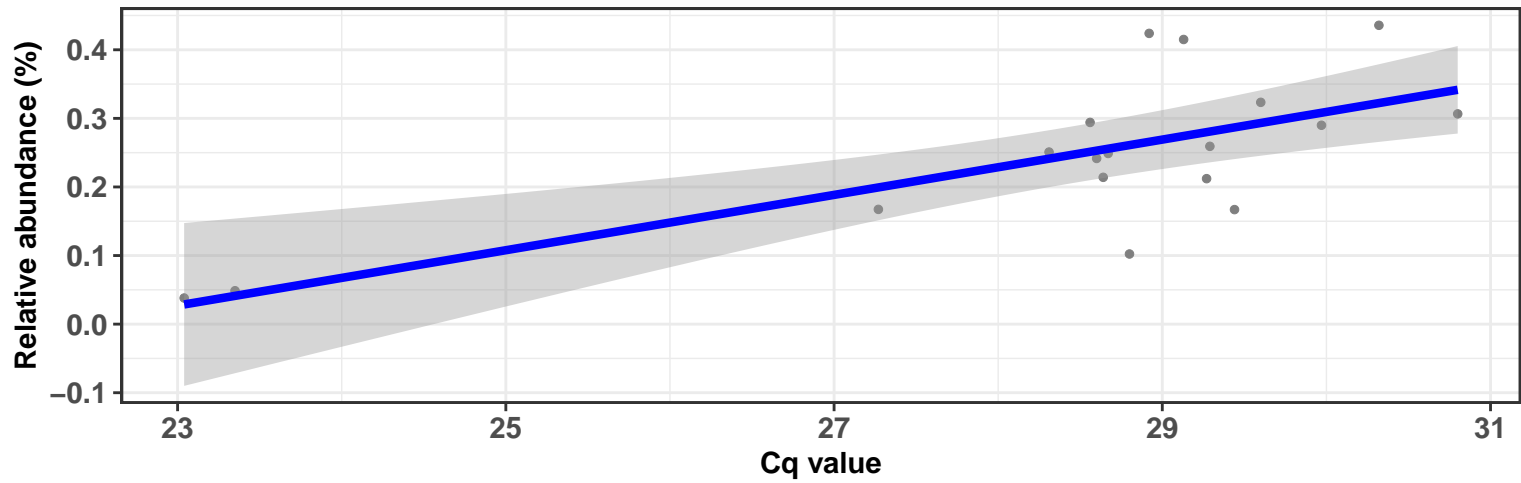
Correlation within: REF-DIM

$\log_e(S) = 5.971$ ,  $p = 0.009$ ,  $\hat{\rho}_{\text{Spearman}} = 0.596$ ,  $\text{CI}_{95\%} [0.224, 1.016]$ ,  $n_{\text{pairs}} = 18$



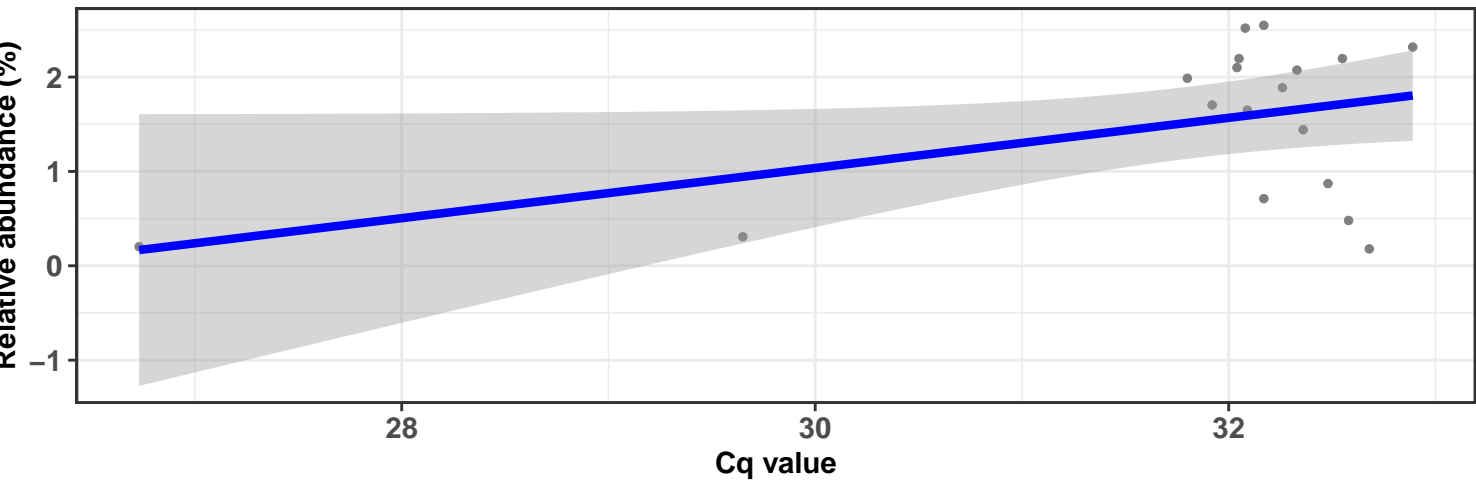
Correlation within: IM-DIC

$\log_e(S) = 5.971$ ,  $p = 0.009$ ,  $\hat{\rho}_{\text{Spearman}} = 0.595$ ,  $\text{CI}_{95\%} [0.267, 0.988]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

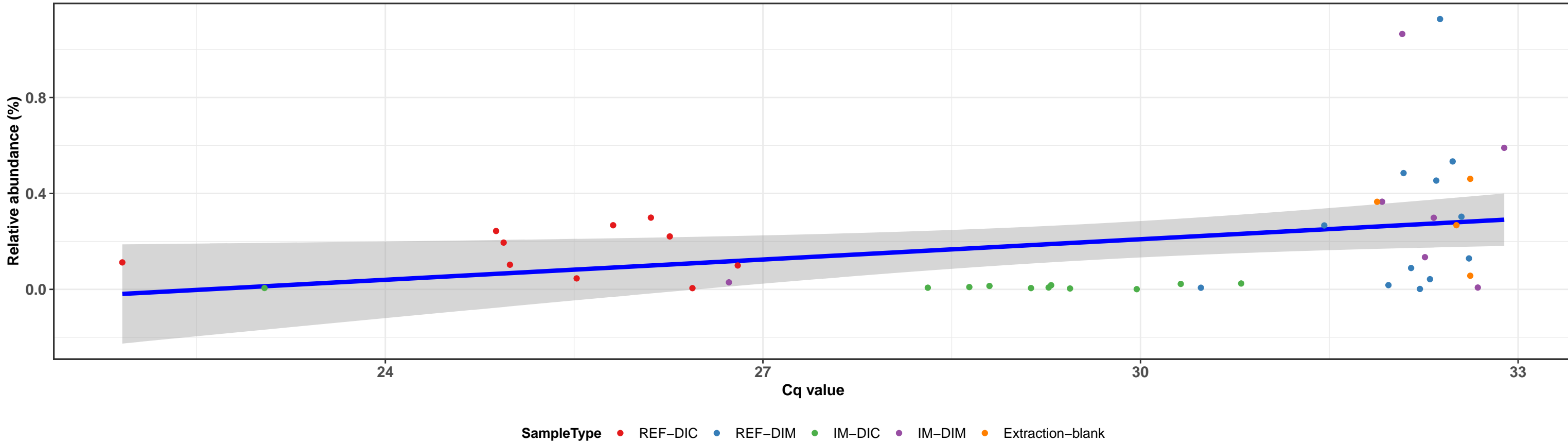
$\log_e(S) = 6.821$ ,  $p = 0.832$ ,  $\hat{\rho}_{\text{Spearman}} = 0.054$ ,  $\text{CI}_{95\%} [-0.508, 0.569]$ ,  $n_{\text{pairs}} = 18$



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

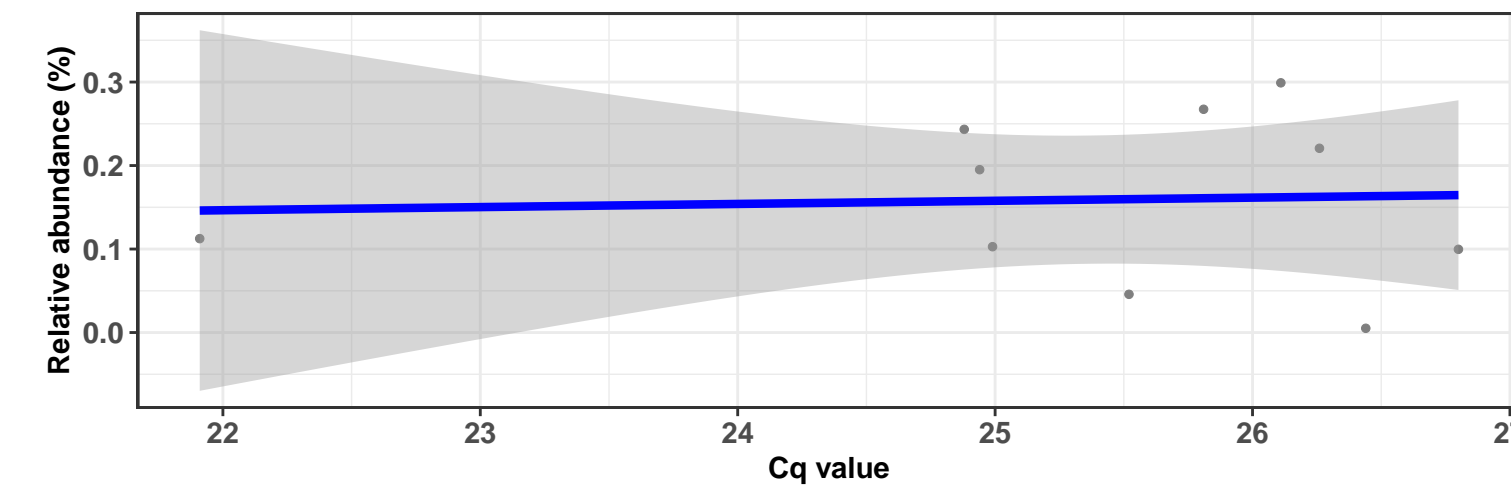
### Correlation with all samples

$\log_e(S) = 9.123$ ,  $p = 0.018$ ,  $\hat{\rho}_{\text{Spearman}} = 0.354$ ,  $\text{CI}_{95\%} [0.106, 0.634]$ ,  $n_{\text{pairs}} = 44$



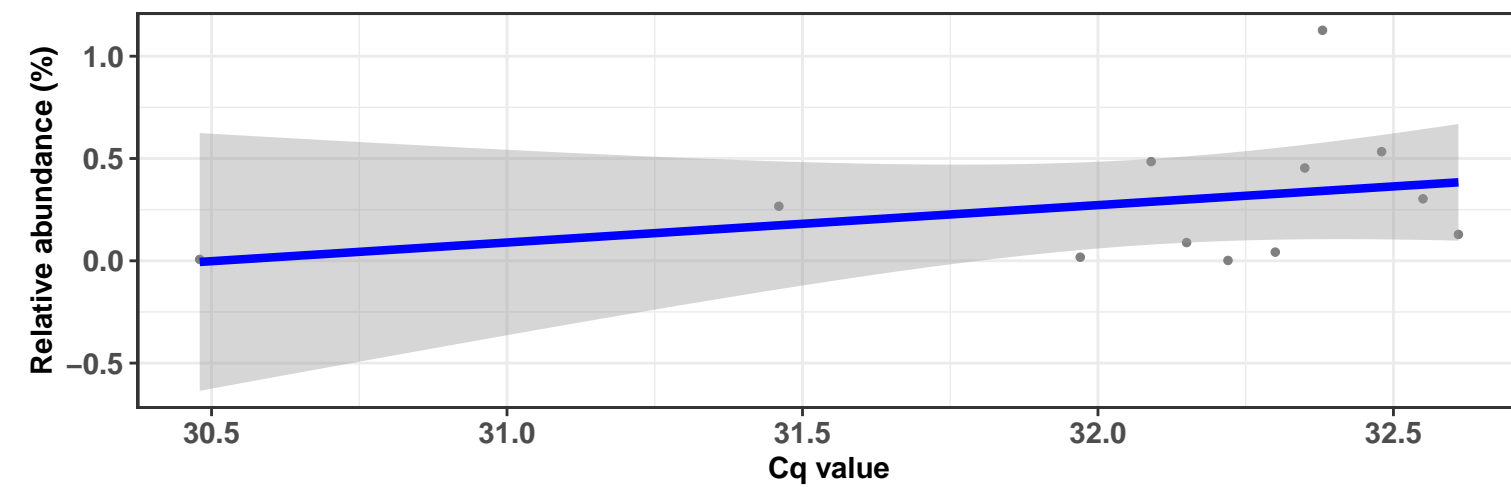
### Correlation within: REF-DIC

$\log_e(S) = 5.308$ ,  $p = 0.533$ ,  $\hat{\rho}_{\text{Spearman}} = -0.224$ ,  $\text{CI}_{95\%} [-0.974, 0.396]$ ,  $n_{\text{pairs}} = 10$



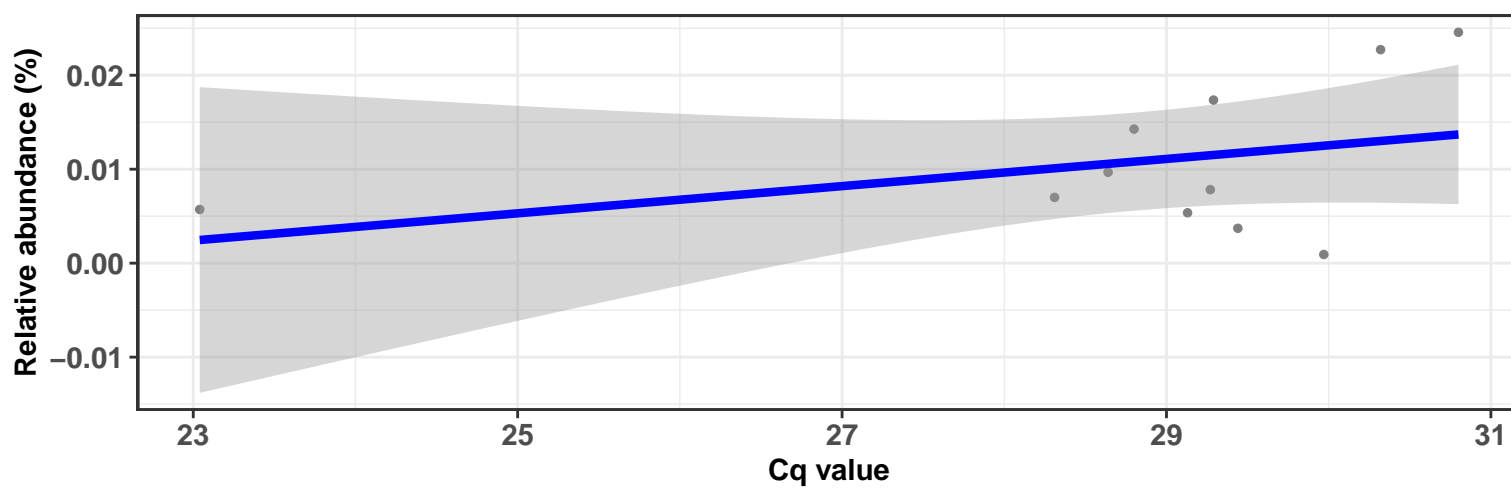
### Correlation within: REF-DIM

$\log_e(S) = 5.024$ ,  $p = 0.124$ ,  $\hat{\rho}_{\text{Spearman}} = 0.469$ ,  $\text{CI}_{95\%} [0.053, 1.060]$ ,  $n_{\text{pairs}} = 12$



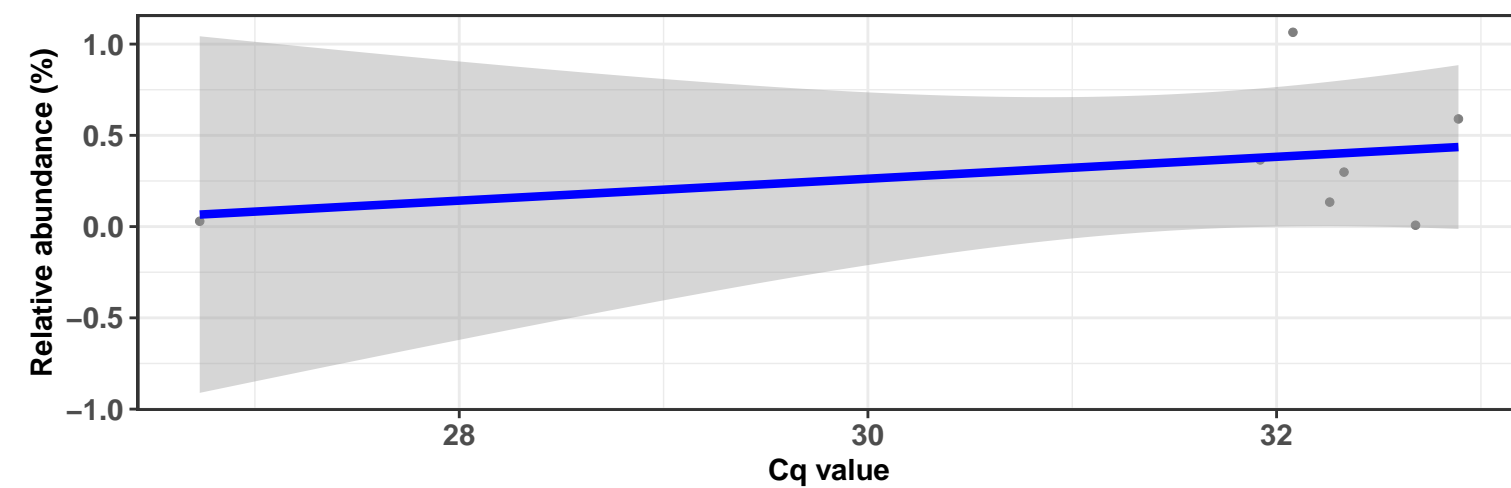
### Correlation within: IM-DIC

$\log_e(S) = 5.063$ ,  $p = 0.401$ ,  $\hat{\rho}_{\text{Spearman}} = 0.282$ ,  $\text{CI}_{95\%} [-0.451, 1.058]$ ,  $n_{\text{pairs}} = 11$



### Correlation within: IM-DIM

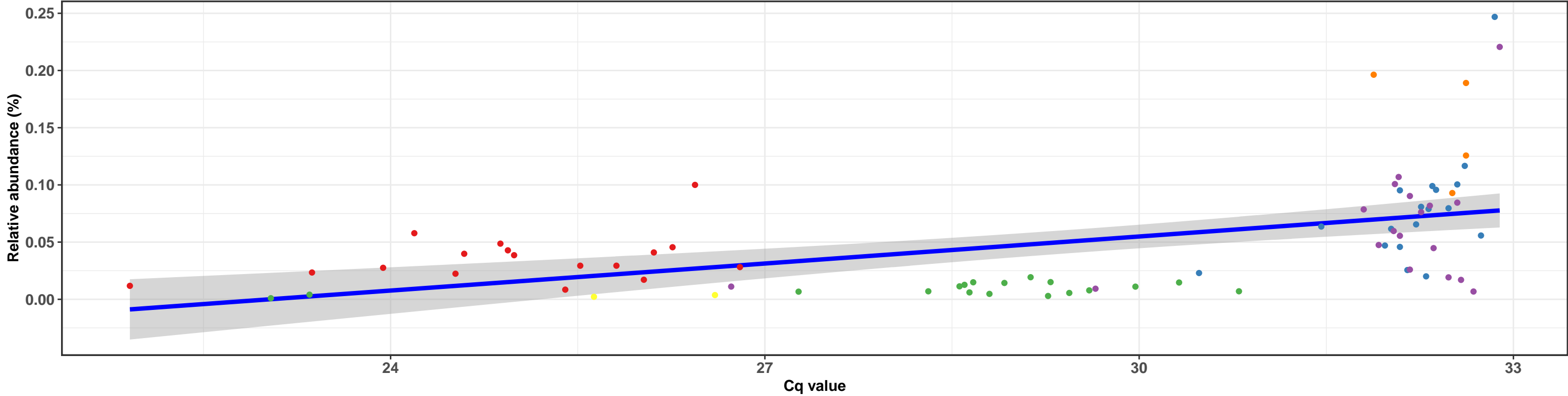
$\log_e(S) = 3.989$ ,  $p = 0.939$ ,  $\hat{\rho}_{\text{Spearman}} = 0.036$ ,  $\text{CI}_{95\%} [-0.872, 0.895]$ ,  $n_{\text{pairs}} = 7$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

Correlation with all samples

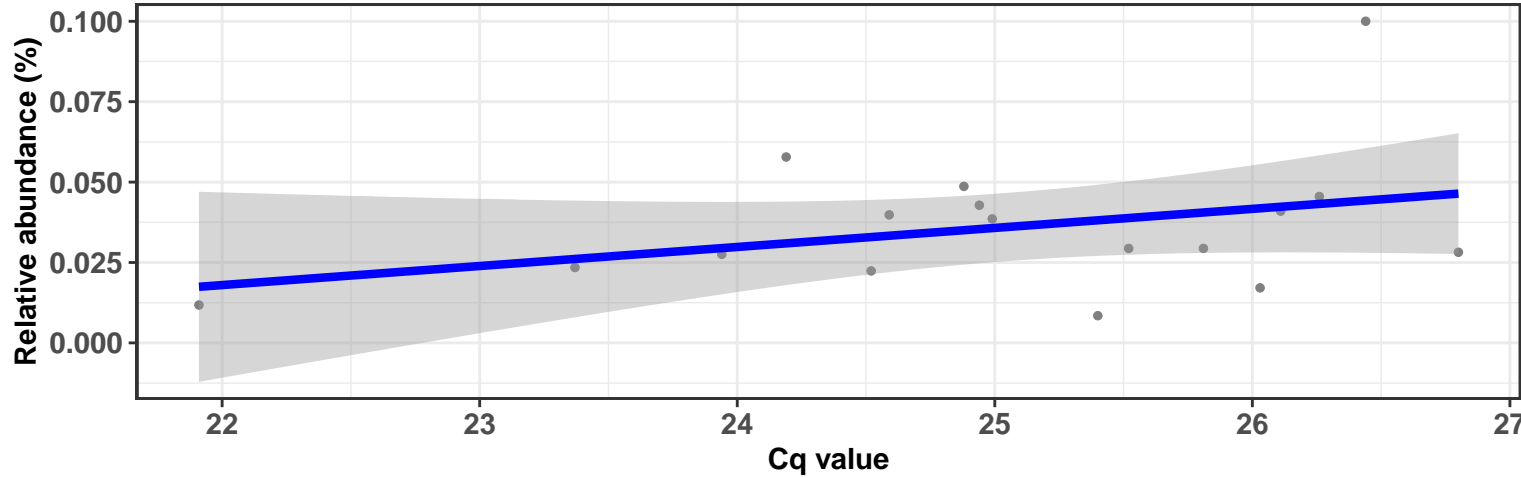
$\log_e(S) = 10.412$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.563$ ,  $CI_{95\%} [0.389, 0.721]$ ,  $n_{\text{pairs}} = 77$



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

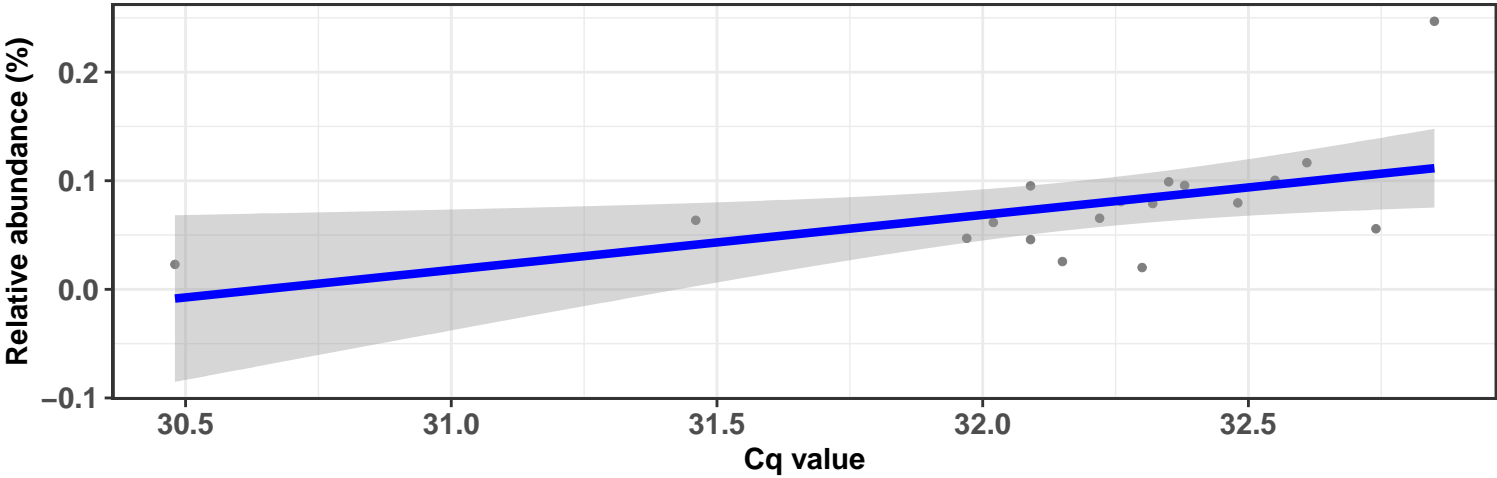
Correlation within: REF-DIC

$\log_e(S) = 6.370$ ,  $p = 0.269$ ,  $\hat{\rho}_{\text{Spearman}} = 0.284$ ,  $CI_{95\%} [-0.187, 0.812]$ ,  $n_{\text{pairs}} = 17$



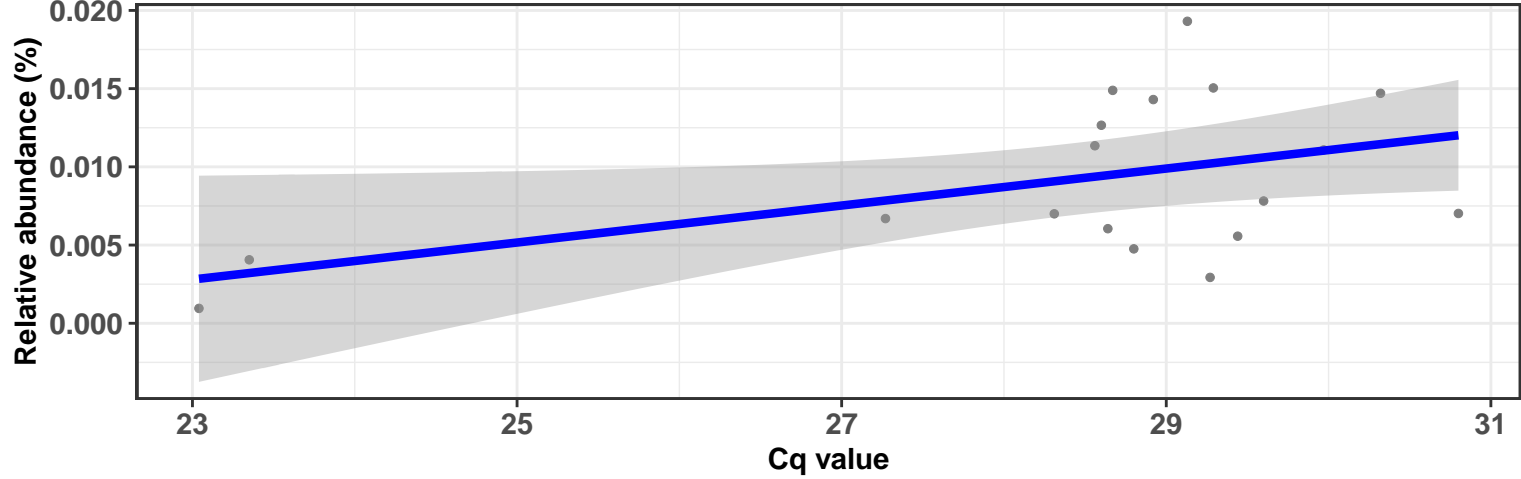
Correlation within: REF-DIM

$\log_e(S) = 5.882$ ,  $p = 0.005$ ,  $\hat{\rho}_{\text{Spearman}} = 0.630$ ,  $CI_{95\%} [0.322, 0.992]$ ,  $n_{\text{pairs}} = 18$



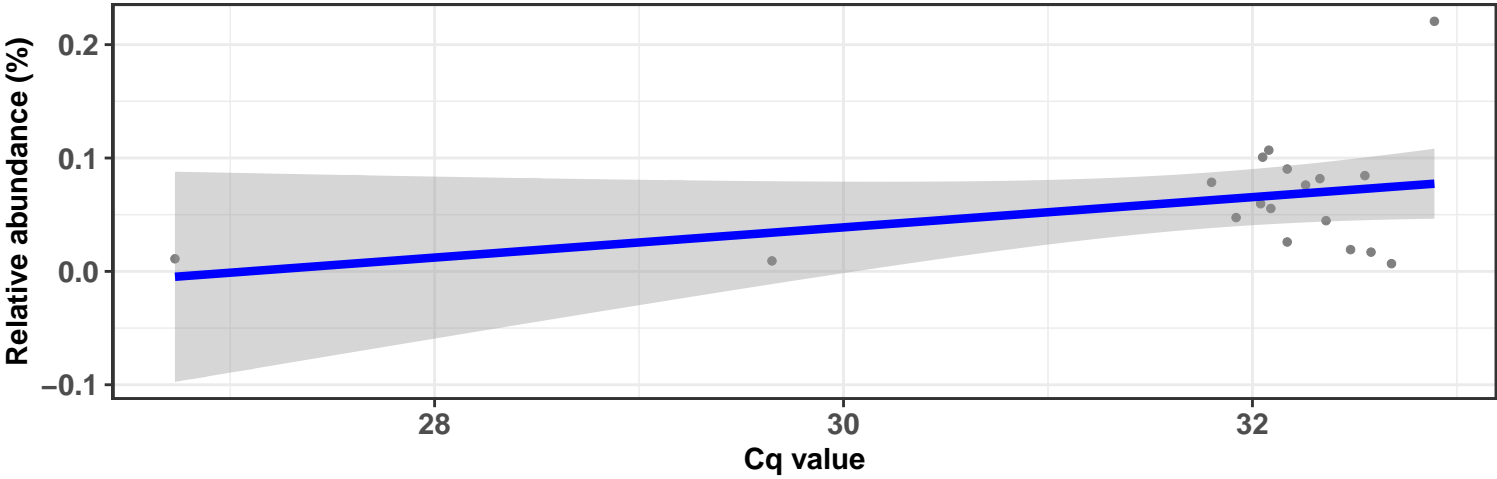
Correlation within: IM-DIC

$\log_e(S) = 6.426$ ,  $p = 0.140$ ,  $\hat{\rho}_{\text{Spearman}} = 0.362$ ,  $CI_{95\%} [-0.012, 0.761]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

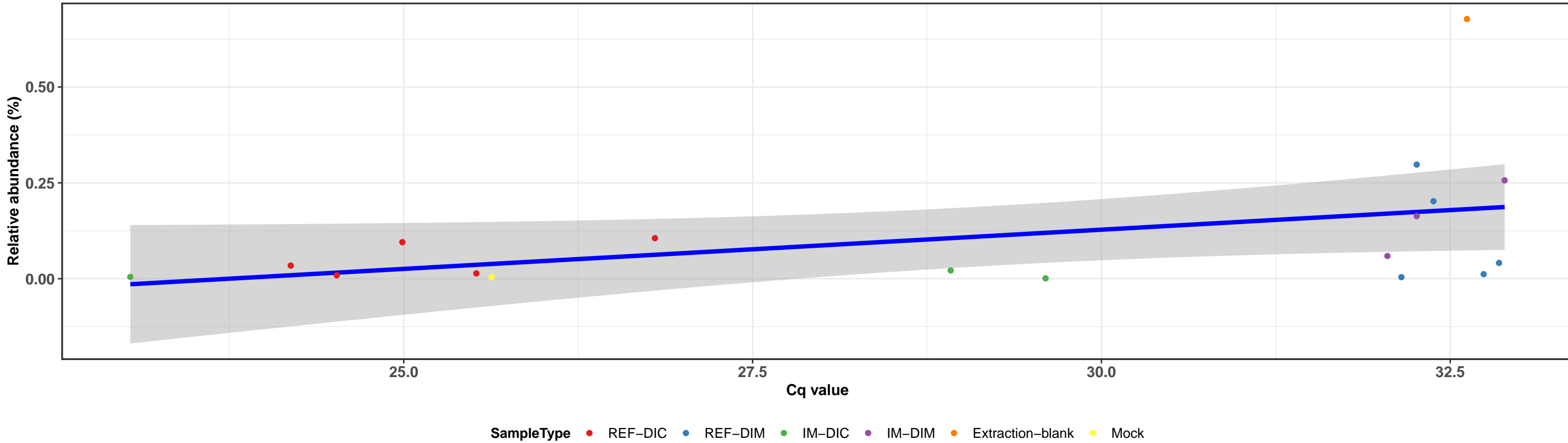
$\log_e(S) = 6.790$ ,  $p = 0.745$ ,  $\hat{\rho}_{\text{Spearman}} = 0.083$ ,  $CI_{95\%} [-0.477, 0.746]$ ,  $n_{\text{pairs}} = 18$



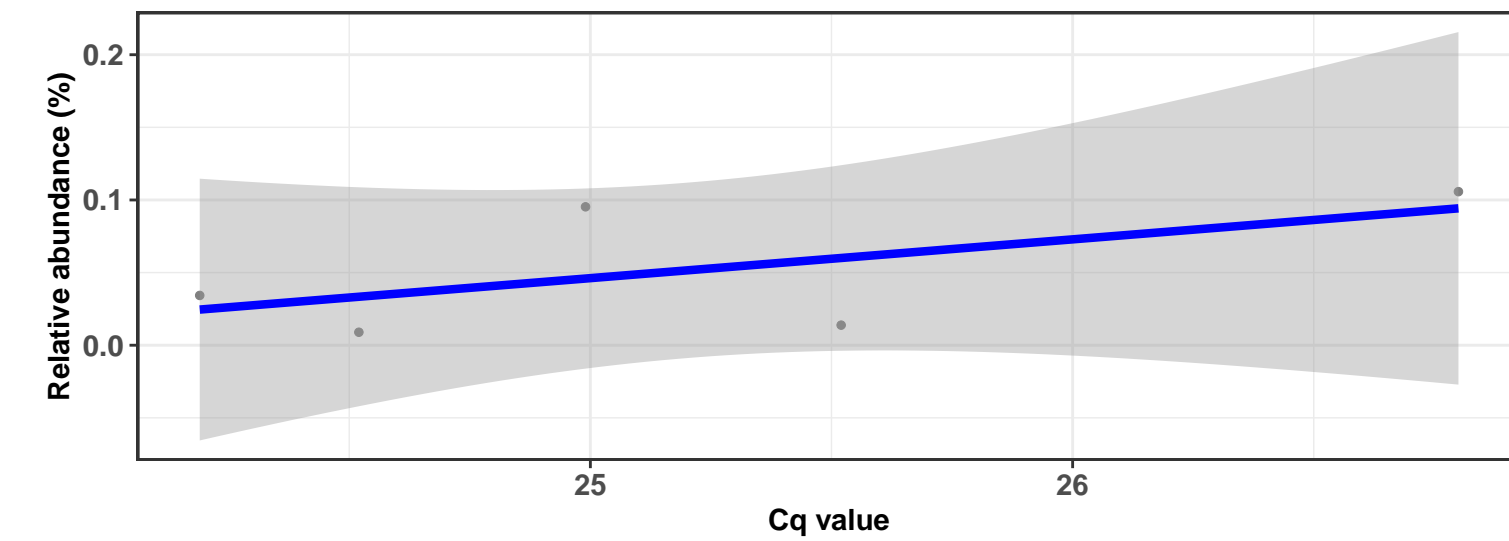
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Microbacteriaceae; g\_\_Curtobacterium; Ambiguous\_taxa

### Correlation with all samples

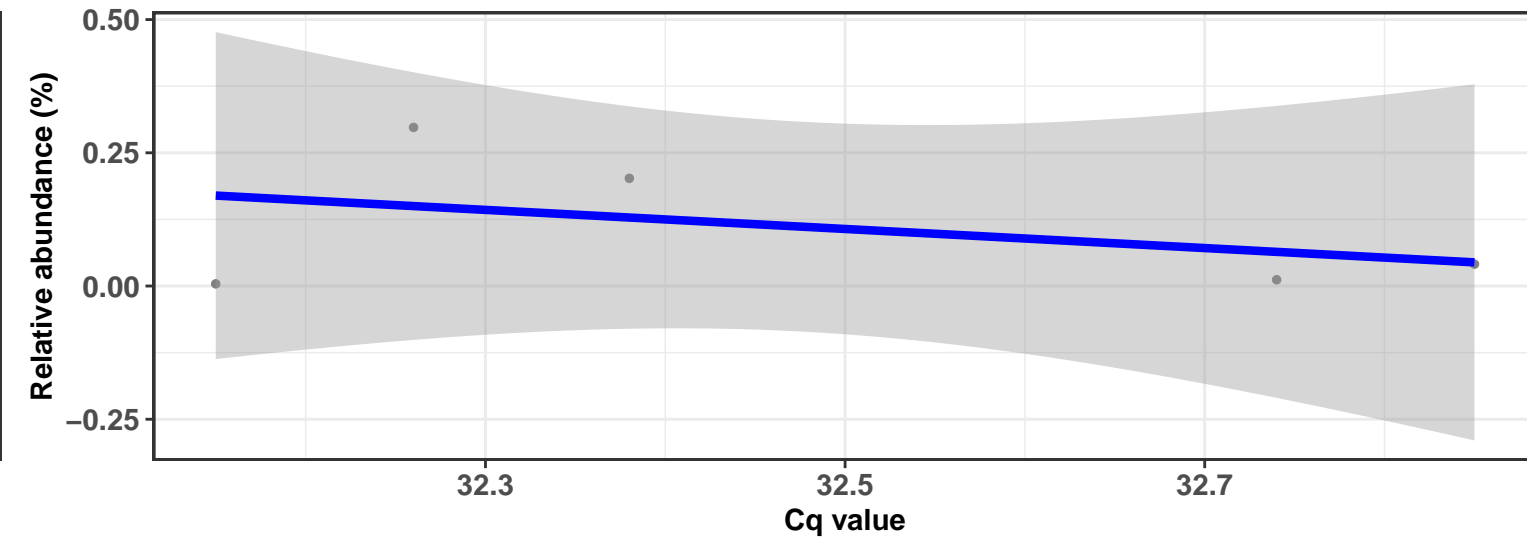
$\log_e(S) = 6.228$ ,  $p = 0.045$ ,  $\hat{\rho}_{\text{Spearman}} = 0.477$ ,  $\text{CI}_{95\%} [0.140, 0.906]$ ,  $n_{\text{pairs}} = 18$



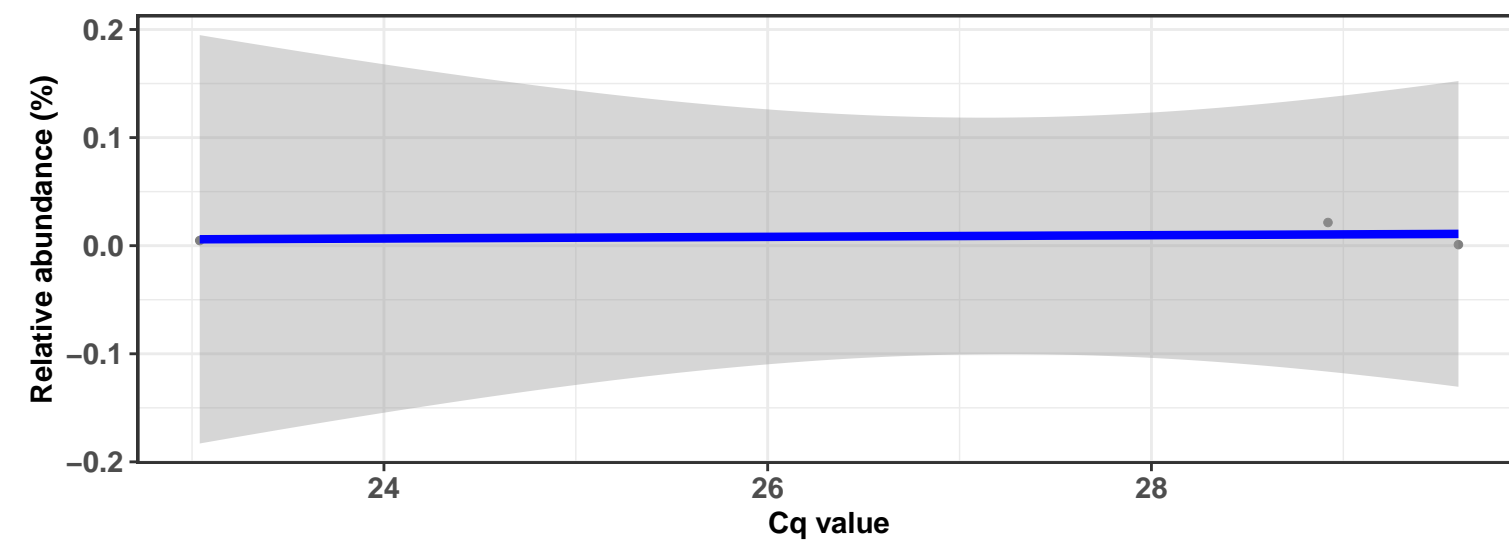
### Correlation within: REF-DIC



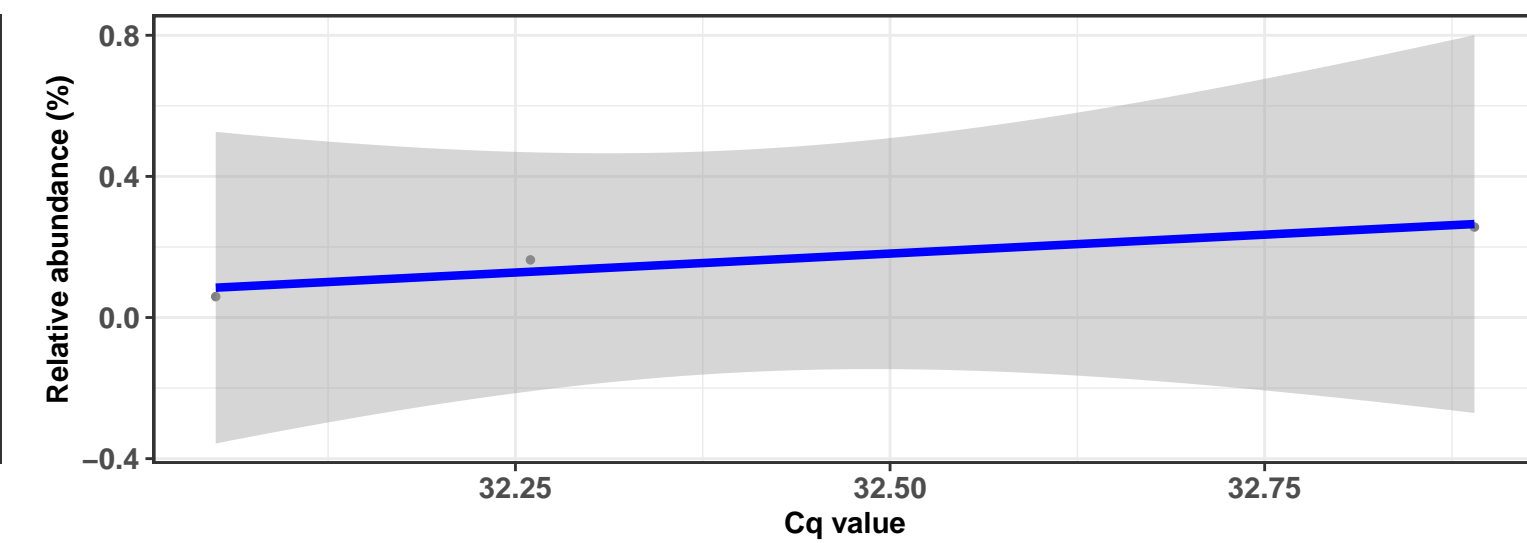
### Correlation within: REF-DIM



### Correlation within: IM-DIC

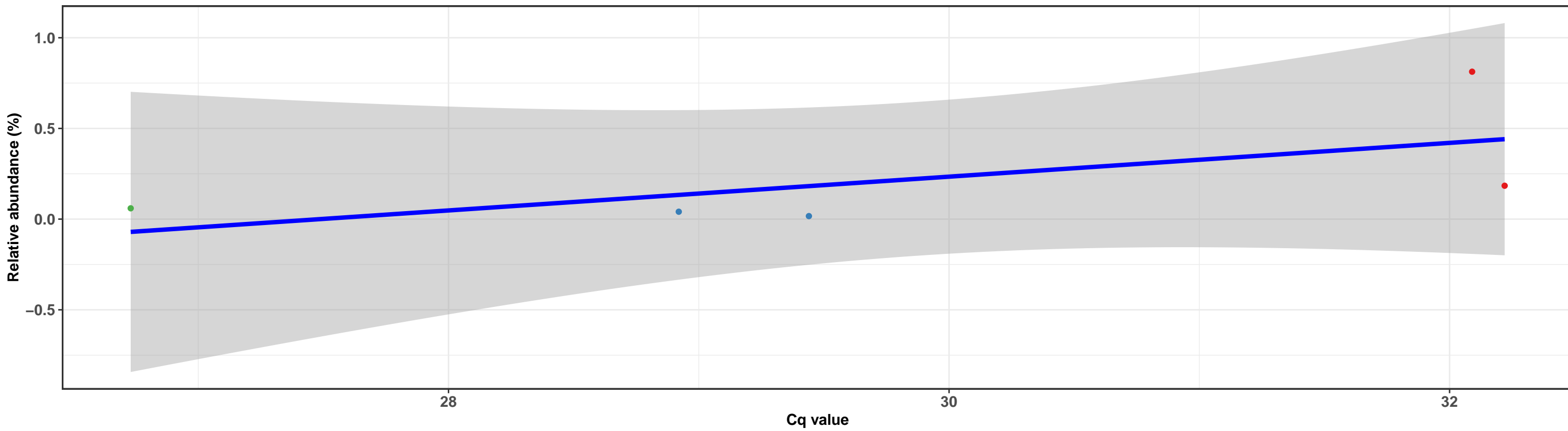


### Correlation within: IM-DIM

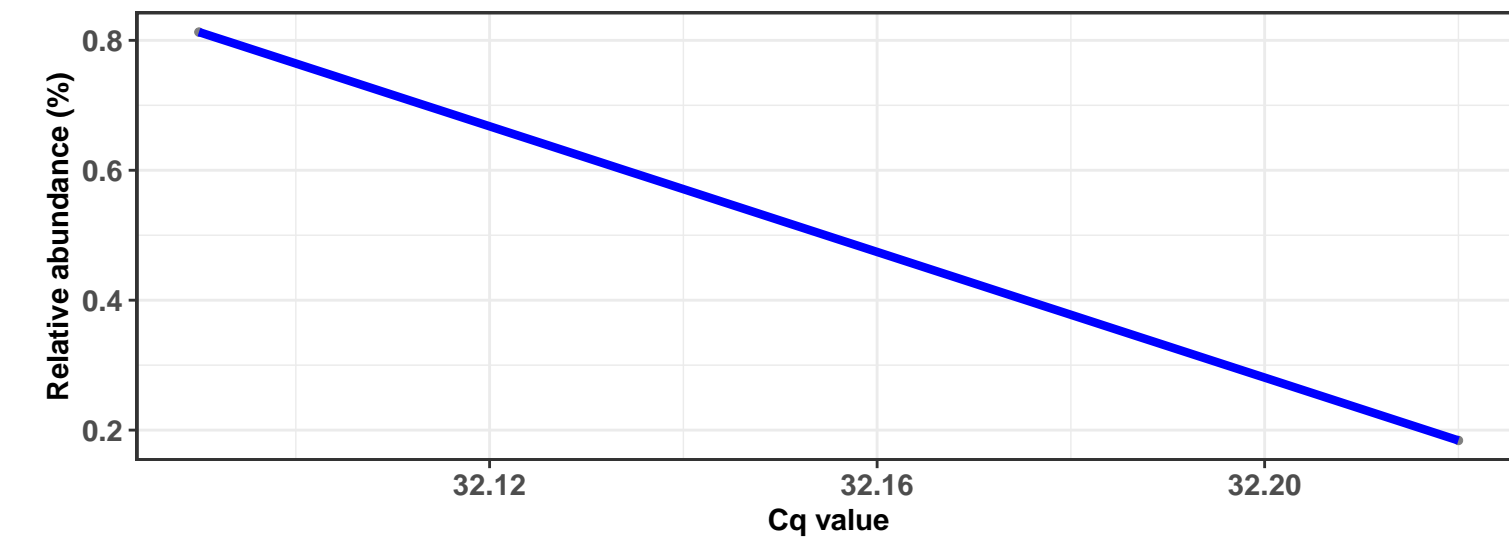


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Jeotgalicoccus; Ambiguous\_taxa

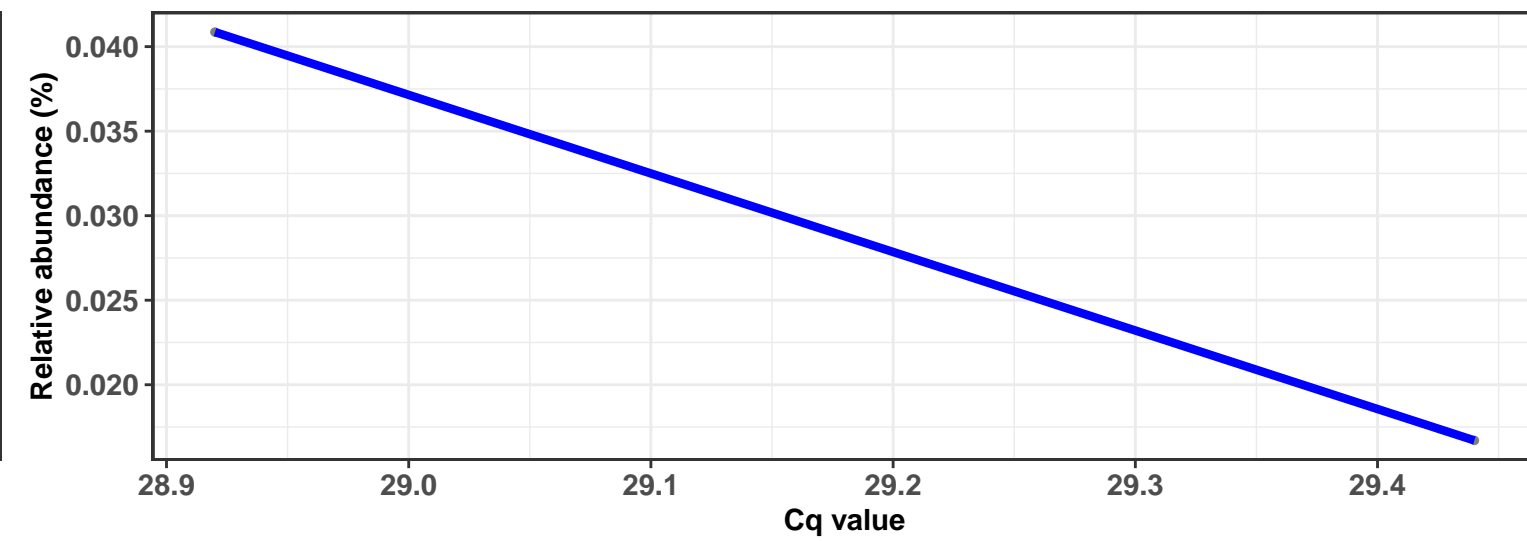
Correlation with all samples



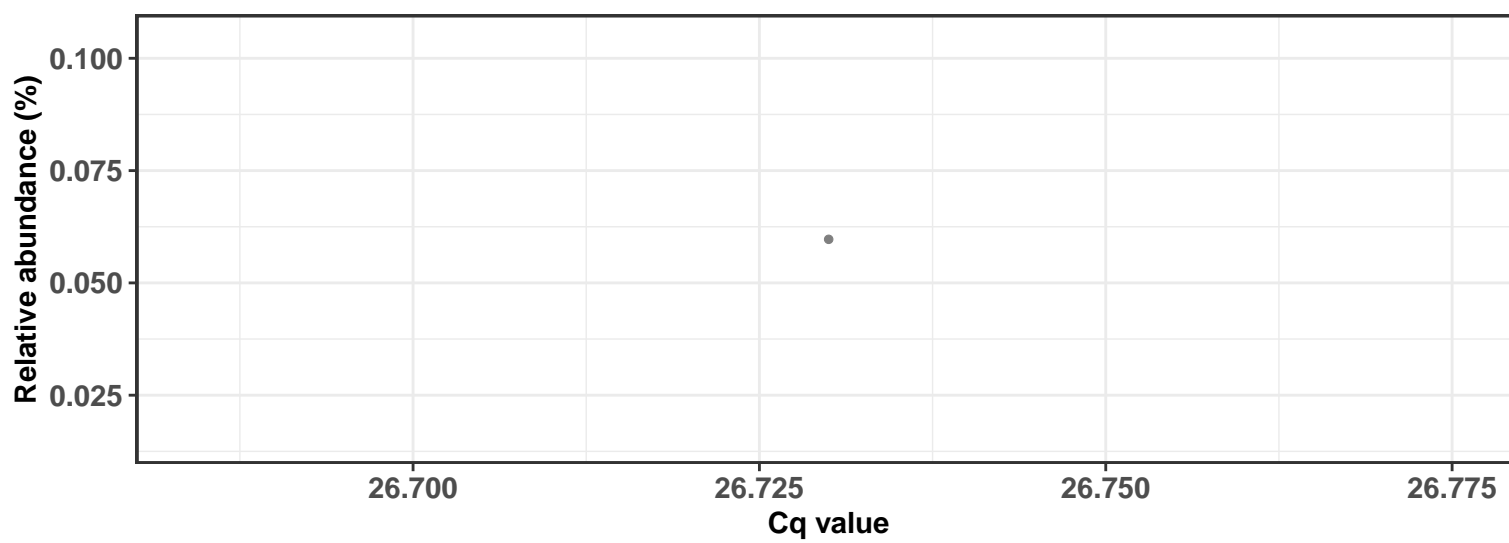
Correlation within: REF-DIM



Correlation within: IM-DIC



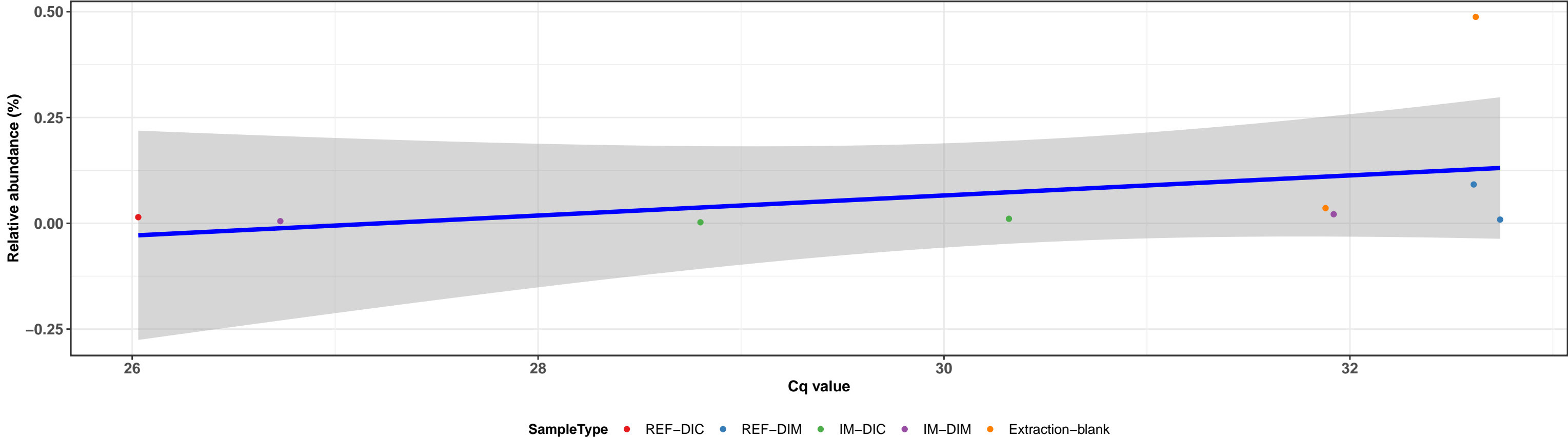
Correlation within: IM-DIM



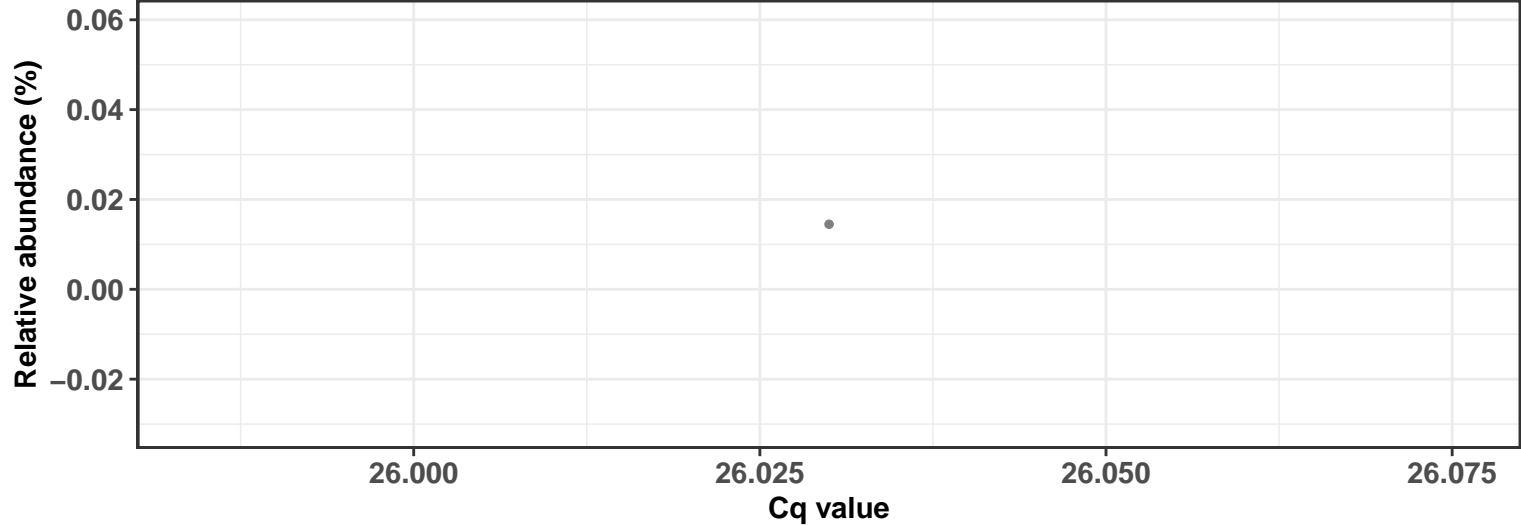
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Frankiales; f\_\_Geodermatophilaceae; g\_\_Modestobacter; Ambiguous\_taxa

Correlation with all samples

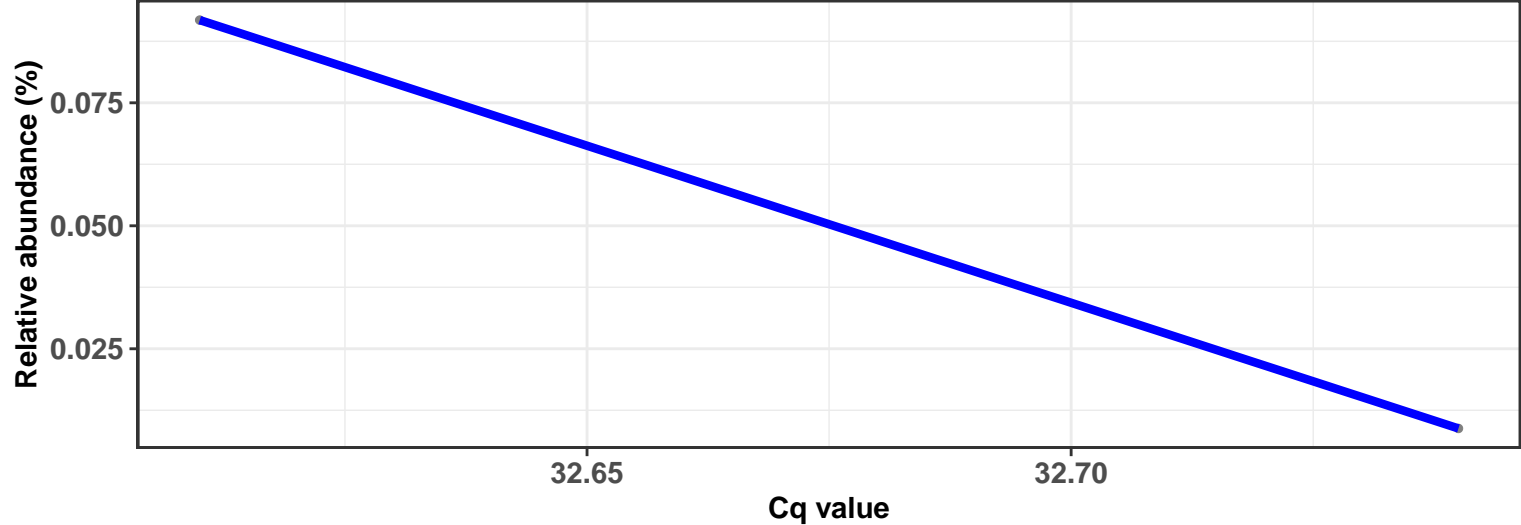
$\log_e(S) = 4.127$ ,  $p = 0.187$ ,  $\hat{\rho}_{\text{Spearman}} = 0.483$ ,  $\text{CI}_{95\%} [-0.102, 1.109]$ ,  $n_{\text{pairs}} = 9$



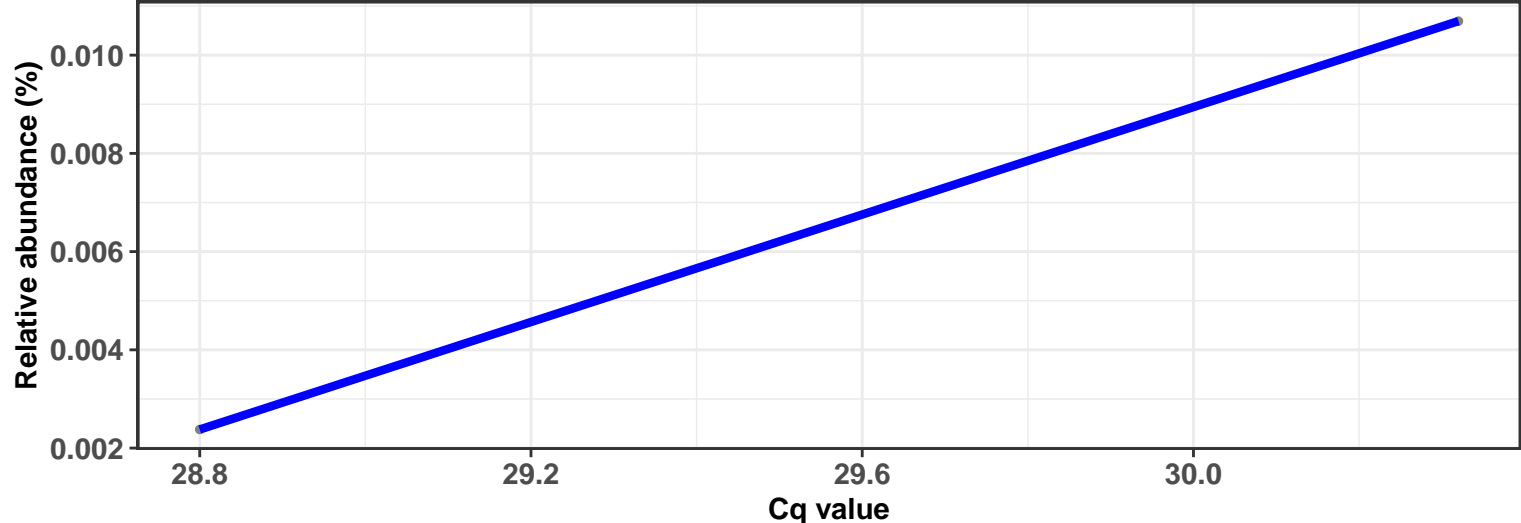
Correlation within: REF-DIC



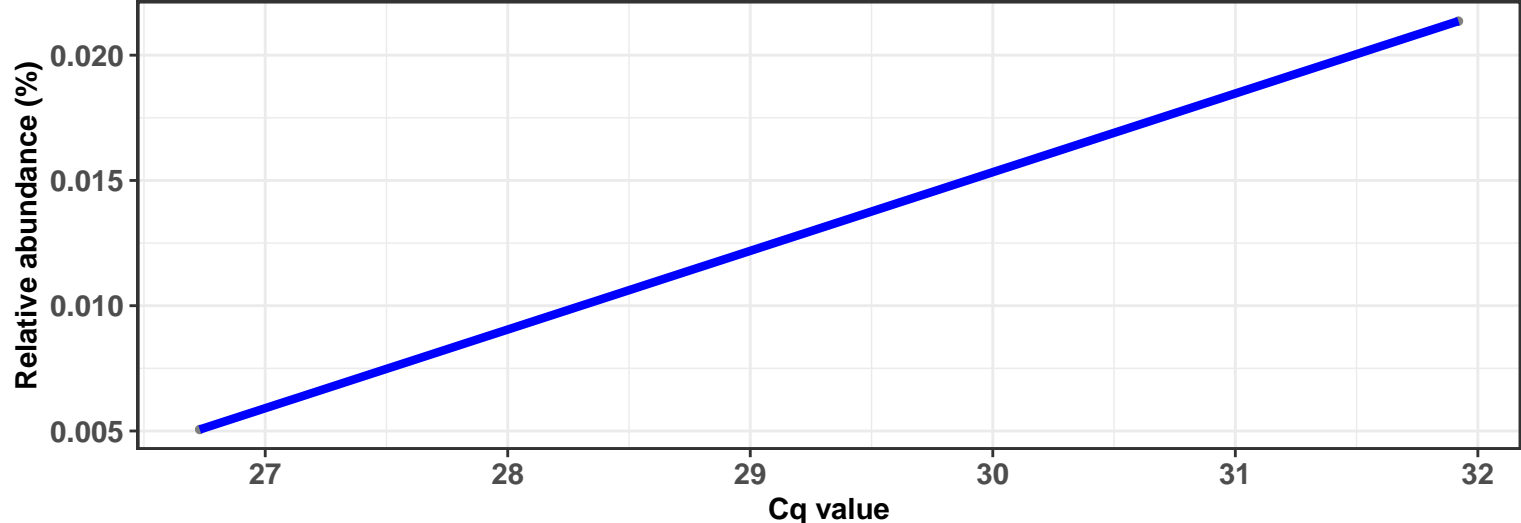
Correlation within: REF-DIM



Correlation within: IM-DIC



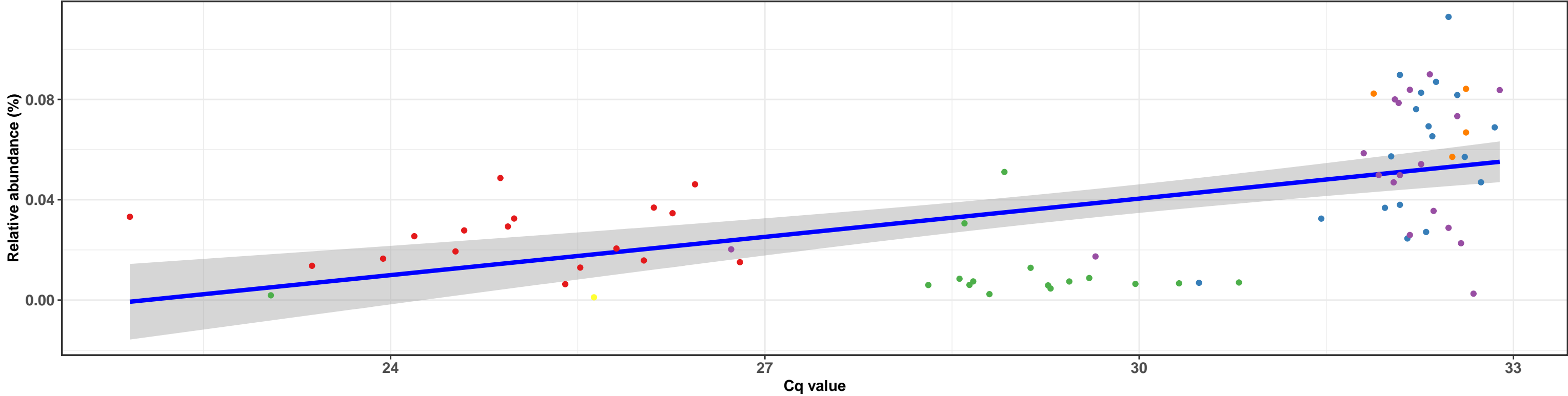
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

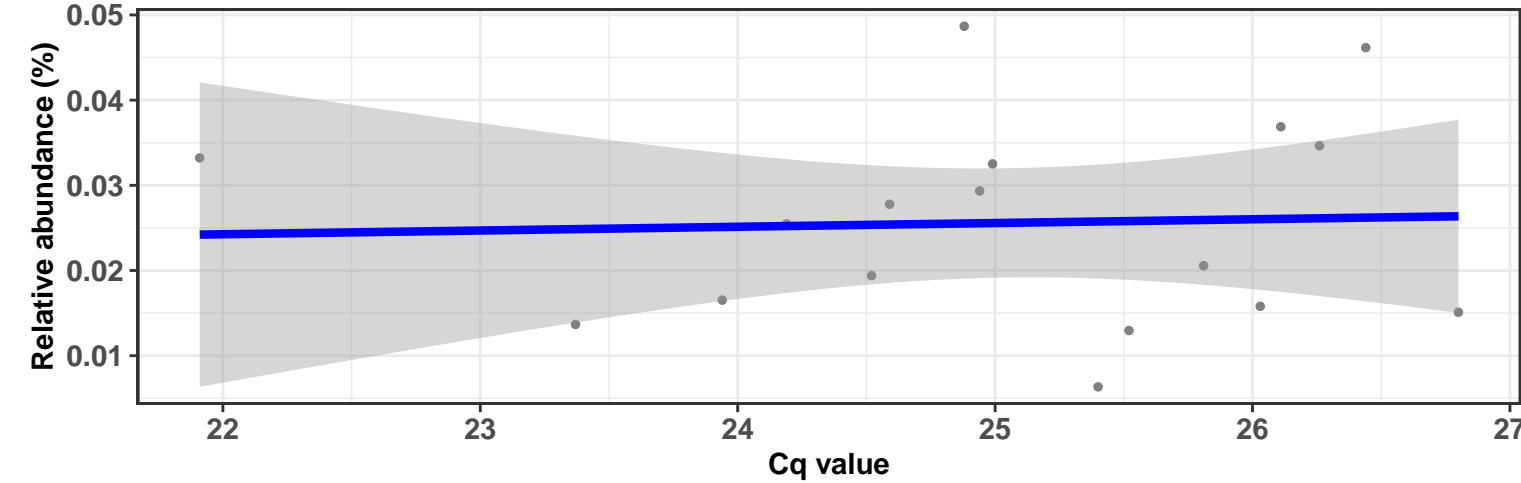
Correlation with all samples

$\log_e(S) = 10.265$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.575$ ,  $\text{CI}_{95\%} [0.416, 0.746]$ ,  $n_{\text{pairs}} = 74$



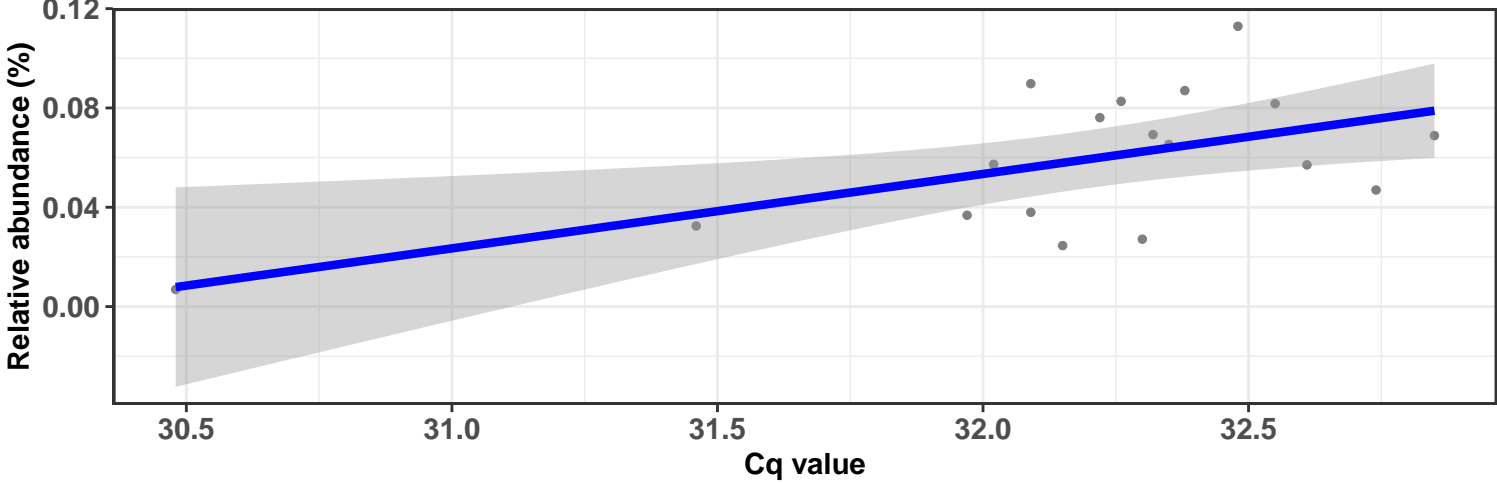
Correlation within: REF-DIC

$\log_e(S) = 6.593$ ,  $p = 0.687$ ,  $\hat{\rho}_{\text{Spearman}} = 0.105$ ,  $\text{CI}_{95\%} [-0.456, 0.646]$ ,  $n_{\text{pairs}} = 17$



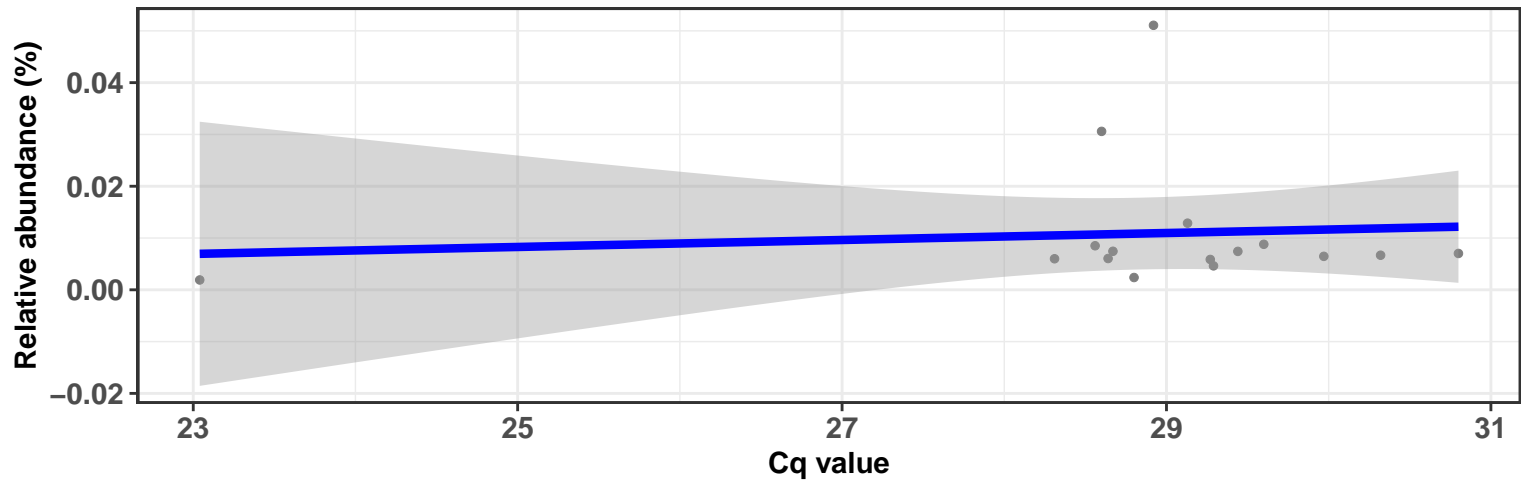
Correlation within: REF-DIM

$\log_e(S) = 6.300$ ,  $p = 0.069$ ,  $\hat{\rho}_{\text{Spearman}} = 0.438$ ,  $\text{CI}_{95\%} [0.056, 0.887]$ ,  $n_{\text{pairs}} = 18$



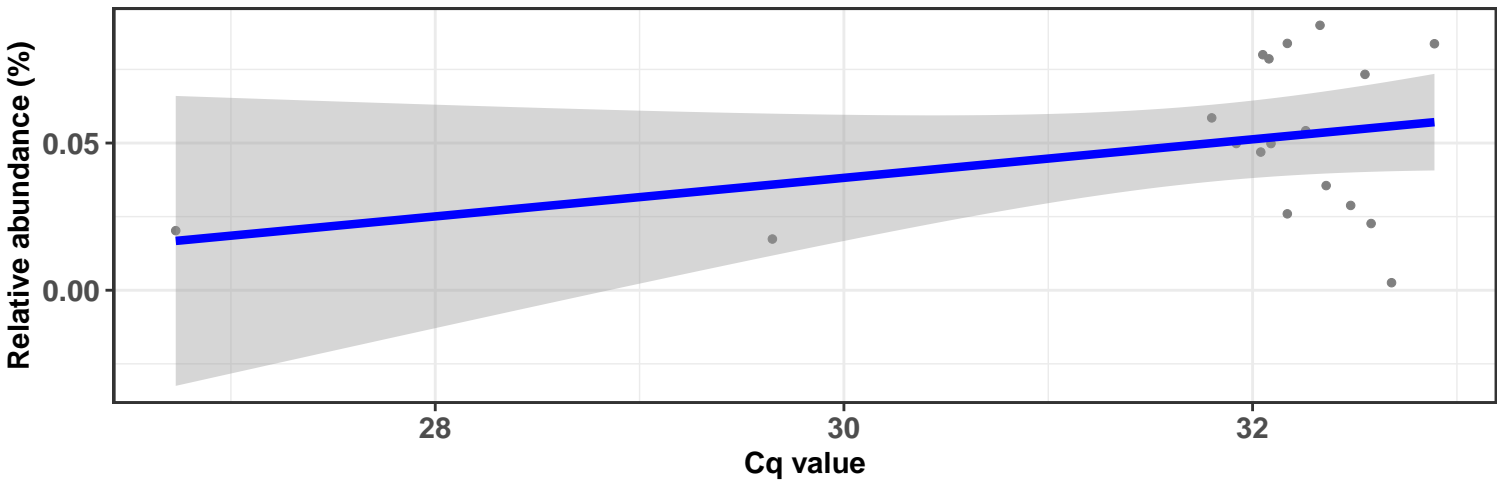
Correlation within: IM-DIC

$\log_e(S) = 6.400$ ,  $p = 0.672$ ,  $\hat{\rho}_{\text{Spearman}} = 0.115$ ,  $\text{CI}_{95\%} [-0.431, 0.680]$ ,  $n_{\text{pairs}} = 16$



Correlation within: IM-DIM

$\log_e(S) = 6.782$ ,  $p = 0.723$ ,  $\hat{\rho}_{\text{Spearman}} = 0.090$ ,  $\text{CI}_{95\%} [-0.392, 0.628]$ ,  $n_{\text{pairs}} = 18$

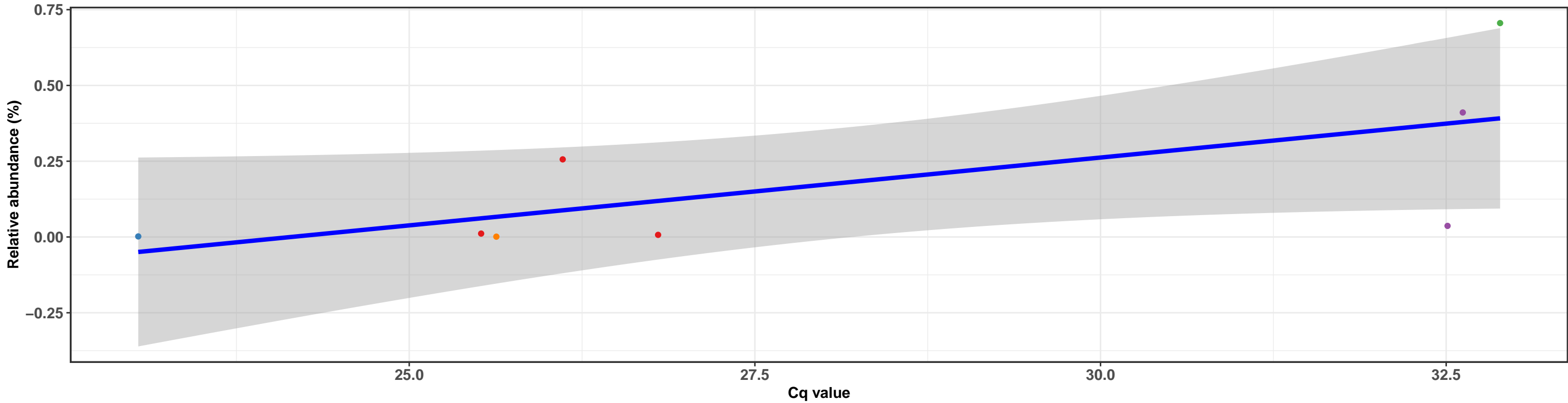




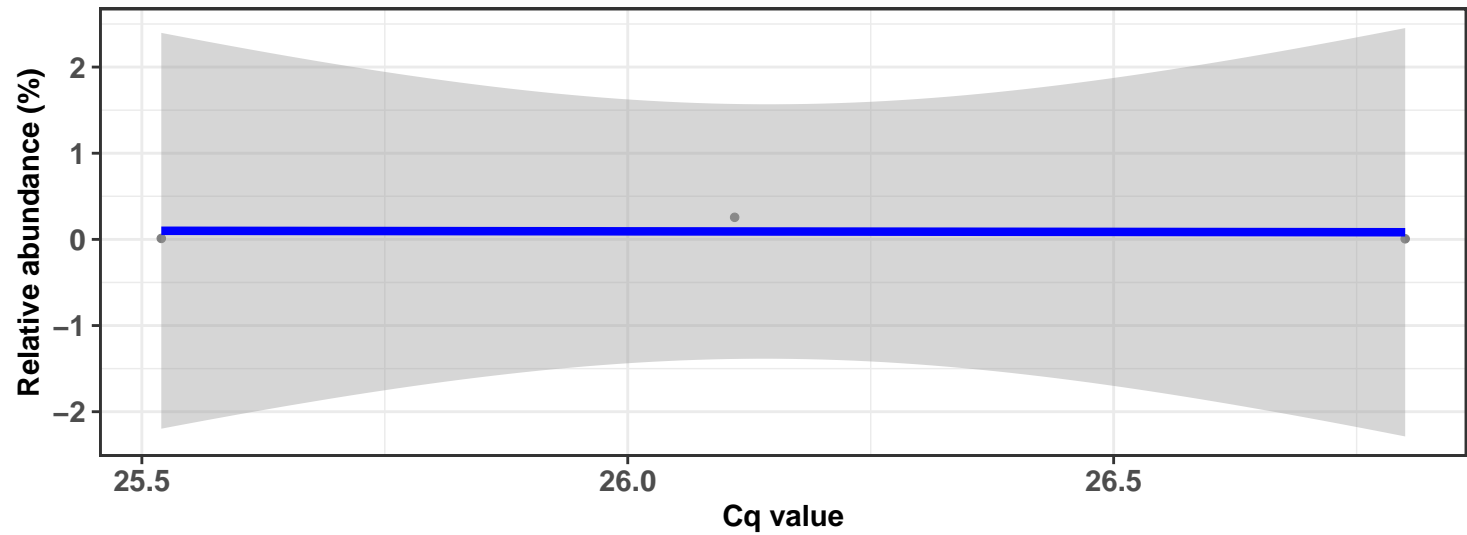
k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Cytophagales; f\_\_Hymenobacteraceae; g\_\_Hymenobacter; s\_\_uncultured bacterium

Correlation with all samples

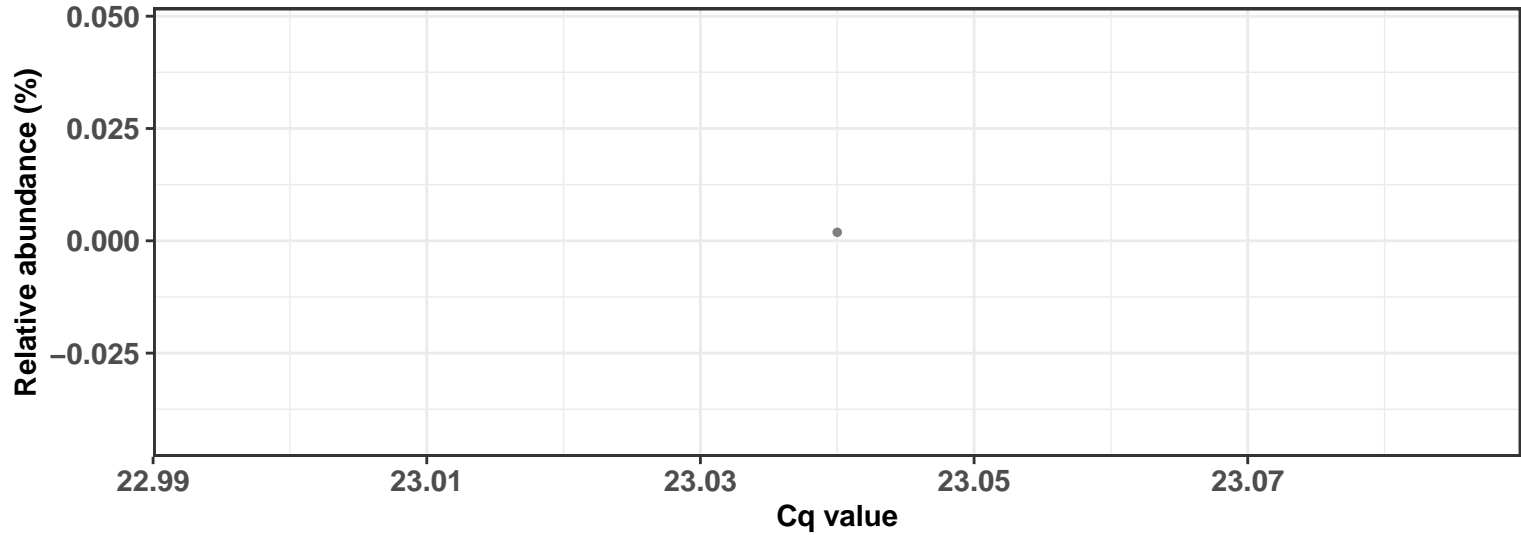
$\log_e(S) = 2.890$ ,  $p = 0.021$ ,  $\hat{\rho}_{\text{Spearman}} = 0.786$ ,  $\text{CI}_{95\%} [0.446, 1.244]$ ,  $n_{\text{pairs}} = 8$



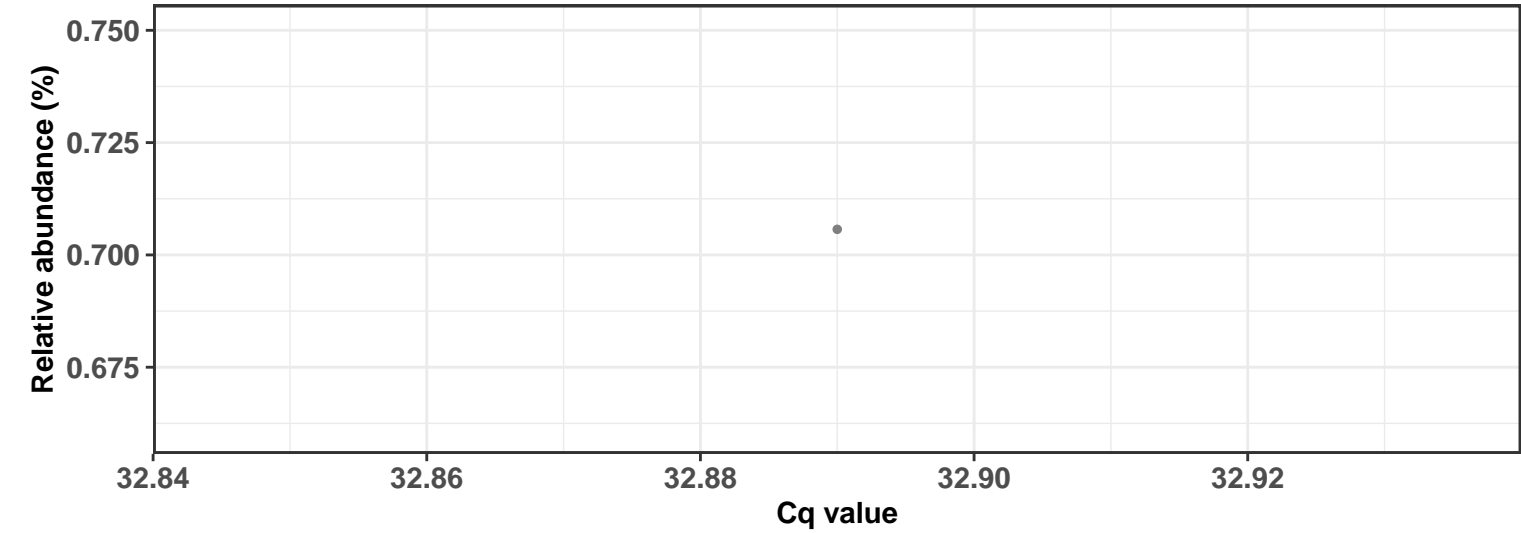
Correlation within: REF-DIC



Correlation within: IM-DIC



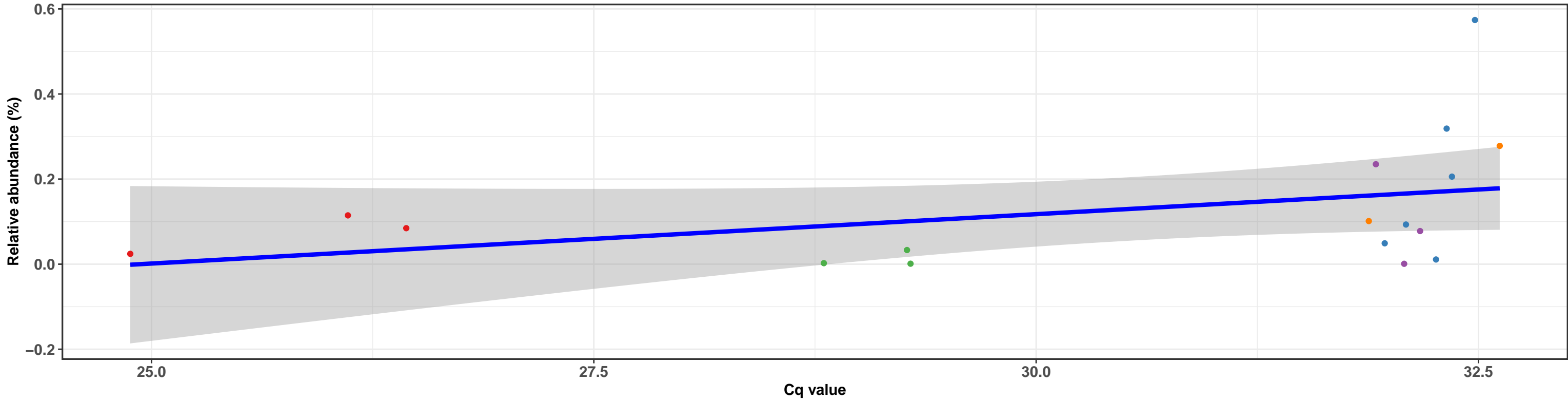
Correlation within: IM-DIM



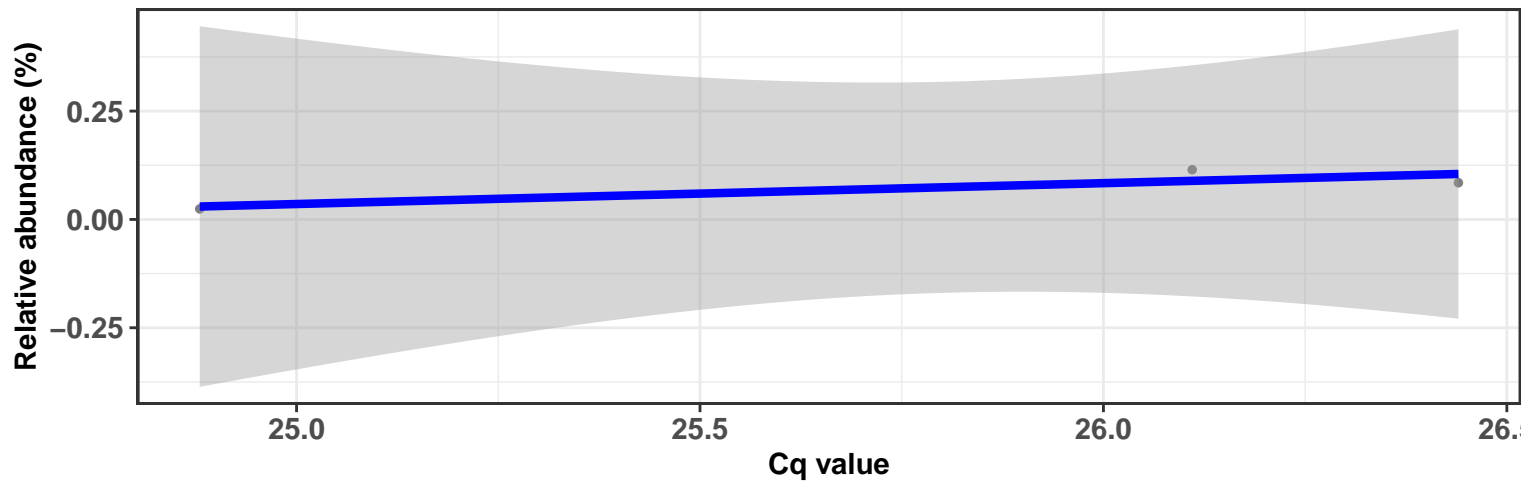
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Caulobacterales; f\_\_Caulobacteraceae; g\_\_Brevundimonas; Ambiguous\_taxa

Correlation with all samples

$\log_e(S) = 6.035$ ,  $p = 0.047$ ,  $\hat{\rho}_{\text{Spearman}} = 0.488$ ,  $\text{CI}_{95\%} [0.091, 0.945]$ ,  $n_{\text{pairs}} = 17$

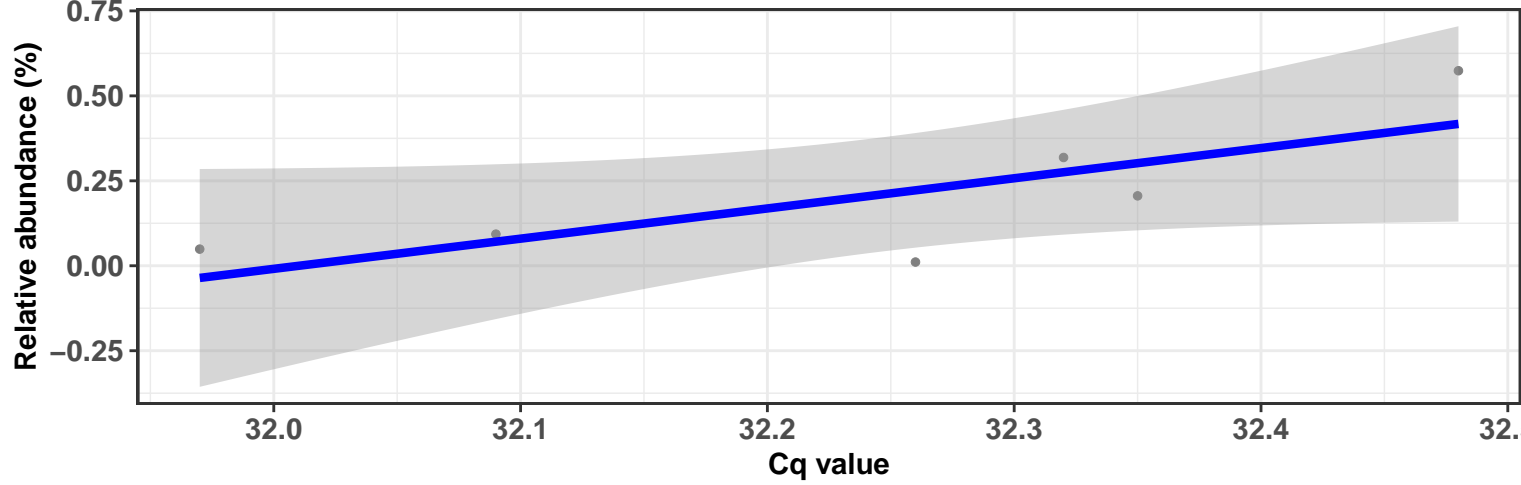


Correlation within: REF-DIC

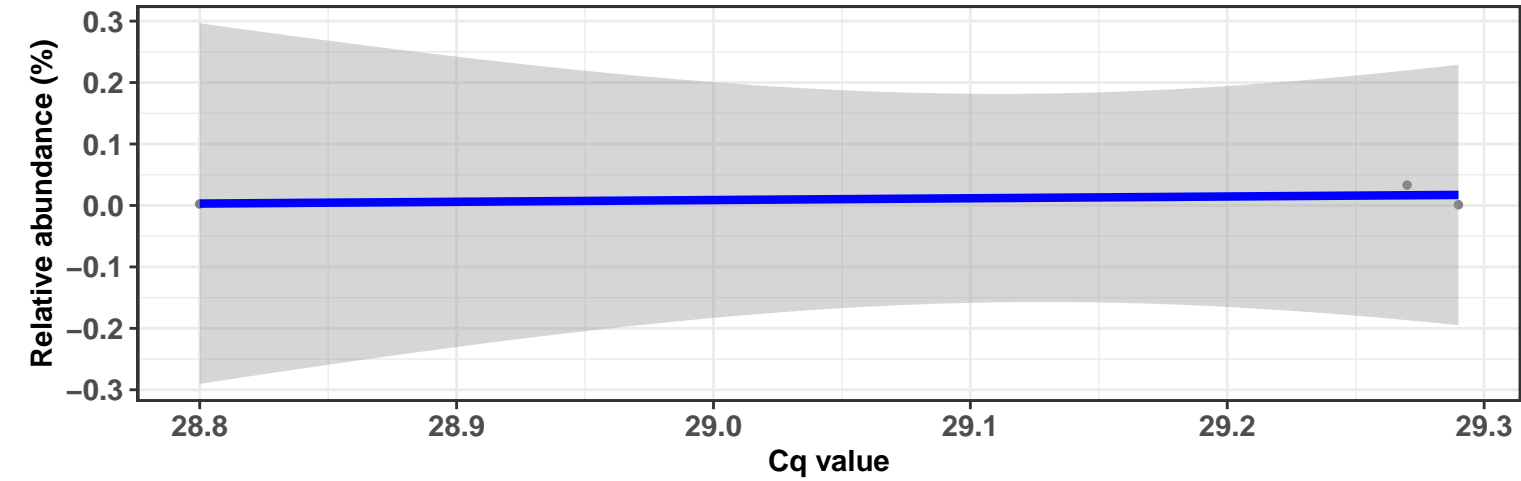


Correlation within: REF-DIM

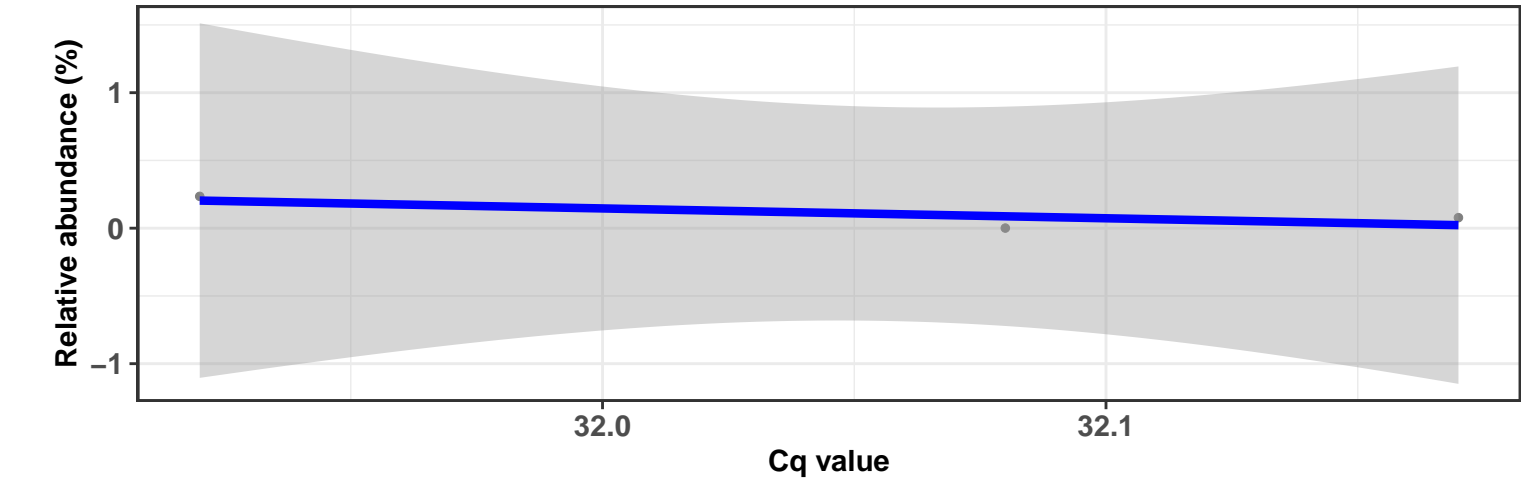
$\log_e(S) = 2.079$ ,  $p = 0.072$ ,  $\hat{\rho}_{\text{Spearman}} = 0.771$ ,  $\text{CI}_{95\%} [0.300, 1.436]$ ,  $n_{\text{pairs}} = 6$



Correlation within: IM-DIC



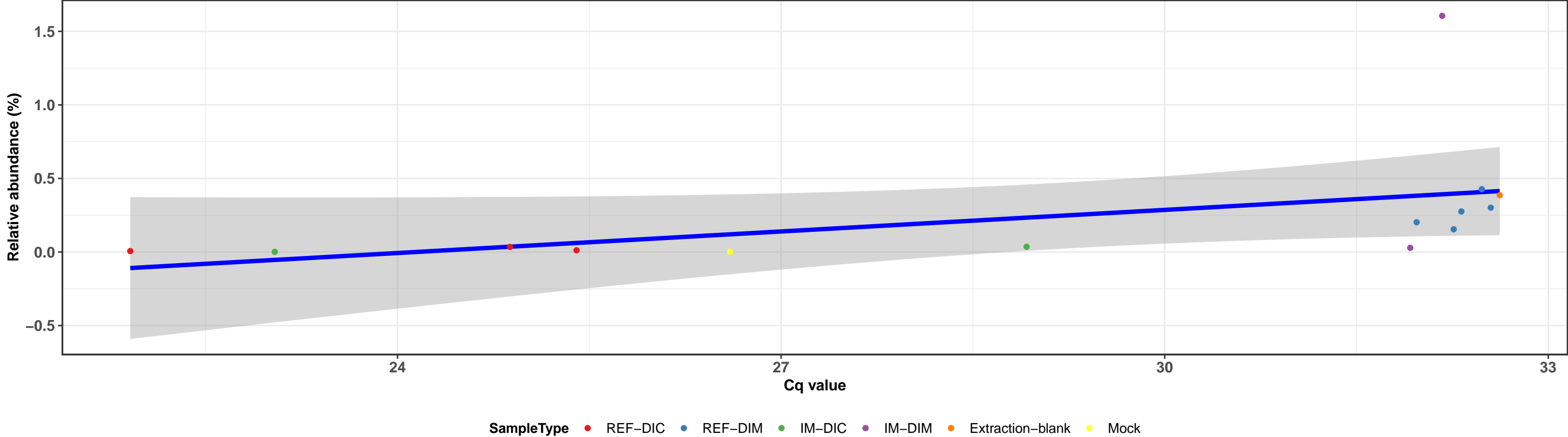
Correlation within: IM-DIM



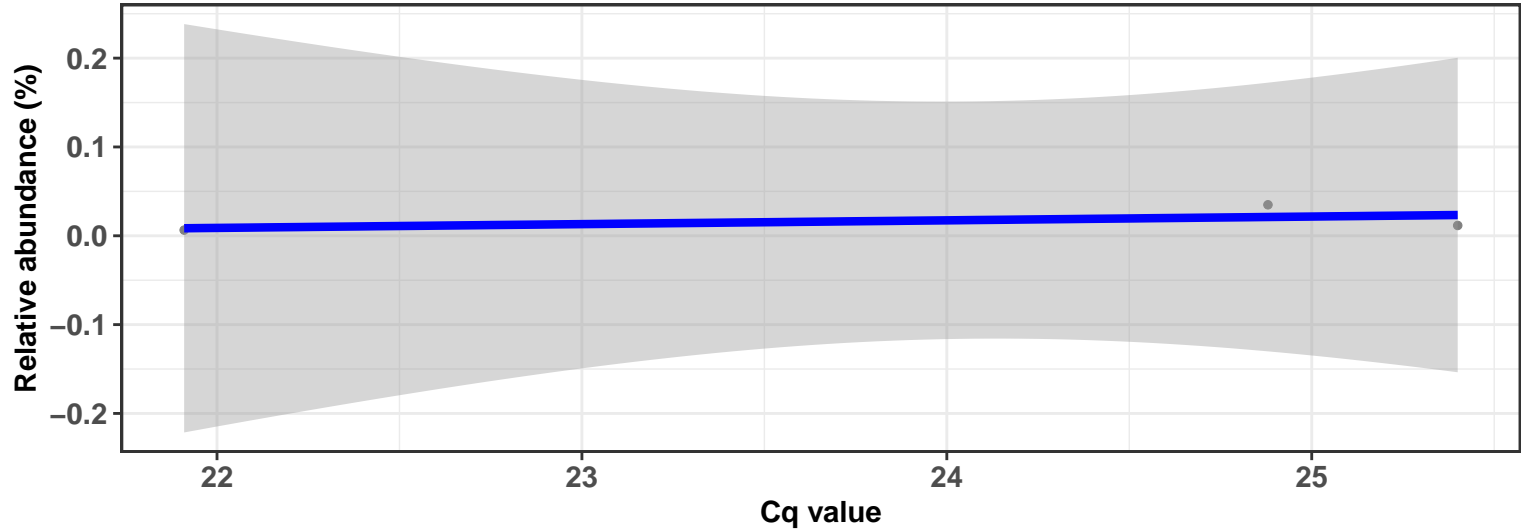
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Caulobacterales; f\_\_Caulobacteraceae; g\_\_Brevundimonas; Ambiguous\_taxa

Correlation with all samples

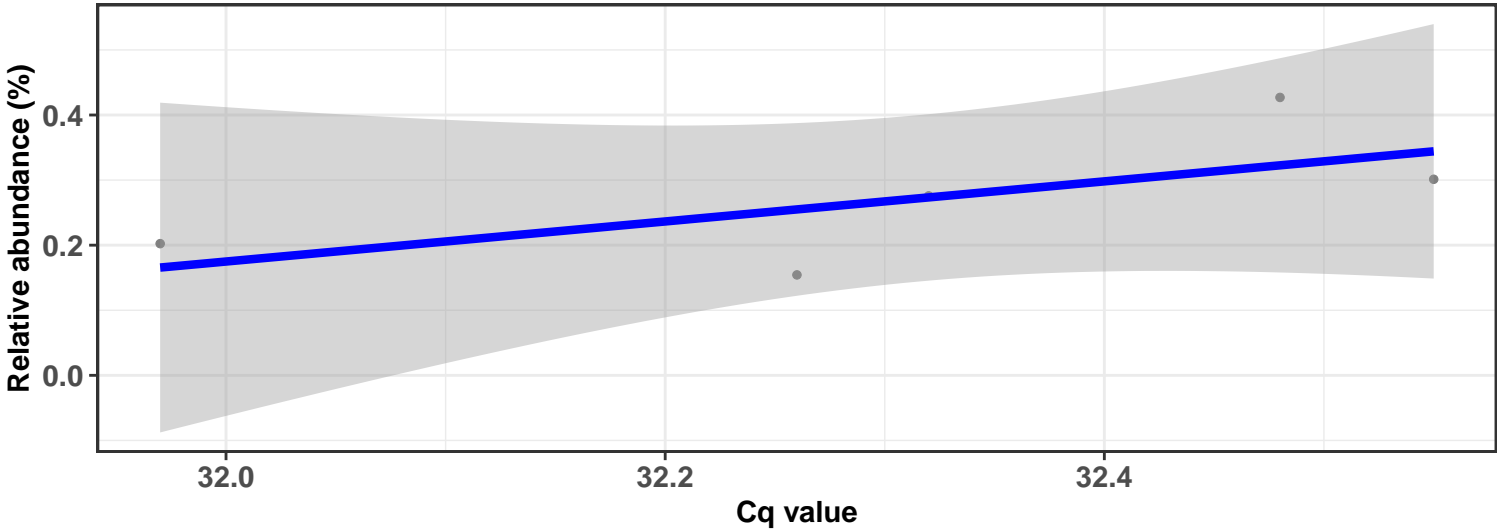
$\log_e(S) = 4.220$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.851$ ,  $CI_{95\%} [0.705, 1.052]$ ,  $n_{\text{pairs}} = 14$



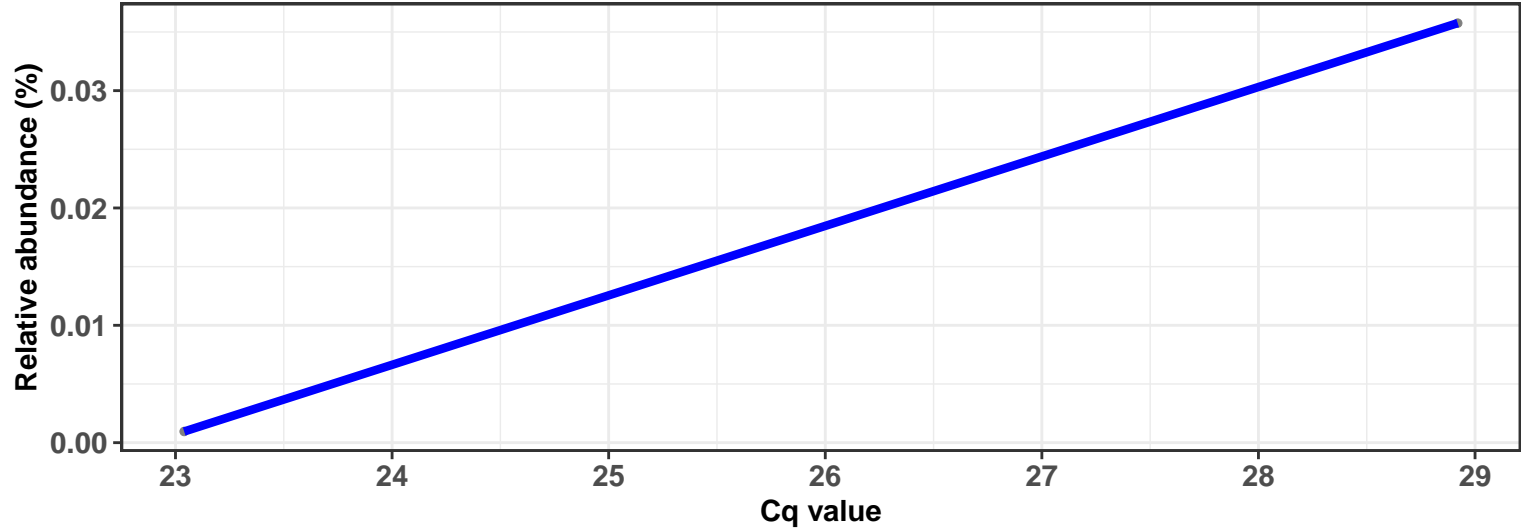
Correlation within: REF-DIC



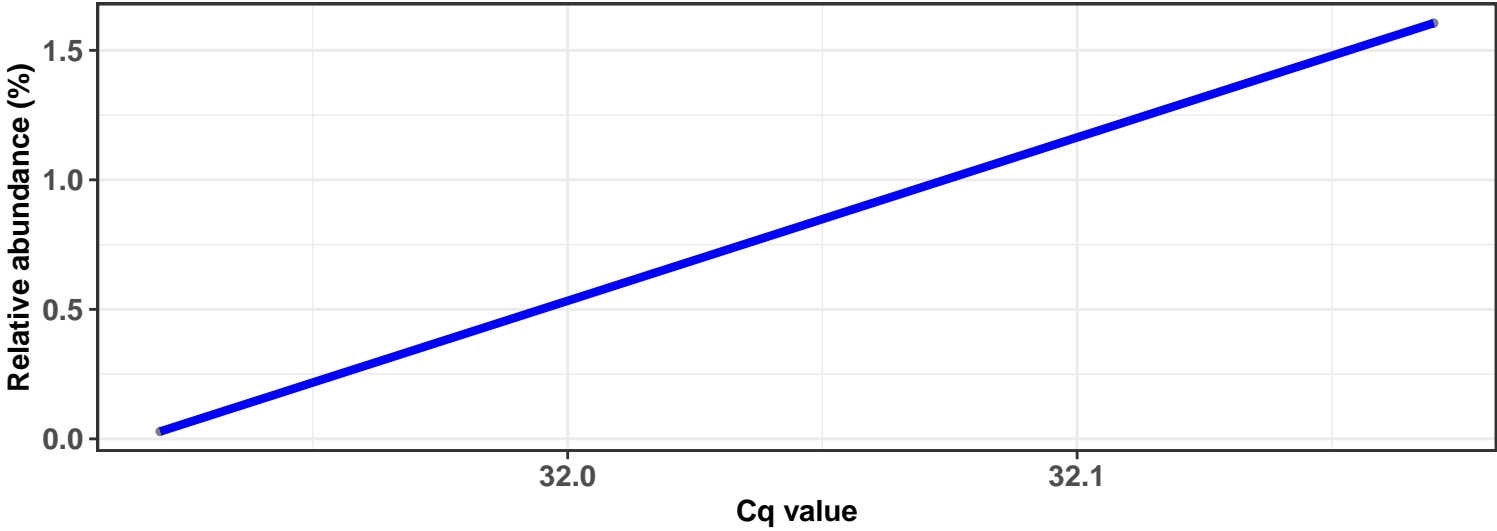
Correlation within: REF-DIM



Correlation within: IM-DIC

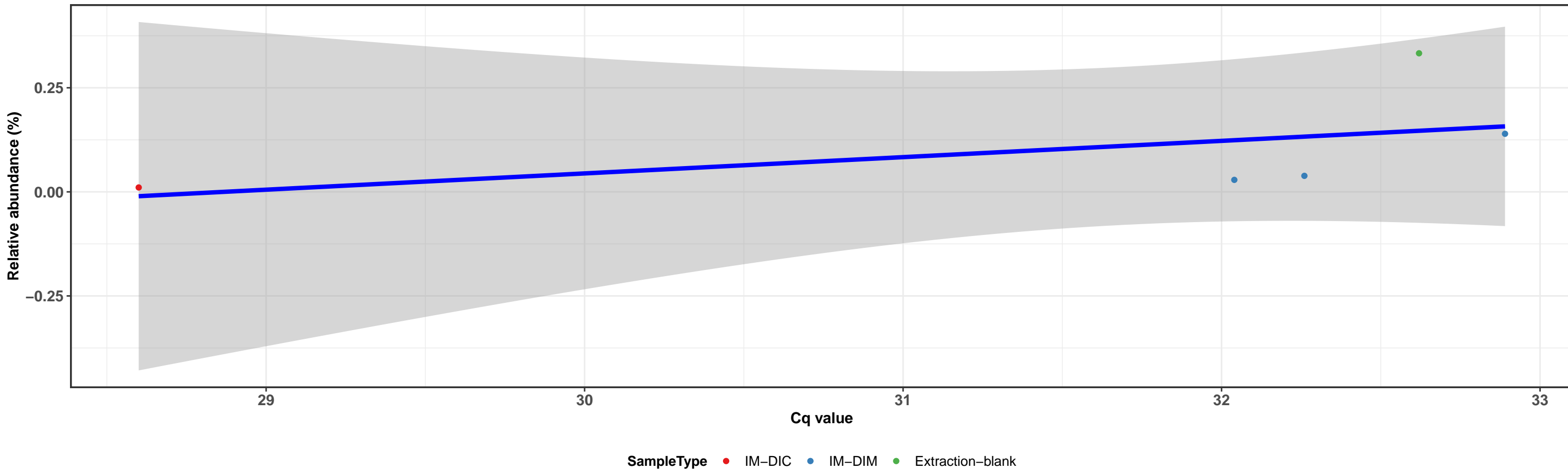


Correlation within: IM-DIM

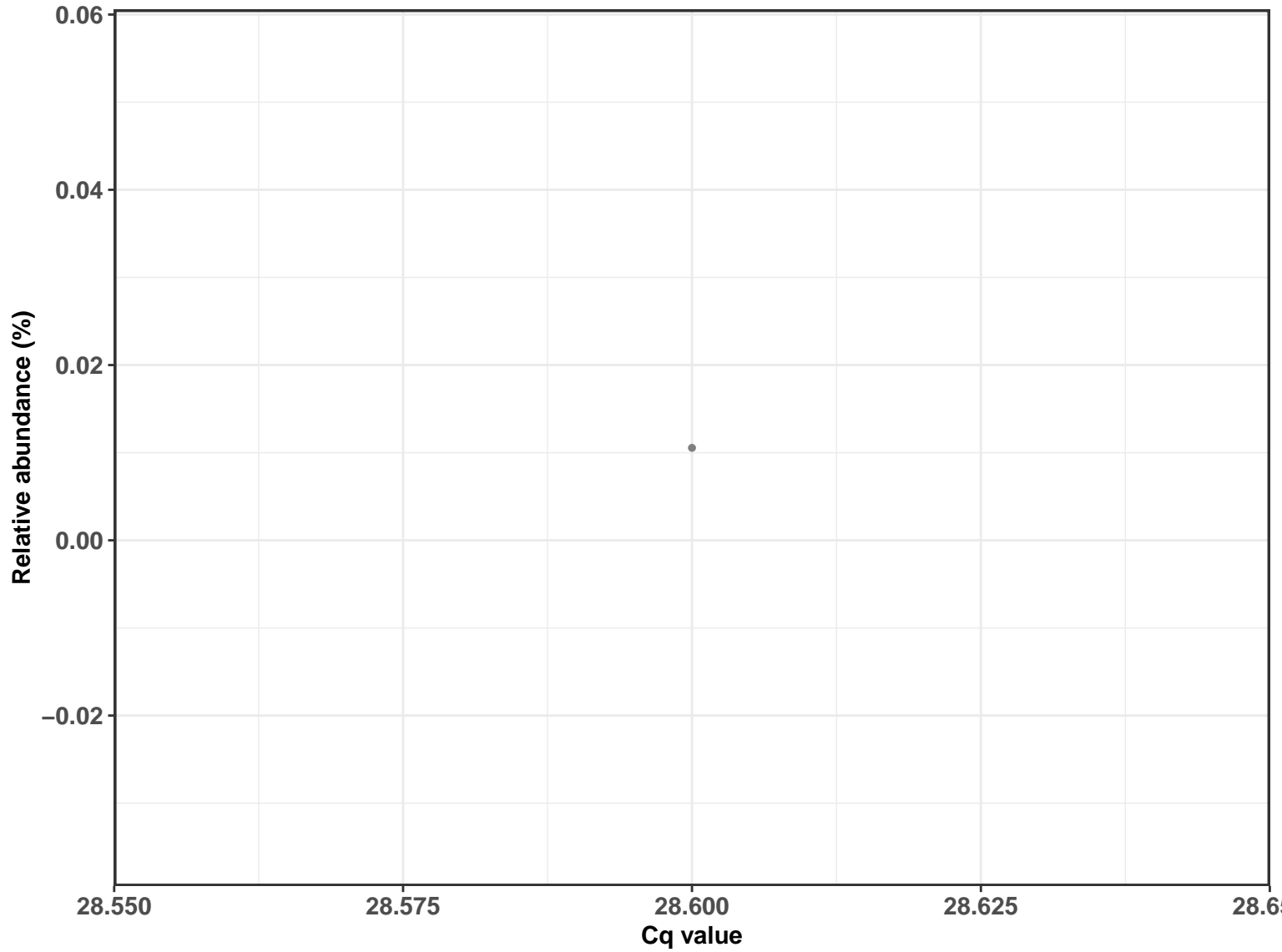


k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Cytophagales; f\_\_Hymenobacteraceae; g\_\_Hymenobacter; s\_\_uncultured bacterium

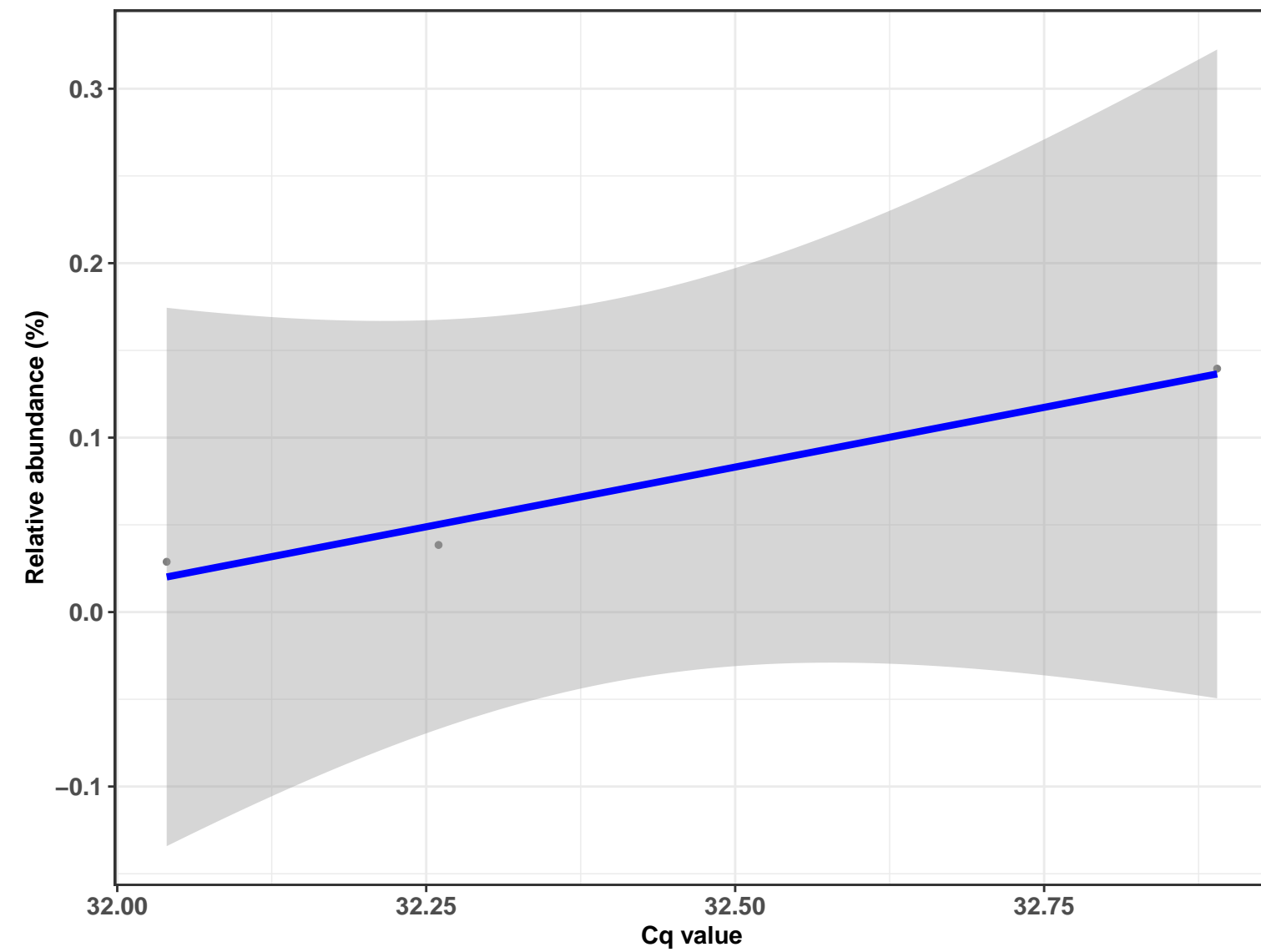
Correlation with all samples



Correlation within: IM-DIC

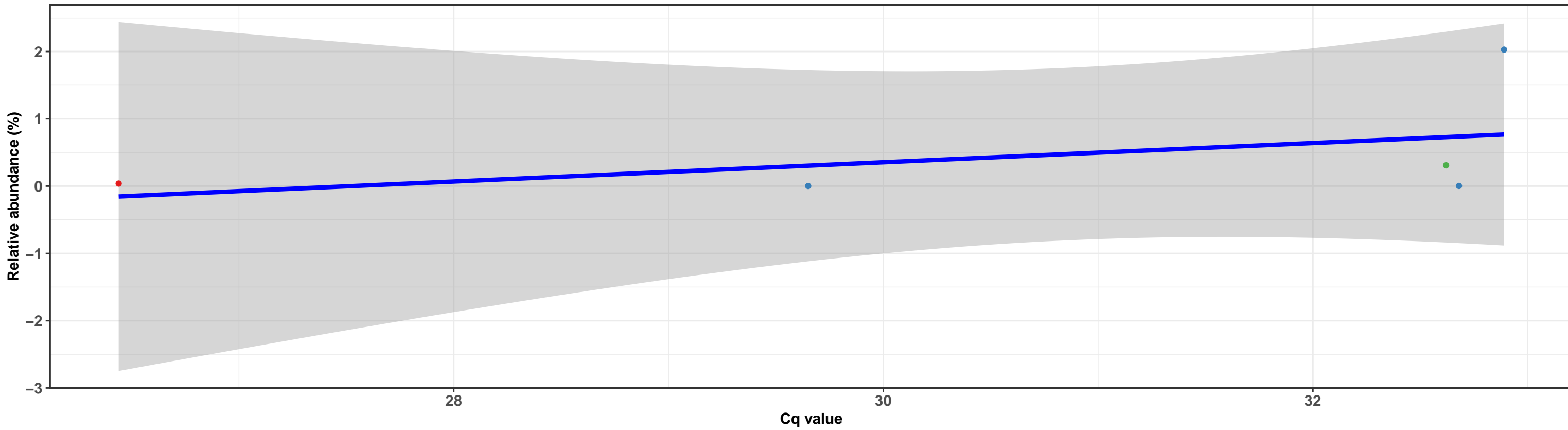


Correlation within: IM-DIM



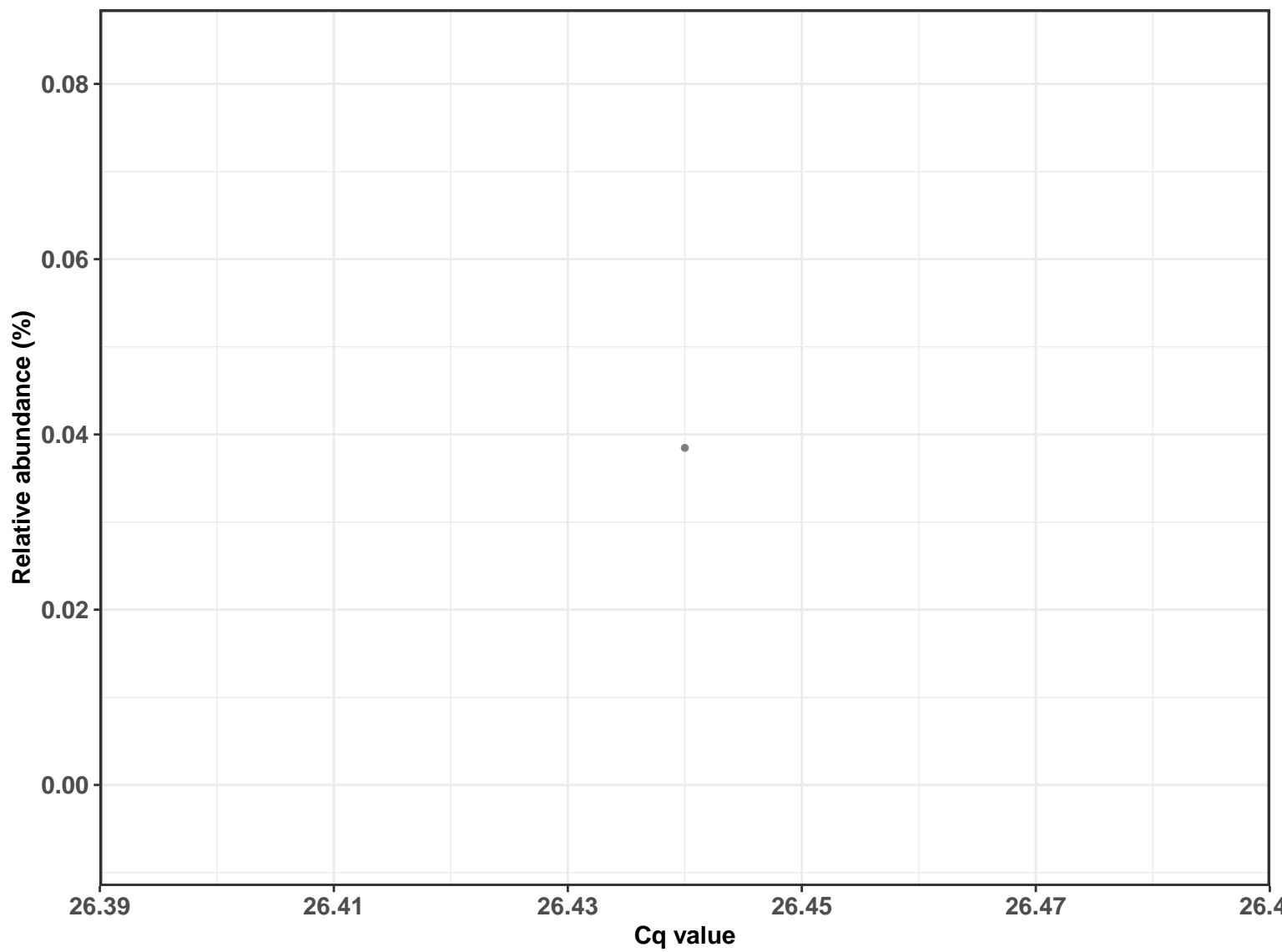
k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Cytophagales; f\_\_Hymenobacteraceae; g\_\_Hymenobacter; s\_\_uncultured bacterium

Correlation with all samples

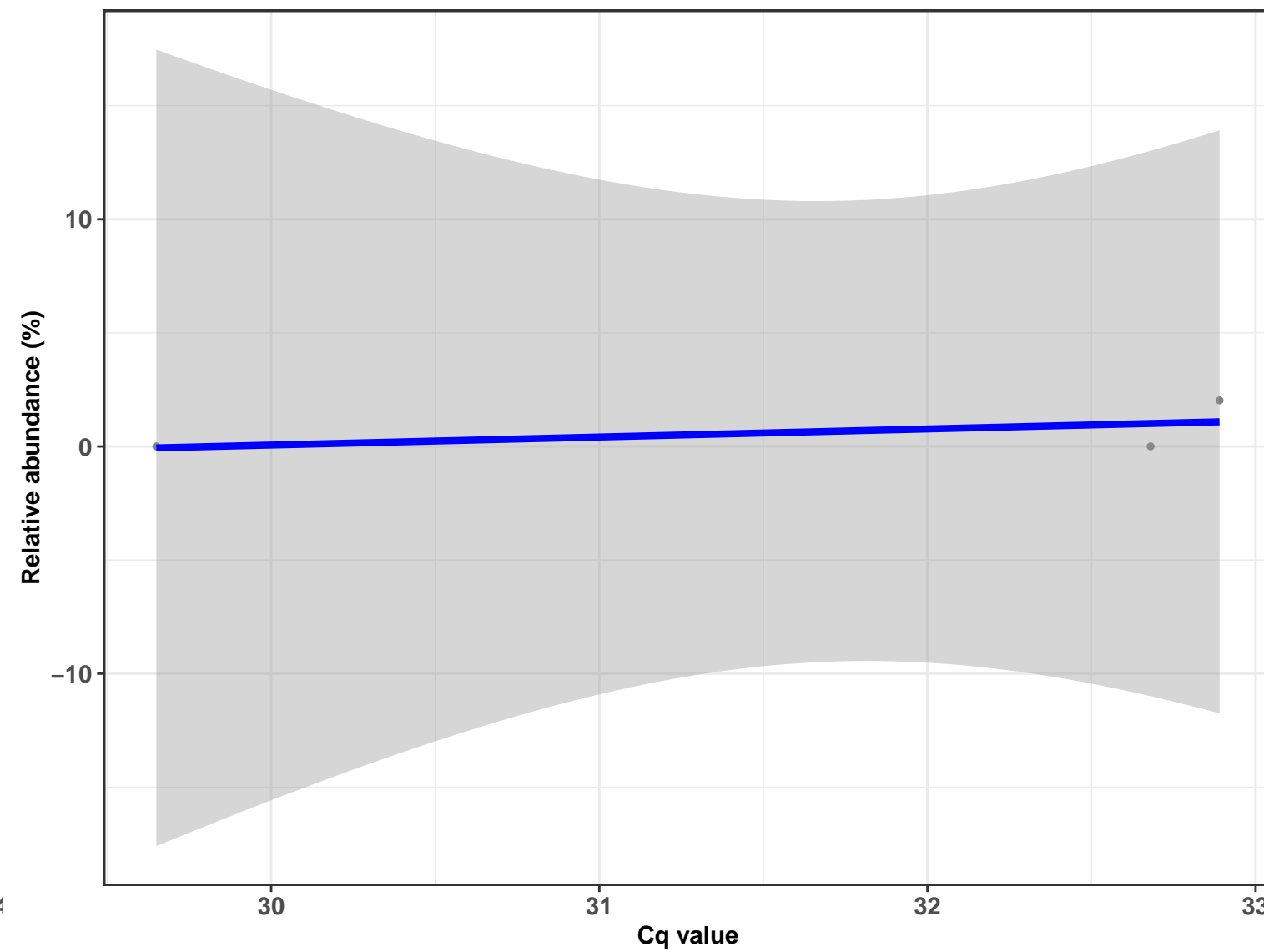


SampleType • REF-DIC • IM-DIM • Extraction-blank

Correlation within: REF-DIC

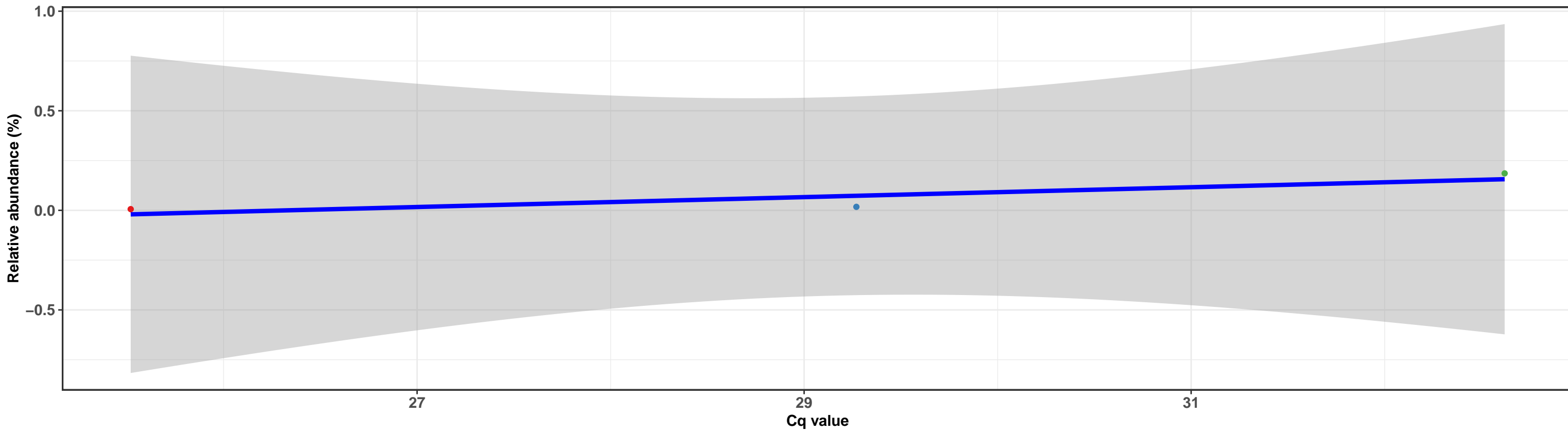


Correlation within: IM-DIM



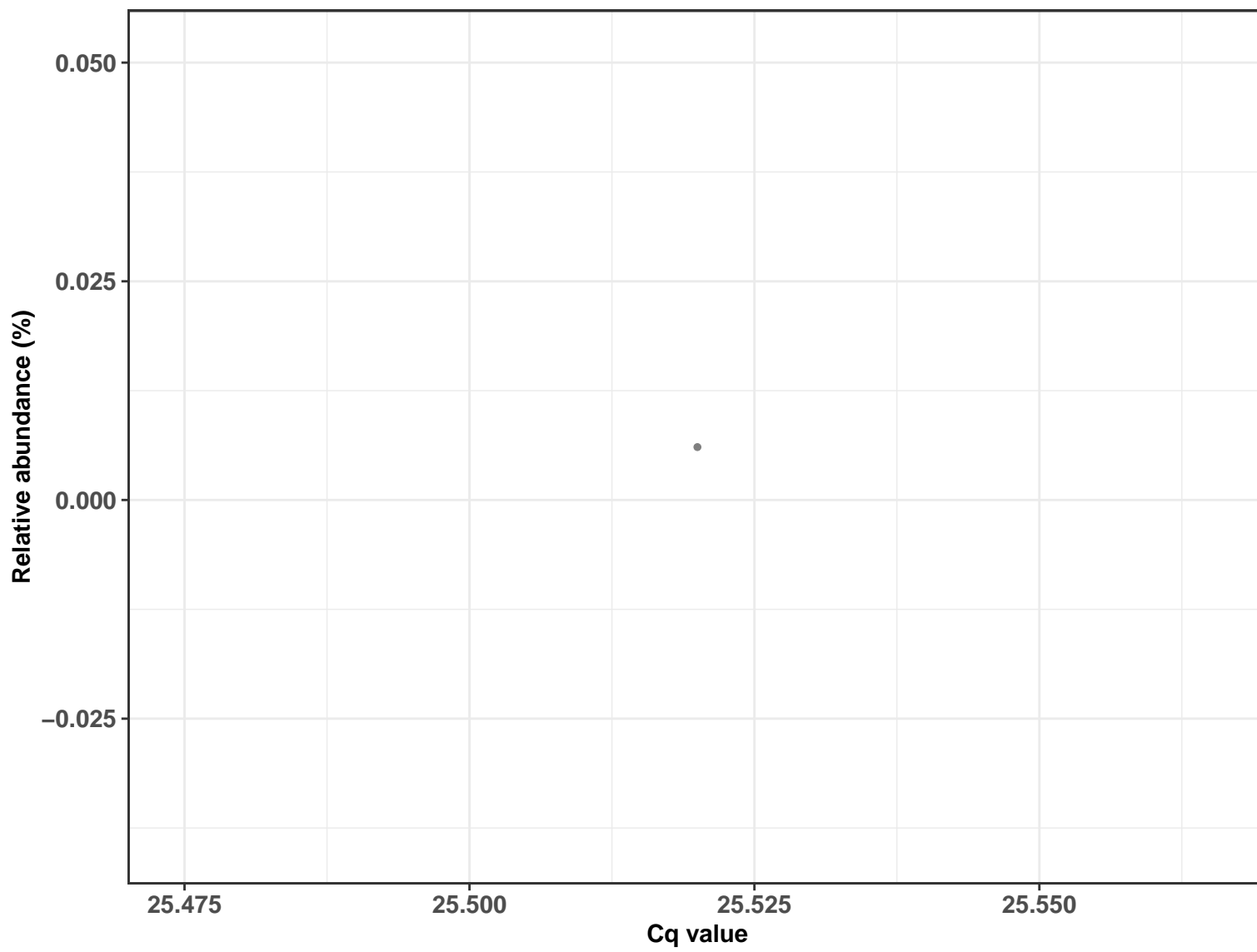
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Micrococcaceae; g\_\_Micrococcus; Ambiguous\_taxa

Correlation with all samples

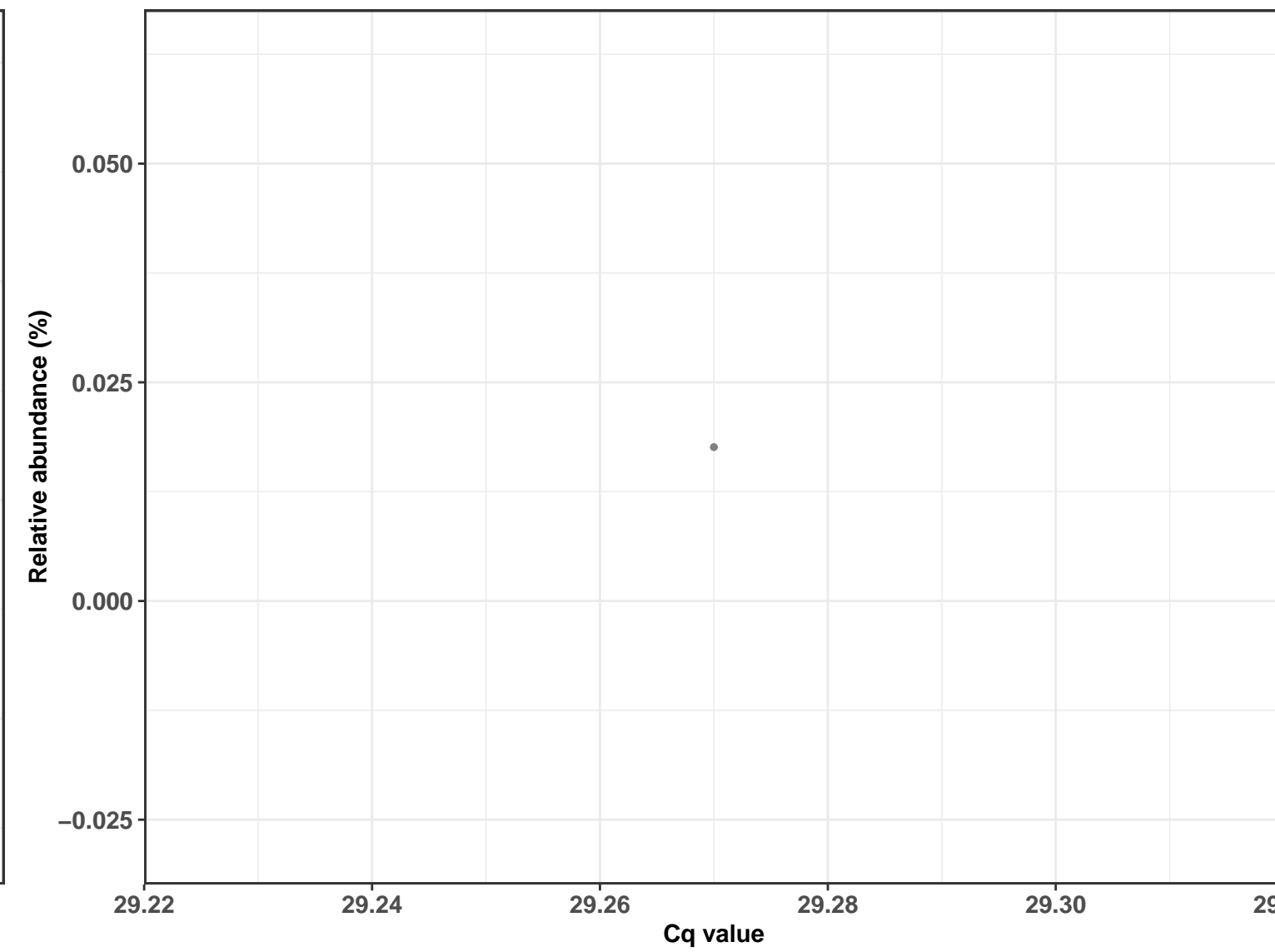


SampleType • REF-DIC • IM-DIC • Extraction-blank

Correlation within: REF-DIC

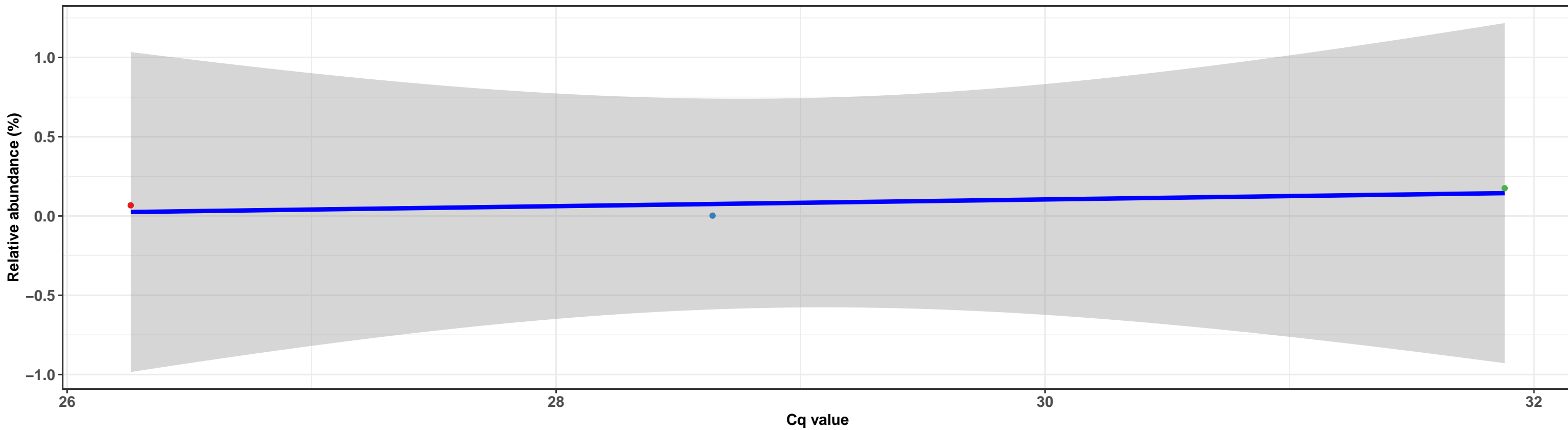


Correlation within: IM-DIC



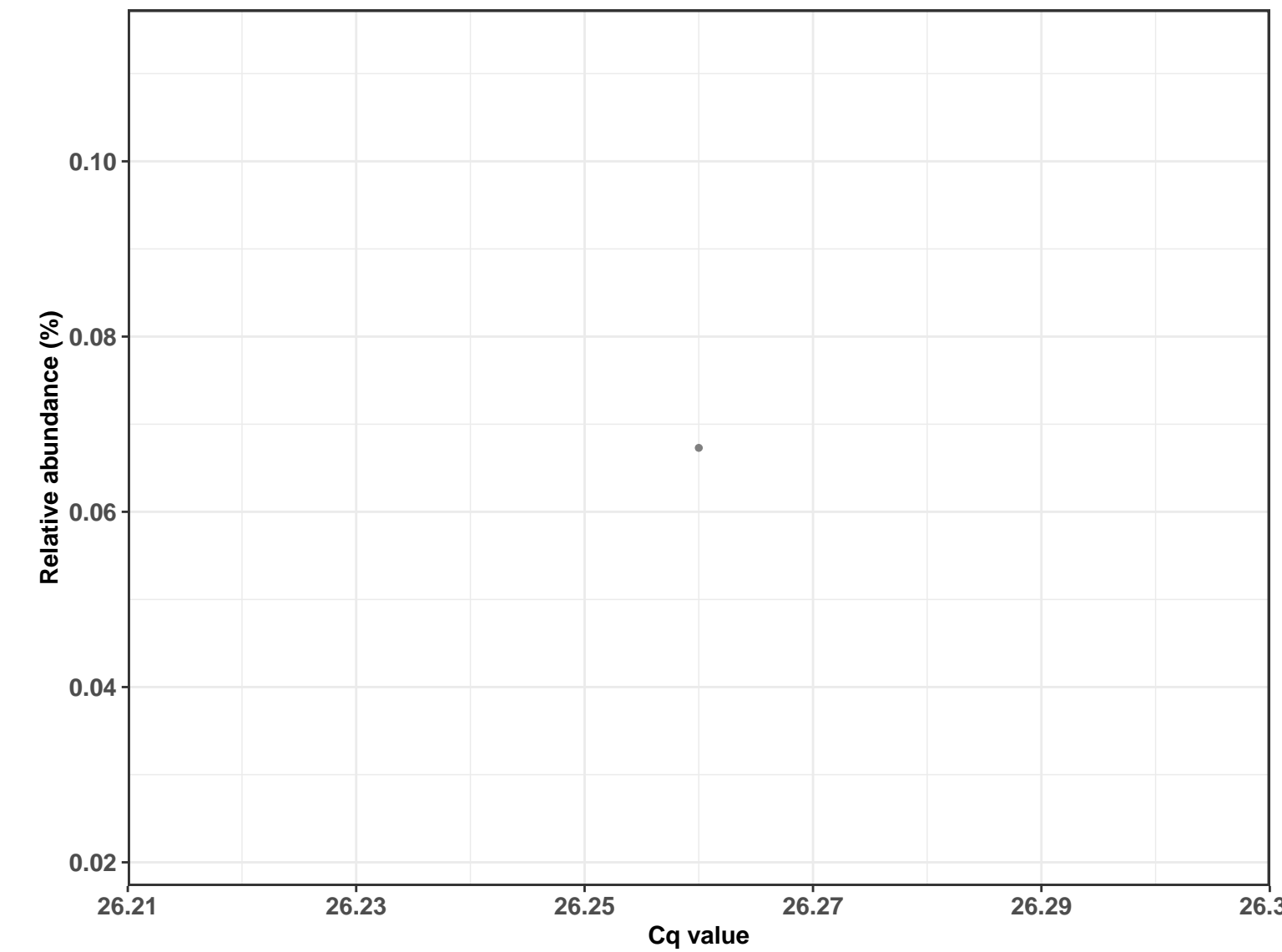
k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Cytophagales; f\_\_Hymenobacteraceae; g\_\_Hymenobacter; s\_\_uncultured bacterium

Correlation with all samples

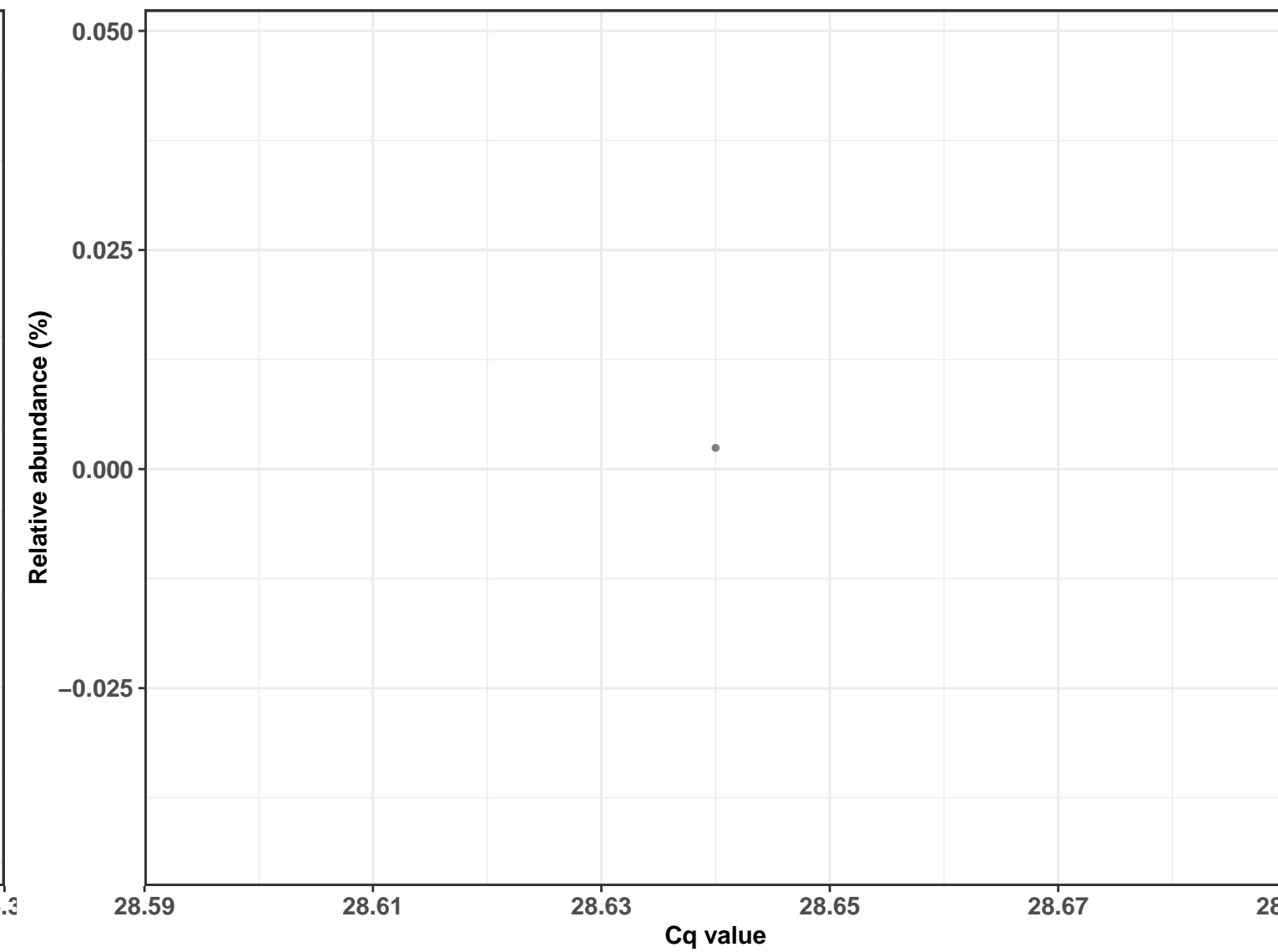


SampleType • REF-DIC • IM-DIC • Extraction-blank

Correlation within: REF-DIC

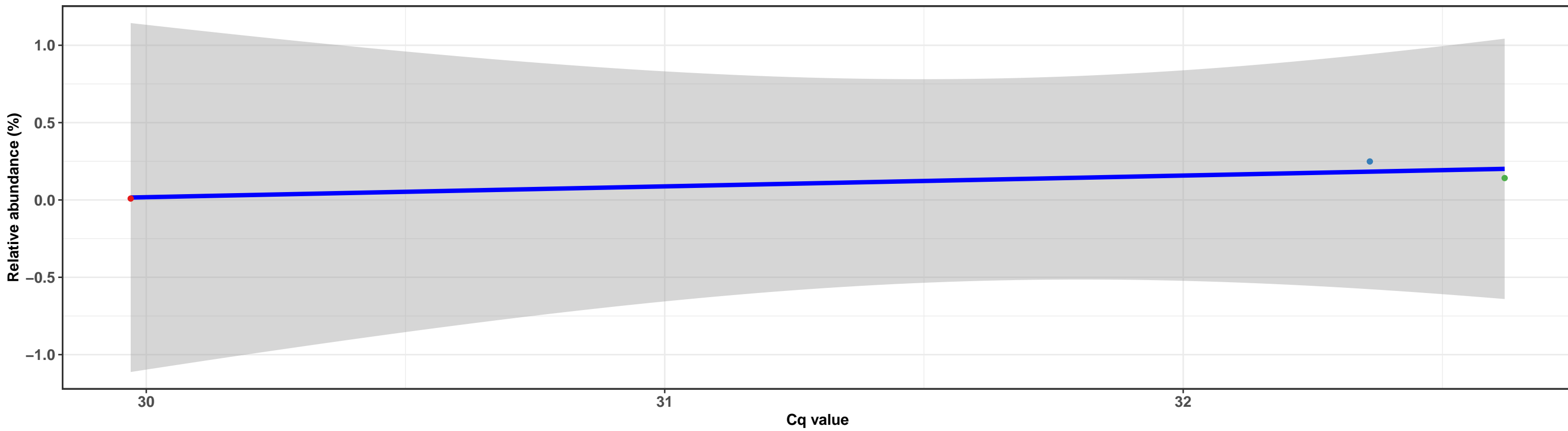


Correlation within: IM-DIC



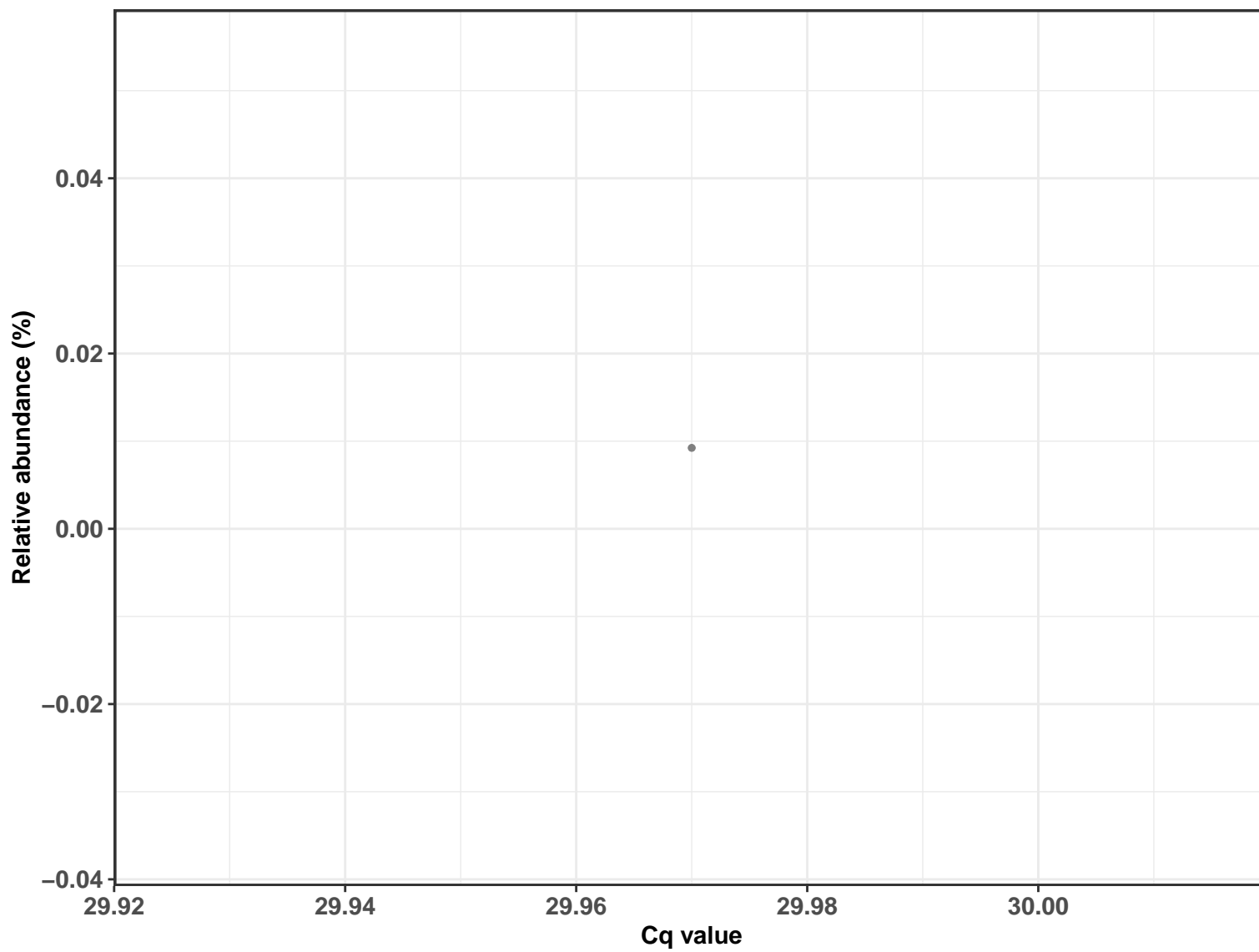
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingomonas; Ambiguous\_taxa

Correlation with all samples

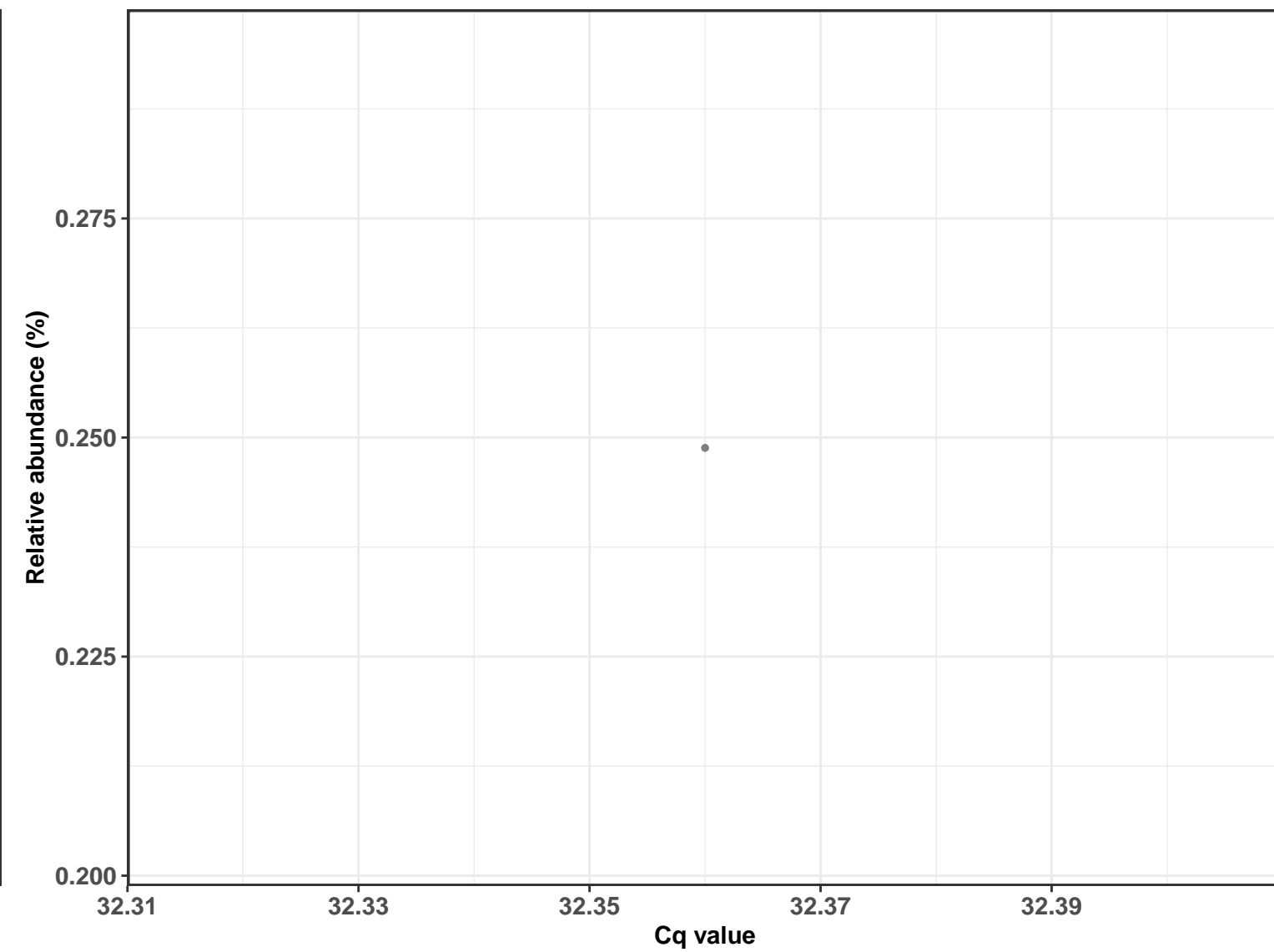


SampleType    • IM-DIC    • IM-DIM    • Extraction-blank

Correlation within: IM-DIC



Correlation within: IM-DIM

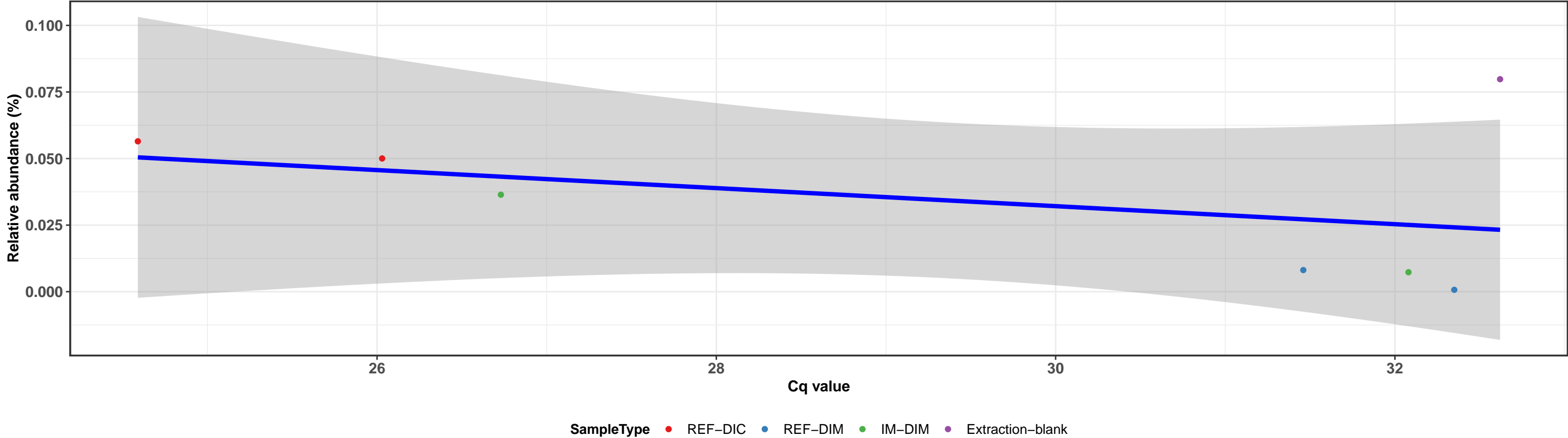




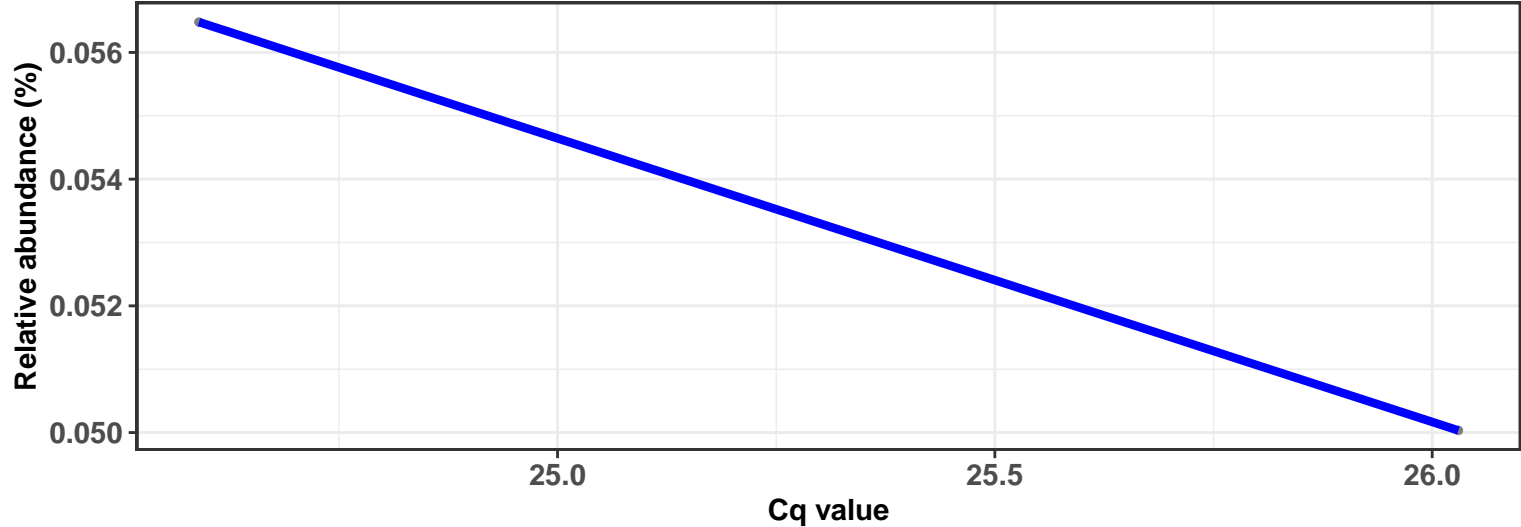
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingomonas; Ambiguous\_taxa

Correlation with all samples

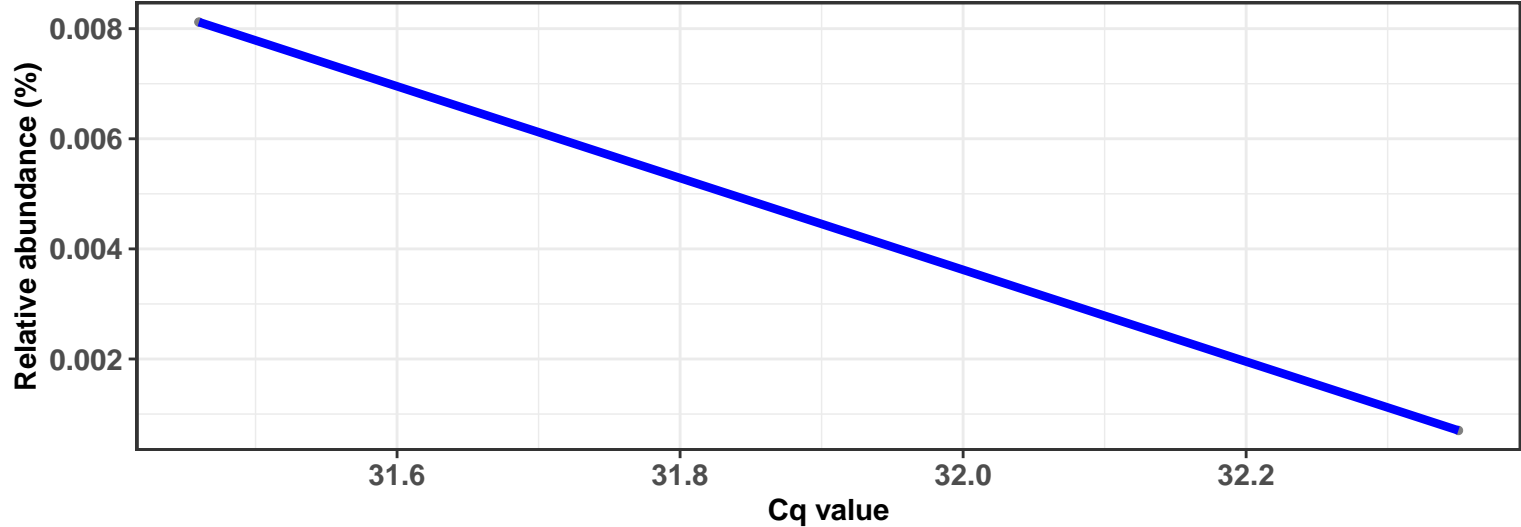
$\log_e(S) = 4.248$ ,  $p = 0.589$ ,  $\hat{\rho}_{\text{Spearman}} = -0.250$ ,  $\text{CI}_{95\%} [-1.205, 0.940]$ ,  $n_{\text{pairs}} = 7$



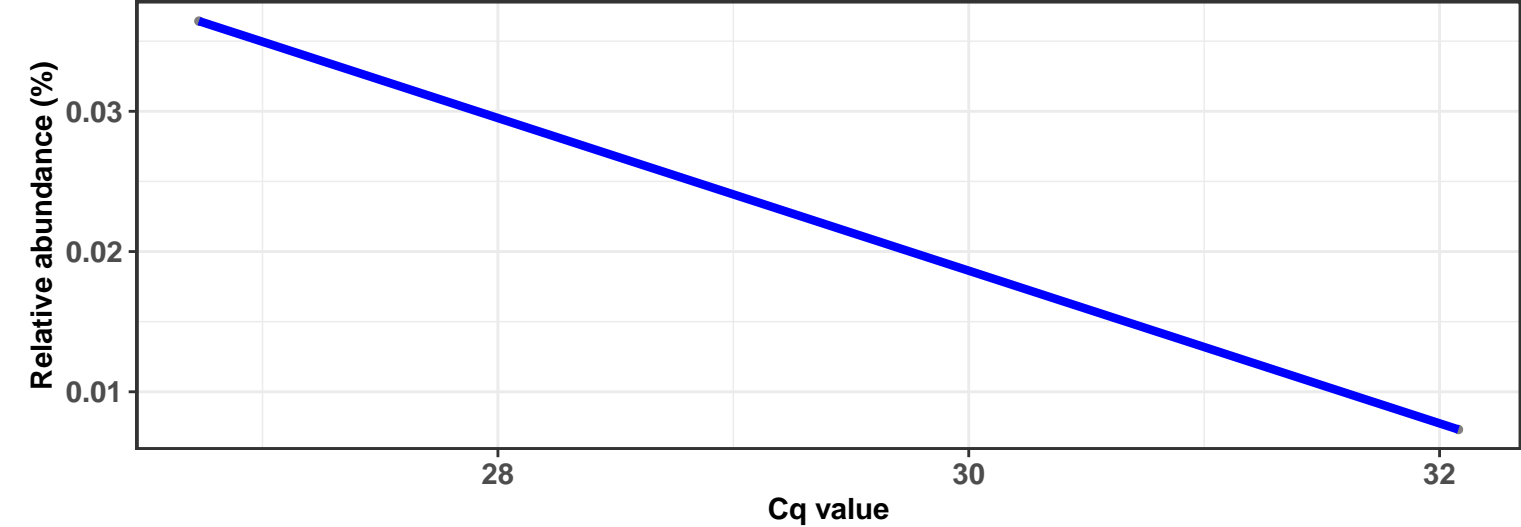
Correlation within: REF-DIC



Correlation within: REF-DIM



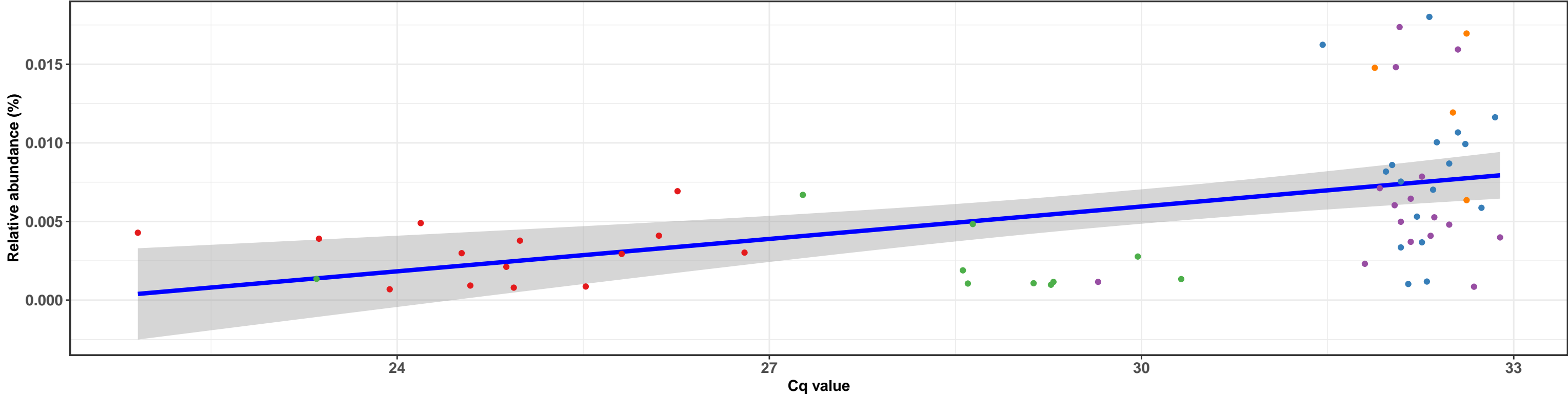
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

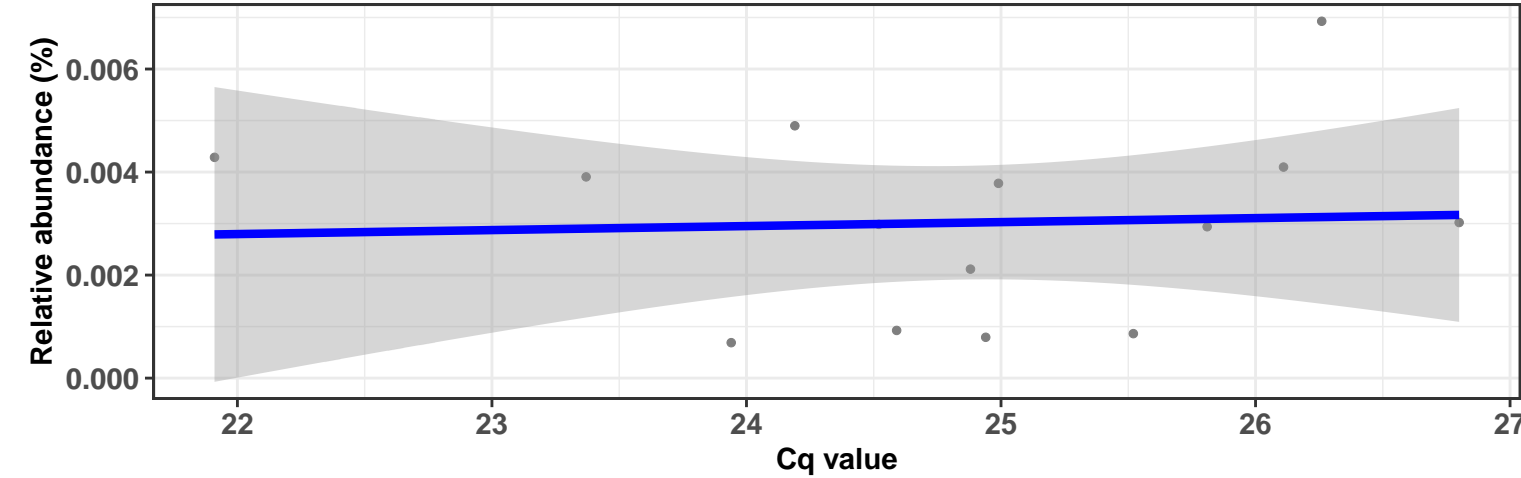
Correlation with all samples

$\log_e(S) = 9.840$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.504$ ,  $\text{CI}_{95\%} [0.319, 0.700]$ ,  $n_{\text{pairs}} = 61$



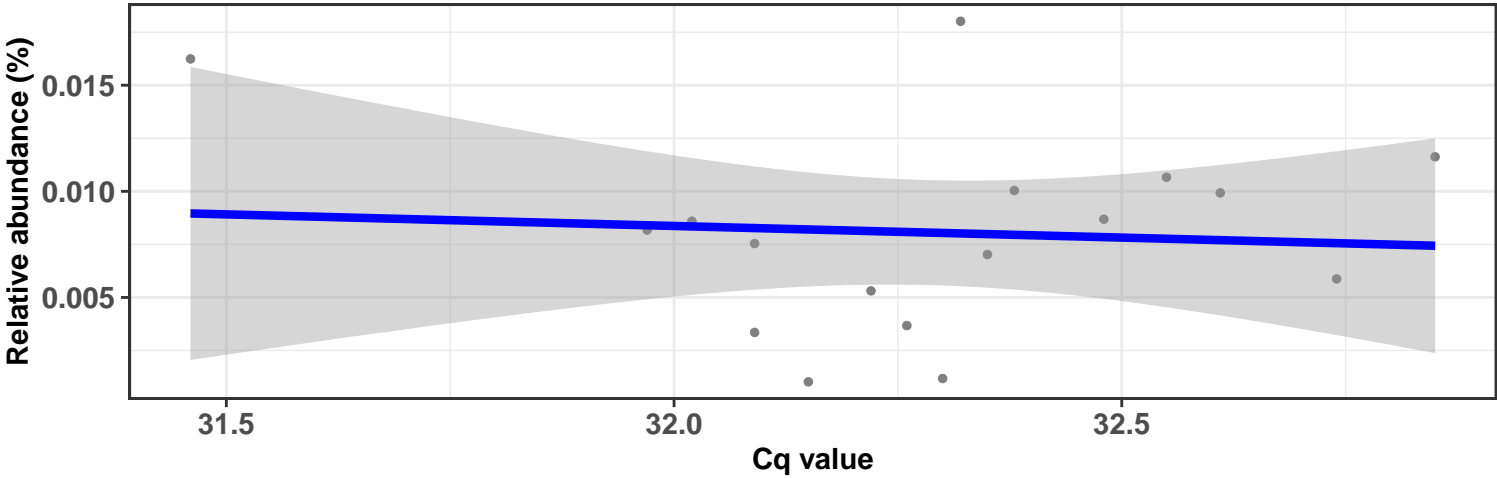
Correlation within: REF-DIC

$\log_e(S) = 6.064$ ,  $p = 0.852$ ,  $\hat{\rho}_{\text{Spearman}} = 0.055$ ,  $\text{CI}_{95\%} [-0.583, 0.652]$ ,  $n_{\text{pairs}} = 14$



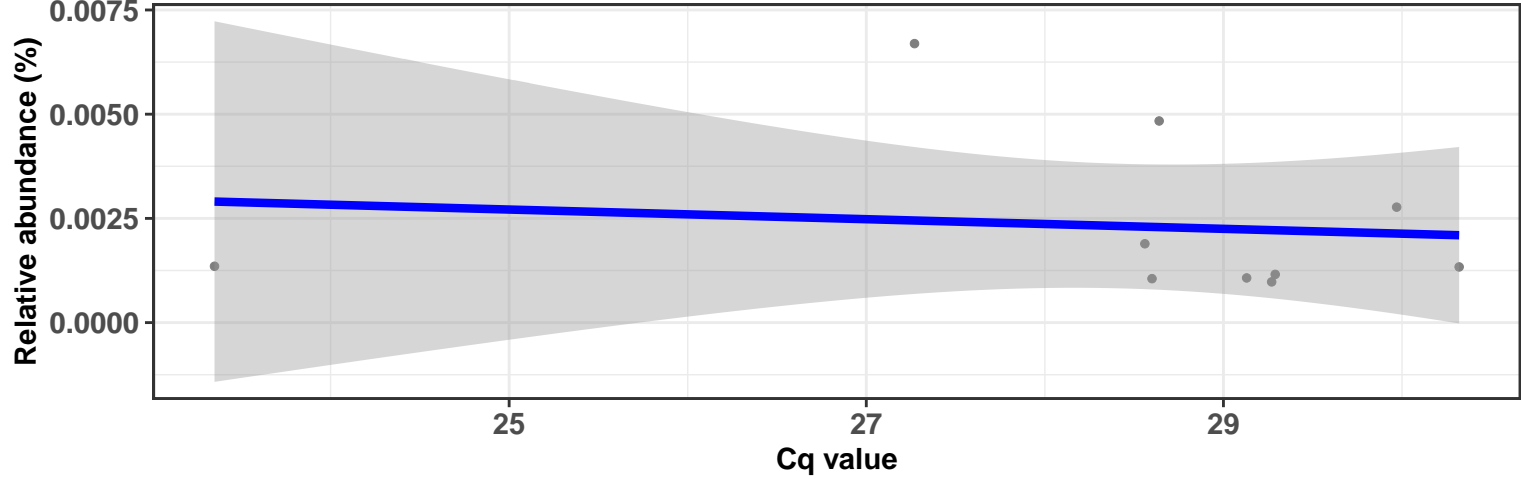
Correlation within: REF-DIM

$\log_e(S) = 6.421$ ,  $p = 0.340$ ,  $\hat{\rho}_{\text{Spearman}} = 0.246$ ,  $\text{CI}_{95\%} [-0.234, 0.738]$ ,  $n_{\text{pairs}} = 17$



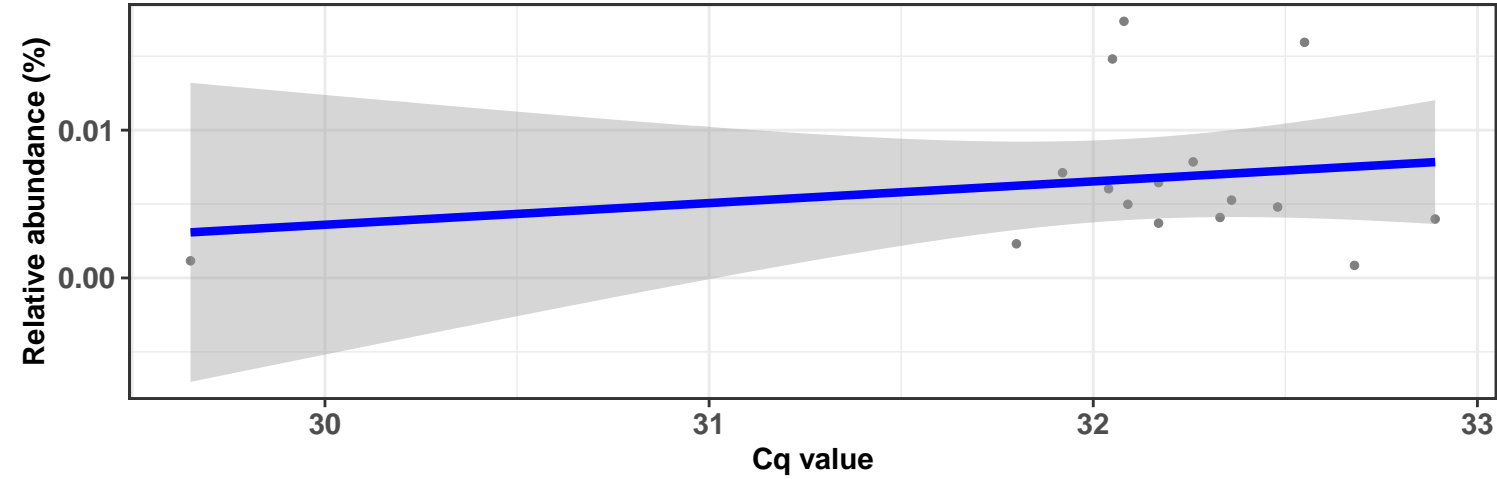
Correlation within: IM-DIC

$\log_e(S) = 5.357$ ,  $p = 0.425$ ,  $\hat{\rho}_{\text{Spearman}} = -0.285$ ,  $\text{CI}_{95\%} [-0.877, 0.351]$ ,  $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

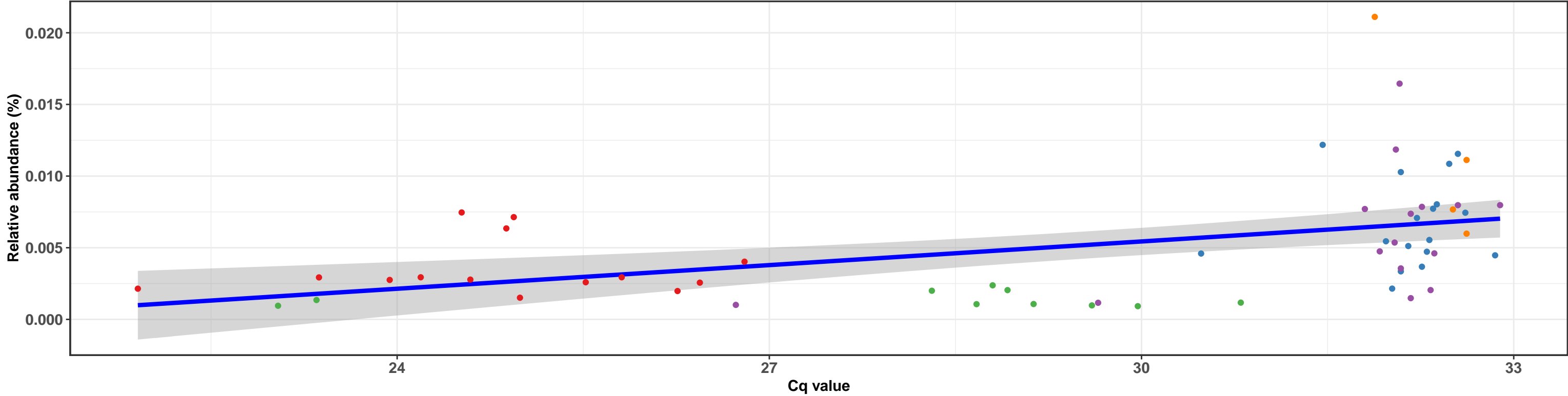
$\log_e(S) = 6.586$ ,  $p = 0.807$ ,  $\hat{\rho}_{\text{Spearman}} = -0.066$ ,  $\text{CI}_{95\%} [-0.607, 0.485]$ ,  $n_{\text{pairs}} = 16$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

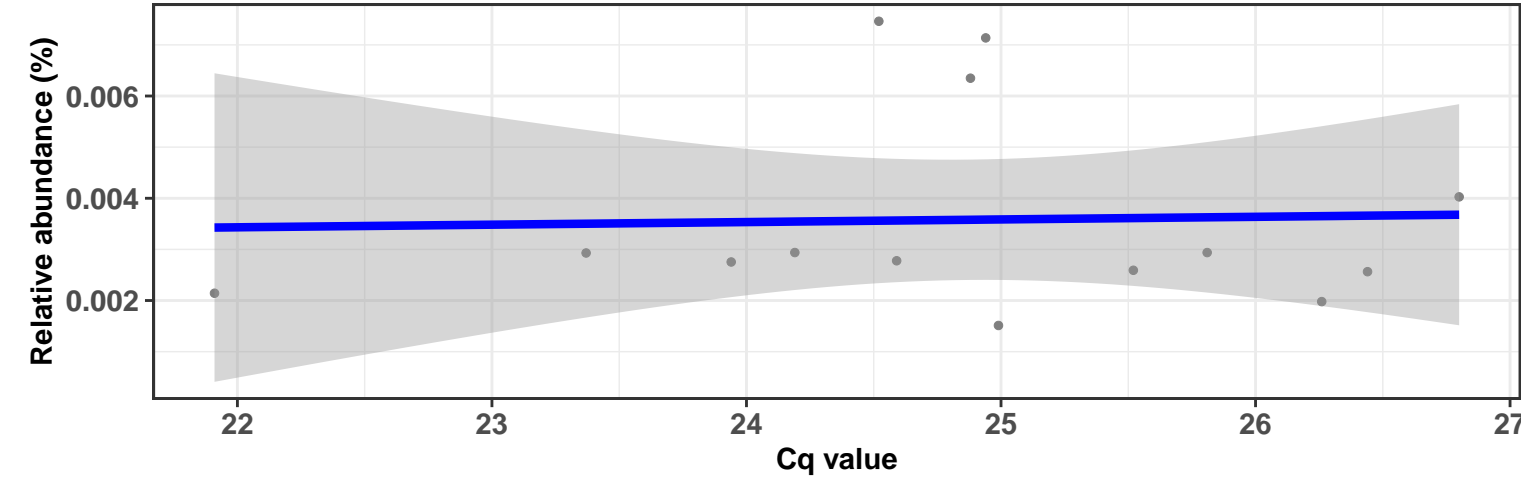
Correlation with all samples

$\log_e(S) = 9.676$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.557$ ,  $\text{CI}_{95\%} [0.410, 0.728]$ ,  $n_{\text{pairs}} = 60$



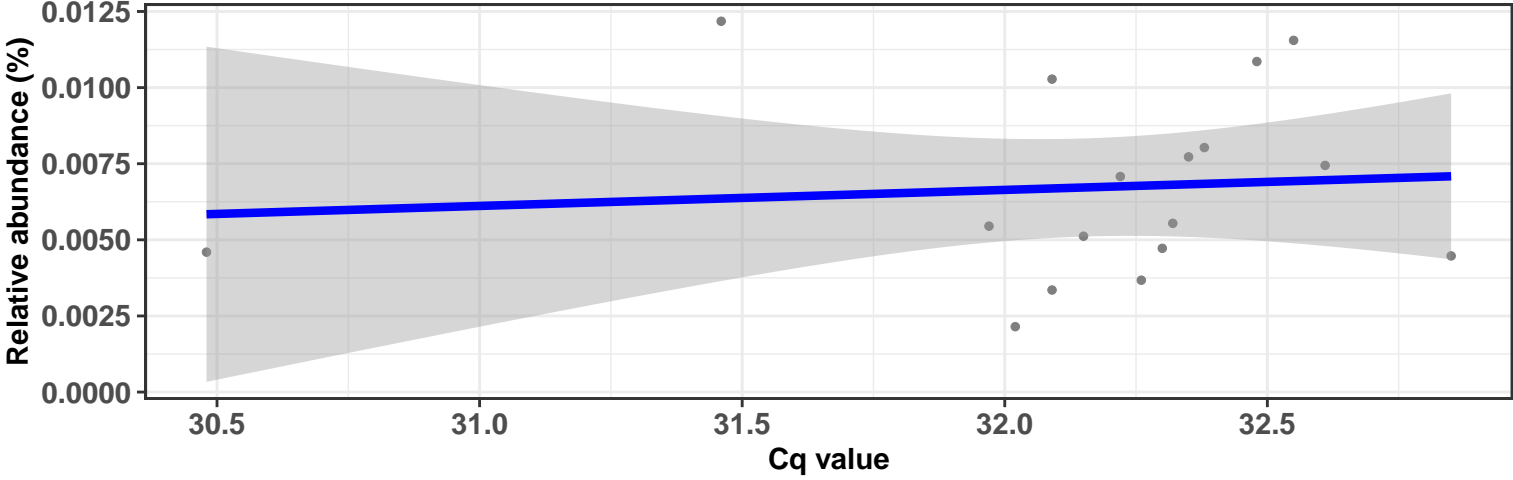
Correlation within: REF-DIC

$\log_e(S) = 6.215$ ,  $p = 0.737$ ,  $\hat{\rho}_{\text{Spearman}} = -0.099$ ,  $\text{CI}_{95\%} [-0.679, 0.458]$ ,  $n_{\text{pairs}} = 14$



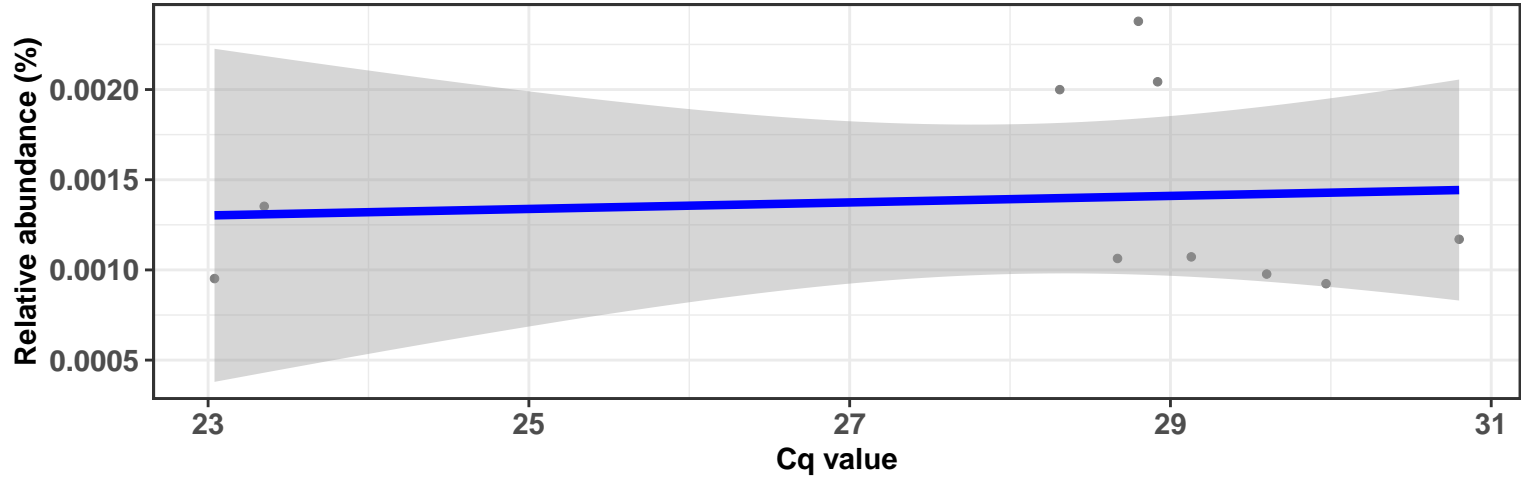
Correlation within: REF-DIM

$\log_e(S) = 6.423$ ,  $p = 0.343$ ,  $\hat{\rho}_{\text{Spearman}} = 0.245$ ,  $\text{CI}_{95\%} [-0.318, 0.783]$ ,  $n_{\text{pairs}} = 17$



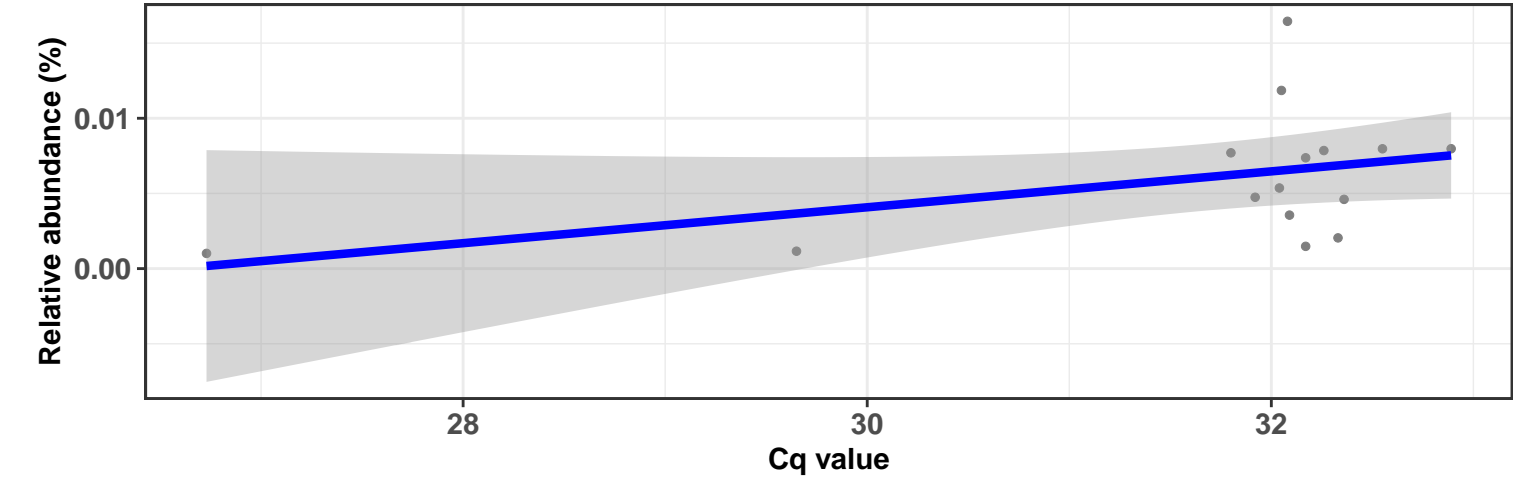
Correlation within: IM-DIC

$\log_e(S) = 5.268$ ,  $p = 0.627$ ,  $\hat{\rho}_{\text{Spearman}} = -0.176$ ,  $\text{CI}_{95\%} [-0.945, 0.380]$ ,  $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

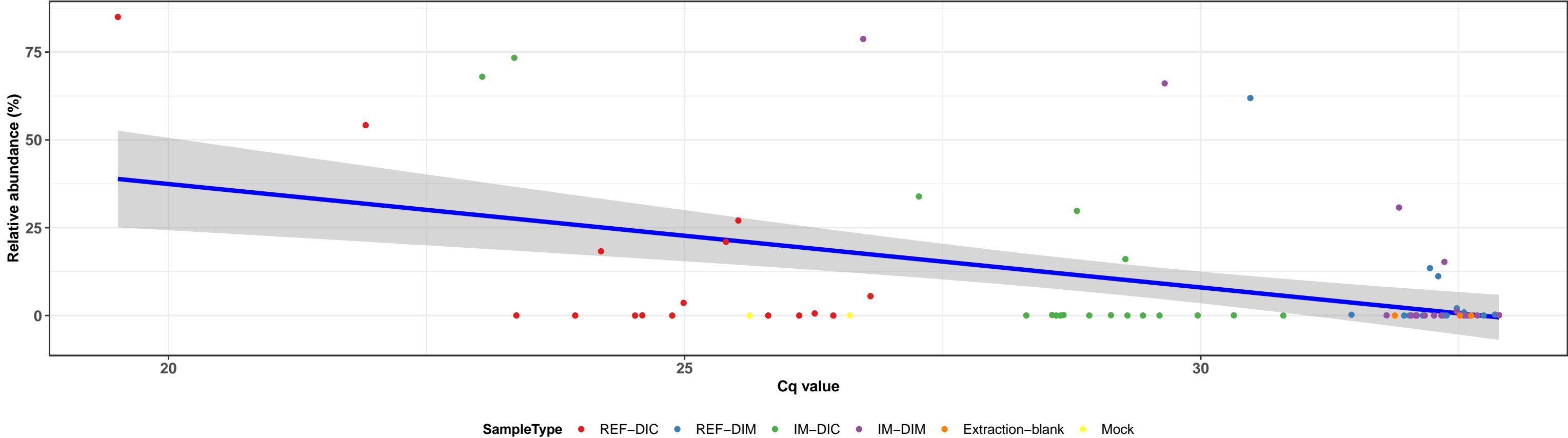
$\log_e(S) = 5.908$ ,  $p = 0.210$ ,  $\hat{\rho}_{\text{Spearman}} = 0.343$ ,  $\text{CI}_{95\%} [-0.178, 0.792]$ ,  $n_{\text{pairs}} = 15$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Aliivibrio; s\_\_uncultured bacterium

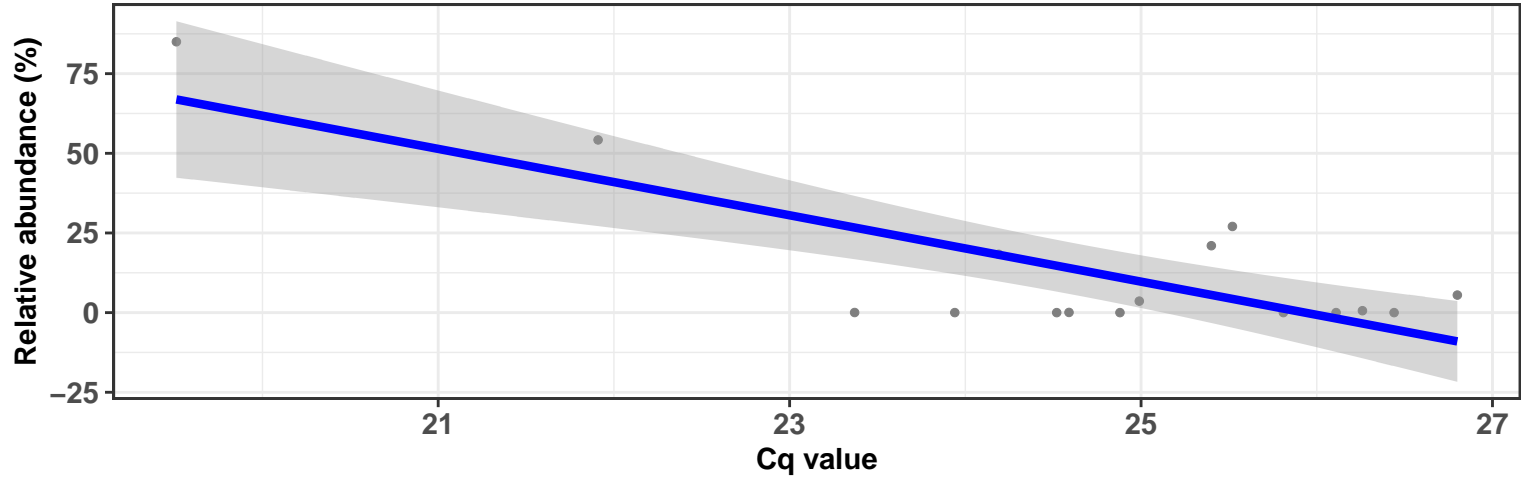
Correlation with all samples

$\log_e(S) = 11.335$ ,  $p = 0.013$ ,  $\hat{\rho}_{\text{Spearman}} = -0.291$ ,  $\text{CI}_{95\%} [-0.505, -0.092]$ ,  $n_{\text{pairs}} = 73$



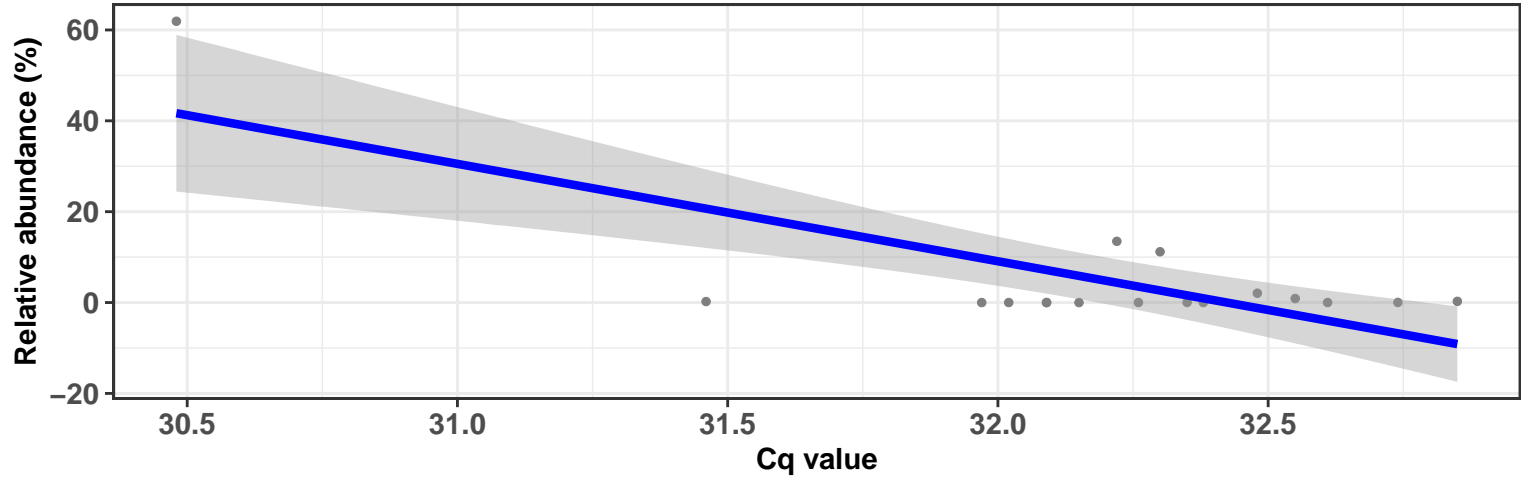
Correlation within: REF-DIC

$\log_e(S) = 6.764$ ,  $p = 0.305$ ,  $\hat{\rho}_{\text{Spearman}} = -0.274$ ,  $\text{CI}_{95\%} [-0.795, 0.248]$ ,  $n_{\text{pairs}} = 16$



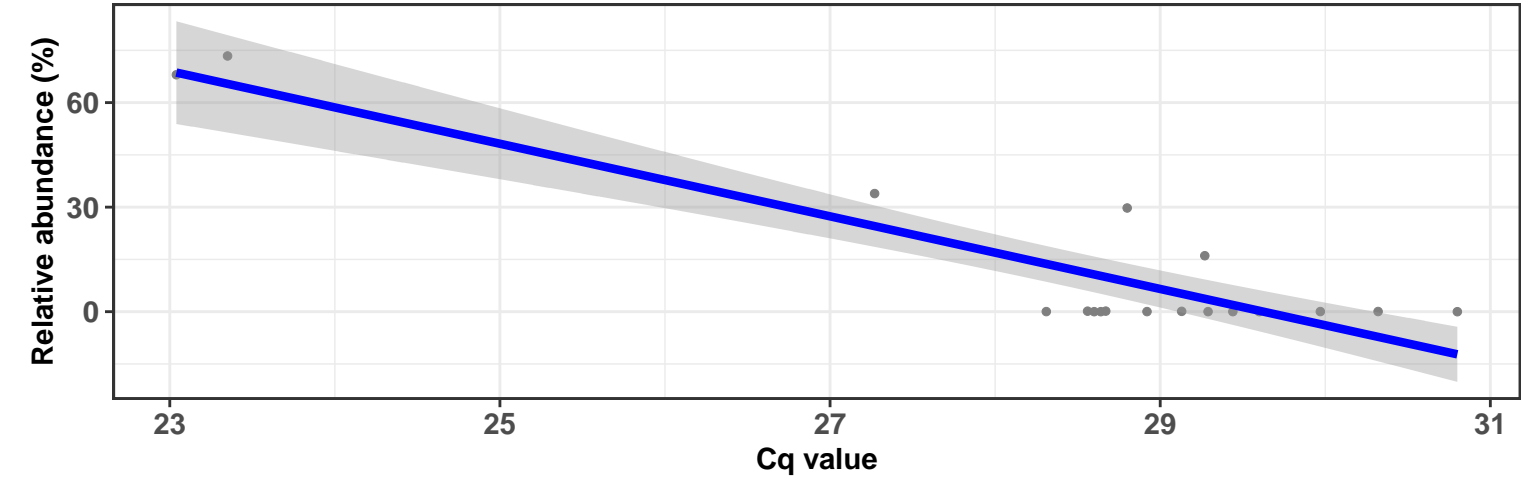
Correlation within: REF-DIM

$\log_e(S) = 6.525$ ,  $p = 0.529$ ,  $\hat{\rho}_{\text{Spearman}} = 0.164$ ,  $\text{CI}_{95\%} [-0.372, 0.685]$ ,  $n_{\text{pairs}} = 17$



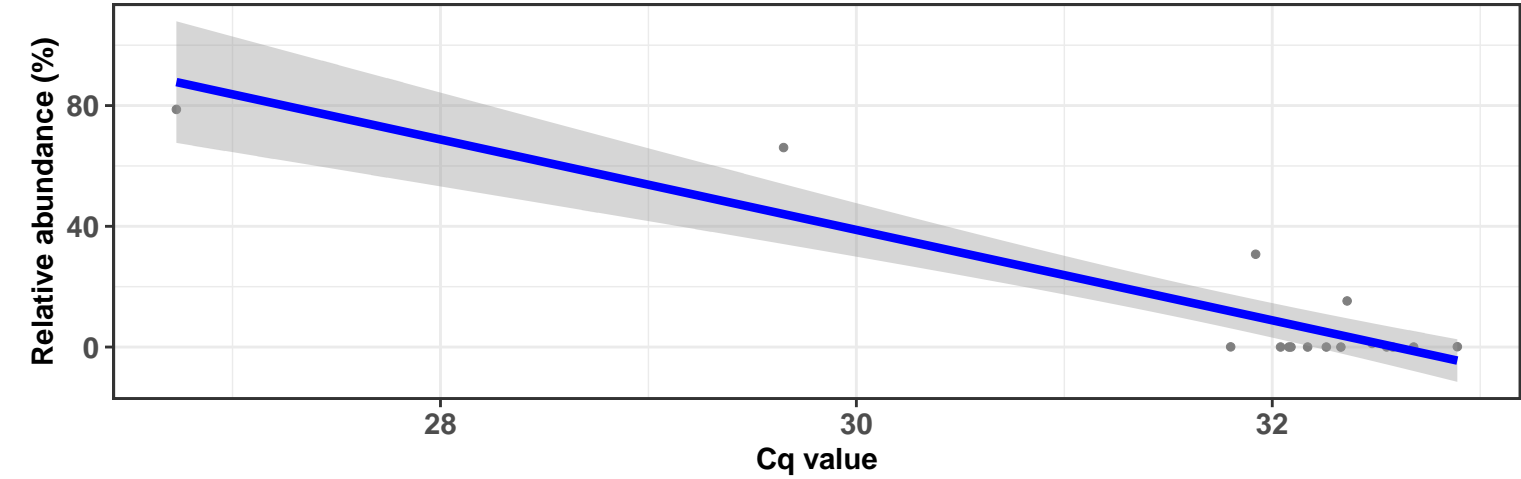
Correlation within: IM-DIC

$\log_e(S) = 7.297$ ,  $p = 0.026$ ,  $\hat{\rho}_{\text{Spearman}} = -0.523$ ,  $\text{CI}_{95\%} [-0.988, -0.124]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

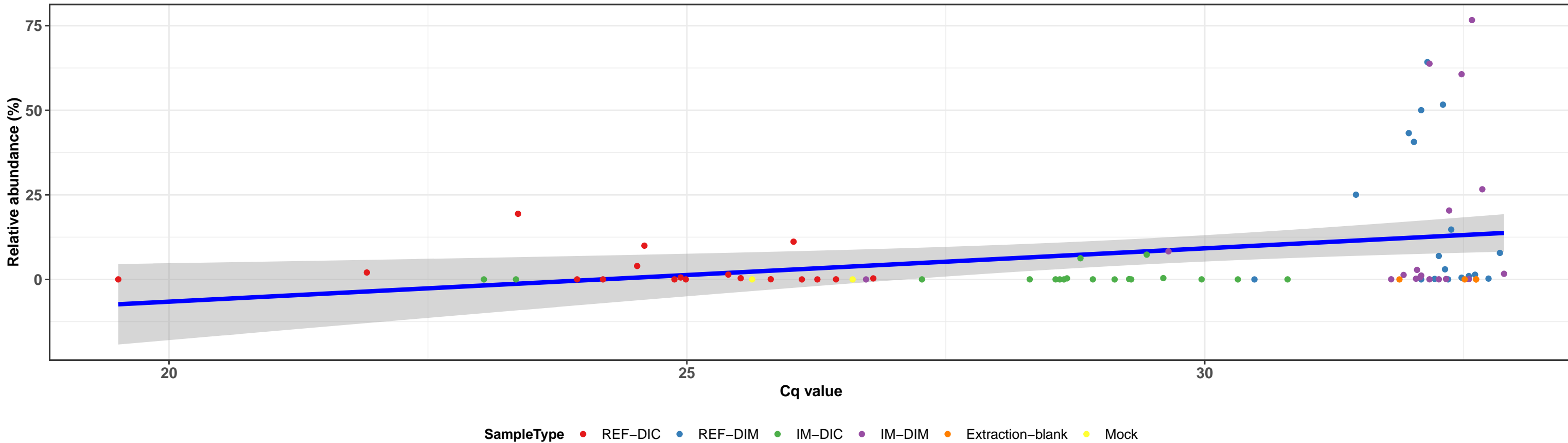
$\log_e(S) = 6.859$ ,  $p = 0.125$ ,  $\hat{\rho}_{\text{Spearman}} = -0.400$ ,  $\text{CI}_{95\%} [-0.945, 0.133]$ ,  $n_{\text{pairs}} = 16$



k\_\_Bacteria; p\_\_Spirochaetes; c\_\_Spirochaetia; o\_\_Brevinematales; f\_\_Brevinemataceae; g\_\_Brevinema; s\_\_Brevinema andersonii

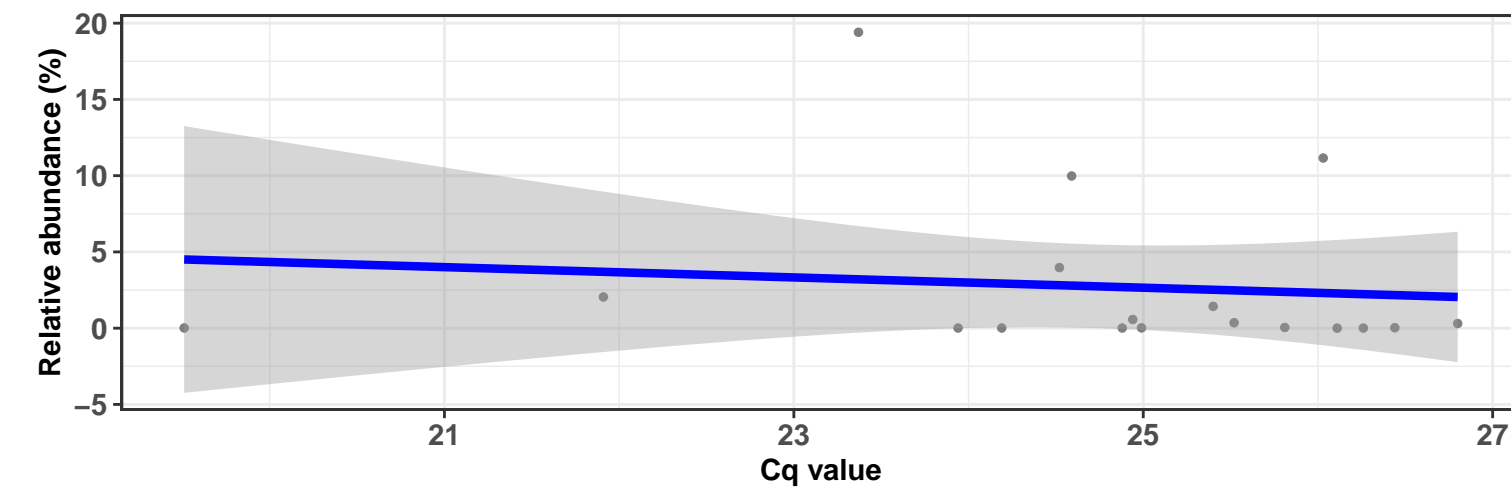
### Correlation with all samples

$\log_e(S) = 10.883$ ,  $p = 0.004$ ,  $\hat{\rho}_{\text{Spearman}} = 0.326$ ,  $CI_{95\%} [0.125, 0.550]$ ,  $n_{\text{pairs}} = 78$



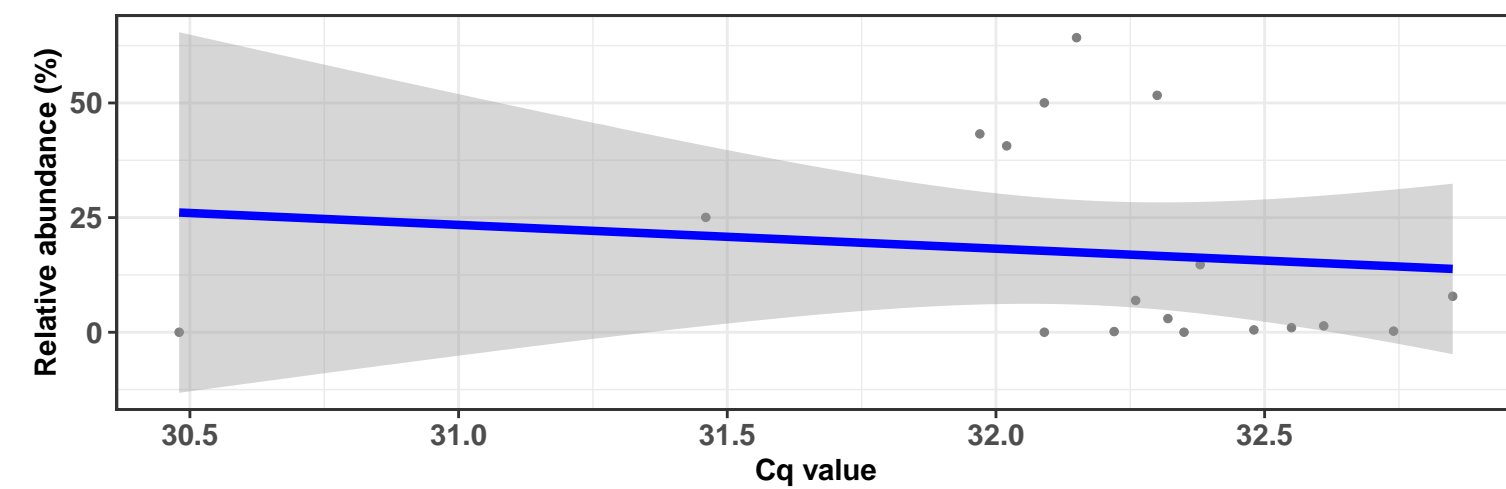
### Correlation within: REF-DIC

$\log_e(S) = 7.063$ ,  $p = 0.414$ ,  $\hat{\rho}_{\text{Spearman}} = -0.205$ ,  $CI_{95\%} [-0.684, 0.194]$ ,  $n_{\text{pairs}} = 18$



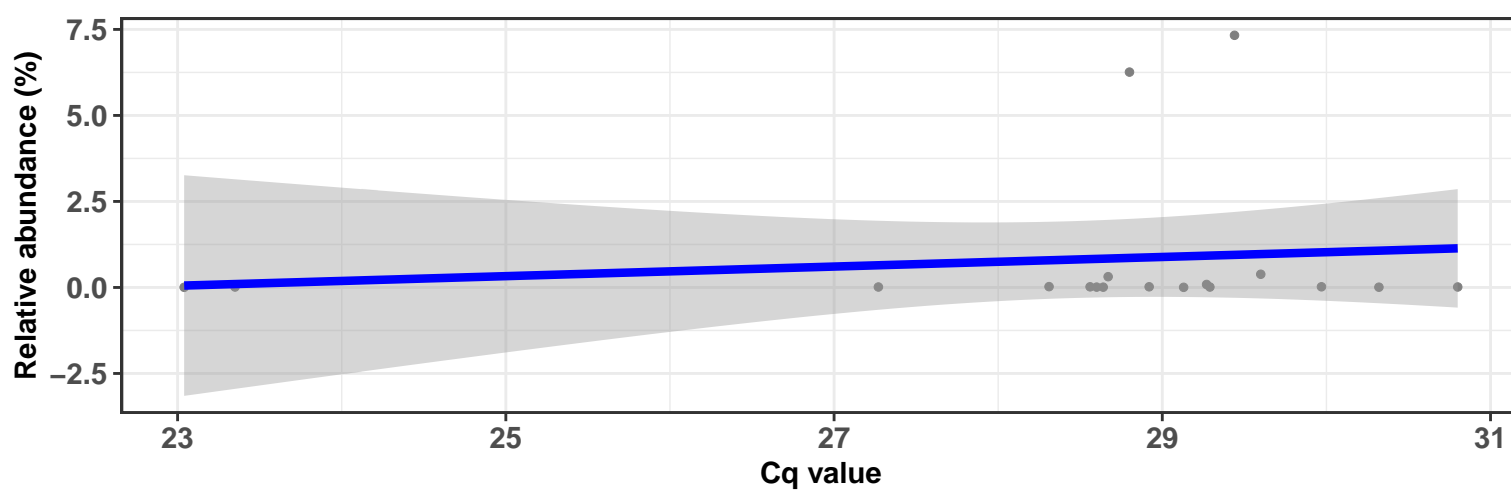
### Correlation within: REF-DIM

$\log_e(S) = 7.044$ ,  $p = 0.468$ ,  $\hat{\rho}_{\text{Spearman}} = -0.183$ ,  $CI_{95\%} [-0.716, 0.350]$ ,  $n_{\text{pairs}} = 18$



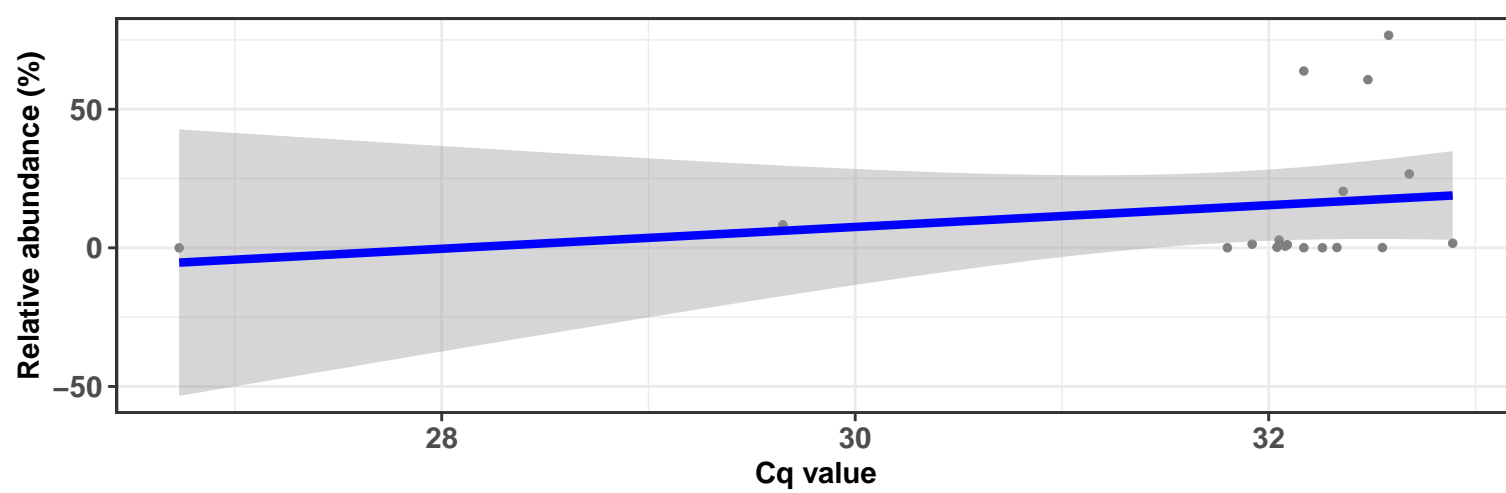
### Correlation within: IM-DIC

$\log_e(S) = 6.631$ ,  $p = 0.385$ ,  $\hat{\rho}_{\text{Spearman}} = 0.218$ ,  $CI_{95\%} [-0.165, 0.776]$ ,  $n_{\text{pairs}} = 18$



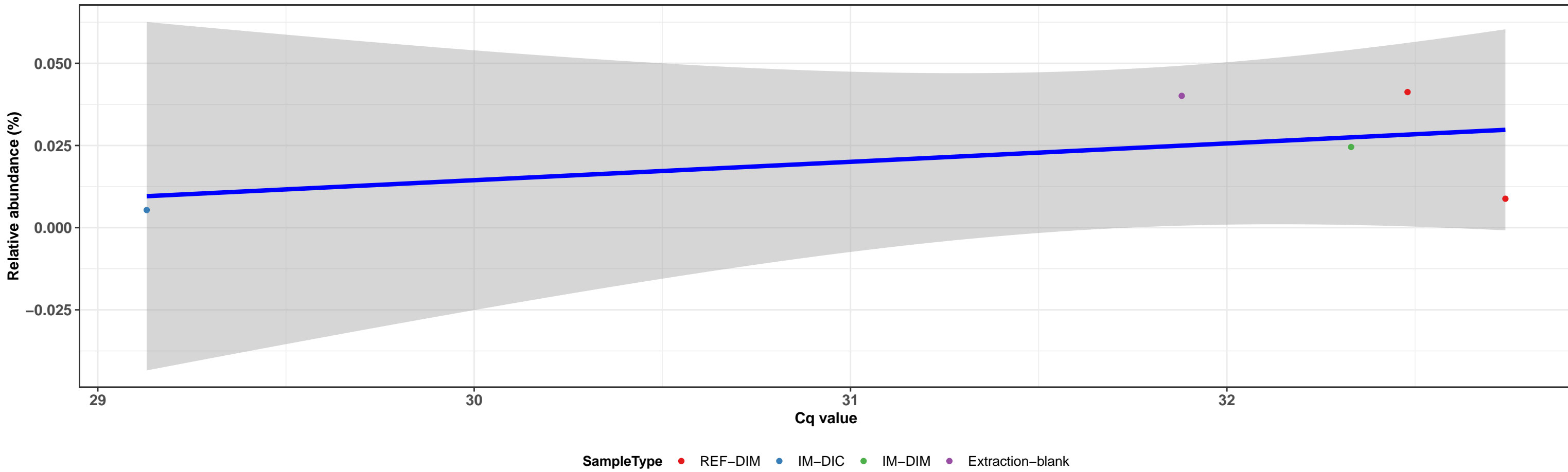
### Correlation within: IM-DIM

$\log_e(S) = 6.359$ ,  $p = 0.097$ ,  $\hat{\rho}_{\text{Spearman}} = 0.404$ ,  $CI_{95\%} [0.012, 0.767]$ ,  $n_{\text{pairs}} = 18$

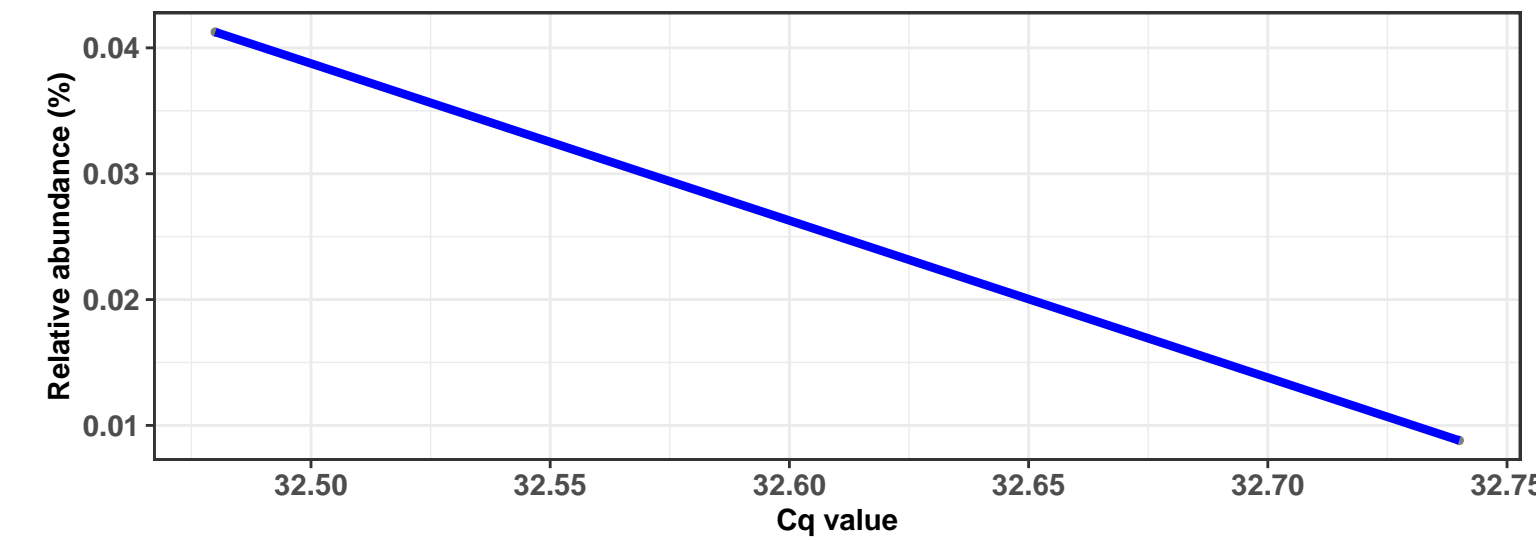


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Rhizobiales; f\_\_Devosiaceae; g\_\_Devosia; NA

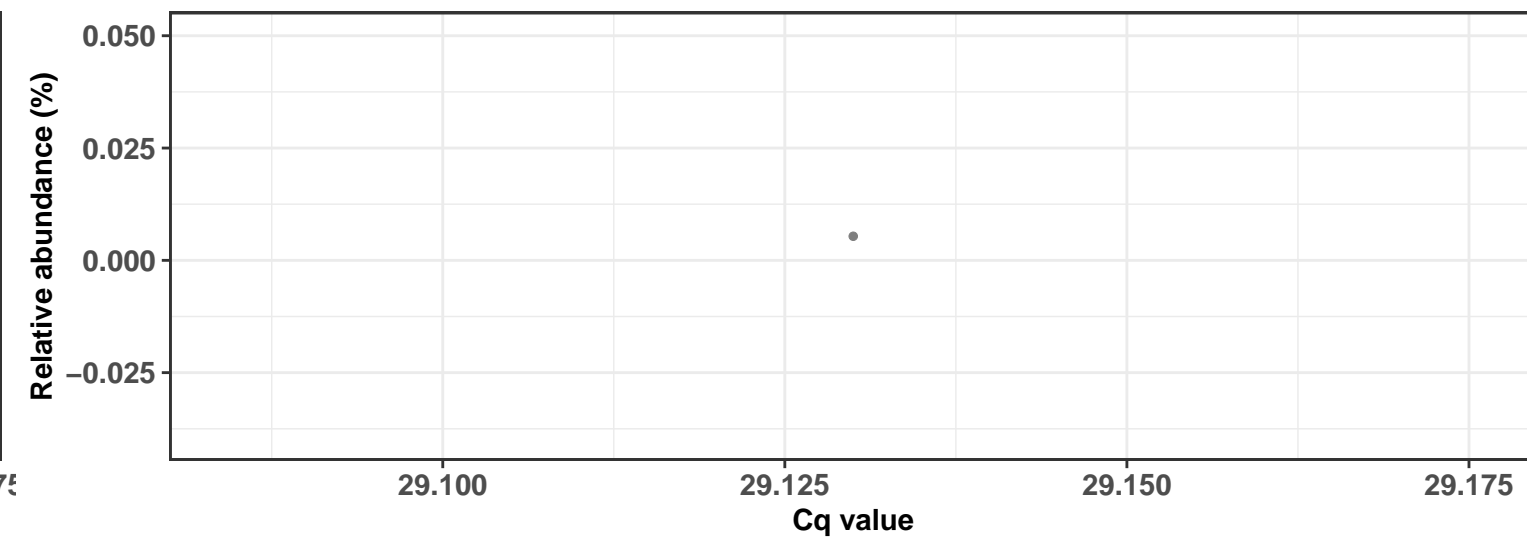
Correlation with all samples



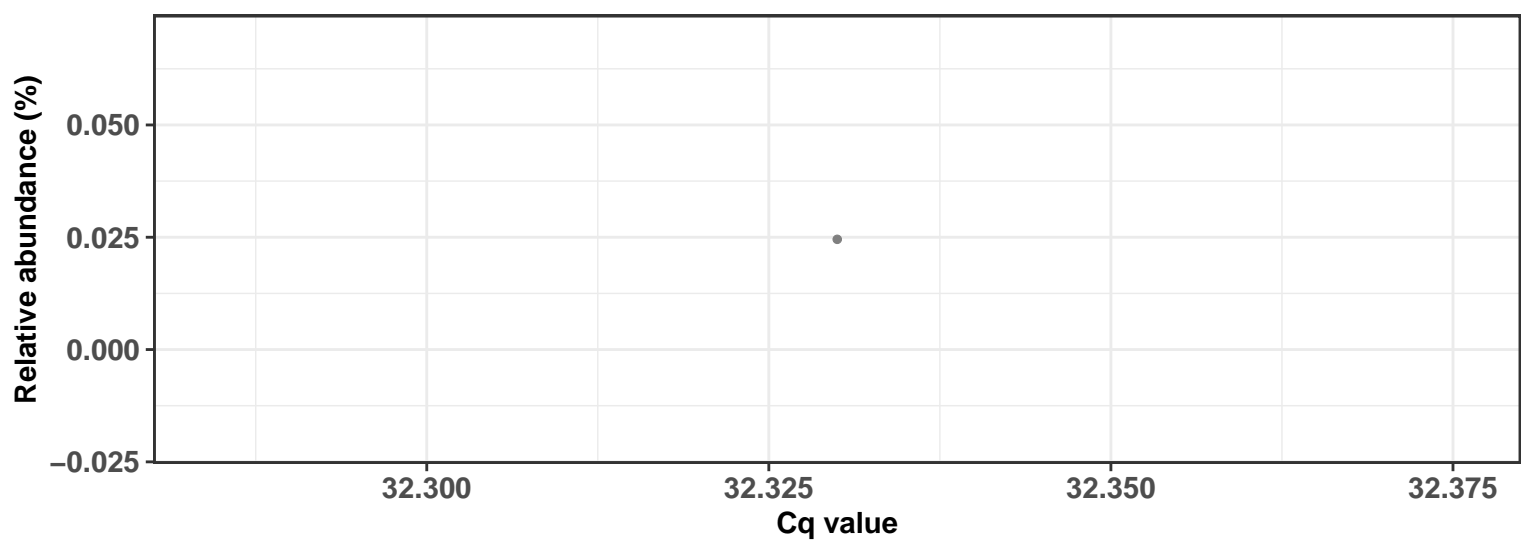
Correlation within: REF-DIM



Correlation within: IM-DIC



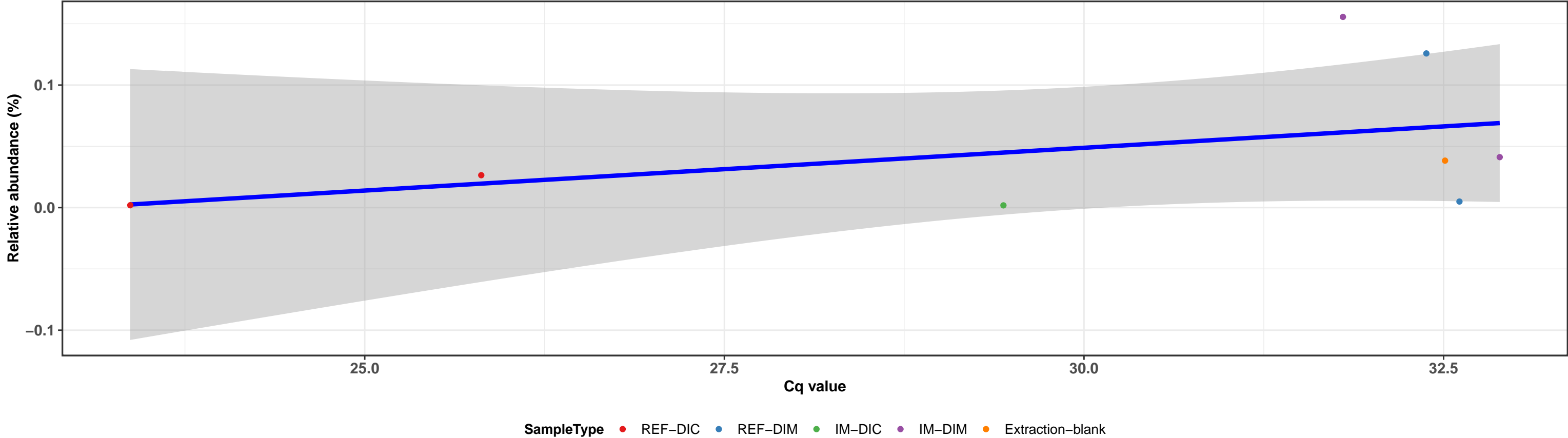
Correlation within: IM-DIM



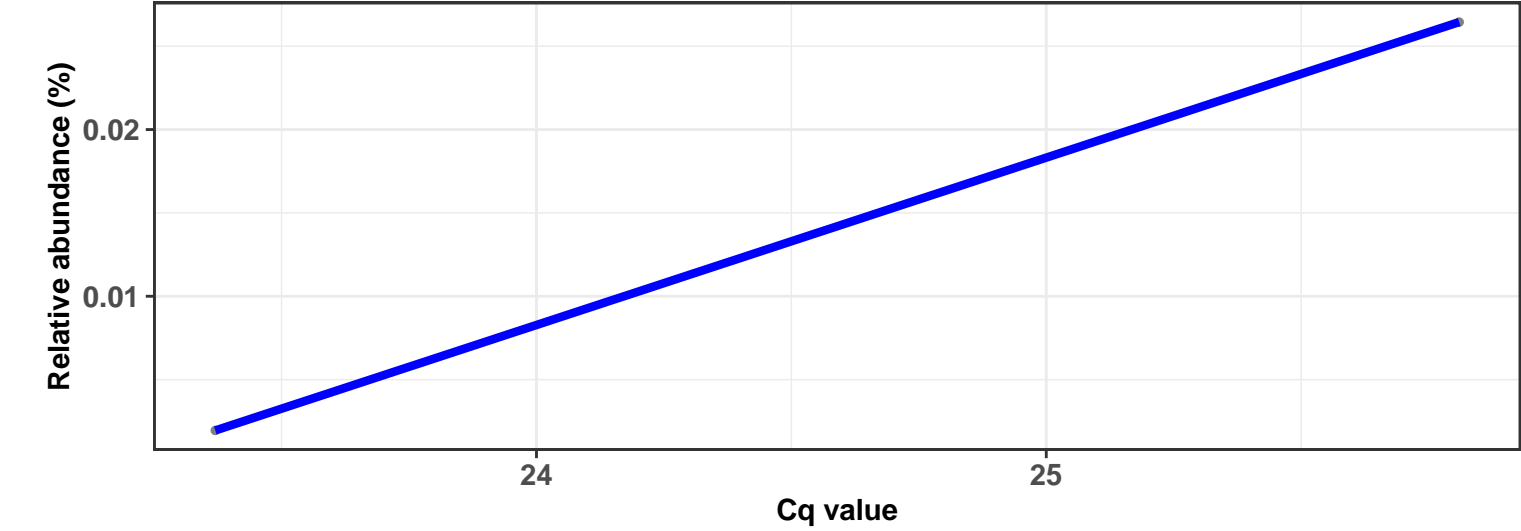
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingomonas; s\_\_Sphingomonas aurantiaca

Correlation with all samples

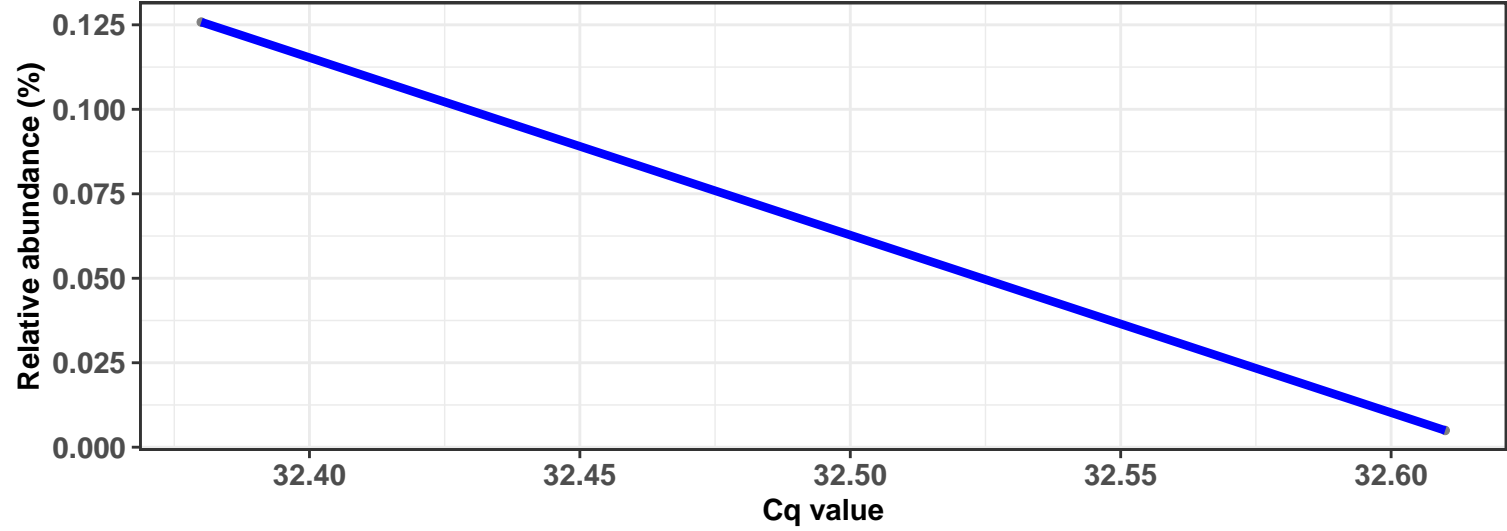
$\log_e(S) = 3.912$ ,  $p = 0.320$ ,  $\hat{\rho}_{\text{Spearman}} = 0.405$ ,  $\text{CI}_{95\%} [-0.197, 1.281]$ ,  $n_{\text{pairs}} = 8$



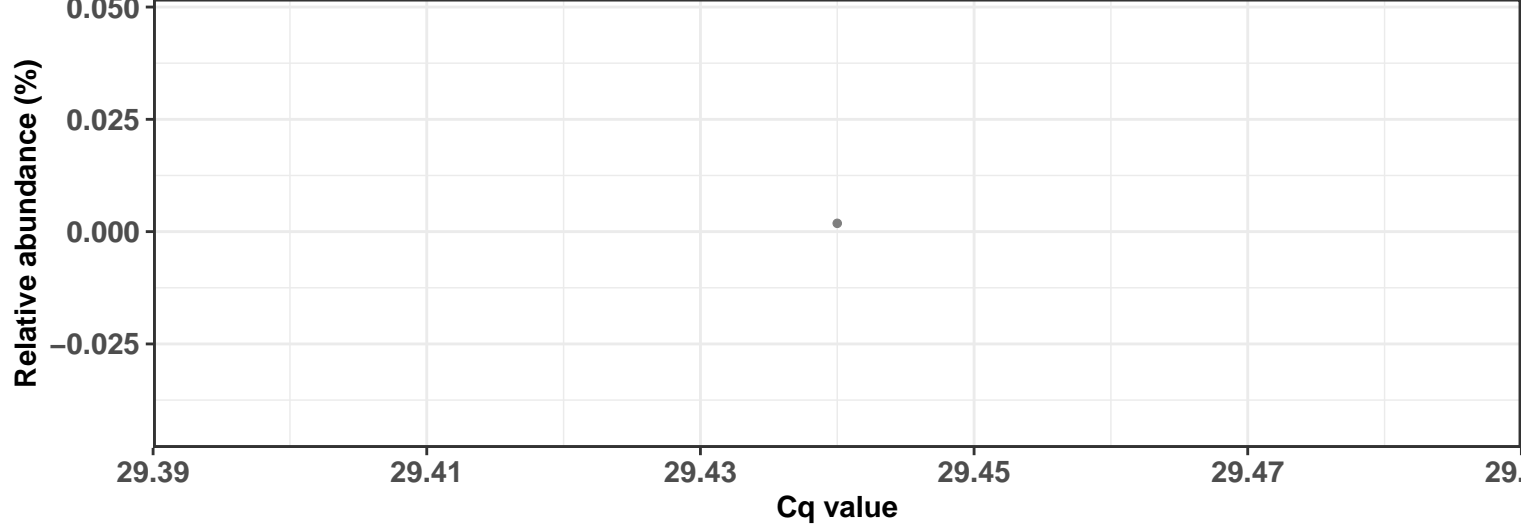
Correlation within: REF-DIC



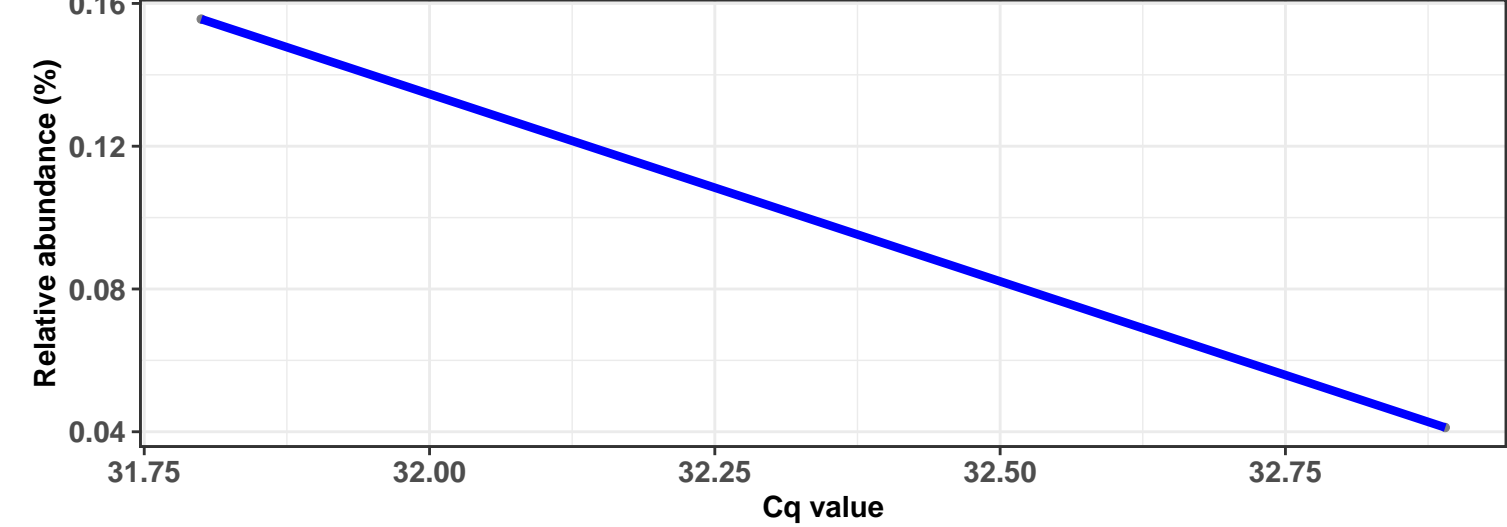
Correlation within: REF-DIM



Correlation within: IM-DIC



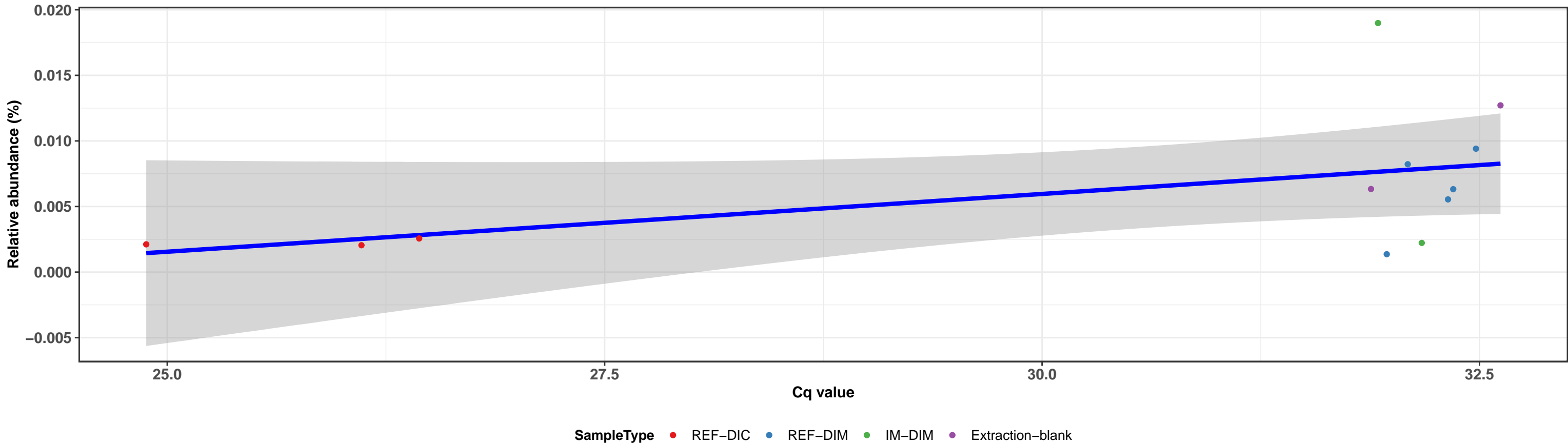
Correlation within: IM-DIM



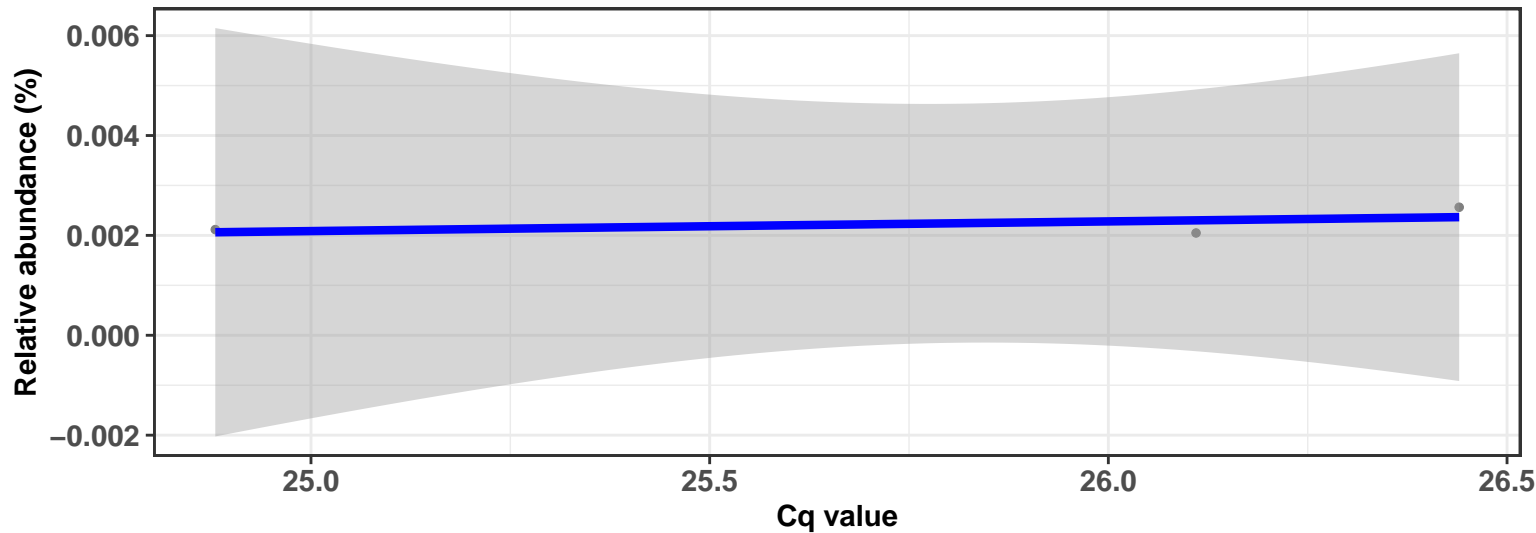
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Caulobacterales; f\_\_Caulobacteraceae; g\_\_Brevundimonas; Ambiguous\_taxa

Correlation with all samples

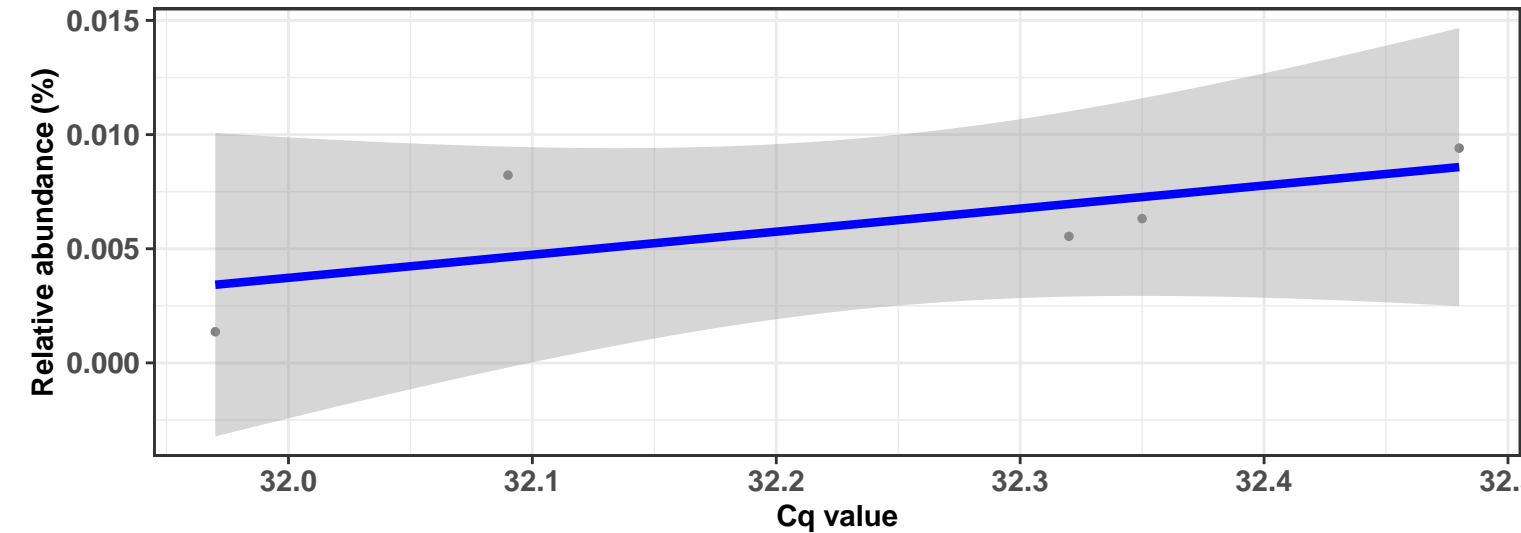
$\log_e(S) = 4.927$ ,  $p = 0.085$ ,  $\hat{\rho}_{\text{Spearman}} = 0.517$ ,  $\text{CI}_{95\%} [0.031, 1.084]$ ,  $n_{\text{pairs}} = 12$



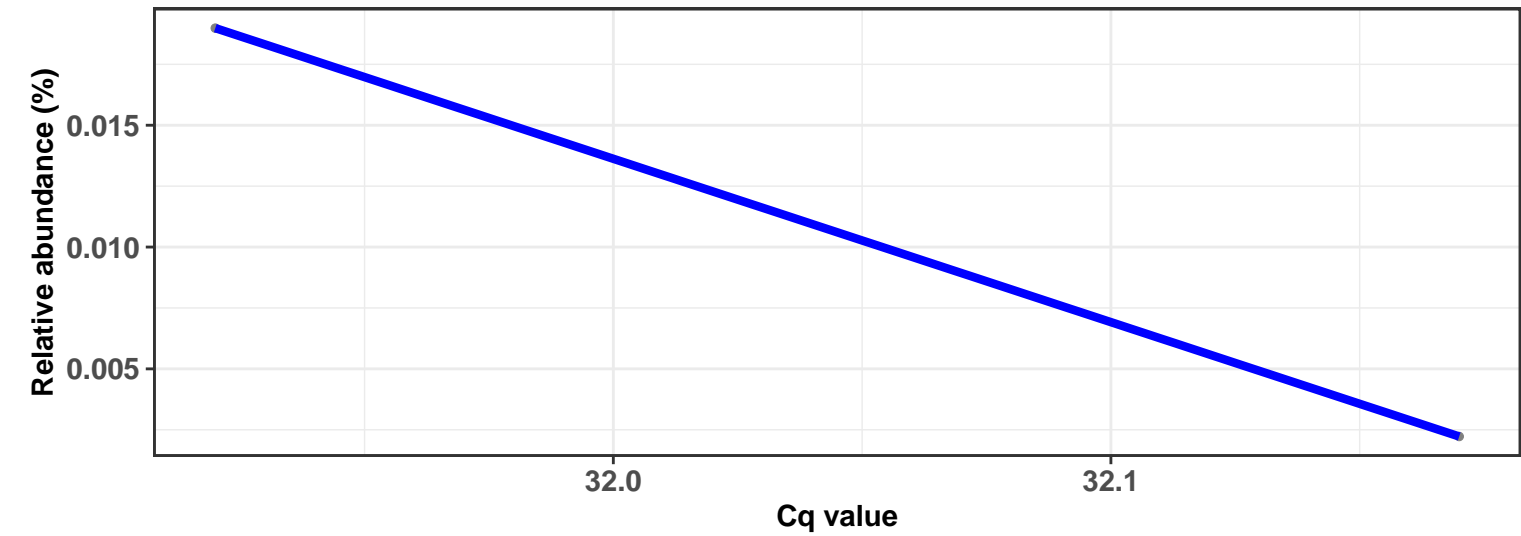
Correlation within: REF-DIC



Correlation within: REF-DIM



Correlation within: IM-DIM

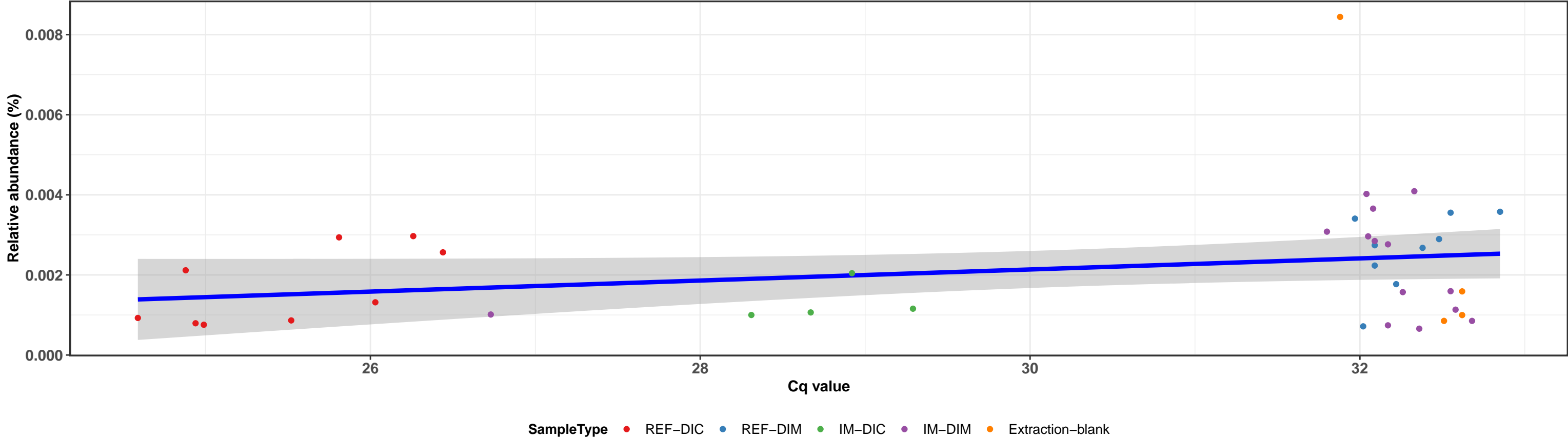




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

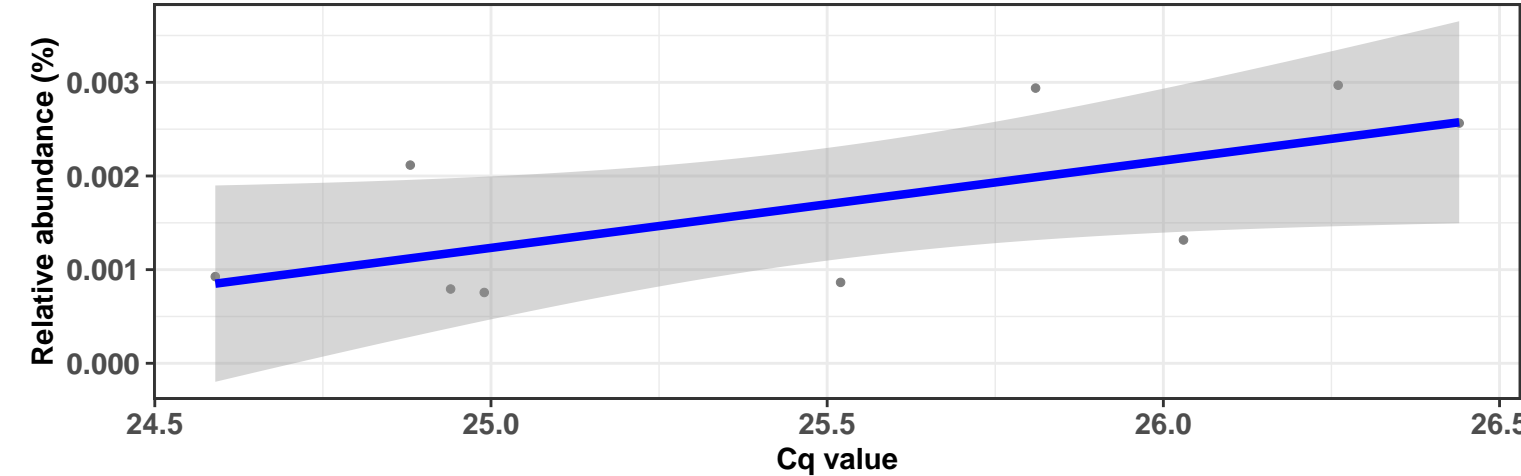
Correlation with all samples

$\log_e(S) = 9.162$ ,  $p = 0.516$ ,  $\hat{\rho}_{\text{Spearman}} = 0.106$ ,  $\text{CI}_{95\%} [-0.187, 0.443]$ ,  $n_{\text{pairs}} = 40$



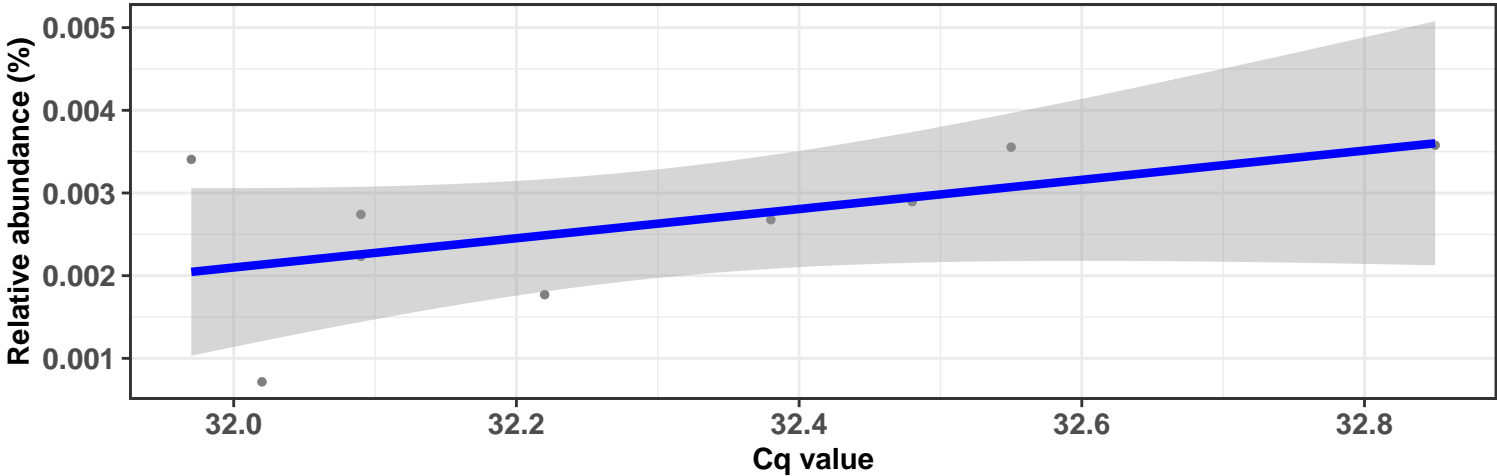
Correlation within: REF-DIC

$\log_e(S) = 3.951$ ,  $p = 0.112$ ,  $\hat{\rho}_{\text{Spearman}} = 0.567$ ,  $\text{CI}_{95\%} [0.112, 1.151]$ ,  $n_{\text{pairs}} = 9$

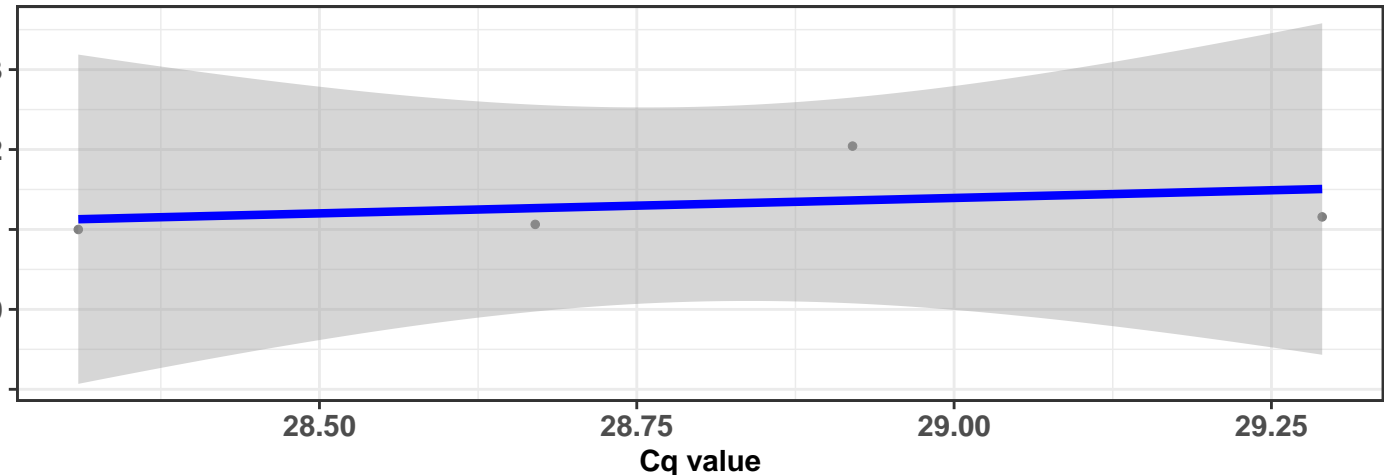


Correlation within: REF-DIM

$\log_e(S) = 3.984$ ,  $p = 0.123$ ,  $\hat{\rho}_{\text{Spearman}} = 0.552$ ,  $\text{CI}_{95\%} [-0.135, 1.195]$ ,  $n_{\text{pairs}} = 9$

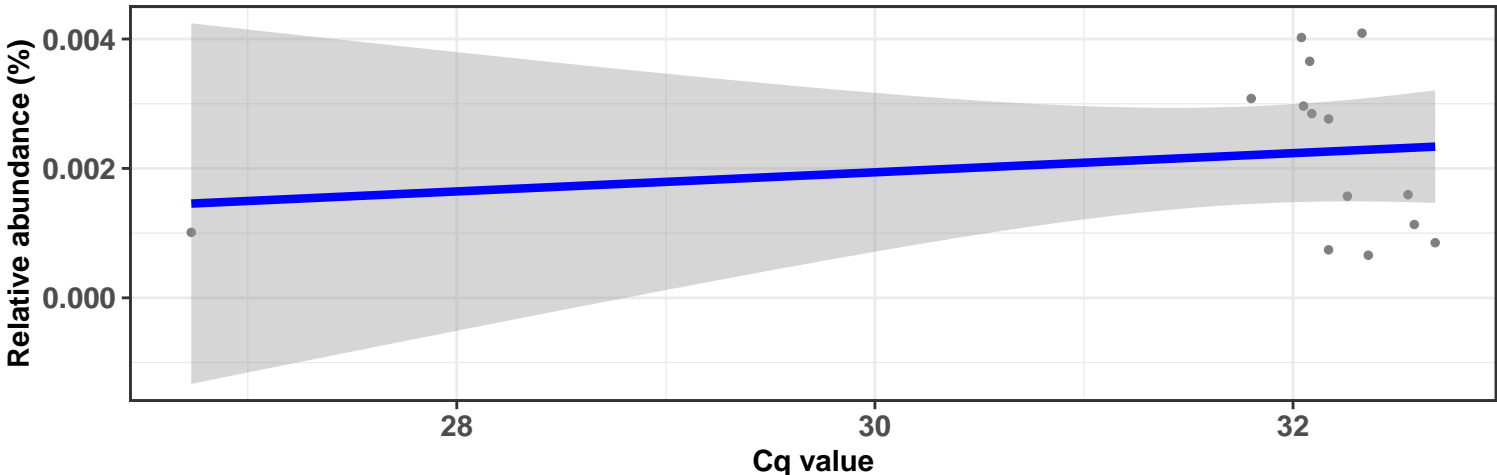


Correlation within: IM-DIC



Correlation within: IM-DIM

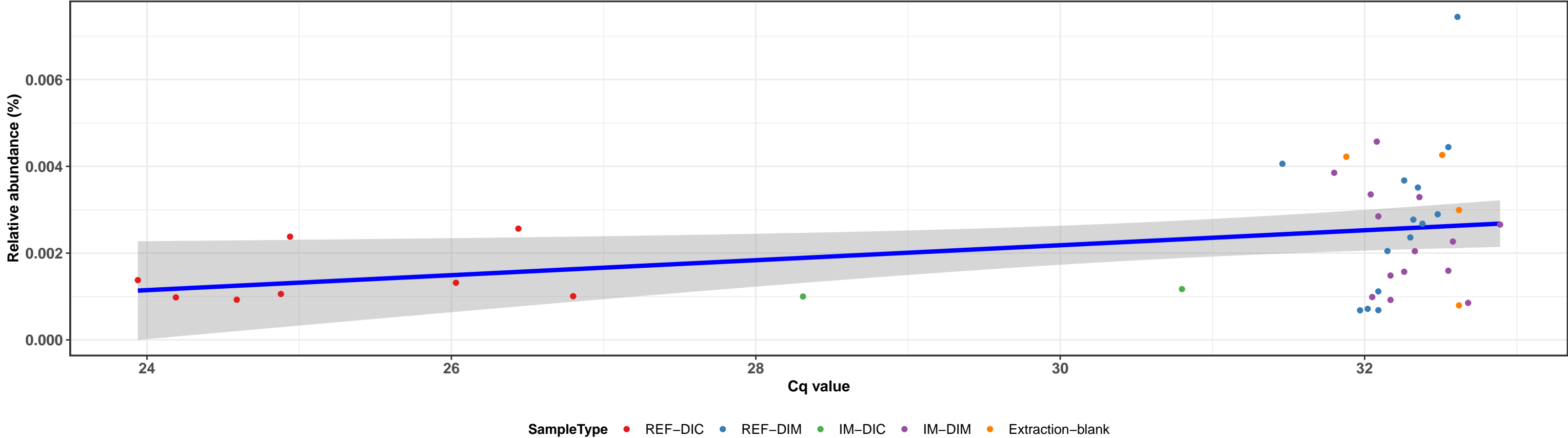
$\log_e(S) = 6.477$ ,  $p = 0.126$ ,  $\hat{\rho}_{\text{Spearman}} = -0.429$ ,  $\text{CI}_{95\%} [-0.860, 0.053]$ ,  $n_{\text{pairs}} = 14$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

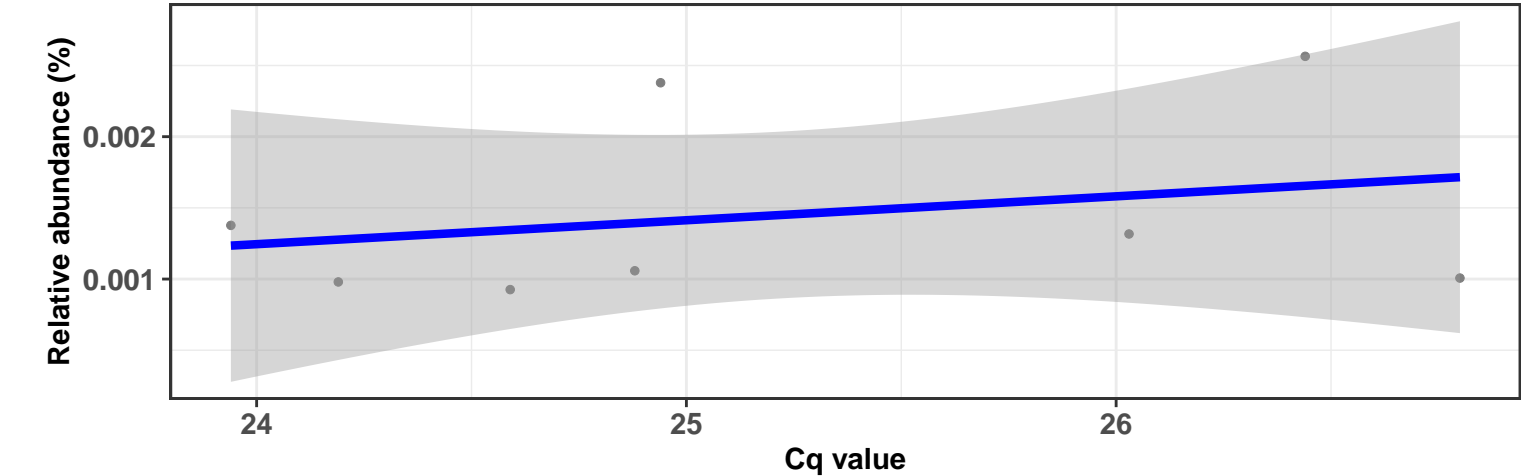
Correlation with all samples

$\log_e(S) = 9.077$ ,  $p = 0.061$ ,  $\hat{\rho}_{\text{Spearman}} = 0.291$ ,  $\text{CI}_{95\%} [0.008, 0.622]$ ,  $n_{\text{pairs}} = 42$



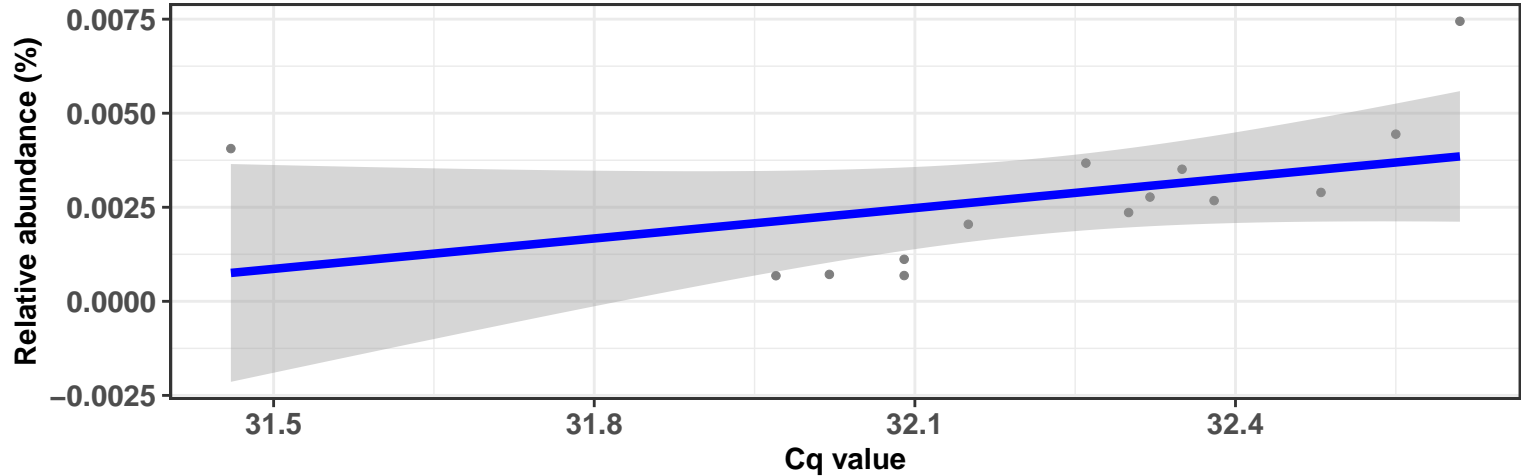
Correlation within: REF-DIC

$\log_e(S) = 4.094$ ,  $p = 0.493$ ,  $\hat{\rho}_{\text{Spearman}} = 0.286$ ,  $\text{CI}_{95\%} [-0.505, 1.119]$ ,  $n_{\text{pairs}} = 8$

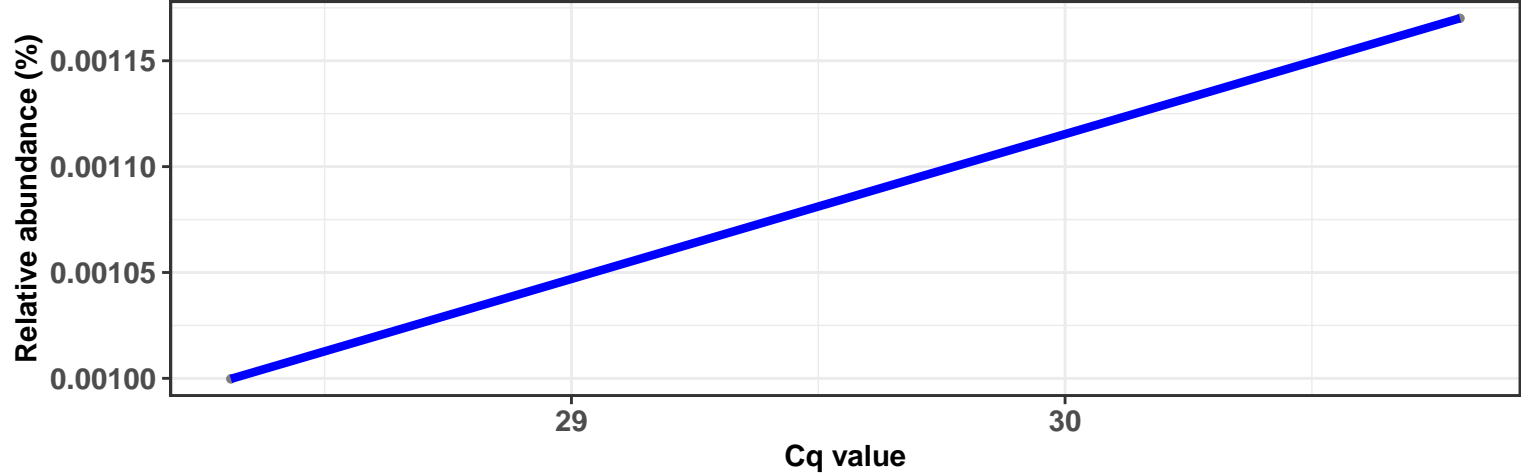


Correlation within: REF-DIM

$\log_e(S) = 5.169$ ,  $p = 0.020$ ,  $\hat{\rho}_{\text{Spearman}} = 0.614$ ,  $\text{CI}_{95\%} [0.127, 1.225]$ ,  $n_{\text{pairs}} = 14$

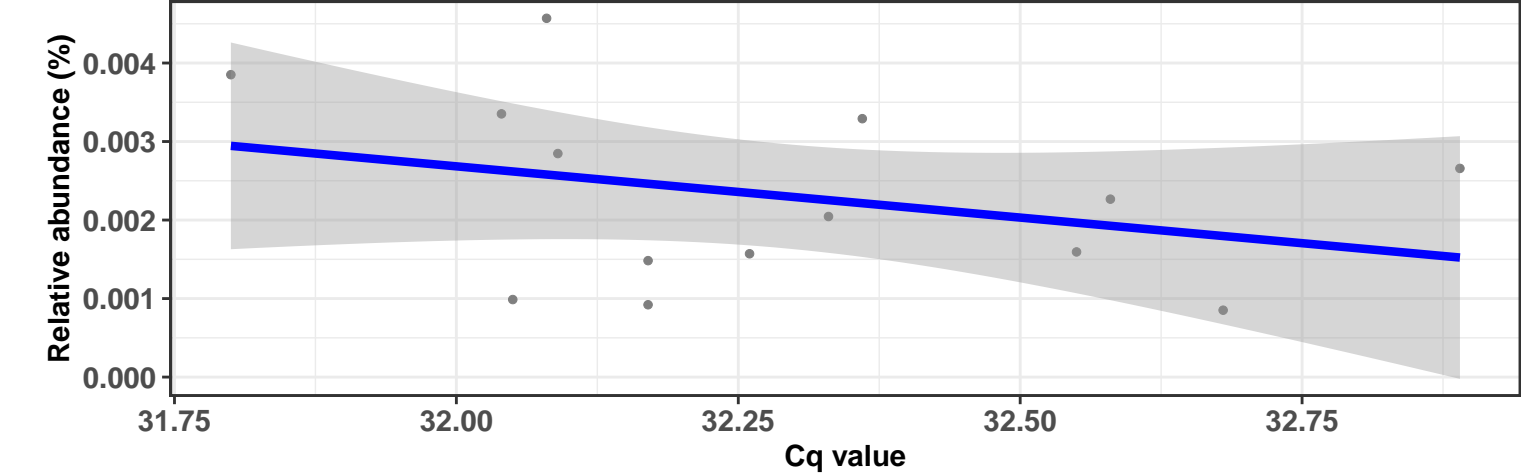


Correlation within: IM-DIC



Correlation within: IM-DIM

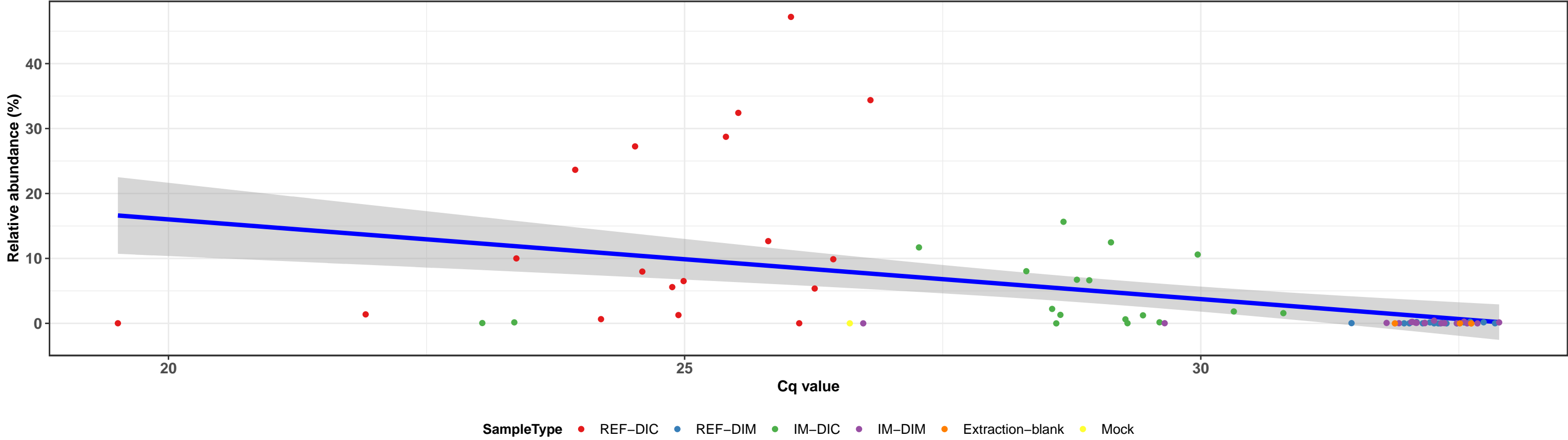
$\log_e(S) = 6.430$ ,  $p = 0.202$ ,  $\hat{\rho}_{\text{Spearman}} = -0.363$ ,  $\text{CI}_{95\%} [-0.910, 0.131]$ ,  $n_{\text{pairs}} = 14$



k\_\_Bacteria; p\_\_Tenericutes; c\_\_Mollicutes; o\_\_Mycoplasmatales; f\_\_Mycoplasmataceae; g\_\_Mycoplasma; s\_\_uncultured bacterium

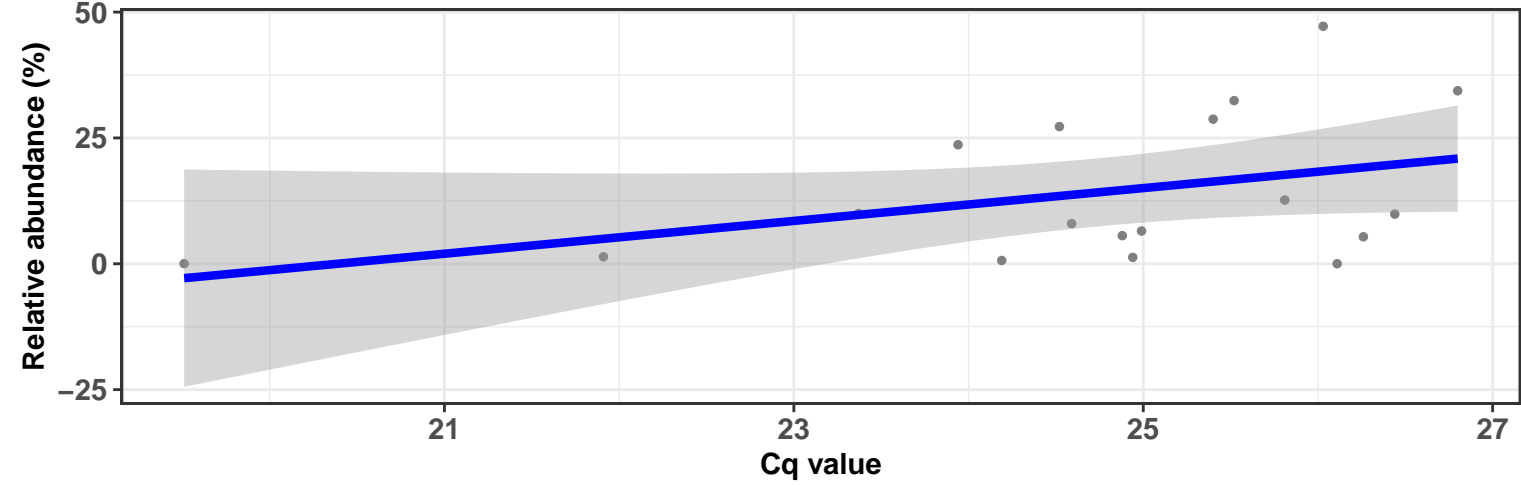
Correlation with all samples

$\log_e(S) = 11.658$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.581$ ,  $\text{CI}_{95\%} [-0.746, -0.429]$ ,  $n_{\text{pairs}} = 76$



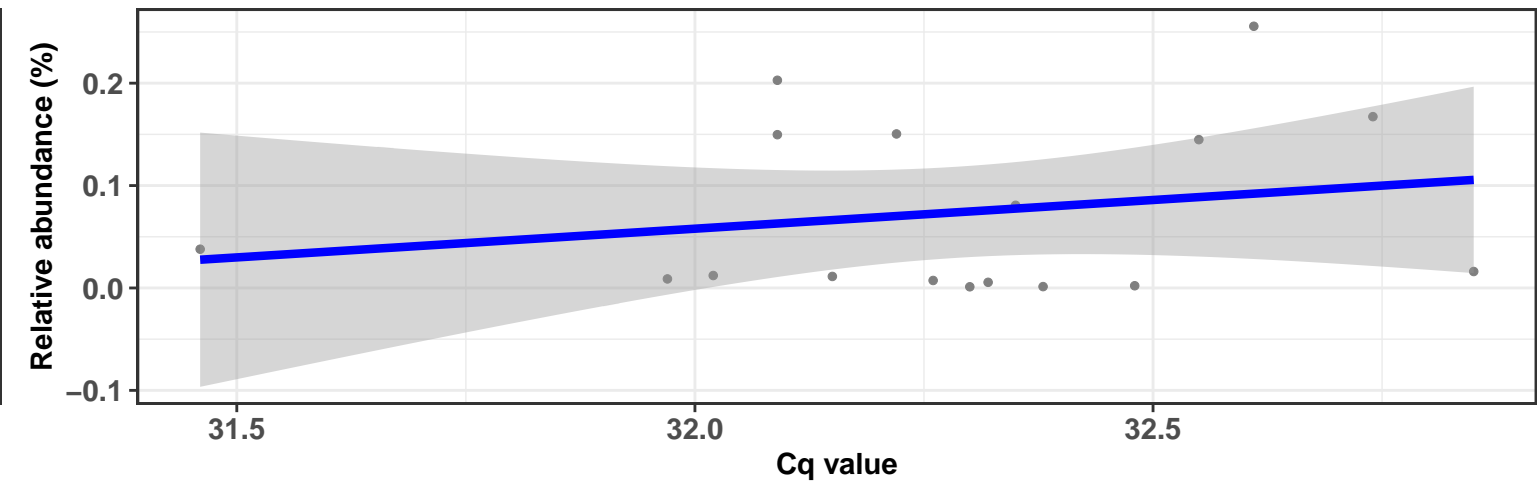
Correlation within: REF-DIC

$\log_e(S) = 6.480$ ,  $p = 0.185$ ,  $\hat{\rho}_{\text{Spearman}} = 0.327$ ,  $\text{CI}_{95\%} [-0.185, 0.798]$ ,  $n_{\text{pairs}} = 18$



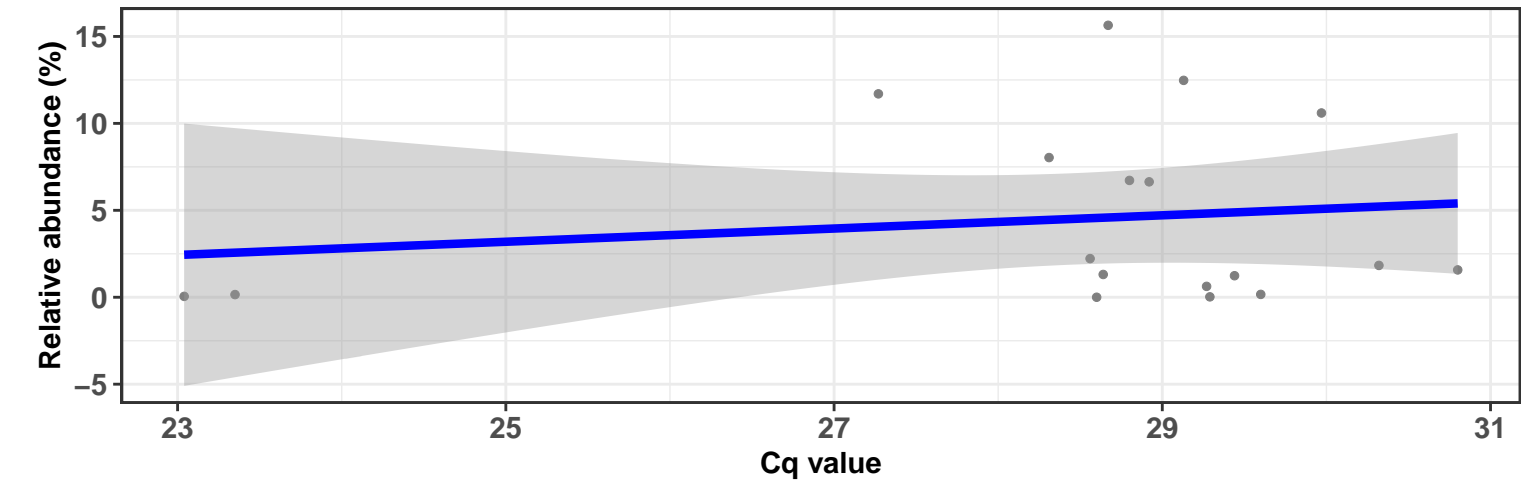
Correlation within: REF-DIM

$\log_e(S) = 6.632$ ,  $p = 0.790$ ,  $\hat{\rho}_{\text{Spearman}} = 0.070$ ,  $\text{CI}_{95\%} [-0.382, 0.514]$ ,  $n_{\text{pairs}} = 17$



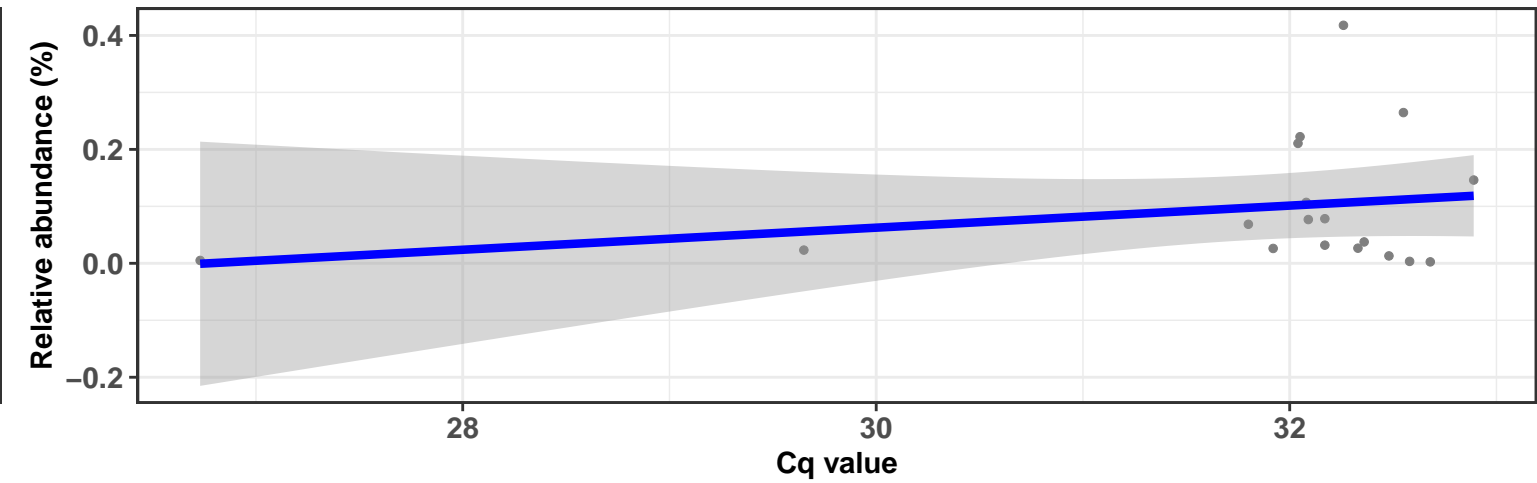
Correlation within: IM-DIC

$\log_e(S) = 6.837$ ,  $p = 0.880$ ,  $\hat{\rho}_{\text{Spearman}} = 0.038$ ,  $\text{CI}_{95\%} [-0.436, 0.548]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

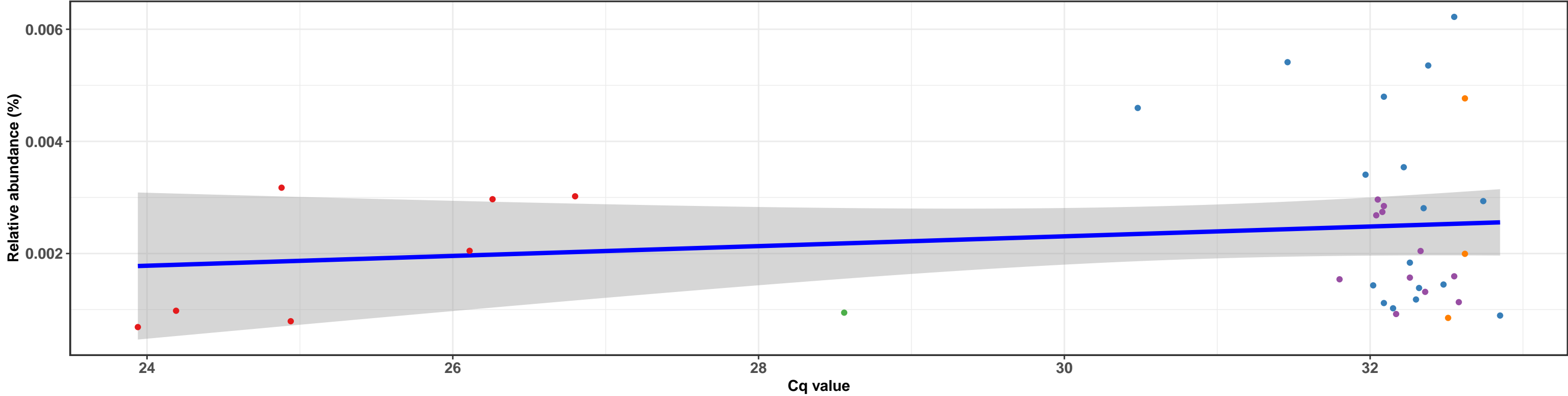
$\log_e(S) = 6.890$ ,  $p = 0.958$ ,  $\hat{\rho}_{\text{Spearman}} = -0.013$ ,  $\text{CI}_{95\%} [-0.595, 0.579]$ ,  $n_{\text{pairs}} = 18$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

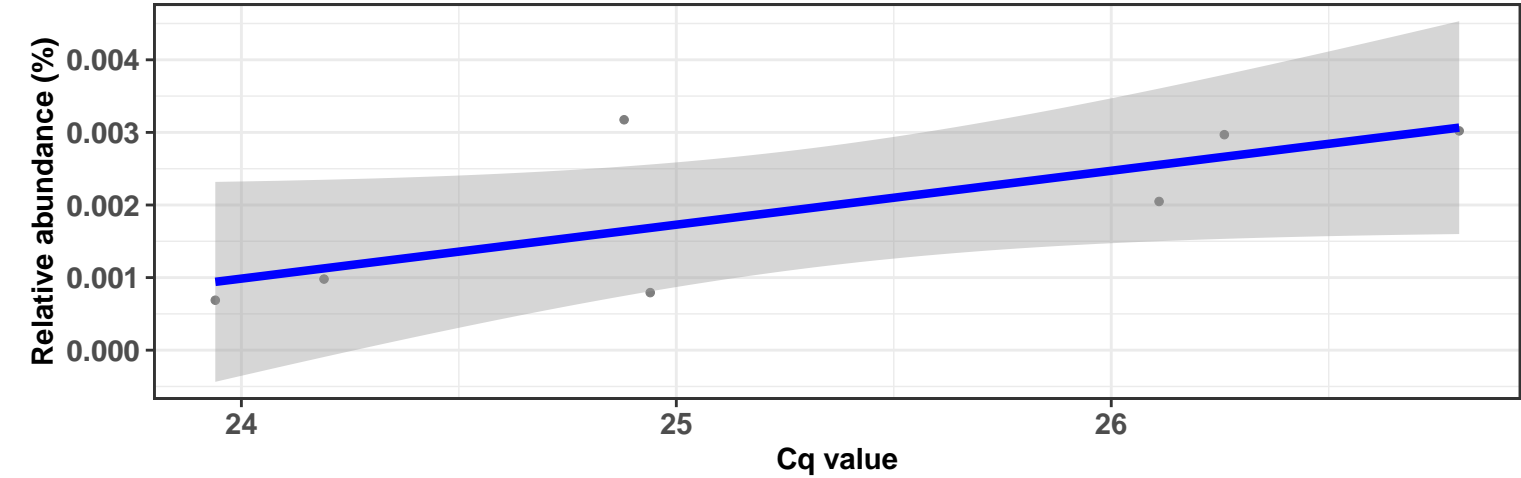
Correlation with all samples

$\log_e(S) = 9.183$ ,  $p = 0.927$ ,  $\hat{\rho}_{\text{Spearman}} = 0.015$ ,  $\text{CI}_{95\%} [-0.376, 0.343]$ ,  $n_{\text{pairs}} = 39$



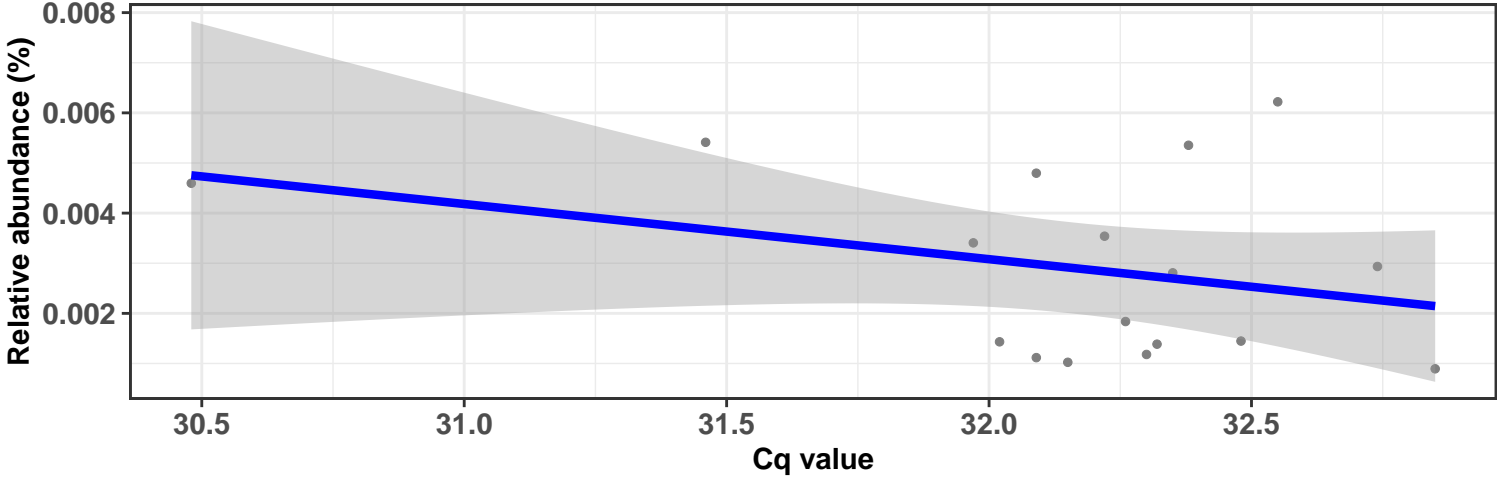
Correlation within: REF-DIC

$\log_e(S) = 3.178$ ,  $p = 0.180$ ,  $\hat{\rho}_{\text{Spearman}} = 0.571$ ,  $\text{CI}_{95\%} [-0.191, 1.258]$ ,  $n_{\text{pairs}} = 7$

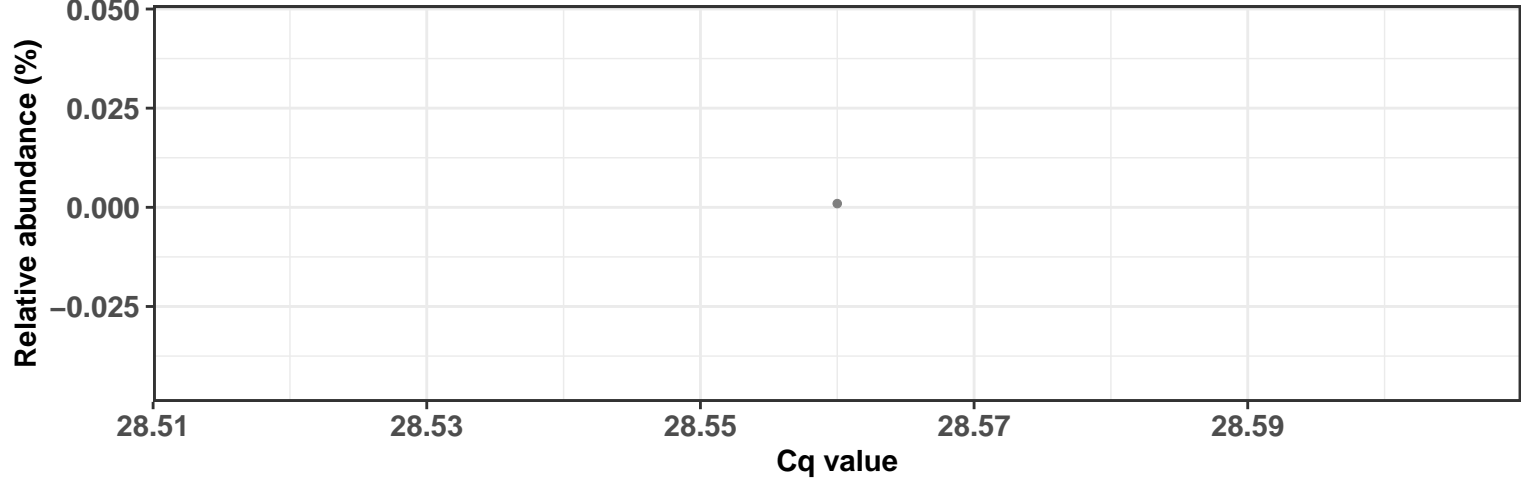


Correlation within: REF-DIM

$\log_e(S) = 6.866$ ,  $p = 0.501$ ,  $\hat{\rho}_{\text{Spearman}} = -0.175$ ,  $\text{CI}_{95\%} [-0.720, 0.399]$ ,  $n_{\text{pairs}} = 17$

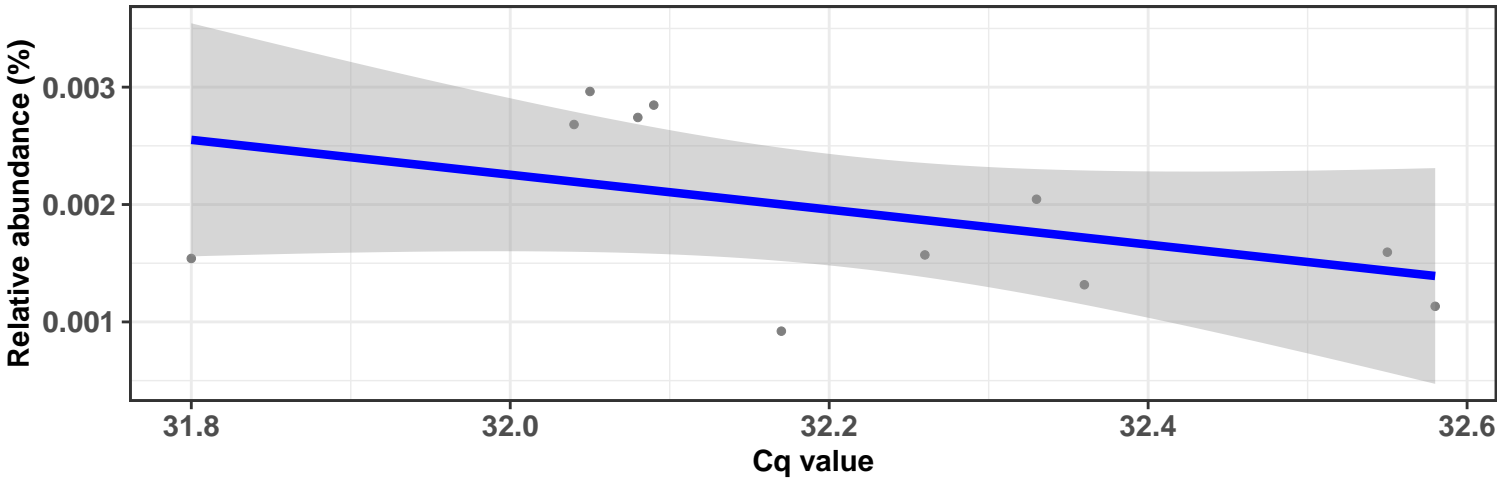


Correlation within: IM-DIC



Correlation within: IM-DIM

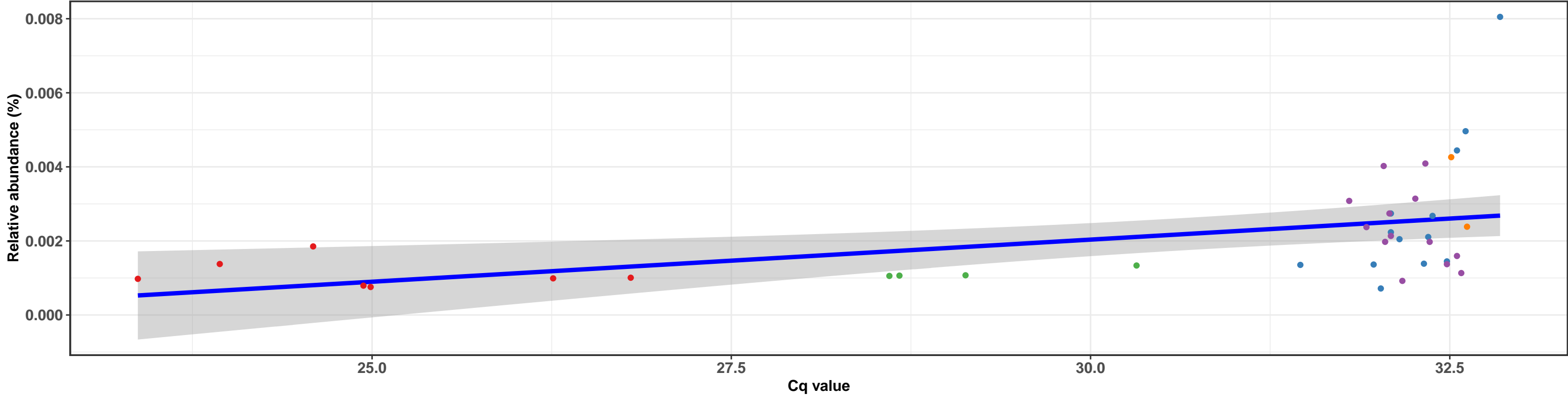
$\log_e(S) = 5.775$ ,  $p = 0.151$ ,  $\hat{\rho}_{\text{Spearman}} = -0.464$ ,  $\text{CI}_{95\%} [-1.067, 0.097]$ ,  $n_{\text{pairs}} = 11$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

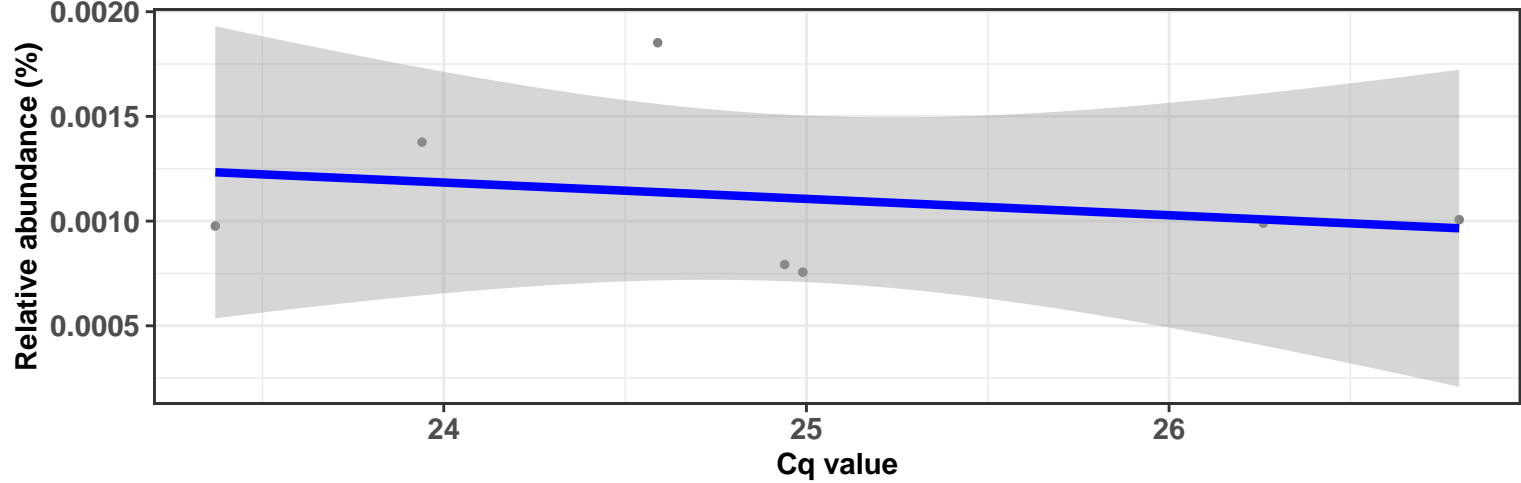
Correlation with all samples

$\log_e(S) = 8.286$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = 0.598$ ,  $\text{CI}_{95\%} [0.338, 0.866]$ ,  $n_{\text{pairs}} = 39$



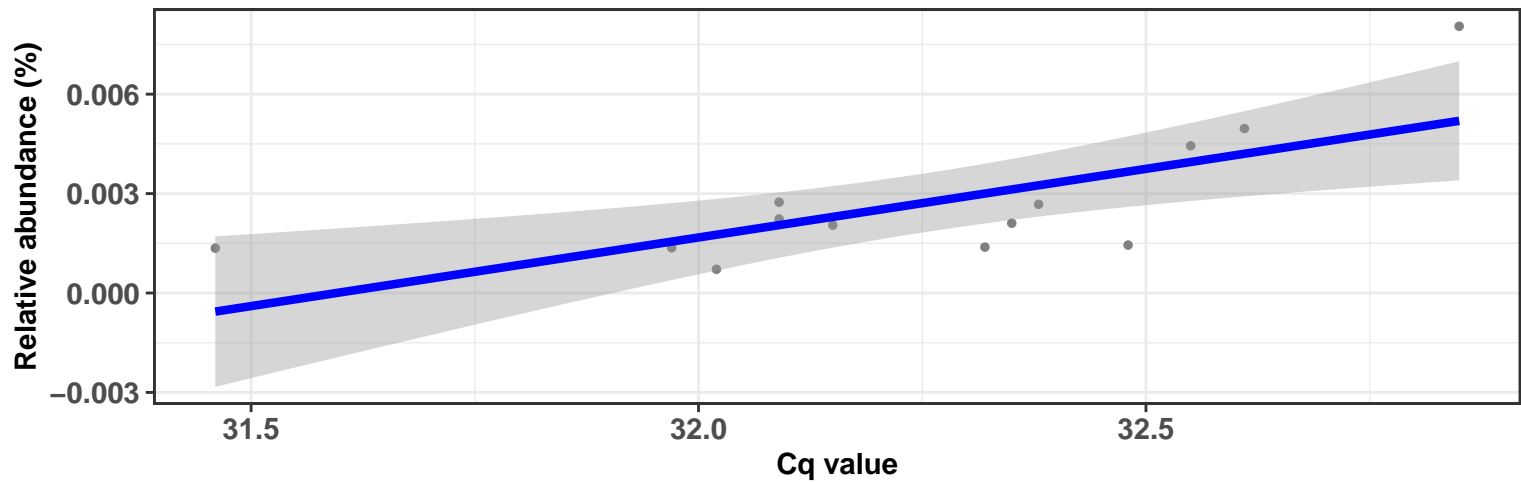
Correlation within: REF-DIC

$\log_e(S) = 4.159$ ,  $p = 0.760$ ,  $\hat{\rho}_{\text{Spearman}} = -0.143$ ,  $\text{CI}_{95\%} [-1.048, 0.617]$ ,  $n_{\text{pairs}} = 7$

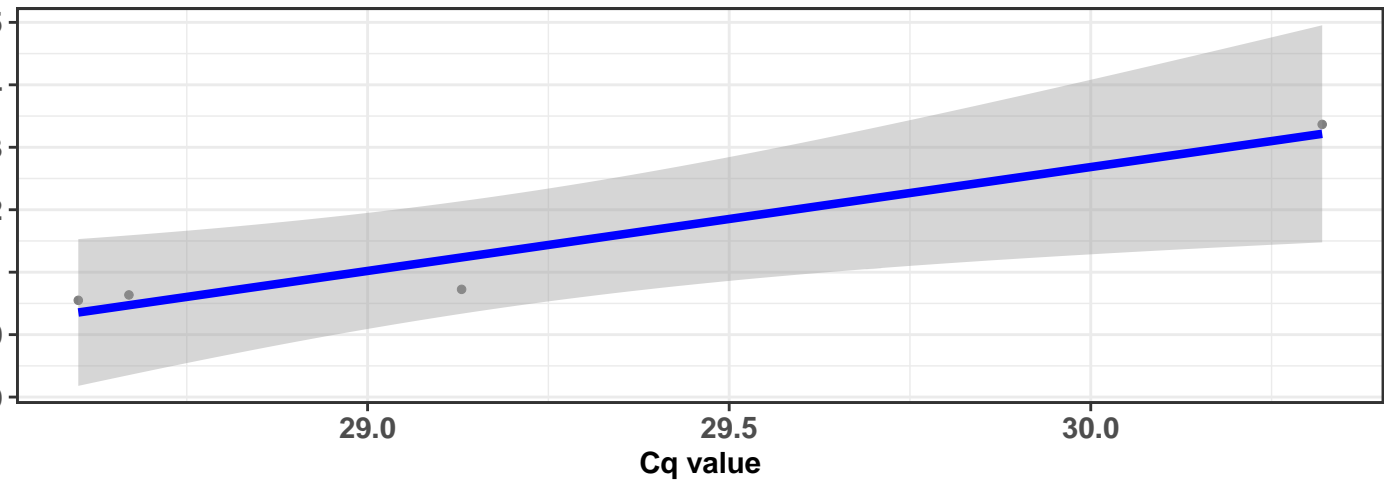


Correlation within: REF-DIM

$\log_e(S) = 4.426$ ,  $p = 0.002$ ,  $\hat{\rho}_{\text{Spearman}} = 0.770$ ,  $\text{CI}_{95\%} [0.491, 1.096]$ ,  $n_{\text{pairs}} = 13$

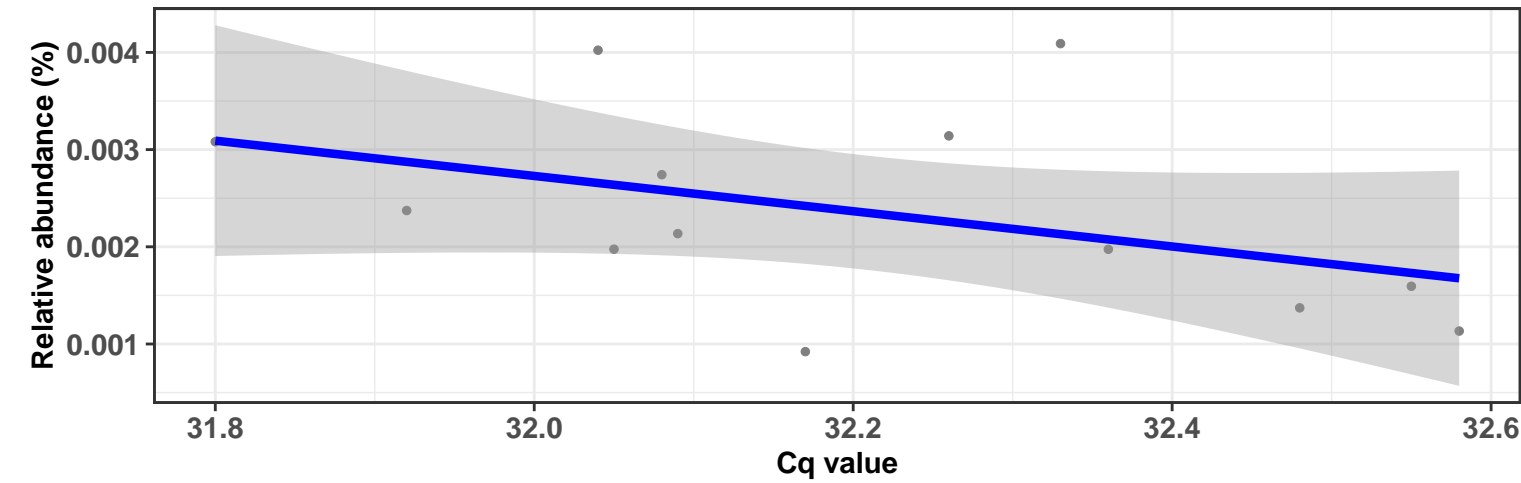


Correlation within: IM-DIC



Correlation within: IM-DIM

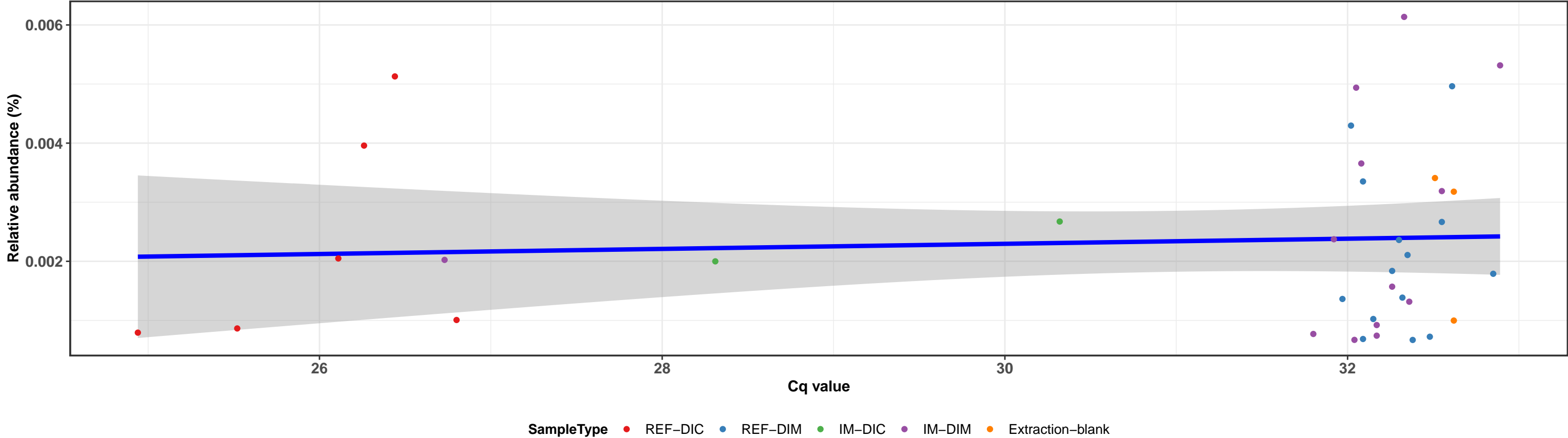
$\log_e(S) = 6.317$ ,  $p = 0.067$ ,  $\hat{\rho}_{\text{Spearman}} = -0.522$ ,  $\text{CI}_{95\%} [-1.050, -0.054]$ ,  $n_{\text{pairs}} = 13$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

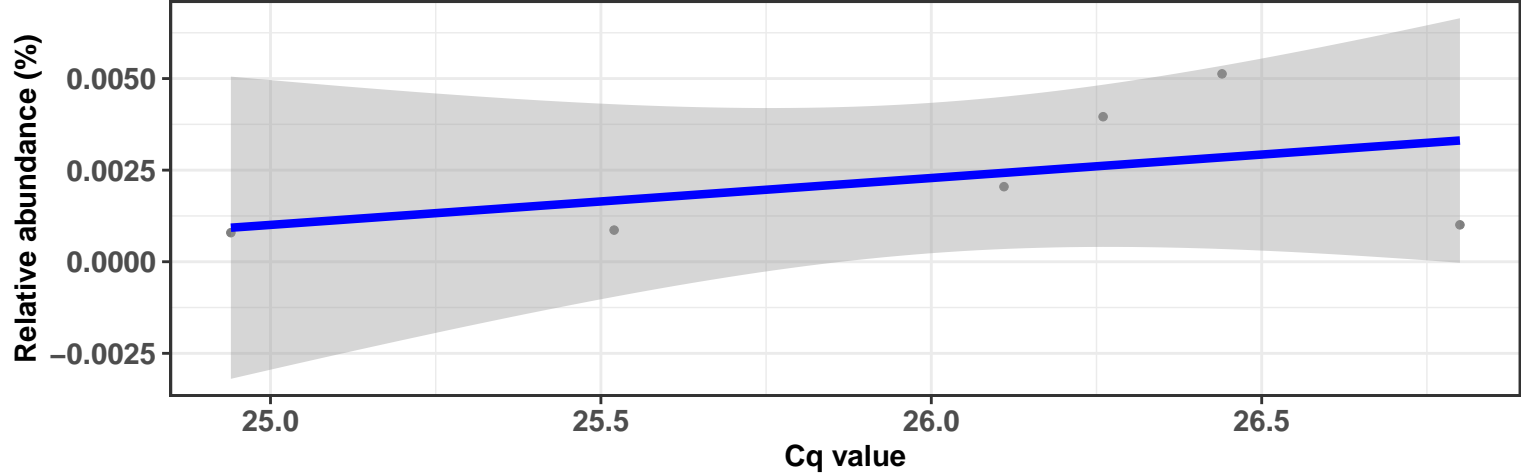
Correlation with all samples

$\log_e(S) = 8.996$ ,  $p = 0.483$ ,  $\hat{\rho}_{\text{Spearman}} = 0.117$ ,  $\text{CI}_{95\%} [-0.201, 0.410]$ ,  $n_{\text{pairs}} = 38$



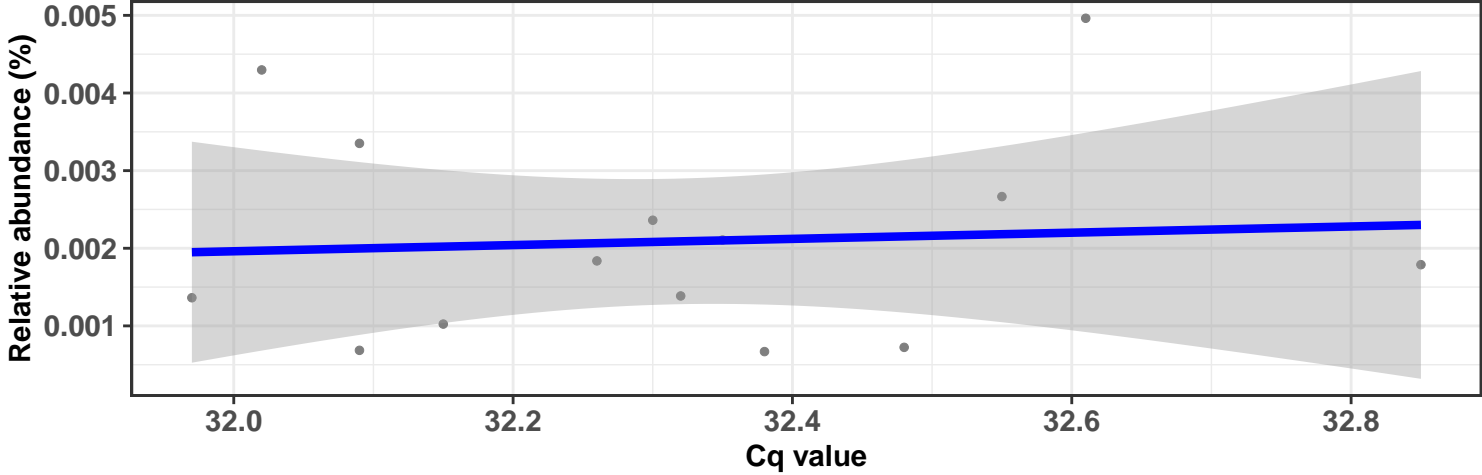
Correlation within: REF-DIC

$\log_e(S) = 2.485$ ,  $p = 0.156$ ,  $\hat{\rho}_{\text{Spearman}} = 0.657$ ,  $\text{CI}_{95\%} [-0.079, 1.271]$ ,  $n_{\text{pairs}} = 6$

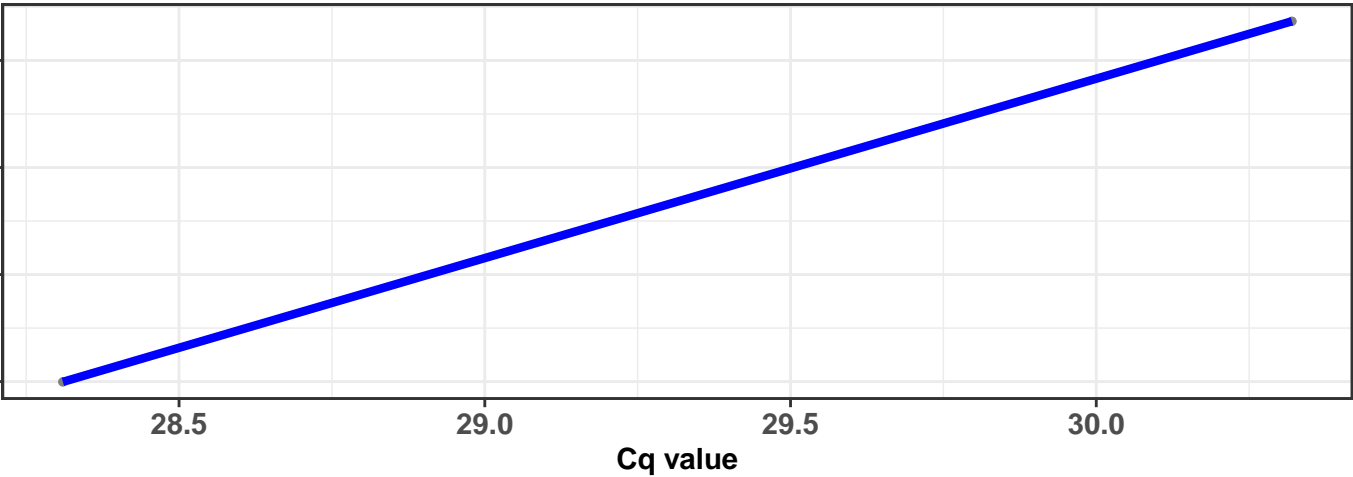


Correlation within: REF-DIM

$\log_e(S) = 6.054$ ,  $p = 0.828$ ,  $\hat{\rho}_{\text{Spearman}} = 0.064$ ,  $\text{CI}_{95\%} [-0.488, 0.641]$ ,  $n_{\text{pairs}} = 14$

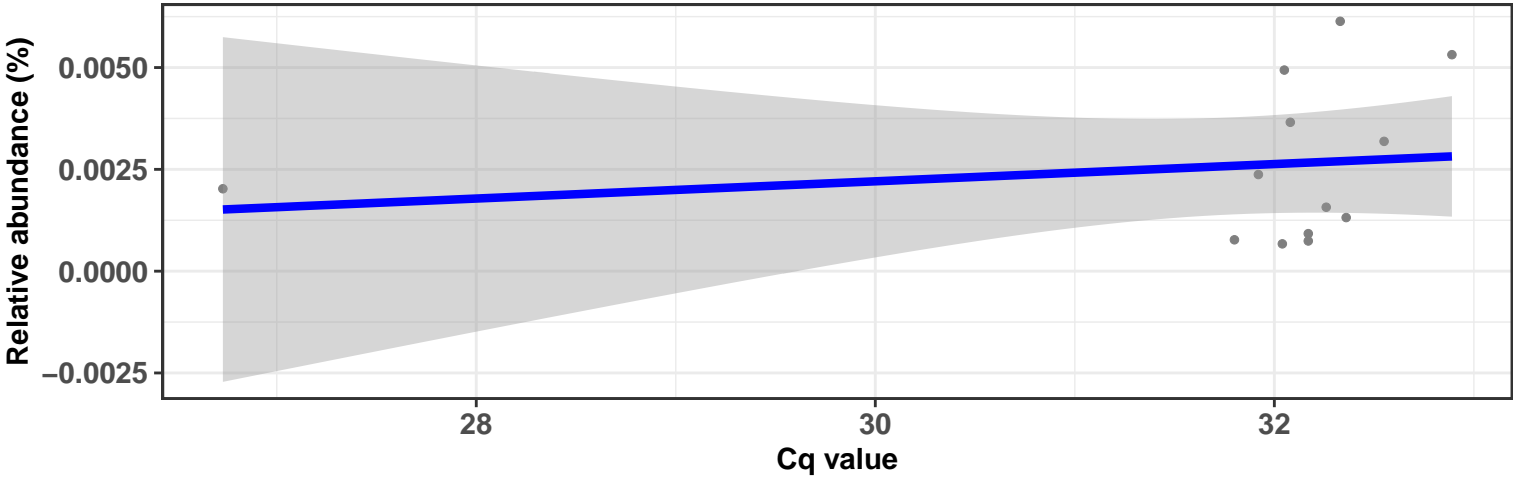


Correlation within: IM-DIC



Correlation within: IM-DIM

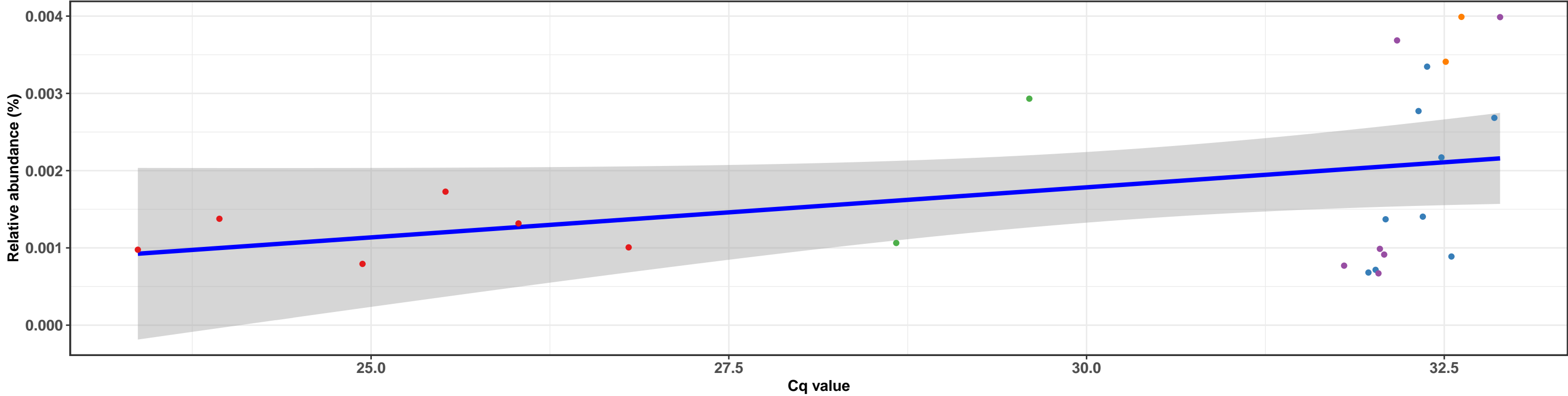
$\log_e(S) = 5.437$ ,  $p = 0.215$ ,  $\hat{\rho}_{\text{Spearman}} = 0.369$ ,  $\text{CI}_{95\%} [-0.111, 0.869]$ ,  $n_{\text{pairs}} = 13$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

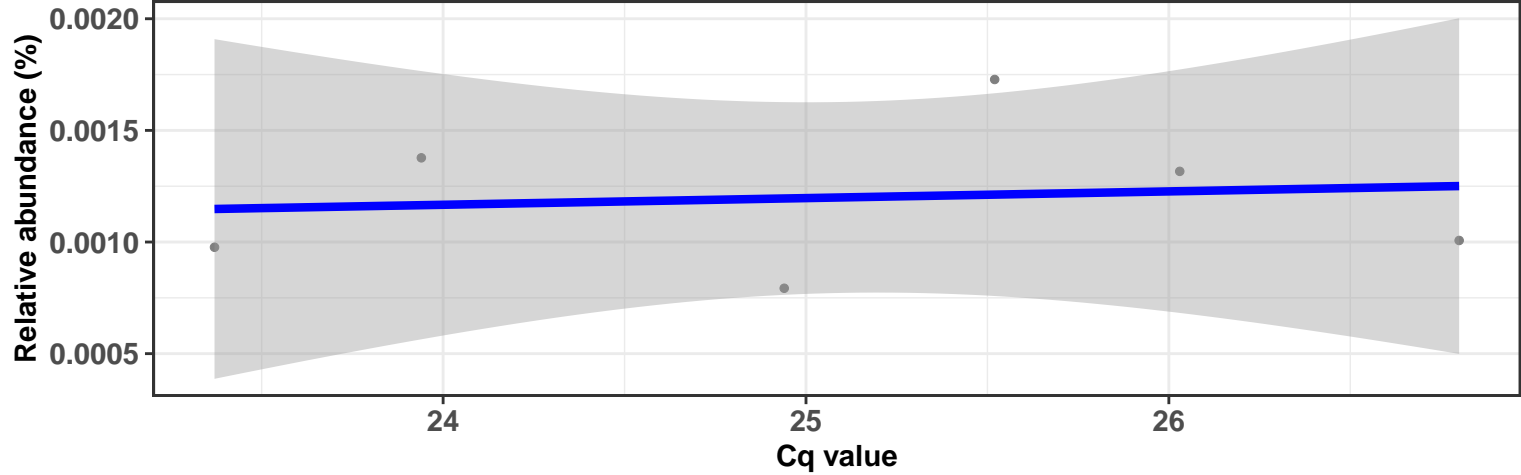
Correlation with all samples

$\log_e(S) = 7.156$ ,  $p = 0.010$ ,  $\hat{\rho}_{\text{Spearman}} = 0.507$ ,  $\text{CI}_{95\%} [0.199, 0.855]$ ,  $n_{\text{pairs}} = 25$



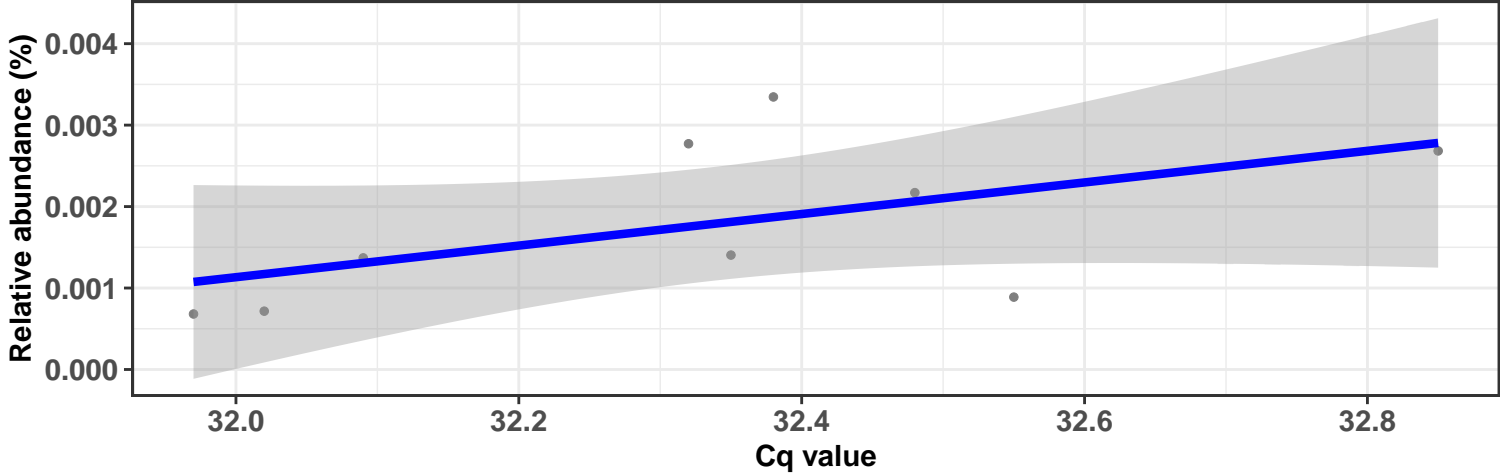
Correlation within: REF-DIC

$\log_e(S) = 3.332$ ,  $p = 0.704$ ,  $\hat{\rho}_{\text{Spearman}} = 0.200$ ,  $\text{CI}_{95\%} [-0.706, 1.269]$ ,  $n_{\text{pairs}} = 6$

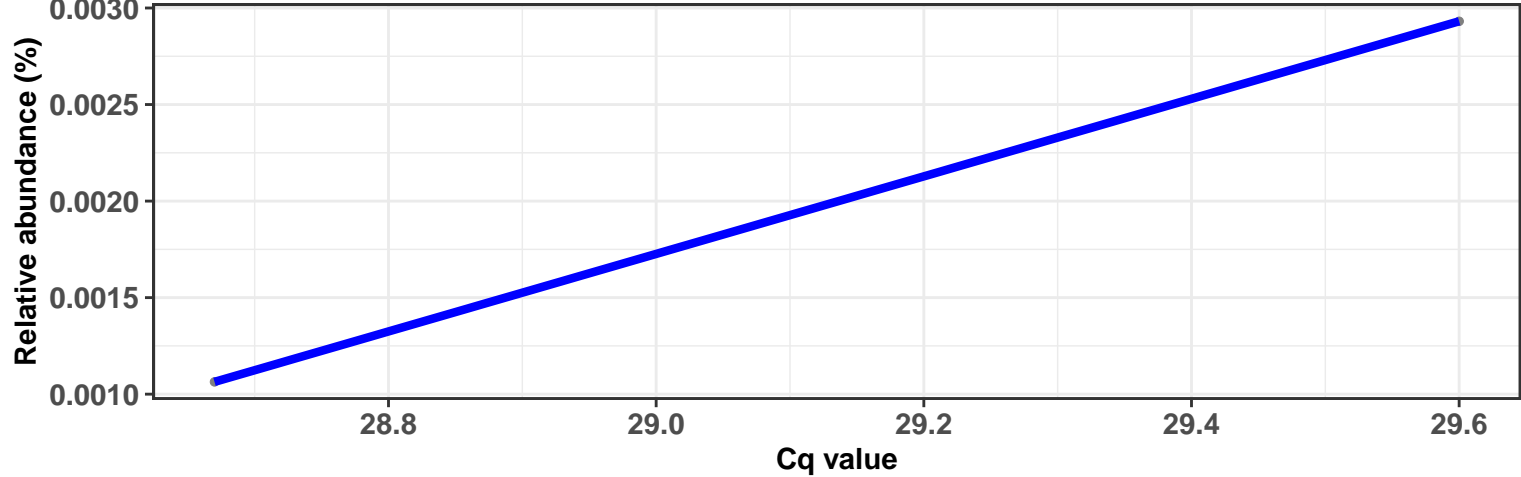


Correlation within: REF-DIM

$\log_e(S) = 4.025$ ,  $p = 0.139$ ,  $\hat{\rho}_{\text{Spearman}} = 0.533$ ,  $\text{CI}_{95\%} [-0.144, 1.215]$ ,  $n_{\text{pairs}} = 9$

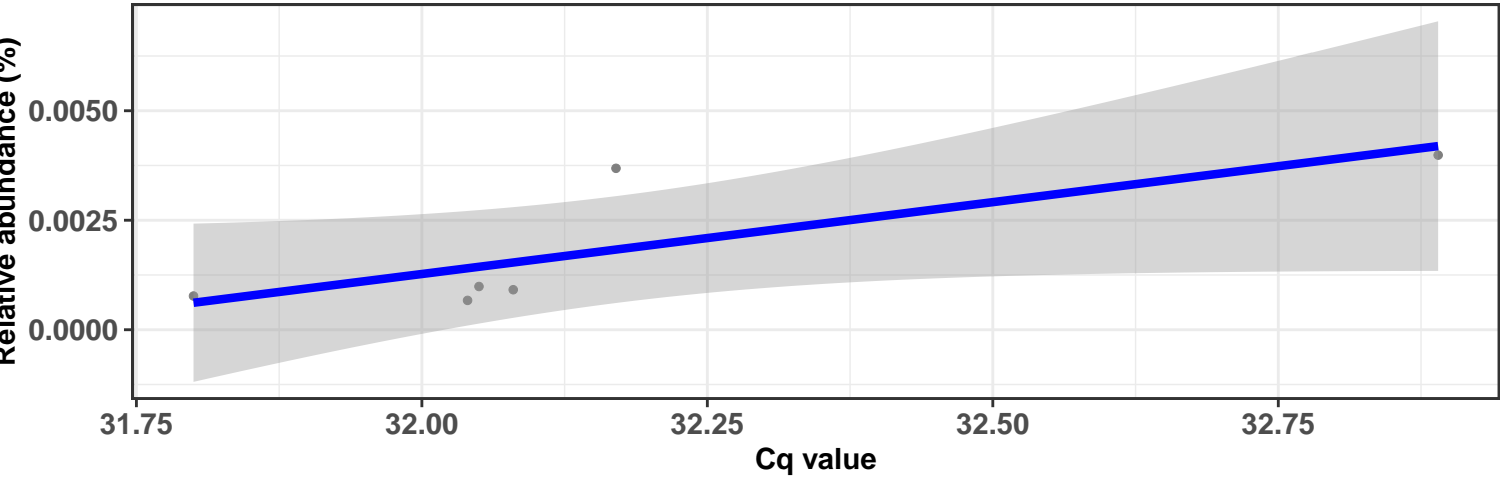


Correlation within: IM-DIC



Correlation within: IM-DIM

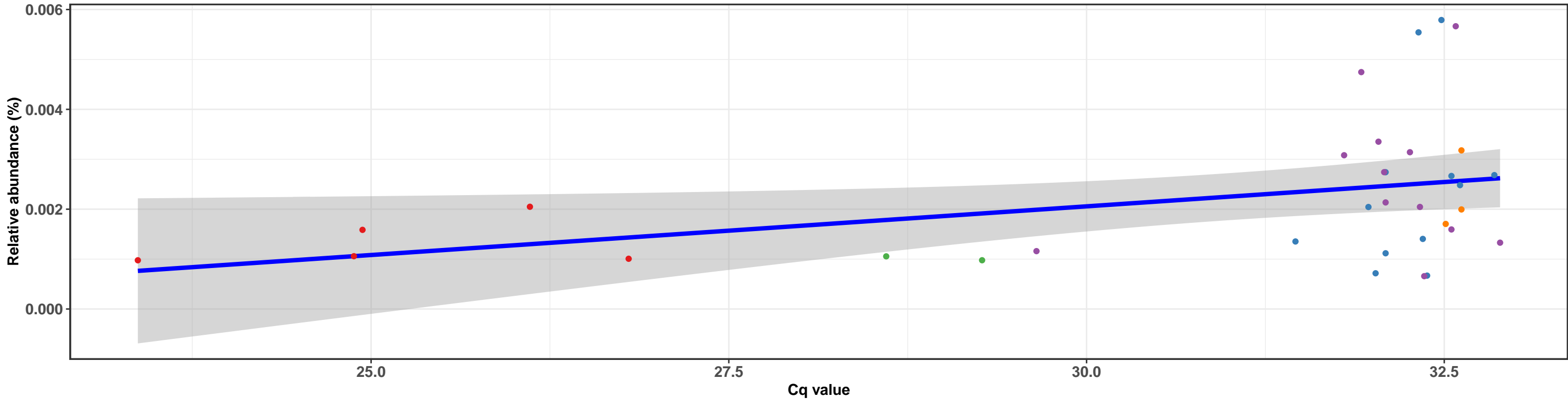
$\log_e(S) = 1.386$ ,  $p = 0.019$ ,  $\hat{\rho}_{\text{Spearman}} = 0.886$ ,  $\text{CI}_{95\%} [0.436, 1.497]$ ,  $n_{\text{pairs}} = 6$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

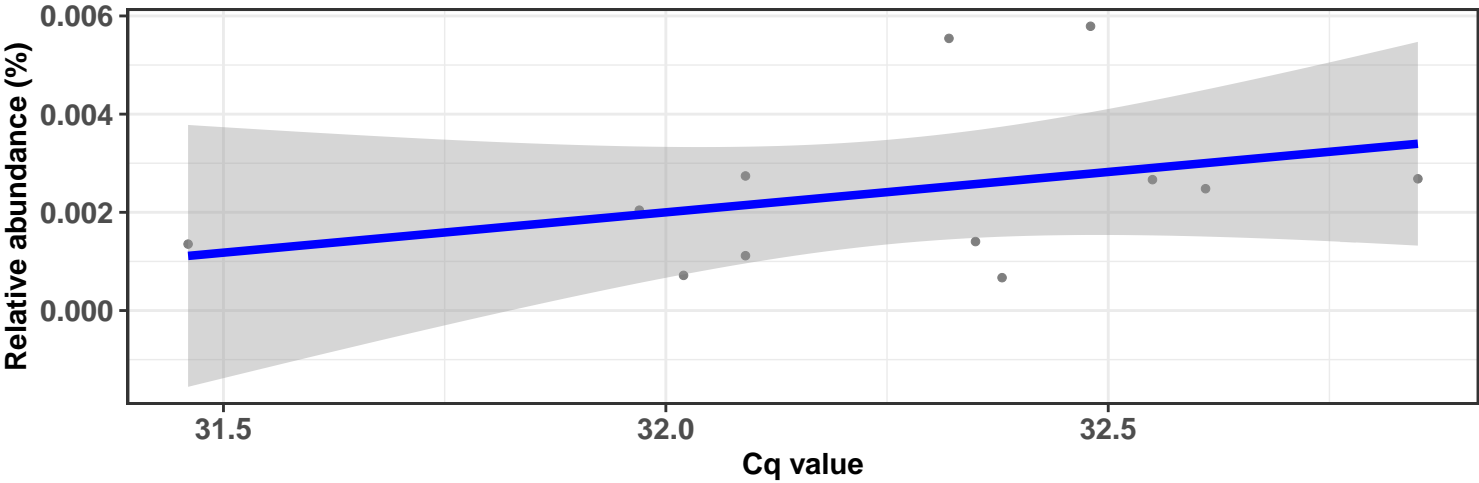
Correlation with all samples

$\log_e(S) = 8.374$ ,  $p = 0.050$ ,  $\hat{\rho}_{\text{Spearman}} = 0.338$ ,  $\text{CI}_{95\%} [0.034, 0.718]$ ,  $n_{\text{pairs}} = 34$



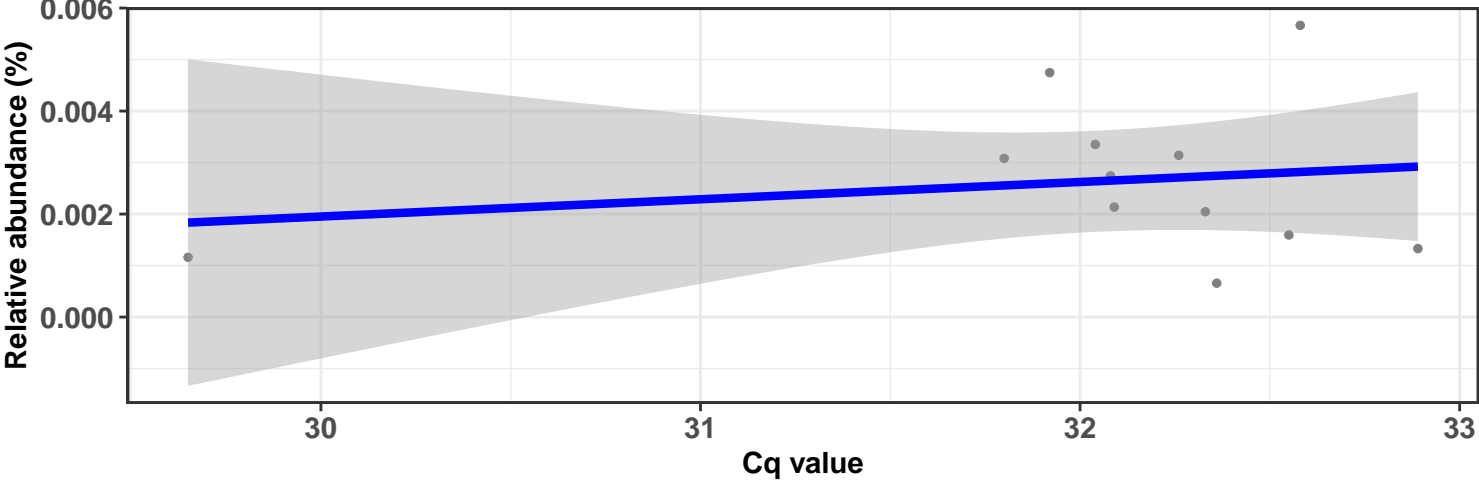
Correlation within: REF-DIM

$\log_e(S) = 5.164$ ,  $p = 0.212$ ,  $\hat{\rho}_{\text{Spearman}} = 0.389$ ,  $\text{CI}_{95\%} [-0.059, 0.887]$ ,  $n_{\text{pairs}} = 12$

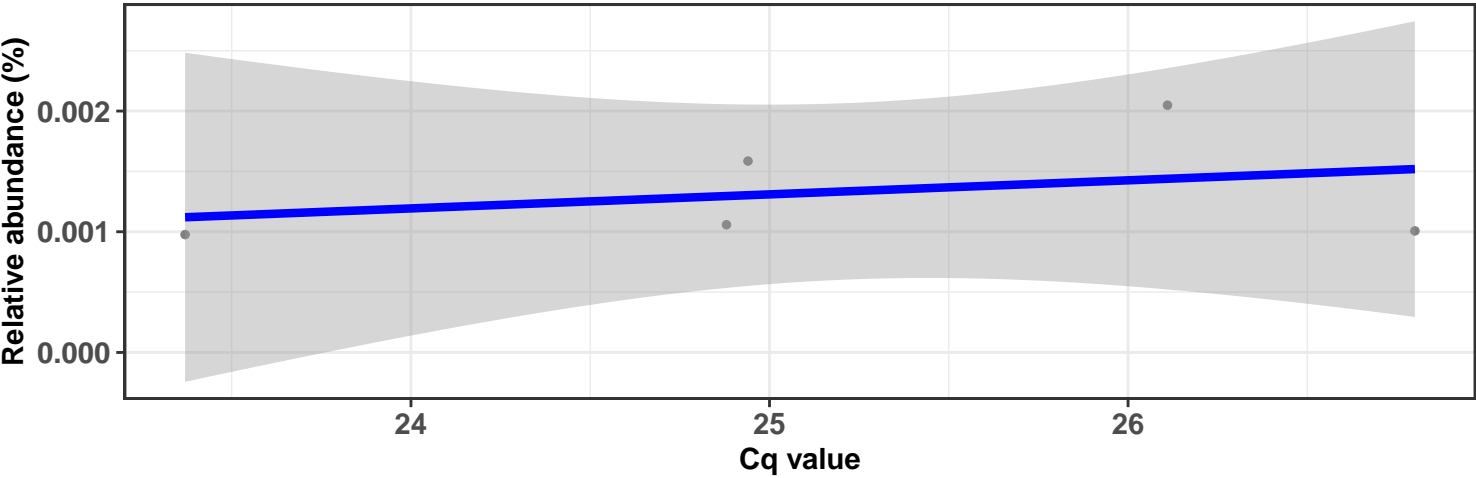


Correlation within: IM-DIM

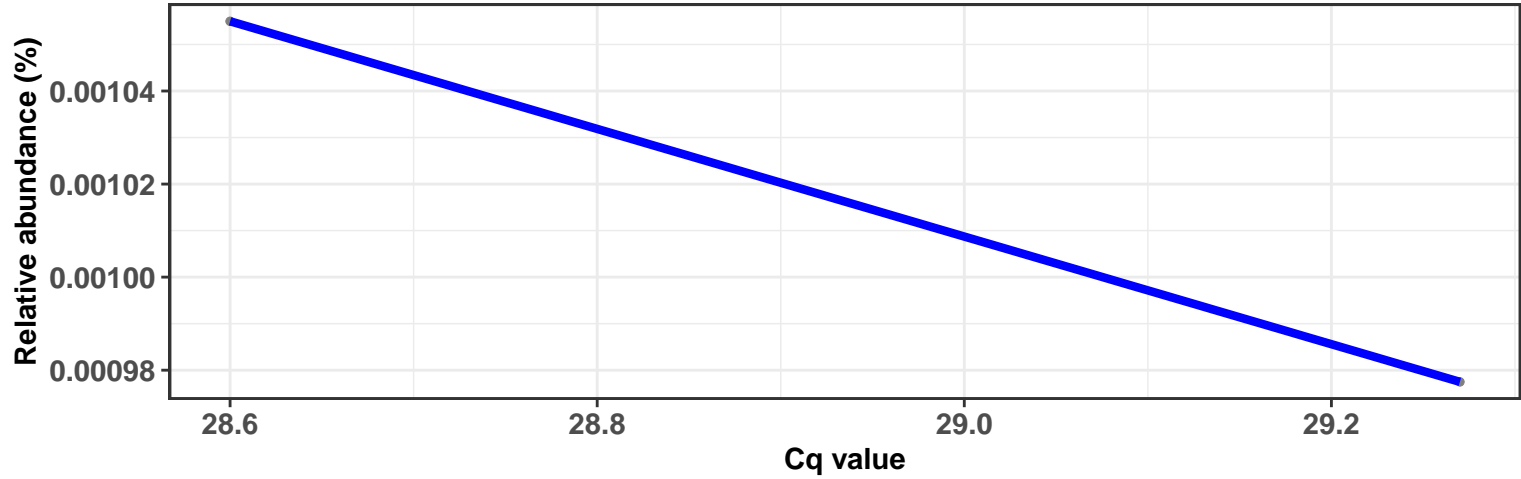
$\log_e(S) = 5.817$ ,  $p = 0.587$ ,  $\hat{\rho}_{\text{Spearman}} = -0.175$ ,  $\text{CI}_{95\%} [-0.874, 0.602]$ ,  $n_{\text{pairs}} = 12$



Correlation within: REF-DIC



Correlation within: IM-DIC

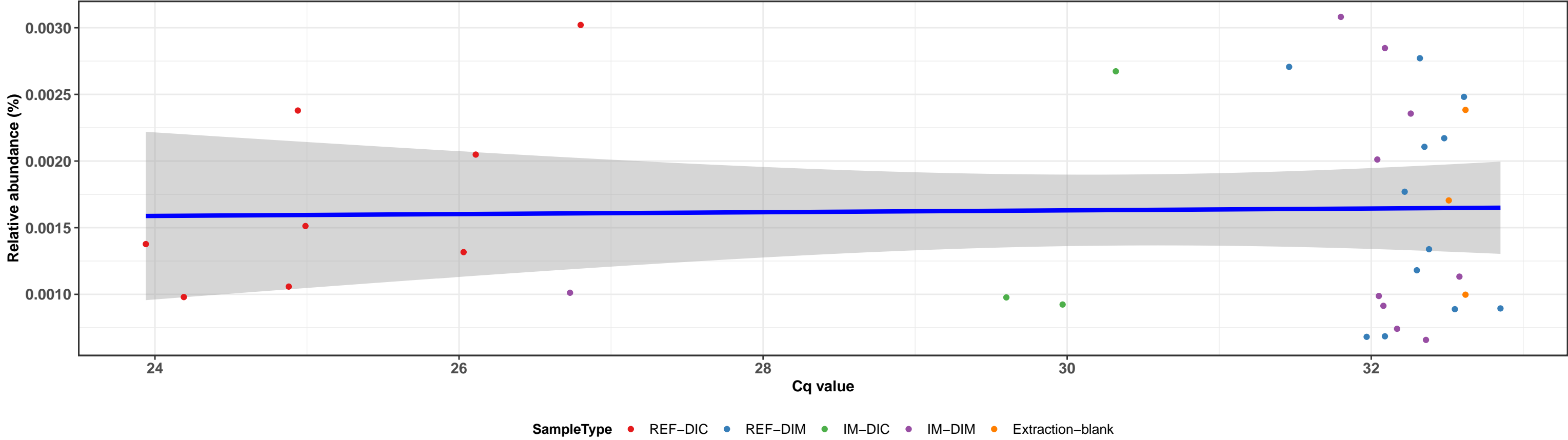




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

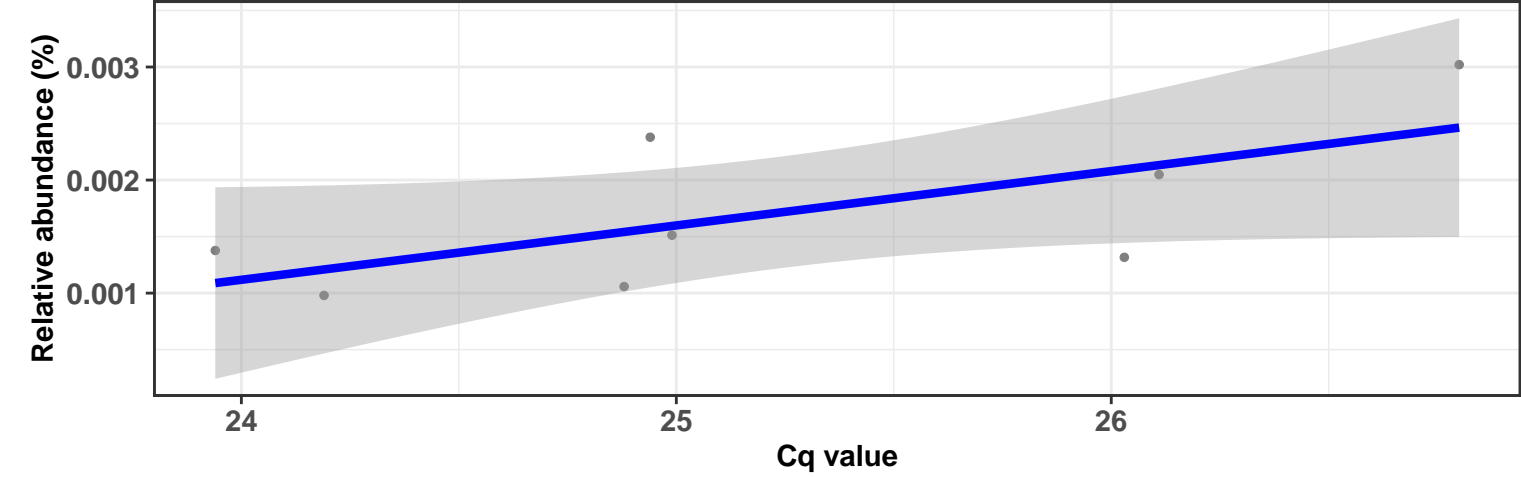
Correlation with all samples

$\log_e(S) = 9.013$ ,  $p = 0.745$ ,  $\hat{\rho}_{\text{Spearman}} = -0.056$ ,  $\text{CI}_{95\%} [-0.369, 0.246]$ ,  $n_{\text{pairs}} = 36$



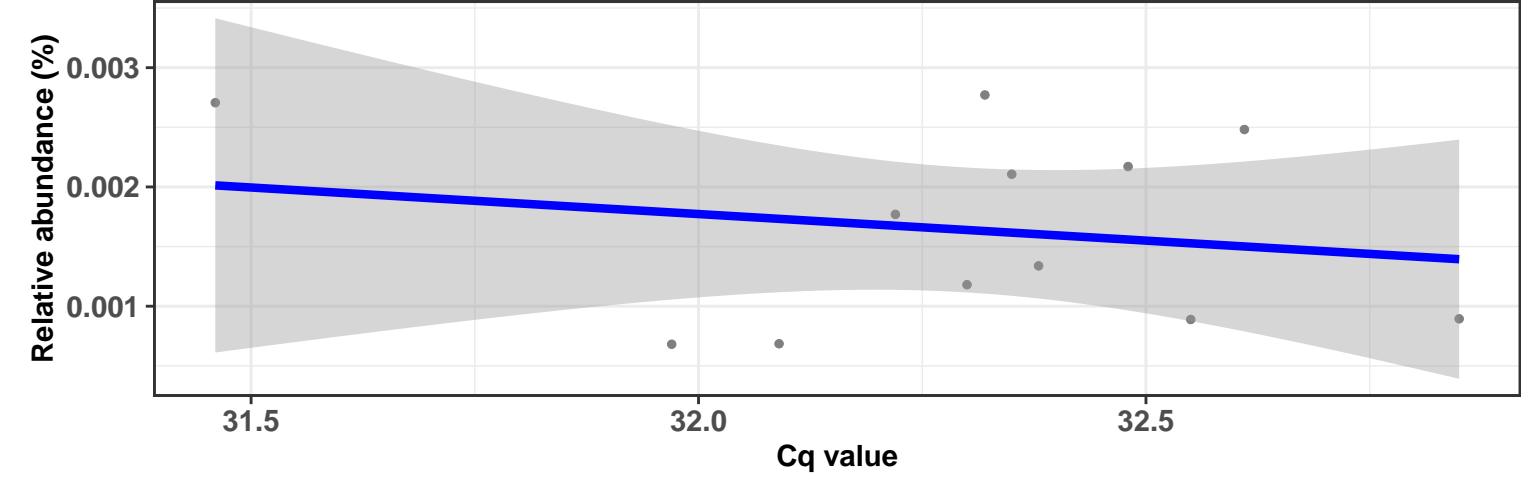
Correlation within: REF-DIC

$\log_e(S) = 3.401$ ,  $p = 0.086$ ,  $\hat{\rho}_{\text{Spearman}} = 0.643$ ,  $\text{CI}_{95\%} [0.139, 1.215]$ ,  $n_{\text{pairs}} = 8$

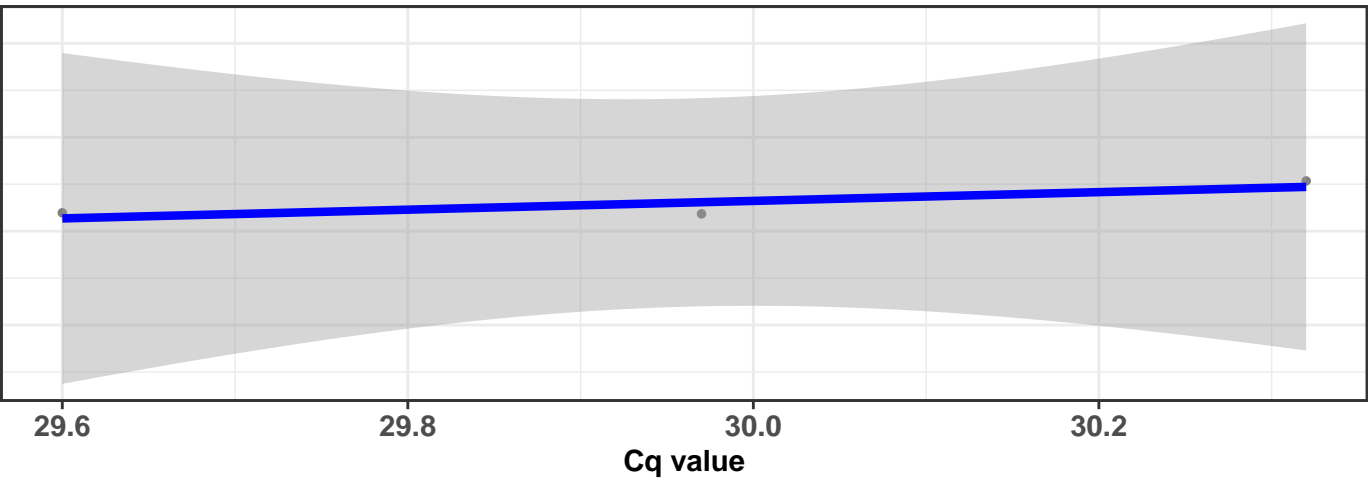


Correlation within: REF-DIM

$\log_e(S) = 5.583$ ,  $p = 0.829$ ,  $\hat{\rho}_{\text{Spearman}} = 0.070$ ,  $\text{CI}_{95\%} [-0.682, 0.685]$ ,  $n_{\text{pairs}} = 12$

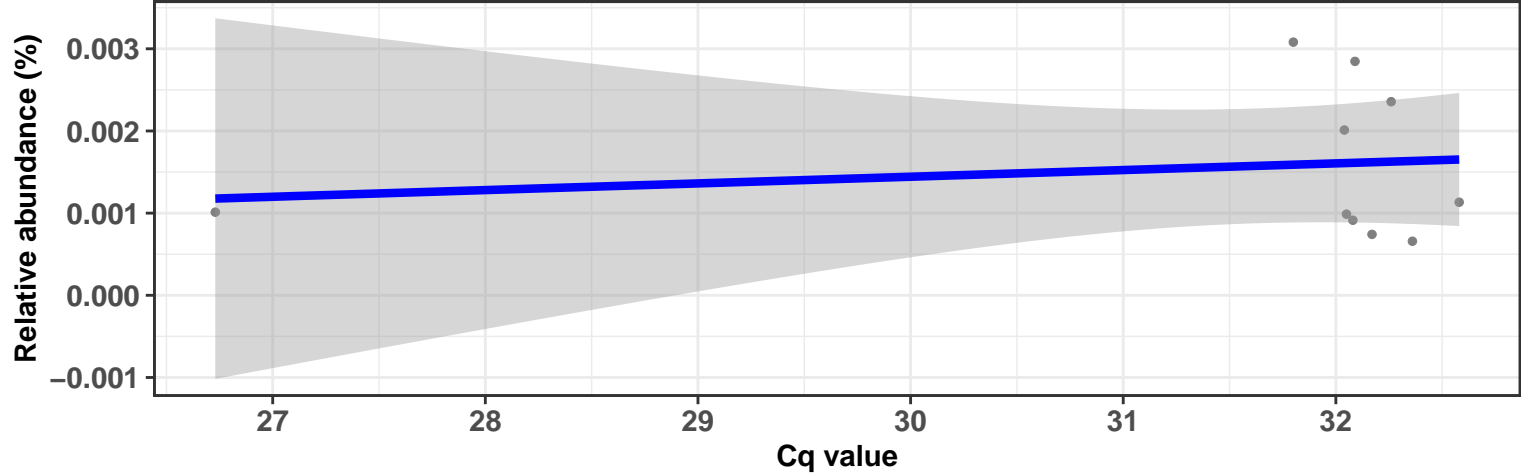


Correlation within: IM-DIC



Correlation within: IM-DIM

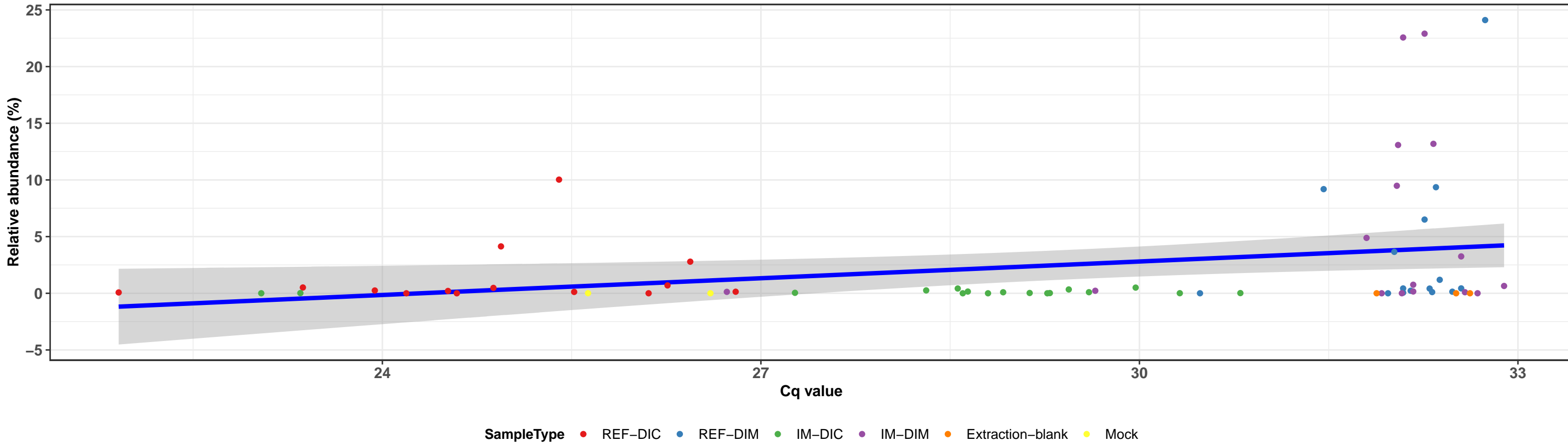
$\log_e(S) = 5.366$ ,  $p = 0.405$ ,  $\hat{\rho}_{\text{Spearman}} = -0.297$ ,  $\text{CI}_{95\%} [-0.994, 0.406]$ ,  $n_{\text{pairs}} = 10$



k\_\_Bacteria; p\_\_Spirochaetes; c\_\_Spirochaetia; o\_\_Spirochaetales; f\_\_Spirochaetaceae; NA; NA

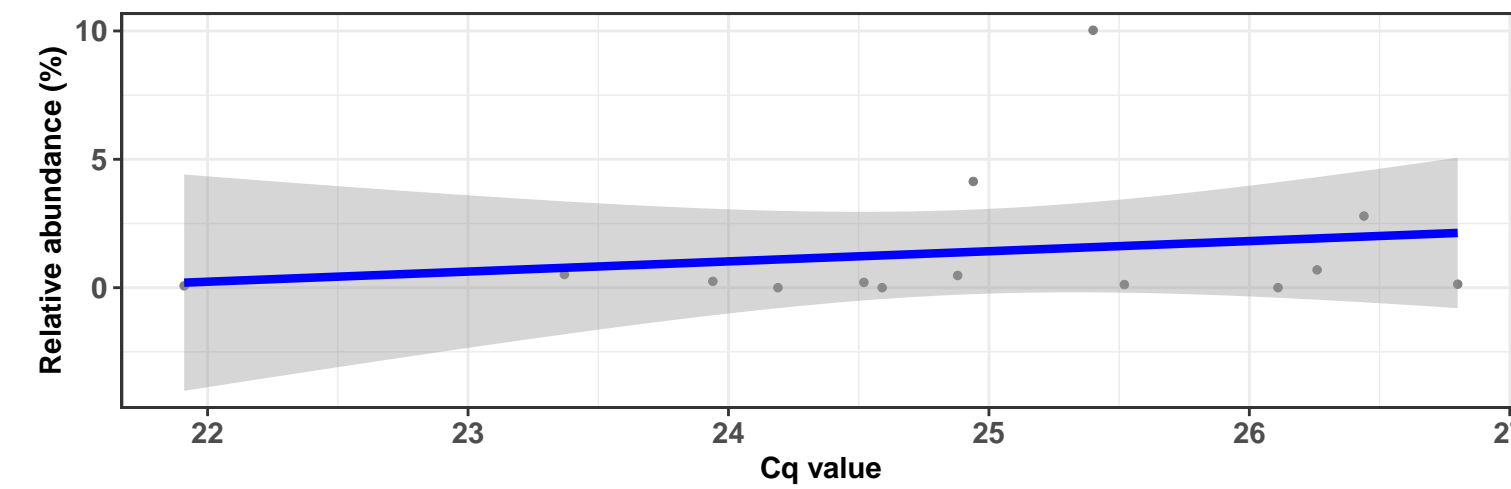
### Correlation with all samples

$\log_e(S) = 10.544$ ,  $p = 0.048$ ,  $\hat{\rho}_{\text{Spearman}} = 0.243$ ,  $\text{CI}_{95\%} [0.003, 0.487]$ ,  $n_{\text{pairs}} = 67$



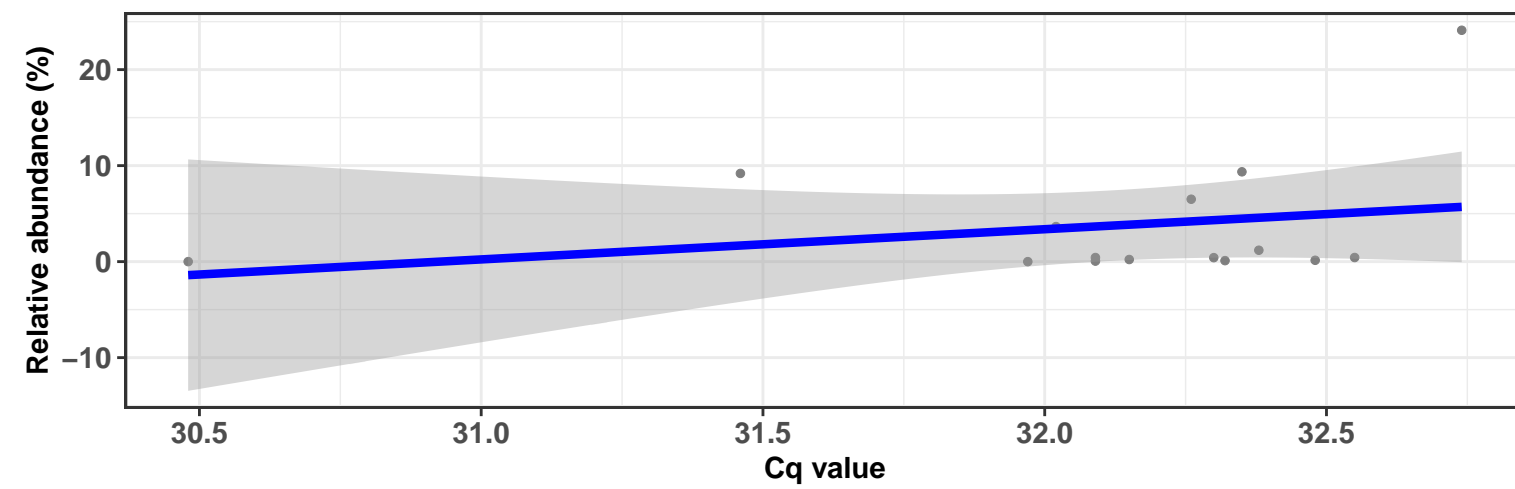
### Correlation within: REF-DIC

$\log_e(S) = 5.829$ ,  $p = 0.383$ ,  $\hat{\rho}_{\text{Spearman}} = 0.253$ ,  $\text{CI}_{95\%} [-0.219, 0.708]$ ,  $n_{\text{pairs}} = 14$



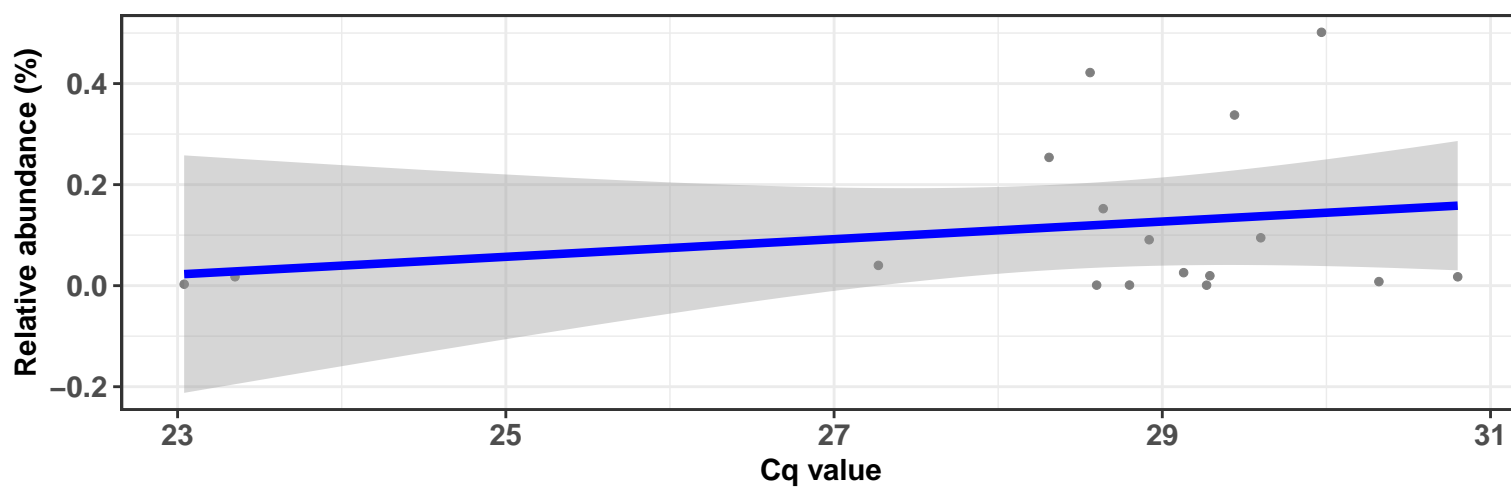
### Correlation within: REF-DIM

$\log_e(S) = 5.849$ ,  $p = 0.162$ ,  $\hat{\rho}_{\text{Spearman}} = 0.381$ ,  $\text{CI}_{95\%} [-0.137, 0.965]$ ,  $n_{\text{pairs}} = 15$



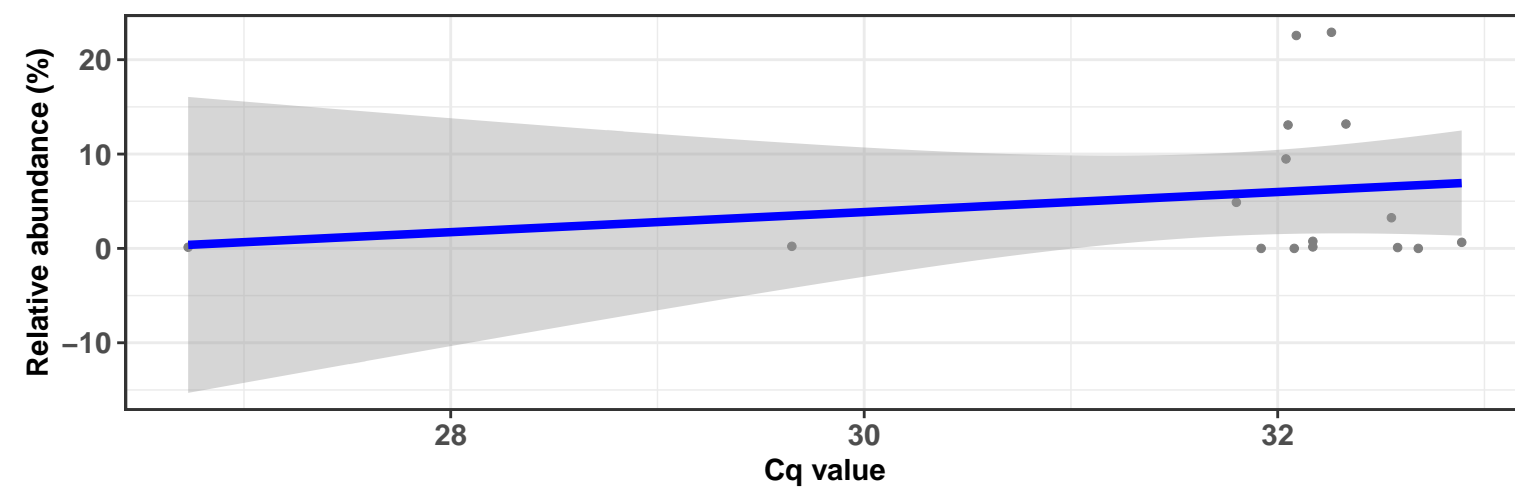
### Correlation within: IM-DIC

$\log_e(S) = 6.628$ ,  $p = 0.779$ ,  $\hat{\rho}_{\text{Spearman}} = 0.074$ ,  $\text{CI}_{95\%} [-0.461, 0.611]$ ,  $n_{\text{pairs}} = 17$



### Correlation within: IM-DIM

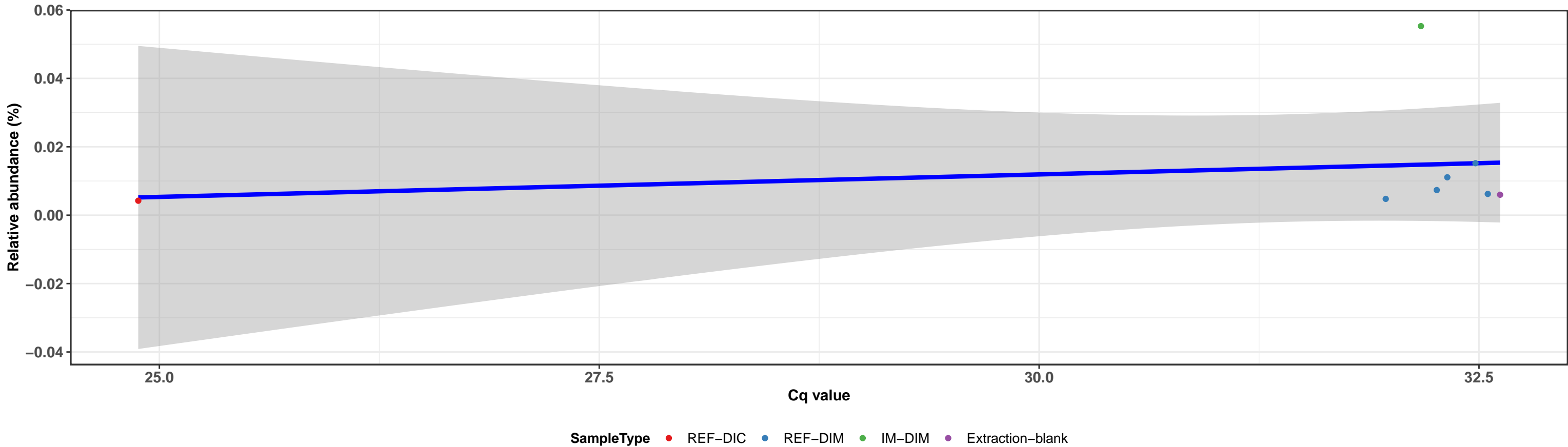
$\log_e(S) = 6.494$ ,  $p = 0.918$ ,  $\hat{\rho}_{\text{Spearman}} = 0.028$ ,  $\text{CI}_{95\%} [-0.509, 0.529]$ ,  $n_{\text{pairs}} = 16$



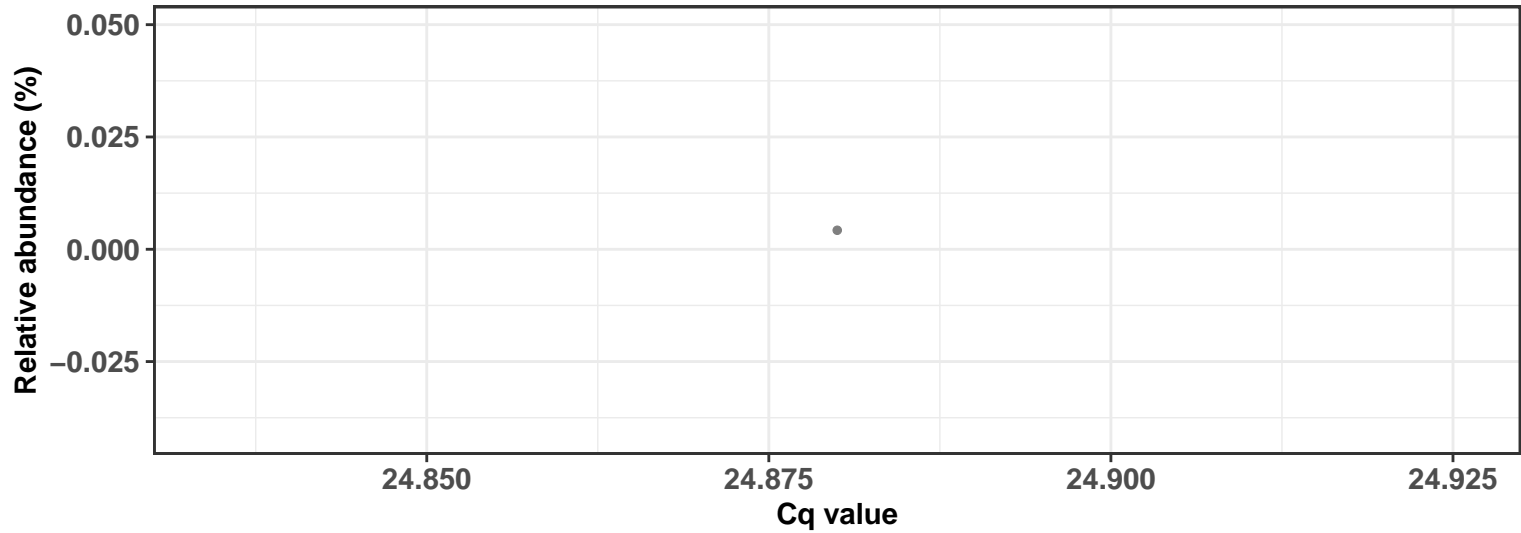
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Caulobacterales; f\_\_Caulobacteraceae; g\_\_Brevundimonas; NA

Correlation with all samples

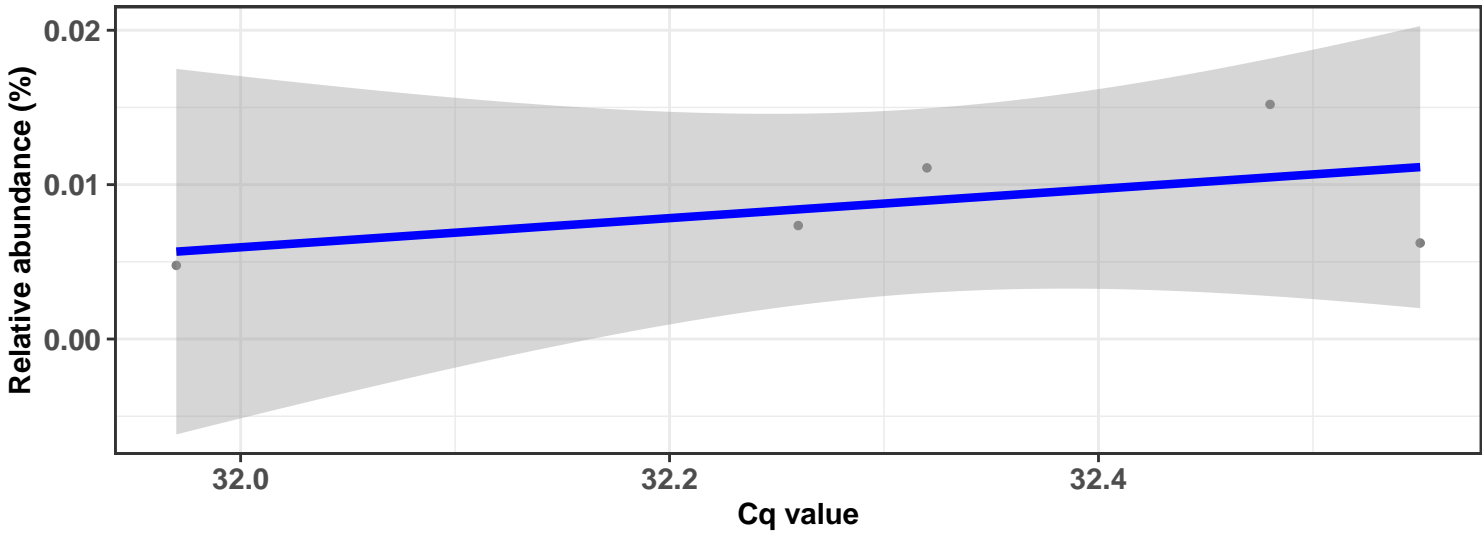
$\log_e(S) = 4.127$ ,  $p = 0.531$ ,  $\hat{\rho}_{\text{Spearman}} = 0.262$ ,  $\text{CI}_{95\%} [-0.683, 1.222]$ ,  $n_{\text{pairs}} = 8$



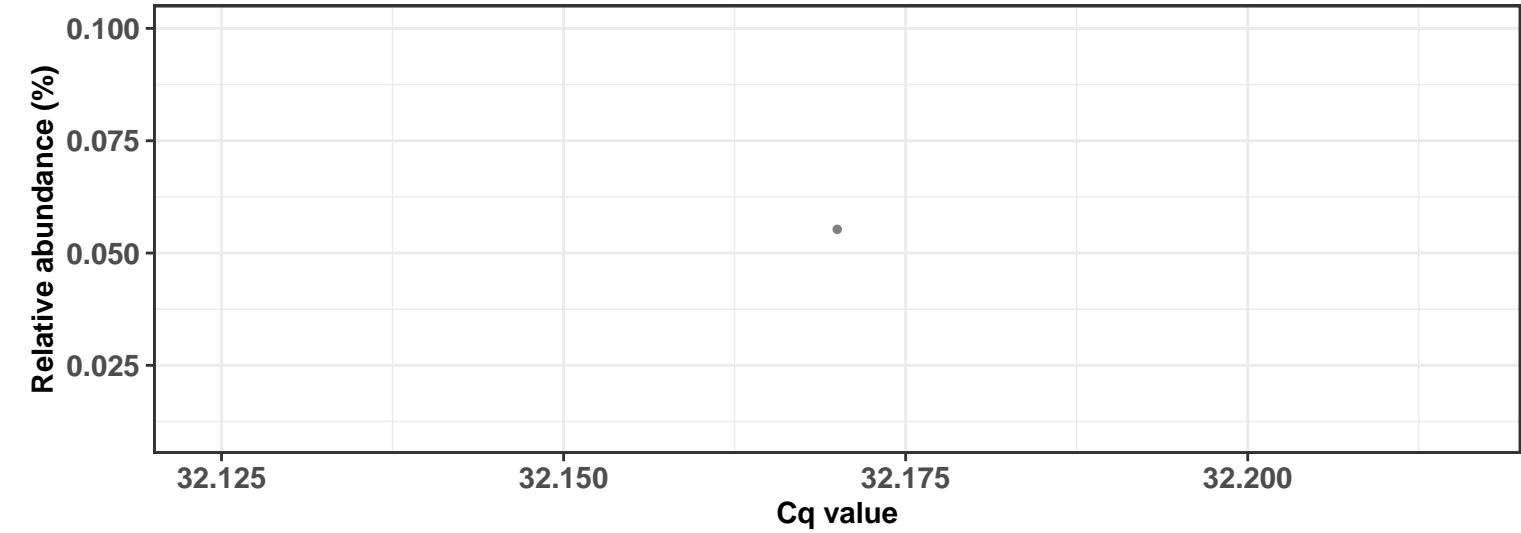
Correlation within: REF-DIC



Correlation within: REF-DIM



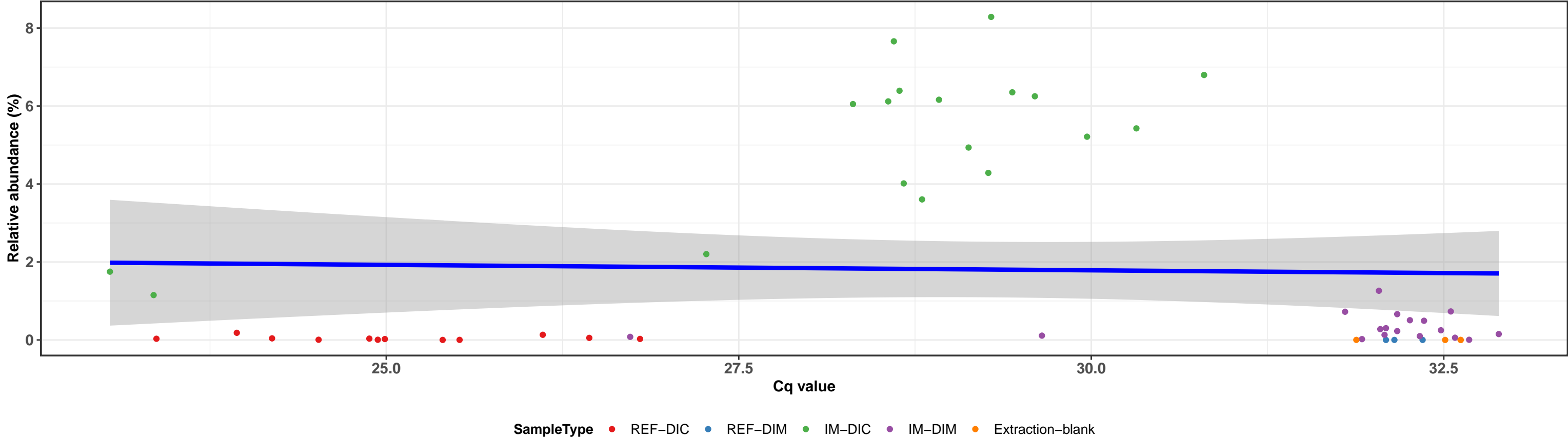
Correlation within: IM-DIM



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

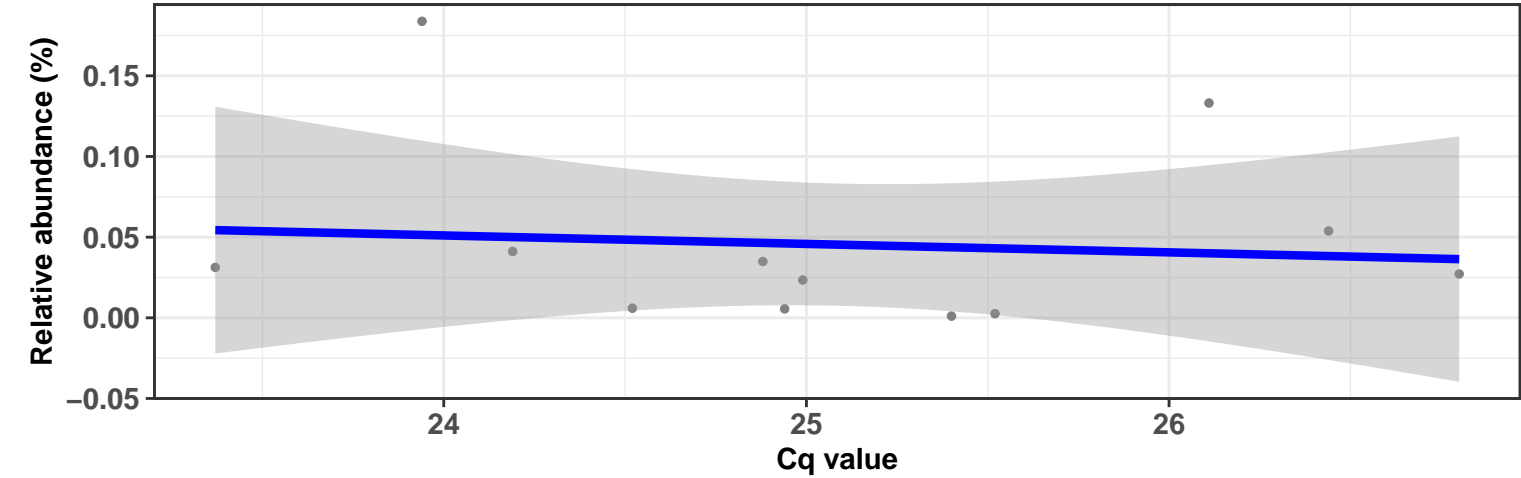
Correlation with all samples

$\log_e(S) = 10.372$ ,  $p = 0.267$ ,  $\hat{\rho}_{\text{Spearman}} = -0.152$ ,  $\text{CI}_{95\%} [-0.444, 0.133]$ ,  $n_{\text{pairs}} = 55$

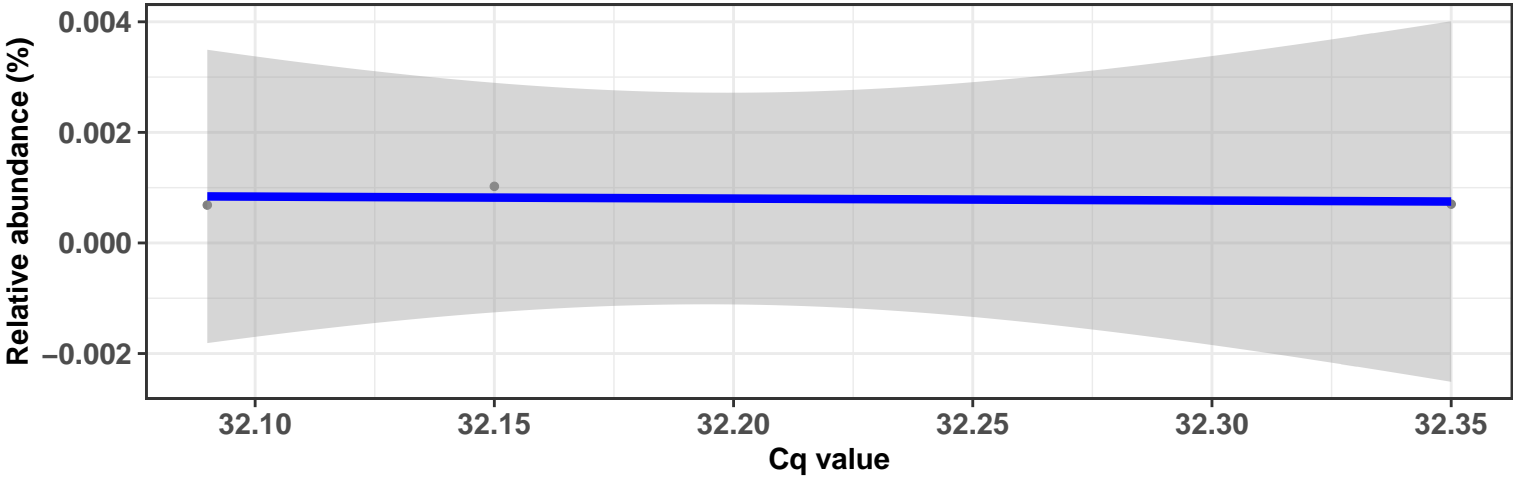


Correlation within: REF-DIC

$\log_e(S) = 5.799$ ,  $p = 0.633$ ,  $\hat{\rho}_{\text{Spearman}} = -0.154$ ,  $\text{CI}_{95\%} [-0.741, 0.406]$ ,  $n_{\text{pairs}} = 12$

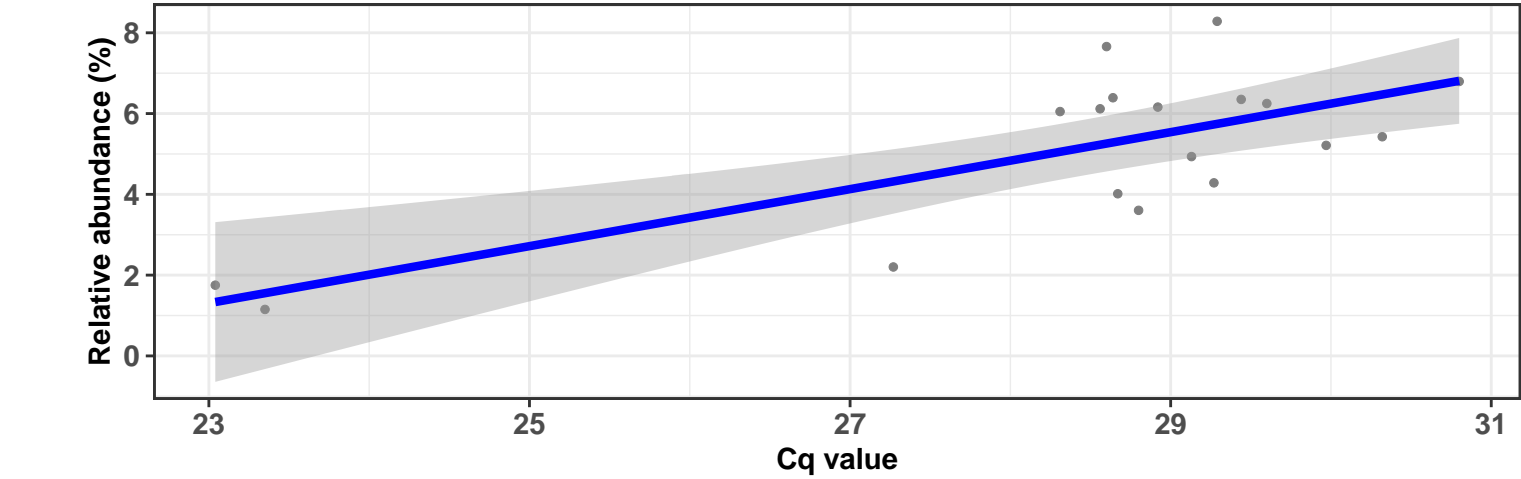


Correlation within: REF-DIM



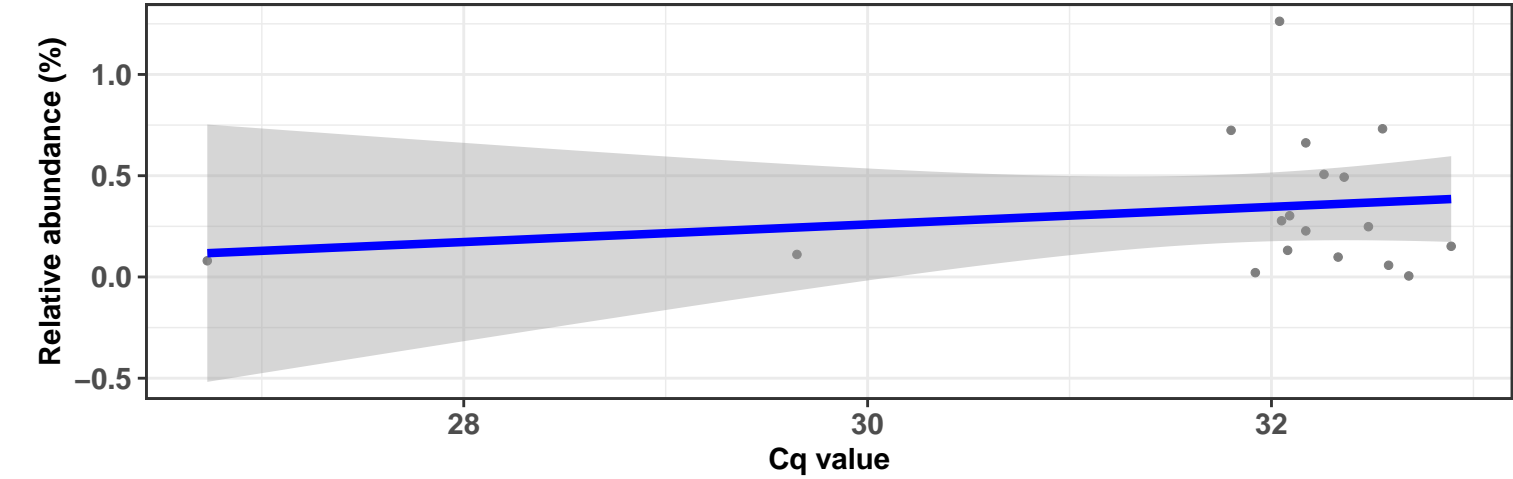
Correlation within: IM-DIC

$\log_e(S) = 6.234$ ,  $p = 0.047$ ,  $\hat{\rho}_{\text{Spearman}} = 0.474$ ,  $\text{CI}_{95\%} [0.127, 0.879]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

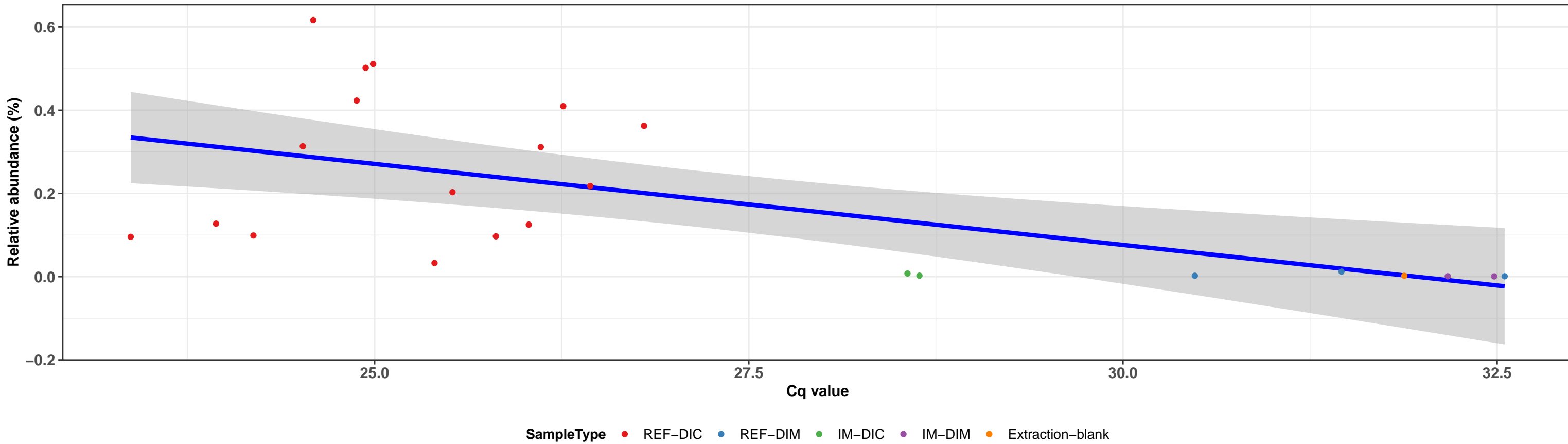
$\log_e(S) = 6.949$ ,  $p = 0.766$ ,  $\hat{\rho}_{\text{Spearman}} = -0.075$ ,  $\text{CI}_{95\%} [-0.545, 0.509]$ ,  $n_{\text{pairs}} = 18$



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Family XI; g\_\_Tepidimicrobium; s\_\_Tepidimicrobium sp. GRC1

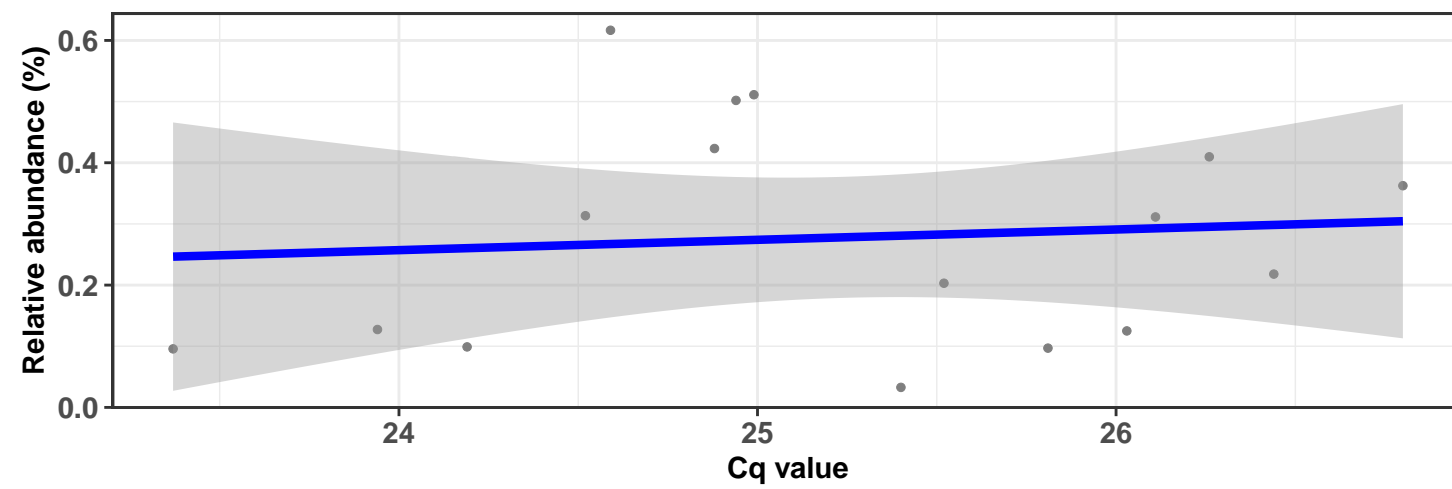
### Correlation with all samples

$\log_e(S) = 8.250$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.664$ ,  $\text{CI}_{95\%} [-0.980, -0.421]$ ,  $n_{\text{pairs}} = 24$

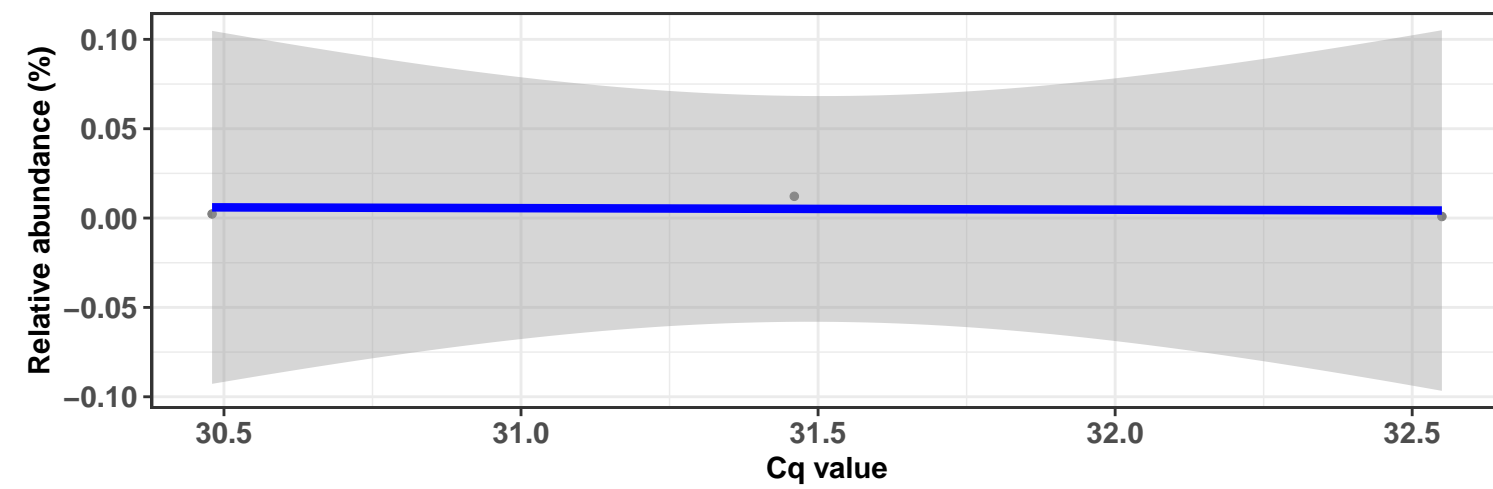


### Correlation within: REF-DIC

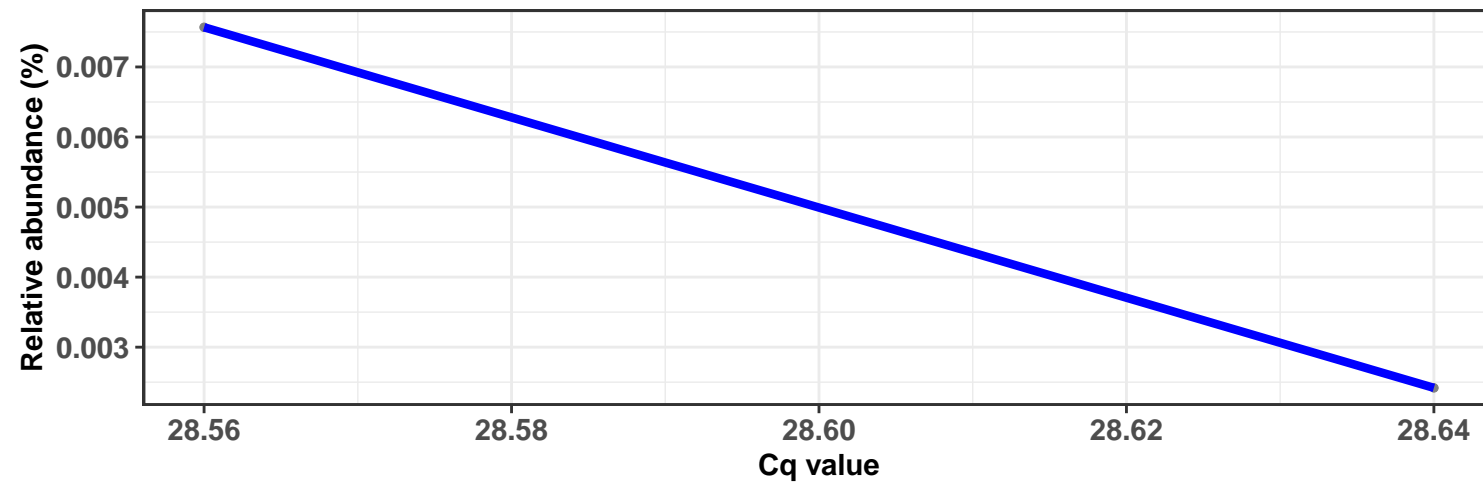
$\log_e(S) = 6.400$ ,  $p = 0.672$ ,  $\hat{\rho}_{\text{Spearman}} = 0.115$ ,  $\text{CI}_{95\%} [-0.330, 0.626]$ ,  $n_{\text{pairs}} = 16$



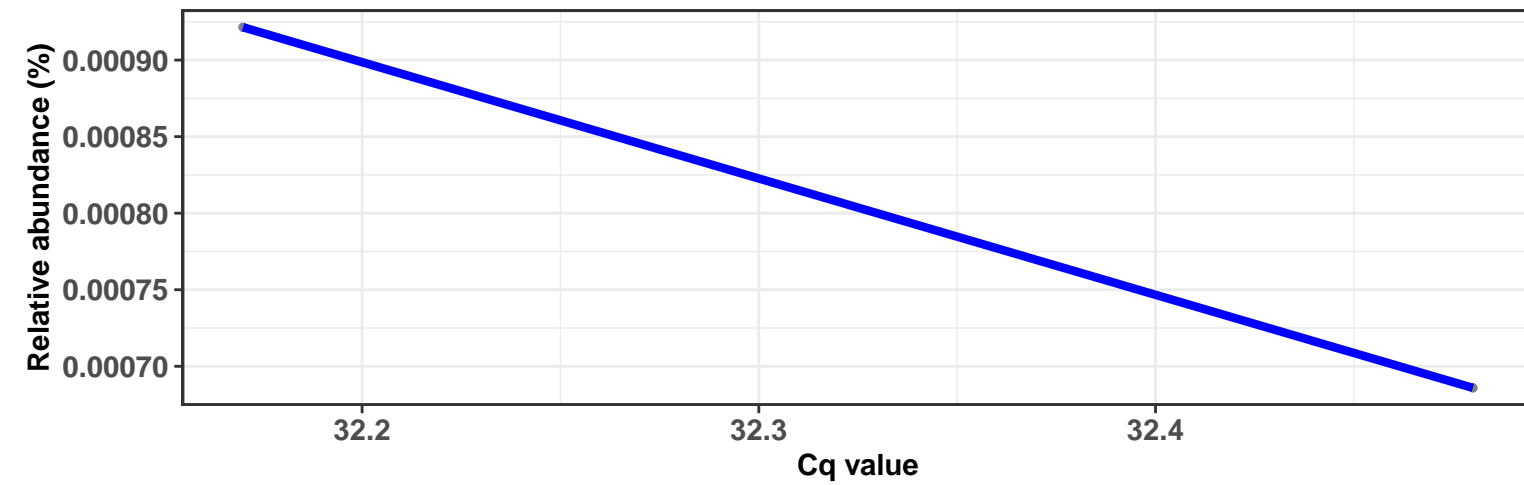
### Correlation within: REF-DIM



### Correlation within: IM-DIC



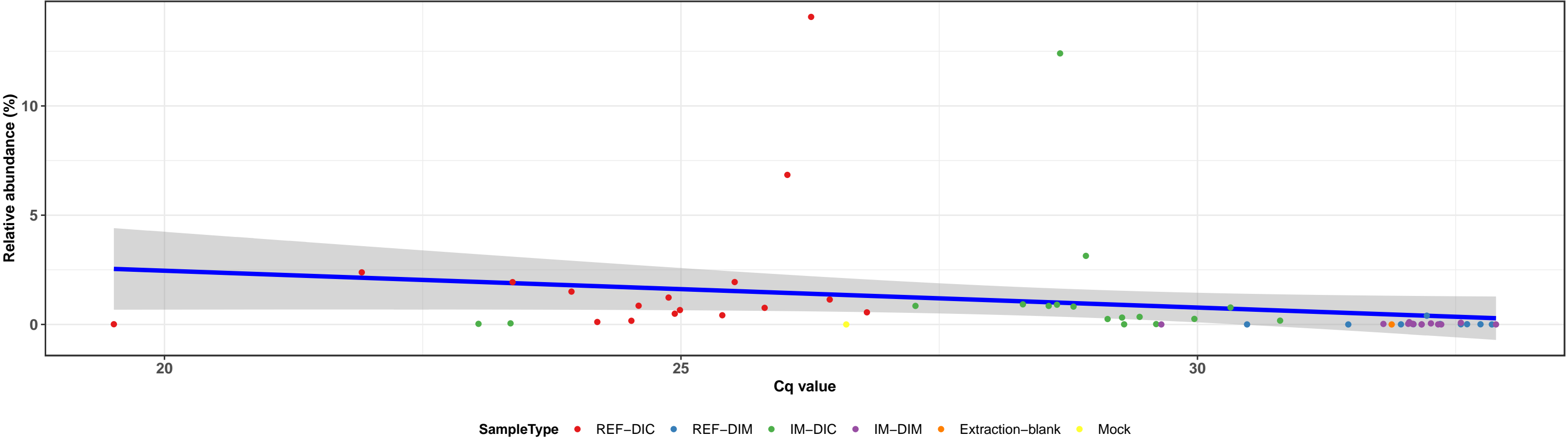
### Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Tenericutes; c\_\_Mollicutes; o\_\_Mycoplasmatales; f\_\_Mycoplasmataceae; g\_\_Mycoplasma; s\_\_uncultured bacterium

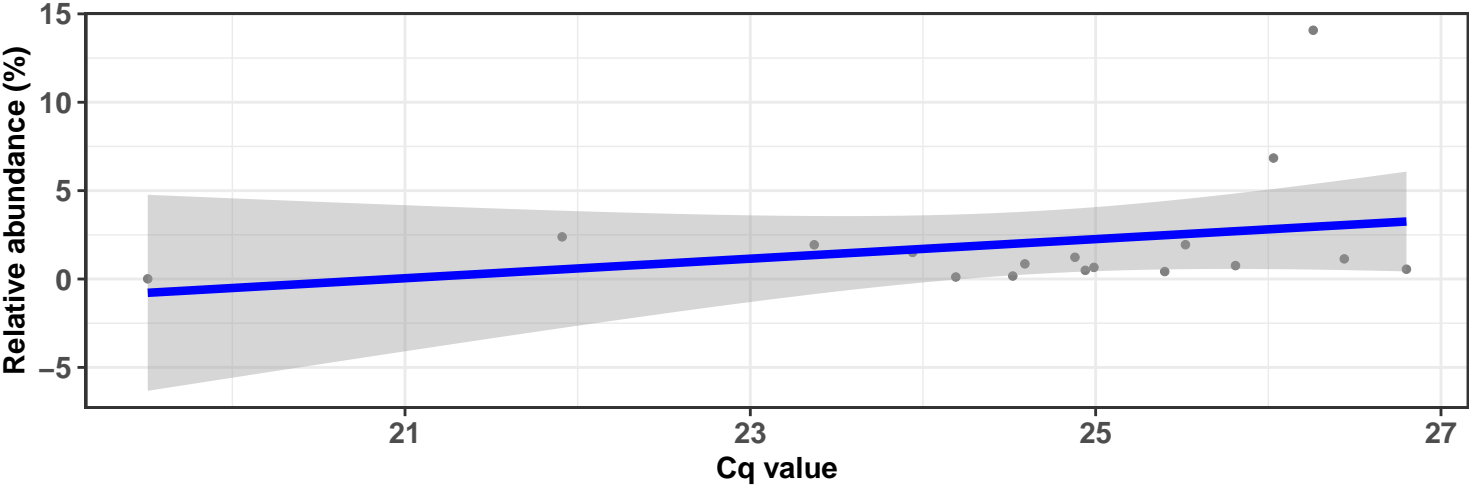
Correlation with all samples

$\log_e(S) = 10.967$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.609$ ,  $CI_{95\%} [-0.766, -0.471]$ ,  $n_{\text{pairs}} = 60$



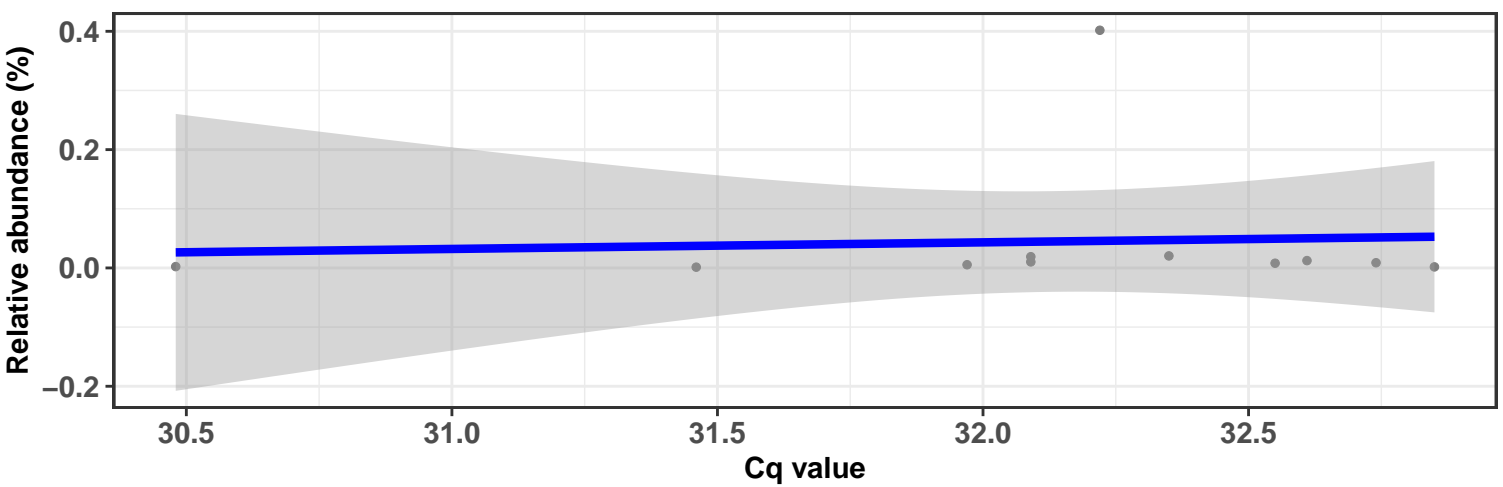
Correlation within: REF-DIC

$\log_e(S) = 6.449$ ,  $p = 0.384$ ,  $\hat{\rho}_{\text{Spearman}} = 0.225$ ,  $CI_{95\%} [-0.402, 0.887]$ ,  $n_{\text{pairs}} = 17$



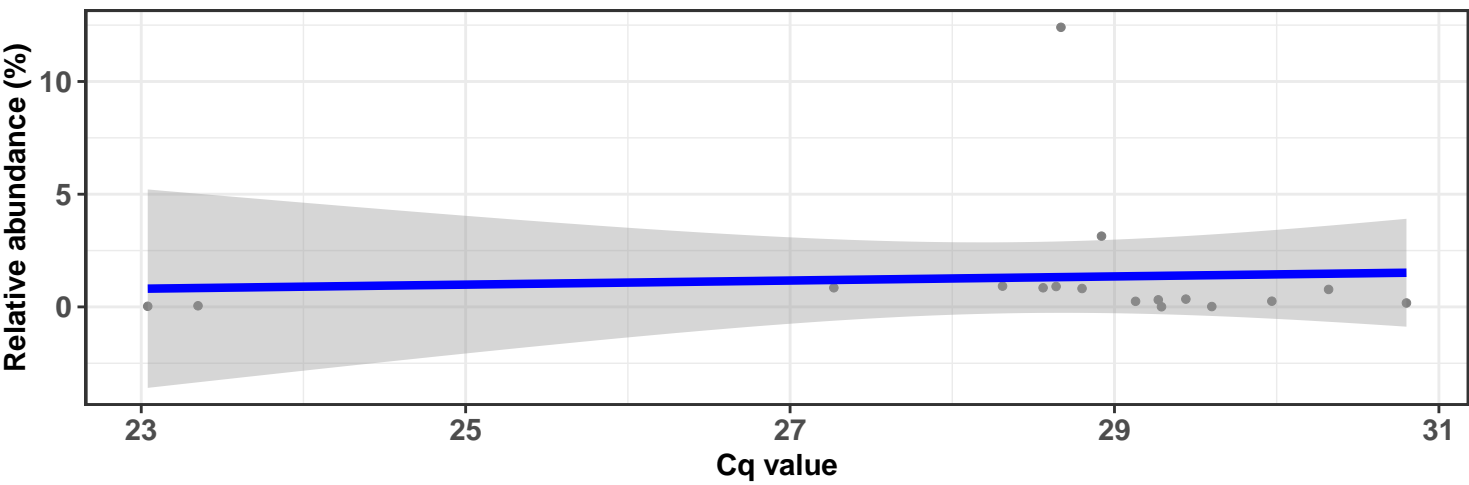
Correlation within: REF-DIM

$\log_e(S) = 5.158$ ,  $p = 0.536$ ,  $\hat{\rho}_{\text{Spearman}} = 0.210$ ,  $CI_{95\%} [-0.567, 1.021]$ ,  $n_{\text{pairs}} = 11$



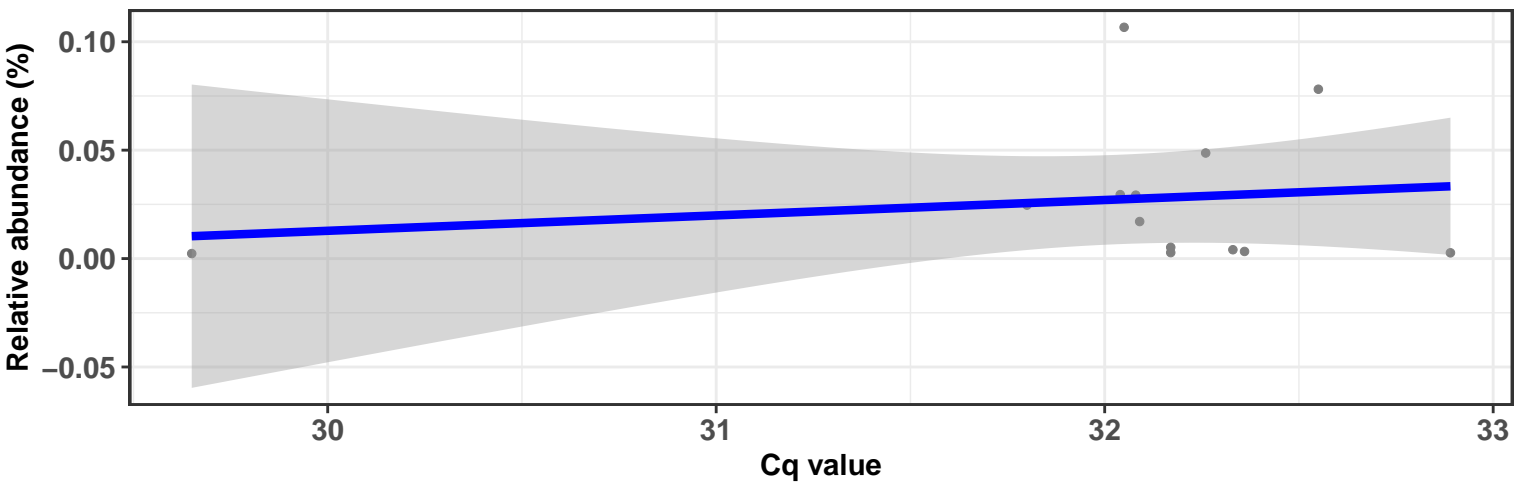
Correlation within: IM-DIC

$\log_e(S) = 6.957$ ,  $p = 0.264$ ,  $\hat{\rho}_{\text{Spearman}} = -0.287$ ,  $CI_{95\%} [-0.867, 0.249]$ ,  $n_{\text{pairs}} = 17$



Correlation within: IM-DIM

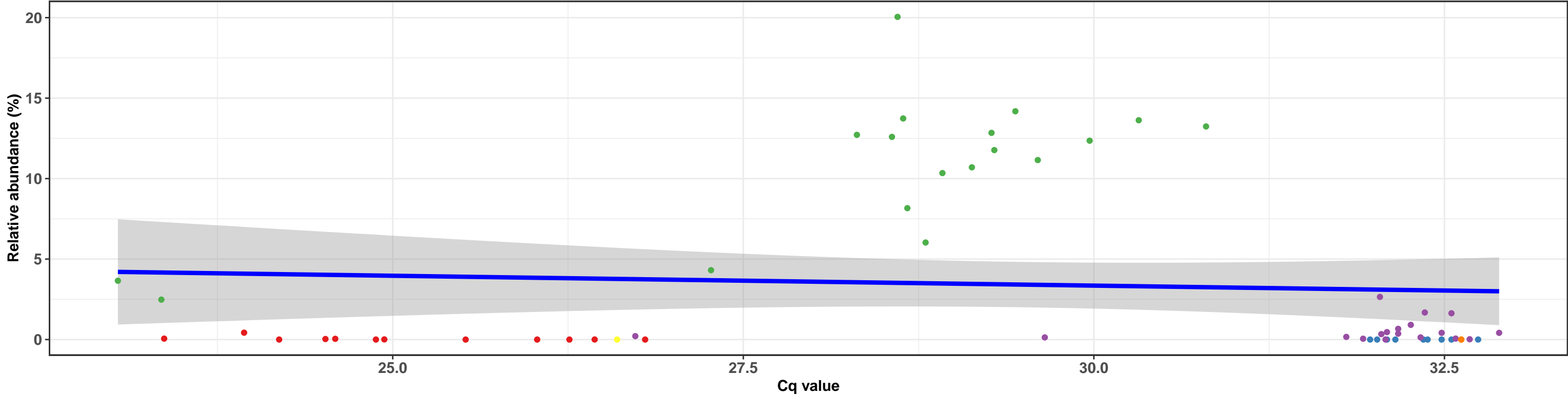
$\log_e(S) = 6.004$ ,  $p = 0.714$ ,  $\hat{\rho}_{\text{Spearman}} = -0.113$ ,  $CI_{95\%} [-0.765, 0.589]$ ,  $n_{\text{pairs}} = 13$



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

Correlation with all samples

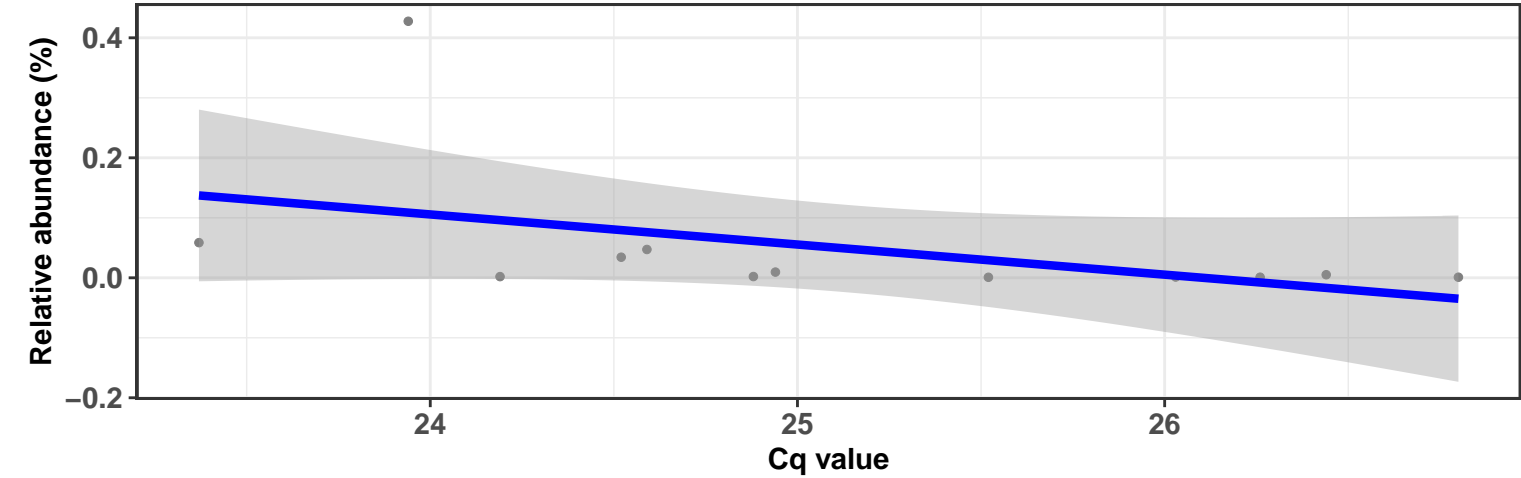
$\log_e(S) = 10.613$ ,  $p = 0.324$ ,  $\hat{\rho}_{\text{Spearman}} = -0.130$ ,  $\text{CI}_{95\%} [-0.384, 0.113]$ ,  $n_{\text{pairs}} = 60$



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

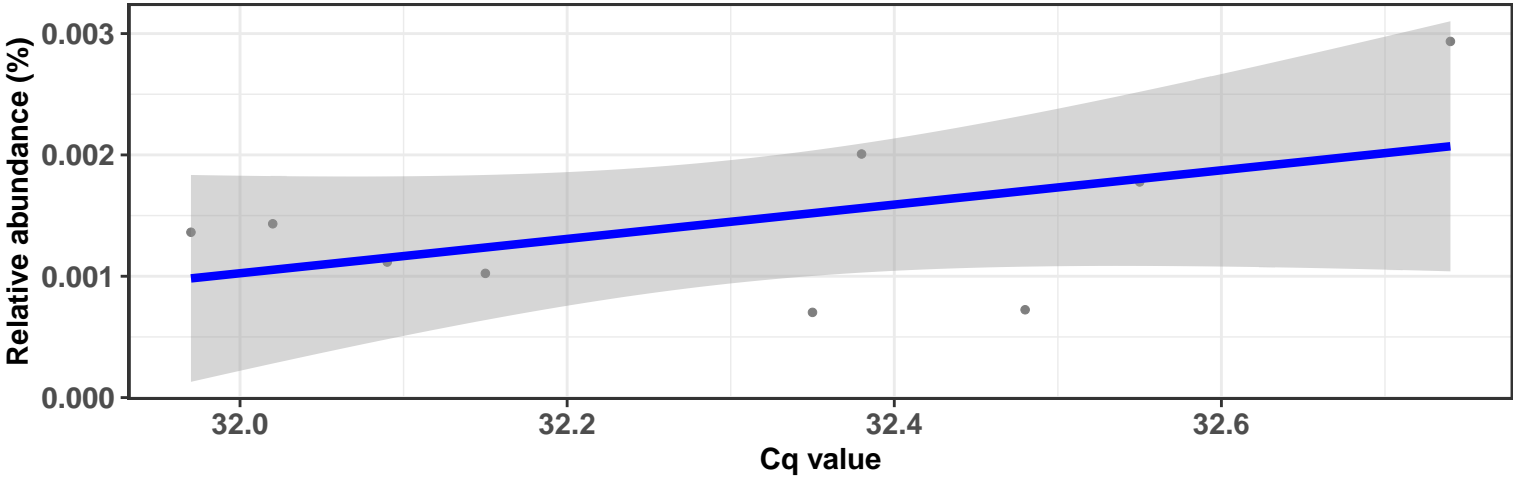
Correlation within: REF-DIC

$\log_e(S) = 6.194$ ,  $p = 0.009$ ,  $\hat{\rho}_{\text{Spearman}} = -0.713$ ,  $\text{CI}_{95\%} [-1.056, -0.457]$ ,  $n_{\text{pairs}} = 12$



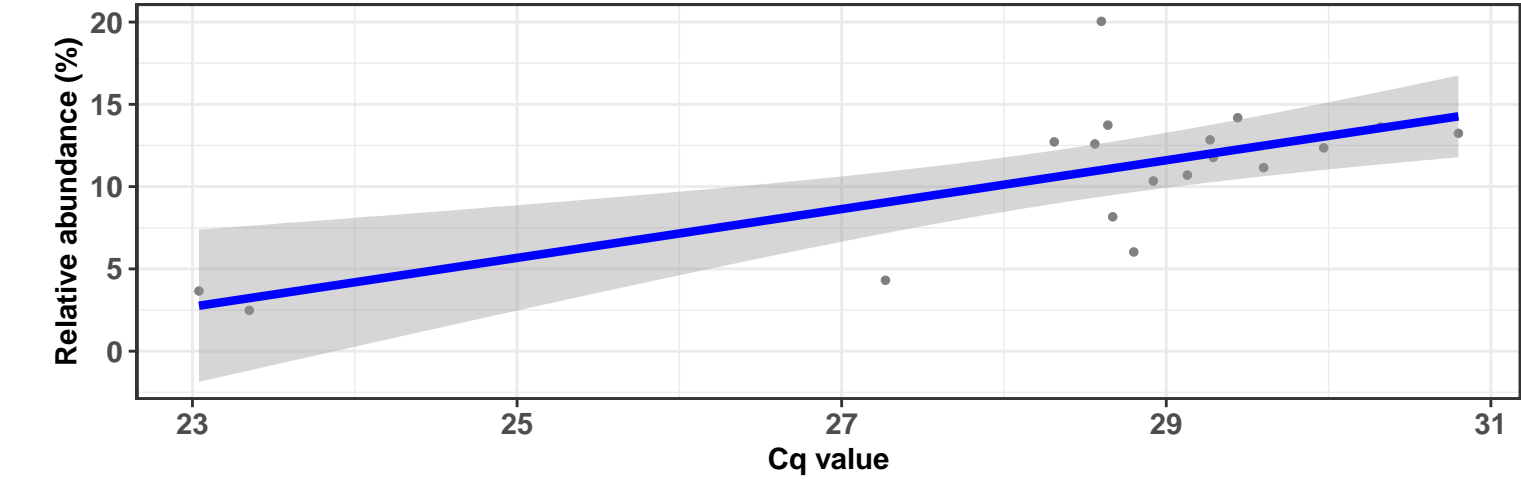
Correlation within: REF-DIM

$\log_e(S) = 4.382$ ,  $p = 0.381$ ,  $\hat{\rho}_{\text{Spearman}} = 0.333$ ,  $\text{CI}_{95\%} [-0.413, 1.046]$ ,  $n_{\text{pairs}} = 9$



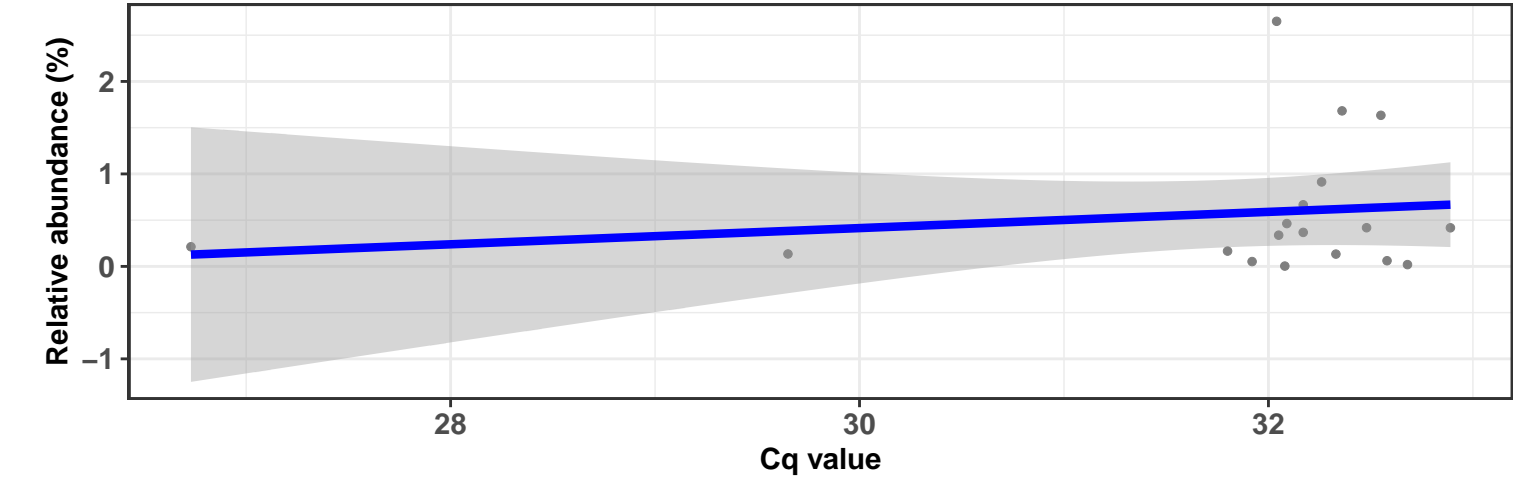
Correlation within: IM-DIC

$\log_e(S) = 6.261$ ,  $p = 0.055$ ,  $\hat{\rho}_{\text{Spearman}} = 0.459$ ,  $\text{CI}_{95\%} [0.069, 0.855]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

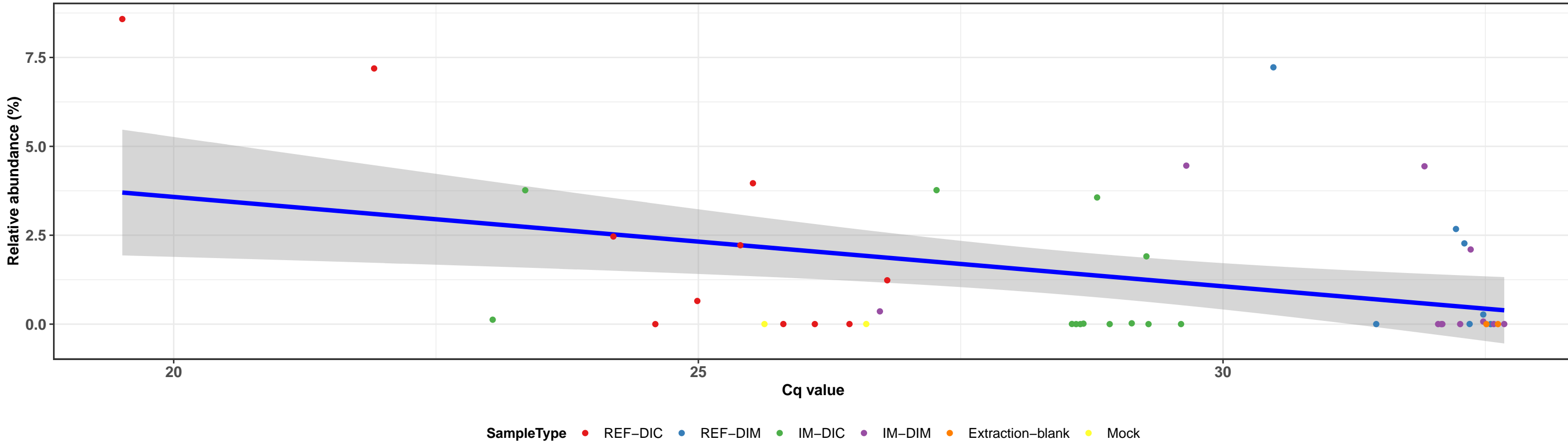
$\log_e(S) = 6.740$ ,  $p = 0.616$ ,  $\hat{\rho}_{\text{Spearman}} = 0.127$ ,  $\text{CI}_{95\%} [-0.409, 0.674]$ ,  $n_{\text{pairs}} = 18$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Aliivibrio; Ambiguous\_taxa

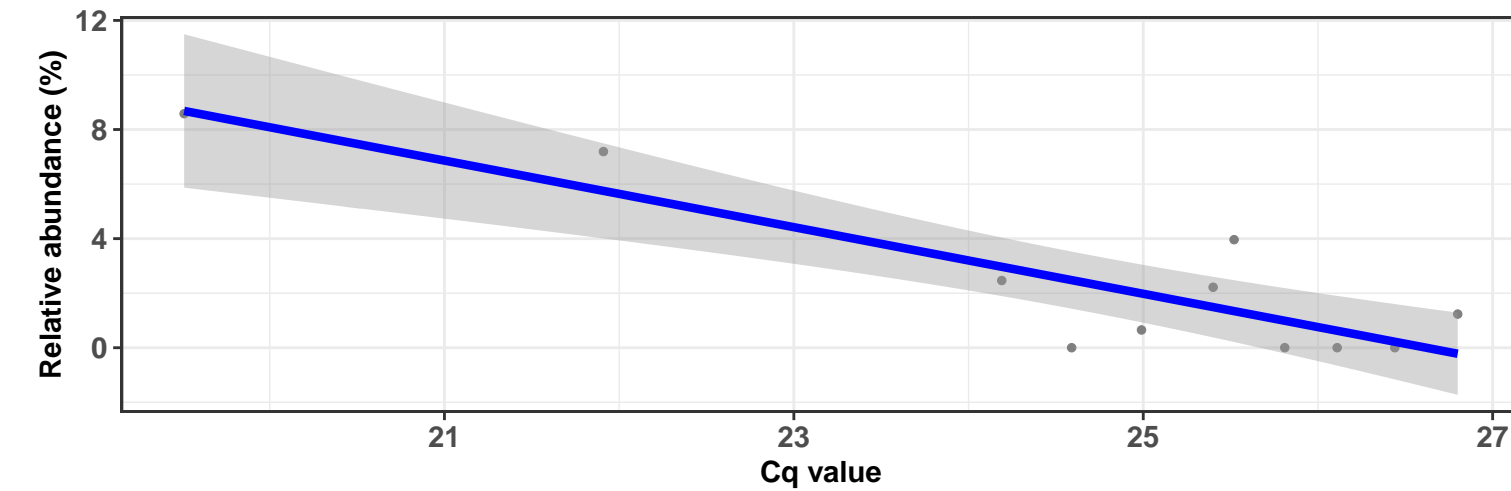
### Correlation with all samples

$\log_e(S) = 9.993$ ,  $p = 0.017$ ,  $\hat{\rho}_{\text{Spearman}} = -0.349$ ,  $\text{CI}_{95\%} [-0.598, -0.087]$ ,  $n_{\text{pairs}} = 46$



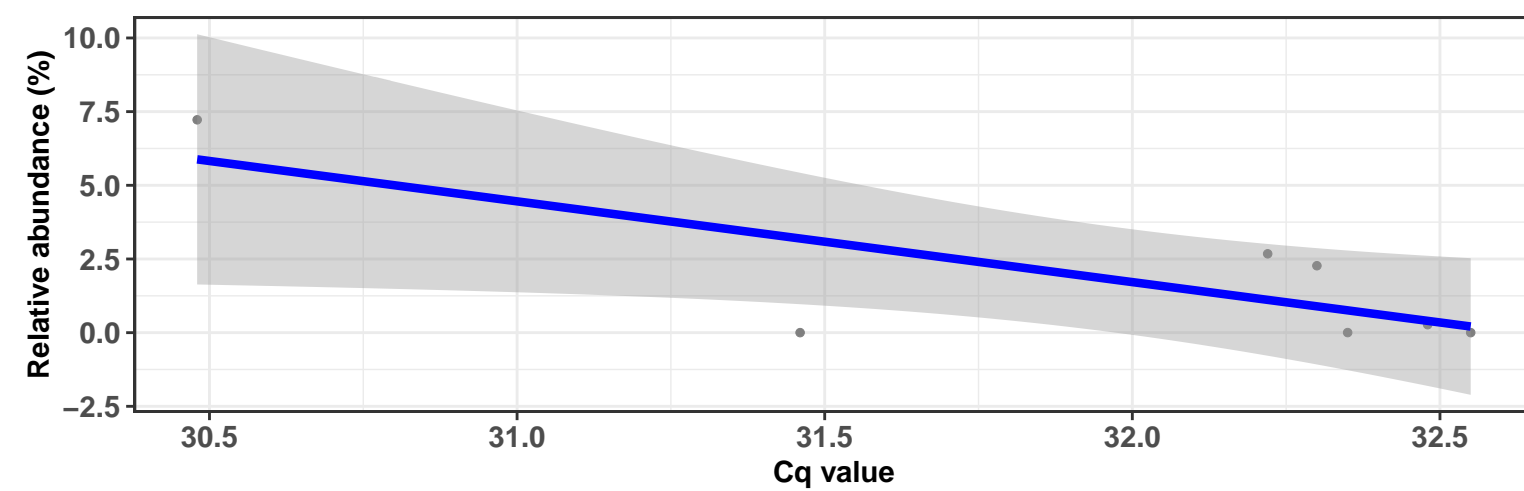
### Correlation within: REF-DIC

$\log_e(S) = 5.835$ ,  $p = 0.077$ ,  $\hat{\rho}_{\text{Spearman}} = -0.555$ ,  $\text{CI}_{95\%} [-1.151, -0.004]$ ,  $n_{\text{pairs}} = 11$



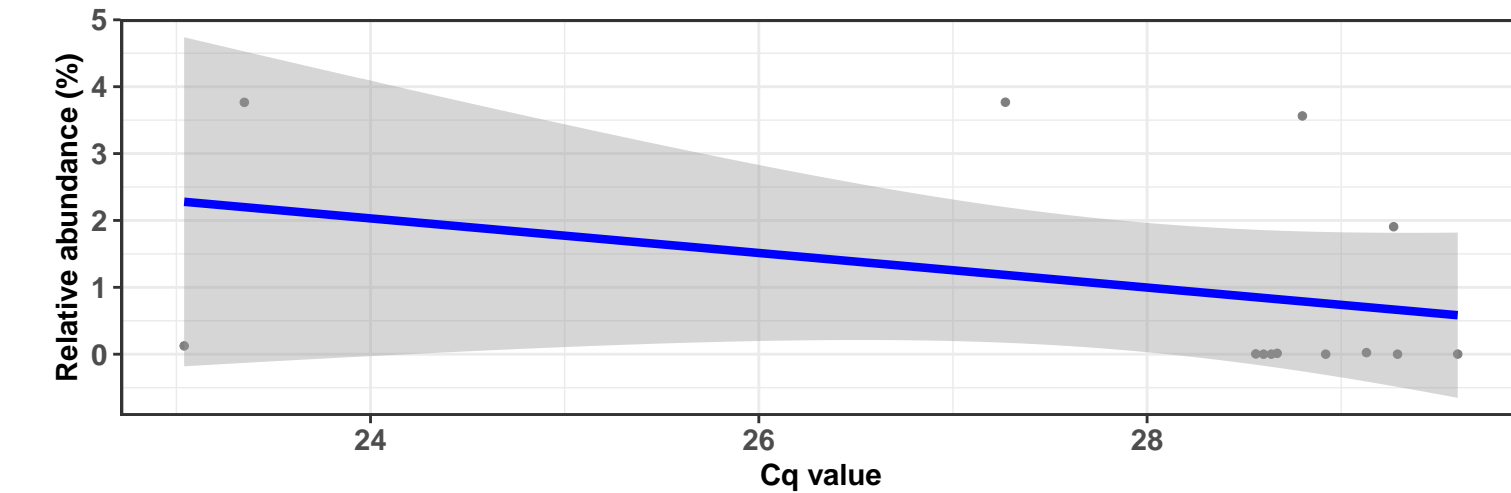
### Correlation within: REF-DIM

$\log_e(S) = 4.500$ ,  $p = 0.148$ ,  $\hat{\rho}_{\text{Spearman}} = -0.607$ ,  $\text{CI}_{95\%} [-1.517, 0.148]$ ,  $n_{\text{pairs}} = 7$



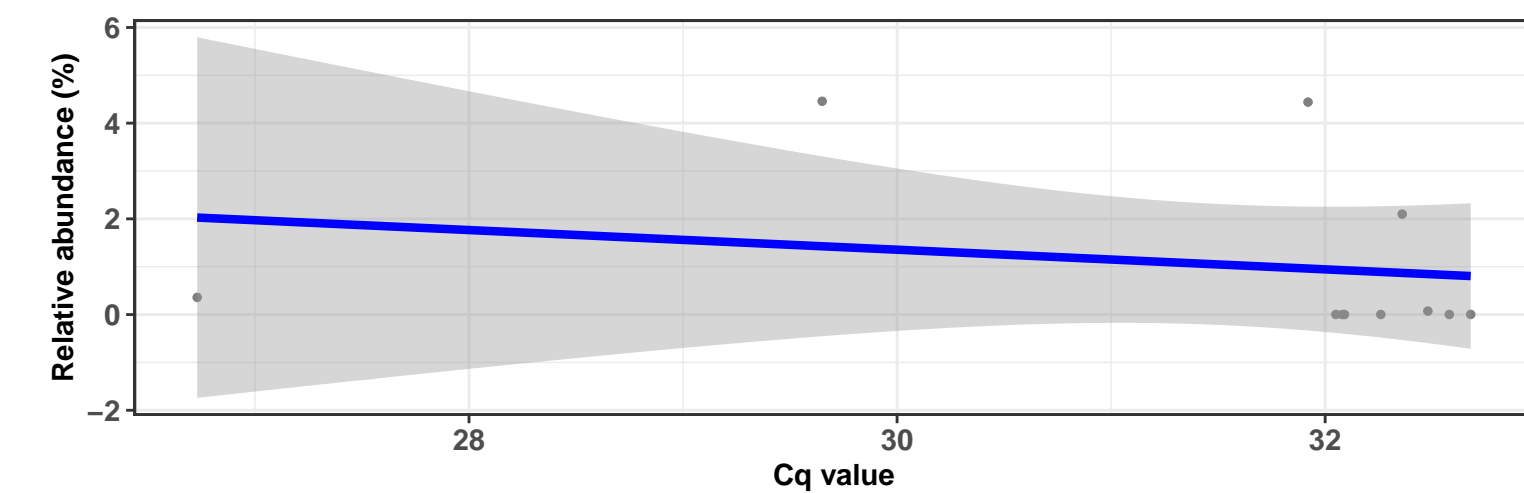
### Correlation within: IM-DIC

$\log_e(S) = 6.223$ ,  $p = 0.194$ ,  $\hat{\rho}_{\text{Spearman}} = -0.385$ ,  $\text{CI}_{95\%} [-0.837, 0.041]$ ,  $n_{\text{pairs}} = 13$



### Correlation within: IM-DIM

$\log_e(S) = 5.642$ ,  $p = 0.401$ ,  $\hat{\rho}_{\text{Spearman}} = -0.282$ ,  $\text{CI}_{95\%} [-0.908, 0.404]$ ,  $n_{\text{pairs}} = 11$

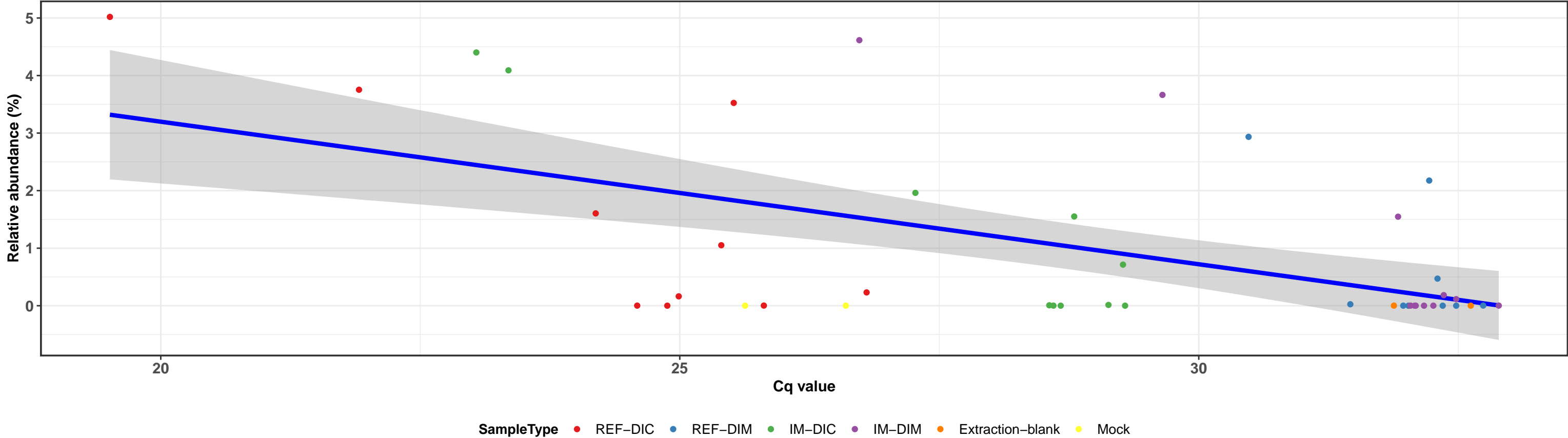




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Aliivibrio; s\_\_uncultured bacterium

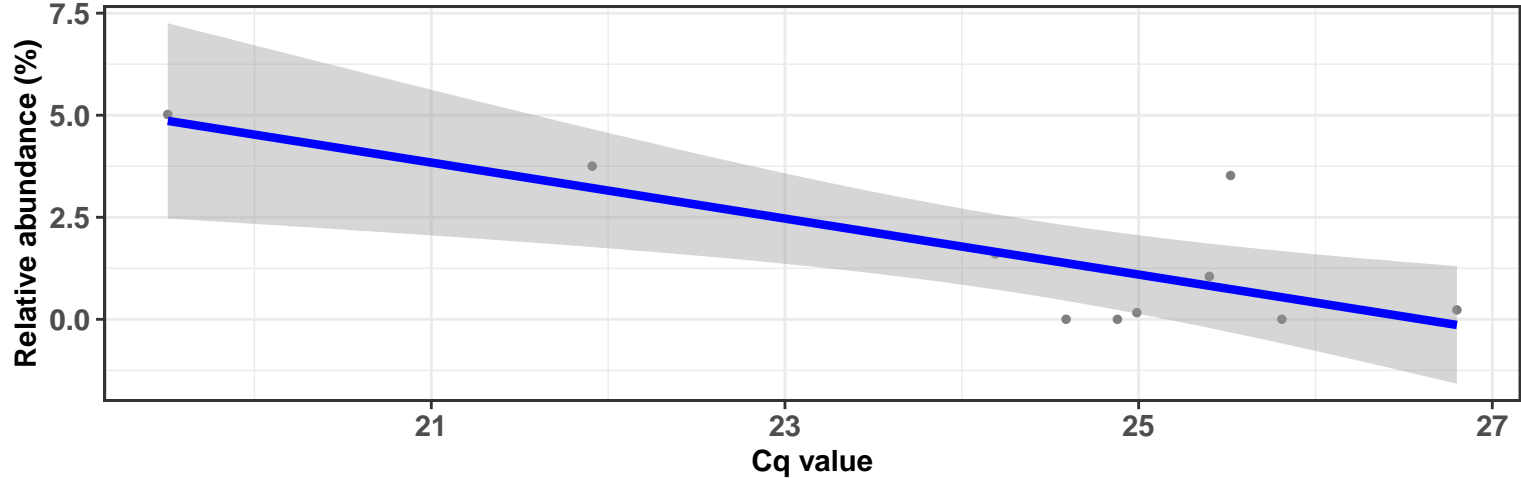
Correlation with all samples

$\log_e(S) = 9.945$ ,  $p = 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.469$ ,  $\text{CI}_{95\%} [-0.749, -0.213]$ ,  $n_{\text{pairs}} = 44$



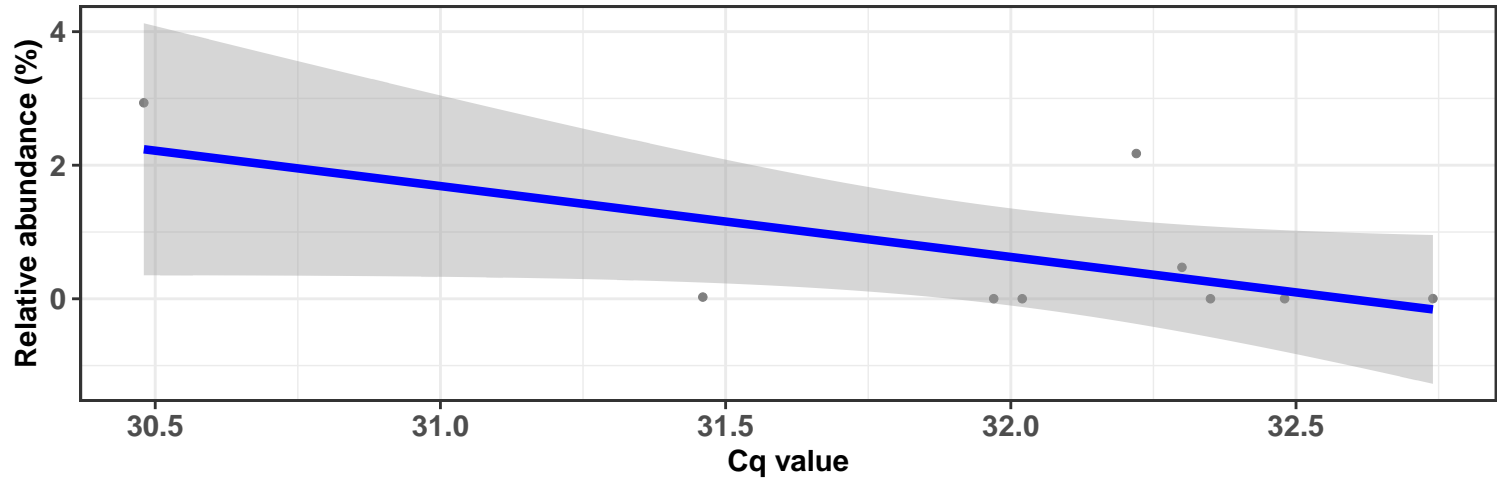
Correlation within: REF-DIC

$\log_e(S) = 5.447$ ,  $p = 0.244$ ,  $\hat{\rho}_{\text{Spearman}} = -0.406$ ,  $\text{CI}_{95\%} [-1.103, 0.216]$ ,  $n_{\text{pairs}} = 10$



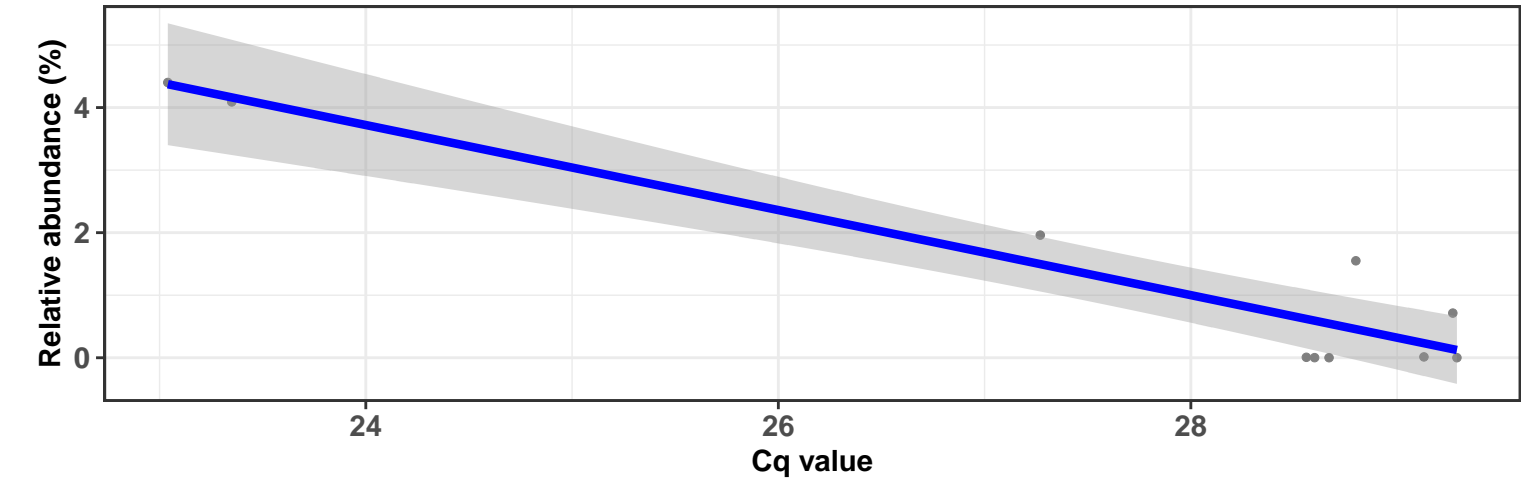
Correlation within: REF-DIM

$\log_e(S) = 5.147$ ,  $p = 0.244$ ,  $\hat{\rho}_{\text{Spearman}} = -0.433$ ,  $\text{CI}_{95\%} [-0.987, 0.073]$ ,  $n_{\text{pairs}} = 9$



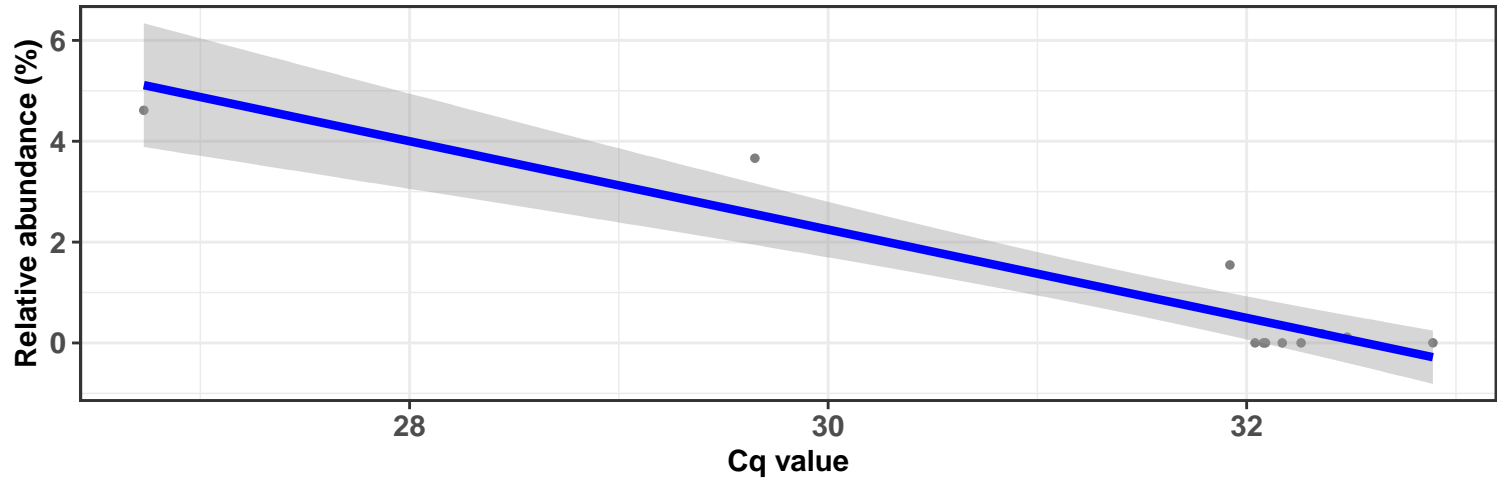
Correlation within: IM-DIC

$\log_e(S) = 5.583$ ,  $p = 0.060$ ,  $\hat{\rho}_{\text{Spearman}} = -0.612$ ,  $\text{CI}_{95\%} [-1.398, 0.007]$ ,  $n_{\text{pairs}} = 10$



Correlation within: IM-DIM

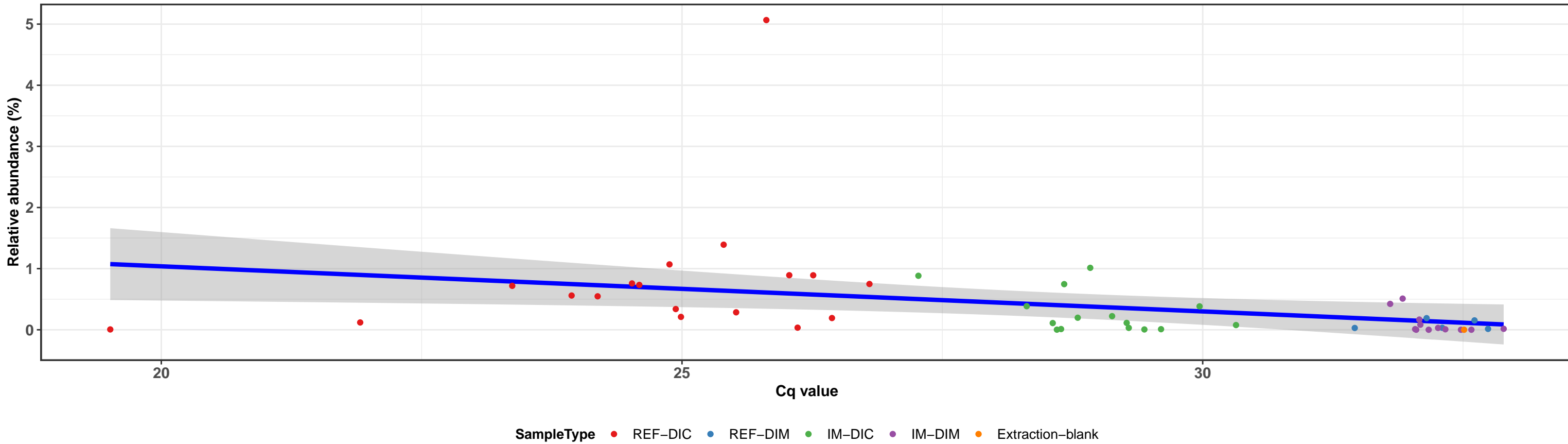
$\log_e(S) = 5.710$ ,  $p = 0.259$ ,  $\hat{\rho}_{\text{Spearman}} = -0.373$ ,  $\text{CI}_{95\%} [-0.995, 0.284]$ ,  $n_{\text{pairs}} = 11$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Photobacterium; NA

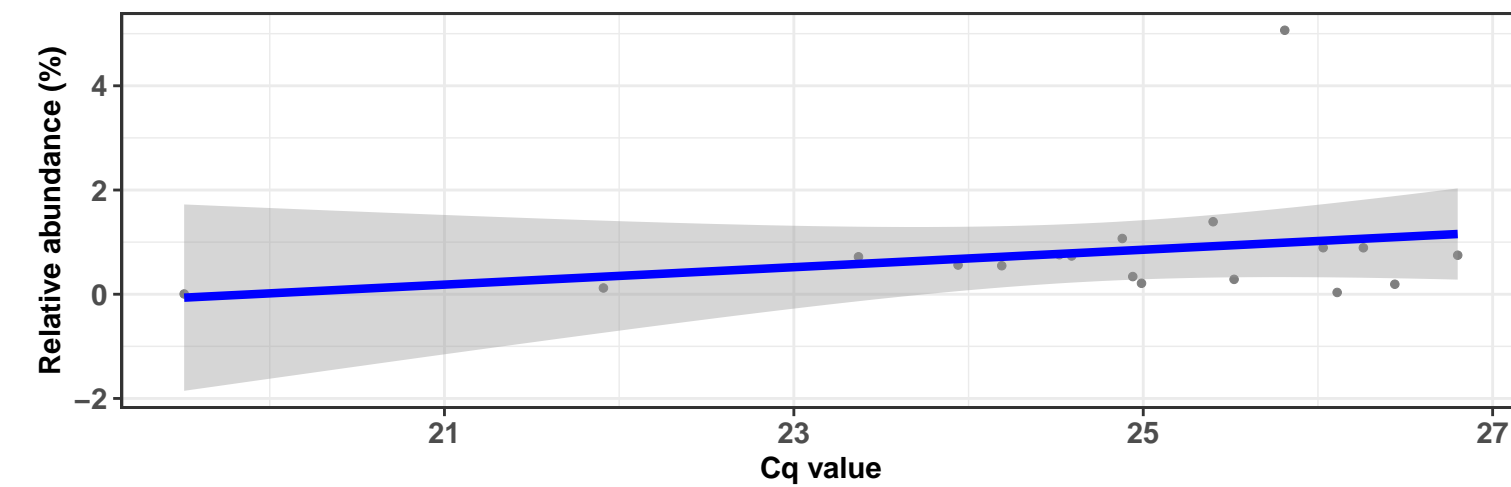
### Correlation with all samples

$\log_e(S) = 10.474$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.600$ ,  $\text{CI}_{95\%} [-0.791, -0.423]$ ,  $n_{\text{pairs}} = 51$

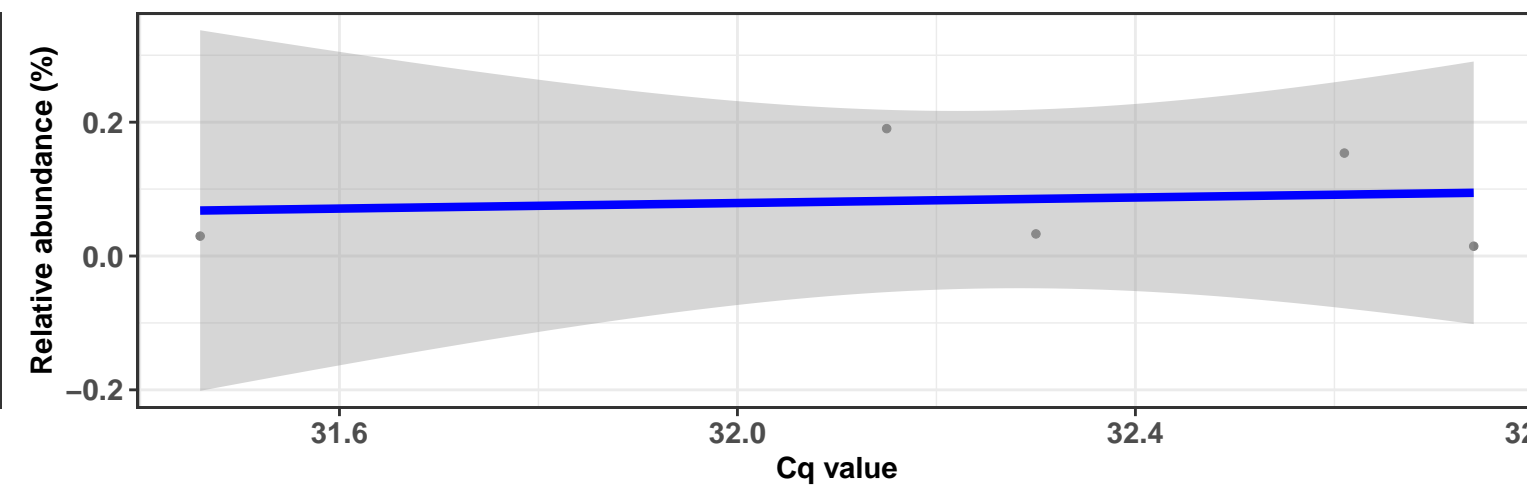


### Correlation within: REF-DIC

$\log_e(S) = 6.576$ ,  $p = 0.299$ ,  $\hat{\rho}_{\text{Spearman}} = 0.259$ ,  $\text{CI}_{95\%} [-0.235, 0.758]$ ,  $n_{\text{pairs}} = 18$

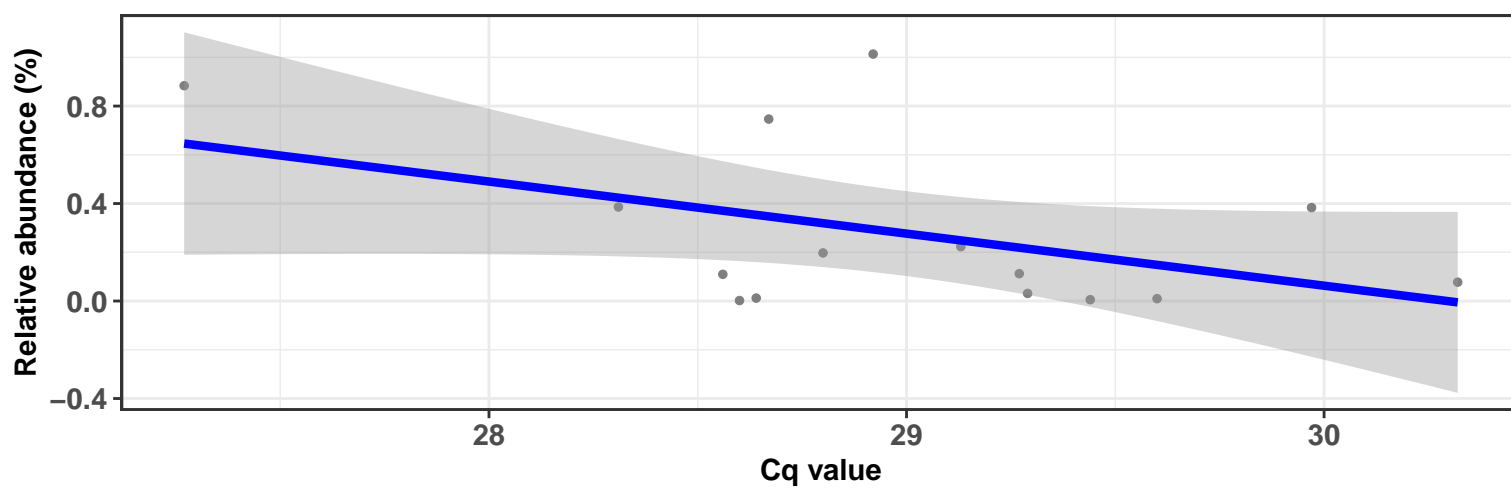


### Correlation within: REF-DIM



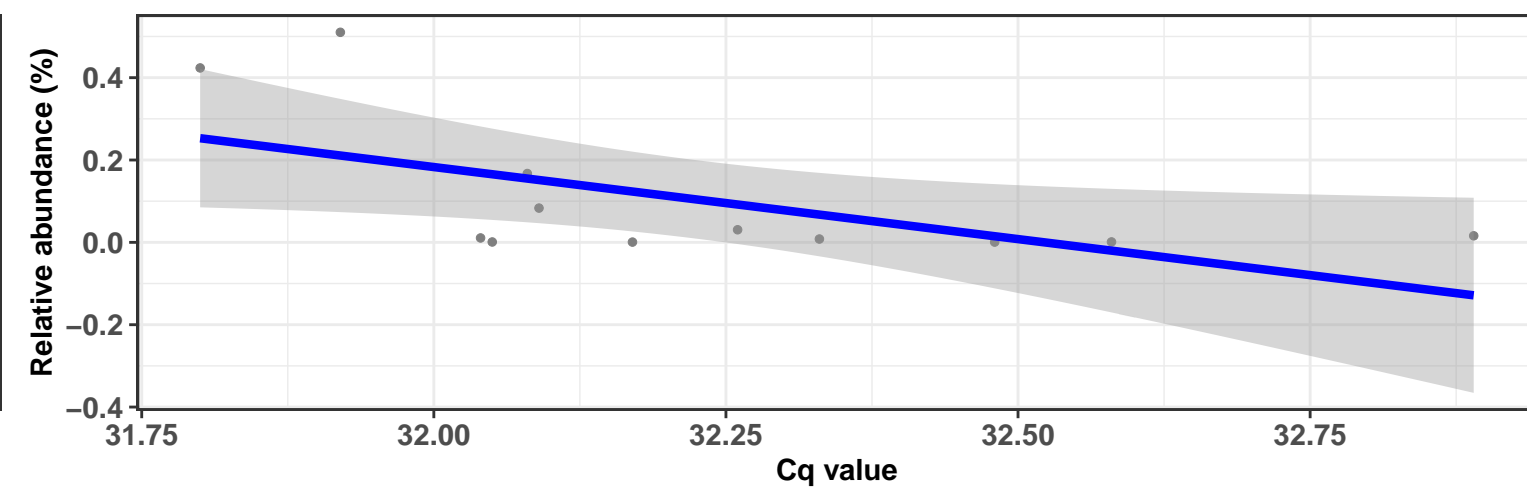
### Correlation within: IM-DIC

$\log_e(S) = 6.590$ ,  $p = 0.277$ ,  $\hat{\rho}_{\text{Spearman}} = -0.300$ ,  $\text{CI}_{95\%} [-0.862, 0.282]$ ,  $n_{\text{pairs}} = 15$



### Correlation within: IM-DIM

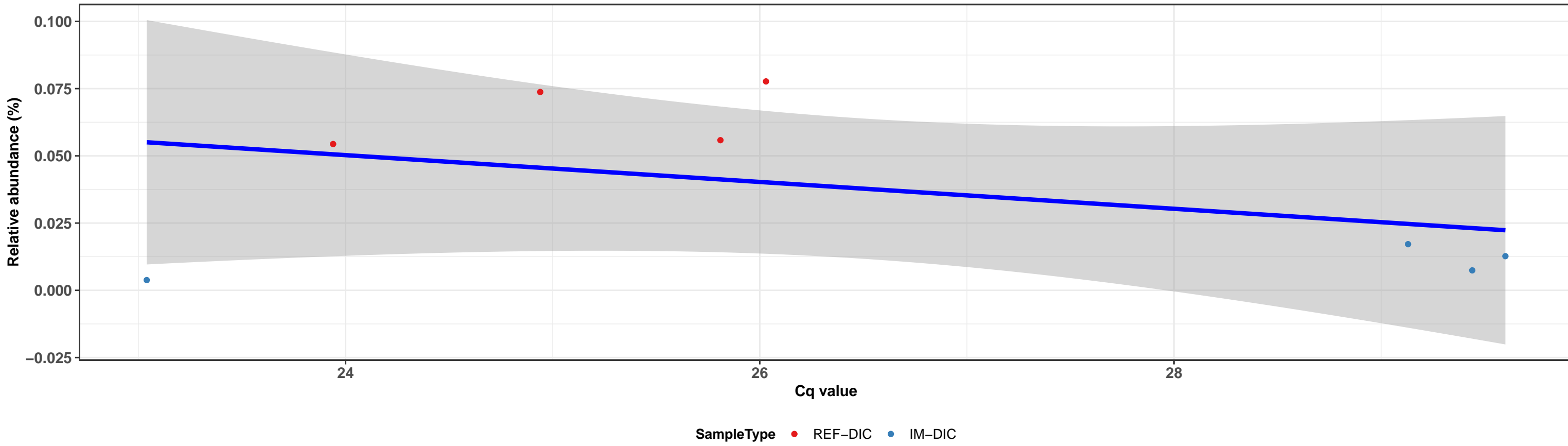
$\log_e(S) = 6.087$ ,  $p = 0.071$ ,  $\hat{\rho}_{\text{Spearman}} = -0.538$ ,  $\text{CI}_{95\%} [-1.011, -0.084]$ ,  $n_{\text{pairs}} = 12$



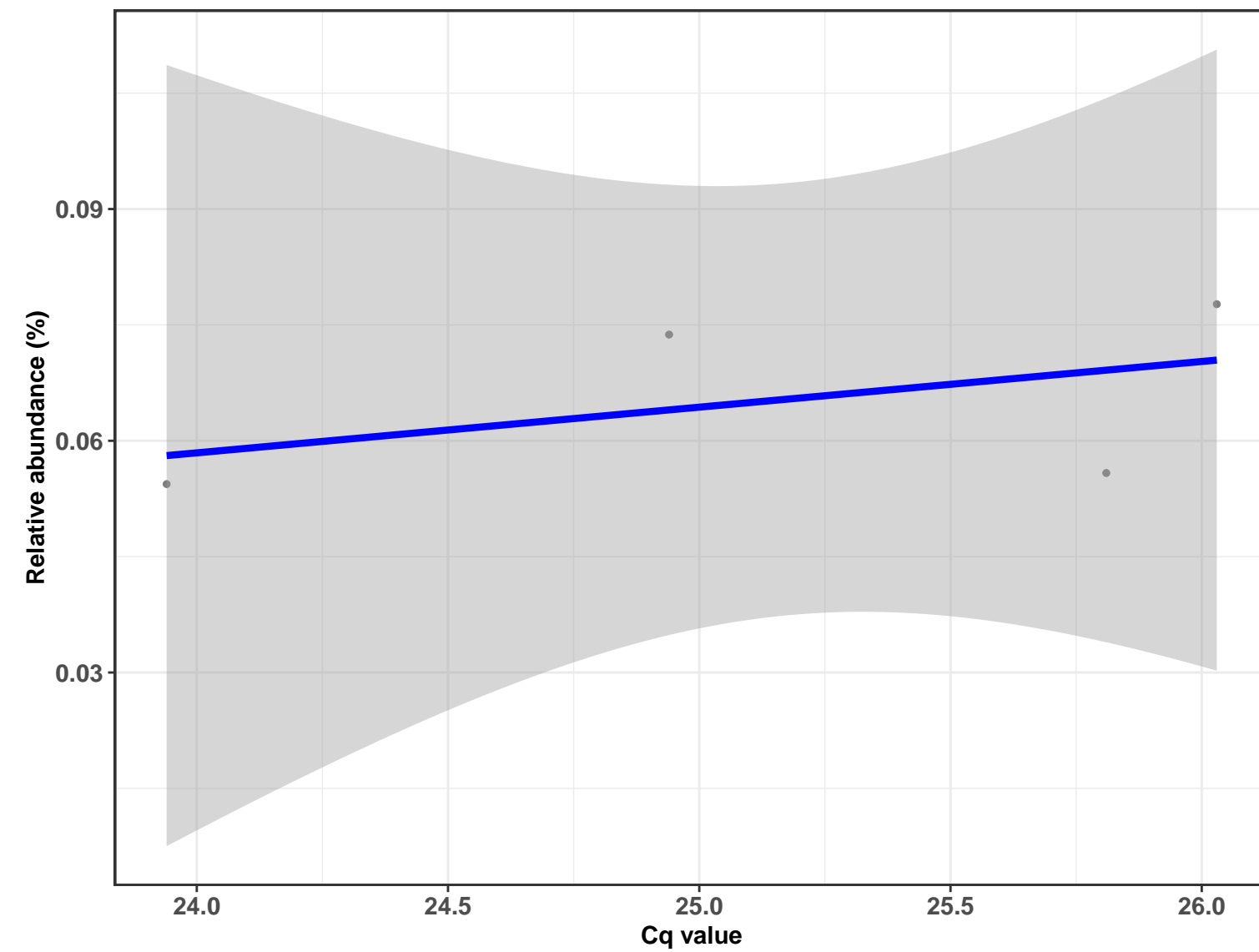
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

### Correlation with all samples

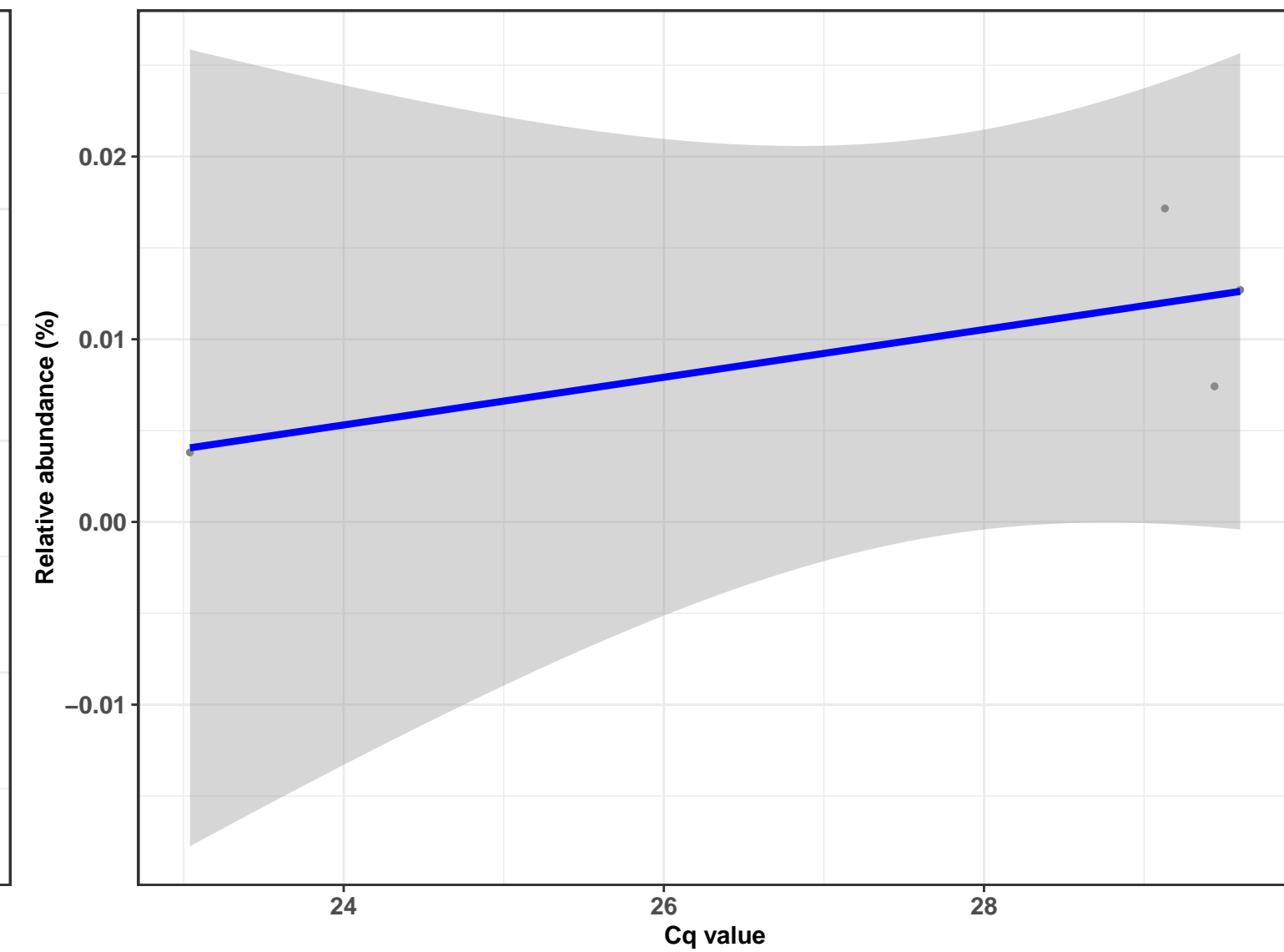
$\log_e(S) = 4.522$ ,  $p = 0.823$ ,  $\hat{\rho}_{\text{Spearman}} = -0.095$ ,  $\text{CI}_{95\%} [-1.073, 0.771]$ ,  $n_{\text{pairs}} = 8$



### Correlation within: REF-DIC



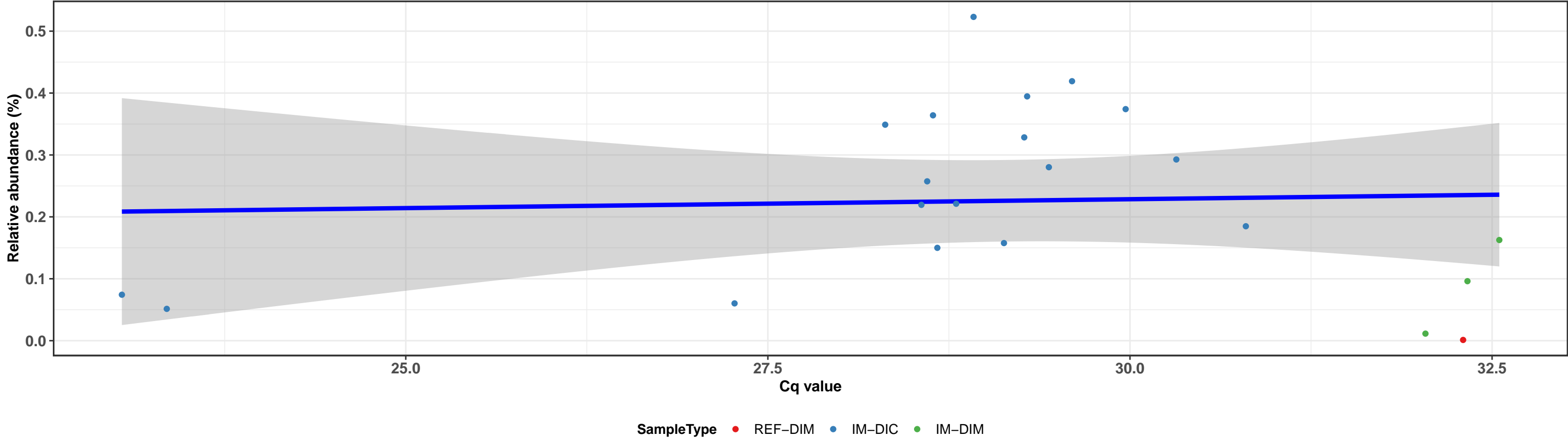
### Correlation within: IM-DIC



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

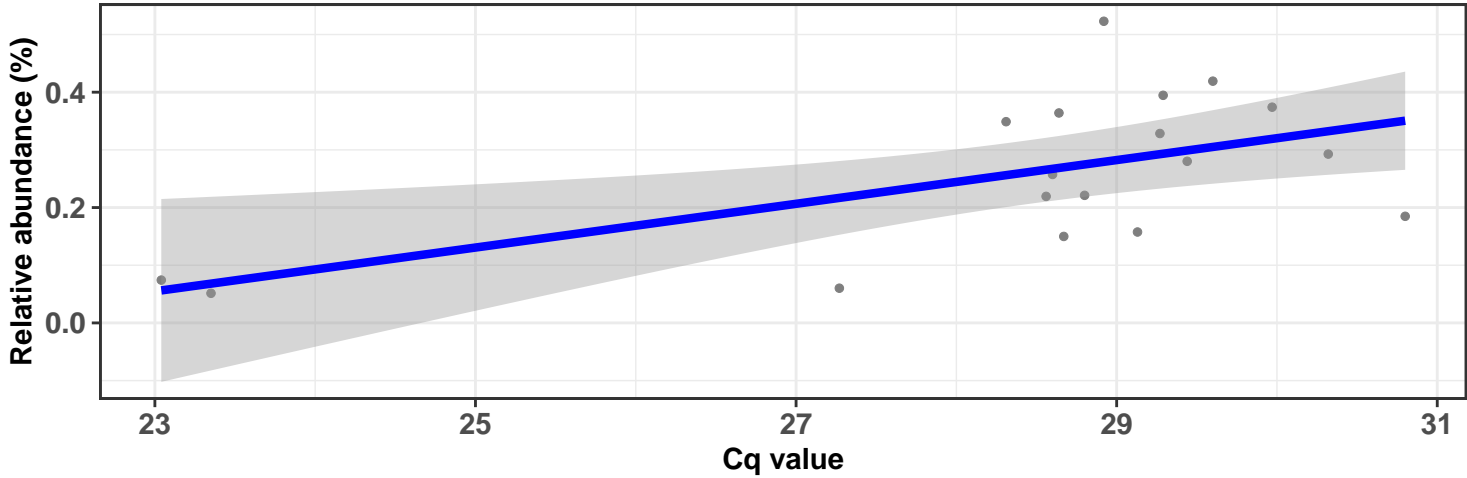
Correlation with all samples

$\log_e(S) = 7.483$ ,  $p = 0.986$ ,  $\hat{\rho}_{\text{Spearman}} = -0.004$ ,  $\text{CI}_{95\%} [-0.479, 0.527]$ ,  $n_{\text{pairs}} = 22$

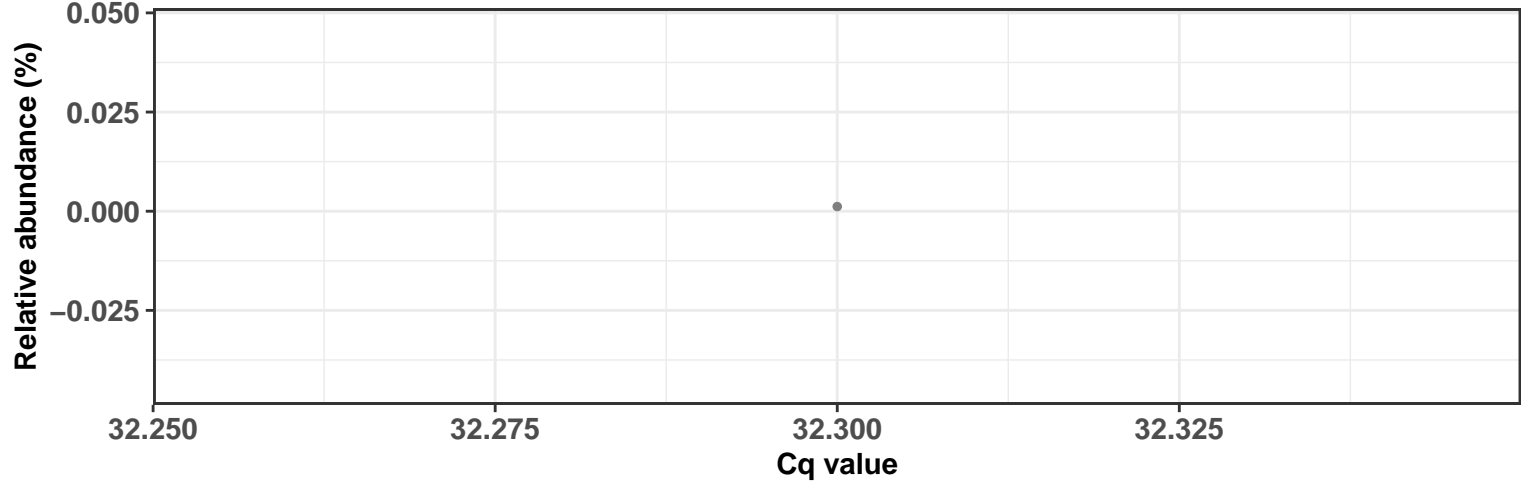


Correlation within: IM-DIC

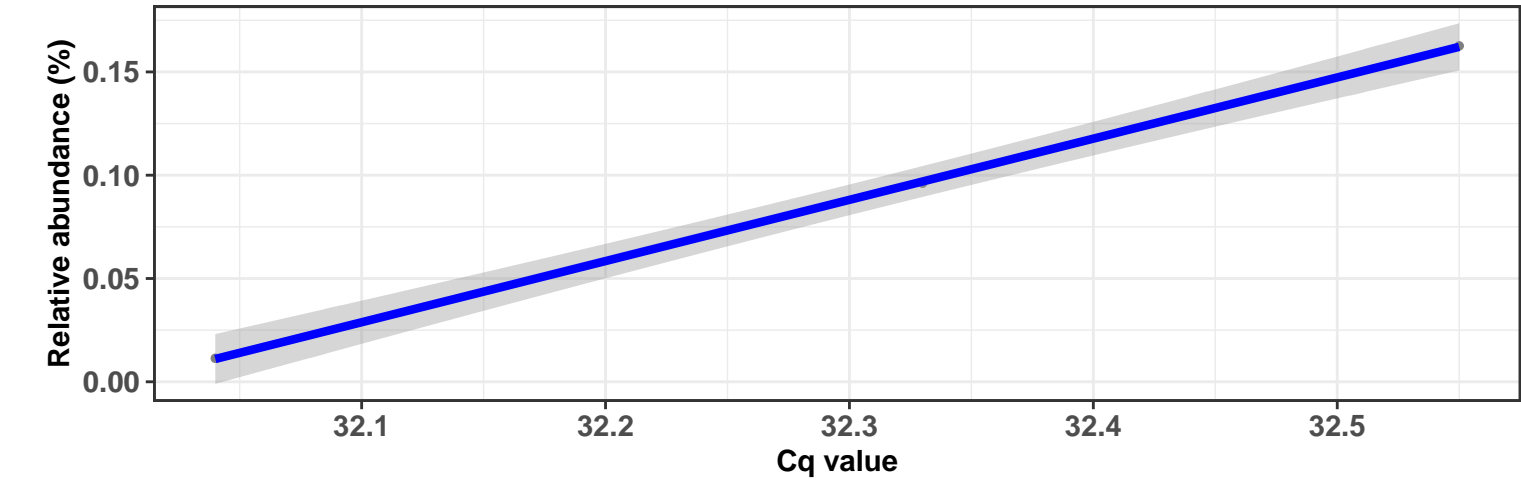
$\log_e(S) = 6.165$ ,  $p = 0.031$ ,  $\hat{\rho}_{\text{Spearman}} = 0.509$ ,  $\text{CI}_{95\%} [0.171, 0.888]$ ,  $n_{\text{pairs}} = 18$



Correlation within: REF-DIM



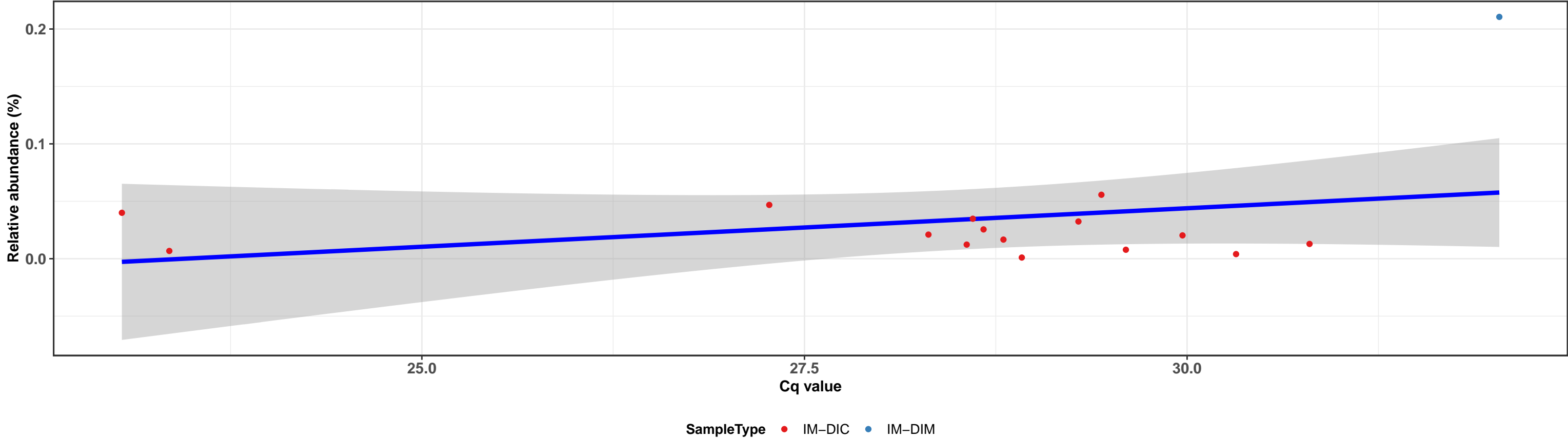
Correlation within: IM-DIM



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

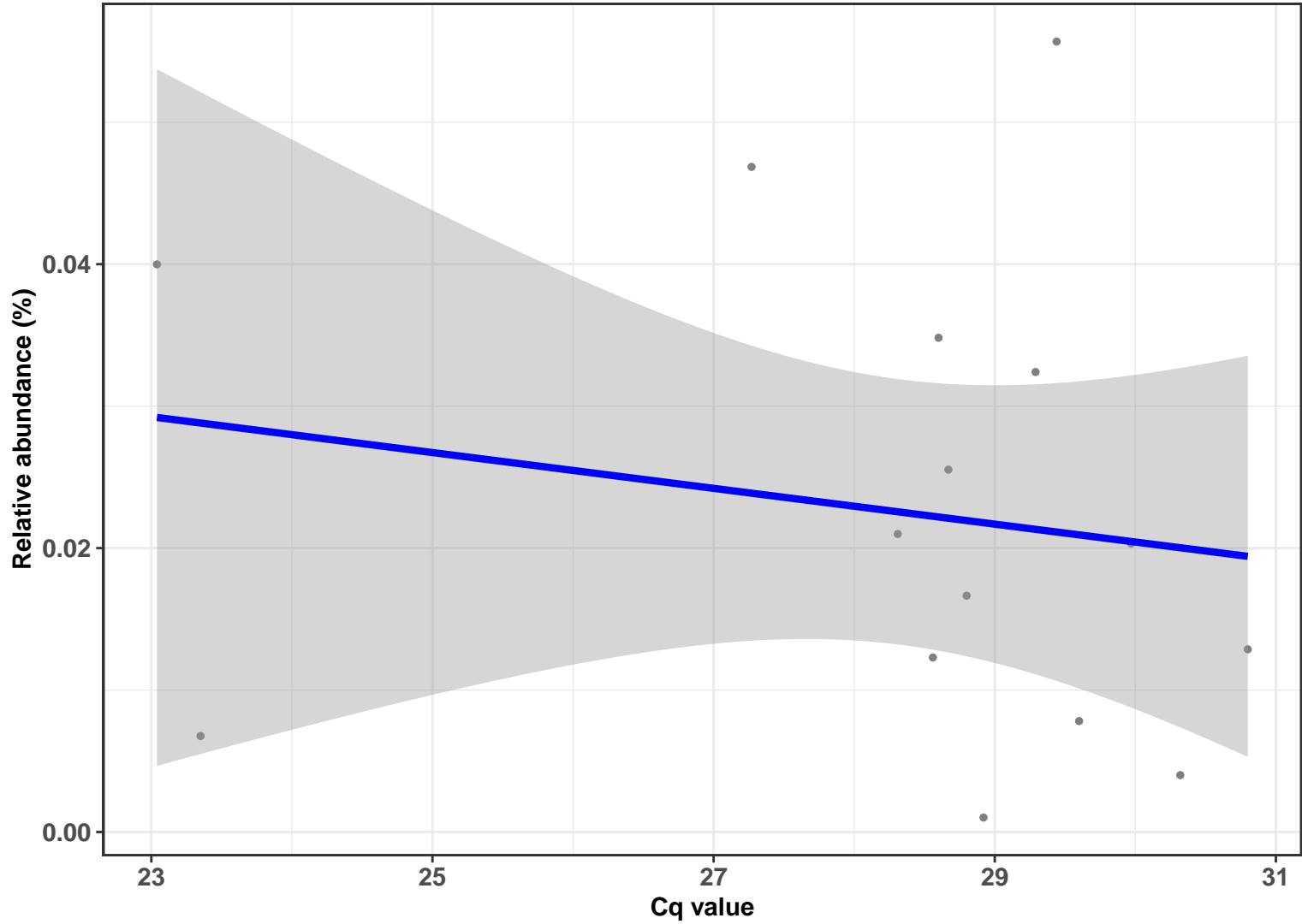
Correlation with all samples

$\log_e(S) = 6.596$ ,  $p = 0.778$ ,  $\hat{\rho}_{\text{Spearman}} = -0.076$ ,  $\text{CI}_{95\%} [-0.722, 0.541]$ ,  $n_{\text{pairs}} = 16$

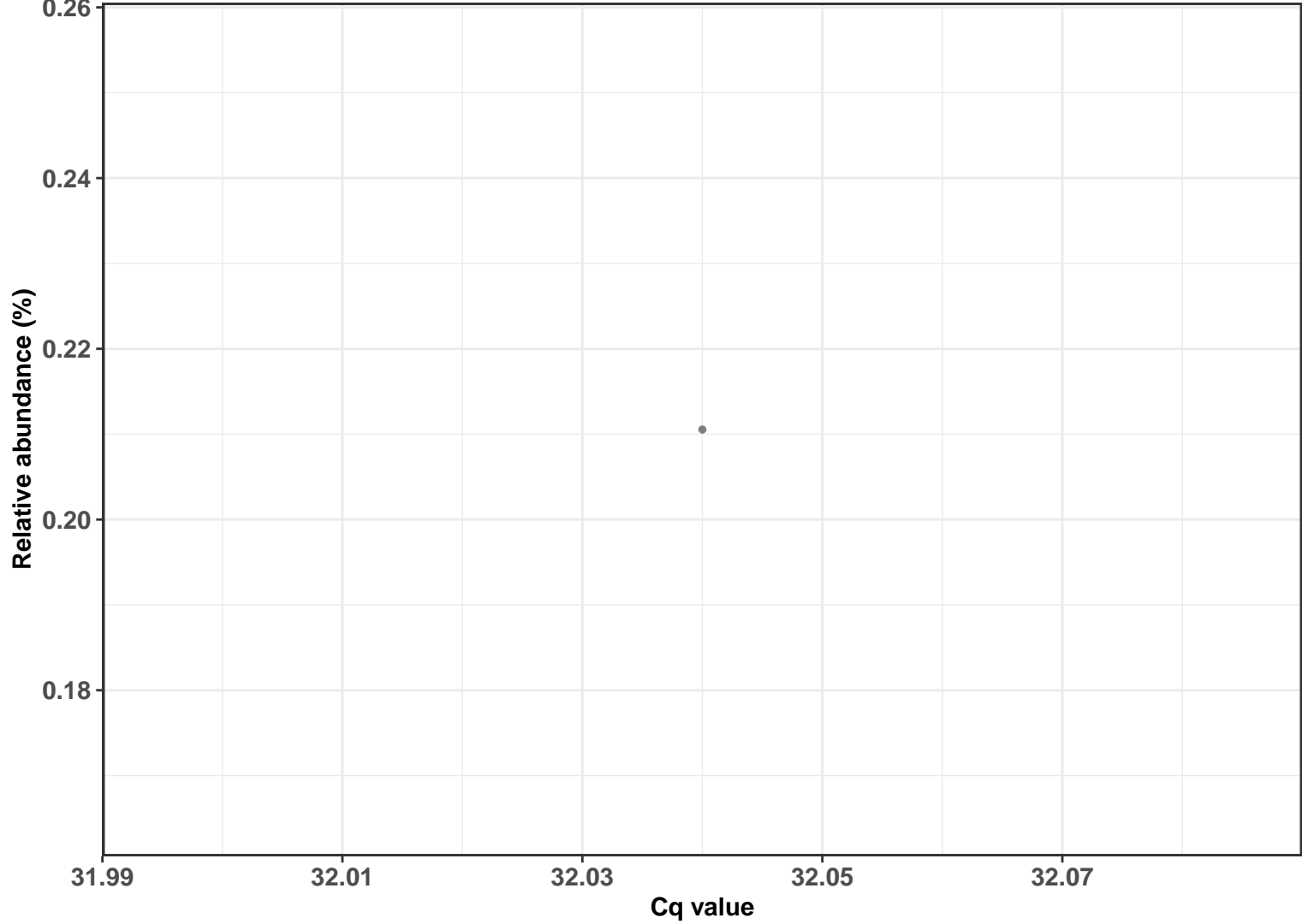


Correlation within: IM-DIC

$\log_e(S) = 6.596$ ,  $p = 0.265$ ,  $\hat{\rho}_{\text{Spearman}} = -0.307$ ,  $\text{CI}_{95\%} [-0.828, 0.241]$ ,  $n_{\text{pairs}} = 15$

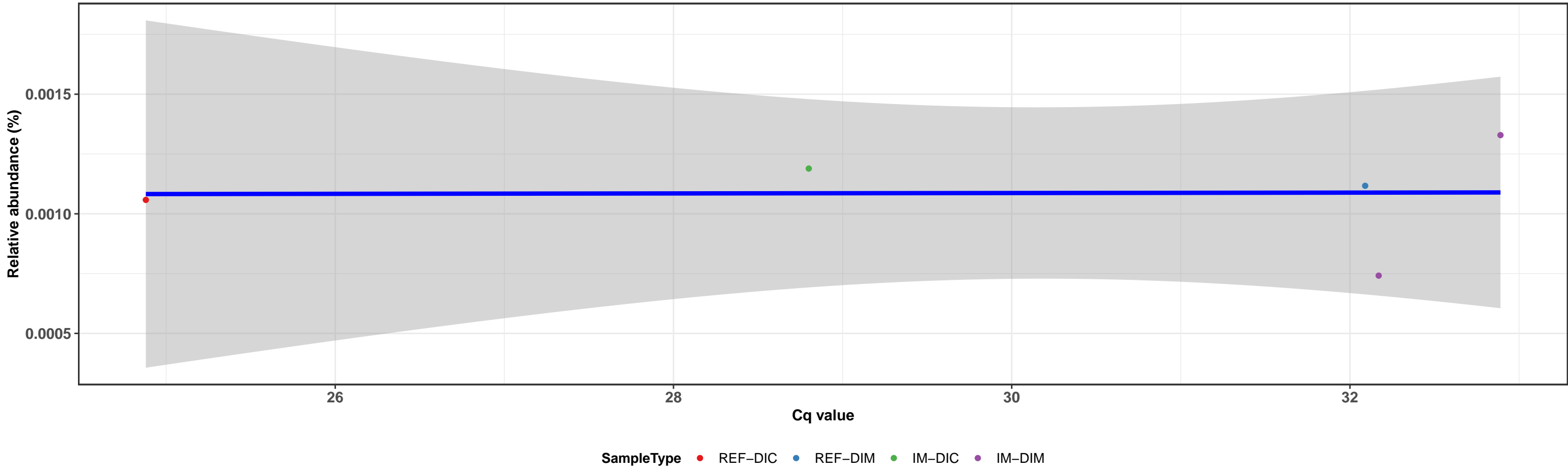


Correlation within: IM-DIM

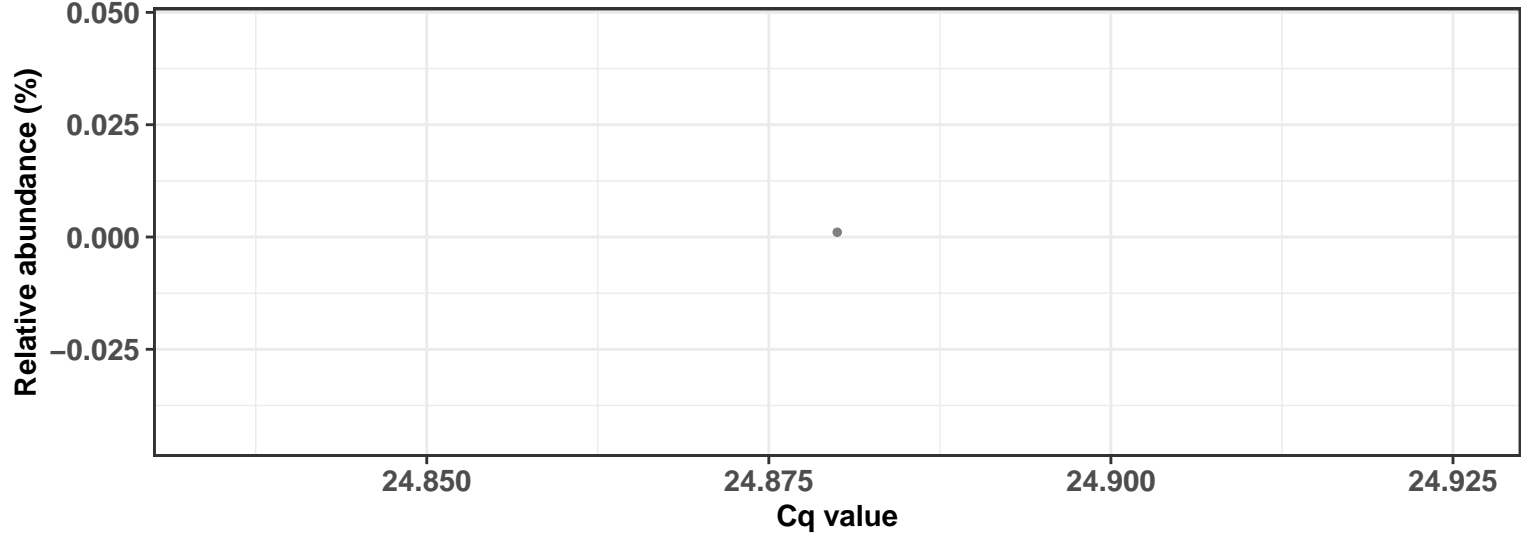


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Alteromonadales; f\_\_Marinobacteraceae; g\_\_Marinobacter; s\_\_Marinobacter adhaerens

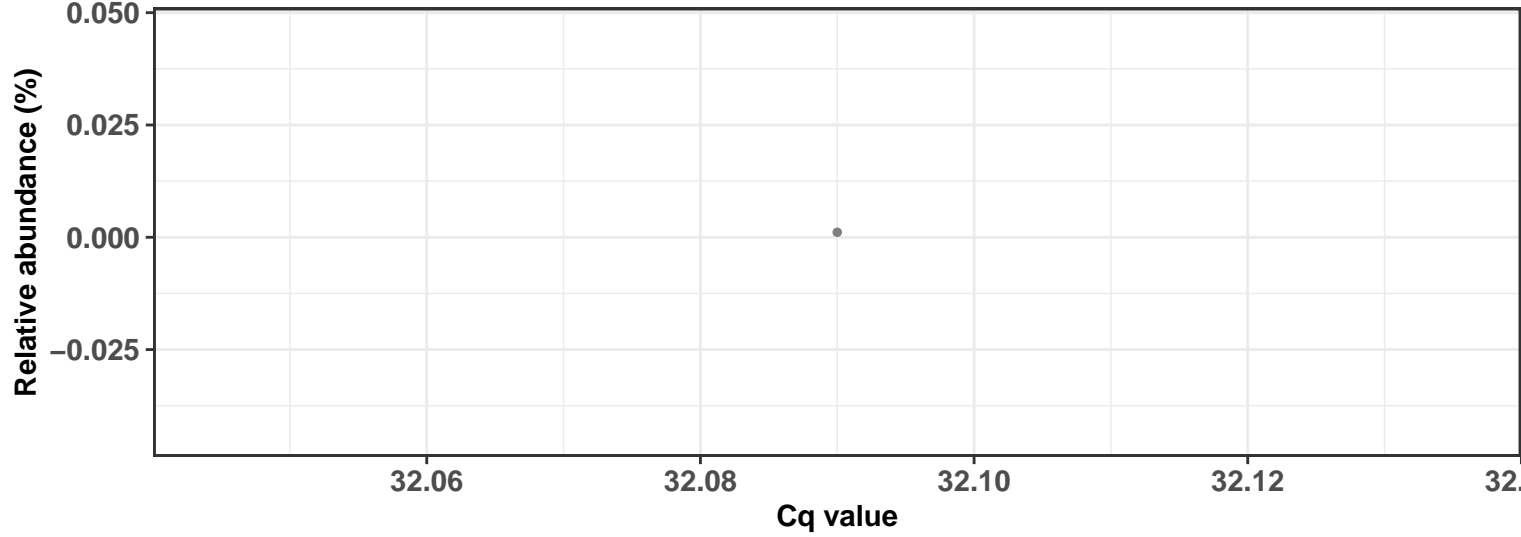
Correlation with all samples



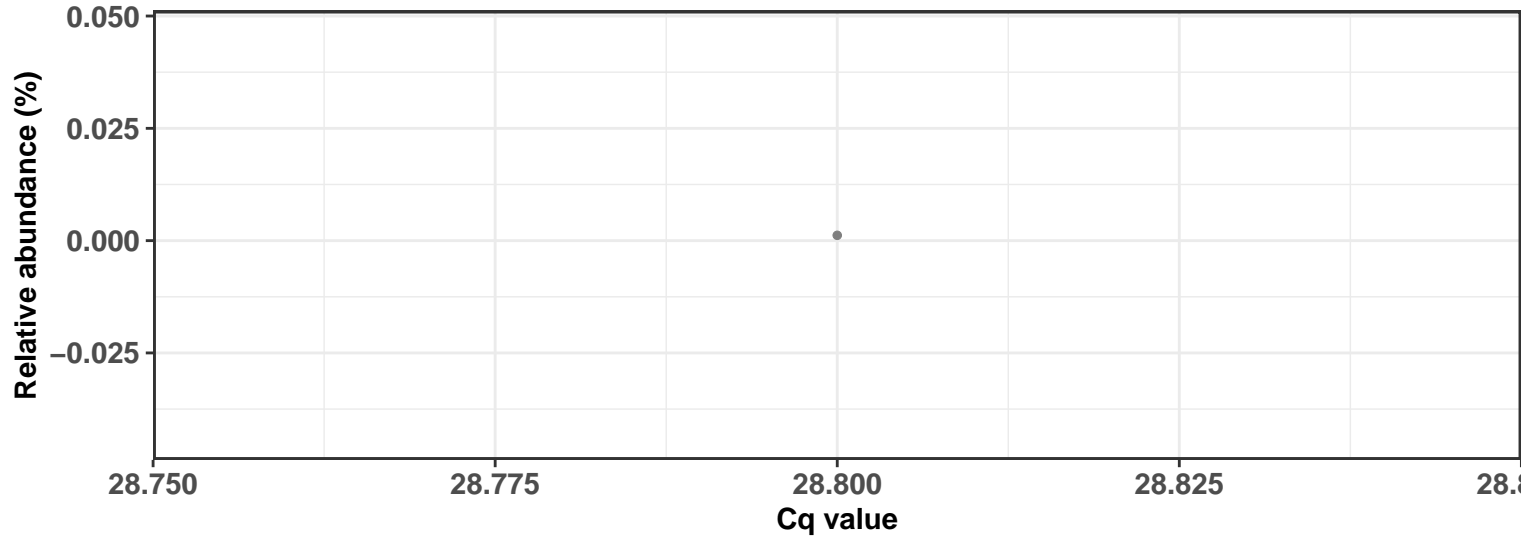
Correlation within: REF-DIC



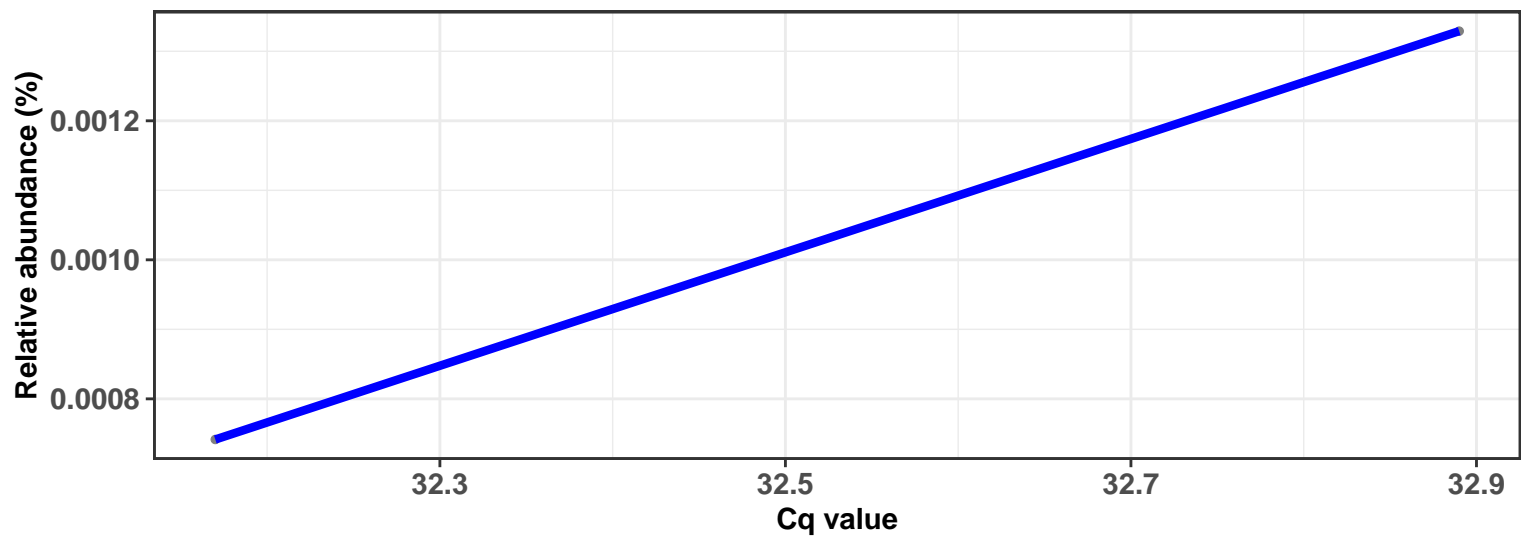
Correlation within: REF-DIM



Correlation within: IM-DIC



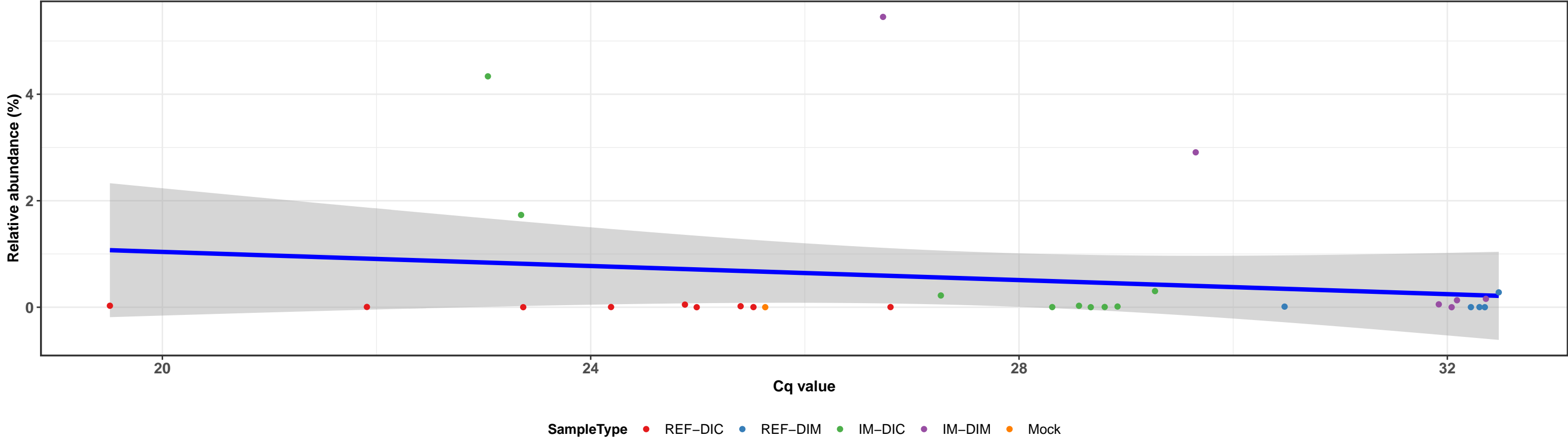
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Aliivibrio; s\_\_uncultured bacterium

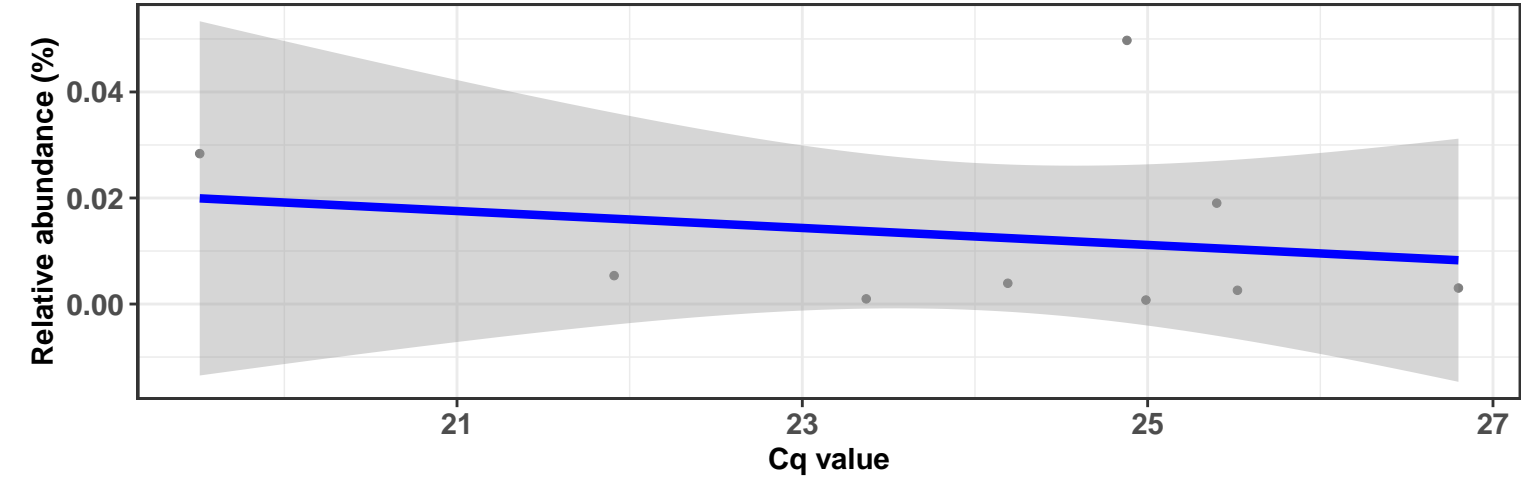
Correlation with all samples

$\log_e(S) = 8.469$ ,  $p = 0.753$ ,  $\hat{\rho}_{\text{Spearman}} = -0.060$ ,  $\text{CI}_{95\%} [-0.432, 0.299]$ ,  $n_{\text{pairs}} = 30$

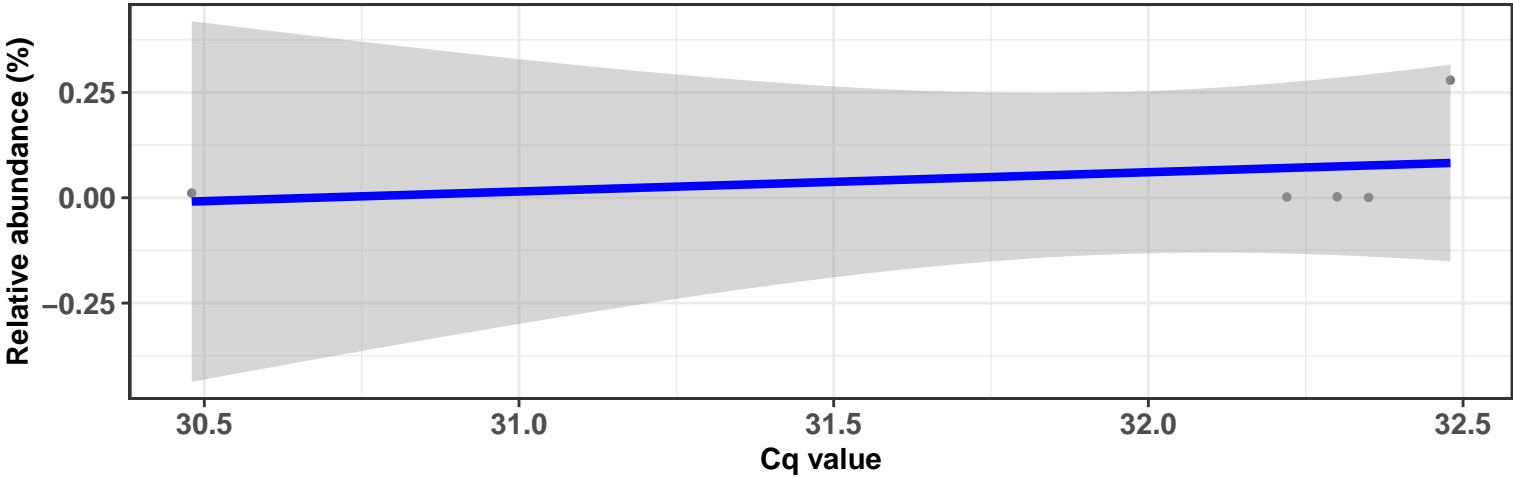


Correlation within: REF-DIC

$\log_e(S) = 5.063$ ,  $p = 0.406$ ,  $\hat{\rho}_{\text{Spearman}} = -0.317$ ,  $\text{CI}_{95\%} [-1.036, 0.281]$ ,  $n_{\text{pairs}} = 9$

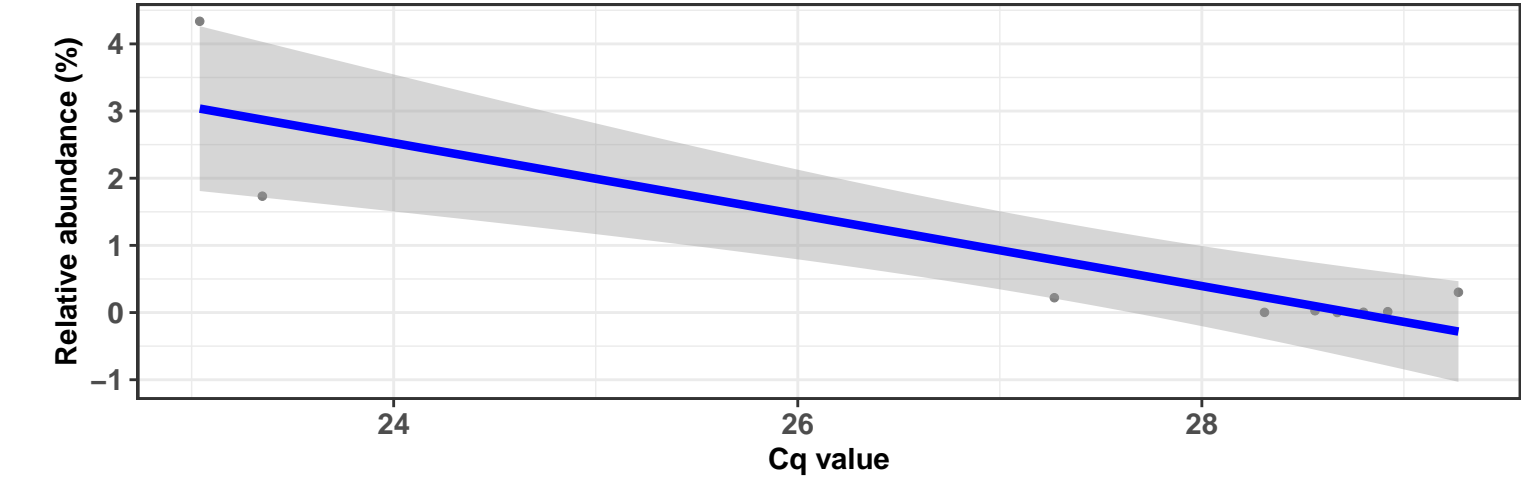


Correlation within: REF-DIM



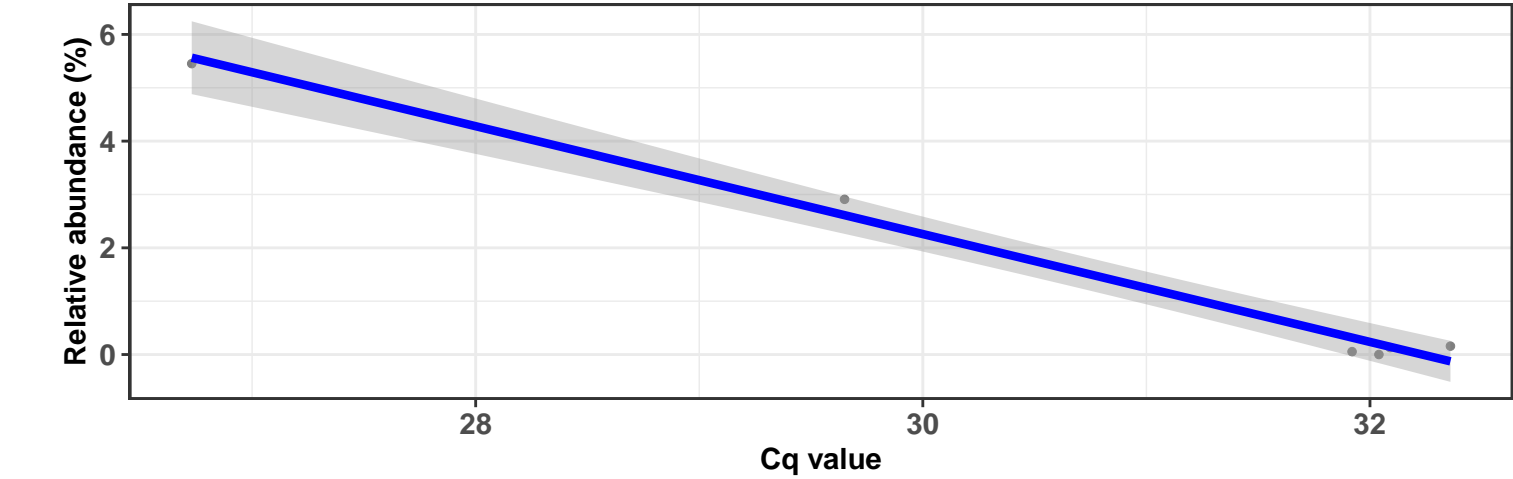
Correlation within: IM-DIC

$\log_e(S) = 5.159$ ,  $p = 0.224$ ,  $\hat{\rho}_{\text{Spearman}} = -0.450$ ,  $\text{CI}_{95\%} [-1.327, 0.318]$ ,  $n_{\text{pairs}} = 9$



Correlation within: IM-DIM

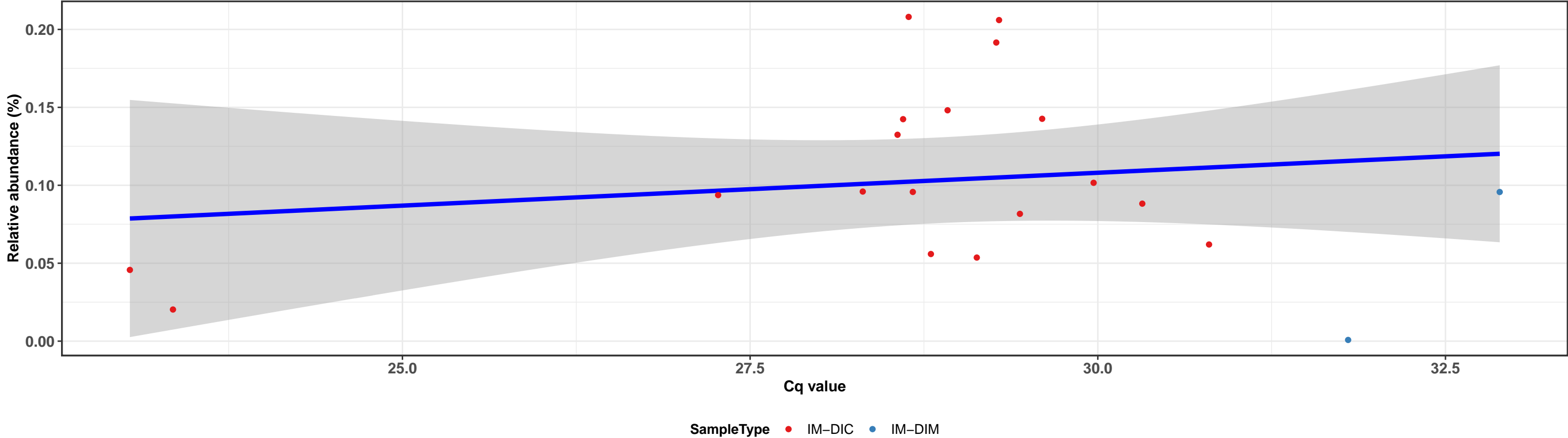
$\log_e(S) = 3.951$ ,  $p = 0.329$ ,  $\hat{\rho}_{\text{Spearman}} = -0.486$ ,  $\text{CI}_{95\%} [-1.611, 0.530]$ ,  $n_{\text{pairs}} = 6$



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

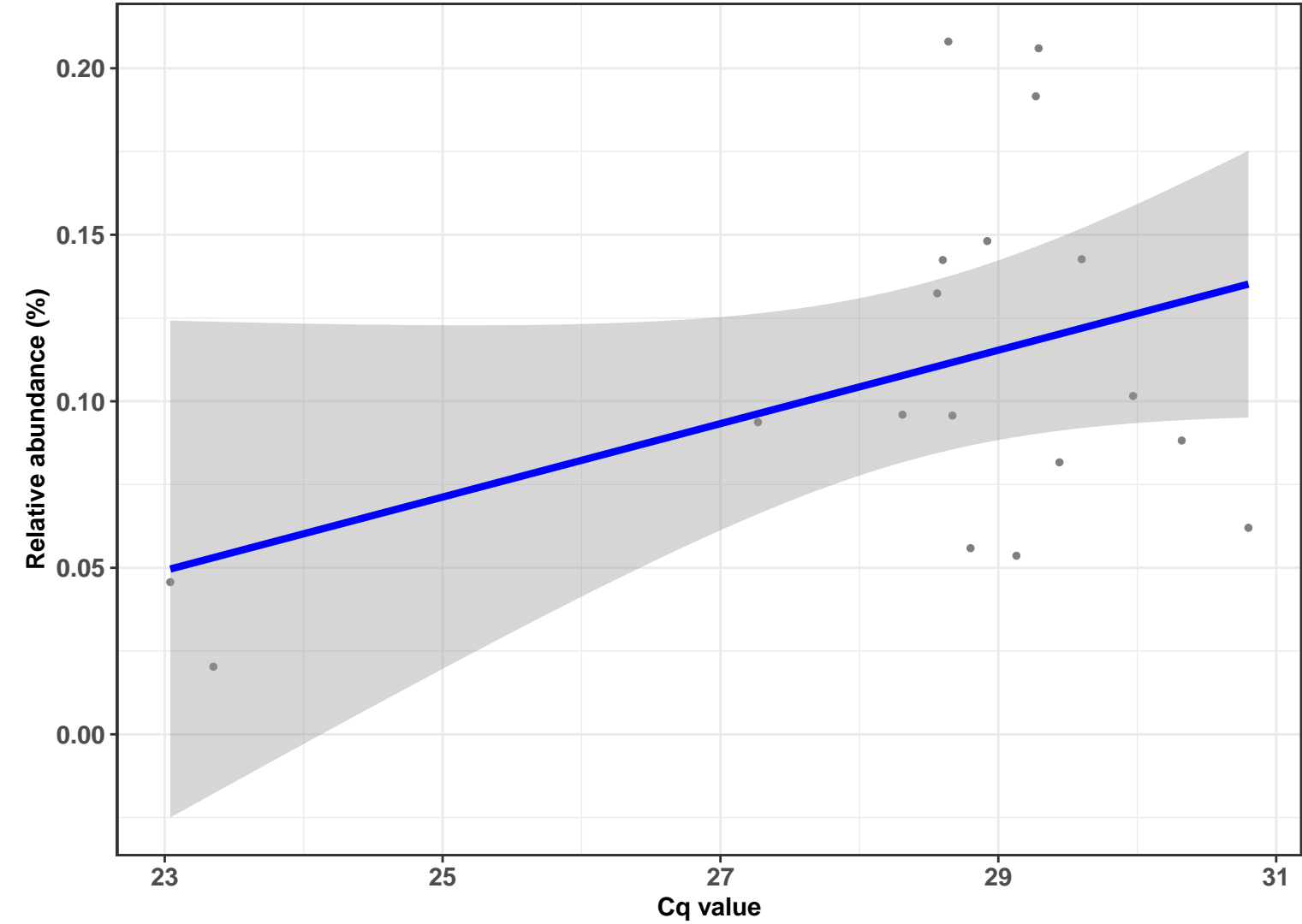
Correlation with all samples

$\log_e(S) = 7.199$ ,  $p = 0.980$ ,  $\hat{\rho}_{\text{Spearman}} = -0.006$ ,  $\text{CI}_{95\%} [-0.512, 0.439]$ ,  $n_{\text{pairs}} = 20$

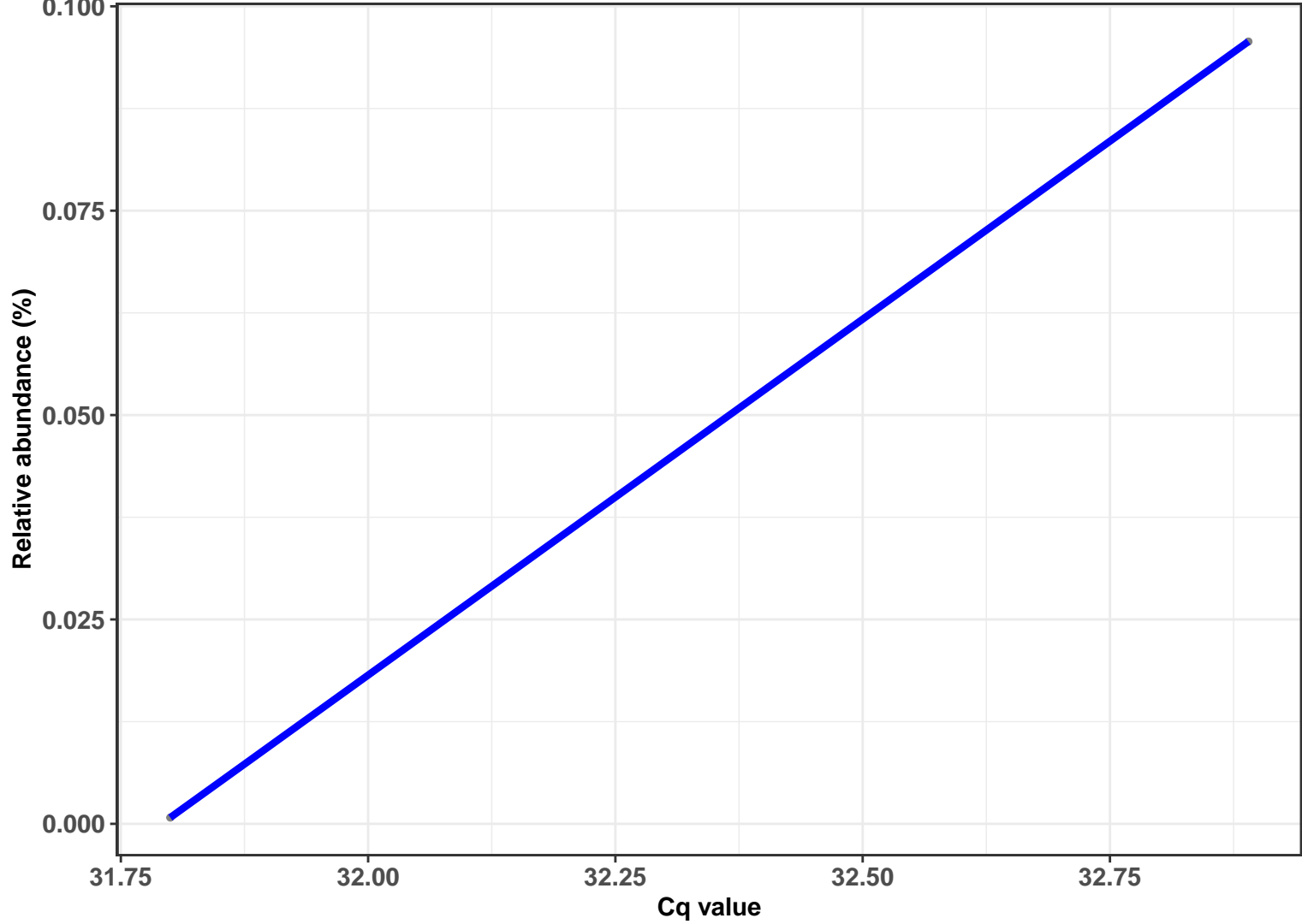


Correlation within: IM-DIC

$\log_e(S) = 6.669$ ,  $p = 0.458$ ,  $\hat{\rho}_{\text{Spearman}} = 0.187$ ,  $\text{CI}_{95\%} [-0.287, 0.788]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

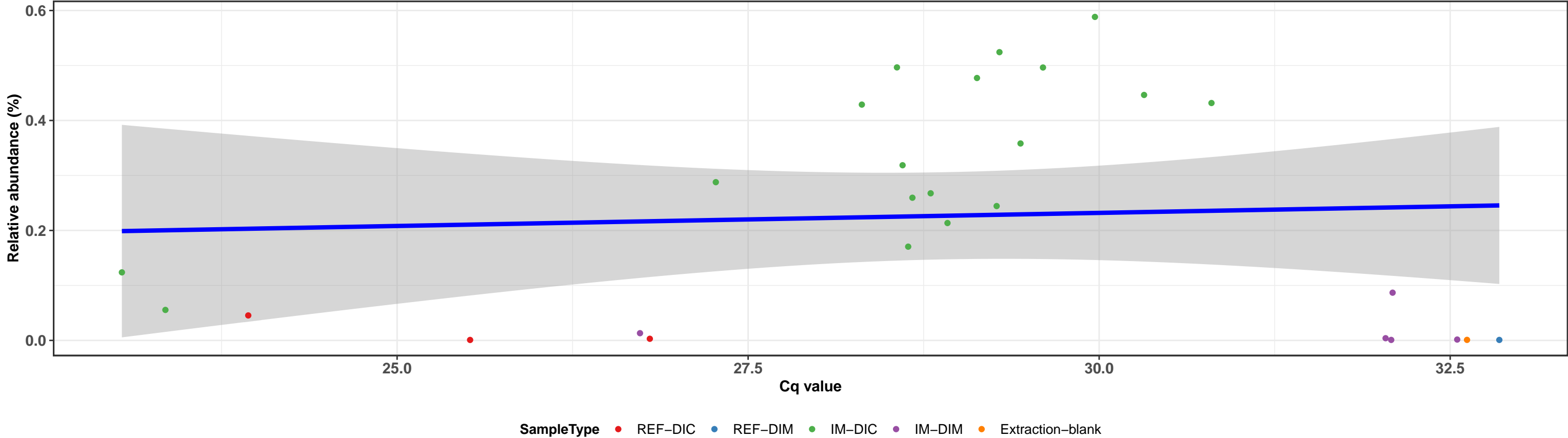




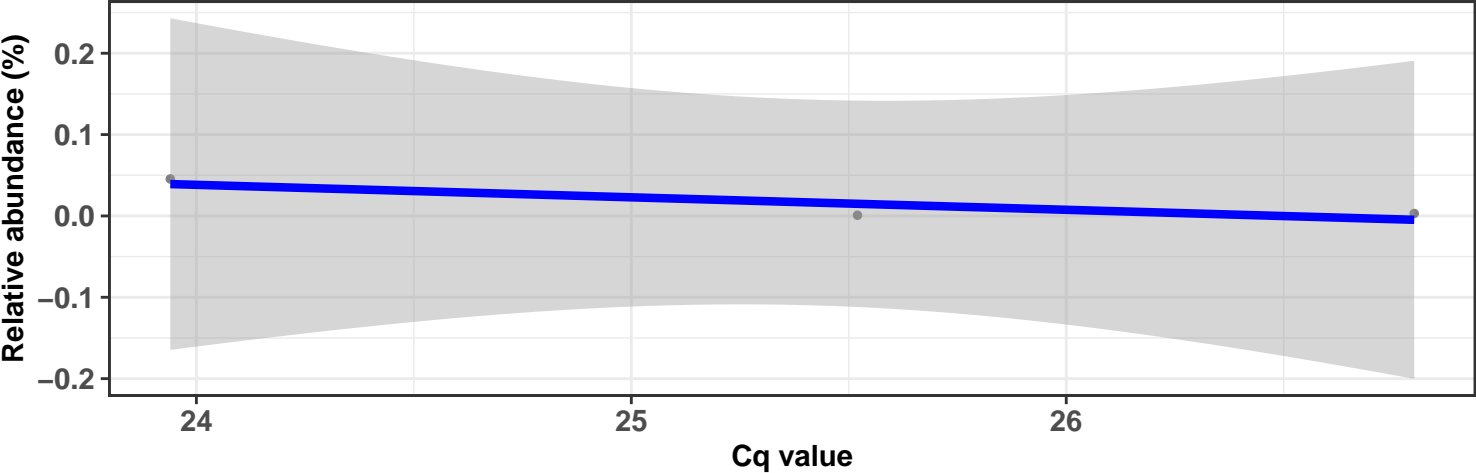
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; Ambiguous\_taxa

Correlation with all samples

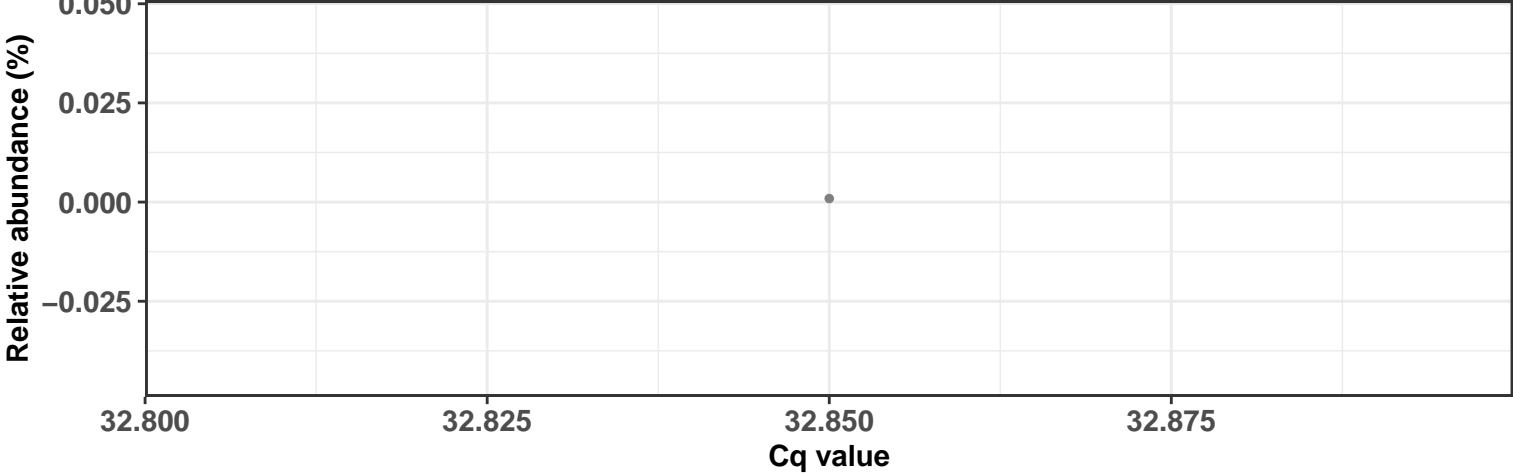
$\log_e(S) = 8.233$ ,  $p = 0.879$ ,  $\hat{\rho}_{\text{Spearman}} = -0.030$ ,  $\text{CI}_{95\%} [-0.472, 0.364]$ ,  $n_{\text{pairs}} = 28$



Correlation within: REF-DIC

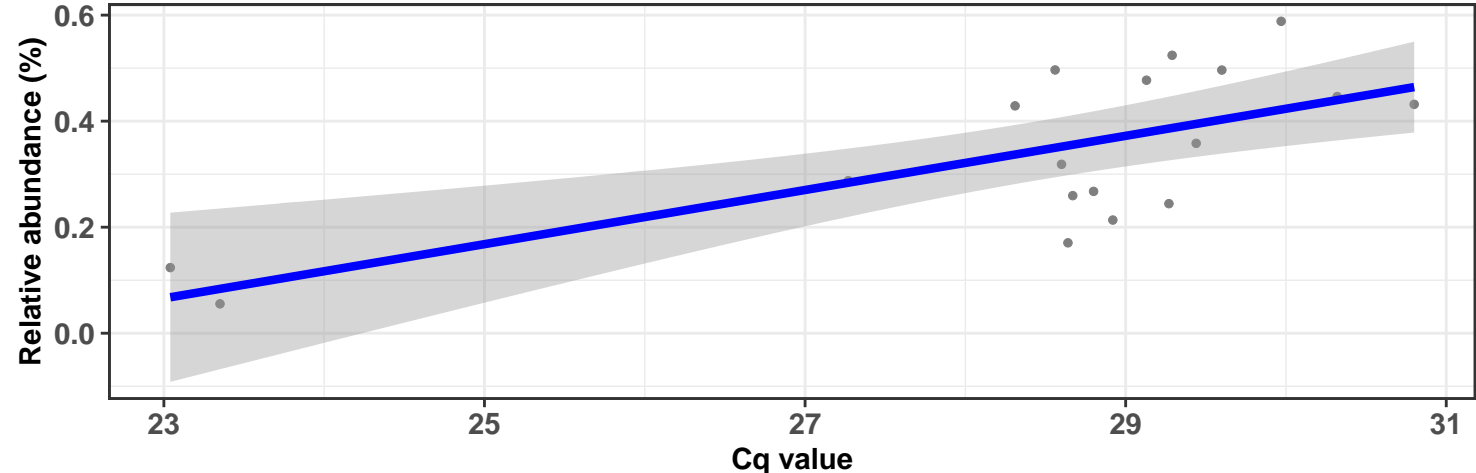


Correlation within: REF-DIM

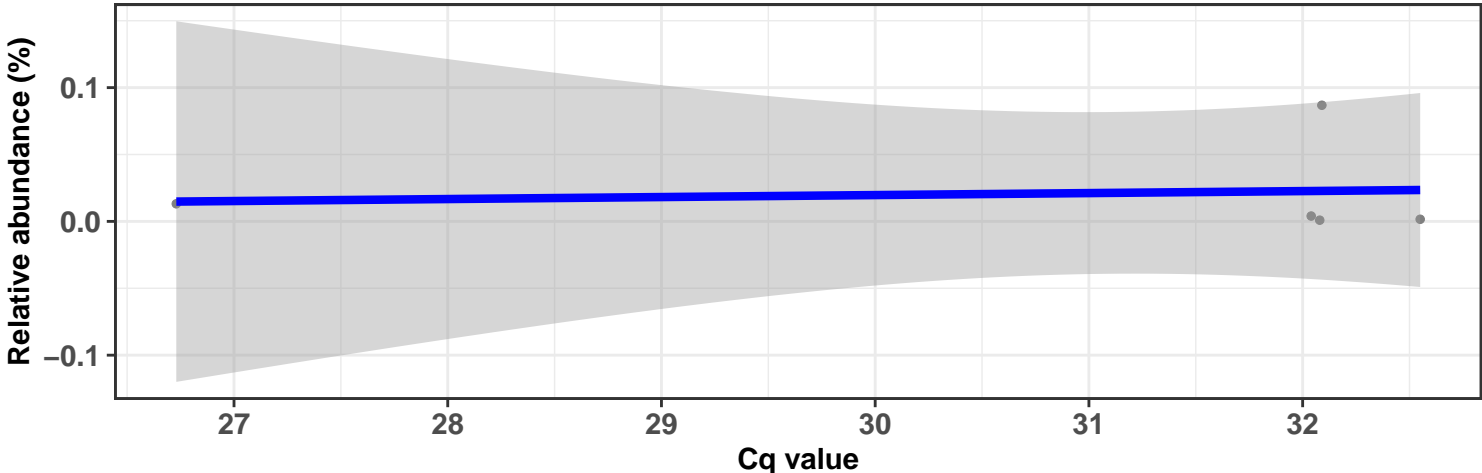


Correlation within: IM-DIC

$\log_e(S) = 6.021$ ,  $p = 0.013$ ,  $\hat{\rho}_{\text{Spearman}} = 0.575$ ,  $\text{CI}_{95\%} [0.226, 0.952]$ ,  $n_{\text{pairs}} = 18$



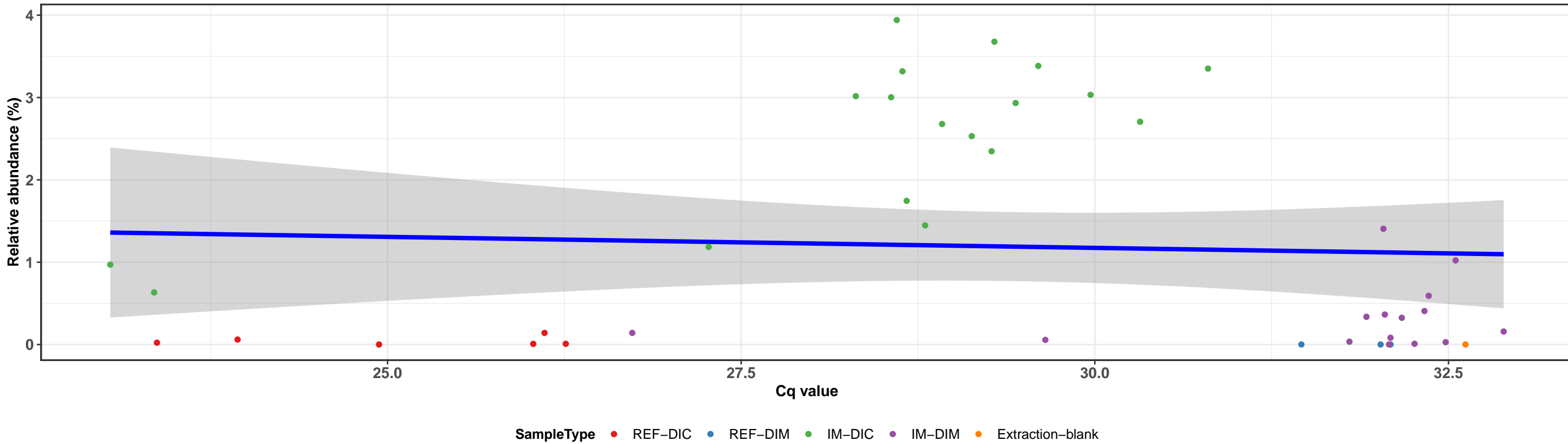
Correlation within: IM-DIM



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

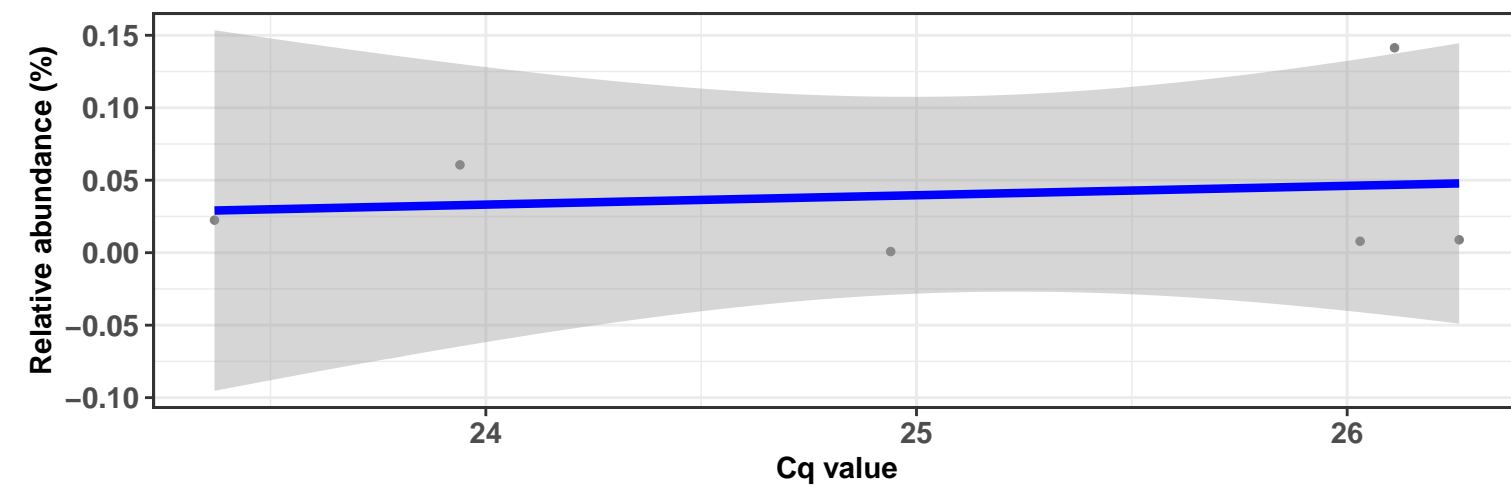
### Correlation with all samples

$\log_e(S) = 9.662$ ,  $p = 0.232$ ,  $\hat{\rho}_{\text{Spearman}} = -0.186$ ,  $\text{CI}_{95\%} [-0.510, 0.148]$ ,  $n_{\text{pairs}} = 43$

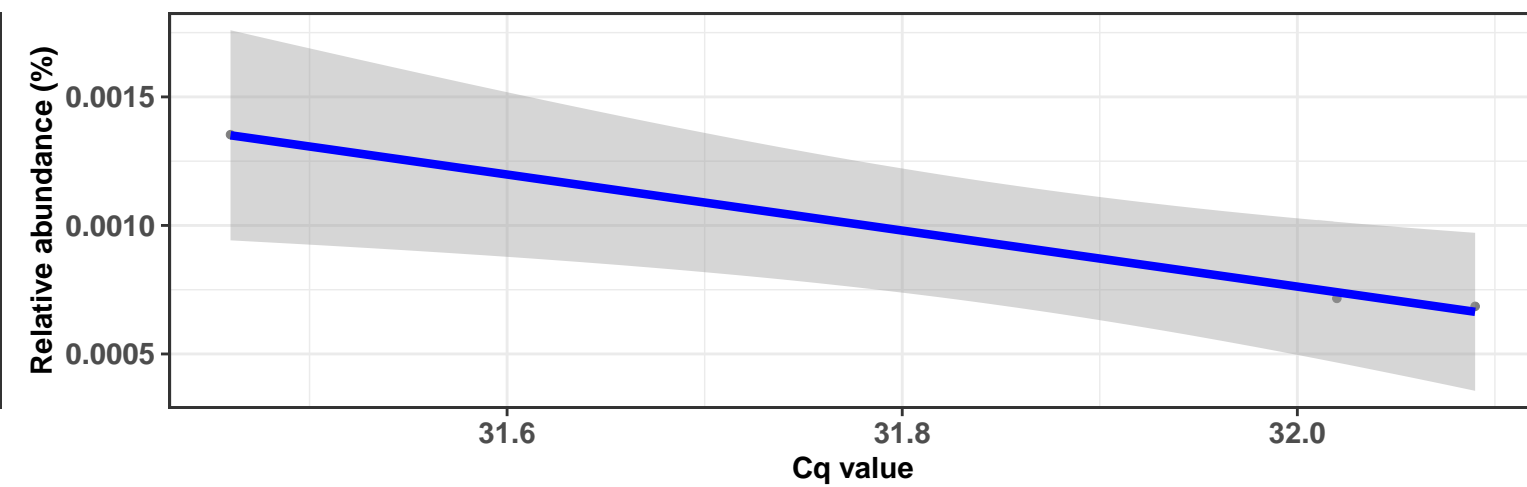


### Correlation within: REF-DIC

$\log_e(S) = 3.584$ ,  $p = 0.957$ ,  $\hat{\rho}_{\text{Spearman}} = -0.029$ ,  $\text{CI}_{95\%} [-1.049, 0.938]$ ,  $n_{\text{pairs}} = 6$

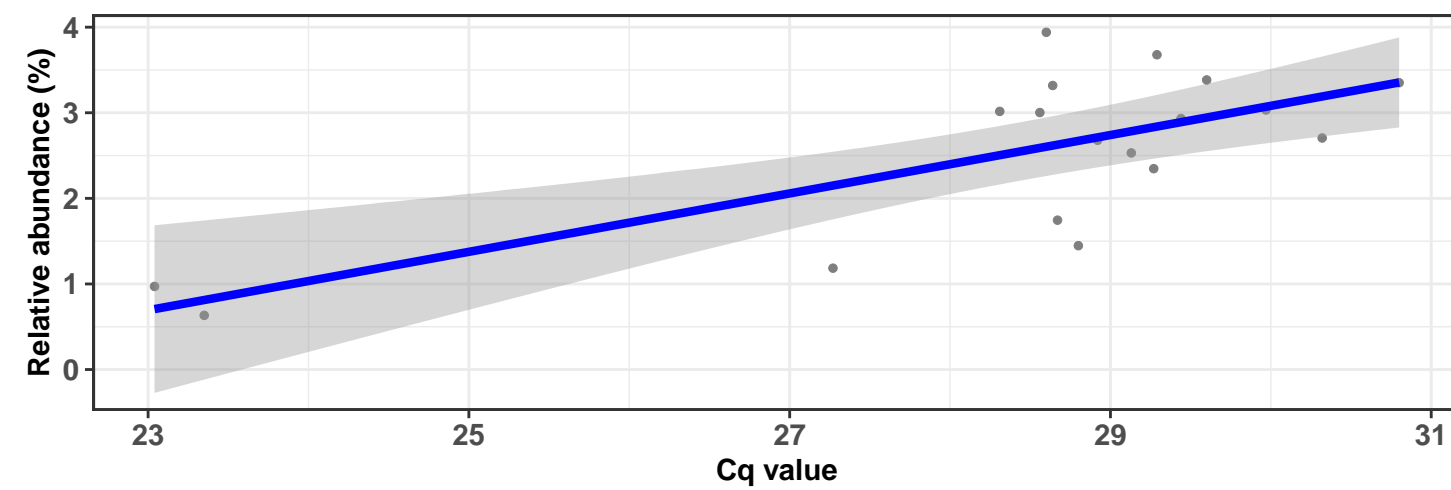


### Correlation within: REF-DIM



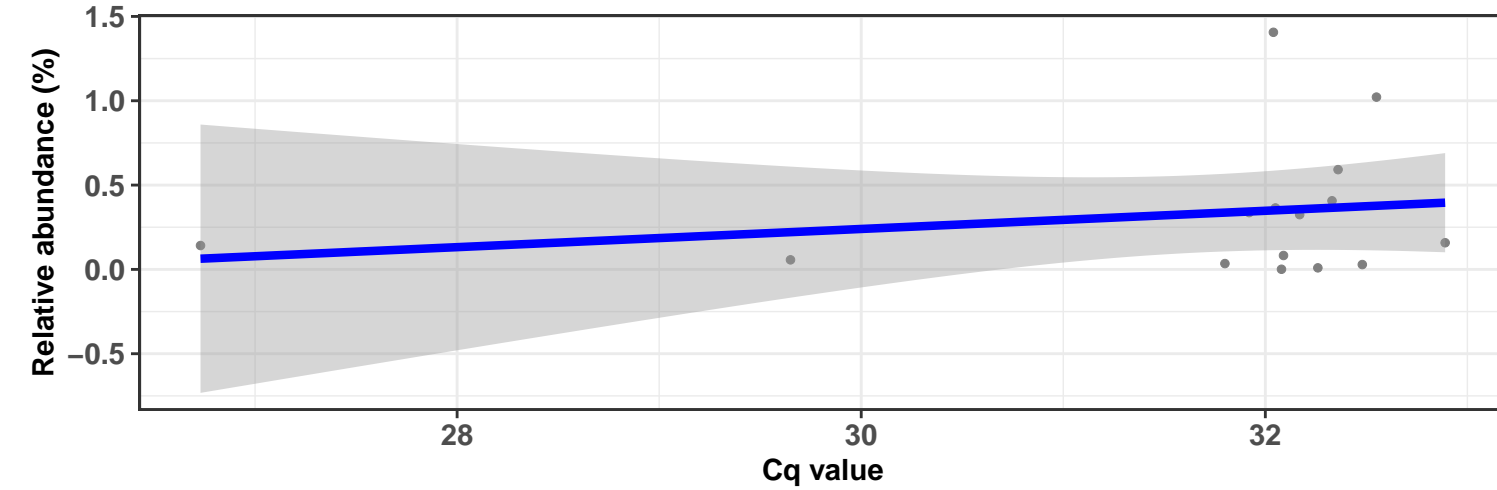
### Correlation within: IM-DIC

$\log_e(S) = 6.215$ ,  $p = 0.042$ ,  $\hat{\rho}_{\text{Spearman}} = 0.484$ ,  $\text{CI}_{95\%} [0.101, 0.921]$ ,  $n_{\text{pairs}} = 18$



### Correlation within: IM-DIM

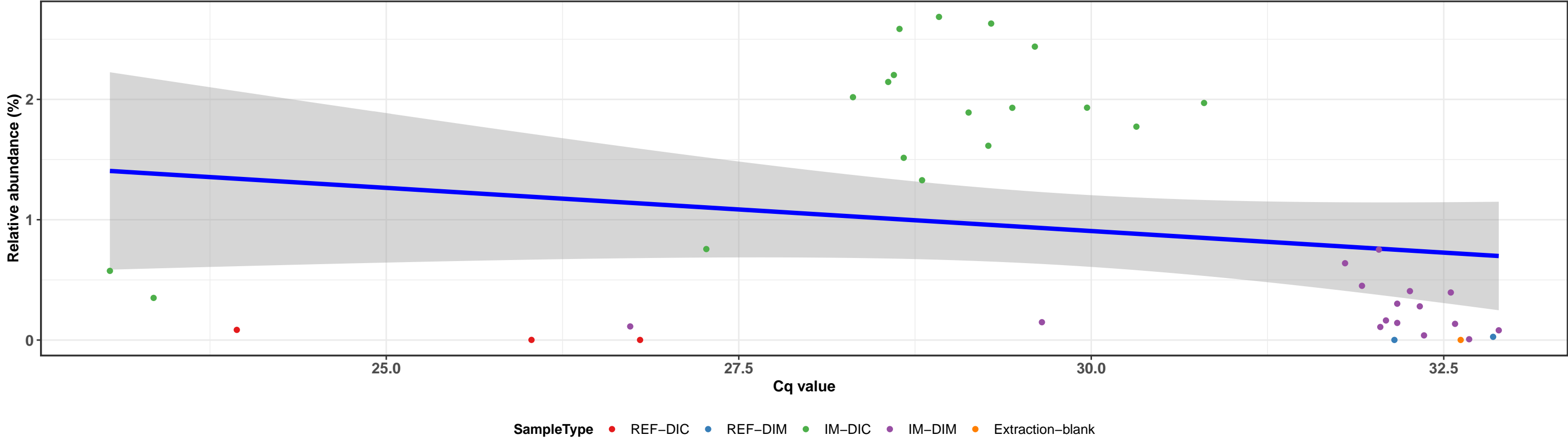
$\log_e(S) = 6.136$ ,  $p = 0.533$ ,  $\hat{\rho}_{\text{Spearman}} = 0.175$ ,  $\text{CI}_{95\%} [-0.372, 0.655]$ ,  $n_{\text{pairs}} = 15$



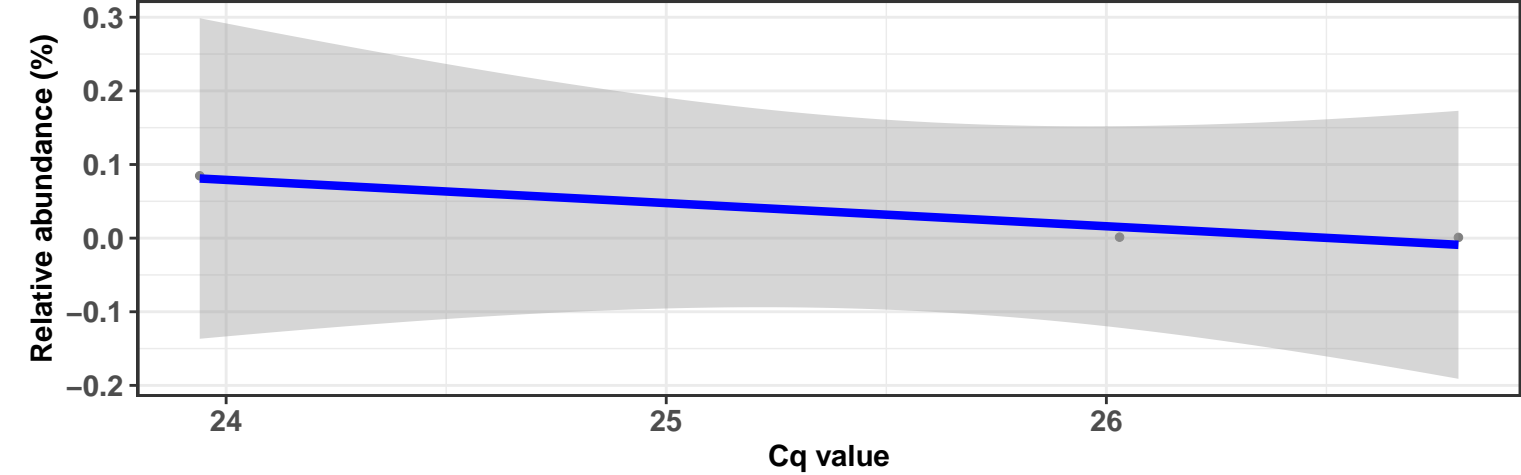
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

Correlation with all samples

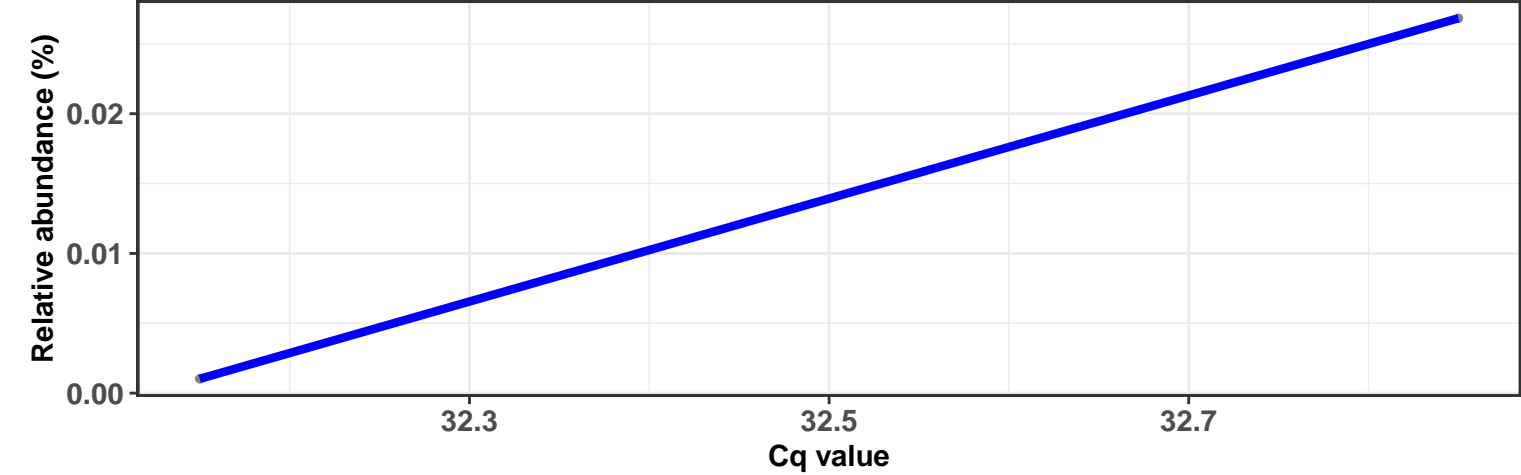
$\log_e(S) = 9.597$ ,  $p = 0.015$ ,  $\hat{\rho}_{\text{Spearman}} = -0.381$ ,  $\text{CI}_{95\%} [-0.700, -0.030]$ ,  $n_{\text{pairs}} = 40$



Correlation within: REF-DIC

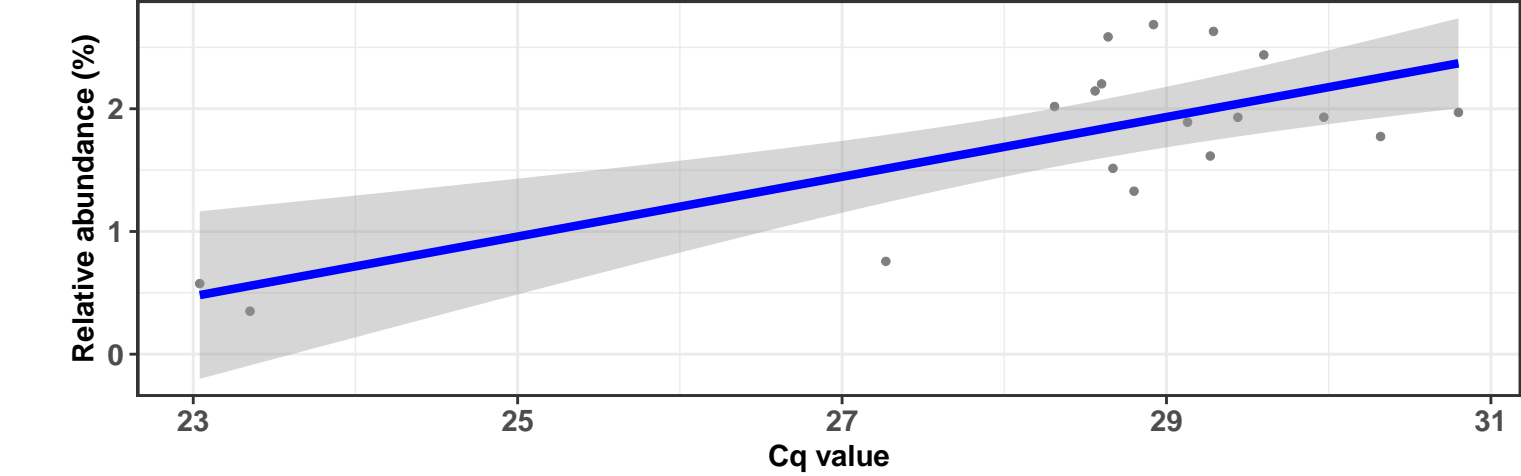


Correlation within: REF-DIM



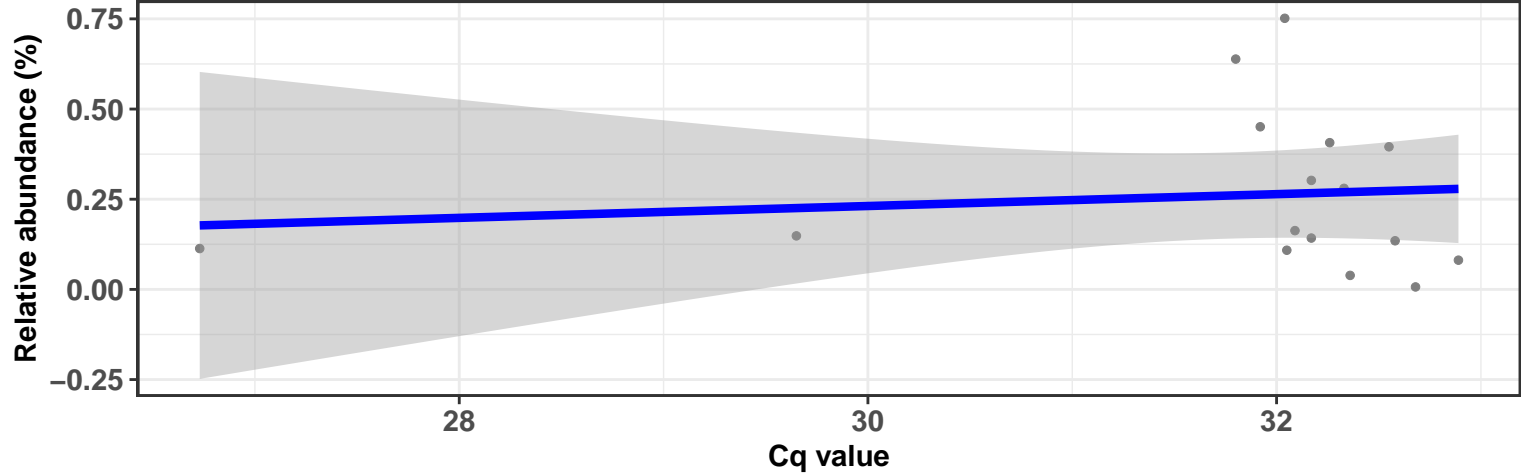
Correlation within: IM-DIC

$\log_e(S) = 6.468$ ,  $p = 0.174$ ,  $\hat{\rho}_{\text{Spearman}} = 0.335$ ,  $\text{CI}_{95\%} [-0.038, 0.747]$ ,  $n_{\text{pairs}} = 18$



Correlation within: IM-DIM

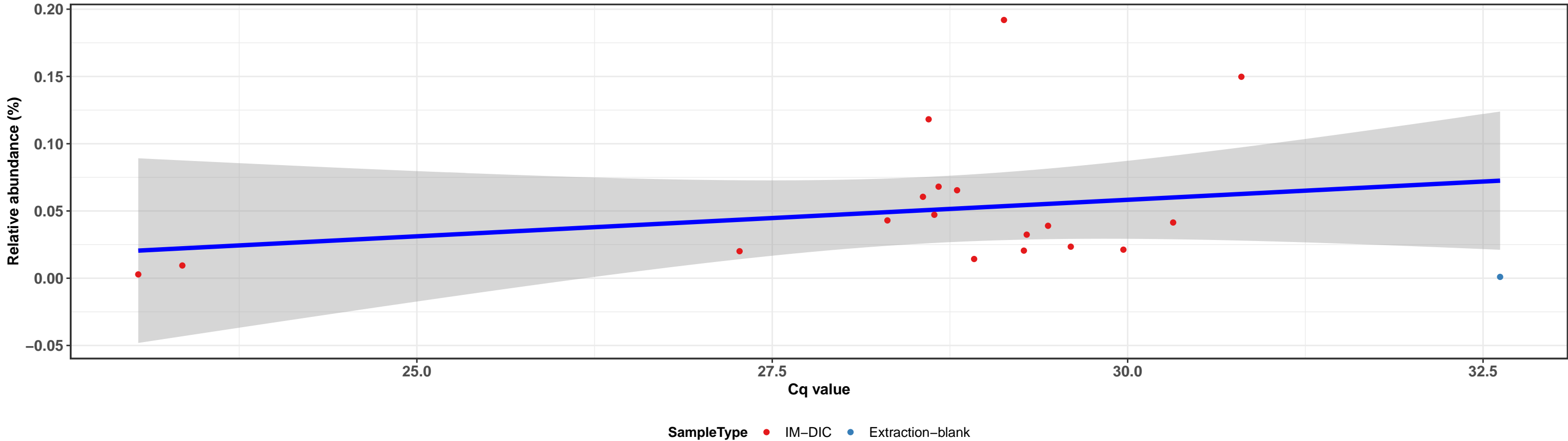
$\log_e(S) = 6.882$ ,  $p = 0.094$ ,  $\hat{\rho}_{\text{Spearman}} = -0.433$ ,  $\text{CI}_{95\%} [-0.936, 0.022]$ ,  $n_{\text{pairs}} = 16$



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

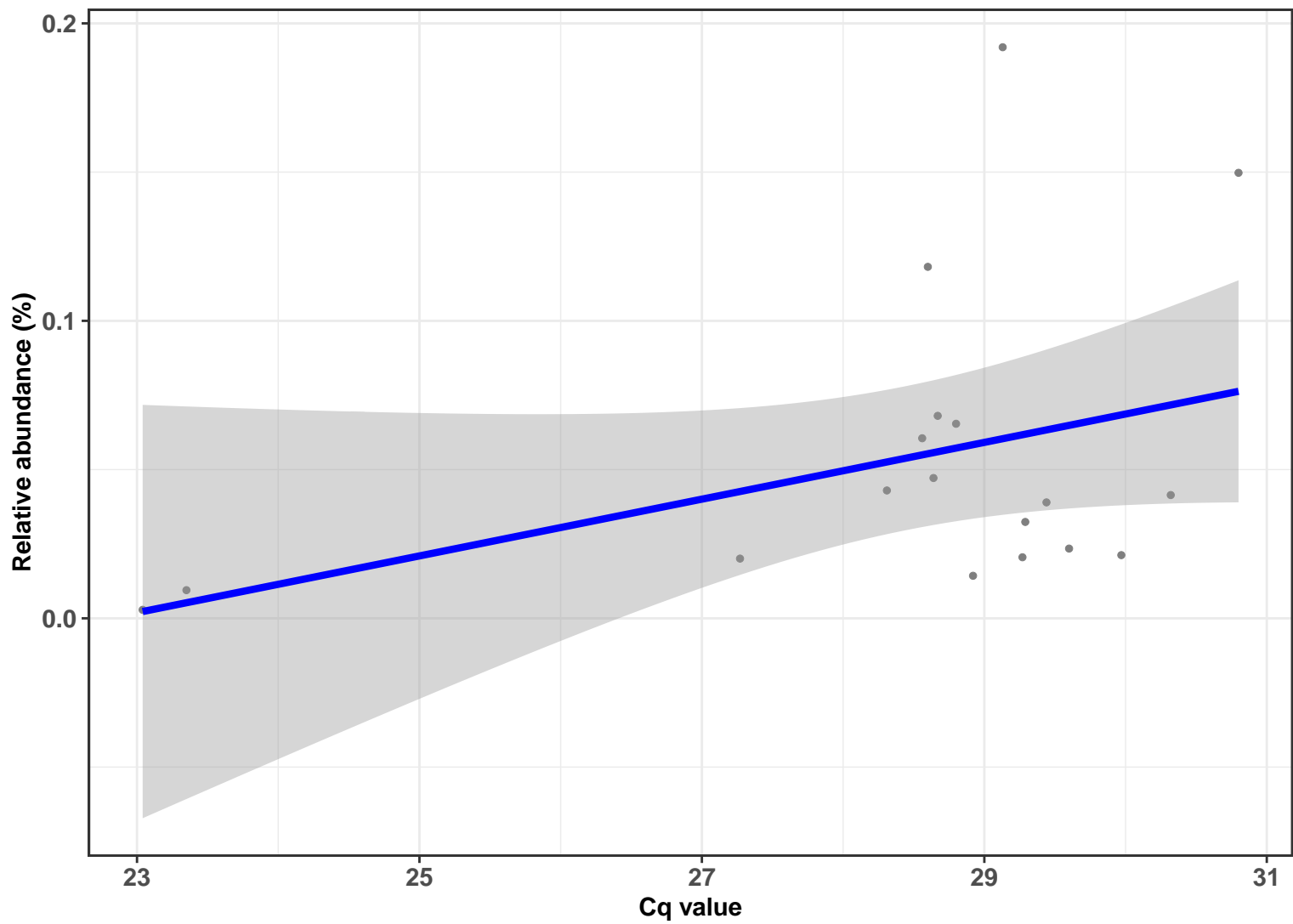
Correlation with all samples

$\log_e(S) = 6.972$ ,  $p = 0.792$ ,  $\hat{\rho}_{\text{Spearman}} = 0.065$ ,  $\text{CI}_{95\%} [-0.523, 0.633]$ ,  $n_{\text{pairs}} = 19$



Correlation within: IM-DIC

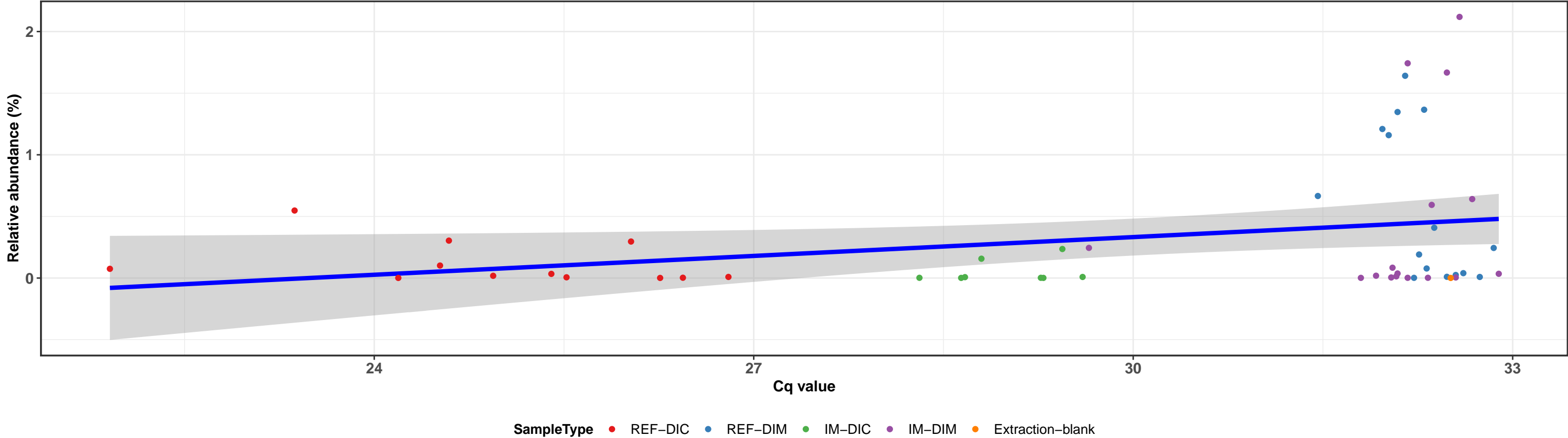
$\log_e(S) = 6.585$ ,  $p = 0.311$ ,  $\hat{\rho}_{\text{Spearman}} = 0.253$ ,  $\text{CI}_{95\%} [-0.268, 0.686]$ ,  $n_{\text{pairs}} = 18$



k\_\_Bacteria; p\_\_Spirochaetes; c\_\_Spirochaetia; o\_\_Brevinematales; f\_\_Brevinemataceae; g\_\_Brevinema; s\_\_Brevinema andersonii

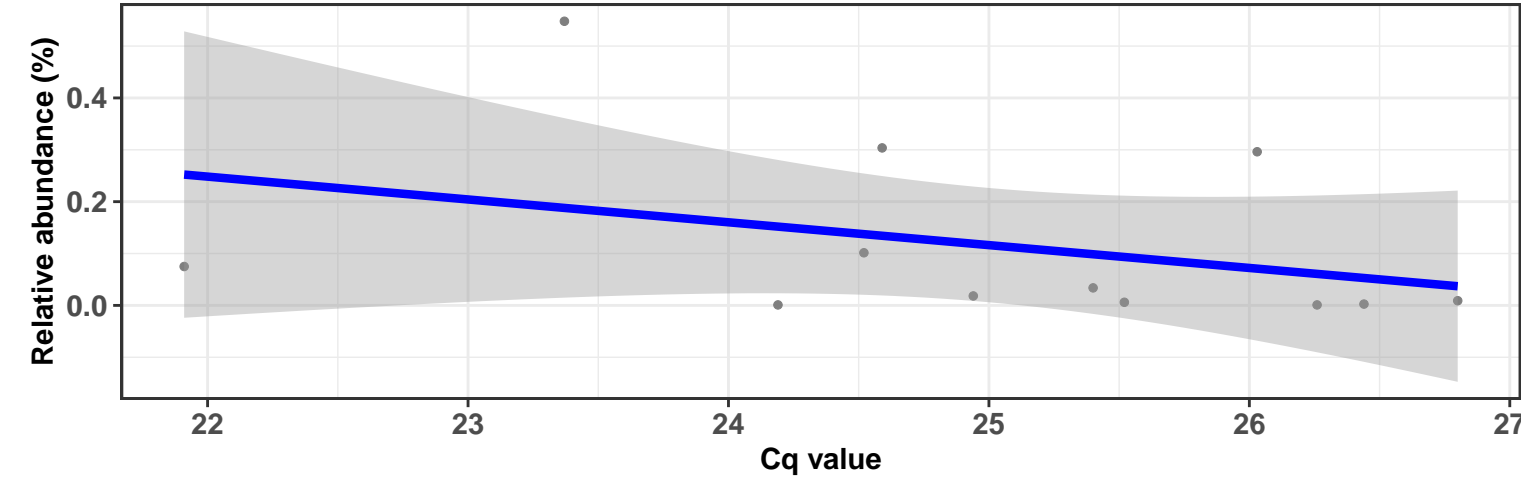
Correlation with all samples

$\log_e(S) = 9.818$ ,  $p = 0.124$ ,  $\hat{\rho}_{\text{Spearman}} = 0.216$ ,  $\text{CI}_{95\%} [-0.017, 0.484]$ ,  $n_{\text{pairs}} = 52$



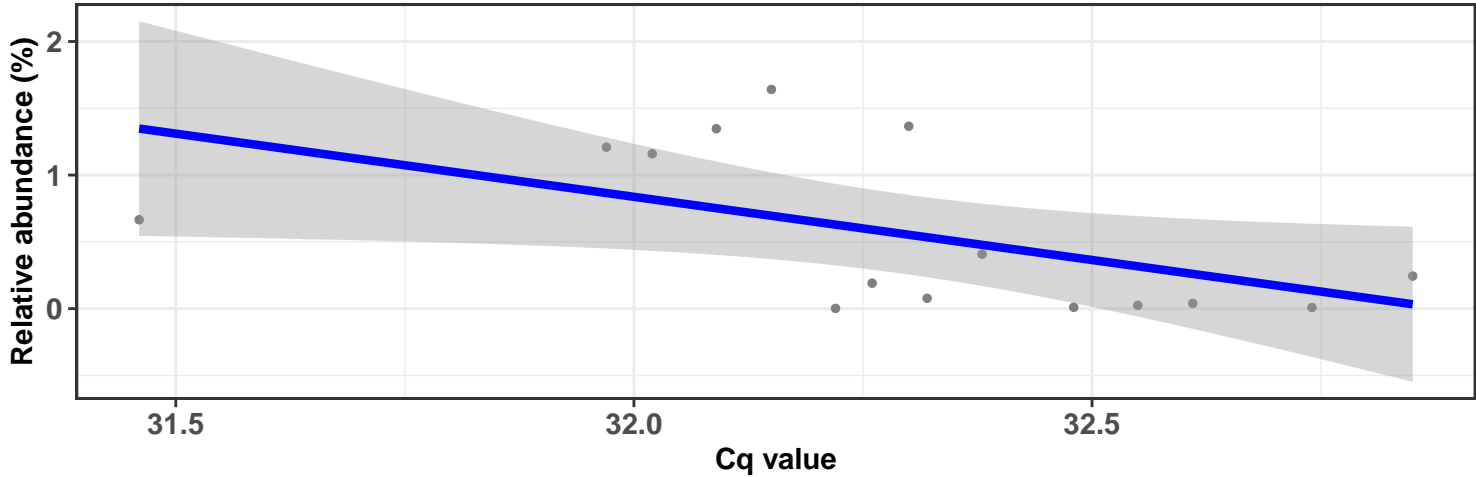
Correlation within: REF-DIC

$\log_e(S) = 6.011$ ,  $p = 0.167$ ,  $\hat{\rho}_{\text{Spearman}} = -0.427$ ,  $\text{CI}_{95\%} [-1.047, 0.137]$ ,  $n_{\text{pairs}} = 12$



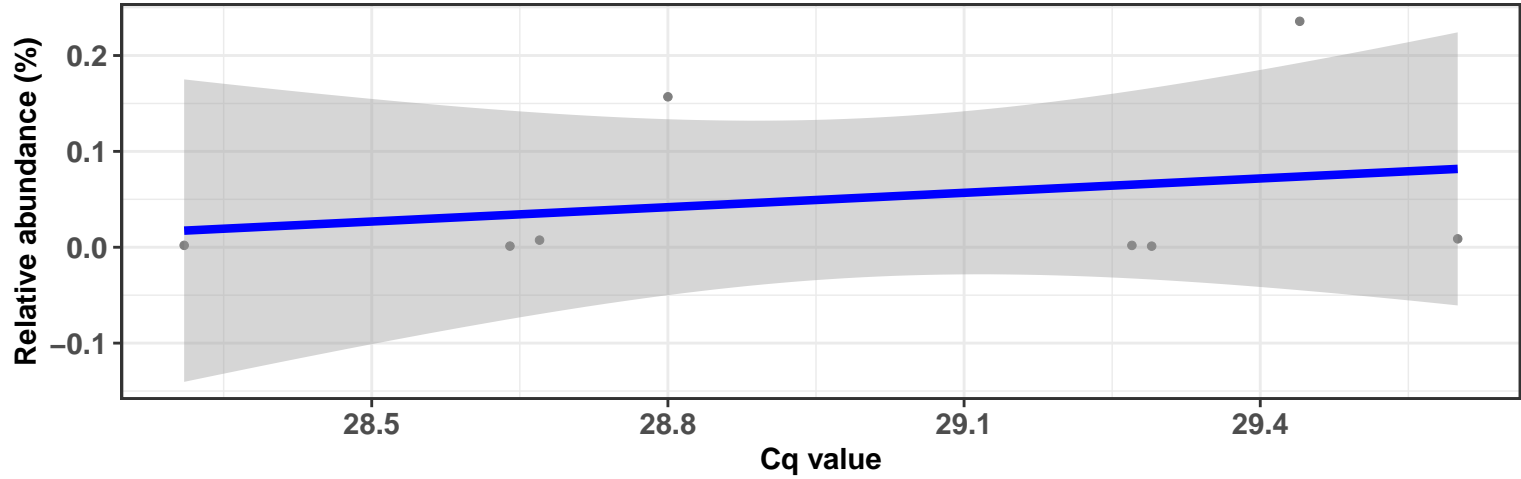
Correlation within: REF-DIM

$\log_e(S) = 6.782$ ,  $p = 0.025$ ,  $\hat{\rho}_{\text{Spearman}} = -0.575$ ,  $\text{CI}_{95\%} [-0.951, -0.305]$ ,  $n_{\text{pairs}} = 15$



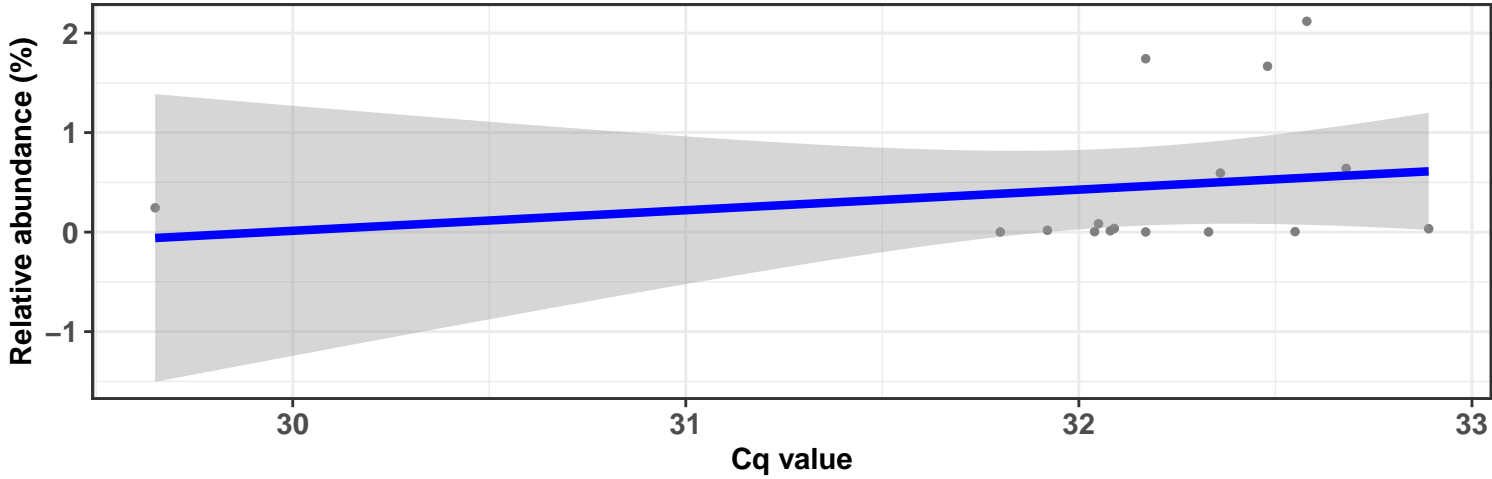
Correlation within: IM-DIC

$\log_e(S) = 4.025$ ,  $p = 0.420$ ,  $\hat{\rho}_{\text{Spearman}} = 0.333$ ,  $\text{CI}_{95\%} [-0.326, 1.149]$ ,  $n_{\text{pairs}} = 8$



Correlation within: IM-DIM

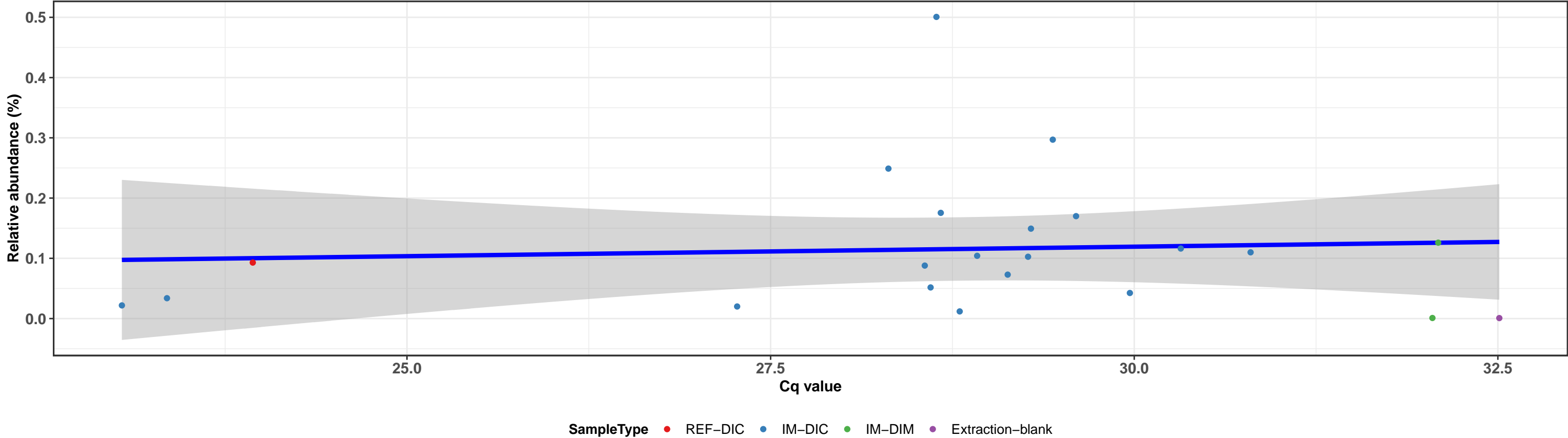
$\log_e(S) = 6.042$ ,  $p = 0.145$ ,  $\hat{\rho}_{\text{Spearman}} = 0.381$ ,  $\text{CI}_{95\%} [-0.047, 0.854]$ ,  $n_{\text{pairs}} = 16$



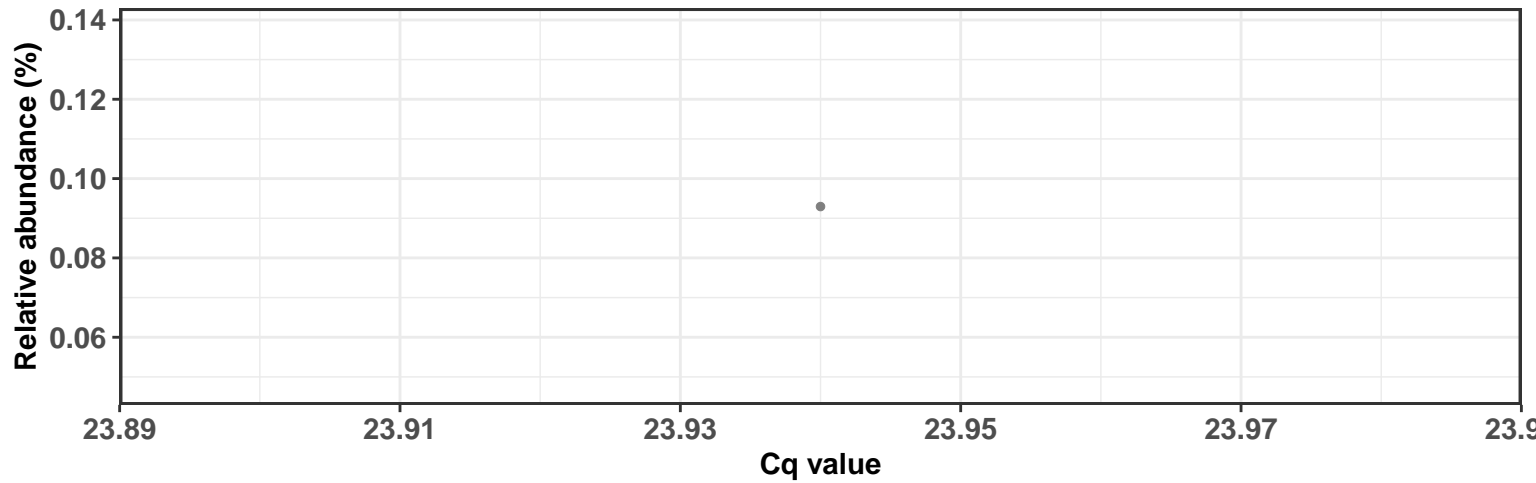
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; s\_\_uncultured bacterium

Correlation with all samples

$\log_e(S) = 7.421$ ,  $p = 0.801$ ,  $\hat{\rho}_{\text{Spearman}} = 0.057$ ,  $\text{CI}_{95\%} [-0.410, 0.592]$ ,  $n_{\text{pairs}} = 22$

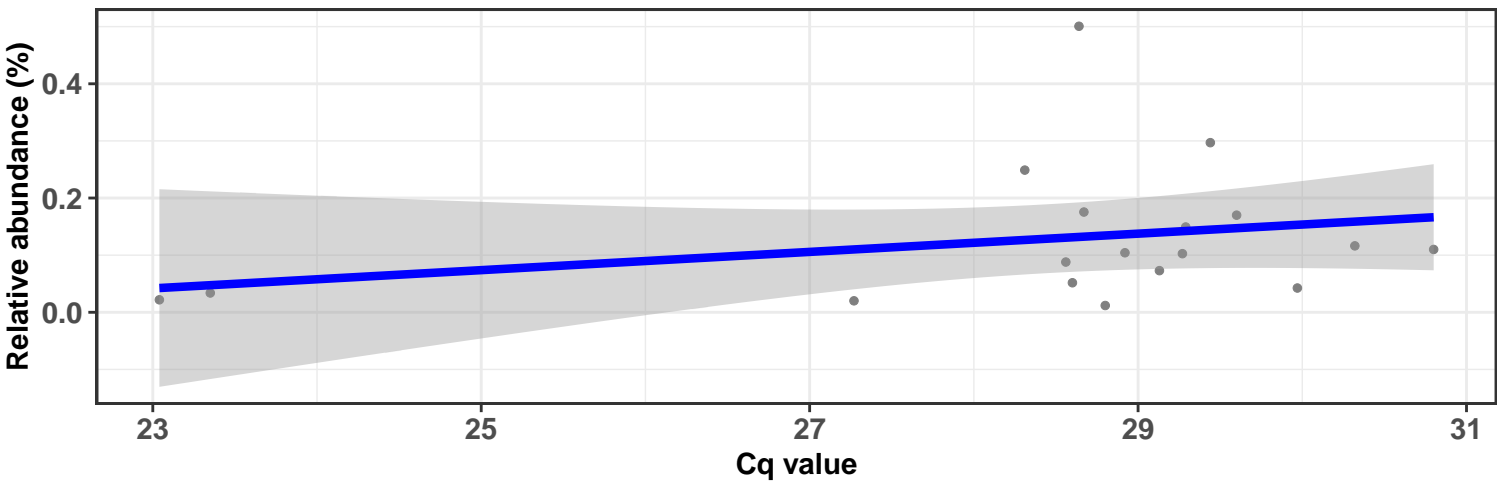


Correlation within: REF-DIC

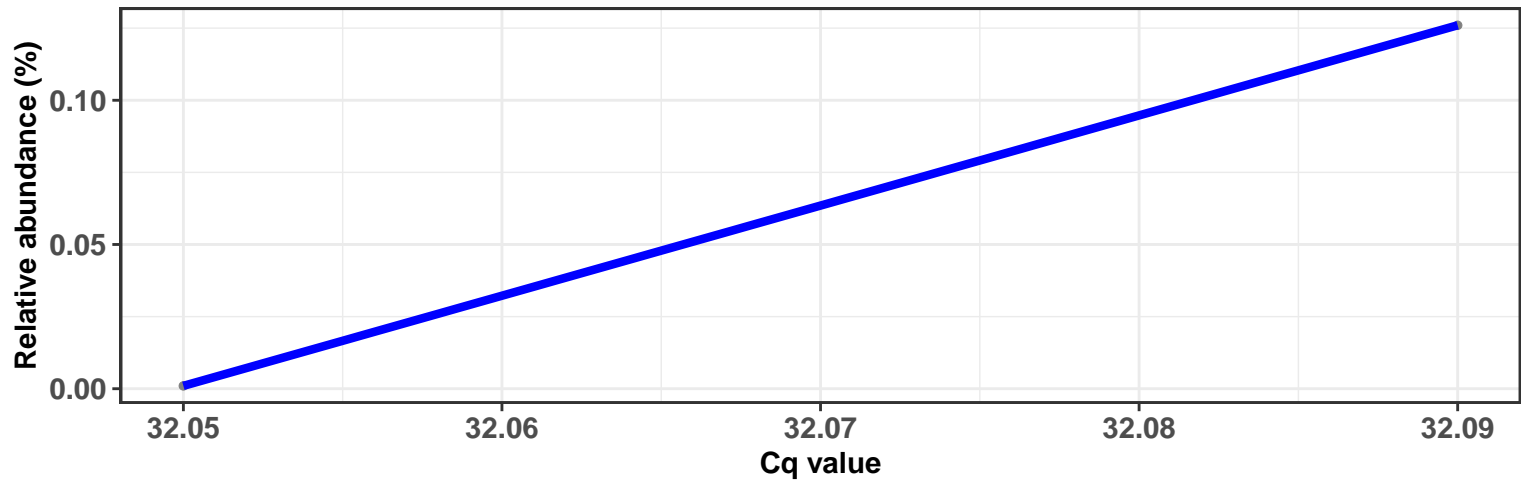


Correlation within: IM-DIC

$\log_e(S) = 6.439$ ,  $p = 0.150$ ,  $\hat{\rho}_{\text{Spearman}} = 0.354$ ,  $\text{CI}_{95\%} [-0.061, 0.781]$ ,  $n_{\text{pairs}} = 18$



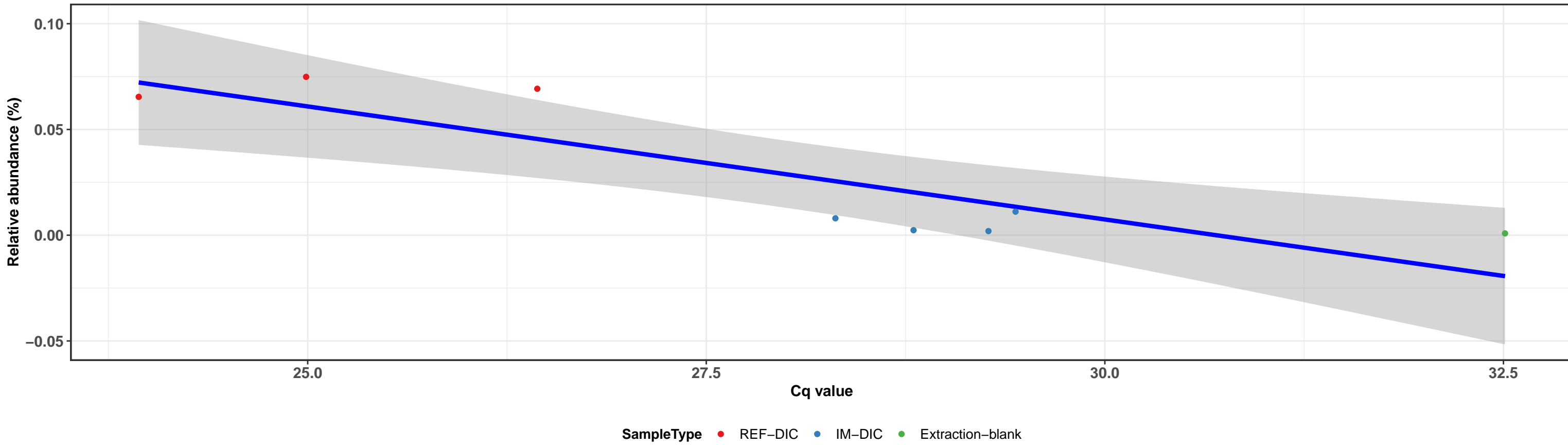
Correlation within: IM-DIM



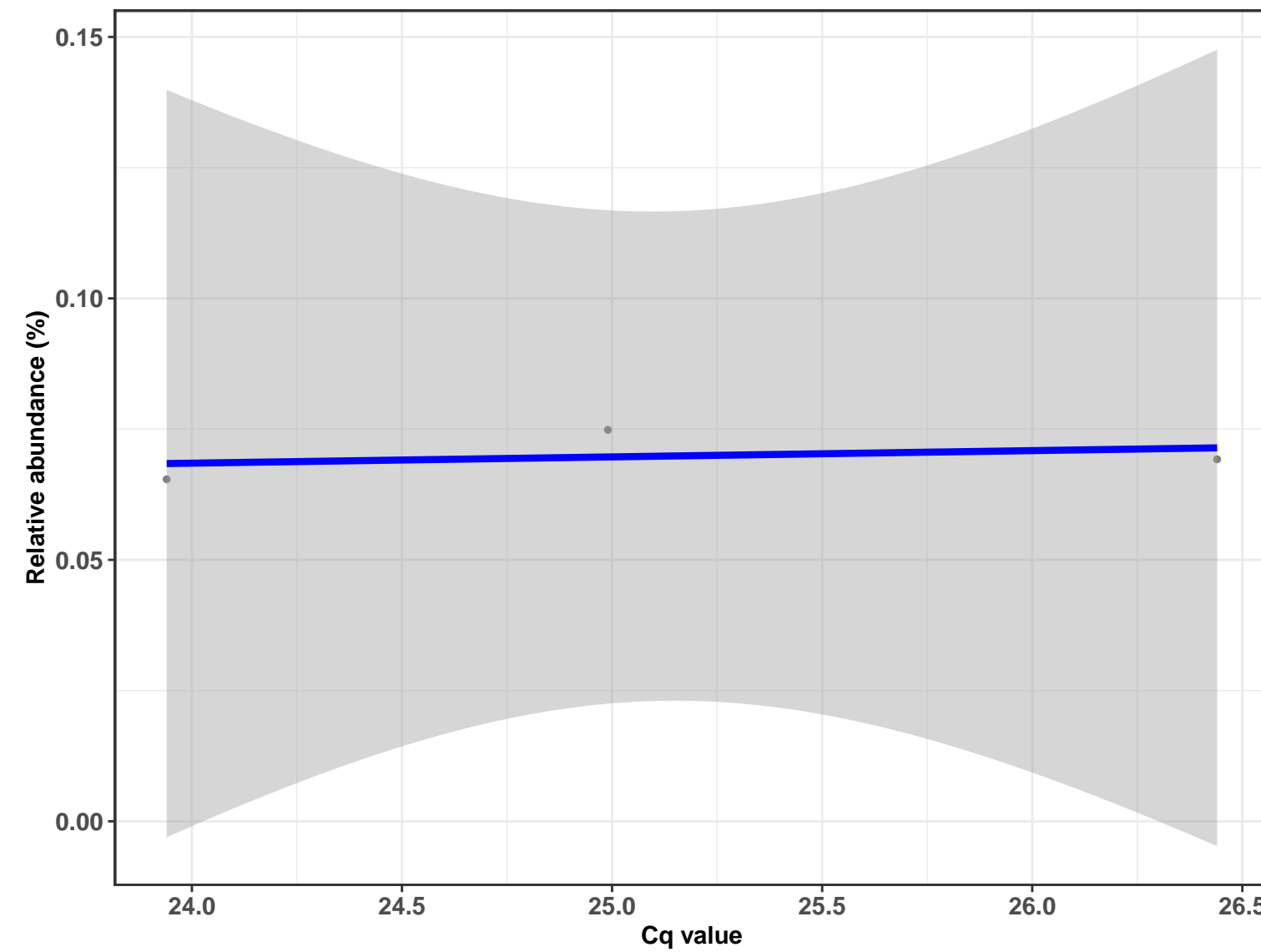
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Erysipelotrichia; o\_\_Erysipelotrichales; f\_\_Erysipelotrichaceae; NA; NA

### Correlation with all samples

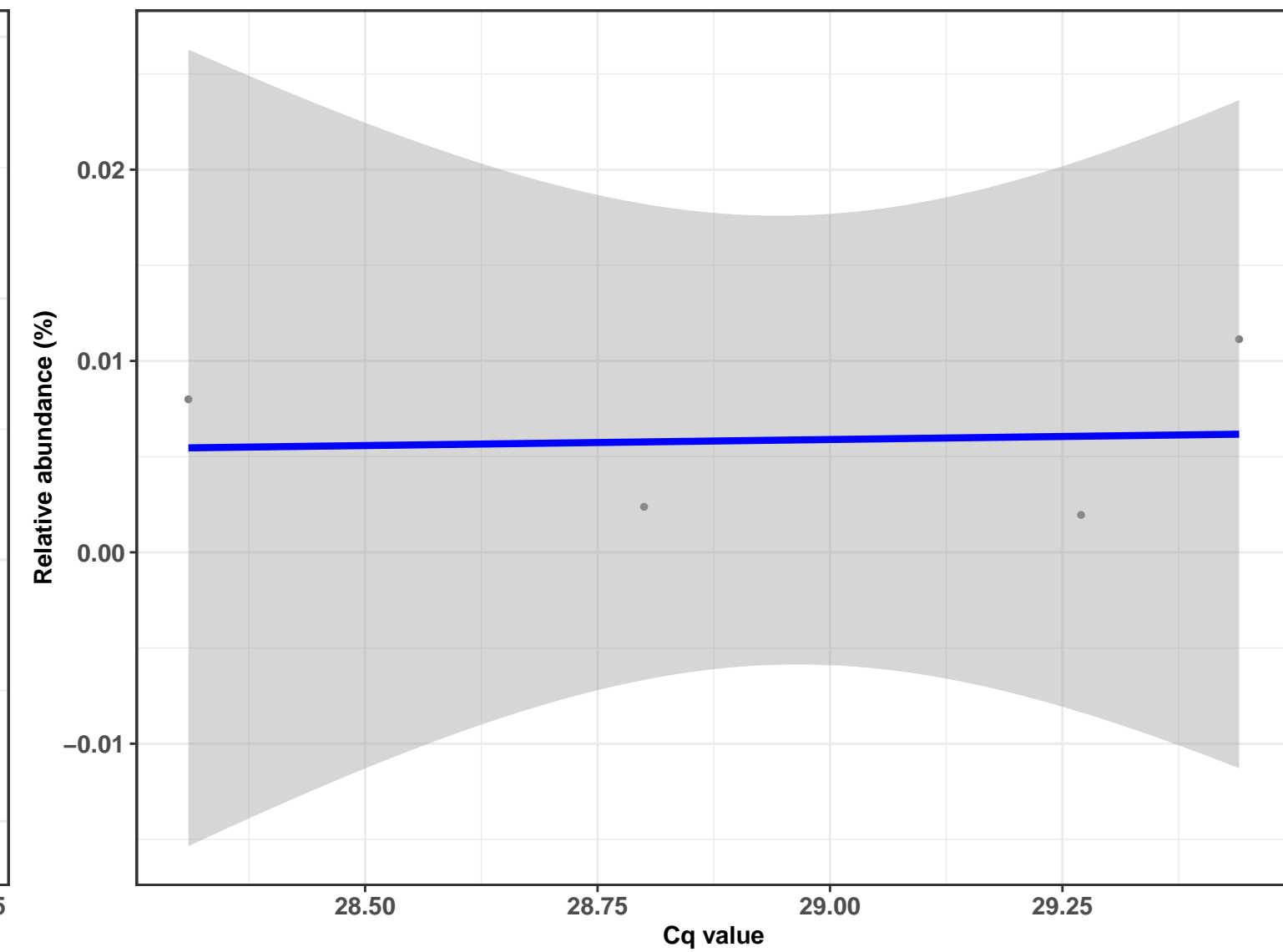
$\log_e(S) = 5.011$ ,  $p = 0.021$ ,  $\hat{\rho}_{\text{Spearman}} = -0.786$ ,  $CI_{95\%} [-1.301, -0.336]$ ,  $n_{\text{pairs}} = 8$



### Correlation within: REF-DIC



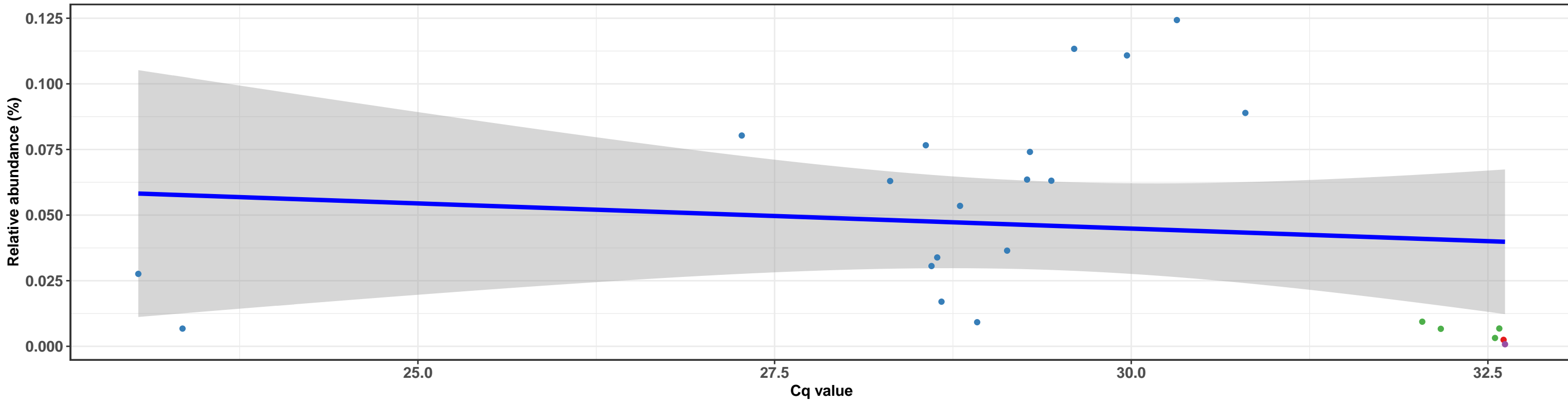
### Correlation within: IM-DIC



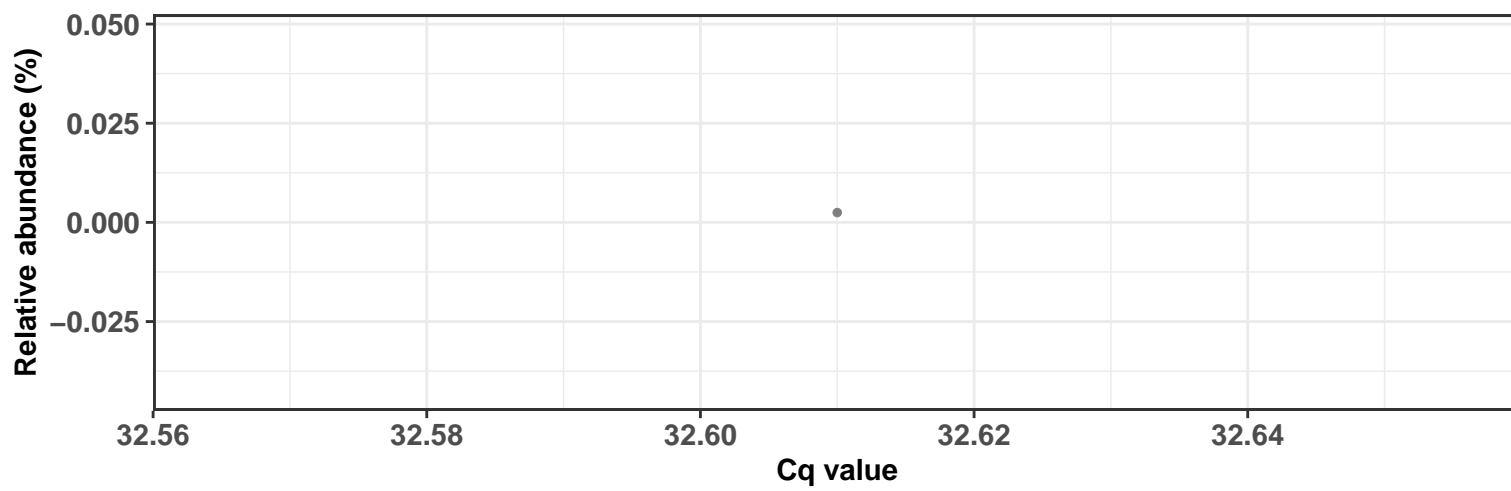
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

### Correlation with all samples

$\log_e(S) = 7.981$ ,  $p = 0.200$ ,  $\hat{\rho}_{\text{Spearman}} = -0.271$ ,  $\text{CI}_{95\%} [-0.750, 0.178]$ ,  $n_{\text{pairs}} = 24$

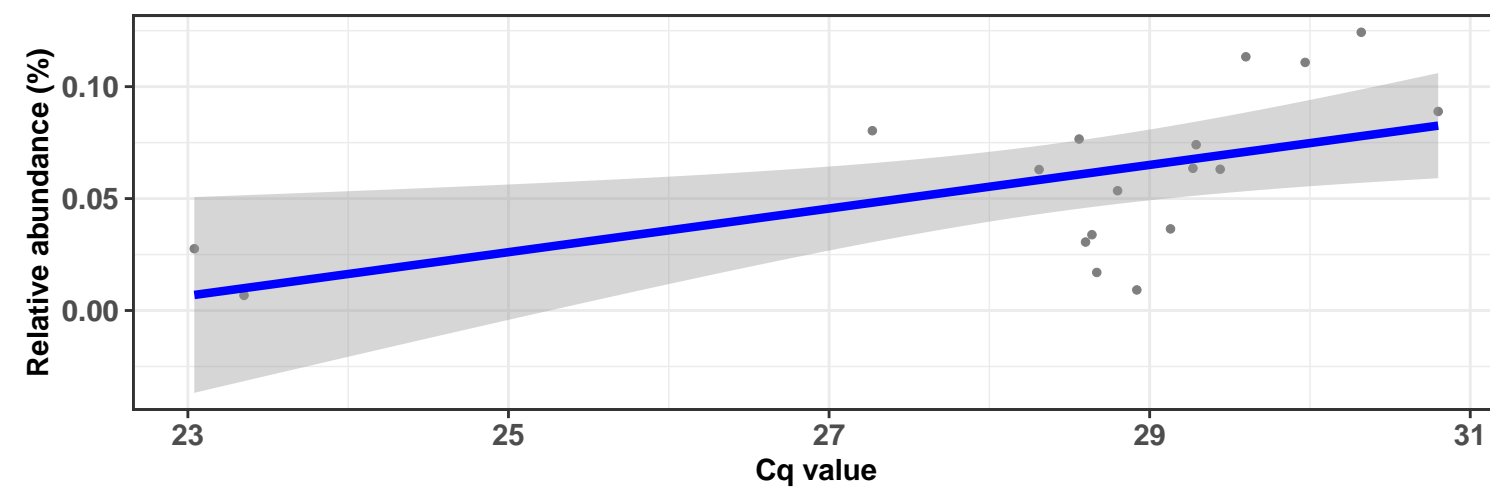


### Correlation within: REF-DIM

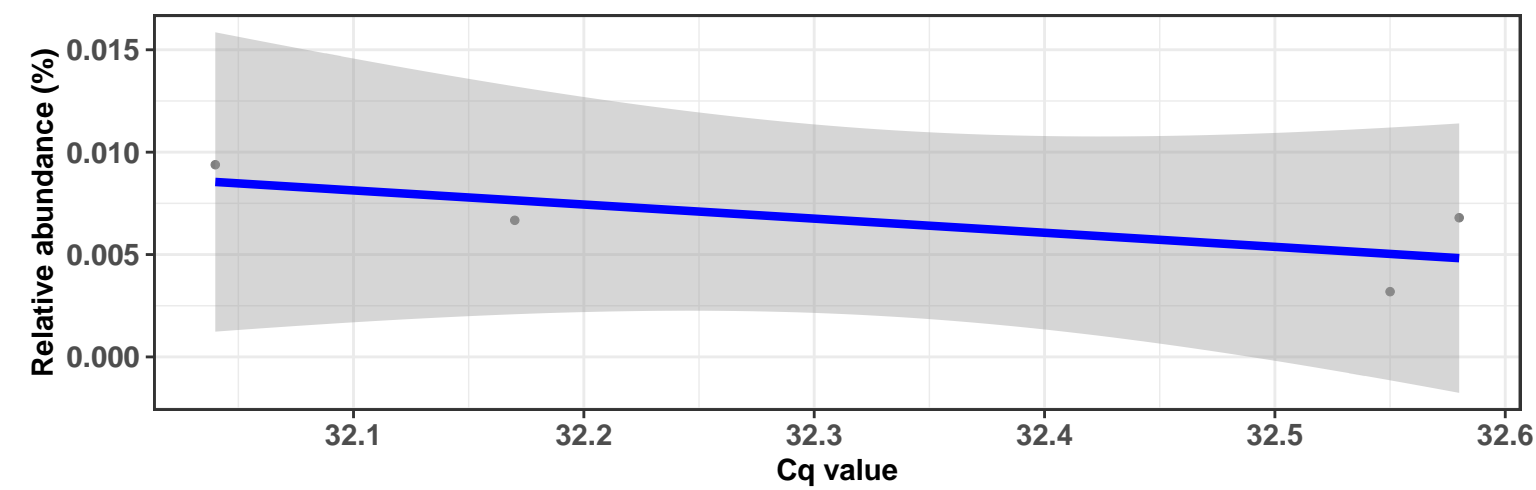


### Correlation within: IM-DIC

$\log_e(S) = 5.886$ ,  $p = 0.005$ ,  $\hat{\rho}_{\text{Spearman}} = 0.628$ ,  $\text{CI}_{95\%} [0.258, 1.057]$ ,  $n_{\text{pairs}} = 18$



### Correlation within: IM-DIM

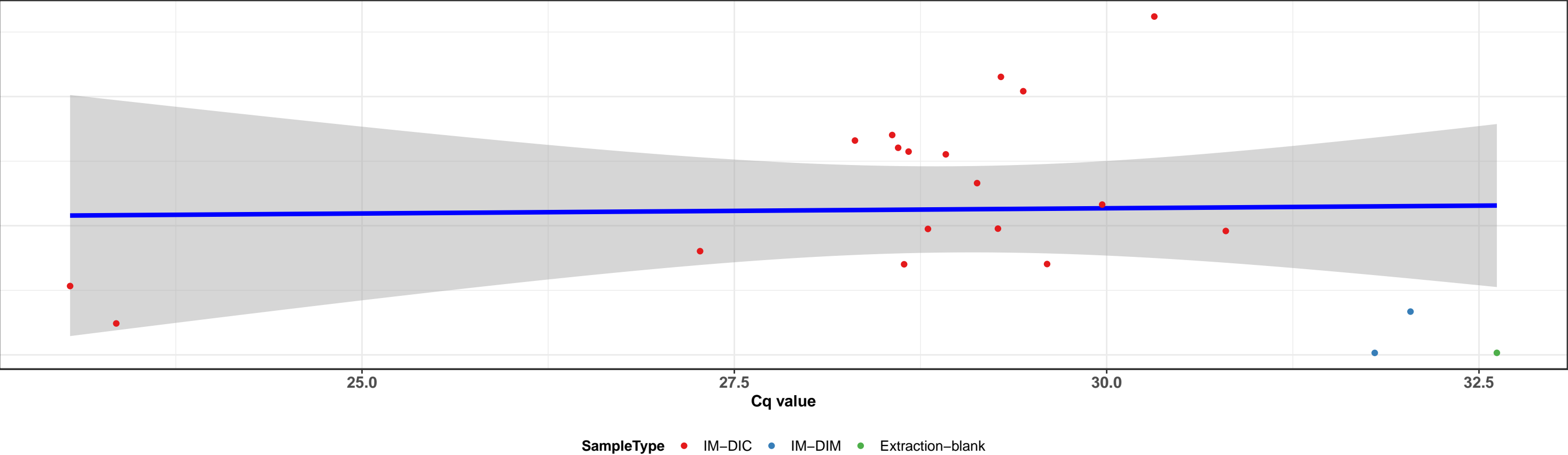




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Gracilibacillus; Ambiguous\_taxa

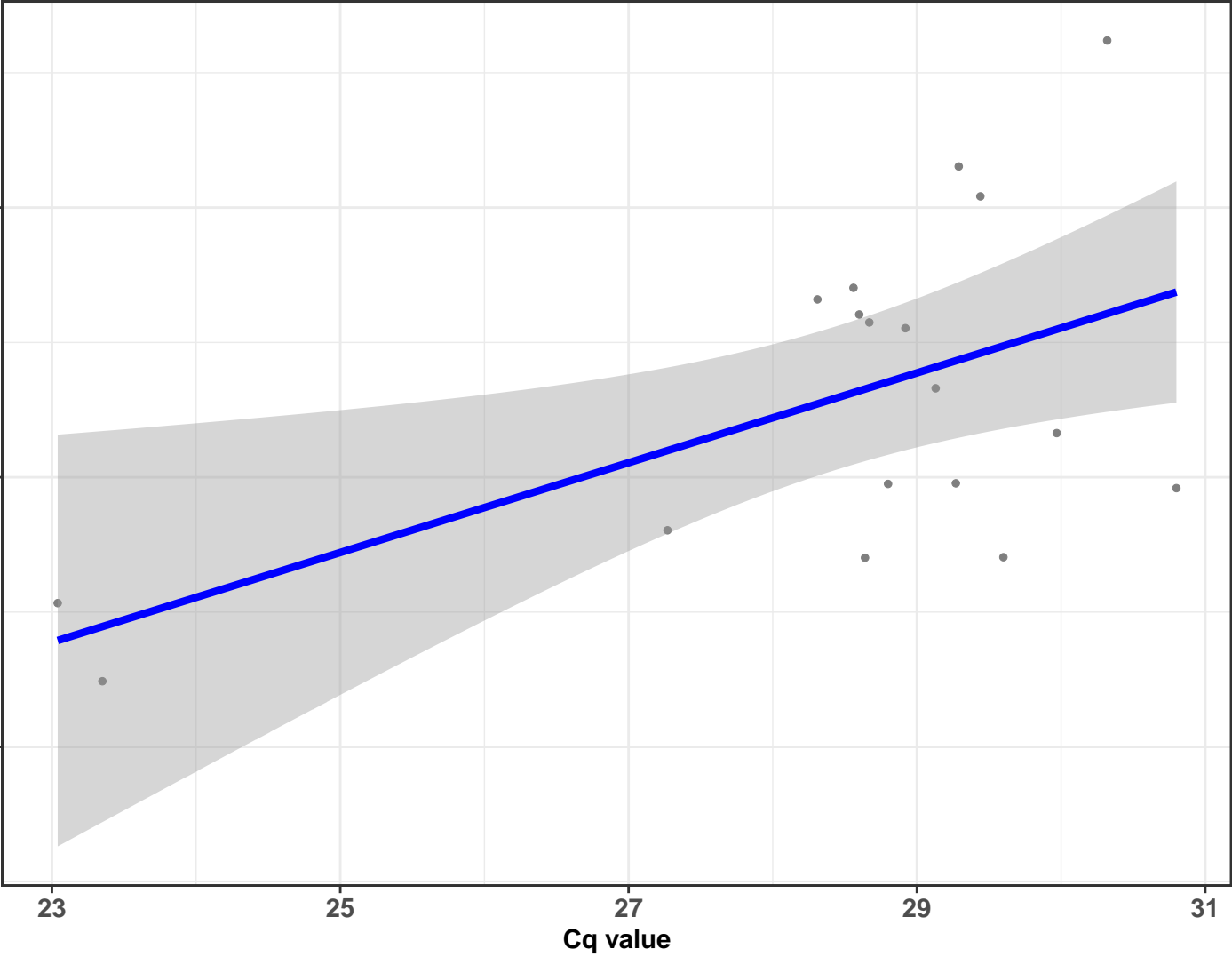
Correlation with all samples

$\log_e(S) = 7.464$ ,  $p = 0.567$ ,  $\hat{\rho}_{\text{Spearman}} = -0.132$ ,  $\text{CI}_{95\%} [-0.683, 0.415]$ ,  $n_{\text{pairs}} = 21$

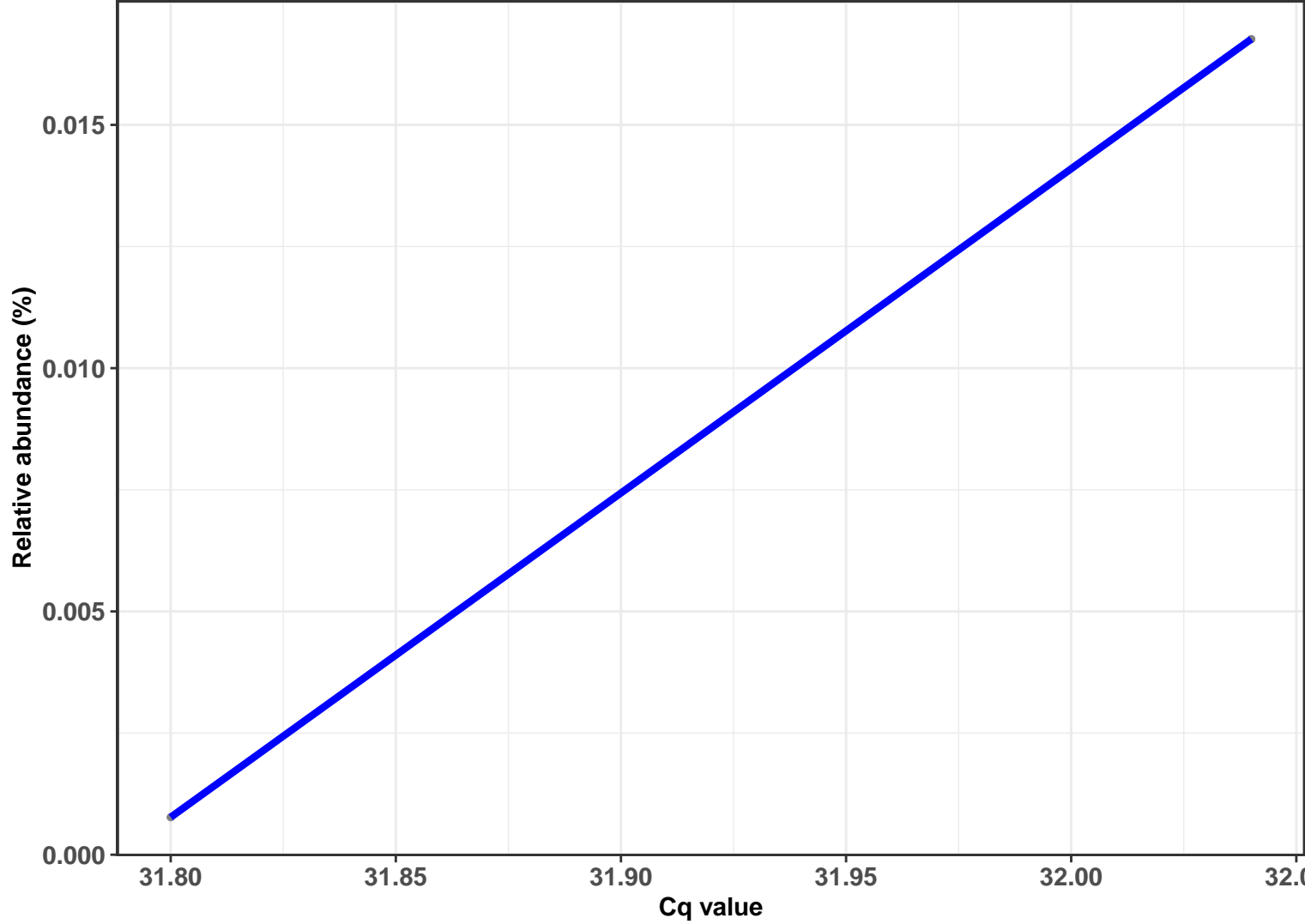


Correlation within: IM-DIC

$\log_e(S) = 6.468$ ,  $p = 0.174$ ,  $\hat{\rho}_{\text{Spearman}} = 0.335$ ,  $\text{CI}_{95\%} [-0.130, 0.888]$ ,  $n_{\text{pairs}} = 18$



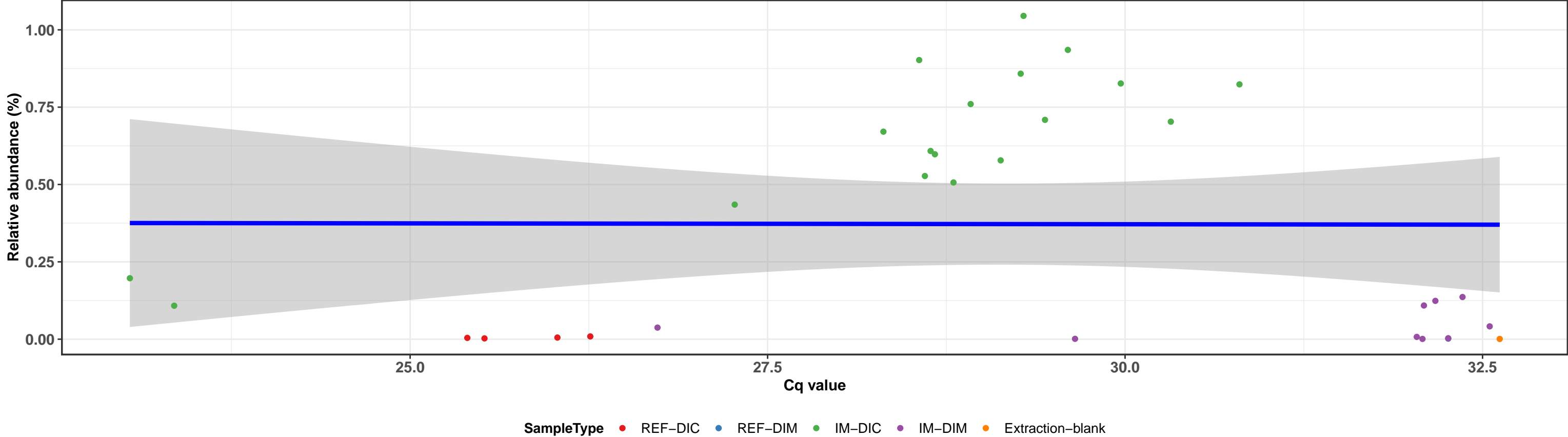
Correlation within: IM-DIM



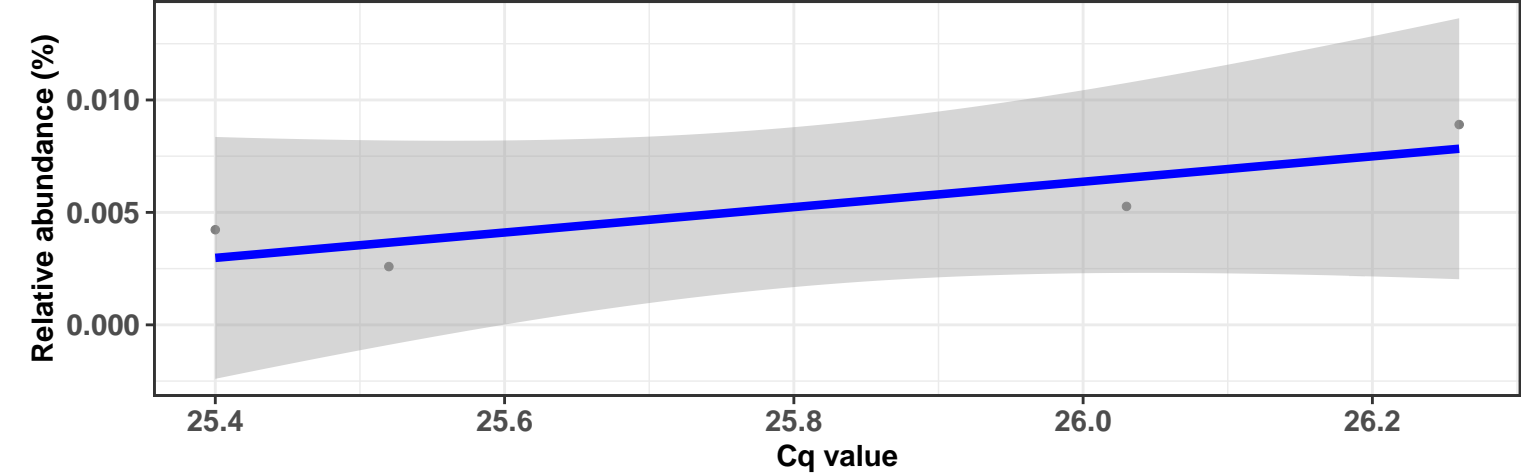
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; s\_\_Oceanobacillus caeni

Correlation with all samples

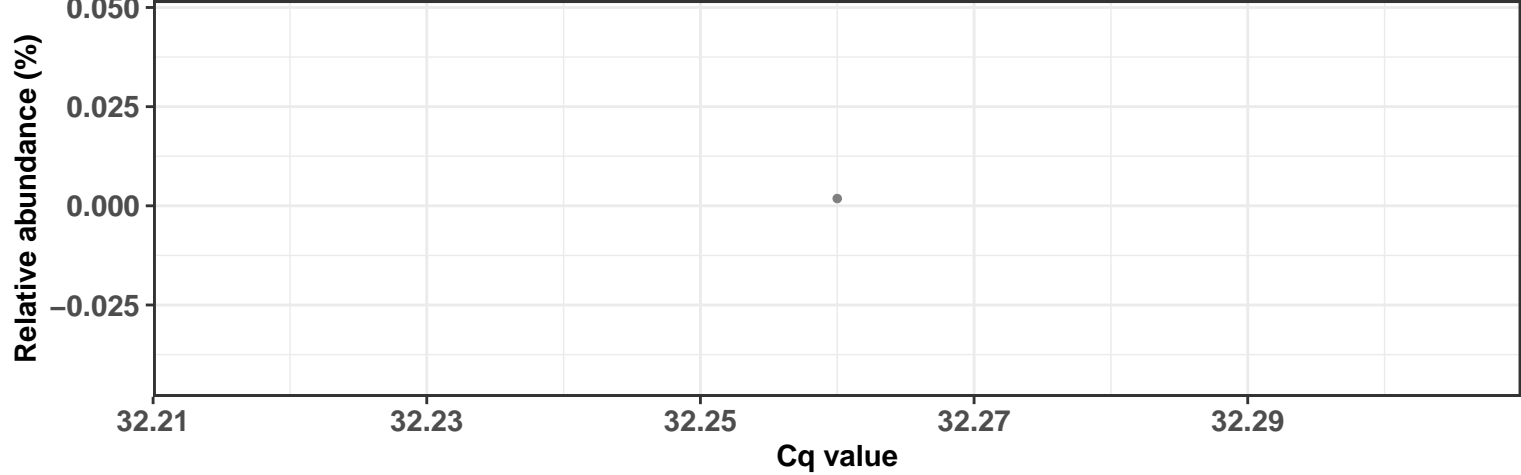
$\log_e(S) = 8.807$ ,  $p = 0.519$ ,  $\hat{\rho}_{\text{Spearman}} = -0.116$ ,  $\text{CI}_{95\%} [-0.514, 0.284]$ ,  $n_{\text{pairs}} = 33$



Correlation within: REF-DIC

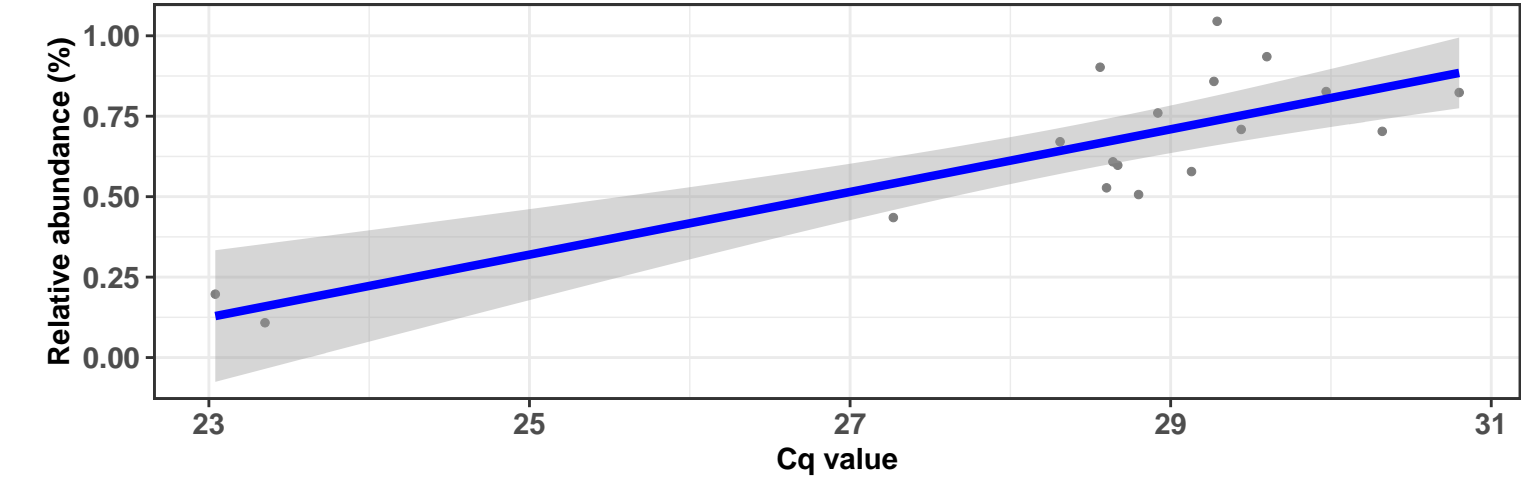


Correlation within: REF-DIM



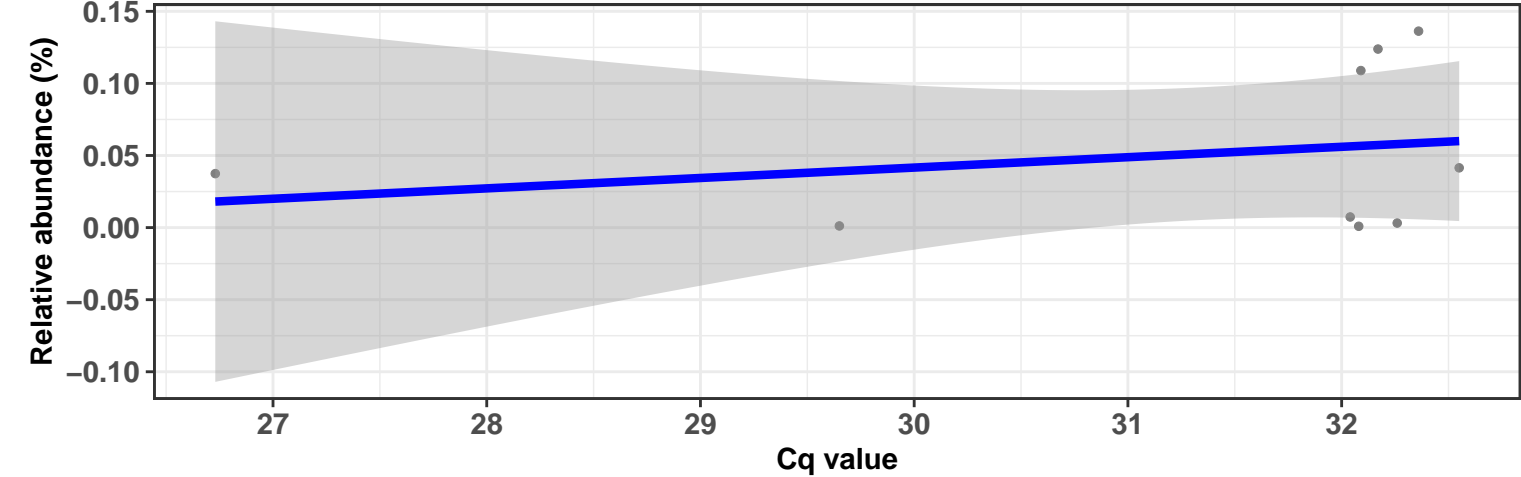
Correlation within: IM-DIC

$\log_e(S) = 5.799$ ,  $p = 0.003$ ,  $\hat{\rho}_{\text{Spearman}} = 0.659$ ,  $\text{CI}_{95\%} [0.349, 1.042]$ ,  $n_{\text{pairs}} = 18$



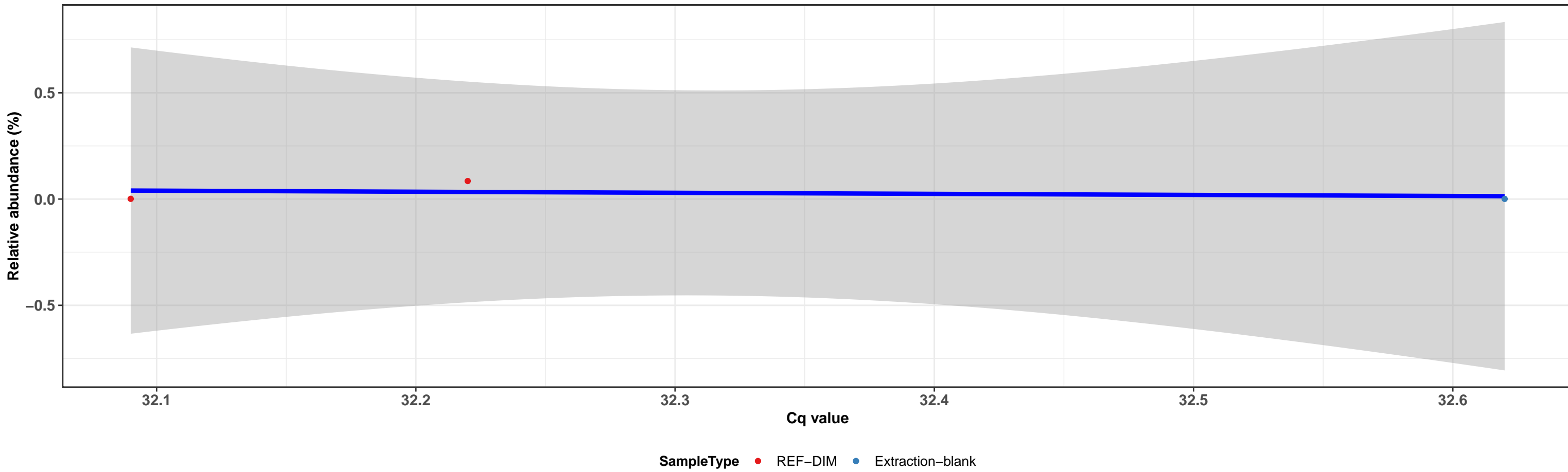
Correlation within: IM-DIM

$\log_e(S) = 4.094$ ,  $p = 0.170$ ,  $\hat{\rho}_{\text{Spearman}} = 0.500$ ,  $\text{CI}_{95\%} [-0.037, 1.127]$ ,  $n_{\text{pairs}} = 9$

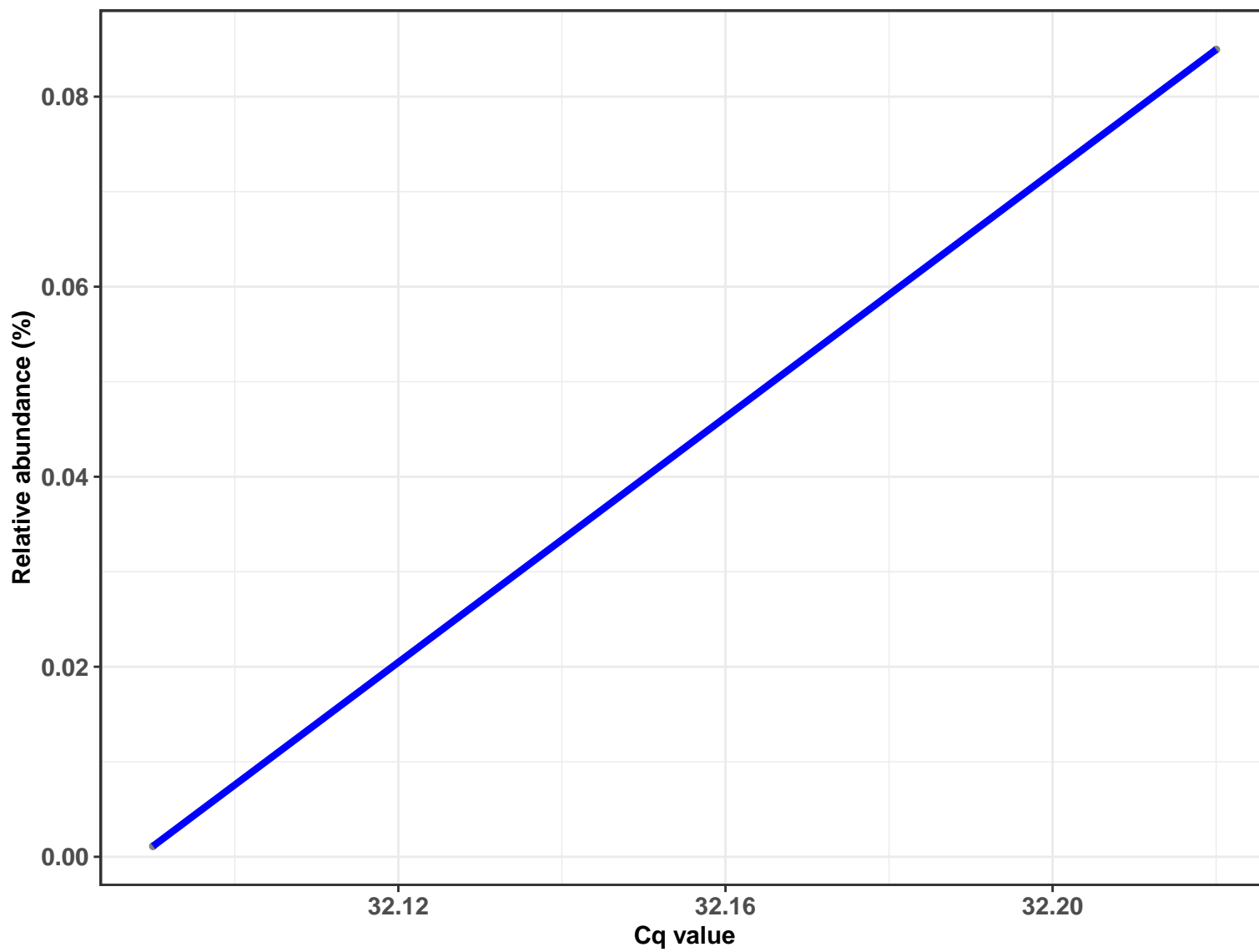


k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Propionibacteriales; f\_\_Propionibacteriaceae; g\_\_Cutibacterium; NA

Correlation with all samples



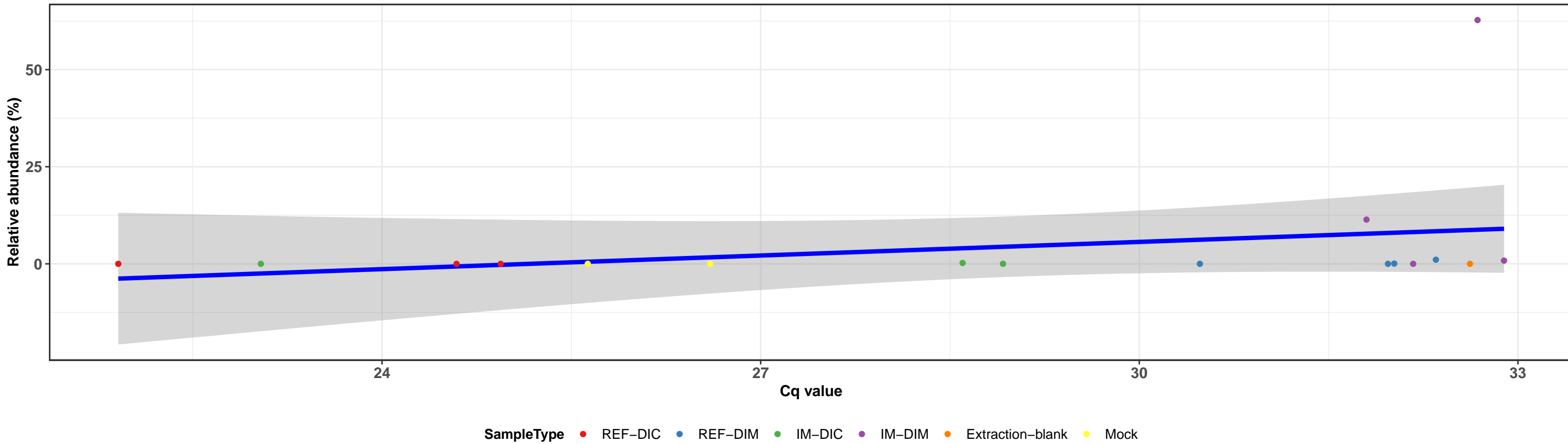
Correlation within: REF-DIM



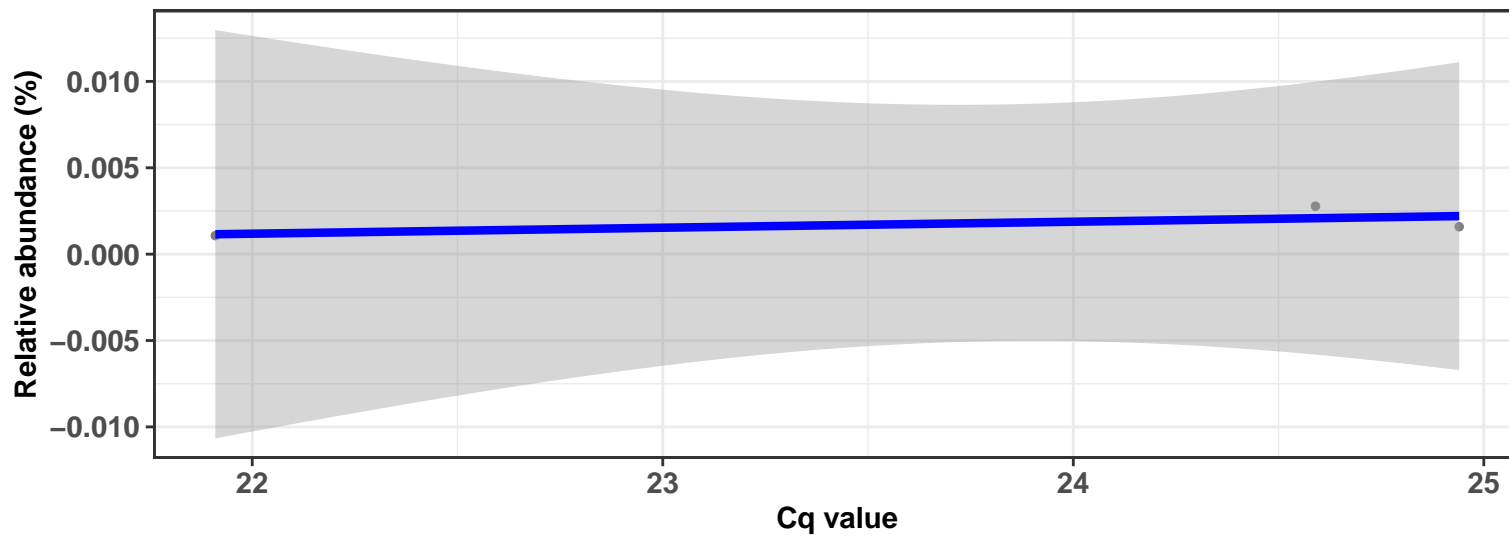
k\_\_Bacteria; p\_\_Tenericutes; c\_\_Mollicutes; o\_\_Mycoplasmatales; f\_\_Mycoplasmataceae; g\_\_Mycoplasma; s\_\_uncultured Mycoplasma sp.

### Correlation with all samples

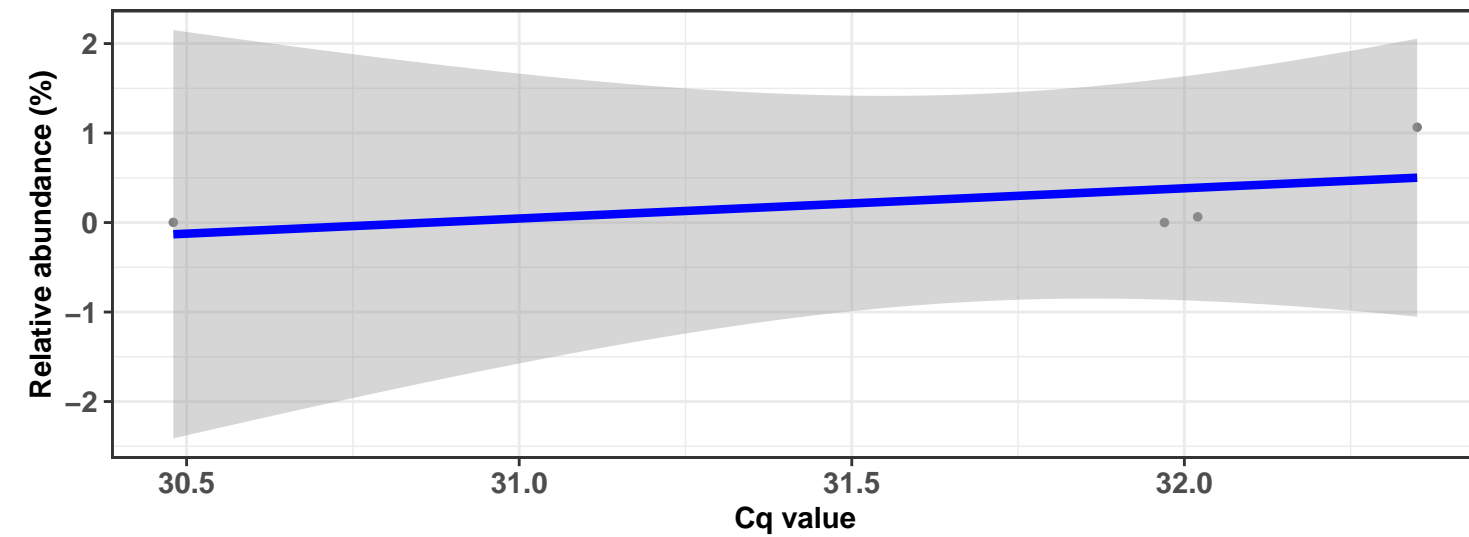
$\log_e(S) = 6.306$ ,  $p = 0.198$ ,  $\hat{\rho}_{\text{Spearman}} = 0.328$ ,  $CI_{95\%} [-0.259, 0.877]$ ,  $n_{\text{pairs}} = 17$



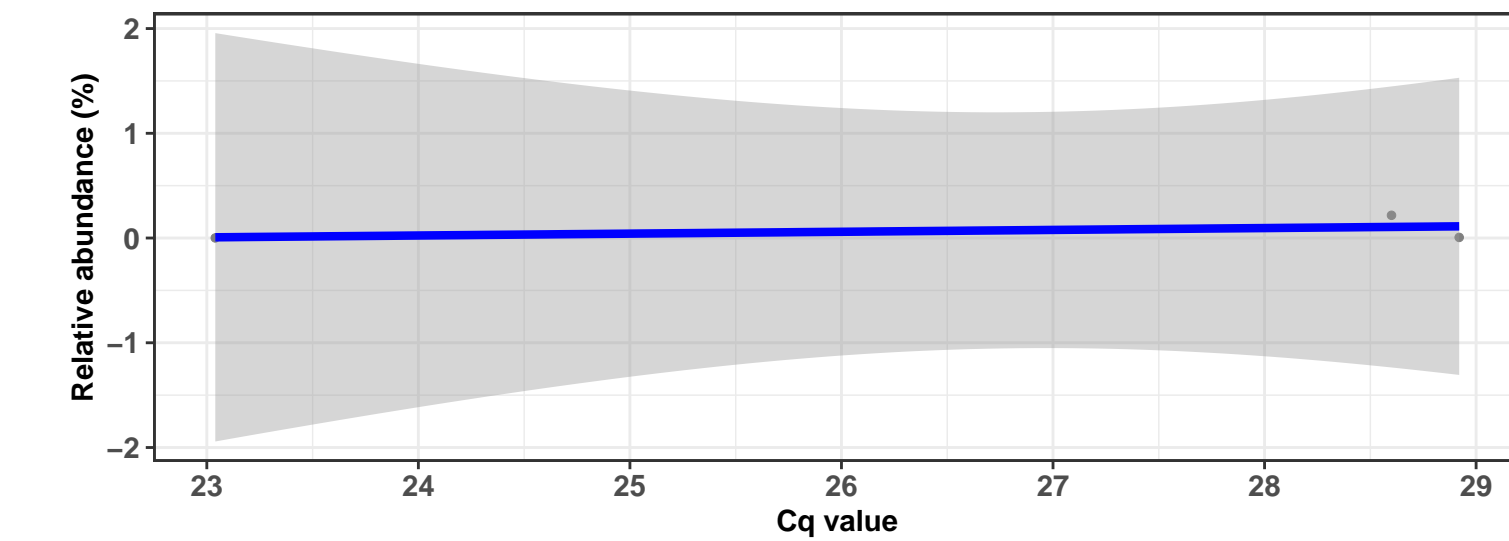
### Correlation within: REF-DIC



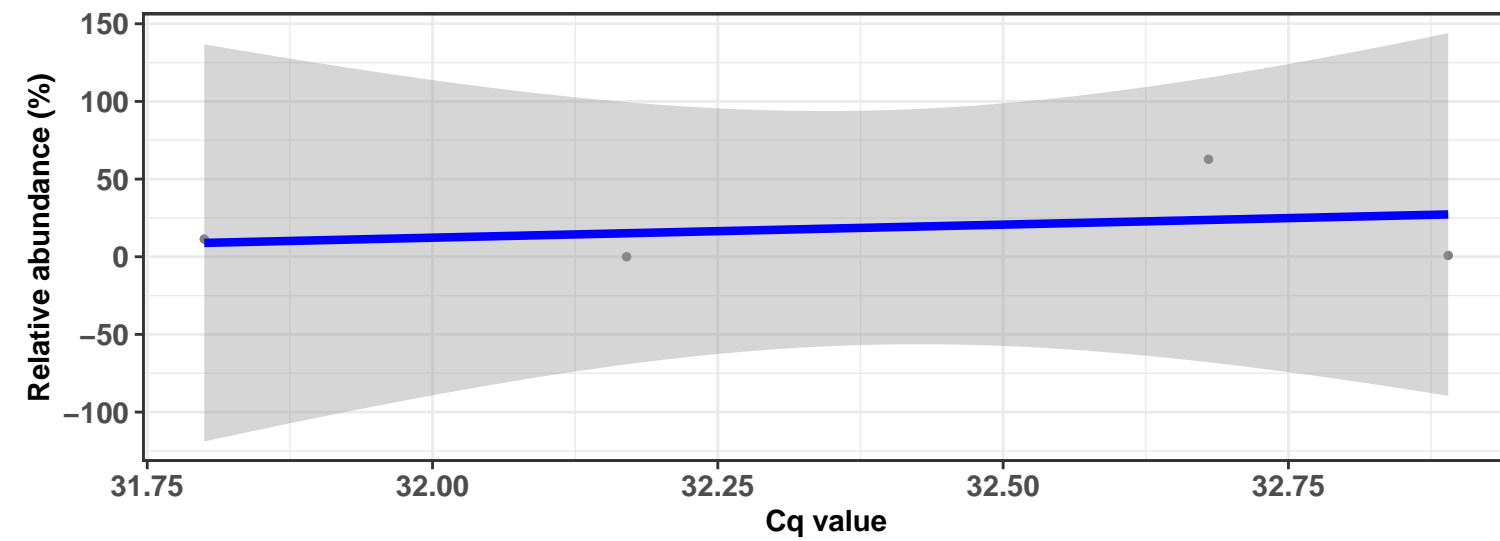
### Correlation within: REF-DIM



### Correlation within: IM-DIC



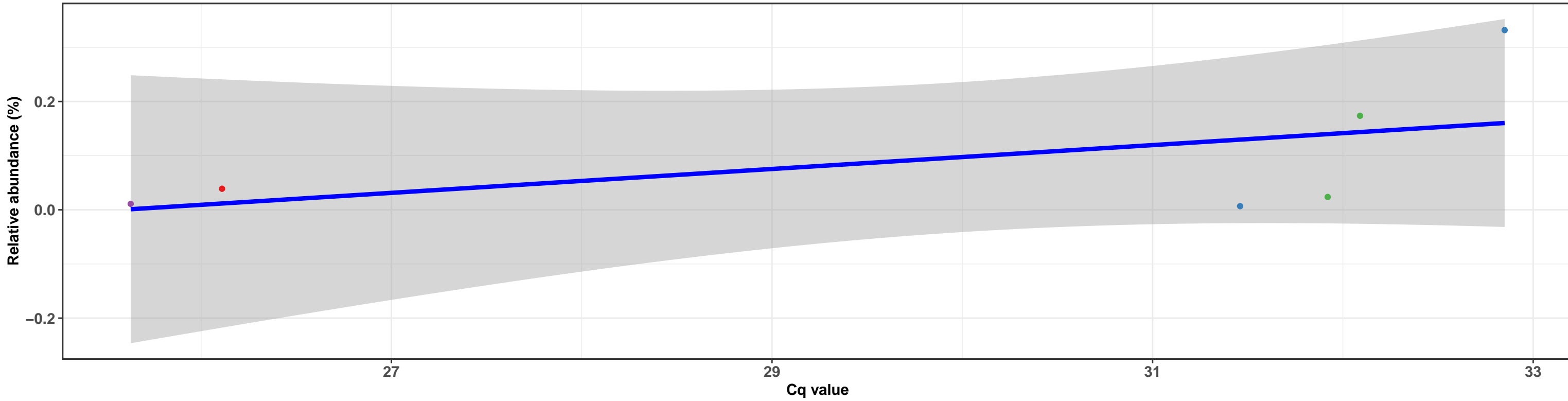
### Correlation within: IM-DIM



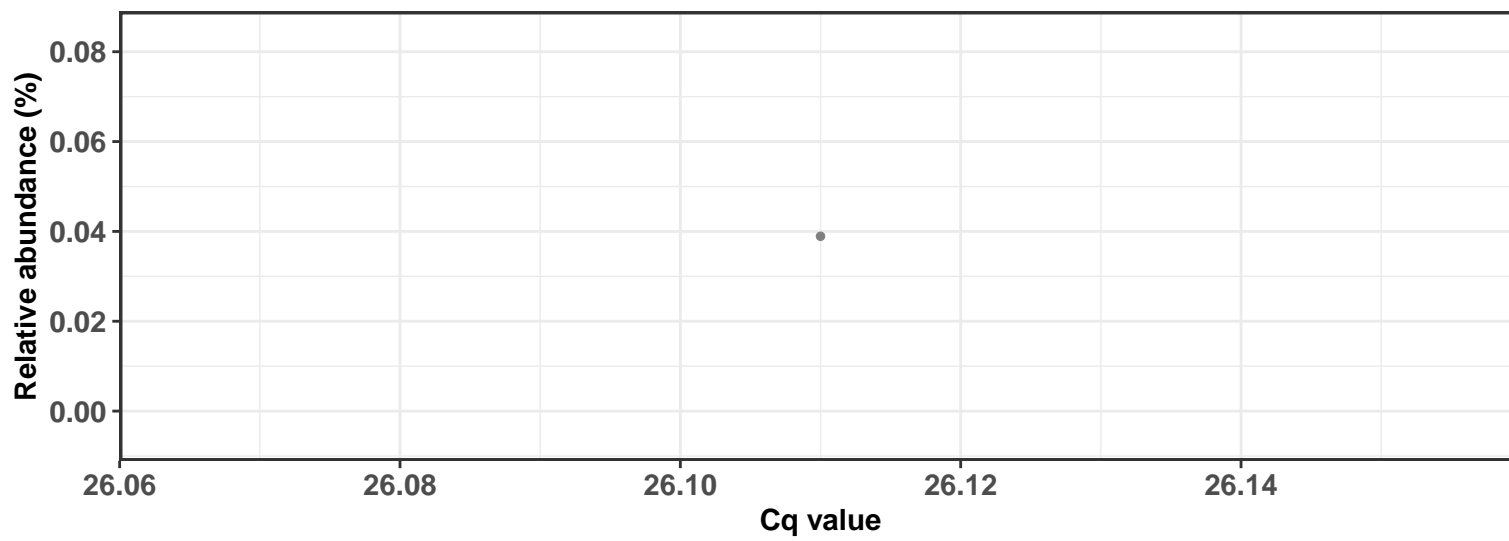
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingomonas; NA

### Correlation with all samples

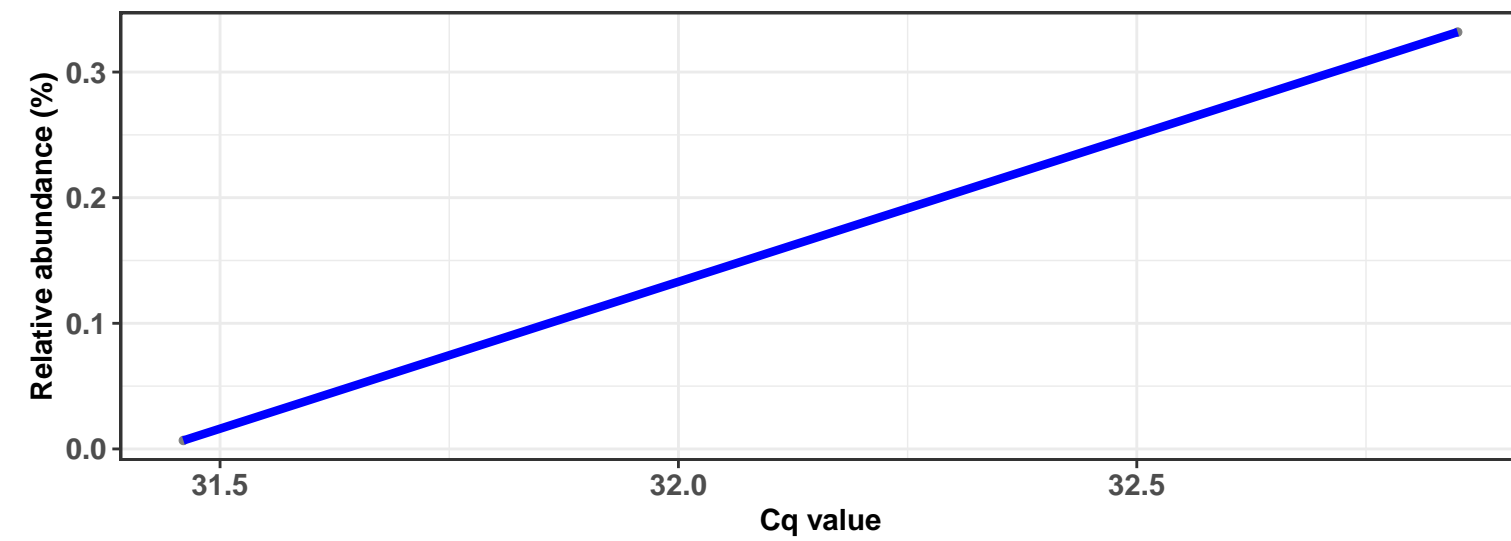
$\log_e(S) = 2.303$ ,  $p = 0.111$ ,  $\hat{\rho}_{\text{Spearman}} = 0.714$ ,  $\text{CI}_{95\%} [0.093, 1.454]$ ,  $n_{\text{pairs}} = 6$



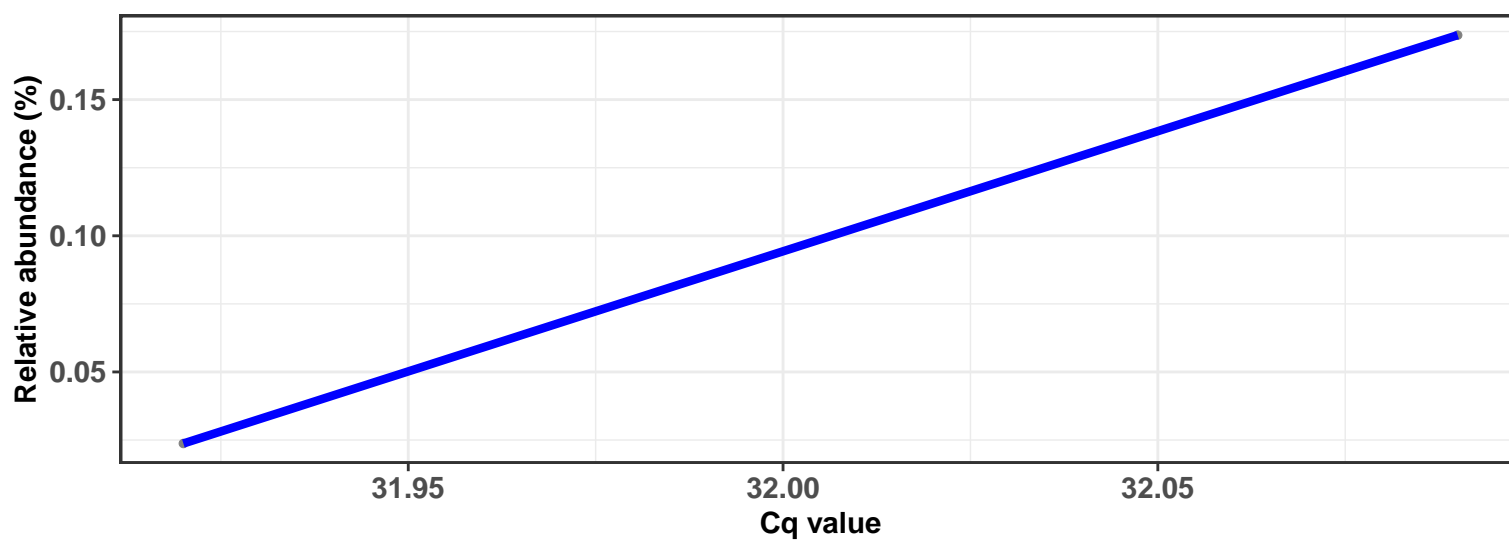
### Correlation within: REF-DIC



### Correlation within: REF-DIM

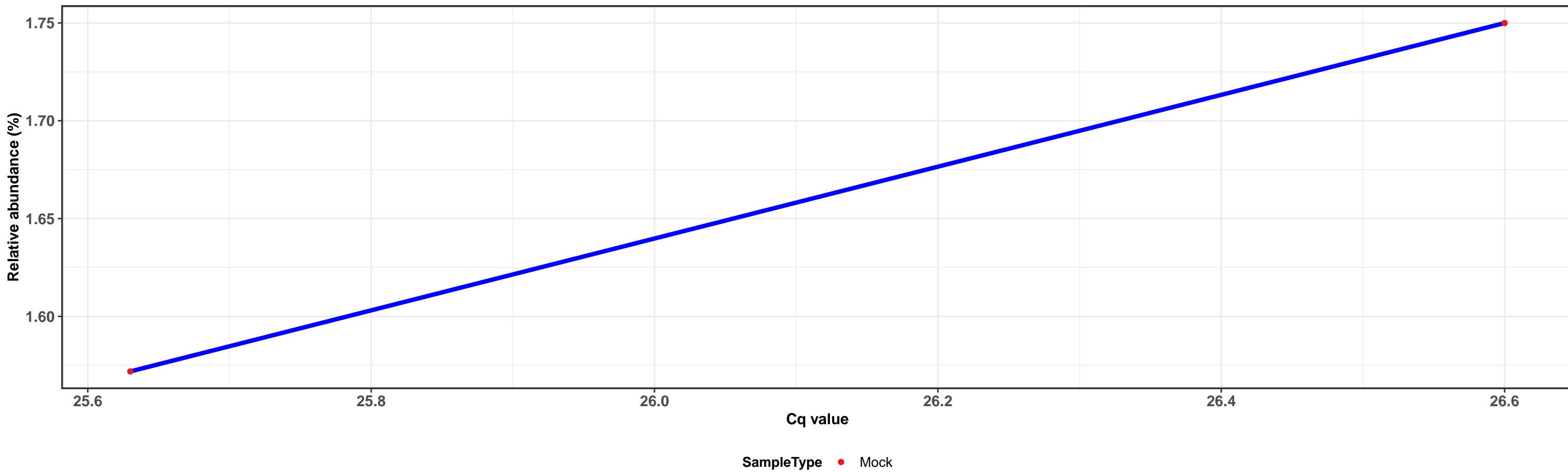


### Correlation within: IM-DIM

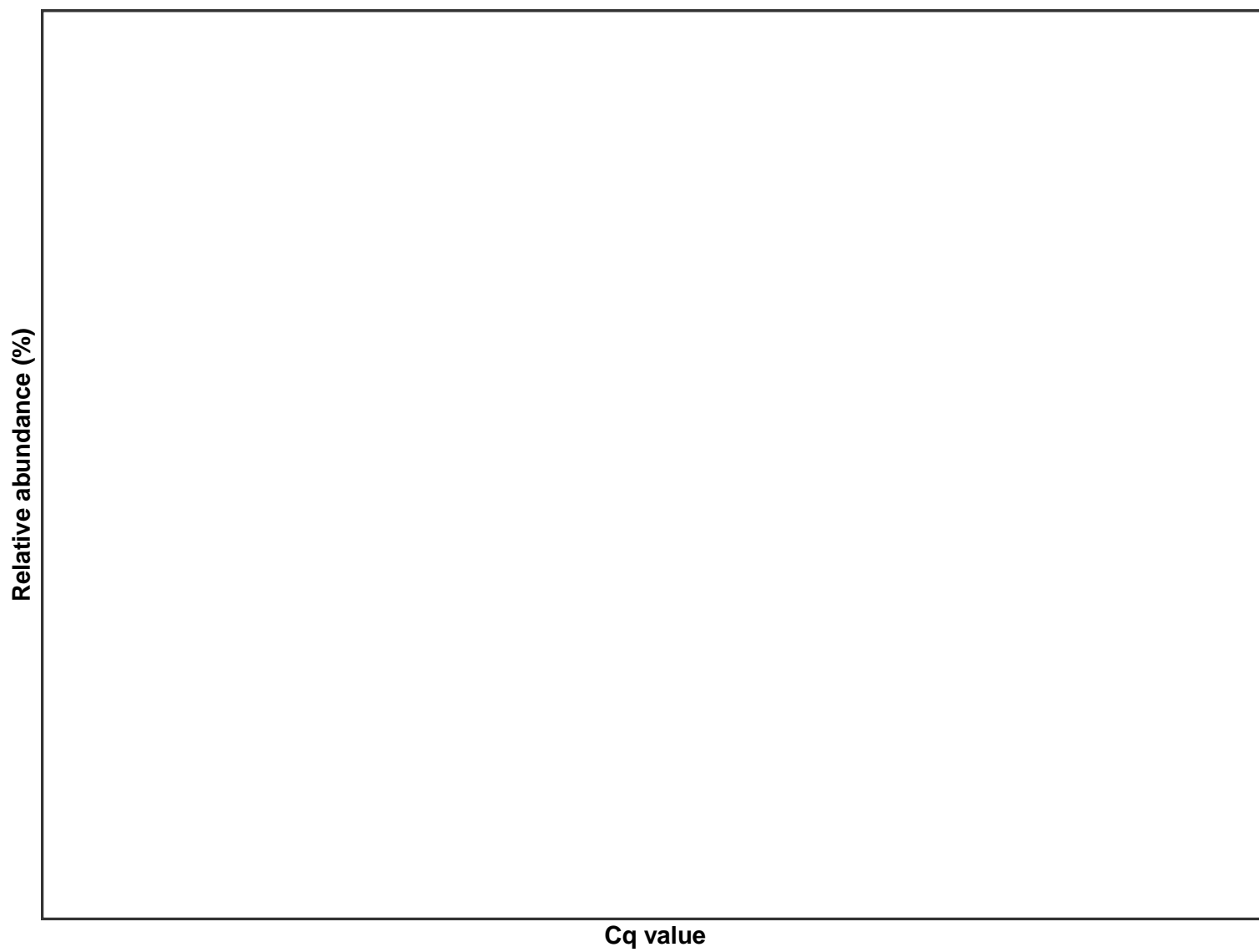


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Staphylococcus; s\_\_Staphylococcus aureus

Correlation with all samples



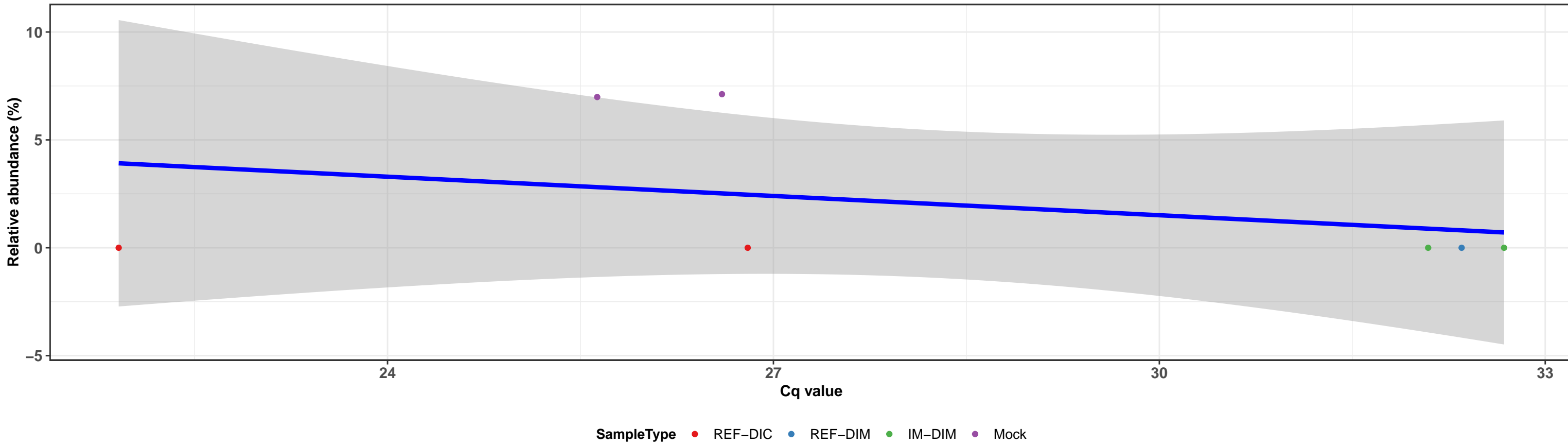
Correlation within:



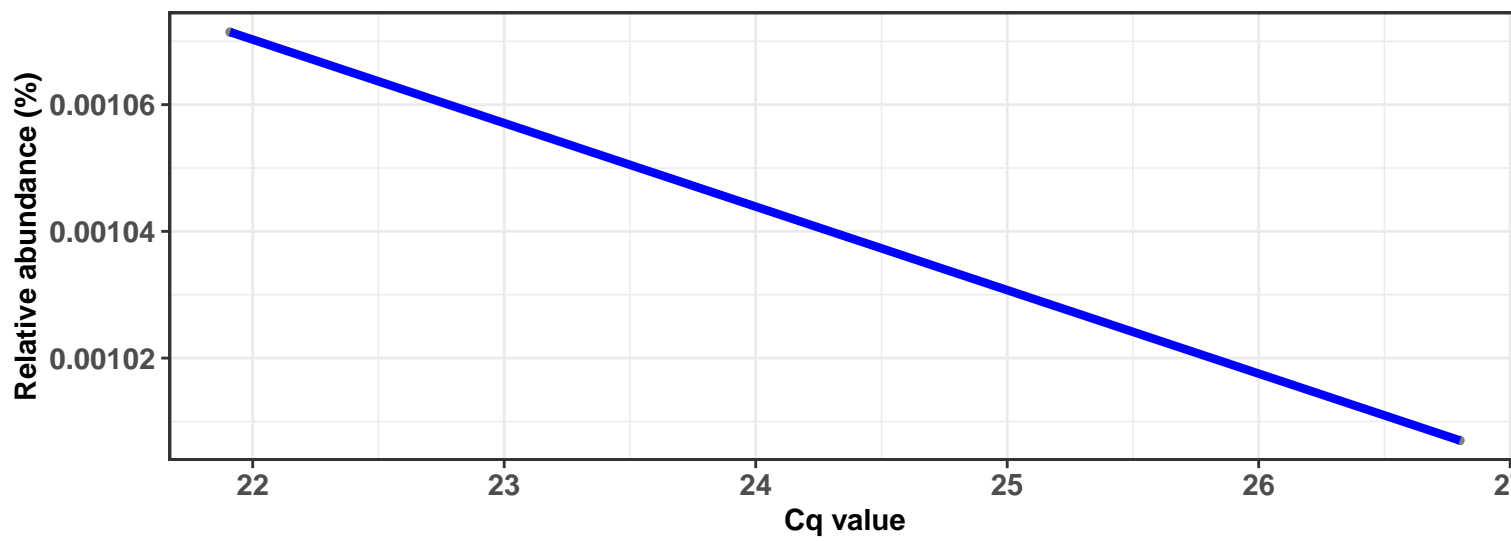
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_Escherichia-Shigella; NA

### Correlation with all samples

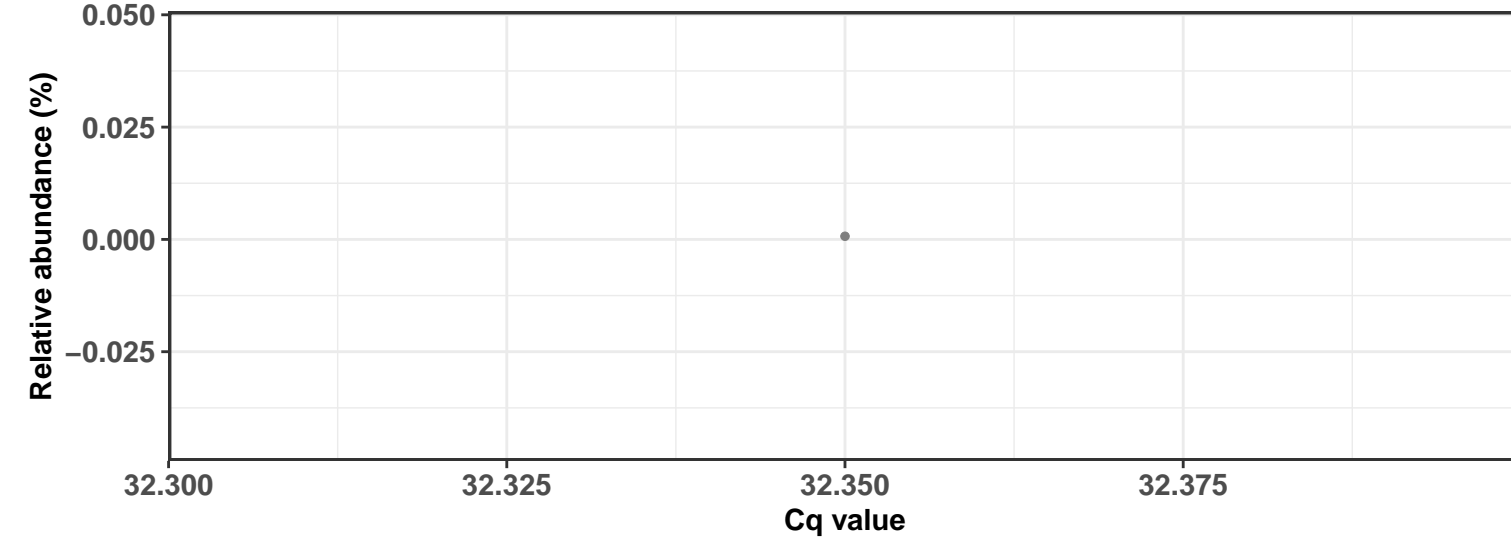
$\log_e(S) = 4.585$ ,  $p = 0.052$ ,  $\hat{\rho}_{\text{Spearman}} = -0.750$ ,  $CI_{95\%} [-1.265, -0.356]$ ,  $n_{\text{pairs}} = 7$



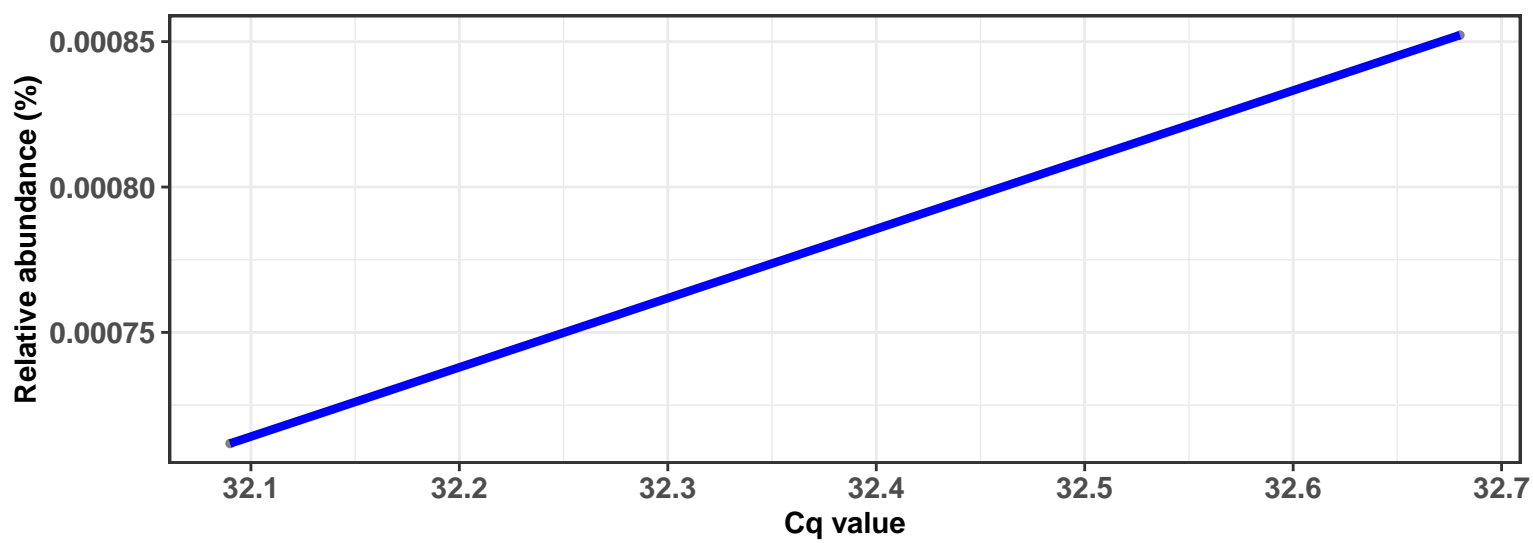
### Correlation within: REF-DIC



### Correlation within: REF-DIM



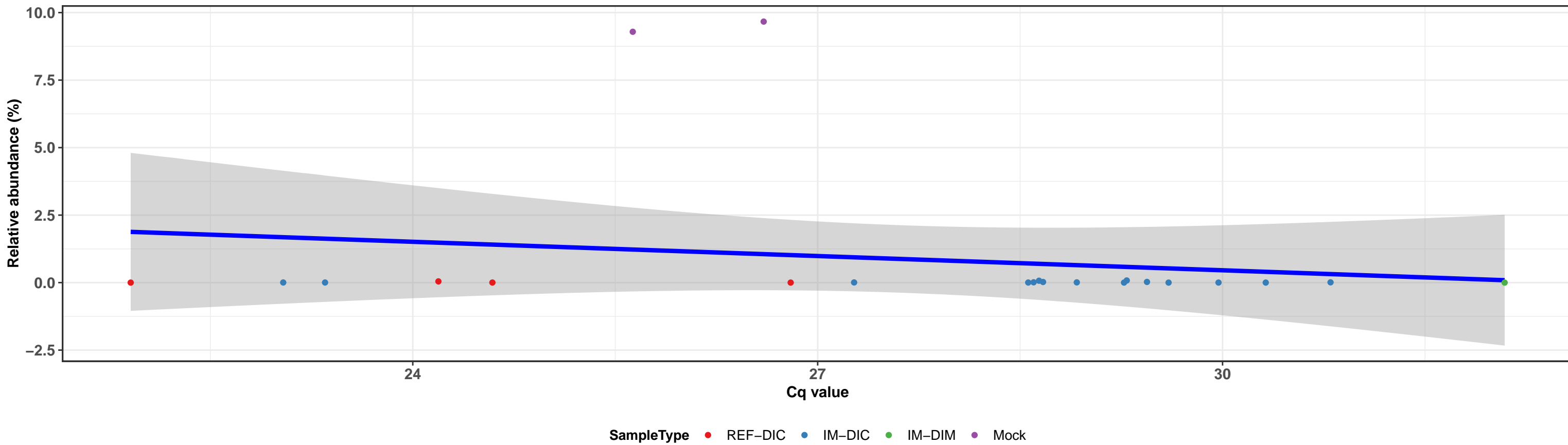
### Correlation within: IM-DIM



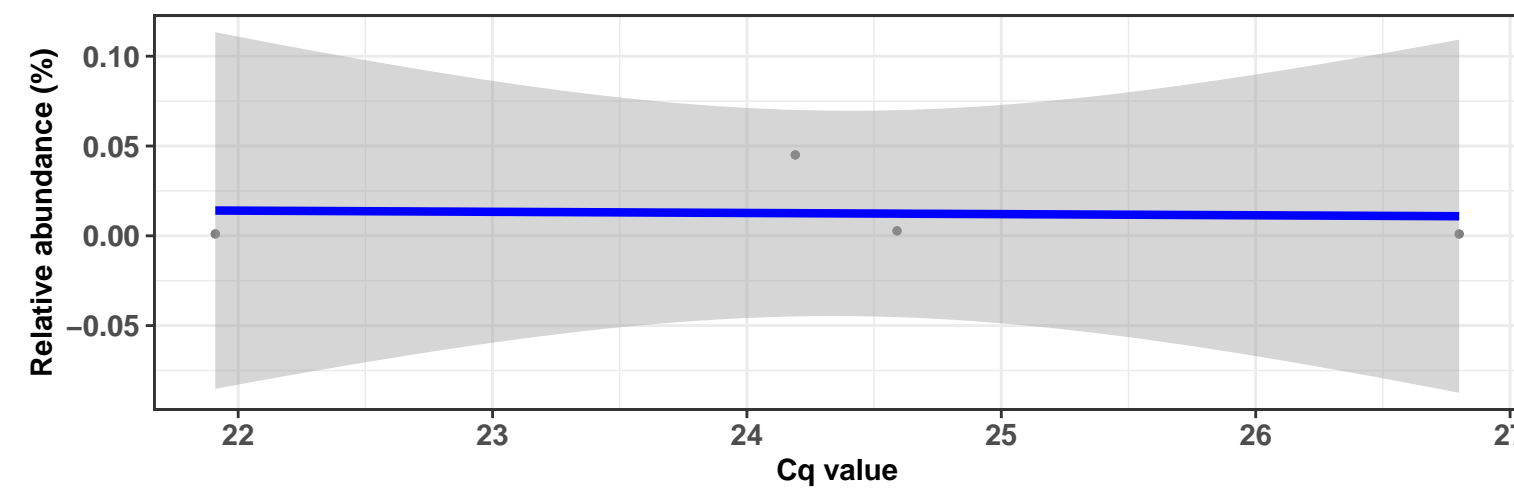
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_Escherichia-Shigella; NA

### Correlation with all samples

$\log_e(S) = 7.672$ ,  $p = 0.342$ ,  $\hat{\rho}_{\text{Spearman}} = -0.213$ ,  $\text{CI}_{95\%} [-0.669, 0.207]$ ,  $n_{\text{pairs}} = 22$

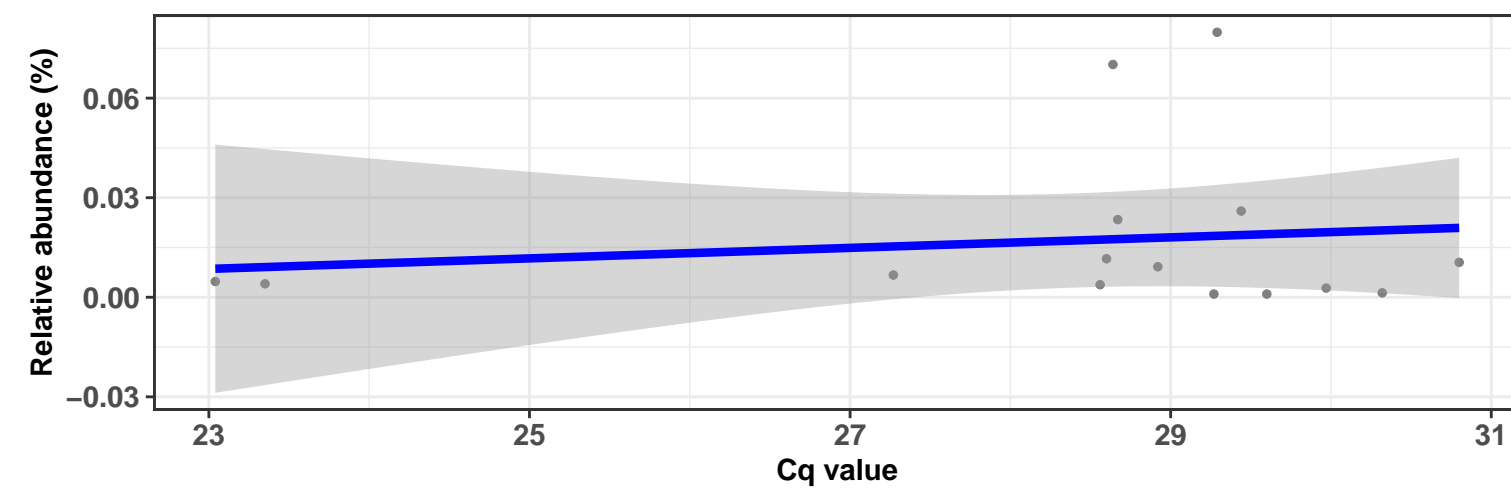


### Correlation within: REF-DIC

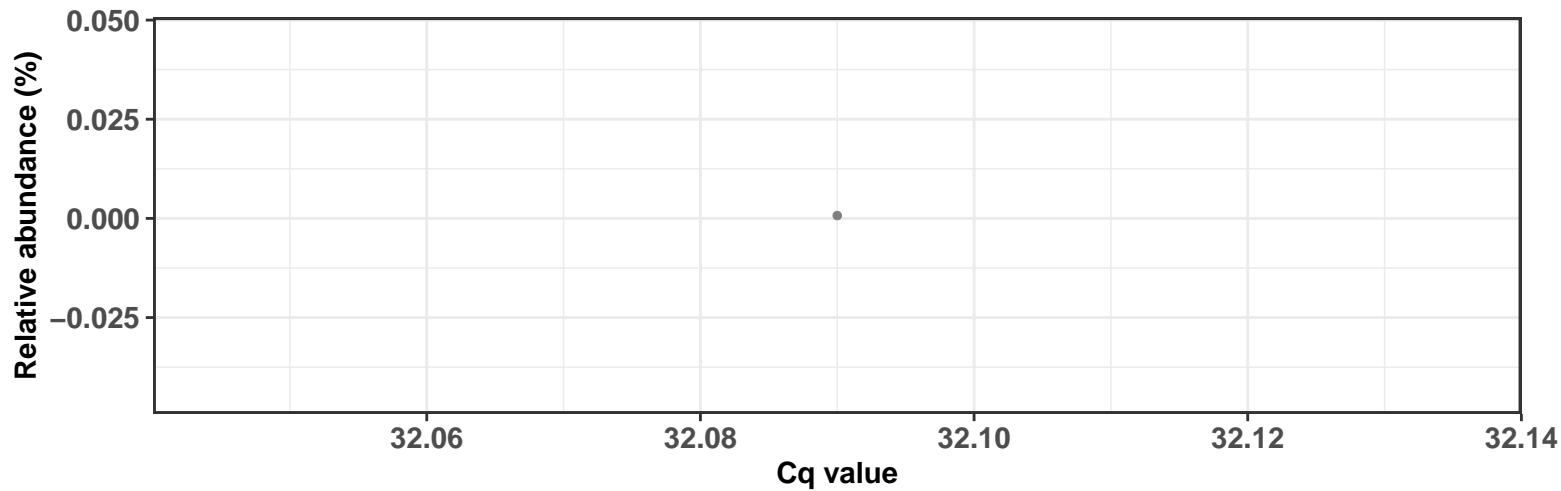


### Correlation within: IM-DIC

$\log_e(S) = 6.446$ ,  $p = 0.657$ ,  $\hat{\rho}_{\text{Spearman}} = -0.125$ ,  $\text{CI}_{95\%} [-0.667, 0.367]$ ,  $n_{\text{pairs}} = 15$



### Correlation within: IM-DIM

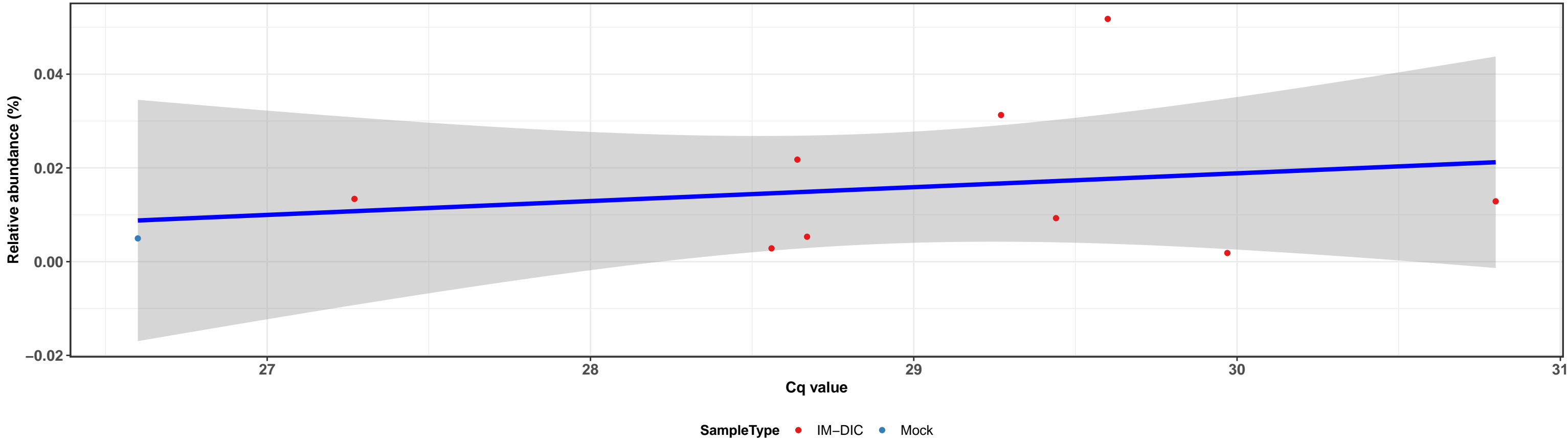




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_Escherichia-Shigella; NA

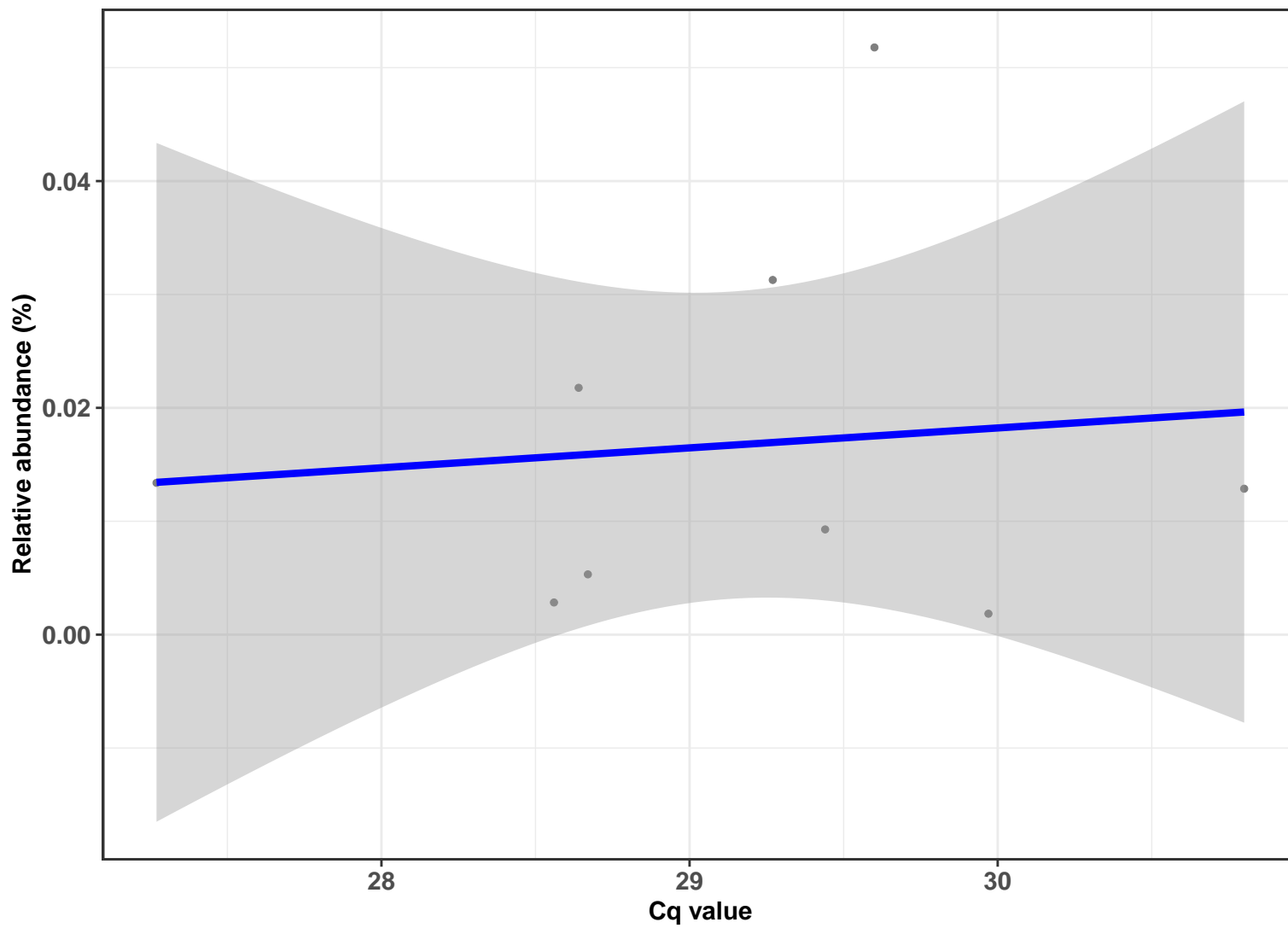
### Correlation with all samples

$\log_e(S) = 4.970$ ,  $p = 0.726$ ,  $\hat{\rho}_{\text{Spearman}} = 0.127$ ,  $\text{CI}_{95\%} [-0.668, 0.818]$ ,  $n_{\text{pairs}} = 10$



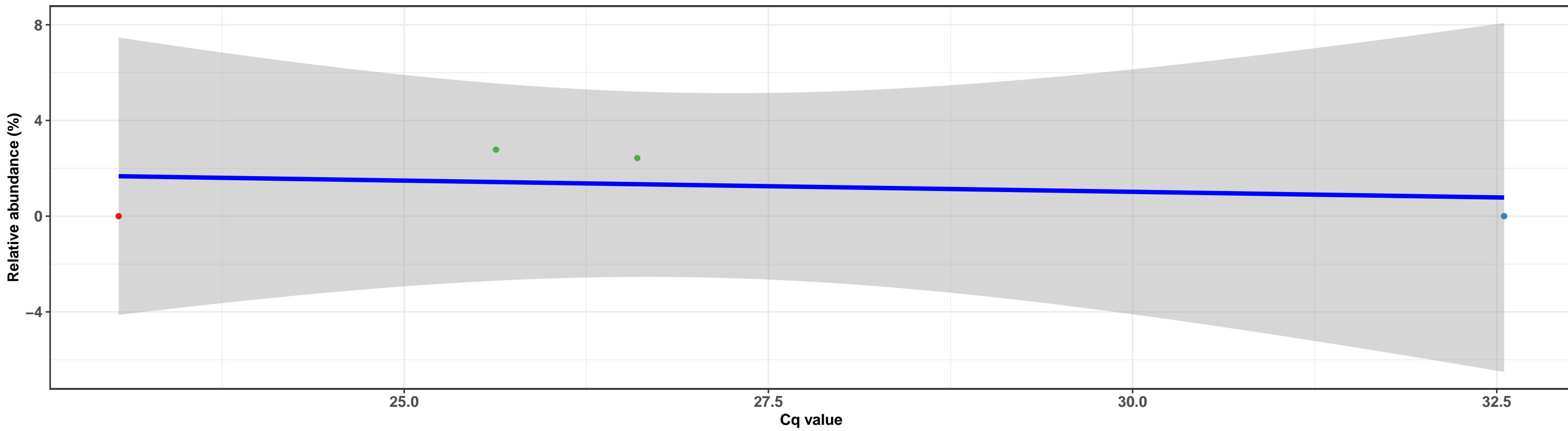
### Correlation within: IM-DIC

$\log_e(S) = 4.820$ ,  $p = 0.932$ ,  $\hat{\rho}_{\text{Spearman}} = -0.033$ ,  $\text{CI}_{95\%} [-0.778, 0.683]$ ,  $n_{\text{pairs}} = 9$



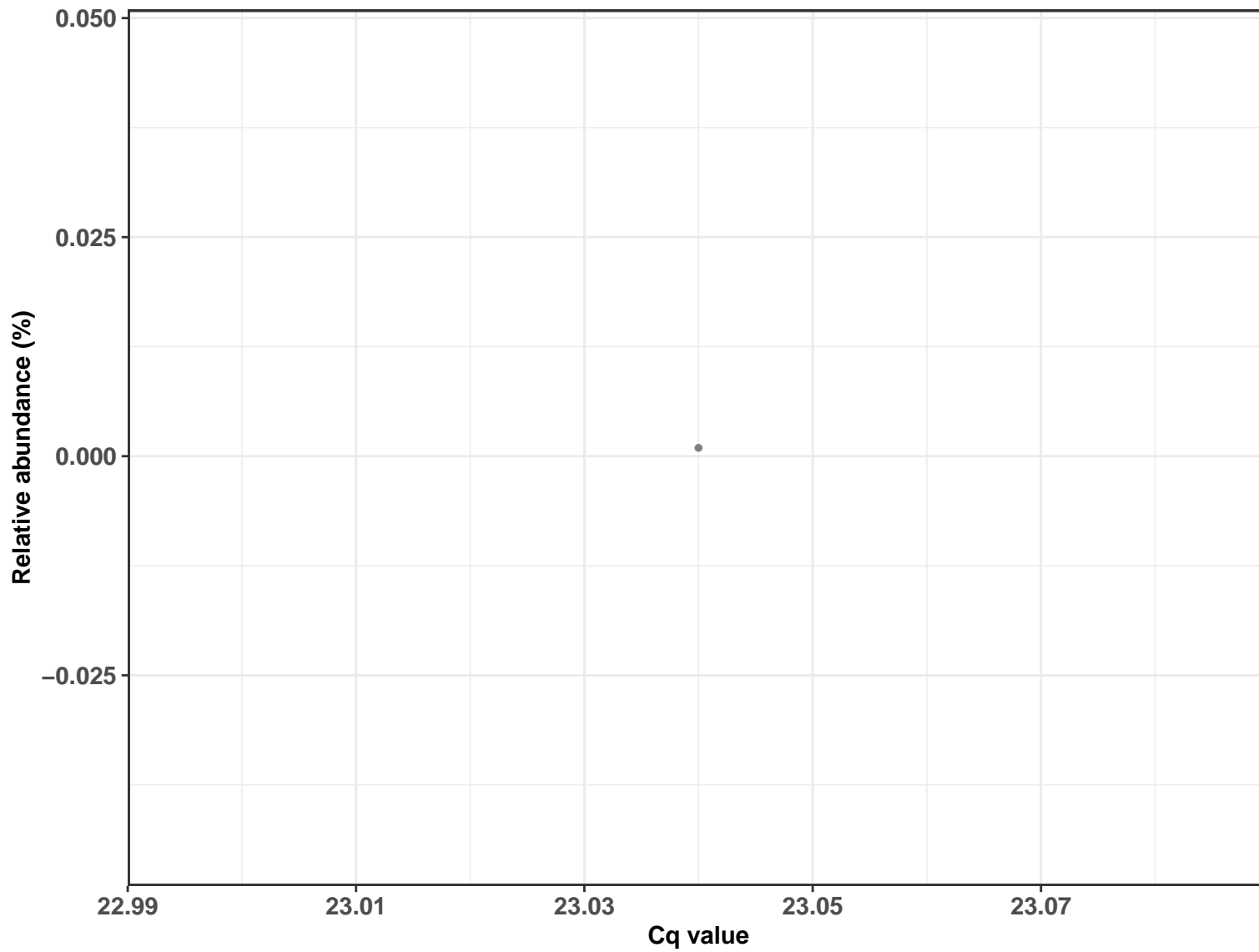
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_Salmonella; NA

Correlation with all samples

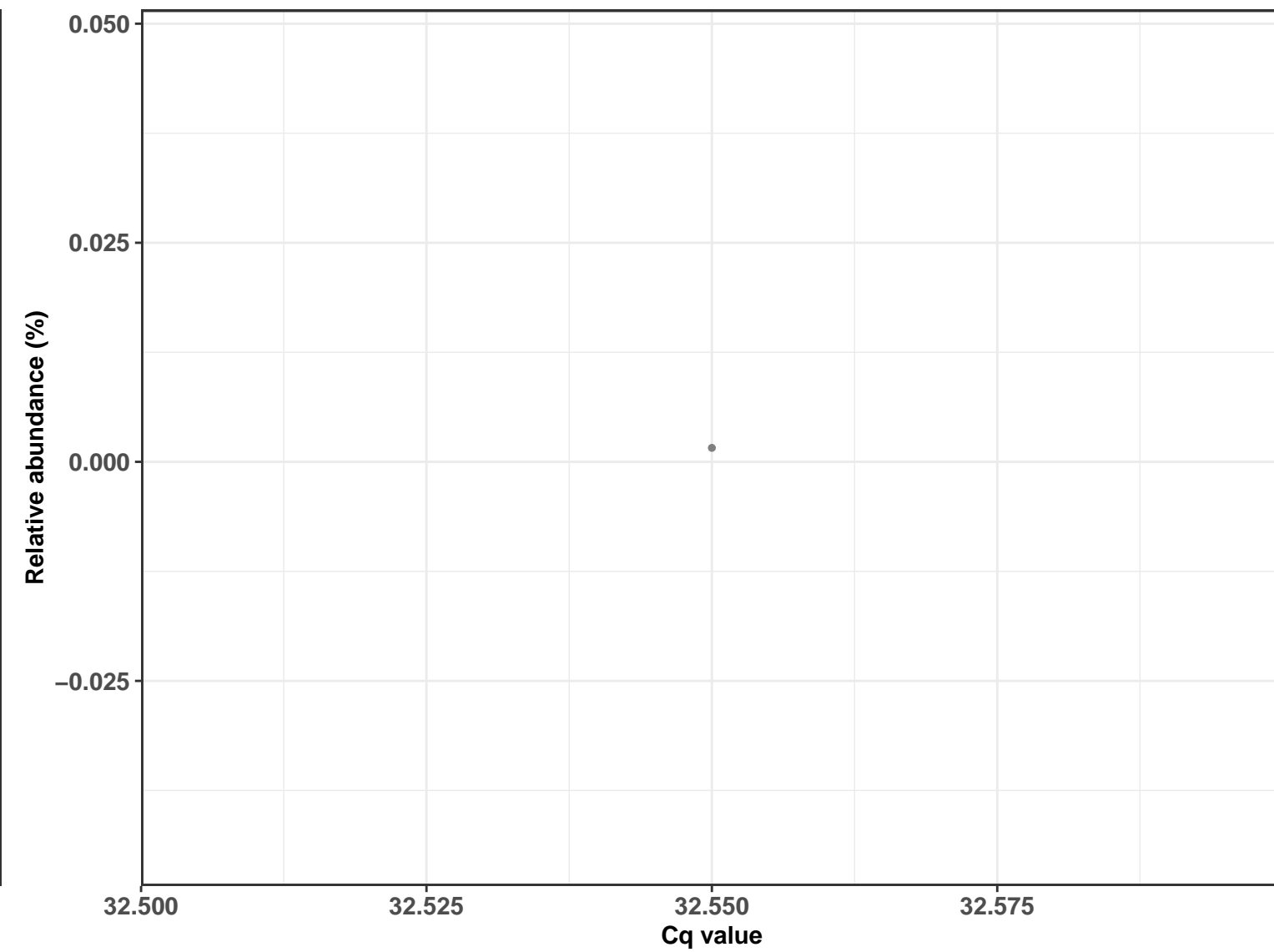


SampleType • IM-DIC • IM-DIM • Mock

Correlation within: IM-DIC



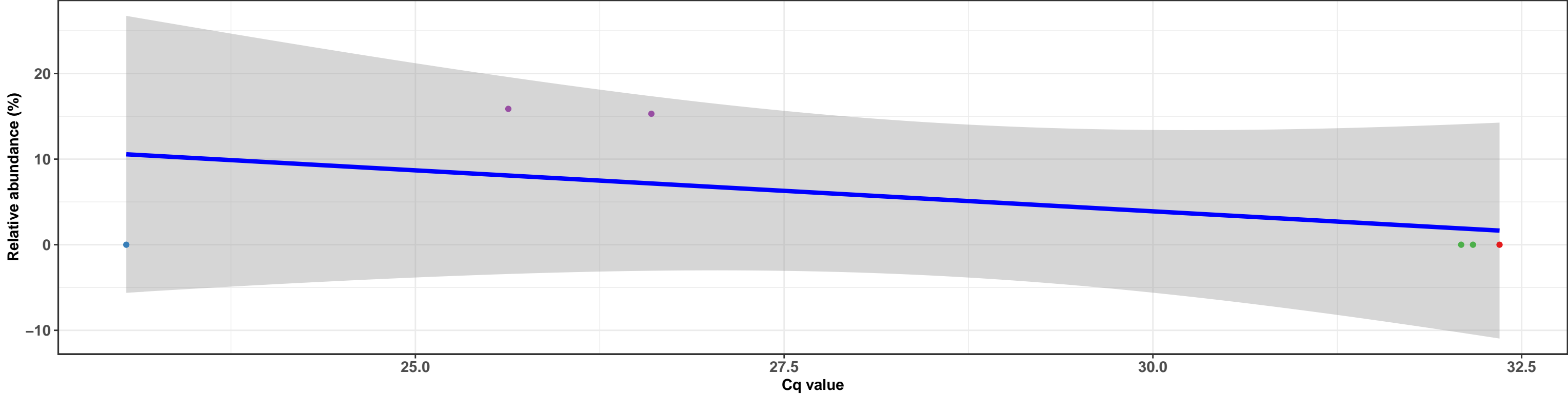
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_Salmonella; NA

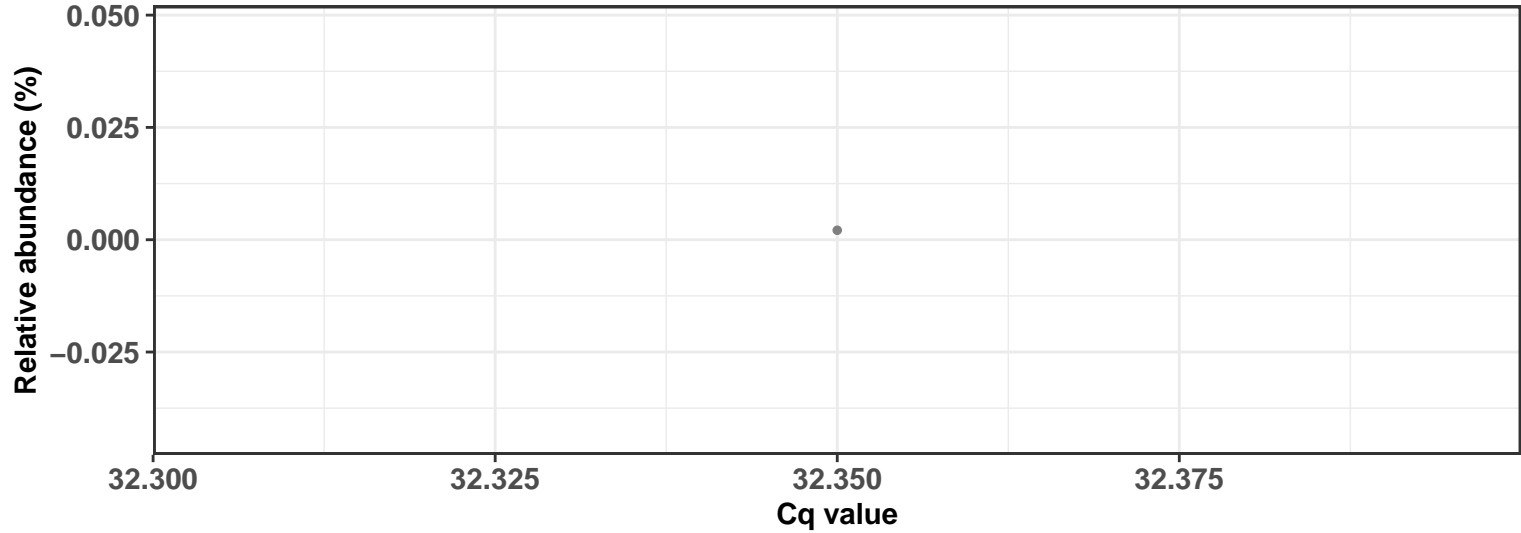
Correlation with all samples

$\log_e(S) = 3.738$ ,  $\rho = 0.704$ ,  $\hat{\rho}_{\text{Spearman}} = -0.200$ ,  $\text{CI}_{95\%} [-1.120, 0.801]$ ,  $n_{\text{pairs}} = 6$

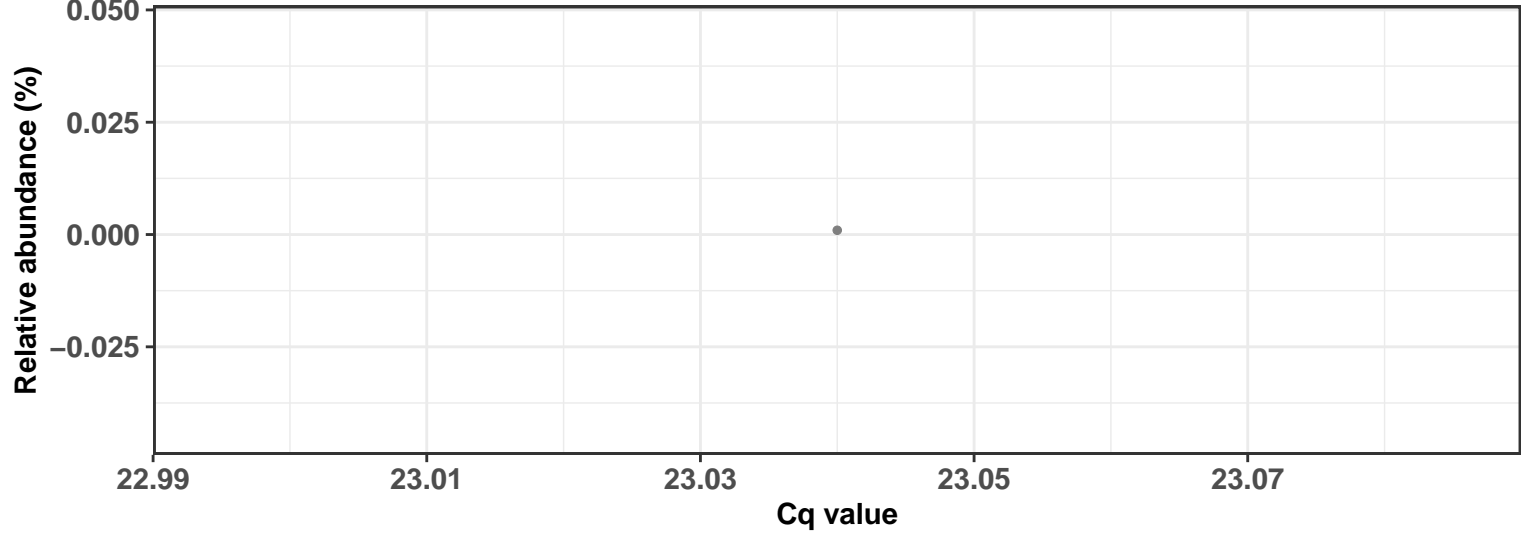


SampleType REF-DIM IM-DIC IM-DIM Mock

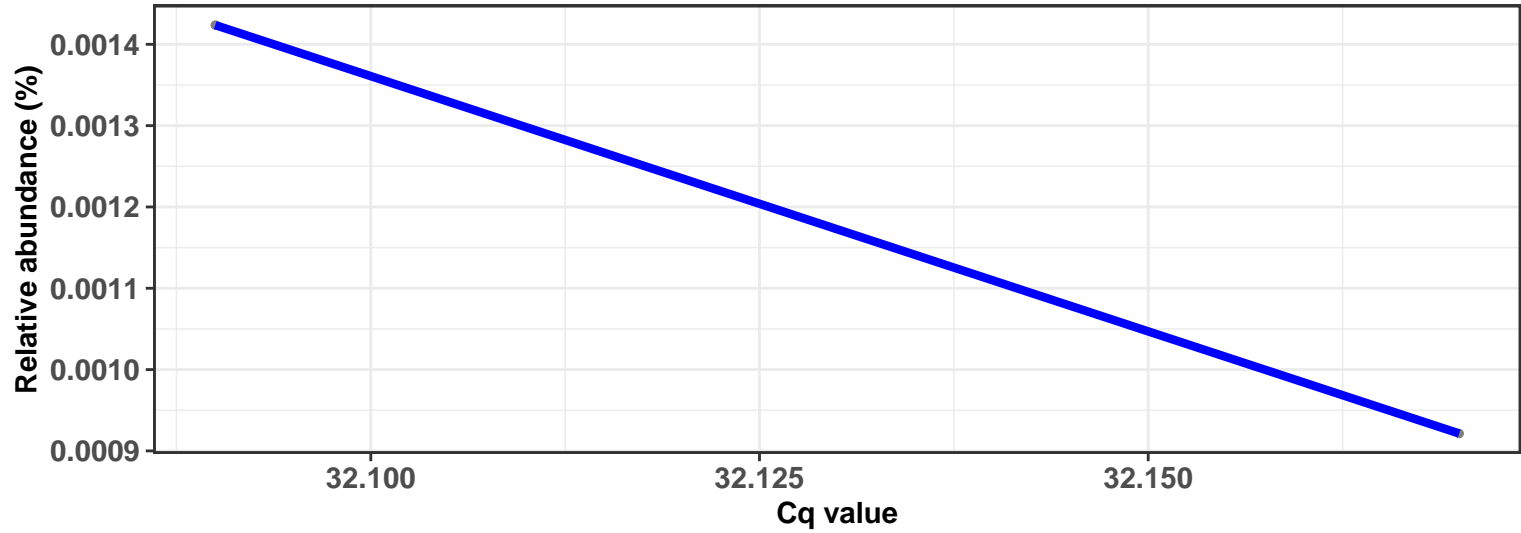
Correlation within: REF-DIM



Correlation within: IM-DIC



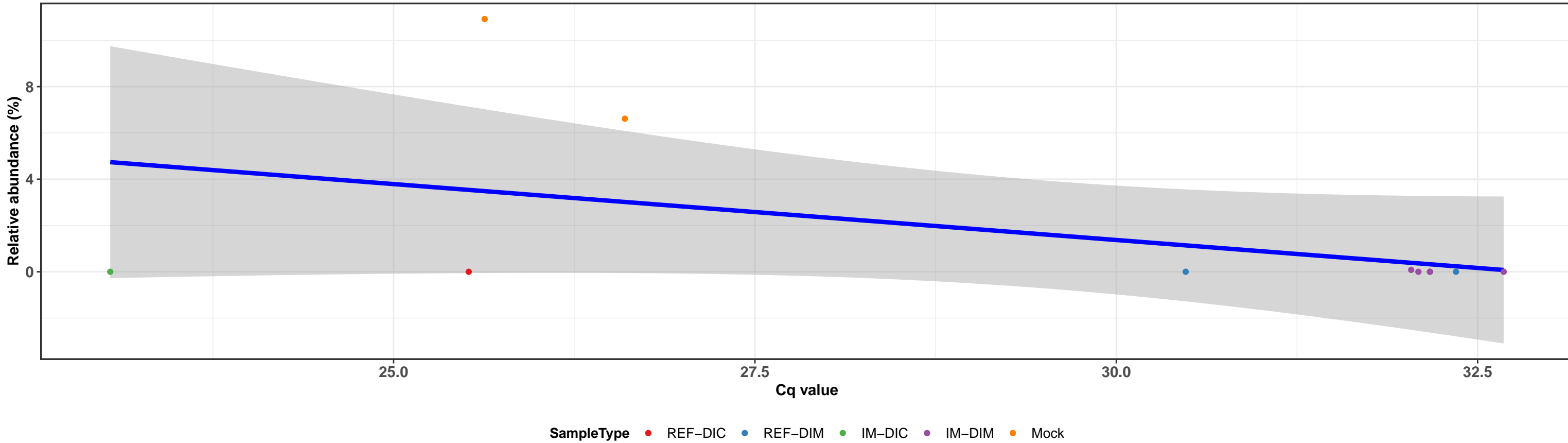
Correlation within: IM-DIM



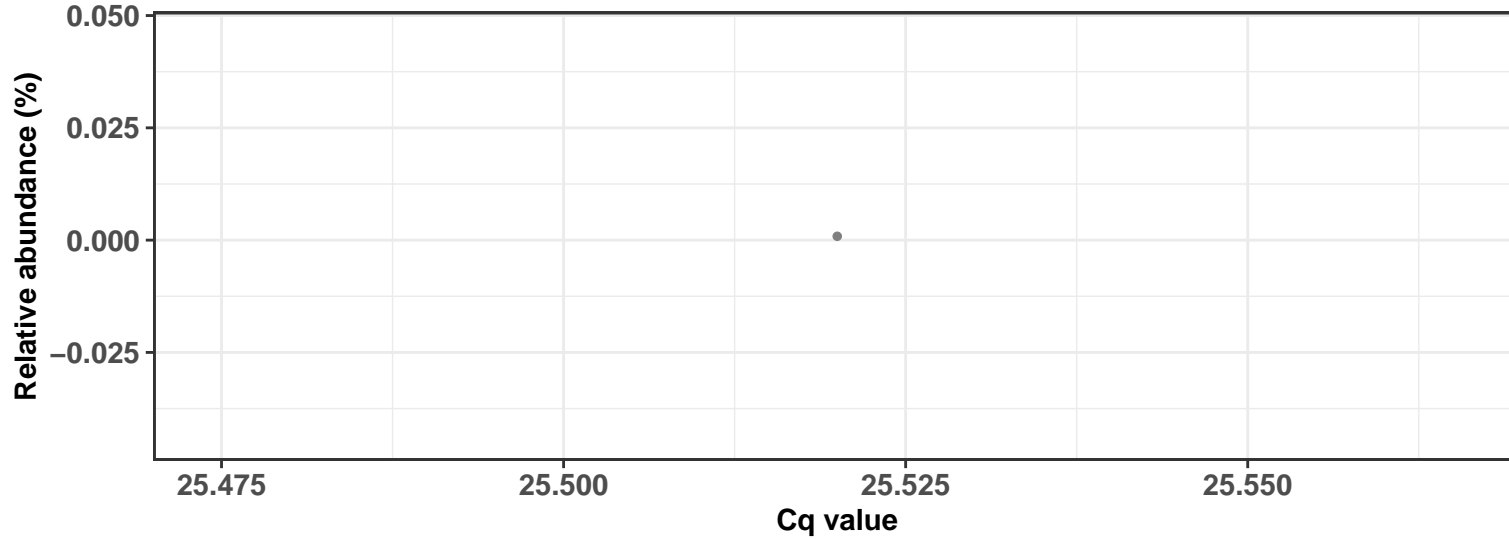
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

### Correlation with all samples

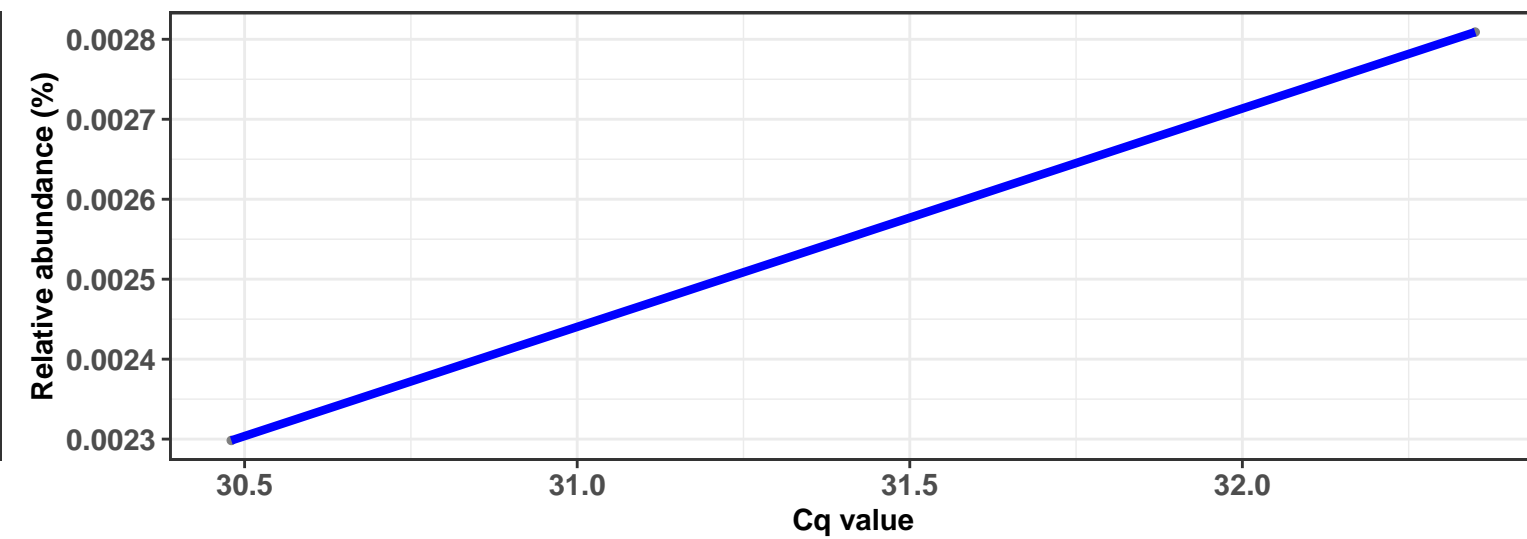
$\log_e(S) = 5.642$ ,  $p = 0.400$ ,  $\hat{\rho}_{\text{Spearman}} = -0.282$ ,  $\text{CI}_{95\%} [-0.911, 0.276]$ ,  $n_{\text{pairs}} = 11$



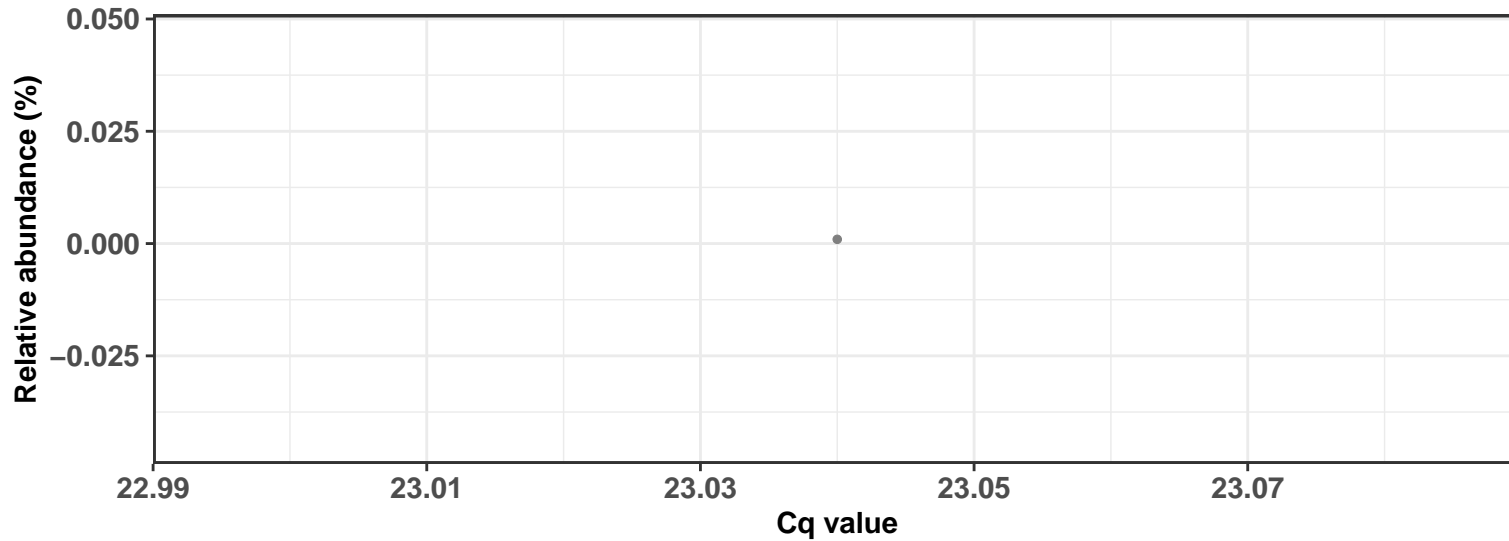
### Correlation within: REF-DIC



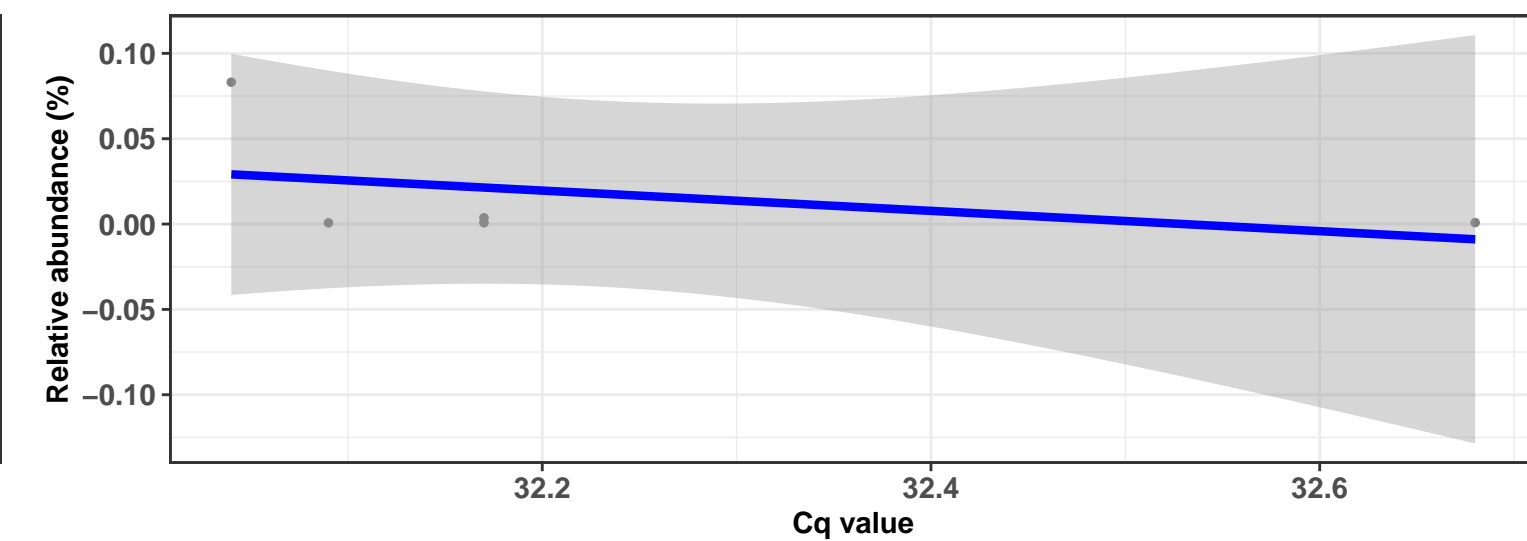
### Correlation within: REF-DIM



### Correlation within: IM-DIC



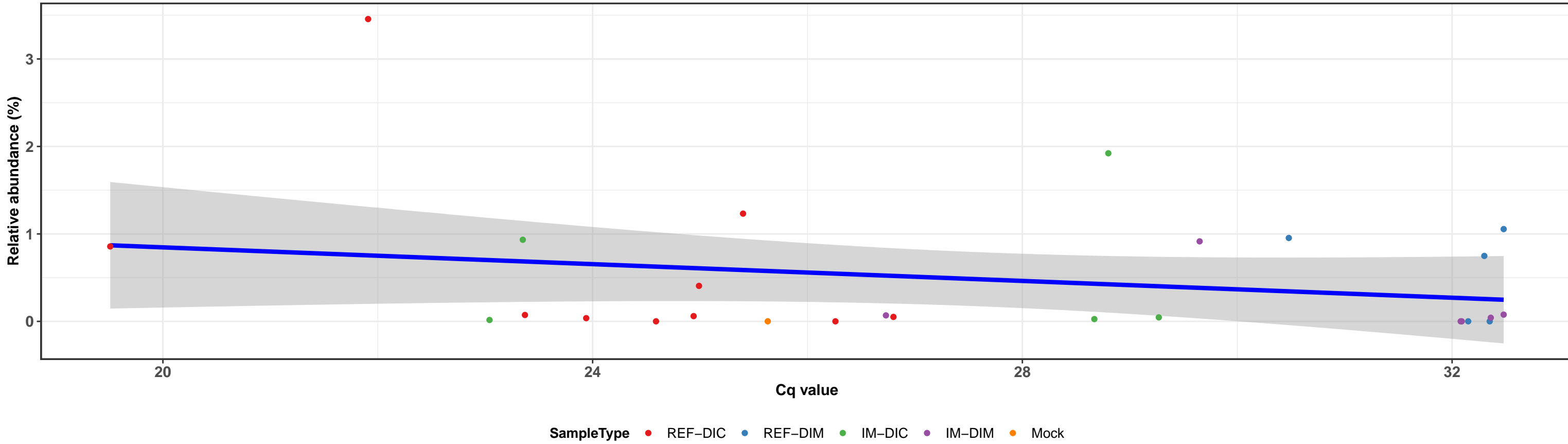
### Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Vibrionales; f\_\_Vibrionaceae; g\_\_Aliivibrio; Ambiguous\_taxa

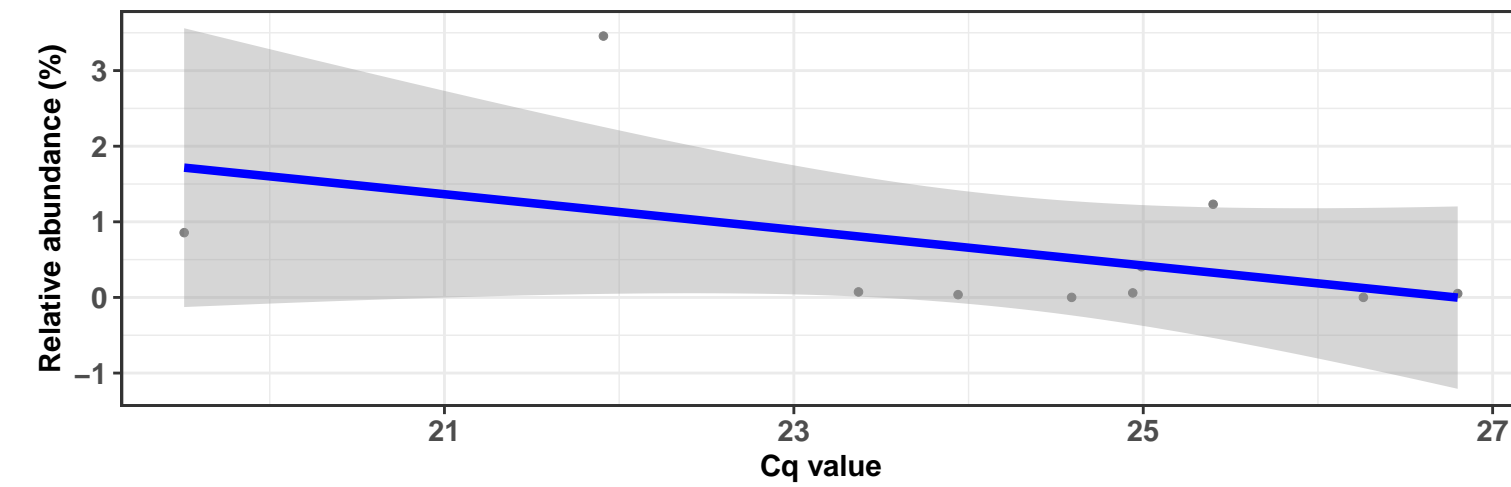
### Correlation with all samples

$\log_e(S) = 8.249$ ,  $p = 0.405$ ,  $\hat{\rho}_{\text{Spearman}} = -0.167$ ,  $\text{CI}_{95\%} [-0.604, 0.252]$ ,  $n_{\text{pairs}} = 27$

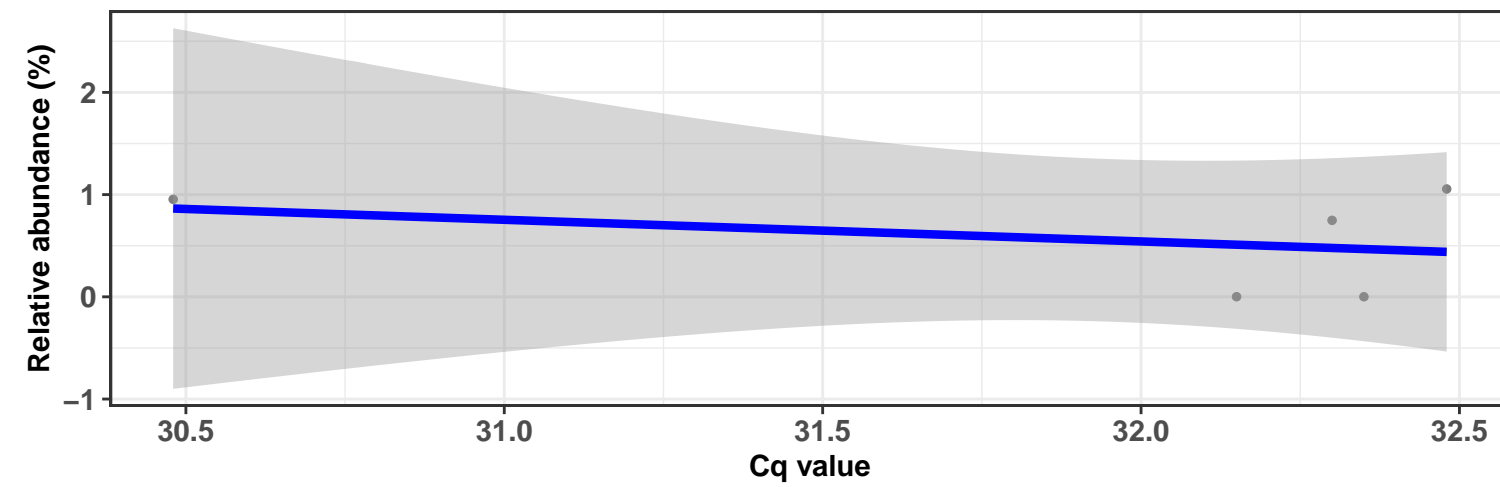


### Correlation within: REF-DIC

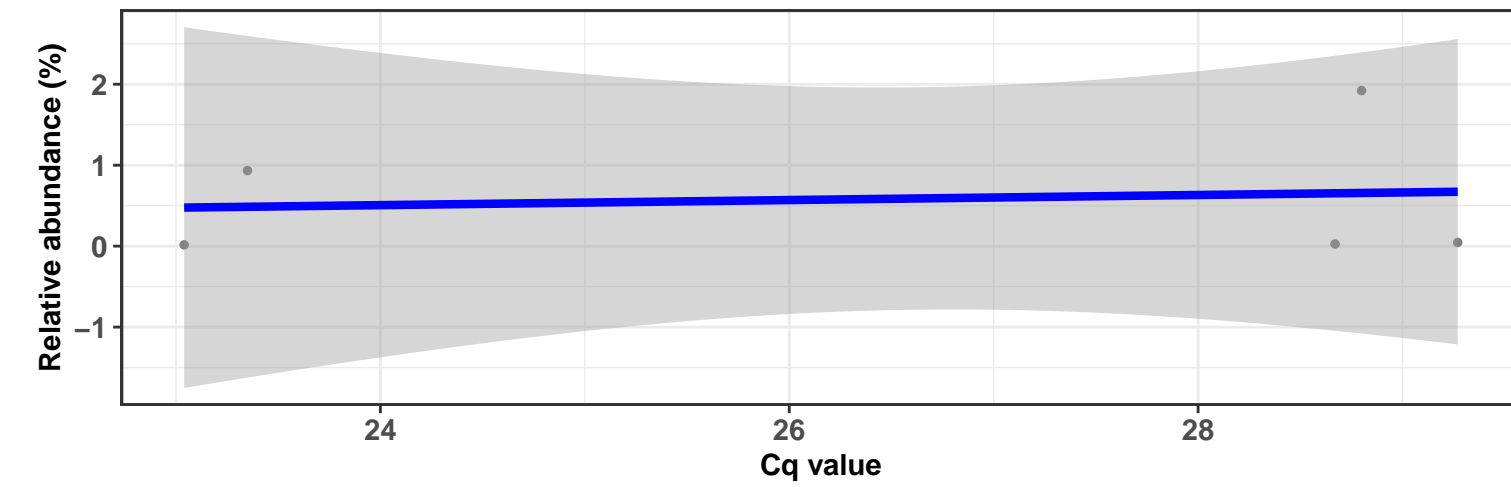
$\log_e(S) = 5.421$ ,  $p = 0.293$ ,  $\hat{\rho}_{\text{Spearman}} = -0.370$ ,  $\text{CI}_{95\%} [-1.094, 0.255]$ ,  $n_{\text{pairs}} = 10$



### Correlation within: REF-DIM

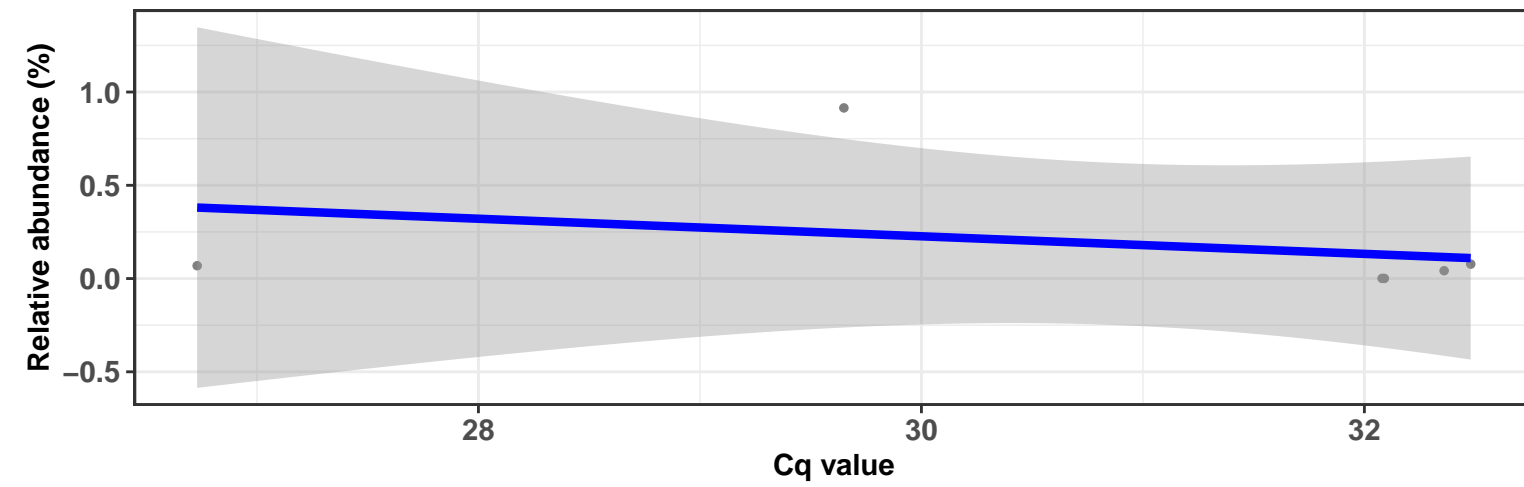


### Correlation within: IM-DIC



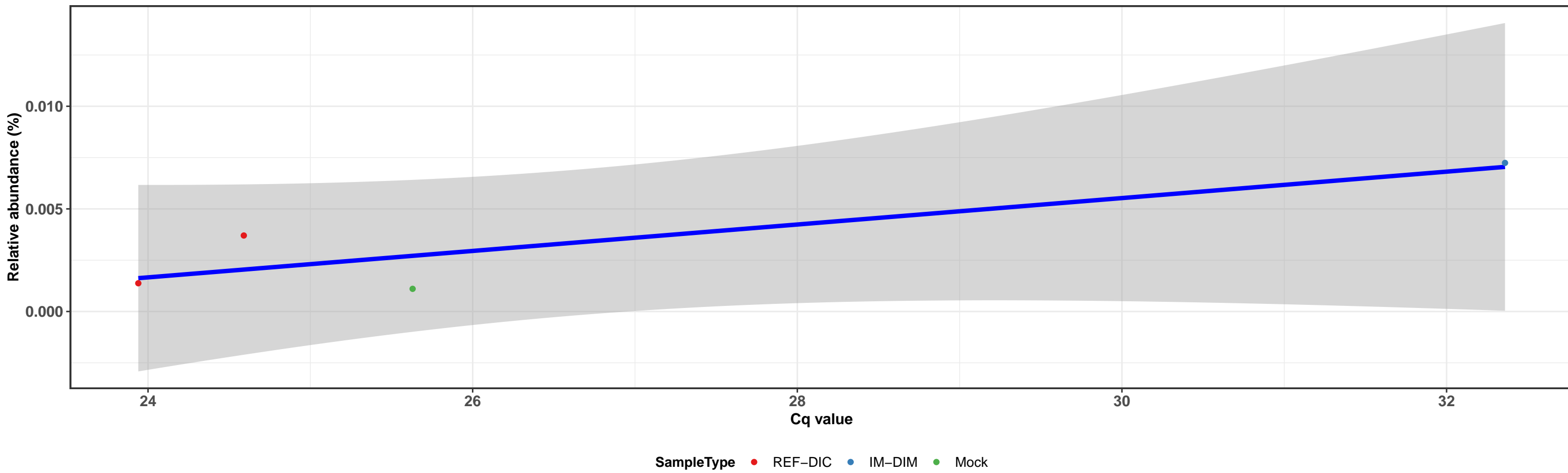
### Correlation within: IM-DIM

$\log_e(S) = 3.689$ ,  $p = 0.787$ ,  $\hat{\rho}_{\text{Spearman}} = -0.143$ ,  $\text{CI}_{95\%} [-1.048, 0.855]$ ,  $n_{\text{pairs}} = 6$

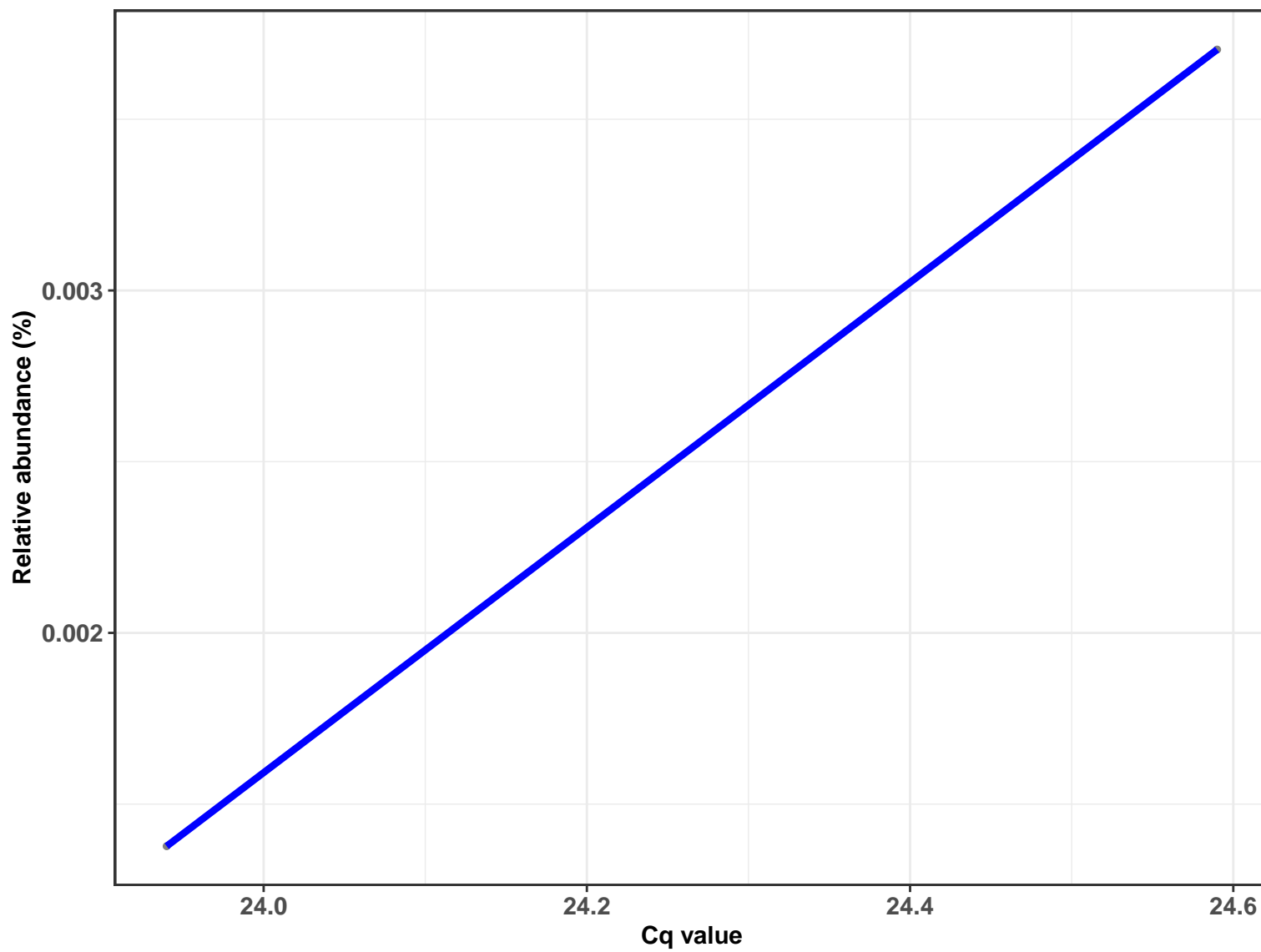


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Acidovorax; NA

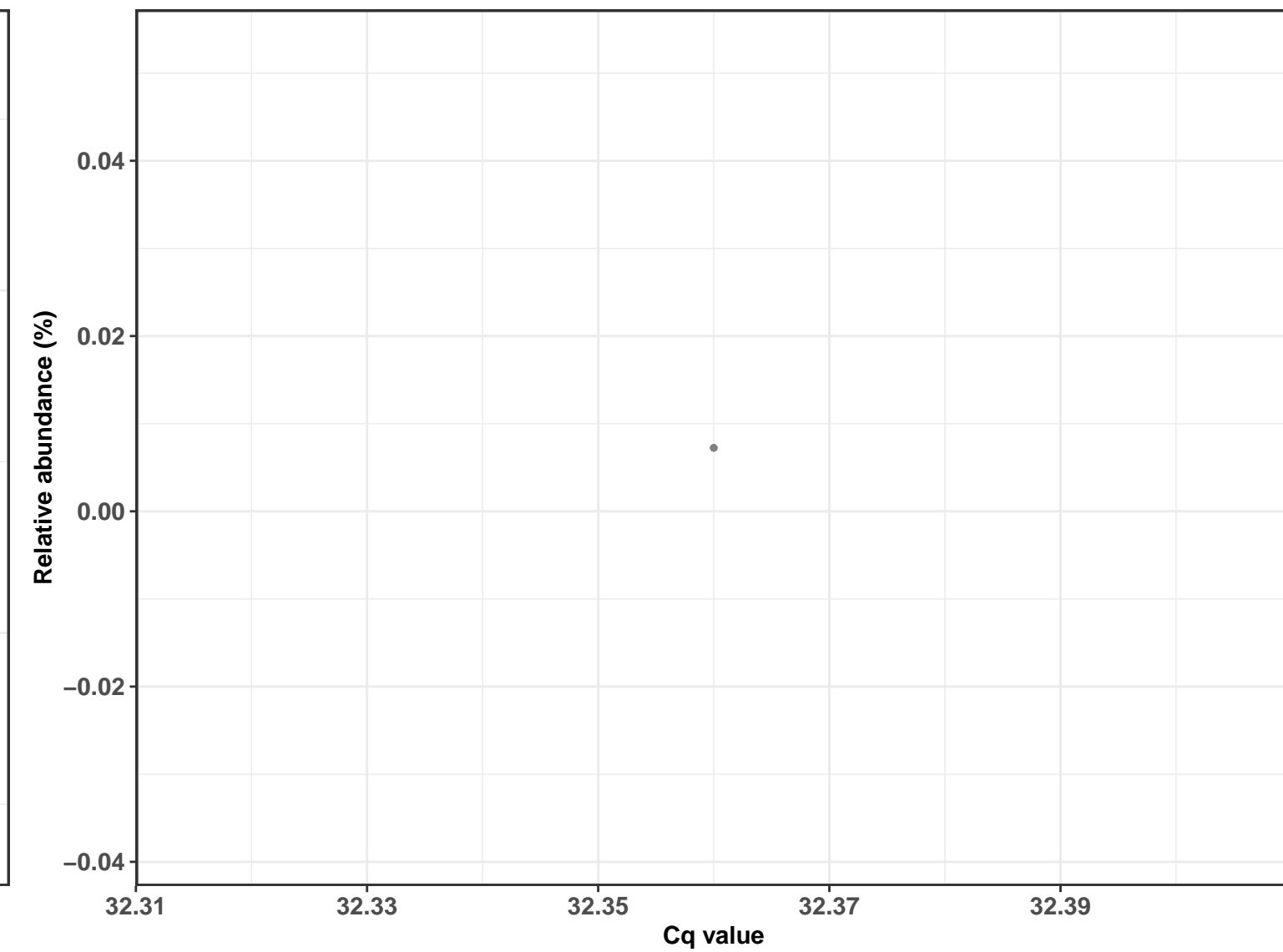
Correlation with all samples



Correlation within: REF-DIC

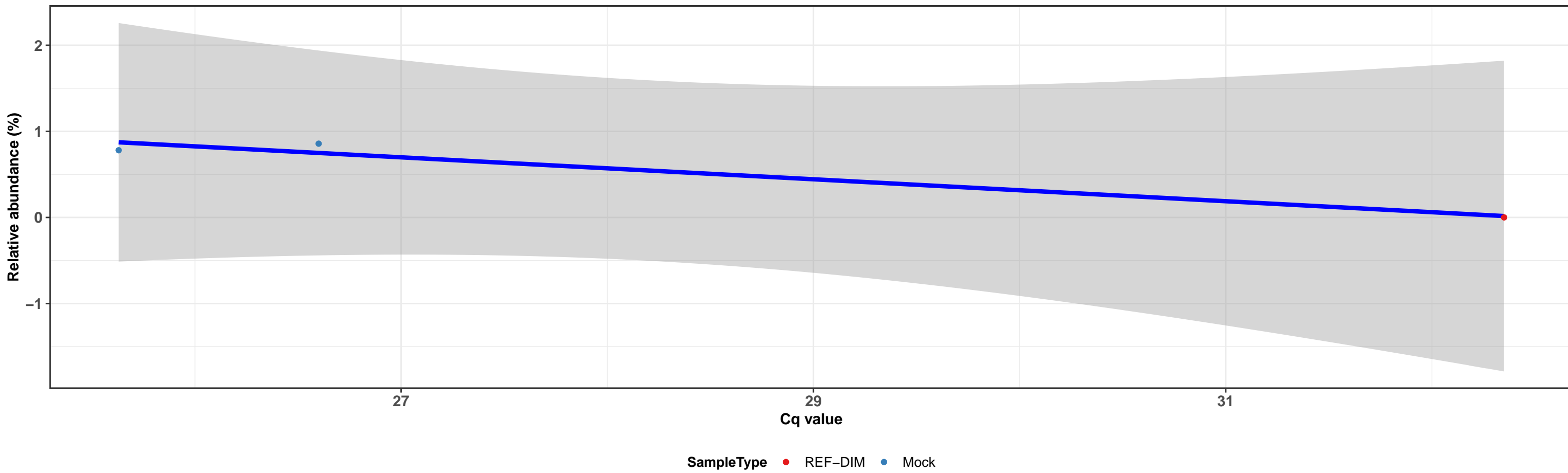


Correlation within: IM-DIM

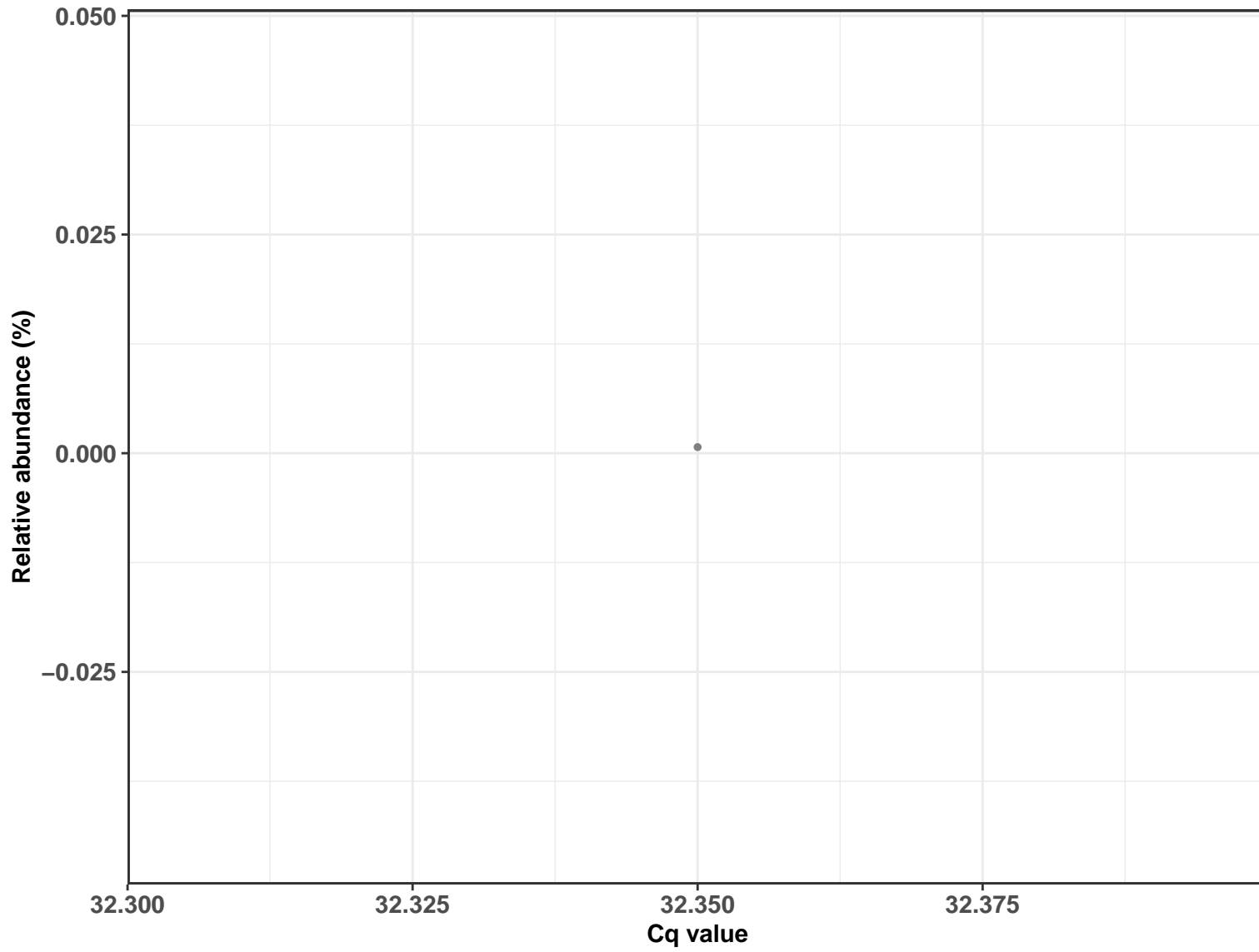


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Listeriaceae; g\_\_Listeria; s\_\_Listeria monocytogenes

Correlation with all samples

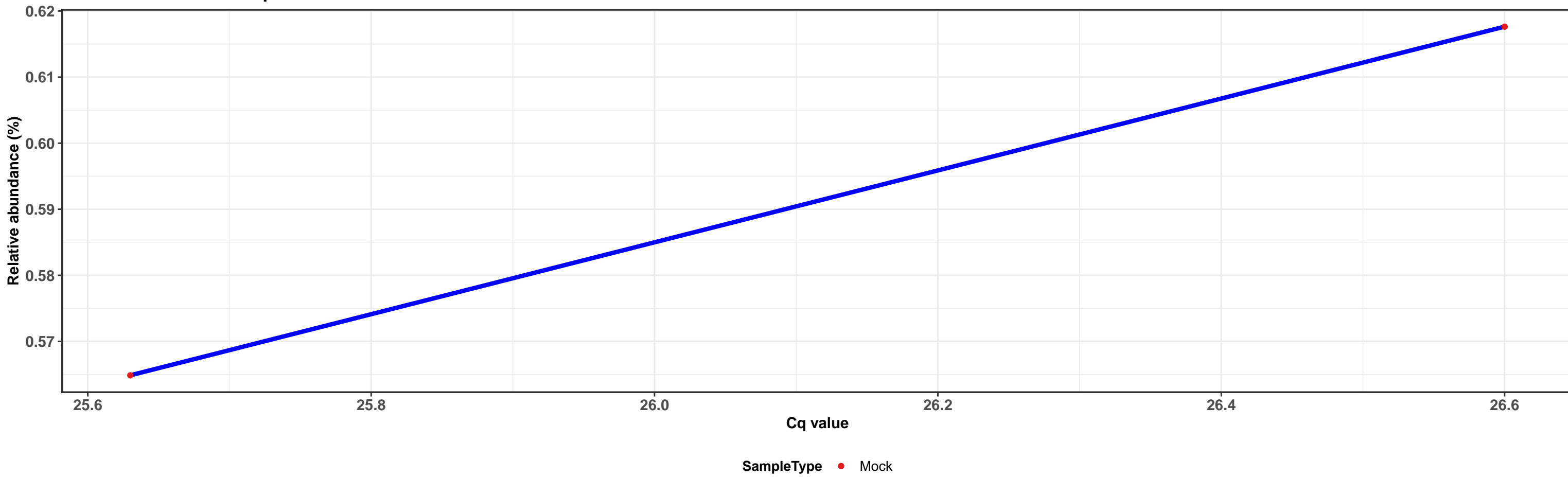


Correlation within: REF-DIM

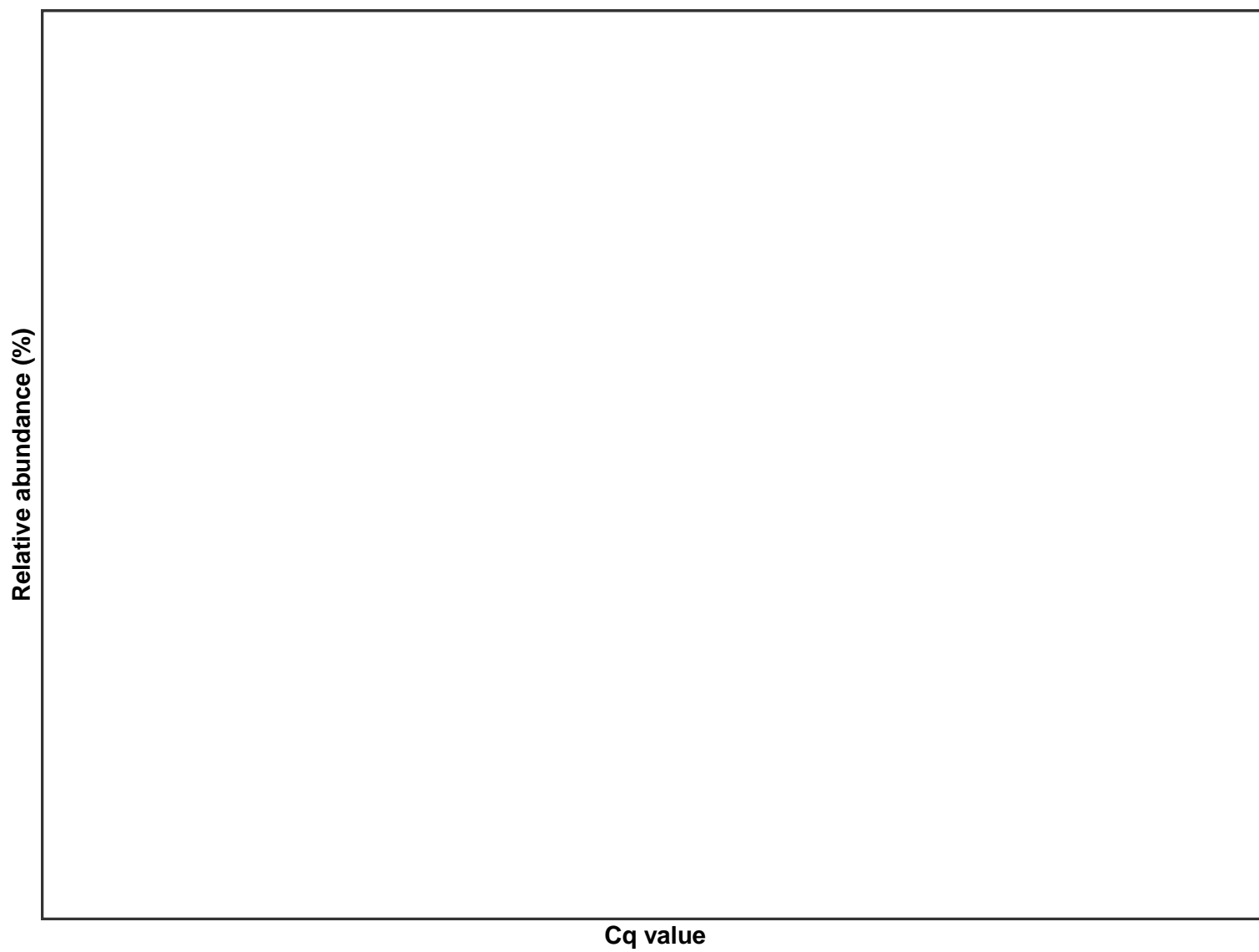


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Listeriaceae; g\_\_Listeria; s\_\_Listeria monocytogenes

Correlation with all samples



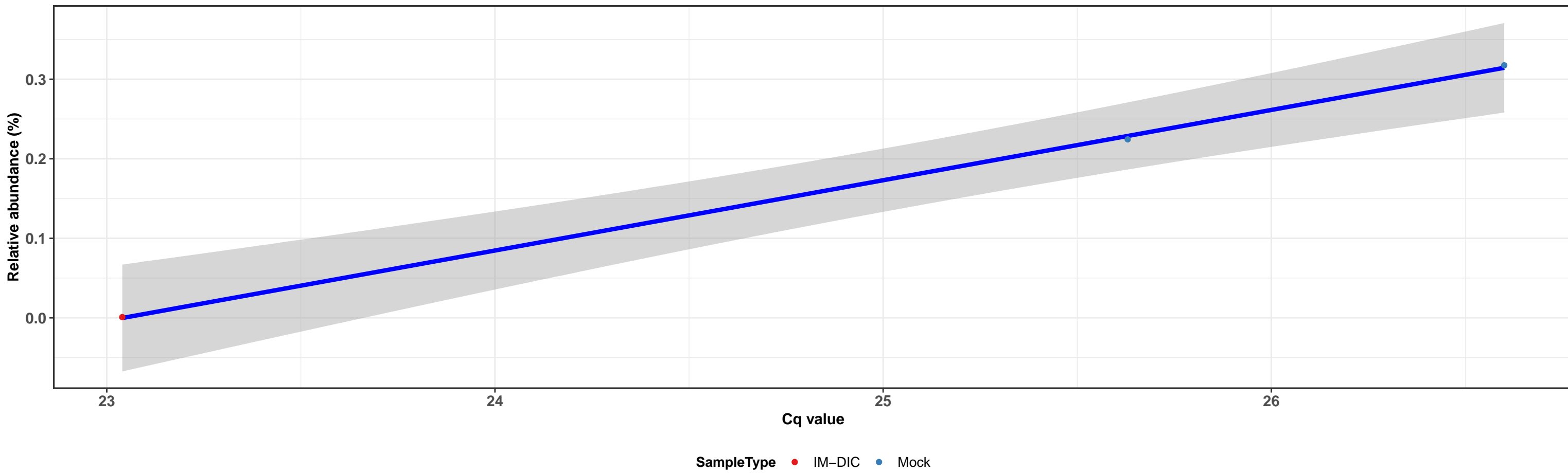
Correlation within:



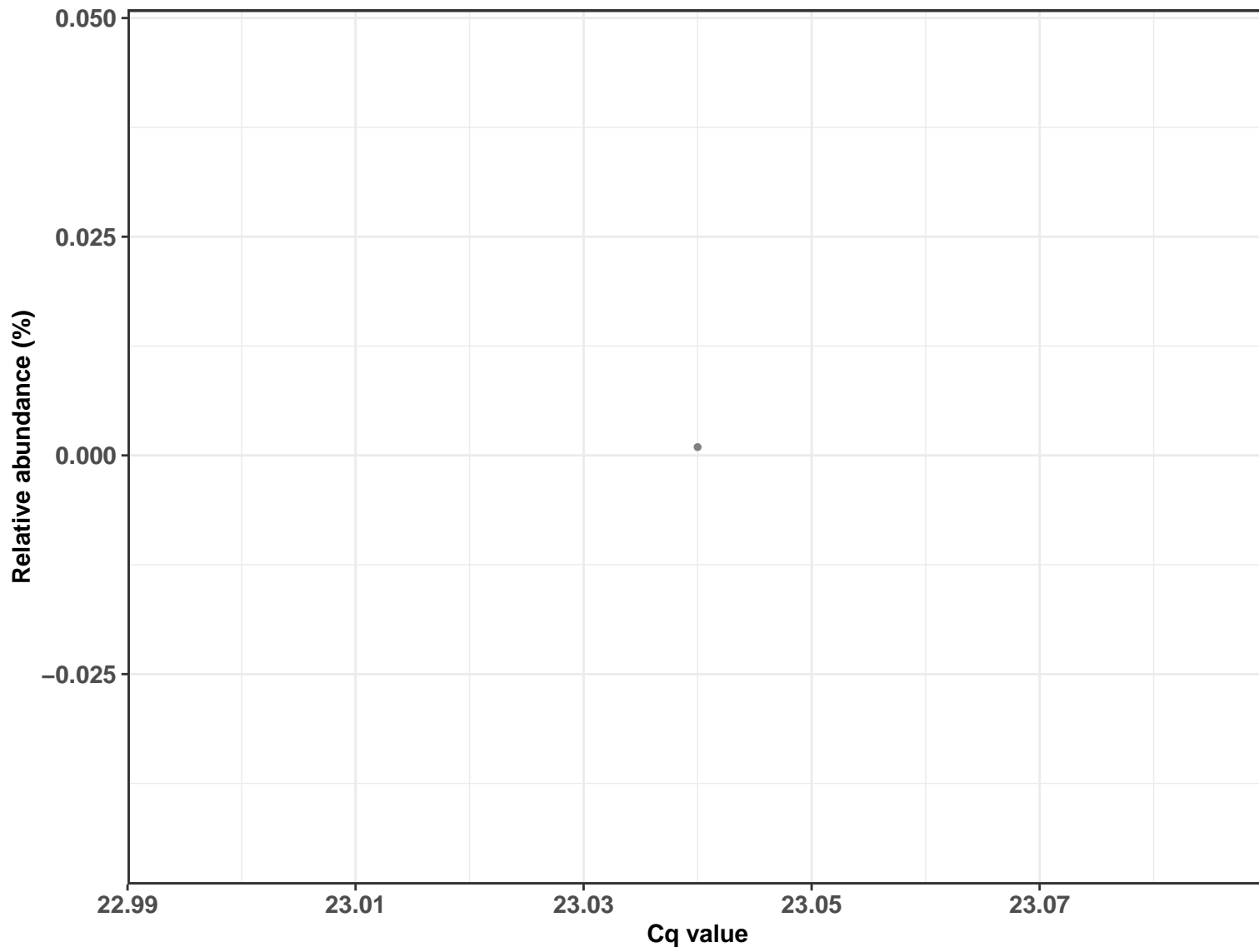


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Listeriaceae; g\_\_Listeria; s\_\_Listeria monocytogenes

Correlation with all samples



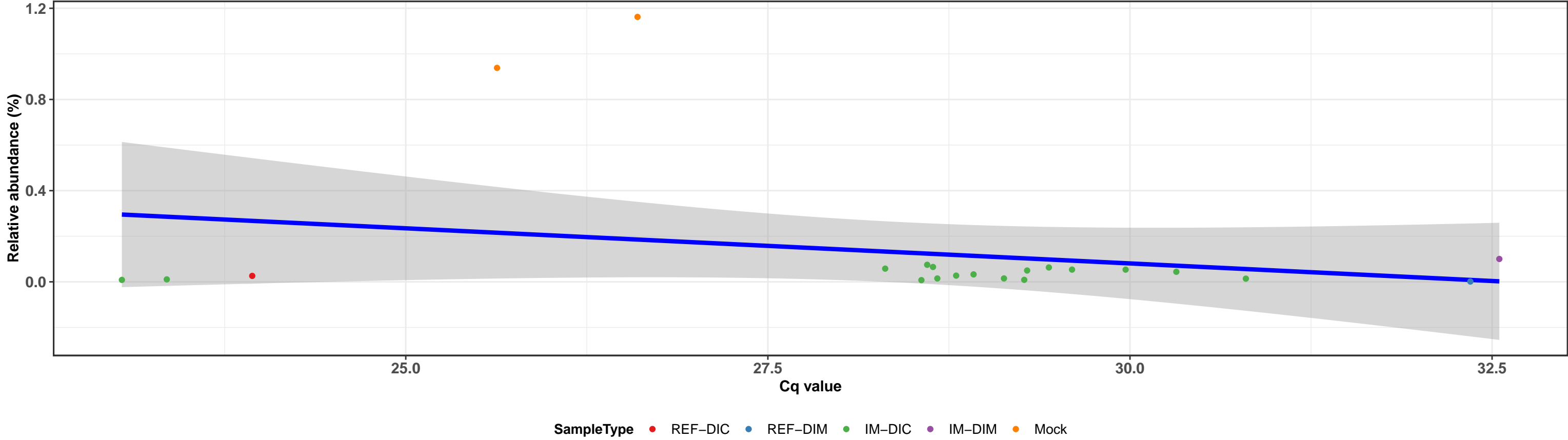
Correlation within: IM-DIC



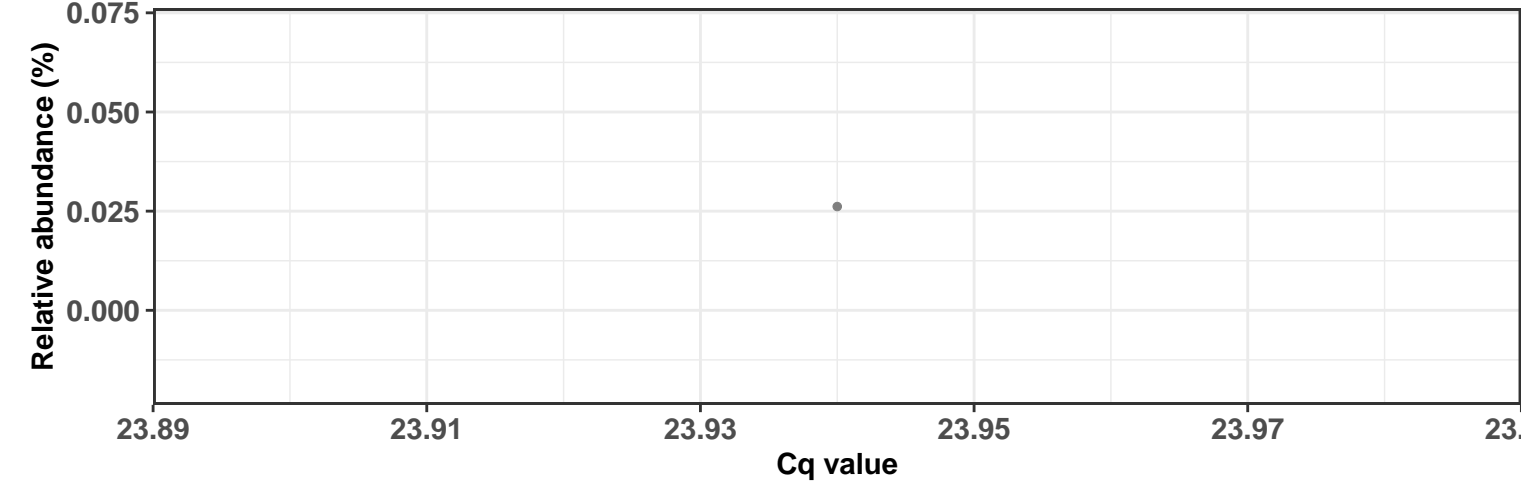
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus faecalis

Correlation with all samples

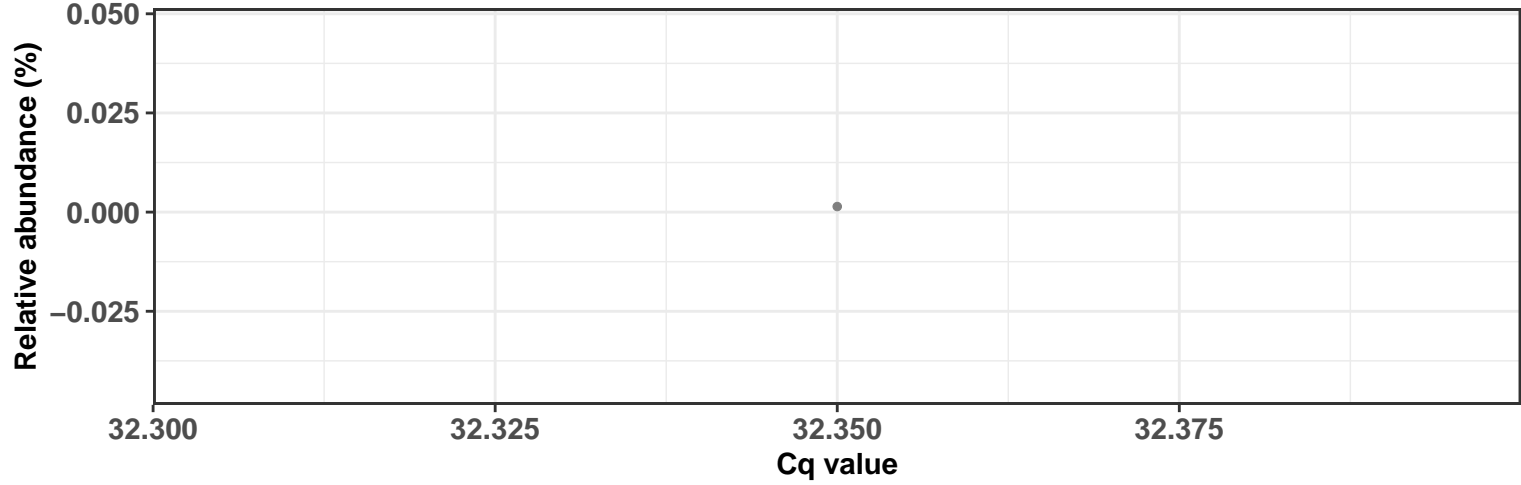
$\log_e(S) = 7.475$ ,  $p = 0.986$ ,  $\hat{\rho}_{\text{Spearman}} = 0.004$ ,  $CI_{95\%} [-0.491, 0.438]$ ,  $n_{\text{pairs}} = 22$



Correlation within: REF-DIC

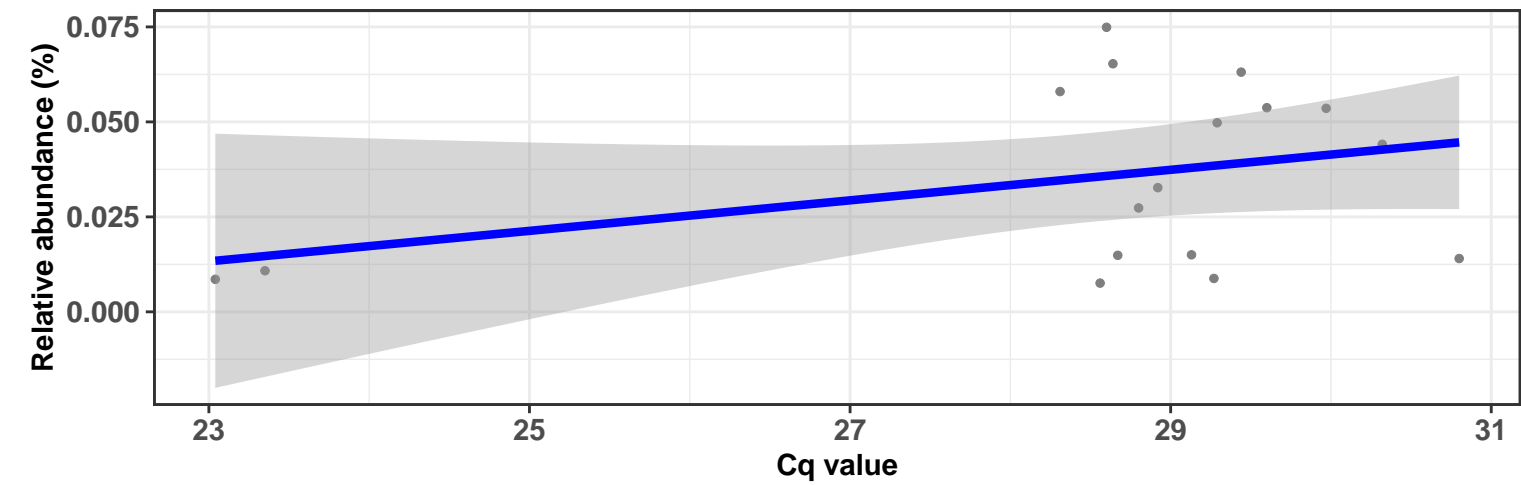


Correlation within: REF-DIM

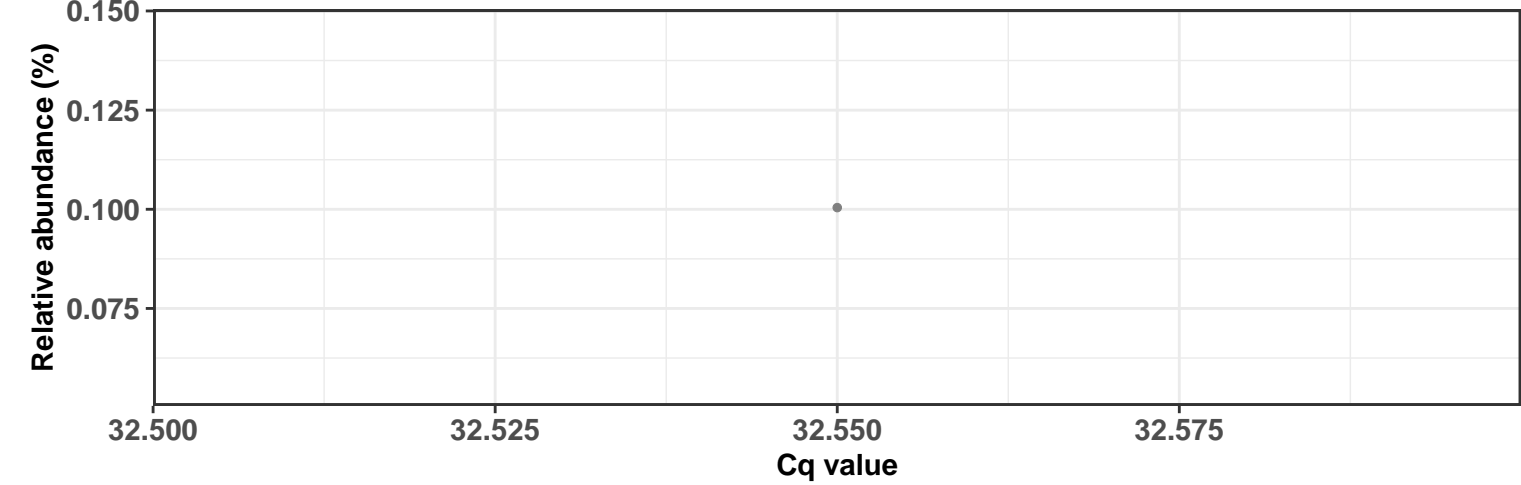


Correlation within: IM-DIC

$\log_e(S) = 6.474$ ,  $p = 0.428$ ,  $\hat{\rho}_{\text{Spearman}} = 0.206$ ,  $CI_{95\%} [-0.312, 0.785]$ ,  $n_{\text{pairs}} = 17$

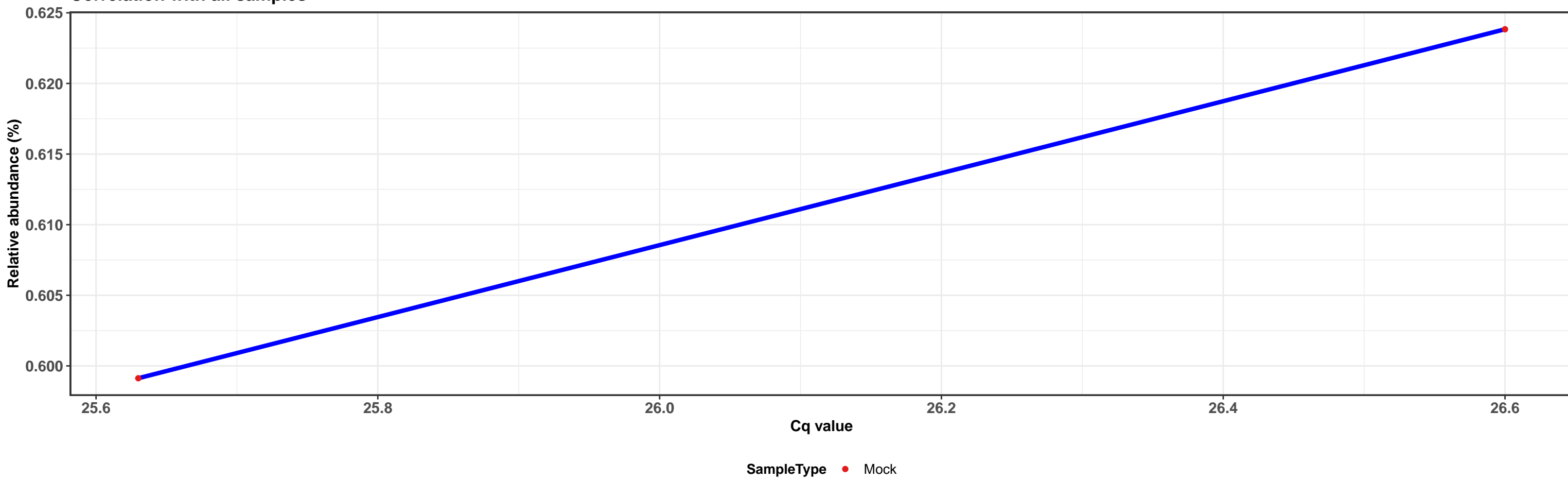


Correlation within: IM-DIM

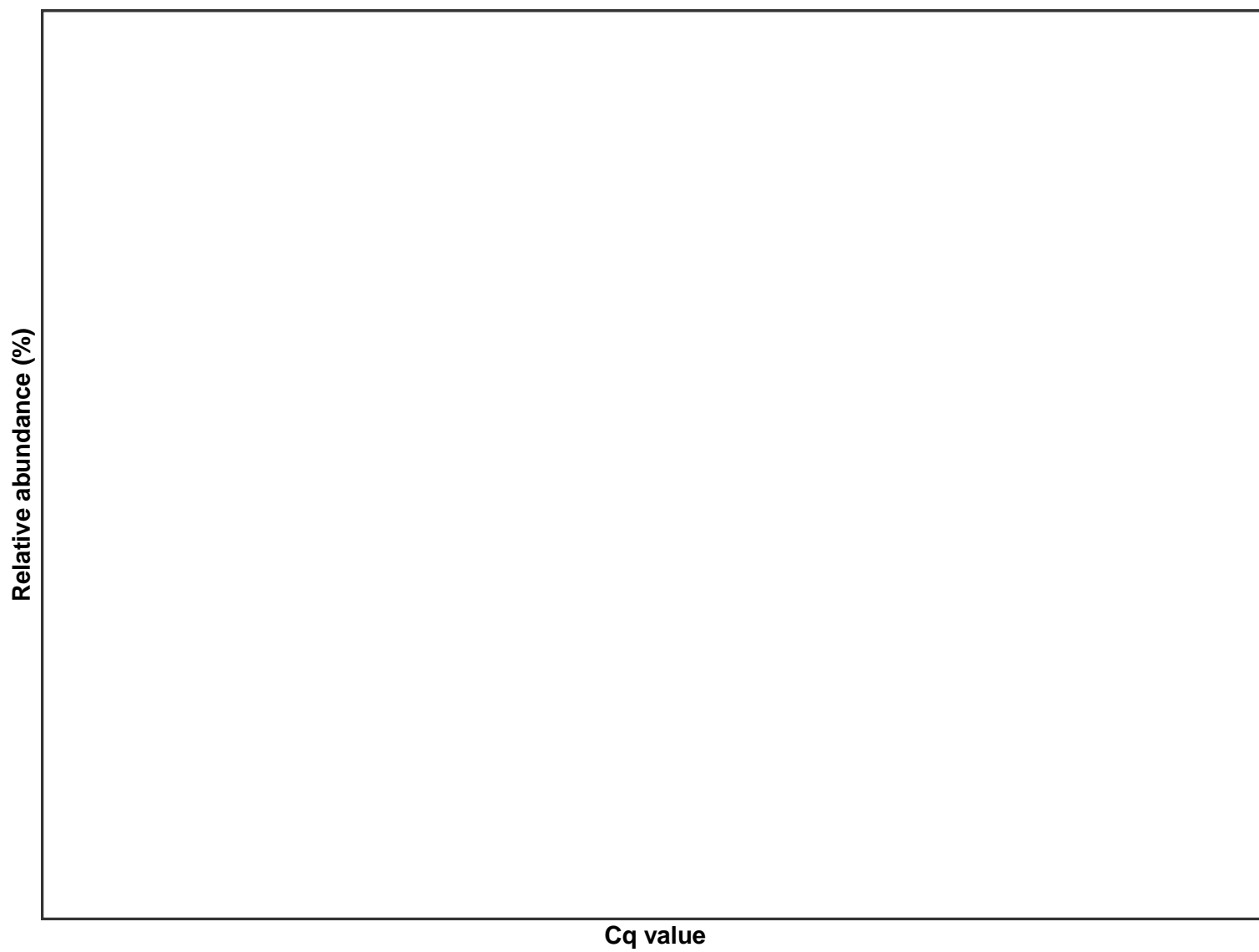


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus faecalis

Correlation with all samples

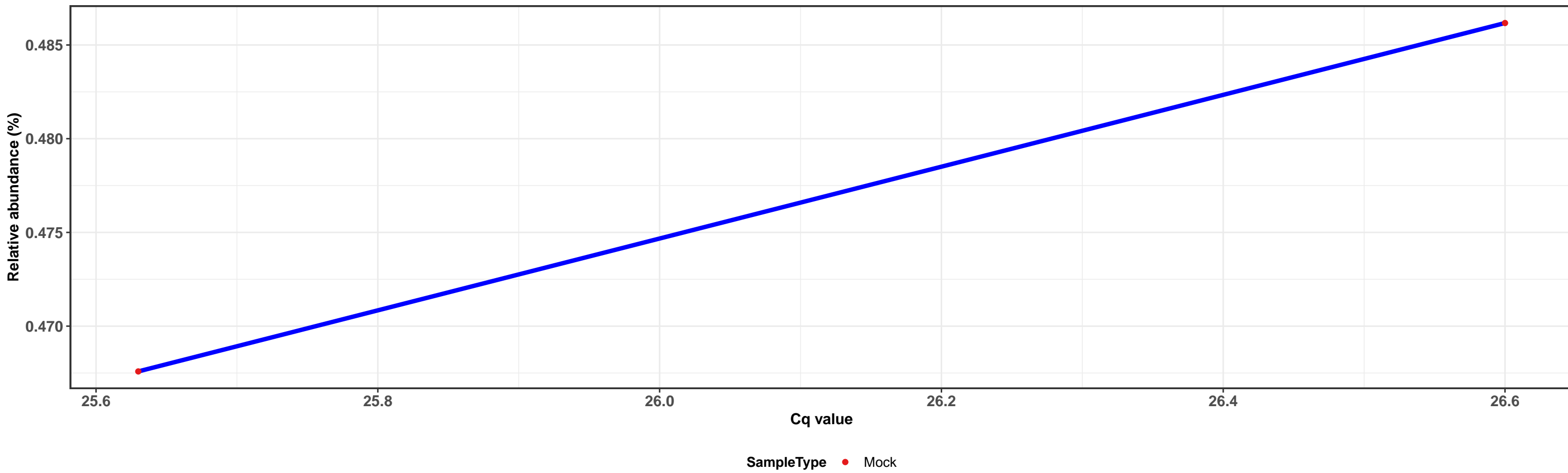


Correlation within:

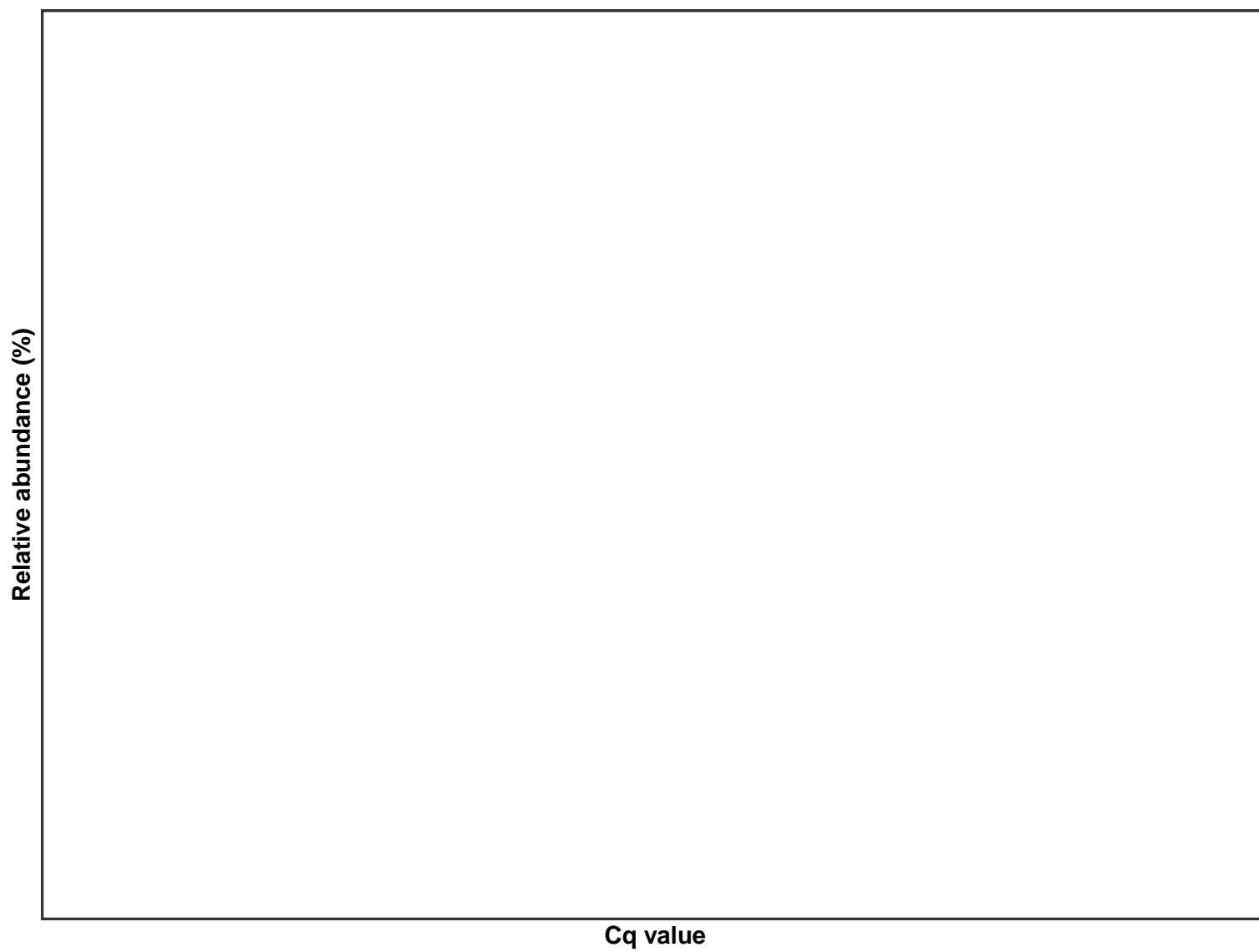


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus faecalis

Correlation with all samples



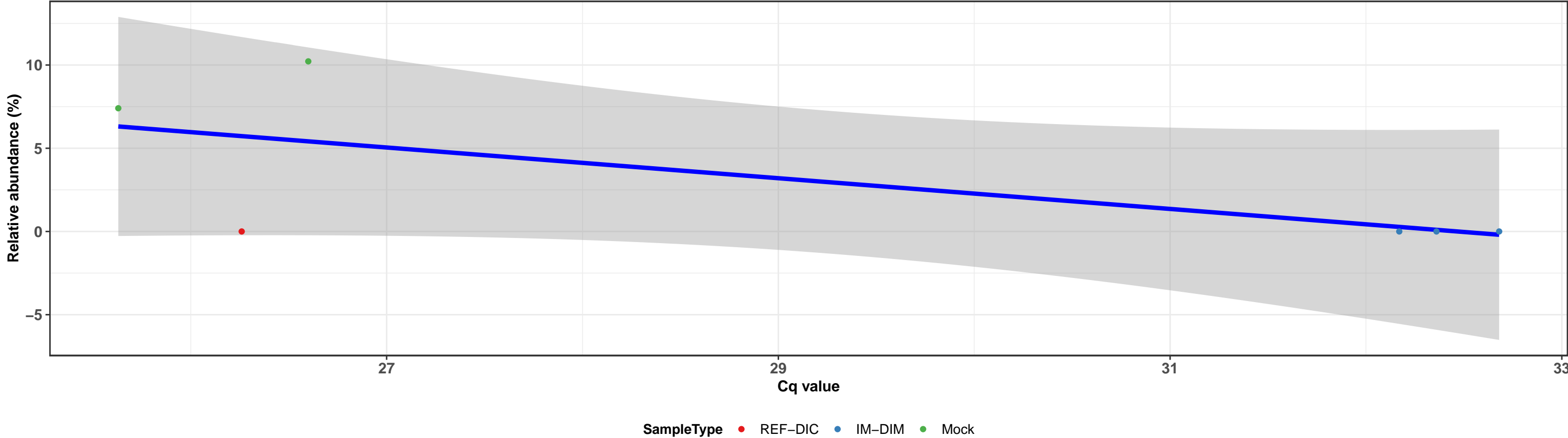
Correlation within:



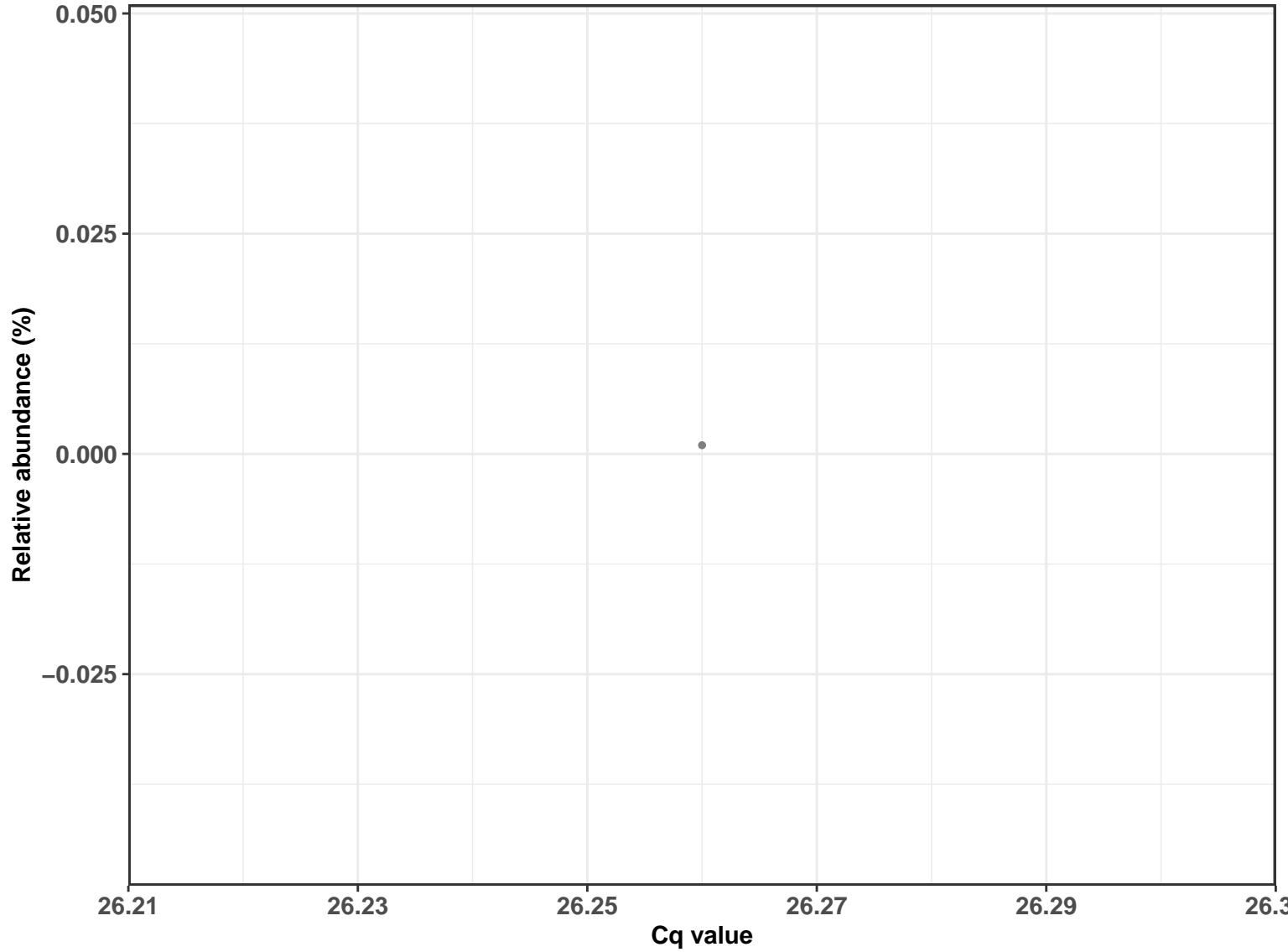
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples

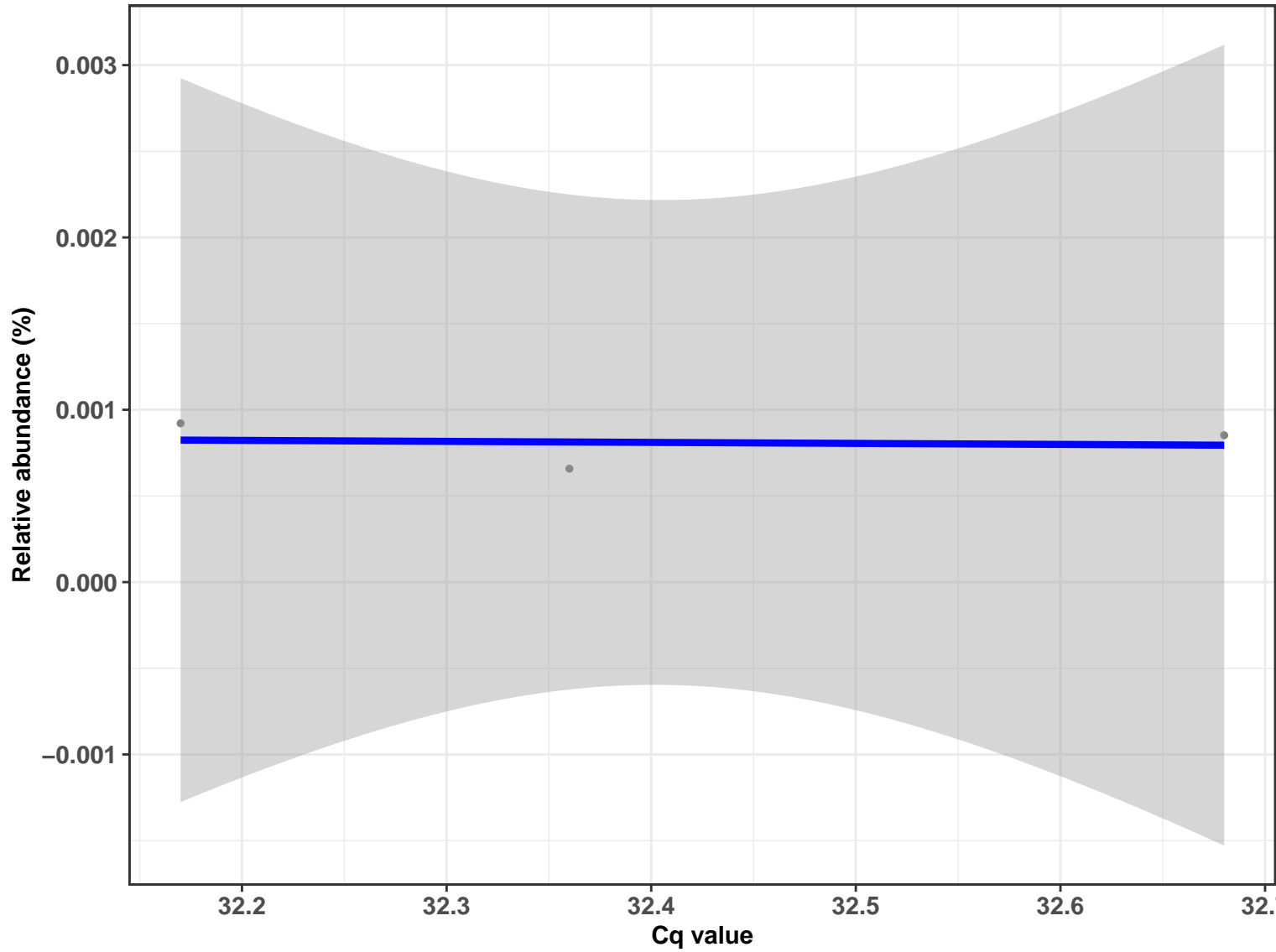
$\log_e(S) = 4.127$ ,  $p = 0.072$ ,  $\hat{\rho}_{\text{Spearman}} = -0.771$ ,  $CI_{95\%} [-1.478, -0.253]$ ,  $n_{\text{pairs}} = 6$



Correlation within: REF-DIC

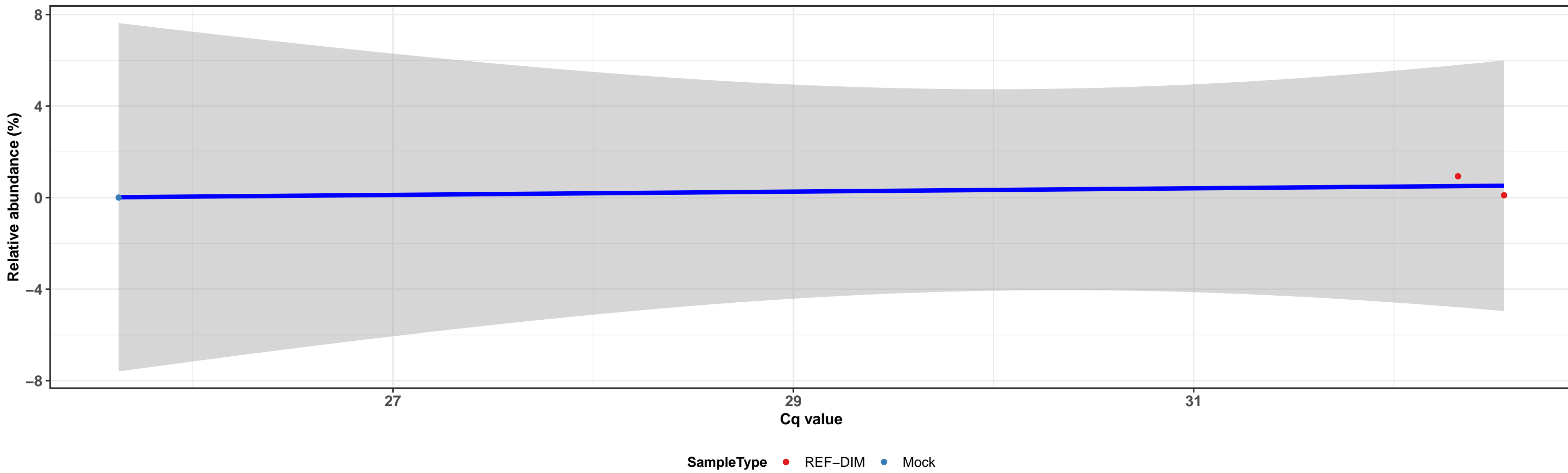


Correlation within: IM-DIM

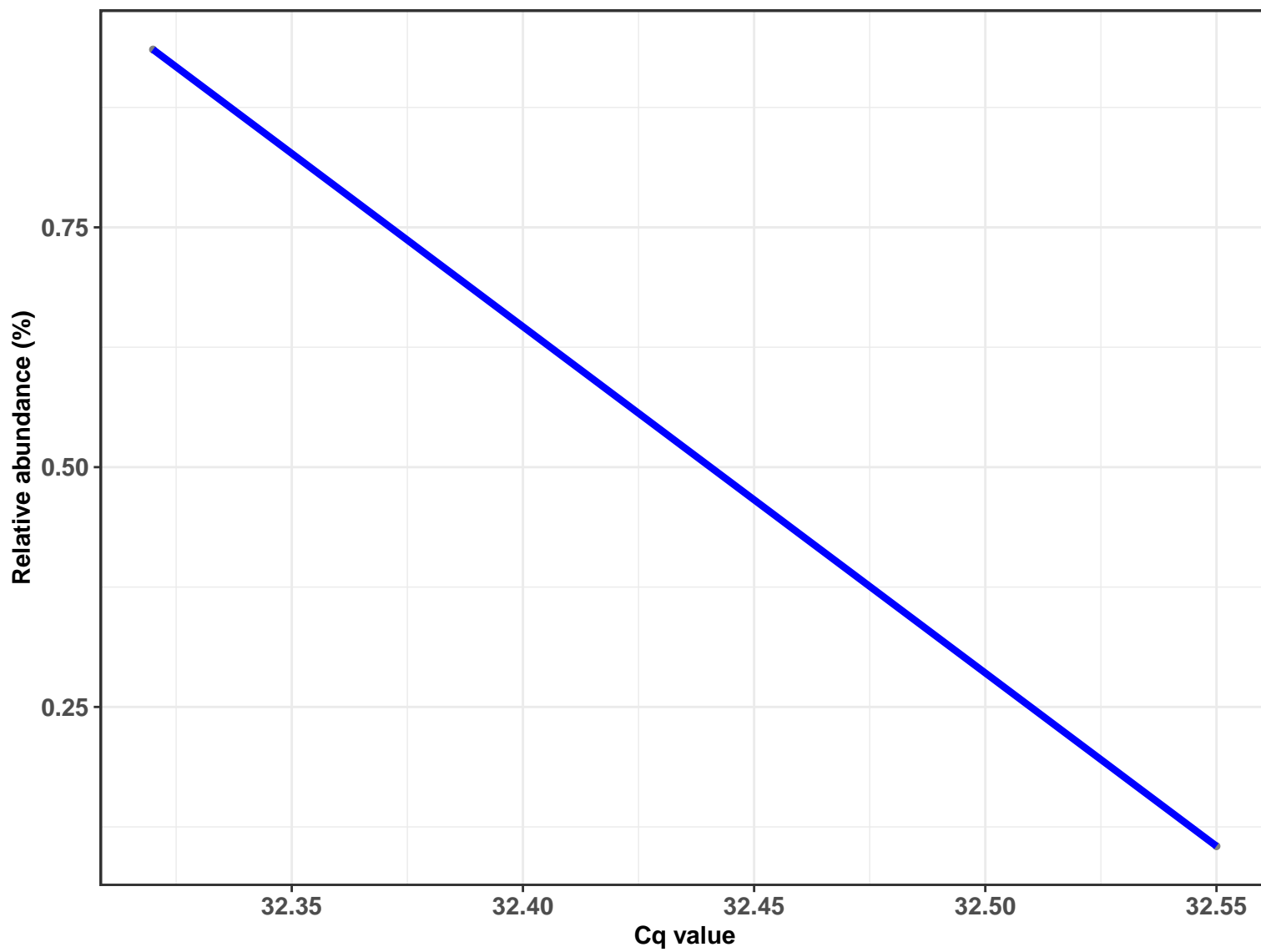


k\_\_Bacteria; p\_\_Cyanobacteria; c\_\_Melainabacteria; o\_\_Obscuribacterales; Ambiguous\_taxa; Ambiguous\_taxa; Ambiguous\_taxa

Correlation with all samples

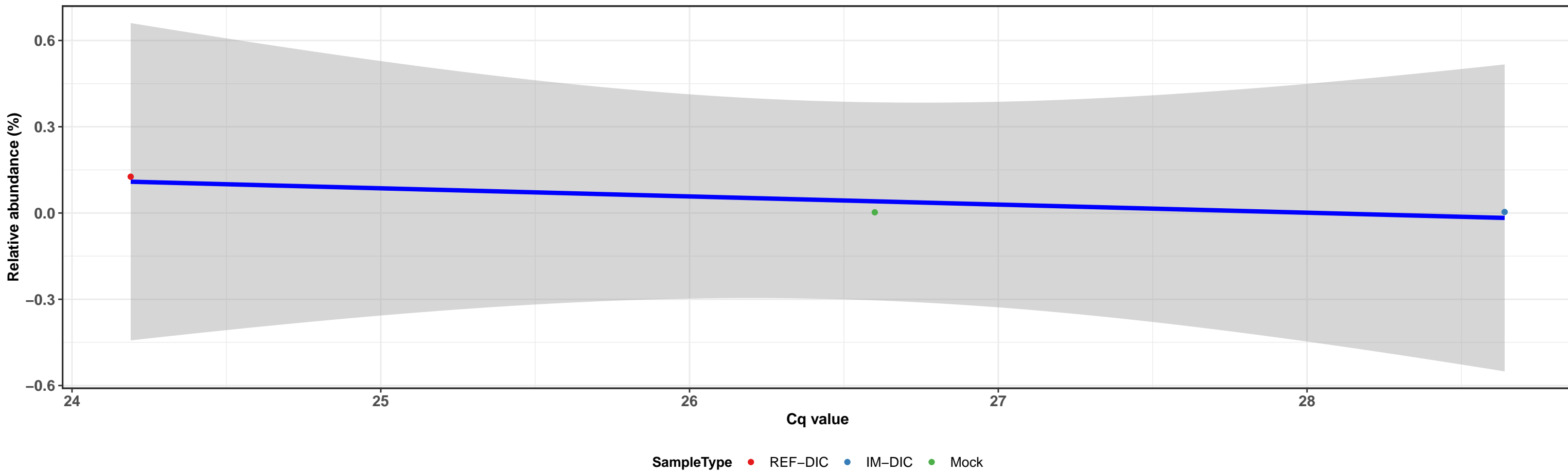


Correlation within: REF-DIM

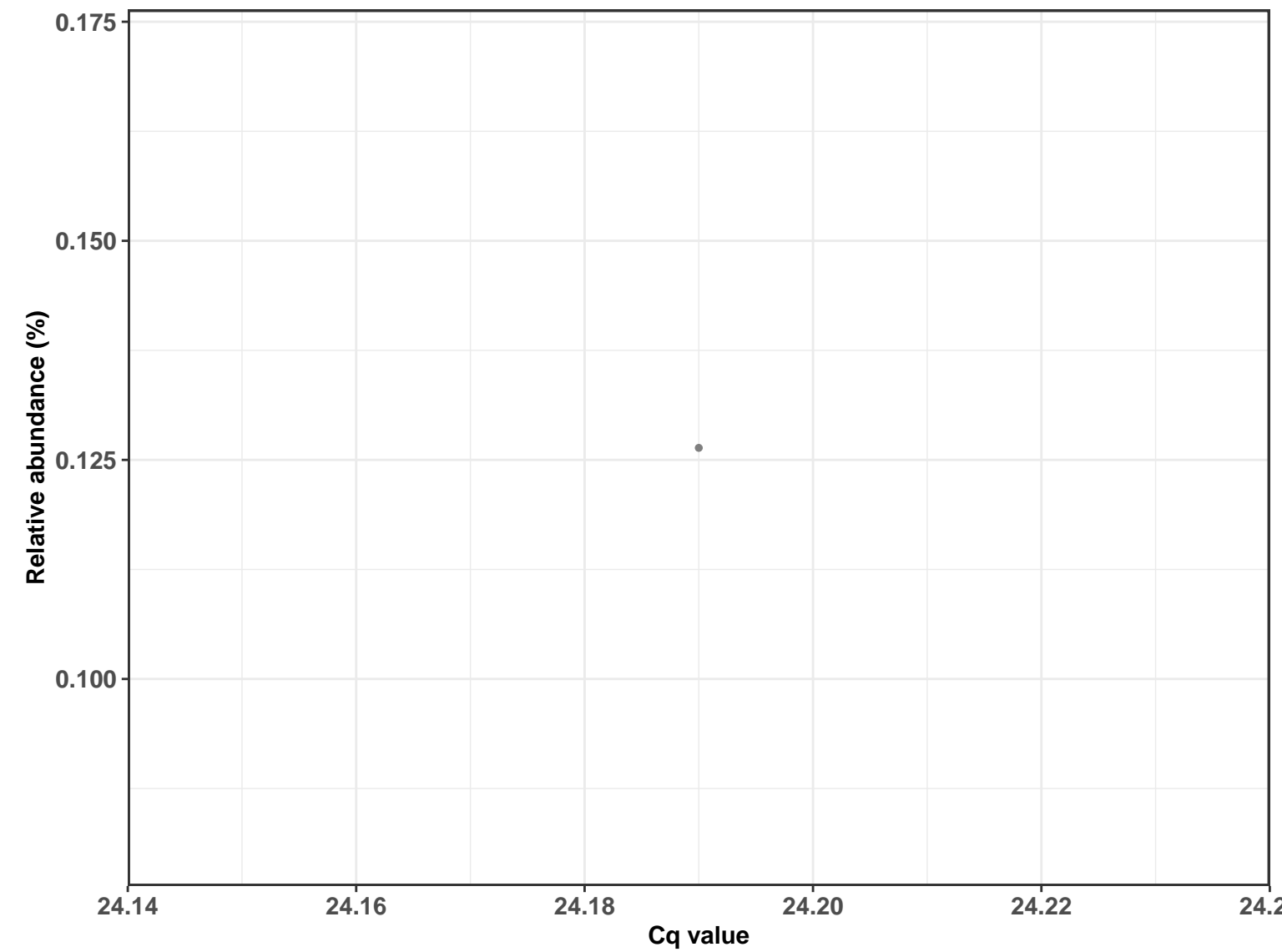


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

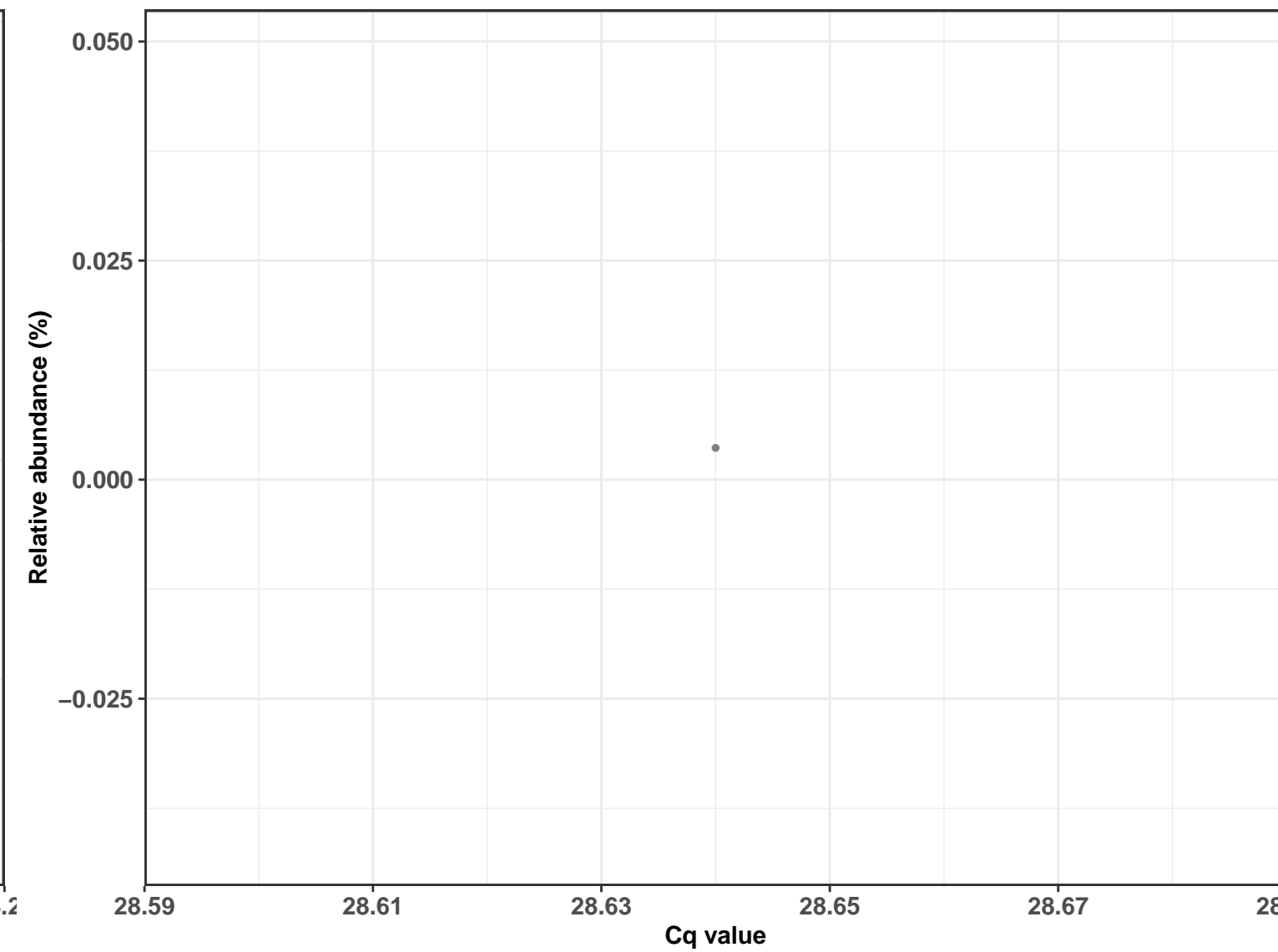
Correlation with all samples



Correlation within: REF-DIC



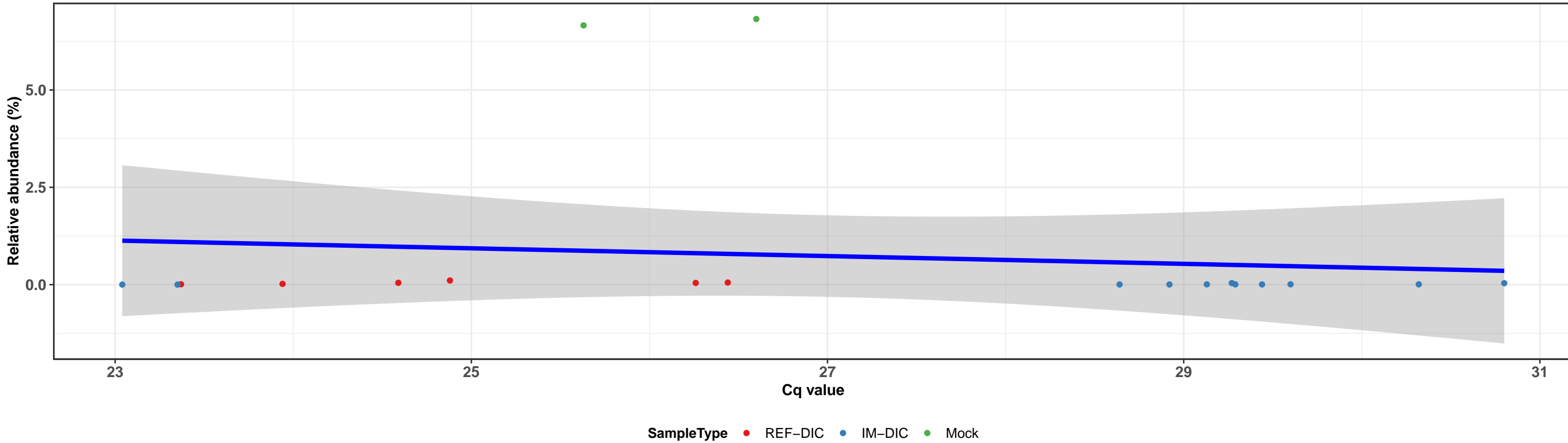
Correlation within: IM-DIC



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

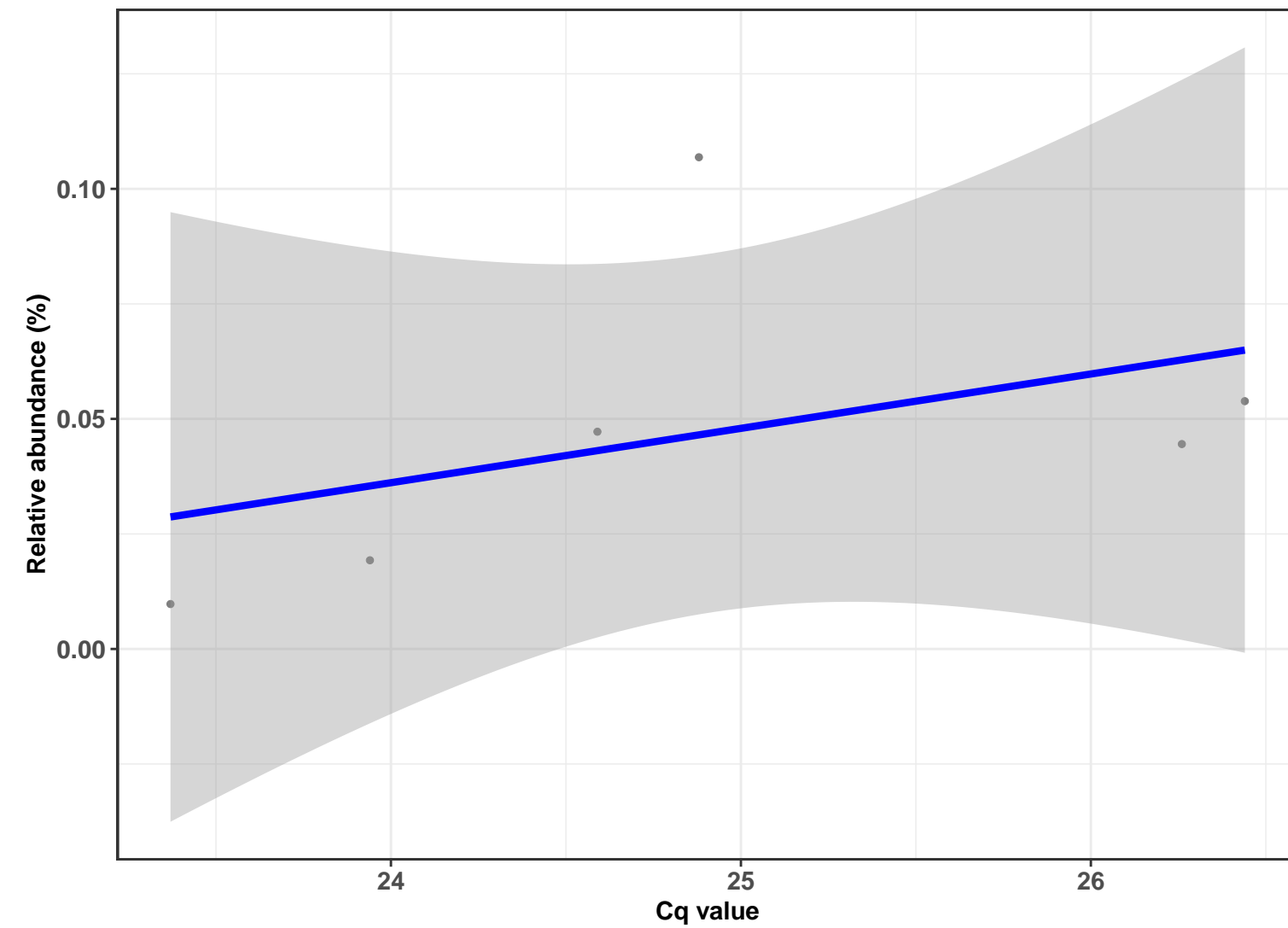
### Correlation with all samples

$\log_e(S) = 7.080$ ,  $p = 0.864$ ,  $\hat{\rho}_{\text{Spearman}} = -0.042$ ,  $\text{CI}_{95\%} [-0.541, 0.441]$ ,  $n_{\text{pairs}} = 19$



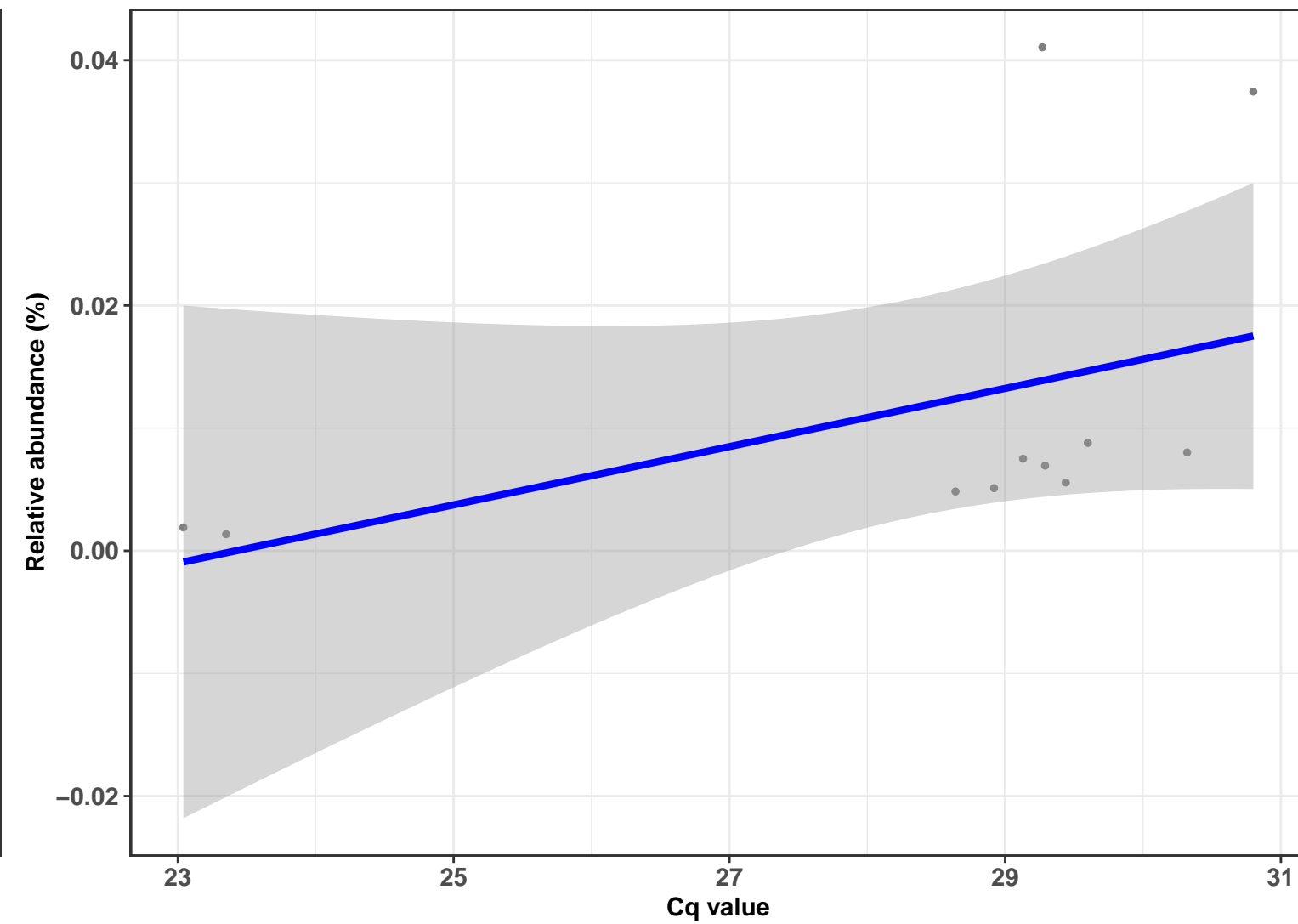
### Correlation within: REF-DIC

$\log_e(S) = 2.303$ ,  $p = 0.111$ ,  $\hat{\rho}_{\text{Spearman}} = 0.714$ ,  $\text{CI}_{95\%} [0.060, 1.427]$ ,  $n_{\text{pairs}} = 6$



### Correlation within: IM-DIC

$\log_e(S) = 3.829$ ,  $p = 0.004$ ,  $\hat{\rho}_{\text{Spearman}} = 0.791$ ,  $\text{CI}_{95\%} [0.448, 1.206]$ ,  $n_{\text{pairs}} = 11$

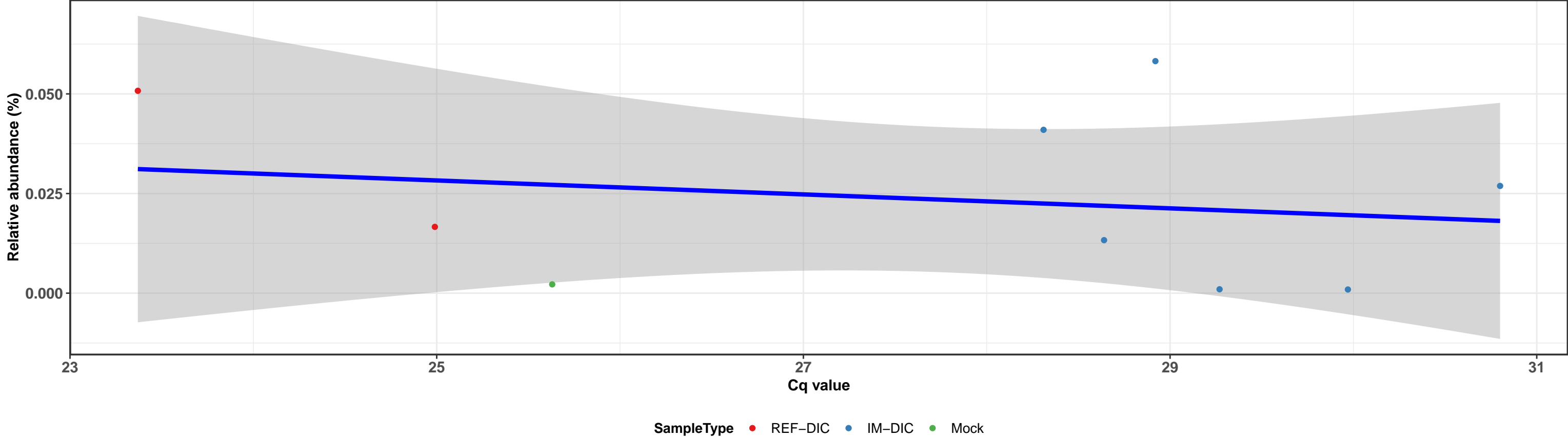




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

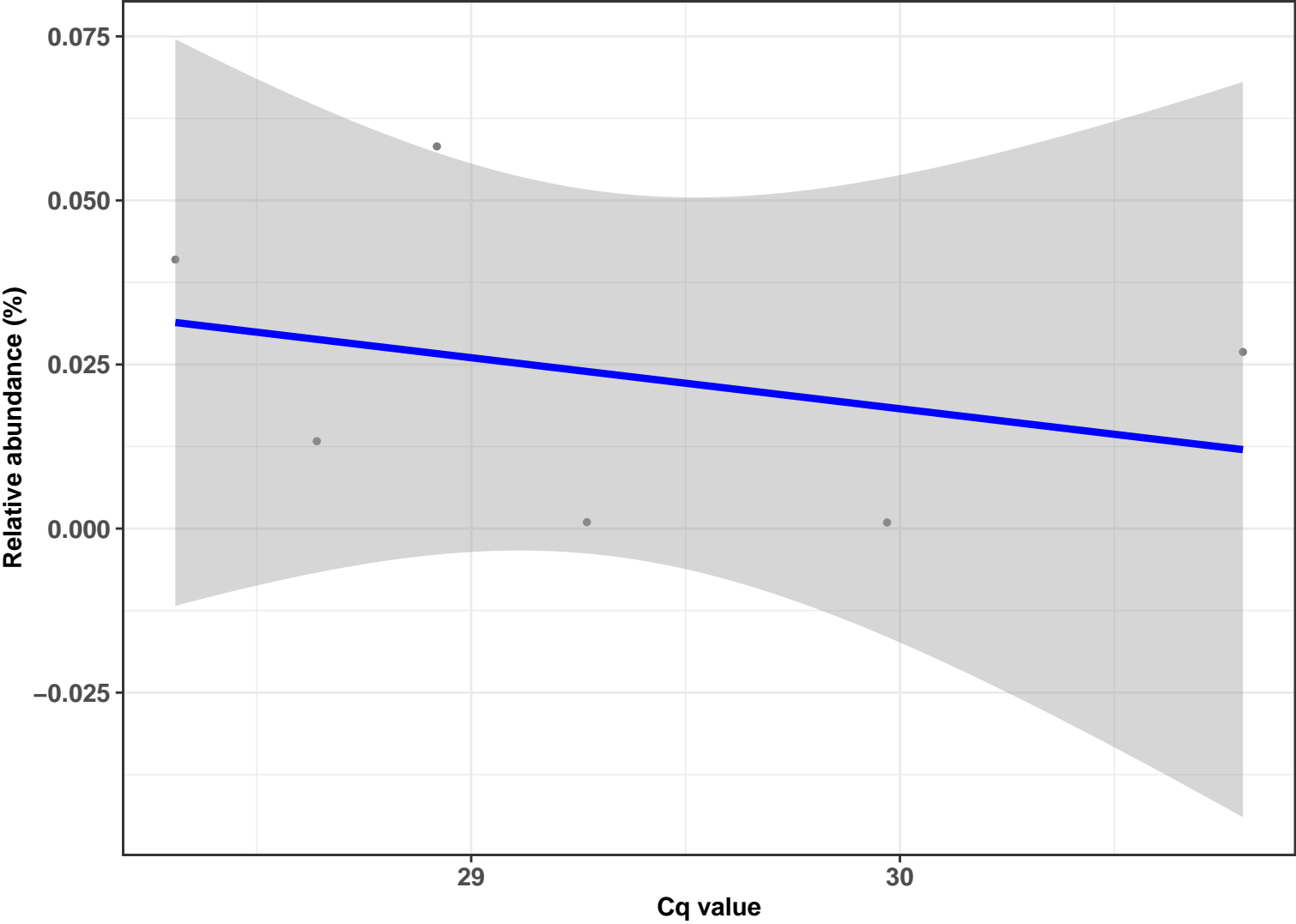
Correlation with all samples

$\log_e(S) = 5.075$ ,  $p = 0.381$ ,  $\hat{\rho}_{\text{Spearman}} = -0.333$ ,  $\text{CI}_{95\%} [-0.986, 0.268]$ ,  $n_{\text{pairs}} = 9$

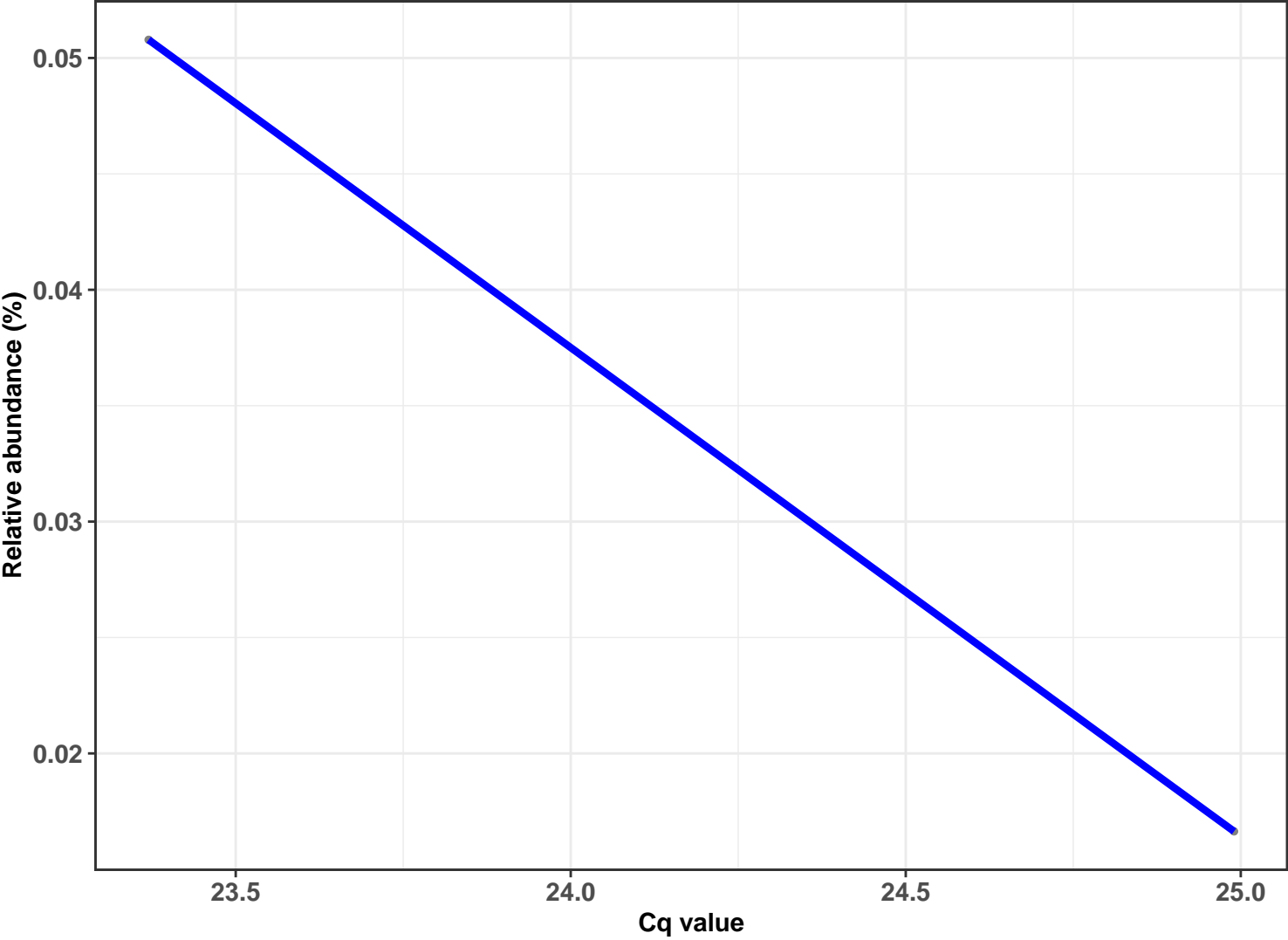


Correlation within: IM-DIC

$\log_e(S) = 3.912$ ,  $p = 0.397$ ,  $\hat{\rho}_{\text{Spearman}} = -0.429$ ,  $\text{CI}_{95\%} [-1.163, 0.310]$ ,  $n_{\text{pairs}} = 6$

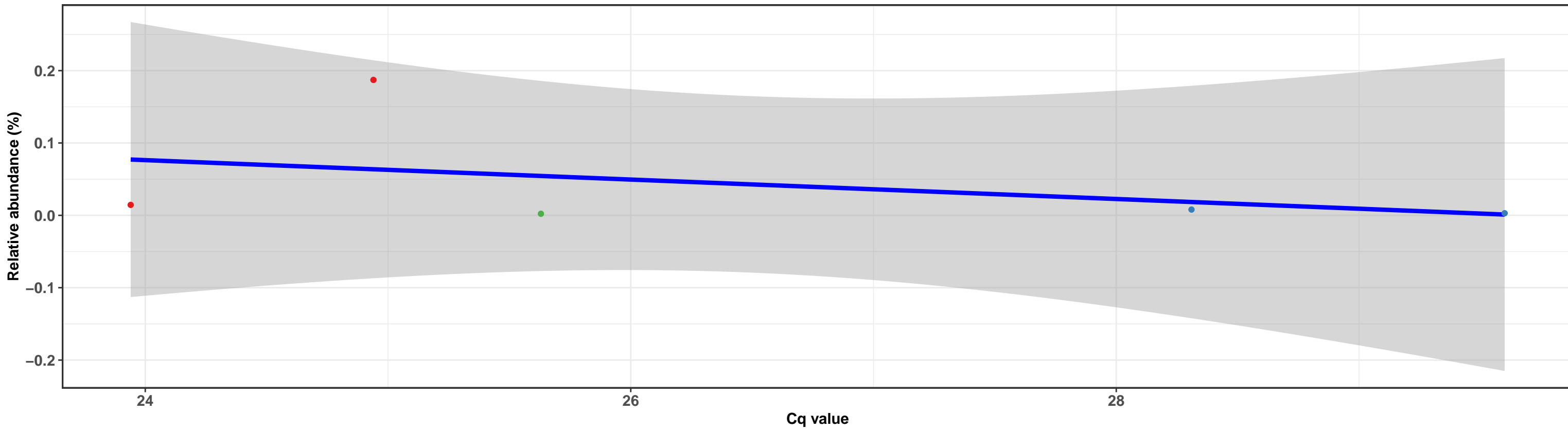


Correlation within: REF-DIC

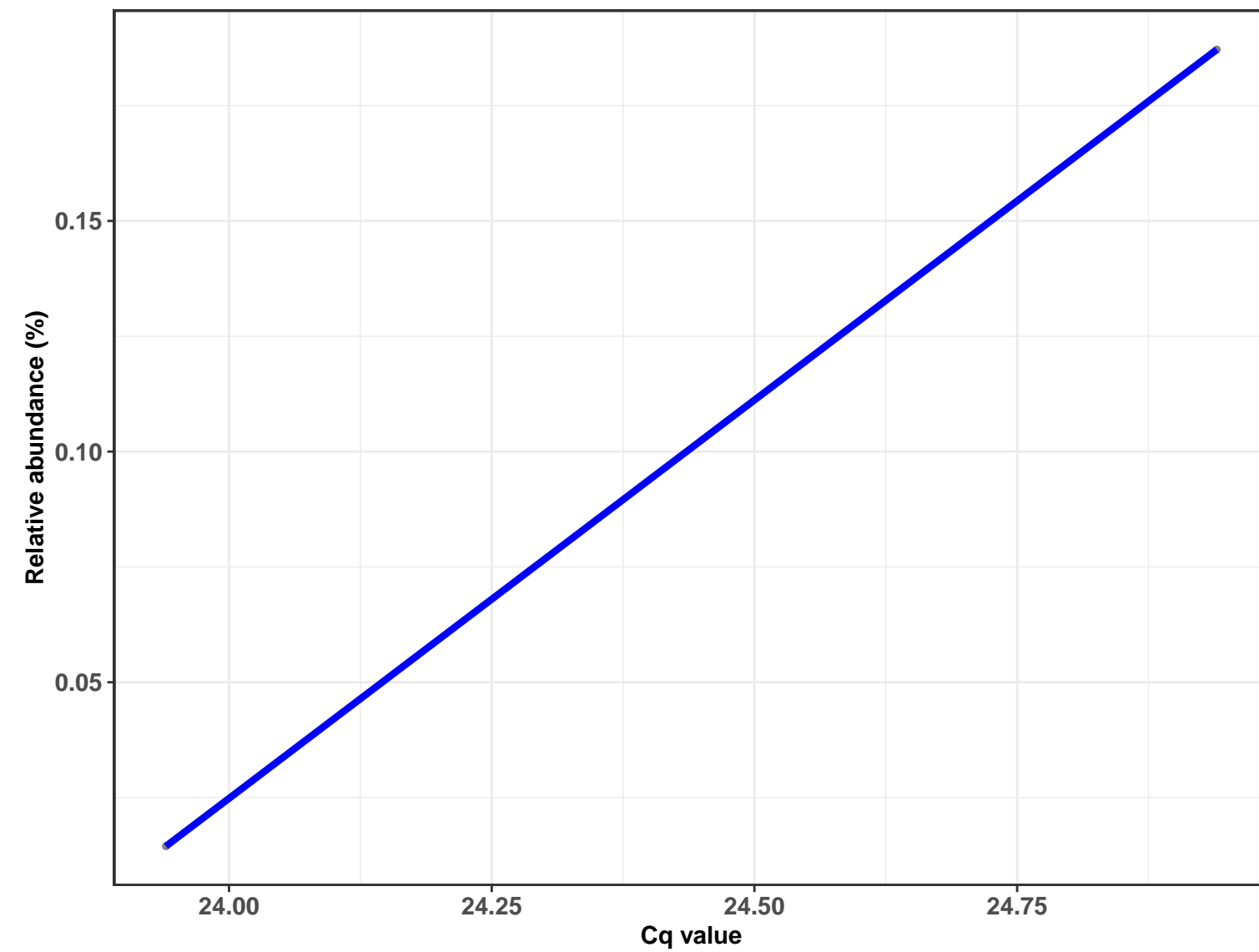


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

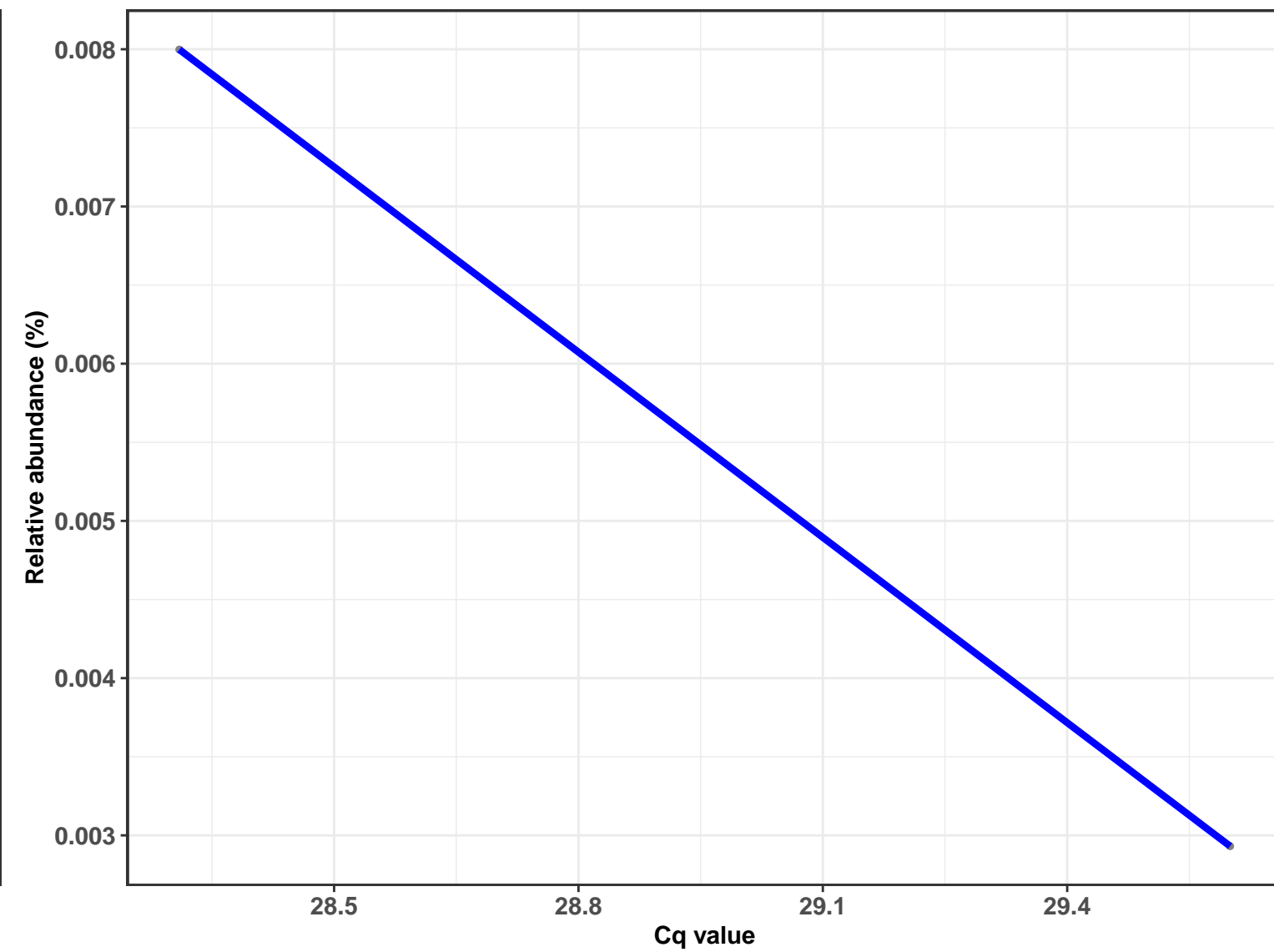
Correlation with all samples



Correlation within: REF-DIC



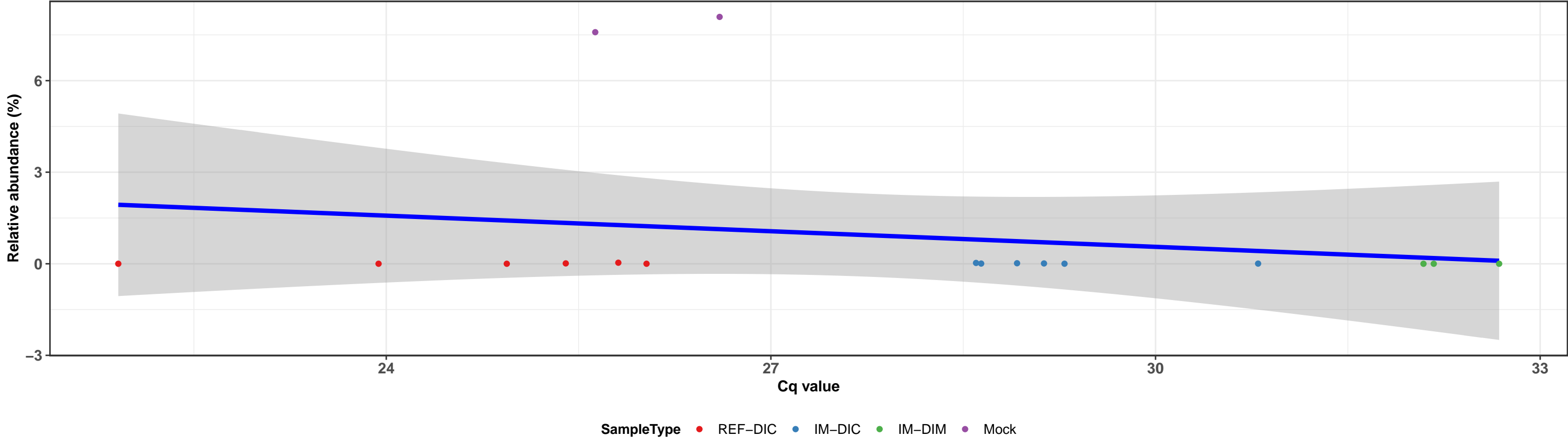
Correlation within: IM-DIC



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

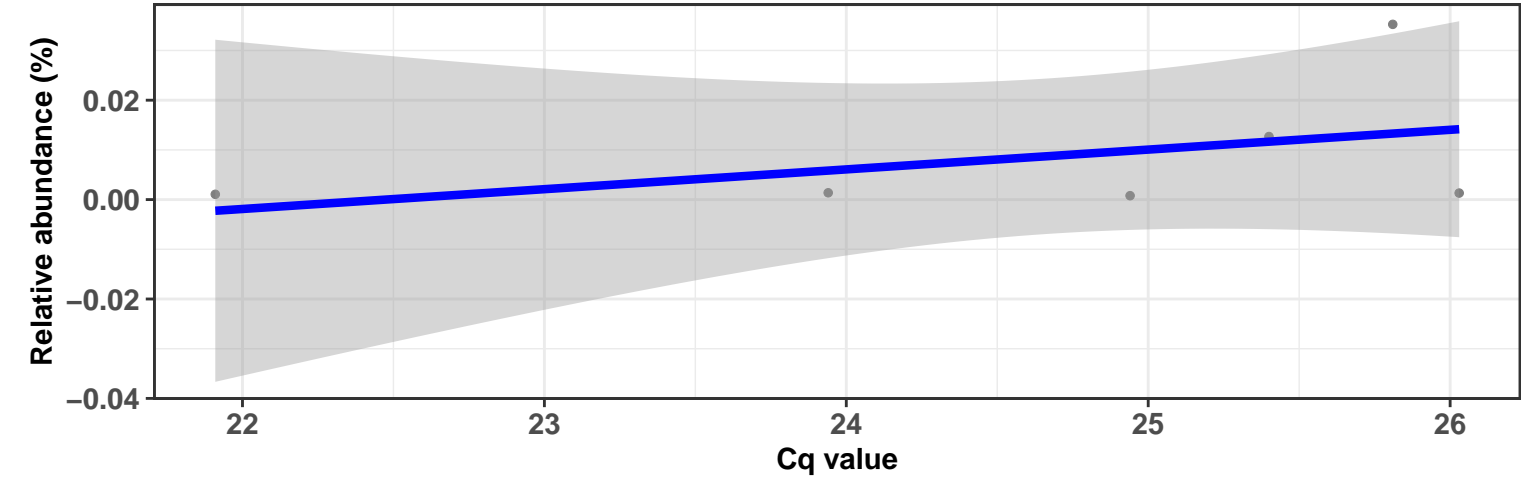
Correlation with all samples

$\log_e(S) = 6.914$ ,  $p = 0.368$ ,  $\hat{\rho}_{\text{Spearman}} = -0.233$ ,  $\text{CI}_{95\%} [-0.806, 0.275]$ ,  $n_{\text{pairs}} = 17$



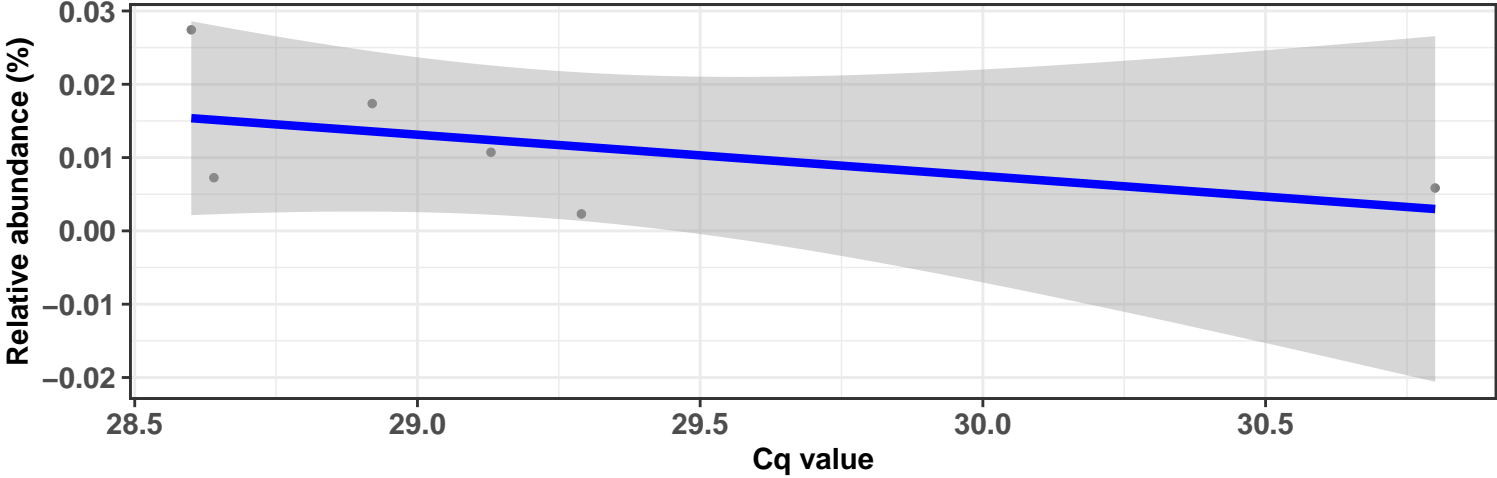
Correlation within: REF-DIC

$\log_e(S) = 2.996$ ,  $p = 0.397$ ,  $\hat{\rho}_{\text{Spearman}} = 0.429$ ,  $\text{CI}_{95\%} [-0.269, 1.376]$ ,  $n_{\text{pairs}} = 6$

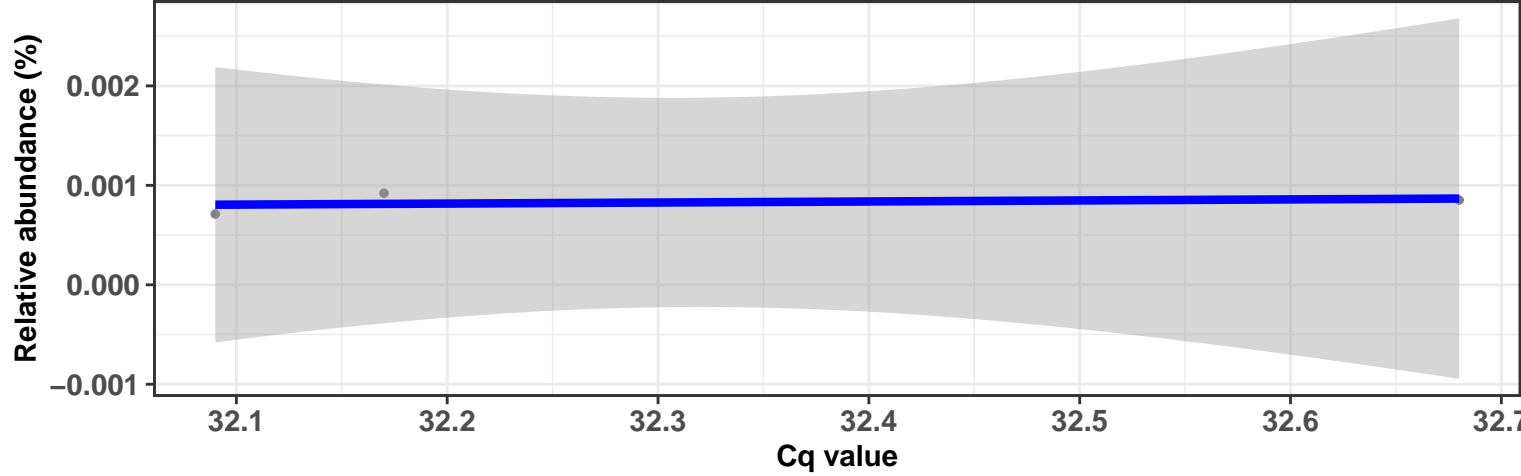


Correlation within: IM-DIC

$\log_e(S) = 4.127$ ,  $p = 0.072$ ,  $\hat{\rho}_{\text{Spearman}} = -0.771$ ,  $\text{CI}_{95\%} [-1.596, -0.161]$ ,  $n_{\text{pairs}} = 6$



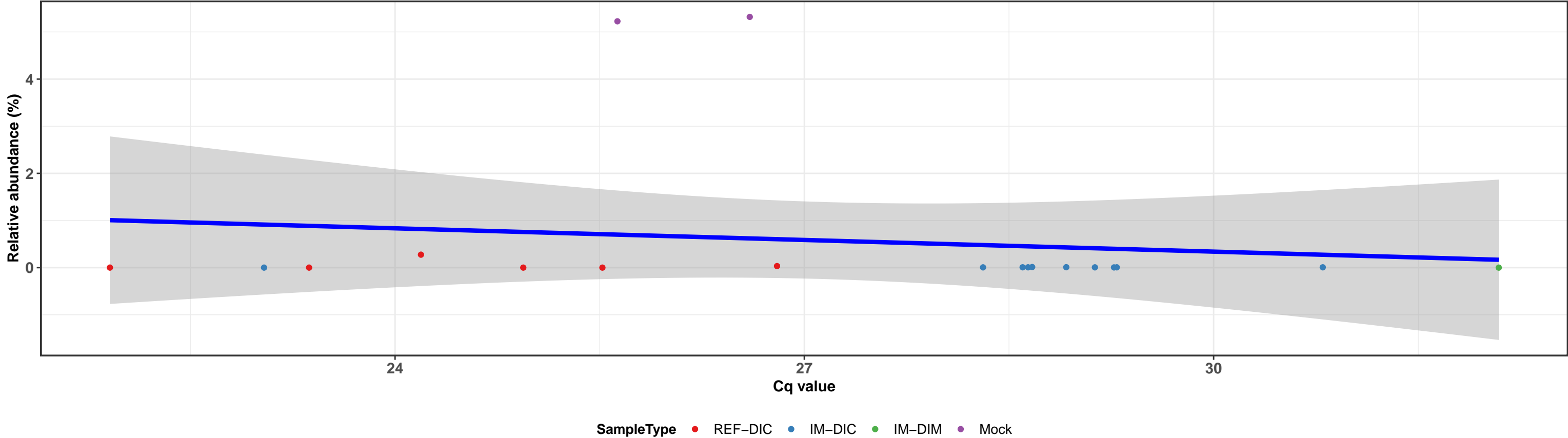
Correlation within: IM-DIM



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

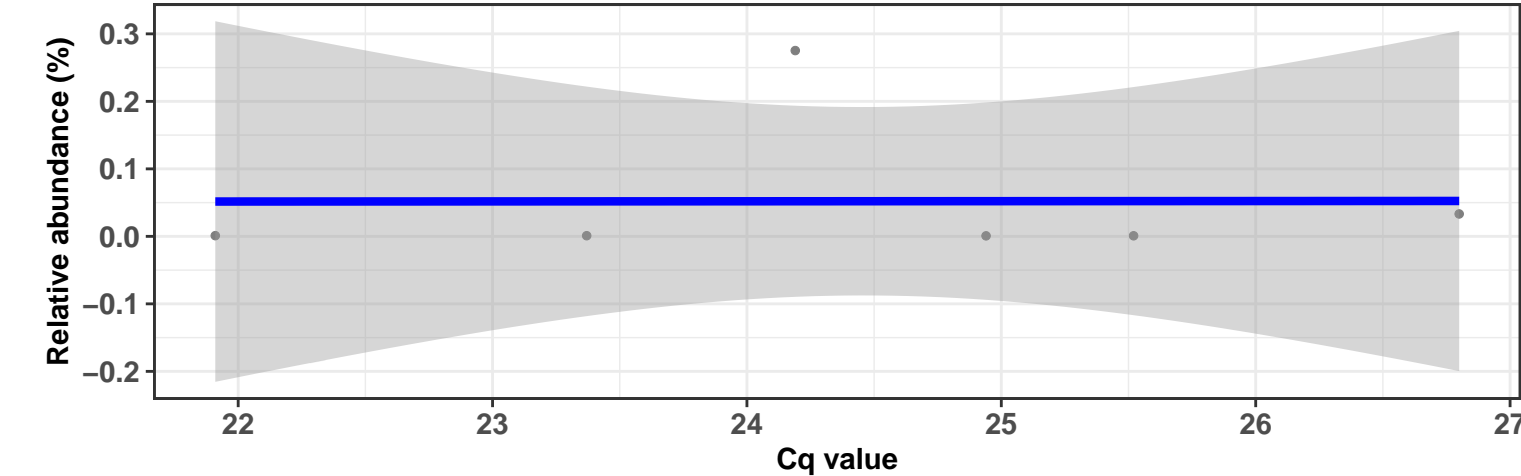
Correlation with all samples

$\log_e(S) = 6.968$ ,  $p = 0.781$ ,  $\hat{\rho}_{\text{Spearman}} = 0.068$ ,  $CI_{95\%} [-0.381, 0.542]$ ,  $n_{\text{pairs}} = 19$



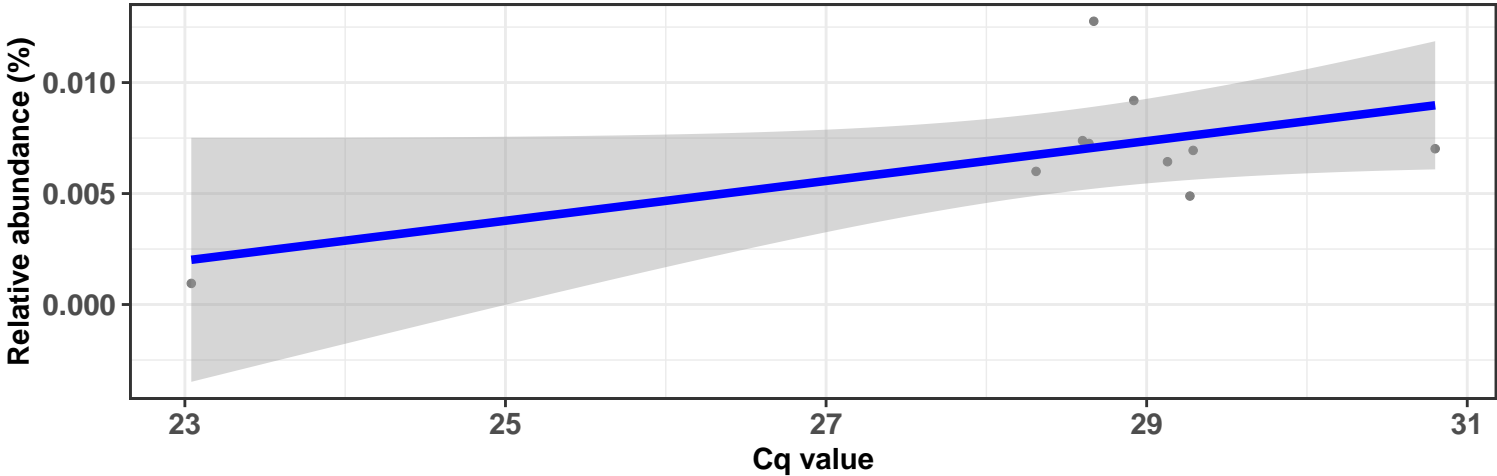
Correlation within: REF-DIC

$\log_e(S) = 3.638$ ,  $p = 0.872$ ,  $\hat{\rho}_{\text{Spearman}} = -0.086$ ,  $CI_{95\%} [-0.996, 0.852]$ ,  $n_{\text{pairs}} = 6$

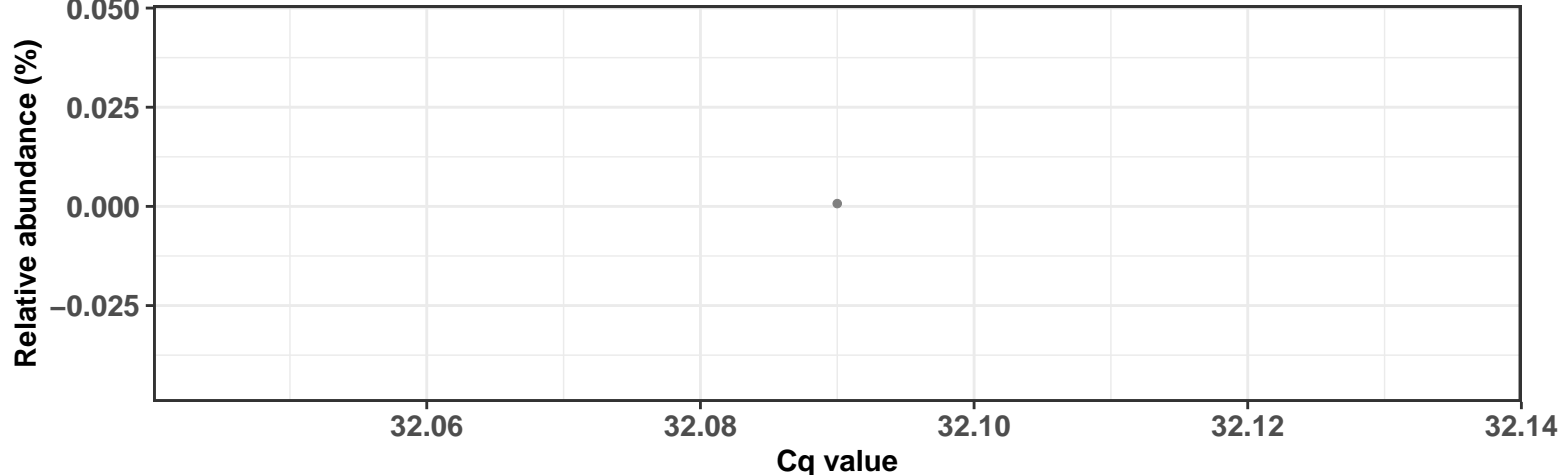


Correlation within: IM-DIC

$\log_e(S) = 4.984$ ,  $p = 0.751$ ,  $\hat{\rho}_{\text{Spearman}} = 0.115$ ,  $CI_{95\%} [-0.591, 0.841]$ ,  $n_{\text{pairs}} = 10$



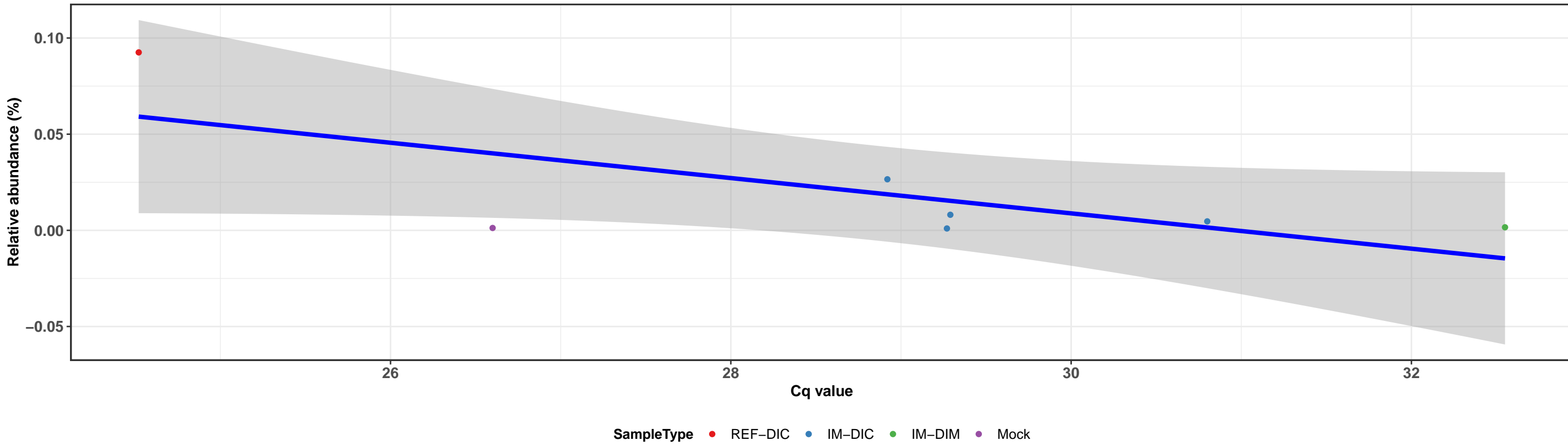
Correlation within: IM-DIM



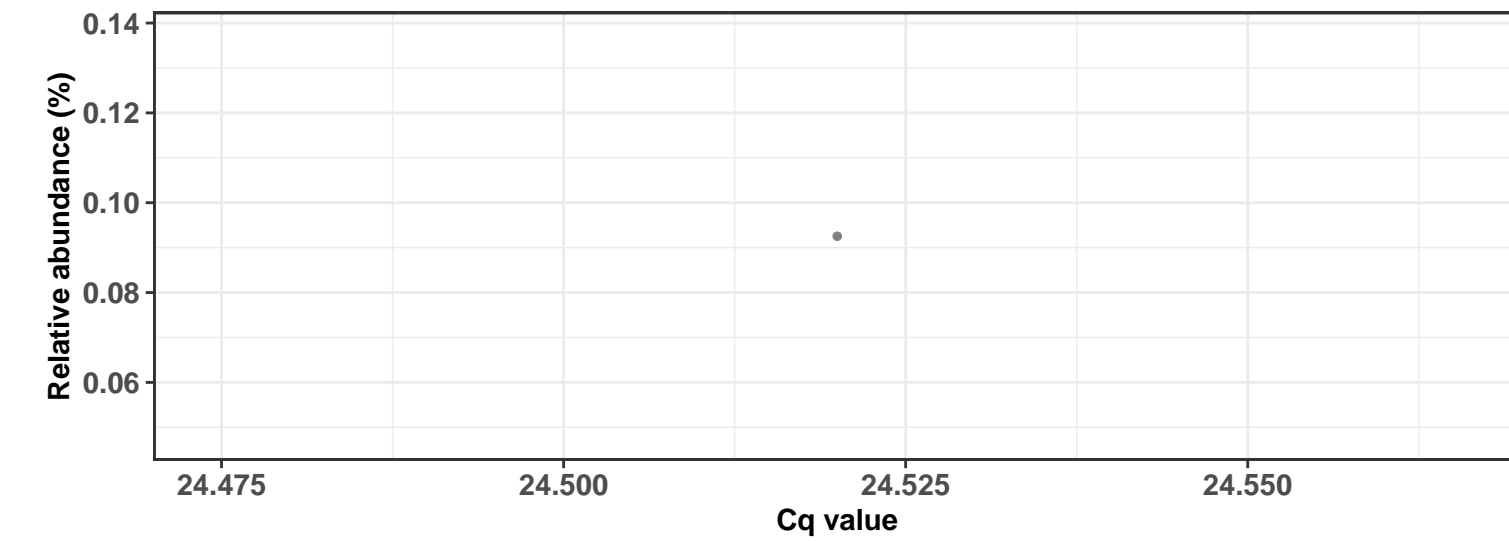
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

### Correlation with all samples

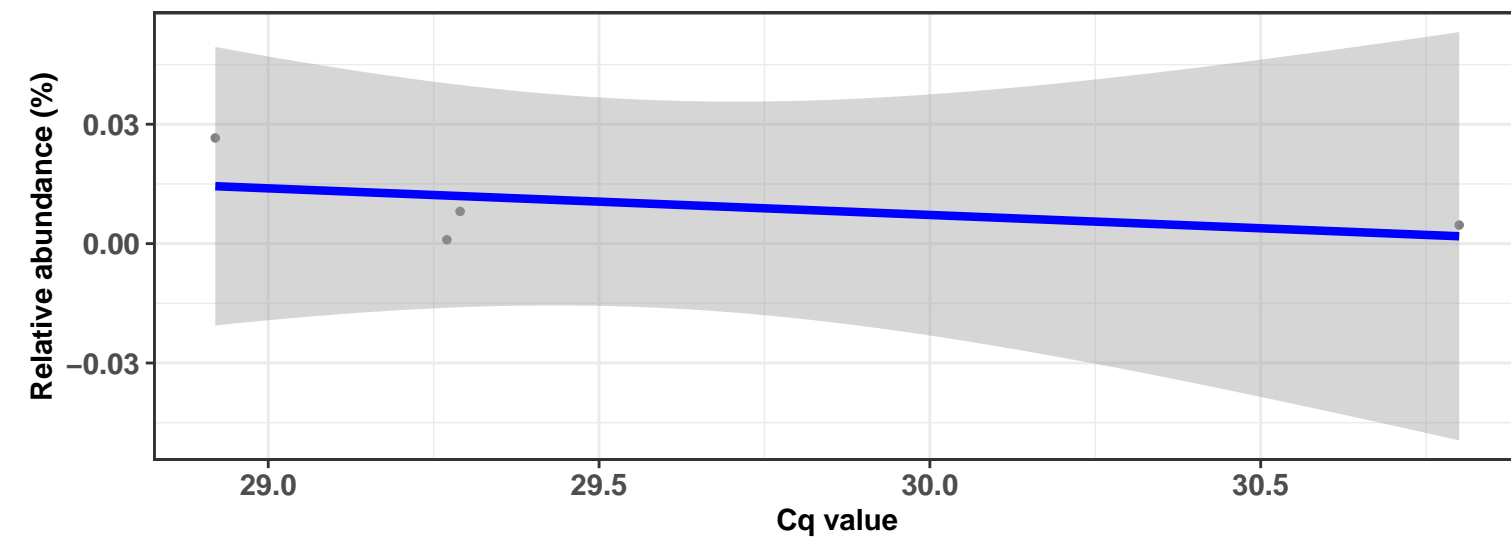
$\log_e(S) = 4.304$ ,  $p = 0.482$ ,  $\hat{\rho}_{\text{Spearman}} = -0.321$ ,  $\text{CI}_{95\%} [-1.221, 0.579]$ ,  $n_{\text{pairs}} = 7$



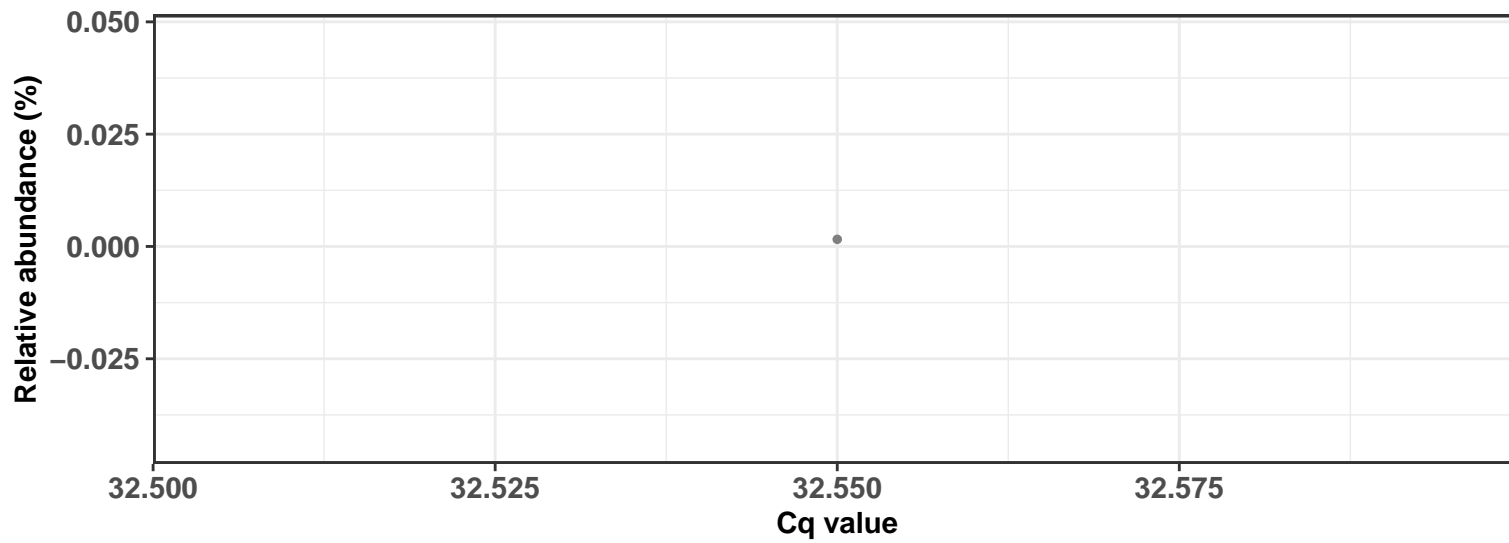
### Correlation within: REF-DIC



### Correlation within: IM-DIC

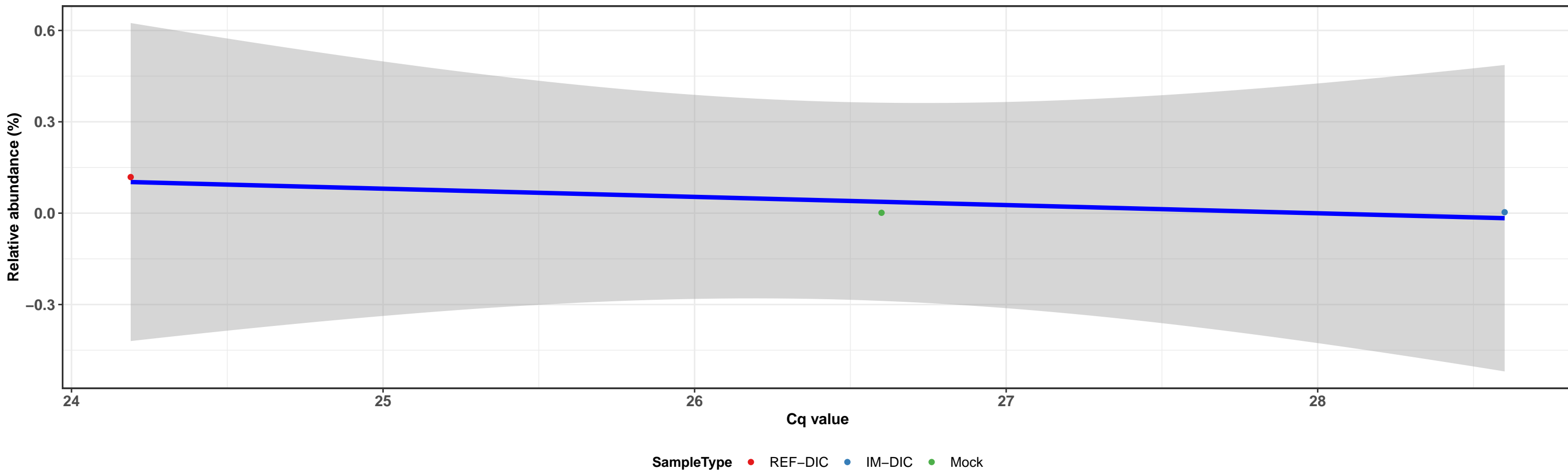


### Correlation within: IM-DIM

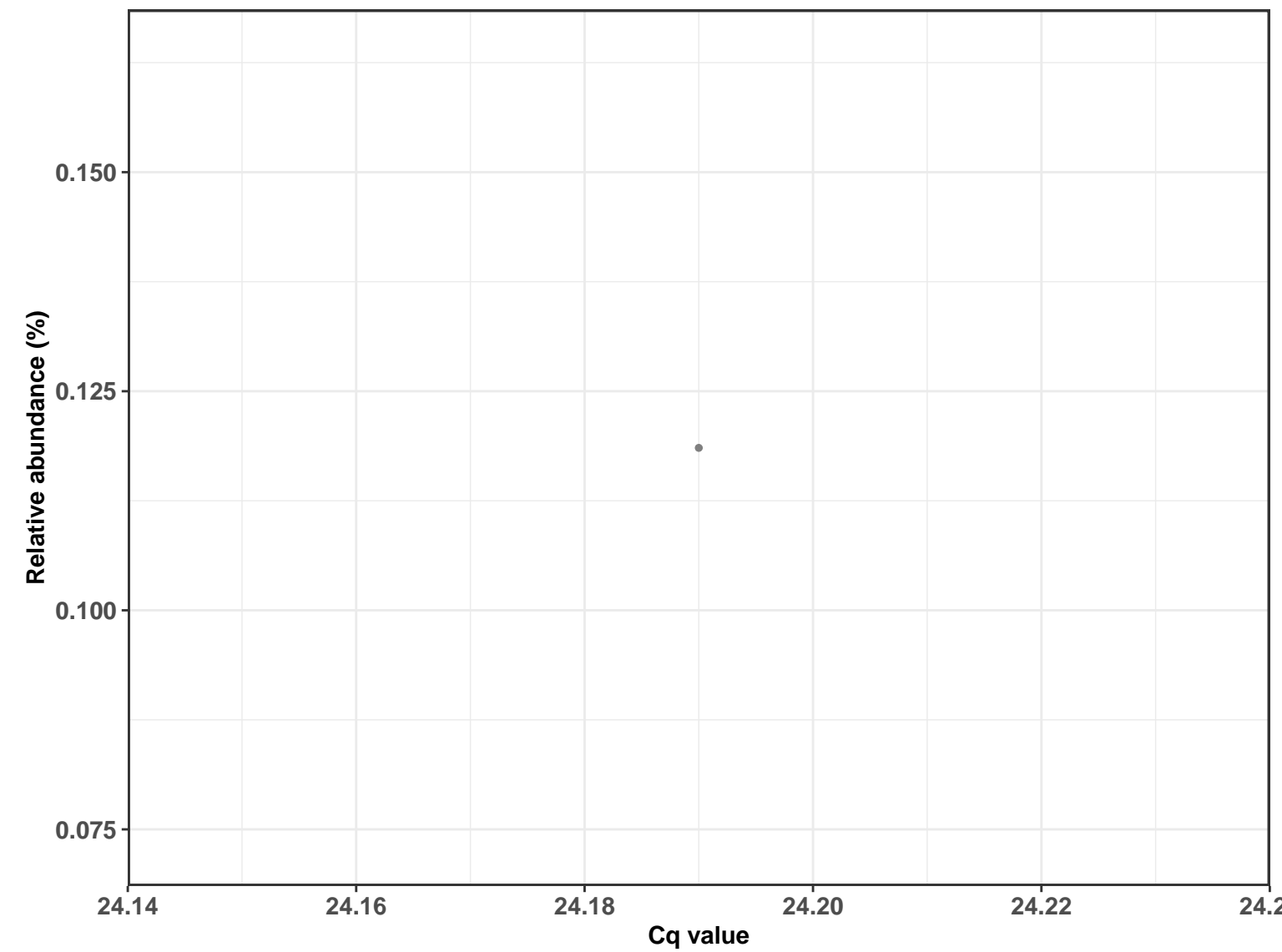


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

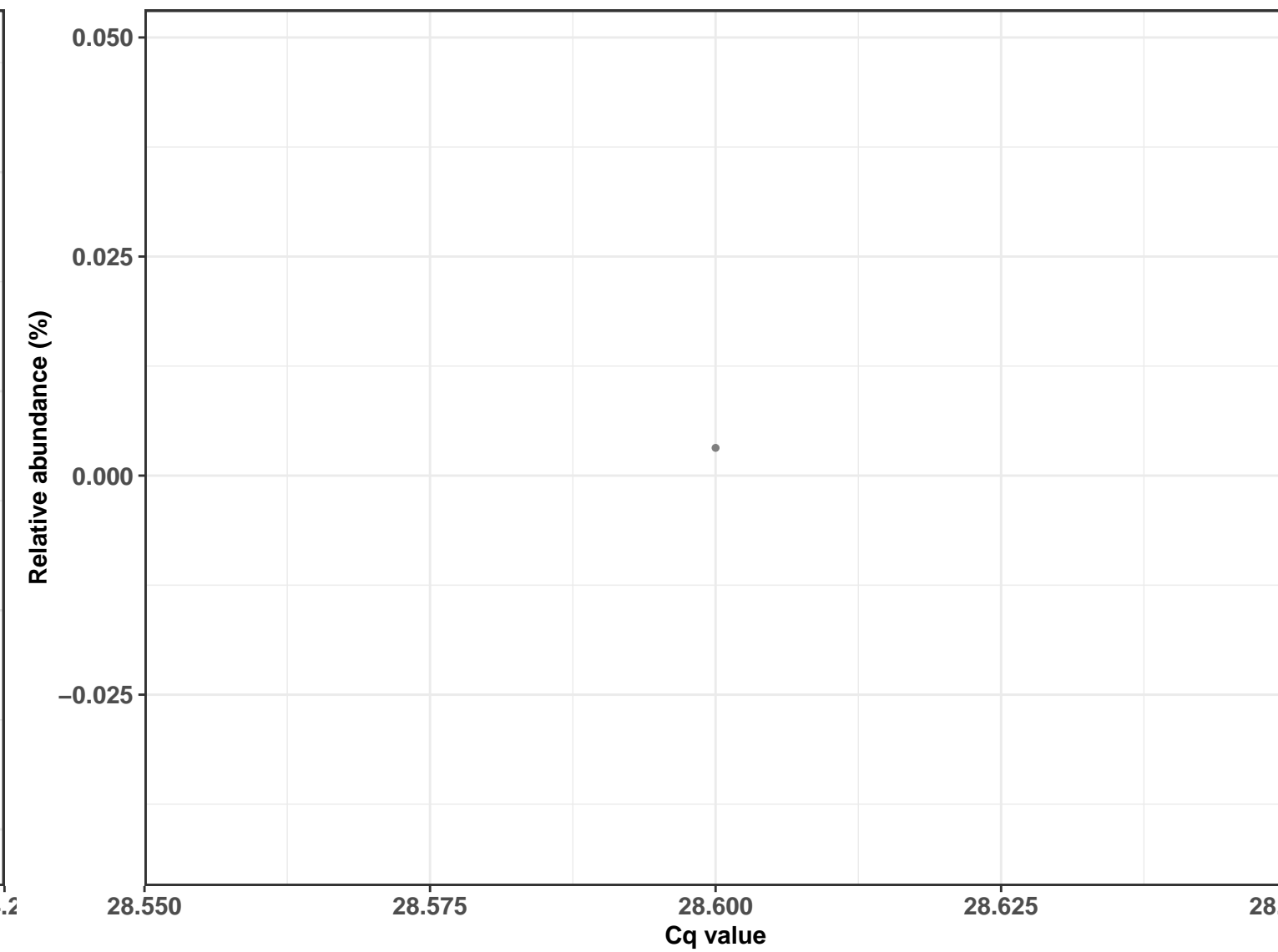
Correlation with all samples



Correlation within: REF-DIC

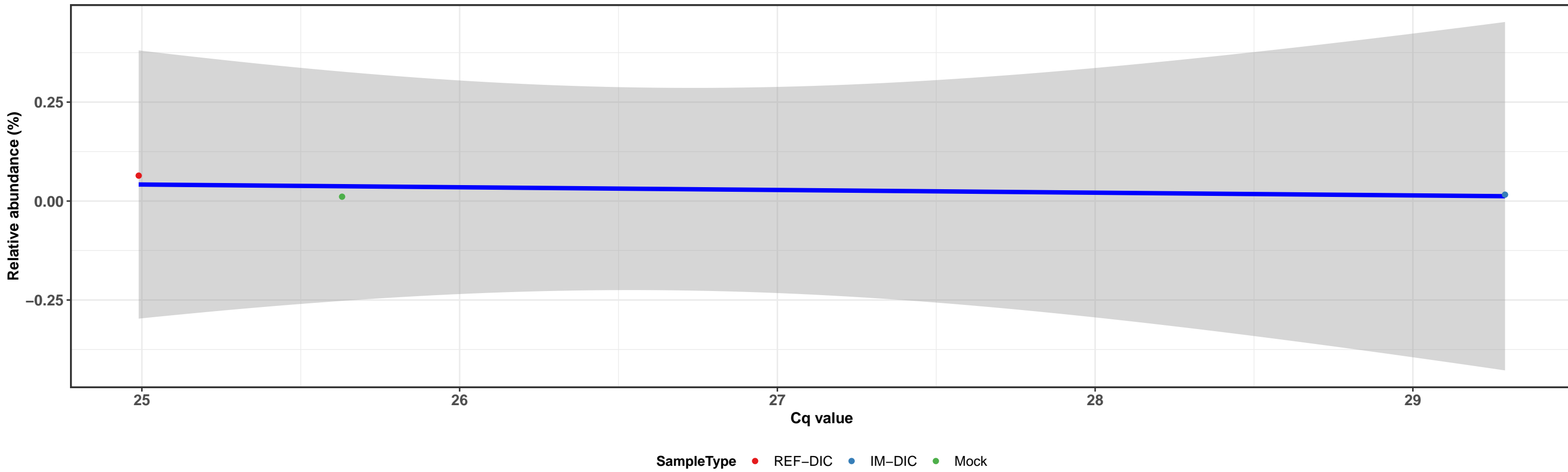


Correlation within: IM-DIC

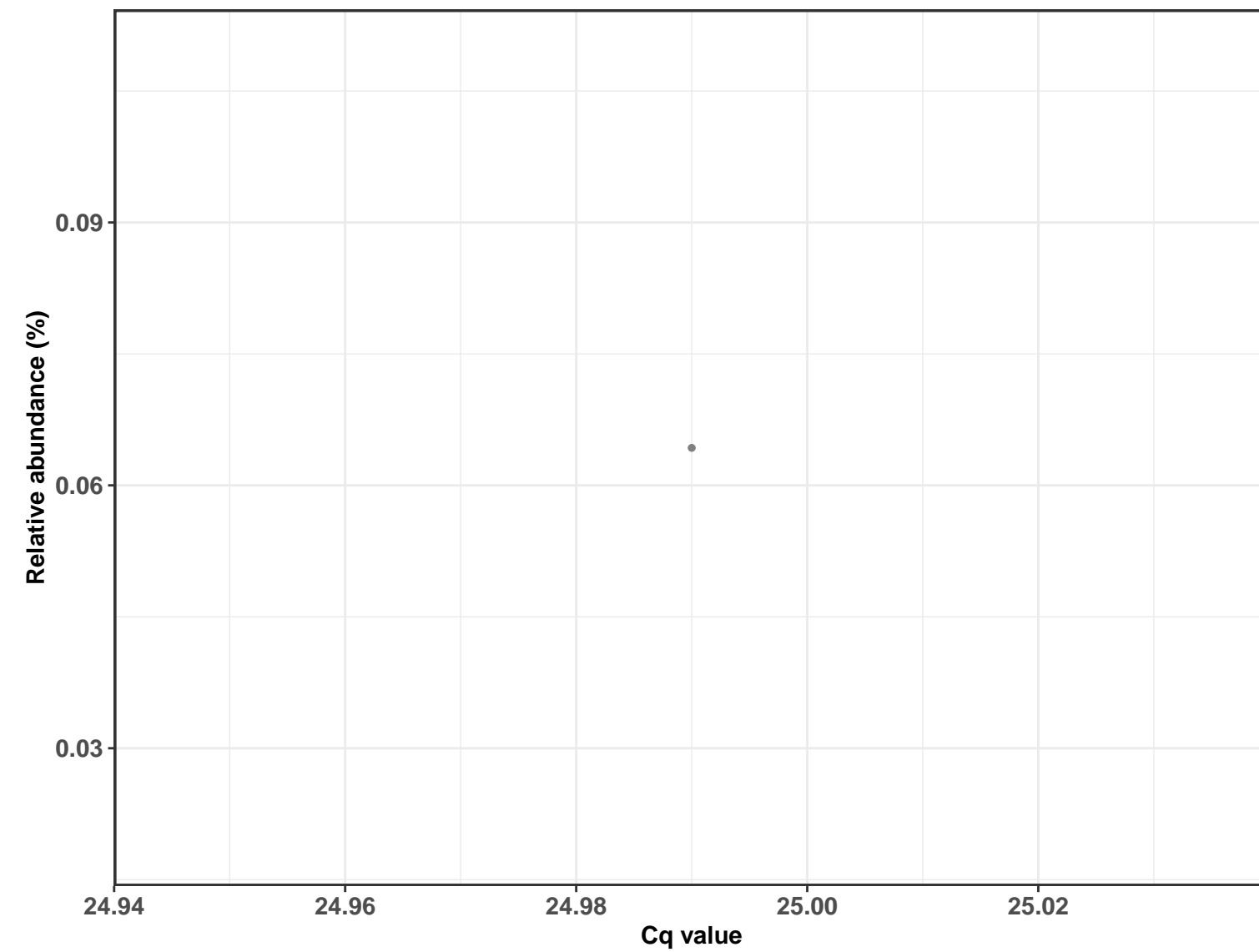


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

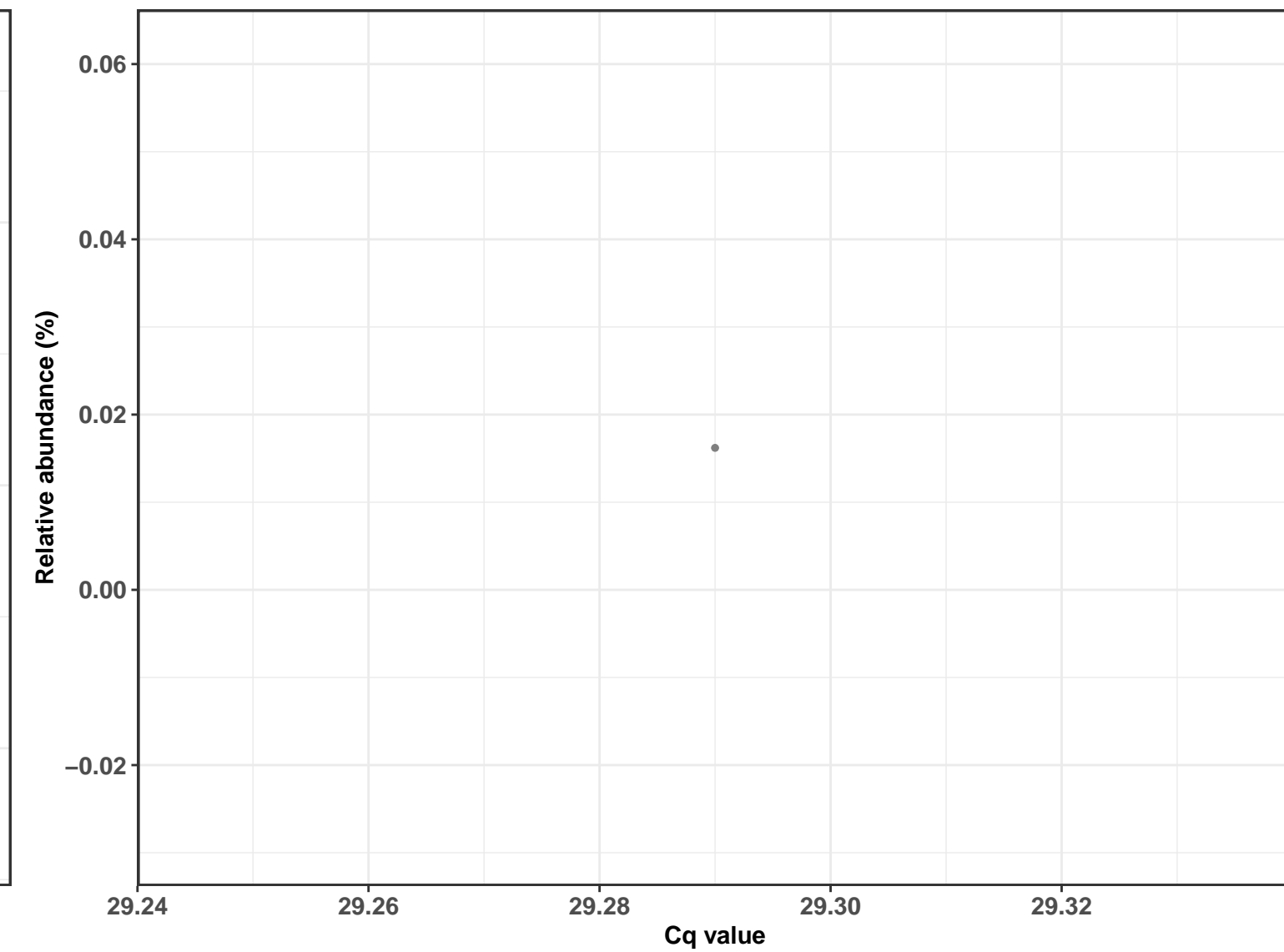
Correlation with all samples



Correlation within: REF-DIC

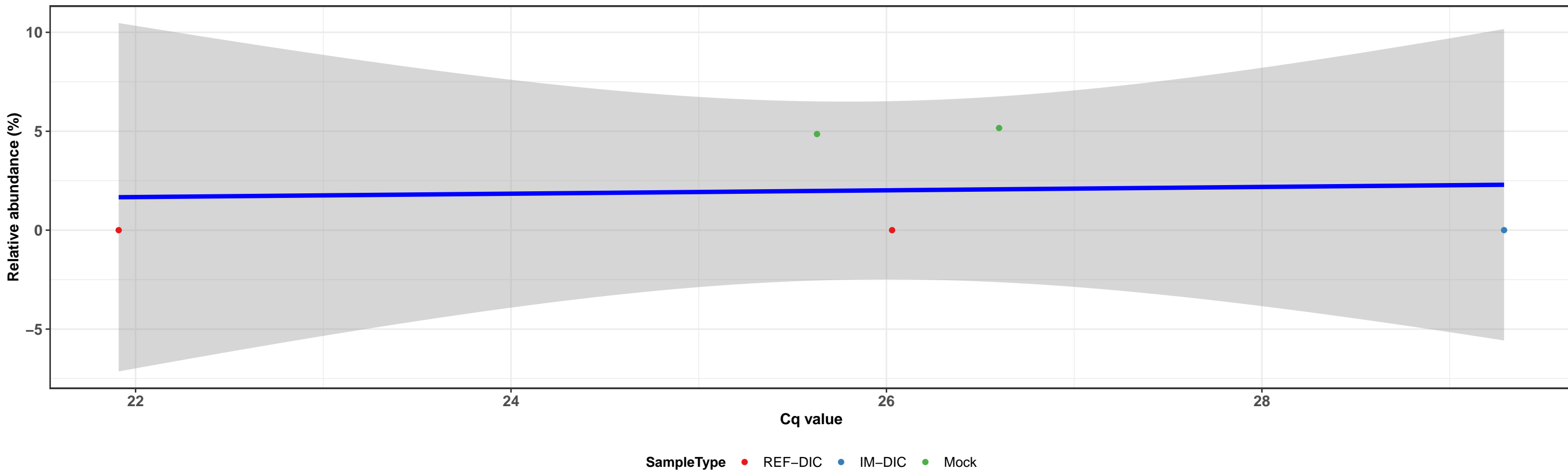


Correlation within: IM-DIC

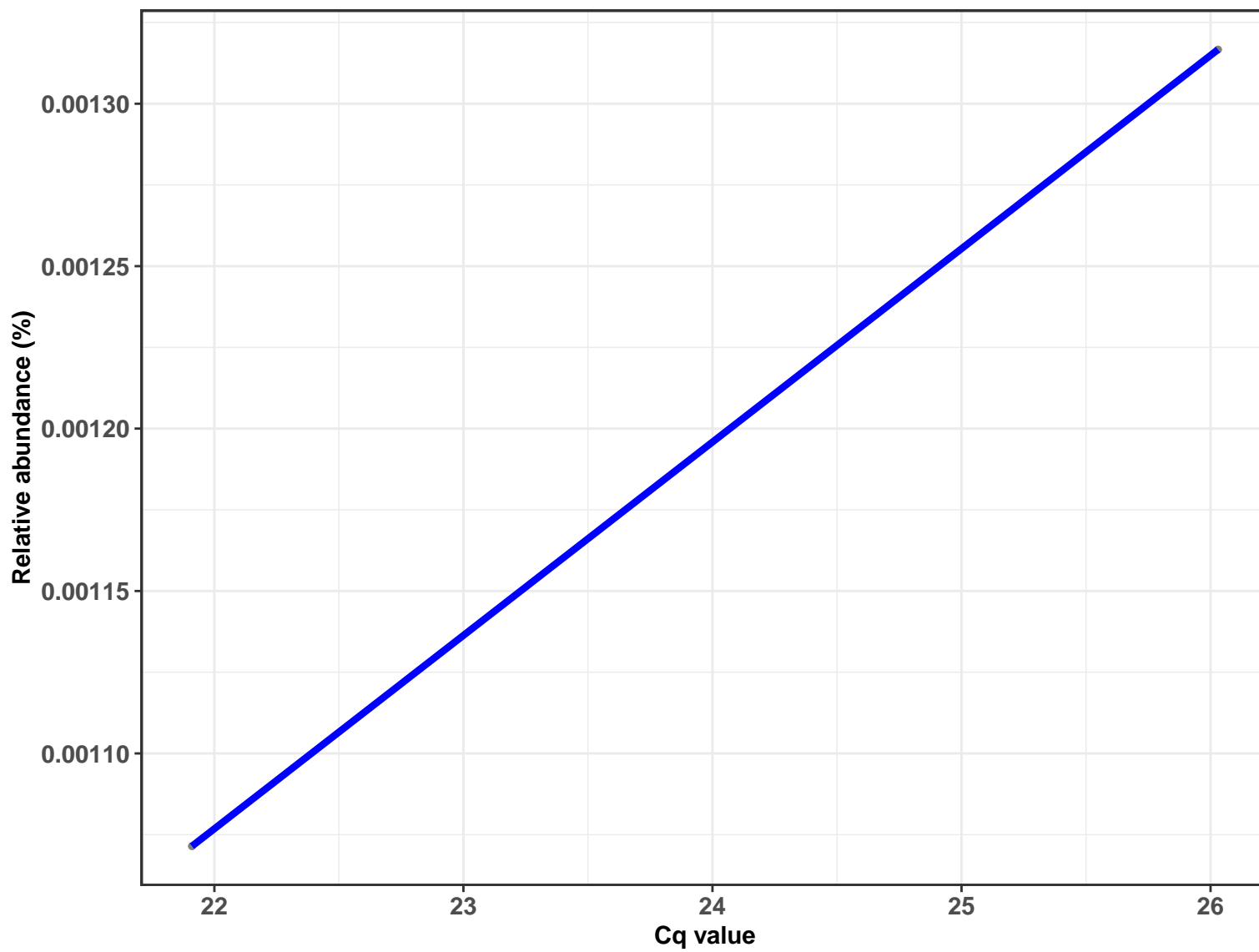


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

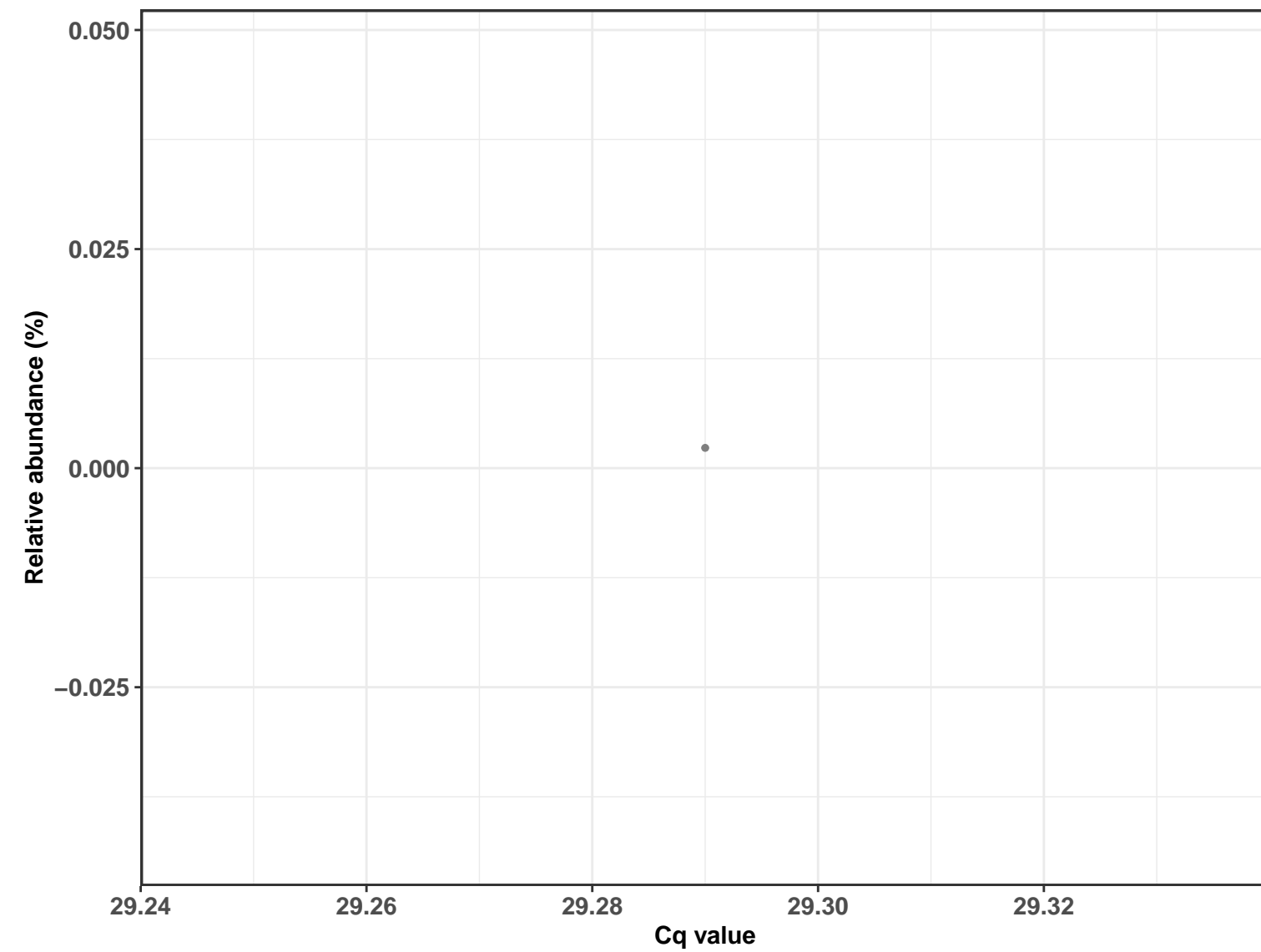
Correlation with all samples



Correlation within: REF-DIC



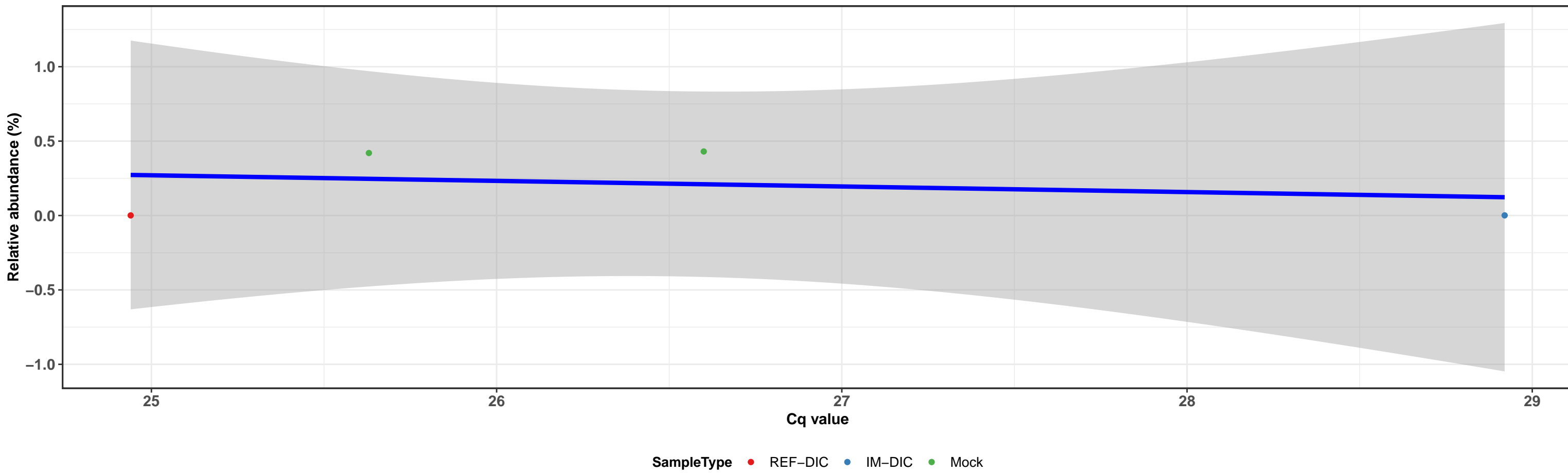
Correlation within: IM-DIC



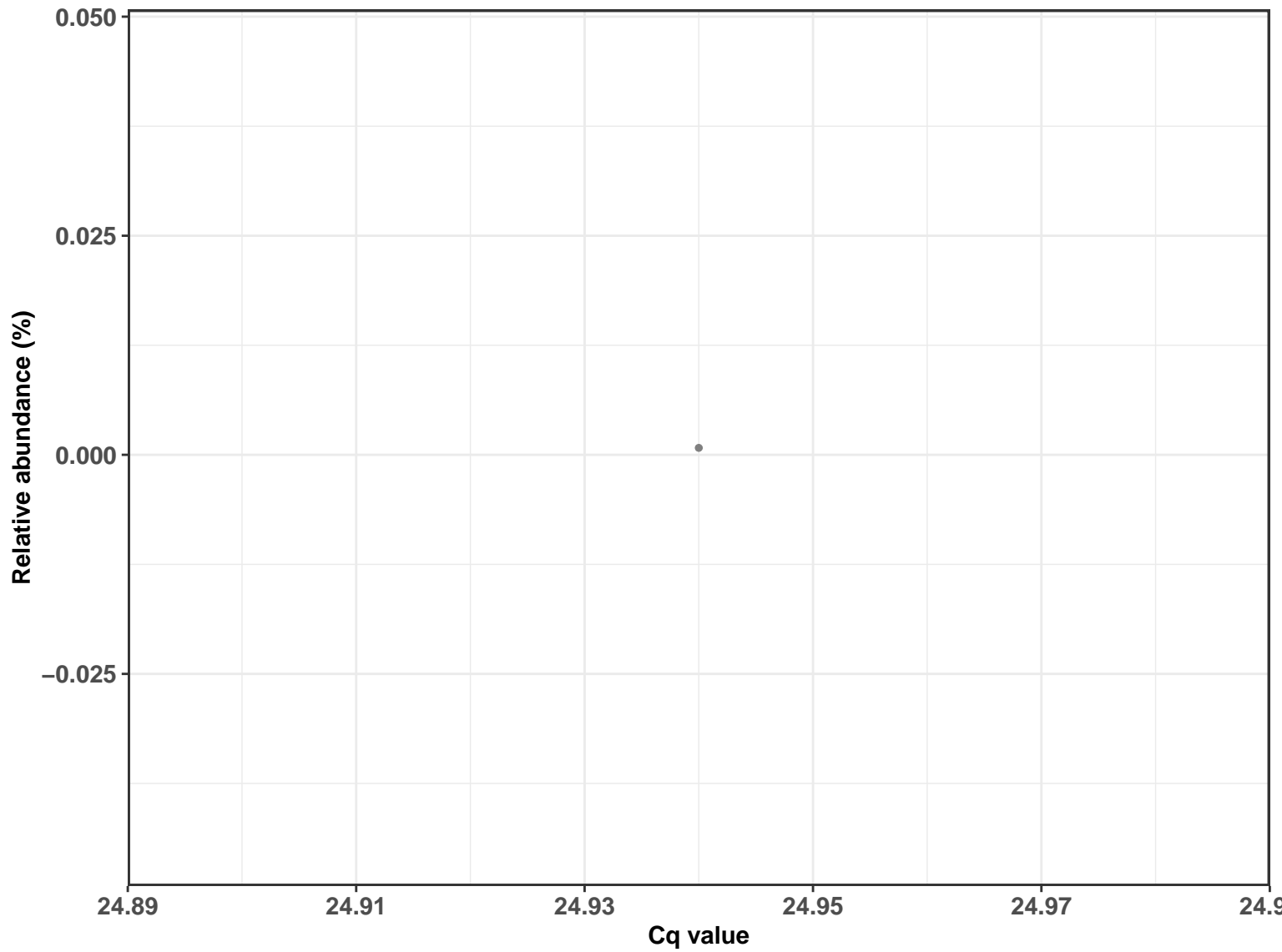


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

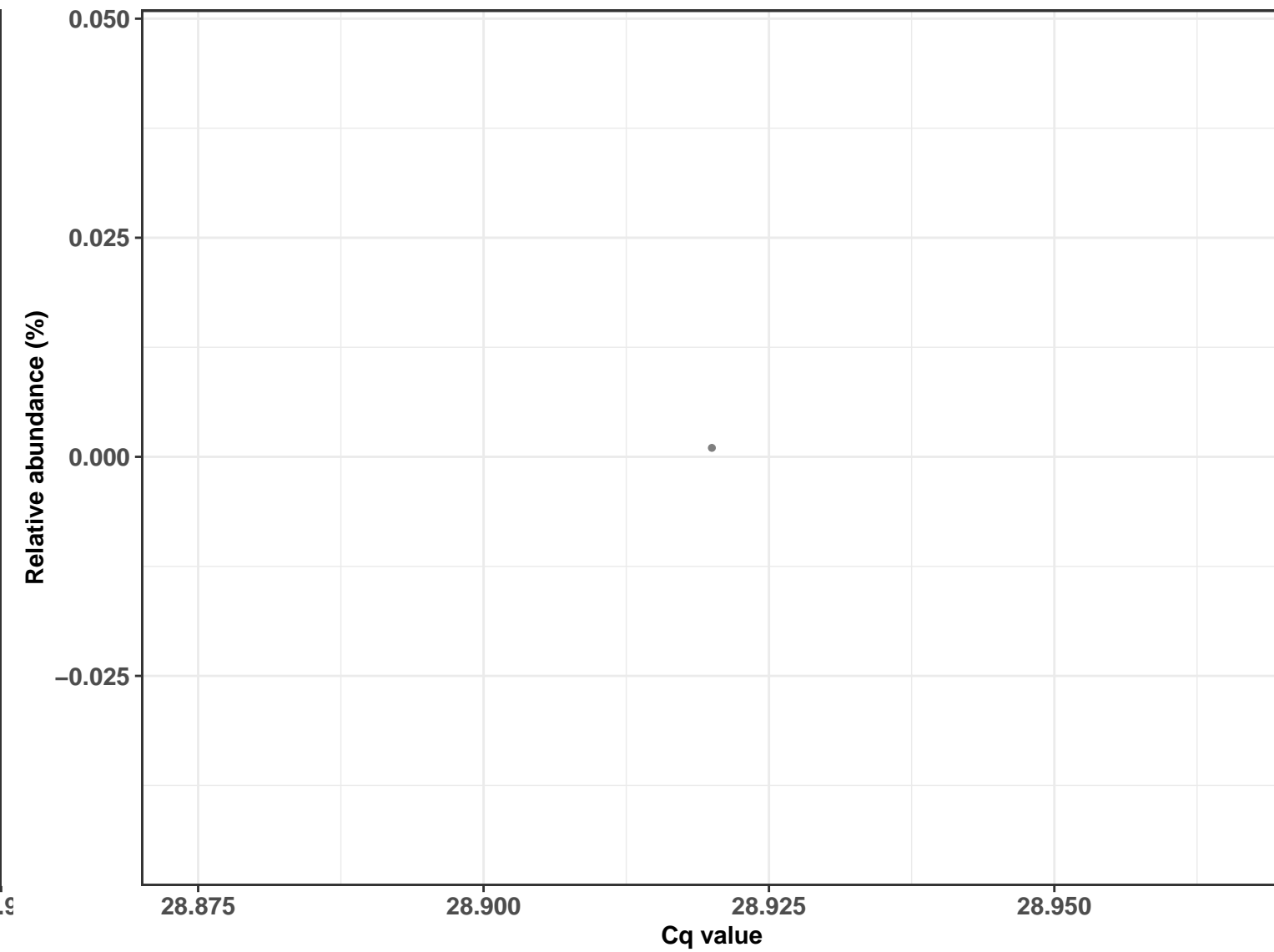
Correlation with all samples



Correlation within: REF-DIC



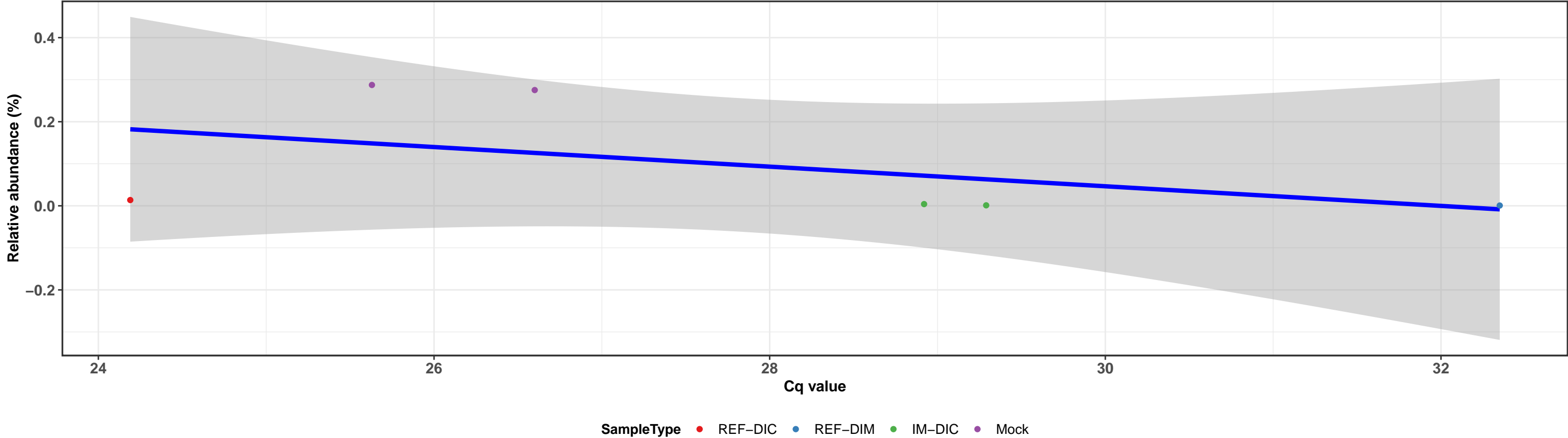
Correlation within: IM-DIC



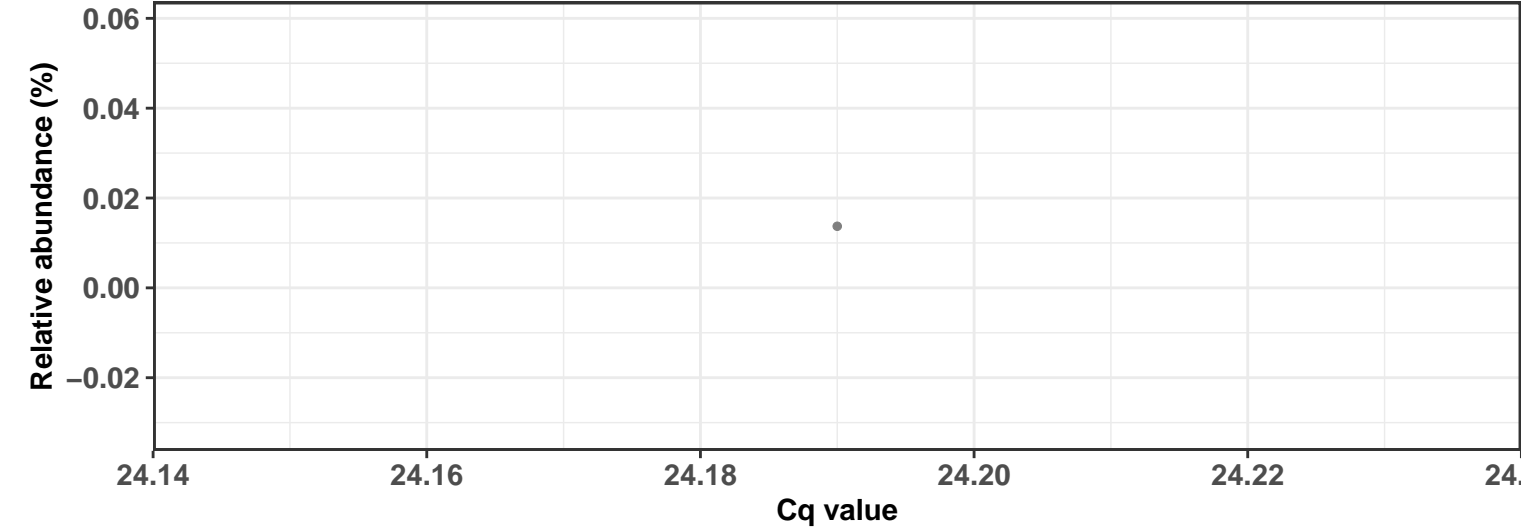
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

Correlation with all samples

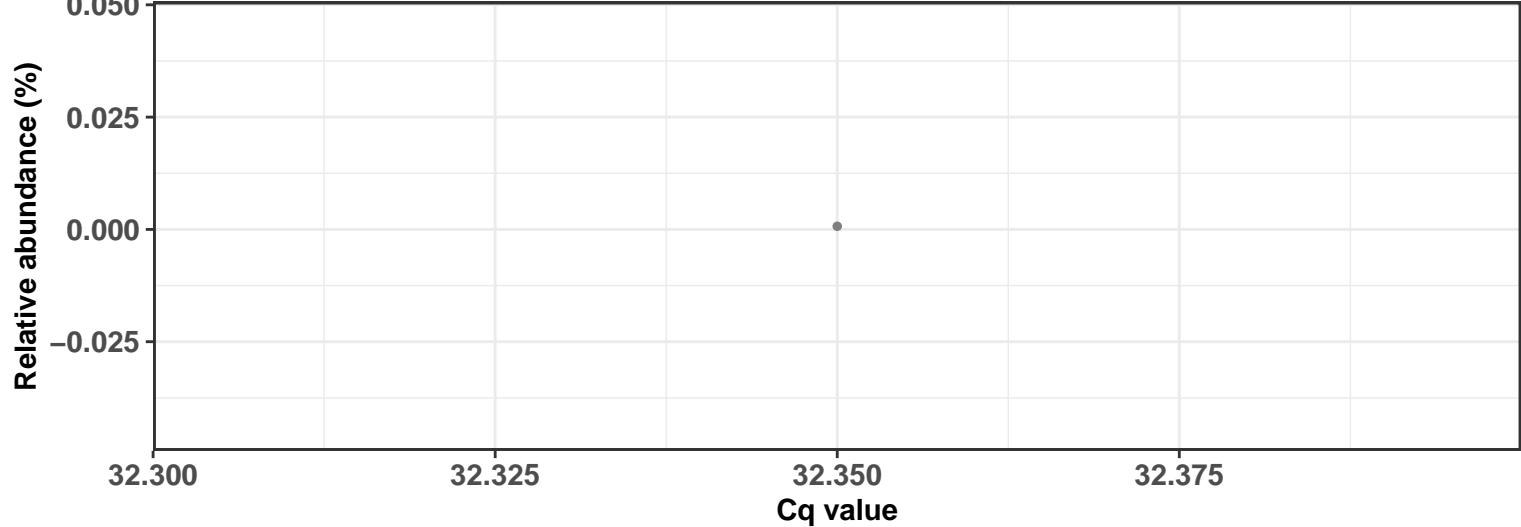
$\log_e(S) = 4.159$ ,  $p = 0.042$ ,  $\hat{\rho}_{\text{Spearman}} = -0.829$ ,  $\text{CI}_{95\%} [-1.354, -0.359]$ ,  $n_{\text{pairs}} = 6$



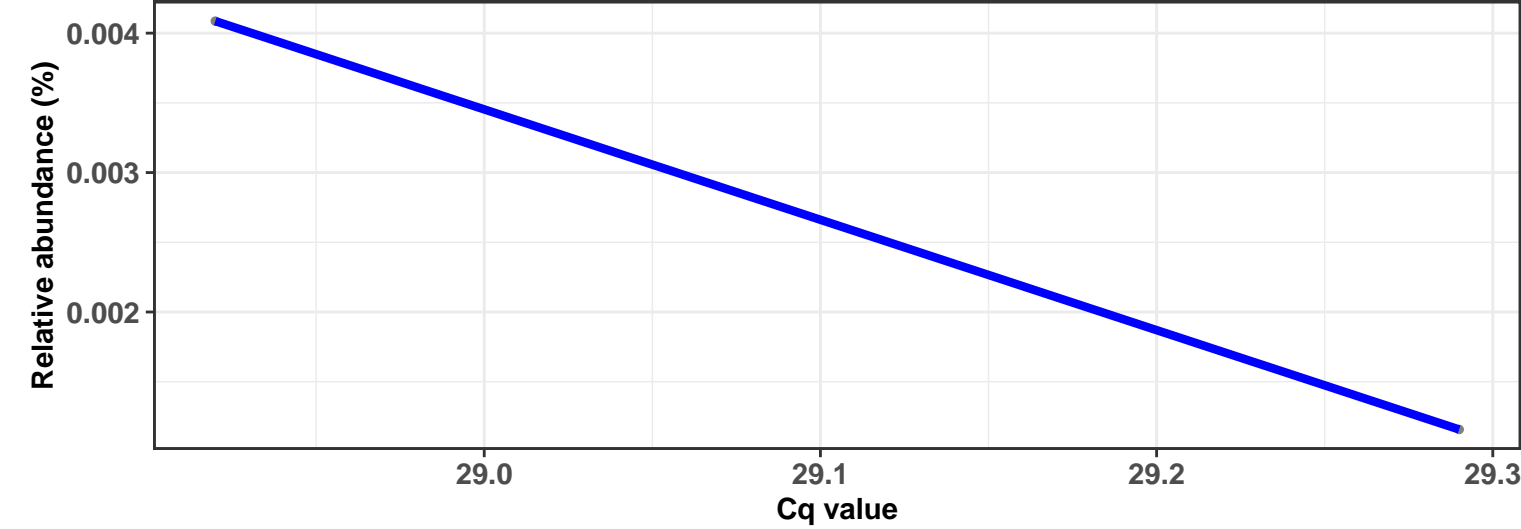
Correlation within: REF-DIC



Correlation within: REF-DIM



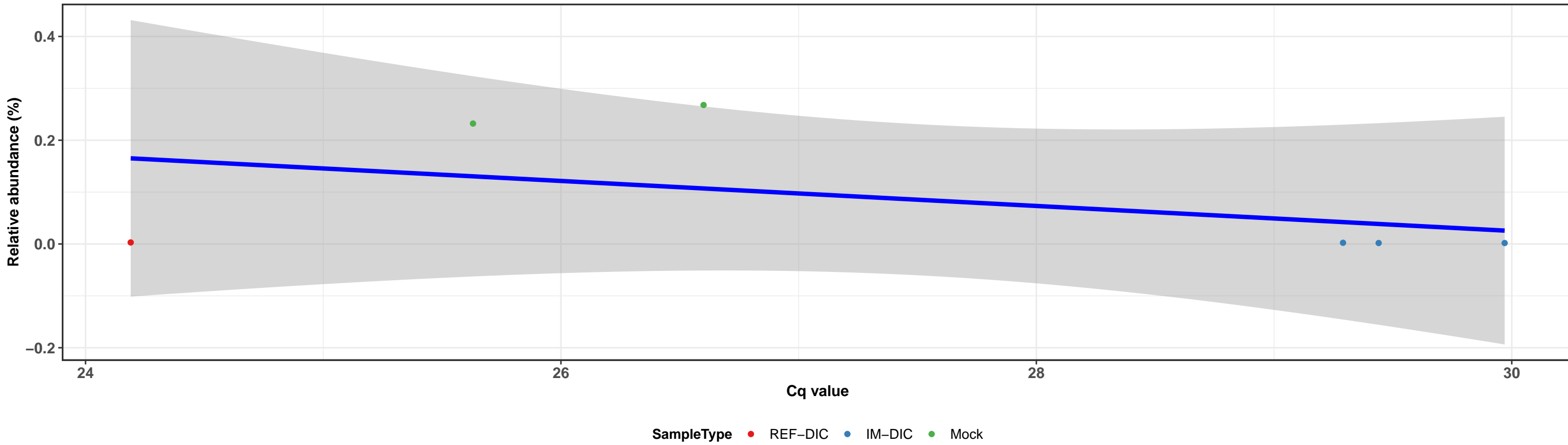
Correlation within: IM-DIC



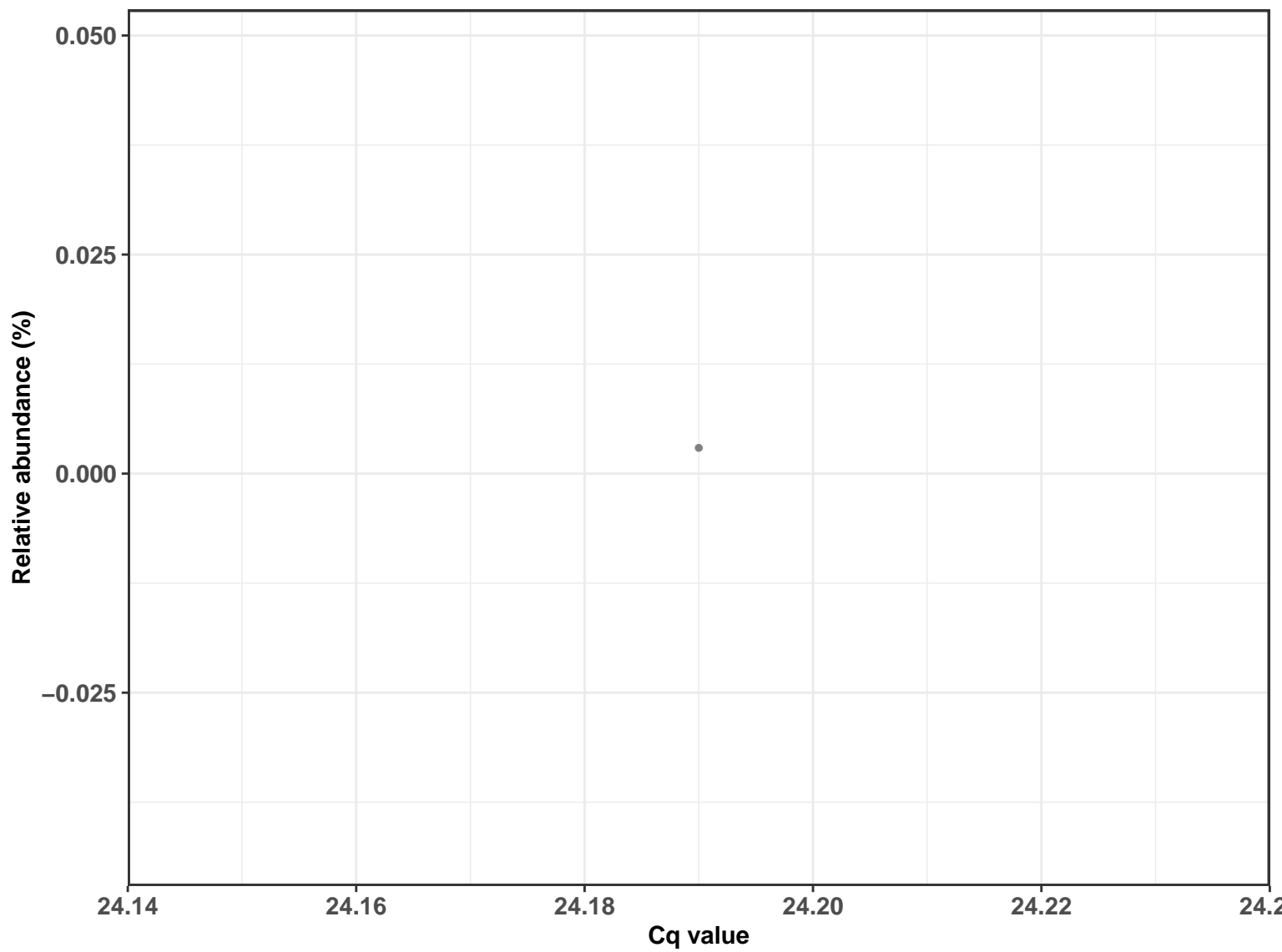
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

### Correlation with all samples

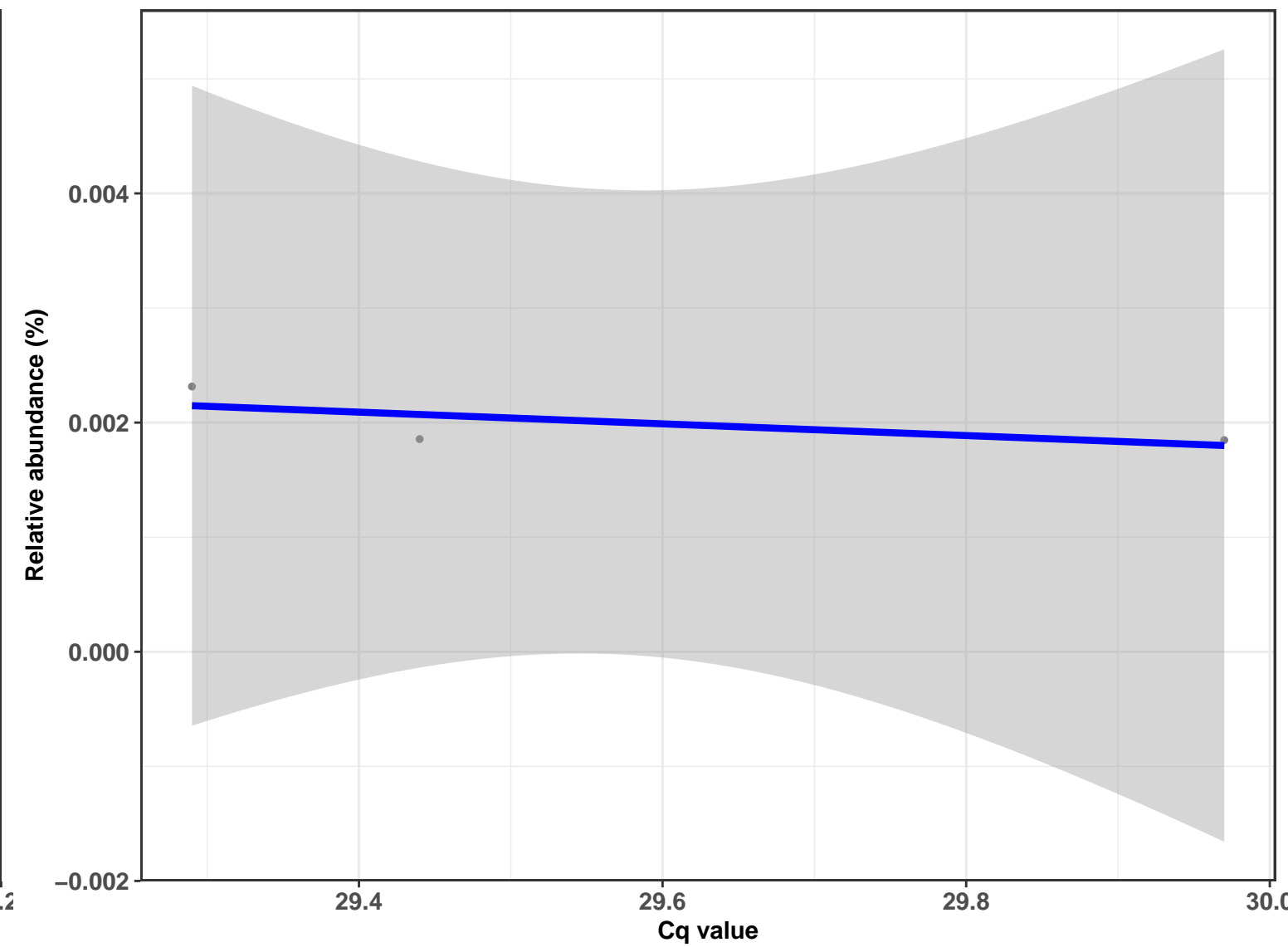
$\log_e(S) = 4.127$ ,  $p = 0.072$ ,  $\hat{\rho}_{\text{Spearman}} = -0.771$ ,  $\text{CI}_{95\%} [-1.421, -0.171]$ ,  $n_{\text{pairs}} = 6$



### Correlation within: REF-DIC



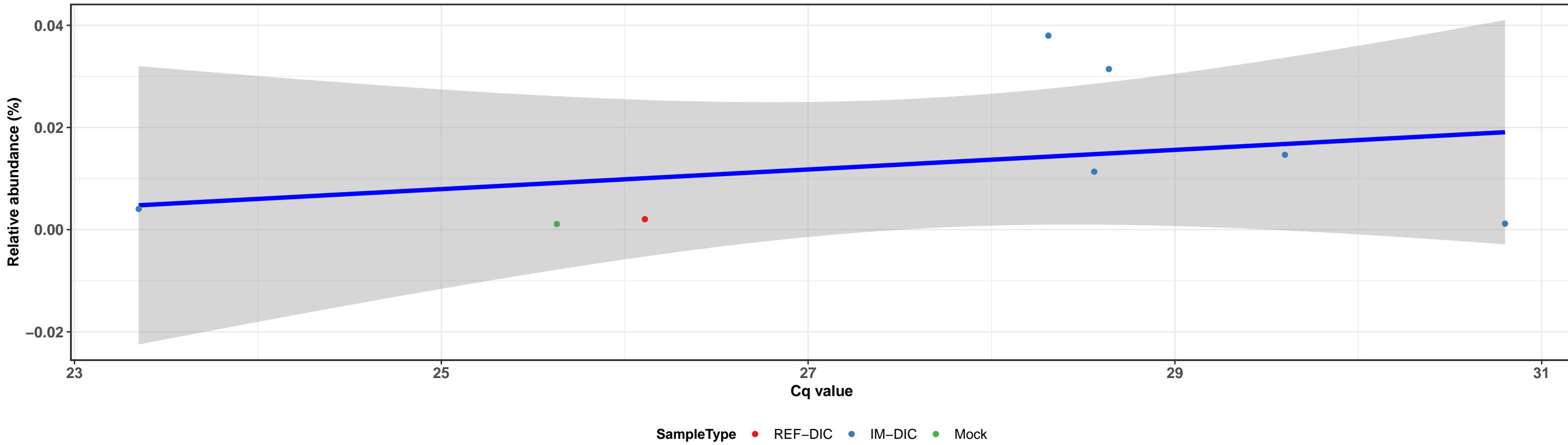
### Correlation within: IM-DIC



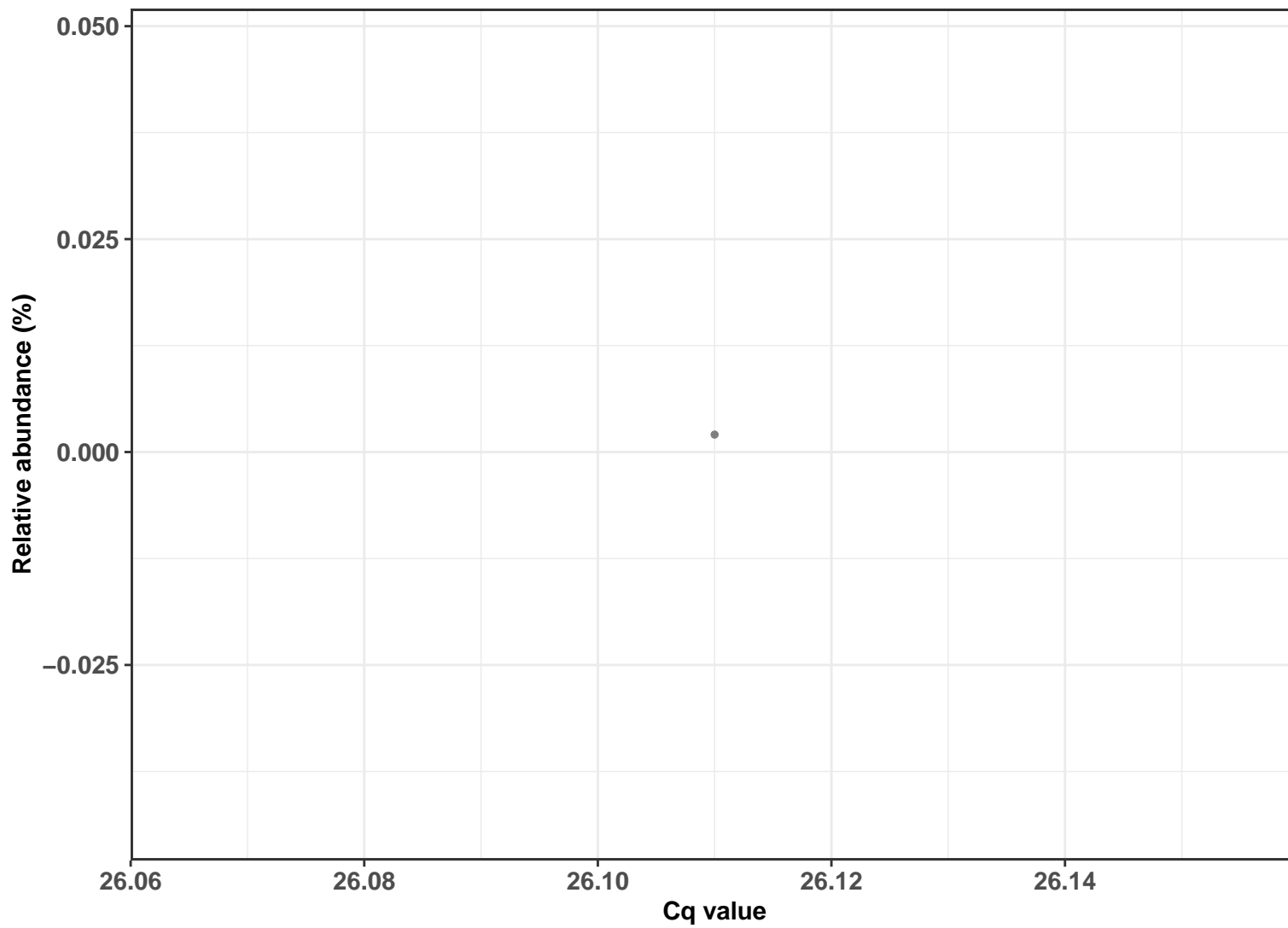
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

### Correlation with all samples

$\log_e(S) = 4.159$ ,  $p = 0.570$ ,  $\hat{\rho}_{\text{Spearman}} = 0.238$ ,  $\text{CI}_{95\%} [-0.567, 1.222]$ ,  $n_{\text{pairs}} = 8$

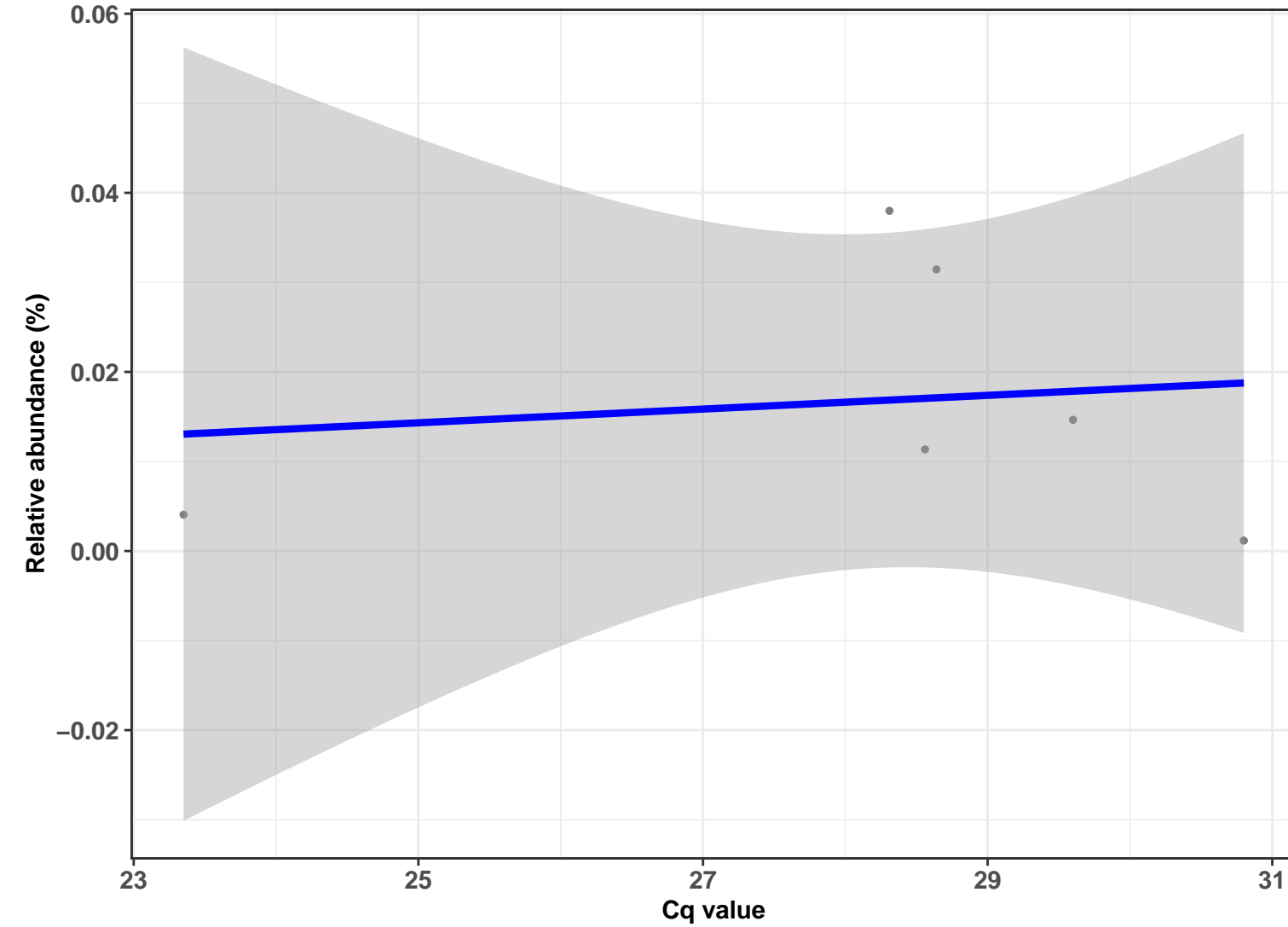


### Correlation within: REF-DIC



### Correlation within: IM-DIC

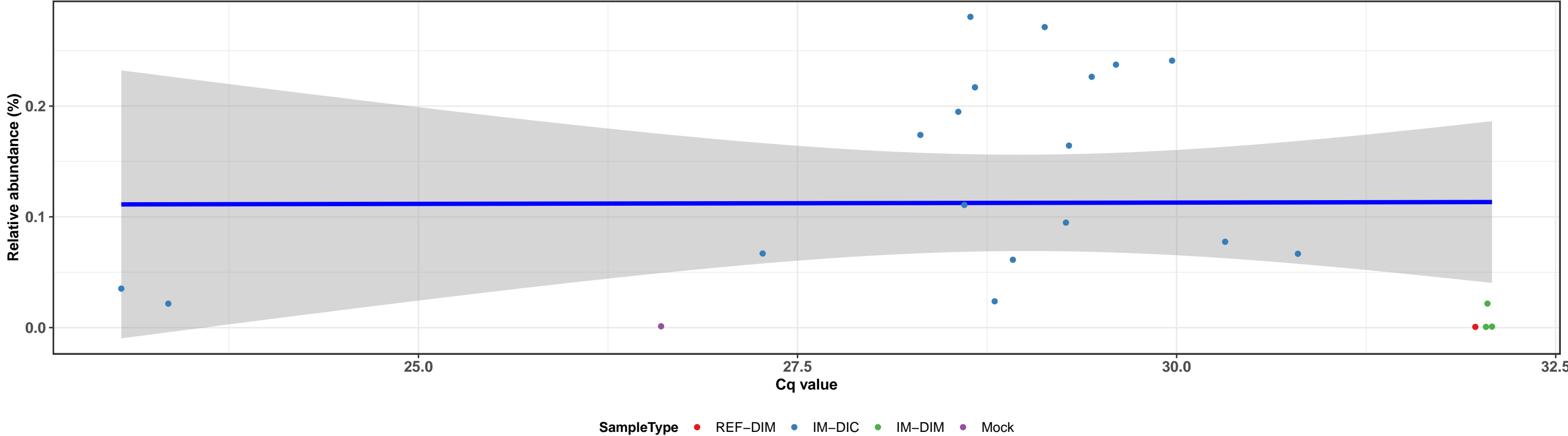
$\log_e(S) = 3.784$ ,  $p = 0.623$ ,  $\hat{\rho}_{\text{Spearman}} = -0.257$ ,  $\text{CI}_{95\%} [-1.338, 0.790]$ ,  $n_{\text{pairs}} = 6$



k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Flavobacteriales; f\_\_Flavobacteriaceae; g\_\_Flavobacterium; NA

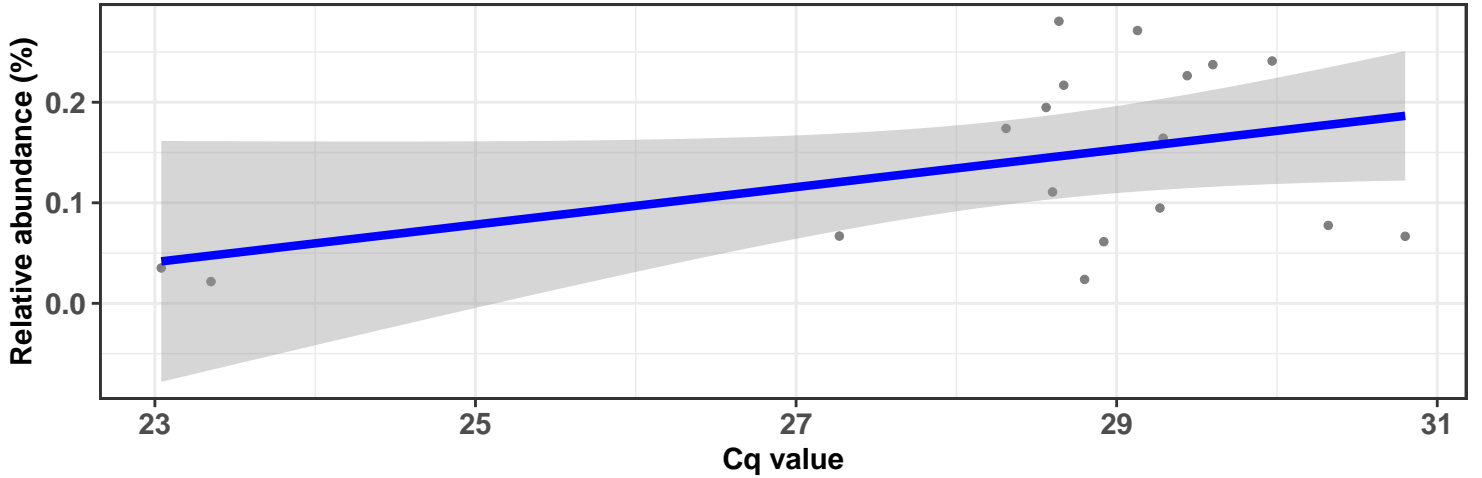
Correlation with all samples

$\log_e(S) = 7.768$ ,  $p = 0.444$ ,  $\hat{\rho}_{\text{Spearman}} = -0.168$ ,  $\text{CI}_{95\%} [-0.731, 0.358]$ ,  $n_{\text{pairs}} = 23$

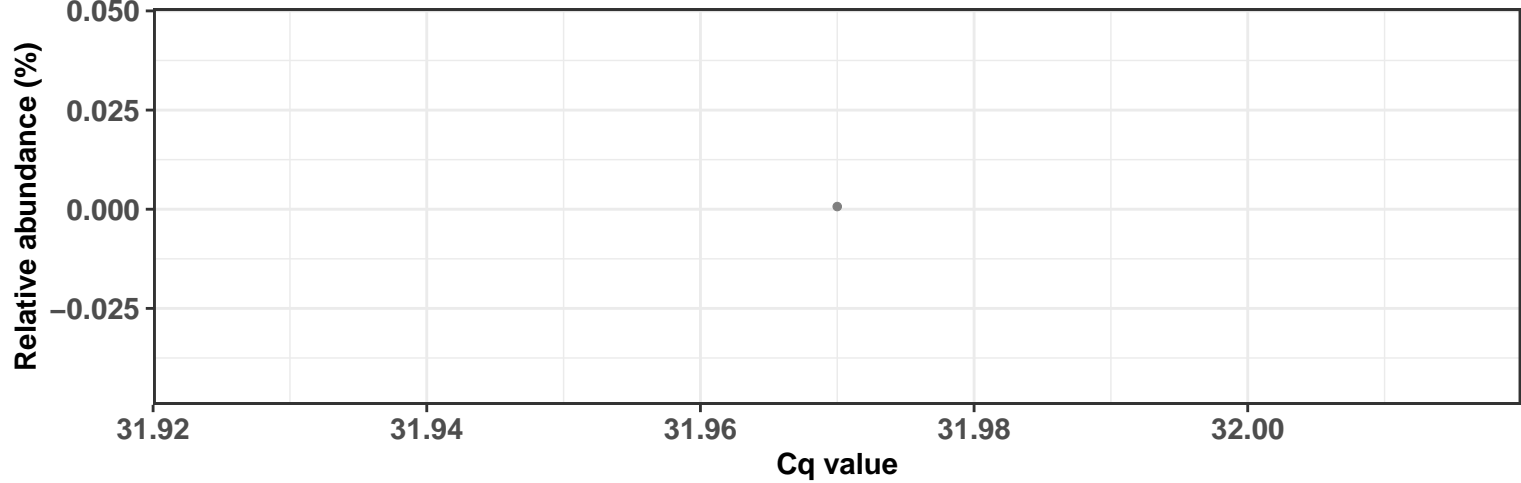


Correlation within: IM-DIC

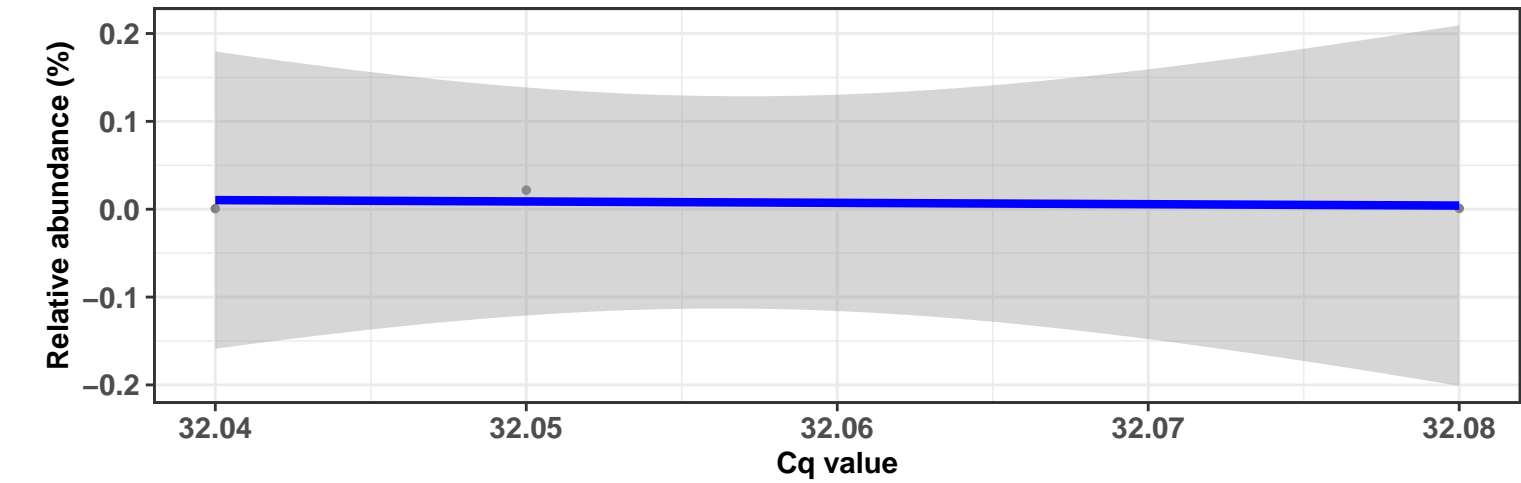
$\log_e(S) = 6.525$ ,  $p = 0.233$ ,  $\hat{\rho}_{\text{Spearman}} = 0.296$ ,  $\text{CI}_{95\%} [-0.217, 0.853]$ ,  $n_{\text{pairs}} = 18$



Correlation within: REF-DIM

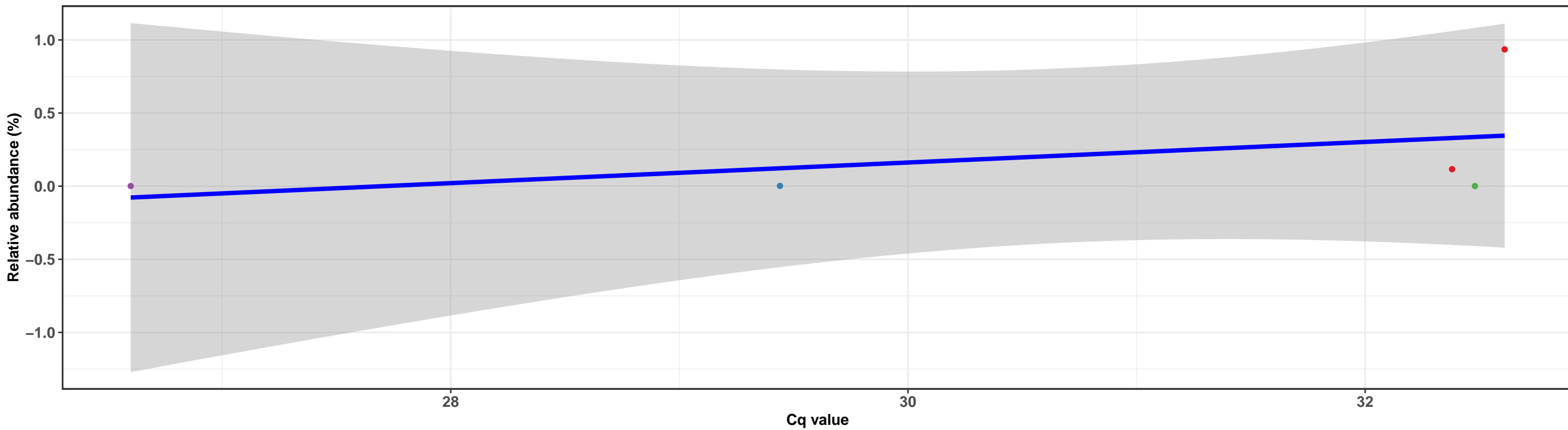


Correlation within: IM-DIM

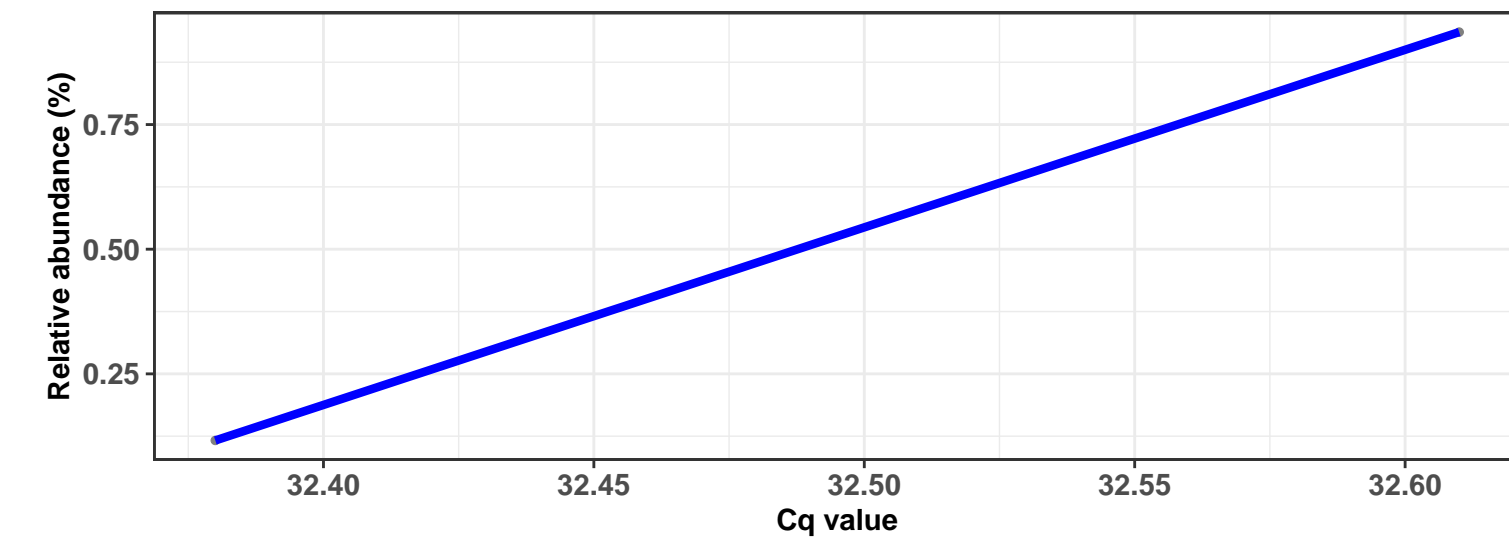


k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Cytophagales; f\_\_Hymenobacteraceae; g\_\_Hymenobacter; s\_\_uncultured bacterium

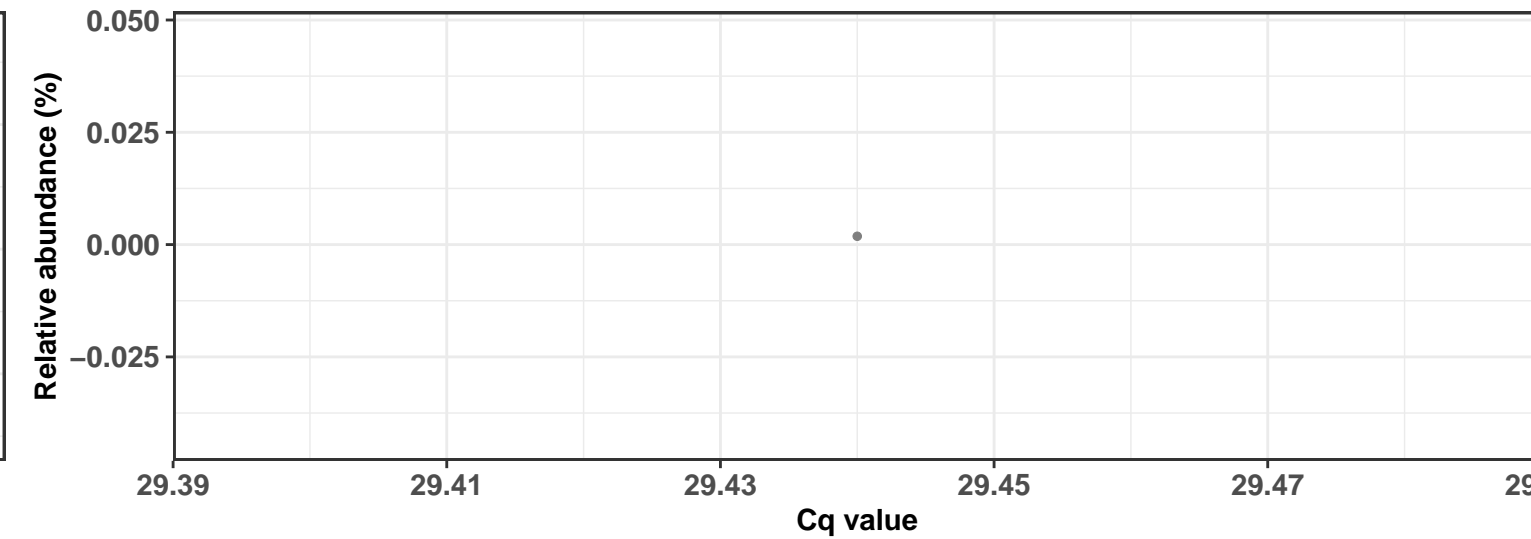
Correlation with all samples



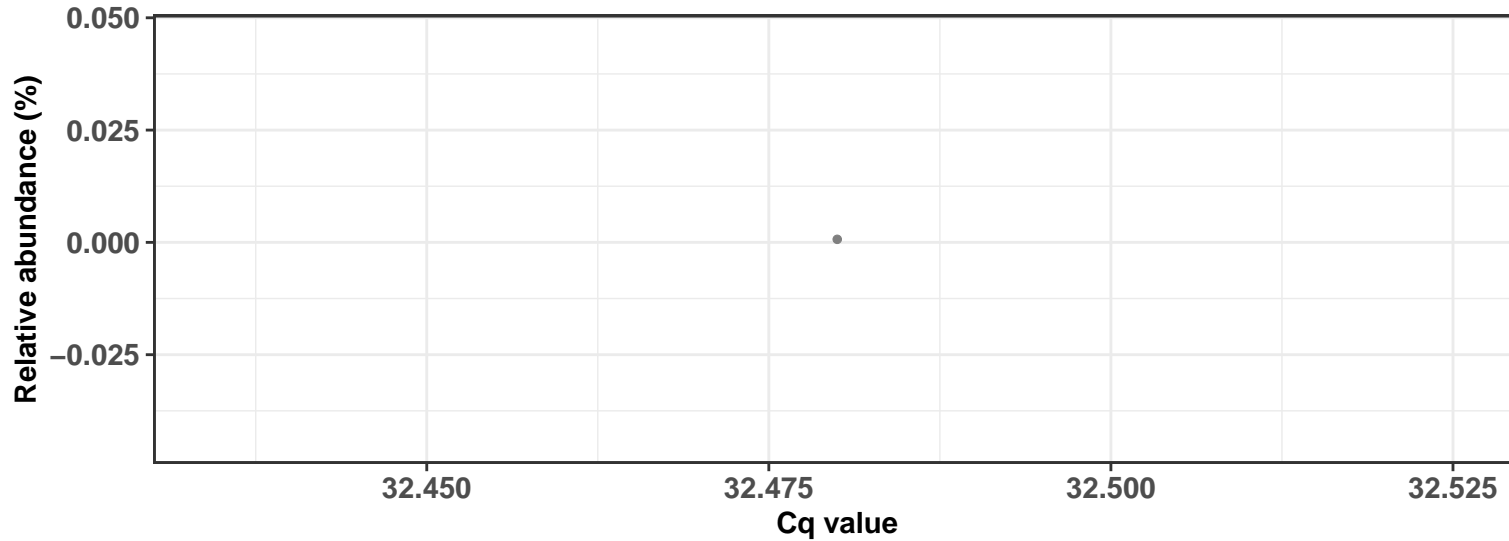
Correlation within: REF-DIM



Correlation within: IM-DIC



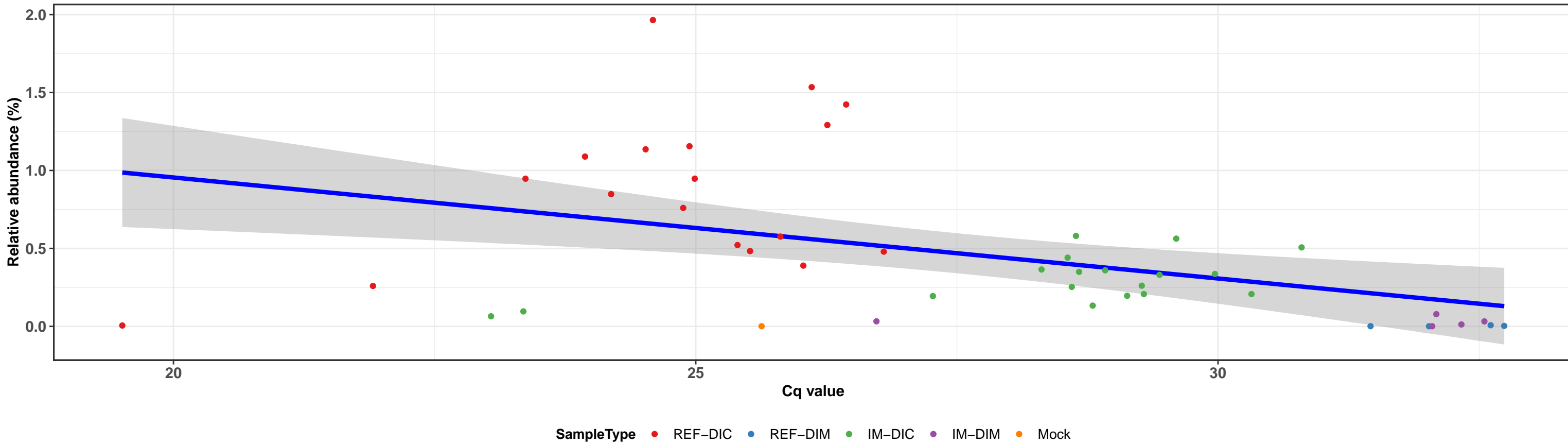
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Leuconostocaceae; g\_\_Weissella; s\_\_uncultured bacterium

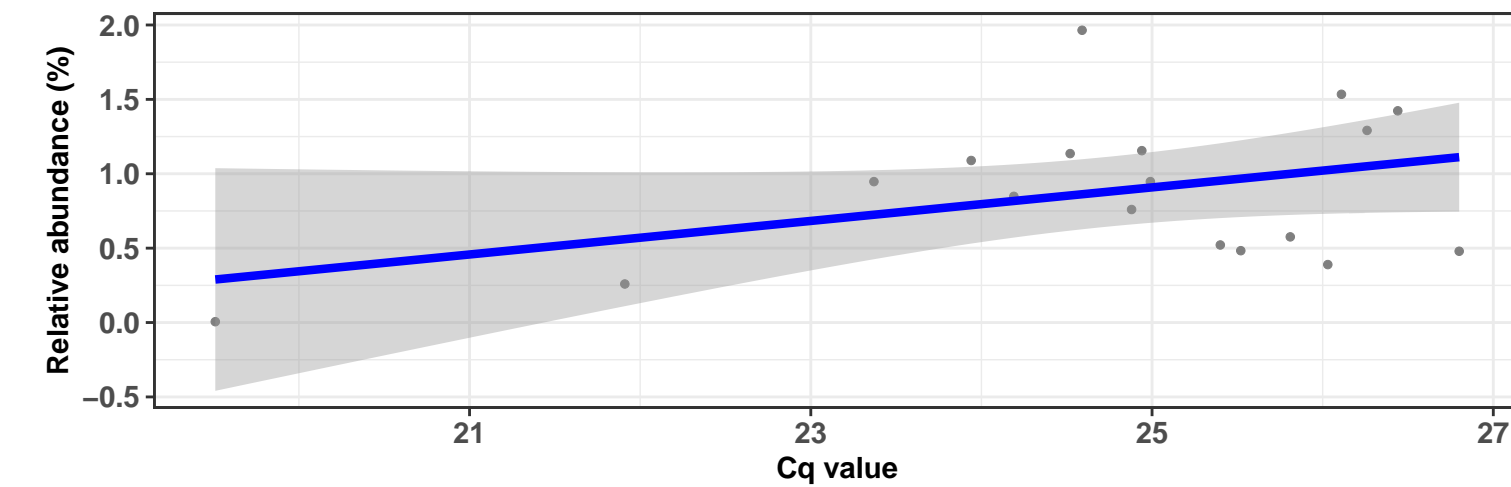
### Correlation with all samples

$\log_e(S) = 10.095$ ,  $p = < 0.001$ ,  $\hat{\rho}_{\text{Spearman}} = -0.494$ ,  $CI_{95\%} [-0.777, -0.245]$ ,  $n_{\text{pairs}} = 46$

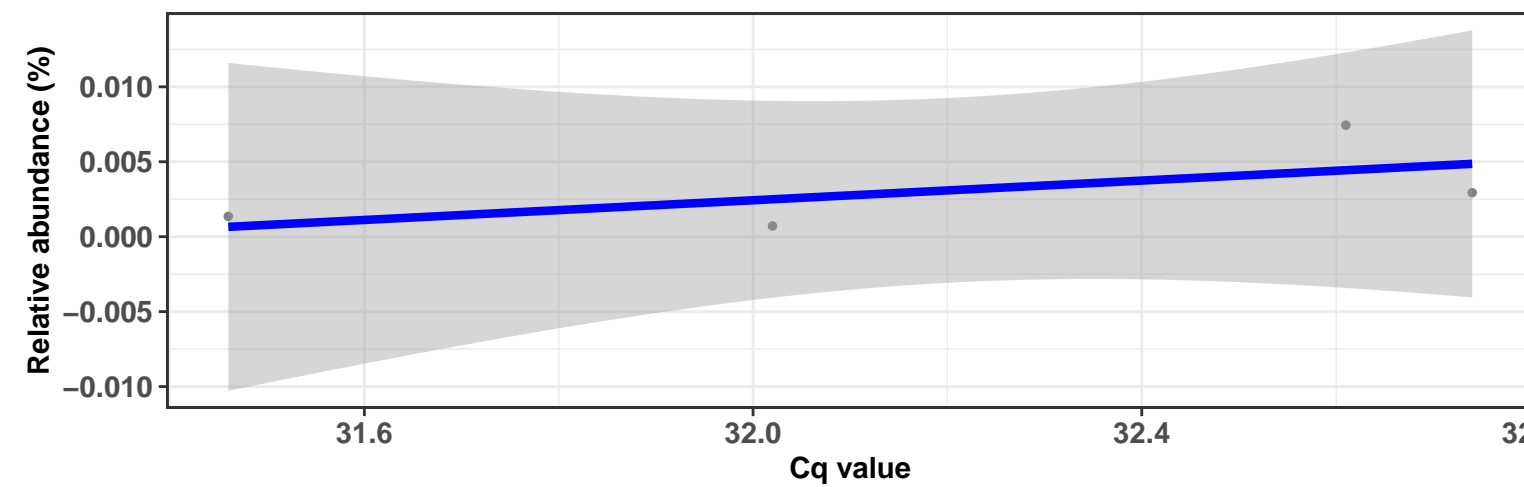


### Correlation within: REF-DIC

$\log_e(S) = 6.631$ ,  $p = 0.385$ ,  $\hat{\rho}_{\text{Spearman}} = 0.218$ ,  $CI_{95\%} [-0.367, 0.806]$ ,  $n_{\text{pairs}} = 18$

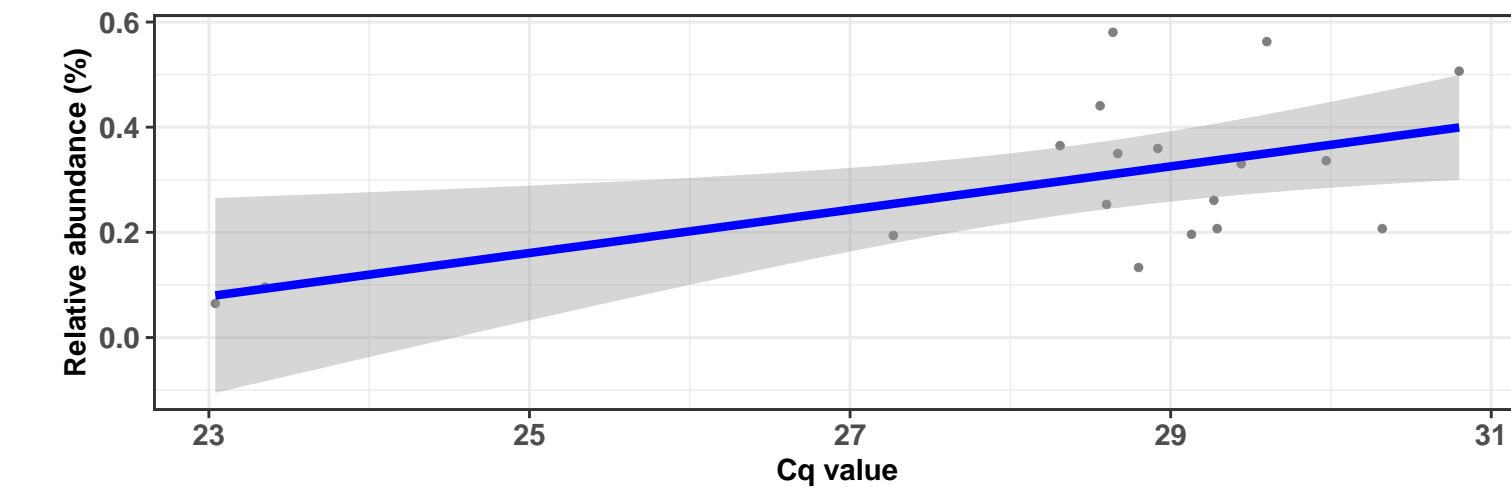


### Correlation within: REF-DIM

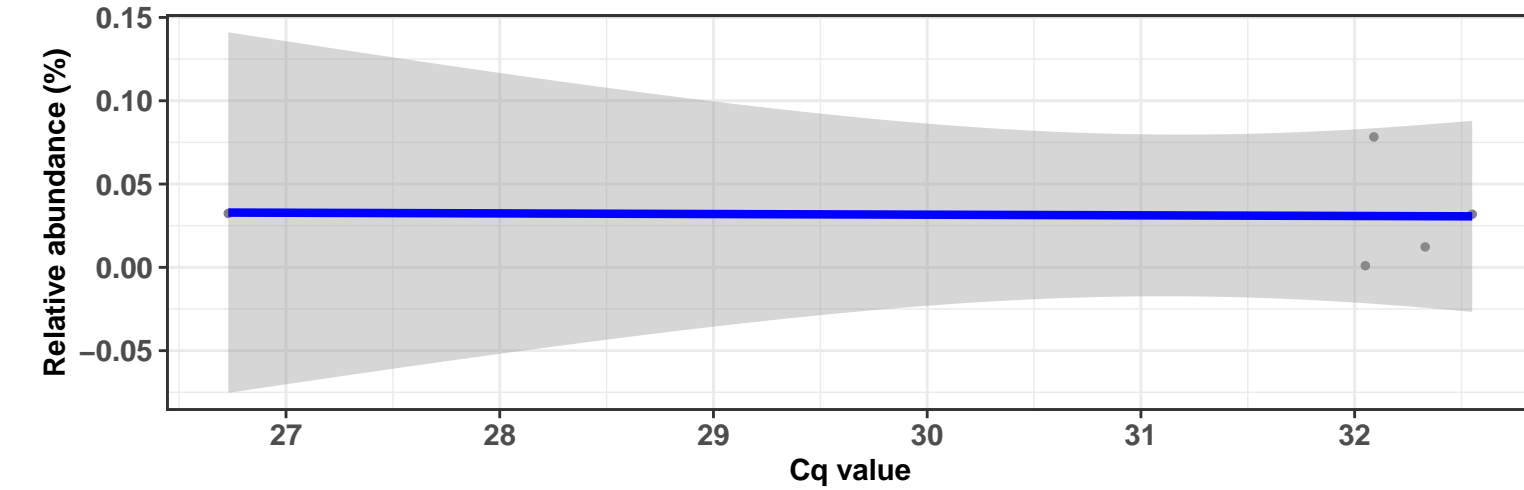


### Correlation within: IM-DIC

$\log_e(S) = 6.446$ ,  $p = 0.155$ ,  $\hat{\rho}_{\text{Spearman}} = 0.350$ ,  $CI_{95\%} [-0.221, 0.876]$ ,  $n_{\text{pairs}} = 18$

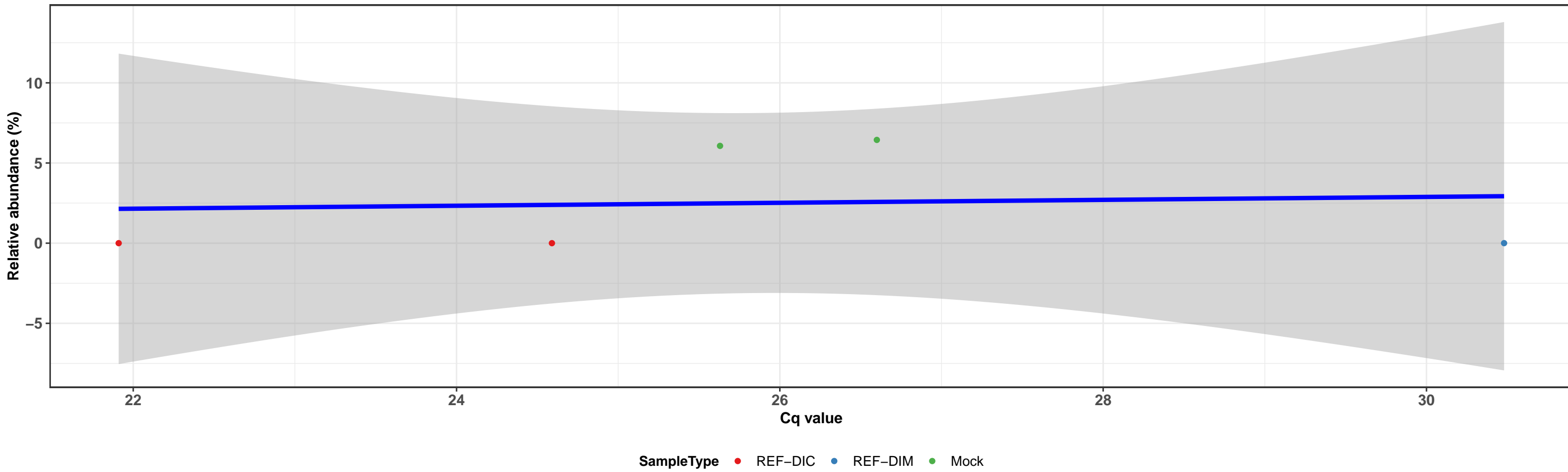


### Correlation within: IM-DIM

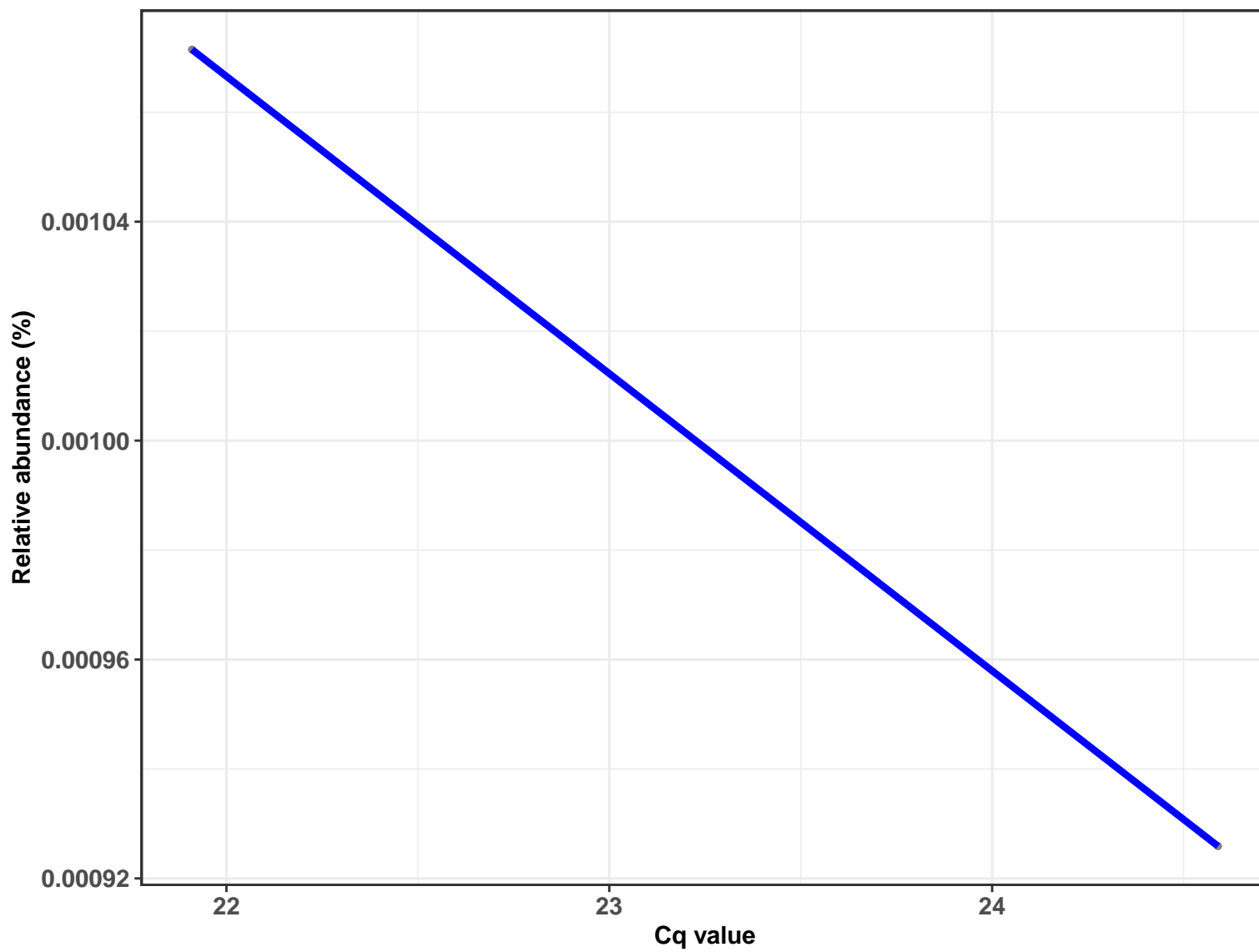


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Staphylococcus; s\_\_Staphylococcus aureus

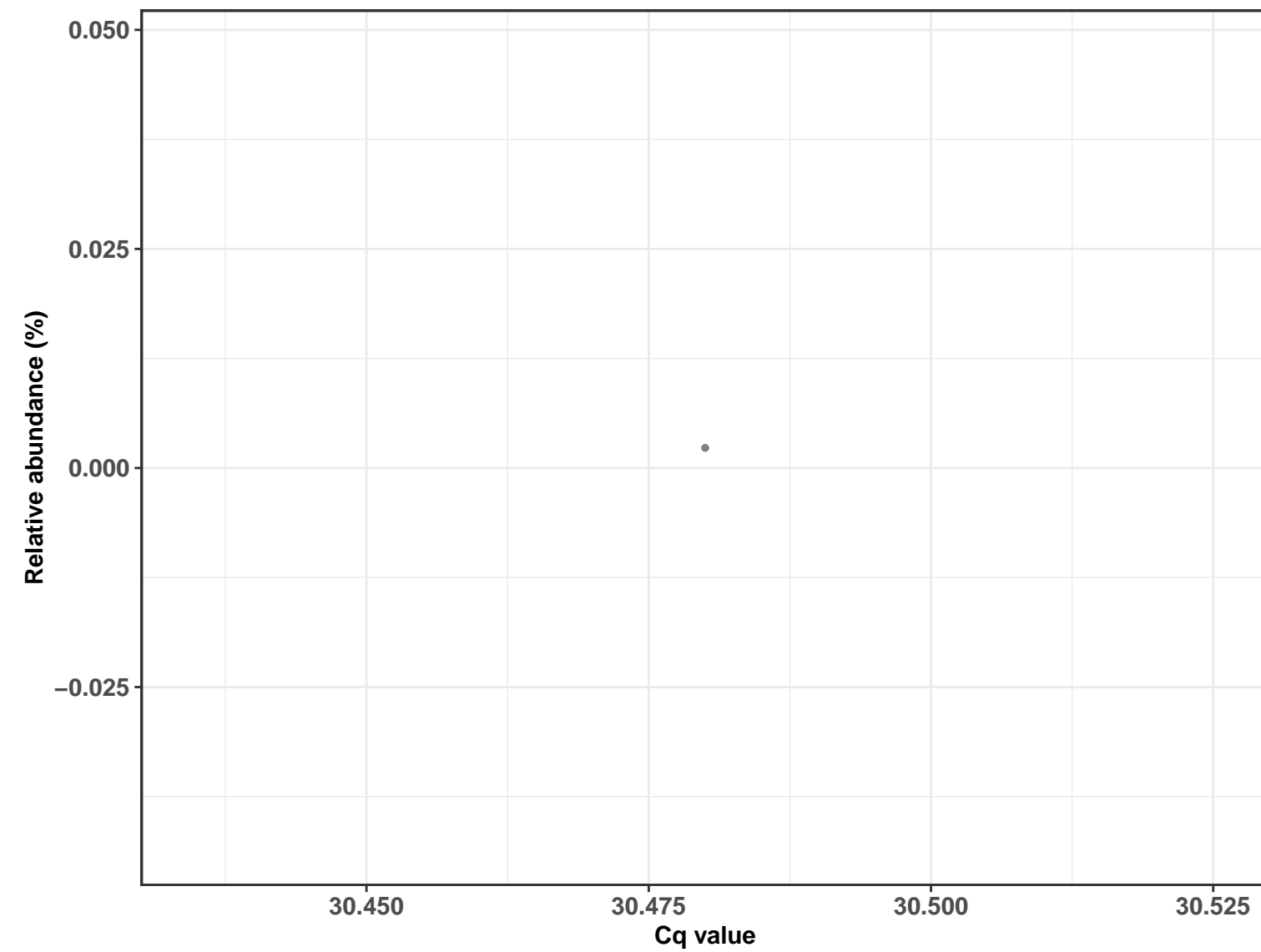
Correlation with all samples



Correlation within: REF-DIC

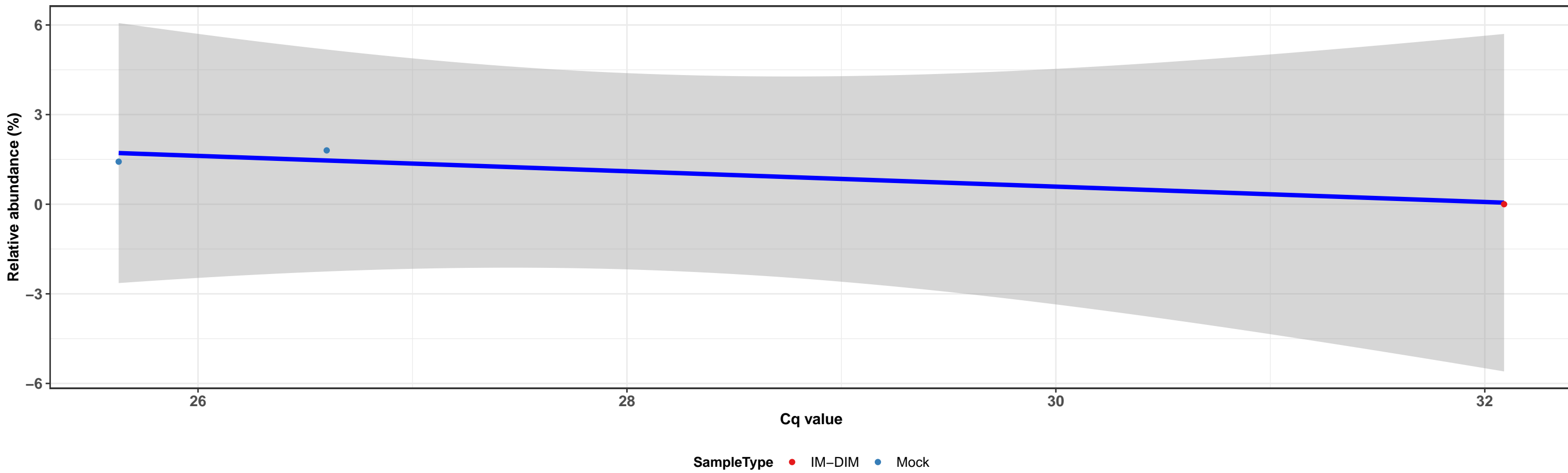


Correlation within: REF-DIM

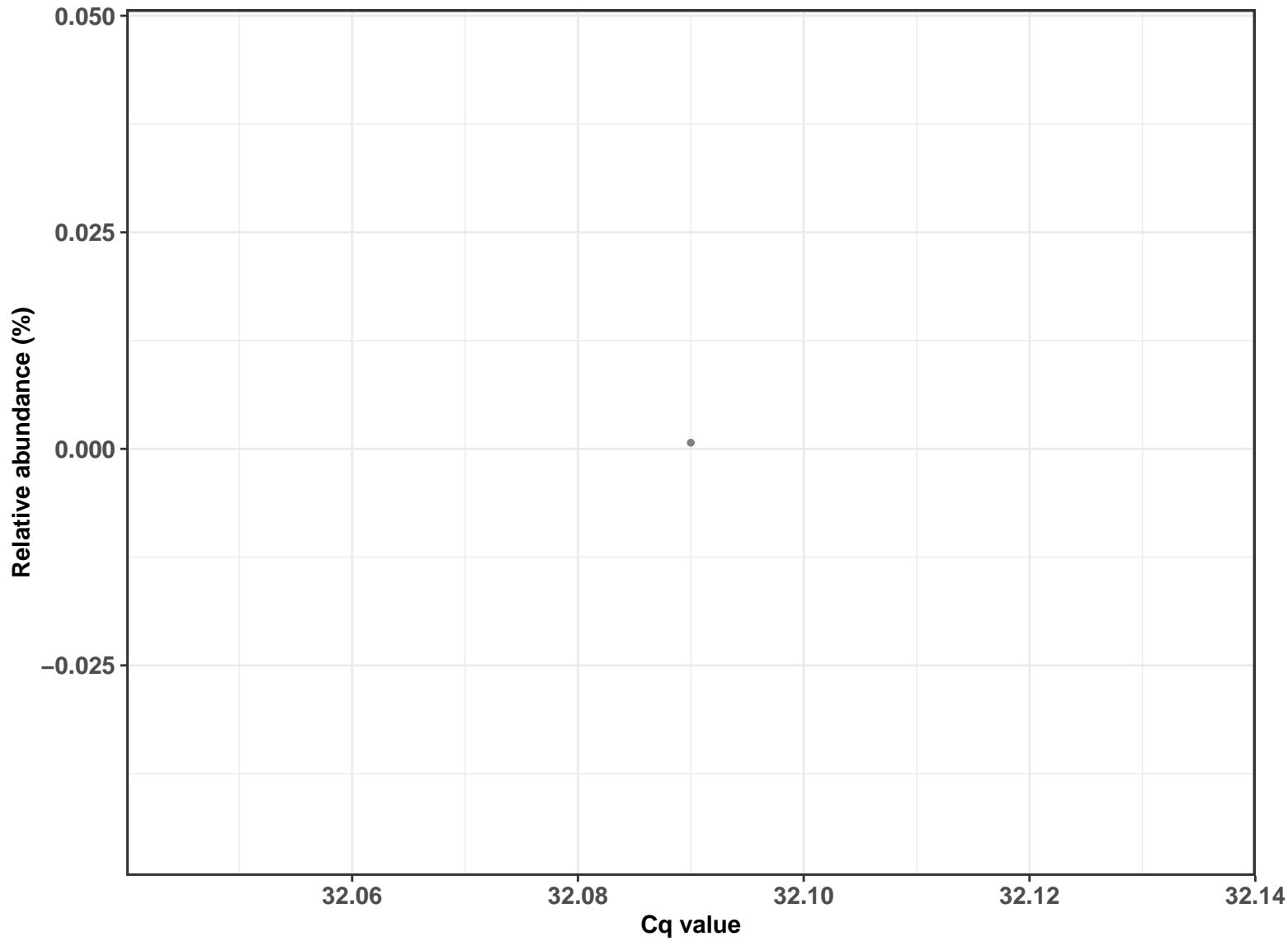




Correlation with all samples

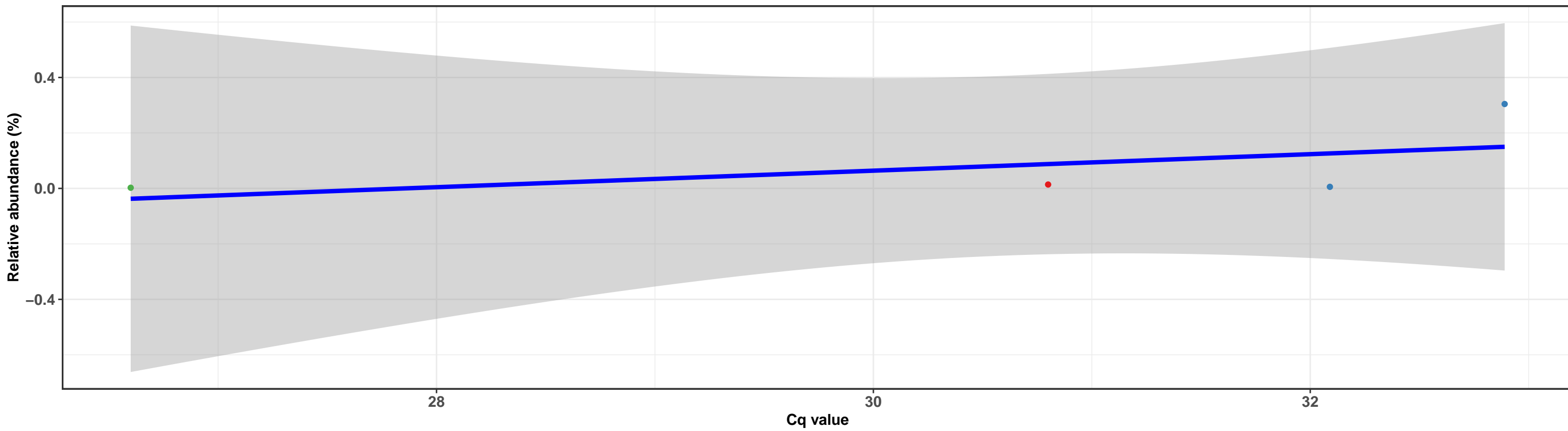


Correlation within: IM-DIM

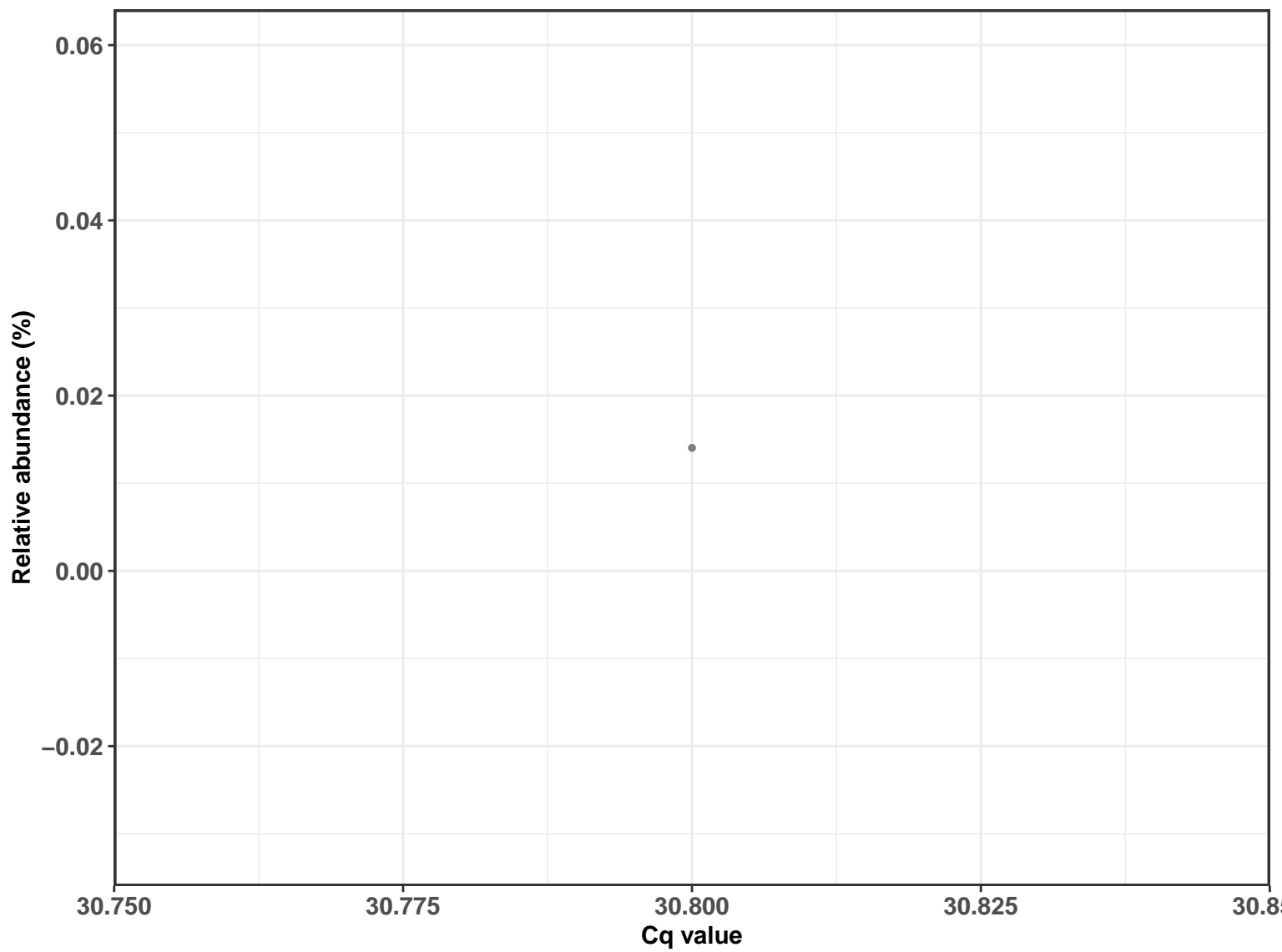


k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Micrococcaceae; g\_\_Arthrobacter; Ambiguous\_taxa

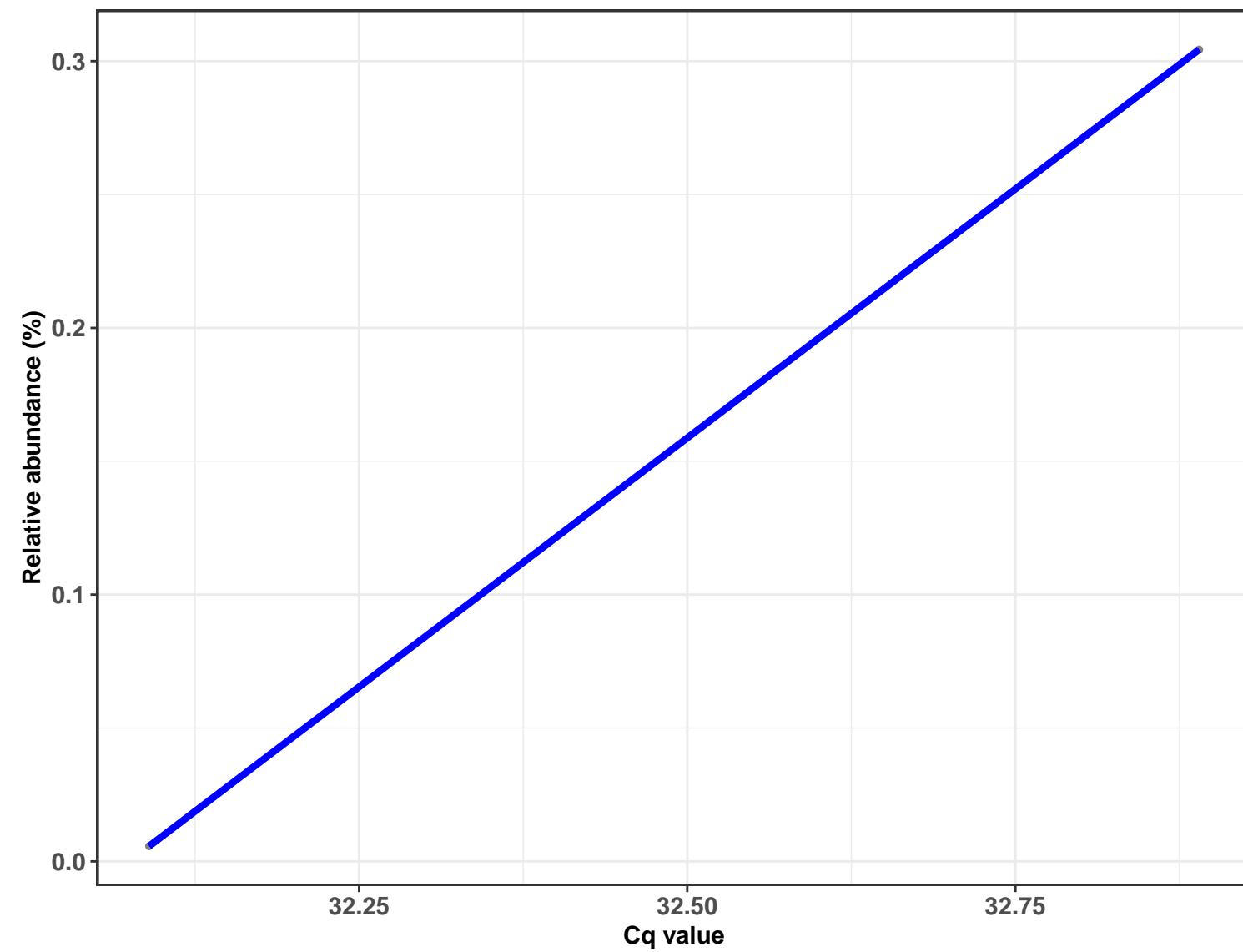
Correlation with all samples



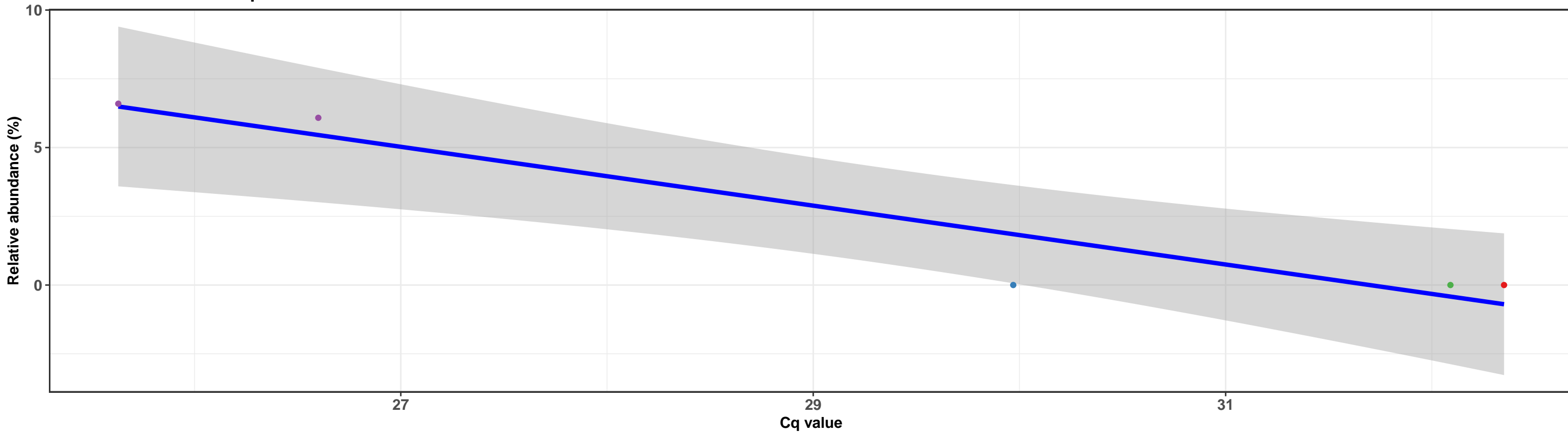
Correlation within: IM-DIC



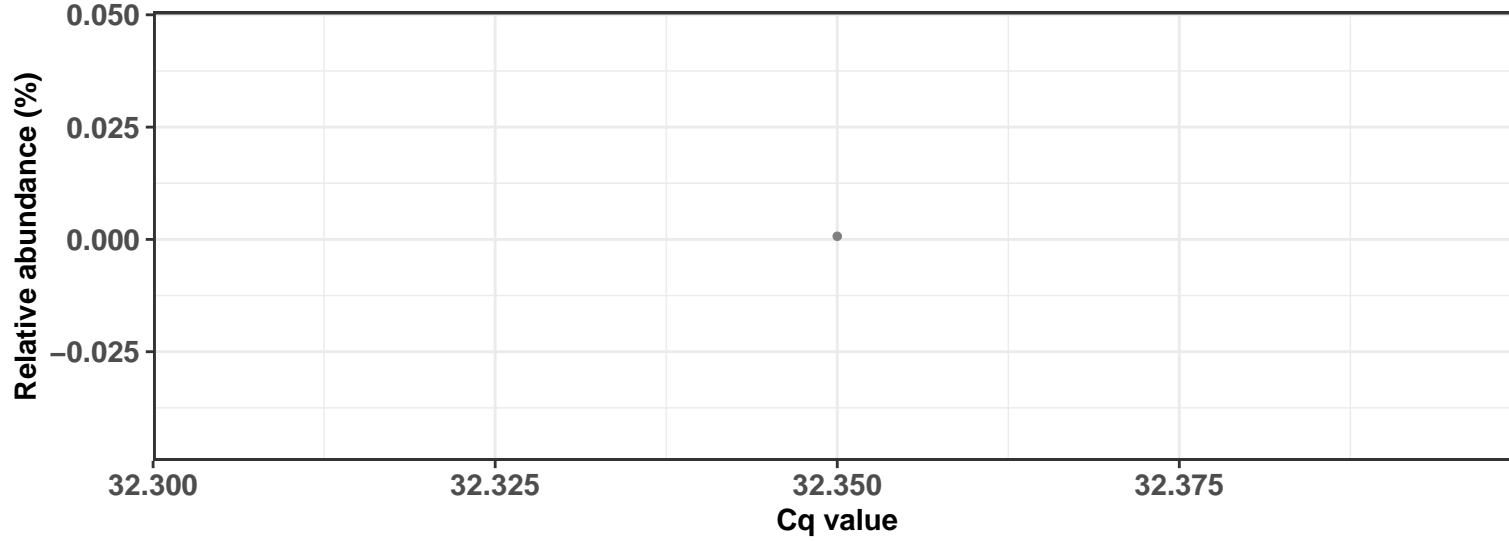
Correlation within: IM-DIM



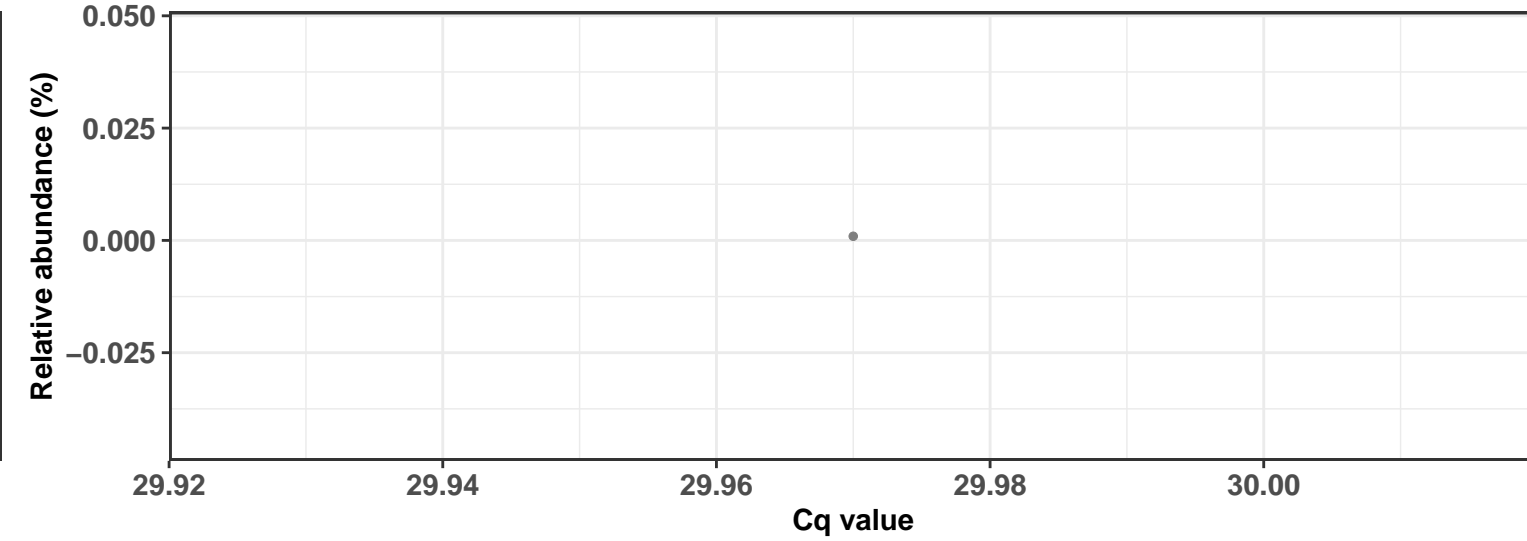
Correlation with all samples



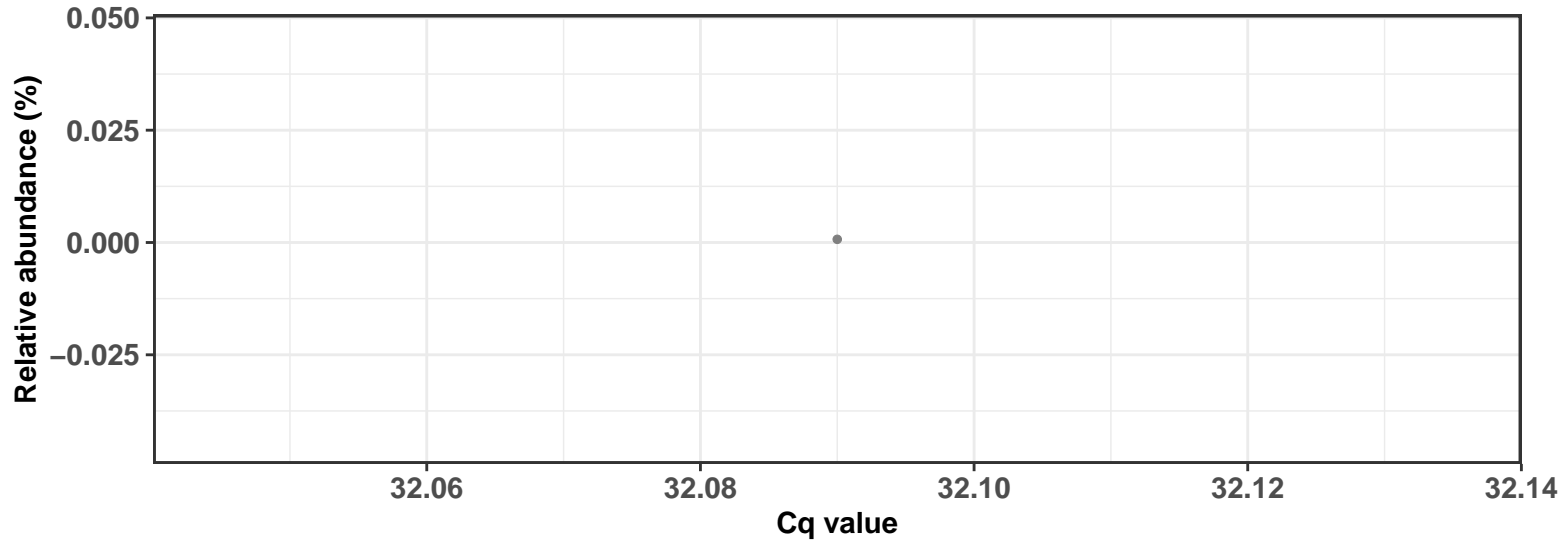
Correlation within: REF-DIM



Correlation within: IM-DIC

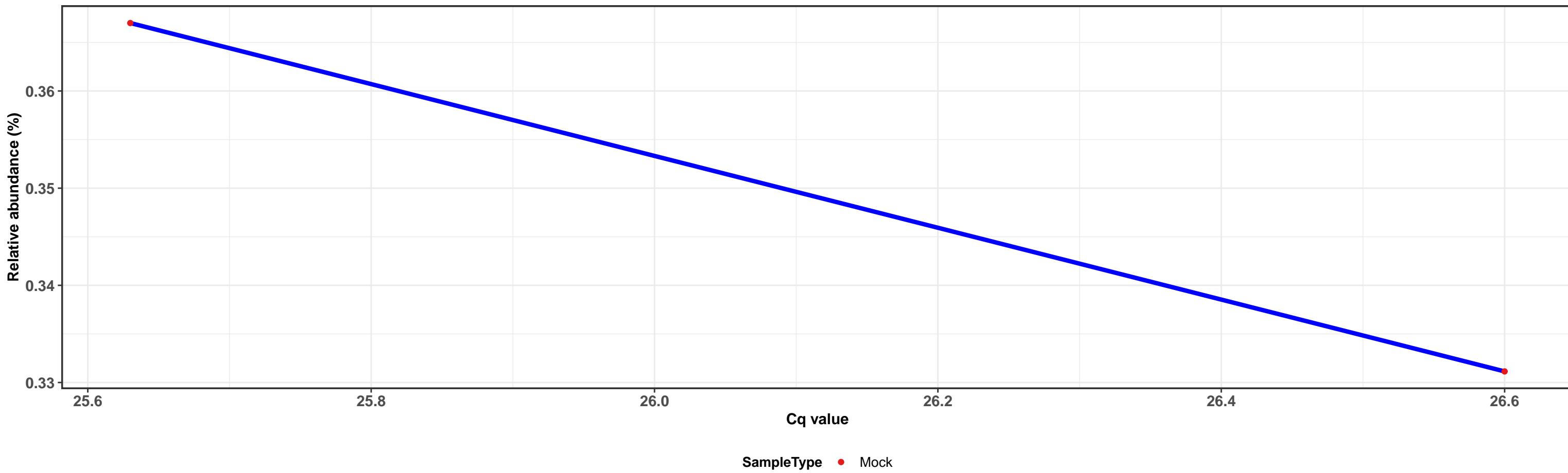


Correlation within: IM-DIM



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

Correlation with all samples



Correlation within:

