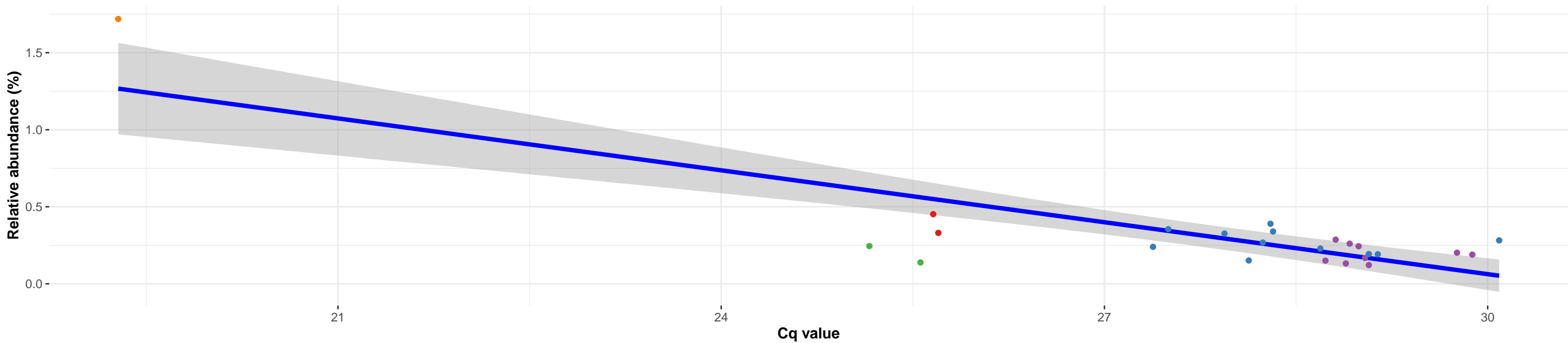


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__Clostridium perfringens

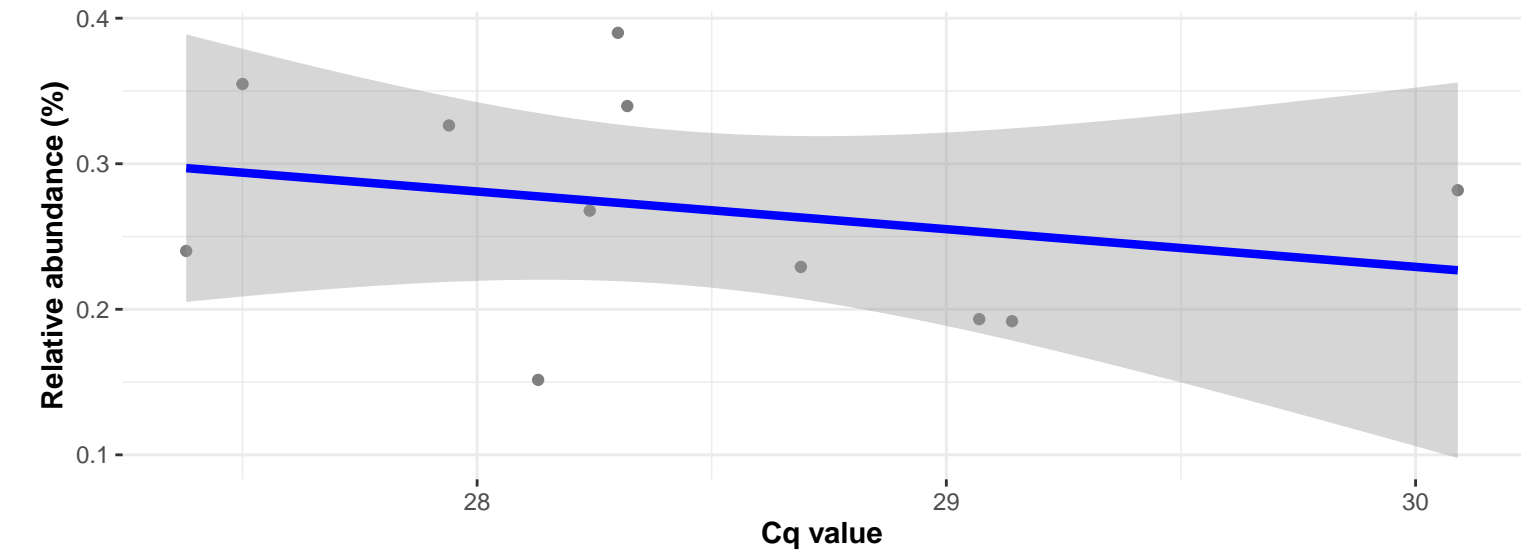
Correlation with all samples

$\log_e(S) = 8.227$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = -0.439$, $\text{CI}_{95\%} [-0.717, -0.041]$, $n_{\text{pairs}} = 25$



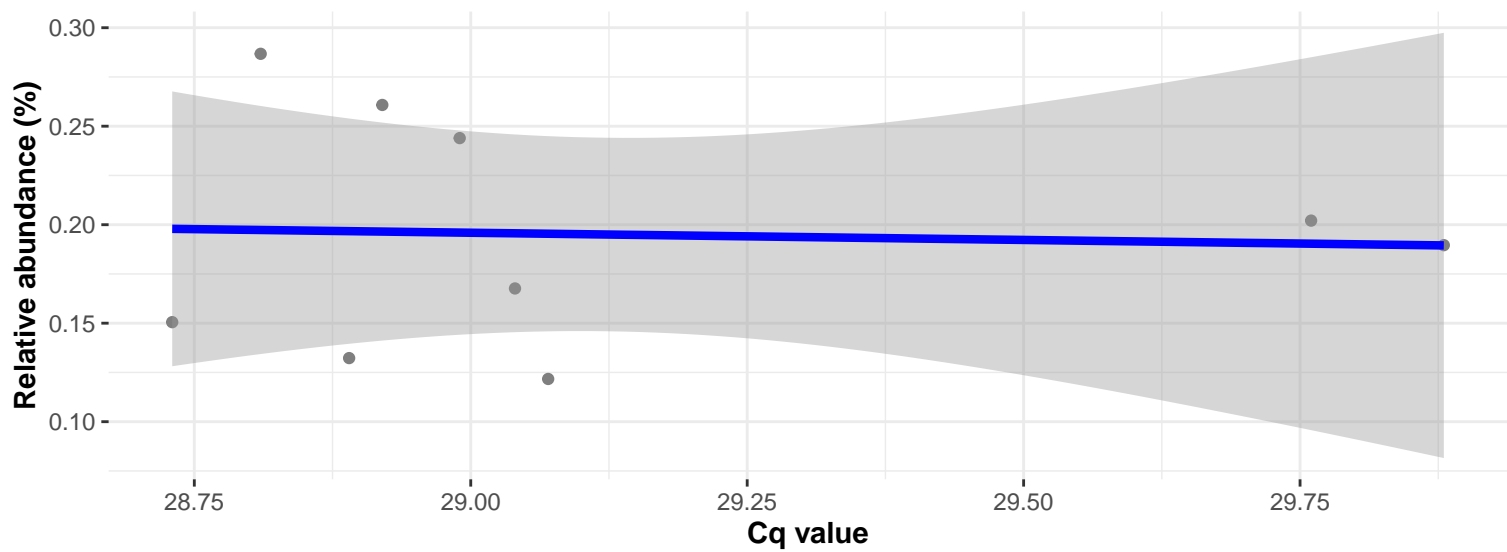
Correlation within: IM-PIM

$\log_e(S) = 5.620$, $p = 0.450$, $\hat{\rho}_{\text{Spearman}} = -0.255$, $\text{CI}_{95\%} [-0.750, 0.425]$, $n_{\text{pairs}} = 11$

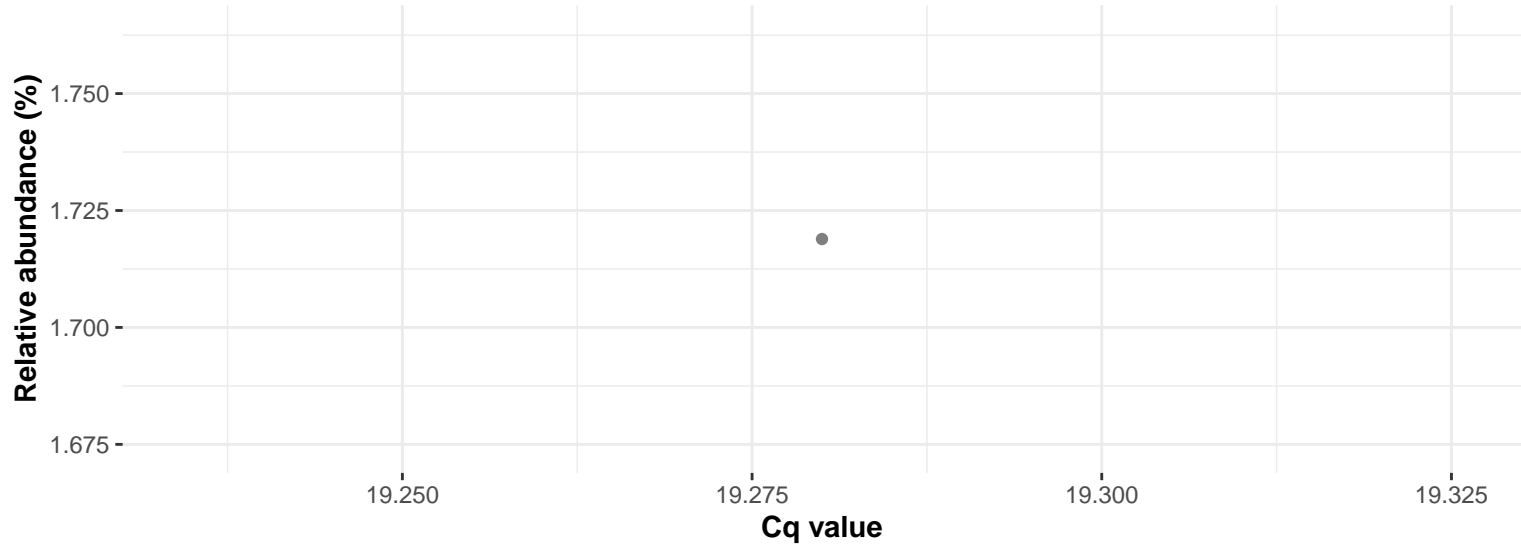


Correlation within: IM-DIM

$\log_e(S) = 4.898$, $p = 0.765$, $\hat{\rho}_{\text{Spearman}} = -0.117$, $\text{CI}_{95\%} [-0.736, 0.609]$, $n_{\text{pairs}} = 9$



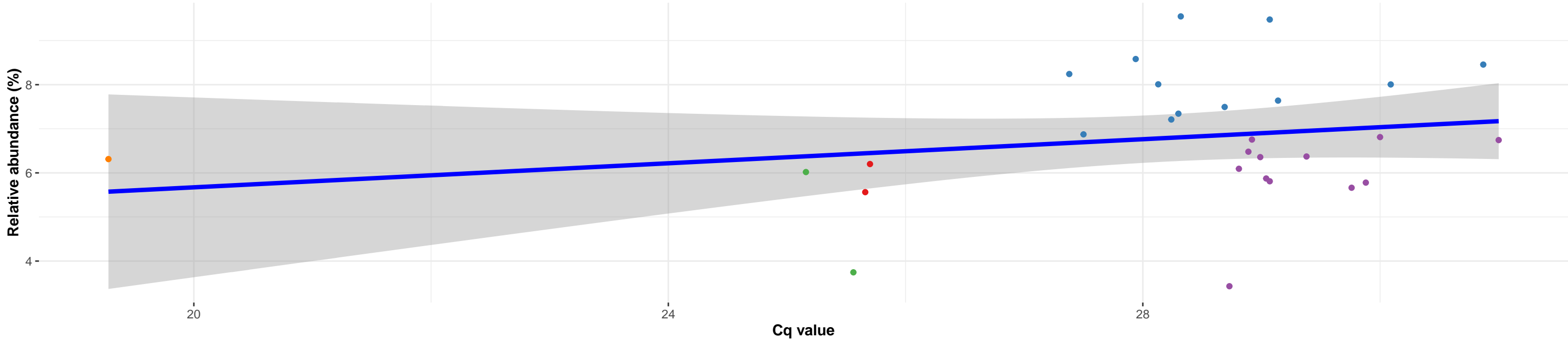
Correlation within: Feed



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

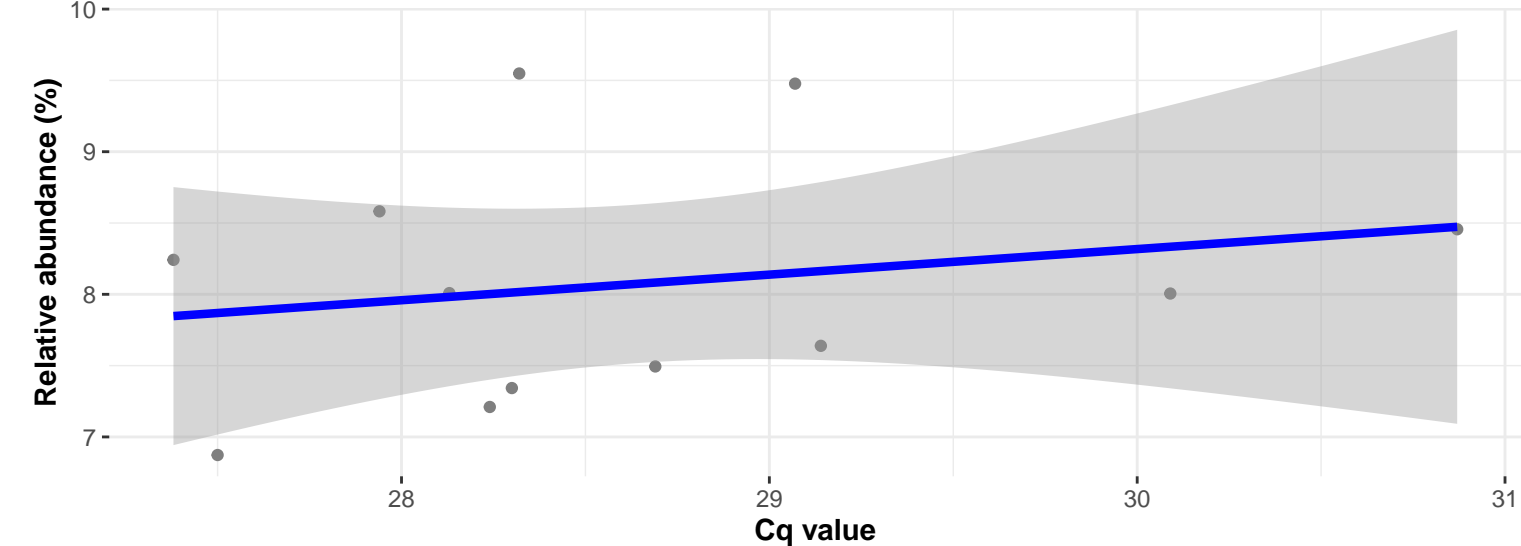
Correlation with all samples

$\log_e(S) = 8.189$, $p = 0.558$, $\hat{\rho}_{\text{Spearman}} = 0.113$, $CI_{95\%} [-0.275, 0.470]$, $n_{\text{pairs}} = 29$



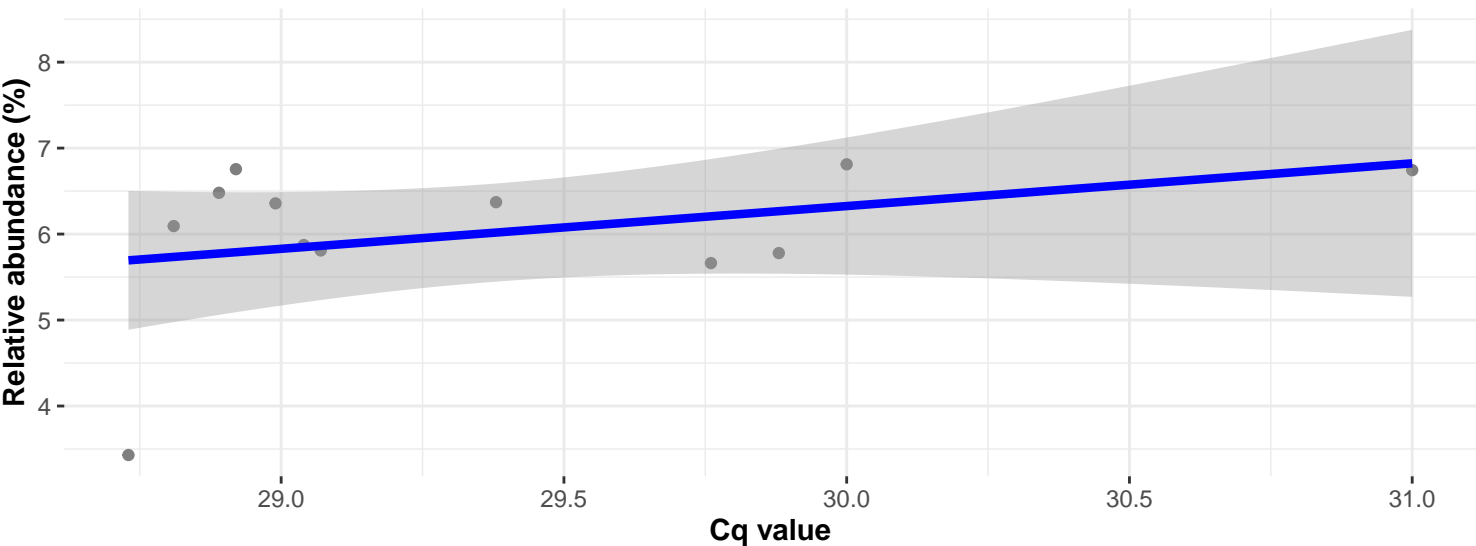
Correlation within: IM-PIM

$\log_e(S) = 5.438$, $p = 0.542$, $\hat{\rho}_{\text{Spearman}} = 0.196$, $CI_{95\%} [-0.442, 0.702]$, $n_{\text{pairs}} = 12$

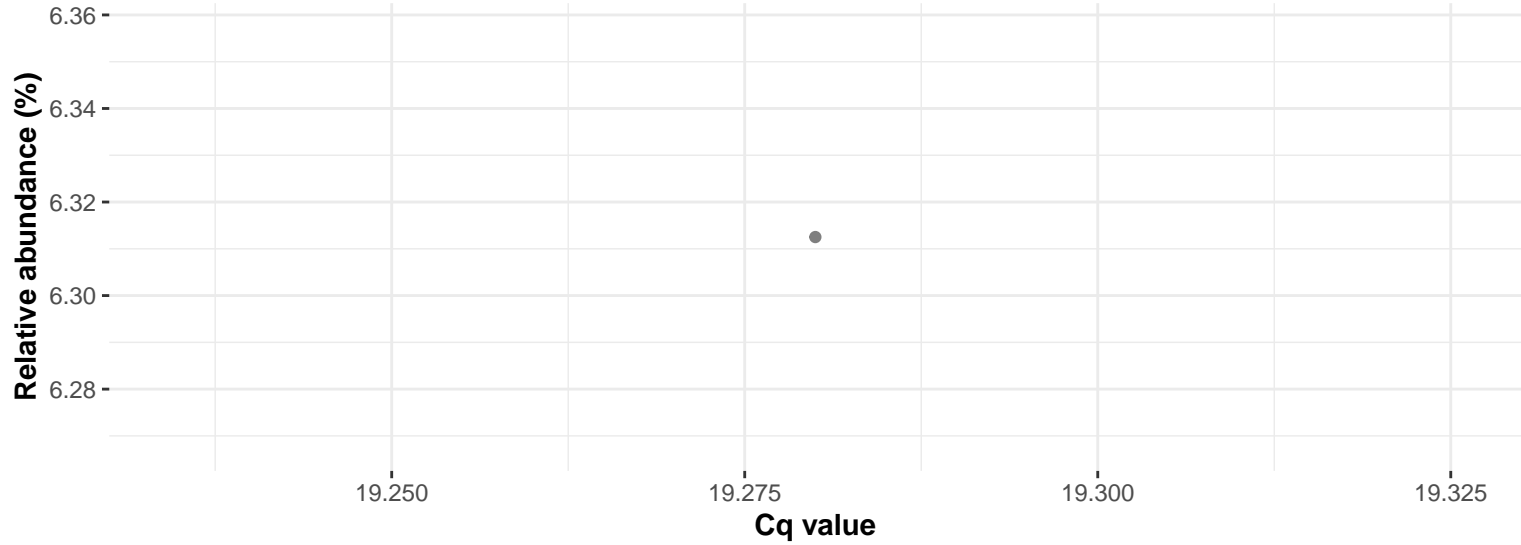


Correlation within: IM-DIM

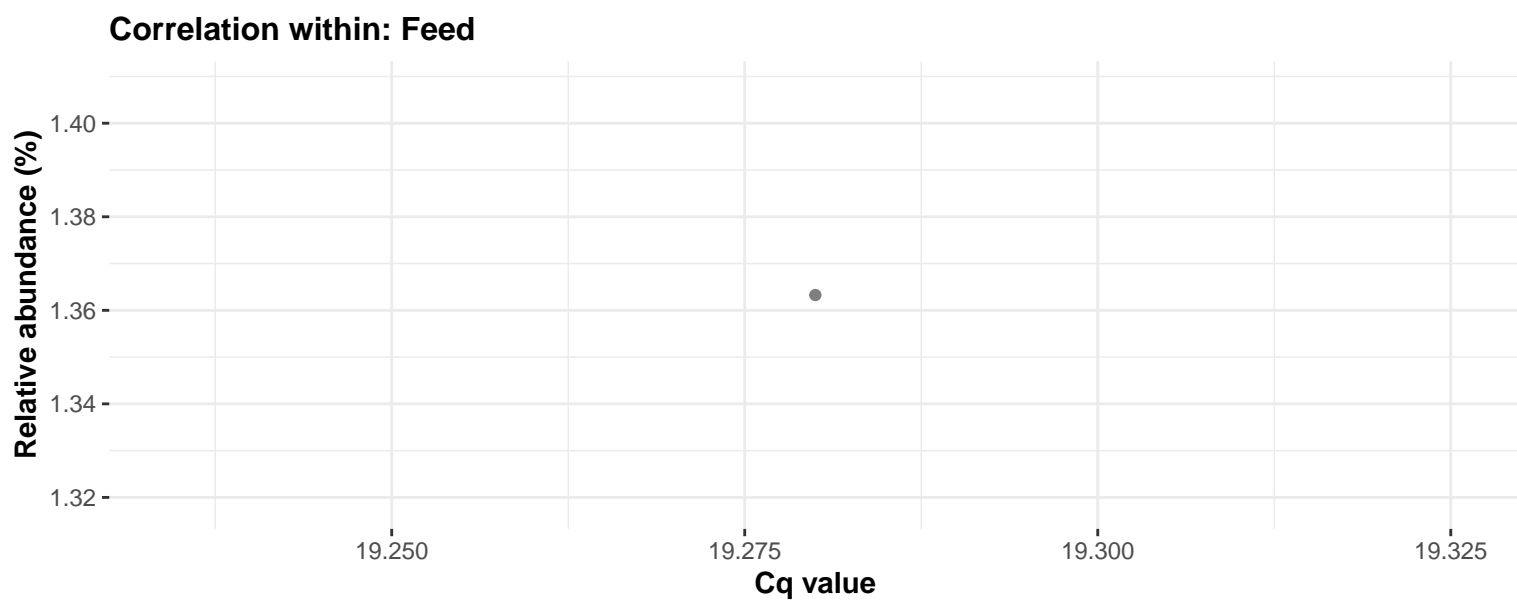
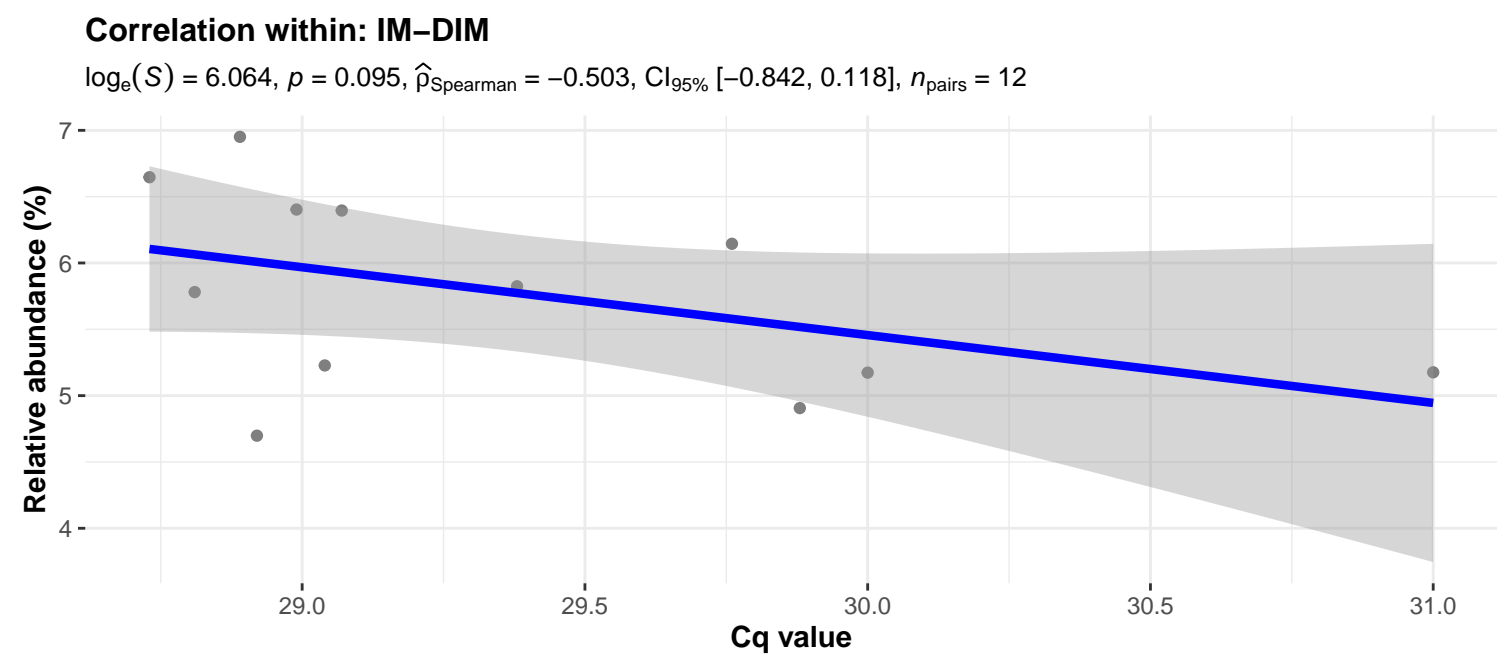
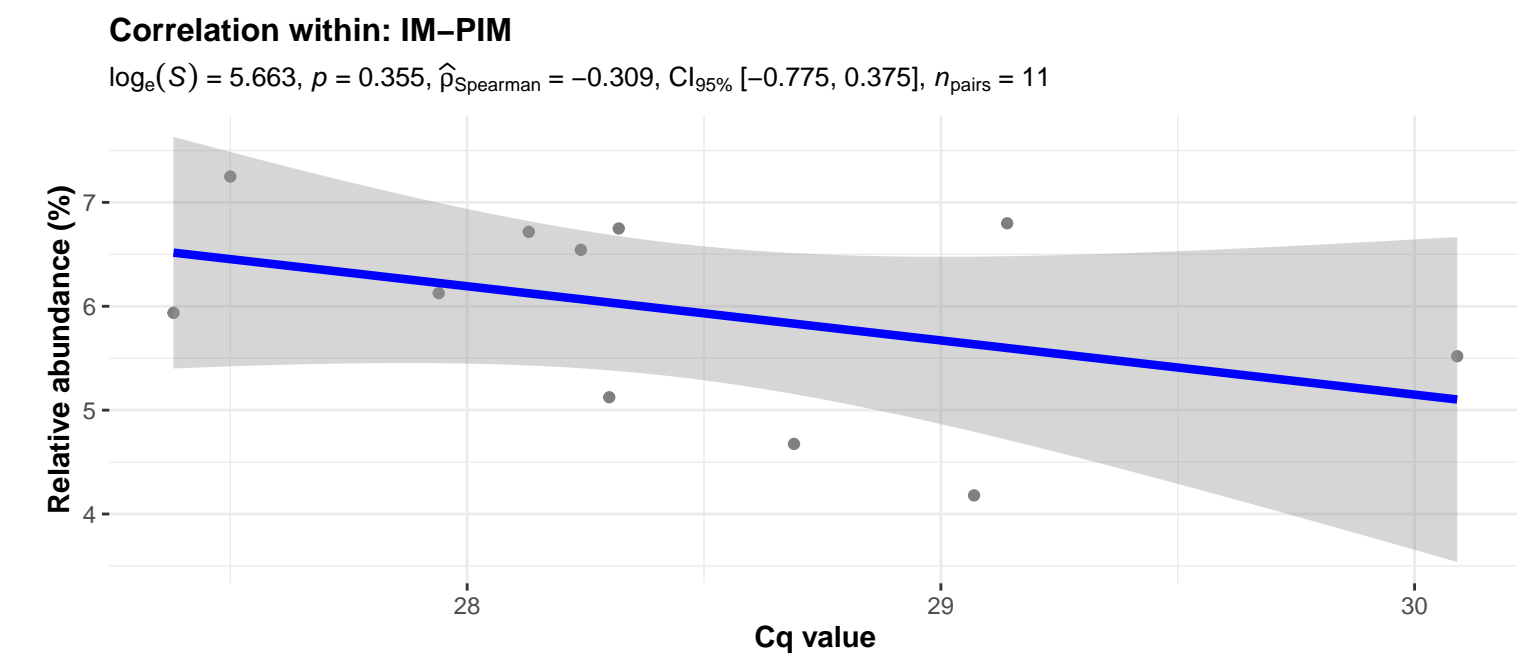
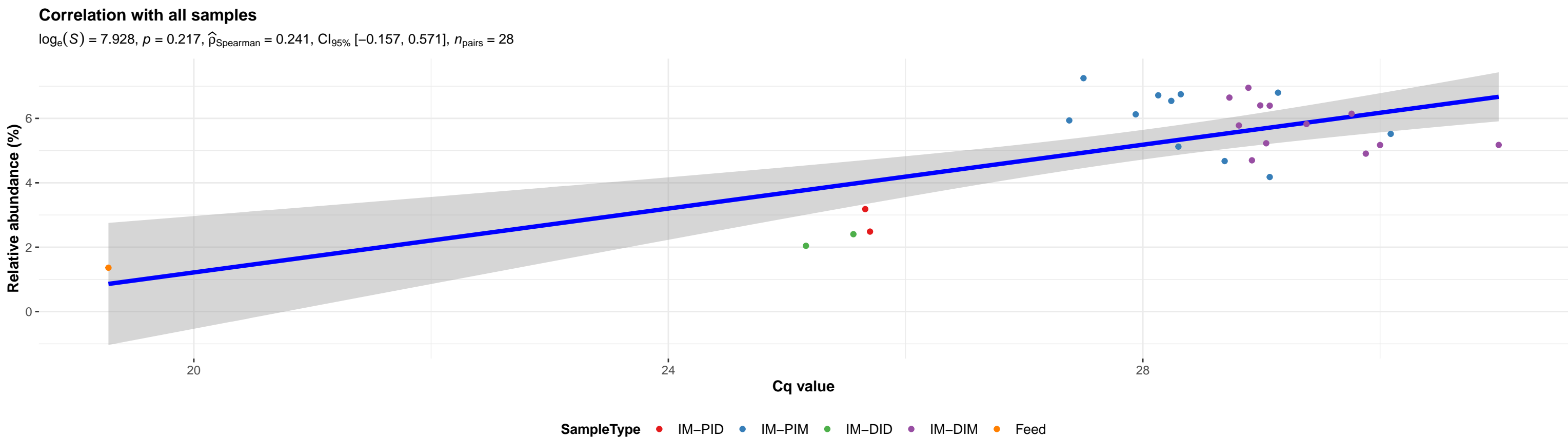
$\log_e(S) = 5.384$, $p = 0.457$, $\hat{\rho}_{\text{Spearman}} = 0.238$, $CI_{95\%} [-0.406, 0.724]$, $n_{\text{pairs}} = 12$



Correlation within: Feed



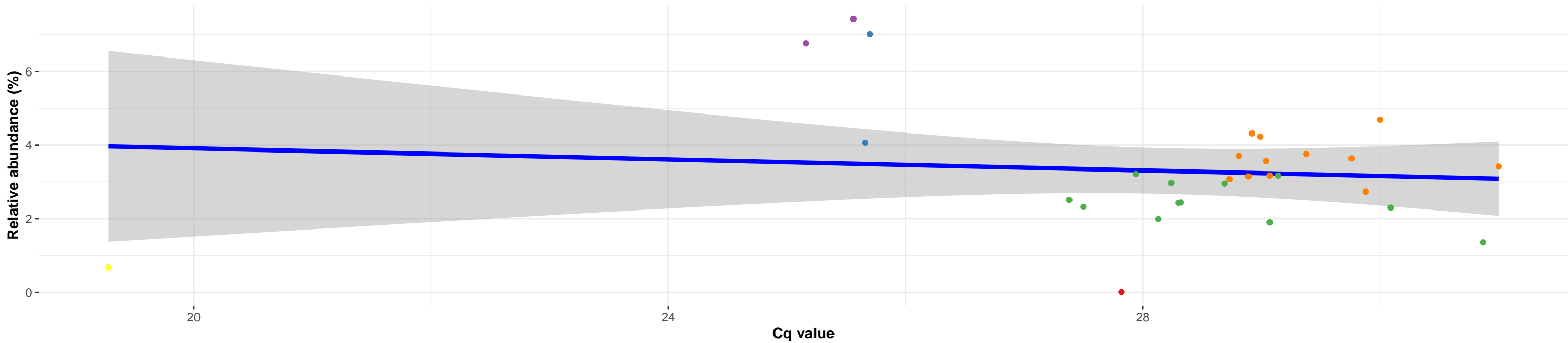
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium aurimucosum ATCC 700975



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

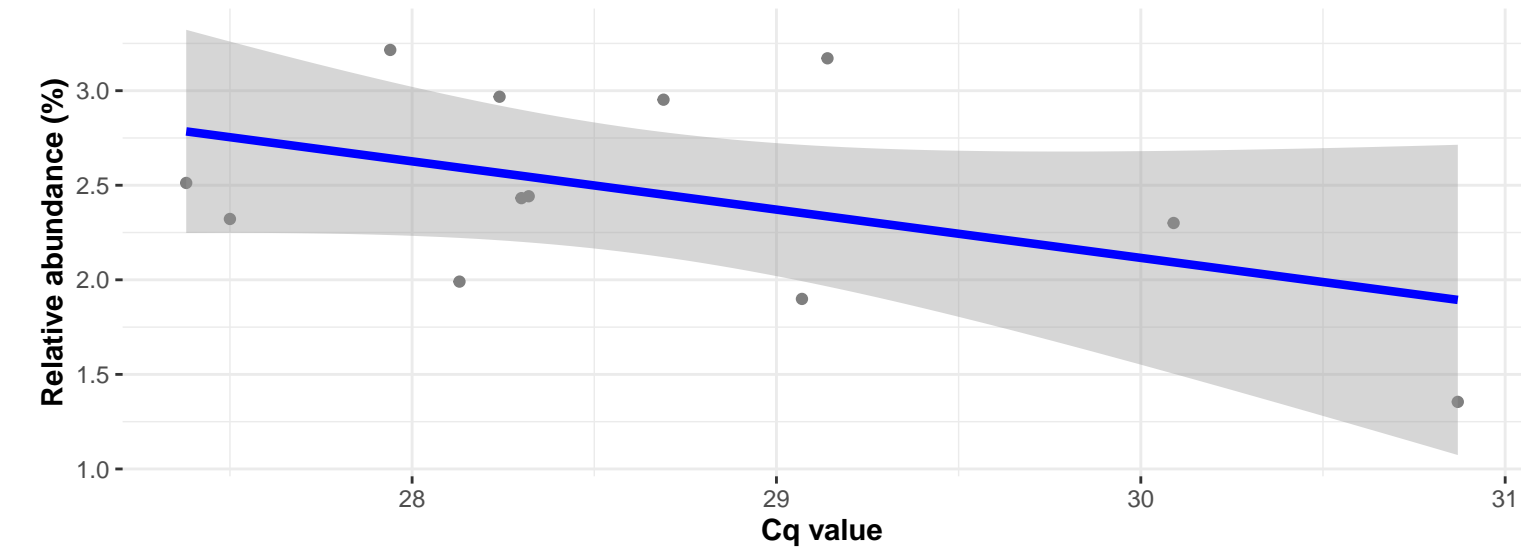
Correlation with all samples

$\log_e(S) = 8.441$, $p = 0.872$, $\hat{\rho}_{\text{Spearman}} = -0.031$, $CI_{95\%} [-0.396, 0.343]$, $n_{\text{pairs}} = 30$



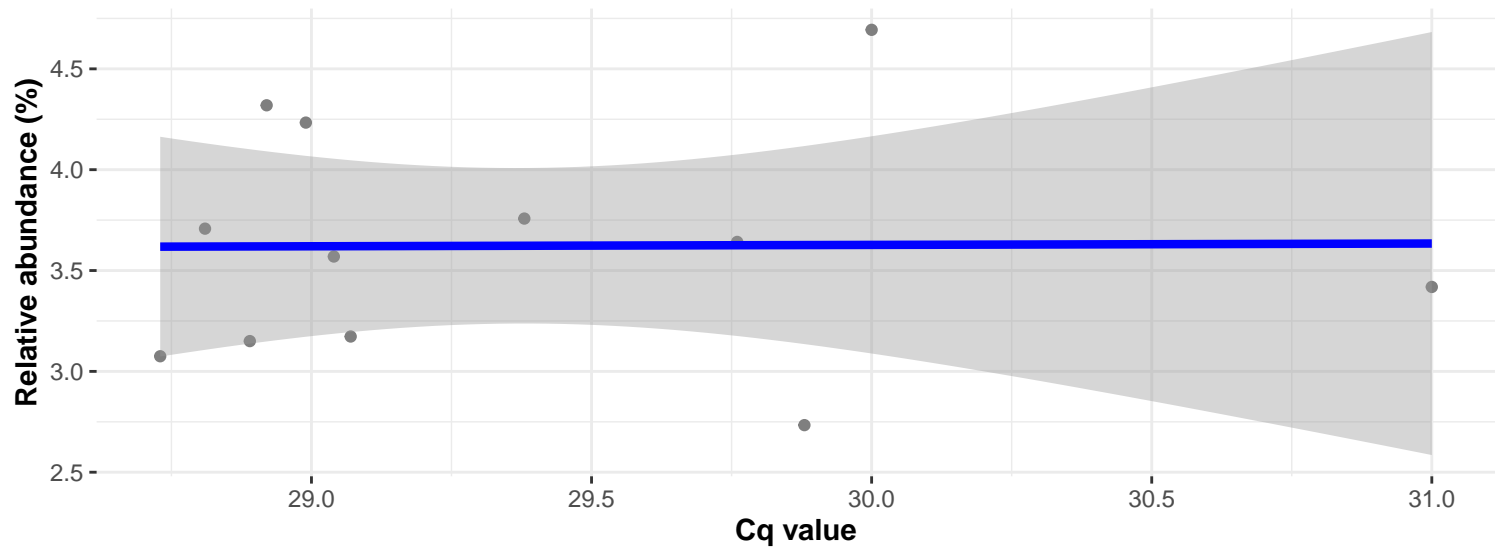
Correlation within: IM-PIM

$\log_e(S) = 5.956$, $p = 0.265$, $\hat{\rho}_{\text{Spearman}} = -0.350$, $CI_{95\%} [-0.777, 0.298]$, $n_{\text{pairs}} = 12$

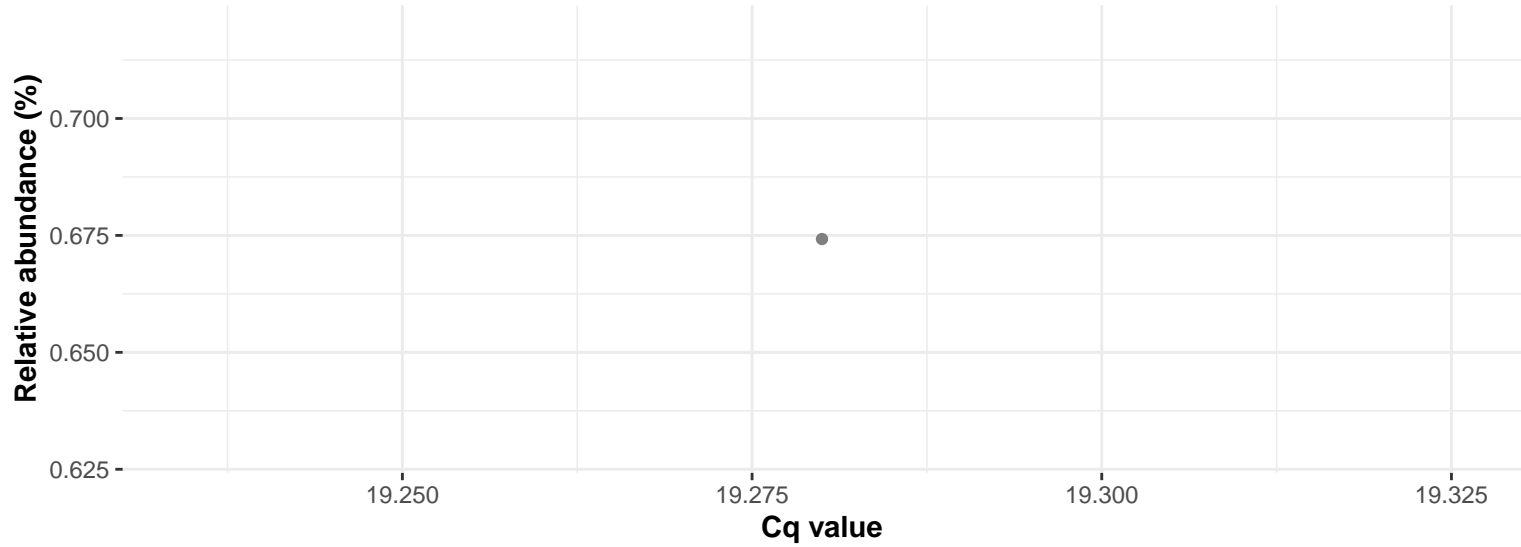


Correlation within: IM-DIM

$\log_e(S) = 5.545$, $p = 0.746$, $\hat{\rho}_{\text{Spearman}} = 0.105$, $CI_{95\%} [-0.513, 0.652]$, $n_{\text{pairs}} = 12$



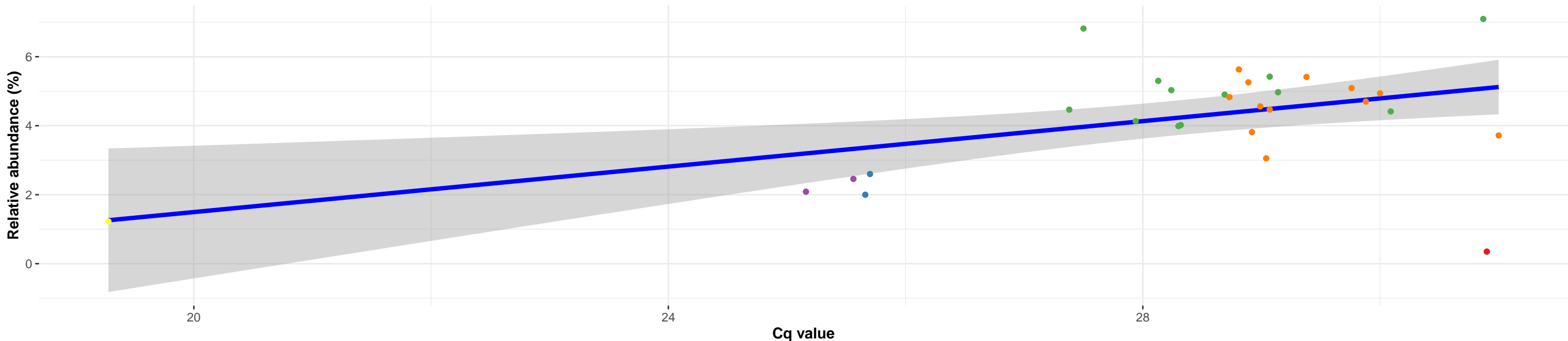
Correlation within: Feed



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

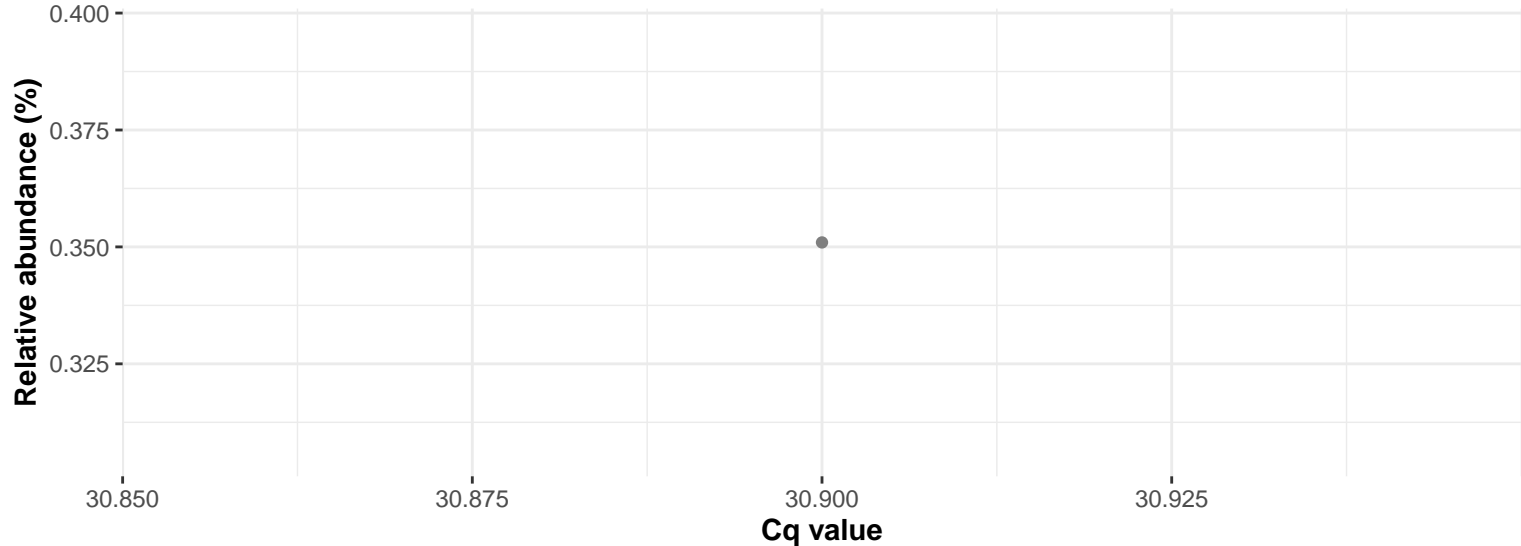
Correlation with all samples

$\log_e(S) = 8.047$, $p = 0.102$, $\hat{\rho}_{\text{Spearman}} = 0.305$, $\text{CI}_{95\%} [-0.074, 0.606]$, $n_{\text{pairs}} = 30$



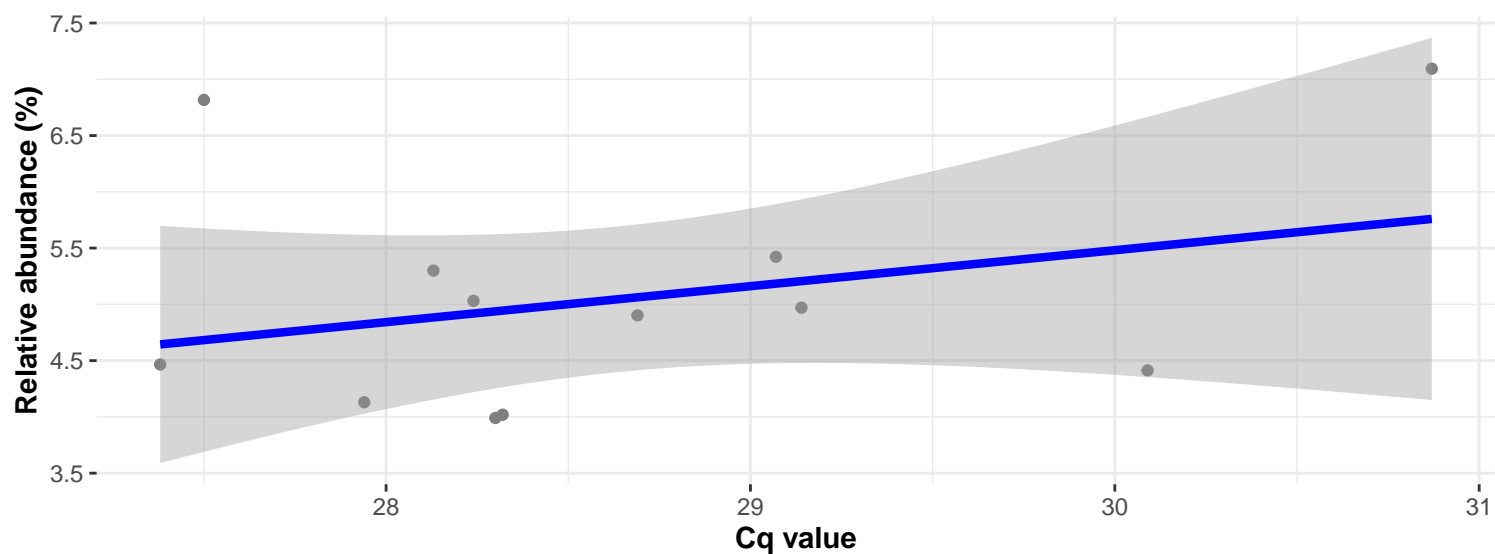
SampleType REF-PIM IM-PID IM-PIM IM-DID IM-DIM Feed

Correlation within: REF-PIM



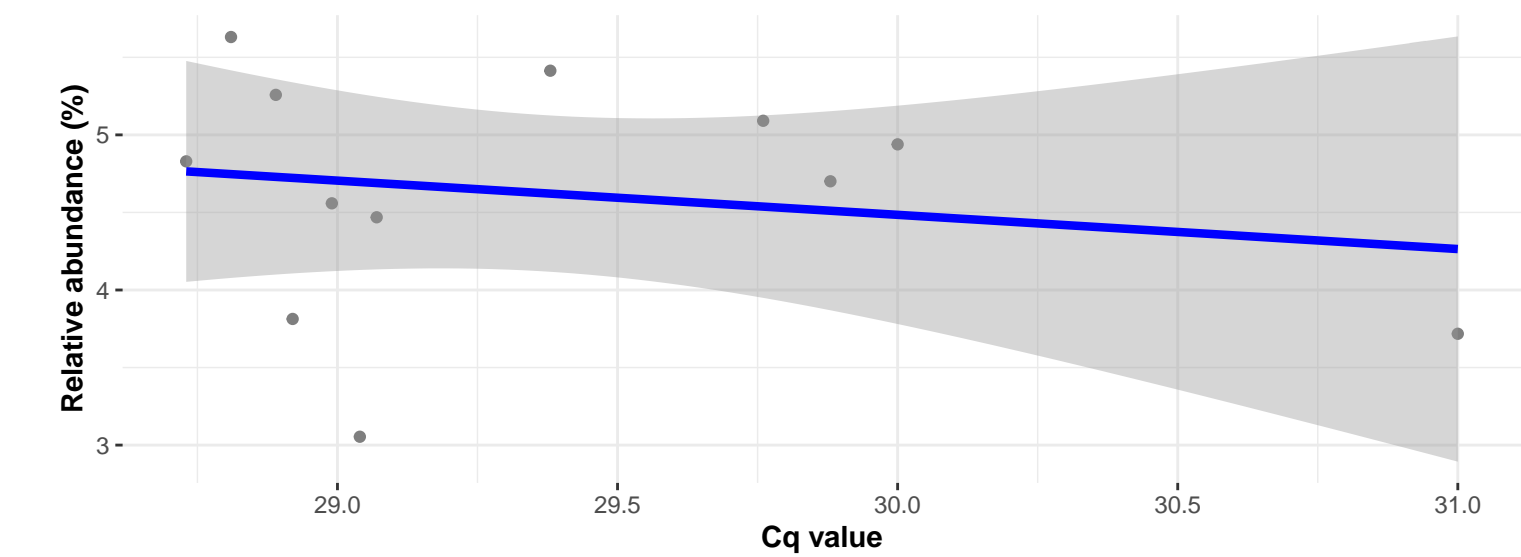
Correlation within: IM-PIM

$\log_e(S) = 5.497$, $p = 0.649$, $\hat{\rho}_{\text{Spearman}} = 0.147$, $\text{CI}_{95\%} [-0.481, 0.675]$, $n_{\text{pairs}} = 12$

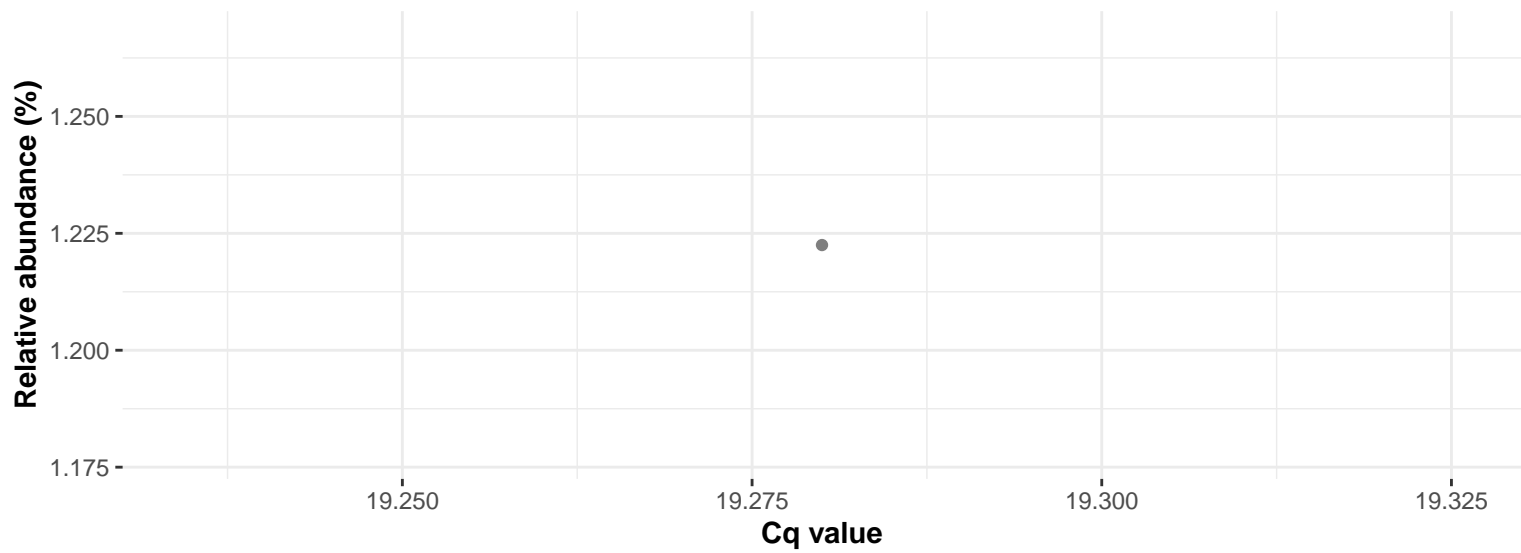


Correlation within: IM-DIM

$\log_e(S) = 5.869$, $p = 0.457$, $\hat{\rho}_{\text{Spearman}} = -0.238$, $\text{CI}_{95\%} [-0.724, 0.406]$, $n_{\text{pairs}} = 12$



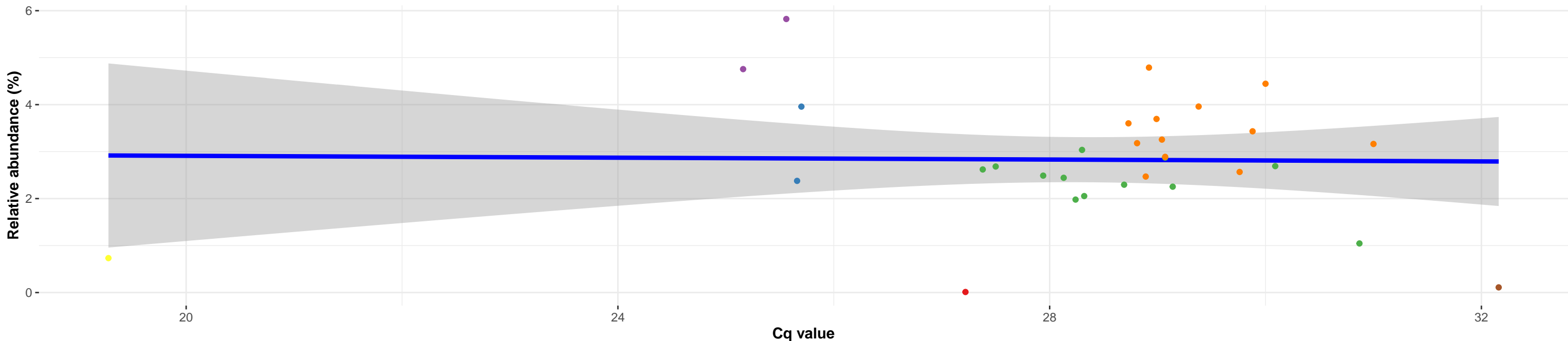
Correlation within: Feed



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

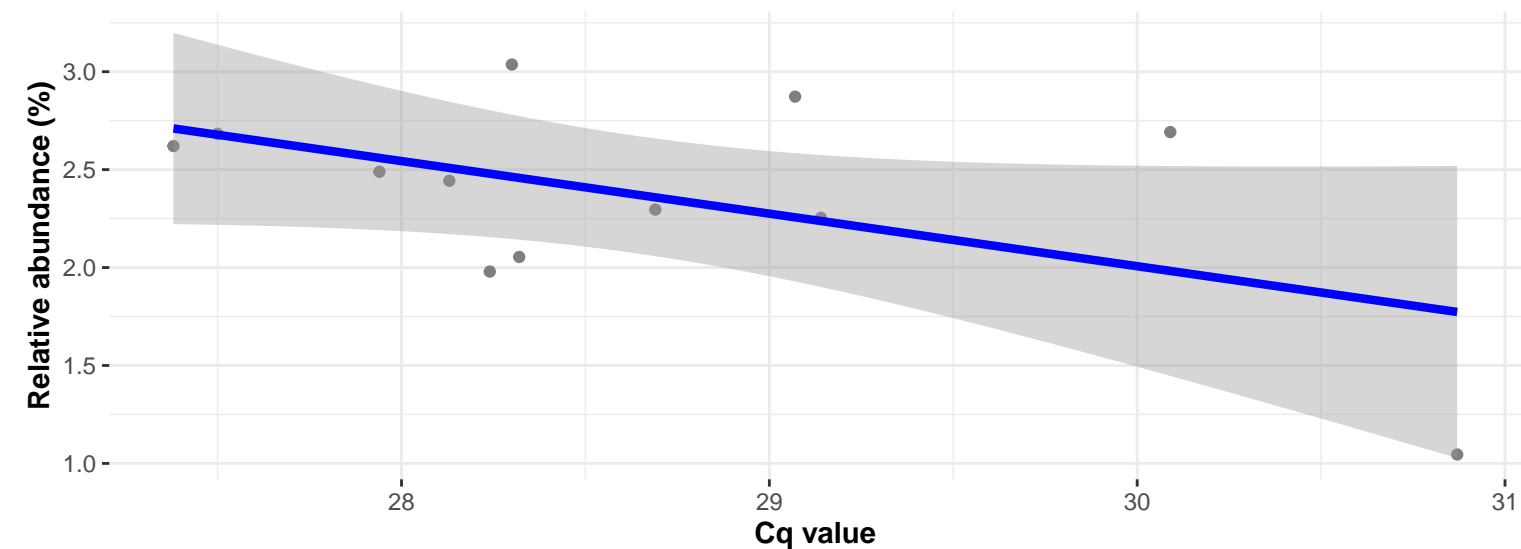
Correlation with all samples

$\log_e(S) = 8.471$, $p = 0.840$, $\hat{\rho}_{\text{Spearman}} = 0.038$, $CI_{95\%} [-0.331, 0.396]$, $n_{\text{pairs}} = 31$



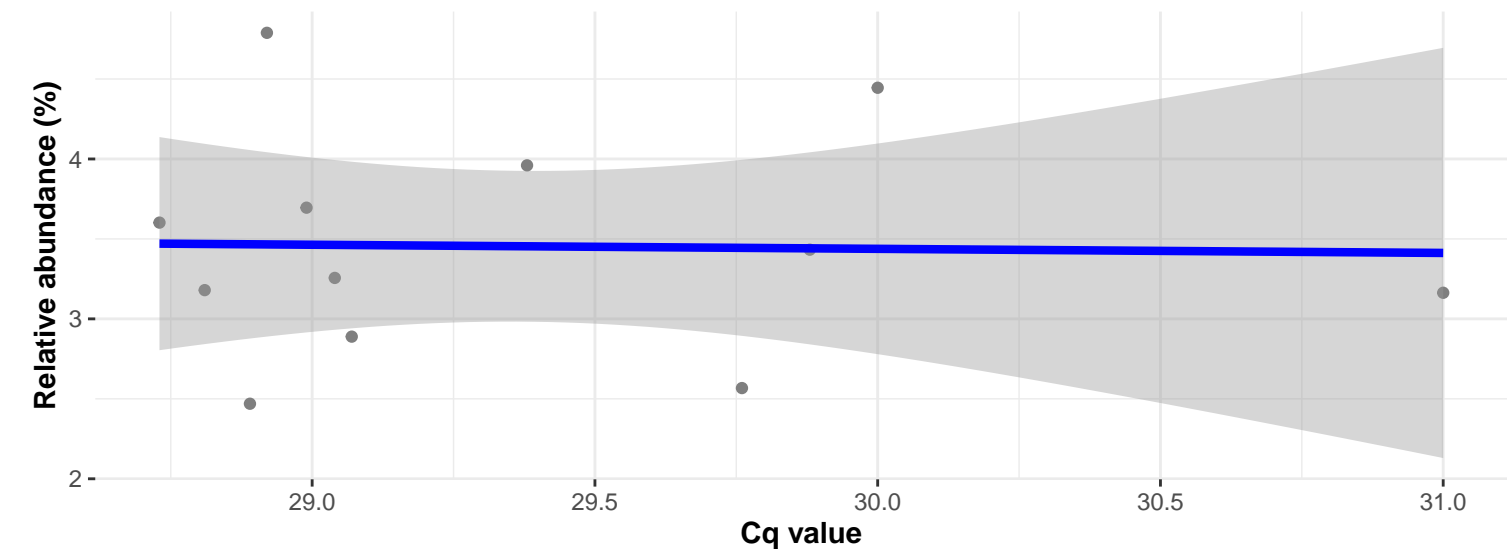
Correlation within: IM-PIM

$\log_e(S) = 5.858$, $p = 0.484$, $\hat{\rho}_{\text{Spearman}} = -0.224$, $CI_{95\%} [-0.716, 0.418]$, $n_{\text{pairs}} = 12$

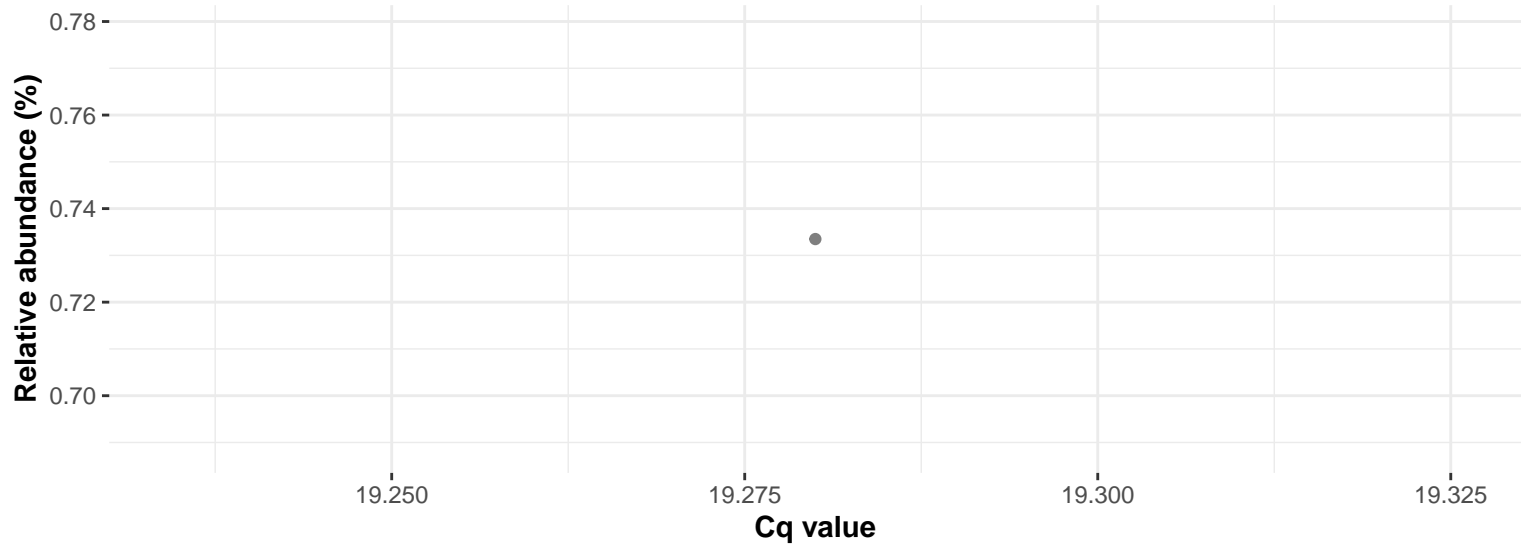


Correlation within: IM-DIM

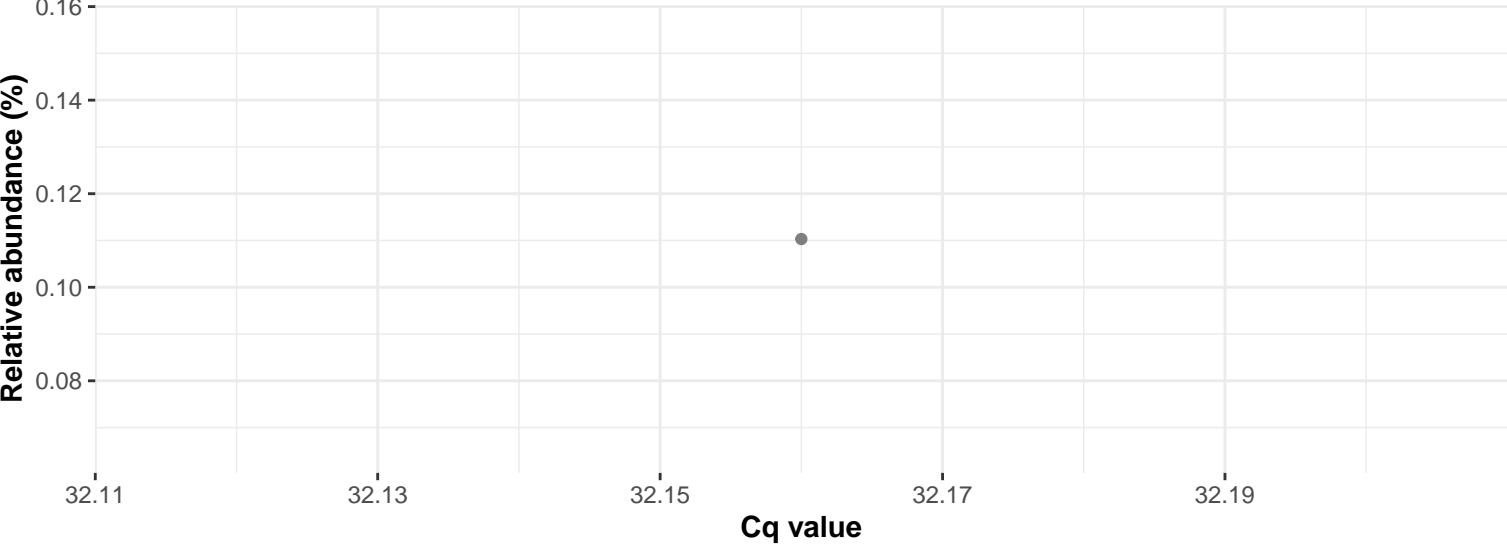
$\log_e(S) = 5.649$, $p = 0.983$, $\hat{\rho}_{\text{Spearman}} = 0.007$, $CI_{95\%} [-0.582, 0.591]$, $n_{\text{pairs}} = 12$



Correlation within: Feed



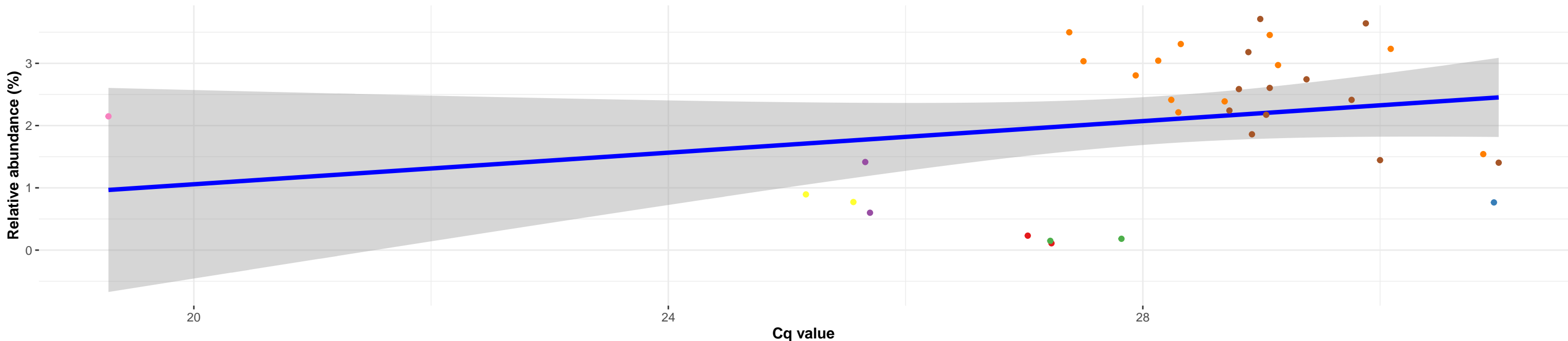
Correlation within: Water



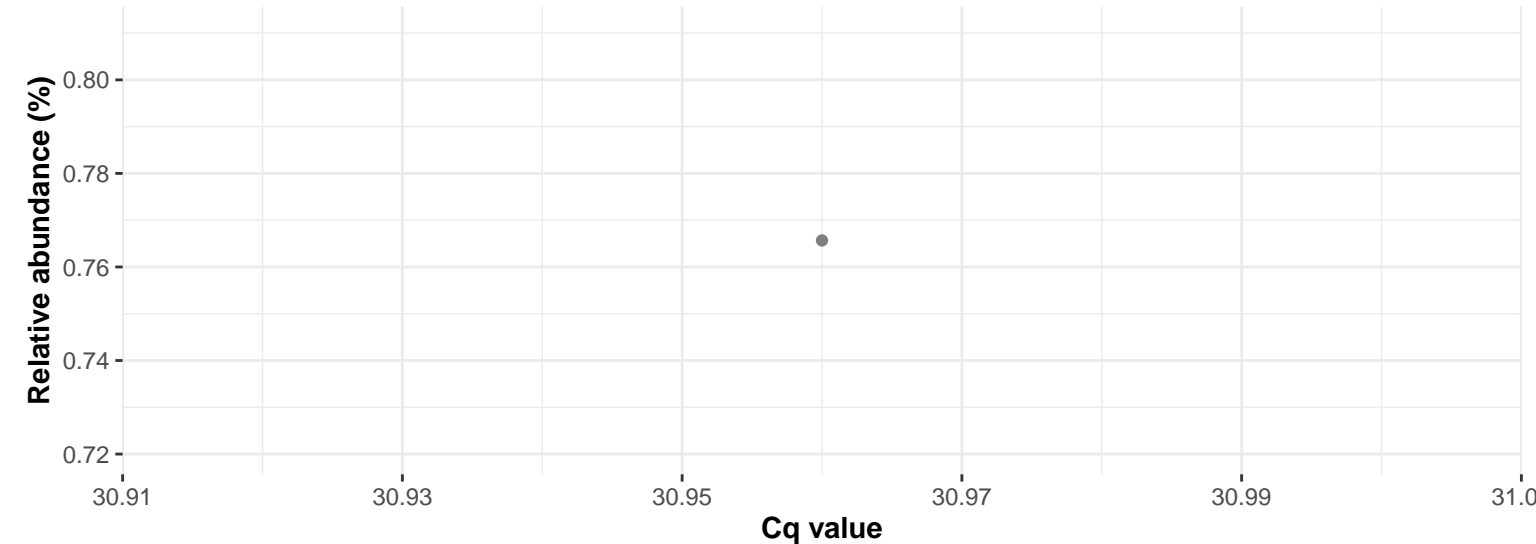
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; NA

Correlation with all samples

$\log_e(S) = 8.379$, $p = 0.053$, $\hat{\rho}_{\text{Spearman}} = 0.335$, $\text{CI}_{95\%} [-0.014, 0.611]$, $n_{\text{pairs}} = 34$

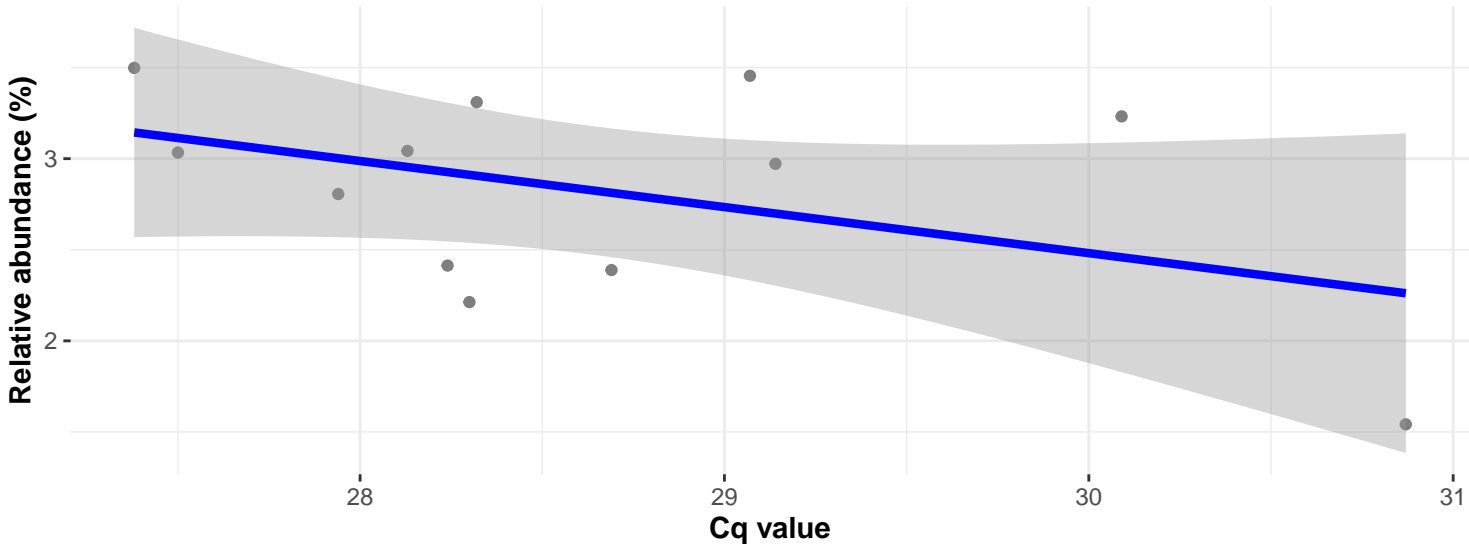


Correlation within: REF-PIM



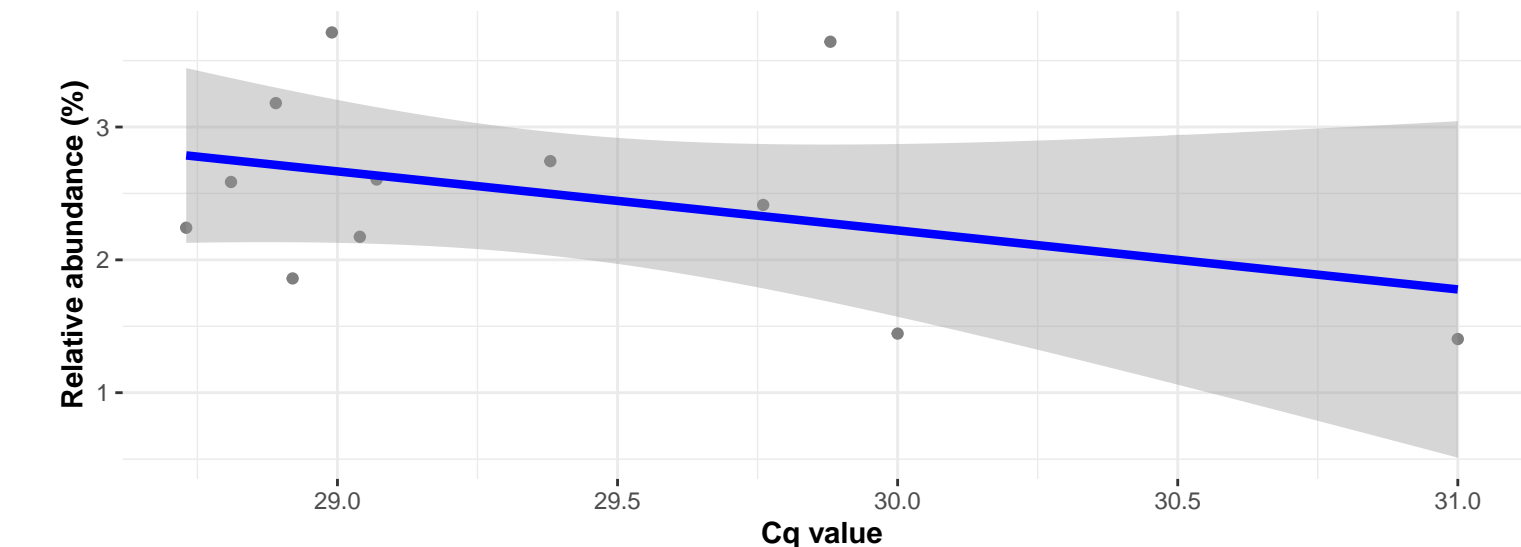
Correlation within: IM-PIM

$\log_e(S) = 5.892$, $p = 0.404$, $\hat{\rho}_{\text{Spearman}} = -0.266$, $\text{CI}_{95\%} [-0.737, 0.380]$, $n_{\text{pairs}} = 12$

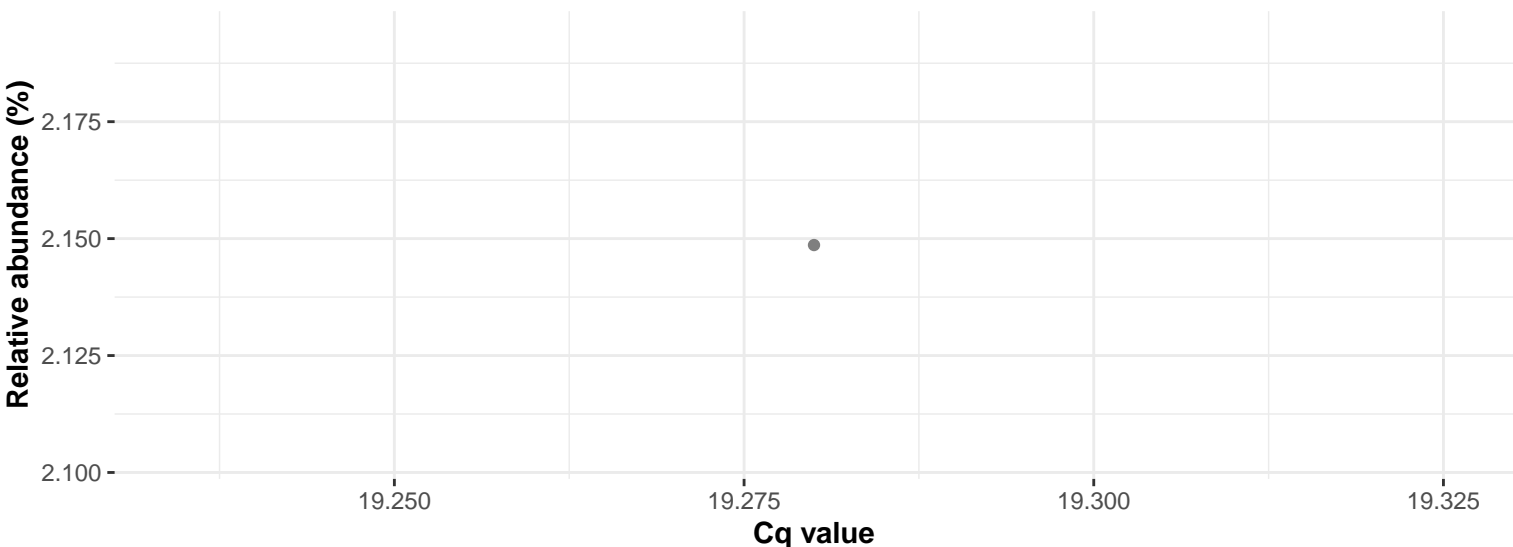


Correlation within: IM-DIM

$\log_e(S) = 5.881$, $p = 0.430$, $\hat{\rho}_{\text{Spearman}} = -0.252$, $\text{CI}_{95\%} [-0.731, 0.393]$, $n_{\text{pairs}} = 12$



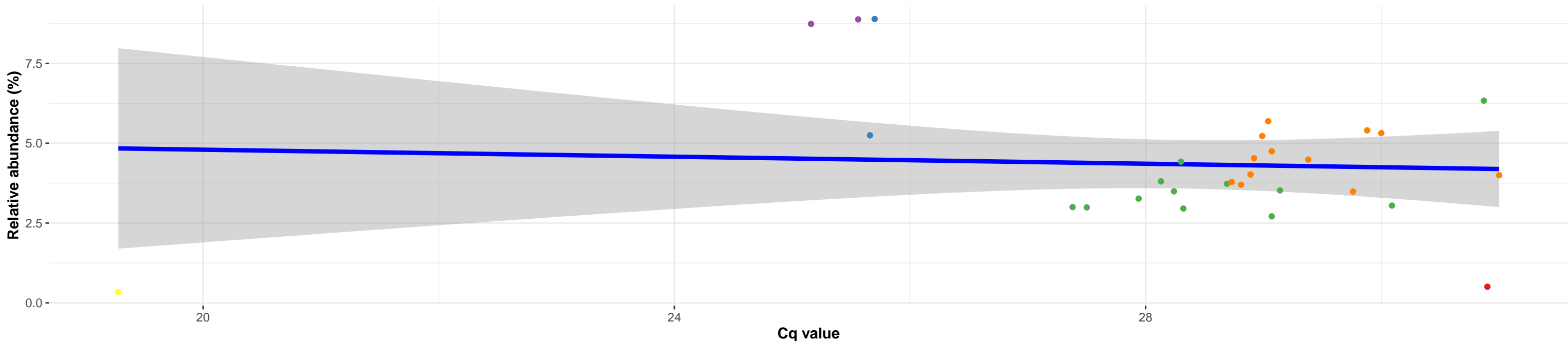
Correlation within: Feed



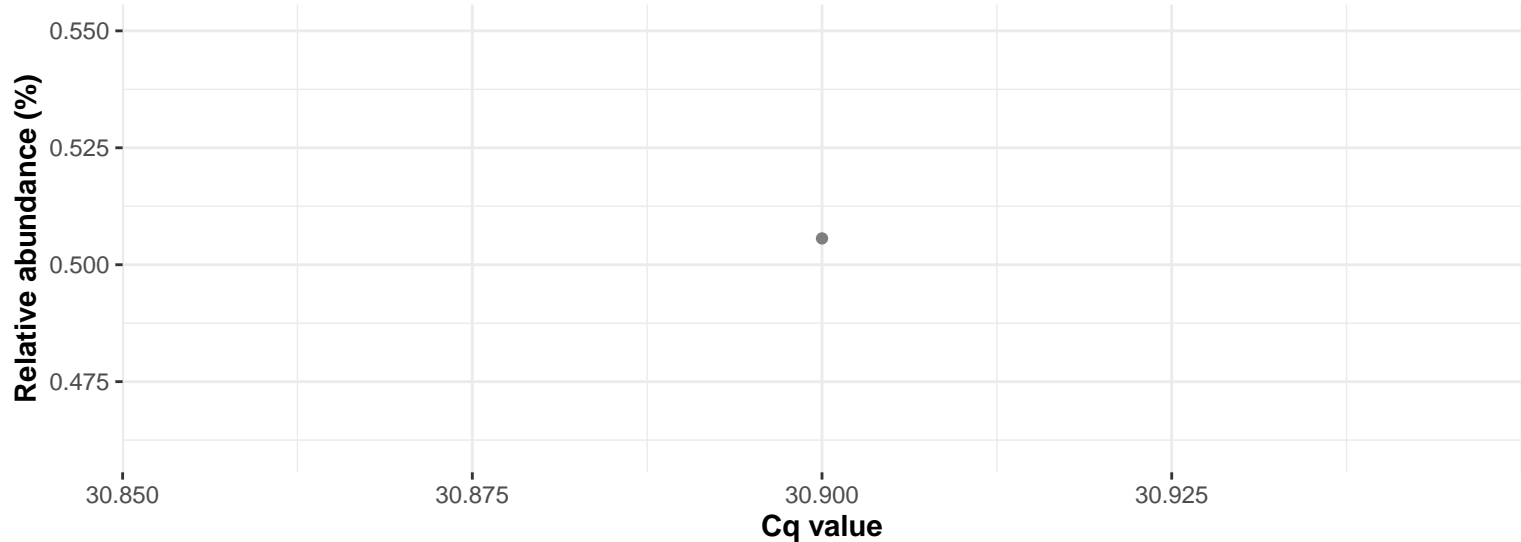
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

Correlation with all samples

$\log_e(S) = 8.428$, $p = 0.927$, $\hat{\rho}_{\text{Spearman}} = -0.018$, $CI_{95\%} [-0.385, 0.355]$, $n_{\text{pairs}} = 30$

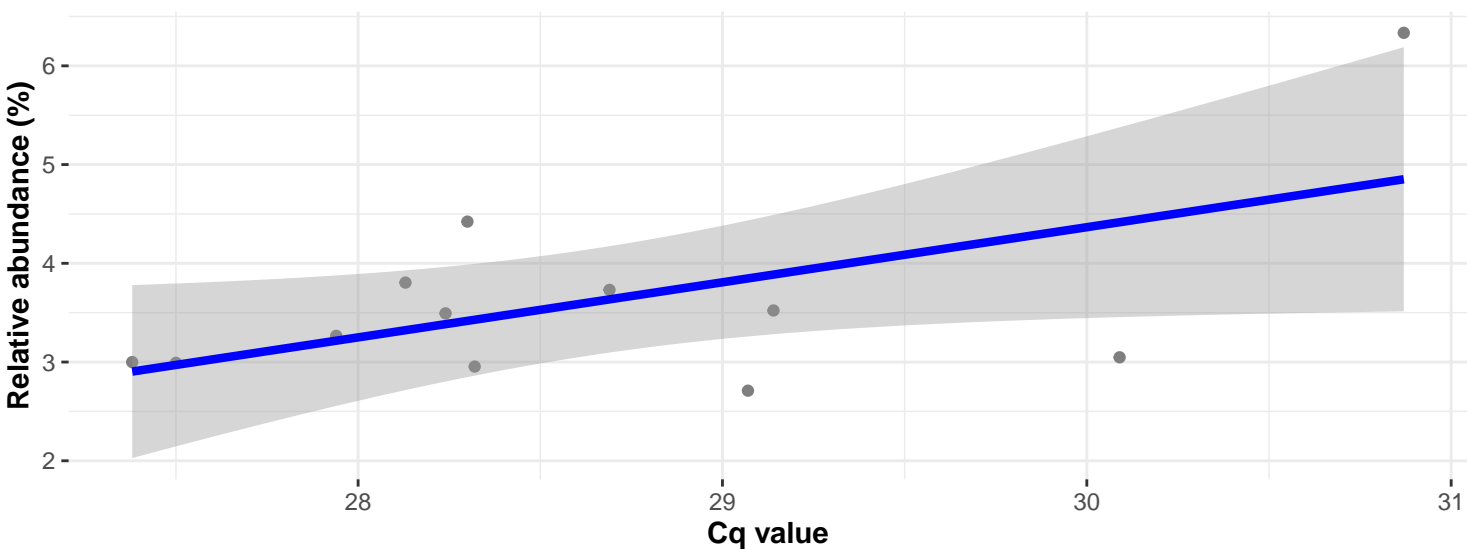


Correlation within: REF-PIM



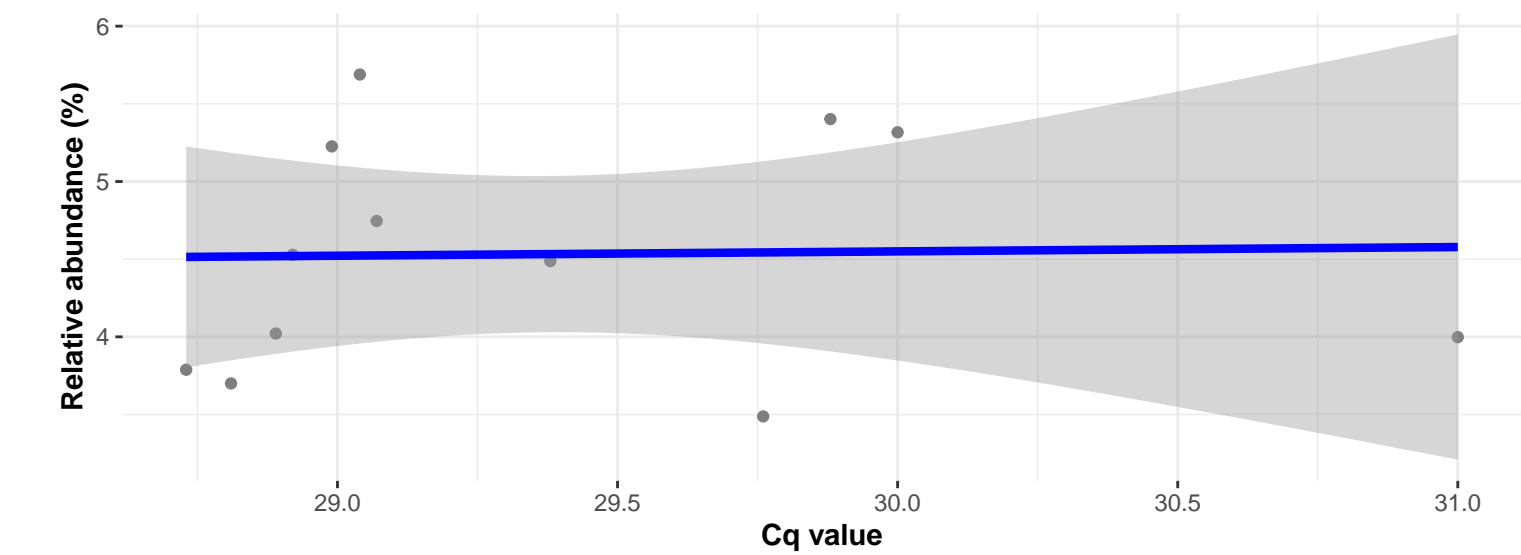
Correlation within: IM-PIM

$\log_e(S) = 5.366$, $p = 0.430$, $\hat{\rho}_{\text{Spearman}} = 0.252$, $CI_{95\%} [-0.393, 0.731]$, $n_{\text{pairs}} = 12$

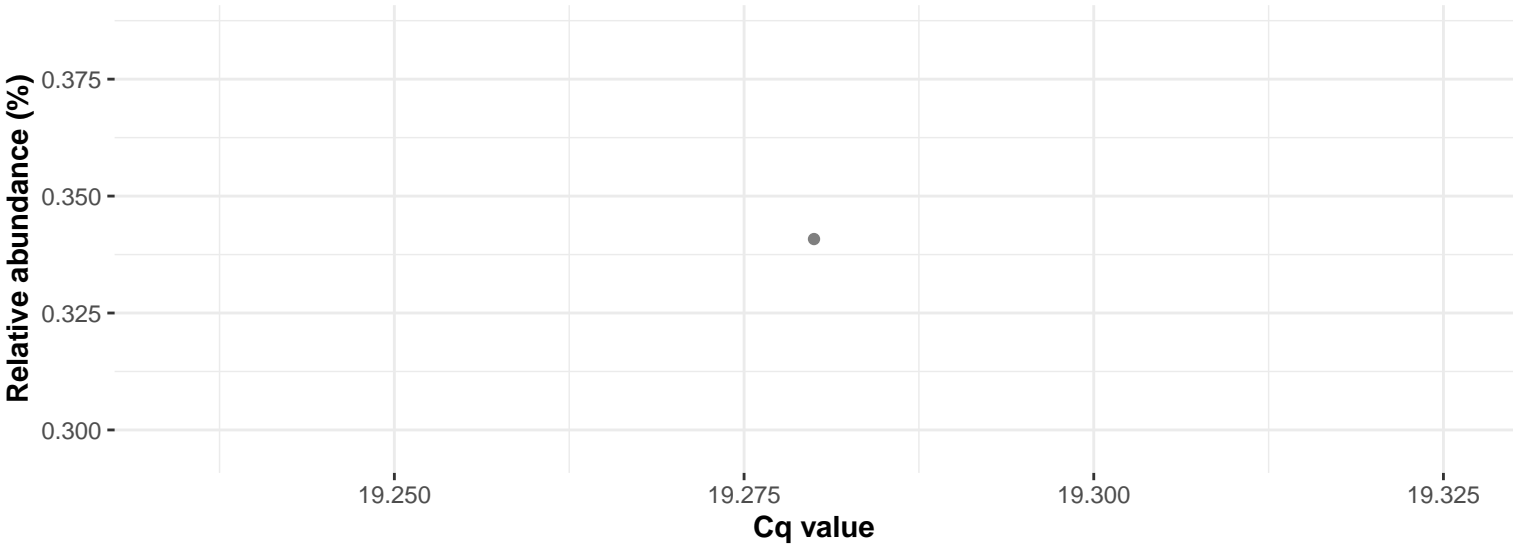


Correlation within: IM-DIM

$\log_e(S) = 5.318$, $p = 0.366$, $\hat{\rho}_{\text{Spearman}} = 0.287$, $CI_{95\%} [-0.361, 0.748]$, $n_{\text{pairs}} = 12$



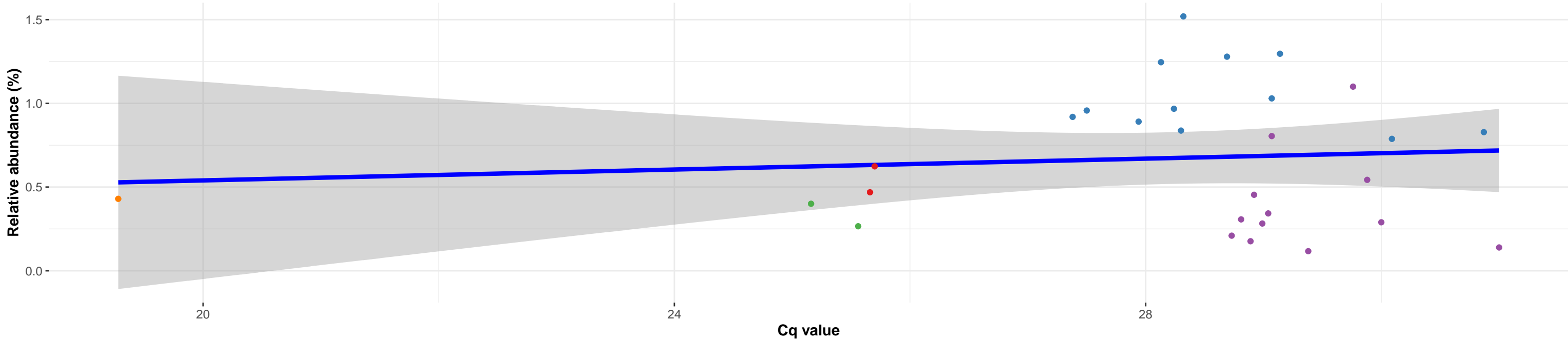
Correlation within: Feed



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

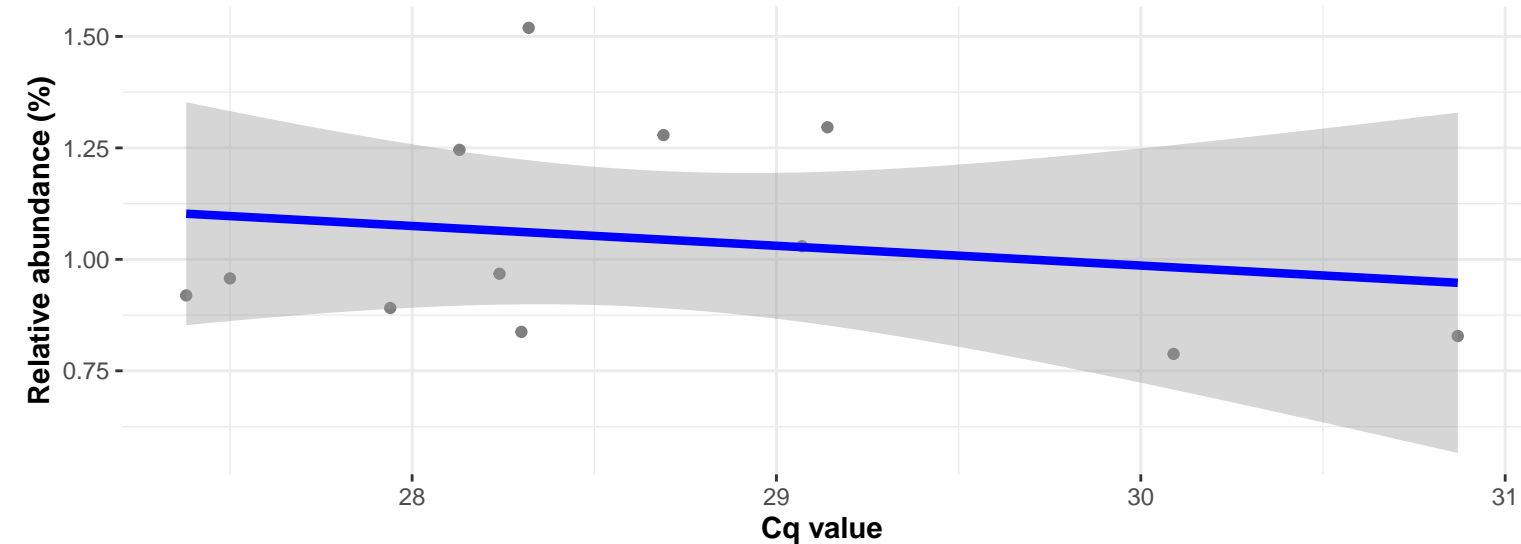
Correlation with all samples

$\log_e(S) = 8.415$, $p = 0.563$, $\hat{\rho}_{\text{Spearman}} = -0.112$, $CI_{95\%} [-0.469, 0.276]$, $n_{\text{pairs}} = 29$



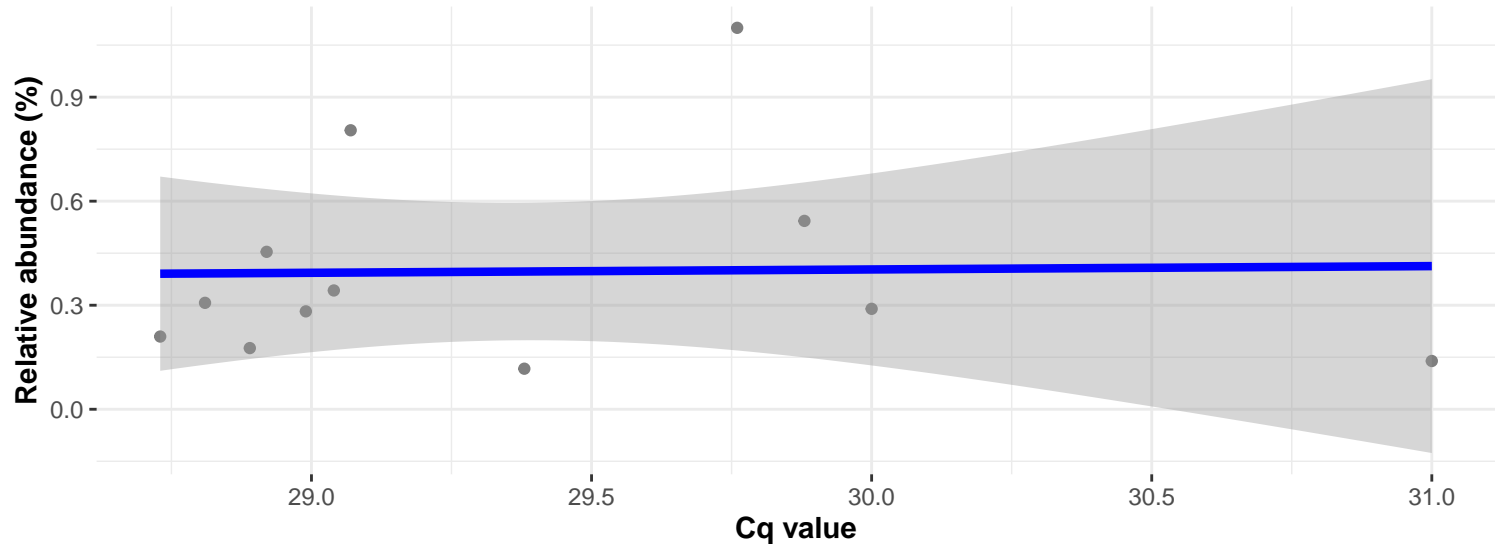
Correlation within: IM-PIM

$\log_e(S) = 5.710$, $p = 0.863$, $\hat{\rho}_{\text{Spearman}} = -0.056$, $CI_{95\%} [-0.622, 0.549]$, $n_{\text{pairs}} = 12$

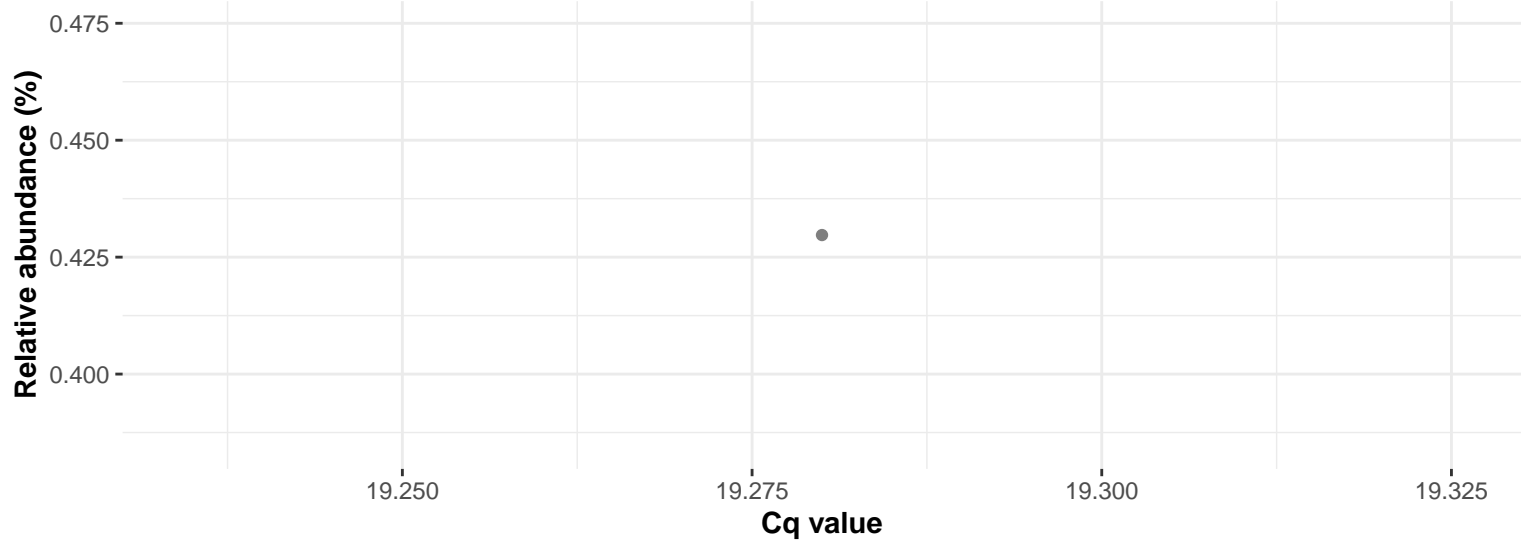


Correlation within: IM-DIM

$\log_e(S) = 5.568$, $p = 0.795$, $\hat{\rho}_{\text{Spearman}} = 0.084$, $CI_{95\%} [-0.529, 0.639]$, $n_{\text{pairs}} = 12$



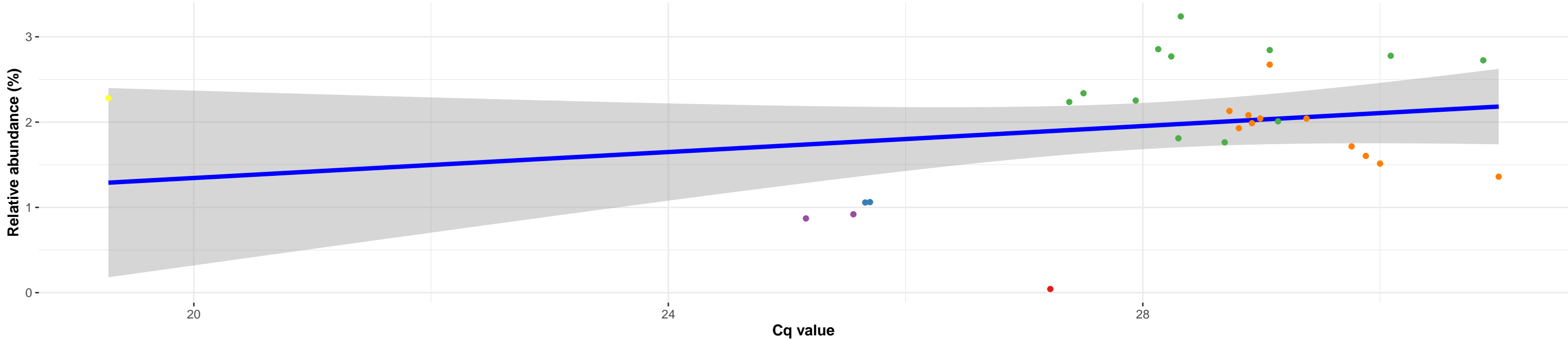
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Beutenbergiaceae; NA; NA

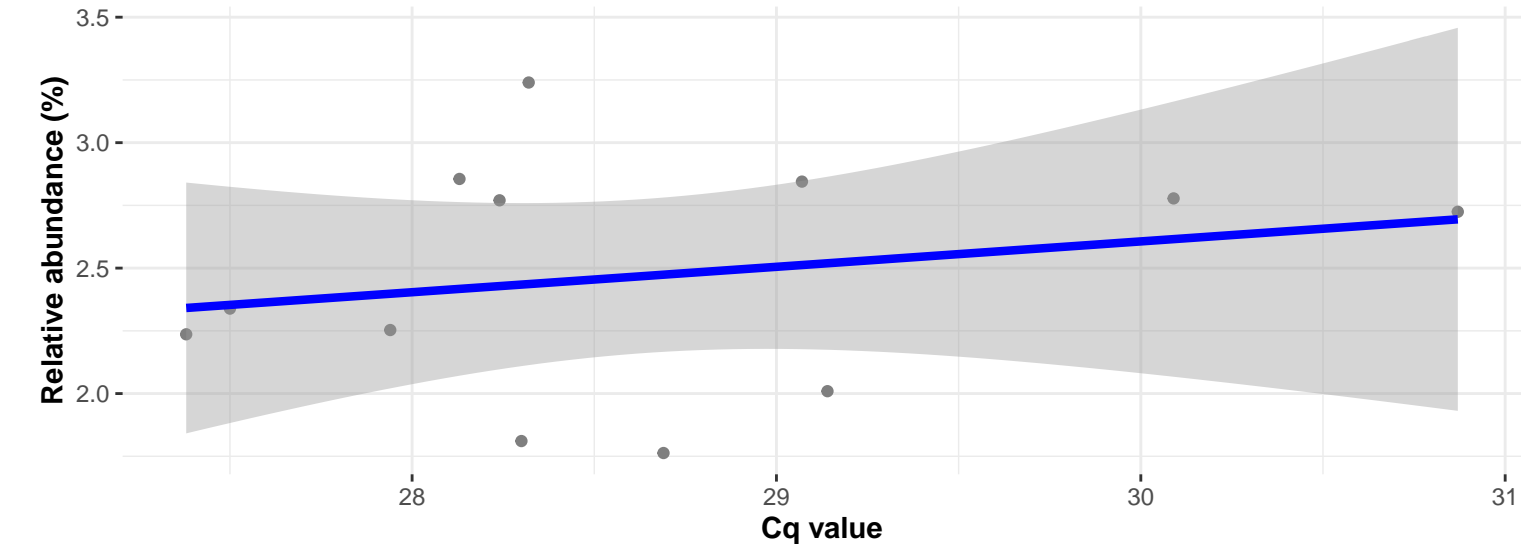
Correlation with all samples

$\log_e(S) = 8.113$, $p = 0.355$, $\hat{\rho}_{\text{Spearman}} = 0.178$, $\text{CI}_{95\%} [-0.212, 0.520]$, $n_{\text{pairs}} = 29$



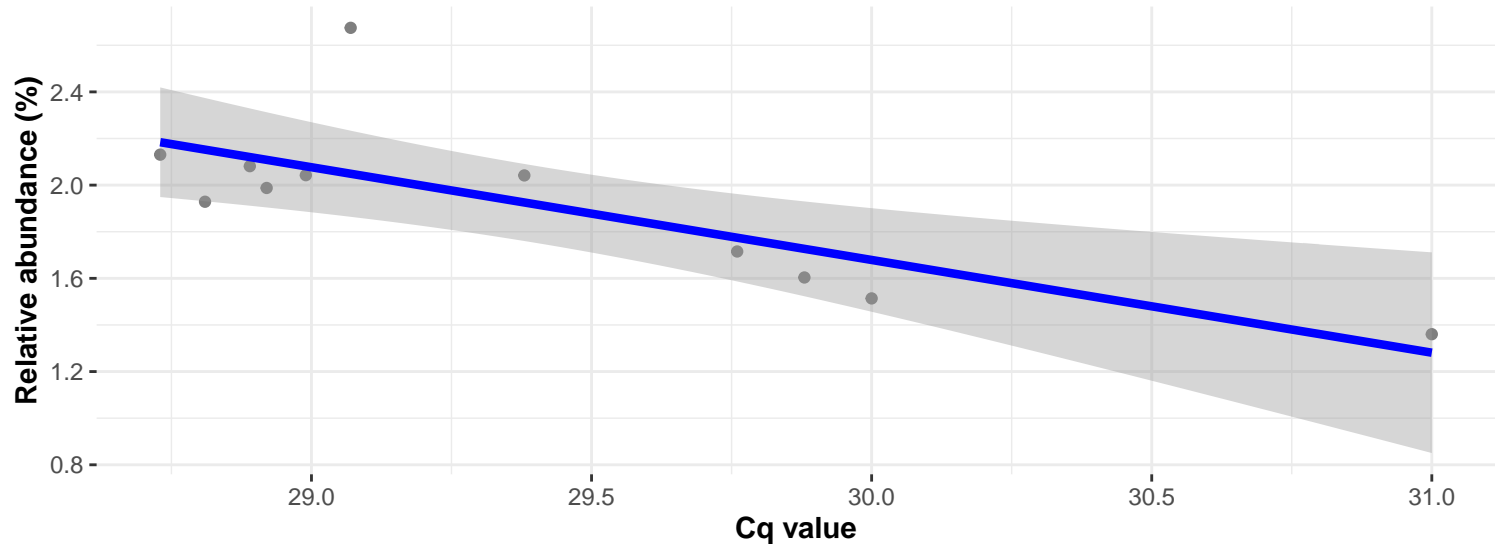
Correlation within: IM-PIM

$\log_e(S) = 5.545$, $p = 0.746$, $\hat{\rho}_{\text{Spearman}} = 0.105$, $\text{CI}_{95\%} [-0.513, 0.652]$, $n_{\text{pairs}} = 12$

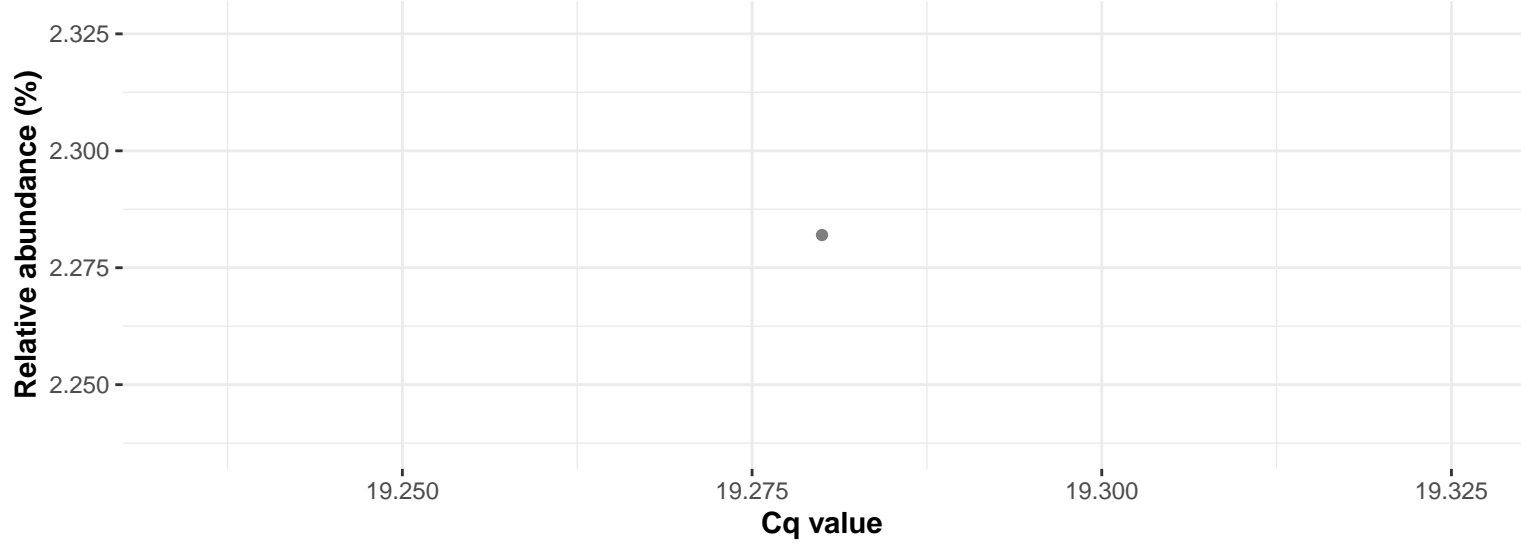


Correlation within: IM-DIM

$\log_e(S) = 5.940$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.727$, $\text{CI}_{95\%} [-0.927, -0.206]$, $n_{\text{pairs}} = 11$



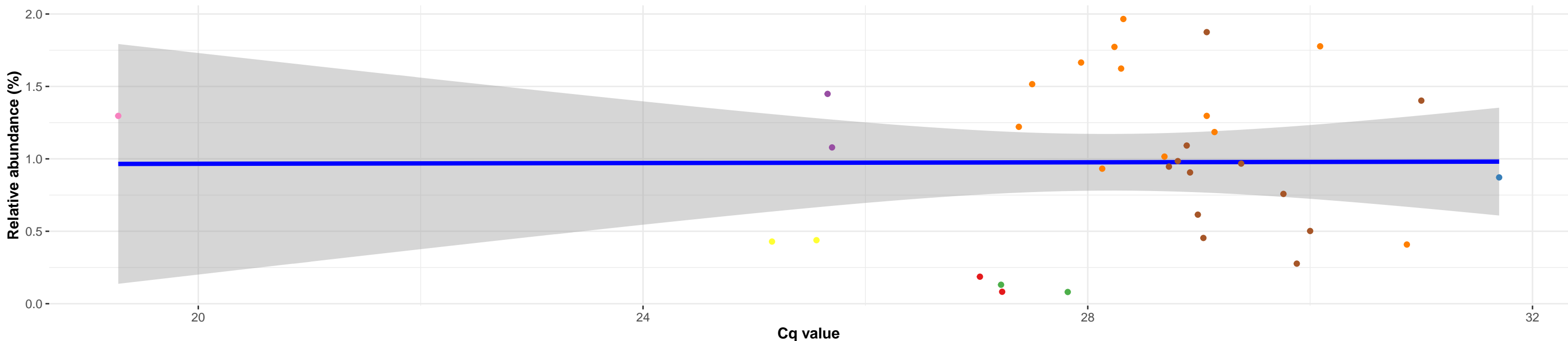
Correlation within: Feed



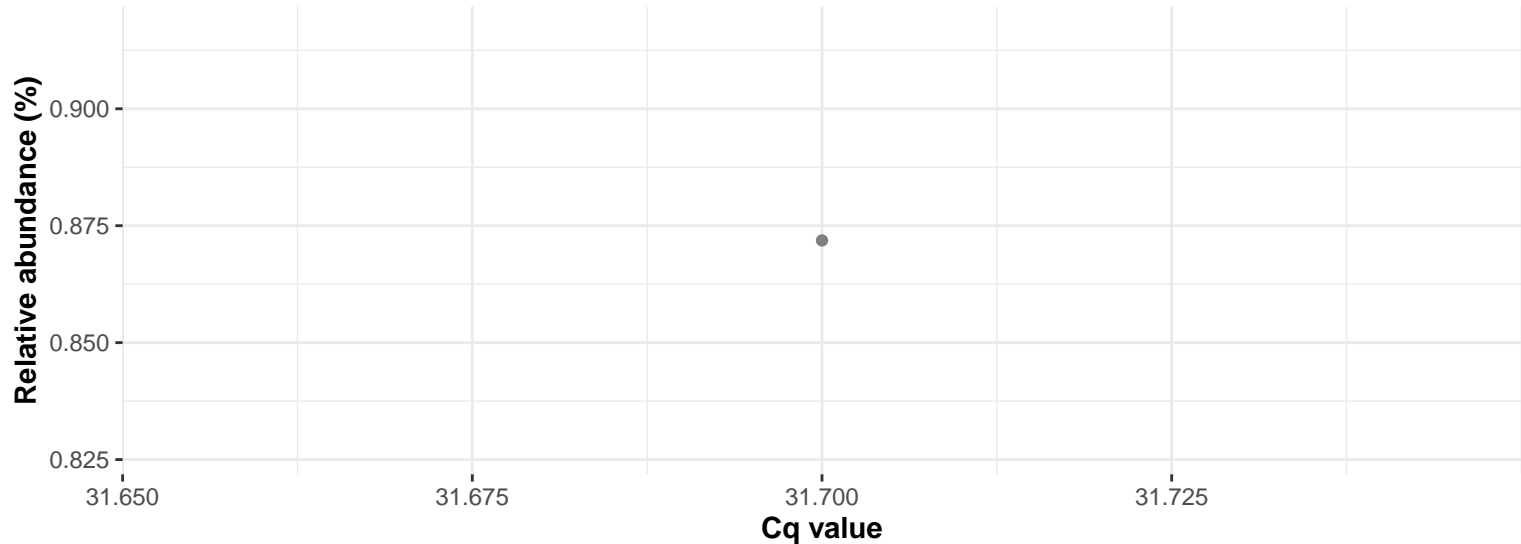
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 8.725$, $p = 0.739$, $\hat{\rho}_{\text{Spearman}} = 0.059$, $CI_{95\%} [-0.294, 0.398]$, $n_{\text{pairs}} = 34$

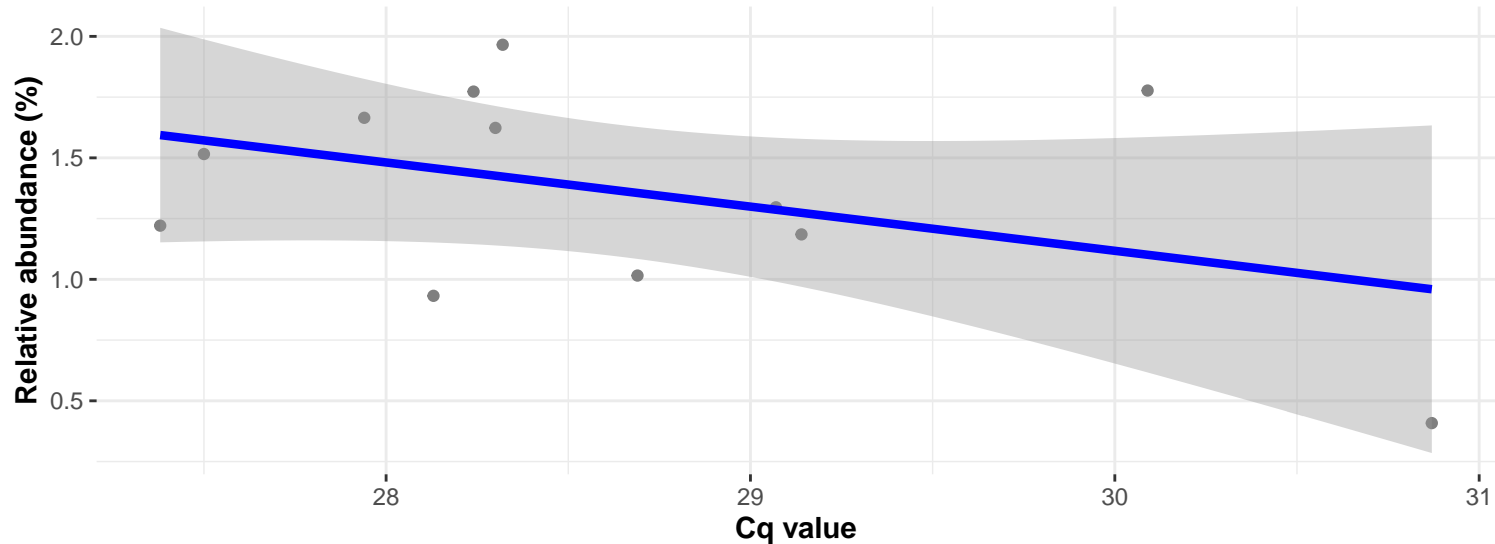


Correlation within: REF-PIM



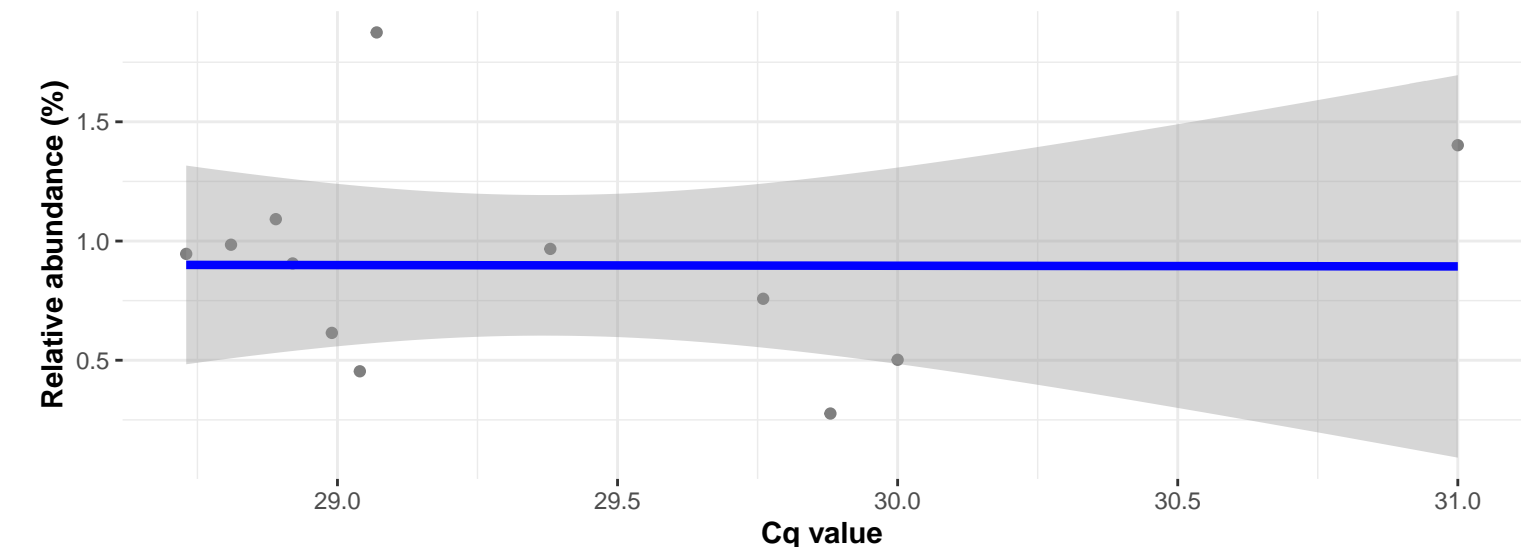
Correlation within: IM-PIM

$\log_e(S) = 5.787$, $p = 0.665$, $\hat{\rho}_{\text{Spearman}} = -0.140$, $CI_{95\%} [-0.671, 0.487]$, $n_{\text{pairs}} = 12$

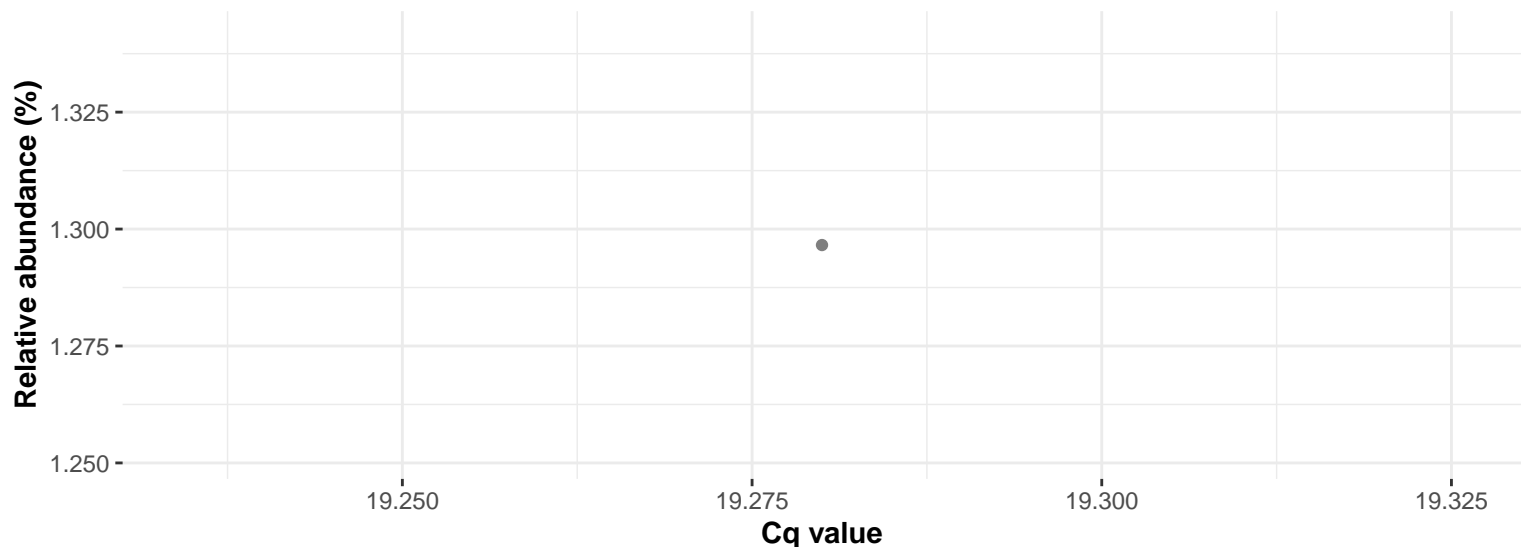


Correlation within: IM-DIM

$\log_e(S) = 5.835$, $p = 0.542$, $\hat{\rho}_{\text{Spearman}} = -0.196$, $CI_{95\%} [-0.702, 0.442]$, $n_{\text{pairs}} = 12$



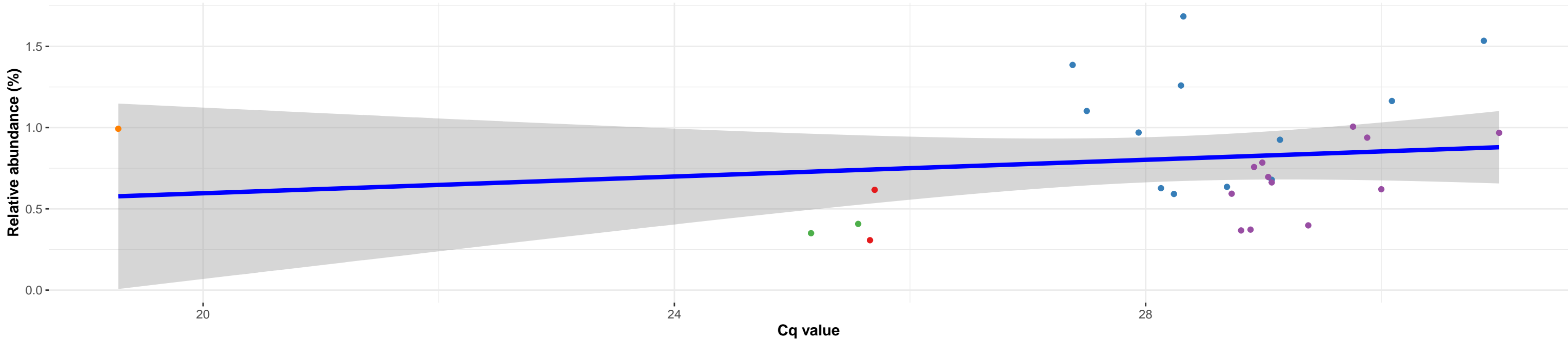
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; NA; NA

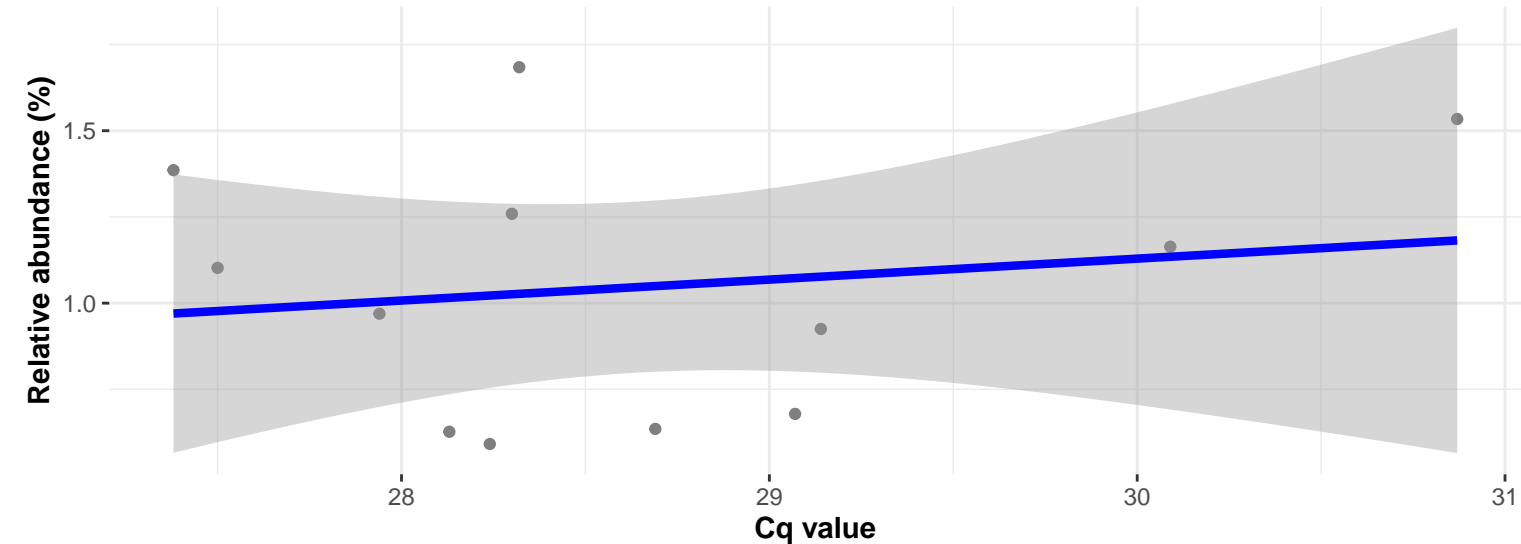
Correlation with all samples

$\log_e(S) = 8.026$, $p = 0.198$, $\hat{\rho}_{\text{Spearman}} = 0.246$, $CI_{95\%} [-0.144, 0.570]$, $n_{\text{pairs}} = 29$



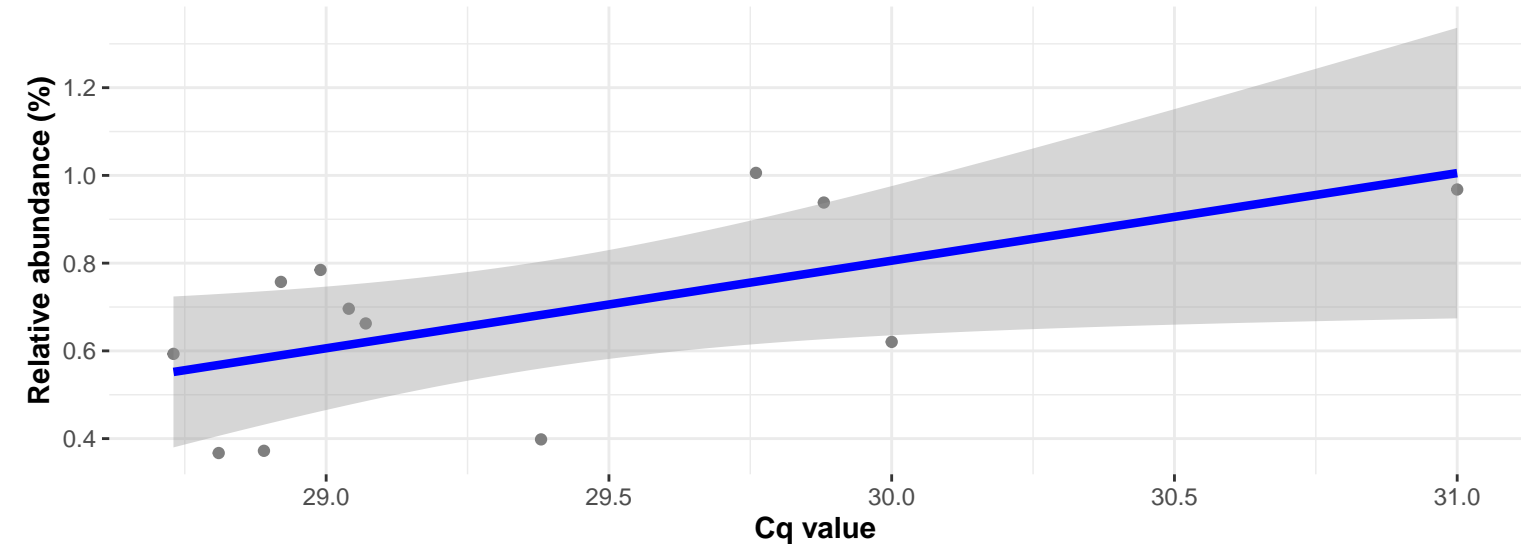
Correlation within: IM-PIM

$\log_e(S) = 5.537$, $p = 0.729$, $\hat{\rho}_{\text{Spearman}} = 0.112$, $CI_{95\%} [-0.508, 0.656]$, $n_{\text{pairs}} = 12$

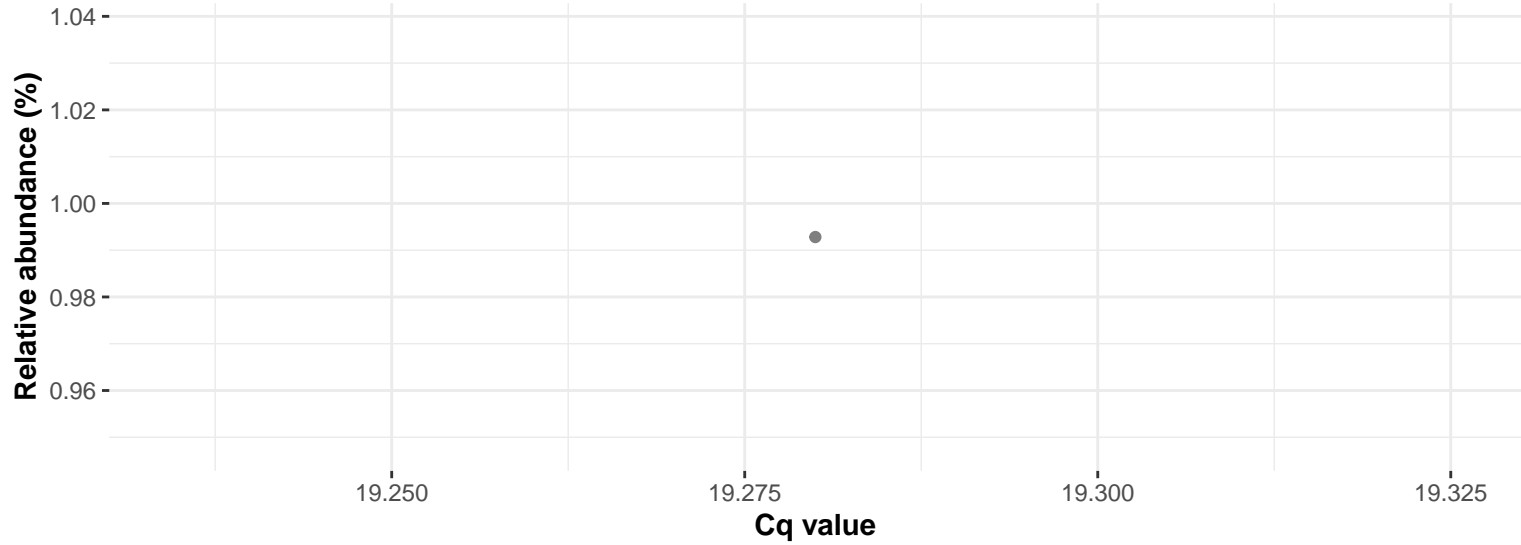


Correlation within: IM-DIM

$\log_e(S) = 4.754$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.594$, $CI_{95\%} [0.012, 0.876]$, $n_{\text{pairs}} = 12$



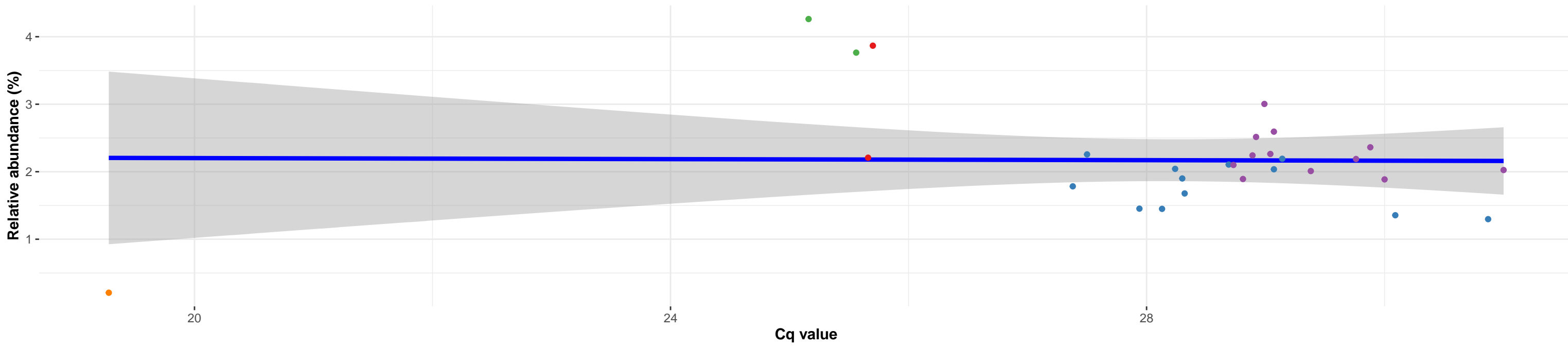
Correlation within: Feed



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

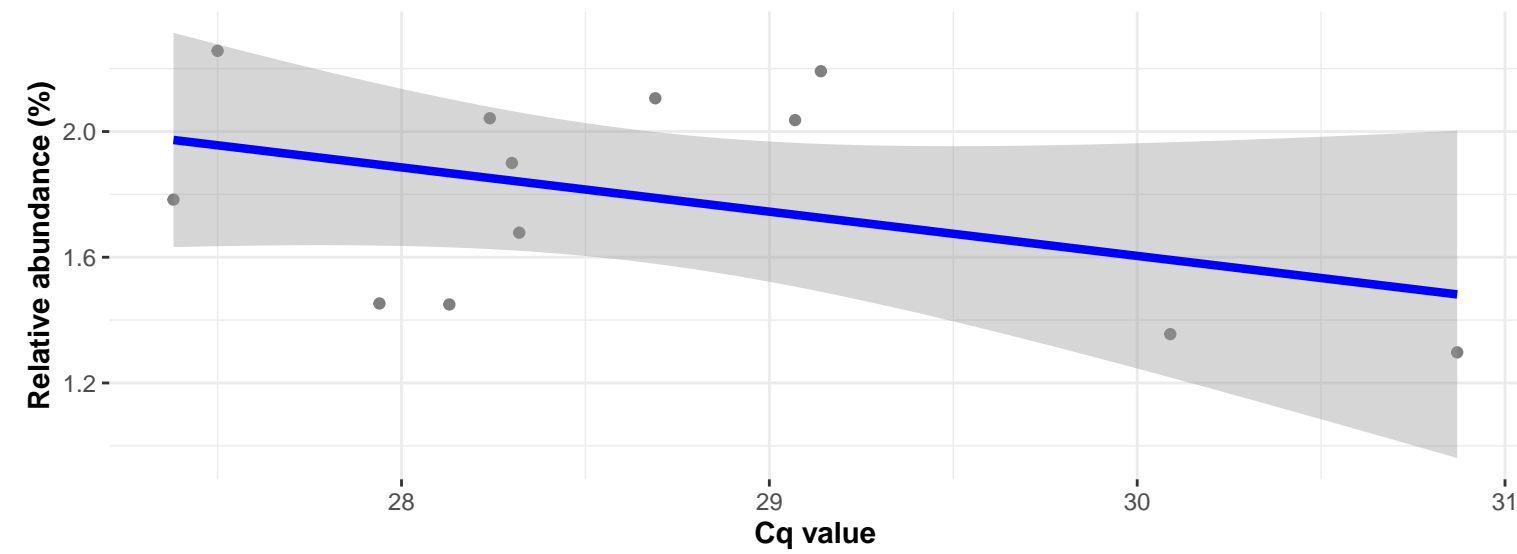
Correlation with all samples

$\log_e(S) = 8.451$, $p = 0.427$, $\hat{\rho}_{\text{Spearman}} = -0.153$, $\text{CI}_{95\%} [-0.501, 0.237]$, $n_{\text{pairs}} = 29$



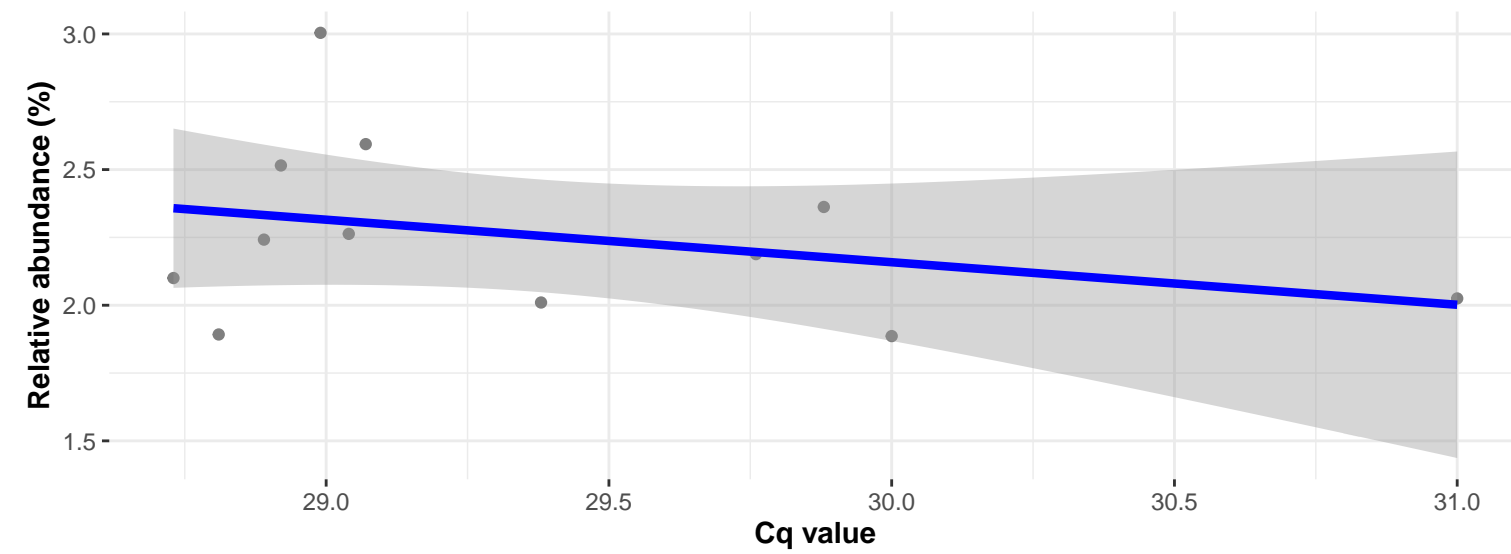
Correlation within: IM-PIM

$\log_e(S) = 5.875$, $p = 0.443$, $\hat{\rho}_{\text{Spearman}} = -0.245$, $\text{CI}_{95\%} [-0.727, 0.399]$, $n_{\text{pairs}} = 12$

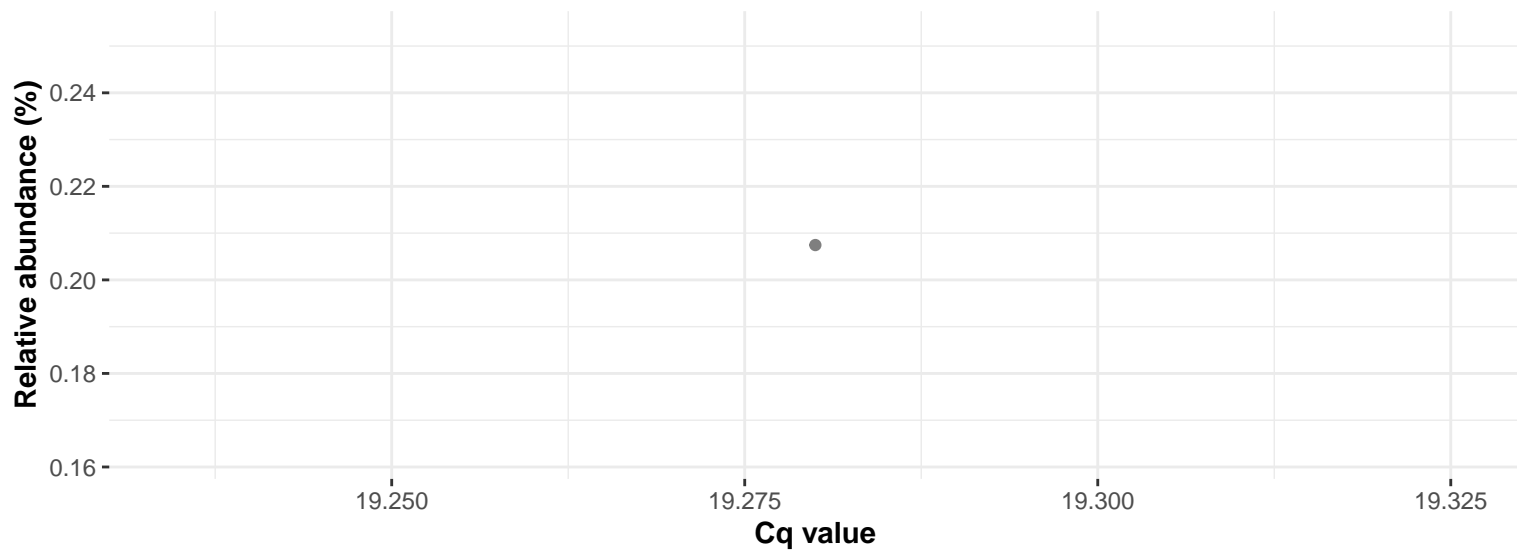


Correlation within: IM-DIM

$\log_e(S) = 5.817$, $p = 0.587$, $\hat{\rho}_{\text{Spearman}} = -0.175$, $\text{CI}_{95\%} [-0.691, 0.459]$, $n_{\text{pairs}} = 12$



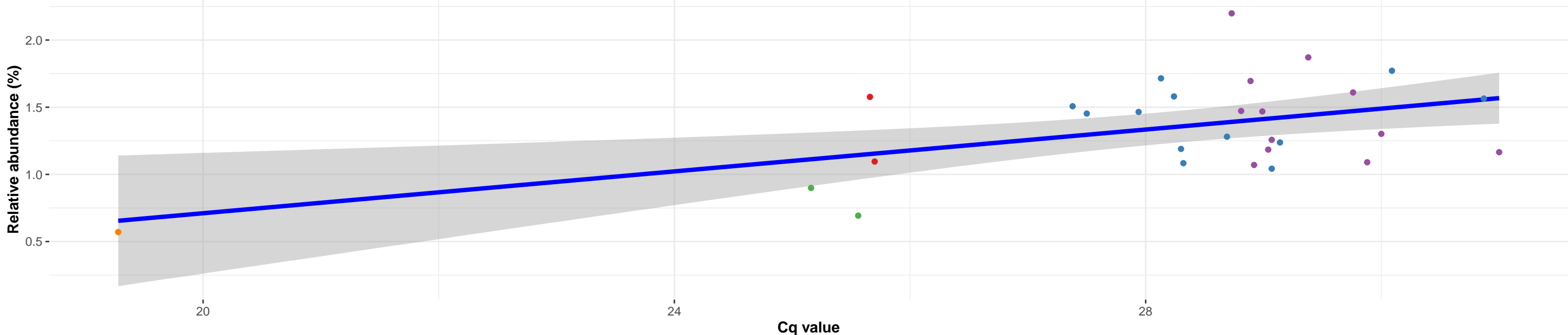
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; Ambiguous_taxa; Ambiguous_taxa

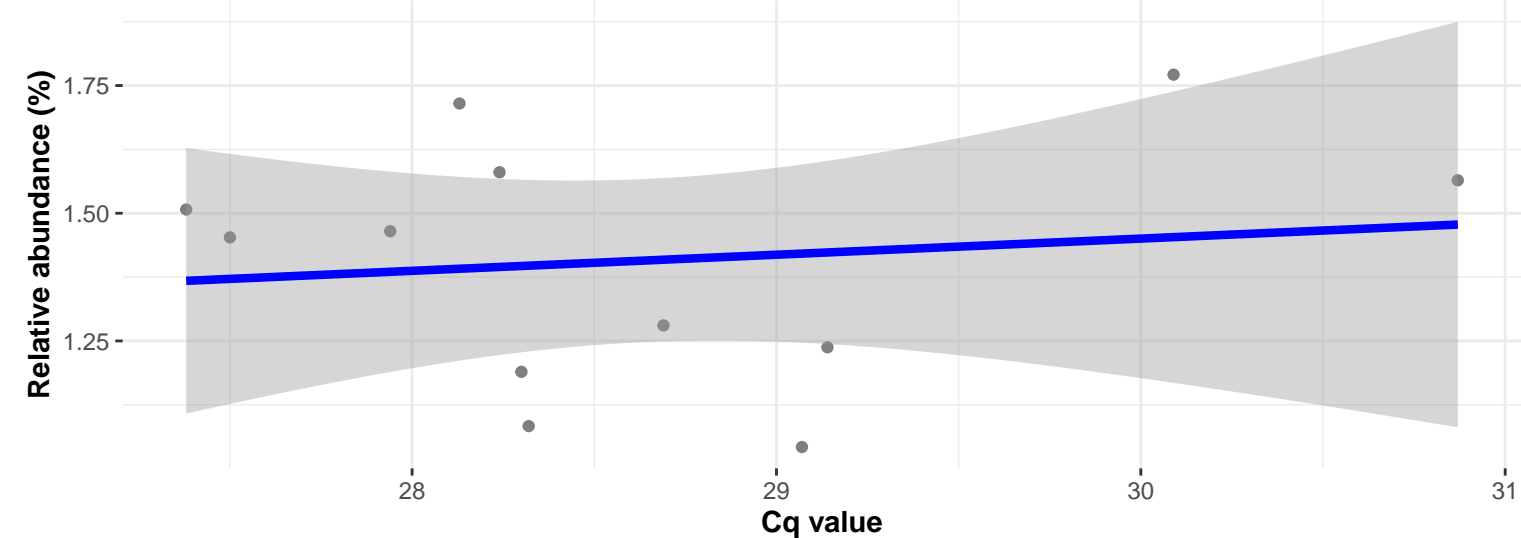
Correlation with all samples

$\log_e(S) = 8.034$, $p = 0.209$, $\hat{\rho}_{\text{Spearman}} = 0.241$, $CI_{95\%} [-0.149, 0.566]$, $n_{\text{pairs}} = 29$



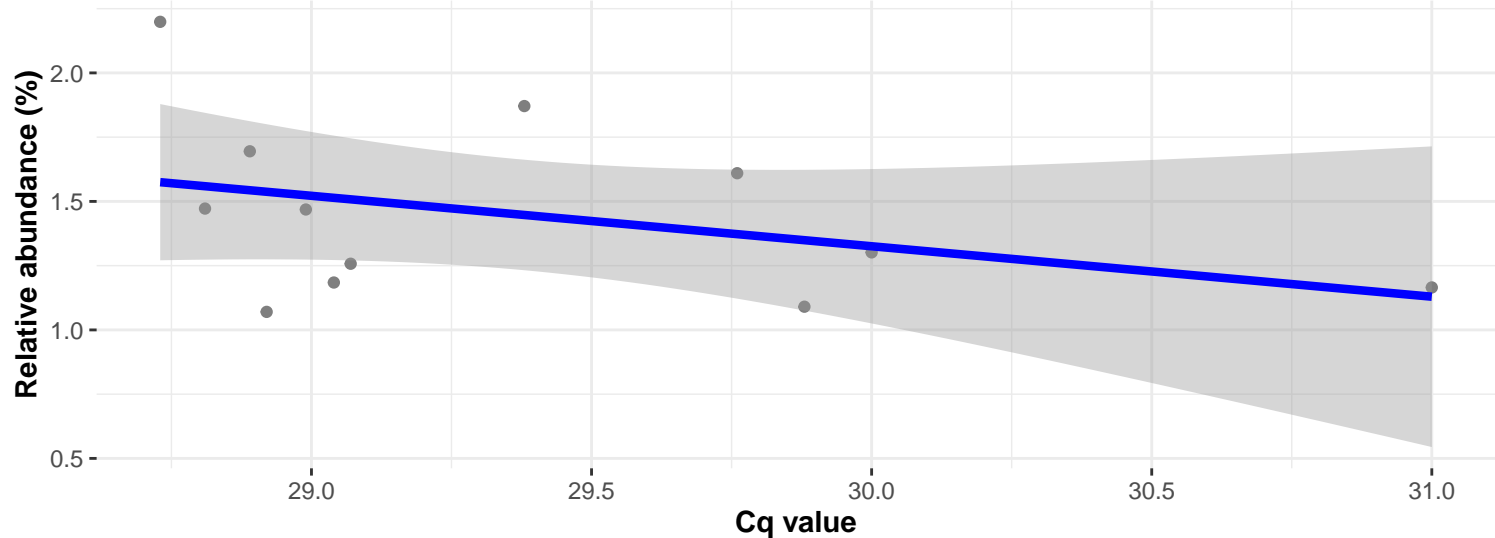
Correlation within: IM-PIM

$\log_e(S) = 5.730$, $p = 0.812$, $\hat{\rho}_{\text{Spearman}} = -0.077$, $CI_{95\%} [-0.635, 0.534]$, $n_{\text{pairs}} = 12$

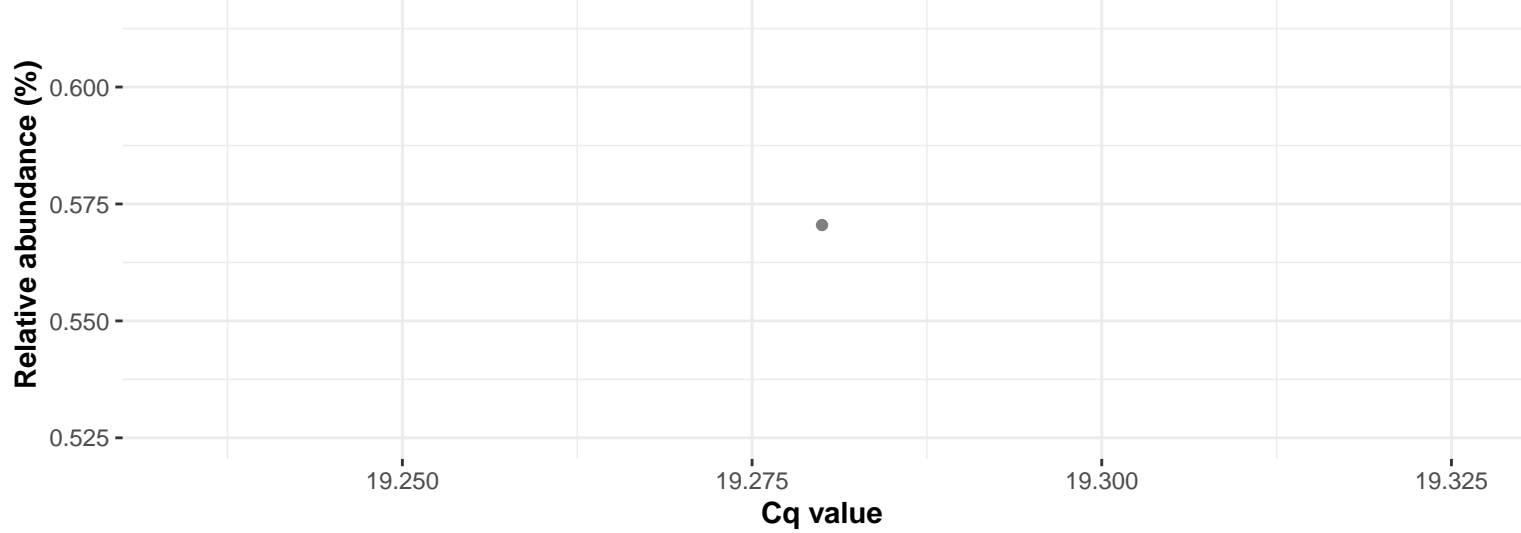


Correlation within: IM-DIM

$\log_e(S) = 6.006$, $p = 0.175$, $\hat{\rho}_{\text{Spearman}} = -0.420$, $CI_{95\%} [-0.808, 0.222]$, $n_{\text{pairs}} = 12$



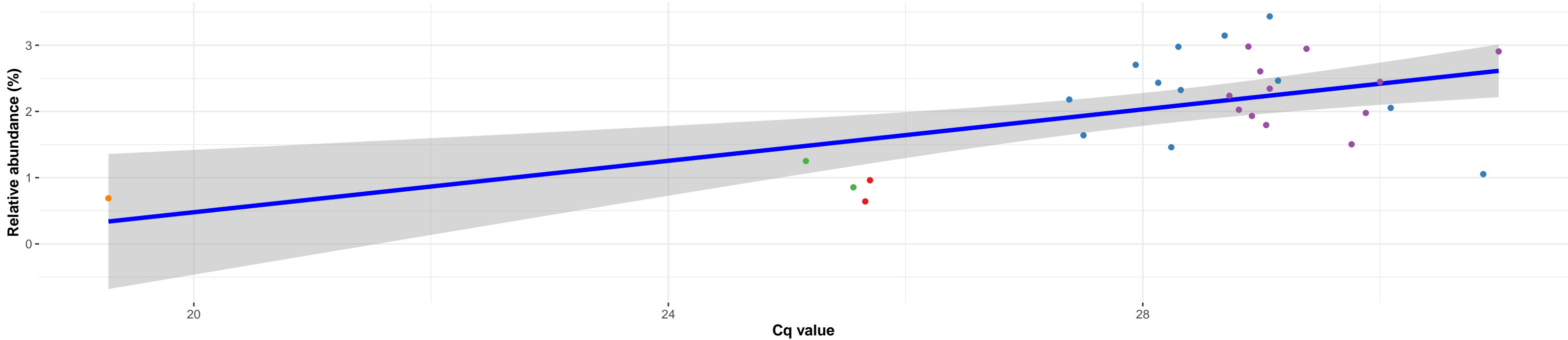
Correlation within: Feed



k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium

Correlation with all samples

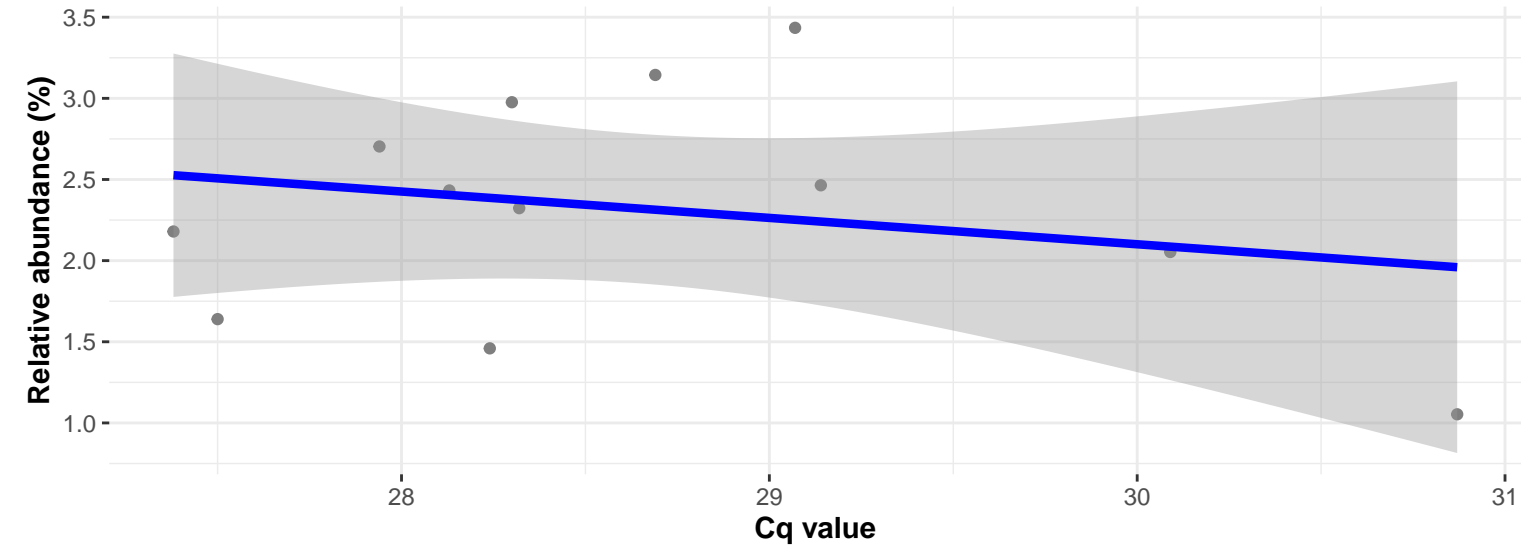
$\log_e(S) = 7.804$, $p = 0.033$, $\hat{\rho}_{\text{Spearman}} = 0.396$, $CI_{95\%} [0.024, 0.672]$, $n_{\text{pairs}} = 29$



SampleType IM-PID IM-PIM IM-DID IM-DIM Feed

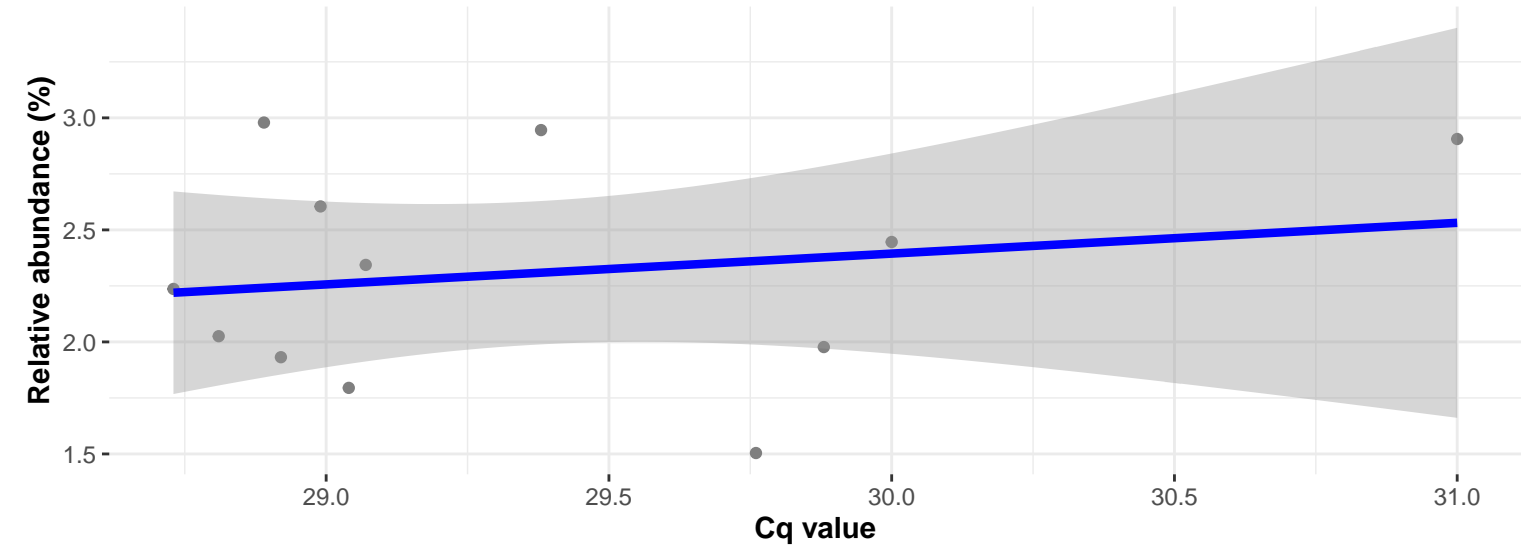
Correlation within: IM-PIM

$\log_e(S) = 5.635$, $p = 0.948$, $\hat{\rho}_{\text{Spearman}} = 0.021$, $CI_{95\%} [-0.573, 0.600]$, $n_{\text{pairs}} = 12$

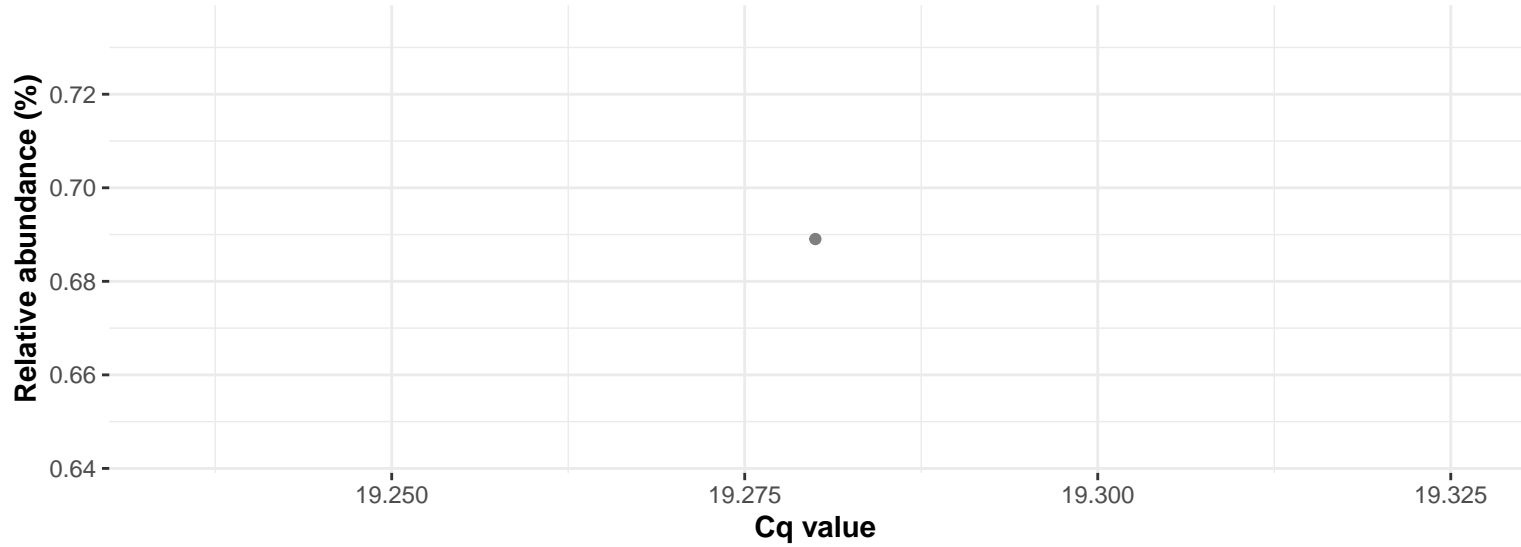


Correlation within: IM-DIM

$\log_e(S) = 5.598$, $p = 0.863$, $\hat{\rho}_{\text{Spearman}} = 0.056$, $CI_{95\%} [-0.549, 0.622]$, $n_{\text{pairs}} = 12$



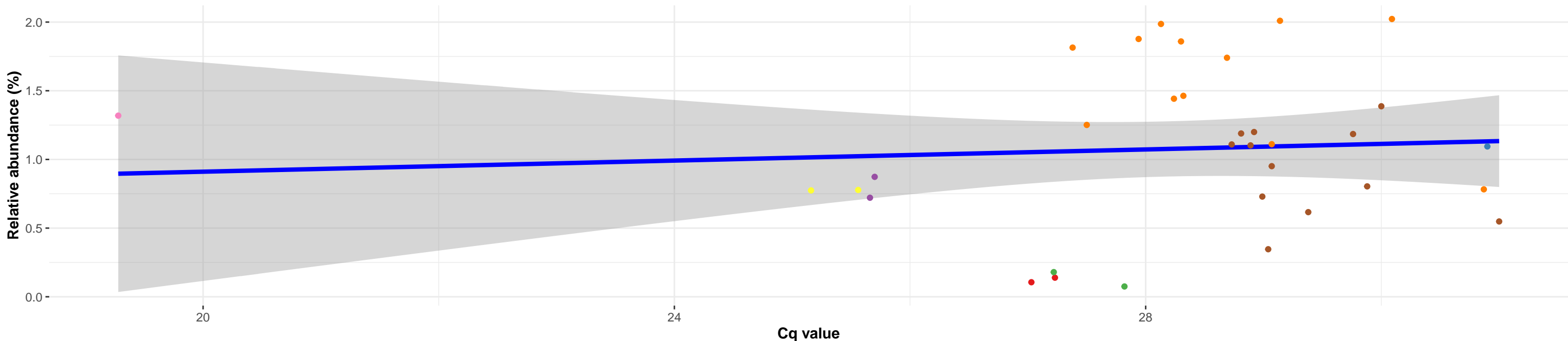
Correlation within: Feed



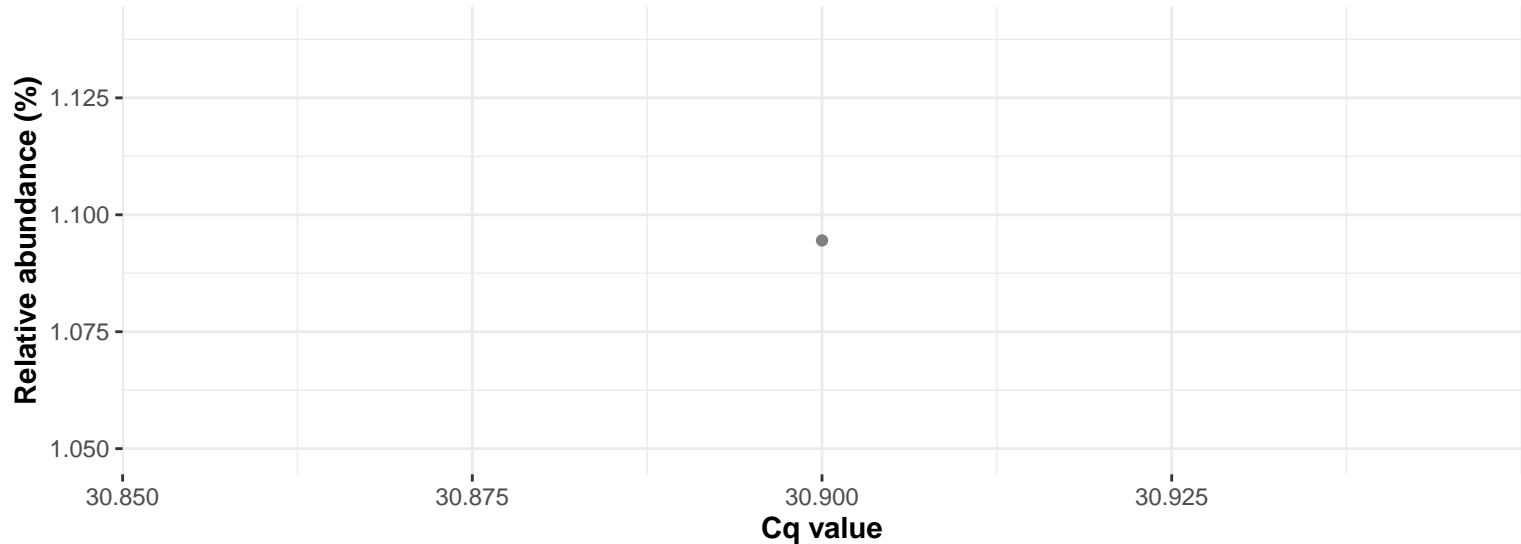
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 8.650$, $p = 0.472$, $\hat{\rho}_{\text{Spearman}} = 0.128$, $CI_{95\%} [-0.230, 0.455]$, $n_{\text{pairs}} = 34$

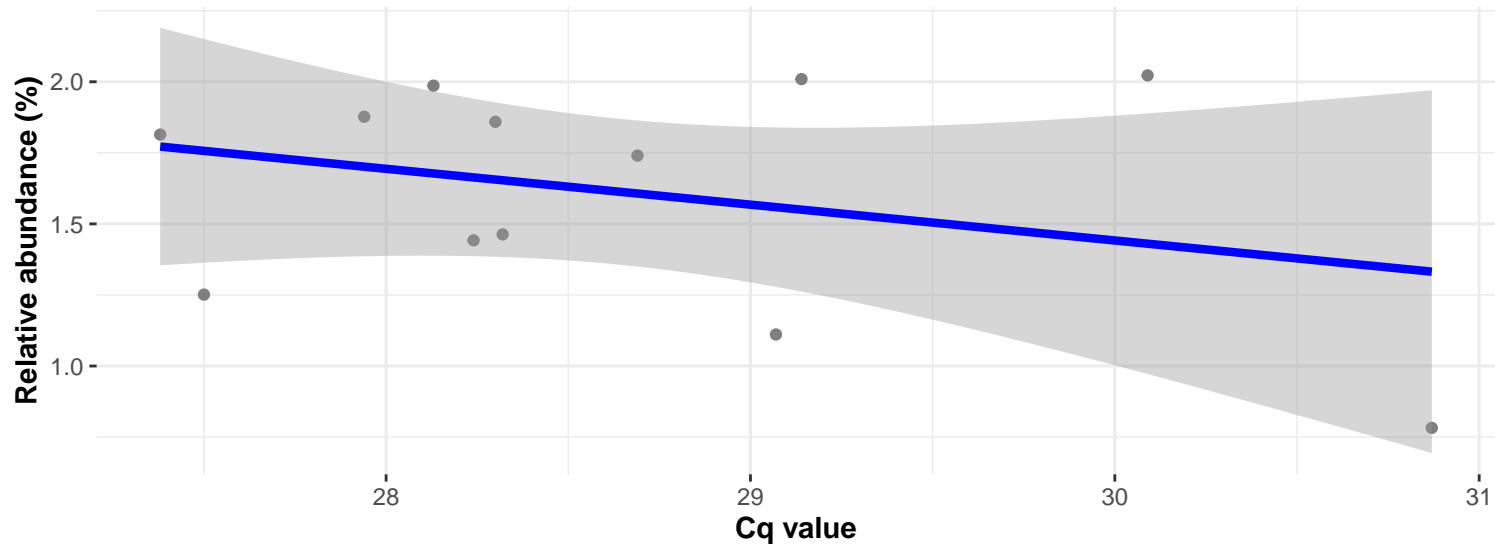


Correlation within: REF-PIM



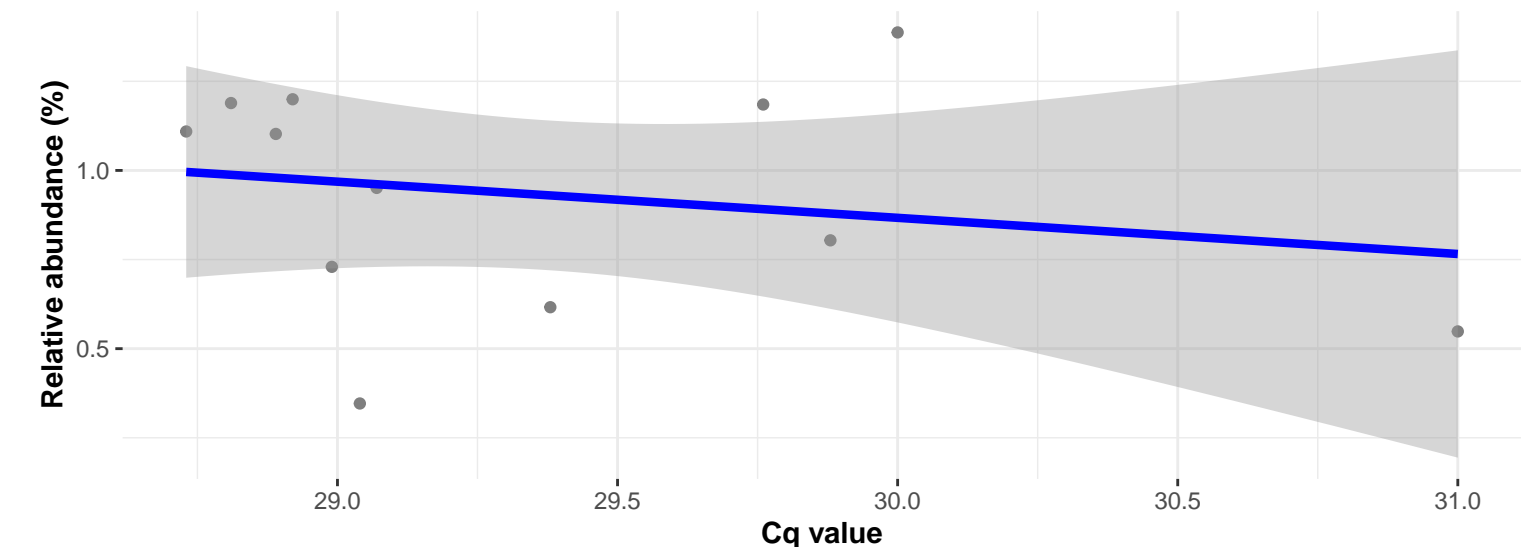
Correlation within: IM-PIM

$\log_e(S) = 5.684$, $p = 0.931$, $\hat{\rho}_{\text{Spearman}} = -0.028$, $CI_{95\%} [-0.605, 0.568]$, $n_{\text{pairs}} = 12$

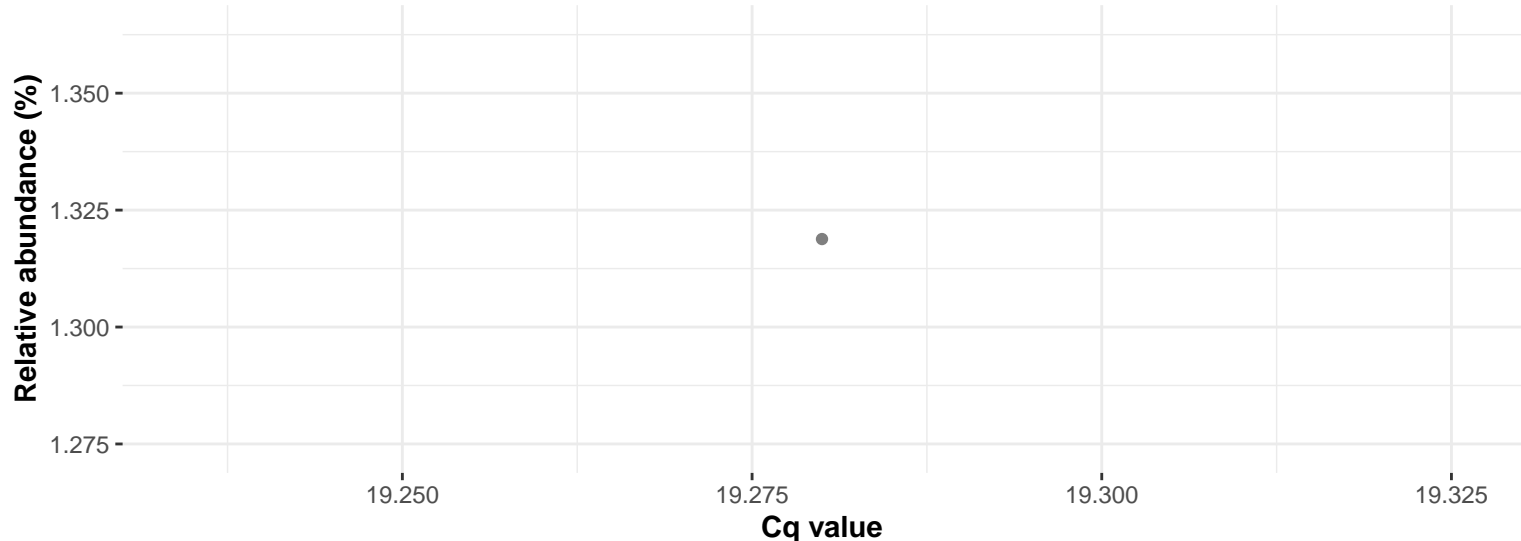


Correlation within: IM-DIM

$\log_e(S) = 5.875$, $p = 0.443$, $\hat{\rho}_{\text{Spearman}} = -0.245$, $CI_{95\%} [-0.727, 0.399]$, $n_{\text{pairs}} = 12$



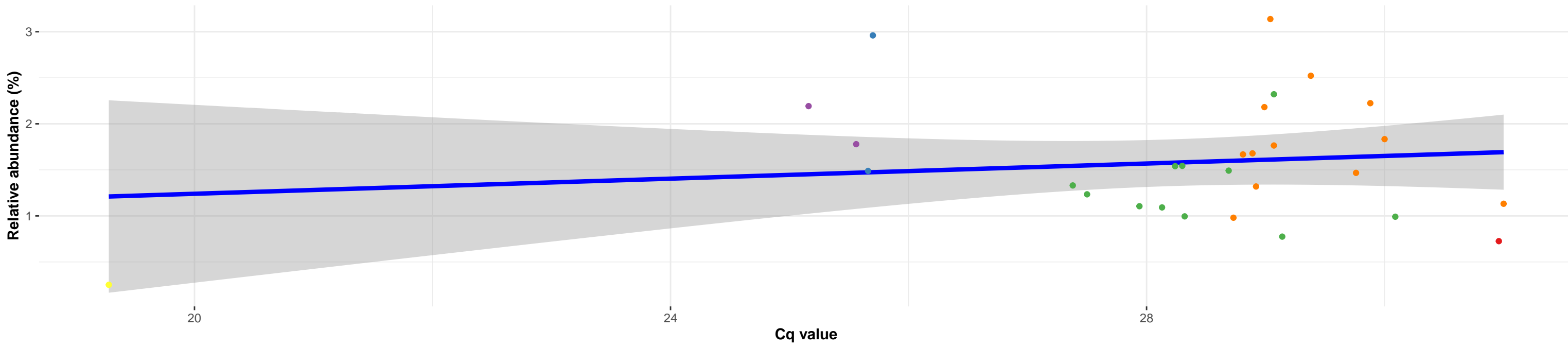
Correlation within: Feed



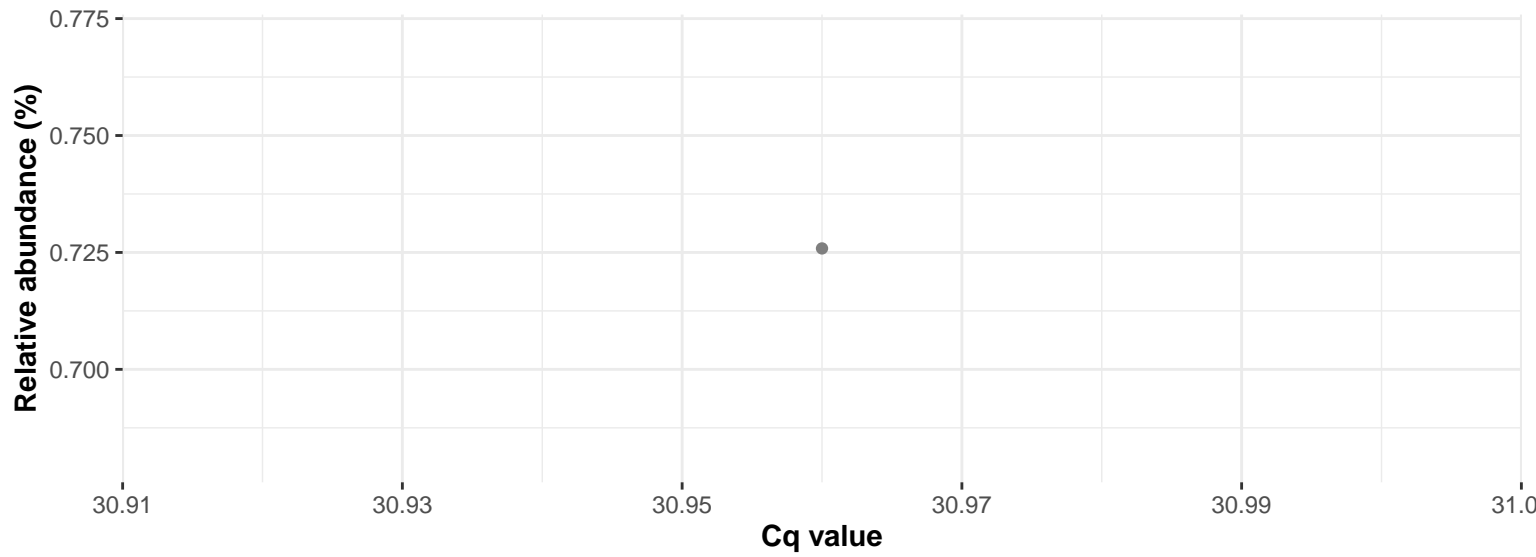
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Lysinibacillus; NA

Correlation with all samples

$\log_e(S) = 8.290$, $p = 0.921$, $\hat{\rho}_{\text{Spearman}} = 0.019$, $\text{CI}_{95\%} [-0.360, 0.393]$, $n_{\text{pairs}} = 29$

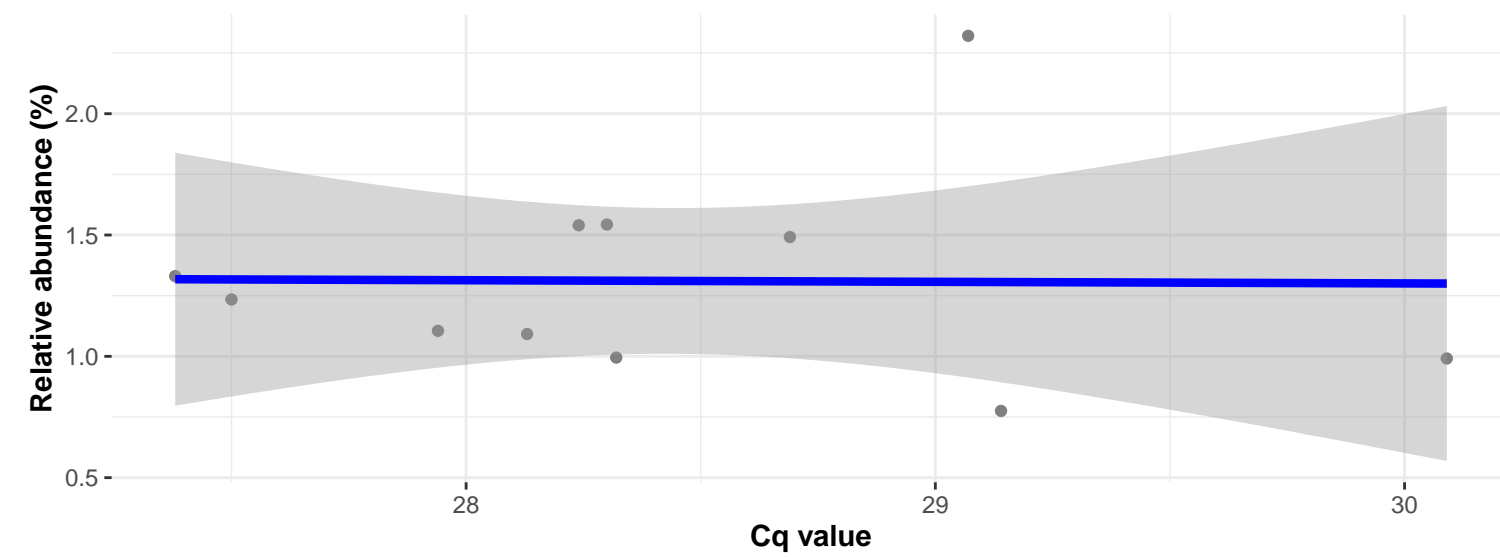


Correlation within: REF-PIM



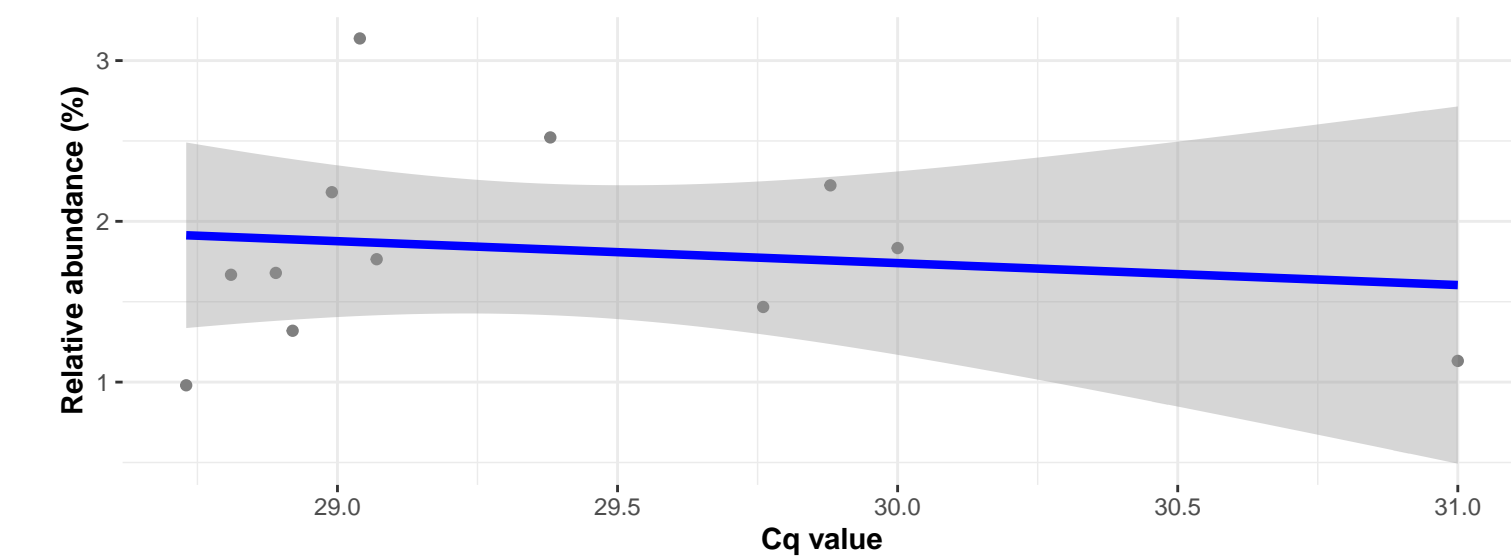
Correlation within: IM-PIM

$\log_e(S) = 5.598$, $p = 0.502$, $\hat{\rho}_{\text{Spearman}} = -0.227$, $\text{CI}_{95\%} [-0.737, 0.448]$, $n_{\text{pairs}} = 11$

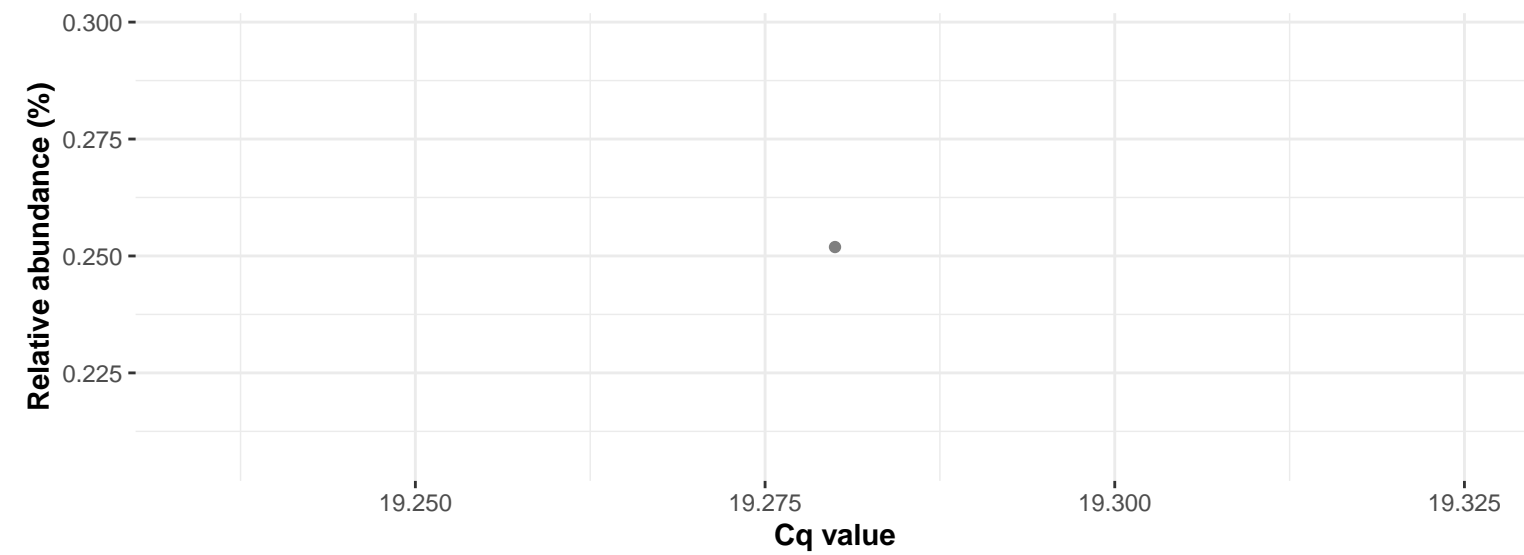


Correlation within: IM-DIM

$\log_e(S) = 5.366$, $p = 0.430$, $\hat{\rho}_{\text{Spearman}} = 0.252$, $\text{CI}_{95\%} [-0.393, 0.731]$, $n_{\text{pairs}} = 12$



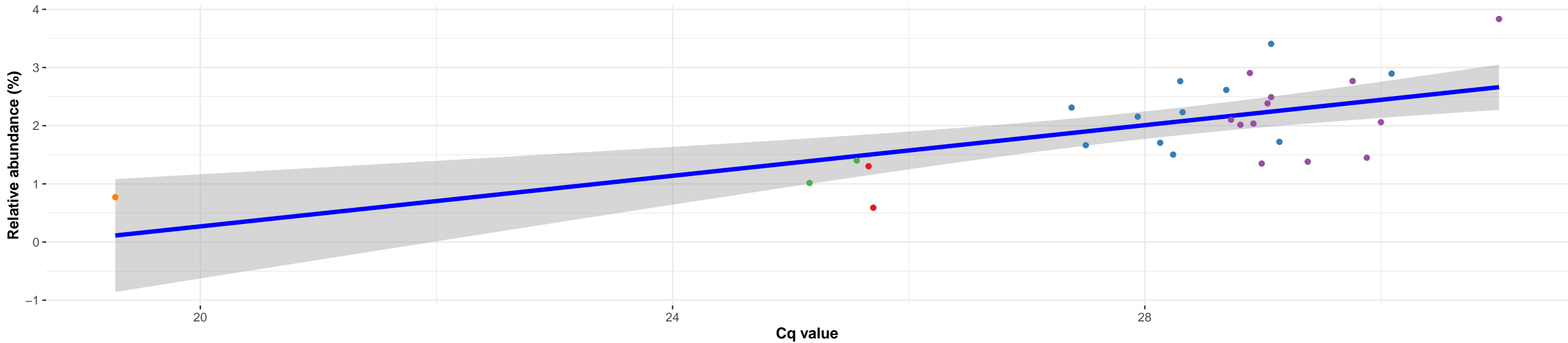
Correlation within: Feed



k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium

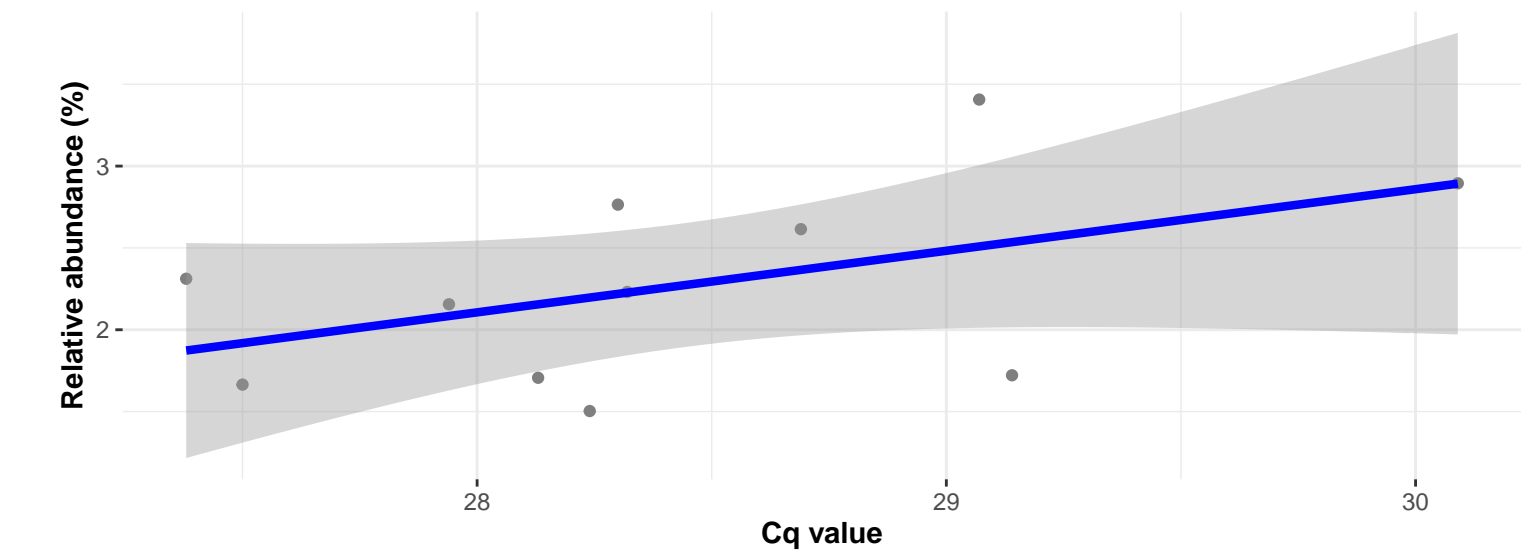
Correlation with all samples

$\log_e(S) = 7.434$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.537$, $CI_{95\%} [0.194, 0.763]$, $n_{\text{pairs}} = 28$



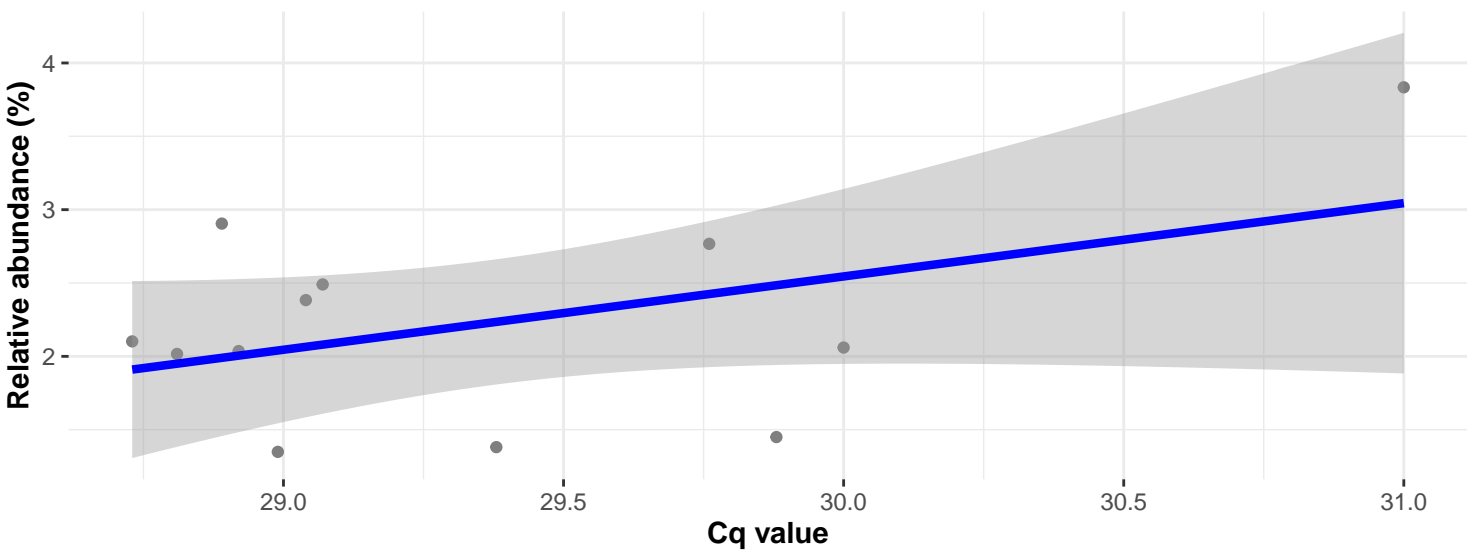
Correlation within: IM-PIM

$\log_e(S) = 4.682$, $p = 0.110$, $\hat{\rho}_{\text{Spearman}} = 0.509$, $CI_{95\%} [-0.151, 0.855]$, $n_{\text{pairs}} = 11$

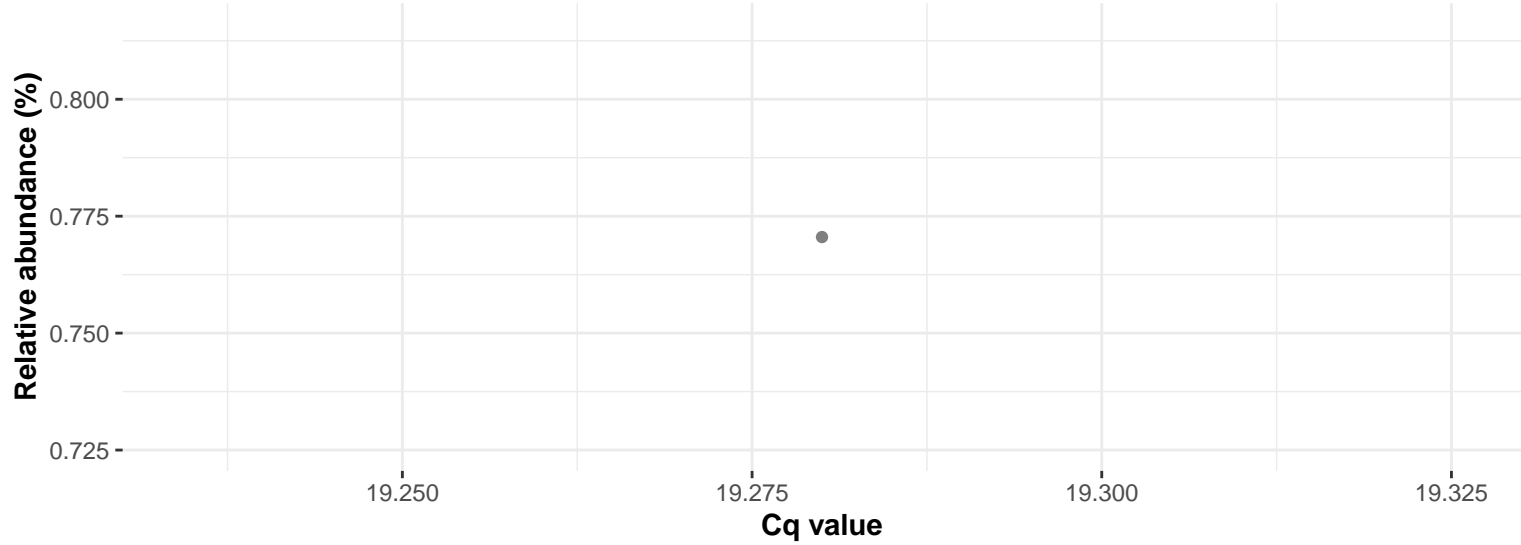


Correlation within: IM-DIM

$\log_e(S) = 5.481$, $p = 0.618$, $\hat{\rho}_{\text{Spearman}} = 0.161$, $CI_{95\%} [-0.470, 0.683]$, $n_{\text{pairs}} = 12$



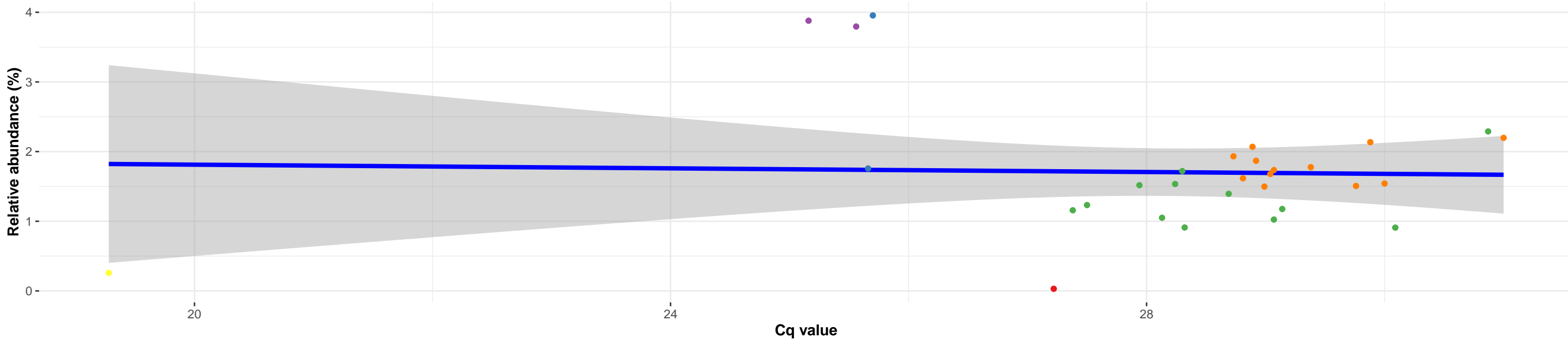
Correlation within: Feed



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

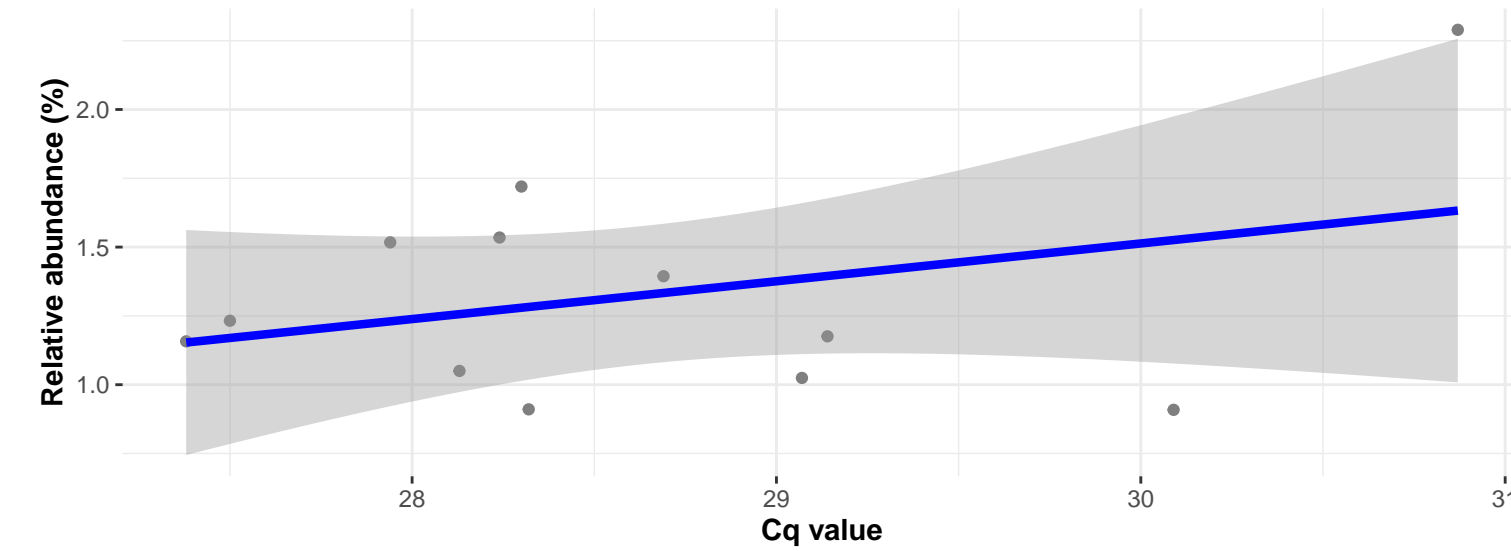
Correlation with all samples

$\log_e(S) = 8.321$, $p = 0.653$, $\hat{\rho}_{\text{Spearman}} = 0.086$, $\text{CI}_{95\%} [-0.294, 0.442]$, $n_{\text{pairs}} = 30$



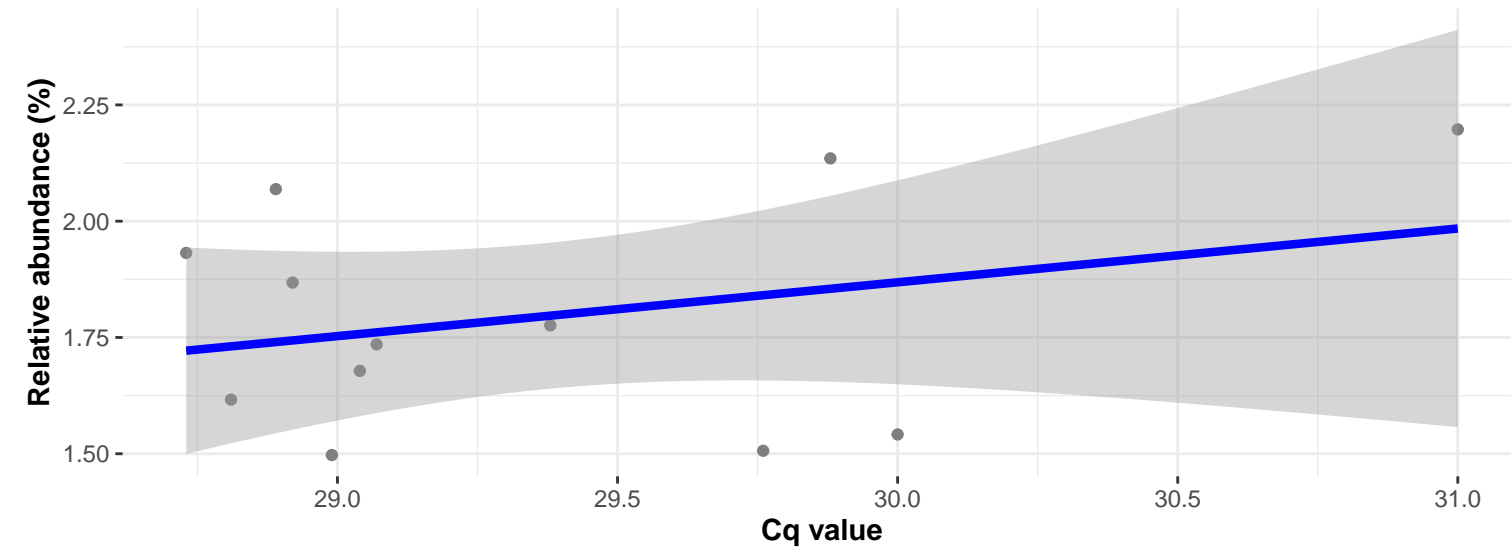
Correlation within: IM-PIM

$\log_e(S) = 5.717$, $p = 0.846$, $\hat{\rho}_{\text{Spearman}} = -0.063$, $\text{CI}_{95\%} [-0.627, 0.544]$, $n_{\text{pairs}} = 12$

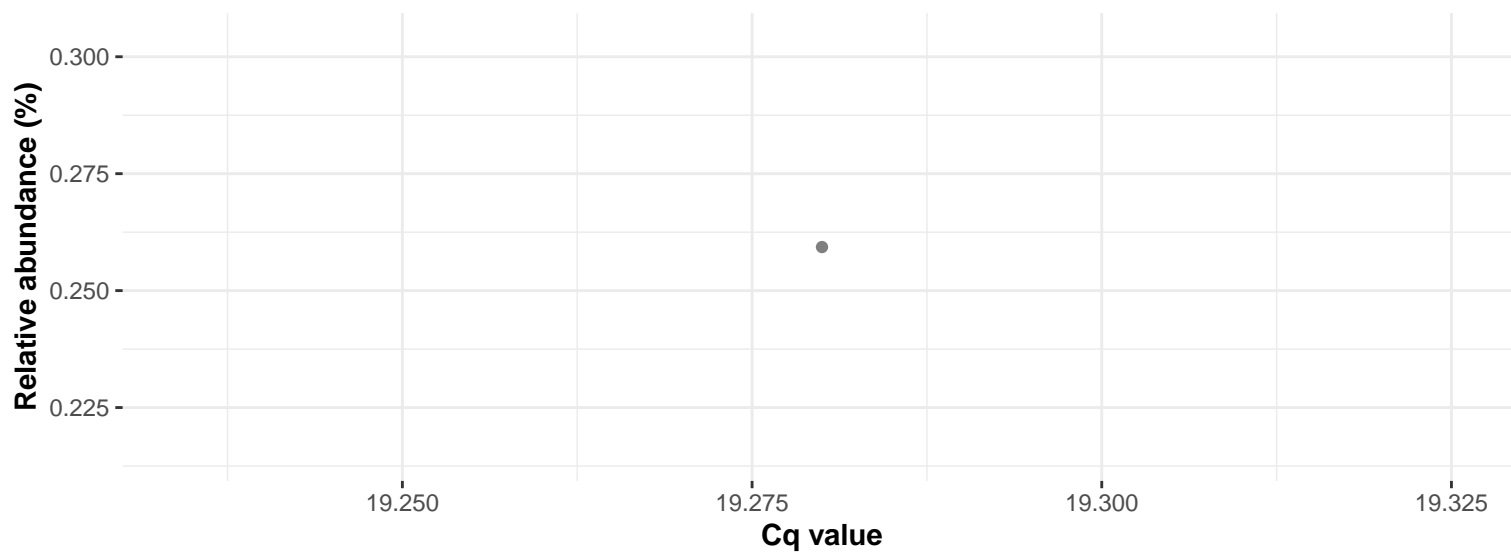


Correlation within: IM-DIM

$\log_e(S) = 5.583$, $p = 0.829$, $\hat{\rho}_{\text{Spearman}} = 0.070$, $\text{CI}_{95\%} [-0.539, 0.631]$, $n_{\text{pairs}} = 12$



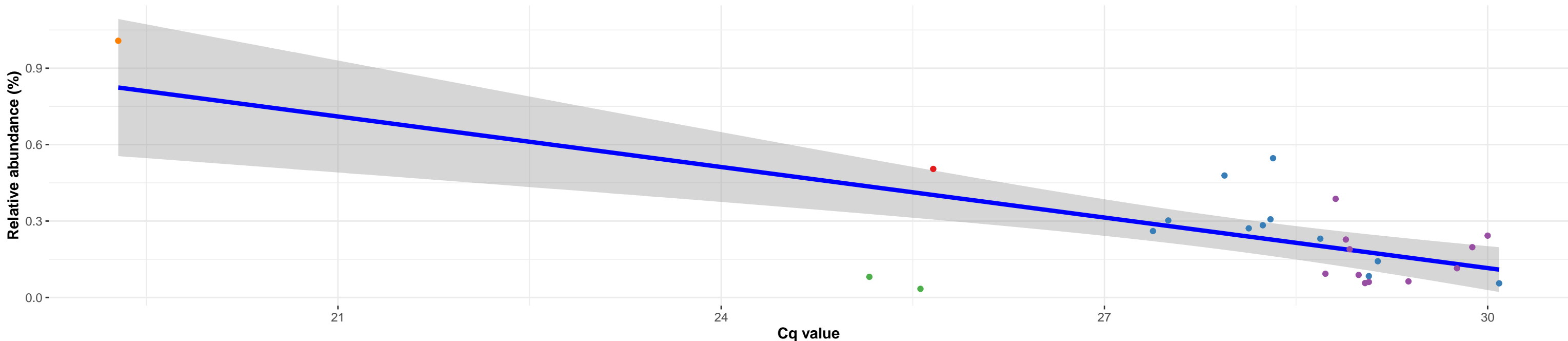
Correlation within: Feed



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

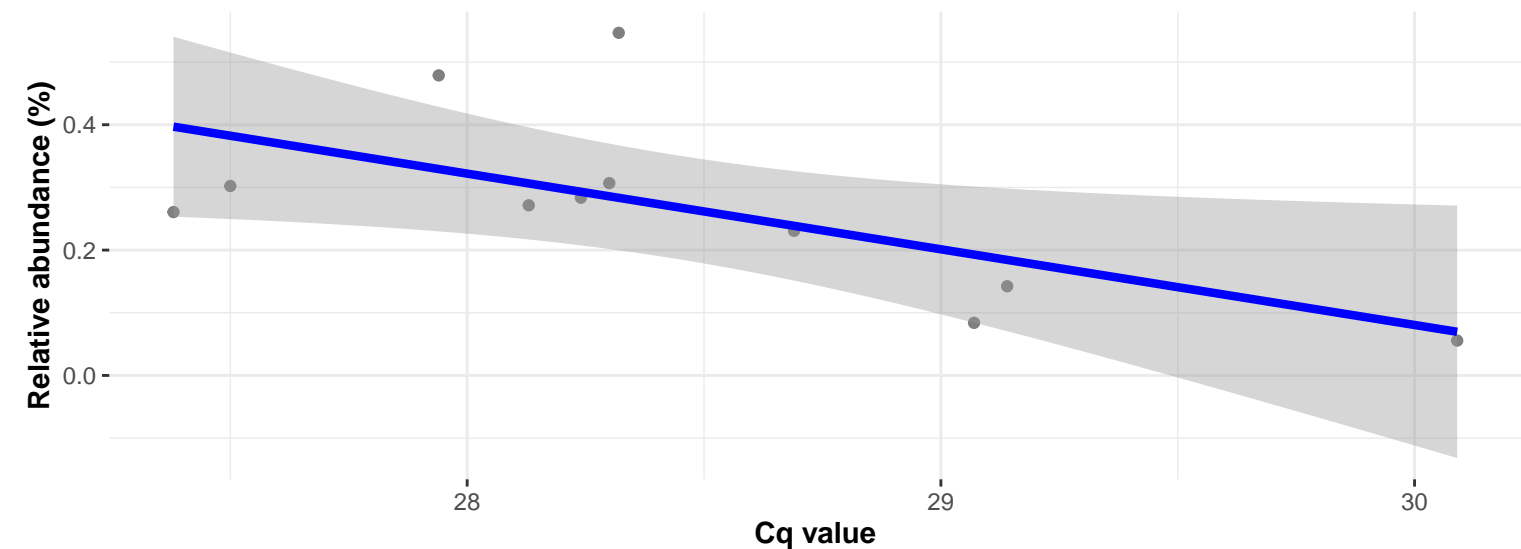
Correlation with all samples

$\log_e(S) = 8.367$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = -0.471$, $CI_{95\%} [-0.732, -0.091]$, $n_{\text{pairs}} = 26$



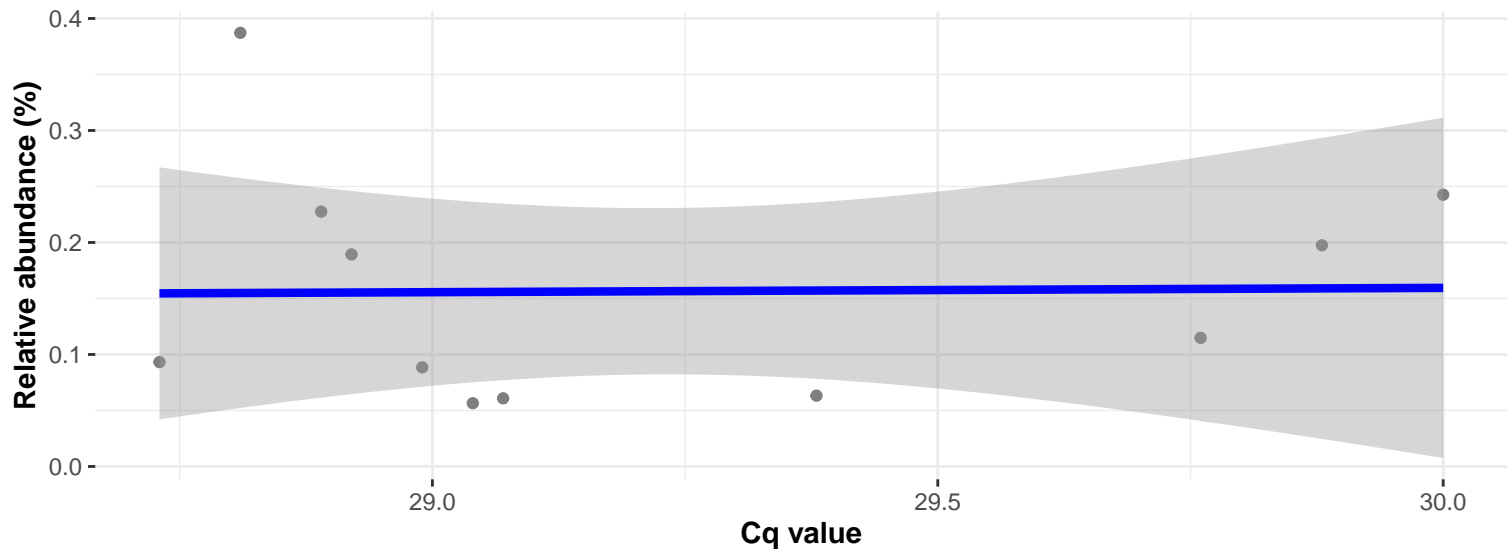
Correlation within: IM-PIM

$\log_e(S) = 5.852$, $p = 0.060$, $\hat{\rho}_{\text{Spearman}} = -0.582$, $CI_{95\%} [-0.881, 0.048]$, $n_{\text{pairs}} = 11$

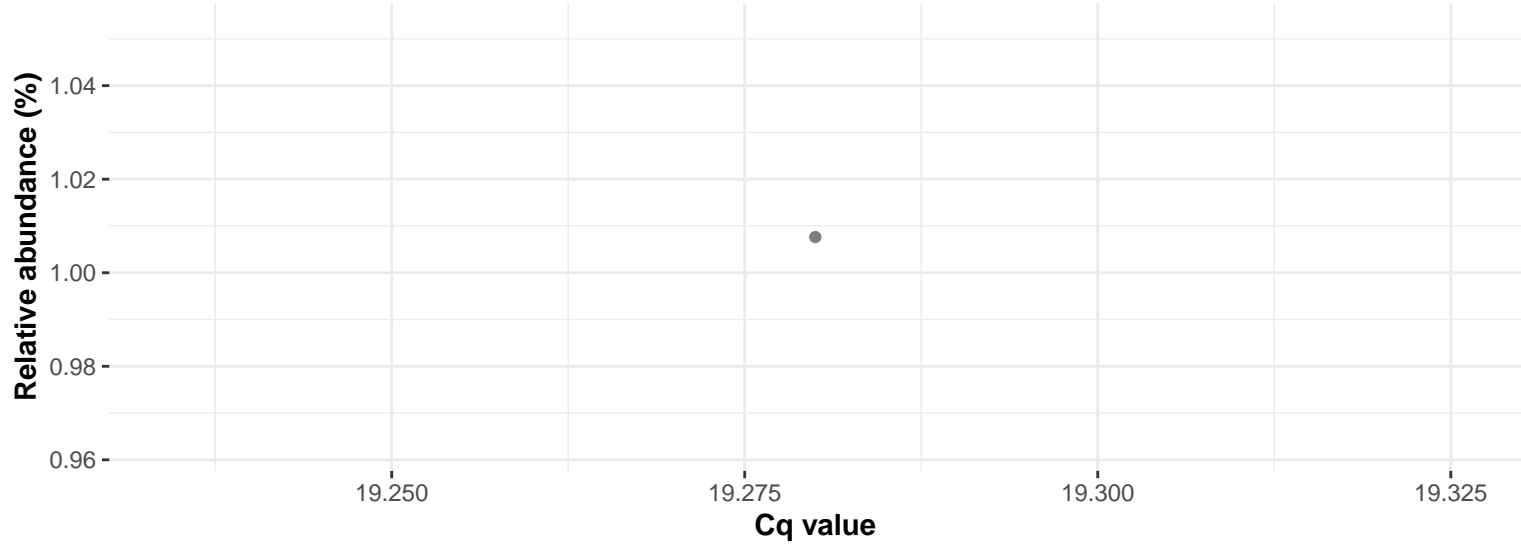


Correlation within: IM-DIM

$\log_e(S) = 5.447$, $p = 0.873$, $\hat{\rho}_{\text{Spearman}} = -0.055$, $CI_{95\%} [-0.646, 0.578]$, $n_{\text{pairs}} = 11$



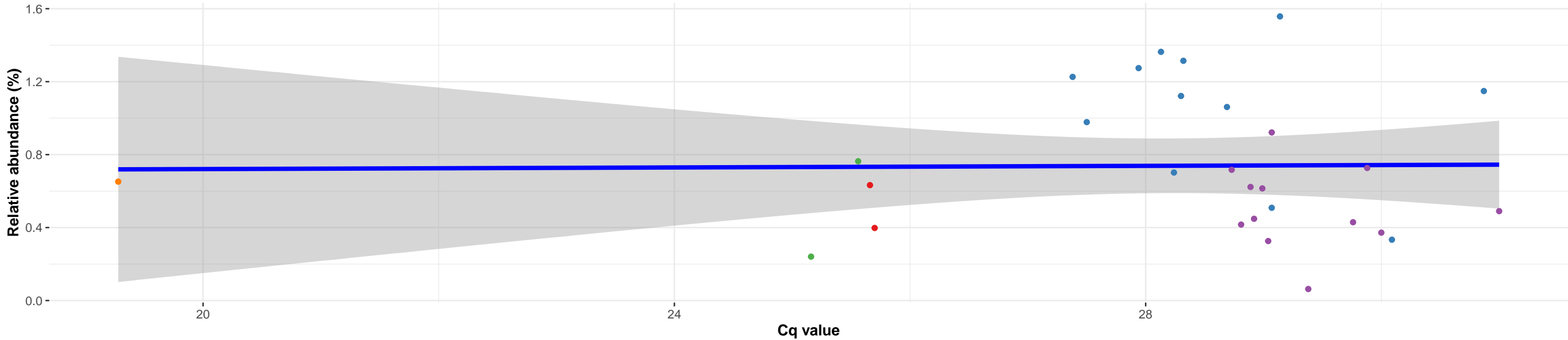
Correlation within: Feed



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

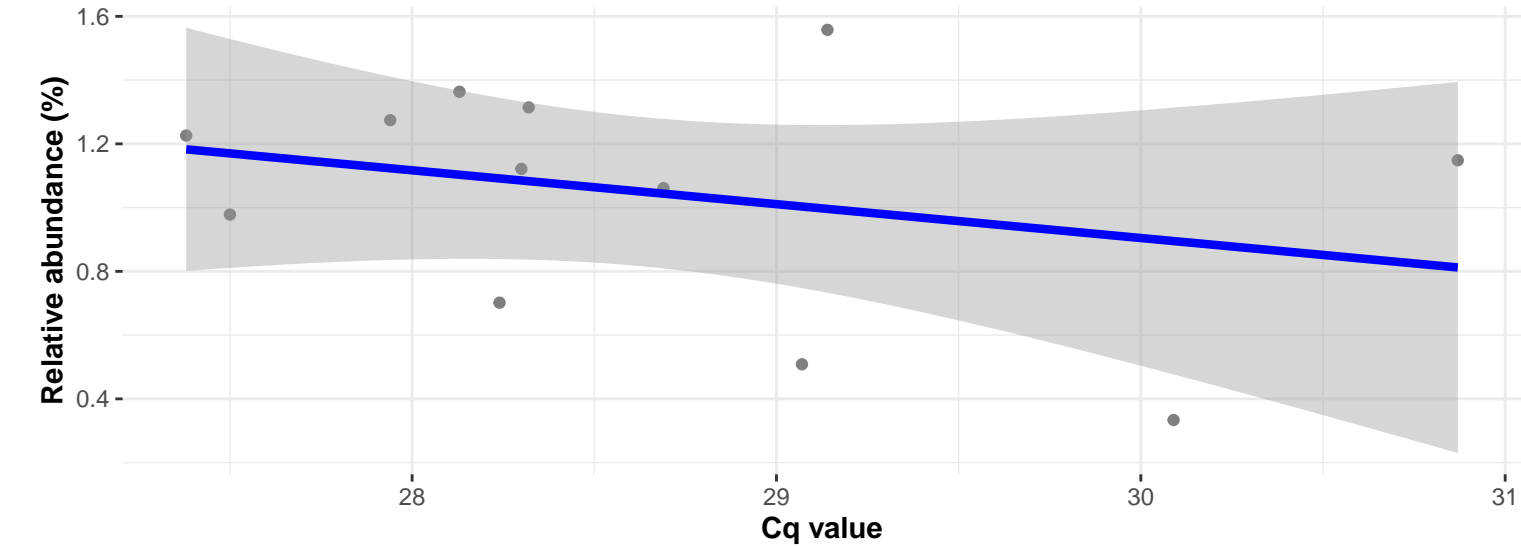
Correlation with all samples

$\log_e(S) = 8.516$, $p = 0.229$, $\hat{\rho}_{\text{Spearman}} = -0.230$, $CI_{95\%} [-0.558, 0.160]$, $n_{\text{pairs}} = 29$



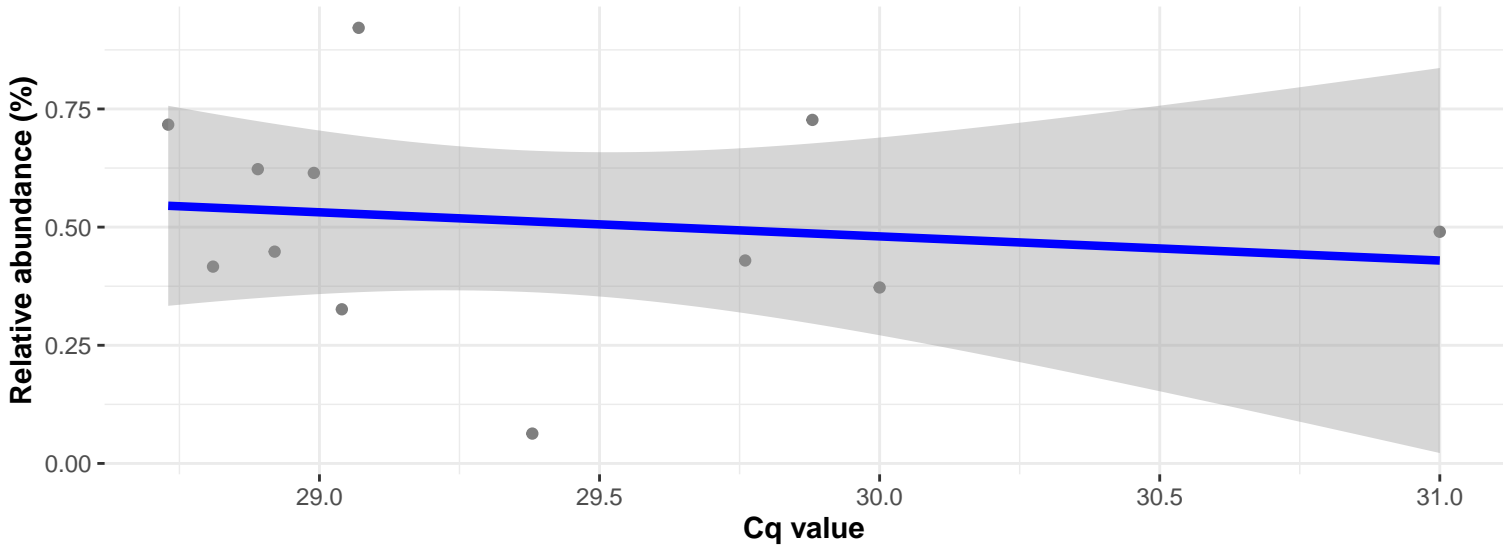
Correlation within: IM-PIM

$\log_e(S) = 5.823$, $p = 0.572$, $\hat{\rho}_{\text{Spearman}} = -0.182$, $CI_{95\%} [-0.694, 0.453]$, $n_{\text{pairs}} = 12$

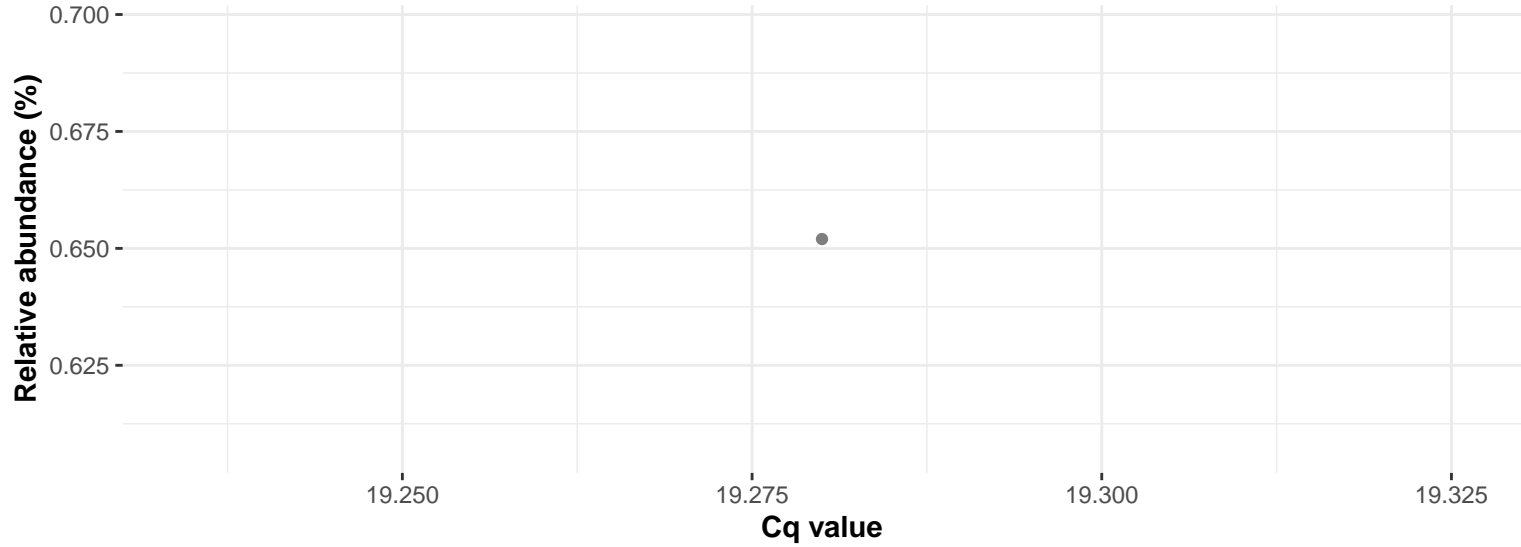


Correlation within: IM-DIM

$\log_e(S) = 5.799$, $p = 0.633$, $\hat{\rho}_{\text{Spearman}} = -0.154$, $CI_{95\%} [-0.679, 0.476]$, $n_{\text{pairs}} = 12$



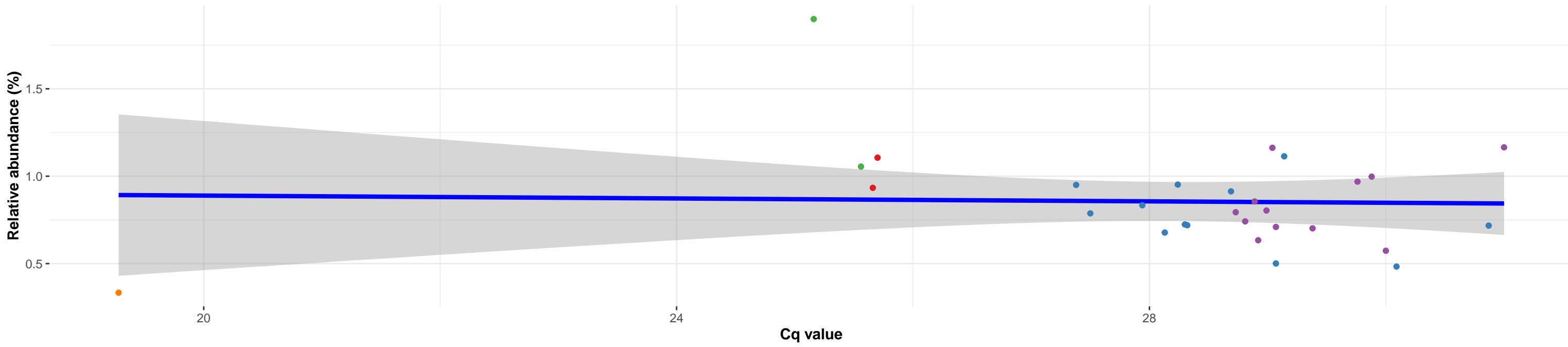
Correlation within: Feed



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

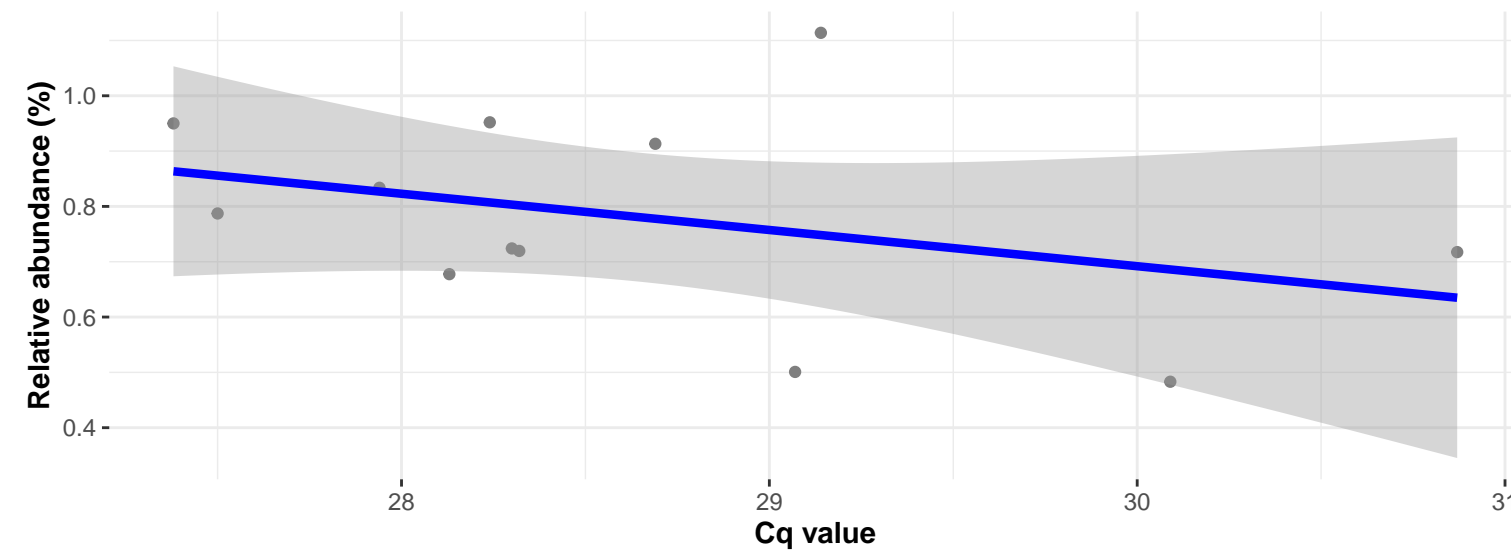
Correlation with all samples

$\log_e(S) = 8.453$, $p = 0.421$, $\hat{\rho}_{\text{Spearman}} = -0.155$, $CI_{95\%} [-0.502, 0.235]$, $n_{\text{pairs}} = 29$



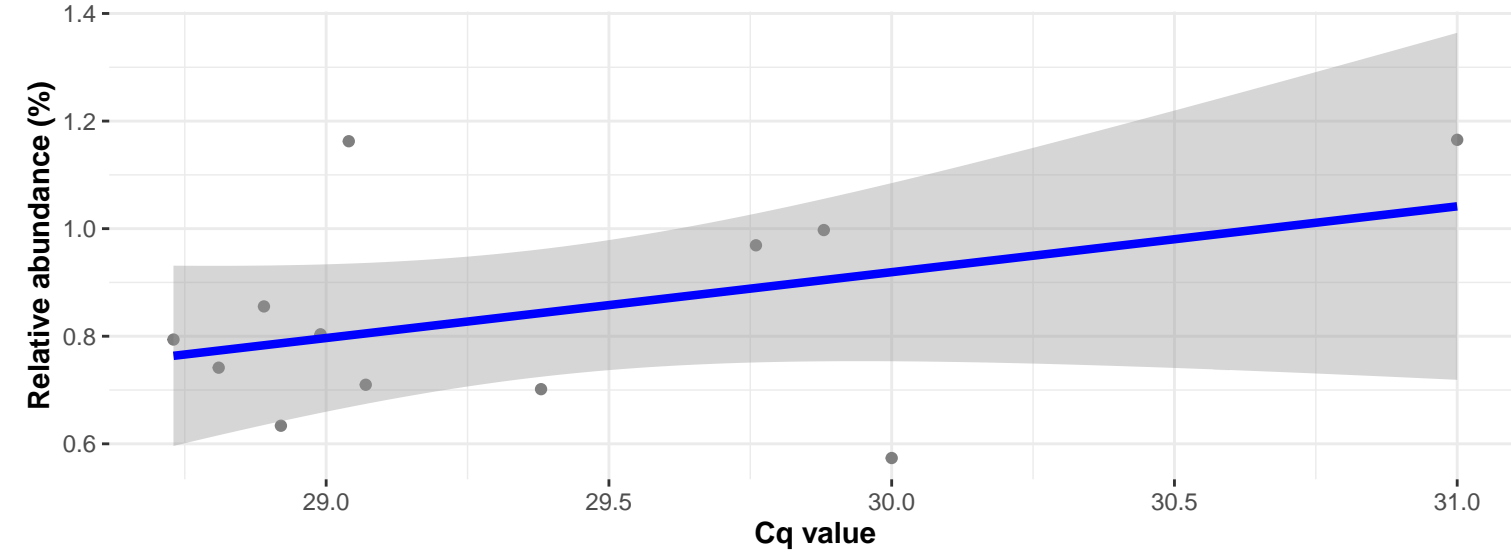
Correlation within: IM-PIM

$\log_e(S) = 5.966$, $p = 0.245$, $\hat{\rho}_{\text{Spearman}} = -0.364$, $CI_{95\%} [-0.783, 0.284]$, $n_{\text{pairs}} = 12$

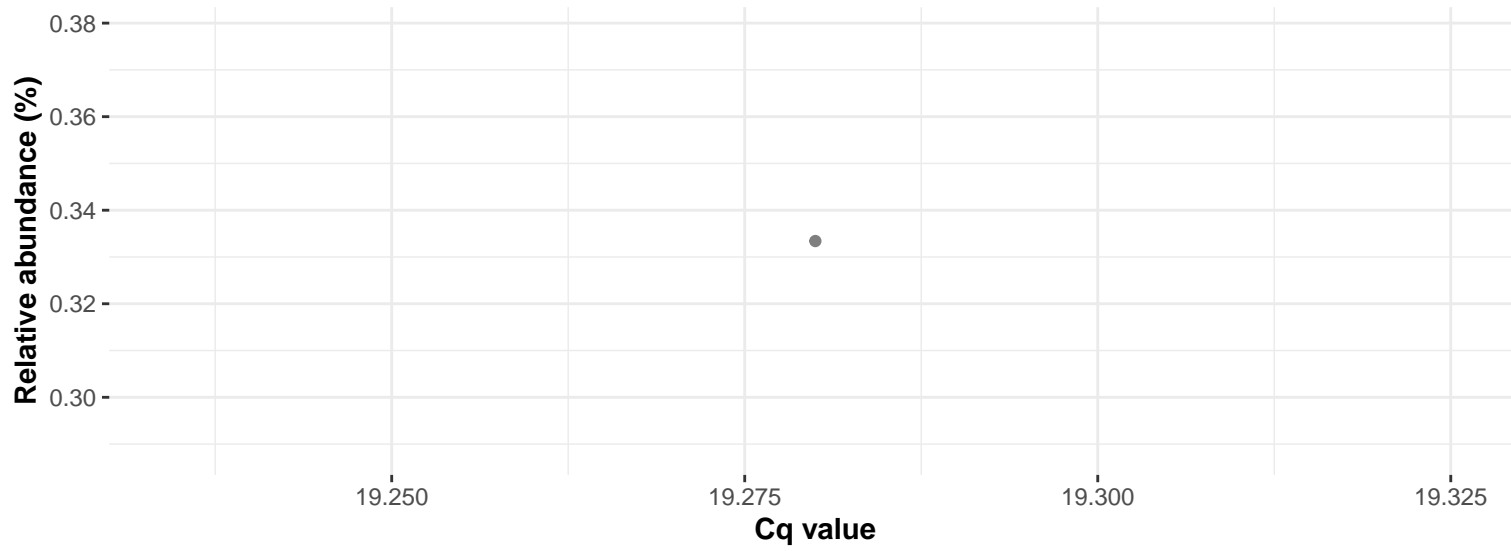


Correlation within: IM-DIM

$\log_e(S) = 5.421$, $p = 0.513$, $\hat{\rho}_{\text{Spearman}} = 0.210$, $CI_{95\%} [-0.430, 0.709]$, $n_{\text{pairs}} = 12$



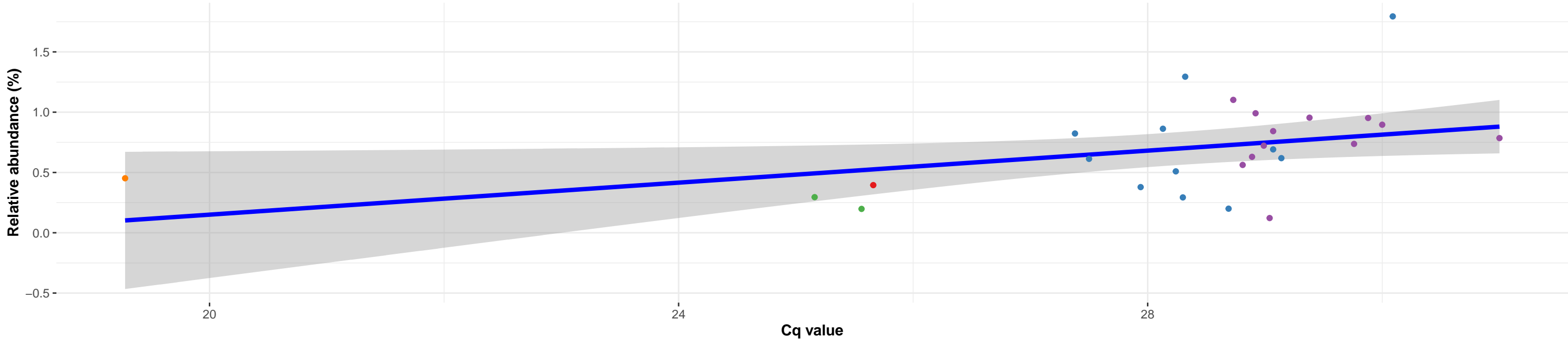
Correlation within: Feed



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

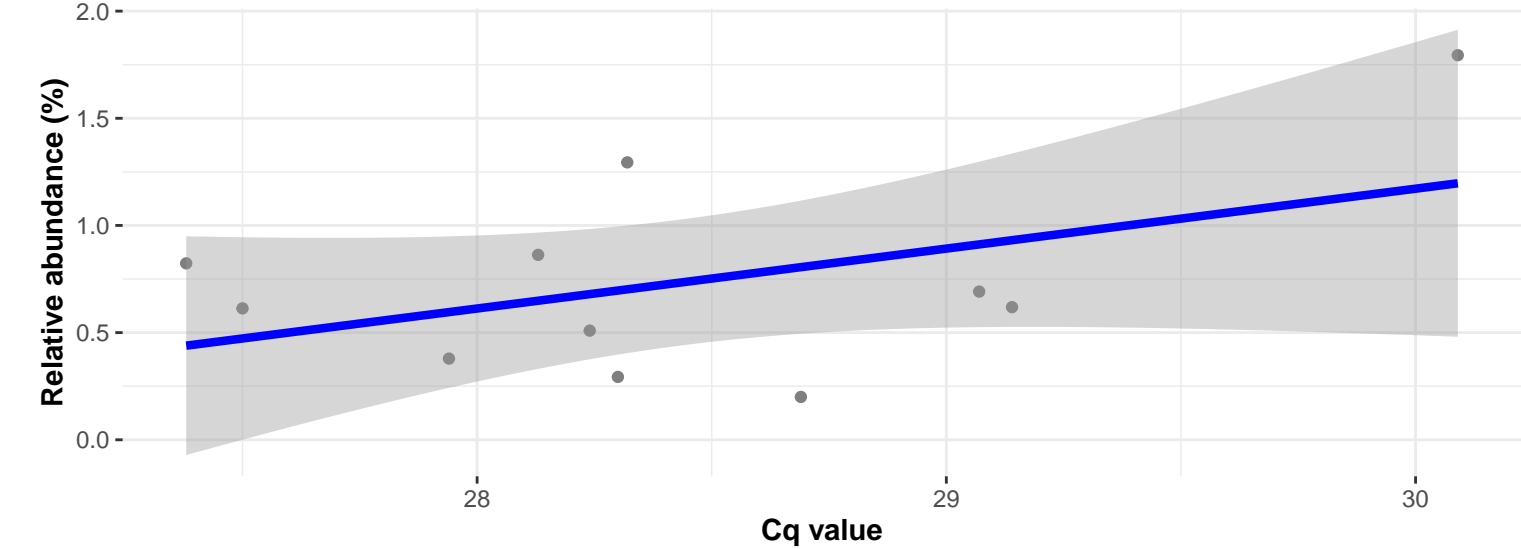
Correlation with all samples

$\log_e(S) = 7.348$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.526$, $CI_{95\%} [0.171, 0.760]$, $n_{\text{pairs}} = 27$



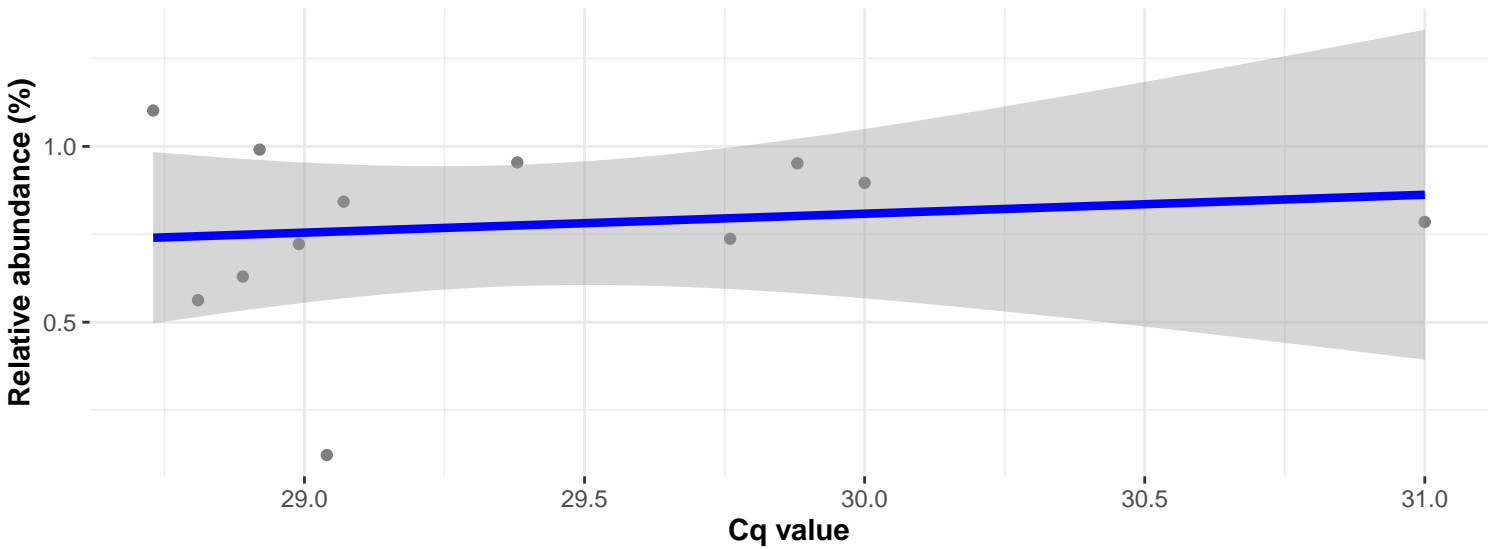
Correlation within: IM-PIM

$\log_e(S) = 5.182$, $p = 0.574$, $\hat{\rho}_{\text{Spearman}} = 0.191$, $CI_{95\%} [-0.478, 0.720]$, $n_{\text{pairs}} = 11$

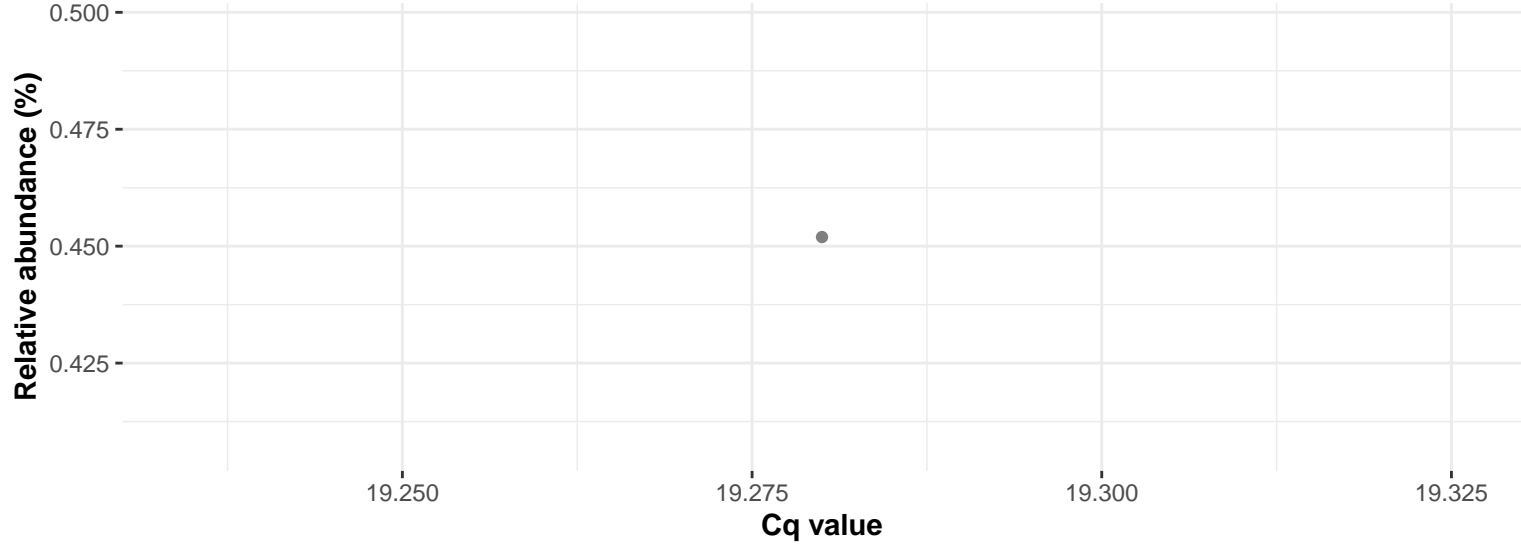


Correlation within: IM-DIM

$\log_e(S) = 5.568$, $p = 0.795$, $\hat{\rho}_{\text{Spearman}} = 0.084$, $CI_{95\%} [-0.529, 0.639]$, $n_{\text{pairs}} = 12$



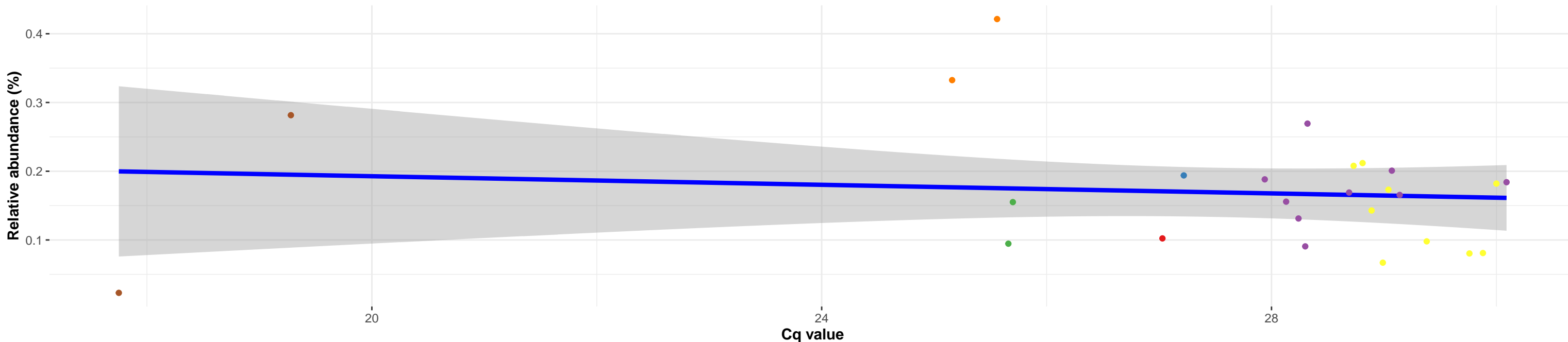
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus thermoamylovorans

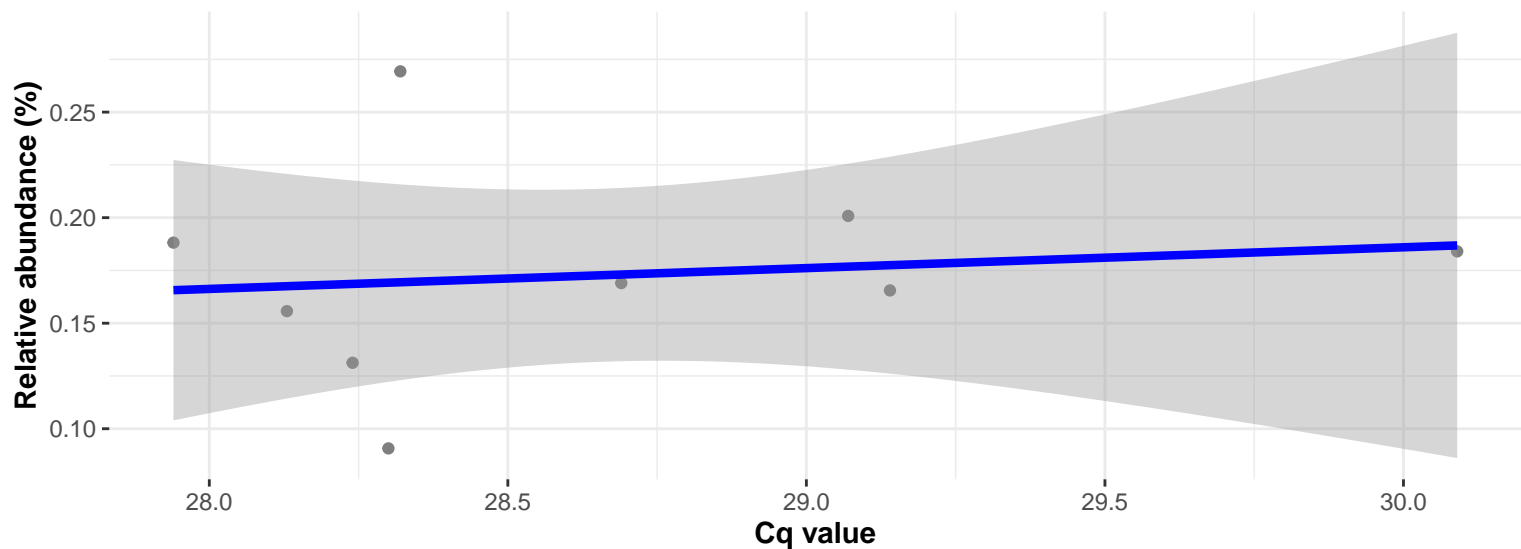
Correlation with all samples

$\log_e(S) = 8.155$, $p = 0.351$, $\hat{\rho}_{\text{Spearman}} = -0.190$, $CI_{95\%} [-0.547, 0.224]$, $n_{\text{pairs}} = 26$



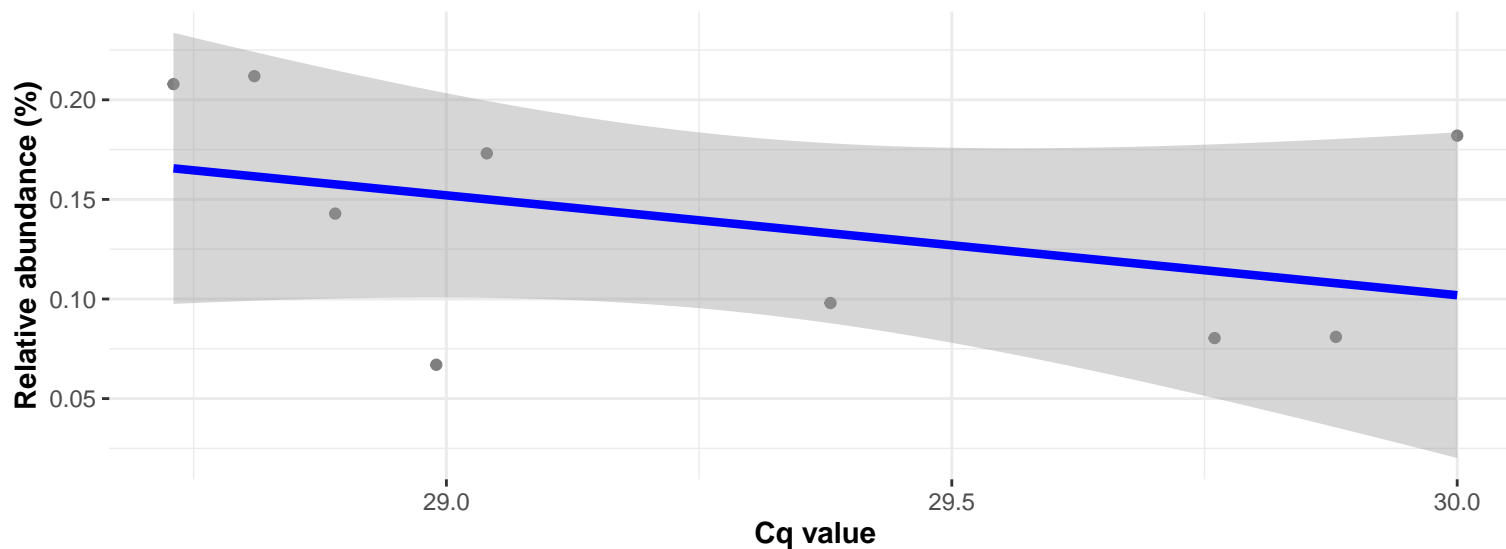
Correlation within: IM-PIM

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

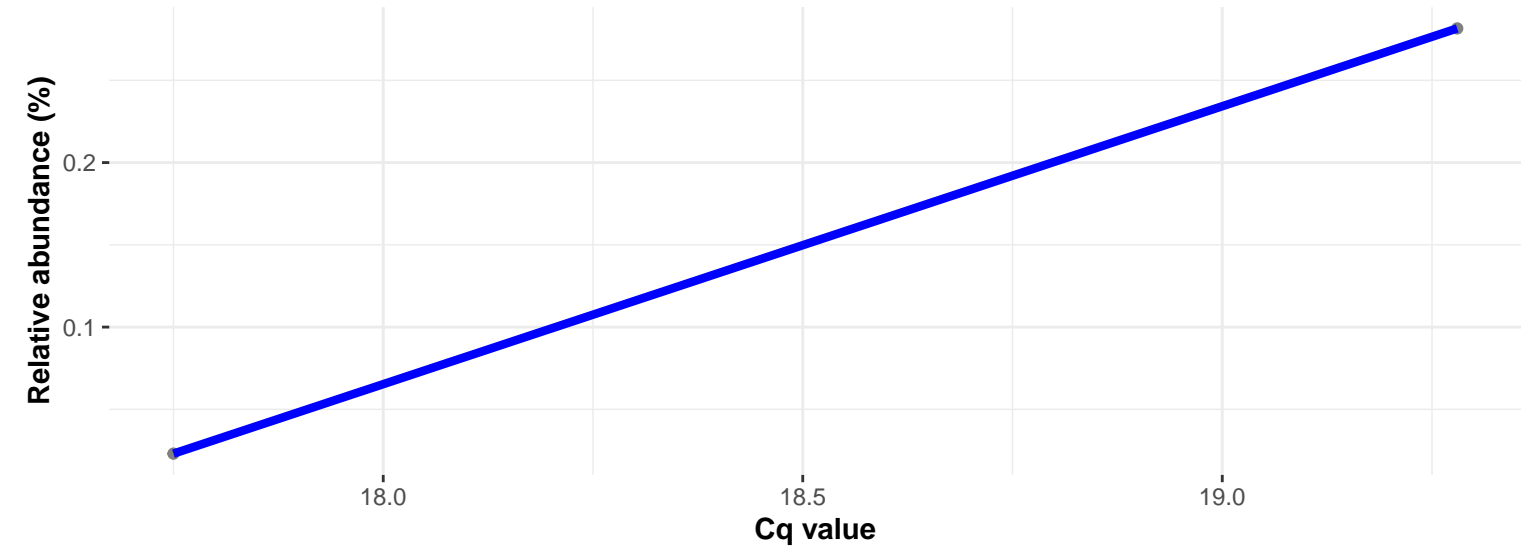


Correlation within: IM-DIM

$\log_e(S) = 5.136$, $p = 0.265$, $\hat{\rho}_{\text{Spearman}} = -0.417$, $CI_{95\%} [-0.853, 0.363]$, $n_{\text{pairs}} = 9$



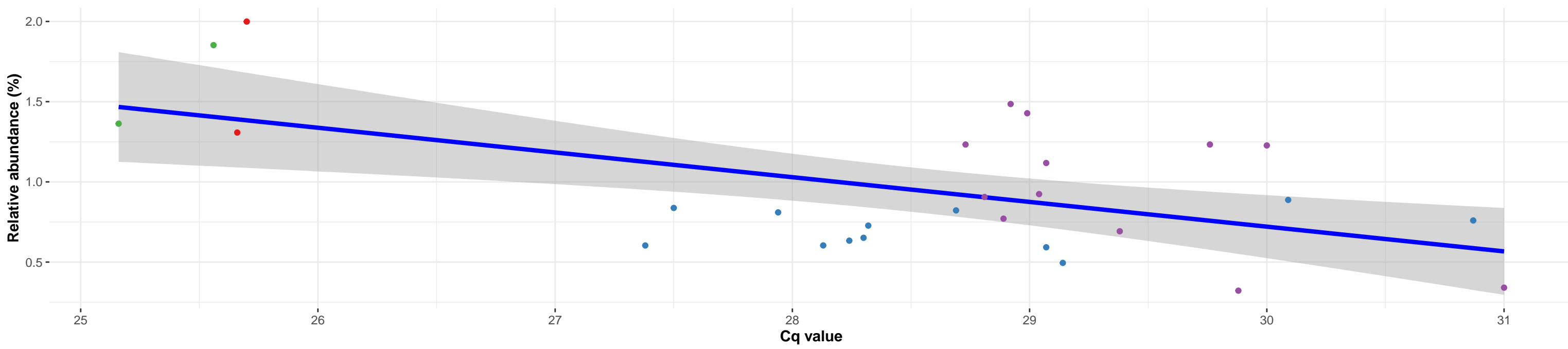
Correlation within: Feed



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

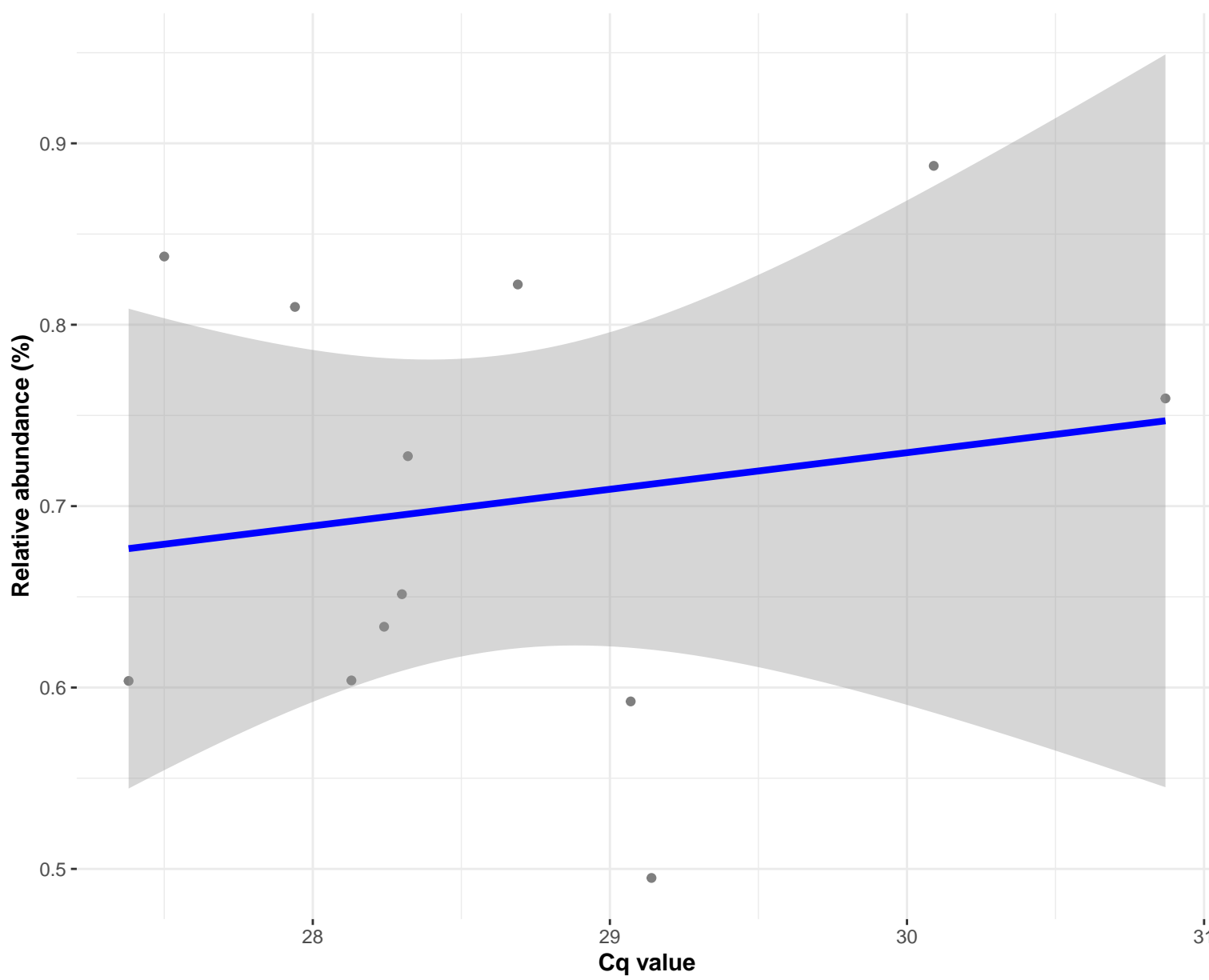
Correlation with all samples

$\log_e(S) = 8.483$, $p = 0.095$, $\hat{\rho}_{\text{Spearman}} = -0.322$, $CI_{95\%} [-0.628, 0.069]$, $n_{\text{pairs}} = 28$



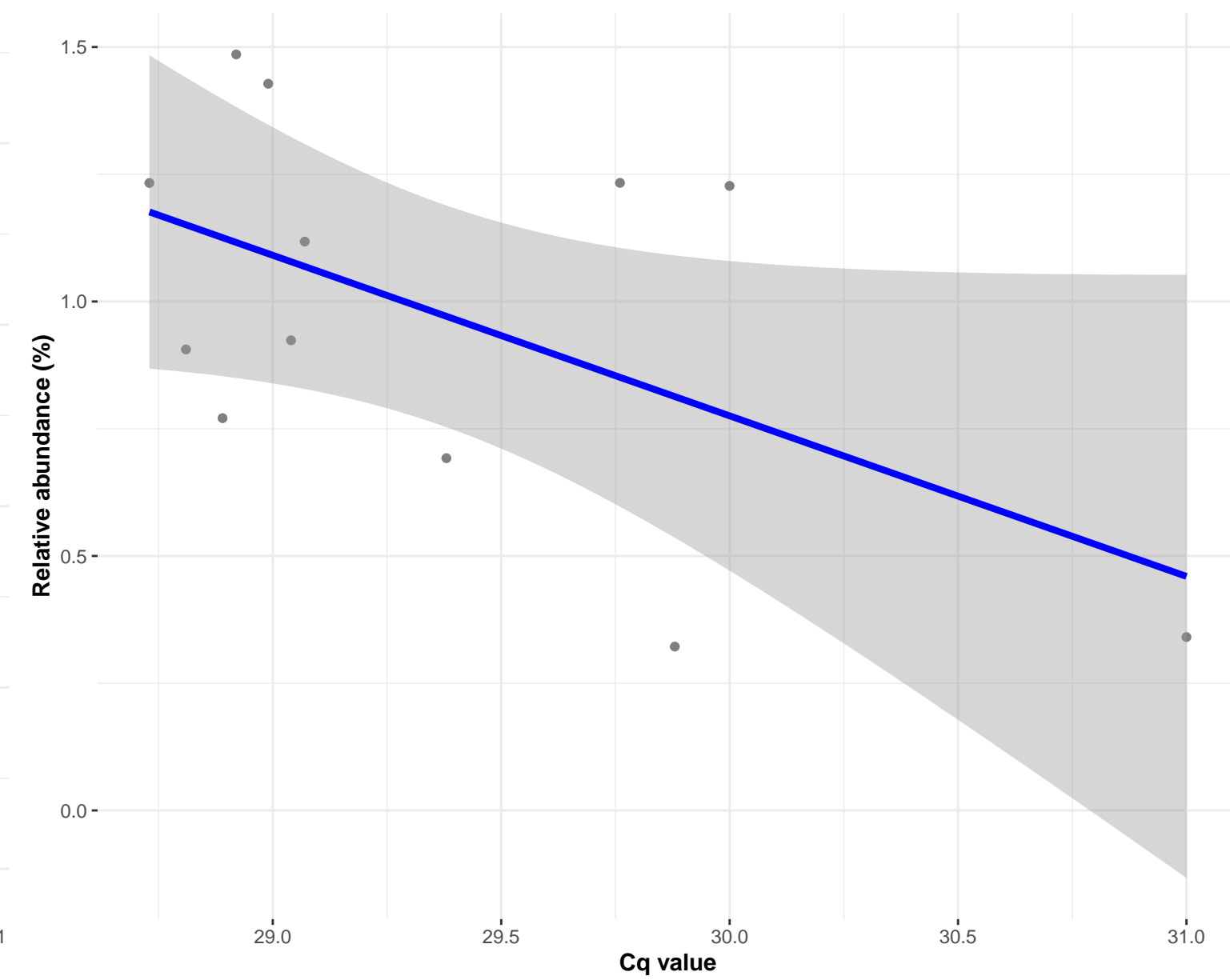
Correlation within: IM-PIM

$\log_e(S) = 5.606$, $p = 0.880$, $\hat{\rho}_{\text{Spearman}} = 0.049$, $CI_{95\%} [-0.554, 0.618]$, $n_{\text{pairs}} = 12$



Correlation within: IM-DIM

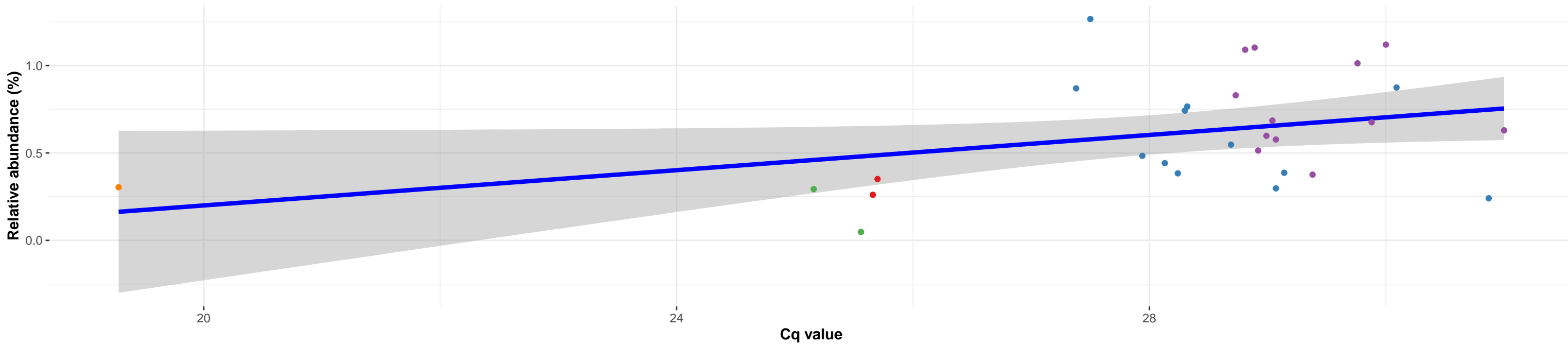
$\log_e(S) = 5.966$, $p = 0.245$, $\hat{\rho}_{\text{Spearman}} = -0.364$, $CI_{95\%} [-0.783, 0.284]$, $n_{\text{pairs}} = 12$



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

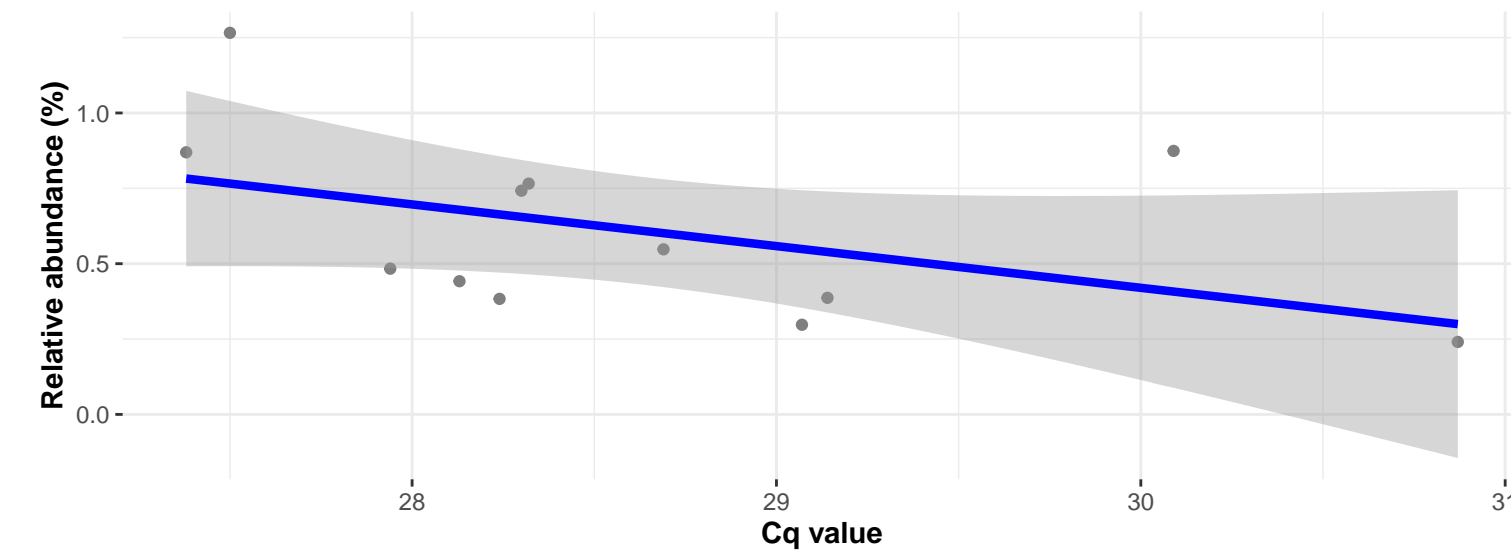
Correlation with all samples

$\log_e(S) = 7.953$, $p = 0.114$, $\hat{\rho}_{\text{Spearman}} = 0.300$, $CI_{95\%} [-0.087, 0.607]$, $n_{\text{pairs}} = 29$



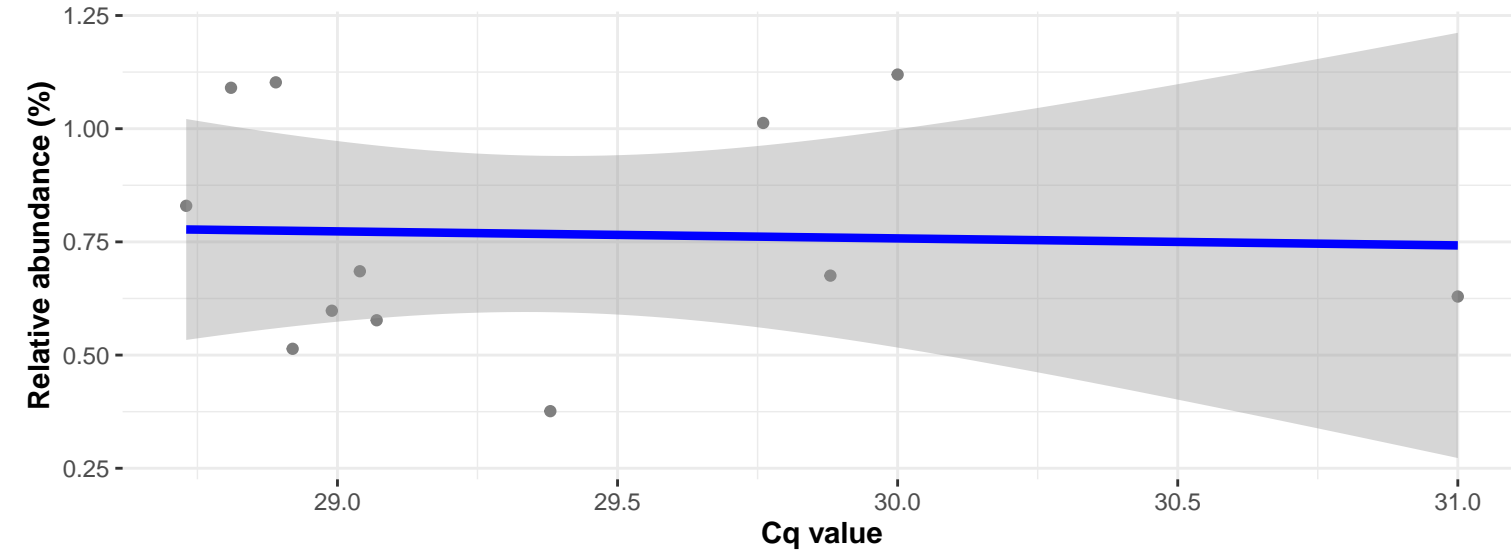
Correlation within: IM-PIM

$\log_e(S) = 6.016$, $p = 0.159$, $\hat{\rho}_{\text{Spearman}} = -0.434$, $CI_{95\%} [-0.813, 0.205]$, $n_{\text{pairs}} = 12$

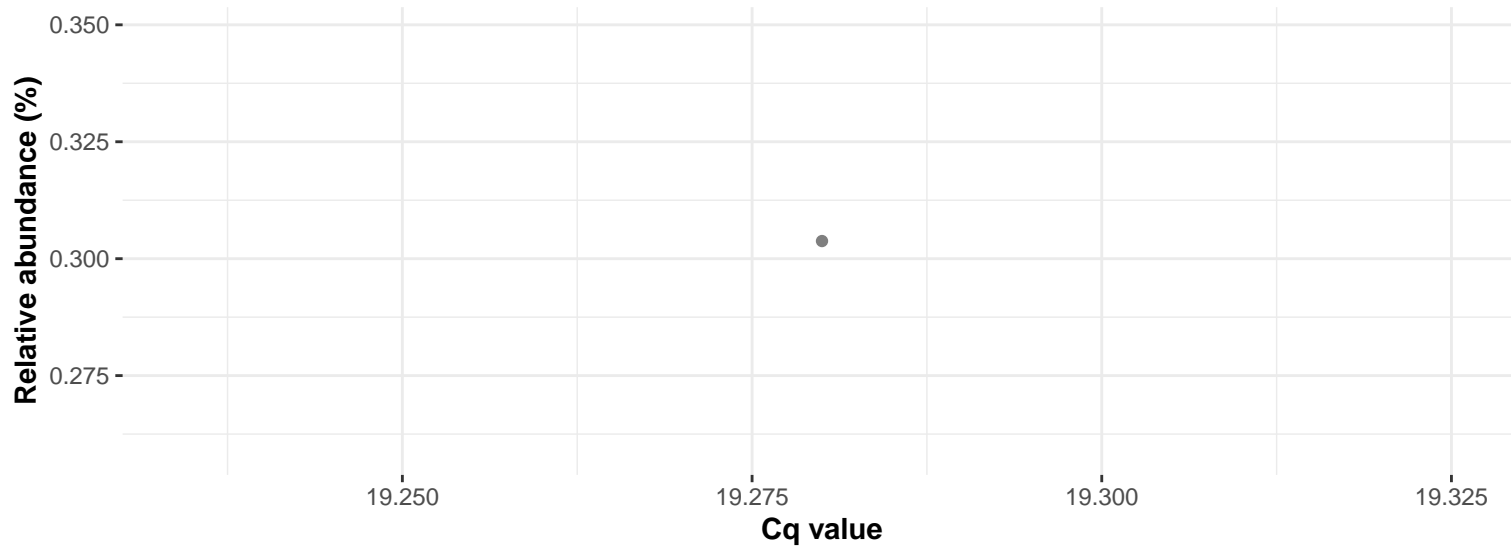


Correlation within: IM-DIM

$\log_e(S) = 5.749$, $p = 0.762$, $\hat{\rho}_{\text{Spearman}} = -0.098$, $CI_{95\%} [-0.647, 0.519]$, $n_{\text{pairs}} = 12$



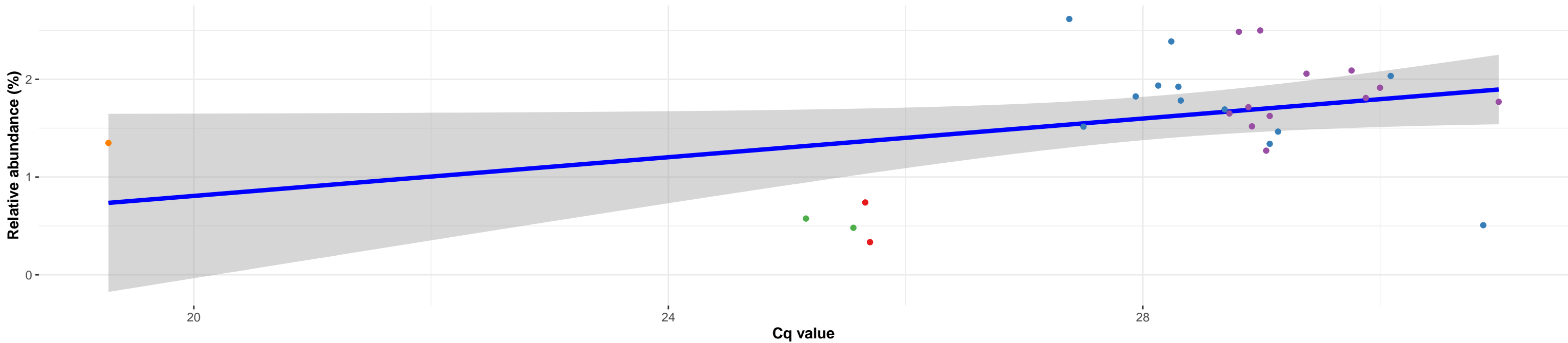
Correlation within: Feed



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

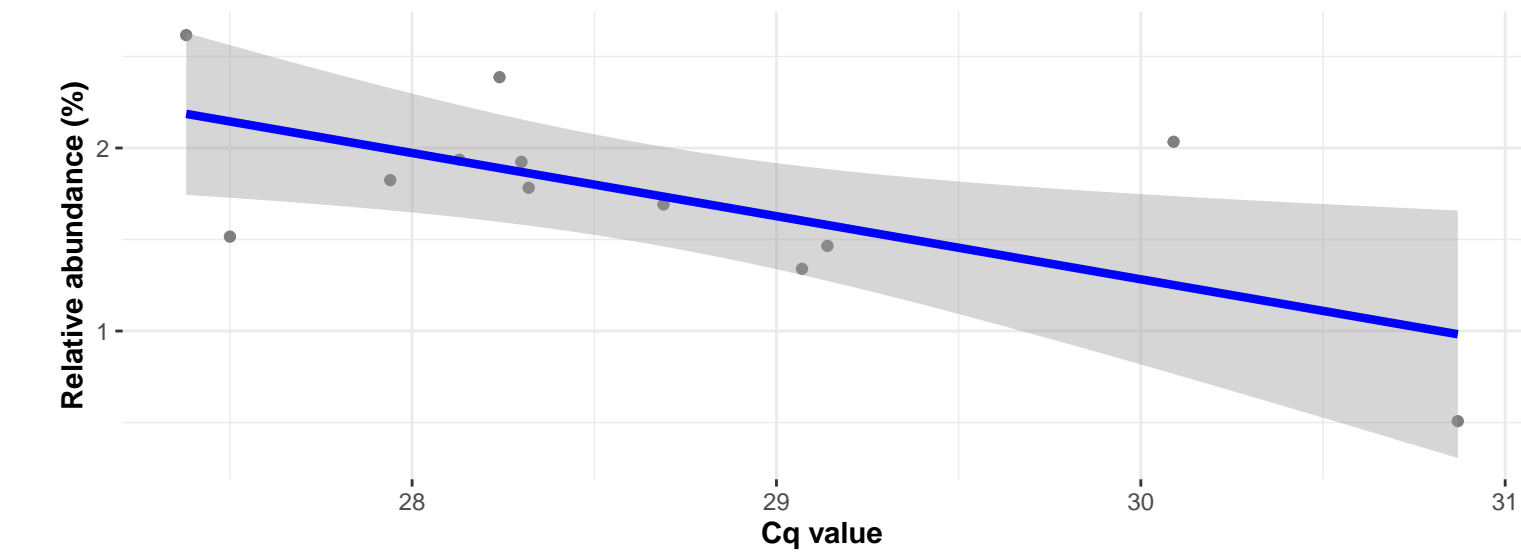
Correlation with all samples

$\log_e(S) = 8.024$, $p = 0.194$, $\hat{\rho}_{\text{Spearman}} = 0.248$, $CI_{95\%} [-0.141, 0.571]$, $n_{\text{pairs}} = 29$



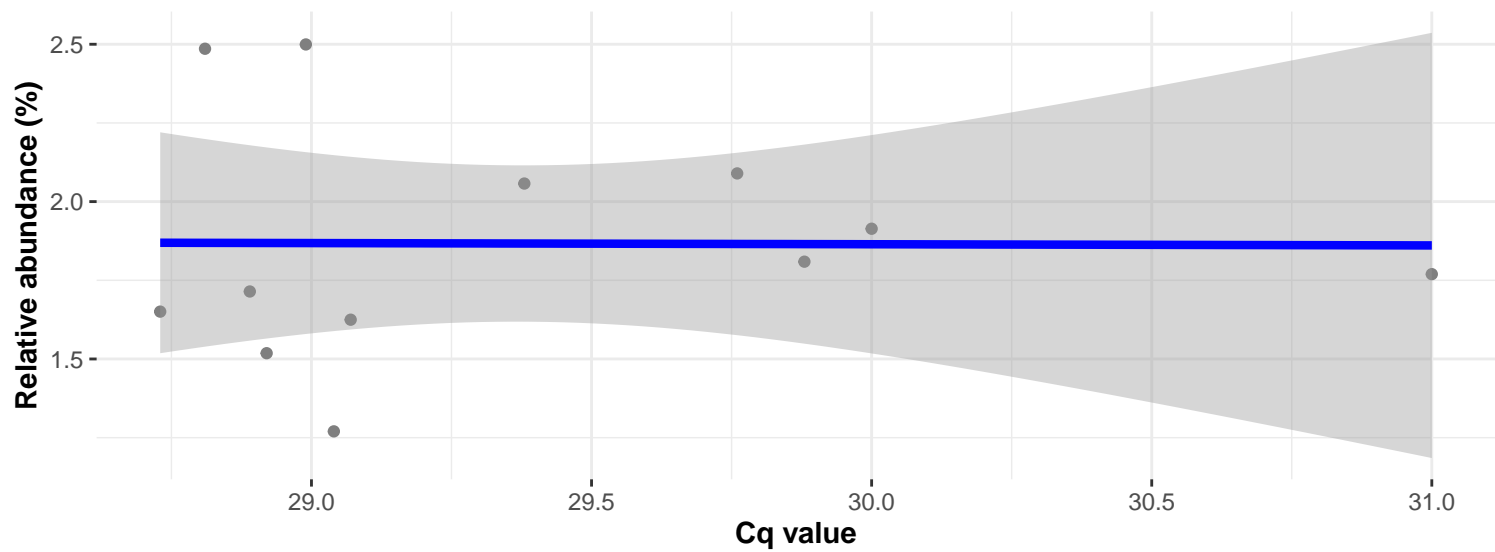
Correlation within: IM-PIM

$\log_e(S) = 6.078$, $p = 0.080$, $\hat{\rho}_{\text{Spearman}} = -0.524$, $CI_{95\%} [-0.850, 0.090]$, $n_{\text{pairs}} = 12$

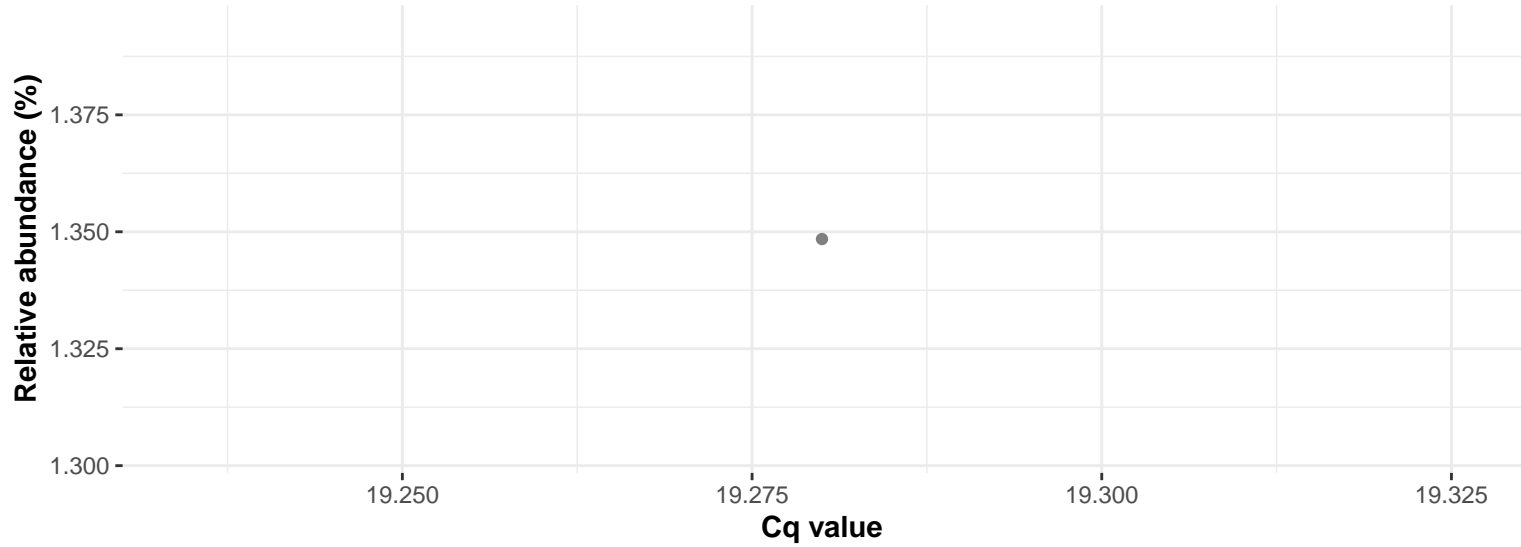


Correlation within: IM-DIM

$\log_e(S) = 5.497$, $p = 0.649$, $\hat{\rho}_{\text{Spearman}} = 0.147$, $CI_{95\%} [-0.481, 0.675]$, $n_{\text{pairs}} = 12$



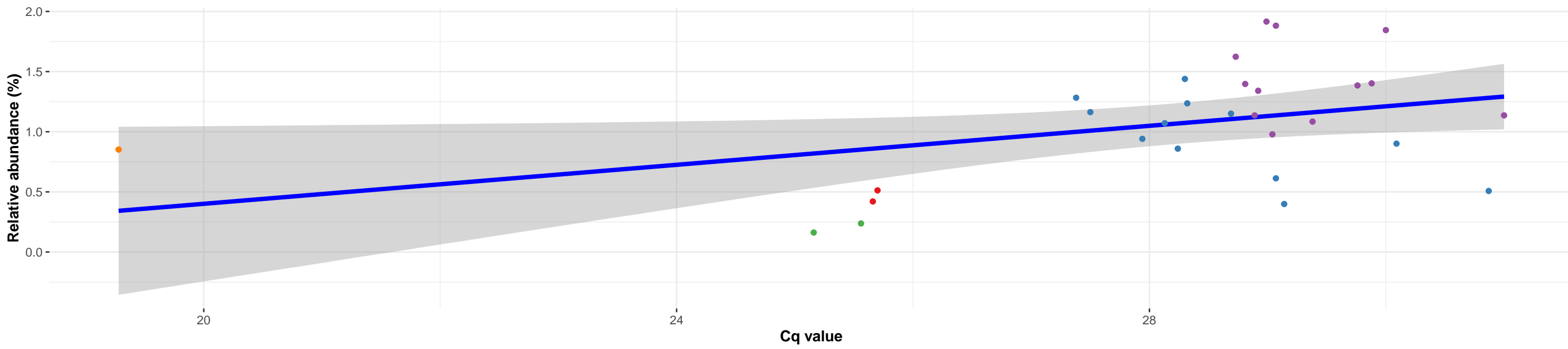
Correlation within: Feed



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

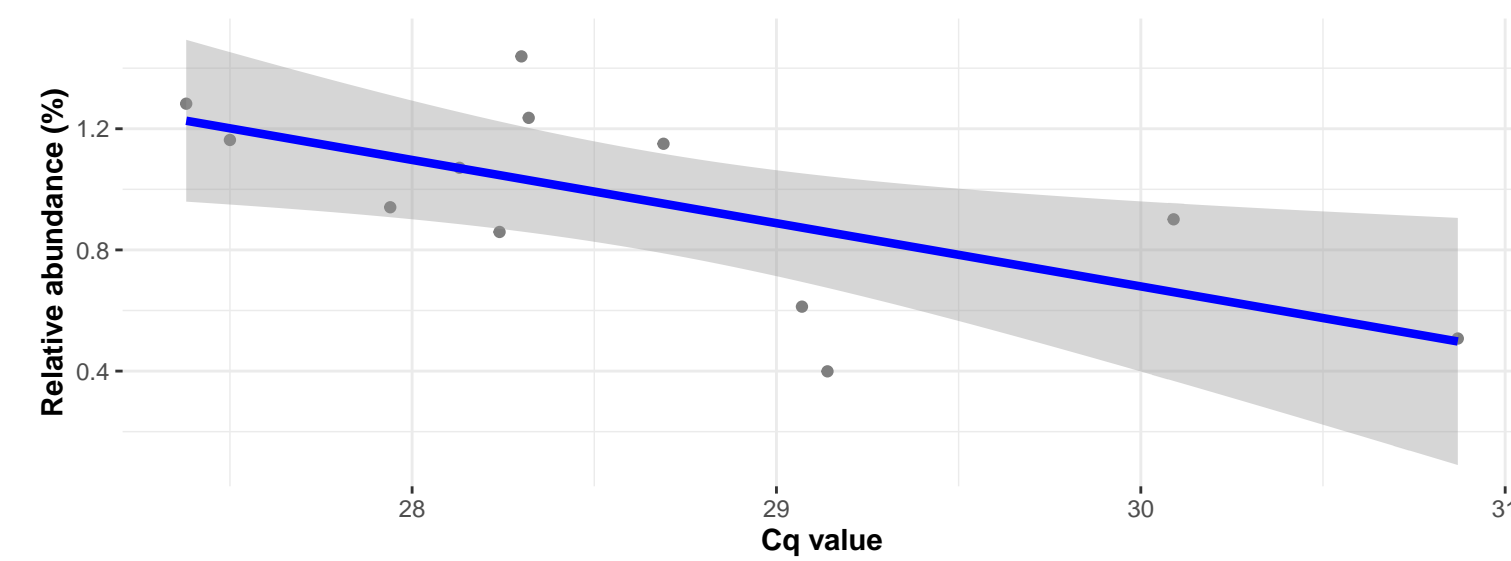
Correlation with all samples

$\log_e(S) = 7.910$, $p = 0.082$, $\hat{\rho}_{\text{Spearman}} = 0.329$, $CI_{95\%} [-0.054, 0.628]$, $n_{\text{pairs}} = 29$



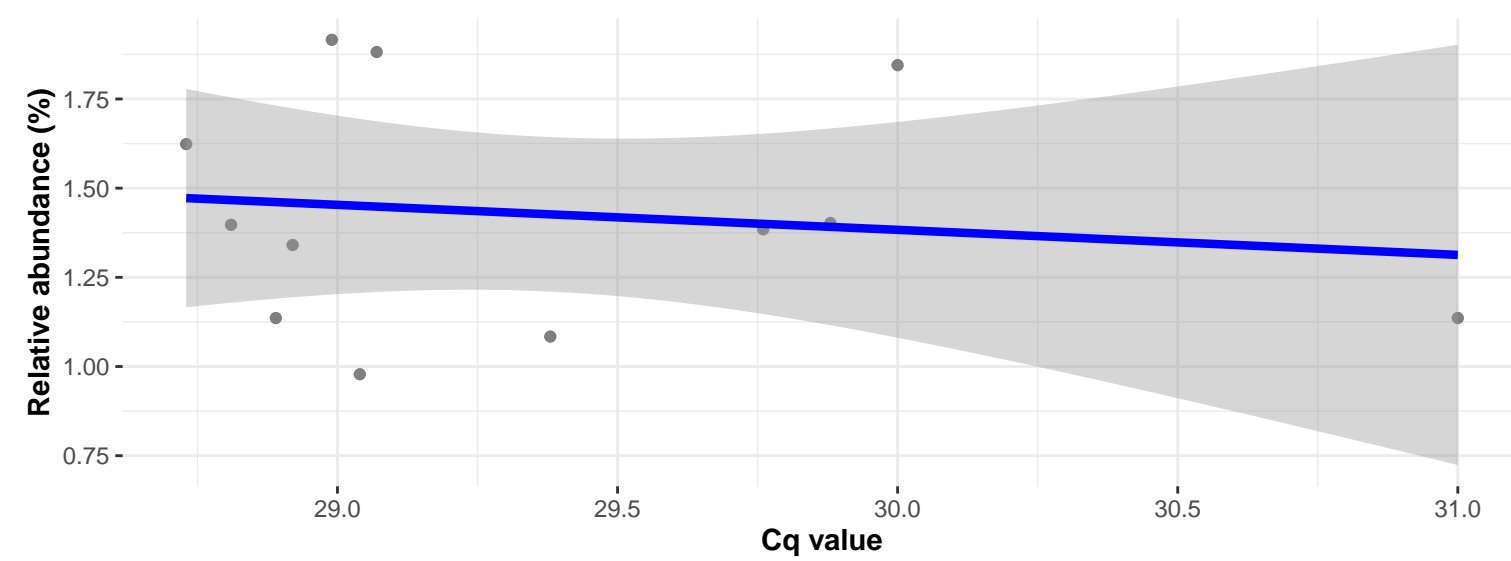
Correlation within: IM-PIM

$\log_e(S) = 6.144$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = -0.629$, $CI_{95\%} [-0.888, -0.068]$, $n_{\text{pairs}} = 12$

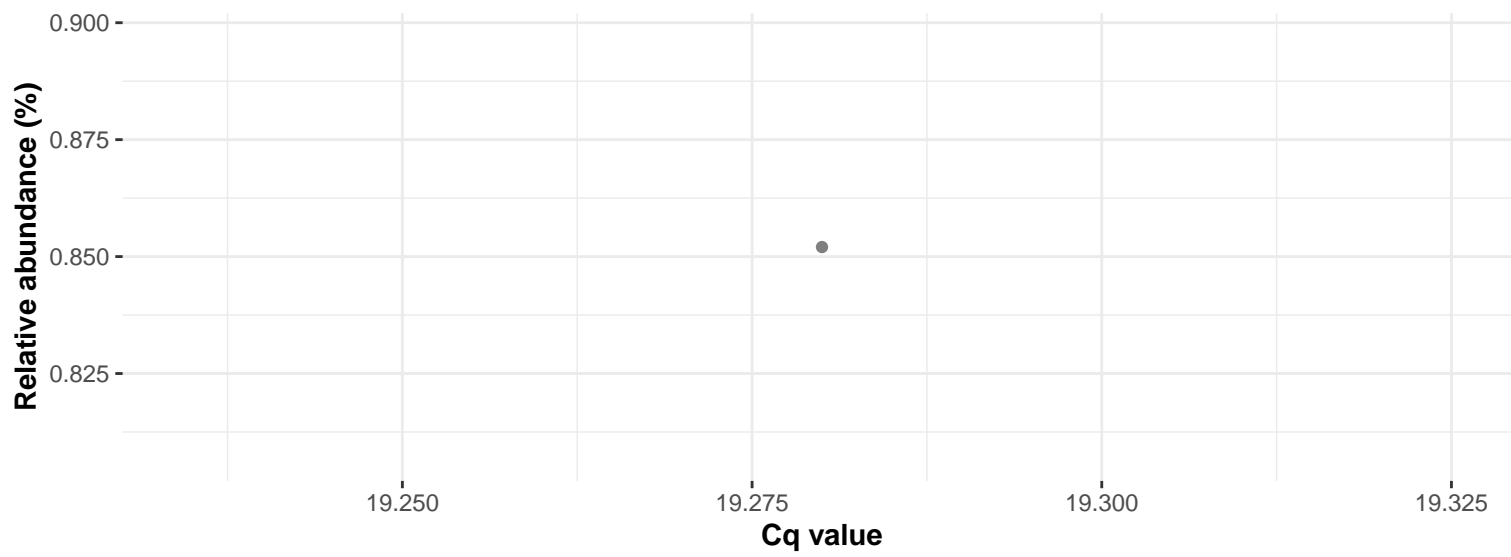


Correlation within: IM-DIM

$\log_e(S) = 5.684$, $p = 0.931$, $\hat{\rho}_{\text{Spearman}} = -0.028$, $CI_{95\%} [-0.605, 0.568]$, $n_{\text{pairs}} = 12$



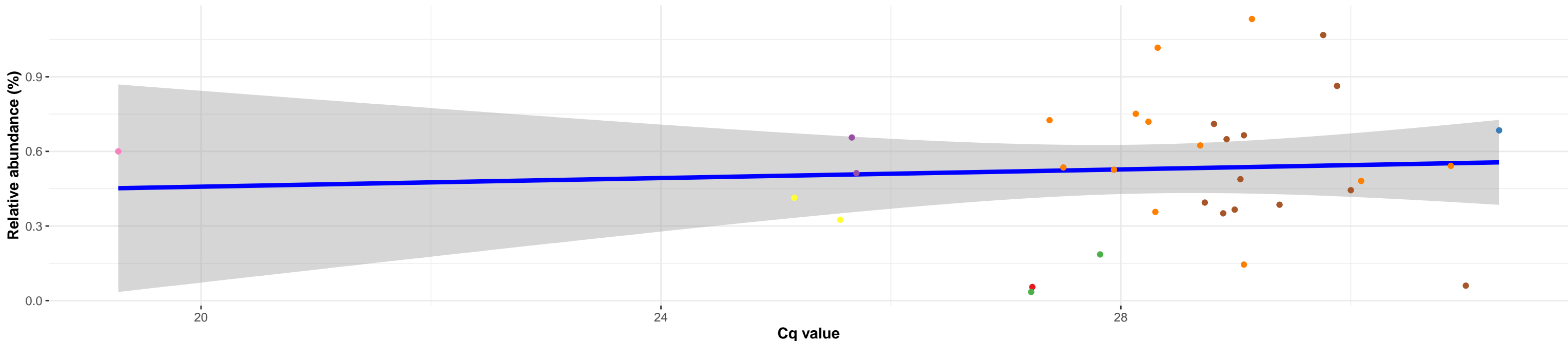
Correlation within: Feed



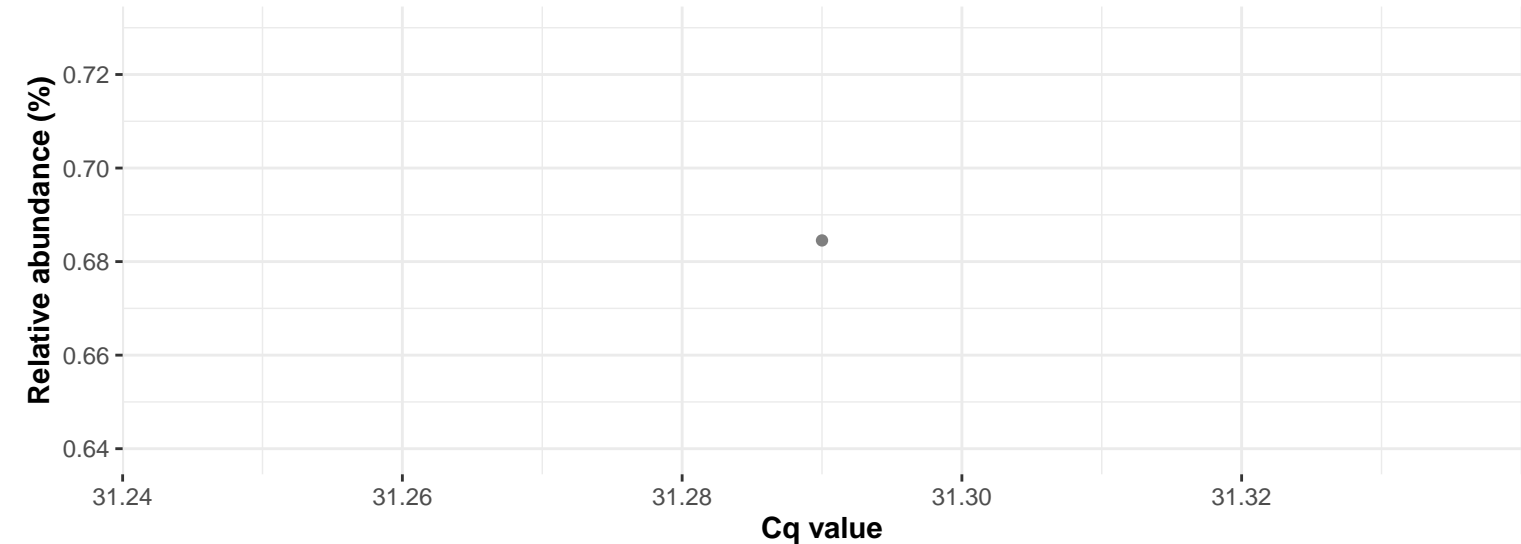
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Macrococcus; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 8.533$, $p = 0.400$, $\hat{\rho}_{\text{Spearman}} = 0.151$, $CI_{95\%} [-0.213, 0.478]$, $n_{\text{pairs}} = 33$

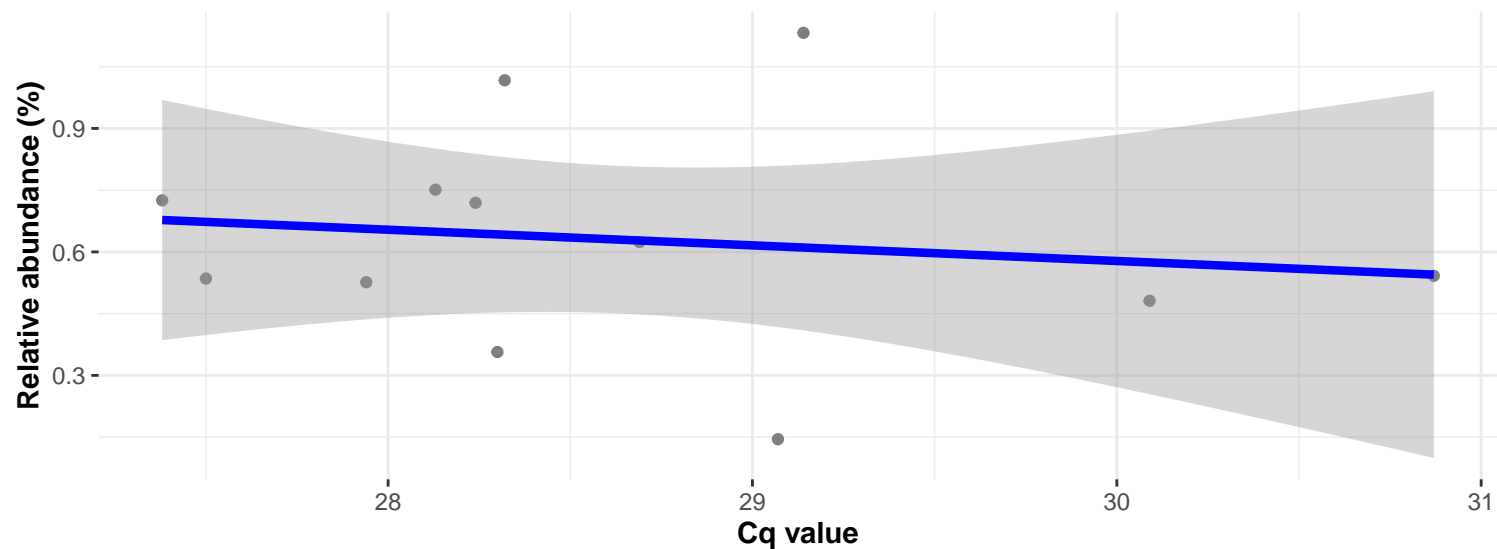


Correlation within: REF-PIM



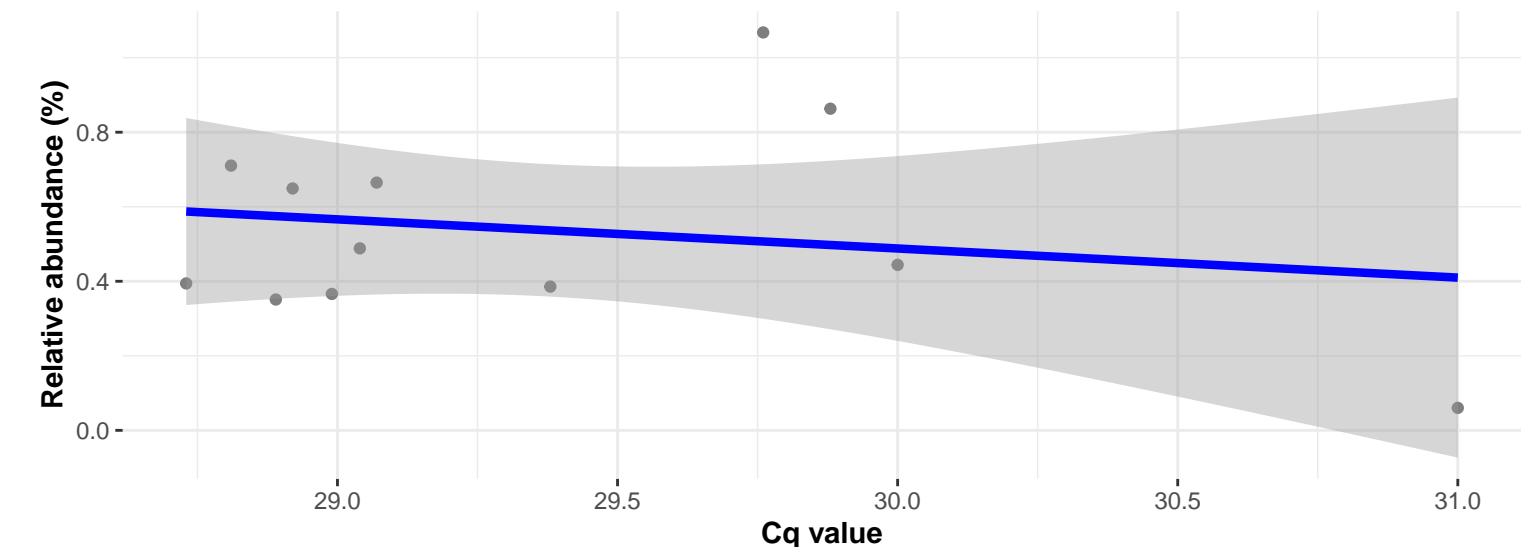
Correlation within: IM-PIM

$\log_e(S) = 5.768$, $p = 0.713$, $\hat{\rho}_{\text{Spearman}} = -0.119$, $CI_{95\%} [-0.660, 0.503]$, $n_{\text{pairs}} = 12$

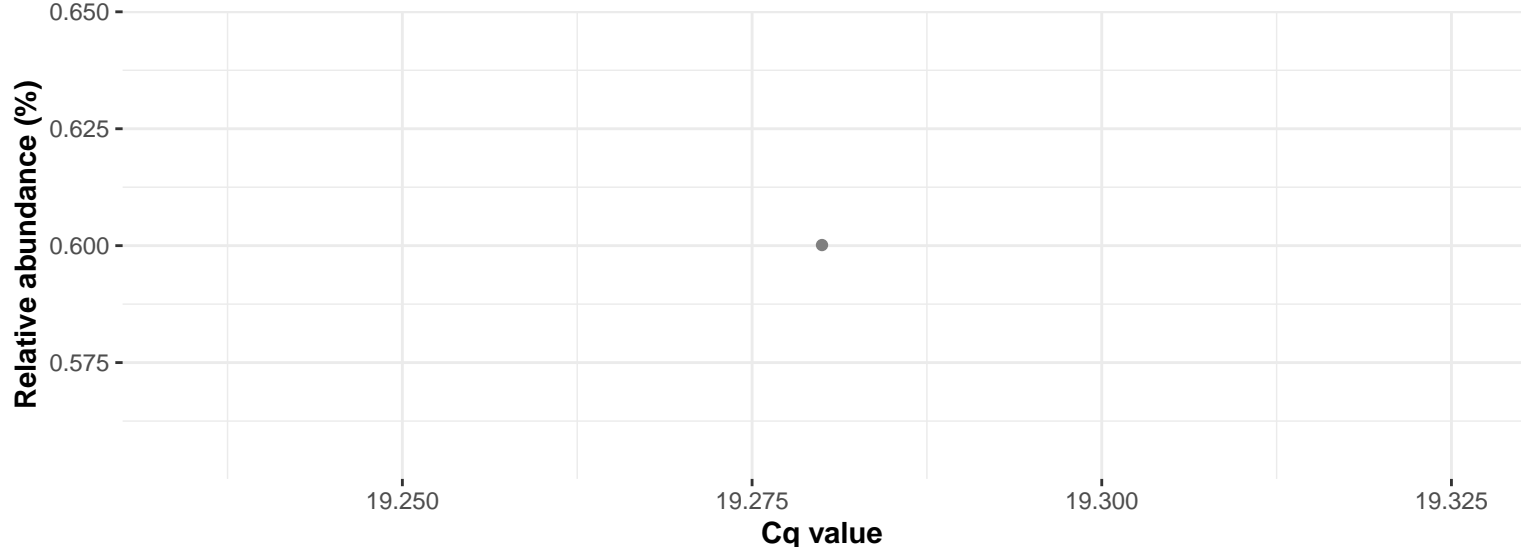


Correlation within: IM-DIM

$\log_e(S) = 5.628$, $p = 0.931$, $\hat{\rho}_{\text{Spearman}} = 0.028$, $CI_{95\%} [-0.568, 0.605]$, $n_{\text{pairs}} = 12$



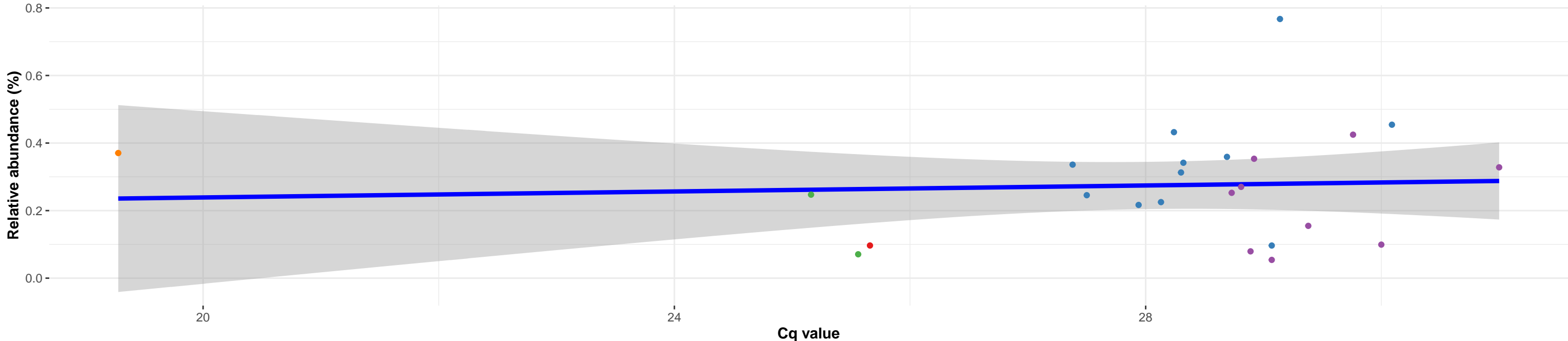
Correlation within: Feed



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

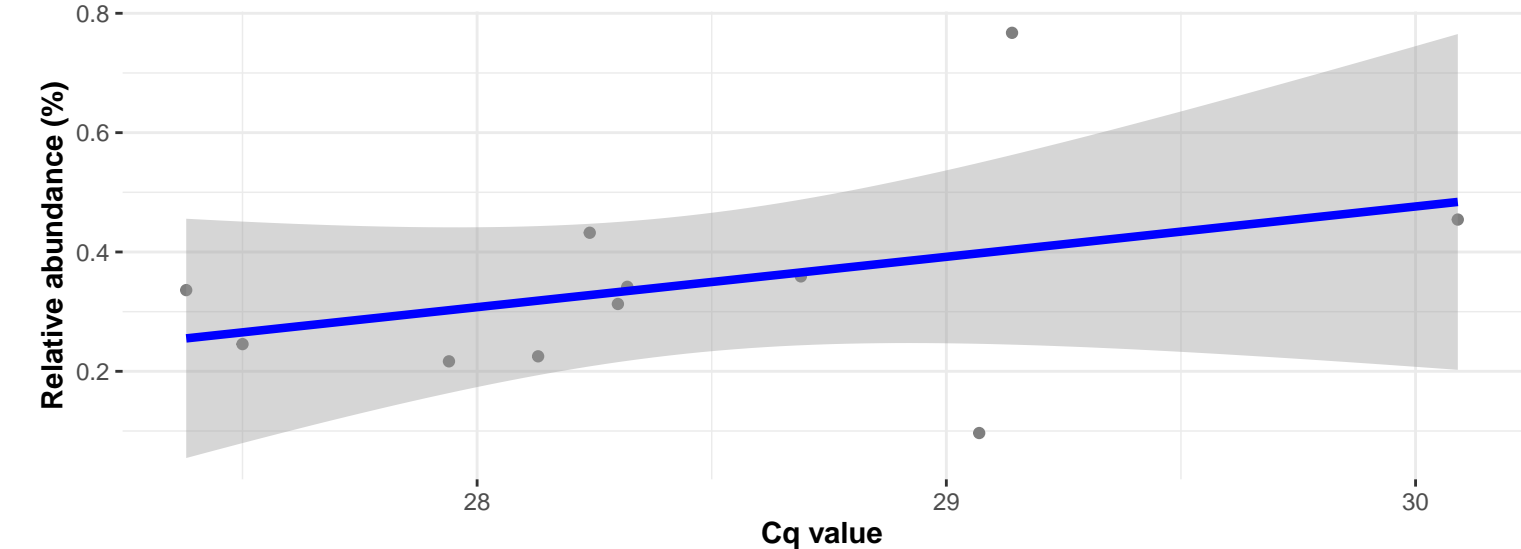
Correlation with all samples

$\log_e(S) = 7.595$, $p = 0.529$, $\hat{\rho}_{\text{Spearman}} = 0.135$, $CI_{95\%} [-0.295, 0.520]$, $n_{\text{pairs}} = 24$



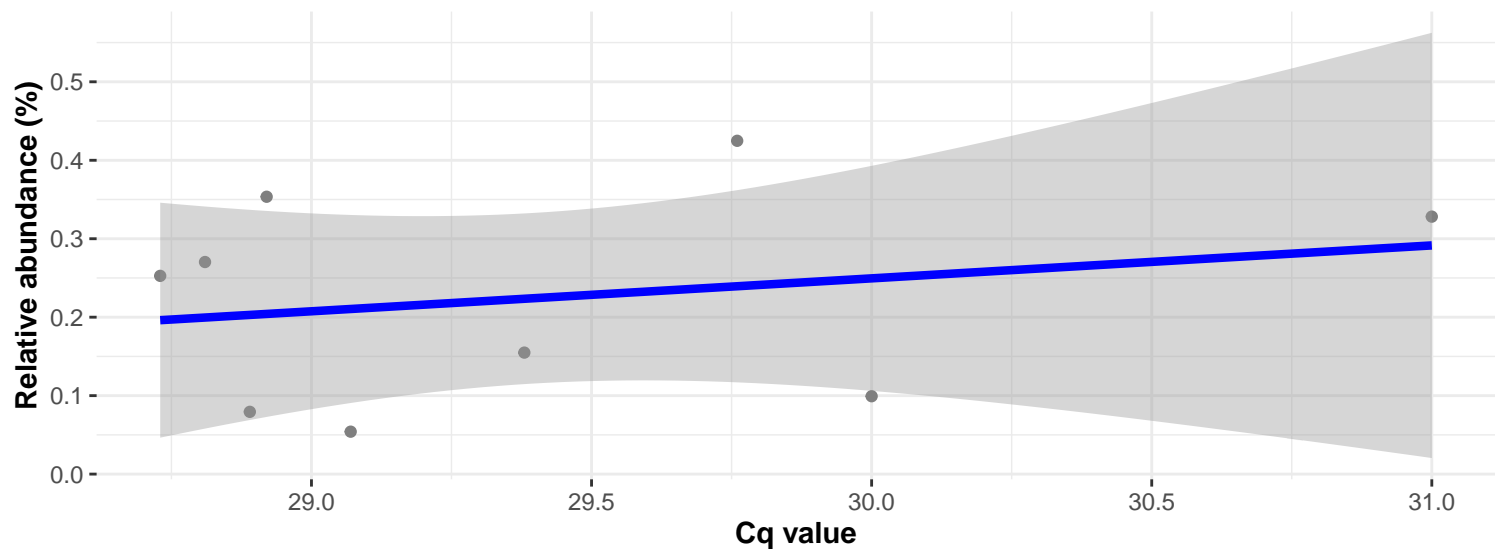
Correlation within: IM-PIM

$\log_e(S) = 4.736$, $p = 0.133$, $\hat{\rho}_{\text{Spearman}} = 0.482$, $CI_{95\%} [-0.186, 0.845]$, $n_{\text{pairs}} = 11$

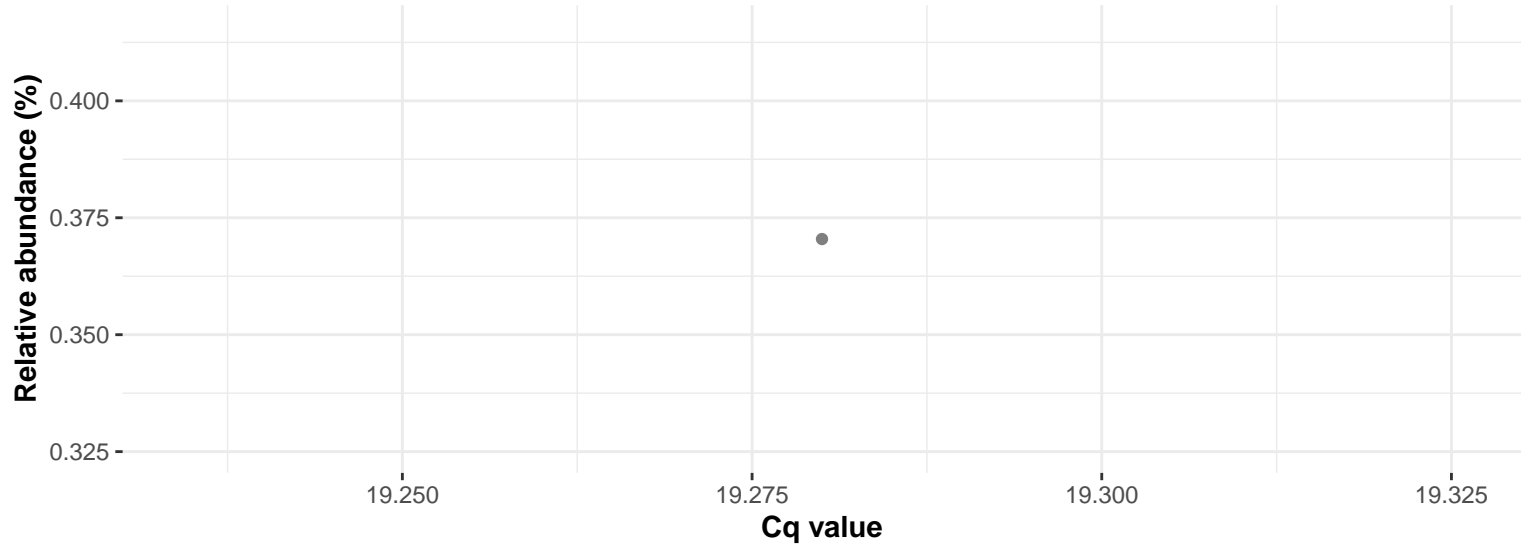


Correlation within: IM-DIM

$\log_e(S) = 4.625$, $p = 0.700$, $\hat{\rho}_{\text{Spearman}} = 0.150$, $CI_{95\%} [-0.587, 0.751]$, $n_{\text{pairs}} = 9$



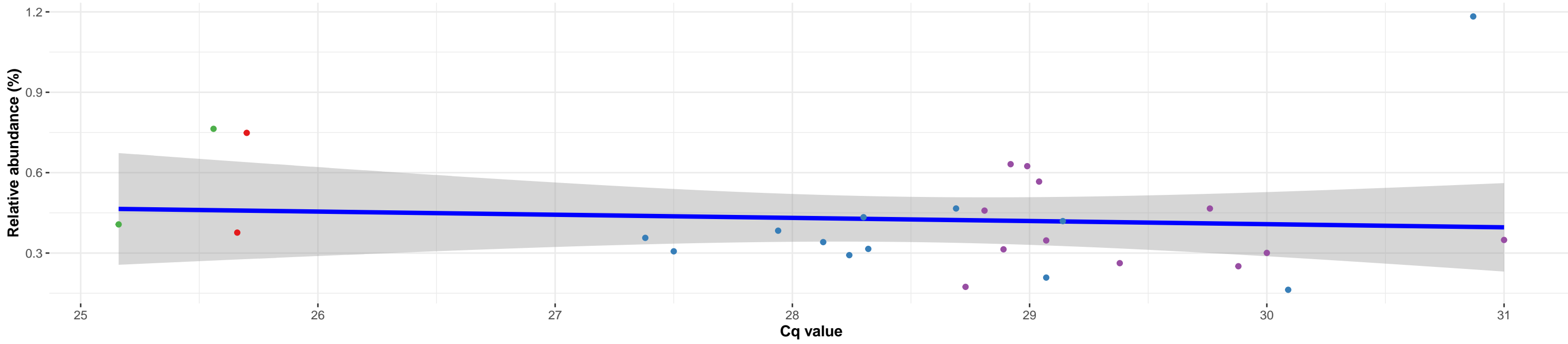
Correlation within: Feed



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

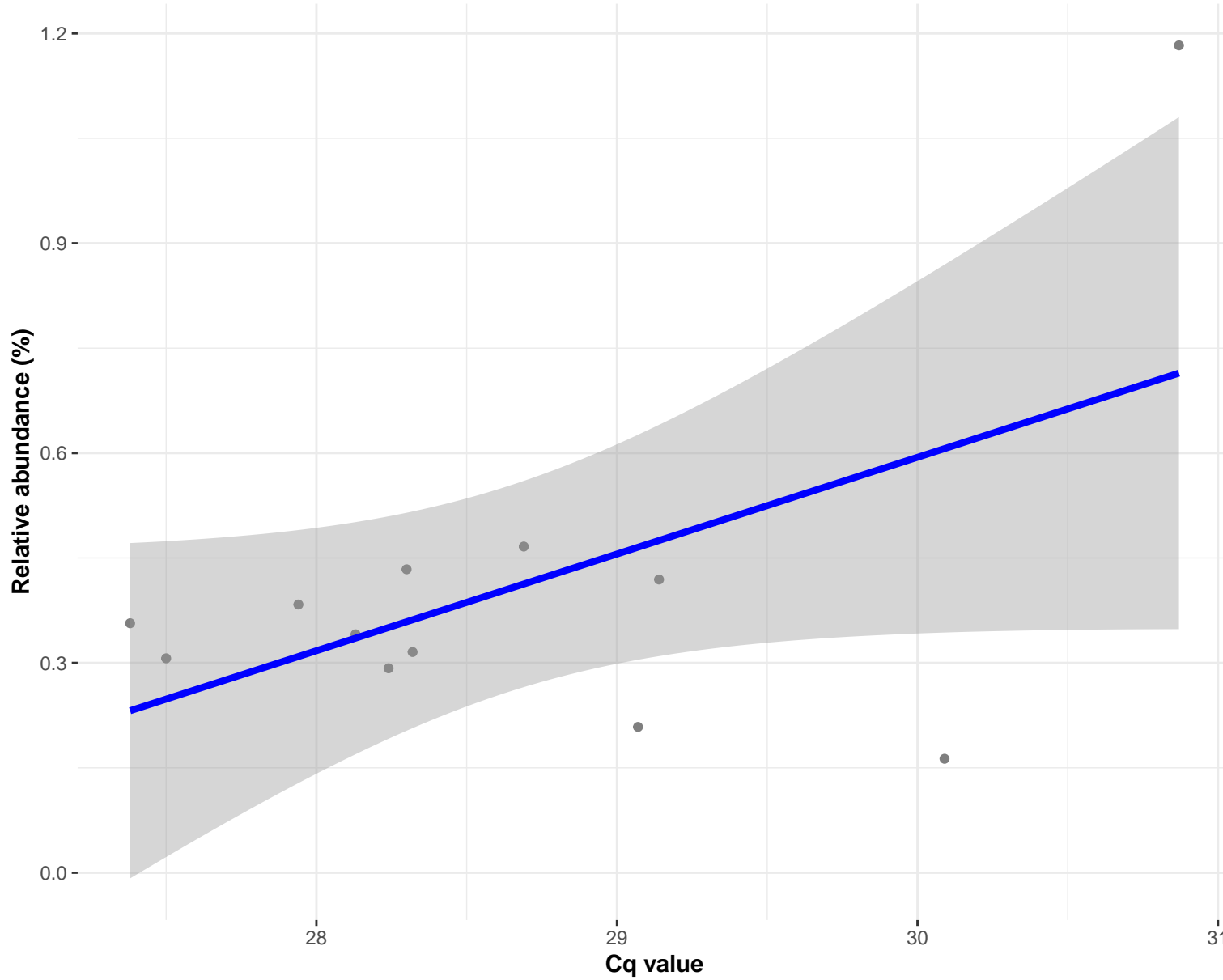
Correlation with all samples

$\log_e(S) = 8.396$, $p = 0.279$, $\hat{\rho}_{\text{Spearman}} = -0.212$, $\text{CI}_{95\%} [-0.550, 0.186]$, $n_{\text{pairs}} = 28$



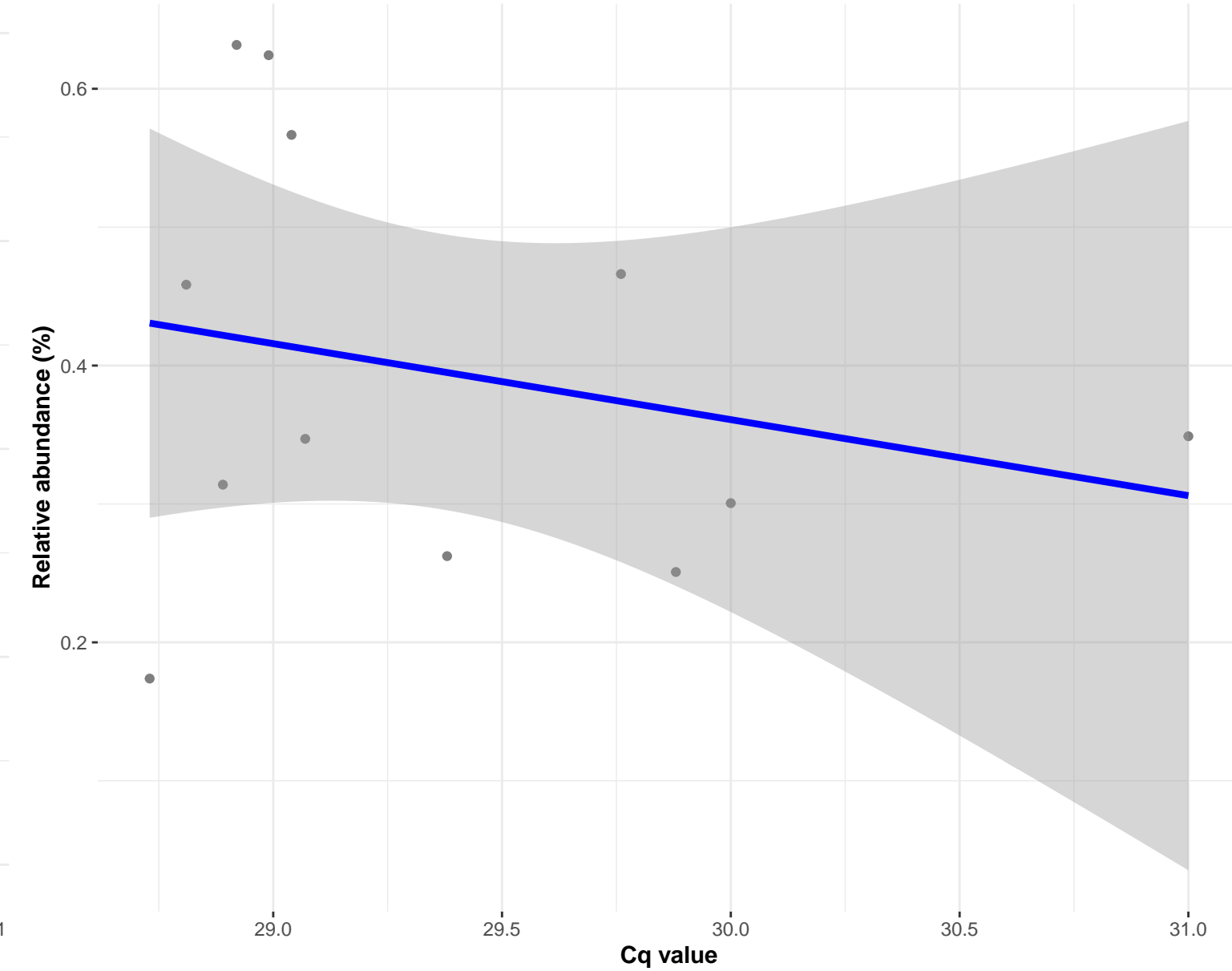
Correlation within: IM-PIM

$\log_e(S) = 5.529$, $p = 0.713$, $\hat{\rho}_{\text{Spearman}} = 0.119$, $\text{CI}_{95\%} [-0.503, 0.660]$, $n_{\text{pairs}} = 12$



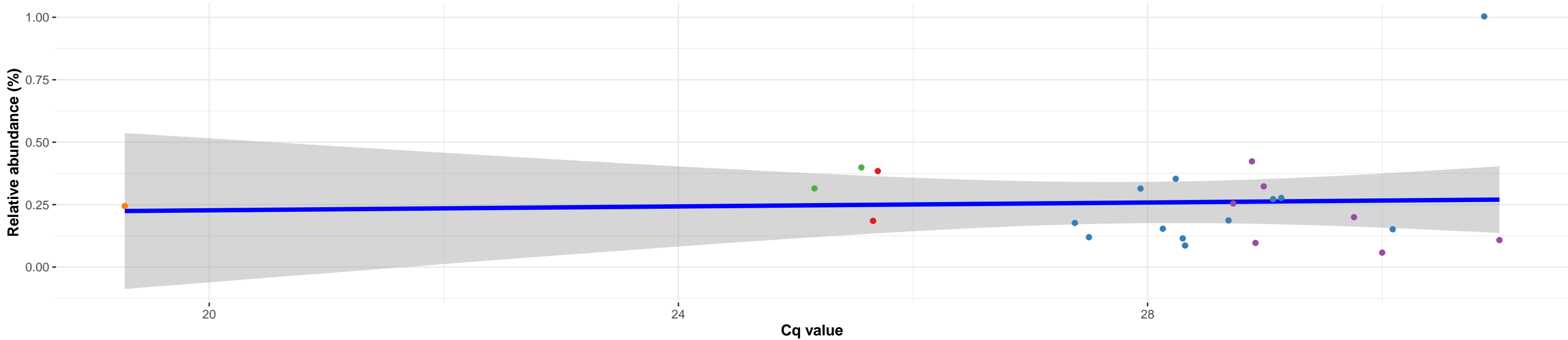
Correlation within: IM-DIM

$\log_e(S) = 5.768$, $p = 0.713$, $\hat{\rho}_{\text{Spearman}} = -0.119$, $\text{CI}_{95\%} [-0.660, 0.503]$, $n_{\text{pairs}} = 12$



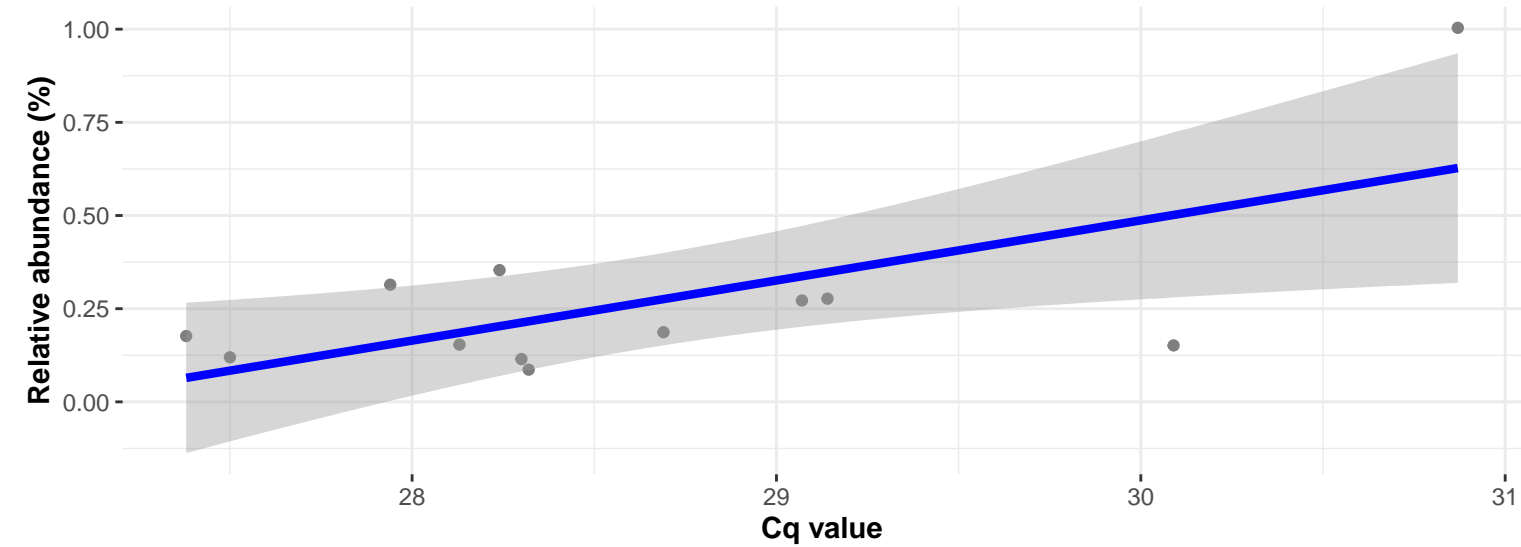
Correlation with all samples

$\log_e(S) = 7.912$, $p = 0.382$, $\hat{\rho}_{\text{Spearman}} = -0.187$, $CI_{95\%} [-0.558, 0.246]$, $n_{\text{pairs}} = 24$



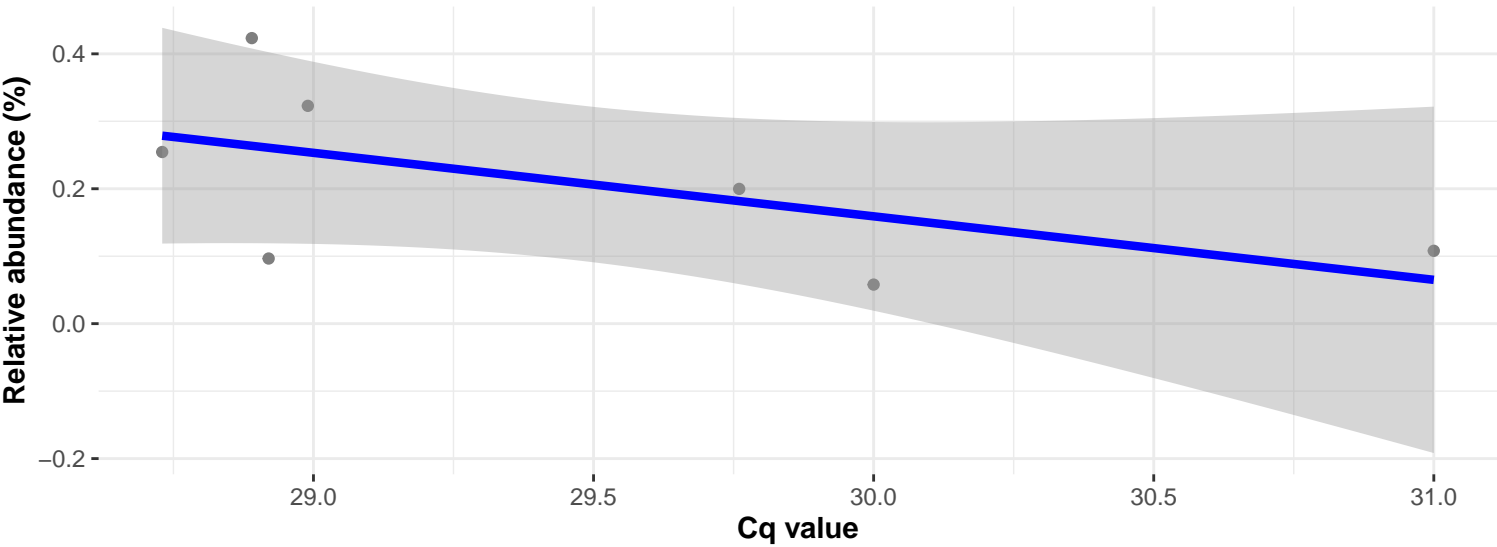
Correlation within: IM-PIM

$\log_e(S) = 5.375$, $p = 0.443$, $\hat{\rho}_{\text{Spearman}} = 0.245$, $CI_{95\%} [-0.399, 0.727]$, $n_{\text{pairs}} = 12$

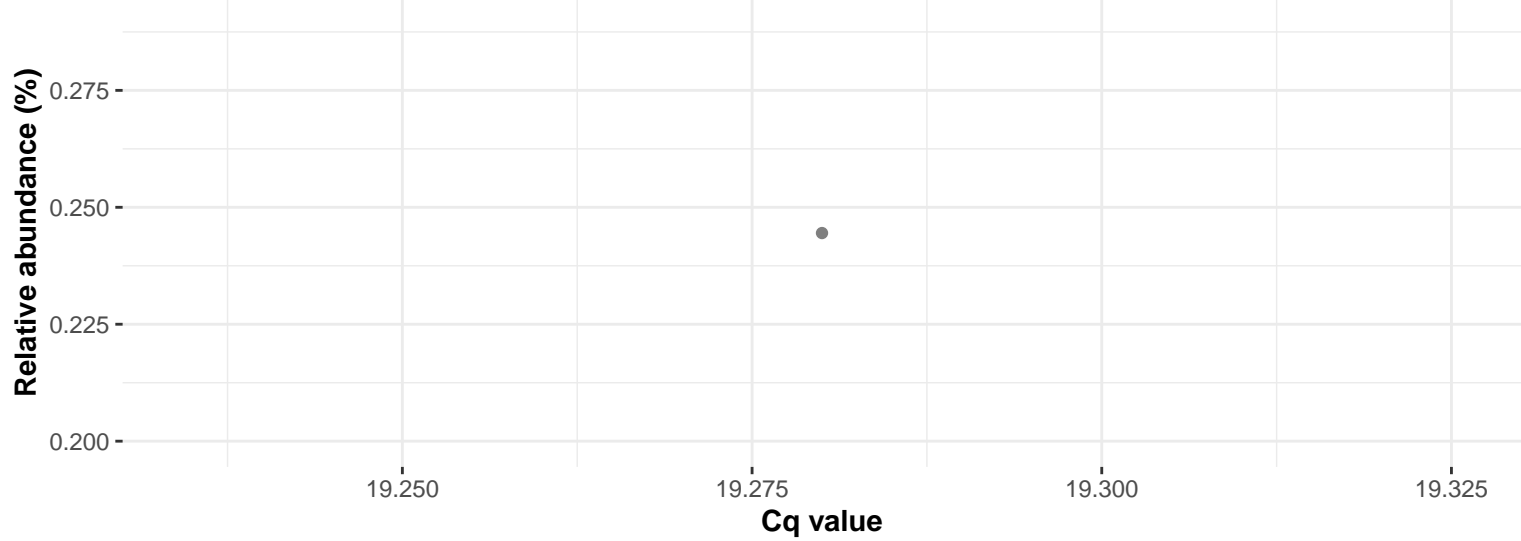


Correlation within: IM-DIM

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



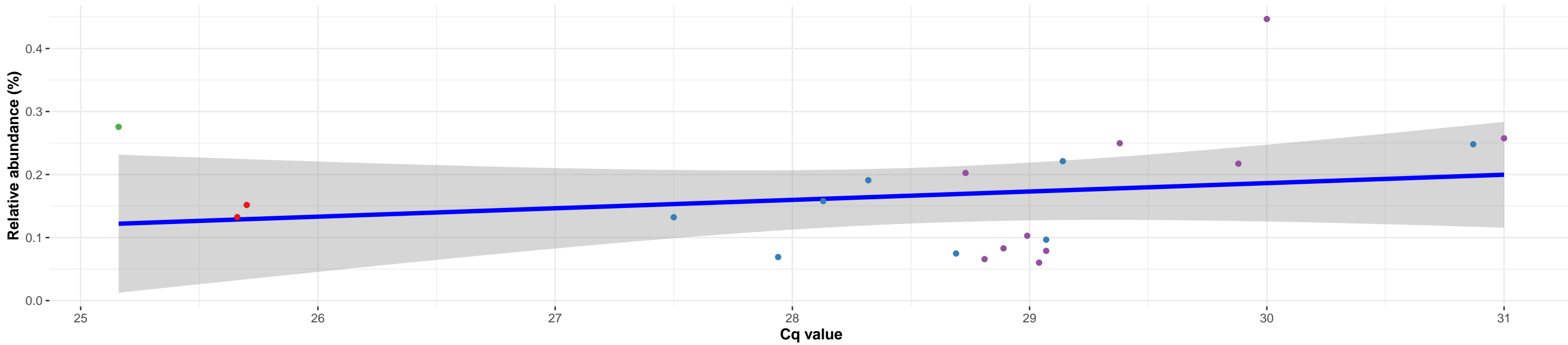
Correlation within: Feed



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

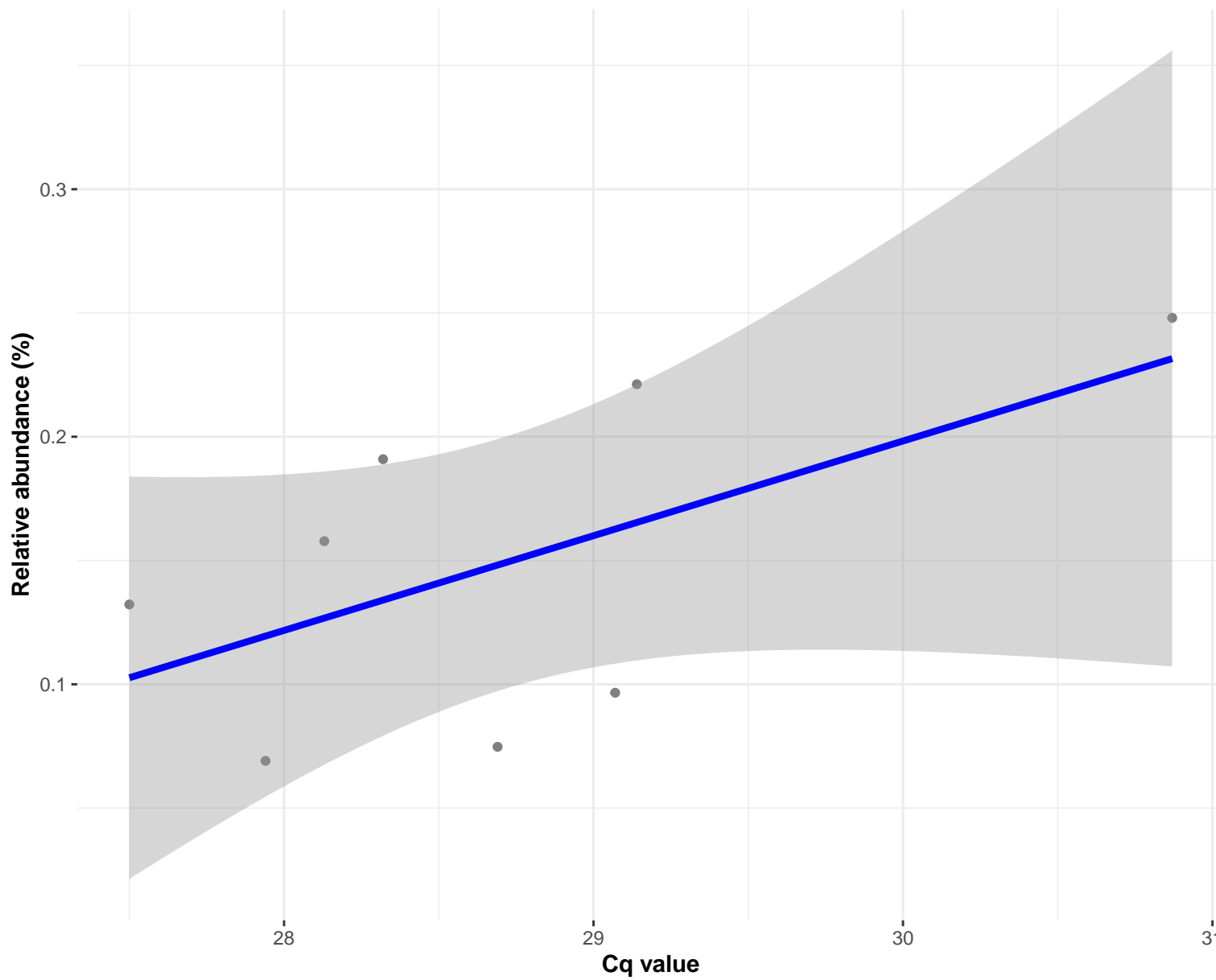
Correlation with all samples

$\log_e(S) = 6.960$, $p = 0.163$, $\hat{\rho}_{\text{Spearman}} = 0.316$, $CI_{95\%} [-0.148, 0.665]$, $n_{\text{pairs}} = 21$



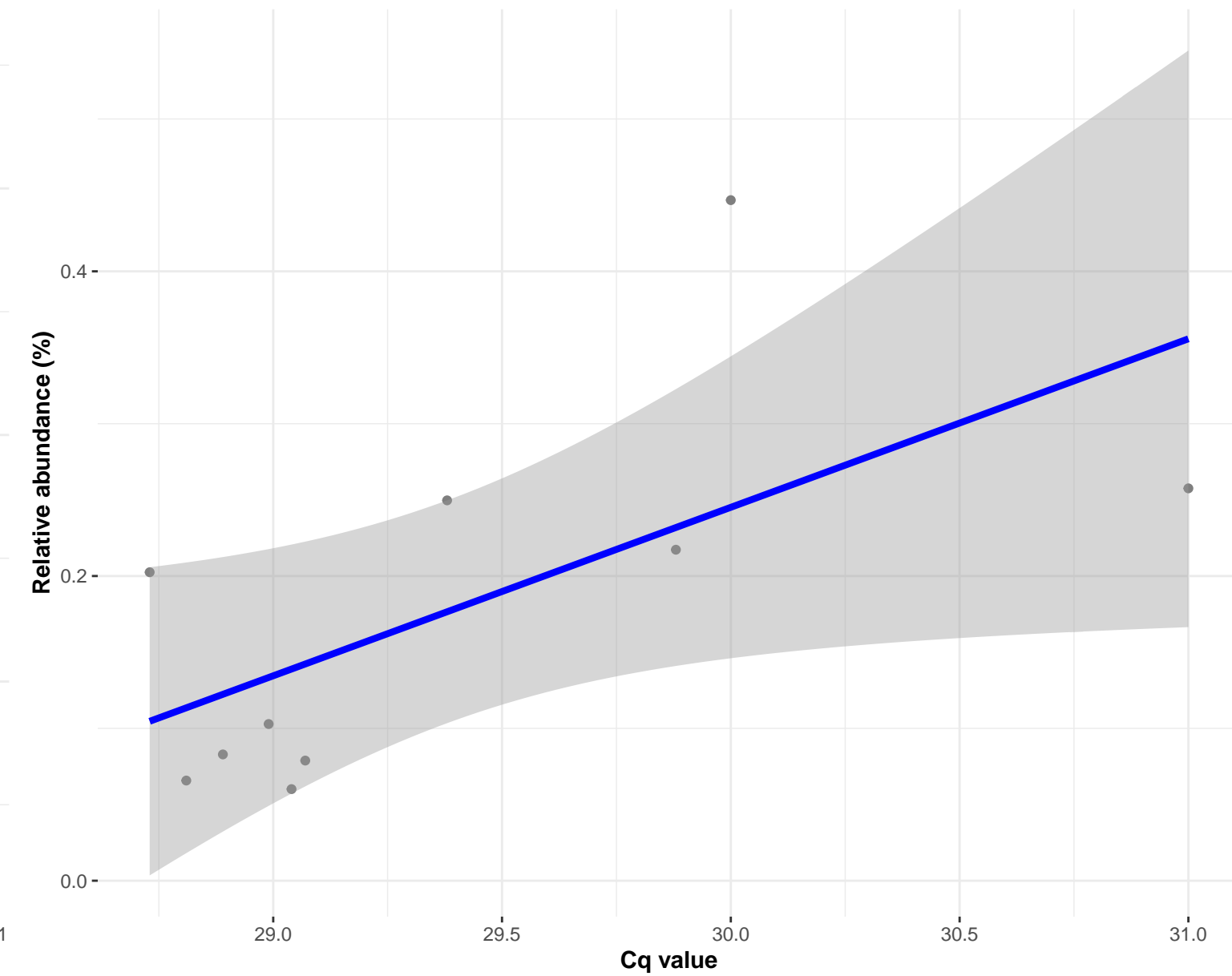
Correlation within: IM-PIM

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



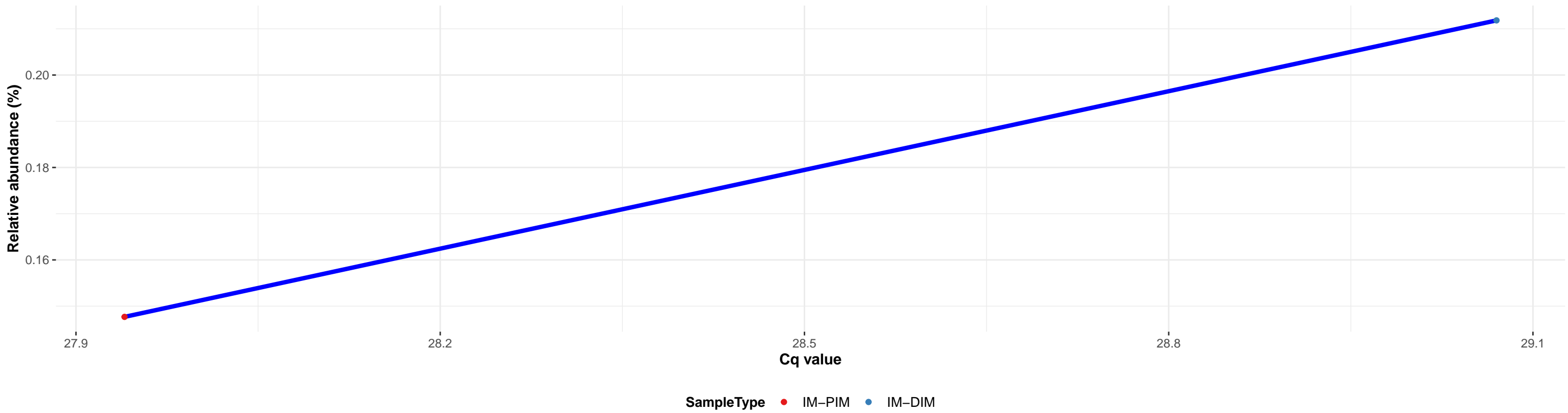
Correlation within: IM-DIM

$\log_e(S) = 4.025$, $p = 0.038$, $\hat{\rho}_{\text{Spearman}} = 0.661$, $CI_{95\%} [0.031, 0.915]$, $n_{\text{pairs}} = 10$

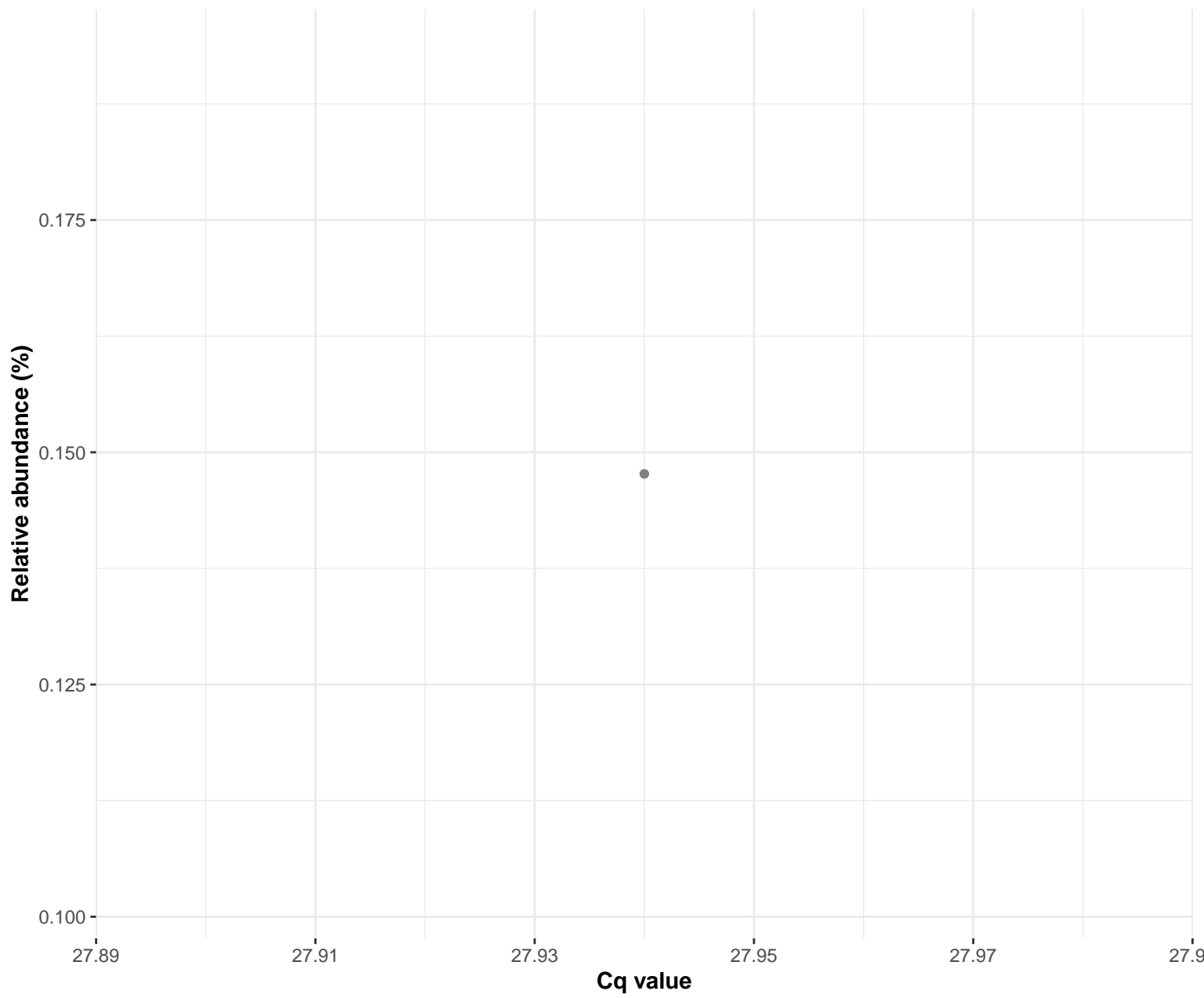


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA

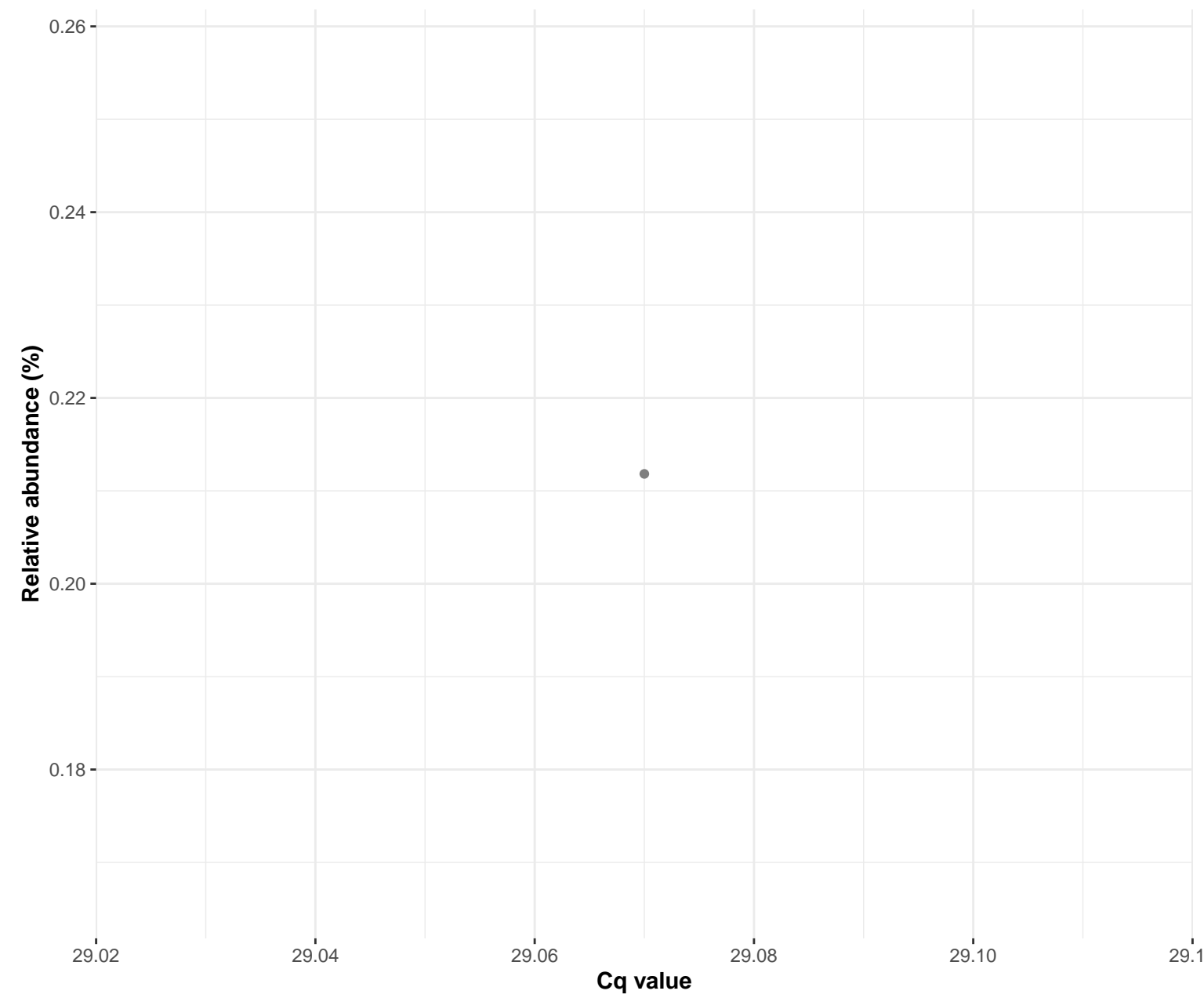
Correlation with all samples



Correlation within: IM-PIM



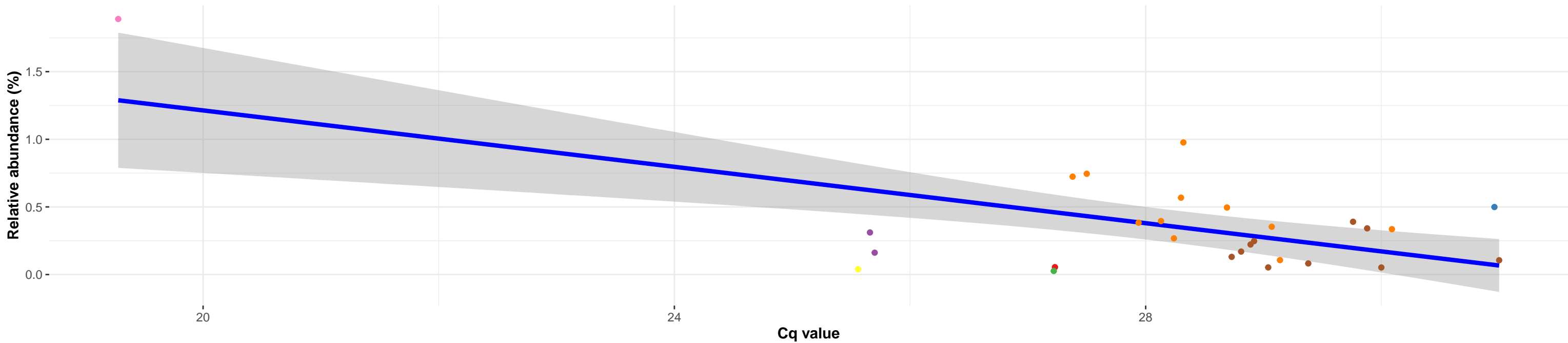
Correlation within: IM-DIM



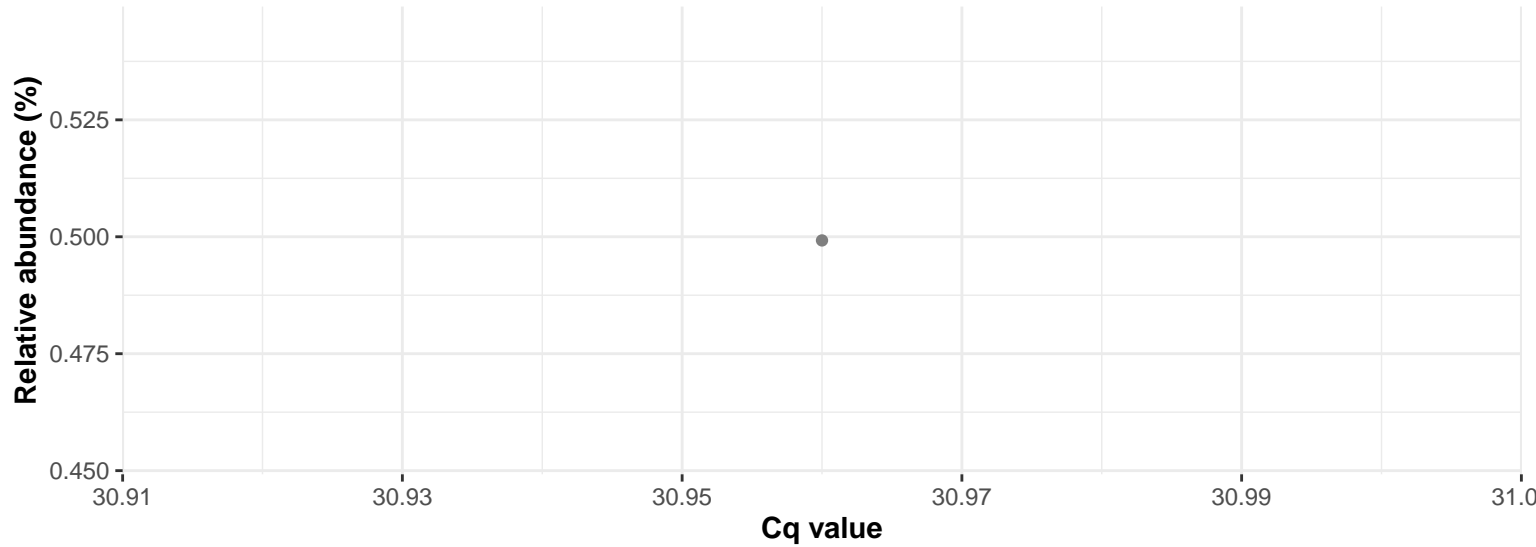
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Savagea; Ambiguous_taxa

Correlation with all samples

$\log_e(S) = 8.312$, $p = 0.562$, $\hat{\rho}_{\text{Spearman}} = -0.114$, $\text{CI}_{95\%} [-0.477, 0.281]$, $n_{\text{pairs}} = 28$

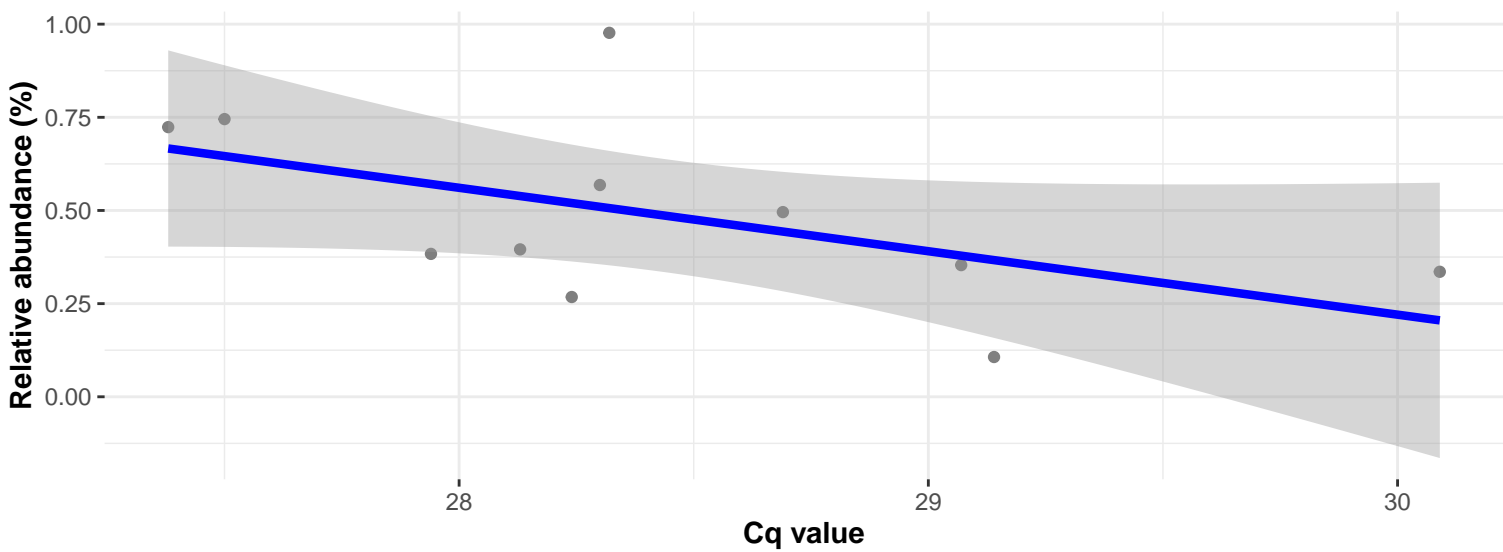


Correlation within: REF-PIM



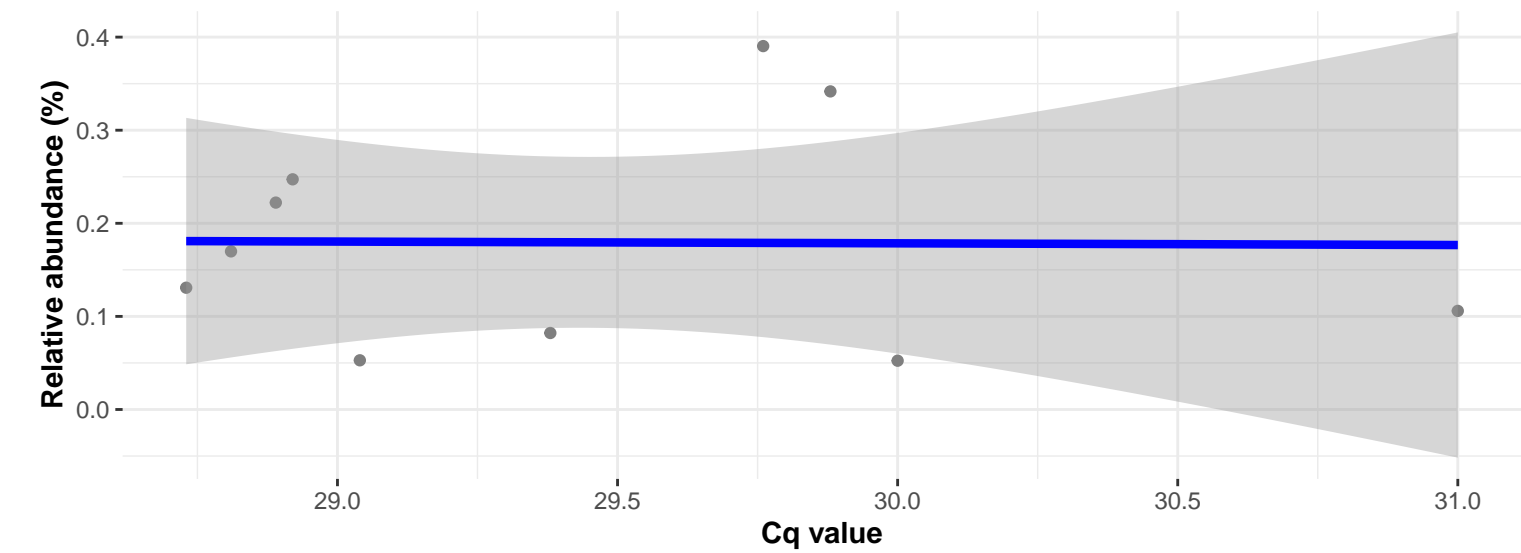
Correlation within: IM-PIM

$\log_e(S) = 5.817$, $p = 0.096$, $\hat{\rho}_{\text{Spearman}} = -0.527$, $\text{CI}_{95\%} [-0.862, 0.126]$, $n_{\text{pairs}} = 11$

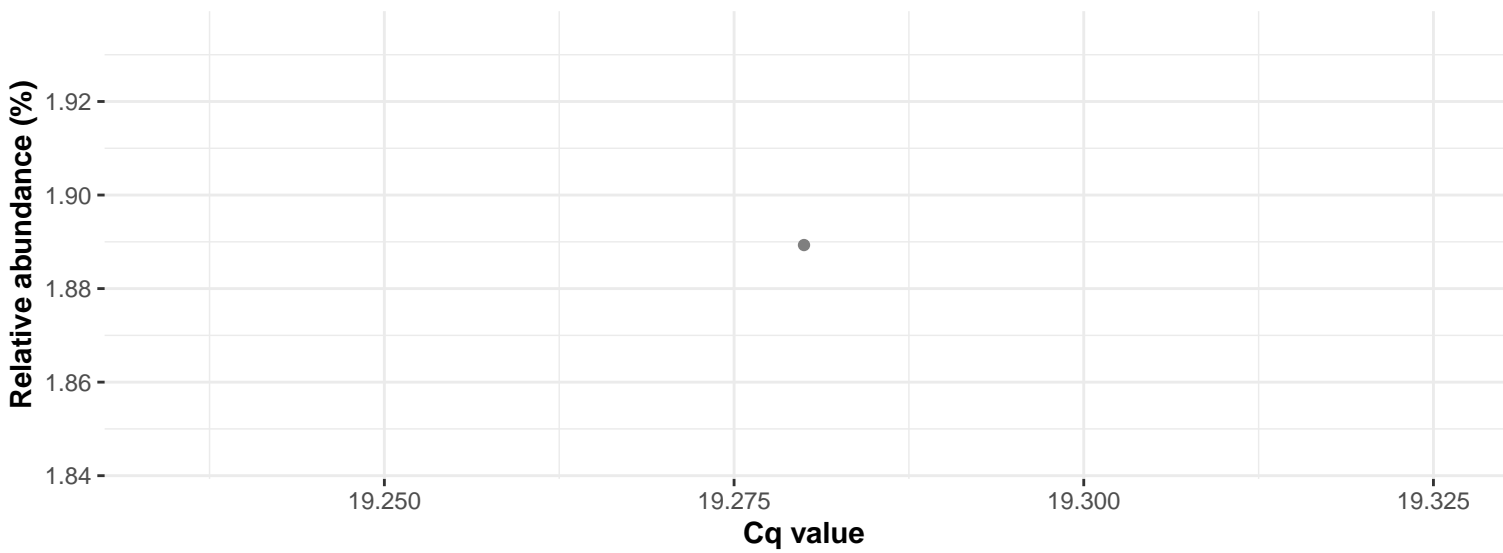


Correlation within: IM-DIM

$\log_e(S) = 5.257$, $p = 0.651$, $\hat{\rho}_{\text{Spearman}} = -0.164$, $\text{CI}_{95\%} [-0.730, 0.535]$, $n_{\text{pairs}} = 10$



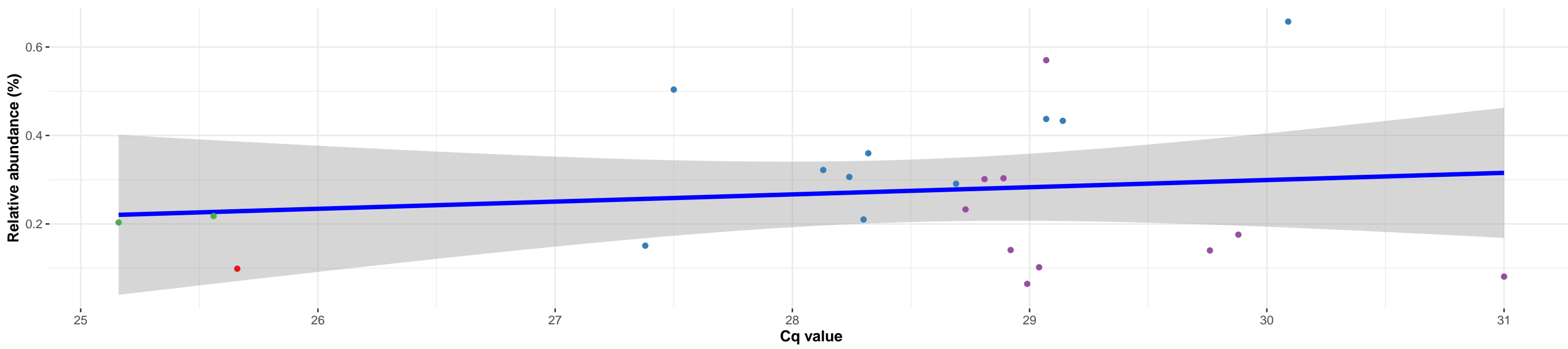
Correlation within: Feed



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

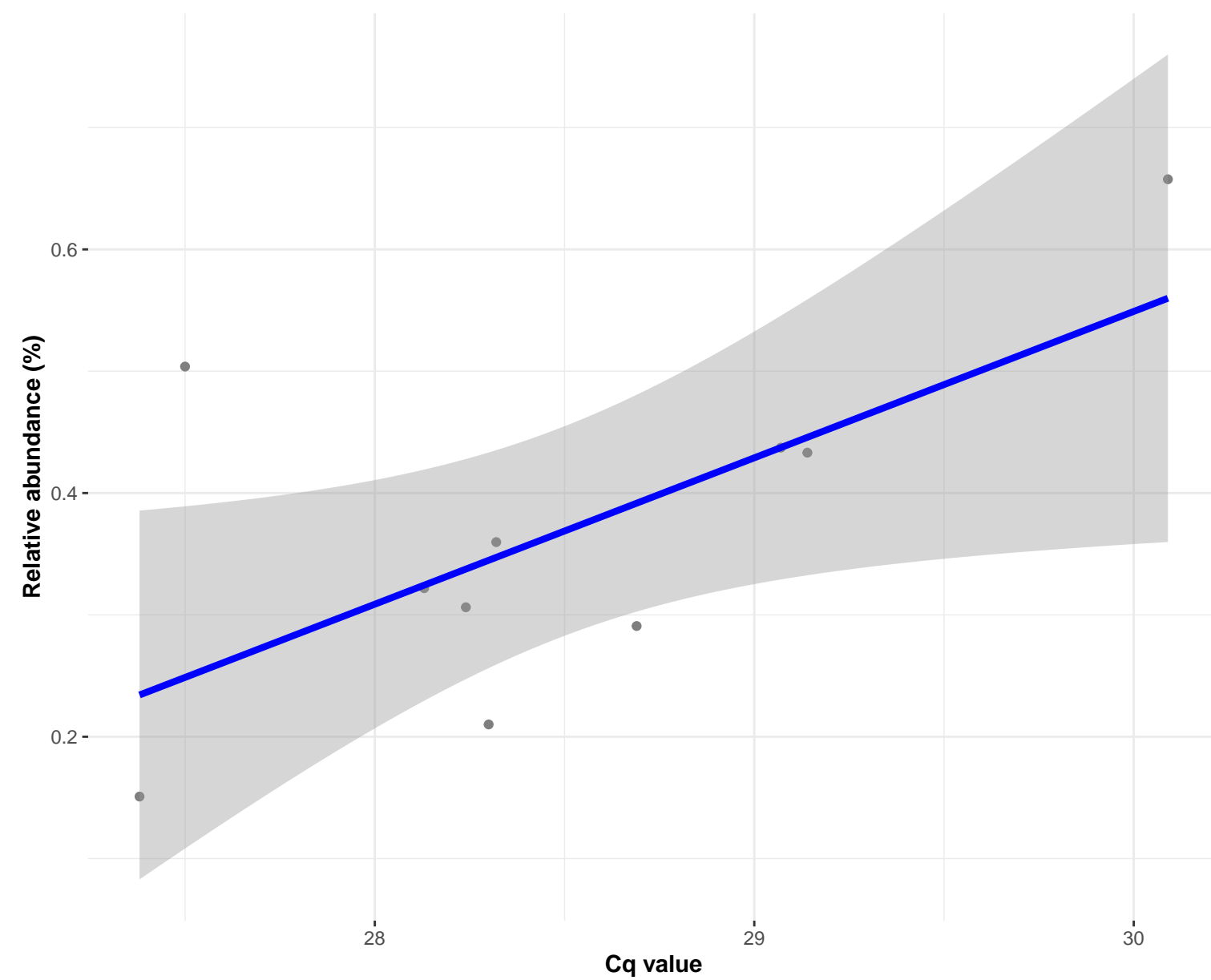
Correlation with all samples

$\log_e(S) = 7.592$, $p = 0.925$, $\hat{\rho}_{\text{Spearman}} = 0.021$, $CI_{95\%} [-0.406, 0.440]$, $n_{\text{pairs}} = 23$



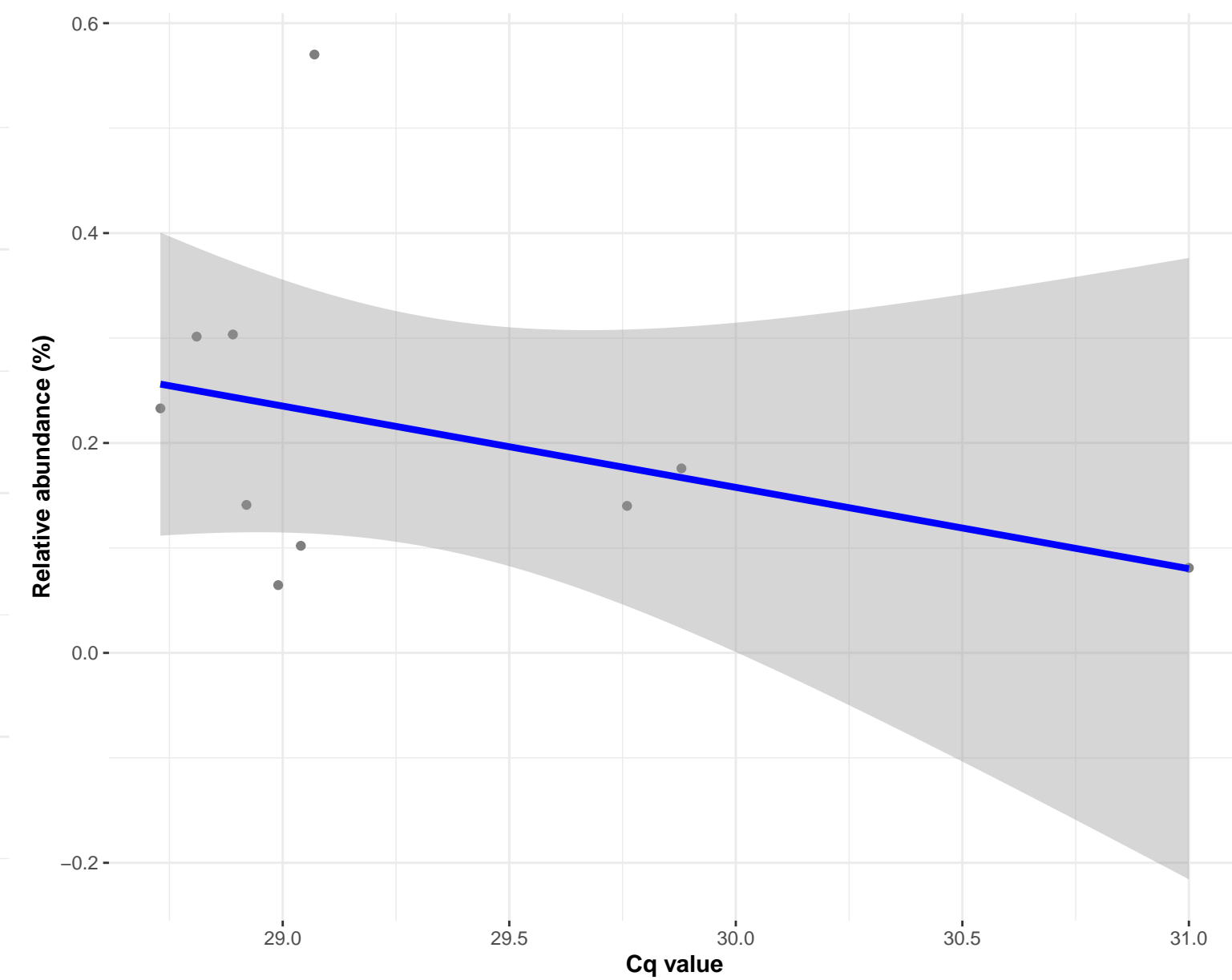
Correlation within: IM-PIM

$\log_e(S) = 4.407$, $p = 0.138$, $\hat{\rho}_{\text{Spearman}} = 0.503$, $CI_{95\%} [-0.206, 0.866]$, $n_{\text{pairs}} = 10$

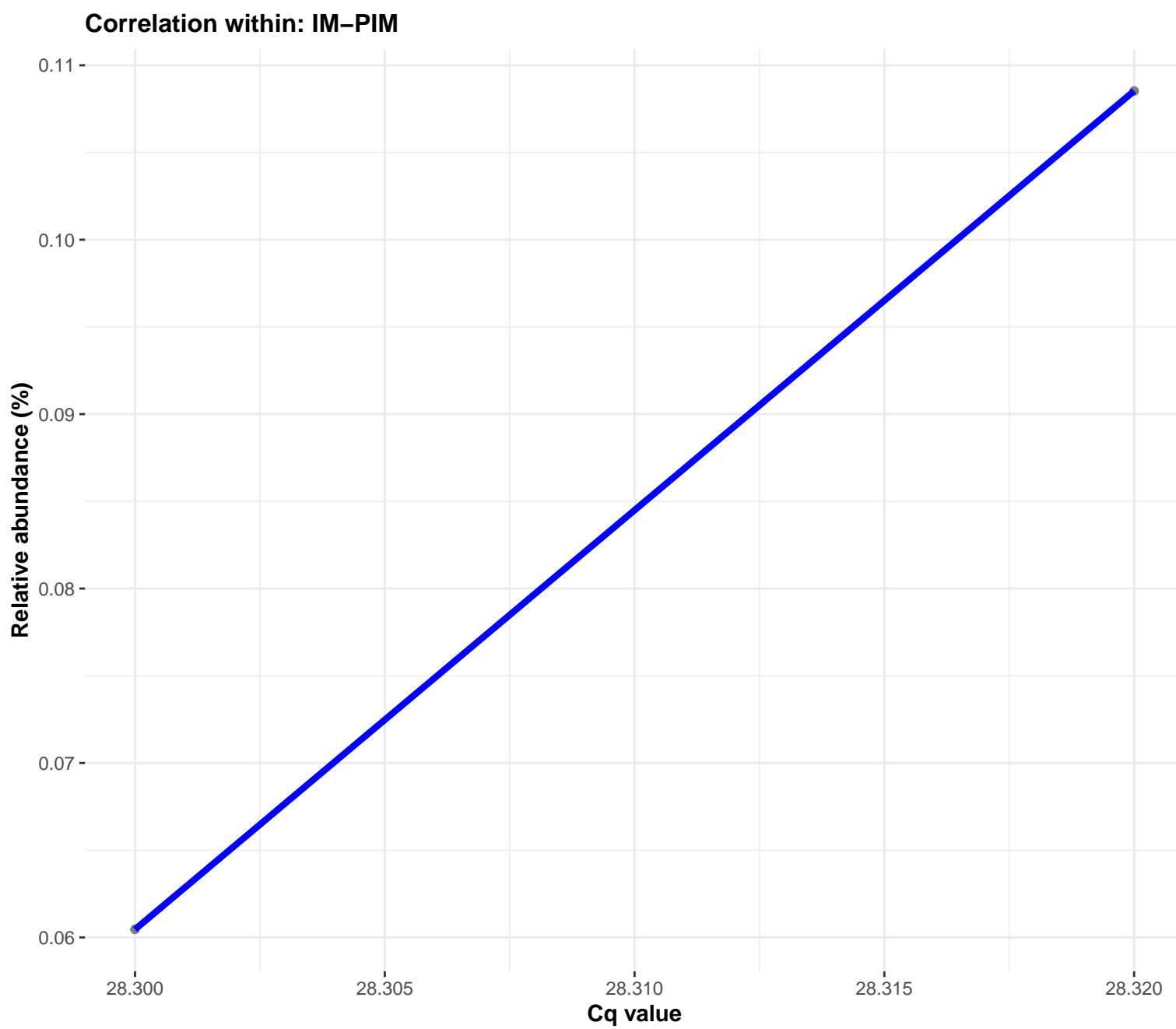
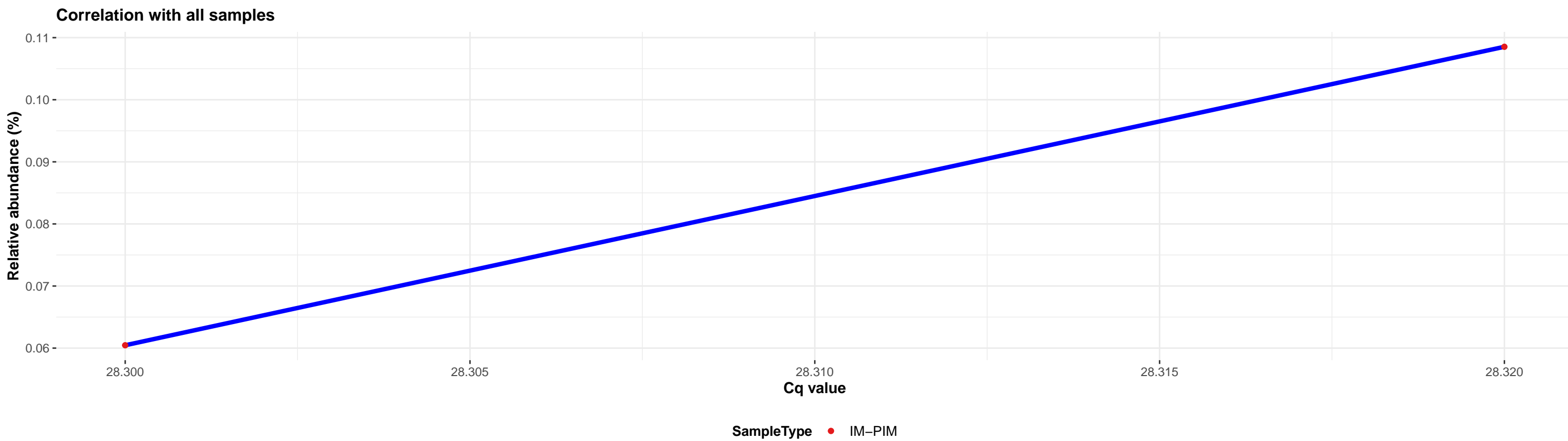


Correlation within: IM-DIM

$\log_e(S) = 5.447$, $p = 0.244$, $\hat{\rho}_{\text{Spearman}} = -0.406$, $CI_{95\%} [-0.832, 0.320]$, $n_{\text{pairs}} = 10$



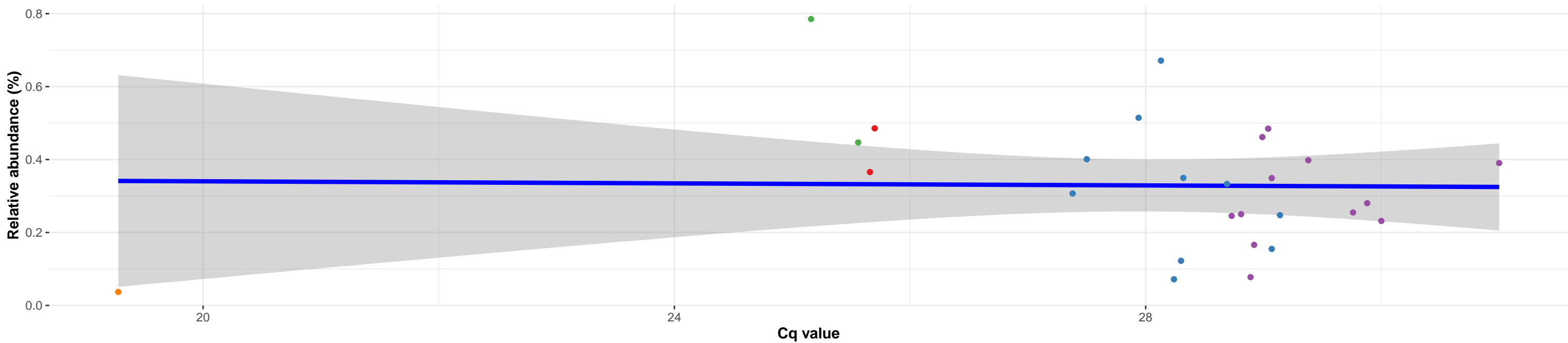
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus licheniformis



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus andreraoultii

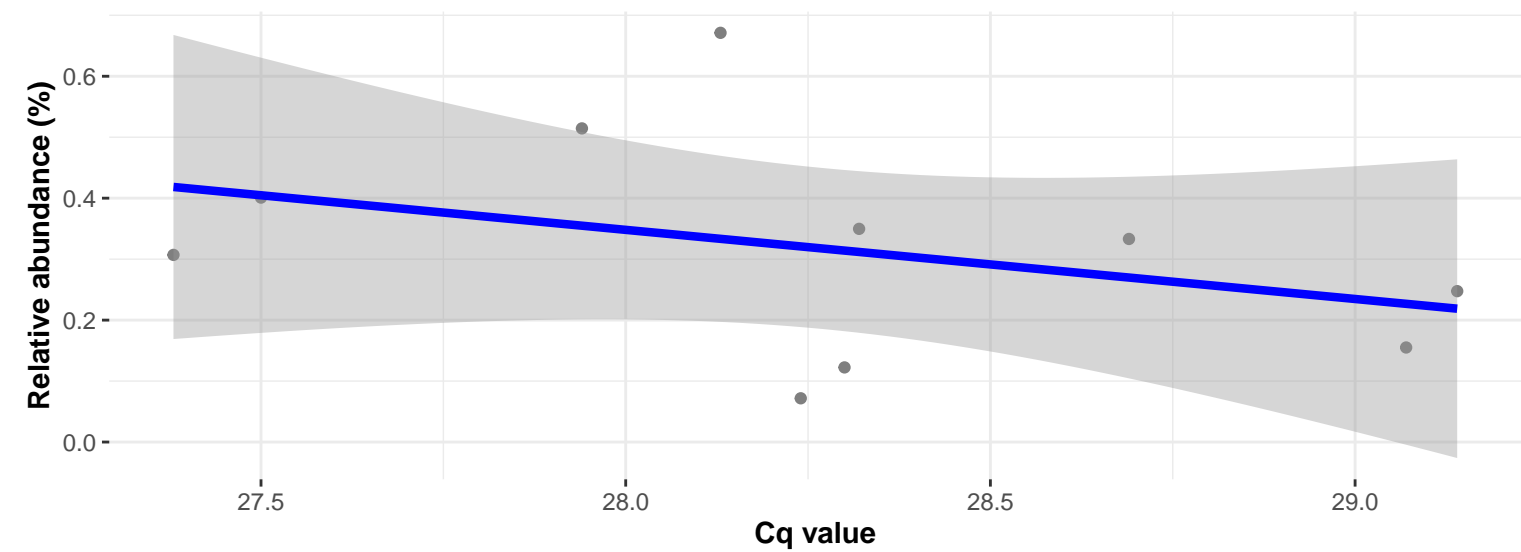
Correlation with all samples

$\log_e(S) = 8.300$, $p = 0.252$, $\hat{\rho}_{\text{Spearman}} = -0.228$, $CI_{95\%} [-0.568, 0.178]$, $n_{\text{pairs}} = 27$



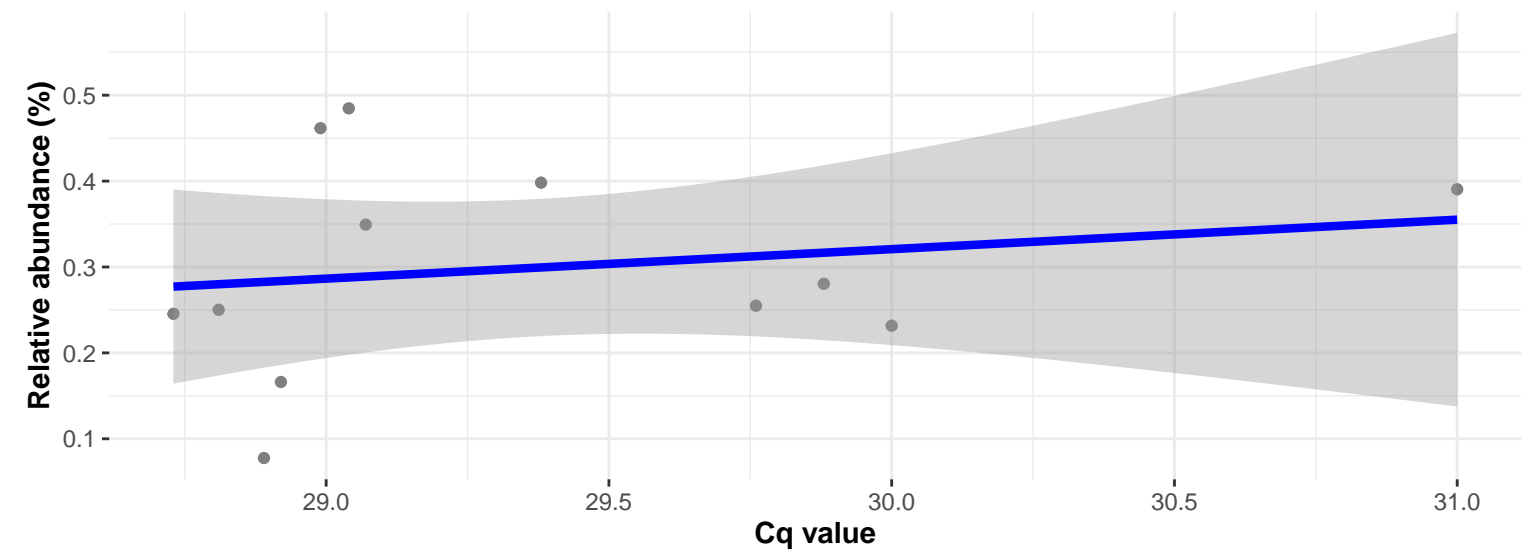
Correlation within: IM-PIM

$\log_e(S) = 5.447$, $p = 0.244$, $\hat{\rho}_{\text{Spearman}} = -0.406$, $CI_{95\%} [-0.832, 0.320]$, $n_{\text{pairs}} = 10$

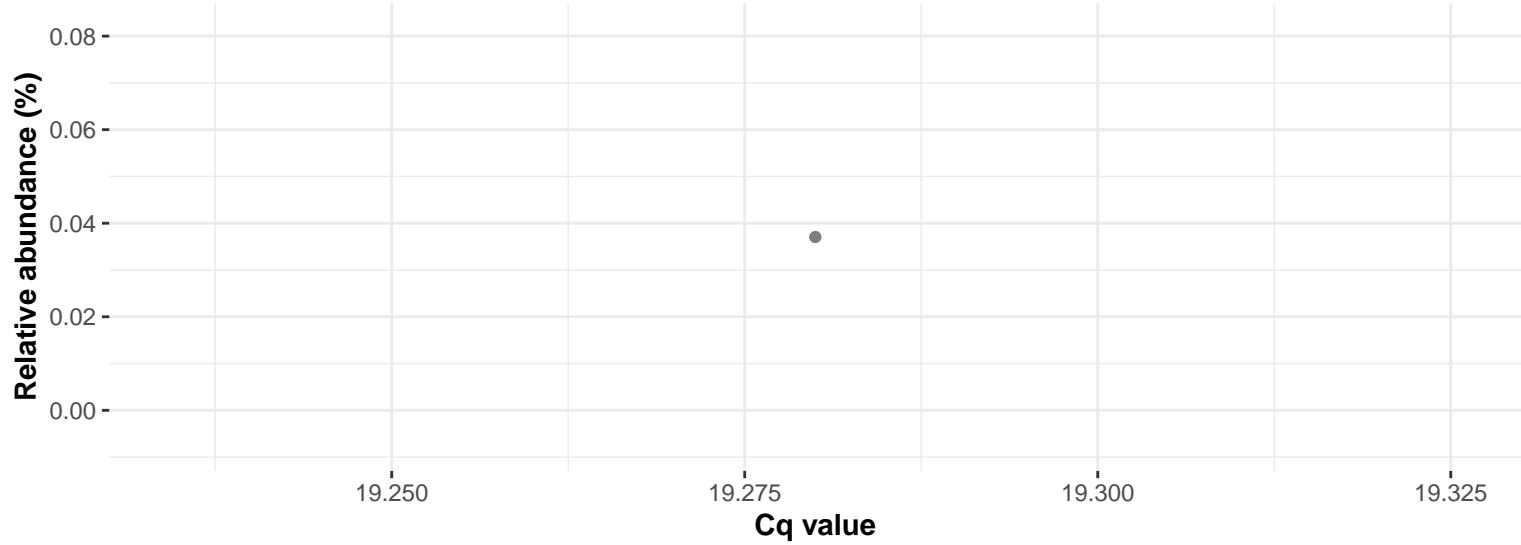


Correlation within: IM-DIM

$\log_e(S) = 5.268$, $p = 0.308$, $\hat{\rho}_{\text{Spearman}} = 0.322$, $CI_{95\%} [-0.327, 0.764]$, $n_{\text{pairs}} = 12$



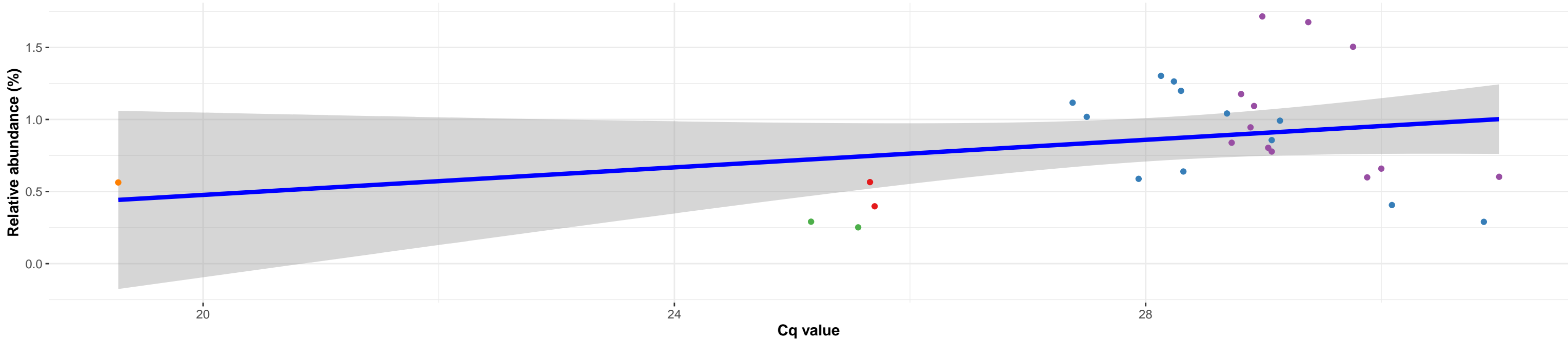
Correlation within: Feed



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

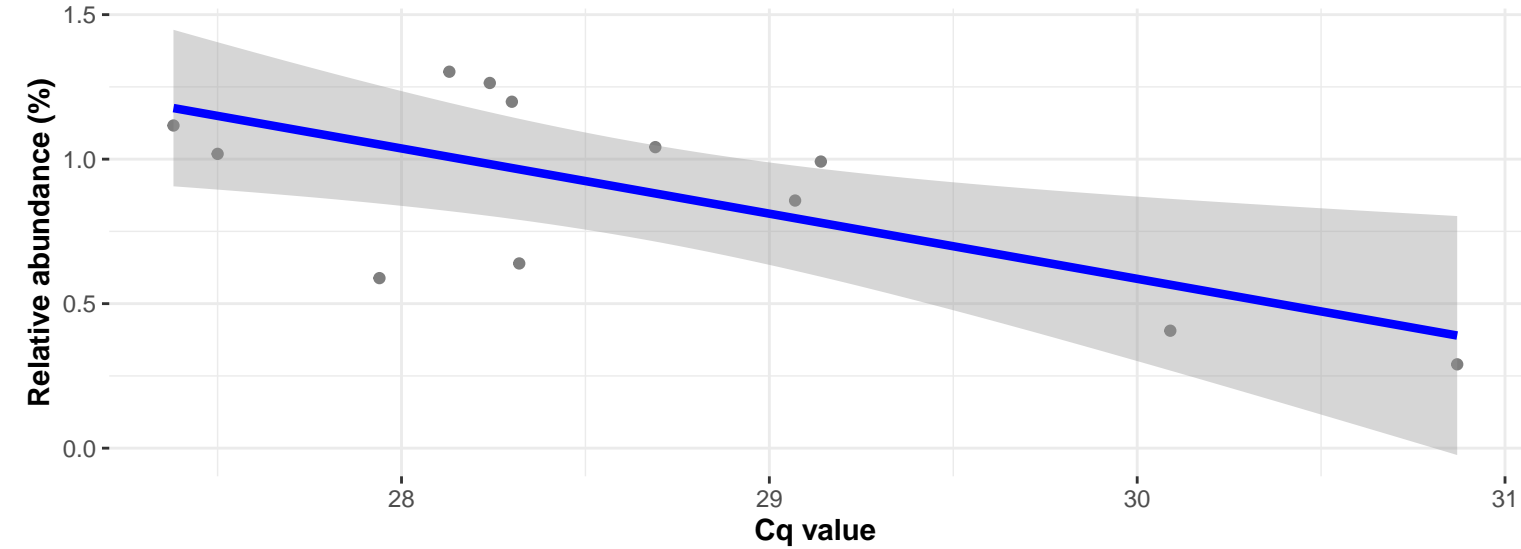
Correlation with all samples

$\log_e(S) = 8.161$, $p = 0.476$, $\hat{\rho}_{\text{Spearman}} = 0.138$, $CI_{95\%} [-0.252, 0.489]$, $n_{\text{pairs}} = 29$



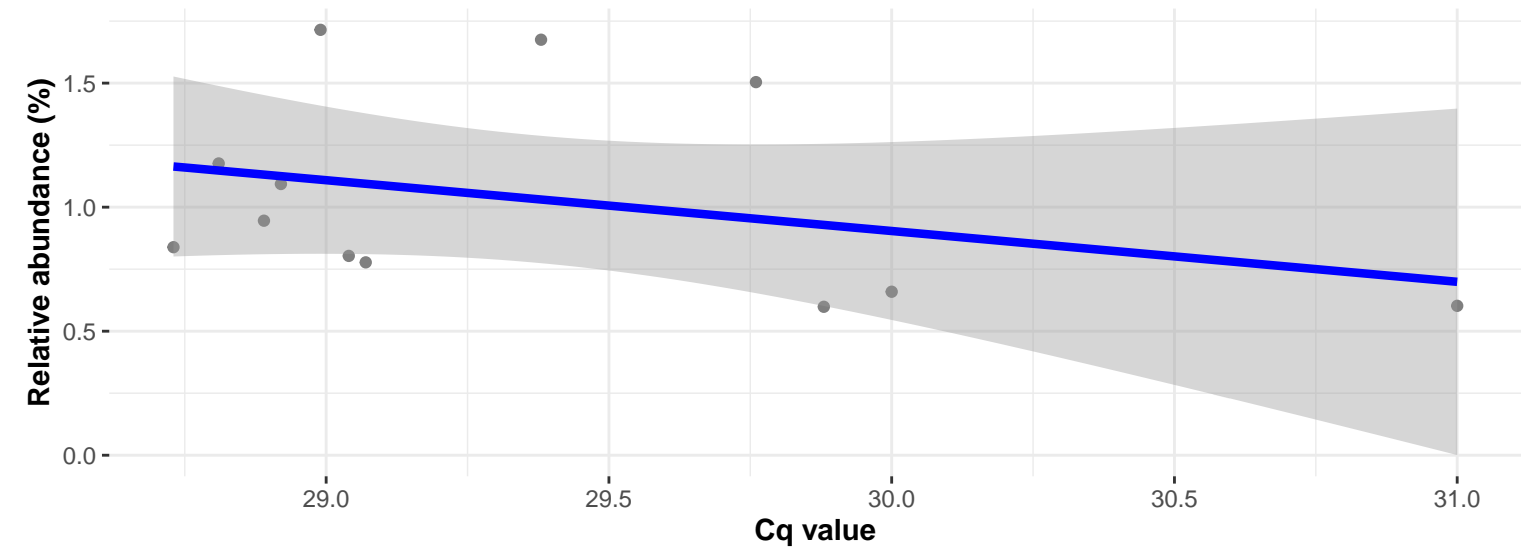
Correlation within: IM-PIM

$\log_e(S) = 6.105$, $p = 0.055$, $\hat{\rho}_{\text{Spearman}} = -0.566$, $CI_{95\%} [-0.866, 0.030]$, $n_{\text{pairs}} = 12$

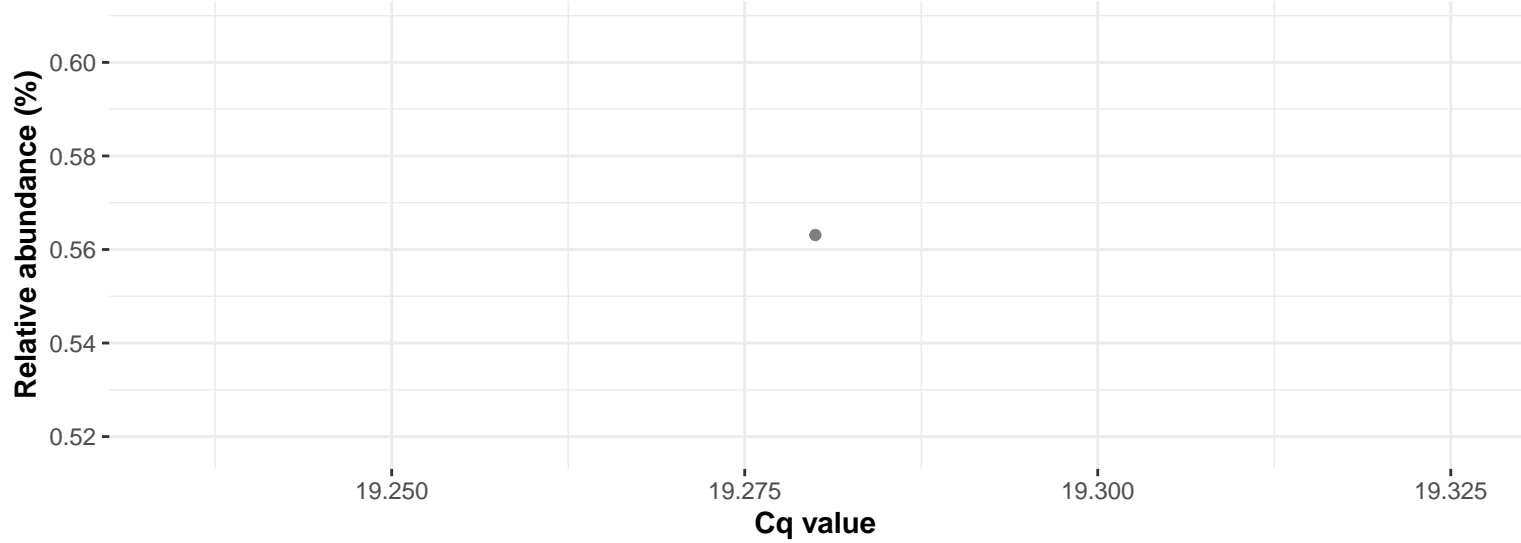


Correlation within: IM-DIM

$\log_e(S) = 6.040$, $p = 0.124$, $\hat{\rho}_{\text{Spearman}} = -0.469$, $CI_{95\%} [-0.828, 0.163]$, $n_{\text{pairs}} = 12$



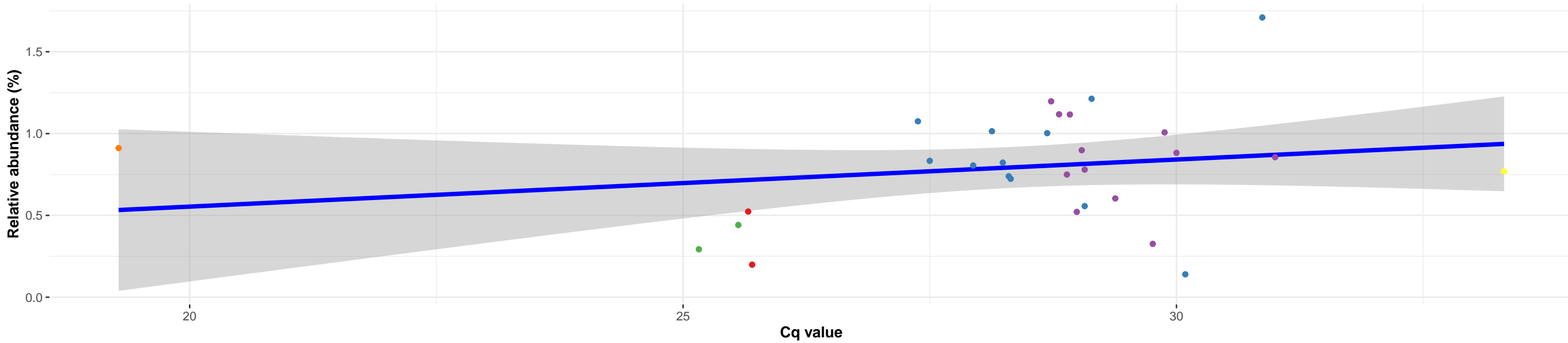
Correlation within: Feed



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

Correlation with all samples

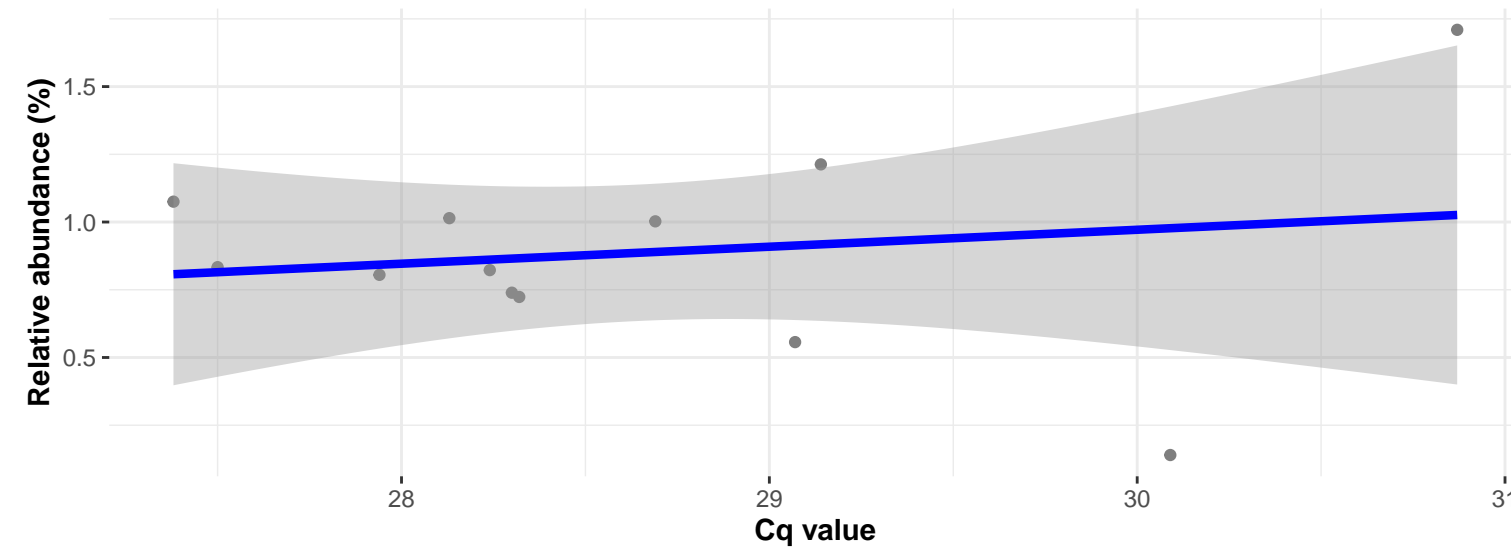
$\log_e(S) = 8.255$, $p = 0.448$, $\hat{\rho}_{\text{Spearman}} = 0.144$, $CI_{95\%} [-0.239, 0.488]$, $n_{\text{pairs}} = 30$



SampleType • IM-PID • IM-PIM • IM-DID • IM-DIM • Feed • Water

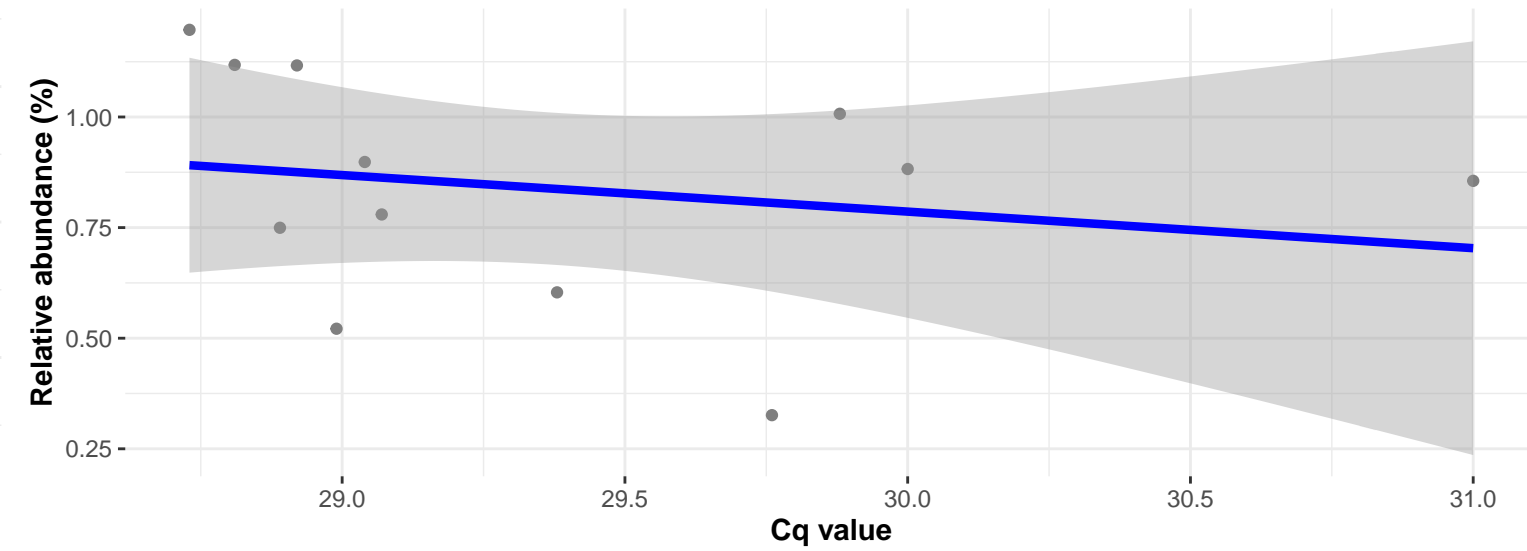
Correlation within: IM-PIM

$\log_e(S) = 5.724$, $p = 0.829$, $\hat{\rho}_{\text{Spearman}} = -0.070$, $CI_{95\%} [-0.631, 0.539]$, $n_{\text{pairs}} = 12$

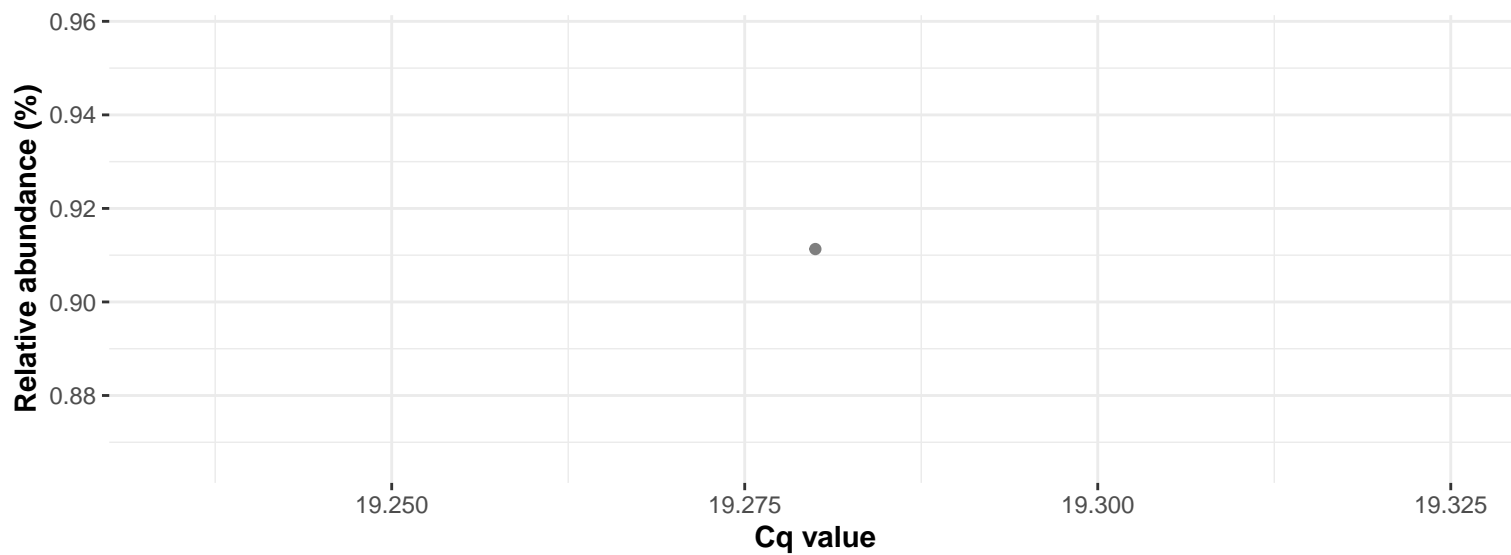


Correlation within: IM-DIM

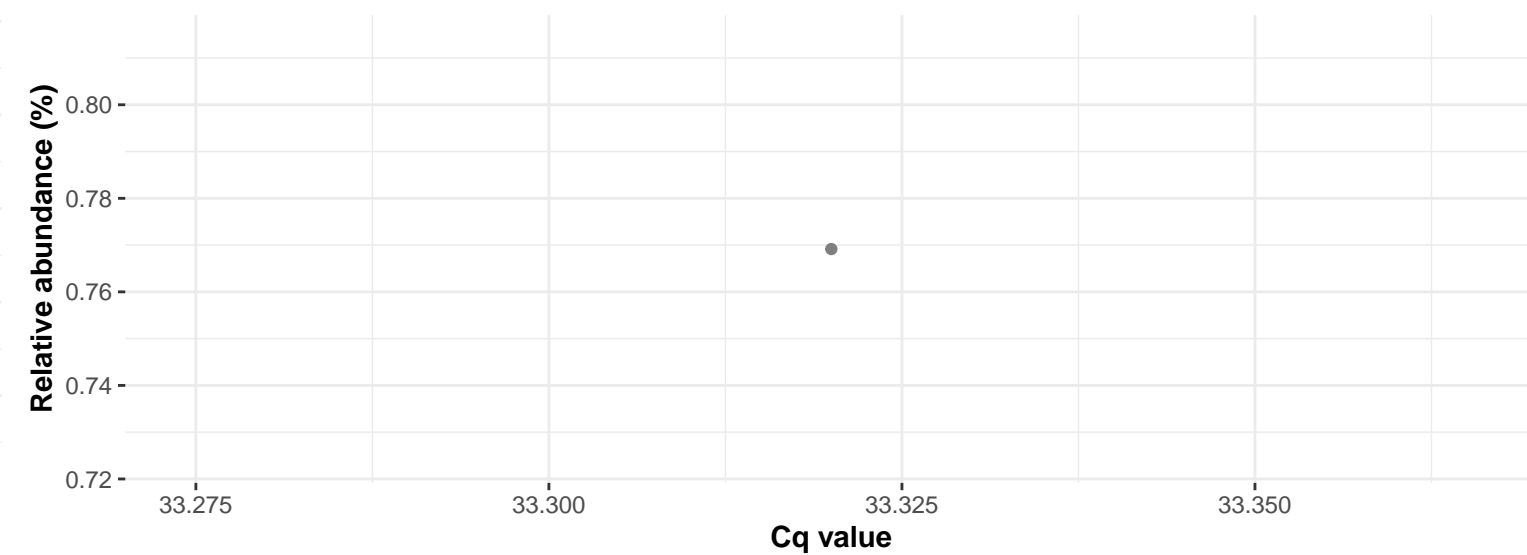
$\log_e(S) = 5.986$, $p = 0.208$, $\hat{\rho}_{\text{Spearman}} = -0.392$, $CI_{95\%} [-0.796, 0.253]$, $n_{\text{pairs}} = 12$



Correlation within: Feed



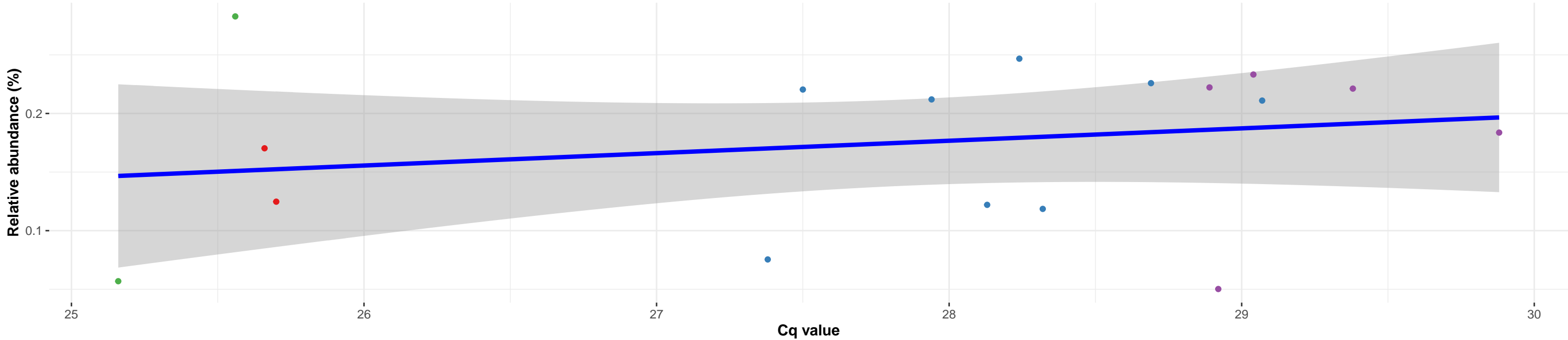
Correlation within: Water



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

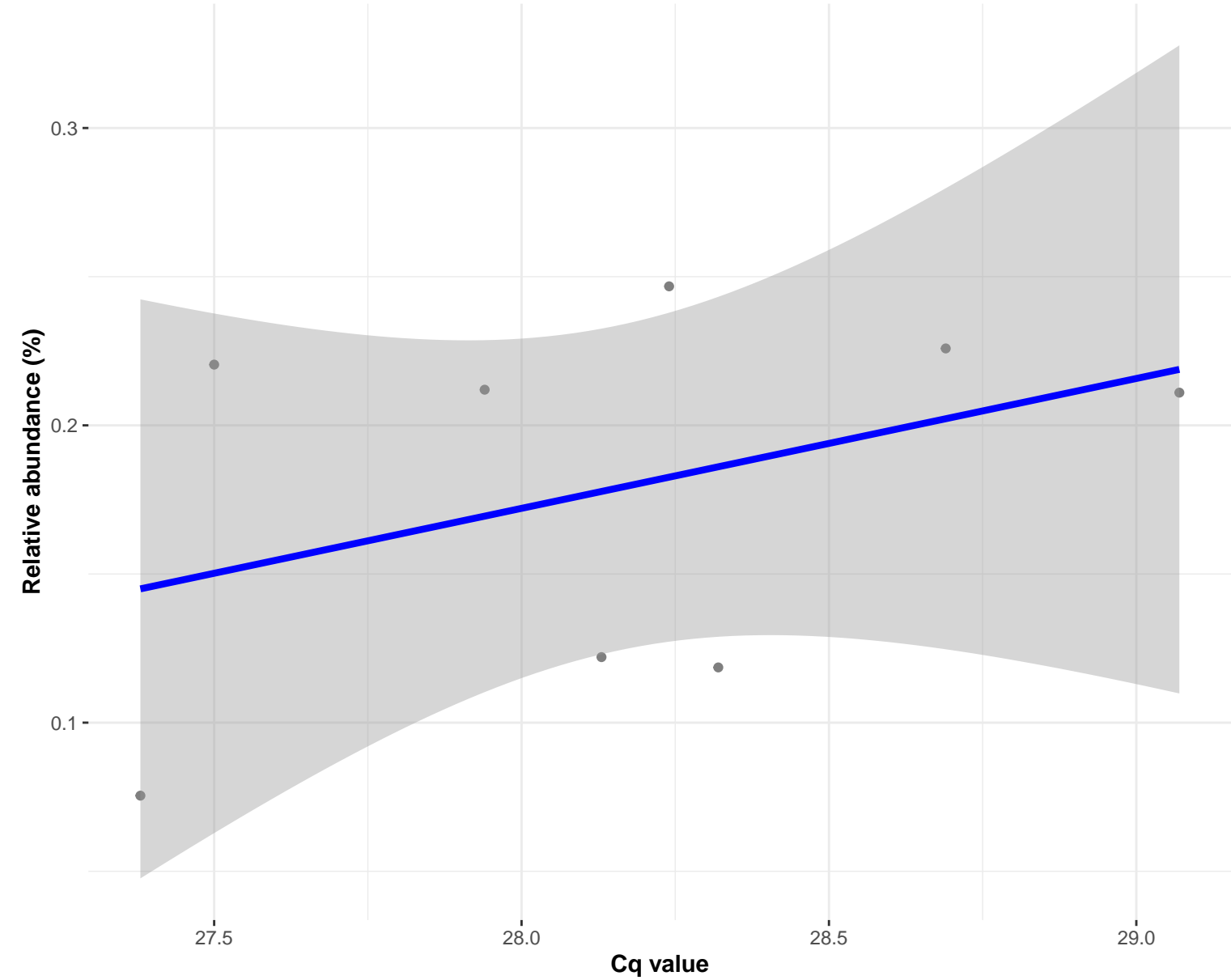
Correlation with all samples

$\log_e(S) = 6.501$, $p = 0.480$, $\hat{\rho}_{\text{Spearman}} = 0.184$, $CI_{95\%} [-0.339, 0.620]$, $n_{\text{pairs}} = 17$

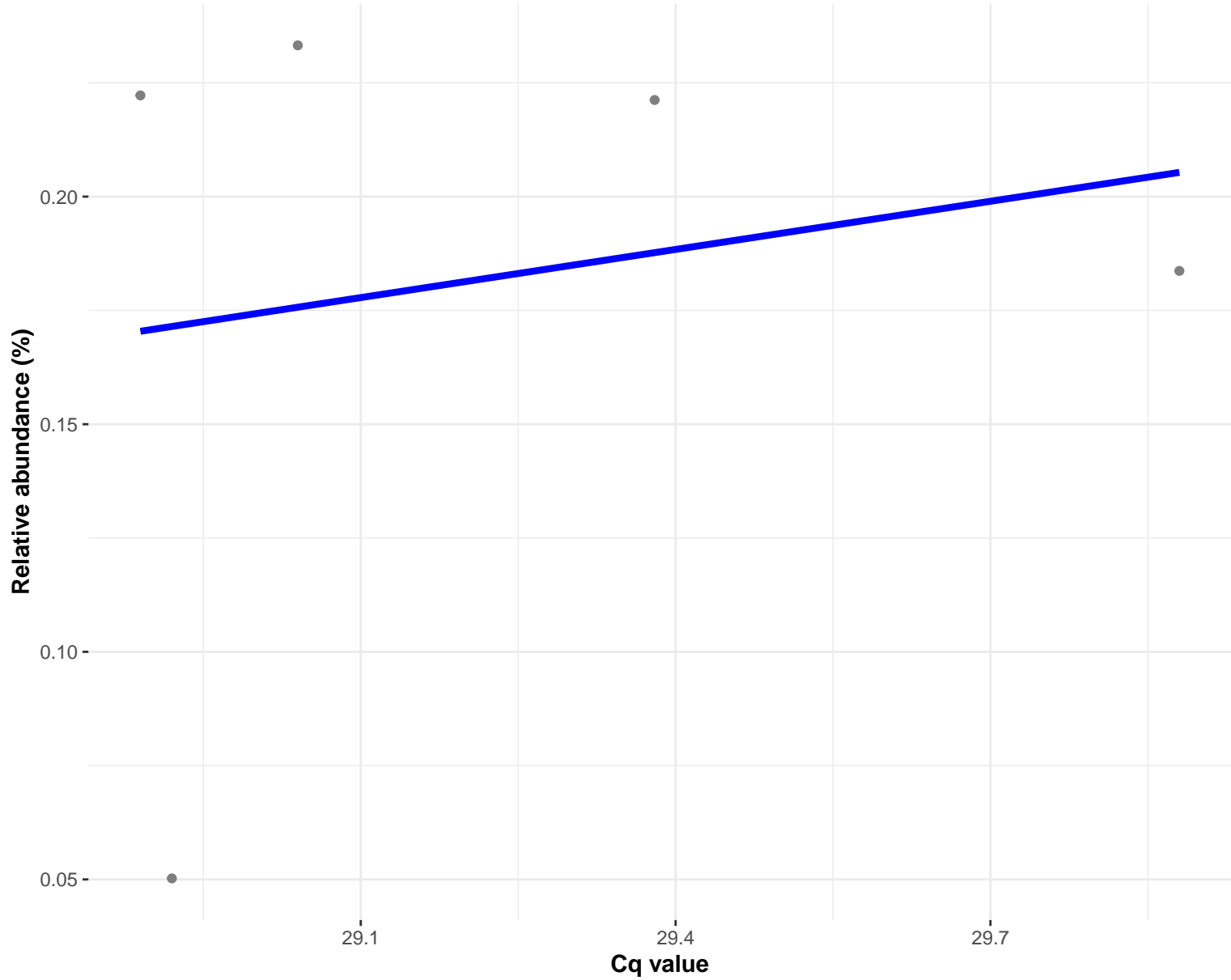


Correlation within: IM-PIM

$\log_e(S) = 4.127$, $p = 0.531$, $\hat{\rho}_{\text{Spearman}} = 0.262$, $CI_{95\%} [-0.561, 0.824]$, $n_{\text{pairs}} = 8$



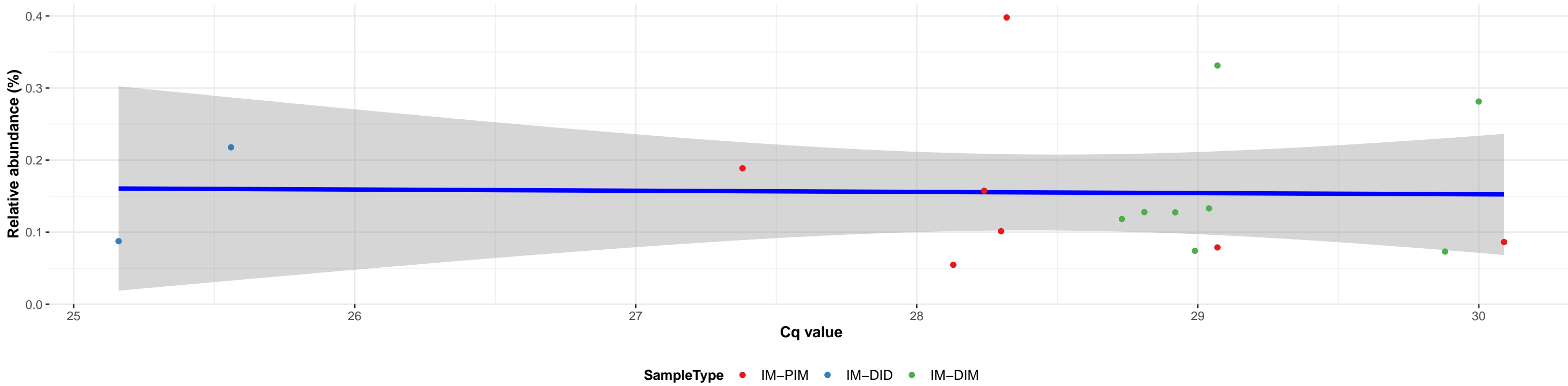
Correlation within: IM-DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus niabensis

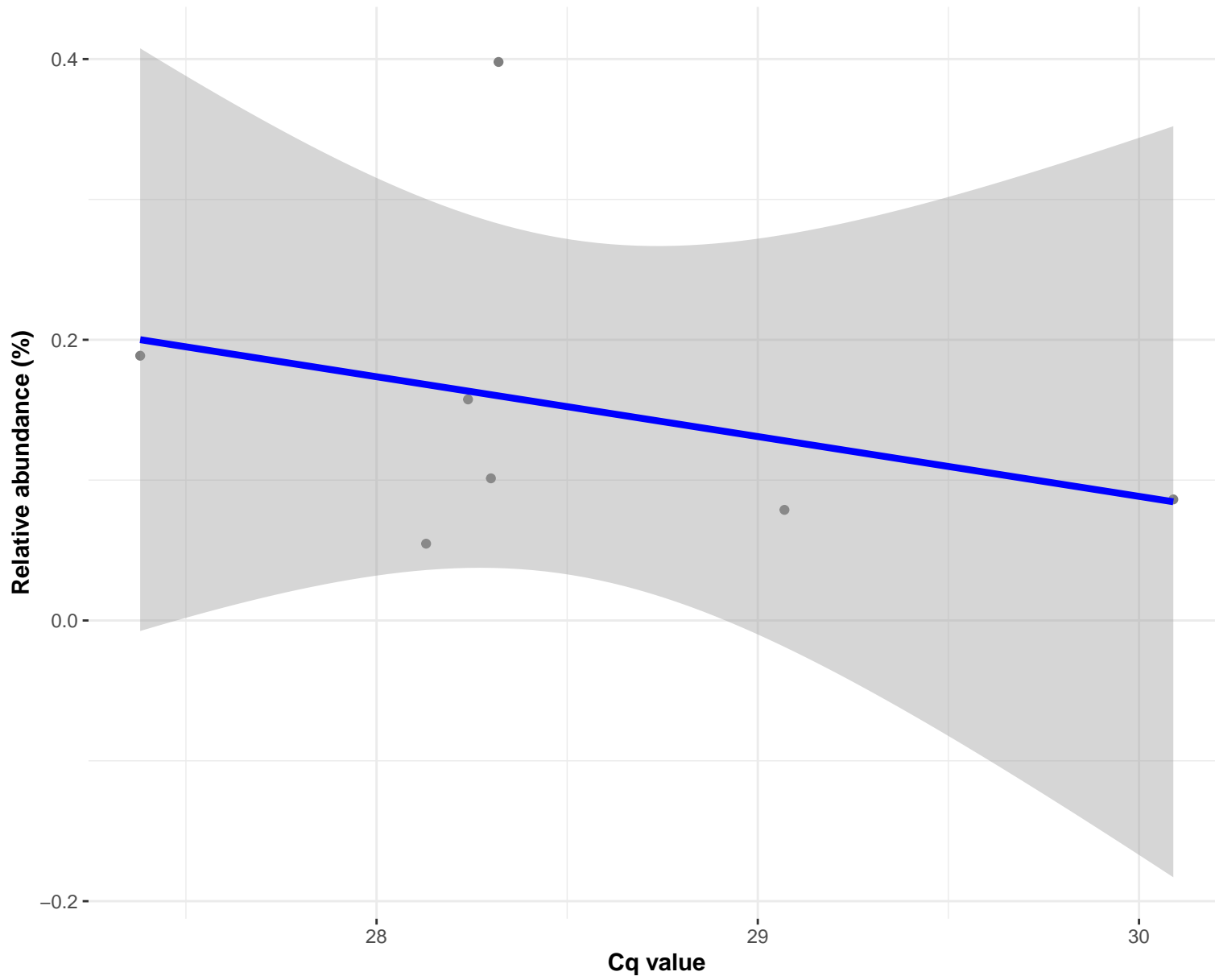
Correlation with all samples

$\log_e(S) = 6.809$, $p = 0.673$, $\hat{\rho}_{\text{Spearman}} = -0.110$, $CI_{95\%} [-0.572, 0.404]$, $n_{\text{pairs}} = 17$



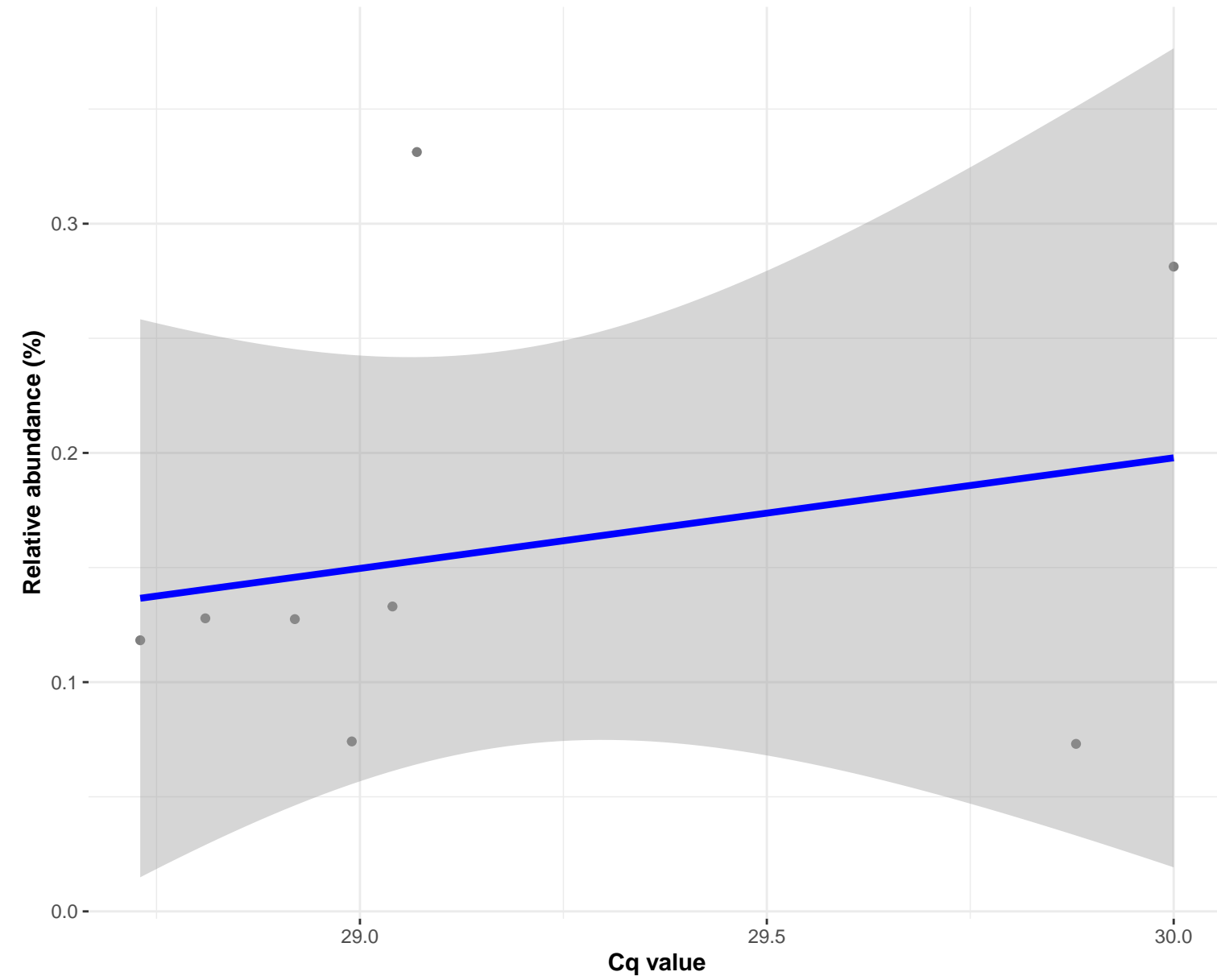
Correlation within: IM-PIM

$\log_e(S) = 4.190$, $p = 0.702$, $\hat{\rho}_{\text{Spearman}} = -0.179$, $CI_{95\%} [-0.830, 0.680]$, $n_{\text{pairs}} = 7$



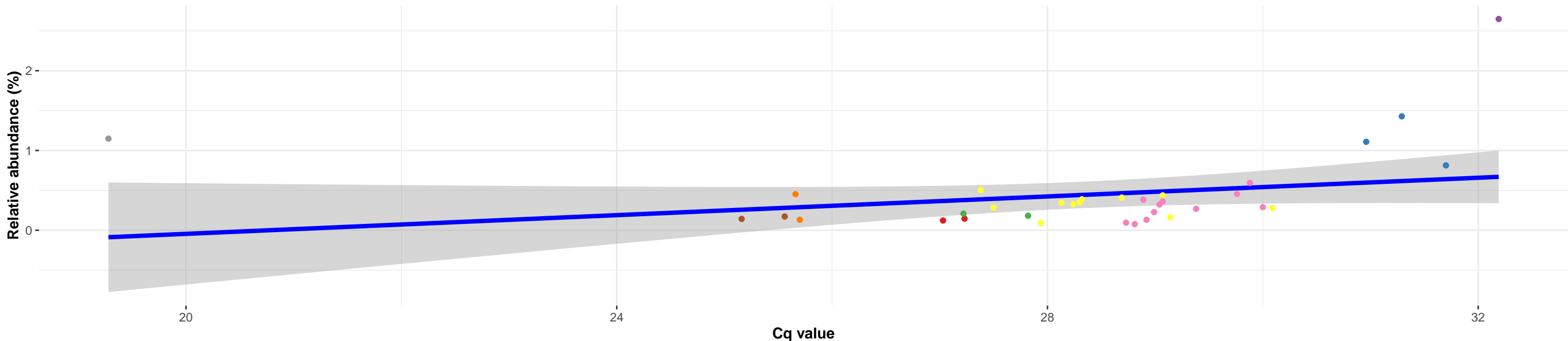
Correlation within: IM-DIM

$\log_e(S) = 4.094$, $p = 0.493$, $\hat{\rho}_{\text{Spearman}} = 0.286$, $CI_{95\%} [-0.543, 0.833]$, $n_{\text{pairs}} = 8$

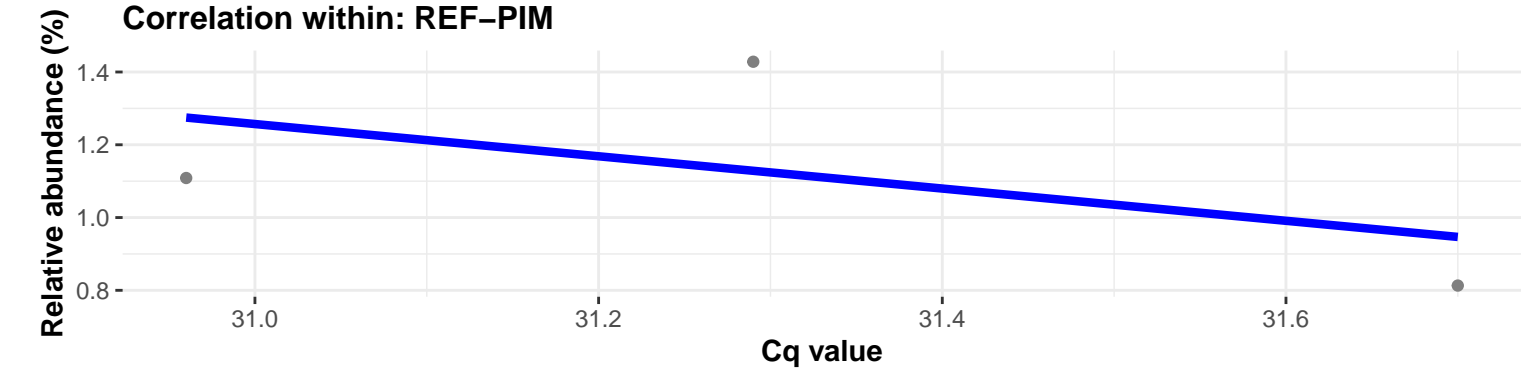


Correlation with all samples

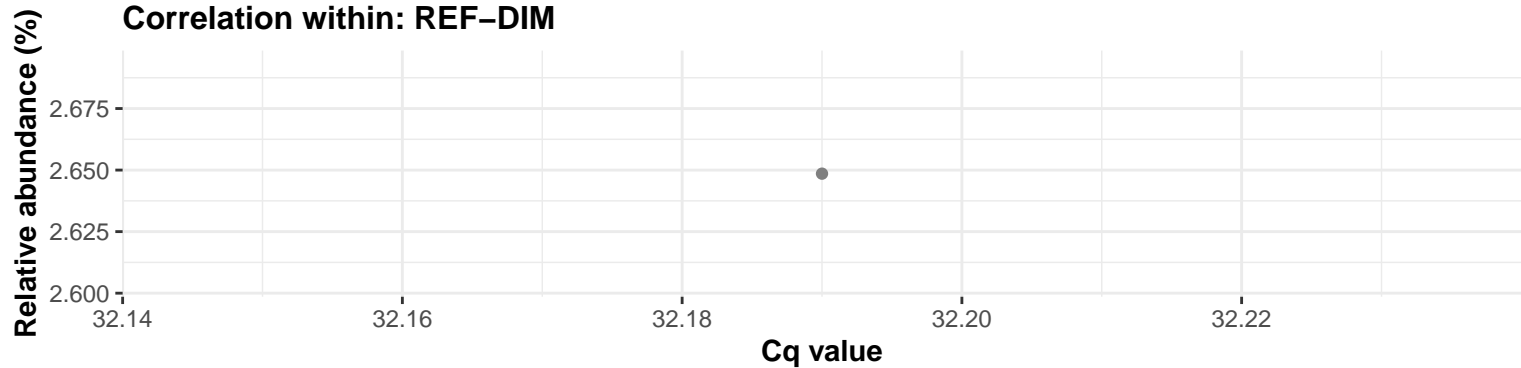
$\log_e(S) = 8.356$, $p = 0.016$, $\hat{\rho}_{\text{Spearman}} = 0.404$, $CI_{95\%} [0.072, 0.656]$, $n_{\text{pairs}} = 35$



Correlation within: REF-PIM

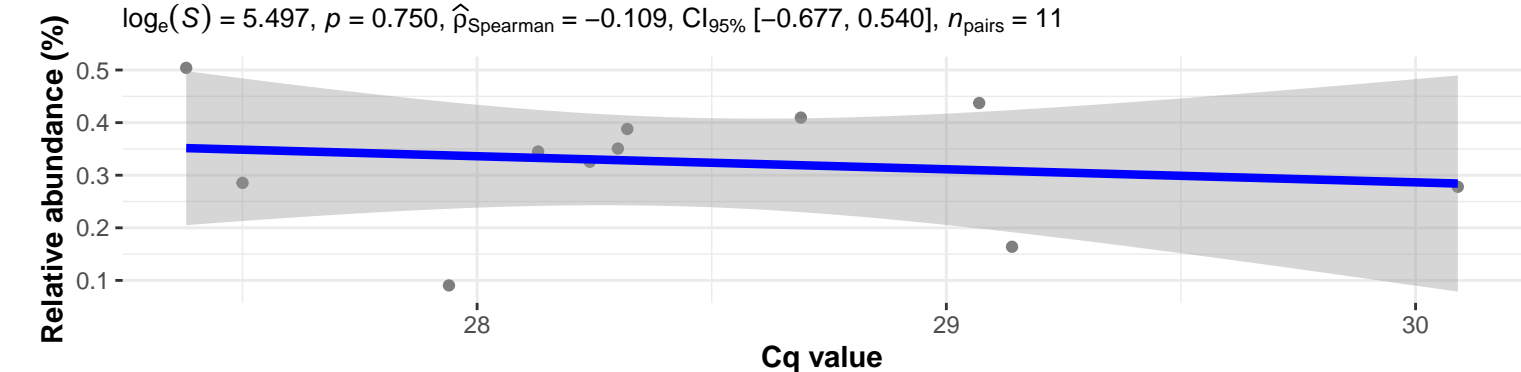


Correlation within: REF-DIM



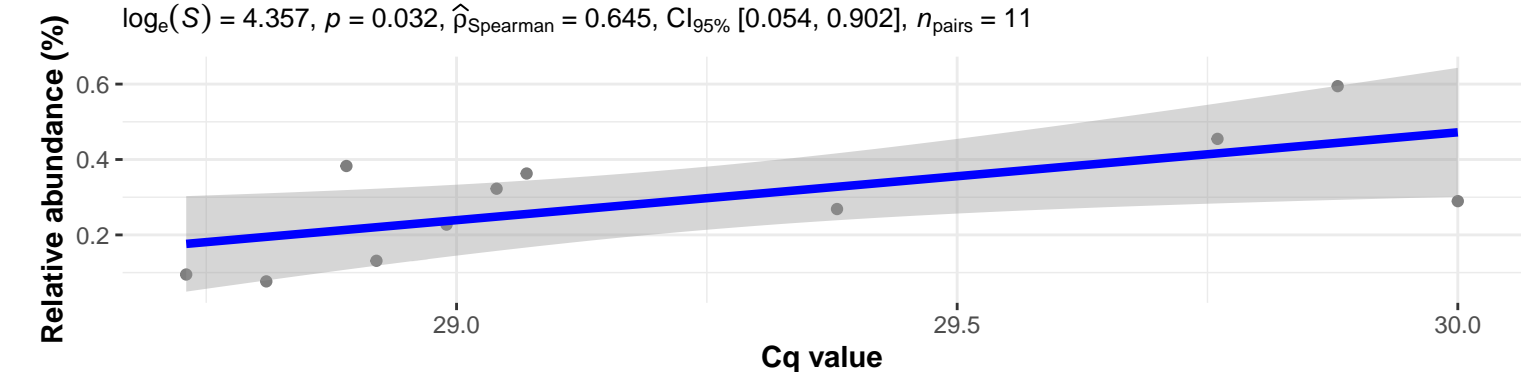
Correlation within: IM-PIM

$\log_e(S) = 5.497$, $p = 0.750$, $\hat{\rho}_{\text{Spearman}} = -0.109$, $CI_{95\%} [-0.677, 0.540]$, $n_{\text{pairs}} = 11$

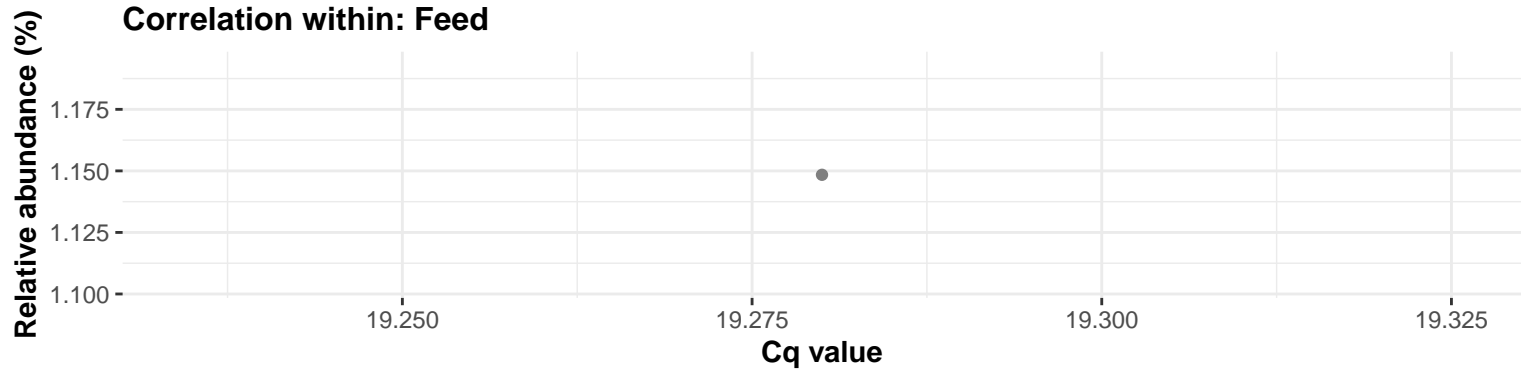


Correlation within: IM-DIM

$\log_e(S) = 4.357$, $p = 0.032$, $\hat{\rho}_{\text{Spearman}} = 0.645$, $CI_{95\%} [0.054, 0.902]$, $n_{\text{pairs}} = 11$



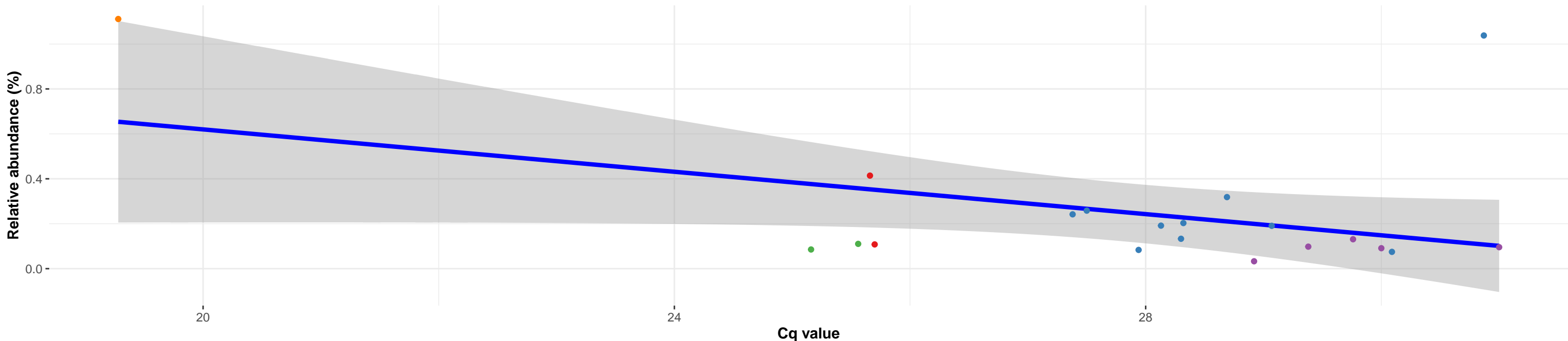
Correlation within: Feed



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

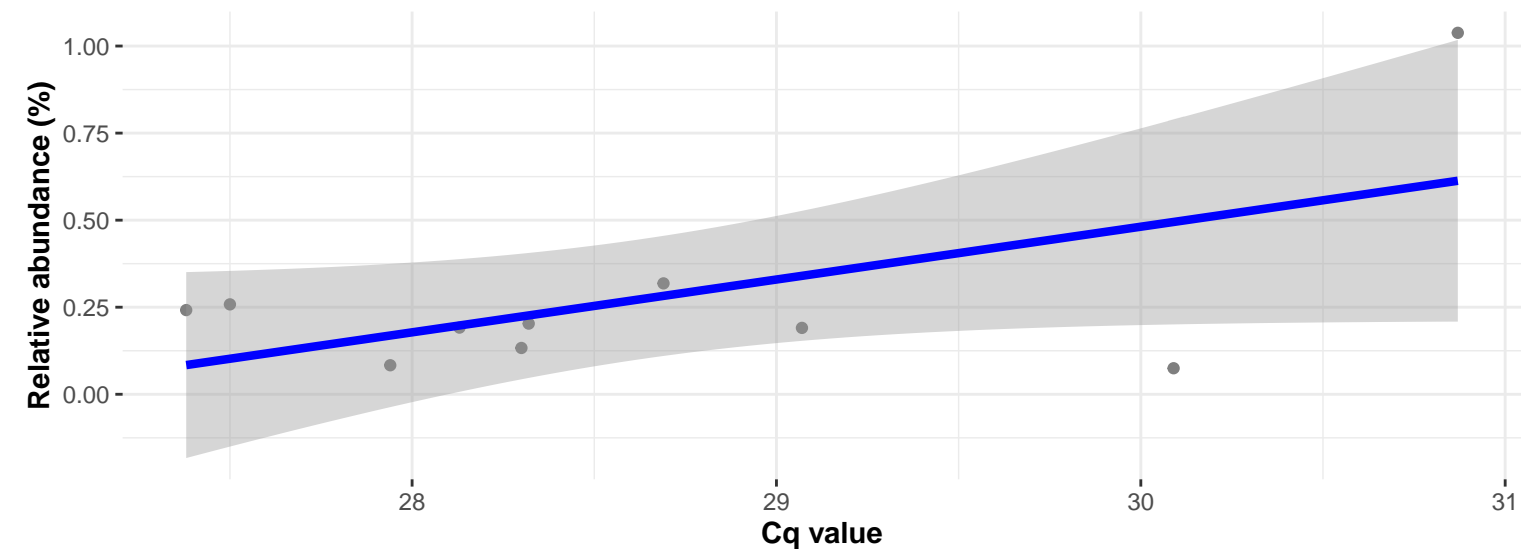
Correlation with all samples

$\log_e(S) = 7.431$, $p = 0.251$, $\hat{\rho}_{\text{Spearman}} = -0.269$, $CI_{95\%} [-0.644, 0.210]$, $n_{\text{pairs}} = 20$

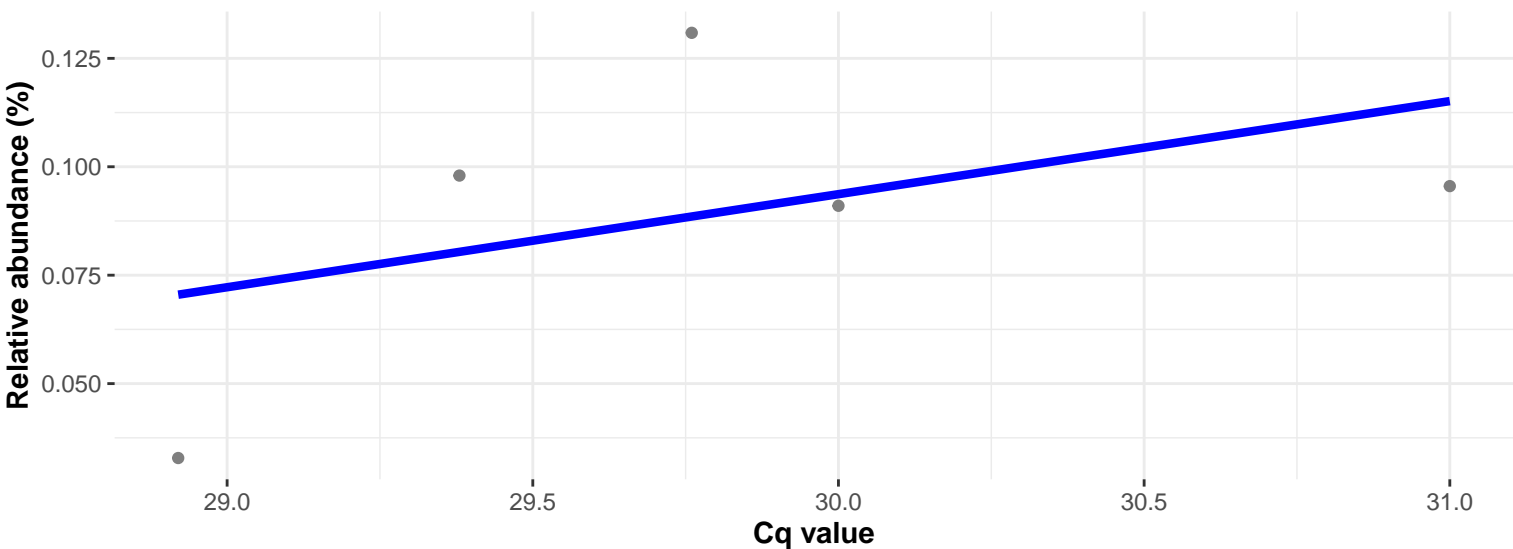


Correlation within: IM-PIM

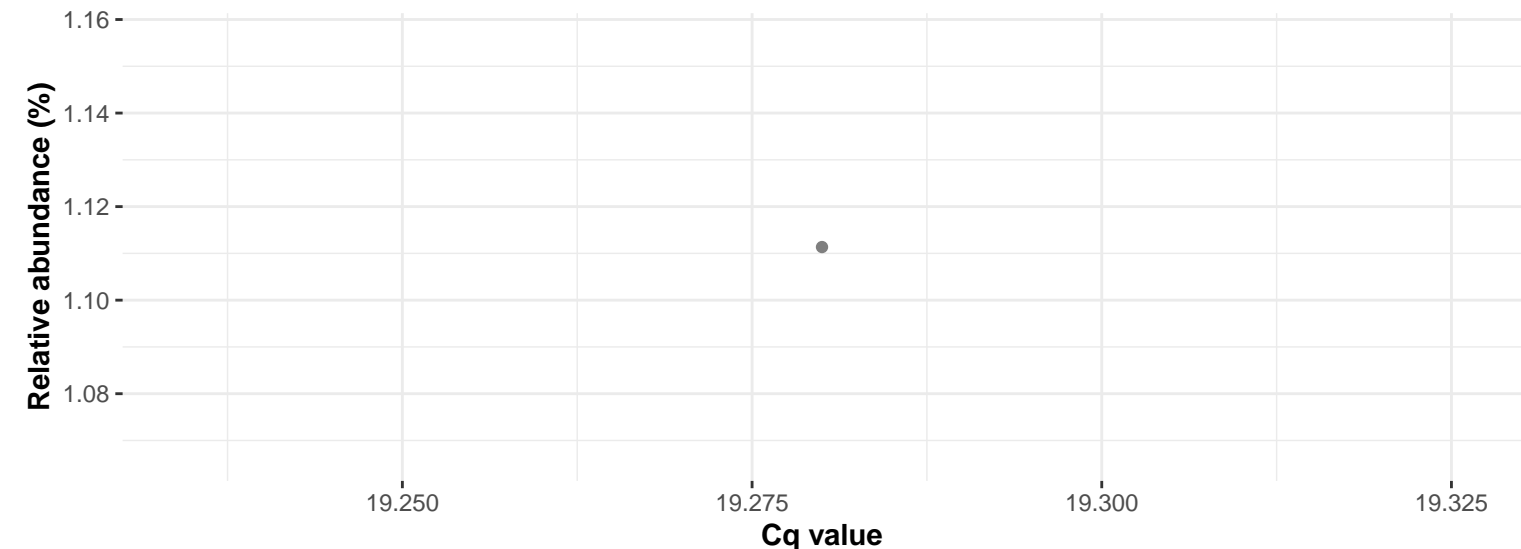
$\log_e(S) = 5.088$, $p = 0.960$, $\hat{\rho}_{\text{Spearman}} = 0.018$, $CI_{95\%} [-0.632, 0.653]$, $n_{\text{pairs}} = 10$



Correlation within: IM-DIM



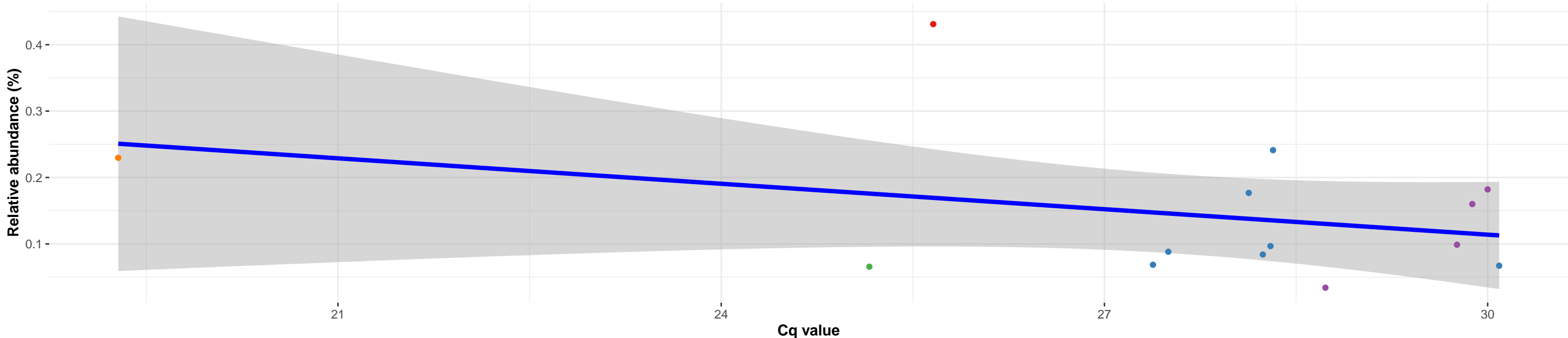
Correlation within: Feed



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

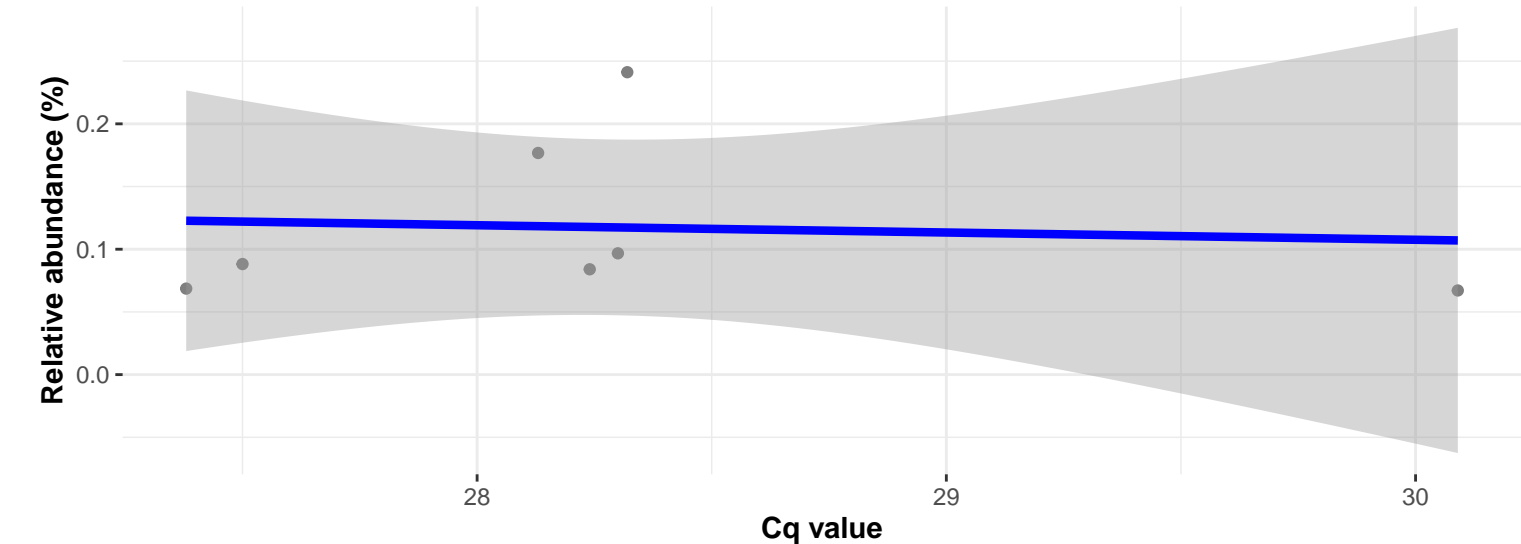
Correlation with all samples

$\log_e(S) = 6.223$, $p = 0.714$, $\hat{\rho}_{\text{Spearman}} = -0.108$, $\text{CI}_{95\%} [-0.615, 0.462]$, $n_{\text{pairs}} = 14$

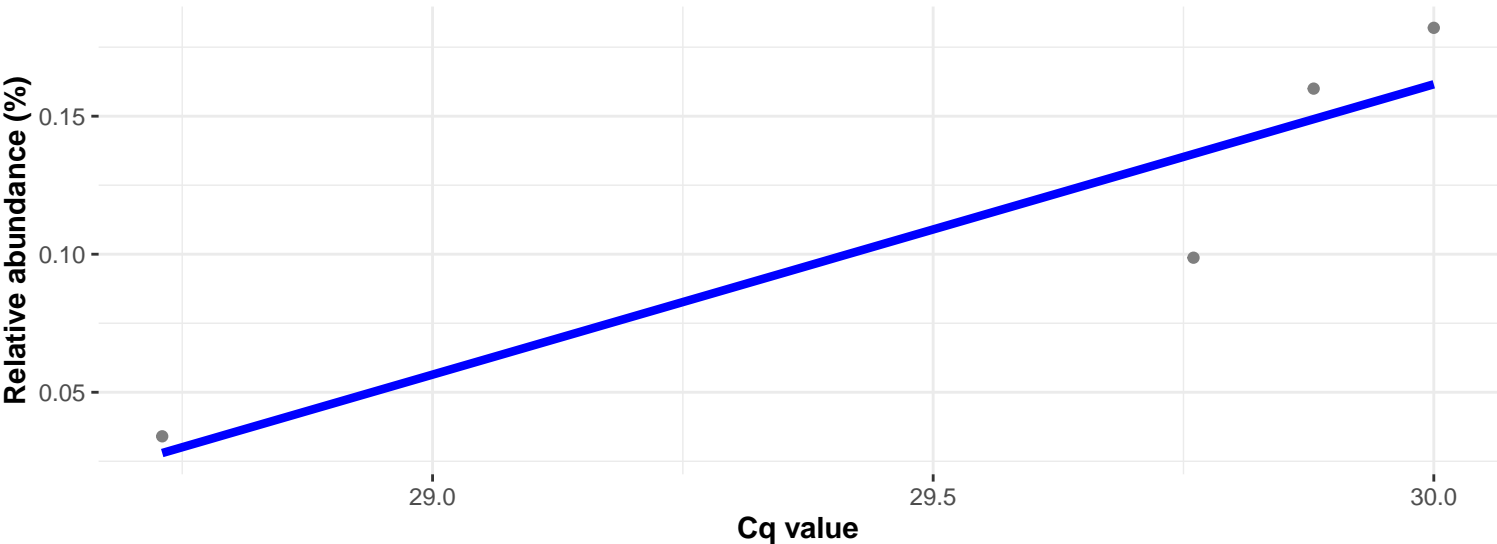


Correlation within: IM-PIM

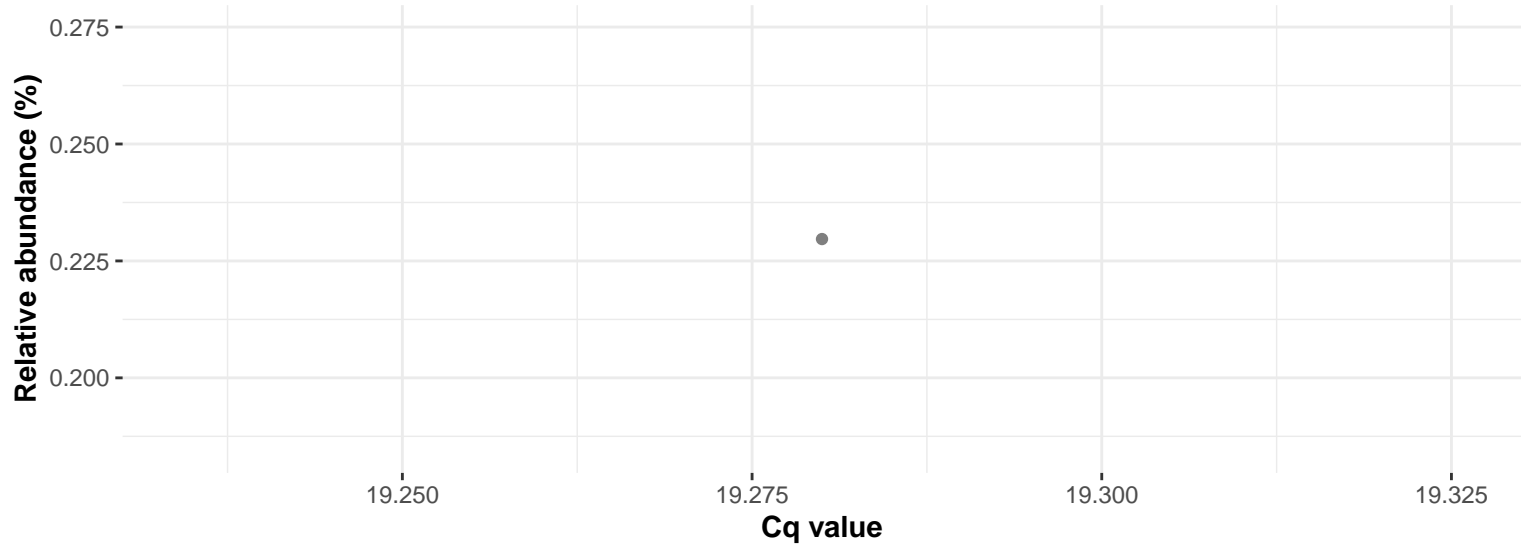
$\log_e(S) = 3.951$, $p = 0.879$, $\hat{\rho}_{\text{Spearman}} = 0.071$, $\text{CI}_{95\%} [-0.734, 0.793]$, $n_{\text{pairs}} = 7$



Correlation within: IM-DIM



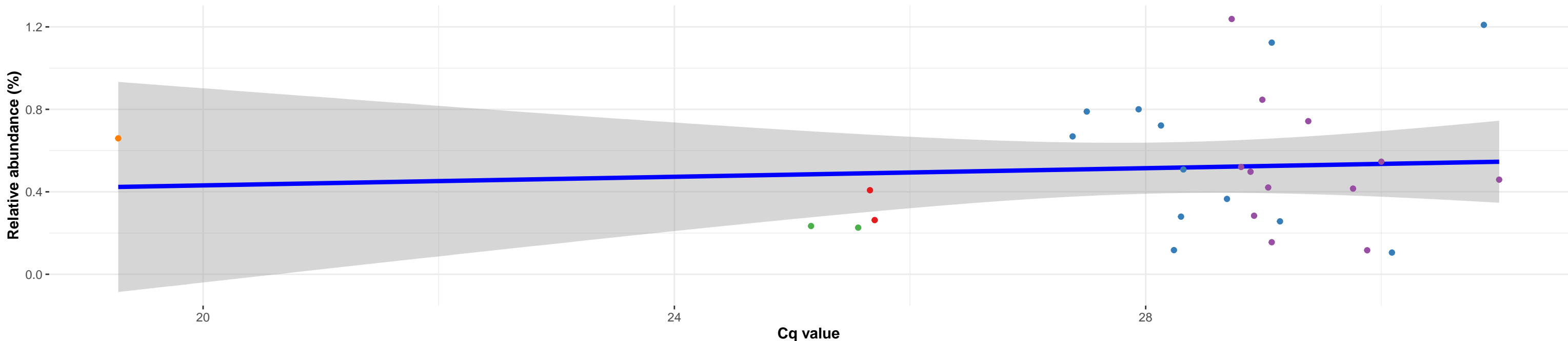
Correlation within: Feed



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

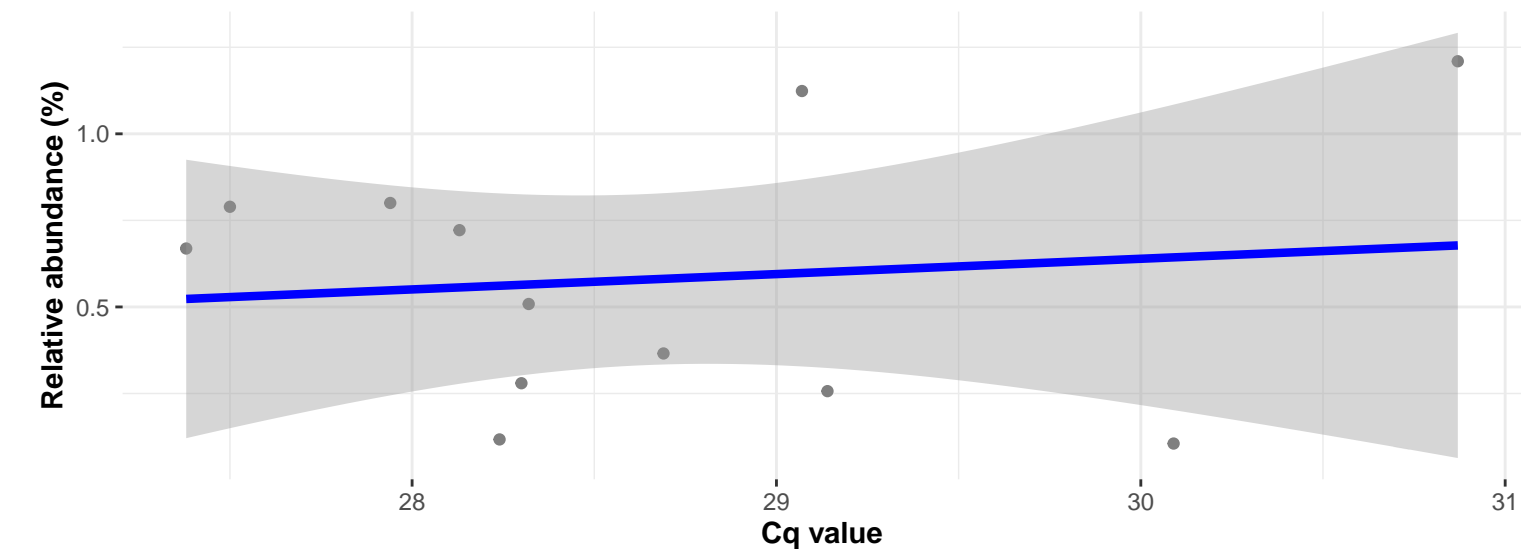
Correlation with all samples

$\log_e(S) = 8.292$, $p = 0.930$, $\hat{\rho}_{\text{Spearman}} = 0.017$, $CI_{95\%} [-0.362, 0.391]$, $n_{\text{pairs}} = 29$



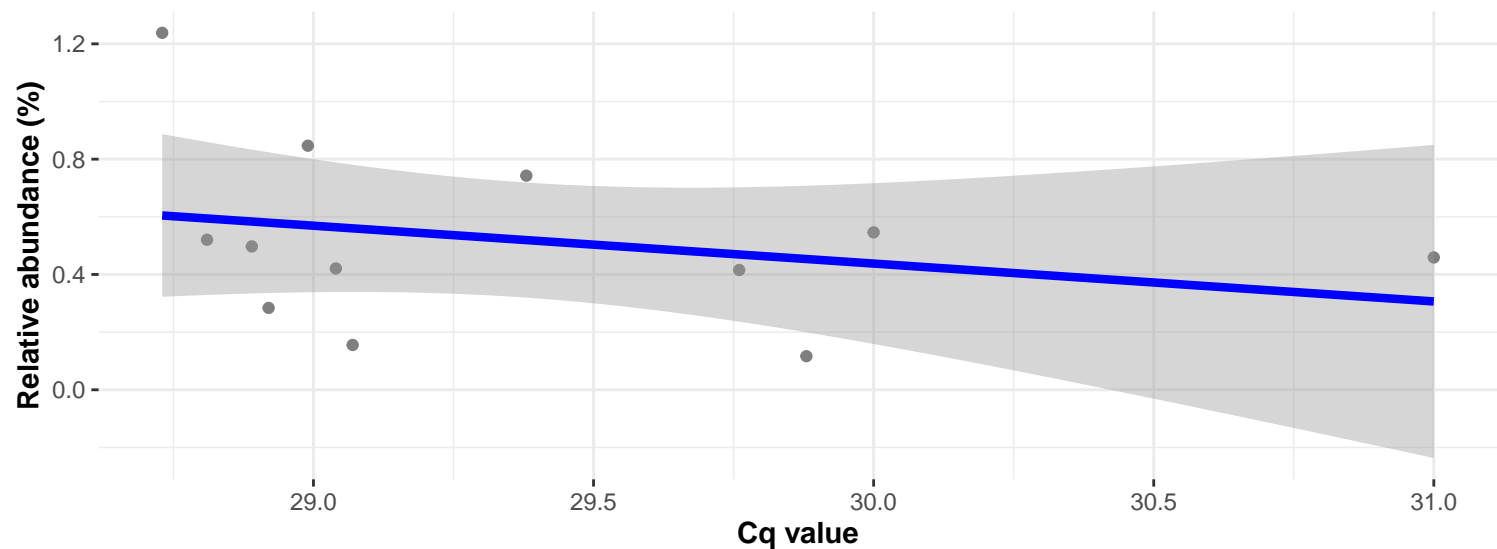
Correlation within: IM-PIM

$\log_e(S) = 5.787$, $p = 0.665$, $\hat{\rho}_{\text{Spearman}} = -0.140$, $CI_{95\%} [-0.671, 0.487]$, $n_{\text{pairs}} = 12$

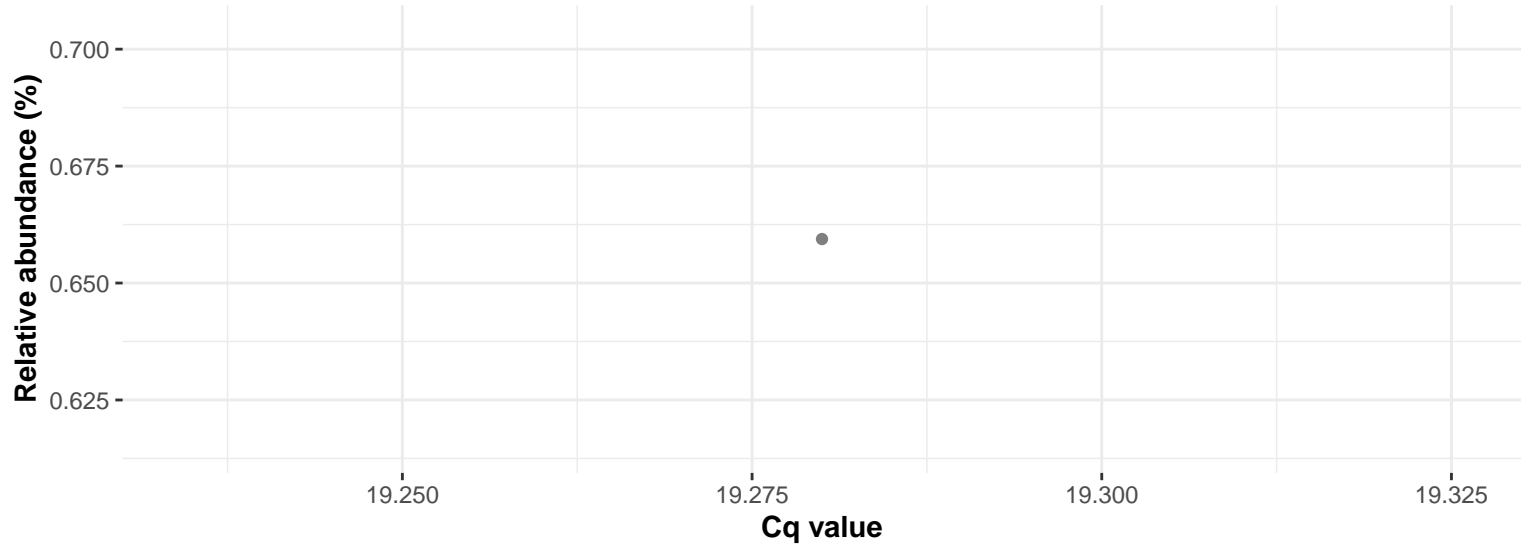


Correlation within: IM-DIM

$\log_e(S) = 5.956$, $p = 0.265$, $\hat{\rho}_{\text{Spearman}} = -0.350$, $CI_{95\%} [-0.777, 0.298]$, $n_{\text{pairs}} = 12$



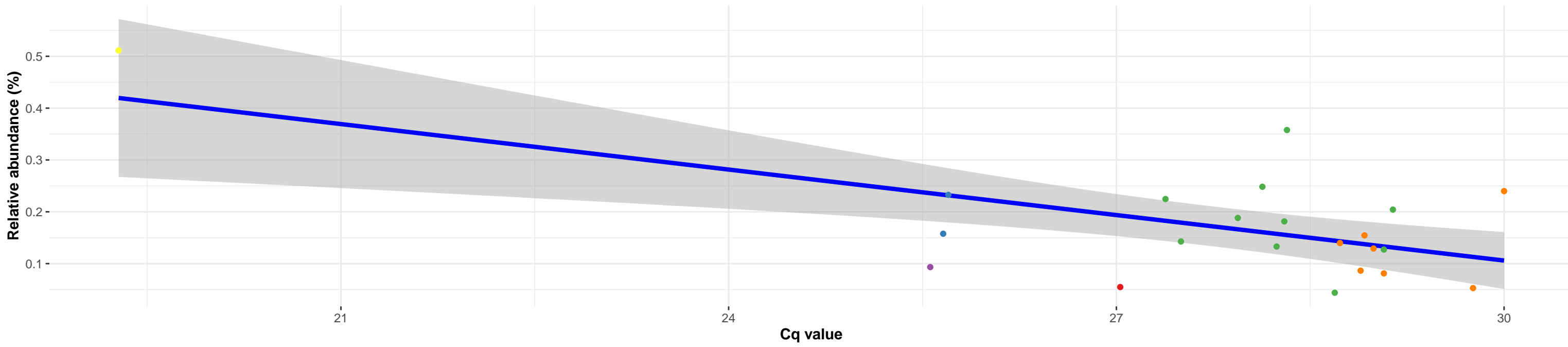
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Vagococcus; Ambiguous_taxa

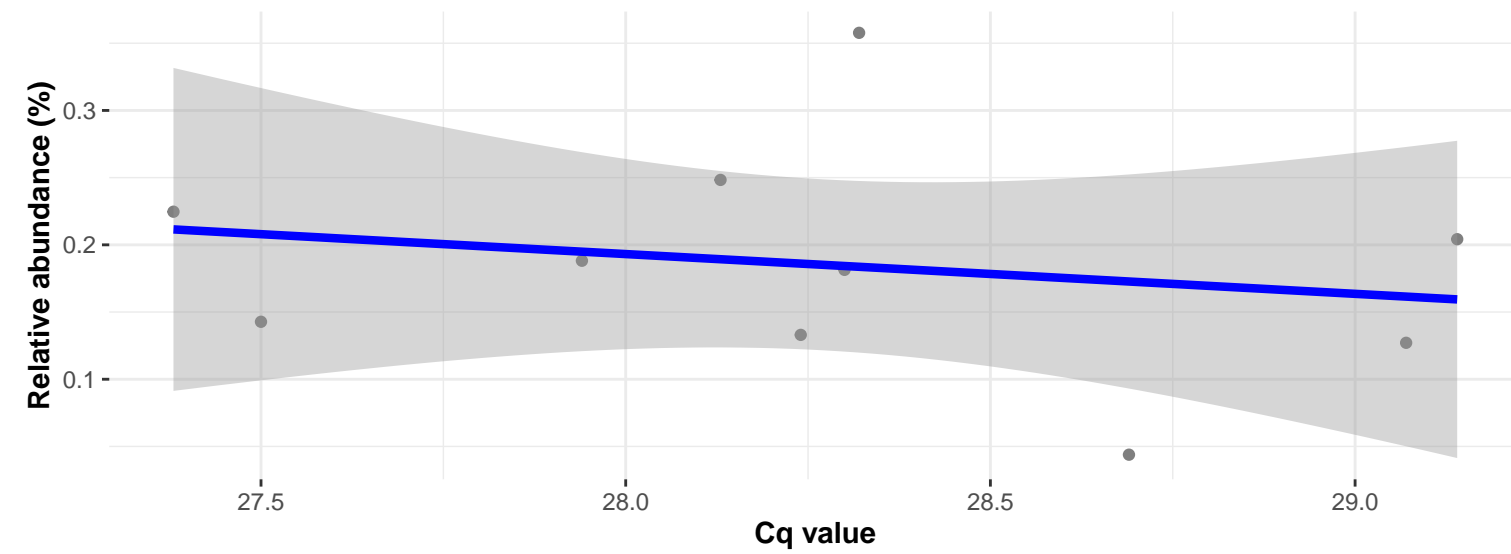
Correlation with all samples

$\log_e(S) = 7.715$, $p = 0.232$, $\hat{\rho}_{\text{Spearman}} = -0.265$, $CI_{95\%} [-0.626, 0.189]$, $n_{\text{pairs}} = 22$



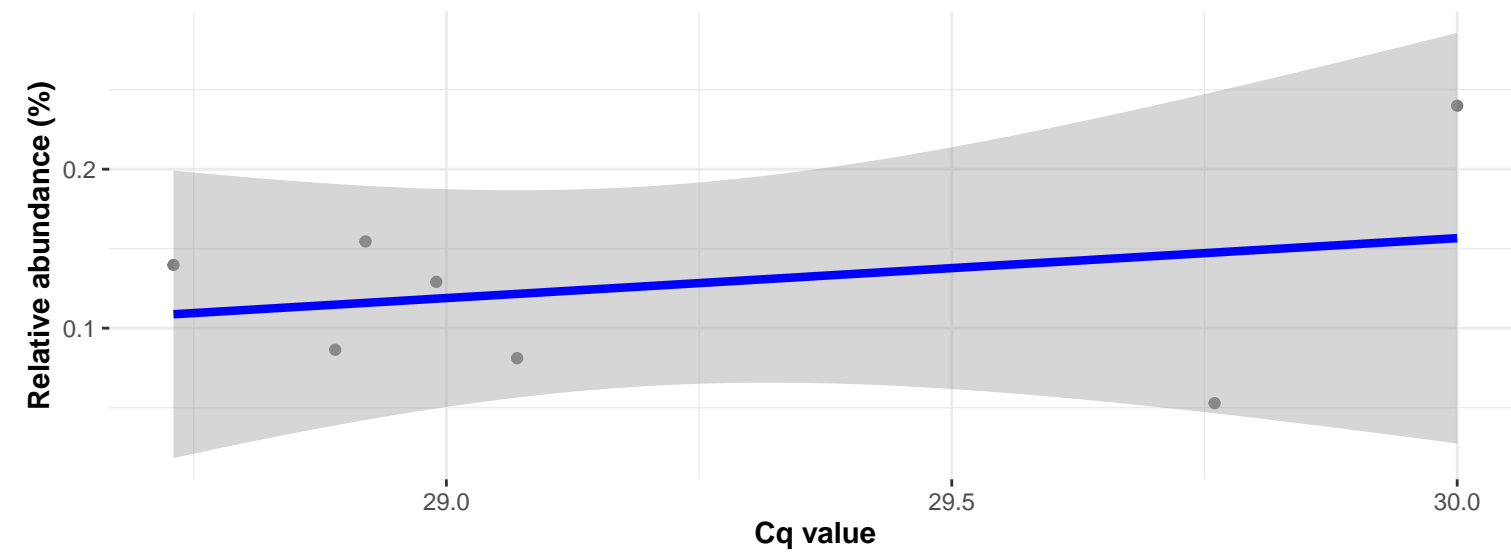
Correlation within: IM-PIM

$\log_e(S) = 5.338$, $p = 0.467$, $\hat{\rho}_{\text{Spearman}} = -0.261$, $CI_{95\%} [-0.774, 0.459]$, $n_{\text{pairs}} = 10$

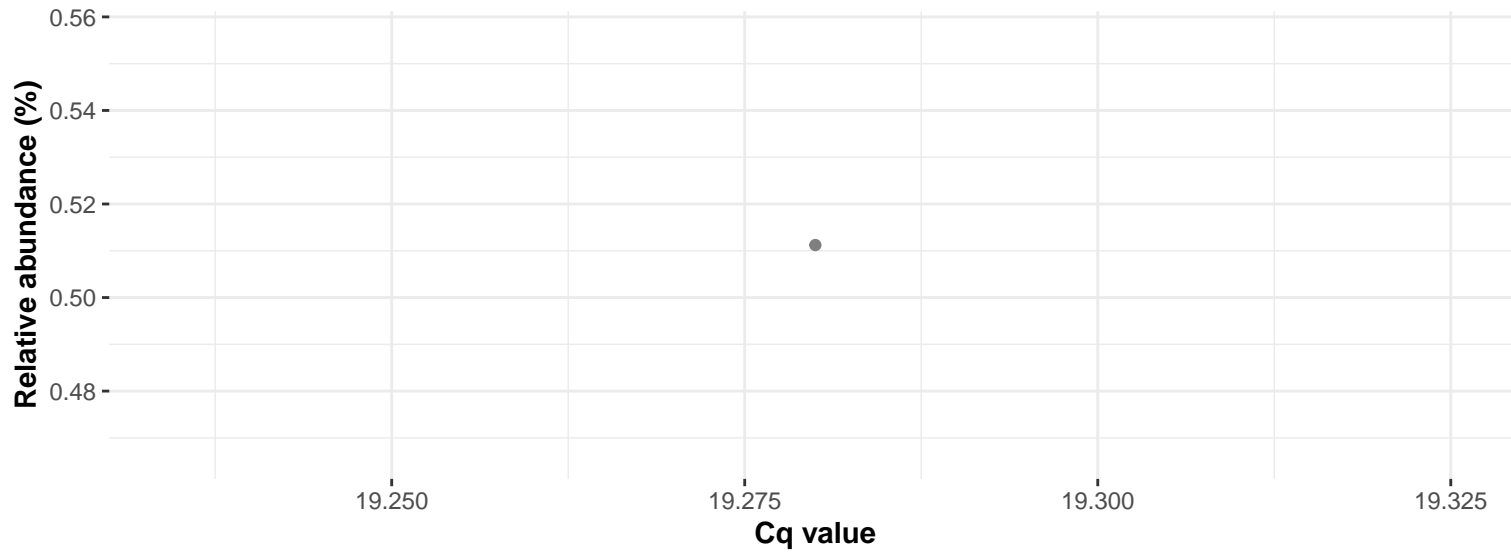


Correlation within: IM-DIM

$\log_e(S) = 4.094$, $p = 0.879$, $\hat{\rho}_{\text{Spearman}} = -0.071$, $CI_{95\%} [-0.793, 0.734]$, $n_{\text{pairs}} = 7$



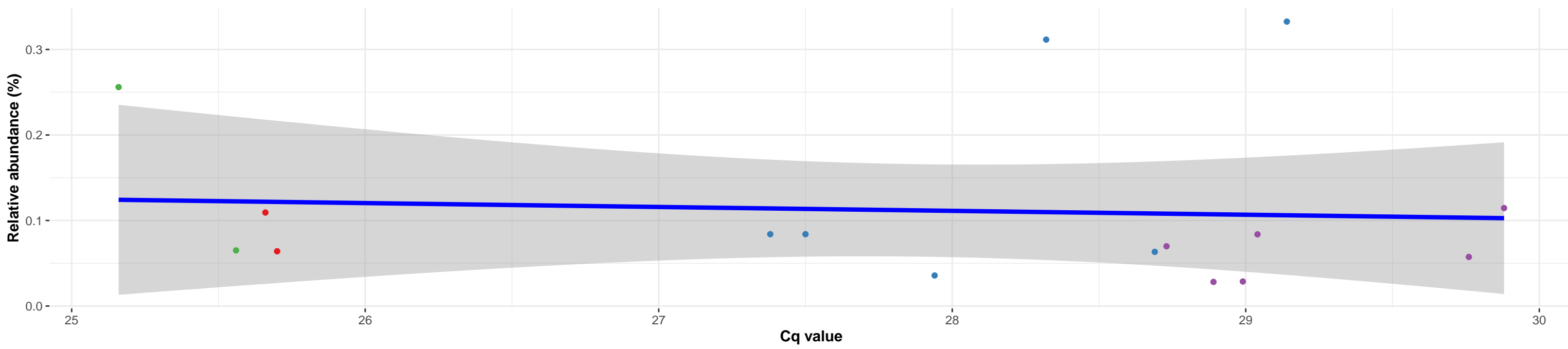
Correlation within: Feed



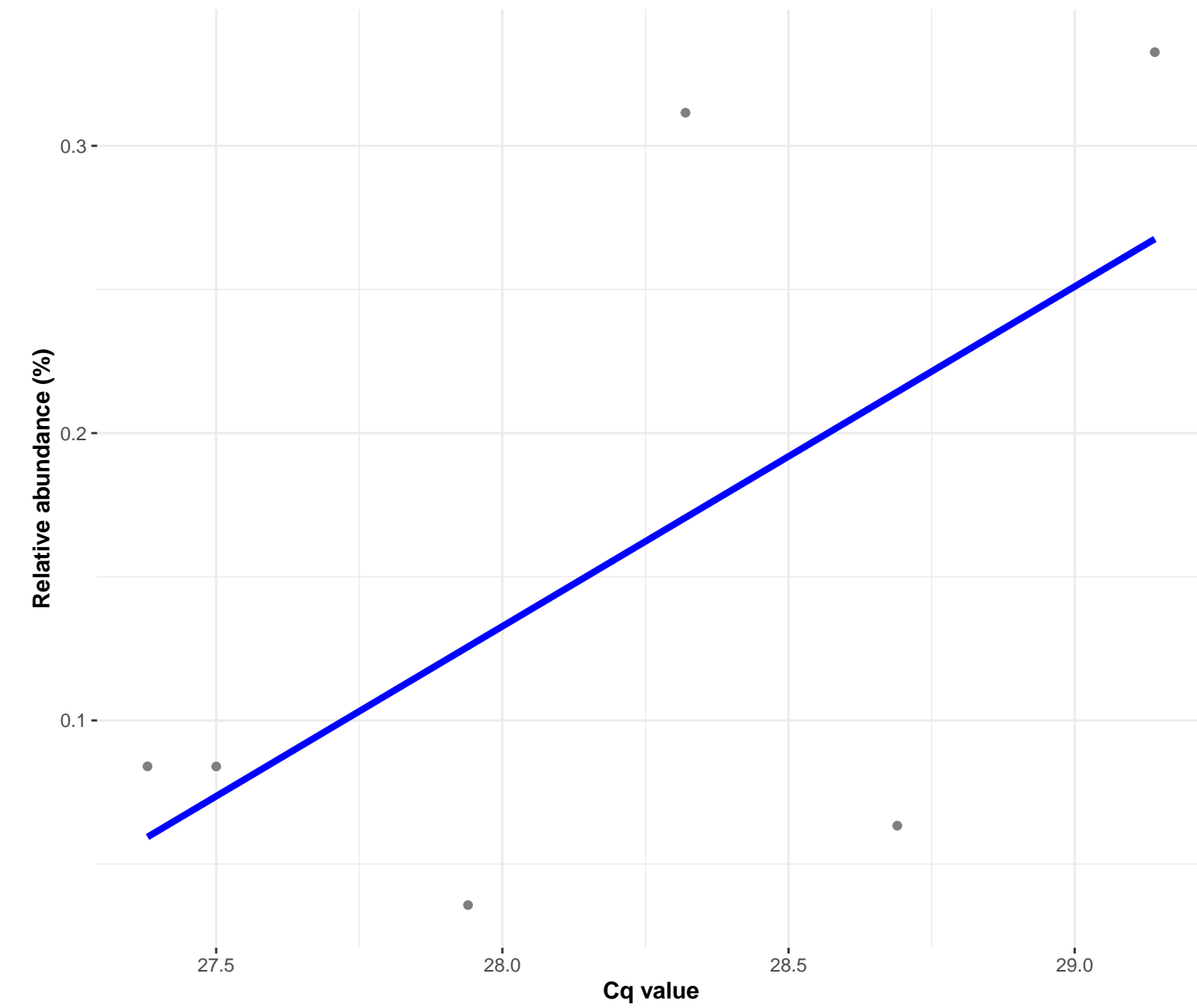
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; Ambiguous_taxa

Correlation with all samples

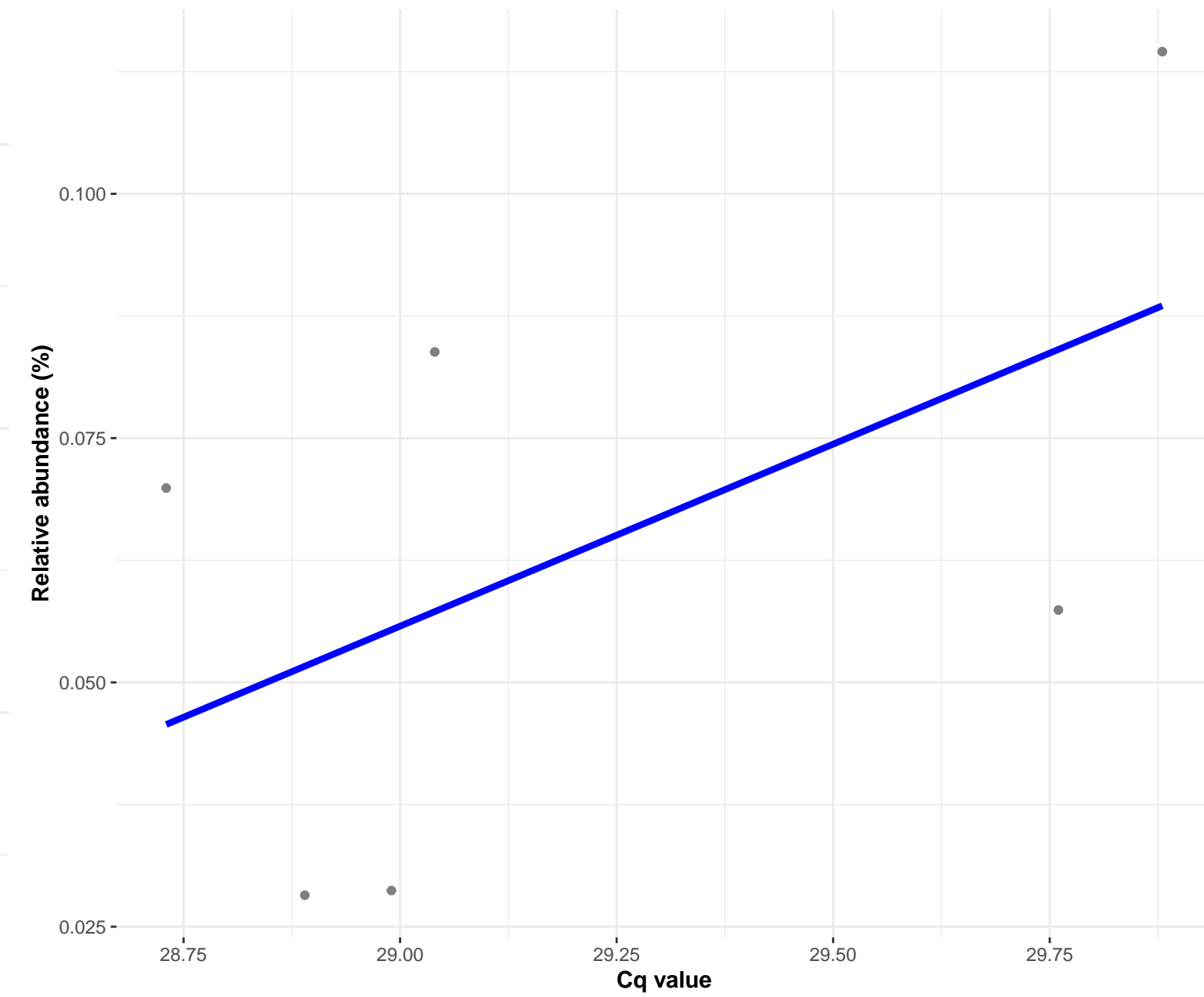
$\log_e(S) = 6.641$, $p = 0.641$, $\hat{\rho}_{\text{Spearman}} = -0.126$, $\text{CI}_{95\%} [-0.596, 0.407]$, $n_{\text{pairs}} = 16$



Correlation within: IM-PIM



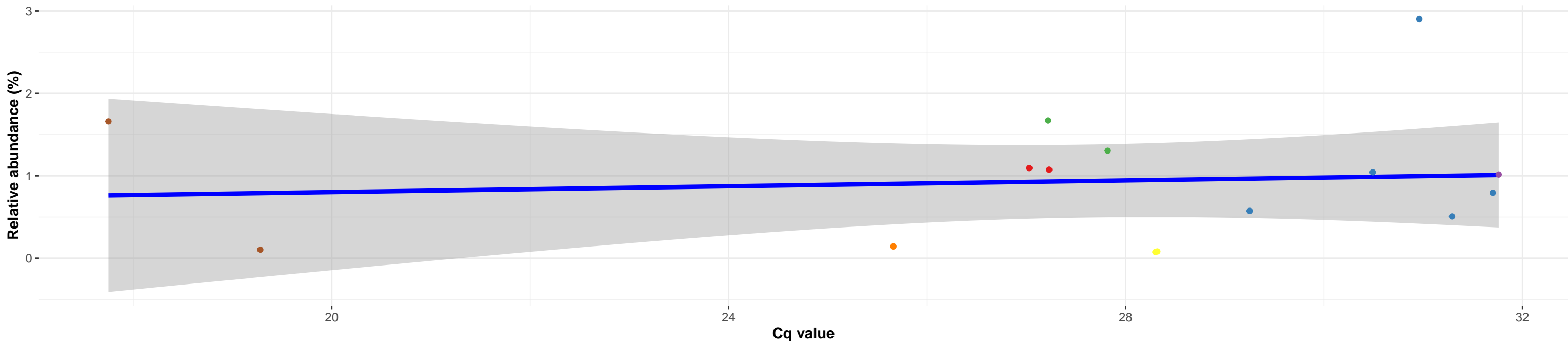
Correlation within: IM-DIM



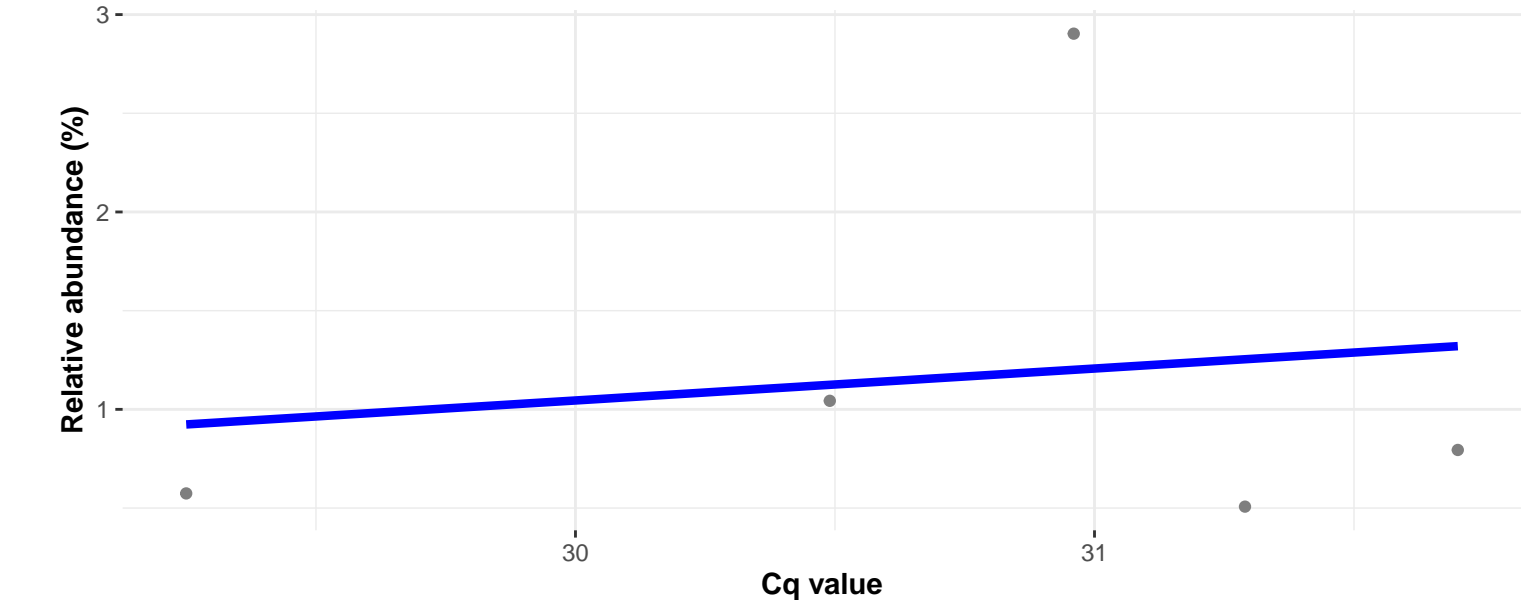
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus helveticus

Correlation with all samples

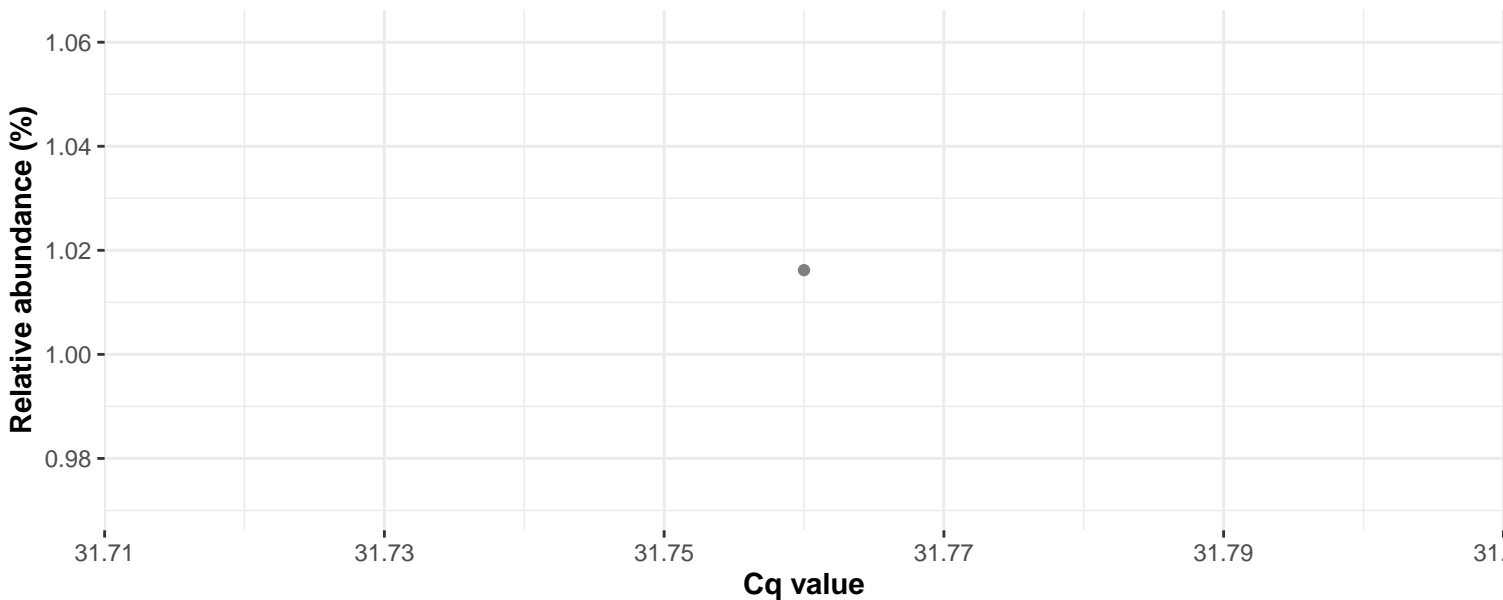
$\log_e(S) = 6.407$, $p = 0.771$, $\hat{\rho}_{\text{Spearman}} = -0.082$, $CI_{95\%} [-0.582, 0.462]$, $n_{\text{pairs}} = 15$



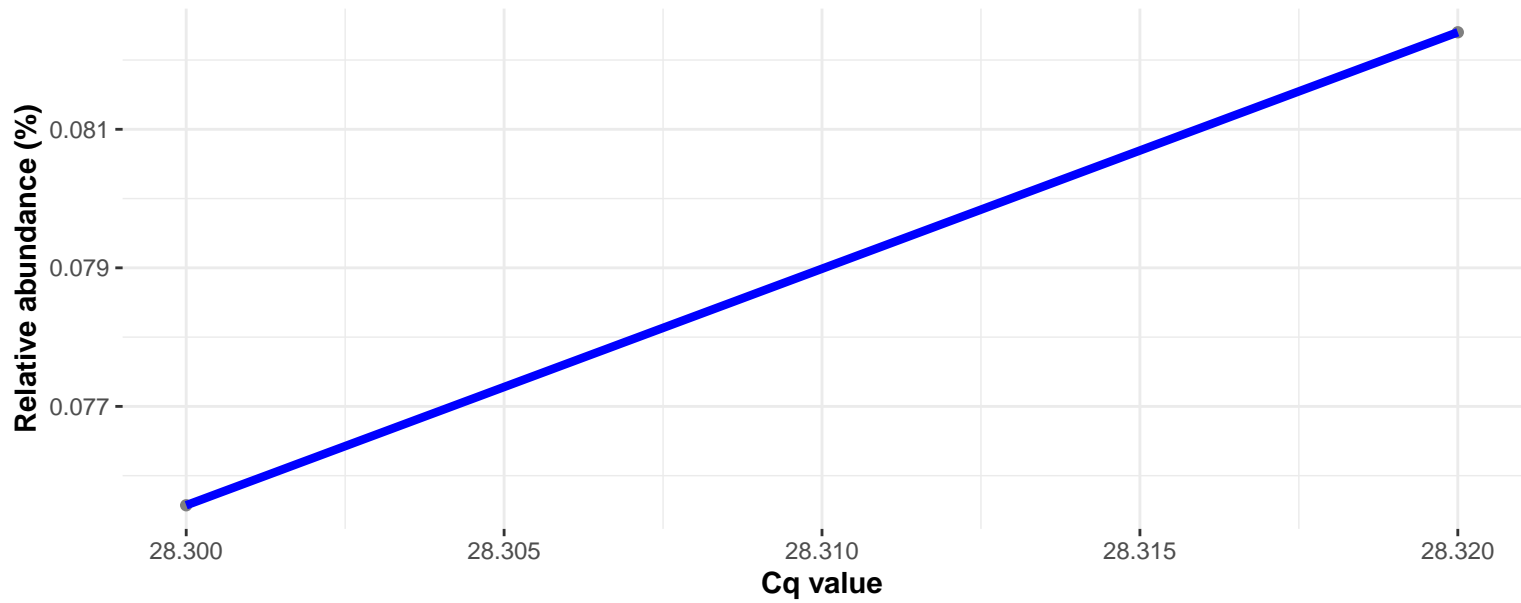
Correlation within: REF-PIM



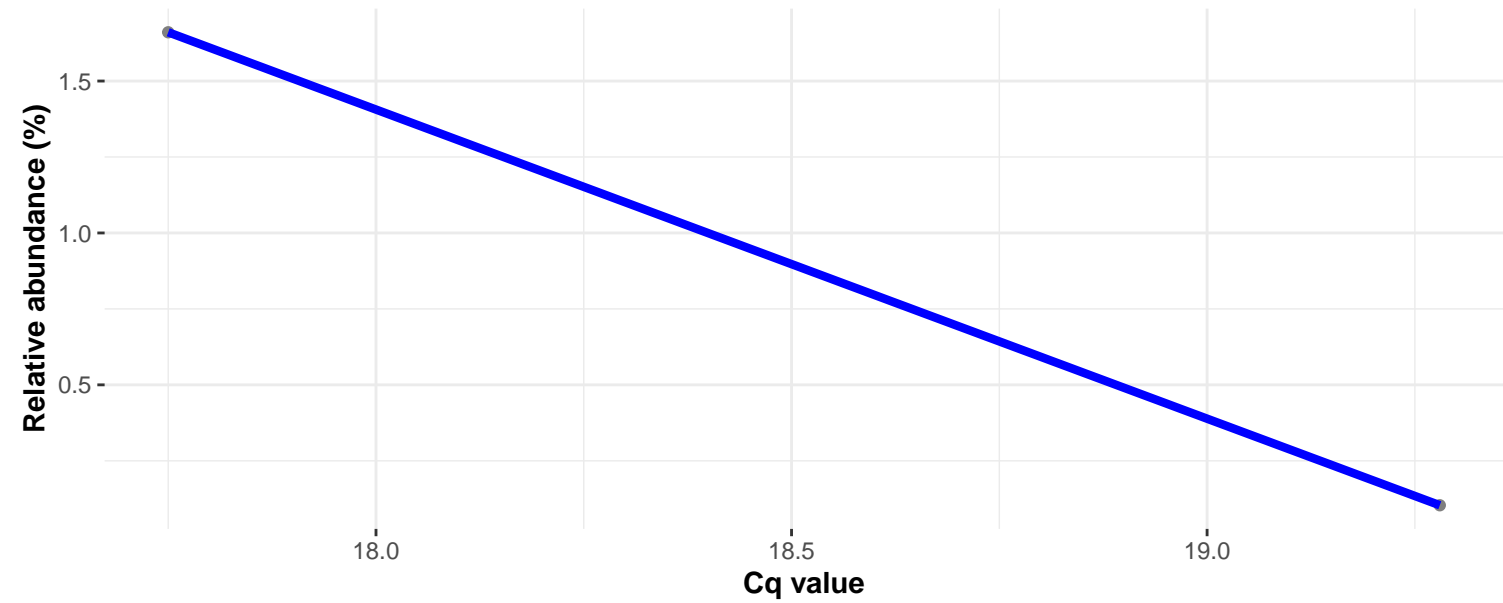
Correlation within: REF-DIM



Correlation within: IM-PIM



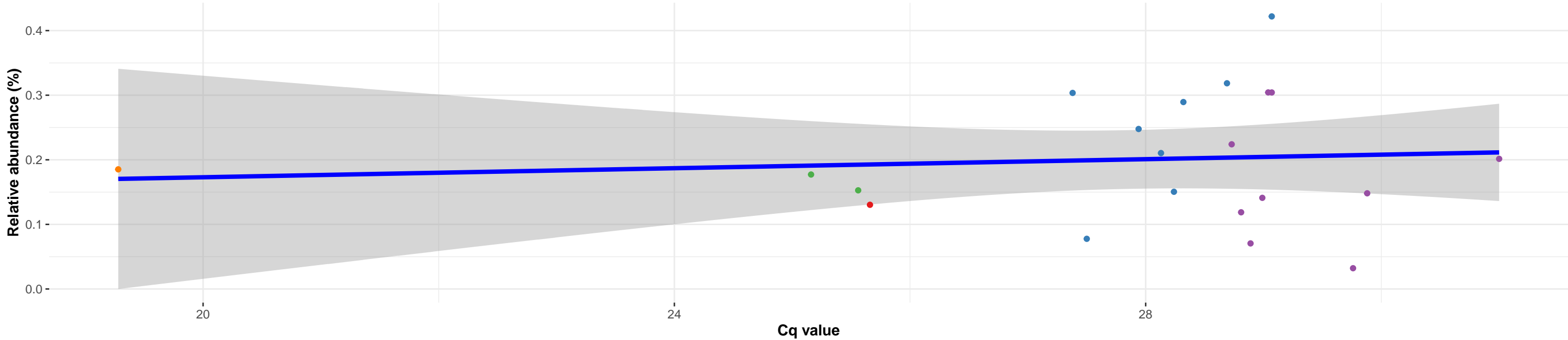
Correlation within: Feed



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

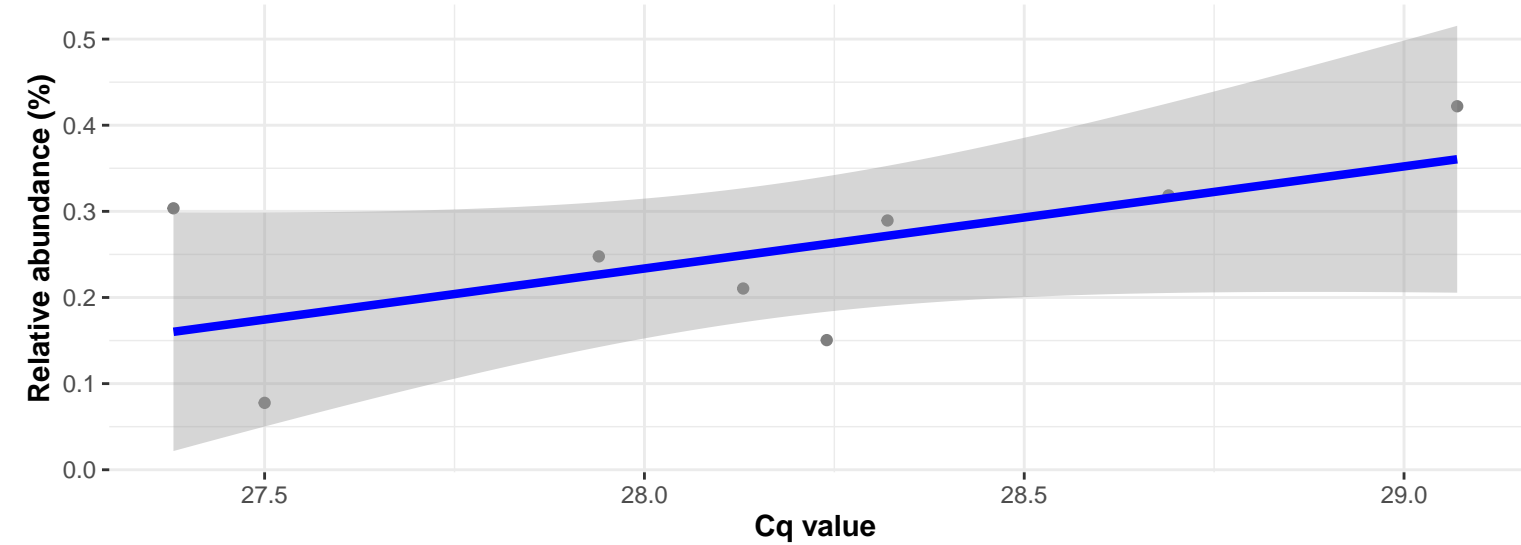
Correlation with all samples

$\log_e(S) = 7.291$, $p = 0.838$, $\hat{\rho}_{\text{Spearman}} = 0.047$, $CI_{95\%} [-0.404, 0.480]$, $n_{\text{pairs}} = 21$



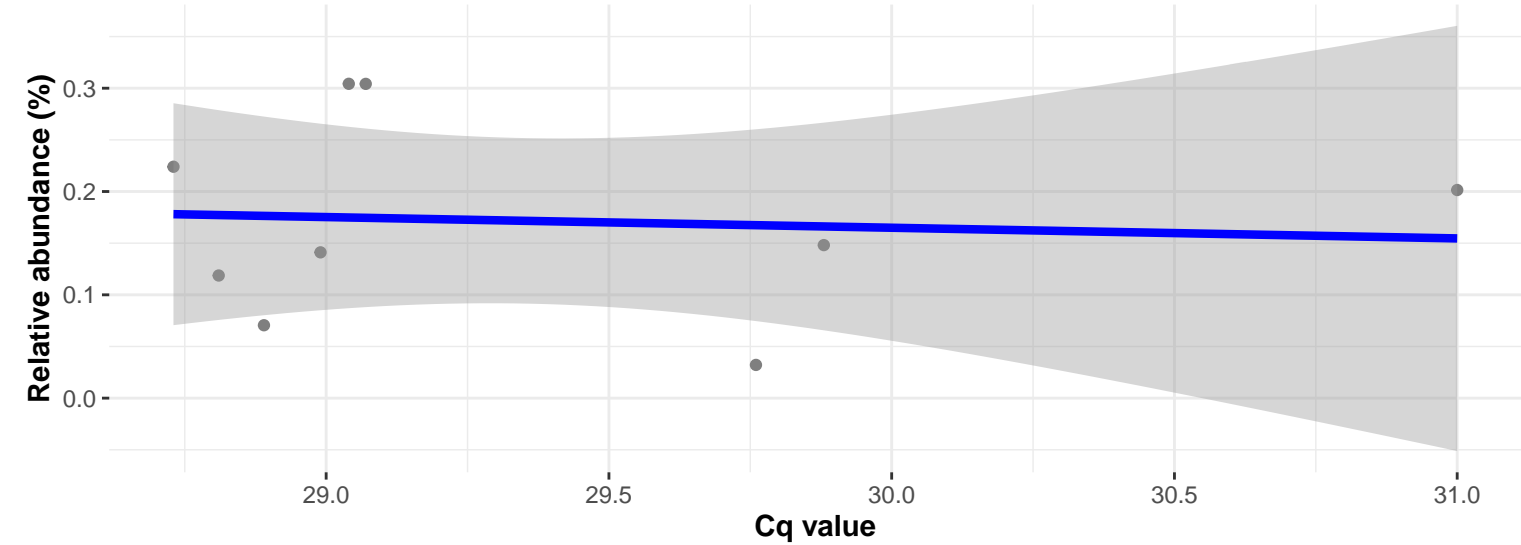
Correlation within: IM-PIM

$\log_e(S) = 3.638$, $p = 0.160$, $\hat{\rho}_{\text{Spearman}} = 0.548$, $CI_{95\%} [-0.280, 0.908]$, $n_{\text{pairs}} = 8$

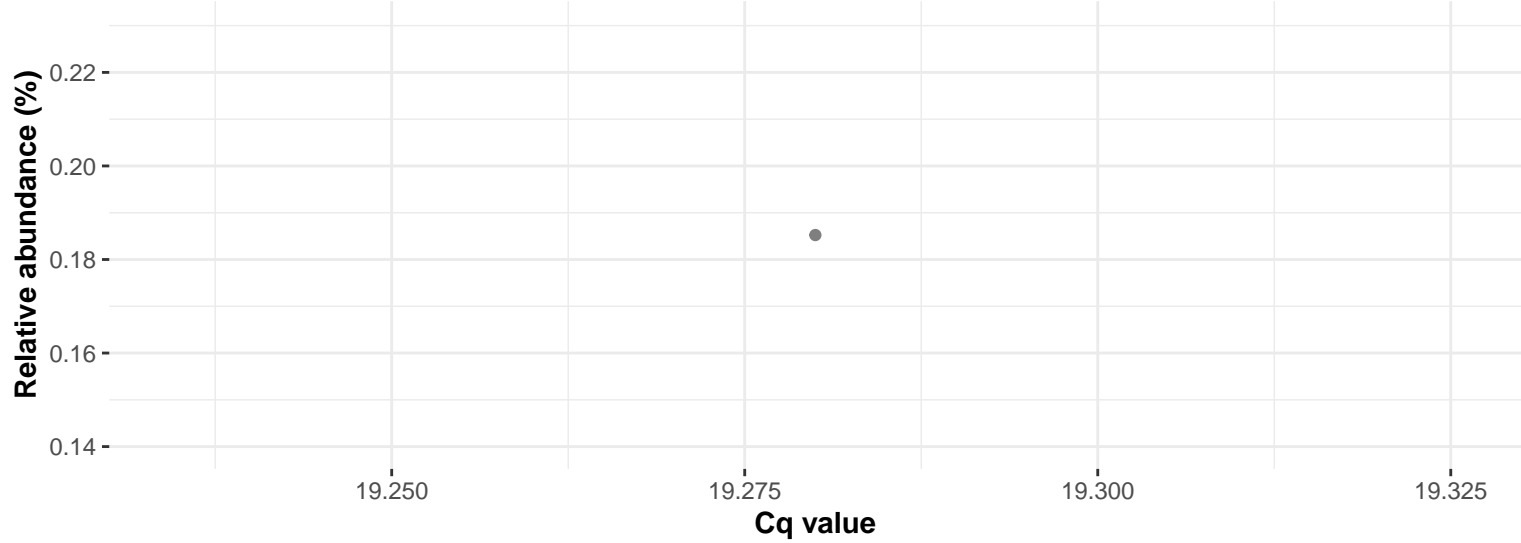


Correlation within: IM-DIM

$\log_e(S) = 4.718$, $p = 0.865$, $\hat{\rho}_{\text{Spearman}} = 0.067$, $CI_{95\%} [-0.639, 0.712]$, $n_{\text{pairs}} = 9$

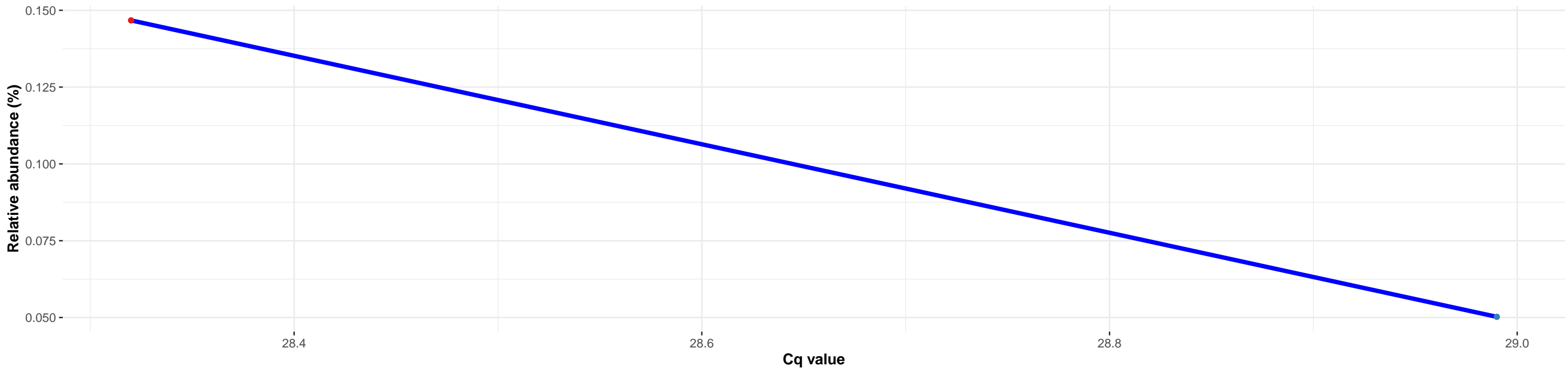


Correlation within: Feed



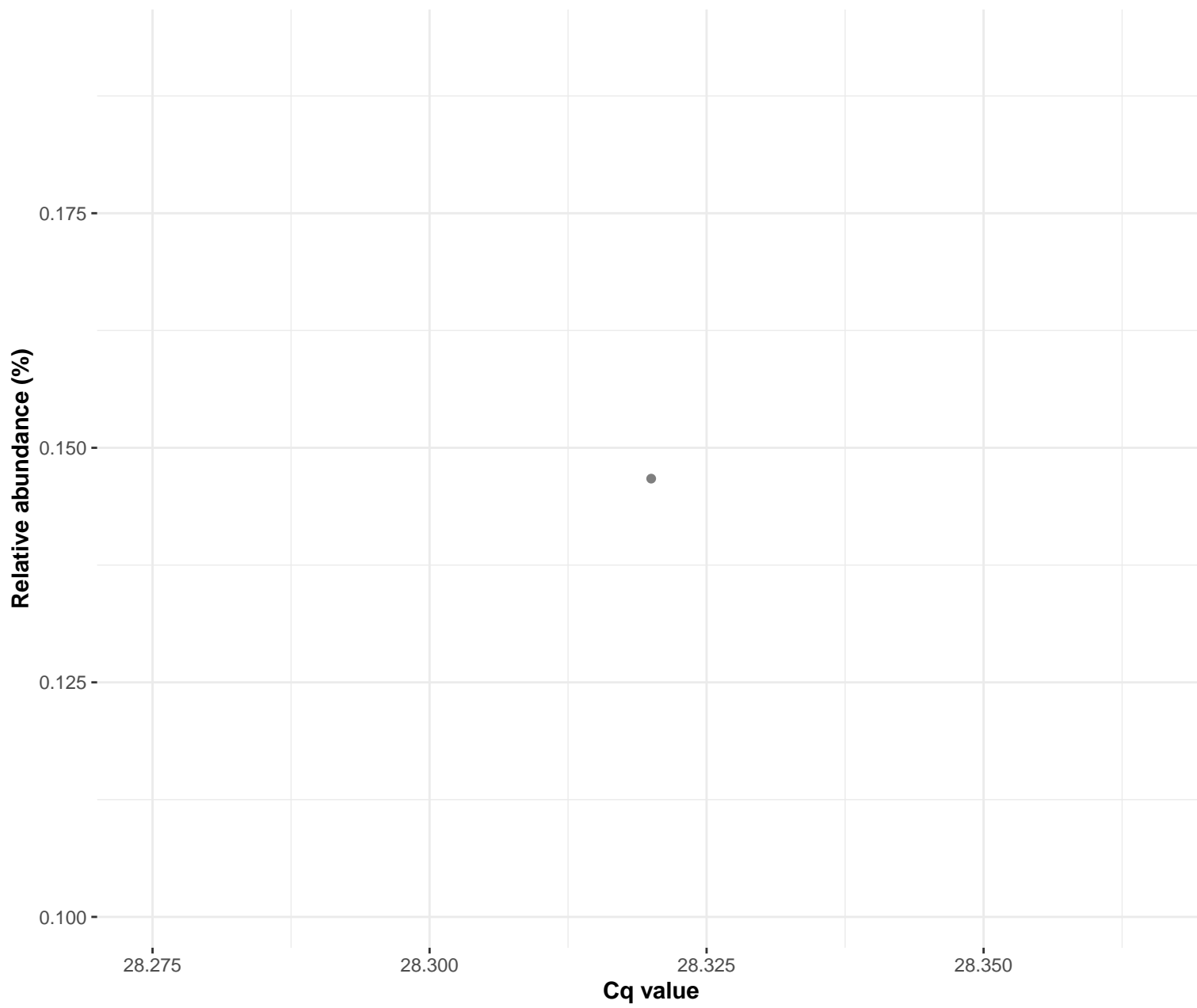
k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingobium; s__alpha proteobacterium PI_GH4.1.H5

Correlation with all samples

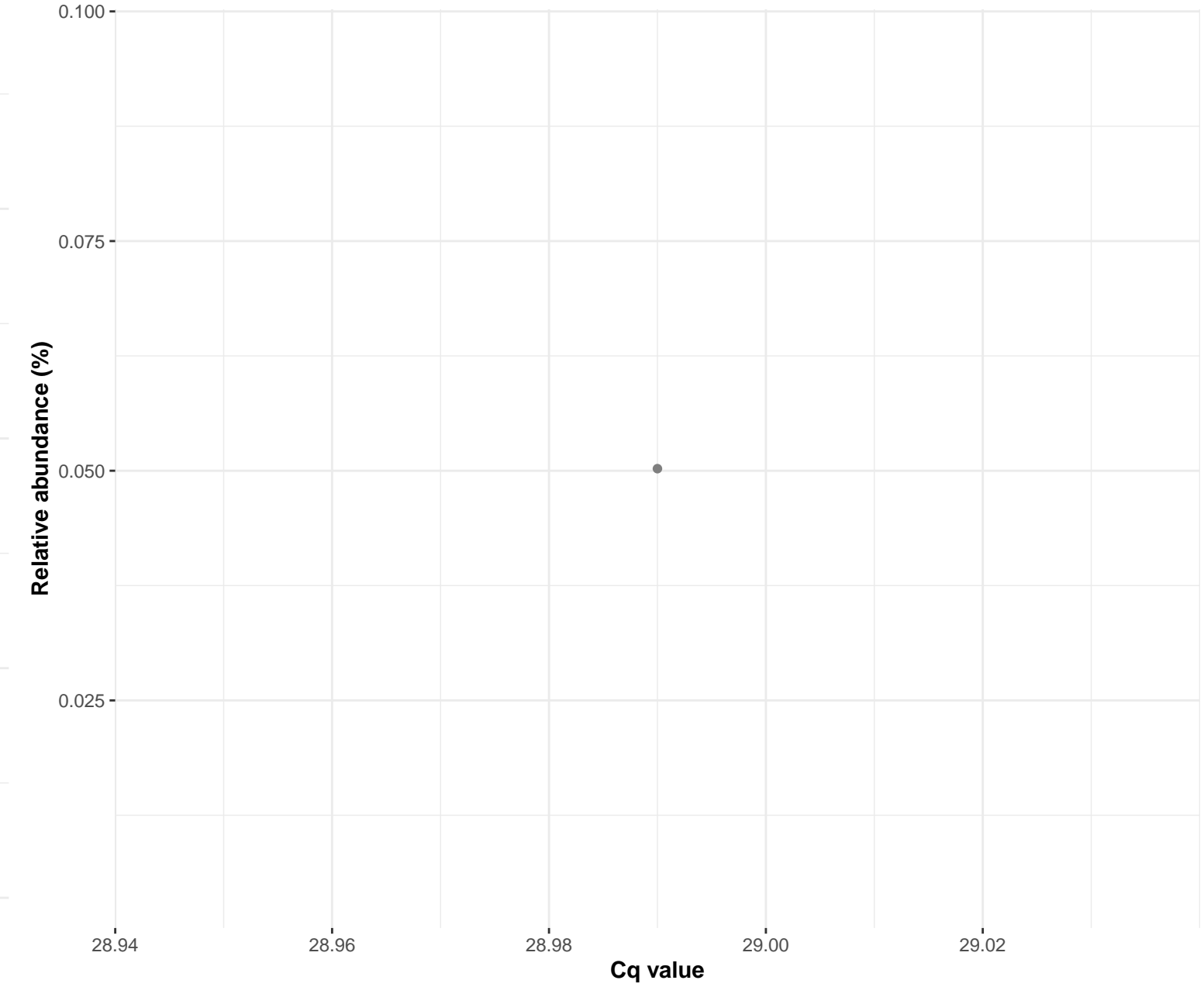


SampleType • IM-PIM • IM-DIM

Correlation within: IM-PIM



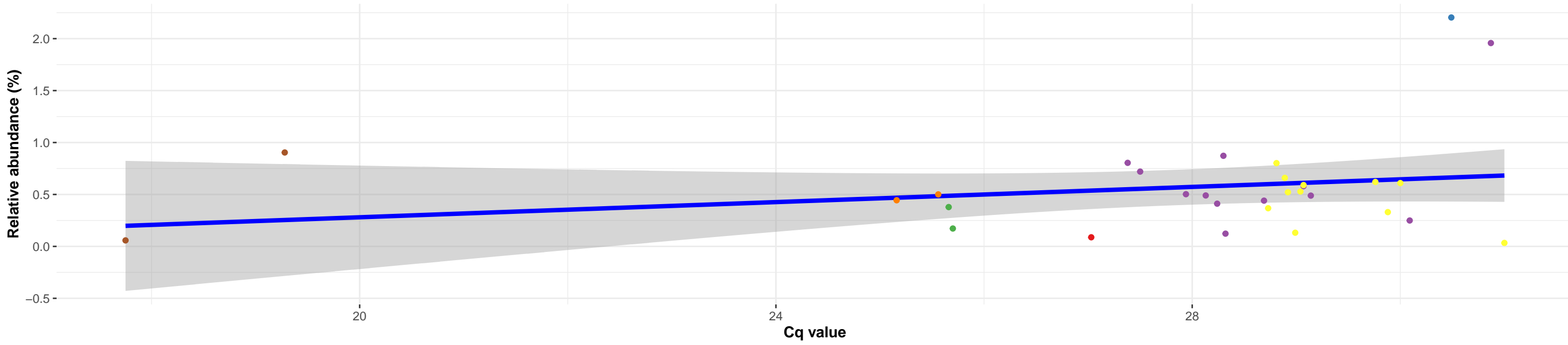
Correlation within: IM-DIM



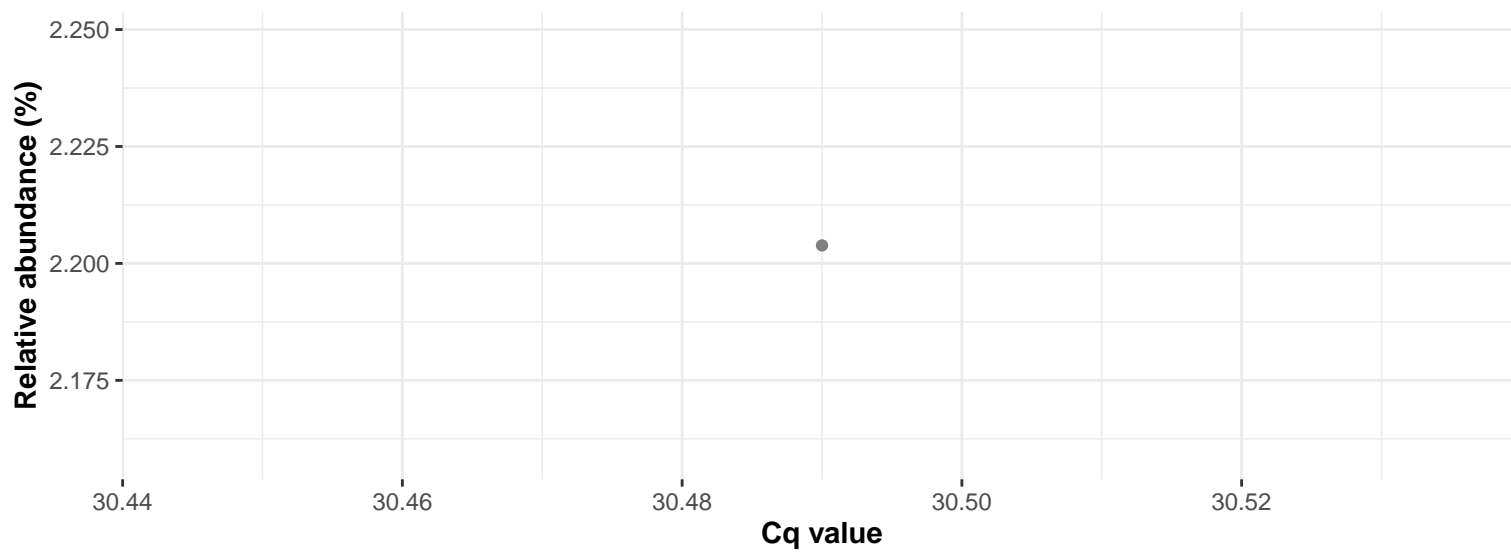
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. DJF_WC57

Correlation with all samples

$\log_e(S) = 8.351$, $p = 0.433$, $\hat{\rho}_{\text{Spearman}} = 0.146$, $\text{CI}_{95\%} [-0.230, 0.484]$, $n_{\text{pairs}} = 31$

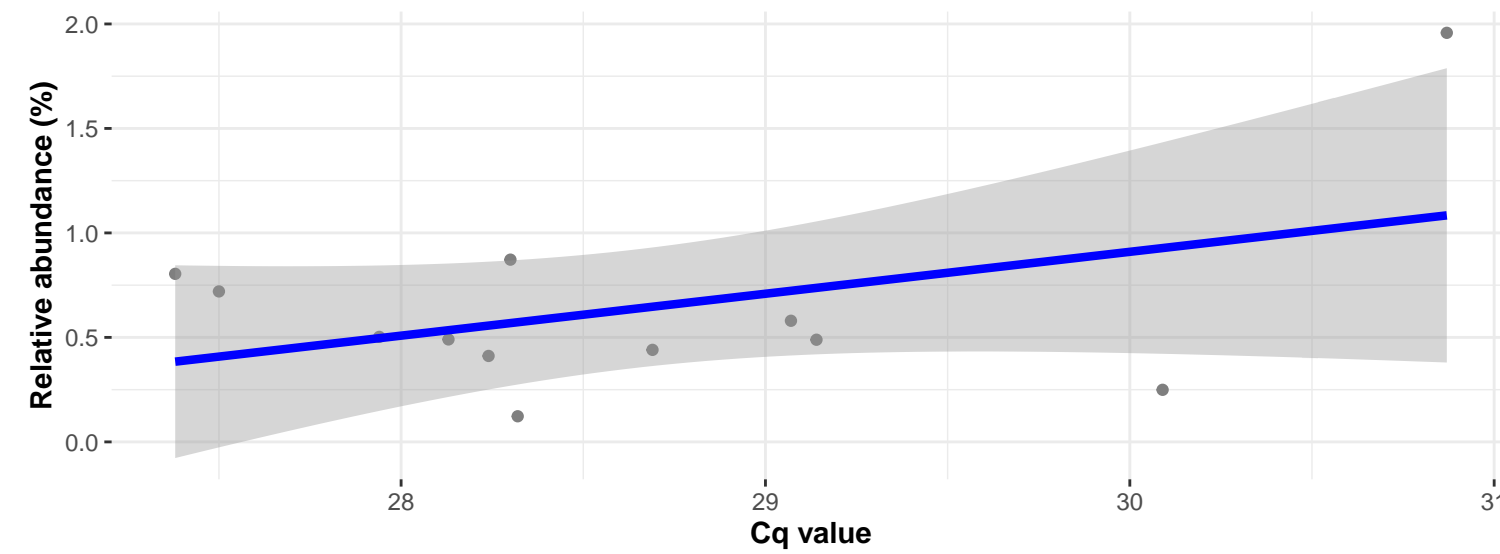


Correlation within: REF-PIM



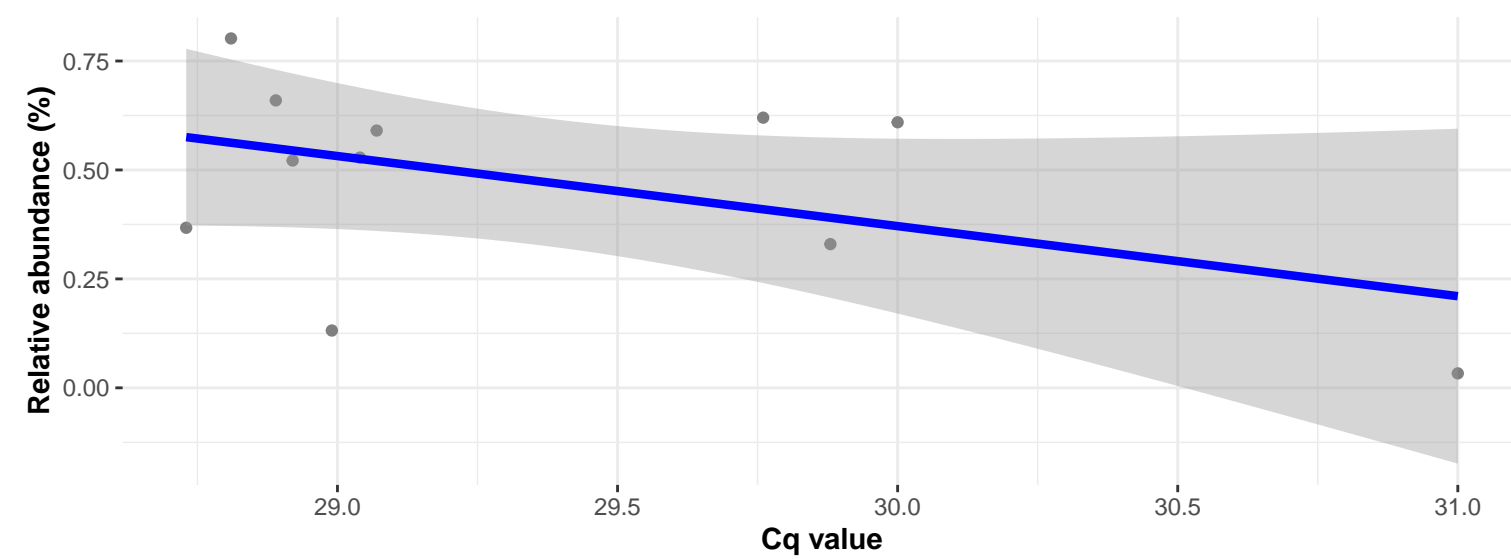
Correlation within: IM-PIM

$\log_e(S) = 5.823$, $p = 0.572$, $\hat{\rho}_{\text{Spearman}} = -0.182$, $\text{CI}_{95\%} [-0.694, 0.453]$, $n_{\text{pairs}} = 12$

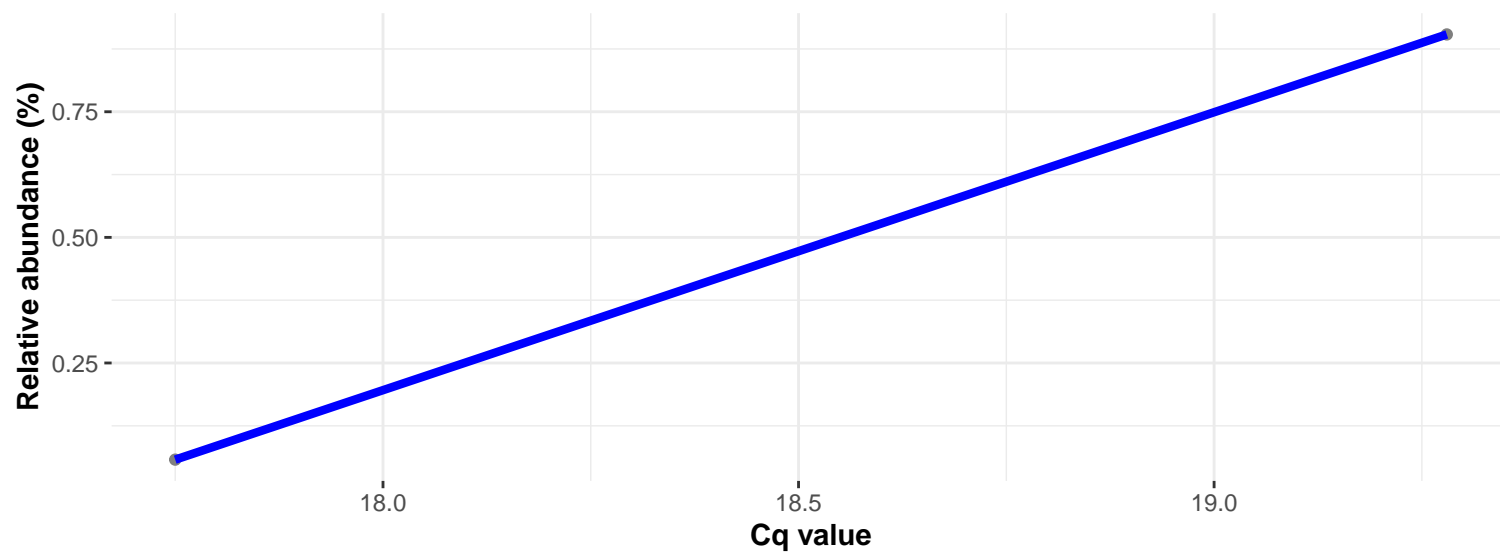


Correlation within: IM-DIM

$\log_e(S) = 5.670$, $p = 0.340$, $\hat{\rho}_{\text{Spearman}} = -0.318$, $\text{CI}_{95\%} [-0.779, 0.366]$, $n_{\text{pairs}} = 11$



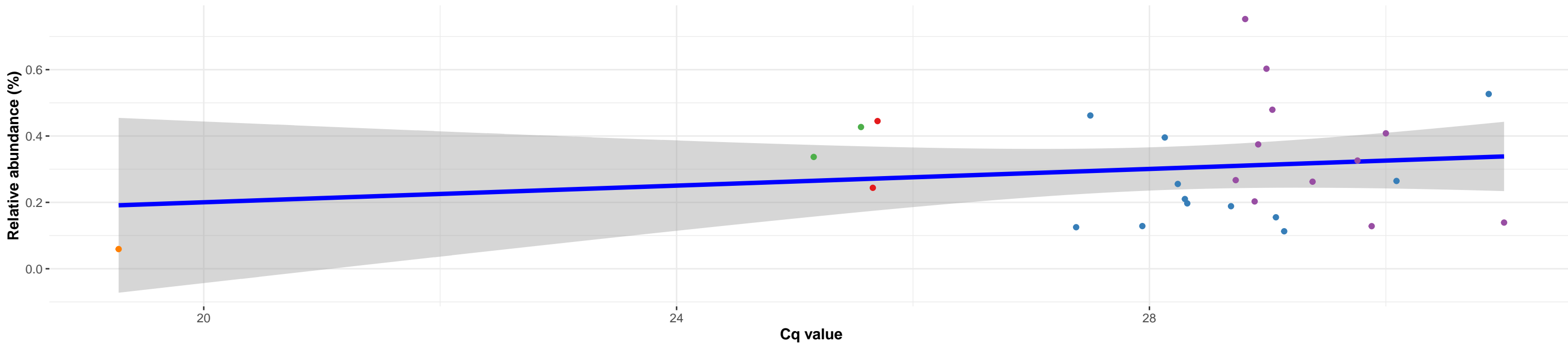
Correlation within: Feed



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

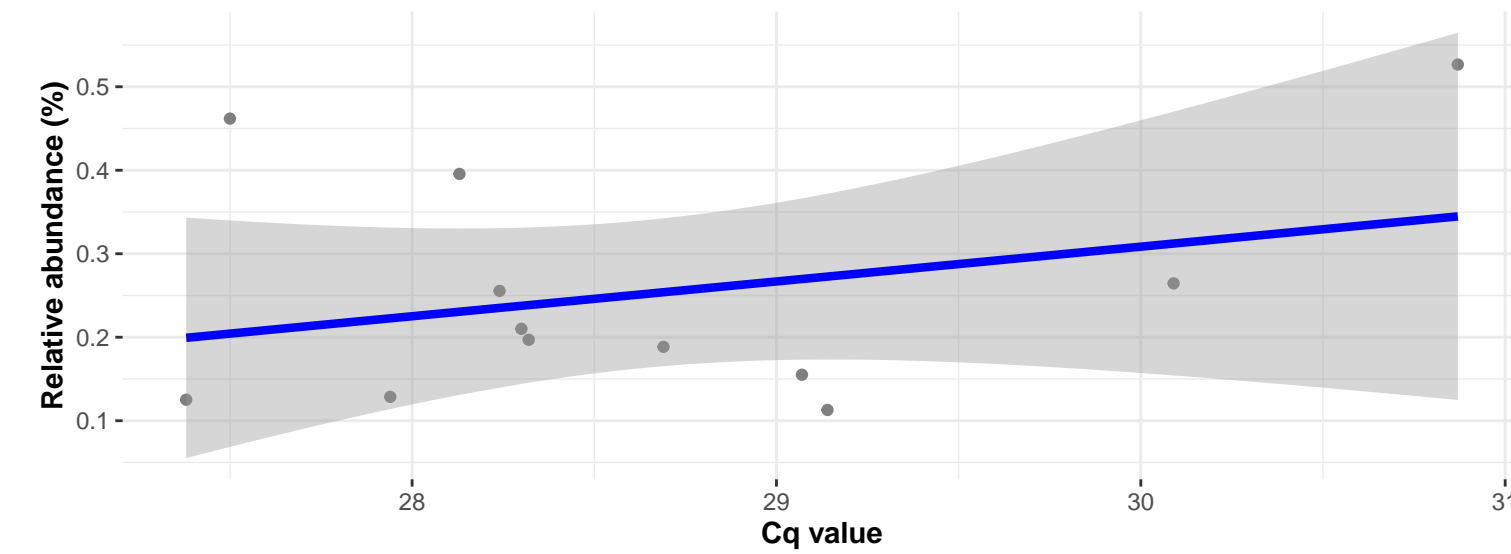
Correlation with all samples

$\log_e(S) = 8.148$, $p = 0.786$, $\hat{\rho}_{\text{Spearman}} = 0.054$, $CI_{95\%} [-0.336, 0.428]$, $n_{\text{pairs}} = 28$



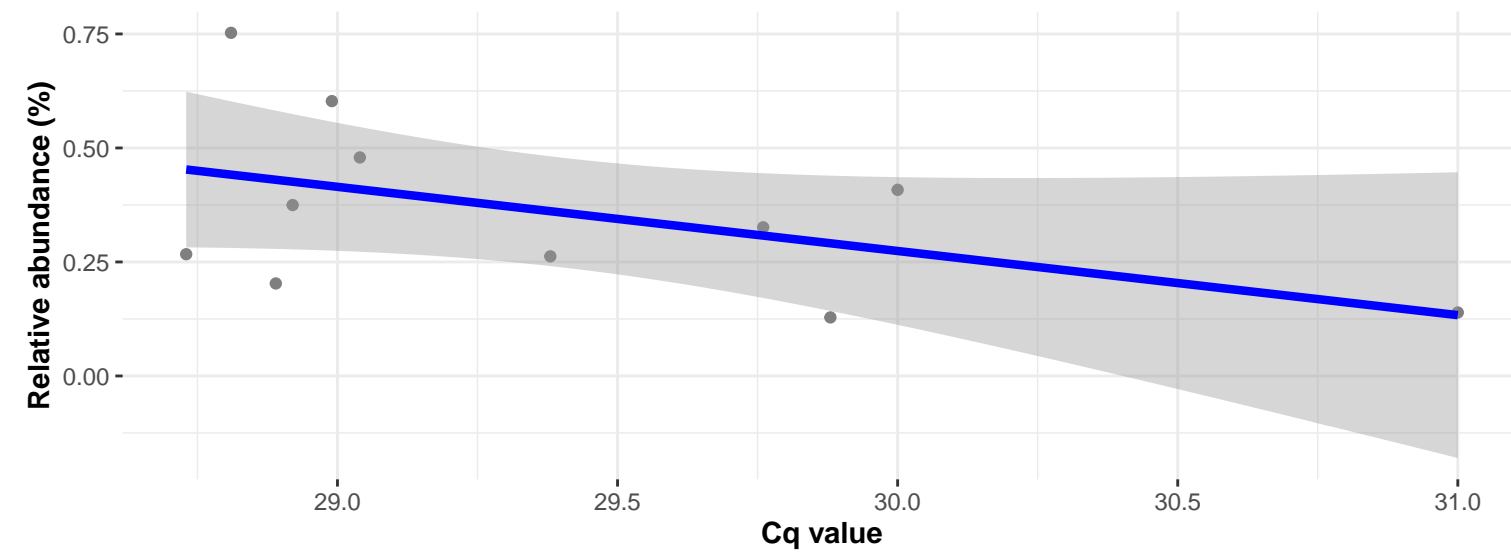
Correlation within: IM-PIM

$\log_e(S) = 5.513$, $p = 0.681$, $\hat{\rho}_{\text{Spearman}} = 0.133$, $CI_{95\%} [-0.492, 0.668]$, $n_{\text{pairs}} = 12$

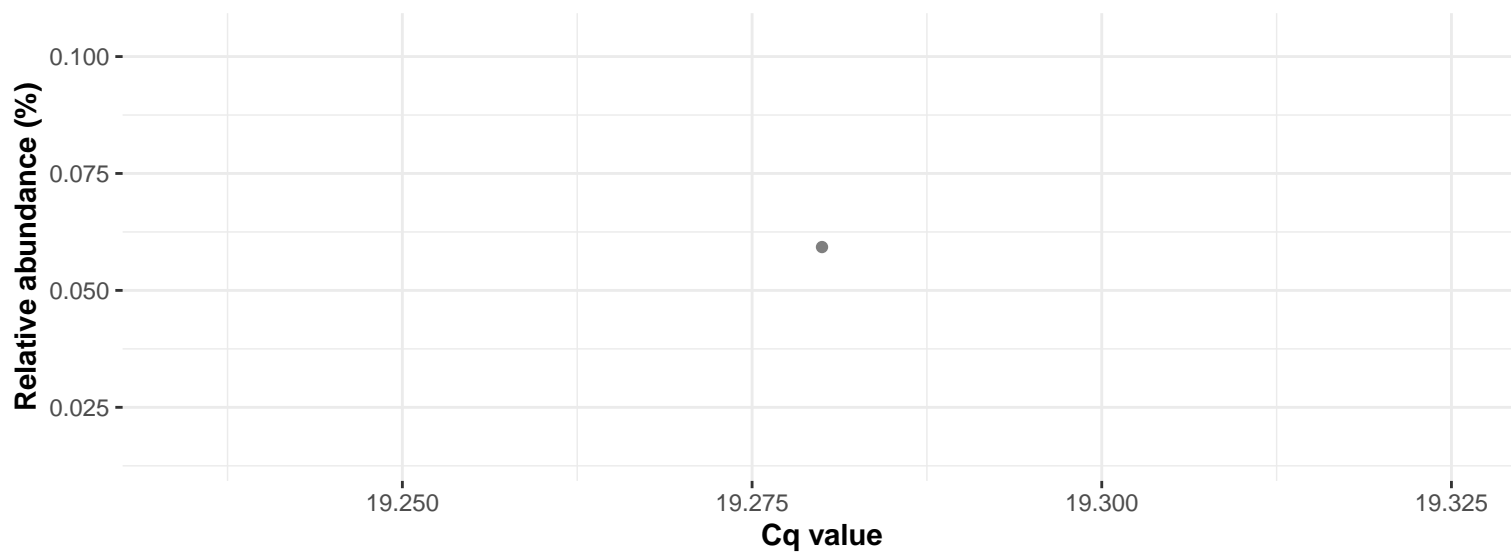


Correlation within: IM-DIM

$\log_e(S) = 5.710$, $p = 0.259$, $\hat{\rho}_{\text{Spearman}} = -0.373$, $CI_{95\%} [-0.802, 0.311]$, $n_{\text{pairs}} = 11$



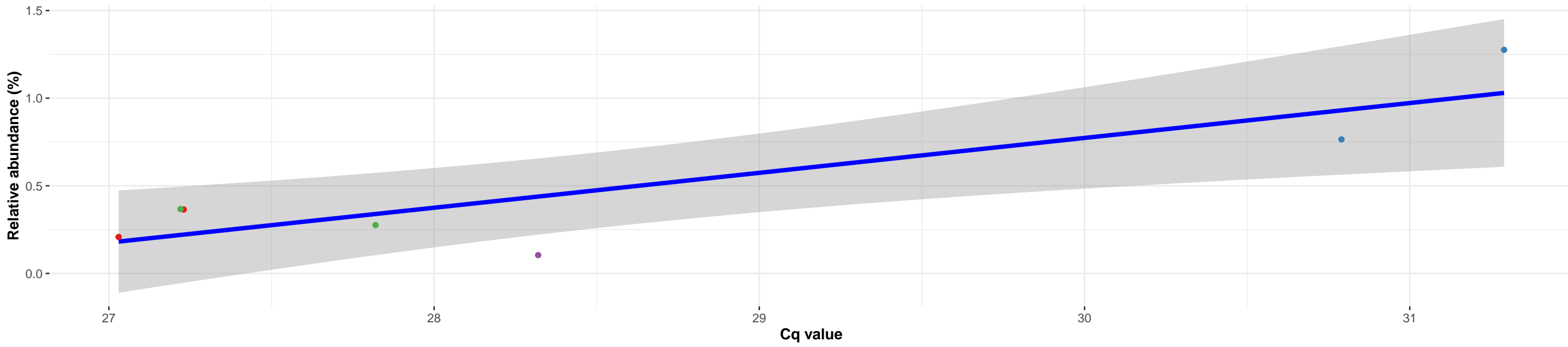
Correlation within: Feed



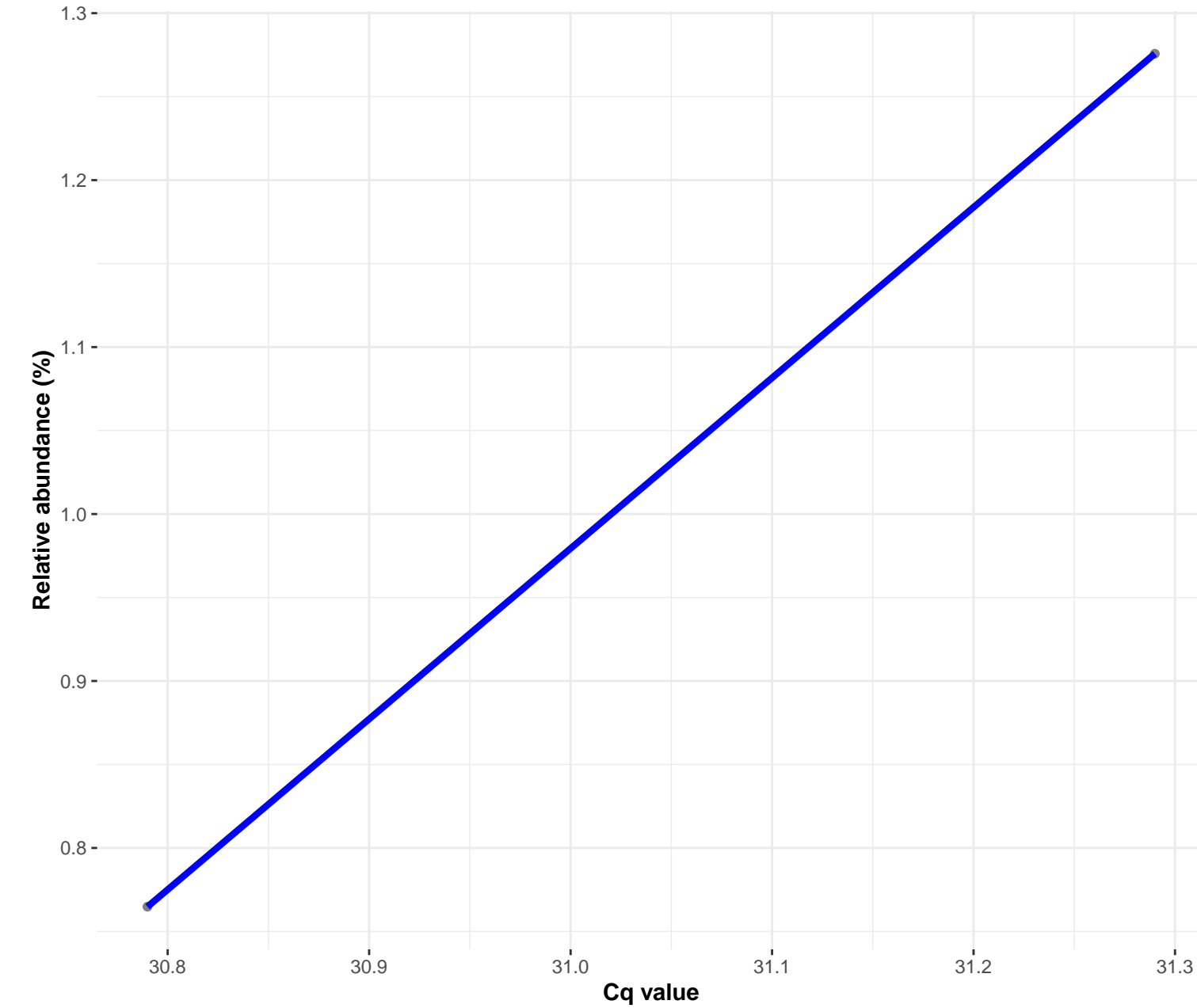
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Kurthia; s__uncultured bacterium

Correlation with all samples

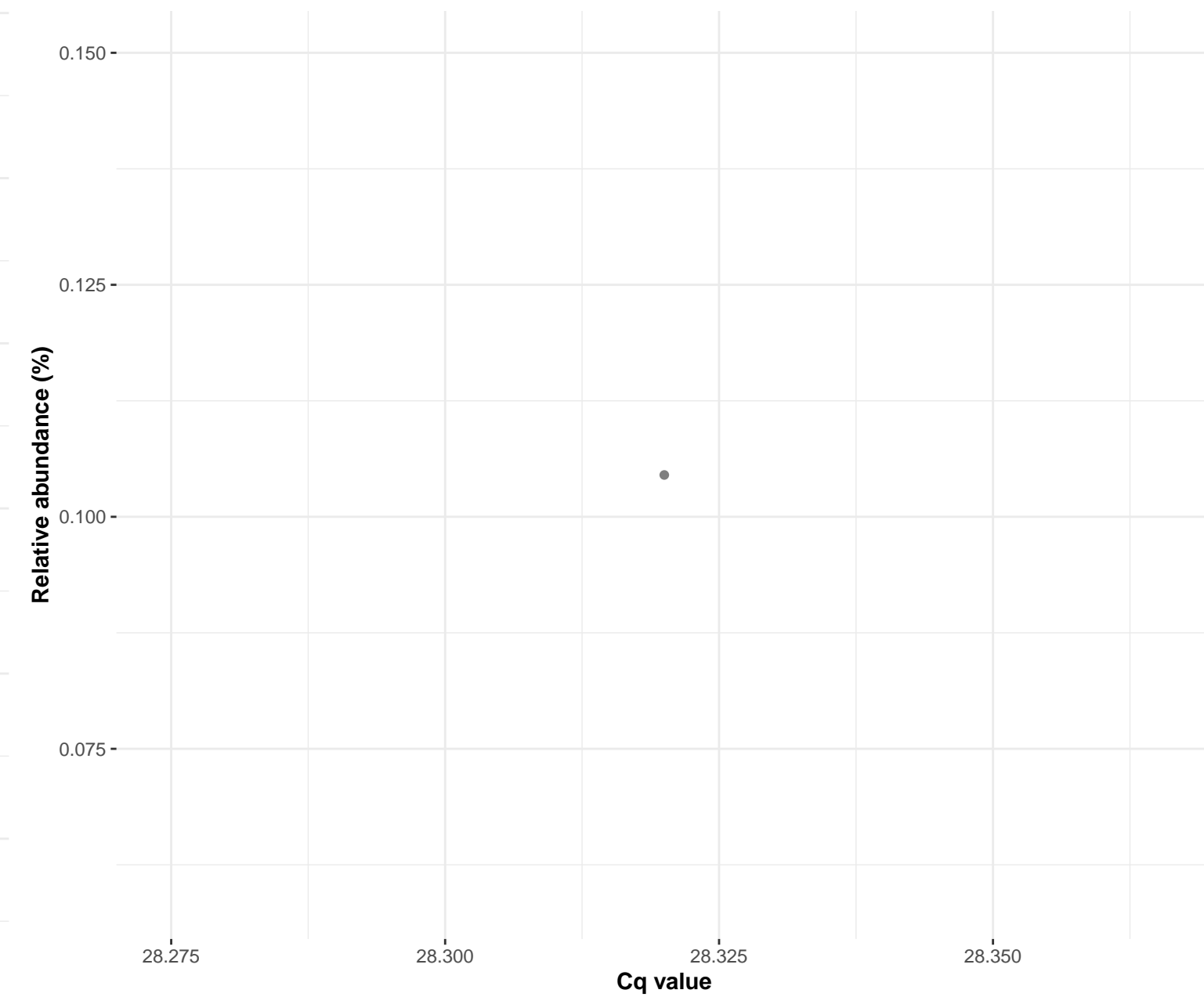
$\log_e(S) = 3.332$, $p = 0.253$, $\hat{\rho}_{\text{Spearman}} = 0.500$, $CI_{95\%} [-0.430, 0.915]$, $n_{\text{pairs}} = 7$



Correlation within: REF-PIM



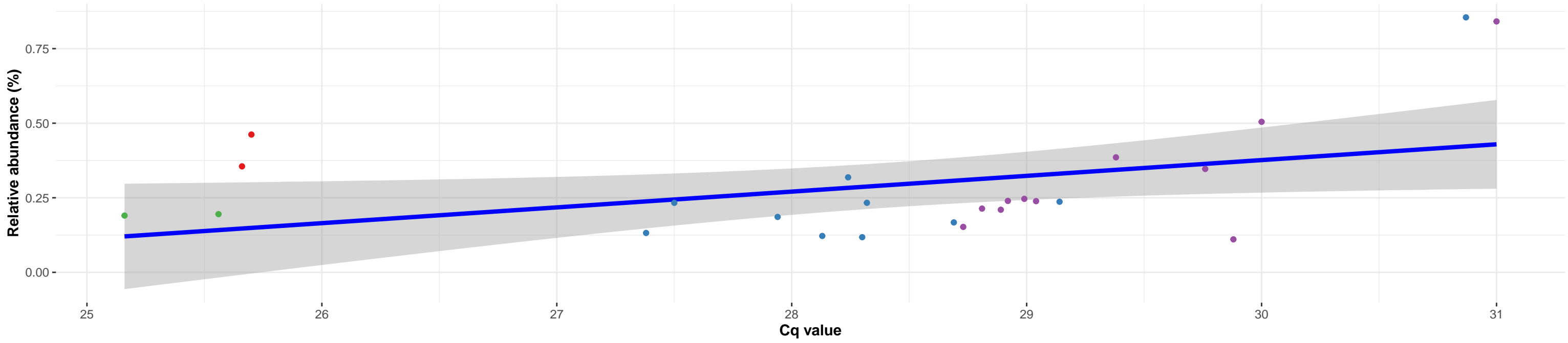
Correlation within: IM-PIM



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

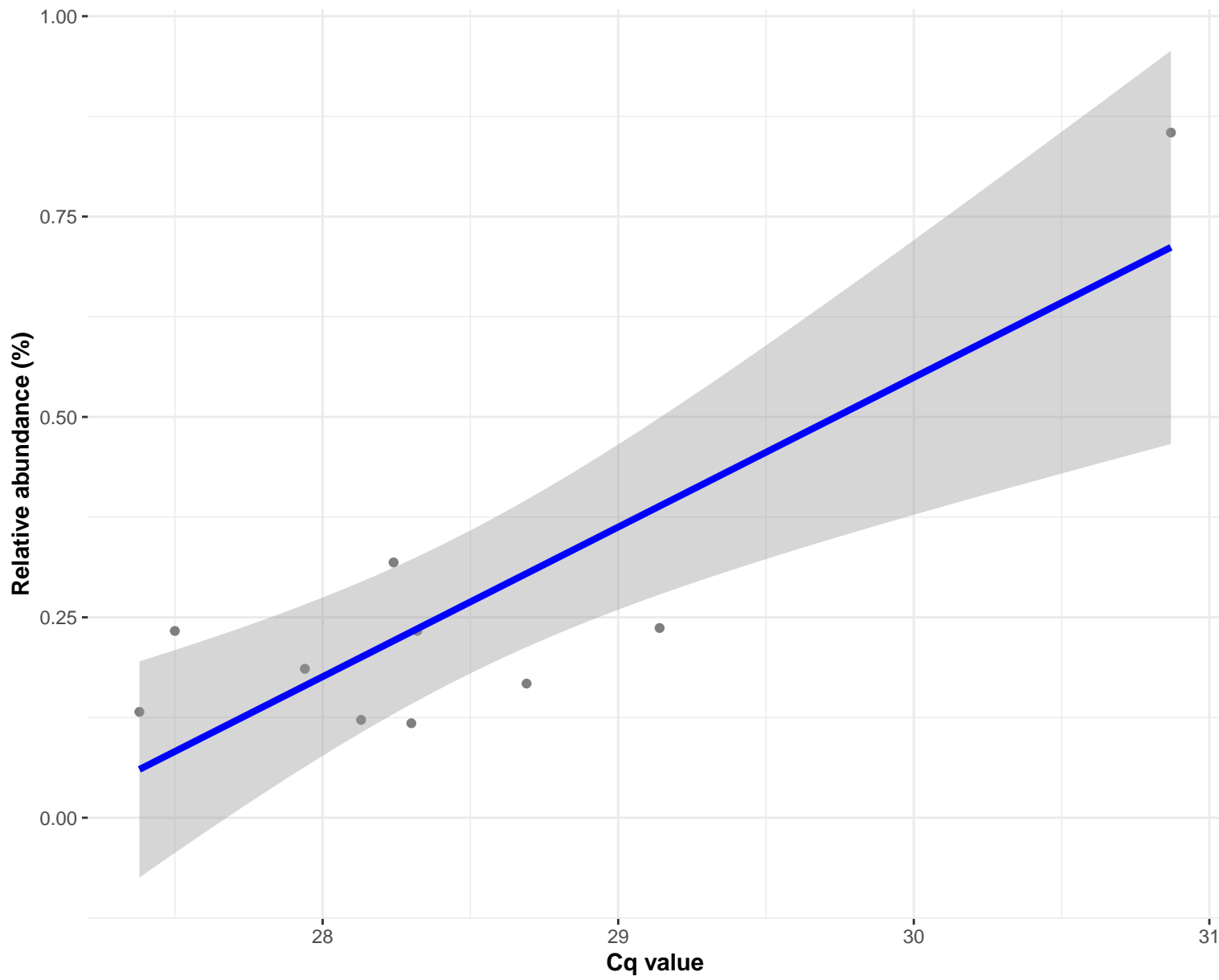
Correlation with all samples

$\log_e(S) = 7.338$, $p = 0.043$, $\hat{\rho}_{\text{Spearman}} = 0.408$, $CI_{95\%} [0.004, 0.698]$, $n_{\text{pairs}} = 25$



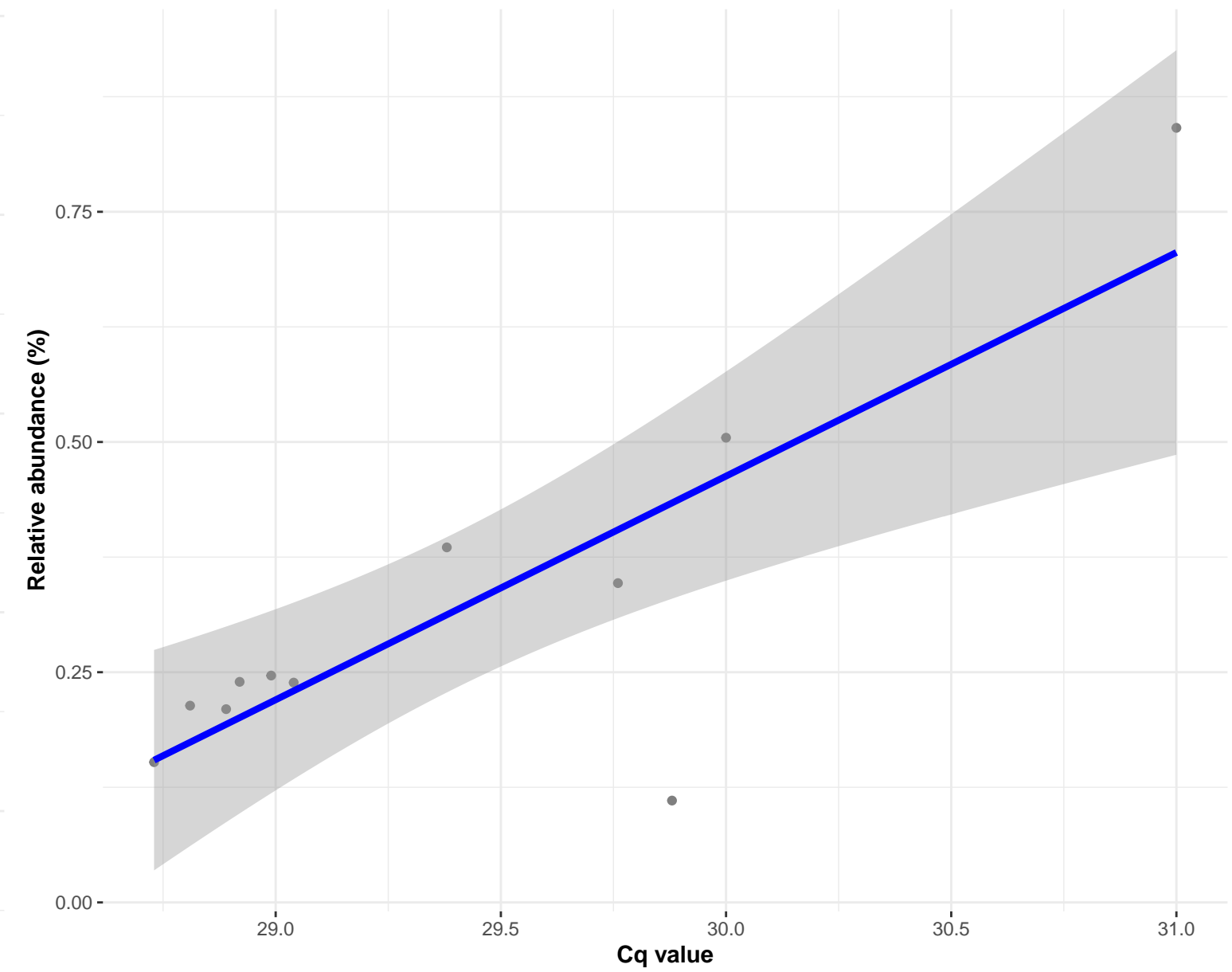
Correlation within: IM-PIM

$\log_e(S) = 4.454$, $p = 0.162$, $\hat{\rho}_{\text{Spearman}} = 0.479$, $CI_{95\%} [-0.237, 0.858]$, $n_{\text{pairs}} = 10$

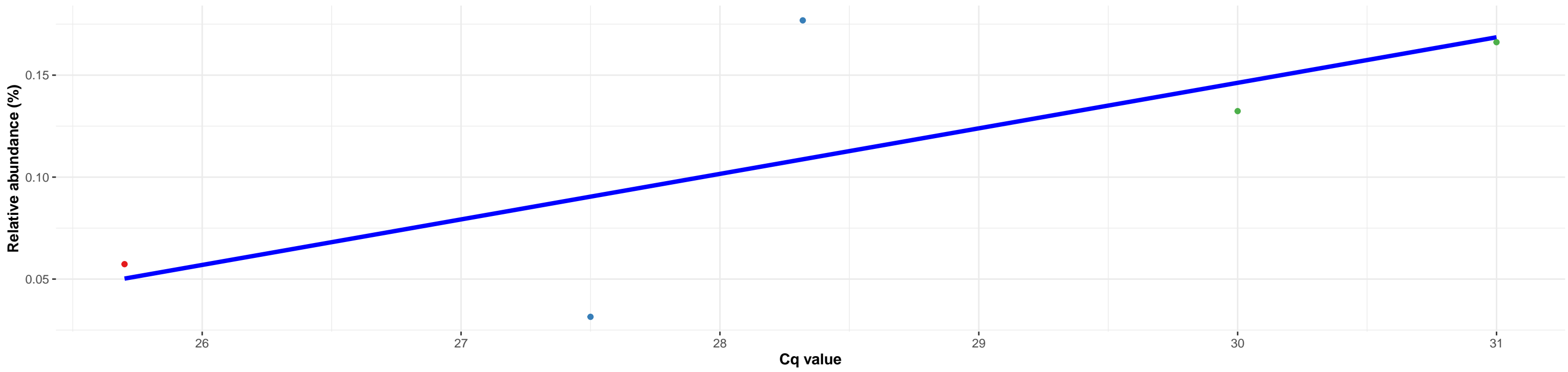


Correlation within: IM-DIM

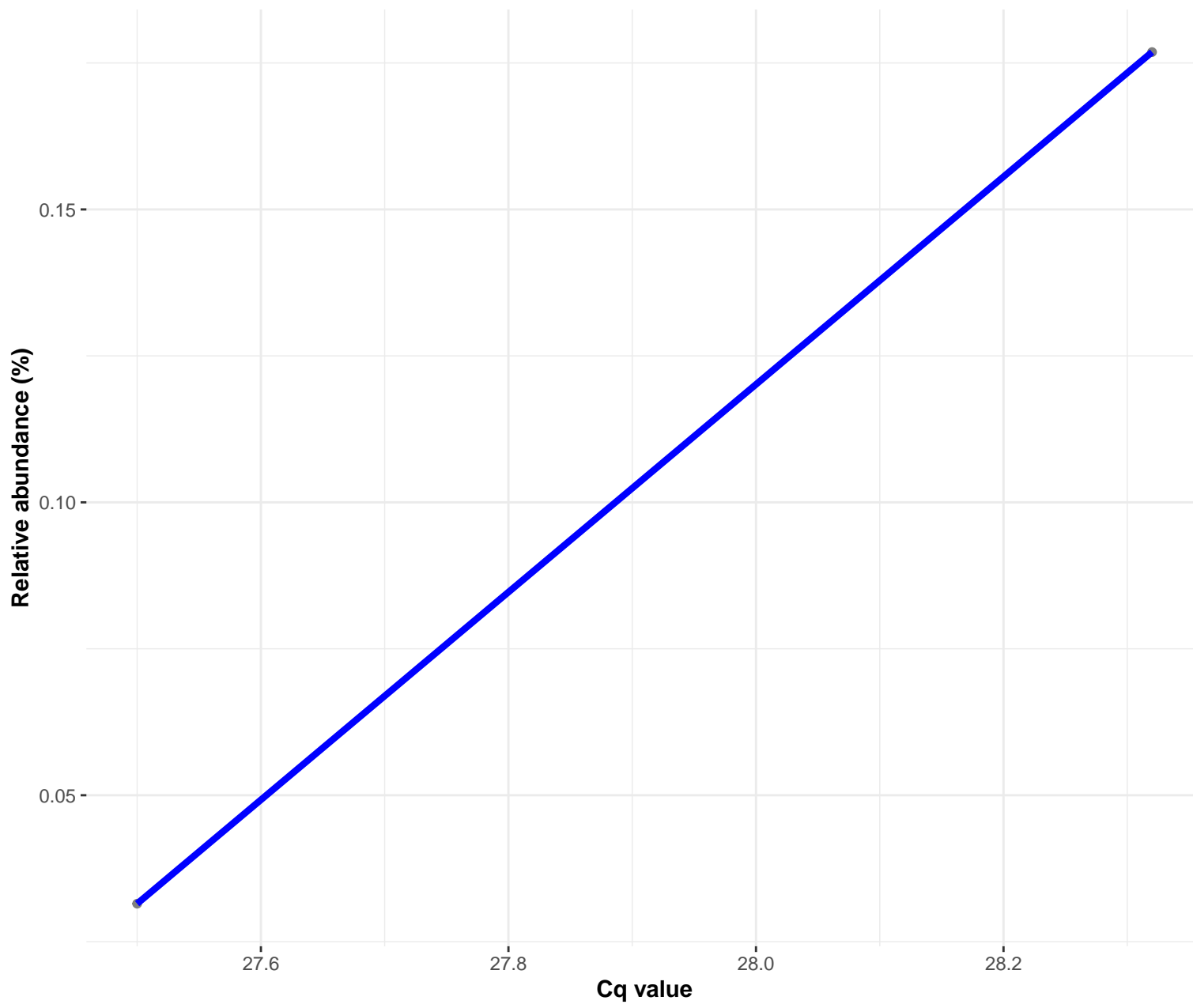
$\log_e(S) = 4.407$, $p = 0.039$, $\hat{\rho}_{\text{Spearman}} = 0.627$, $CI_{95\%} [0.023, 0.896]$, $n_{\text{pairs}} = 11$



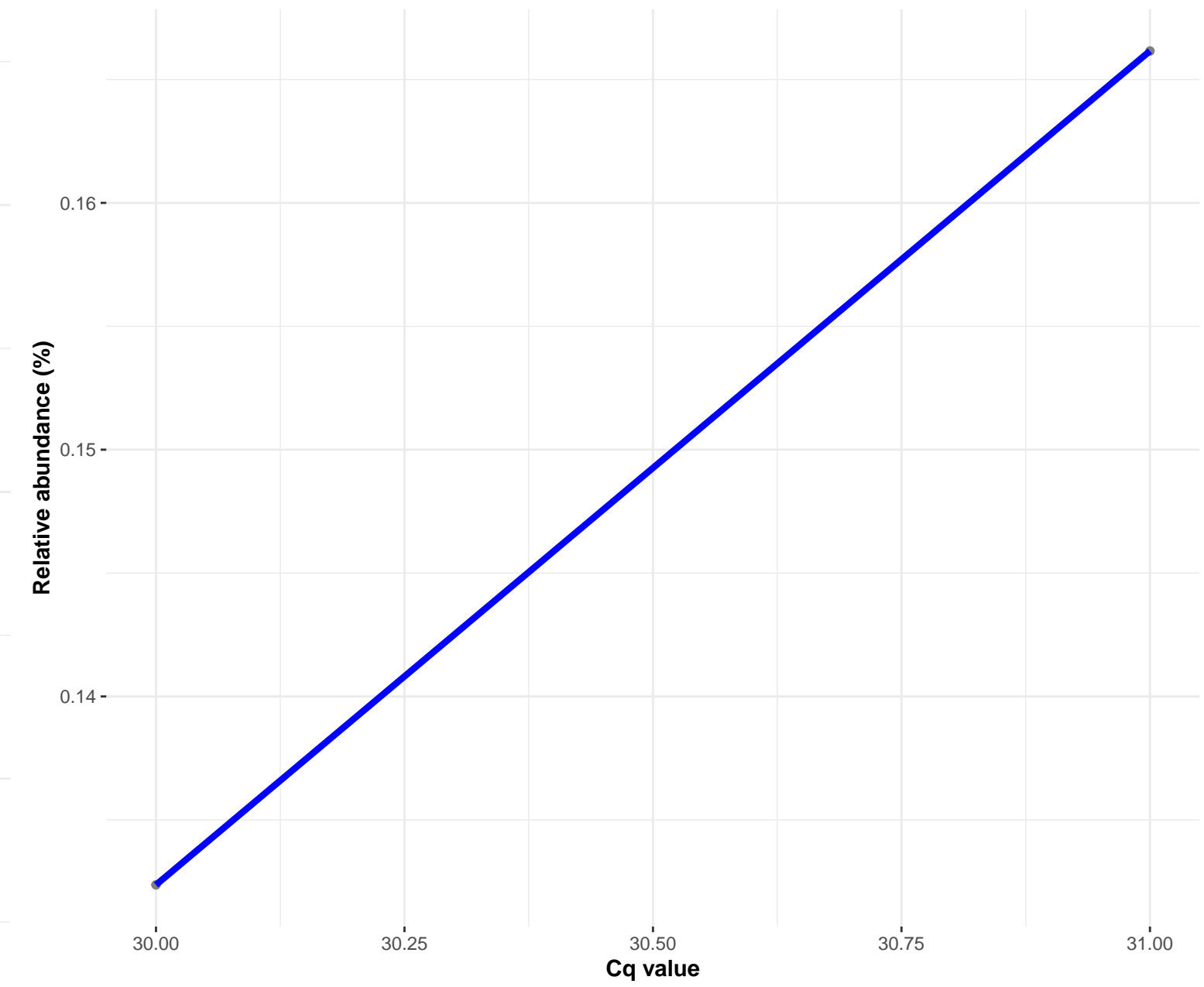
Correlation with all samples



Correlation within: IM-PIM



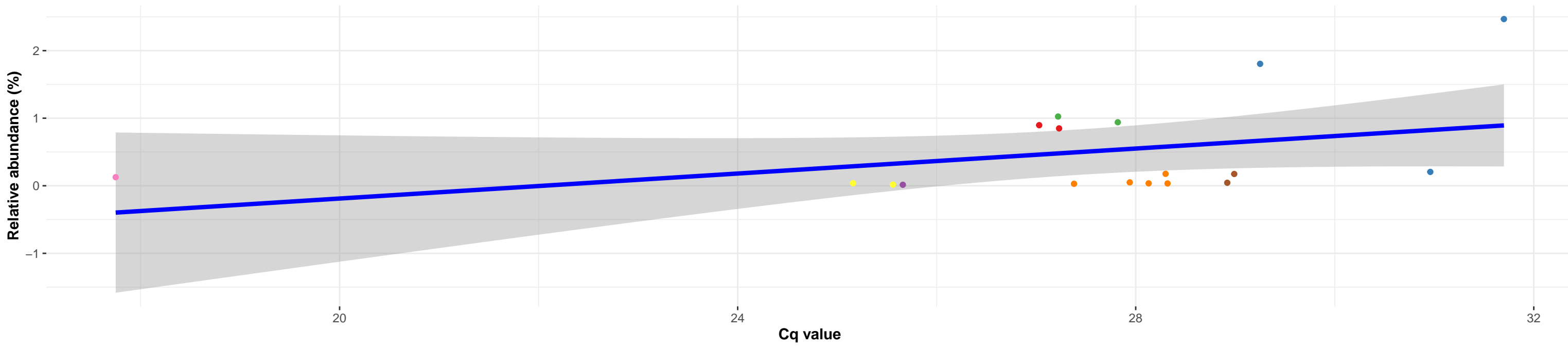
Correlation within: IM-DIM



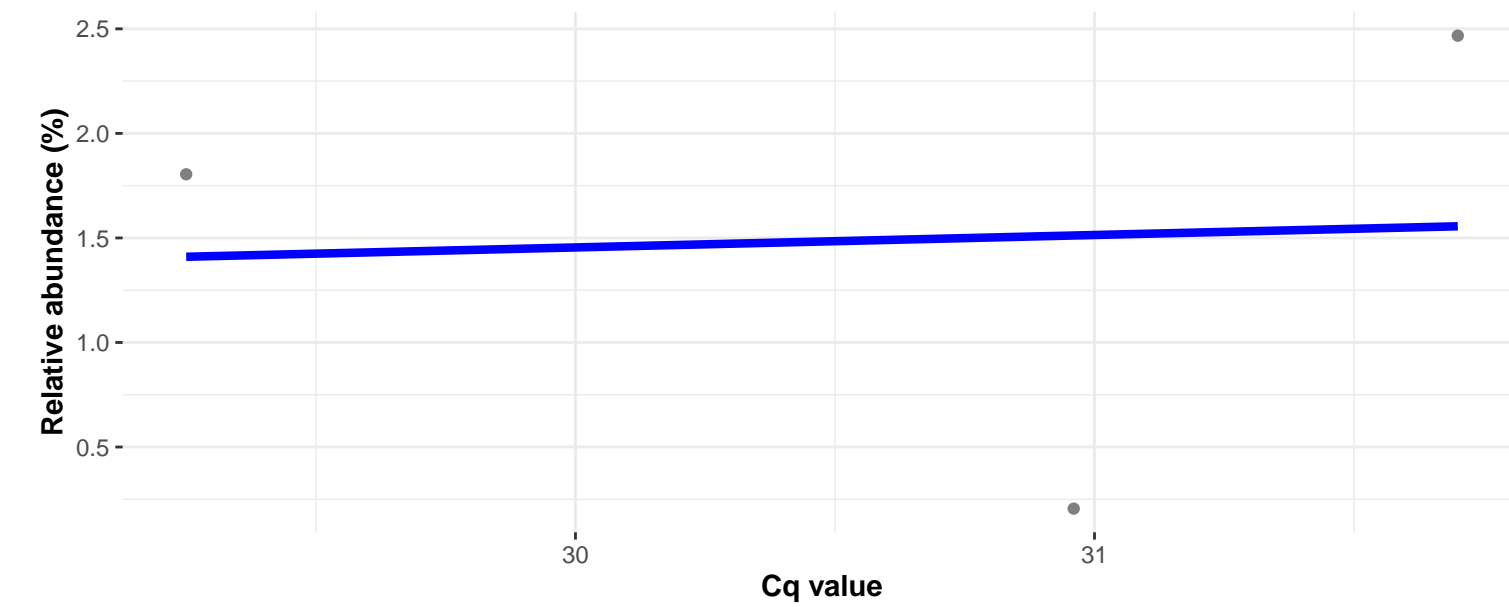
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; Ambiguous_taxa

Correlation with all samples

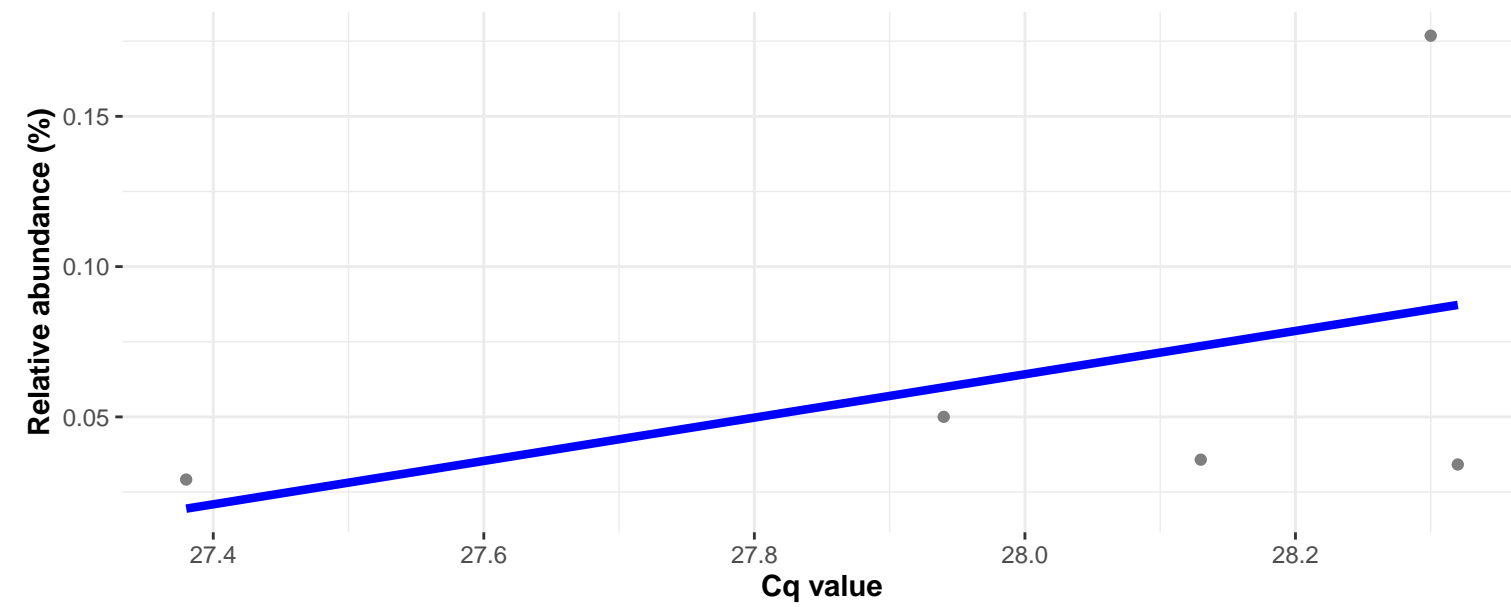
$\log_e(S) = 6.380$, $p = 0.108$, $\hat{\rho}_{\text{Spearman}} = 0.391$, $CI_{95\%} [-0.107, 0.733]$, $n_{\text{pairs}} = 18$



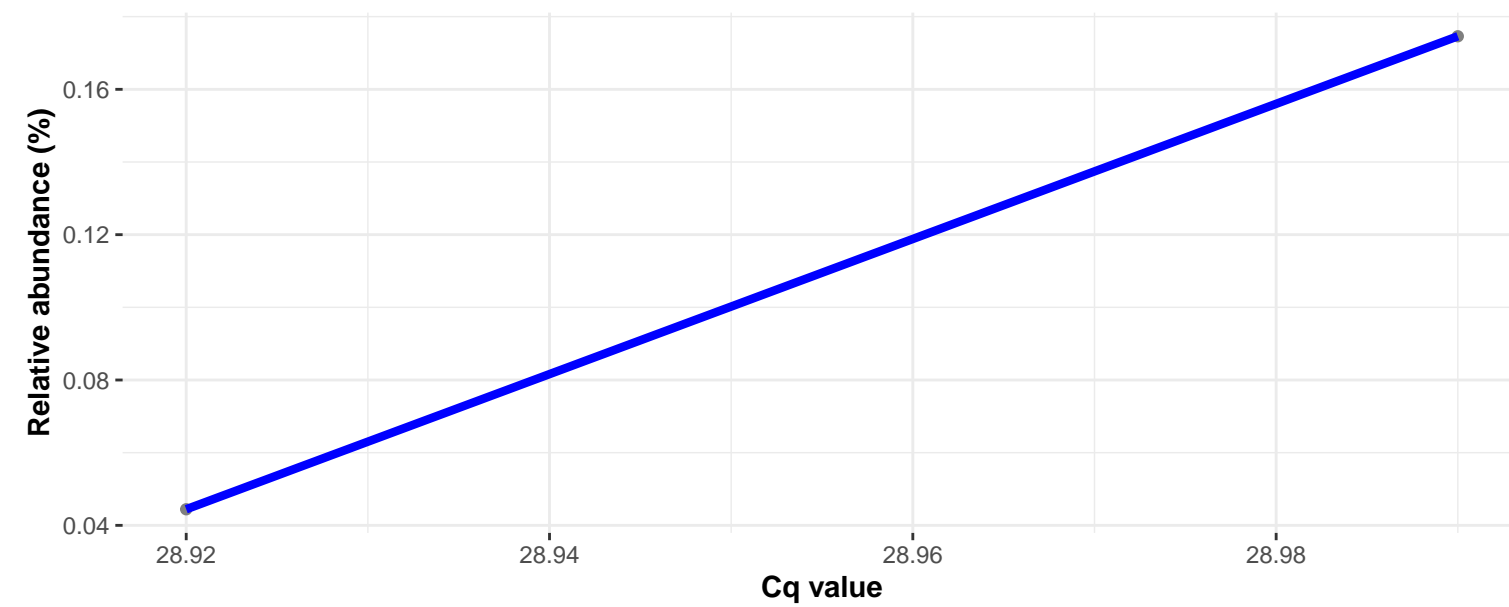
Correlation within: REF-PIM



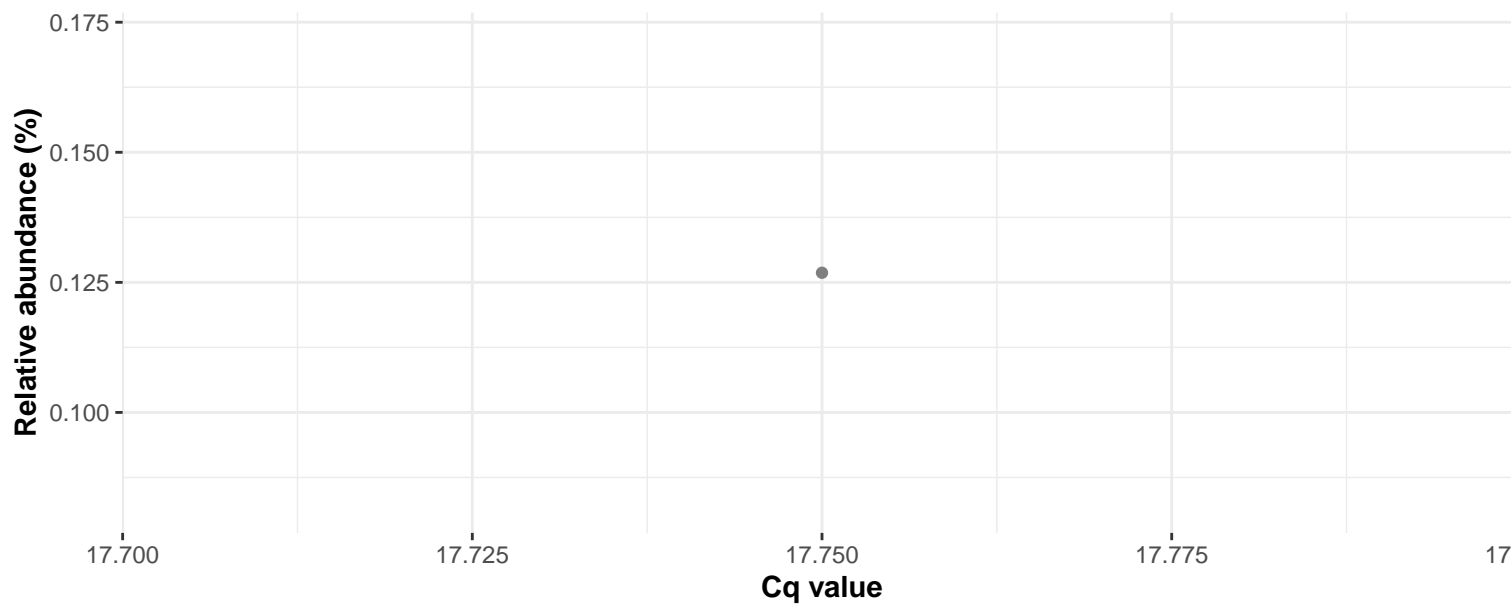
Correlation within: IM-PIM



Correlation within: IM-DIM



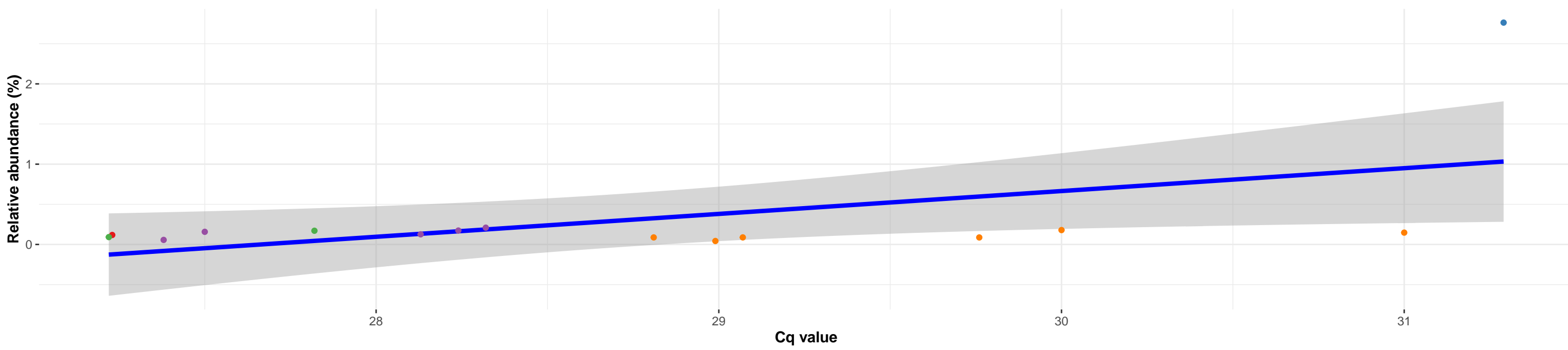
Correlation within: Feed



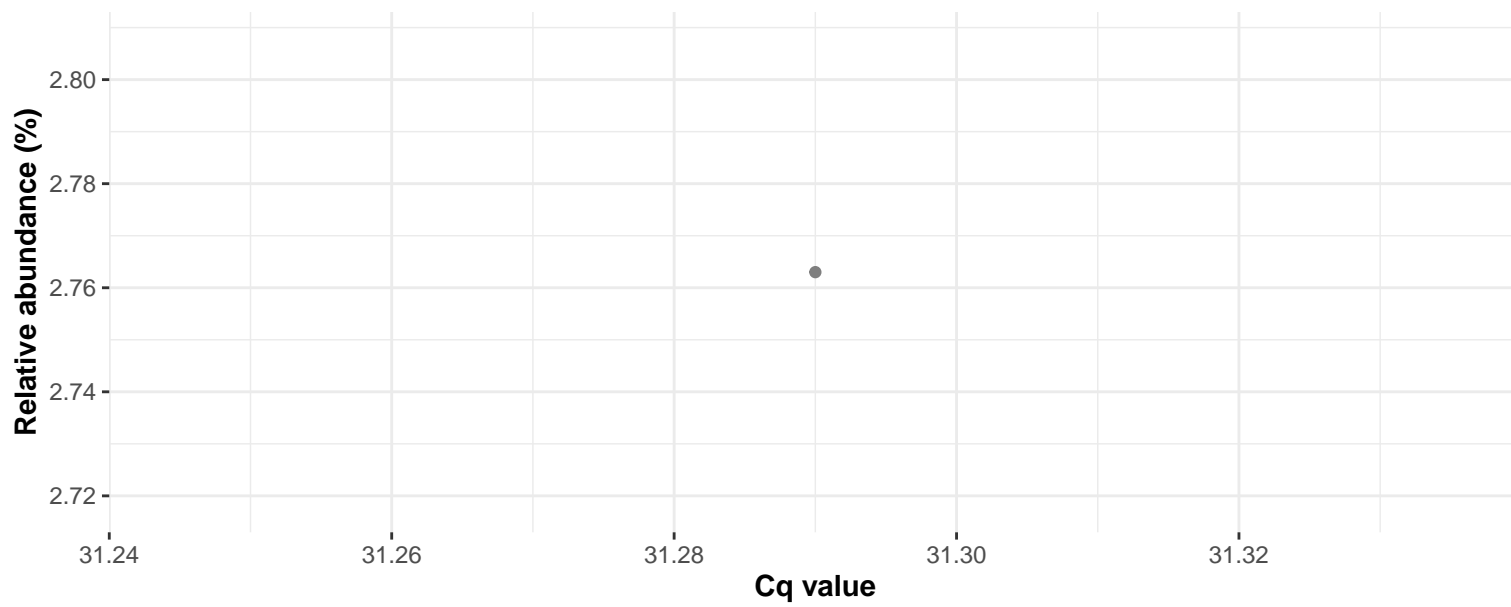
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

Correlation with all samples

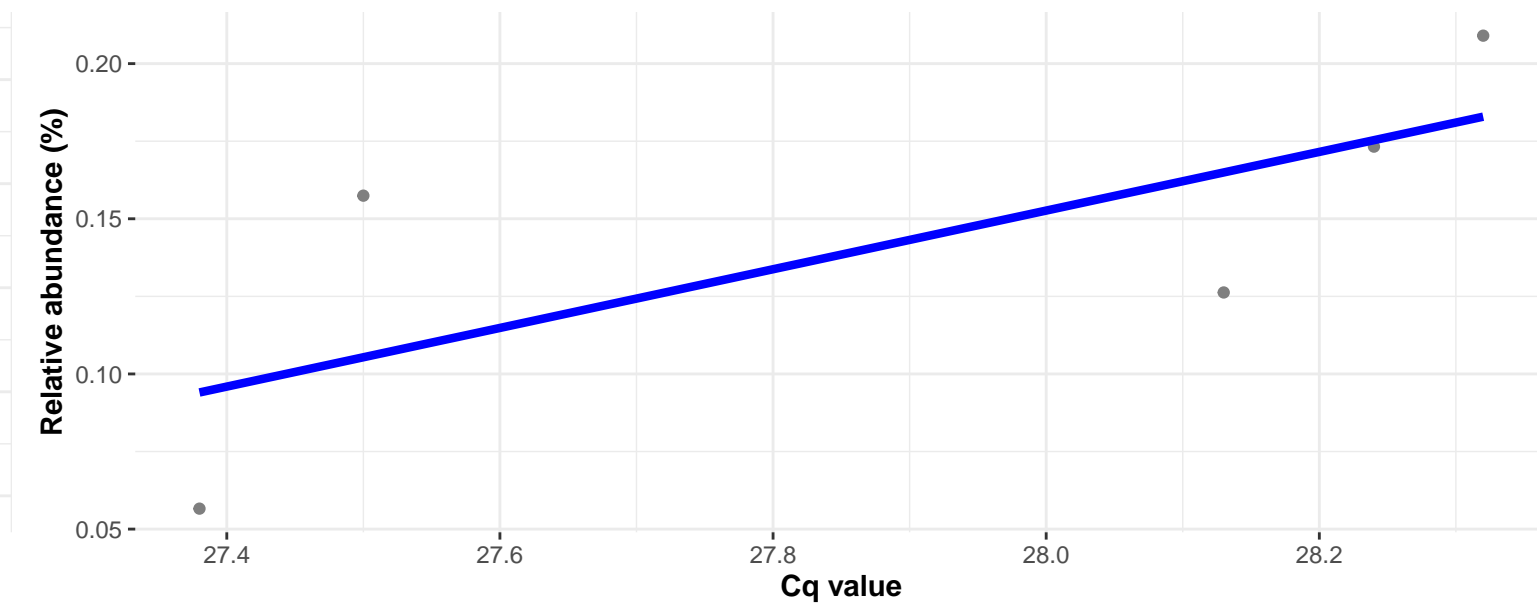
$\log_e(S) = 6.078$, $p = 0.428$, $\hat{\rho}_{\text{Spearman}} = 0.221$, $\text{CI}_{95\%} [-0.343, 0.668]$, $n_{\text{pairs}} = 15$



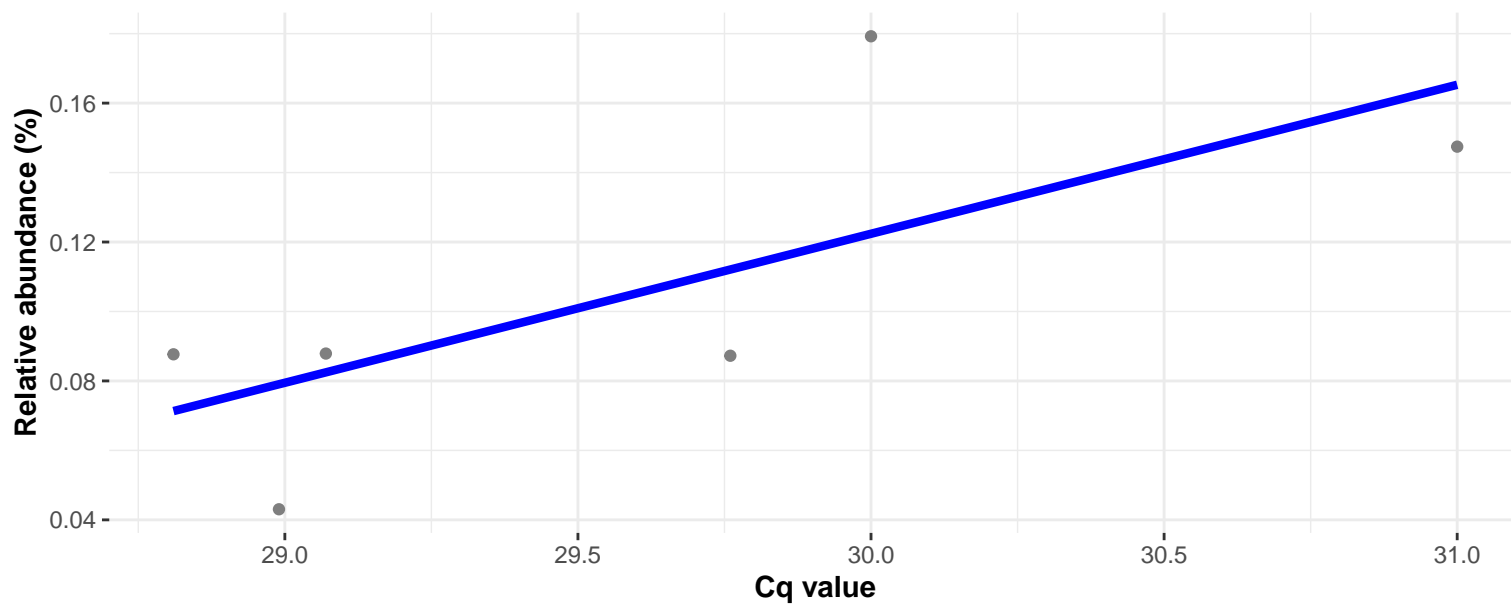
Correlation within: REF-PIM



Correlation within: IM-PIM



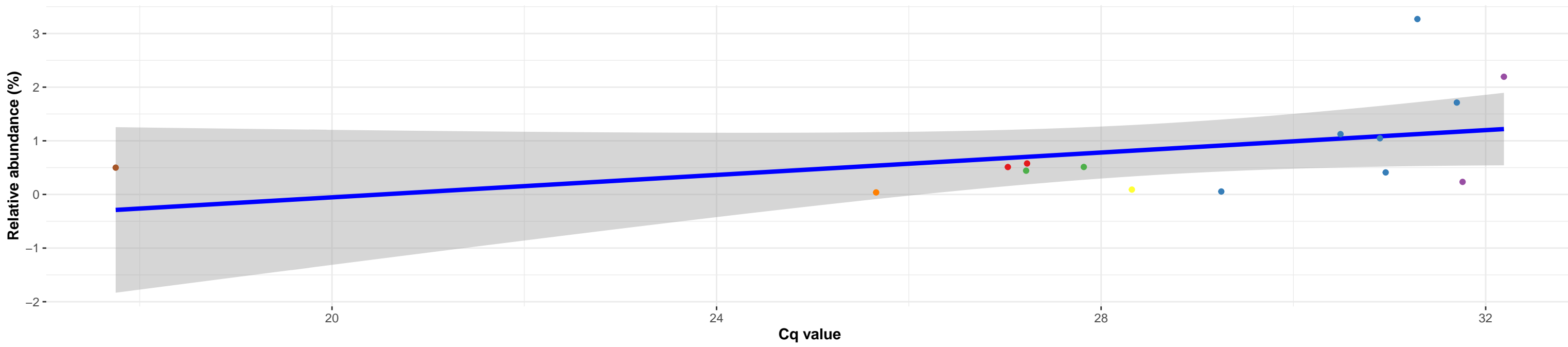
Correlation within: IM-DIM



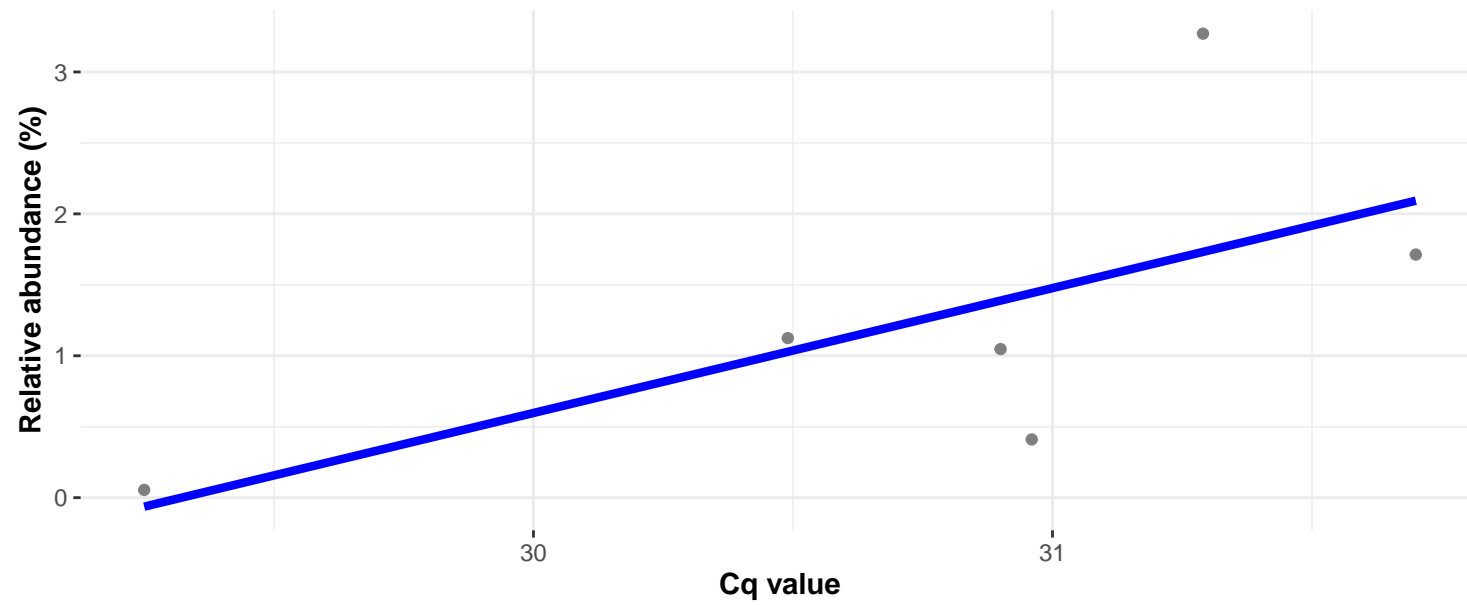
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. LA-6

Correlation with all samples

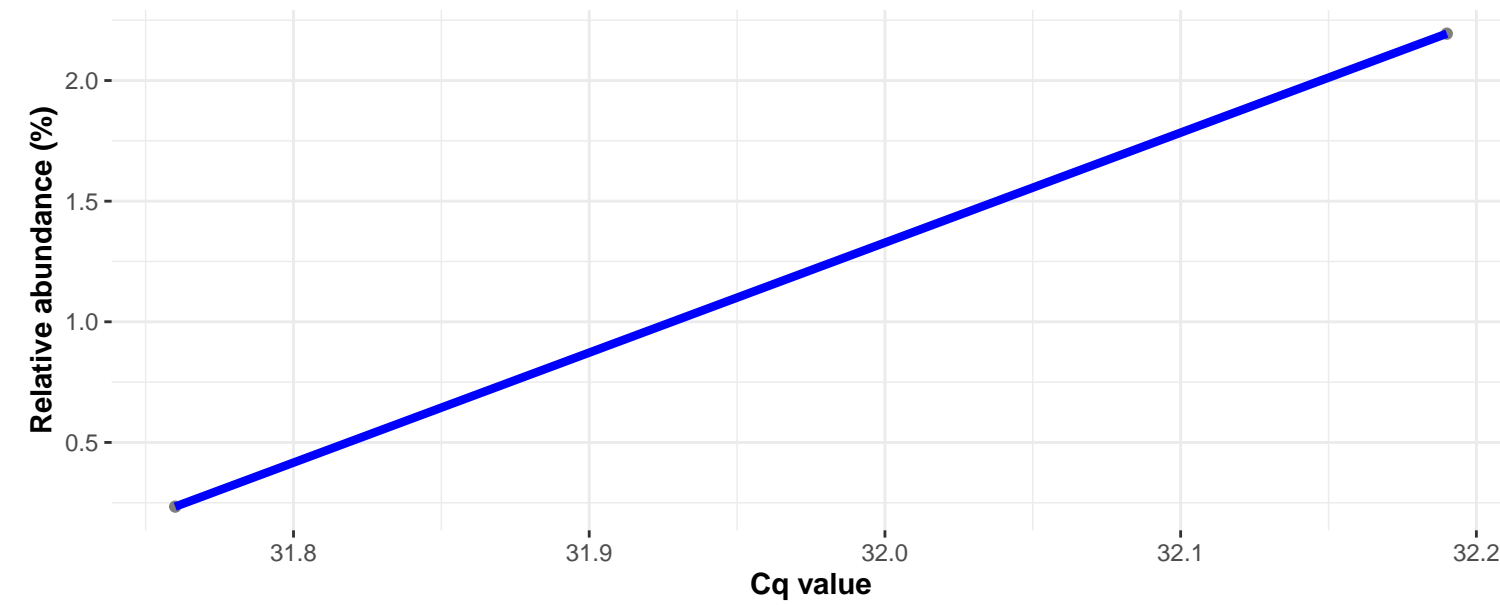
$\log_e(S) = 5.730$, $p = 0.092$, $\hat{\rho}_{\text{Spearman}} = 0.450$, $CI_{95\%} [-0.098, 0.788]$, $n_{\text{pairs}} = 15$



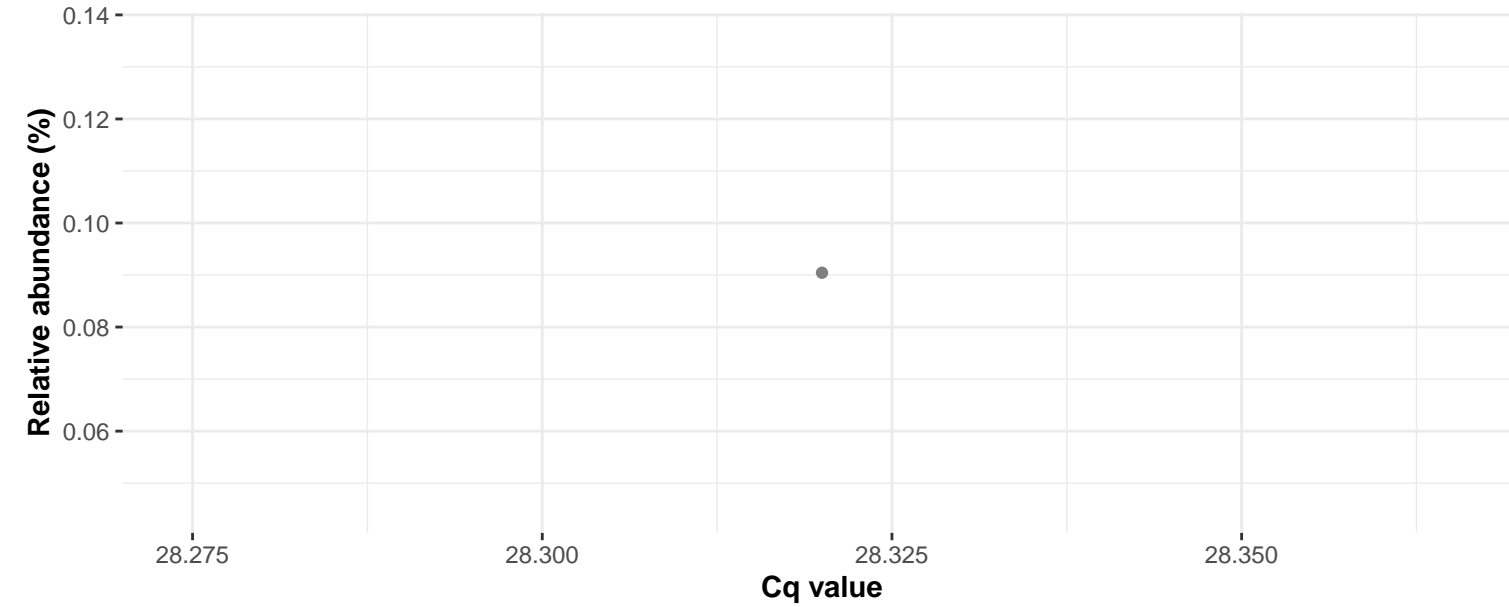
Correlation within: REF-PIM



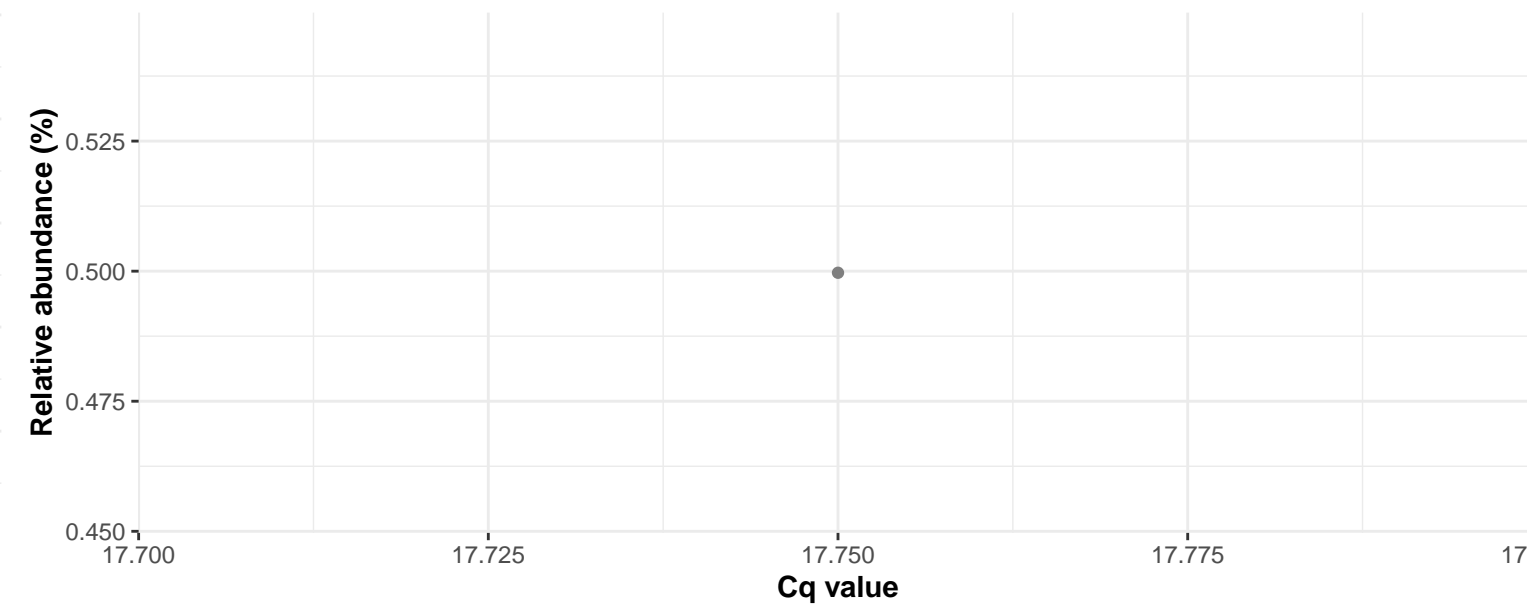
Correlation within: REF-DIM



Correlation within: IM-PIM

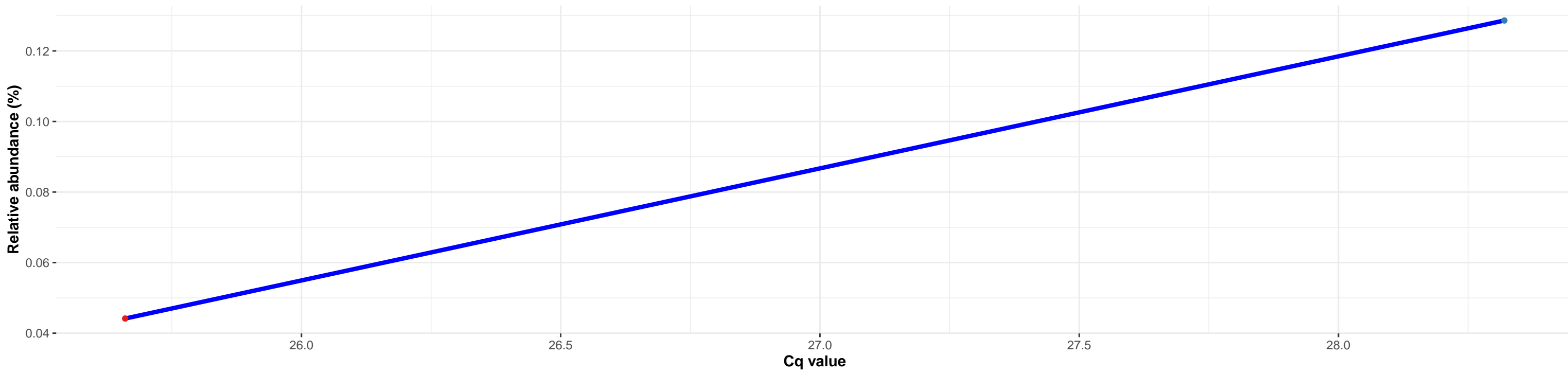


Correlation within: Feed



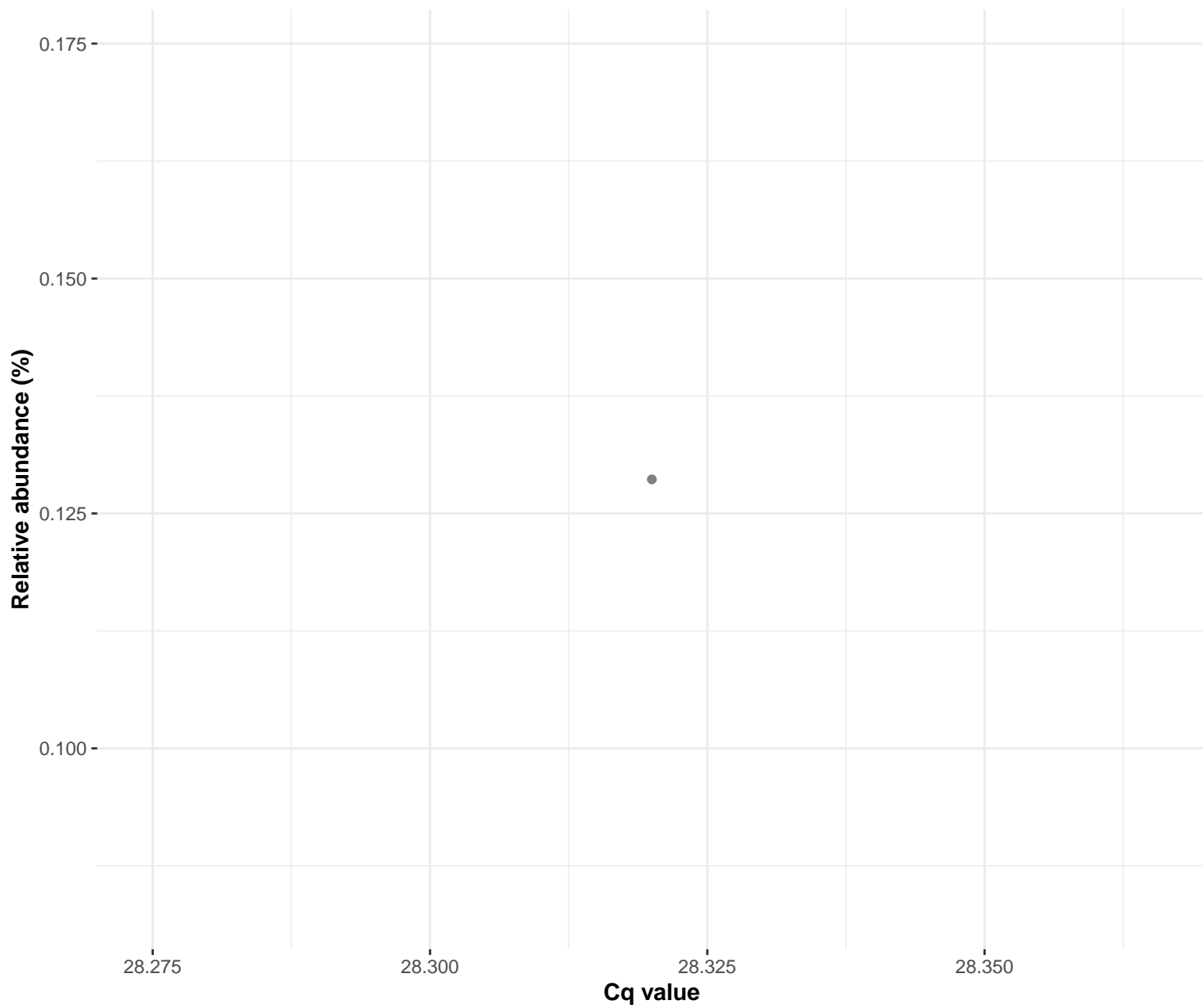
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples

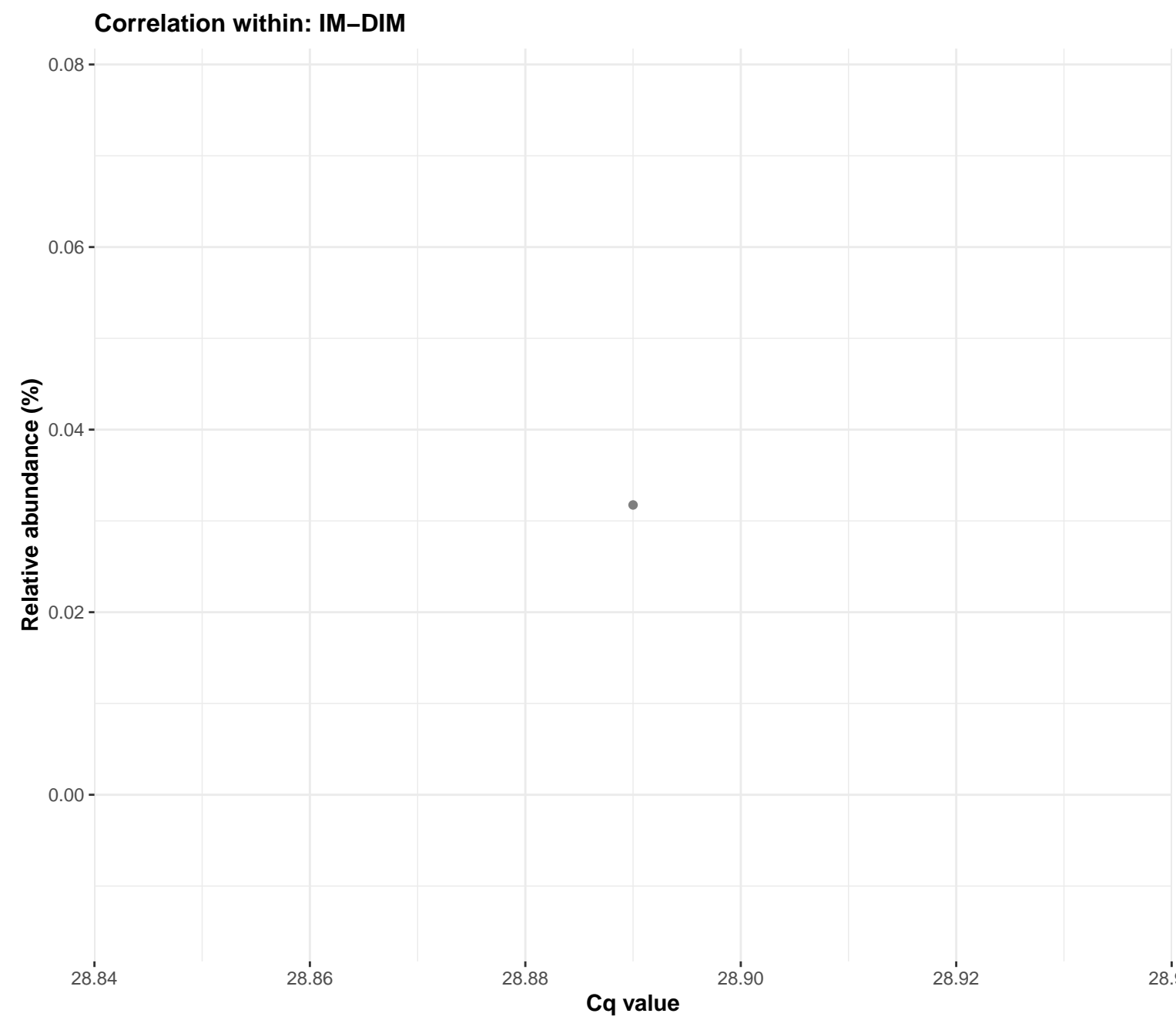
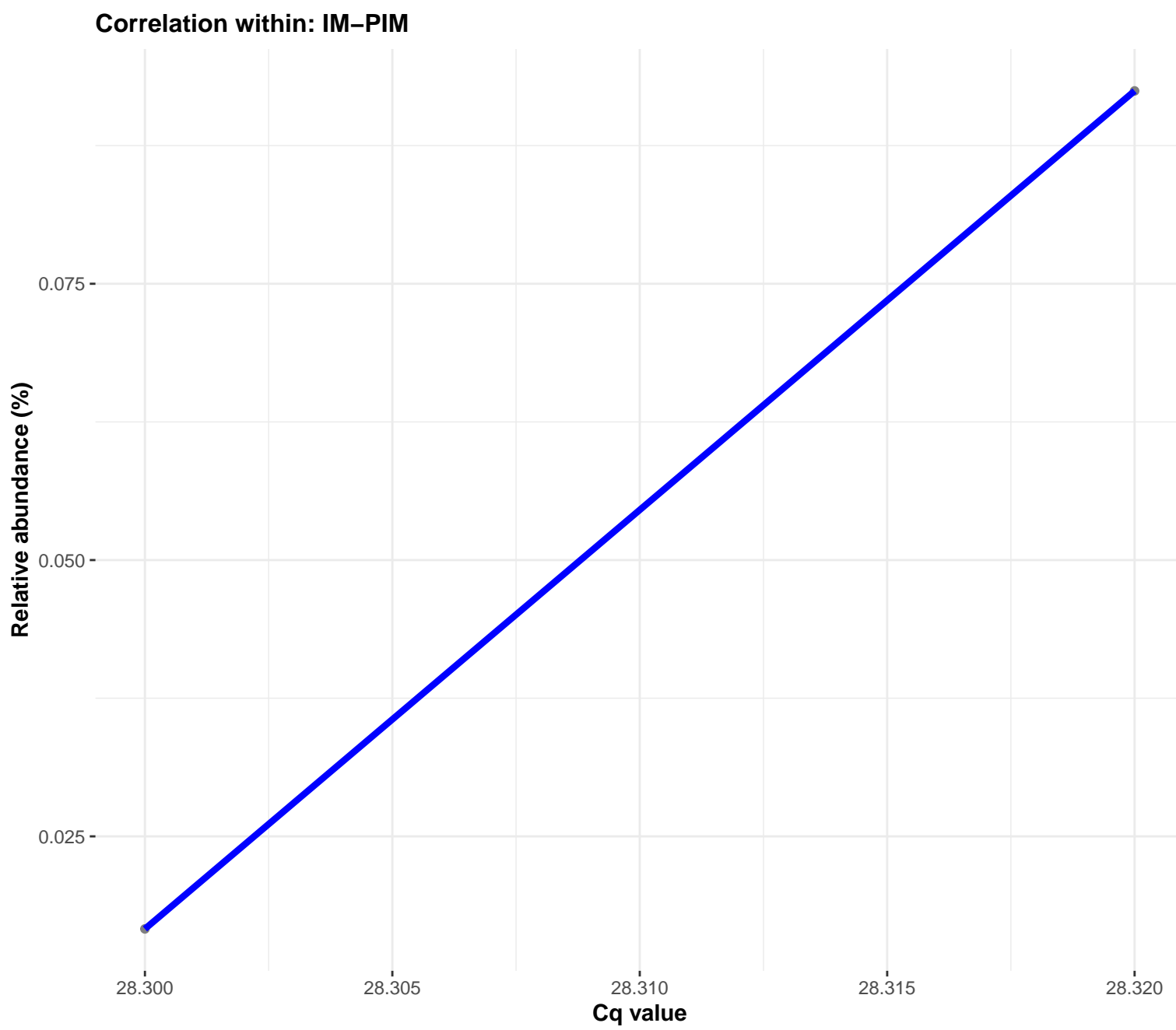
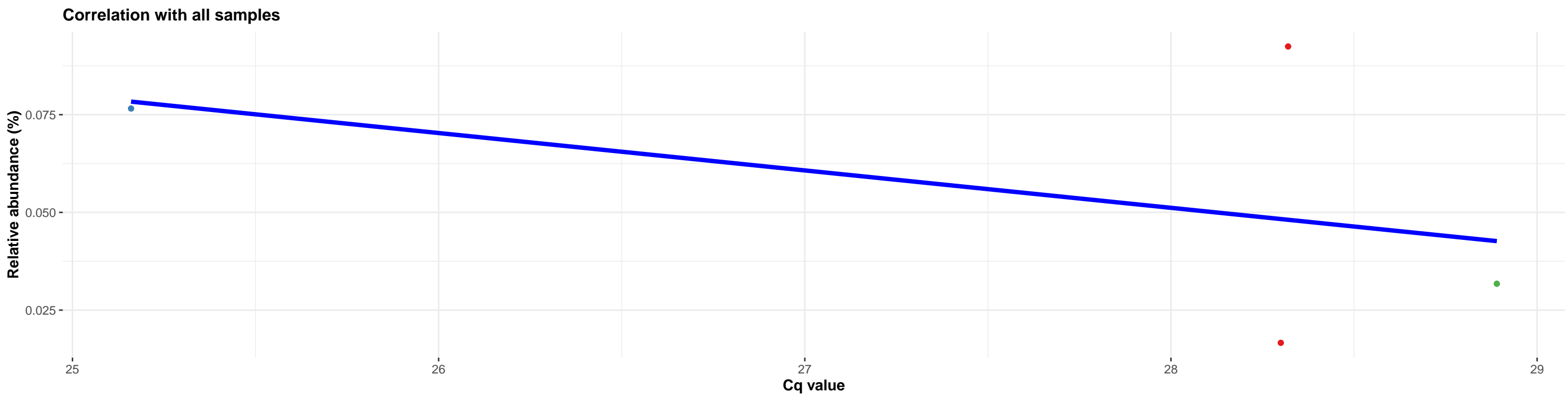


SampleType • IM-PID • IM-PIM

Correlation within: IM-PIM



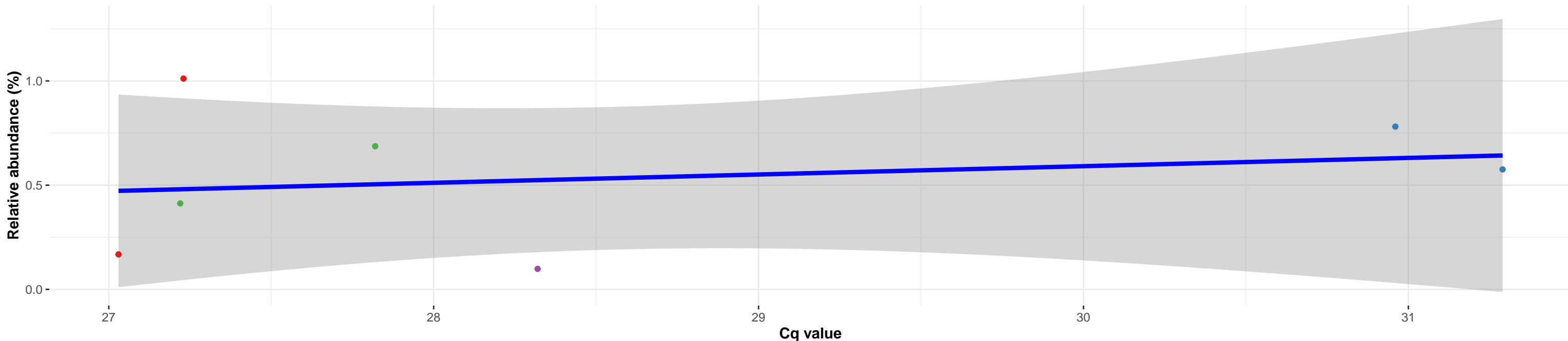
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA



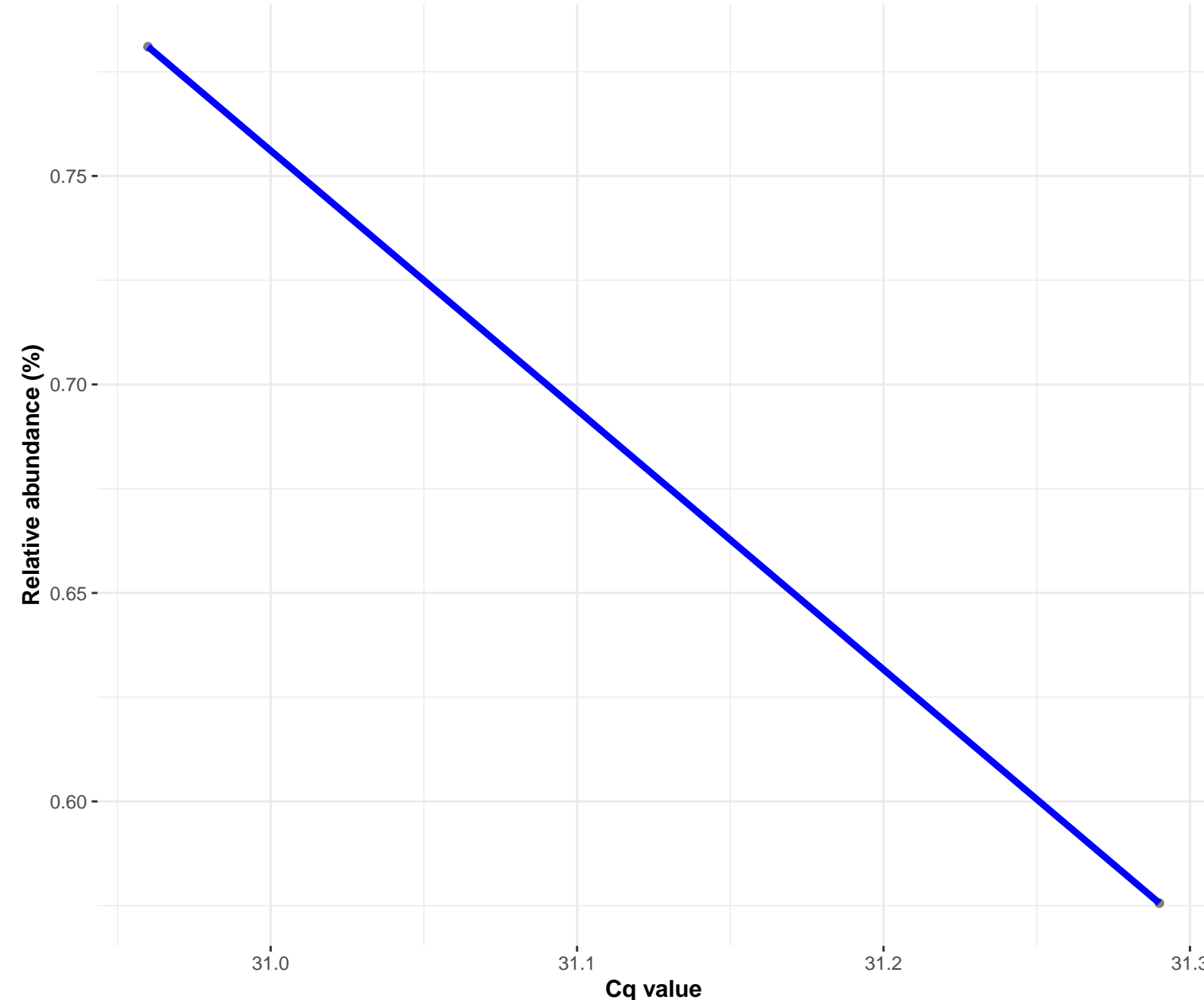
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; NA

Correlation with all samples

$\log_e(S) = 3.784$, $p = 0.645$, $\hat{\rho}_{\text{Spearman}} = 0.214$, $CI_{95\%} [-0.659, 0.842]$, $n_{\text{pairs}} = 7$



Correlation within: REF-PIM



Correlation within: IM-PIM

