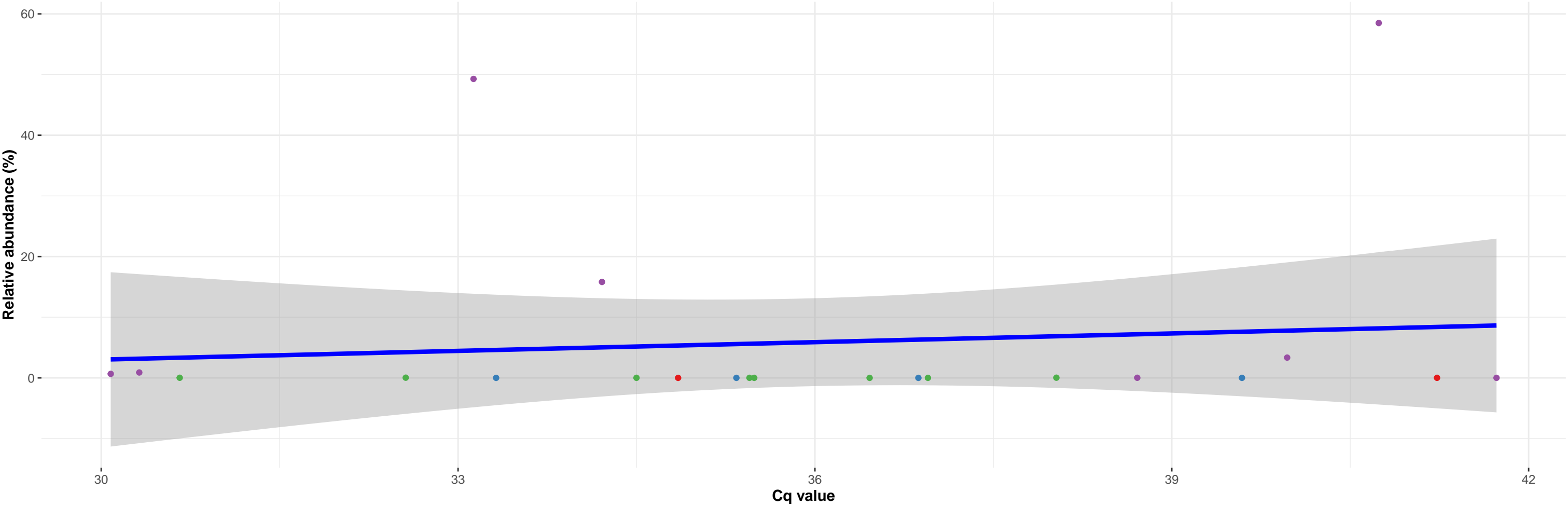


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

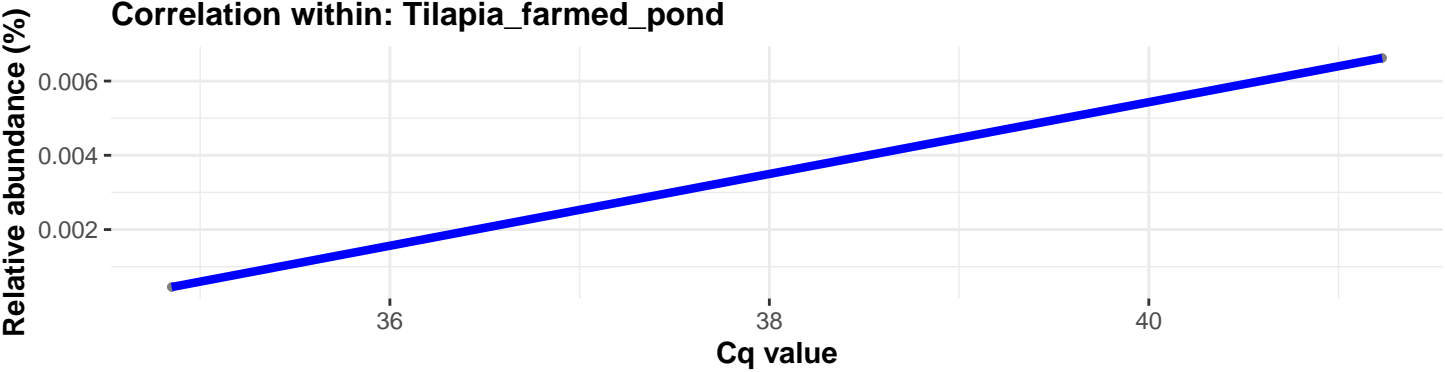
featureID: 30cd2eb39b81e92ac815ec19fd6ccdee

Correlation with all samples

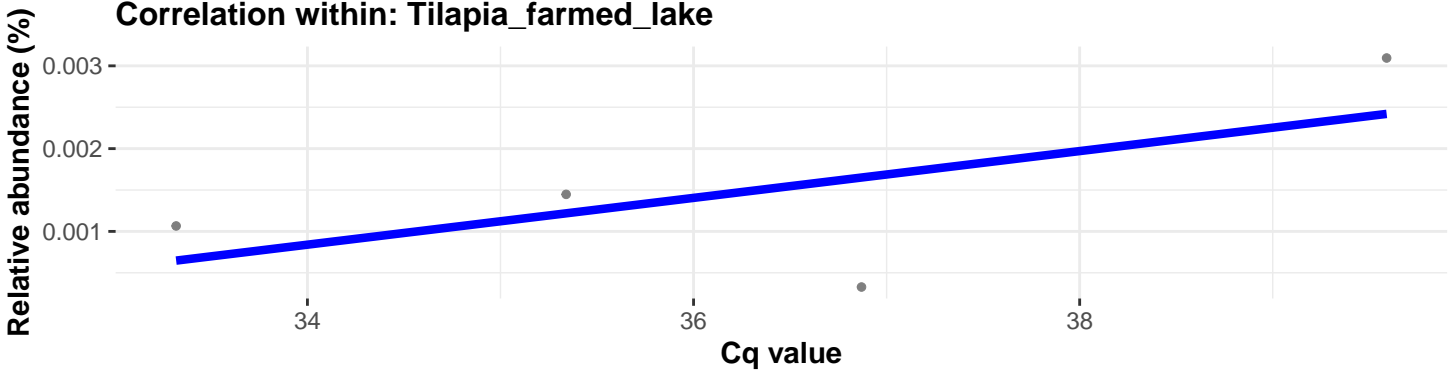
$\log_e(S) = 7.631$, $p = 0.465$, $\hat{\rho}_{\text{Spearman}} = -0.164$, $CI_{95\%} [-0.557, 0.289]$, $n_{\text{pairs}} = 22$



Correlation within: Tilapia_farmed_pond

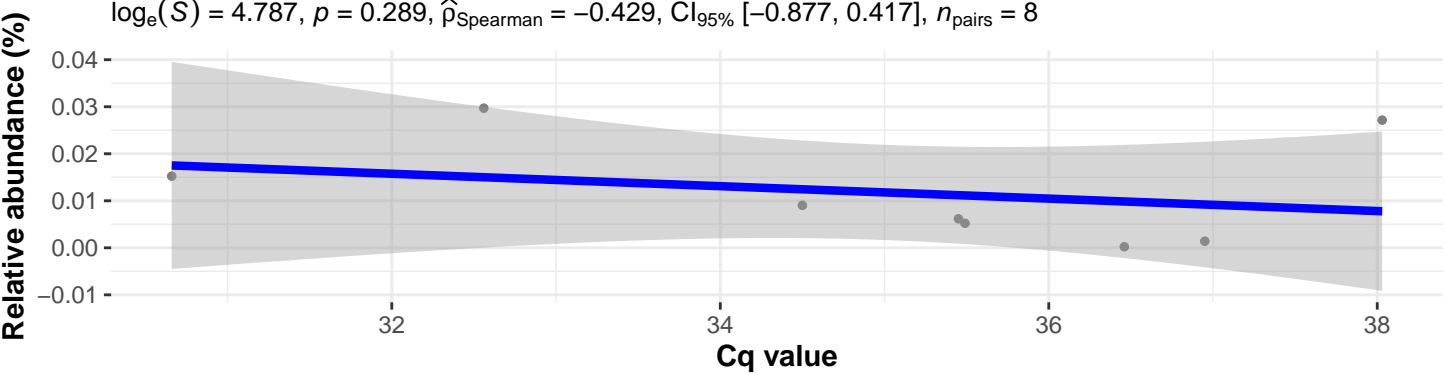


Correlation within: Tilapia_farmed_lake



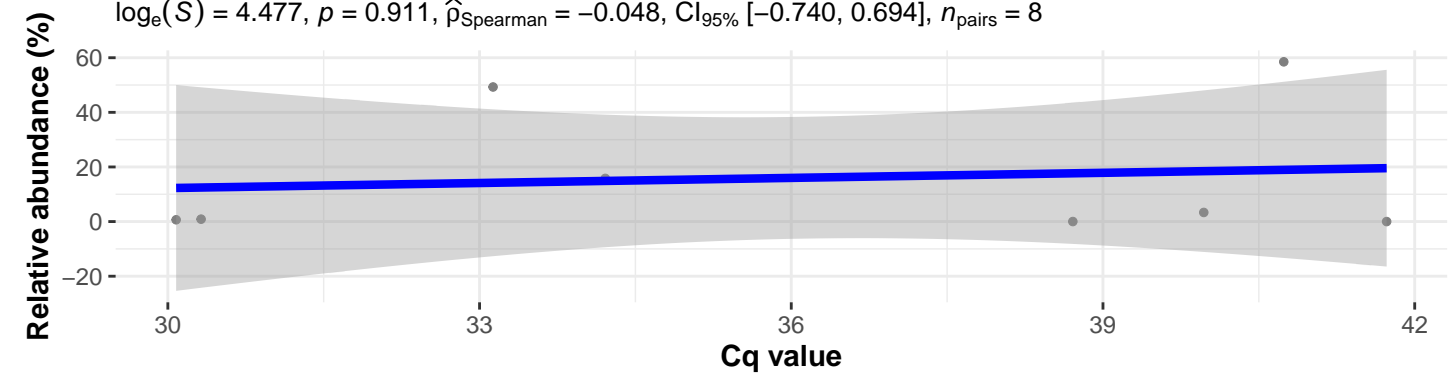
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.787$, $p = 0.289$, $\hat{\rho}_{\text{Spearman}} = -0.429$, $CI_{95\%} [-0.877, 0.417]$, $n_{\text{pairs}} = 8$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.477$, $p = 0.911$, $\hat{\rho}_{\text{Spearman}} = -0.048$, $CI_{95\%} [-0.740, 0.694]$, $n_{\text{pairs}} = 8$

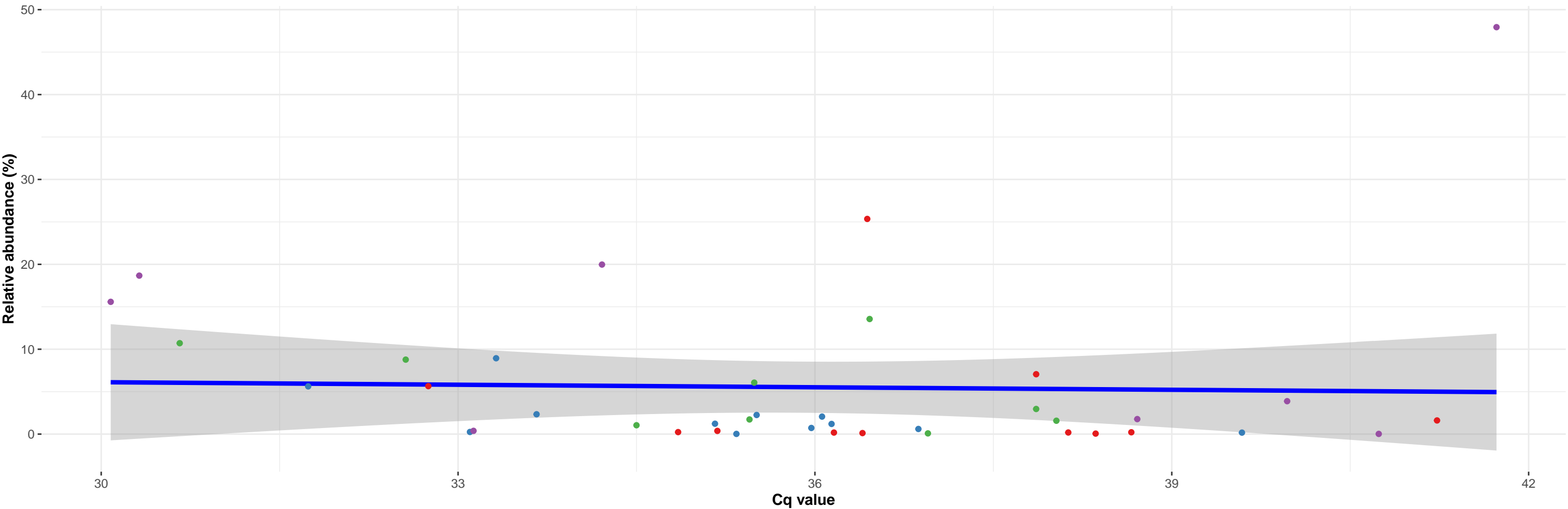


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 9039275571577e03e38d718f59db0e1f

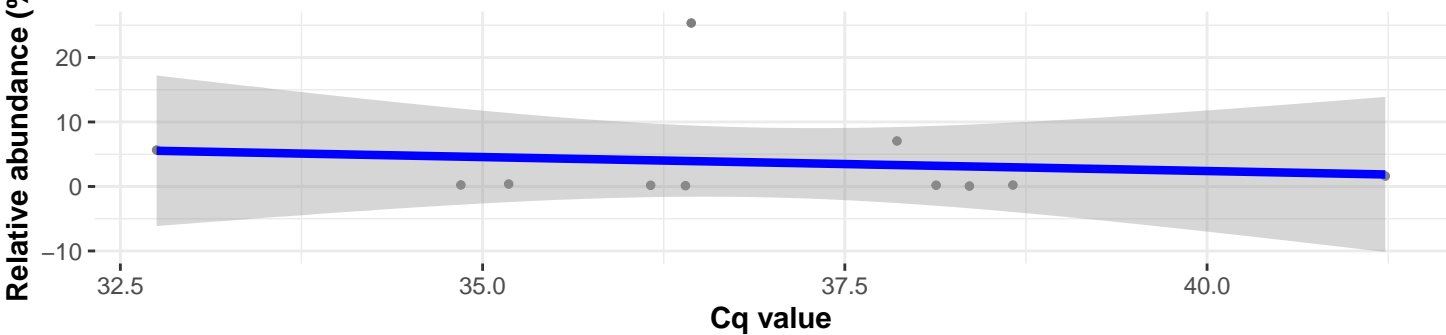
Correlation with all samples

$\log_e(S) = 9.554$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = -0.323$, $\text{CI}_{95\%} [-0.583, -0.003]$, $n_{\text{pairs}} = 40$



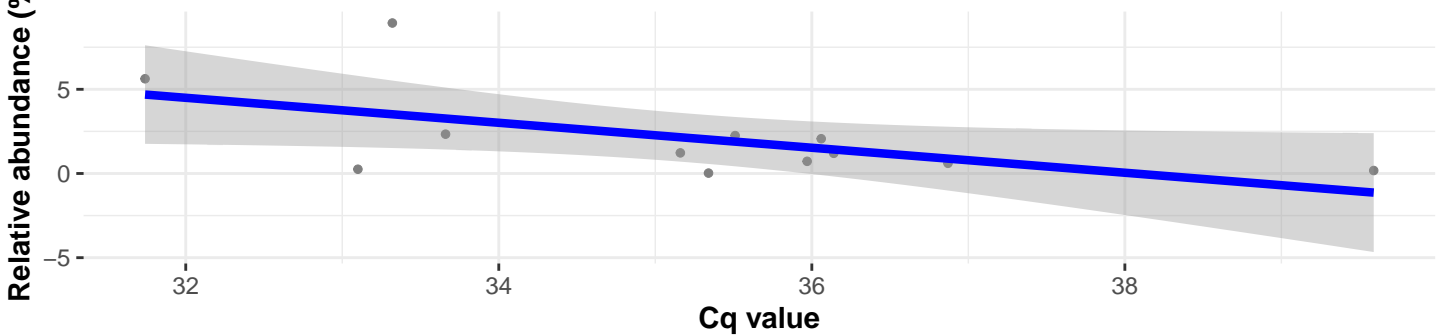
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.537$, $p = 0.650$, $\hat{\rho}_{\text{Spearman}} = -0.155$, $\text{CI}_{95\%} [-0.701, 0.506]$, $n_{\text{pairs}} = 11$



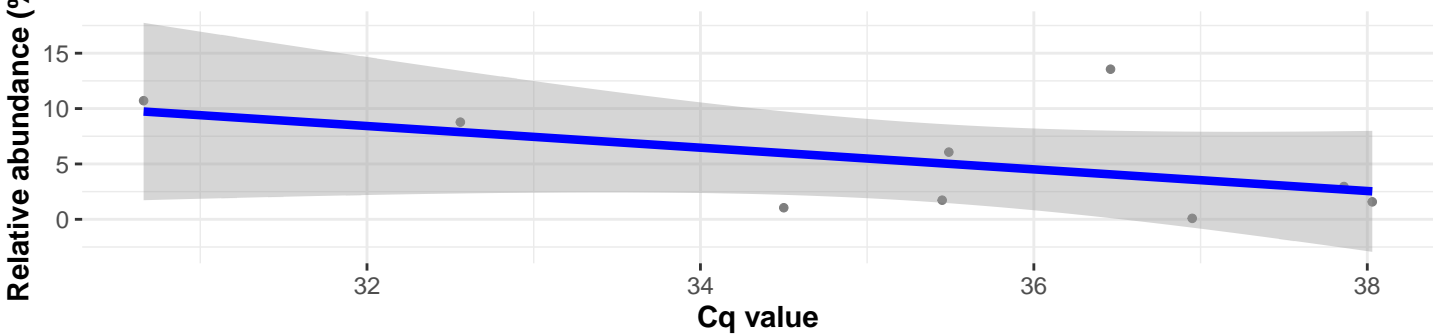
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 6.054$, $p = 0.106$, $\hat{\rho}_{\text{Spearman}} = -0.490$, $\text{CI}_{95\%} [-0.836, 0.136]$, $n_{\text{pairs}} = 12$



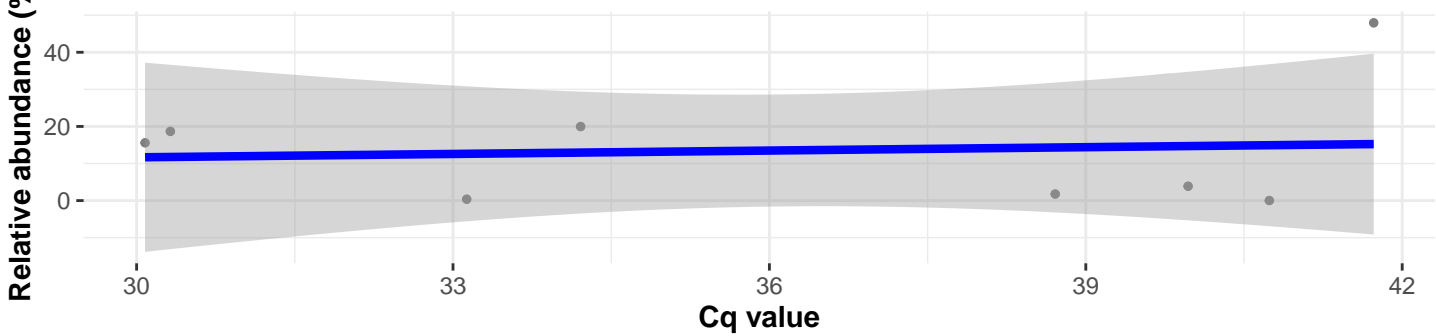
Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.112$, $p = 0.308$, $\hat{\rho}_{\text{Spearman}} = -0.383$, $\text{CI}_{95\%} [-0.842, 0.397]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.454$, $p = 0.955$, $\hat{\rho}_{\text{Spearman}} = -0.024$, $\text{CI}_{95\%} [-0.729, 0.706]$, $n_{\text{pairs}} = 8$

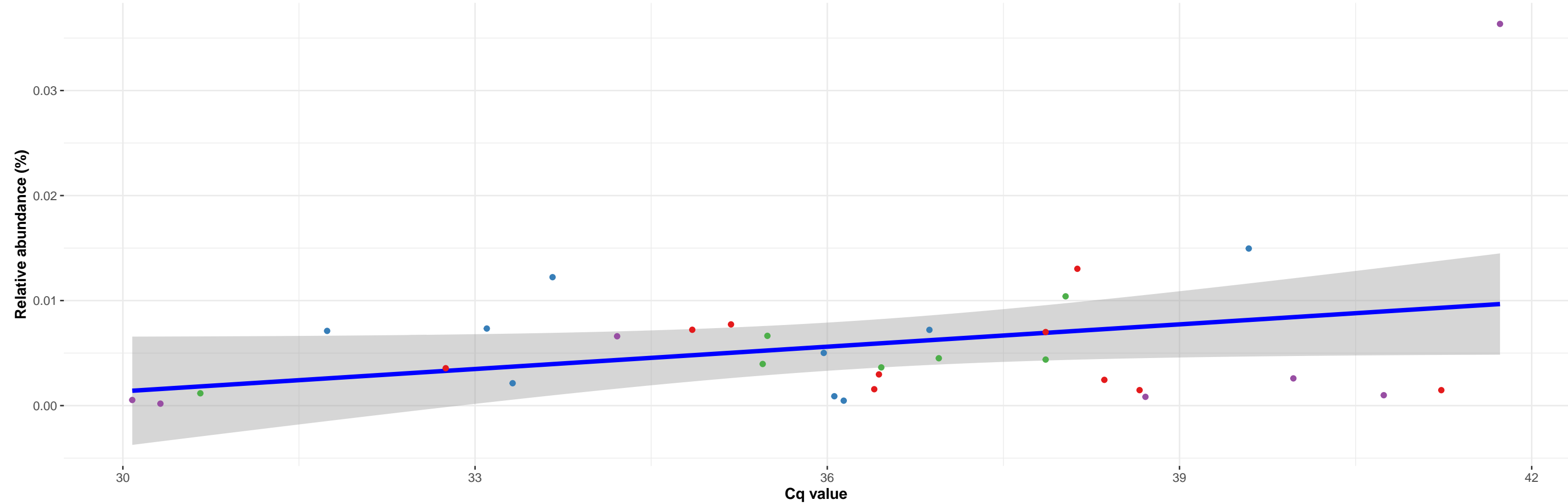


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Curvibacter; NA

featureID: e0fcddfb9012f2ef3fe5165e818f651

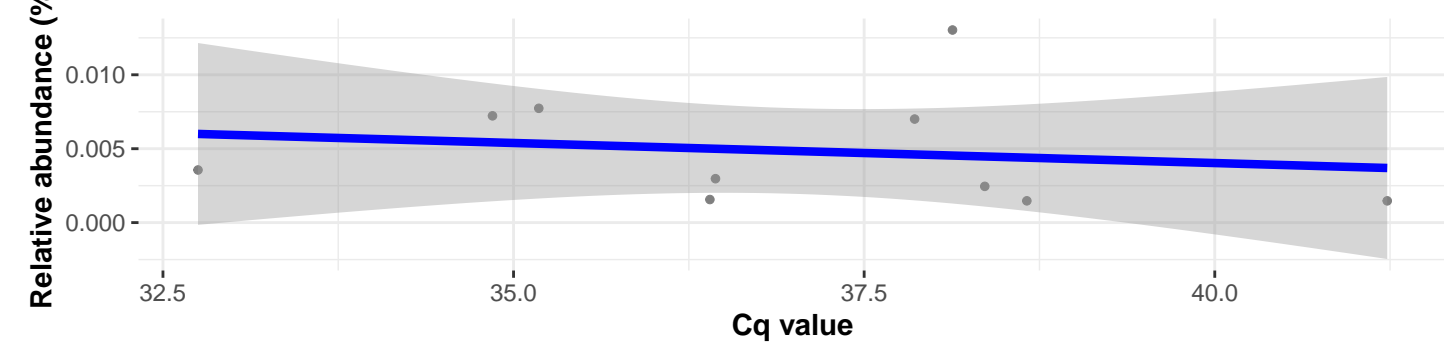
Correlation with all samples

$\log_e(S) = 8.588$, $p = 0.569$, $\hat{\rho}_{\text{Spearman}} = 0.103$, $CI_{95\%} [-0.259, 0.439]$, $n_{\text{pairs}} = 33$



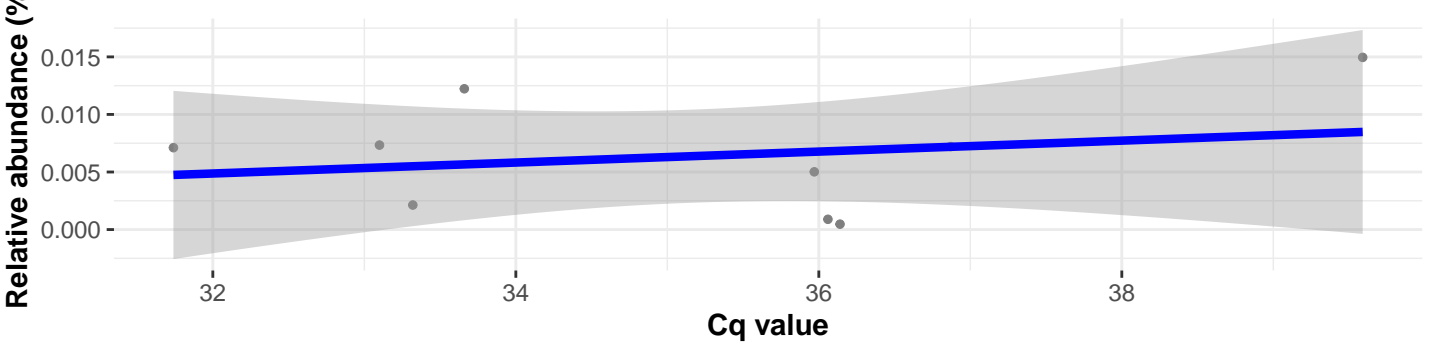
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.537$, $p = 0.108$, $\hat{\rho}_{\text{Spearman}} = -0.539$, $CI_{95\%} [-0.878, 0.158]$, $n_{\text{pairs}} = 10$



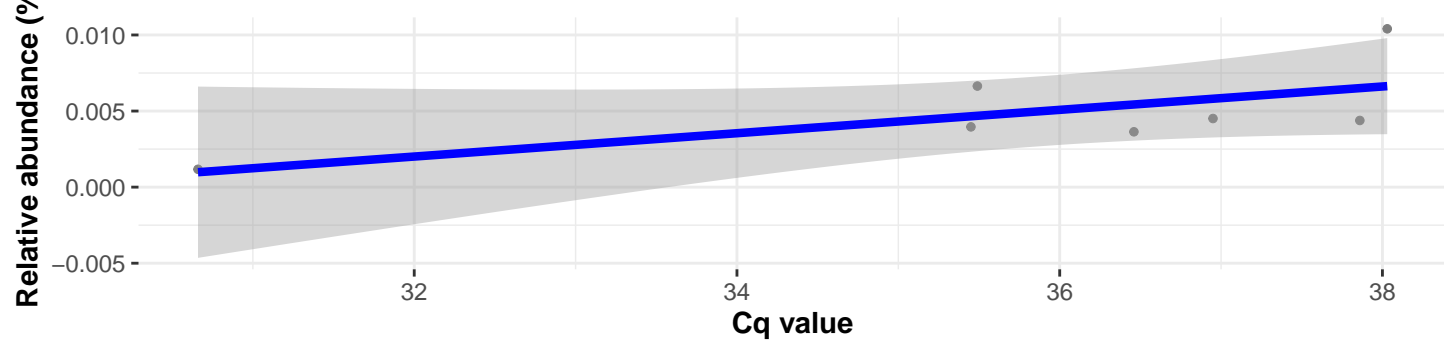
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 4.736$, $p = 0.898$, $\hat{\rho}_{\text{Spearman}} = 0.050$, $CI_{95\%} [-0.649, 0.703]$, $n_{\text{pairs}} = 9$



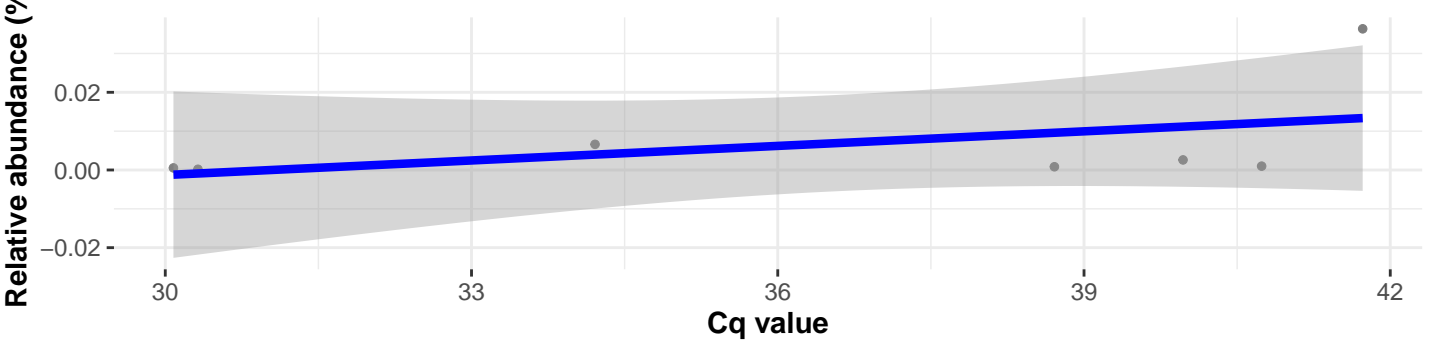
Correlation within: Tilapia_wild_lake

$\log_e(S) = 2.890$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = 0.679$, $CI_{95\%} [-0.180, 0.950]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

$\log_e(S) = 2.773$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $CI_{95\%} [-0.113, 0.957]$, $n_{\text{pairs}} = 7$

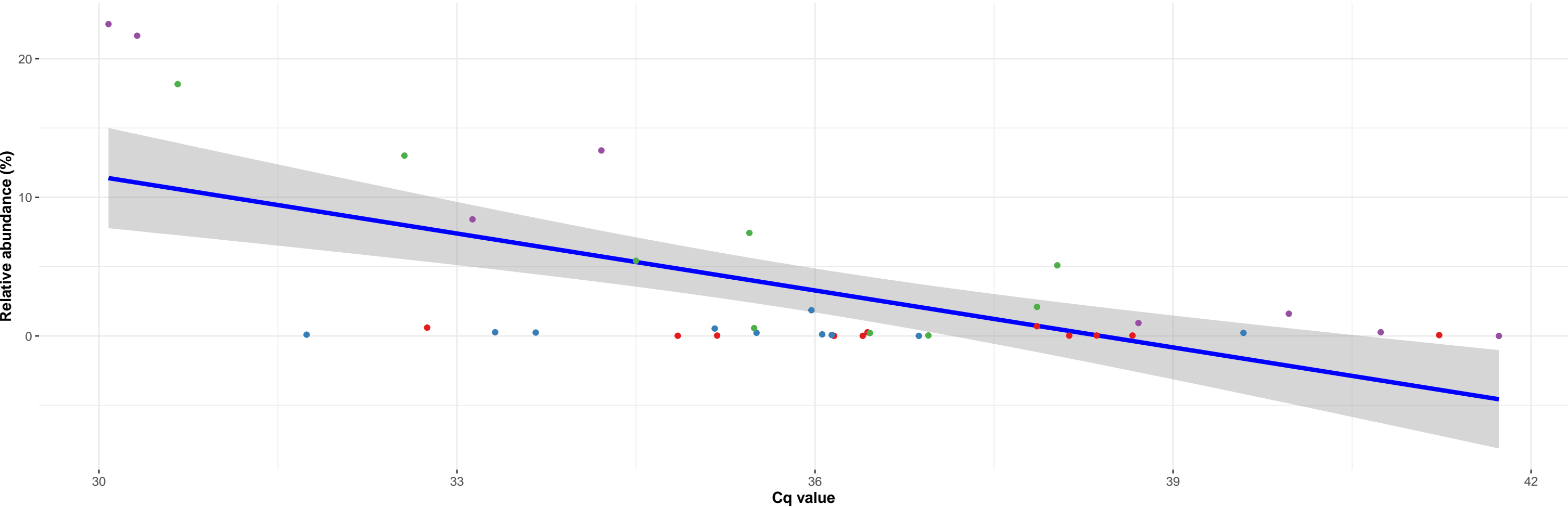


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 4f52c06bab364867d8911147cbccbc38

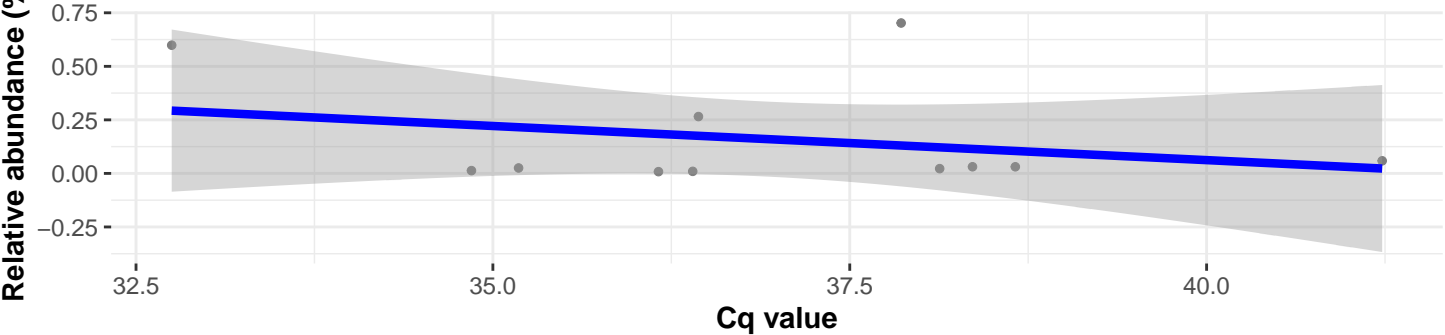
Correlation with all samples

$\log_e(S) = 9.506$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = -0.471$, $CI_{95\%} [-0.692, -0.169]$, $n_{\text{pairs}} = 38$



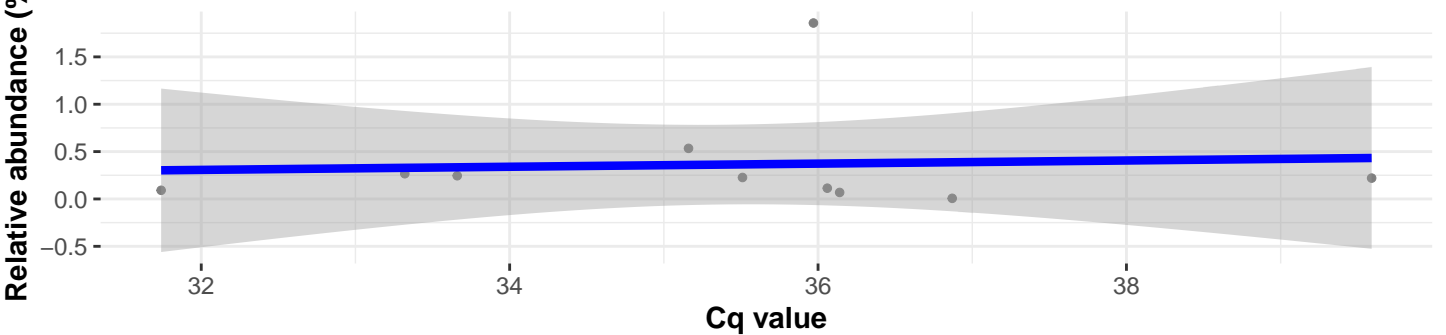
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.159$, $p = 0.537$, $\hat{\rho}_{\text{Spearman}} = 0.209$, $CI_{95\%} [-0.463, 0.729]$, $n_{\text{pairs}} = 11$



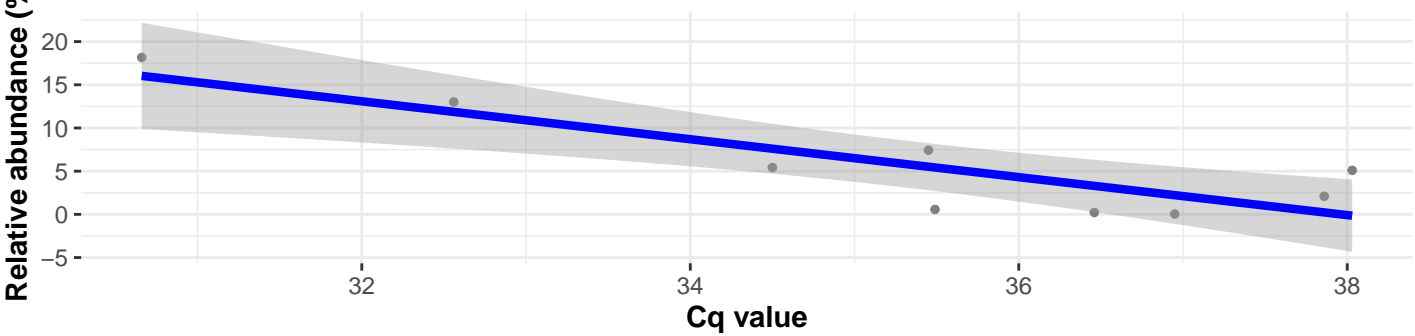
Correlation within: Tilapia_farmed_lake

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



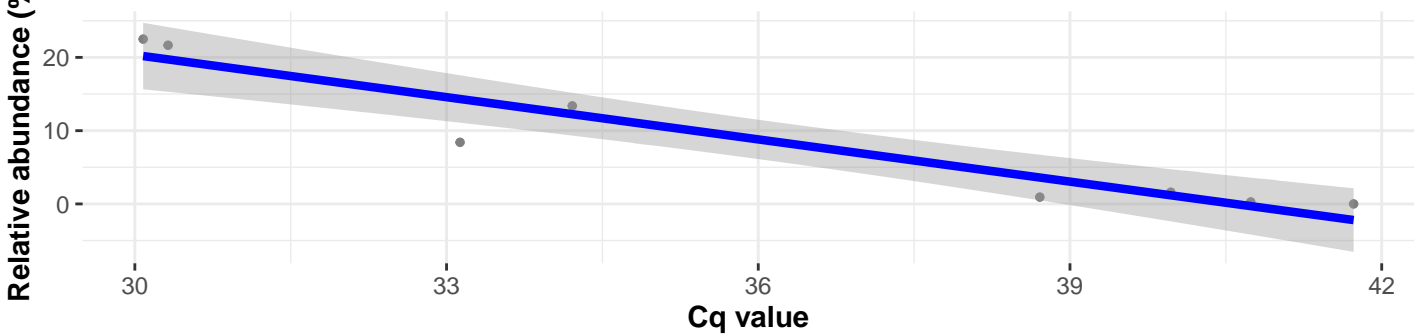
Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.328$, $p = 0.030$, $\hat{\rho}_{\text{Spearman}} = -0.717$, $CI_{95\%} [-0.938, -0.077]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

$\log_e(S) = 5.100$, $p = 2.6e-04$, $\hat{\rho}_{\text{Spearman}} = -0.952$, $CI_{95\%} [-0.992, -0.742]$, $n_{\text{pairs}} = 8$

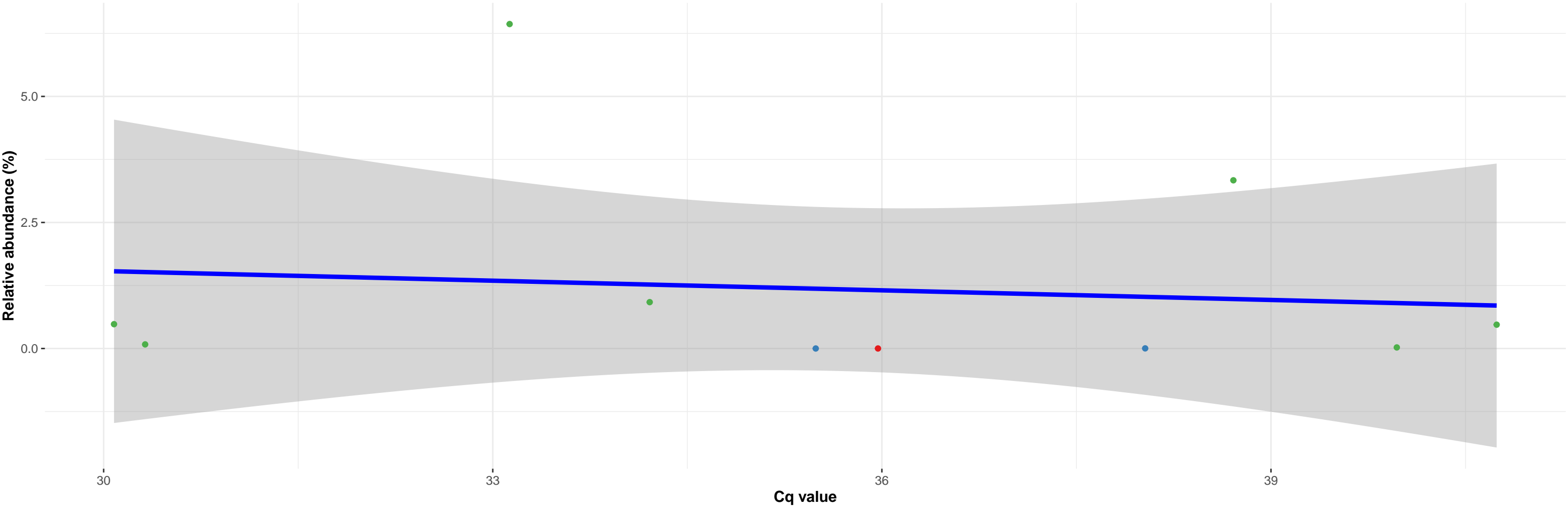


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

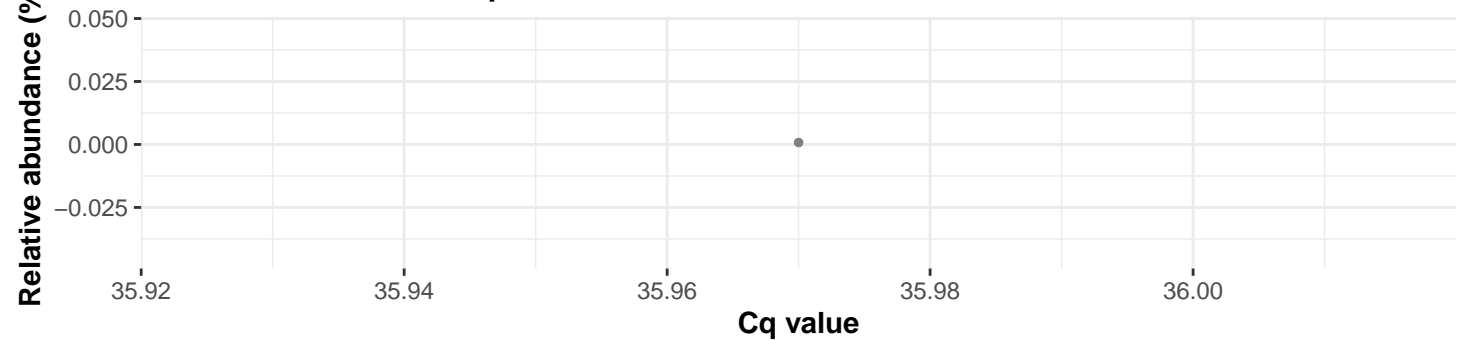
featureID: 2e13ada579831ad7bc85cacea069bcb4

Correlation with all samples

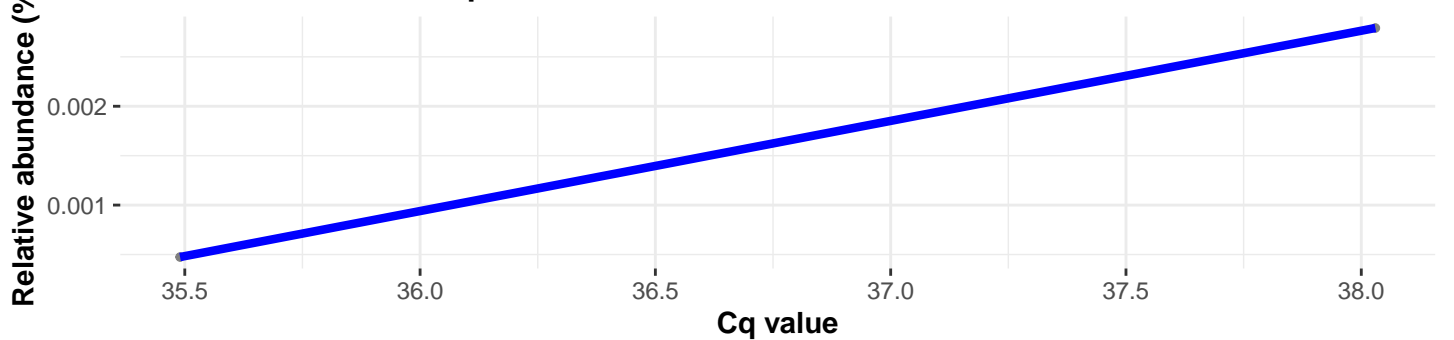
$\log_e(S) = 5.298$, $\rho = 0.556$, $\hat{\rho}_{\text{Spearman}} = -0.212$, $CI_{95\%} [-0.752, 0.498]$, $n_{\text{pairs}} = 10$



Correlation within: Tilapia_farmed_lake

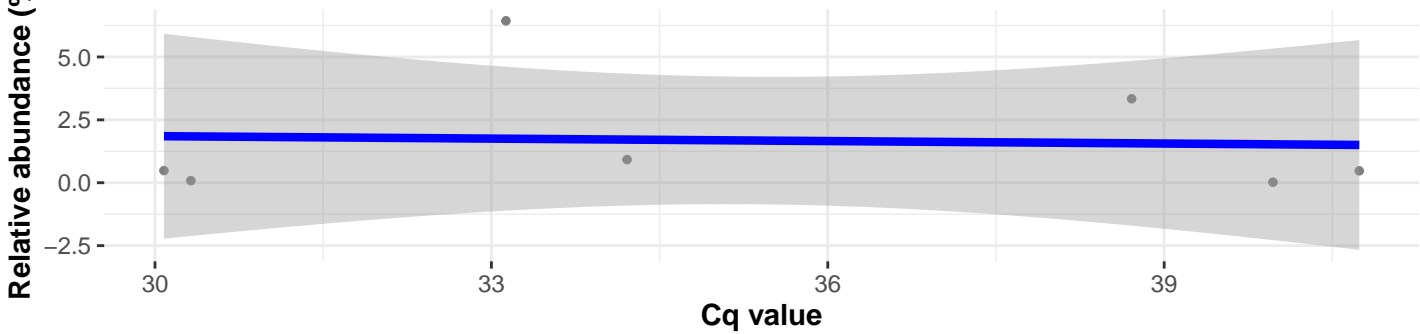


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

$\log_e(S) = 4.220$, $\rho = 0.645$, $\hat{\rho}_{\text{Spearman}} = -0.214$, $CI_{95\%} [-0.842, 0.659]$, $n_{\text{pairs}} = 7$

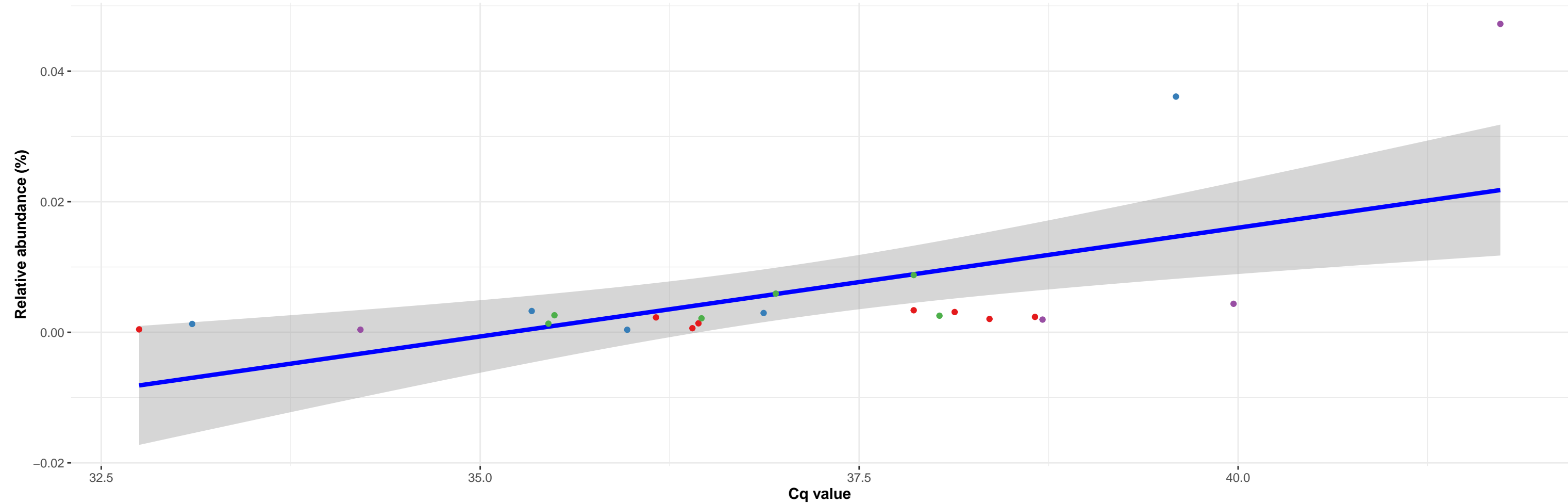


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; NA

featureID: 11c192ca47293df7d3c26138fd796fe1

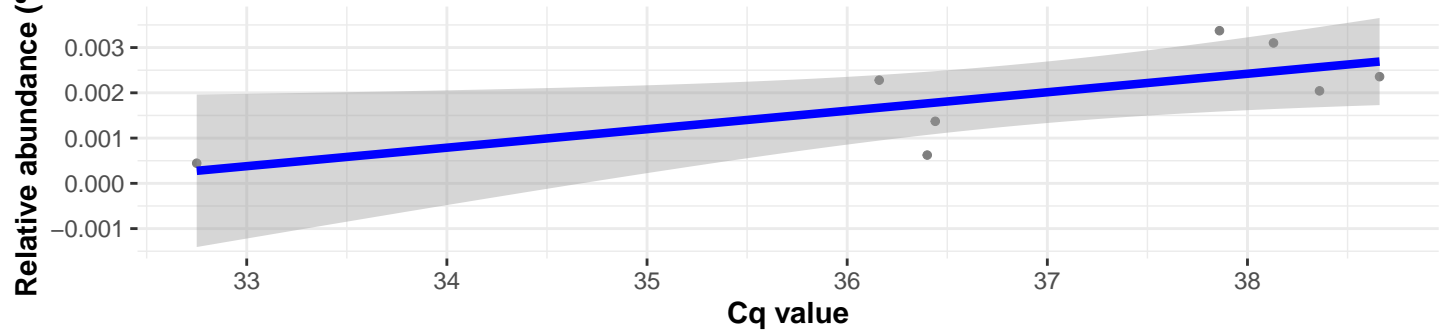
Correlation with all samples

$\log_e(S) = 6.599$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.637$, $\text{CI}_{95\%} [0.293, 0.835]$, $n_{\text{pairs}} = 23$

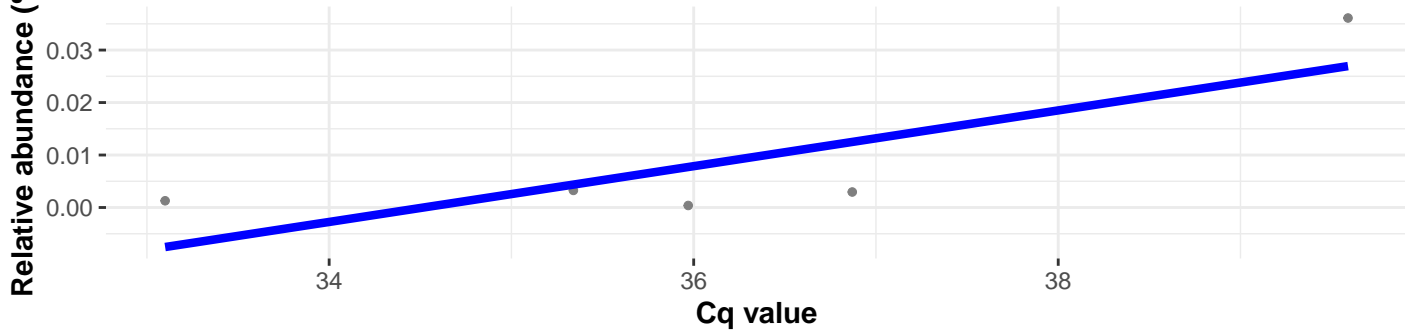


Correlation within: Tilapia_farmed_pond

$\log_e(S) = 3.526$, $p = 0.120$, $\hat{\rho}_{\text{Spearman}} = 0.595$, $\text{CI}_{95\%} [-0.213, 0.920]$, $n_{\text{pairs}} = 8$

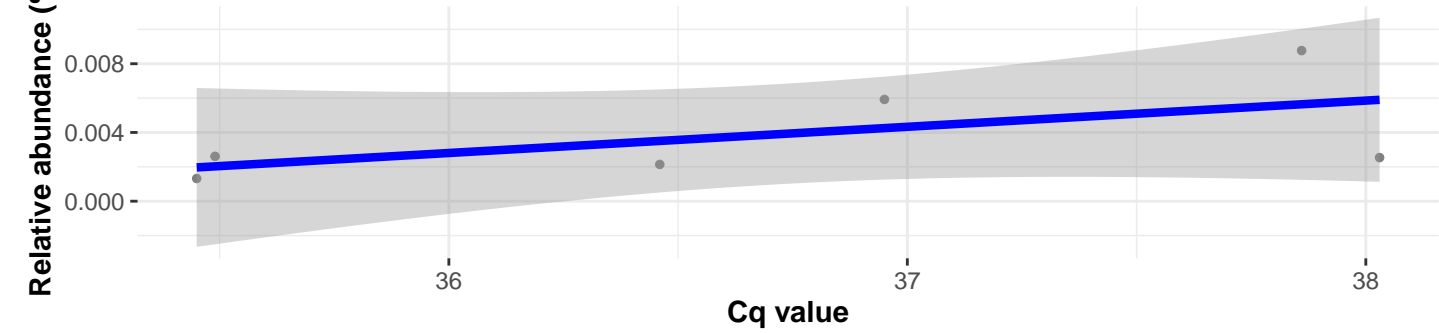


Correlation within: Tilapia_farmed_lake

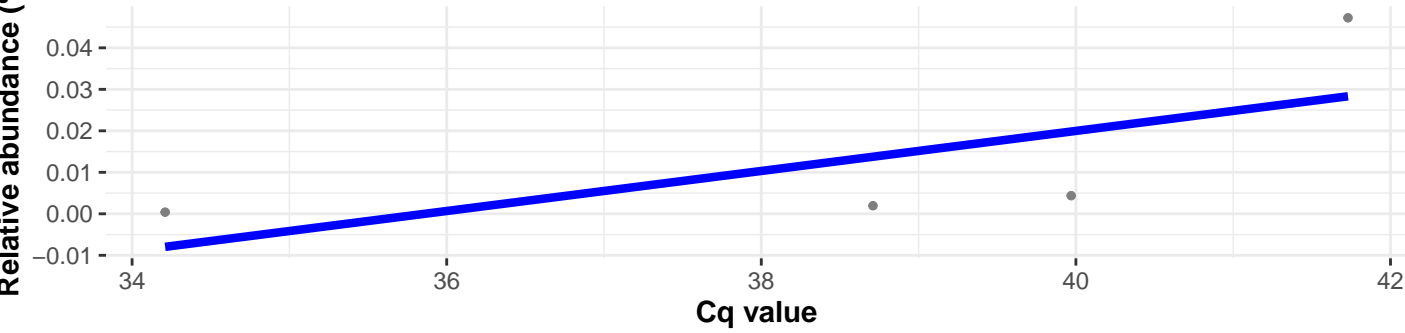


Correlation within: Tilapia_wild_lake

$\log_e(S) = 2.773$, $p = 0.266$, $\hat{\rho}_{\text{Spearman}} = 0.543$, $\text{CI}_{95\%} [-0.506, 0.944]$, $n_{\text{pairs}} = 6$



Correlation within: Perch_wild_lake

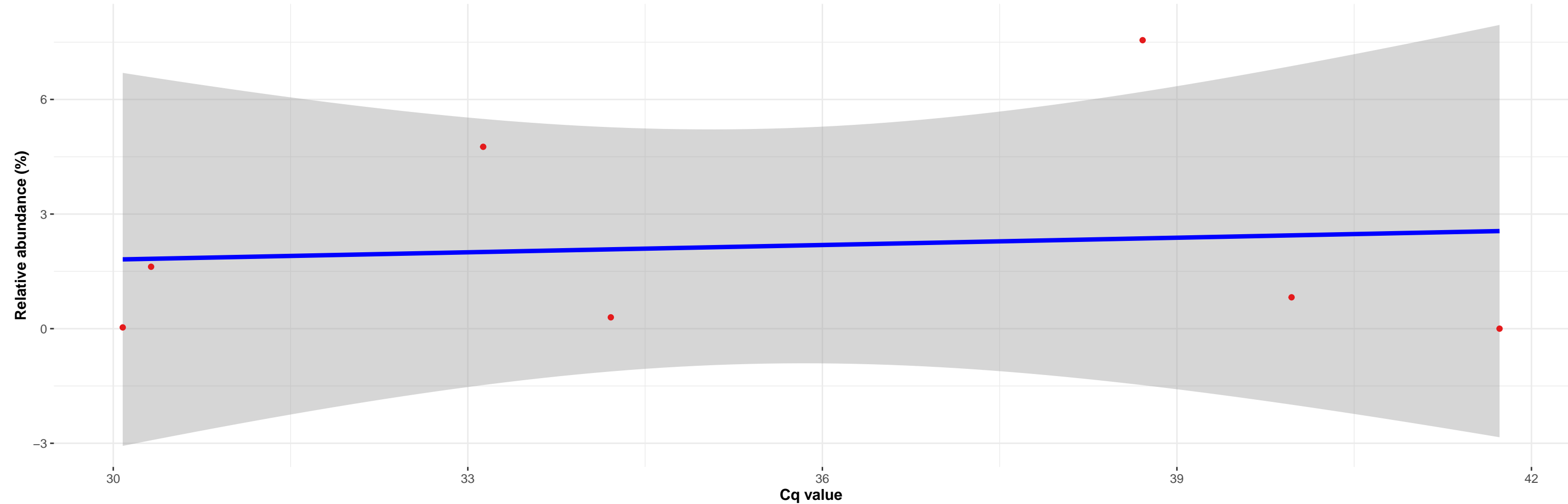


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 1f1ddbae27b2e40cd4947dc079b0021e

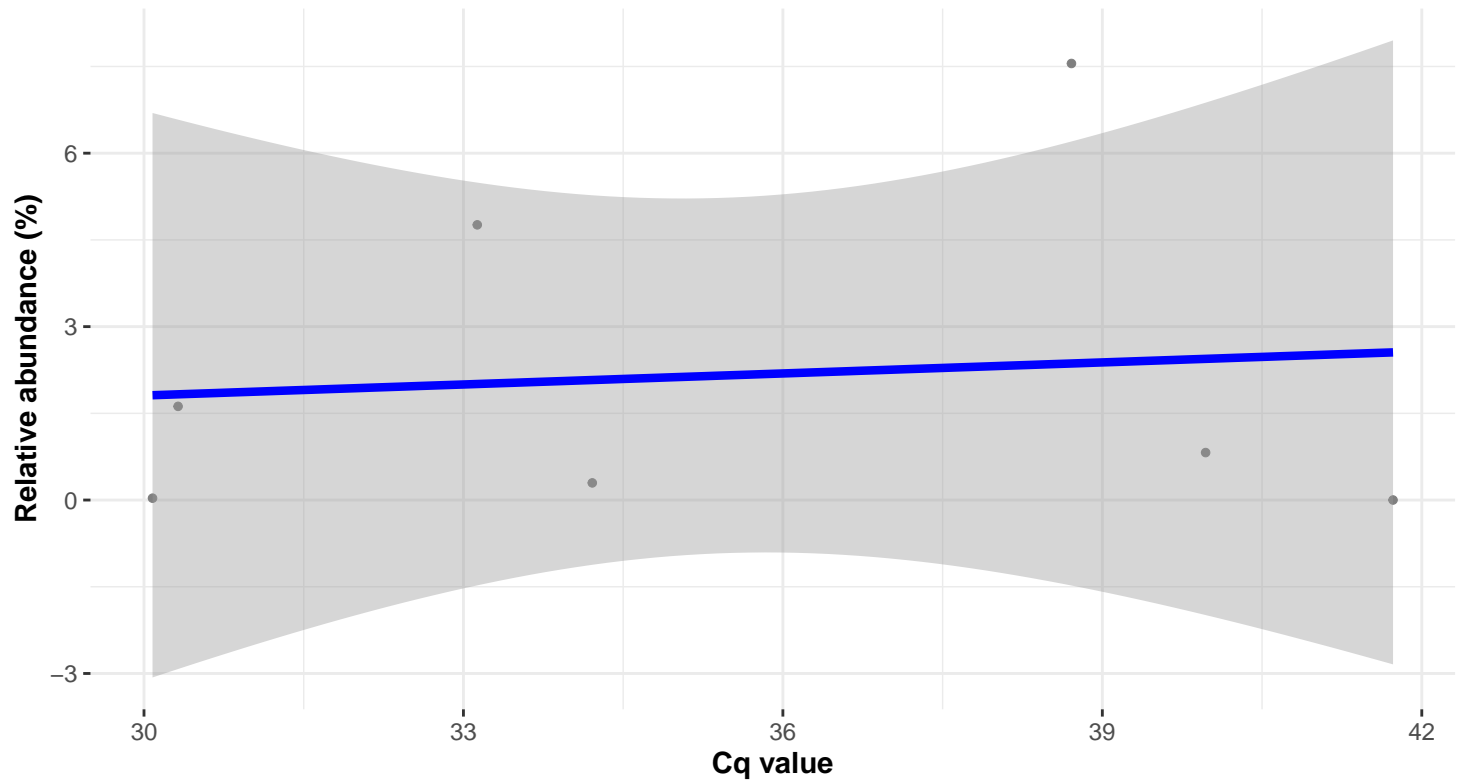
Correlation with all samples

$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-0.819, 0.699]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-0.819, 0.699]$, $n_{\text{pairs}} = 7$

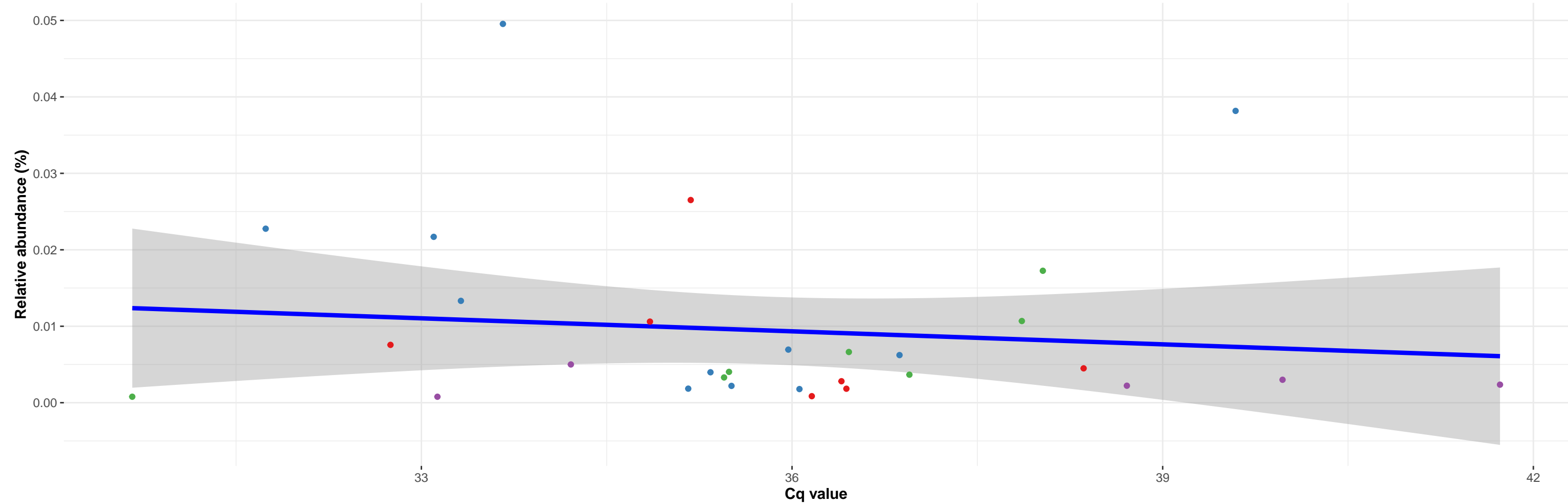


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: af190b852cec0d6eb78c15eb0e8777e0

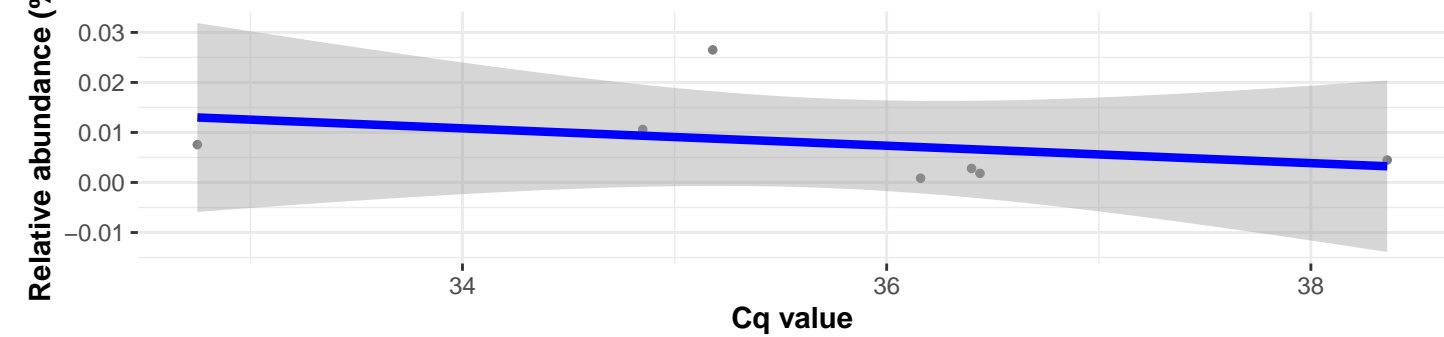
Correlation with all samples

$\log_e(S) = 8.516$, $p = 0.561$, $\hat{\rho}_{\text{Spearman}} = -0.111$, $\text{CI}_{95\%} [-0.462, 0.270]$, $n_{\text{pairs}} = 30$



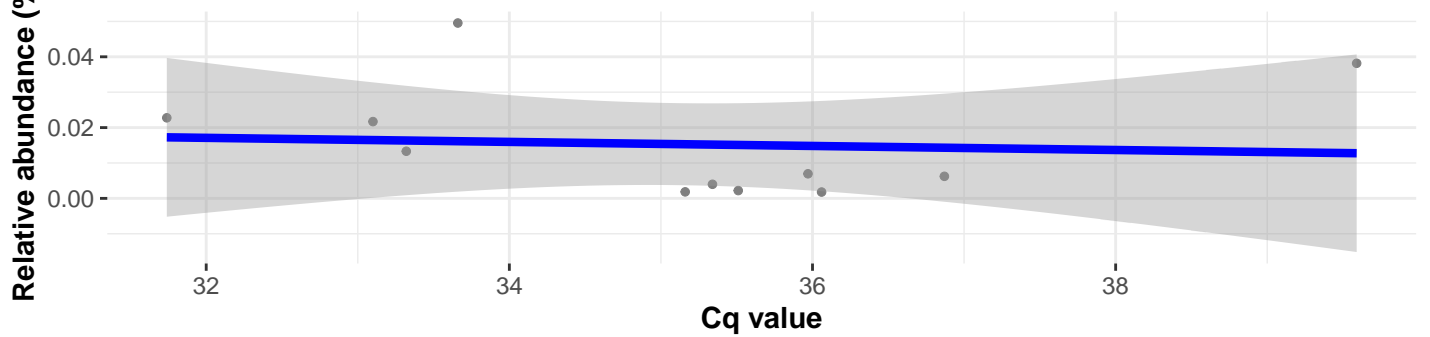
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.454$, $p = 0.215$, $\hat{\rho}_{\text{Spearman}} = -0.536$, $\text{CI}_{95\%} [-0.923, 0.389]$, $n_{\text{pairs}} = 7$



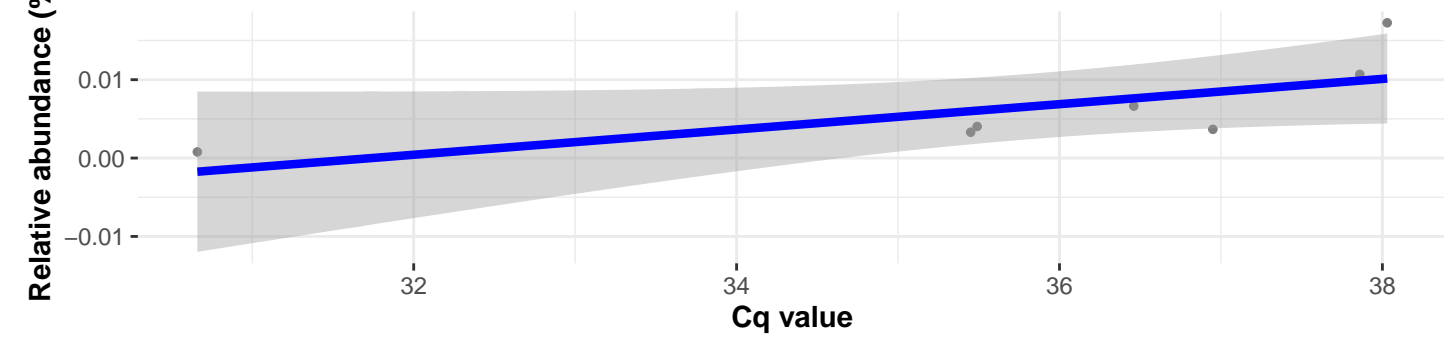
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.663$, $p = 0.355$, $\hat{\rho}_{\text{Spearman}} = -0.309$, $\text{CI}_{95\%} [-0.775, 0.375]$, $n_{\text{pairs}} = 11$



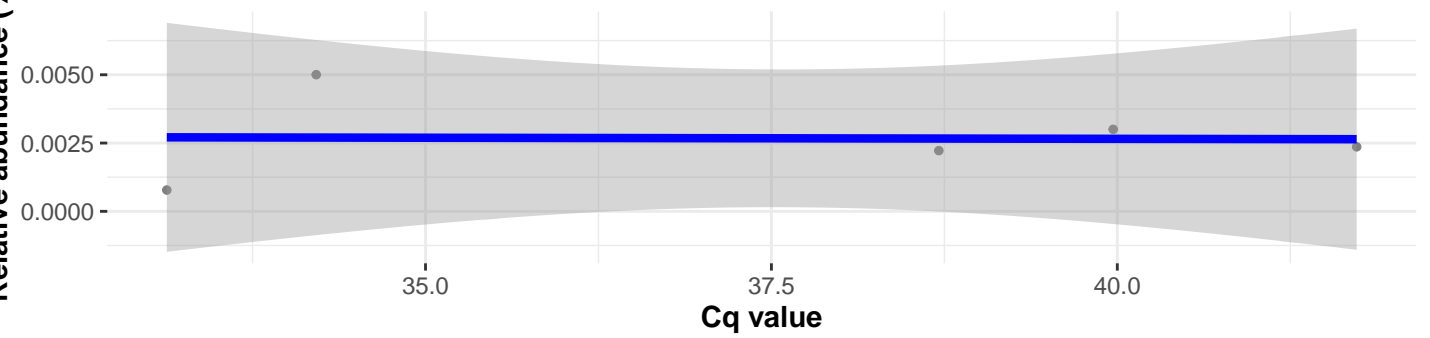
Correlation within: Tilapia_wild_lake

$\log_e(S) = 1.792$, $p = 0.007$, $\hat{\rho}_{\text{Spearman}} = 0.893$, $\text{CI}_{95\%} [0.403, 0.985]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

$\log_e(S) = 2.639$, $p = 0.624$, $\hat{\rho}_{\text{Spearman}} = 0.300$, $\text{CI}_{95\%} [-0.807, 0.940]$, $n_{\text{pairs}} = 5$

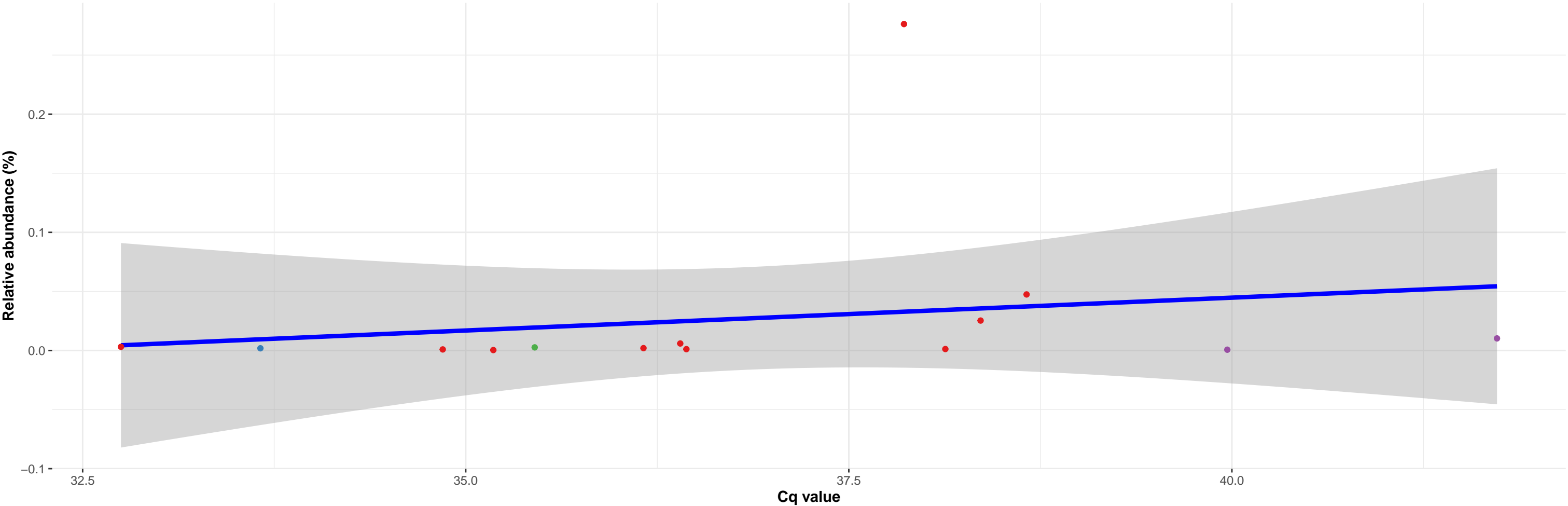


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA

featureID: 9db2817f5c42be6a7bcbca662959982d

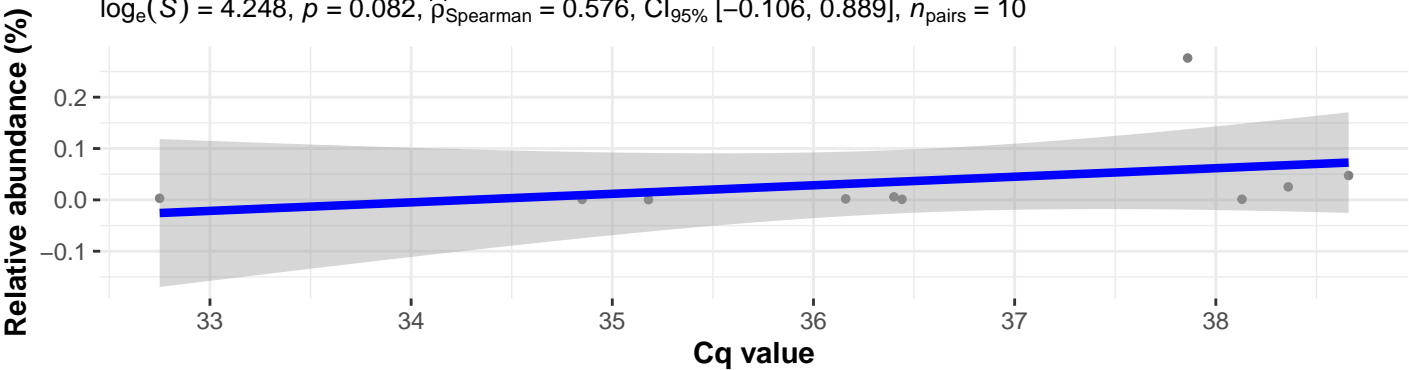
Correlation with all samples

$\log_e(S) = 5.724$, $p = 0.253$, $\hat{\rho}_{\text{Spearman}} = 0.327$, $CI_{95\%} [-0.262, 0.739]$, $n_{\text{pairs}} = 14$

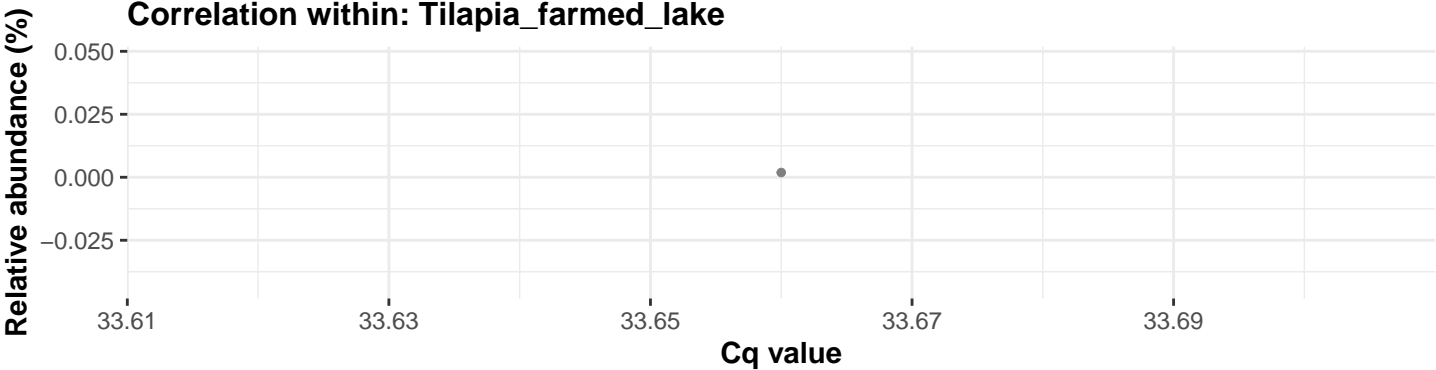


Correlation within: Tilapia_farmed_pond

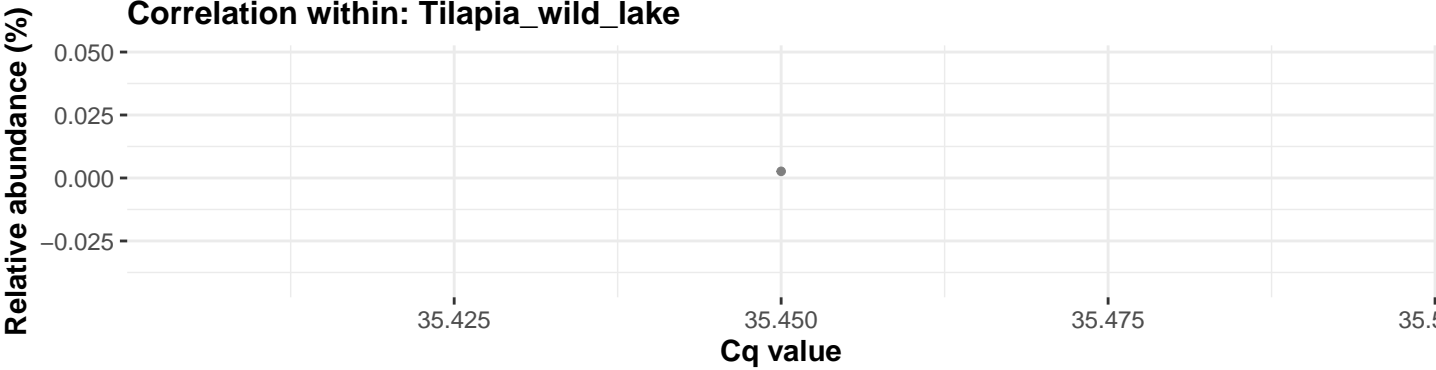
$\log_e(S) = 4.248$, $p = 0.082$, $\hat{\rho}_{\text{Spearman}} = 0.576$, $CI_{95\%} [-0.106, 0.889]$, $n_{\text{pairs}} = 10$



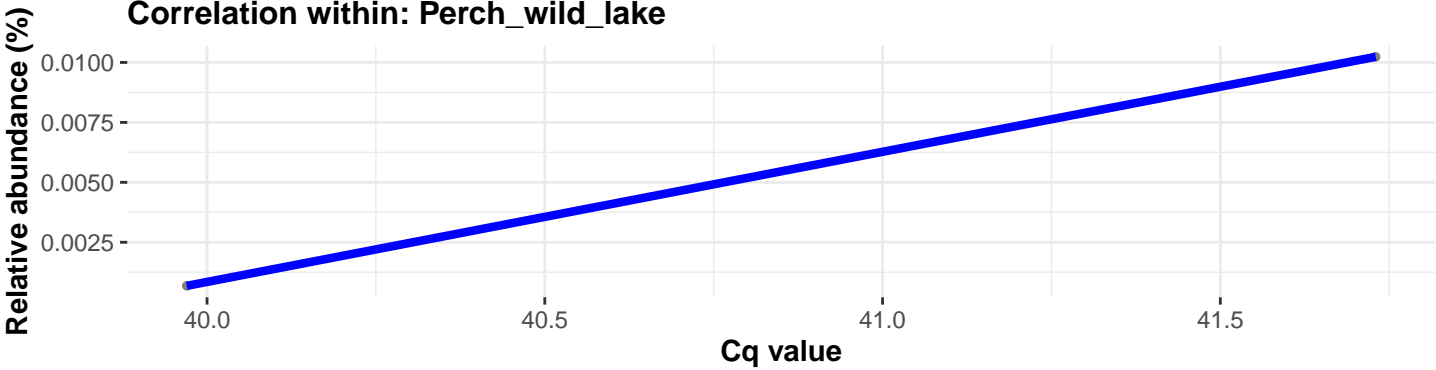
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

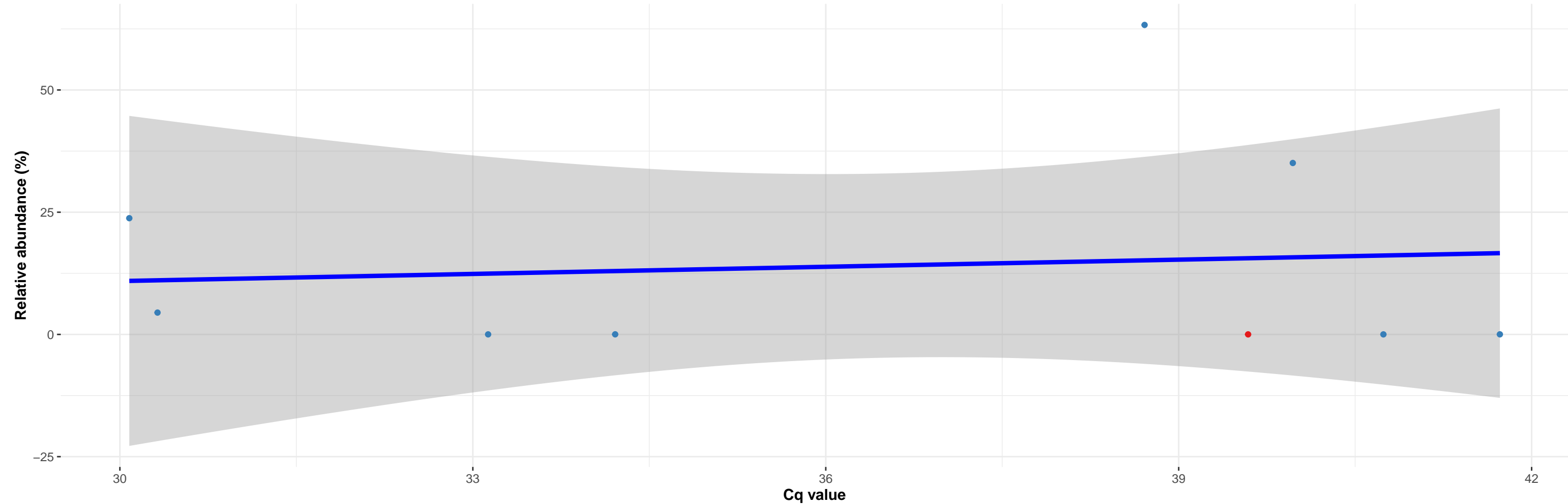


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

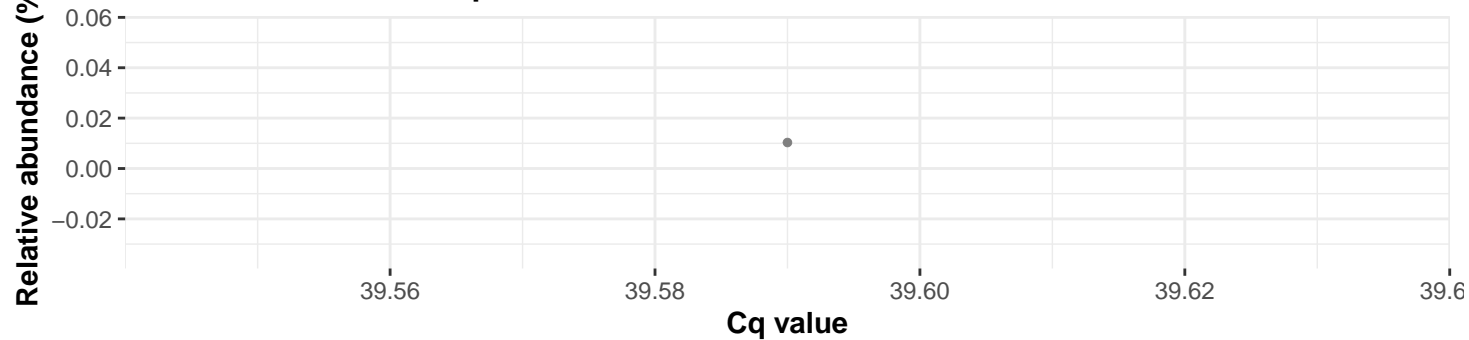
featureID: 750438ef469a6a58cdf16b89f540188b

Correlation with all samples

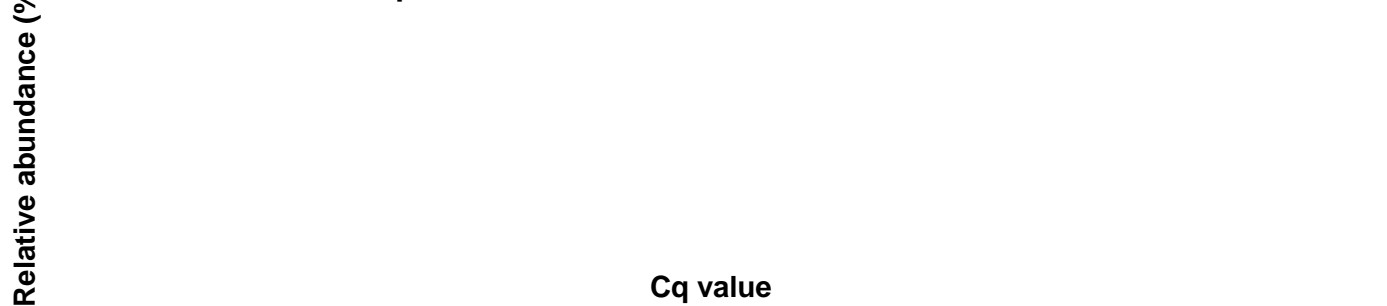
$\log_e(S) = 5.075$, $p = 0.381$, $\hat{\rho}_{\text{Spearman}} = -0.333$, $\text{CI}_{95\%} [-0.824, 0.444]$, $n_{\text{pairs}} = 9$



Correlation within: Tilapia_farmed_lake

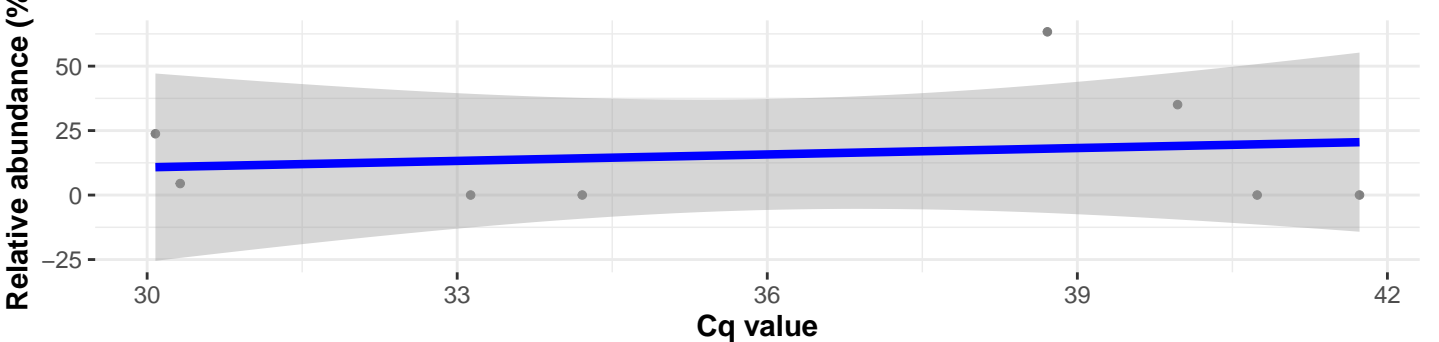


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

$\log_e(S) = 4.663$, $p = 0.531$, $\hat{\rho}_{\text{Spearman}} = -0.262$, $\text{CI}_{95\%} [-0.824, 0.561]$, $n_{\text{pairs}} = 8$

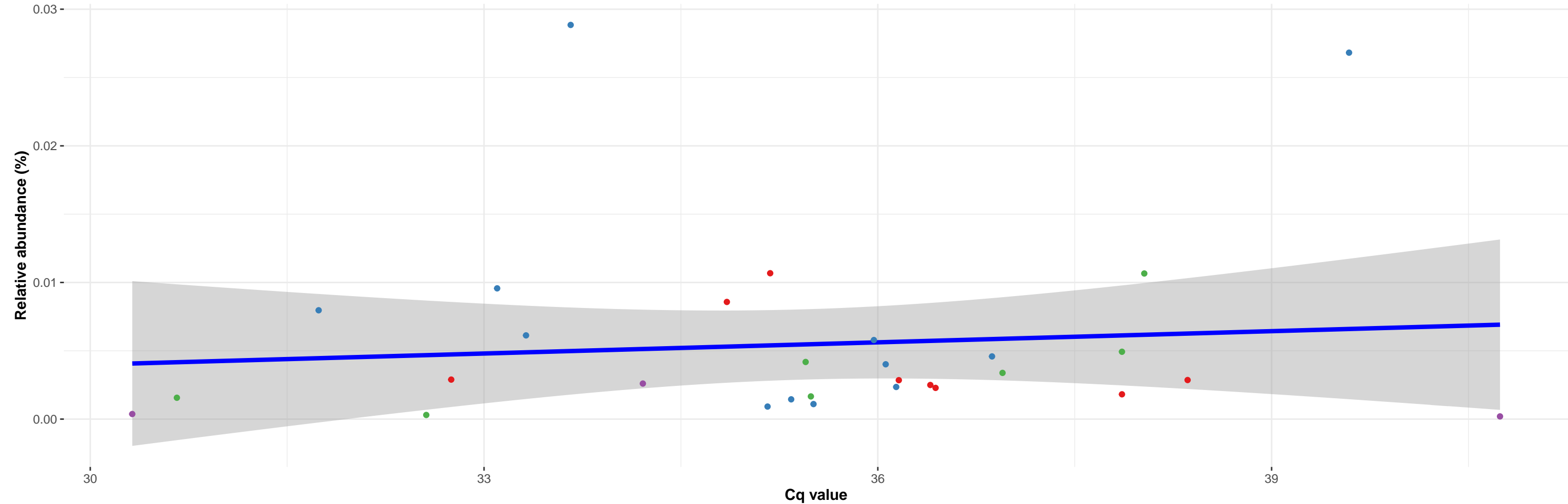


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: 5a90e7fe242256a5c625bd072bb3337

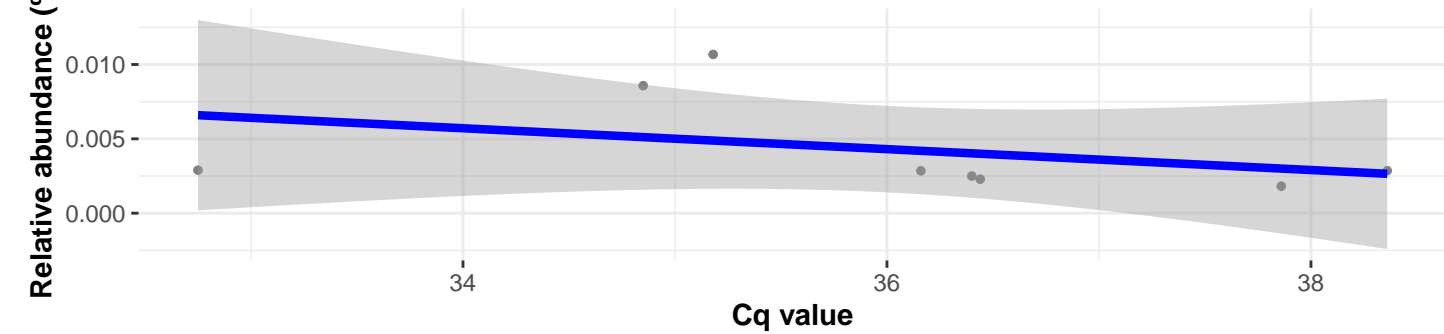
Correlation with all samples

$\log_e(S) = 8.351$, $p = 0.762$, $\hat{\rho}_{\text{Spearman}} = 0.058$, $\text{CI}_{95\%} [-0.319, 0.419]$, $n_{\text{pairs}} = 30$



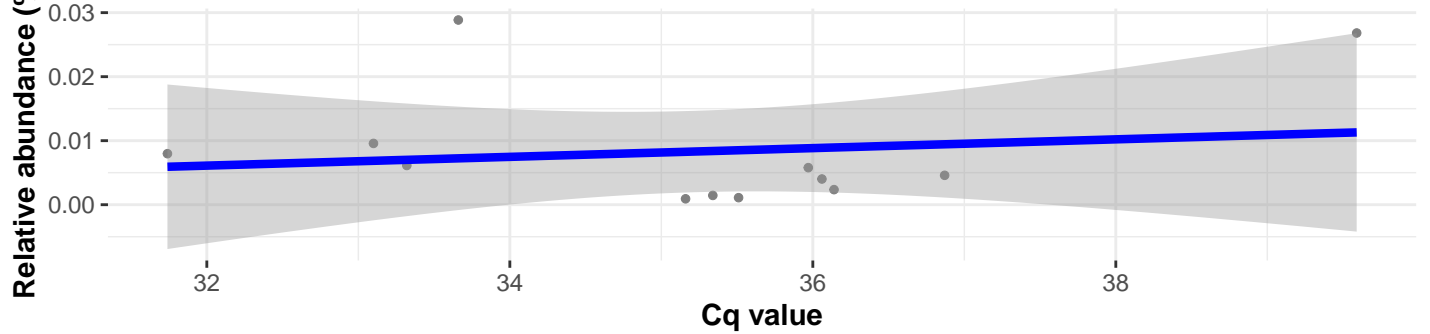
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.942$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = -0.667$, $\text{CI}_{95\%} [-0.936, 0.097]$, $n_{\text{pairs}} = 8$



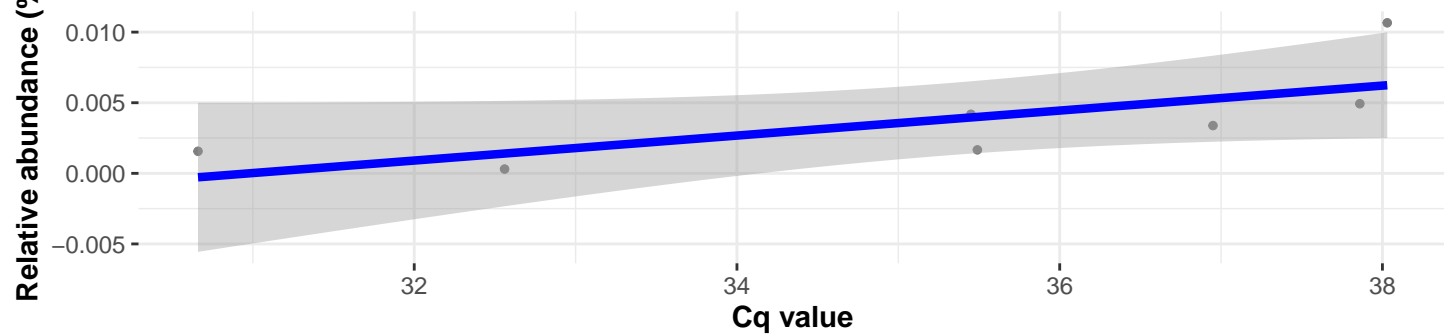
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.846$, $p = 0.513$, $\hat{\rho}_{\text{Spearman}} = -0.210$, $\text{CI}_{95\%} [-0.709, 0.430]$, $n_{\text{pairs}} = 12$

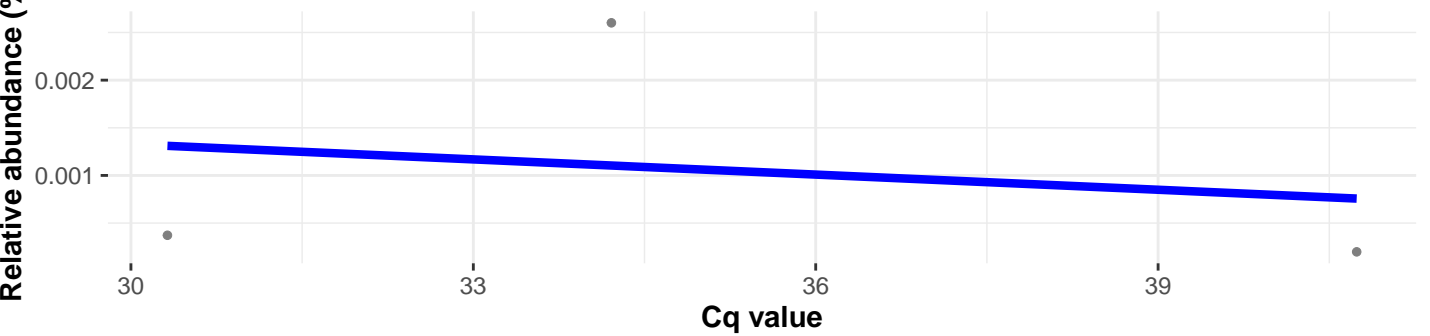


Correlation within: Tilapia_wild_lake

$\log_e(S) = 2.079$, $p = 0.014$, $\hat{\rho}_{\text{Spearman}} = 0.857$, $\text{CI}_{95\%} [0.267, 0.980]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

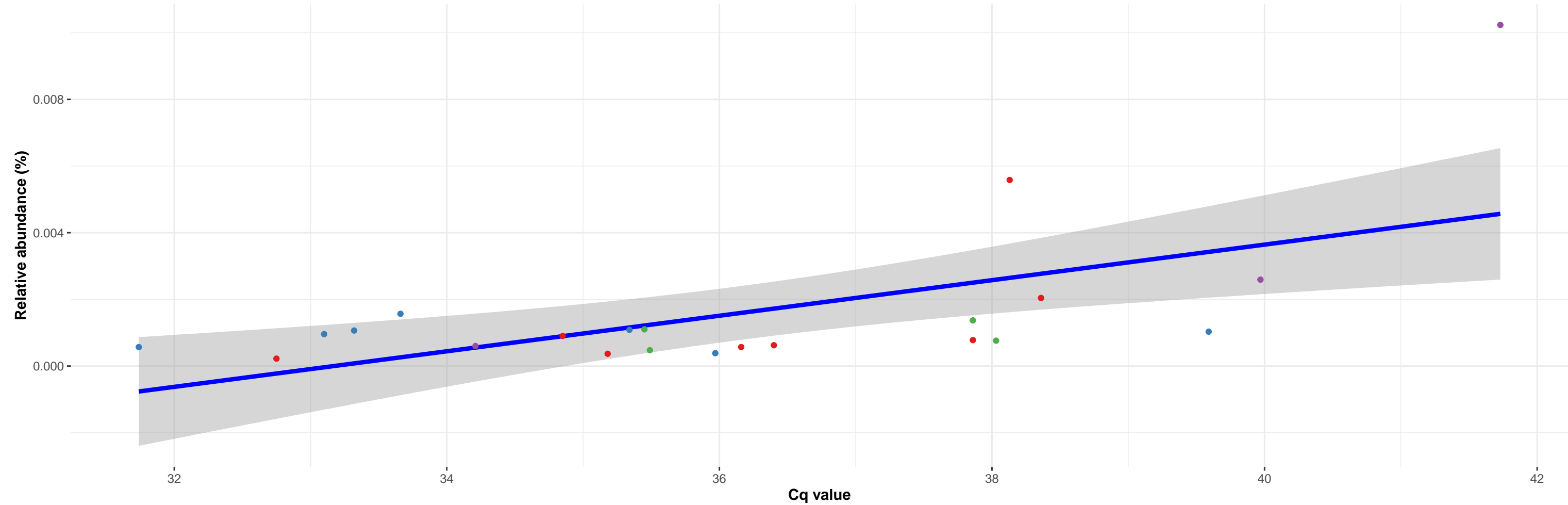


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; NA; NA

featureID: 8f2bbe692f7aca0f2c3959c3cf312b1d

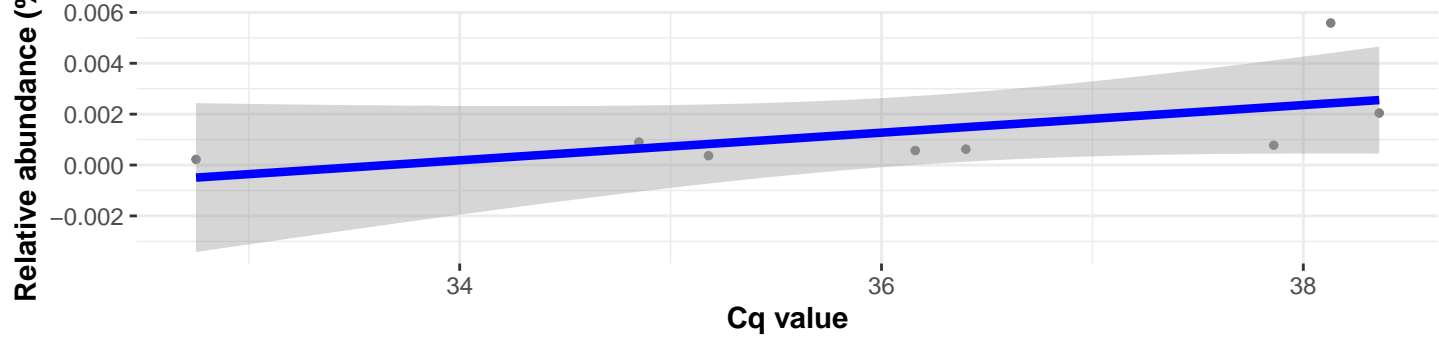
Correlation with all samples

$\log_e(S) = 6.760$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = 0.513$, $CI_{95\%} [0.103, 0.774]$, $n_{\text{pairs}} = 22$



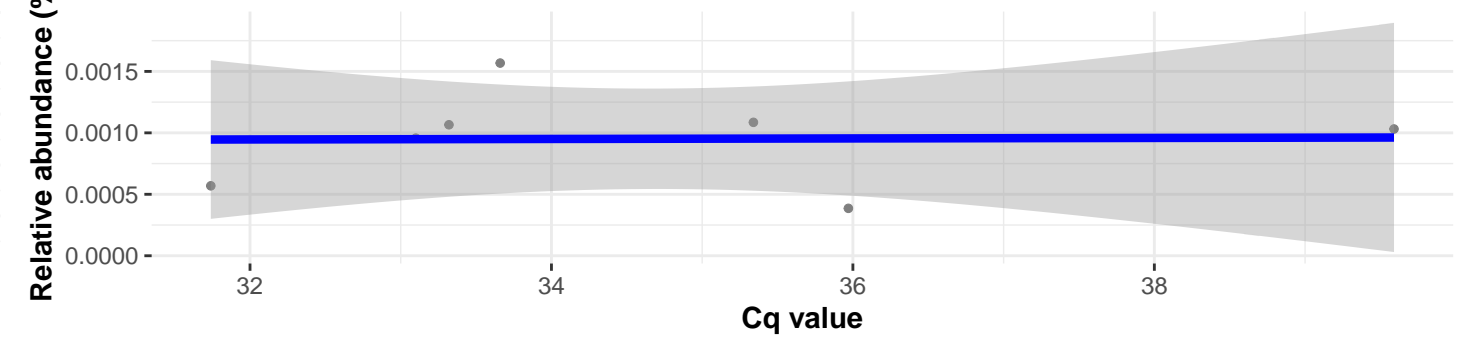
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 3.091$, $p = 0.037$, $\hat{\rho}_{\text{Spearman}} = 0.738$, $CI_{95\%} [0.044, 0.952]$, $n_{\text{pairs}} = 8$

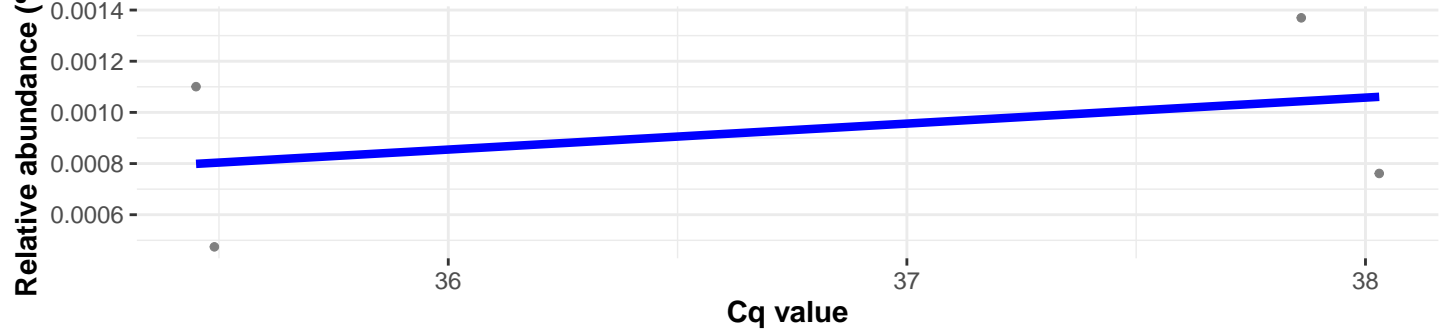


Correlation within: Tilapia_farmed_lake

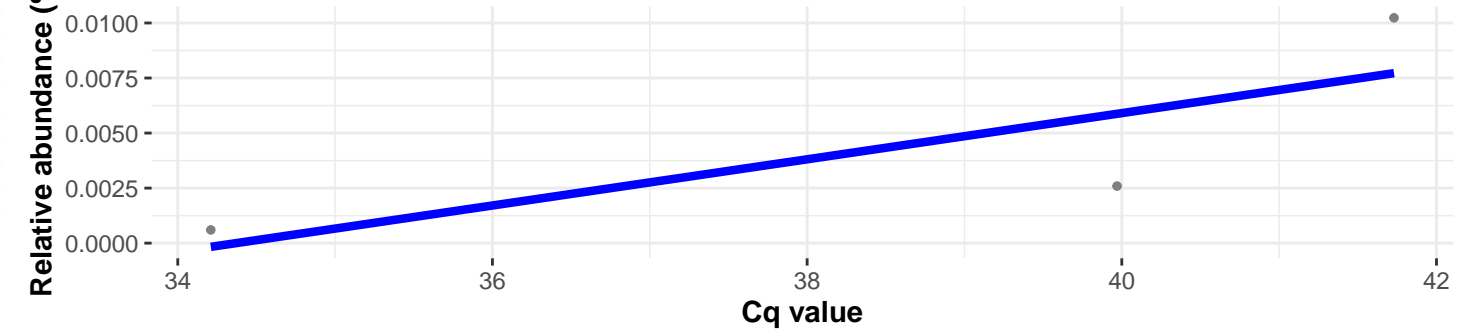
$\log_e(S) = 3.912$, $p = 0.819$, $\hat{\rho}_{\text{Spearman}} = 0.107$, $CI_{95\%} [-0.717, 0.806]$, $n_{\text{pairs}} = 7$



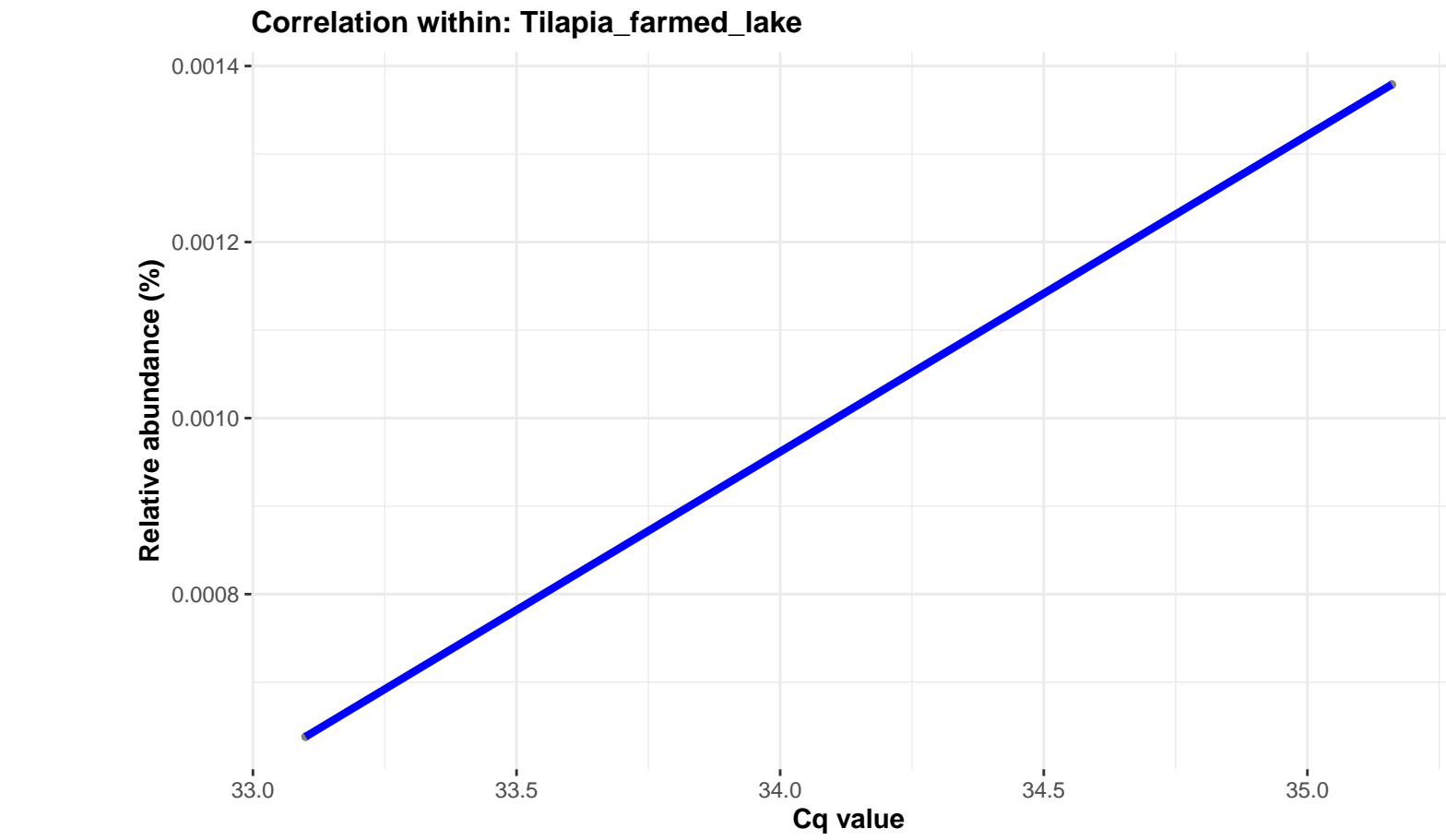
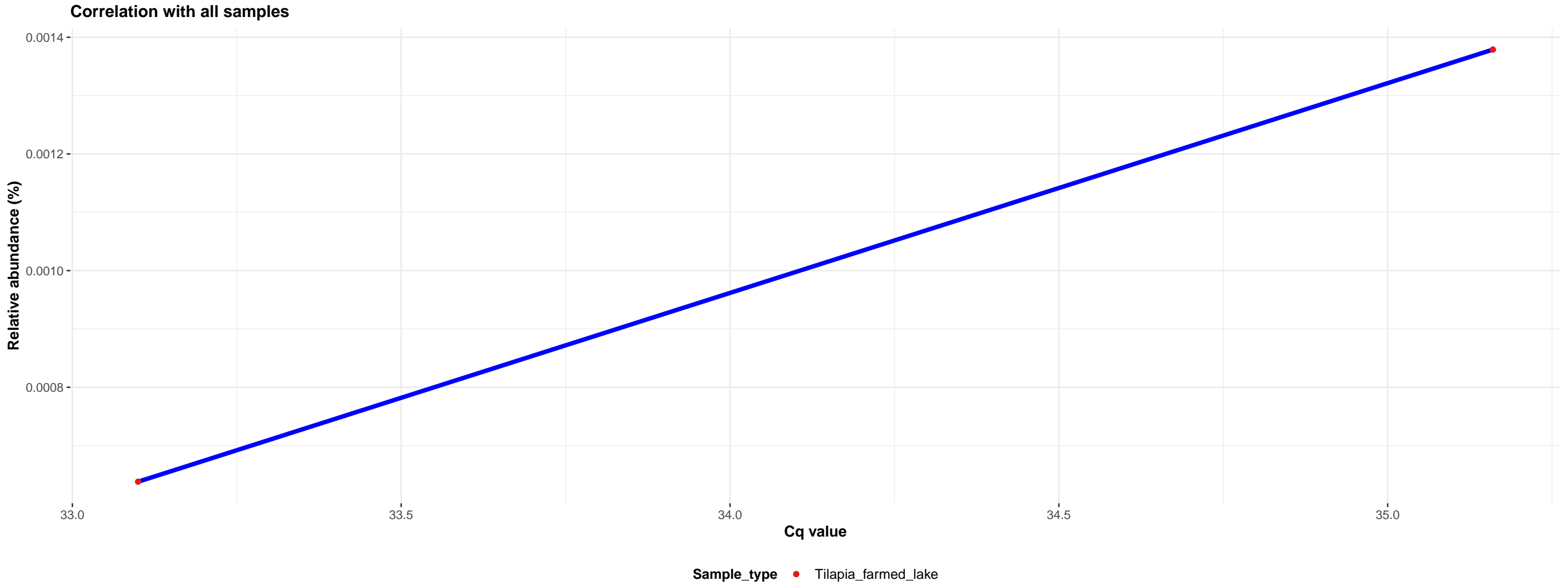
Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake



featureID: 4a7f867d55034fd3b2b4b28e0b1dda36

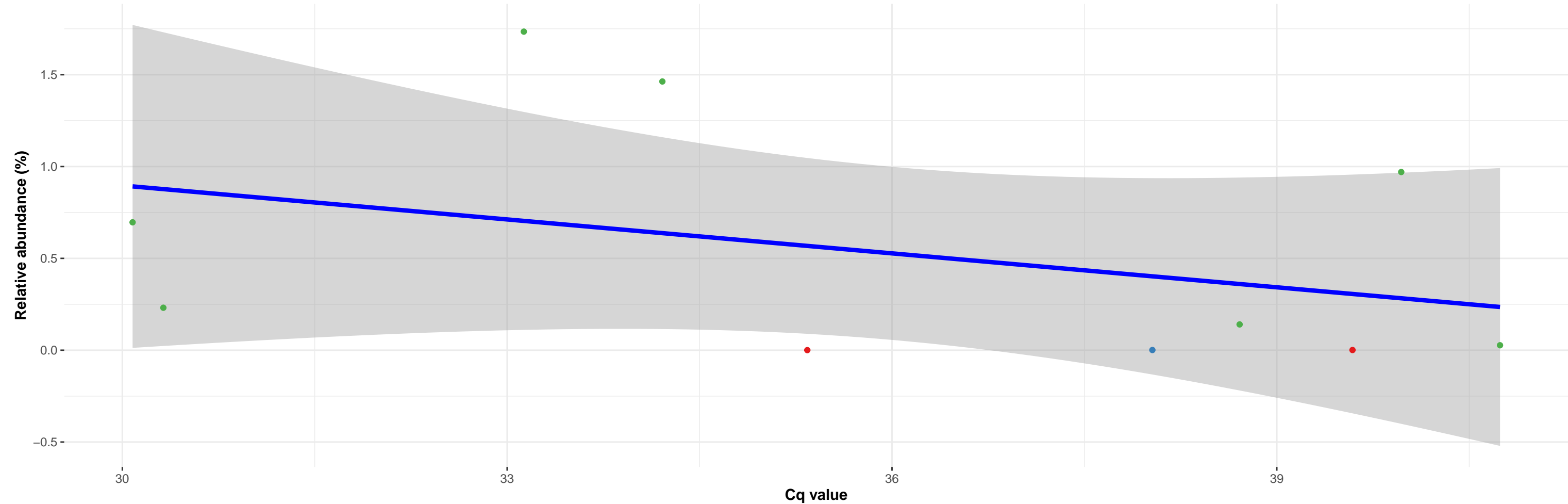


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

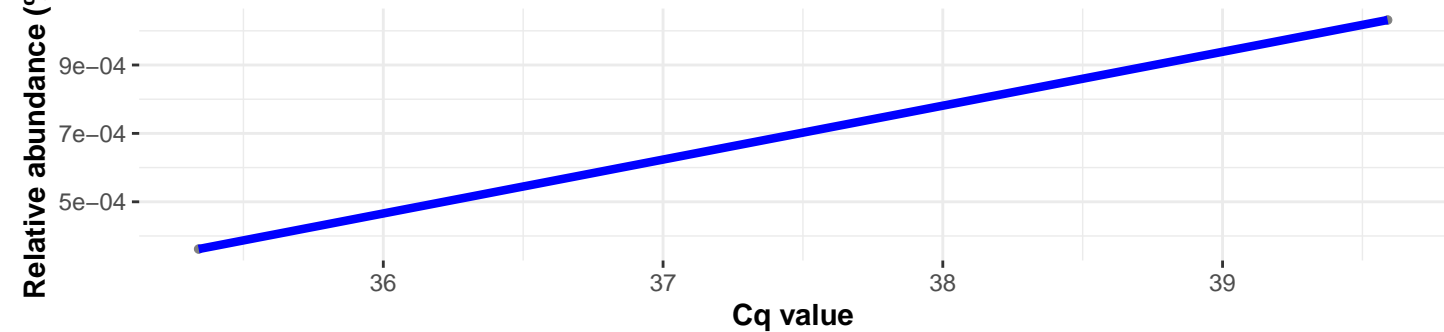
featureID: 8f6ff8174262993339a29e403091e900

Correlation with all samples

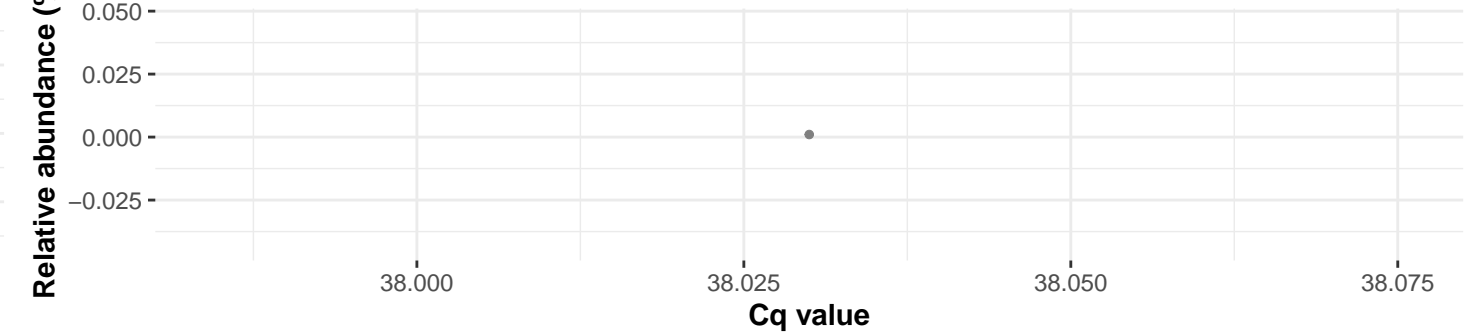
$\log_e(S) = 5.412$, $p = 0.310$, $\hat{\rho}_{\text{Spearman}} = -0.358$, $\text{CI}_{95\%} [-0.813, 0.370]$, $n_{\text{pairs}} = 10$



Correlation within: Tilapia_farmed_lake

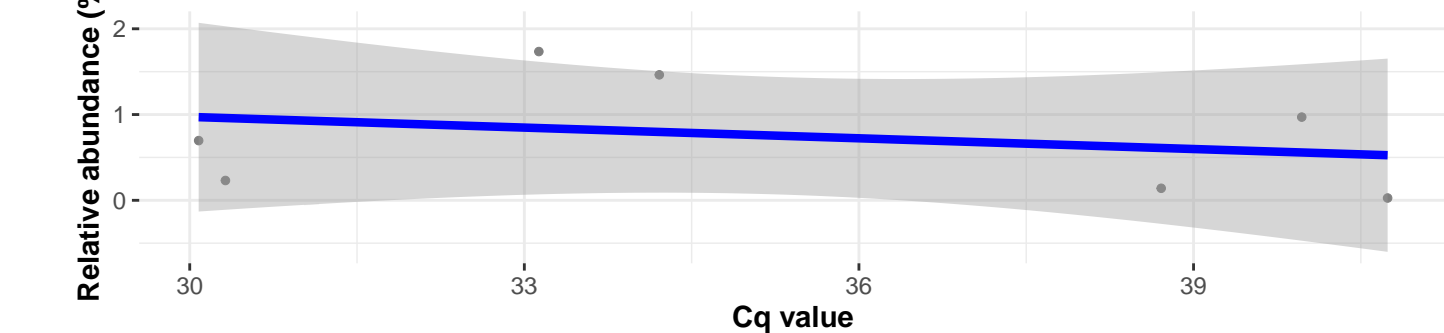


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

$\log_e(S) = 4.331$, $p = 0.432$, $\hat{\rho}_{\text{Spearman}} = -0.357$, $\text{CI}_{95\%} [-0.882, 0.562]$, $n_{\text{pairs}} = 7$

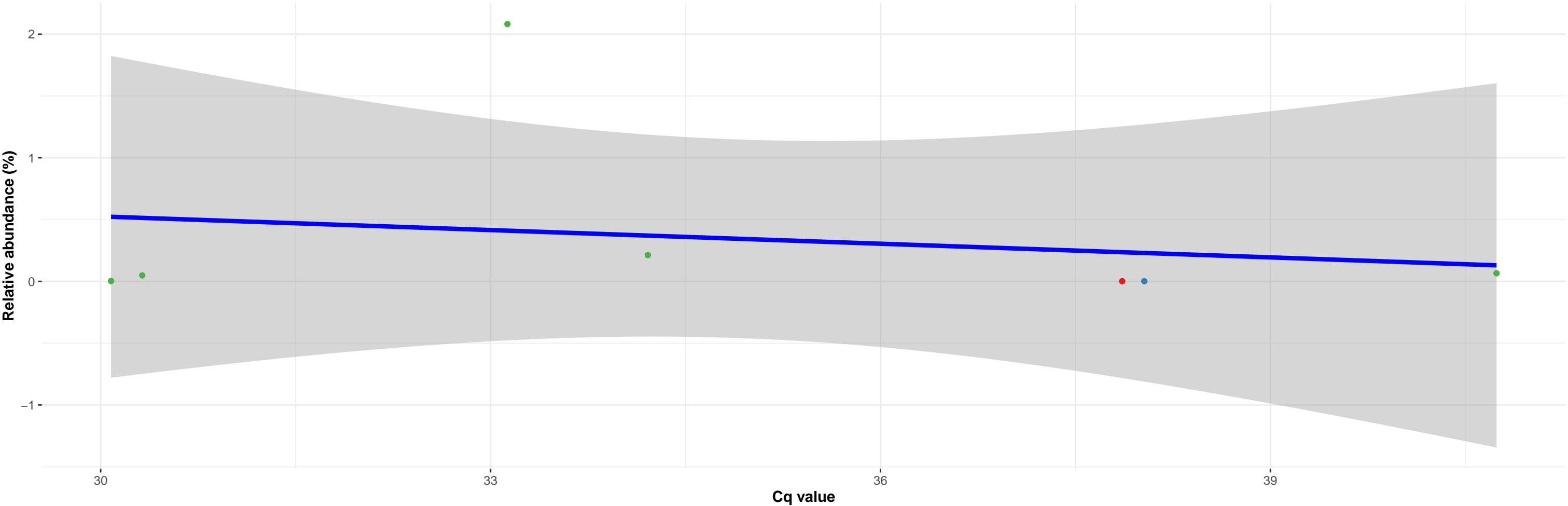


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

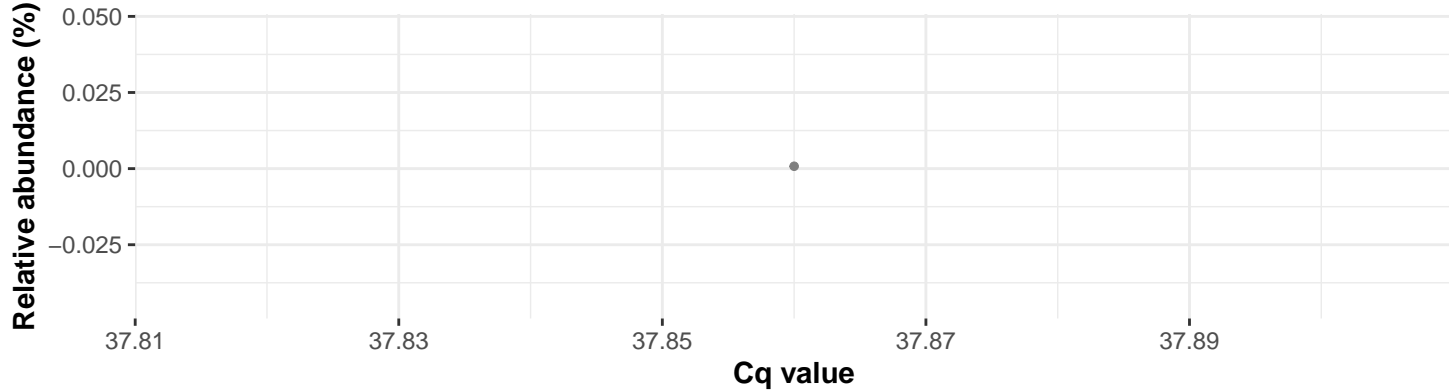
featureID: 444cb870909dcd447934e3eb70c73738

Correlation with all samples

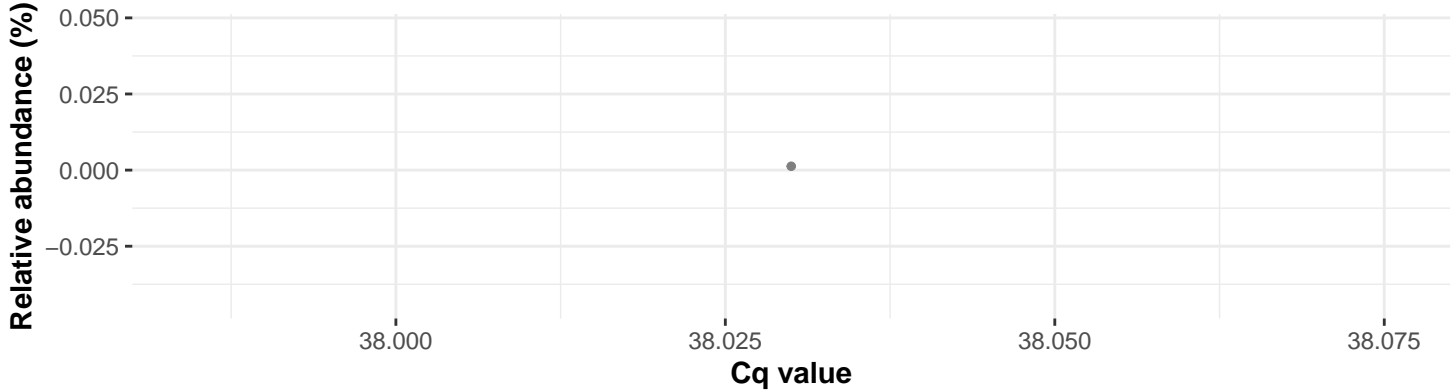
$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-0.819, 0.699]$, $n_{\text{pairs}} = 7$



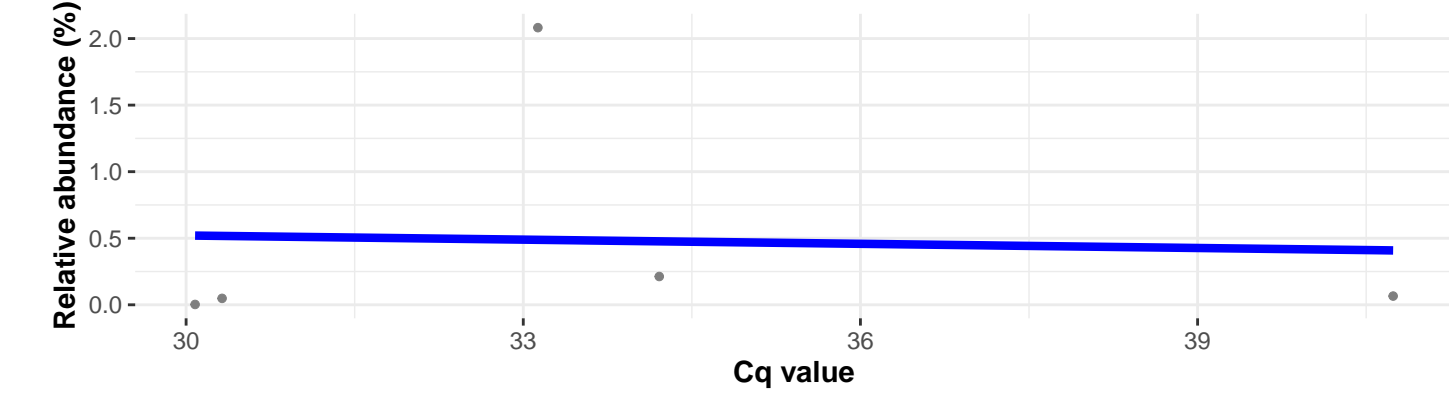
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_wild_lake



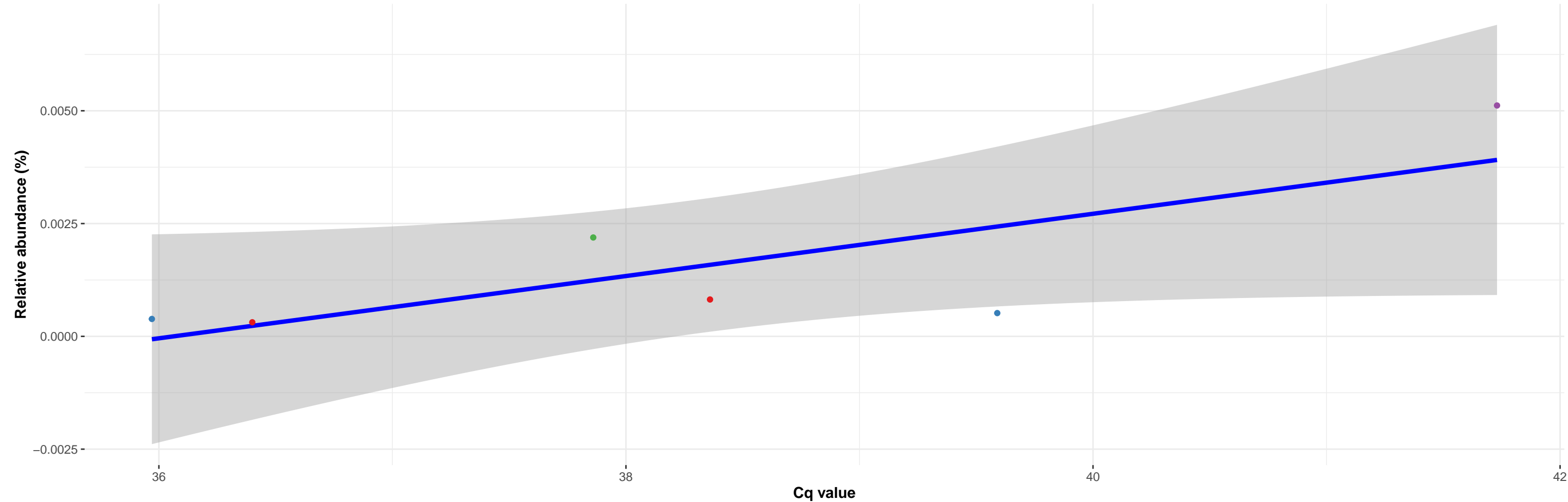
Correlation within: Perch_wild_lake



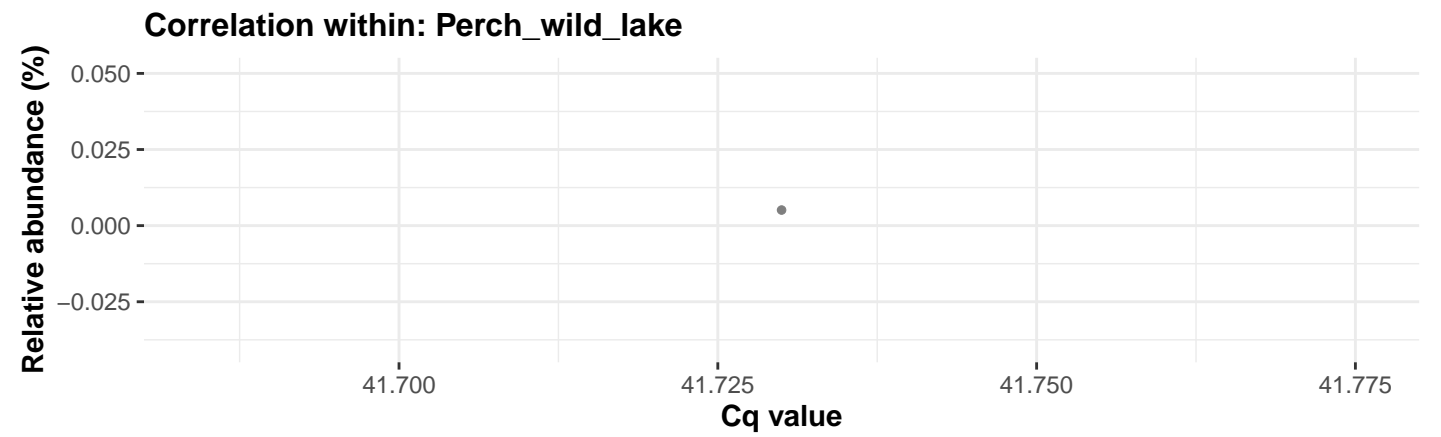
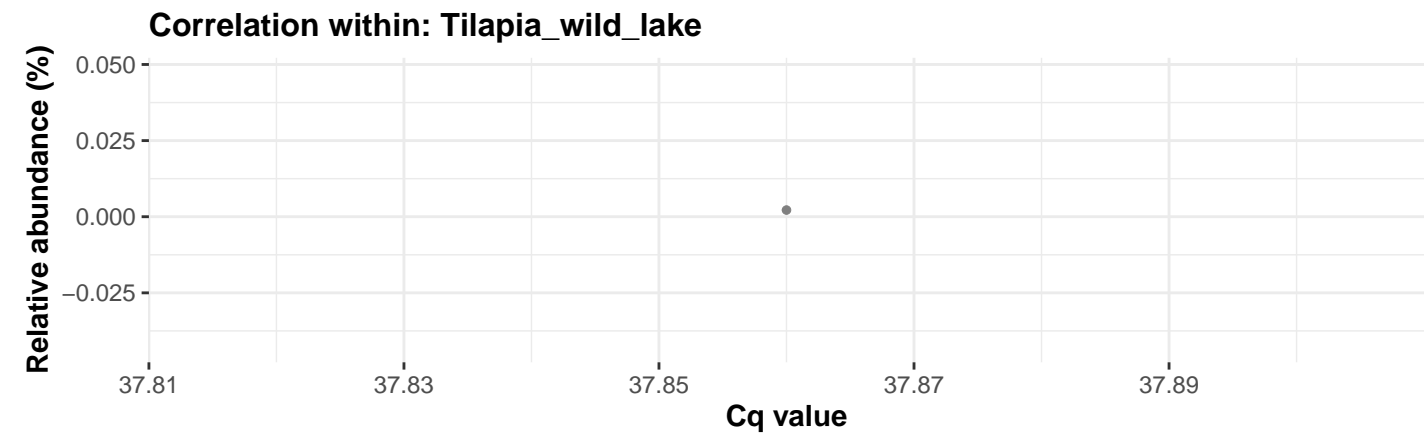
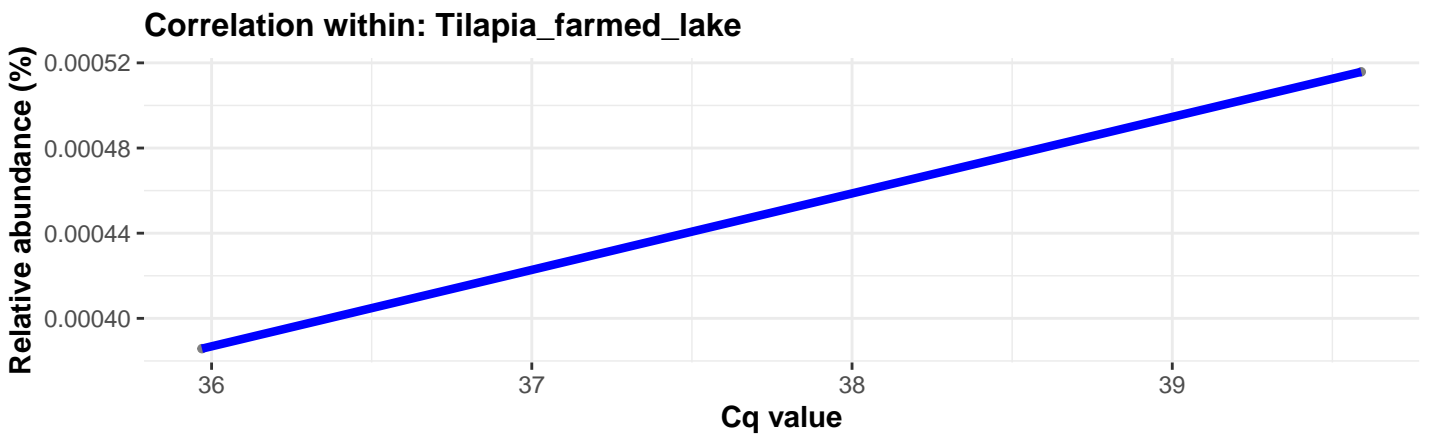
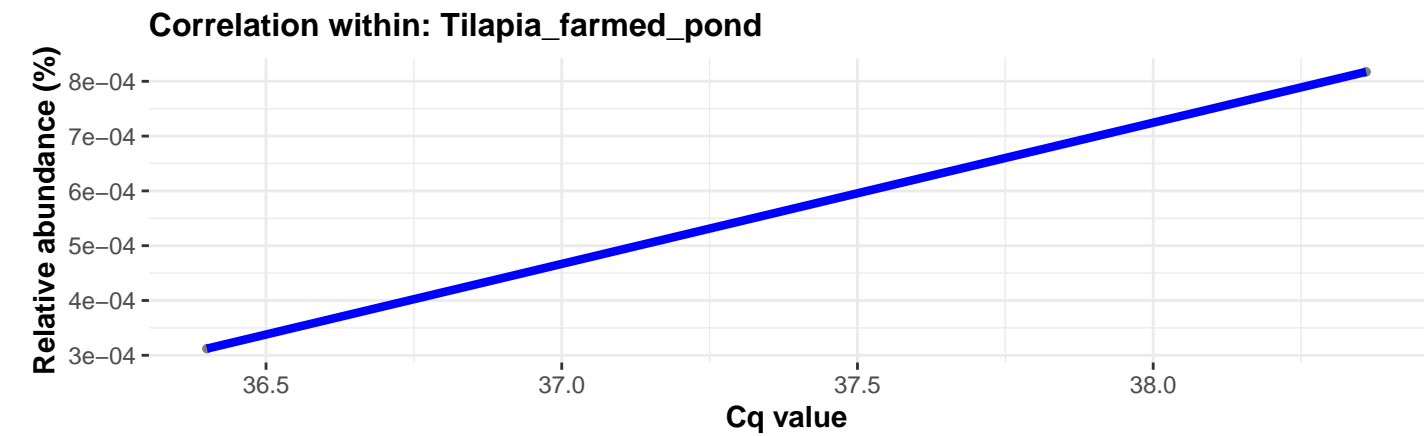
featureID: 10a4ba9050a60c9880edf695bd202b6e

Correlation with all samples

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $CI_{95\%} [-0.263, 0.968]$, $n_{\text{pairs}} = 6$

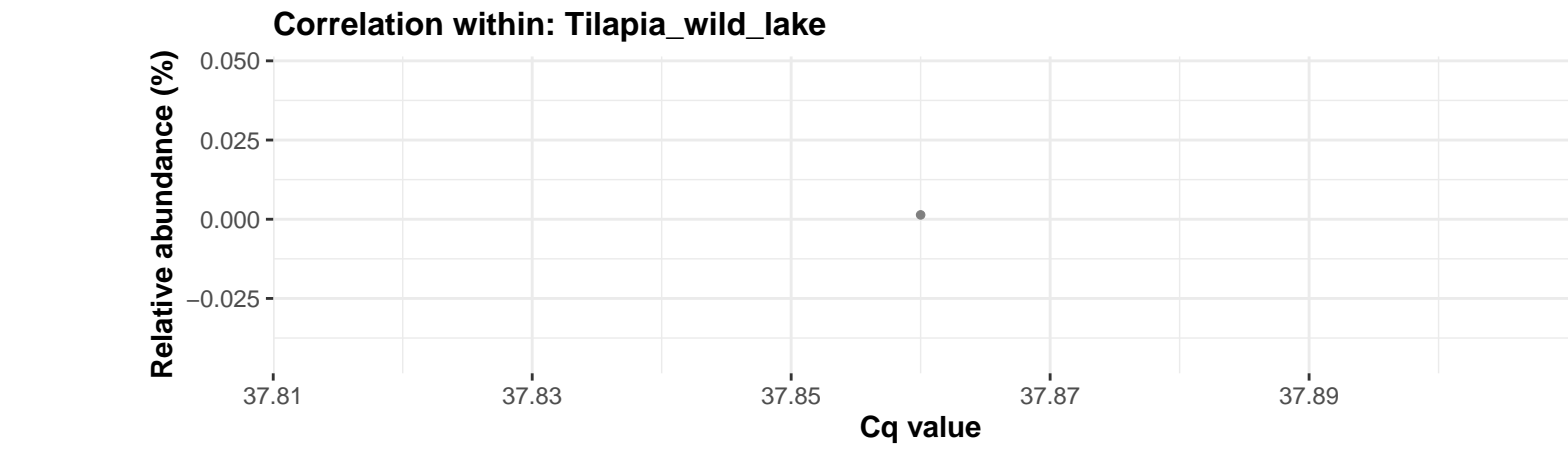
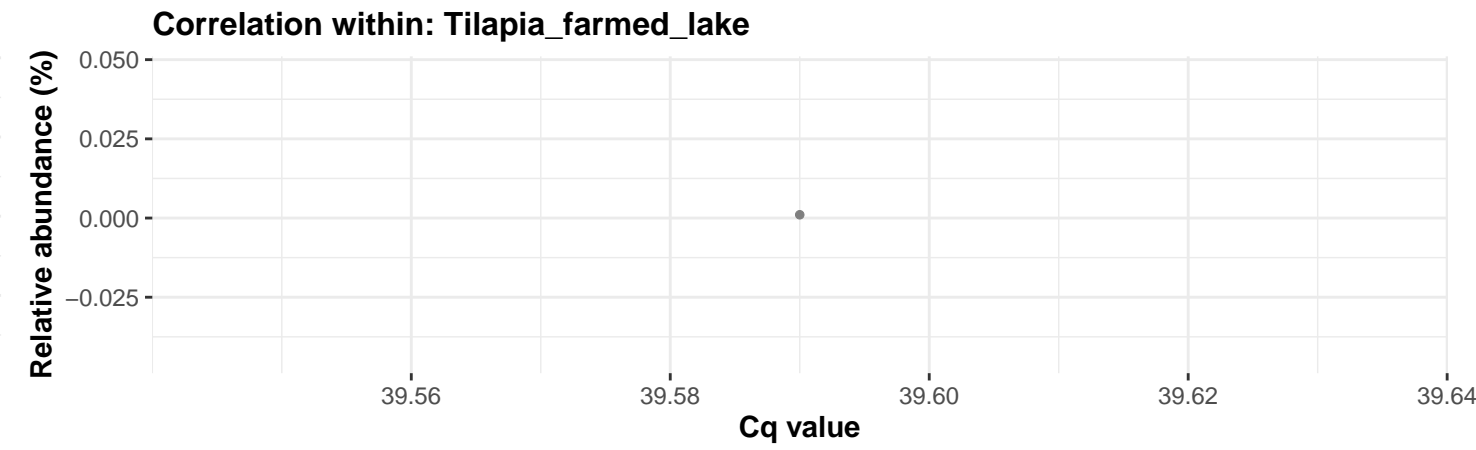
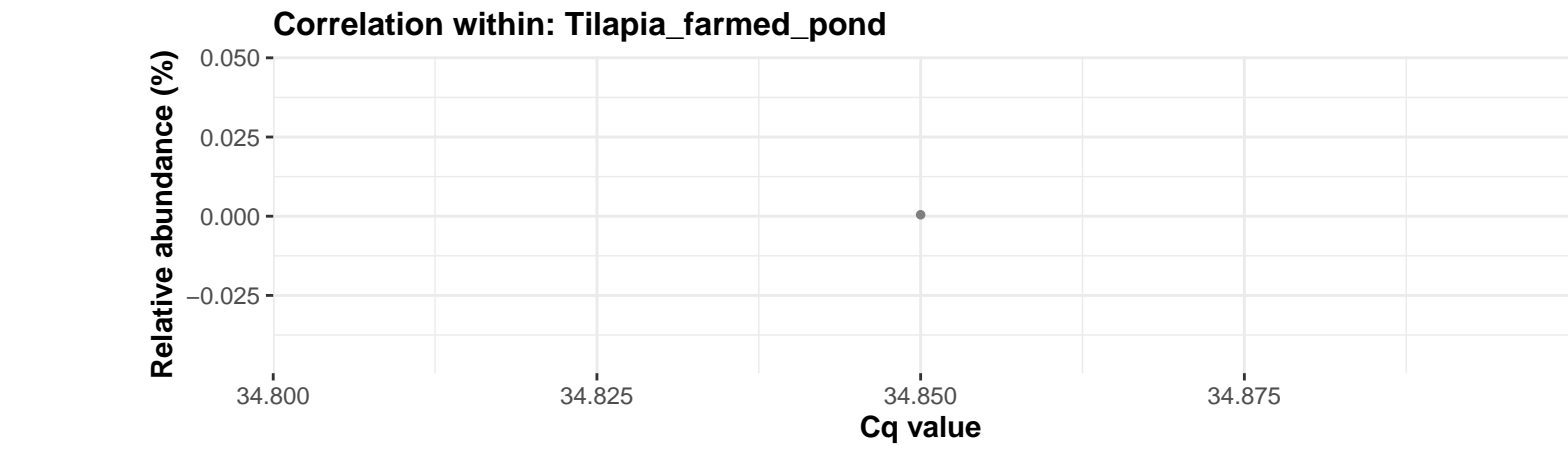
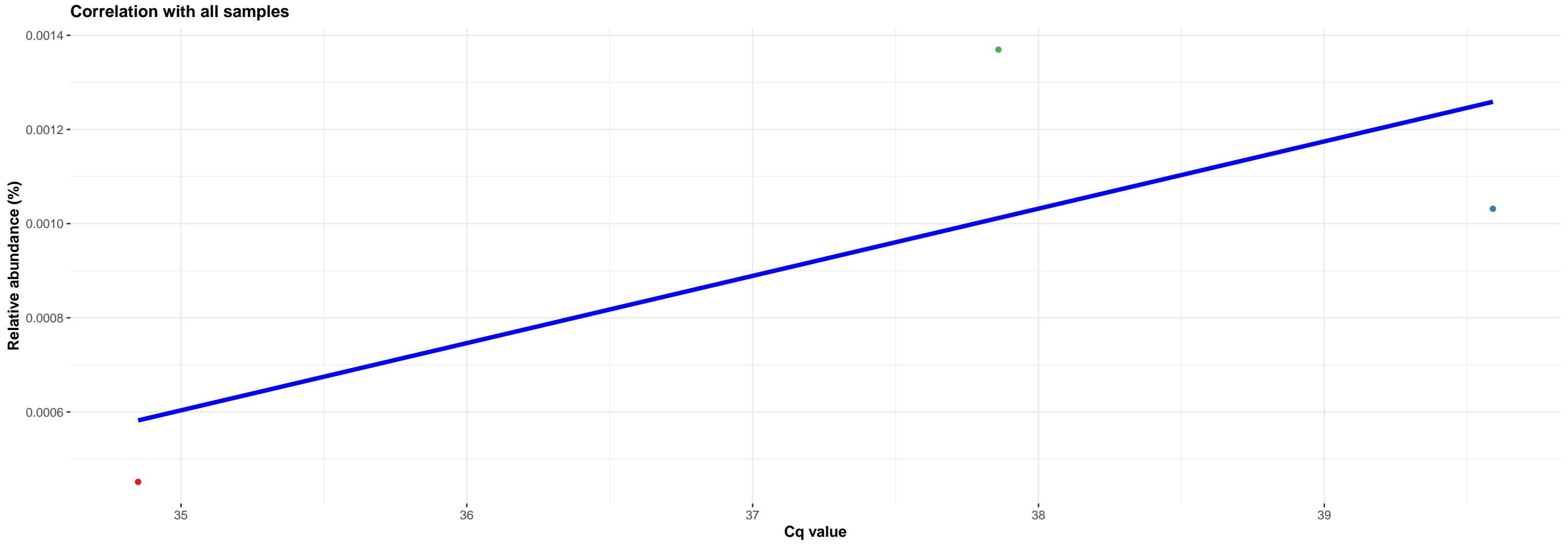


Sample_type • Tilapia_farmed_pond • Tilapia_farmed_lake • Tilapia_wild_lake • Perch_wild_lake



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Kocuria; s__Kocuria marina

featureID: 19c88c43cefc0efae399898111815666

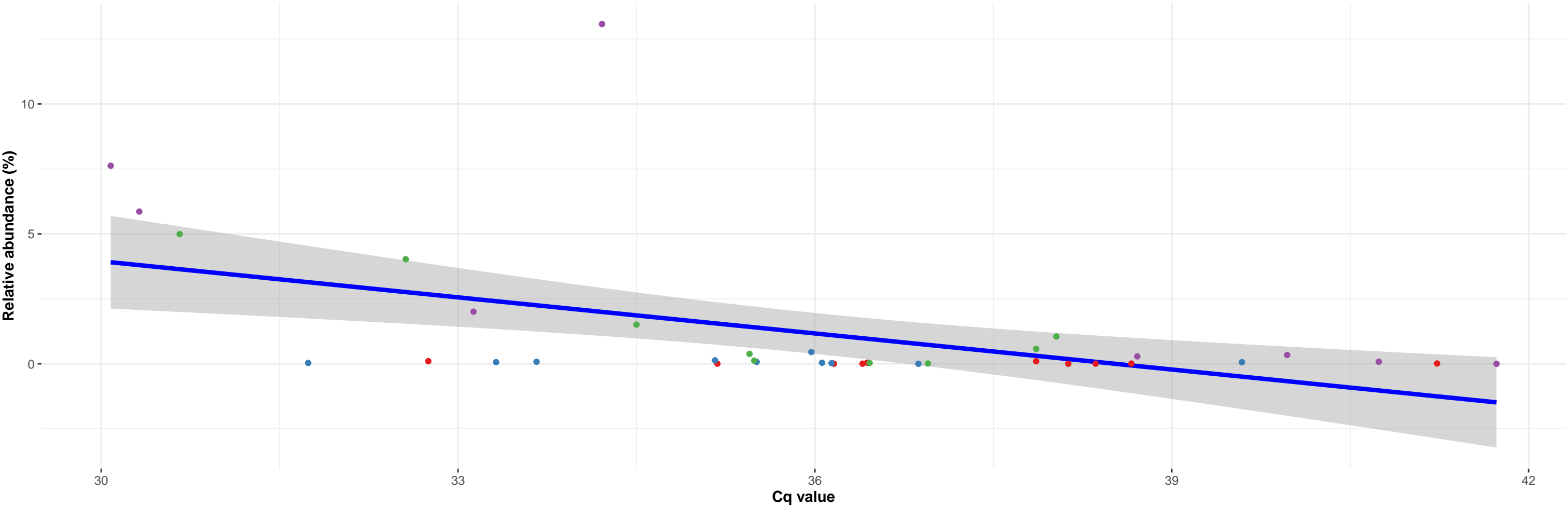


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 7438db900c870a0d550a34920b927788

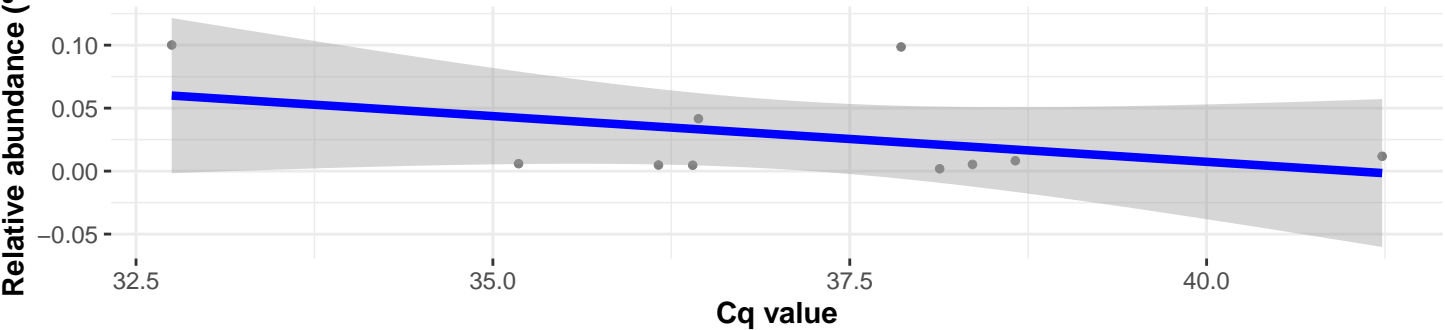
Correlation with all samples

$\log_e(S) = 9.457$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = -0.517$, $CI_{95\%} [-0.725, -0.222]$, $n_{\text{pairs}} = 37$



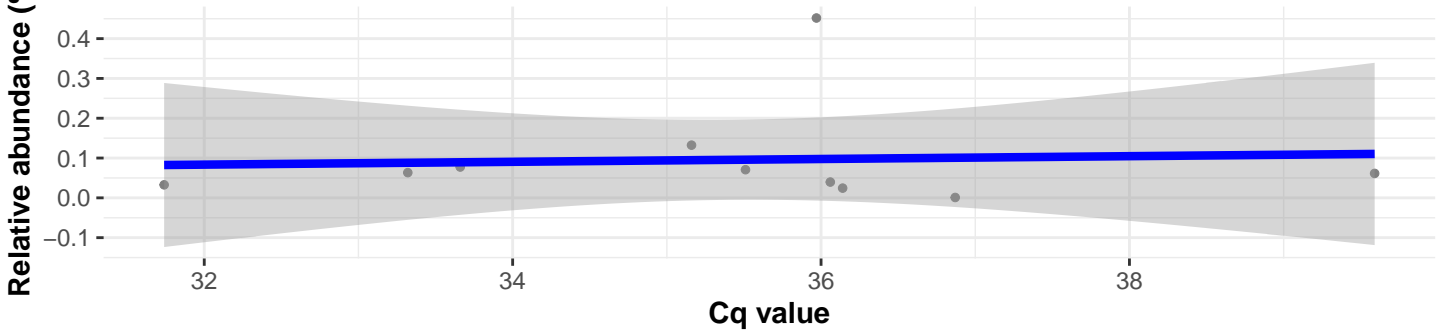
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.204$, $p = 0.777$, $\hat{\rho}_{\text{Spearman}} = -0.103$, $CI_{95\%} [-0.699, 0.578]$, $n_{\text{pairs}} = 10$



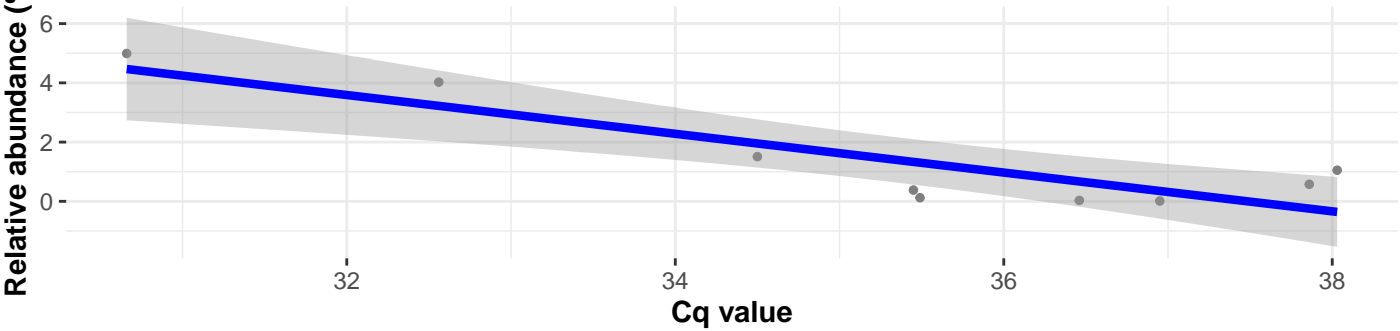
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.412$, $p = 0.310$, $\hat{\rho}_{\text{Spearman}} = -0.358$, $CI_{95\%} [-0.813, 0.370]$, $n_{\text{pairs}} = 10$



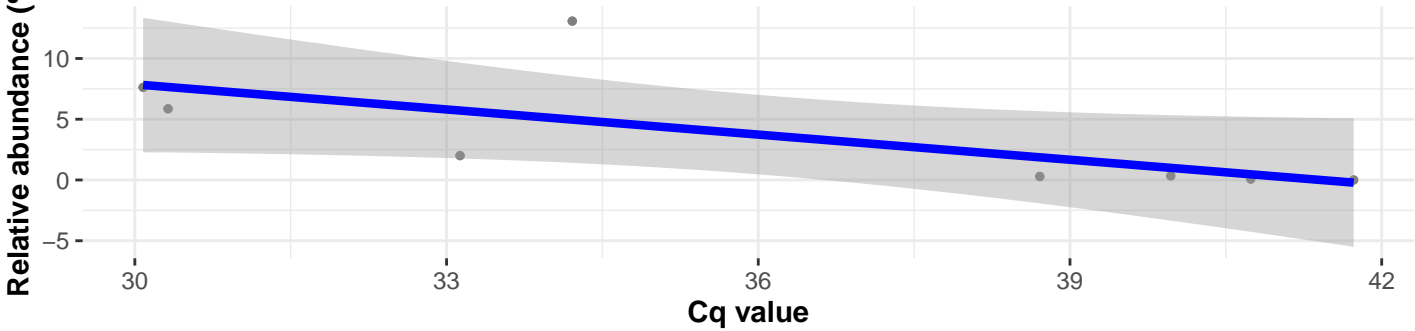
Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.247$, $p = 0.099$, $\hat{\rho}_{\text{Spearman}} = -0.583$, $CI_{95\%} [-0.904, 0.155]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

$\log_e(S) = 5.037$, $p = 0.010$, $\hat{\rho}_{\text{Spearman}} = -0.833$, $CI_{95\%} [-0.971, -0.288]$, $n_{\text{pairs}} = 8$

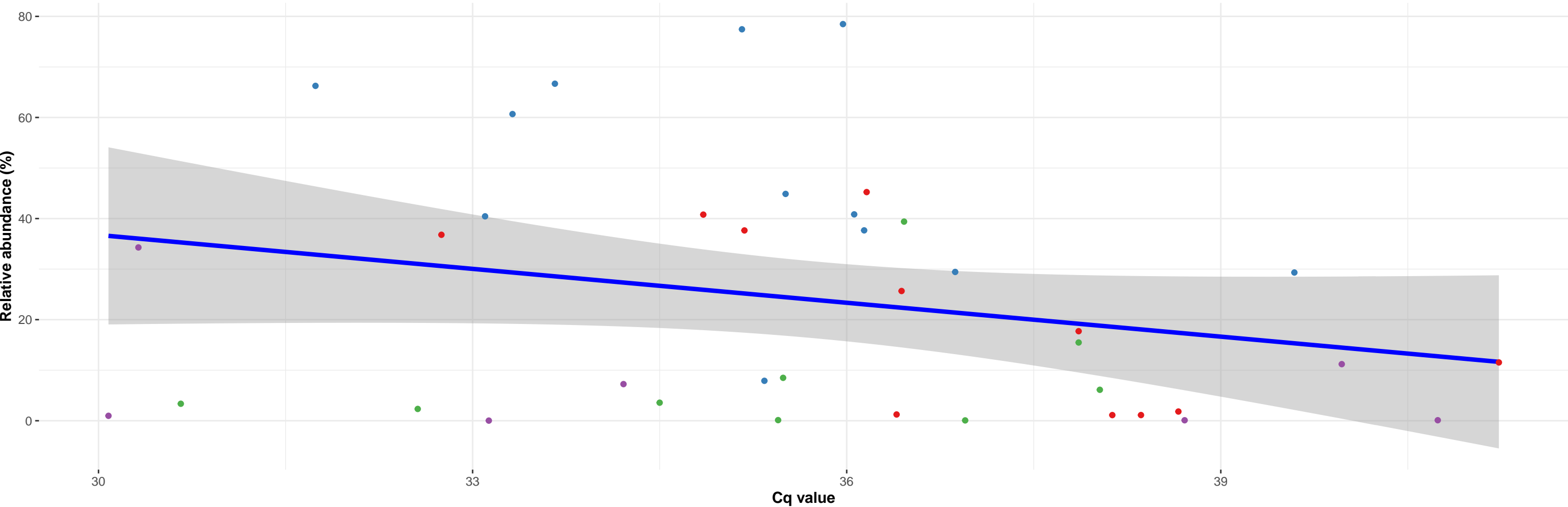


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 03f0f9af305de66090e757aaa19b09fd

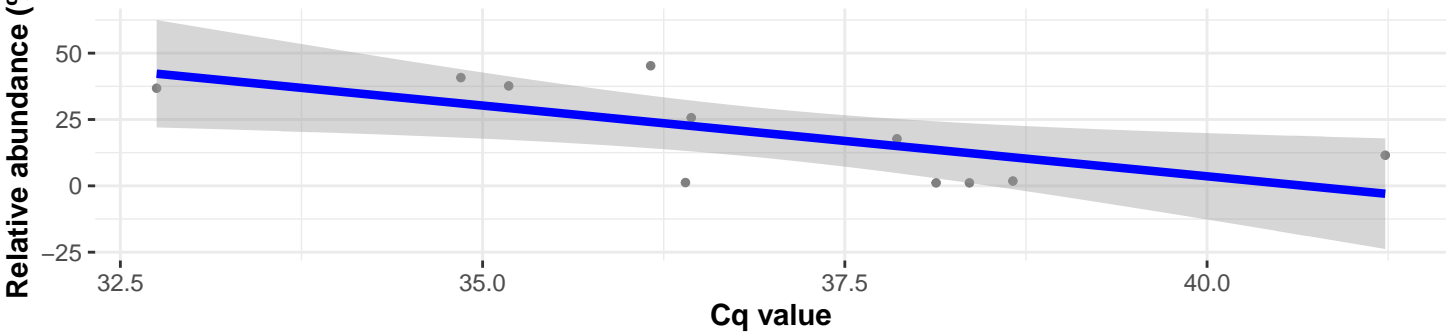
Correlation with all samples

$\log_e(S) = 9.428$, $p = 0.112$, $\hat{\rho}_{\text{Spearman}} = -0.259$, $\text{CI}_{95\%} [-0.538, 0.072]$, $n_{\text{pairs}} = 39$



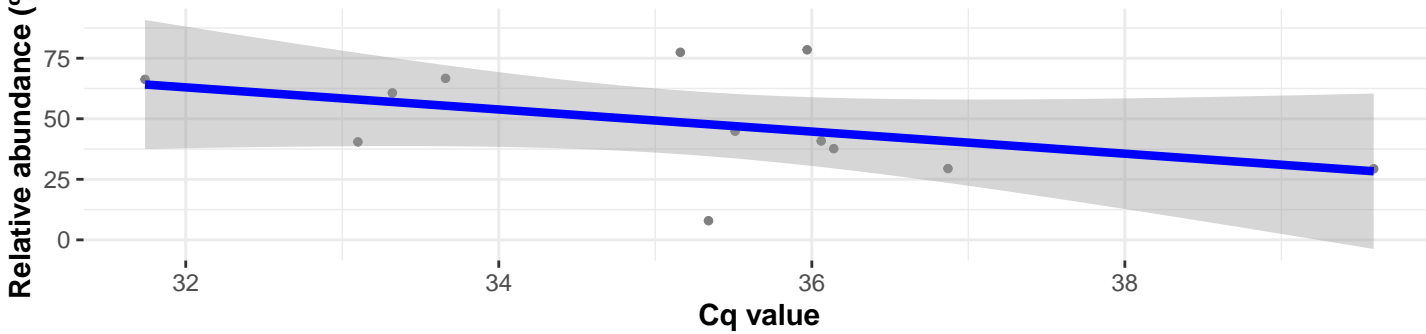
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.924$, $p = 0.016$, $\hat{\rho}_{\text{Spearman}} = -0.700$, $\text{CI}_{95\%} [-0.919, -0.153]$, $n_{\text{pairs}} = 11$



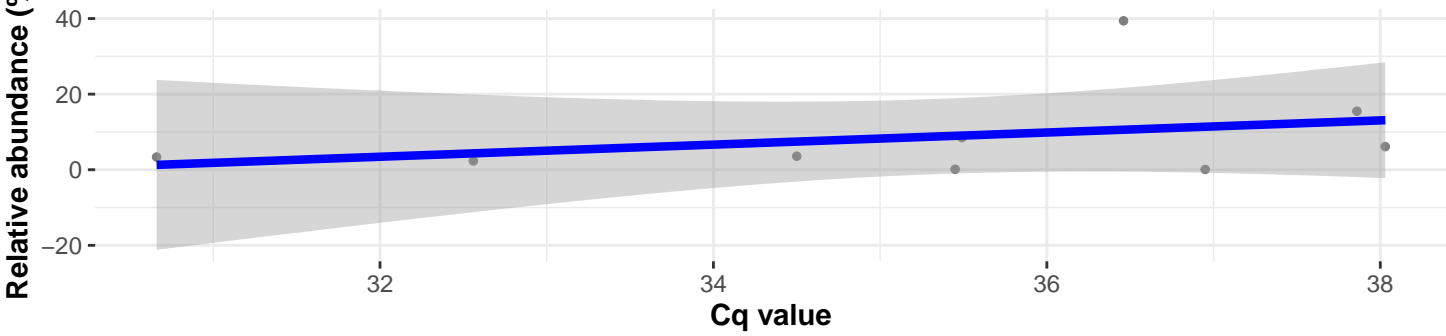
Correlation within: Tilapia_farmed_lake

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



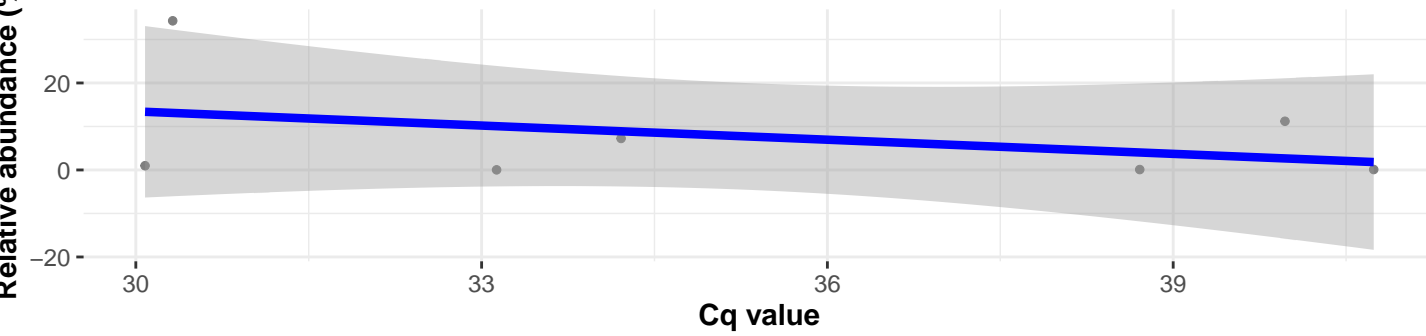
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.331$, $p = 0.332$, $\hat{\rho}_{\text{Spearman}} = 0.367$, $\text{CI}_{95\%} [-0.413, 0.836]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-0.819, 0.699]$, $n_{\text{pairs}} = 7$

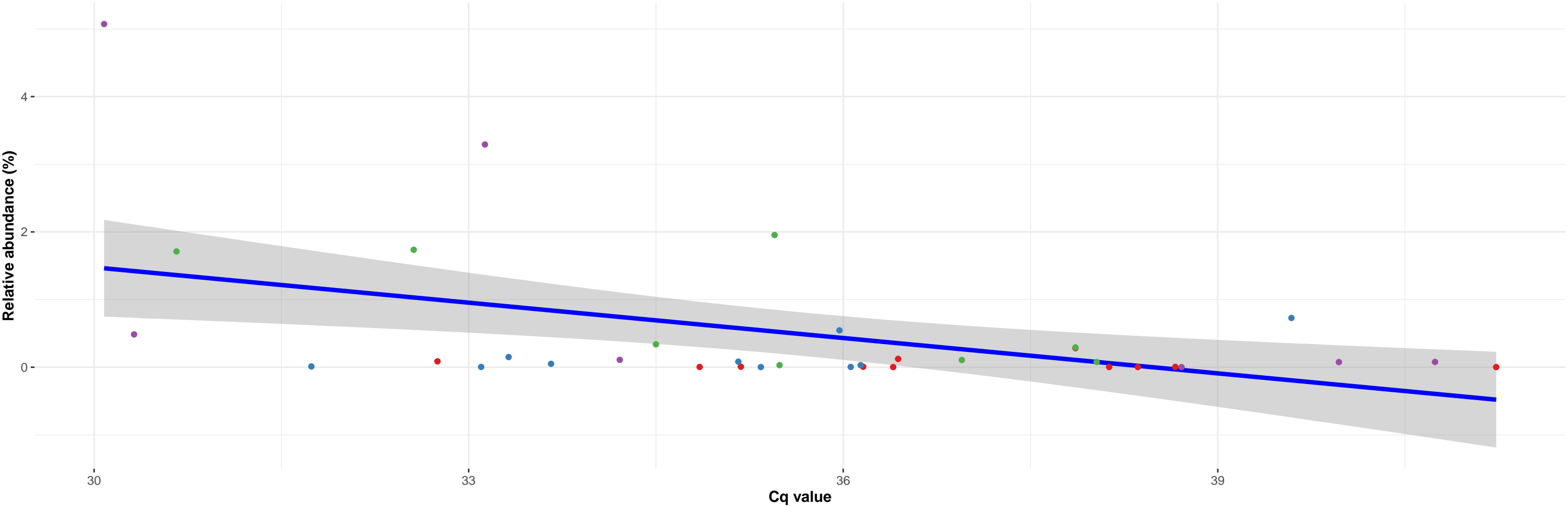


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paraclostridium; NA

featureID: f4b4dbd070c3296a6040e51b1e2aacfa

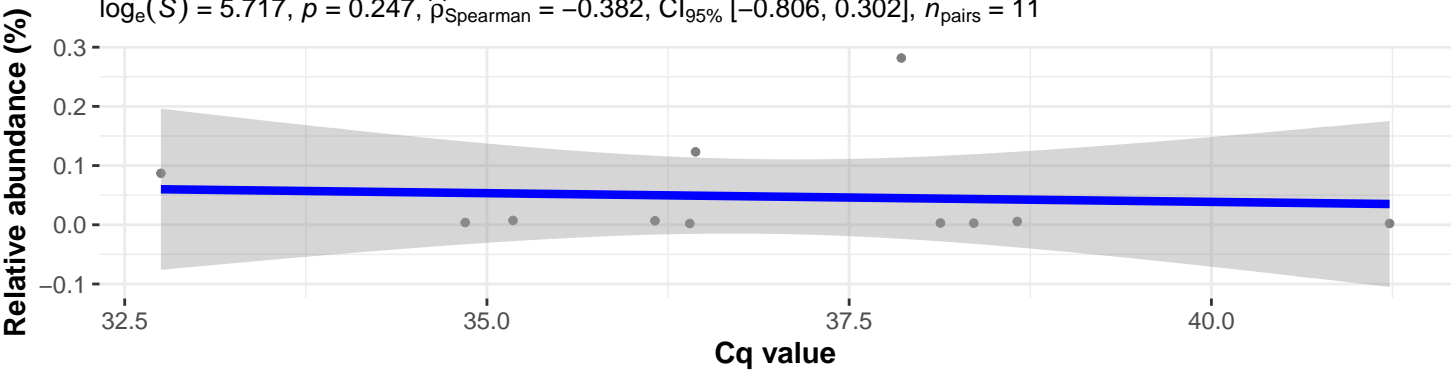
Correlation with all samples

$\log_e(S) = 9.307$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.417$, $\text{CI}_{95\%} [-0.662, -0.093]$, $n_{\text{pairs}} = 36$



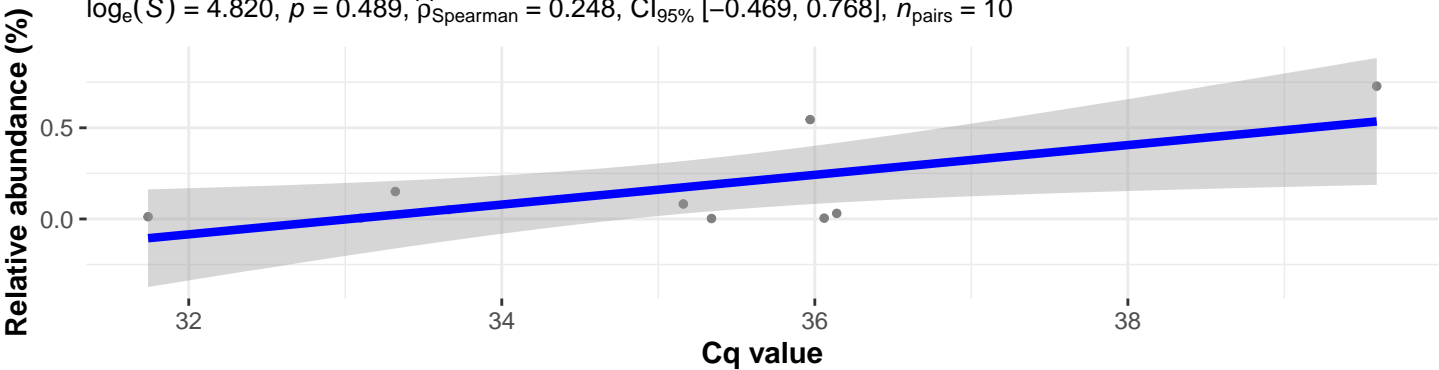
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.717$, $p = 0.247$, $\hat{\rho}_{\text{Spearman}} = -0.382$, $\text{CI}_{95\%} [-0.806, 0.302]$, $n_{\text{pairs}} = 11$



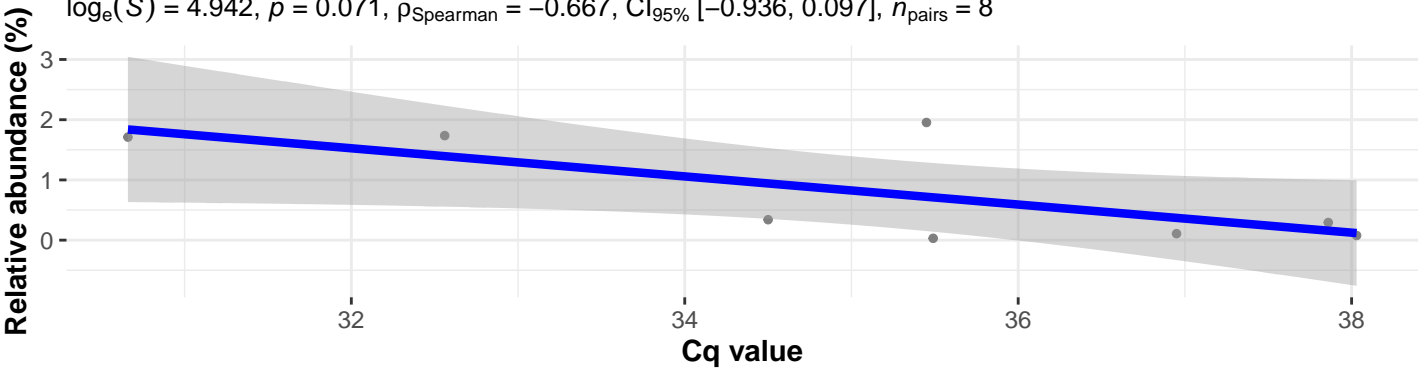
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 4.820$, $p = 0.489$, $\hat{\rho}_{\text{Spearman}} = 0.248$, $\text{CI}_{95\%} [-0.469, 0.768]$, $n_{\text{pairs}} = 10$



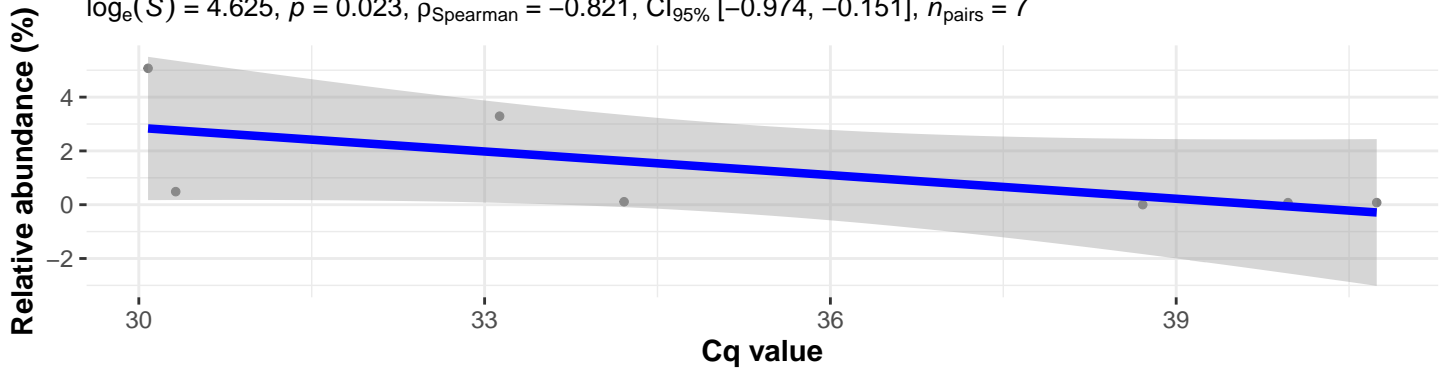
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.942$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = -0.667$, $\text{CI}_{95\%} [-0.936, 0.097]$, $n_{\text{pairs}} = 8$



Correlation within: Perch_wild_lake

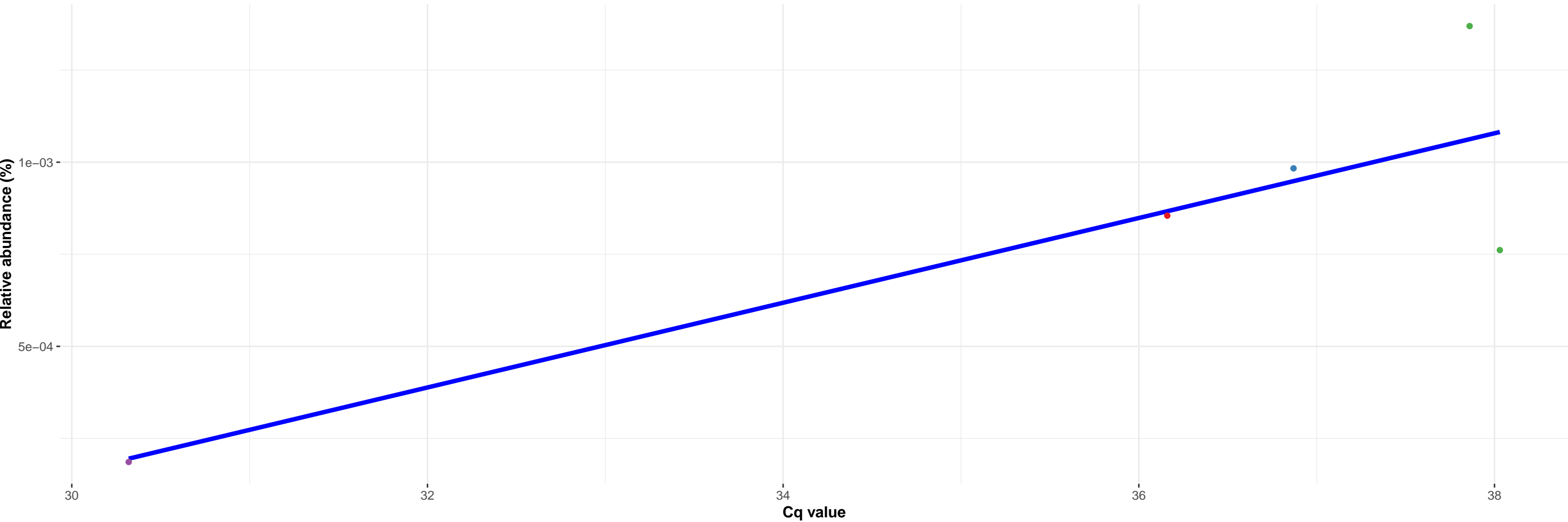
$\log_e(S) = 4.625$, $p = 0.023$, $\hat{\rho}_{\text{Spearman}} = -0.821$, $\text{CI}_{95\%} [-0.974, -0.151]$, $n_{\text{pairs}} = 7$



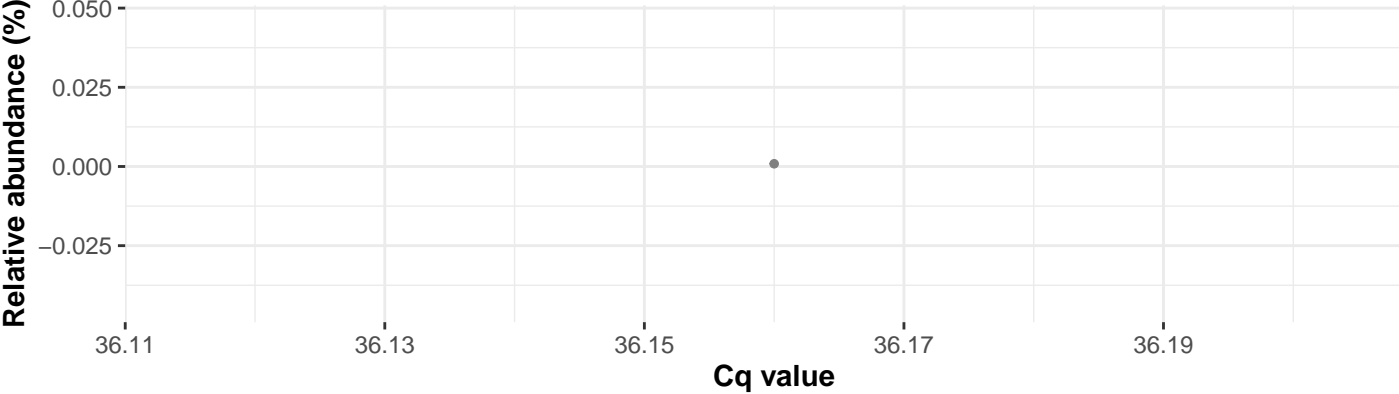
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

featureID: fadf78bc47e055f59328c8f565155ea5

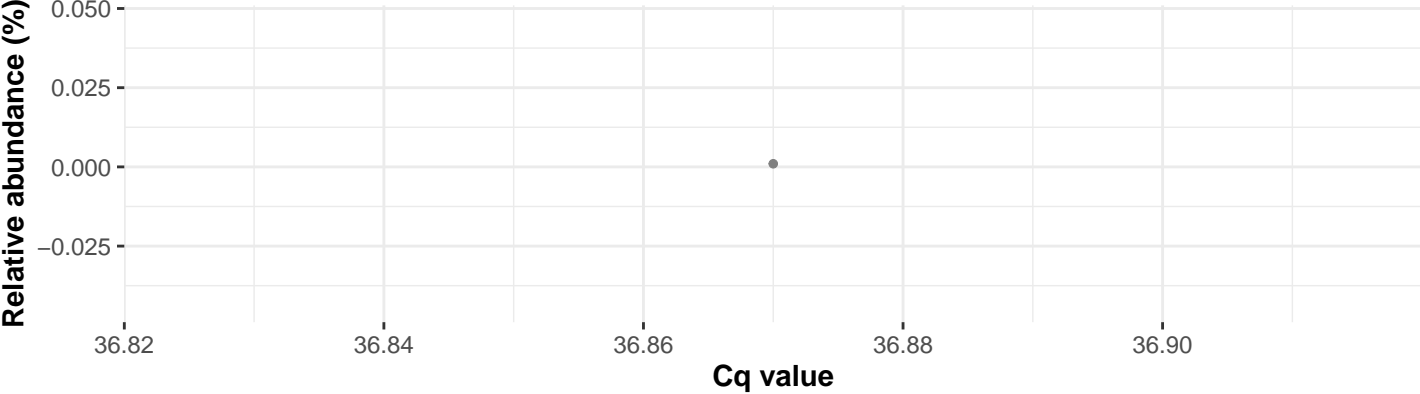
Correlation with all samples



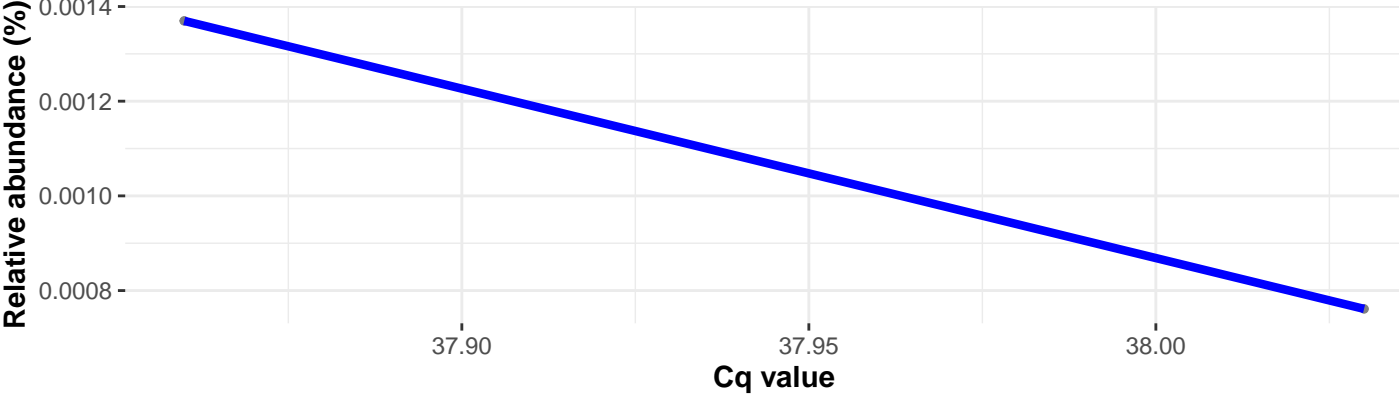
Correlation within: Tilapia_farmed_pond



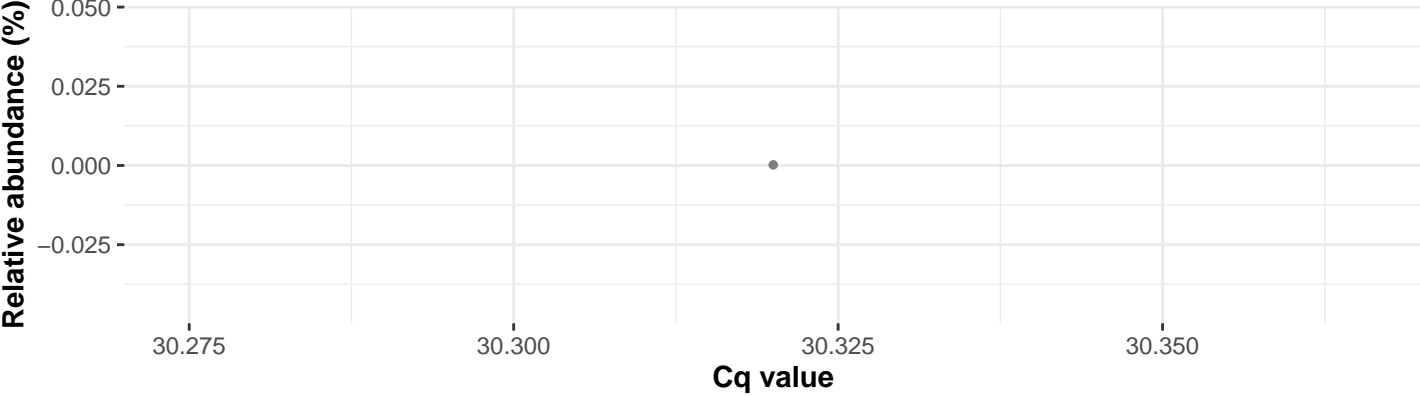
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

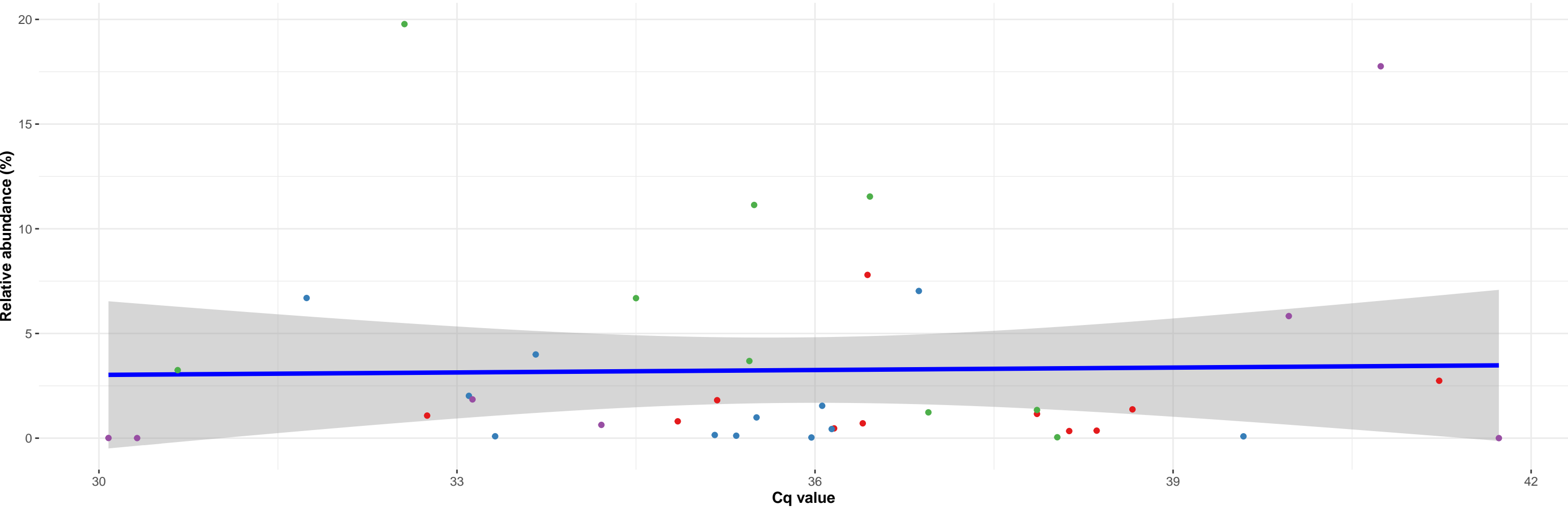


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Romboutsia; NA

featureID: efa98c673cef7e11e51b27d01167c2af

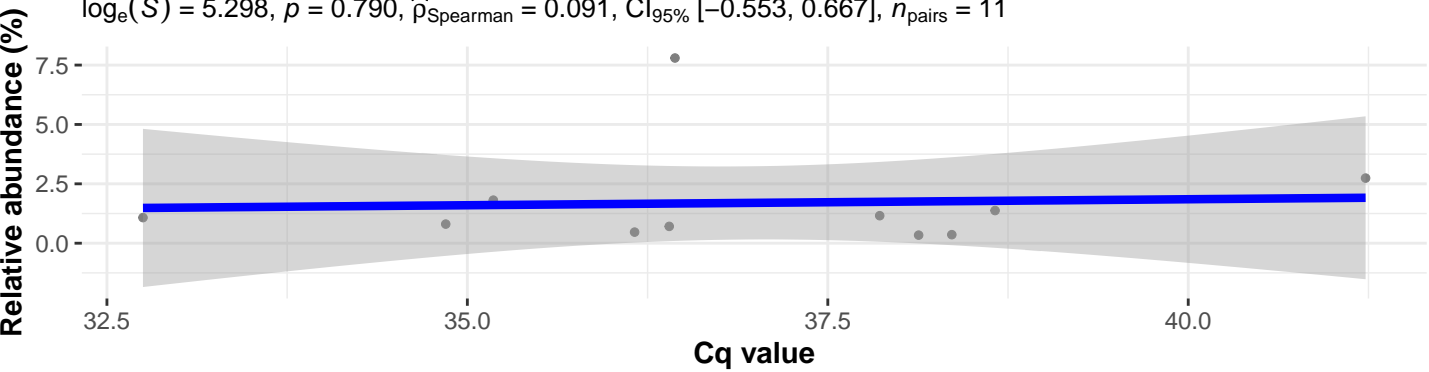
Correlation with all samples

$\log_e(S) = 9.226$, $p = 0.863$, $\hat{\rho}_{\text{Spearman}} = -0.029$, $CI_{95\%} [-0.349, 0.298]$, $n_{\text{pairs}} = 39$



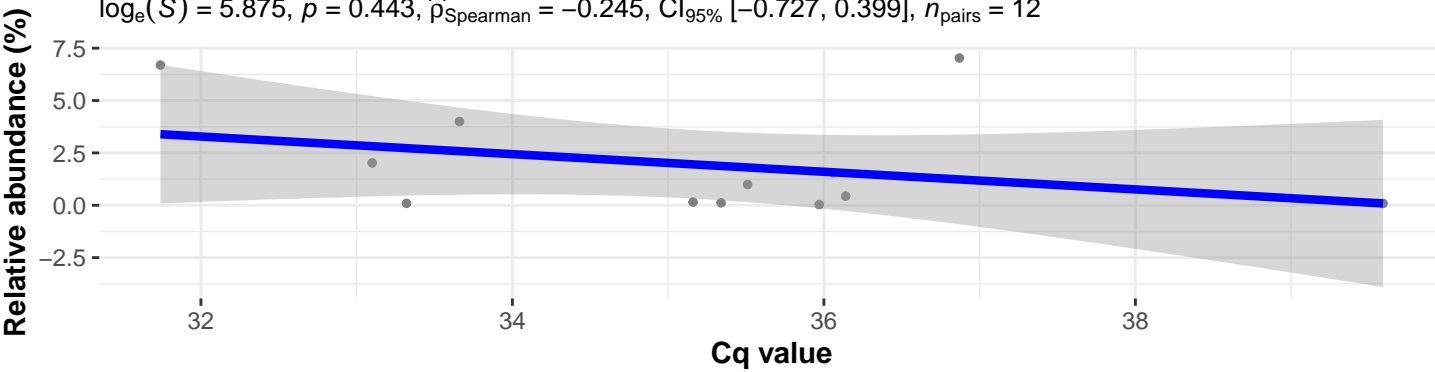
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.298$, $p = 0.790$, $\hat{\rho}_{\text{Spearman}} = 0.091$, $CI_{95\%} [-0.553, 0.667]$, $n_{\text{pairs}} = 11$



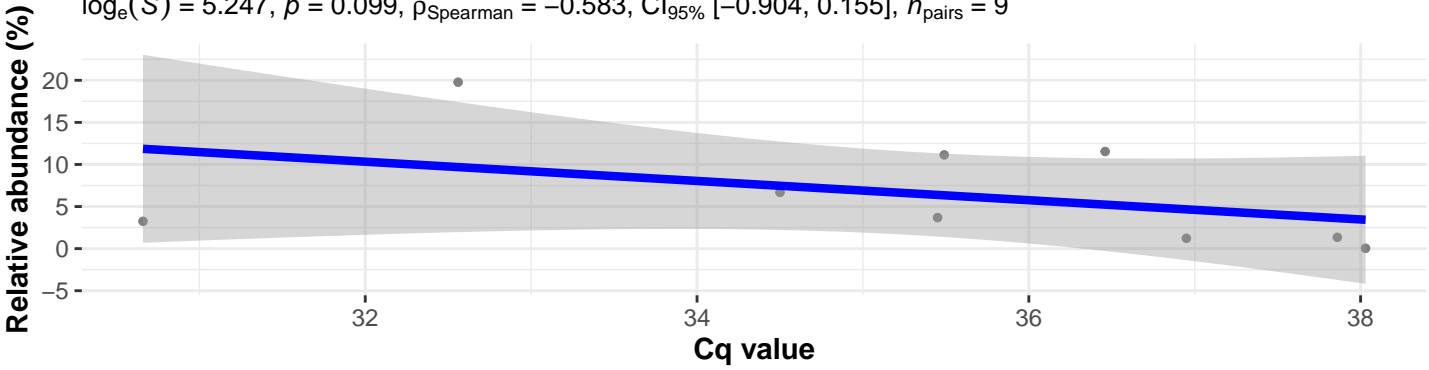
Correlation within: Tilapia_farmed_lake

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



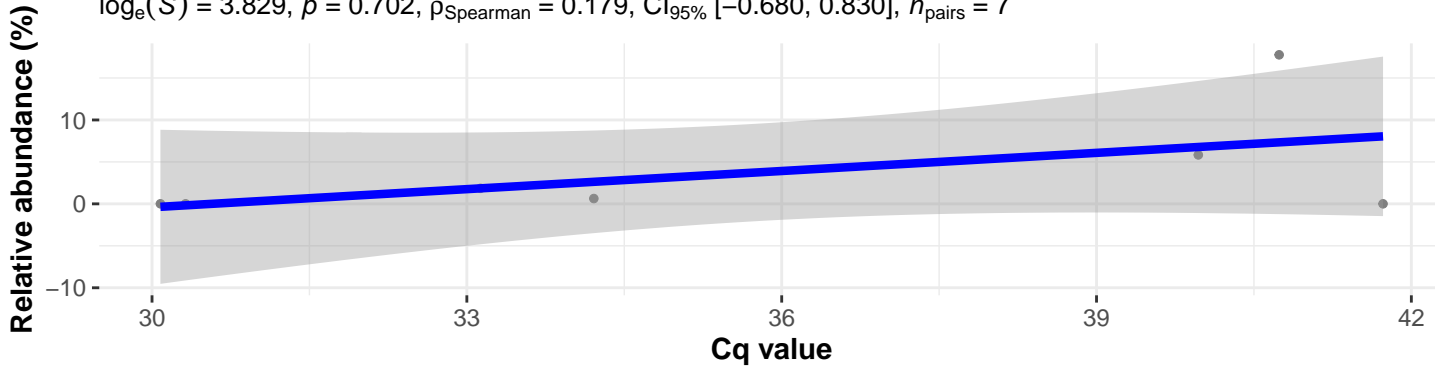
Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.247$, $p = 0.099$, $\hat{\rho}_{\text{Spearman}} = -0.583$, $CI_{95\%} [-0.904, 0.155]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

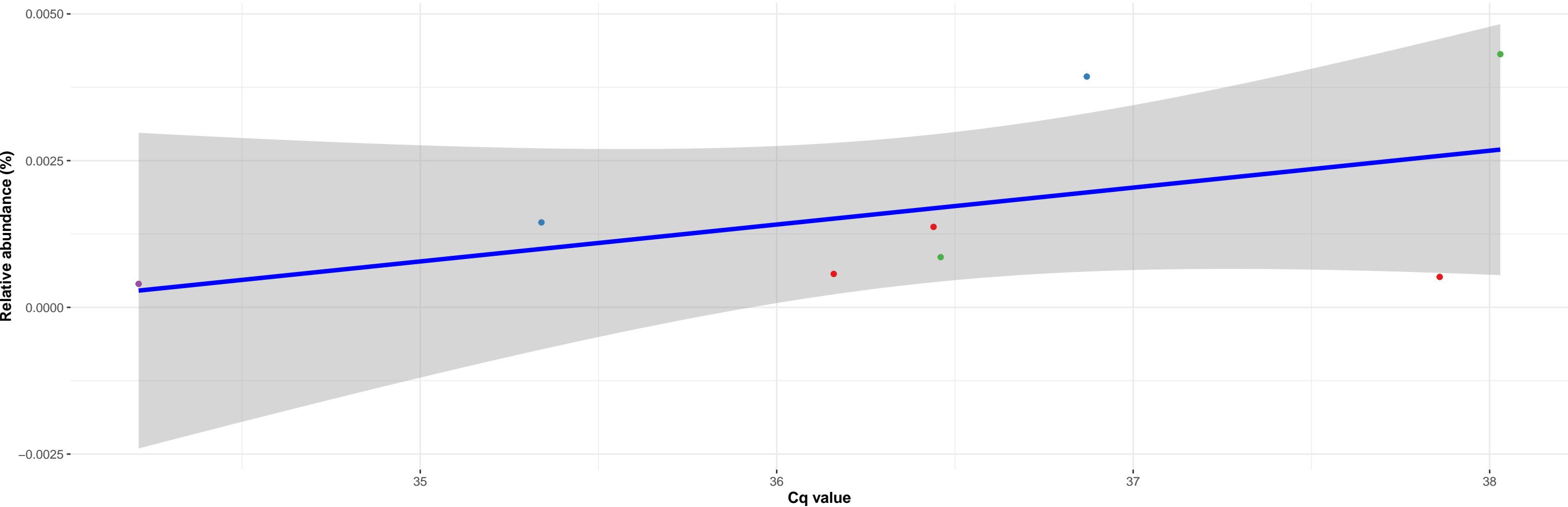
$\log_e(S) = 3.829$, $p = 0.702$, $\hat{\rho}_{\text{Spearman}} = 0.179$, $CI_{95\%} [-0.680, 0.830]$, $n_{\text{pairs}} = 7$



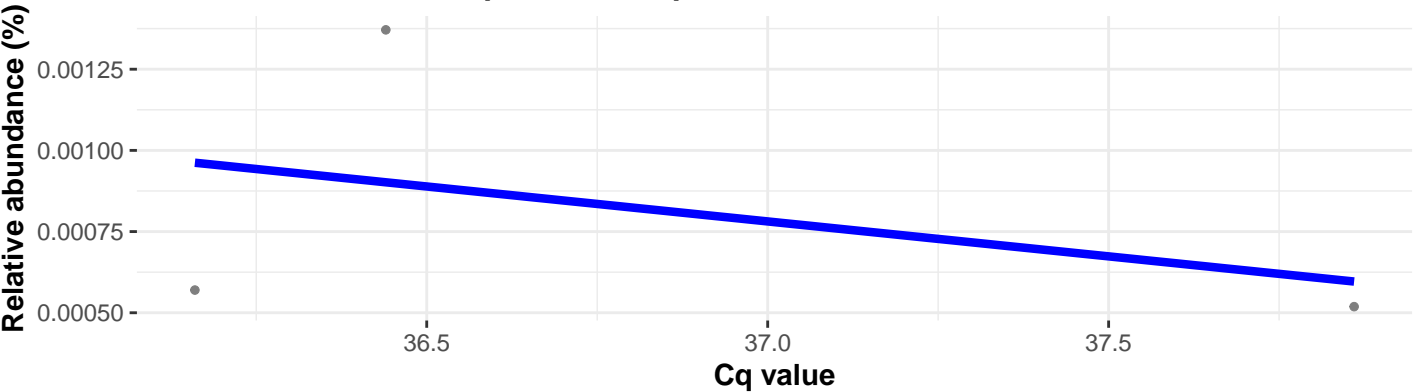
featureID: 7f46b7ea18aa6ed4244429796401c660

Correlation with all samples

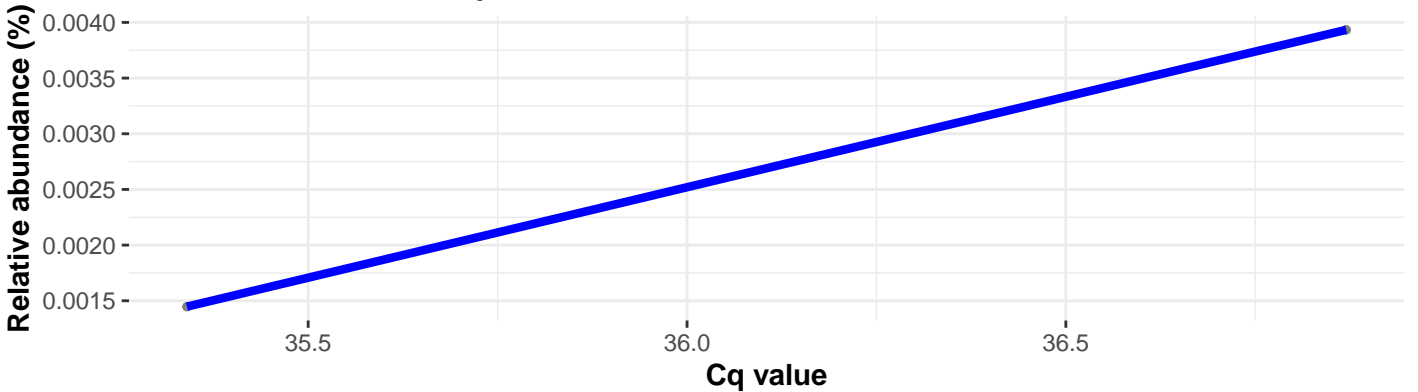
$\log_e(S) = 3.784$, $p = 0.233$, $\hat{\rho}_{\text{Spearman}} = 0.476$, $CI_{95\%} [-0.367, 0.890]$, $n_{\text{pairs}} = 8$



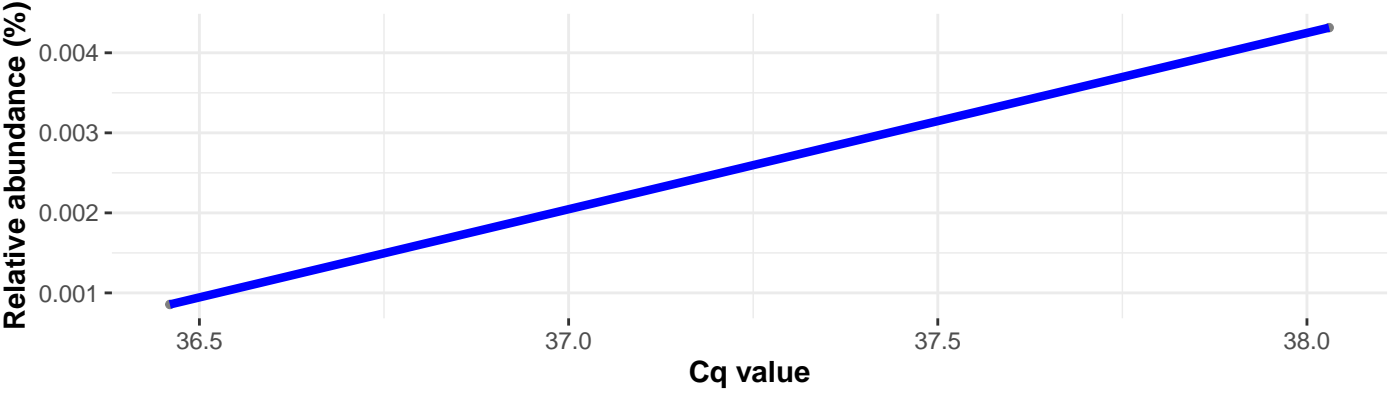
Correlation within: Tilapia_farmed_pond



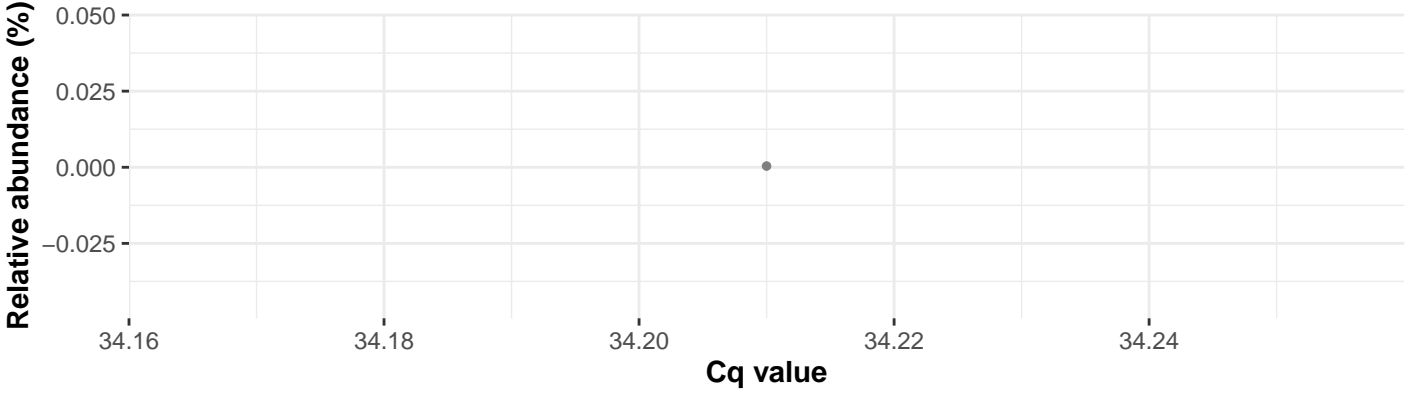
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

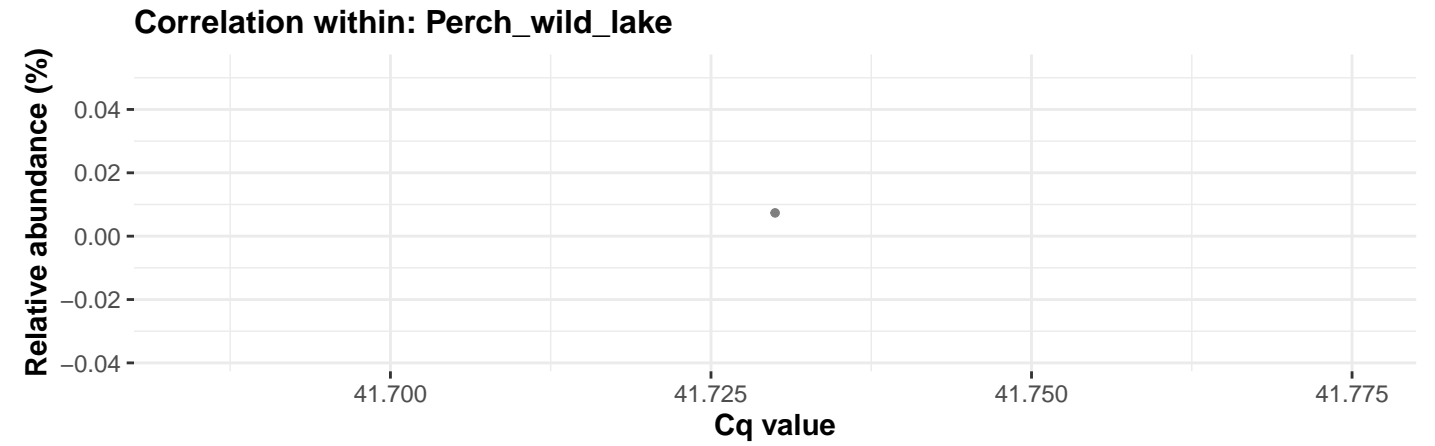
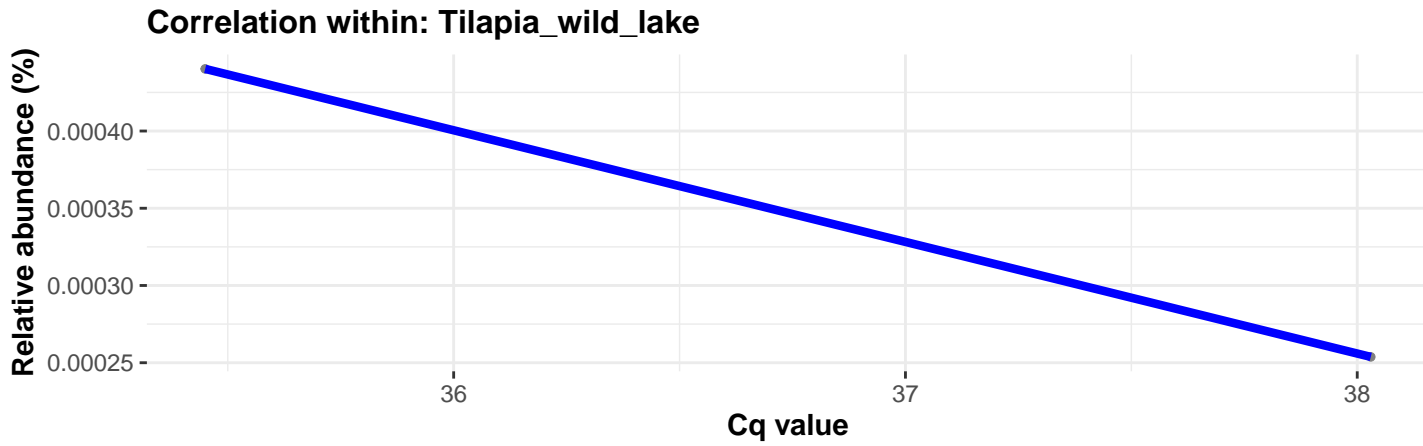
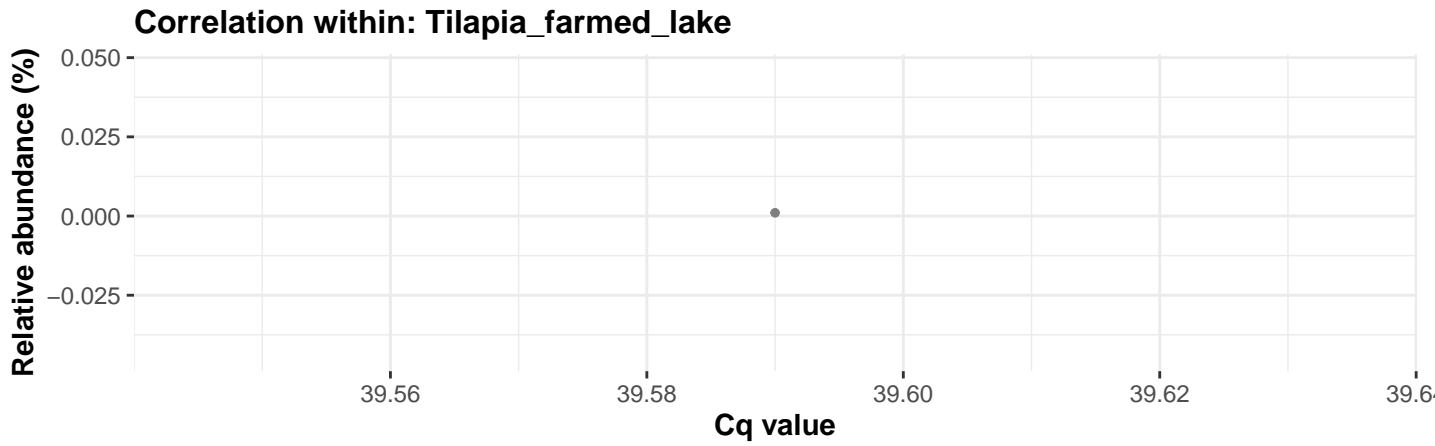
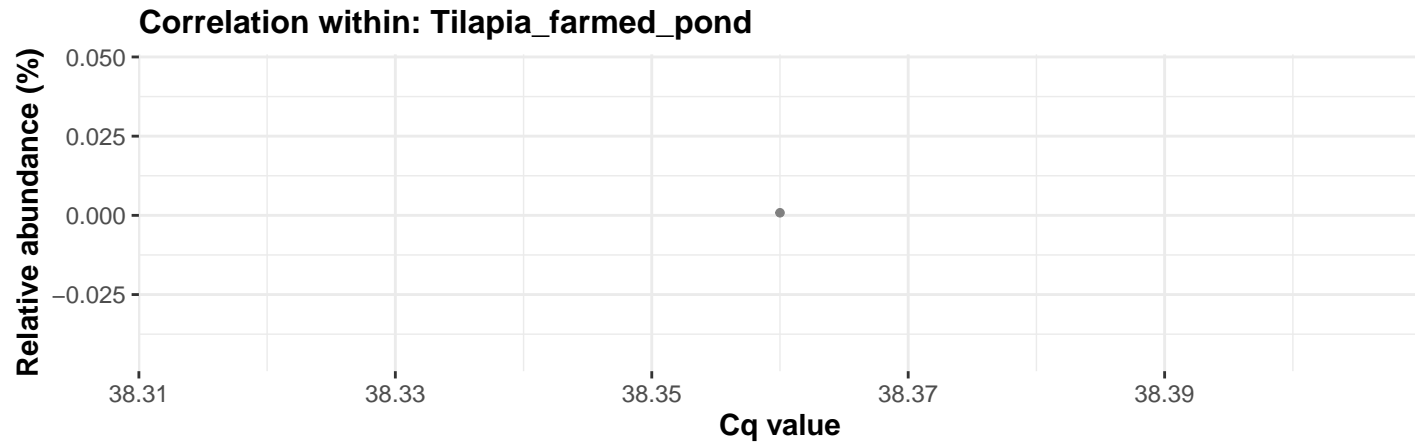
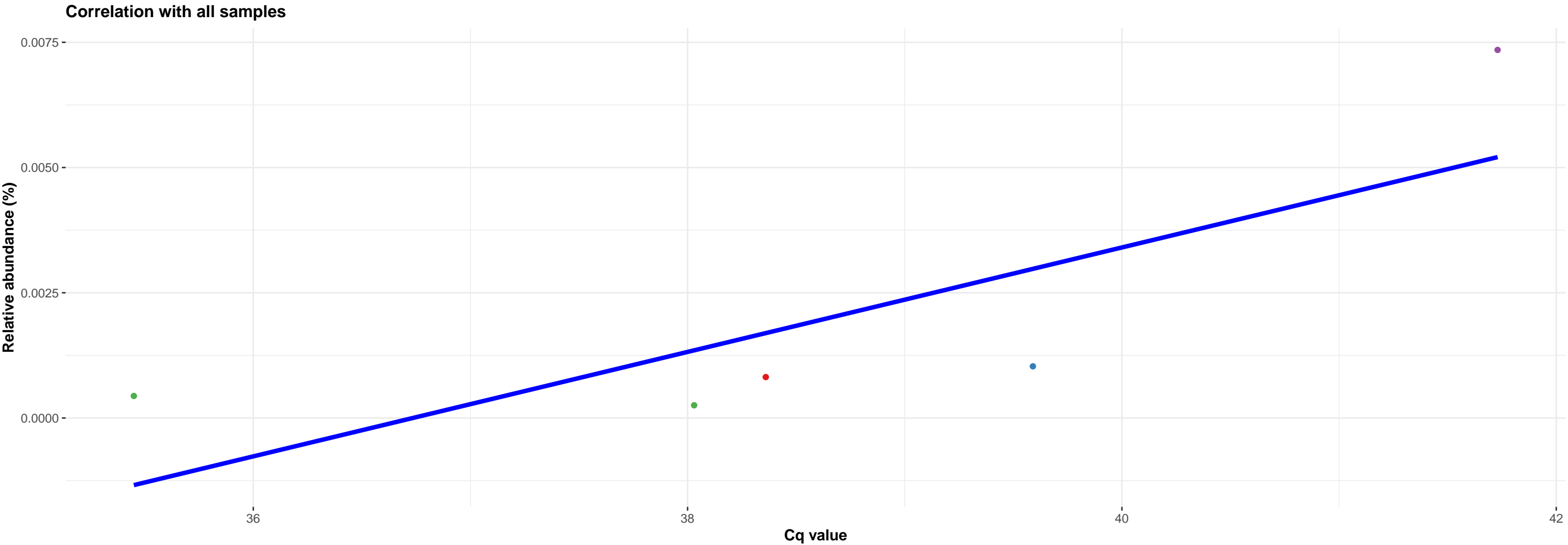


Correlation within: Perch_wild_lake



k__Bacteria; p__Patescibacteria; c__Gracilibacteria; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa

featureID: 6bd3f3df4073826645c0bfe560765004

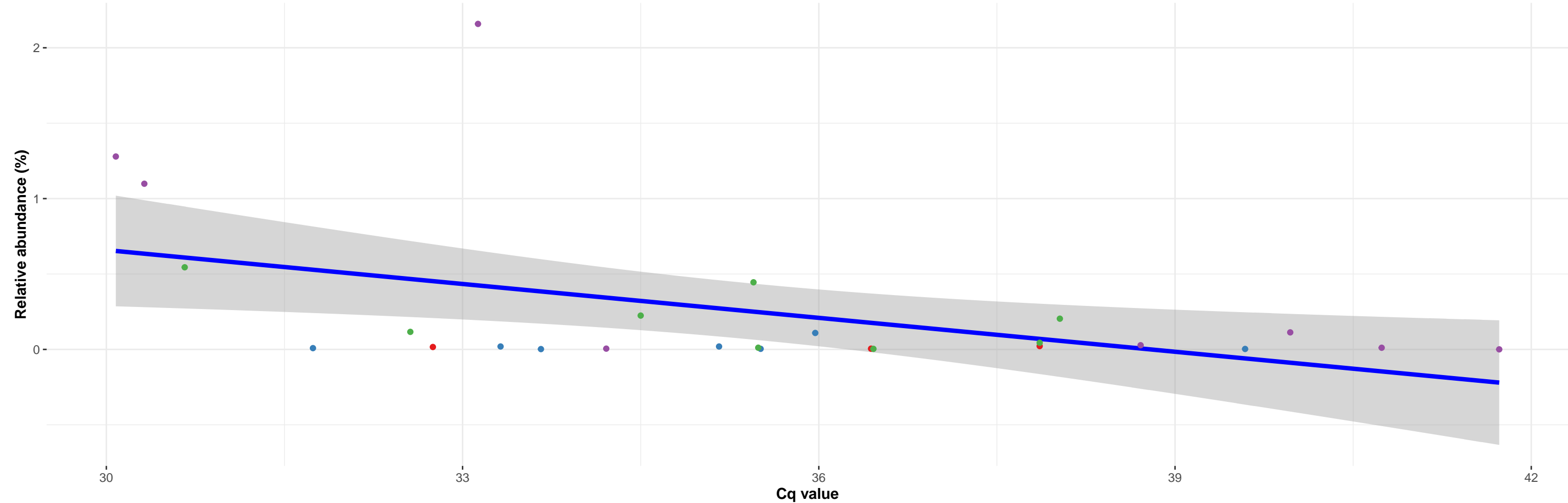


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

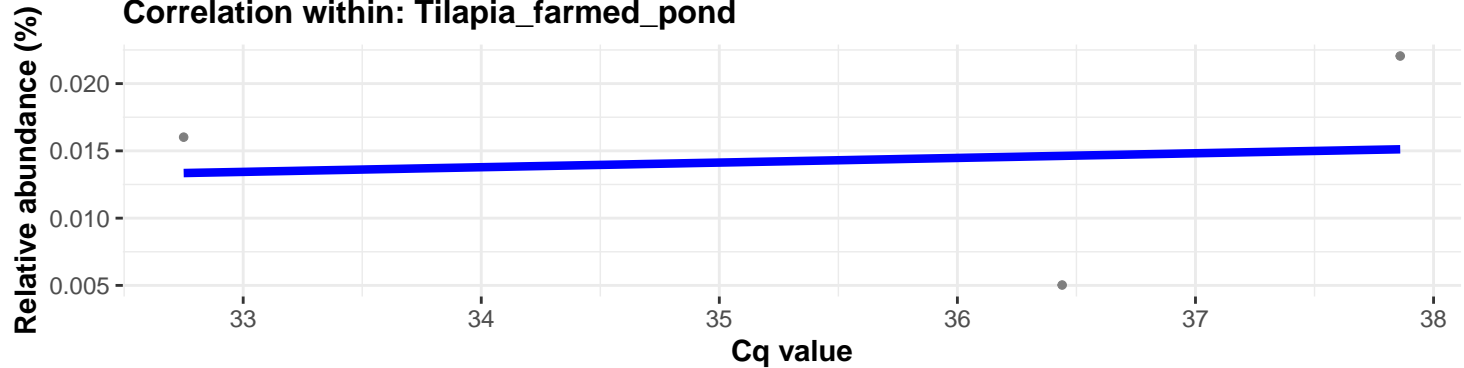
featureID: 4d951a112c225bc3bdfd2d0cfec2b2d3

Correlation with all samples

$\log_e(S) = 8.335$, $p = 0.031$, $\hat{\rho}_{\text{Spearman}} = -0.424$, $\text{CI}_{95\%} [-0.703, -0.032]$, $n_{\text{pairs}} = 26$

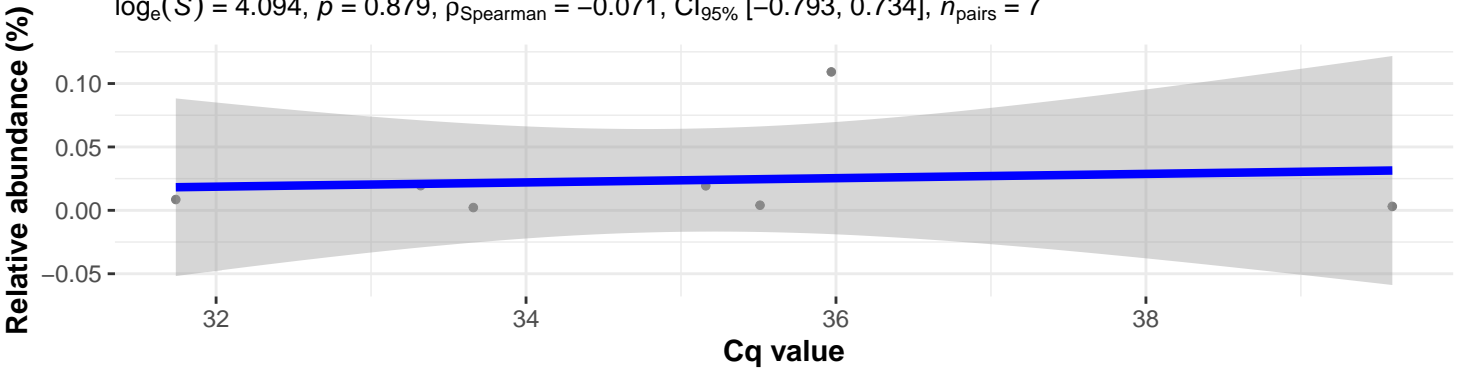


Correlation within: Tilapia_farmed_pond

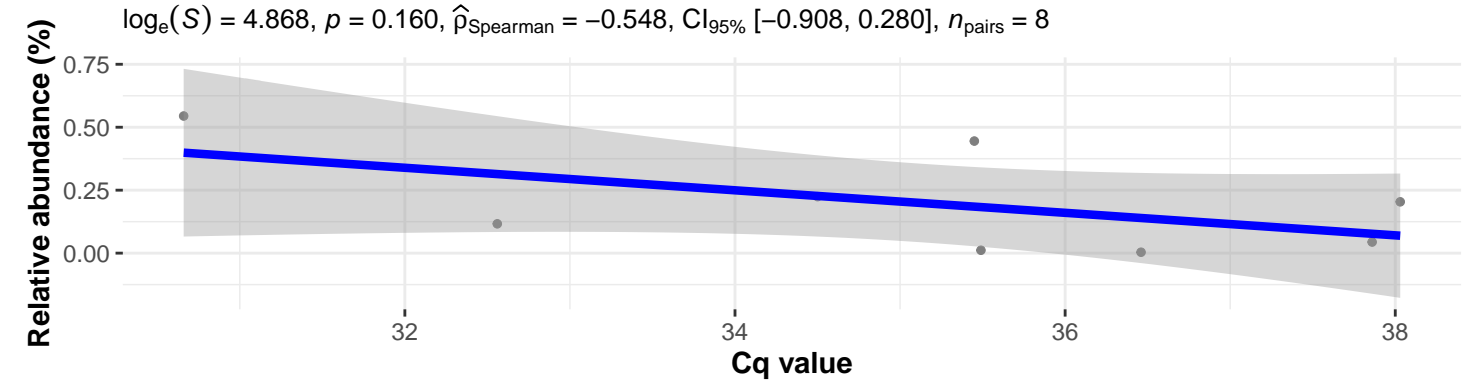


Correlation within: Tilapia_farmed_lake

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

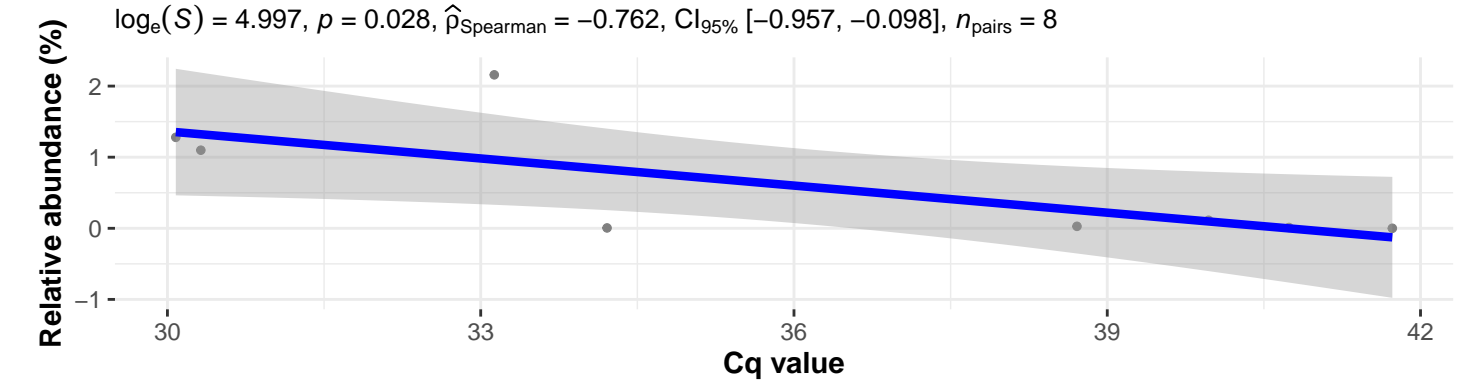


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

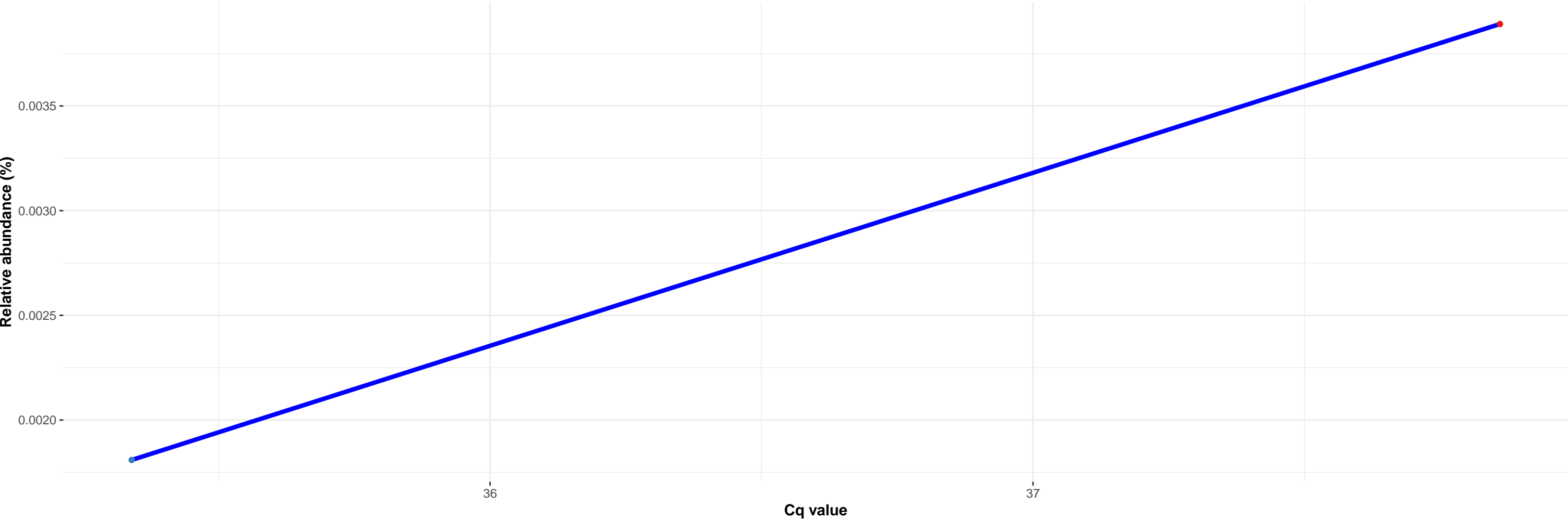
$\log_e(S) = 4.997$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = -0.762$, $\text{CI}_{95\%} [-0.957, -0.098]$, $n_{\text{pairs}} = 8$



k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae (Subgroup 1); g__Bryocella; s__uncultured bacterium

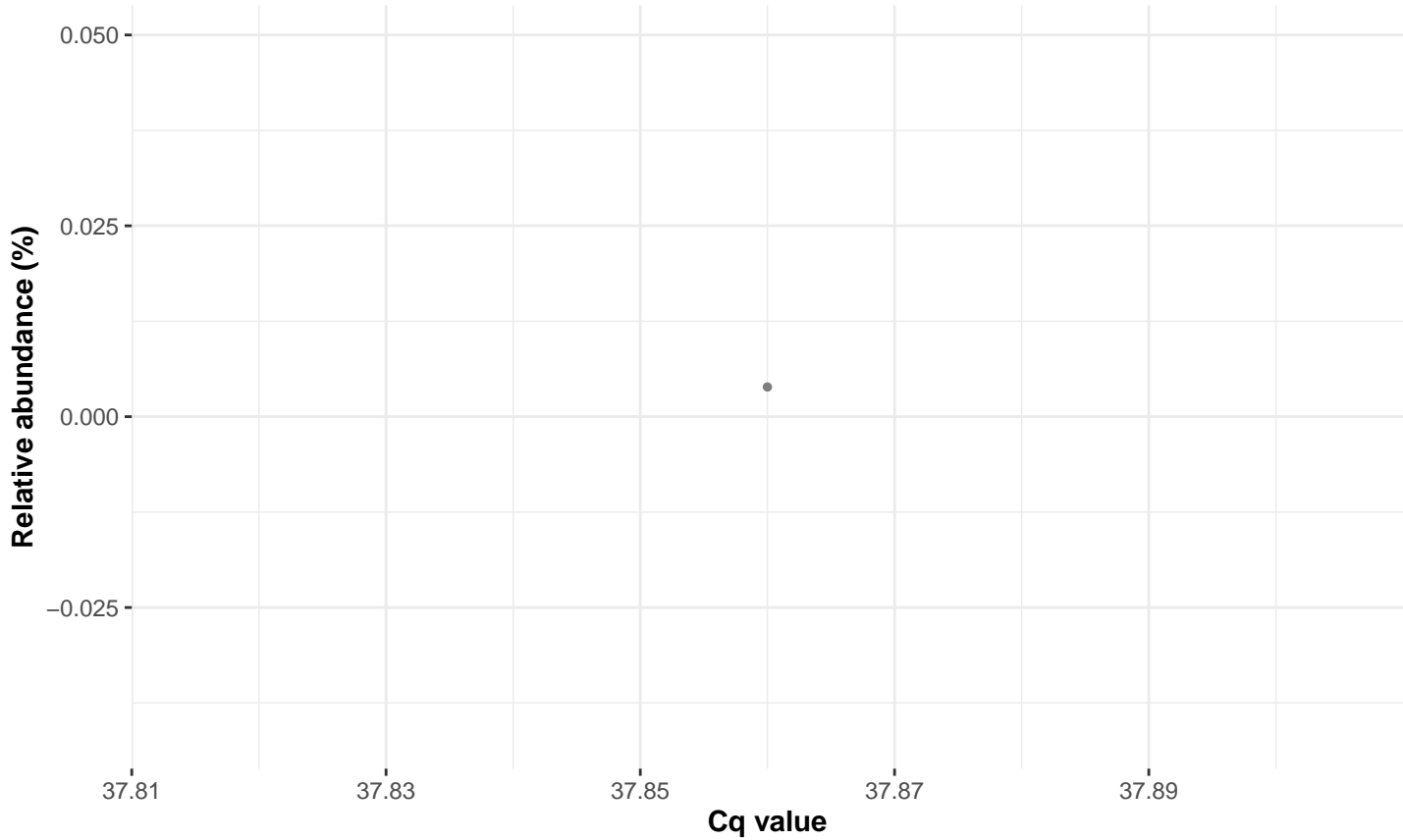
featureID: 92eda480cf7a77d3e7b6890877207fe6

Correlation with all samples

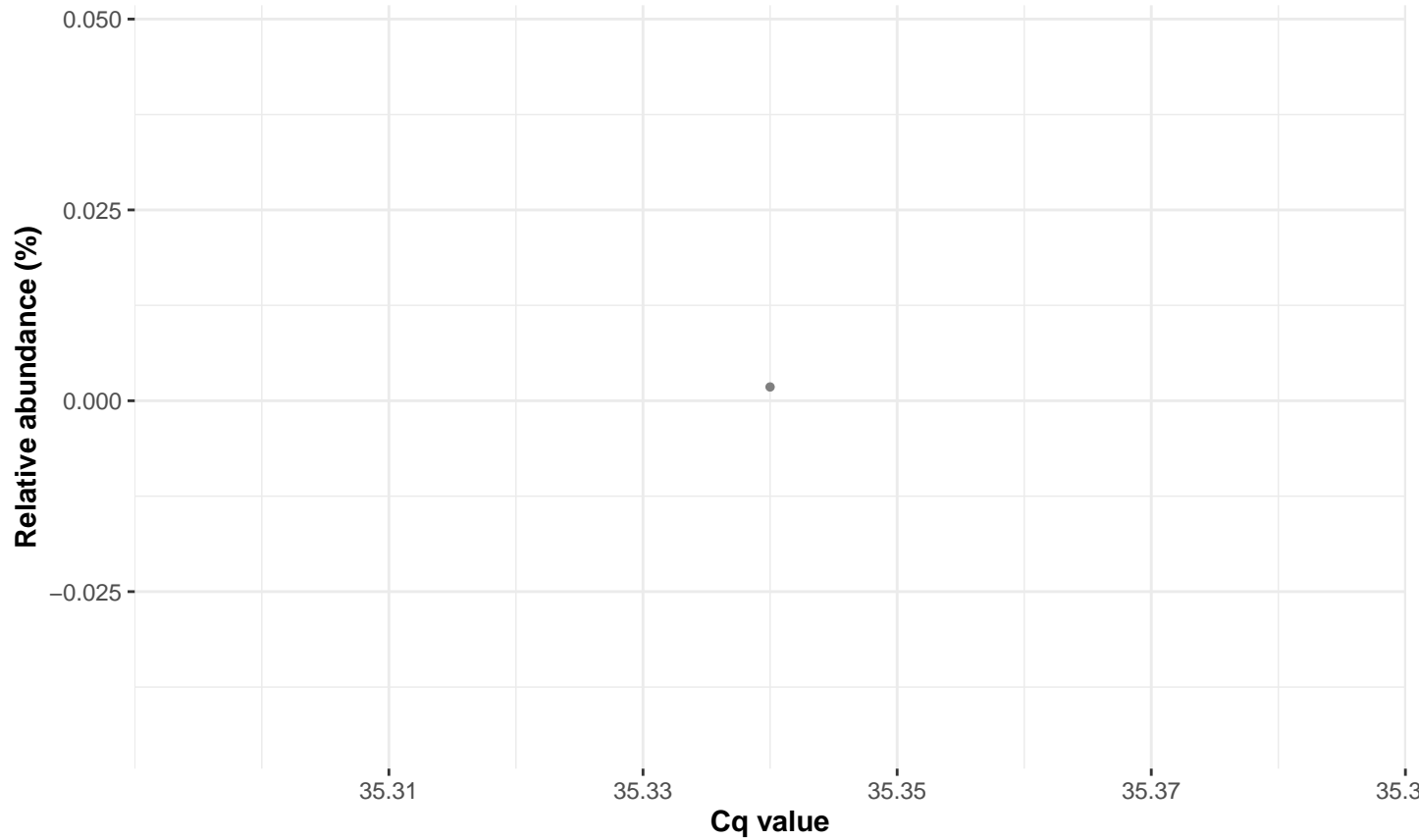


Sample_type • Tilapia_farmed_pond • Tilapia_farmed_lake

Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_farmed_lake

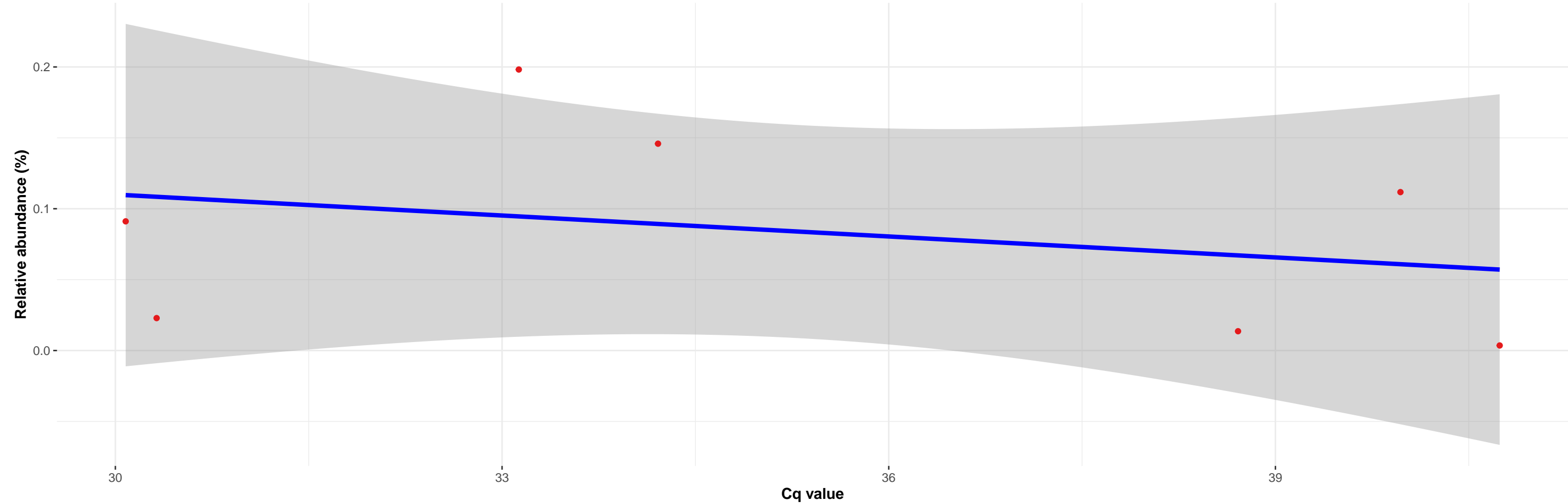


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 98368b3901045189f93ca86afab6cc2b

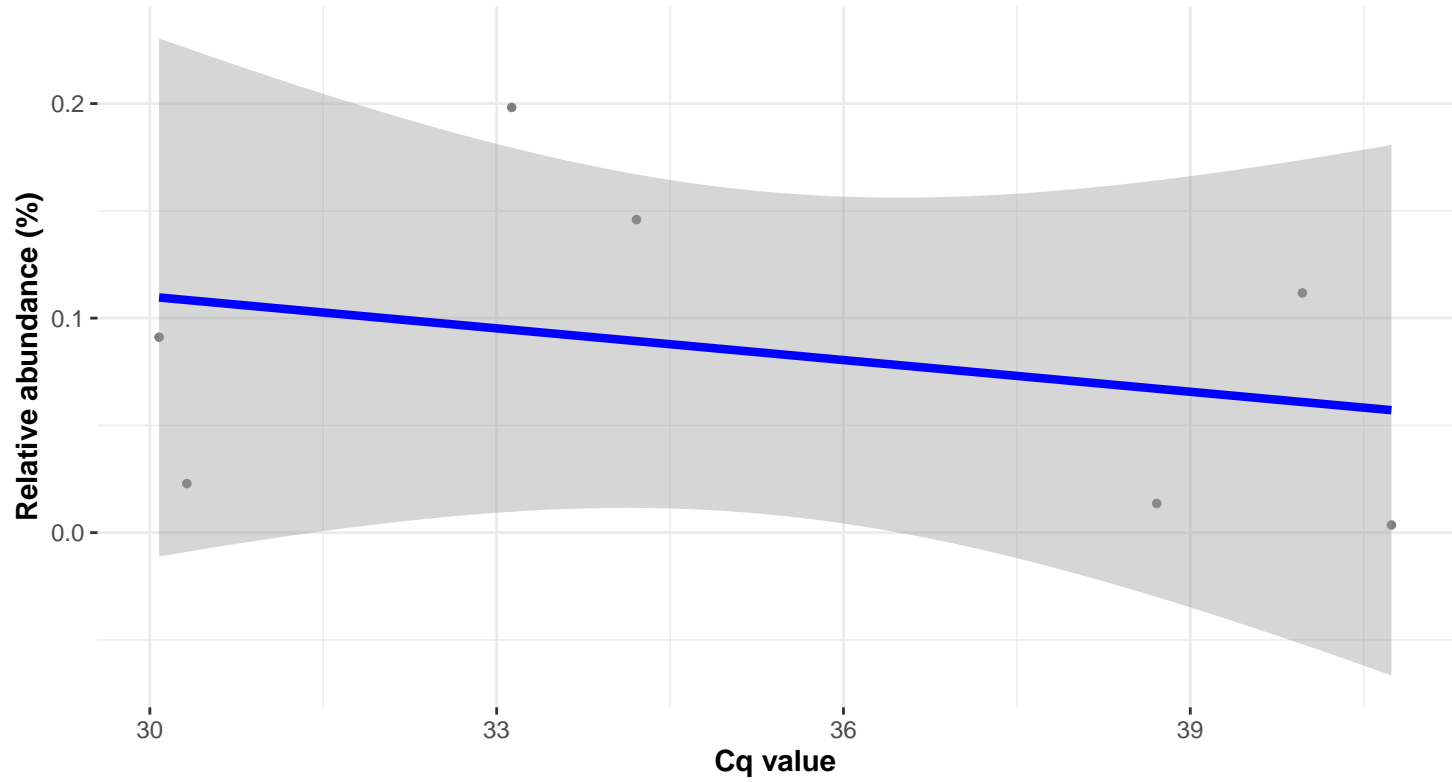
Correlation with all samples

$\log_e(S) = 4.331$, $p = 0.432$, $\hat{\rho}_{\text{Spearman}} = -0.357$, $CI_{95\%} [-0.882, 0.562]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.331$, $p = 0.432$, $\hat{\rho}_{\text{Spearman}} = -0.357$, $CI_{95\%} [-0.882, 0.562]$, $n_{\text{pairs}} = 7$

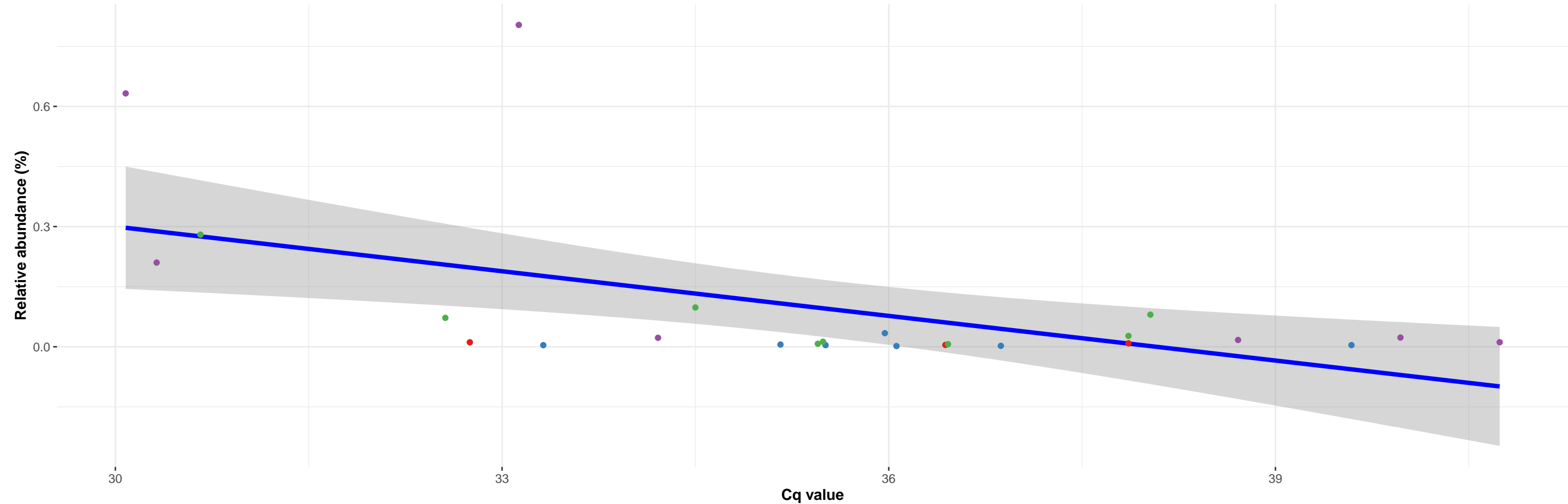


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

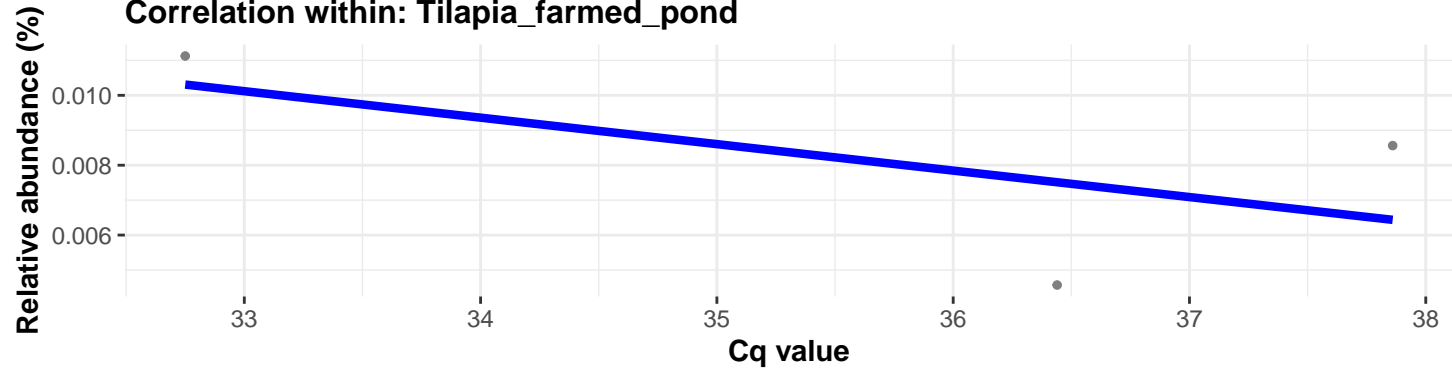
featureID: 913a3599bef09a615b00dee32ead1f48

Correlation with all samples

$\log_e(S) = 8.195$, $p = 0.052$, $\hat{\rho}_{\text{Spearman}} = -0.394$, $CI_{95\%} [-0.689, 0.014]$, $n_{\text{pairs}} = 25$

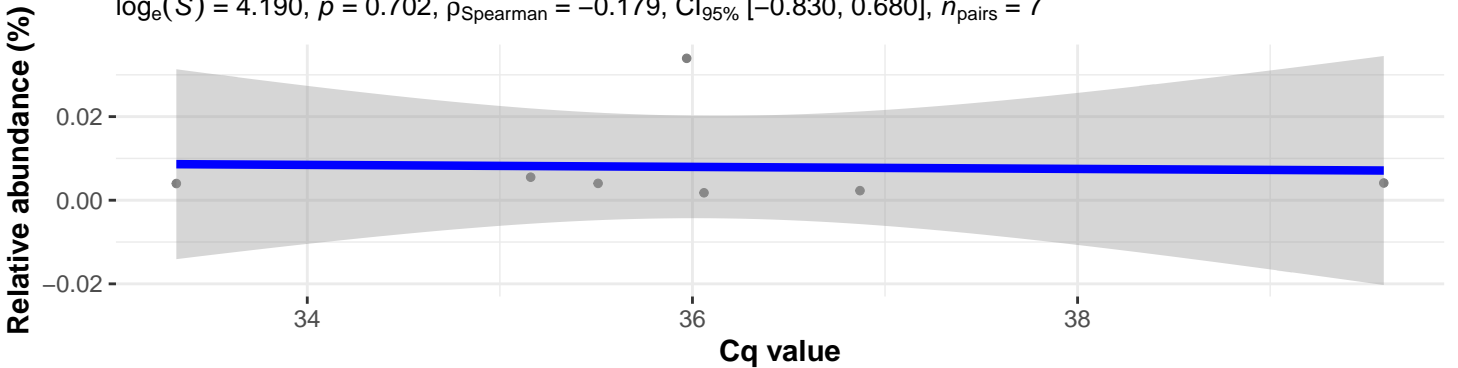


Correlation within: Tilapia_farmed_pond



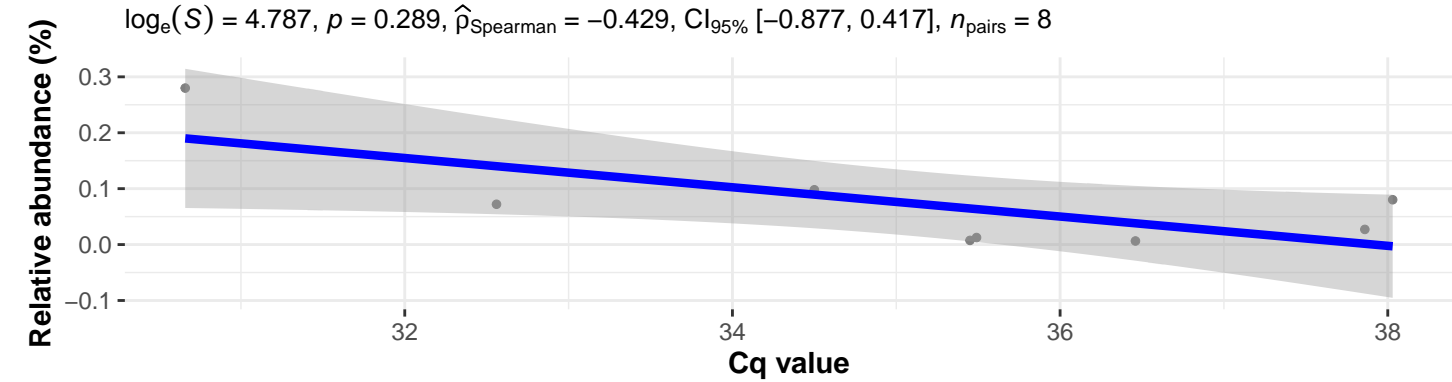
Correlation within: Tilapia_farmed_lake

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



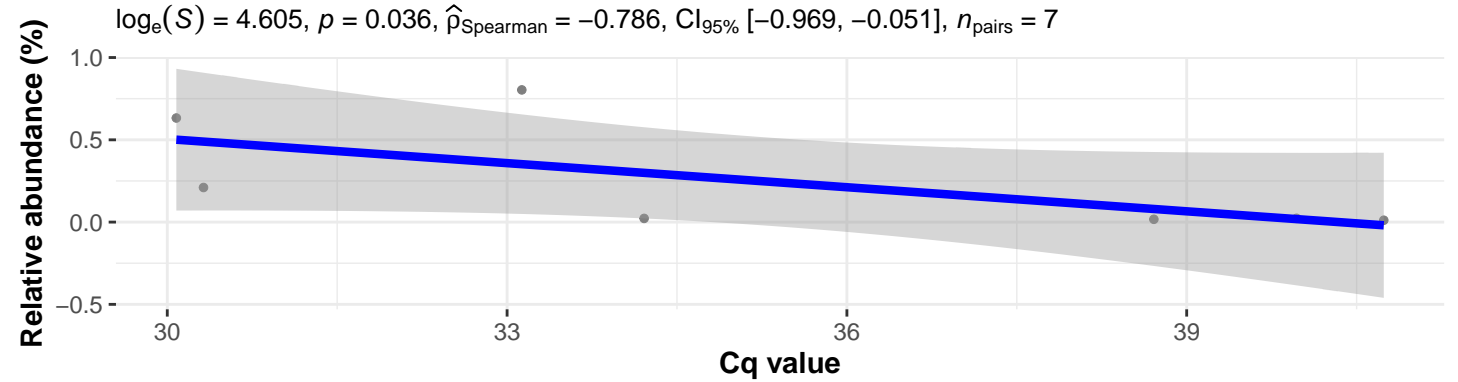
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.787$, $p = 0.289$, $\hat{\rho}_{\text{Spearman}} = -0.429$, $CI_{95\%} [-0.877, 0.417]$, $n_{\text{pairs}} = 8$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.605$, $p = 0.036$, $\hat{\rho}_{\text{Spearman}} = -0.786$, $CI_{95\%} [-0.969, -0.051]$, $n_{\text{pairs}} = 7$

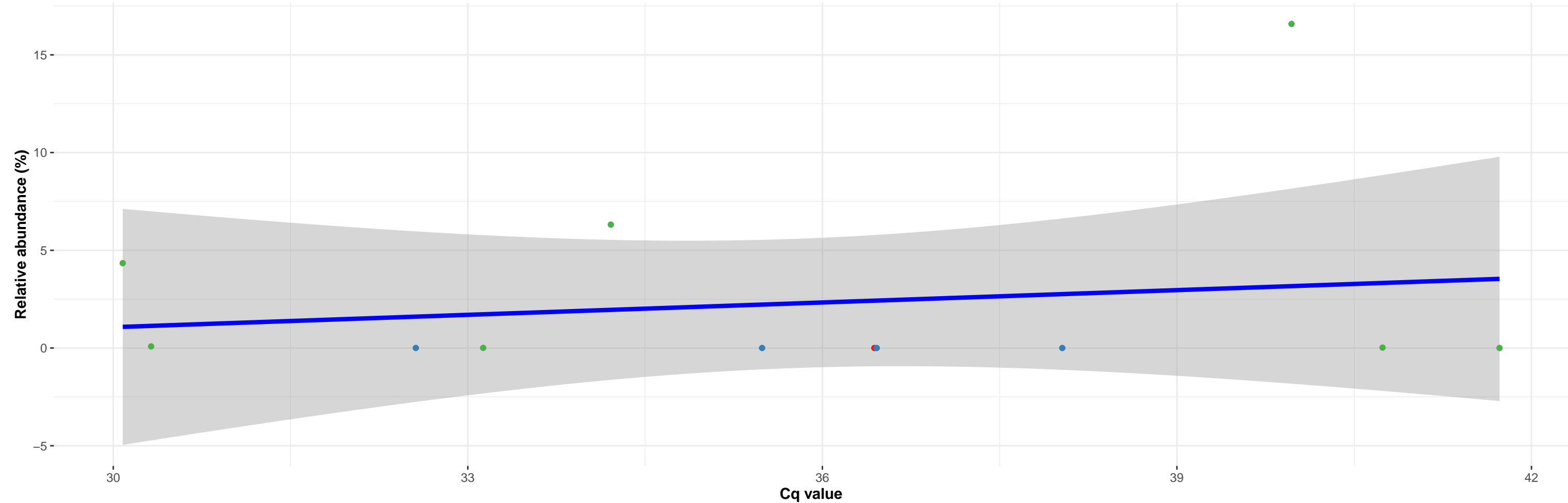


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

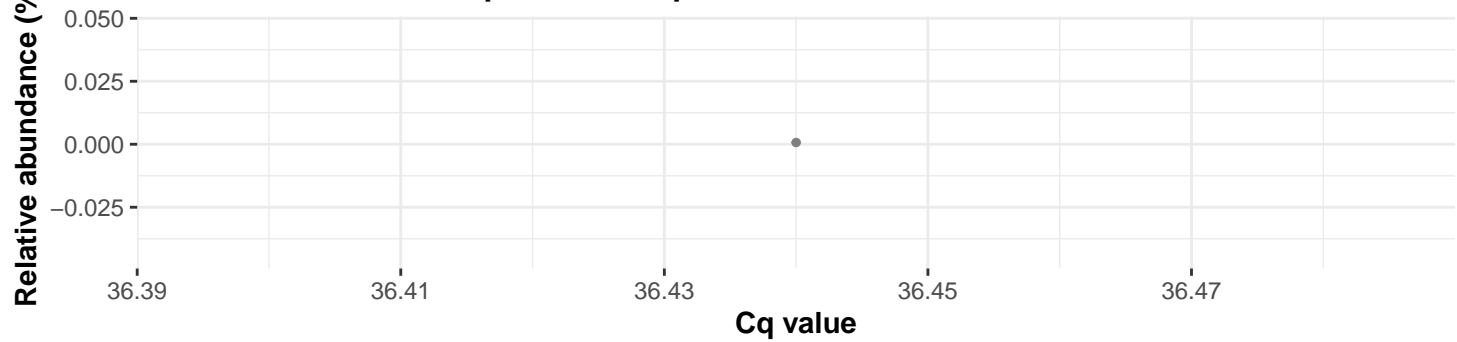
featureID: d36c9fdfa26099ffe57512e6dfbe0b8

Correlation with all samples

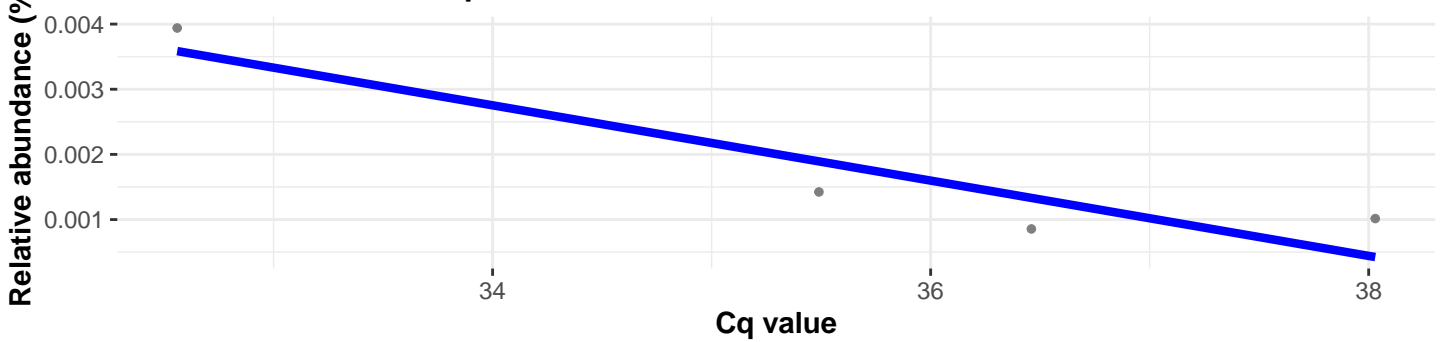
$\log_e(S) = 5.881$, $p = 0.430$, $\hat{\rho}_{\text{Spearman}} = -0.252$, $\text{CI}_{95\%} [-0.731, 0.393]$, $n_{\text{pairs}} = 12$



Correlation within: Tilapia_farmed_pond

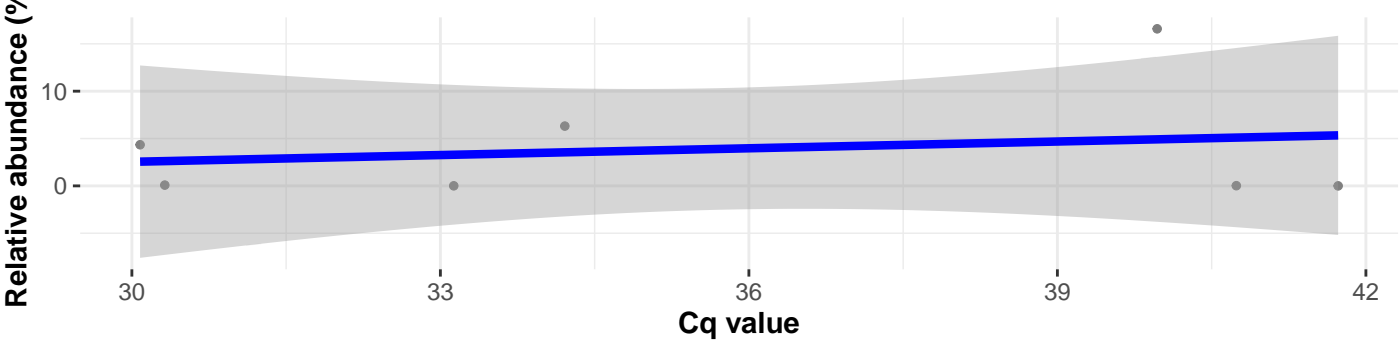


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

$\log_e(S) = 4.304$, $p = 0.482$, $\hat{\rho}_{\text{Spearman}} = -0.321$, $\text{CI}_{95\%} [-0.872, 0.589]$, $n_{\text{pairs}} = 7$

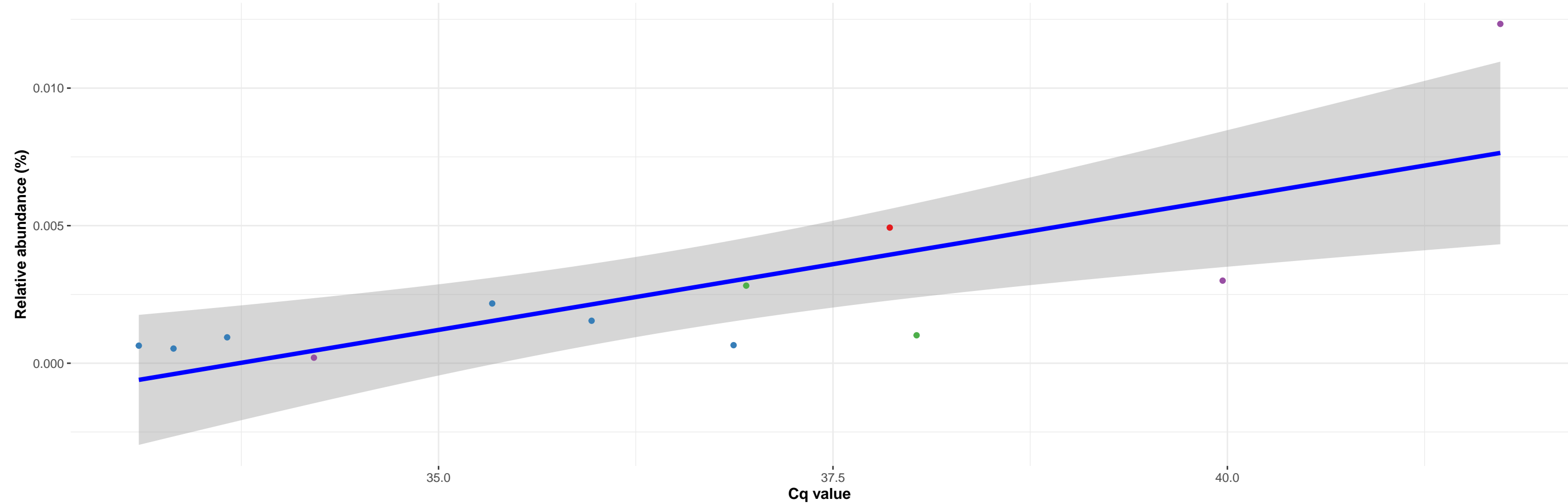


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

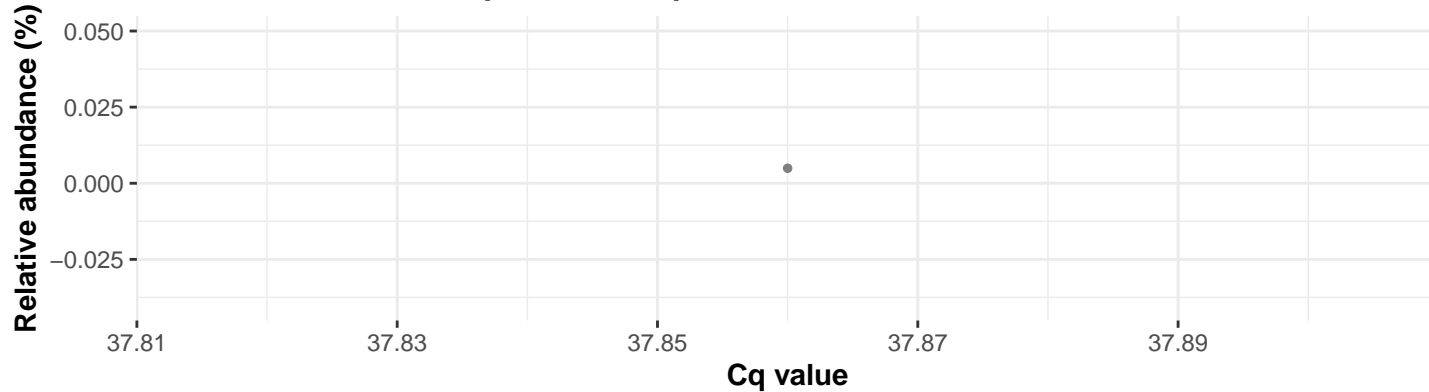
featureID: 3638f2062c305c79df283ef573a10b97

Correlation with all samples

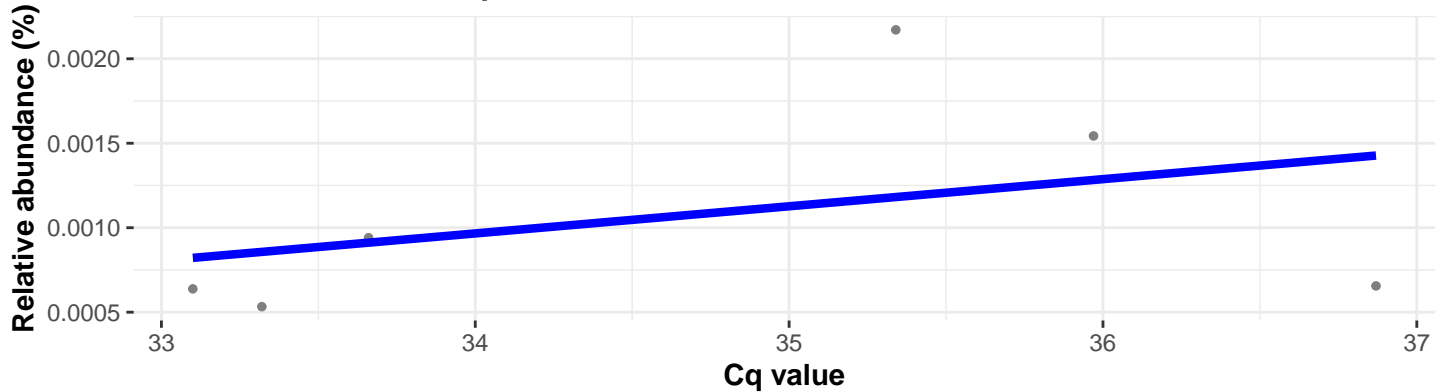
$\log_e(S) = 4.060$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.797$, $CI_{95\%} [0.395, 0.943]$, $n_{\text{pairs}} = 12$



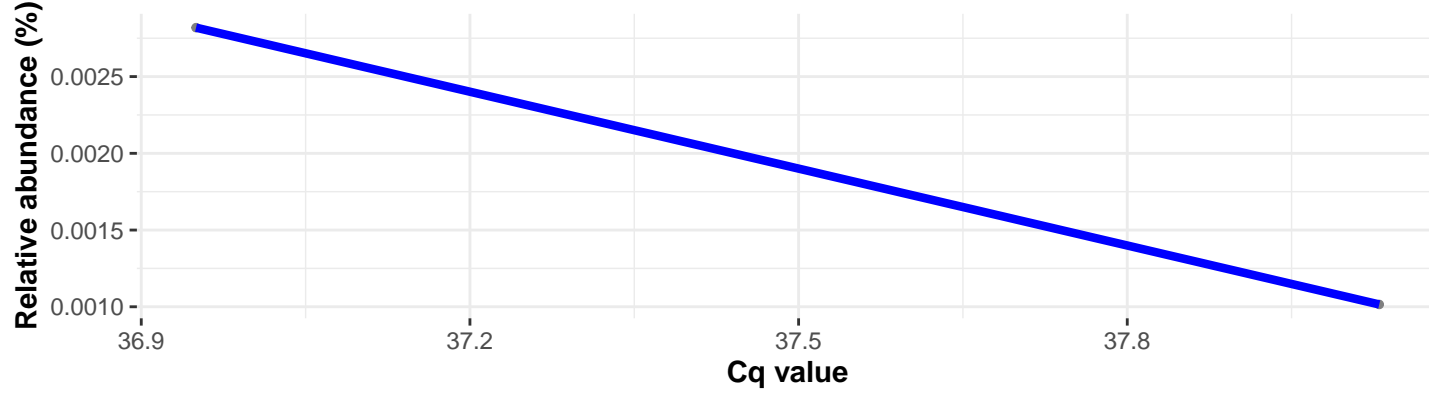
Correlation within: Tilapia_farmed_pond



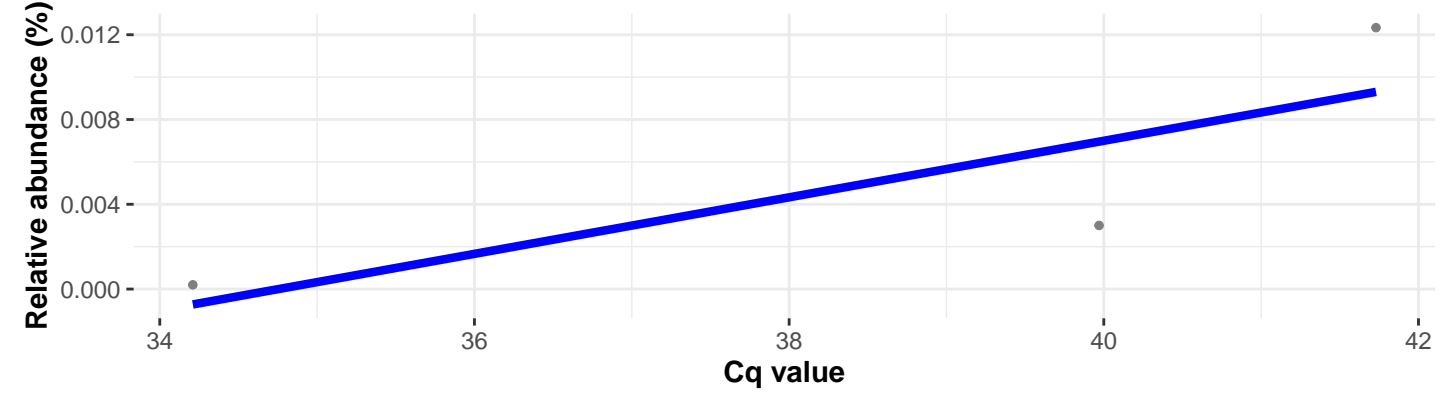
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

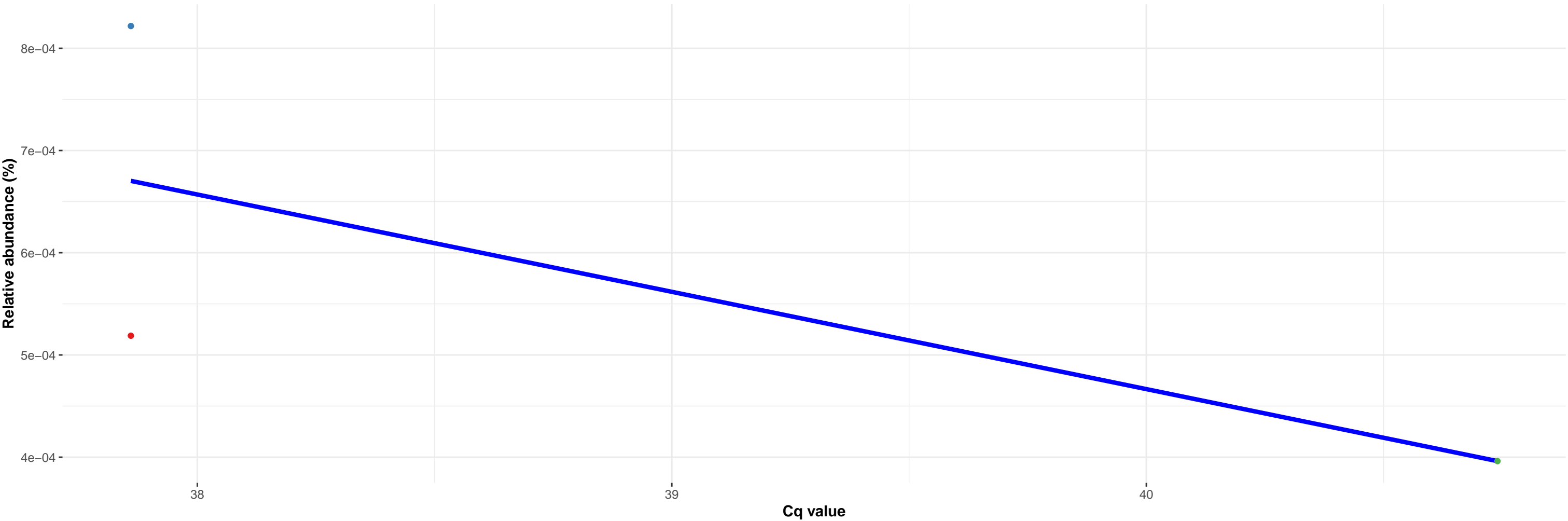


Correlation within: Perch_wild_lake

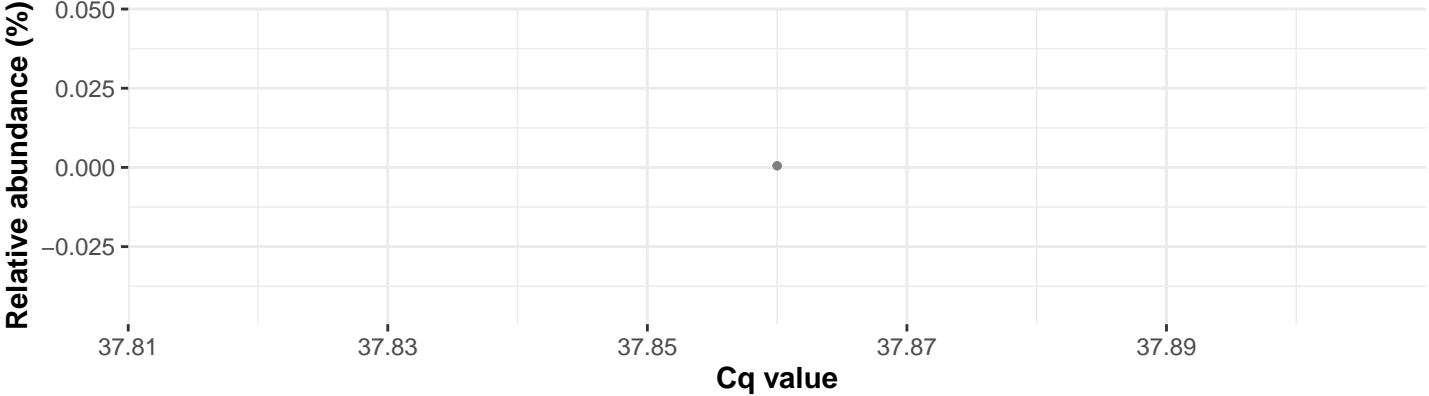


featureID: 8f2ddde9ccf2d7afe5abf35614fe5b43

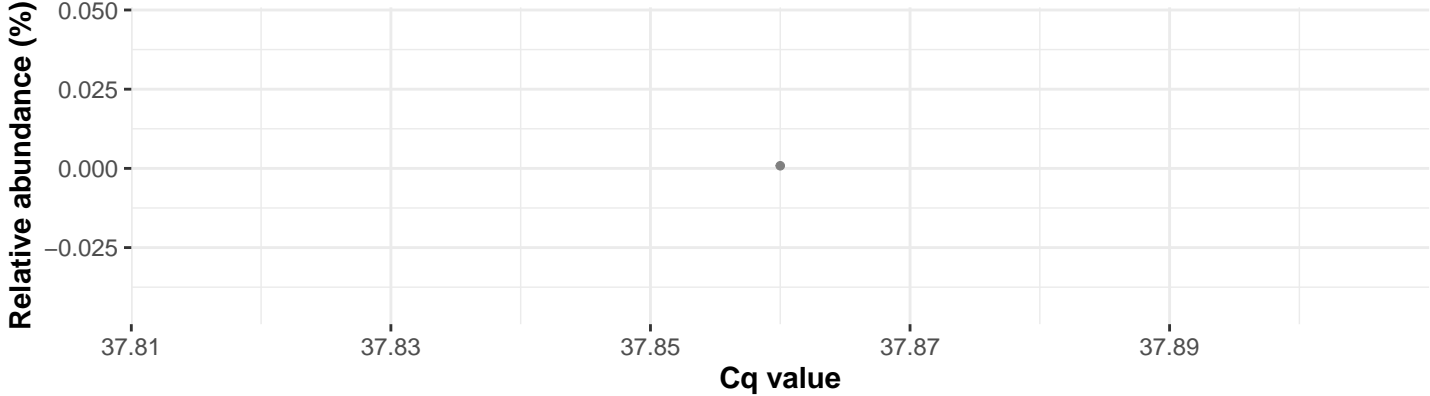
Correlation with all samples



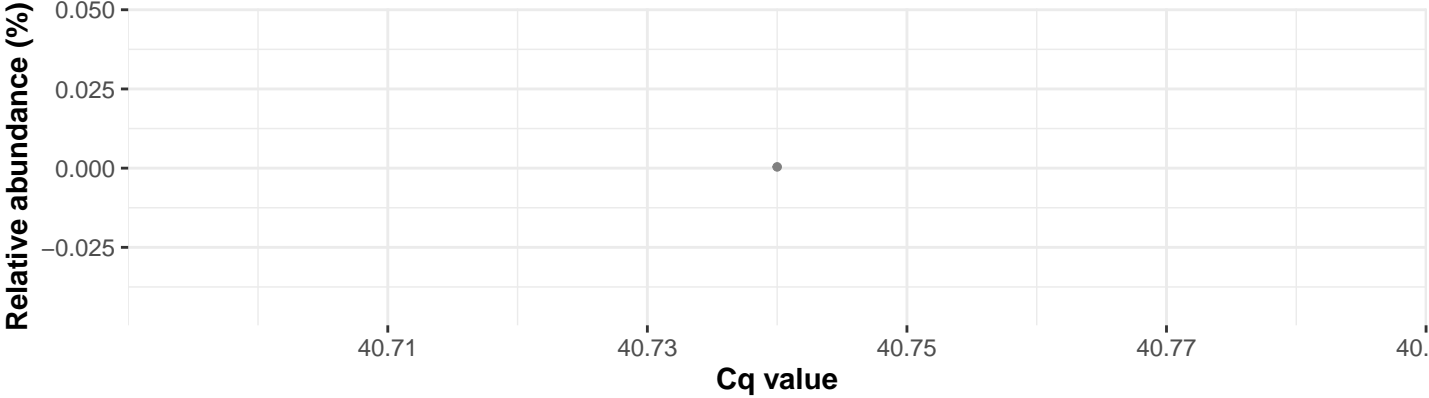
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_wild_lake



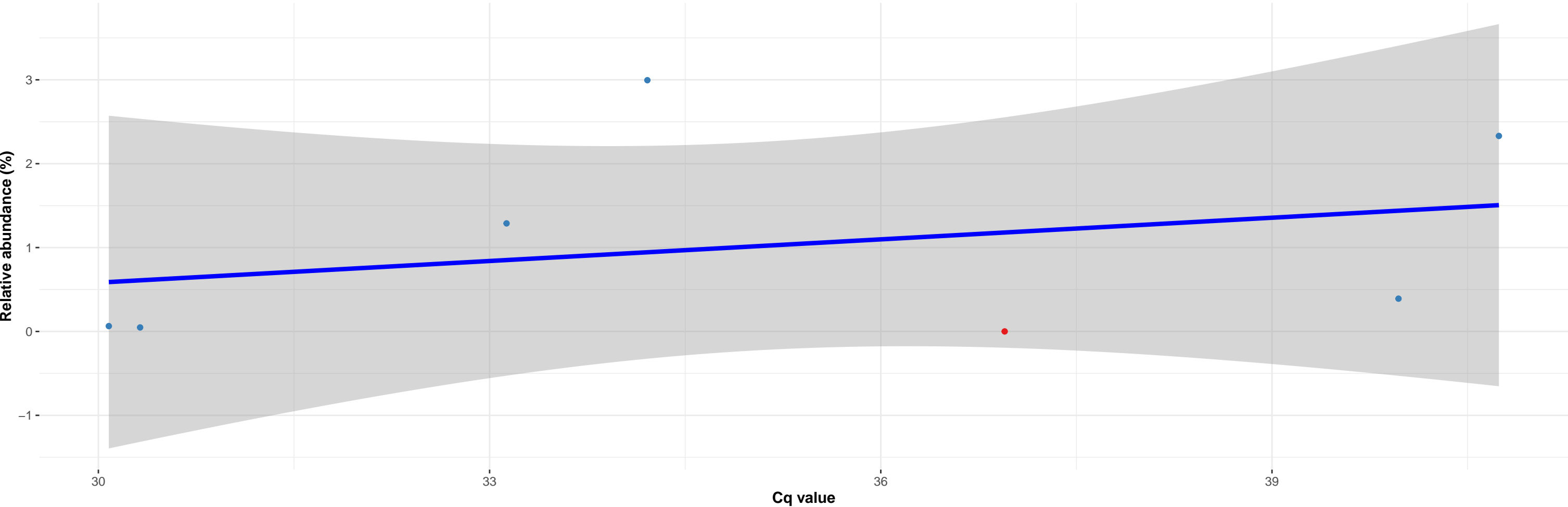
Correlation within: Perch_wild_lake



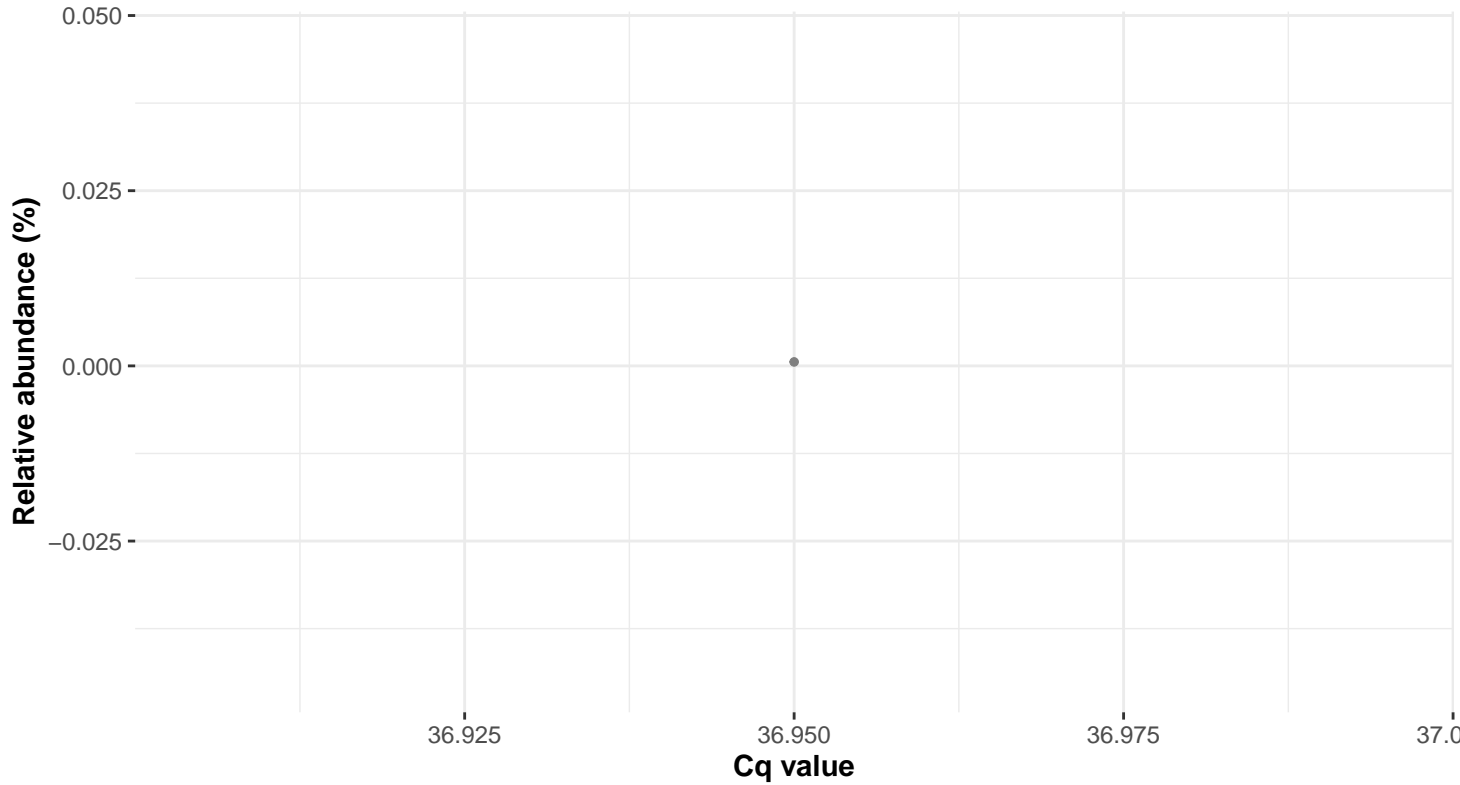
featureID: 249270189cd8e1c30eb0d62d77589cb8

Correlation with all samples

$\log_e(S) = 3.638$, $p = 0.482$, $\hat{\rho}_{\text{Spearman}} = 0.321$, $CI_{95\%} [-0.589, 0.872]$, $n_{\text{pairs}} = 7$

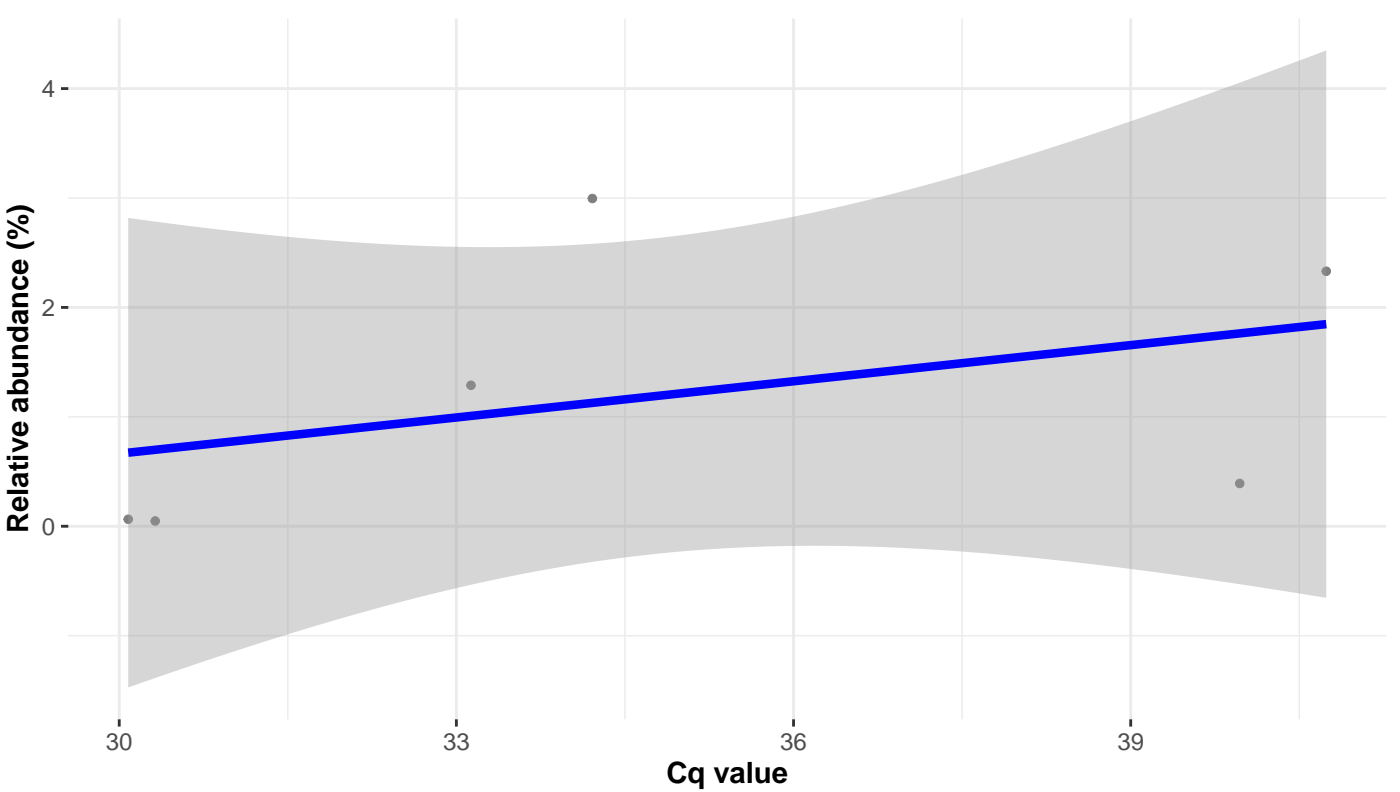


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

$\log_e(S) = 2.485$, $p = 0.156$, $\hat{\rho}_{\text{Spearman}} = 0.657$, $CI_{95\%} [-0.360, 0.961]$, $n_{\text{pairs}} = 6$

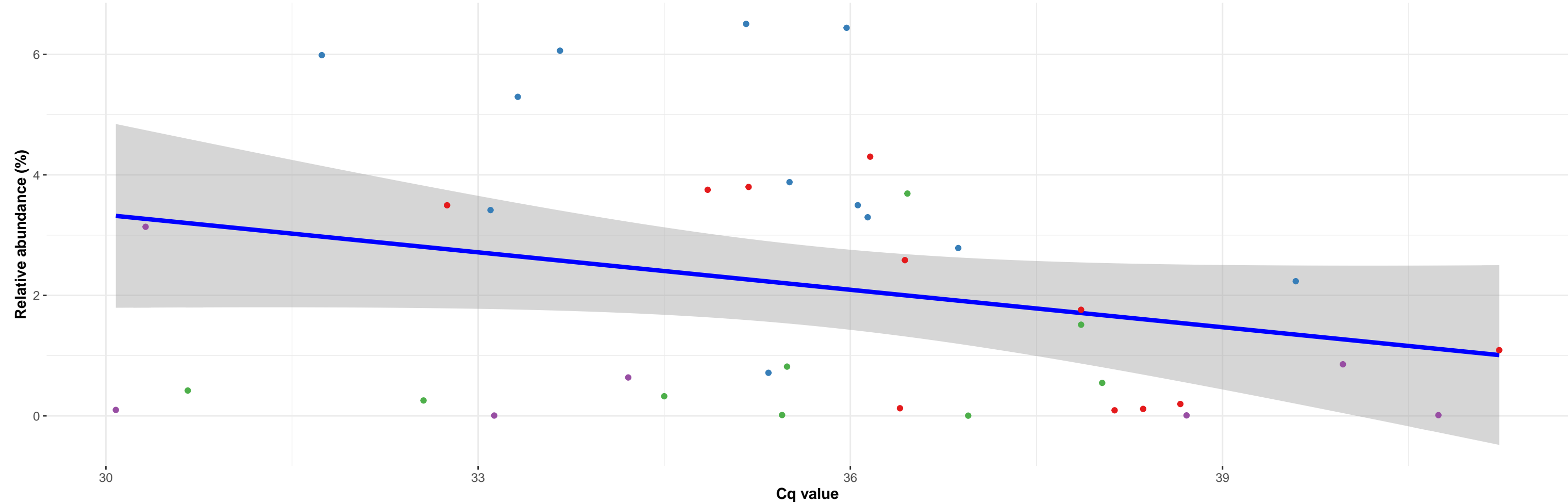


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 7732d6712ceae4666bd66aba7880c6f1

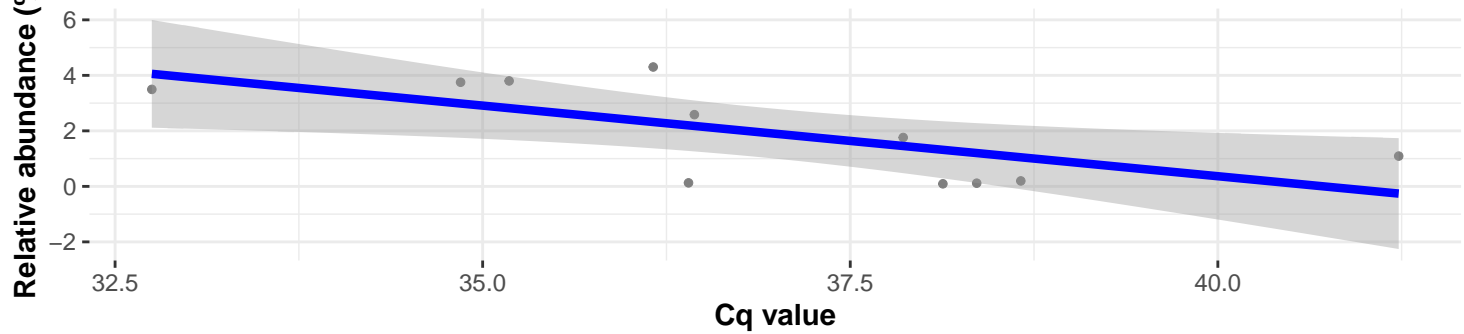
Correlation with all samples

$\log_e(S) = 9.443$, $p = 0.088$, $\hat{\rho}_{\text{Spearman}} = -0.277$, $\text{CI}_{95\%} [-0.552, 0.052]$, $n_{\text{pairs}} = 39$



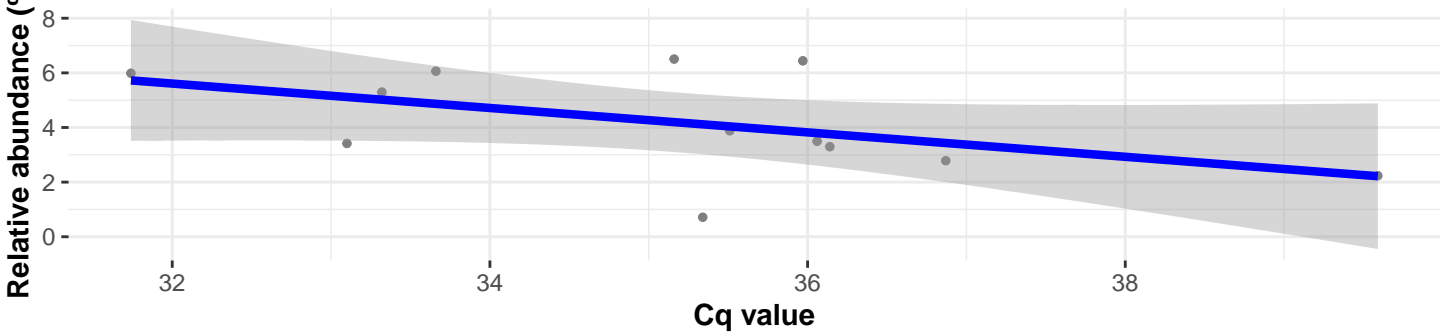
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.919$, $p = 0.019$, $\hat{\rho}_{\text{Spearman}} = -0.691$, $\text{CI}_{95\%} [-0.916, -0.135]$, $n_{\text{pairs}} = 11$



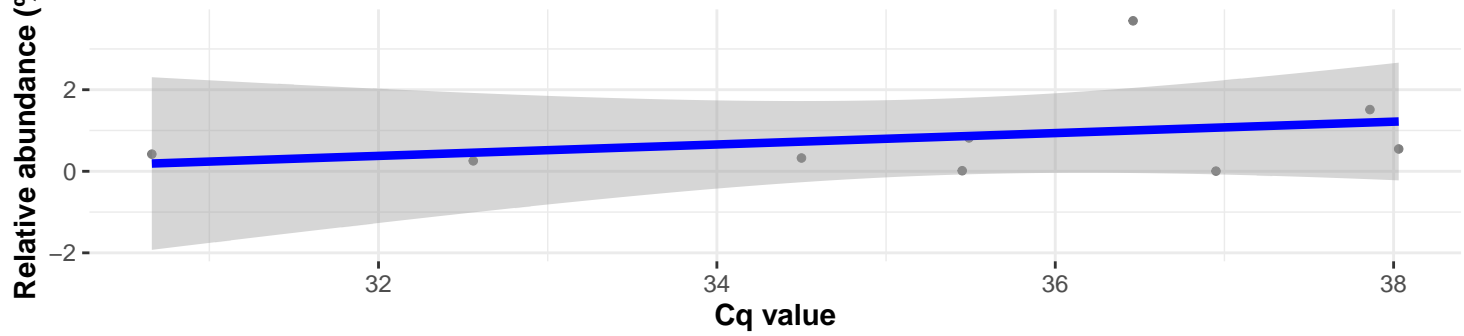
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 6.054$, $p = 0.106$, $\hat{\rho}_{\text{Spearman}} = -0.490$, $\text{CI}_{95\%} [-0.836, 0.136]$, $n_{\text{pairs}} = 12$



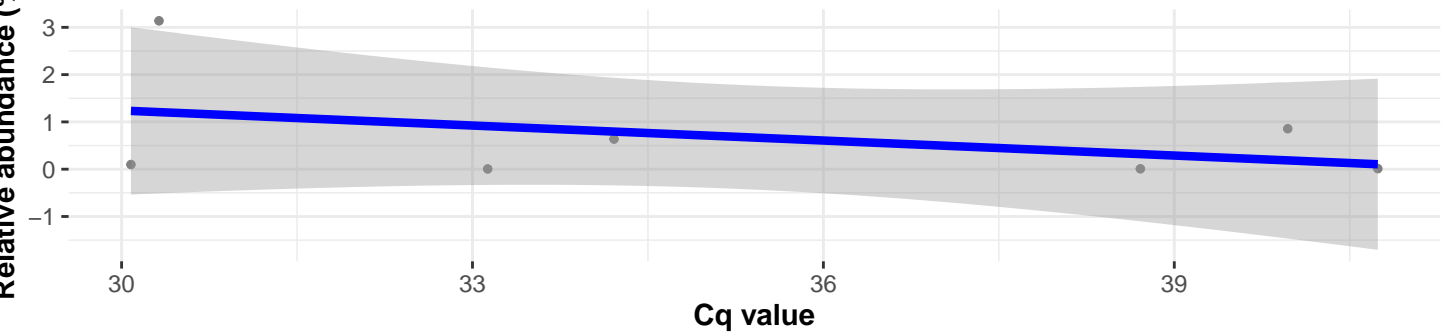
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.382$, $p = 0.381$, $\hat{\rho}_{\text{Spearman}} = 0.333$, $\text{CI}_{95\%} [-0.444, 0.824]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

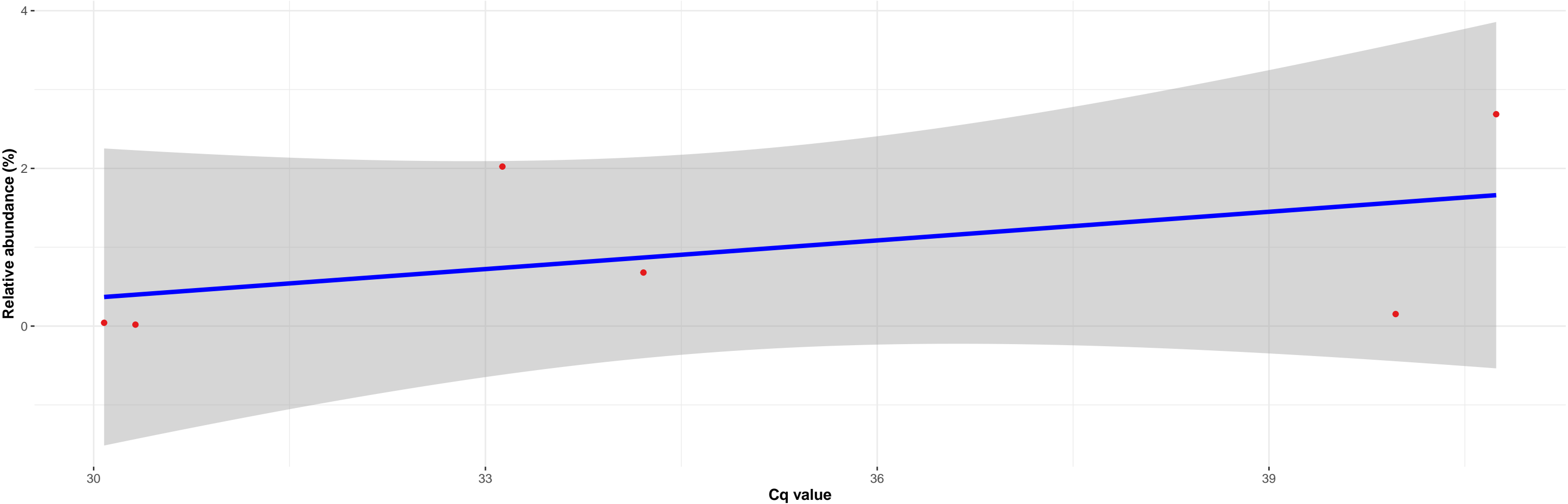
$\log_e(S) = 4.159$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $\text{CI}_{95\%} [-0.819, 0.699]$, $n_{\text{pairs}} = 7$



featureID: 4c5af046872782b10af8fff902cdf641

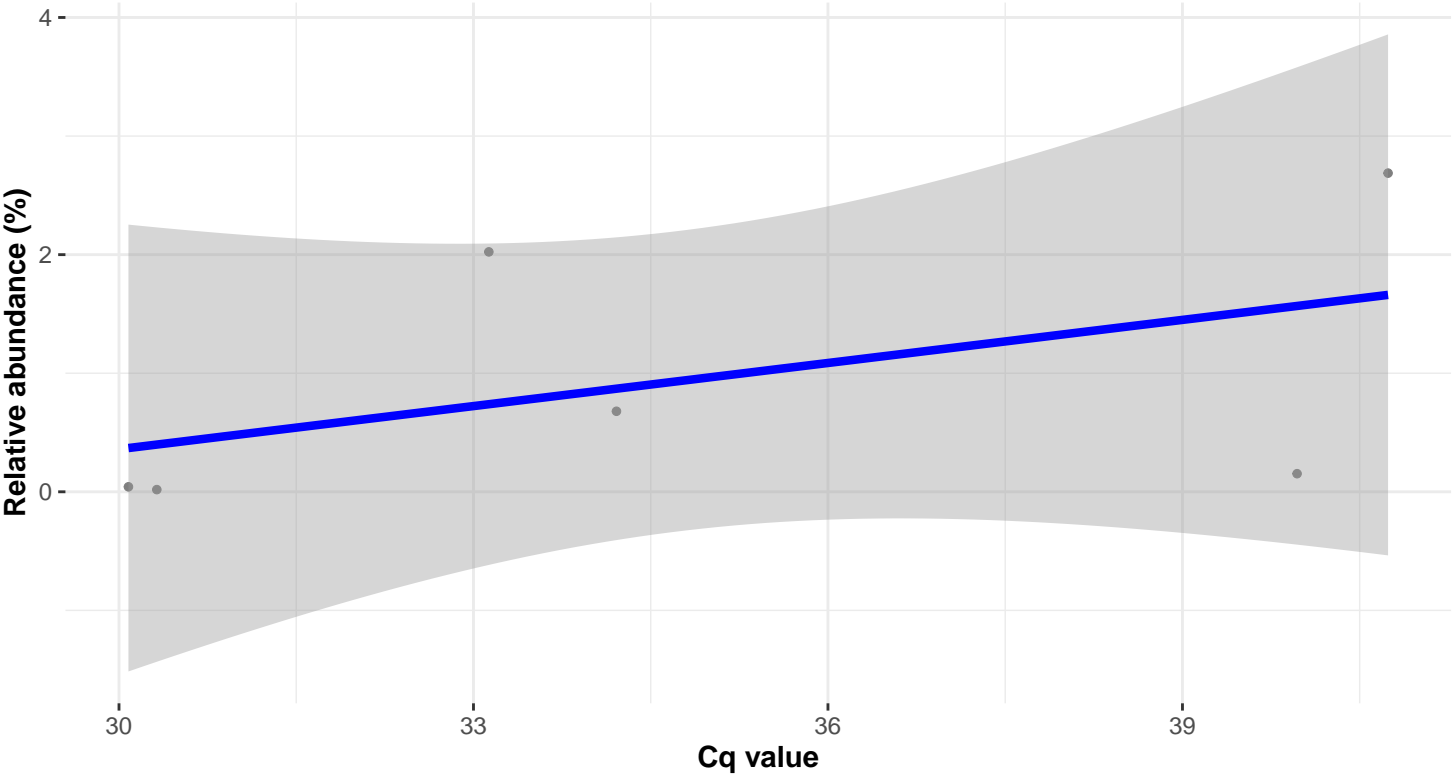
Correlation with all samples

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $\text{CI}_{95\%} [-0.263, 0.968]$, $n_{\text{pairs}} = 6$



Correlation within: Perch_wild_lake

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $\text{CI}_{95\%} [-0.263, 0.968]$, $n_{\text{pairs}} = 6$

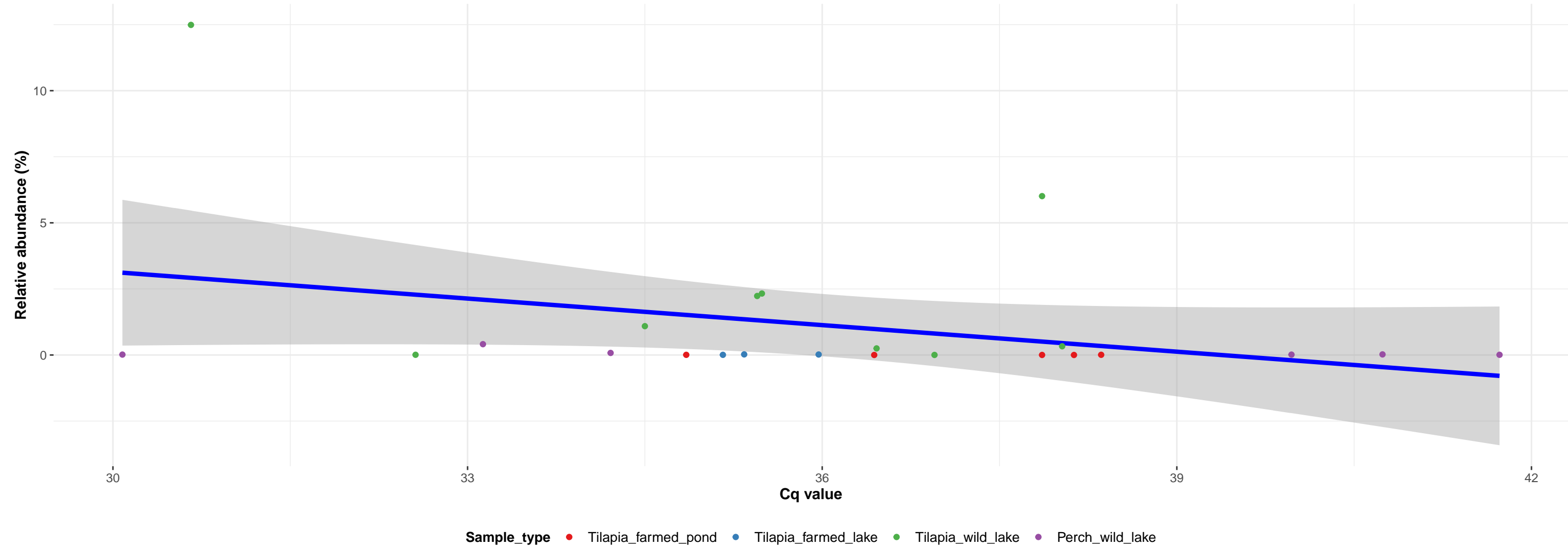


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

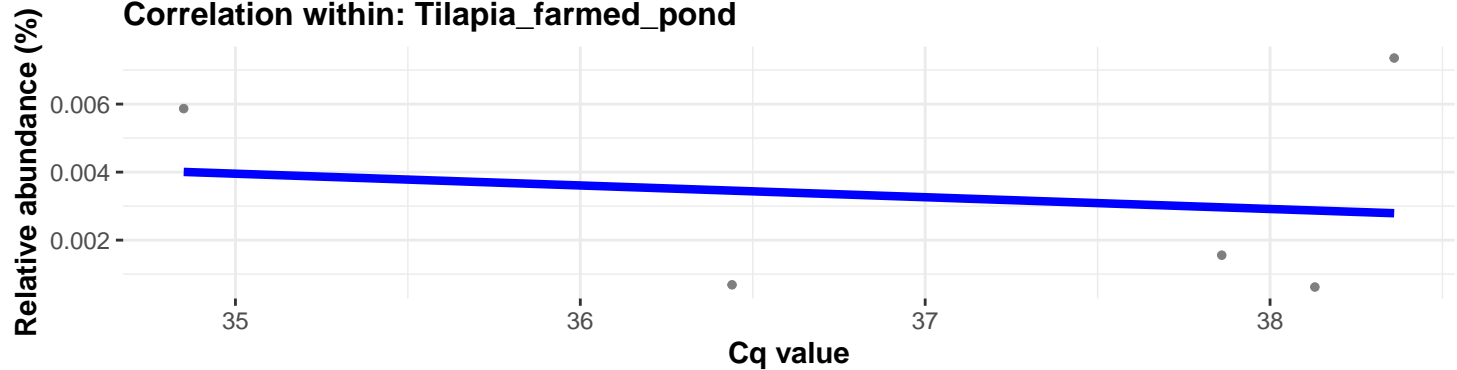
featureID: dacf22eb1a2065568c1175d1a76c9dc7

Correlation with all samples

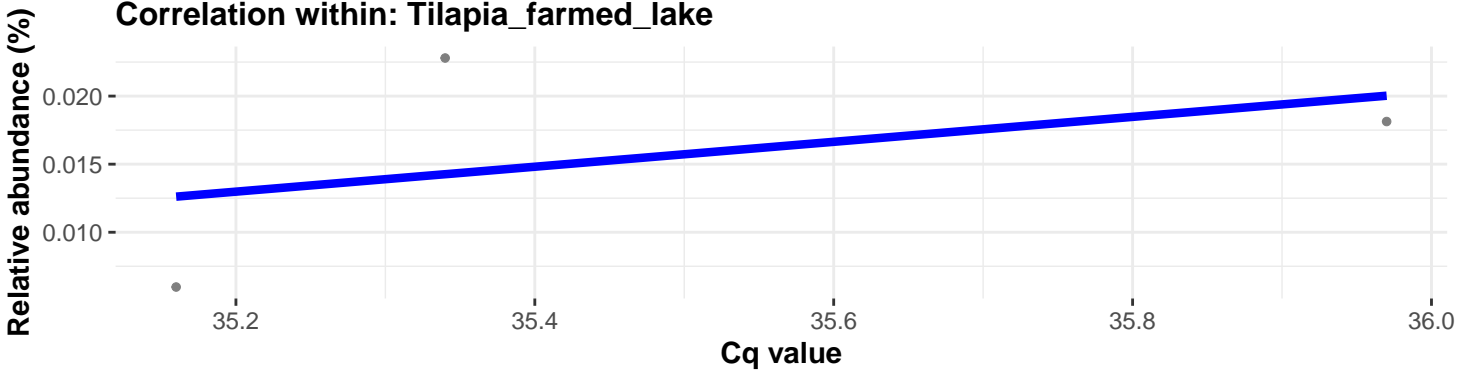
$\log_e(S) = 7.887$, $p = 0.143$, $\hat{\rho}_{\text{Spearman}} = -0.315$, $CI_{95\%} [-0.651, 0.125]$, $n_{\text{pairs}} = 23$



Correlation within: Tilapia_farmed_pond

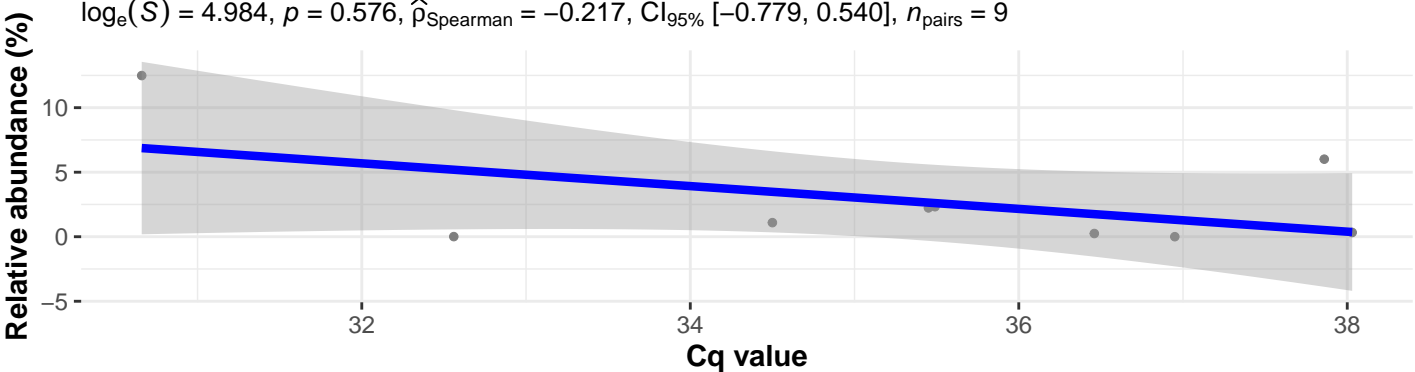


Correlation within: Tilapia_farmed_lake



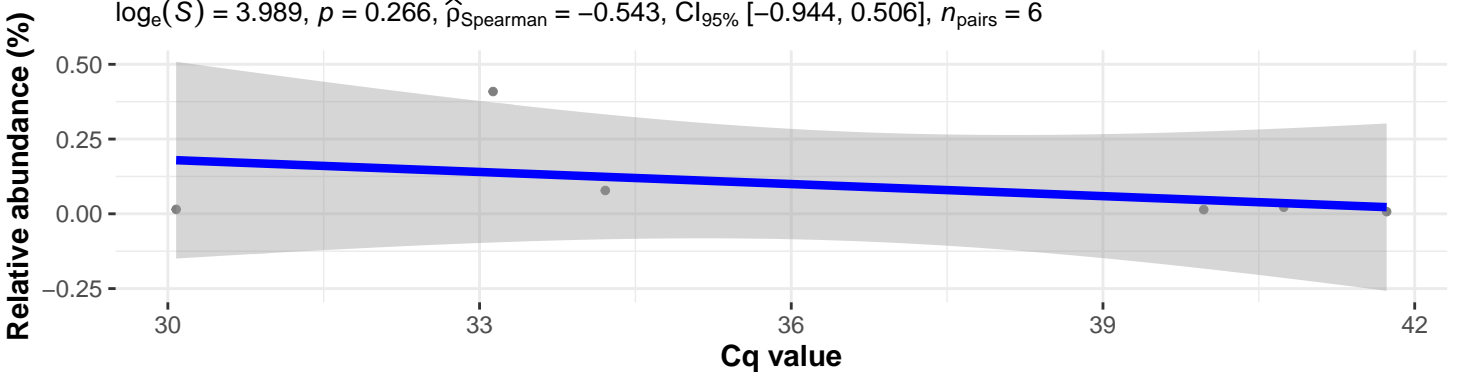
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.984$, $p = 0.576$, $\hat{\rho}_{\text{Spearman}} = -0.217$, $CI_{95\%} [-0.779, 0.540]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

$\log_e(S) = 3.989$, $p = 0.266$, $\hat{\rho}_{\text{Spearman}} = -0.543$, $CI_{95\%} [-0.944, 0.506]$, $n_{\text{pairs}} = 6$

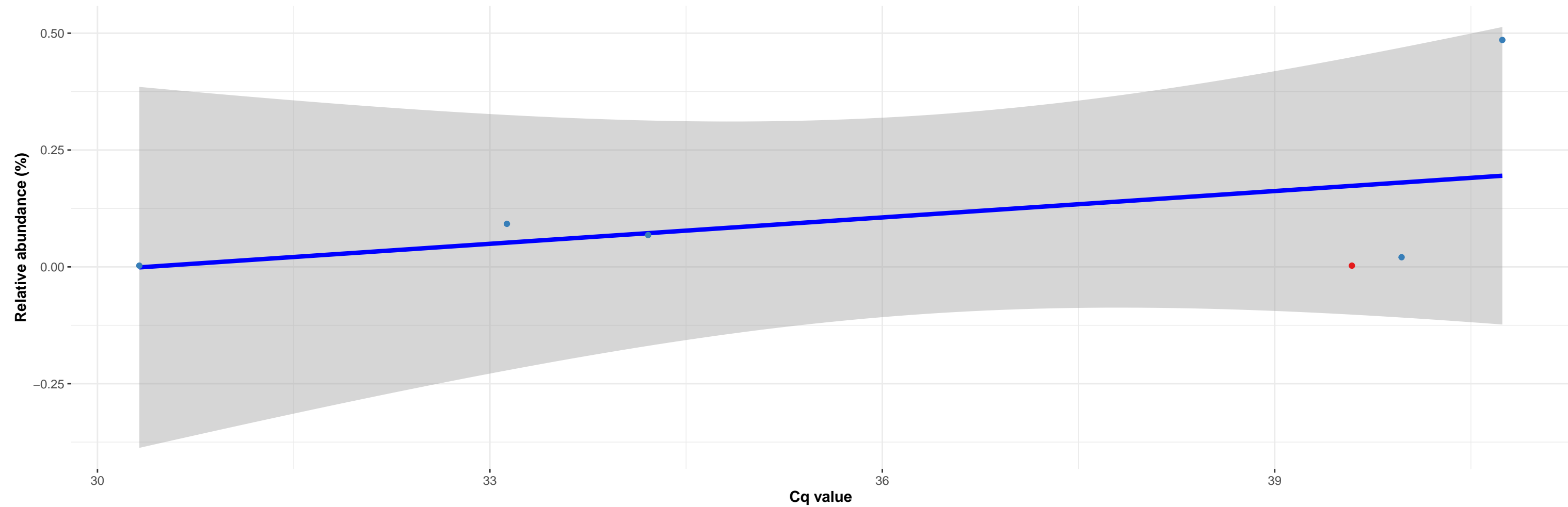


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__uncultured bacterium

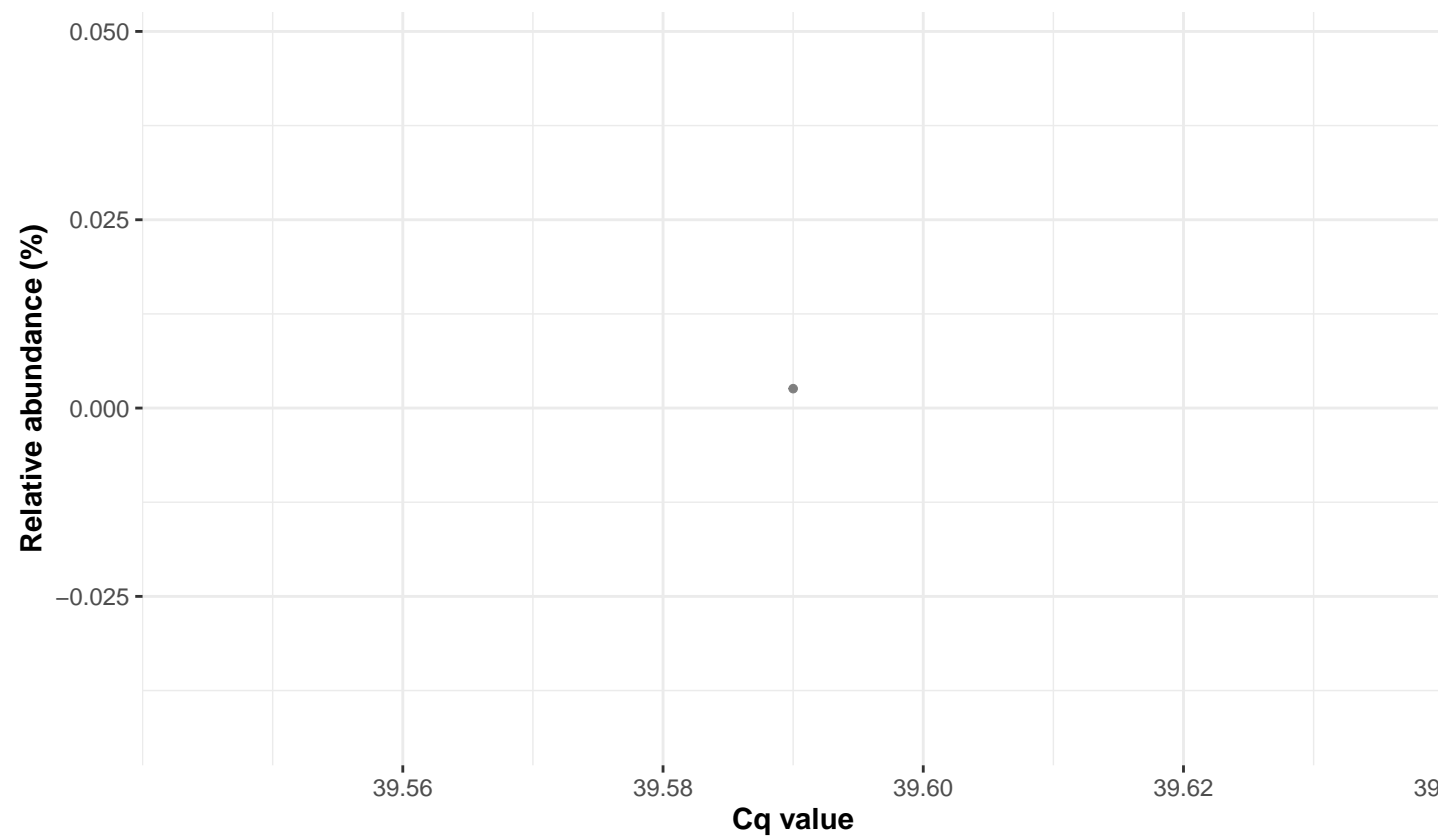
featureID: 4852811146dcf523a9ecf810088a2da5

Correlation with all samples

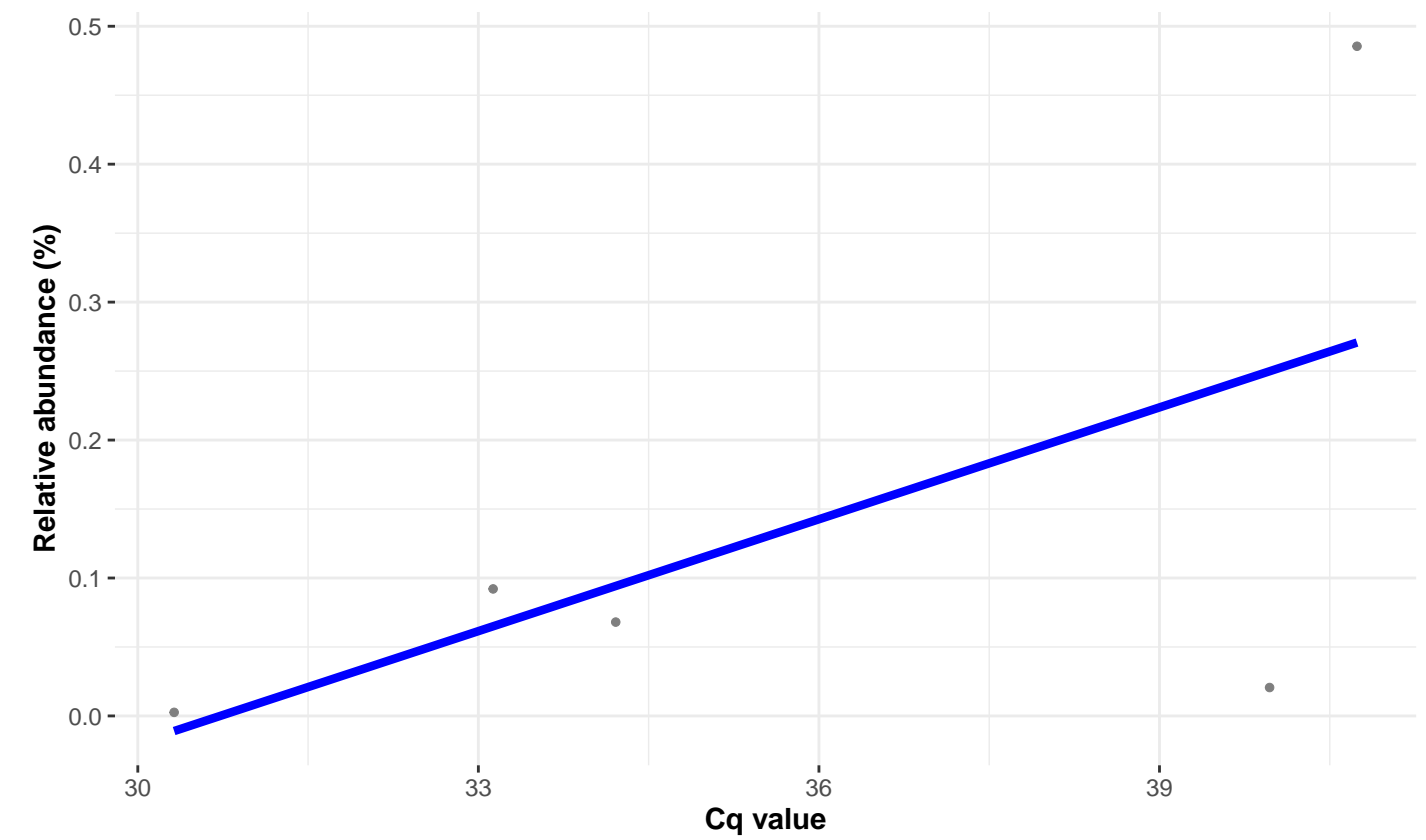
$\log_e(S) = 3.178$, $p = 0.544$, $\hat{\rho}_{\text{Spearman}} = 0.314$, $\text{CI}_{95\%} [-0.686, 0.903]$, $n_{\text{pairs}} = 6$



Correlation within: Tilapia_farmed_lake



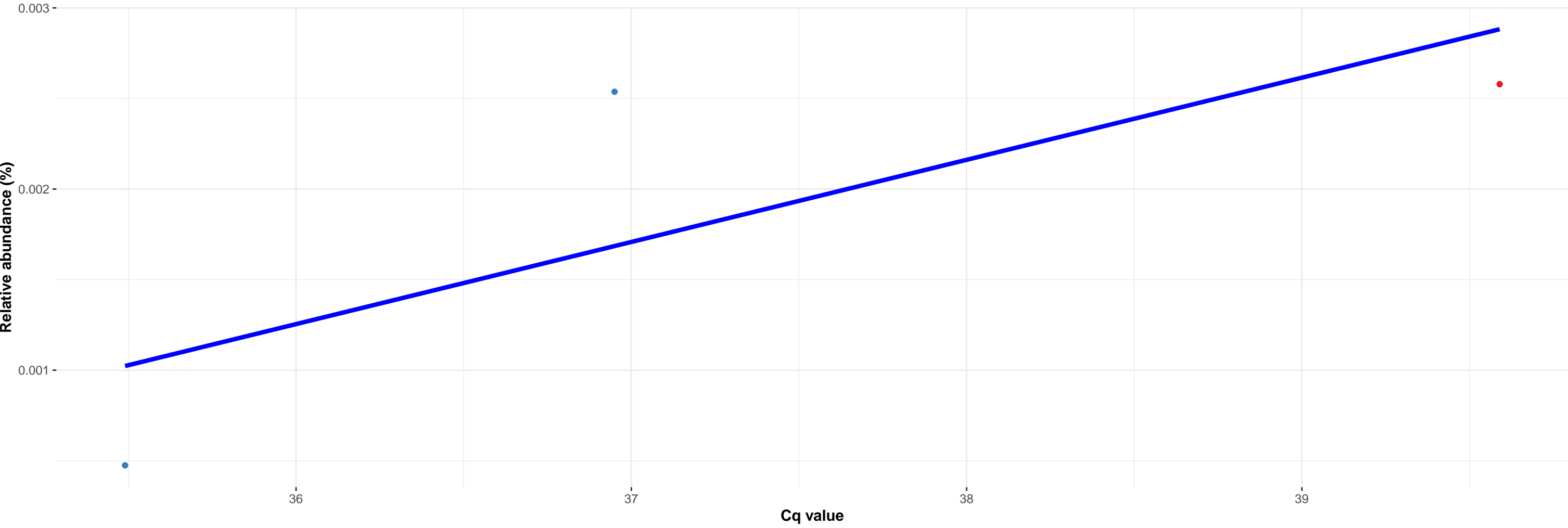
Correlation within: Perch_wild_lake



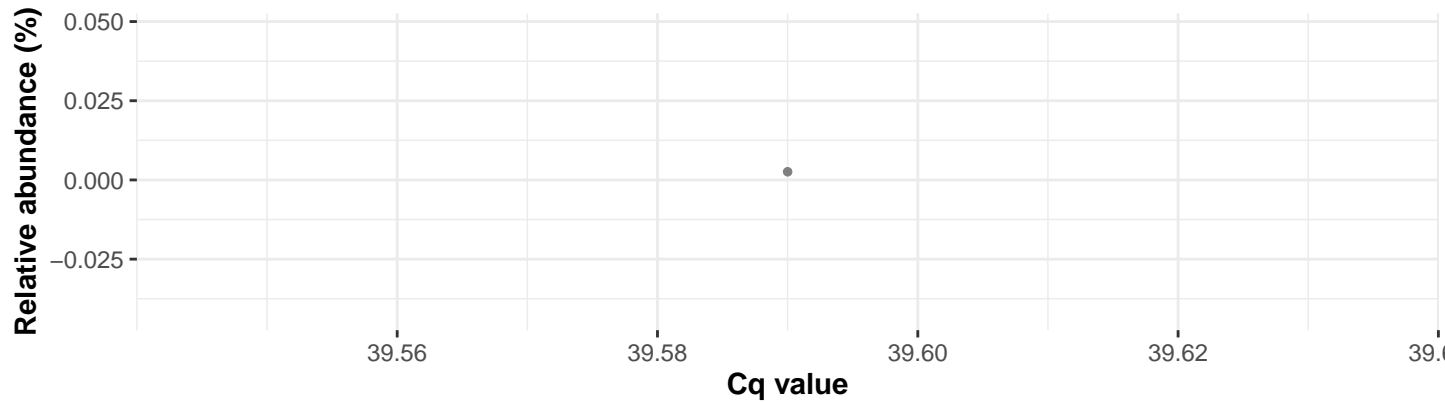
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; NA

featureID: 62611dedc42201591d0c89973f903dde

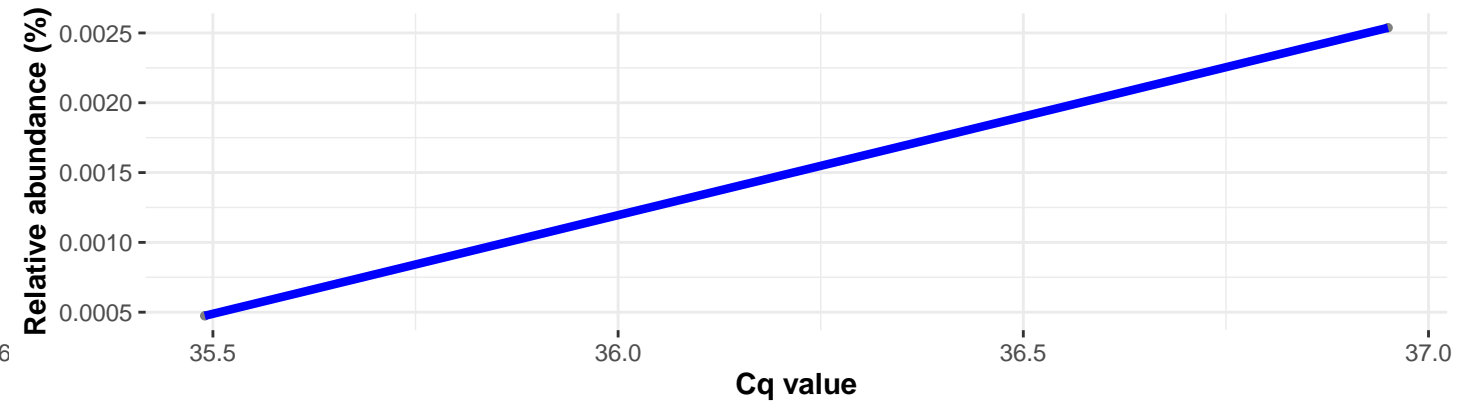
Correlation with all samples



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

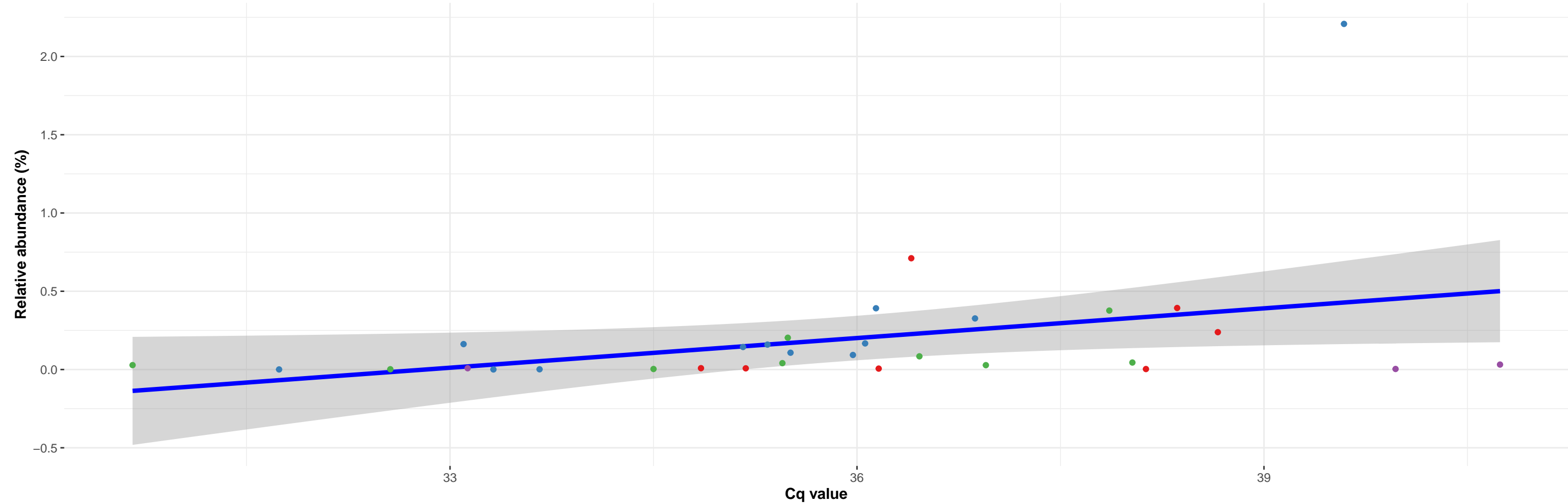


k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiae; o__Chthoniobacterales; f__Chthoniobacteraceae; g__LD29; Ambiguous_taxa

featureID: 550884702aea7eaa9461b76e8ef9da16

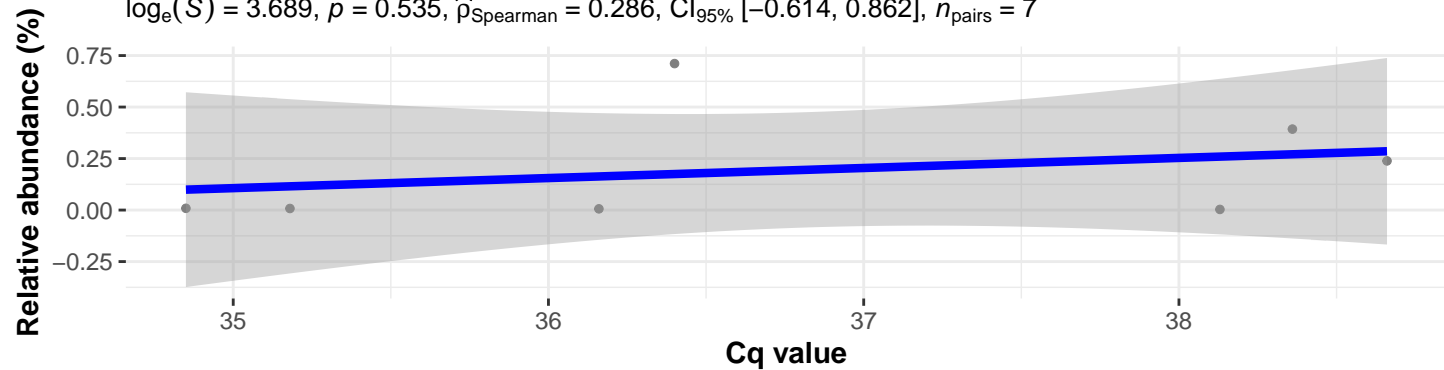
Correlation with all samples

$\log_e(S) = 7.911$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = 0.450$, $\text{CI}_{95\%} [0.103, 0.699]$, $n_{\text{pairs}} = 31$



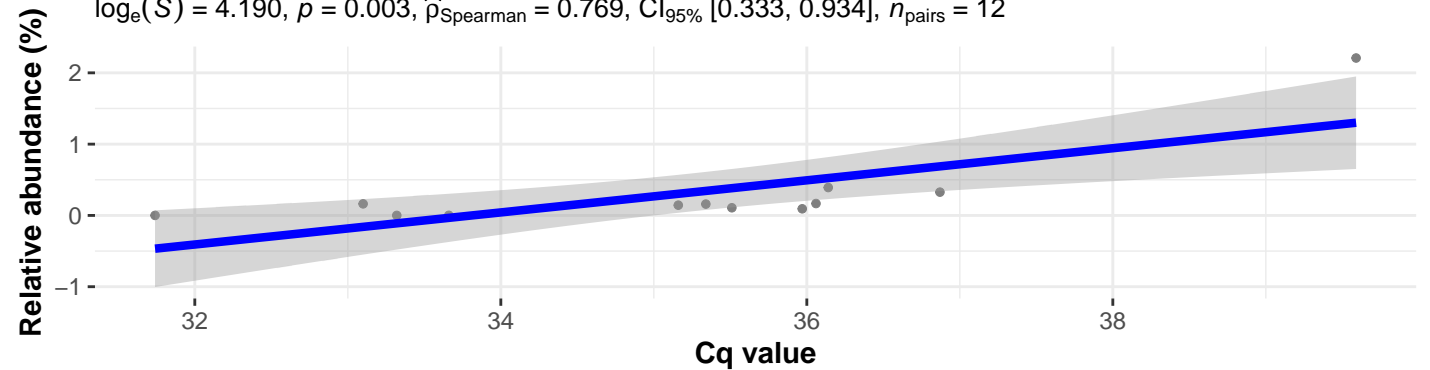
Correlation within: Tilapia_farmed_pond

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



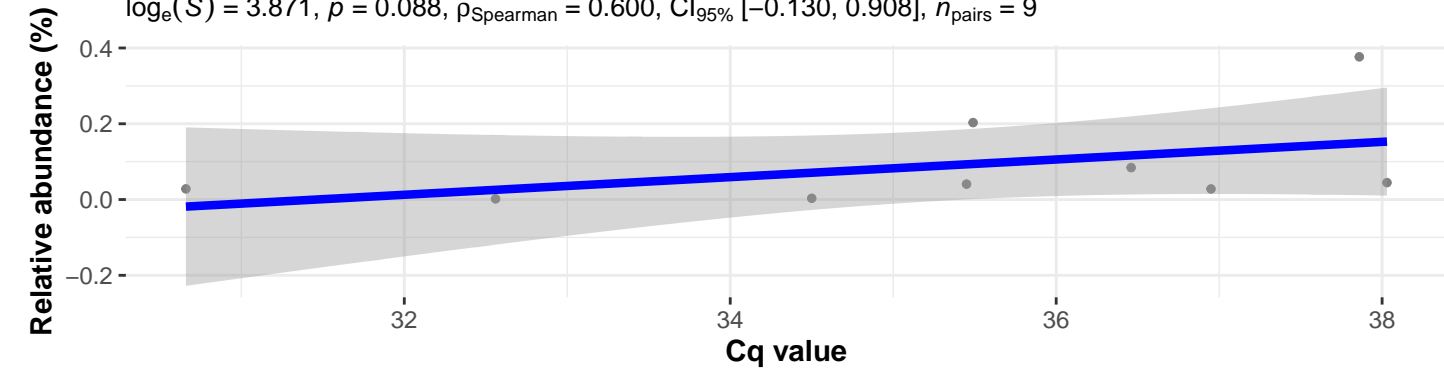
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 4.190$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.769$, $\text{CI}_{95\%} [0.333, 0.934]$, $n_{\text{pairs}} = 12$

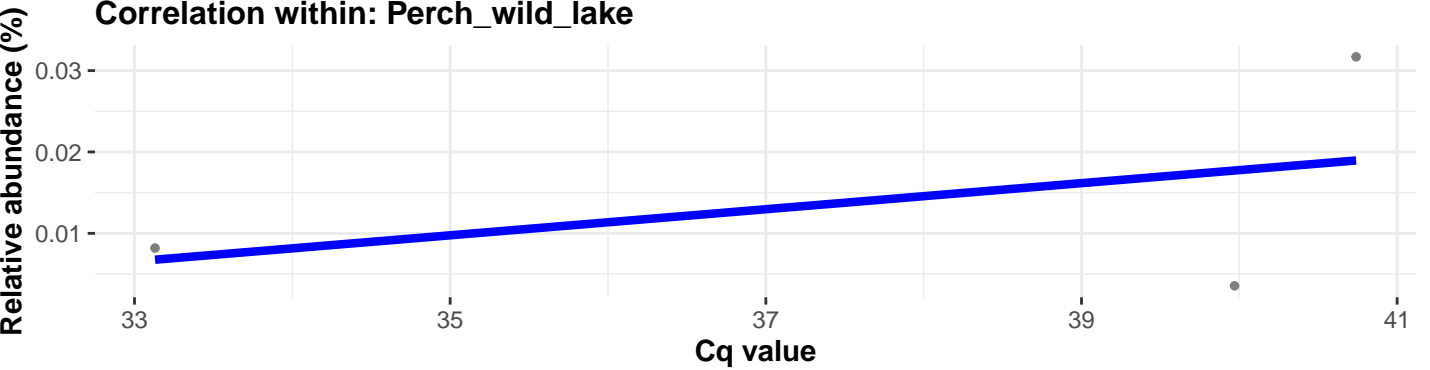


Correlation within: Tilapia_wild_lake

$\log_e(S) = 3.871$, $p = 0.088$, $\hat{\rho}_{\text{Spearman}} = 0.600$, $\text{CI}_{95\%} [-0.130, 0.908]$, $n_{\text{pairs}} = 9$

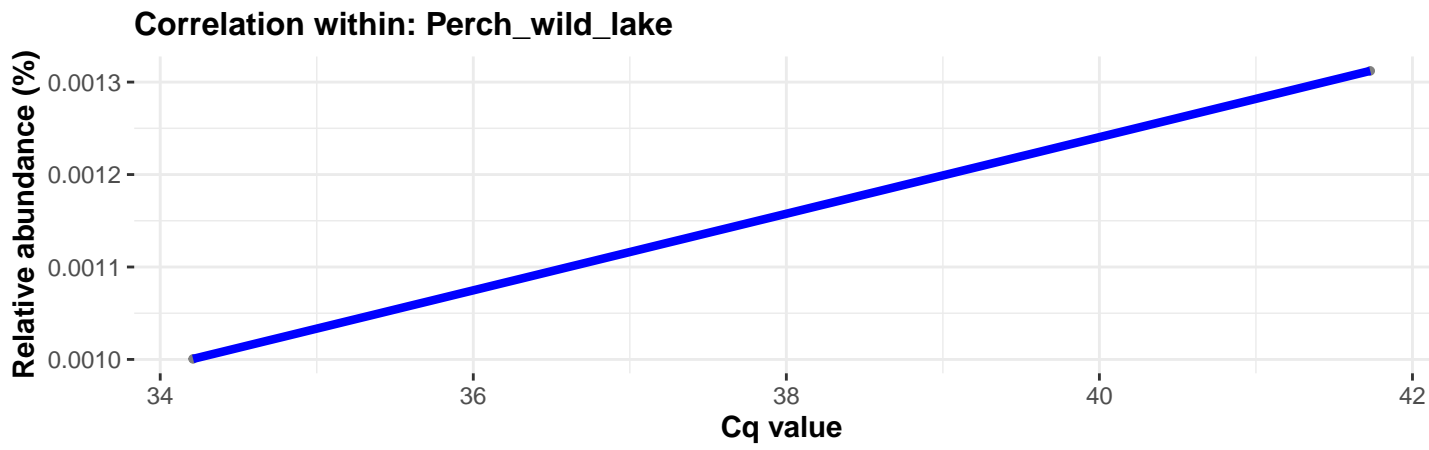
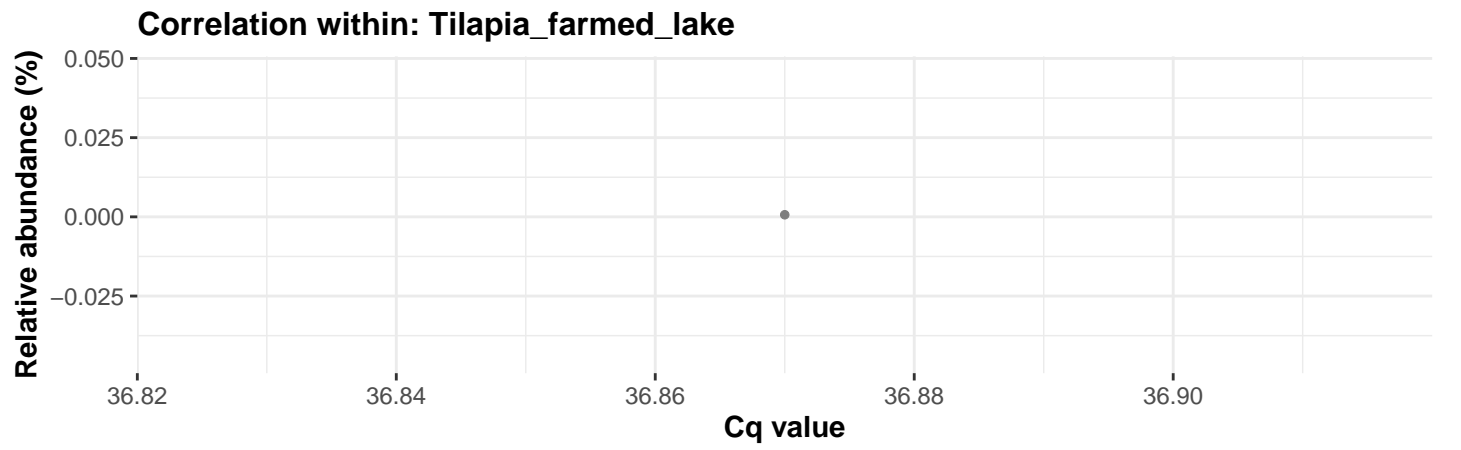
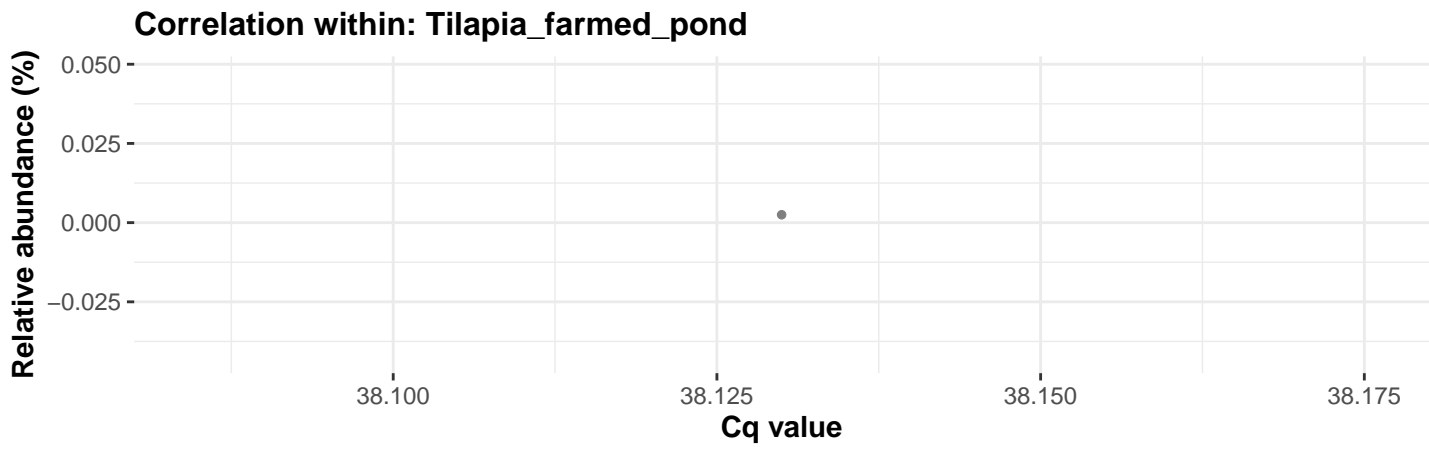
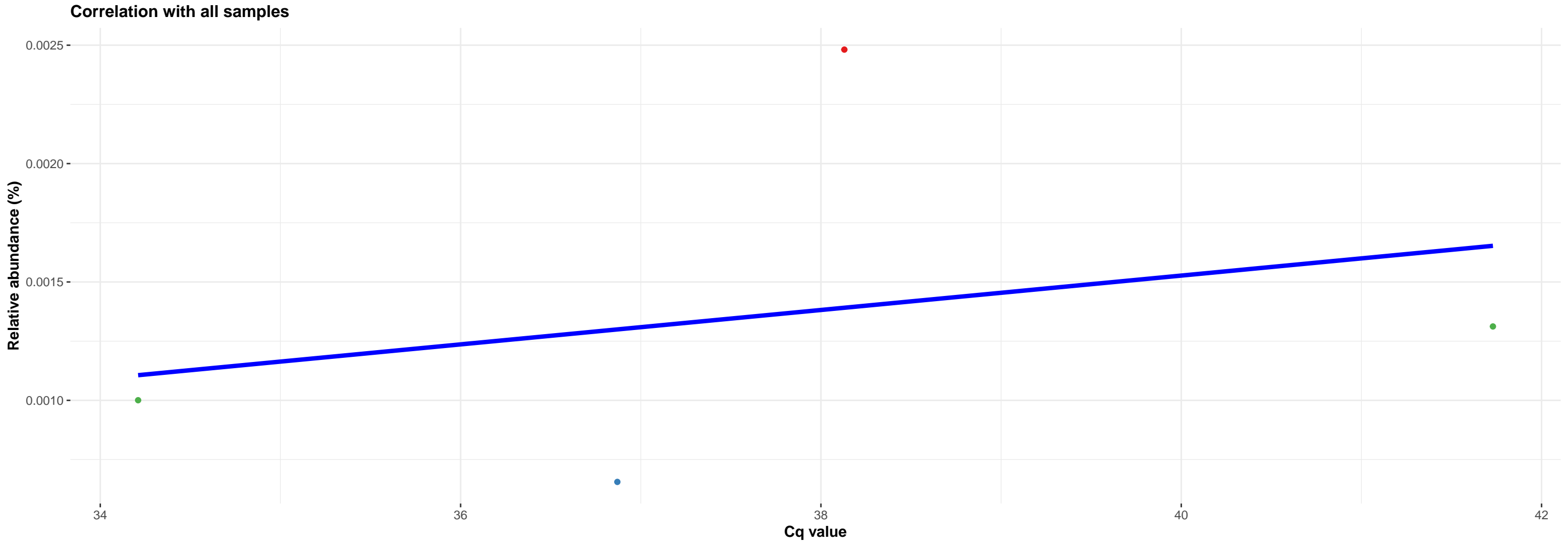


Correlation within: Perch_wild_lake



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; NA

featureID: 43a54829cc0d7a58a61ad7f833cc2b22

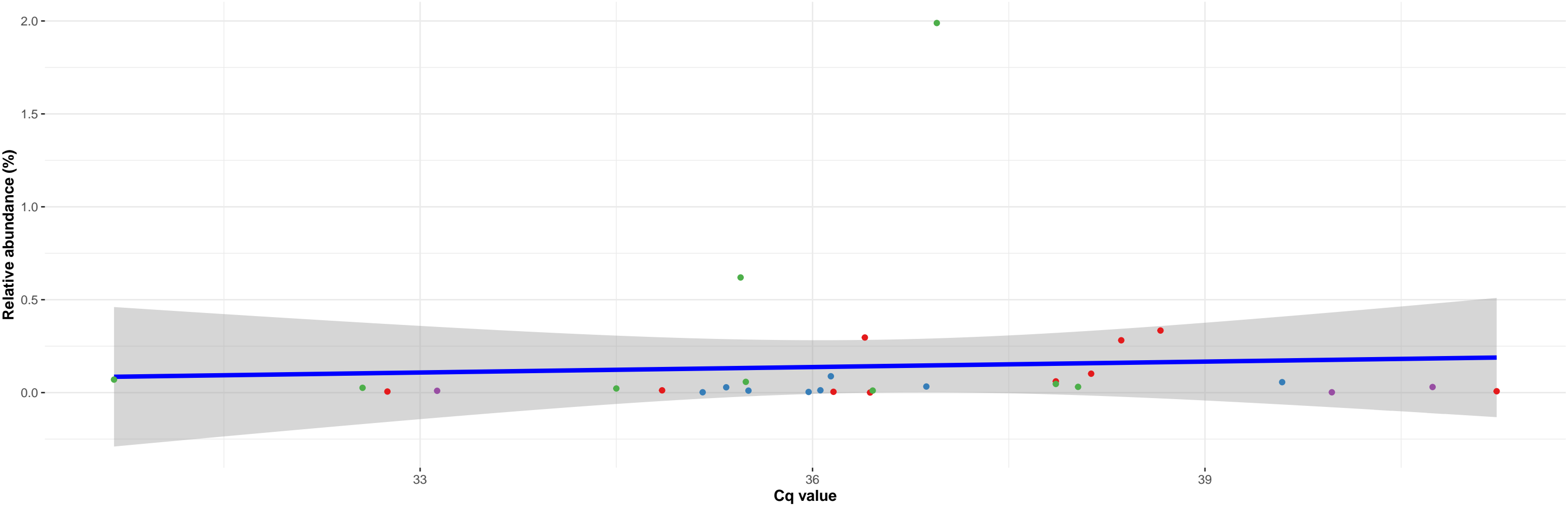


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Methylocystis; NA

featureID: 675f287d70a622c1c4cd8e1b634e8aed

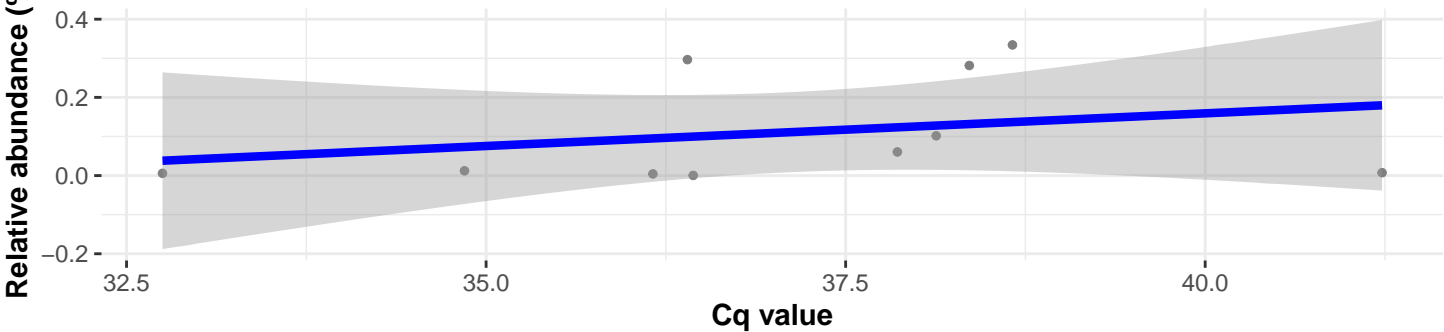
Correlation with all samples

$\log_e(S) = 8.192$, $p = 0.298$, $\hat{\rho}_{\text{Spearman}} = 0.197$, $\text{CI}_{95\%} [-0.187, 0.528]$, $n_{\text{pairs}} = 30$



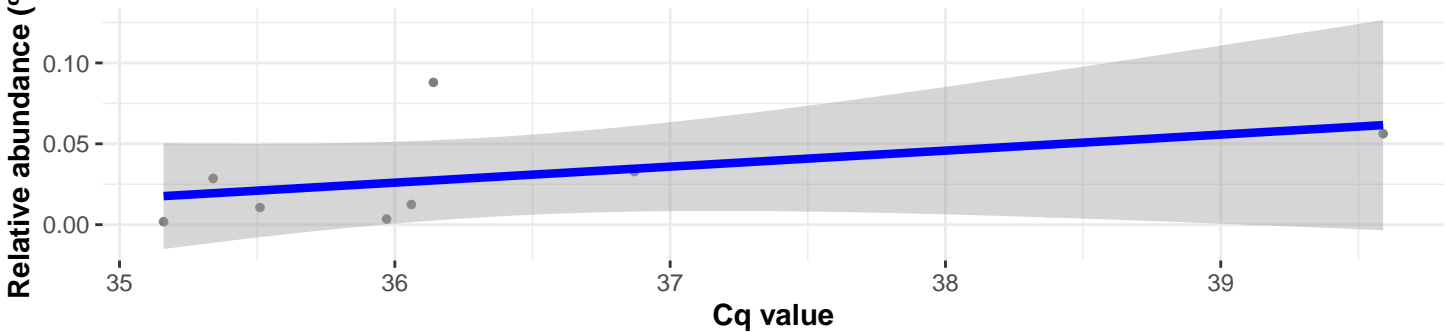
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.522$, $p = 0.200$, $\hat{\rho}_{\text{Spearman}} = 0.442$, $\text{CI}_{95\%} [-0.280, 0.845]$, $n_{\text{pairs}} = 10$



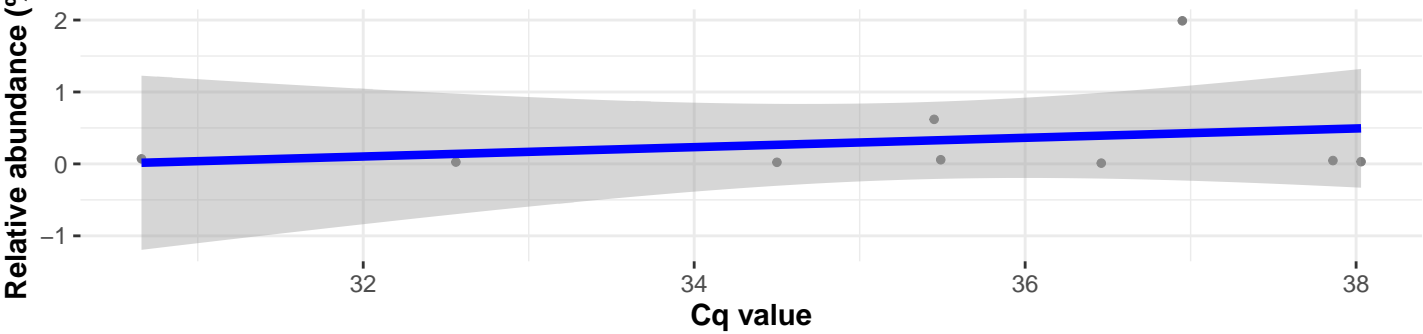
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 2.996$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = 0.762$, $\text{CI}_{95\%} [0.098, 0.957]$, $n_{\text{pairs}} = 8$

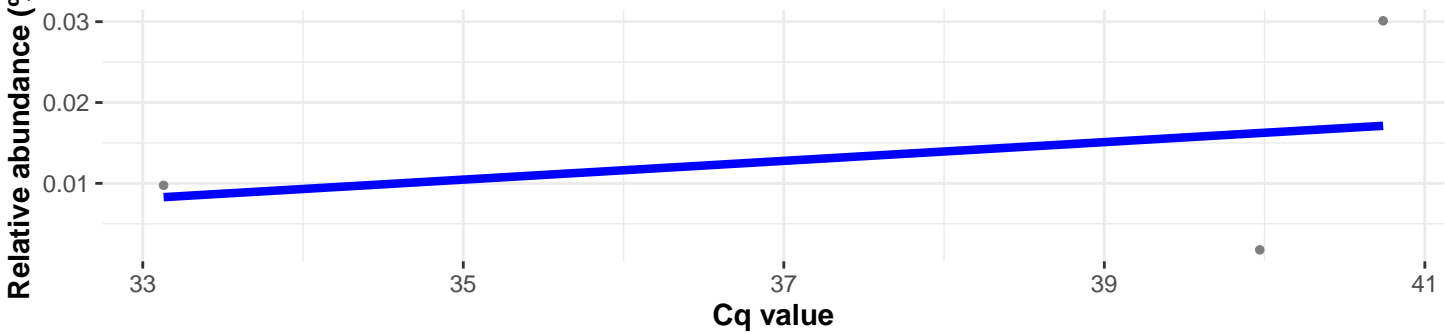


Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.771$, $p = 0.966$, $\hat{\rho}_{\text{Spearman}} = 0.017$, $\text{CI}_{95\%} [-0.668, 0.686]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

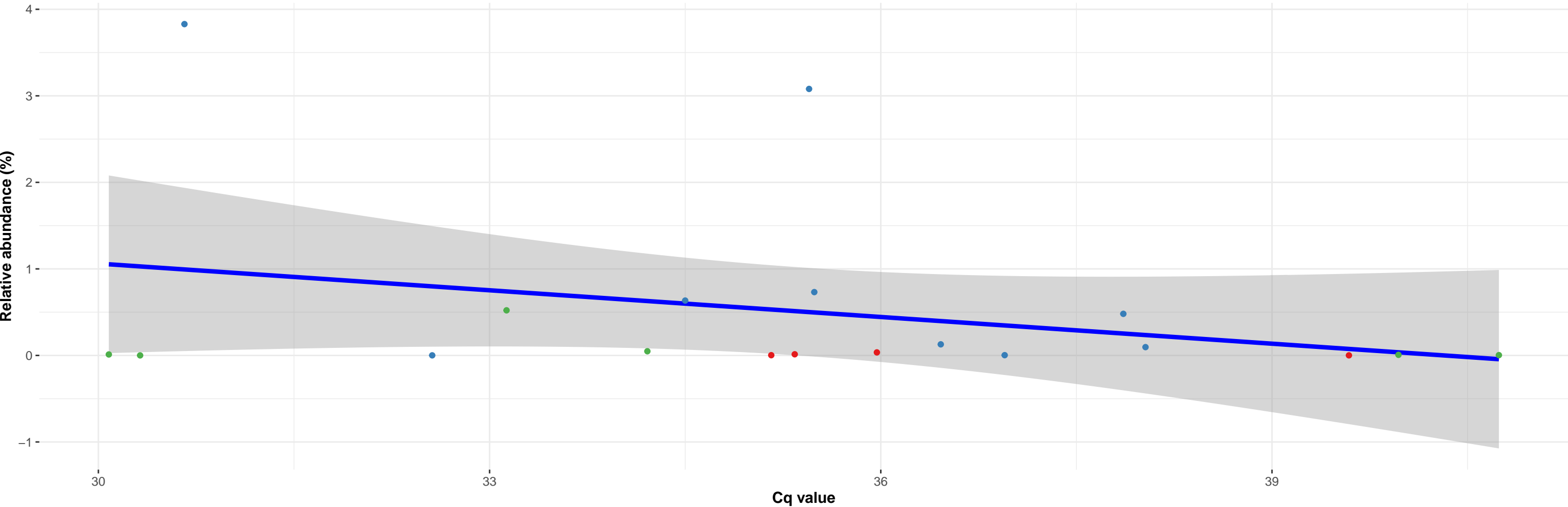


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: f4ddba285154bdd47f4dc510c2038305

Correlation with all samples

$\log_e(S) = 7.107$, $p = 0.775$, $\hat{\rho}_{\text{Spearman}} = -0.070$, $\text{CI}_{95\%} [-0.519, 0.409]$, $n_{\text{pairs}} = 19$



Correlation within: Tilapia_farmed_pond

Relative abundance (%)

Cq value

Correlation within: Tilapia_farmed_lake

Relative abundance (%)

Cq value

Correlation within: Tilapia_wild_lake

Relative abundance (%)

Cq value

Correlation within: Perch_wild_lake

Relative abundance (%)

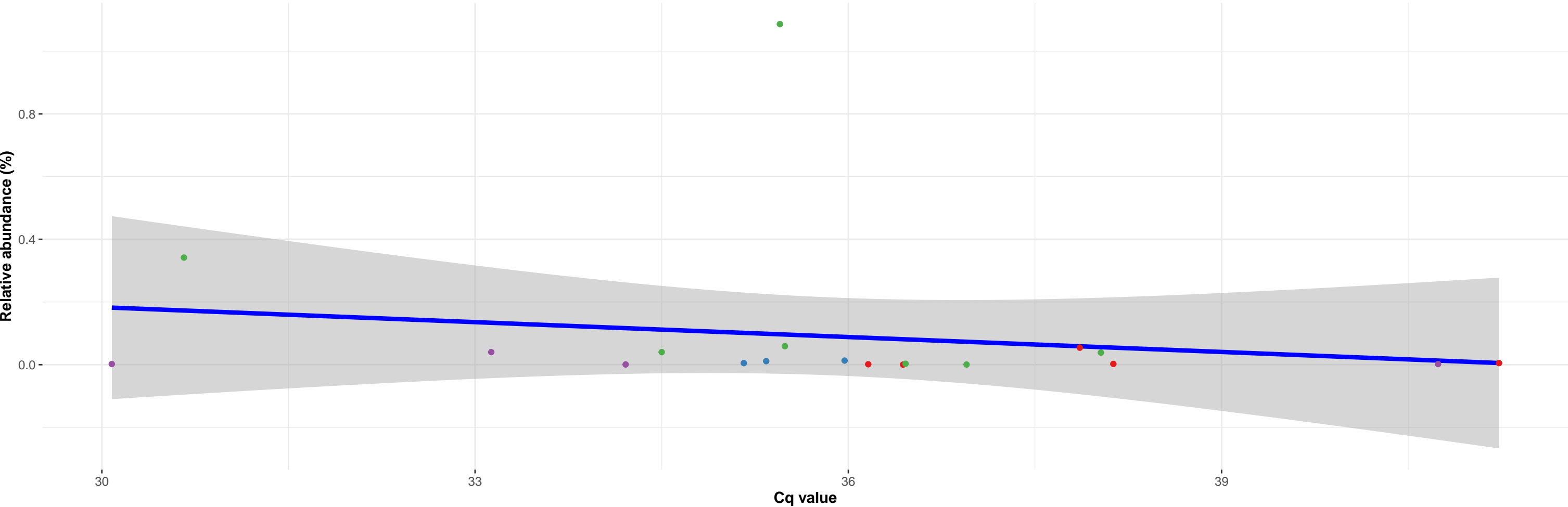
Cq value

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

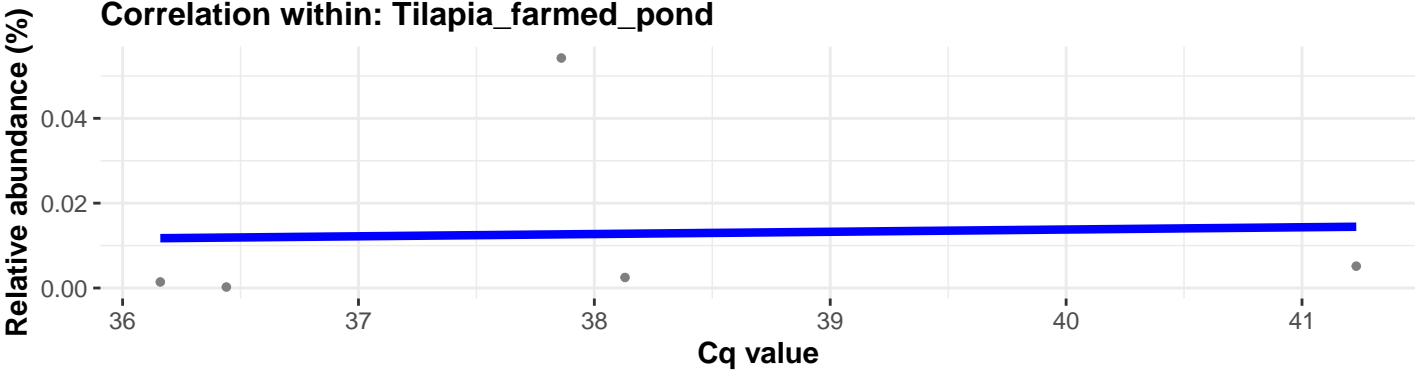
featureID: 2e119ce67894fe00027176e52f17a225

Correlation with all samples

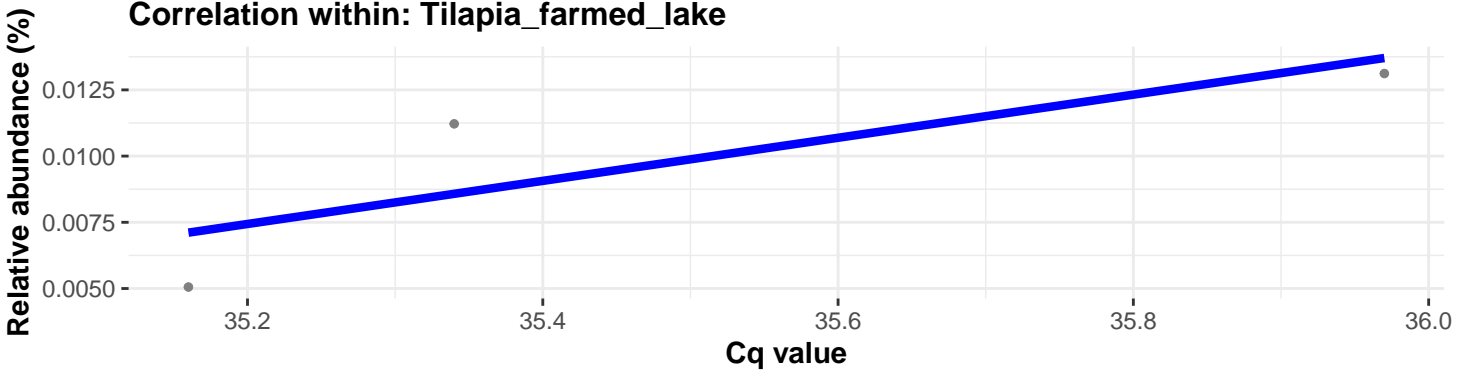
$\log_e(S) = 7.256$, $p = 0.318$, $\hat{\rho}_{\text{Spearman}} = -0.242$, $CI_{95\%} [-0.636, 0.252]$, $n_{\text{pairs}} = 19$



Correlation within: Tilapia_farmed_pond

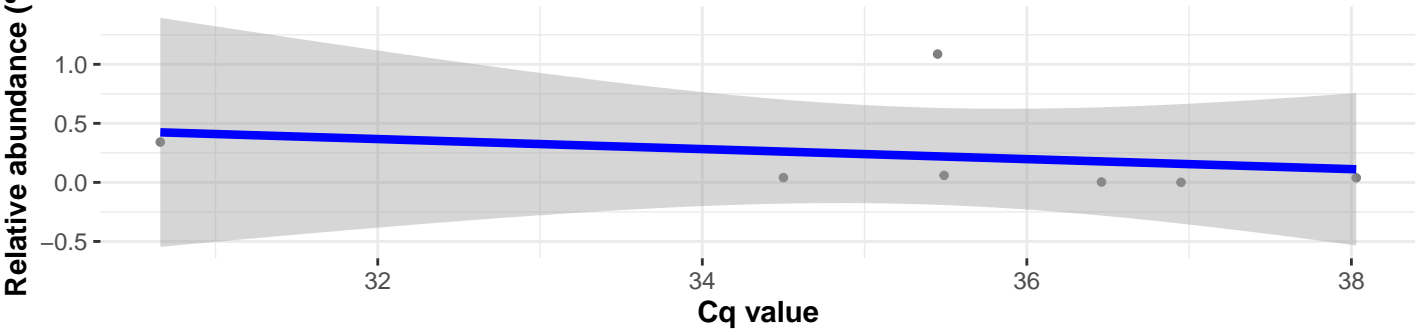


Correlation within: Tilapia_farmed_lake



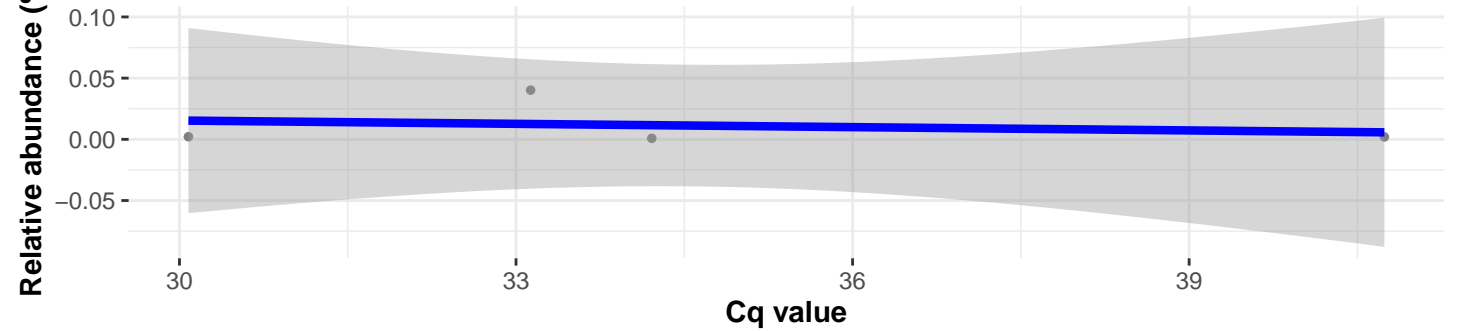
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.564$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = -0.714$, $CI_{95\%} [-0.957, 0.113]$, $n_{\text{pairs}} = 7$



Correlation within: Perch_wild_lake

$\log_e(S) = 2.773$, $p = 0.400$, $\hat{\rho}_{\text{Spearman}} = -0.600$, $CI_{95\%} [-0.991, 0.868]$, $n_{\text{pairs}} = 4$

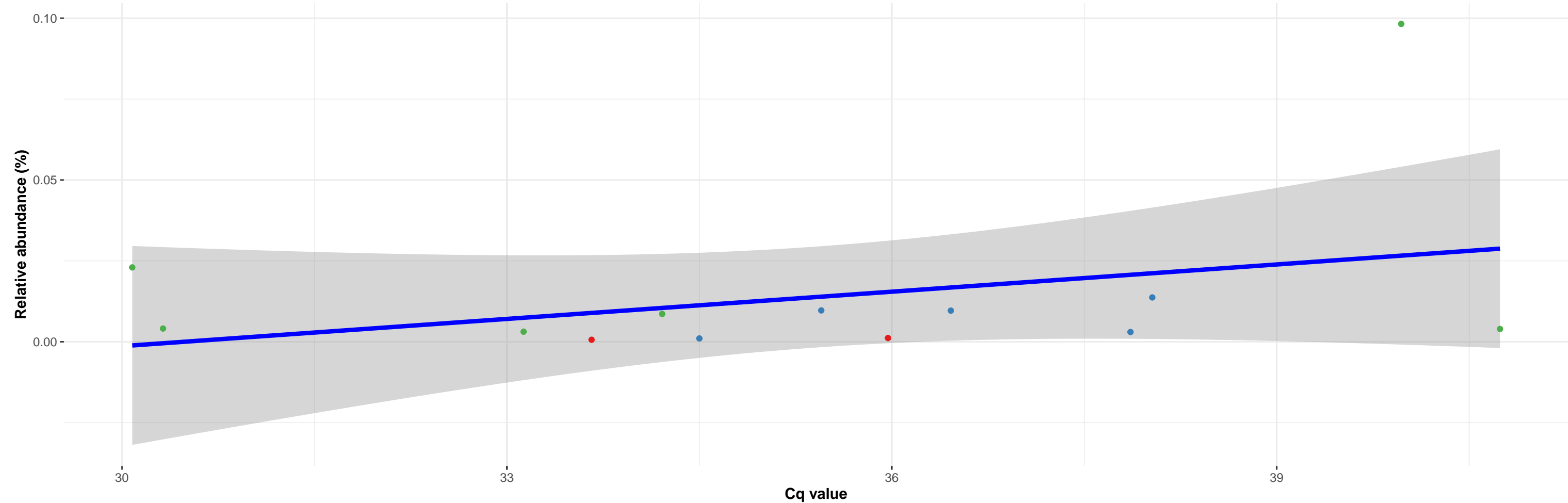


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

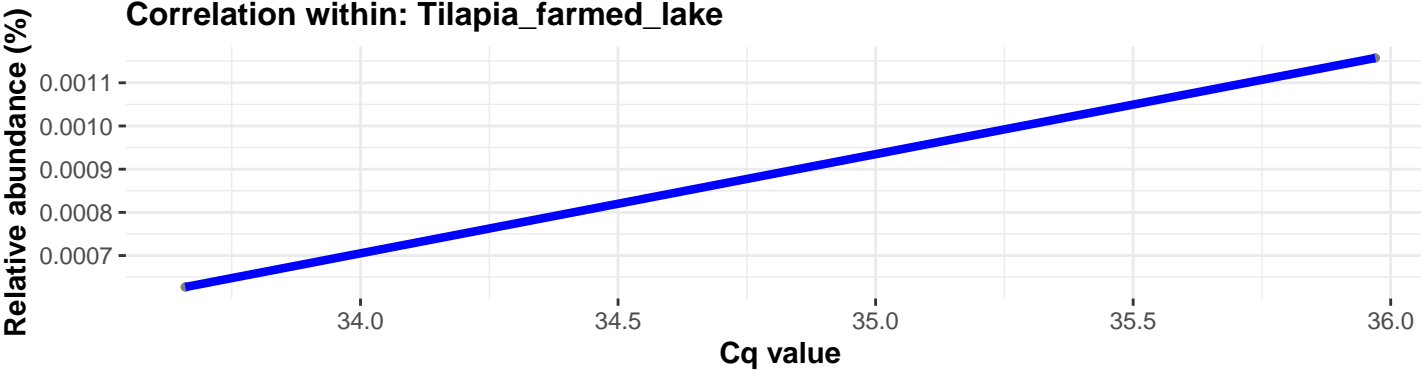
featureID: 8cc0e176d680aac1a413121d8633c30d

Correlation with all samples

$\log_e(S) = 5.717$, $p = 0.590$, $\hat{\rho}_{\text{Spearman}} = 0.165$, $CI_{95\%} [-0.440, 0.667]$, $n_{\text{pairs}} = 13$

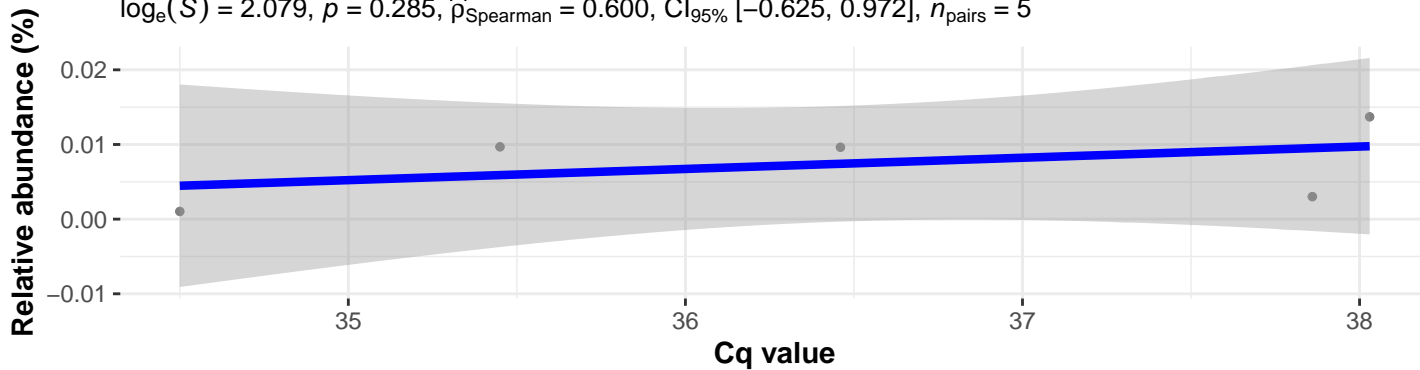


Correlation within: Tilapia_farmed_lake



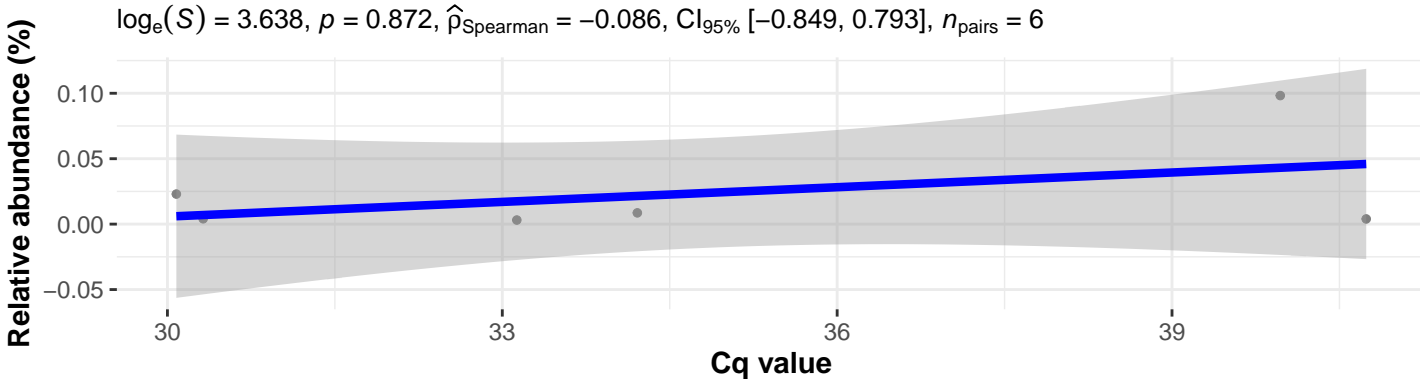
Correlation within: Tilapia_wild_lake

$\log_e(S) = 2.079$, $p = 0.285$, $\hat{\rho}_{\text{Spearman}} = 0.600$, $CI_{95\%} [-0.625, 0.972]$, $n_{\text{pairs}} = 5$



Correlation within: Perch_wild_lake

$\log_e(S) = 3.638$, $p = 0.872$, $\hat{\rho}_{\text{Spearman}} = -0.086$, $CI_{95\%} [-0.849, 0.793]$, $n_{\text{pairs}} = 6$

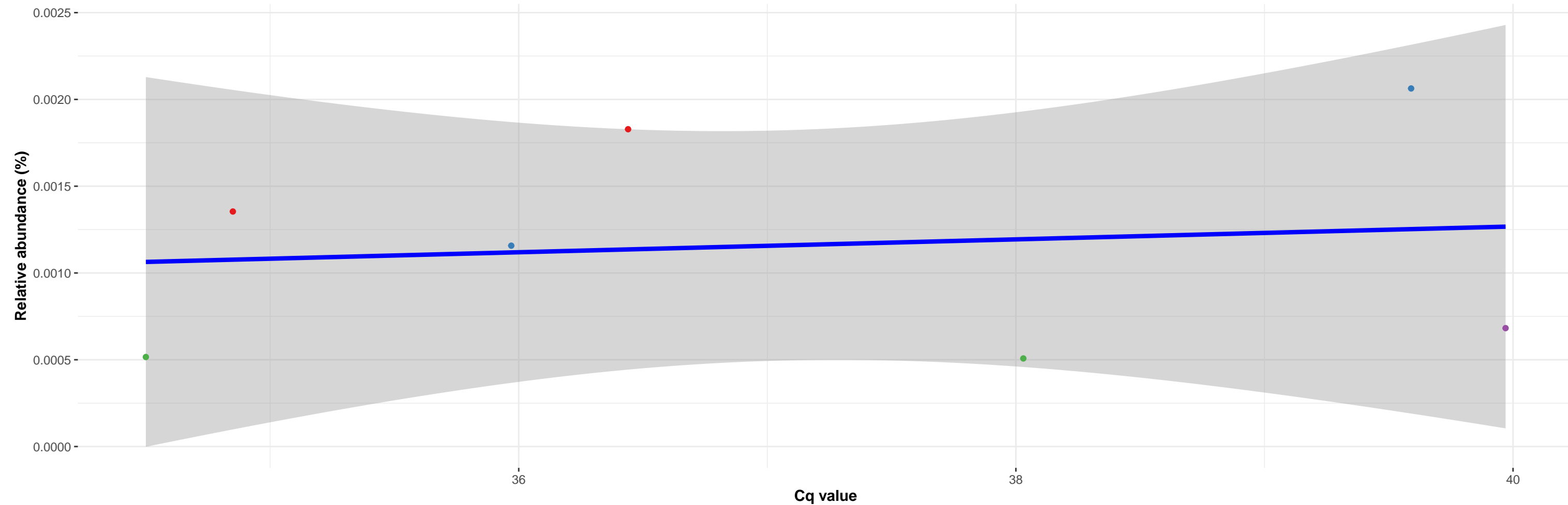


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Micrococcus; NA

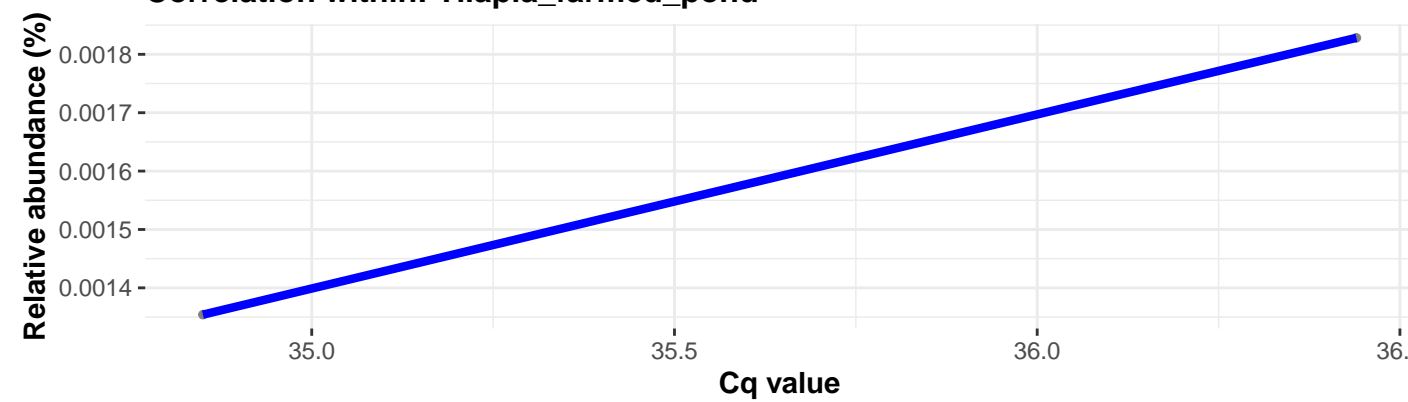
featureID: 09403870435de24e0d1079059a287957

Correlation with all samples

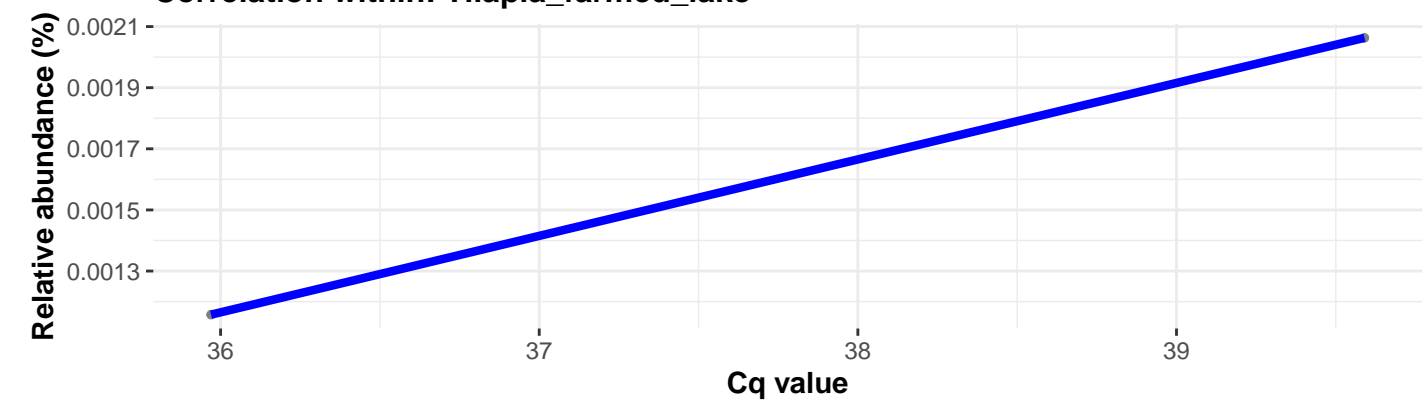
$\log_e(S) = 3.871$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = 0.143$, $CI_{95\%} [-0.699, 0.819]$, $n_{\text{pairs}} = 7$



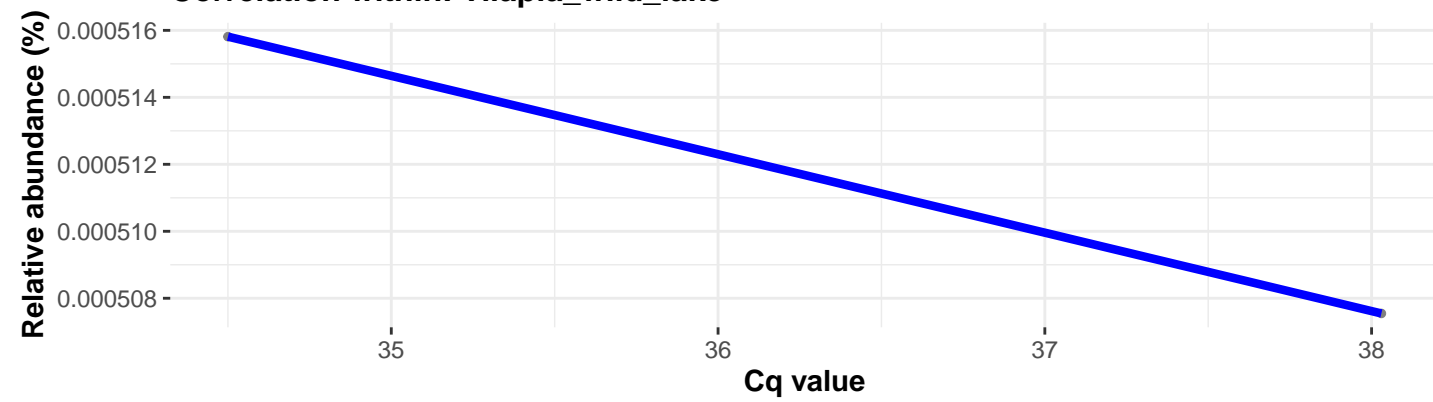
Correlation within: Tilapia_farmed_pond



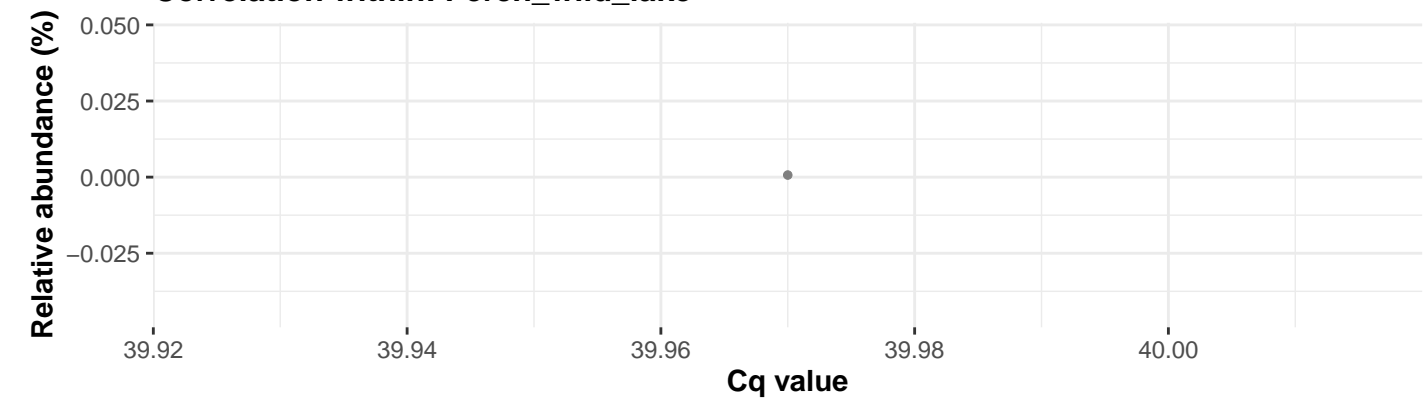
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



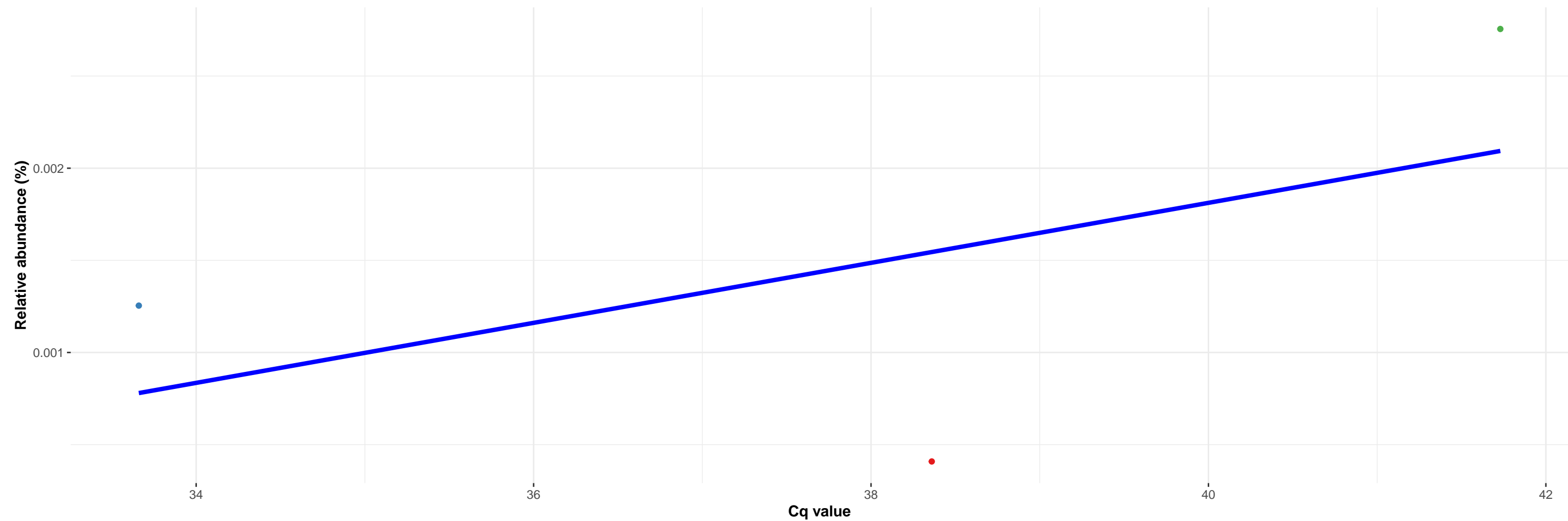
Correlation within: Perch_wild_lake



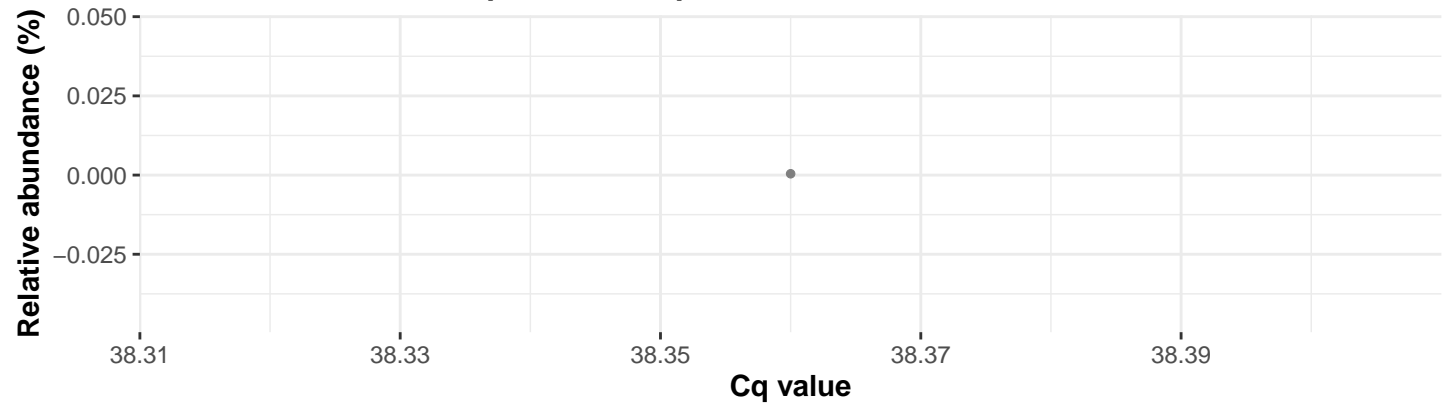
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

featureID: 07c3160551922faa7be5740ea3adc189

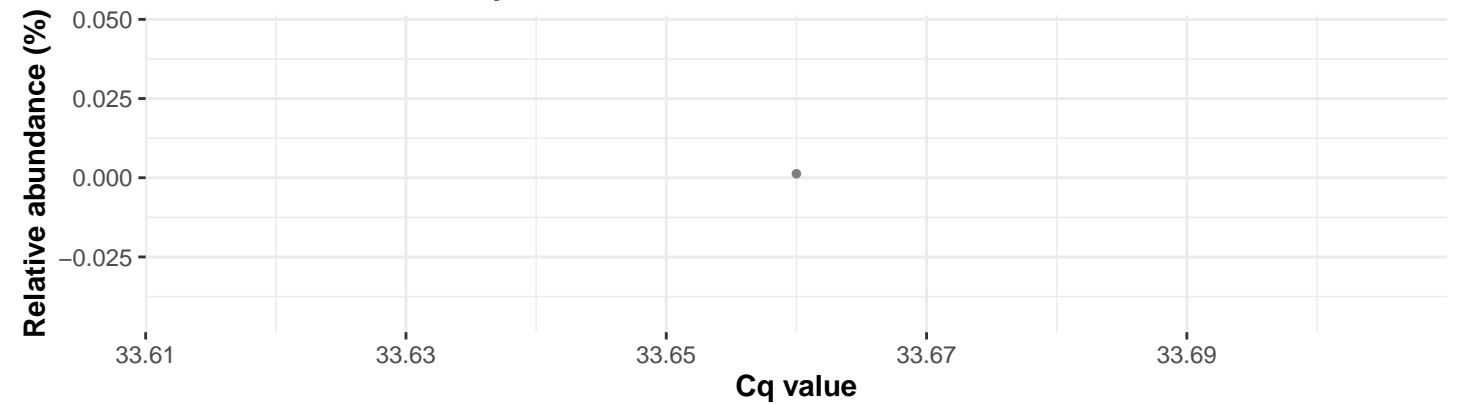
Correlation with all samples



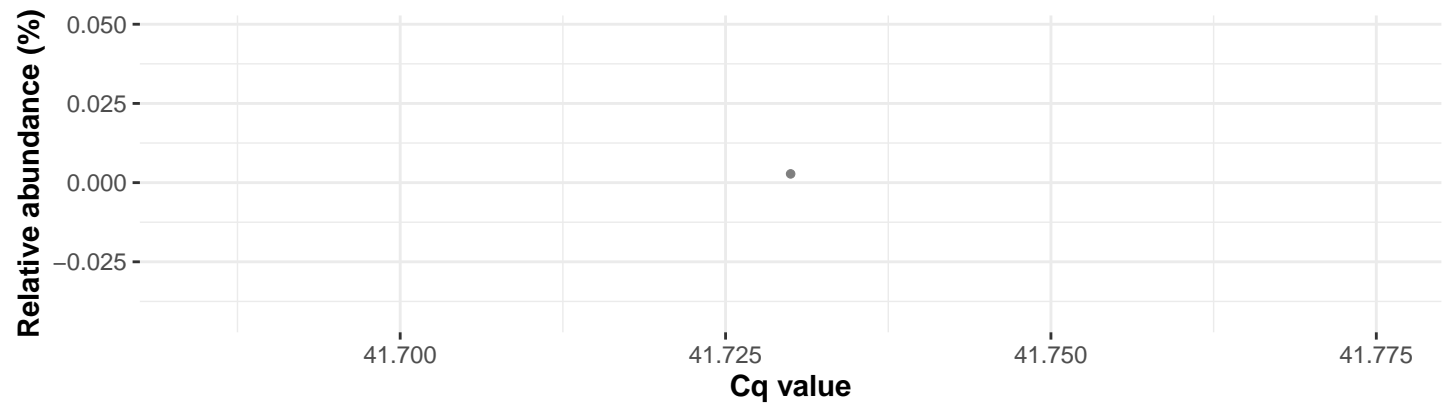
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_farmed_lake



Correlation within: Perch_wild_lake

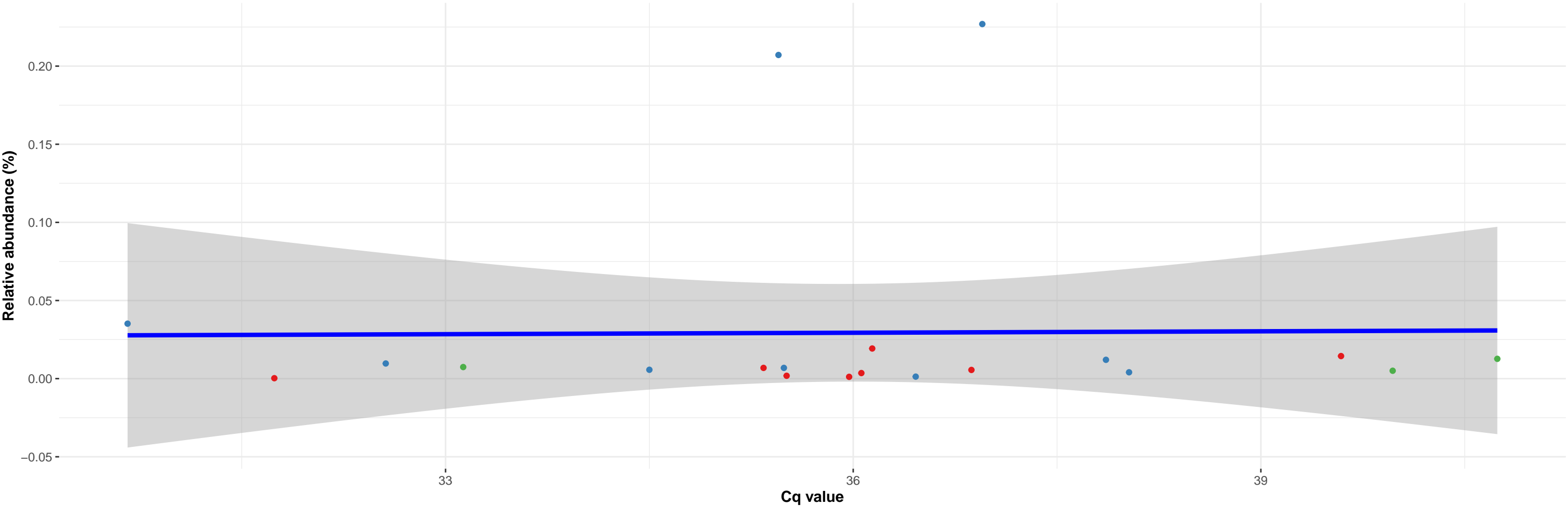


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methylocaldum; s__uncultured bacterium

featureID: 572e092b99869f99a6ae2c111893fbc5

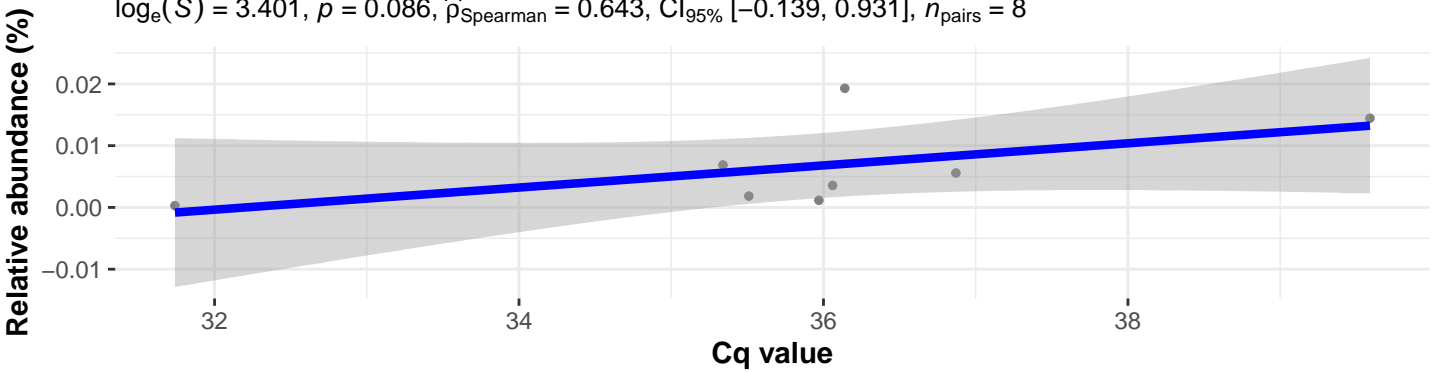
Correlation with all samples

$\log_e(S) = 7.129$, $p = 0.796$, $\hat{\rho}_{\text{Spearman}} = 0.062$, $CI_{95\%} [-0.403, 0.501]$, $n_{\text{pairs}} = 20$



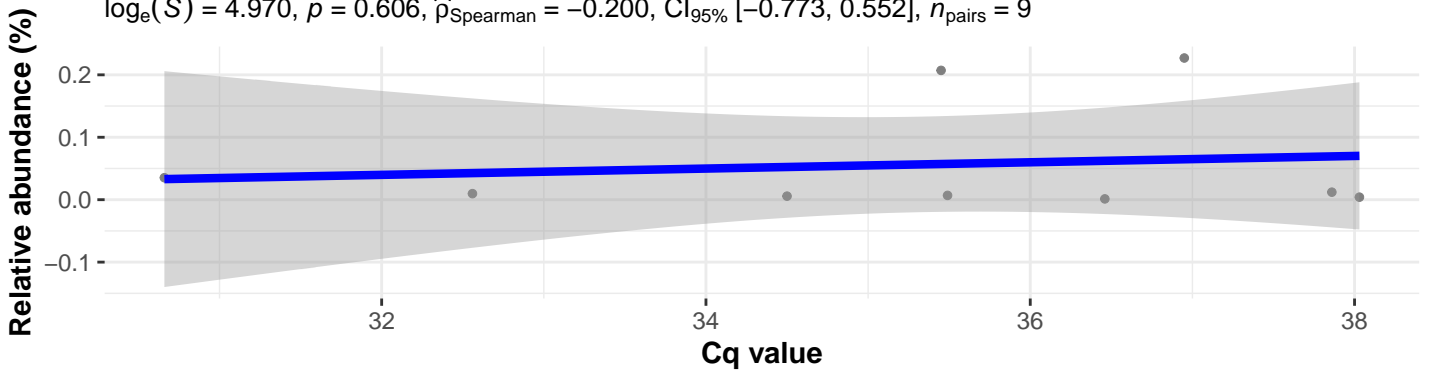
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 3.401$, $p = 0.086$, $\hat{\rho}_{\text{Spearman}} = 0.643$, $CI_{95\%} [-0.139, 0.931]$, $n_{\text{pairs}} = 8$

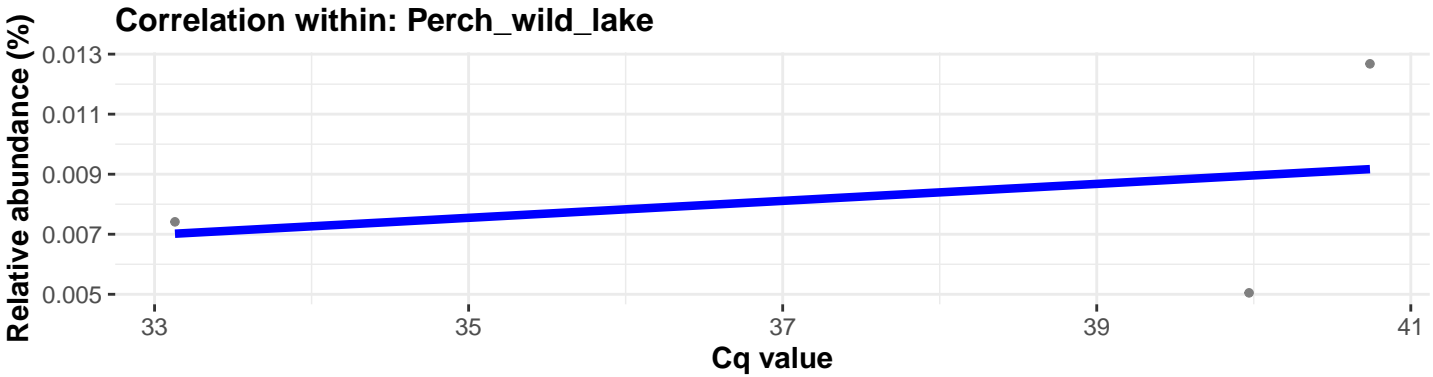


Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.970$, $p = 0.606$, $\hat{\rho}_{\text{Spearman}} = -0.200$, $CI_{95\%} [-0.773, 0.552]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

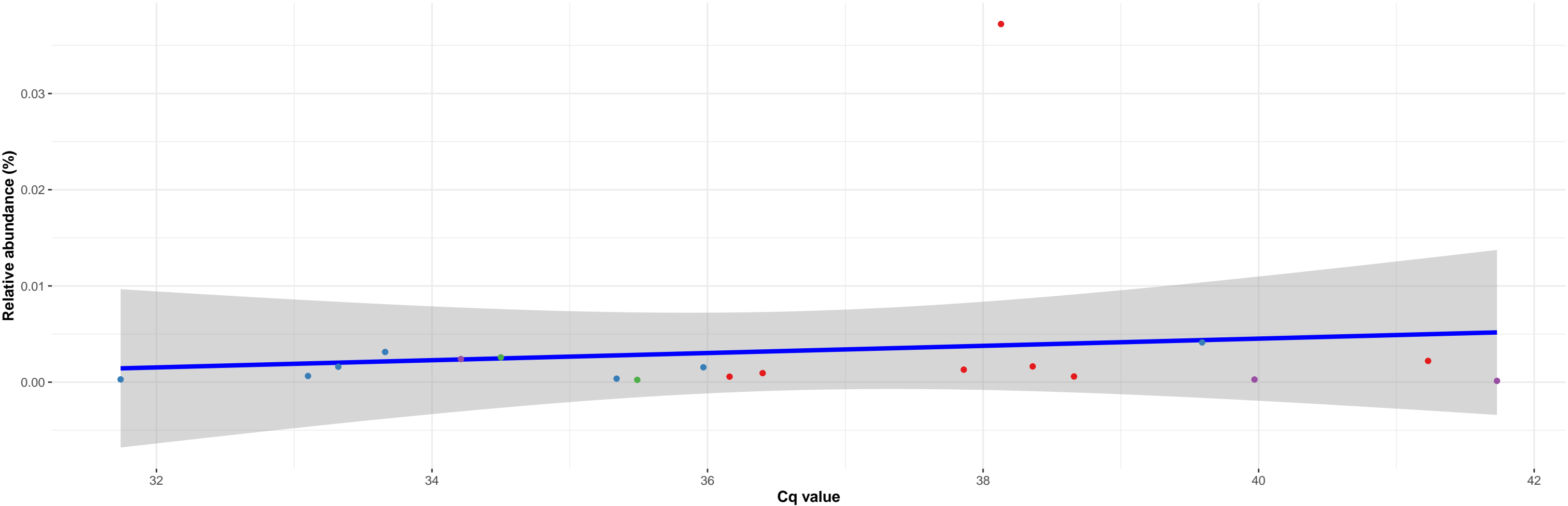


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

featureID: b02a8d33d018119dedb2db15db887bfd

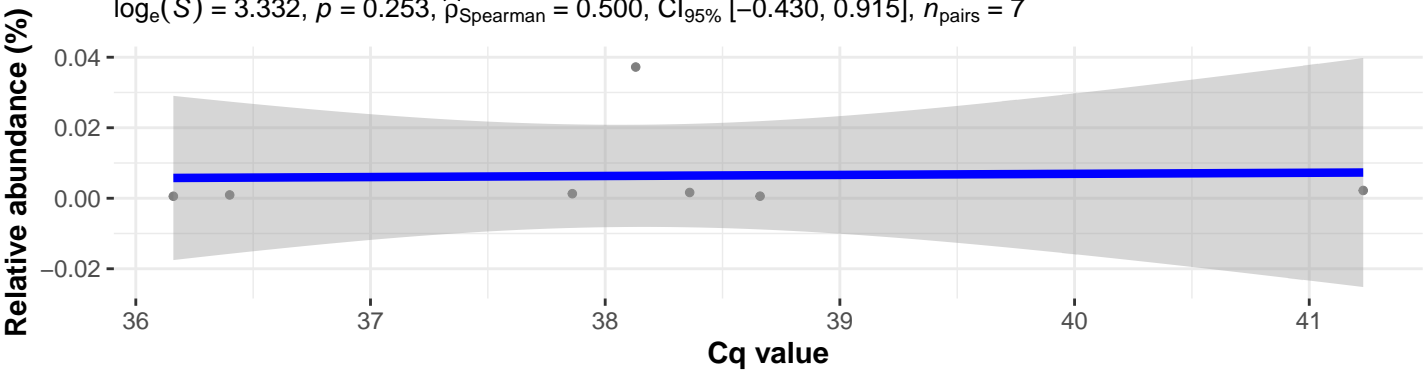
Correlation with all samples

$\log_e(S) = 7.093$, $p = 0.819$, $\hat{\rho}_{\text{Spearman}} = -0.056$, $CI_{95\%} [-0.508, 0.420]$, $n_{\text{pairs}} = 19$



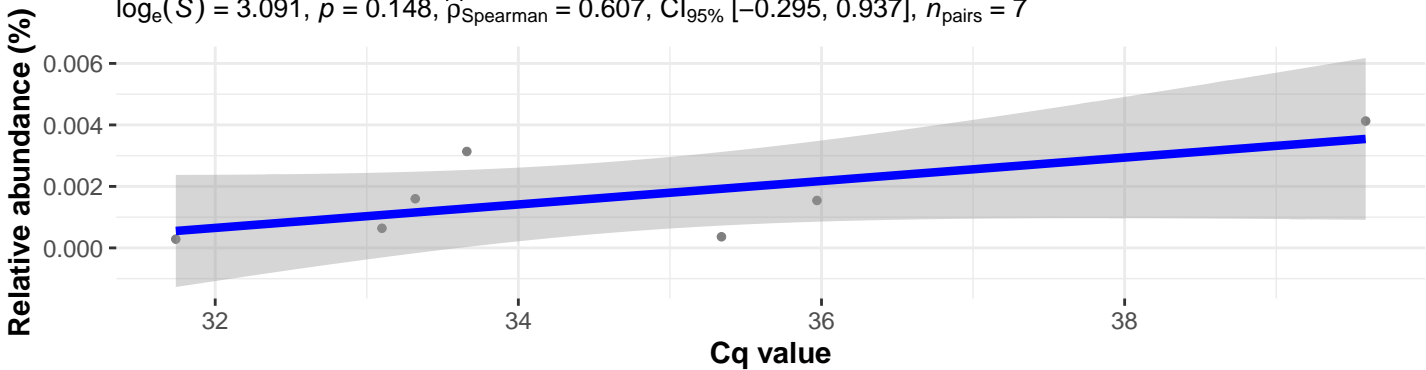
Correlation within: Tilapia_farmed_pond

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

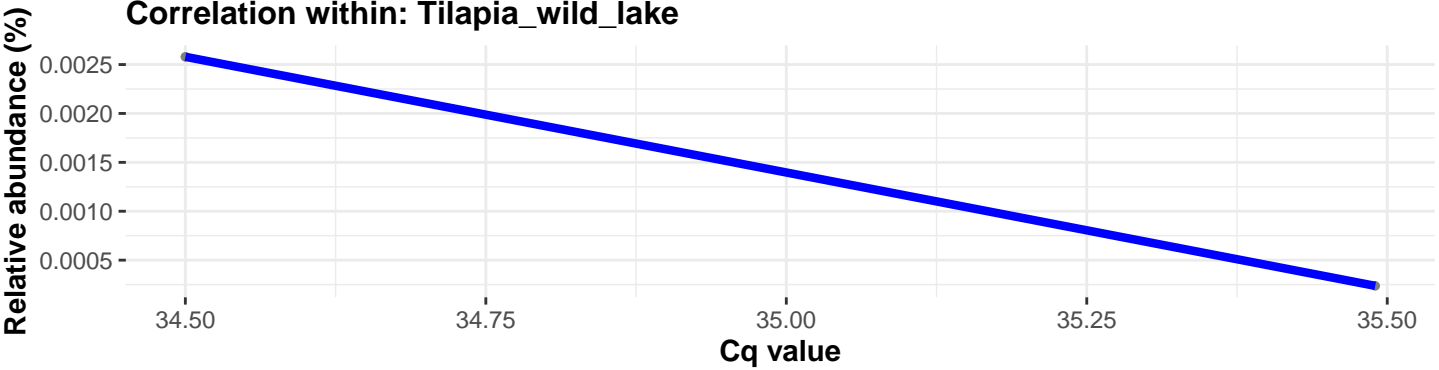


Correlation within: Tilapia_farmed_lake

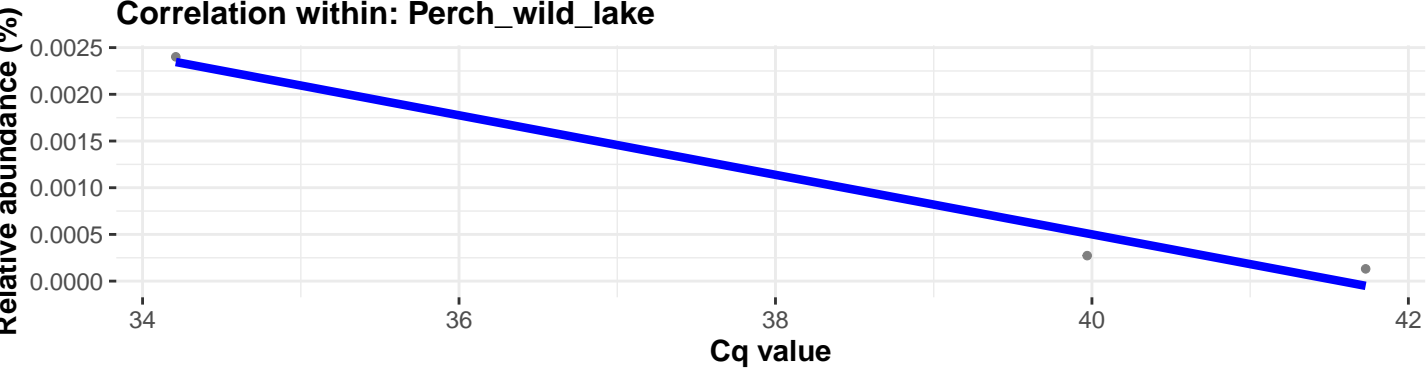
$\log_e(S) = 3.091$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = 0.607$, $CI_{95\%} [-0.295, 0.937]$, $n_{\text{pairs}} = 7$



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

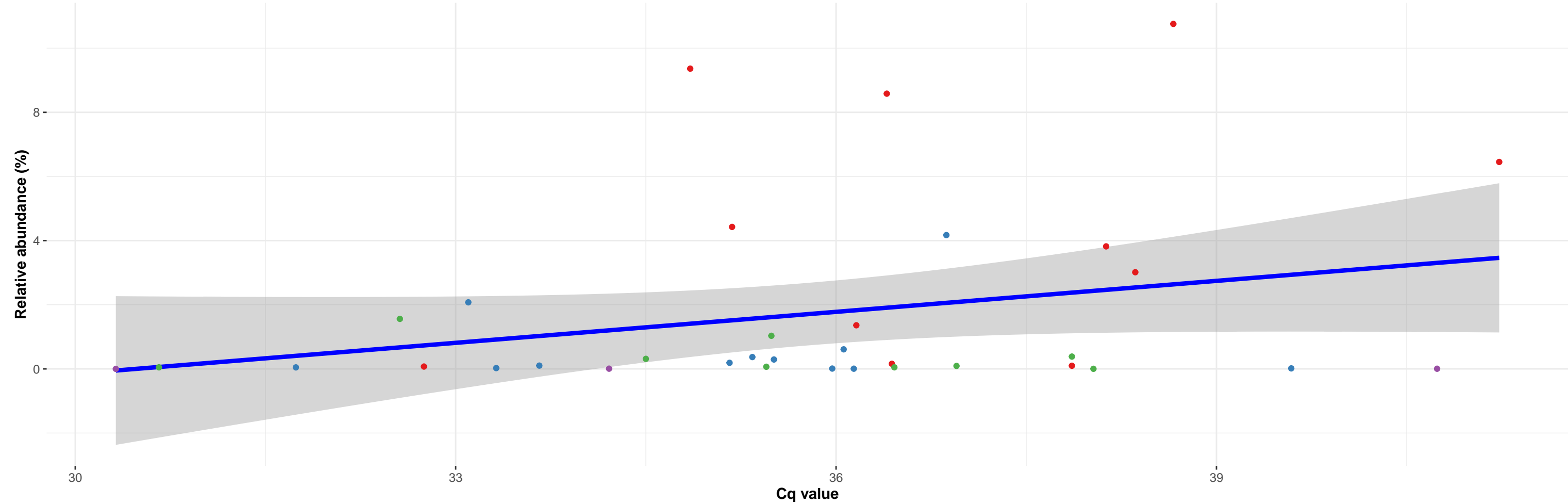


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 17d5a49452a6ccbe4473c55b3f818efc

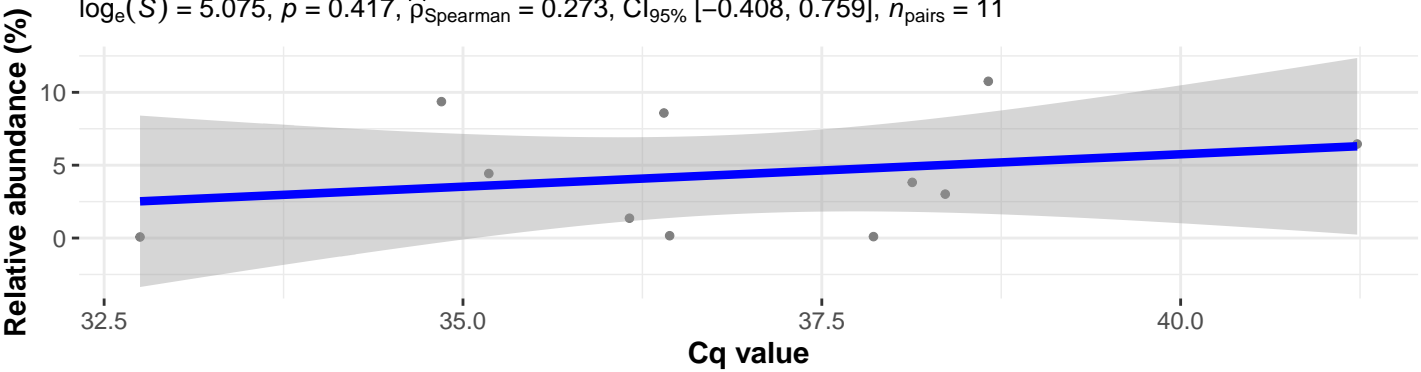
Correlation with all samples

$\log_e(S) = 8.664$, $p = 0.278$, $\hat{\rho}_{\text{Spearman}} = 0.189$, $\text{CI}_{95\%} [-0.164, 0.499]$, $n_{\text{pairs}} = 35$



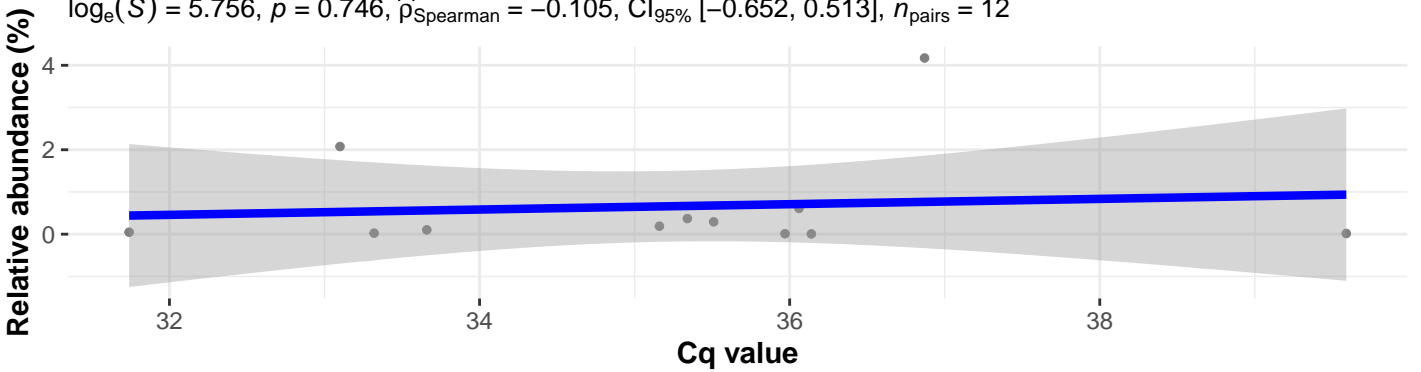
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.075$, $p = 0.417$, $\hat{\rho}_{\text{Spearman}} = 0.273$, $\text{CI}_{95\%} [-0.408, 0.759]$, $n_{\text{pairs}} = 11$



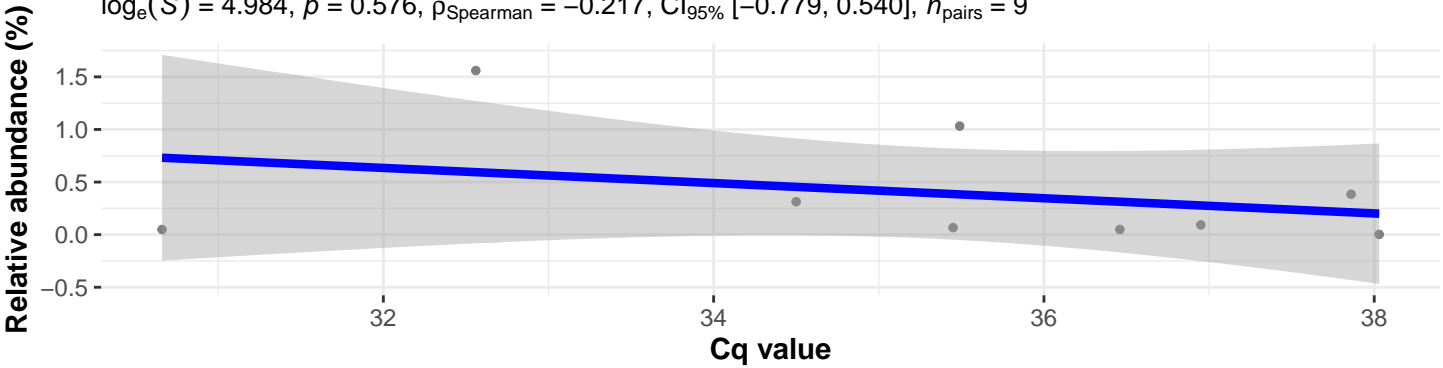
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.756$, $p = 0.746$, $\hat{\rho}_{\text{Spearman}} = -0.105$, $\text{CI}_{95\%} [-0.652, 0.513]$, $n_{\text{pairs}} = 12$

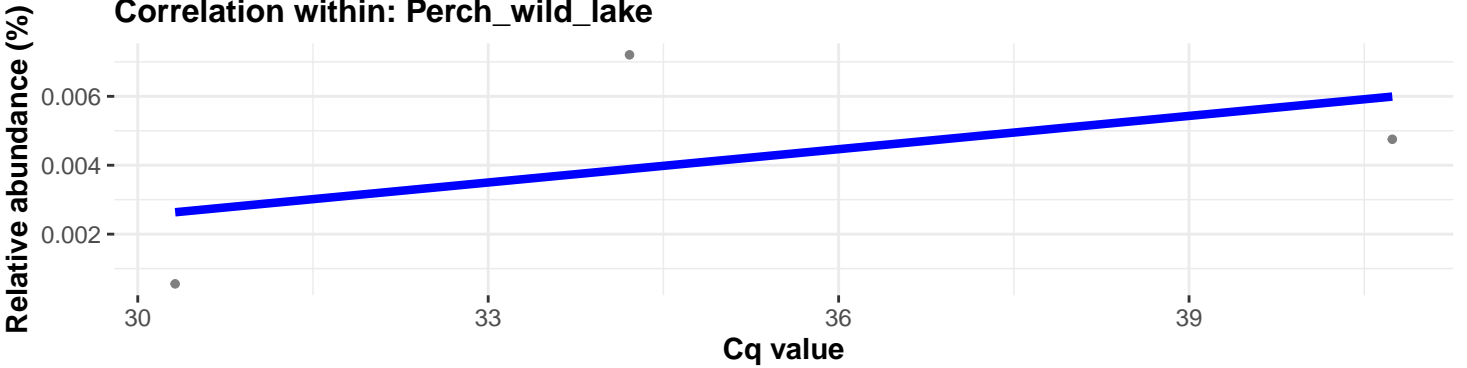


Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.984$, $p = 0.576$, $\hat{\rho}_{\text{Spearman}} = -0.217$, $\text{CI}_{95\%} [-0.779, 0.540]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

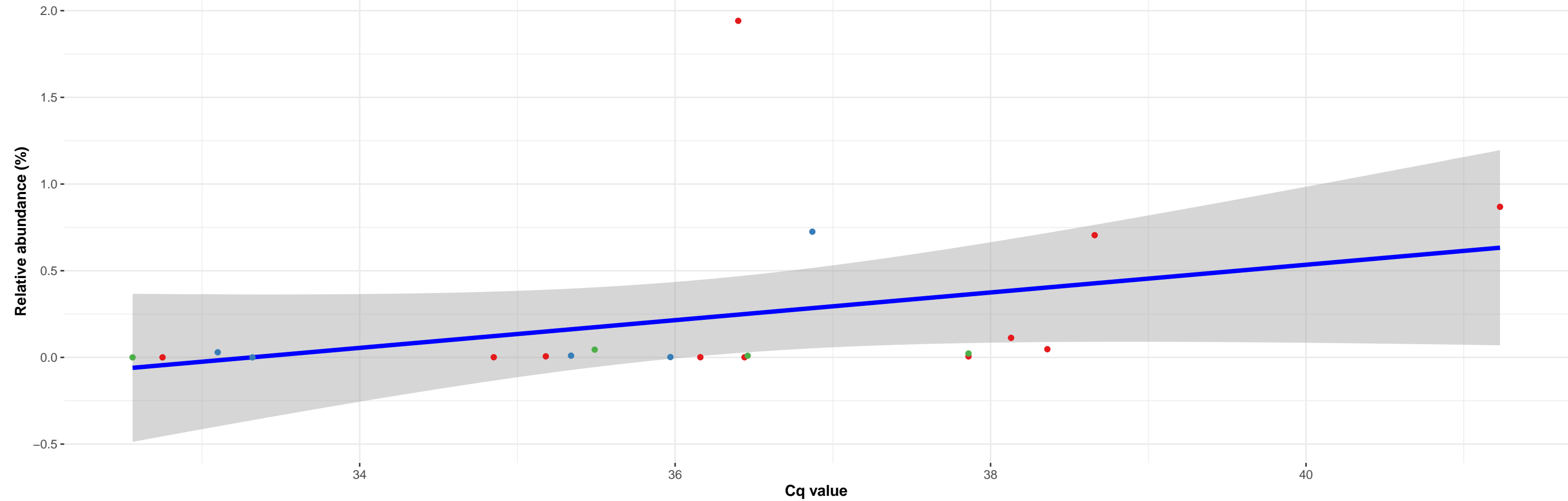


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paeniclostridium; s__uncultured bacterium

featureID: 1b00cdeda74eca68518123e3b3036f1f

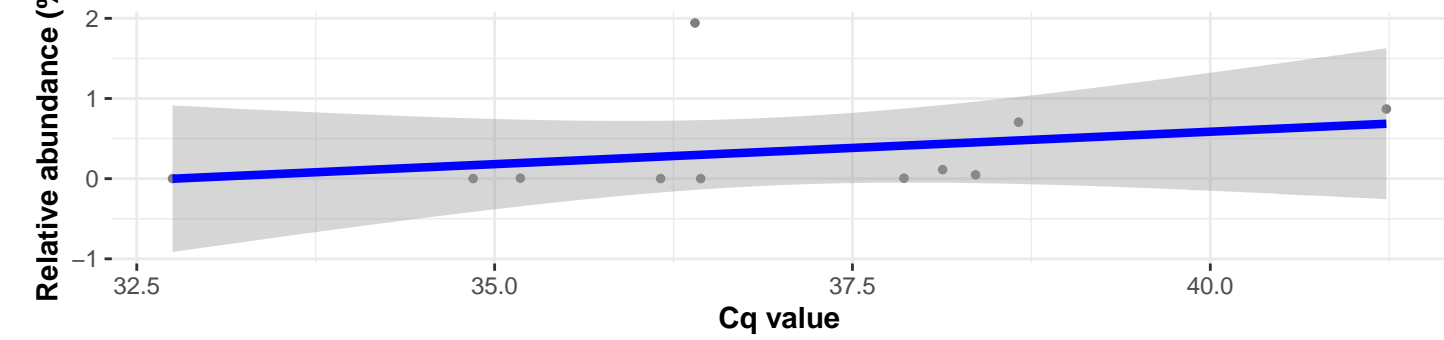
Correlation with all samples

$\log_e(S) = 6.100$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.665$, $CI_{95\%} [0.302, 0.859]$, $n_{\text{pairs}} = 20$

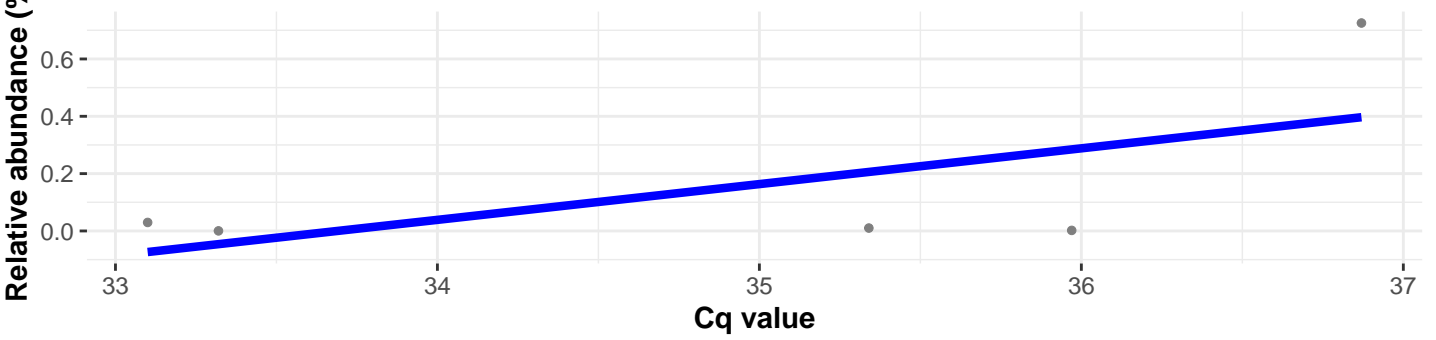


Correlation within: Tilapia_farmed_pond

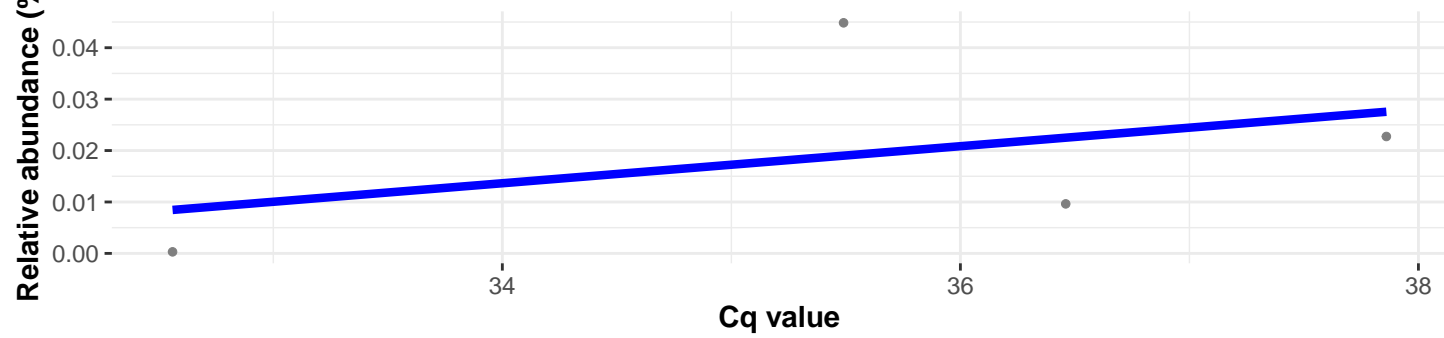
$\log_e(S) = 4.277$, $p = 0.023$, $\hat{\rho}_{\text{Spearman}} = 0.673$, $CI_{95\%} [0.102, 0.910]$, $n_{\text{pairs}} = 11$



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

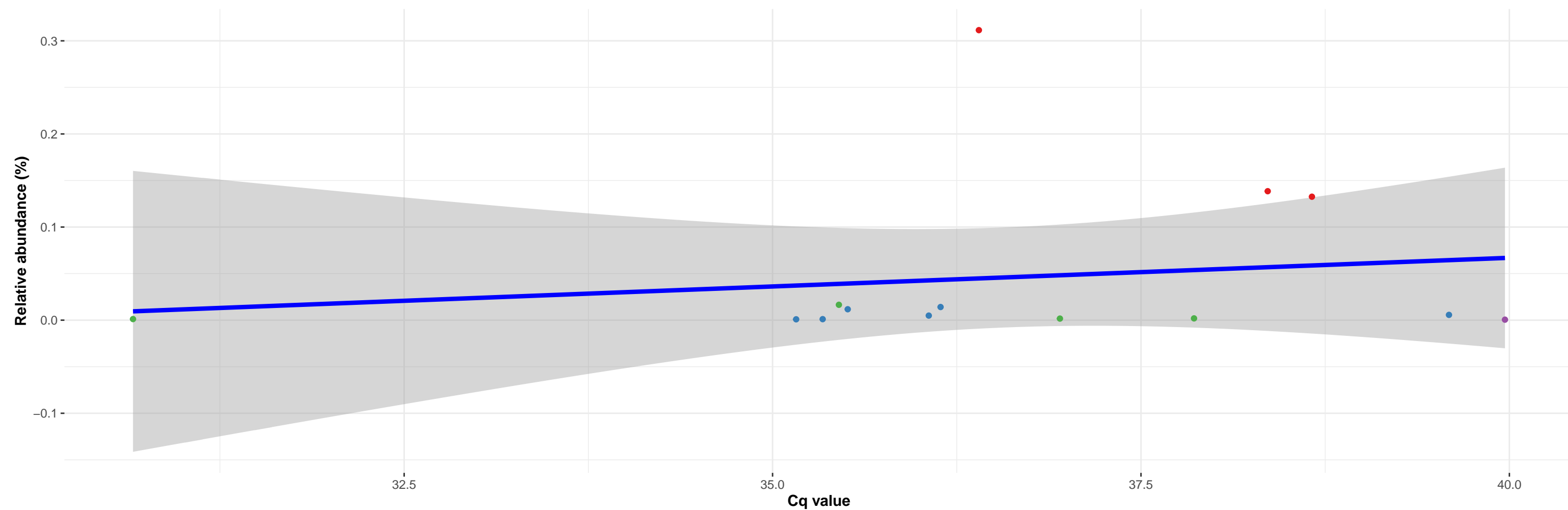


k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC-6307; NA

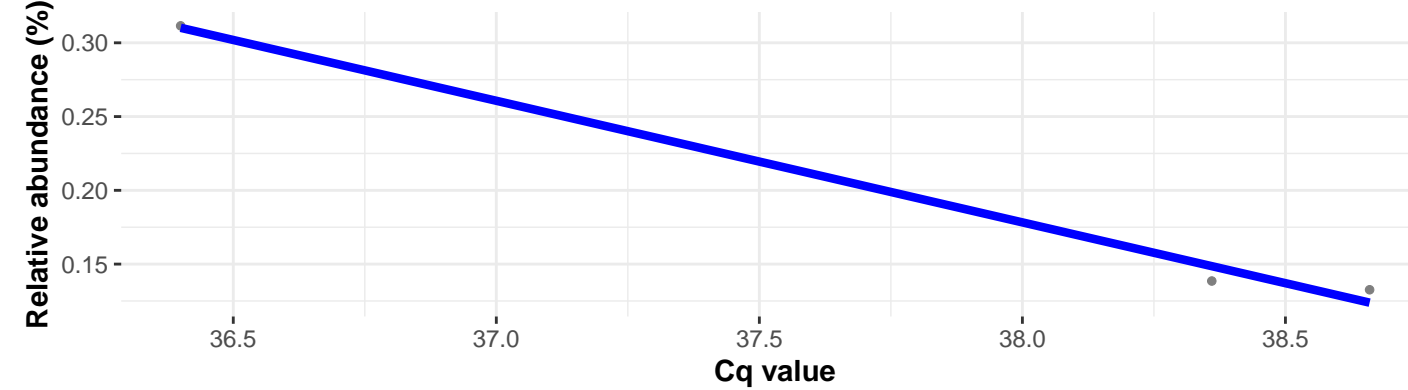
featureID: e7ce2cd99fee0bb346892bd41d5aae49

Correlation with all samples

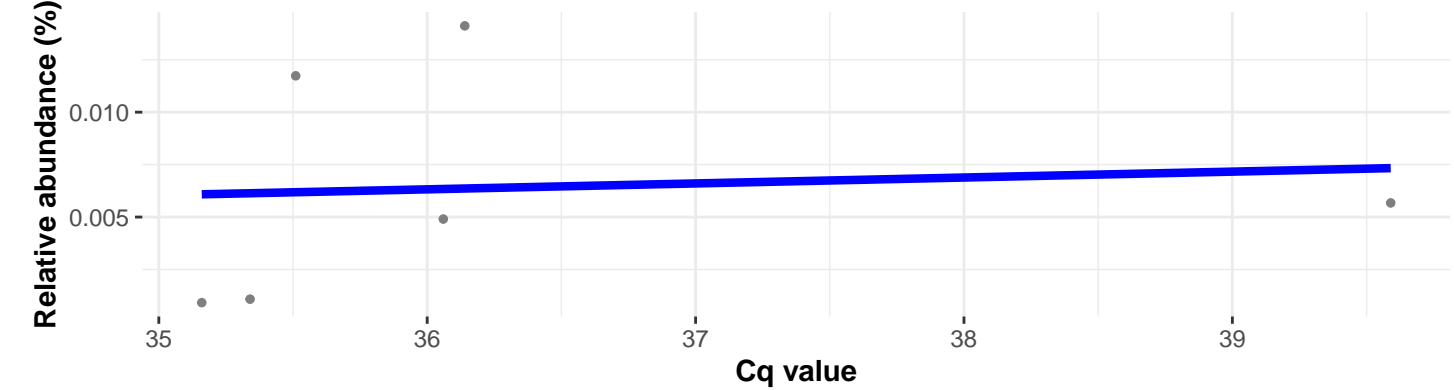
$\log_e(S) = 5.858$, $p = 0.427$, $\hat{\rho}_{\text{Spearman}} = 0.231$, $\text{CI}_{95\%} [-0.357, 0.688]$, $n_{\text{pairs}} = 14$



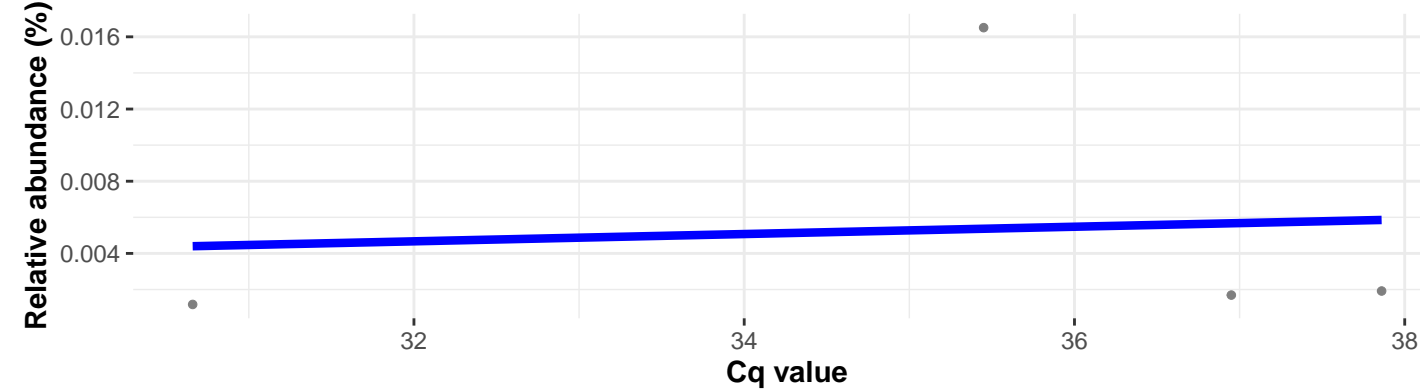
Correlation within: Tilapia_farmed_pond



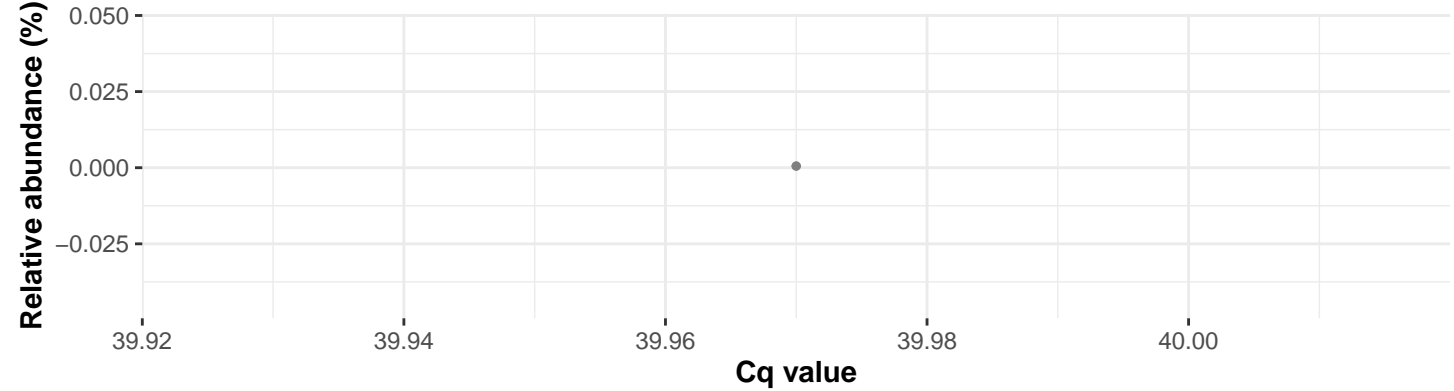
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

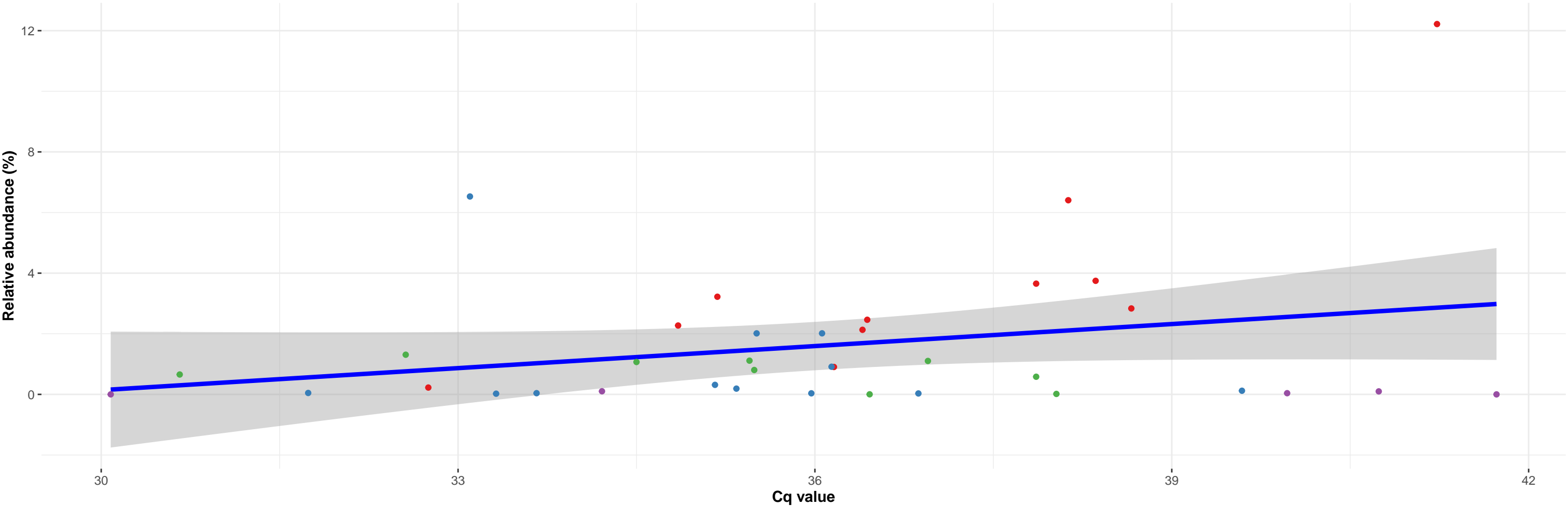


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: b7d96ace8aeb2c69a218149ac26a6ce9

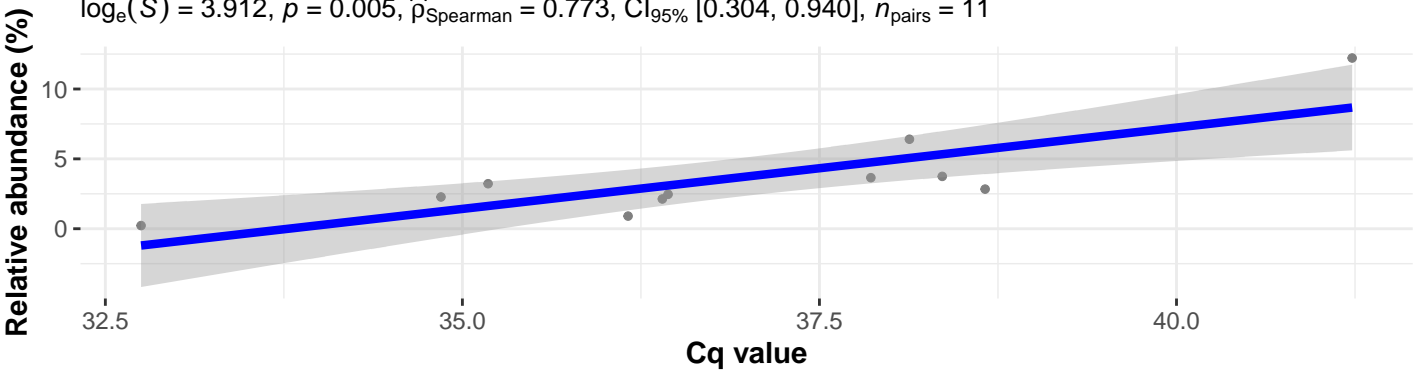
Correlation with all samples

$\log_e(S) = 8.937$, $p = 0.564$, $\hat{\rho}_{\text{Spearman}} = 0.098$, $CI_{95\%} [-0.243, 0.417]$, $n_{\text{pairs}} = 37$



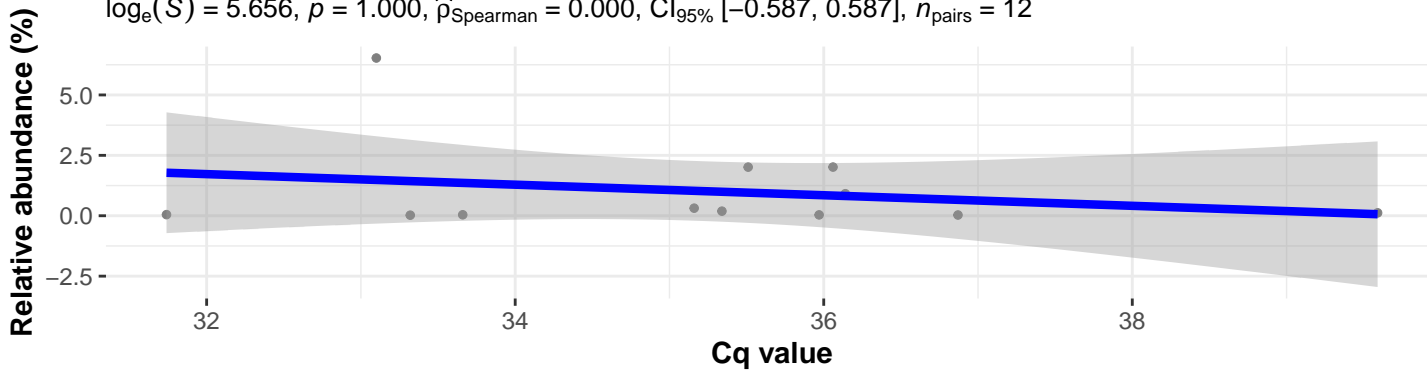
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 3.912$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.773$, $CI_{95\%} [0.304, 0.940]$, $n_{\text{pairs}} = 11$



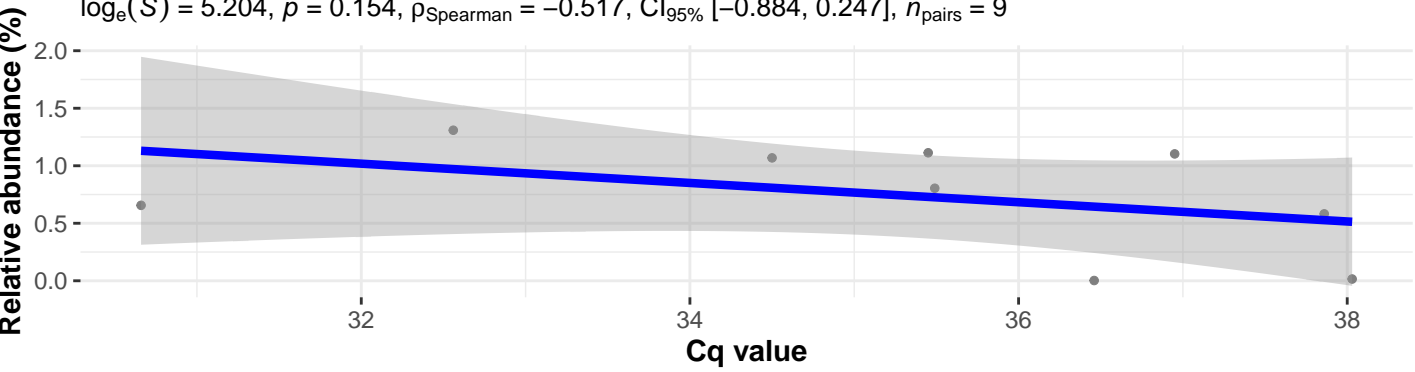
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.656$, $p = 1.000$, $\hat{\rho}_{\text{Spearman}} = 0.000$, $CI_{95\%} [-0.587, 0.587]$, $n_{\text{pairs}} = 12$

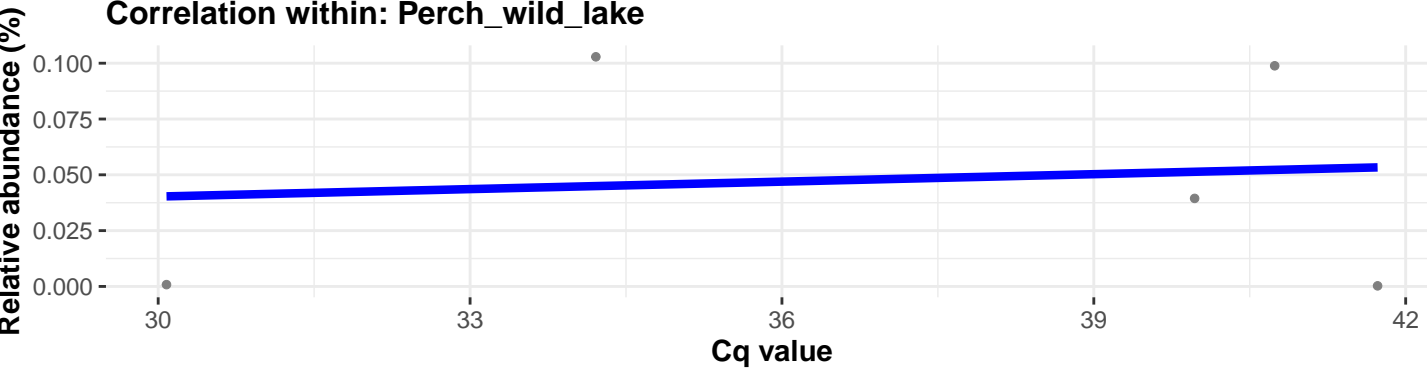


Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.204$, $p = 0.154$, $\hat{\rho}_{\text{Spearman}} = -0.517$, $CI_{95\%} [-0.884, 0.247]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

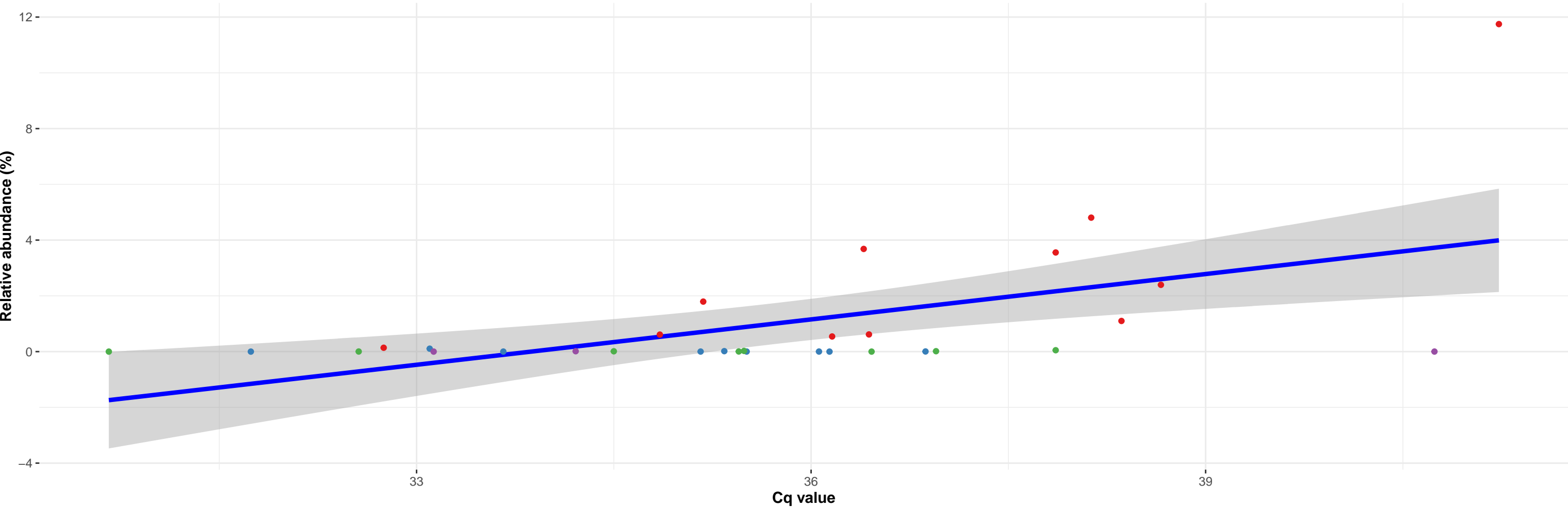


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: eeb27bcd7d7aaa8b5bd04631b5bea486

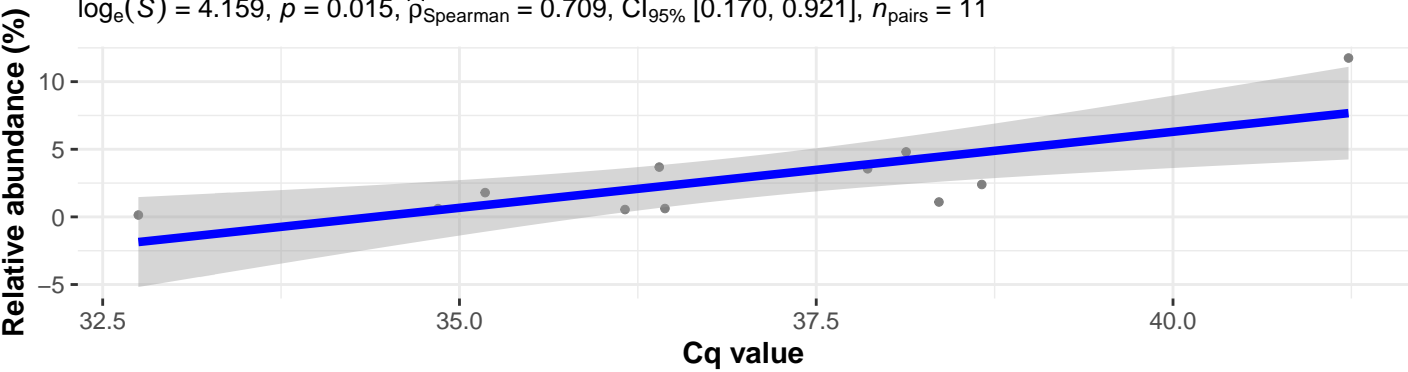
Correlation with all samples

$\log_e(S) = 7.836$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.490$, $\text{CI}_{95\%} [0.153, 0.725]$, $n_{\text{pairs}} = 31$



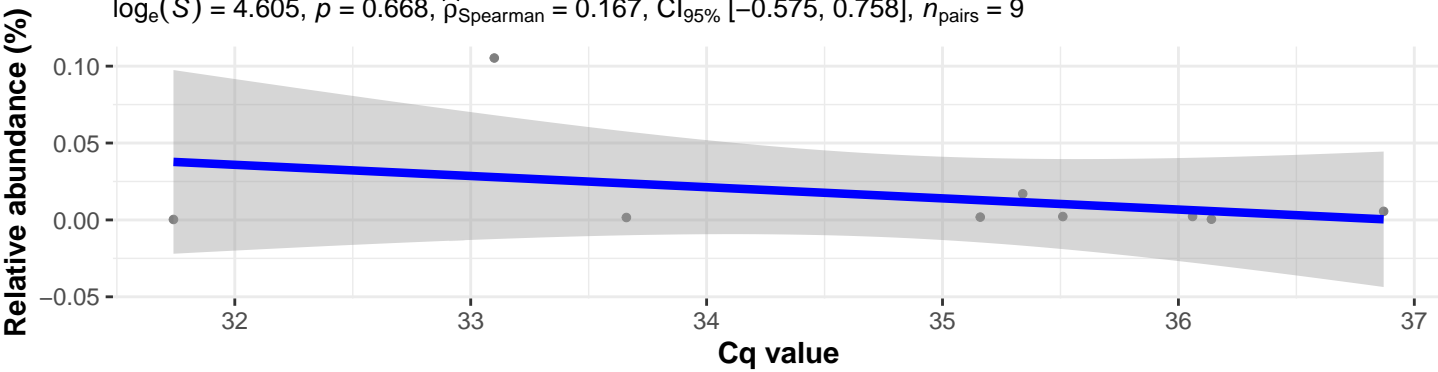
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.159$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = 0.709$, $\text{CI}_{95\%} [0.170, 0.921]$, $n_{\text{pairs}} = 11$



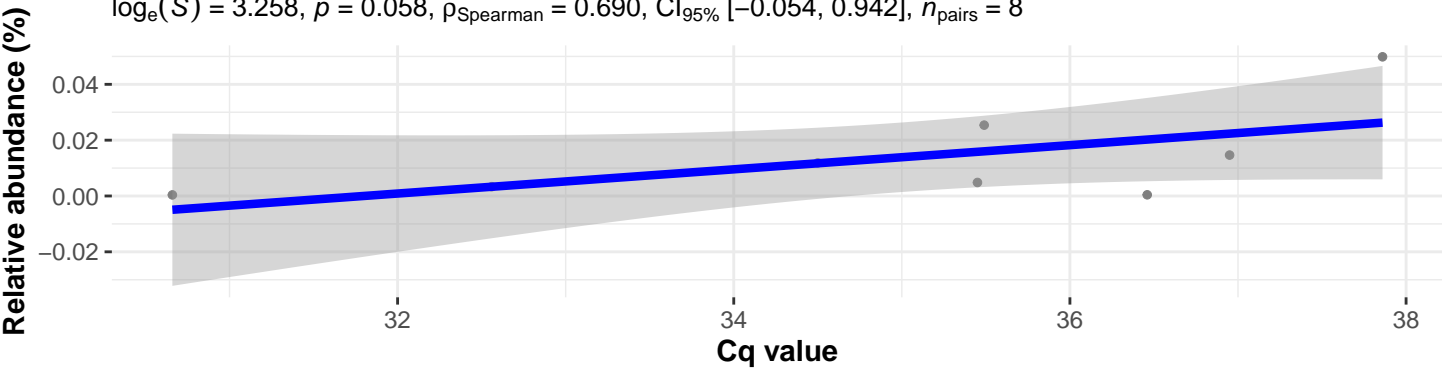
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 4.605$, $p = 0.668$, $\hat{\rho}_{\text{Spearman}} = 0.167$, $\text{CI}_{95\%} [-0.575, 0.758]$, $n_{\text{pairs}} = 9$

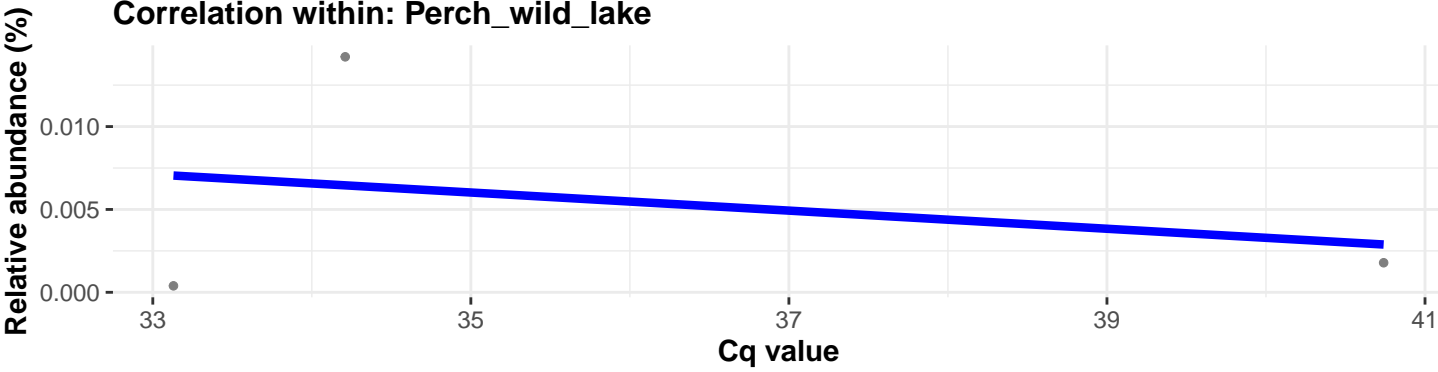


Correlation within: Tilapia_wild_lake

$\log_e(S) = 3.258$, $p = 0.058$, $\hat{\rho}_{\text{Spearman}} = 0.690$, $\text{CI}_{95\%} [-0.054, 0.942]$, $n_{\text{pairs}} = 8$



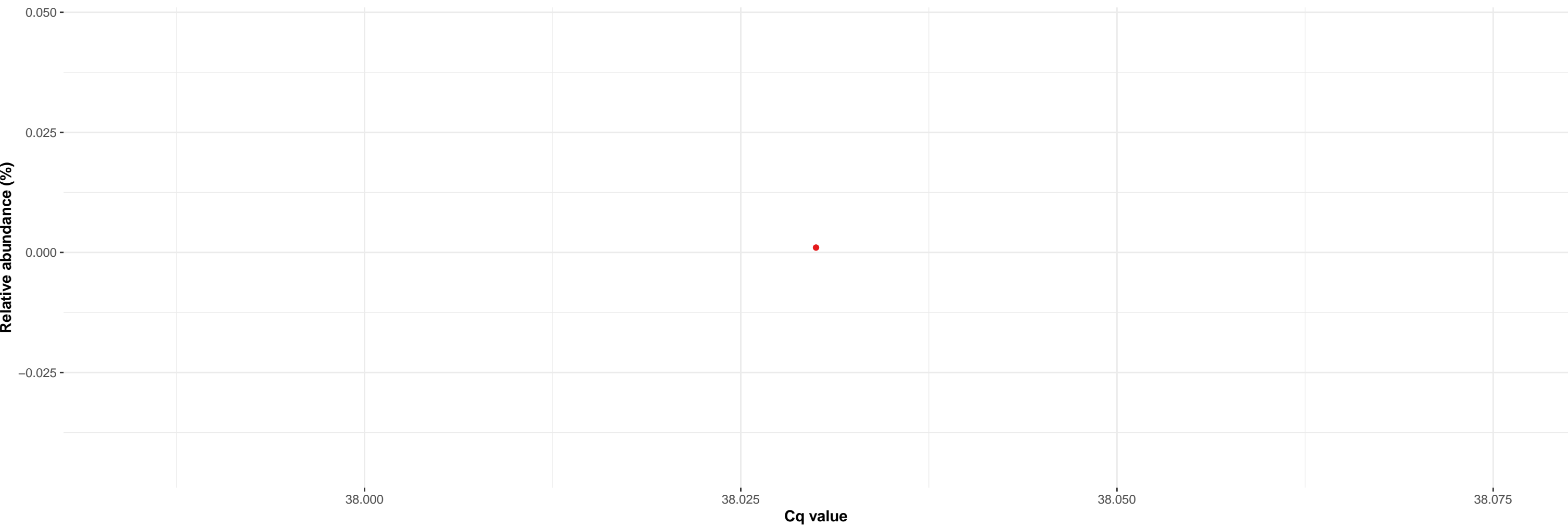
Correlation within: Perch_wild_lake



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; NA

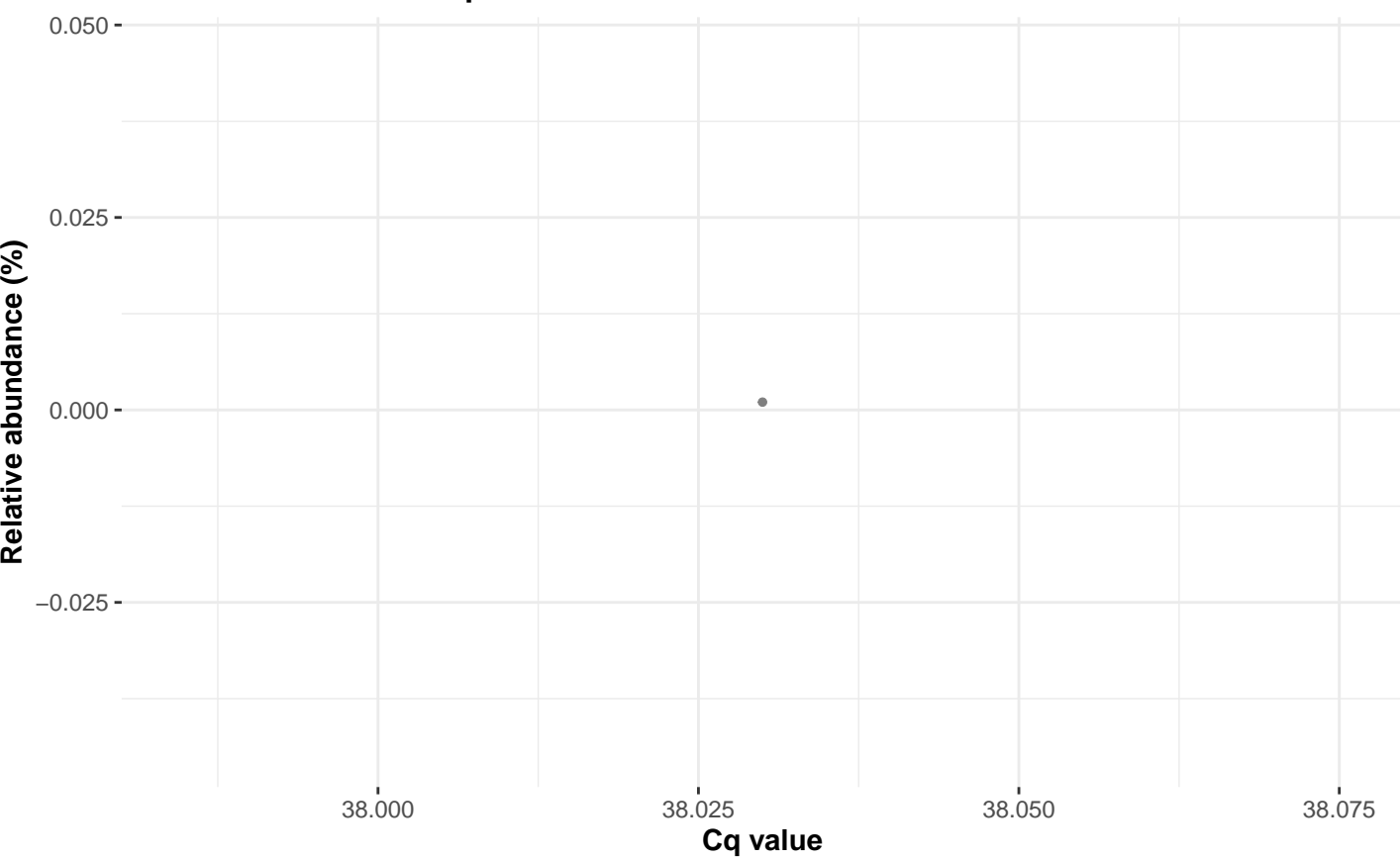
featureID: ba4ab8dea6b4223dbc9ed5bbf3ea60ea

Correlation with all samples



Sample_type • Tilapia_wild_lake

Correlation within: Tilapia_wild_lake

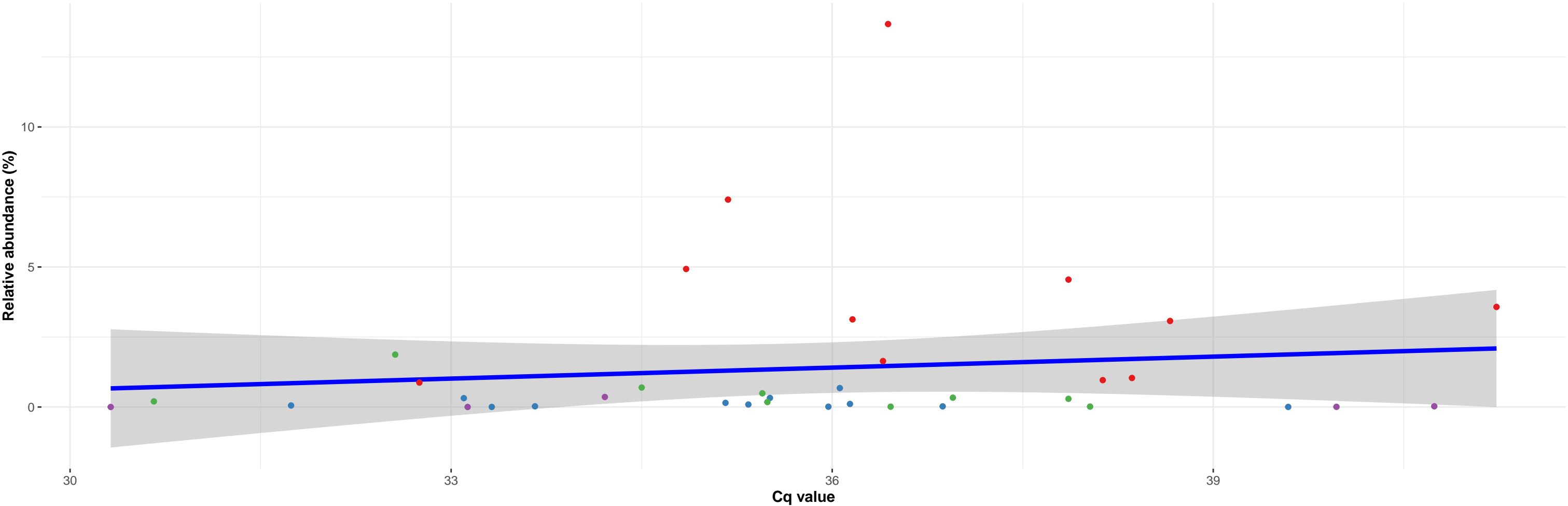


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: d112db53cc44b1be8395e16355a2109d

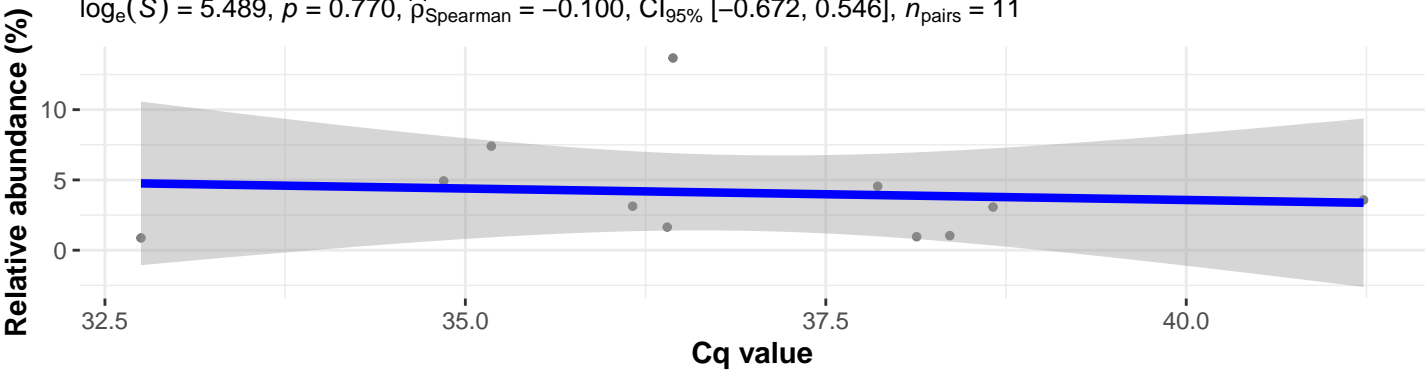
Correlation with all samples

$\log_e(S) = 8.909$, $p = 0.469$, $\hat{\rho}_{\text{Spearman}} = 0.123$, $\text{CI}_{95\%} [-0.219, 0.438]$, $n_{\text{pairs}} = 37$



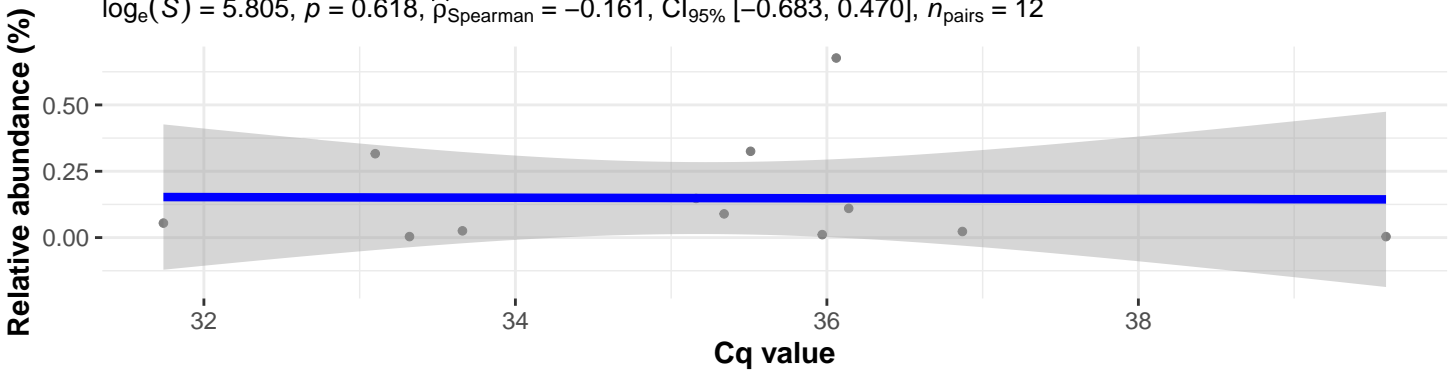
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 5.489$, $p = 0.770$, $\hat{\rho}_{\text{Spearman}} = -0.100$, $\text{CI}_{95\%} [-0.672, 0.546]$, $n_{\text{pairs}} = 11$



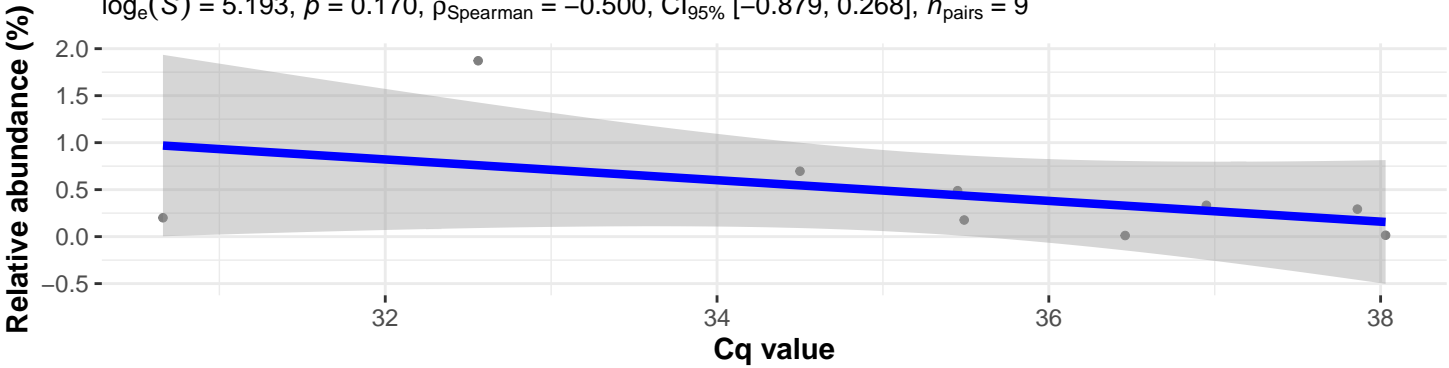
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.805$, $p = 0.618$, $\hat{\rho}_{\text{Spearman}} = -0.161$, $\text{CI}_{95\%} [-0.683, 0.470]$, $n_{\text{pairs}} = 12$

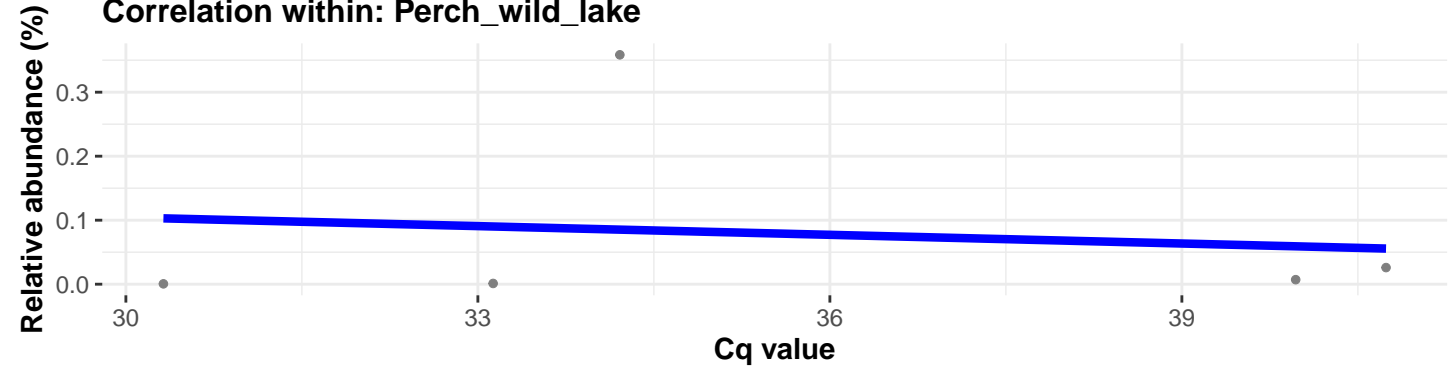


Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.193$, $p = 0.170$, $\hat{\rho}_{\text{Spearman}} = -0.500$, $\text{CI}_{95\%} [-0.879, 0.268]$, $n_{\text{pairs}} = 9$



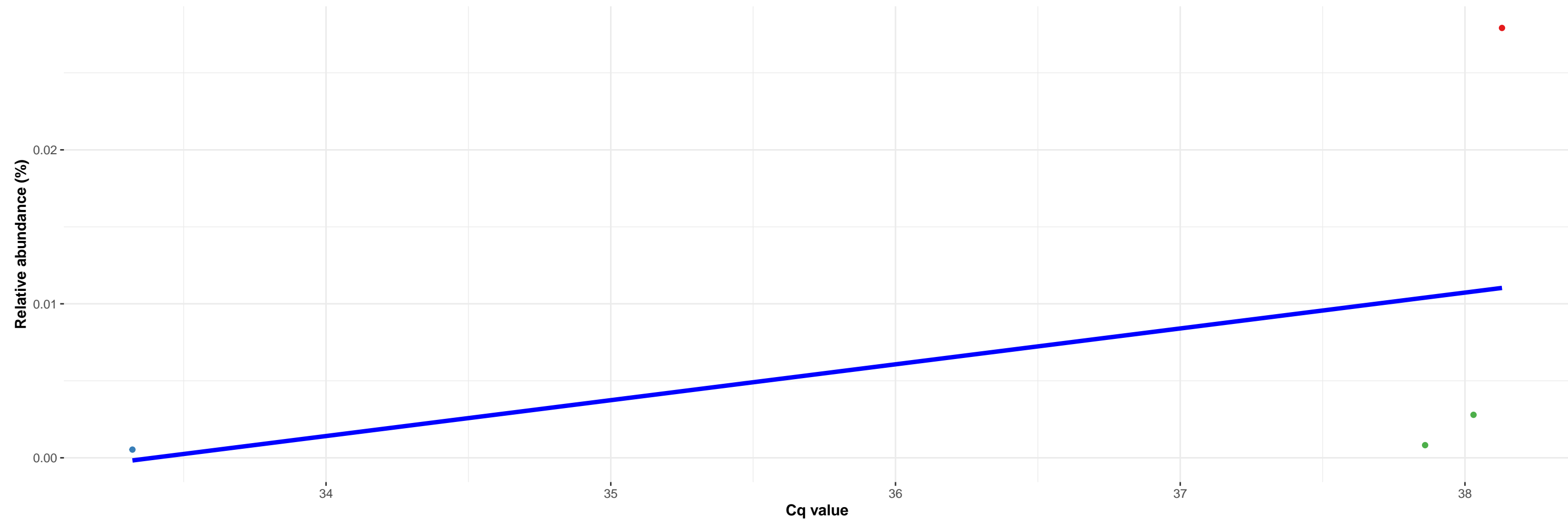
Correlation within: Perch_wild_lake



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

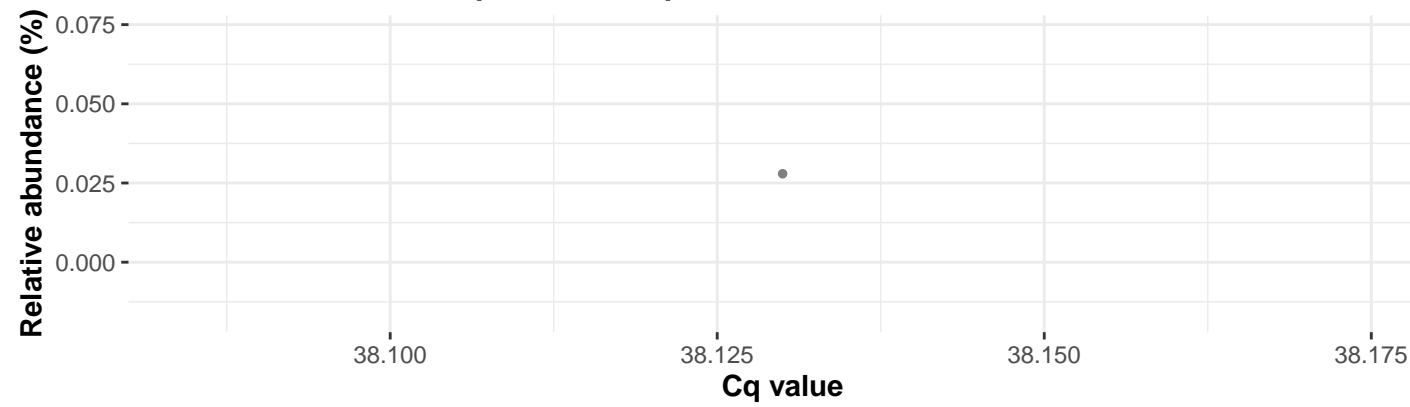
featureID: d4e740bc5c2587cbbb188e8e30026611

Correlation with all samples

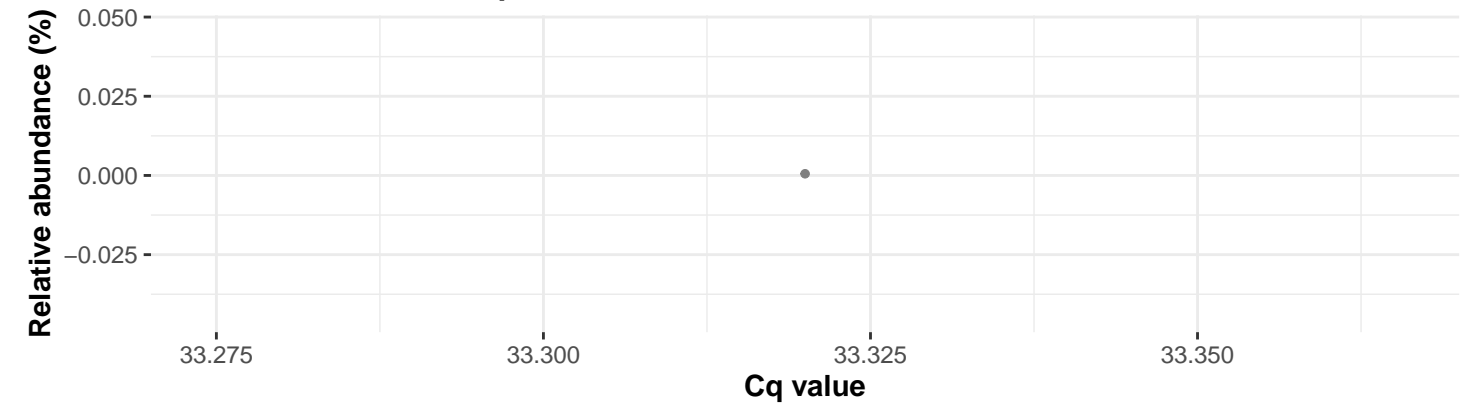


Sample_type ● Tilapia_farmed_pond ● Tilapia_farmed_lake ● Tilapia_wild_lake

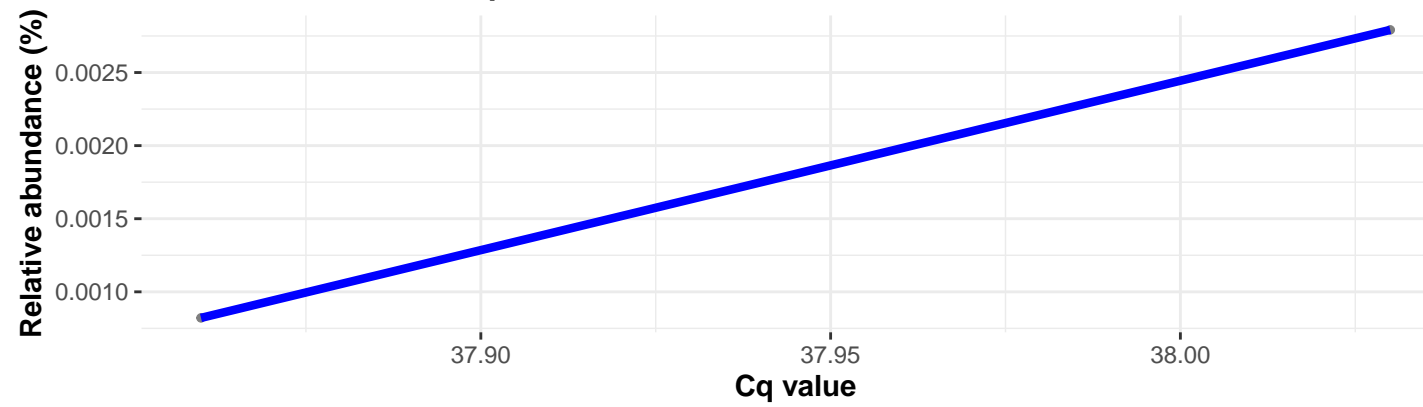
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

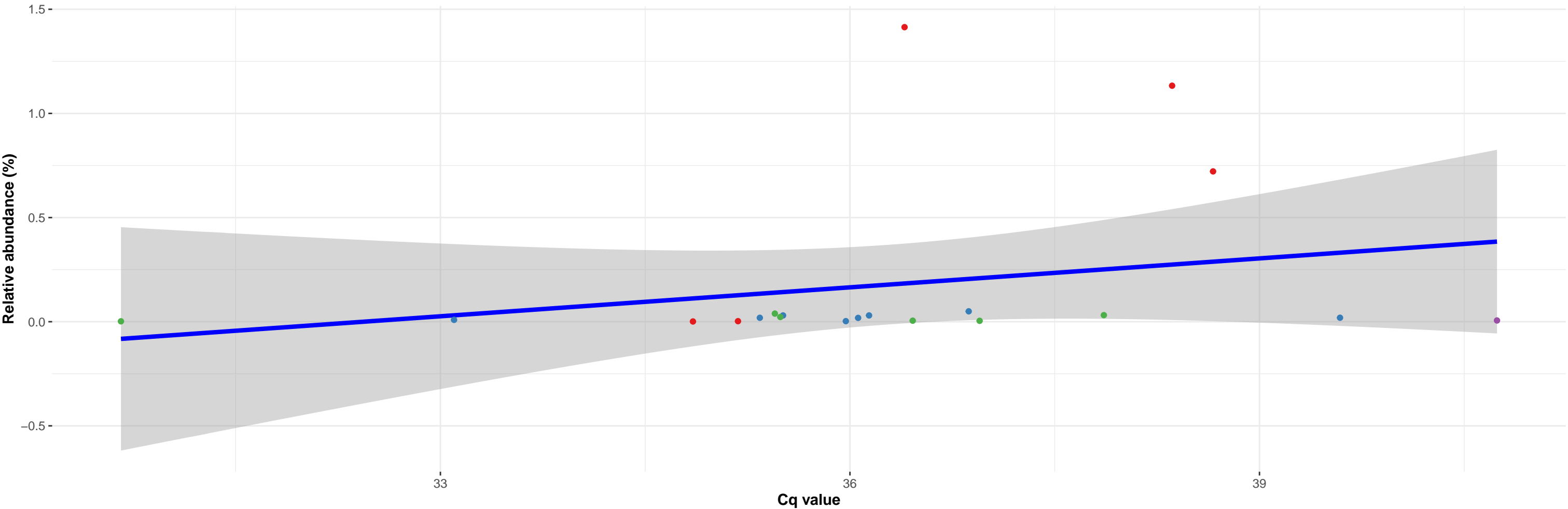


k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC-6307; NA

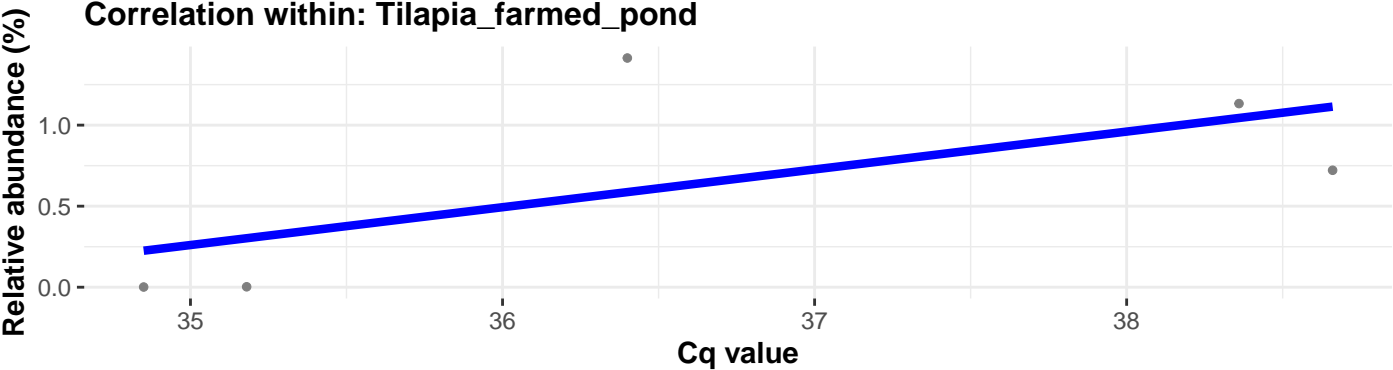
featureID: 12e90f65e34a30ad48d9e3f3b842b30d

Correlation with all samples

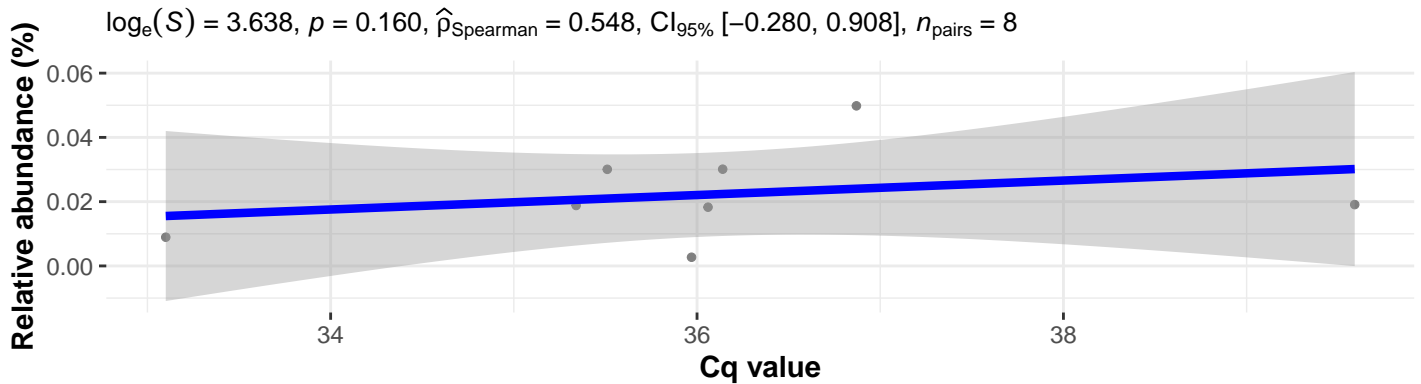
$\log_e(S) = 6.568$, $p = 0.039$, $\hat{\rho}_{\text{Spearman}} = 0.465$, $\text{CI}_{95\%} [0.014, 0.758]$, $n_{\text{pairs}} = 20$



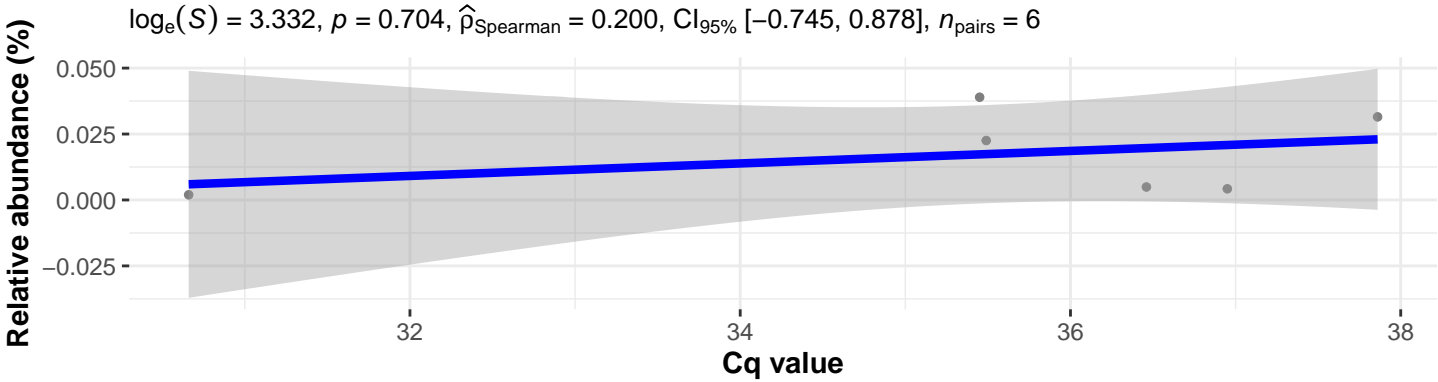
Correlation within: Tilapia_farmed_pond



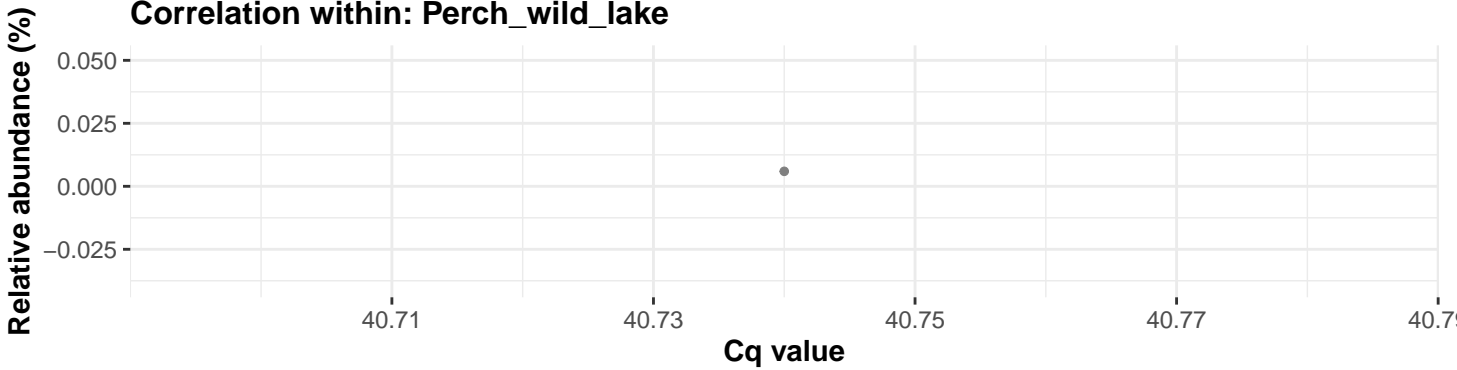
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



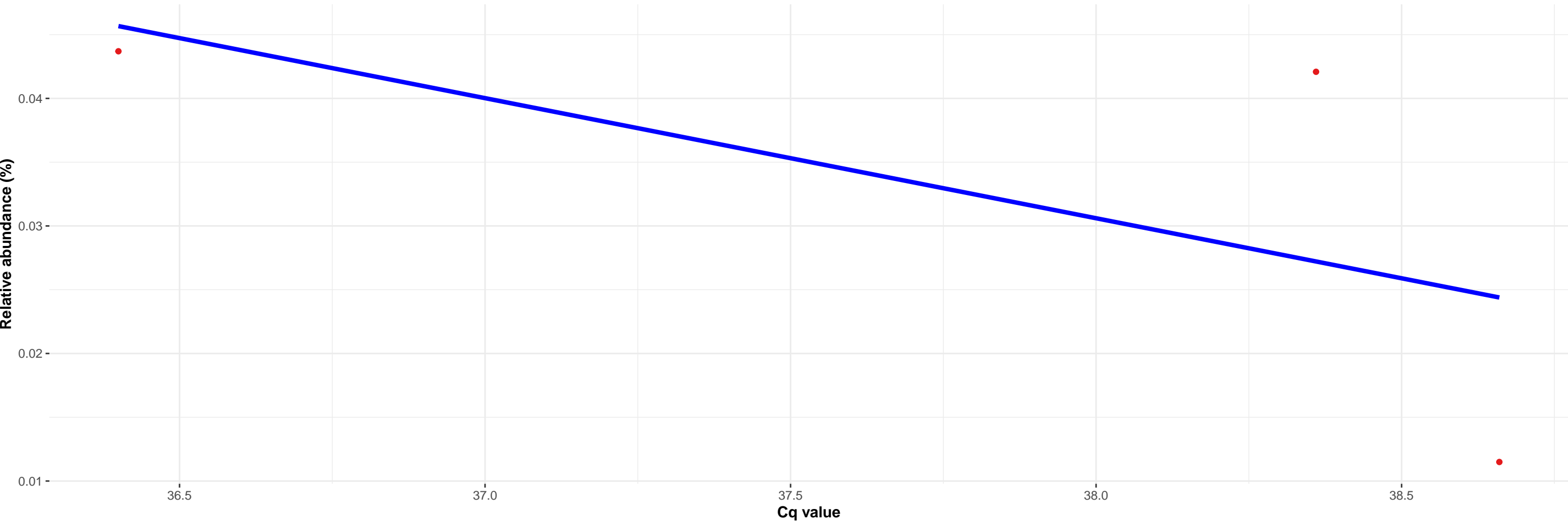
Correlation within: Perch_wild_lake



k__Bacteria; p__Chlamydiae; c__Chlamydiae; o__Chlamydiales; f__Parachlamydiaceae; g__Neochlamydia; NA

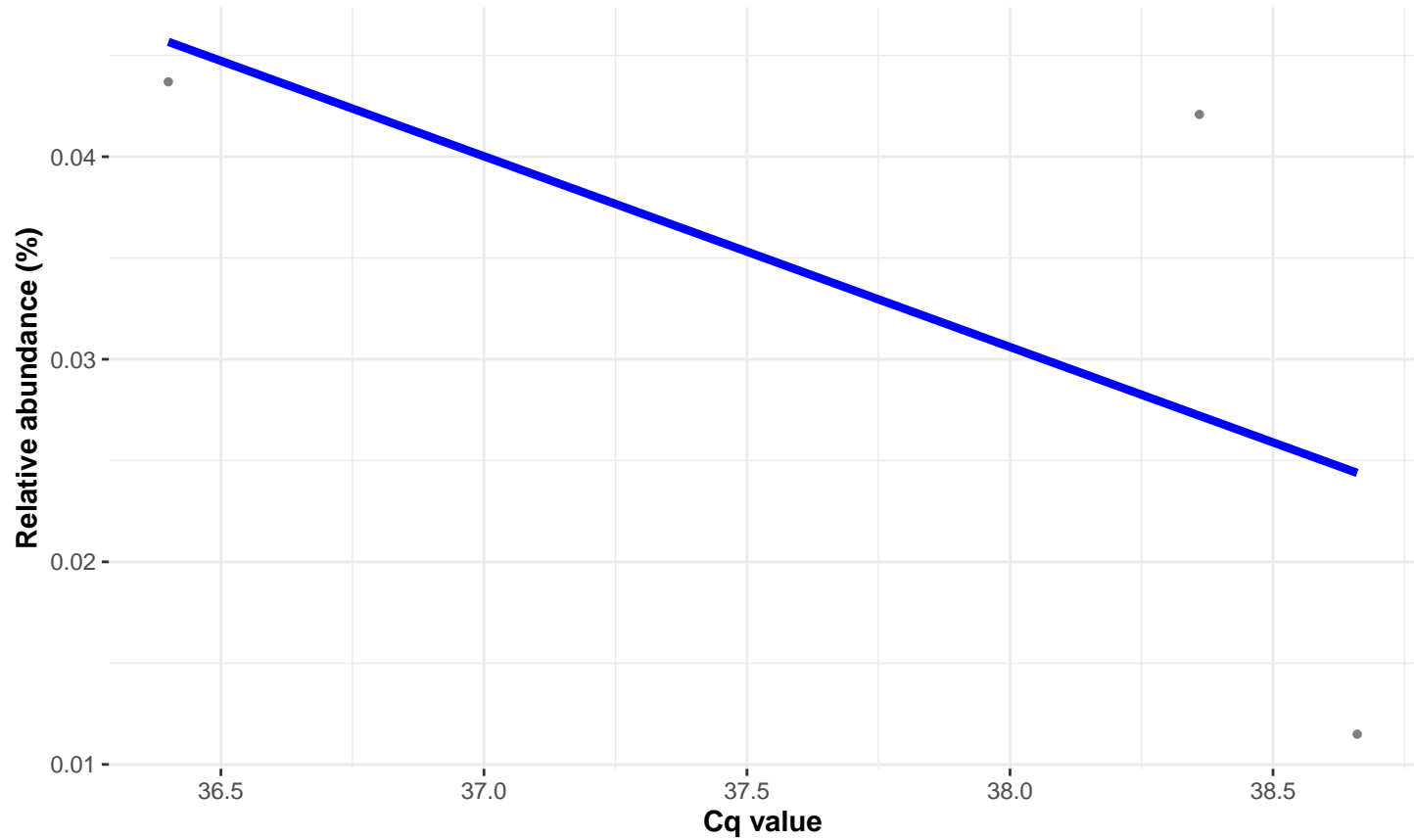
featureID: 35e38ee9b5dff68dbd41115b73741414

Correlation with all samples



Sample_type • Tilapia_farmed_pond

Correlation within: Tilapia_farmed_pond

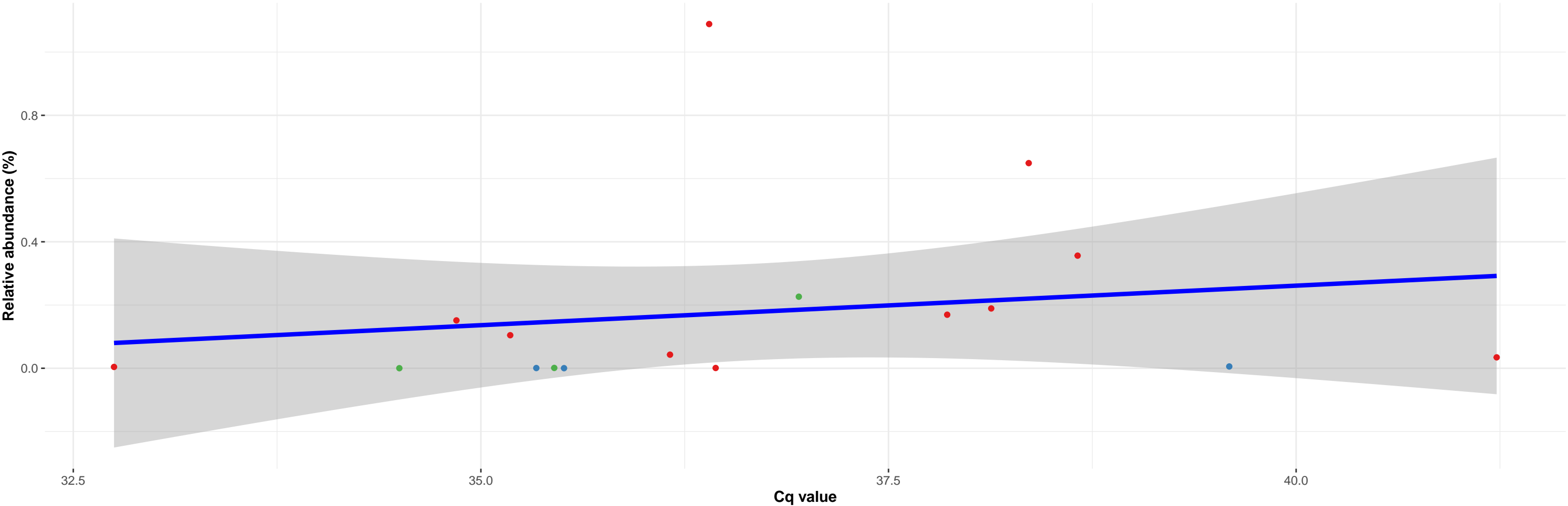


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methyloparacoccus; s__uncultured bacterium

featureID: 66c3e0b10570a19d613f692d701da8d0

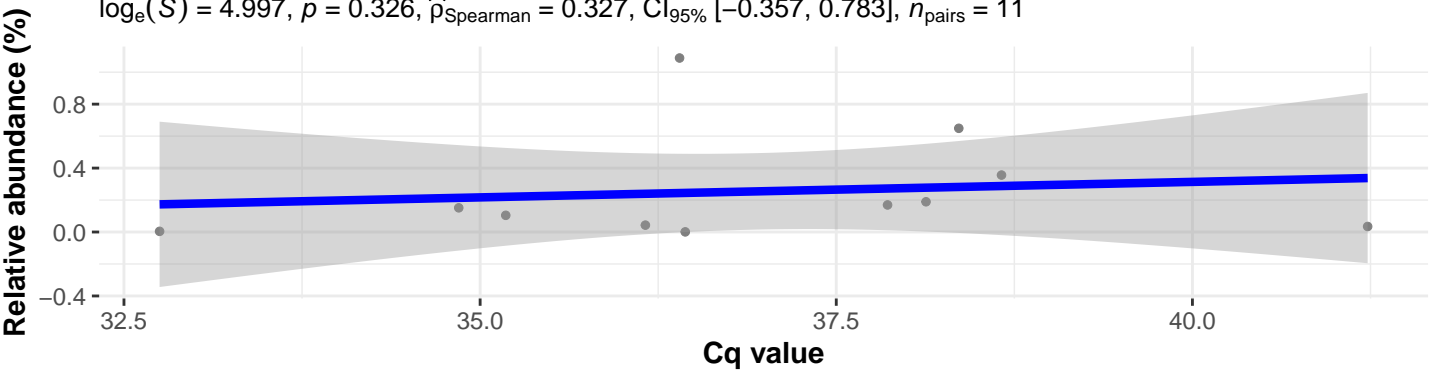
Correlation with all samples

$\log_e(S) = 6.068$, $p = 0.057$, $\hat{\rho}_{\text{Spearman}} = 0.471$, $CI_{95\%} [-0.028, 0.782]$, $n_{\text{pairs}} = 17$

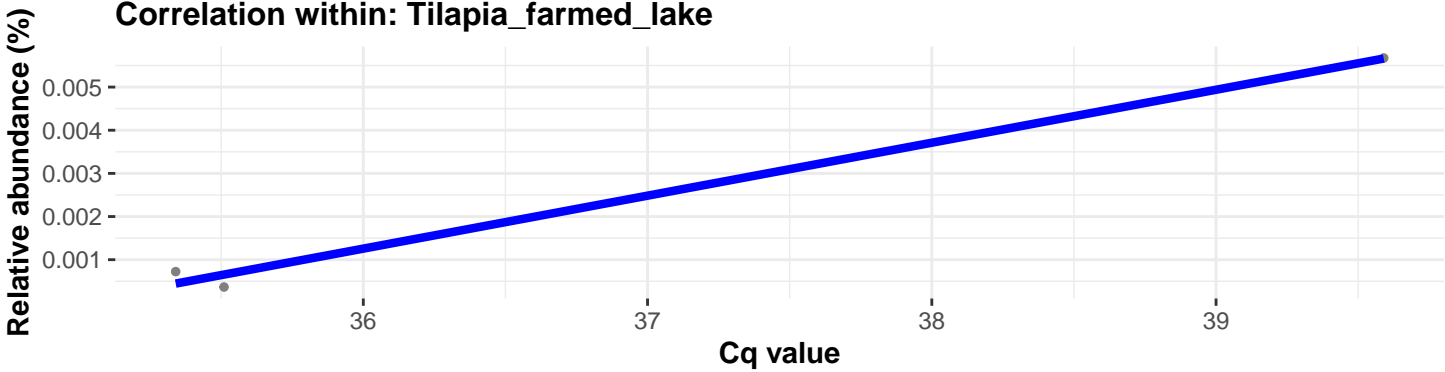


Correlation within: Tilapia_farmed_pond

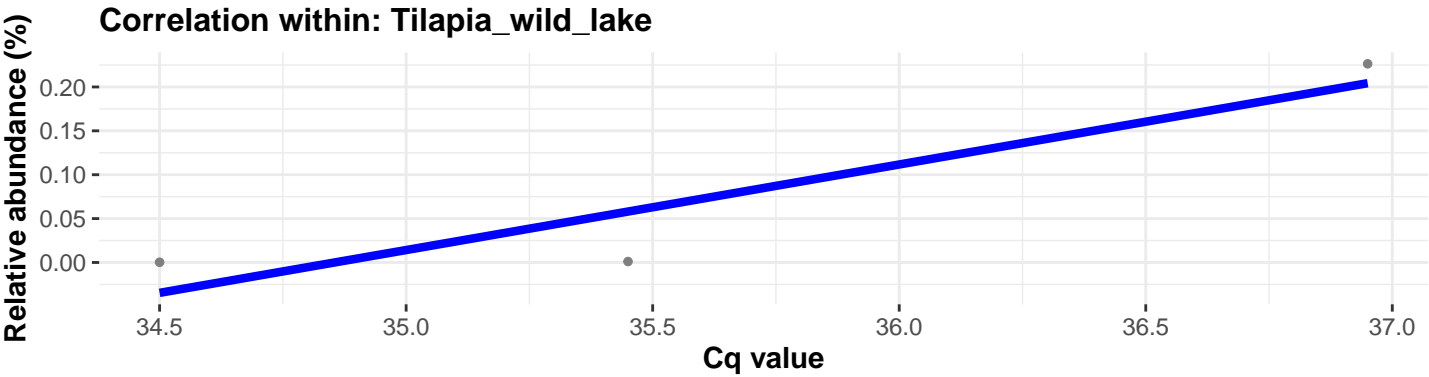
$\log_e(S) = 4.997$, $p = 0.326$, $\hat{\rho}_{\text{Spearman}} = 0.327$, $CI_{95\%} [-0.357, 0.783]$, $n_{\text{pairs}} = 11$



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

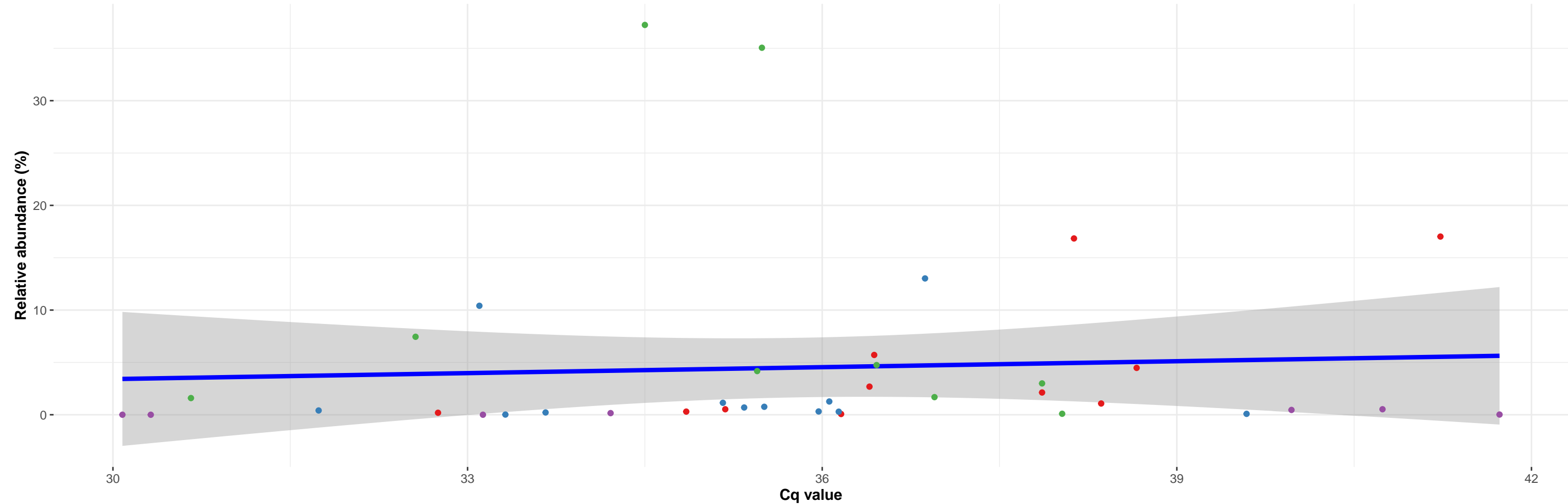


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; NA; NA

featureID: 8ebe63f7e7dd6bd4ca4dca5a66df57c2

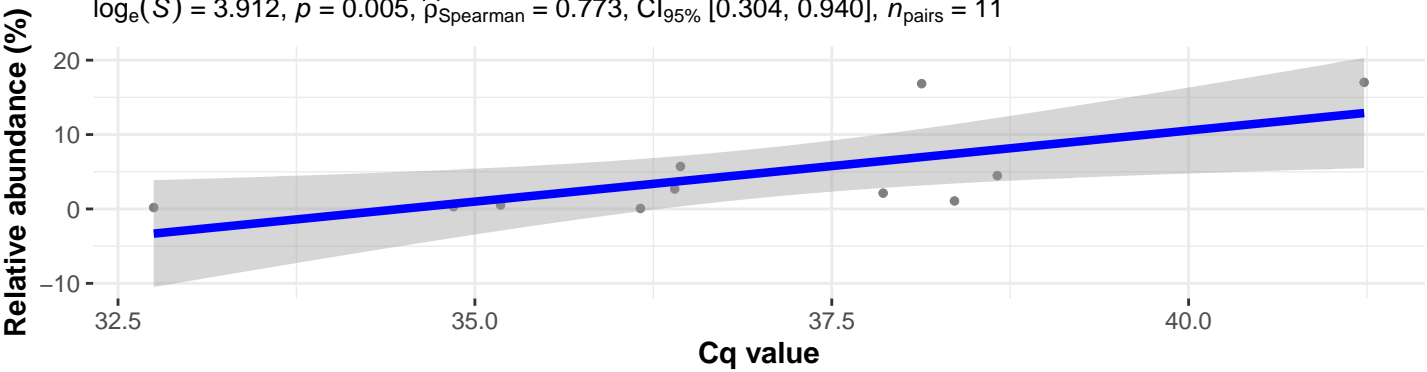
Correlation with all samples

$\log_e(S) = 8.925$, $p = 0.143$, $\hat{\rho}_{\text{Spearman}} = 0.239$, $\text{CI}_{95\%} [-0.092, 0.523]$, $n_{\text{pairs}} = 39$



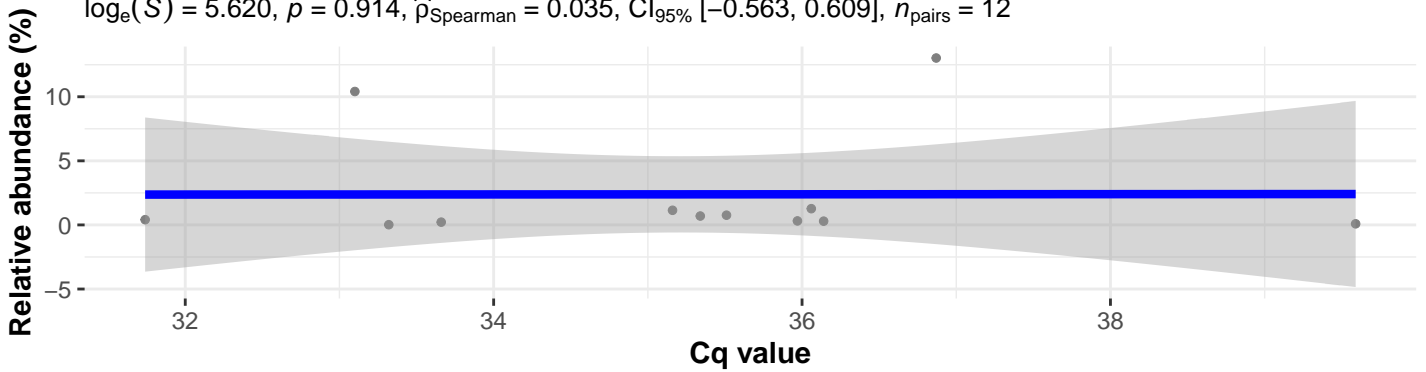
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 3.912$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.773$, $\text{CI}_{95\%} [0.304, 0.940]$, $n_{\text{pairs}} = 11$



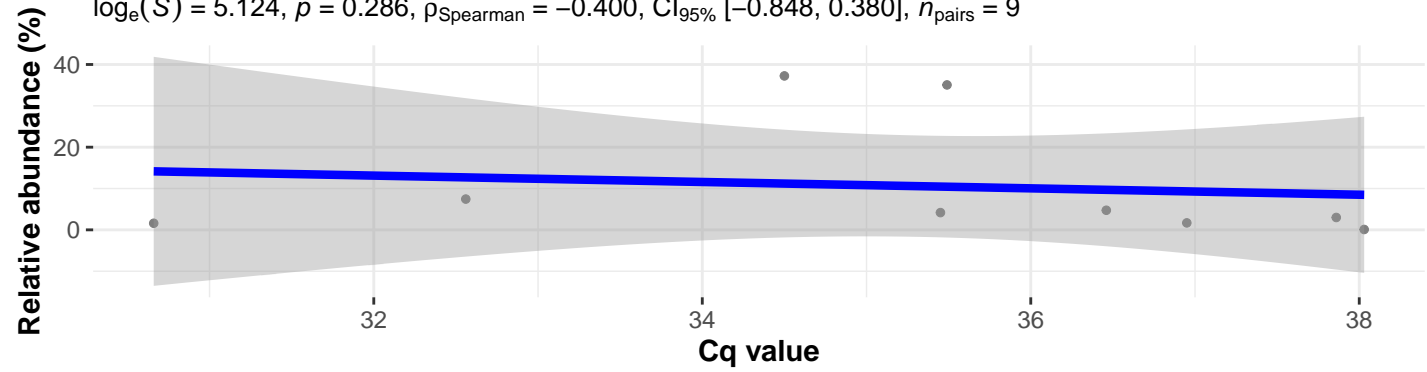
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.620$, $p = 0.914$, $\hat{\rho}_{\text{Spearman}} = 0.035$, $\text{CI}_{95\%} [-0.563, 0.609]$, $n_{\text{pairs}} = 12$



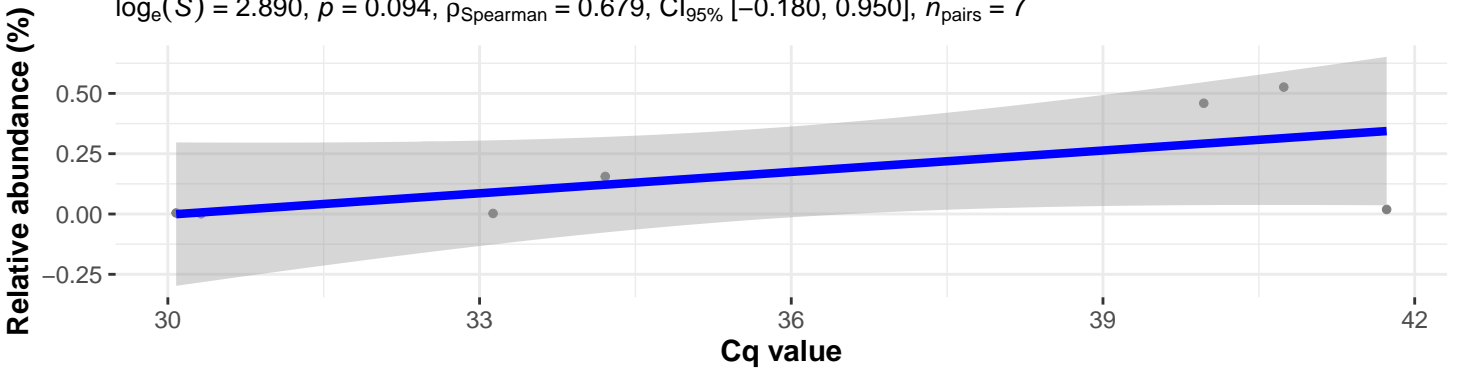
Correlation within: Tilapia_wild_lake

$\log_e(S) = 5.124$, $p = 0.286$, $\hat{\rho}_{\text{Spearman}} = -0.400$, $\text{CI}_{95\%} [-0.848, 0.380]$, $n_{\text{pairs}} = 9$



Correlation within: Perch_wild_lake

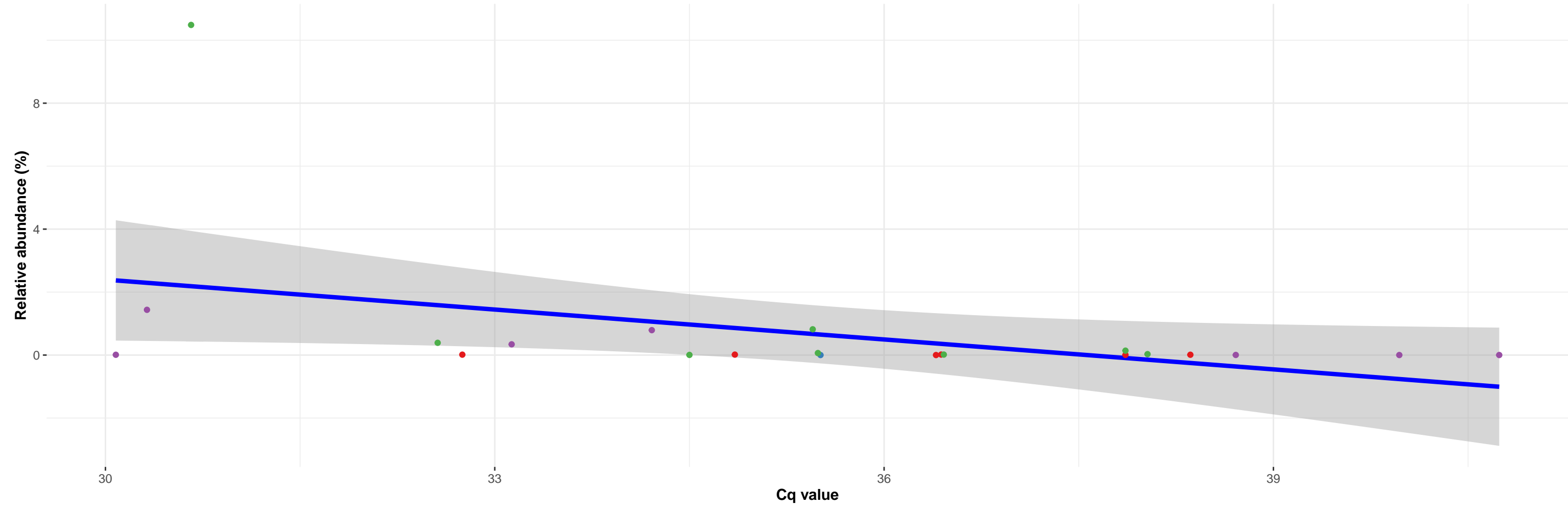
$\log_e(S) = 2.890$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = 0.679$, $\text{CI}_{95\%} [-0.180, 0.950]$, $n_{\text{pairs}} = 7$



featureID: 50b18b94311c09ff882fda744bc15200

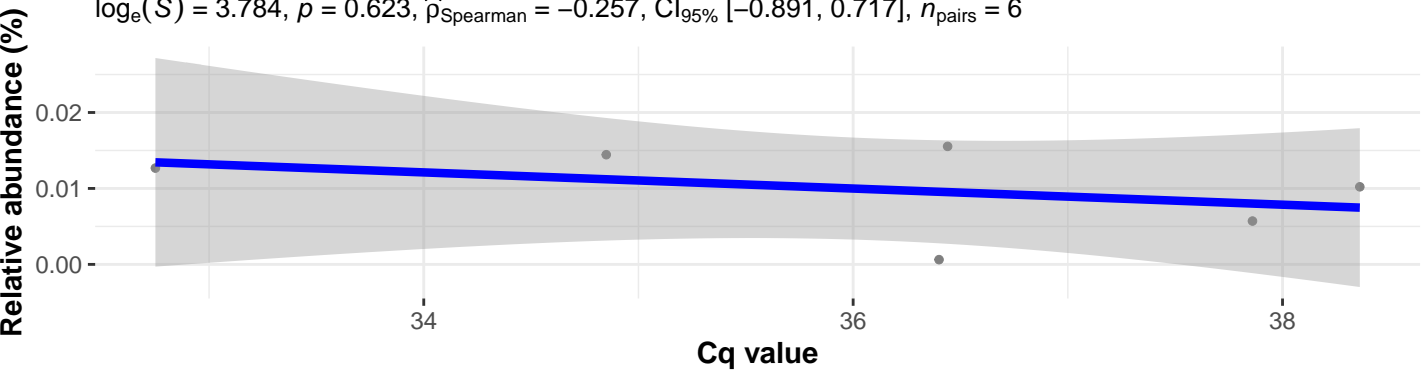
Correlation with all samples

$\log_e(S) = 7.907$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.533$, $\text{CI}_{95\%} [-0.785, -0.131]$, $n_{\text{pairs}} = 22$

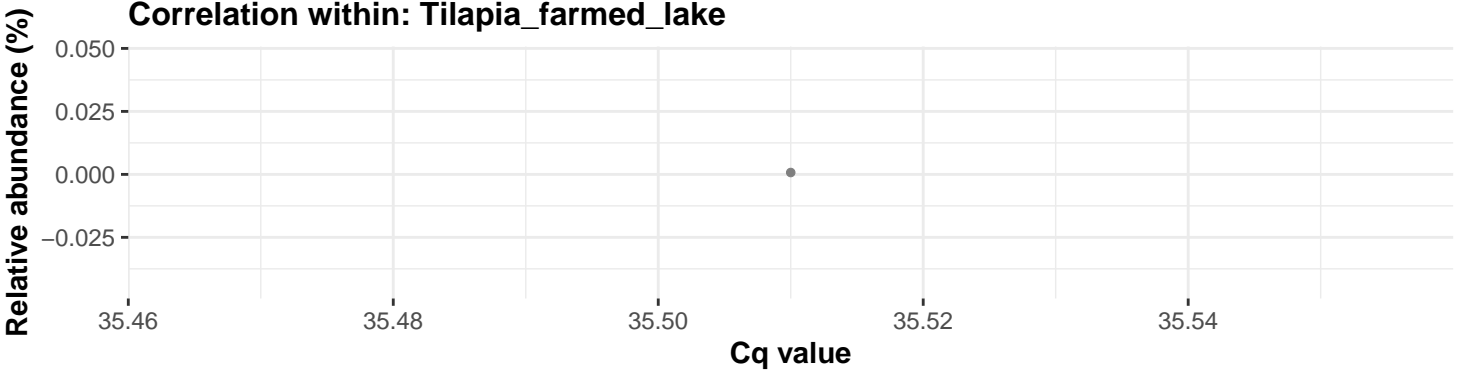


Correlation within: Tilapia_farmed_pond

$\log_e(S) = 3.784$, $p = 0.623$, $\hat{\rho}_{\text{Spearman}} = -0.257$, $\text{CI}_{95\%} [-0.891, 0.717]$, $n_{\text{pairs}} = 6$

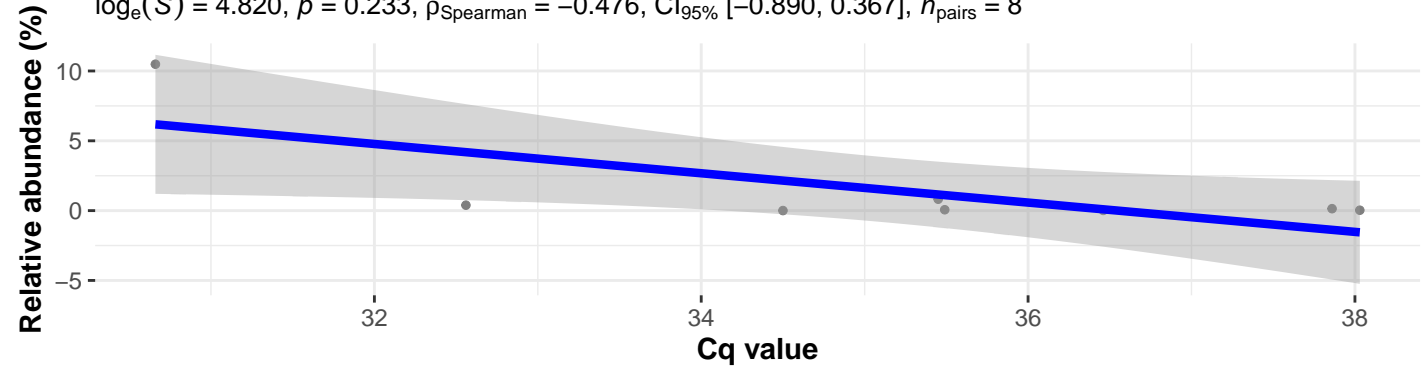


Correlation within: Tilapia_farmed_lake



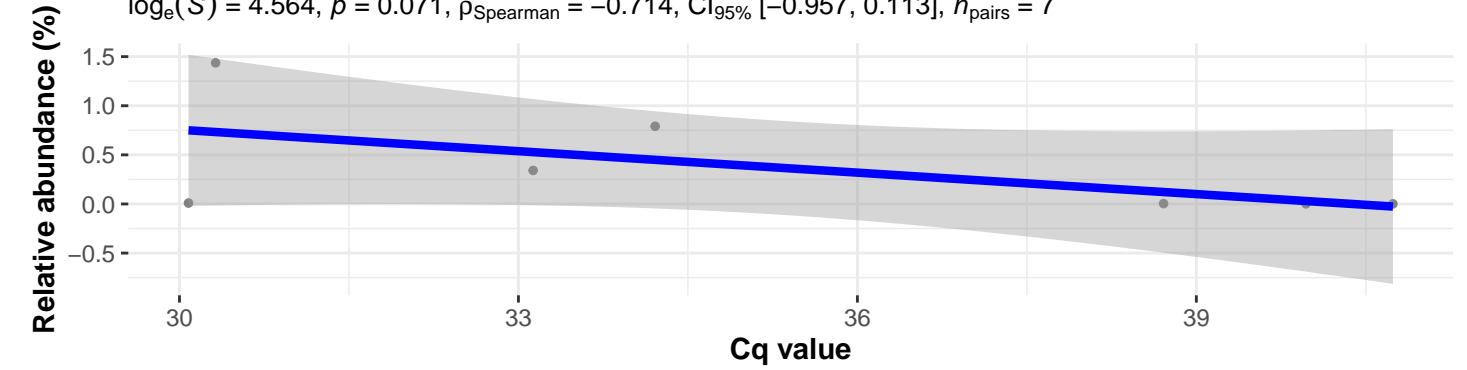
Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.820$, $p = 0.233$, $\hat{\rho}_{\text{Spearman}} = -0.476$, $\text{CI}_{95\%} [-0.890, 0.367]$, $n_{\text{pairs}} = 8$



Correlation within: Perch_wild_lake

$\log_e(S) = 4.564$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = -0.714$, $\text{CI}_{95\%} [-0.957, 0.113]$, $n_{\text{pairs}} = 7$

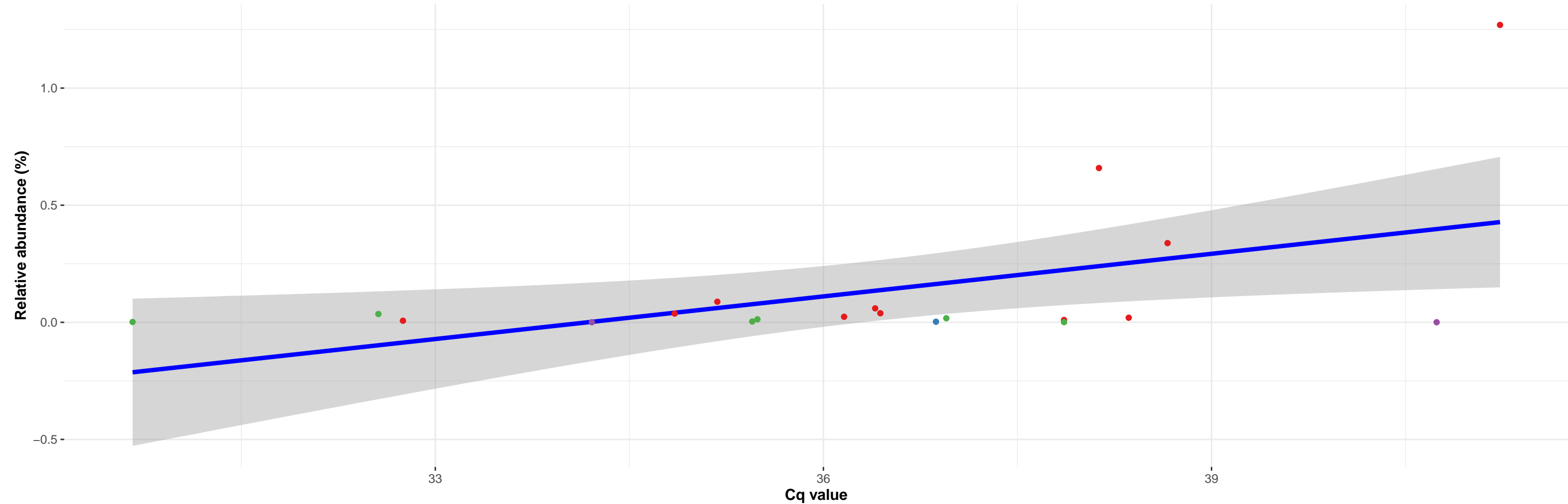


k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Turicibacter; s__uncultured bacterium

featureID: 8440d53055be17f665533f3bf79970b8

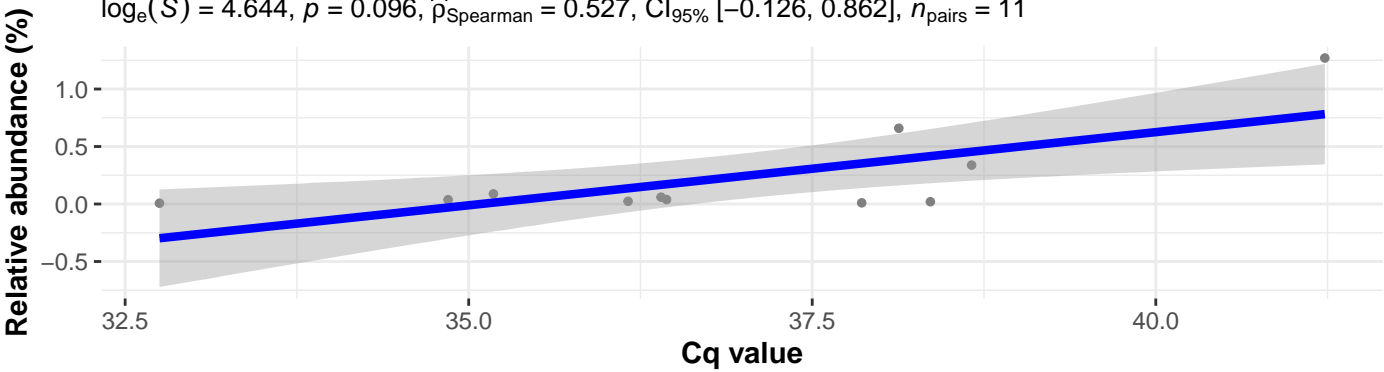
Correlation with all samples

$\log_e(S) = 6.924$, $p = 0.318$, $\hat{\rho}_{\text{Spearman}} = 0.235$, $\text{CI}_{95\%} [-0.244, 0.623]$, $n_{\text{pairs}} = 20$

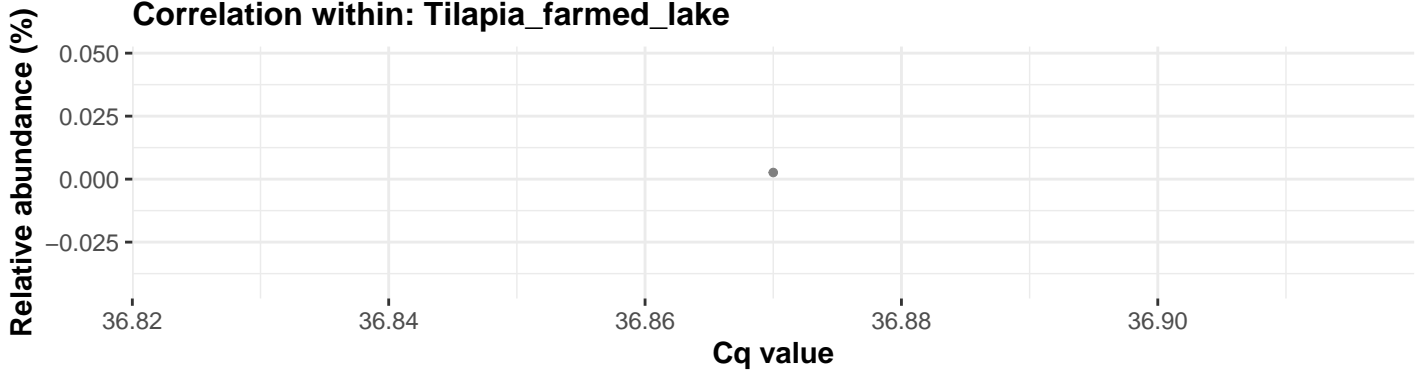


Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.644$, $p = 0.096$, $\hat{\rho}_{\text{Spearman}} = 0.527$, $\text{CI}_{95\%} [-0.126, 0.862]$, $n_{\text{pairs}} = 11$

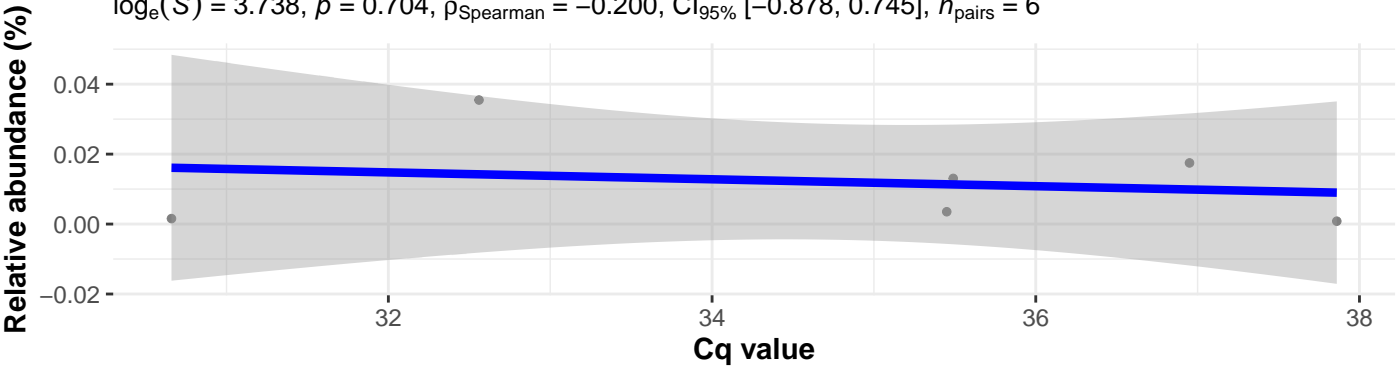


Correlation within: Tilapia_farmed_lake

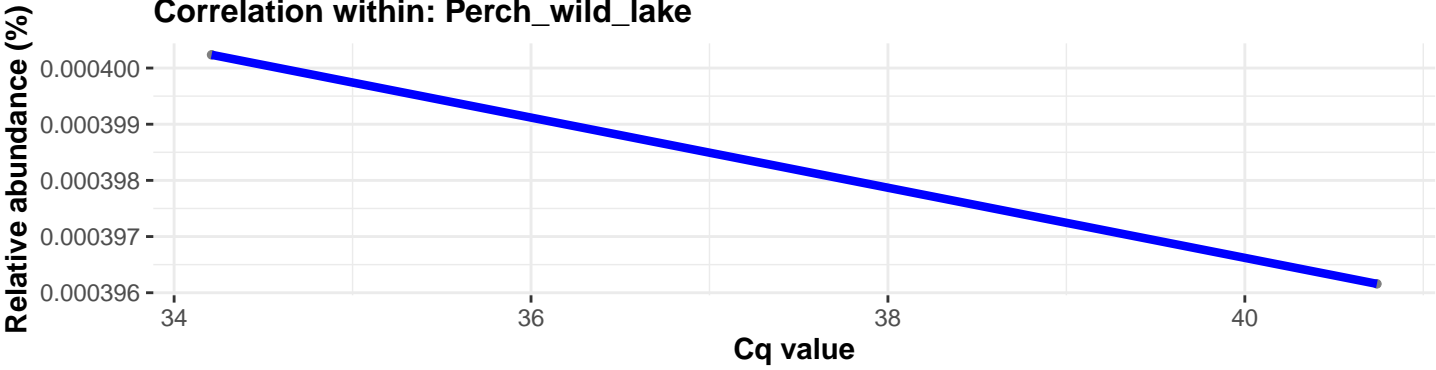


Correlation within: Tilapia_wild_lake

$\log_e(S) = 3.738$, $p = 0.704$, $\hat{\rho}_{\text{Spearman}} = -0.200$, $\text{CI}_{95\%} [-0.878, 0.745]$, $n_{\text{pairs}} = 6$



Correlation within: Perch_wild_lake

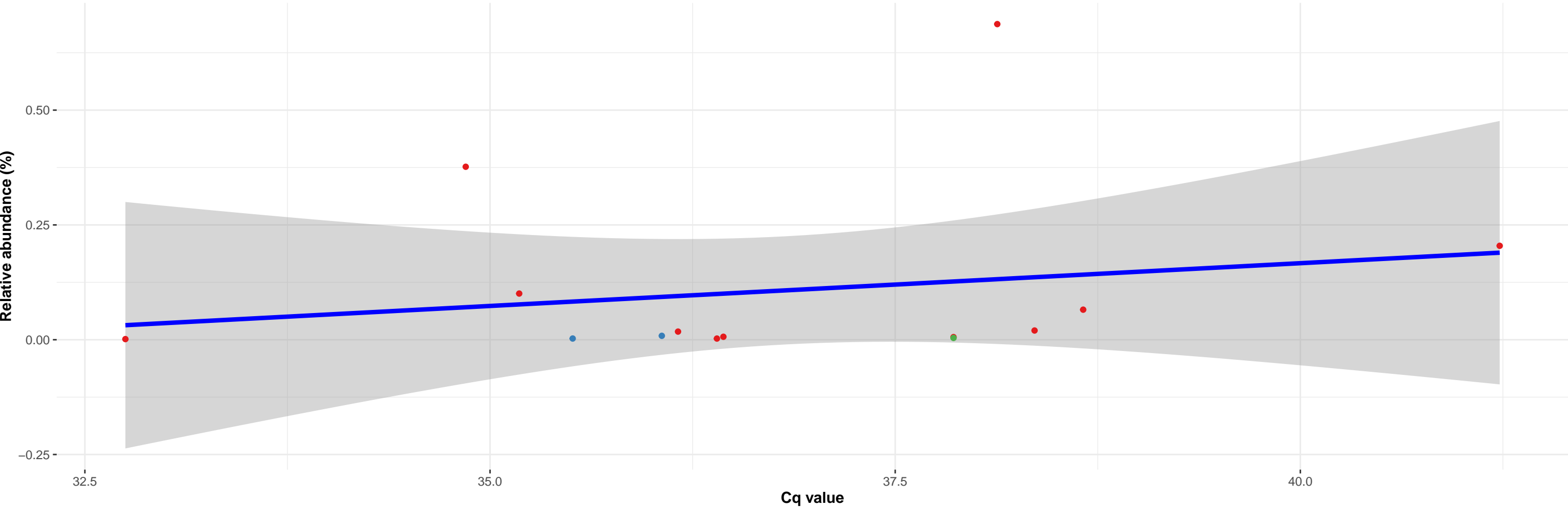


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__uncultured; Ambiguous_taxa; Ambiguous_taxa

featureID: c63bd7419c3dcdbff038ae017cba123c

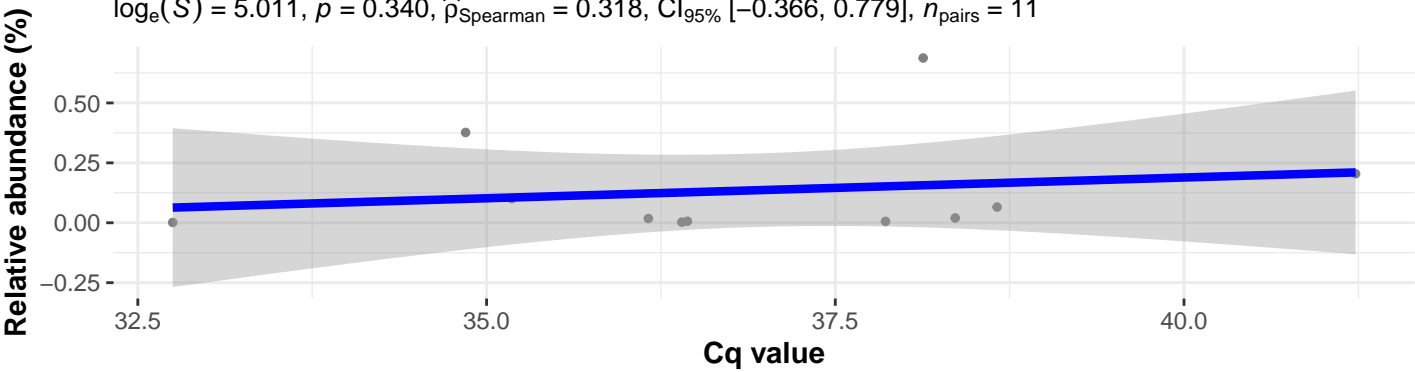
Correlation with all samples

$\log_e(S) = 5.720$, $p = 0.249$, $\hat{\rho}_{\text{Spearman}} = 0.330$, $\text{CI}_{95\%} [-0.259, 0.740]$, $n_{\text{pairs}} = 14$

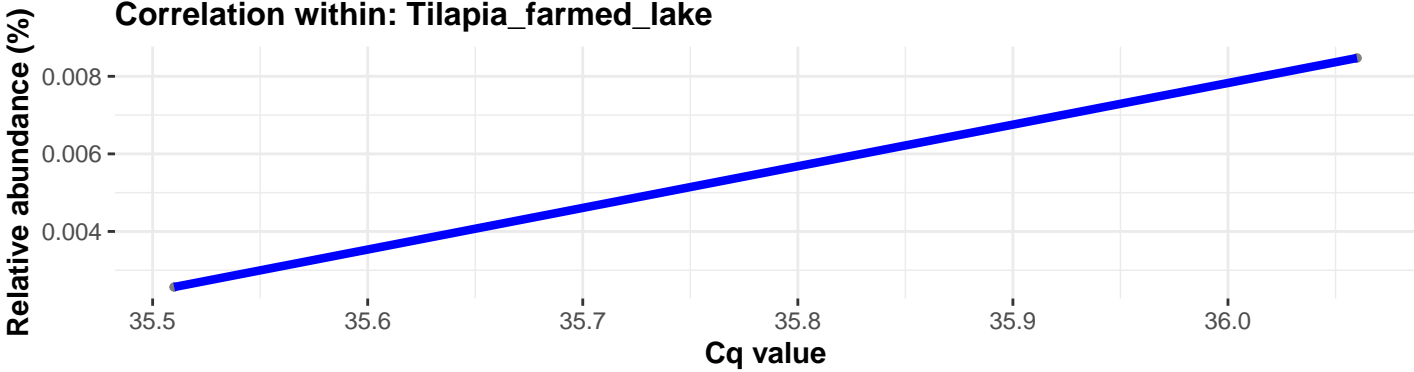


Correlation within: Tilapia_farmed_pond

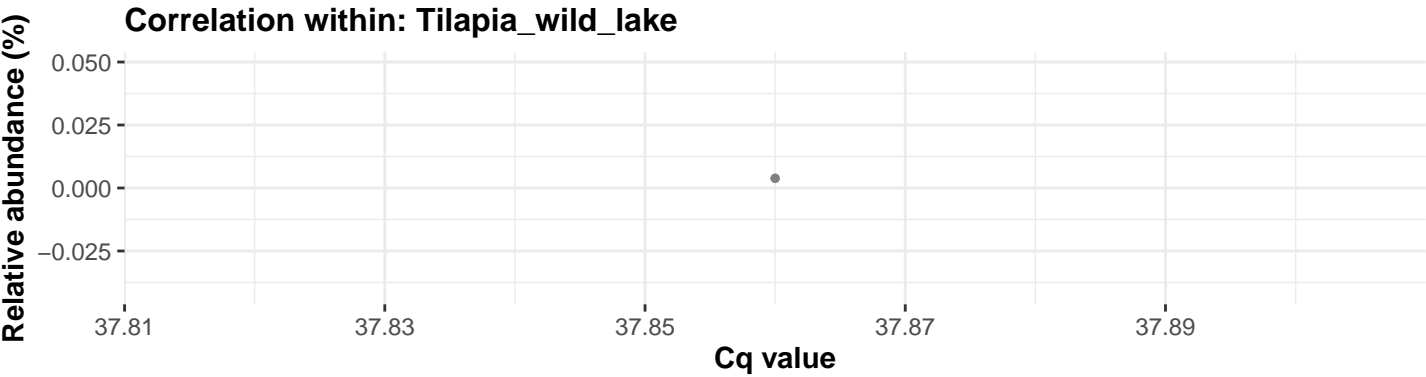
$\log_e(S) = 5.011$, $p = 0.340$, $\hat{\rho}_{\text{Spearman}} = 0.318$, $\text{CI}_{95\%} [-0.366, 0.779]$, $n_{\text{pairs}} = 11$



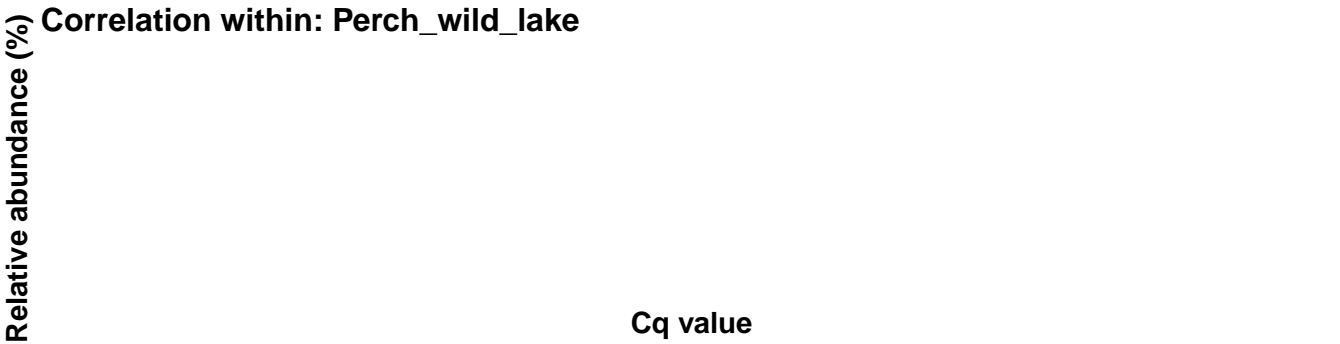
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

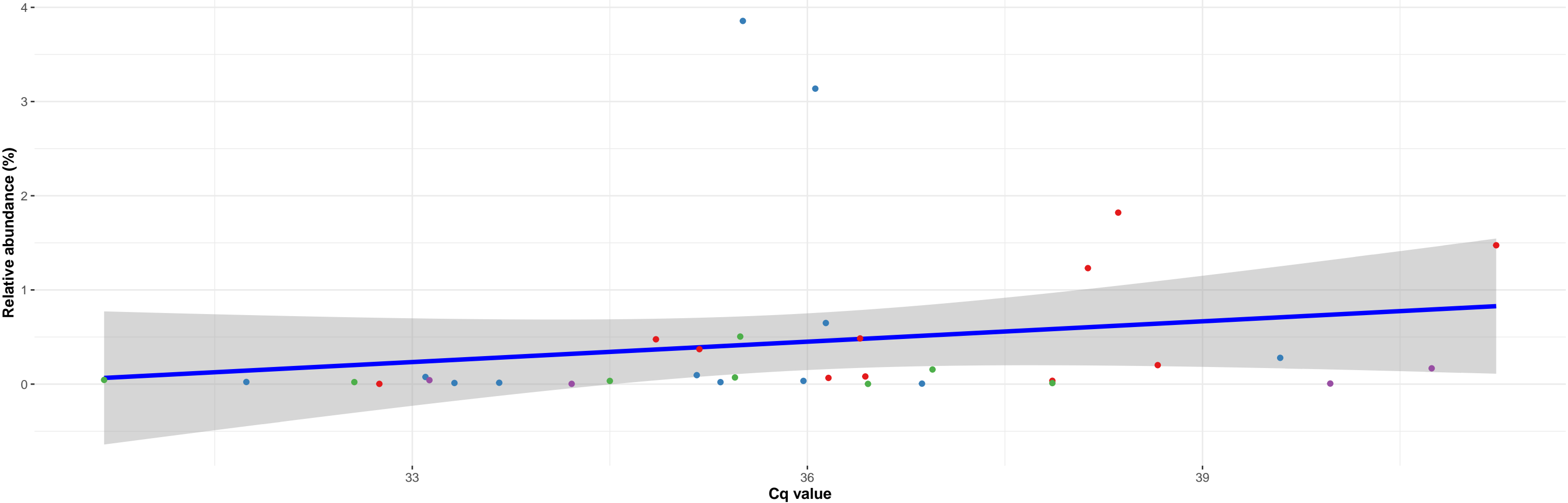


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: e576356609fe0b38cefff9ad3b12816a

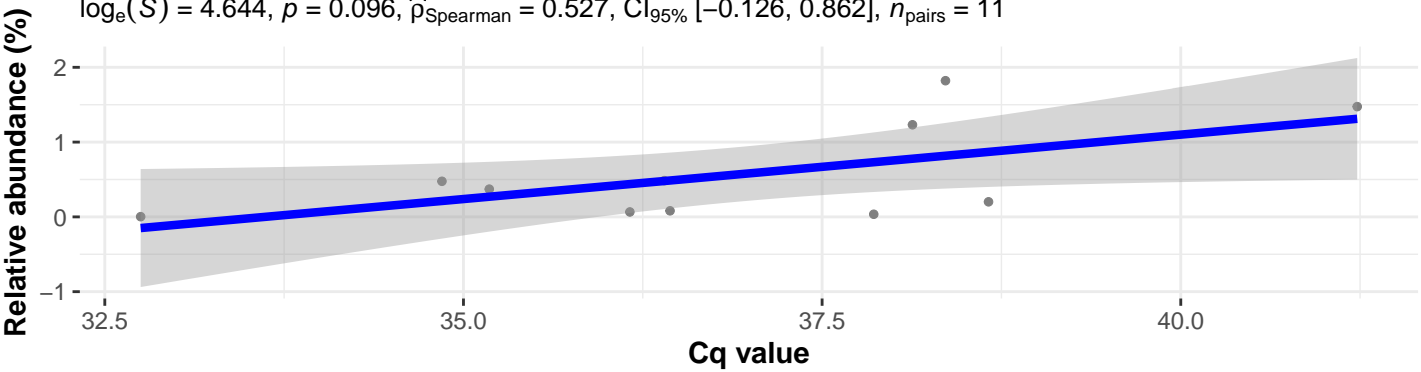
Correlation with all samples

$\log_e(S) = 8.475$, $p = 0.054$, $\hat{\rho}_{\text{Spearman}} = 0.329$, $\text{CI}_{95\%} [-0.015, 0.603]$, $n_{\text{pairs}} = 35$



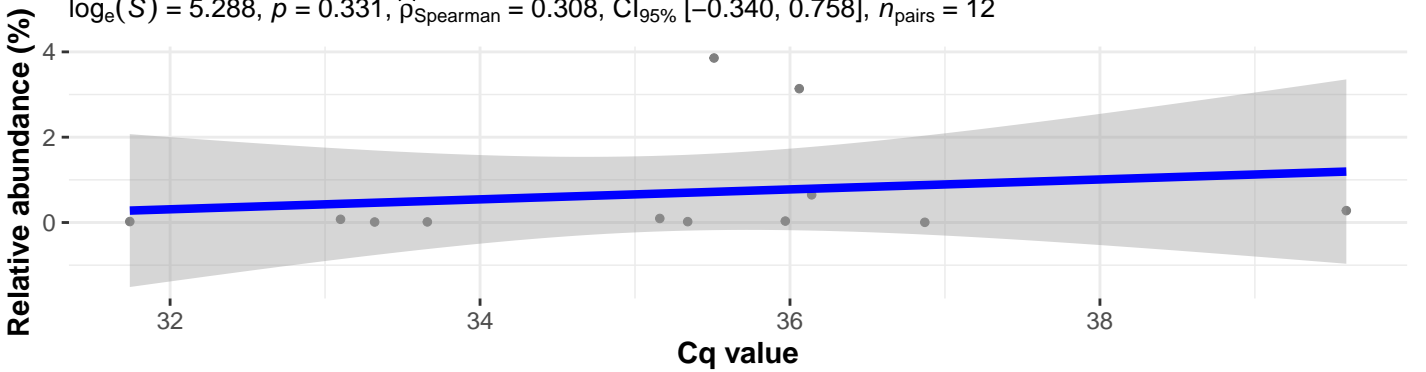
Correlation within: Tilapia_farmed_pond

$\log_e(S) = 4.644$, $p = 0.096$, $\hat{\rho}_{\text{Spearman}} = 0.527$, $\text{CI}_{95\%} [-0.126, 0.862]$, $n_{\text{pairs}} = 11$



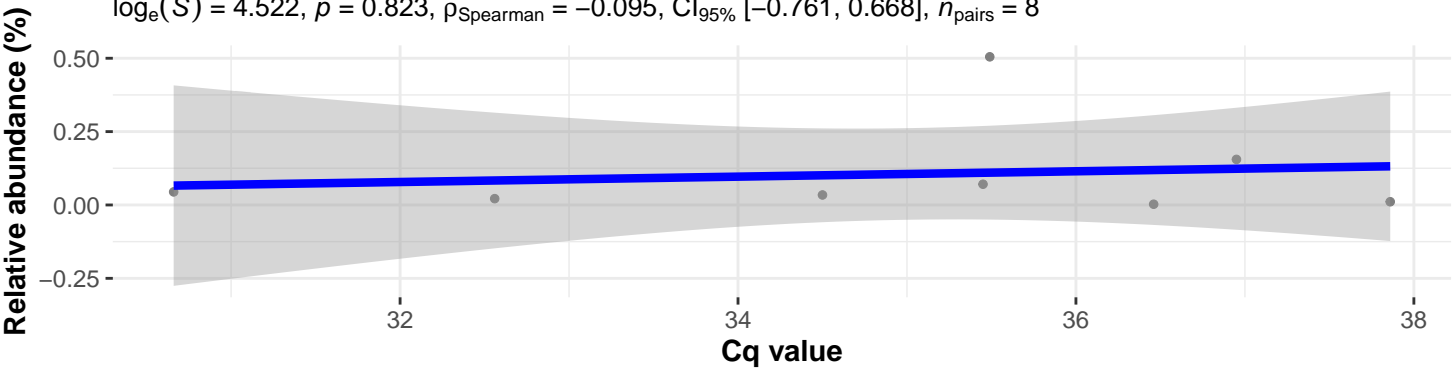
Correlation within: Tilapia_farmed_lake

$\log_e(S) = 5.288$, $p = 0.331$, $\hat{\rho}_{\text{Spearman}} = 0.308$, $\text{CI}_{95\%} [-0.340, 0.758]$, $n_{\text{pairs}} = 12$



Correlation within: Tilapia_wild_lake

$\log_e(S) = 4.522$, $p = 0.823$, $\hat{\rho}_{\text{Spearman}} = -0.095$, $\text{CI}_{95\%} [-0.761, 0.668]$, $n_{\text{pairs}} = 8$



Correlation within: Perch_wild_lake

