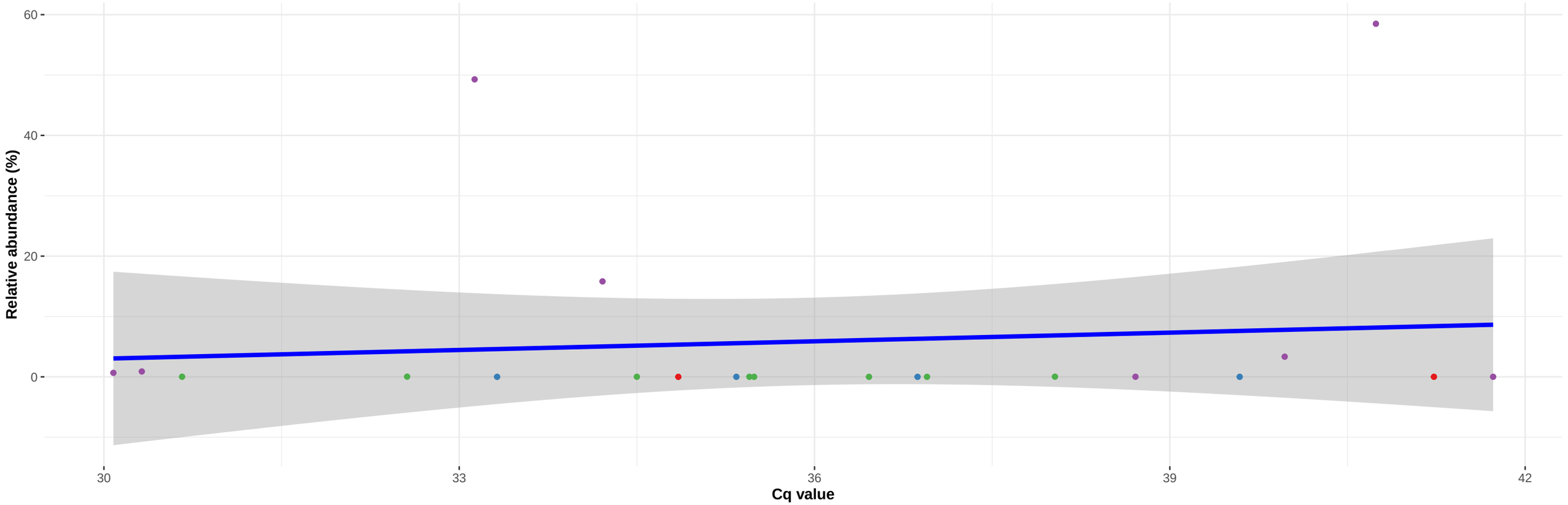
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 30cd2eb39b81e92ac815ec19fd6ccdee

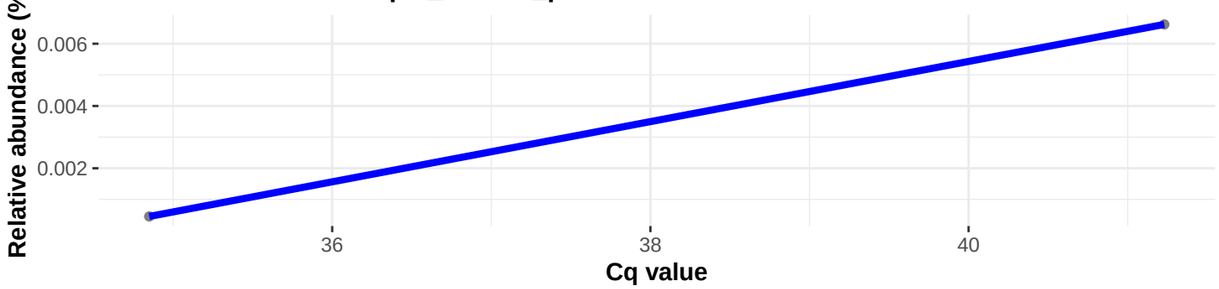
Correlation with all samples

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

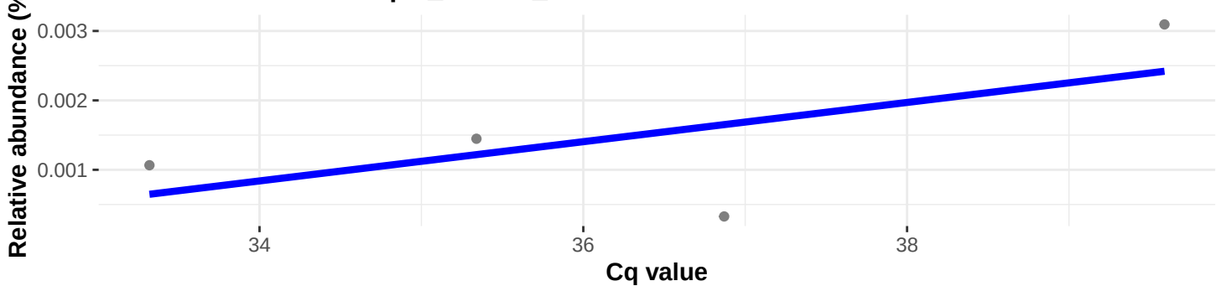


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

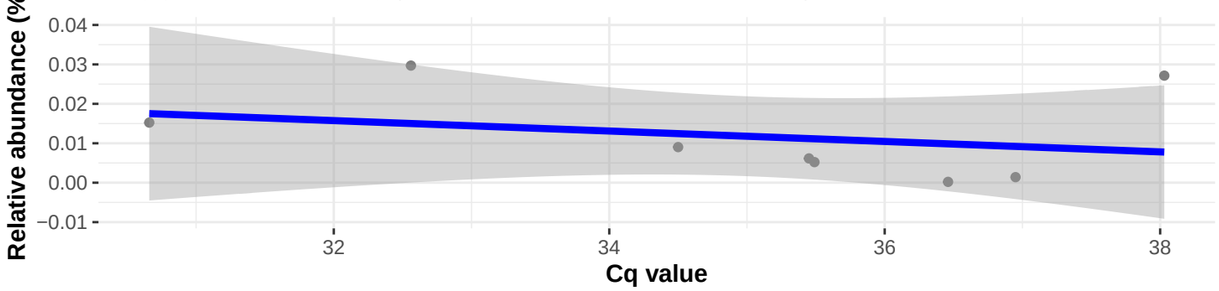


Correlation within: Tilapia_farmed_lake



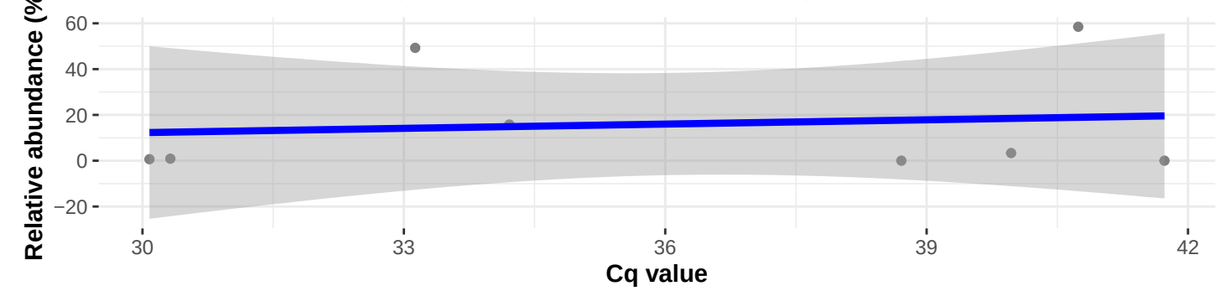
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

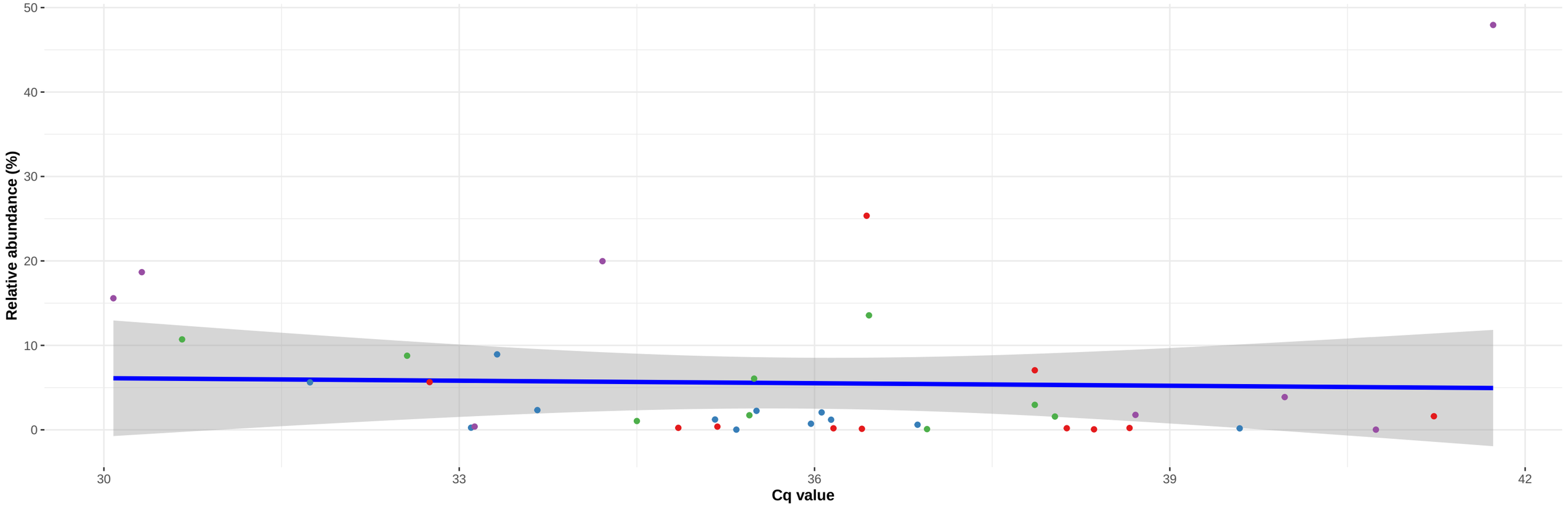


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 9039275571577e03e38d718f59db0e1f

Correlation with all samples

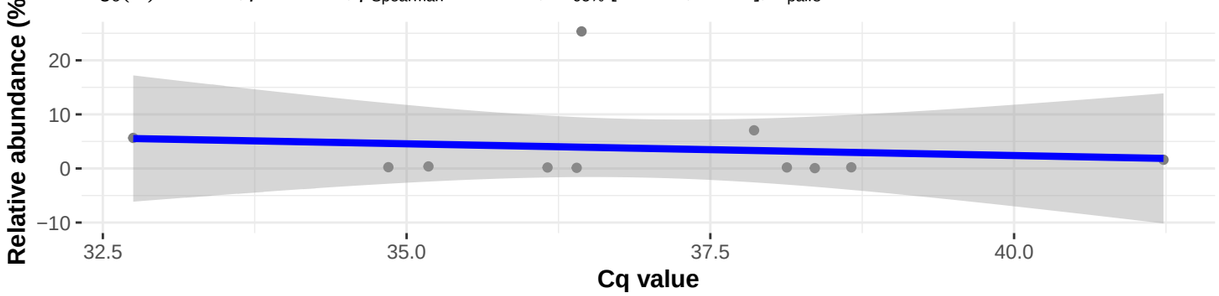
$\log_e(S) = 9.554$, $p = 0.042$, $\hat{\rho}_{Spearman} = -0.323$, $CI_{95\%}$ [−0.583, −0.003], $n_{pairs} = 40$



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

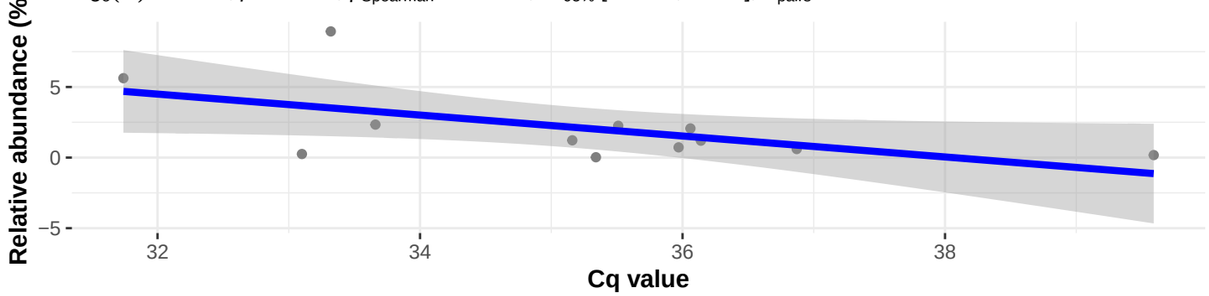
Correlation within: Tilapia_farmed_pond

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



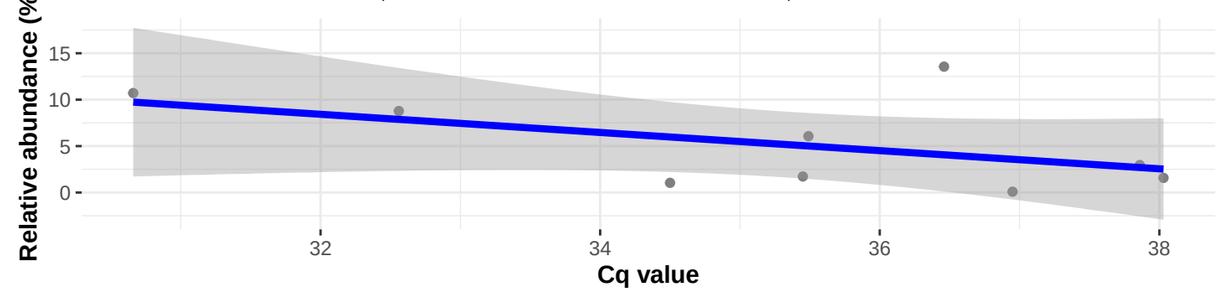
Correlation within: Tilapia_farmed_lake

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



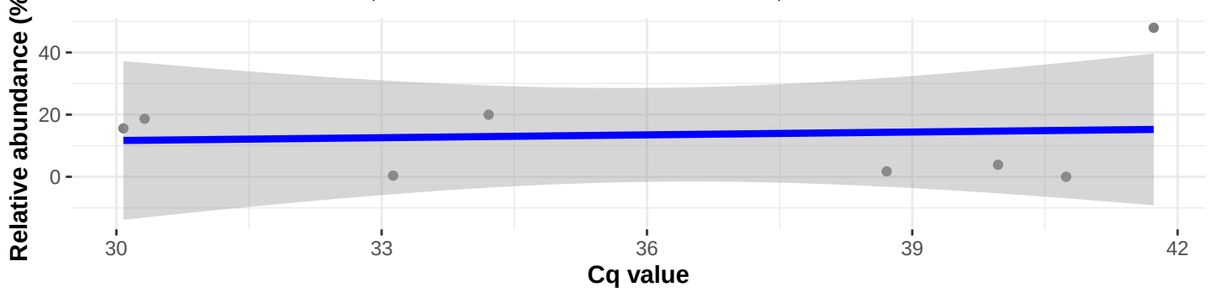
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

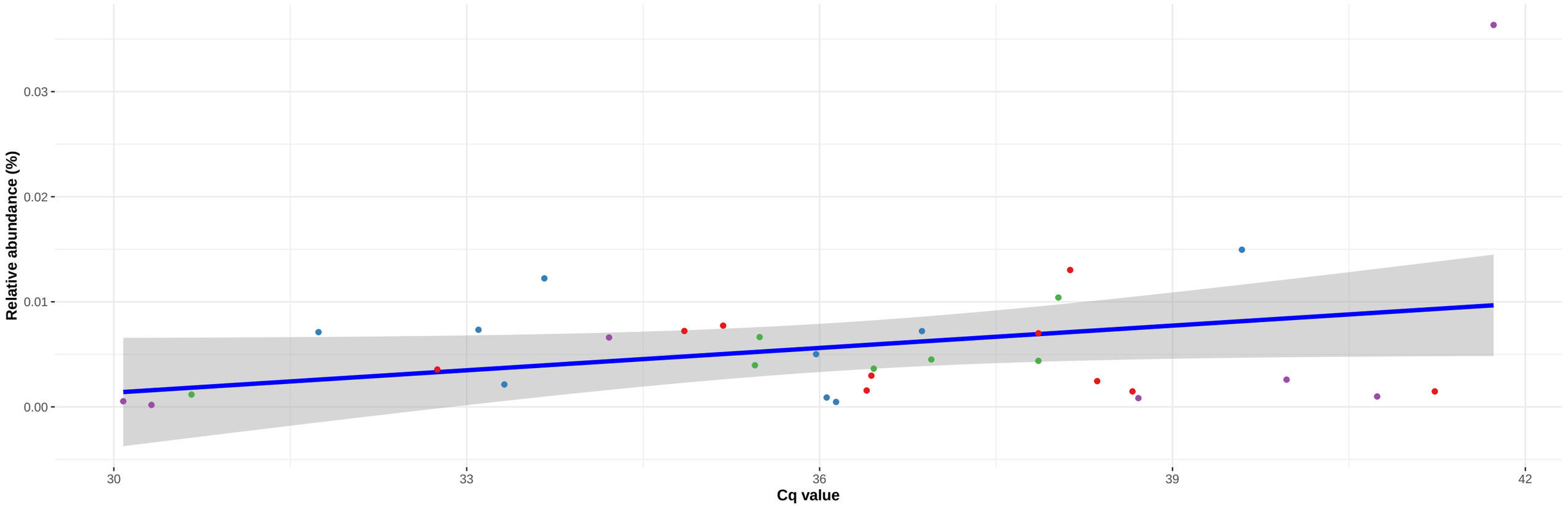


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Curvibacter; NA

featureID: e0fcddfbd9012f2ef3fe5165e818f651

Correlation with all samples

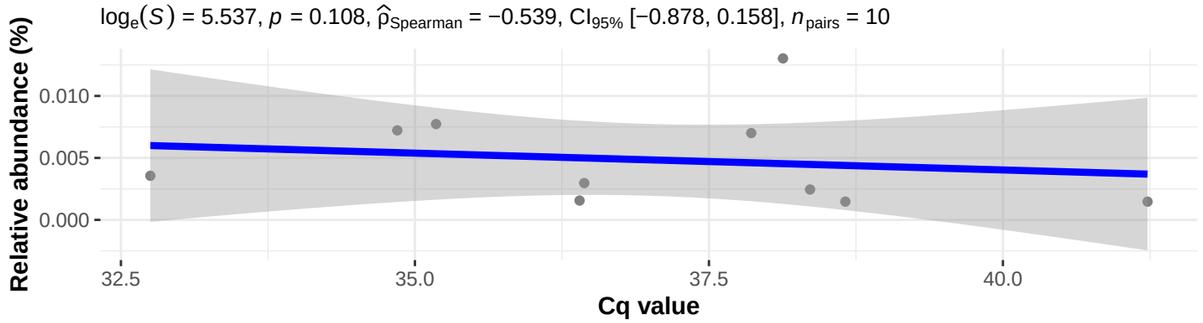
$\log_e(S)$ = 8.588, p = 0.569, $\hat{\rho}_{Spearman}$ = 0.103, $CI_{95\%}$ [−0.259, 0.439], n_{pairs} = 33



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

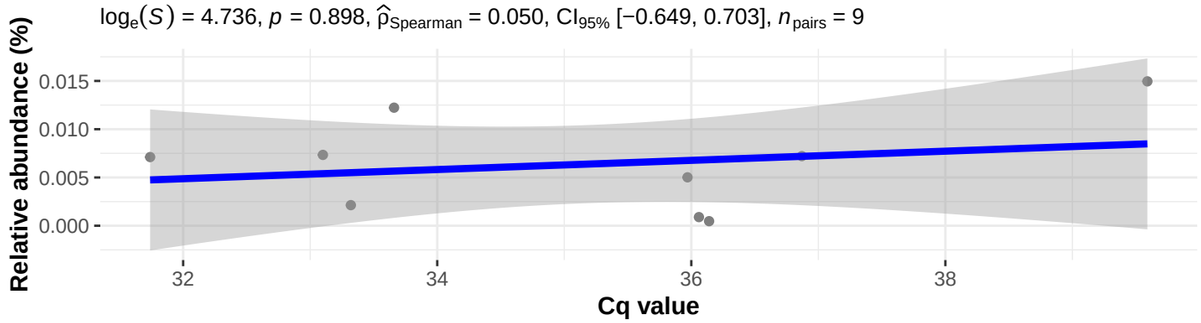
Correlation within: Tilapia_farmed_pond

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



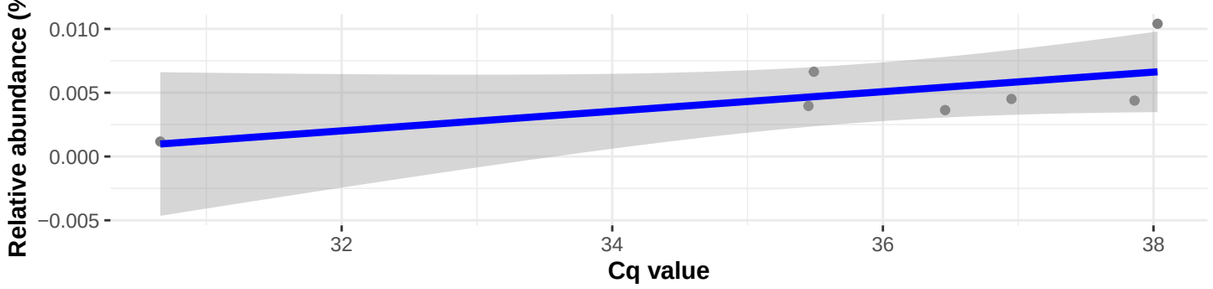
Correlation within: Tilapia_farmed_lake

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



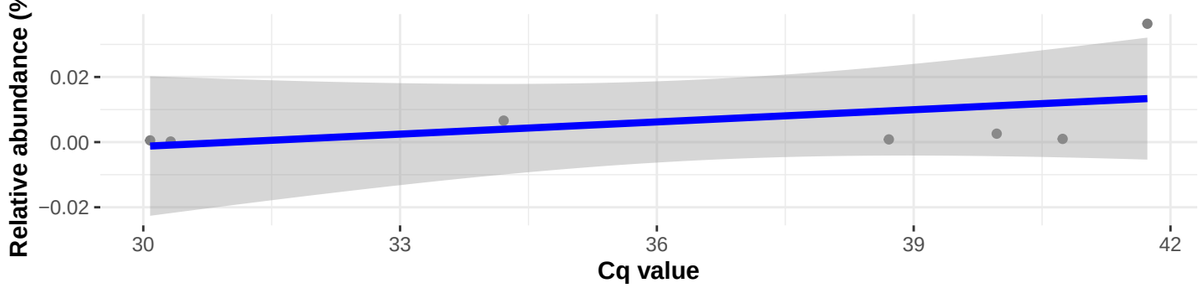
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

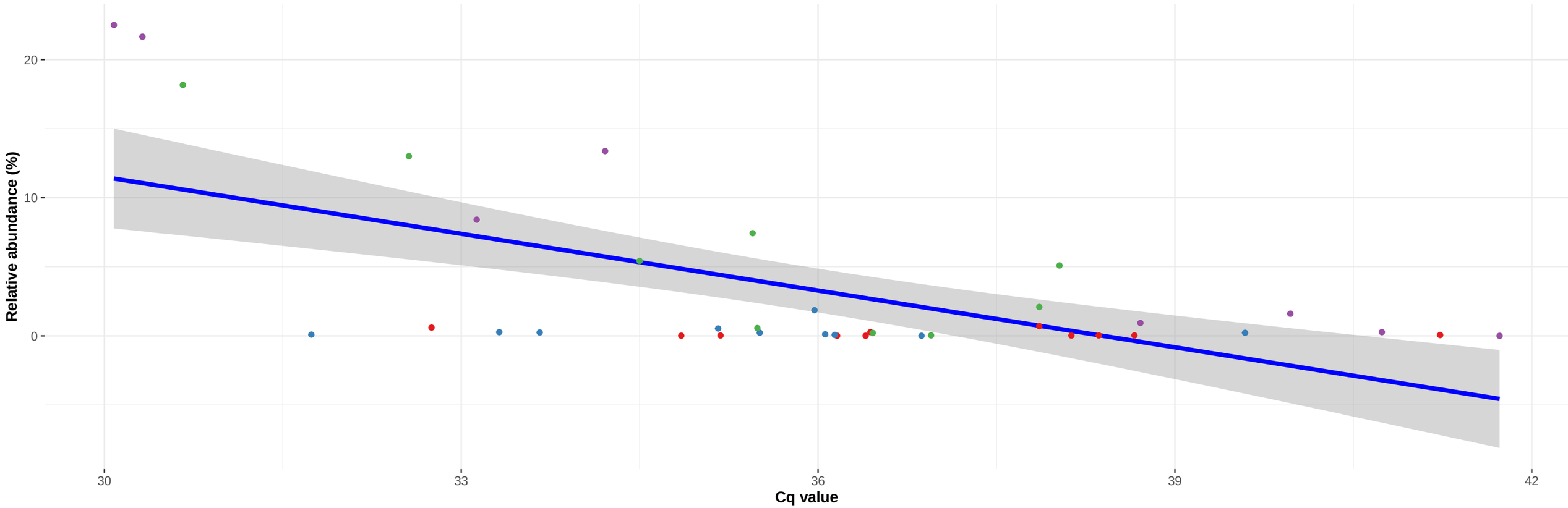


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

featureID: 4f52c06bab364867d8911147cbccbc38

Correlation with all samples

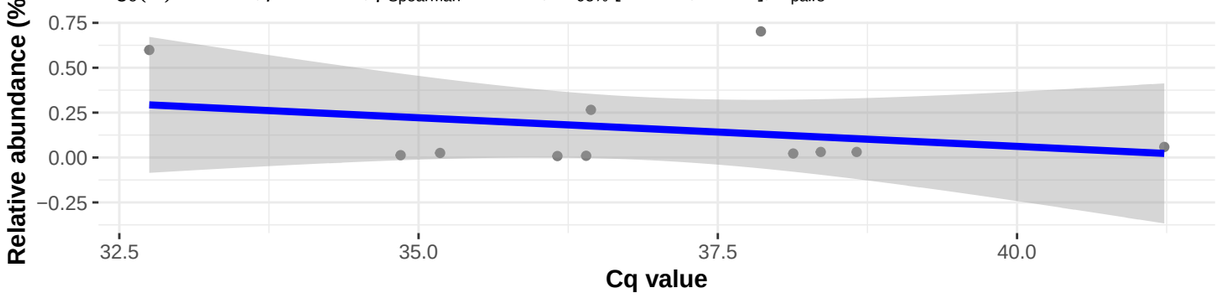
$\log_e(S)$ = 9.506, p = 0.003, $\hat{\rho}_{Spearman}$ = −0.471, $CI_{95\%}$ [−0.692, −0.169], n_{pairs} = 38



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

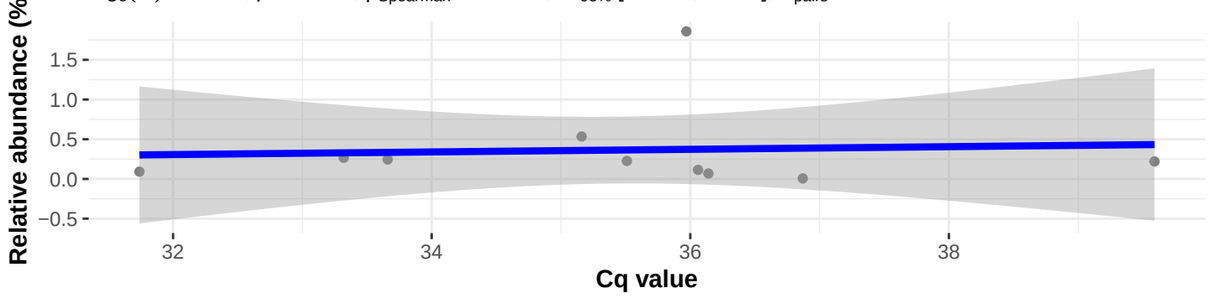
Correlation within: Tilapia_farmed_pond

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



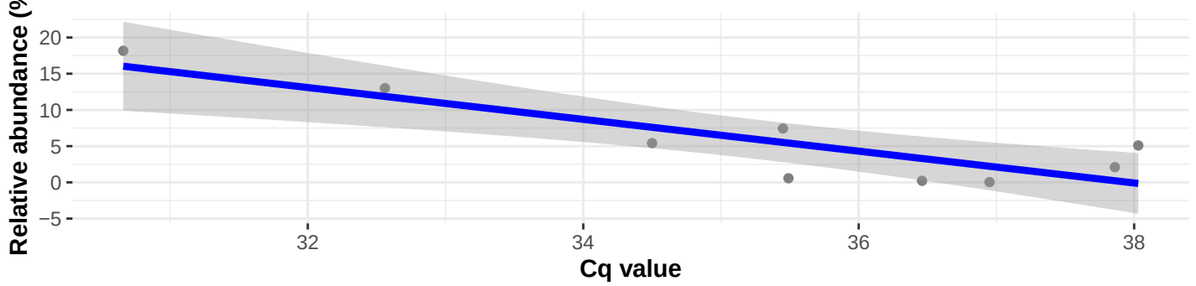
Correlation within: Tilapia_farmed_lake

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



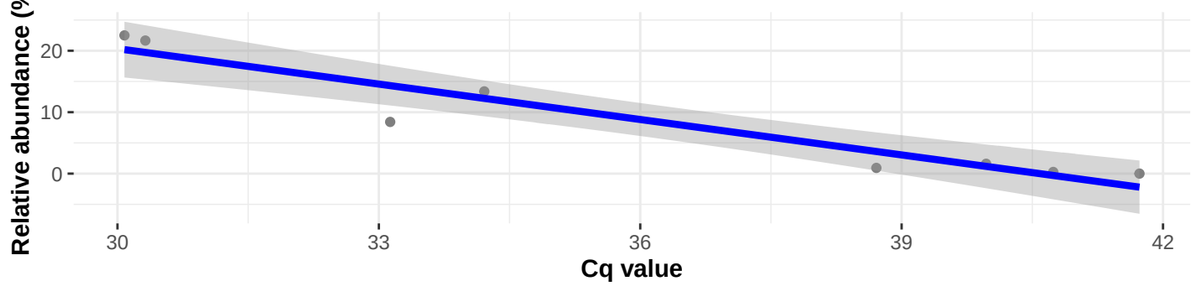
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

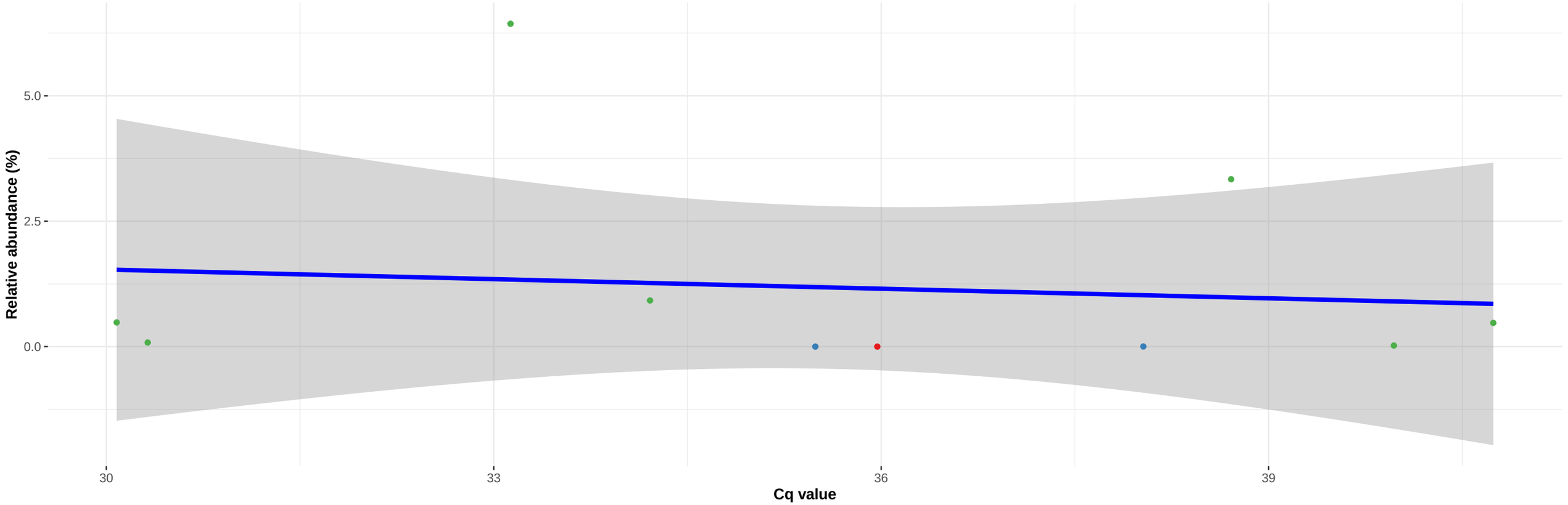


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

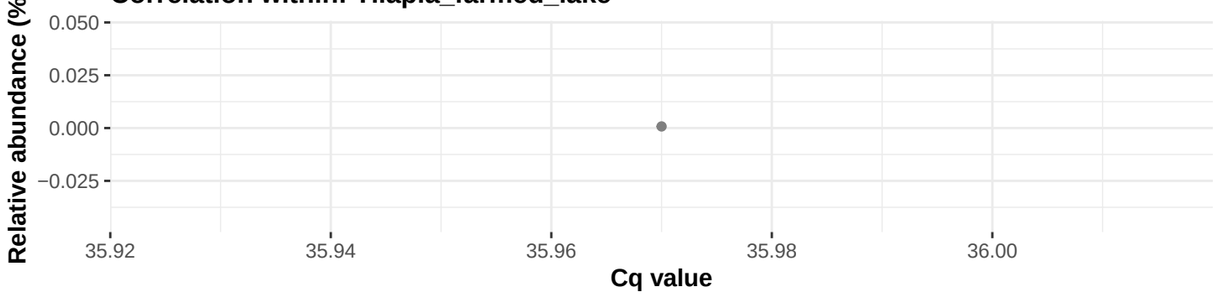
featureID: 2e13ada579831ad7bc85cacea069bcb4

Correlation with all samples

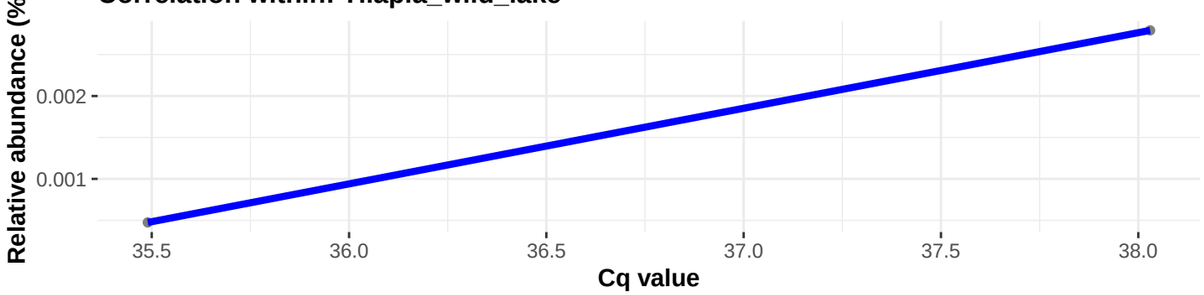
$\log_e(S)$ = 5.298, p = 0.556, $\hat{\rho}_{Spearman}$ = −0.212, $CI_{95\%}$ [−0.752, 0.498], n_{pairs} = 10



Correlation within: Tilapia_farmed_lake

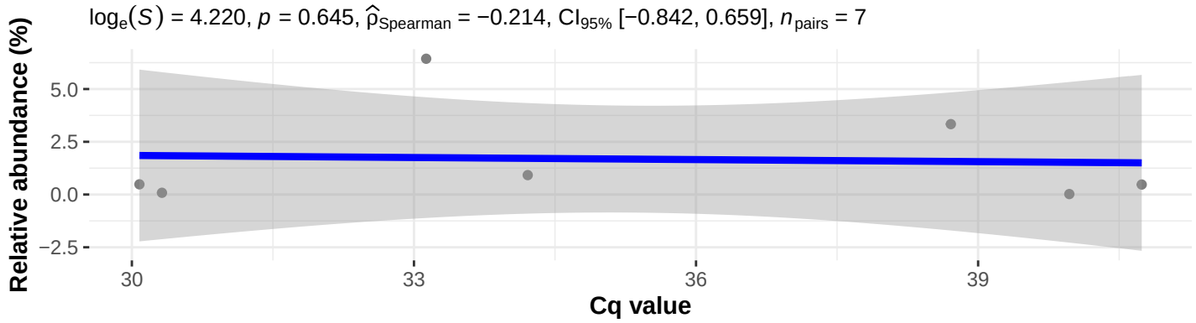


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

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

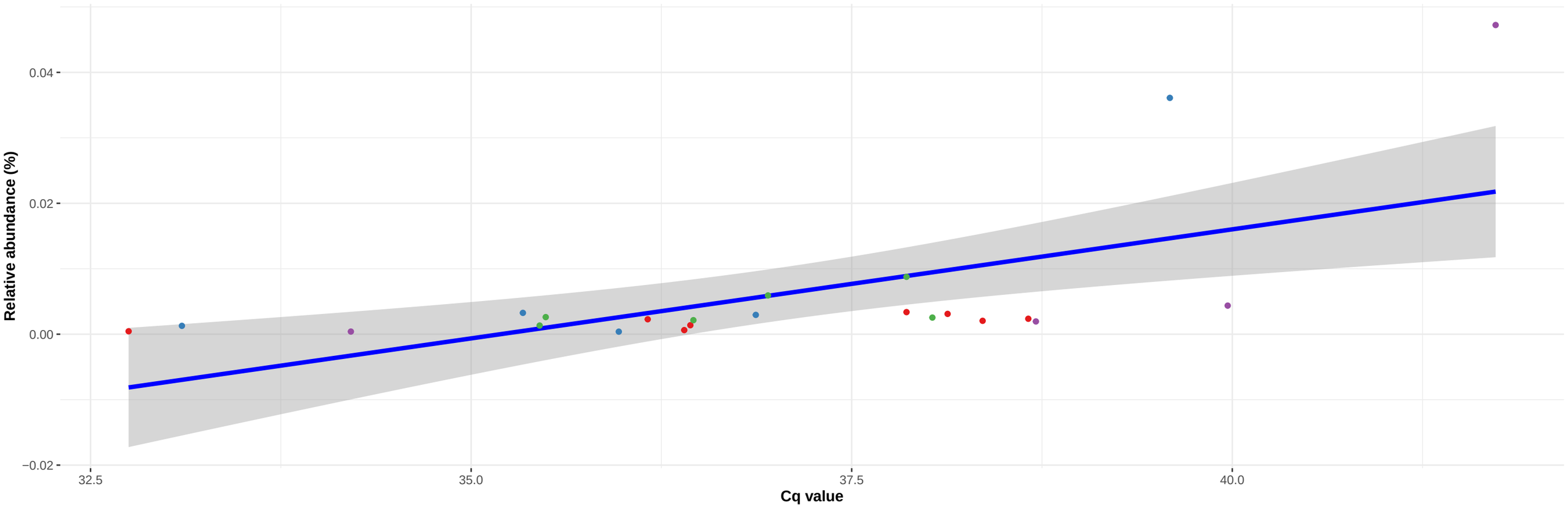


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; NA

featureID: 11c192ca47293df7d3c26138fd796fe1

Correlation with all samples

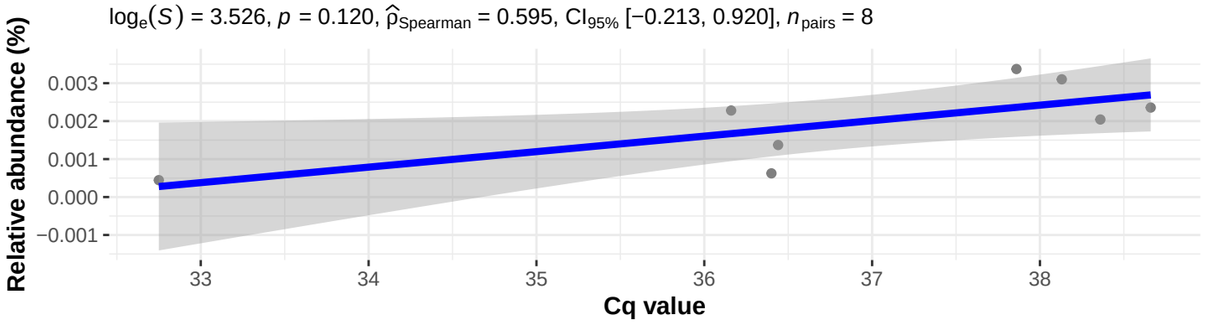
$\log_e(S)$ = 6.599, p = 0.001, $\hat{\rho}_{Spearman}$ = 0.637, $CI_{95\%}$ [0.293, 0.835], n_{pairs} = 23



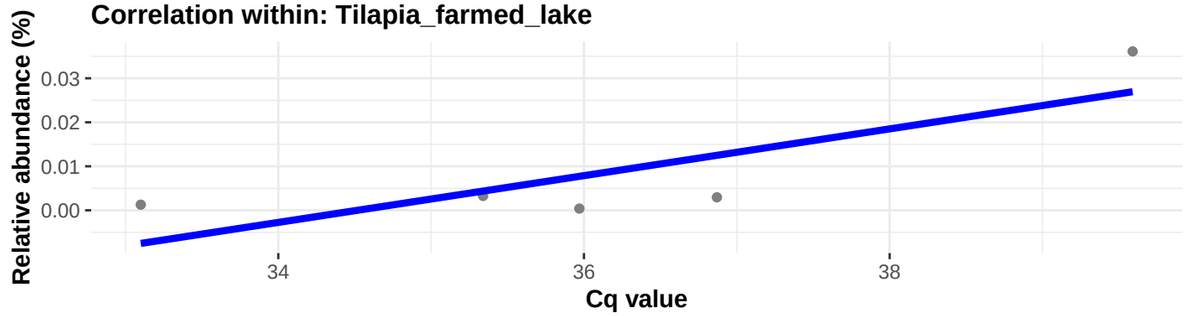
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

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

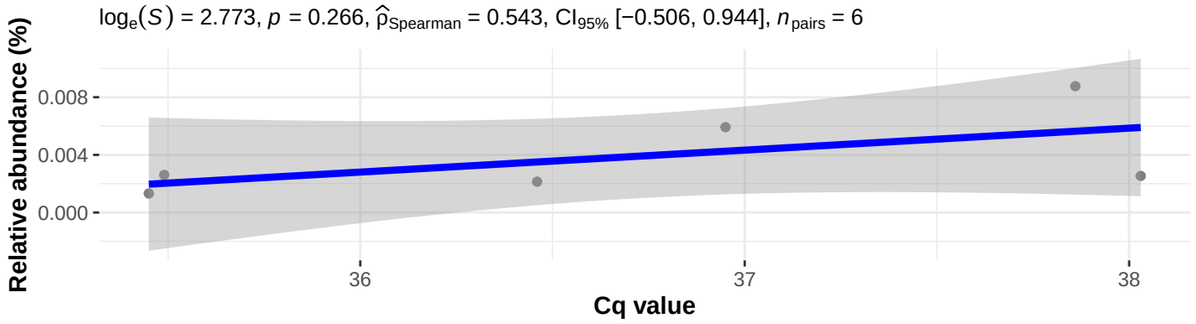


Correlation within: Tilapia_farmed_lake

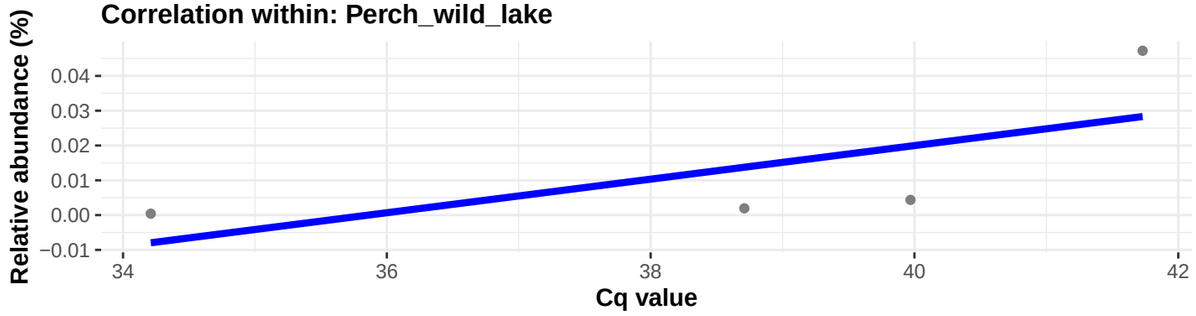


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

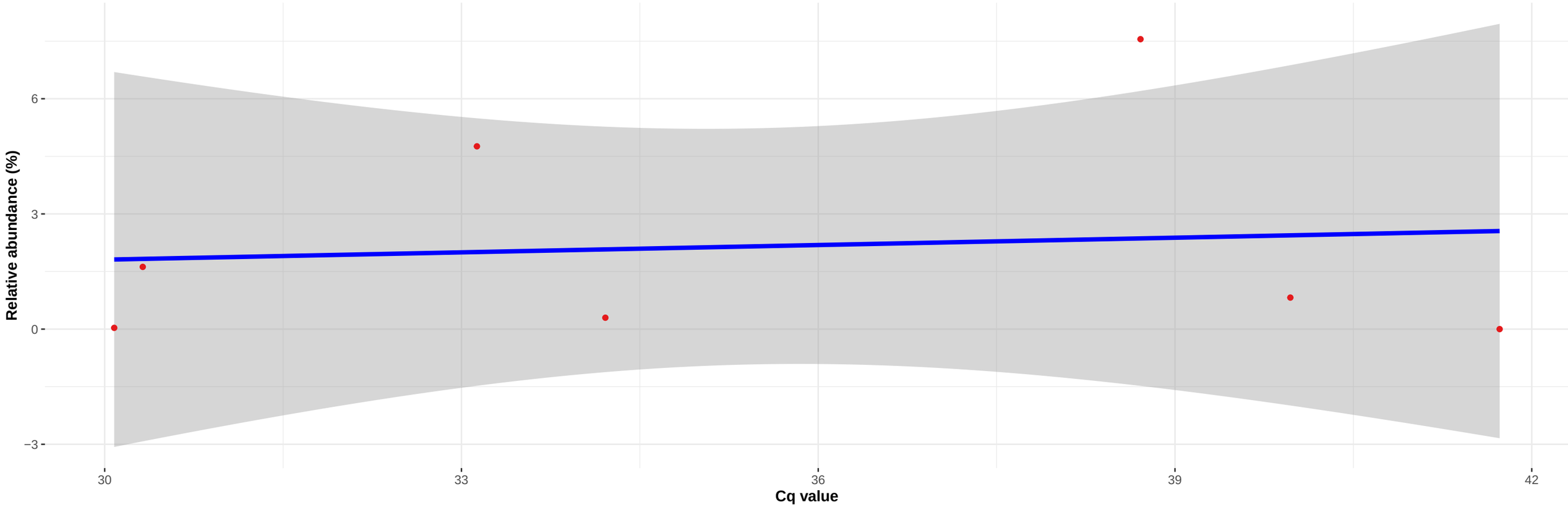


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 1f1ddbae27b2e40cd4947dc079b0021e

Correlation with all samples

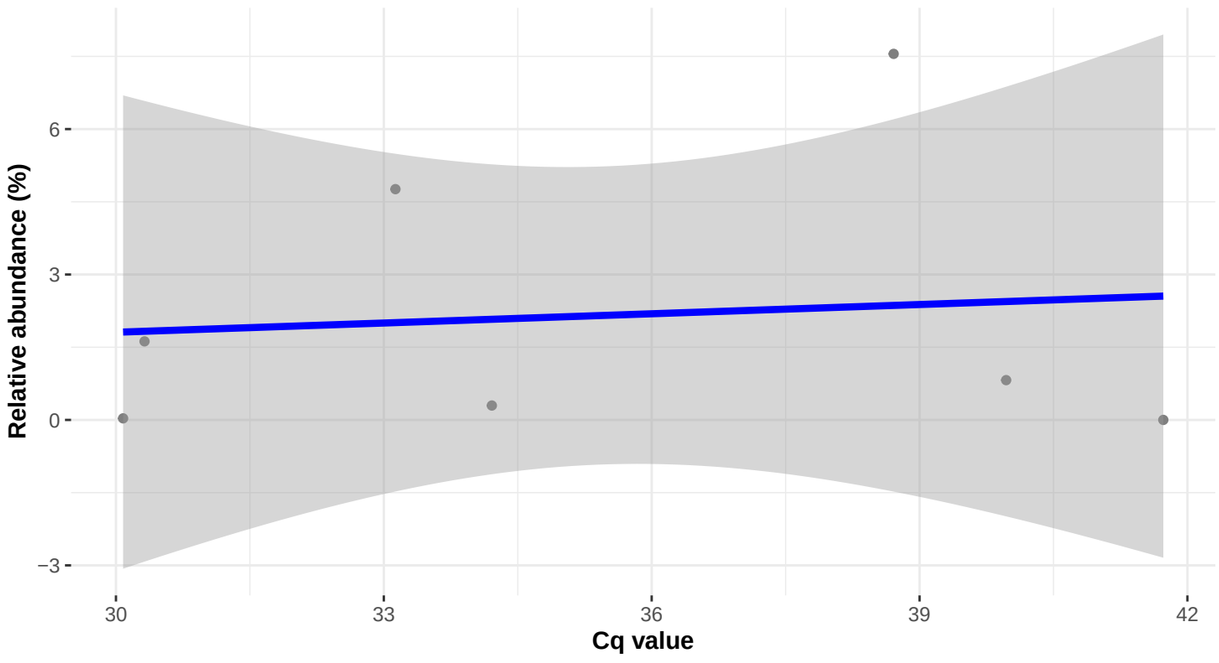
$\log_e(S)$ = 4.159, p = 0.760, $\hat{\rho}_{Spearman}$ = −0.143, $CI_{95\%}$ [−0.819, 0.699], n_{pairs} = 7



Sample_type ● Perch_wild_lake

Correlation within: Perch_wild_lake

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

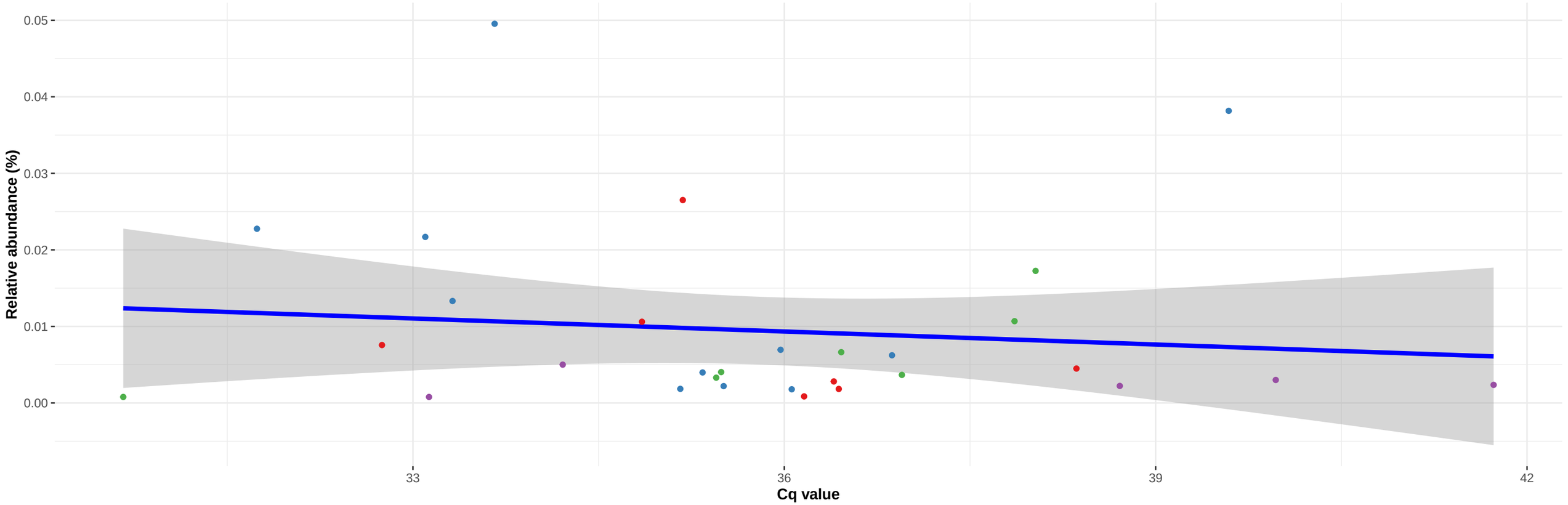


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: af190b852cec0d6eb78c15eb0e8777e0

Correlation with all samples

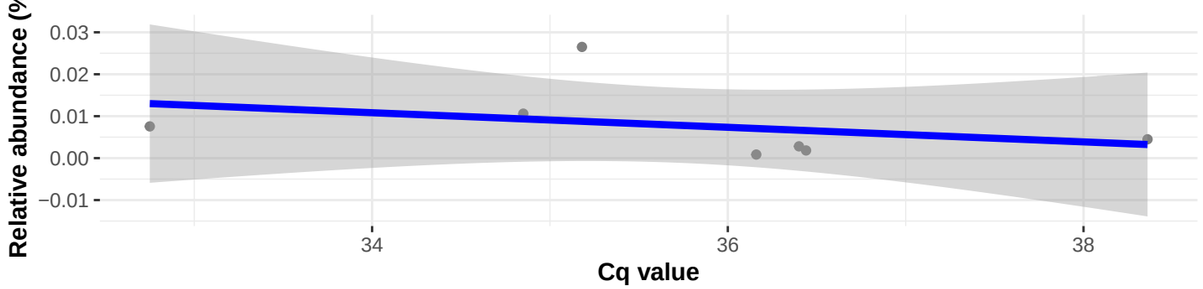
$\log_e(S)$ = 8.516, p = 0.561, $\hat{\rho}_{Spearman}$ = −0.111, $CI_{95\%}$ [−0.462, 0.270], n_{pairs} = 30



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

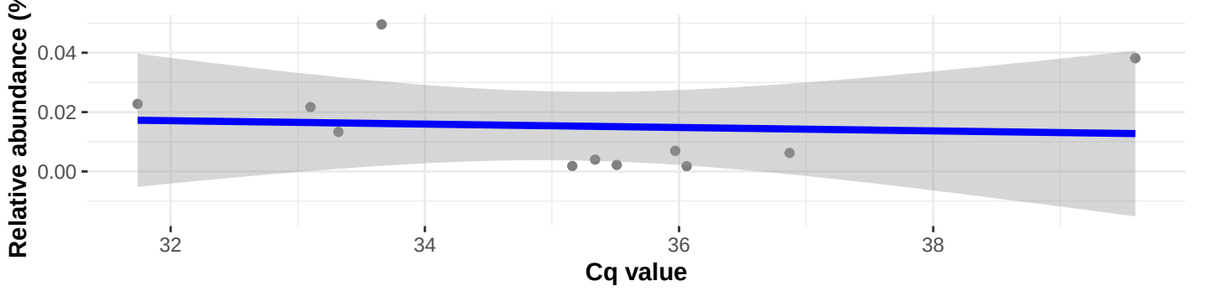
Correlation within: Tilapia_farmed_pond

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



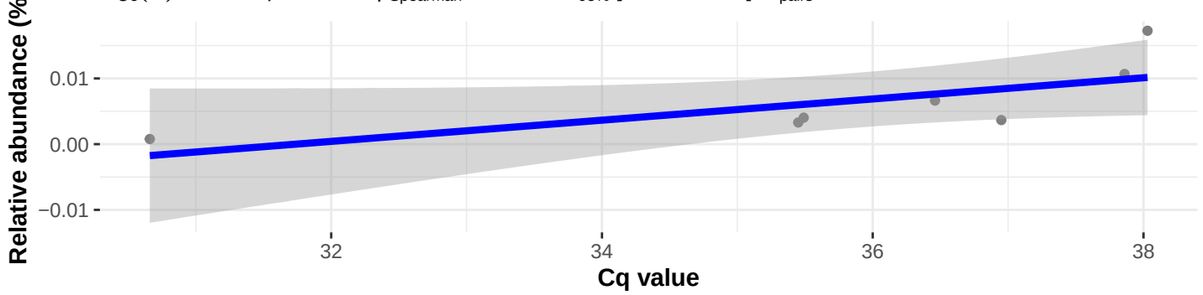
Correlation within: Tilapia_farmed_lake

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



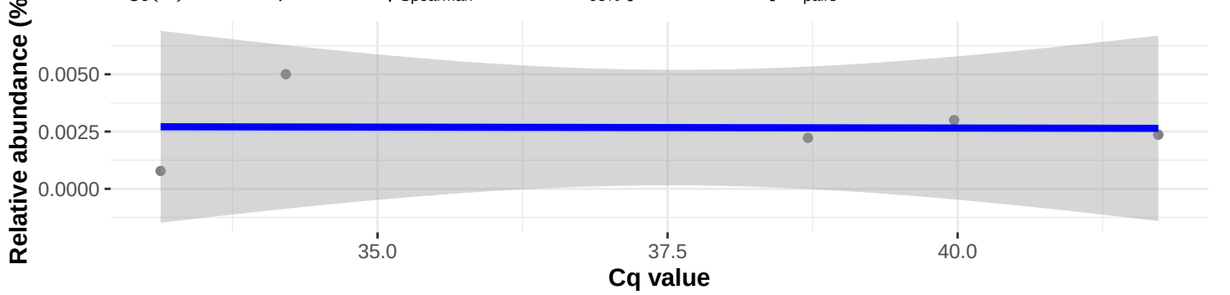
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

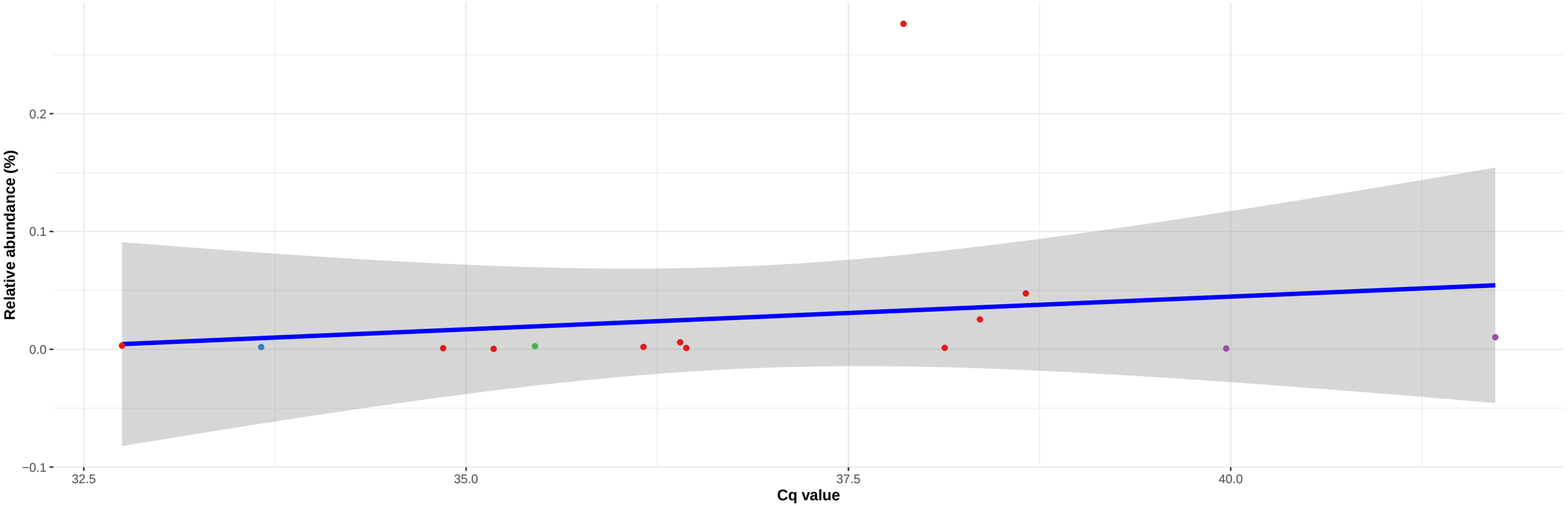


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA

featureID: 9db2817f5c42be6a7bcbca662959982d

Correlation with all samples

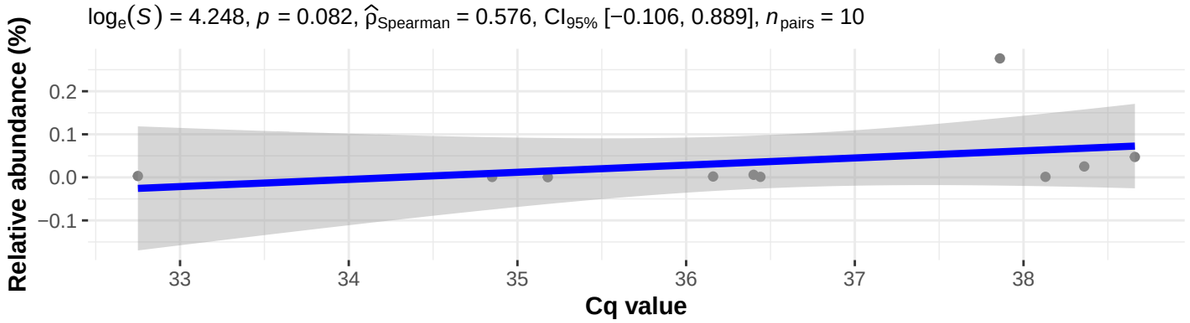
$\log_e(S)$ = 5.724, p = 0.253, $\hat{\rho}_{Spearman}$ = 0.327, $CI_{95\%}$ [−0.262, 0.739], n_{pairs} = 14



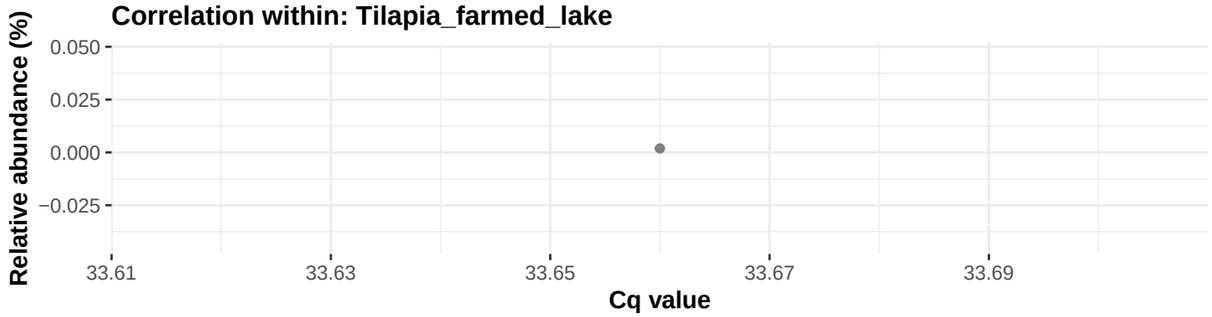
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

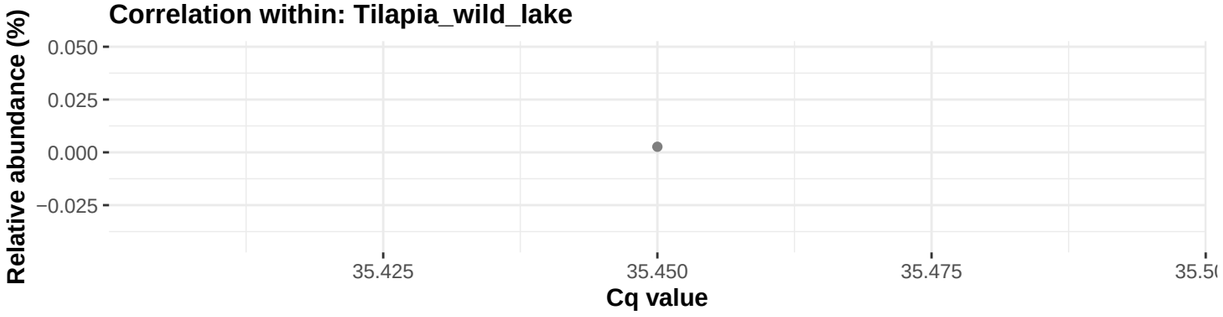
$\log_e(S)$ = 4.248, p = 0.082, $\hat{\rho}_{Spearman}$ = 0.576, $CI_{95\%}$ [−0.106, 0.889], n_{pairs} = 10



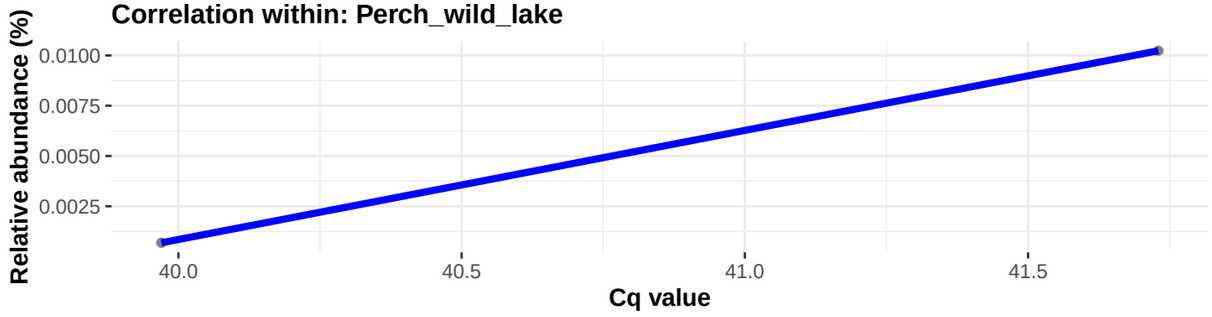
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

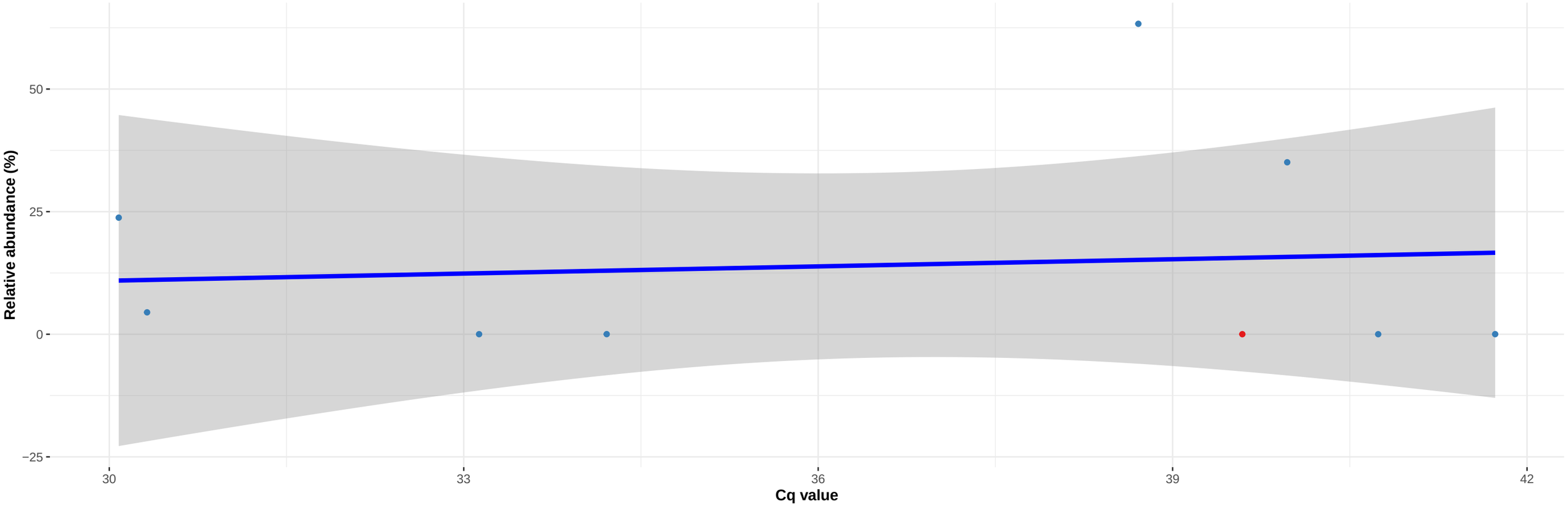


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: 750438ef469a6a58cdf16b89f540188b

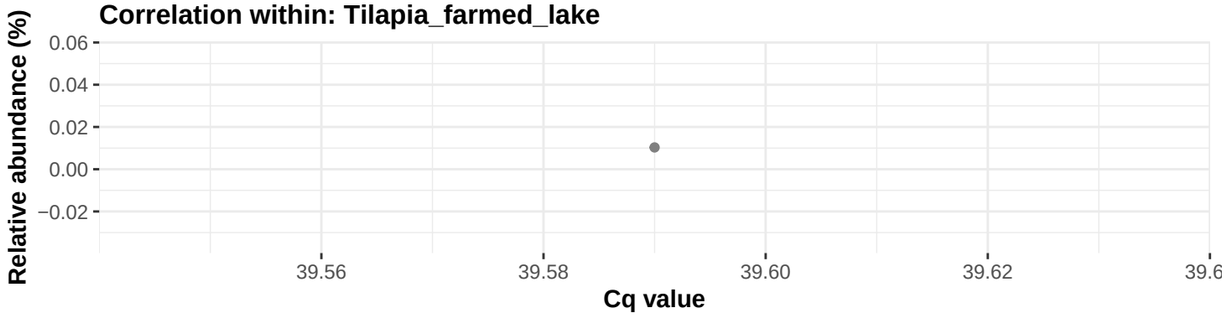
Correlation with all samples

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

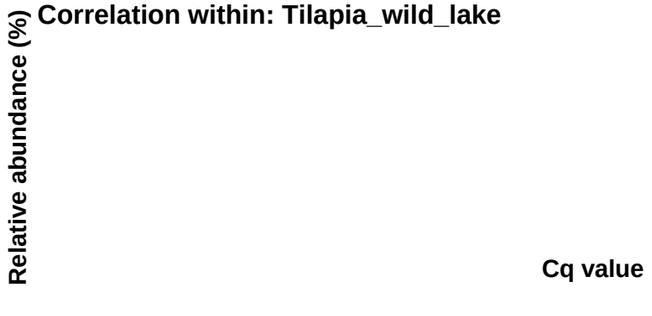


Sample_type ● Tilapia_farmed_lake ● Perch_wild_lake

Correlation within: Tilapia_farmed_lake

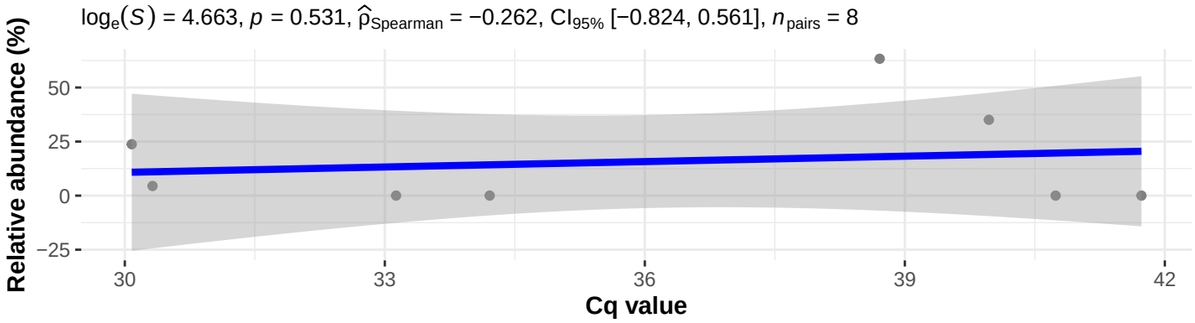


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

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

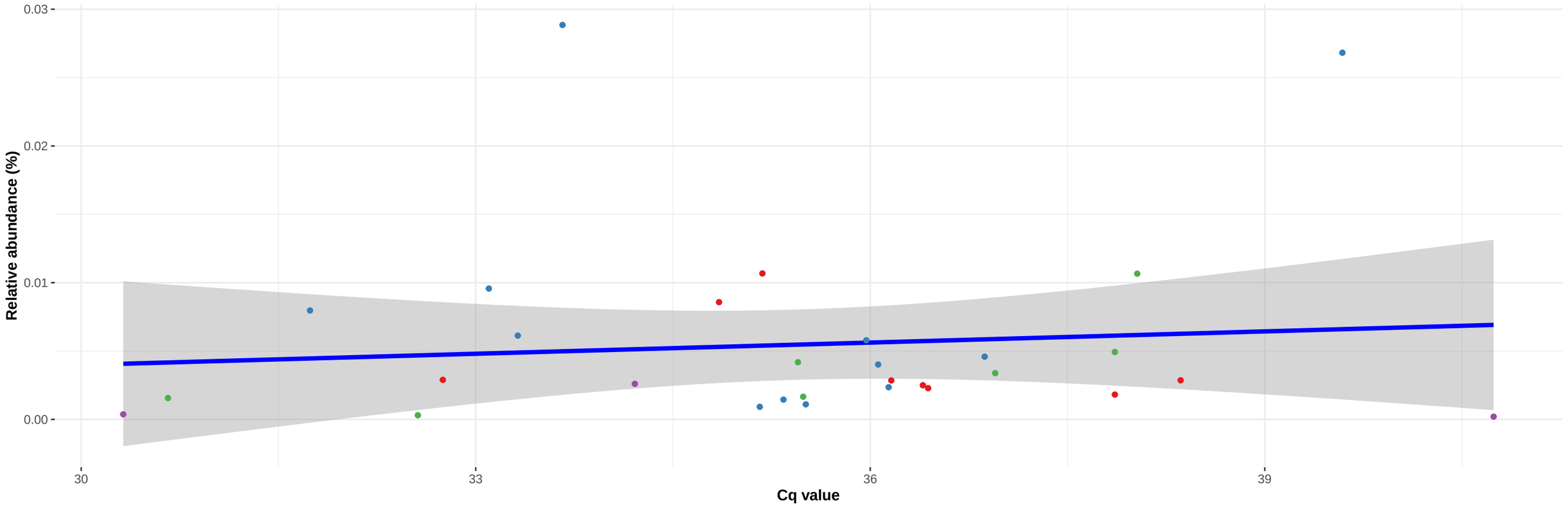


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

featureID: 5a90e7ffe242256a5c625bd072bb3337

Correlation with all samples

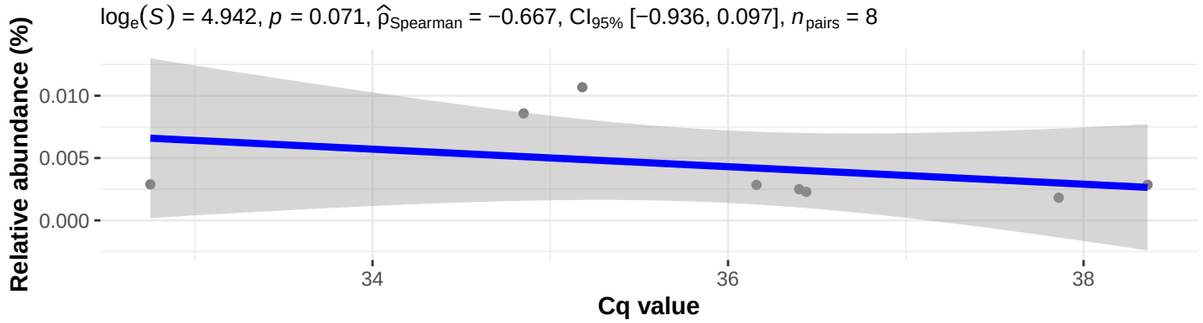
$\log_e(S)$ = 8.351, p = 0.762, $\hat{\rho}_{Spearman}$ = 0.058, $CI_{95\%}$ [−0.319, 0.419], n_{pairs} = 30



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

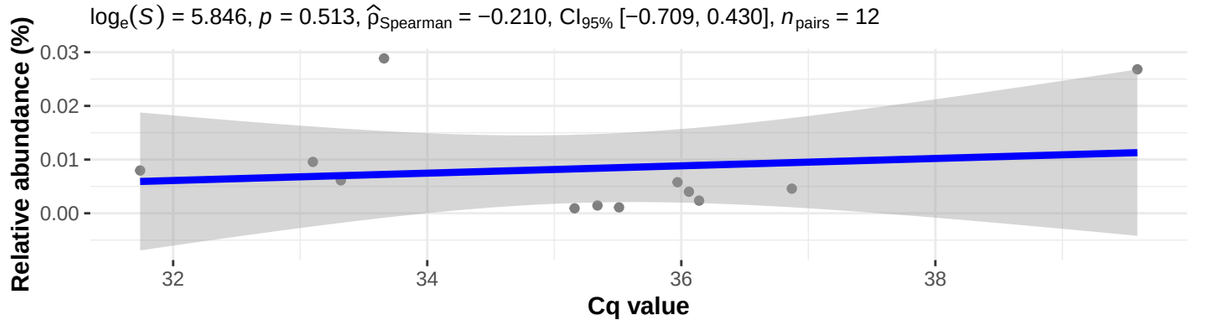
Correlation within: Tilapia_farmed_pond

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



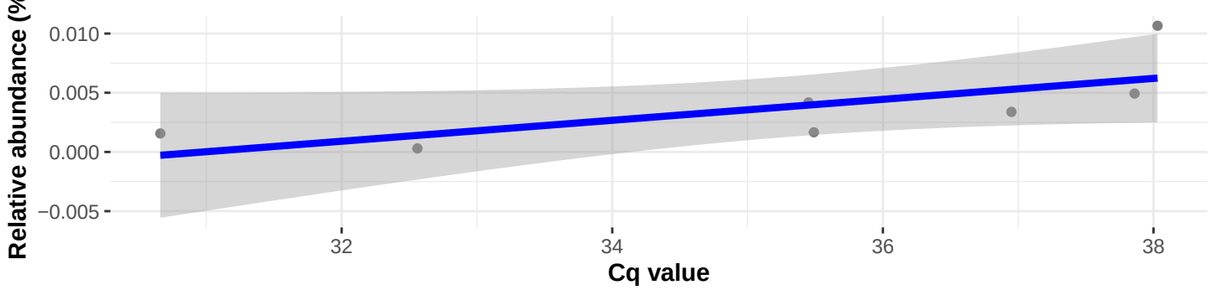
Correlation within: Tilapia_farmed_lake

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

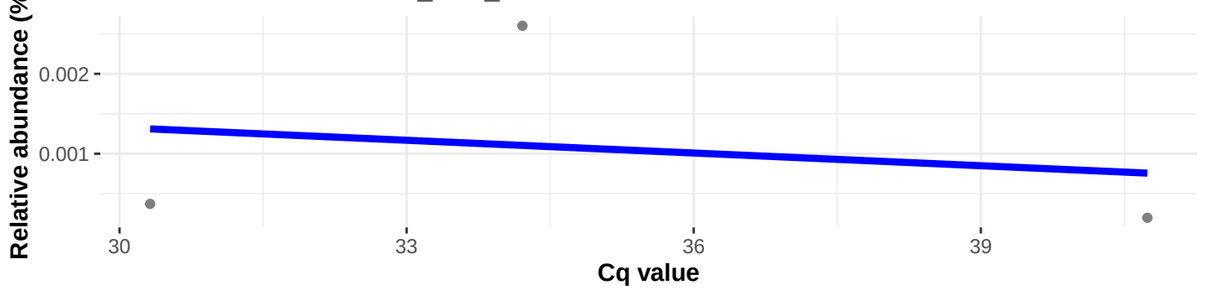


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

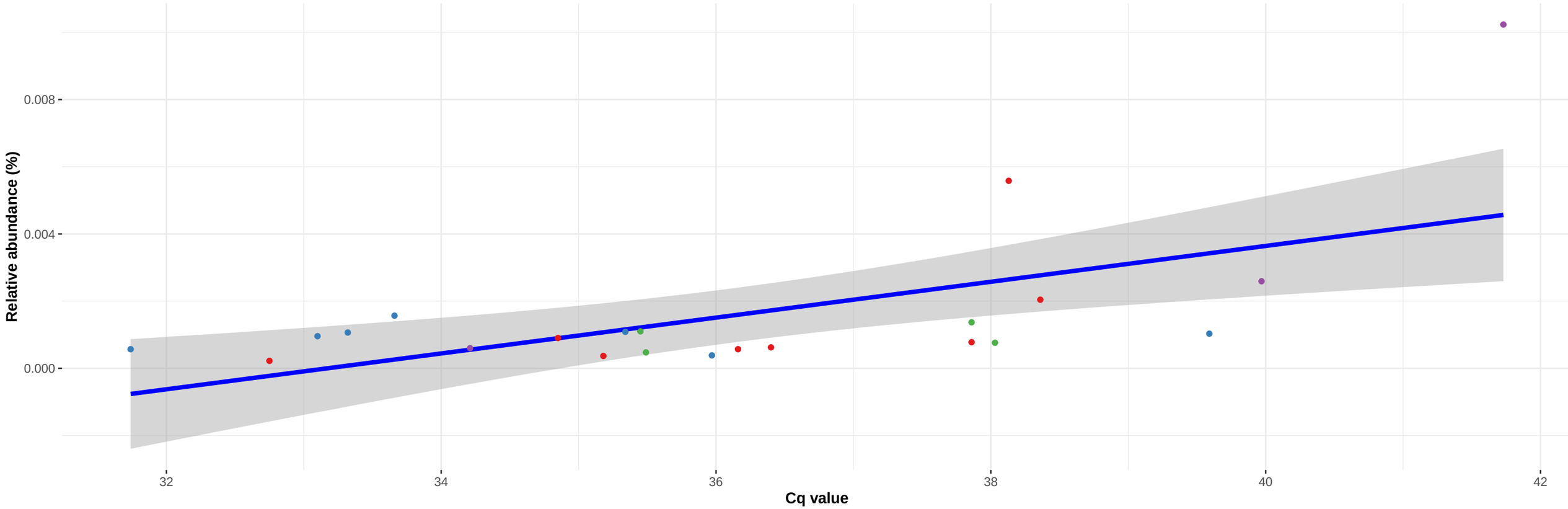


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; NA; NA

featureID: 8f2bbe692f7aca0f2c3959c3cf312b1d

Correlation with all samples

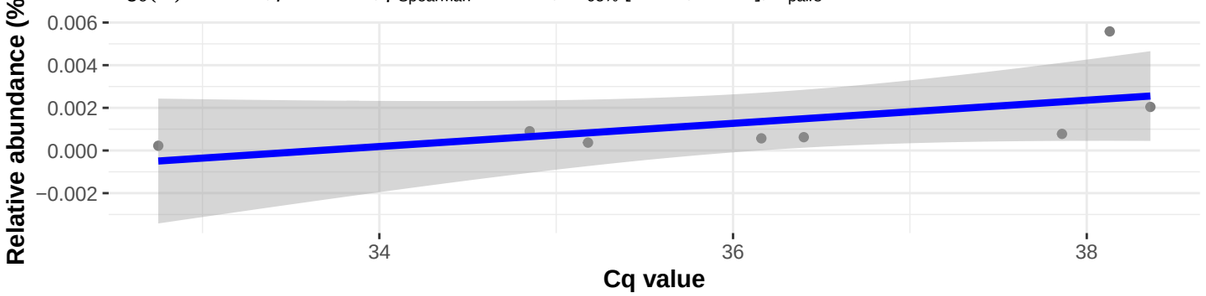
$\log_e(S)$ = 6.760, p = 0.015, $\hat{\rho}_{Spearman}$ = 0.513, $CI_{95\%}$ [0.103, 0.774], n_{pairs} = 22



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

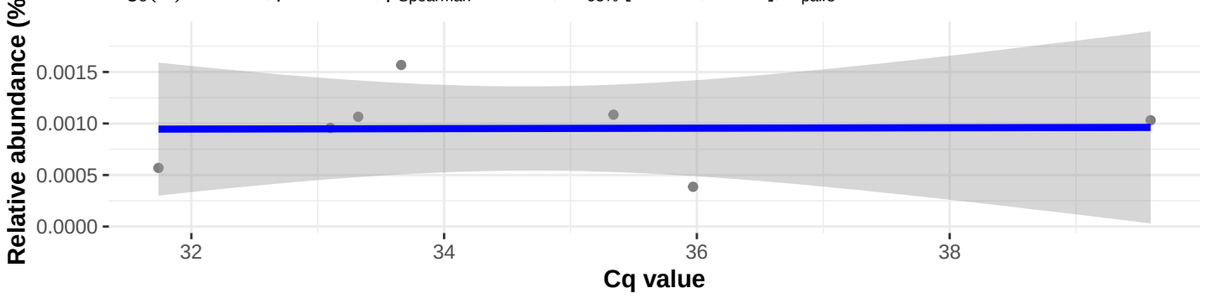
Correlation within: Tilapia_farmed_pond

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

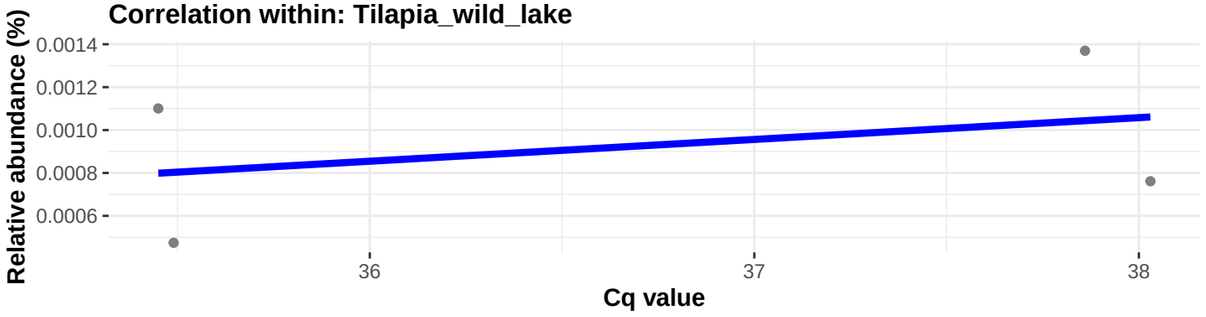


Correlation within: Tilapia_farmed_lake

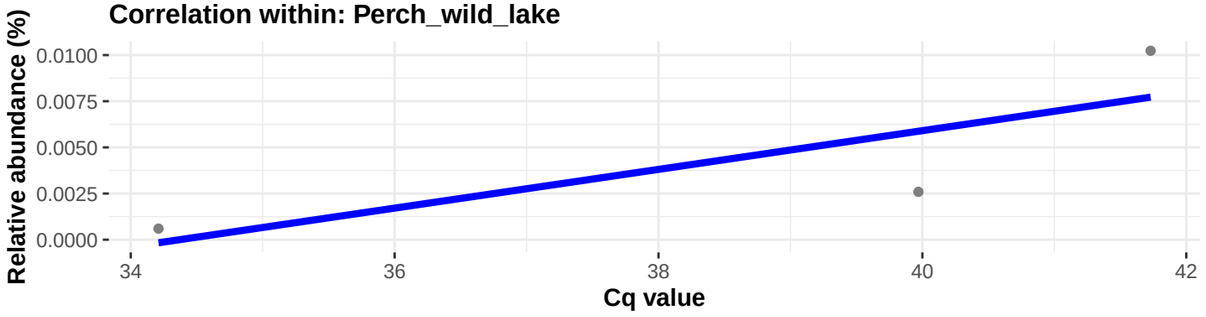
$\log_e(S)$ = 3.912, p = 0.819, $\hat{\rho}_{Spearman}$ = 0.107, $CI_{95\%}$ [−0.717, 0.806], n_{pairs} = 7



Correlation within: Tilapia_wild_lake

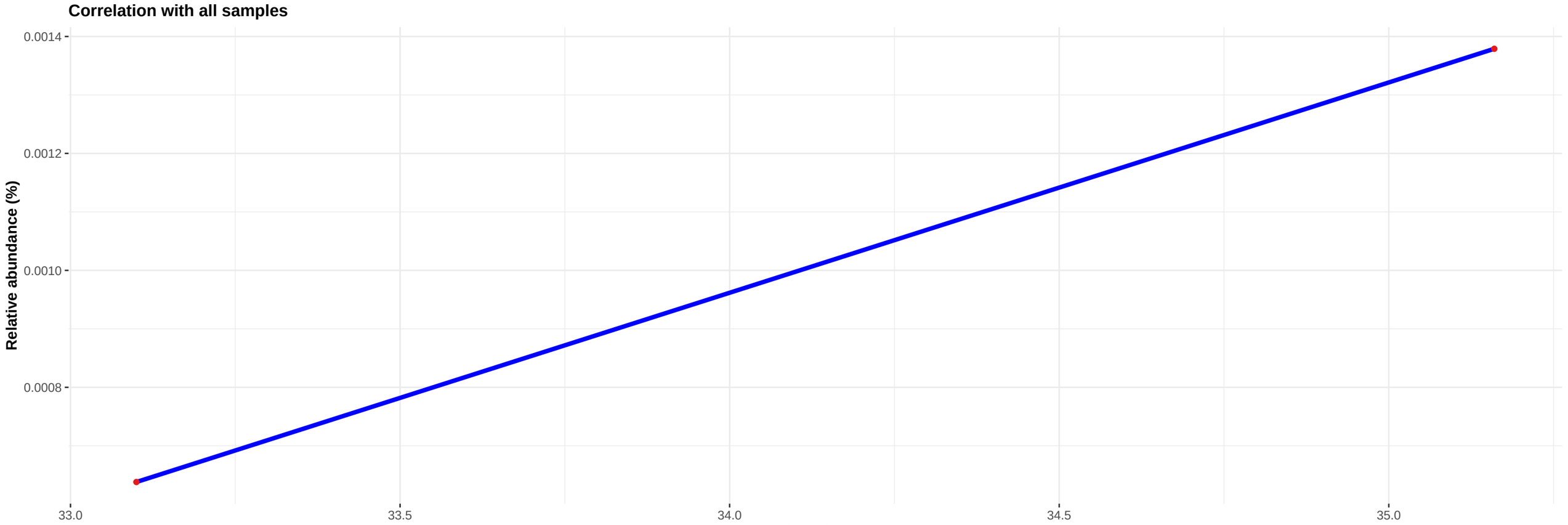


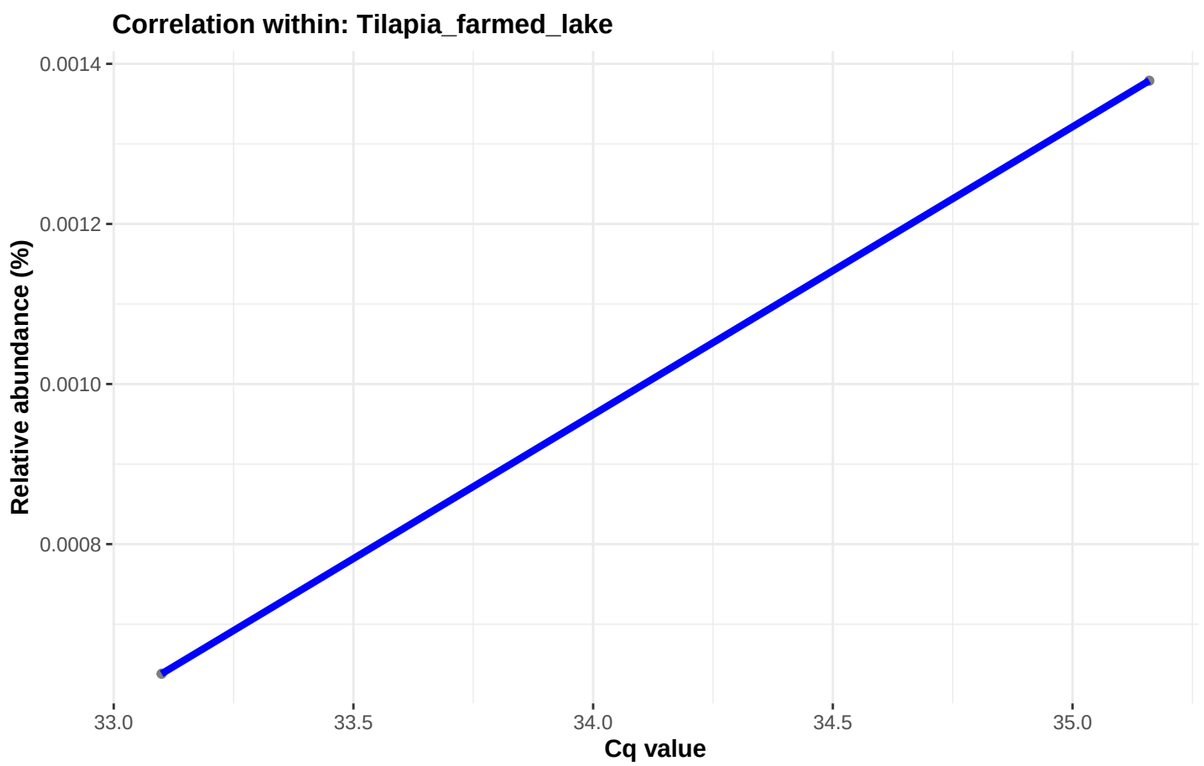
Correlation within: Perch_wild_lake



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Nocardiaceae; g__Rhodococcus; NA

featureID: 4a7f867d55034fd3b2b4b28e0b1dda36



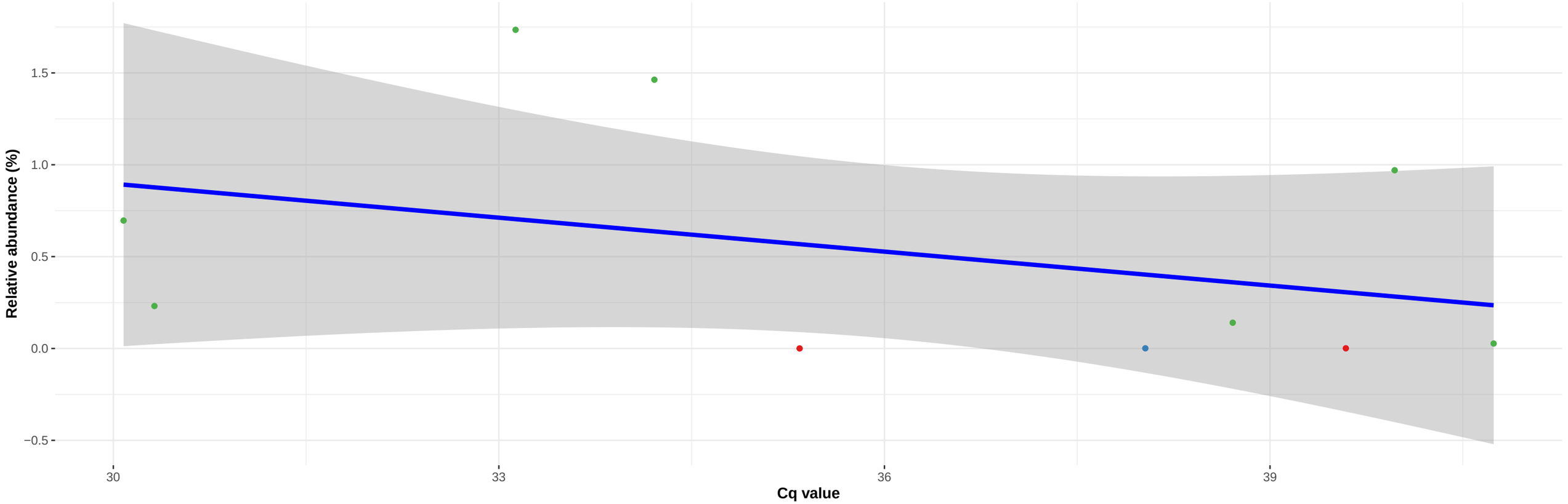


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 8f6ff8174262993339a29e403091e900

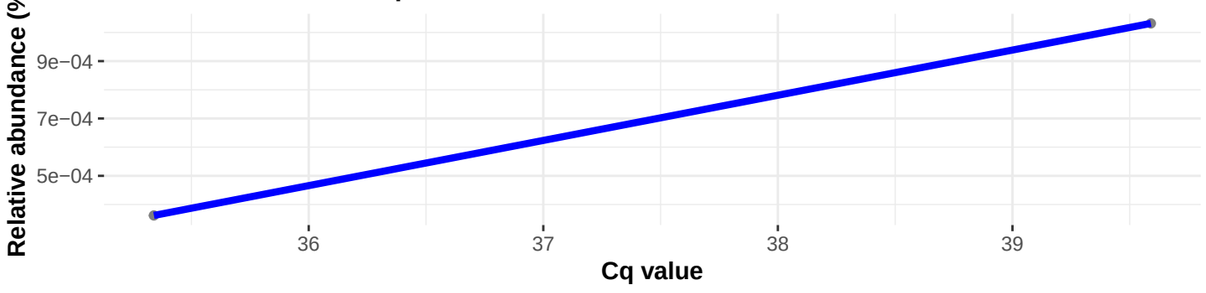
Correlation with all samples

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

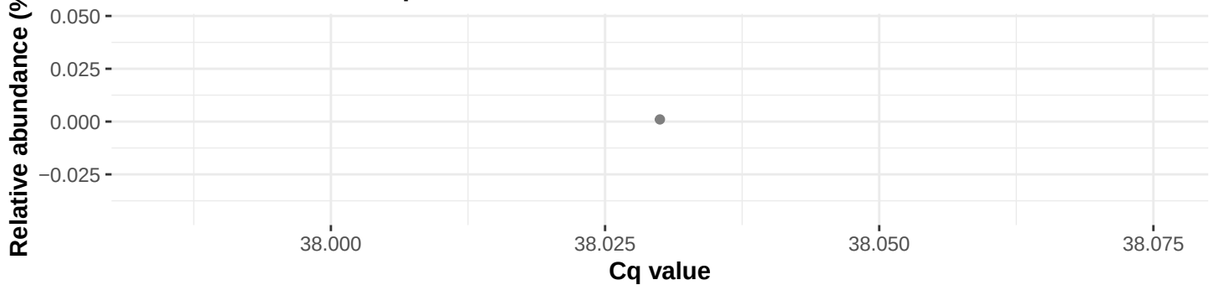


Sample_type Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_lake

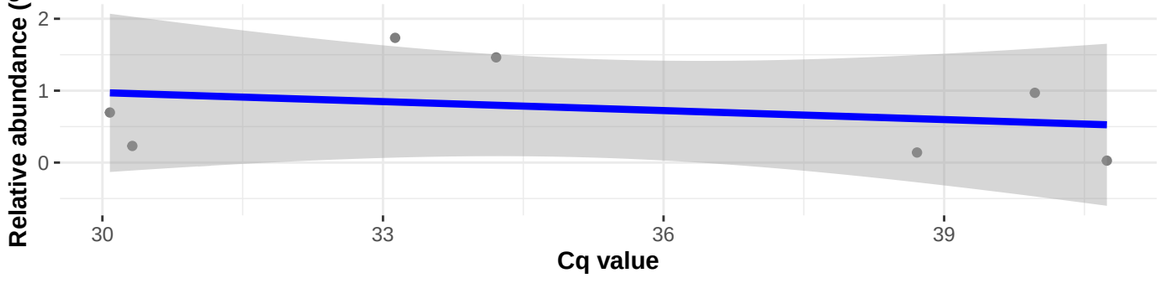


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

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

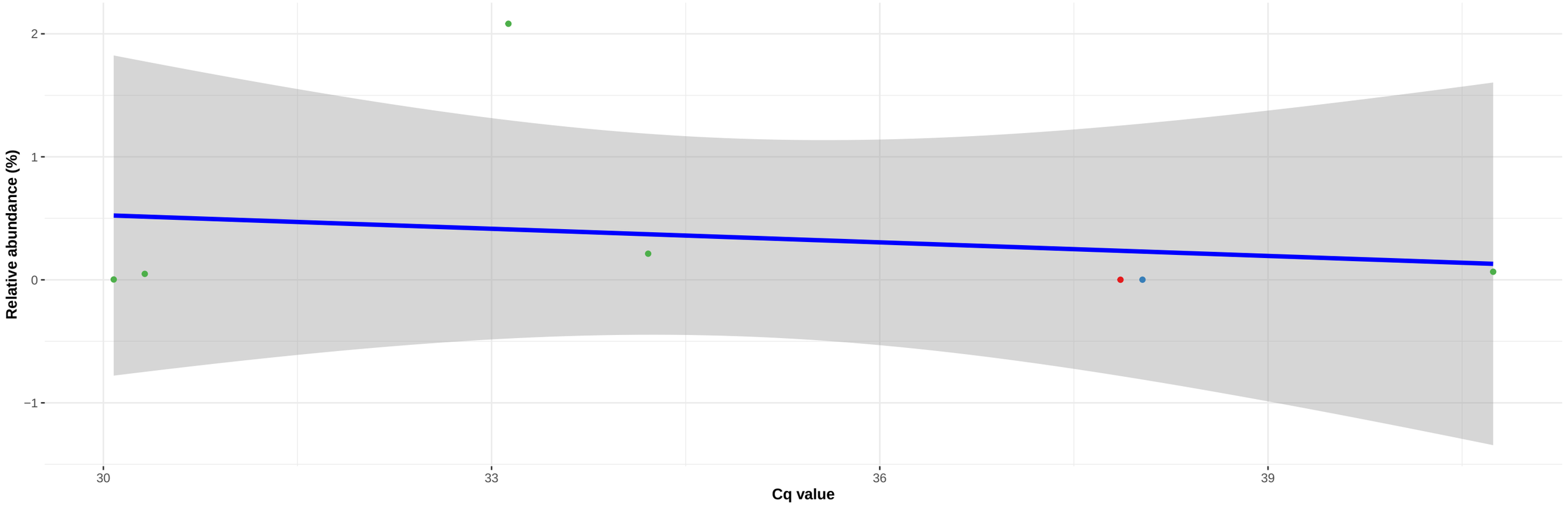


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 444cb870909dcd447934e3eb70c73738

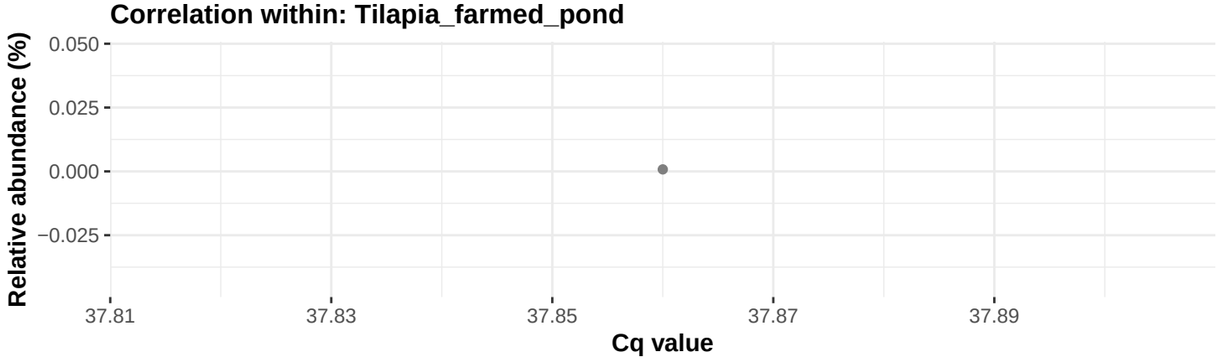
Correlation with all samples

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

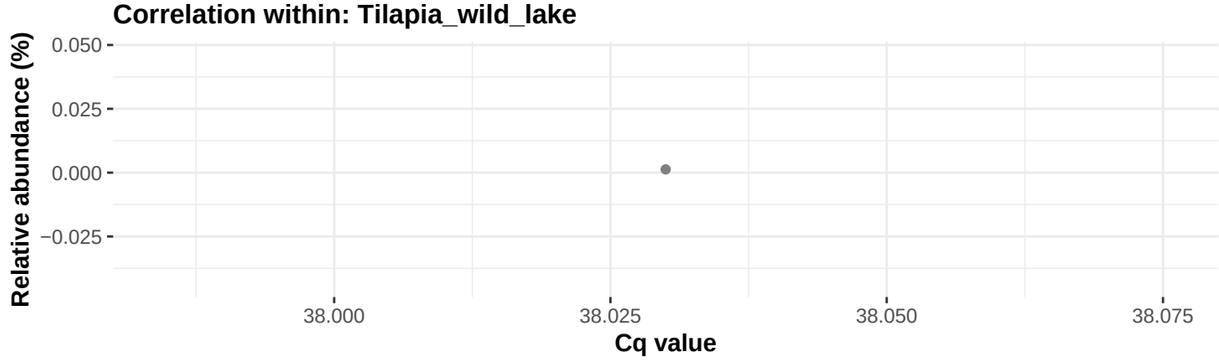


Sample_type Tilapia_farmed_pond Tilapia_wild_lake Perch_wild_lake

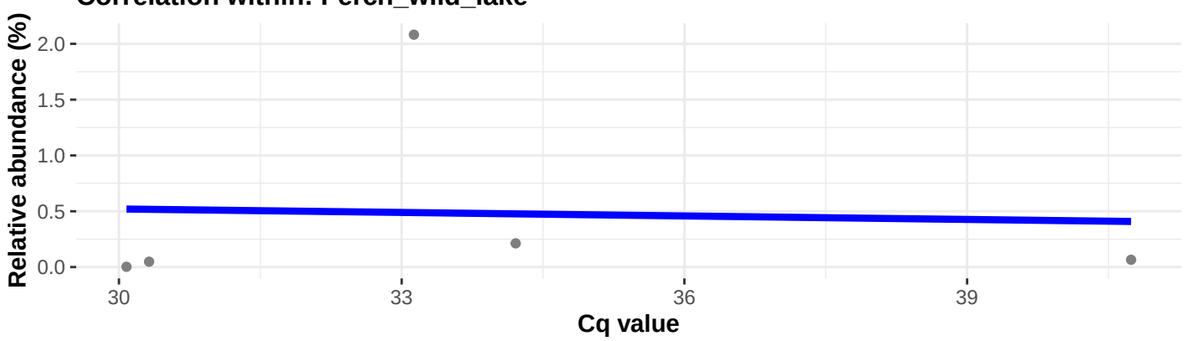
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

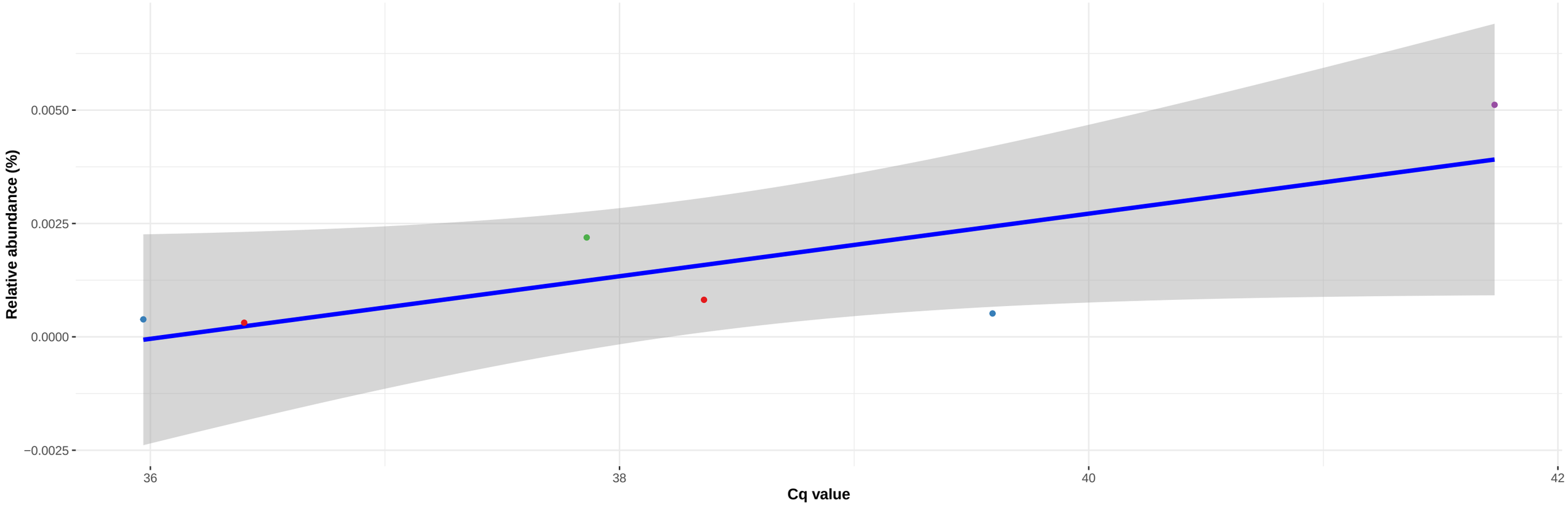


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Candidatus Aquiluna; NA

featureID: 10a4ba9050a60c9880edf695bd202b6e

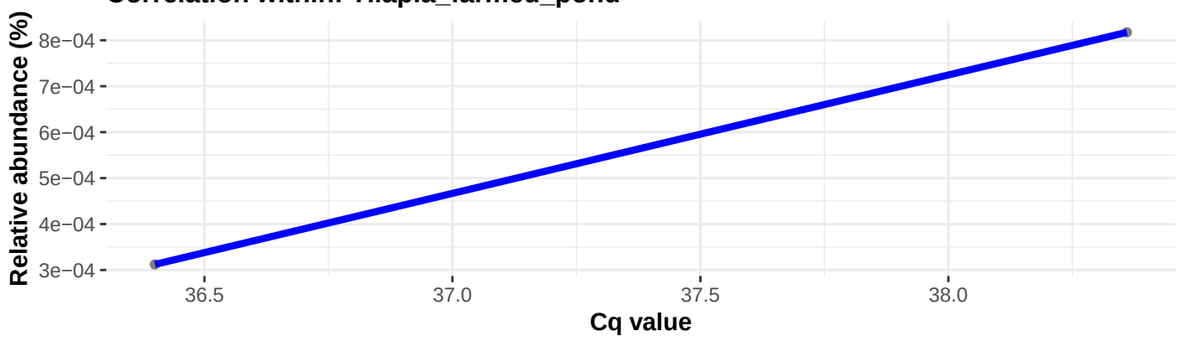
Correlation with all samples

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

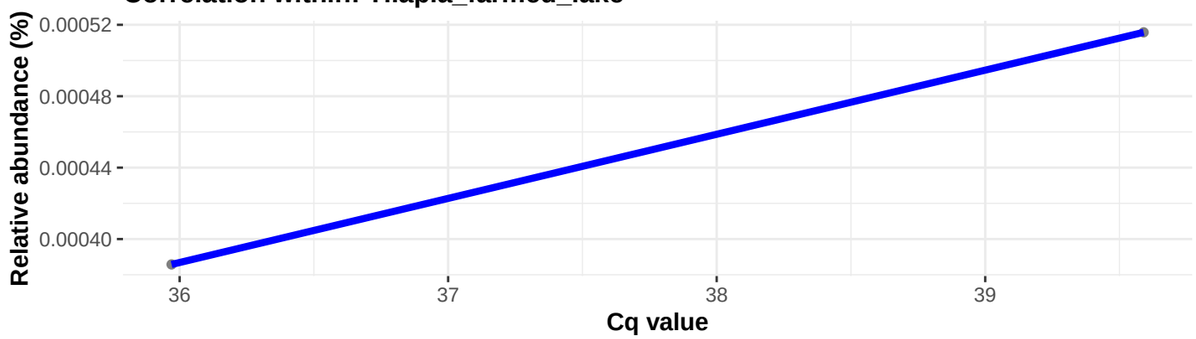


Sample_type ● Tilapia_farmed_pond ● Tilapia_farmed_lake ● Tilapia_wild_lake ● Perch_wild_lake

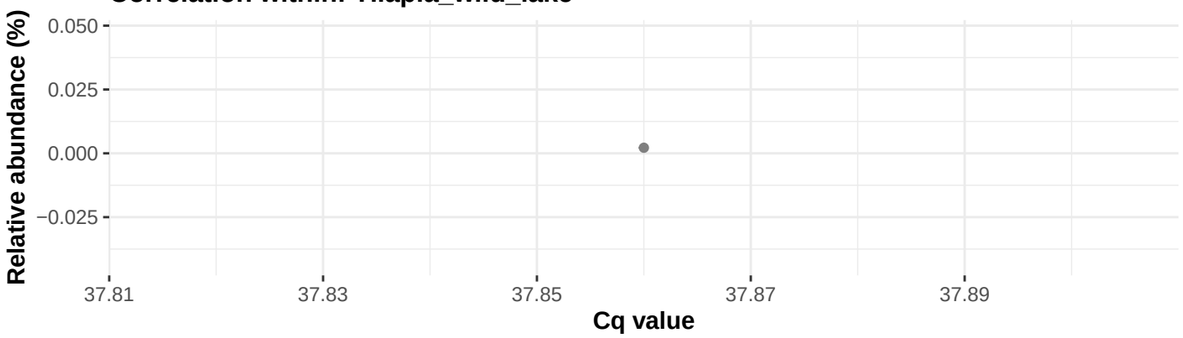
Correlation within: Tilapia_farmed_pond



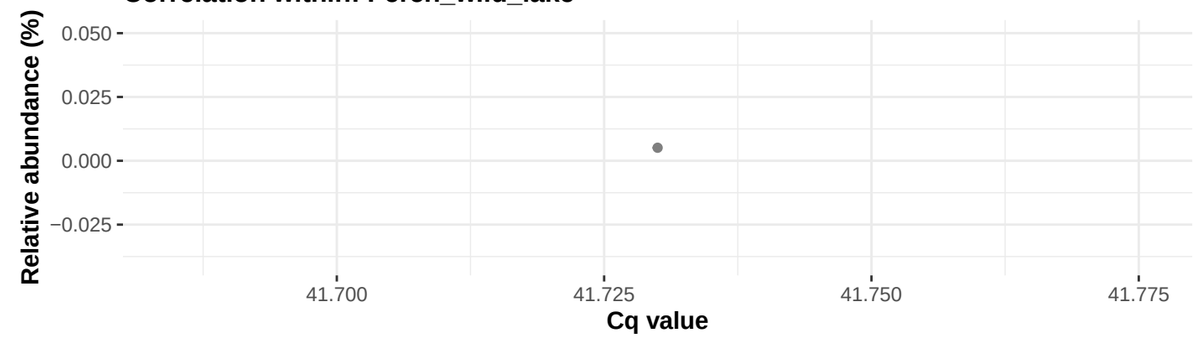
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

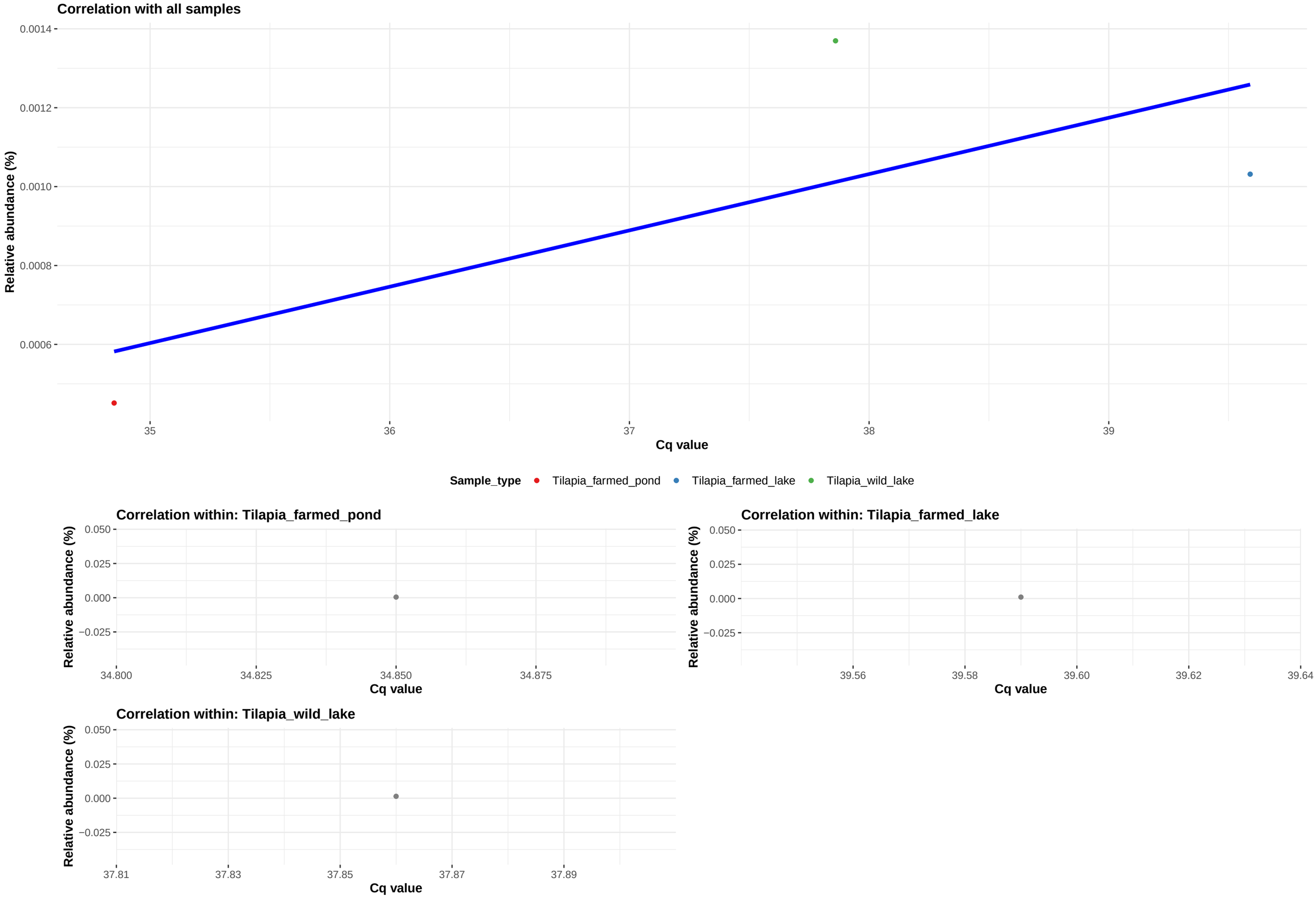


Correlation within: Perch_wild_lake



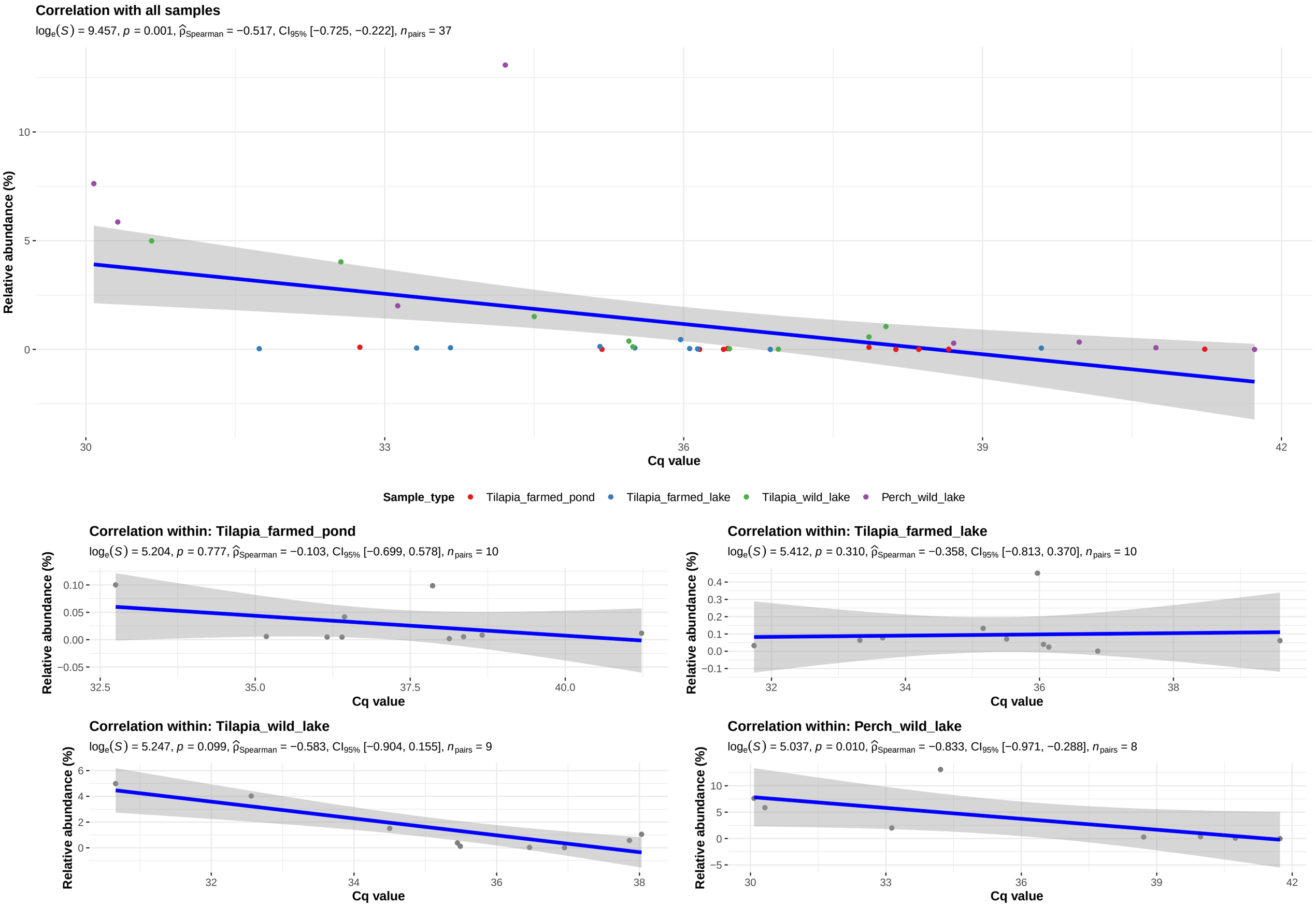
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Kocuria; s__Kocuria marina

featureID: 19c88c43cefc0efae399898111815666



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

featureID: 7438db900c870a0d550a34920b927788

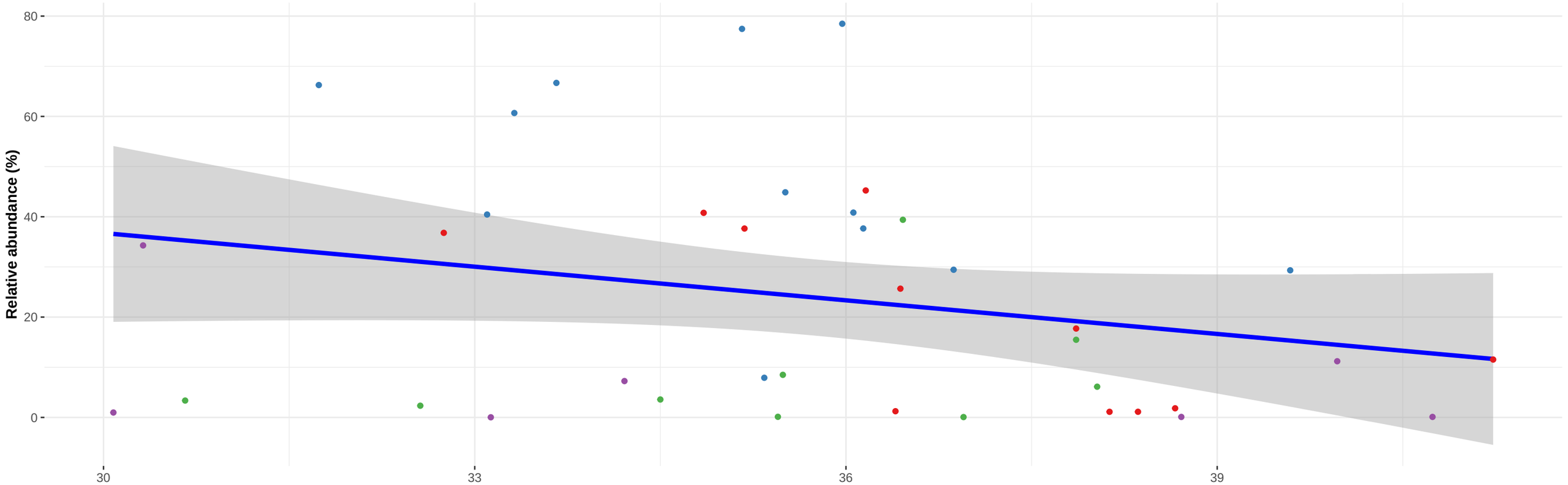


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 03f0f9af305de66090e757aaa19b09fd

Correlation with all samples

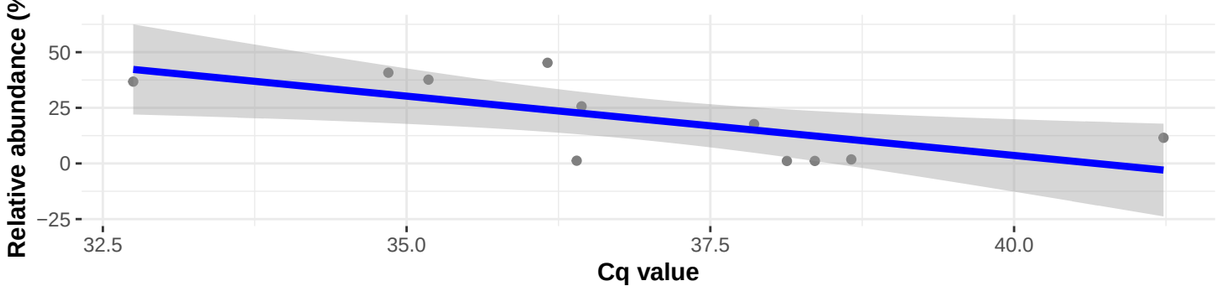
$\log_e(S)$ = 9.428, p = 0.112, $\hat{\rho}_{Spearman}$ = −0.259, $CI_{95\%}$ [−0.538, 0.072], n_{pairs} = 39



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

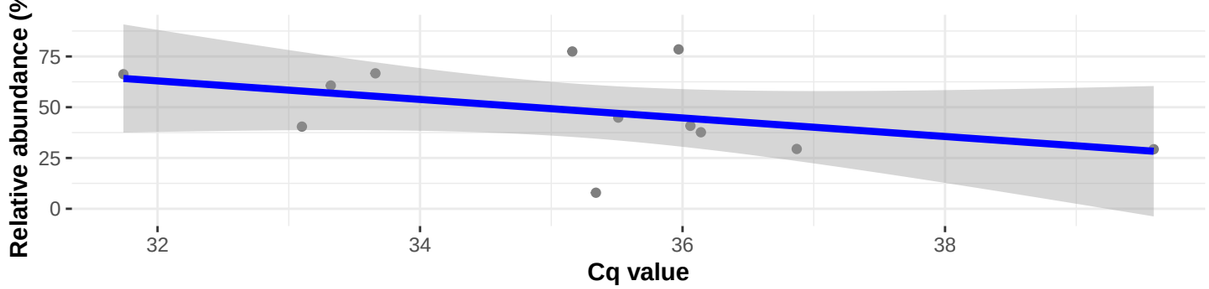
Correlation within: Tilapia_farmed_pond

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



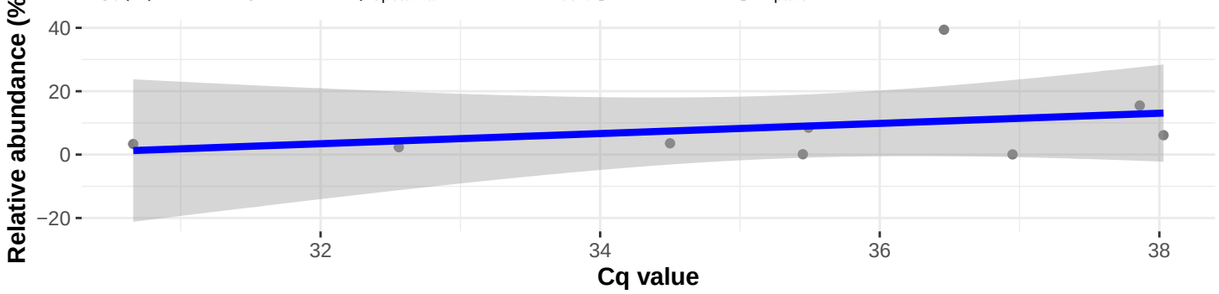
Correlation within: Tilapia_farmed_lake

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



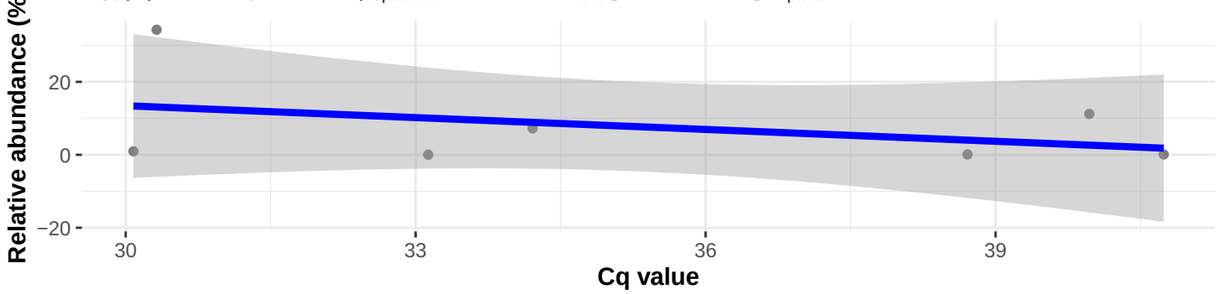
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

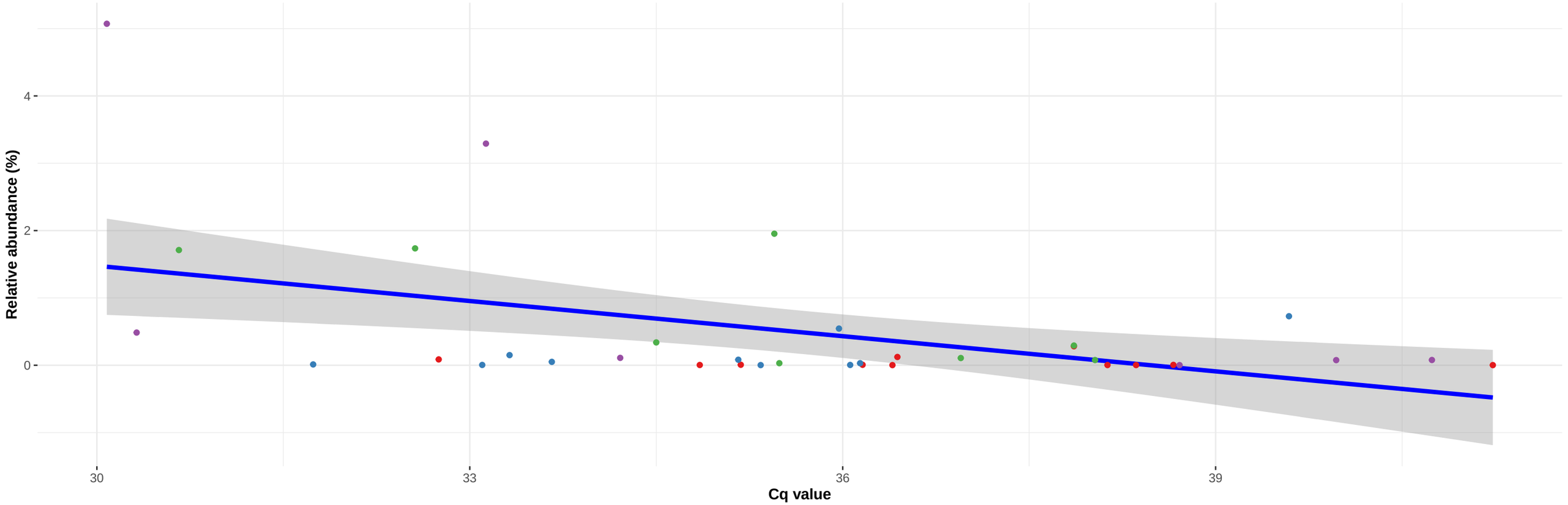


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paraclostridium; NA

featureID: f4b4dbd070c3296a6040e51b1e2aacfa

Correlation with all samples

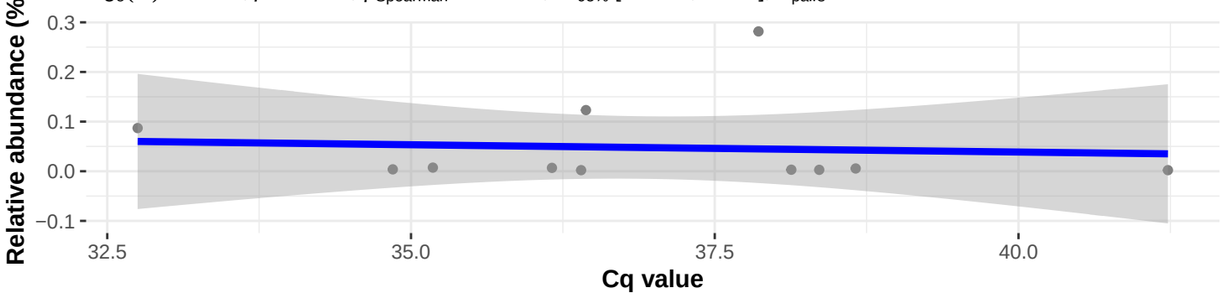
$\log_e(S)$ = 9.307, p = 0.011, $\hat{\rho}_{Spearman}$ = −0.417, $CI_{95\%}$ [−0.662, −0.093], n_{pairs} = 36



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

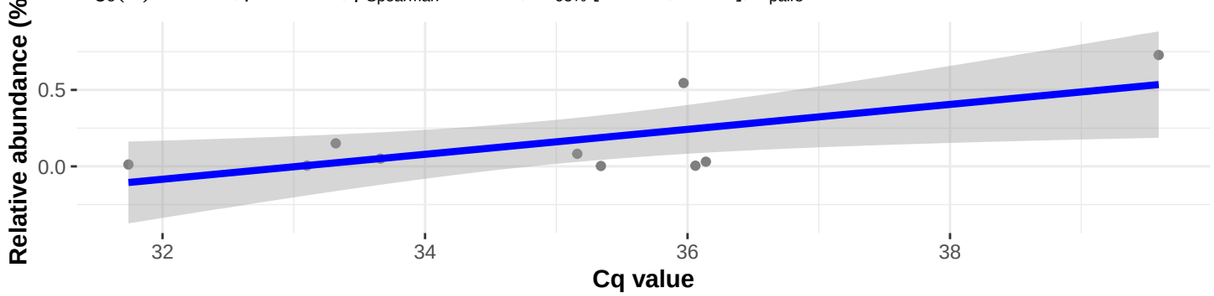
Correlation within: Tilapia_farmed_pond

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



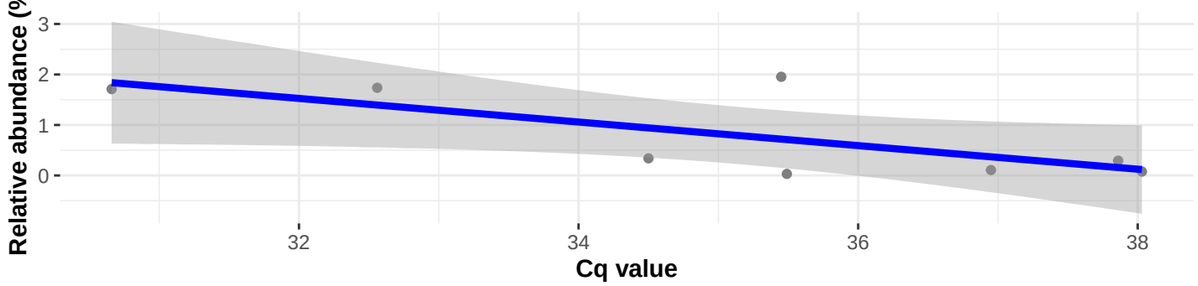
Correlation within: Tilapia_farmed_lake

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



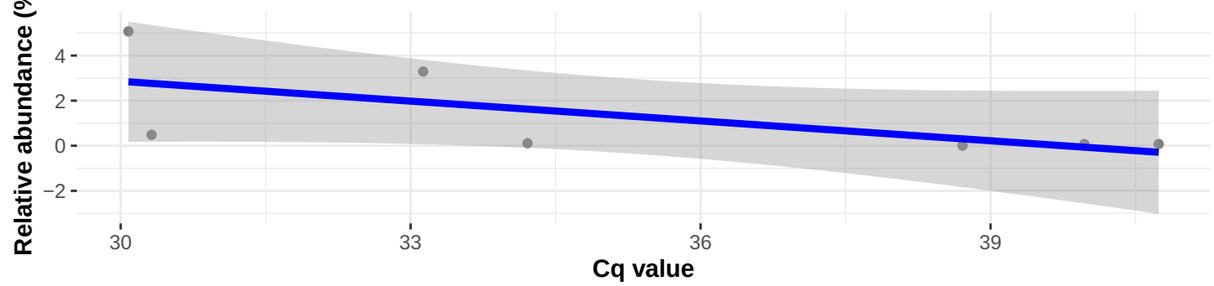
Correlation within: Tilapia_wild_lake

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



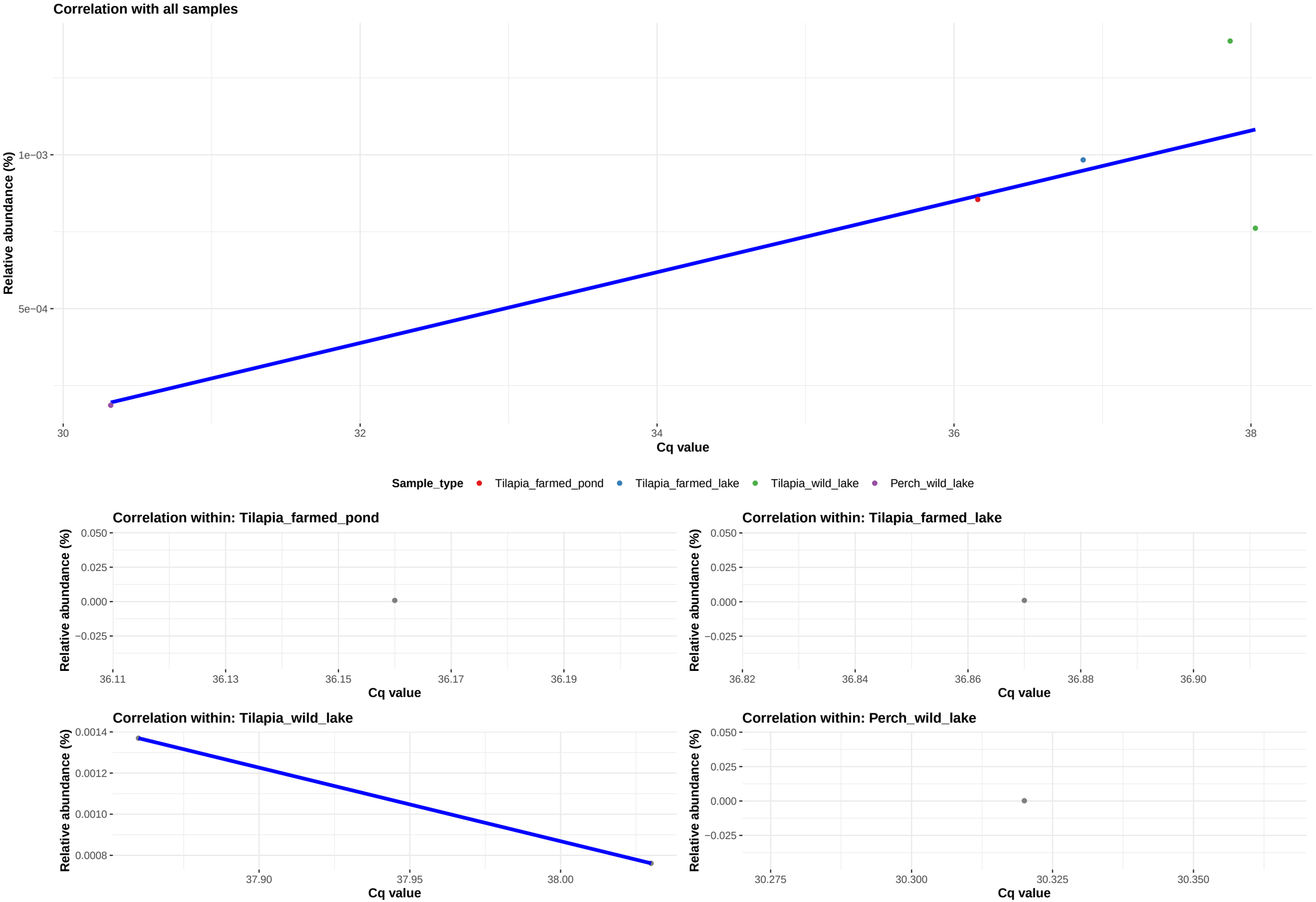
Correlation within: Perch_wild_lake

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



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

featureID: fadf78bc47e055f59328c8f565155ea5

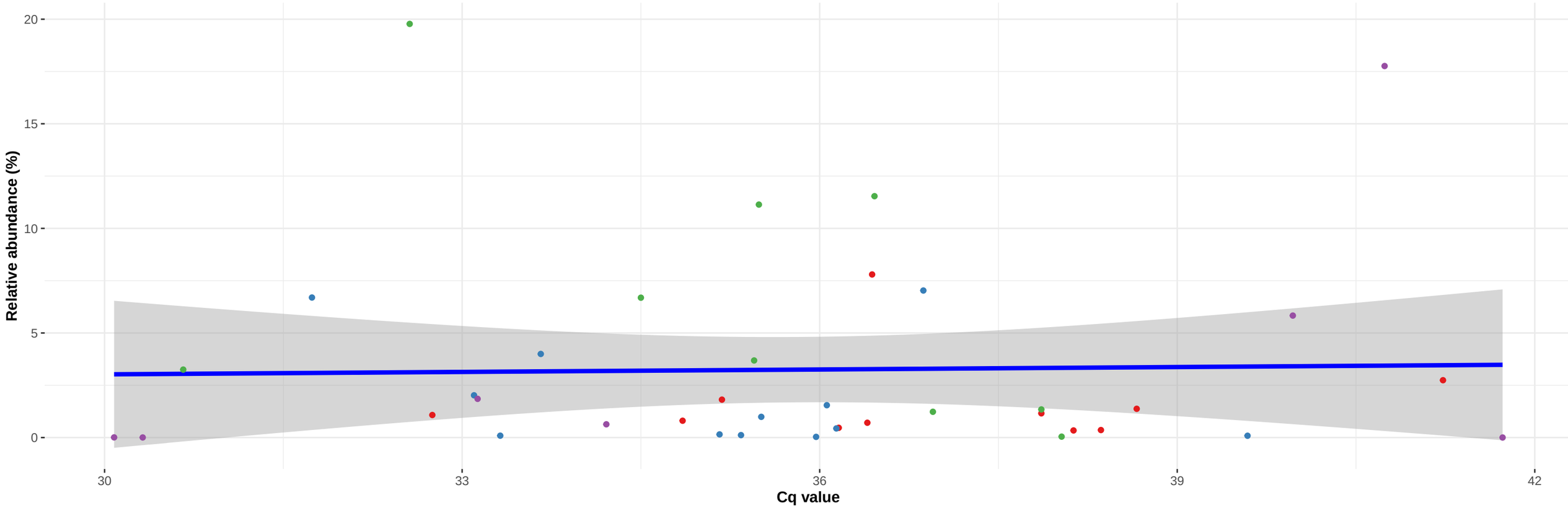


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Romboutsia; NA

featureID: efa98c673cef7e11e51b27d01167c2af

Correlation with all samples

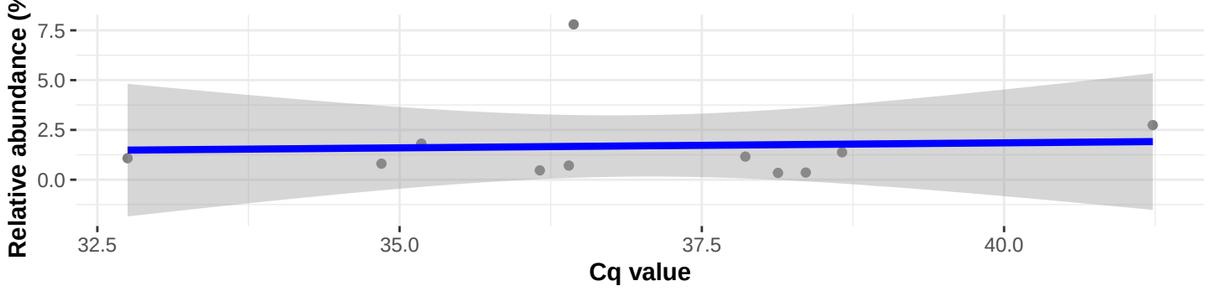
$\log_e(S) = 9.226$, $p = 0.863$, $\hat{\rho}_{Spearman} = -0.029$, $CI_{95\%}$ [−0.349, 0.298], $n_{pairs} = 39$



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

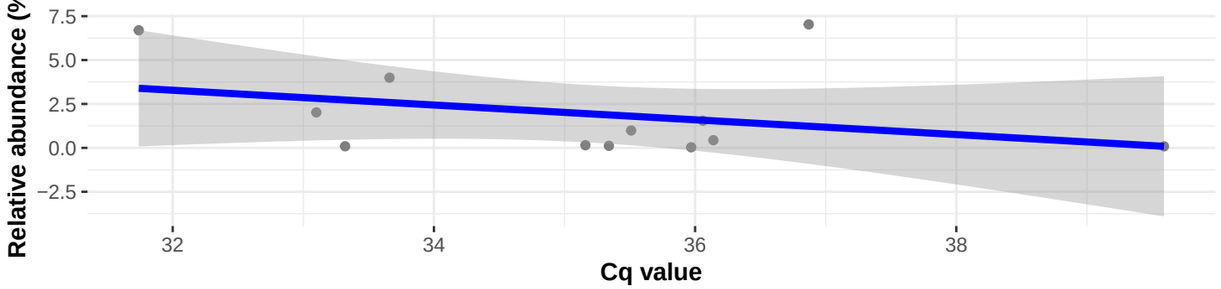
Correlation within: Tilapia_farmed_pond

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



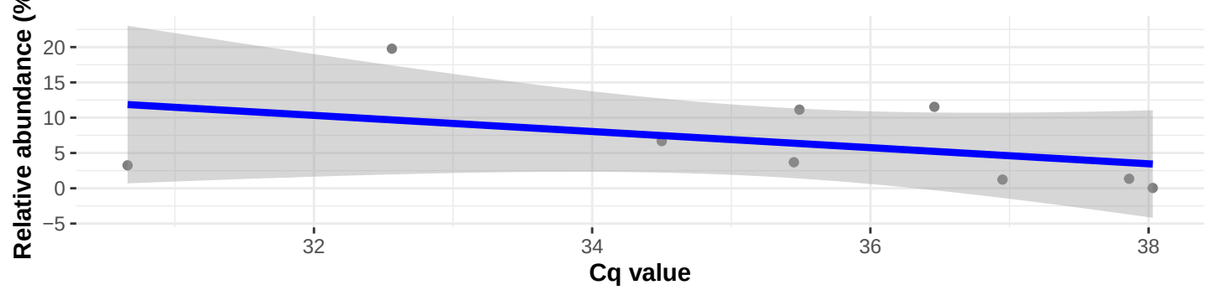
Correlation within: Tilapia_farmed_lake

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



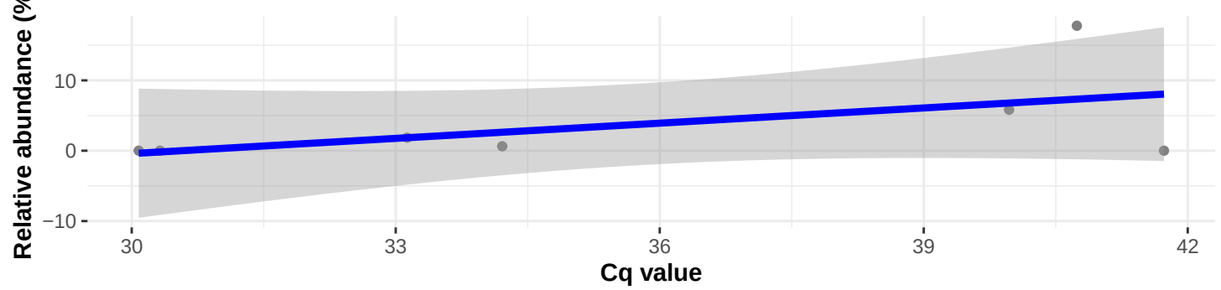
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

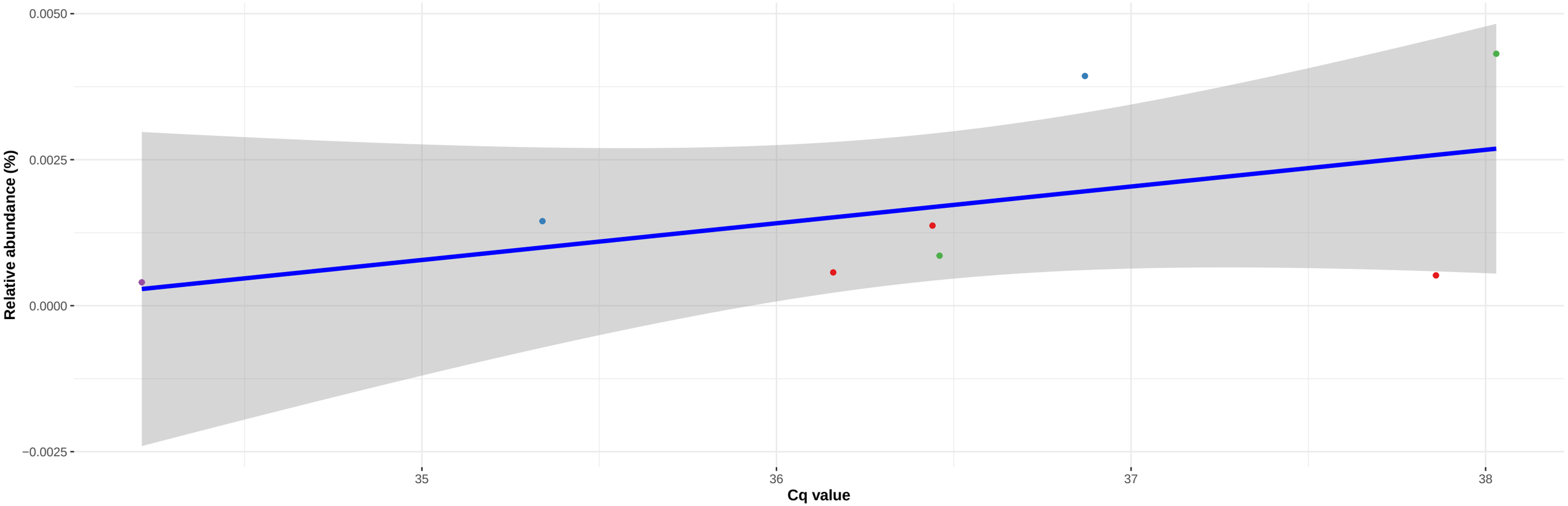


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; NA

featureID: 7f46b7ea18aa6ed4244429796401c660

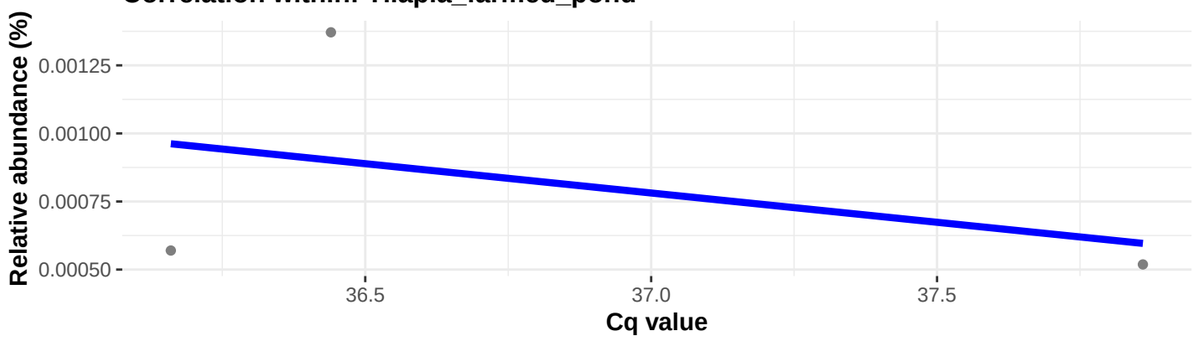
Correlation with all samples

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

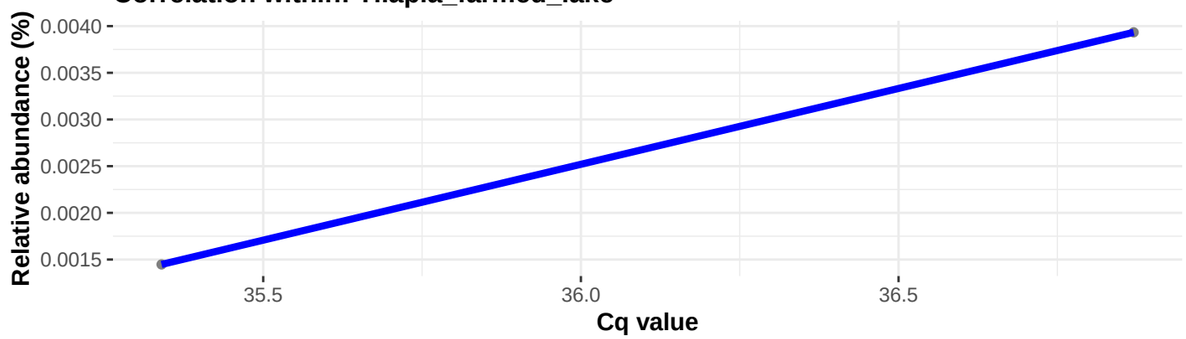


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

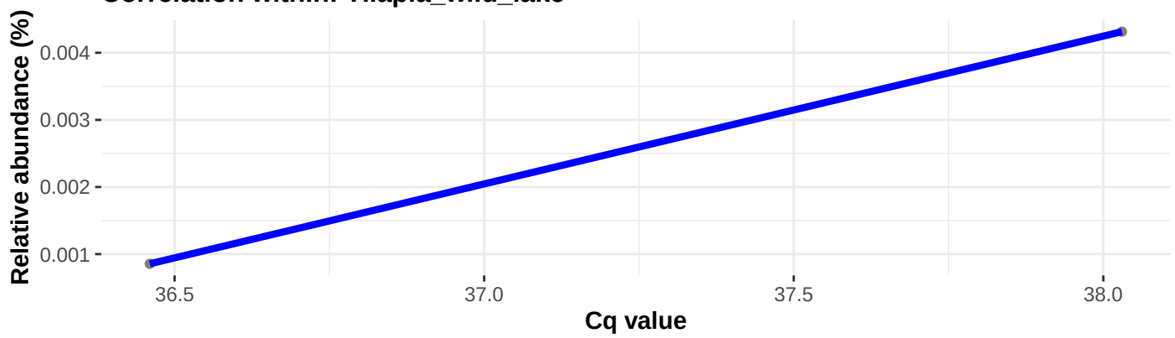
Correlation within: Tilapia_farmed_pond



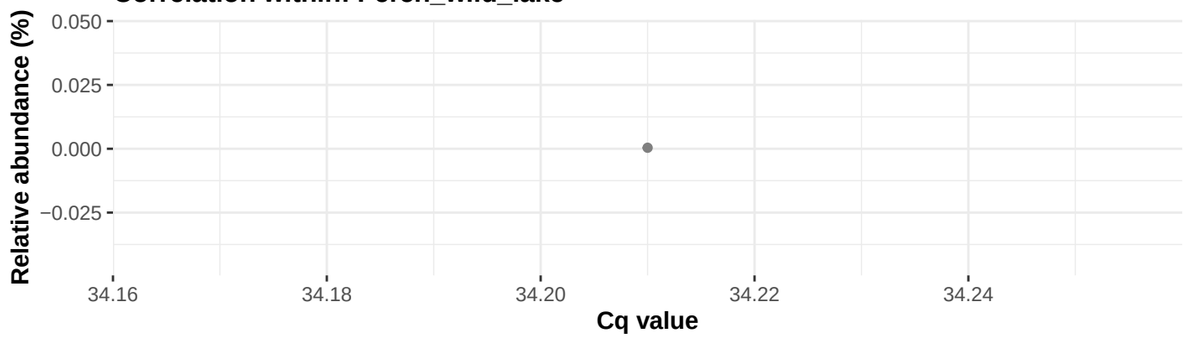
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

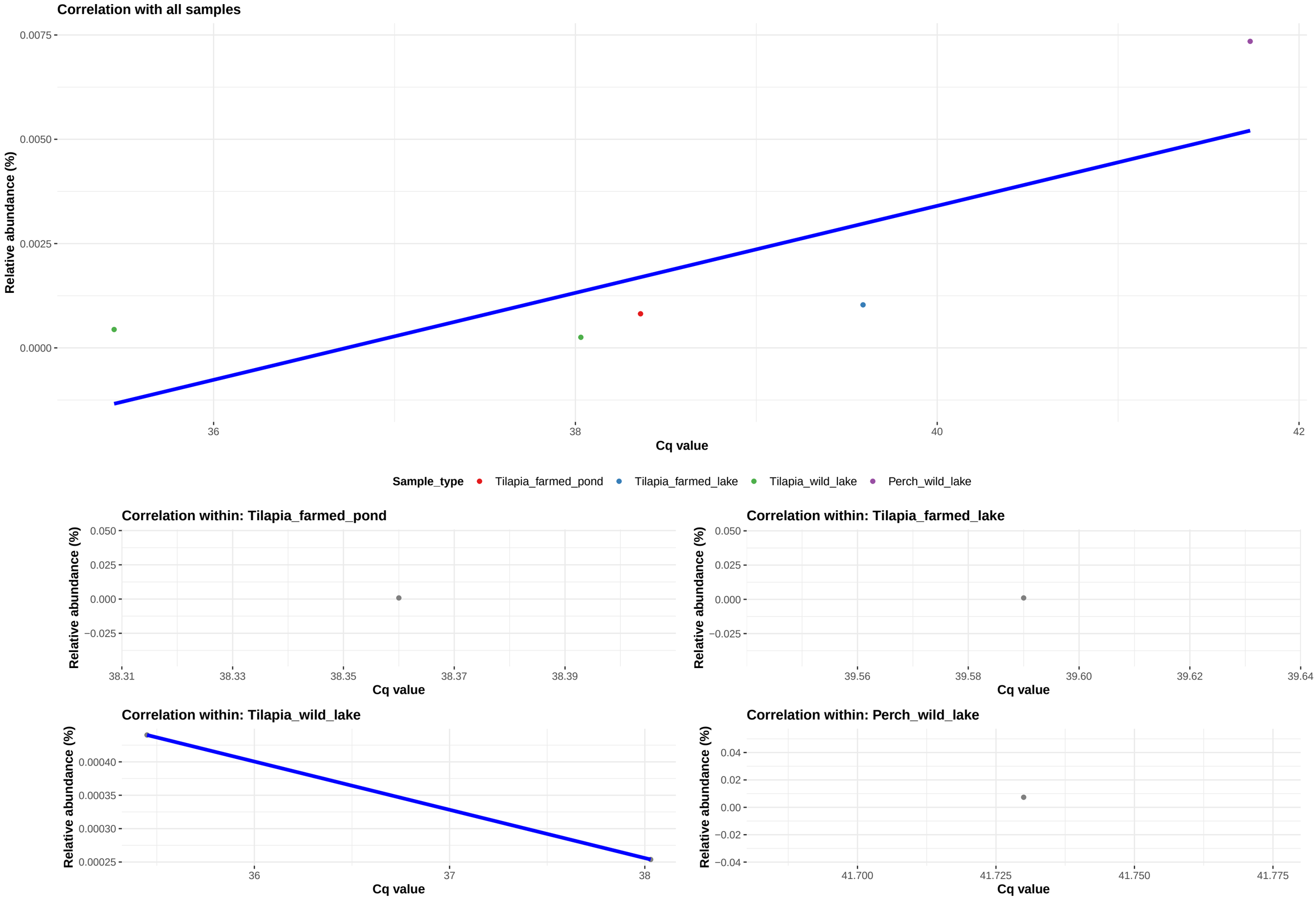


Correlation within: Perch_wild_lake



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

featureID: 6bd3f3df4073826645c0bfe560765004

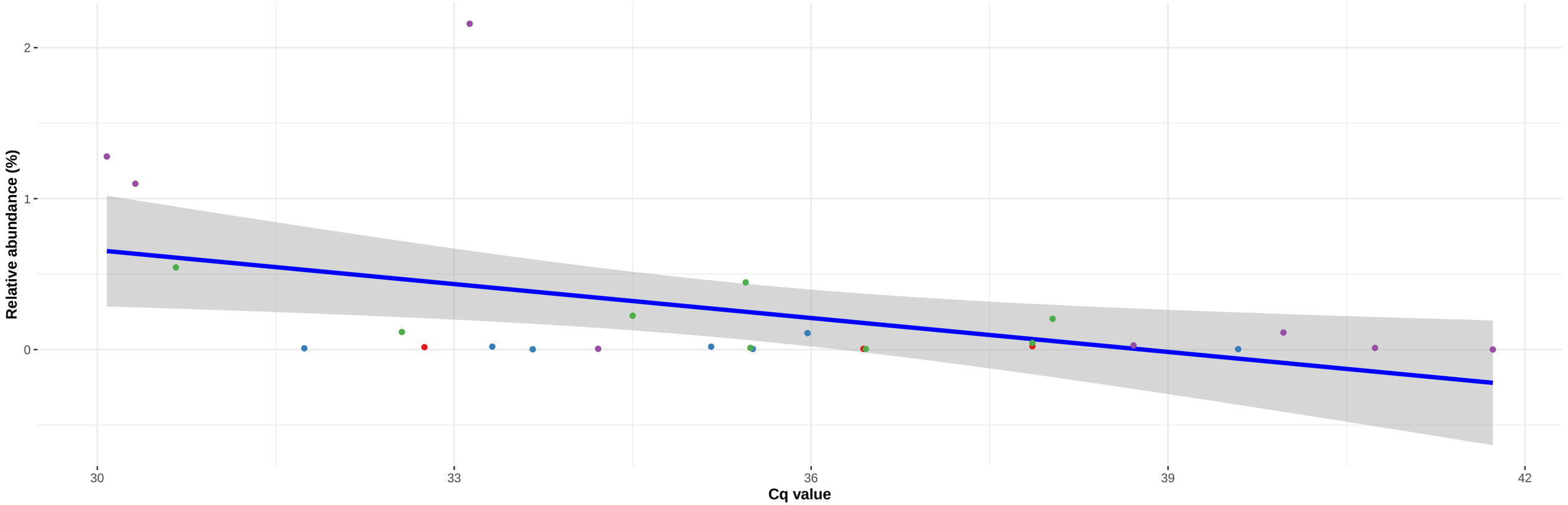


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

featureID: 4d951a112c225bc3bdfd2d0cfec2b2d3

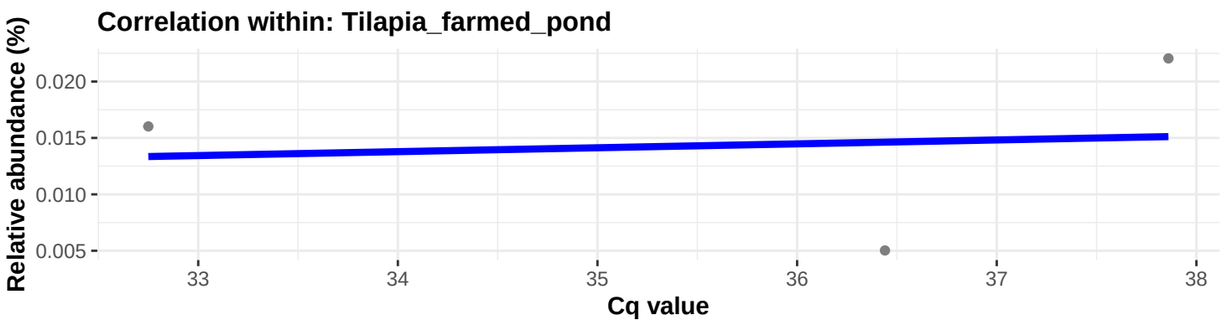
Correlation with all samples

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



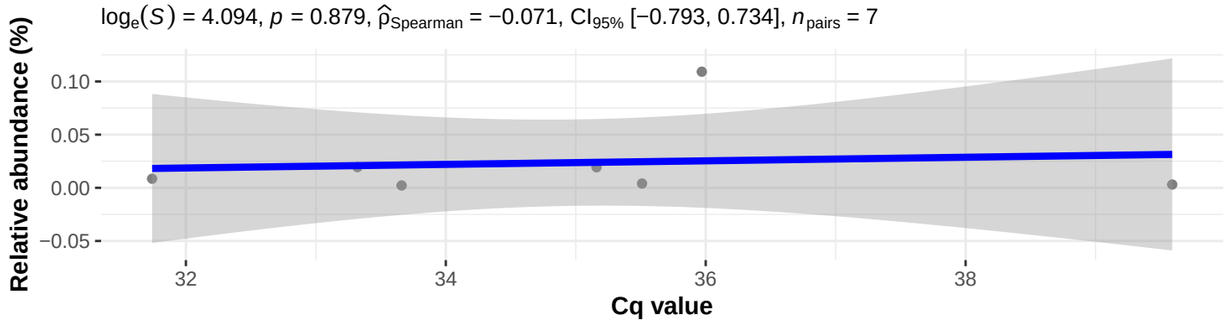
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond



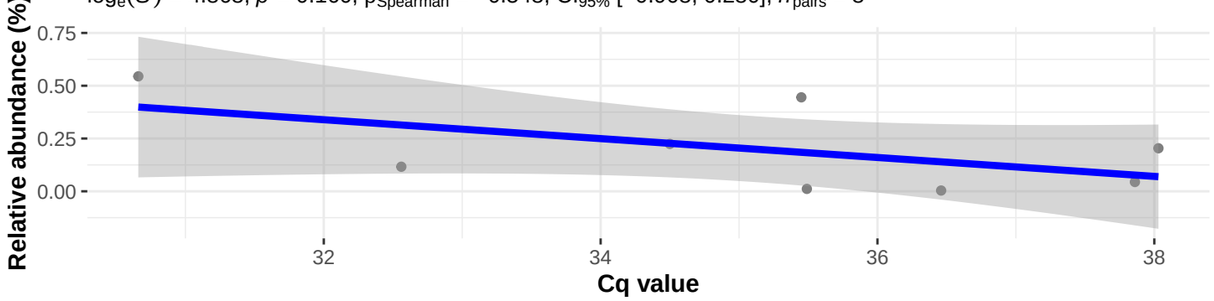
Correlation within: Tilapia_farmed_lake

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



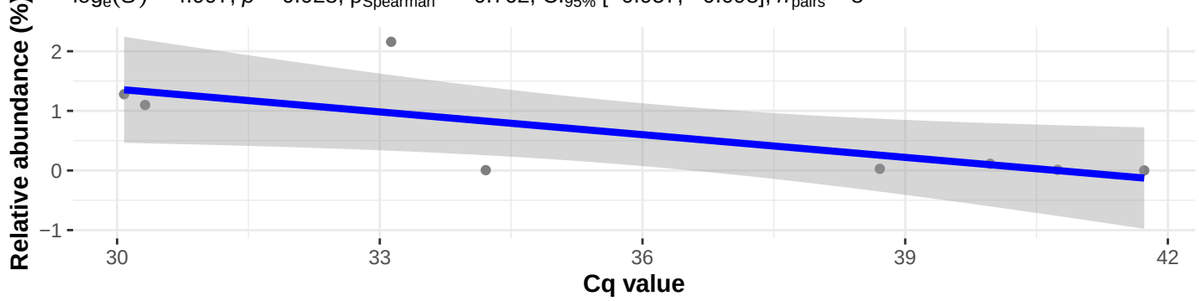
Correlation within: Tilapia_wild_lake

$\log_e(S)$ = 4.868, p = 0.160, $\hat{\rho}_{Spearman}$ = −0.548, $CI_{95\%}$ [−0.908, 0.280], n_{pairs} = 8



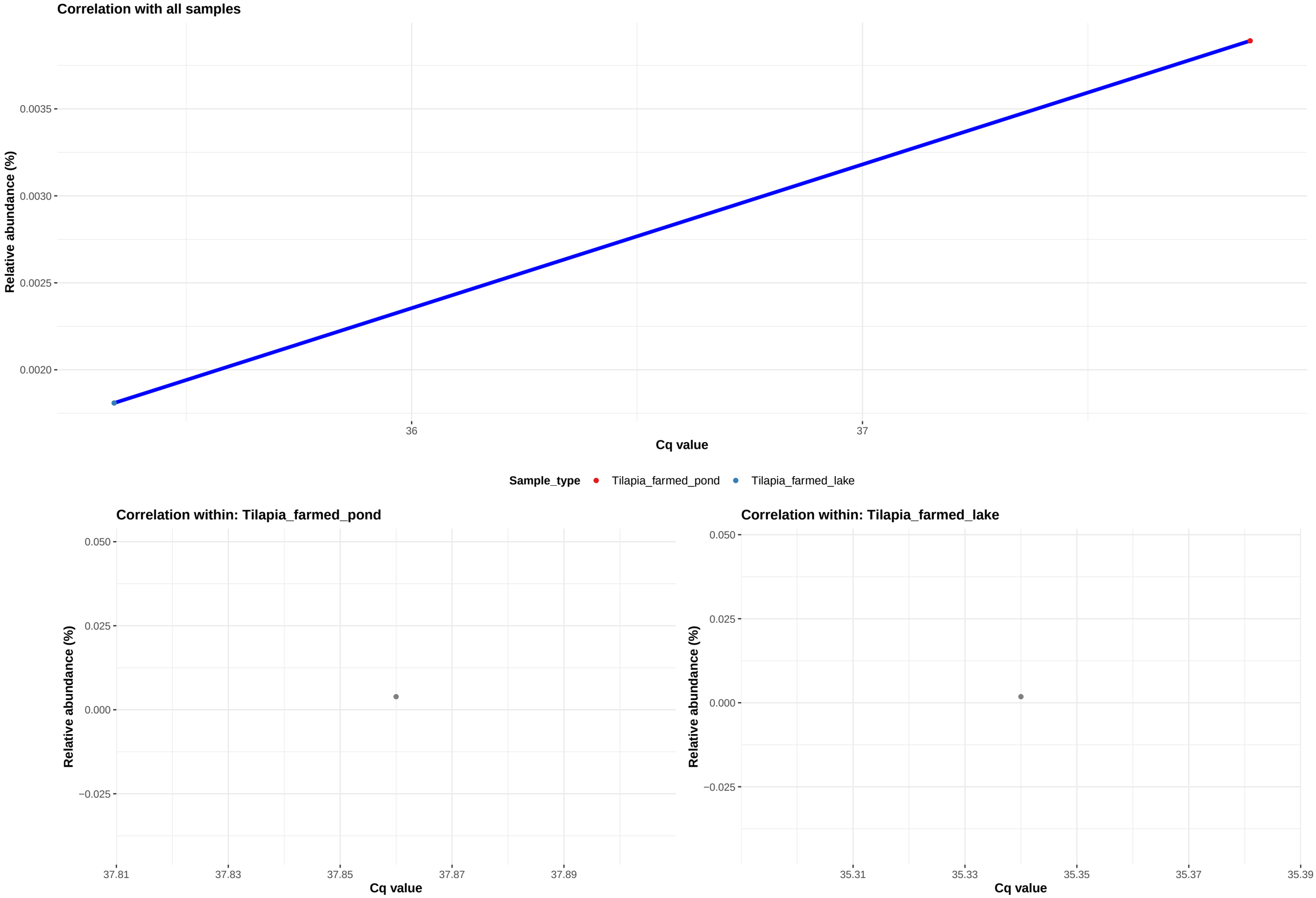
Correlation within: Perch_wild_lake

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



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

featureID: 92eda480cf7a77d3e7b6890877207fe6

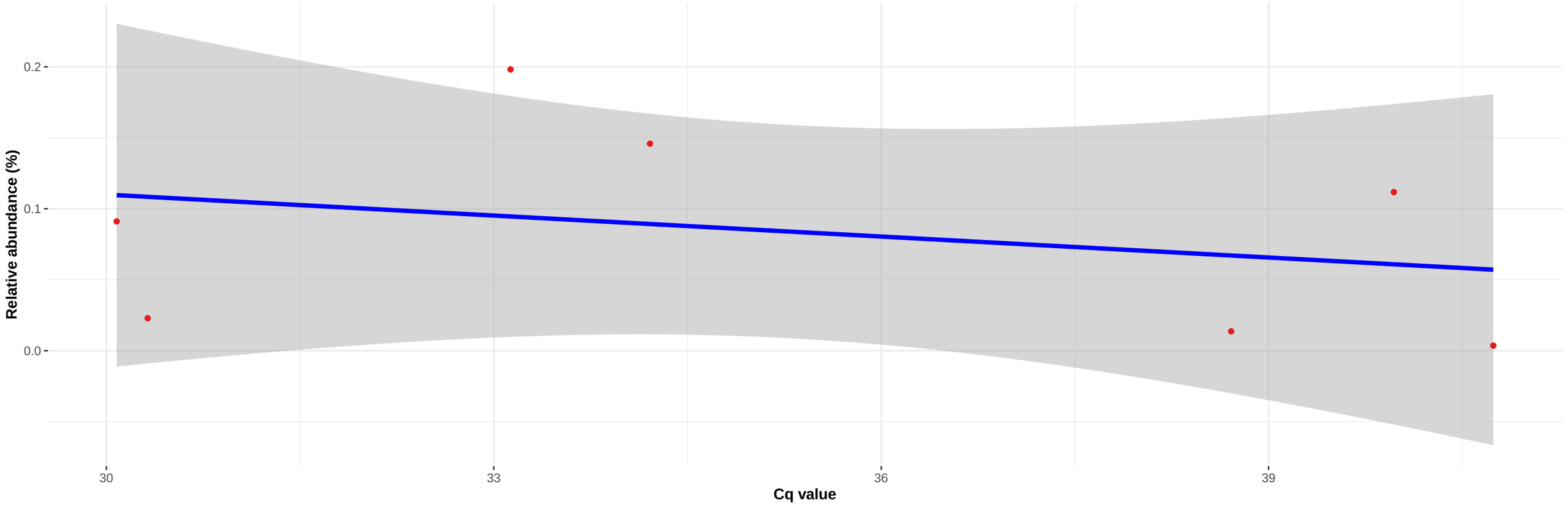


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 98368b3901045189f93ca86afab6cc2b

Correlation with all samples

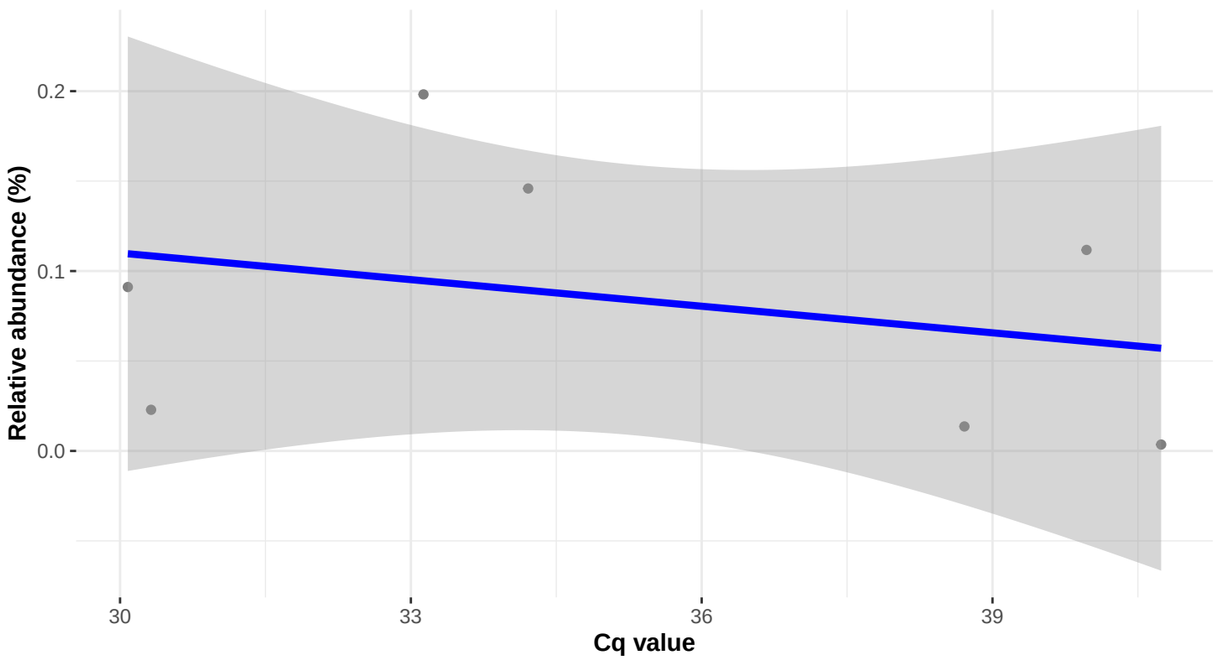
$\log_e(S)$ = 4.331, p = 0.432, $\hat{\rho}_{Spearman}$ = −0.357, $CI_{95\%}$ [−0.882, 0.562], n_{pairs} = 7



Sample_type Perch_wild_lake

Correlation within: Perch_wild_lake

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

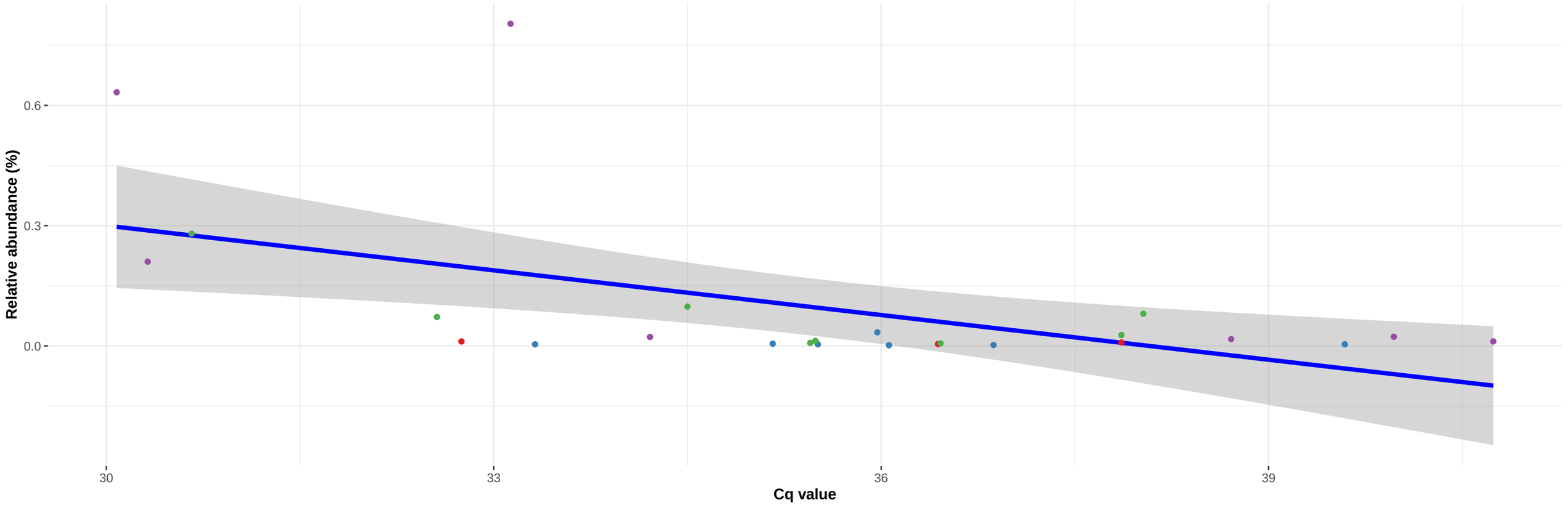


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; Ambiguous_taxa

featureID: 913a3599bef09a615b00dee32ead1f48

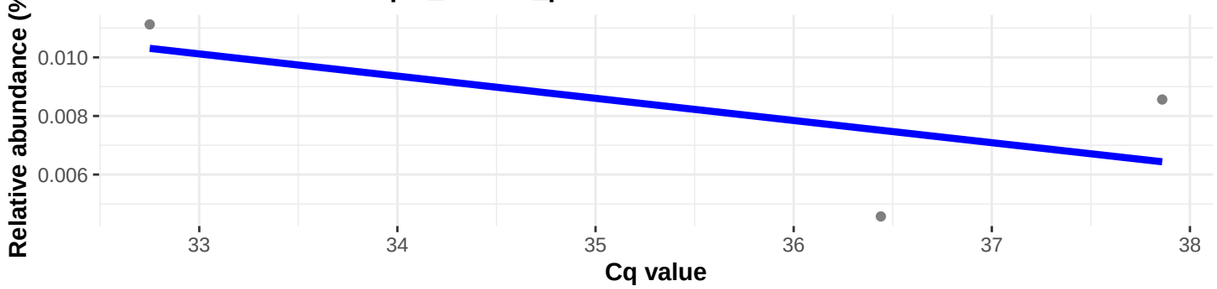
Correlation with all samples

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



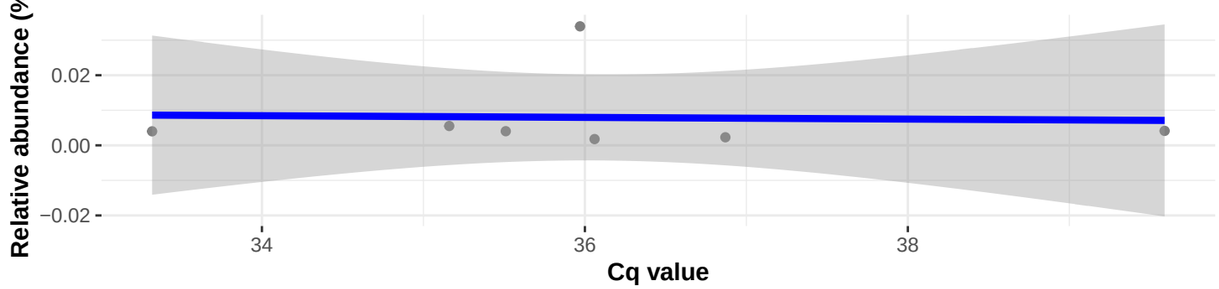
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond



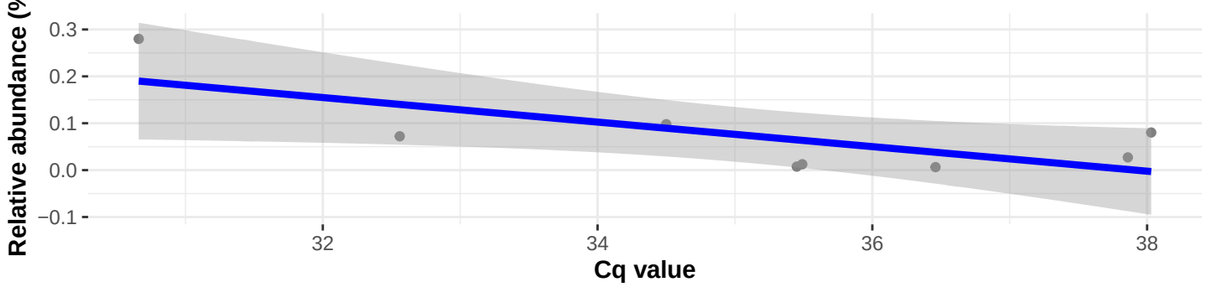
Correlation within: Tilapia_farmed_lake

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



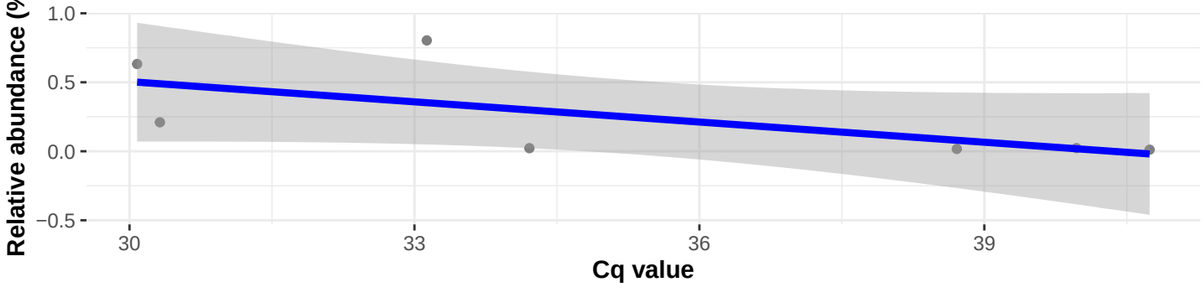
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

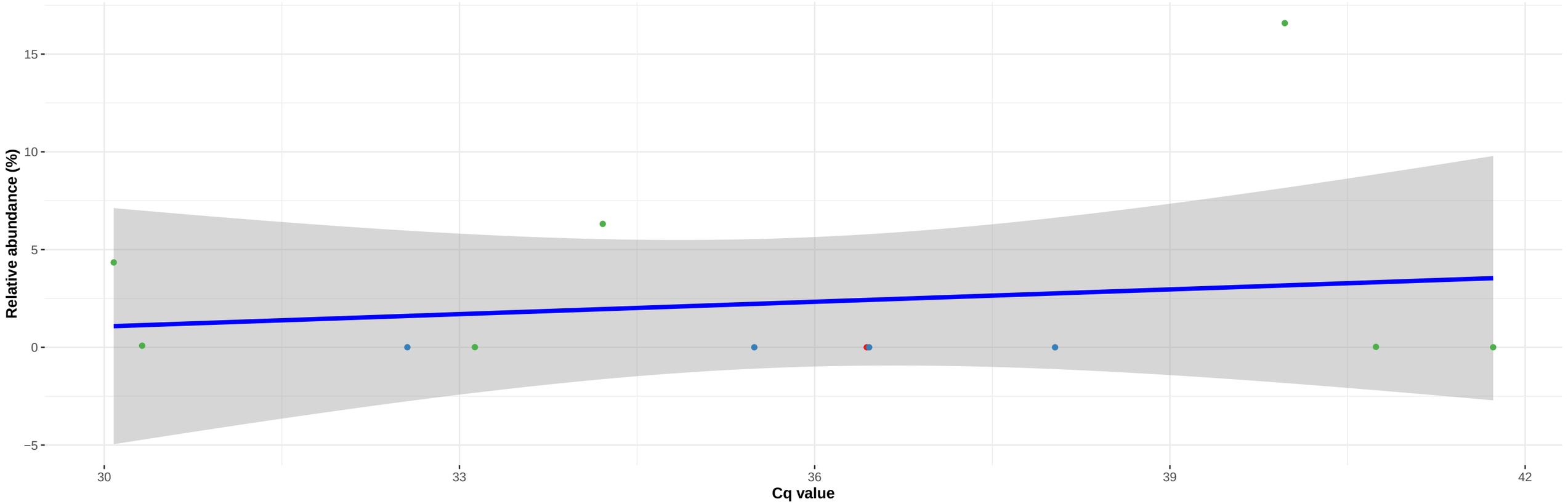


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: d36c9fdfa26099fffe57512e6dfbe0b8

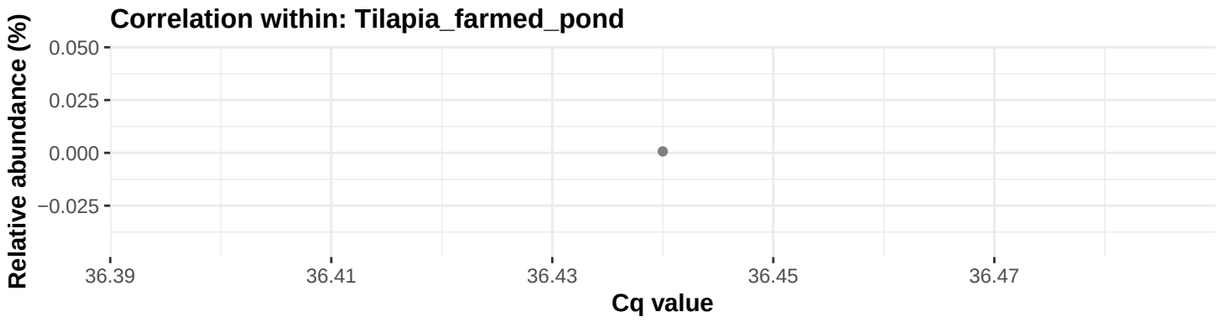
Correlation with all samples

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

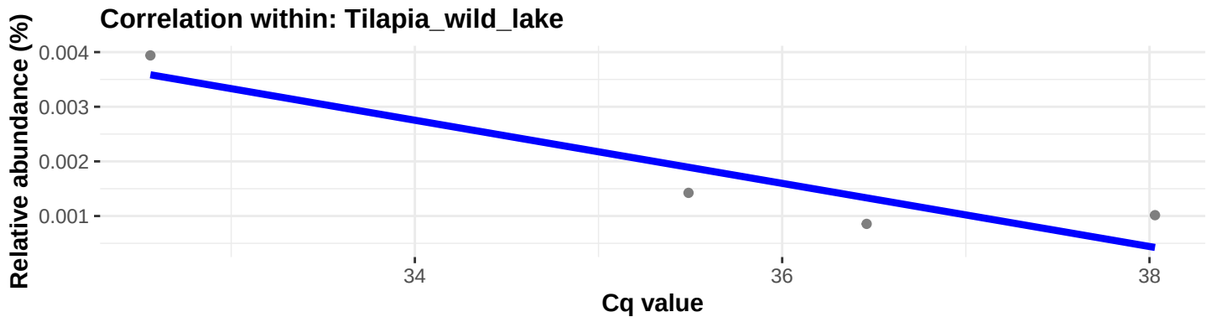


Sample_type Tilapia_farmed_pond Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

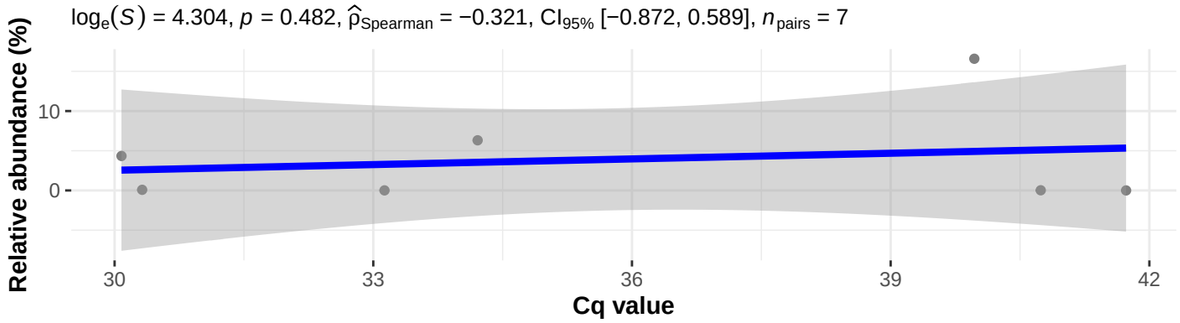


Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

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

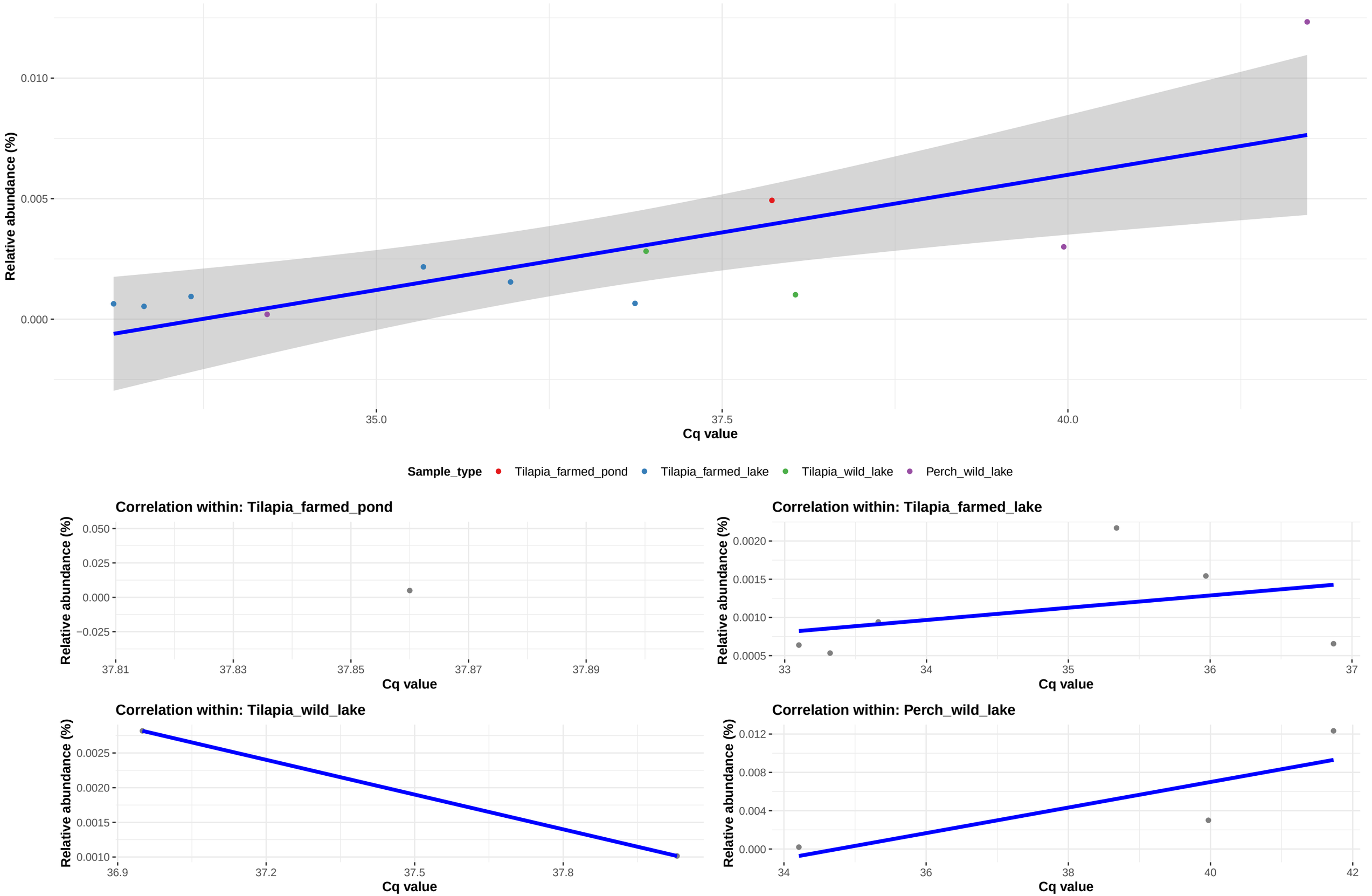


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; NA

featureID: 3638f2062c305c79df283ef573a10b97

Correlation with all samples

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



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

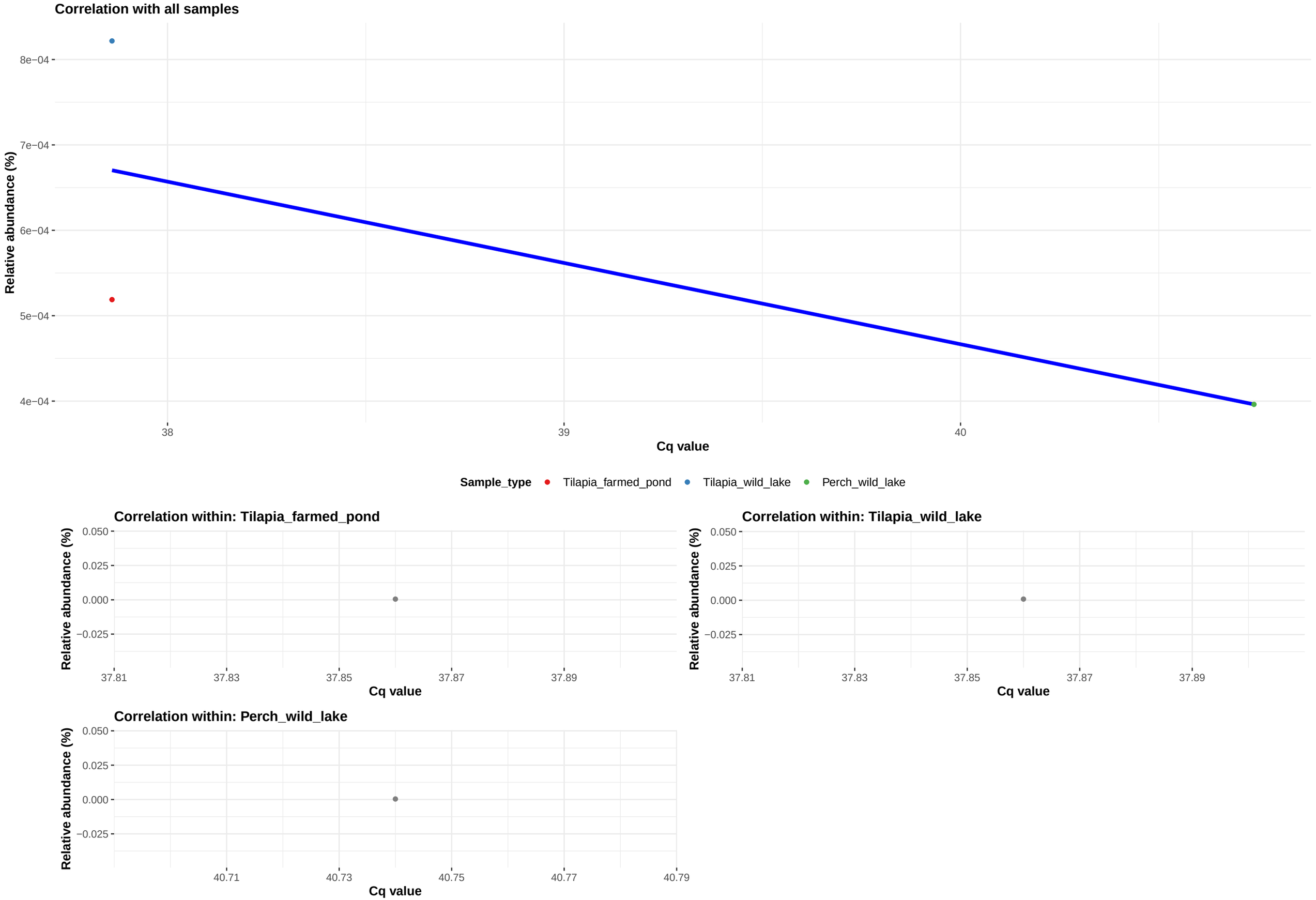
Correlation within: Tilapia_farmed_lake

Correlation within: Tilapia_wild_lake

Correlation within: Perch_wild_lake

k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Comamonas; NA

featureID: 8f2ddde9ccf2d7afe5abf35614fe5b43

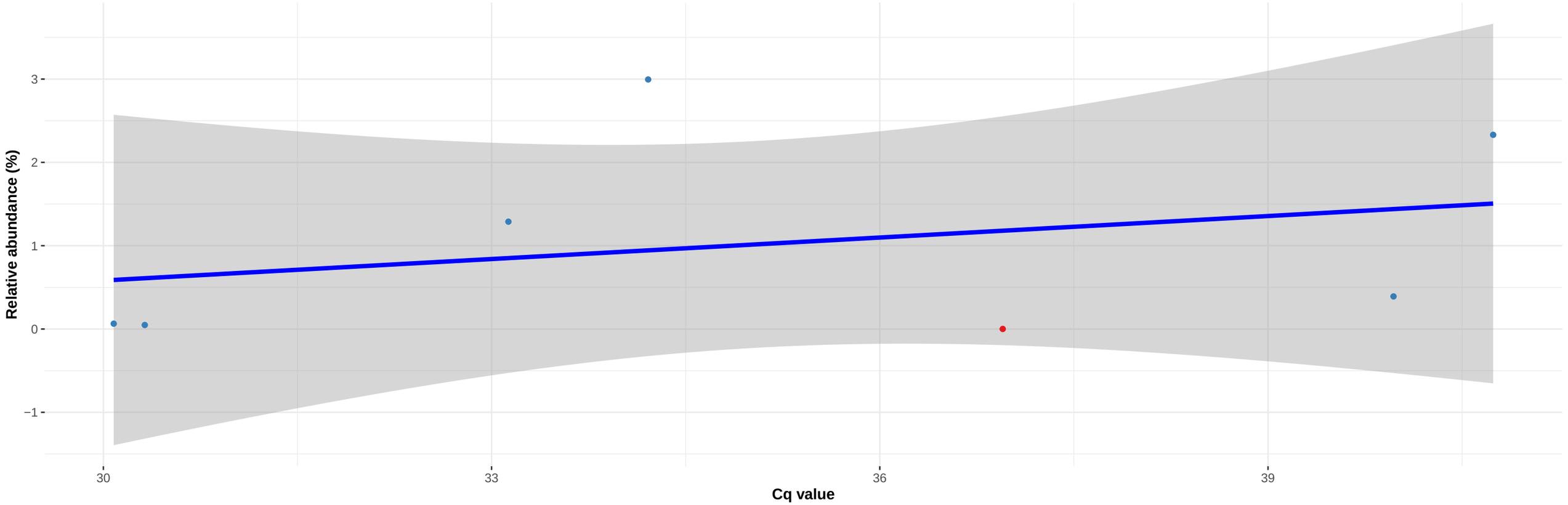


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Candidatus Arthromitus; NA

featureID: 249270189cd8e1c30eb0d62d77589cb8

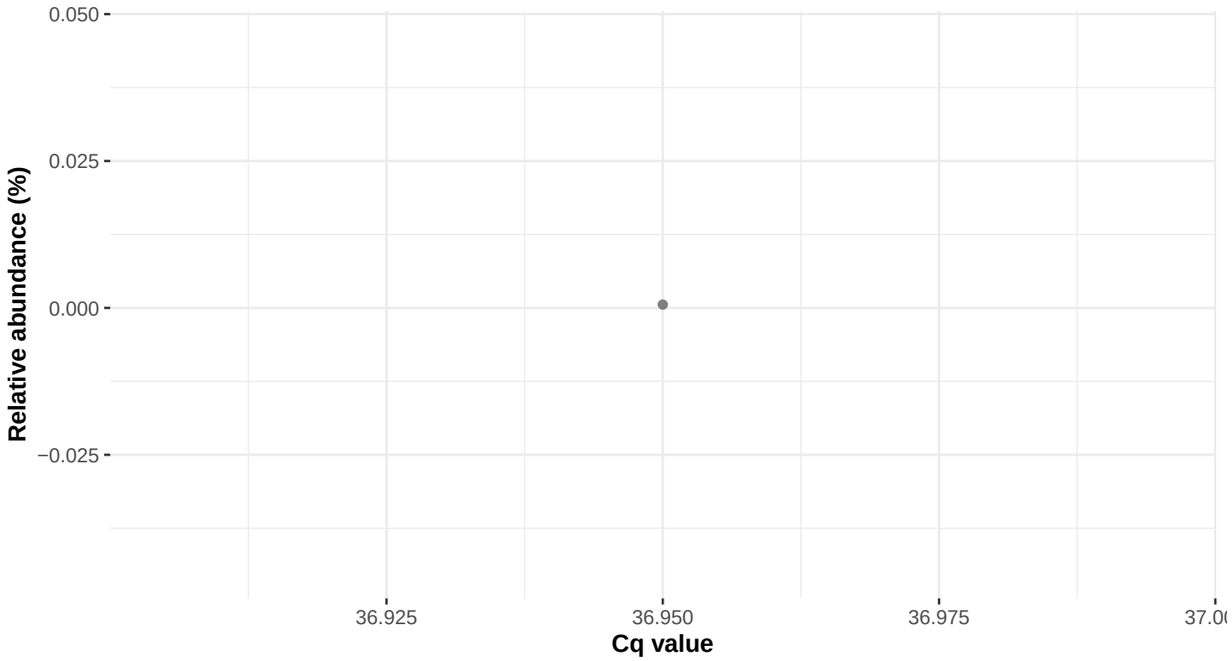
Correlation with all samples

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



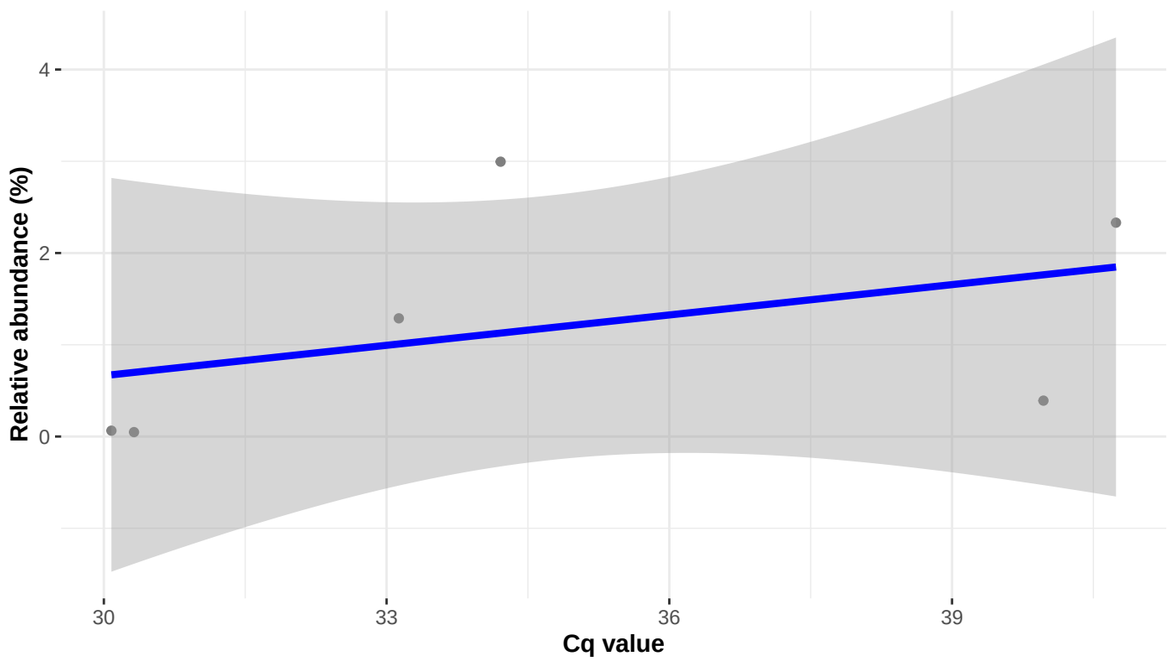
Sample_type Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

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

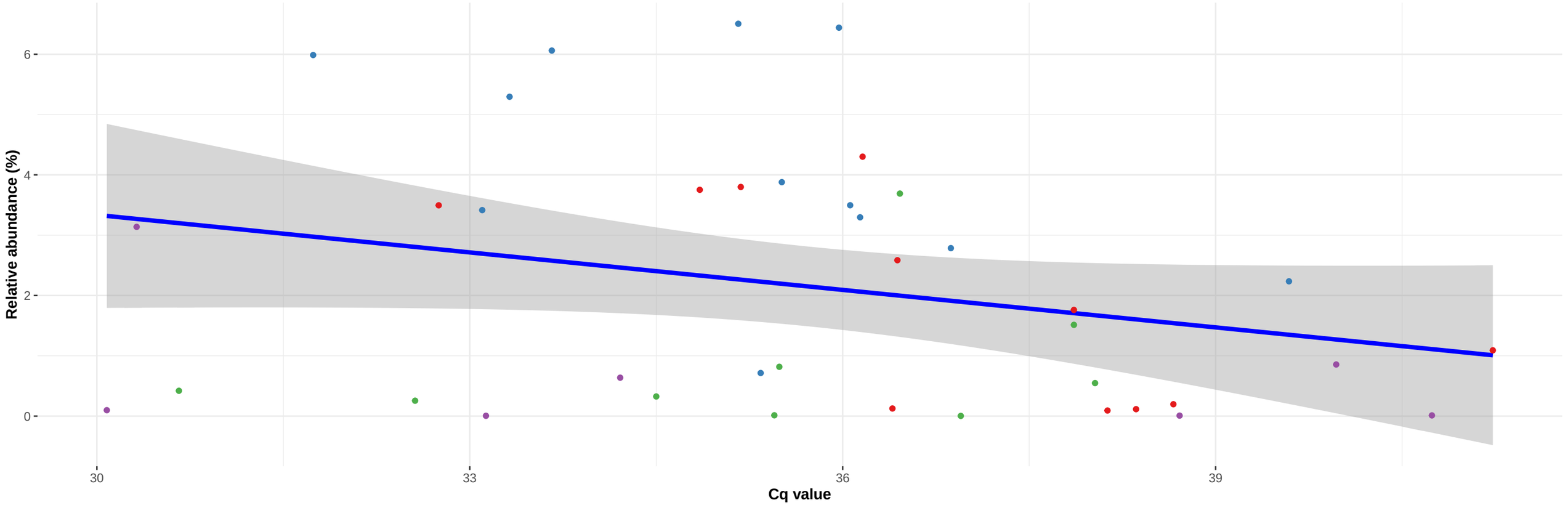


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 7732d6712ceae4666bd66aba7880c6f1

Correlation with all samples

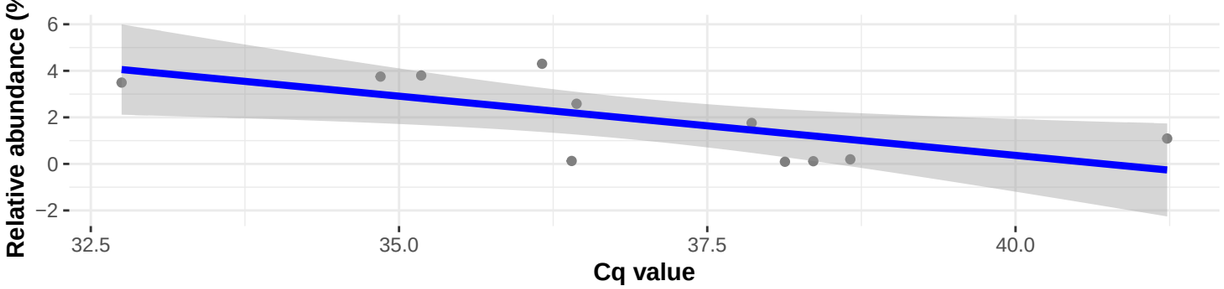
$\log_e(S)$ = 9.443, p = 0.088, $\hat{\rho}_{Spearman}$ = −0.277, $CI_{95\%}$ [−0.552, 0.052], n_{pairs} = 39



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

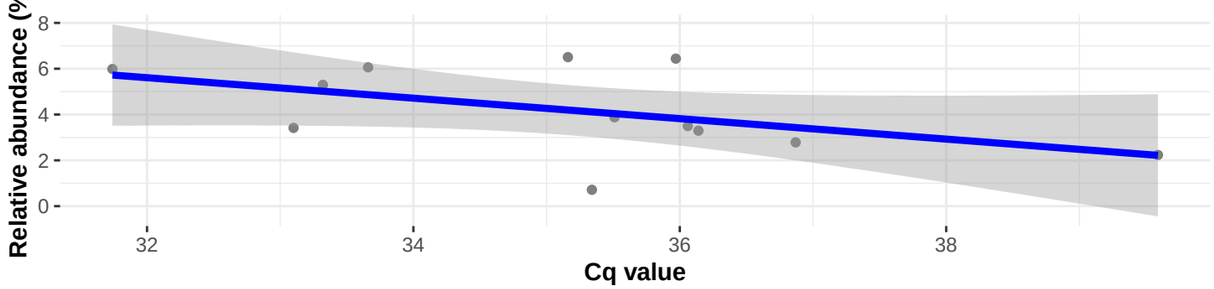
Correlation within: Tilapia_farmed_pond

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



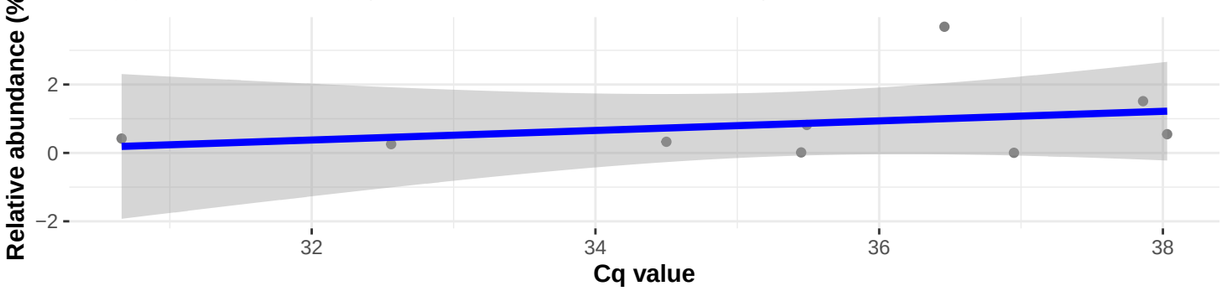
Correlation within: Tilapia_farmed_lake

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



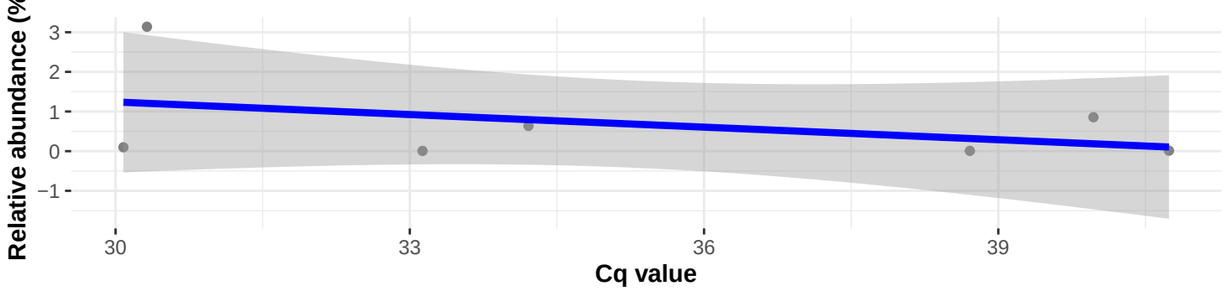
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

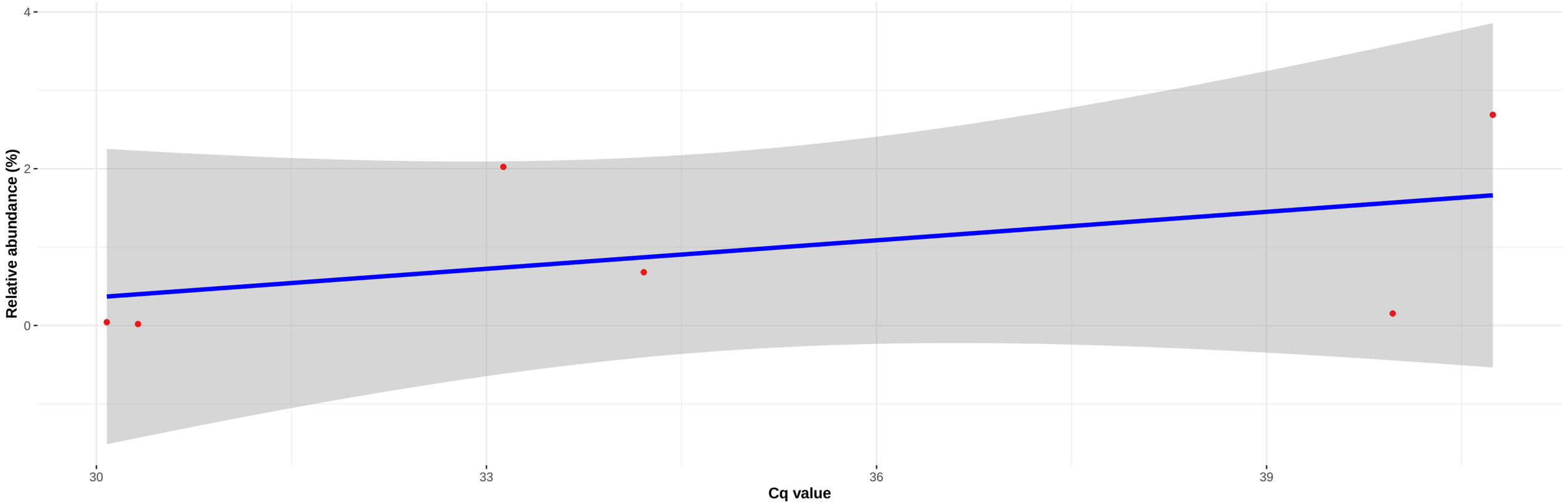


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: 4c5af046872782b10af8fff902cdf641

Correlation with all samples

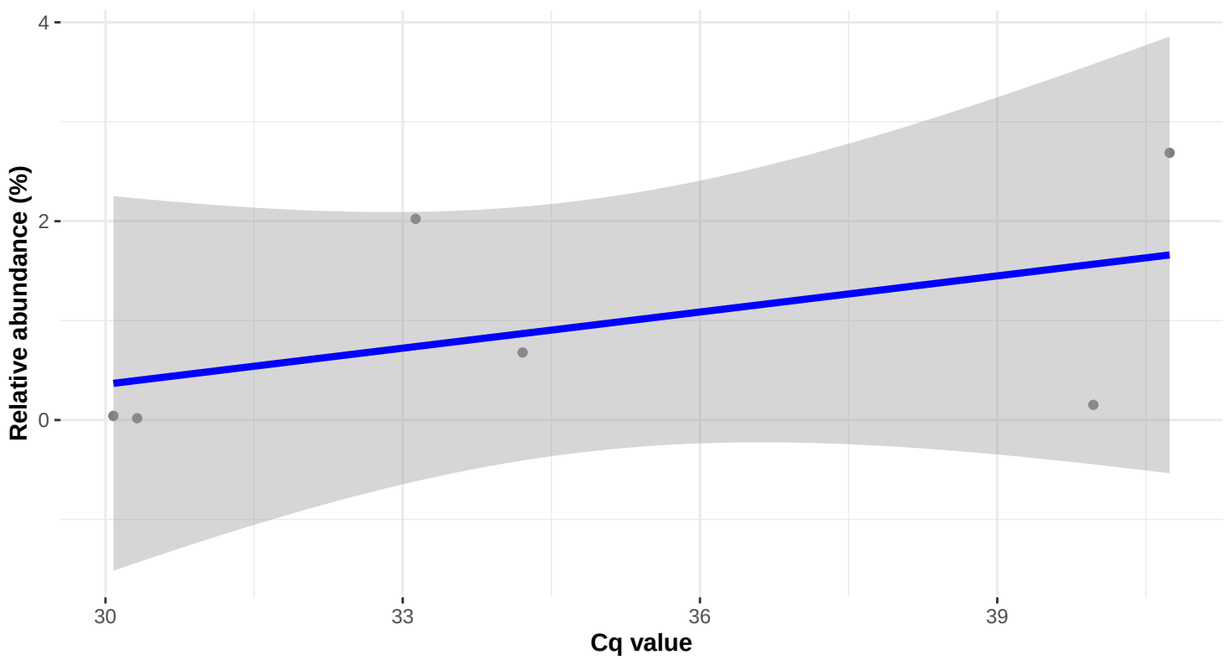
$\log_e(S)$ = 2.303, p = 0.111, $\hat{\rho}_{Spearman}$ = 0.714, $CI_{95\%}$ [−0.263, 0.968], n_{pairs} = 6



Sample_type Perch_wild_lake

Correlation within: Perch_wild_lake

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

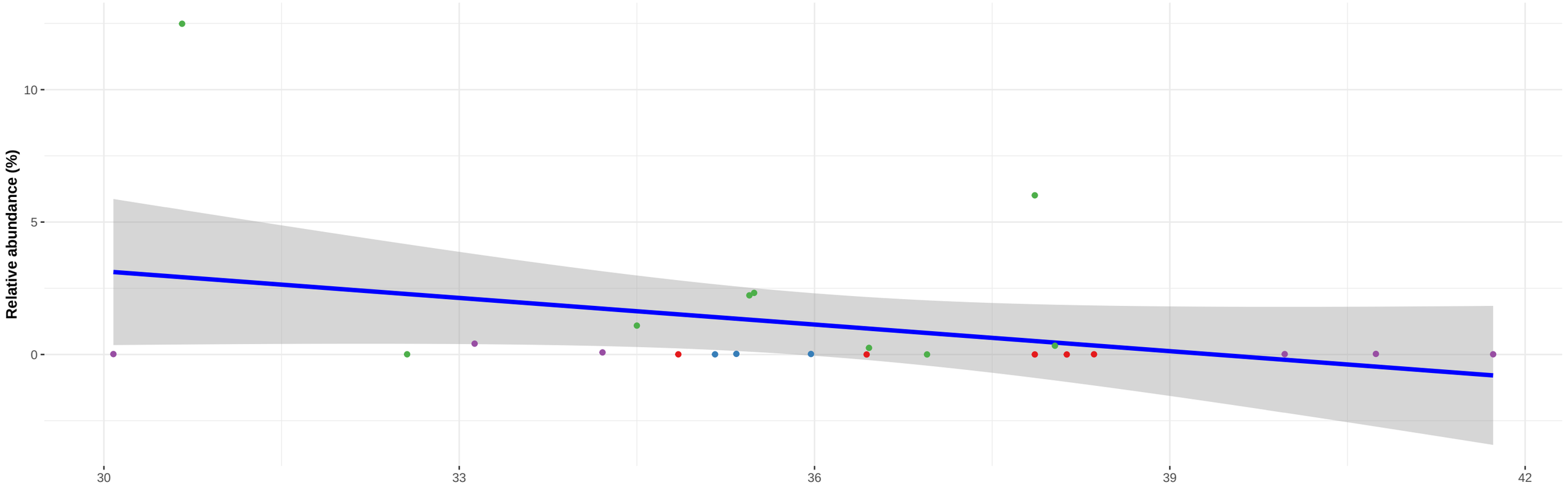


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: dacf22eb1a2065568c1175d1a76c9dc7

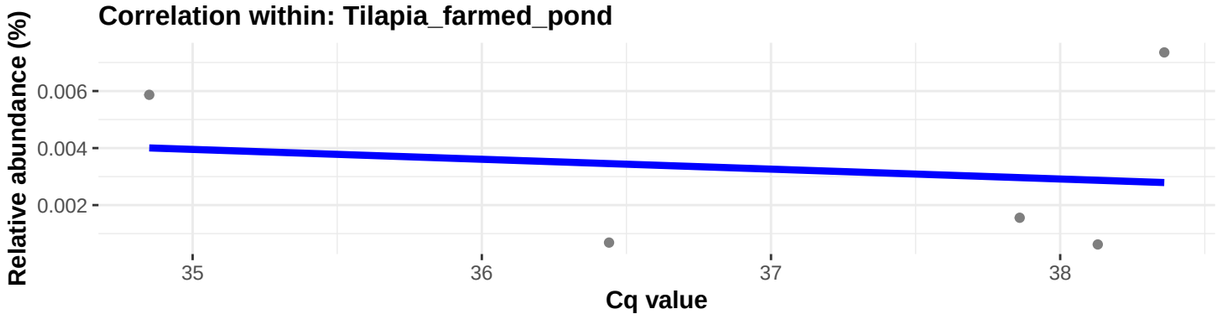
Correlation with all samples

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

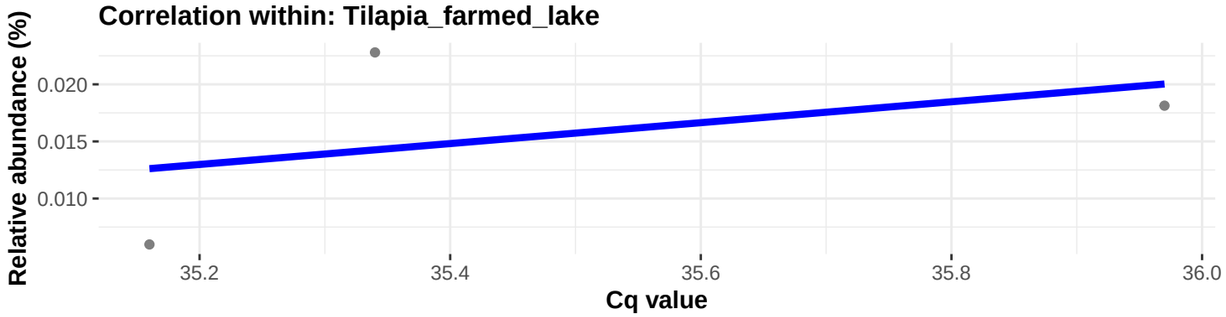


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

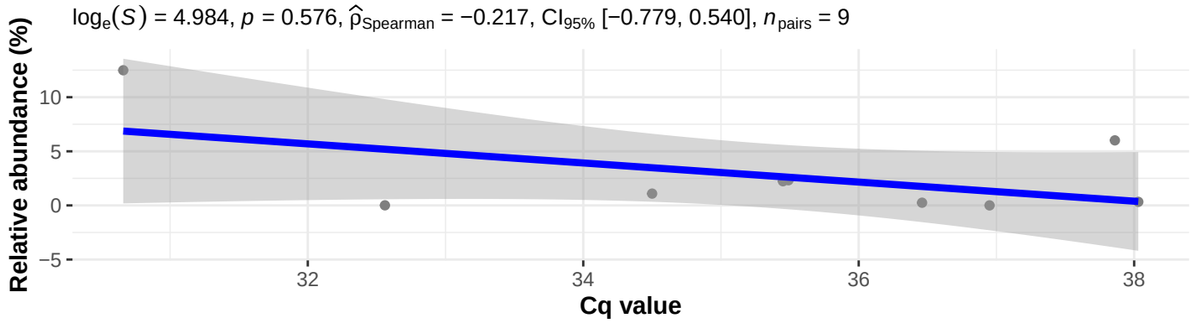


Correlation within: Tilapia_farmed_lake



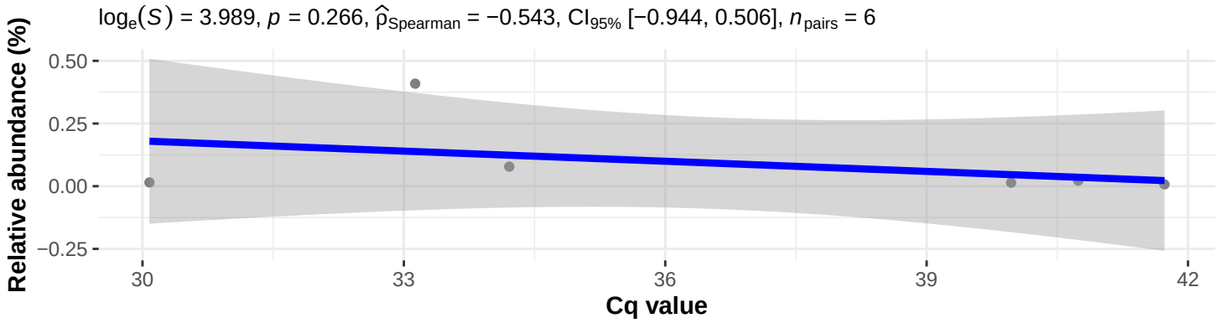
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

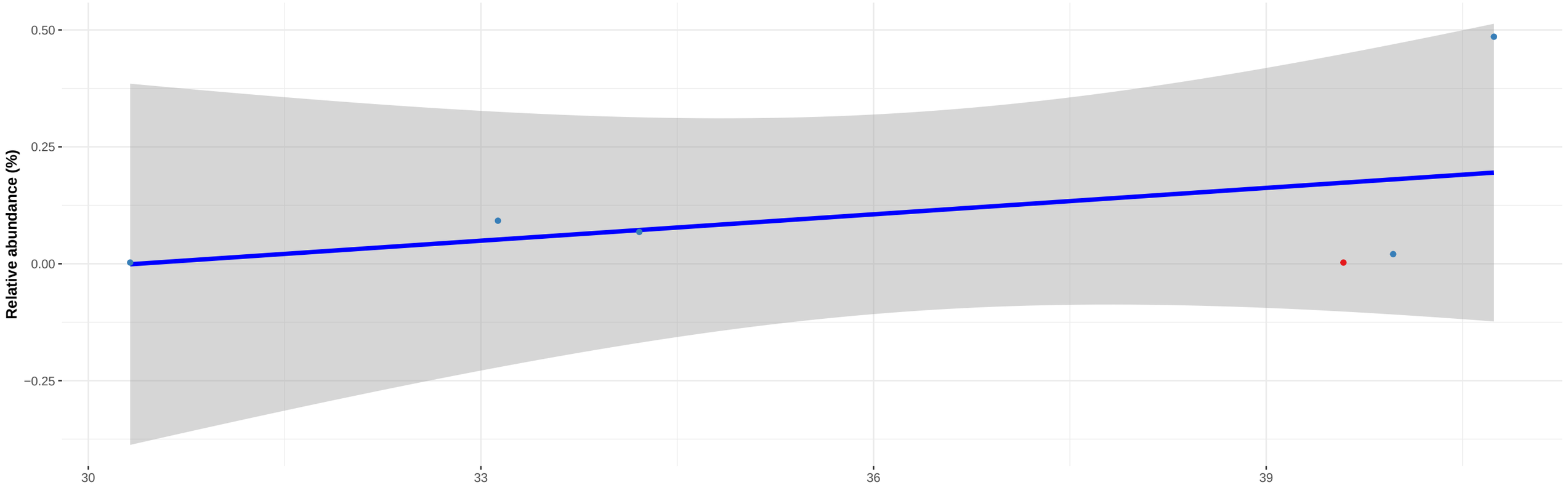


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__uncultured bacterium

featureID: 4852811146dcf523a9ecf810088a2da5

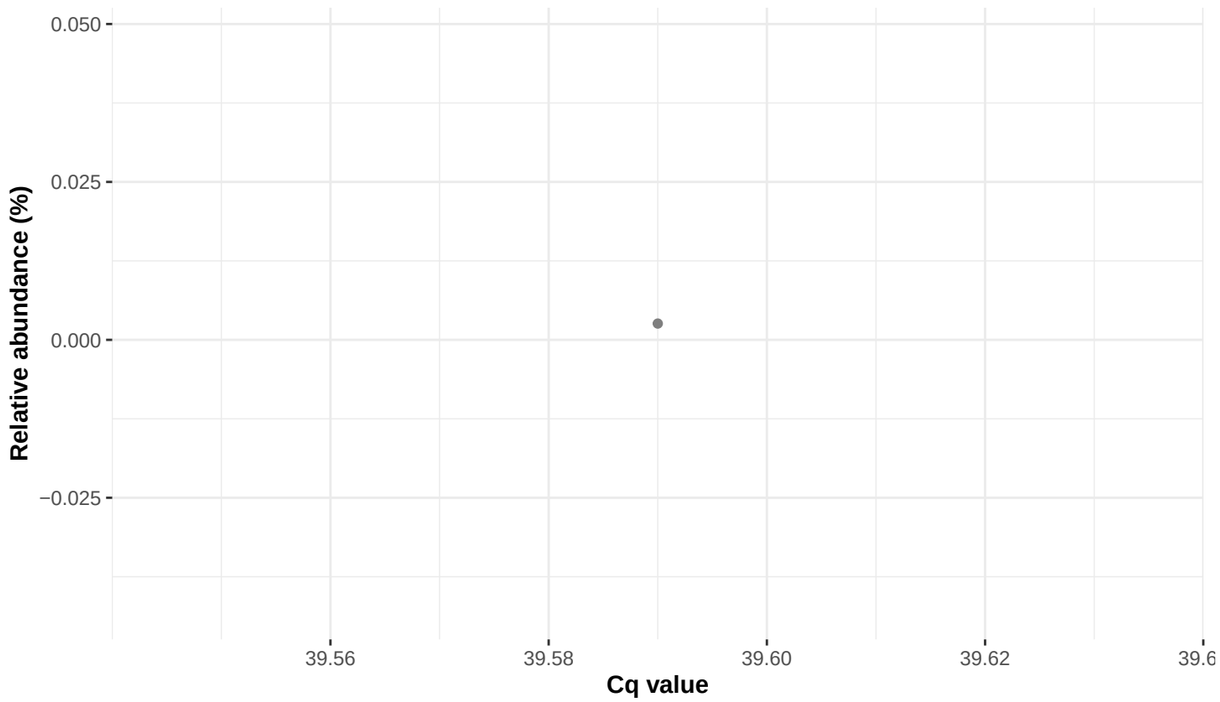
Correlation with all samples

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

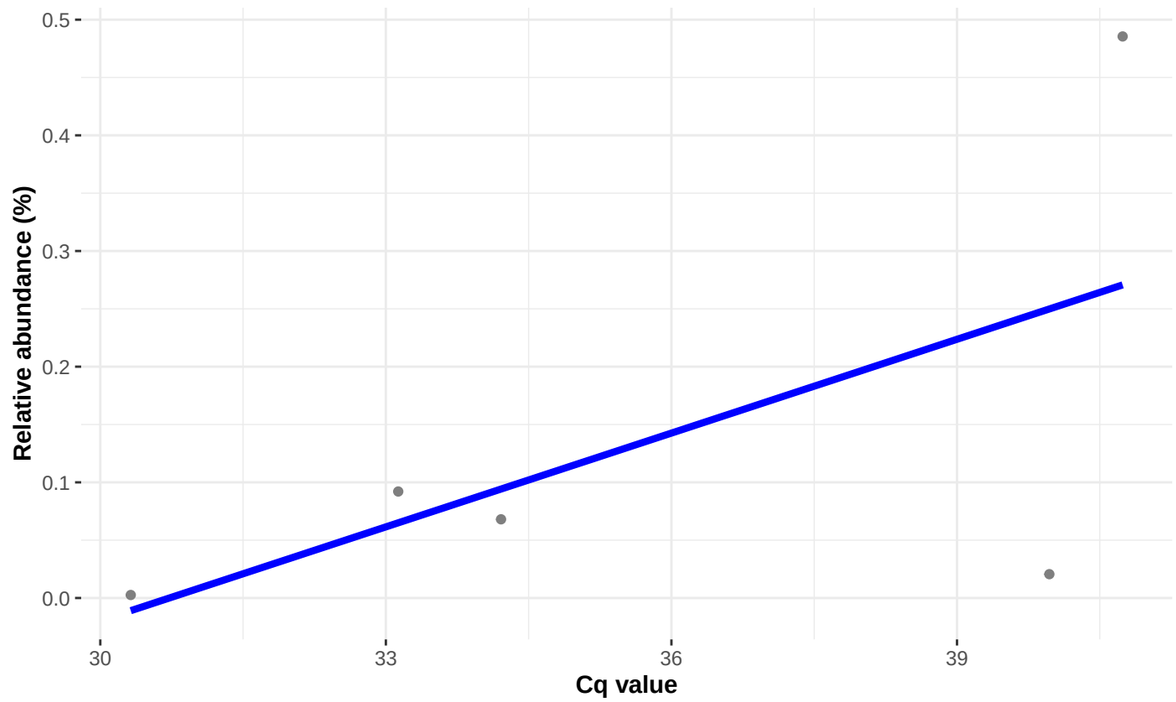


Sample_type Tilapia_farmed_lake Perch_wild_lake

Correlation within: Tilapia_farmed_lake



Correlation within: Perch_wild_lake



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

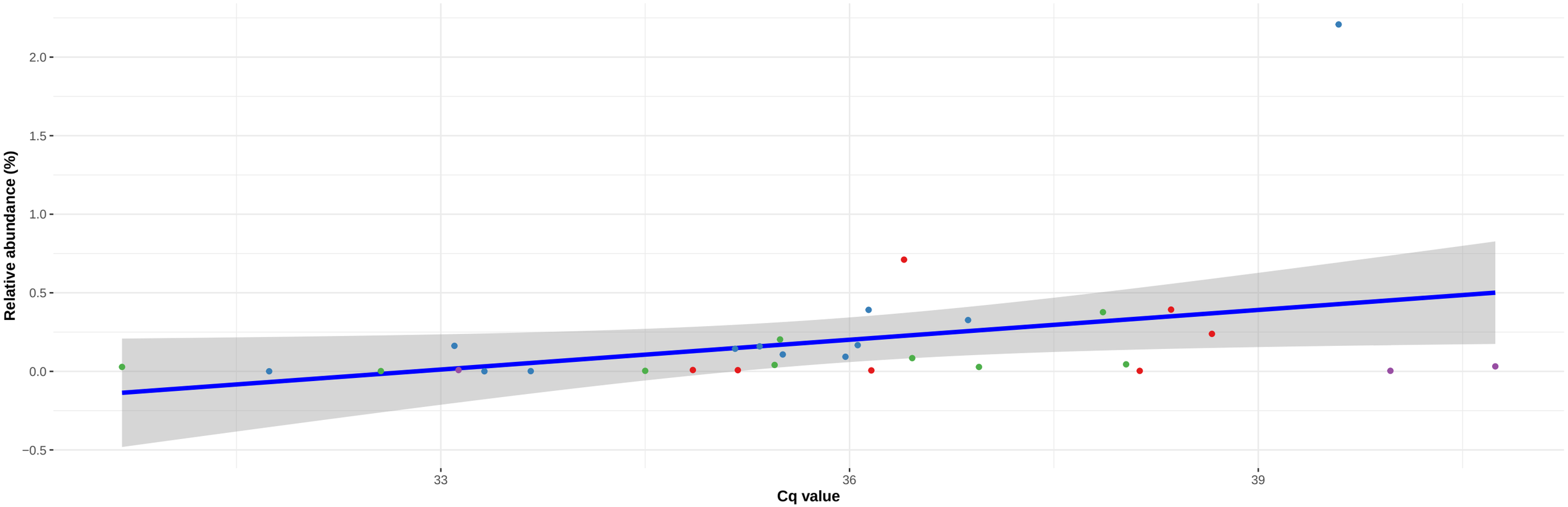
featureID: 62611dedc42201591d0c89973f903dde

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

featureID: 550884702aea7eaa9461b76e8ef9da16

Correlation with all samples

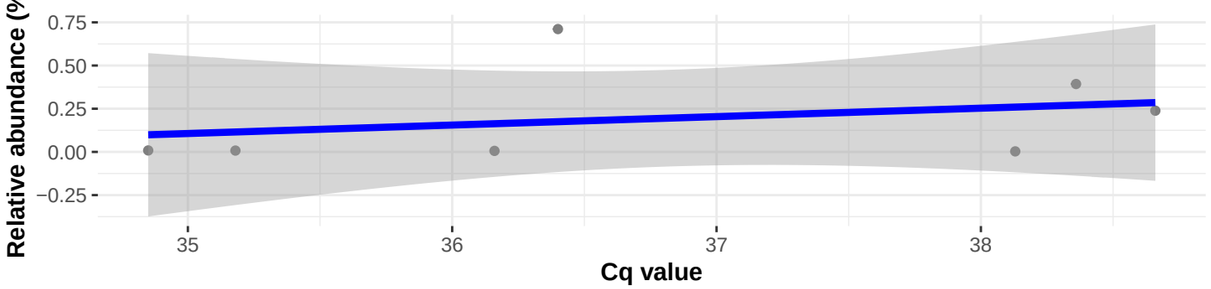
$\log_e(S)$ = 7.911, p = 0.011, $\hat{\rho}_{Spearman}$ = 0.450, $CI_{95\%}$ [0.103, 0.699], n_{pairs} = 31



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

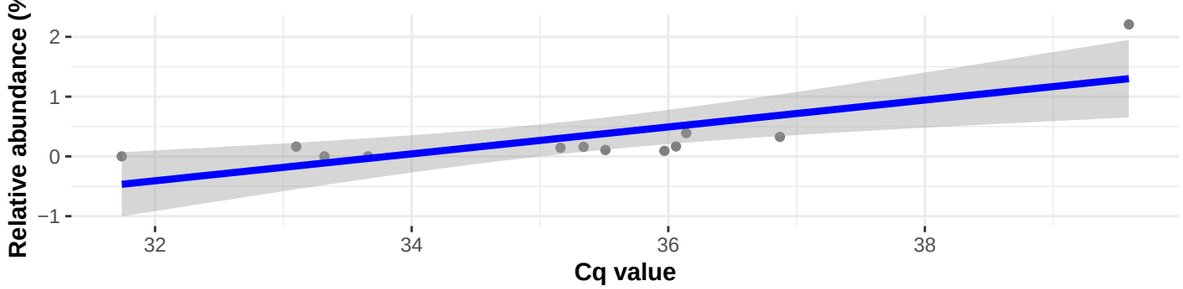
Correlation within: Tilapia_farmed_pond

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



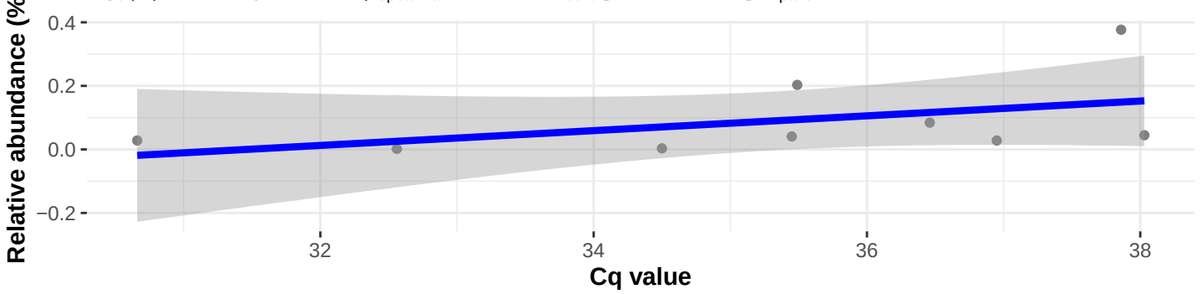
Correlation within: Tilapia_farmed_lake

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

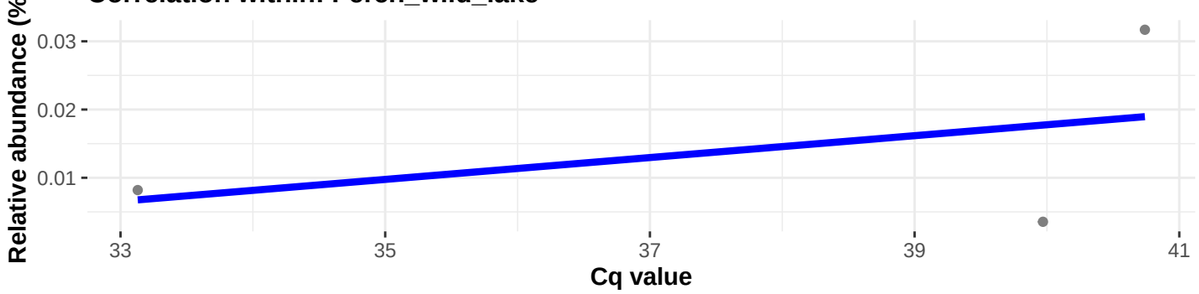


Correlation within: Tilapia_wild_lake

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

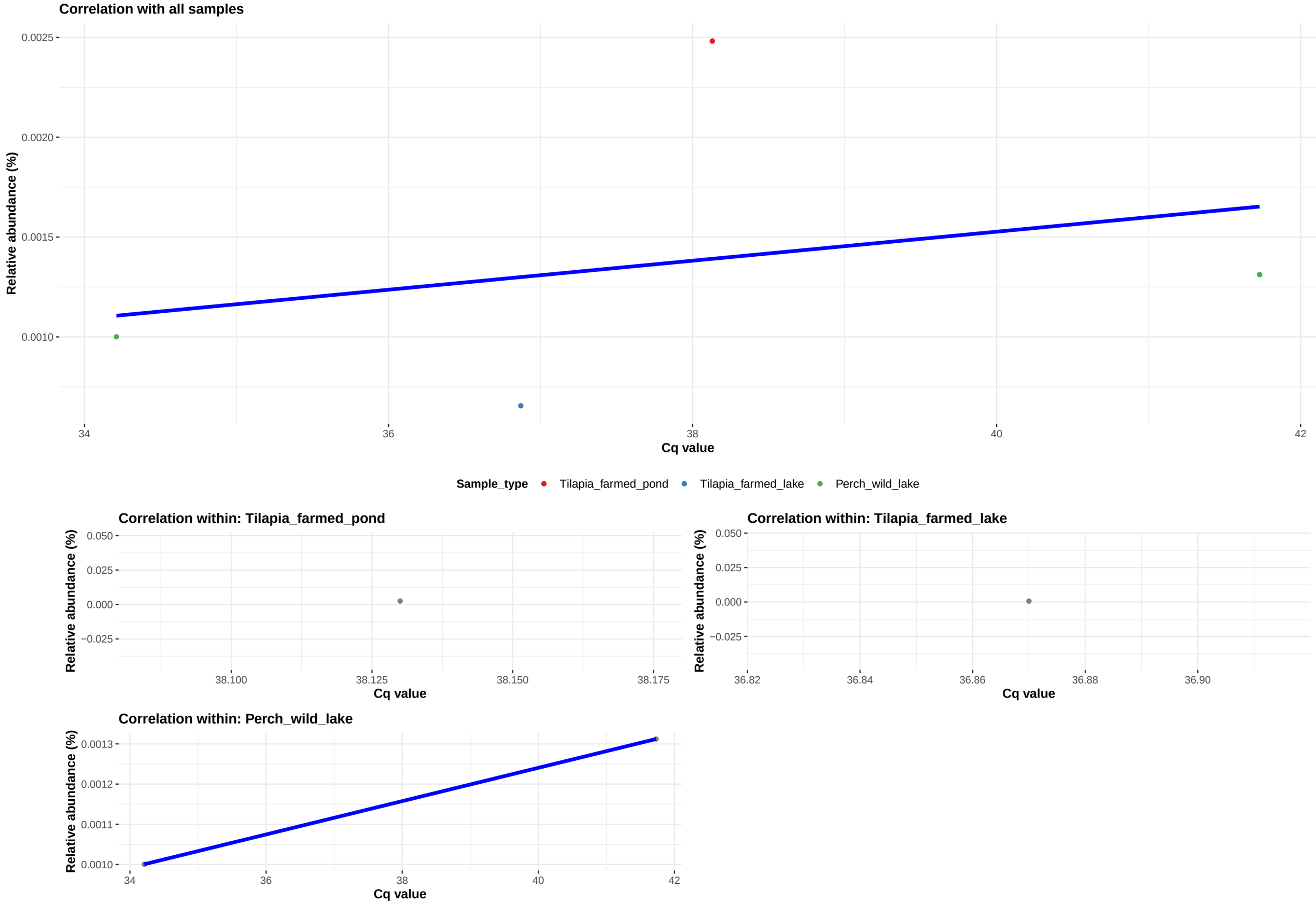


Correlation within: Perch_wild_lake



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

featureID: 43a54829cc0d7a58a61ad7f833cc2b22

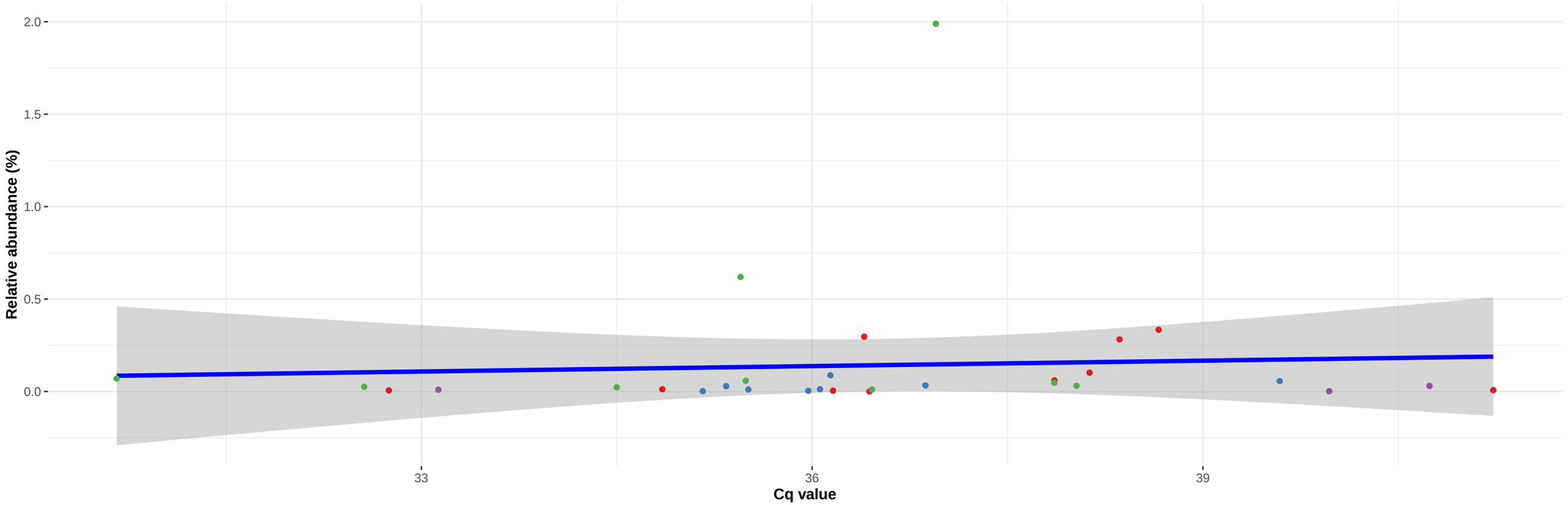


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Methylocystis; NA

featureID: 675f287d70a622c1c4cd8e1b634e8aed

Correlation with all samples

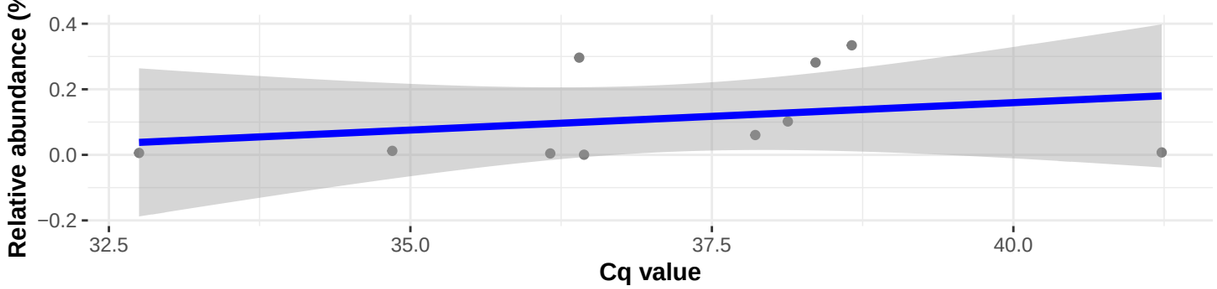
$\log_e(S)$ = 8.192, p = 0.298, $\hat{\rho}_{Spearman}$ = 0.197, $CI_{95\%}$ [−0.187, 0.528], n_{pairs} = 30



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

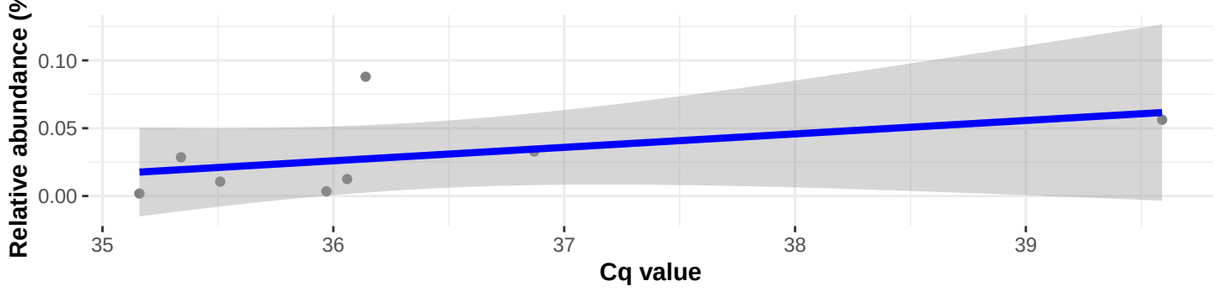
Correlation within: Tilapia_farmed_pond

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



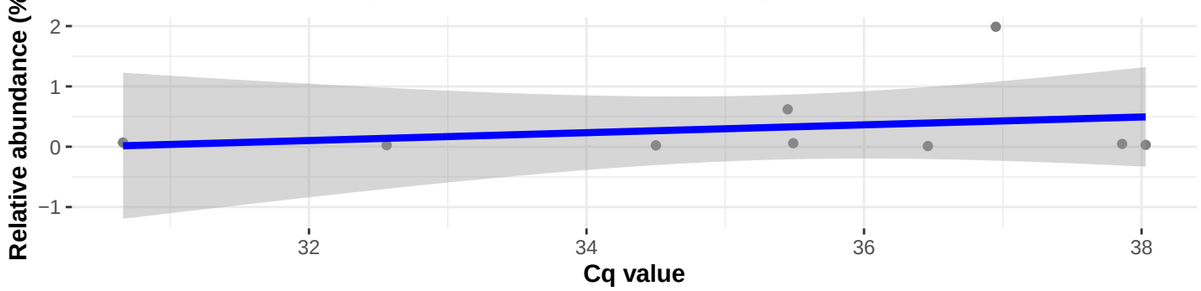
Correlation within: Tilapia_farmed_lake

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

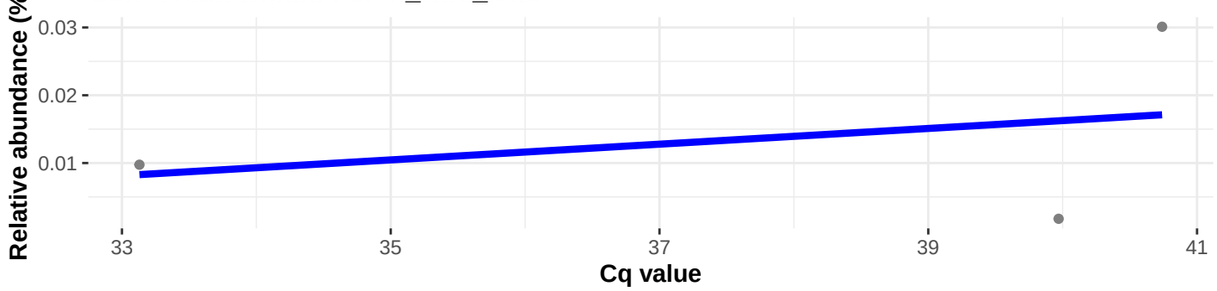


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

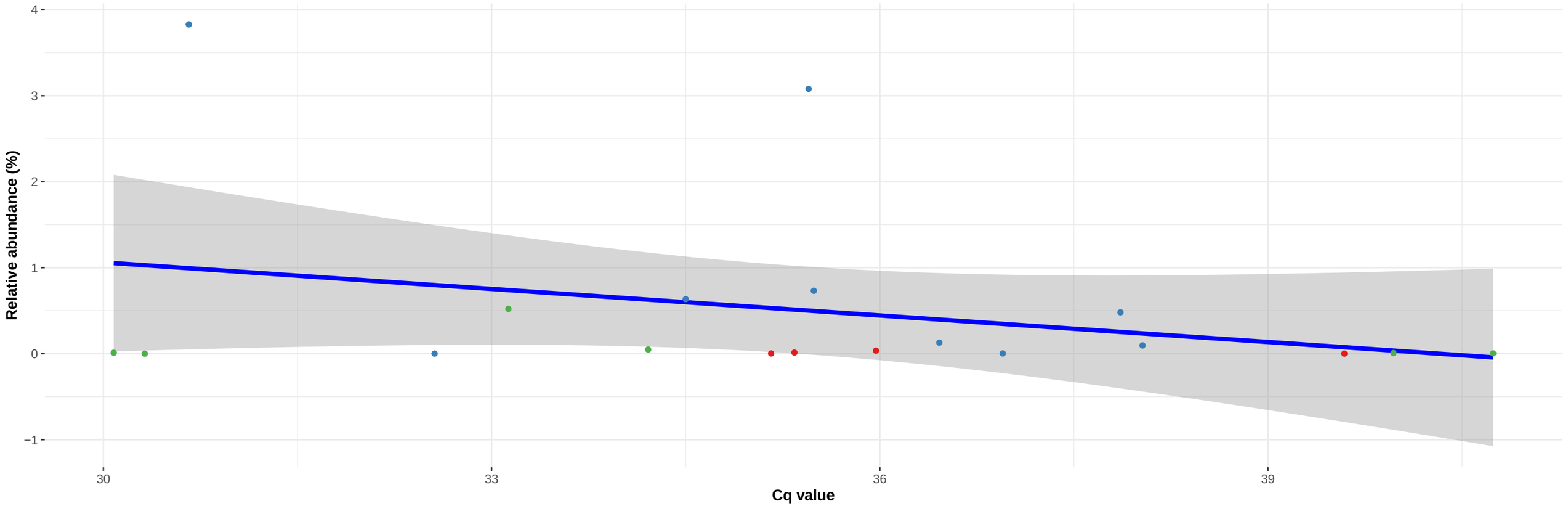


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: f4ddba285154bdd47f4dc510c2038305

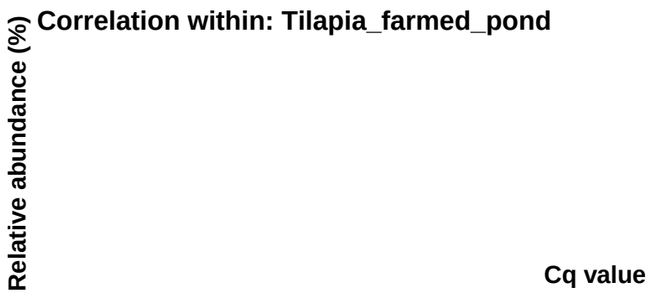
Correlation with all samples

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

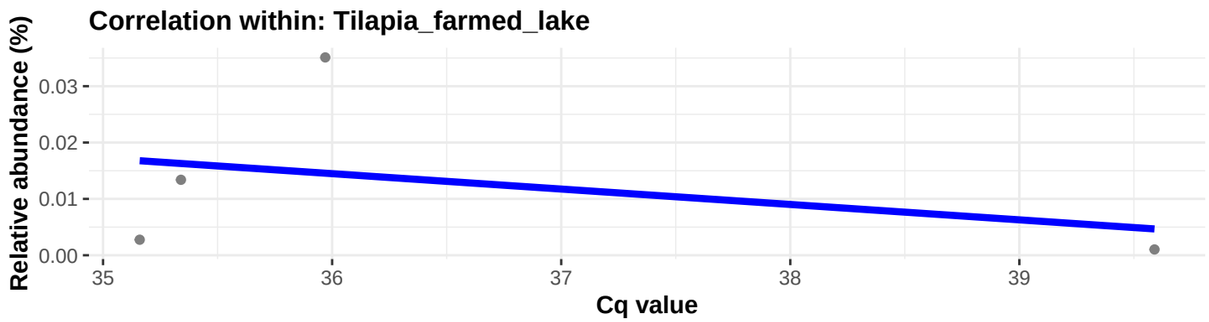


Sample_type Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

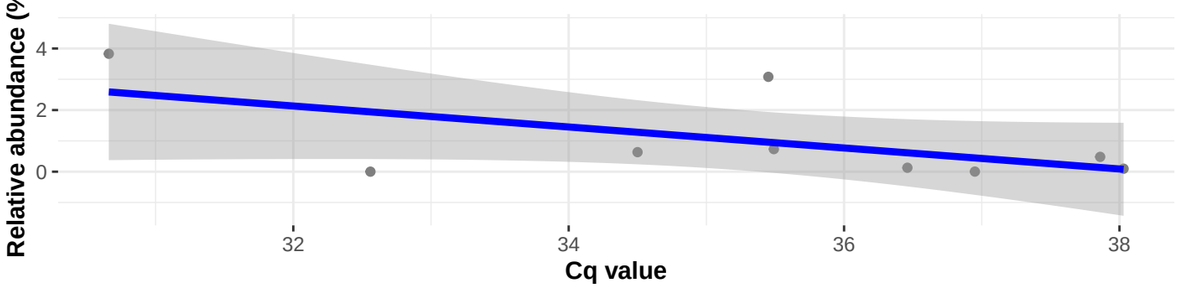


Correlation within: Tilapia_farmed_lake



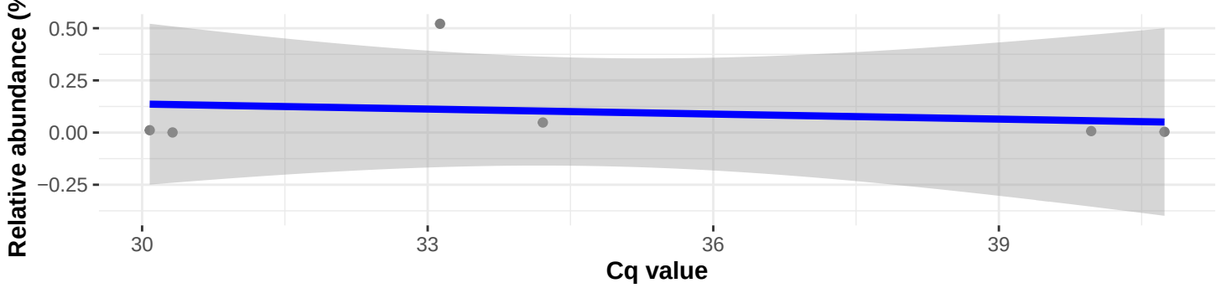
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

$\log_e(S)$ = 3.689, p = 0.787, $\hat{\rho}_{Spearman}$ = −0.143, $CI_{95\%}$ [−0.864, 0.770], n_{pairs} = 6

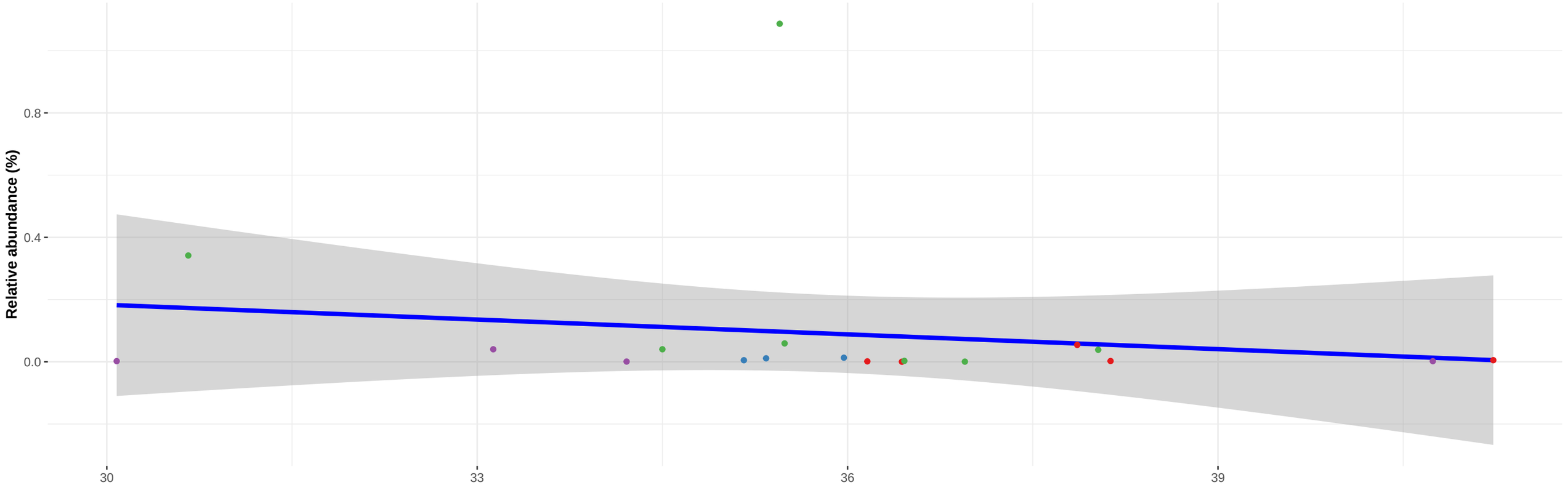


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; NA

featureID: 2e119ce67894fe00027176e52f17a225

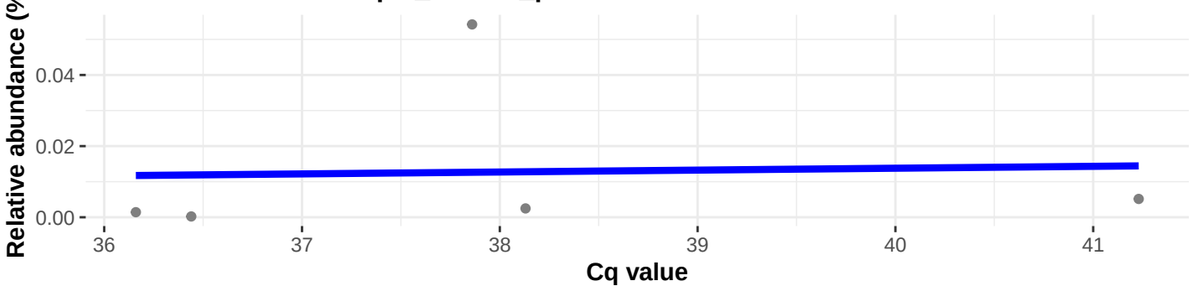
Correlation with all samples

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

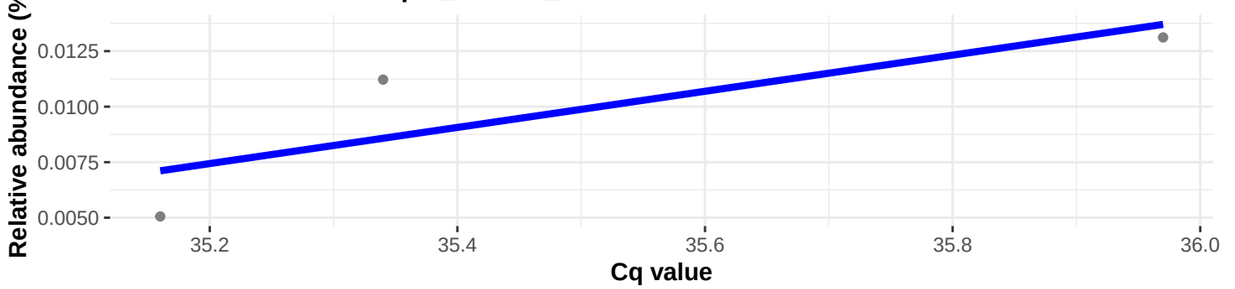


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

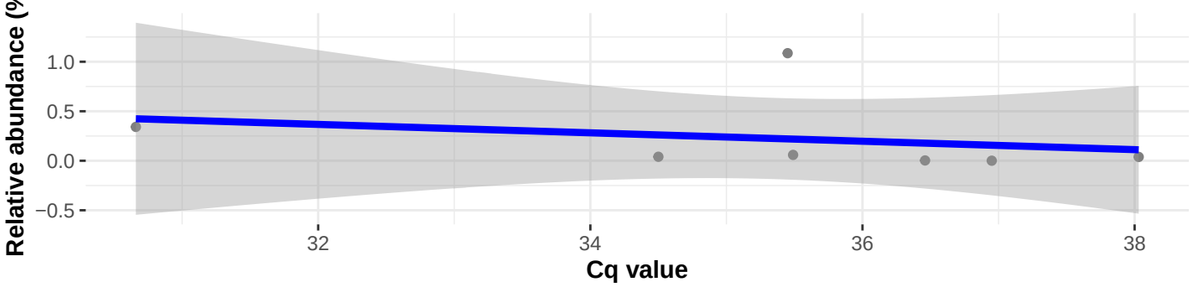


Correlation within: Tilapia_farmed_lake



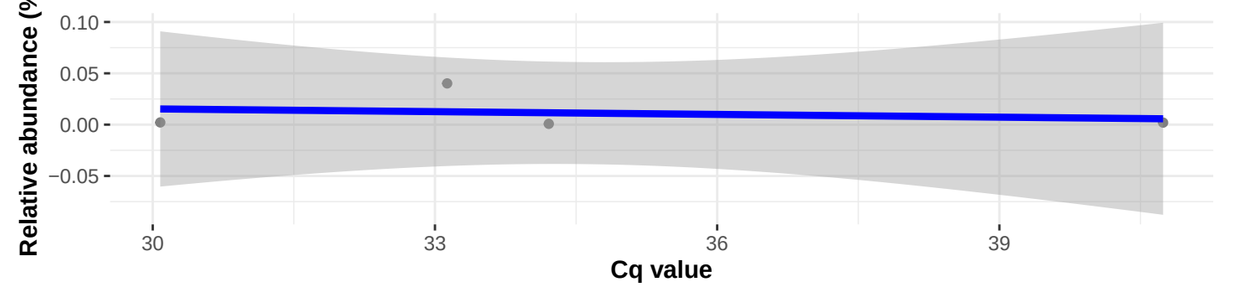
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

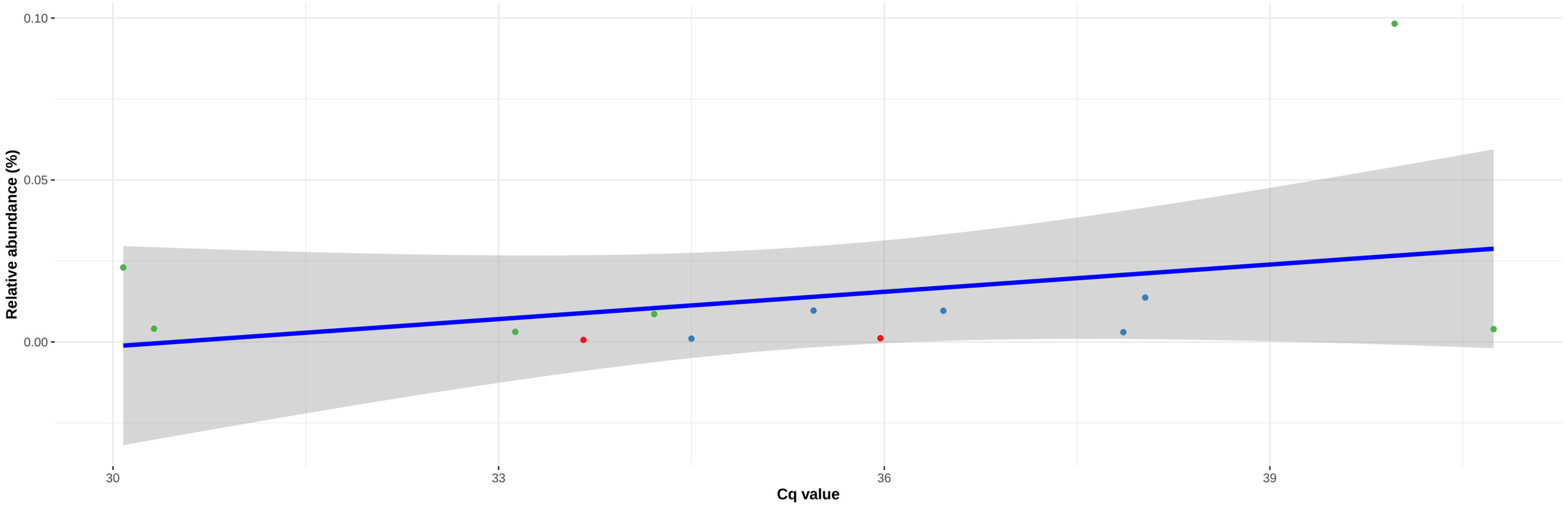


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Plesiomonas; NA

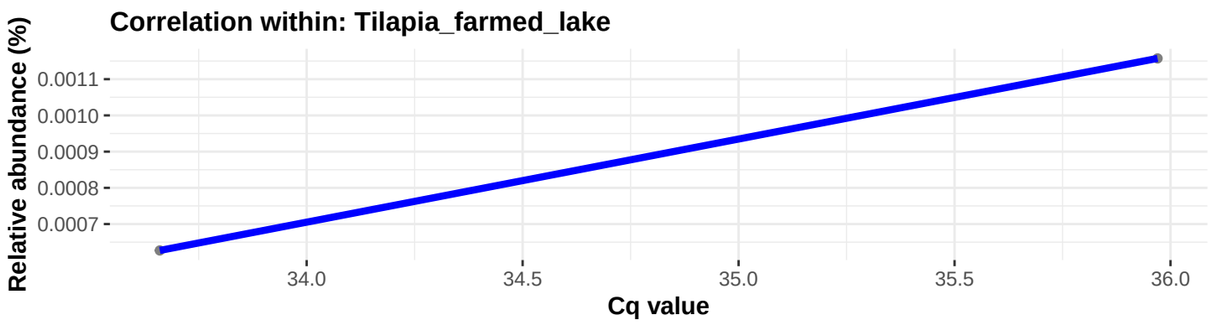
featureID: 8cc0e176d680aac1a413121d8633c30d

Correlation with all samples

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

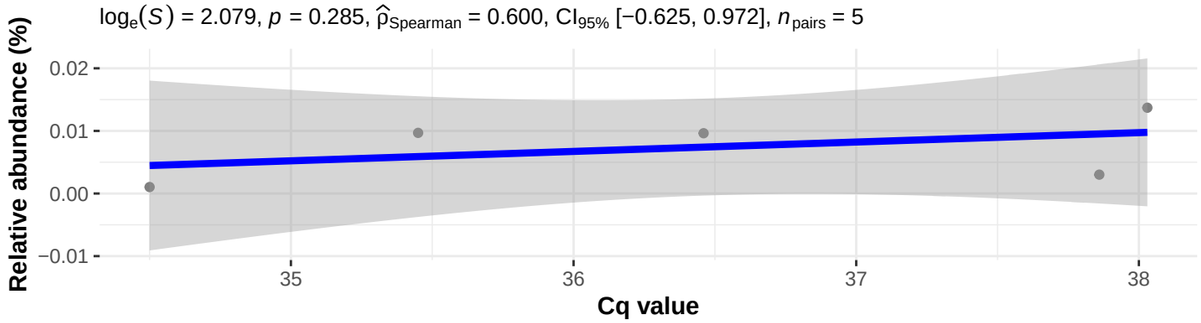


Correlation within: Tilapia_farmed_lake



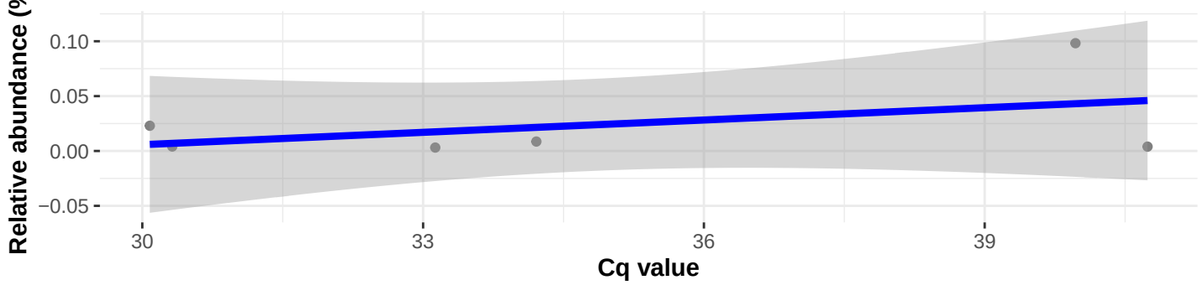
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

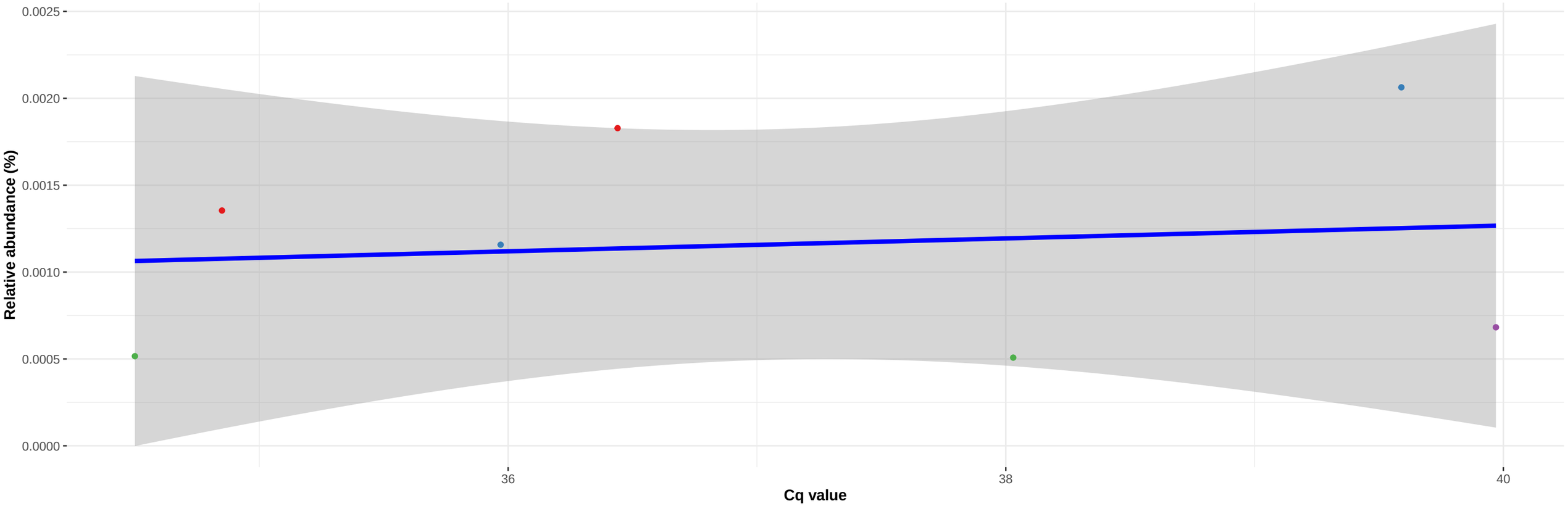


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Micrococcaceae; g__Micrococcus; NA

featureID: 09403870435de24e0d1079059a287957

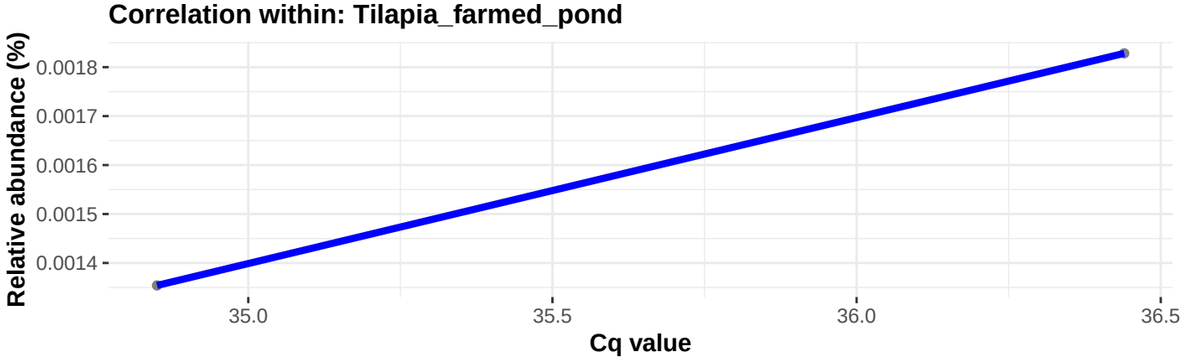
Correlation with all samples

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

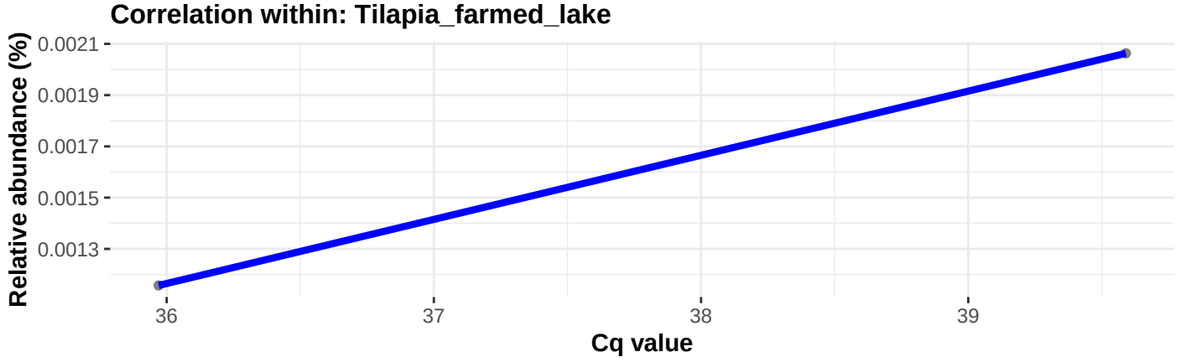


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

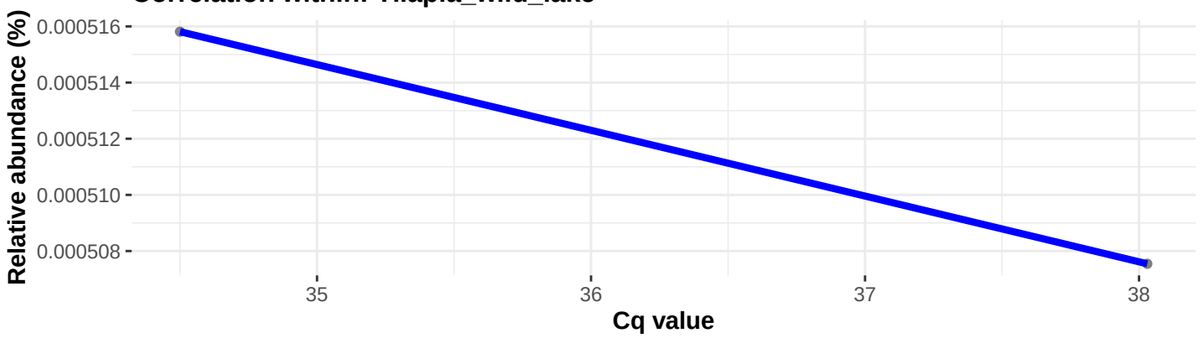
Correlation within: Tilapia_farmed_pond



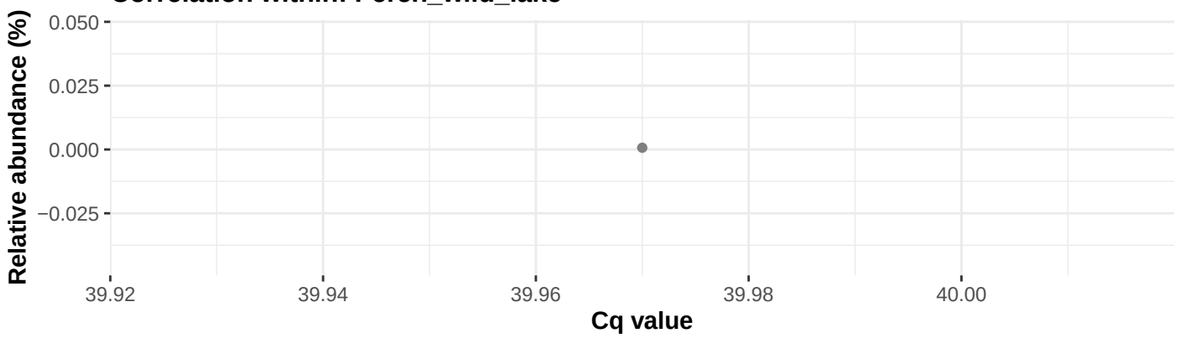
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

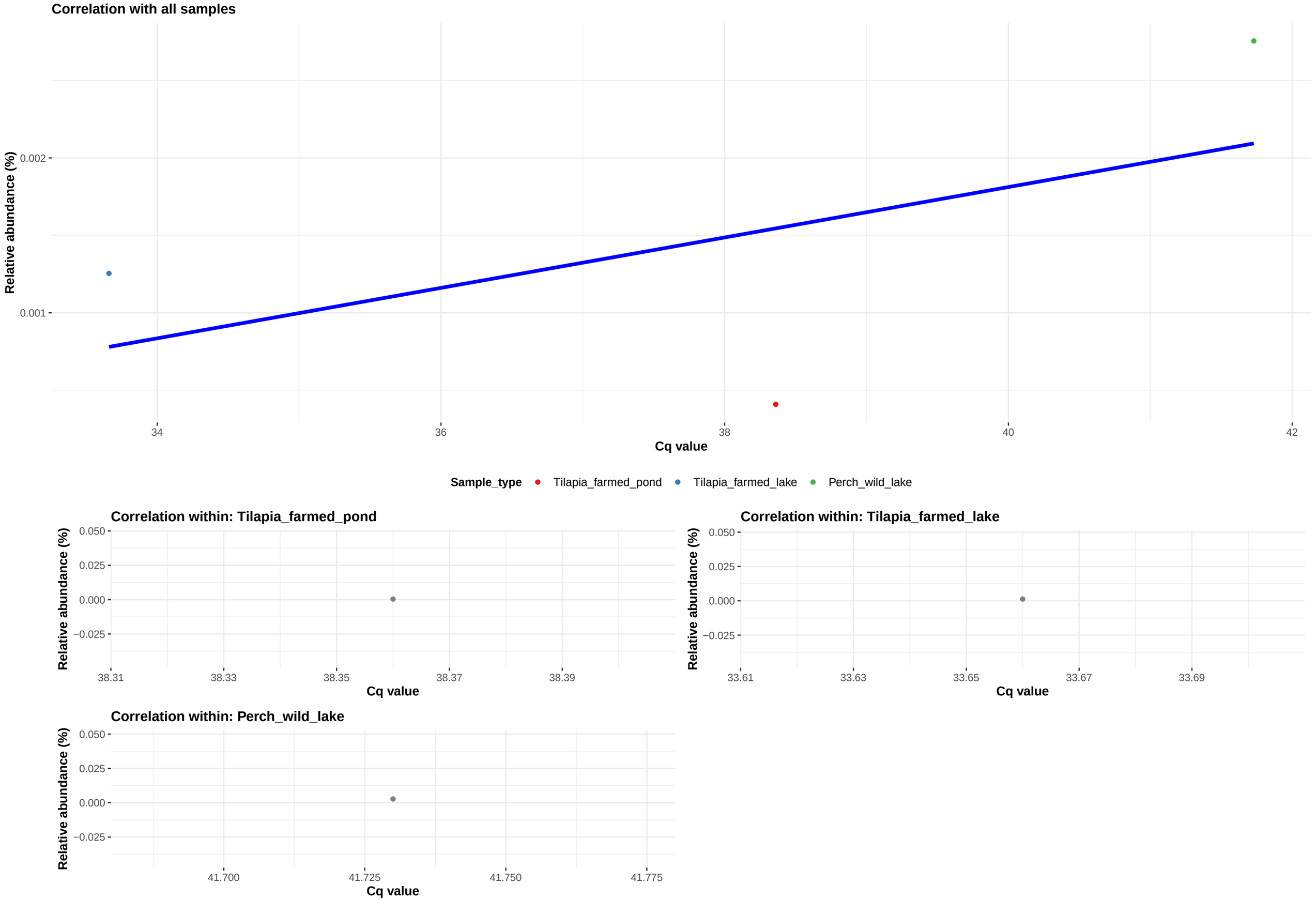


Correlation within: Perch_wild_lake



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

featureID: 07c3160551922faa7be5740ea3adc189

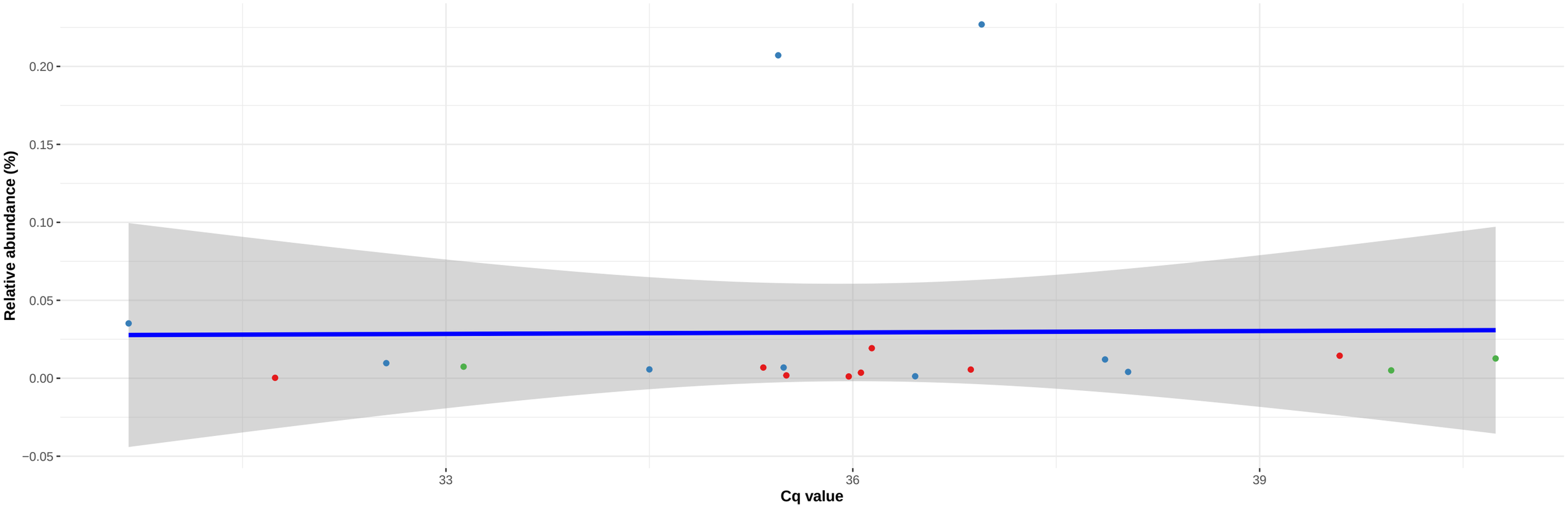


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methylocaldum; s__uncultured bacterium

featureID: 572e092b99869f99a6ae2c111893fbc5

Correlation with all samples

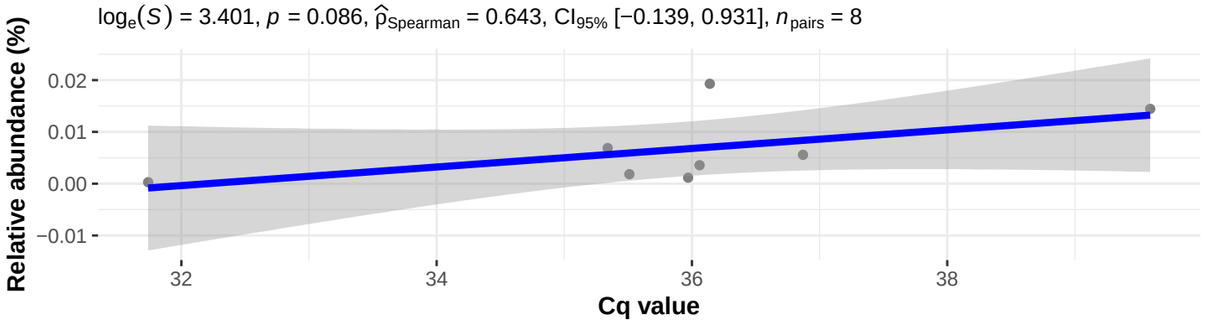
$\log_e(S)$ = 7.129, p = 0.796, $\hat{\rho}_{Spearman}$ = 0.062, $CI_{95\%}$ [−0.403, 0.501], n_{pairs} = 20



Sample_type ● Tilapia_farmed_lake ● Tilapia_wild_lake ● Perch_wild_lake

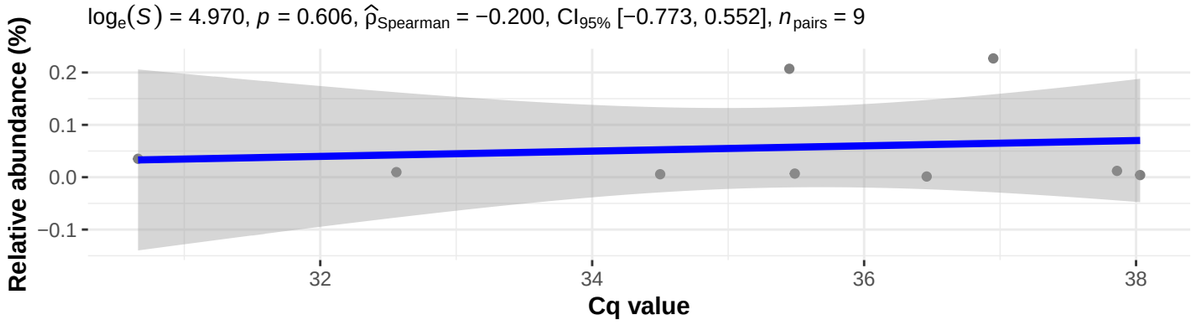
Correlation within: Tilapia_farmed_lake

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

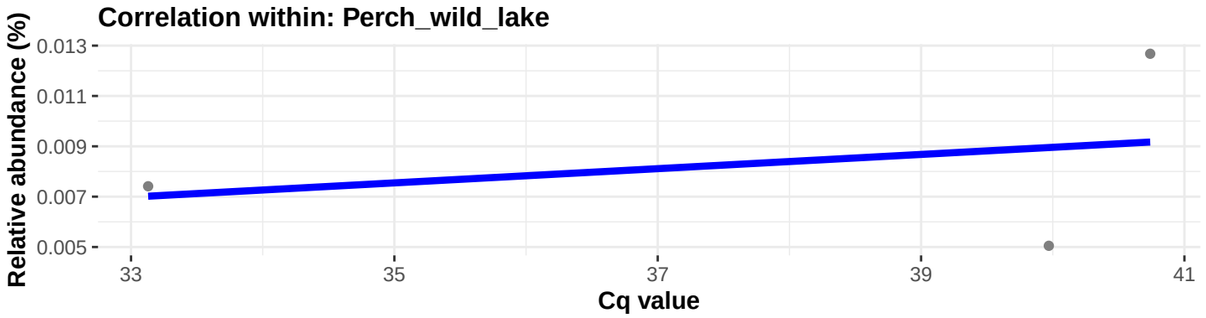


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

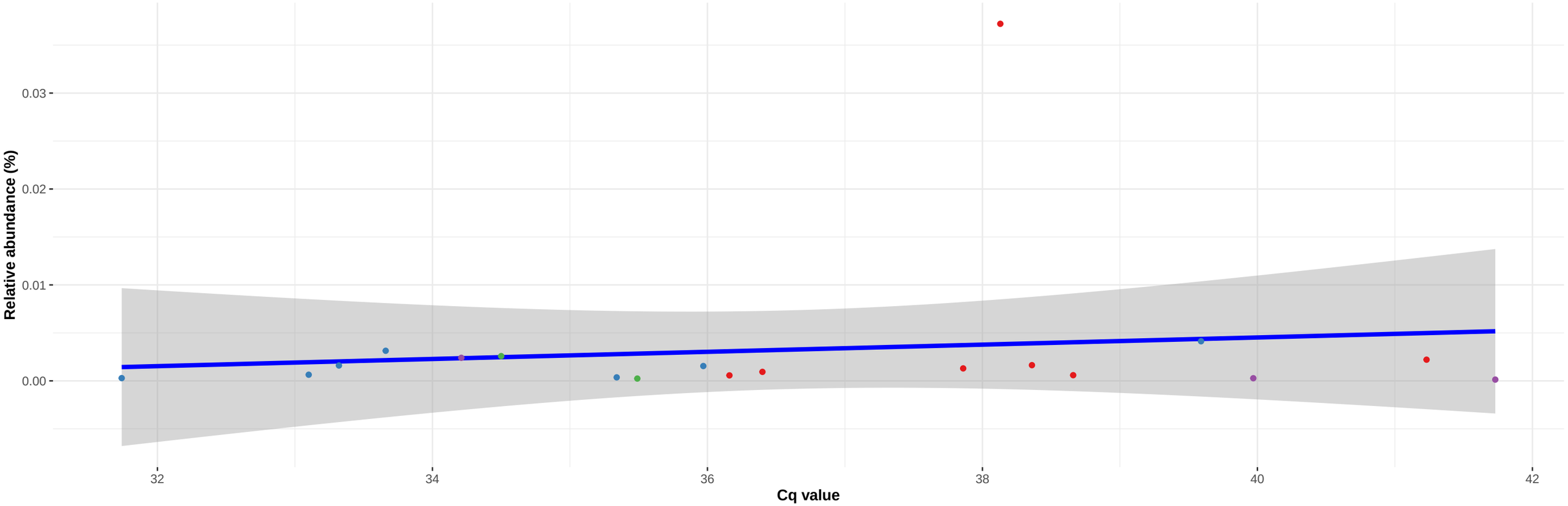


k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Propionibacteriales; f__Propionibacteriaceae; g__Cutibacterium; NA

featureID: b02a8d33d018119dedb2db15db887bfd

Correlation with all samples

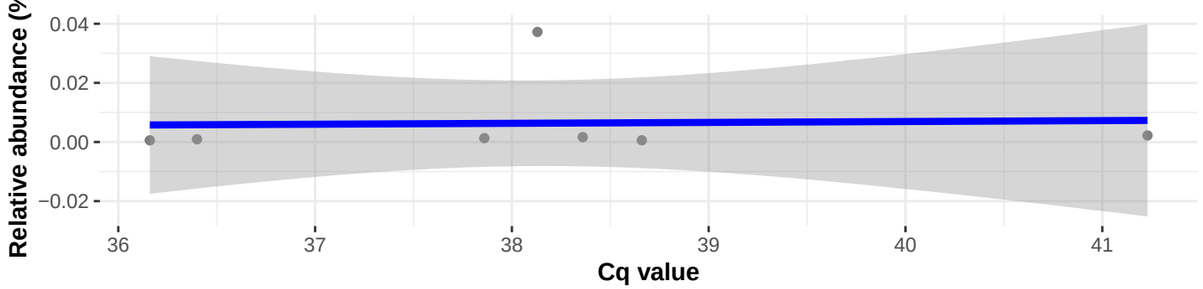
$\log_e(S)$ = 7.093, p = 0.819, $\hat{\rho}_{Spearman}$ = −0.056, $CI_{95\%}$ [−0.508, 0.420], n_{pairs} = 19



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

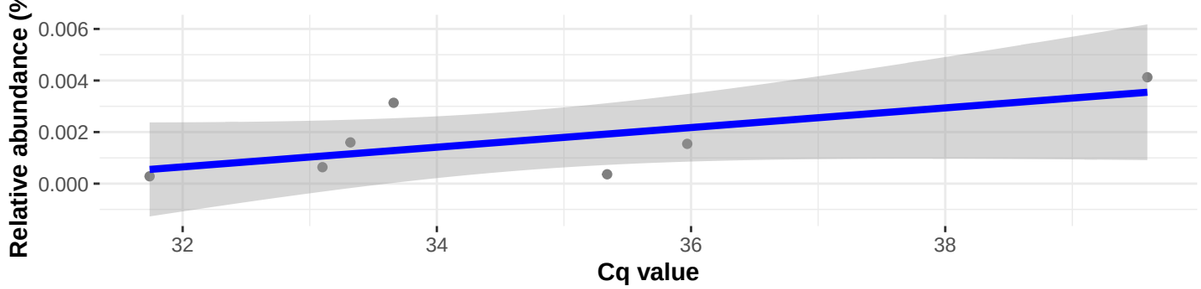
Correlation within: Tilapia_farmed_pond

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

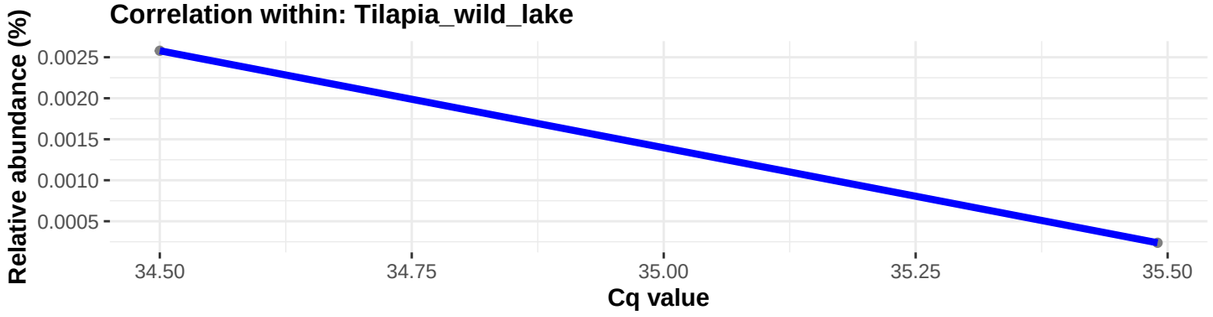


Correlation within: Tilapia_farmed_lake

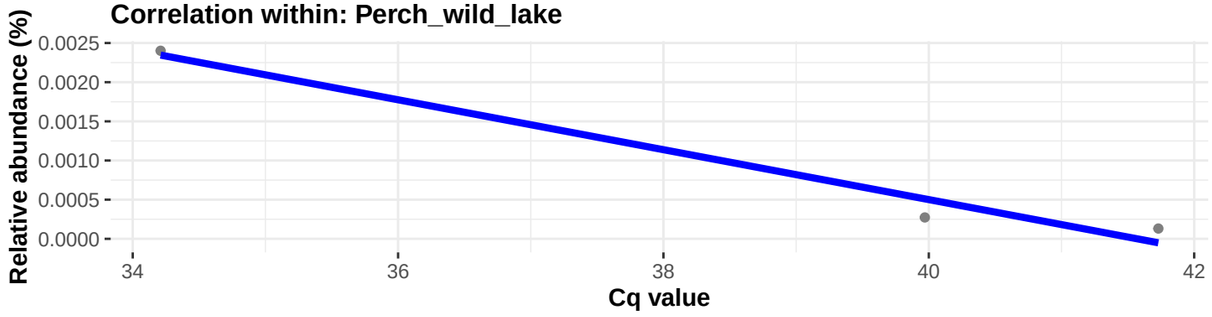
$\log_e(S)$ = 3.091, p = 0.148, $\hat{\rho}_{Spearman}$ = 0.607, $CI_{95\%}$ [−0.295, 0.937], n_{pairs} = 7



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

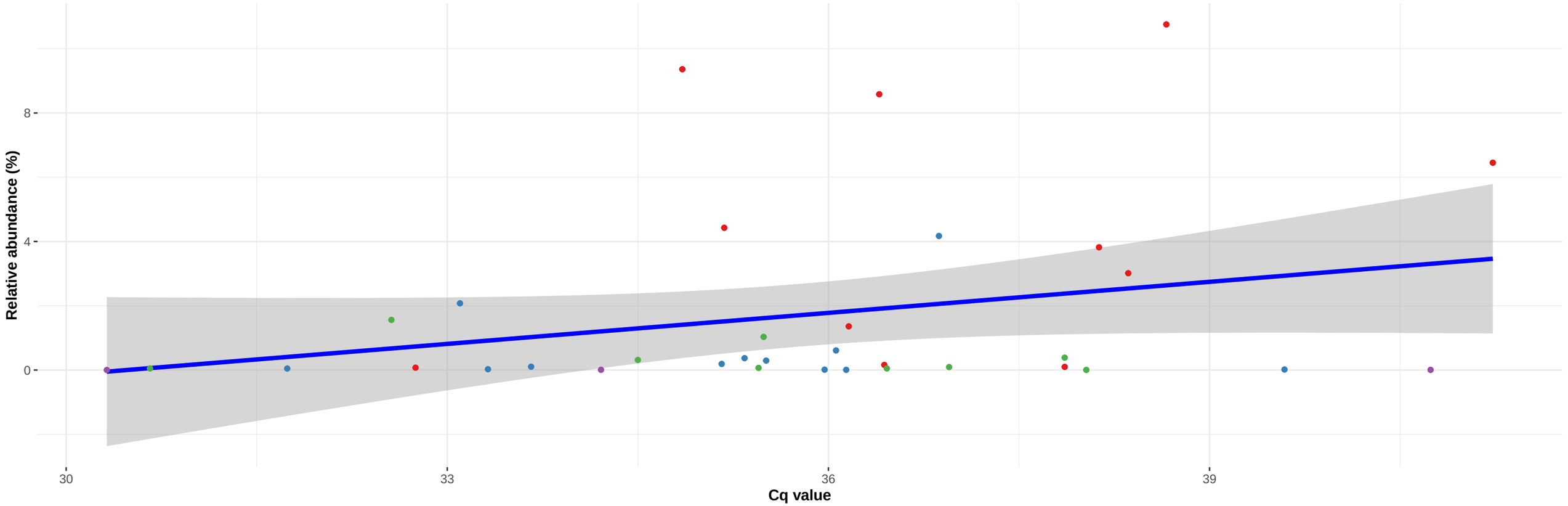


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; s__uncultured bacterium

featureID: 17d5a49452a6ccbe4473c55b3f818efc

Correlation with all samples

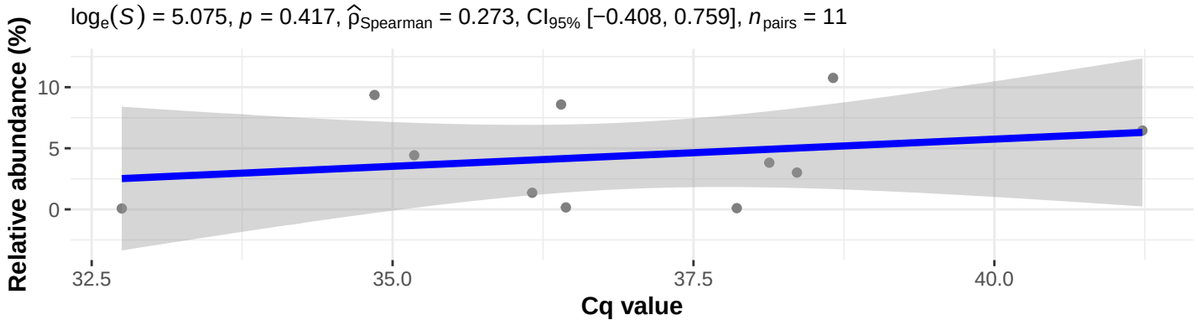
$\log_e(S)$ = 8.664, p = 0.278, $\hat{\rho}_{Spearman}$ = 0.189, $CI_{95\%}$ [−0.164, 0.499], n_{pairs} = 35



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

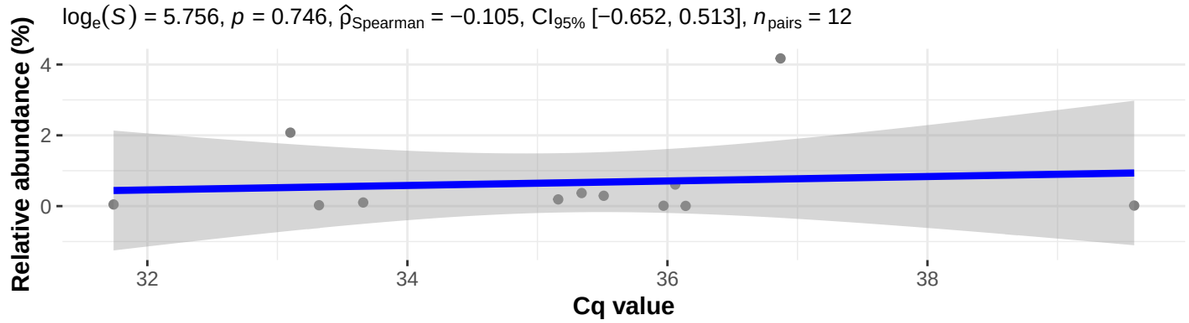
Correlation within: Tilapia_farmed_pond

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



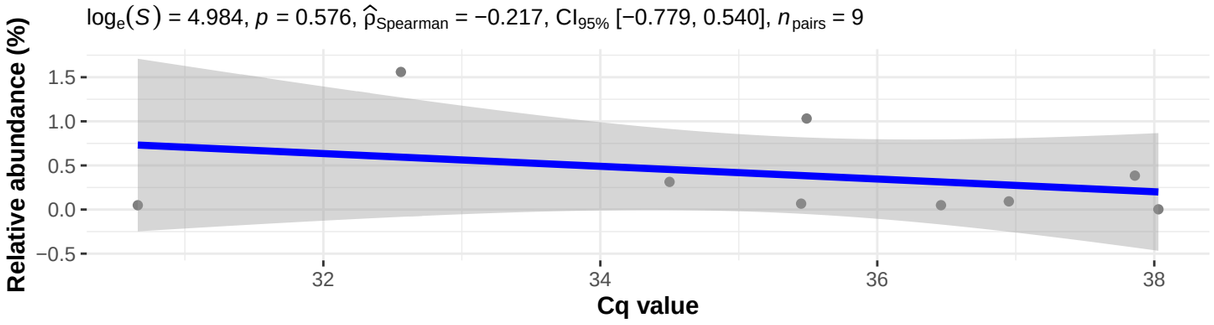
Correlation within: Tilapia_farmed_lake

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

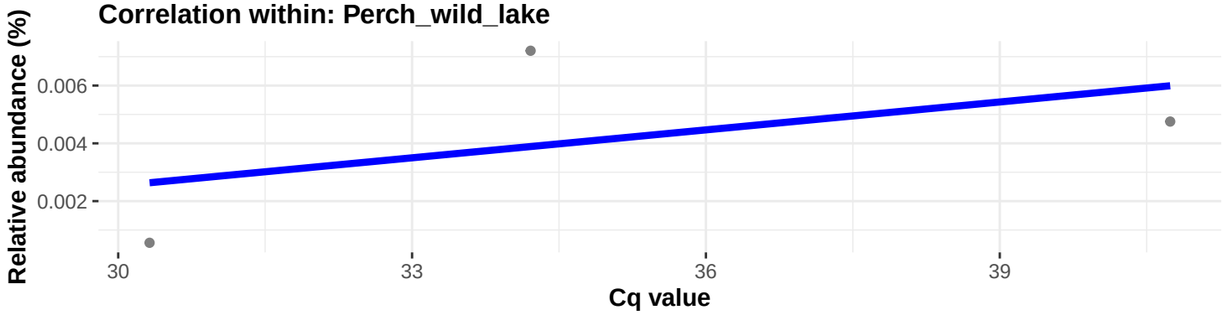


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

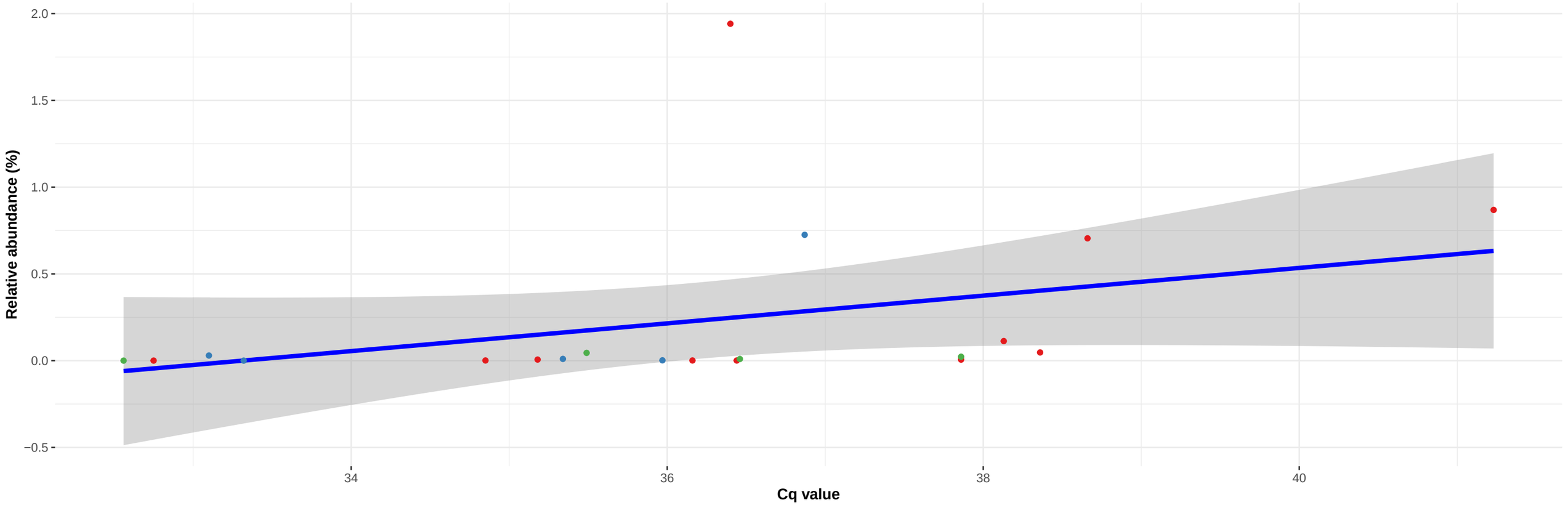


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; g__Paeniclostridium; s__uncultured bacterium

featureID: 1b00cdeda74eca68518123e3b3036f1f

Correlation with all samples

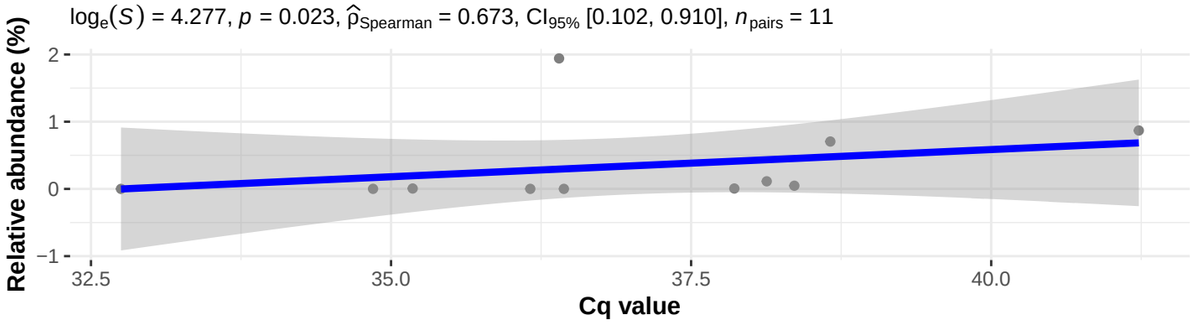
$\log_e(S)$ = 6.100, p = 0.001, $\hat{\rho}_{Spearman}$ = 0.665, $CI_{95\%}$ [0.302, 0.859], n_{pairs} = 20



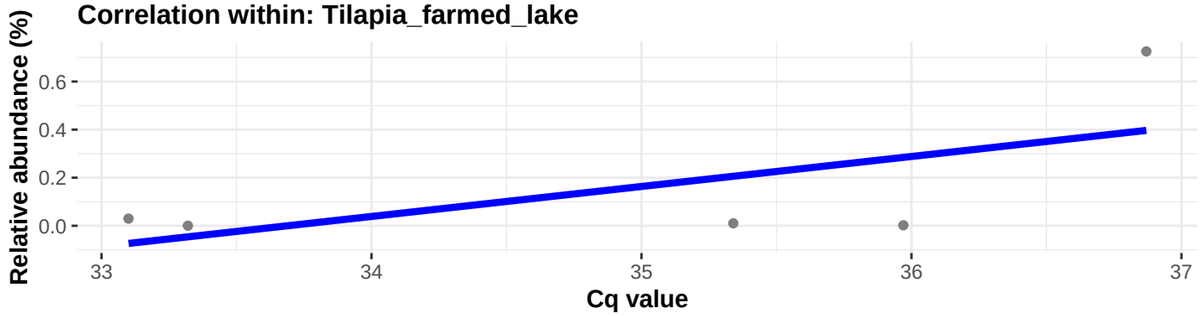
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake

Correlation within: Tilapia_farmed_pond

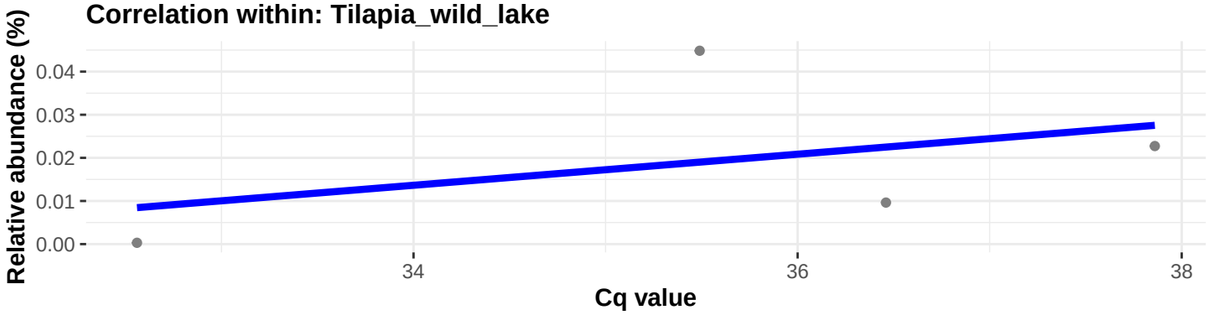
$\log_e(S)$ = 4.277, p = 0.023, $\hat{\rho}_{Spearman}$ = 0.673, $CI_{95\%}$ [0.102, 0.910], n_{pairs} = 11



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

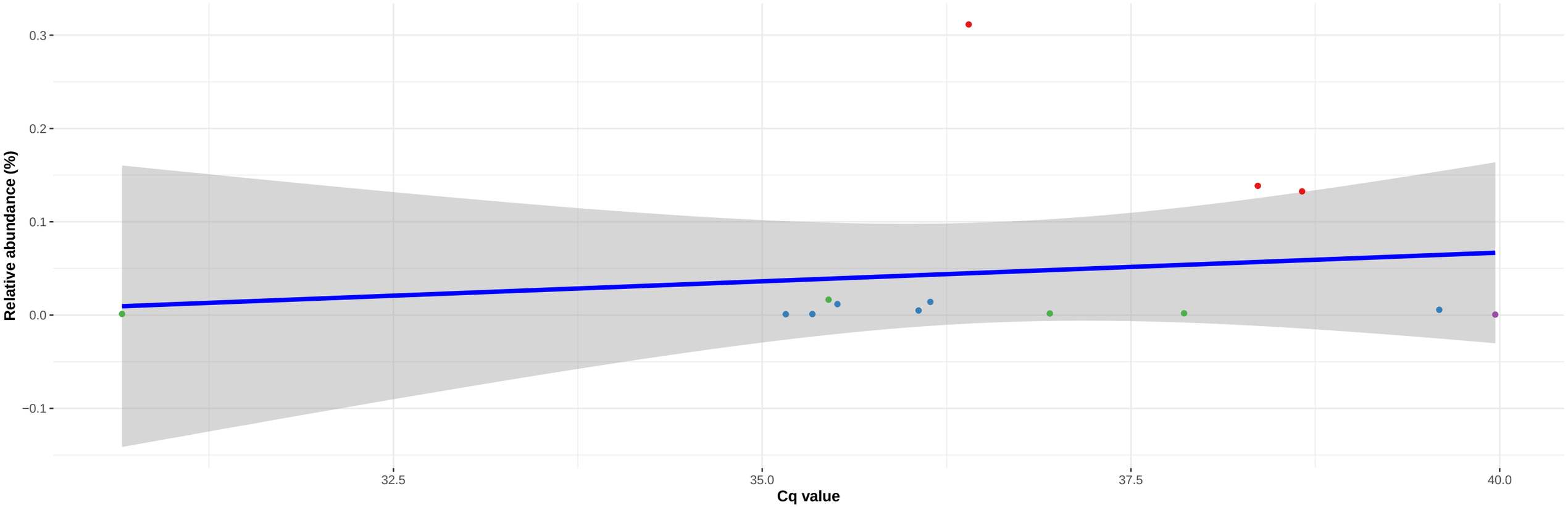


k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC−6307; NA

featureID: e7ce2cd99fee0bb346892bd41d5aae49

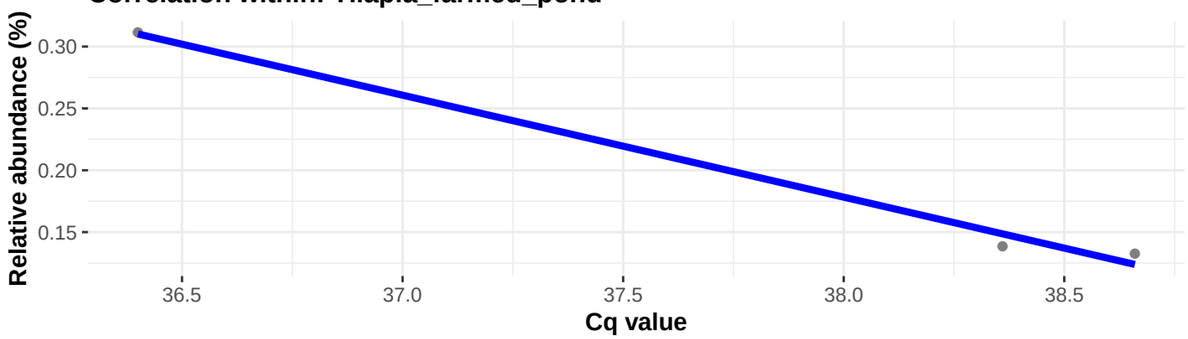
Correlation with all samples

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

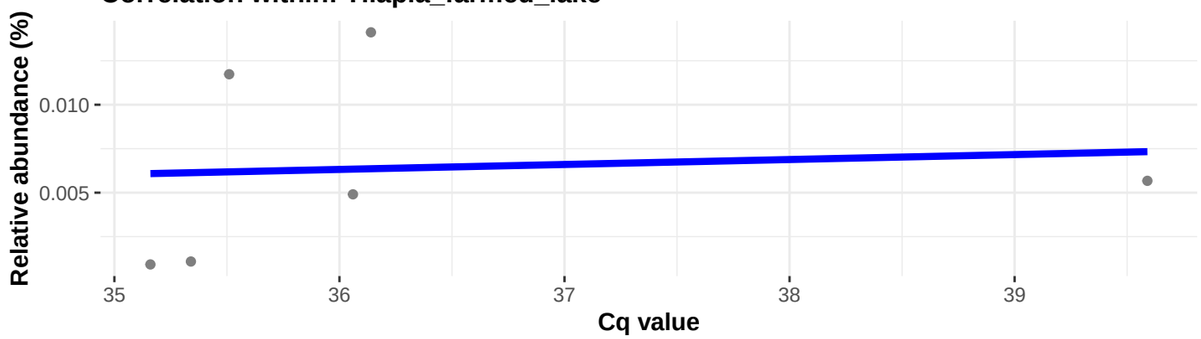


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

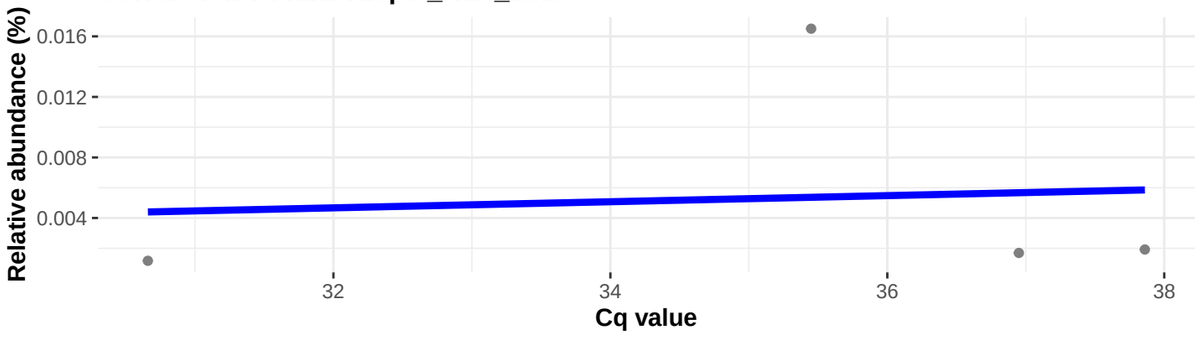
Correlation within: Tilapia_farmed_pond



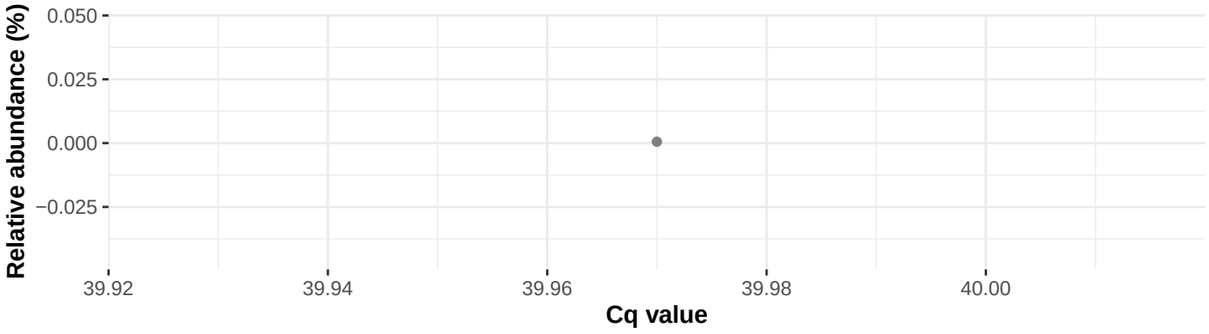
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

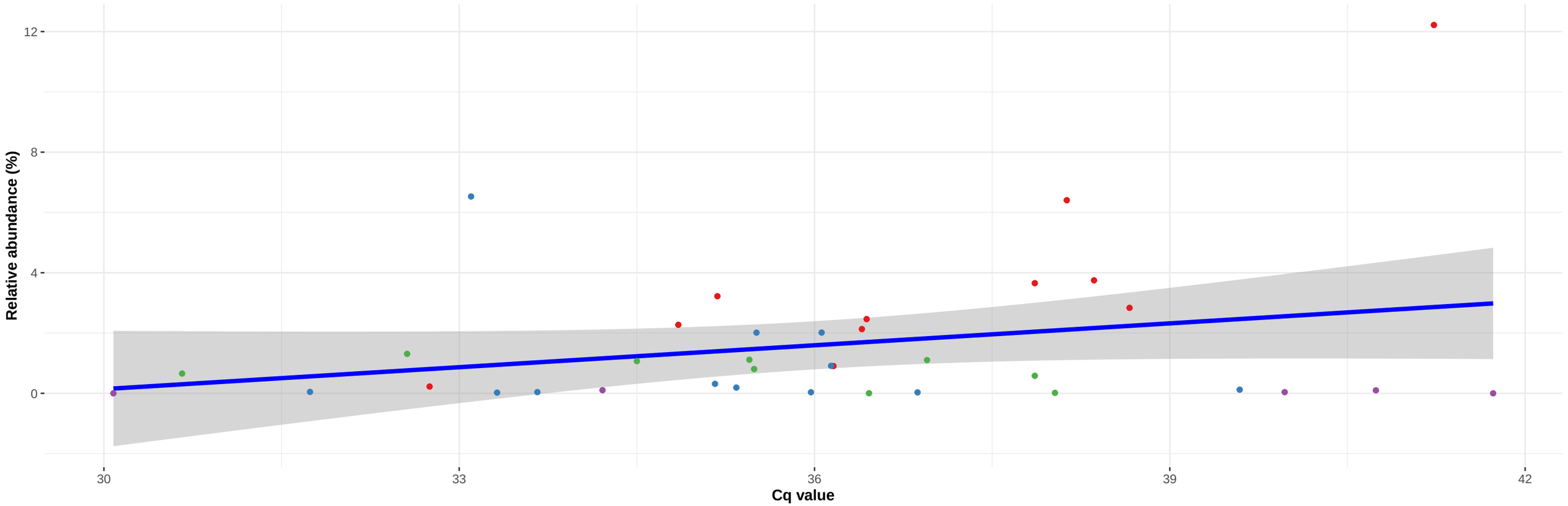


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: b7d96ace8aeb2c69a218149ac26a6ce9

Correlation with all samples

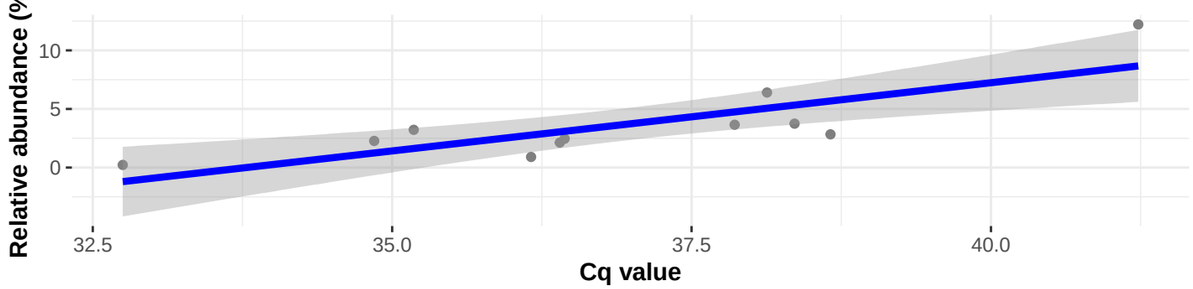
$\log_e(S)$ = 8.937, p = 0.564, $\hat{\rho}_{Spearman}$ = 0.098, $CI_{95\%}$ [−0.243, 0.417], n_{pairs} = 37



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

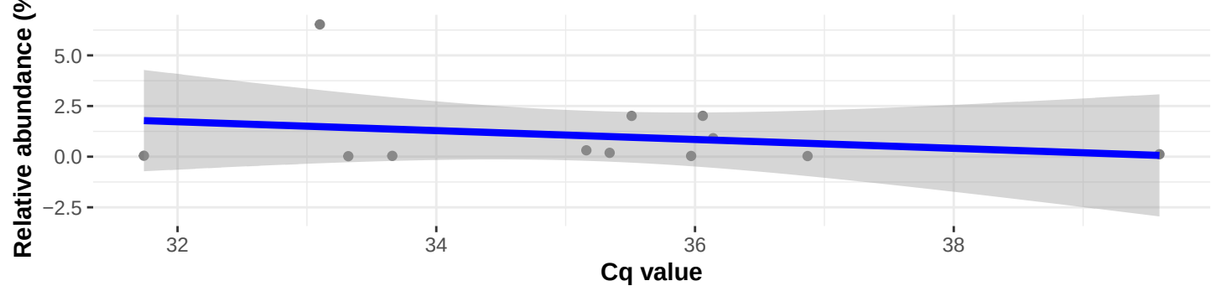
Correlation within: Tilapia_farmed_pond

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



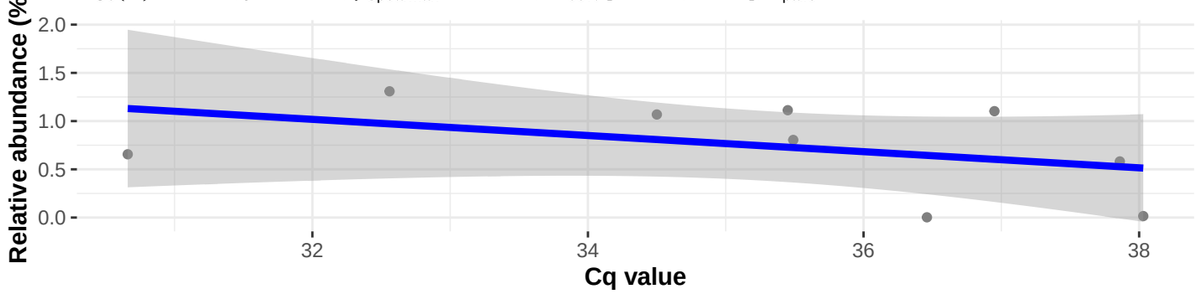
Correlation within: Tilapia_farmed_lake

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

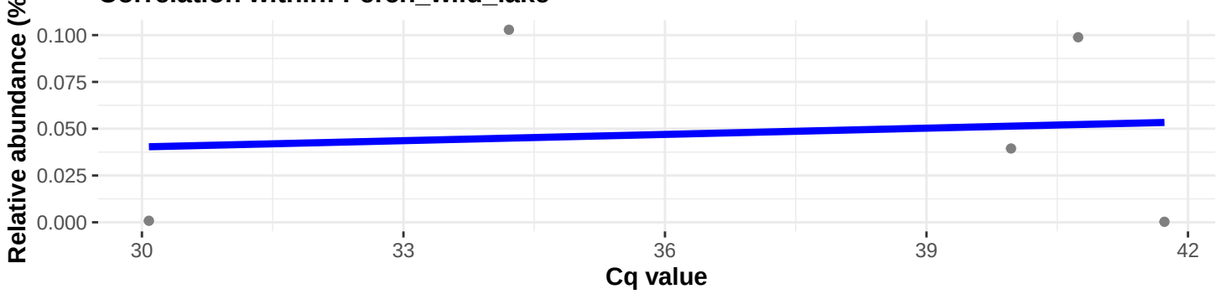


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

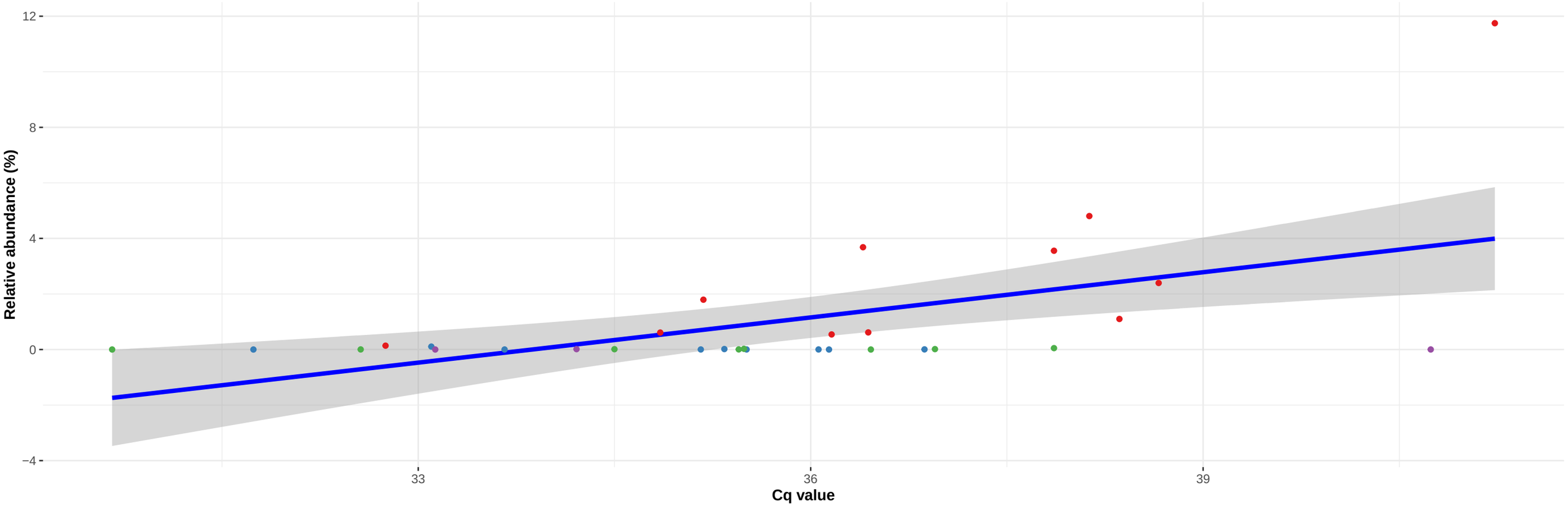


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; NA; NA

featureID: eeb27bcdfd7aaa8b5bd04631b5bea486

Correlation with all samples

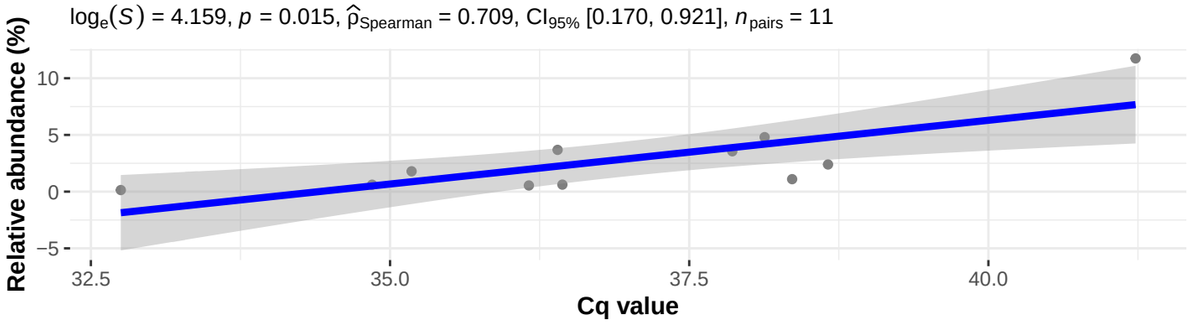
$\log_e(S)$ = 7.836, p = 0.005, $\hat{\rho}_{Spearman}$ = 0.490, $CI_{95\%}$ [0.153, 0.725], n_{pairs} = 31



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

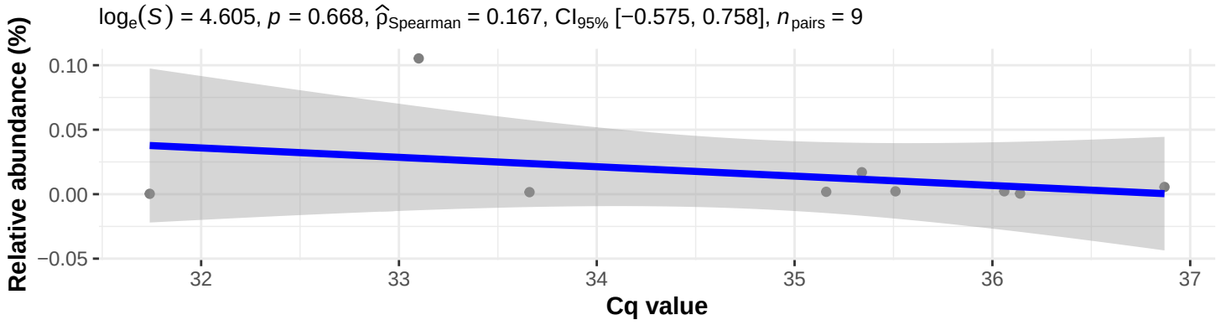
Correlation within: Tilapia_farmed_pond

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



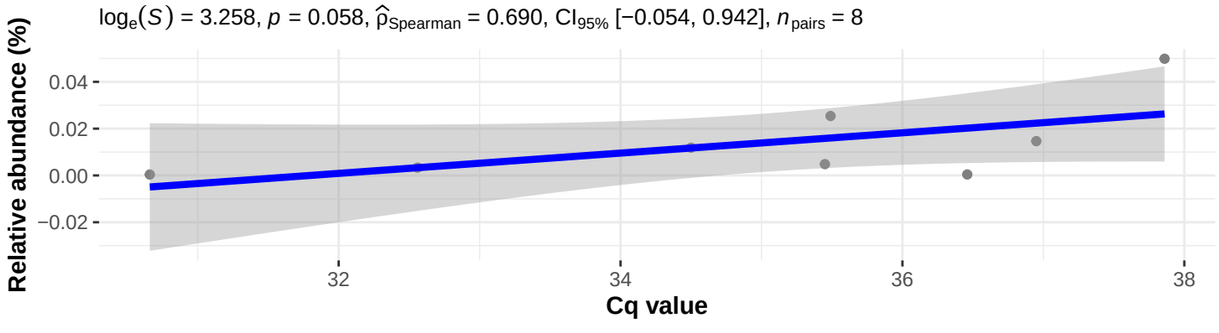
Correlation within: Tilapia_farmed_lake

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

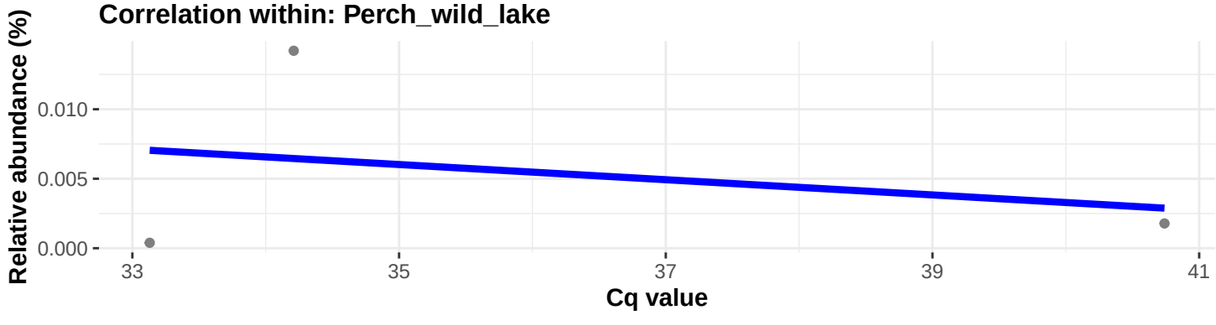


Correlation within: Tilapia_wild_lake

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

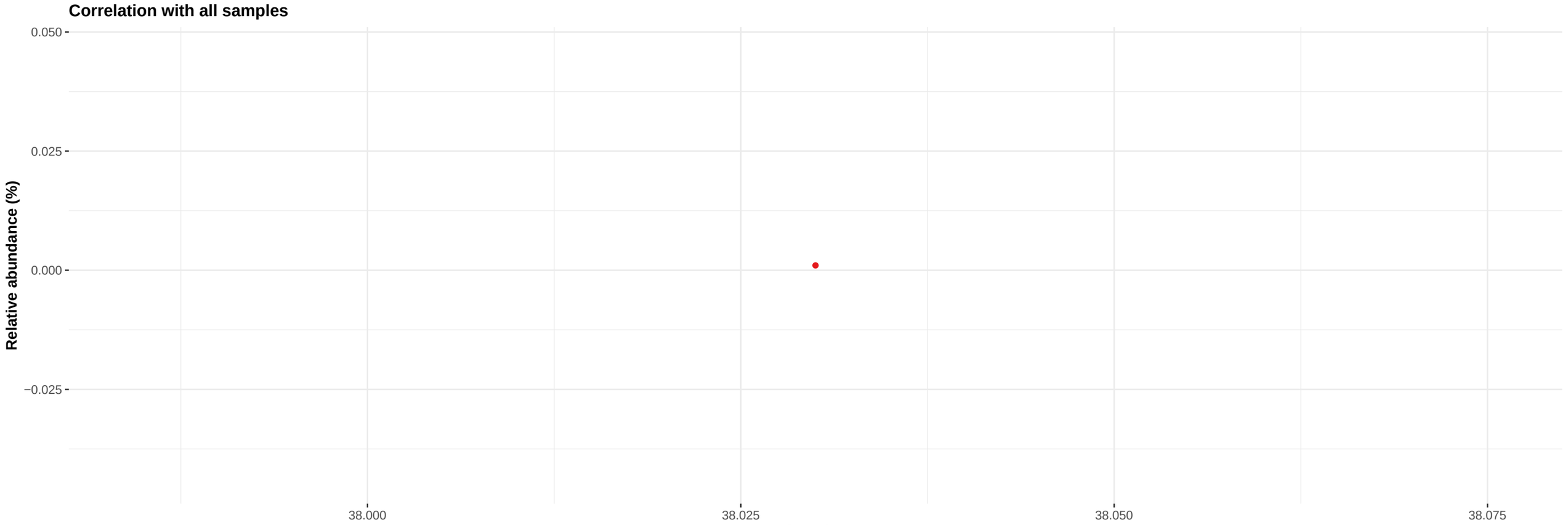


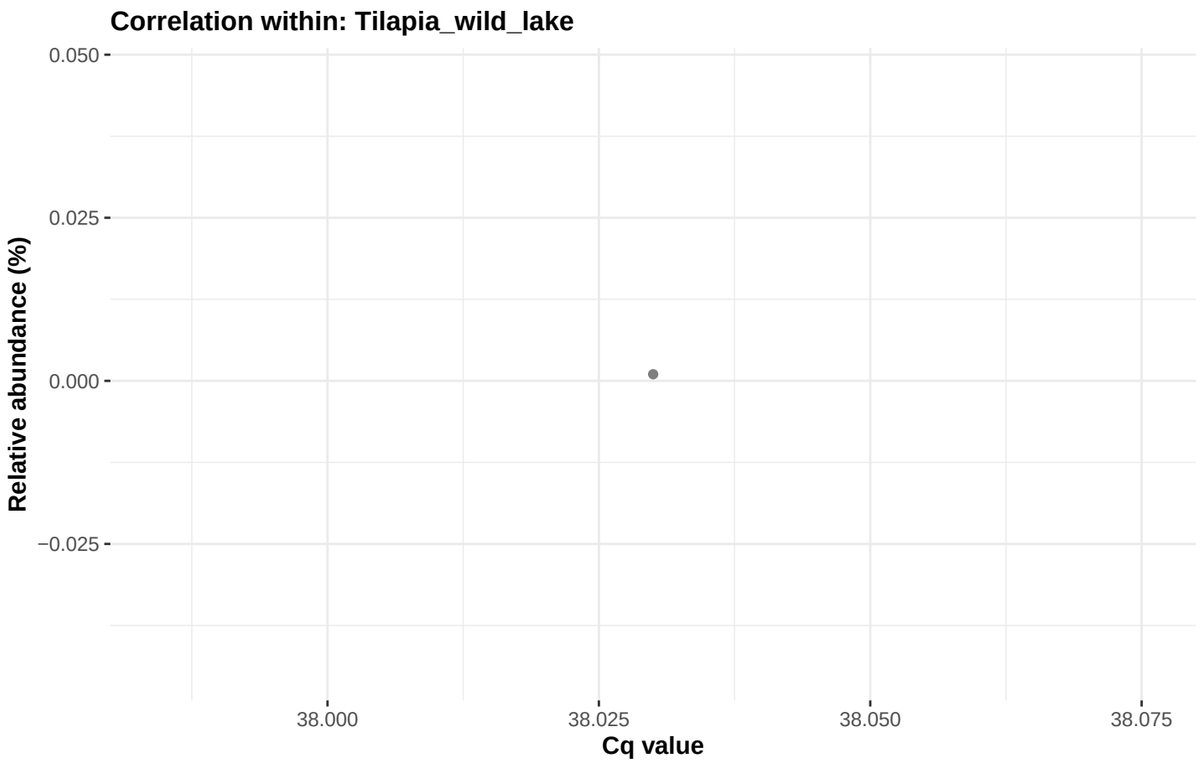
Correlation within: Perch_wild_lake



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

featureID: ba4ab8dea6b4223dbc9ed5bbf3ea60ea



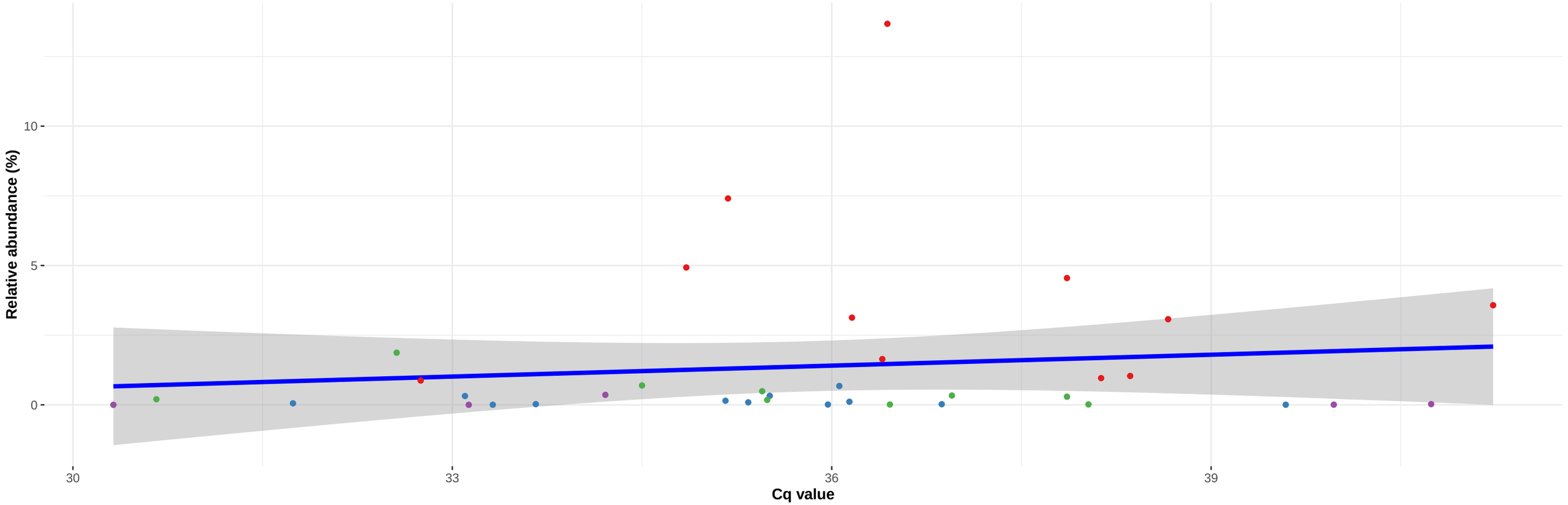


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: d112db53cc44b1be8395e16355a2109d

Correlation with all samples

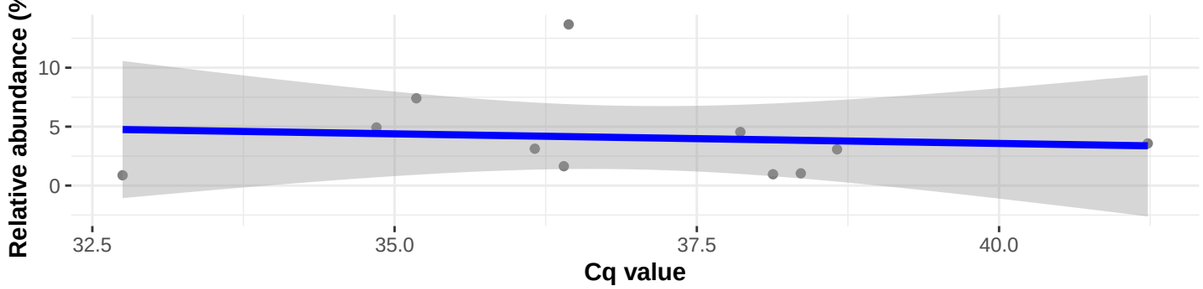
$\log_e(S)$ = 8.909, p = 0.469, $\hat{\rho}_{Spearman}$ = 0.123, $CI_{95\%}$ [−0.219, 0.438], n_{pairs} = 37



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

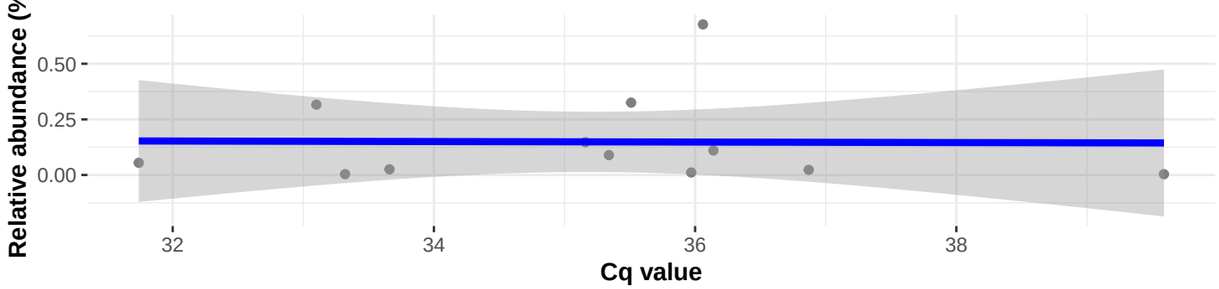
Correlation within: Tilapia_farmed_pond

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



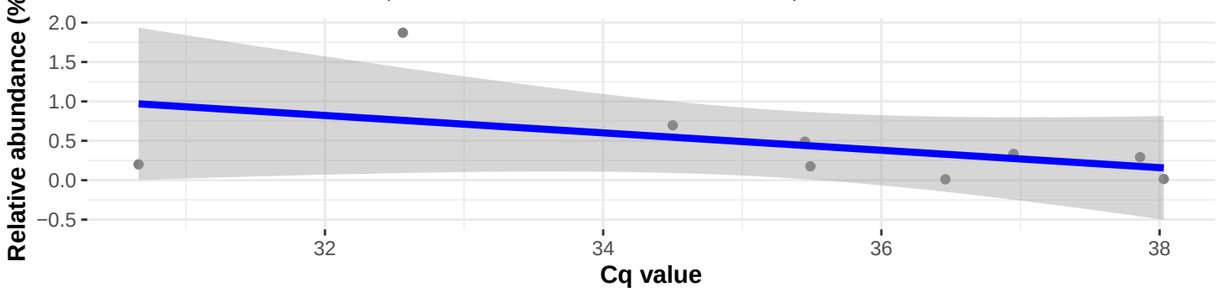
Correlation within: Tilapia_farmed_lake

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

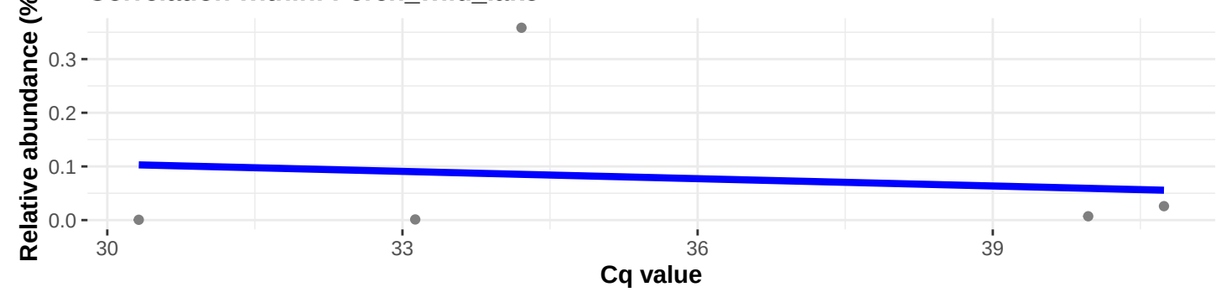


Correlation within: Tilapia_wild_lake

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



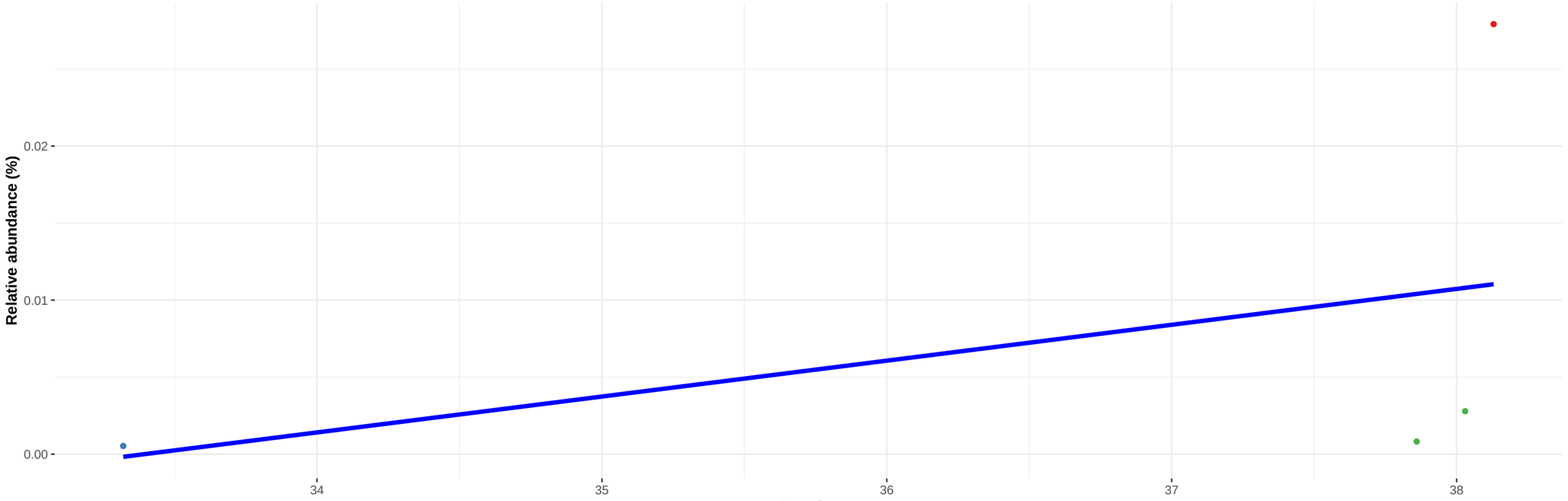
Correlation within: Perch_wild_lake



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

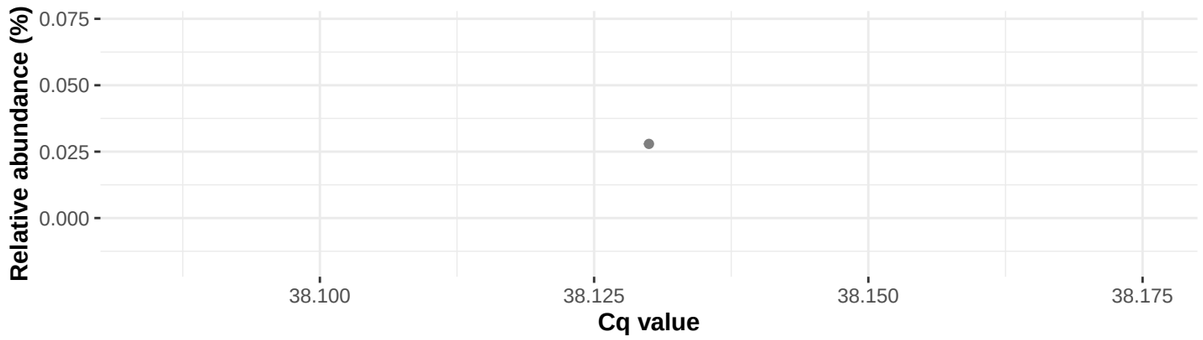
featureID: d4e740bc5c2587cbbb188e8e30026611

Correlation with all samples

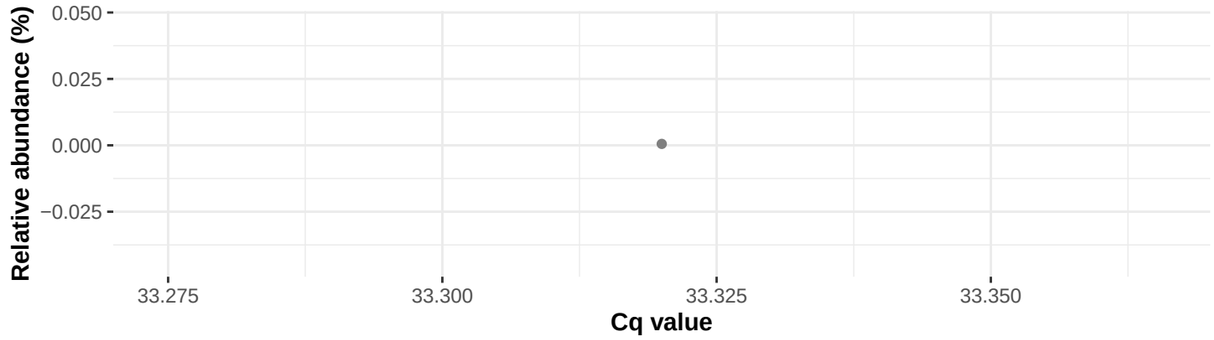


Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake

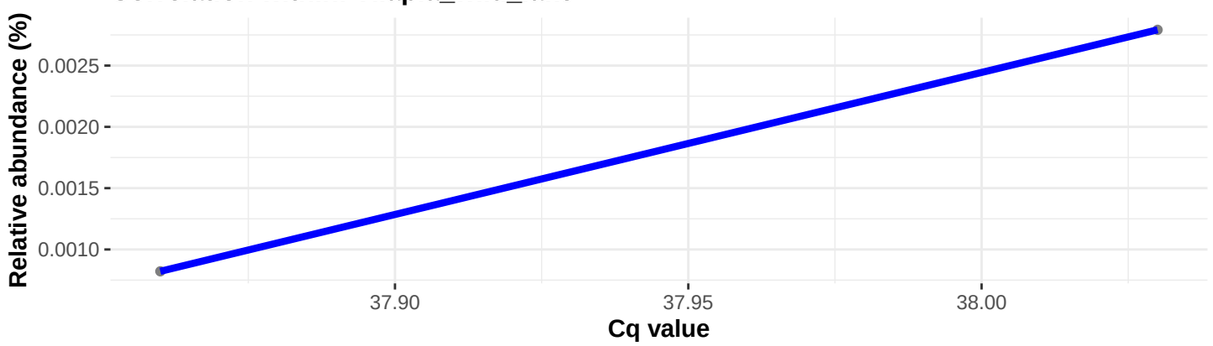
Correlation within: Tilapia_farmed_pond



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

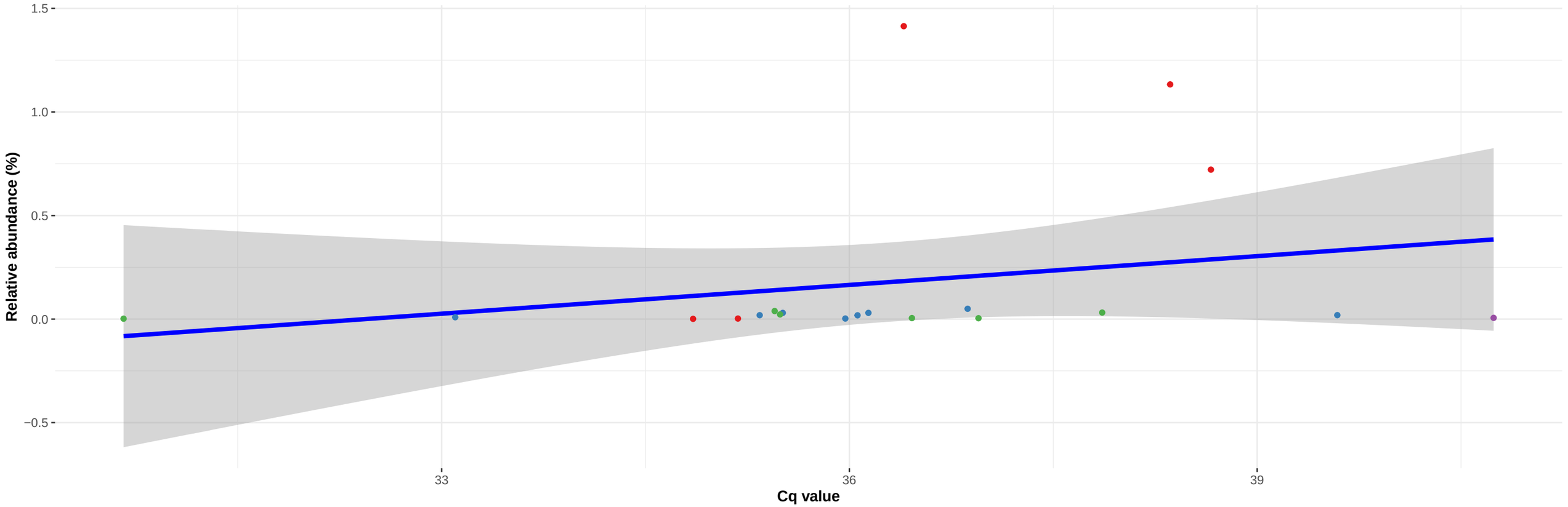


k__Bacteria; p__Cyanobacteria; c__Oxyphotobacteria; o__Synechococcales; f__Cyanobiaceae; g__Cyanobium PCC−6307; NA

featureID: 12e90f65e34a30ad48d9e3f3b842b30d

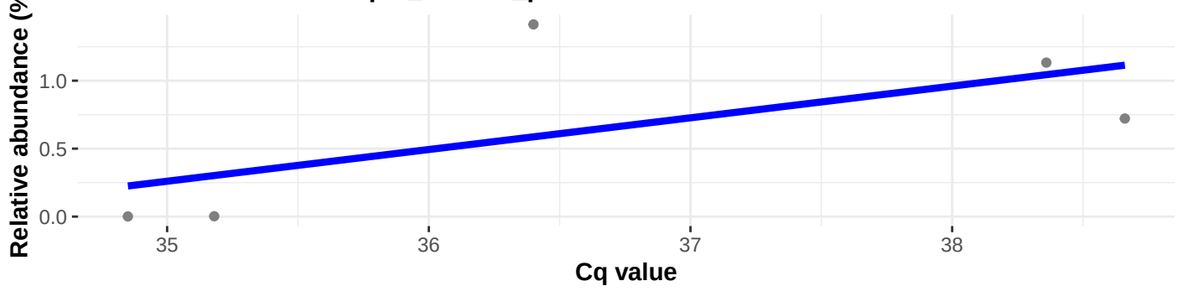
Correlation with all samples

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



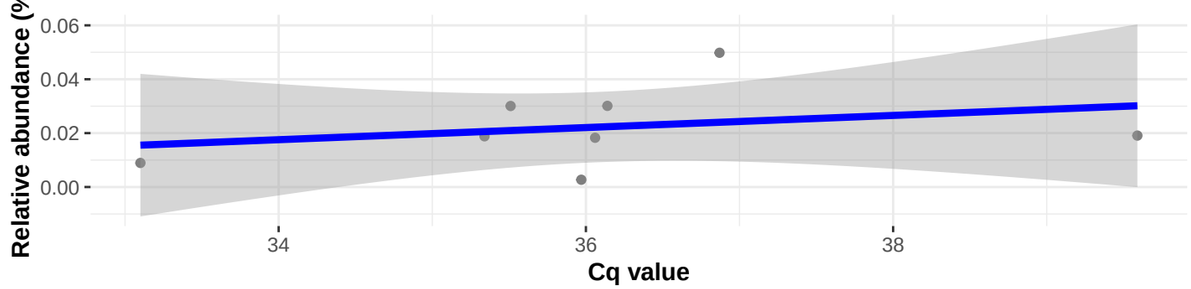
Sample_type Tilapia_farmed_pond · Tilapia_farmed_lake · Tilapia_wild_lake · Perch_wild_lake

Correlation within: Tilapia_farmed_pond



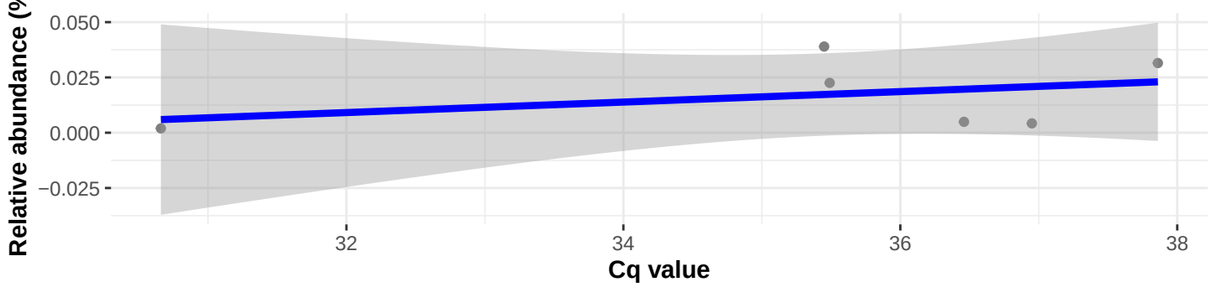
Correlation within: Tilapia_farmed_lake

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

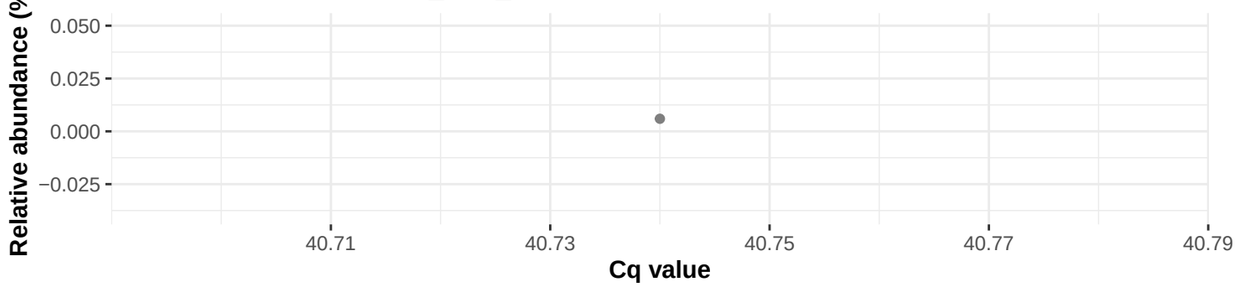


Correlation within: Tilapia_wild_lake

$\log_e(S)$ = 3.332, p = 0.704, $\hat{\rho}_{Spearman}$ = 0.200, $CI_{95\%}$ [−0.745, 0.878], n_{pairs} = 6



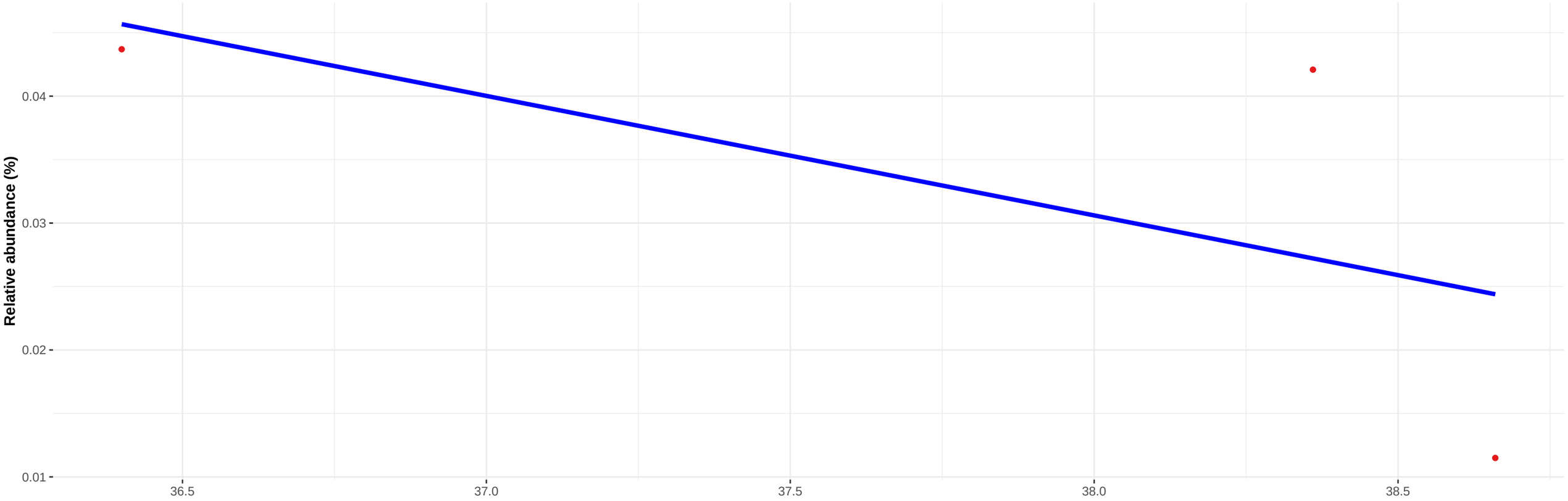
Correlation within: Perch_wild_lake



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

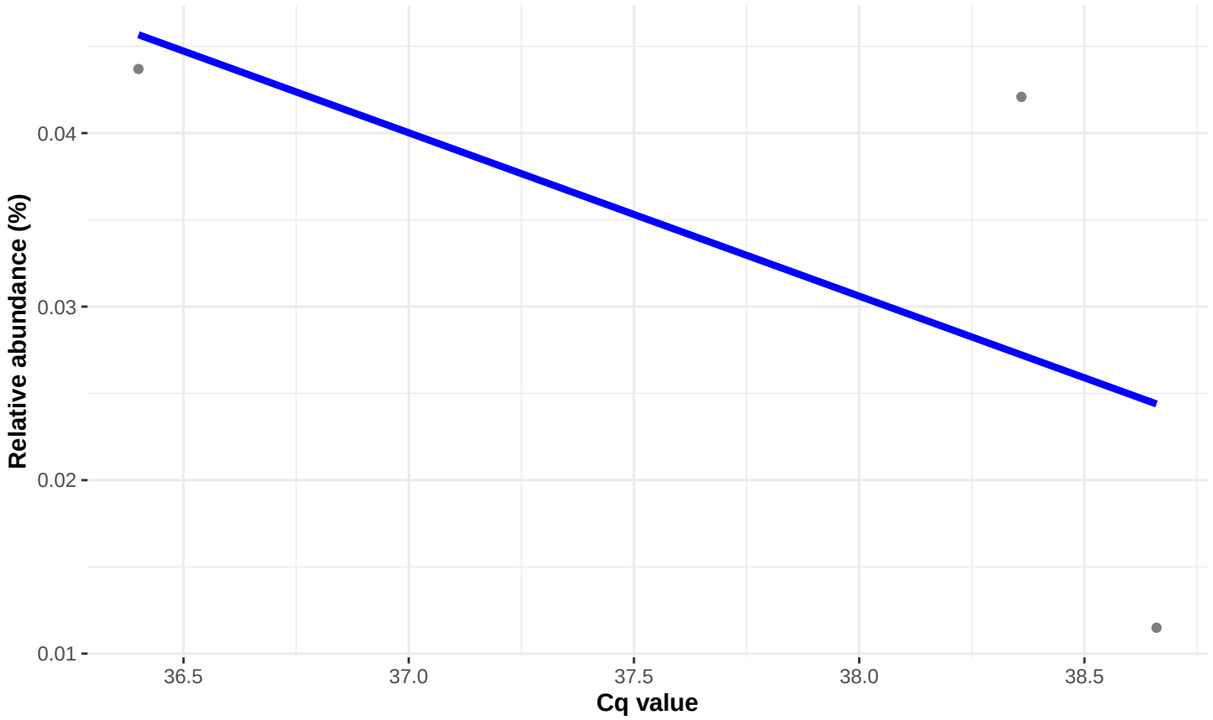
featureID: 35e38ee9b5dff68dbd41115b73741414

Correlation with all samples



Sample_type Tilapia_farmed_pond

Correlation within: Tilapia_farmed_pond

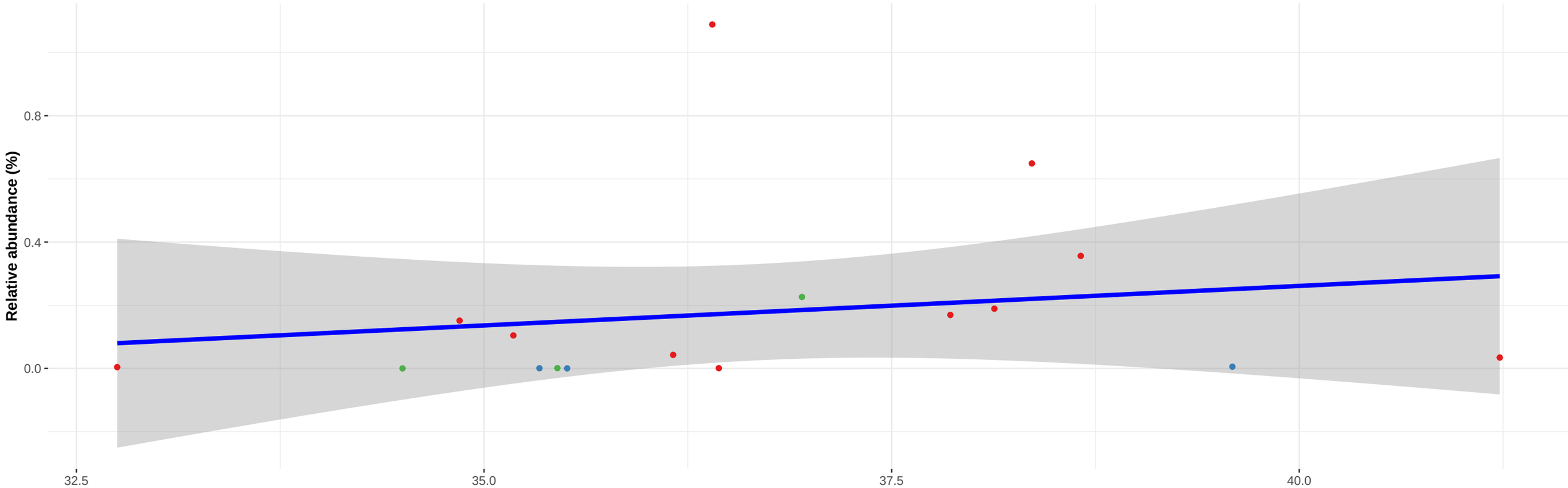


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Methylococcales; f__Methylococcaceae; g__Methyloparacoccus; s__uncultured bacterium

featureID: 66c3e0b10570a19d613f692d701da8d0

Correlation with all samples

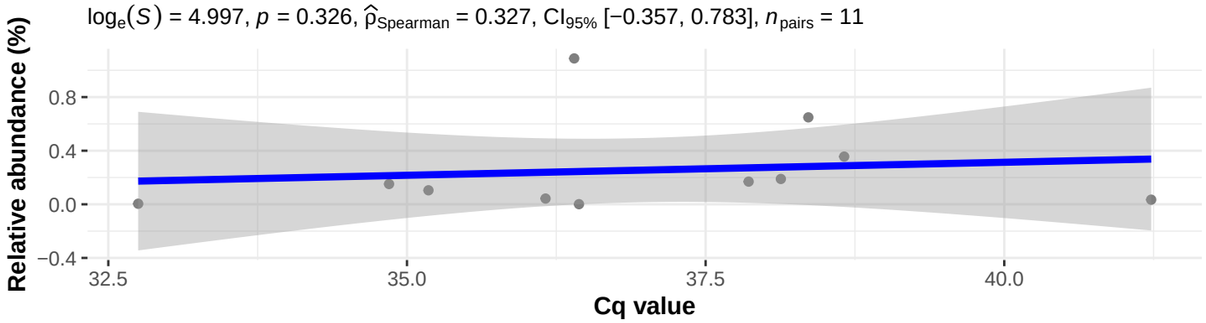
$\log_e(S)$ = 6.068, p = 0.057, $\hat{\rho}_{Spearman}$ = 0.471, $CI_{95\%}$ [−0.028, 0.782], n_{pairs} = 17



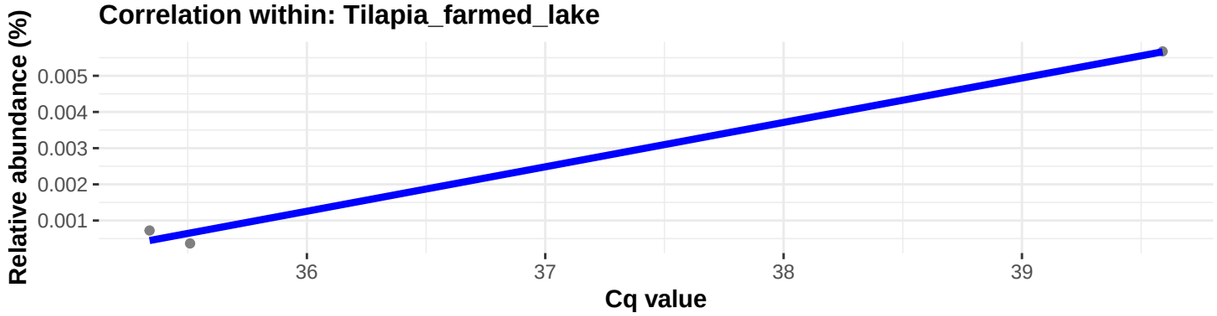
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake

Correlation within: Tilapia_farmed_pond

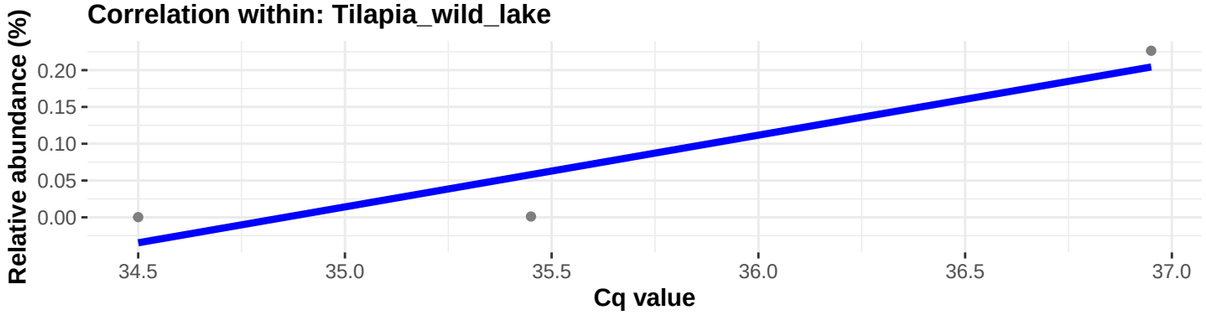
$\log_e(S)$ = 4.997, p = 0.326, $\hat{\rho}_{Spearman}$ = 0.327, $CI_{95\%}$ [−0.357, 0.783], n_{pairs} = 11



Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake

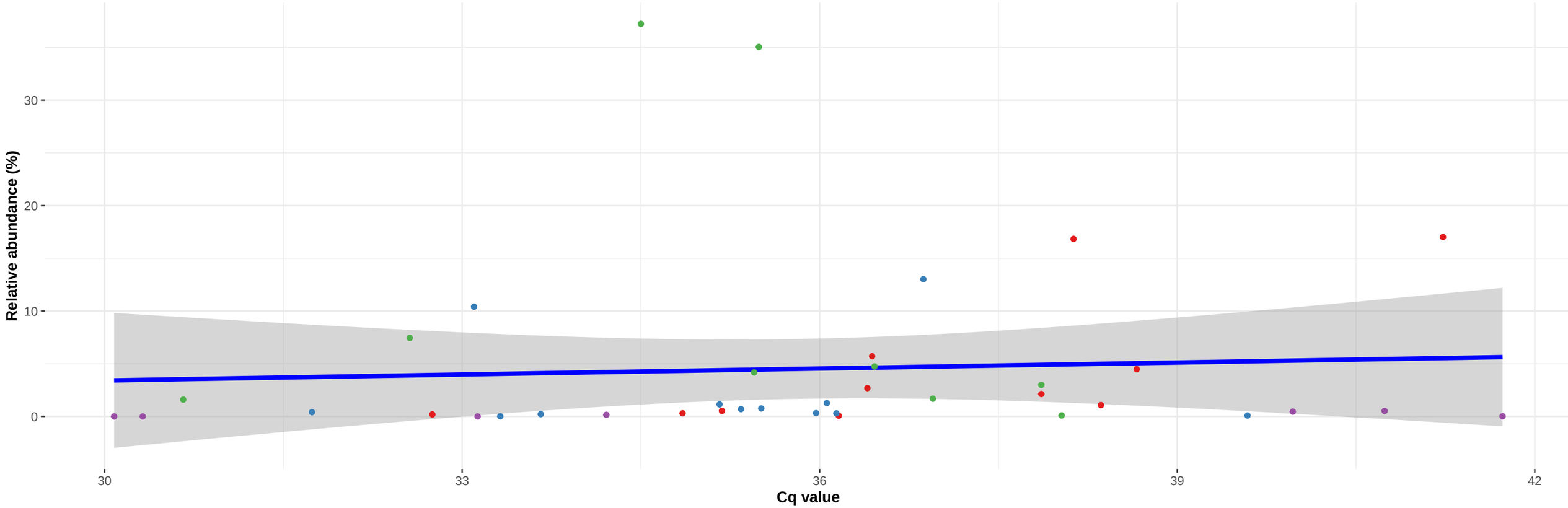


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Peptostreptococcaceae; NA; NA

featureID: 8ebe63f7e7dd6bd4ca4dca5a66df57c2

Correlation with all samples

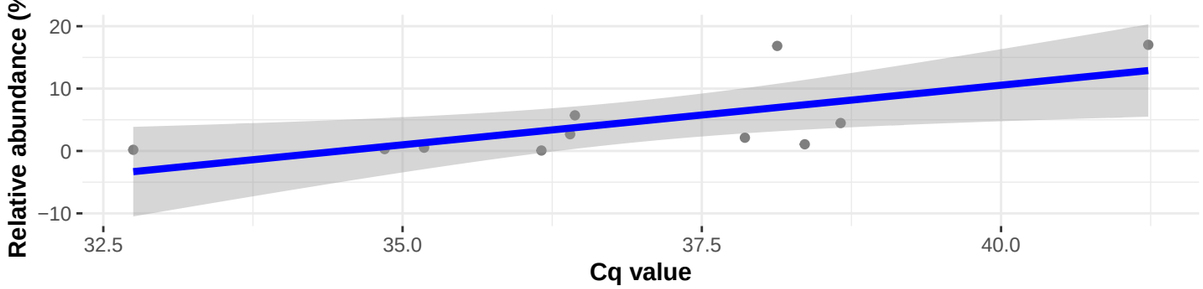
$\log_e(S)$ = 8.925, p = 0.143, $\hat{\rho}_{Spearman}$ = 0.239, $CI_{95\%}$ [−0.092, 0.523], n_{pairs} = 39



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

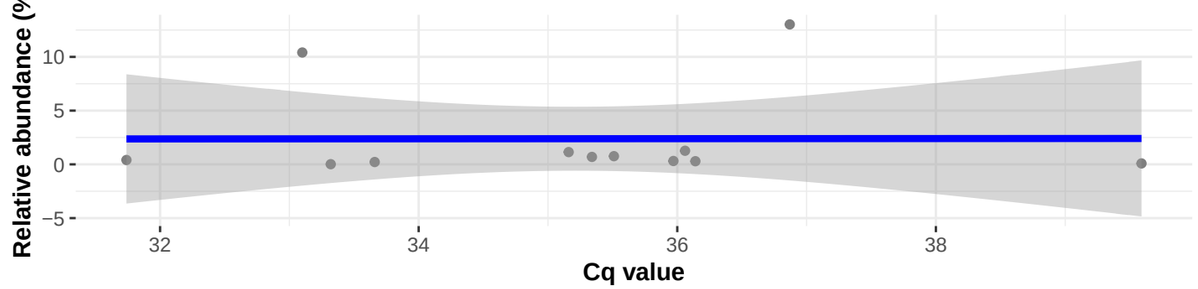
Correlation within: Tilapia_farmed_pond

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



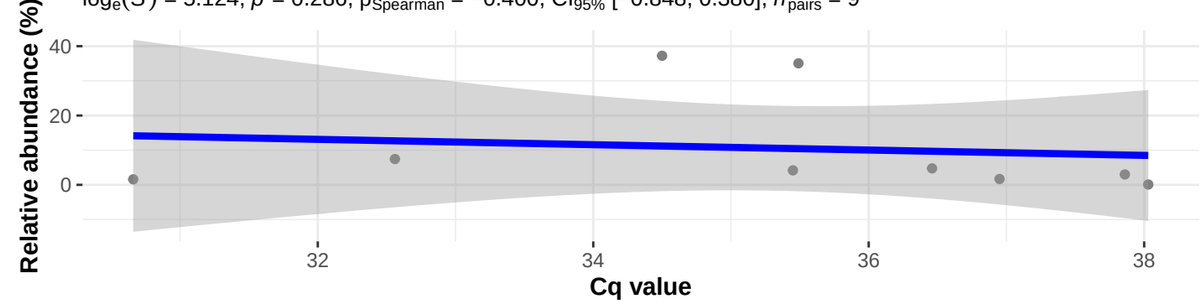
Correlation within: Tilapia_farmed_lake

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



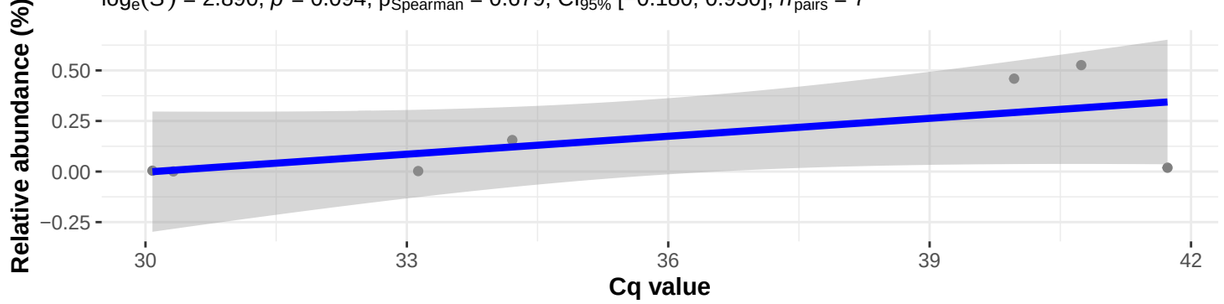
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

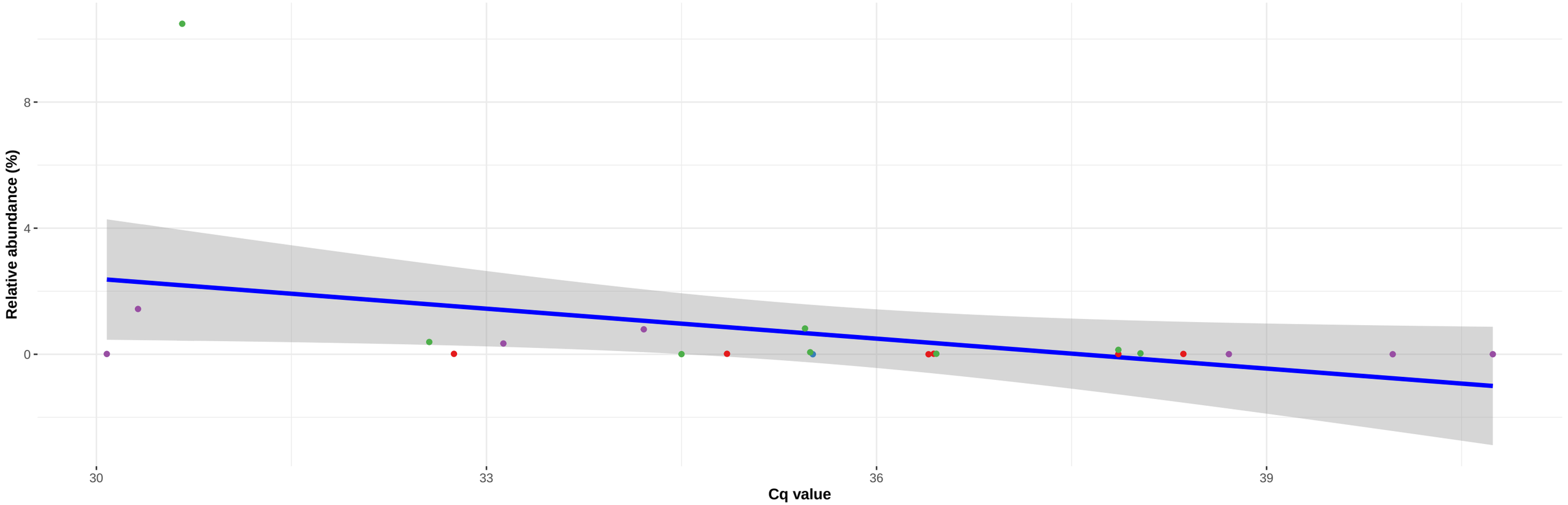


k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Cetobacterium; NA

featureID: 50b18b94311c09ff882fda744bc15200

Correlation with all samples

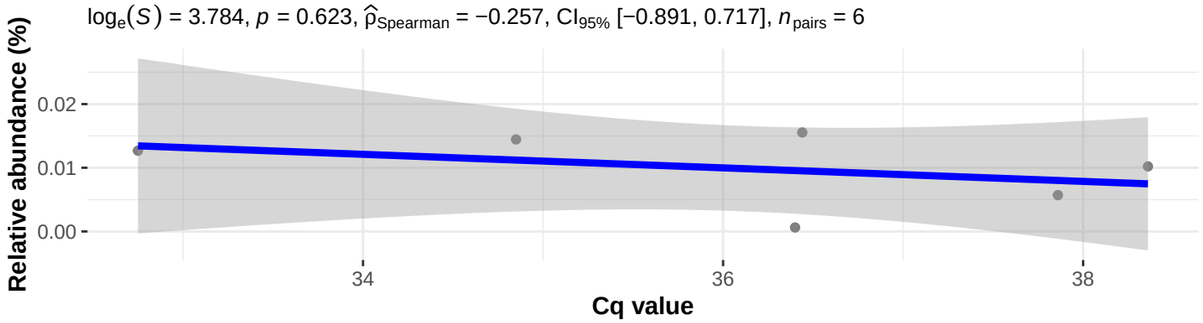
$\log_e(S)$ = 7.907, p = 0.011, $\hat{\rho}_{Spearman}$ = −0.533, $CI_{95\%}$ [−0.785, −0.131], n_{pairs} = 22



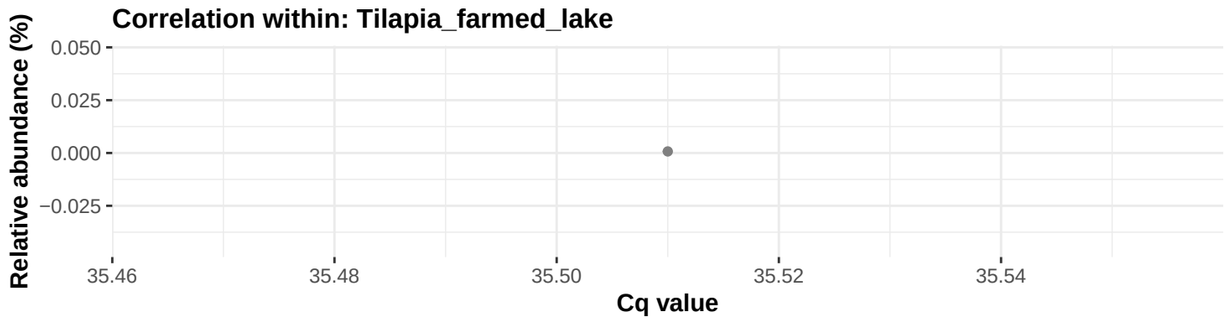
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

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

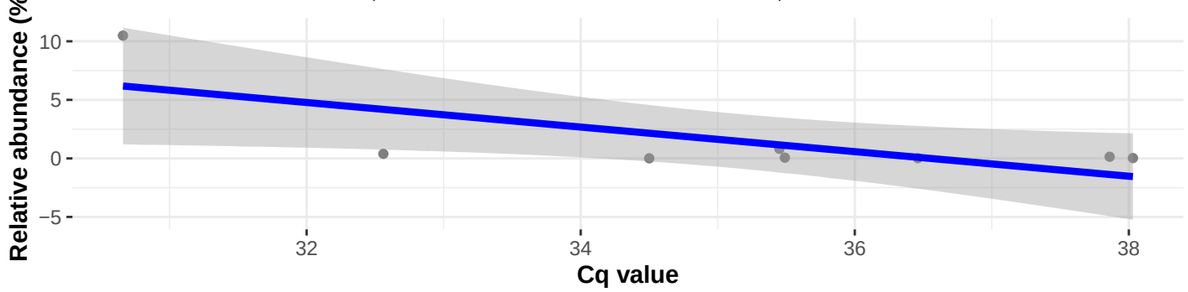


Correlation within: Tilapia_farmed_lake



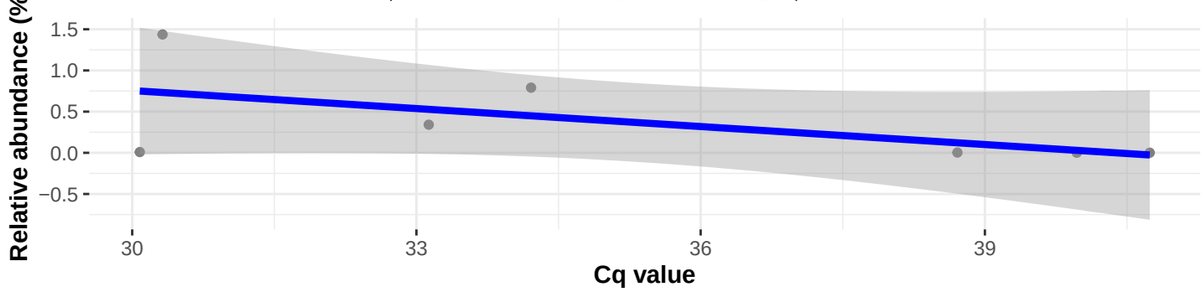
Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

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

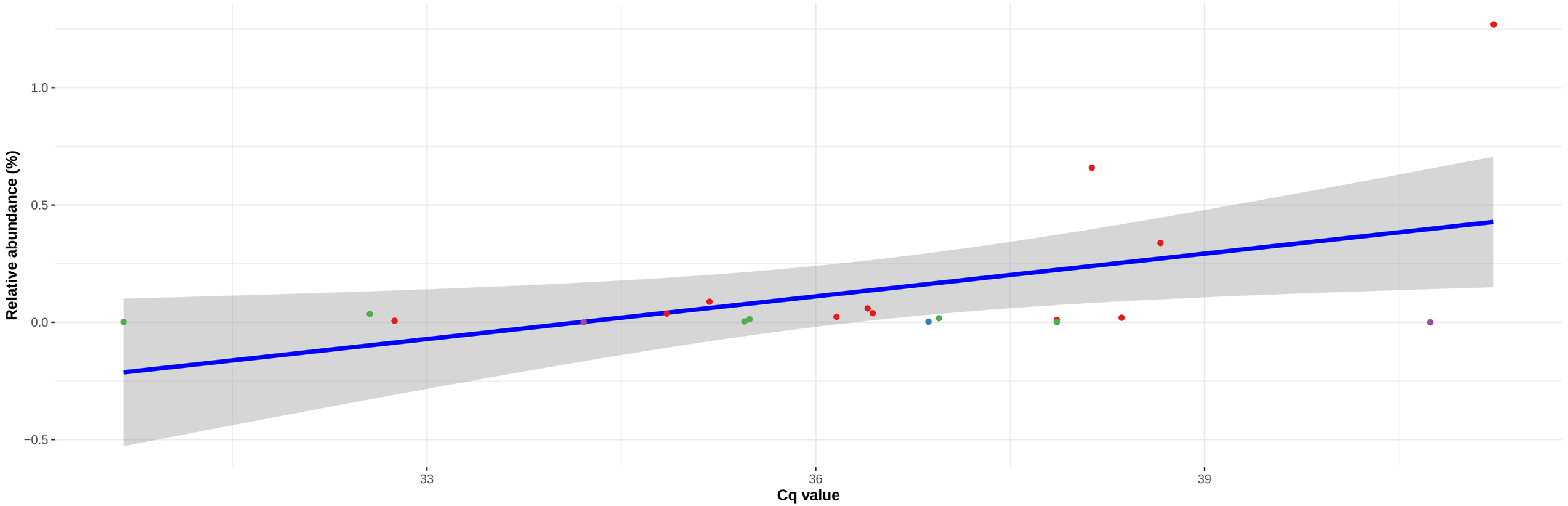


k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Turicibacter; s__uncultured bacterium

featureID: 8440d53055be17f665533f3bf79970b8

Correlation with all samples

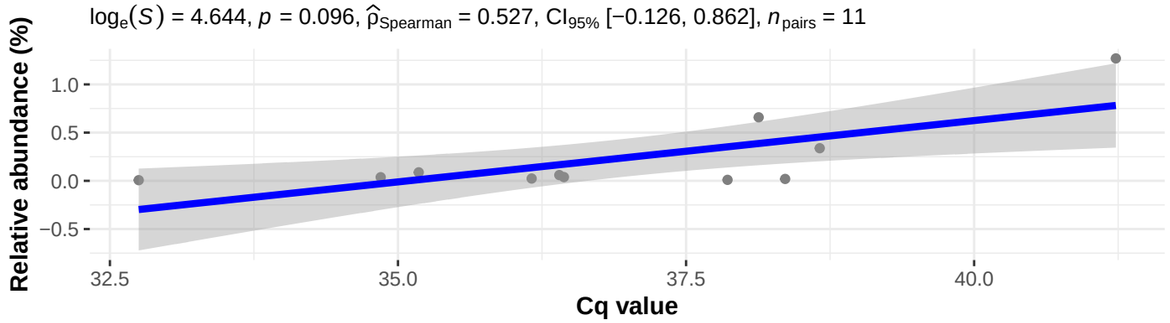
$\log_e(S)$ = 6.924, p = 0.318, $\hat{\rho}_{Spearman}$ = 0.235, $CI_{95\%}$ [−0.244, 0.623], n_{pairs} = 20



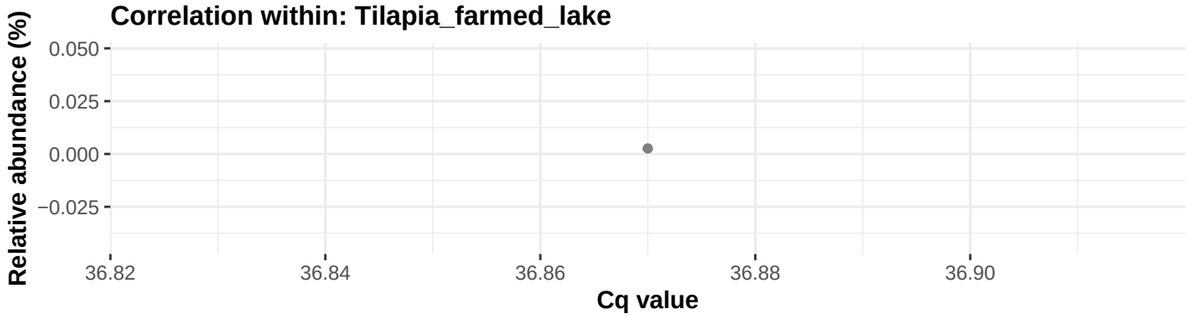
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

Correlation within: Tilapia_farmed_pond

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

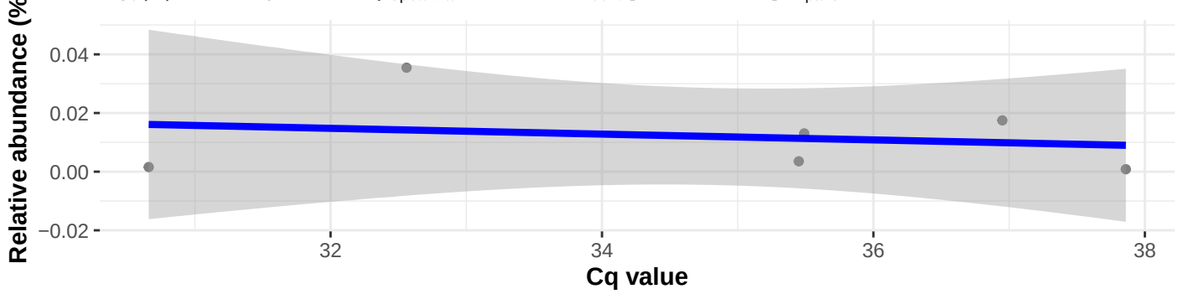


Correlation within: Tilapia_farmed_lake

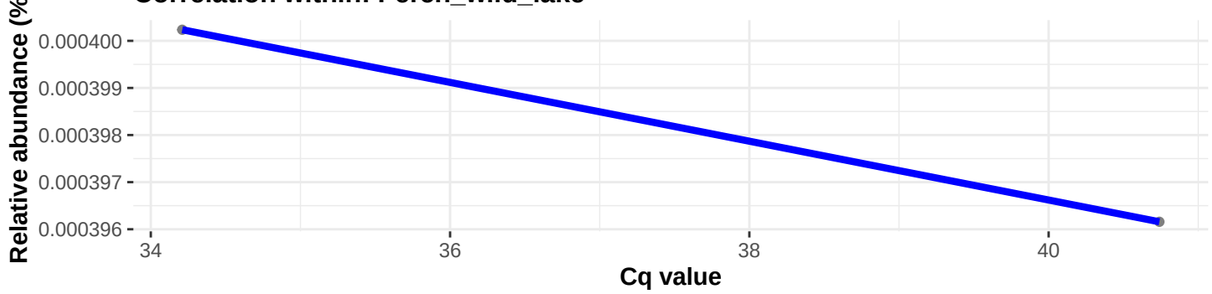


Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake

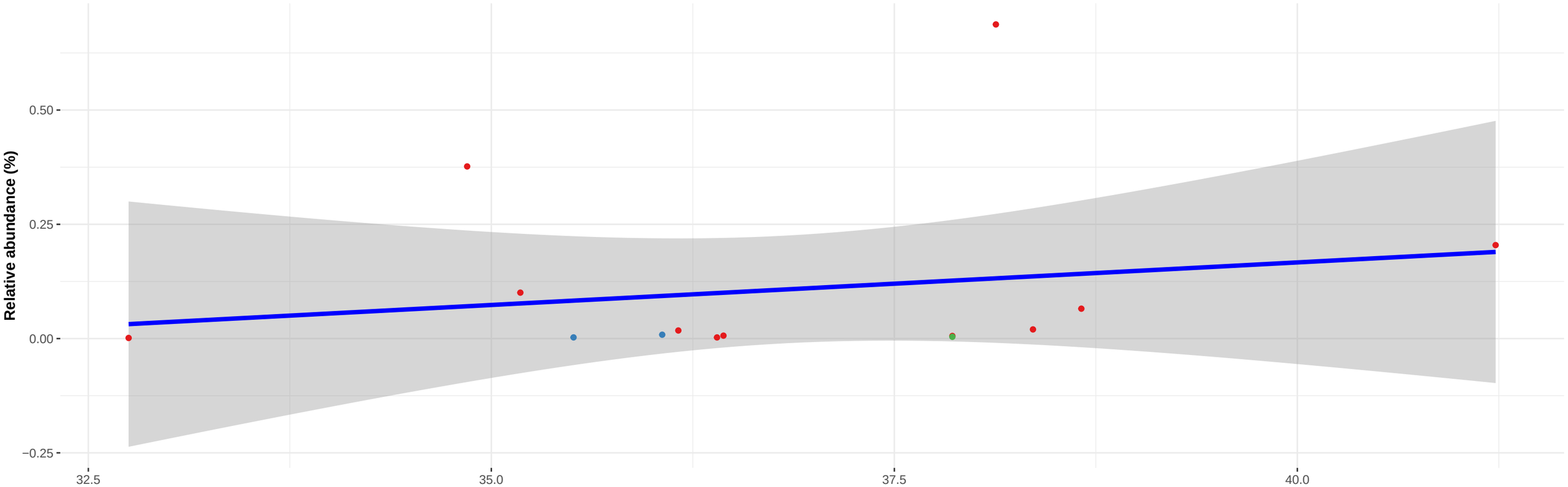


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__uncultured; Ambiguous_taxa; Ambiguous_taxa

featureID: c63bd7419c3dcdbff038ae017cba123c

Correlation with all samples

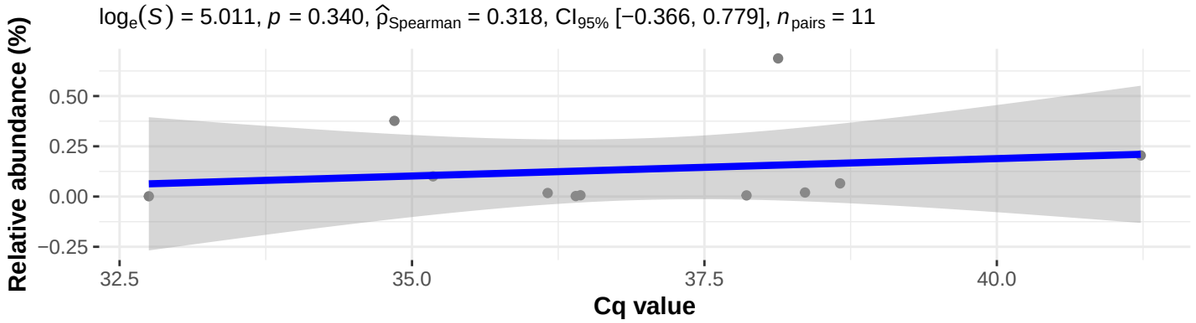
$\log_e(S)$ = 5.720, p = 0.249, $\hat{\rho}_{Spearman}$ = 0.330, $CI_{95\%}$ [−0.259, 0.740], n_{pairs} = 14



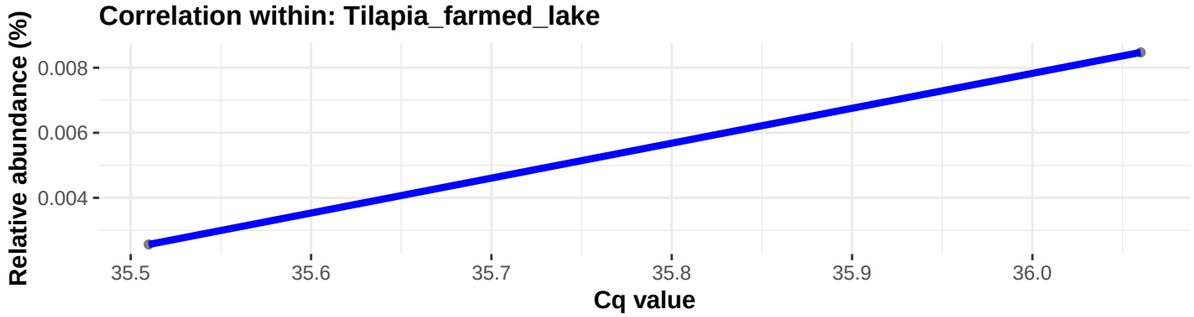
Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake

Correlation within: Tilapia_farmed_pond

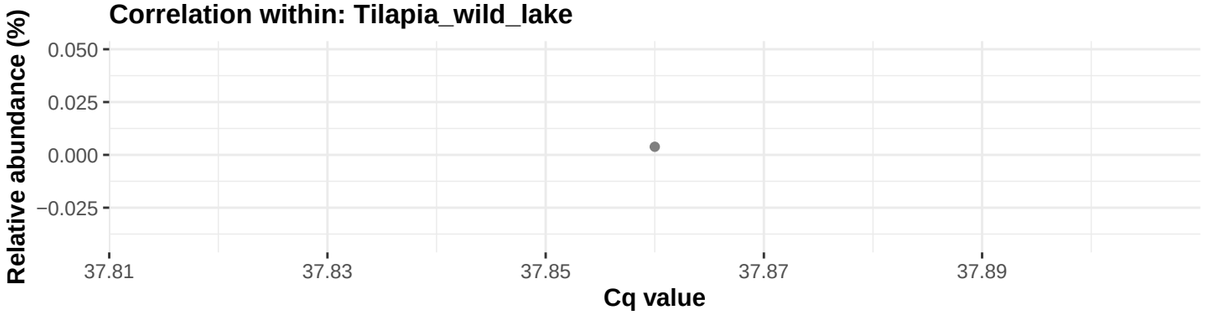
$\log_e(S)$ = 5.011, p = 0.340, $\hat{\rho}_{Spearman}$ = 0.318, $CI_{95\%}$ [−0.366, 0.779], n_{pairs} = 11



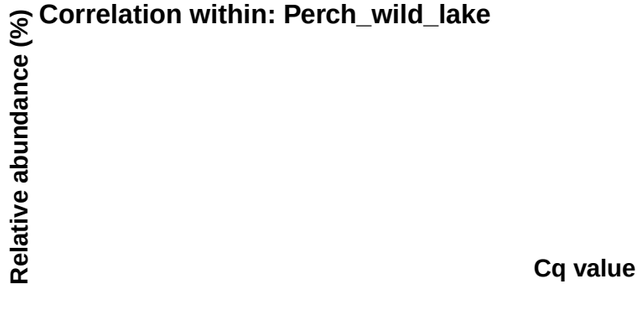
Correlation within: Tilapia_farmed_lake



Correlation within: Tilapia_wild_lake



Correlation within: Perch_wild_lake

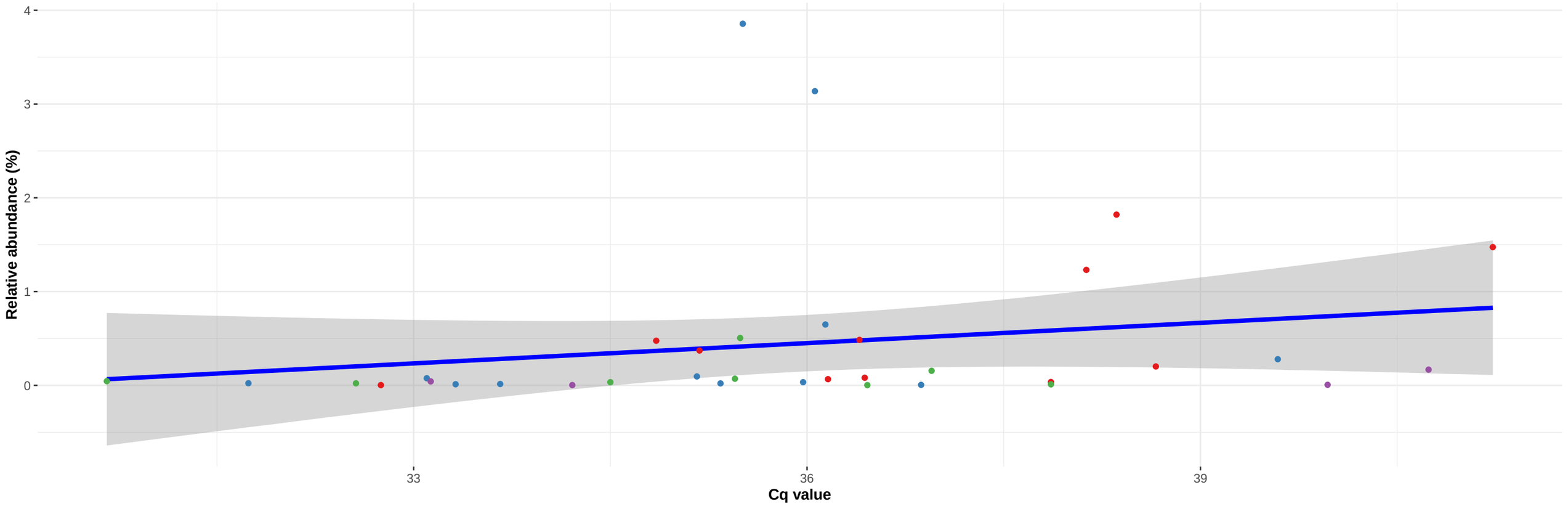


k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; NA

featureID: e576356609fe0b38cefff9ad3b12816a

Correlation with all samples

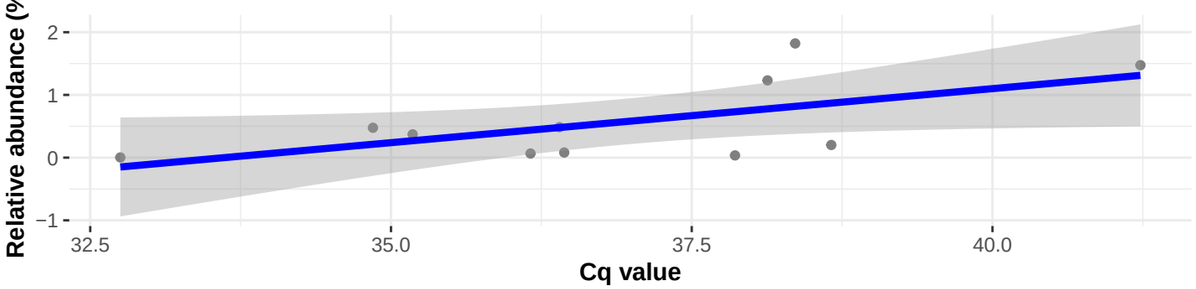
$\log_e(S)$ = 8.475, p = 0.054, $\hat{\rho}_{Spearman}$ = 0.329, $CI_{95\%}$ [−0.015, 0.603], n_{pairs} = 35



Sample_type Tilapia_farmed_pond Tilapia_farmed_lake Tilapia_wild_lake Perch_wild_lake

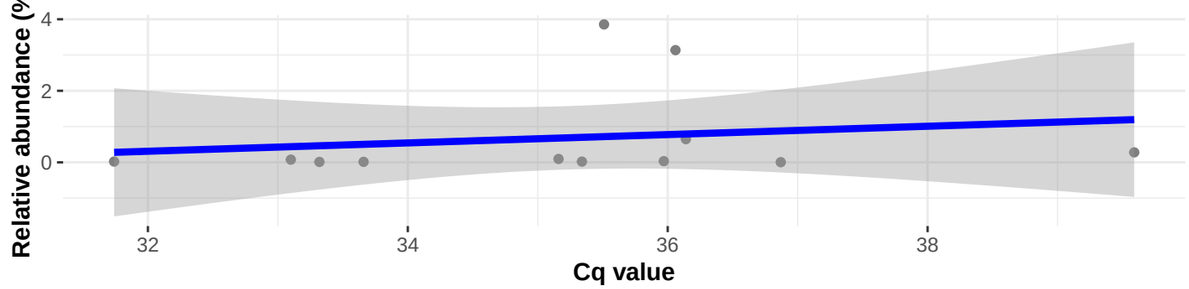
Correlation within: Tilapia_farmed_pond

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



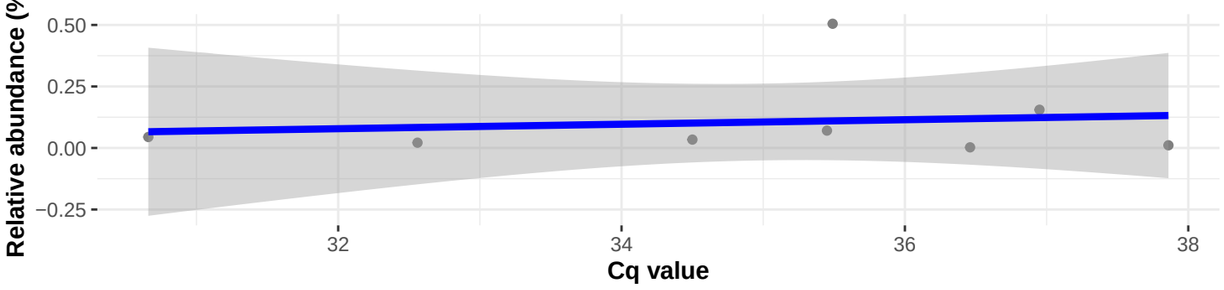
Correlation within: Tilapia_farmed_lake

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



Correlation within: Tilapia_wild_lake

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



Correlation within: Perch_wild_lake