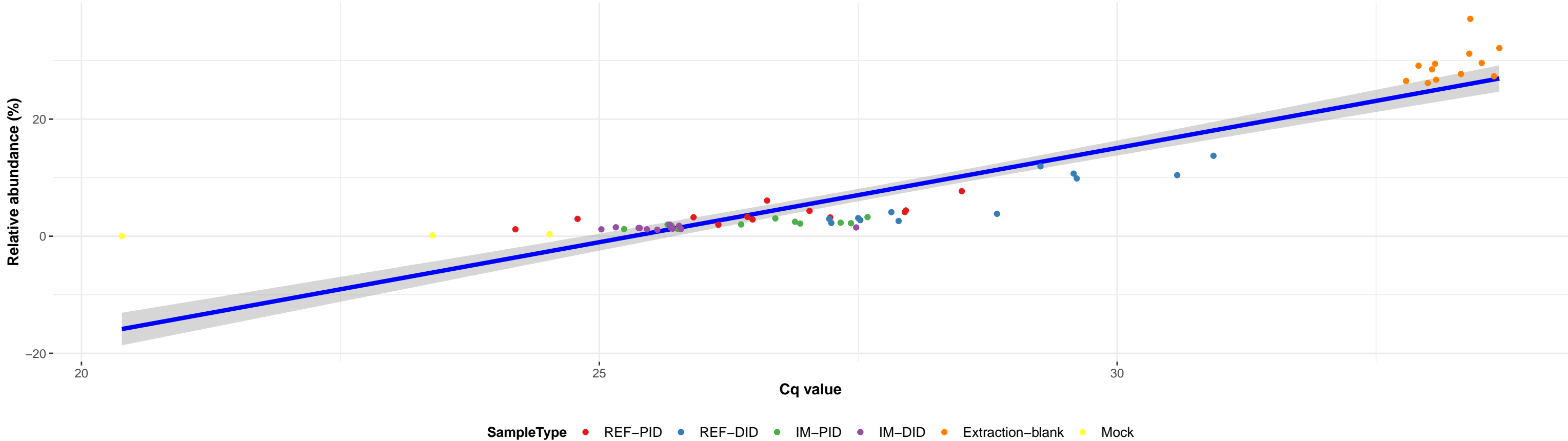


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

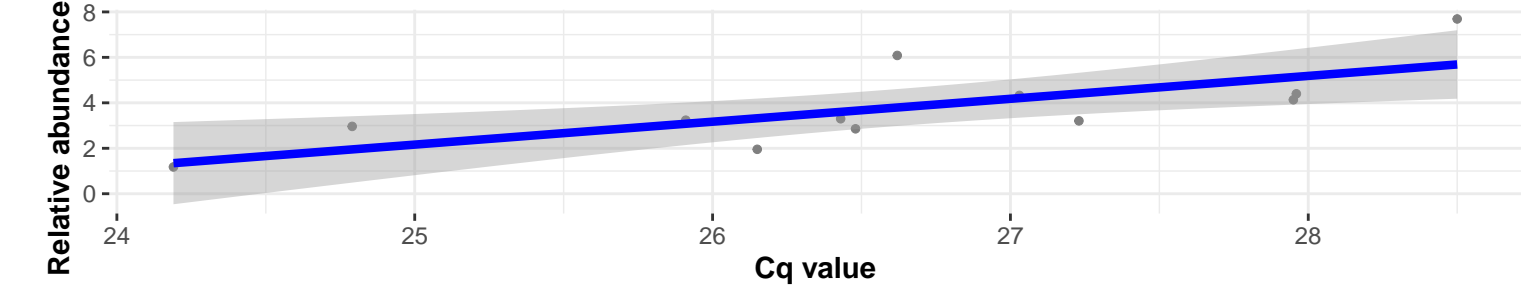
Correlation with all samples

$\log_e(S) = 8.130$, $p = 2.96e-25$, $\hat{\rho}_{\text{Spearman}} = 0.914$, $CI_{95\%} [0.860, 0.949]$, $n_{\text{pairs}} = 62$



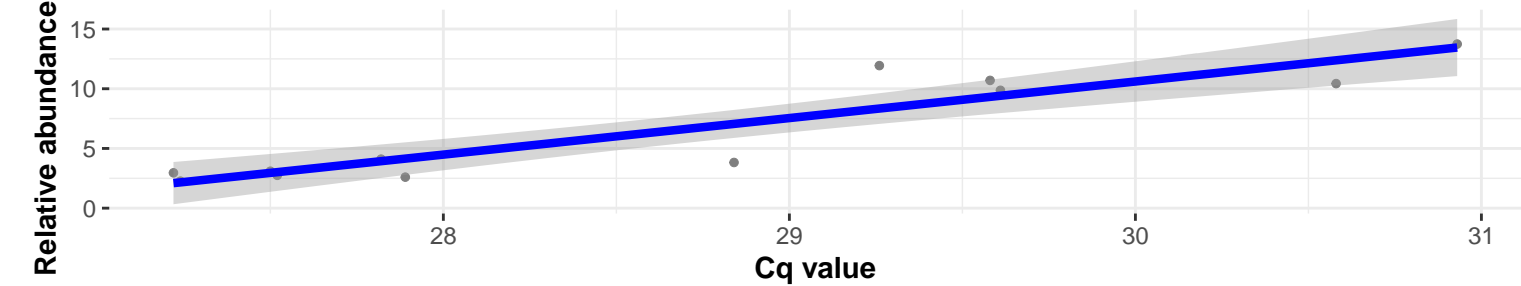
Correlation within: REF-PID

$\log_e(S) = 4.220$, $p = 0.004$, $\hat{\rho}_{\text{Spearman}} = 0.762$, $CI_{95\%} [0.318, 0.932]$, $n_{\text{pairs}} = 12$



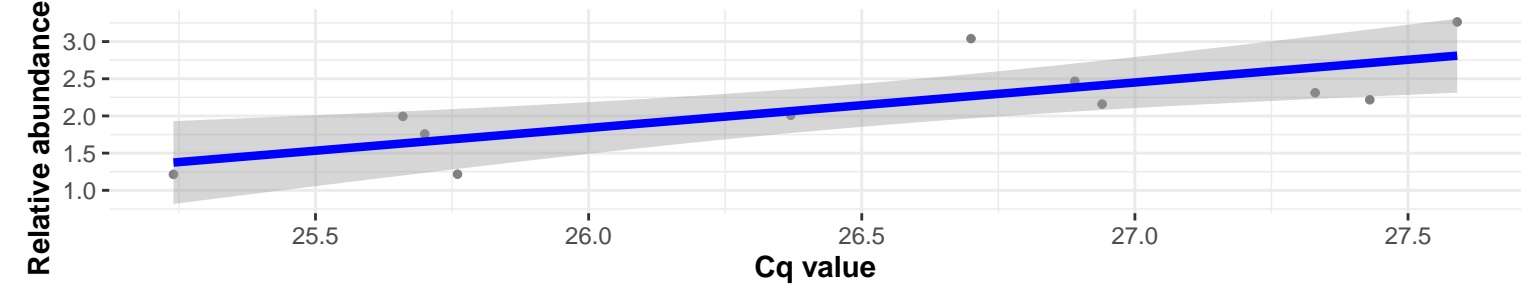
Correlation within: REF-DID

$\log_e(S) = 3.989$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.811$, $CI_{95\%} [0.428, 0.947]$, $n_{\text{pairs}} = 12$



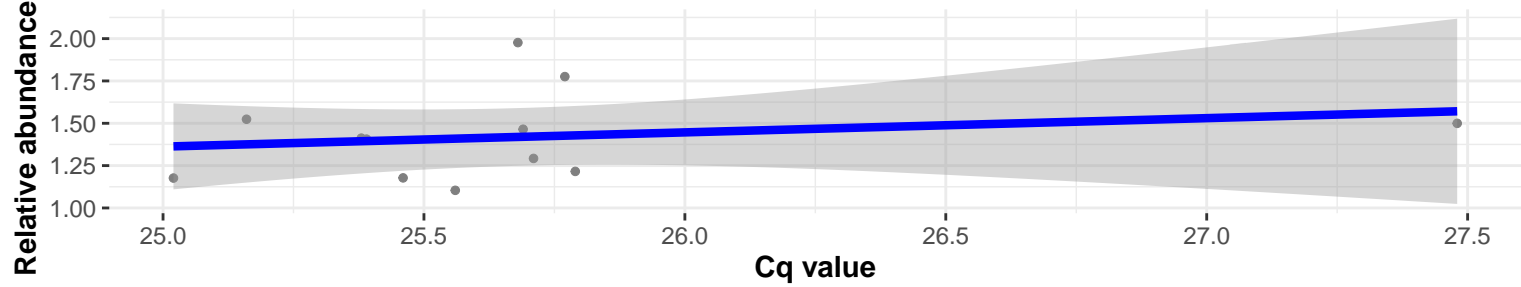
Correlation within: IM-PID

$\log_e(S) = 3.738$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.809$, $CI_{95\%} [0.389, 0.951]$, $n_{\text{pairs}} = 11$



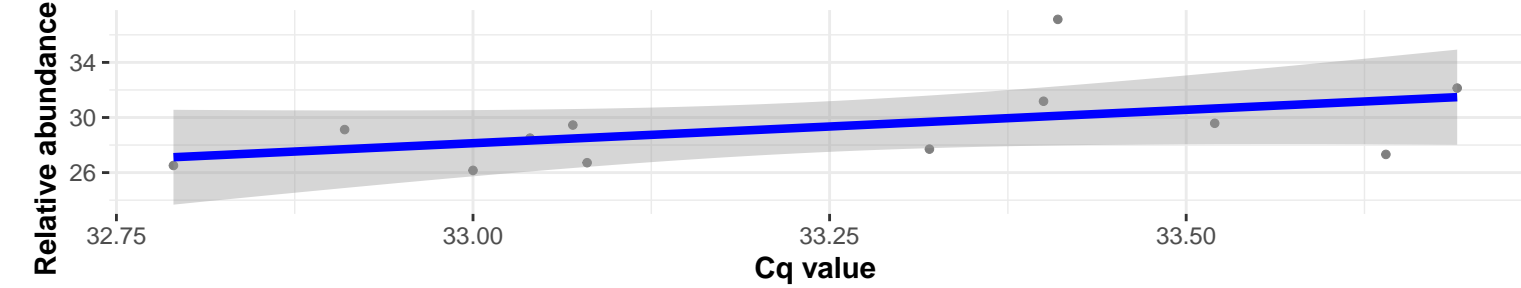
Correlation within: IM-DID

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

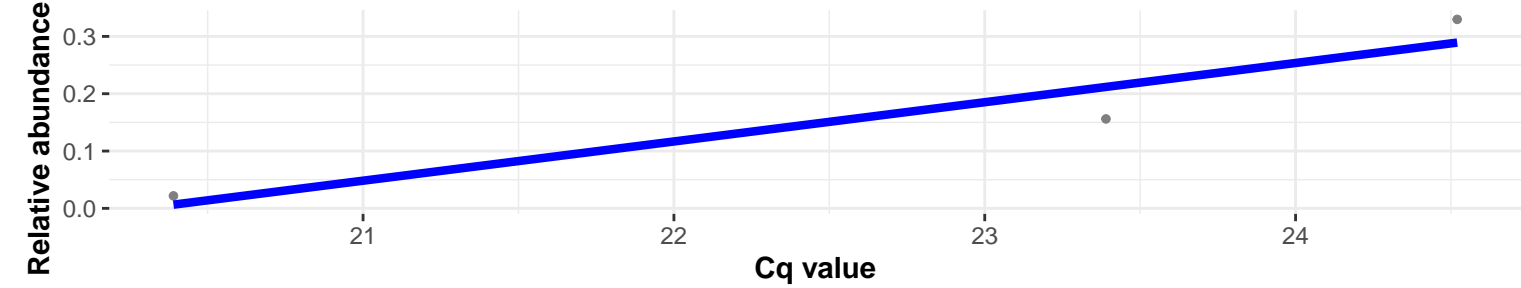


Correlation within: Extraction-blank

$\log_e(S) = 4.787$, $p = 0.048$, $\hat{\rho}_{\text{Spearman}} = 0.580$, $CI_{95\%} [-0.010, 0.871]$, $n_{\text{pairs}} = 12$



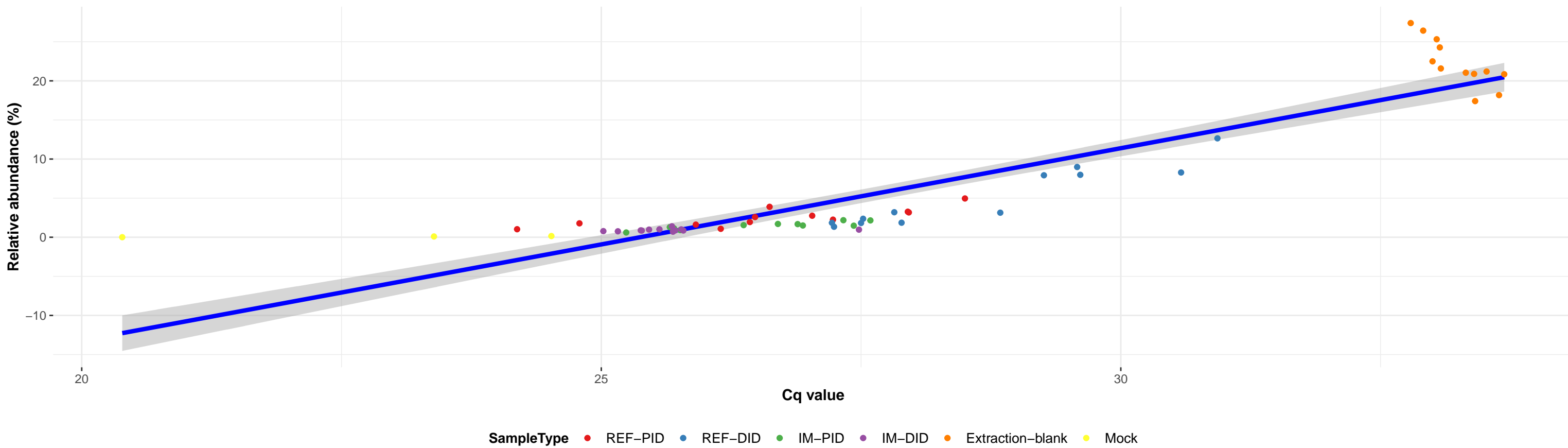
Correlation within: Mock



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

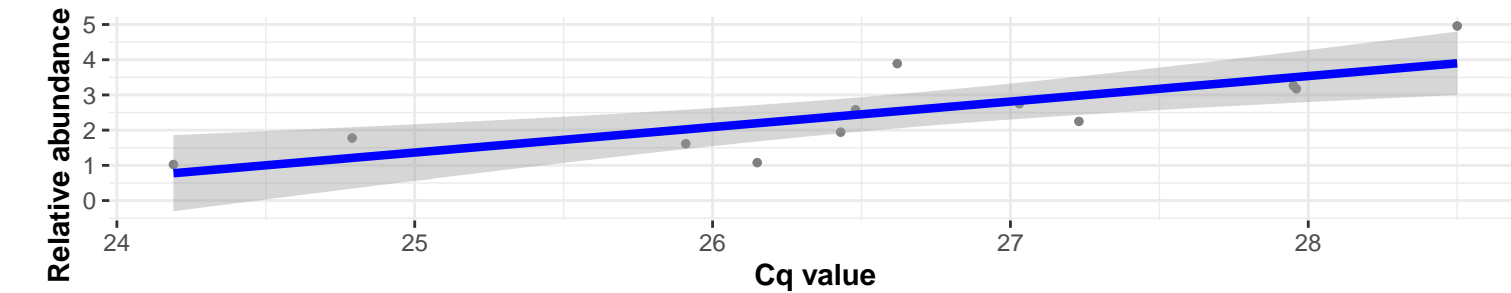
Correlation with all samples

$\log_e(S) = 8.180$, $p = 1.22\text{e-}24$, $\hat{\rho}_{\text{Spearman}} = 0.910$, $\text{CI}_{95\%} [0.853, 0.946]$, $n_{\text{pairs}} = 62$



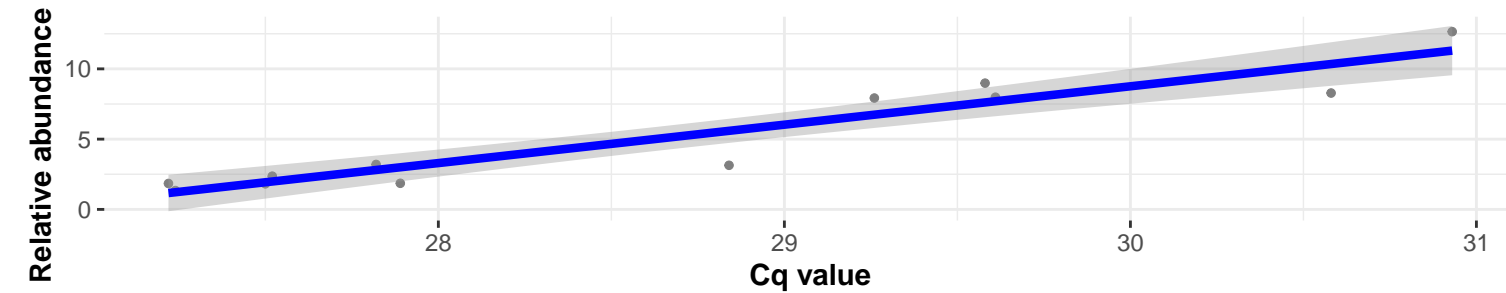
Correlation within: REF-PID

$\log_e(S) = 3.638$, $p = 2.6\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = 0.867$, $\text{CI}_{95\%} [0.571, 0.964]$, $n_{\text{pairs}} = 12$



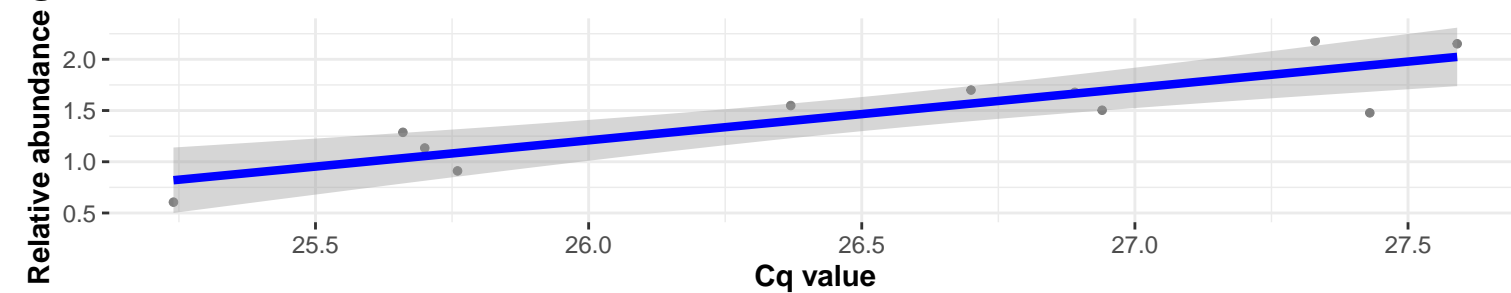
Correlation within: REF-DID

$\log_e(S) = 3.091$, $p = 1.86\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = 0.923$, $\text{CI}_{95\%} [0.734, 0.979]$, $n_{\text{pairs}} = 12$



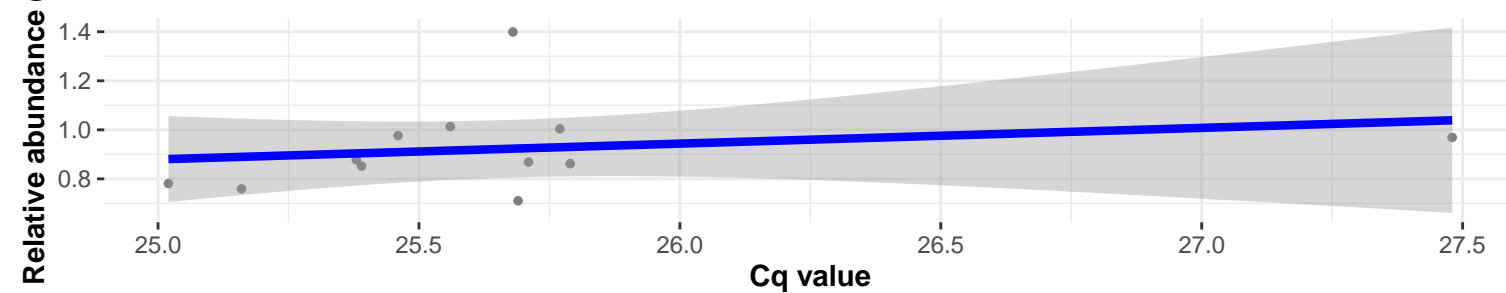
Correlation within: IM-PID

$\log_e(S) = 4.025$, $p = 0.008$, $\hat{\rho}_{\text{Spearman}} = 0.745$, $\text{CI}_{95\%} [0.244, 0.932]$, $n_{\text{pairs}} = 11$



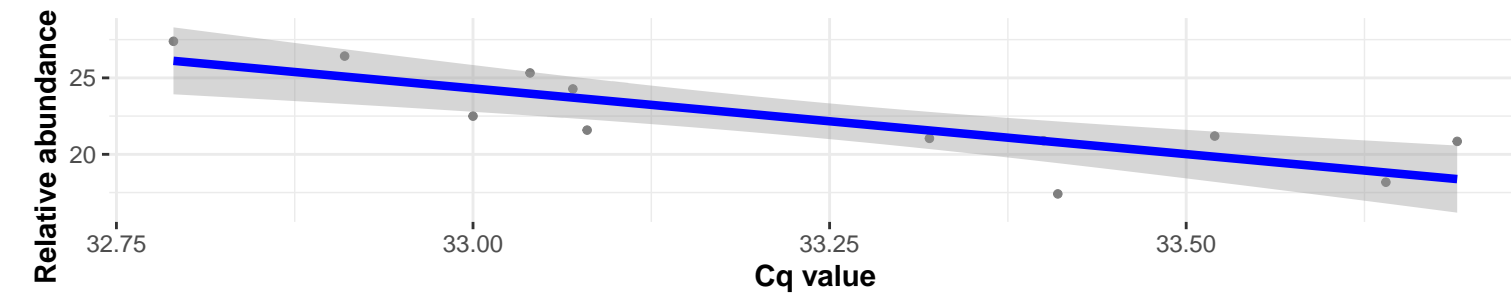
Correlation within: IM-DID

$\log_e(S) = 5.278$, $p = 0.319$, $\hat{\rho}_{\text{Spearman}} = 0.315$, $\text{CI}_{95\%} [-0.334, 0.761]$, $n_{\text{pairs}} = 12$

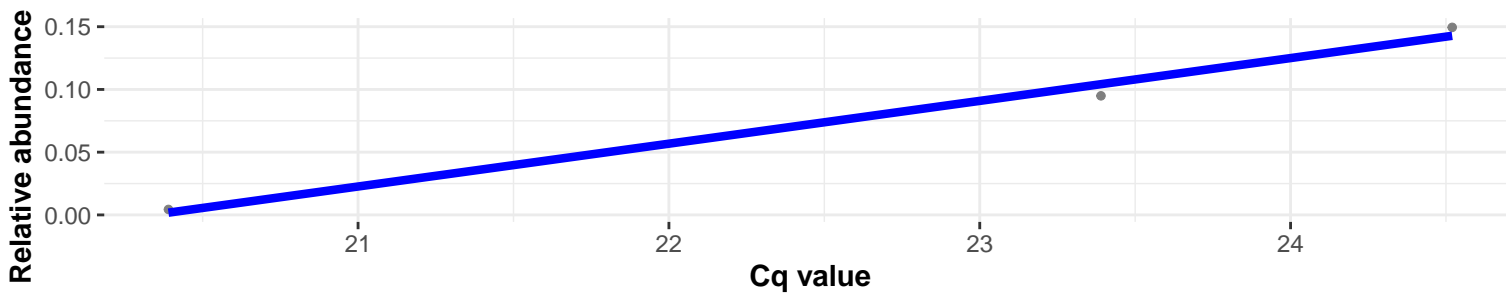


Correlation within: Extraction-blank

$\log_e(S) = 6.295$, $p = 8.37\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = -0.895$, $\text{CI}_{95\%} [-0.972, -0.649]$, $n_{\text{pairs}} = 12$



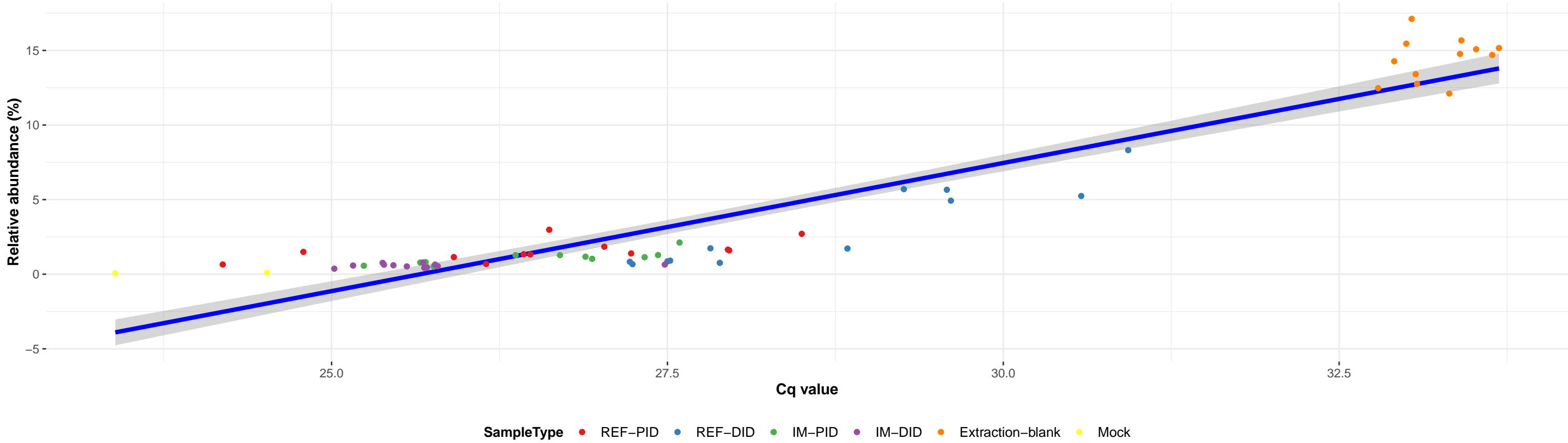
Correlation within: Mock



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

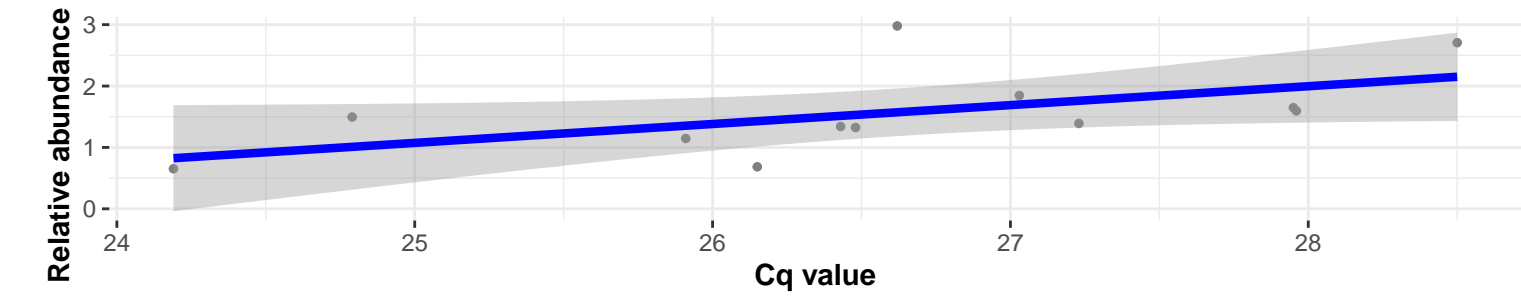
Correlation with all samples

$\log_e(S) = 8.475$, $p = 4.47e-20$, $\hat{\rho}_{\text{Spearman}} = 0.873$, $CI_{95\%} [0.794, 0.923]$, $n_{\text{pairs}} = 61$



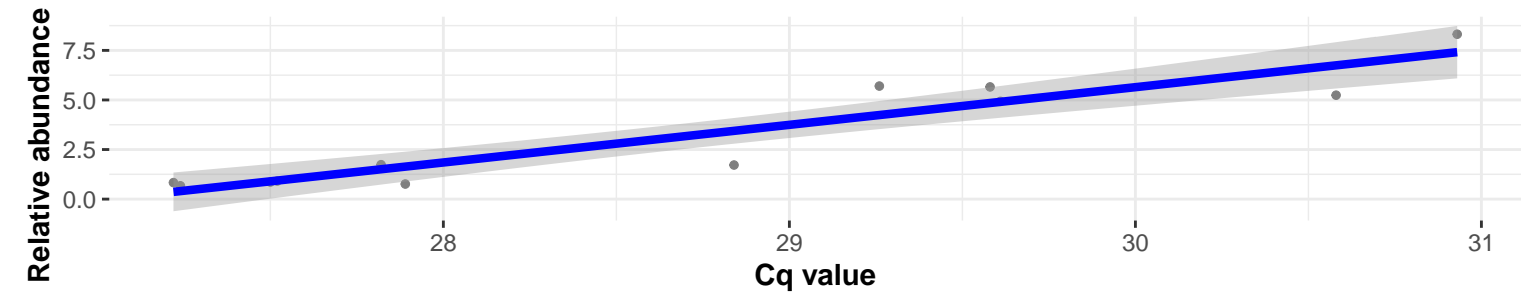
Correlation within: REF-PID

$\log_e(S) = 4.407$, $p = 0.009$, $\hat{\rho}_{\text{Spearman}} = 0.713$, $CI_{95\%} [0.218, 0.916]$, $n_{\text{pairs}} = 12$



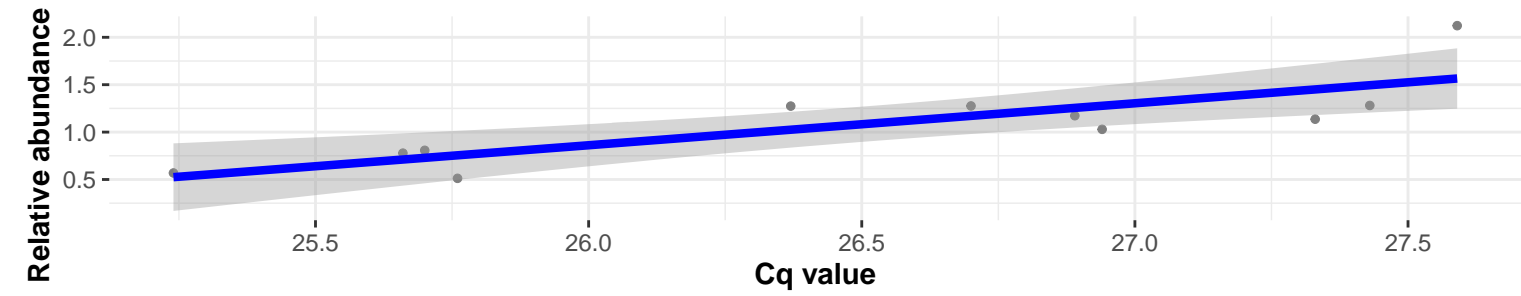
Correlation within: REF-DID

$\log_e(S) = 3.829$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.839$, $CI_{95\%} [0.497, 0.955]$, $n_{\text{pairs}} = 12$



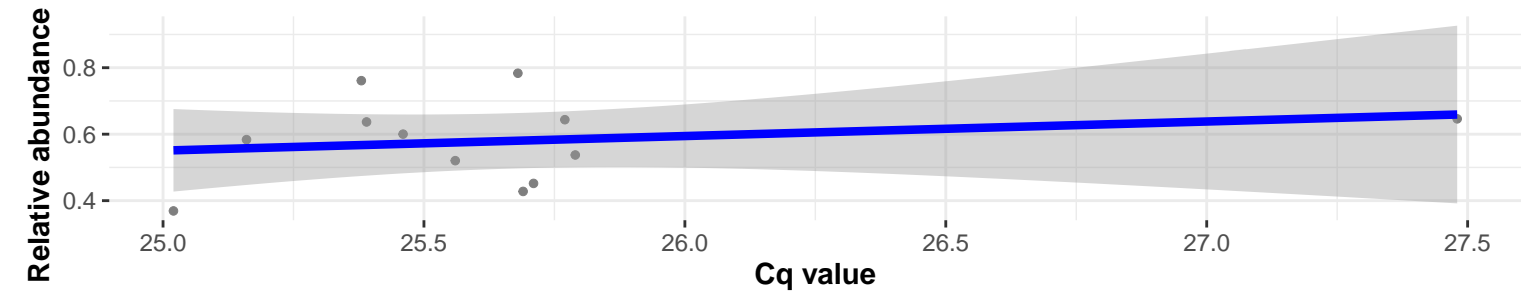
Correlation within: IM-PID

$\log_e(S) = 3.871$, $p = 0.004$, $\hat{\rho}_{\text{Spearman}} = 0.782$, $CI_{95\%} [0.324, 0.943]$, $n_{\text{pairs}} = 11$



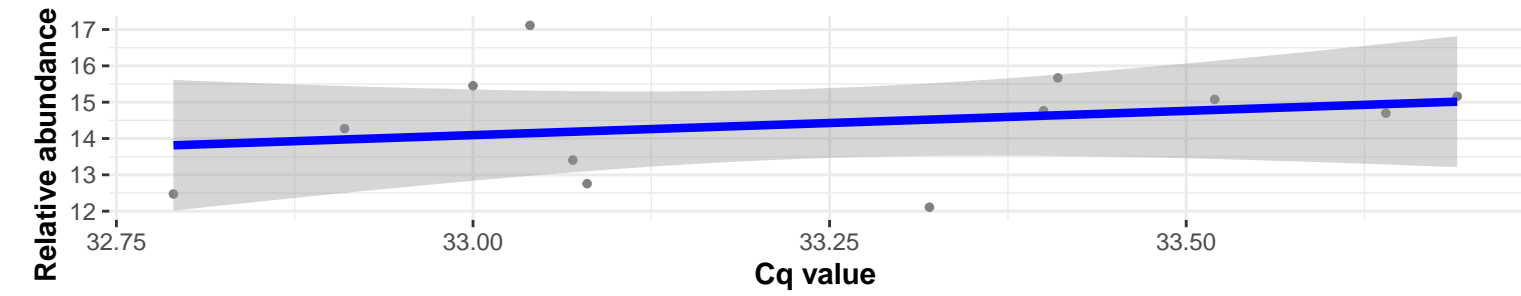
Correlation within: IM-DID

$\log_e(S) = 5.489$, $p = 0.633$, $\hat{\rho}_{\text{Spearman}} = 0.154$, $CI_{95\%} [-0.476, 0.679]$, $n_{\text{pairs}} = 12$

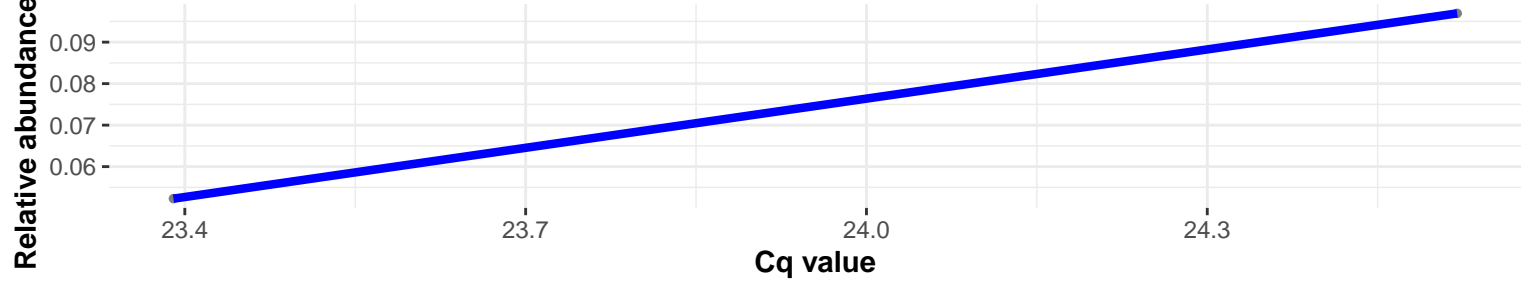


Correlation within: Extraction-blank

$\log_e(S) = 5.357$, $p = 0.417$, $\hat{\rho}_{\text{Spearman}} = 0.259$, $CI_{95\%} [-0.387, 0.734]$, $n_{\text{pairs}} = 12$



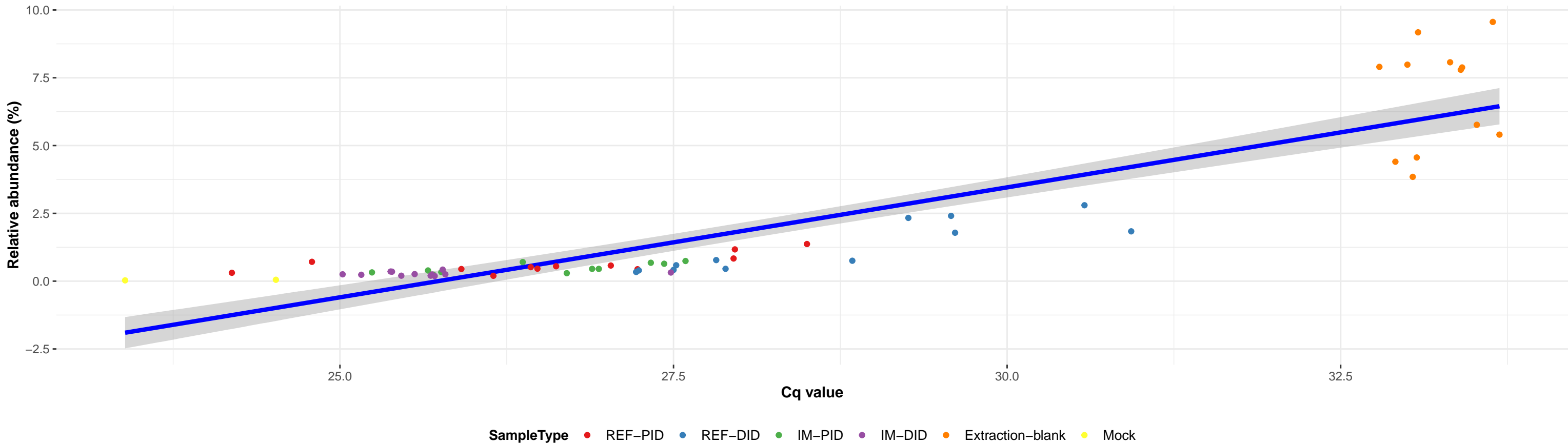
Correlation within: Mock



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

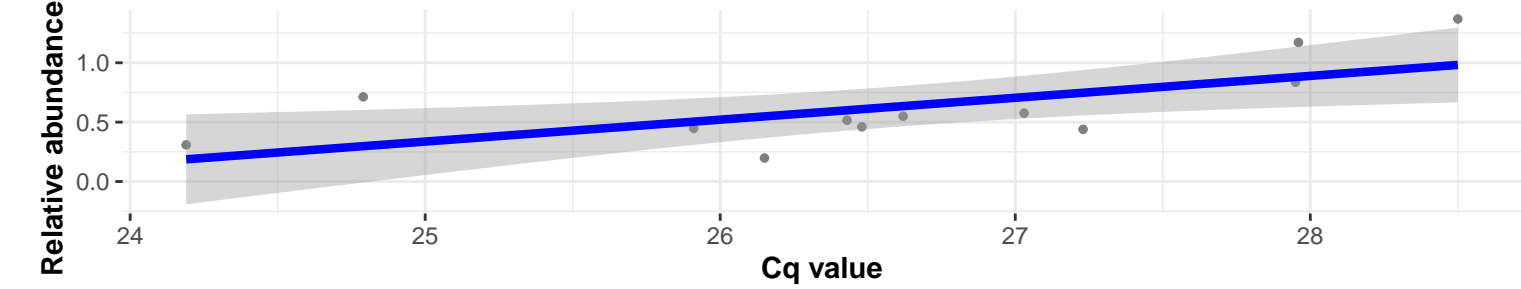
Correlation with all samples

$\log_e(S) = 8.373$, $p = 2.66\text{e-}21$, $\hat{\rho}_{\text{Spearman}} = 0.886$, $\text{CI}_{95\%} [0.813, 0.931]$, $n_{\text{pairs}} = 61$



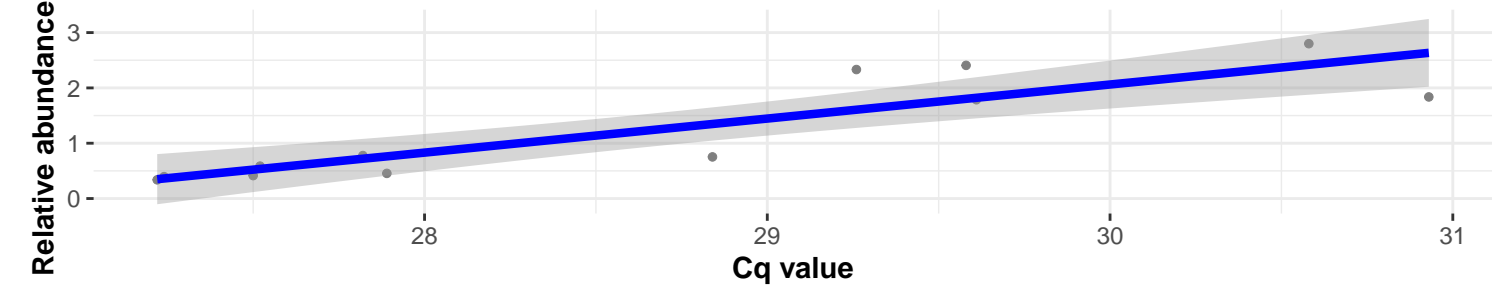
Correlation within: REF-PID

$\log_e(S) = 4.585$, $p = 0.020$, $\hat{\rho}_{\text{Spearman}} = 0.657$, $\text{CI}_{95\%} [0.115, 0.898]$, $n_{\text{pairs}} = 12$



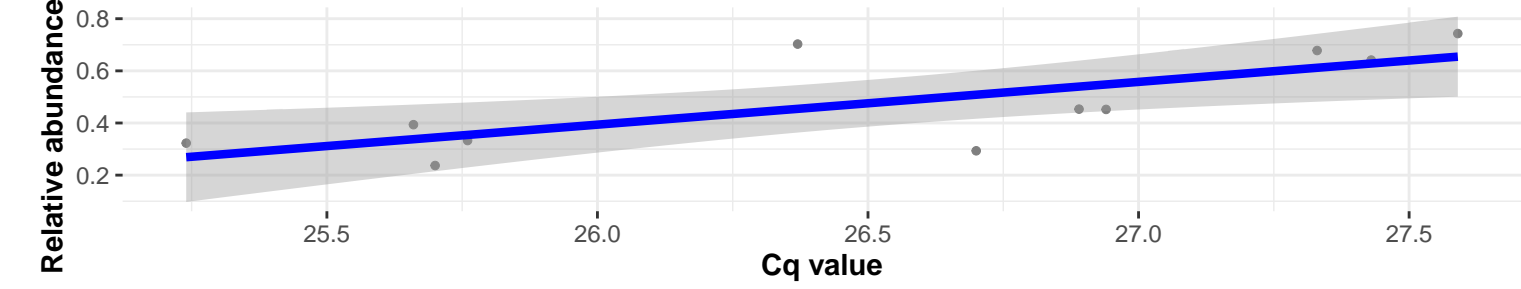
Correlation within: REF-DID

$\log_e(S) = 3.466$, $p = 1.14\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = 0.888$, $\text{CI}_{95\%} [0.629, 0.970]$, $n_{\text{pairs}} = 12$



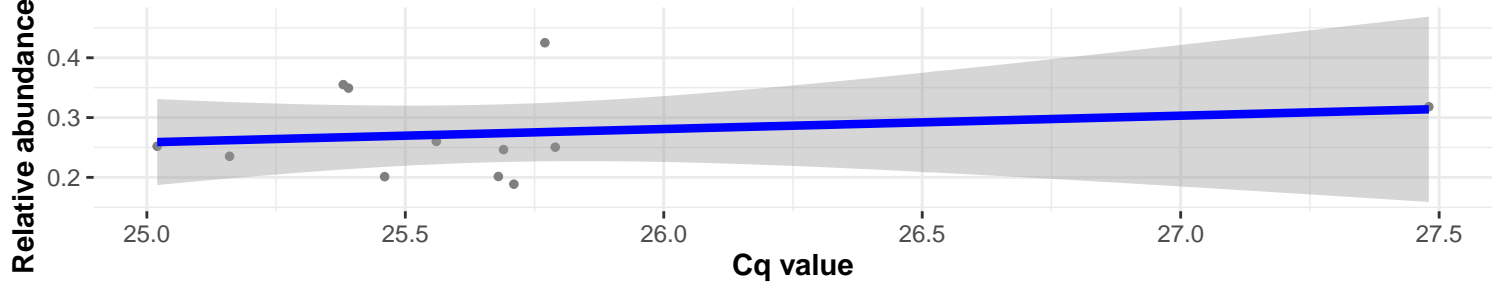
Correlation within: IM-PID

$\log_e(S) = 4.190$, $p = 0.016$, $\hat{\rho}_{\text{Spearman}} = 0.700$, $\text{CI}_{95\%} [0.153, 0.919]$, $n_{\text{pairs}} = 11$



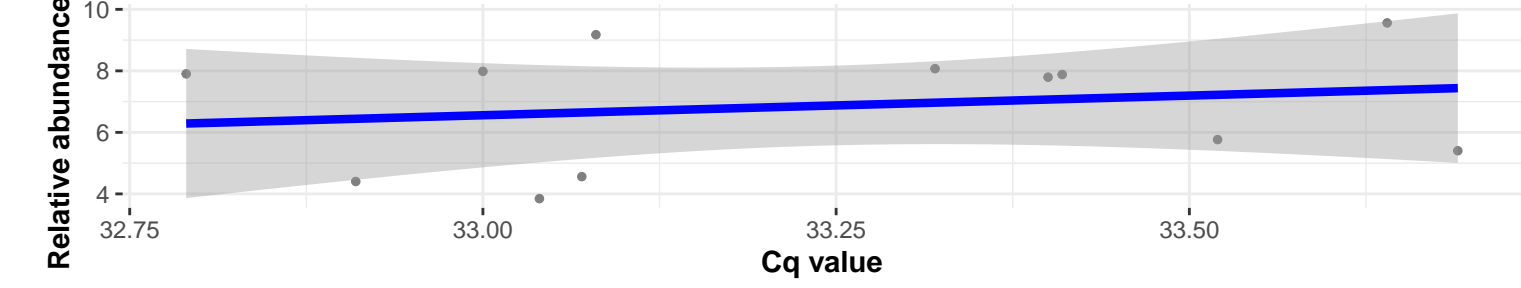
Correlation within: IM-DID

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

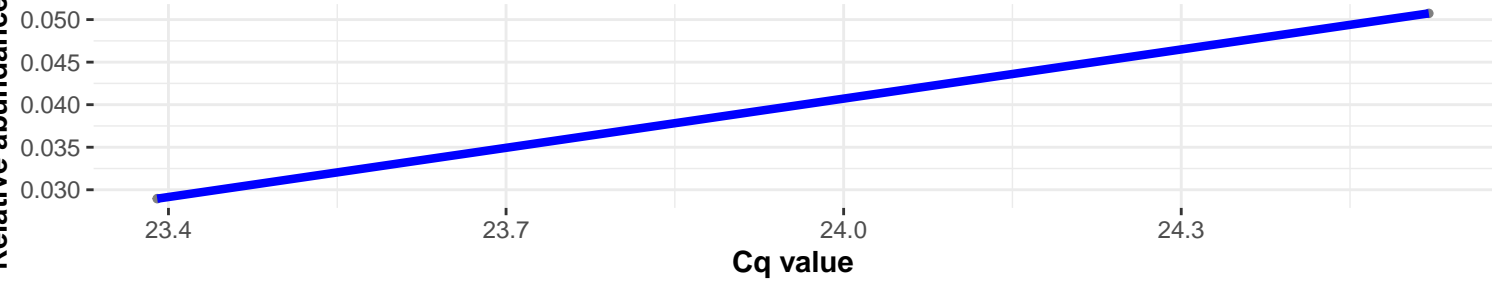


Correlation within: Extraction-blank

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



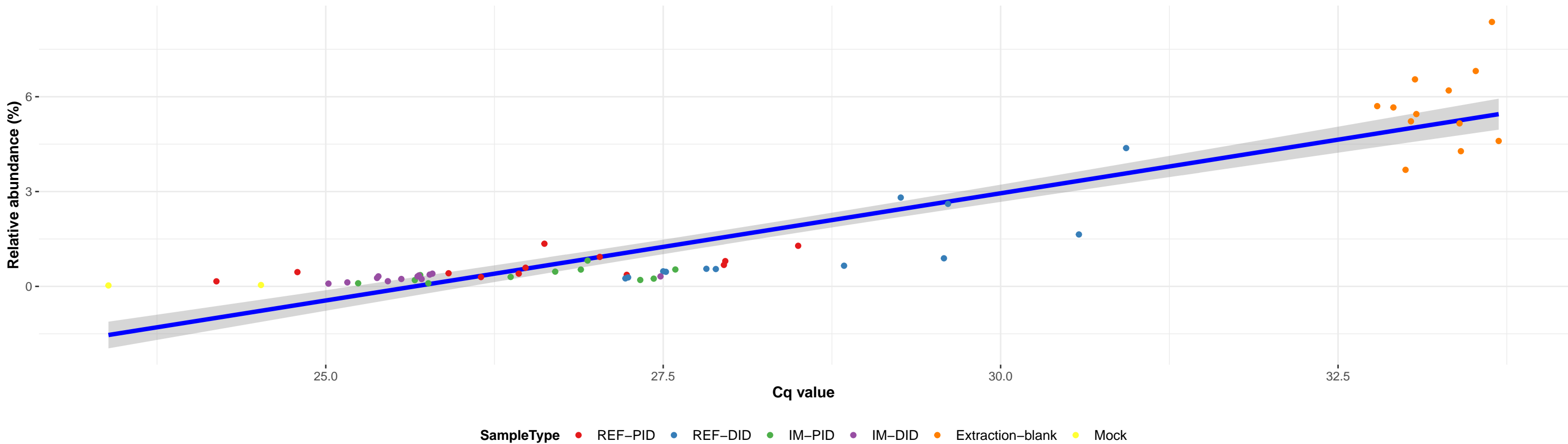
Correlation within: Mock



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

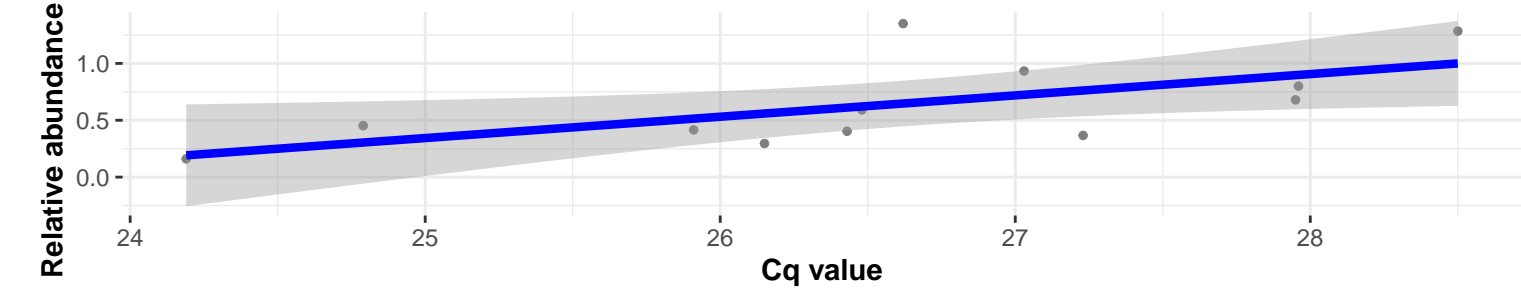
Correlation with all samples

$\log_e(S) = 8.447$, $p = 2.07\text{e-}20$, $\hat{\rho}_{\text{Spearman}} = 0.877$, $\text{CI}_{95\%} [0.799, 0.926]$, $n_{\text{pairs}} = 61$



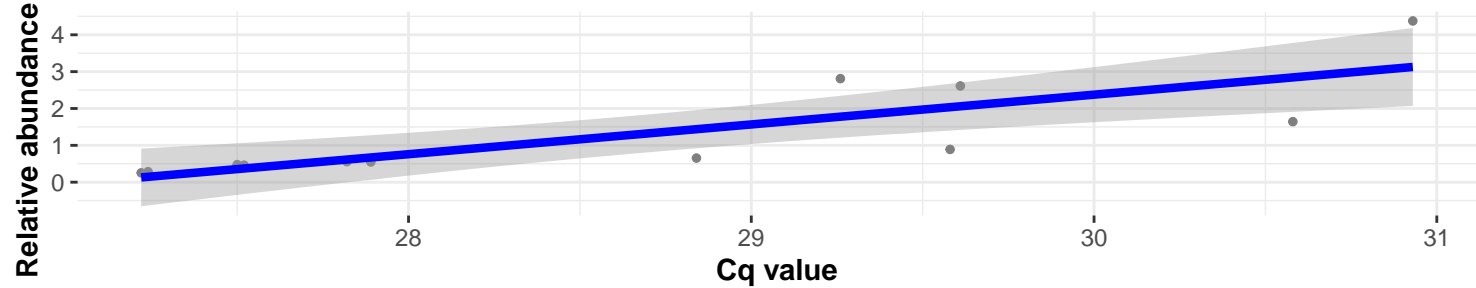
Correlation within: REF-PID

$\log_e(S) = 4.605$, $p = 0.022$, $\hat{\rho}_{\text{Spearman}} = 0.650$, $\text{CI}_{95\%} [0.103, 0.895]$, $n_{\text{pairs}} = 12$



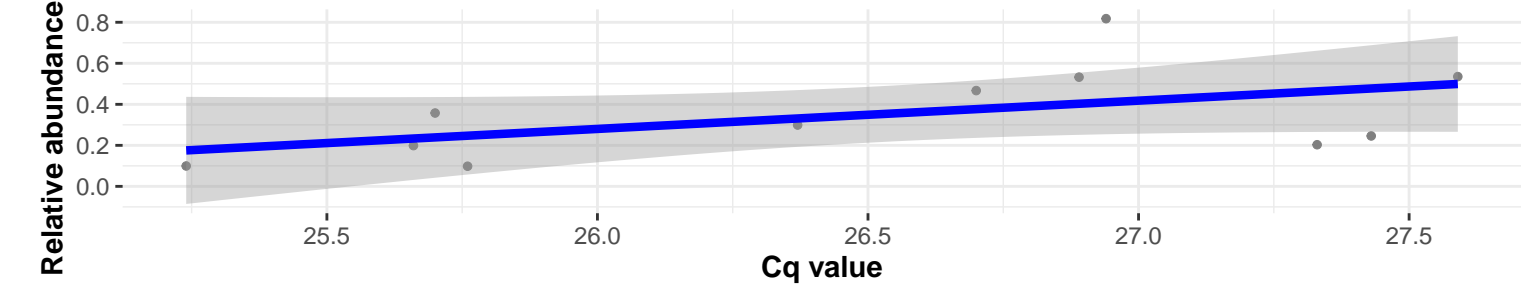
Correlation within: REF-DID

$\log_e(S) = 2.890$, $p = 6.99\text{e-}06$, $\hat{\rho}_{\text{Spearman}} = 0.937$, $\text{CI}_{95\%} [0.778, 0.983]$, $n_{\text{pairs}} = 12$



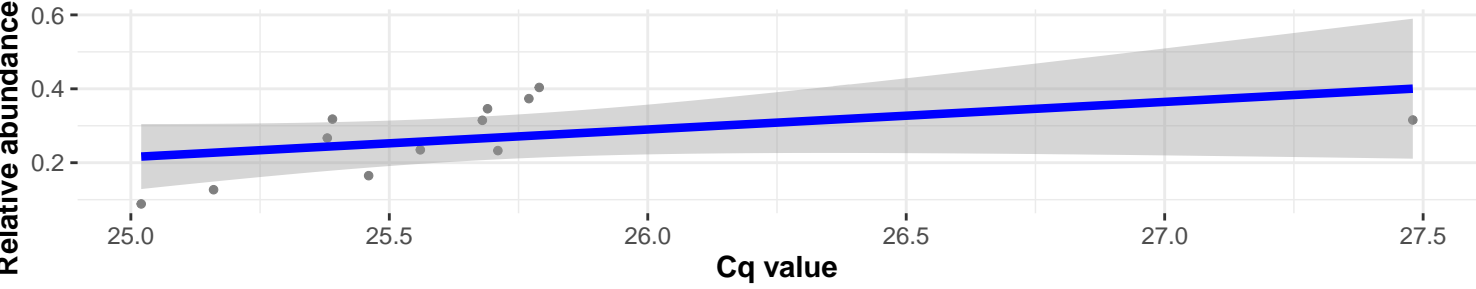
Correlation within: IM-PID

$\log_e(S) = 4.564$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = 0.564$, $\text{CI}_{95\%} [-0.075, 0.874]$, $n_{\text{pairs}} = 11$



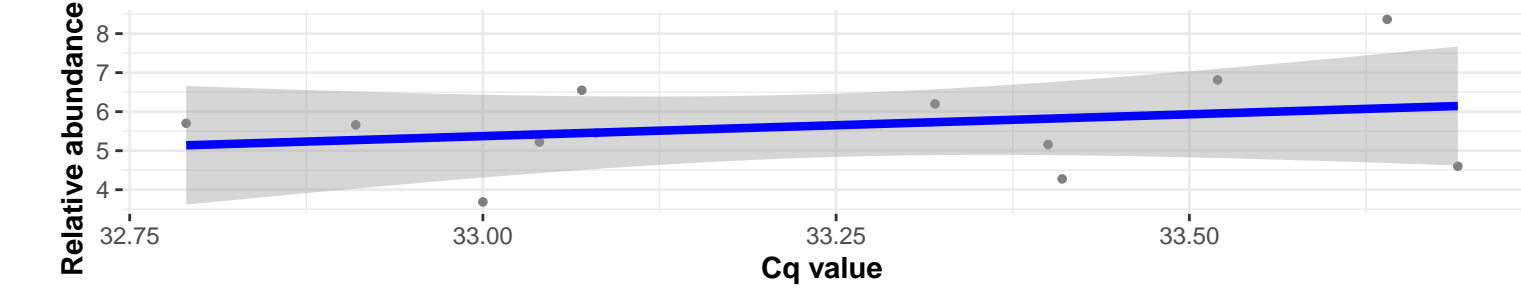
Correlation within: IM-DID

$\log_e(S) = 4.454$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = 0.699$, $\text{CI}_{95\%} [0.191, 0.912]$, $n_{\text{pairs}} = 12$

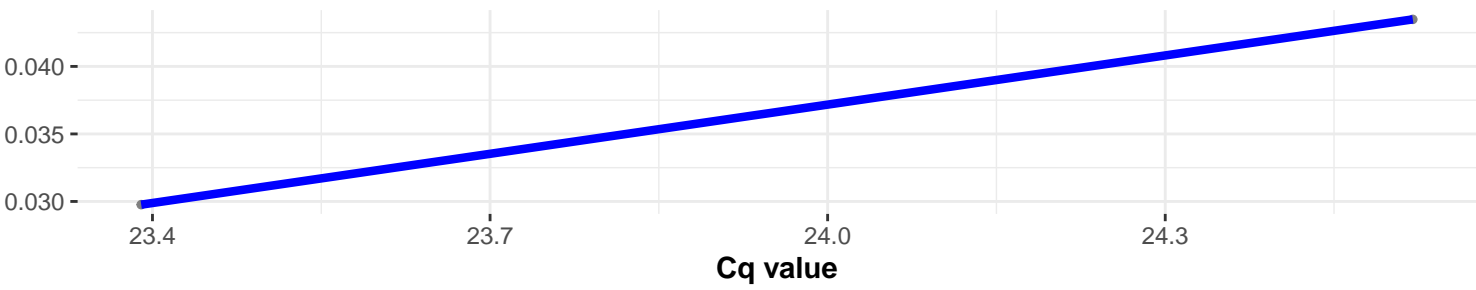


Correlation within: Extraction-blank

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



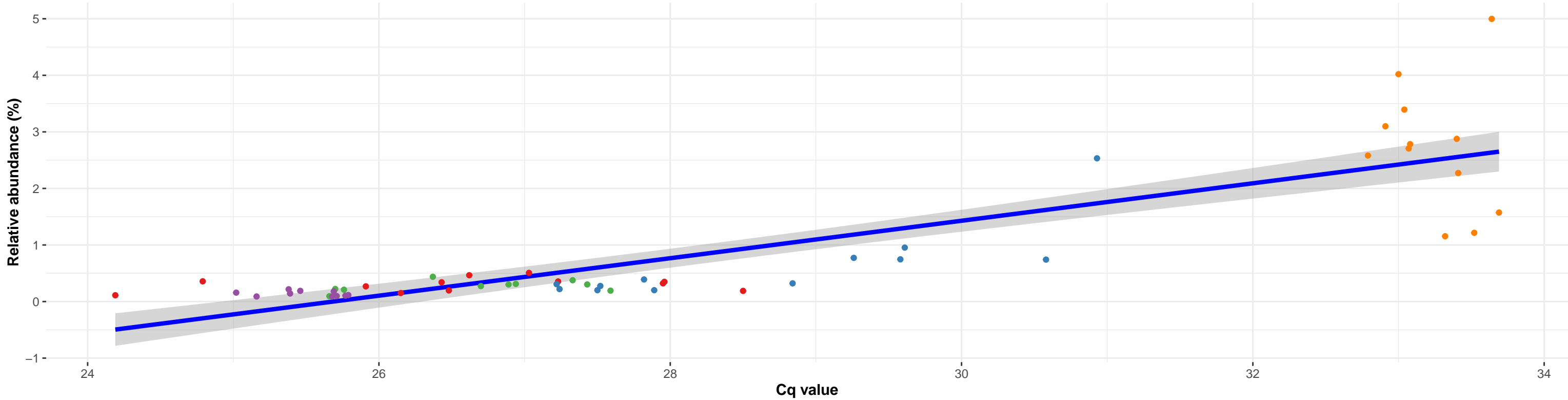
Correlation within: Mock



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

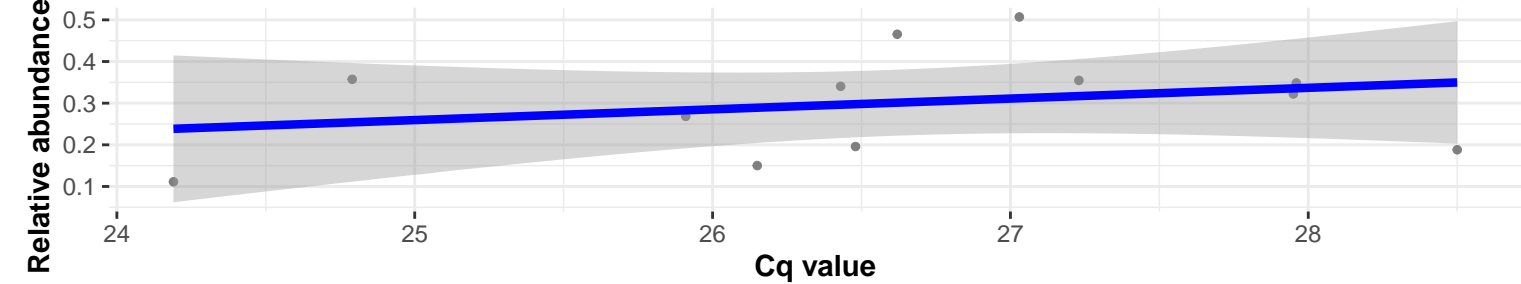
Correlation with all samples

$\log_e(S) = 8.581$, $p = 1.44e-14$, $\hat{\rho}_{\text{Spearman}} = 0.818$, $CI_{95\%} [0.703, 0.891]$, $n_{\text{pairs}} = 56$



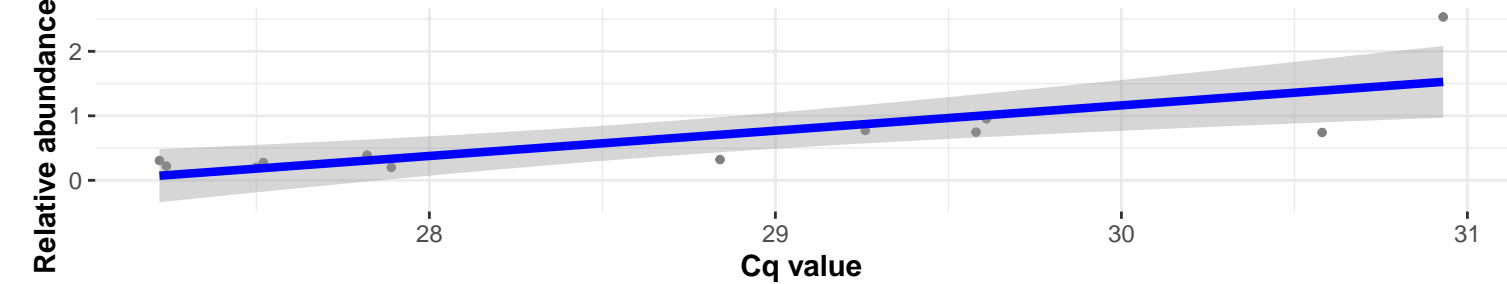
Correlation within: REF-PID

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



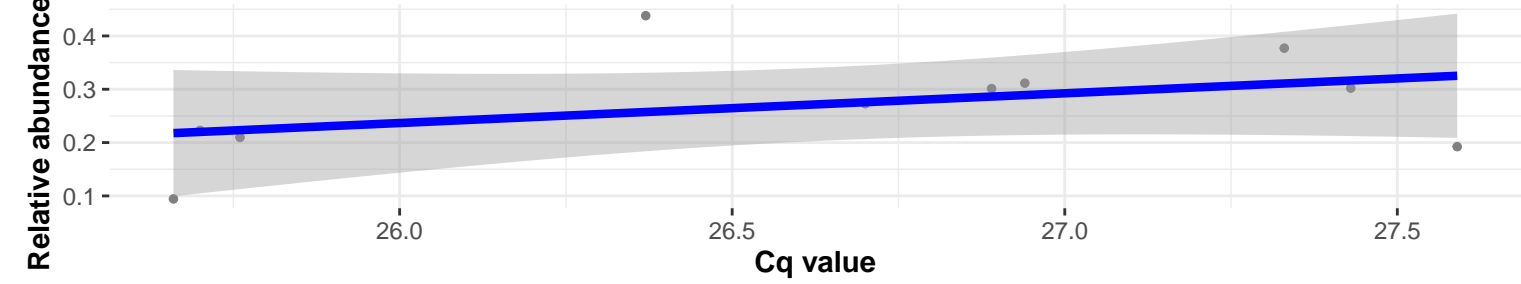
Correlation within: REF-DID

$\log_e(S) = 4.025$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.804$, $CI_{95\%} [0.412, 0.945]$, $n_{\text{pairs}} = 12$



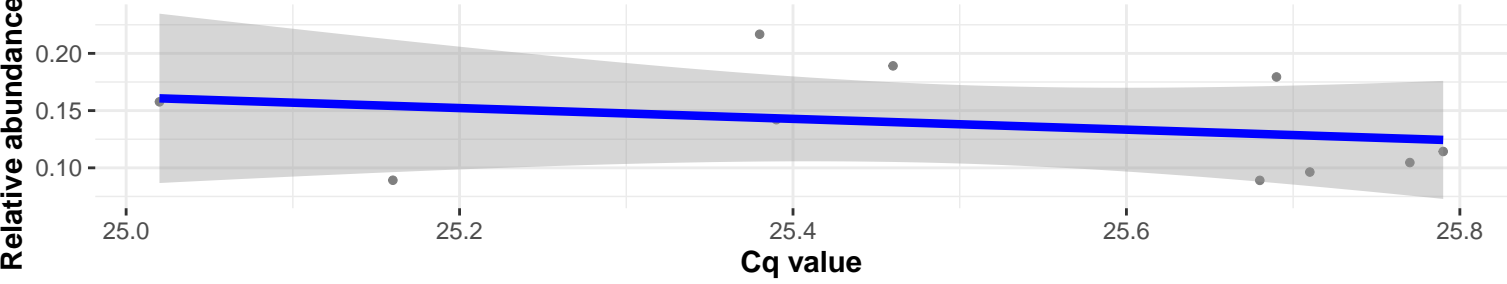
Correlation within: IM-PID

$\log_e(S) = 4.700$, $p = 0.347$, $\hat{\rho}_{\text{Spearman}} = 0.333$, $CI_{95\%} [-0.394, 0.804]$, $n_{\text{pairs}} = 10$



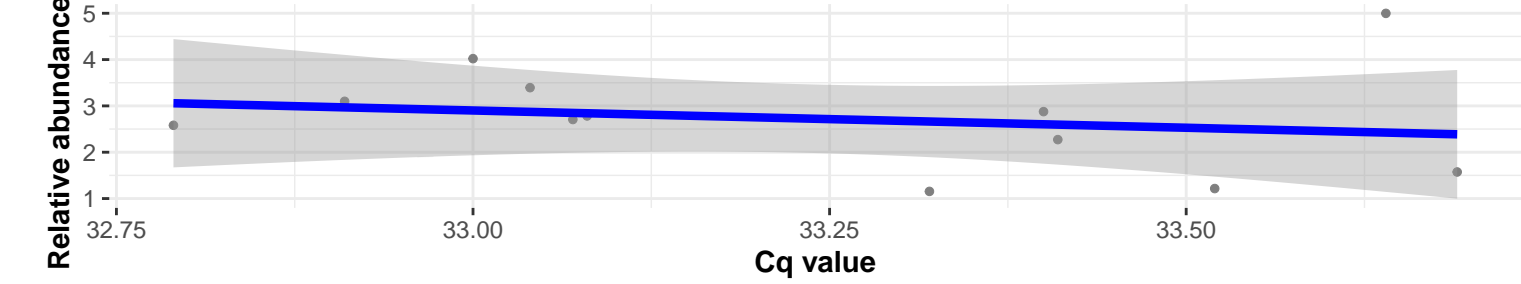
Correlation within: IM-DID

$\log_e(S) = 5.328$, $p = 0.489$, $\hat{\rho}_{\text{Spearman}} = -0.248$, $CI_{95\%} [-0.768, 0.469]$, $n_{\text{pairs}} = 10$



Correlation within: Extraction-blank

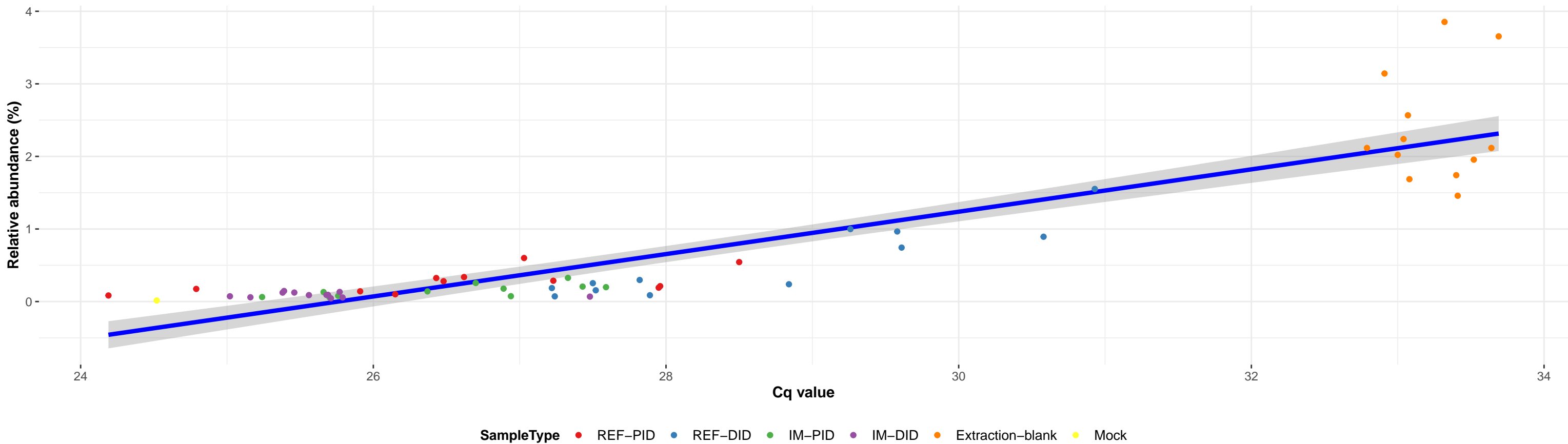
$\log_e(S) = 5.924$, $p = 0.331$, $\hat{\rho}_{\text{Spearman}} = -0.308$, $CI_{95\%} [-0.758, 0.340]$, $n_{\text{pairs}} = 12$



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

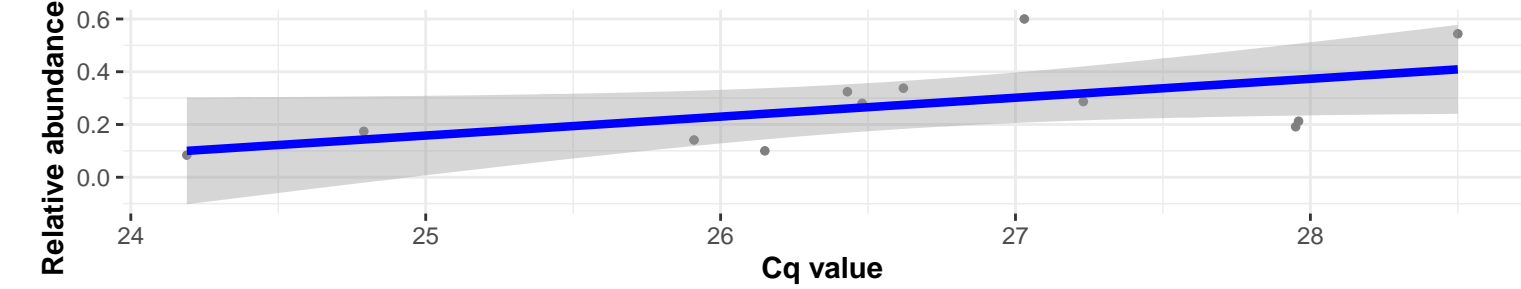
Correlation with all samples

$\log_e(S) = 8.709$, $p = 1.91\text{e-}16$, $\hat{\rho}_{\text{Spearman}} = 0.832$, $\text{CI}_{95\%} [0.729, 0.898]$, $n_{\text{pairs}} = 60$



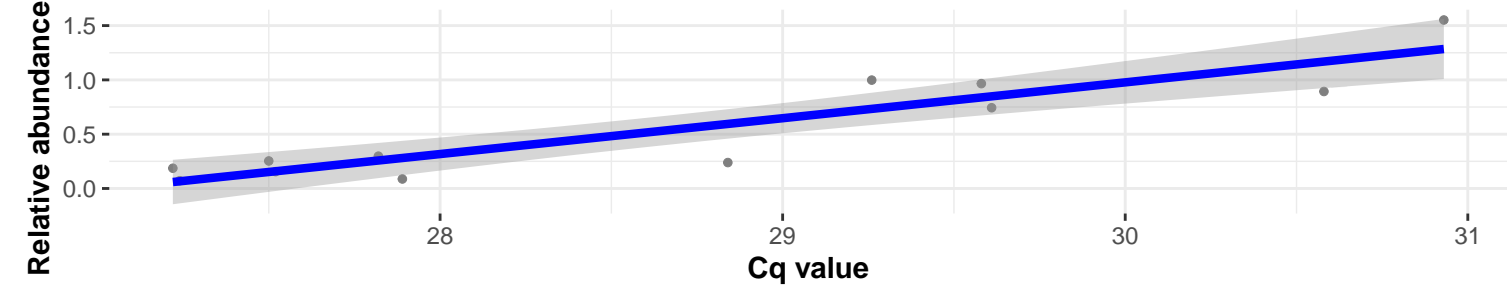
Correlation within: REF-PID

$\log_e(S) = 4.625$, $p = 0.024$, $\hat{\rho}_{\text{Spearman}} = 0.643$, $\text{CI}_{95\%} [0.091, 0.893]$, $n_{\text{pairs}} = 12$



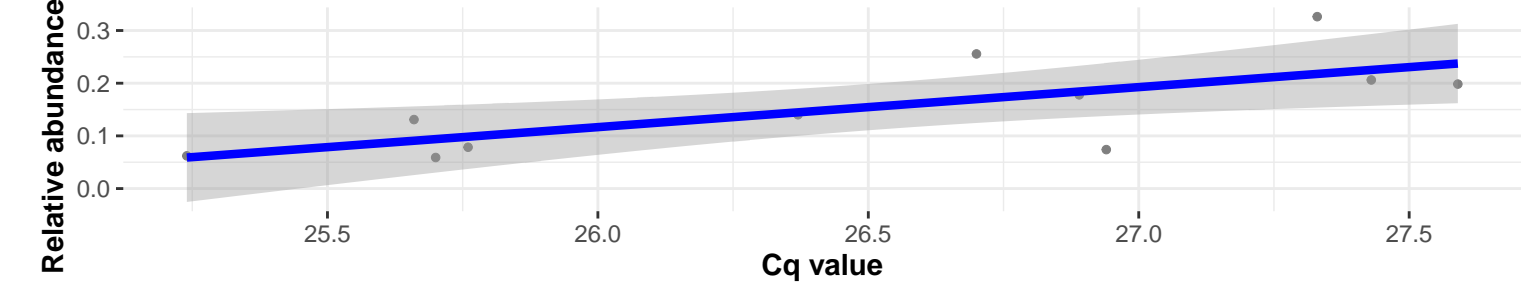
Correlation within: REF-DID

$\log_e(S) = 4.127$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.783$, $\text{CI}_{95\%} [0.364, 0.939]$, $n_{\text{pairs}} = 12$



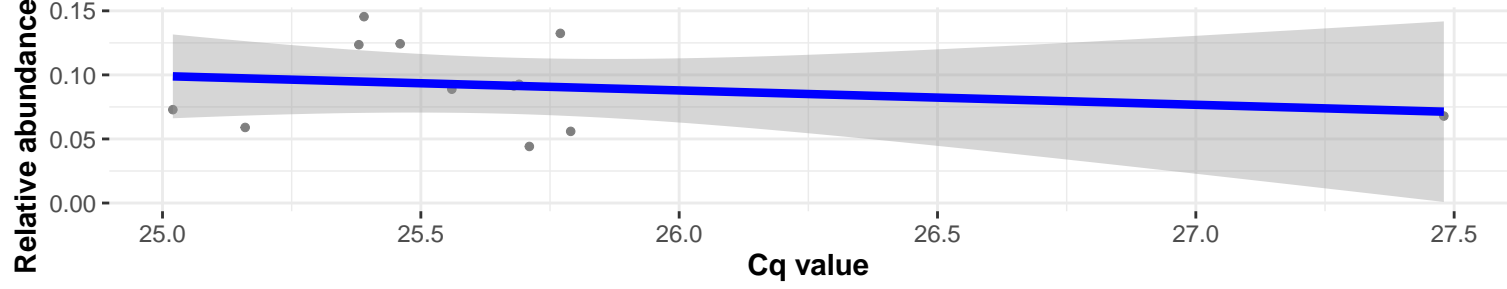
Correlation within: IM-PID

$\log_e(S) = 4.248$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = 0.682$, $\text{CI}_{95\%} [0.119, 0.913]$, $n_{\text{pairs}} = 11$



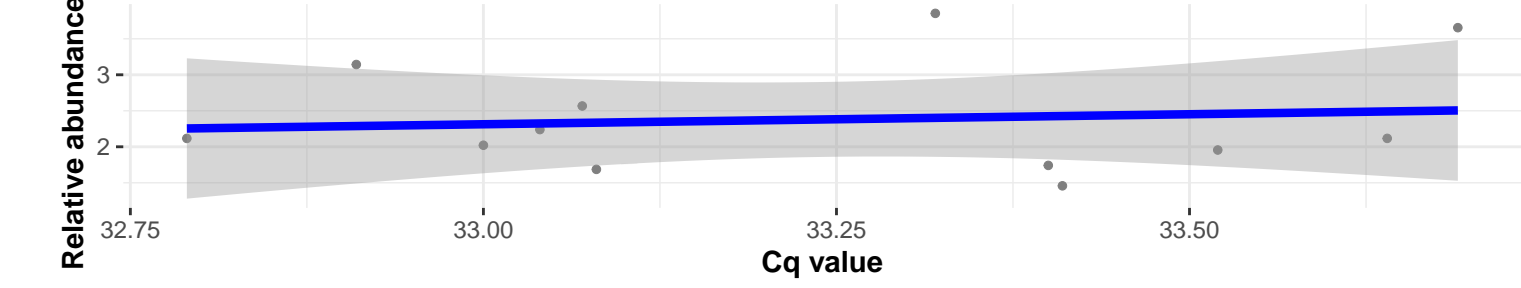
Correlation within: IM-DID

$\log_e(S) = 5.864$, $p = 0.471$, $\hat{\rho}_{\text{Spearman}} = -0.231$, $\text{CI}_{95\%} [-0.720, 0.412]$, $n_{\text{pairs}} = 12$

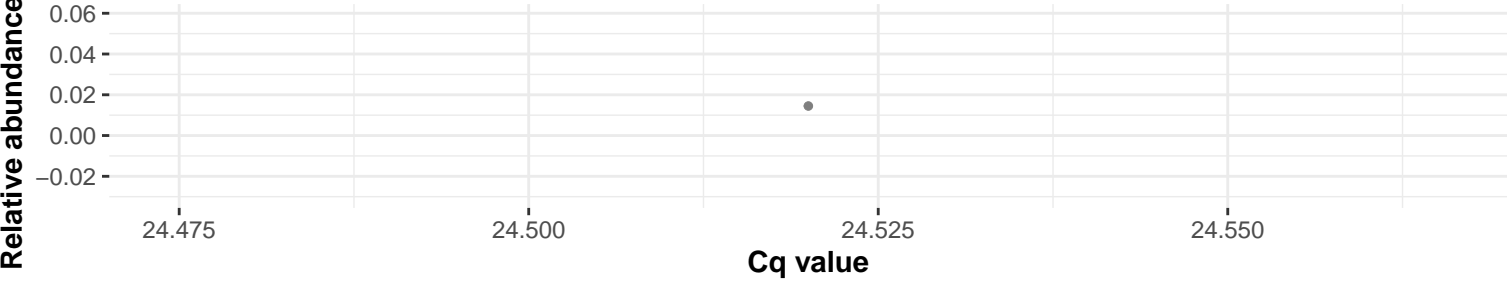


Correlation within: Extraction-blank

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



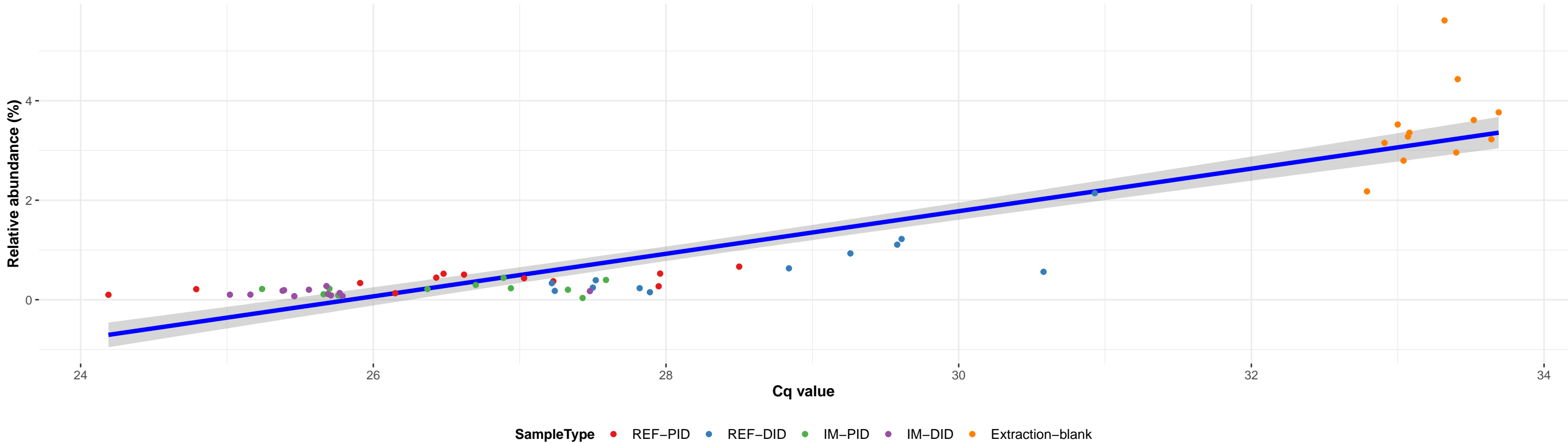
Correlation within: Mock



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

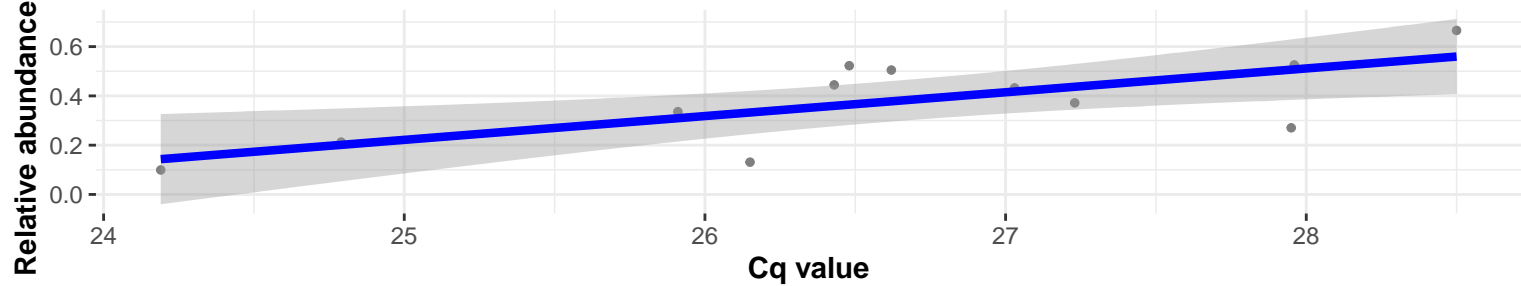
Correlation with all samples

$\log_e(S) = 8.684$, $p = 6.64e-16$, $\hat{\rho}_{\text{Spearman}} = 0.827$, $CI_{95\%} [0.721, 0.896]$, $n_{\text{pairs}} = 59$



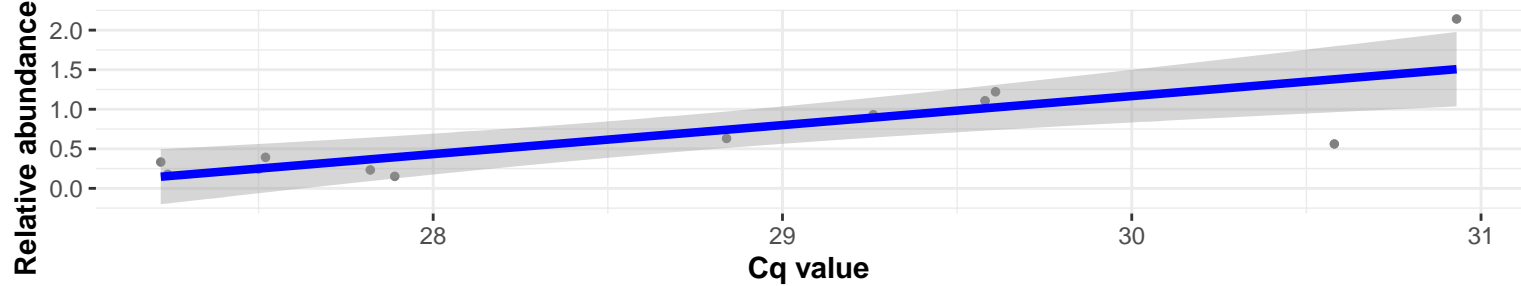
Correlation within: REF-PID

$\log_e(S) = 4.431$, $p = 0.010$, $\hat{\rho}_{\text{Spearman}} = 0.706$, $CI_{95\%} [0.204, 0.914]$, $n_{\text{pairs}} = 12$



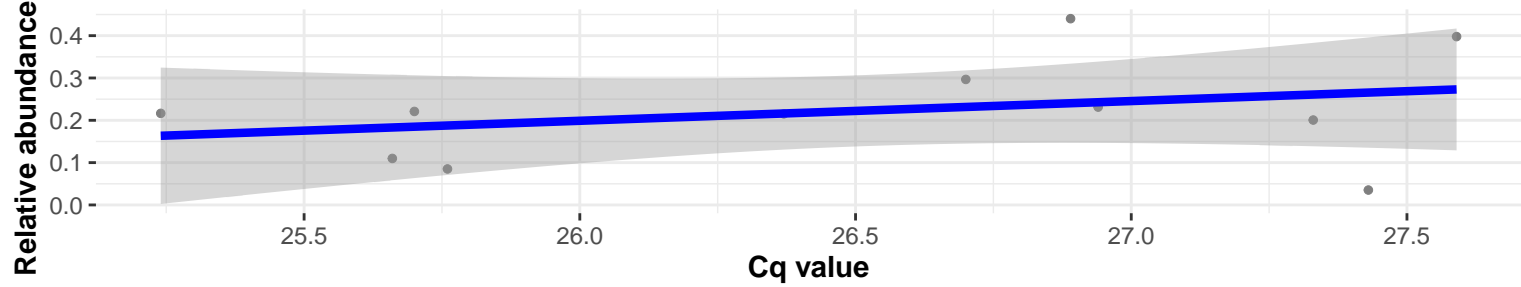
Correlation within: REF-DID

$\log_e(S) = 4.248$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.755$, $CI_{95\%} [0.303, 0.930]$, $n_{\text{pairs}} = 12$



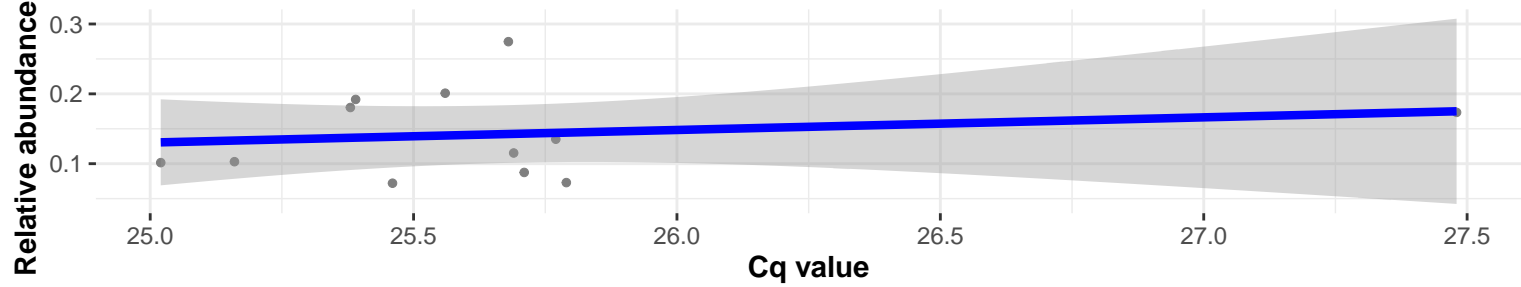
Correlation within: IM-PID

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



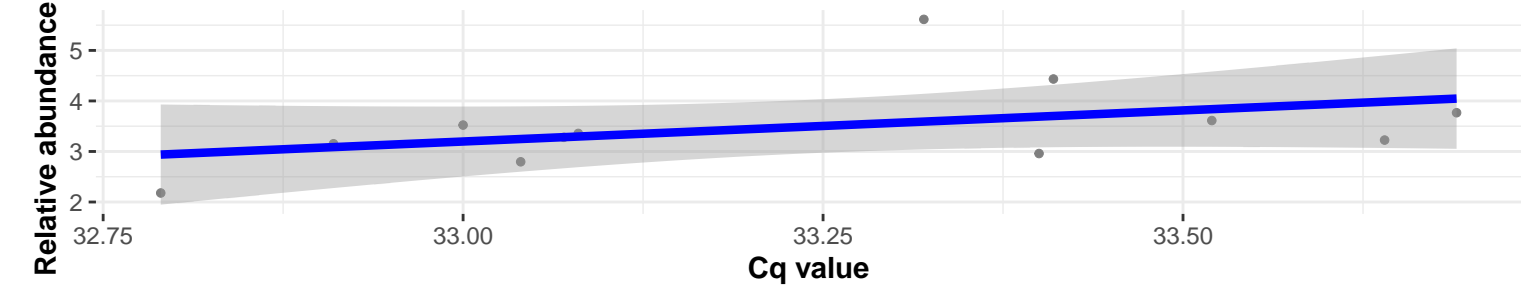
Correlation within: IM-DID

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



Correlation within: Extraction-blank

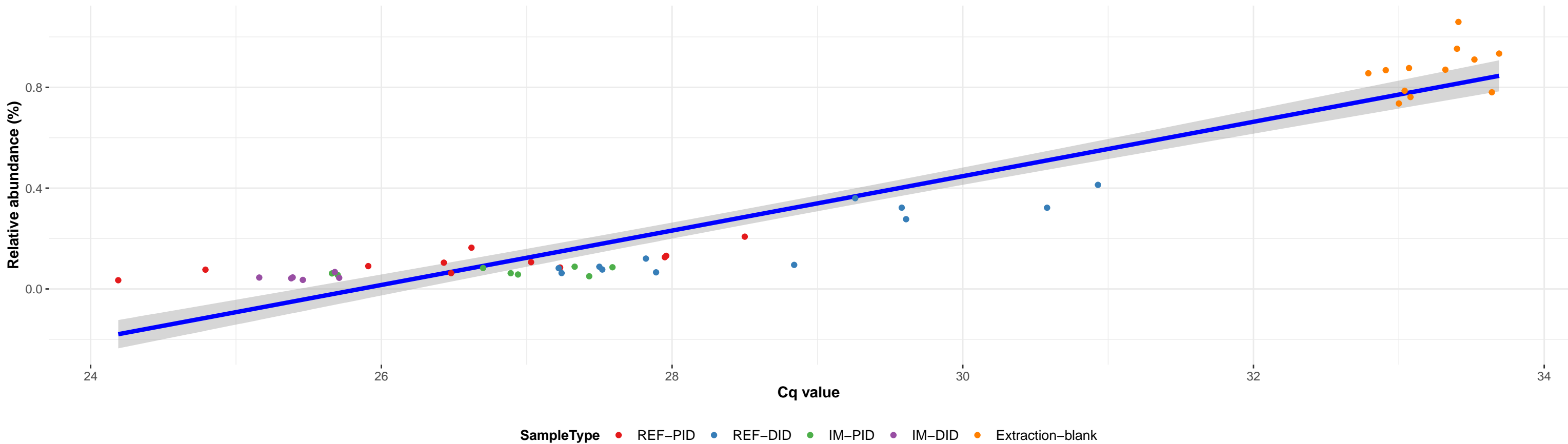
$\log_e(S) = 4.868$, $p = 0.067$, $\hat{\rho}_{\text{Spearman}} = 0.545$, $CI_{95\%} [-0.061, 0.858]$, $n_{\text{pairs}} = 12$



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

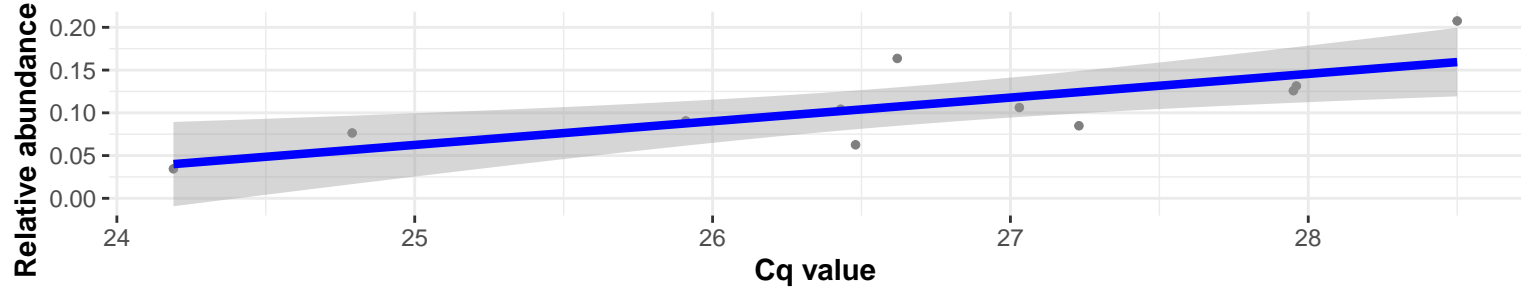
Correlation with all samples

$\log_e(S) = 7.592$, $p = 1.85e-18$, $\hat{\rho}_{\text{Spearman}} = 0.899$, $CI_{95\%} [0.824, 0.943]$, $n_{\text{pairs}} = 49$



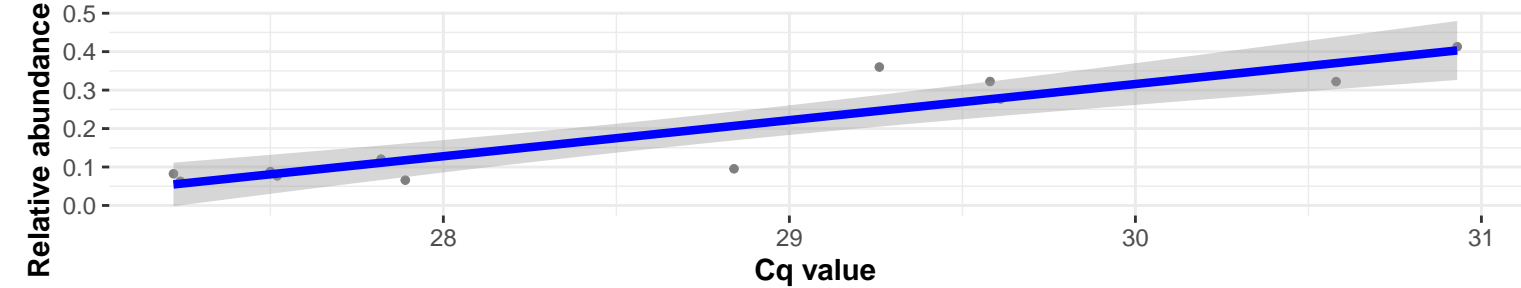
Correlation within: REF-PID

$\log_e(S) = 3.951$, $p = 0.006$, $\hat{\rho}_{\text{Spearman}} = 0.764$, $CI_{95\%} [0.283, 0.938]$, $n_{\text{pairs}} = 11$



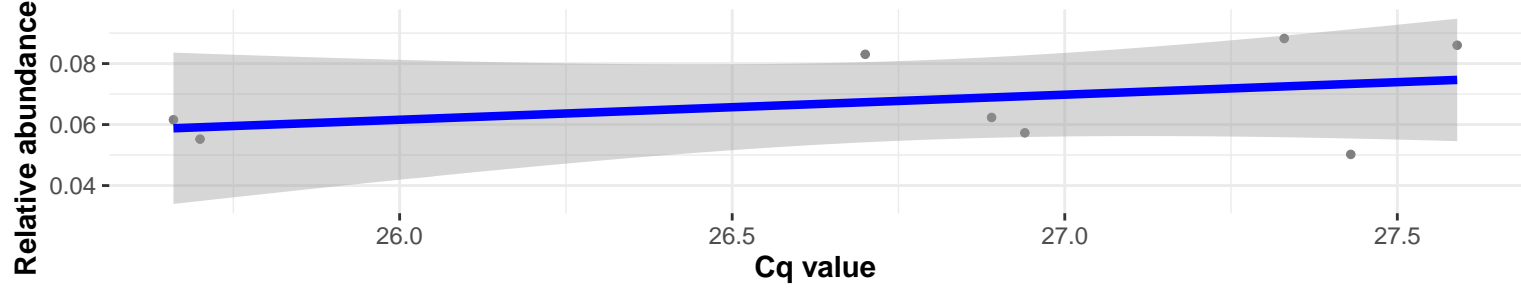
Correlation within: REF-DID

$\log_e(S) = 3.989$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.811$, $CI_{95\%} [0.428, 0.947]$, $n_{\text{pairs}} = 12$

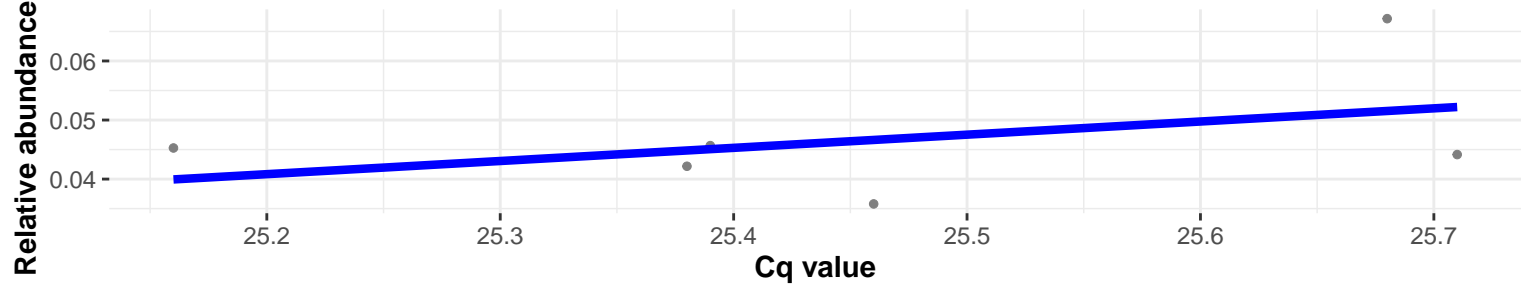


Correlation within: IM-PID

$\log_e(S) = 4.159$, $p = 0.570$, $\hat{\rho}_{\text{Spearman}} = 0.238$, $CI_{95\%} [-0.578, 0.816]$, $n_{\text{pairs}} = 8$

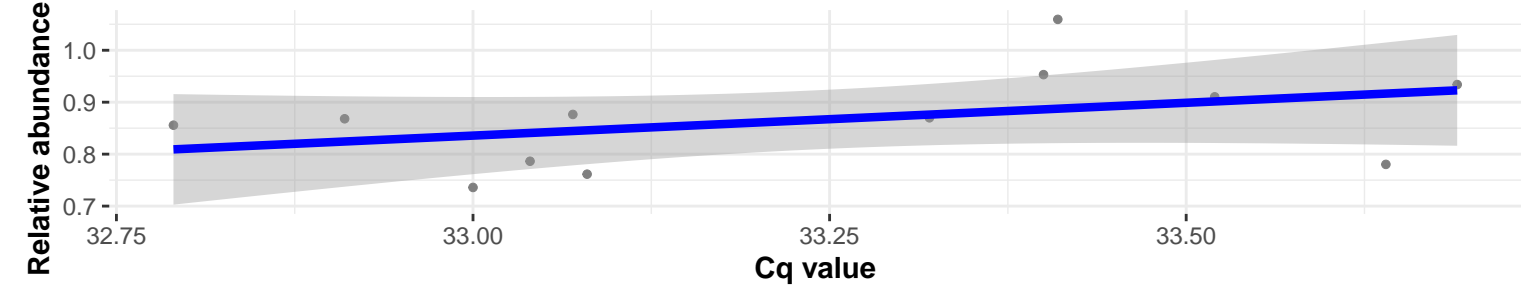


Correlation within: IM-DID



Correlation within: Extraction-blank

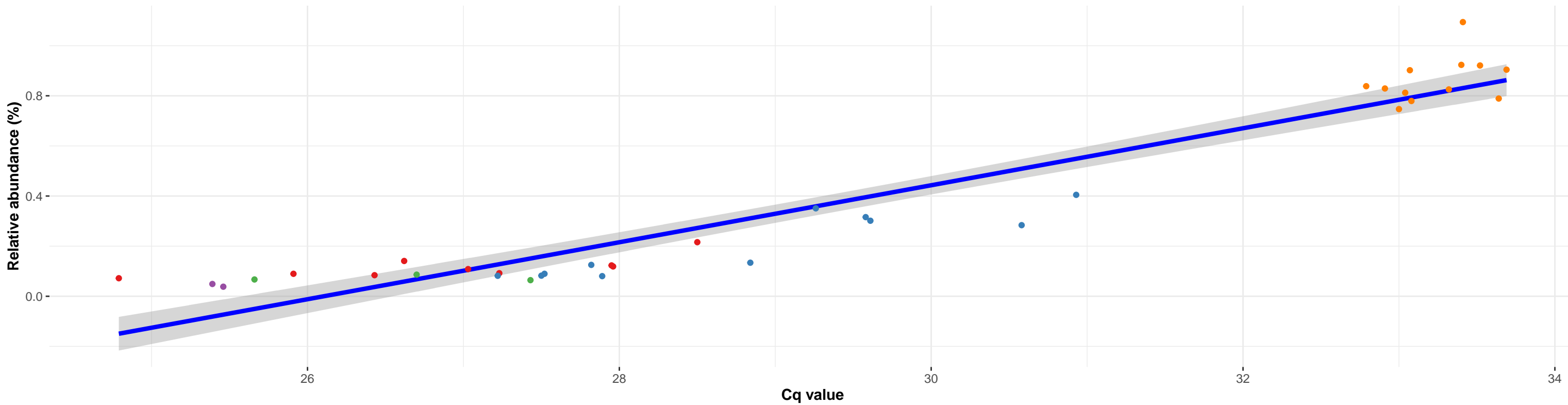
$\log_e(S) = 4.997$, $p = 0.112$, $\hat{\rho}_{\text{Spearman}} = 0.483$, $CI_{95\%} [-0.145, 0.833]$, $n_{\text{pairs}} = 12$



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

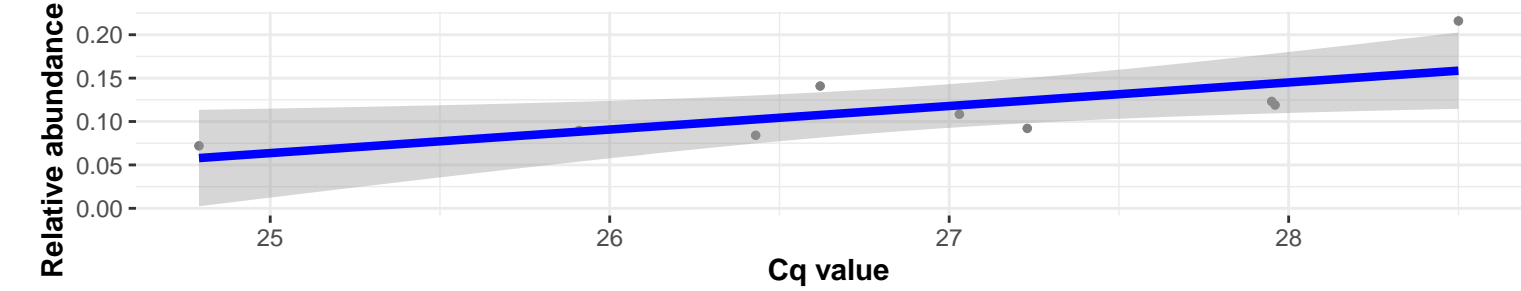
Correlation with all samples

$\log_e(S) = 6.516$, $p = 8.61\text{e-}16$, $\hat{\rho}_{\text{Spearman}} = 0.920$, $\text{CI}_{95\%} [0.846, 0.959]$, $n_{\text{pairs}} = 37$



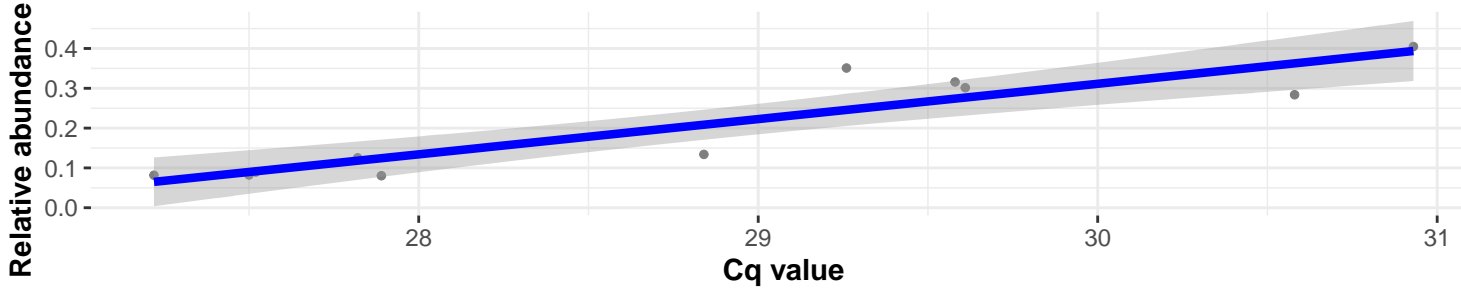
Correlation within: REF-PID

$\log_e(S) = 3.258$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = 0.783$, $\text{CI}_{95\%} [0.226, 0.954]$, $n_{\text{pairs}} = 9$

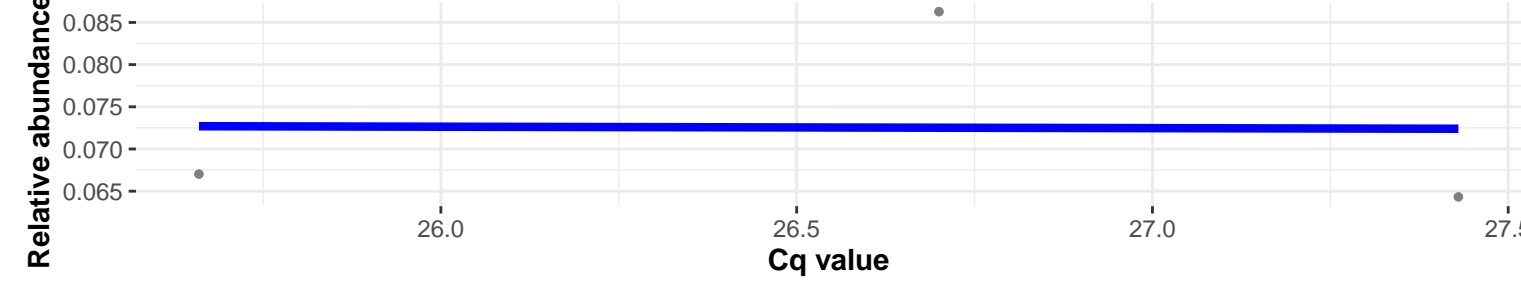


Correlation within: REF-DID

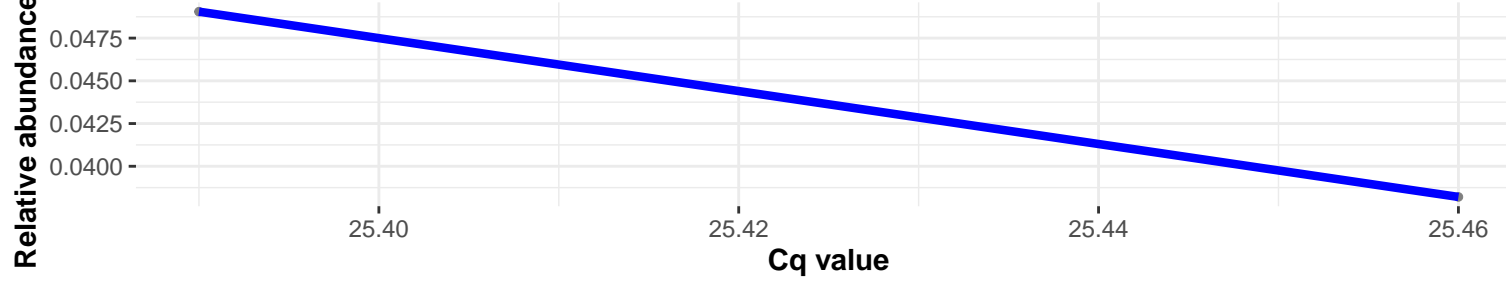
$\log_e(S) = 3.689$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.818$, $\text{CI}_{95\%} [0.412, 0.953]$, $n_{\text{pairs}} = 11$



Correlation within: IM-PID

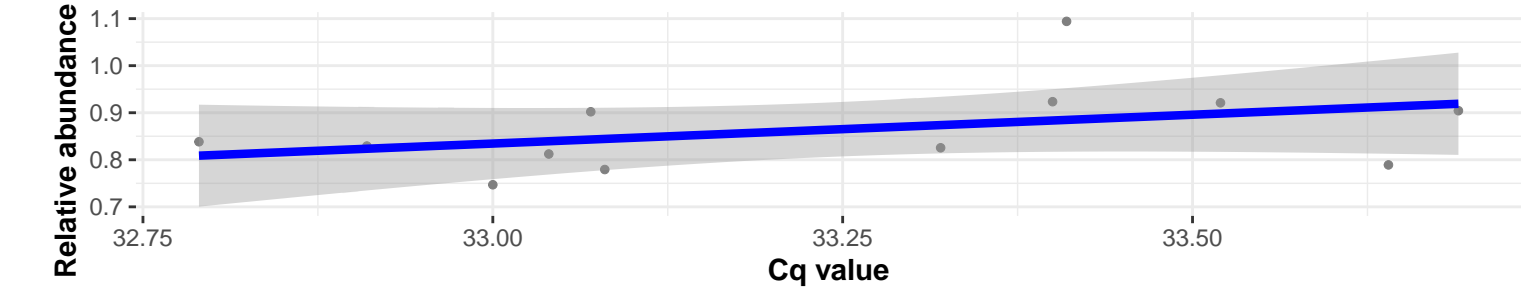


Correlation within: IM-DID



Correlation within: Extraction-blank

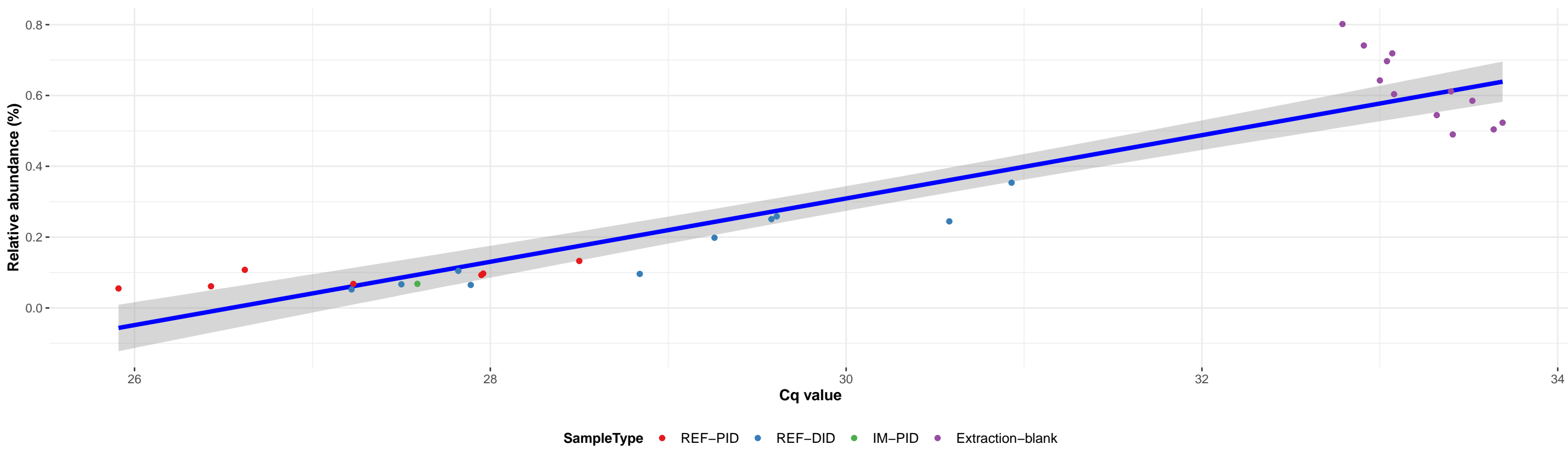
$\log_e(S) = 5.170$, $p = 0.217$, $\hat{\rho}_{\text{Spearman}} = 0.385$, $\text{CI}_{95\%} [-0.261, 0.792]$, $n_{\text{pairs}} = 12$



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

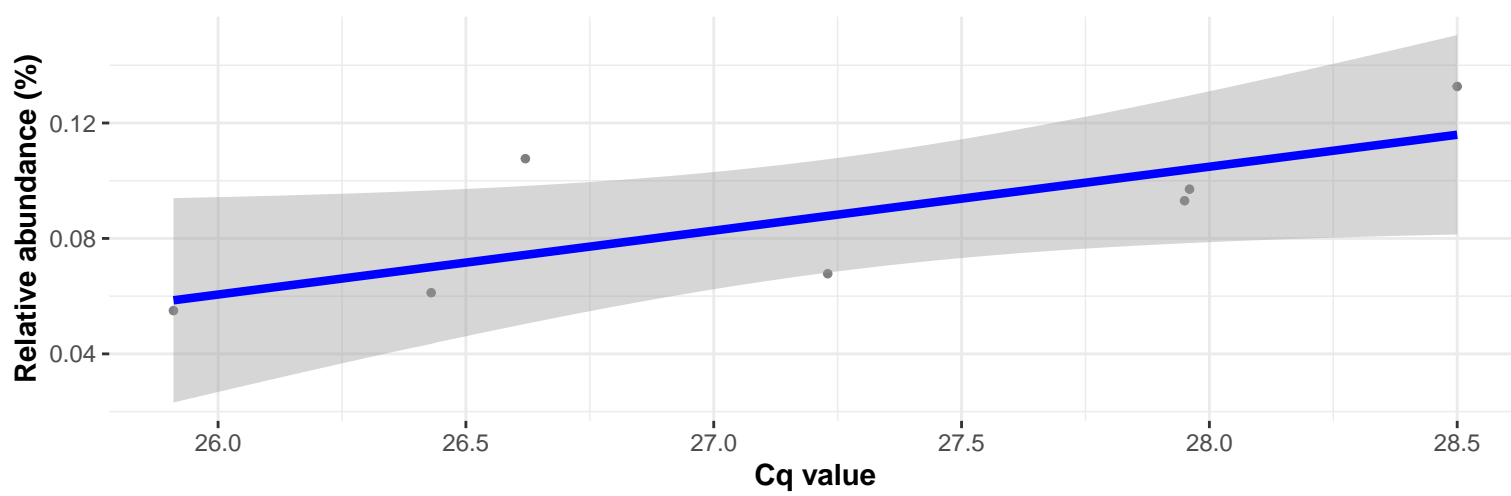
Correlation with all samples

$\log_e(S) = 6.542$, $p = 4.06\text{e-}09$, $\hat{\rho}_{\text{Spearman}} = 0.846$, $\text{CI}_{95\%} [0.692, 0.926]$, $n_{\text{pairs}} = 30$



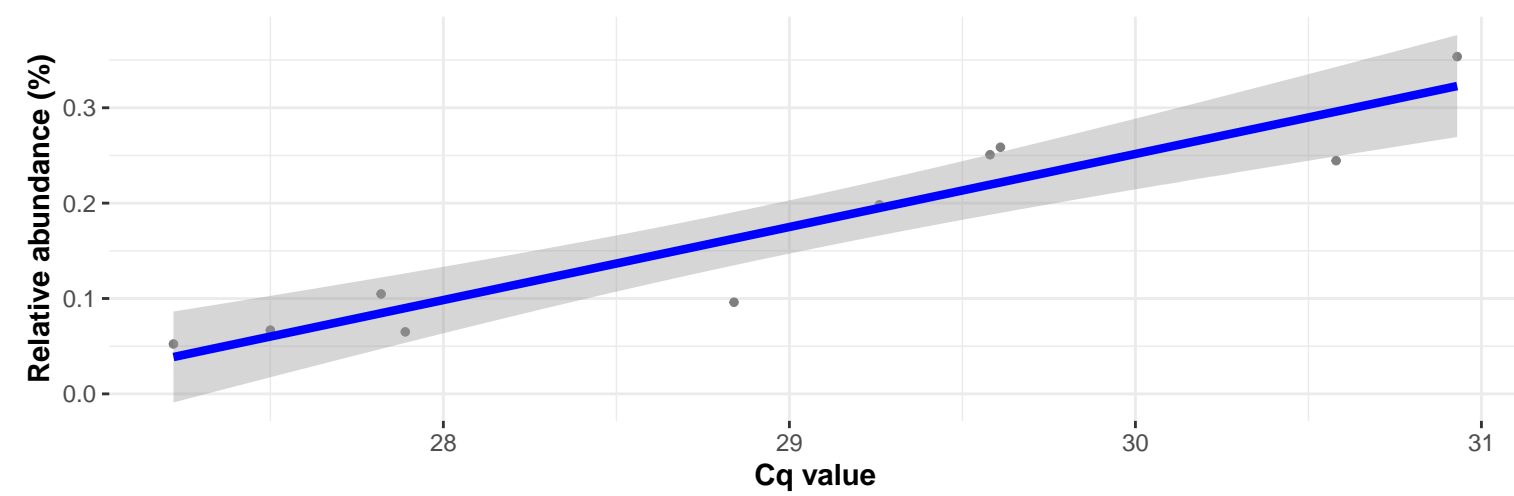
Correlation within: REF-PID

$\log_e(S) = 2.485$, $p = 0.036$, $\hat{\rho}_{\text{Spearman}} = 0.786$, $\text{CI}_{95\%} [0.051, 0.969]$, $n_{\text{pairs}} = 7$

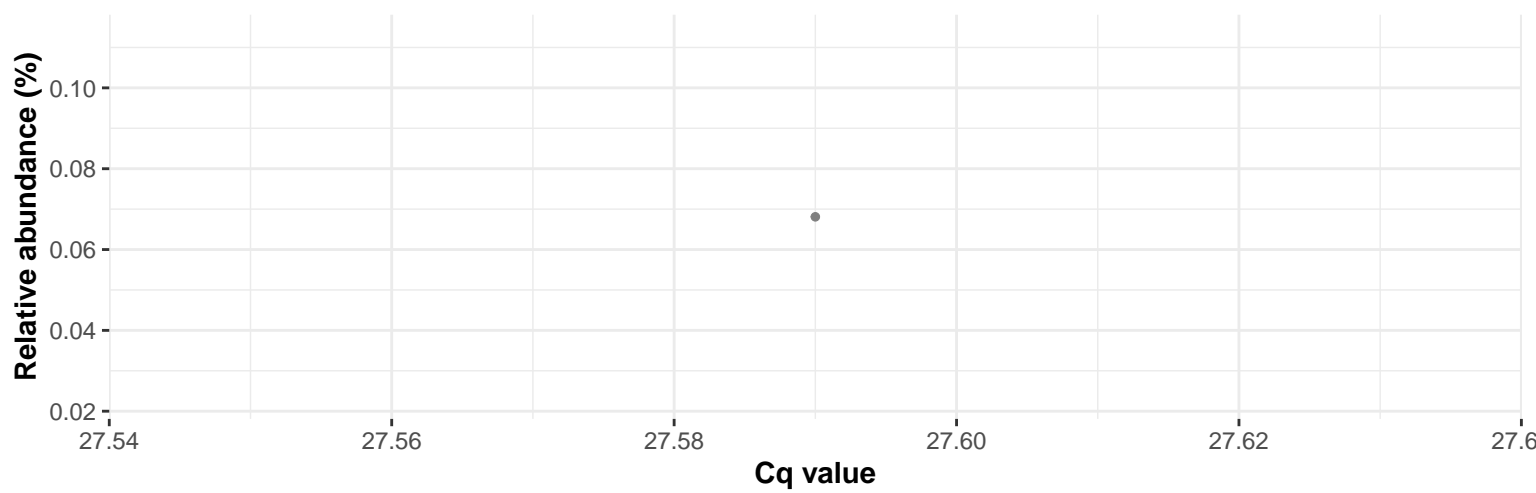


Correlation within: REF-DID

$\log_e(S) = 2.773$, $p = 3.44\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = 0.903$, $\text{CI}_{95\%} [0.620, 0.978]$, $n_{\text{pairs}} = 10$

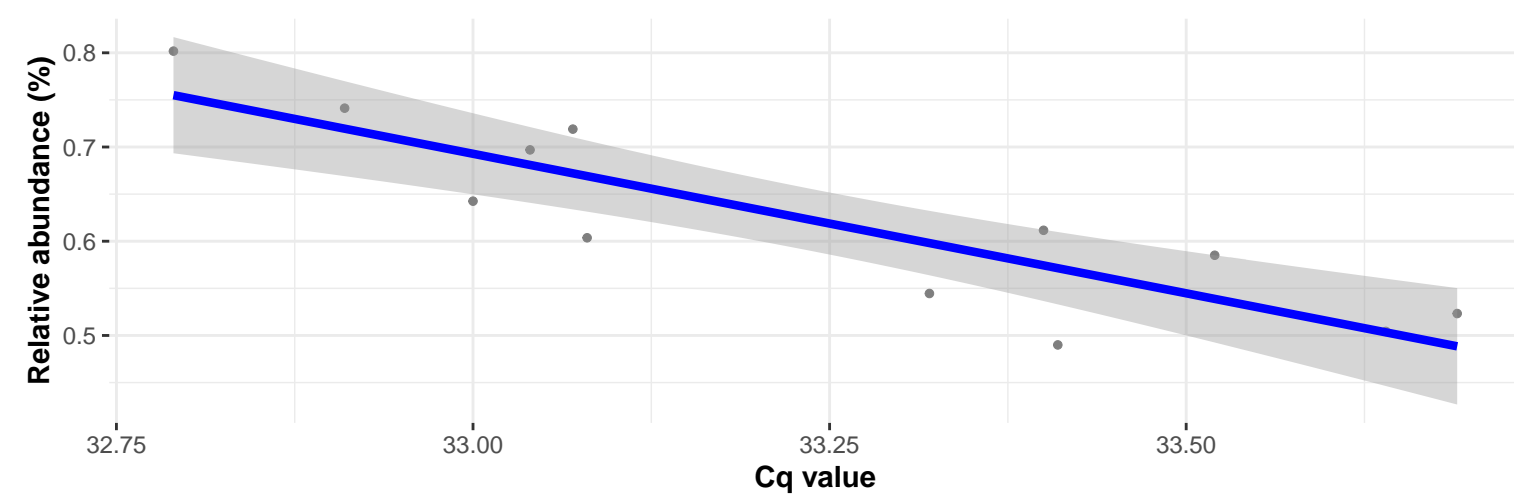


Correlation within: IM-PID



Correlation within: Extraction-blank

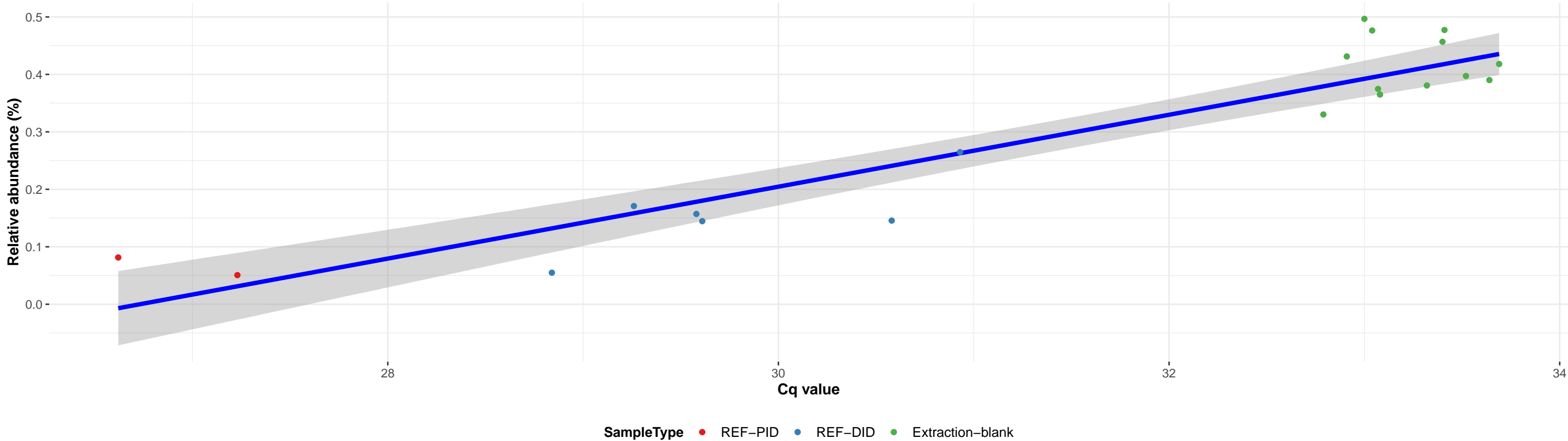
$\log_e(S) = 6.288$, $p = 1.53\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = -0.881$, $\text{CI}_{95\%} [-0.968, -0.609]$, $n_{\text{pairs}} = 12$



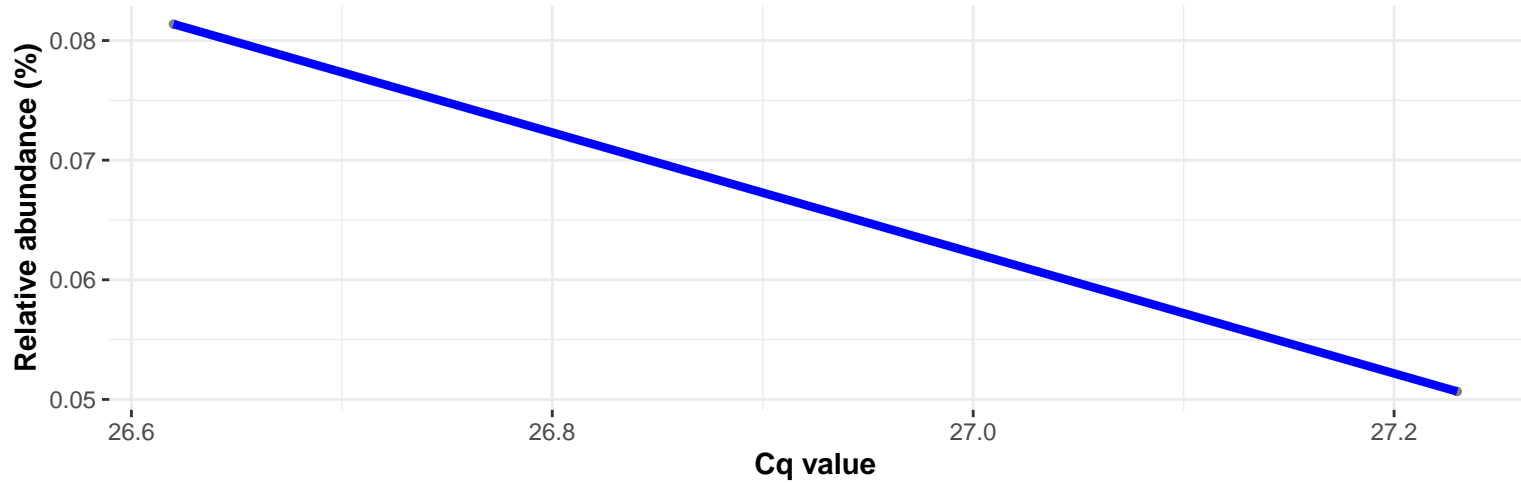
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; NA

Correlation with all samples

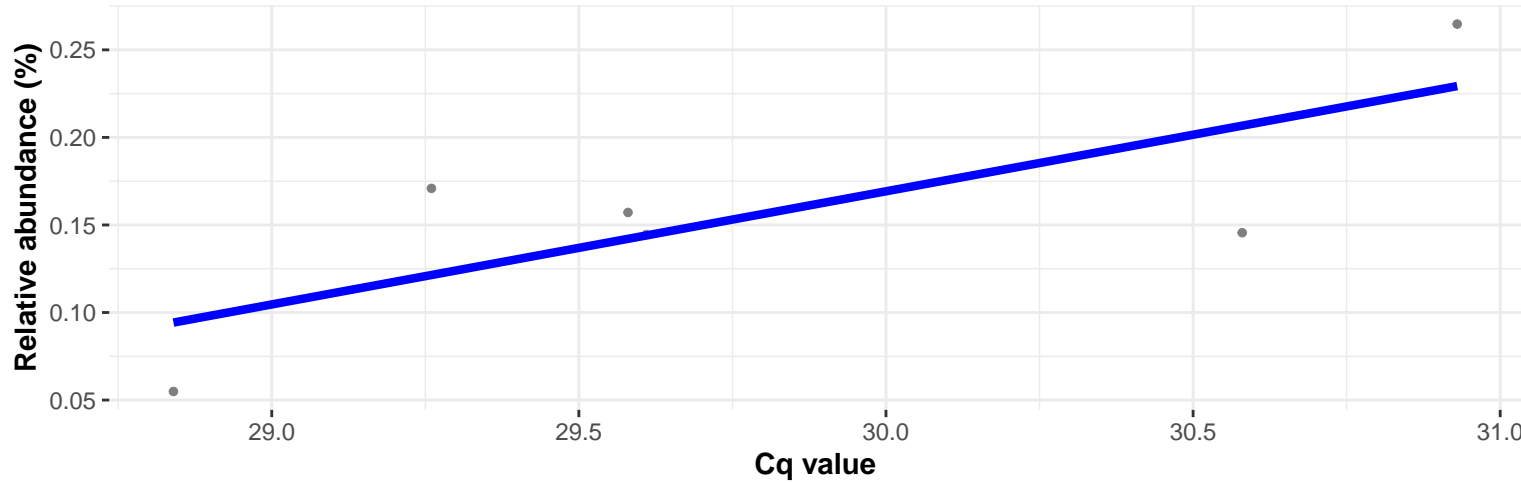
$\log_e(S) = 5.663$, $p = 4.39\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = 0.783$, $\text{CI}_{95\%} [0.512, 0.913]$, $n_{\text{pairs}} = 20$



Correlation within: REF-PID

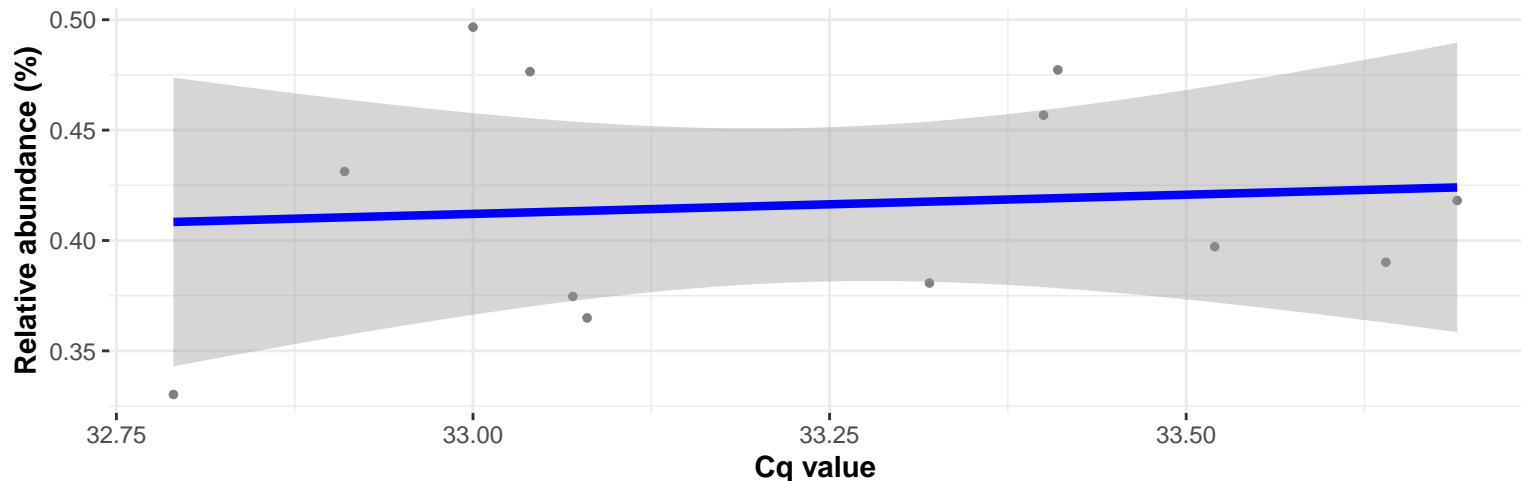


Correlation within: REF-DID



Correlation within: Extraction-blank

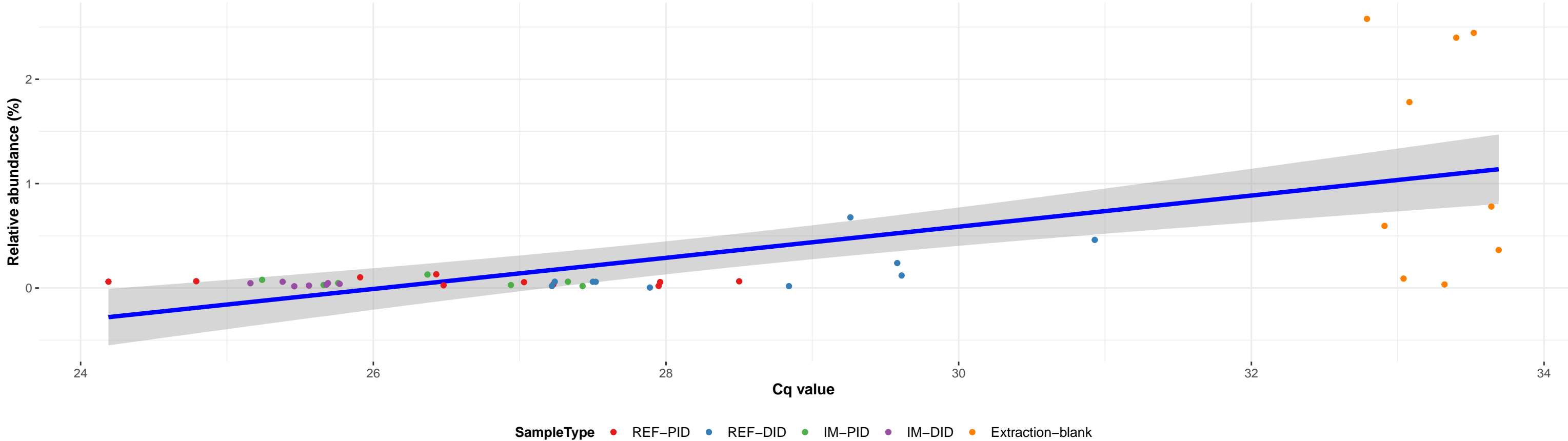
$\log_e(S) = 5.576$, $p = 0.812$, $\hat{\rho}_{\text{Spearman}} = 0.077$, $\text{CI}_{95\%} [-0.534, 0.635]$, $n_{\text{pairs}} = 12$



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Ralstonia; s__uncultured Ralstonia sp.

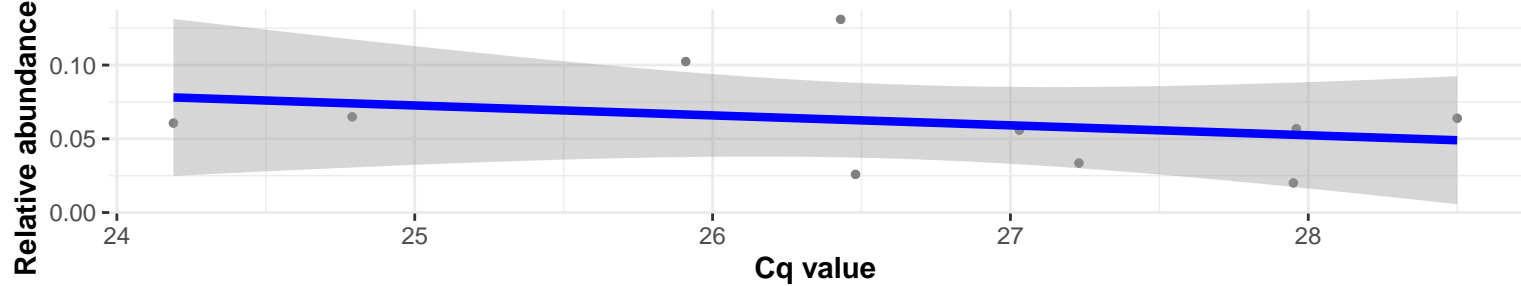
Correlation with all samples

$\log_e(S) = 8.835$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.481$, $\text{CI}_{95\%} [0.203, 0.688]$, $n_{\text{pairs}} = 43$



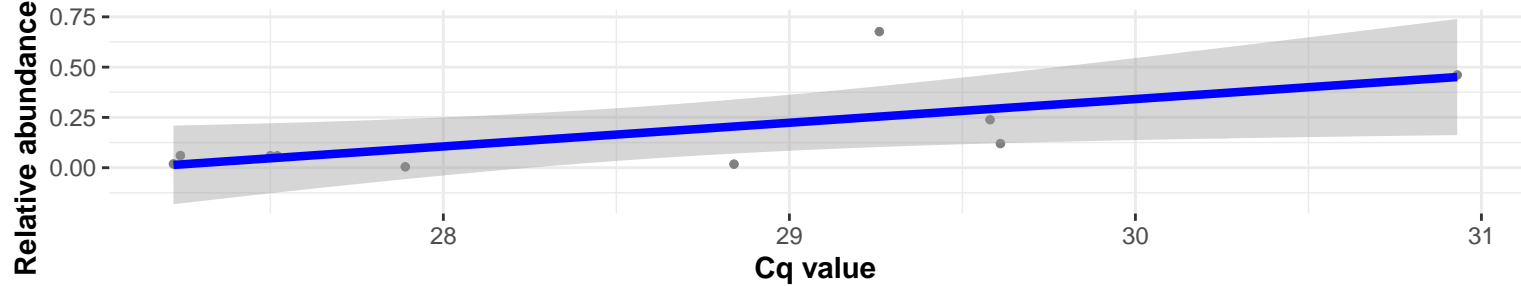
Correlation within: REF-PID

$\log_e(S) = 5.464$, $p = 0.214$, $\hat{\rho}_{\text{Spearman}} = -0.430$, $\text{CI}_{95\%} [-0.841, 0.294]$, $n_{\text{pairs}} = 10$



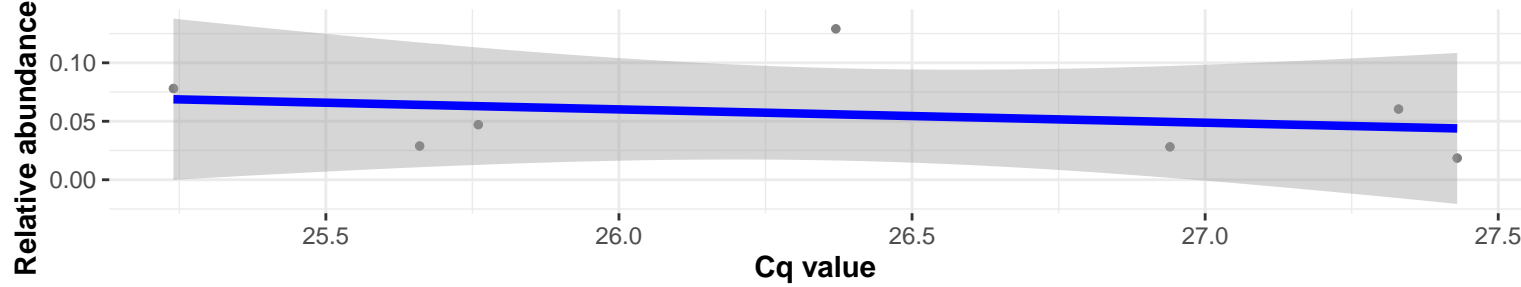
Correlation within: REF-DID

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



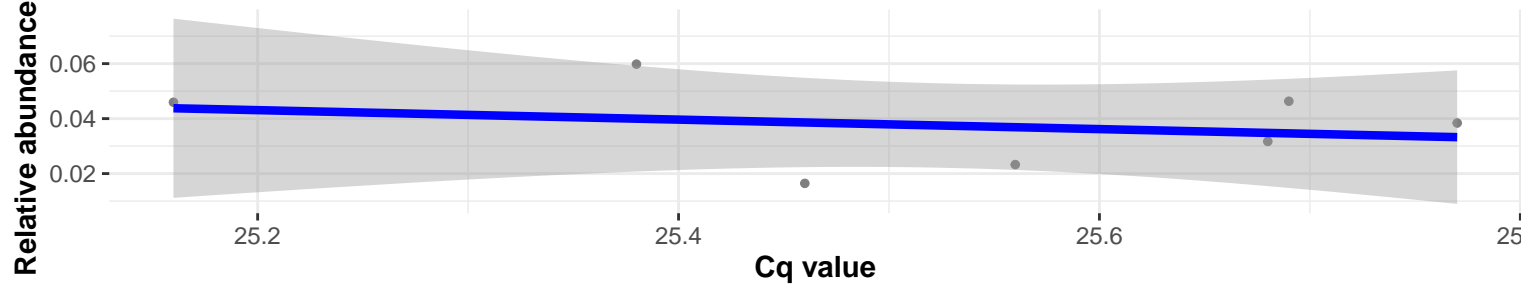
Correlation within: IM-PID

$\log_e(S) = 4.407$, $p = 0.294$, $\hat{\rho}_{\text{Spearman}} = -0.464$, $\text{CI}_{95\%} [-0.907, 0.467]$, $n_{\text{pairs}} = 7$



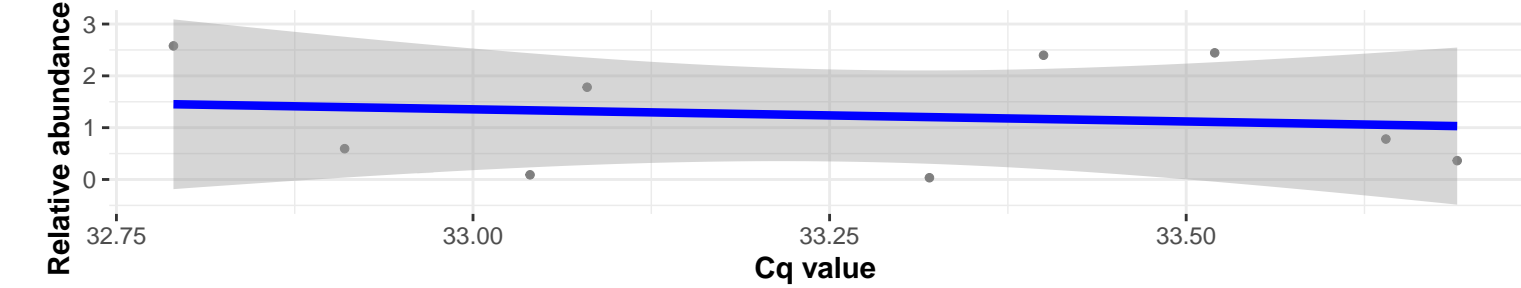
Correlation within: IM-DID

$\log_e(S) = 4.127$, $p = 0.819$, $\hat{\rho}_{\text{Spearman}} = -0.107$, $\text{CI}_{95\%} [-0.806, 0.717]$, $n_{\text{pairs}} = 7$



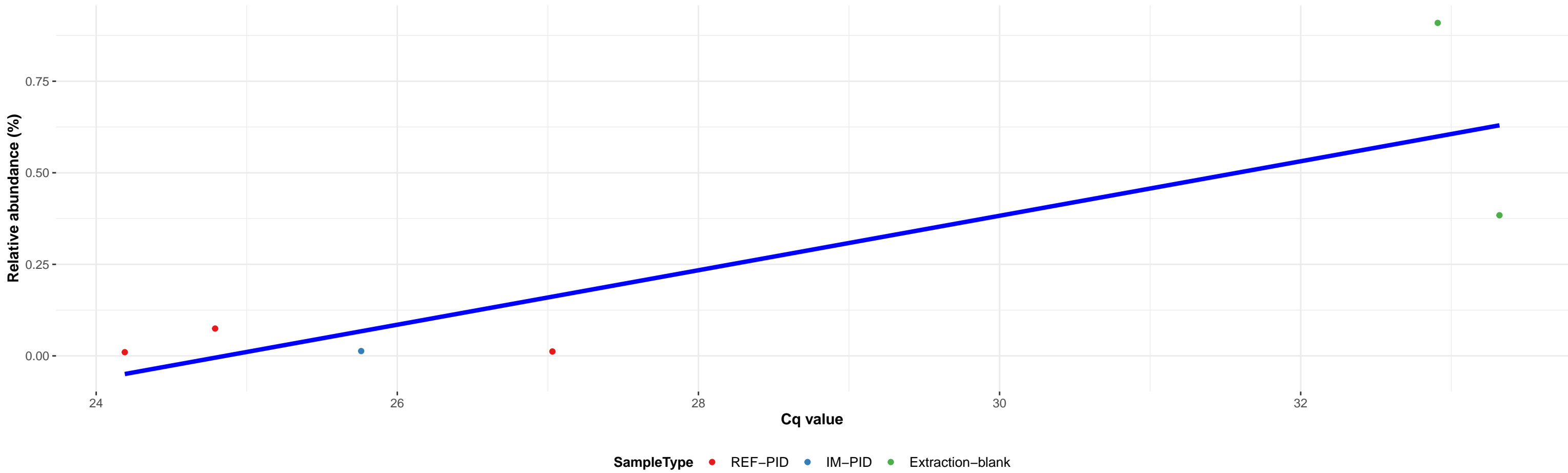
Correlation within: Extraction-blank

$\log_e(S) = 4.913$, $p = 0.732$, $\hat{\rho}_{\text{Spearman}} = -0.133$, $\text{CI}_{95\%} [-0.743, 0.598]$, $n_{\text{pairs}} = 9$

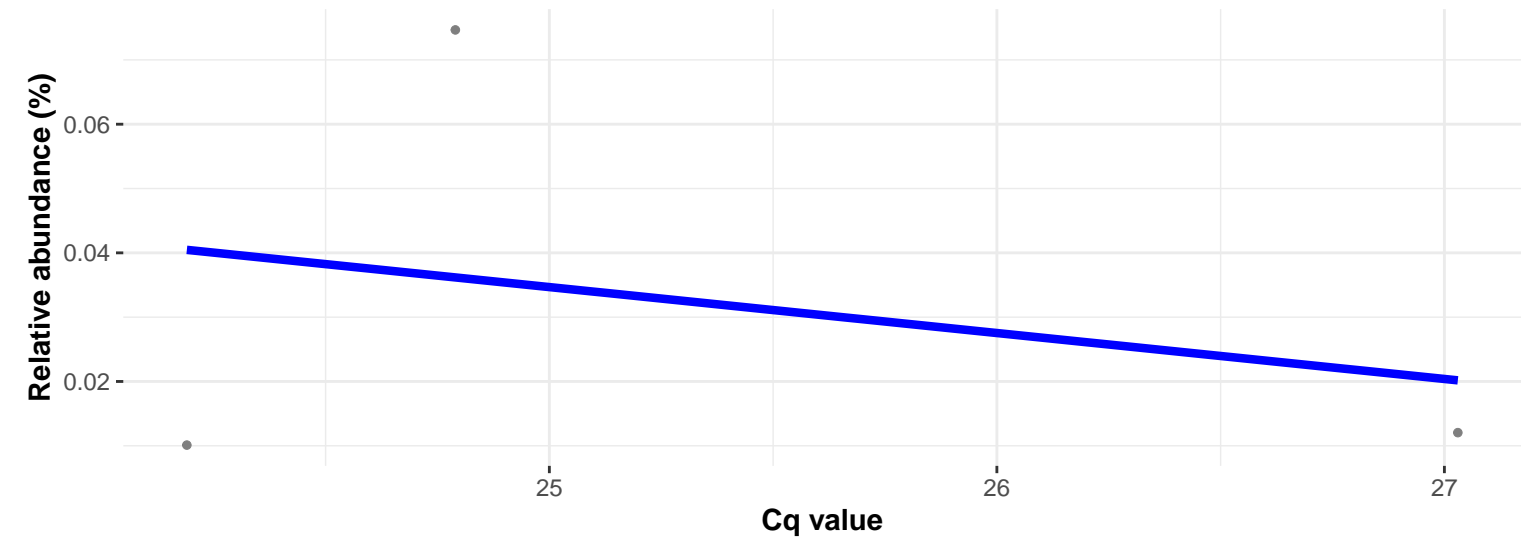


k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfuromonadales; f__Desulfuromonadaceae; g__Pelobacter; s__uncultured bacterium

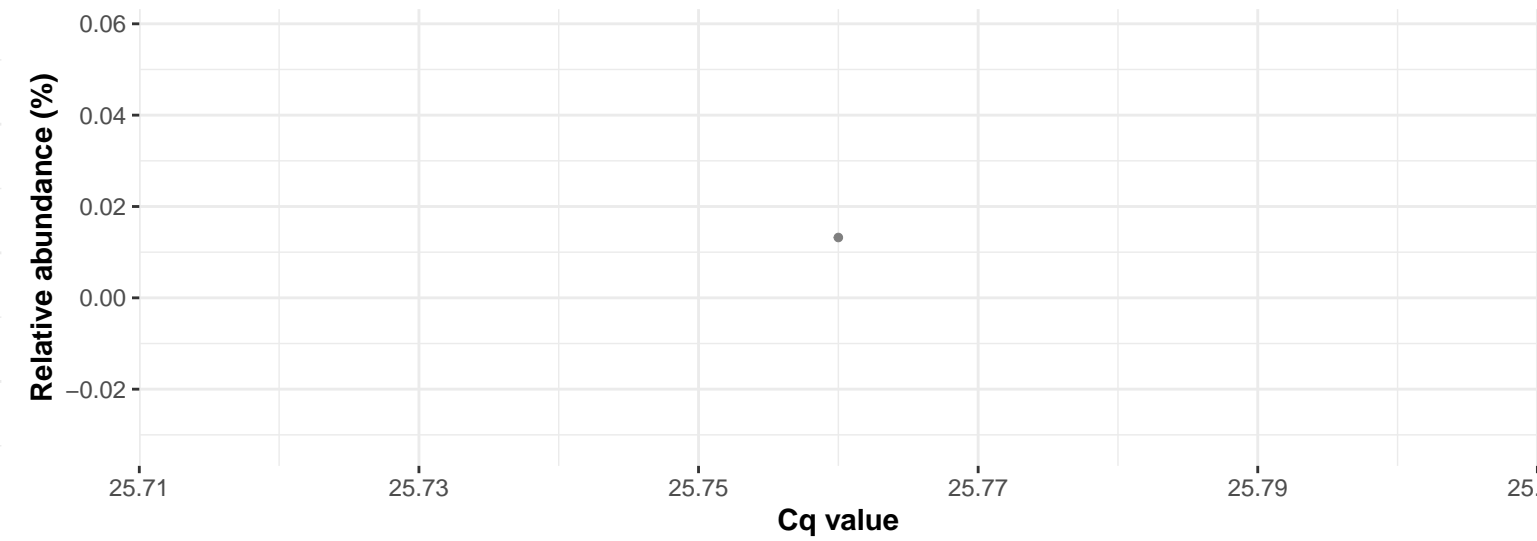
Correlation with all samples



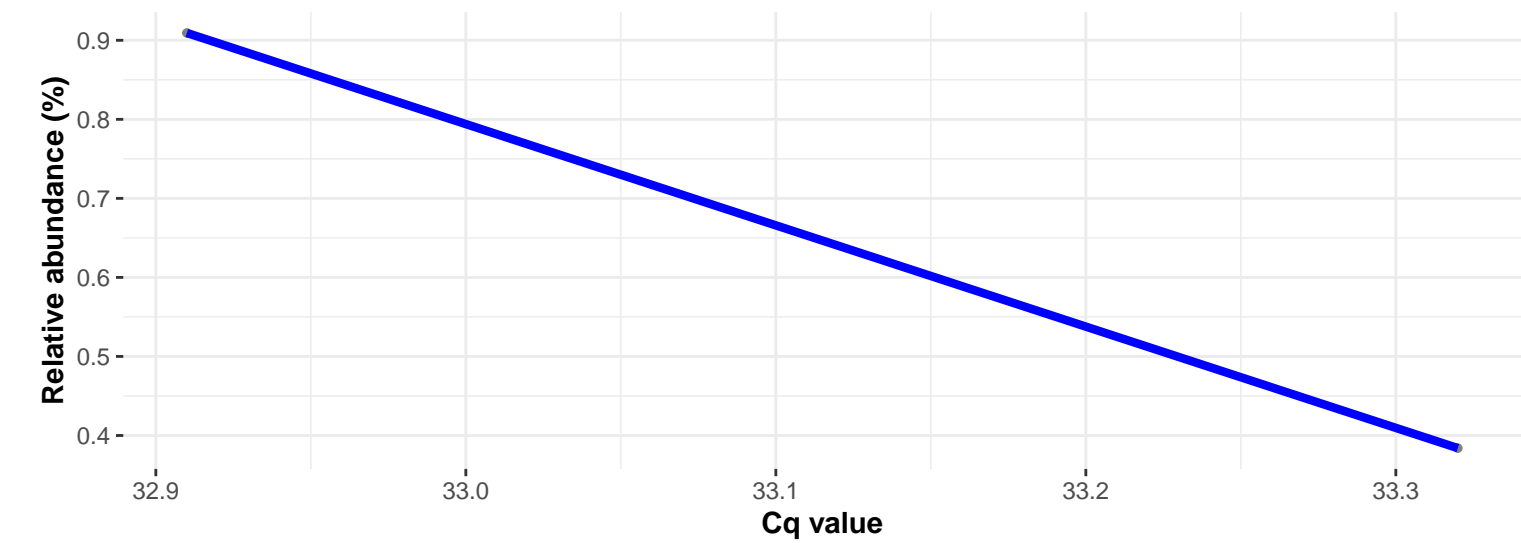
Correlation within: REF-PID



Correlation within: IM-PID



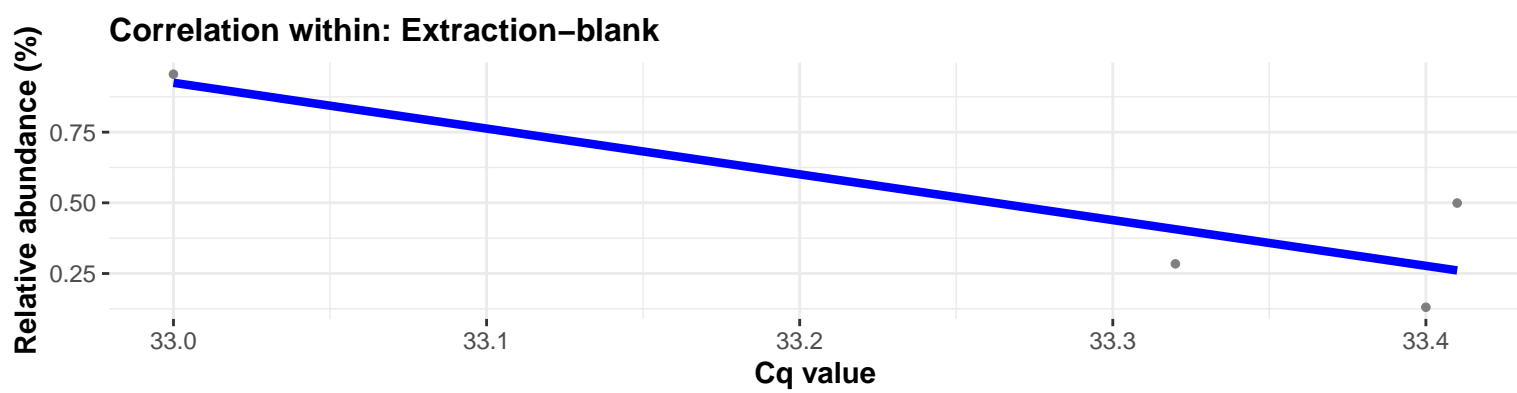
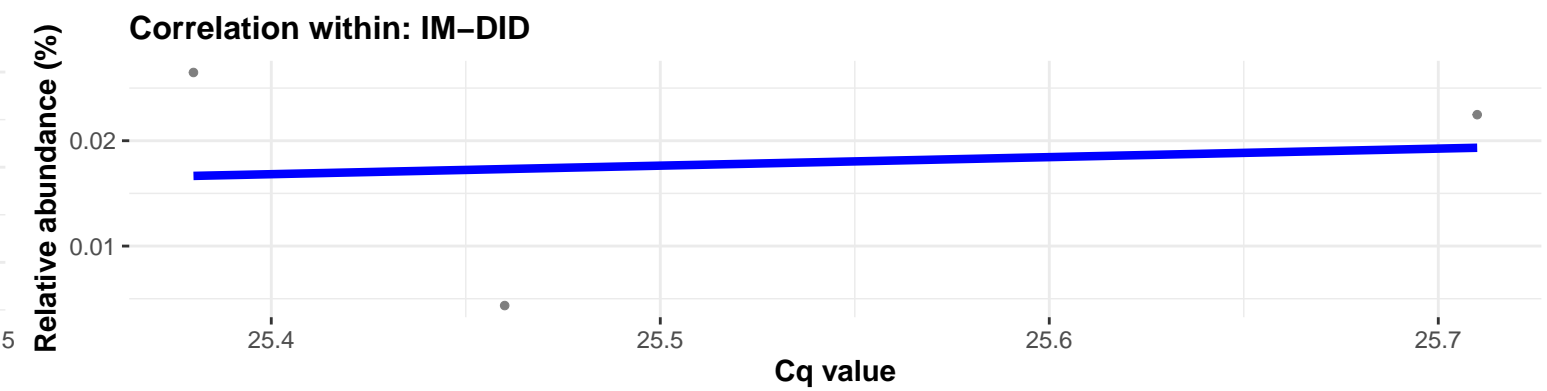
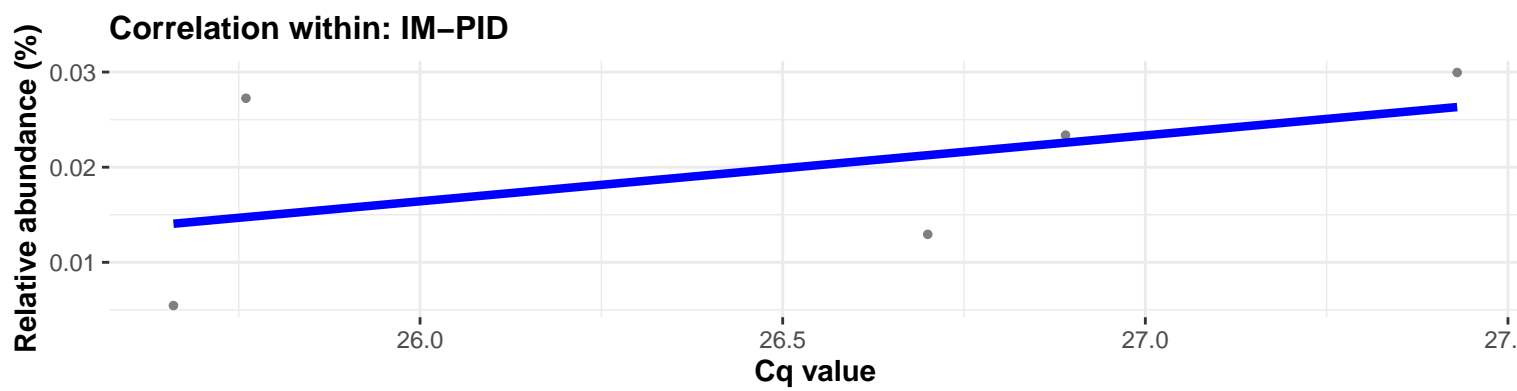
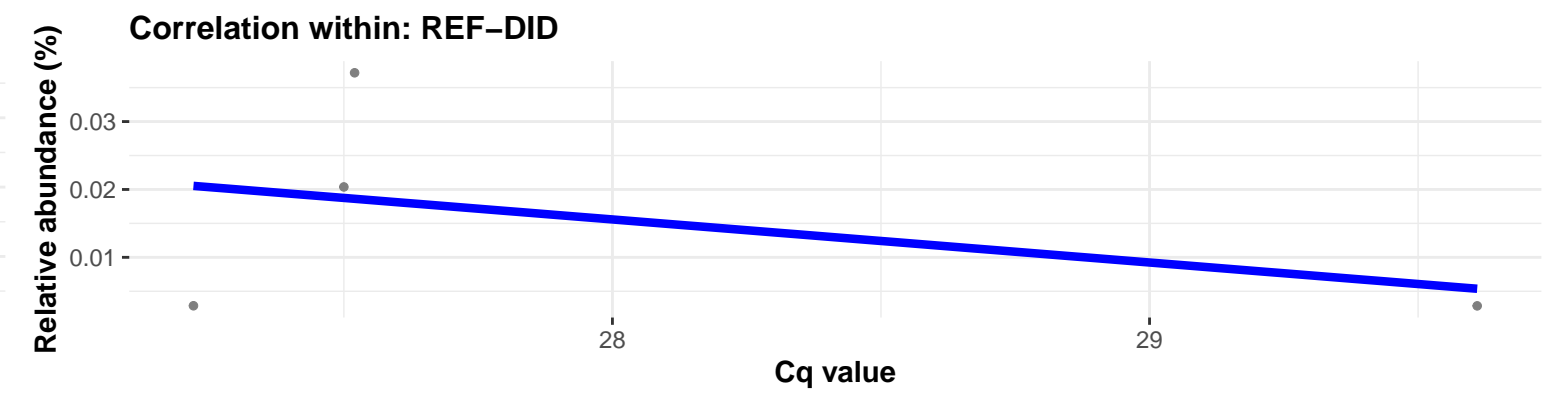
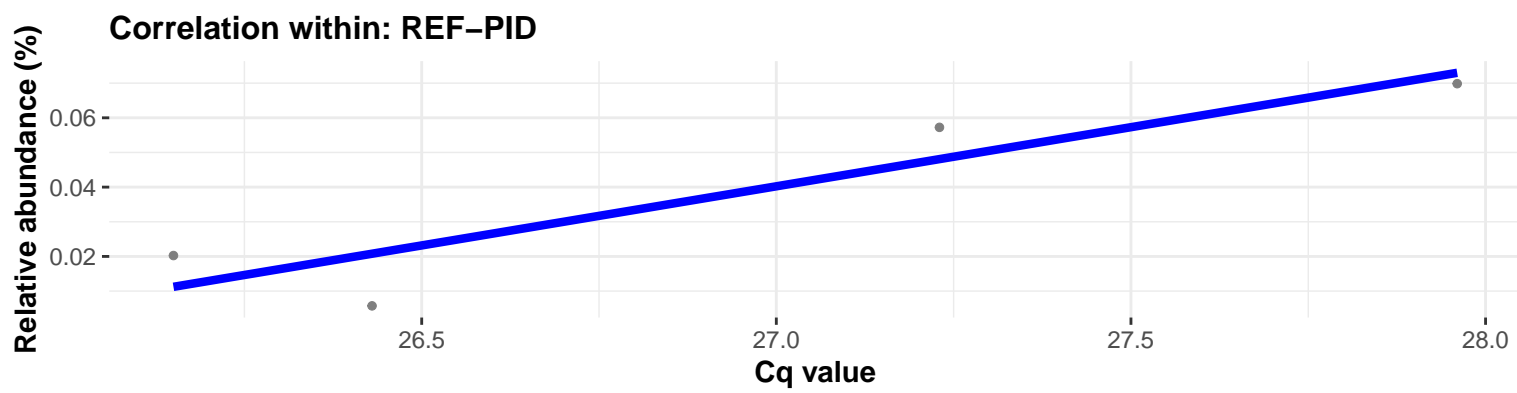
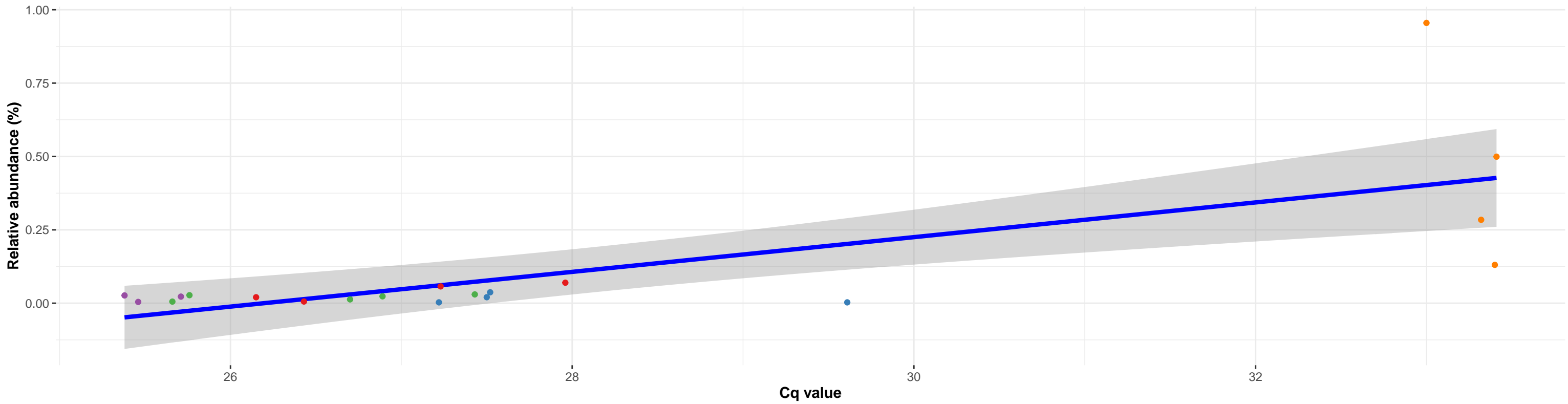
Correlation within: Extraction-blank



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

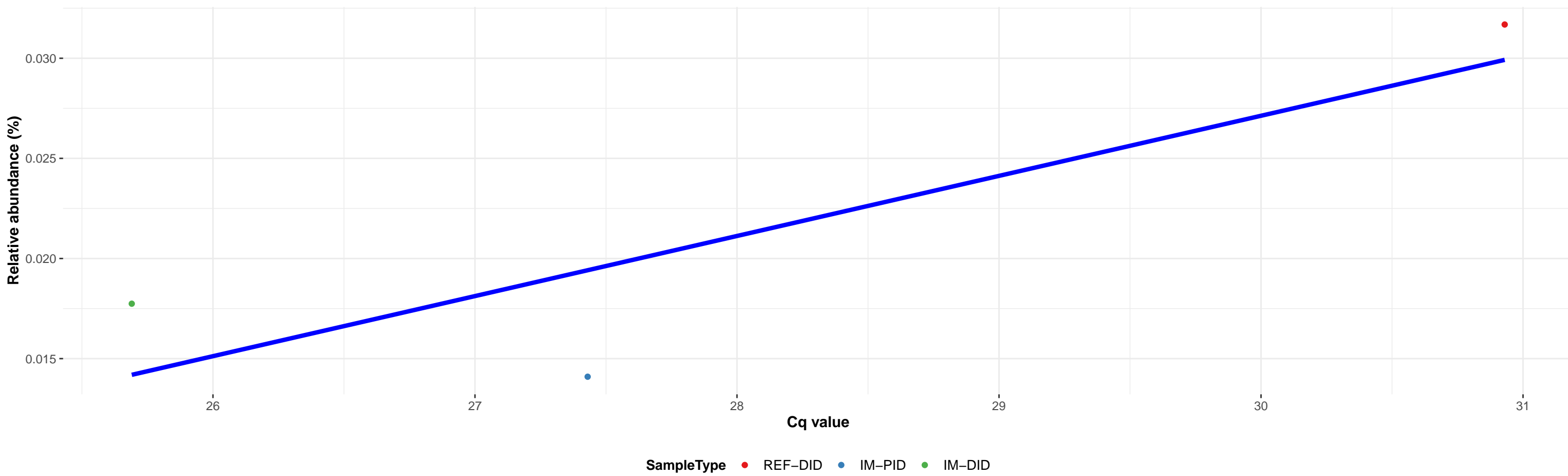
Correlation with all samples

$\log_e(S) = 6.277$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.600$, $CI_{95\%} [0.201, 0.828]$, $n_{\text{pairs}} = 20$

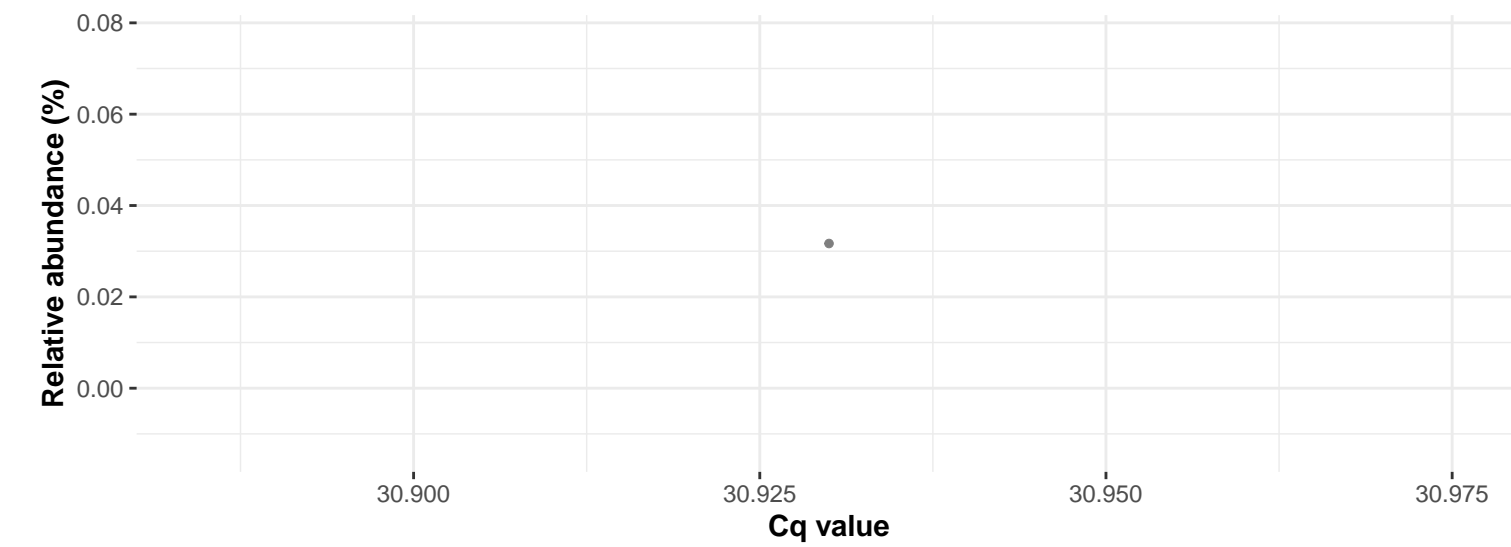


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Cupriavidus; NA

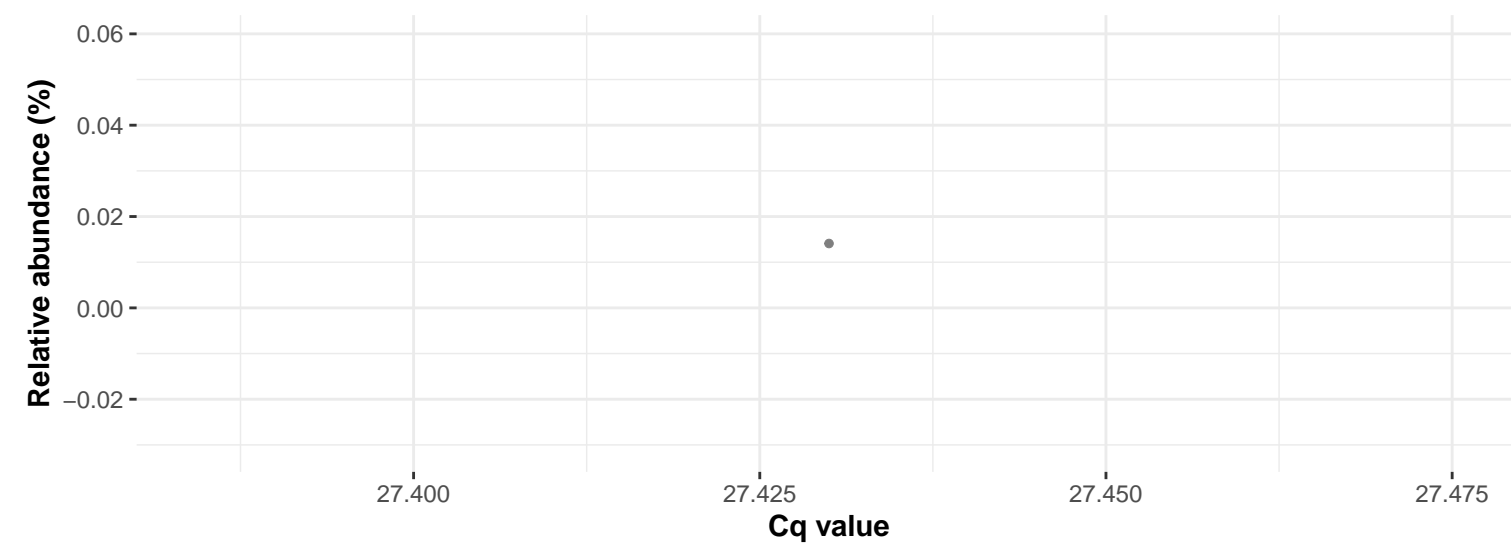
Correlation with all samples



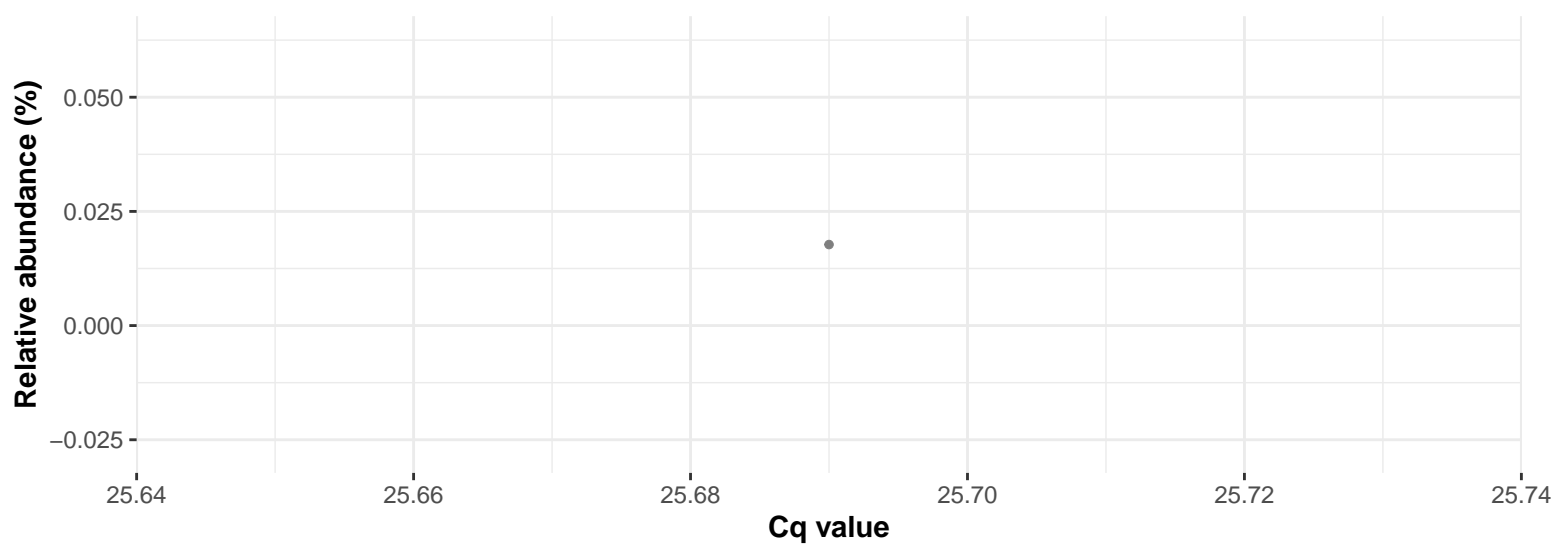
Correlation within: REF-DID



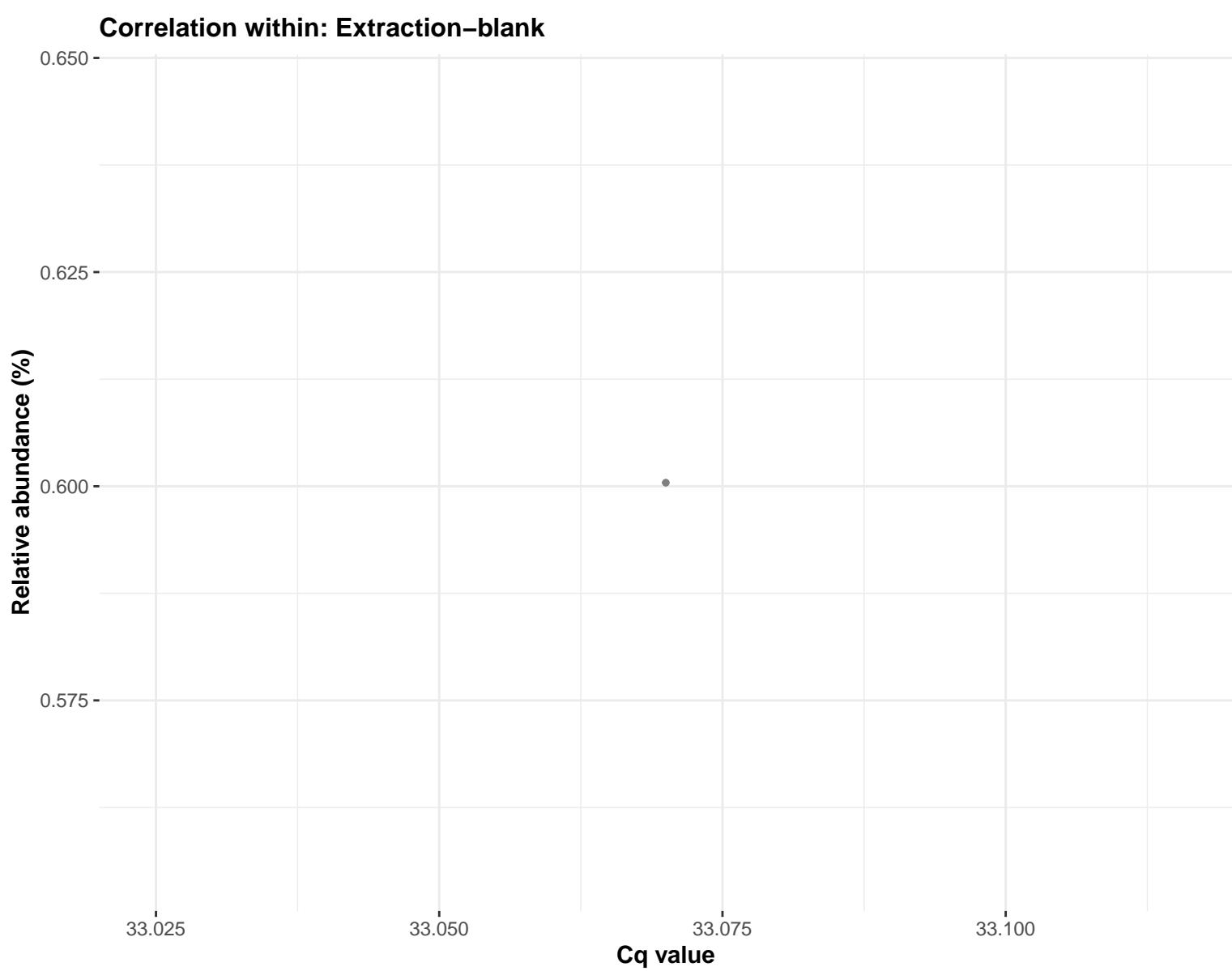
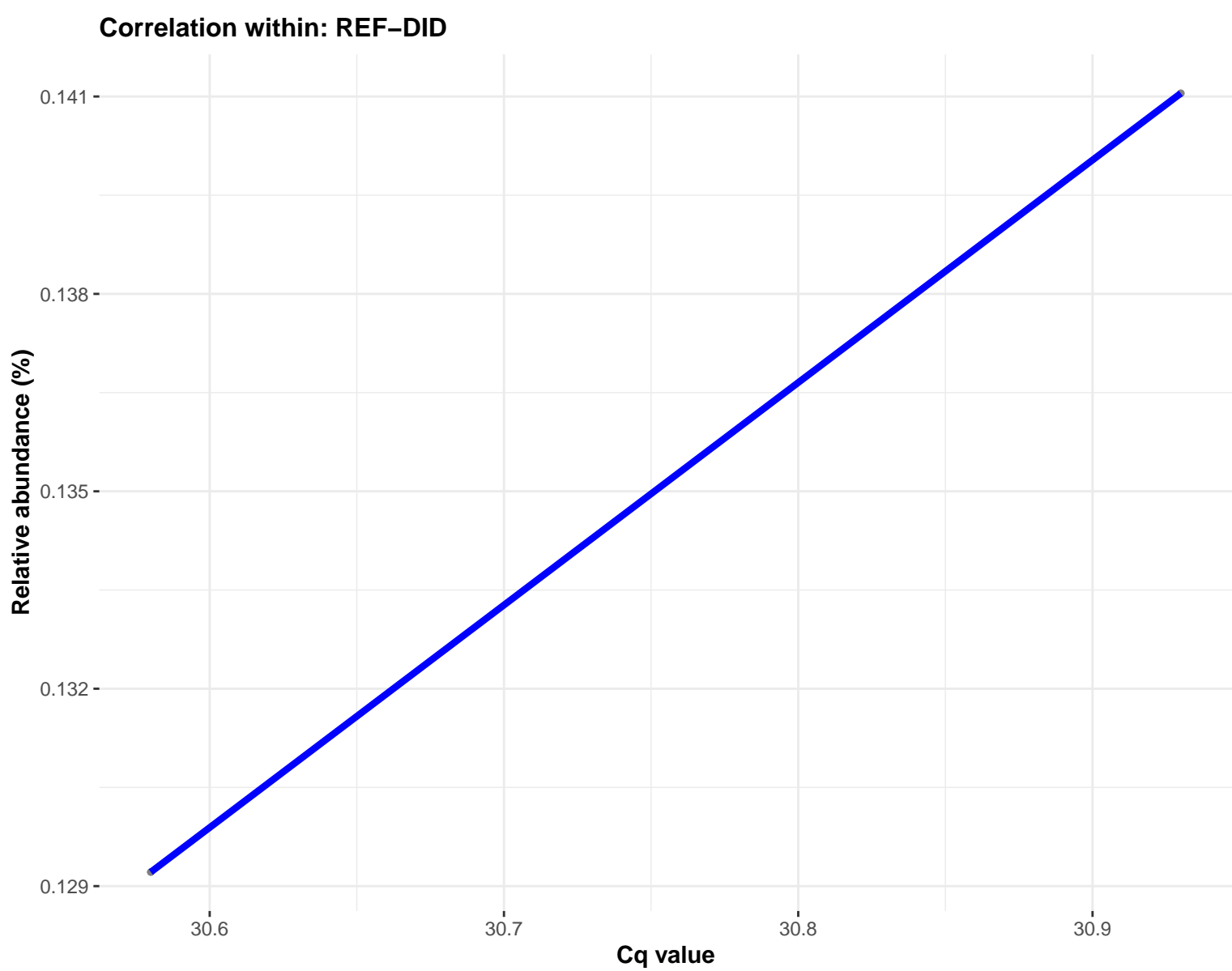
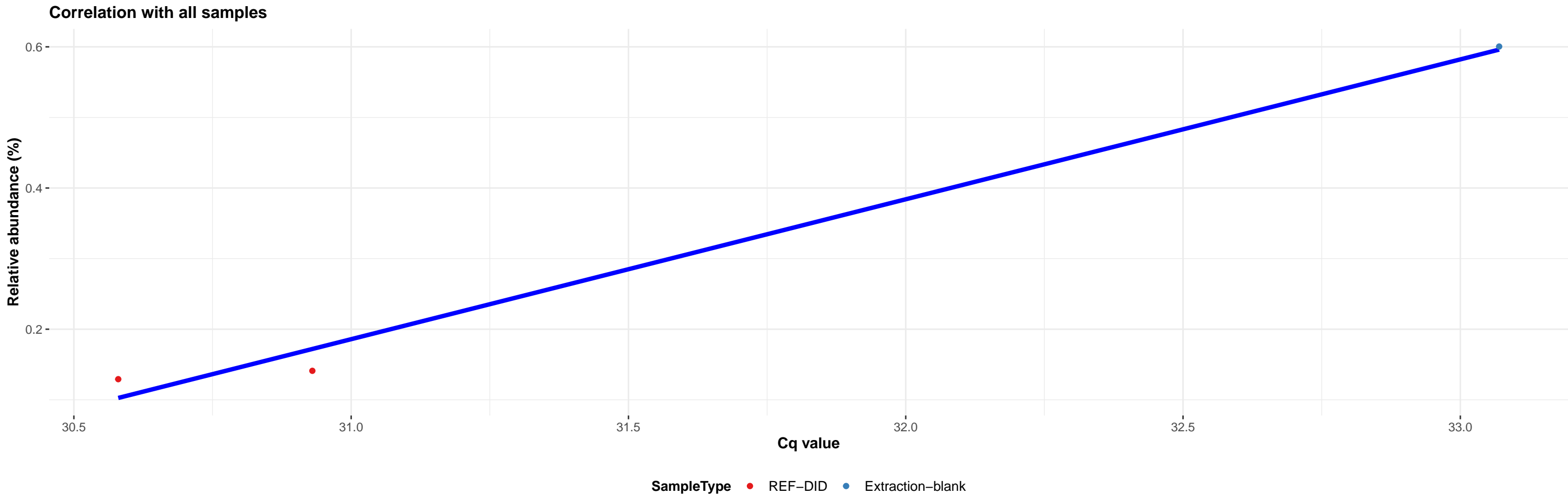
Correlation within: IM-PID



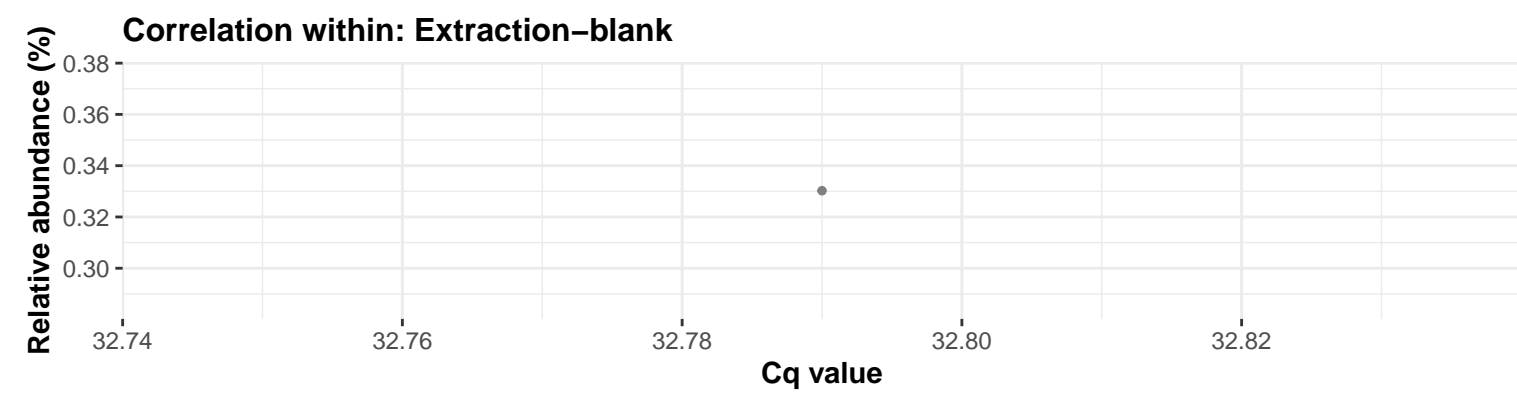
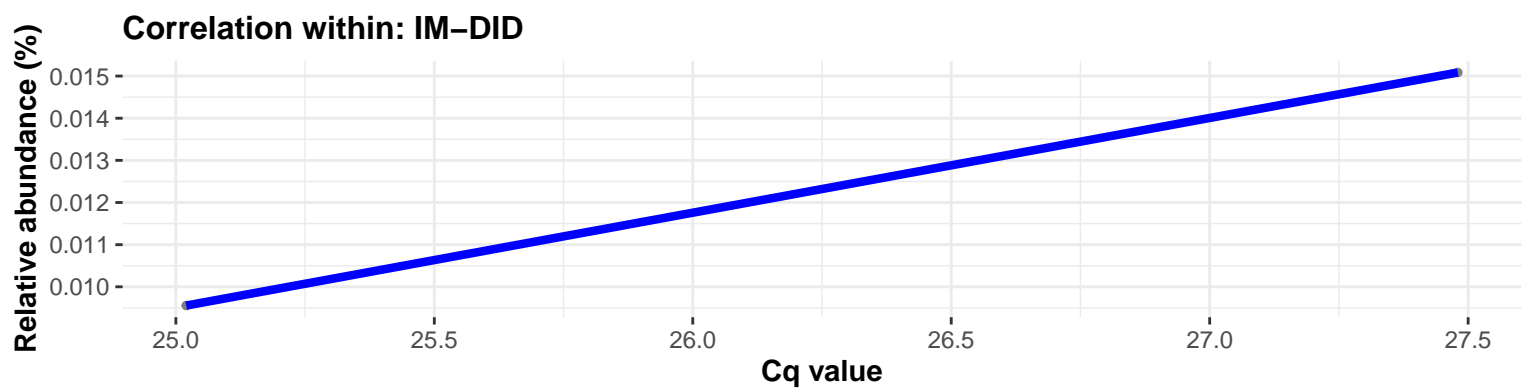
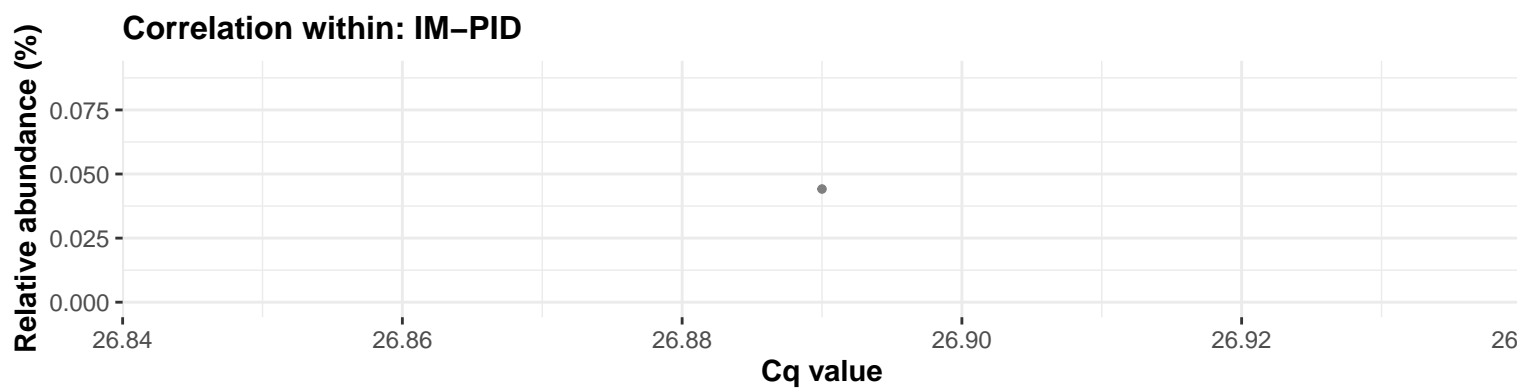
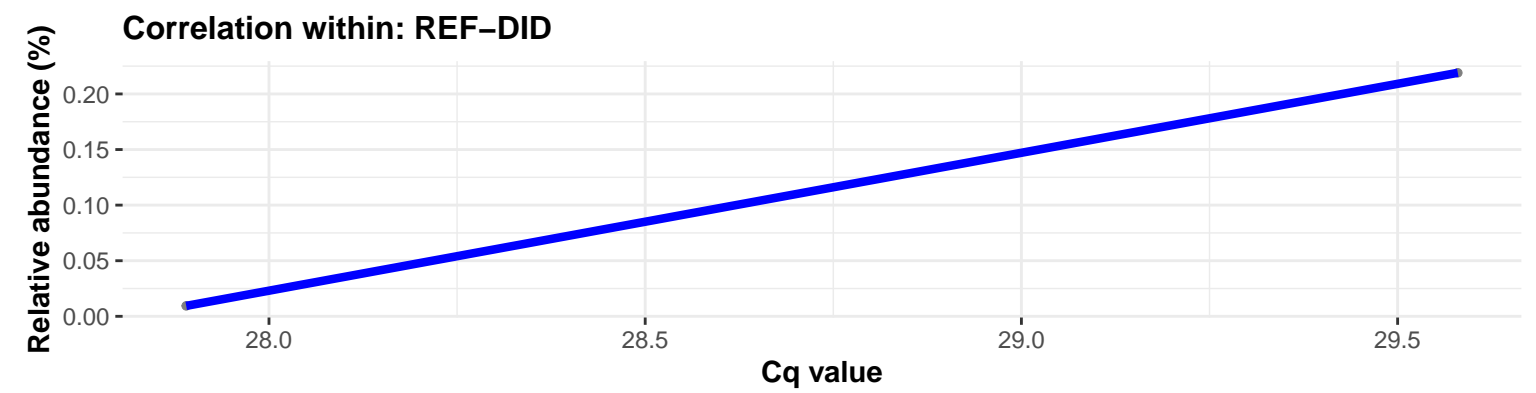
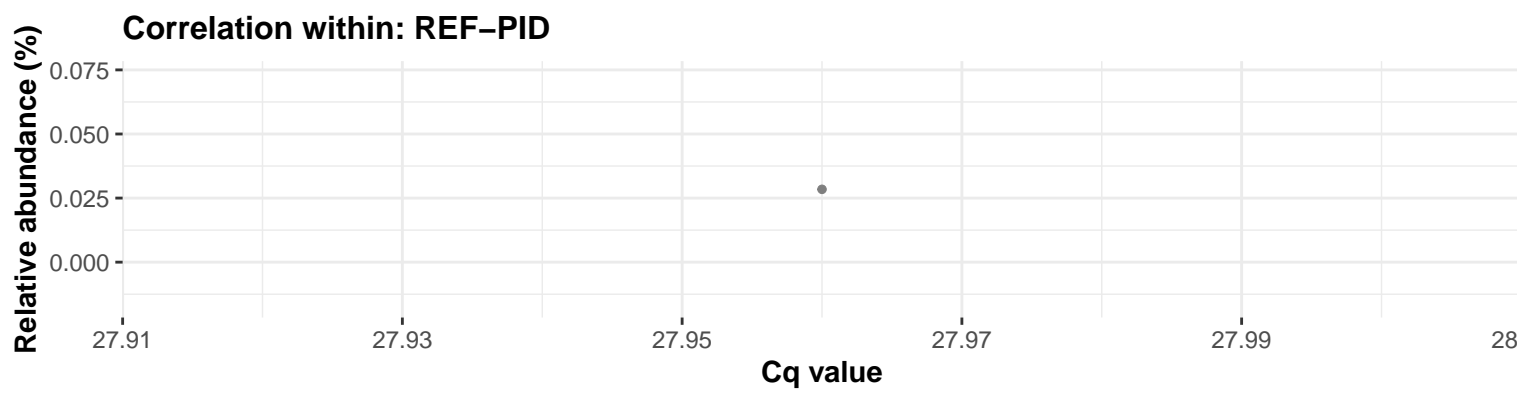
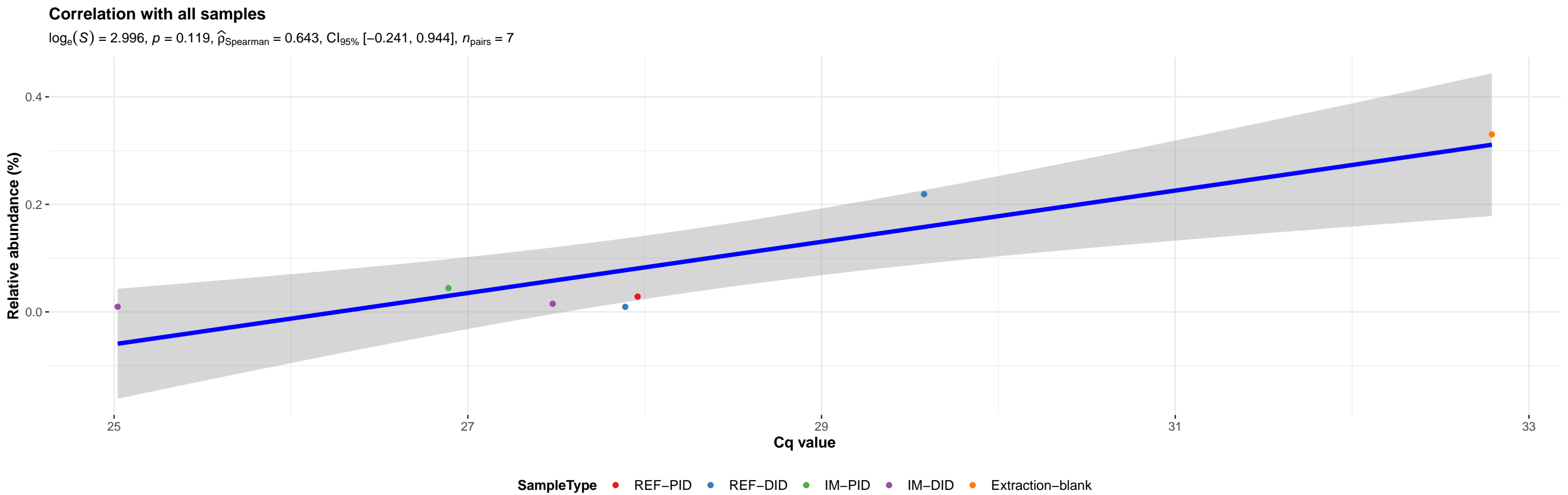
Correlation within: IM-DID



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

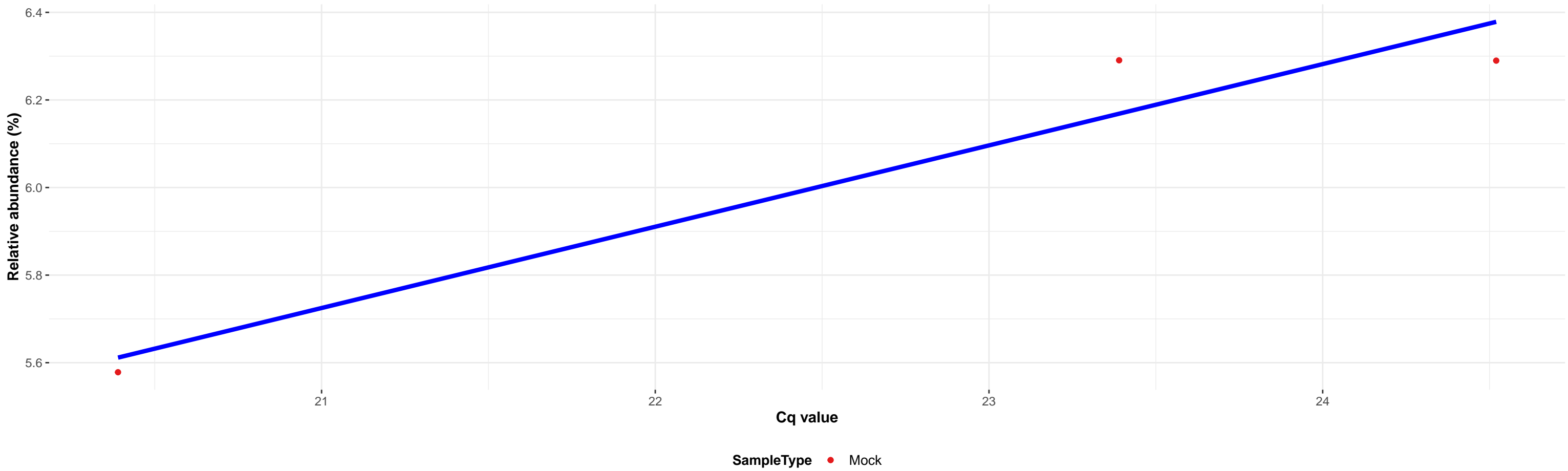


a; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Burkholderia–Caballeronia–Paraburkholderia; s__uncultured beta prote

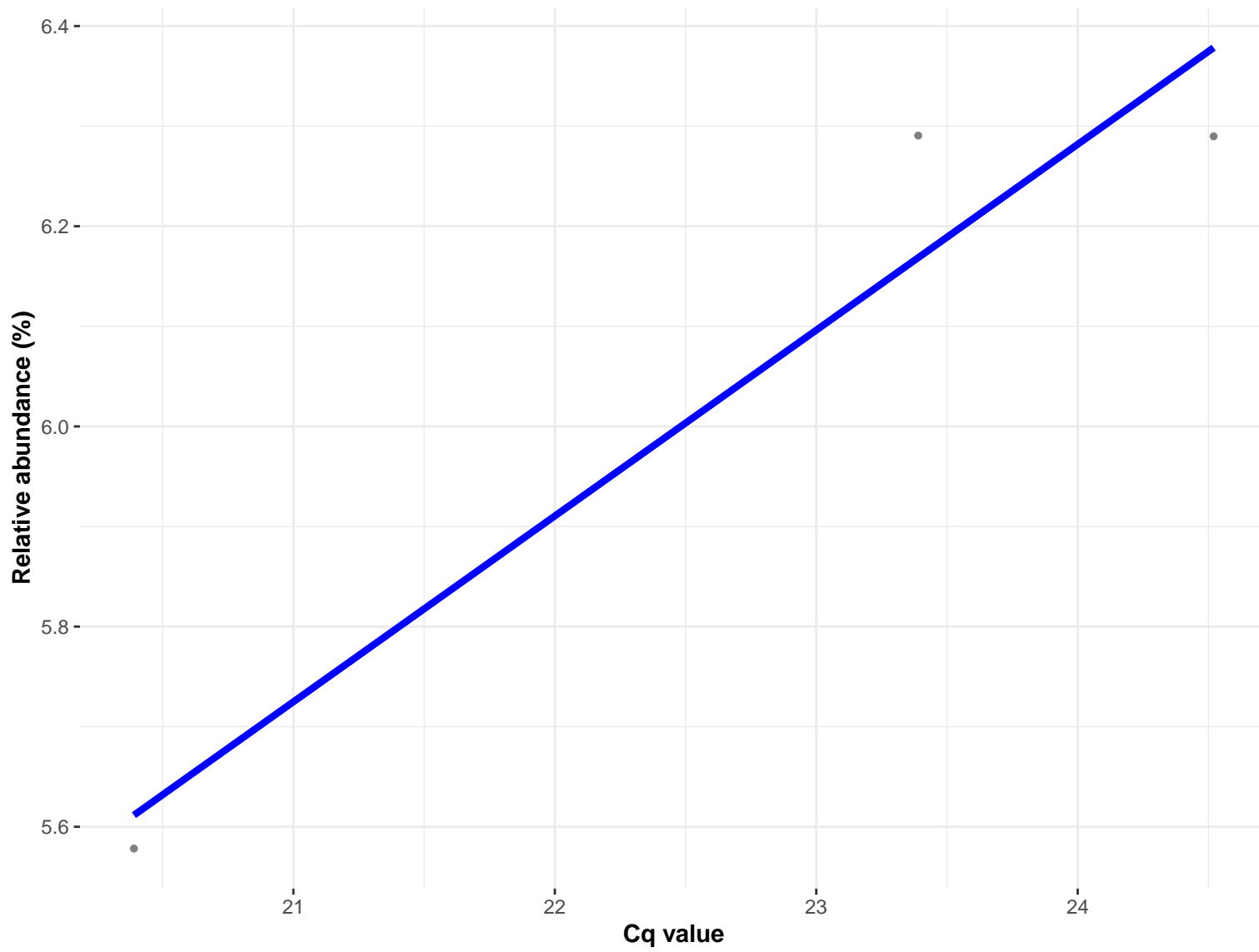


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus fermentum

Correlation with all samples



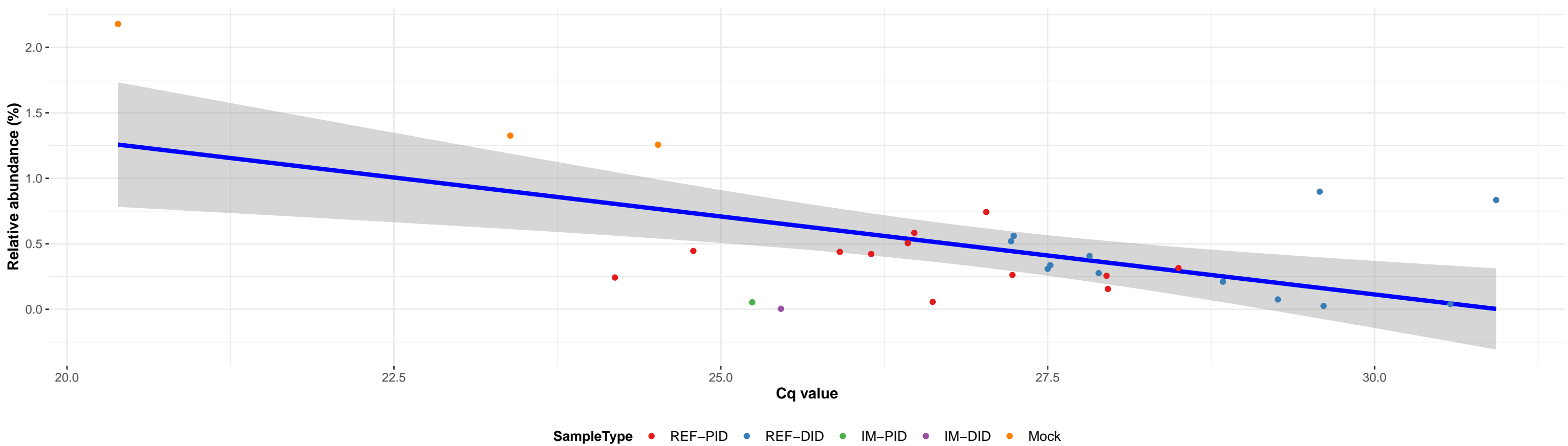
Correlation within: Mock



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

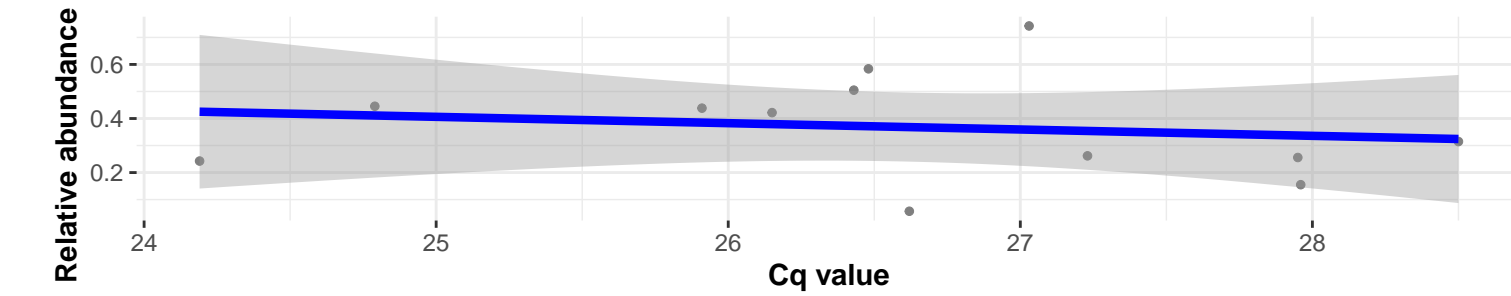
Correlation with all samples

$\log_e(S) = 8.584$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = -0.317$, $\text{CI}_{95\%} [-0.620, 0.067]$, $n_{\text{pairs}} = 29$



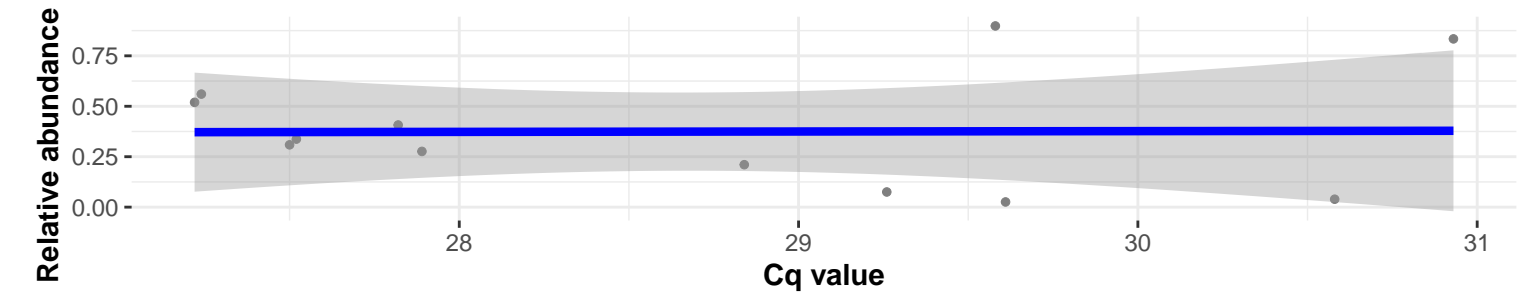
Correlation within: REF-PID

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

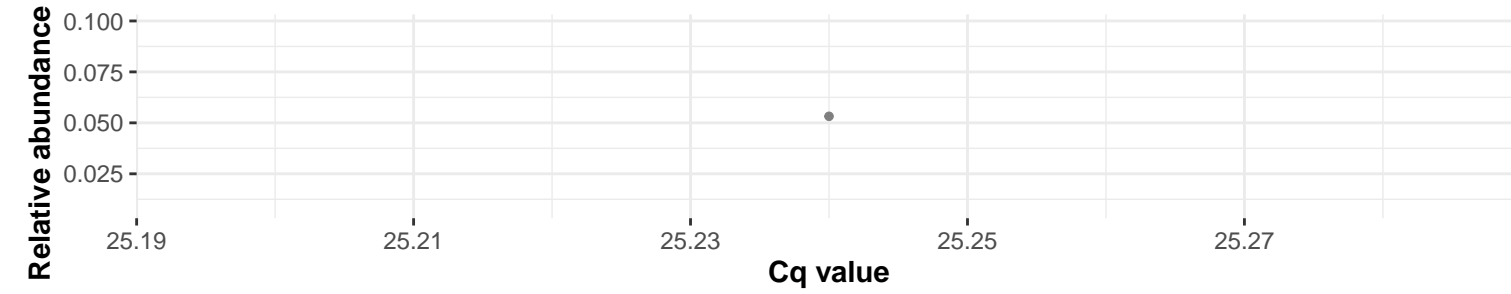


Correlation within: REF-DID

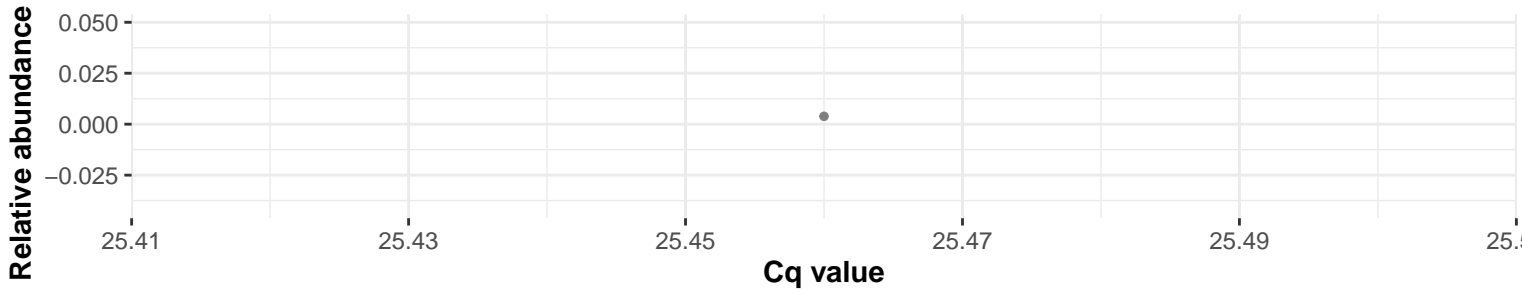
$\log_e(S) = 5.892$, $p = 0.404$, $\hat{\rho}_{\text{Spearman}} = -0.266$, $\text{CI}_{95\%} [-0.737, 0.380]$, $n_{\text{pairs}} = 12$



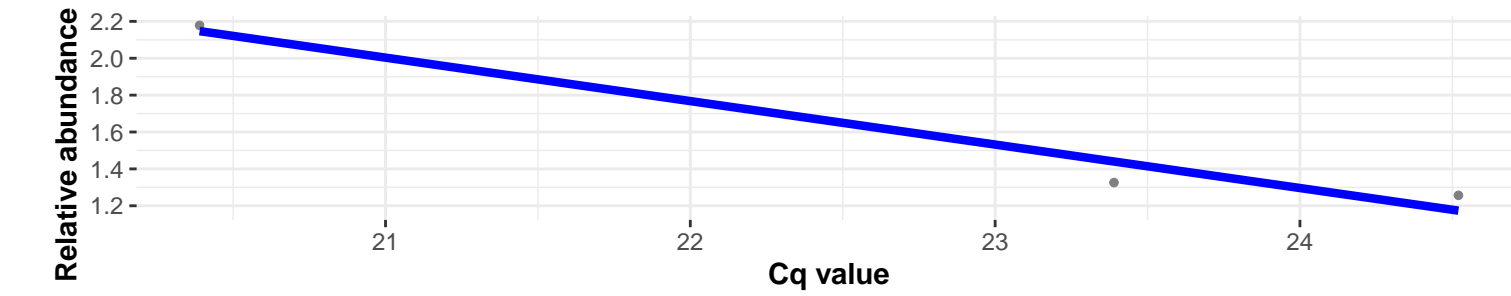
Correlation within: IM-PID



Correlation within: IM-DID

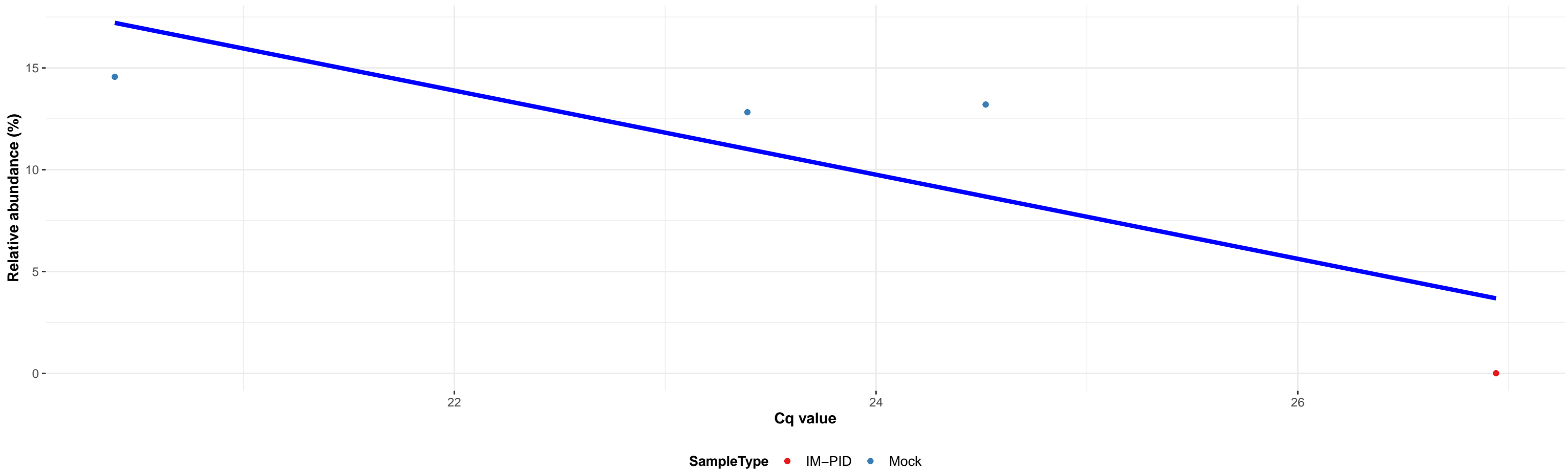


Correlation within: Mock

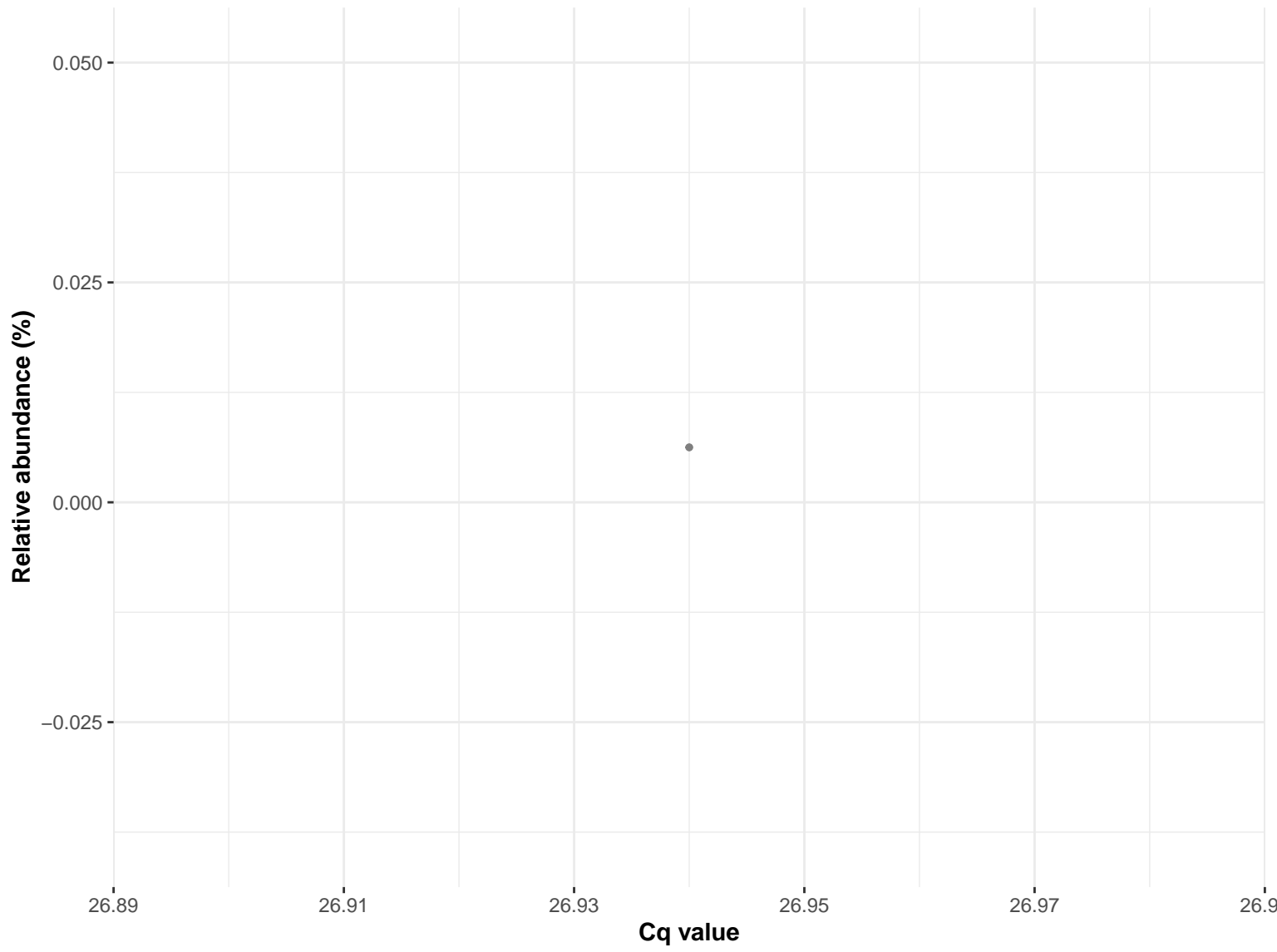


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

Correlation with all samples



Correlation within: IM-PID



Correlation within: Mock

