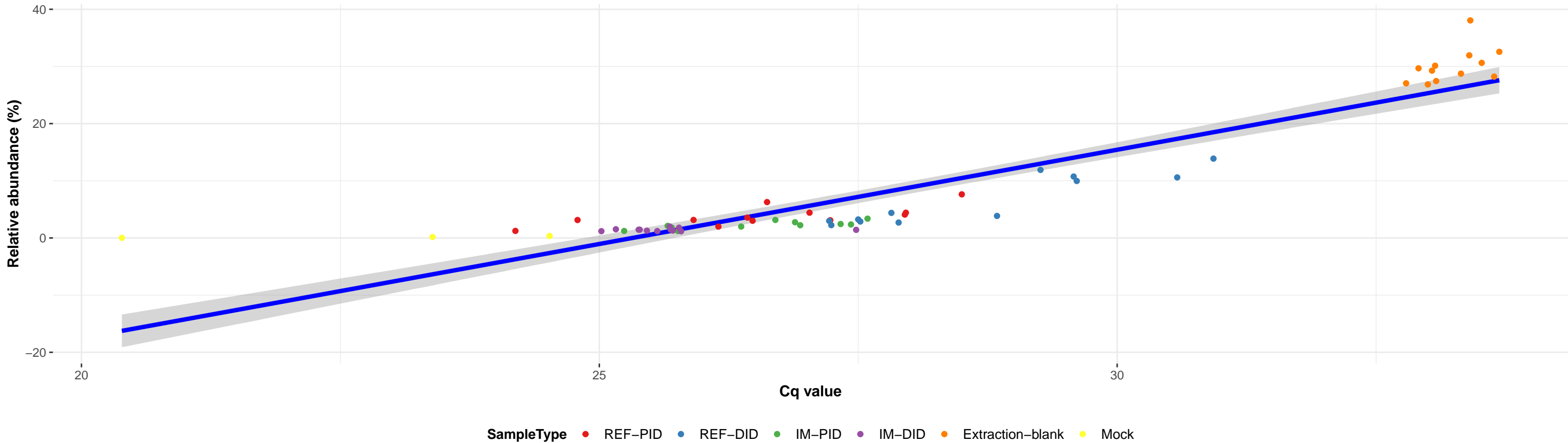


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

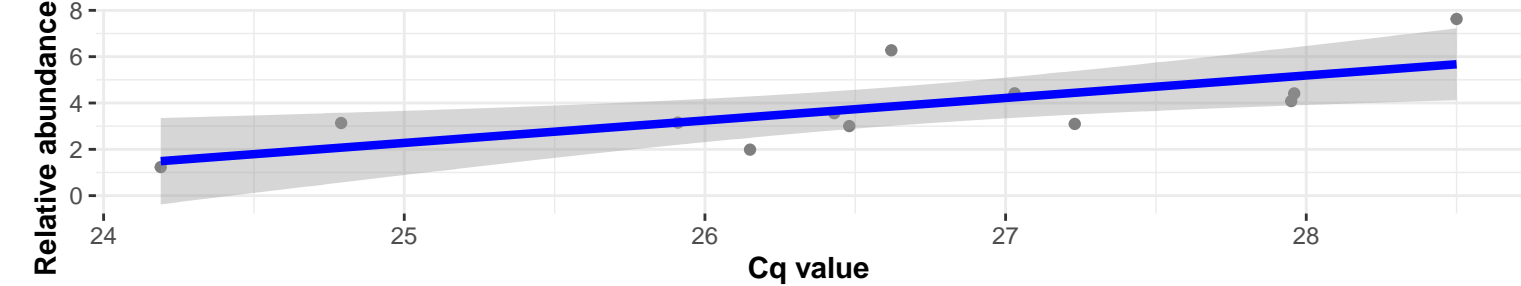
Correlation with all samples

$\log_e(S) = 8.249$, $p = 8.91\text{e-}24$, $\hat{\rho}_{\text{Spearman}} = 0.904$, $\text{CI}_{95\%} [0.842, 0.942]$, $n_{\text{pairs}} = 62$



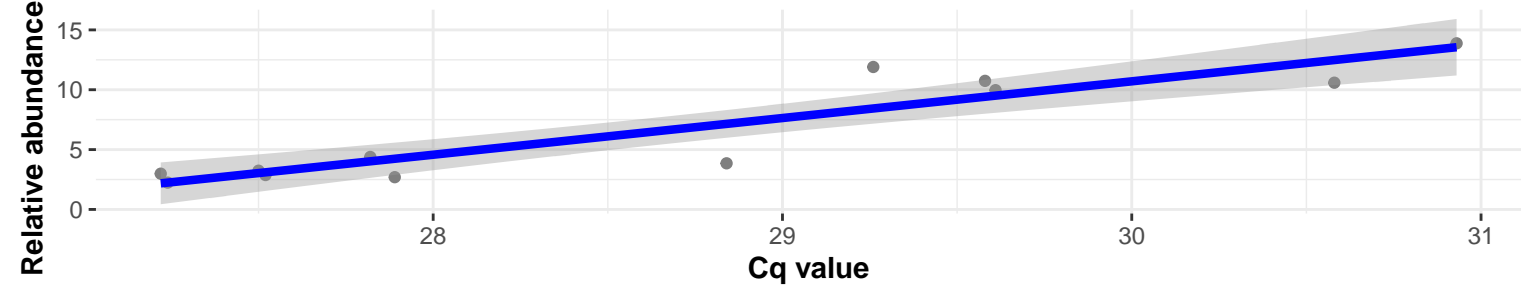
Correlation within: REF-PID

$\log_e(S) = 4.477$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = 0.692$, $\text{CI}_{95\%} [0.178, 0.910]$, $n_{\text{pairs}} = 12$



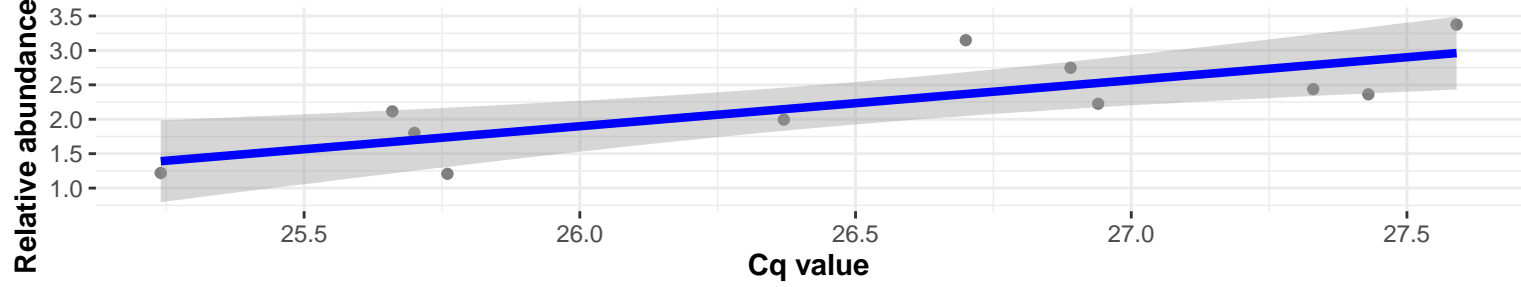
Correlation within: REF-DID

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



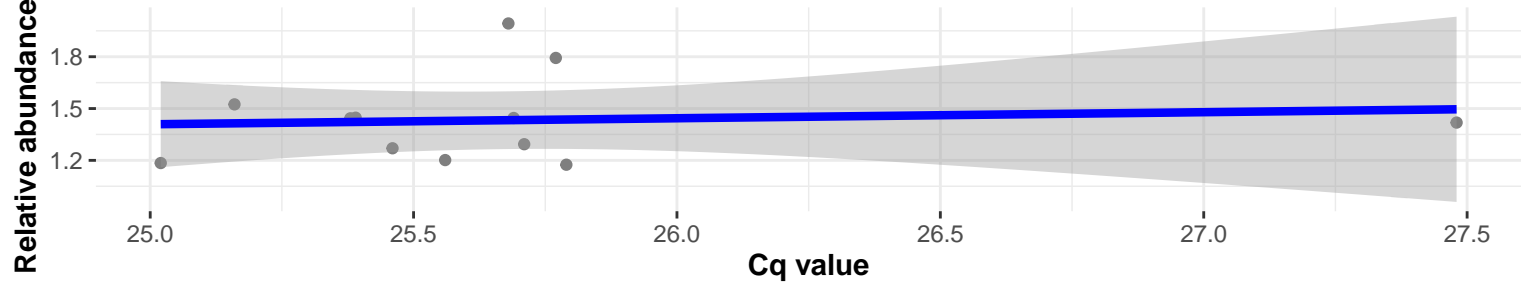
Correlation within: IM-PID

$\log_e(S) = 3.989$, $p = 0.007$, $\hat{\rho}_{\text{Spearman}} = 0.755$, $\text{CI}_{95\%} [0.264, 0.935]$, $n_{\text{pairs}} = 11$



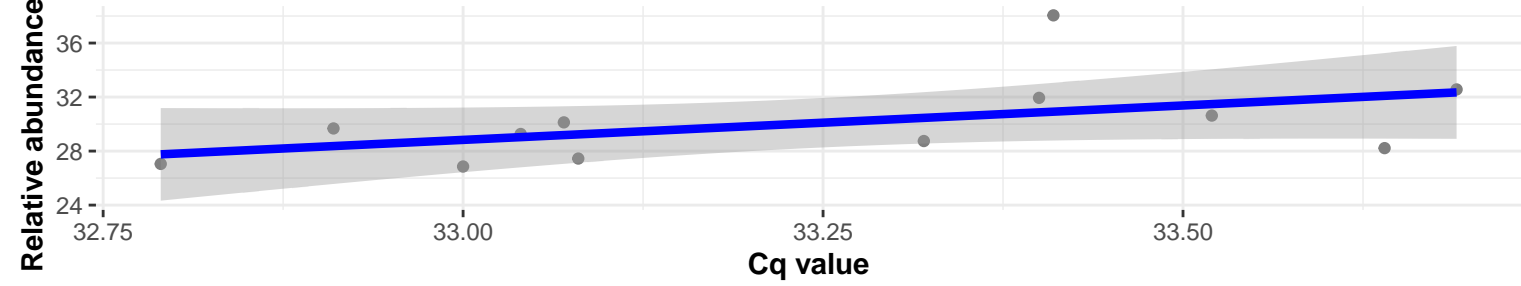
Correlation within: IM-DID

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

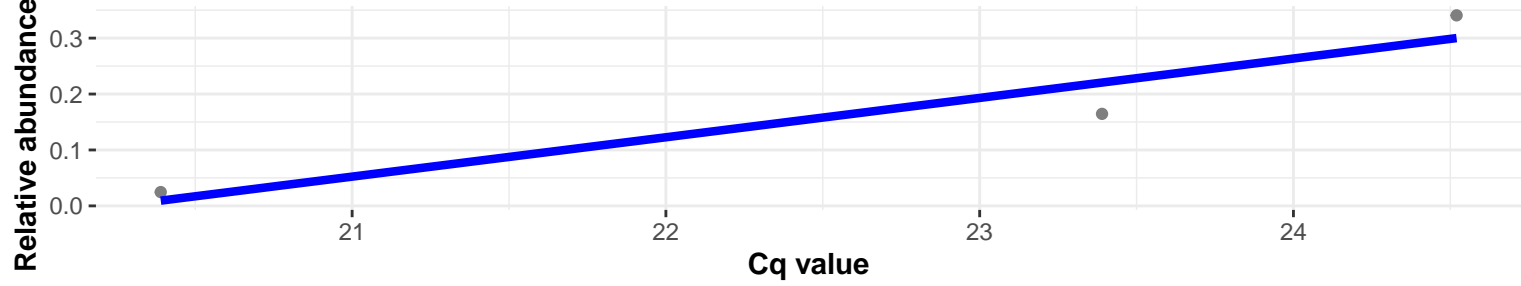


Correlation within: Extraction-blank

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



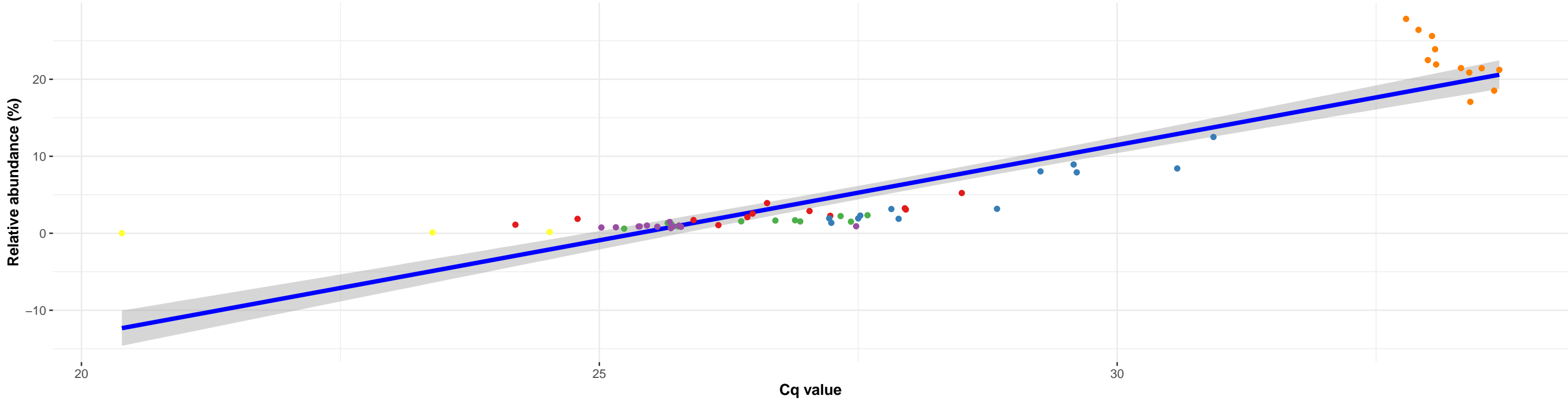
Correlation within: Mock



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

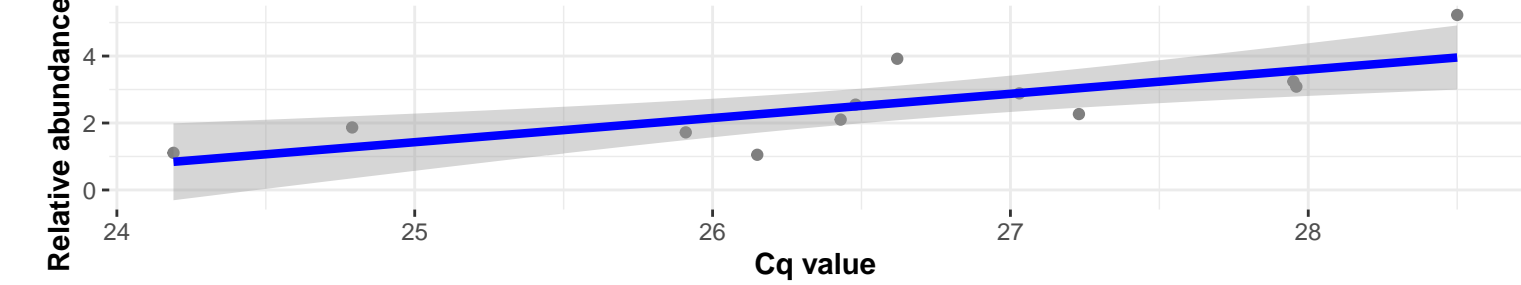
Correlation with all samples

$\log_e(S) = 8.191$, $p = 1.71\text{e-}24$, $\hat{\rho}_{\text{Spearman}} = 0.909$, $\text{CI}_{95\%} [0.851, 0.945]$, $n_{\text{pairs}} = 62$



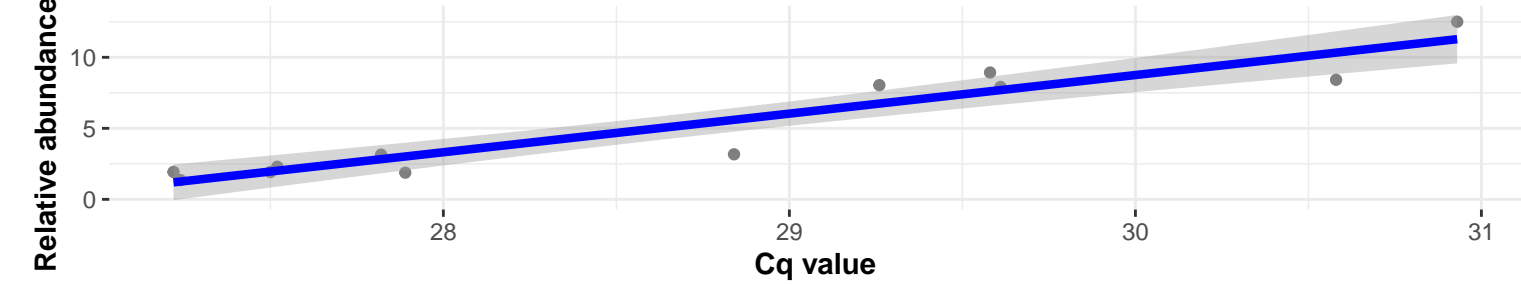
Correlation within: REF-PID

$\log_e(S) = 3.784$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.846$, $\text{CI}_{95\%} [0.515, 0.958]$, $n_{\text{pairs}} = 12$



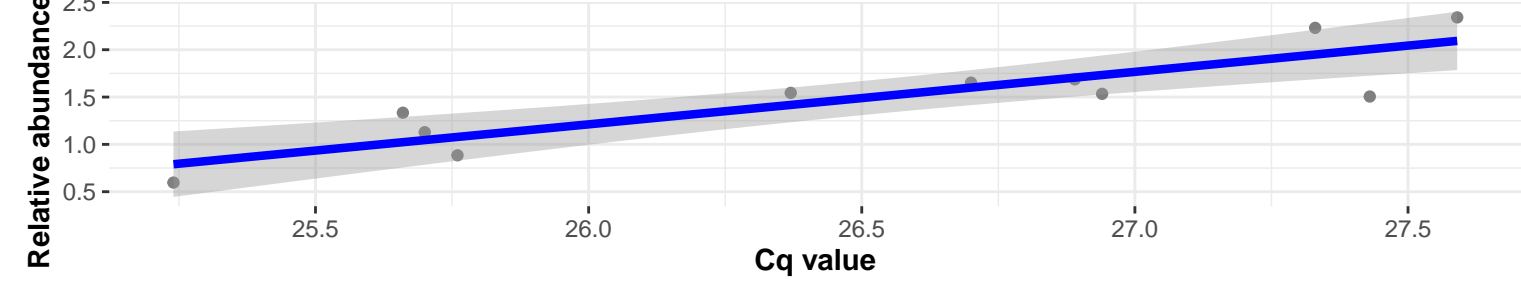
Correlation within: REF-DID

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



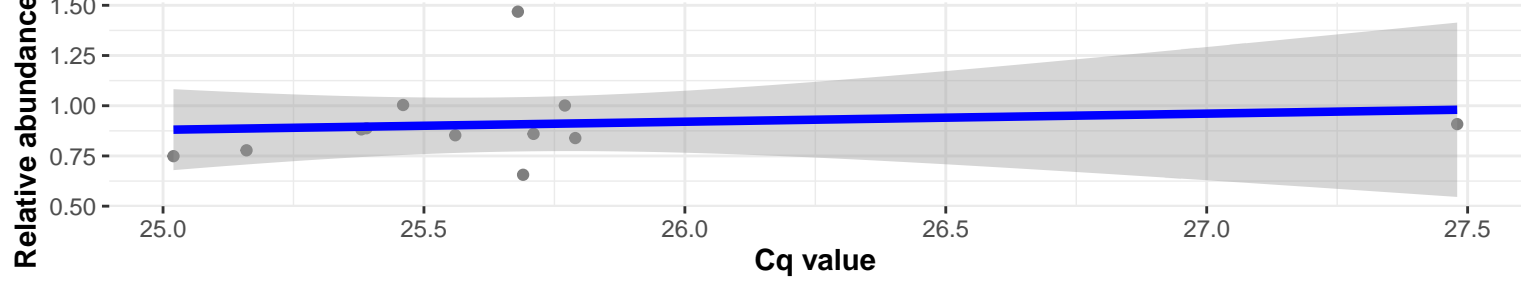
Correlation within: IM-PID

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



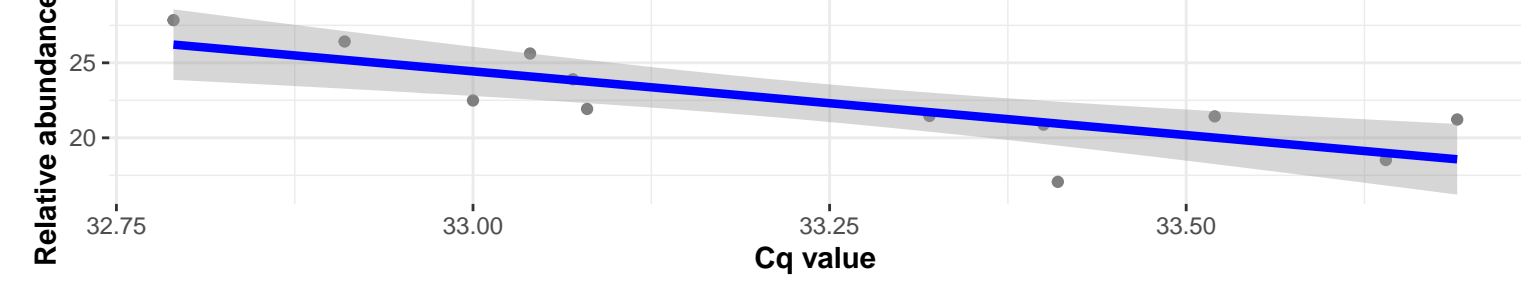
Correlation within: IM-DID

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

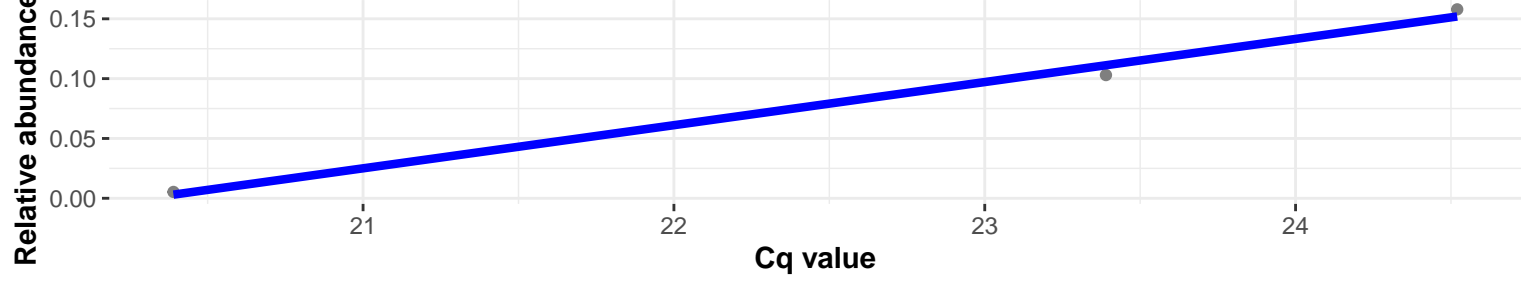


Correlation within: Extraction-blank

$\log_e(S) = 6.292$, $p = 1.14\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = -0.888$, $\text{CI}_{95\%} [-0.970, -0.629]$, $n_{\text{pairs}} = 12$



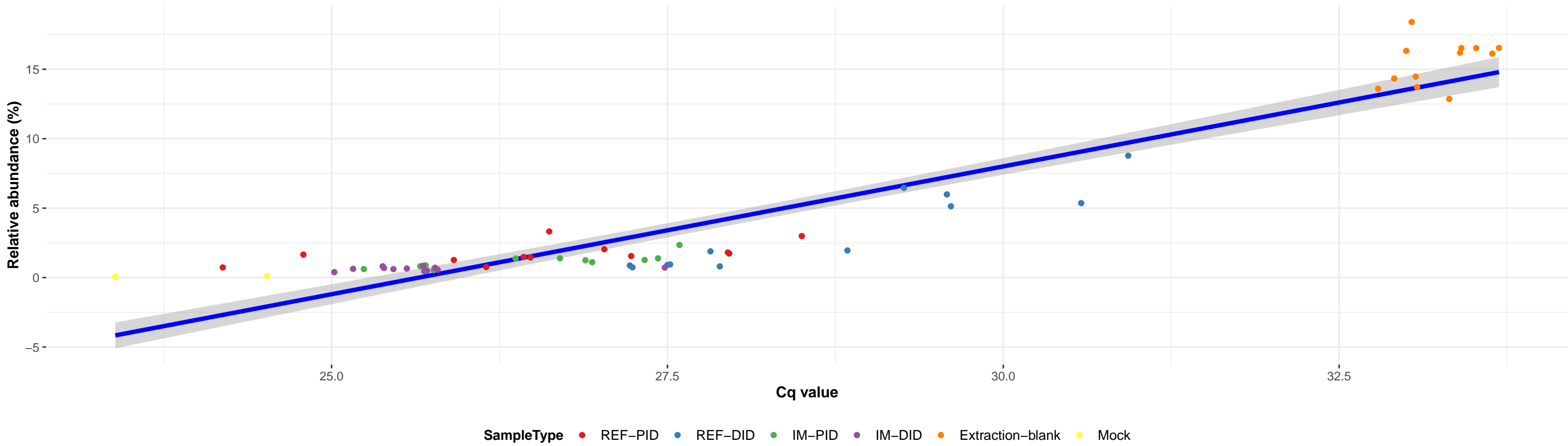
Correlation within: Mock



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

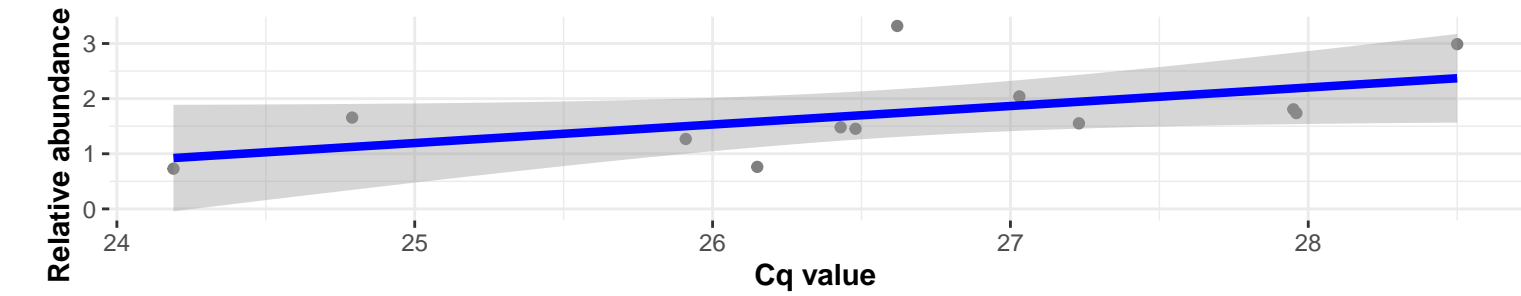
Correlation with all samples

$\log_e(S) = 8.470$, $p = 3.89e-20$, $\hat{\rho}_{\text{Spearman}} = 0.874$, $CI_{95\%} [0.795, 0.924]$, $n_{\text{pairs}} = 61$



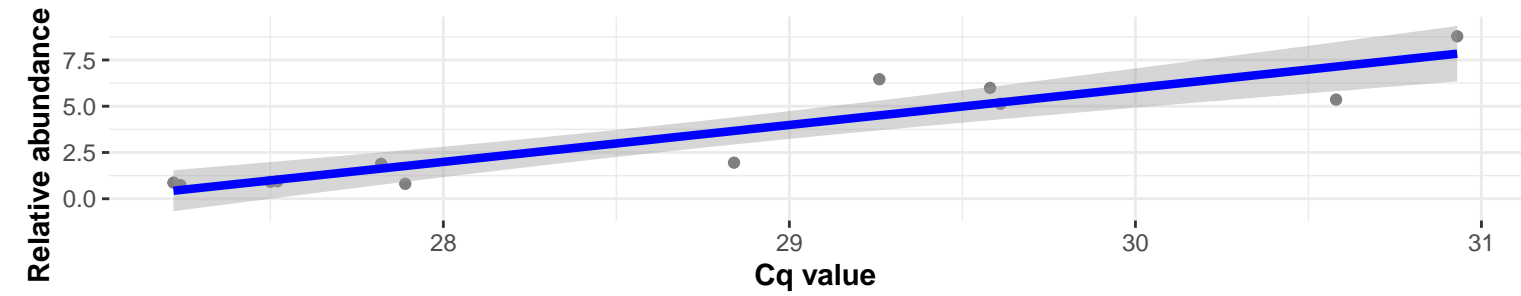
Correlation within: REF-PID

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



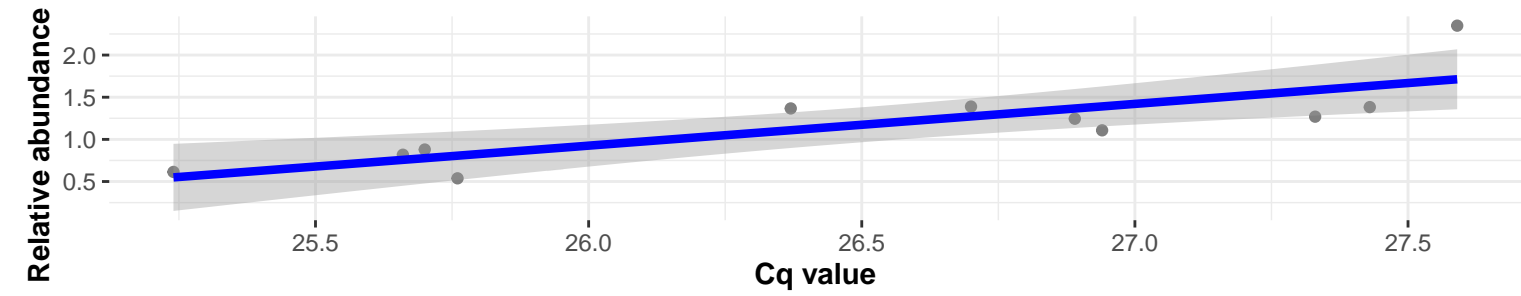
Correlation within: REF-DID

$\log_e(S) = 3.738$, $p = 4.18e-04$, $\hat{\rho}_{\text{Spearman}} = 0.853$, $CI_{95\%} [0.533, 0.960]$, $n_{\text{pairs}} = 12$



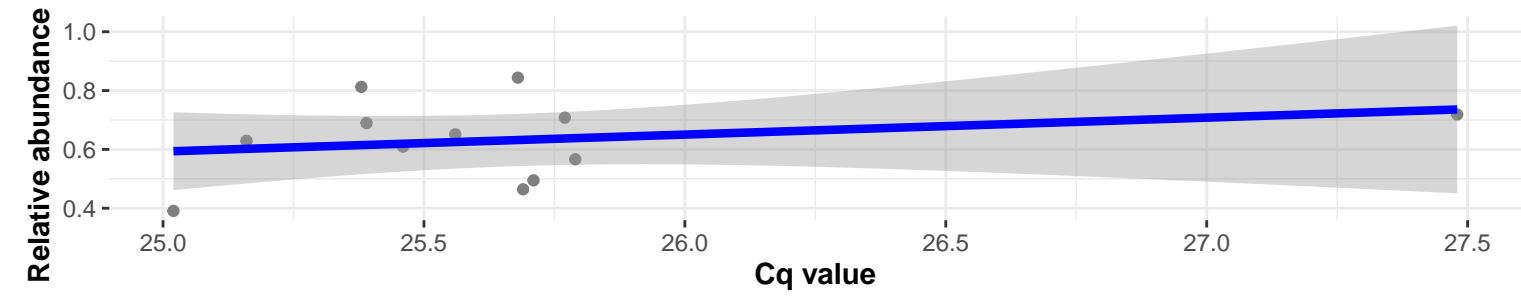
Correlation within: IM-PID

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



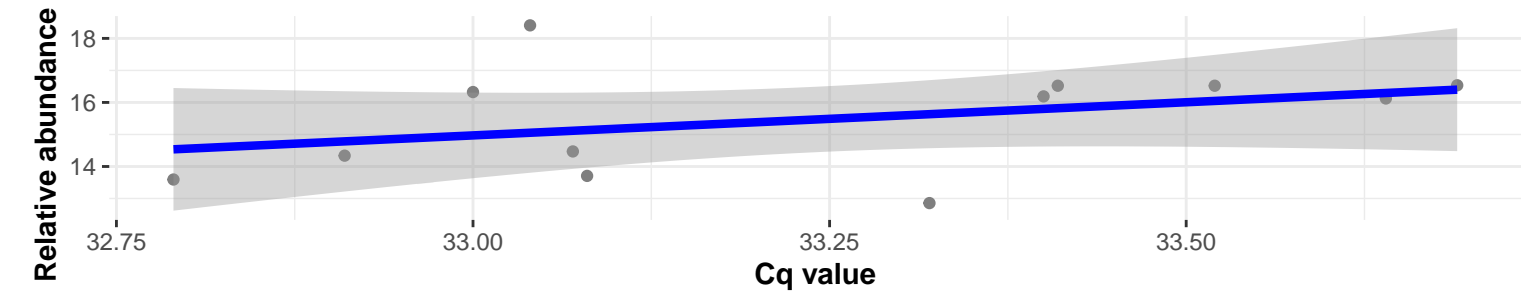
Correlation within: IM-DID

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

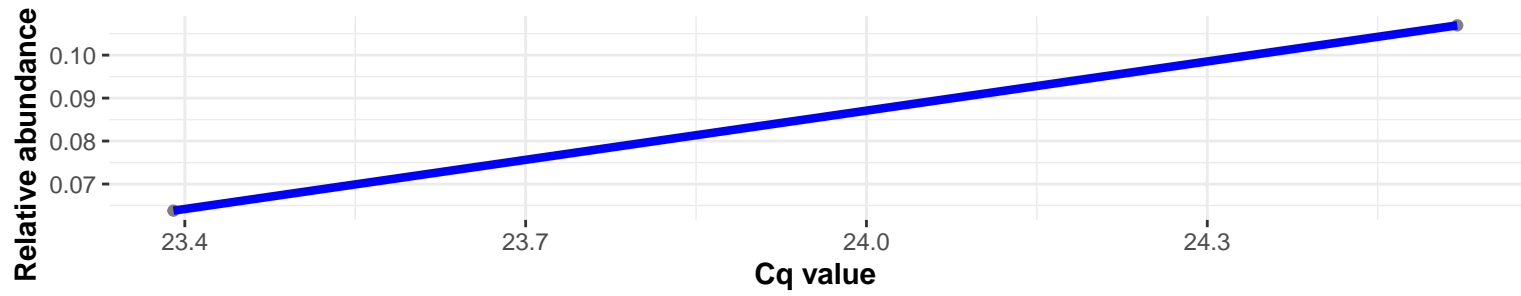


Correlation within: Extraction-blank

$\log_e(S) = 5.112$, $p = 0.175$, $\hat{\rho}_{\text{Spearman}} = 0.420$, $CI_{95\%} [-0.222, 0.808]$, $n_{\text{pairs}} = 12$



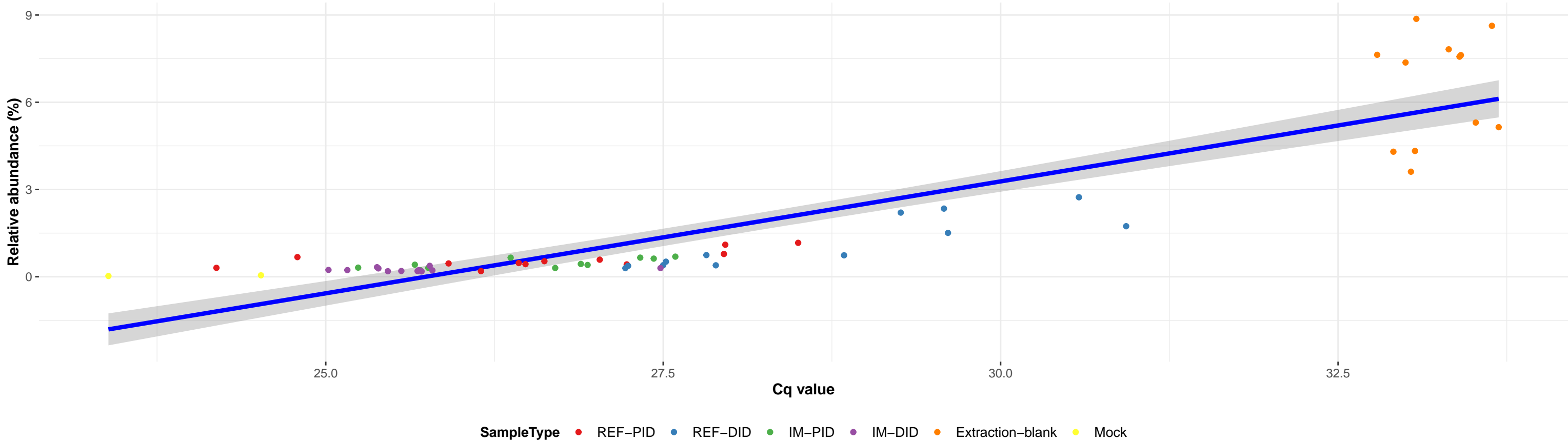
Correlation within: Mock



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

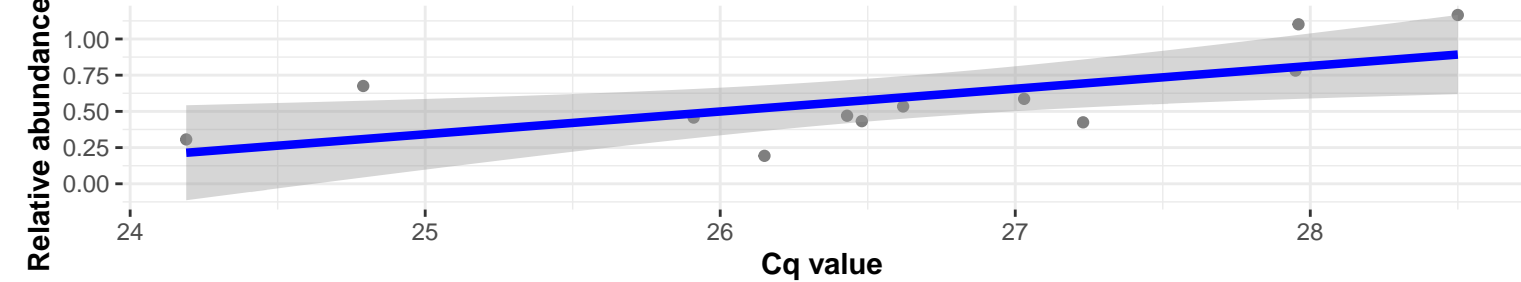
Correlation with all samples

$\log_e(S) = 8.479$, $p = 5.02\text{e-}20$, $\hat{\rho}_{\text{Spearman}} = 0.873$, $\text{CI}_{95\%} [0.793, 0.923]$, $n_{\text{pairs}} = 61$



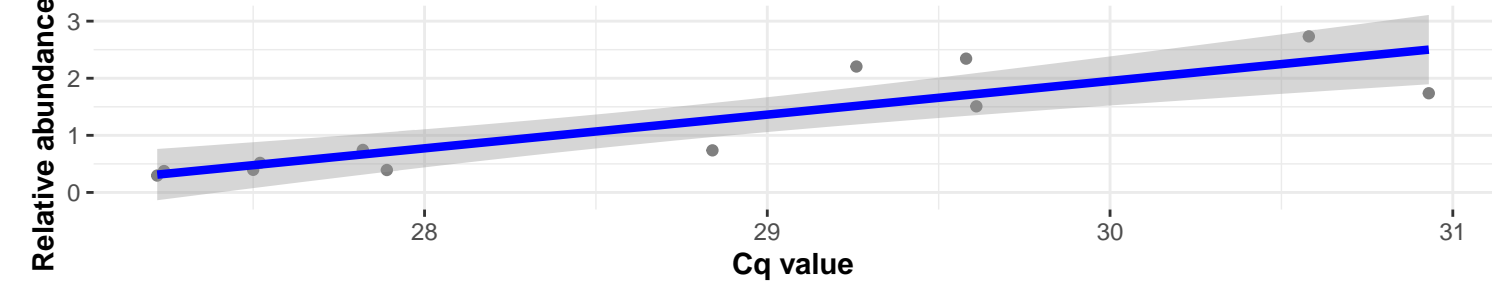
Correlation within: REF-PID

$\log_e(S) = 4.644$, $p = 0.026$, $\hat{\rho}_{\text{Spearman}} = 0.636$, $\text{CI}_{95\%} [0.079, 0.891]$, $n_{\text{pairs}} = 12$



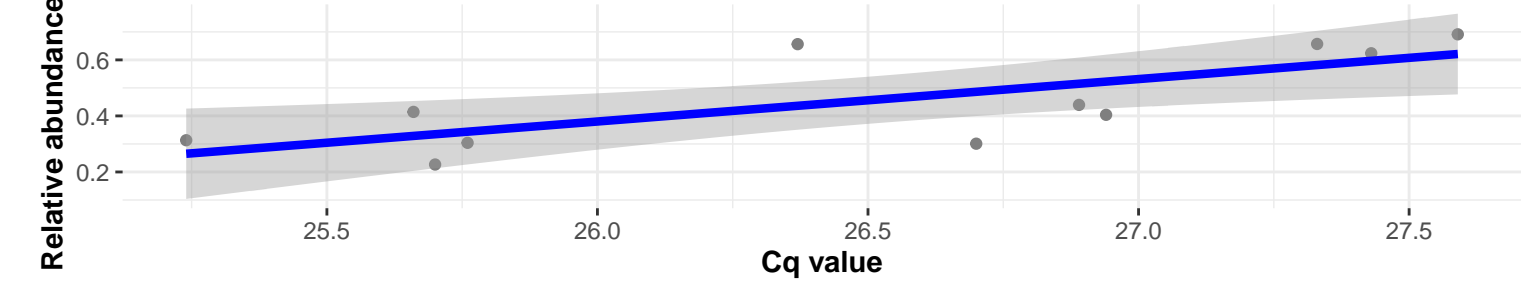
Correlation within: REF-DID

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



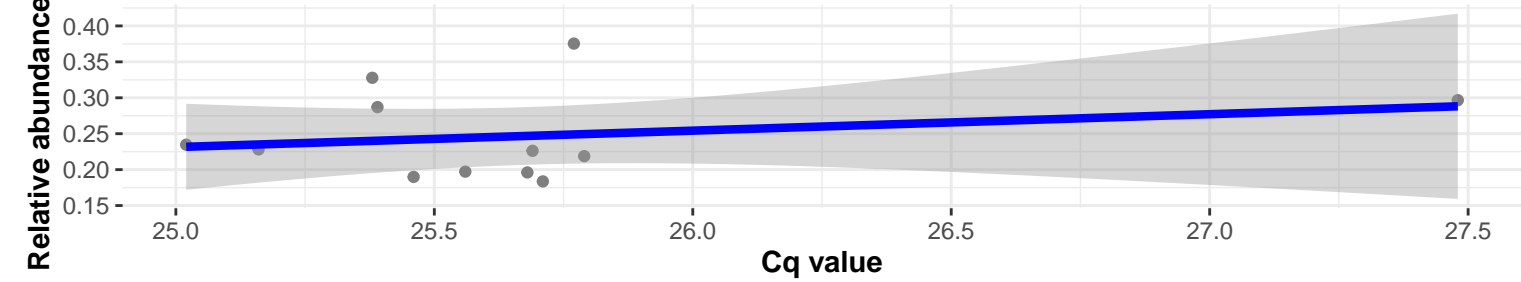
Correlation within: IM-PID

$\log_e(S) = 4.331$, $p = 0.029$, $\hat{\rho}_{\text{Spearman}} = 0.655$, $\text{CI}_{95\%} [0.070, 0.905]$, $n_{\text{pairs}} = 11$



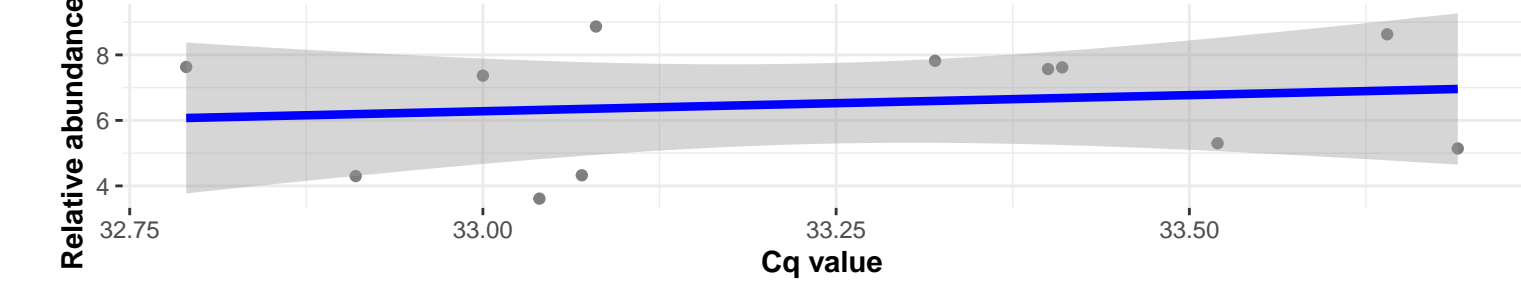
Correlation within: IM-DID

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

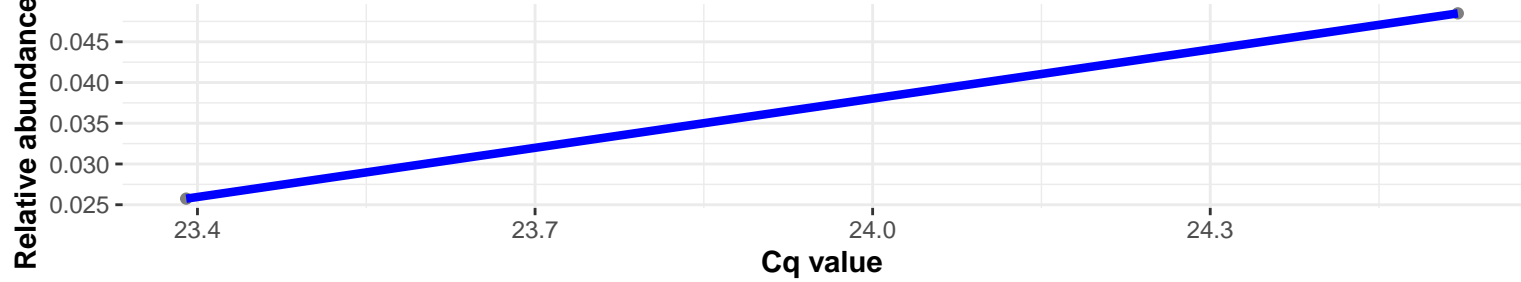


Correlation within: Extraction-blank

$\log_e(S) = 5.403$, $p = 0.484$, $\hat{\rho}_{\text{Spearman}} = 0.224$, $\text{CI}_{95\%} [-0.418, 0.716]$, $n_{\text{pairs}} = 12$



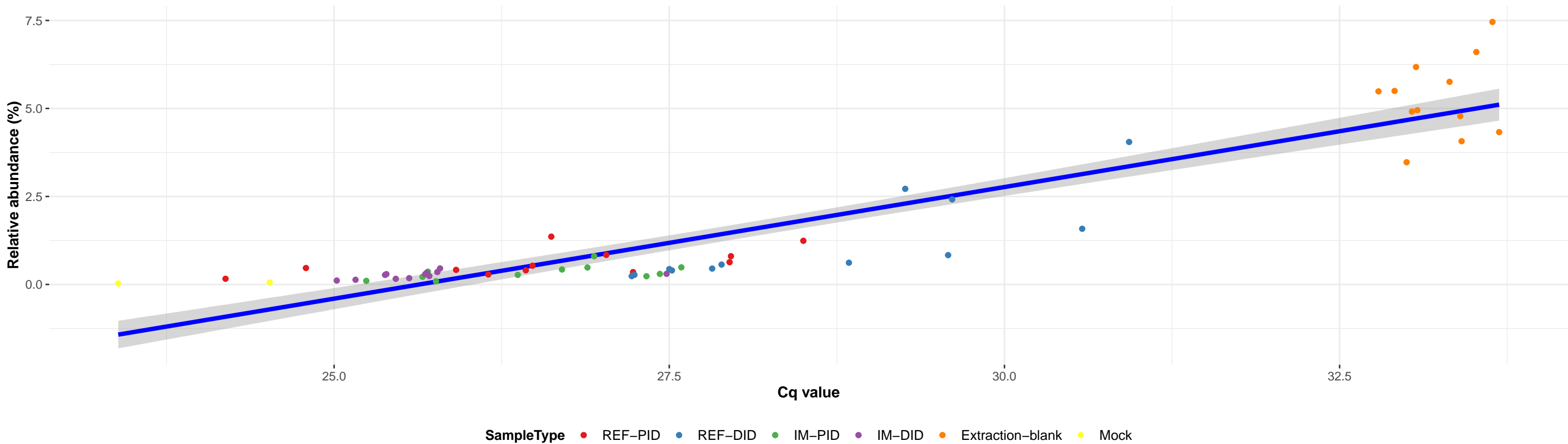
Correlation within: Mock



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

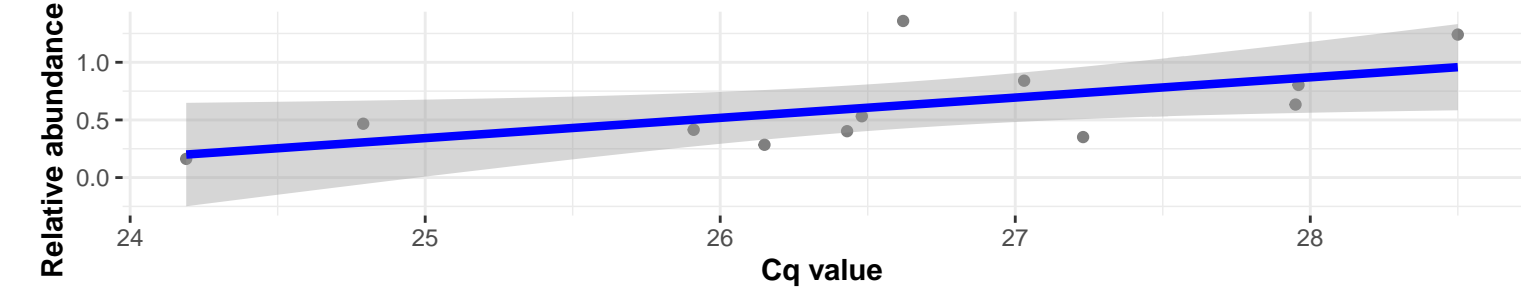
Correlation with all samples

$\log_e(S) = 8.478$, $p = 4.85e-20$, $\hat{\rho}_{\text{Spearman}} = 0.873$, $CI_{95\%} [0.793, 0.923]$, $n_{\text{pairs}} = 61$



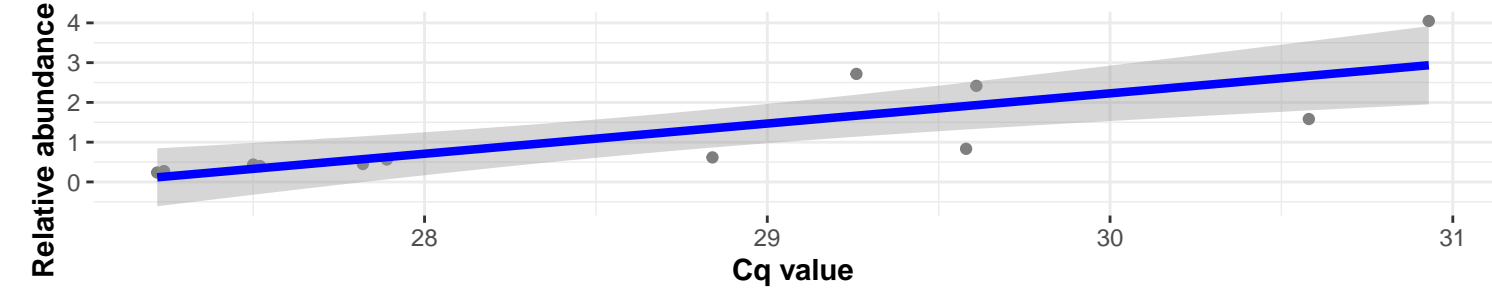
Correlation within: REF-PID

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



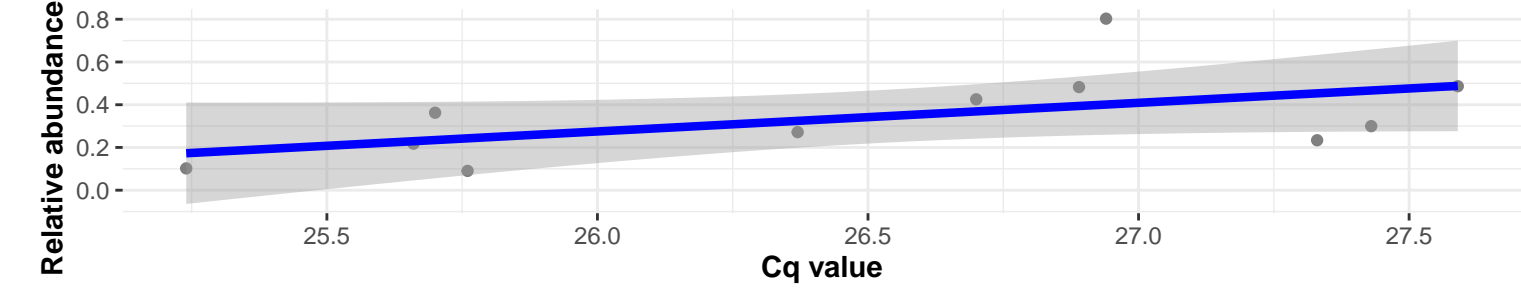
Correlation within: REF-DID

$\log_e(S) = 2.773$, $p = 3.93e-06$, $\hat{\rho}_{\text{Spearman}} = 0.944$, $CI_{95\%} [0.801, 0.985]$, $n_{\text{pairs}} = 12$



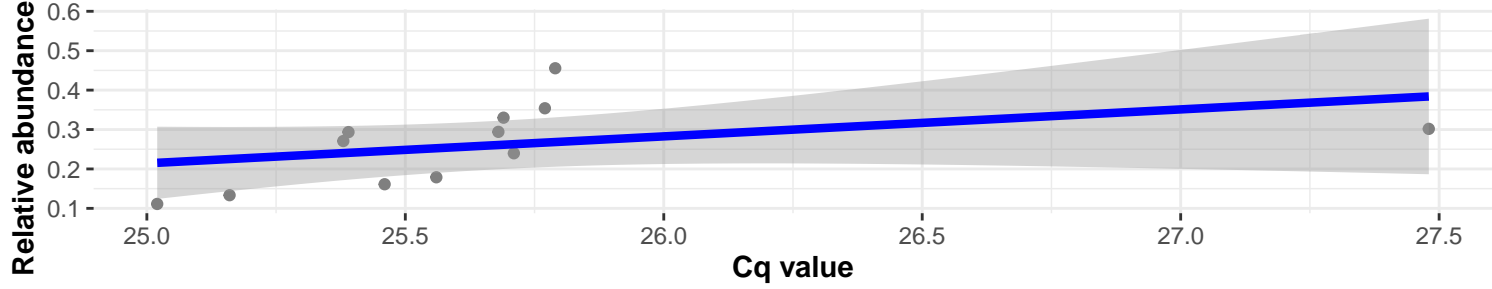
Correlation within: IM-PID

$\log_e(S) = 4.454$, $p = 0.047$, $\hat{\rho}_{\text{Spearman}} = 0.609$, $CI_{95\%} [-0.006, 0.890]$, $n_{\text{pairs}} = 11$



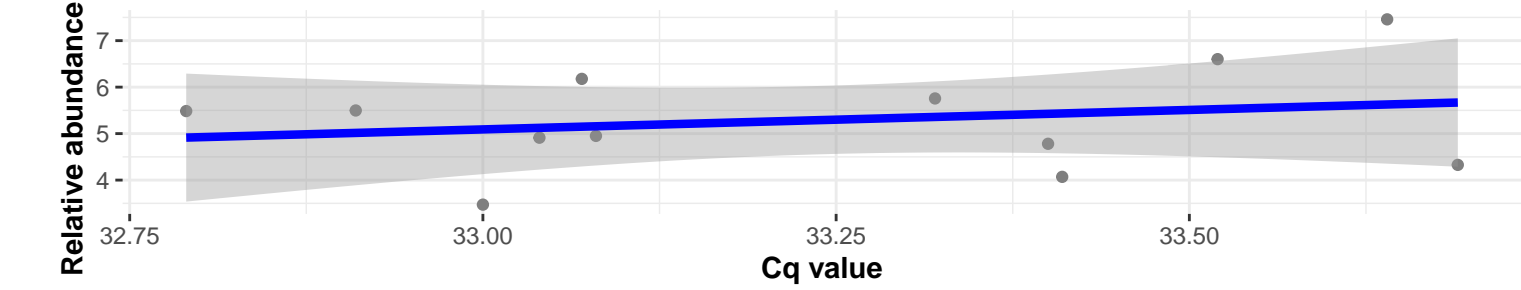
Correlation within: IM-DID

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

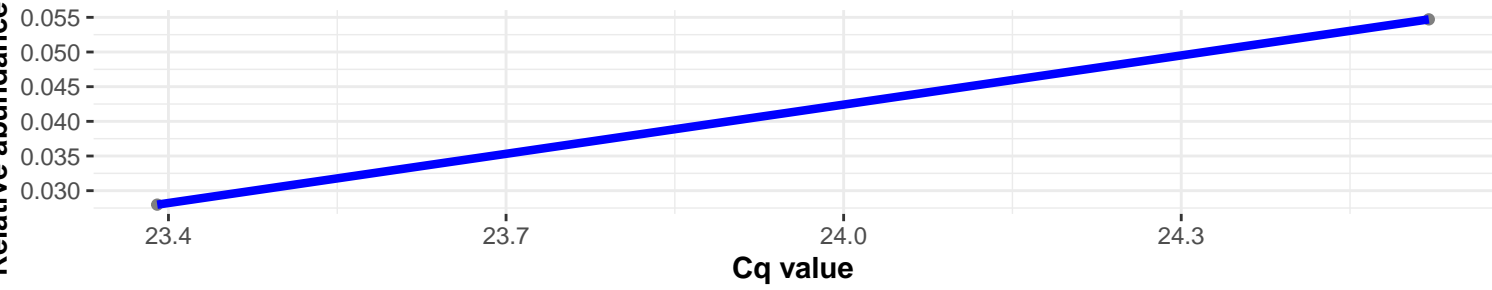


Correlation within: Extraction-blank

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



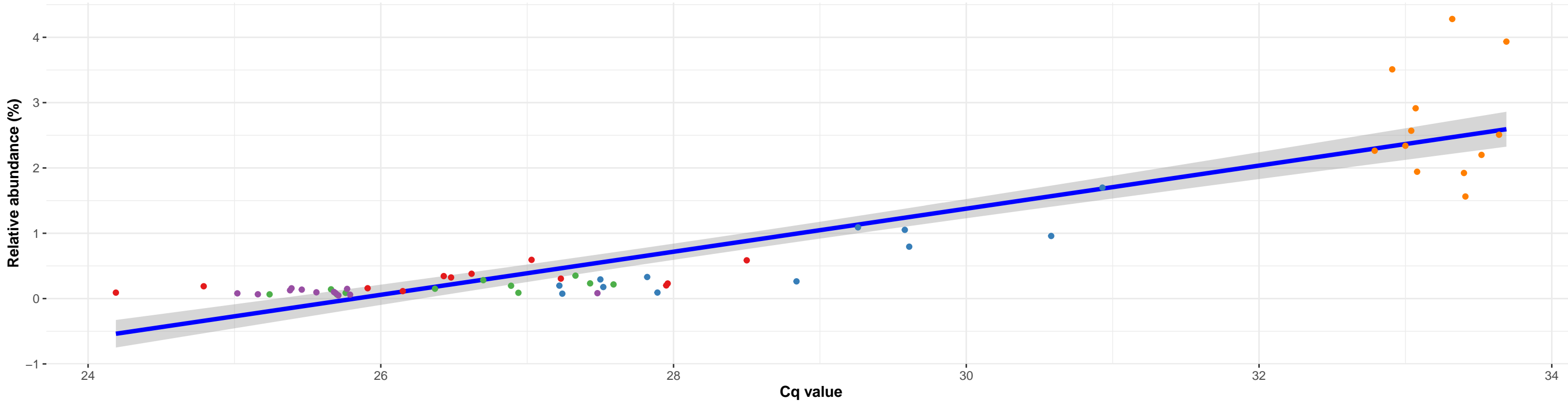
Correlation within: Mock



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

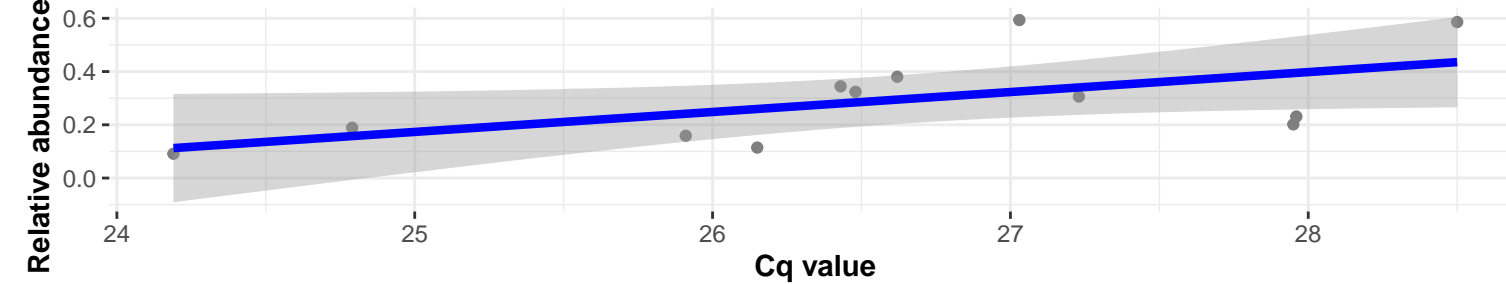
Correlation with all samples

$\log_e(S) = 8.680$, $p = 5.97e-16$, $\hat{\rho}_{\text{Spearman}} = 0.828$, $CI_{95\%} [0.722, 0.896]$, $n_{\text{pairs}} = 59$



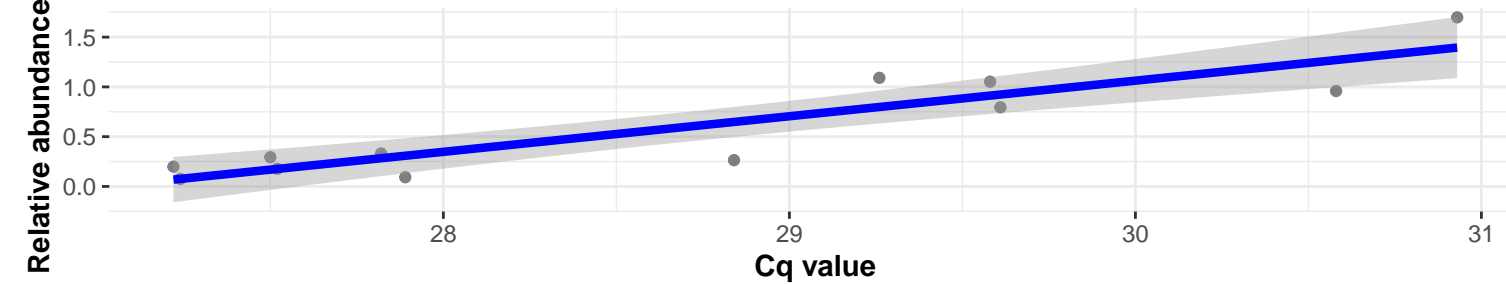
Correlation within: REF-PID

$\log_e(S) = 4.682$, $p = 0.031$, $\hat{\rho}_{\text{Spearman}} = 0.622$, $CI_{95\%} [0.056, 0.886]$, $n_{\text{pairs}} = 12$



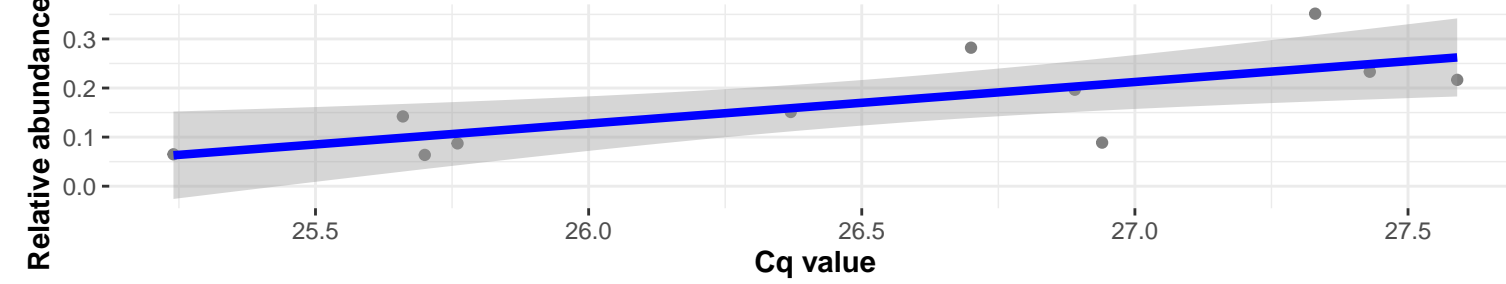
Correlation within: REF-DID

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



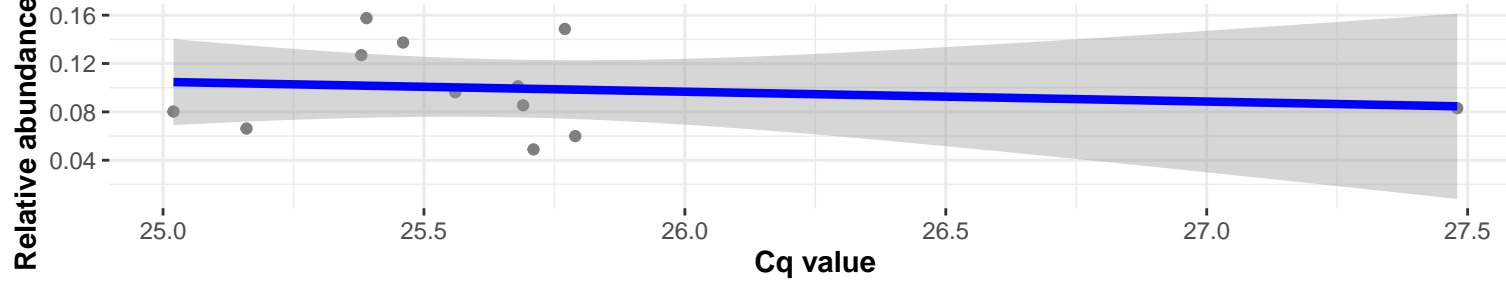
Correlation within: IM-PID

$\log_e(S) = 4.127$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = 0.718$, $CI_{95\%} [0.188, 0.924]$, $n_{\text{pairs}} = 11$



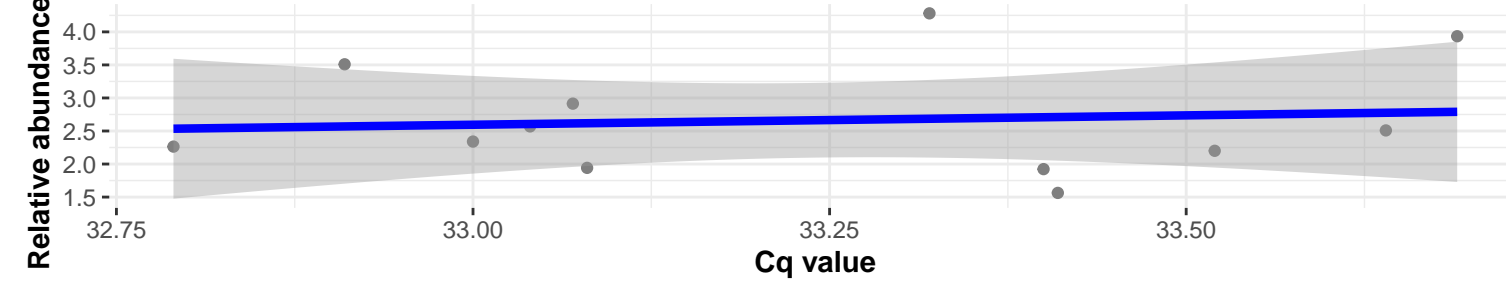
Correlation within: IM-DID

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



Correlation within: Extraction-blank

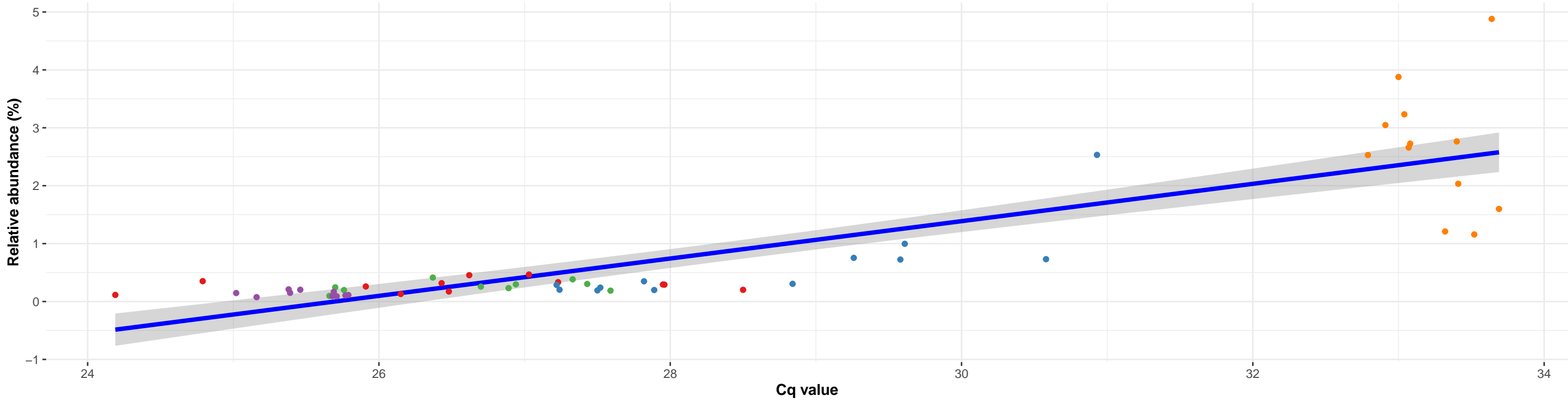
$\log_e(S) = 5.730$, $p = 0.812$, $\hat{\rho}_{\text{Spearman}} = -0.077$, $CI_{95\%} [-0.635, 0.534]$, $n_{\text{pairs}} = 12$



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

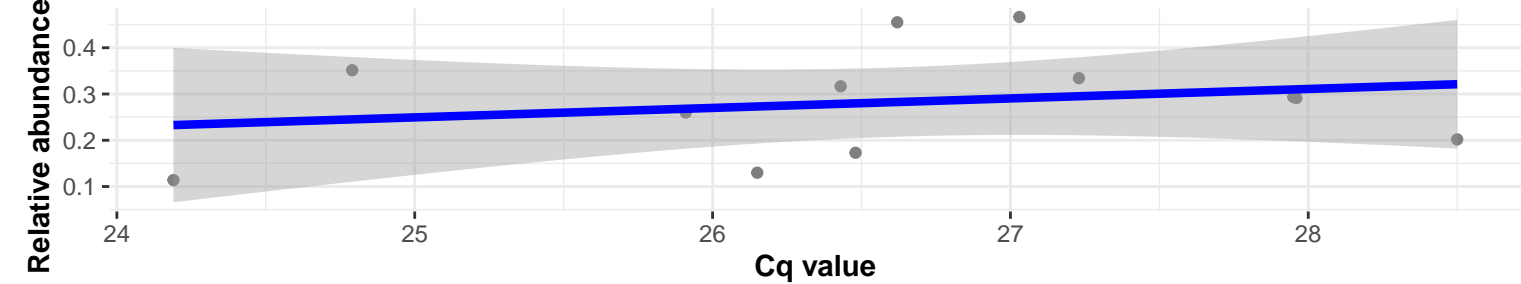
Correlation with all samples

$\log_e(S) = 8.652$, $p = 8.12e-14$, $\hat{\rho}_{\text{Spearman}} = 0.804$, $CI_{95\%} [0.683, 0.883]$, $n_{\text{pairs}} = 56$



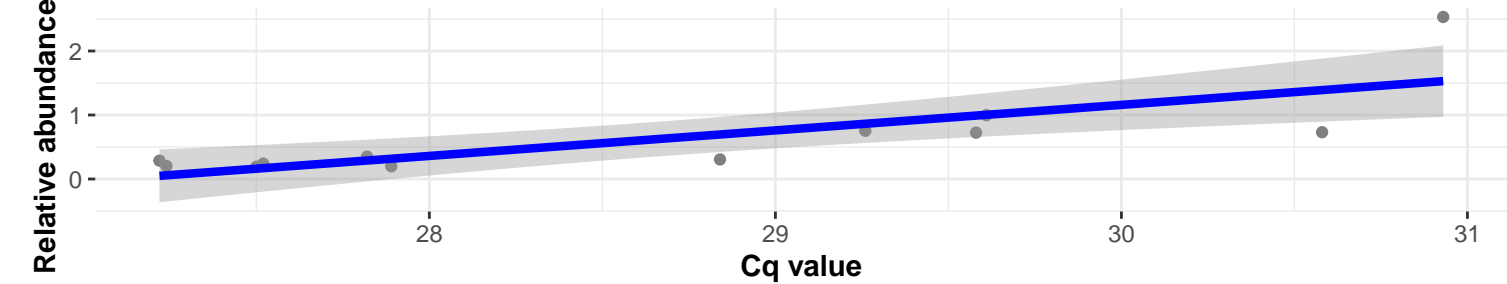
Correlation within: REF-PID

$\log_e(S) = 5.394$, $p = 0.471$, $\hat{\rho}_{\text{Spearman}} = 0.231$, $CI_{95\%} [-0.412, 0.720]$, $n_{\text{pairs}} = 12$



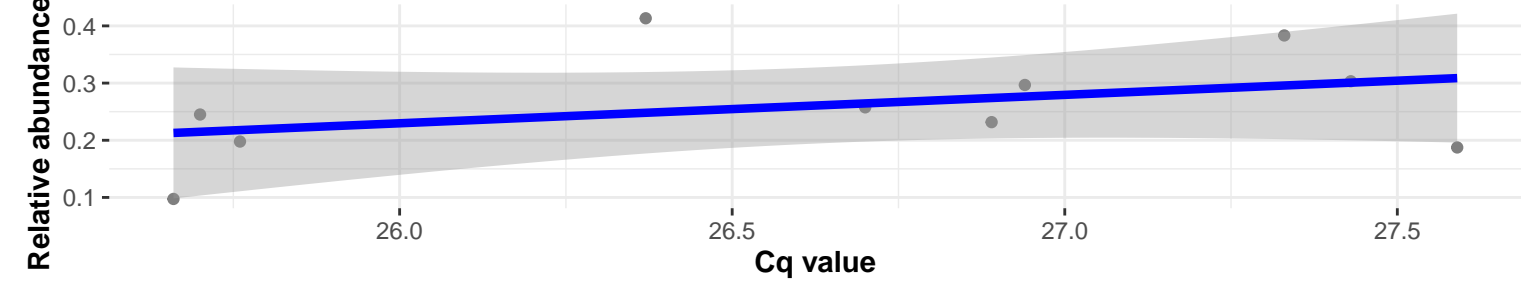
Correlation within: REF-DID

$\log_e(S) = 3.951$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.818$, $CI_{95\%} [0.445, 0.949]$, $n_{\text{pairs}} = 12$



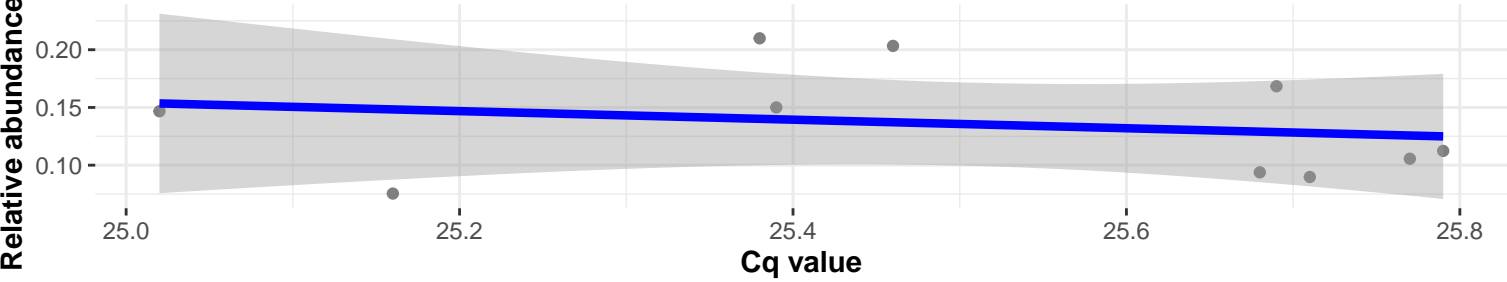
Correlation within: IM-PID

$\log_e(S) = 4.754$, $p = 0.405$, $\hat{\rho}_{\text{Spearman}} = 0.297$, $CI_{95\%} [-0.427, 0.789]$, $n_{\text{pairs}} = 10$



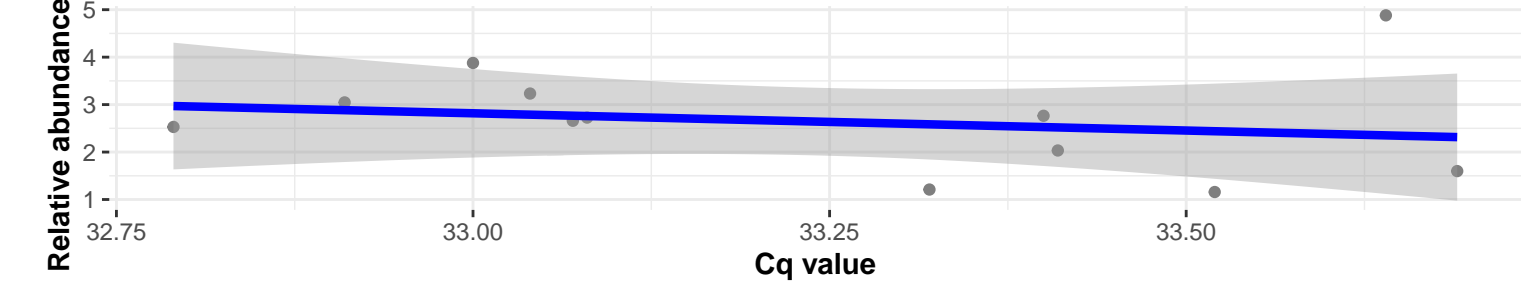
Correlation within: IM-DID

$\log_e(S) = 5.278$, $p = 0.603$, $\hat{\rho}_{\text{Spearman}} = -0.188$, $CI_{95\%} [-0.741, 0.517]$, $n_{\text{pairs}} = 10$



Correlation within: Extraction-blank

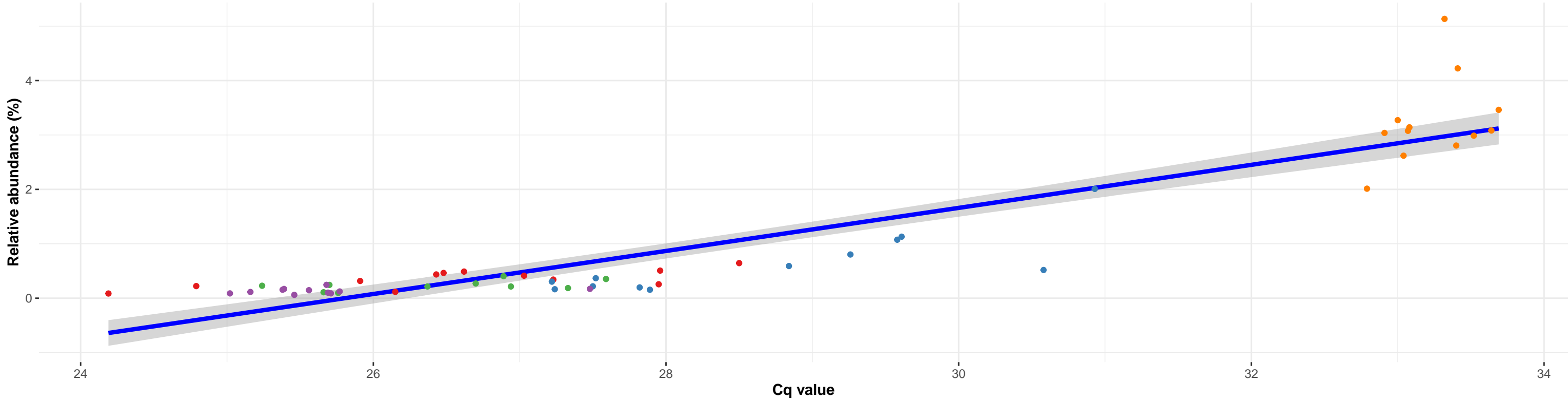
$\log_e(S) = 5.940$, $p = 0.297$, $\hat{\rho}_{\text{Spearman}} = -0.329$, $CI_{95\%} [-0.767, 0.320]$, $n_{\text{pairs}} = 12$



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

Correlation with all samples

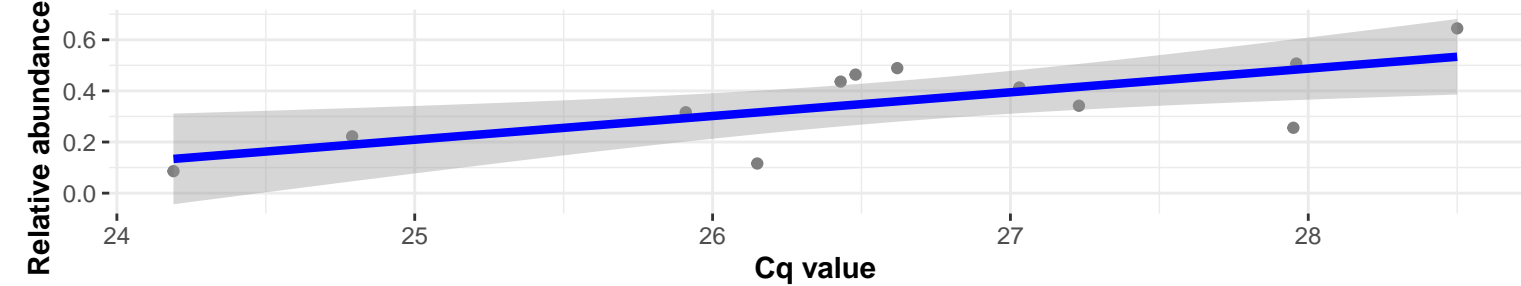
$\log_e(S) = 8.421$, $p = 3.75e-17$, $\hat{\rho}_{\text{Spearman}} = 0.853$, $CI_{95\%} [0.758, 0.912]$, $n_{\text{pairs}} = 57$



SampleType ● REF-PID ● REF-DID ● IM-PID ● IM-DID ● Extraction-blank

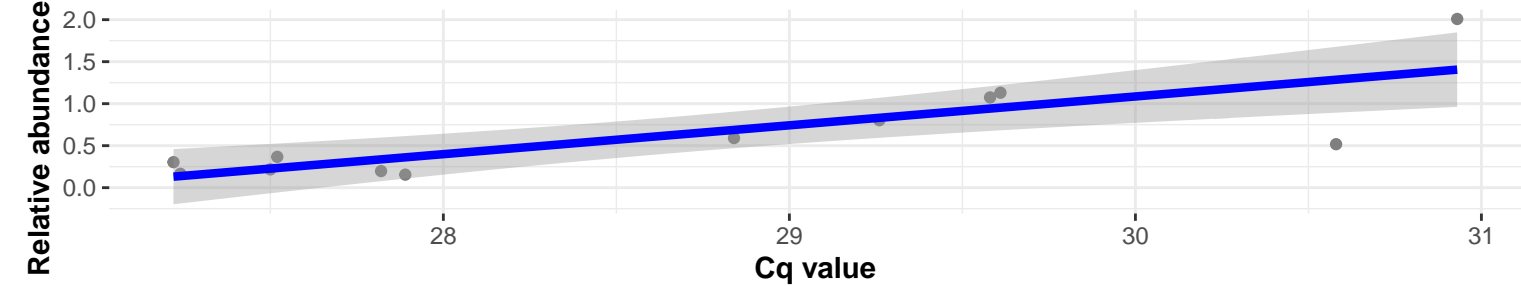
Correlation within: REF-PID

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



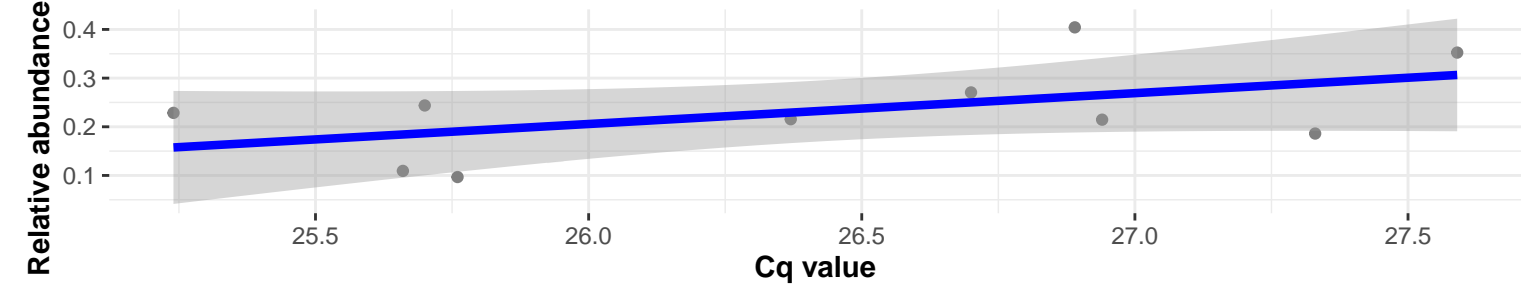
Correlation within: REF-DID

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



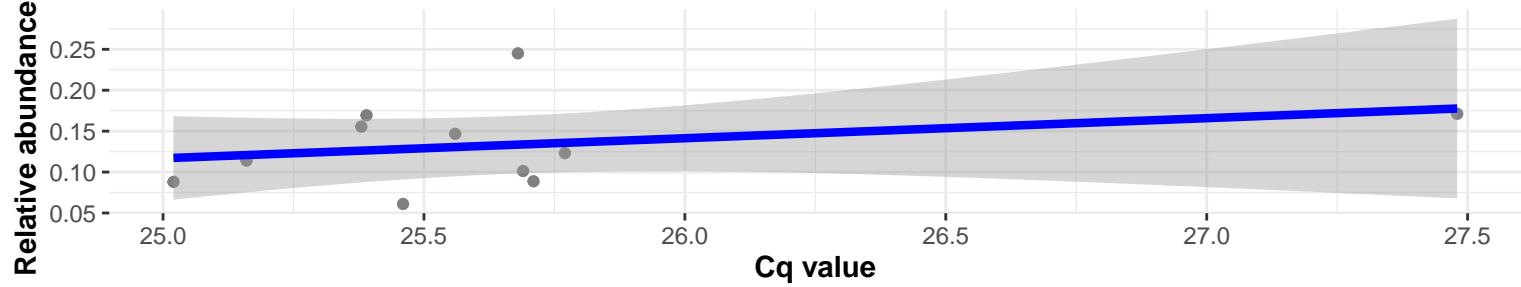
Correlation within: IM-PID

$\log_e(S) = 4.754$, $p = 0.405$, $\hat{\rho}_{\text{Spearman}} = 0.297$, $CI_{95\%} [-0.427, 0.789]$, $n_{\text{pairs}} = 10$



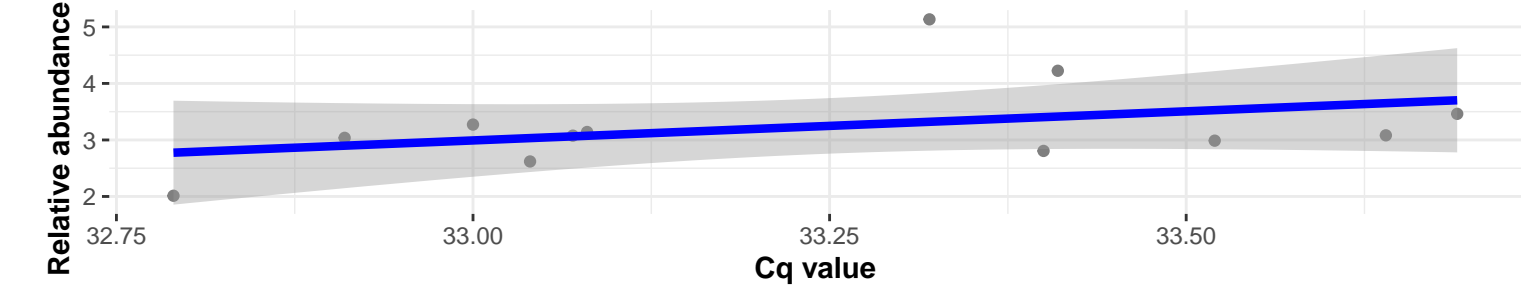
Correlation within: IM-DID

$\log_e(S) = 5.088$, $p = 0.433$, $\hat{\rho}_{\text{Spearman}} = 0.264$, $CI_{95\%} [-0.416, 0.755]$, $n_{\text{pairs}} = 11$



Correlation within: Extraction-blank

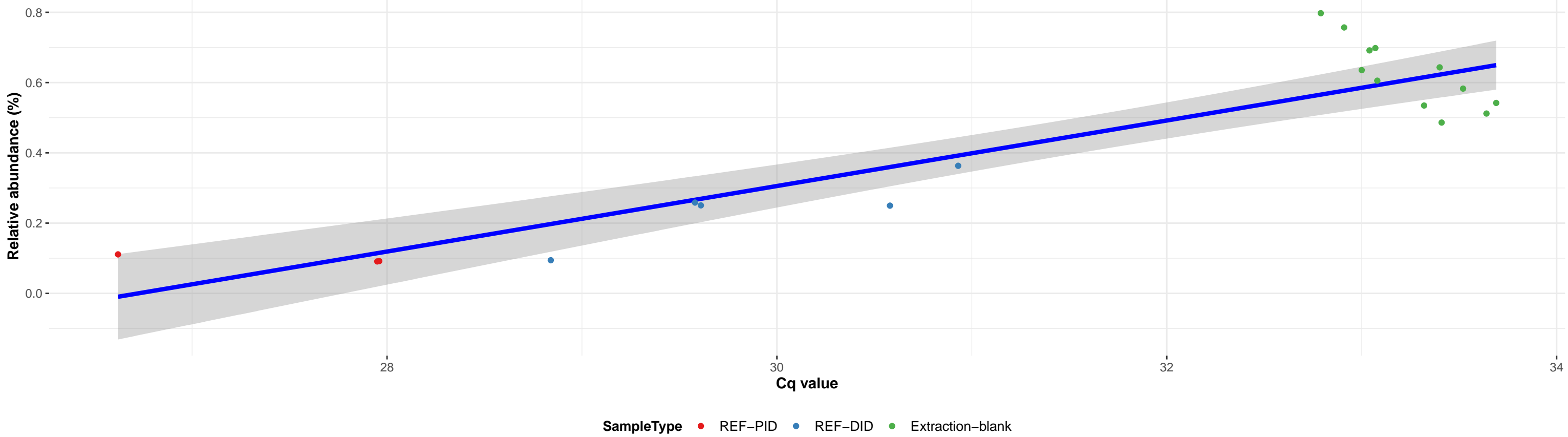
$\log_e(S) = 5.100$, $p = 0.167$, $\hat{\rho}_{\text{Spearman}} = 0.427$, $CI_{95\%} [-0.214, 0.810]$, $n_{\text{pairs}} = 12$



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

Correlation with all samples

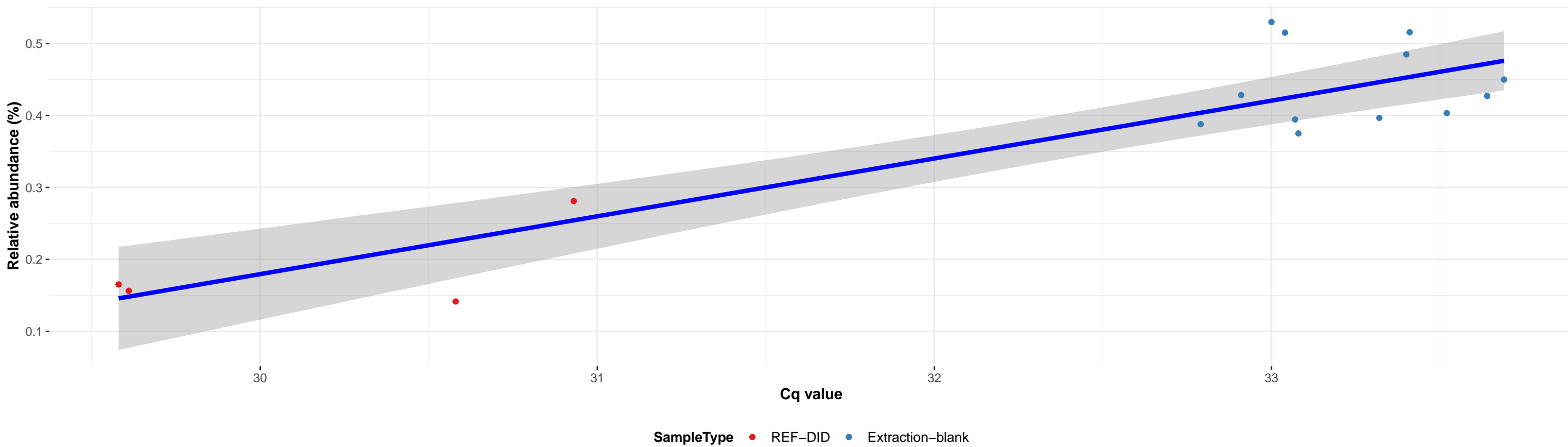
$\log_e(S) = 6.288$, $p = 0.006$, $\hat{\rho}_{\text{Spearman}} = 0.595$, $\text{CI}_{95\%} [0.194, 0.826]$, $n_{\text{pairs}} = 20$



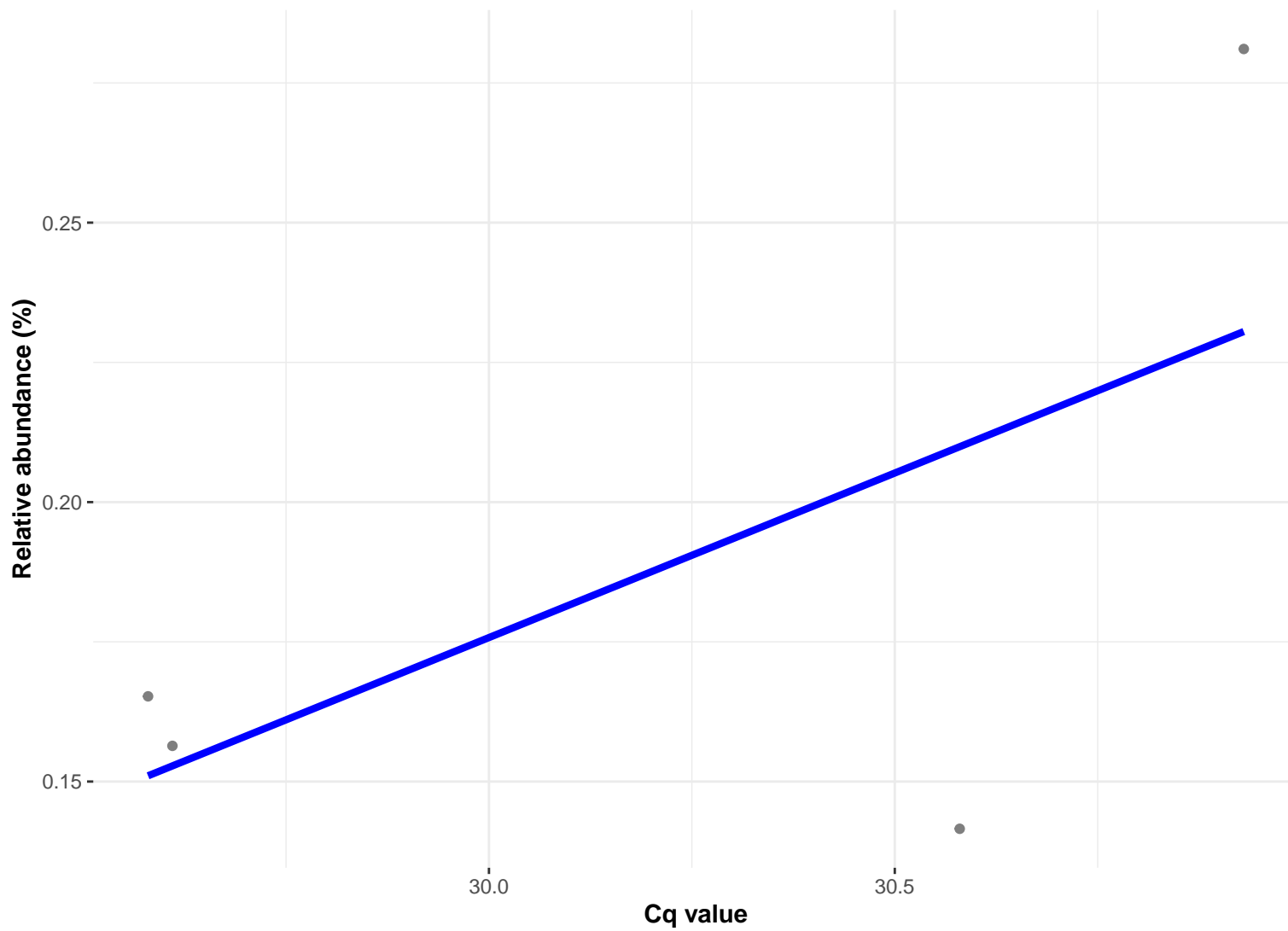
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

Correlation with all samples

$\log_e(S) = 5.561$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = 0.618$, $\text{CI}_{95\%} [0.160, 0.857]$, $n_{\text{pairs}} = 16$

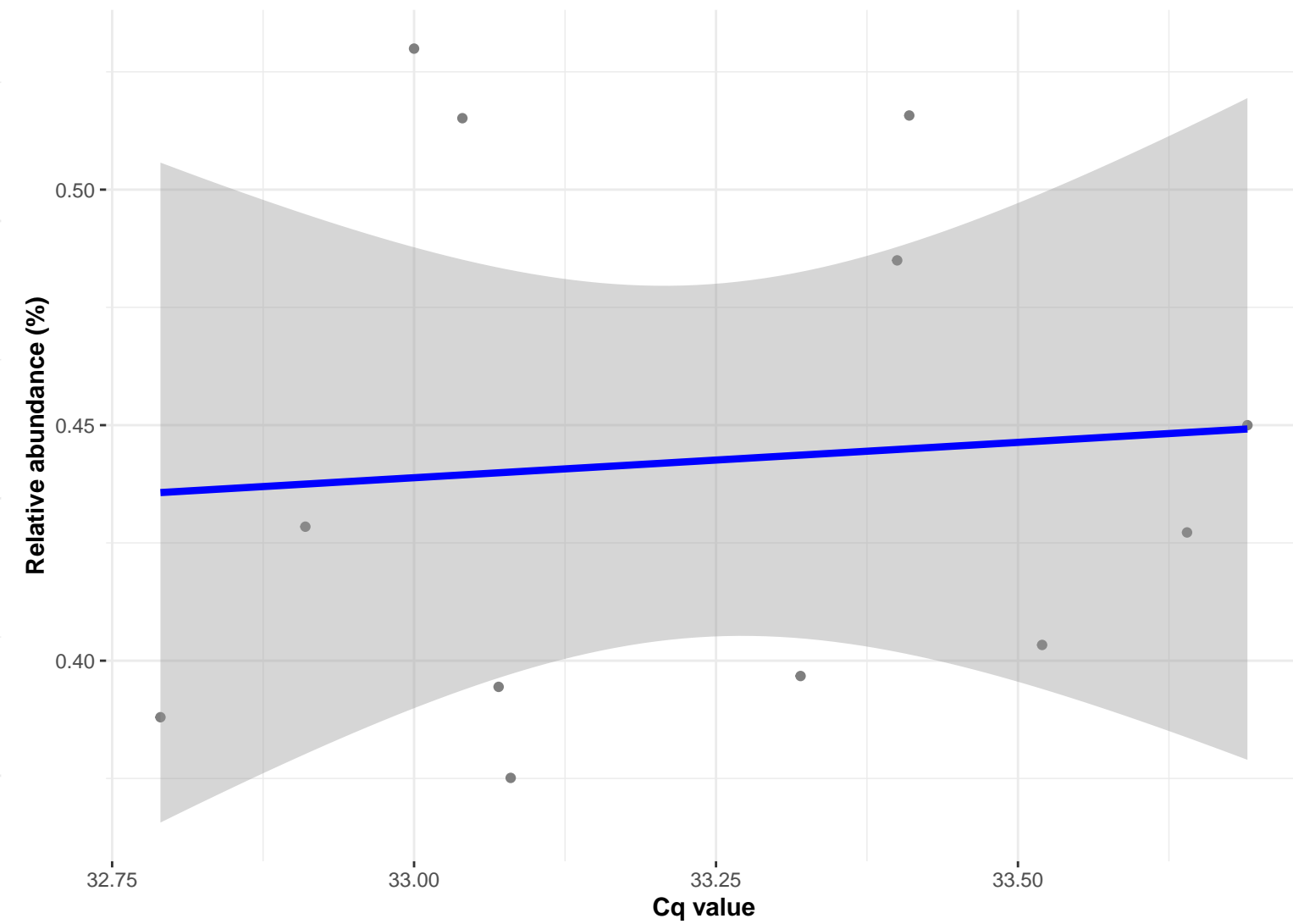


Correlation within: REF-DID



Correlation within: Extraction-blank

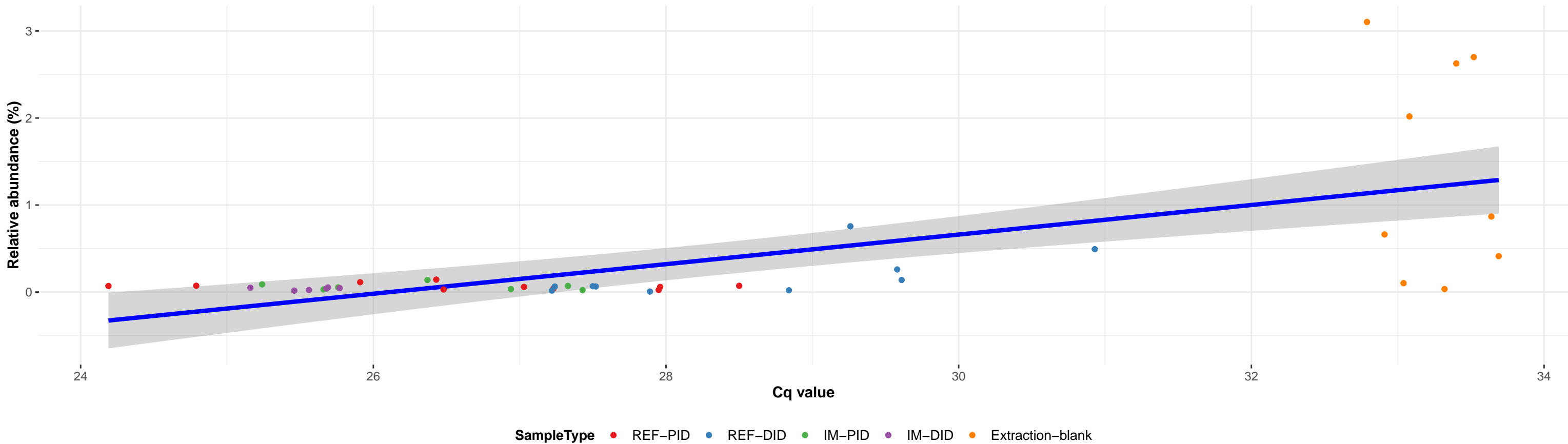
$\log_e(S) = 5.529$, $p = 0.713$, $\hat{\rho}_{\text{Spearman}} = 0.119$, $\text{CI}_{95\%} [-0.503, 0.660]$, $n_{\text{pairs}} = 12$



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

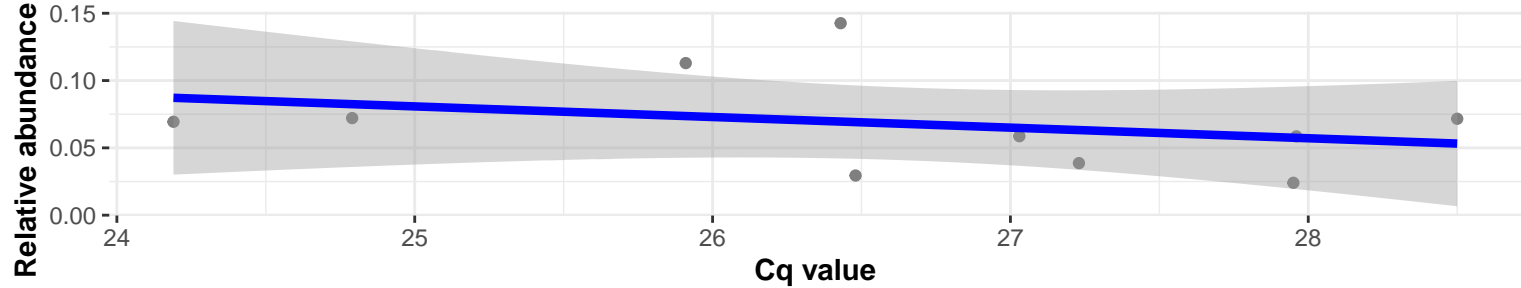
Correlation with all samples

$\log_e(S) = 8.716$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.506$, $\text{CI}_{95\%} [0.230, 0.707]$, $n_{\text{pairs}} = 42$



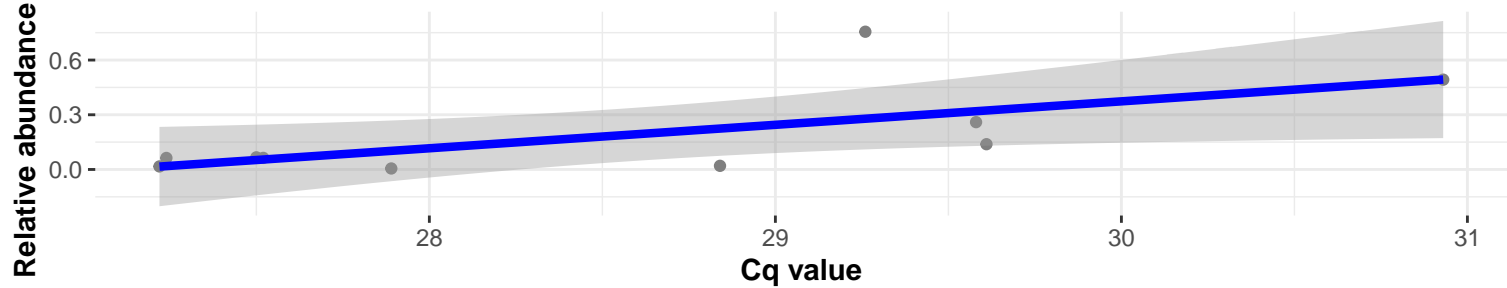
Correlation within: REF-PID

$\log_e(S) = 5.489$, $p = 0.174$, $\hat{\rho}_{\text{Spearman}} = -0.467$, $\text{CI}_{95\%} [-0.853, 0.251]$, $n_{\text{pairs}} = 10$



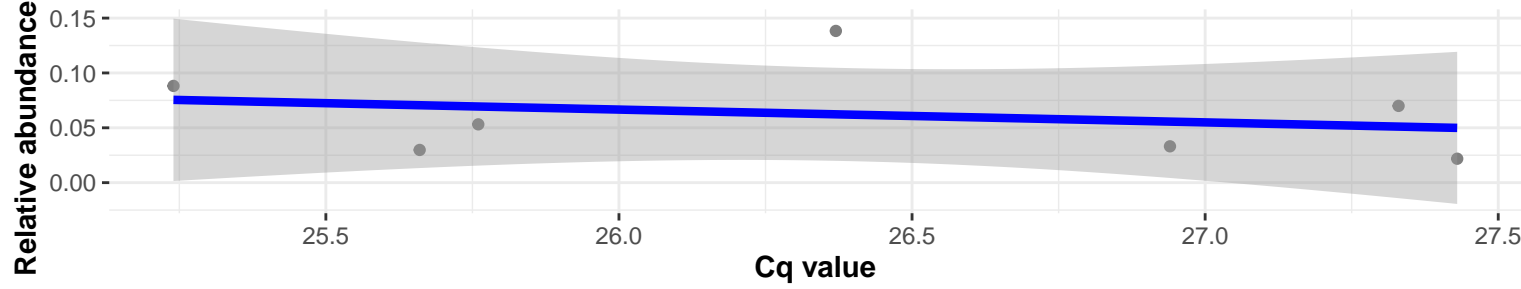
Correlation within: REF-DID

$\log_e(S) = 3.989$, $p = 0.033$, $\hat{\rho}_{\text{Spearman}} = 0.673$, $\text{CI}_{95\%} [0.053, 0.918]$, $n_{\text{pairs}} = 10$

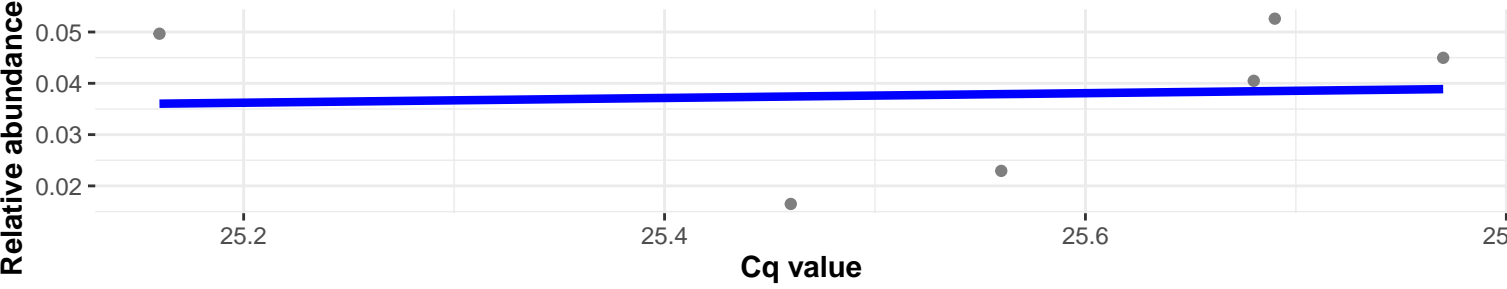


Correlation within: IM-PID

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

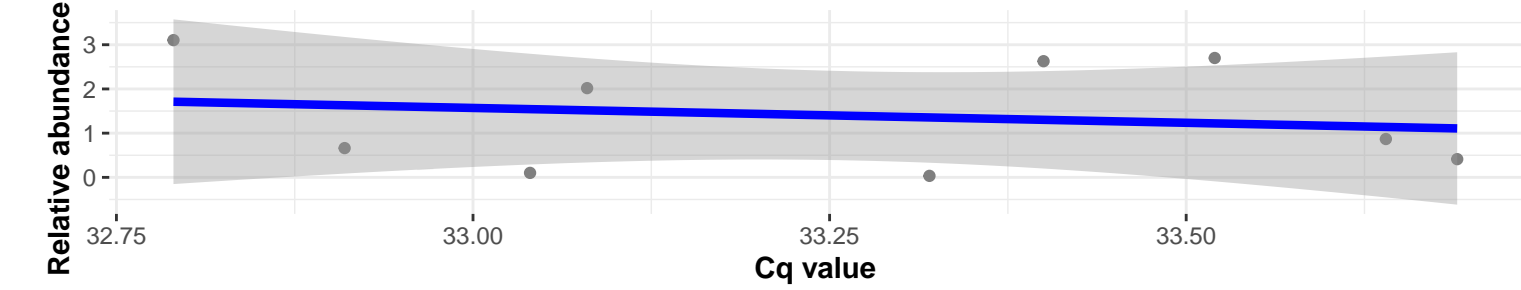


Correlation within: IM-DID

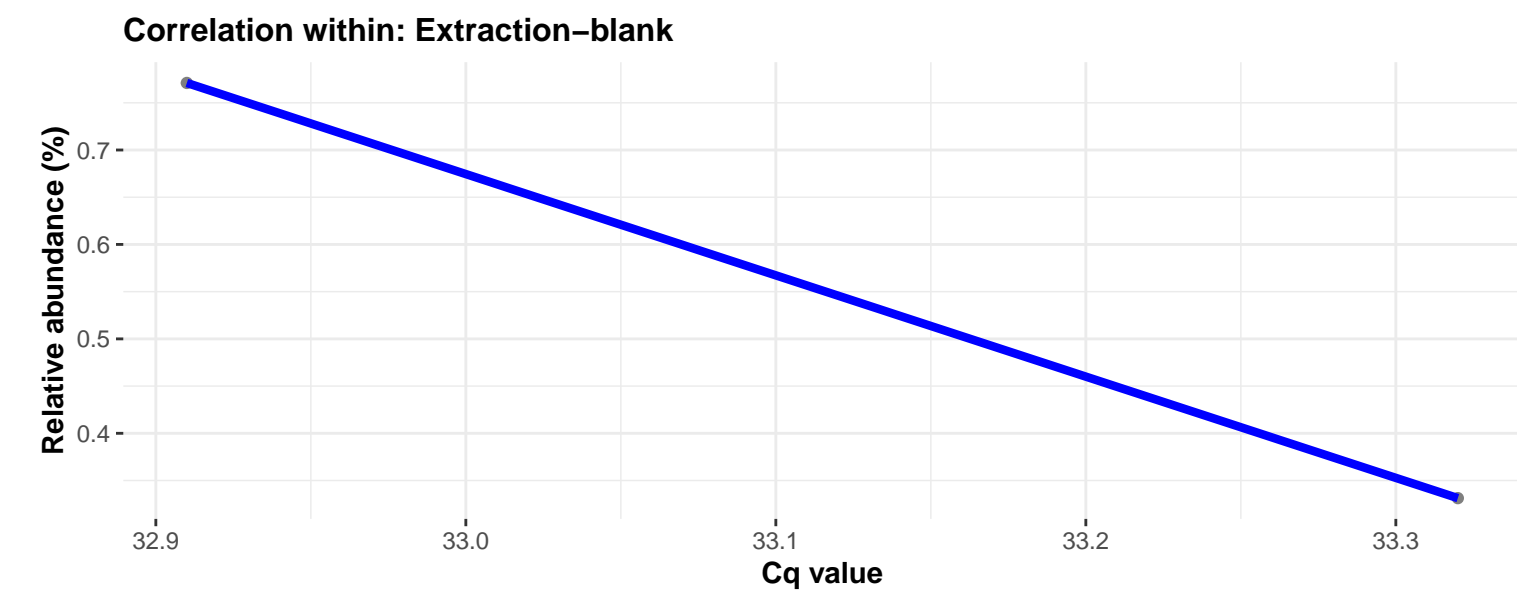
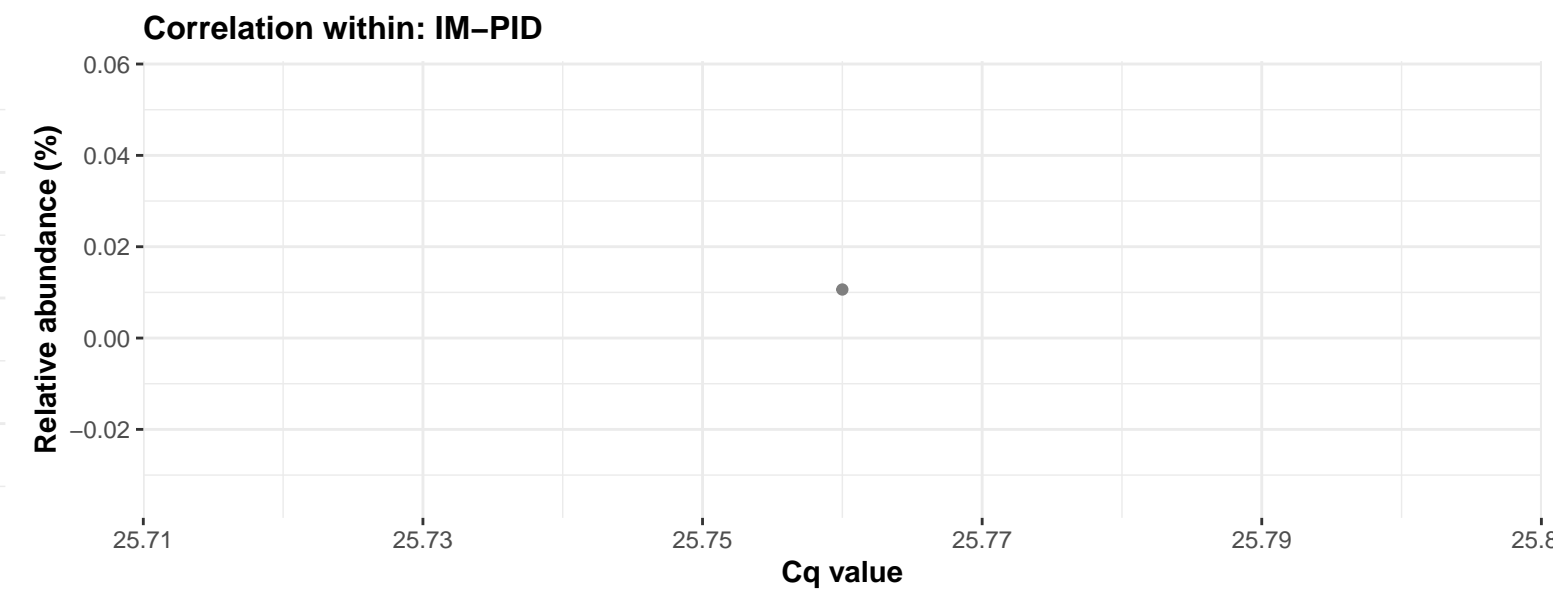
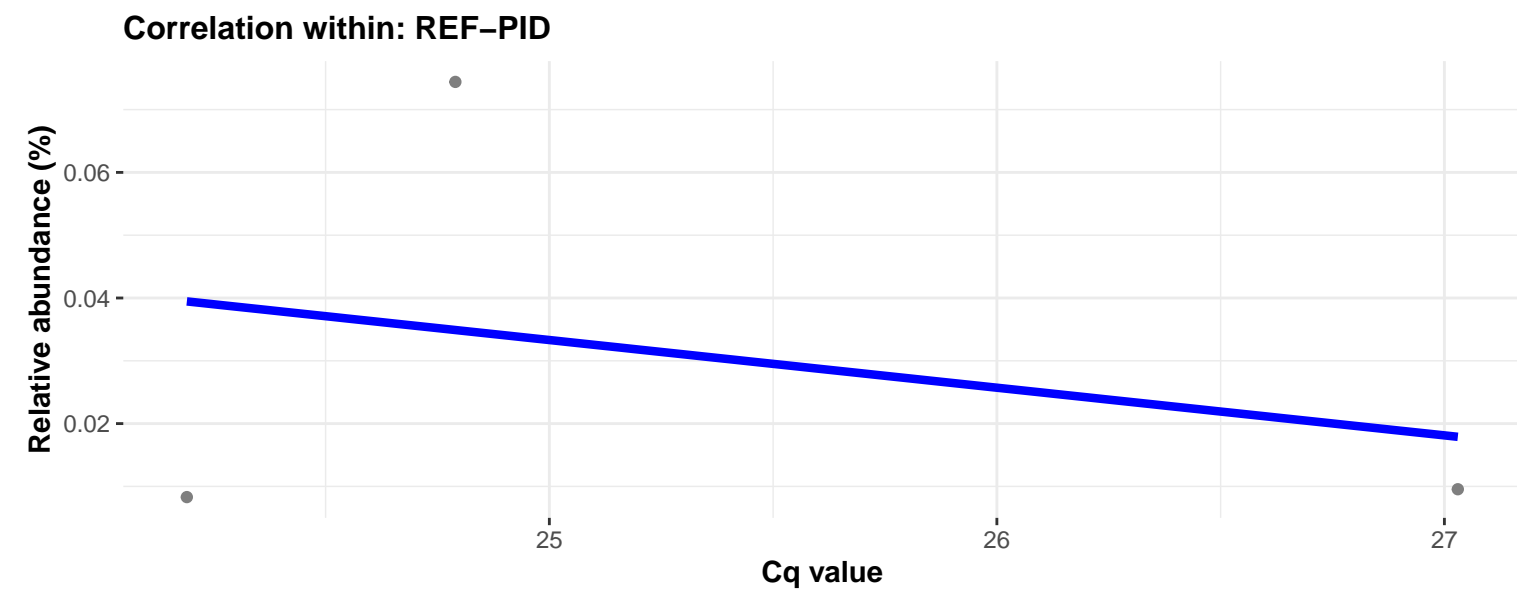
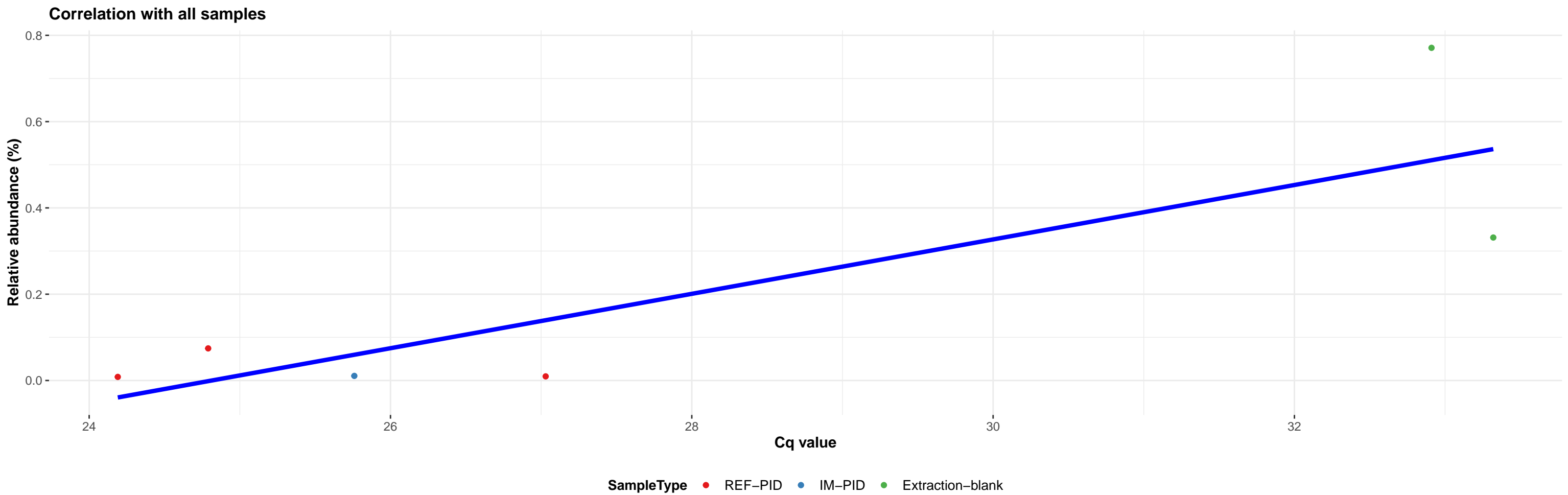


Correlation within: Extraction-blank

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



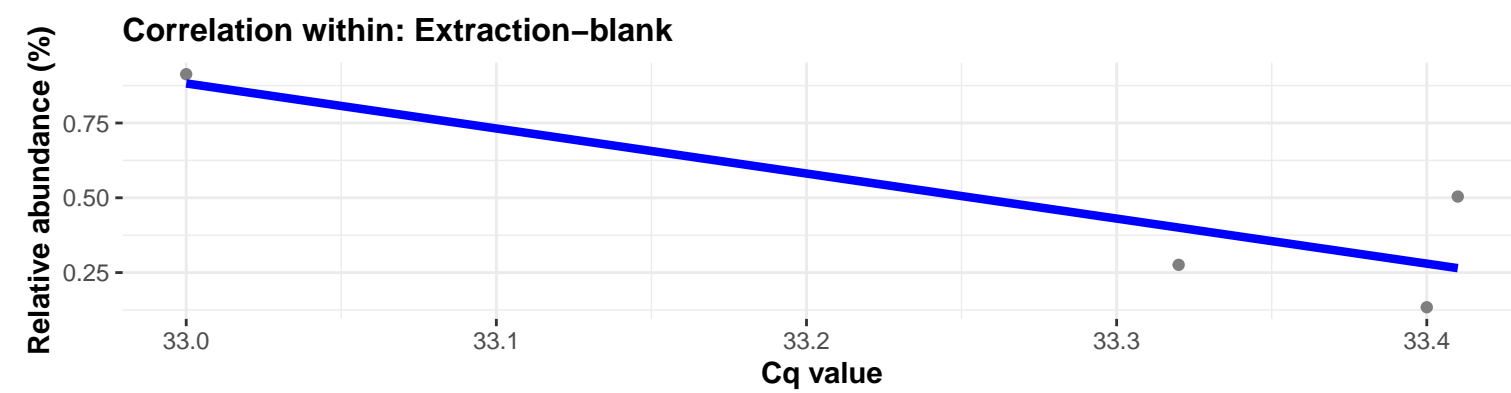
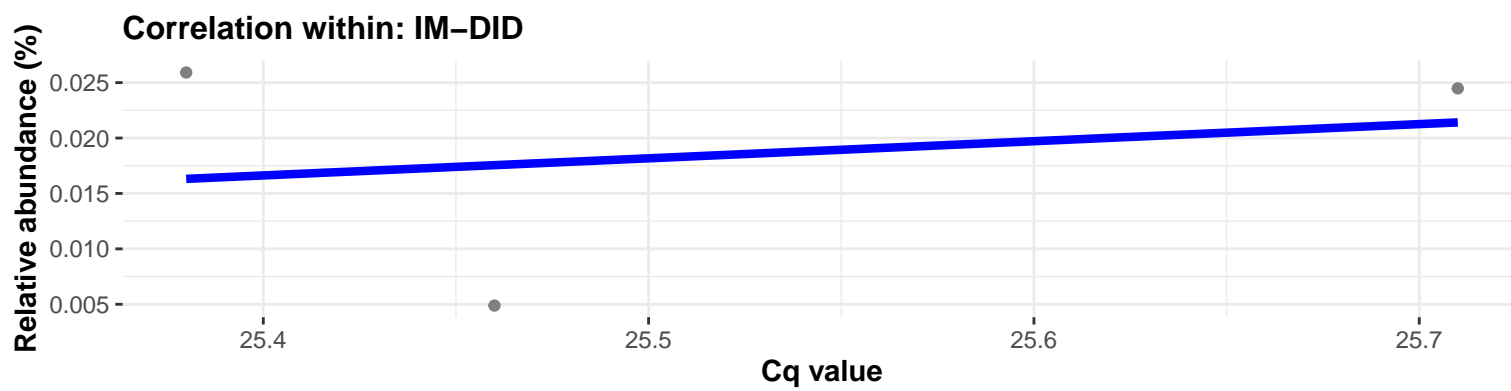
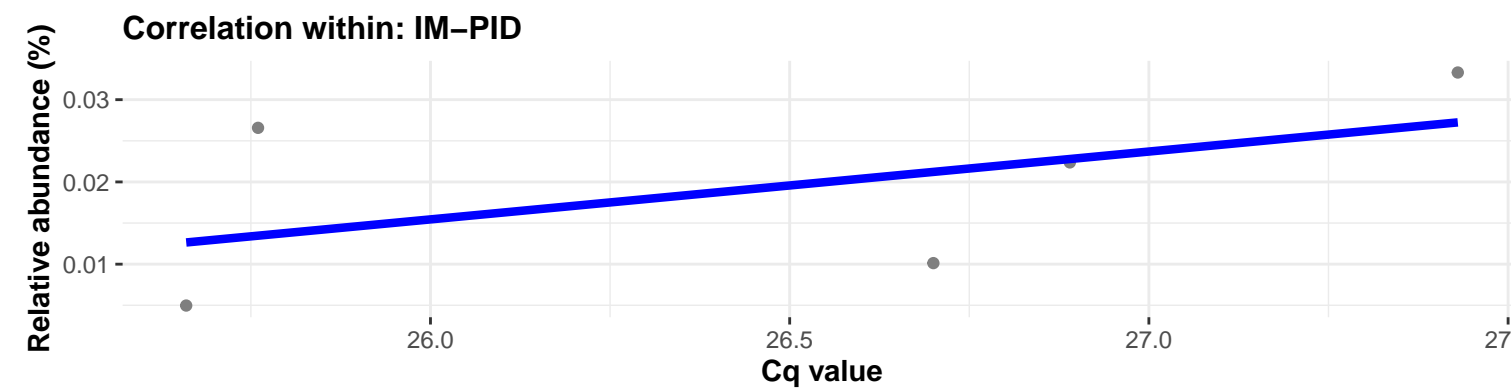
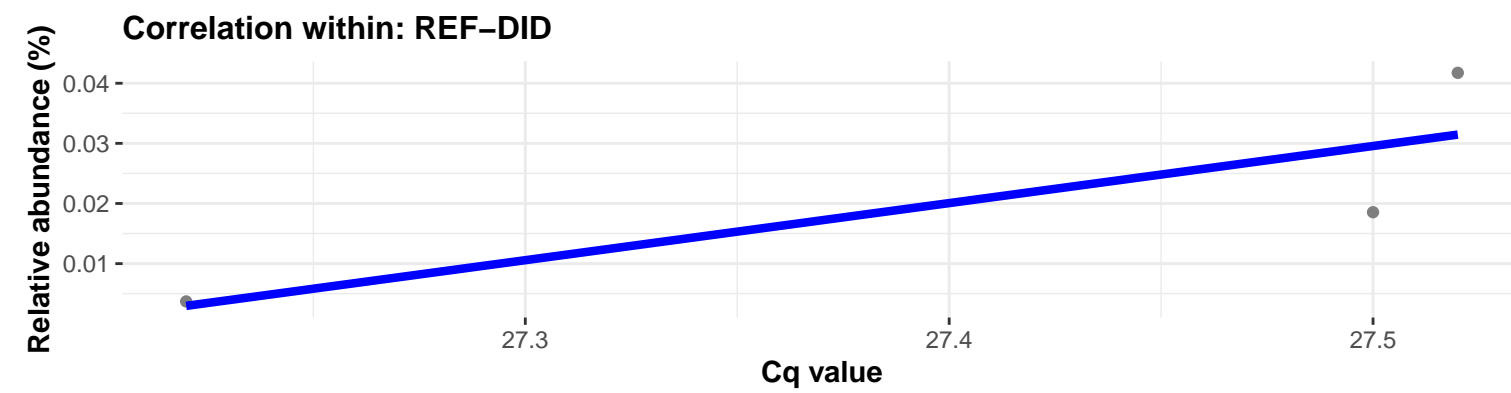
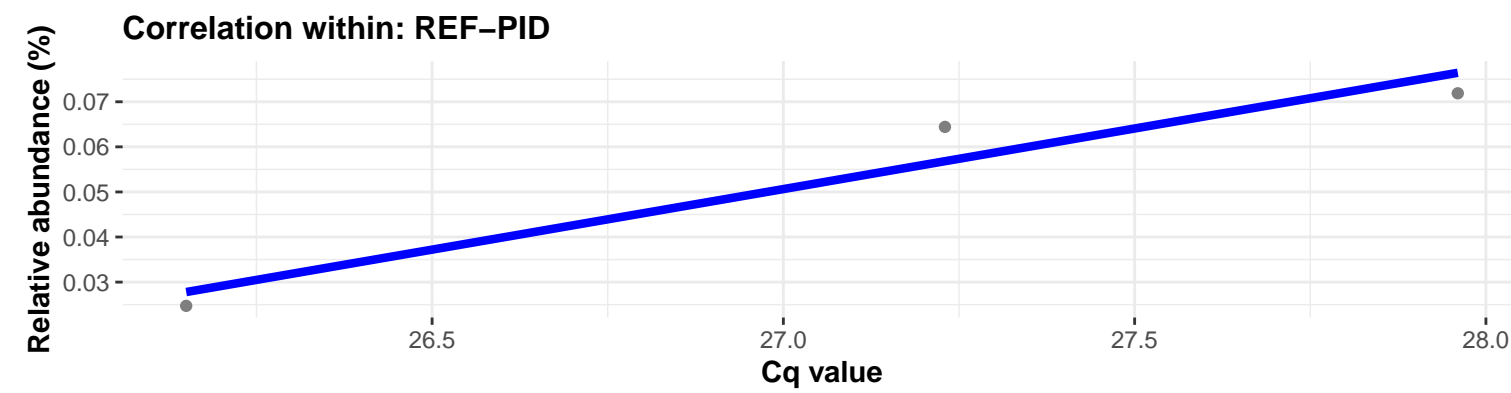
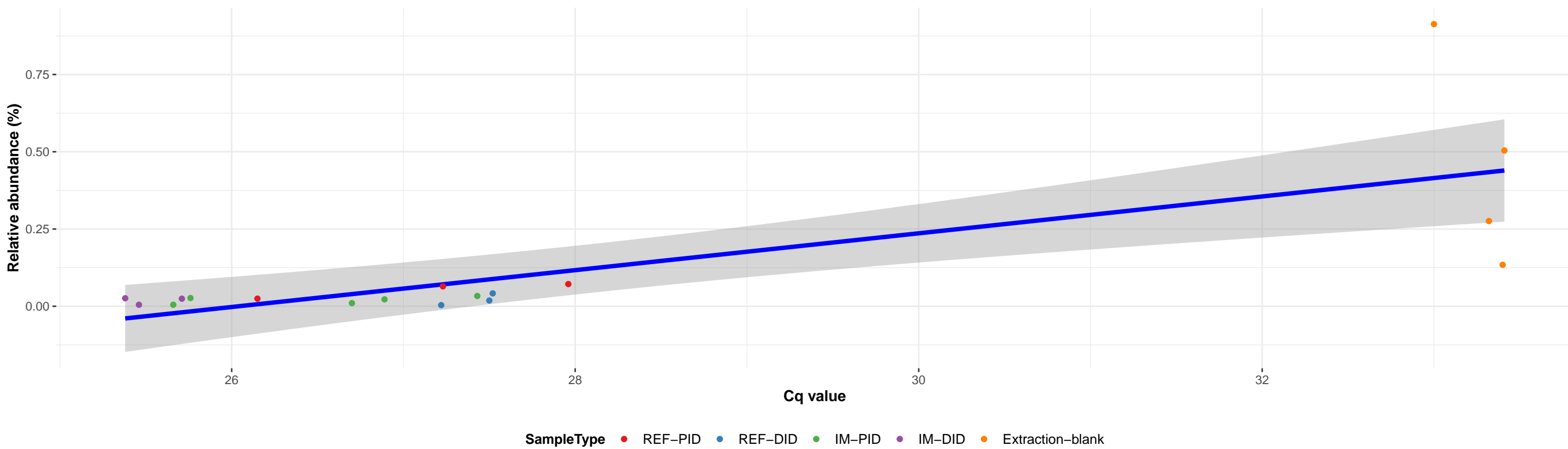
k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfuromonadales; f__Desulfuromonadaceae; g__Pelobacter; s__uncultured bacterium



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

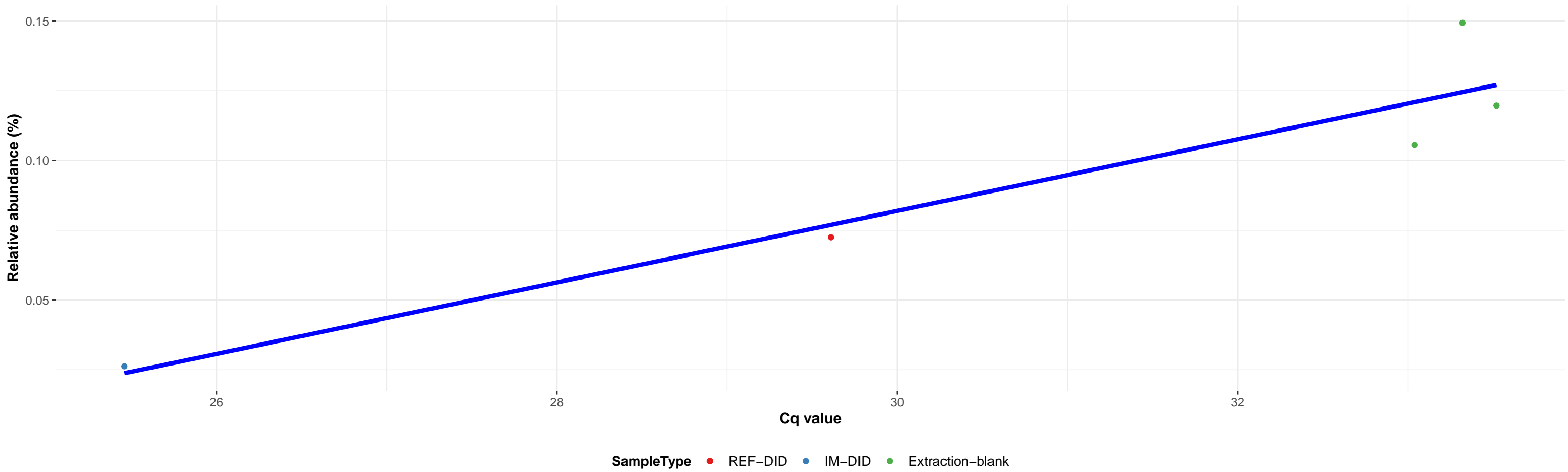
Correlation with all samples

$\log_e(S) = 5.529$, $p = 4.47\text{e-}04$, $\hat{\rho}_{\text{Spearman}} = 0.740$, $\text{CI}_{95\%} [0.405, 0.900]$, $n_{\text{pairs}} = 18$

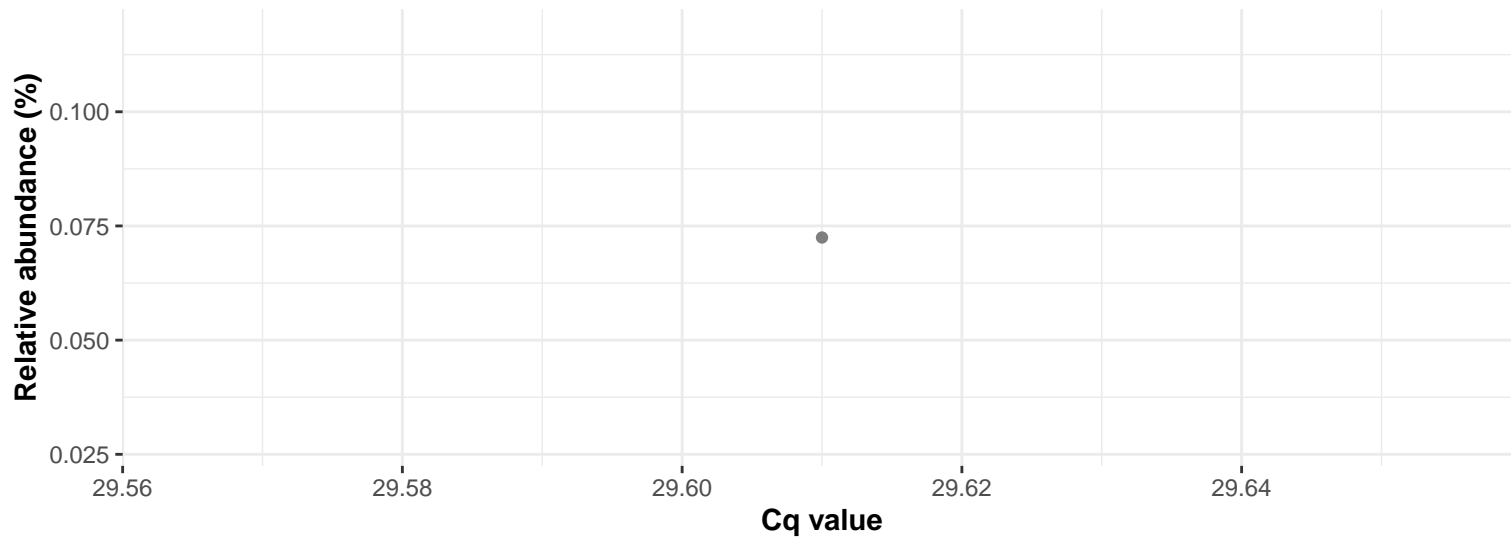


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

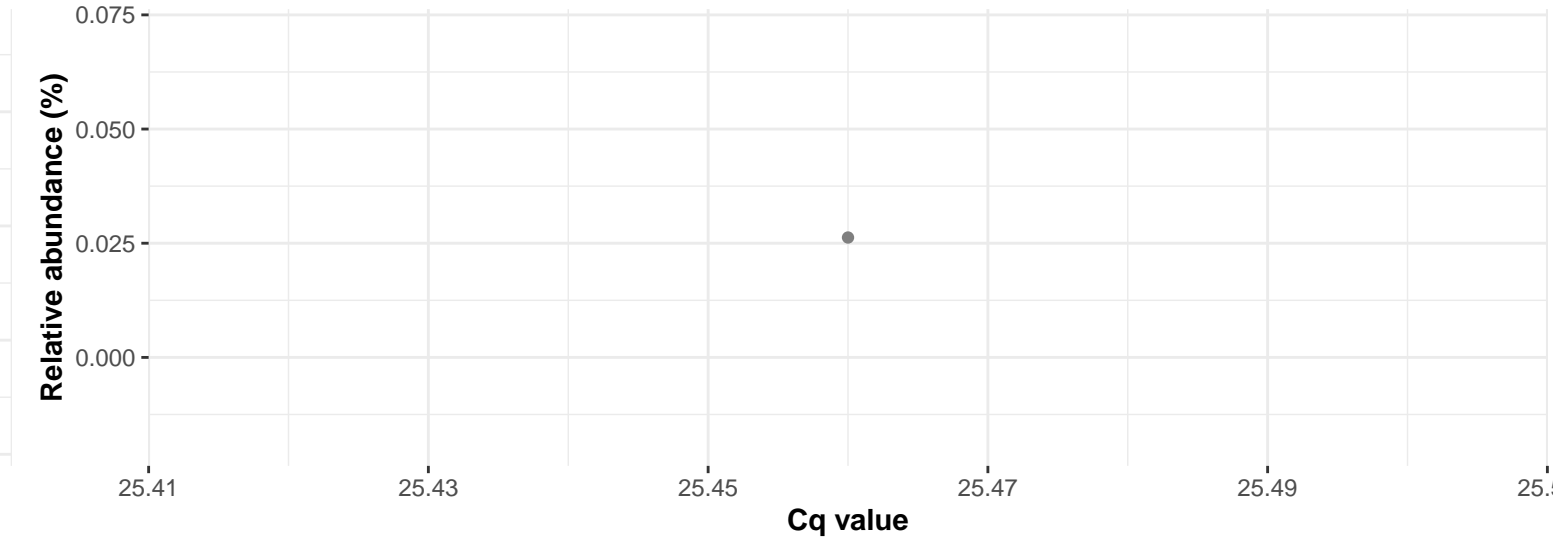
Correlation with all samples



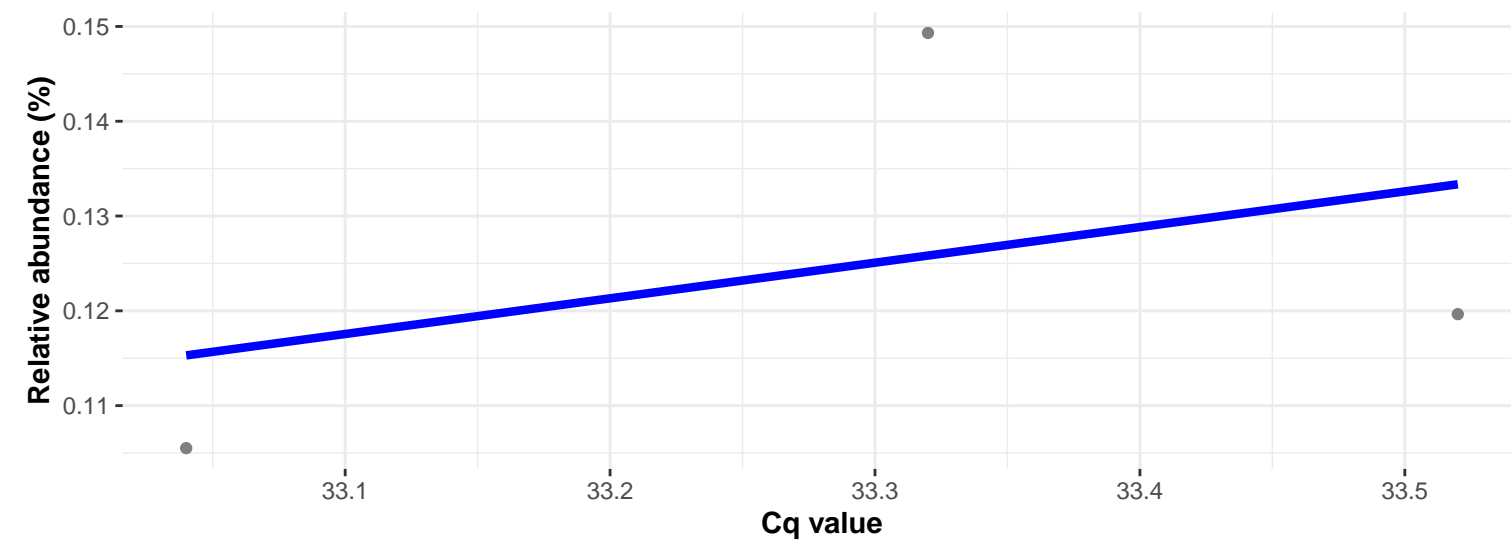
Correlation within: REF-DID



Correlation within: IM-DID

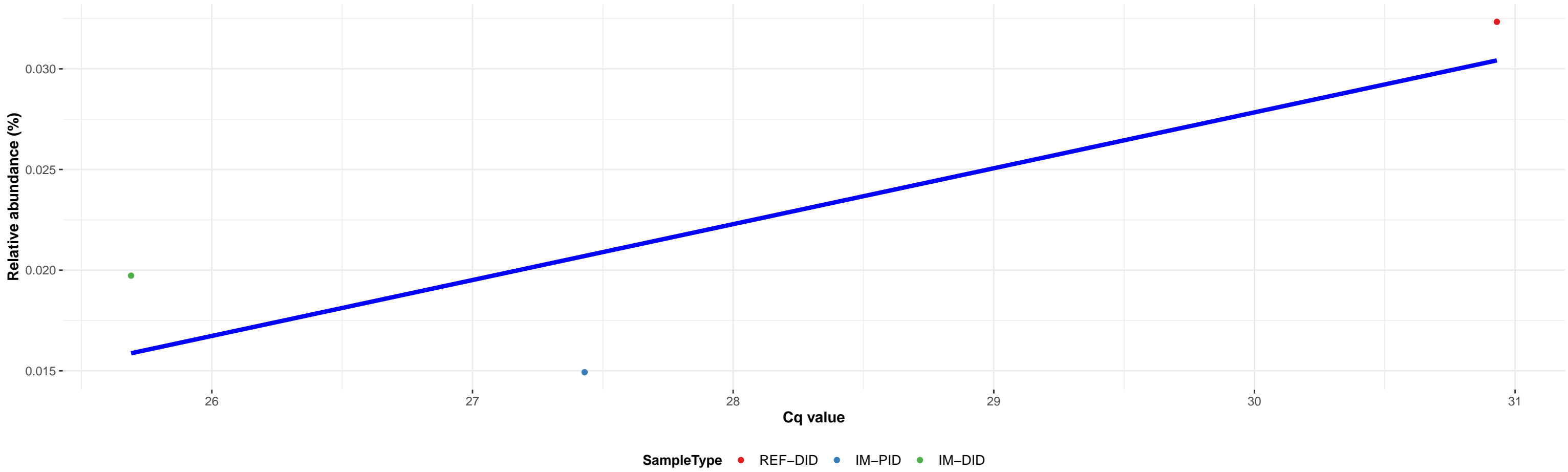


Correlation within: Extraction-blank

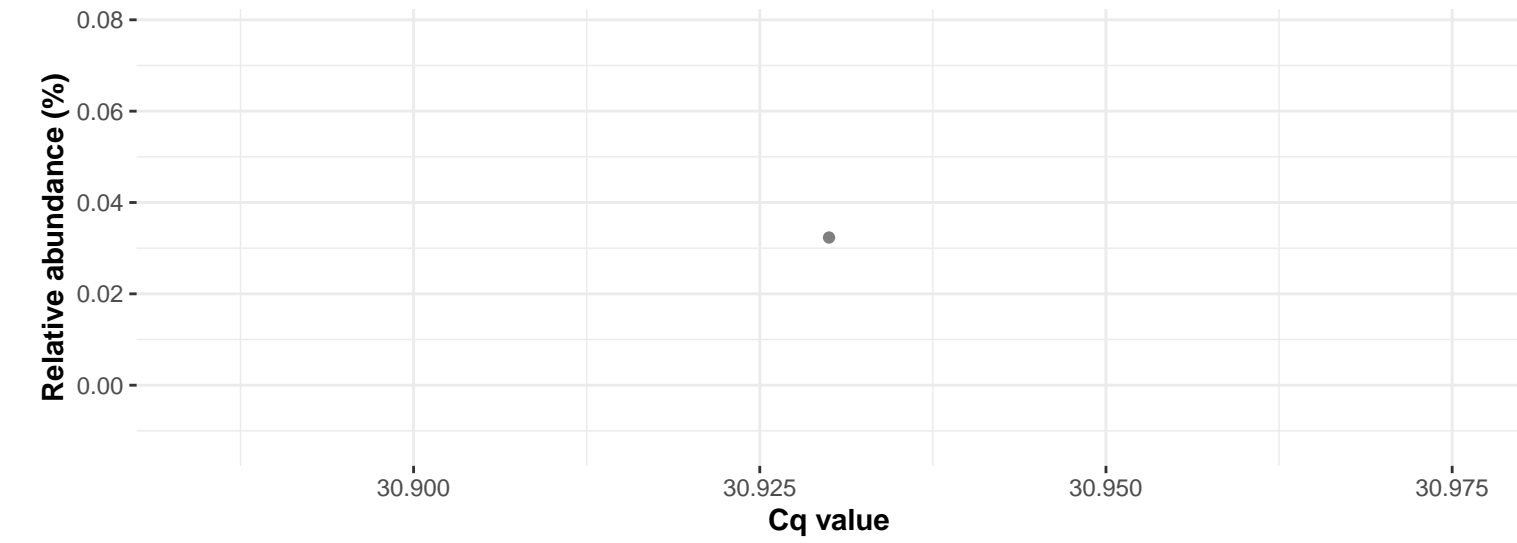


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Cupriavidus; NA

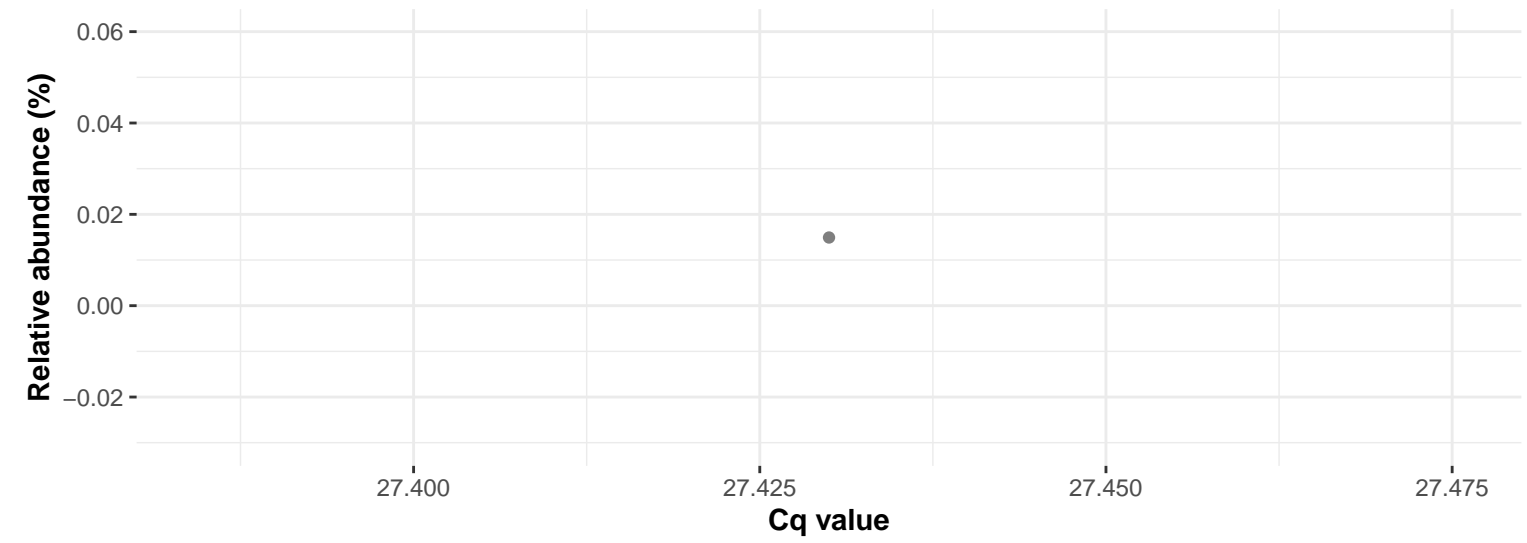
Correlation with all samples



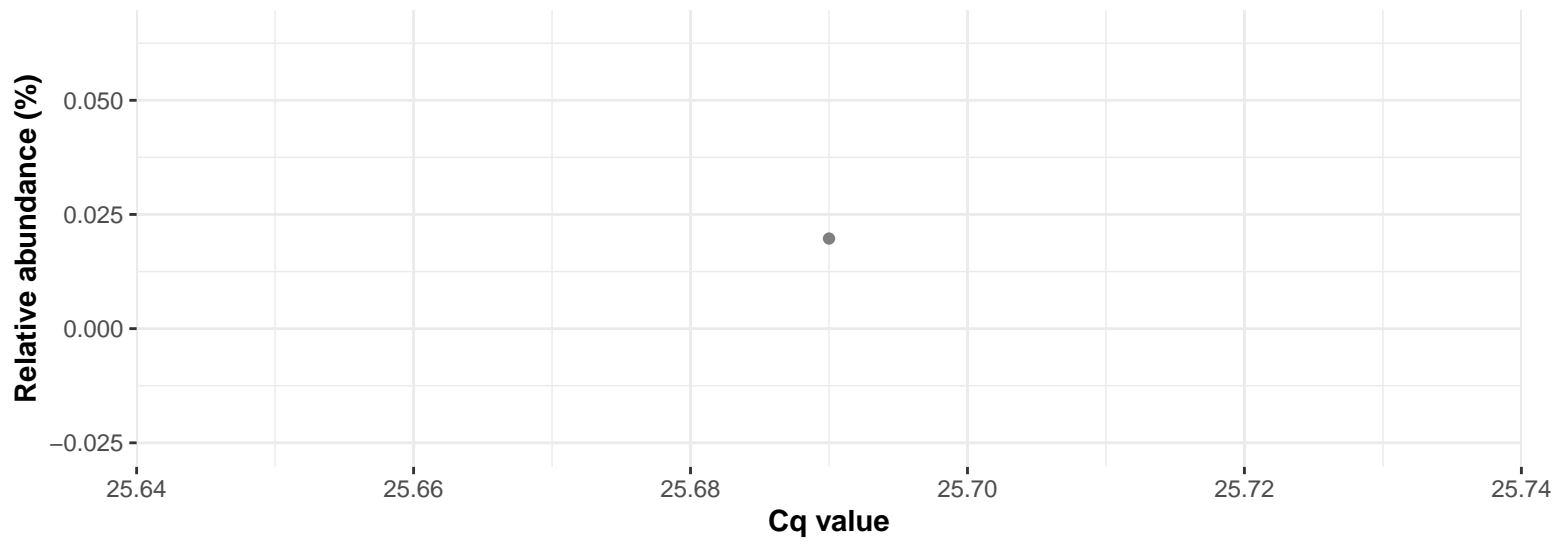
Correlation within: REF-DID



Correlation within: IM-PID



Correlation within: IM-DID



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

