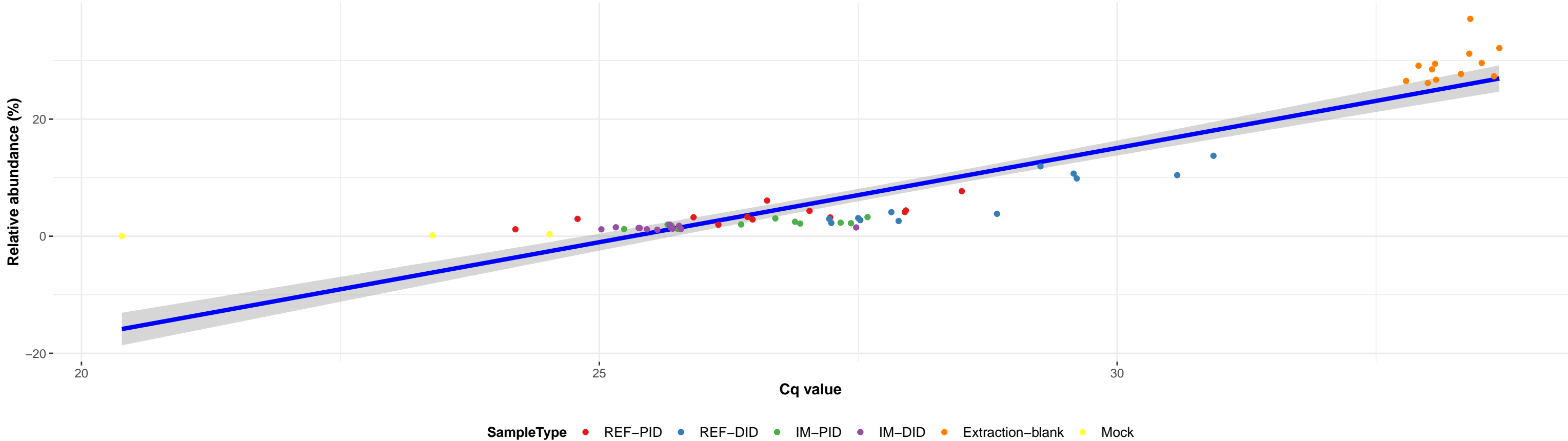


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

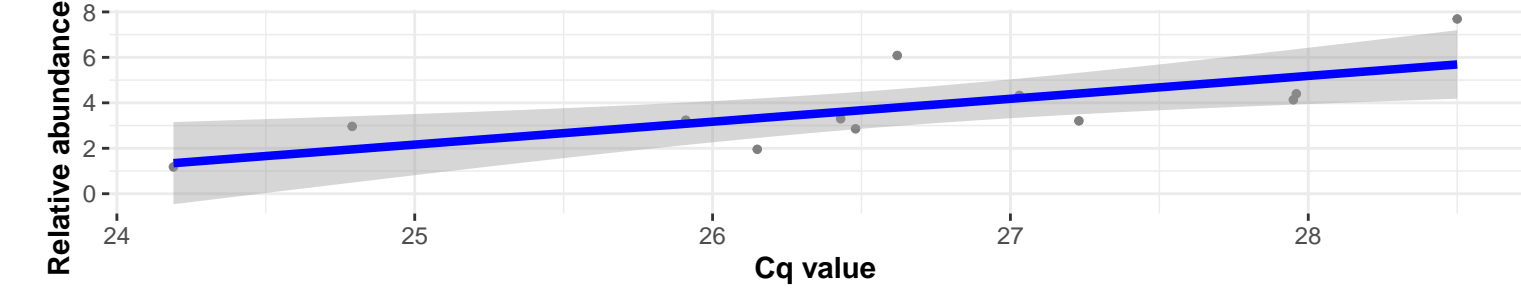
Correlation with all samples

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



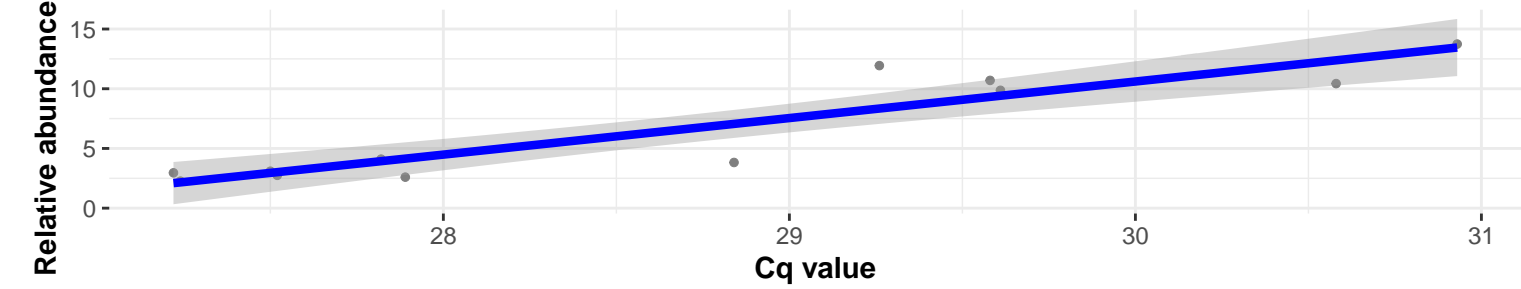
Correlation within: REF-PID

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



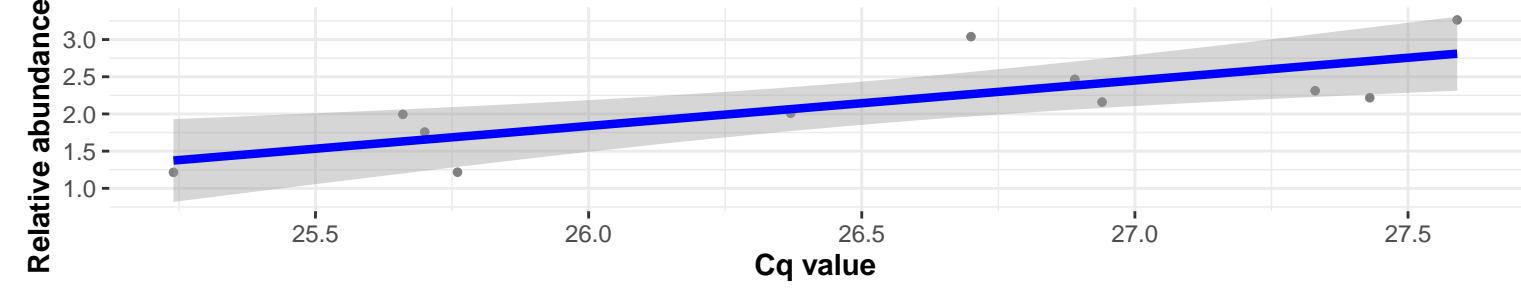
Correlation within: REF-DID

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



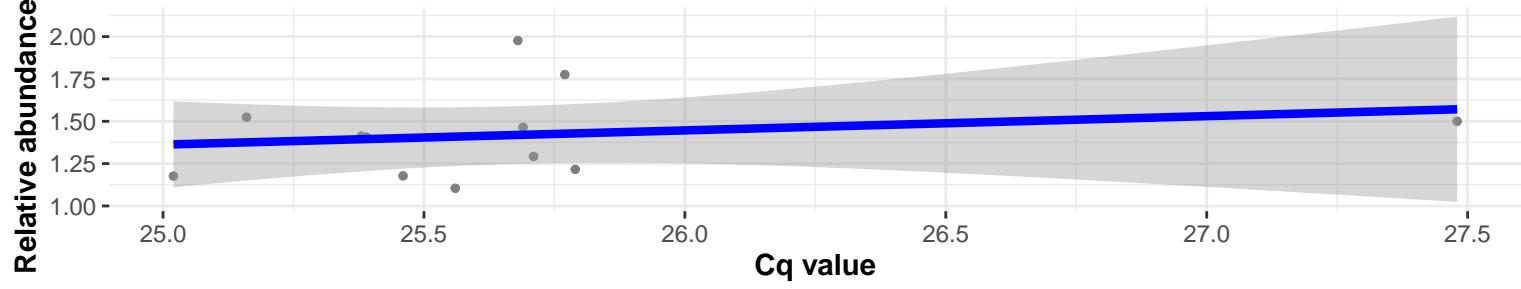
Correlation within: IM-PID

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



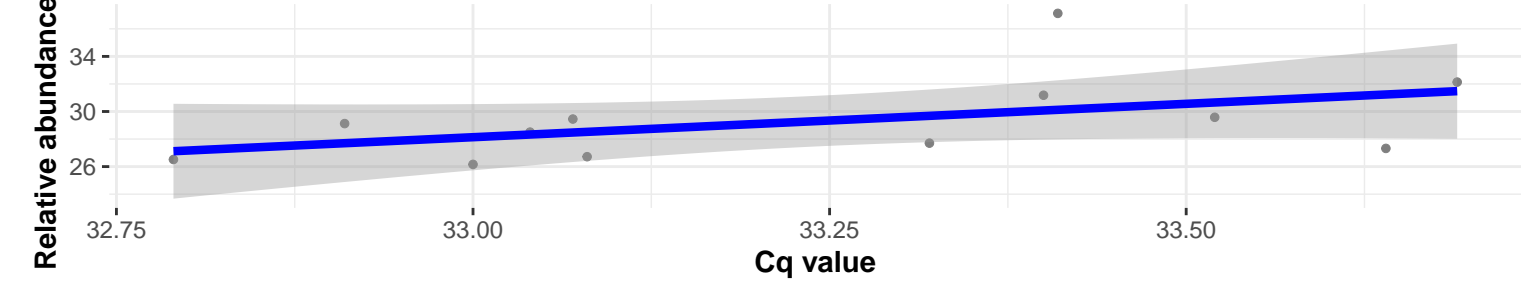
Correlation within: IM-DID

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

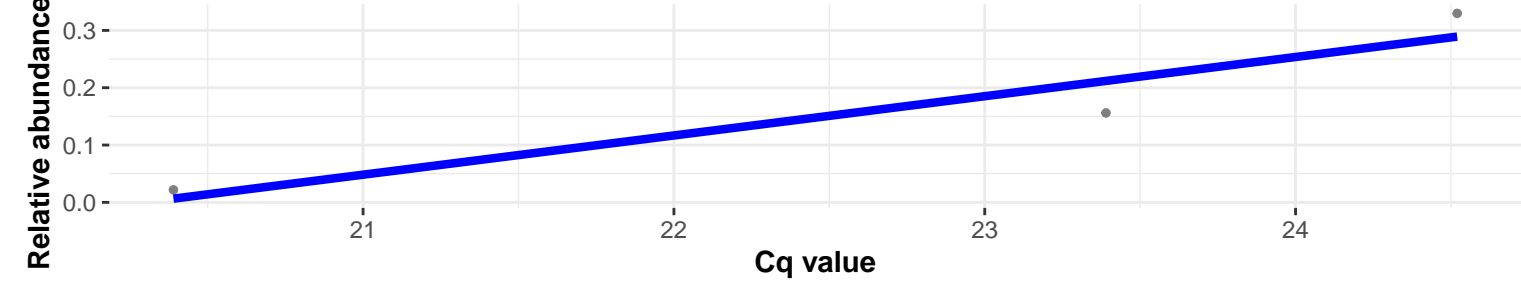


Correlation within: Extraction-blank

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



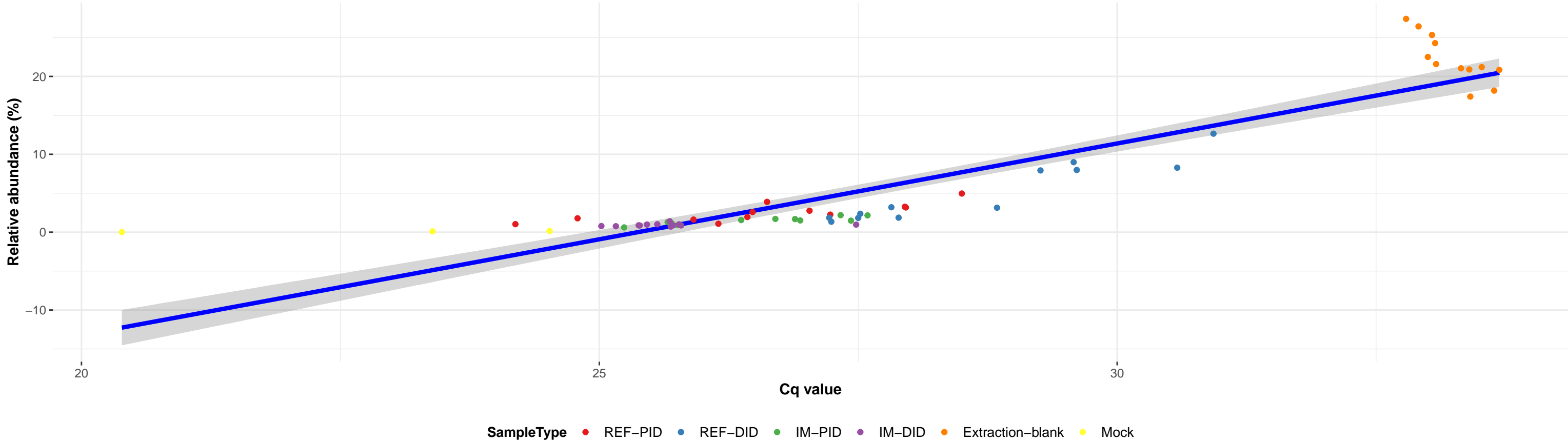
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

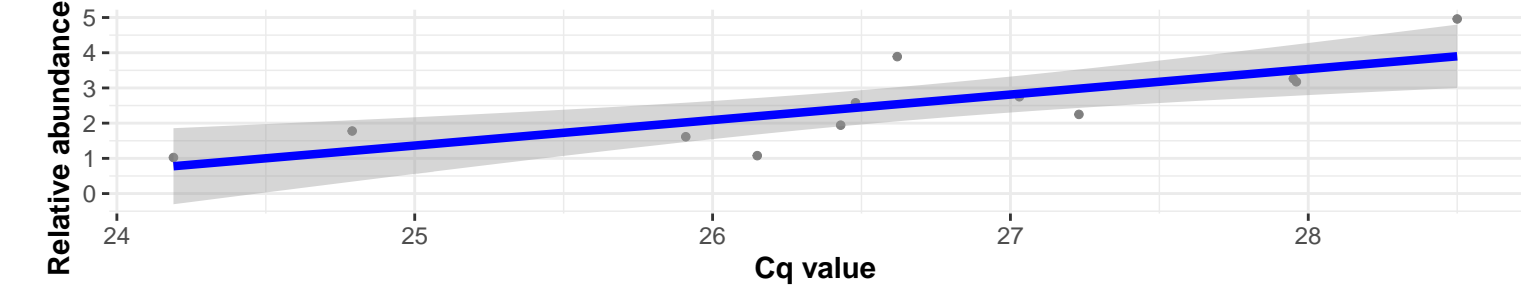
Correlation with all samples

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



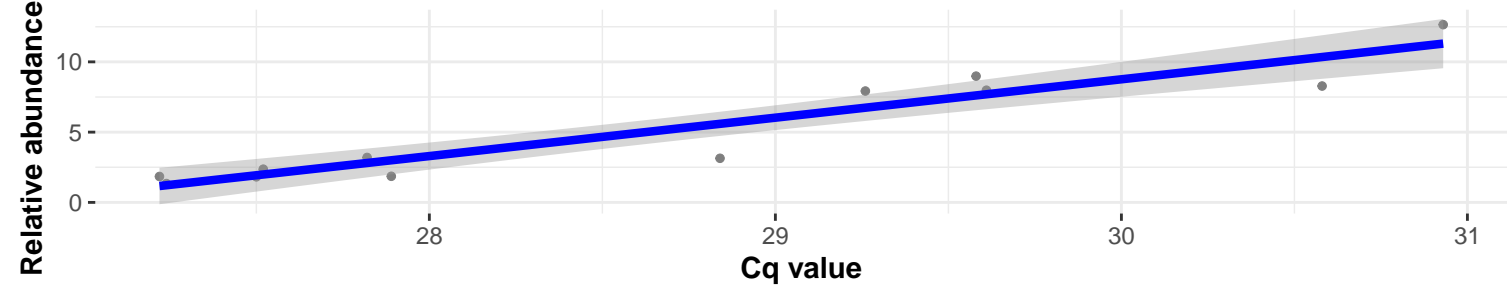
Correlation within: REF-PID

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



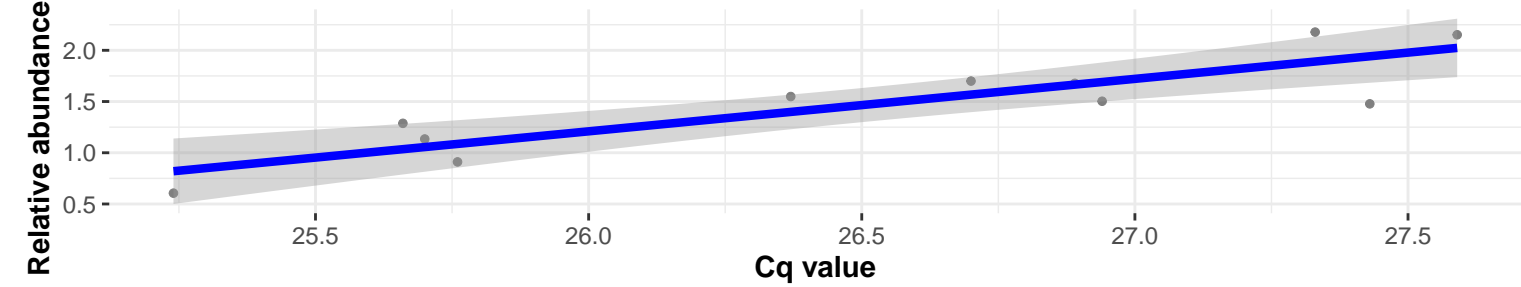
Correlation within: REF-DID

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



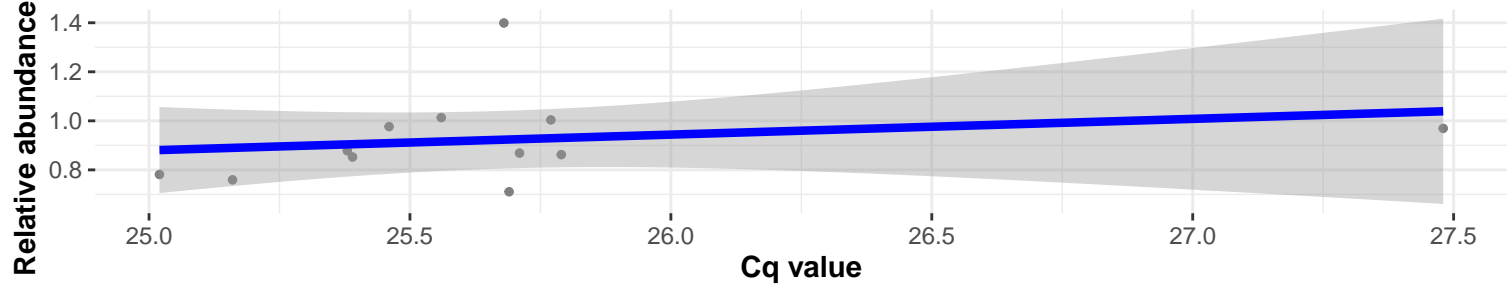
Correlation within: IM-PID

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



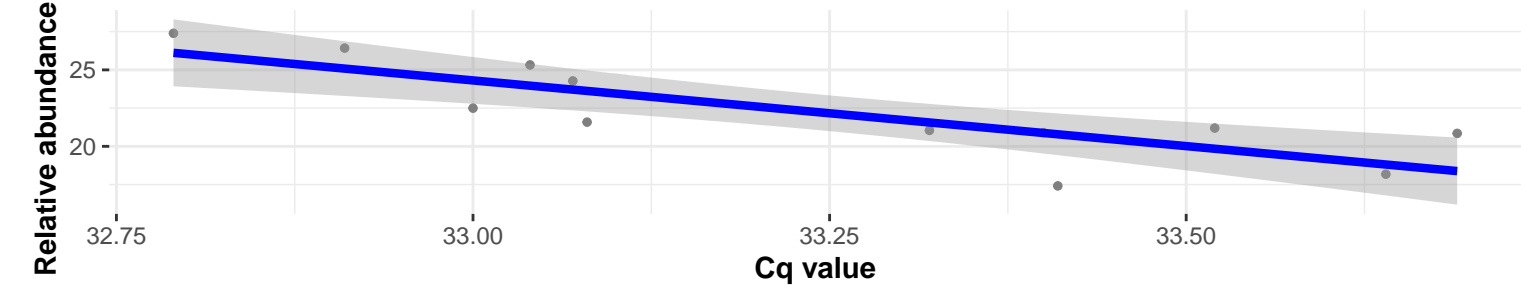
Correlation within: IM-DID

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

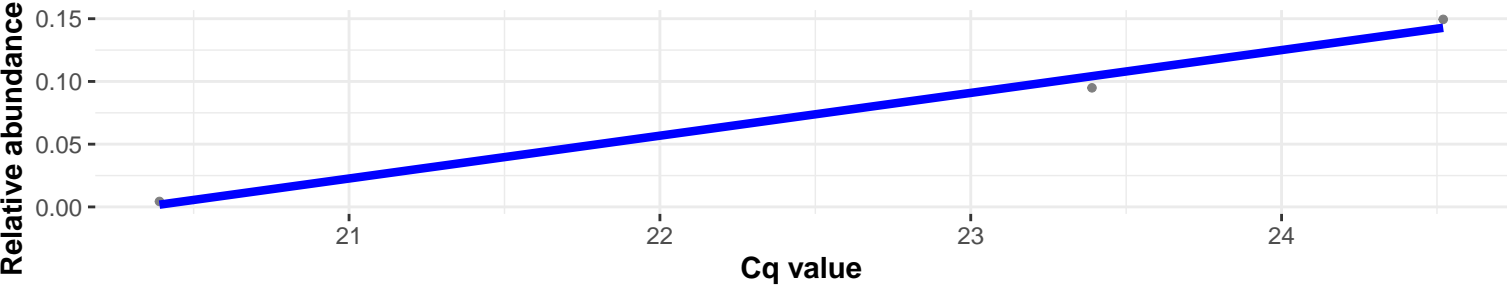


Correlation within: Extraction-blank

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



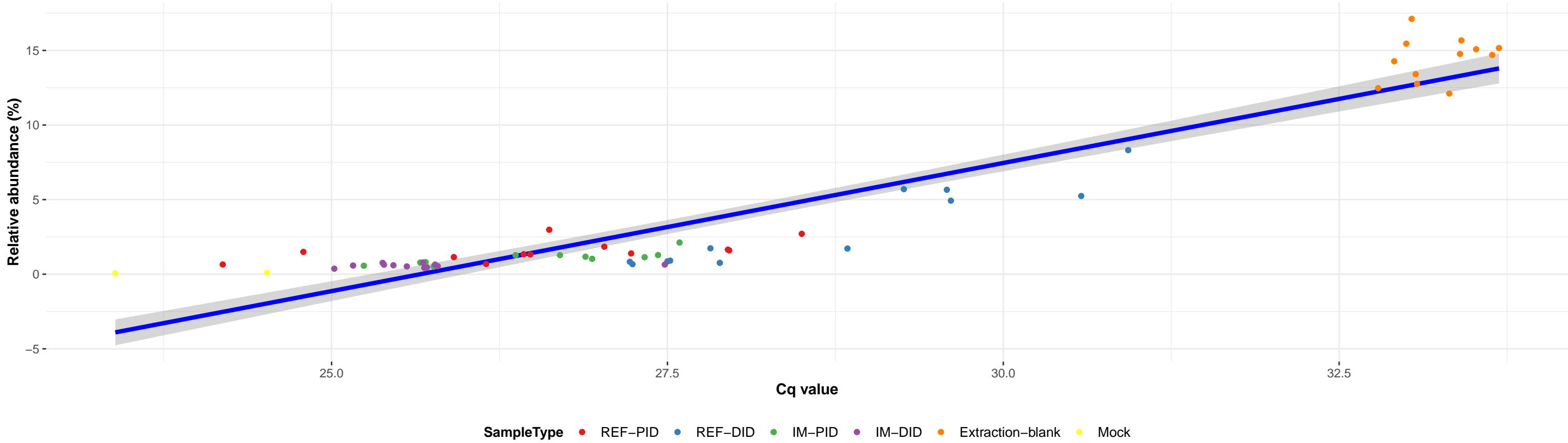
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Alteromonadales; f\_\_Shewanellaceae; g\_\_Shewanella; s\_\_Shewanella algae

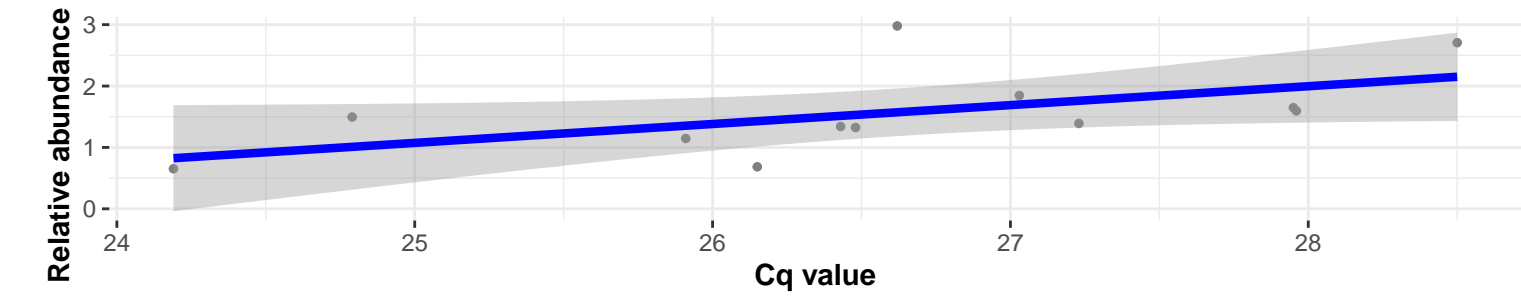
Correlation with all samples

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



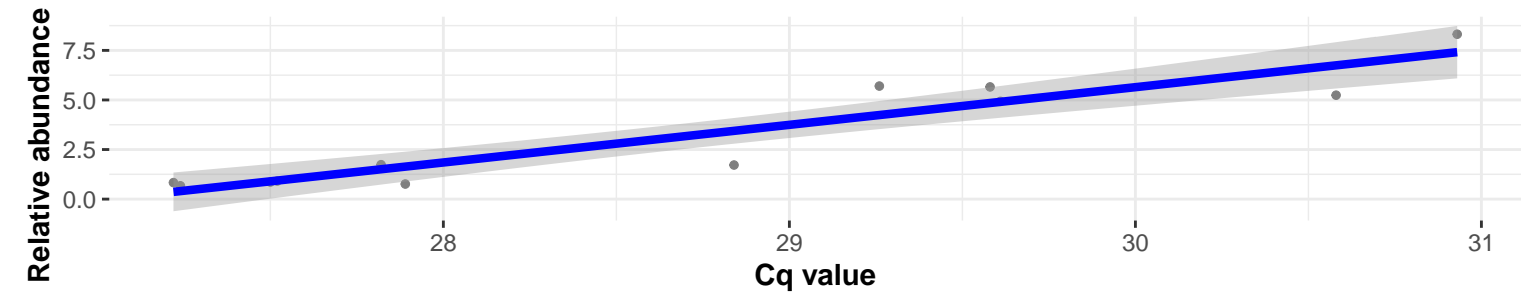
Correlation within: REF-PID

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



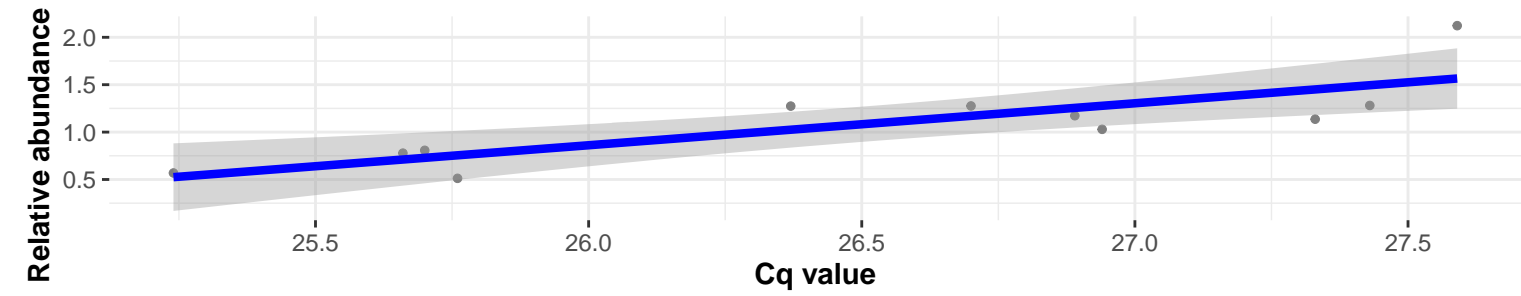
Correlation within: REF-DID

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



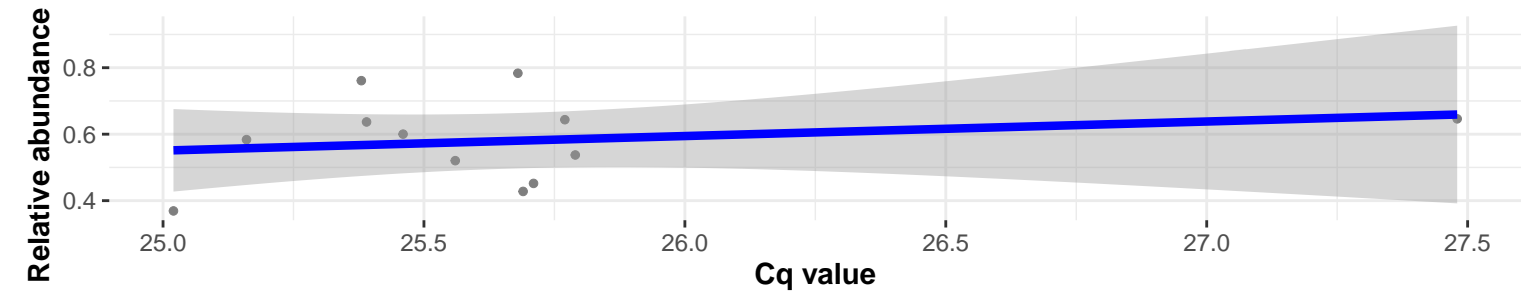
Correlation within: IM-PID

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



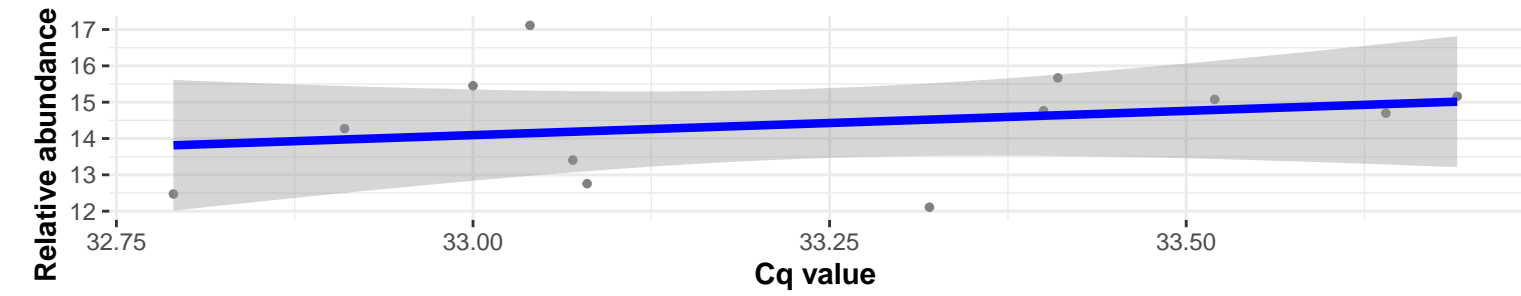
Correlation within: IM-DID

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

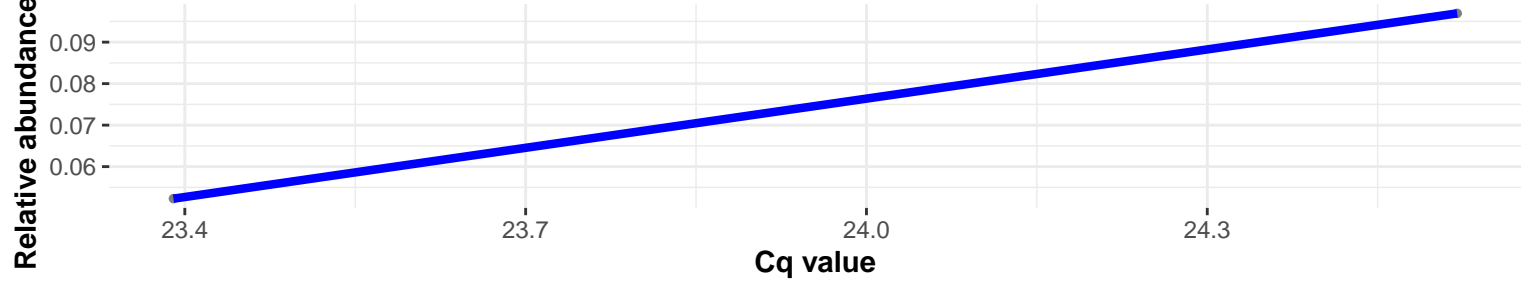


Correlation within: Extraction-blank

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



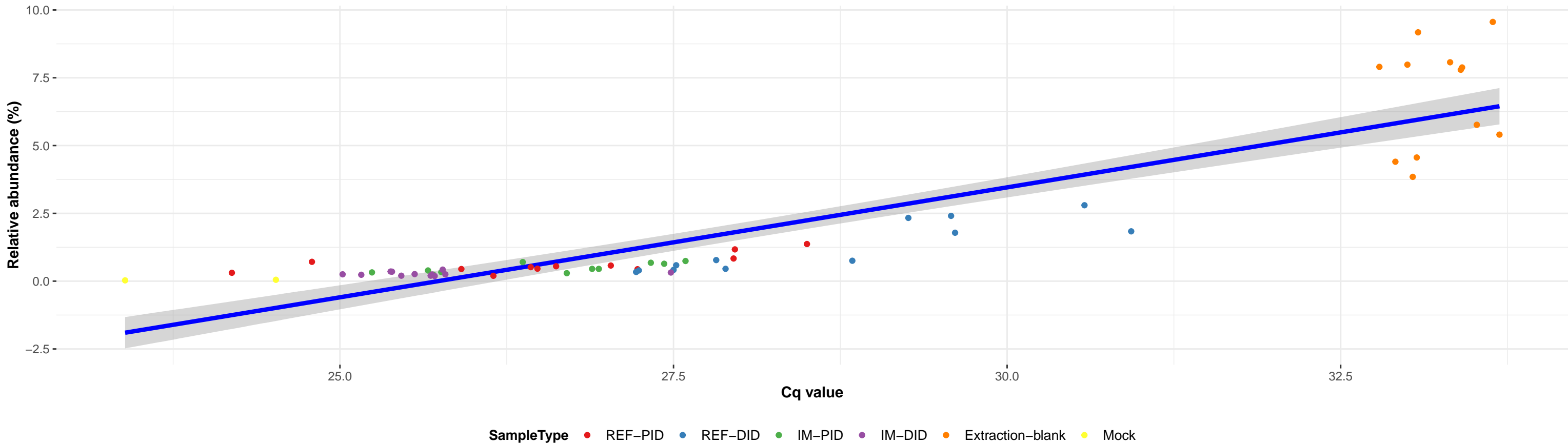
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

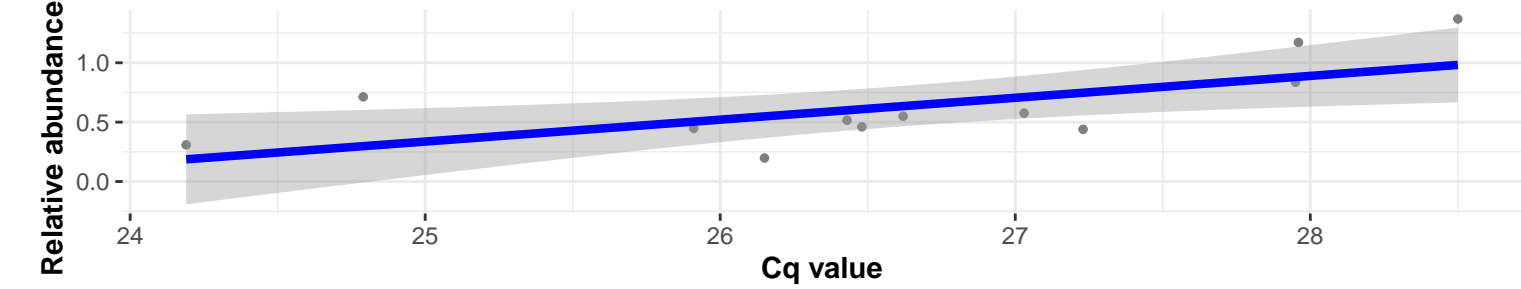
Correlation with all samples

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



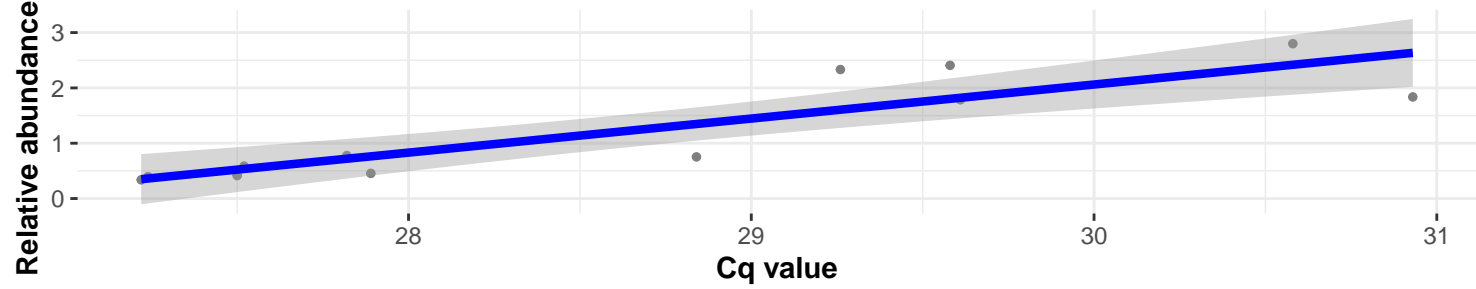
Correlation within: REF-PID

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



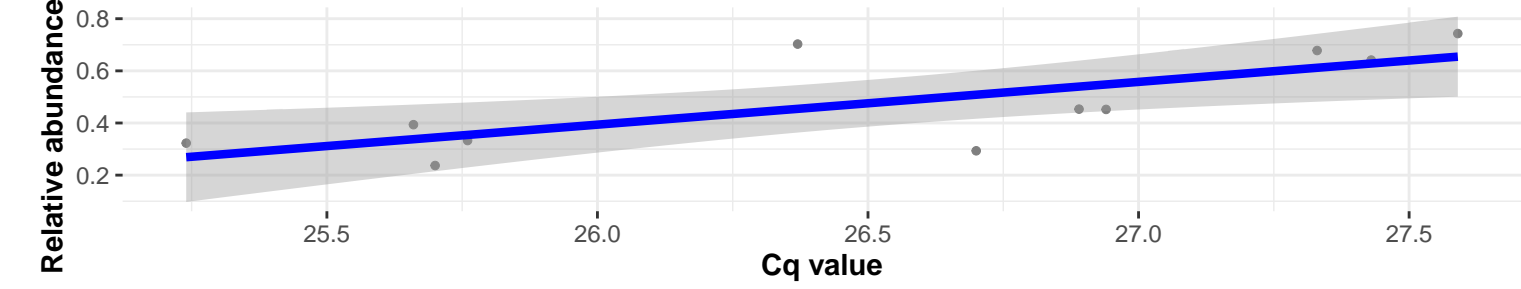
Correlation within: REF-DID

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



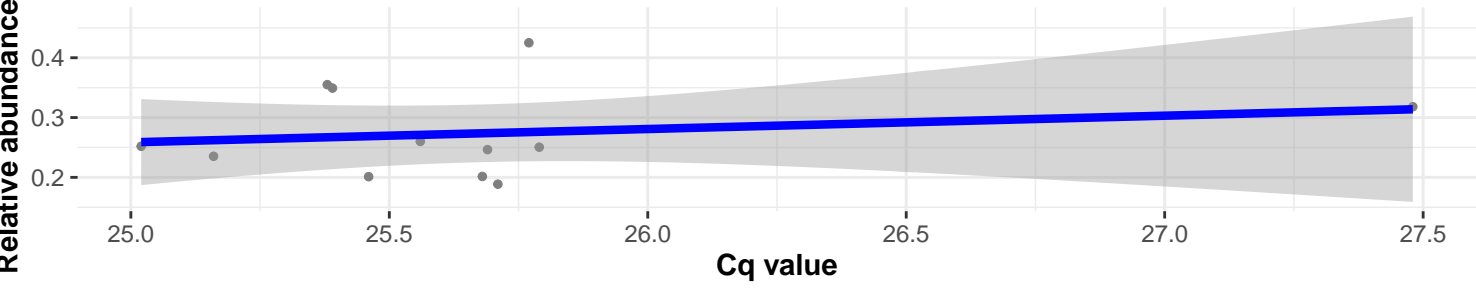
Correlation within: IM-PID

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



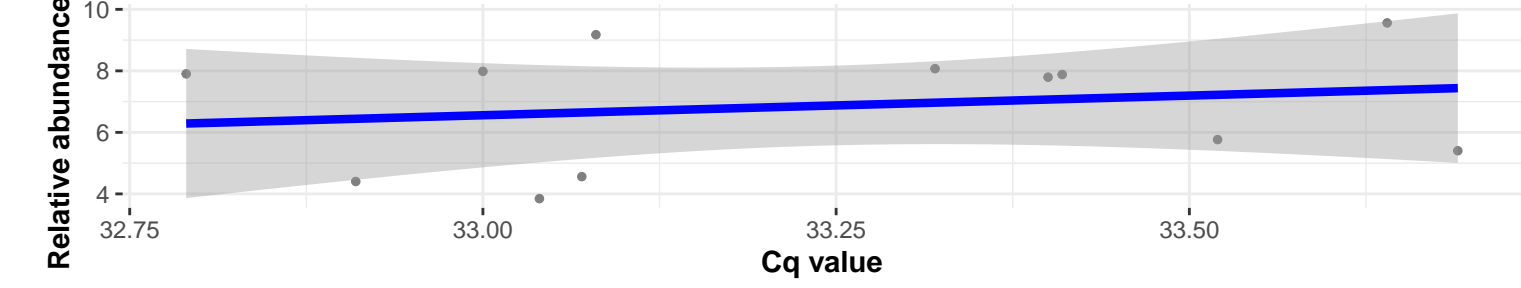
Correlation within: IM-DID

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

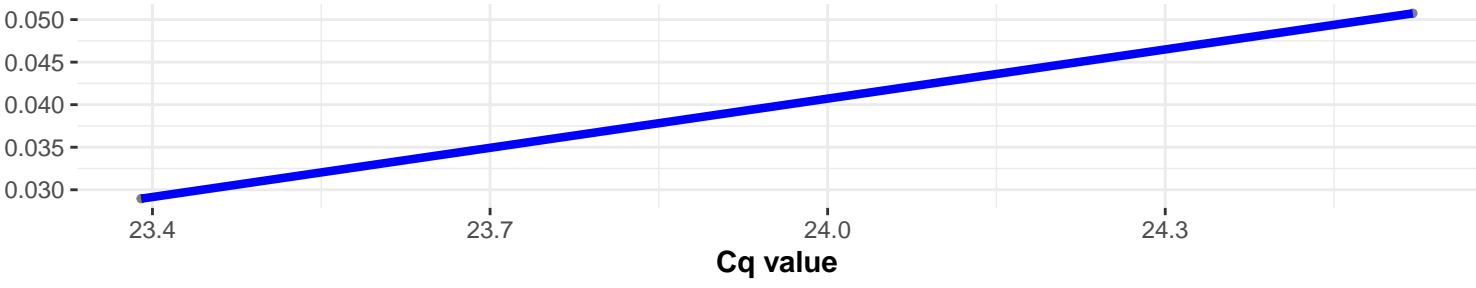


Correlation within: Extraction-blank

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



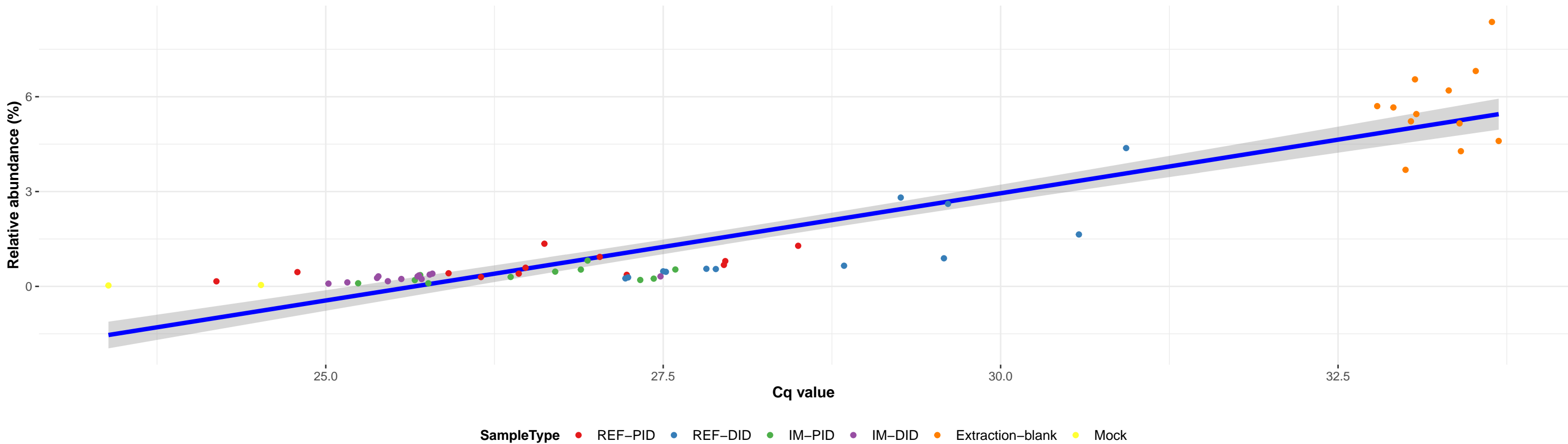
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

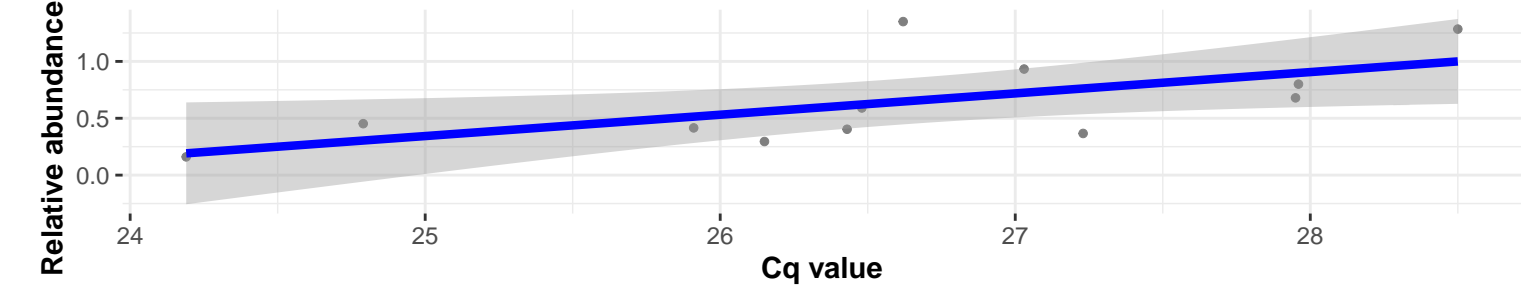
Correlation with all samples

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



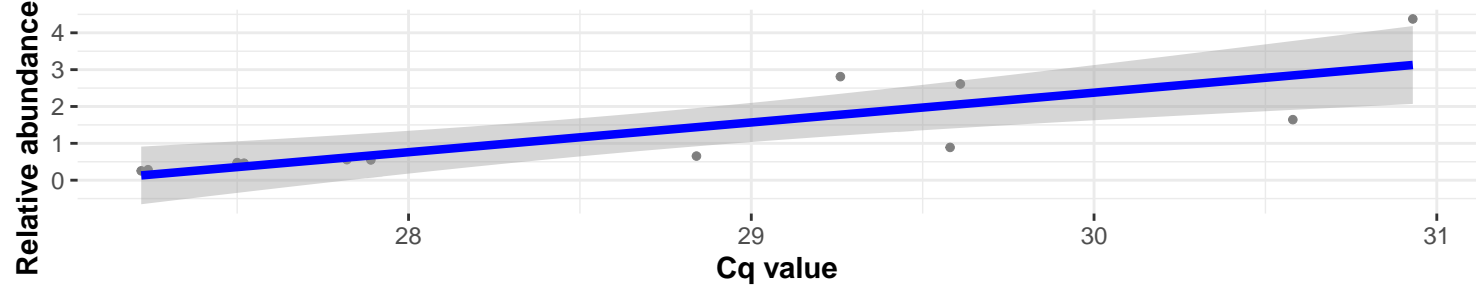
Correlation within: REF-PID

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



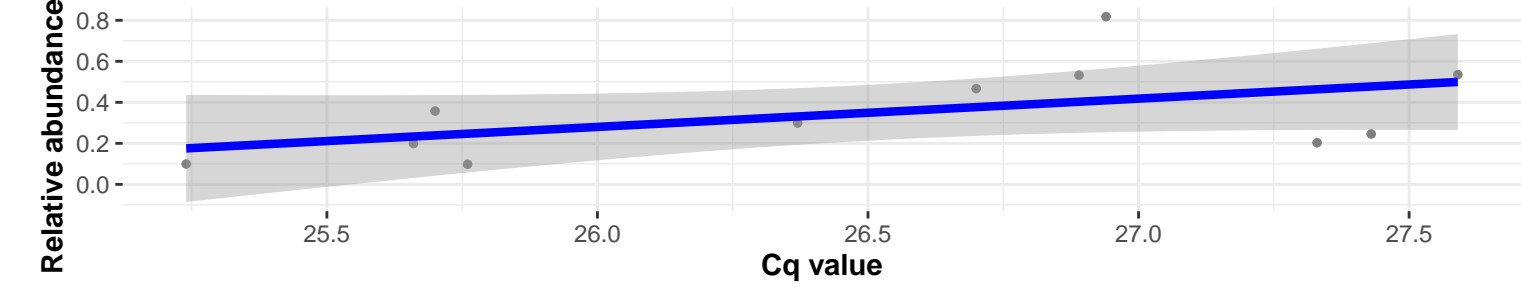
Correlation within: REF-DID

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



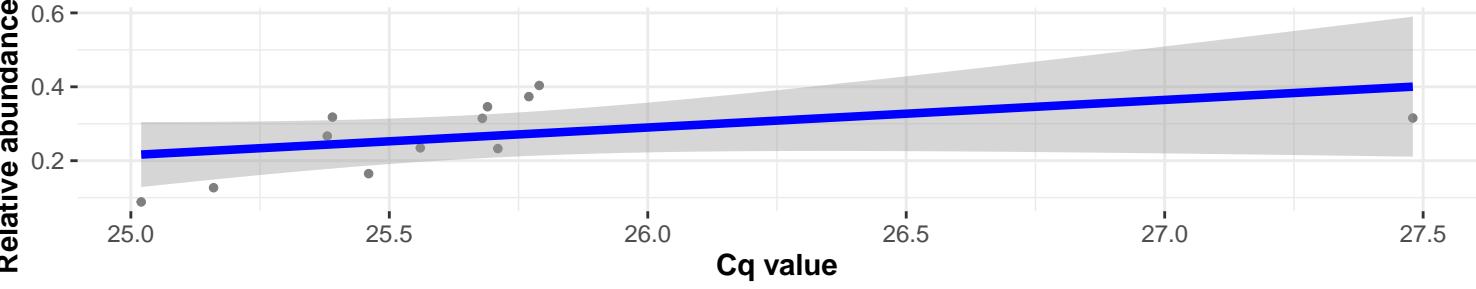
Correlation within: IM-PID

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



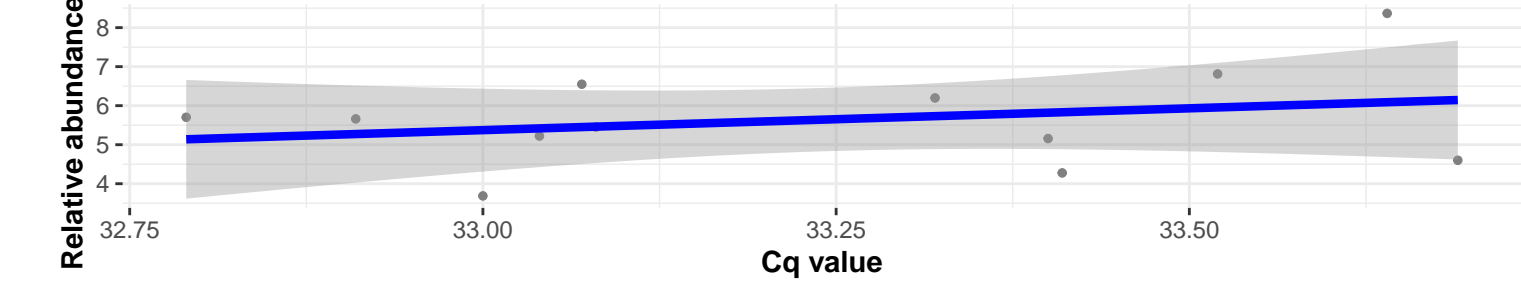
Correlation within: IM-DID

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

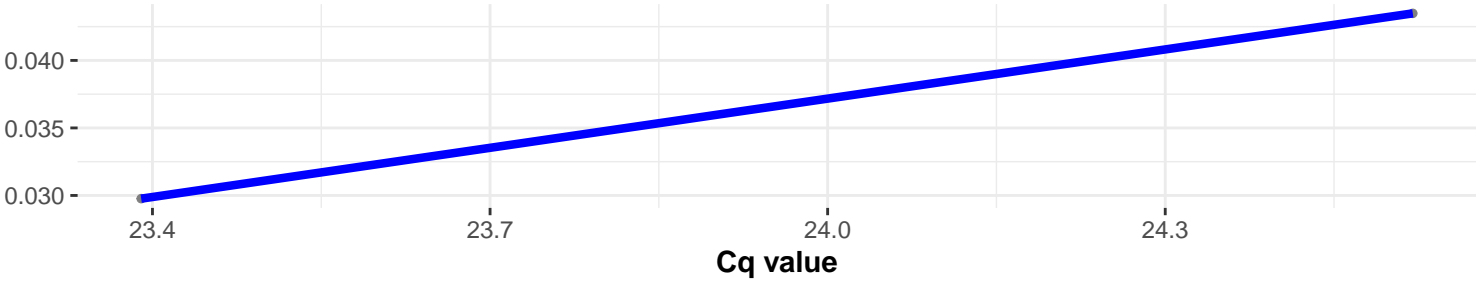


Correlation within: Extraction-blank

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



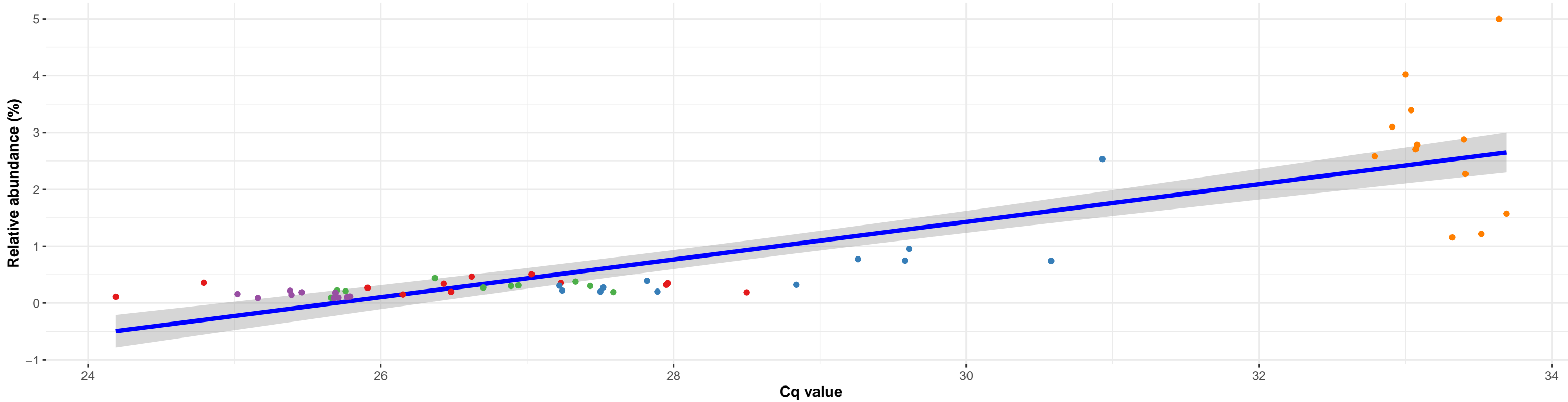
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

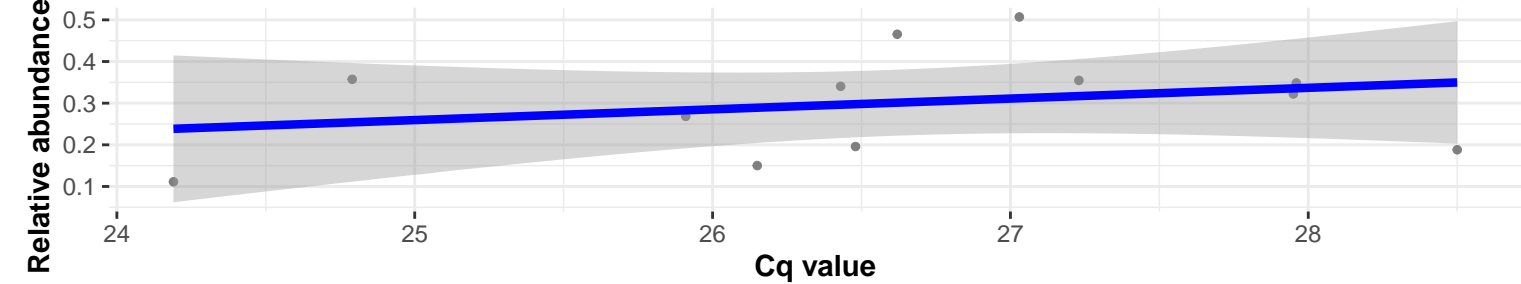
Correlation with all samples

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



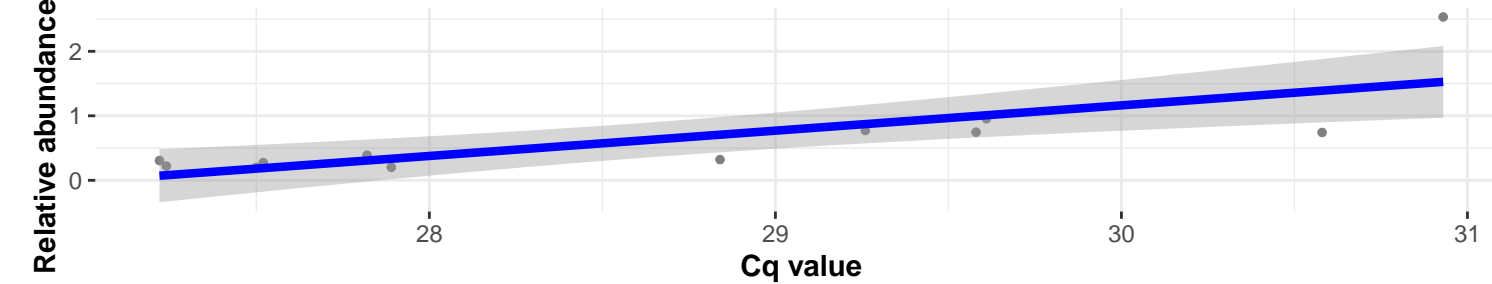
Correlation within: REF-PID

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



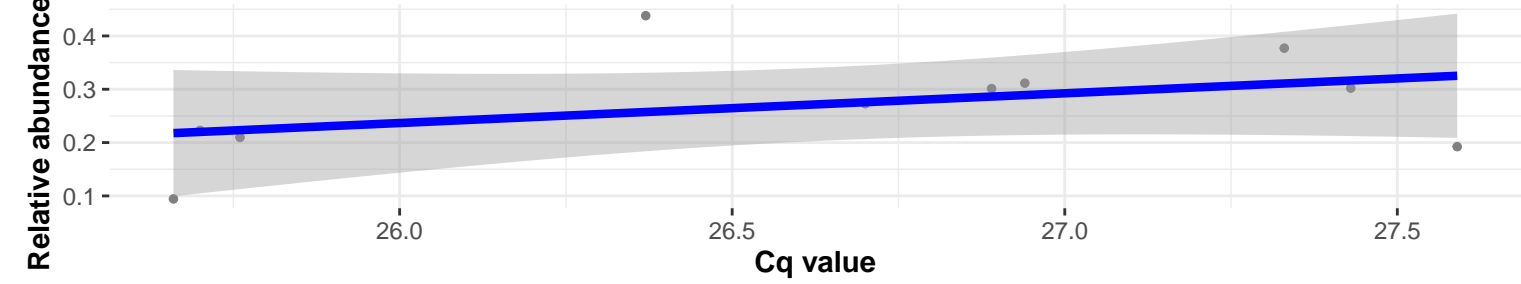
Correlation within: REF-DID

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



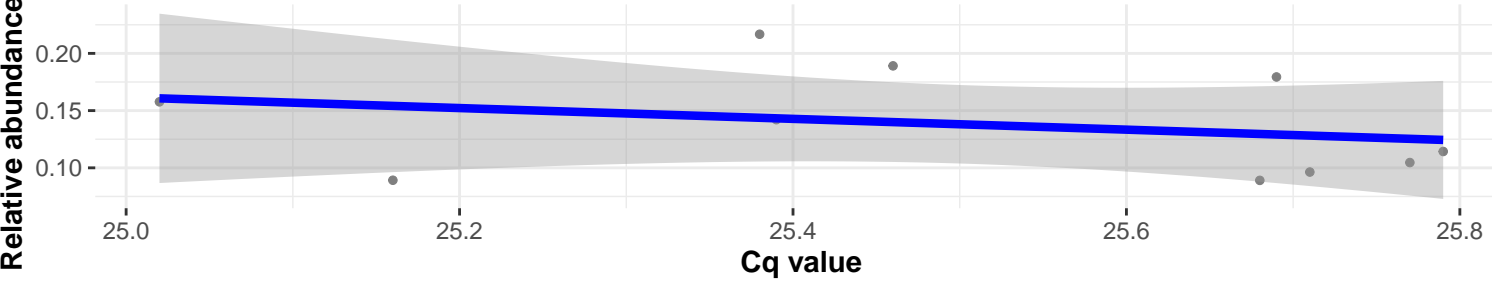
Correlation within: IM-PID

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



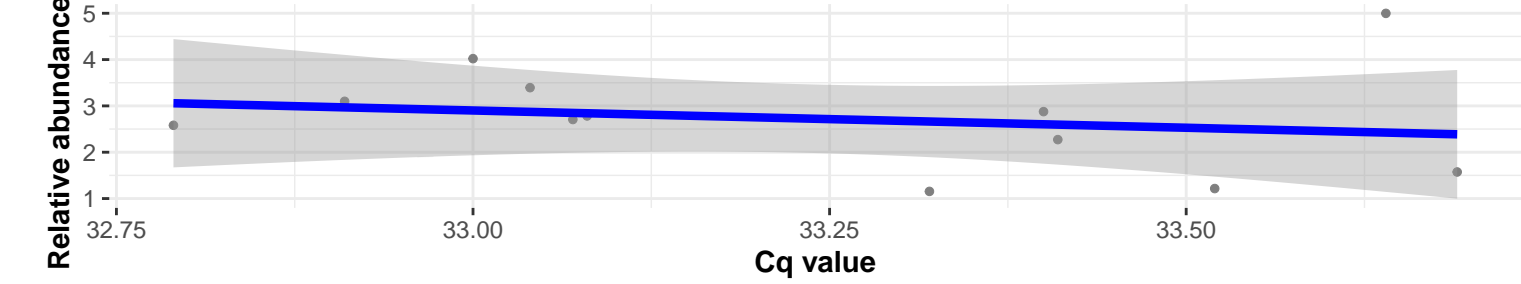
Correlation within: IM-DID

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



Correlation within: Extraction-blank

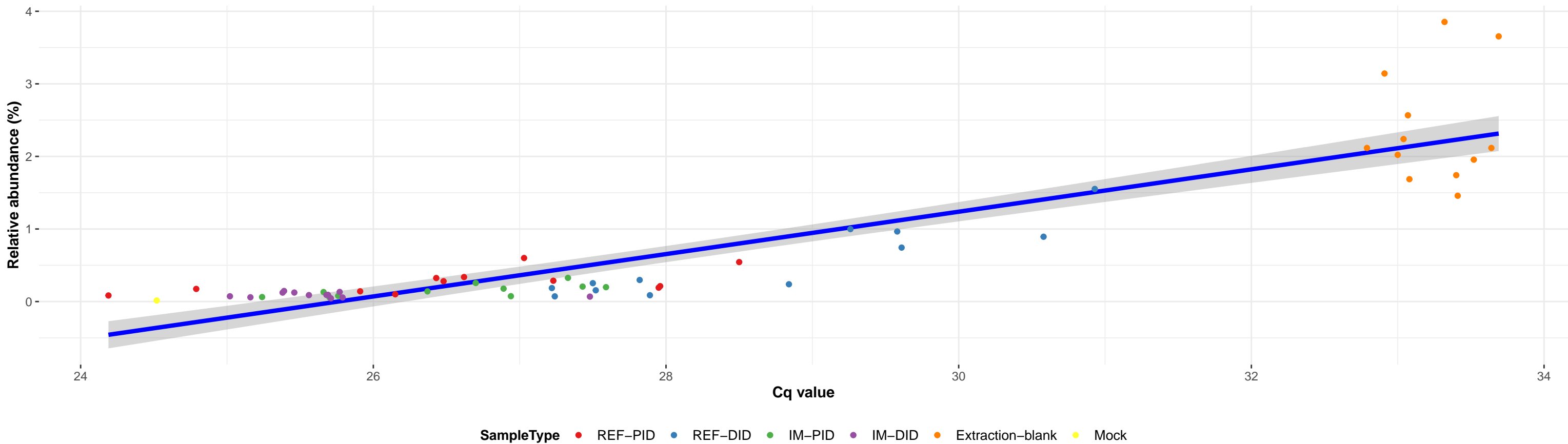
$\log_e(S) = 5.924$ ,  $p = 0.331$ ,  $\hat{\rho}_{\text{Spearman}} = -0.308$ ,  $CI_{95\%} [-0.758, 0.340]$ ,  $n_{\text{pairs}} = 12$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Alteromonadales; f\_\_Shewanellaceae; g\_\_Shewanella; s\_\_Shewanella algae

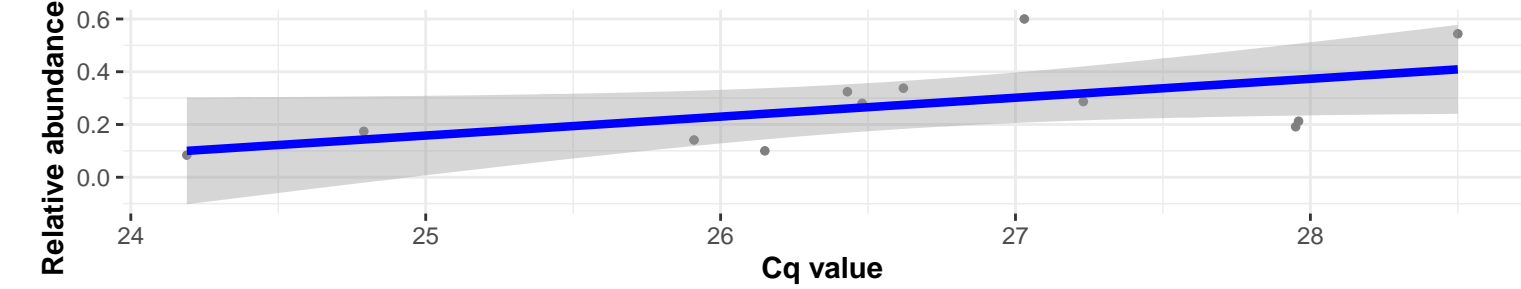
Correlation with all samples

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



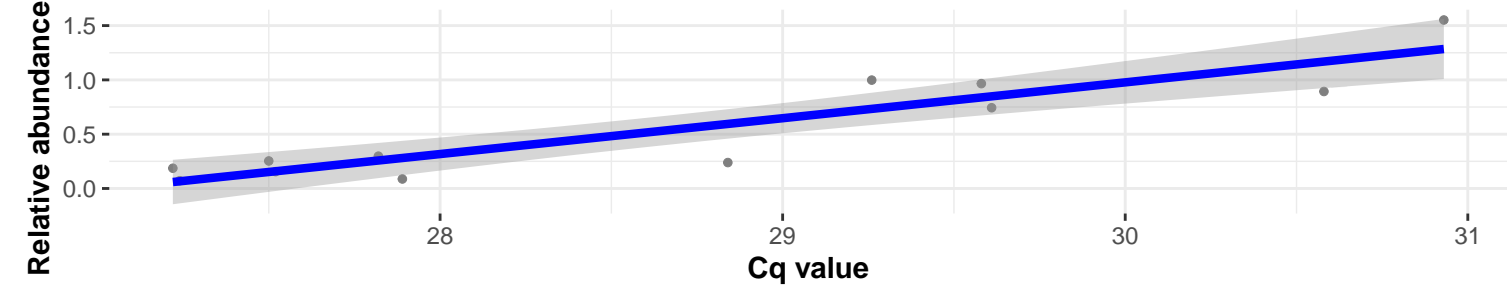
Correlation within: REF-PID

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



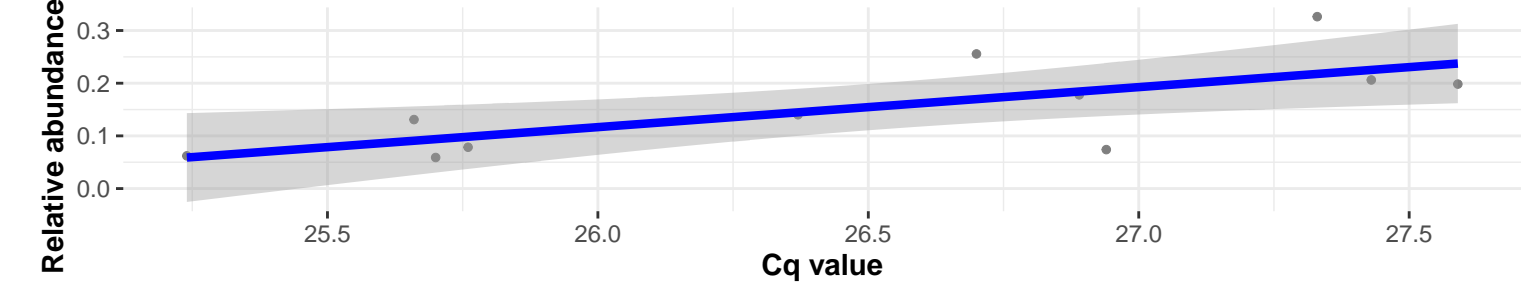
Correlation within: REF-DID

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



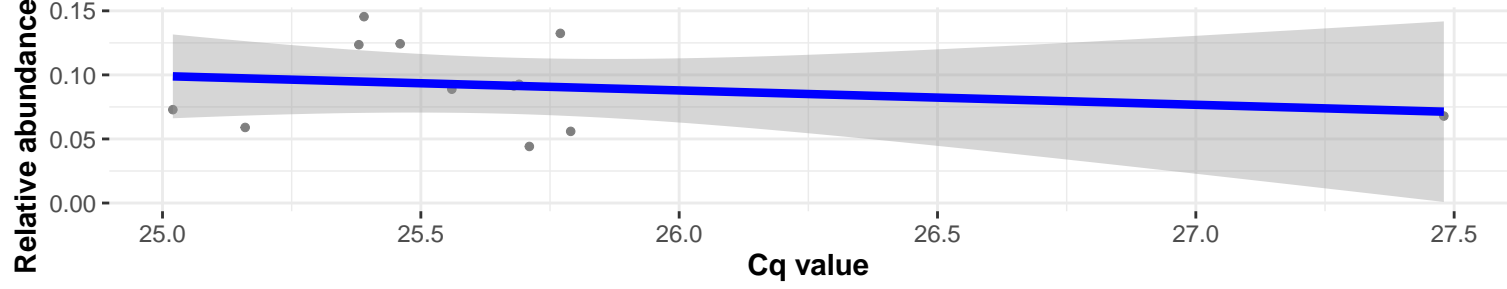
Correlation within: IM-PID

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



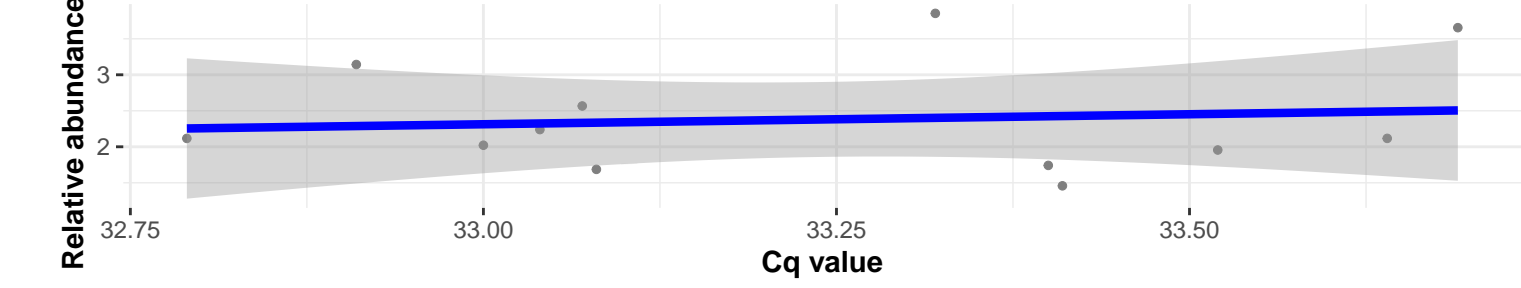
Correlation within: IM-DID

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

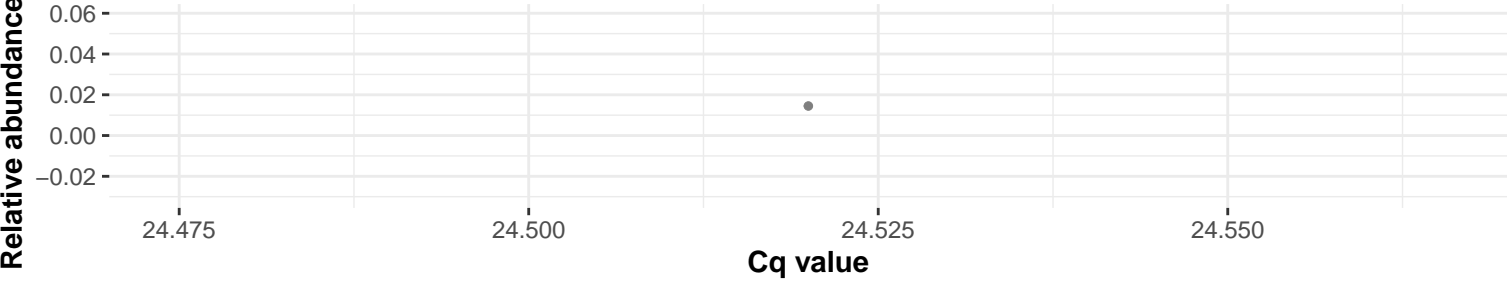


Correlation within: Extraction-blank

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



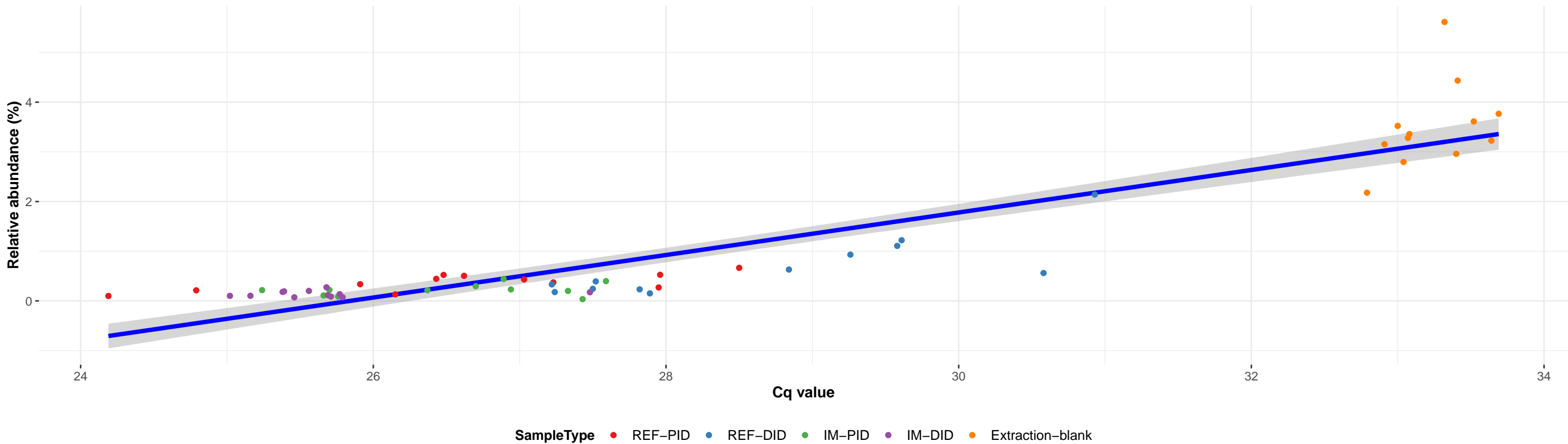
Correlation within: Mock



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

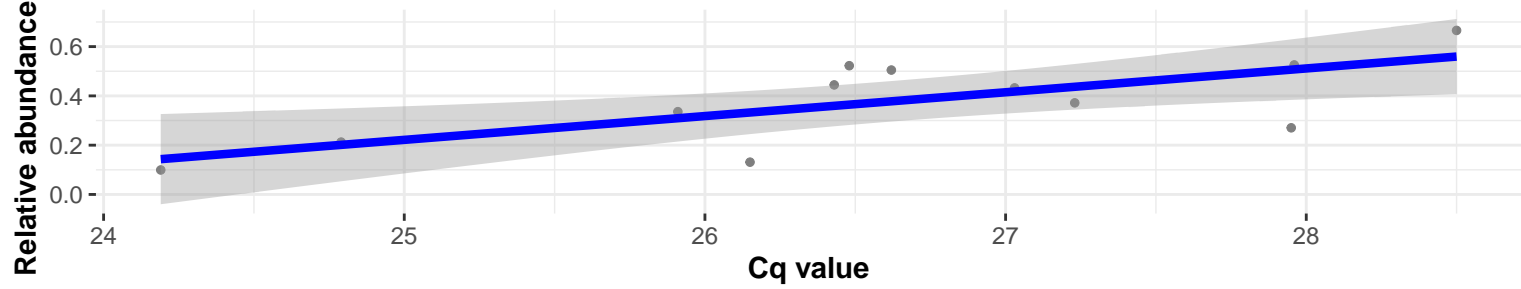
Correlation with all samples

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



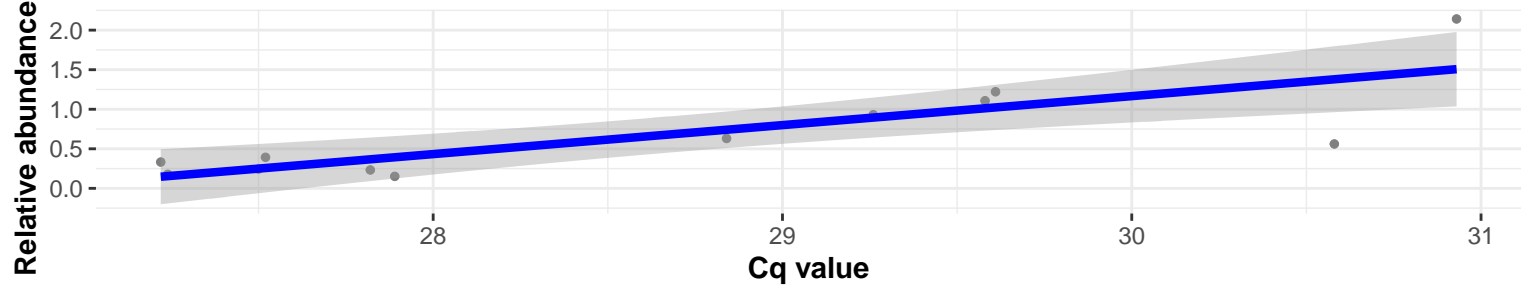
Correlation within: REF-PID

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



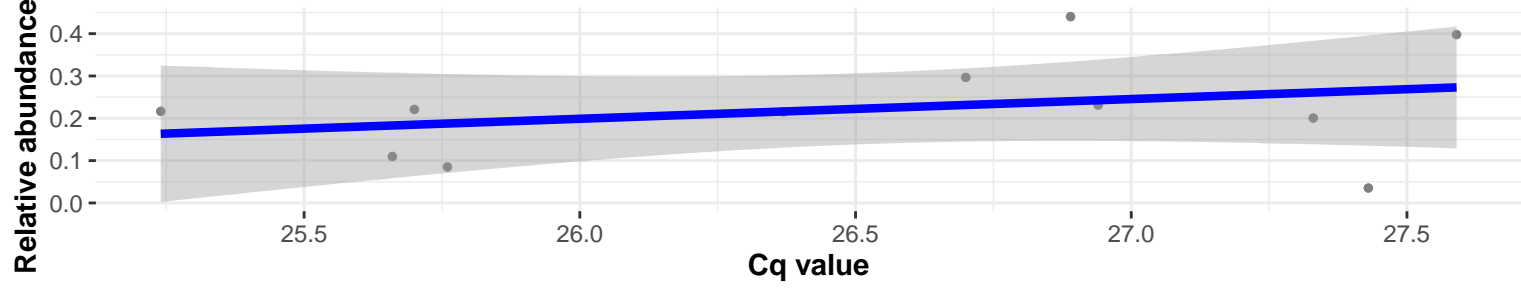
Correlation within: REF-DID

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



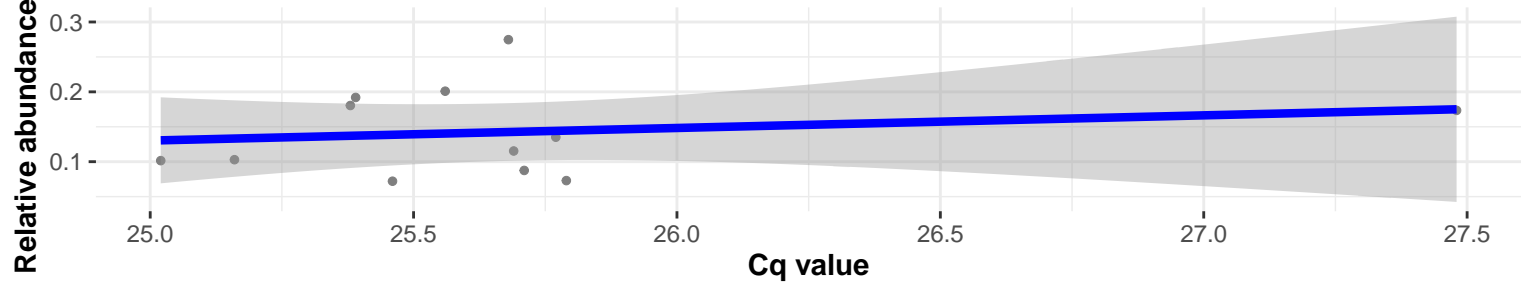
Correlation within: IM-PID

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



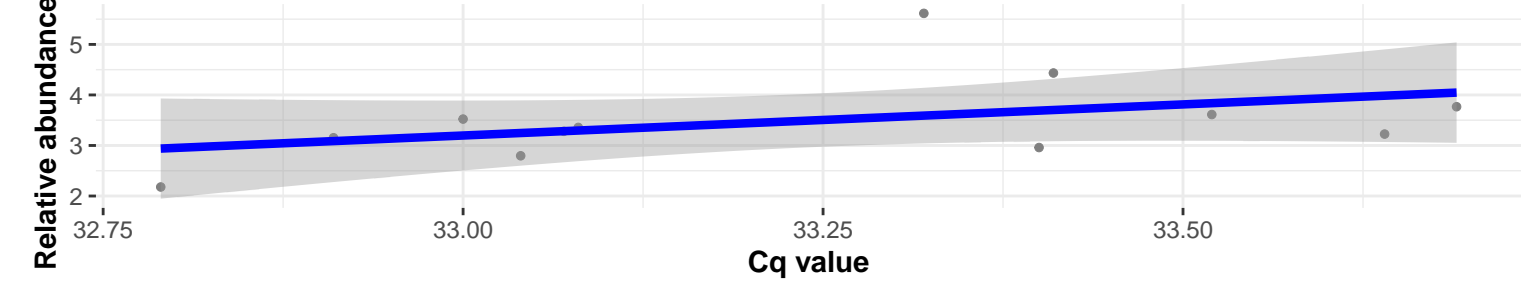
Correlation within: IM-DID

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



Correlation within: Extraction-blank

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

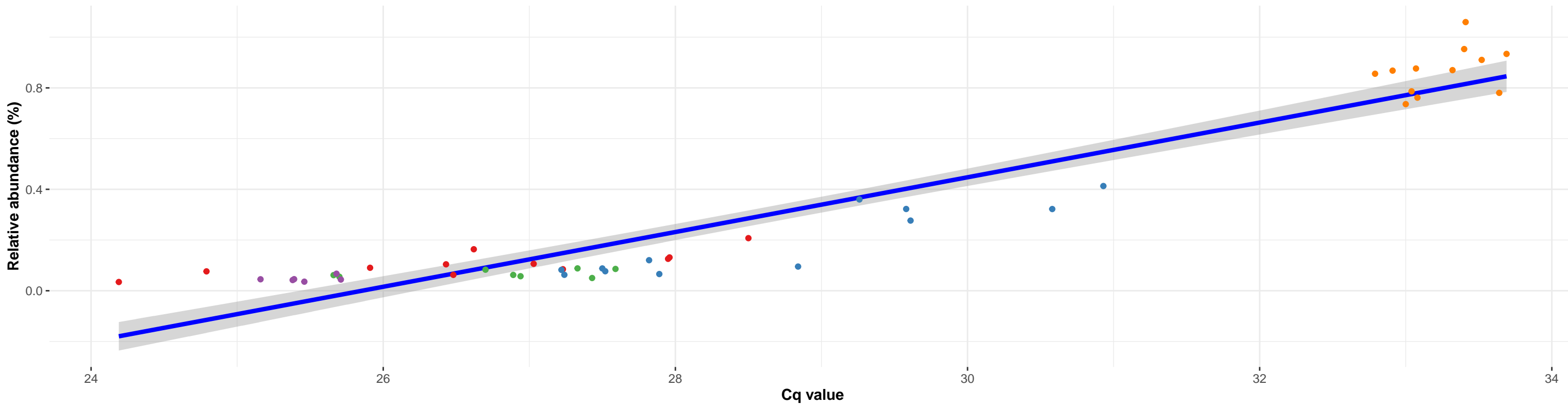




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

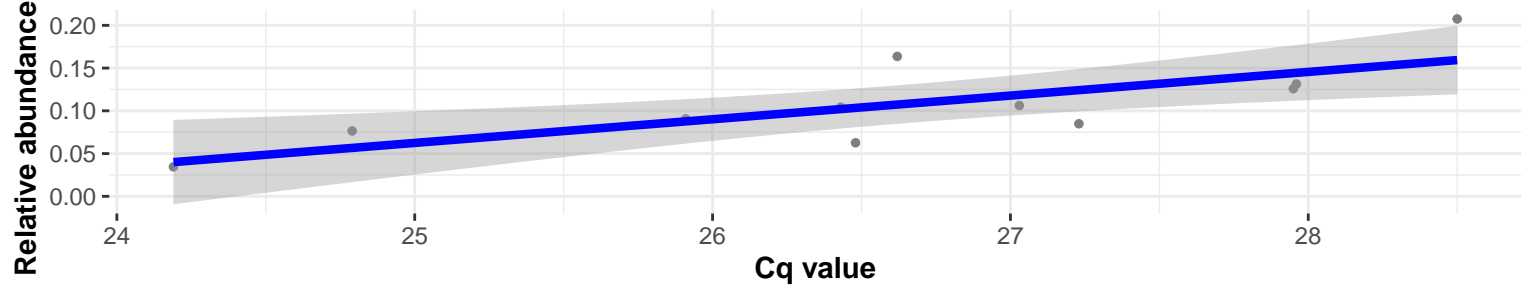
Correlation with all samples

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



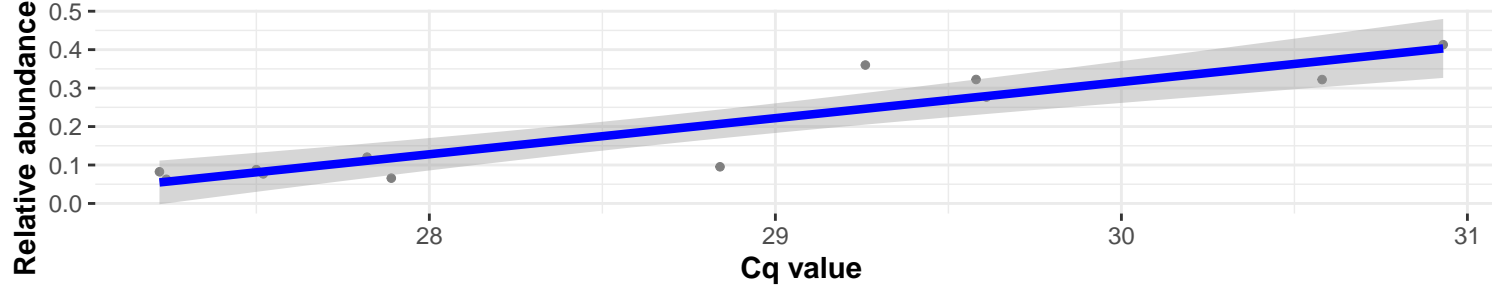
Correlation within: REF-PID

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



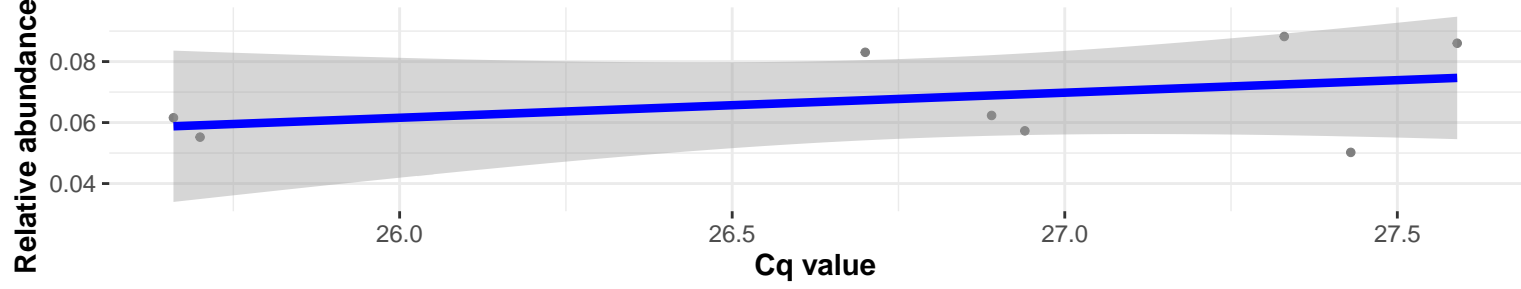
Correlation within: REF-DID

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

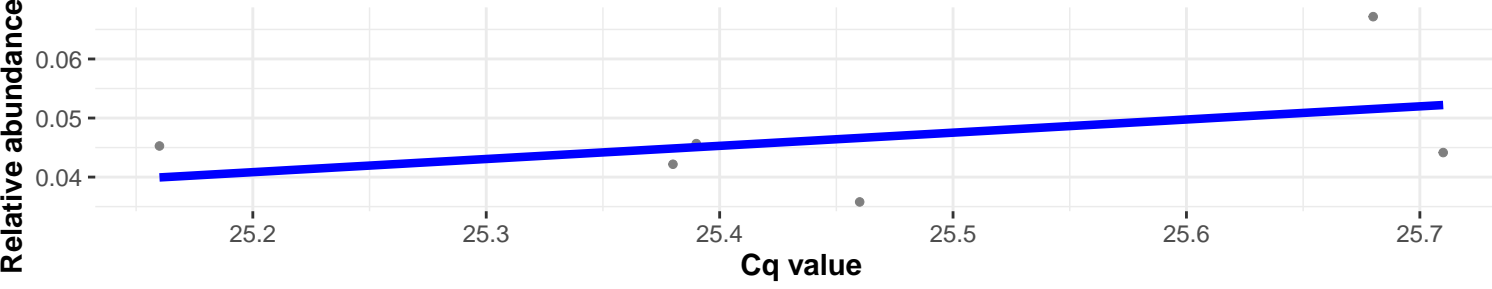


Correlation within: IM-PID

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

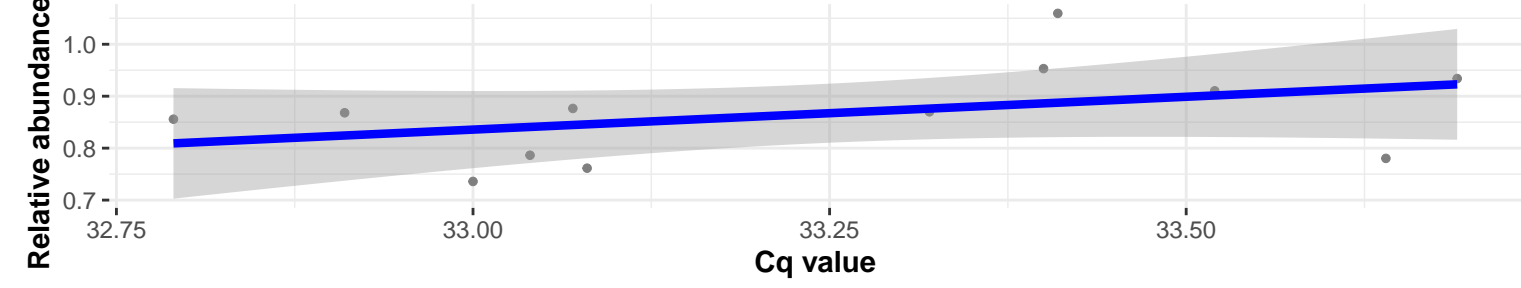


Correlation within: IM-DID



Correlation within: Extraction-blank

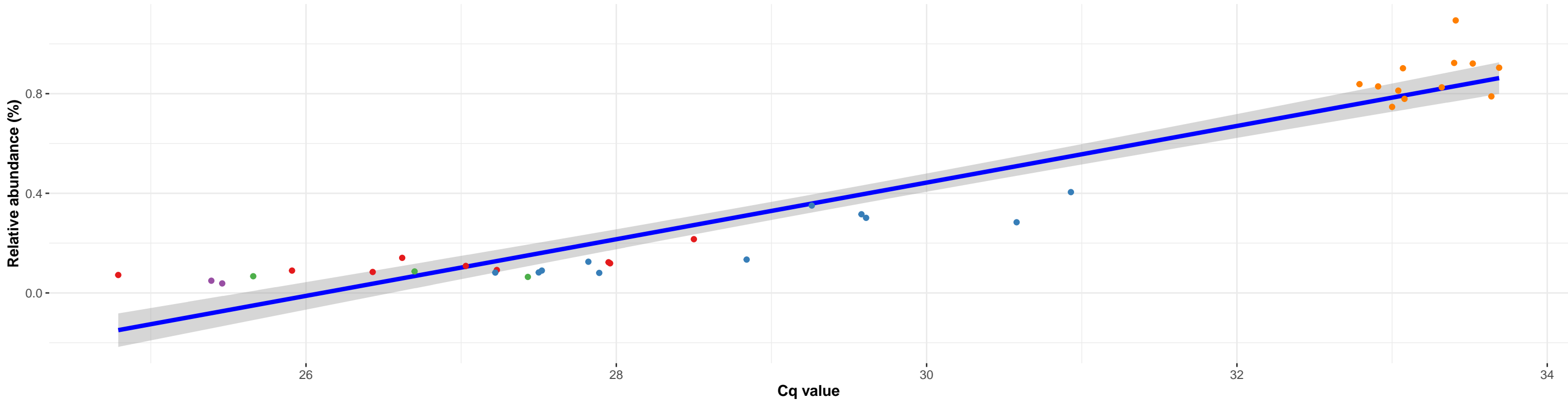
$\log_e(S) = 4.997$ ,  $p = 0.112$ ,  $\hat{\rho}_{\text{Spearman}} = 0.483$ ,  $CI_{95\%} [-0.145, 0.833]$ ,  $n_{\text{pairs}} = 12$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Pseudomonadales; f\_\_Pseudomonadaceae; g\_\_Pseudomonas; NA

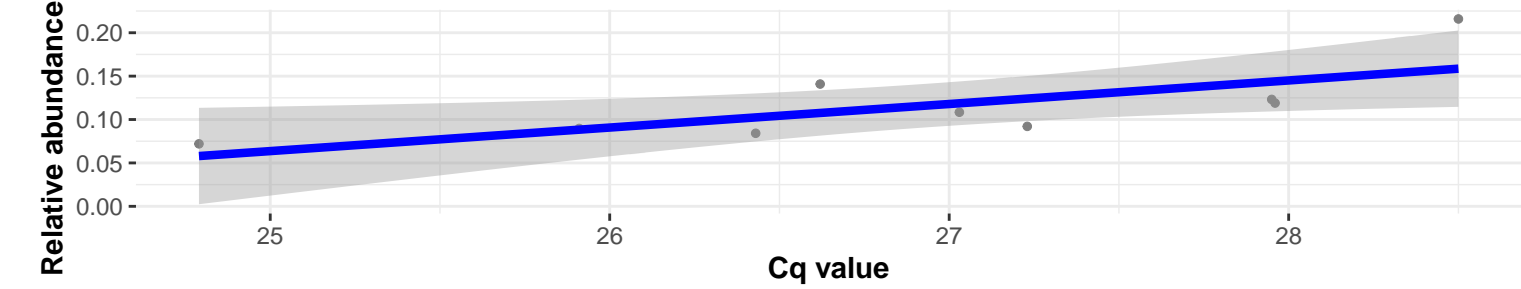
Correlation with all samples

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



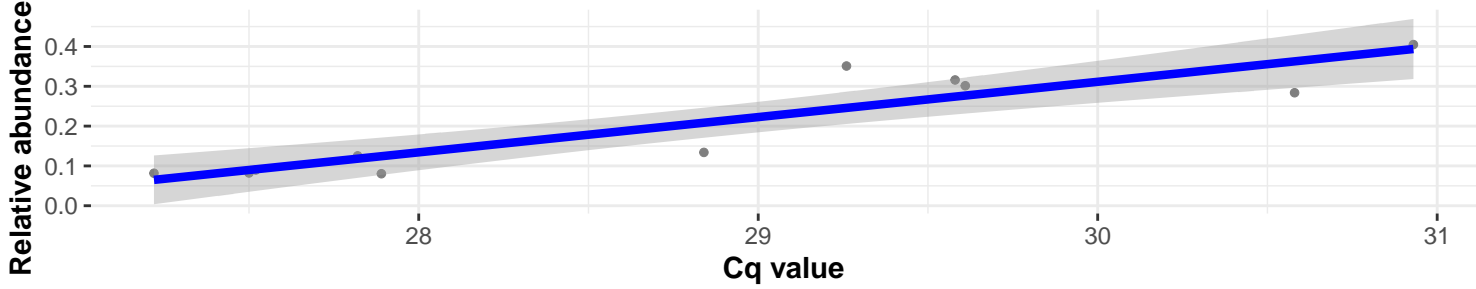
Correlation within: REF-PID

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

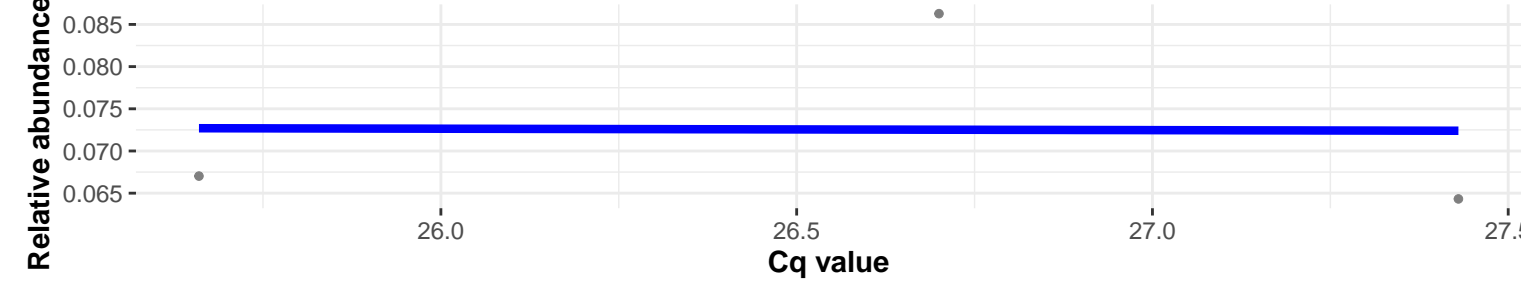


Correlation within: REF-DID

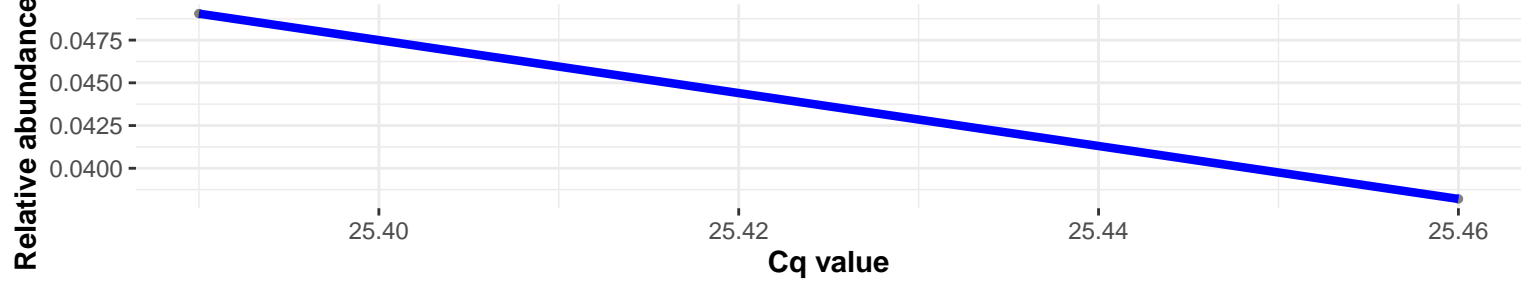
$\log_e(S) = 3.689$ ,  $p = 0.002$ ,  $\hat{\rho}_{\text{Spearman}} = 0.818$ ,  $\text{CI}_{95\%} [0.412, 0.953]$ ,  $n_{\text{pairs}} = 11$



Correlation within: IM-PID

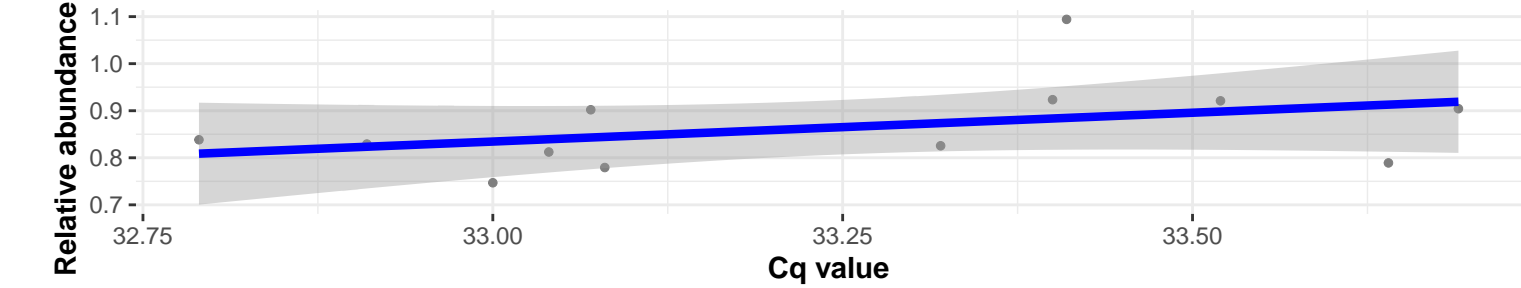


Correlation within: IM-DID



Correlation within: Extraction-blank

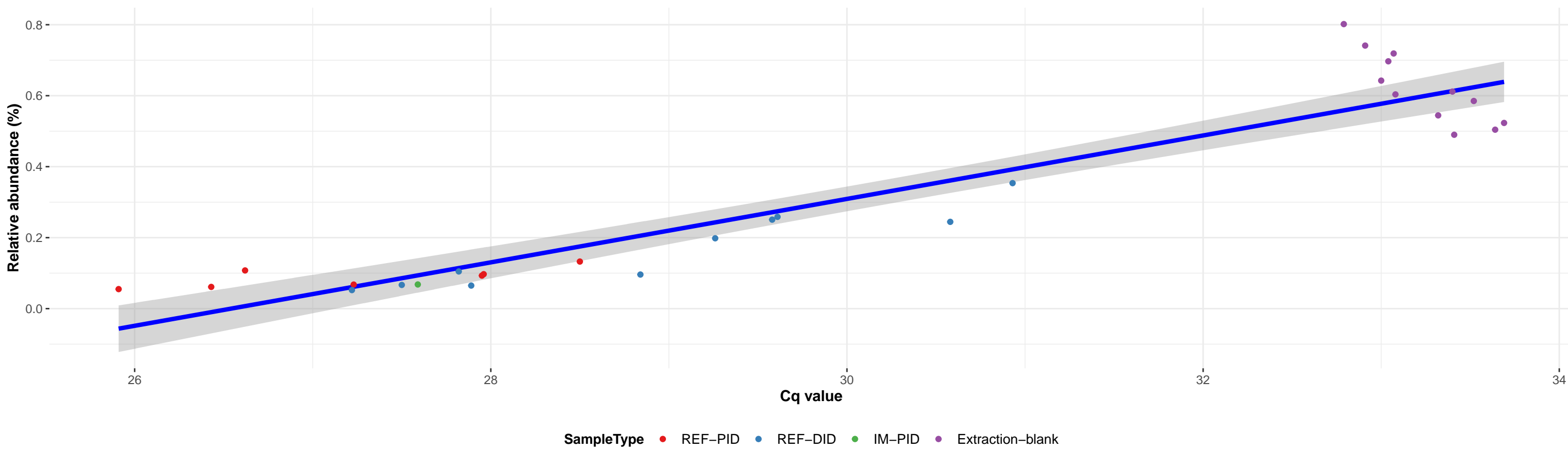
$\log_e(S) = 5.170$ ,  $p = 0.217$ ,  $\hat{\rho}_{\text{Spearman}} = 0.385$ ,  $\text{CI}_{95\%} [-0.261, 0.792]$ ,  $n_{\text{pairs}} = 12$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

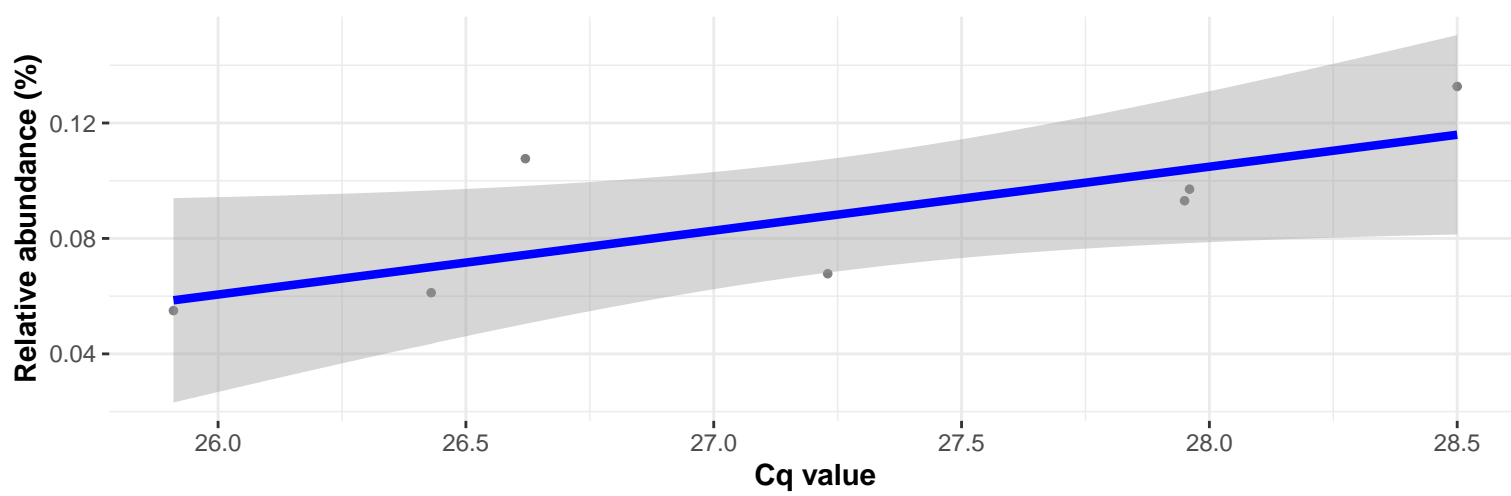
### Correlation with all samples

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



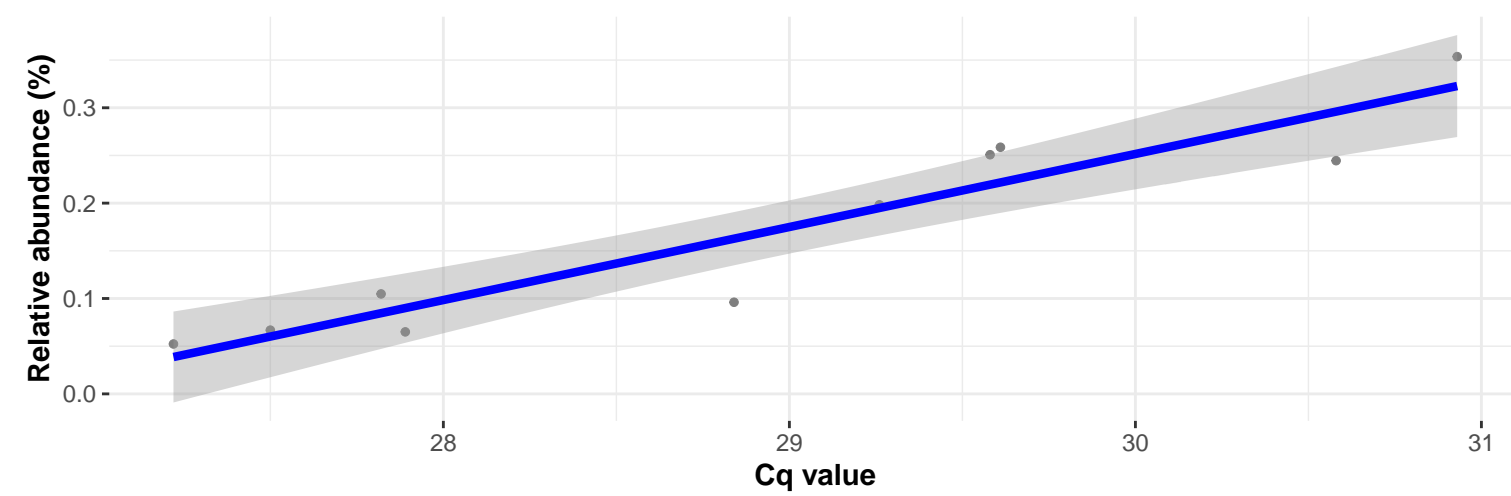
### Correlation within: REF-PID

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

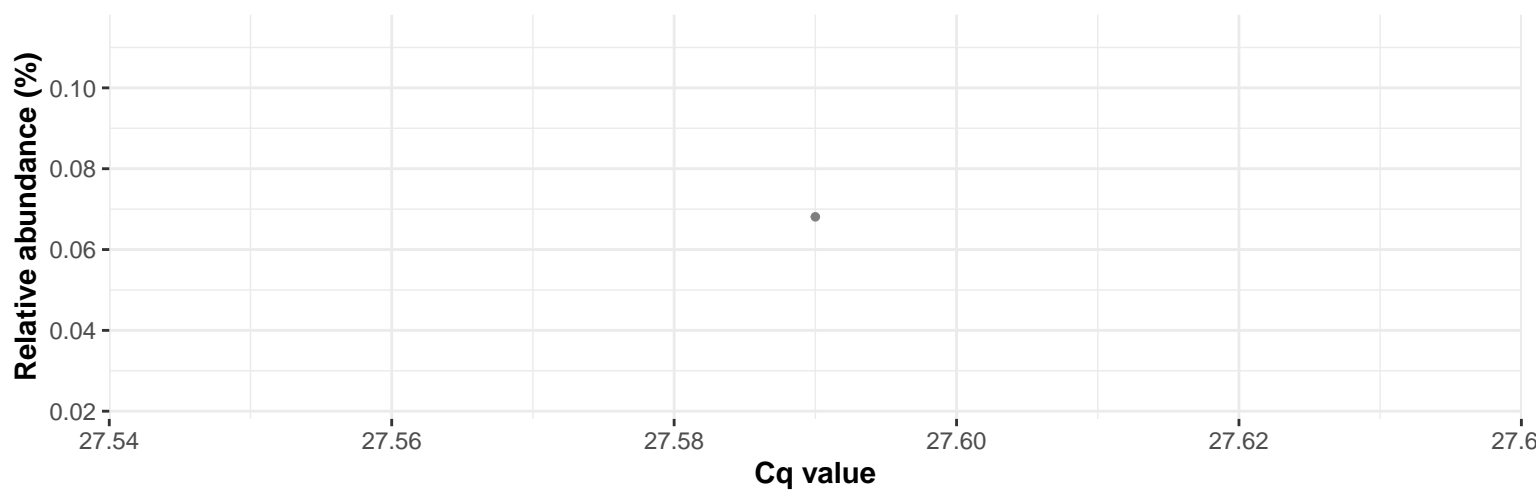


### Correlation within: REF-DID

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

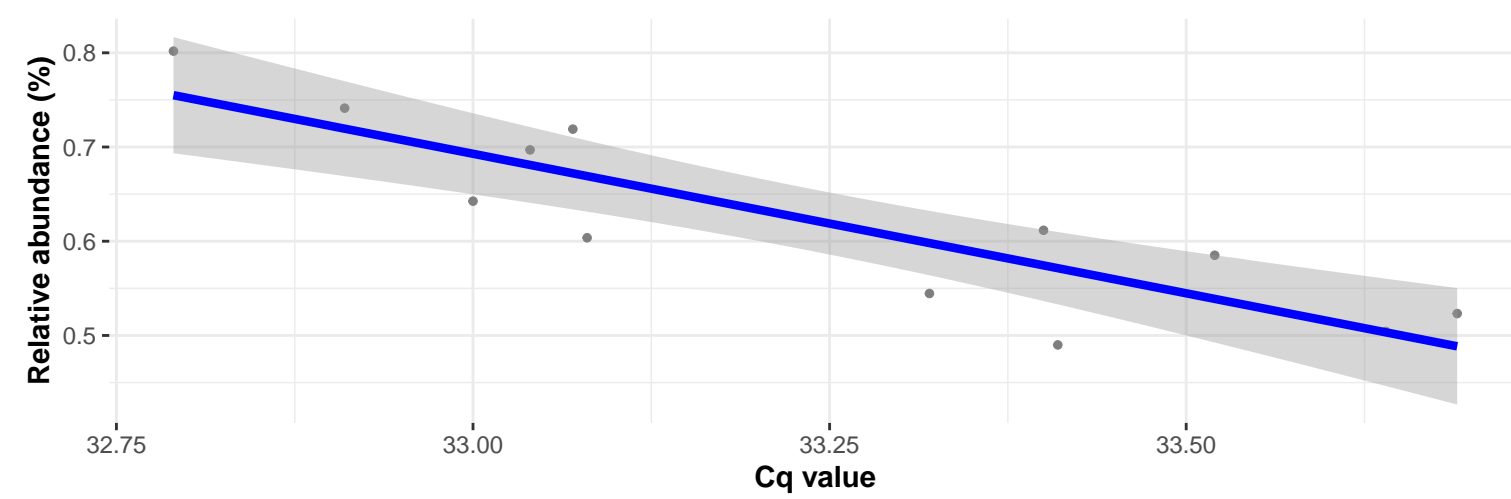


### Correlation within: IM-PID



### Correlation within: Extraction-blank

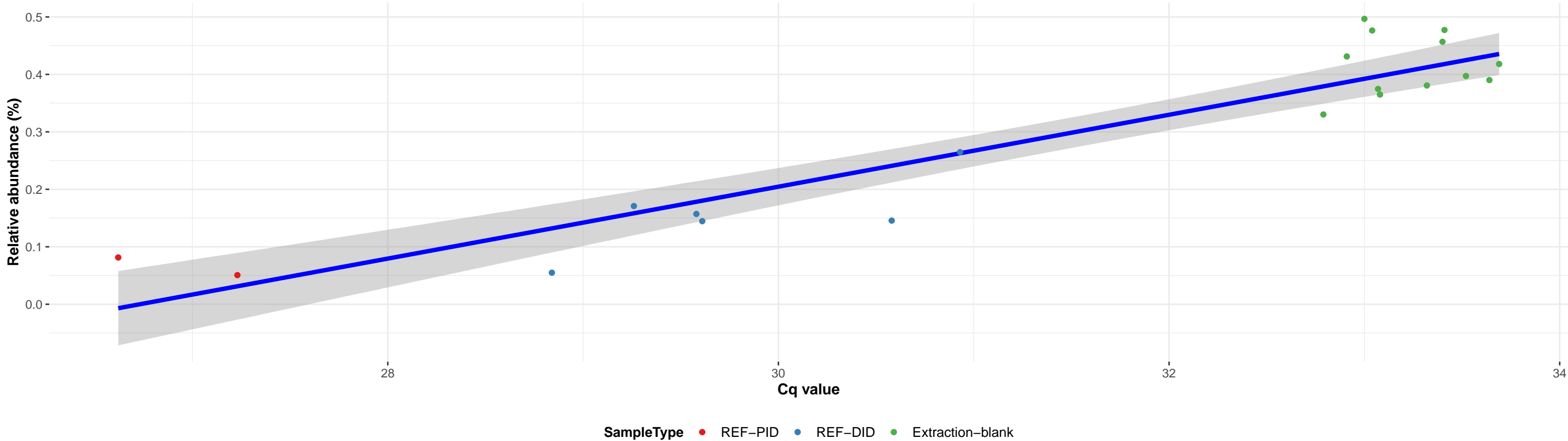
$\log_e(S) = 6.288$ ,  $p = 1.53\text{e-}04$ ,  $\hat{\rho}_{\text{Spearman}} = -0.881$ ,  $\text{CI}_{95\%} [-0.968, -0.609]$ ,  $n_{\text{pairs}} = 12$



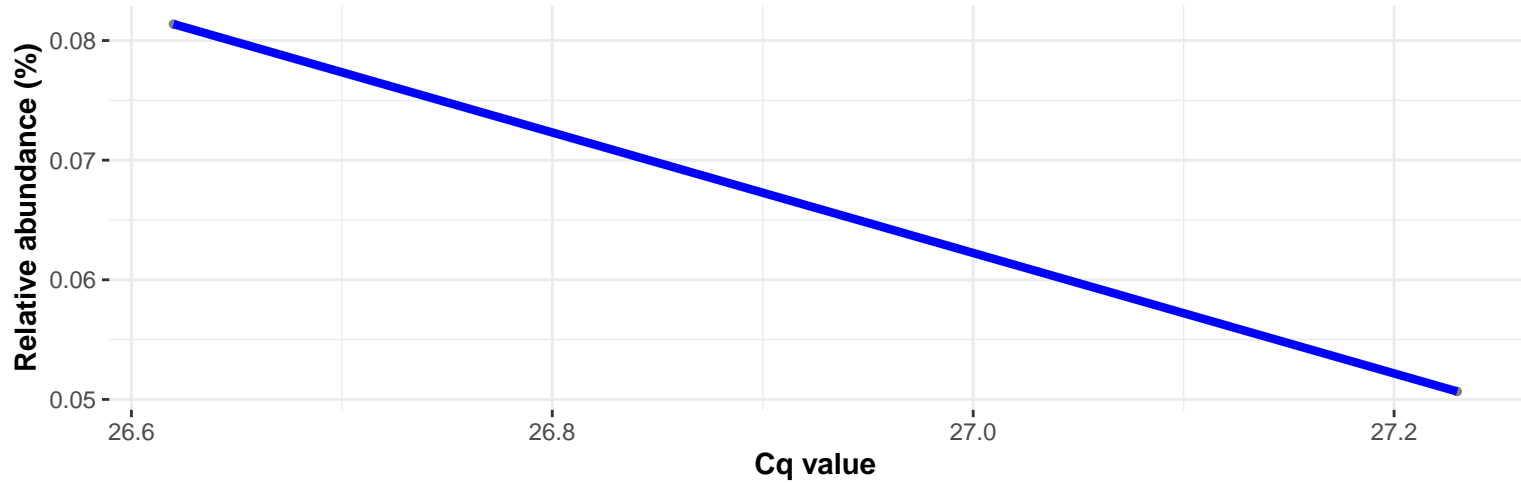
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Alteromonadales; f\_\_Shewanellaceae; g\_\_Shewanella; NA

Correlation with all samples

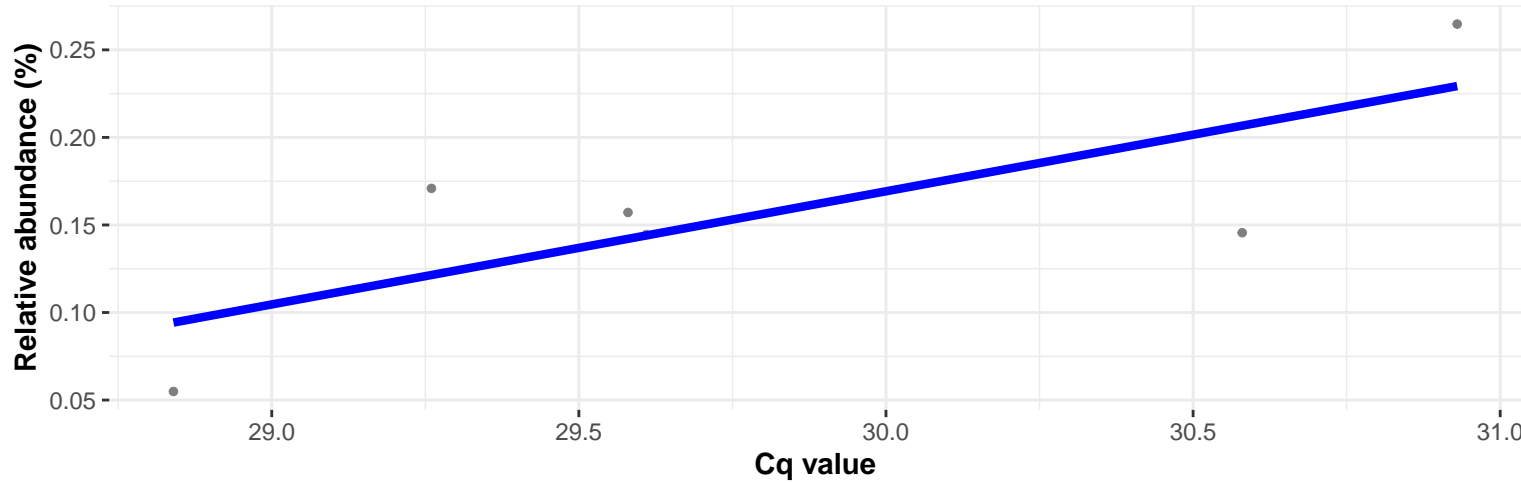
$\log_e(S) = 5.663$ ,  $p = 4.39\text{e-}05$ ,  $\hat{\rho}_{\text{Spearman}} = 0.783$ ,  $\text{CI}_{95\%} [0.512, 0.913]$ ,  $n_{\text{pairs}} = 20$



Correlation within: REF-PID

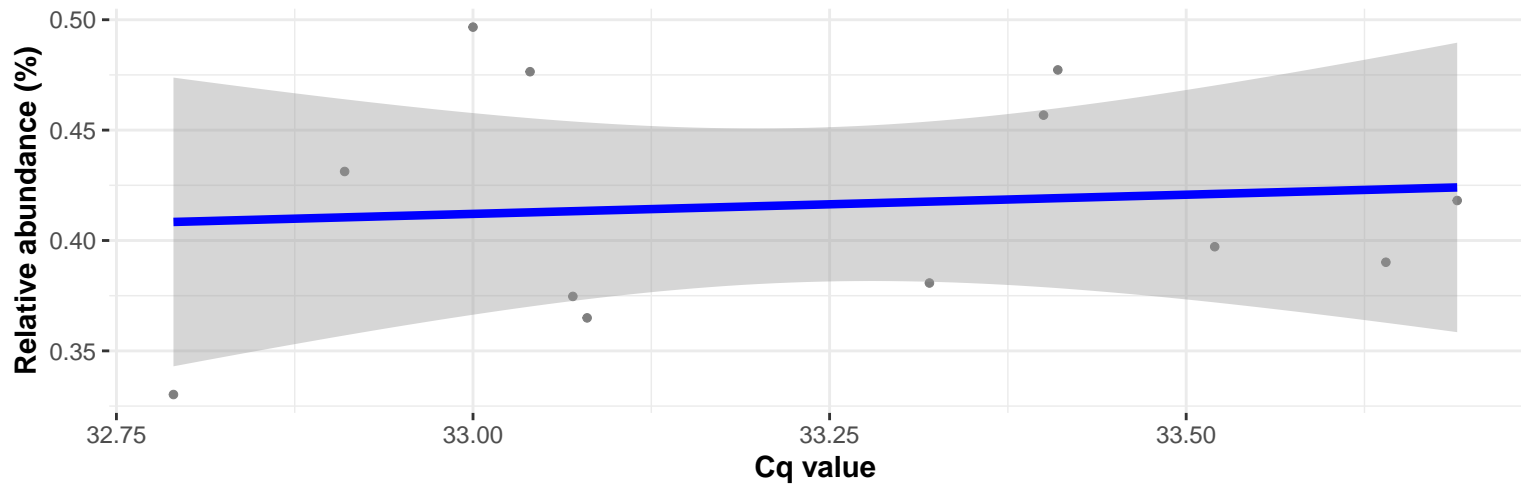


Correlation within: REF-DID



Correlation within: Extraction-blank

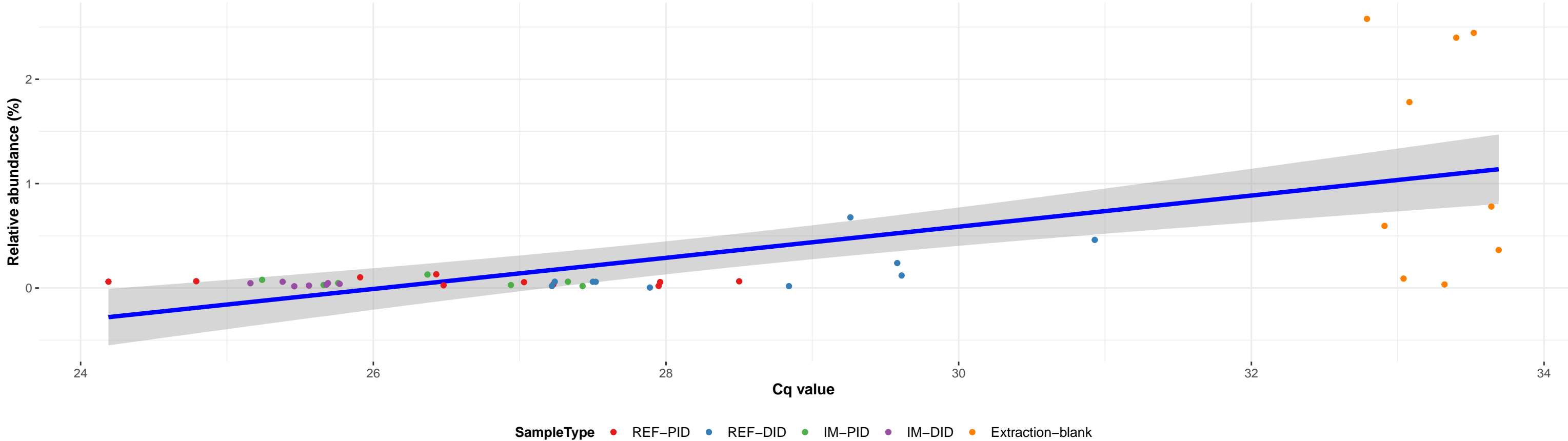
$\log_e(S) = 5.576$ ,  $p = 0.812$ ,  $\hat{\rho}_{\text{Spearman}} = 0.077$ ,  $\text{CI}_{95\%} [-0.534, 0.635]$ ,  $n_{\text{pairs}} = 12$



k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Ralstonia; s\_\_uncultured Ralstonia sp.

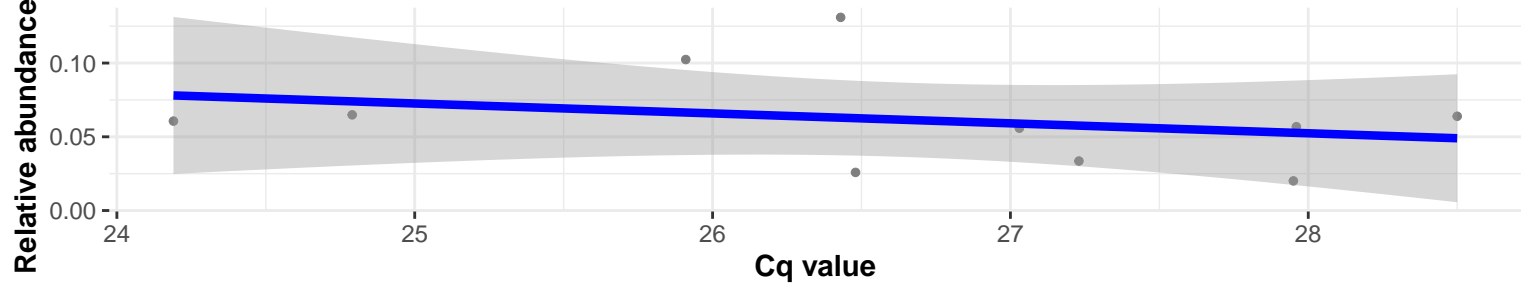
Correlation with all samples

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



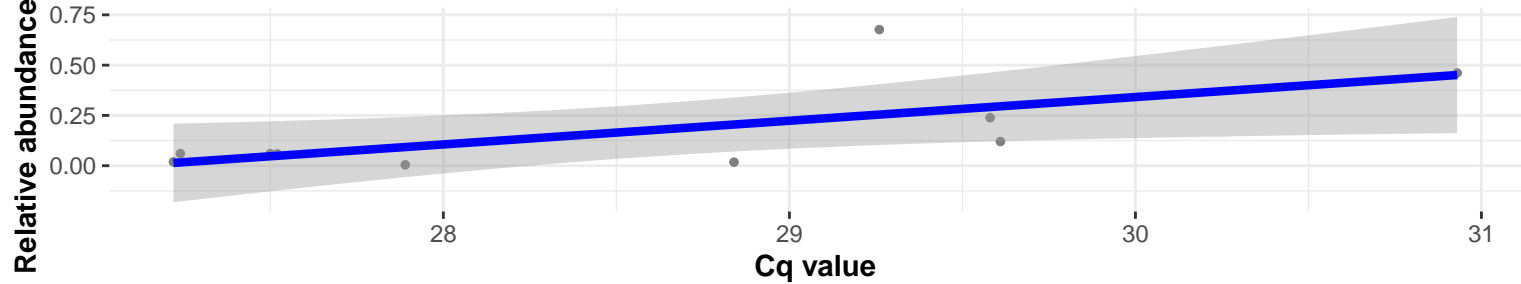
Correlation within: REF-PID

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



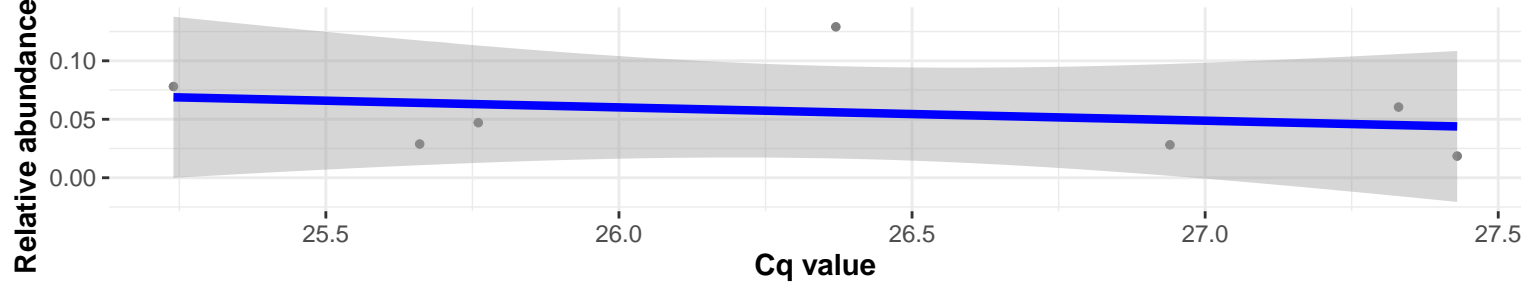
Correlation within: REF-DID

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



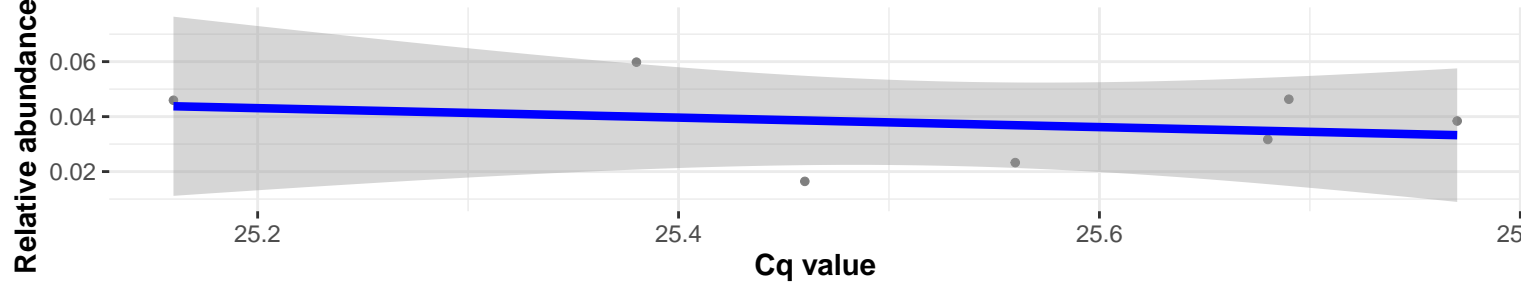
Correlation within: IM-PID

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



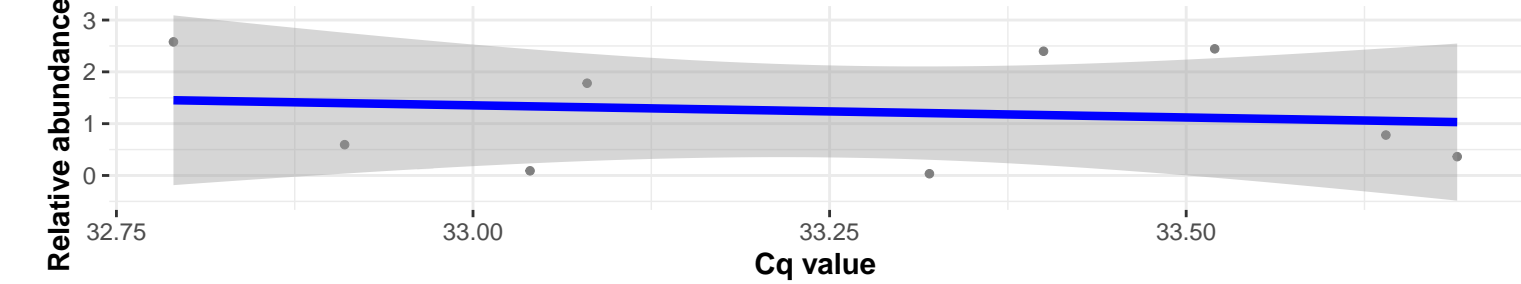
Correlation within: IM-DID

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



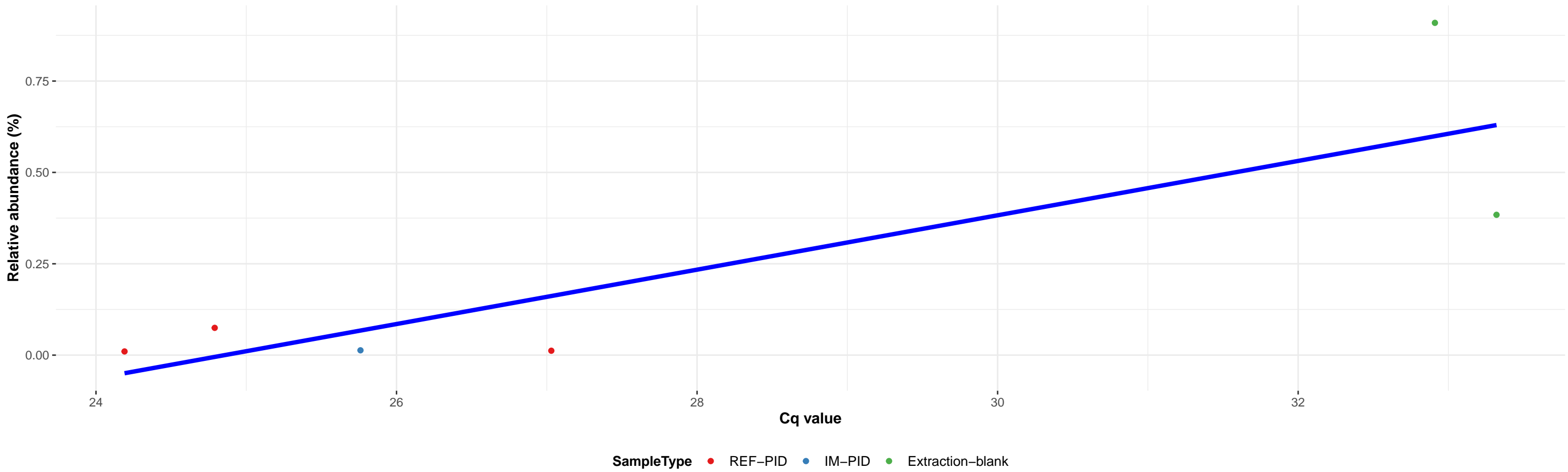
Correlation within: Extraction-blank

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

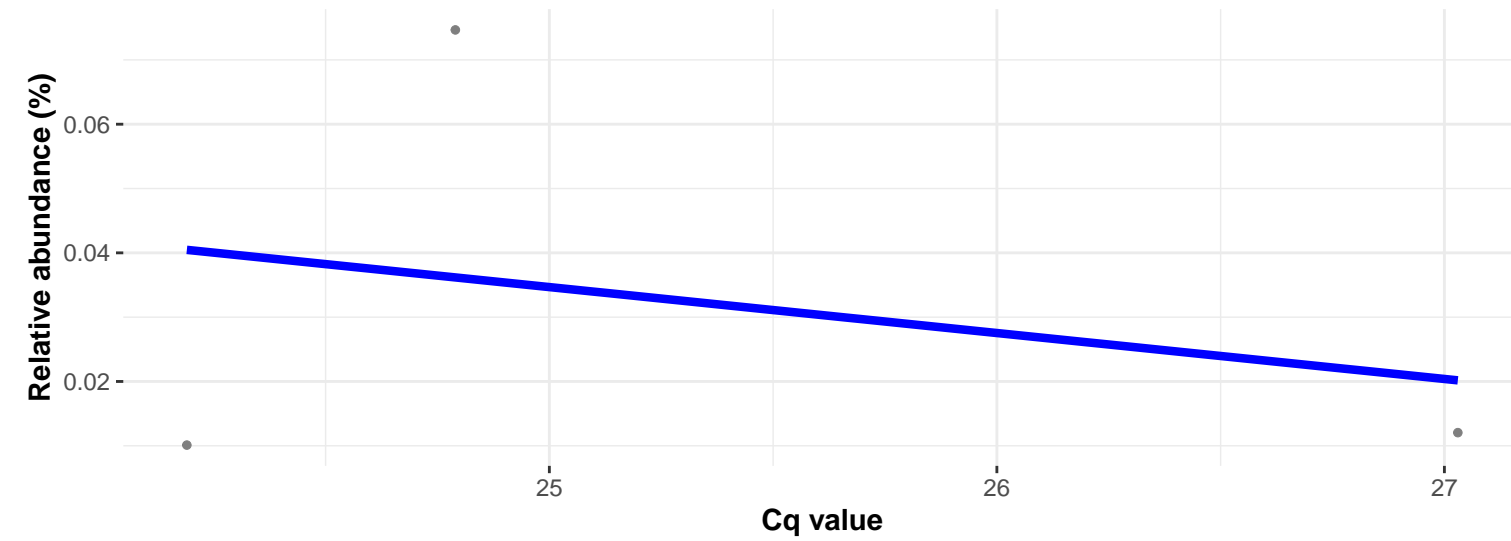


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Deltaproteobacteria; o\_\_Desulfuromonadales; f\_\_Desulfuromonadaceae; g\_\_Pelobacter; s\_\_uncultured bacterium

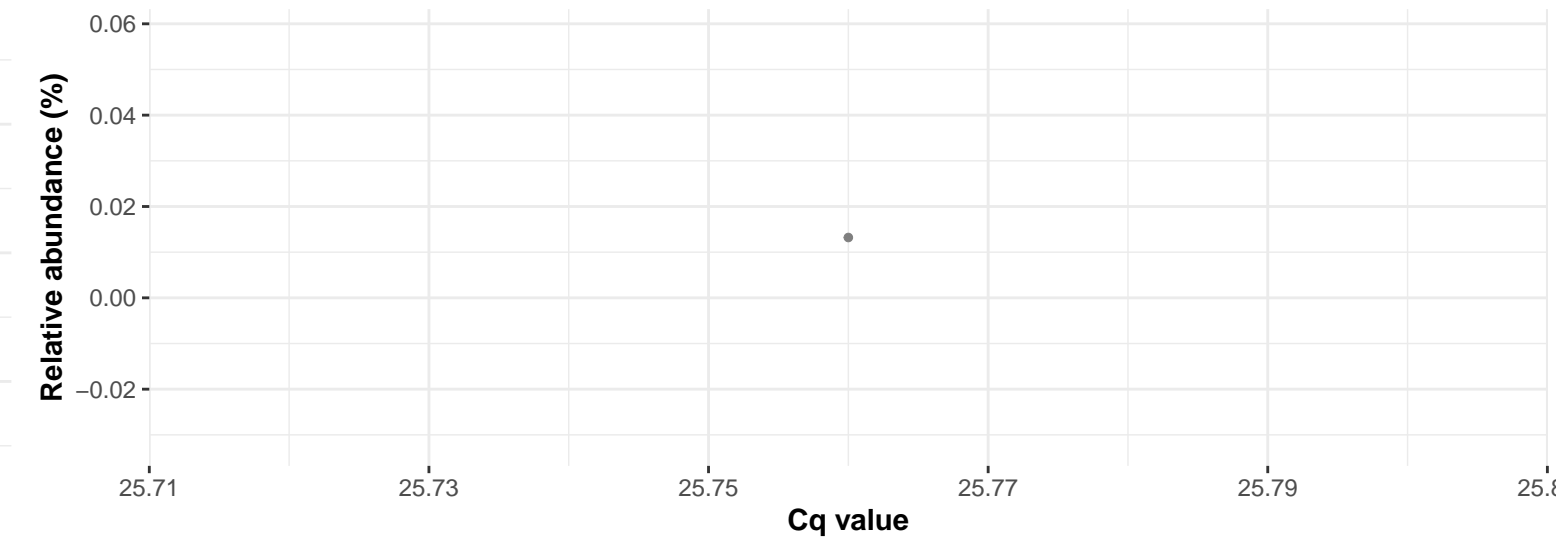
Correlation with all samples



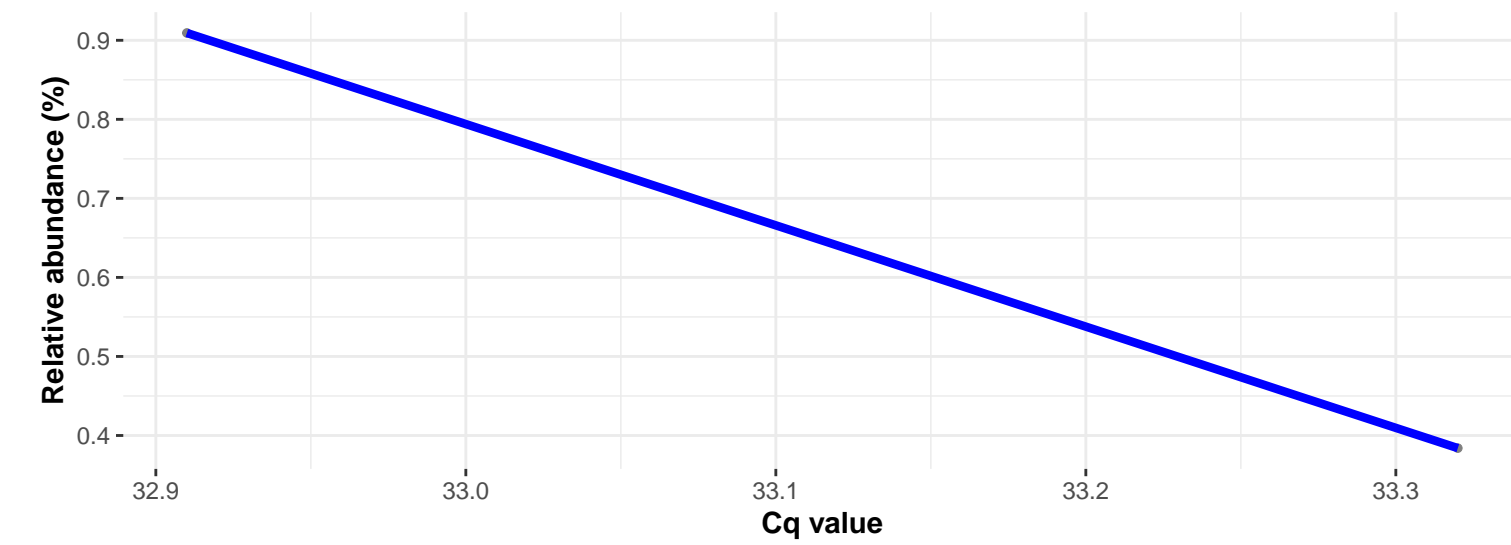
Correlation within: REF-PID



Correlation within: IM-PID



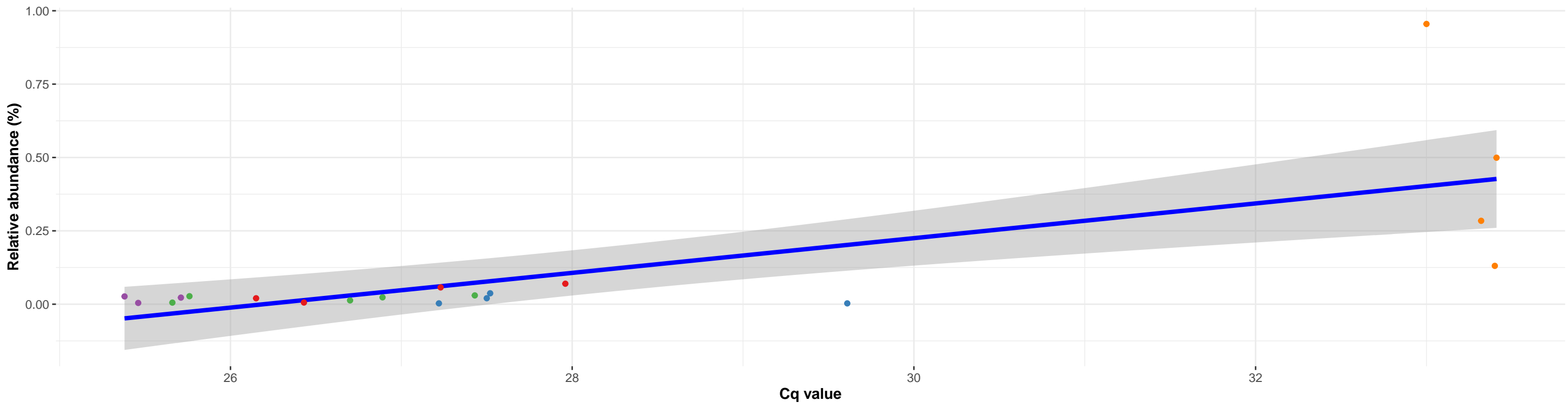
Correlation within: Extraction-blank



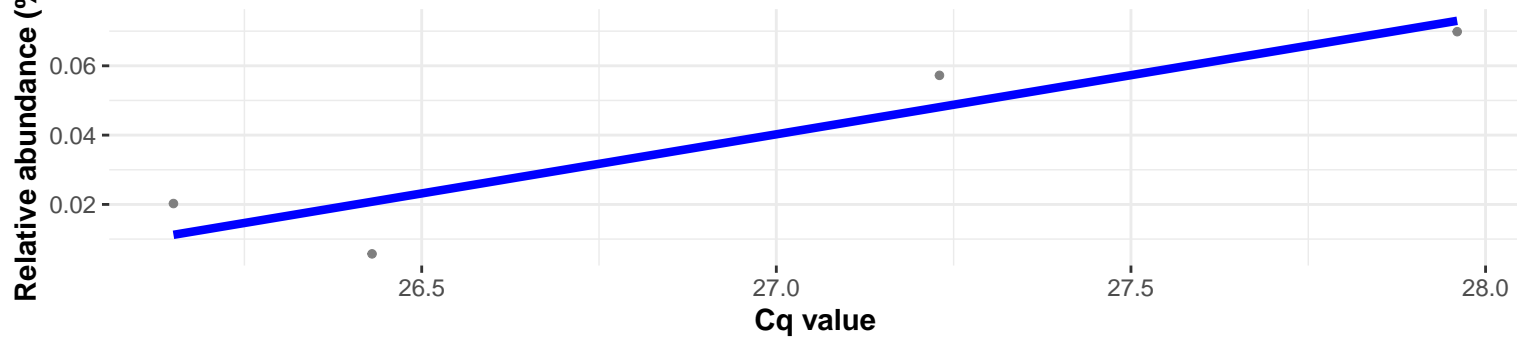
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Propionibacteriales; f\_\_Propionibacteriaceae; g\_\_Cutibacterium; NA

### Correlation with all samples

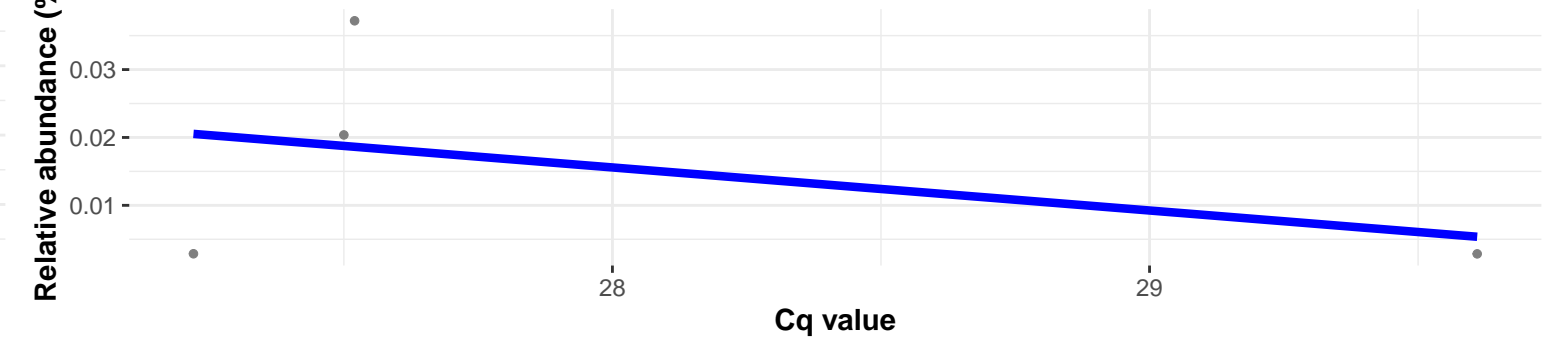
$\log_e(S) = 6.277$ ,  $p = 0.005$ ,  $\hat{\rho}_{\text{Spearman}} = 0.600$ ,  $CI_{95\%} [0.201, 0.828]$ ,  $n_{\text{pairs}} = 20$



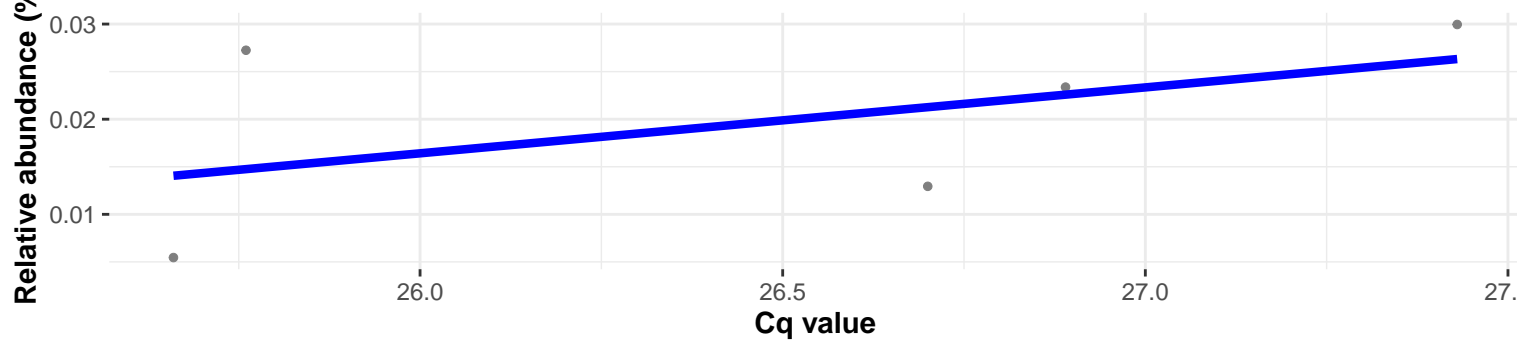
### Correlation within: REF-PID



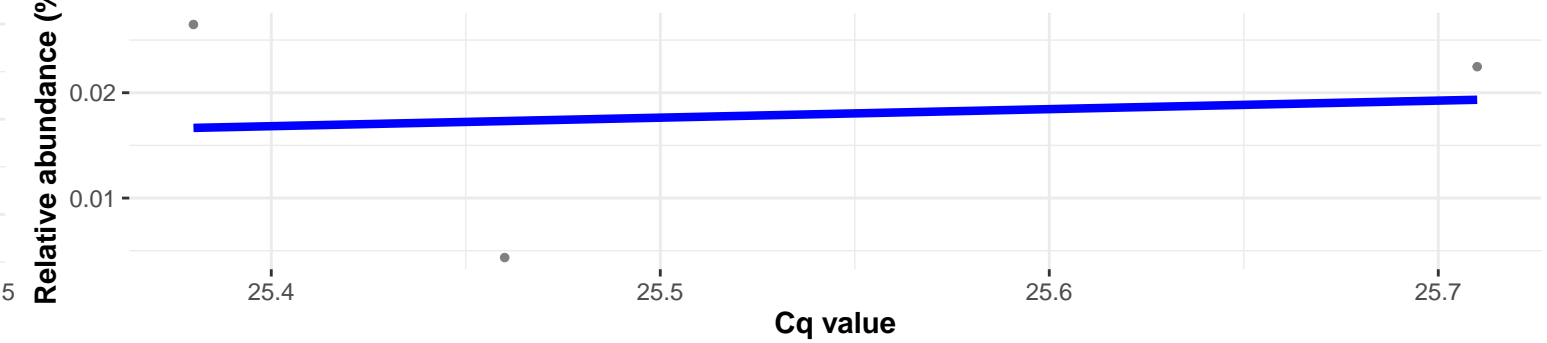
### Correlation within: REF-DID



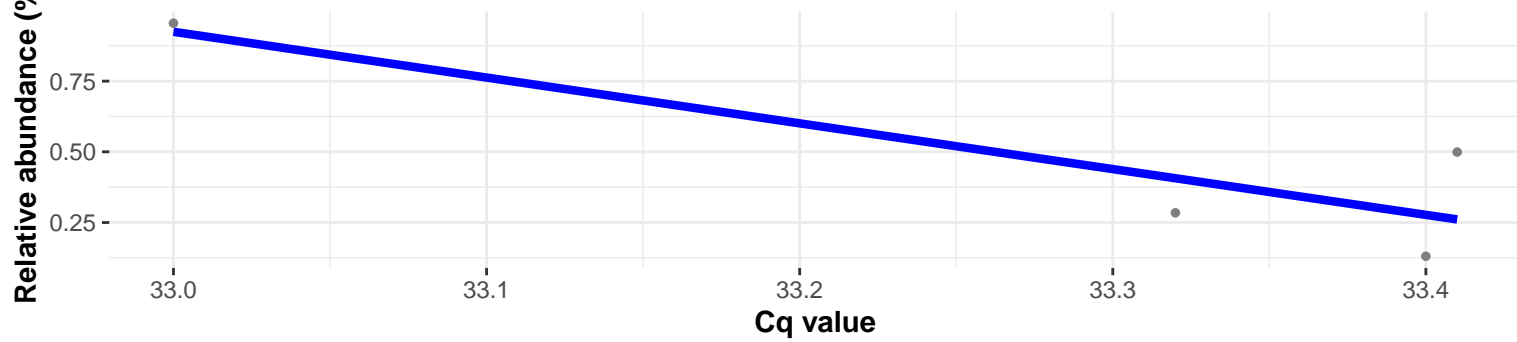
### Correlation within: IM-PID



### Correlation within: IM-DID

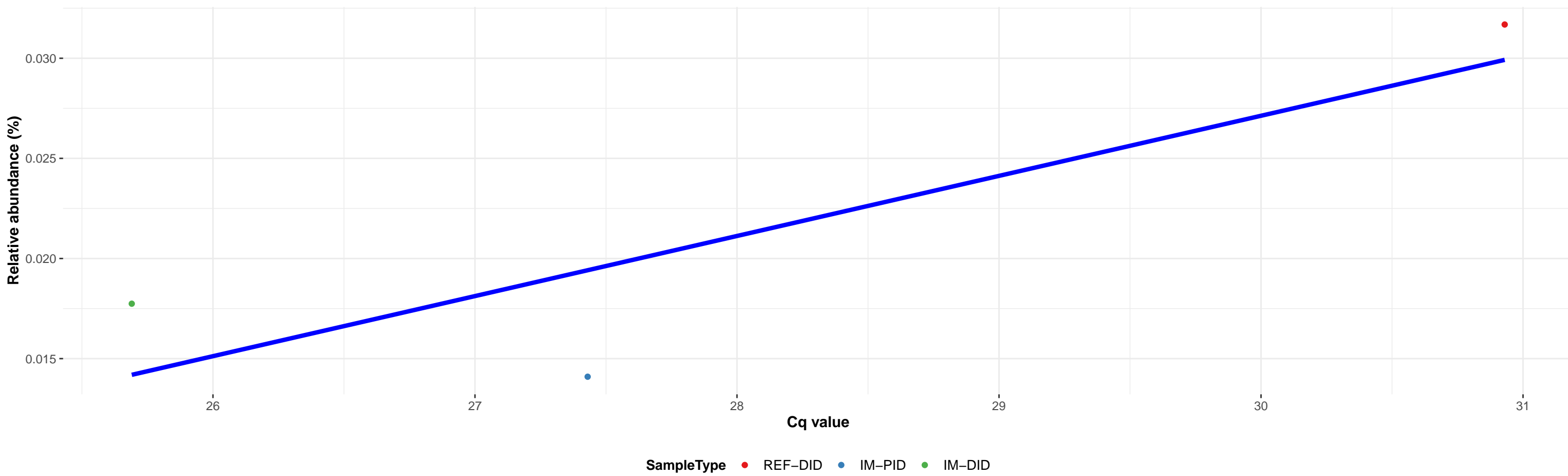


### Correlation within: Extraction-blank

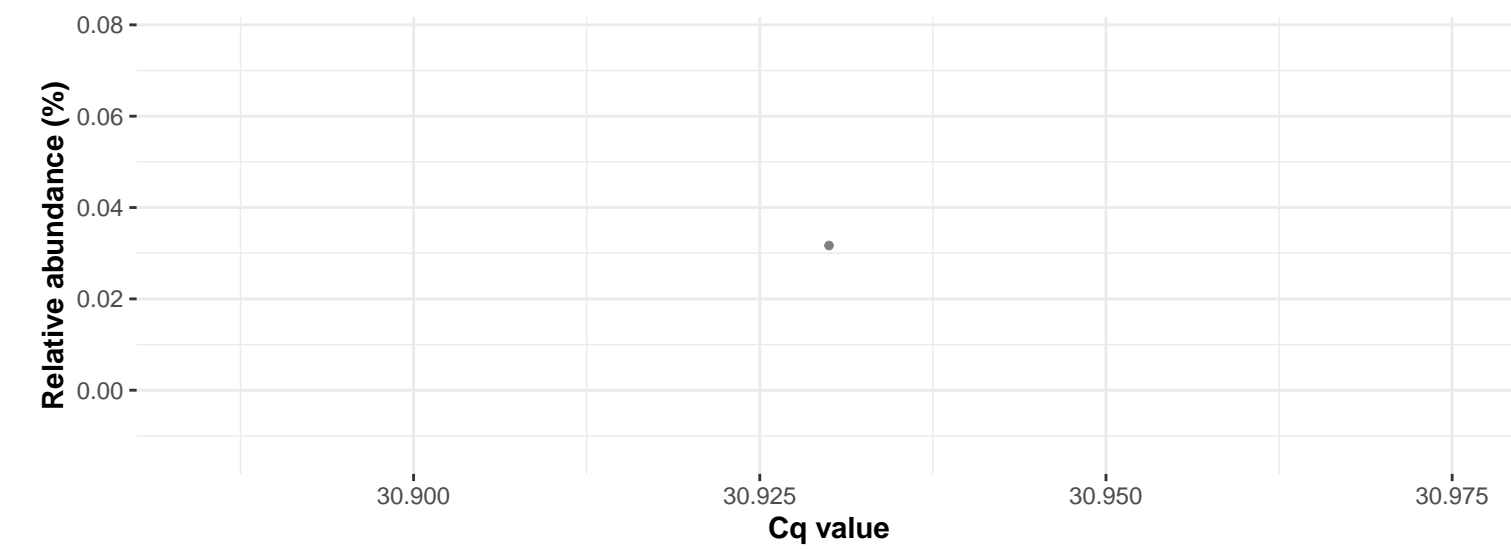


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Cupriavidus; NA

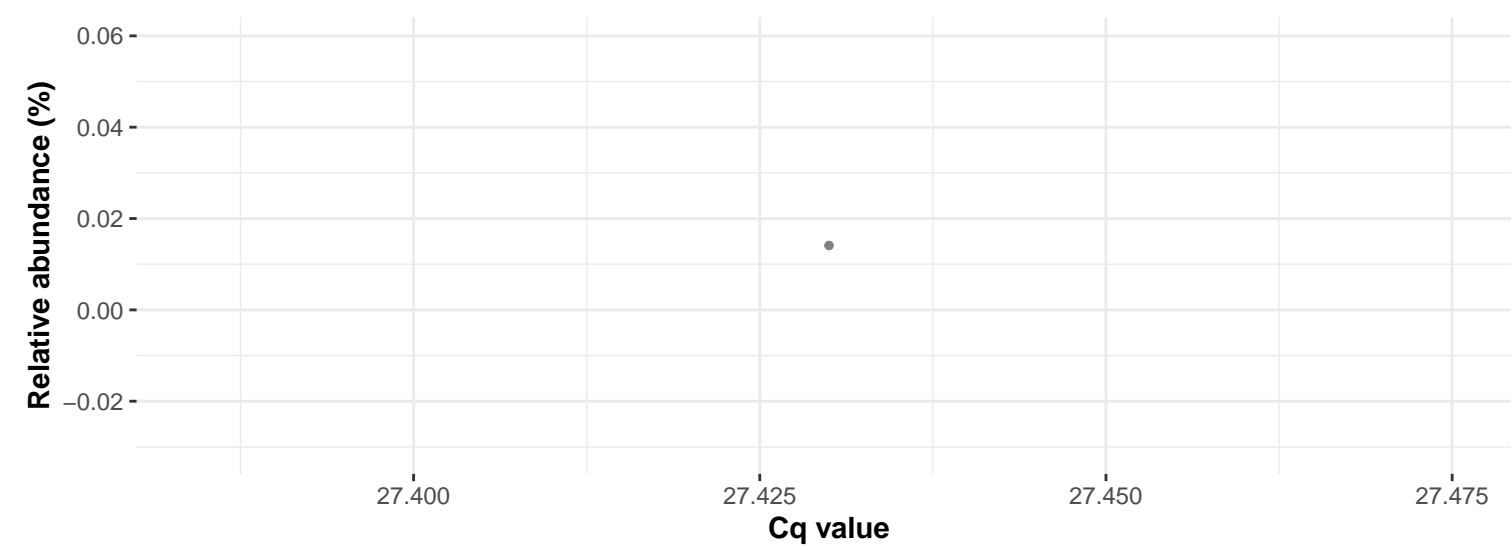
Correlation with all samples



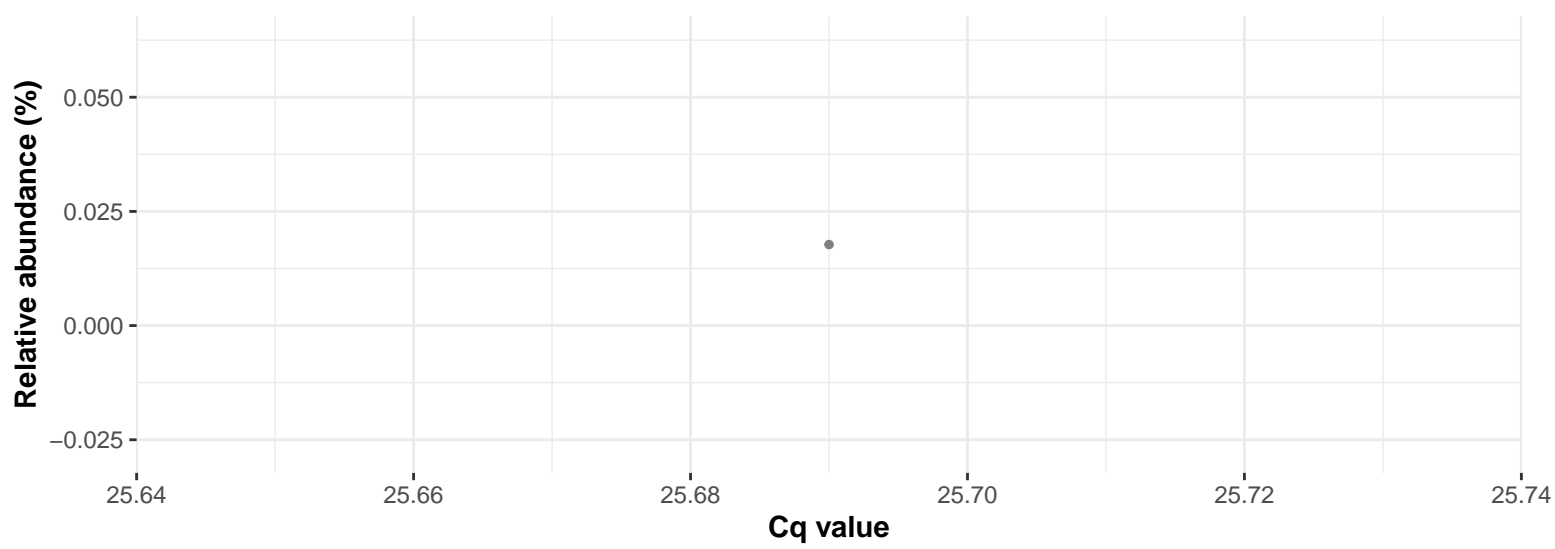
Correlation within: REF-DID



Correlation within: IM-PID

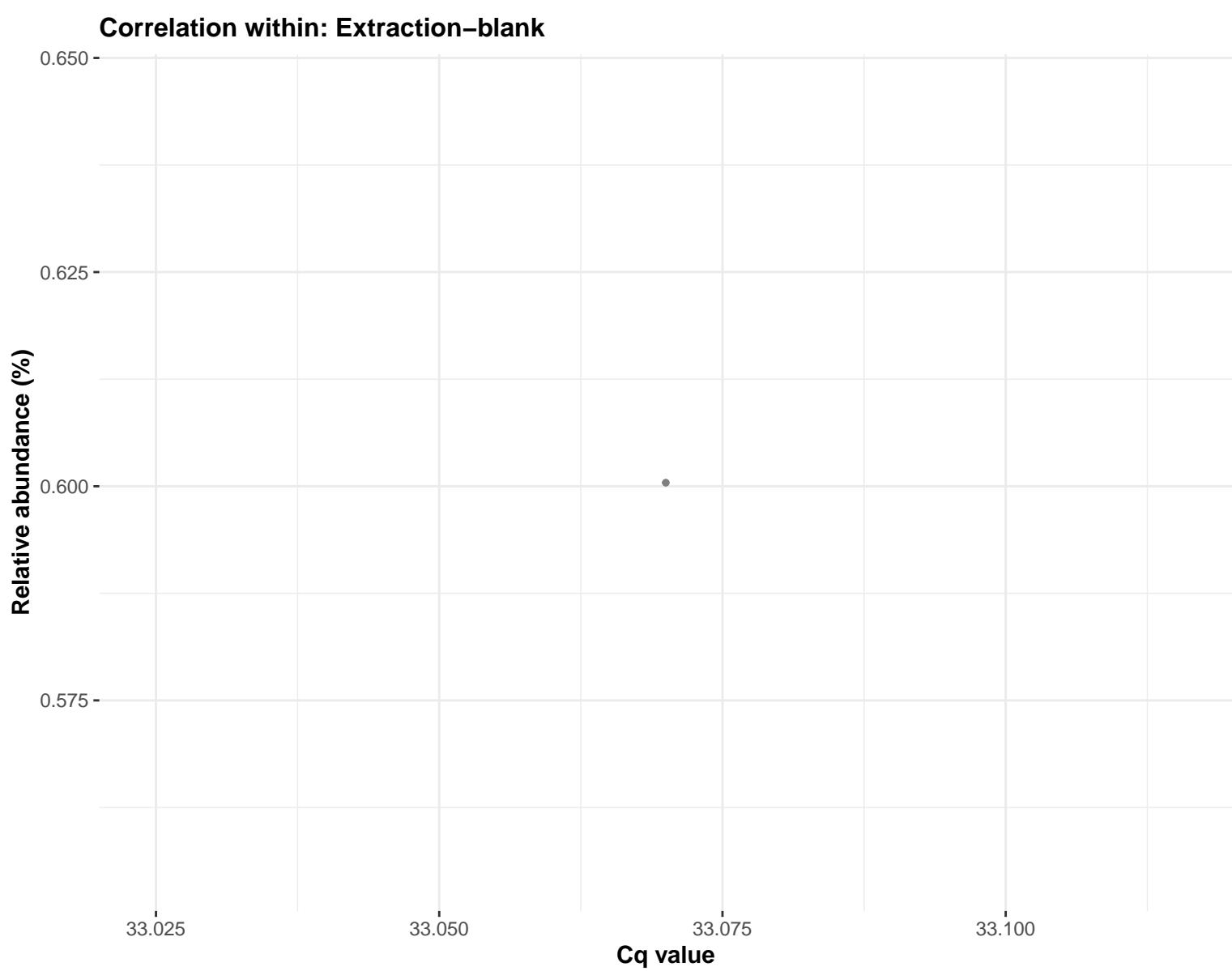
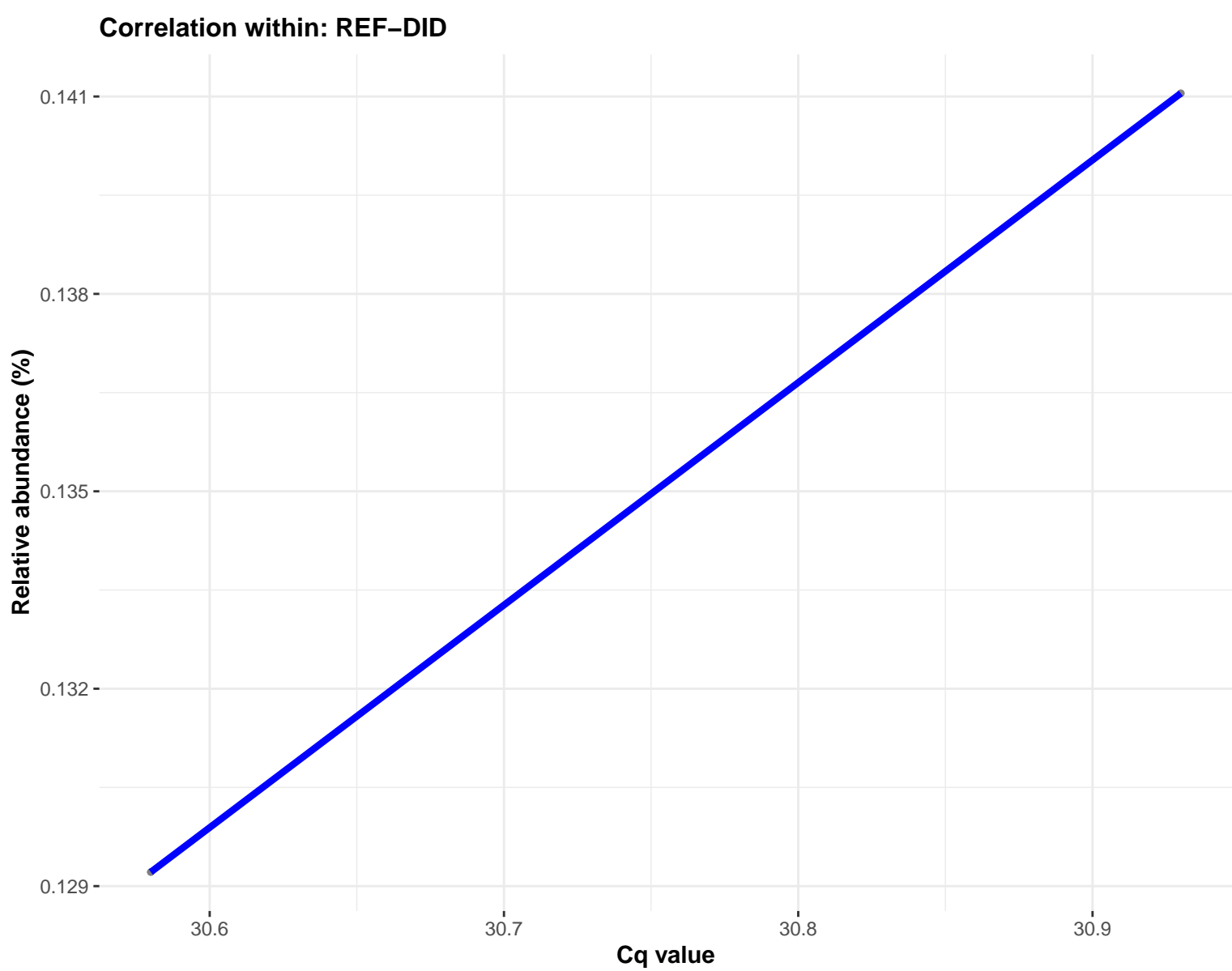
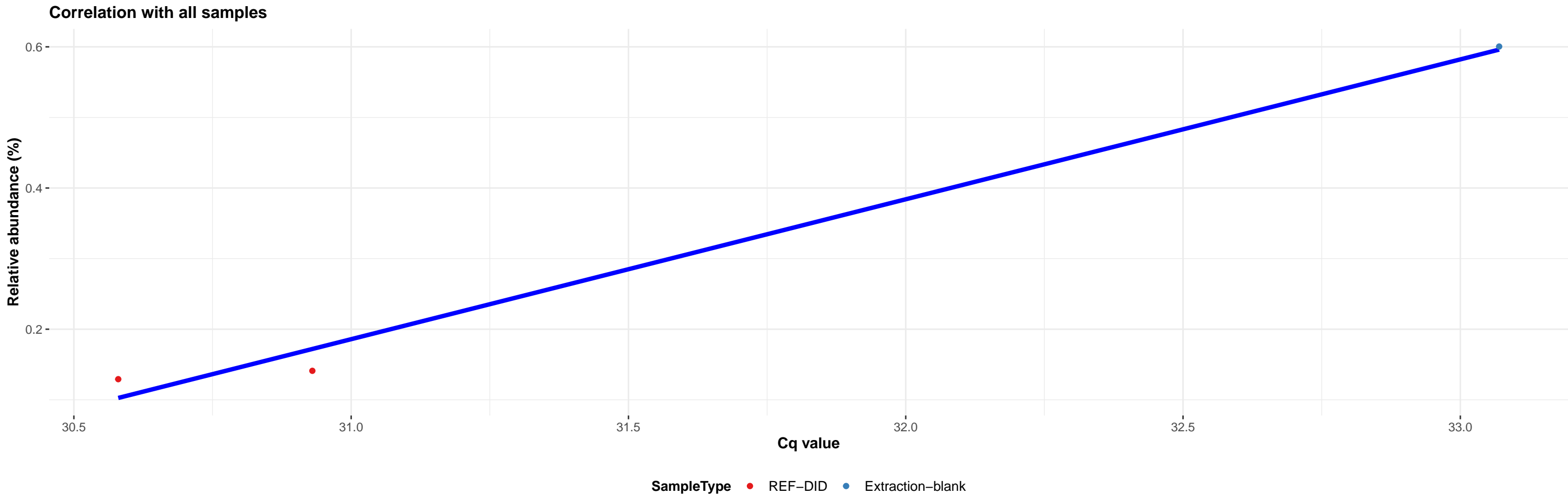


Correlation within: IM-DID

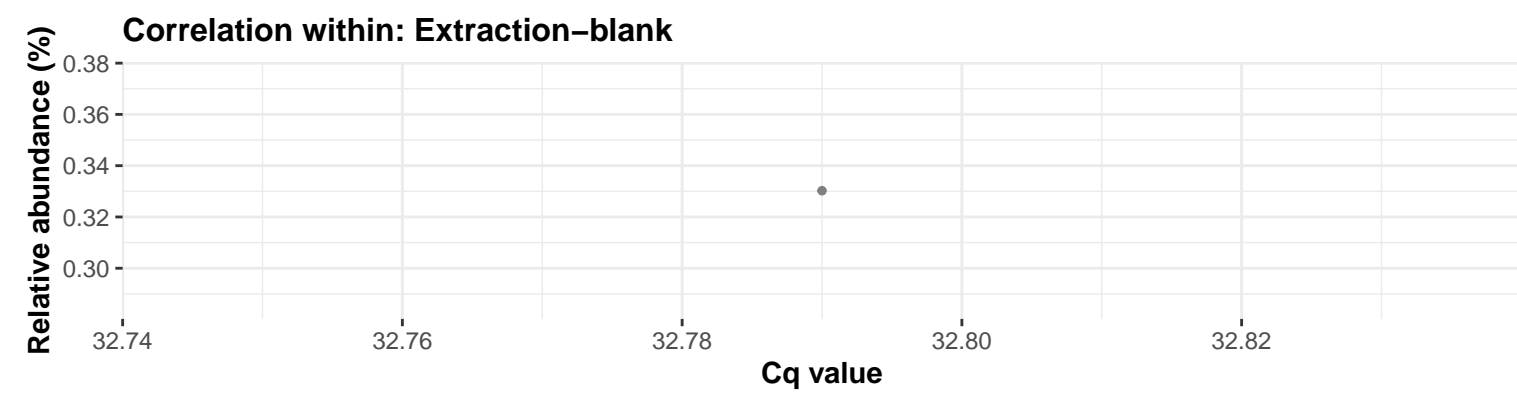
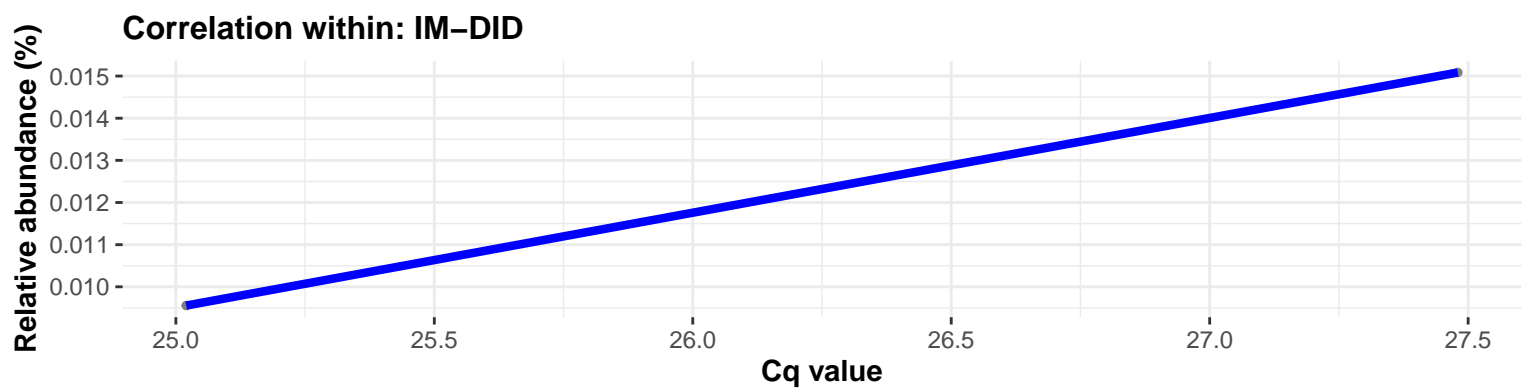
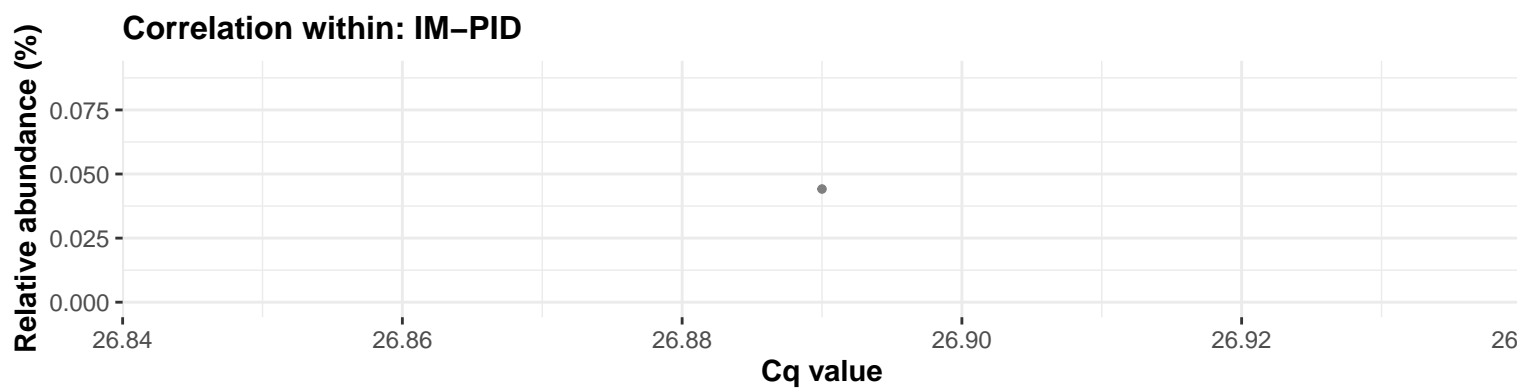
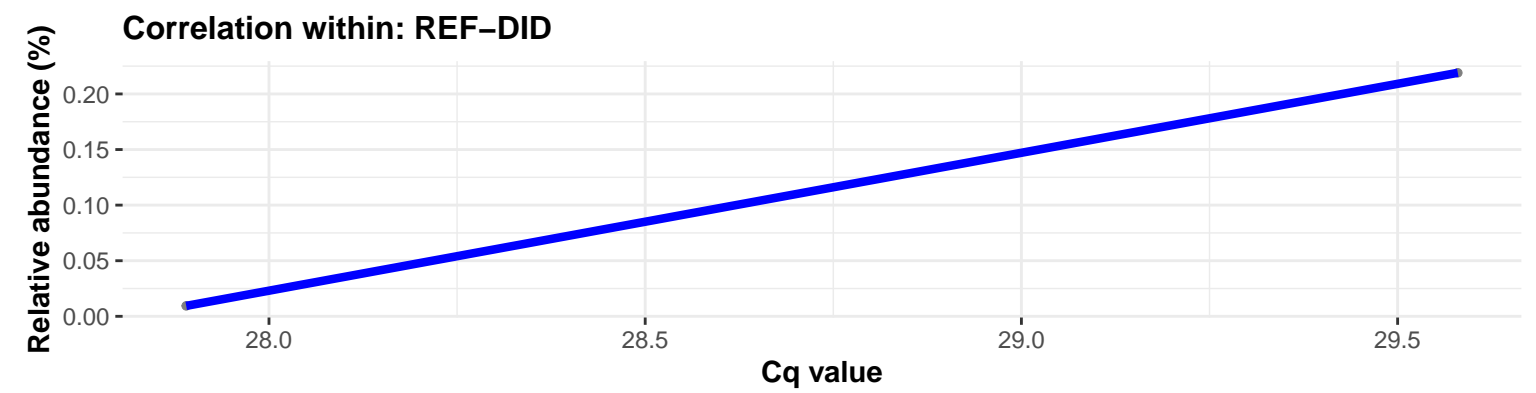
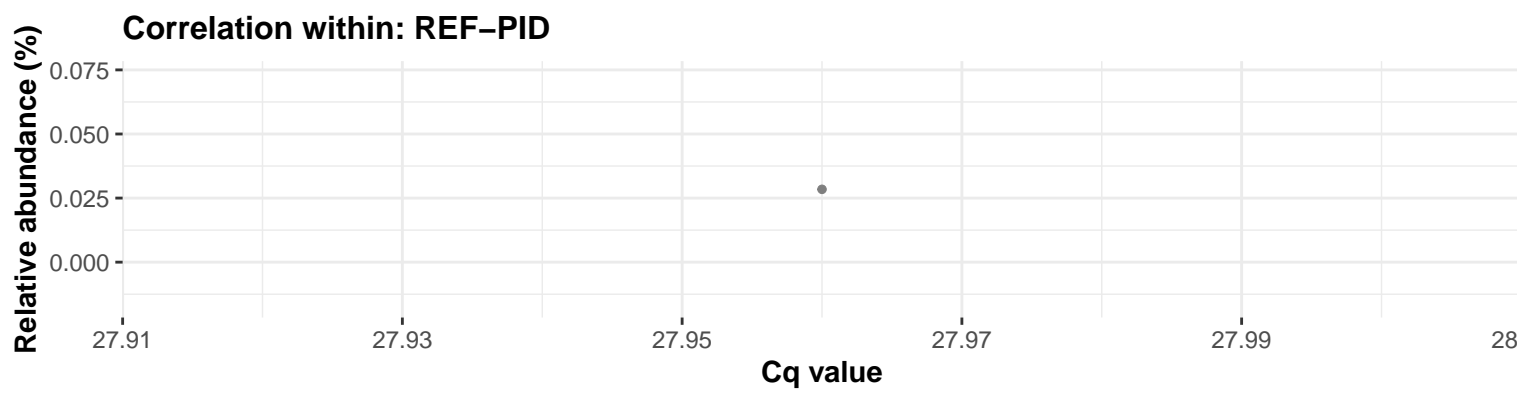
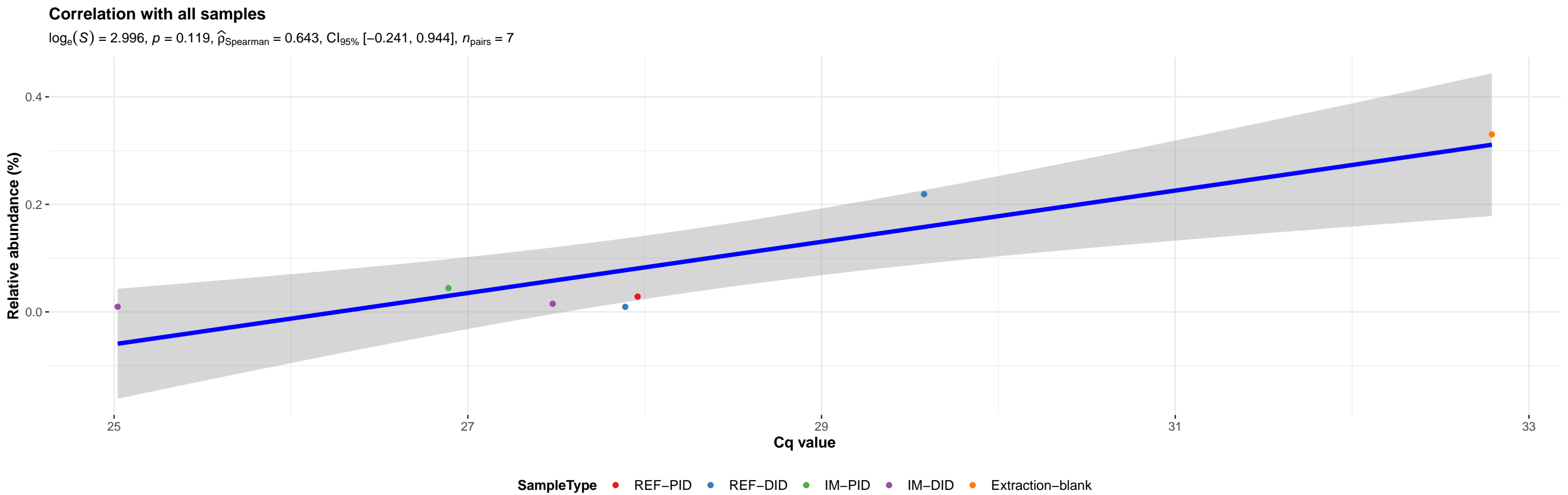




k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Oceanospirillales; f\_\_Halomonadaceae; g\_\_Halomonas; NA

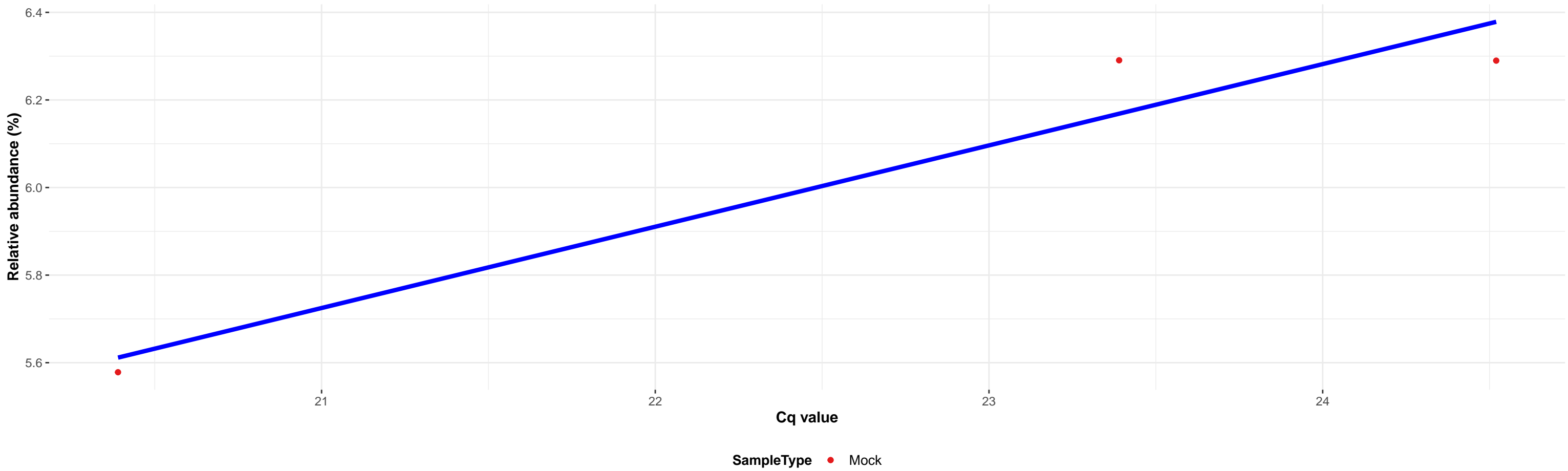


a; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Betaproteobacteriales; f\_\_Burkholderiaceae; g\_\_Burkholderia–Caballeronia–Paraburkholderia; s\_\_uncultured beta prote

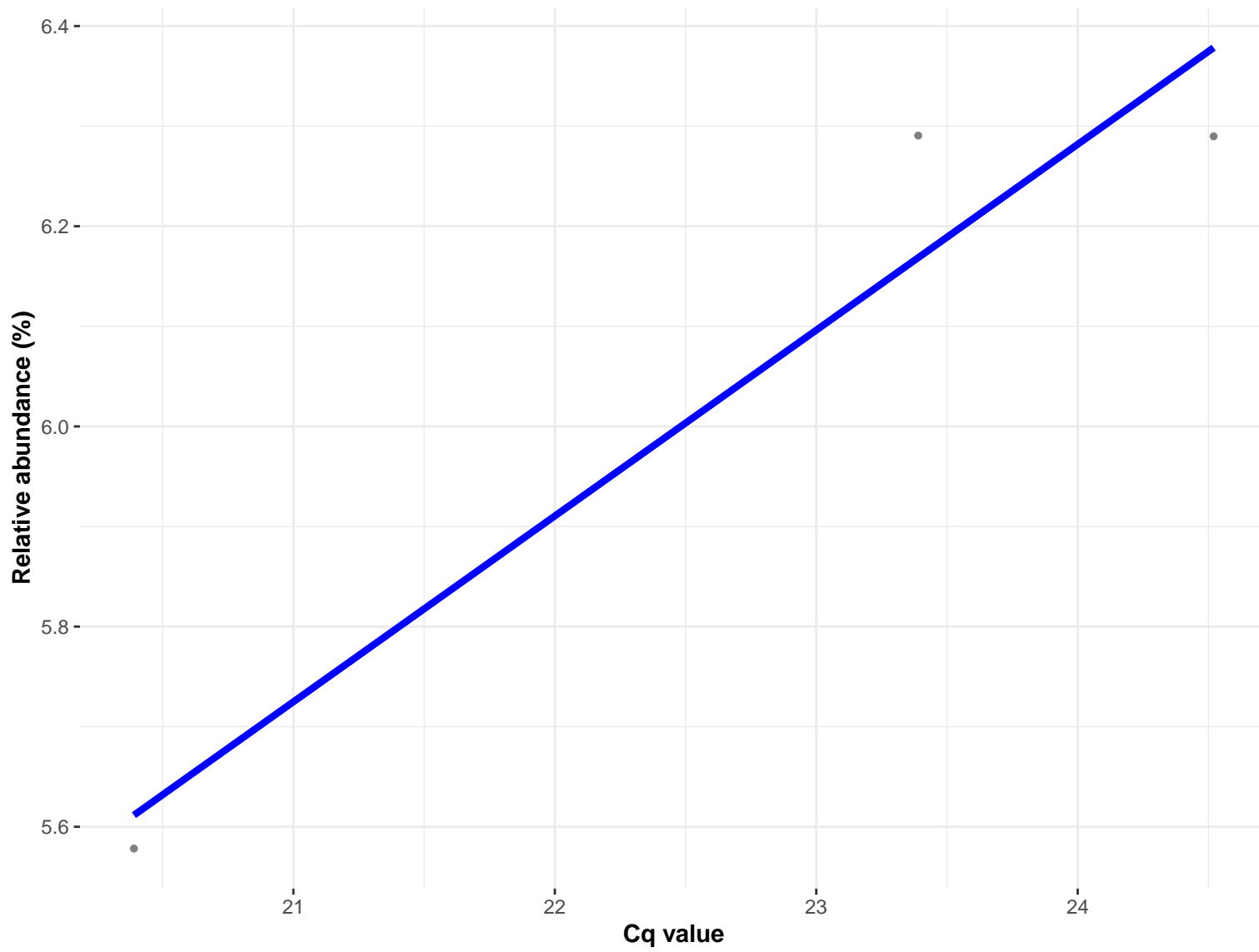


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

Correlation with all samples



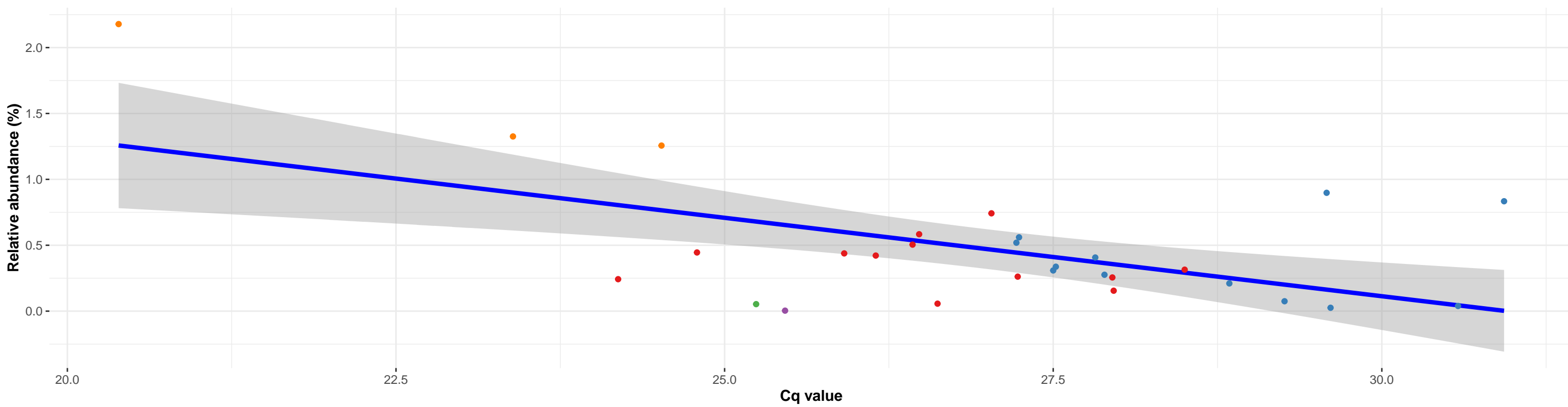
Correlation within: Mock



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus fermentum

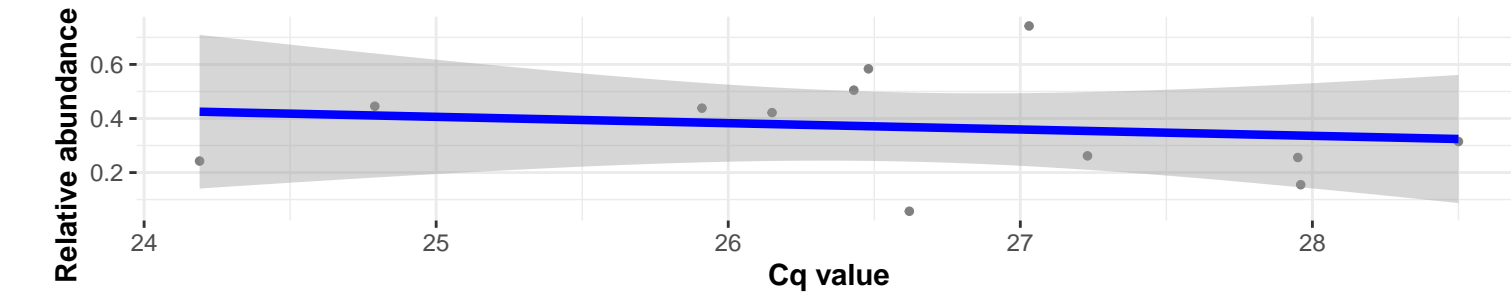
### Correlation with all samples

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



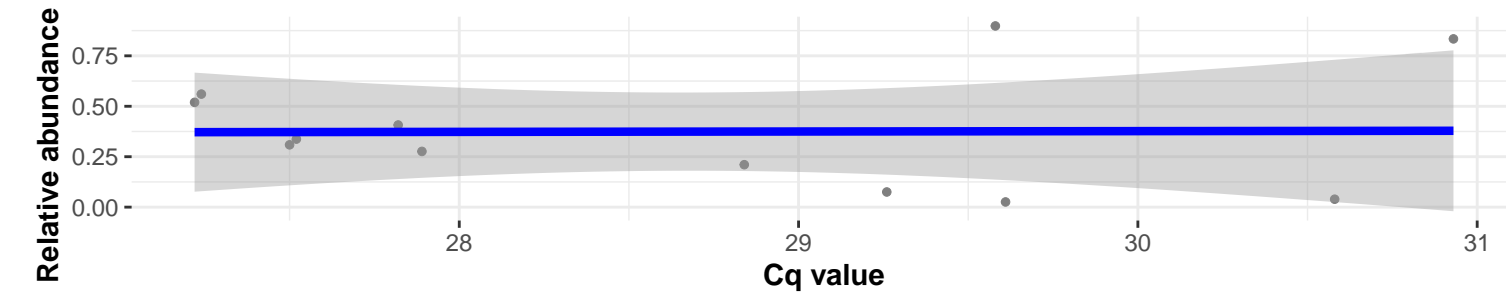
### Correlation within: REF-PID

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

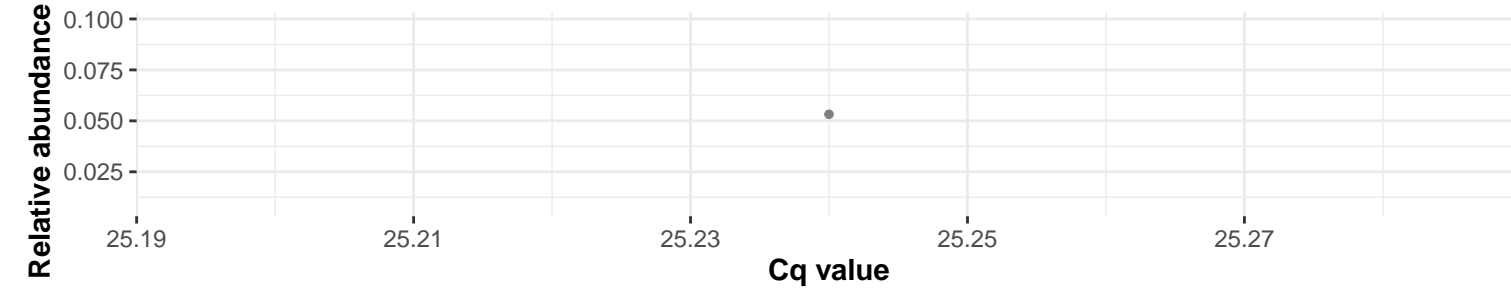


### Correlation within: REF-DID

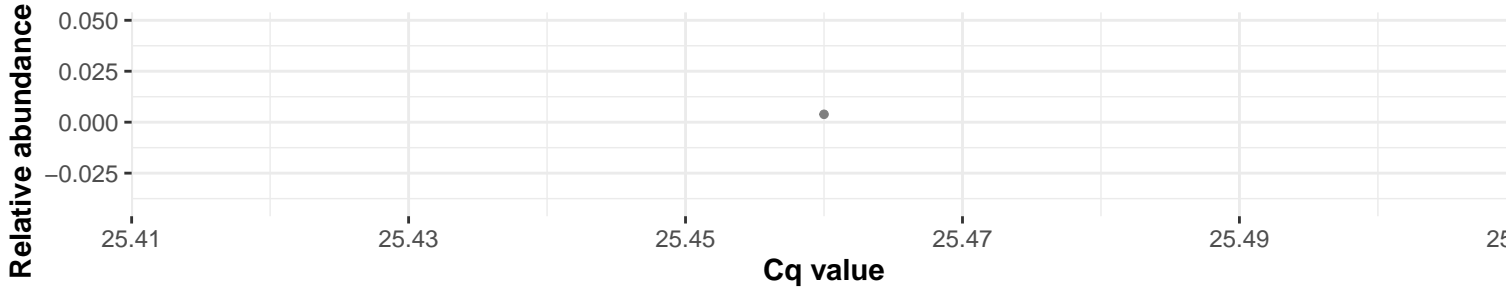
$\log_e(S) = 5.892$ ,  $p = 0.404$ ,  $\hat{\rho}_{\text{Spearman}} = -0.266$ ,  $\text{CI}_{95\%} [-0.737, 0.380]$ ,  $n_{\text{pairs}} = 12$



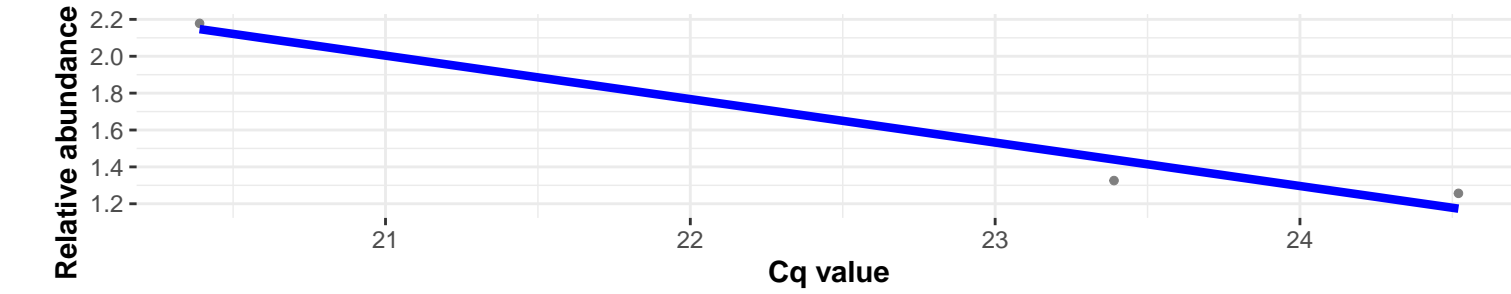
### Correlation within: IM-PID



### Correlation within: IM-DID

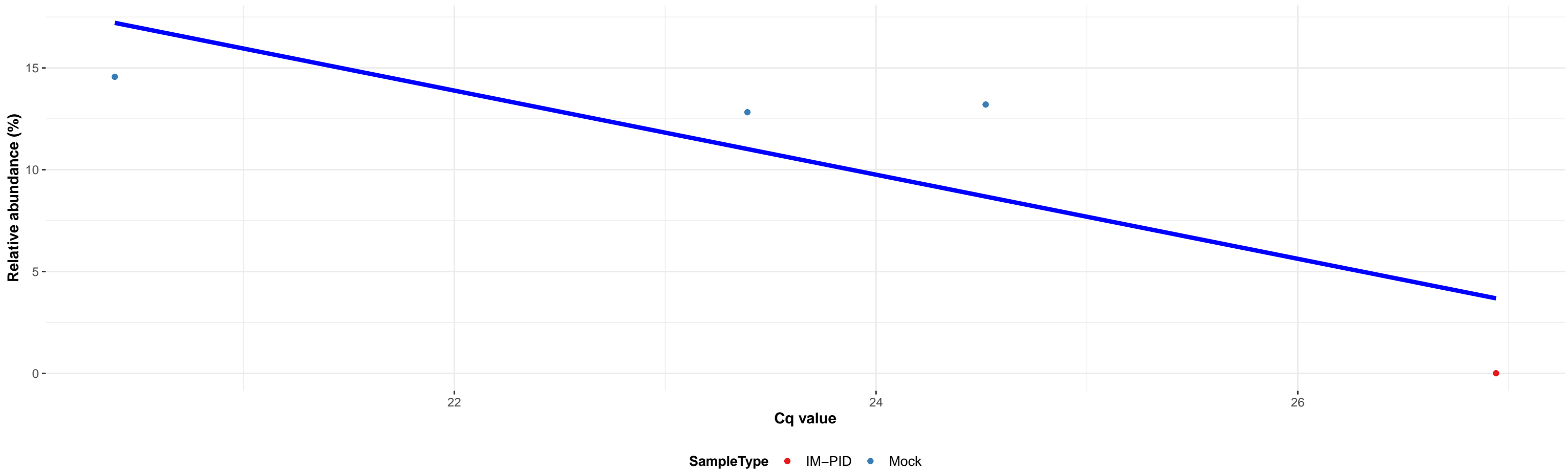


### Correlation within: Mock

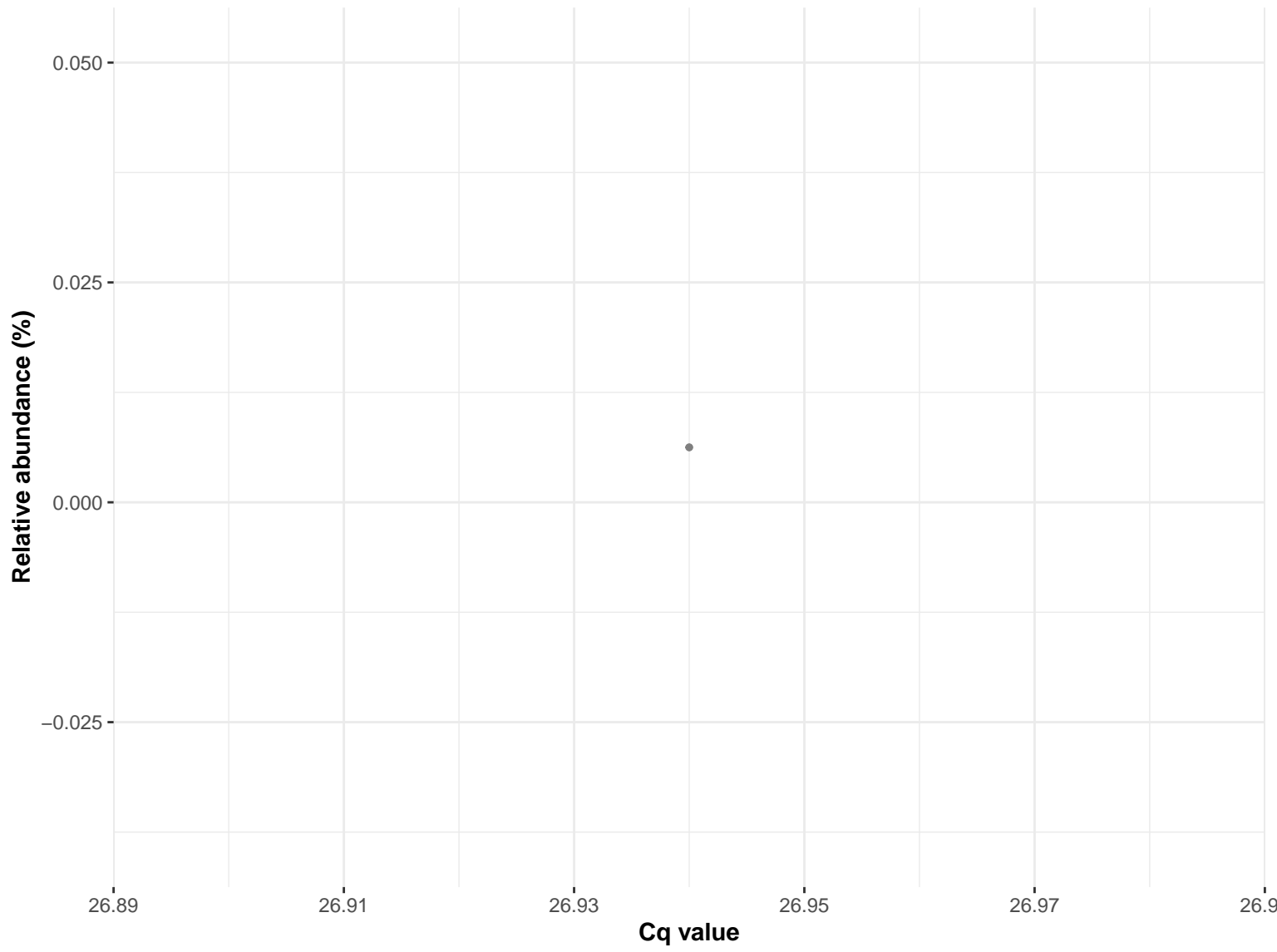


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

Correlation with all samples



Correlation within: IM-PID



Correlation within: Mock

