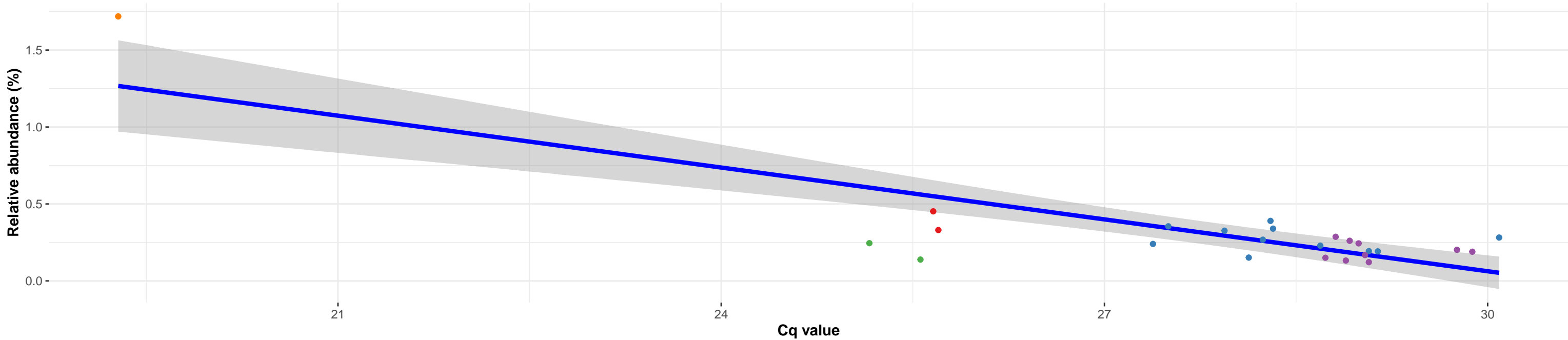


k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Clostridiaceae 1; g\_\_Clostridium sensu stricto 1; s\_\_Clostridium perfringens

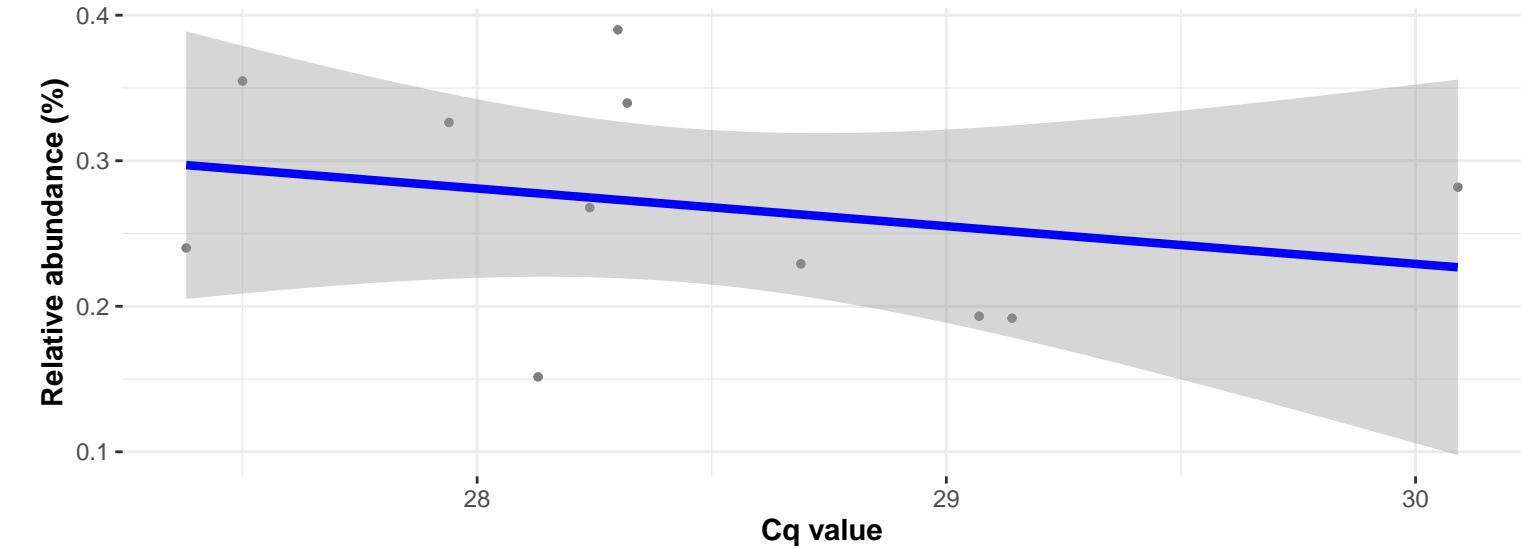
Correlation with all samples

$\log_e(S) = 8.227$ ,  $p = 0.028$ ,  $\hat{\rho}_{\text{Spearman}} = -0.439$ ,  $\text{CI}_{95\%} [-0.717, -0.041]$ ,  $n_{\text{pairs}} = 25$



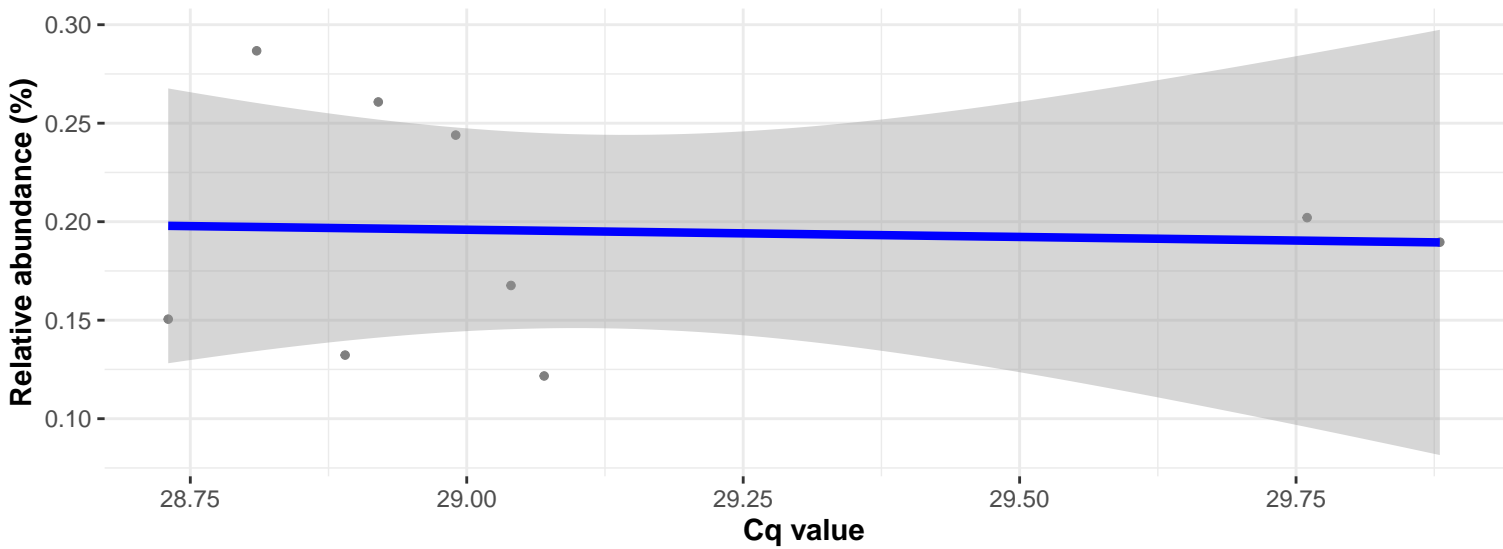
Correlation within: IM-PIM

$\log_e(S) = 5.620$ ,  $p = 0.450$ ,  $\hat{\rho}_{\text{Spearman}} = -0.255$ ,  $\text{CI}_{95\%} [-0.750, 0.425]$ ,  $n_{\text{pairs}} = 11$

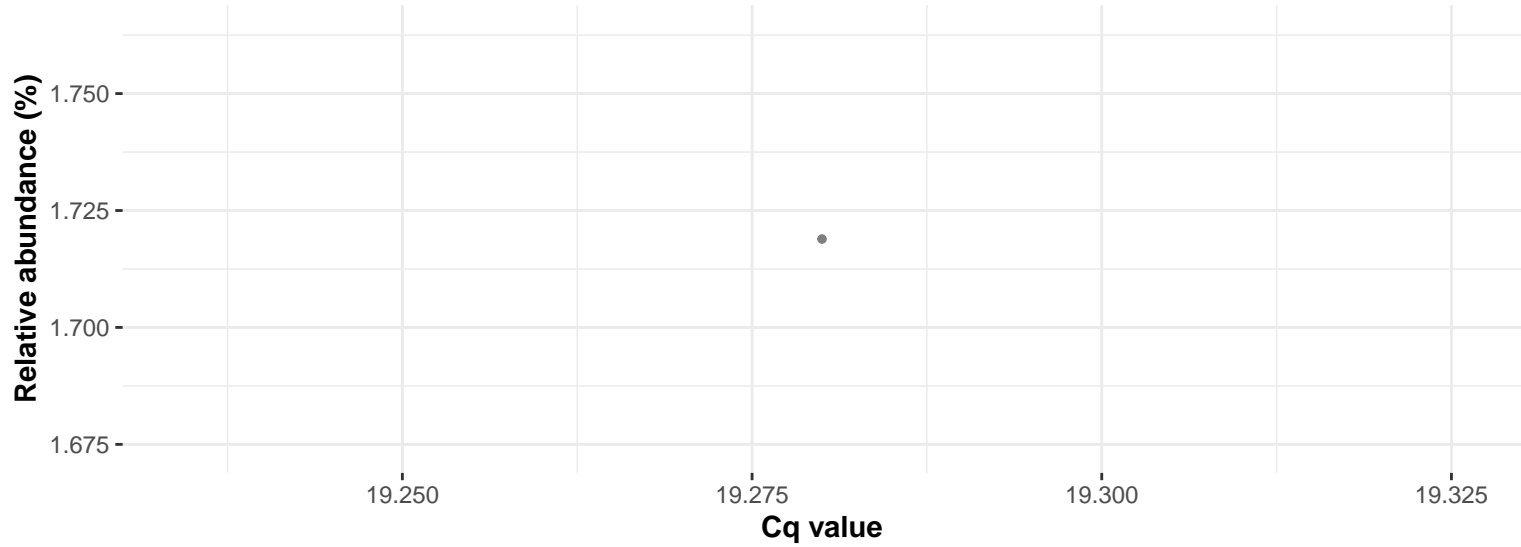


Correlation within: IM-DIM

$\log_e(S) = 4.898$ ,  $p = 0.765$ ,  $\hat{\rho}_{\text{Spearman}} = -0.117$ ,  $\text{CI}_{95\%} [-0.736, 0.609]$ ,  $n_{\text{pairs}} = 9$



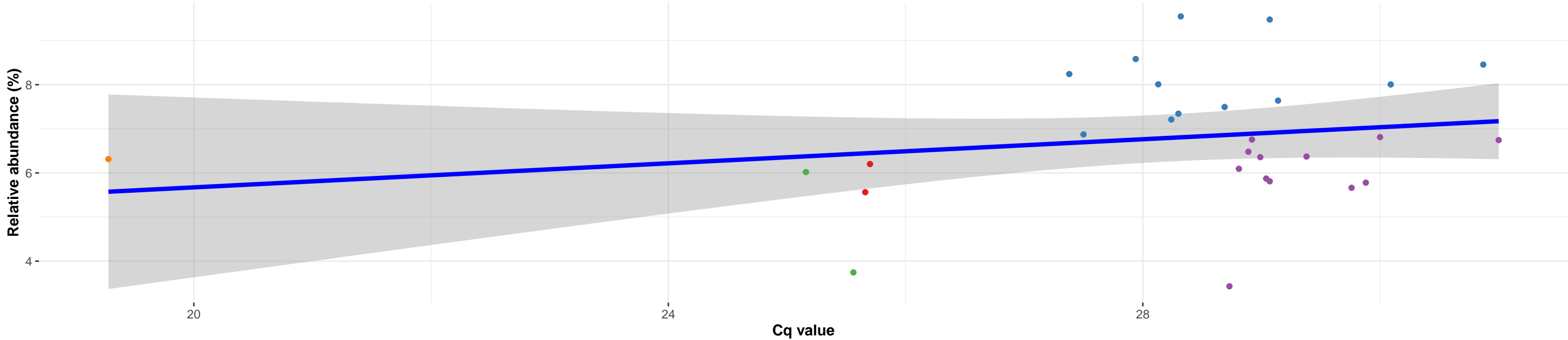
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; NA; NA; NA

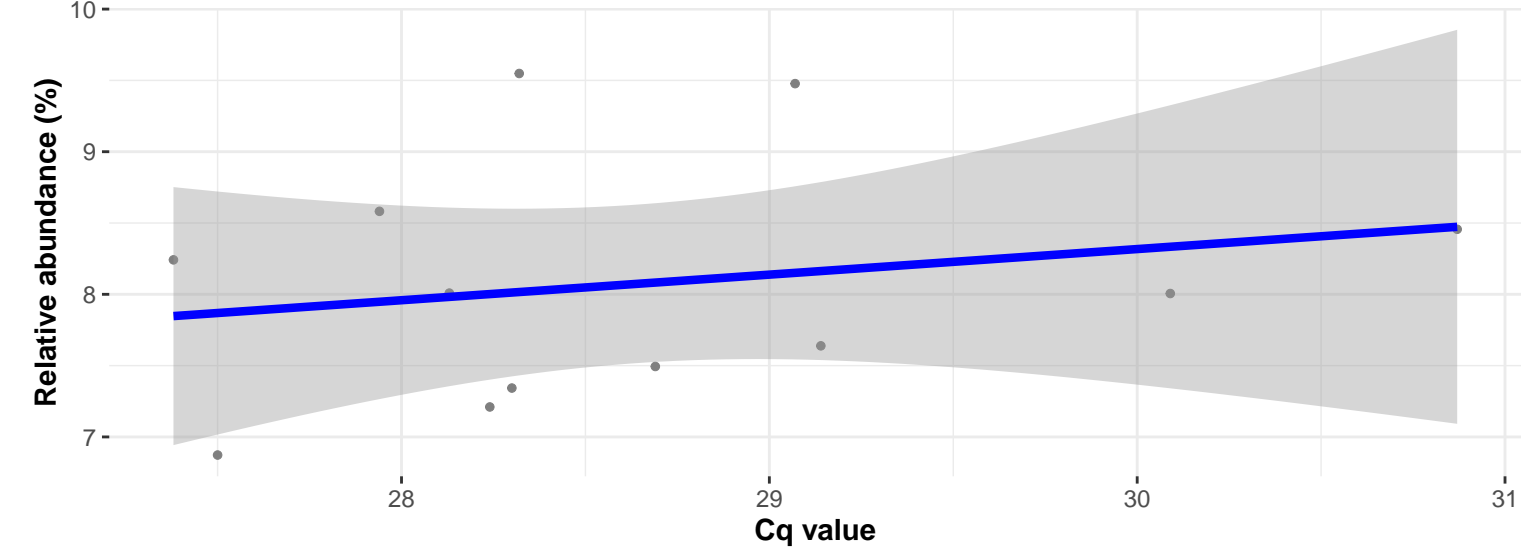
Correlation with all samples

$\log_e(S) = 8.189$ ,  $p = 0.558$ ,  $\hat{\rho}_{\text{Spearman}} = 0.113$ ,  $CI_{95\%} [-0.275, 0.470]$ ,  $n_{\text{pairs}} = 29$



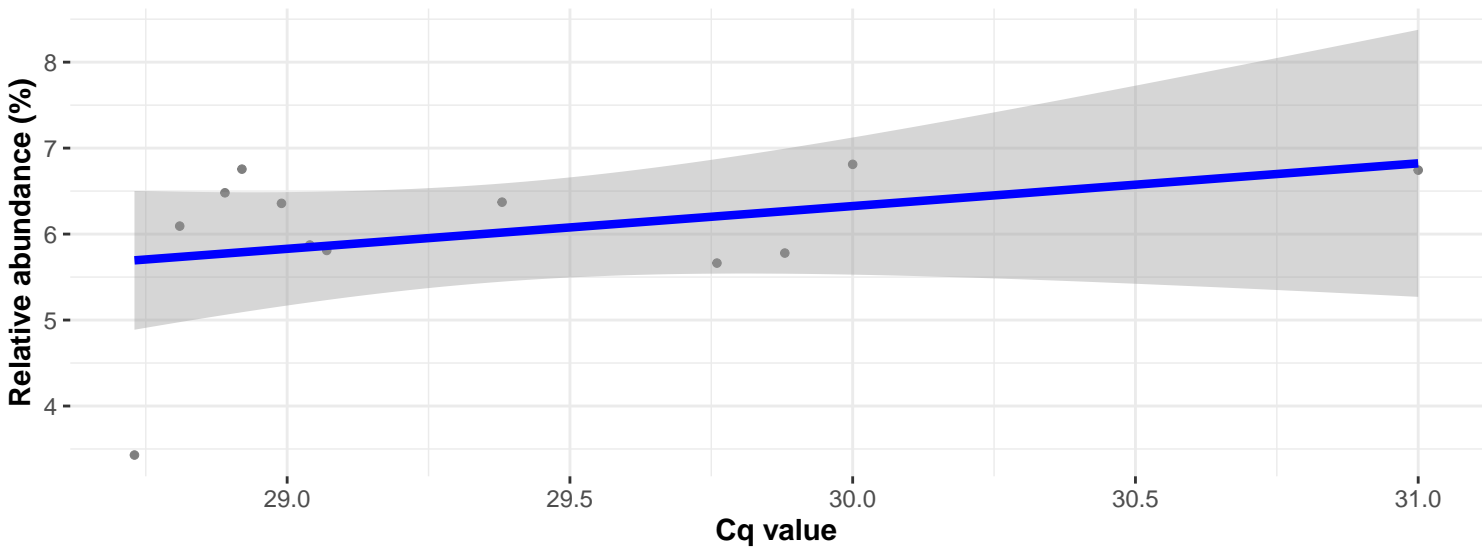
Correlation within: IM-PIM

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

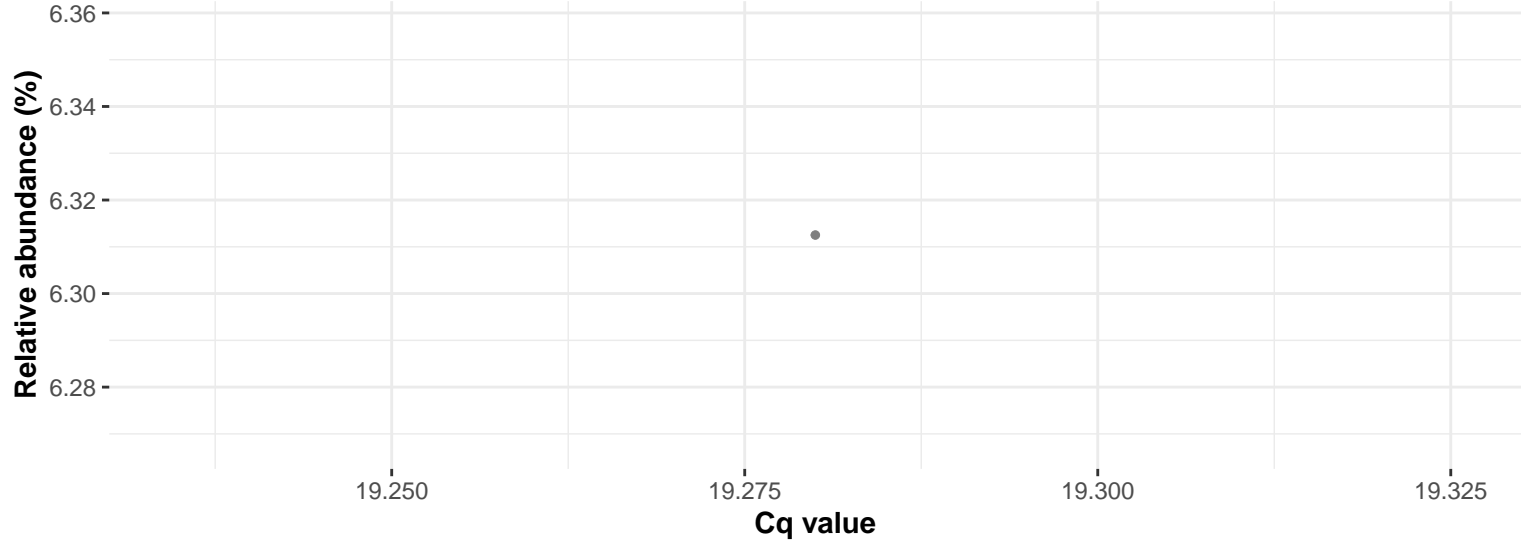


Correlation within: IM-DIM

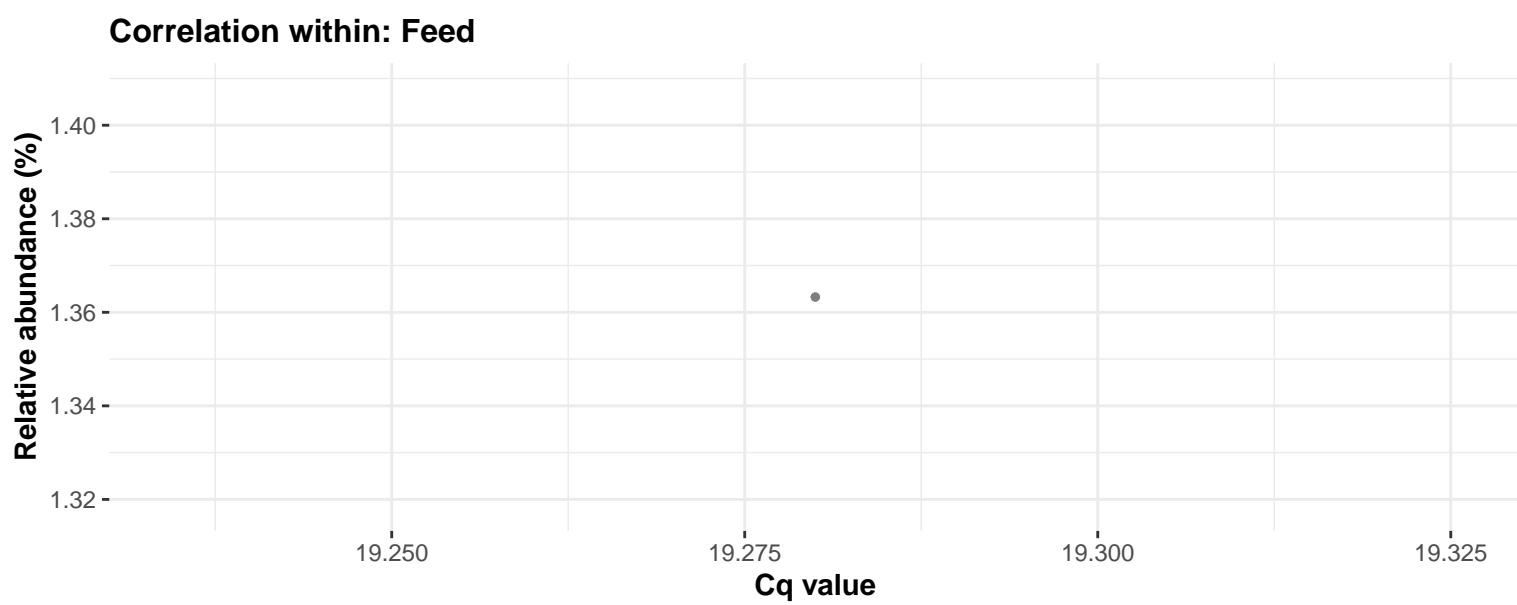
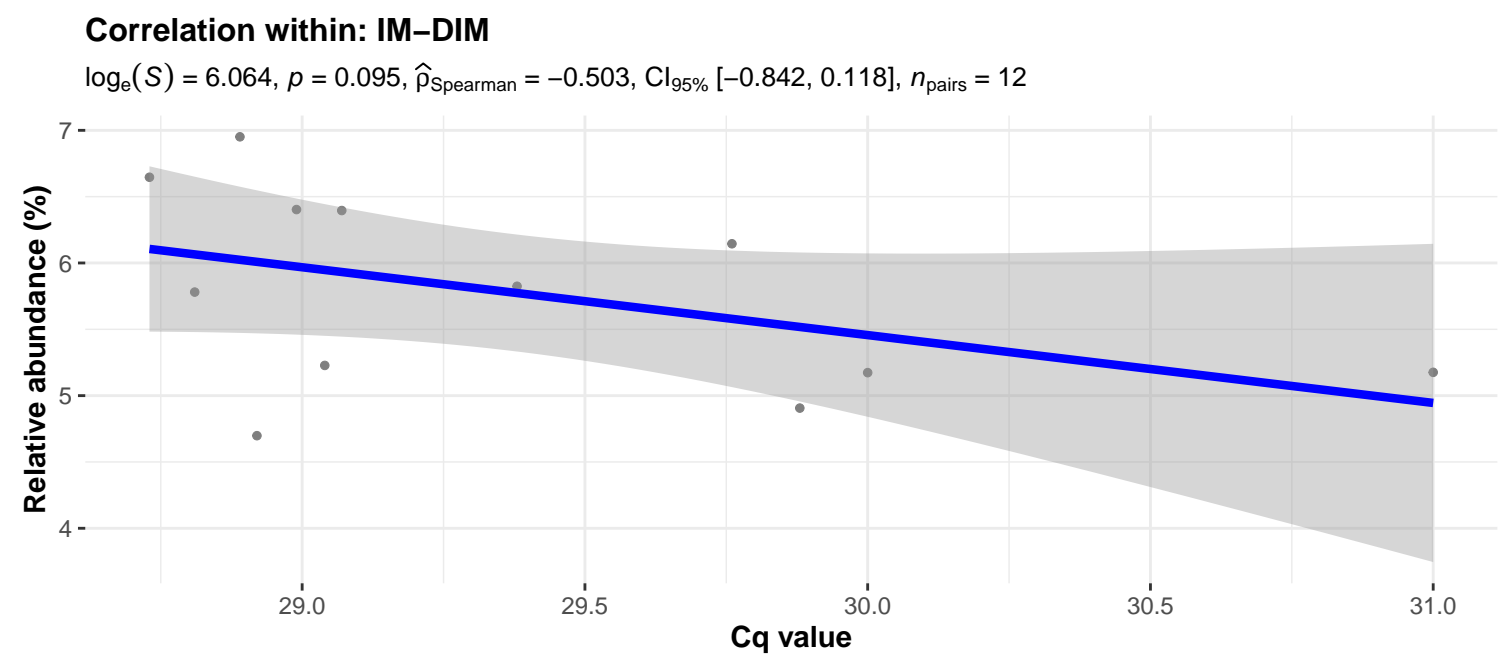
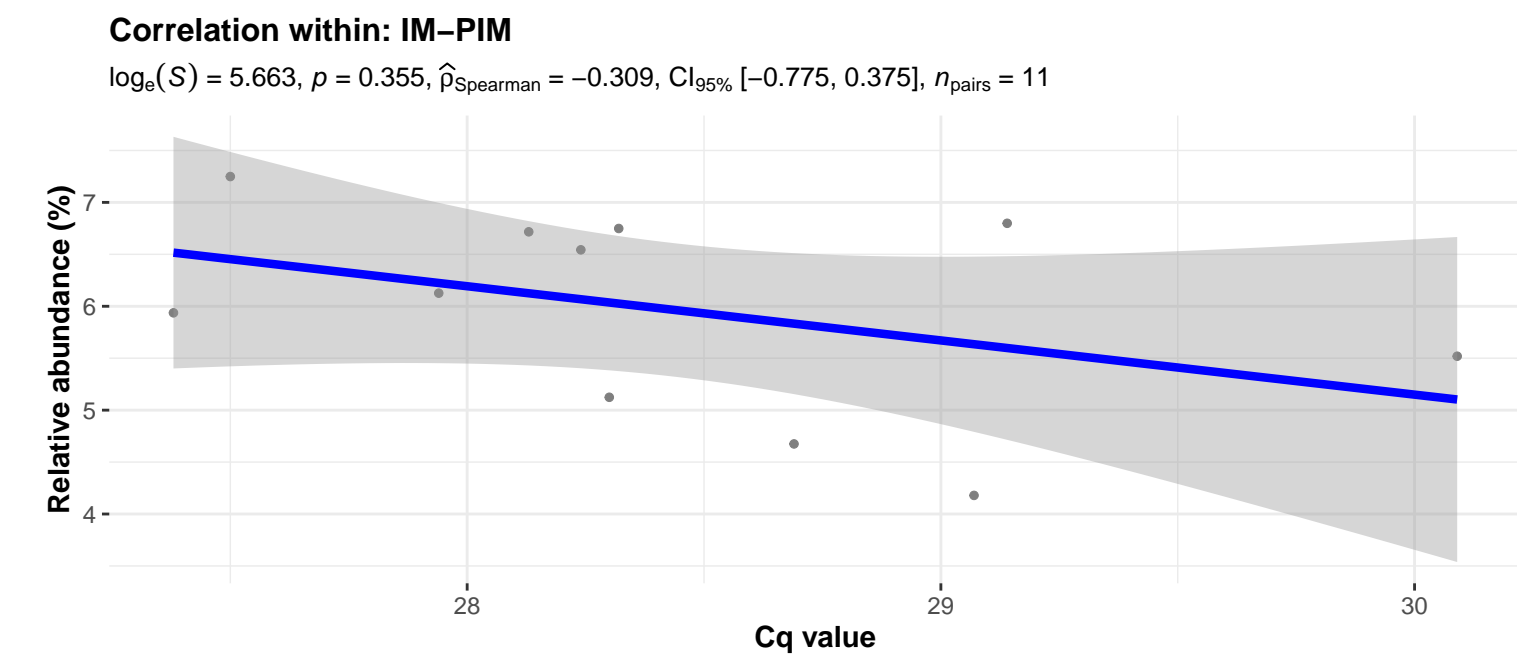
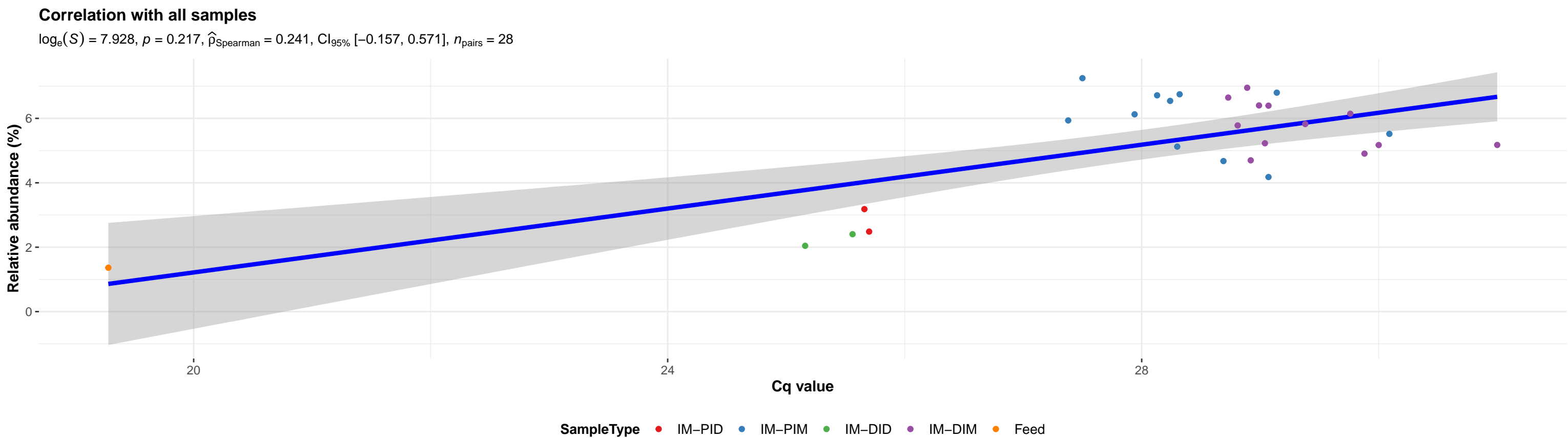
$\log_e(S) = 5.384$ ,  $p = 0.457$ ,  $\hat{\rho}_{\text{Spearman}} = 0.238$ ,  $CI_{95\%} [-0.406, 0.724]$ ,  $n_{\text{pairs}} = 12$



Correlation within: Feed



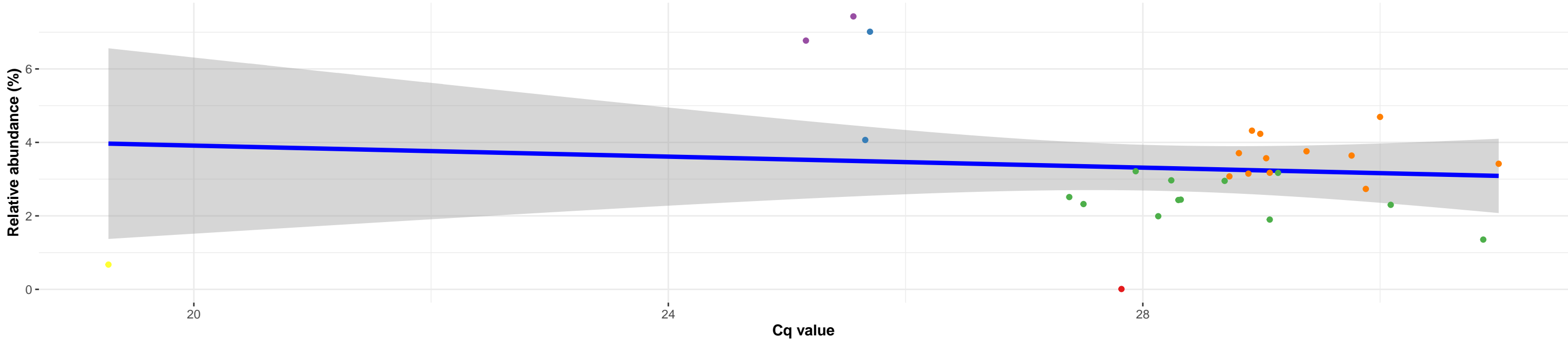
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; s\_\_Corynebacterium aurimucosum ATCC 700975



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; s\_\_Oceanobacillus caeni

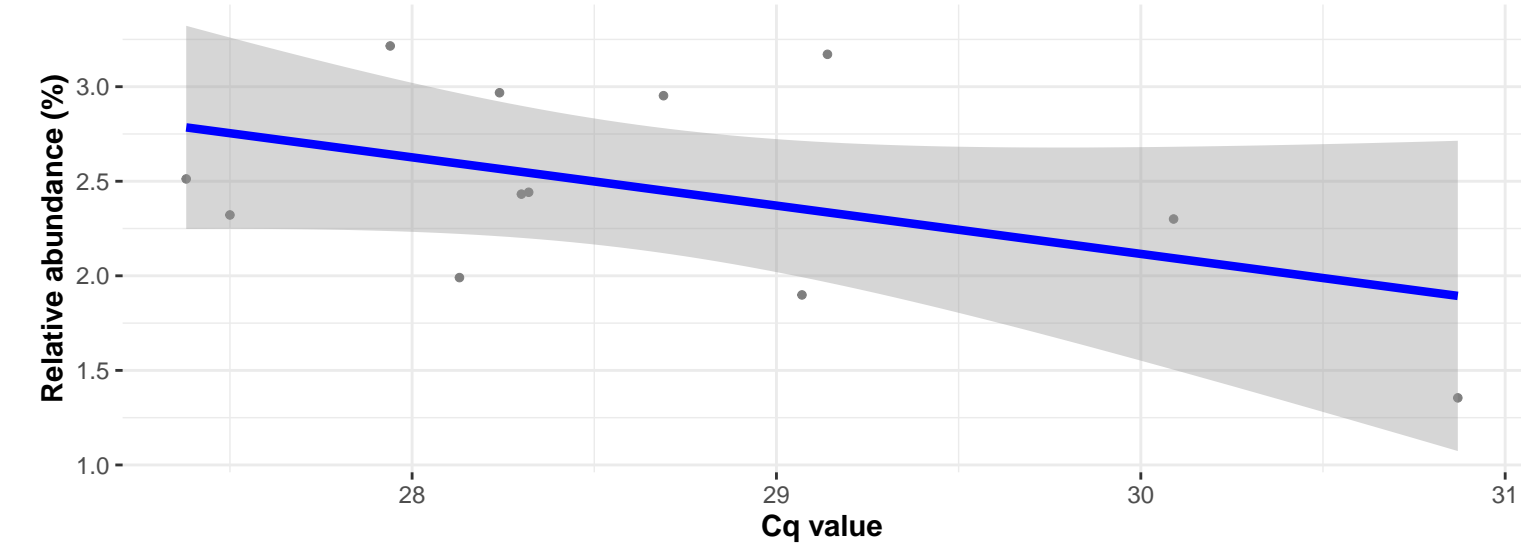
Correlation with all samples

$\log_e(S) = 8.441$ ,  $p = 0.872$ ,  $\hat{\rho}_{\text{Spearman}} = -0.031$ ,  $CI_{95\%} [-0.396, 0.343]$ ,  $n_{\text{pairs}} = 30$



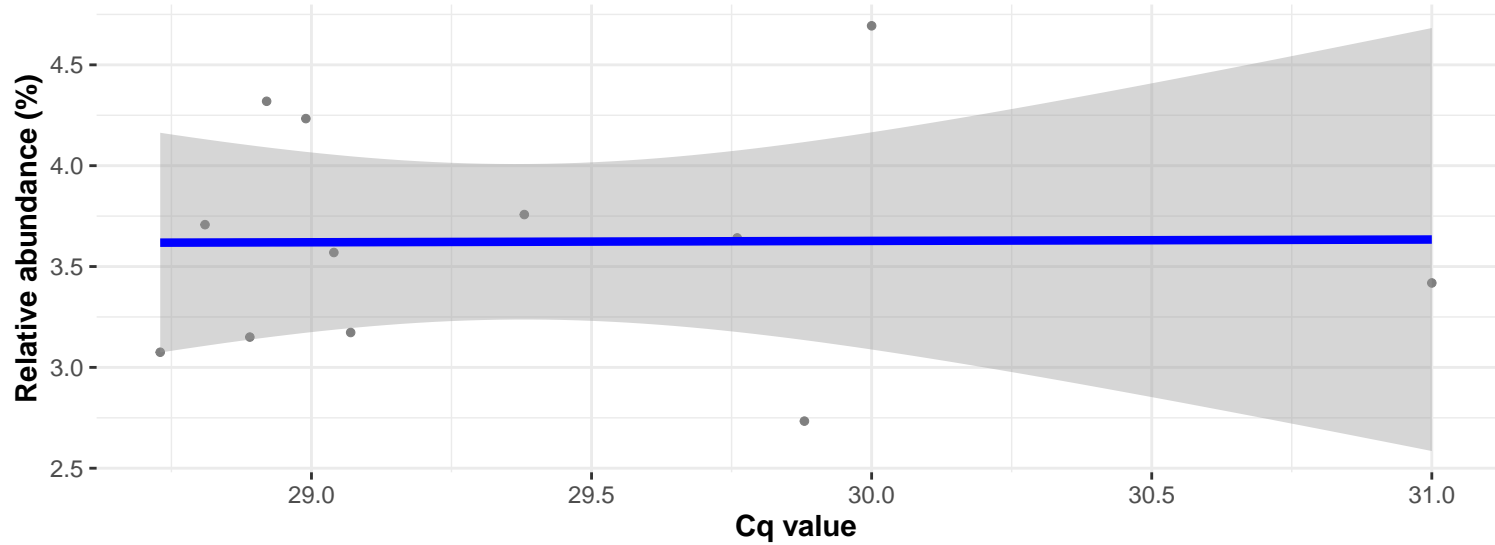
Correlation within: IM-PIM

$\log_e(S) = 5.956$ ,  $p = 0.265$ ,  $\hat{\rho}_{\text{Spearman}} = -0.350$ ,  $CI_{95\%} [-0.777, 0.298]$ ,  $n_{\text{pairs}} = 12$

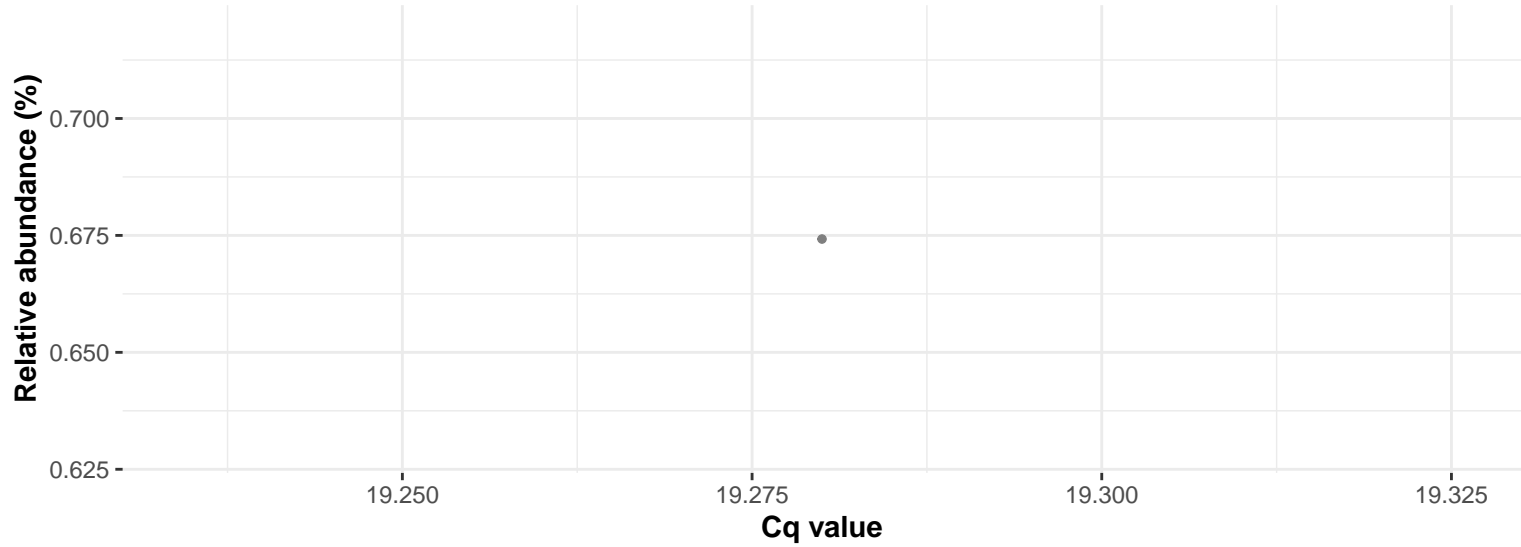


Correlation within: IM-DIM

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



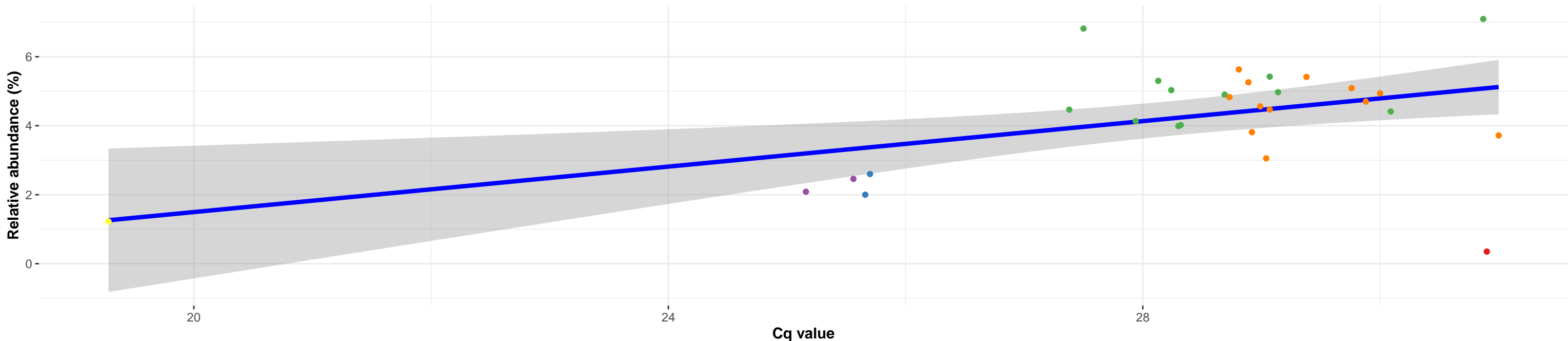
Correlation within: Feed



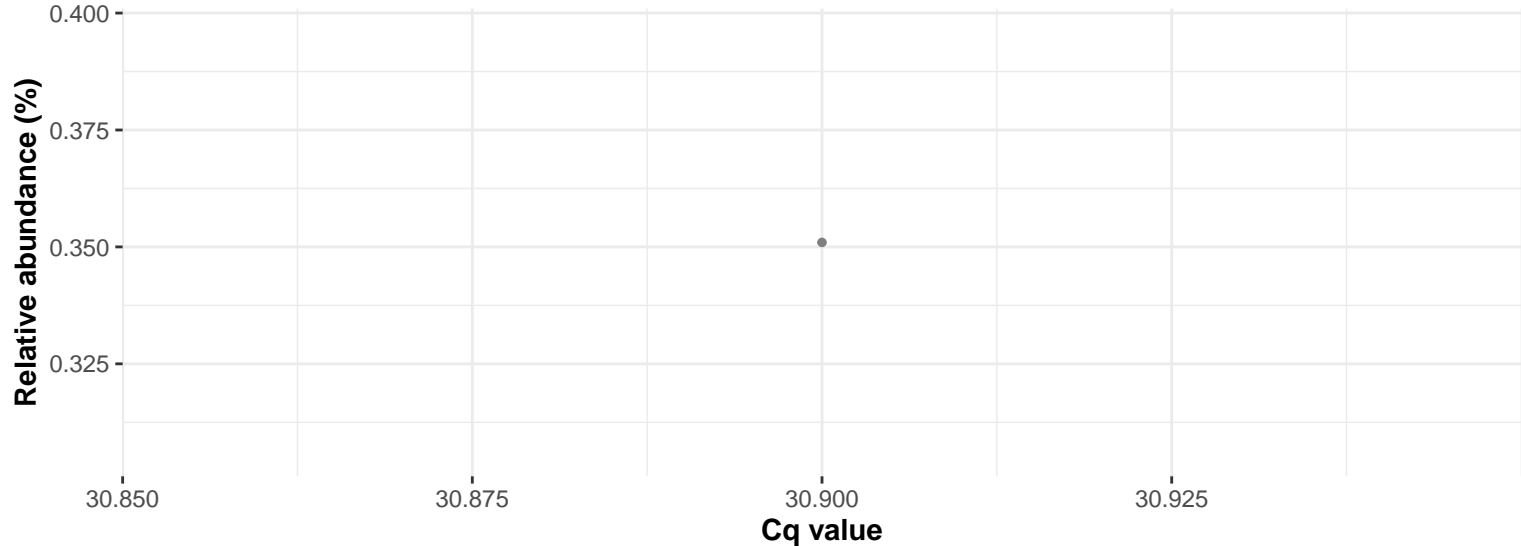
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

Correlation with all samples

$\log_e(S) = 8.047$ ,  $p = 0.102$ ,  $\hat{\rho}_{\text{Spearman}} = 0.305$ ,  $\text{CI}_{95\%} [-0.074, 0.606]$ ,  $n_{\text{pairs}} = 30$

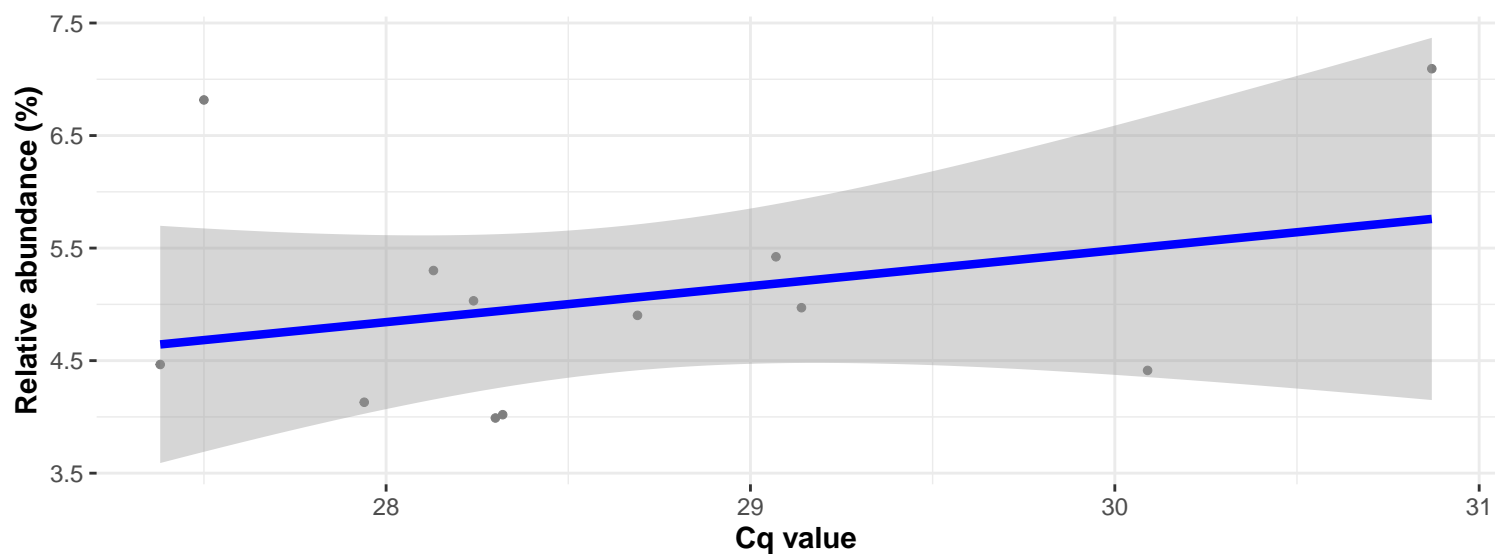


Correlation within: REF-PIM



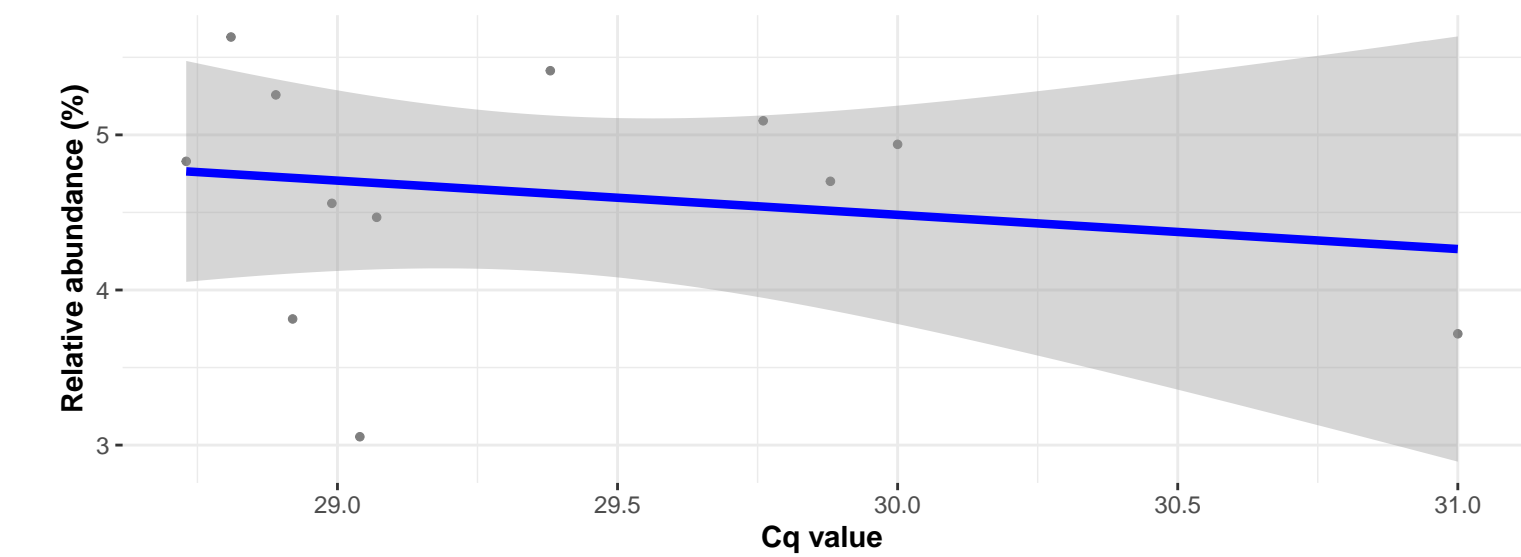
Correlation within: IM-PIM

$\log_e(S) = 5.497$ ,  $p = 0.649$ ,  $\hat{\rho}_{\text{Spearman}} = 0.147$ ,  $\text{CI}_{95\%} [-0.481, 0.675]$ ,  $n_{\text{pairs}} = 12$

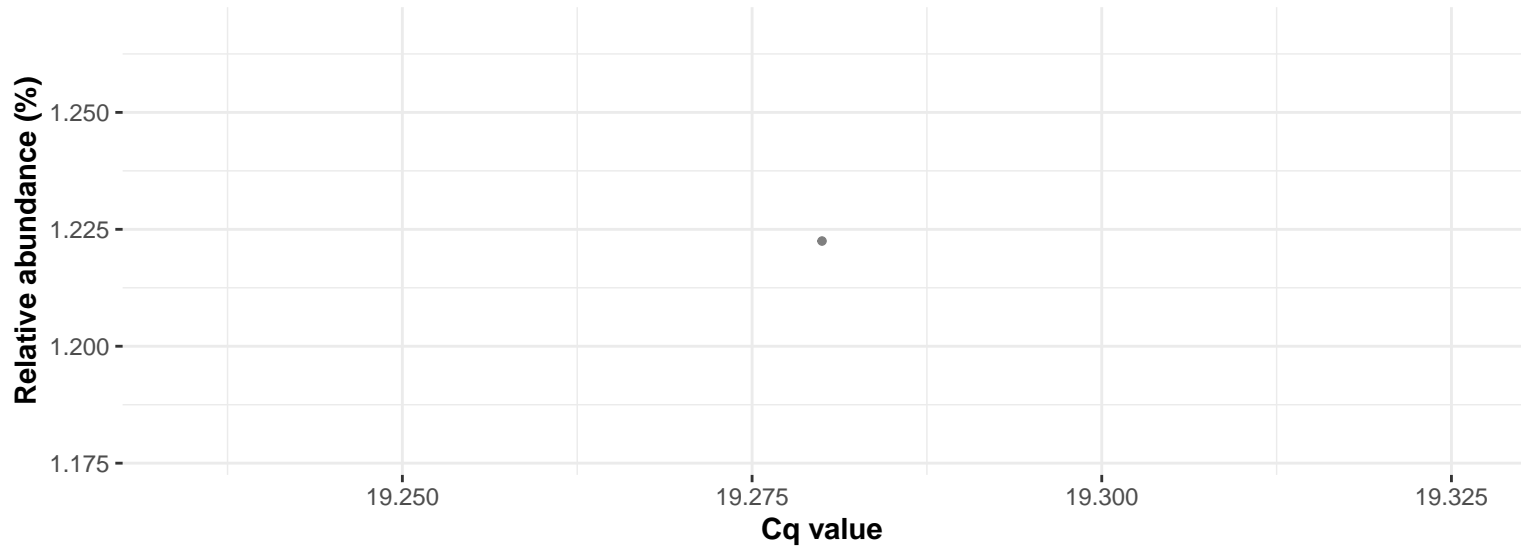


Correlation within: IM-DIM

$\log_e(S) = 5.869$ ,  $p = 0.457$ ,  $\hat{\rho}_{\text{Spearman}} = -0.238$ ,  $\text{CI}_{95\%} [-0.724, 0.406]$ ,  $n_{\text{pairs}} = 12$



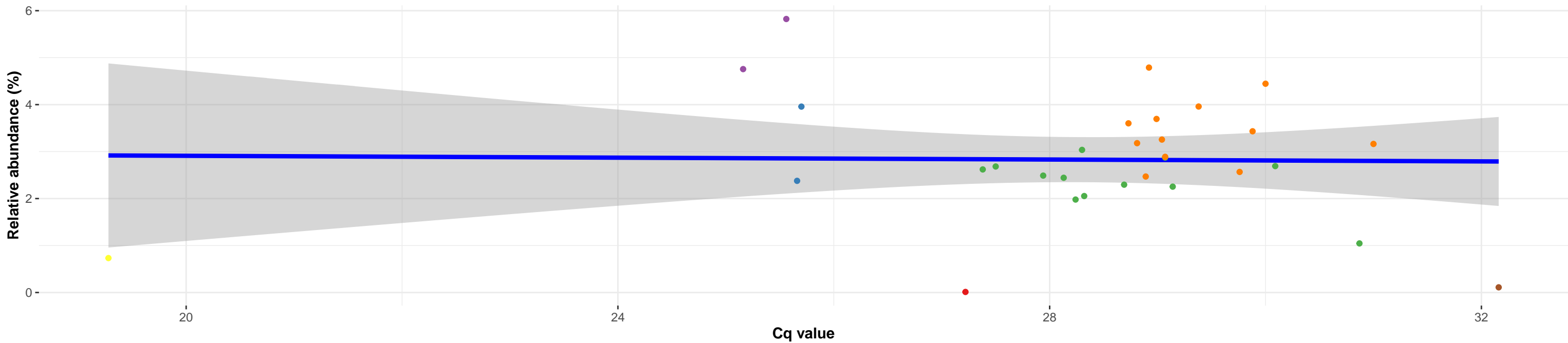
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; Ambiguous\_taxa

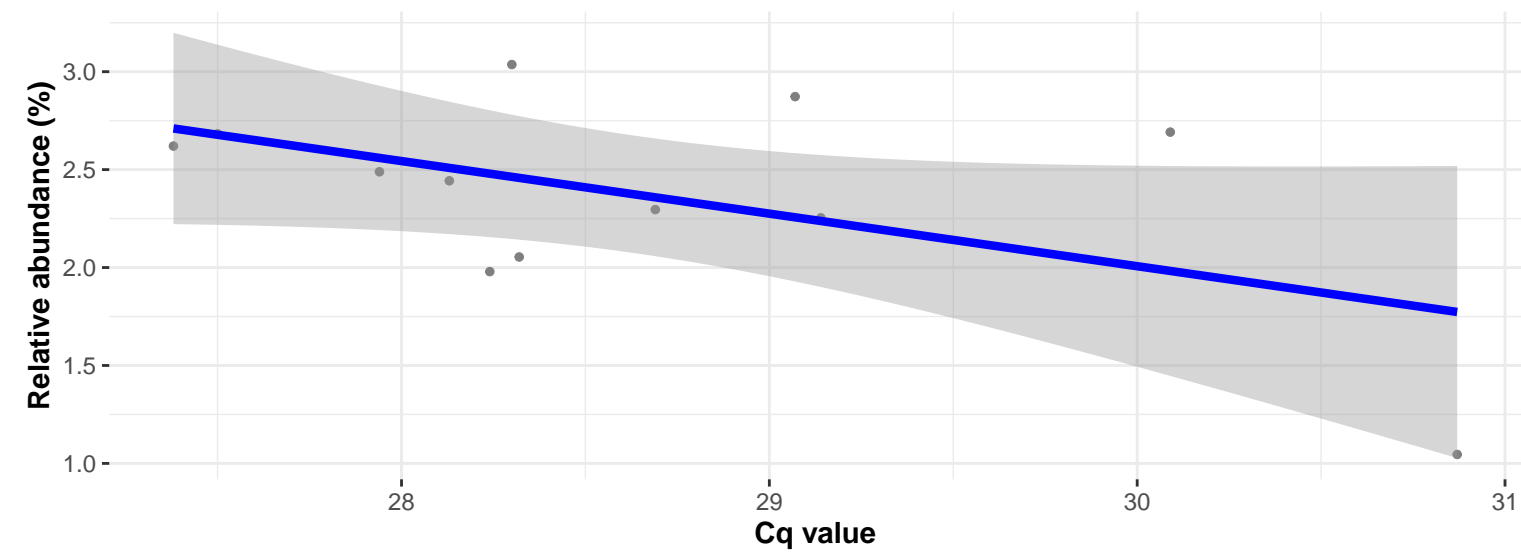
Correlation with all samples

$\log_e(S) = 8.471$ ,  $p = 0.840$ ,  $\hat{\rho}_{\text{Spearman}} = 0.038$ ,  $CI_{95\%} [-0.331, 0.396]$ ,  $n_{\text{pairs}} = 31$



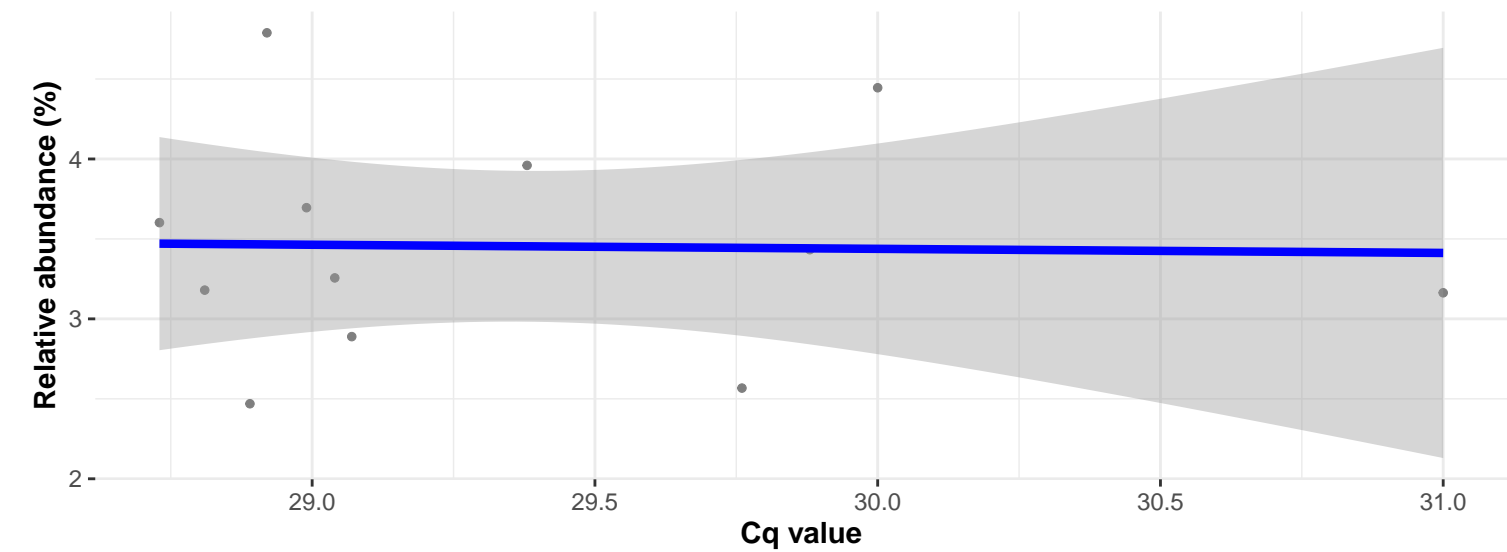
Correlation within: IM-PIM

$\log_e(S) = 5.858$ ,  $p = 0.484$ ,  $\hat{\rho}_{\text{Spearman}} = -0.224$ ,  $CI_{95\%} [-0.716, 0.418]$ ,  $n_{\text{pairs}} = 12$

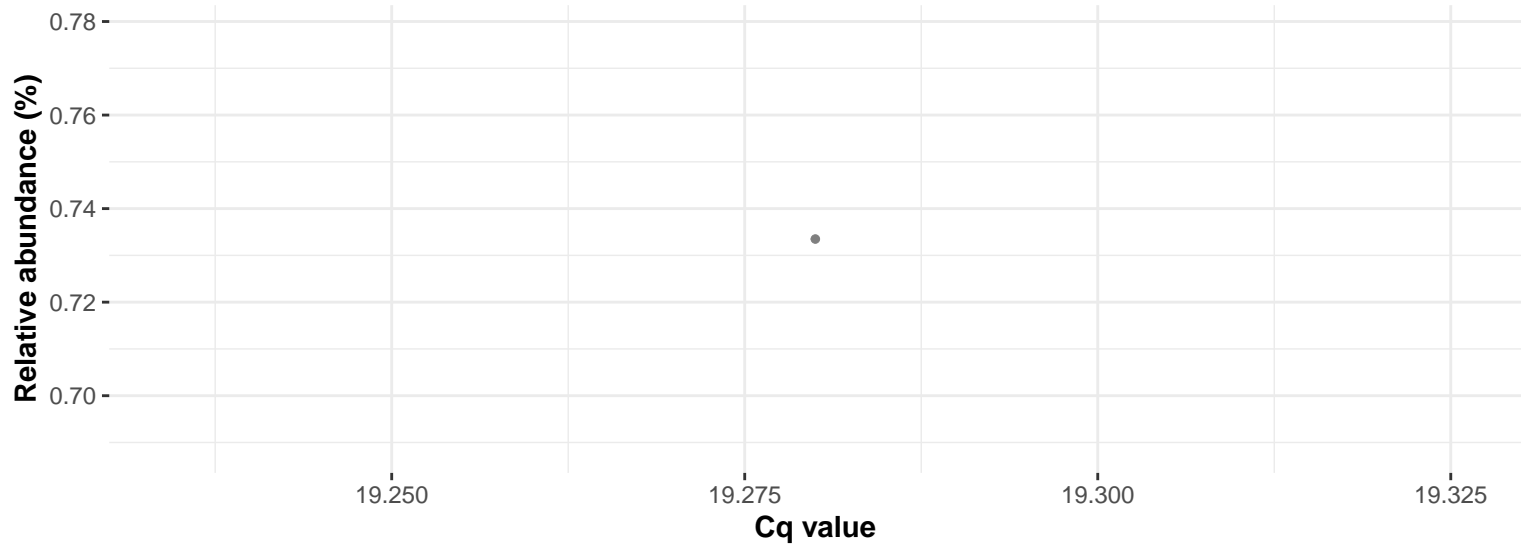


Correlation within: IM-DIM

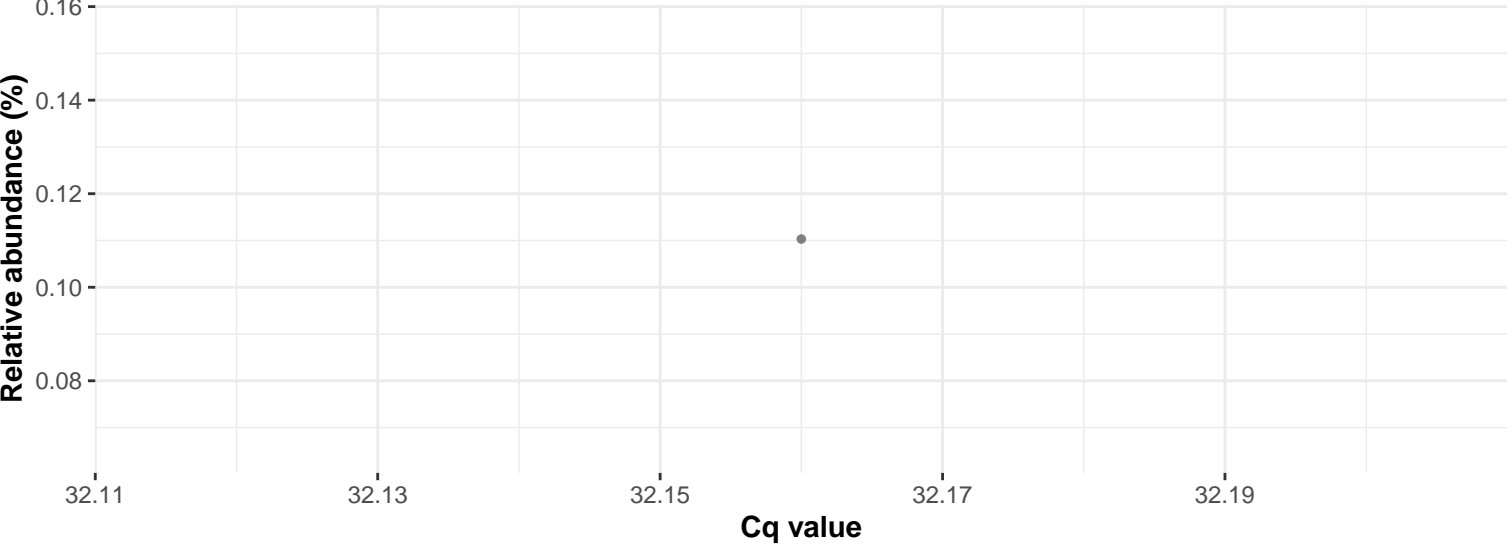
$\log_e(S) = 5.649$ ,  $p = 0.983$ ,  $\hat{\rho}_{\text{Spearman}} = 0.007$ ,  $CI_{95\%} [-0.582, 0.591]$ ,  $n_{\text{pairs}} = 12$



Correlation within: Feed



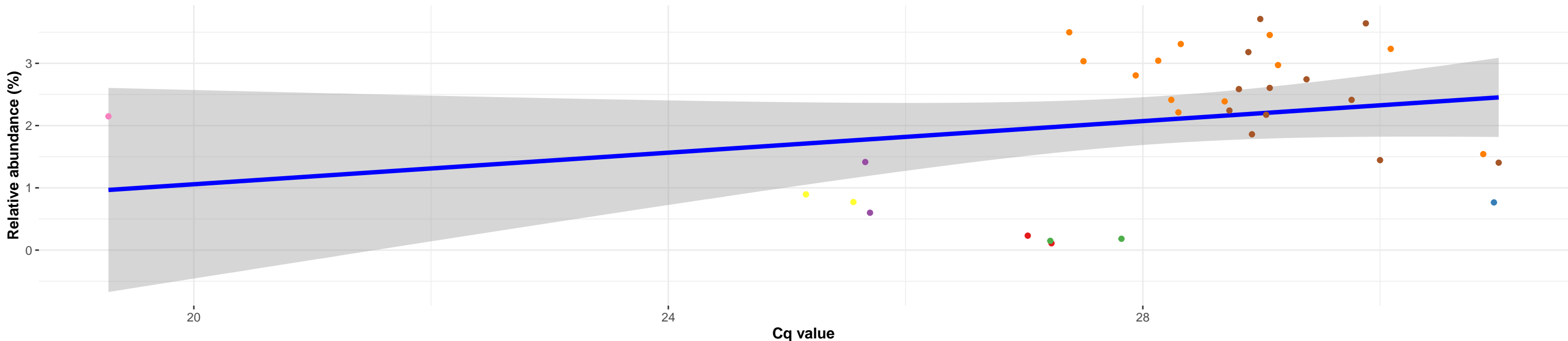
Correlation within: Water



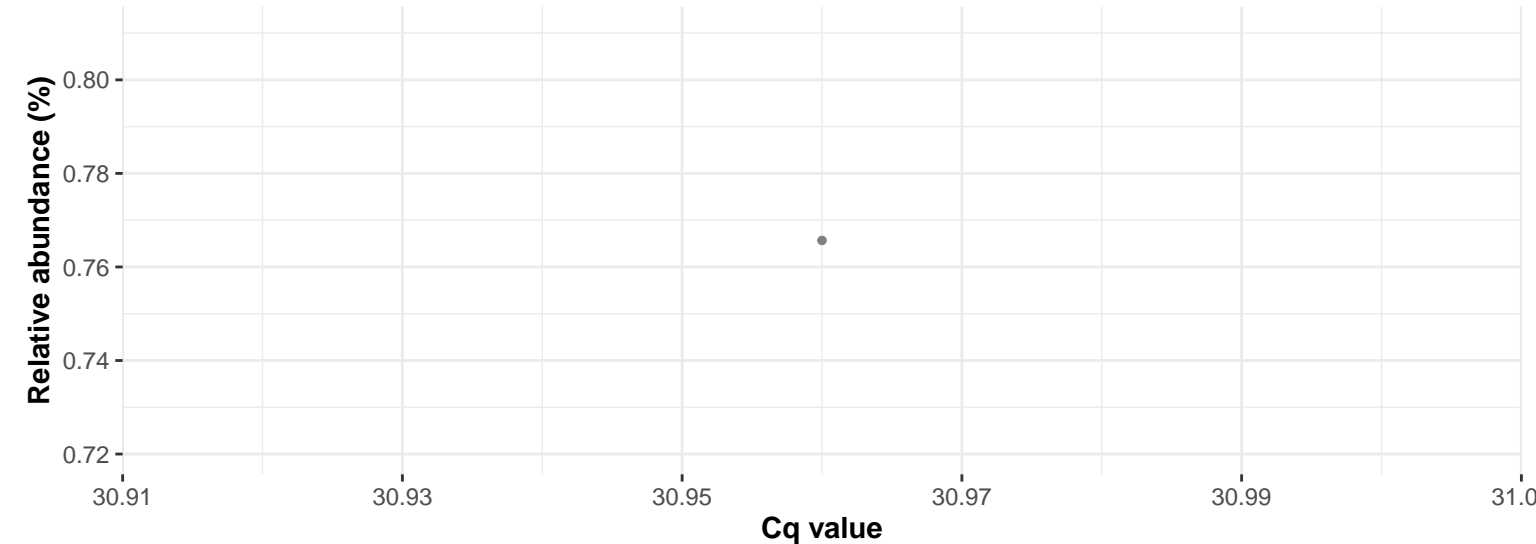
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Brevibacteriaceae; g\_\_Brevibacterium; NA

Correlation with all samples

$\log_e(S) = 8.379$ ,  $p = 0.053$ ,  $\hat{\rho}_{\text{Spearman}} = 0.335$ ,  $\text{CI}_{95\%} [-0.014, 0.611]$ ,  $n_{\text{pairs}} = 34$

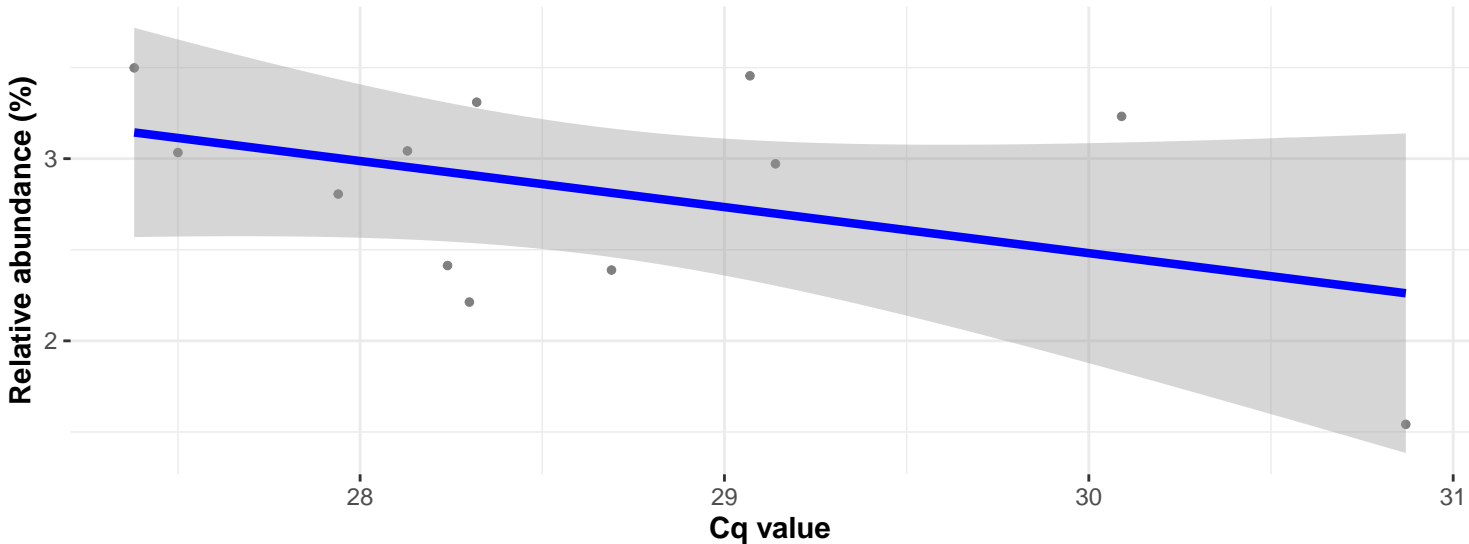


Correlation within: REF-PIM



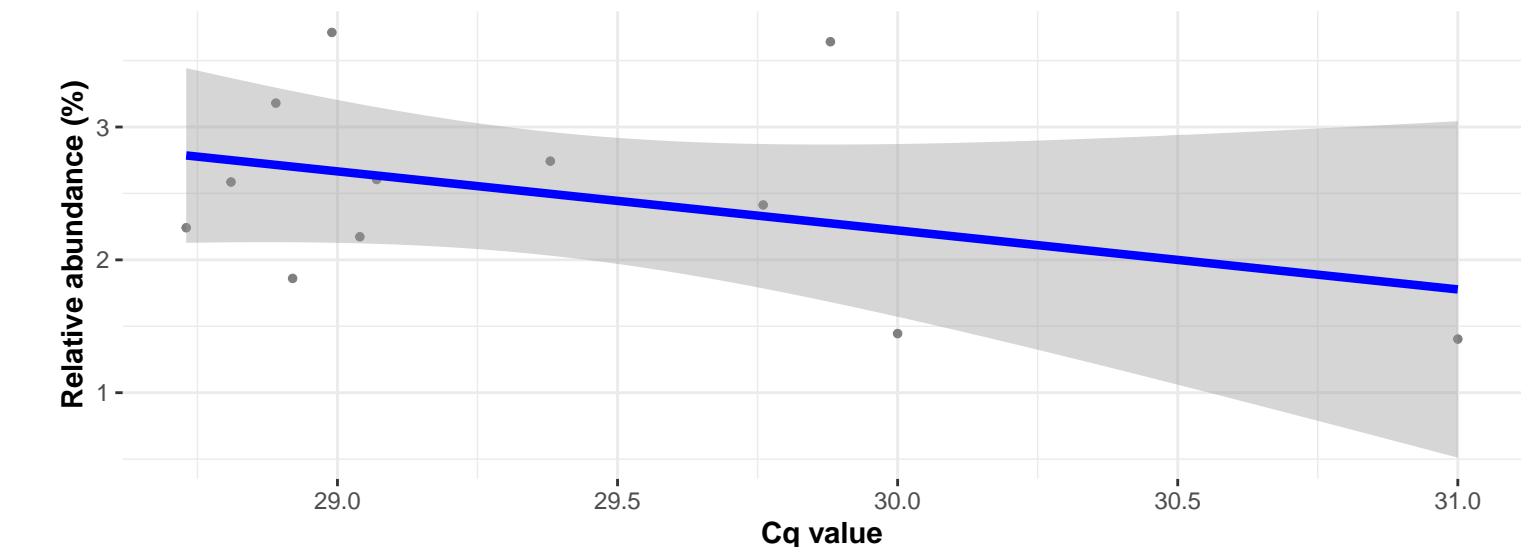
Correlation within: IM-PIM

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

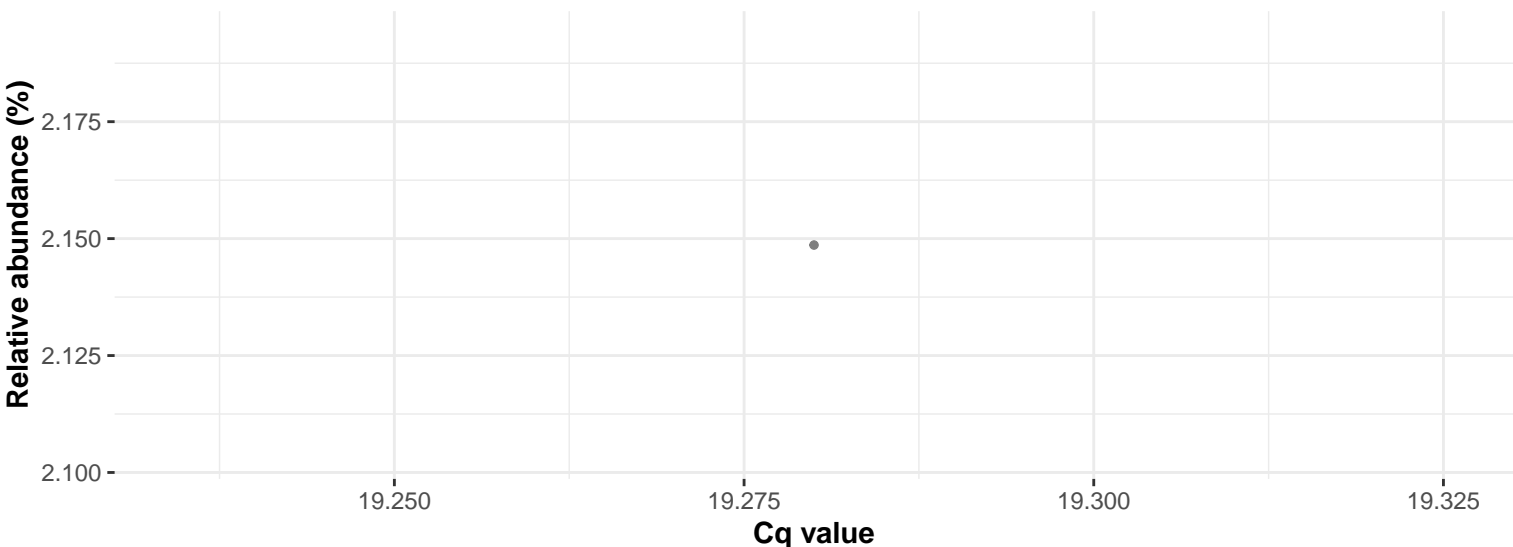


Correlation within: IM-DIM

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



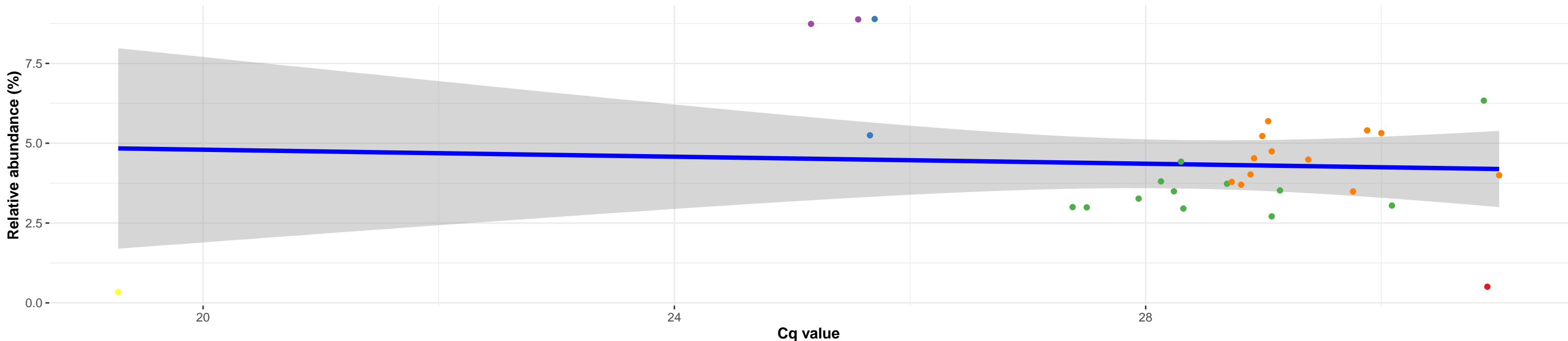
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; s\_\_Oceanobacillus caeni

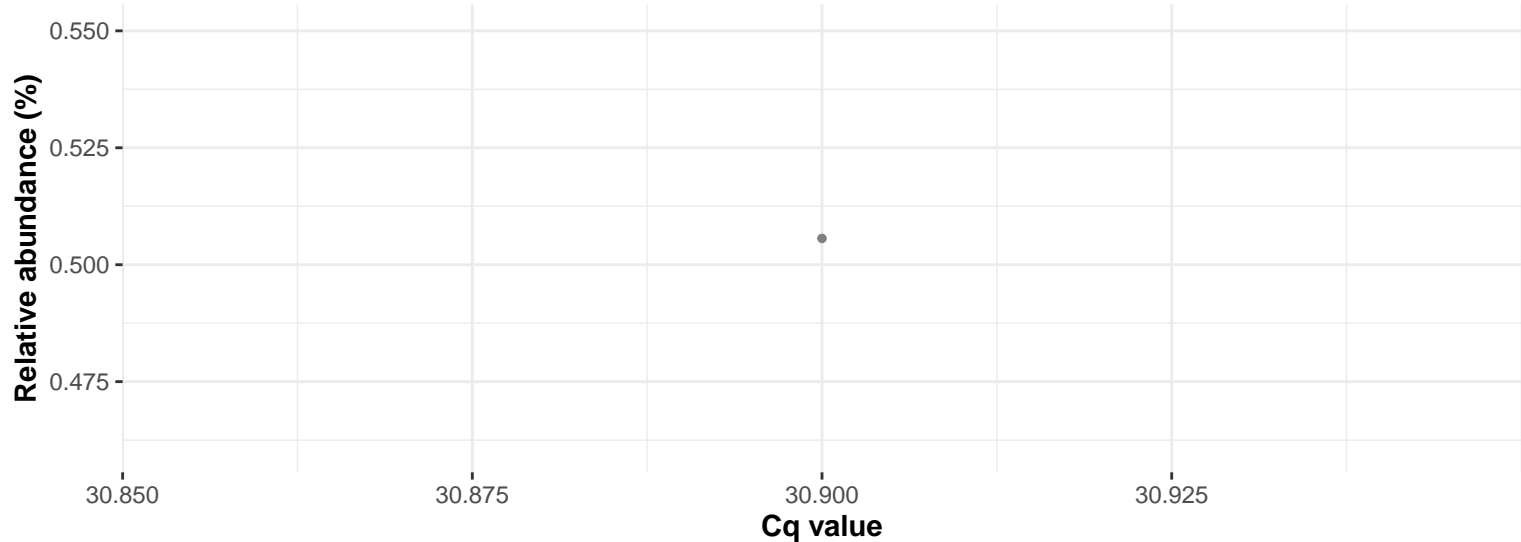
Correlation with all samples

$\log_e(S) = 8.428$ ,  $p = 0.927$ ,  $\hat{\rho}_{\text{Spearman}} = -0.018$ ,  $\text{CI}_{95\%} [-0.385, 0.355]$ ,  $n_{\text{pairs}} = 30$



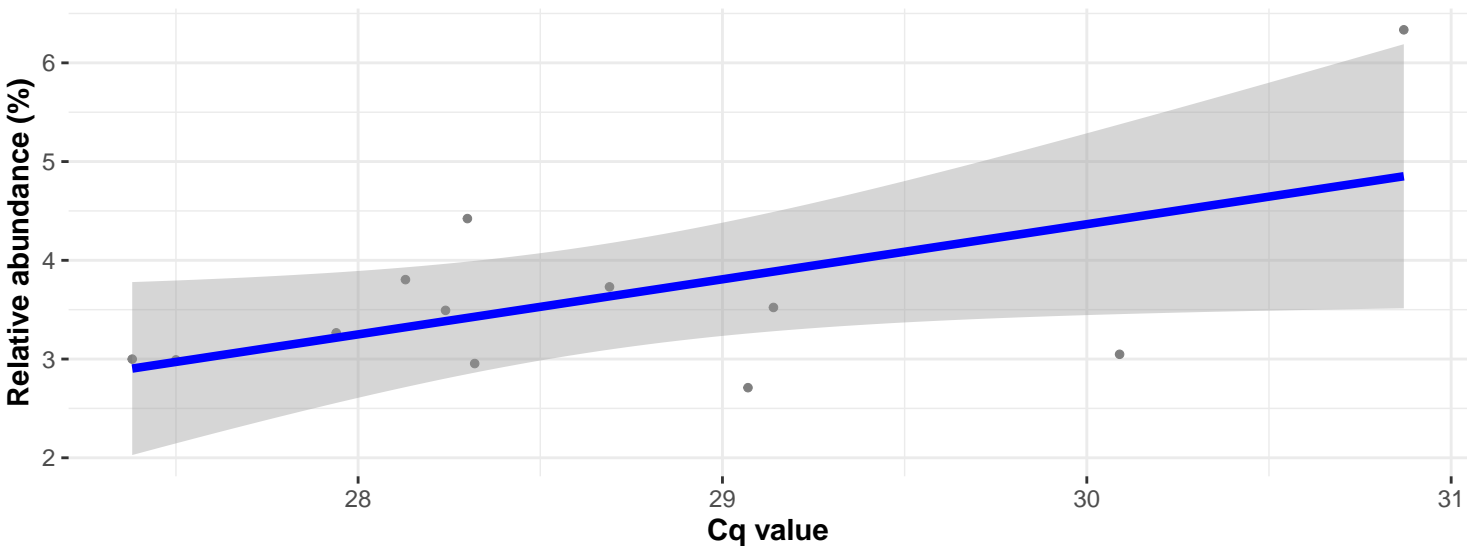
SampleType REF-PIM IM-PID IM-PIM IM-DID IM-DIM Feed

Correlation within: REF-PIM



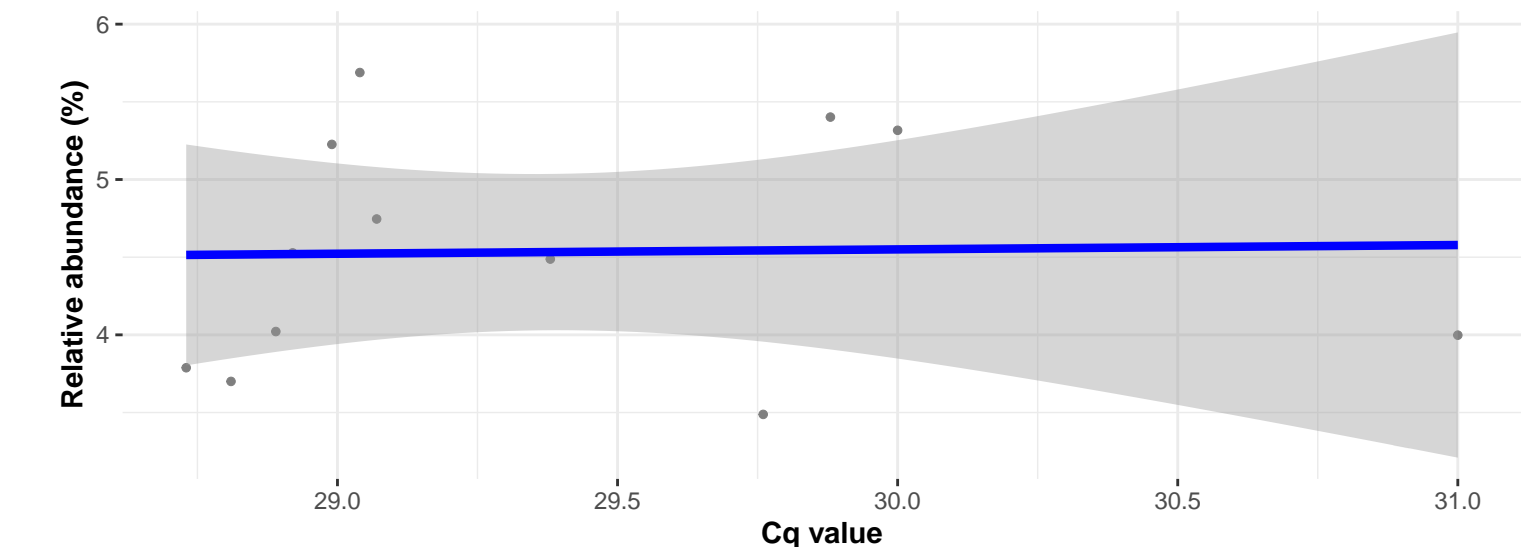
Correlation within: IM-PIM

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

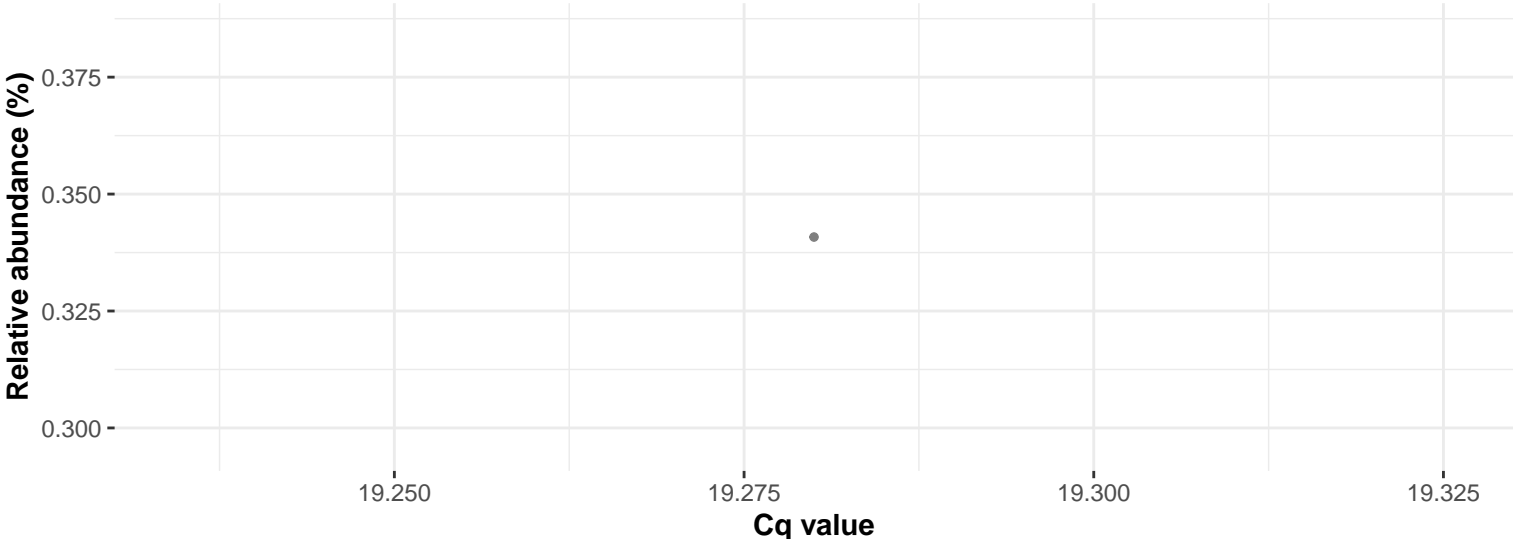


Correlation within: IM-DIM

$\log_e(S) = 5.318$ ,  $p = 0.366$ ,  $\hat{\rho}_{\text{Spearman}} = 0.287$ ,  $\text{CI}_{95\%} [-0.361, 0.748]$ ,  $n_{\text{pairs}} = 12$



Correlation within: Feed

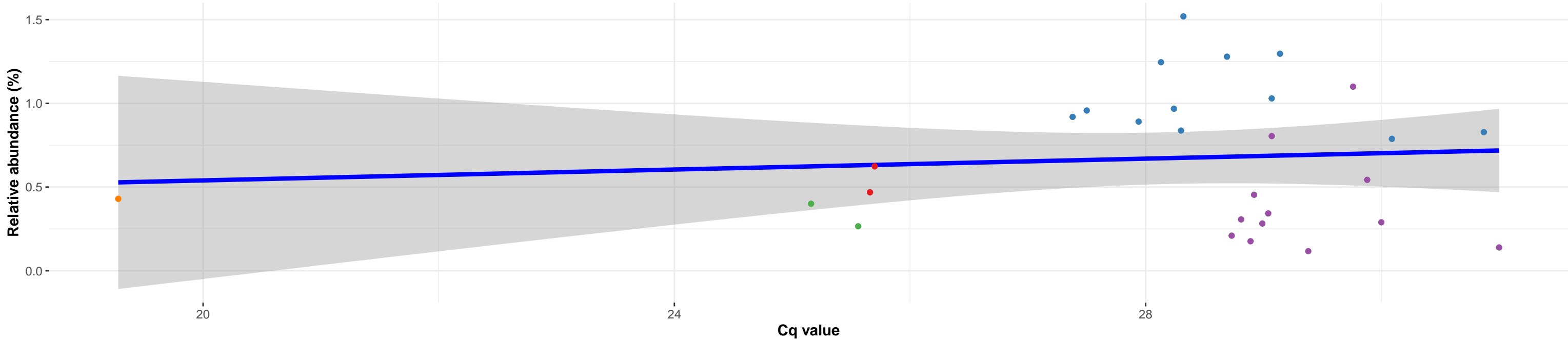




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; NA

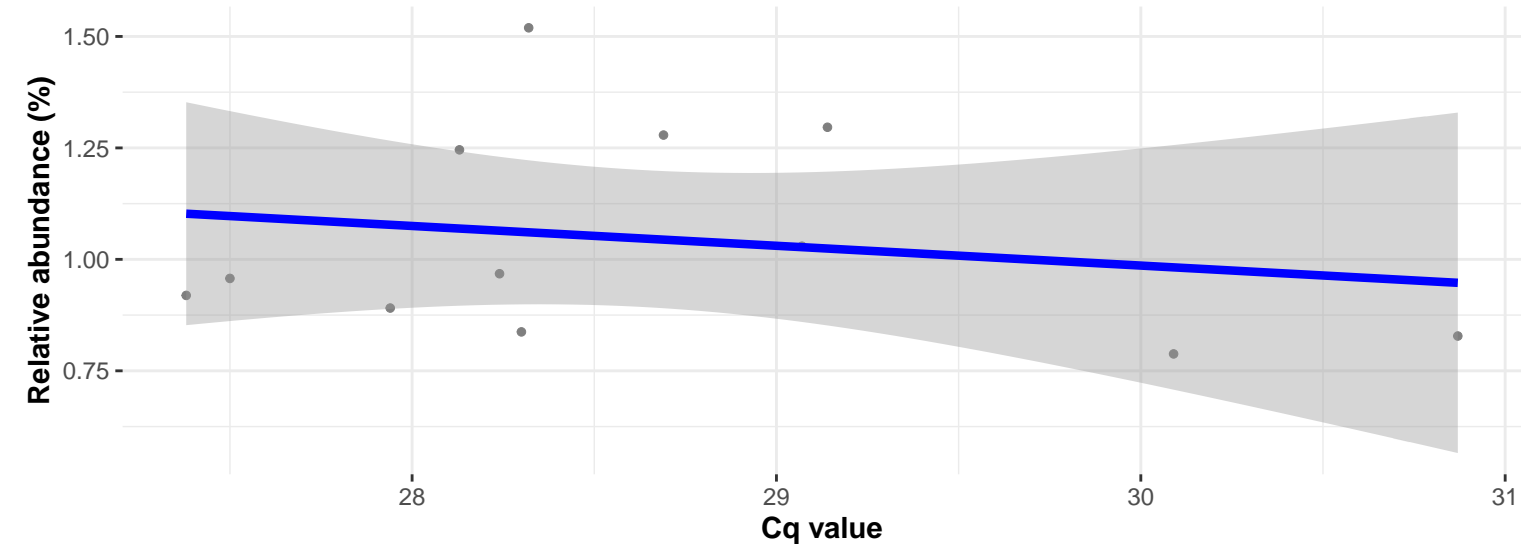
Correlation with all samples

$\log_e(S) = 8.415$ ,  $p = 0.563$ ,  $\hat{\rho}_{\text{Spearman}} = -0.112$ ,  $CI_{95\%} [-0.469, 0.276]$ ,  $n_{\text{pairs}} = 29$



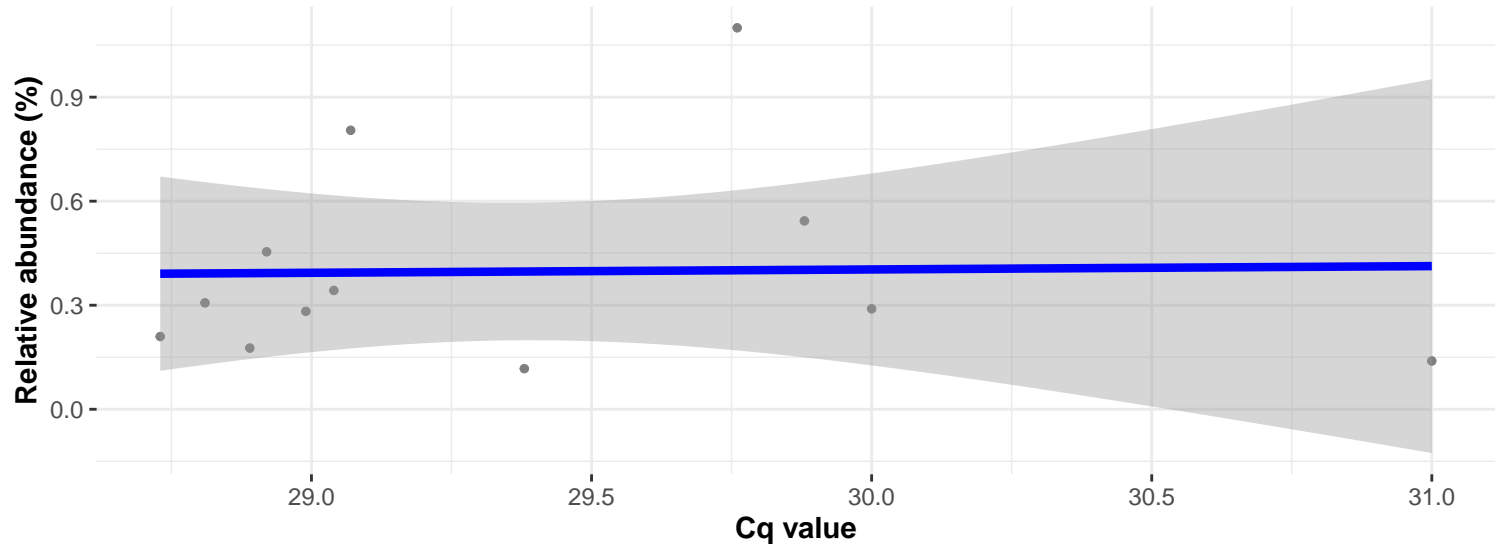
Correlation within: IM-PIM

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

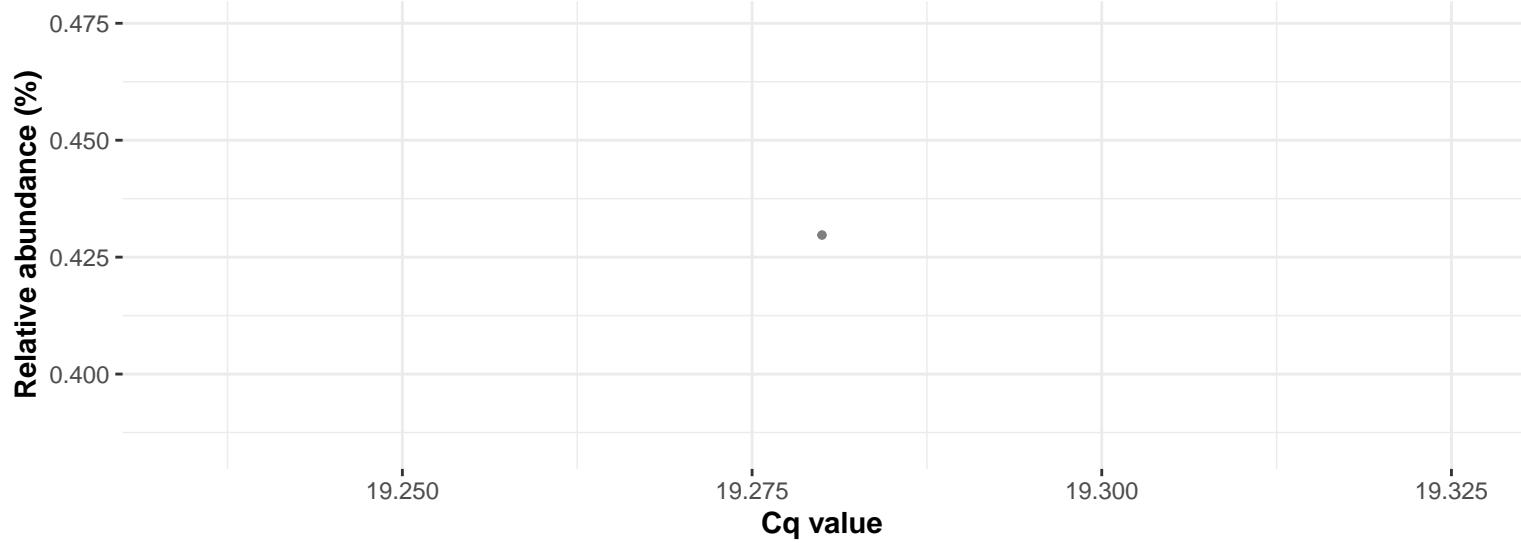


Correlation within: IM-DIM

$\log_e(S) = 5.568$ ,  $p = 0.795$ ,  $\hat{\rho}_{\text{Spearman}} = 0.084$ ,  $CI_{95\%} [-0.529, 0.639]$ ,  $n_{\text{pairs}} = 12$



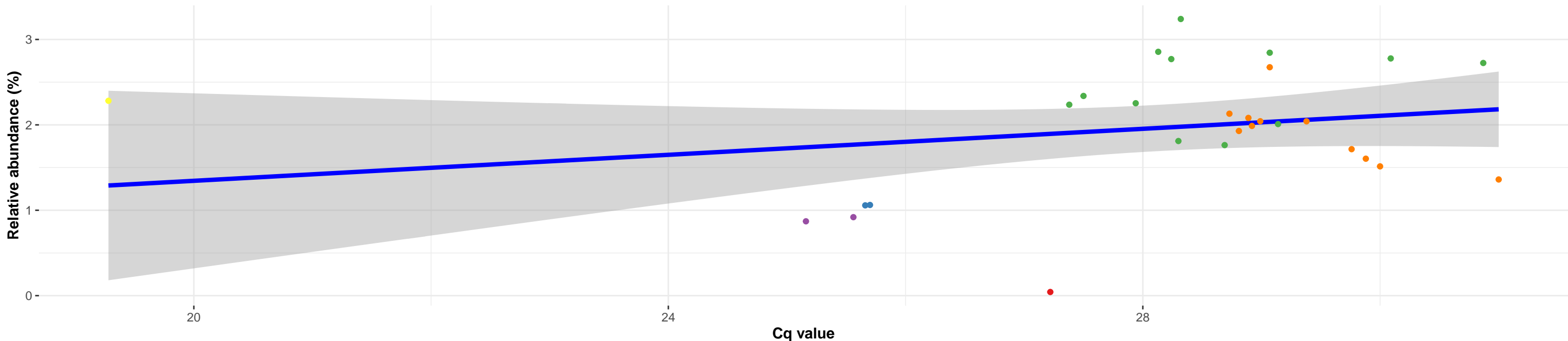
Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Beutenbergiaceae; NA; NA

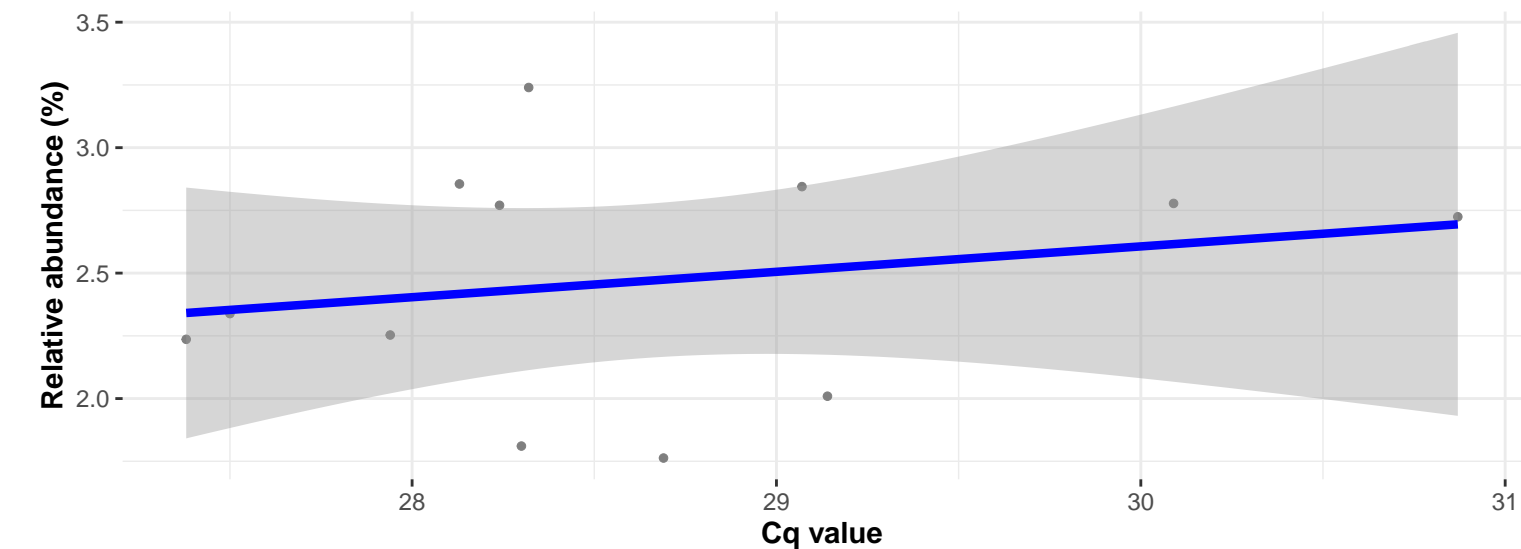
Correlation with all samples

$\log_e(S) = 8.113$ ,  $p = 0.355$ ,  $\hat{\rho}_{\text{Spearman}} = 0.178$ ,  $\text{CI}_{95\%} [-0.212, 0.520]$ ,  $n_{\text{pairs}} = 29$



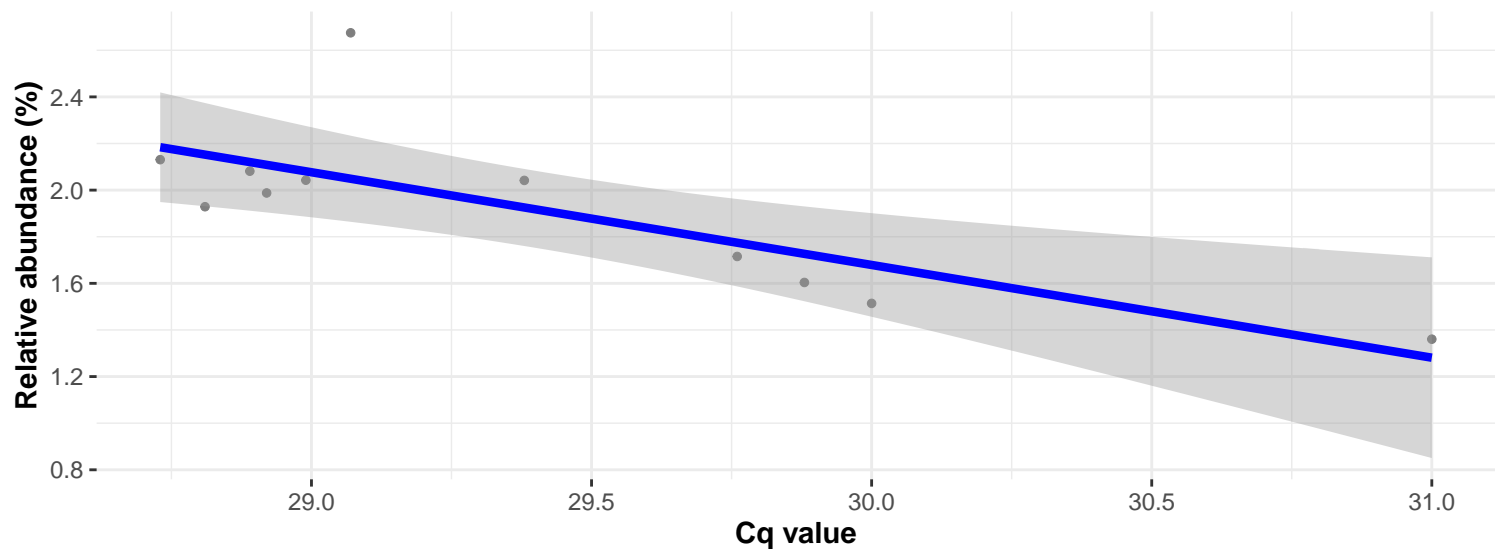
Correlation within: IM-PIM

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

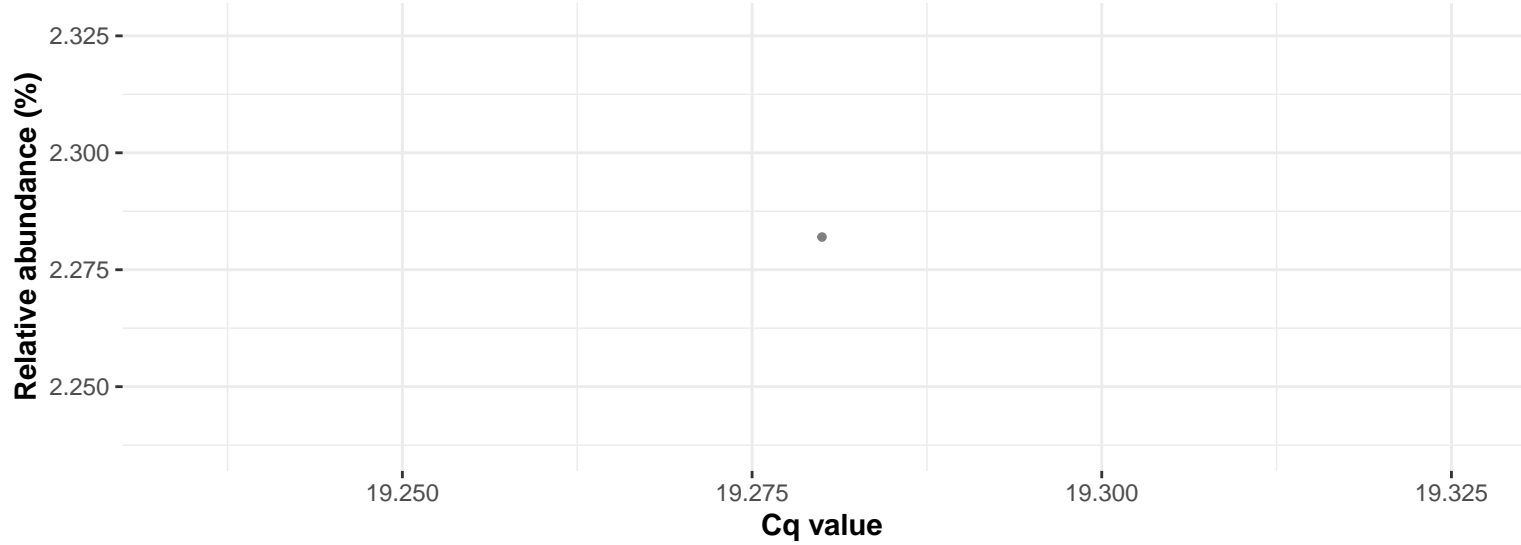


Correlation within: IM-DIM

$\log_e(S) = 5.940$ ,  $p = 0.011$ ,  $\hat{\rho}_{\text{Spearman}} = -0.727$ ,  $\text{CI}_{95\%} [-0.927, -0.206]$ ,  $n_{\text{pairs}} = 11$



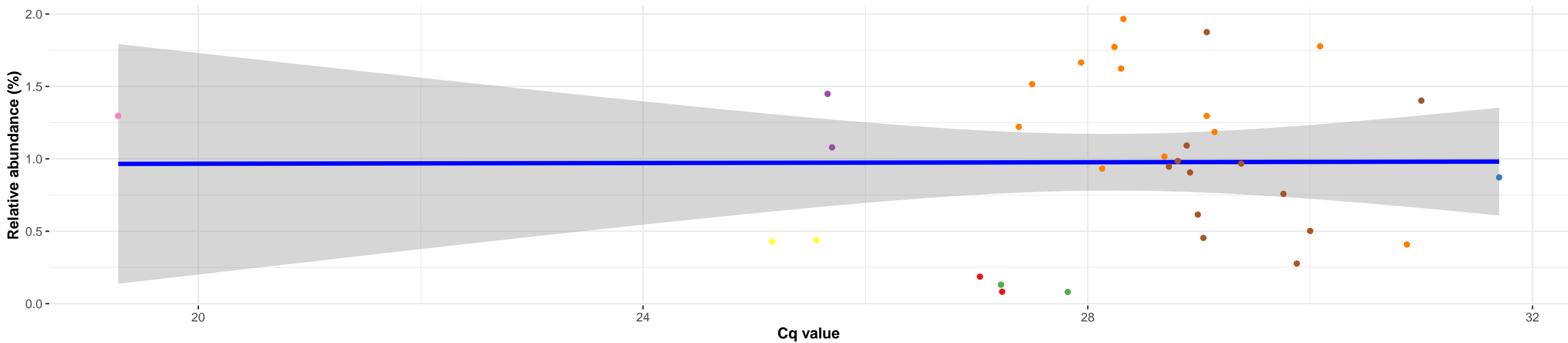
Correlation within: Feed



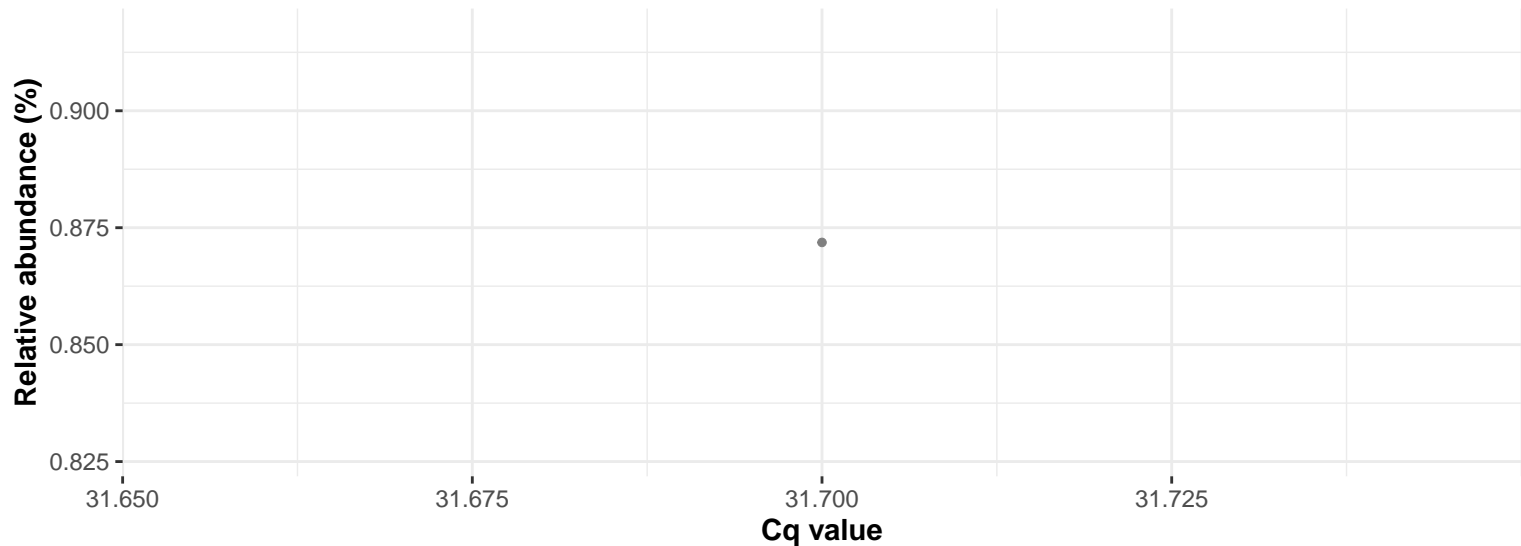
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Aerococcaceae; g\_\_Globicatella; Ambiguous\_taxa

Correlation with all samples

$\log_e(S) = 8.725$ ,  $p = 0.739$ ,  $\hat{\rho}_{\text{Spearman}} = 0.059$ ,  $CI_{95\%} [-0.294, 0.398]$ ,  $n_{\text{pairs}} = 34$

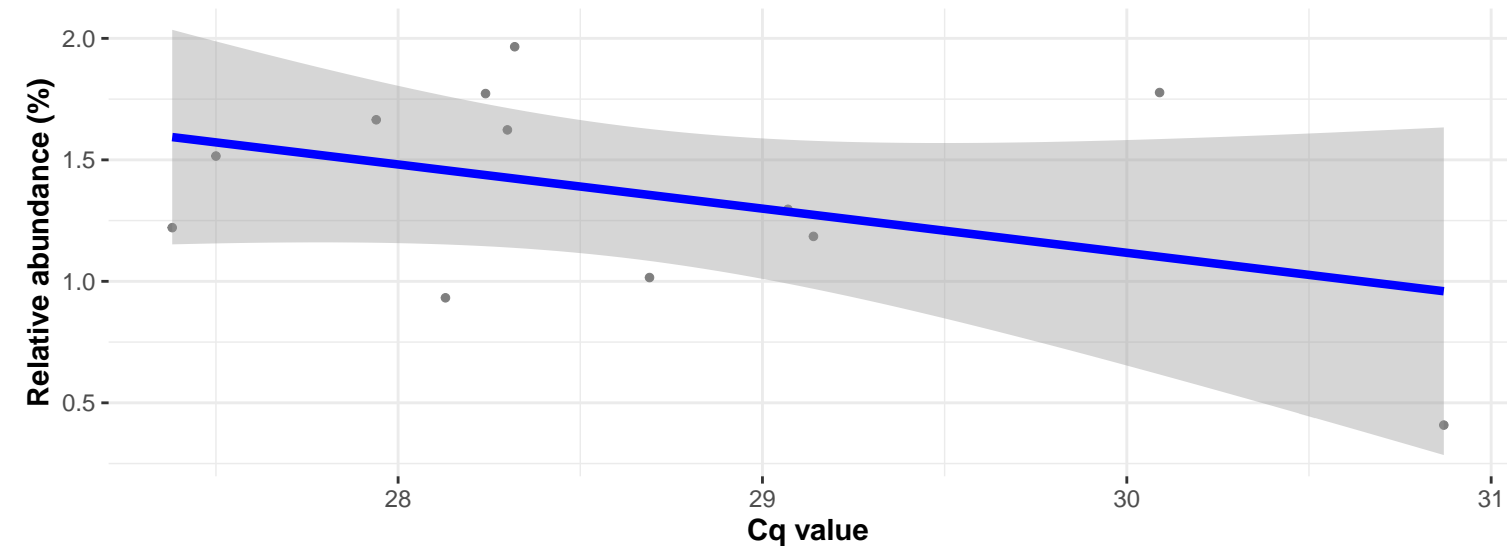


Correlation within: REF-PIM



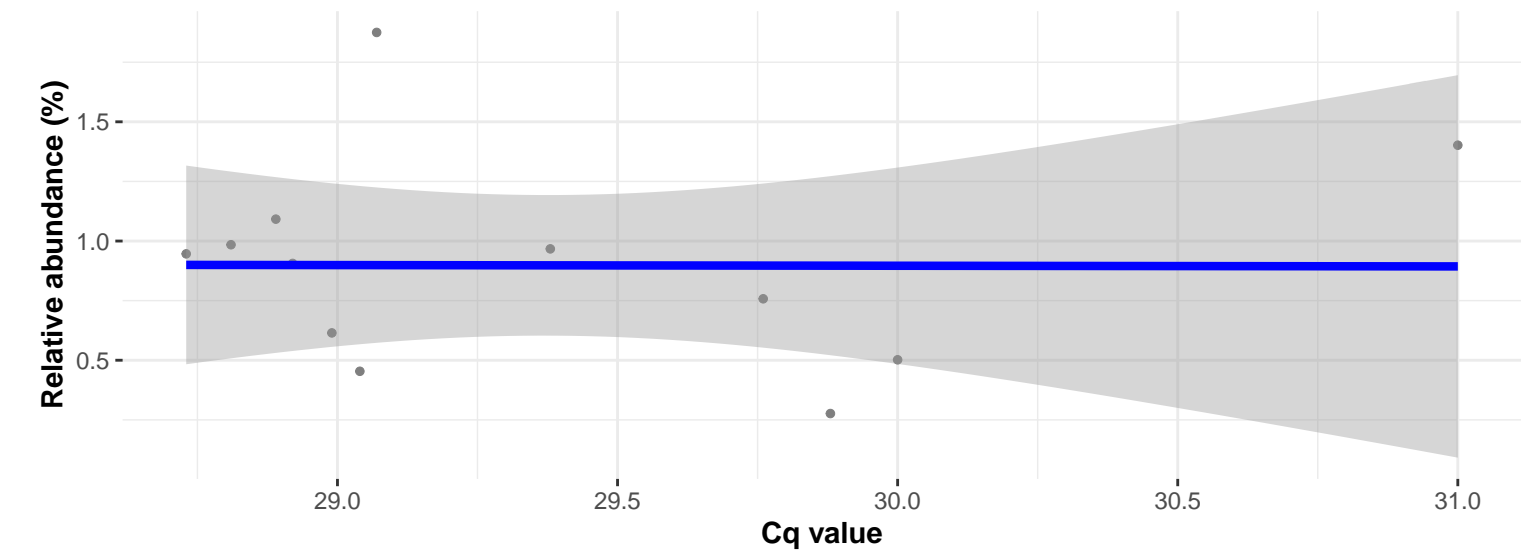
Correlation within: IM-PIM

$\log_e(S) = 5.787$ ,  $p = 0.665$ ,  $\hat{\rho}_{\text{Spearman}} = -0.140$ ,  $CI_{95\%} [-0.671, 0.487]$ ,  $n_{\text{pairs}} = 12$

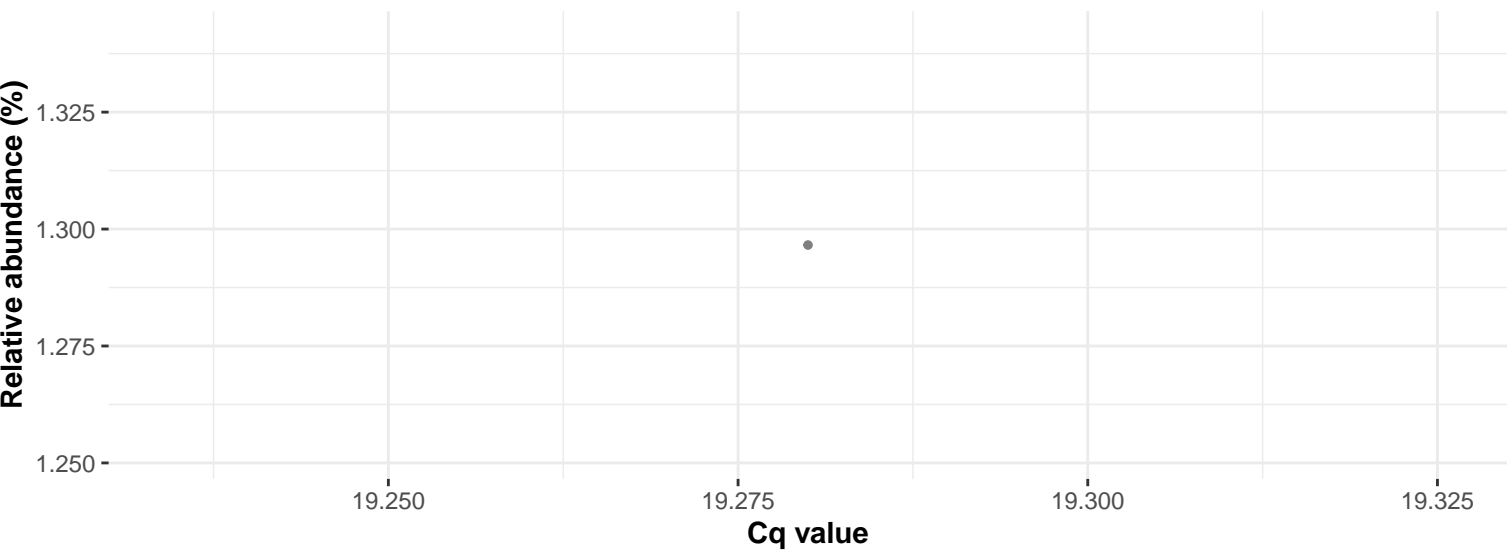


Correlation within: IM-DIM

$\log_e(S) = 5.835$ ,  $p = 0.542$ ,  $\hat{\rho}_{\text{Spearman}} = -0.196$ ,  $CI_{95\%} [-0.702, 0.442]$ ,  $n_{\text{pairs}} = 12$



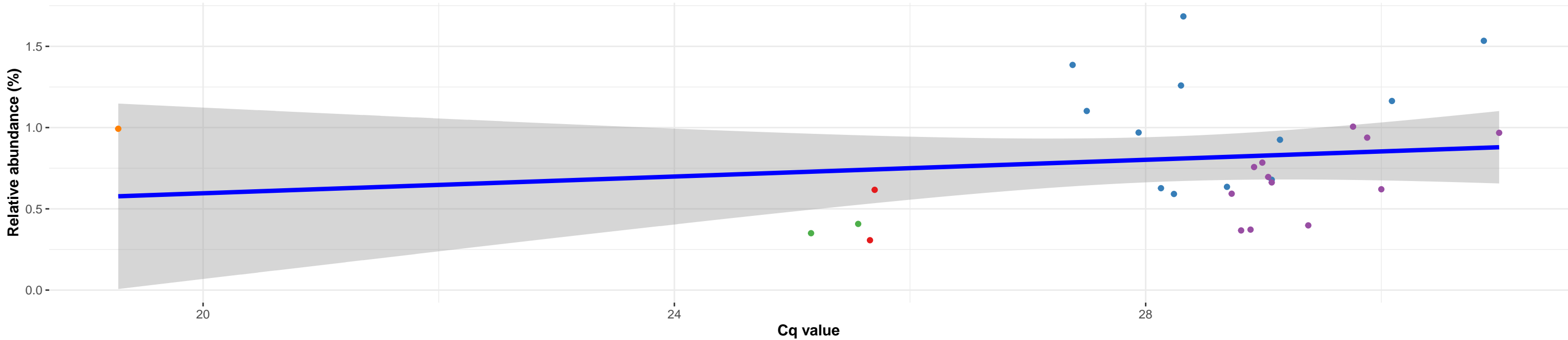
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; NA; NA

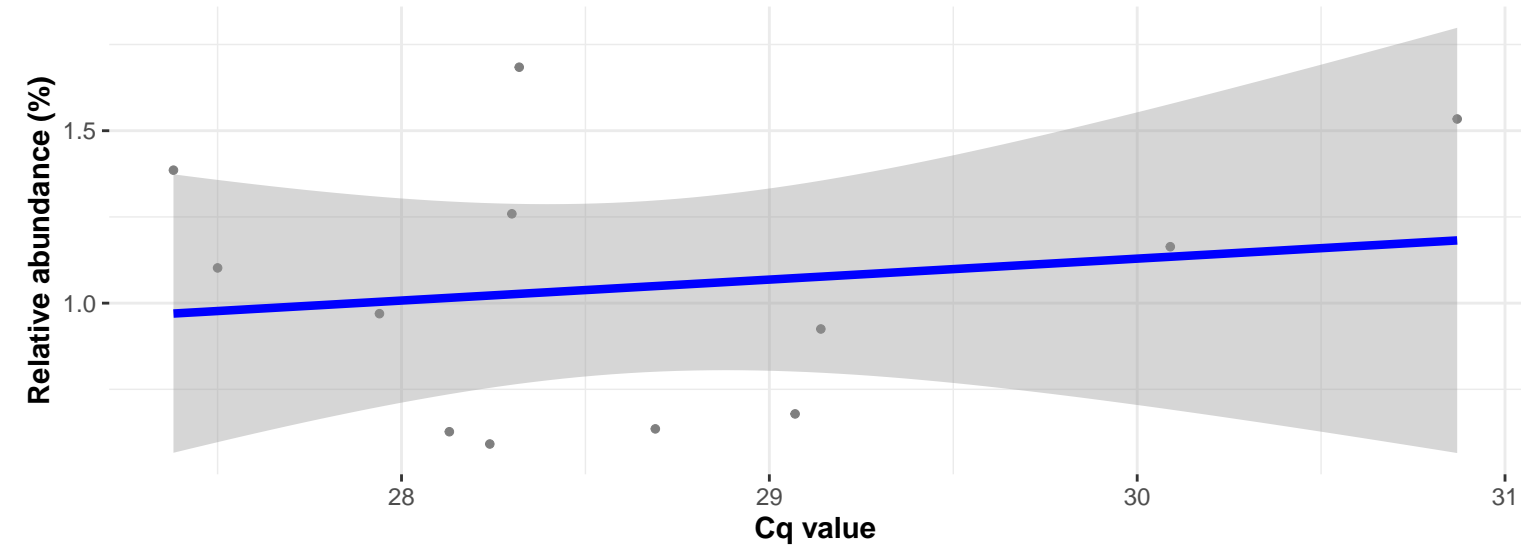
Correlation with all samples

$\log_e(S) = 8.026$ ,  $p = 0.198$ ,  $\hat{\rho}_{\text{Spearman}} = 0.246$ ,  $CI_{95\%} [-0.144, 0.570]$ ,  $n_{\text{pairs}} = 29$



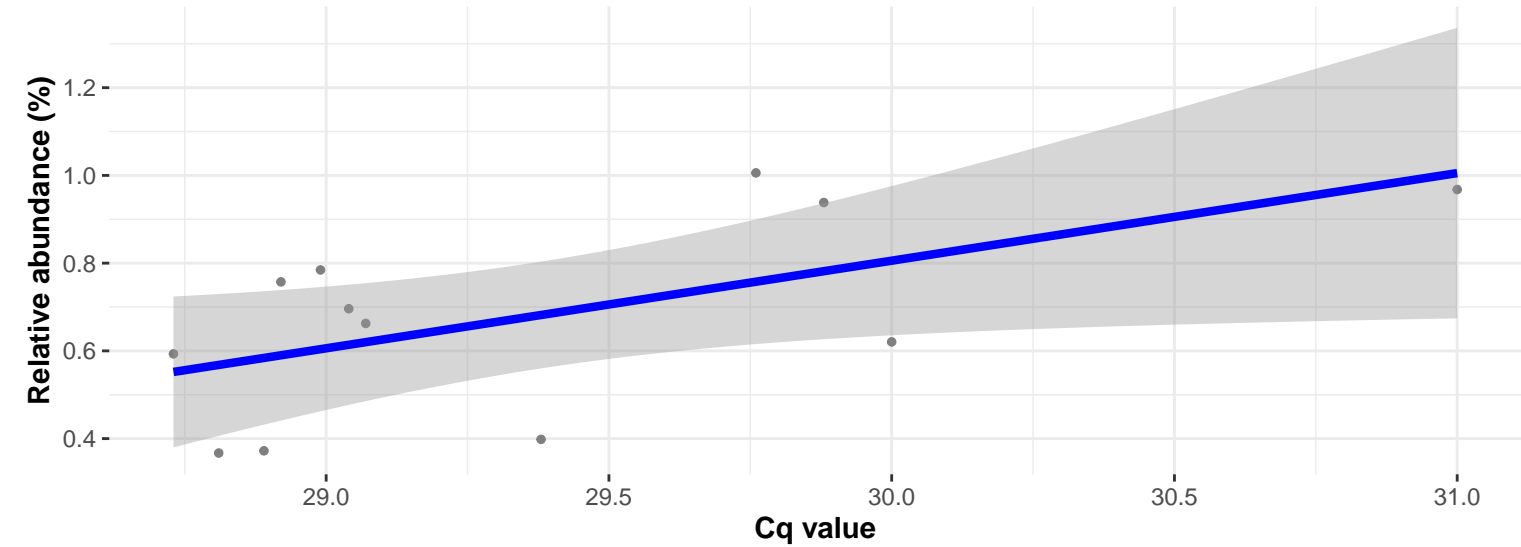
Correlation within: IM-PIM

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

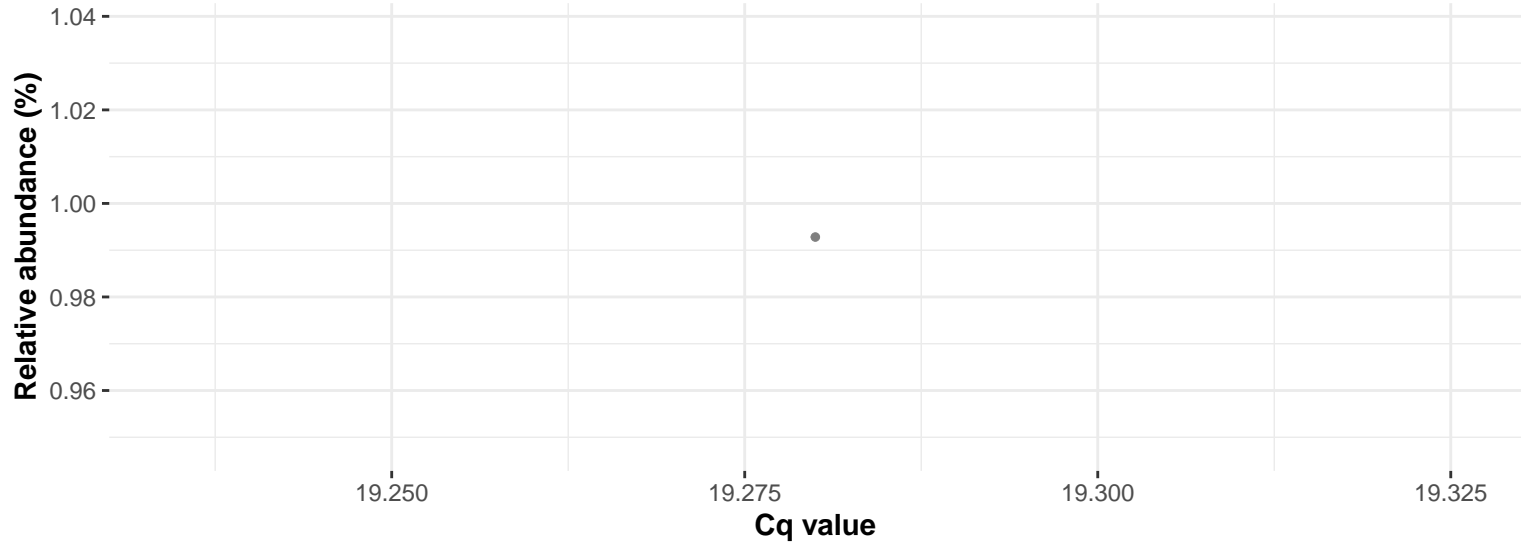


Correlation within: IM-DIM

$\log_e(S) = 4.754$ ,  $p = 0.042$ ,  $\hat{\rho}_{\text{Spearman}} = 0.594$ ,  $CI_{95\%} [0.012, 0.876]$ ,  $n_{\text{pairs}} = 12$



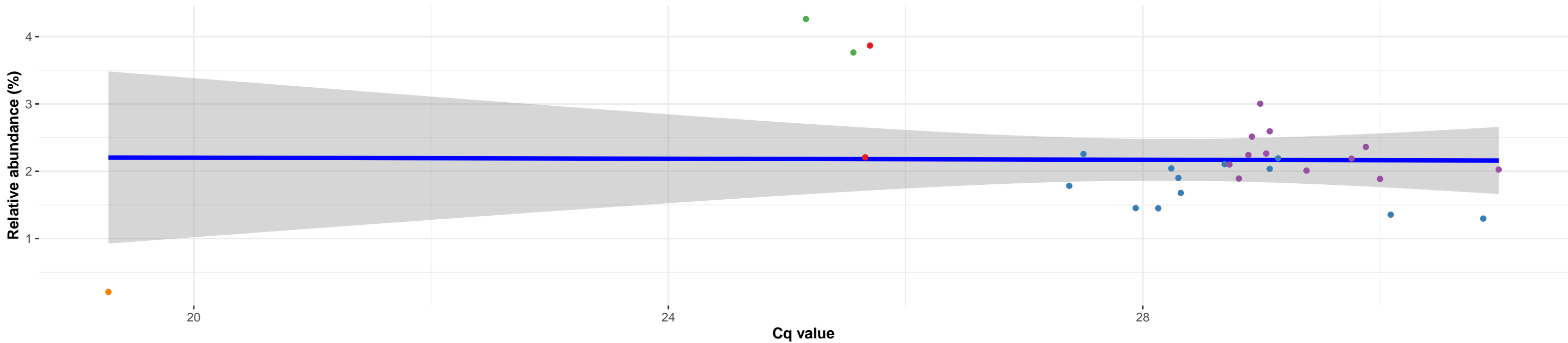
Correlation within: Feed



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

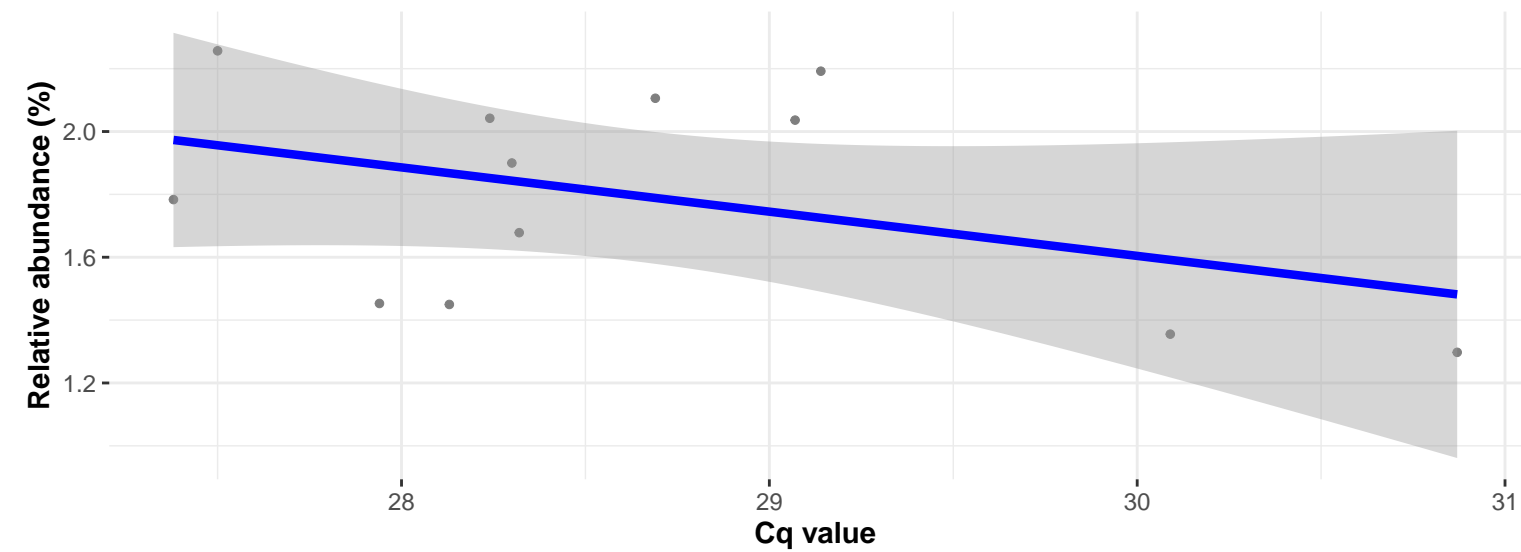
Correlation with all samples

$\log_e(S) = 8.451$ ,  $p = 0.427$ ,  $\hat{\rho}_{\text{Spearman}} = -0.153$ ,  $CI_{95\%} [-0.501, 0.237]$ ,  $n_{\text{pairs}} = 29$



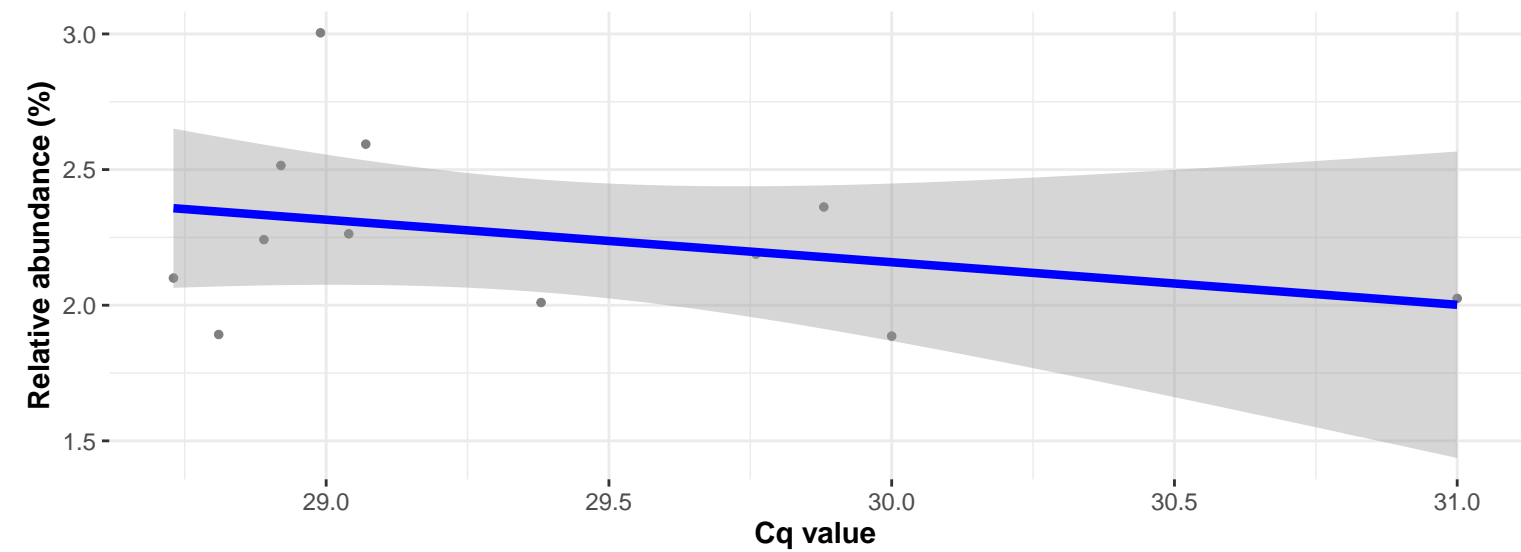
Correlation within: IM-PIM

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

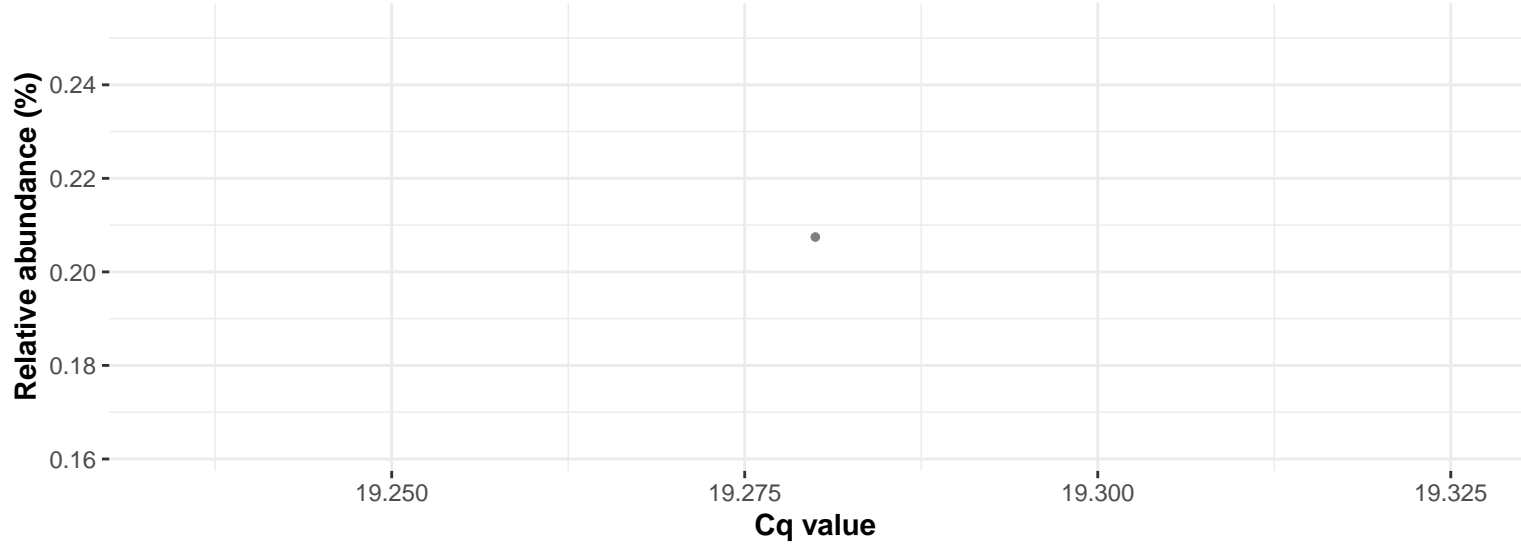


Correlation within: IM-DIM

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



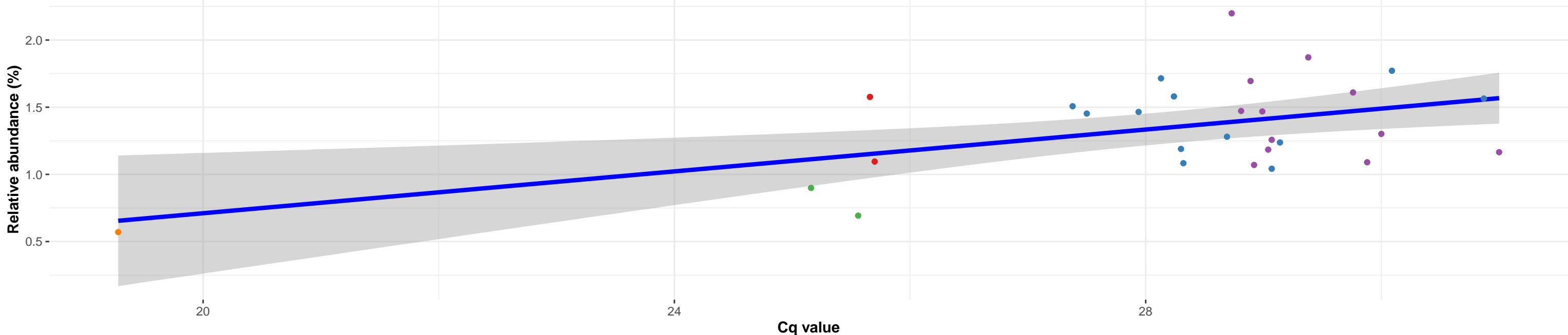
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; Ambiguous\_taxa; Ambiguous\_taxa

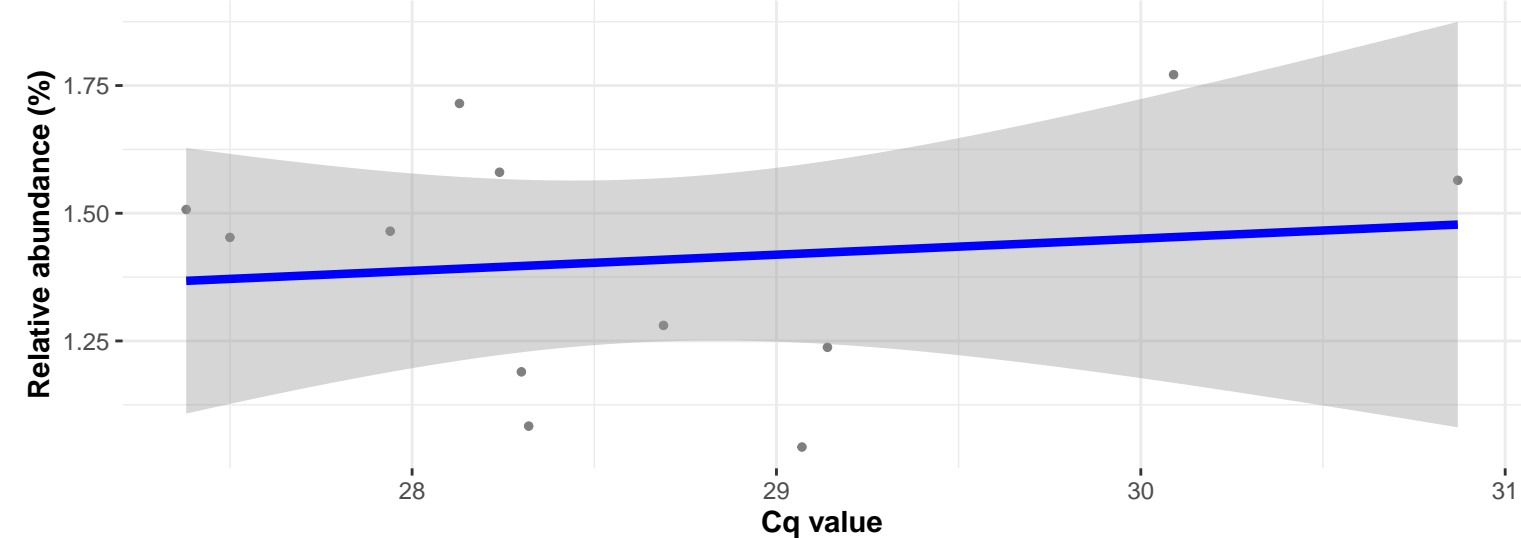
Correlation with all samples

$\log_e(S) = 8.034$ ,  $p = 0.209$ ,  $\hat{\rho}_{\text{Spearman}} = 0.241$ ,  $CI_{95\%} [-0.149, 0.566]$ ,  $n_{\text{pairs}} = 29$



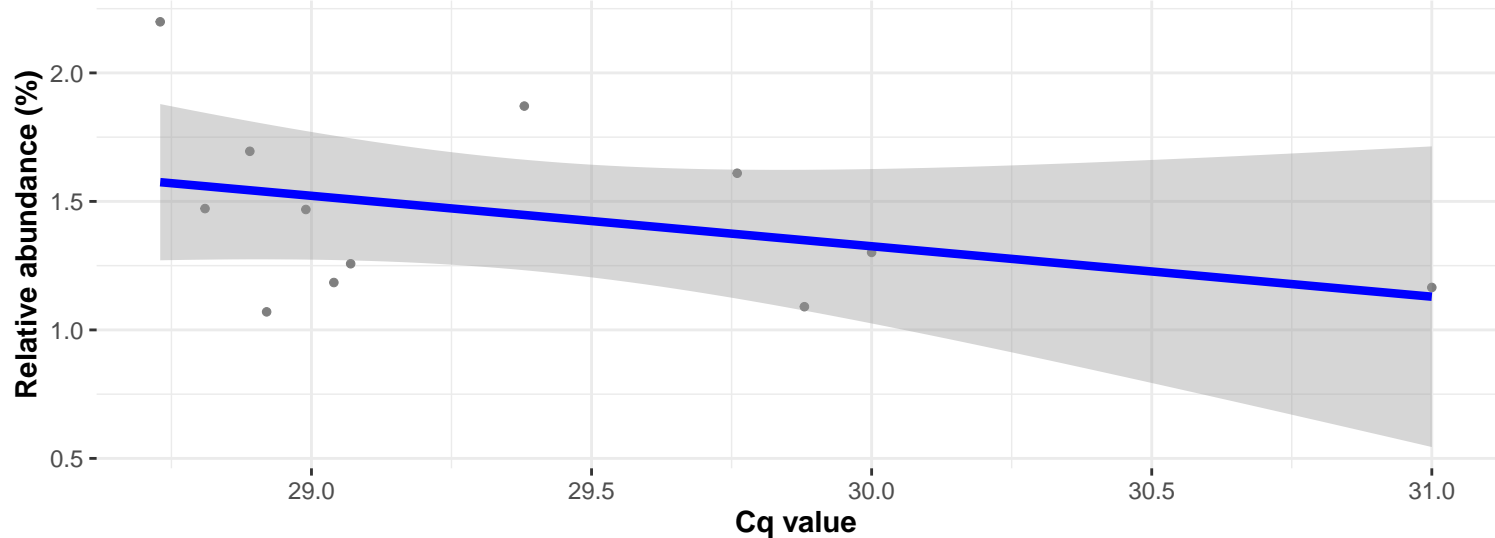
Correlation within: IM-PIM

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

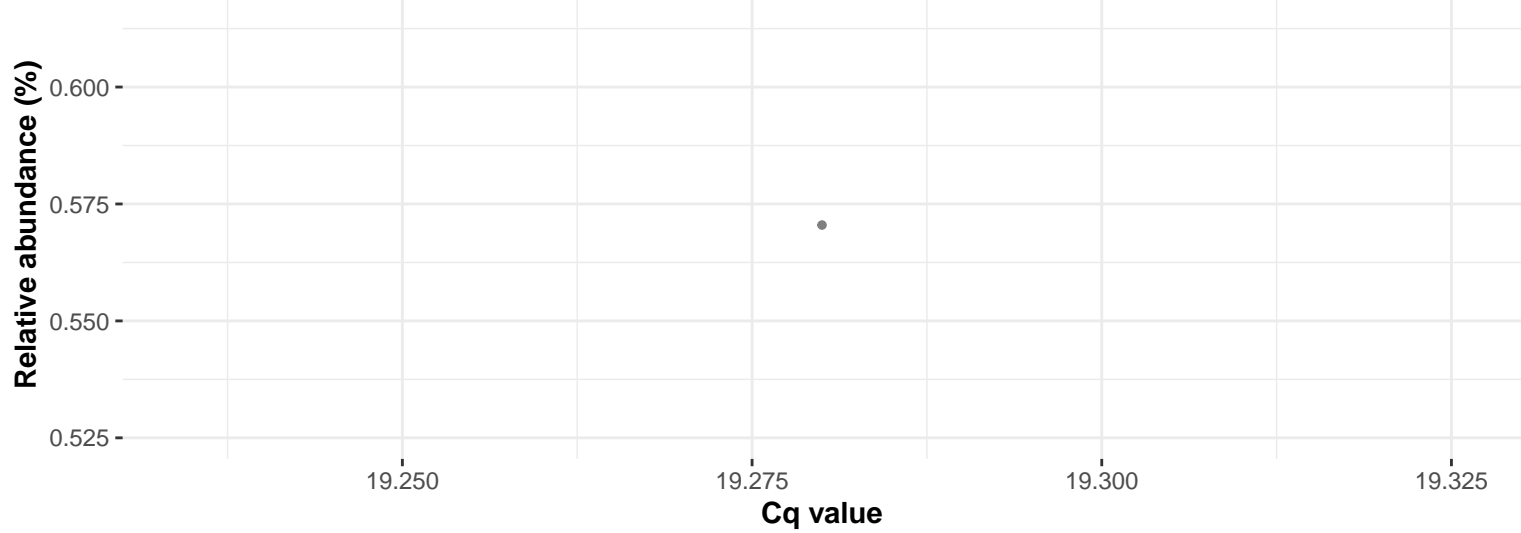


Correlation within: IM-DIM

$\log_e(S) = 6.006$ ,  $p = 0.175$ ,  $\hat{\rho}_{\text{Spearman}} = -0.420$ ,  $CI_{95\%} [-0.808, 0.222]$ ,  $n_{\text{pairs}} = 12$



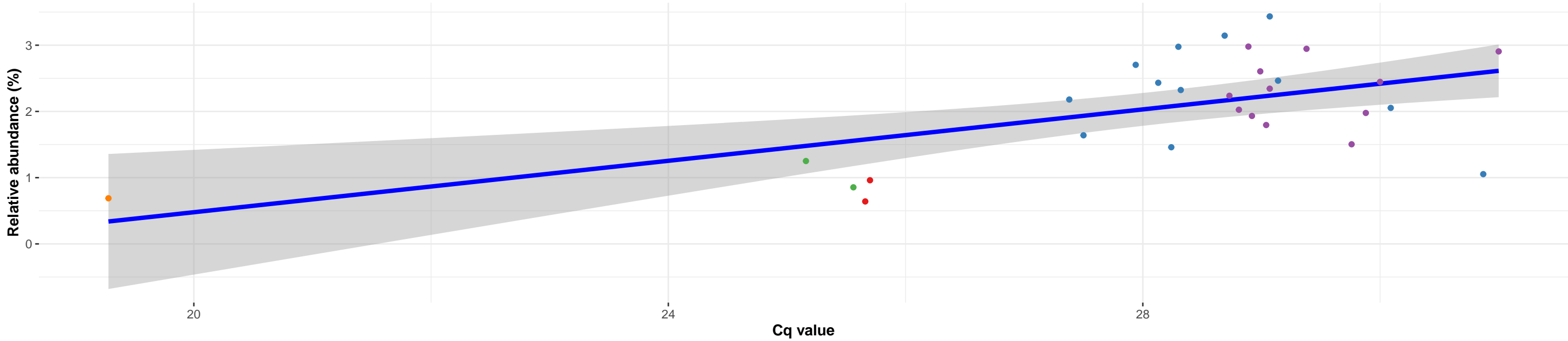
Correlation within: Feed



k\_\_Bacteria; p\_\_RsaHF231; c\_\_uncultured bacterium; o\_\_uncultured bacterium; f\_\_uncultured bacterium; g\_\_uncultured bacterium; s\_\_uncultured bacterium

Correlation with all samples

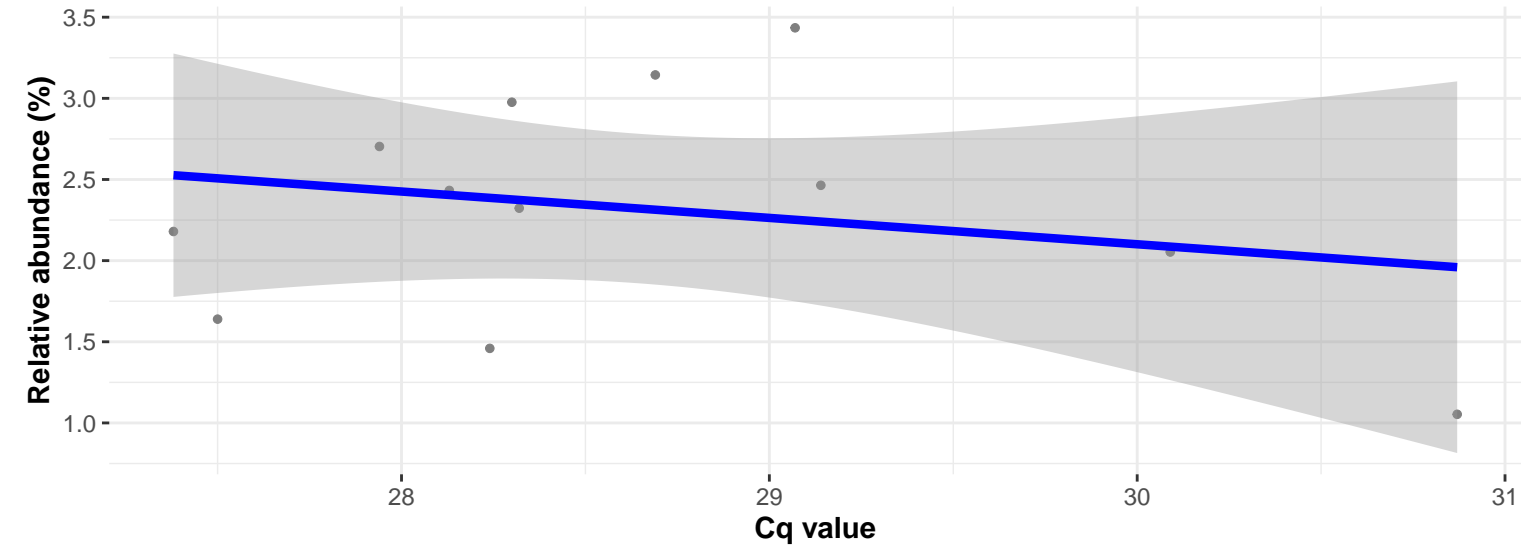
$\log_e(S) = 7.804$ ,  $p = 0.033$ ,  $\hat{\rho}_{\text{Spearman}} = 0.396$ ,  $CI_{95\%} [0.024, 0.672]$ ,  $n_{\text{pairs}} = 29$



SampleType IM-PID IM-PIM IM-DID IM-DIM Feed

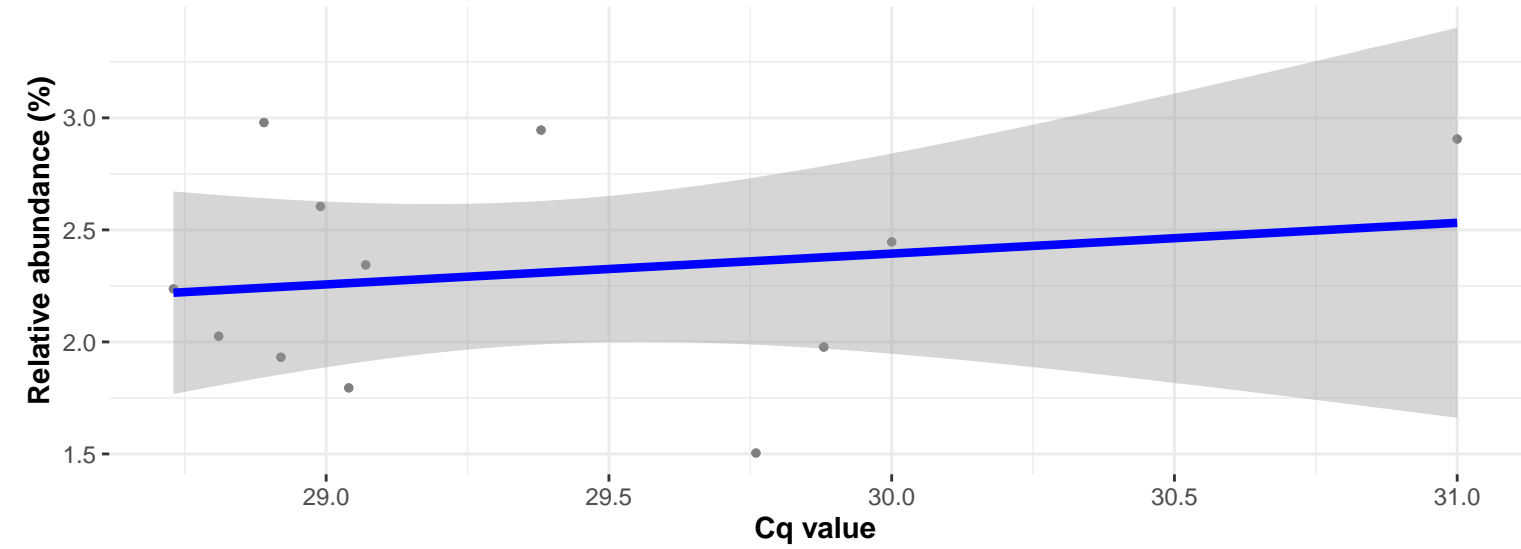
Correlation within: IM-PIM

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

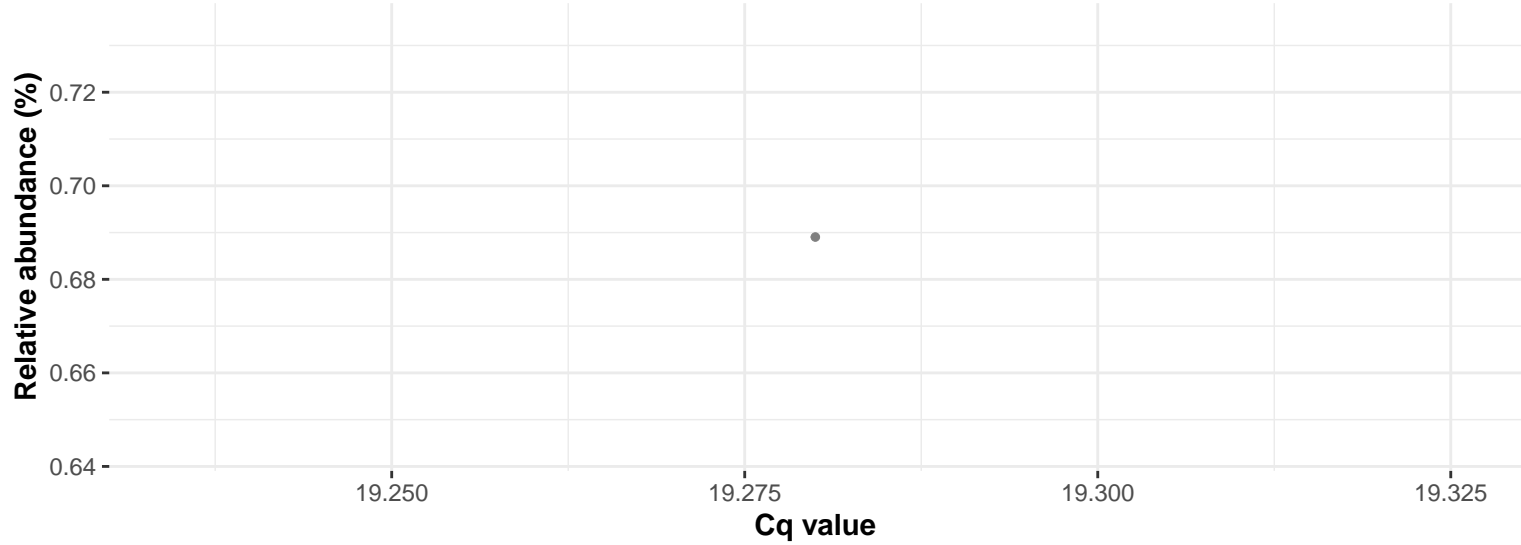


Correlation within: IM-DIM

$\log_e(S) = 5.598$ ,  $p = 0.863$ ,  $\hat{\rho}_{\text{Spearman}} = 0.056$ ,  $CI_{95\%} [-0.549, 0.622]$ ,  $n_{\text{pairs}} = 12$



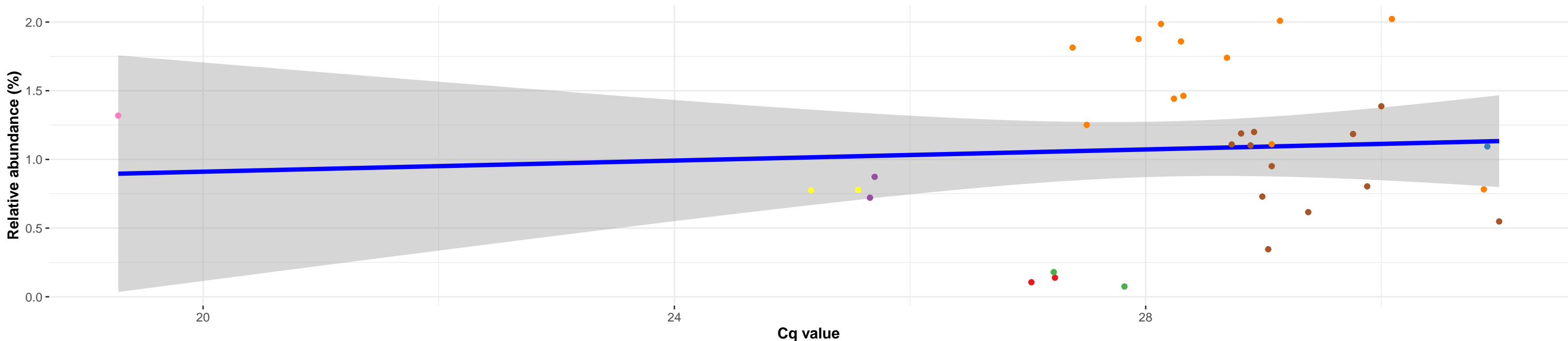
Correlation within: Feed



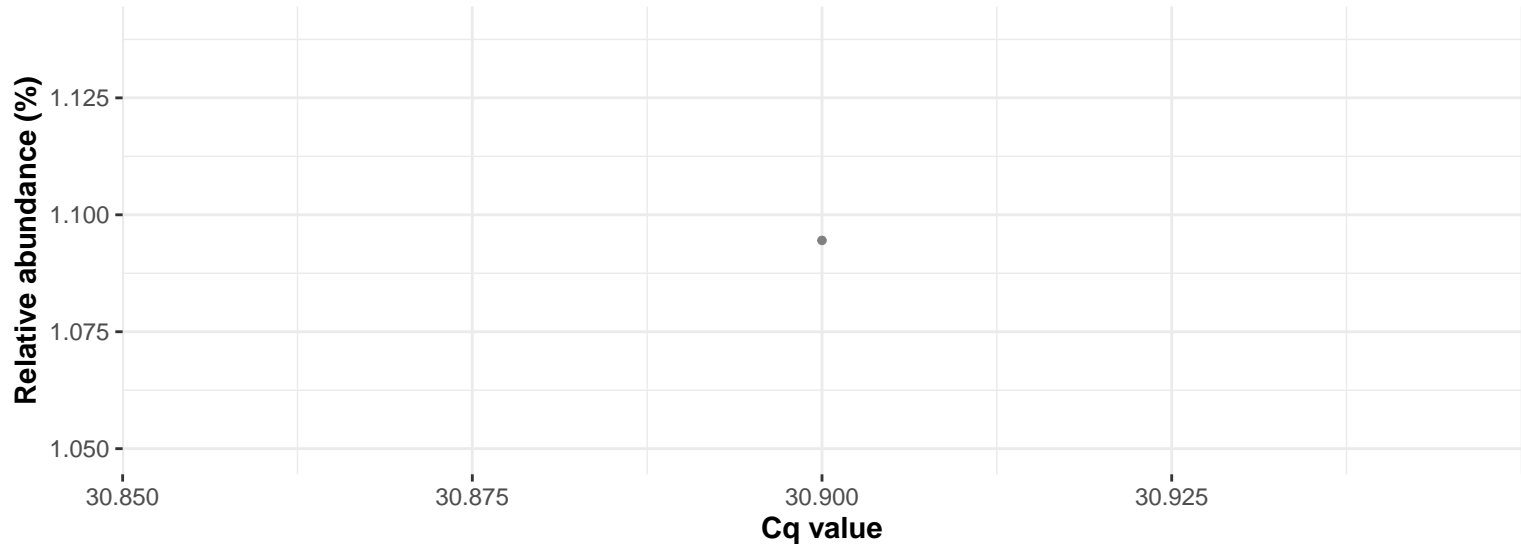
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Aerococcaceae; g\_\_Globicatella; Ambiguous\_taxa

Correlation with all samples

$\log_e(S) = 8.650$ ,  $p = 0.472$ ,  $\hat{\rho}_{\text{Spearman}} = 0.128$ ,  $CI_{95\%} [-0.230, 0.455]$ ,  $n_{\text{pairs}} = 34$

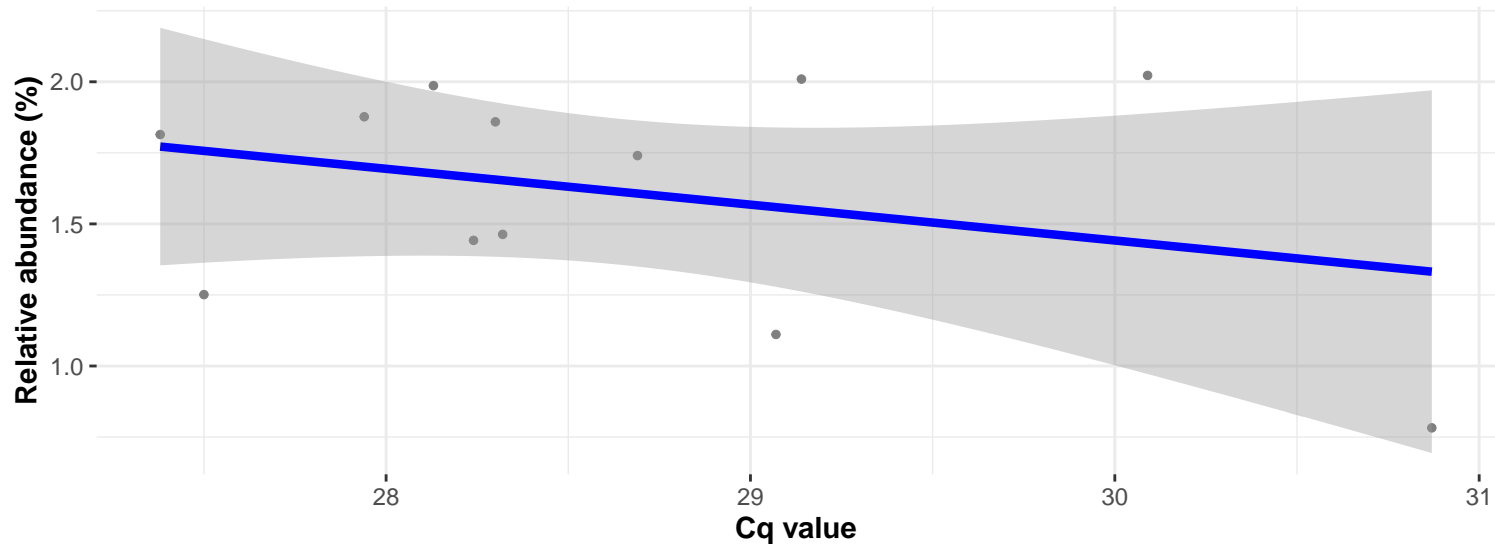


Correlation within: REF-PIM



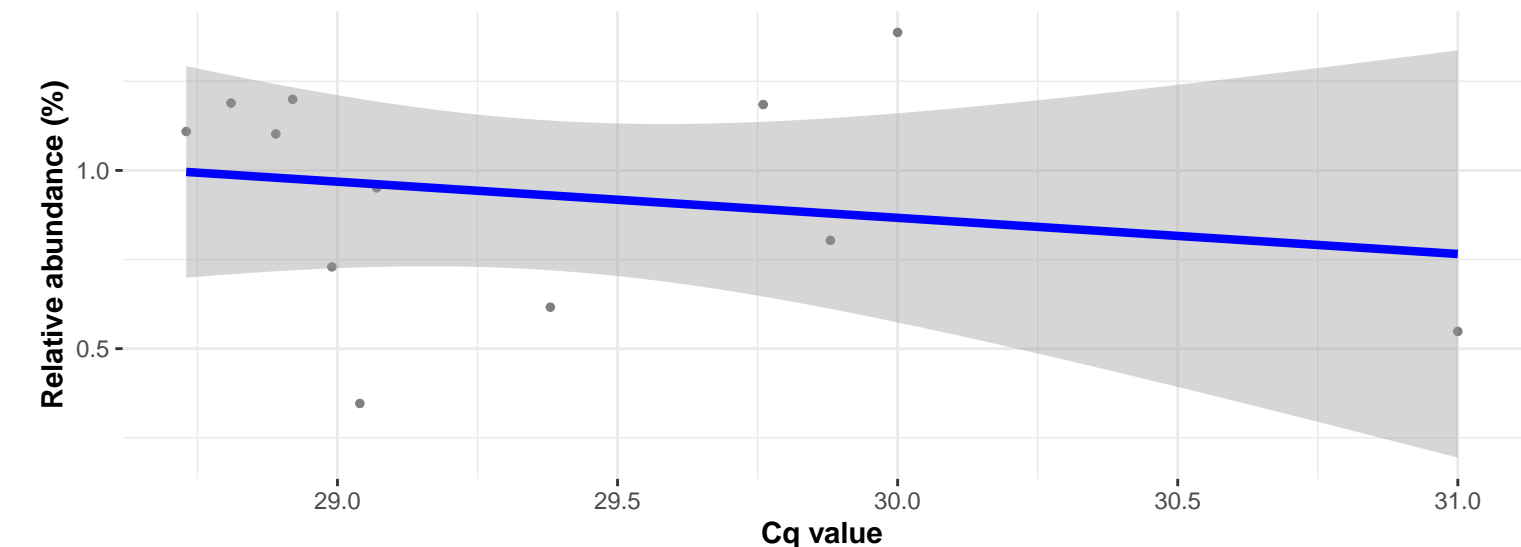
Correlation within: IM-PIM

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

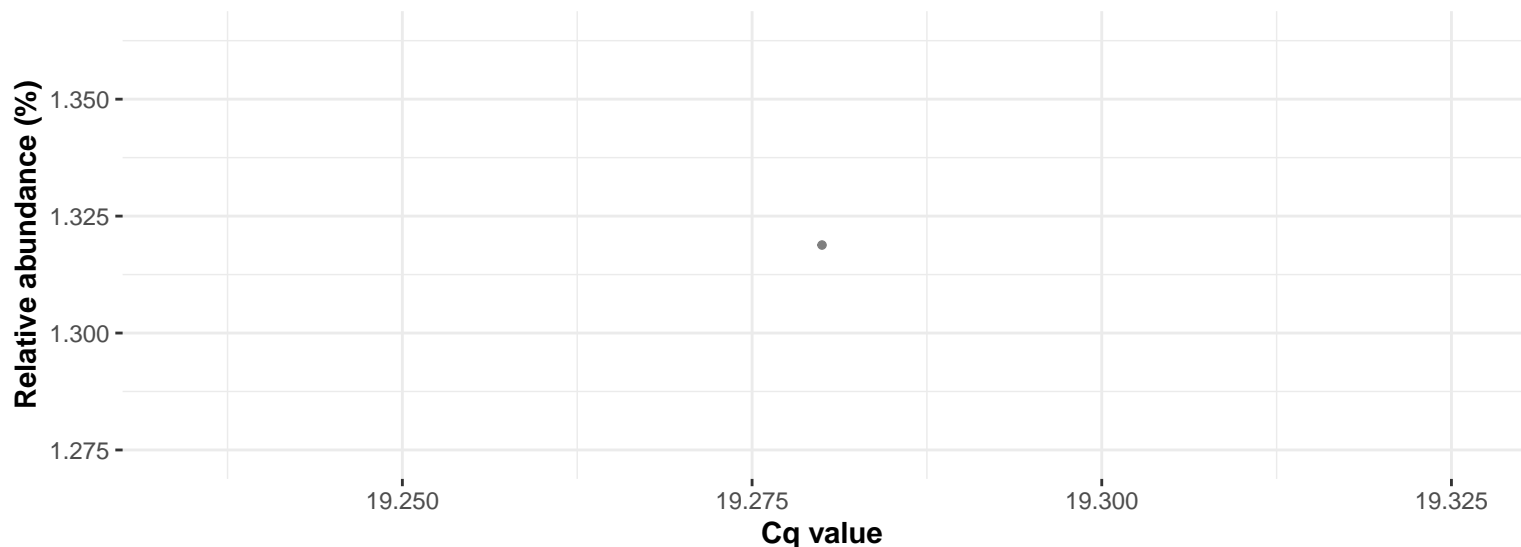


Correlation within: IM-DIM

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



Correlation within: Feed

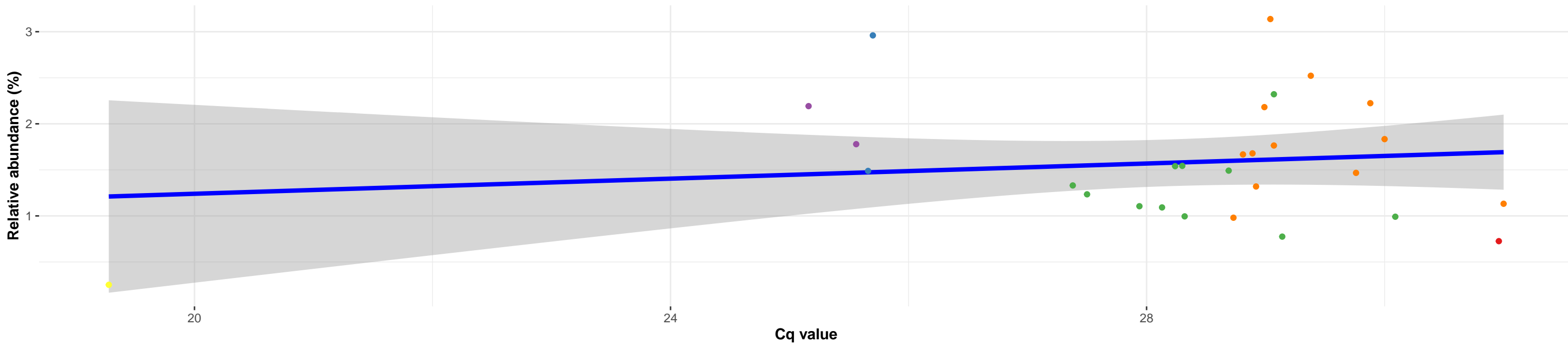




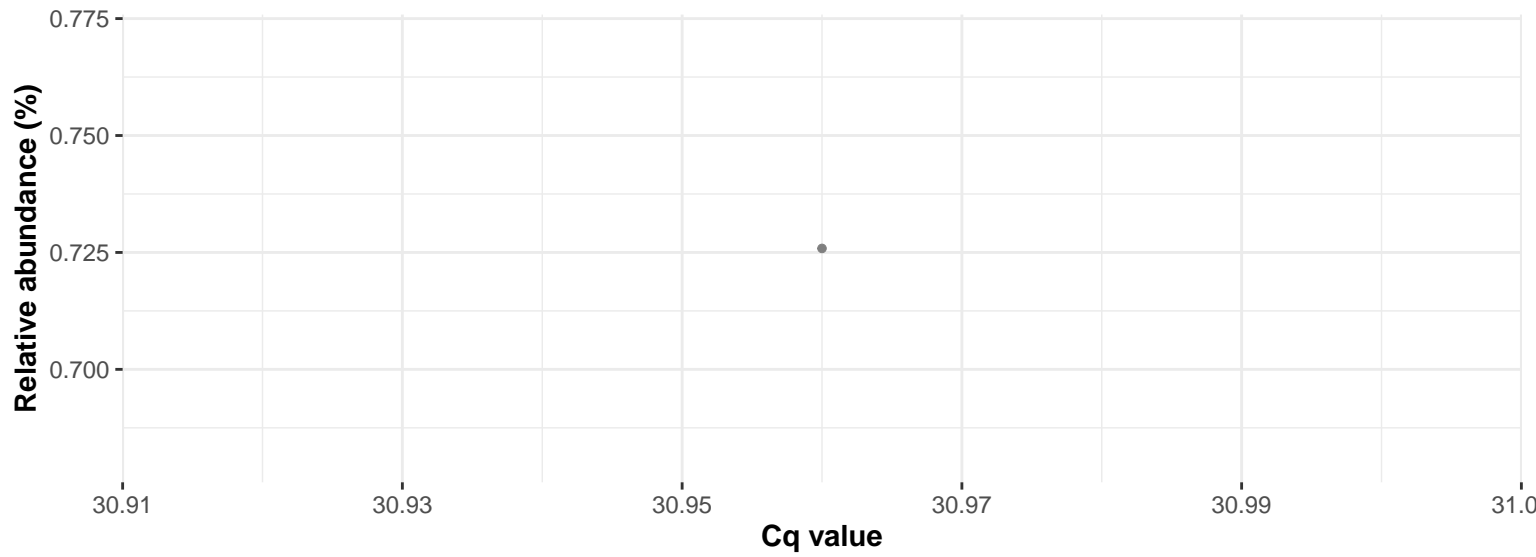
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Lysinibacillus; NA

### Correlation with all samples

$\log_e(S) = 8.290$ ,  $p = 0.921$ ,  $\hat{\rho}_{\text{Spearman}} = 0.019$ ,  $\text{CI}_{95\%} [-0.360, 0.393]$ ,  $n_{\text{pairs}} = 29$

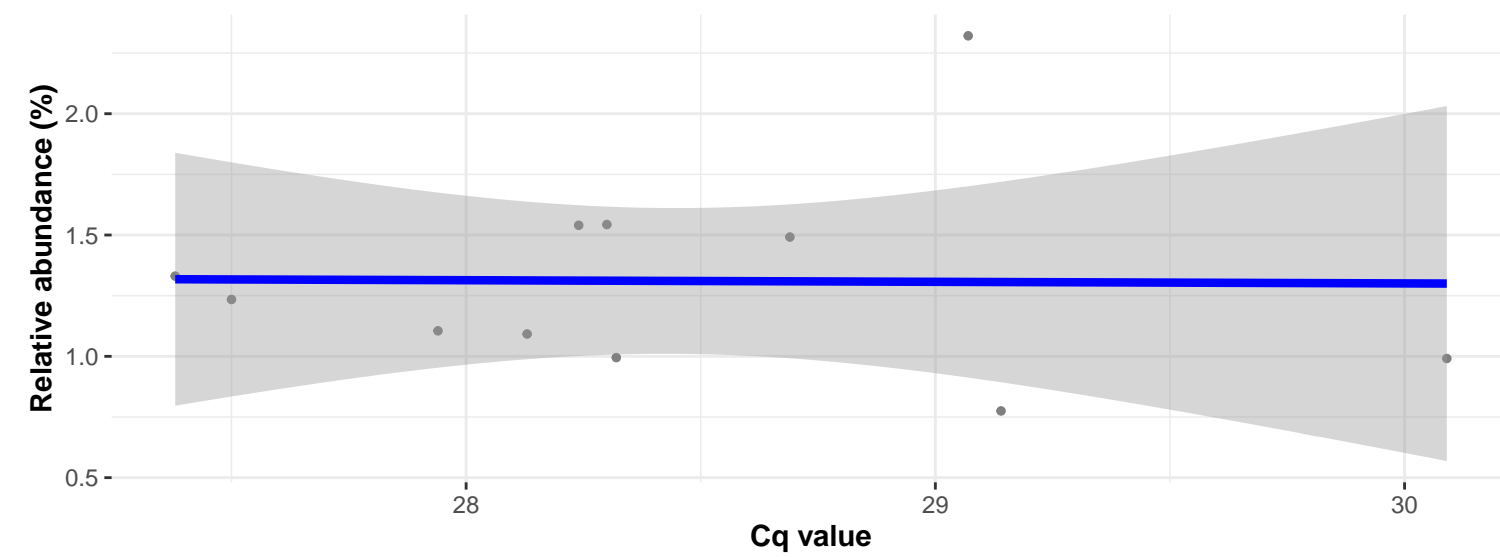


### Correlation within: REF-PIM



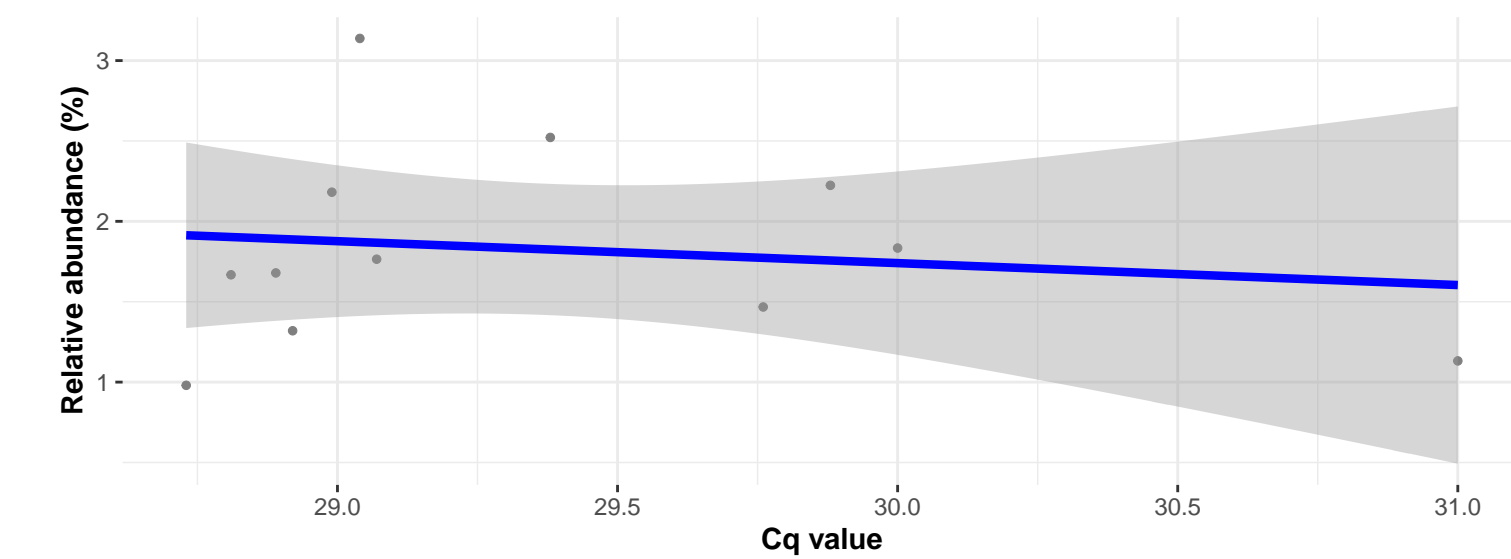
### Correlation within: IM-PIM

$\log_e(S) = 5.598$ ,  $p = 0.502$ ,  $\hat{\rho}_{\text{Spearman}} = -0.227$ ,  $\text{CI}_{95\%} [-0.737, 0.448]$ ,  $n_{\text{pairs}} = 11$

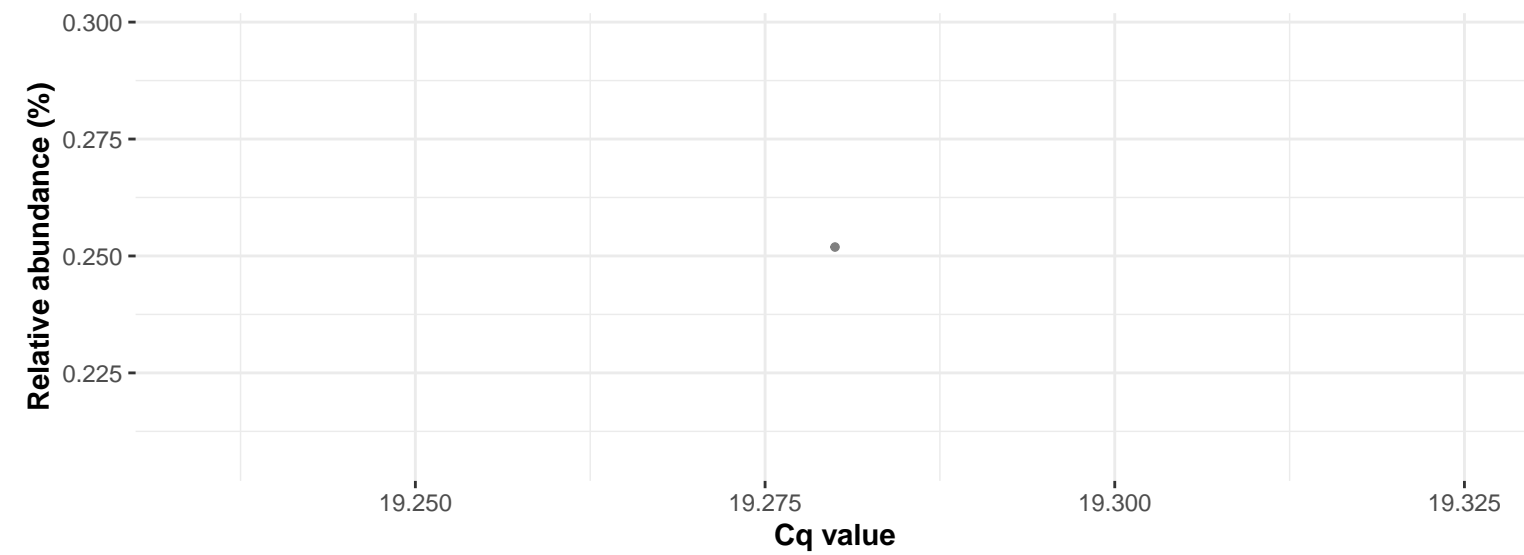


### Correlation within: IM-DIM

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



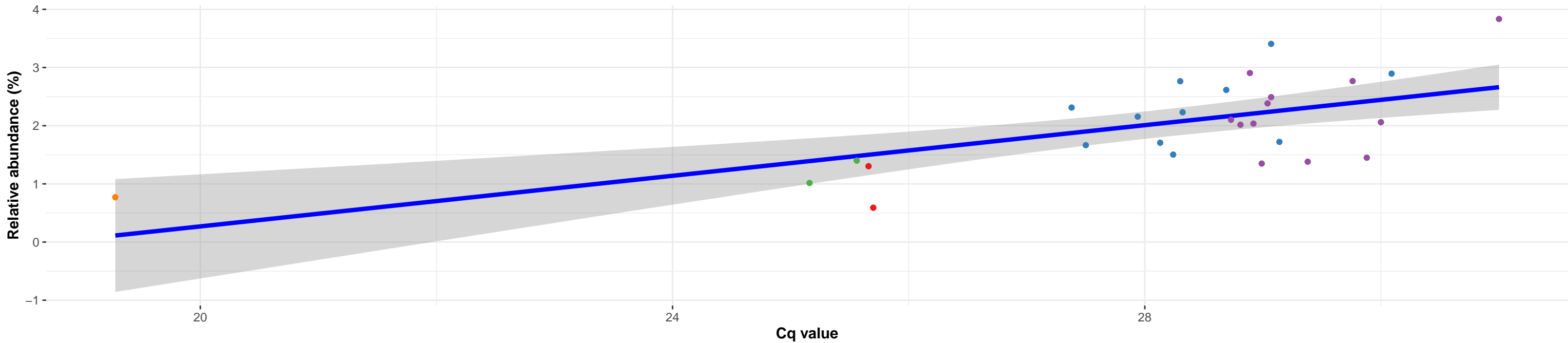
### Correlation within: Feed



k\_\_Bacteria; p\_\_RsaHF231; c\_\_uncultured bacterium; o\_\_uncultured bacterium; f\_\_uncultured bacterium; g\_\_uncultured bacterium; s\_\_uncultured bacterium

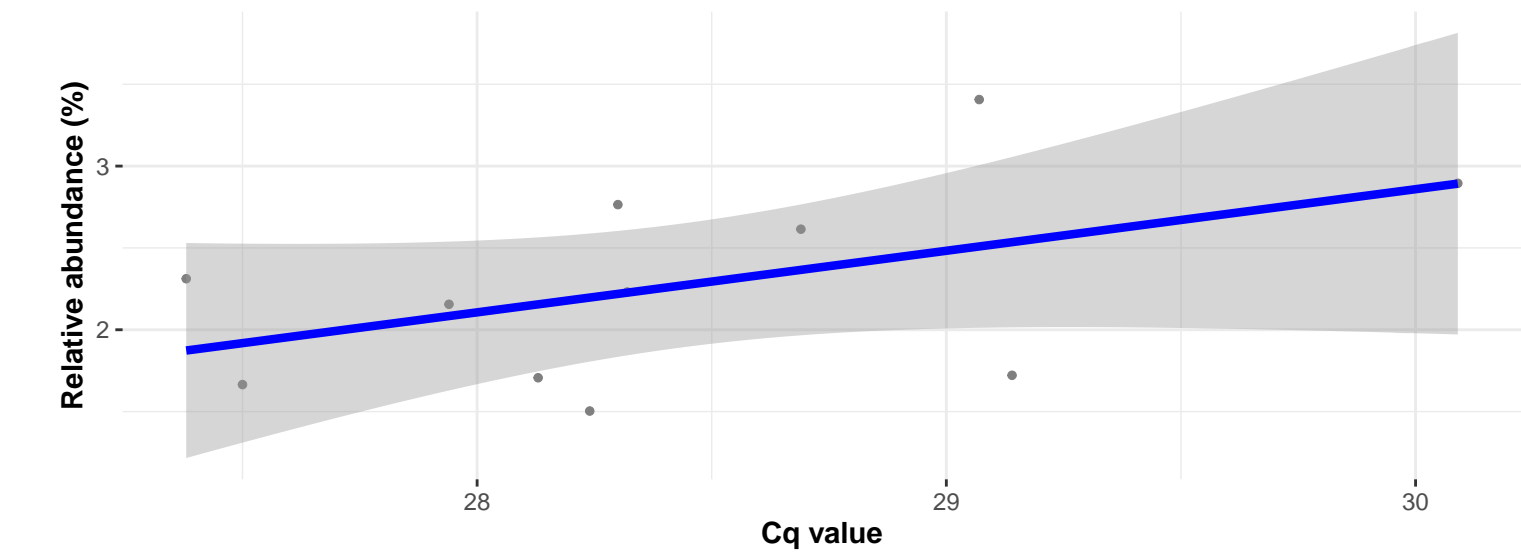
Correlation with all samples

$\log_e(S) = 7.434$ ,  $p = 0.003$ ,  $\hat{\rho}_{\text{Spearman}} = 0.537$ ,  $CI_{95\%} [0.194, 0.763]$ ,  $n_{\text{pairs}} = 28$



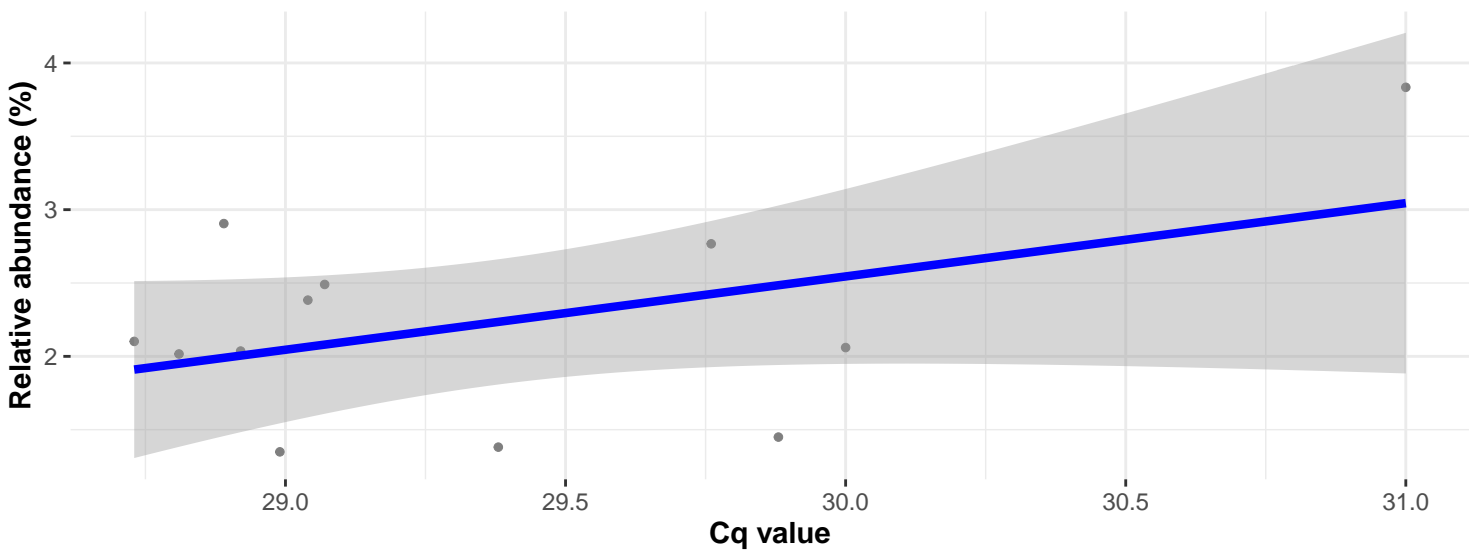
Correlation within: IM-PIM

$\log_e(S) = 4.682$ ,  $p = 0.110$ ,  $\hat{\rho}_{\text{Spearman}} = 0.509$ ,  $CI_{95\%} [-0.151, 0.855]$ ,  $n_{\text{pairs}} = 11$

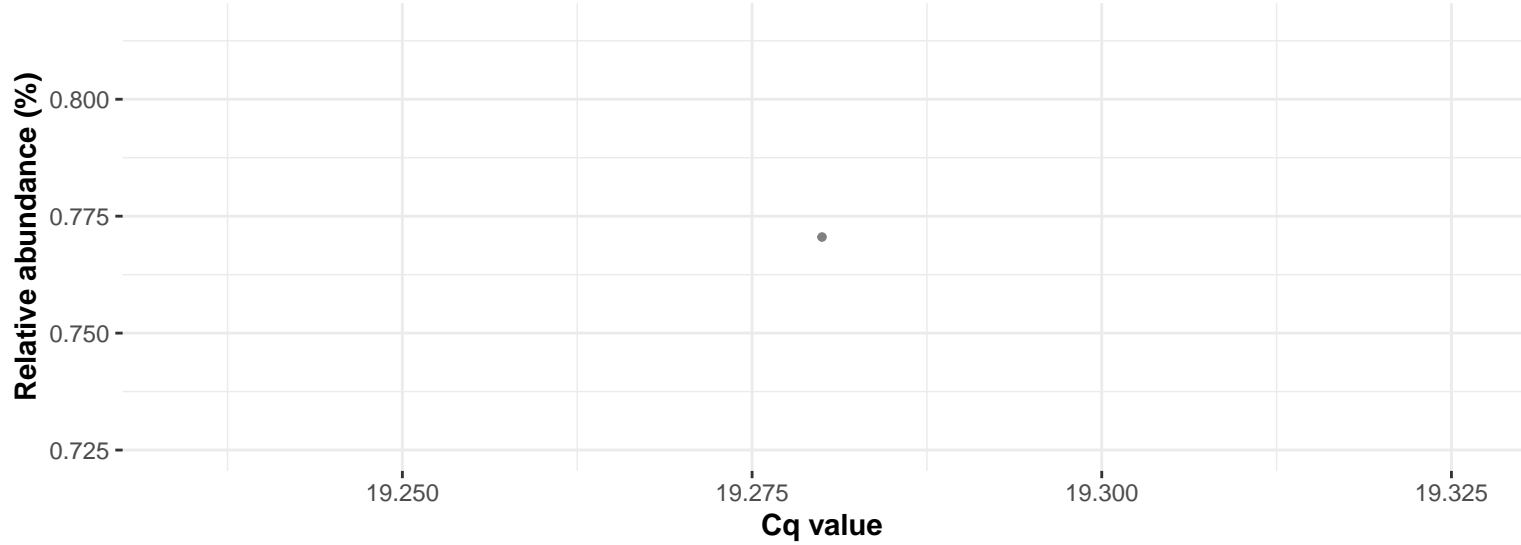


Correlation within: IM-DIM

$\log_e(S) = 5.481$ ,  $p = 0.618$ ,  $\hat{\rho}_{\text{Spearman}} = 0.161$ ,  $CI_{95\%} [-0.470, 0.683]$ ,  $n_{\text{pairs}} = 12$



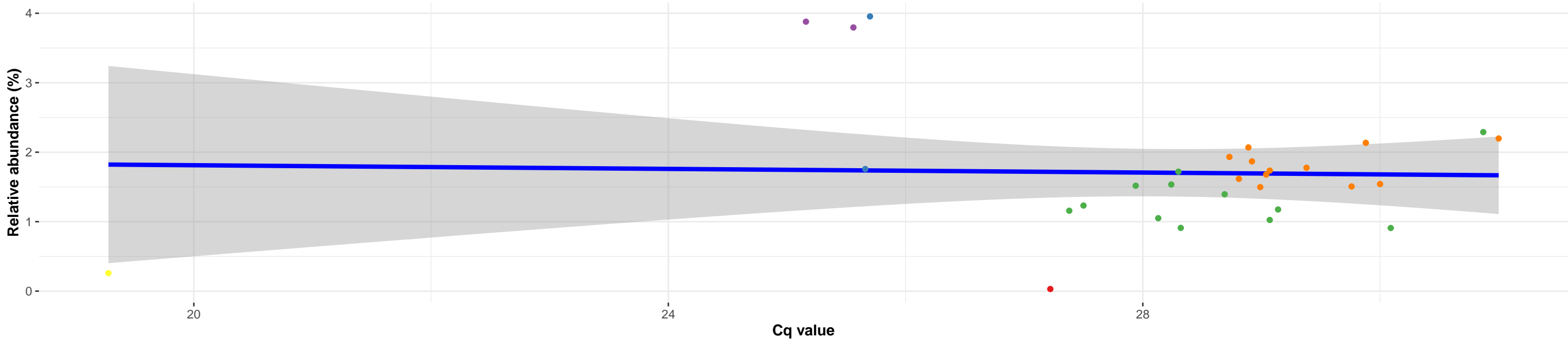
Correlation within: Feed



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

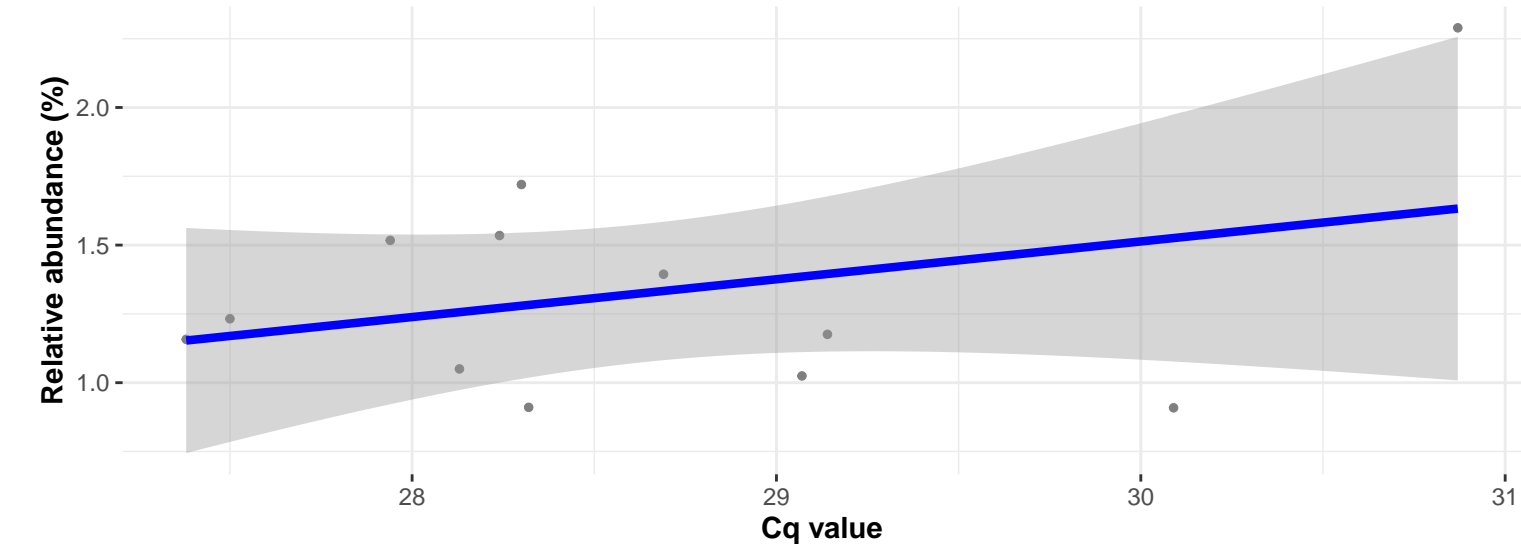
Correlation with all samples

$\log_e(S) = 8.321$ ,  $p = 0.653$ ,  $\hat{\rho}_{\text{Spearman}} = 0.086$ ,  $CI_{95\%} [-0.294, 0.442]$ ,  $n_{\text{pairs}} = 30$



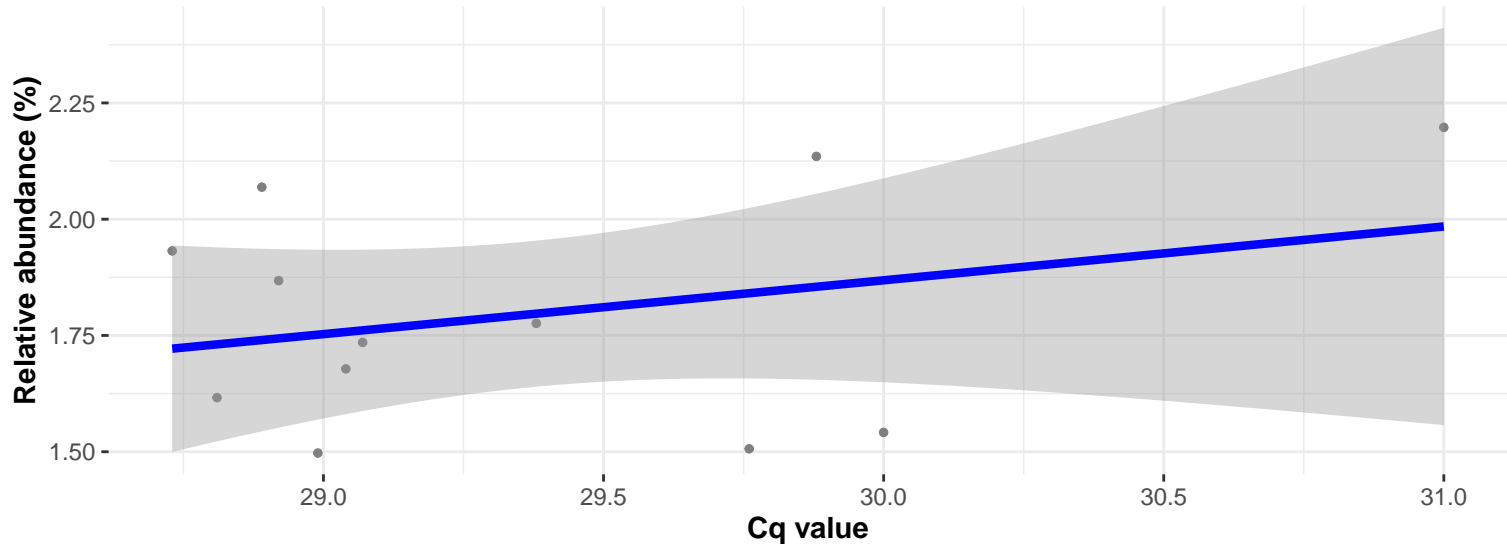
Correlation within: IM-PIM

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

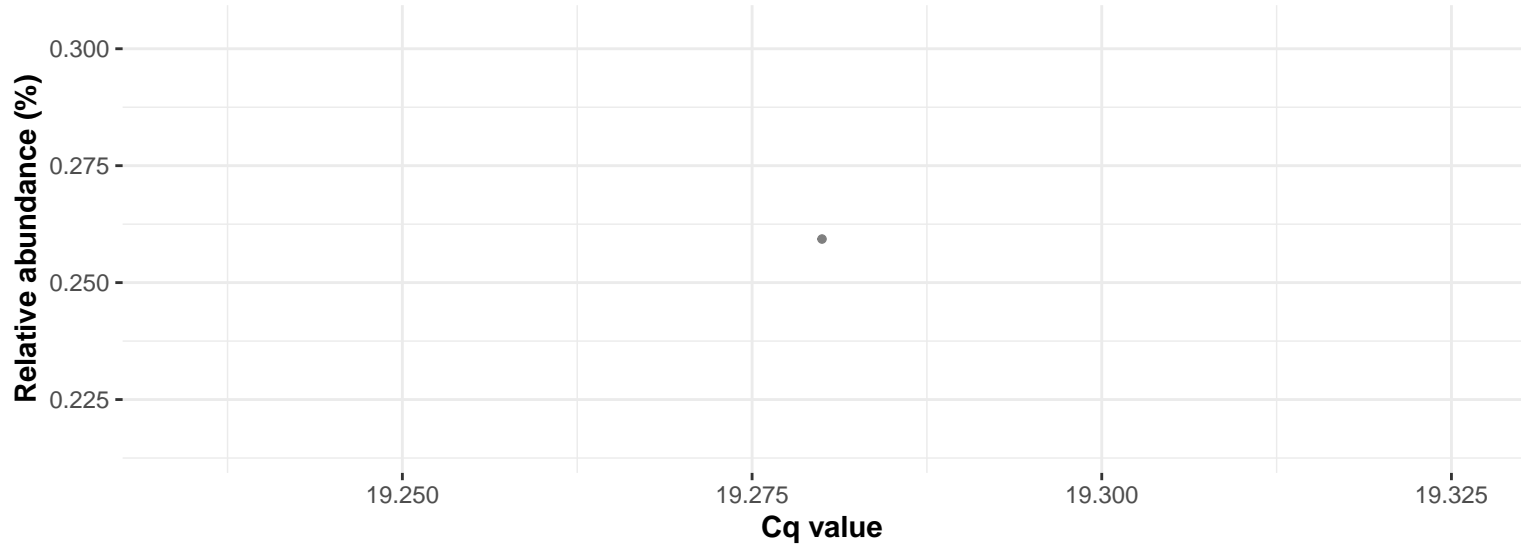


Correlation within: IM-DIM

$\log_e(S) = 5.583$ ,  $p = 0.829$ ,  $\hat{\rho}_{\text{Spearman}} = 0.070$ ,  $CI_{95\%} [-0.539, 0.631]$ ,  $n_{\text{pairs}} = 12$



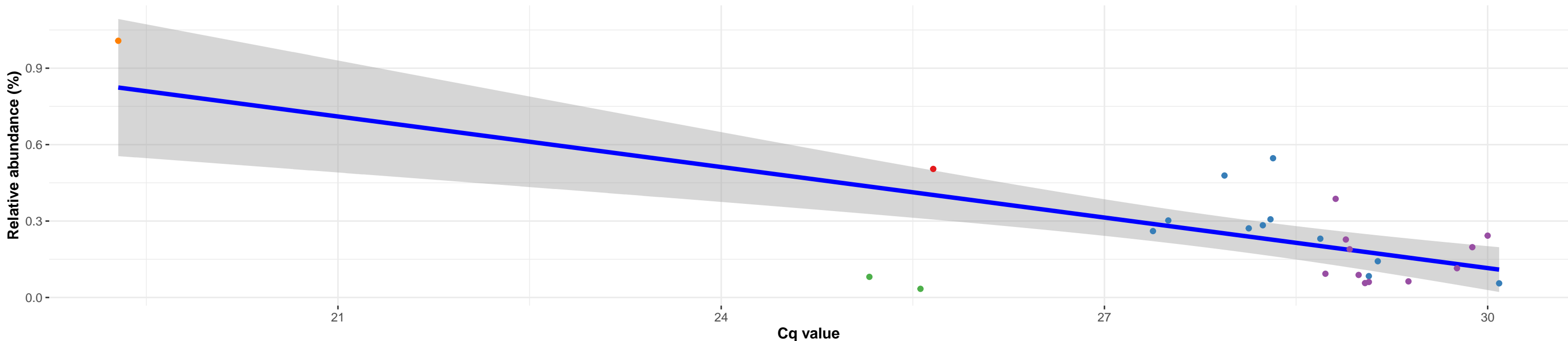
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; s\_\_Enterococcus cecorum

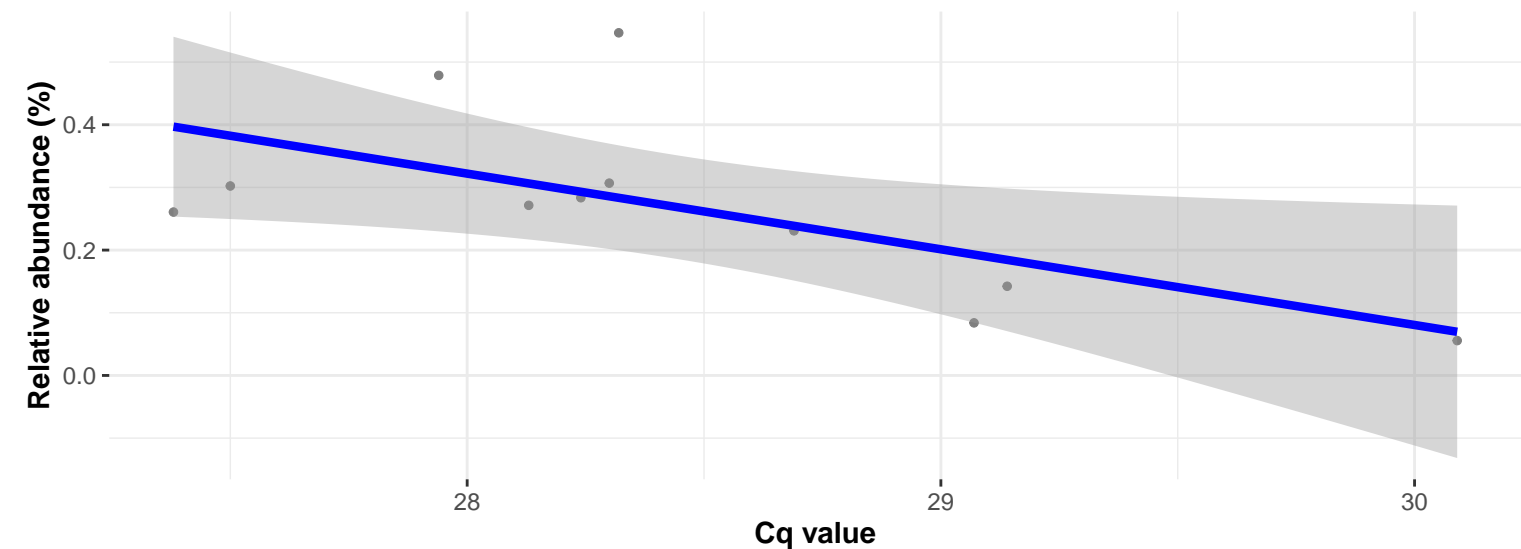
Correlation with all samples

$\log_e(S) = 8.367$ ,  $p = 0.015$ ,  $\hat{\rho}_{\text{Spearman}} = -0.471$ ,  $CI_{95\%} [-0.732, -0.091]$ ,  $n_{\text{pairs}} = 26$



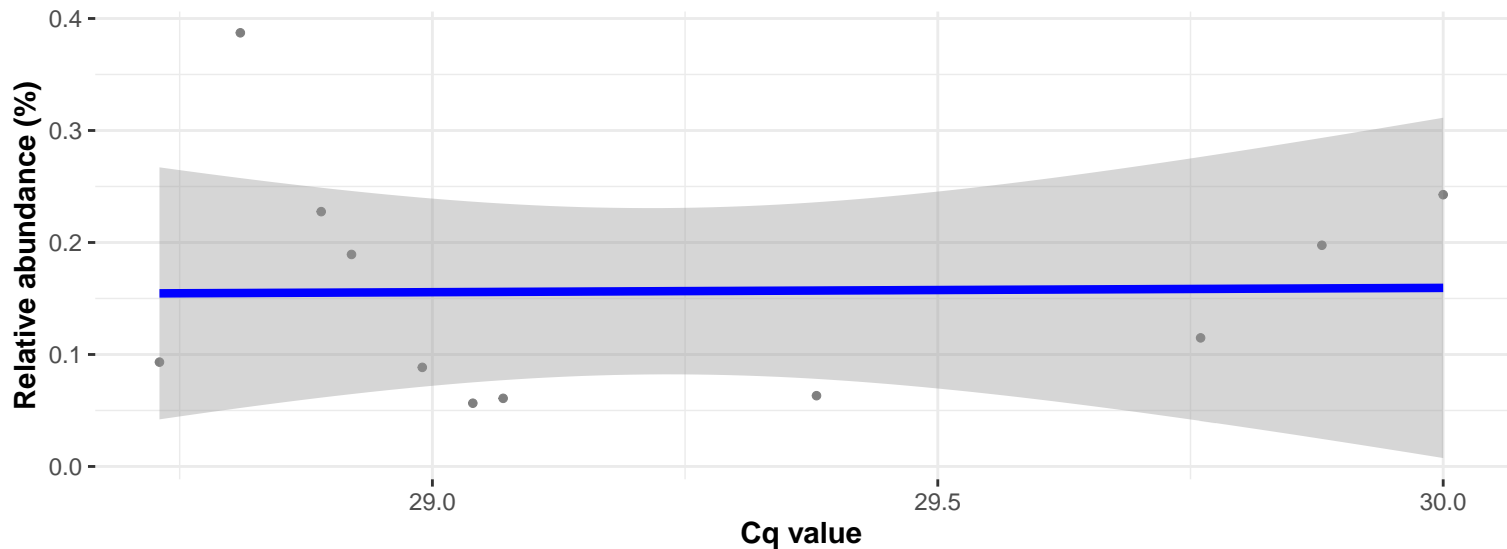
Correlation within: IM-PIM

$\log_e(S) = 5.852$ ,  $p = 0.060$ ,  $\hat{\rho}_{\text{Spearman}} = -0.582$ ,  $CI_{95\%} [-0.881, 0.048]$ ,  $n_{\text{pairs}} = 11$

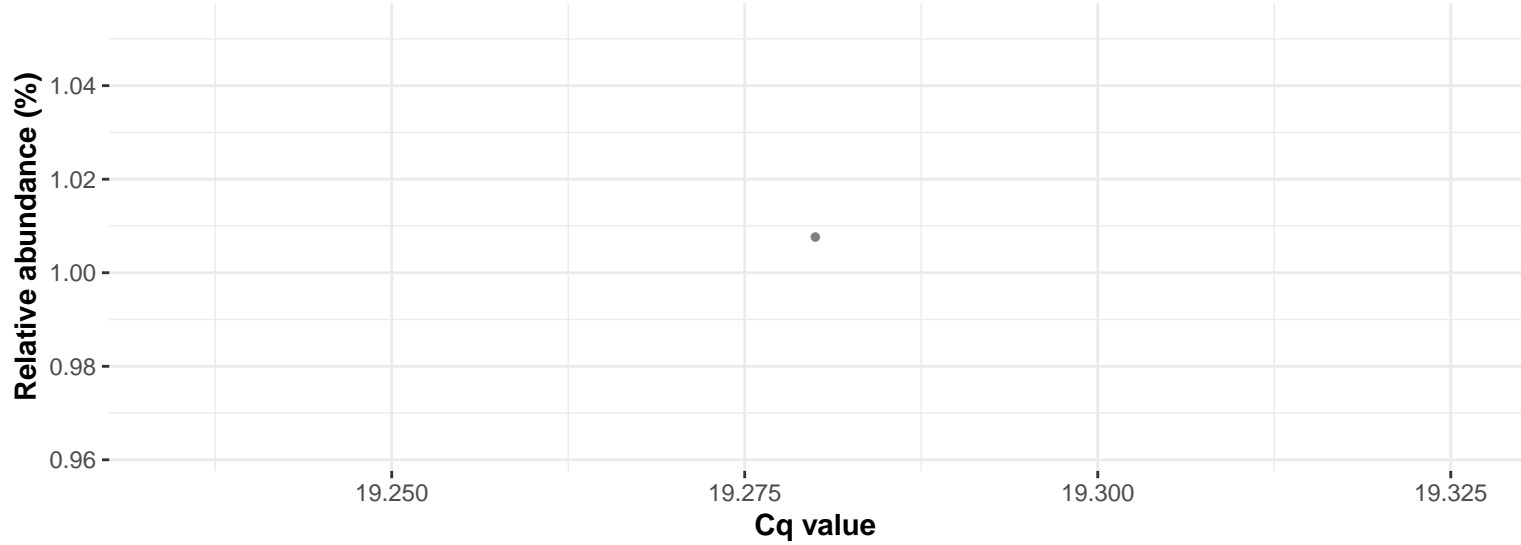


Correlation within: IM-DIM

$\log_e(S) = 5.447$ ,  $p = 0.873$ ,  $\hat{\rho}_{\text{Spearman}} = -0.055$ ,  $CI_{95\%} [-0.646, 0.578]$ ,  $n_{\text{pairs}} = 11$



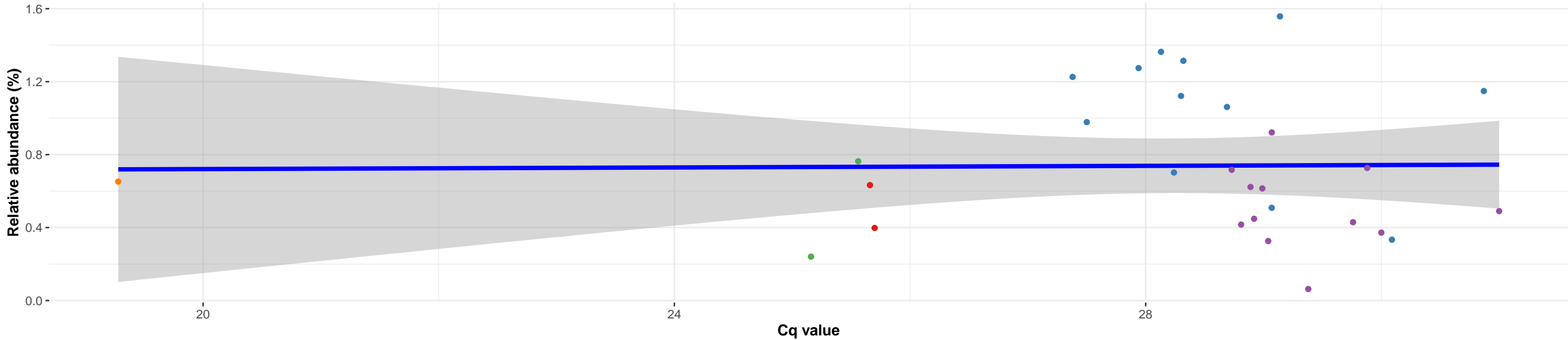
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; NA

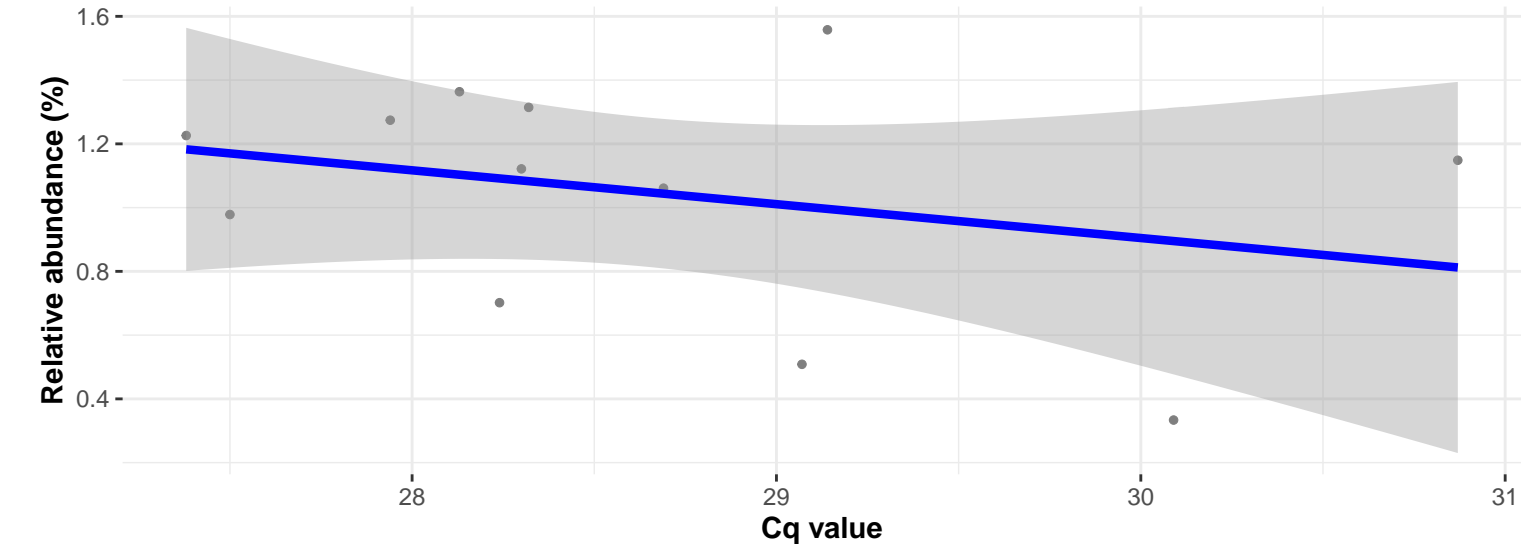
Correlation with all samples

$\log_e(S) = 8.516$ ,  $p = 0.229$ ,  $\hat{\rho}_{\text{Spearman}} = -0.230$ ,  $\text{CI}_{95\%} [-0.558, 0.160]$ ,  $n_{\text{pairs}} = 29$



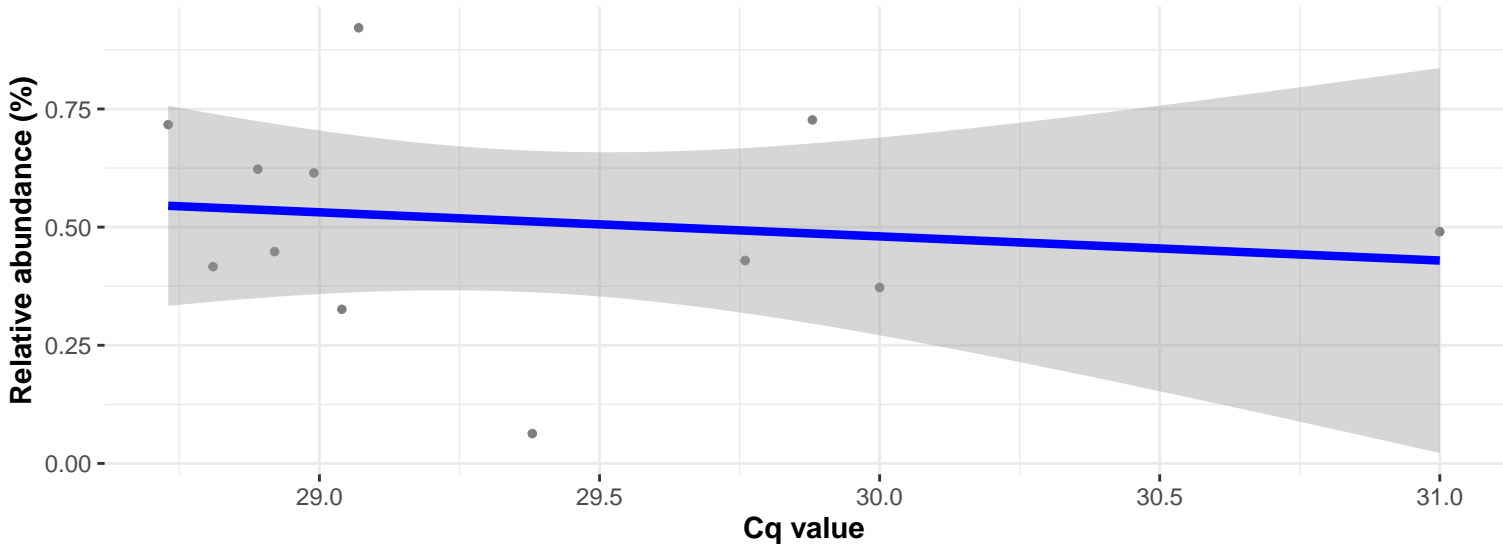
Correlation within: IM-PIM

$\log_e(S) = 5.823$ ,  $p = 0.572$ ,  $\hat{\rho}_{\text{Spearman}} = -0.182$ ,  $\text{CI}_{95\%} [-0.694, 0.453]$ ,  $n_{\text{pairs}} = 12$

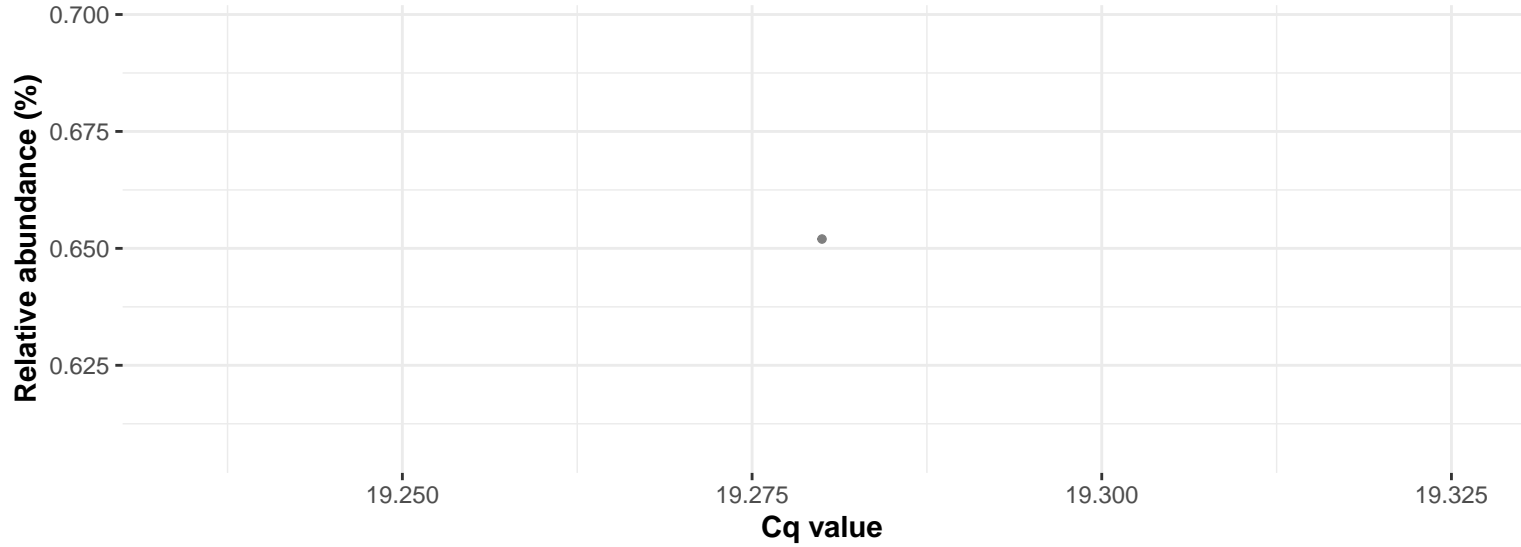


Correlation within: IM-DIM

$\log_e(S) = 5.799$ ,  $p = 0.633$ ,  $\hat{\rho}_{\text{Spearman}} = -0.154$ ,  $\text{CI}_{95\%} [-0.679, 0.476]$ ,  $n_{\text{pairs}} = 12$



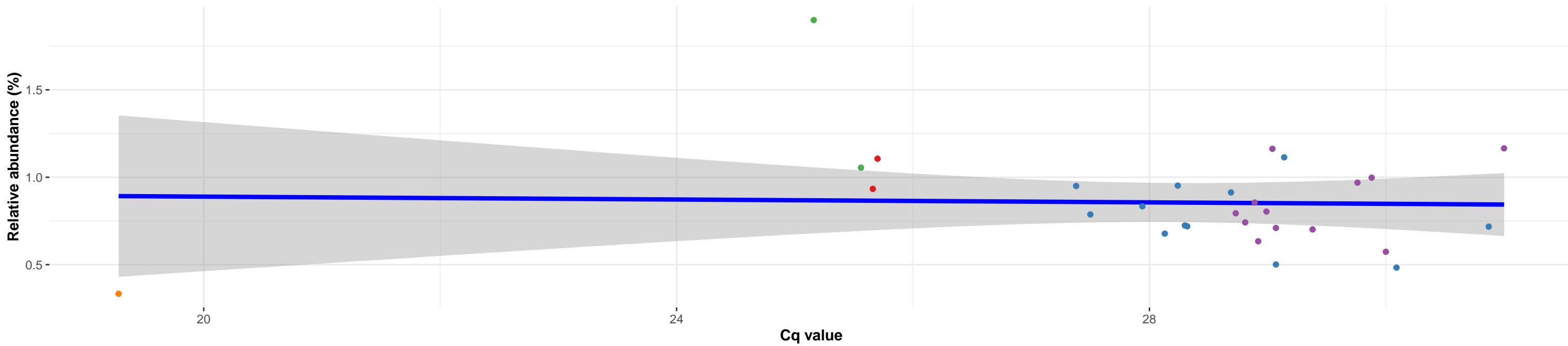
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; s\_\_uncultured Virgibacillus sp.

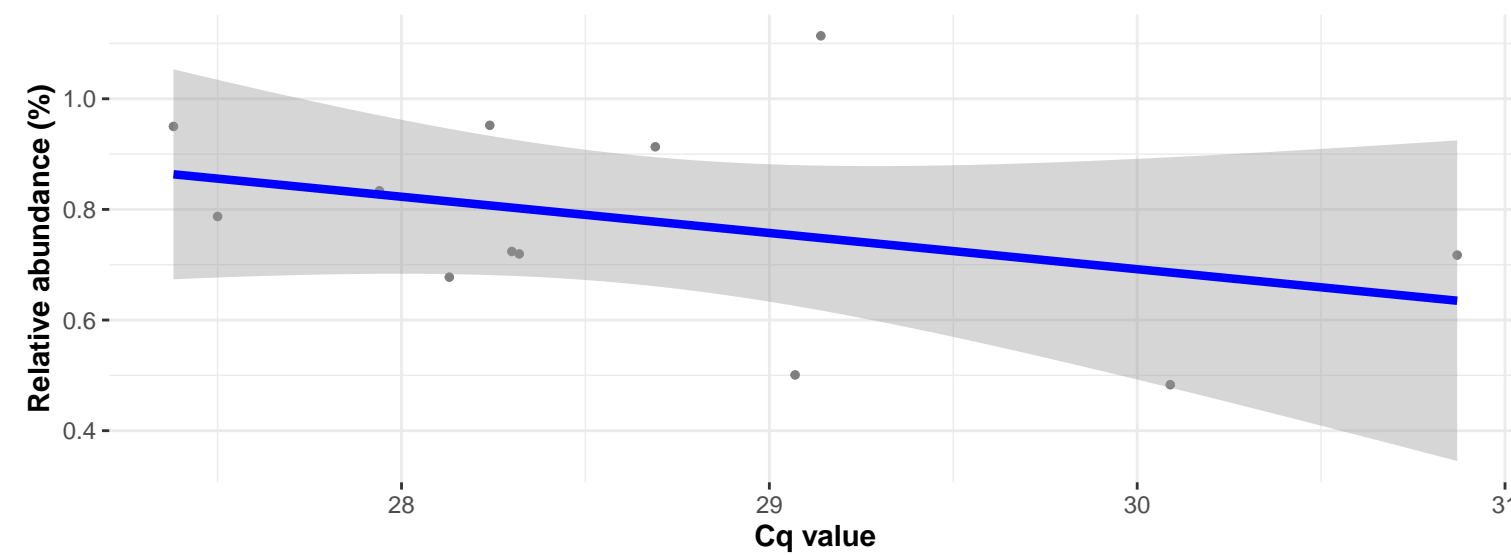
### Correlation with all samples

$\log_e(S) = 8.453$ ,  $p = 0.421$ ,  $\hat{\rho}_{\text{Spearman}} = -0.155$ ,  $\text{CI}_{95\%} [-0.502, 0.235]$ ,  $n_{\text{pairs}} = 29$



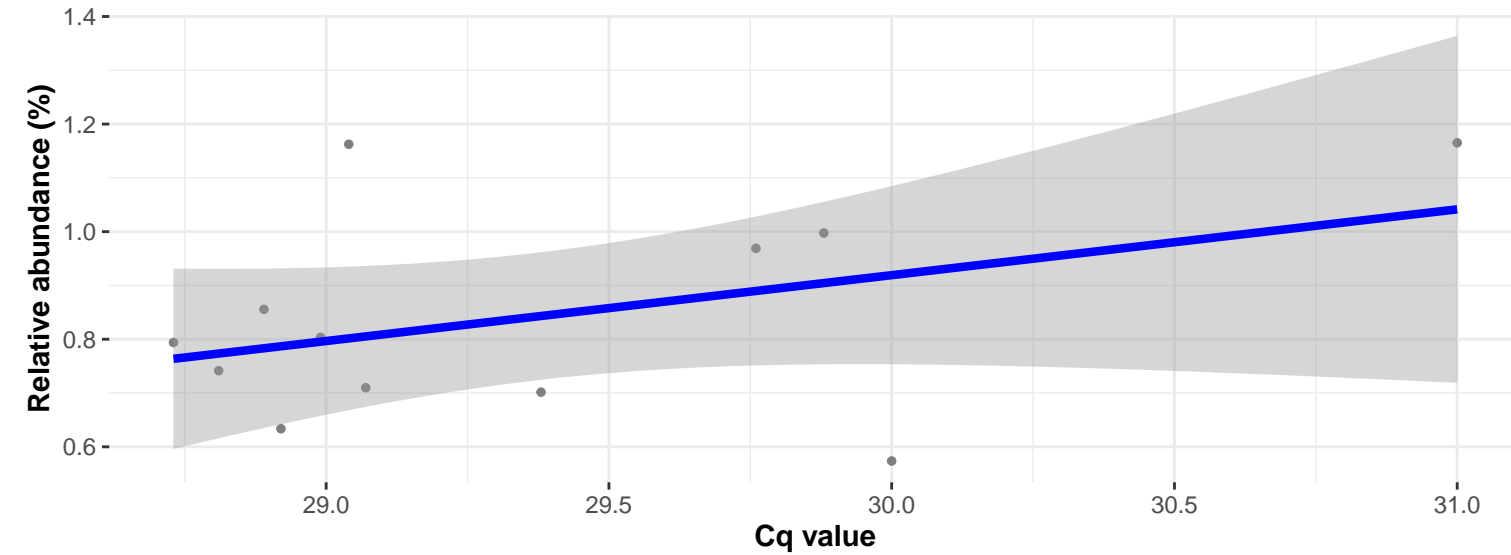
### Correlation within: IM-PIM

$\log_e(S) = 5.966$ ,  $p = 0.245$ ,  $\hat{\rho}_{\text{Spearman}} = -0.364$ ,  $\text{CI}_{95\%} [-0.783, 0.284]$ ,  $n_{\text{pairs}} = 12$

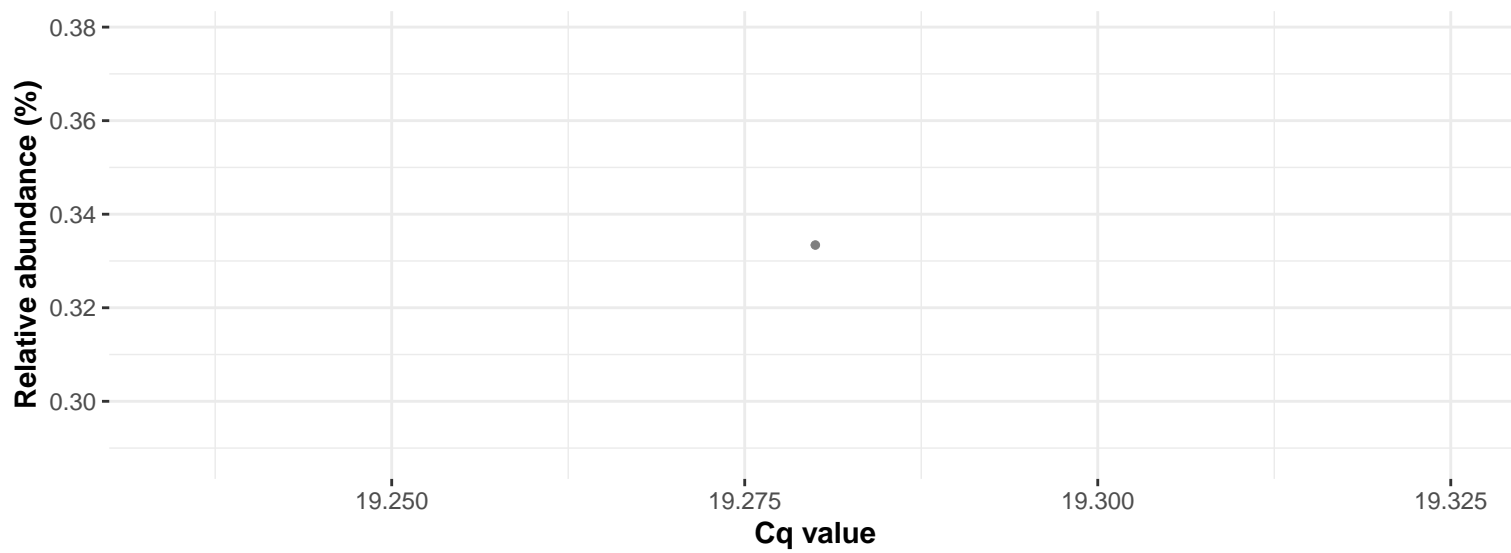


### Correlation within: IM-DIM

$\log_e(S) = 5.421$ ,  $p = 0.513$ ,  $\hat{\rho}_{\text{Spearman}} = 0.210$ ,  $\text{CI}_{95\%} [-0.430, 0.709]$ ,  $n_{\text{pairs}} = 12$



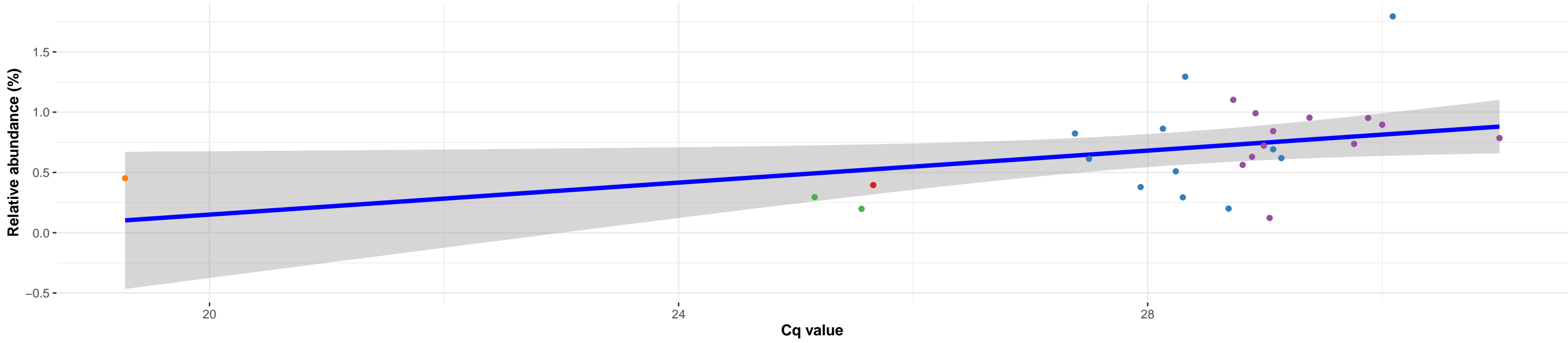
### Correlation within: Feed



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

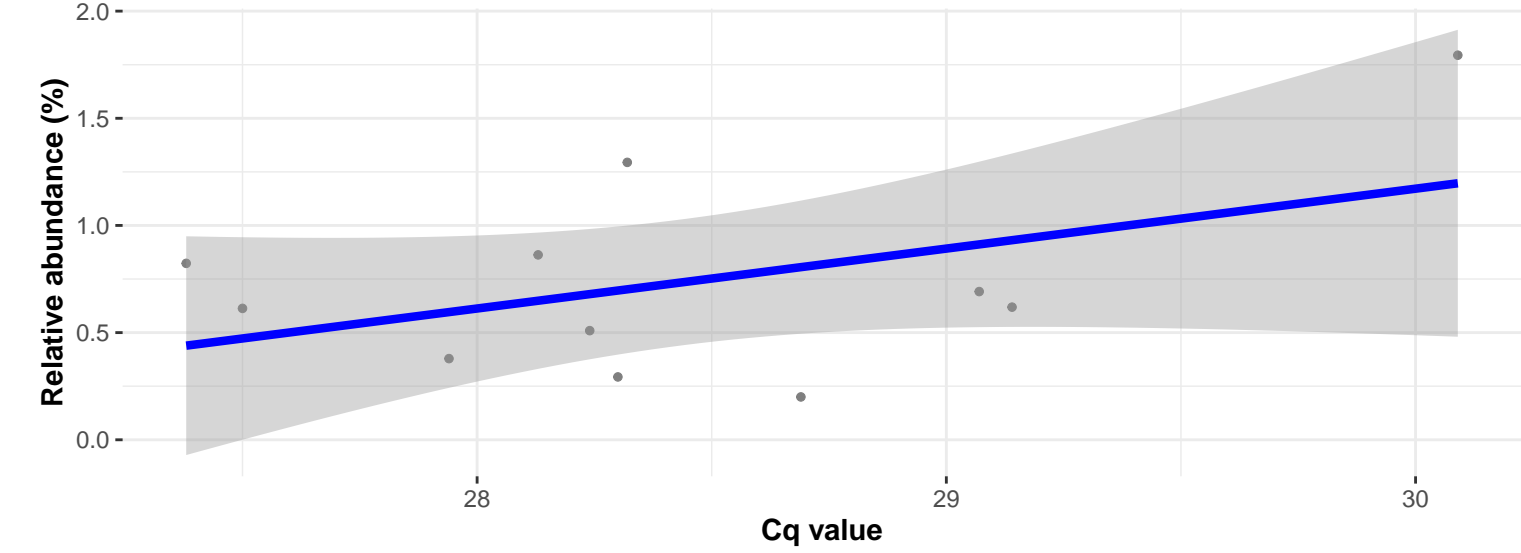
Correlation with all samples

$\log_e(S) = 7.348$ ,  $p = 0.005$ ,  $\hat{\rho}_{\text{Spearman}} = 0.526$ ,  $CI_{95\%} [0.171, 0.760]$ ,  $n_{\text{pairs}} = 27$



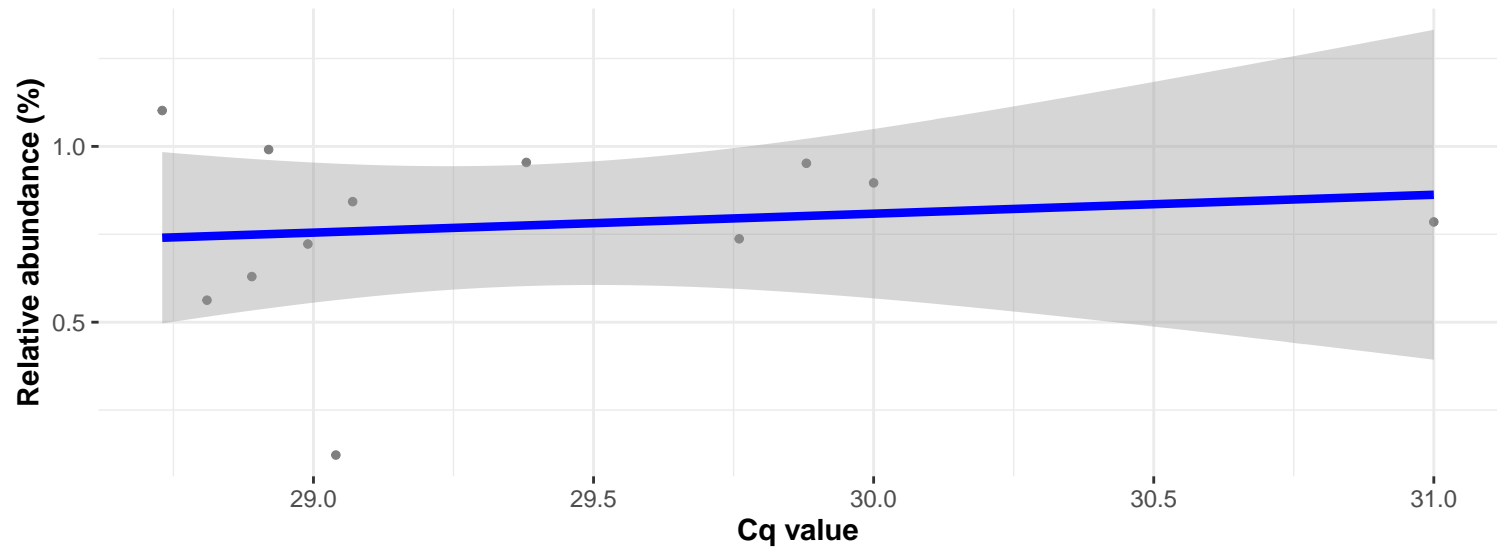
Correlation within: IM-PIM

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

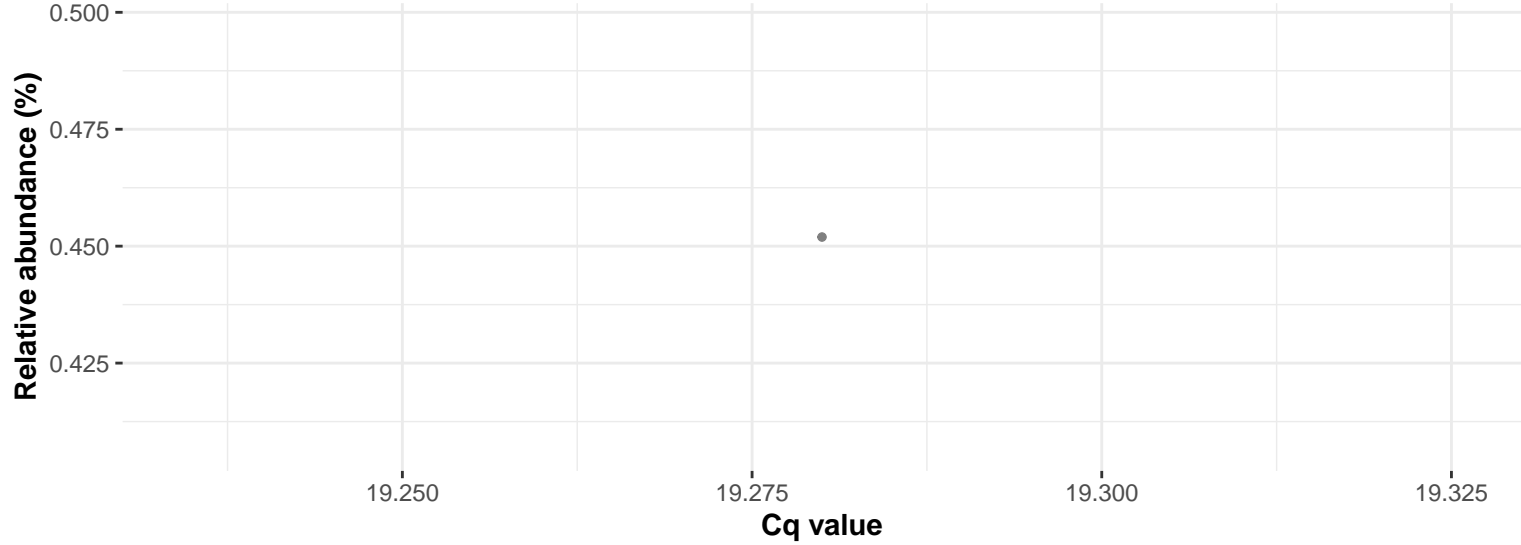


Correlation within: IM-DIM

$\log_e(S) = 5.568$ ,  $p = 0.795$ ,  $\hat{\rho}_{\text{Spearman}} = 0.084$ ,  $CI_{95\%} [-0.529, 0.639]$ ,  $n_{\text{pairs}} = 12$



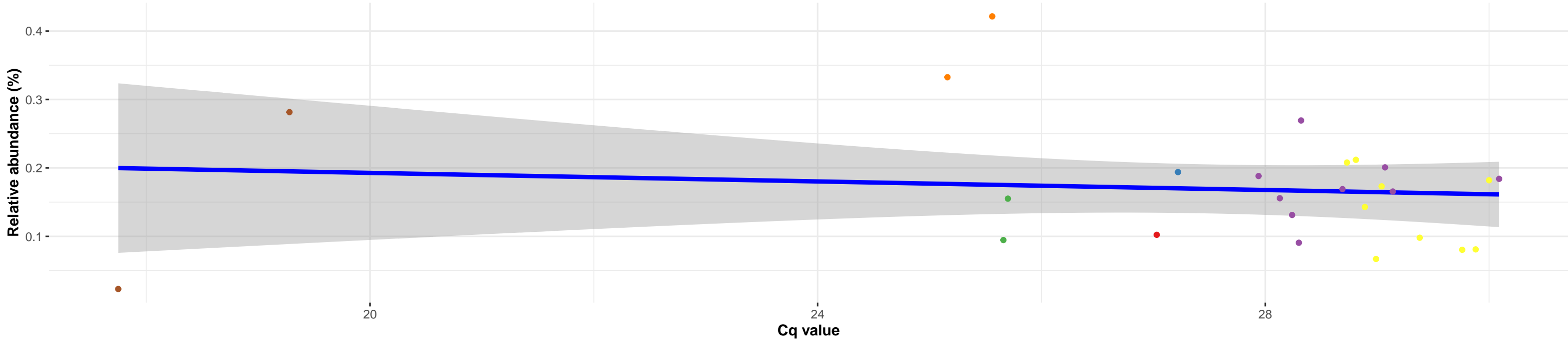
Correlation within: Feed



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

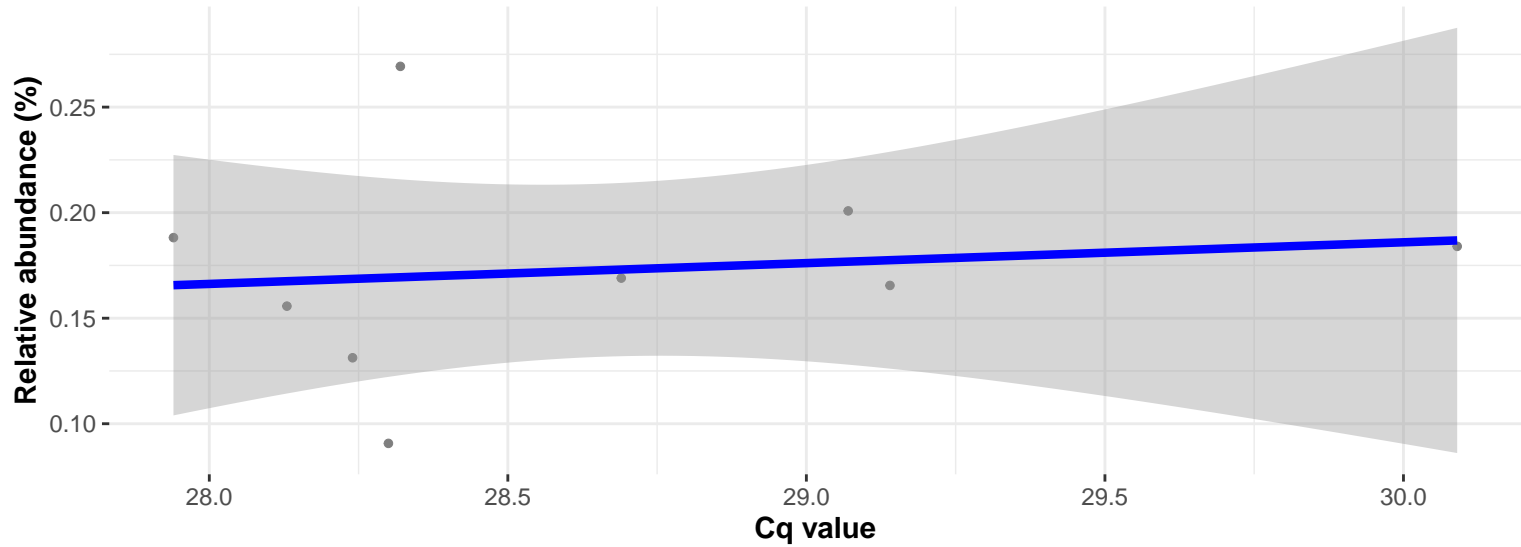
Correlation with all samples

$\log_e(S) = 8.155$ ,  $p = 0.351$ ,  $\hat{\rho}_{\text{Spearman}} = -0.190$ ,  $CI_{95\%} [-0.547, 0.224]$ ,  $n_{\text{pairs}} = 26$



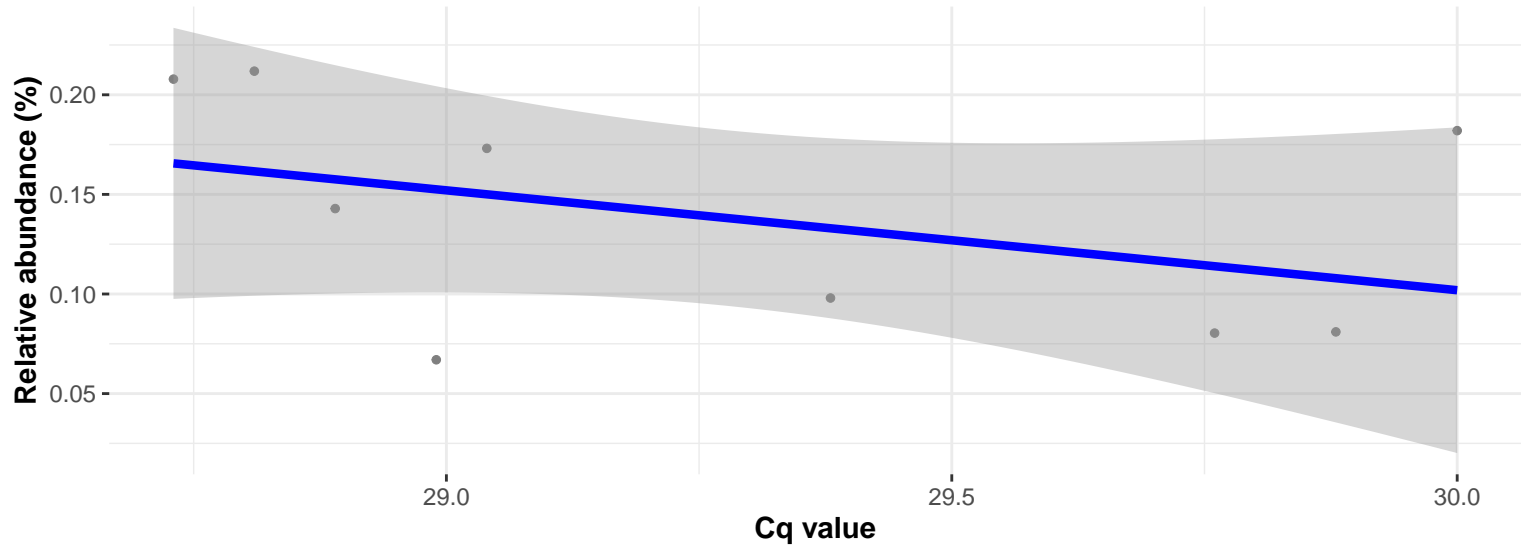
Correlation within: IM-PIM

$\log_e(S) = 4.500$ ,  $p = 0.516$ ,  $\hat{\rho}_{\text{Spearman}} = 0.250$ ,  $CI_{95\%} [-0.514, 0.793]$ ,  $n_{\text{pairs}} = 9$

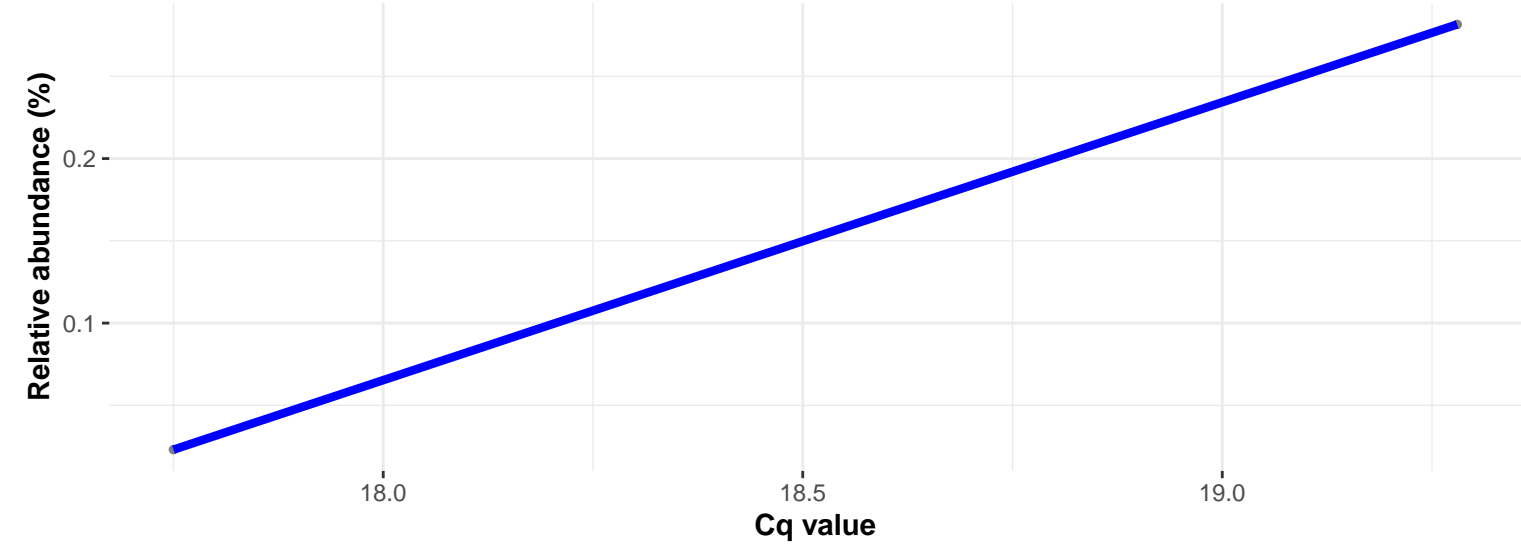


Correlation within: IM-DIM

$\log_e(S) = 5.136$ ,  $p = 0.265$ ,  $\hat{\rho}_{\text{Spearman}} = -0.417$ ,  $CI_{95\%} [-0.853, 0.363]$ ,  $n_{\text{pairs}} = 9$



Correlation within: Feed

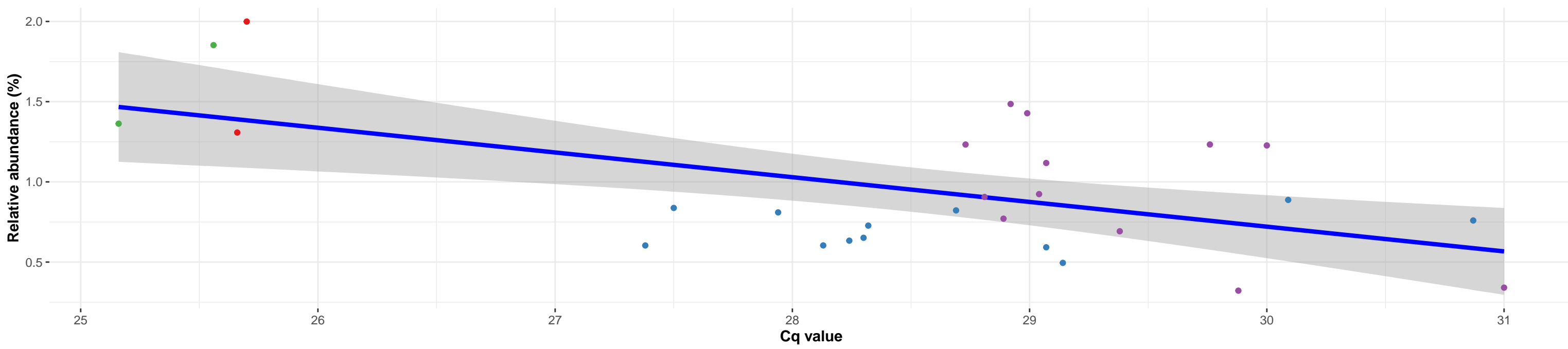




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

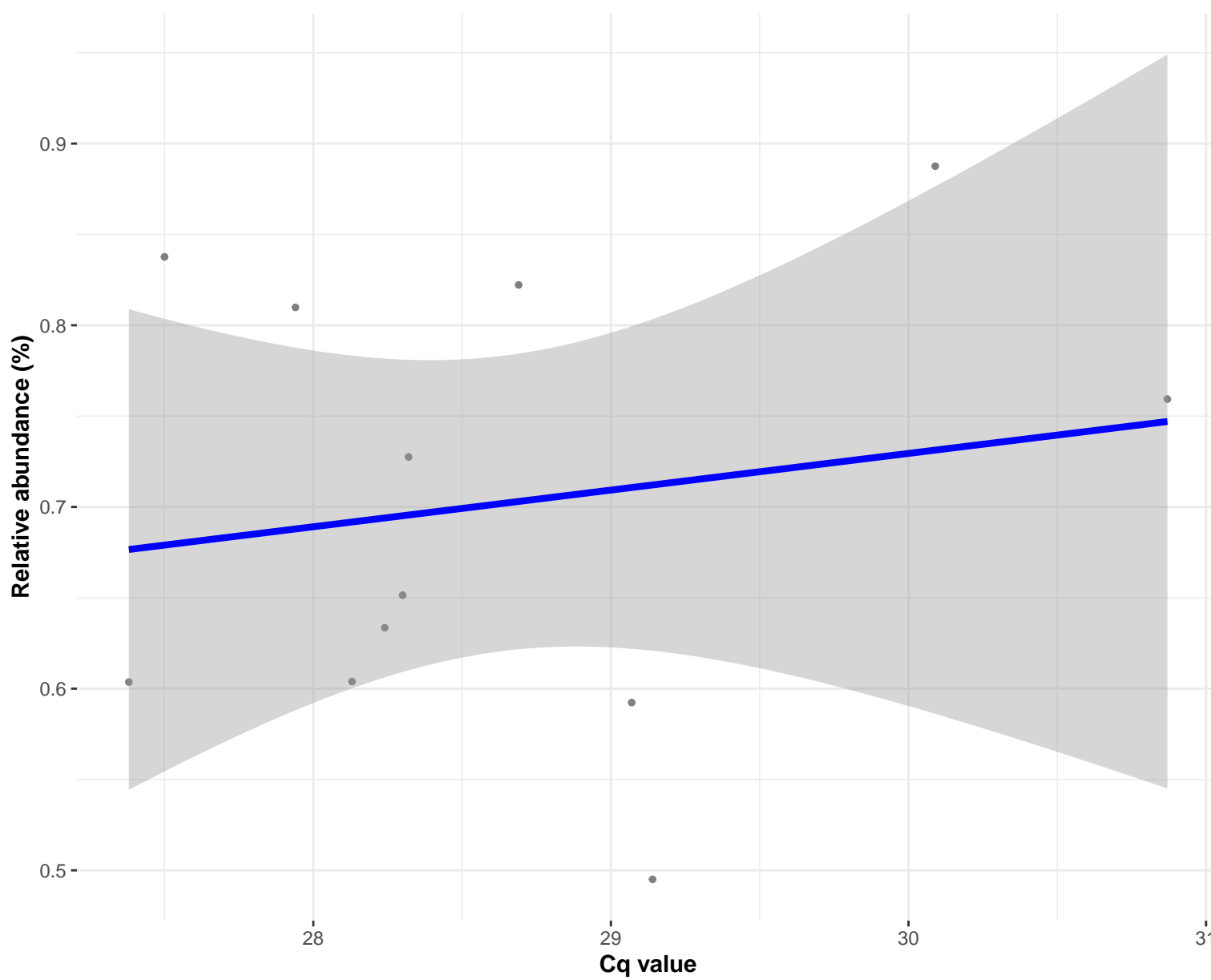
### Correlation with all samples

$\log_e(S) = 8.483$ ,  $p = 0.095$ ,  $\hat{\rho}_{\text{Spearman}} = -0.322$ ,  $CI_{95\%} [-0.628, 0.069]$ ,  $n_{\text{pairs}} = 28$



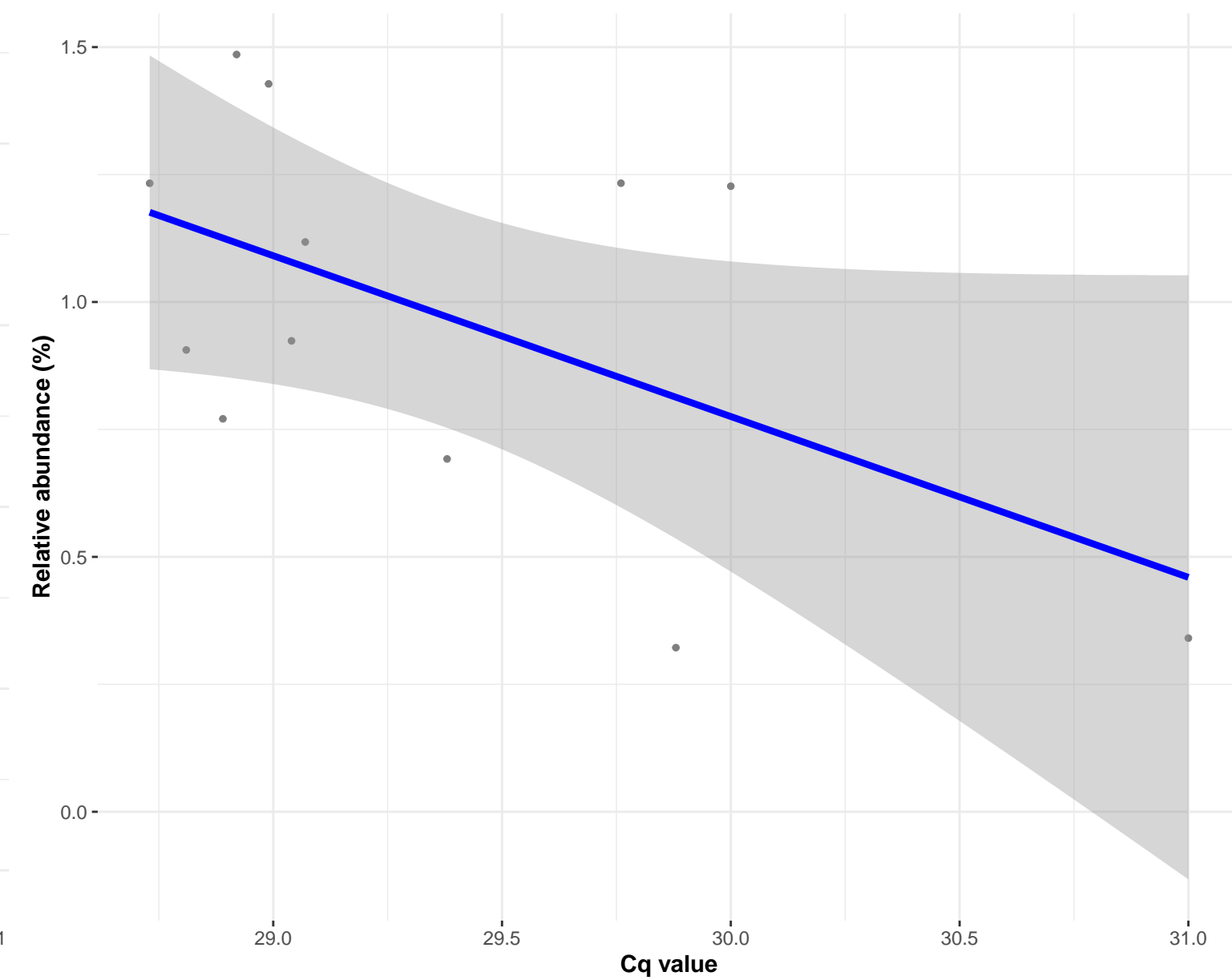
### Correlation within: IM-PIM

$\log_e(S) = 5.606$ ,  $p = 0.880$ ,  $\hat{\rho}_{\text{Spearman}} = 0.049$ ,  $CI_{95\%} [-0.554, 0.618]$ ,  $n_{\text{pairs}} = 12$



### Correlation within: IM-DIM

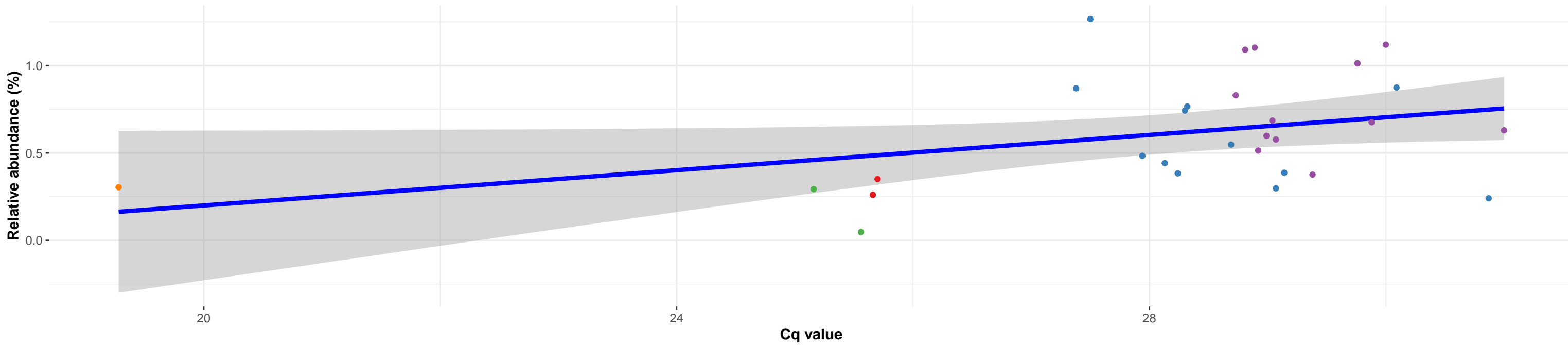
$\log_e(S) = 5.966$ ,  $p = 0.245$ ,  $\hat{\rho}_{\text{Spearman}} = -0.364$ ,  $CI_{95\%} [-0.783, 0.284]$ ,  $n_{\text{pairs}} = 12$



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; s\_\_Corynebacterium xerosis

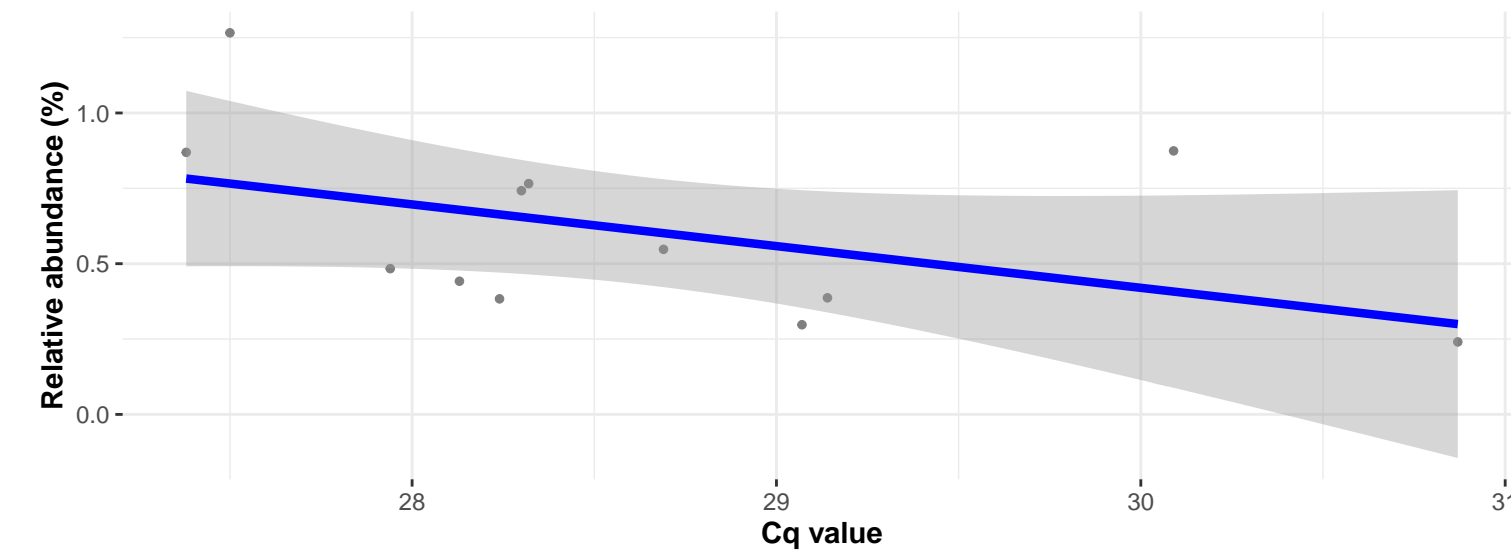
### Correlation with all samples

$\log_e(S) = 7.953$ ,  $p = 0.114$ ,  $\hat{\rho}_{\text{Spearman}} = 0.300$ ,  $CI_{95\%} [-0.087, 0.607]$ ,  $n_{\text{pairs}} = 29$



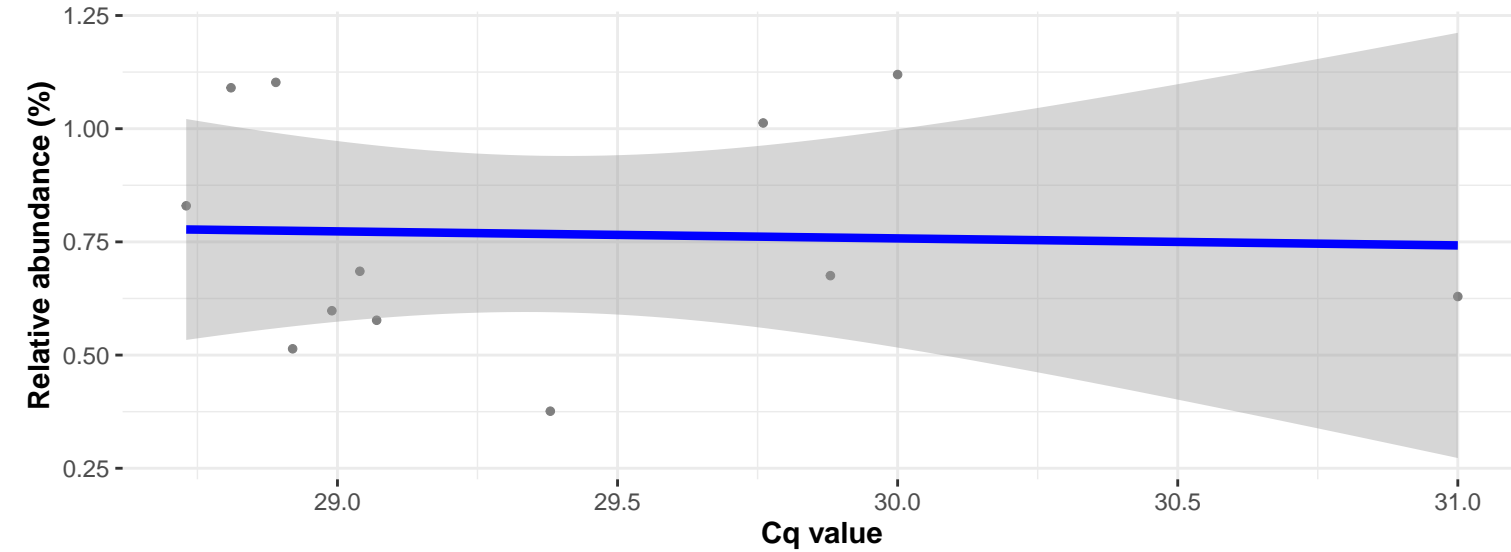
### Correlation within: IM-PIM

$\log_e(S) = 6.016$ ,  $p = 0.159$ ,  $\hat{\rho}_{\text{Spearman}} = -0.434$ ,  $CI_{95\%} [-0.813, 0.205]$ ,  $n_{\text{pairs}} = 12$

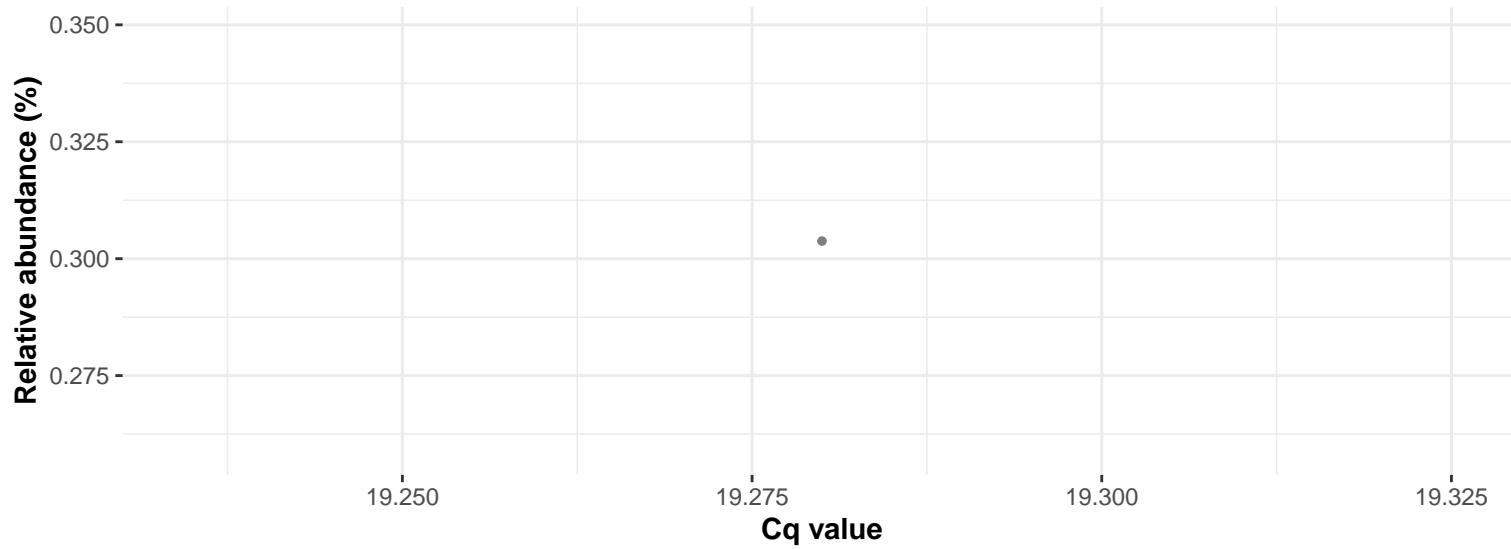


### Correlation within: IM-DIM

$\log_e(S) = 5.749$ ,  $p = 0.762$ ,  $\hat{\rho}_{\text{Spearman}} = -0.098$ ,  $CI_{95\%} [-0.647, 0.519]$ ,  $n_{\text{pairs}} = 12$



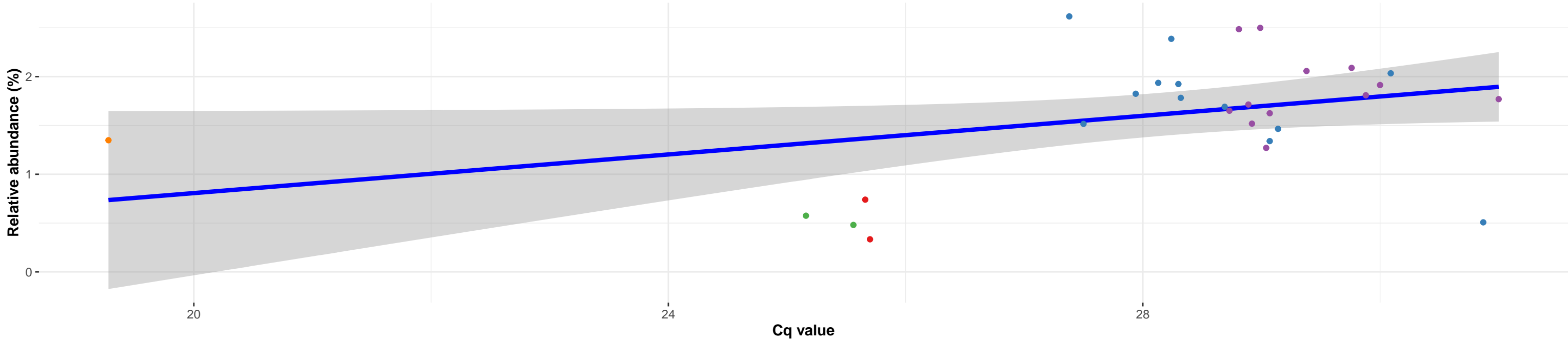
### Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

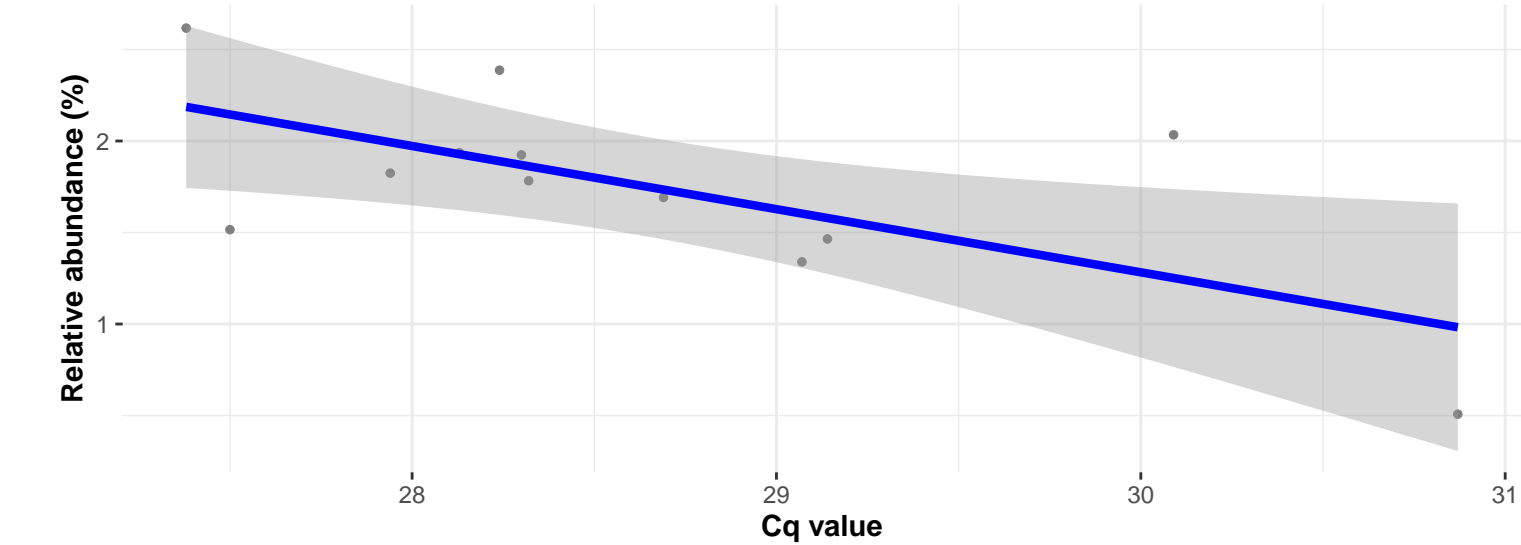
Correlation with all samples

$\log_e(S) = 8.024$ ,  $p = 0.194$ ,  $\hat{\rho}_{\text{Spearman}} = 0.248$ ,  $CI_{95\%} [-0.141, 0.571]$ ,  $n_{\text{pairs}} = 29$



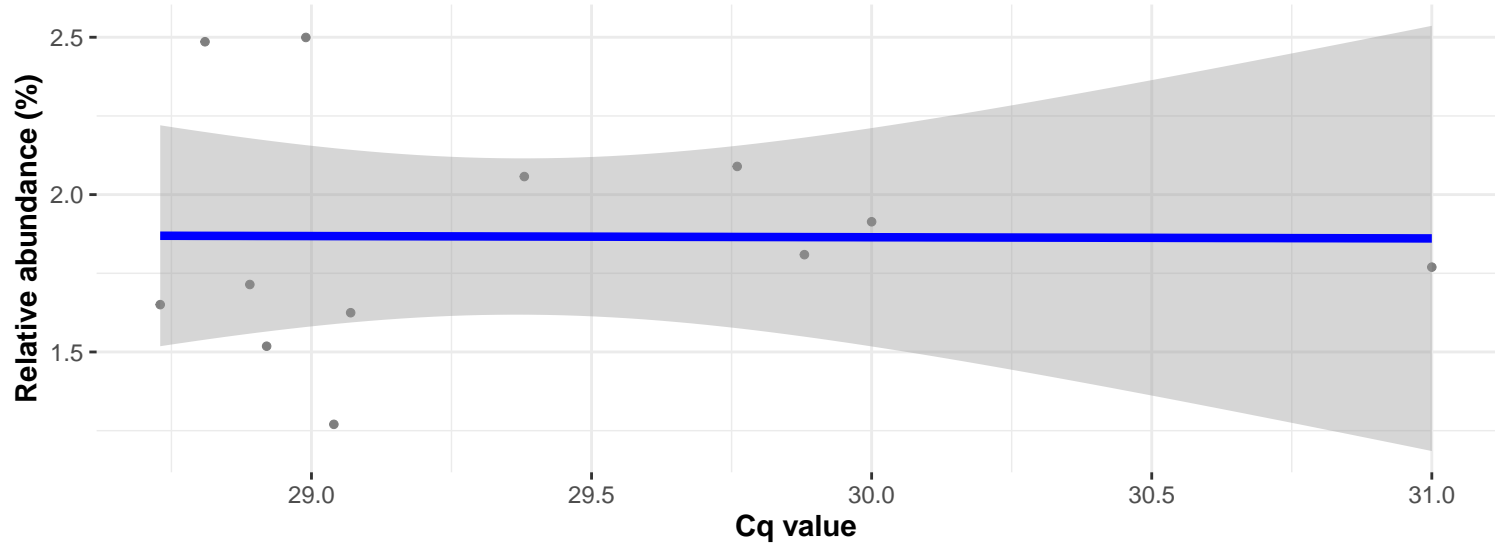
Correlation within: IM-PIM

$\log_e(S) = 6.078$ ,  $p = 0.080$ ,  $\hat{\rho}_{\text{Spearman}} = -0.524$ ,  $CI_{95\%} [-0.850, 0.090]$ ,  $n_{\text{pairs}} = 12$

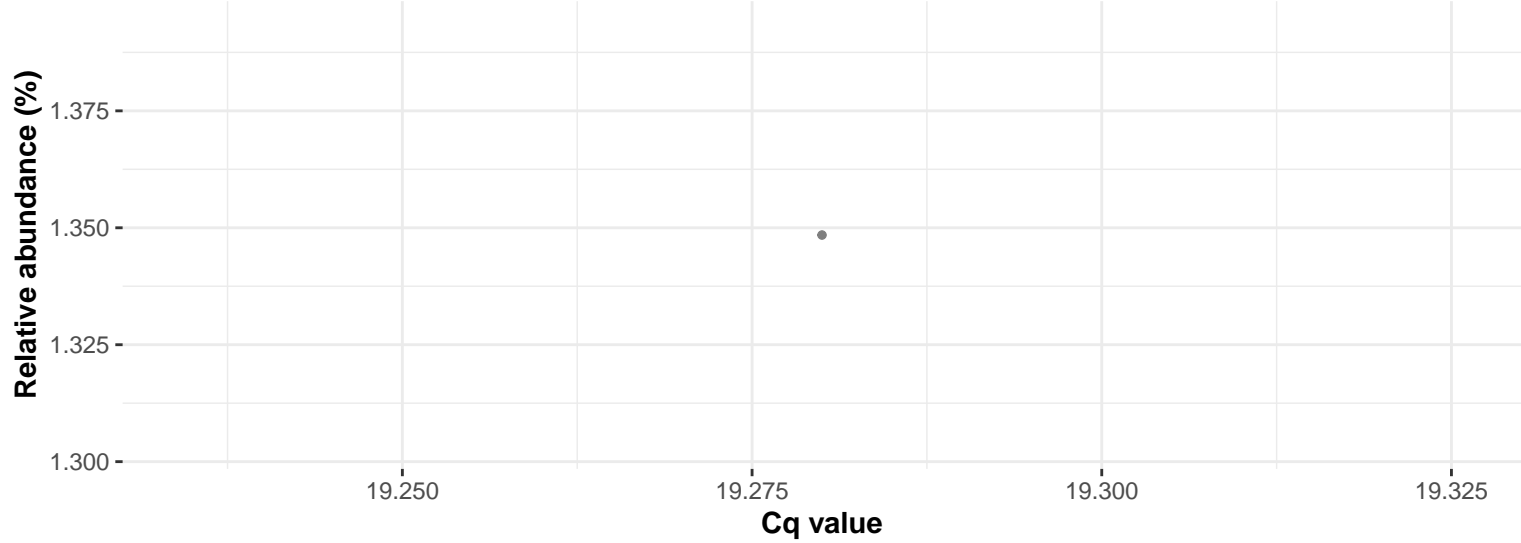


Correlation within: IM-DIM

$\log_e(S) = 5.497$ ,  $p = 0.649$ ,  $\hat{\rho}_{\text{Spearman}} = 0.147$ ,  $CI_{95\%} [-0.481, 0.675]$ ,  $n_{\text{pairs}} = 12$



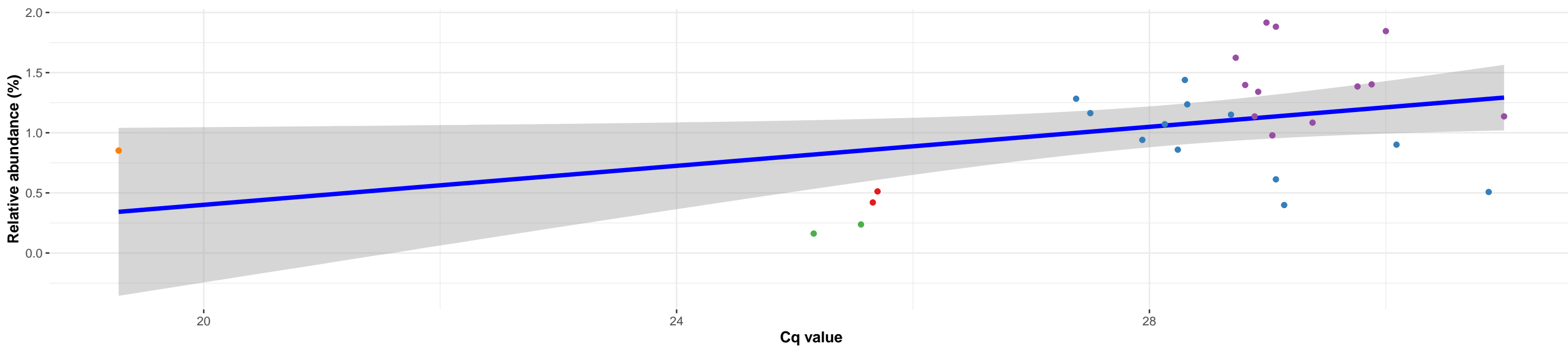
Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Microbacteriaceae; g\_\_Microbacterium; Ambiguous\_taxa

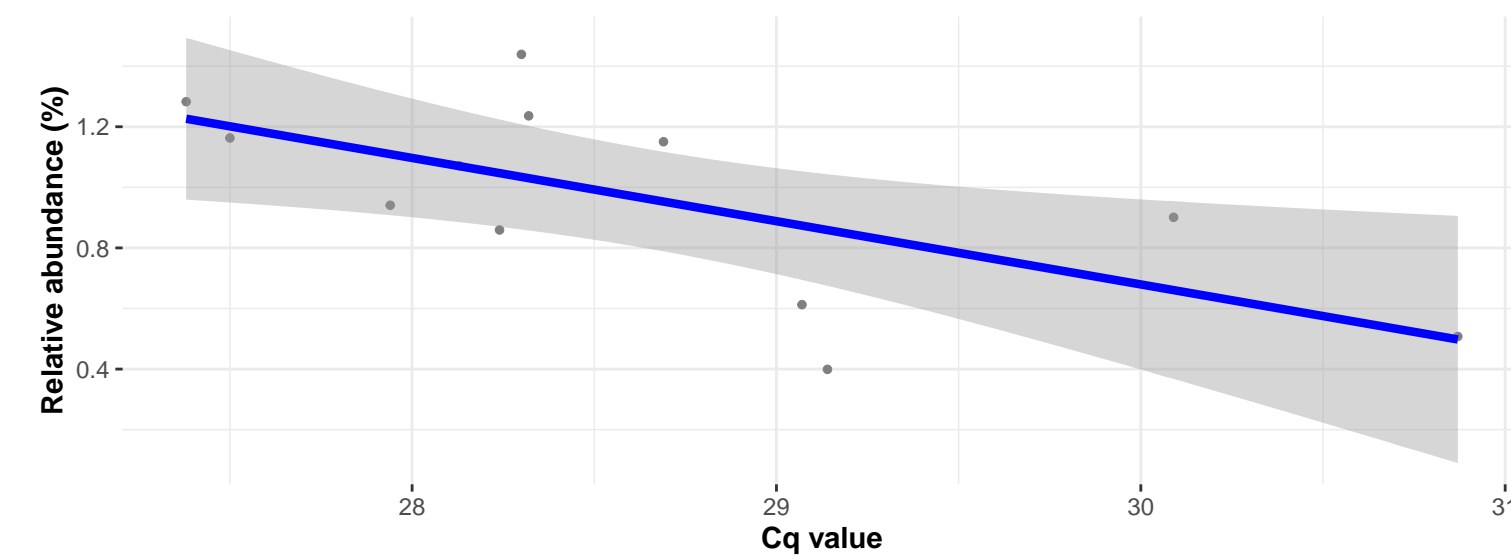
### Correlation with all samples

$\log_e(S) = 7.910$ ,  $p = 0.082$ ,  $\hat{\rho}_{\text{Spearman}} = 0.329$ ,  $CI_{95\%} [-0.054, 0.628]$ ,  $n_{\text{pairs}} = 29$



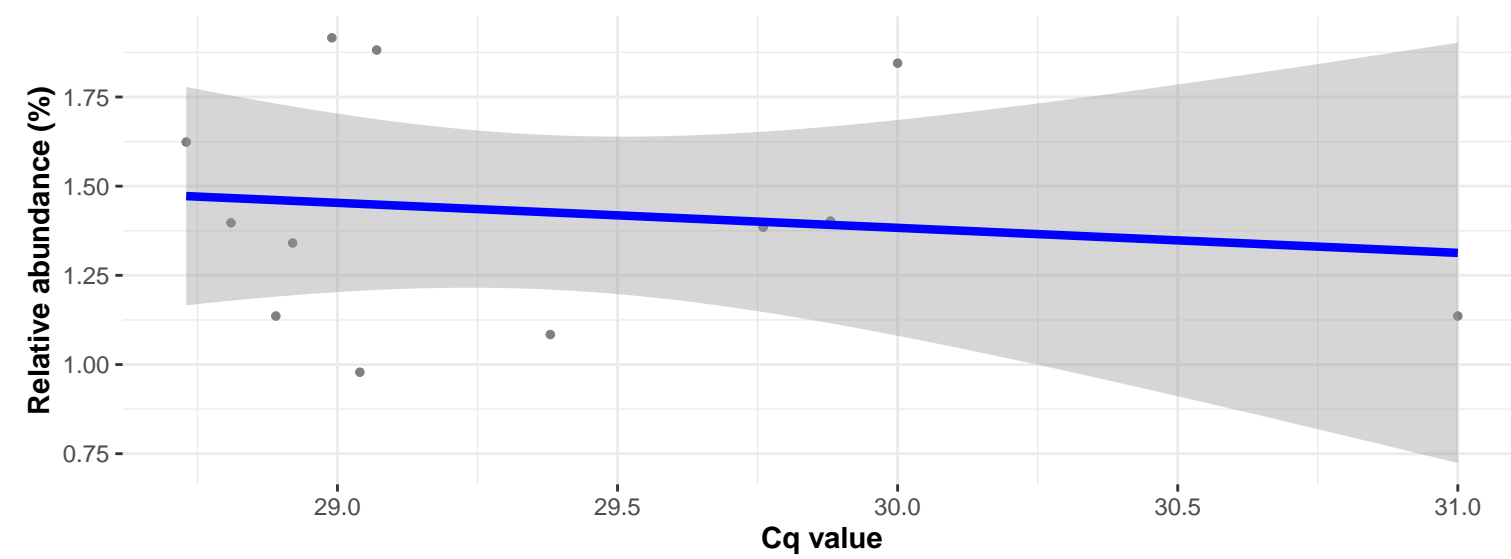
### Correlation within: IM-PIM

$\log_e(S) = 6.144$ ,  $p = 0.028$ ,  $\hat{\rho}_{\text{Spearman}} = -0.629$ ,  $CI_{95\%} [-0.888, -0.068]$ ,  $n_{\text{pairs}} = 12$

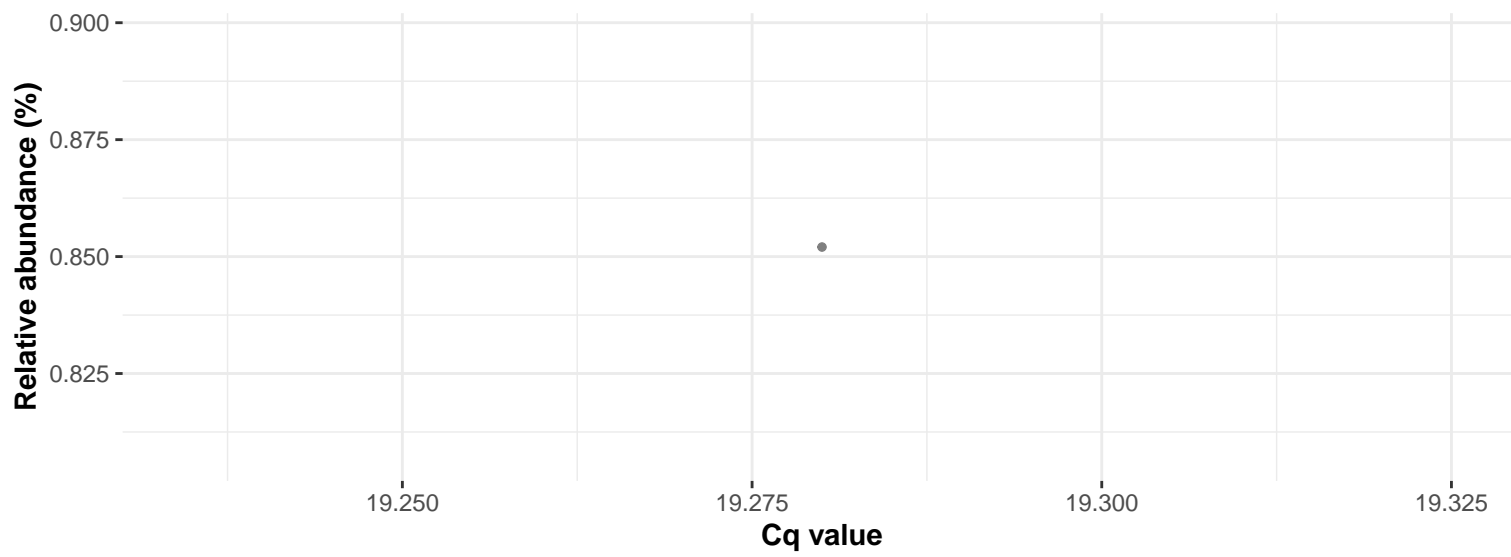


### Correlation within: IM-DIM

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



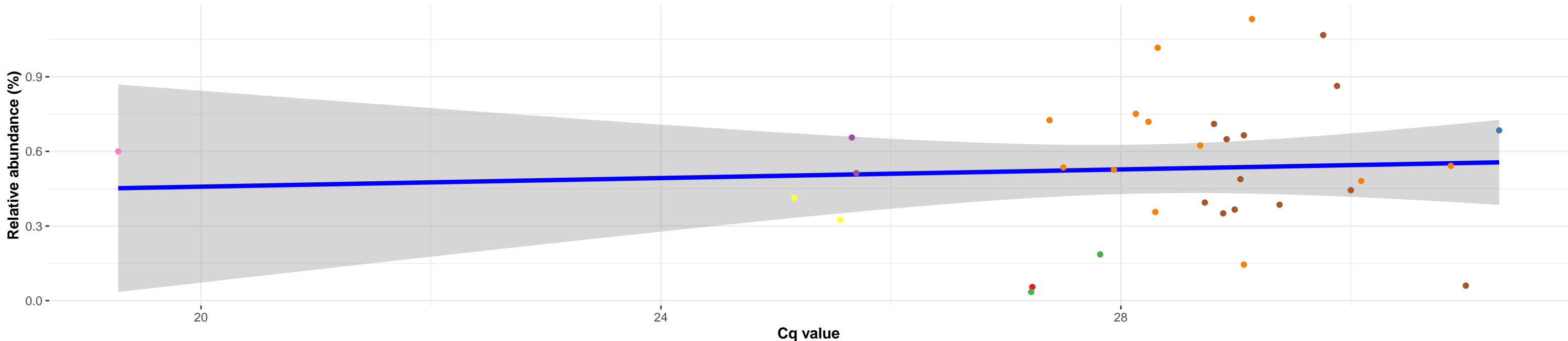
### Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Macrococcus; Ambiguous\_taxa

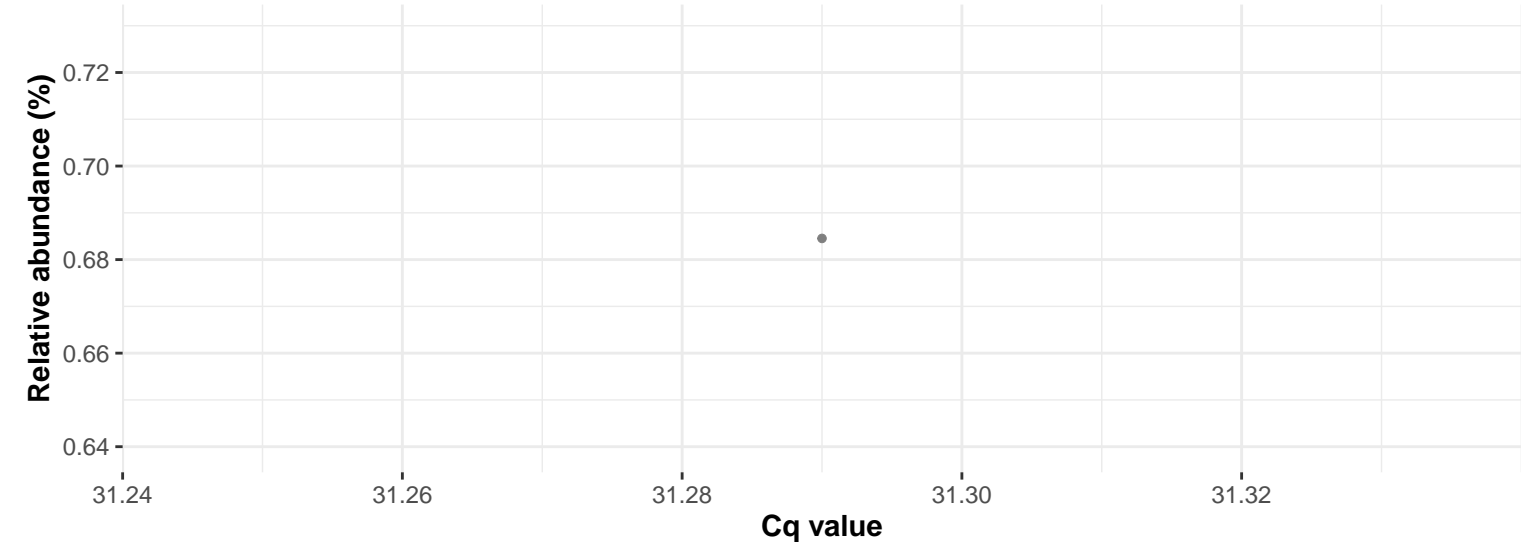
Correlation with all samples

$\log_e(S) = 8.533$ ,  $p = 0.400$ ,  $\hat{\rho}_{\text{Spearman}} = 0.151$ ,  $CI_{95\%} [-0.213, 0.478]$ ,  $n_{\text{pairs}} = 33$



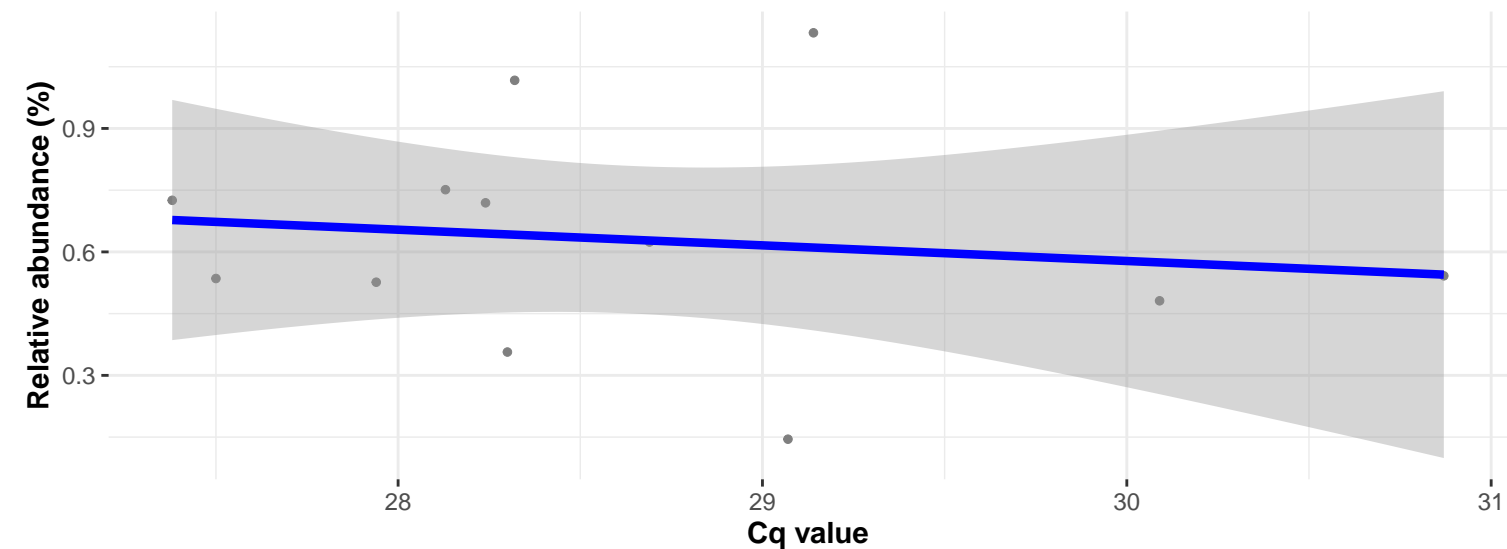
SampleType REF-PID REF-PIM REF-DID IM-PID IM-PIM IM-DID IM-DIM Feed

Correlation within: REF-PIM



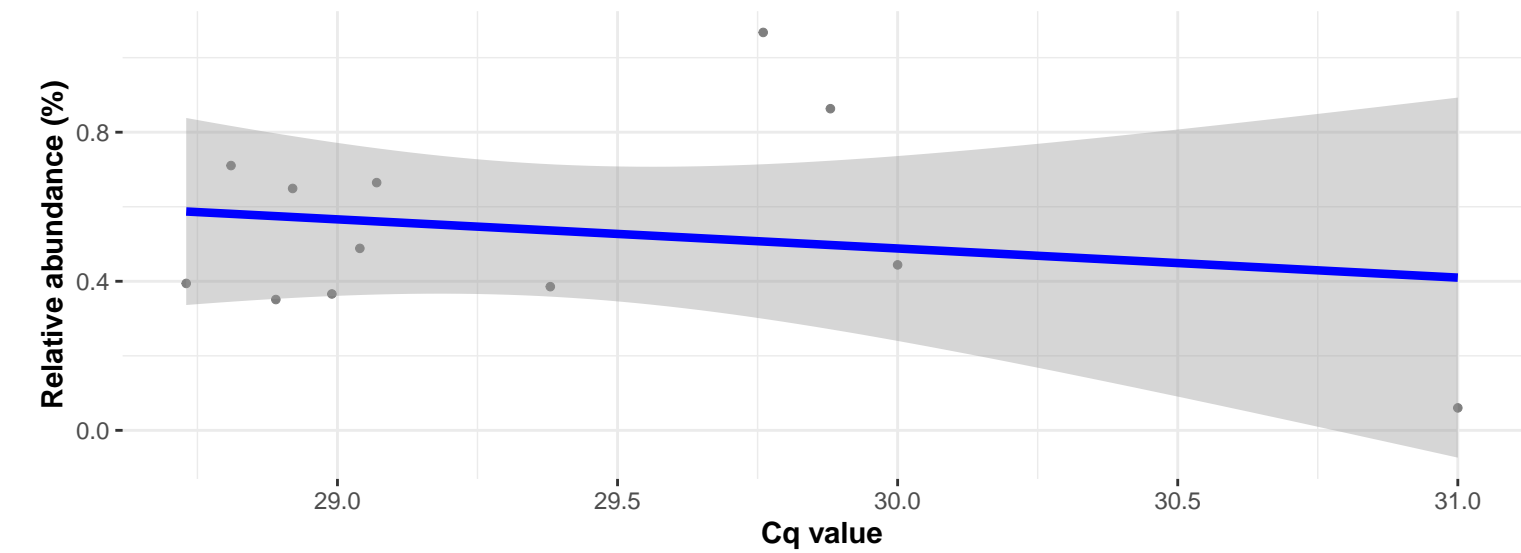
Correlation within: IM-PIM

$\log_e(S) = 5.768$ ,  $p = 0.713$ ,  $\hat{\rho}_{\text{Spearman}} = -0.119$ ,  $CI_{95\%} [-0.660, 0.503]$ ,  $n_{\text{pairs}} = 12$

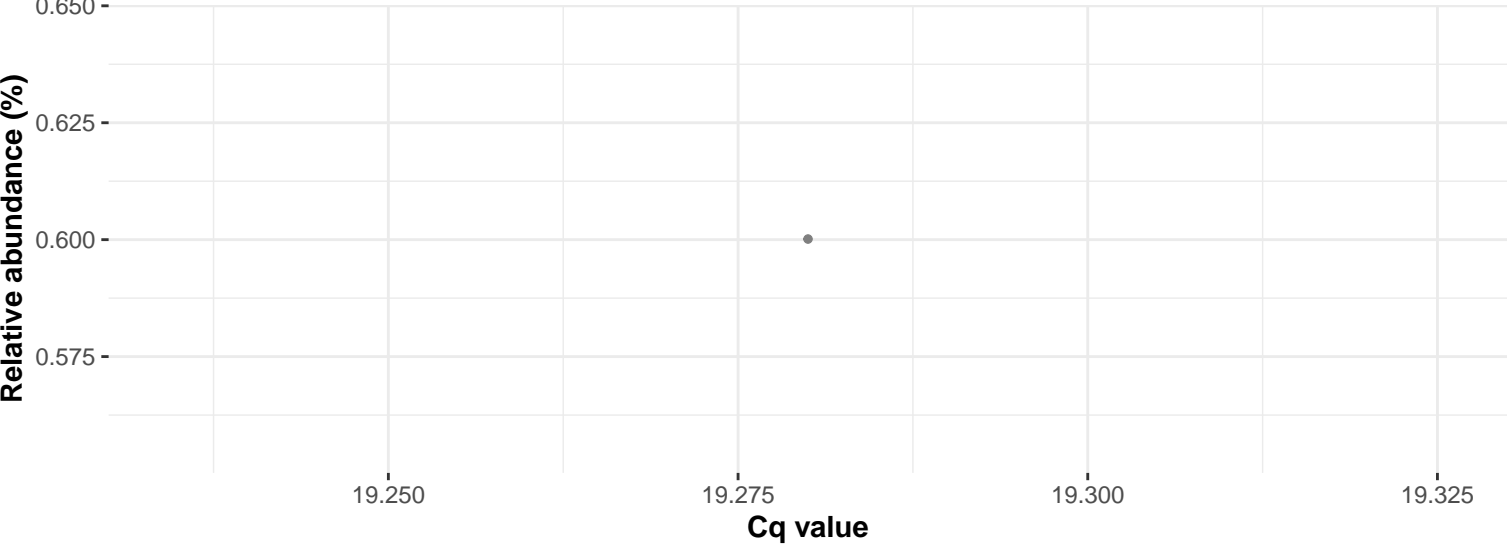


Correlation within: IM-DIM

$\log_e(S) = 5.628$ ,  $p = 0.931$ ,  $\hat{\rho}_{\text{Spearman}} = 0.028$ ,  $CI_{95\%} [-0.568, 0.605]$ ,  $n_{\text{pairs}} = 12$



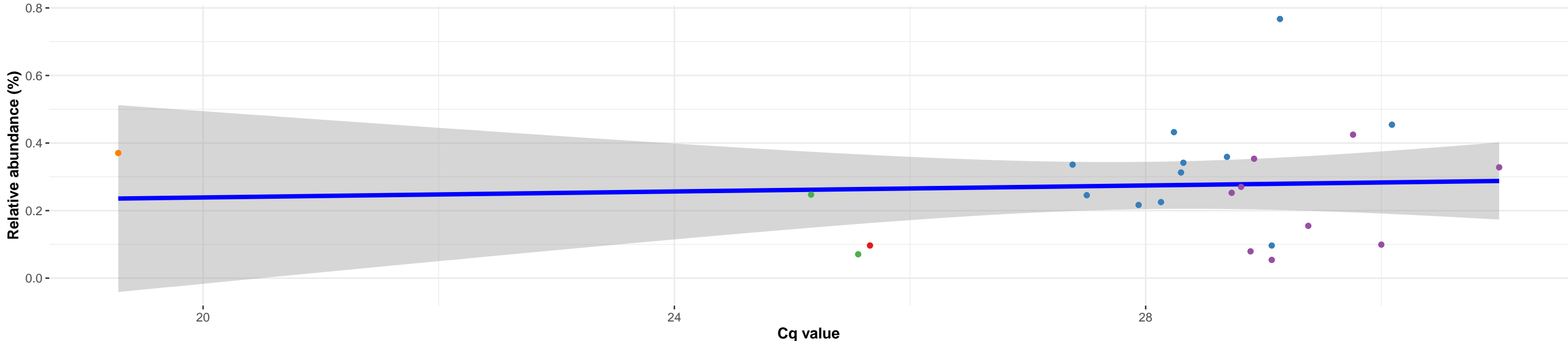
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; NA

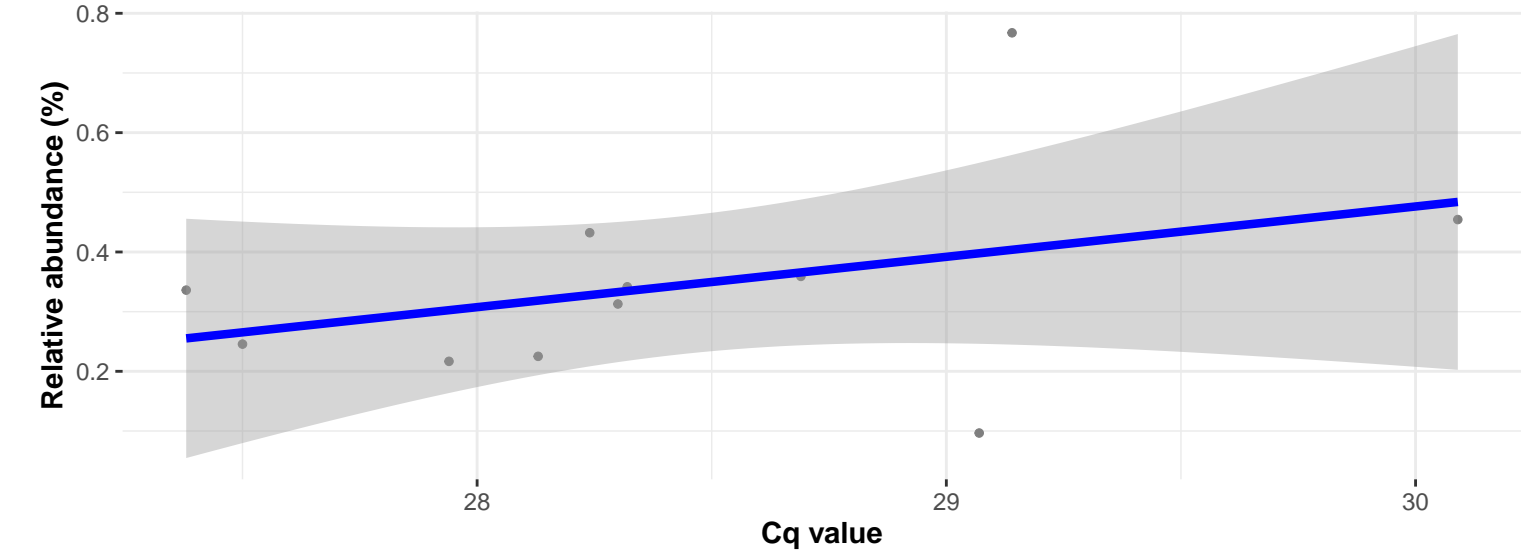
Correlation with all samples

$\log_e(S) = 7.595$ ,  $p = 0.529$ ,  $\hat{\rho}_{\text{Spearman}} = 0.135$ ,  $CI_{95\%} [-0.295, 0.520]$ ,  $n_{\text{pairs}} = 24$



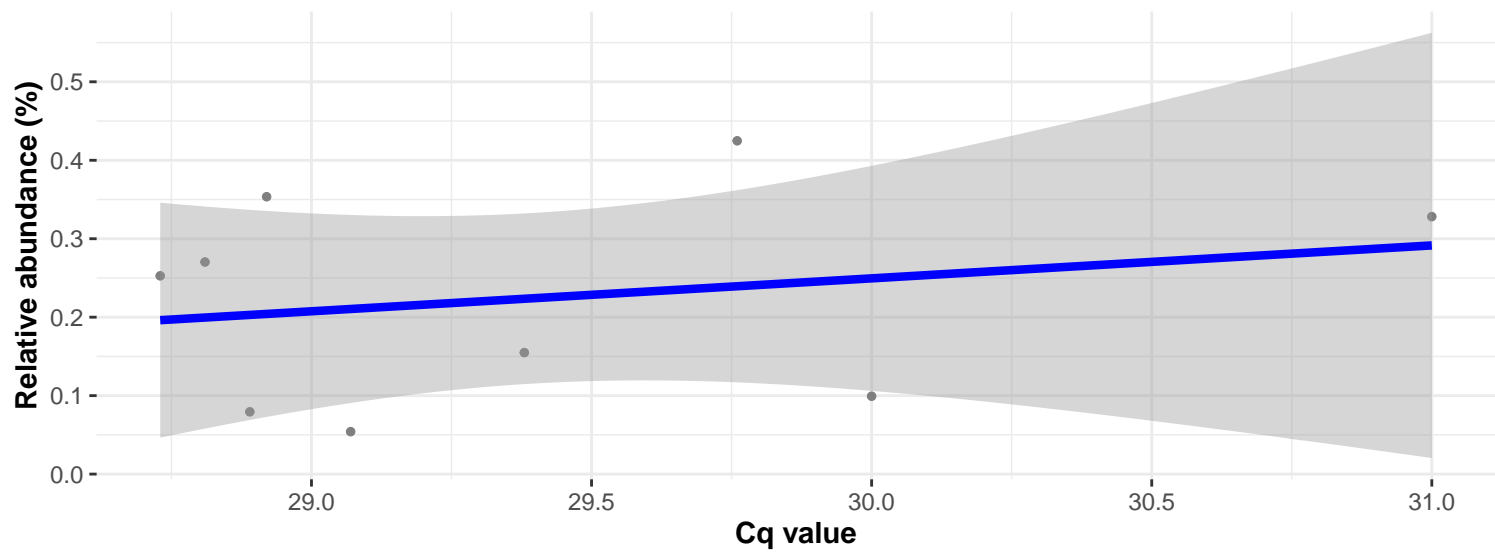
Correlation within: IM-PIM

$\log_e(S) = 4.736$ ,  $p = 0.133$ ,  $\hat{\rho}_{\text{Spearman}} = 0.482$ ,  $CI_{95\%} [-0.186, 0.845]$ ,  $n_{\text{pairs}} = 11$

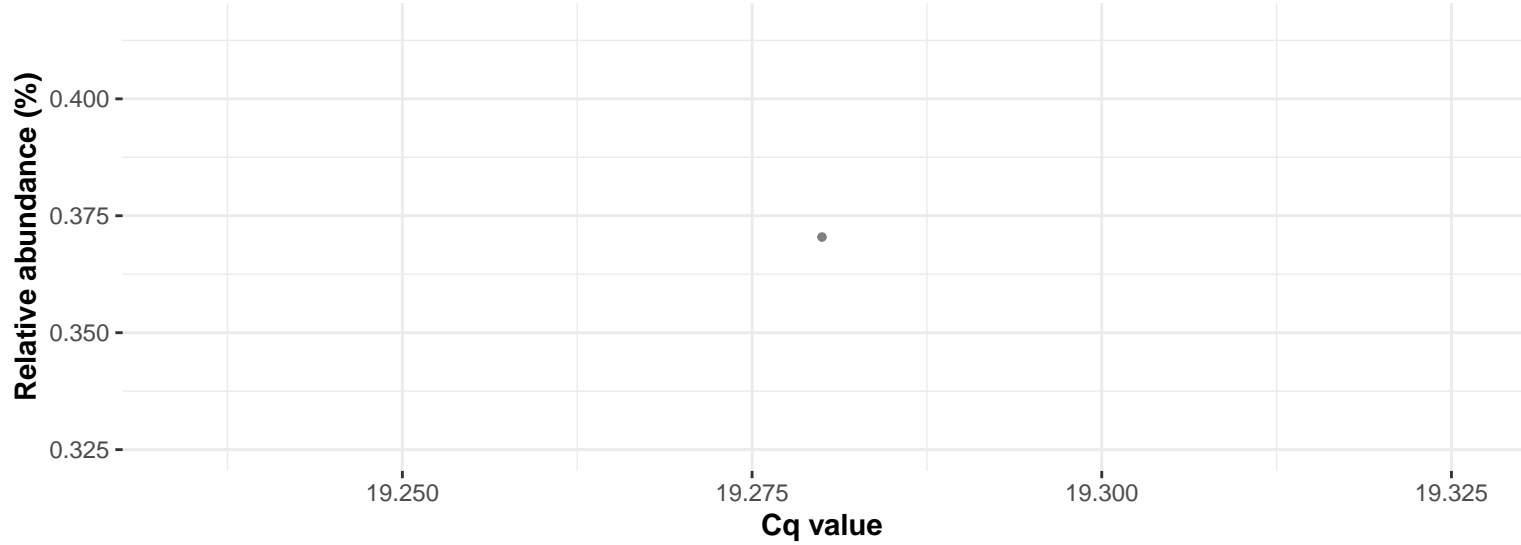


Correlation within: IM-DIM

$\log_e(S) = 4.625$ ,  $p = 0.700$ ,  $\hat{\rho}_{\text{Spearman}} = 0.150$ ,  $CI_{95\%} [-0.587, 0.751]$ ,  $n_{\text{pairs}} = 9$



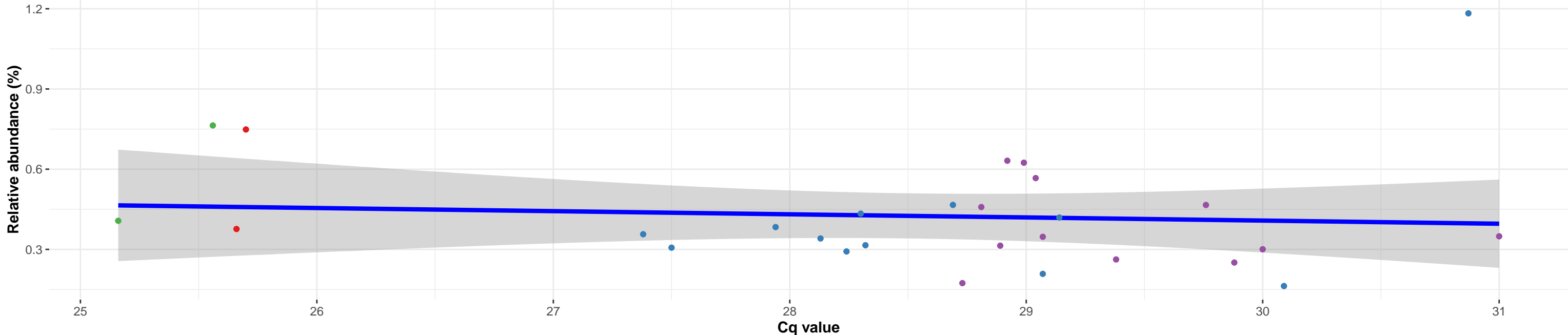
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Ornithinibacillus; Ambiguous\_taxa

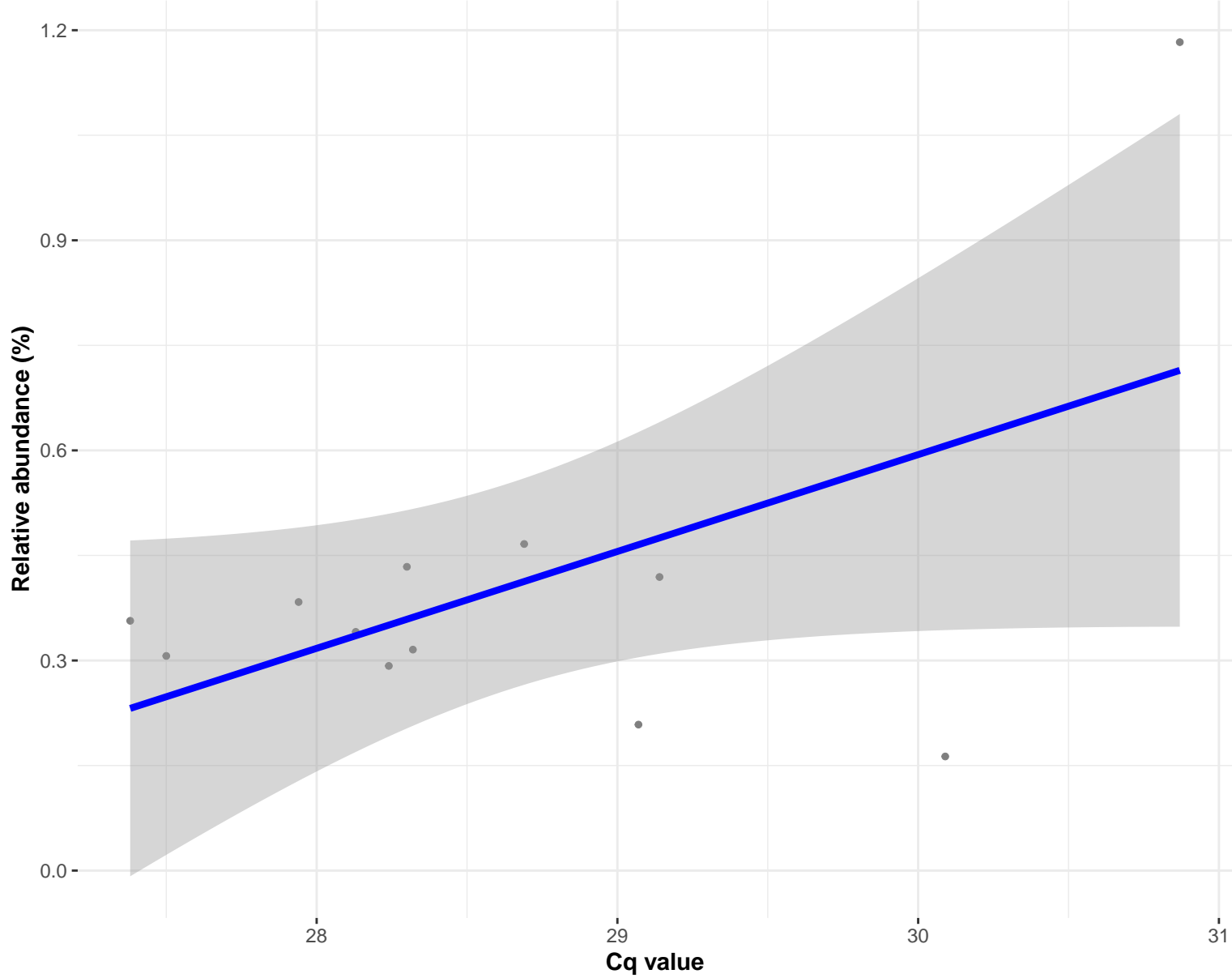
Correlation with all samples

$\log_e(S) = 8.396$ ,  $p = 0.279$ ,  $\hat{\rho}_{\text{Spearman}} = -0.212$ ,  $\text{CI}_{95\%} [-0.550, 0.186]$ ,  $n_{\text{pairs}} = 28$



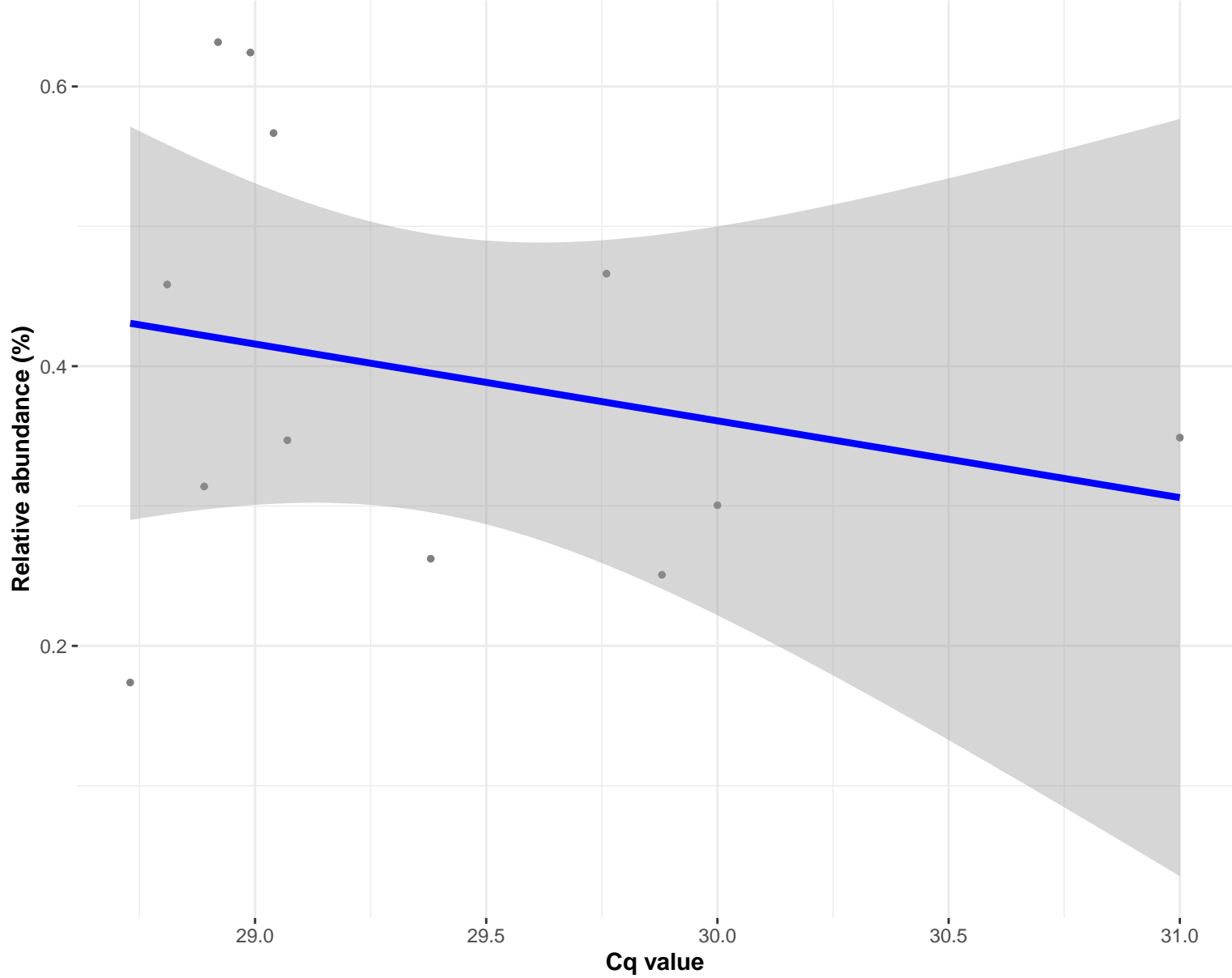
Correlation within: IM-PIM

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



Correlation within: IM-DIM

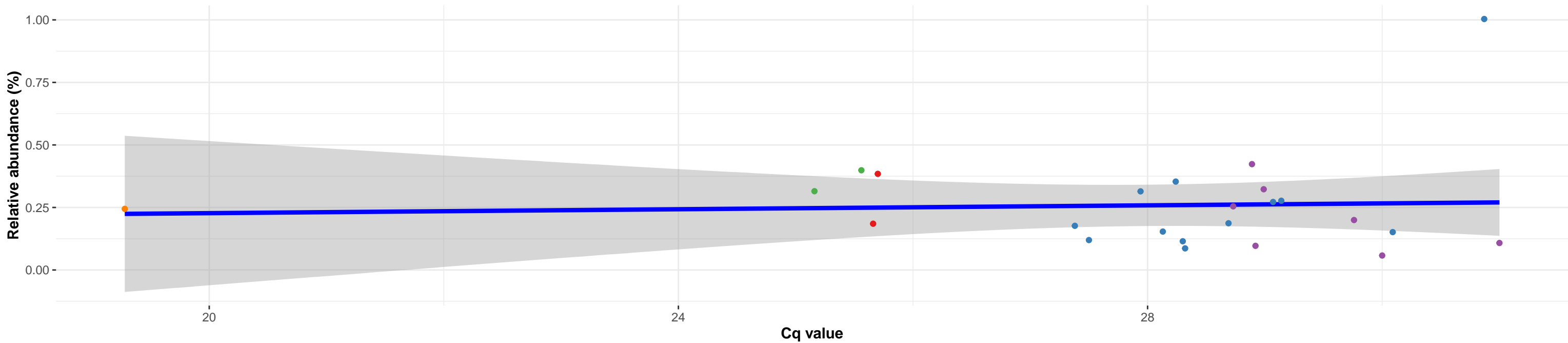
$\log_e(S) = 5.768$ ,  $p = 0.713$ ,  $\hat{\rho}_{\text{Spearman}} = -0.119$ ,  $\text{CI}_{95\%} [-0.660, 0.503]$ ,  $n_{\text{pairs}} = 12$



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

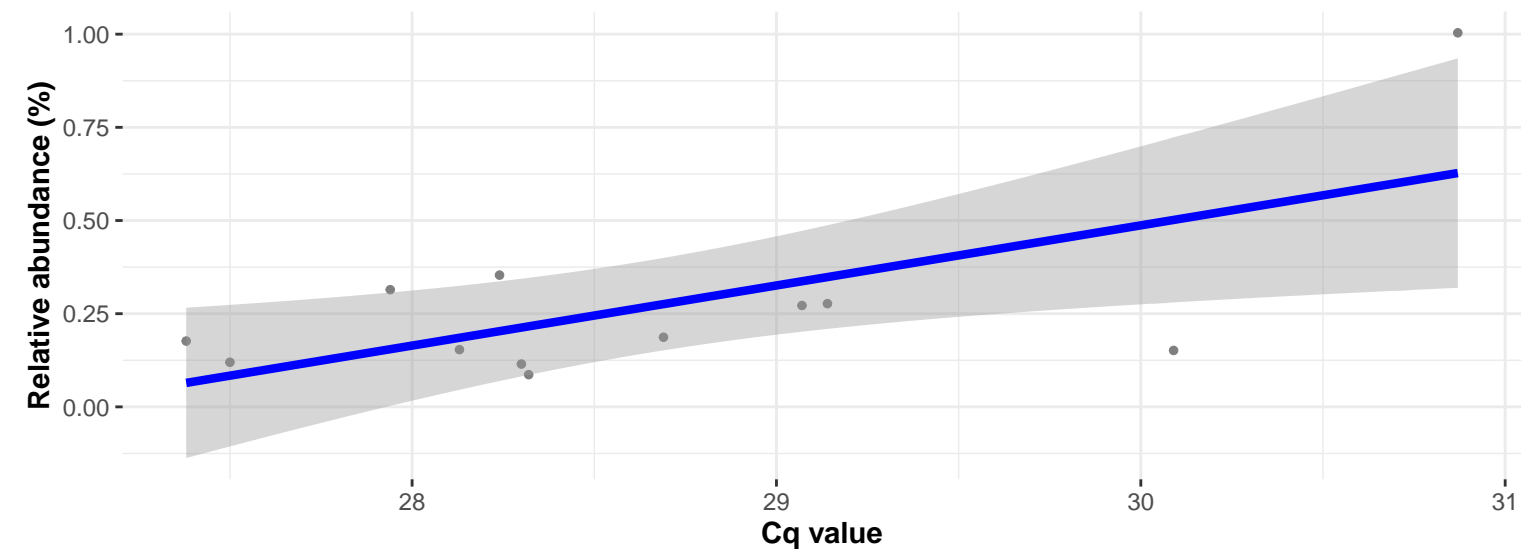
Correlation with all samples

$\log_e(S) = 7.912$ ,  $p = 0.382$ ,  $\hat{\rho}_{\text{Spearman}} = -0.187$ ,  $CI_{95\%} [-0.558, 0.246]$ ,  $n_{\text{pairs}} = 24$



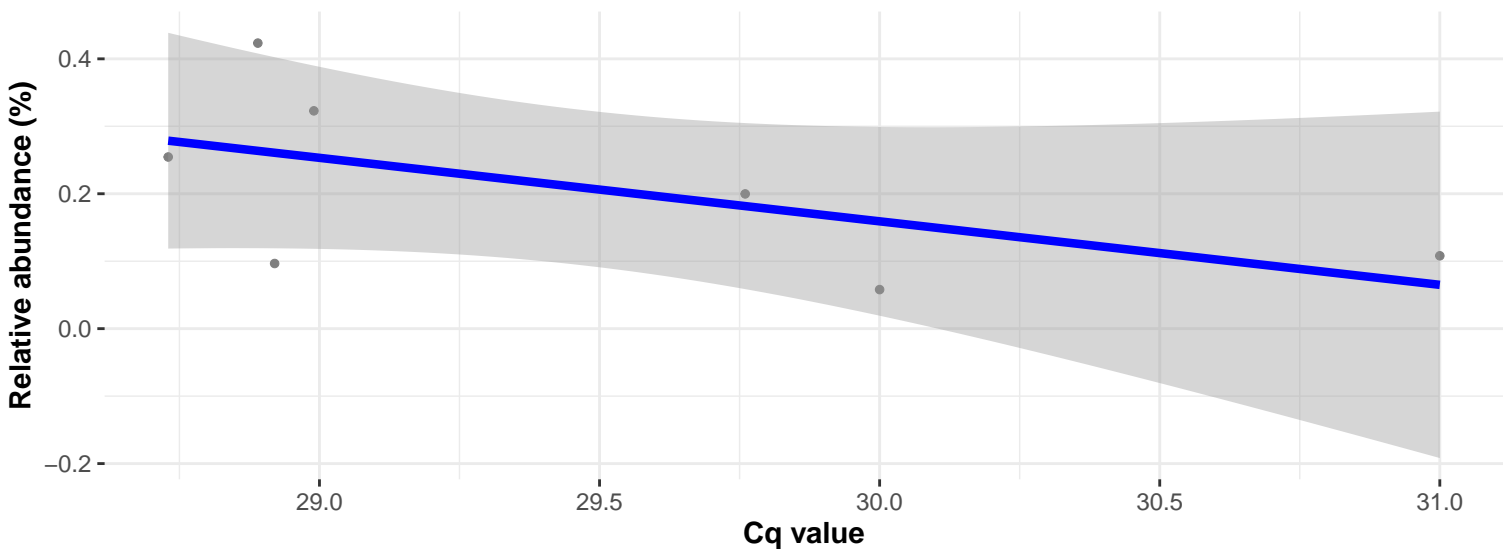
Correlation within: IM-PIM

$\log_e(S) = 5.375$ ,  $p = 0.443$ ,  $\hat{\rho}_{\text{Spearman}} = 0.245$ ,  $CI_{95\%} [-0.399, 0.727]$ ,  $n_{\text{pairs}} = 12$

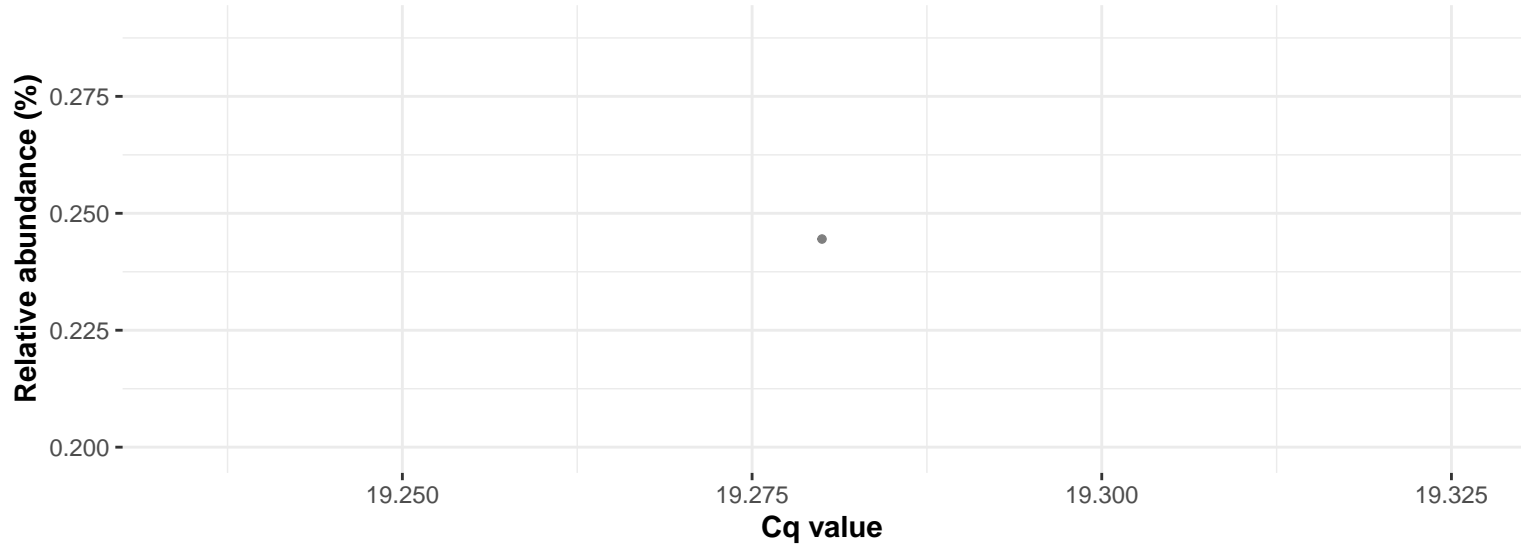


Correlation within: IM-DIM

$\log_e(S) = 4.477$ ,  $p = 0.180$ ,  $\hat{\rho}_{\text{Spearman}} = -0.571$ ,  $CI_{95\%} [-0.930, 0.345]$ ,  $n_{\text{pairs}} = 7$



Correlation within: Feed

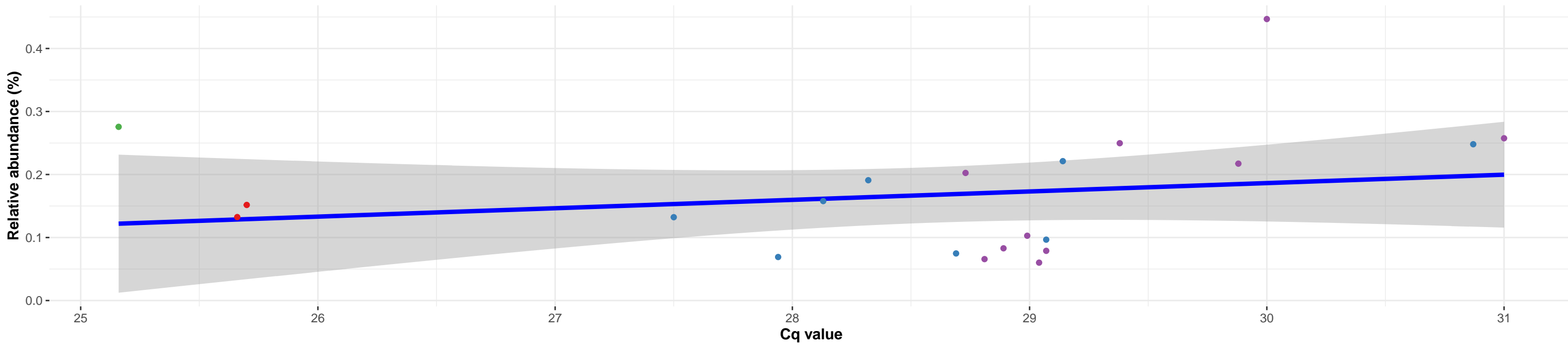




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Gracilibacillus; Ambiguous\_taxa

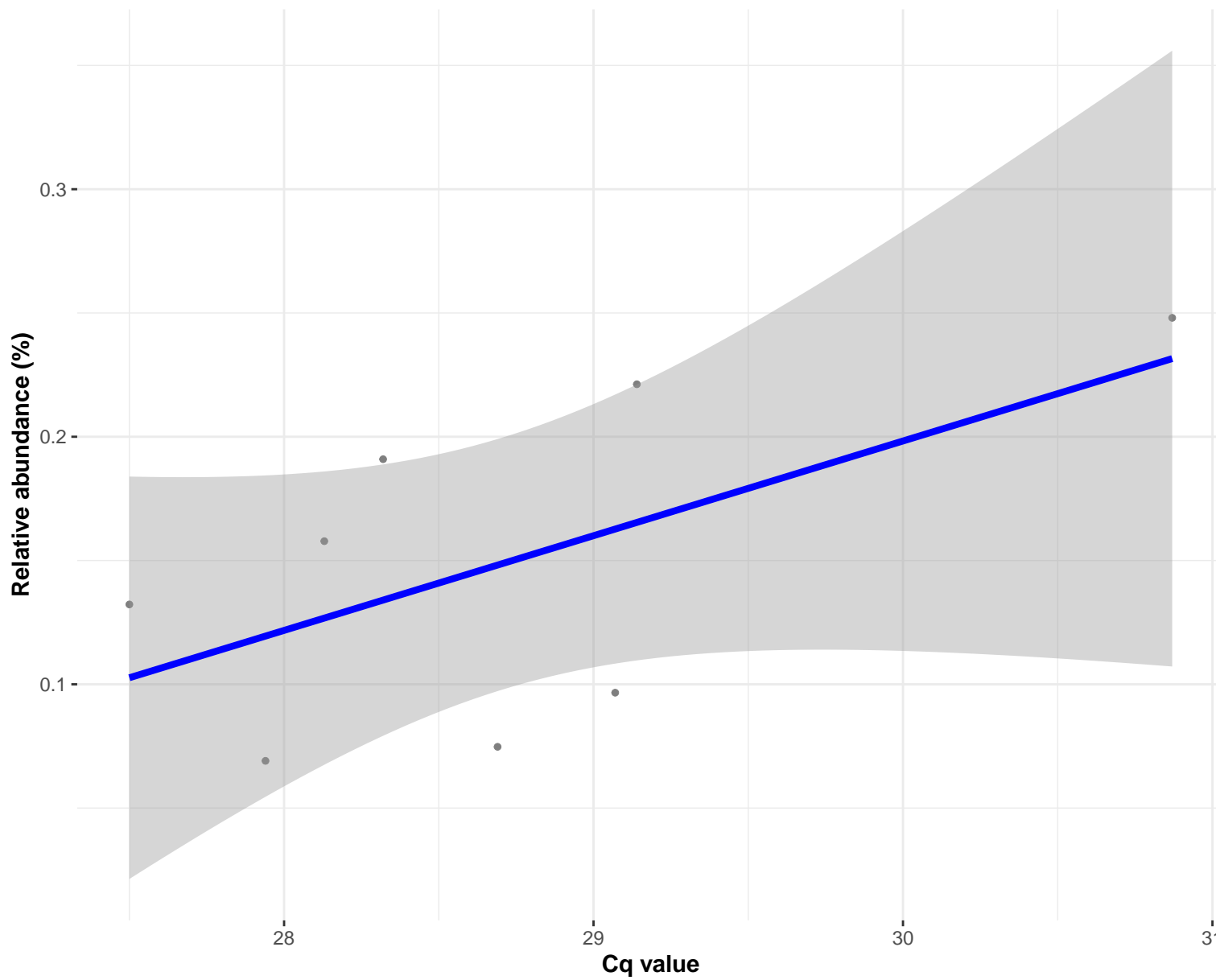
### Correlation with all samples

$\log_e(S) = 6.960$ ,  $p = 0.163$ ,  $\hat{\rho}_{\text{Spearman}} = 0.316$ ,  $CI_{95\%} [-0.148, 0.665]$ ,  $n_{\text{pairs}} = 21$



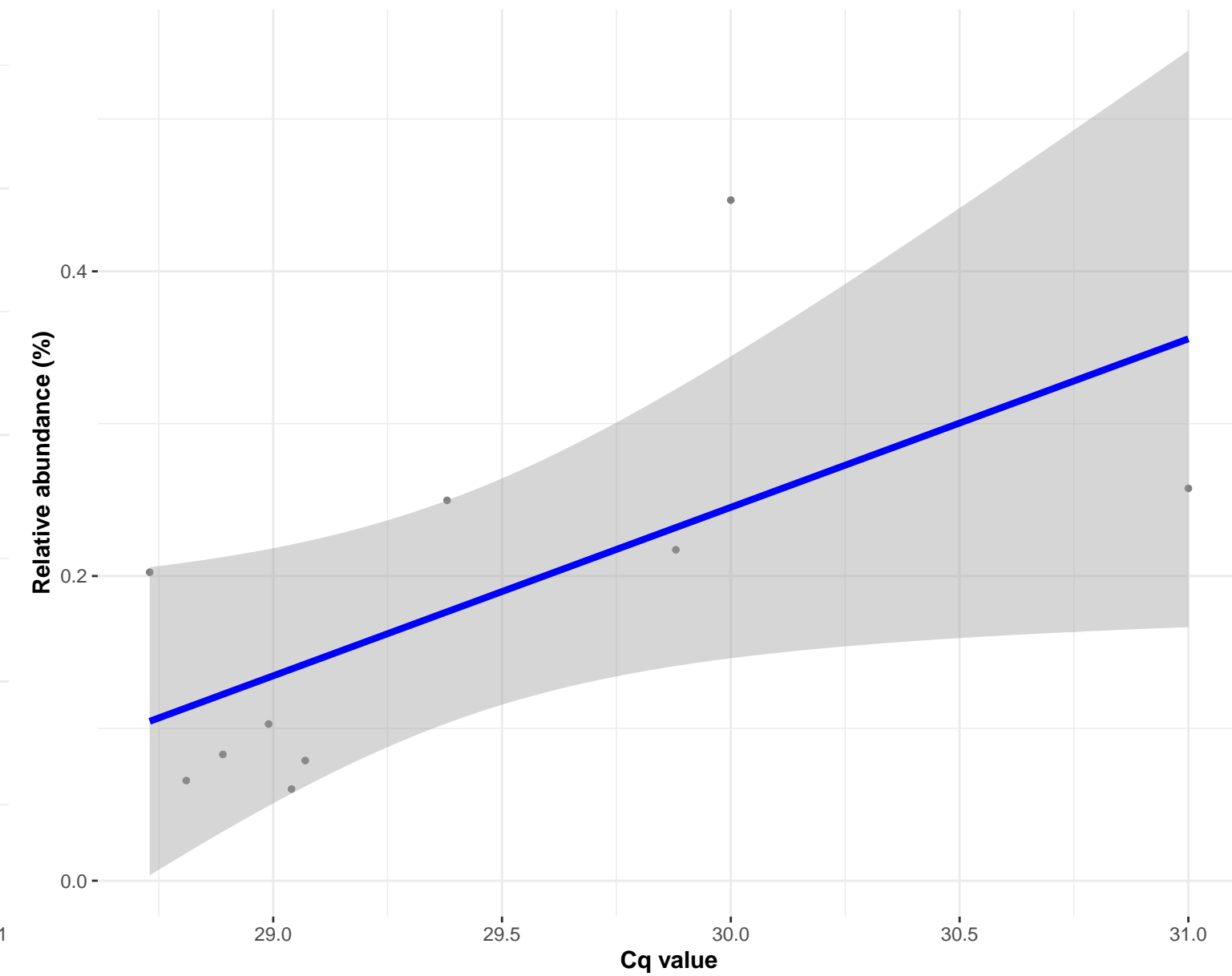
### Correlation within: IM-PIM

$\log_e(S) = 3.584$ ,  $p = 0.139$ ,  $\hat{\rho}_{\text{Spearman}} = 0.571$ ,  $CI_{95\%} [-0.248, 0.914]$ ,  $n_{\text{pairs}} = 8$



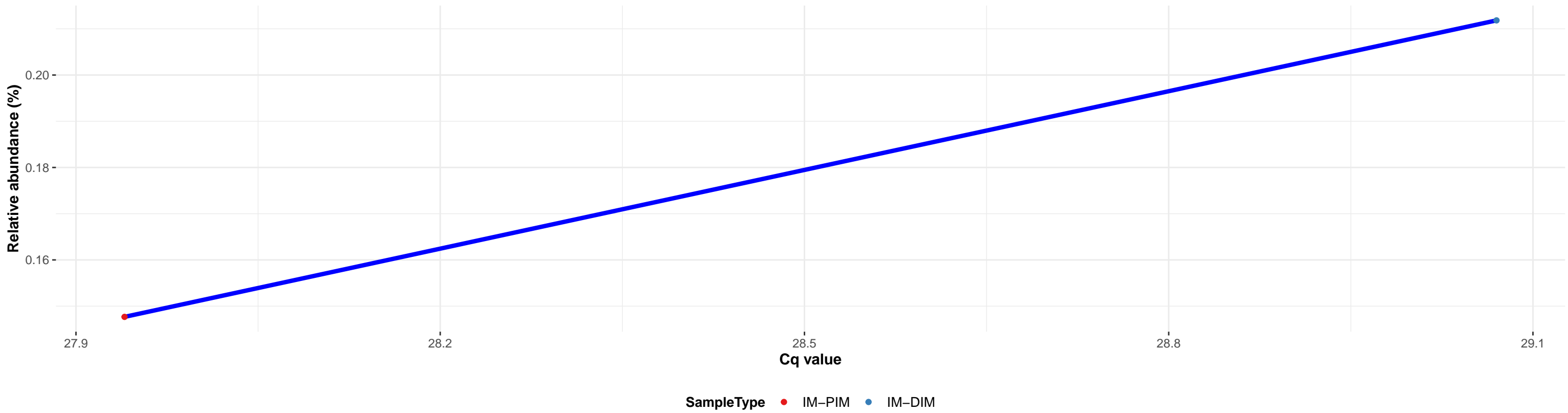
### Correlation within: IM-DIM

$\log_e(S) = 4.025$ ,  $p = 0.038$ ,  $\hat{\rho}_{\text{Spearman}} = 0.661$ ,  $CI_{95\%} [0.031, 0.915]$ ,  $n_{\text{pairs}} = 10$

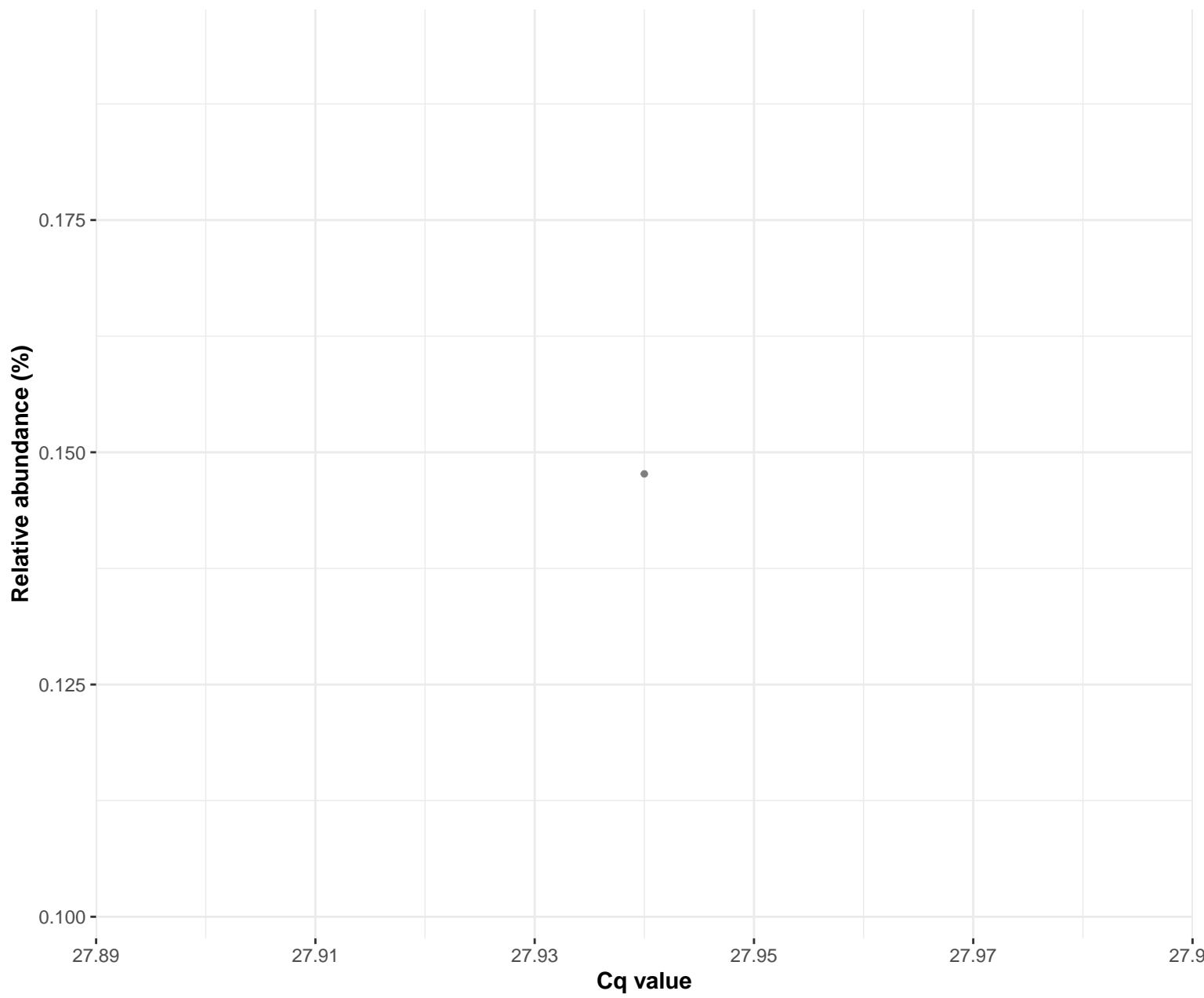


k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Rhizobiales; f\_\_Xanthobacteraceae; g\_\_Bradyrhizobium; NA

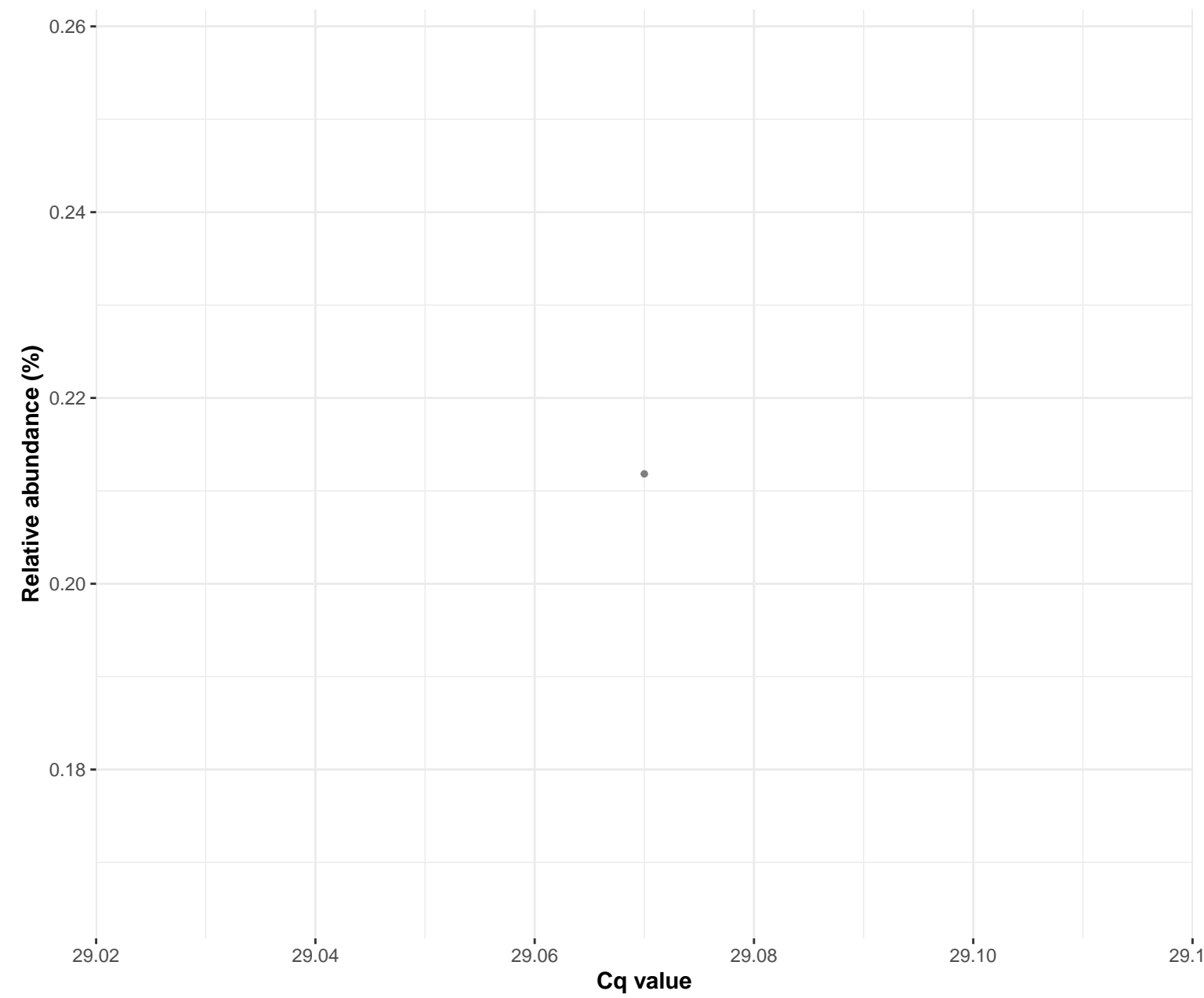
Correlation with all samples



Correlation within: IM-PIM



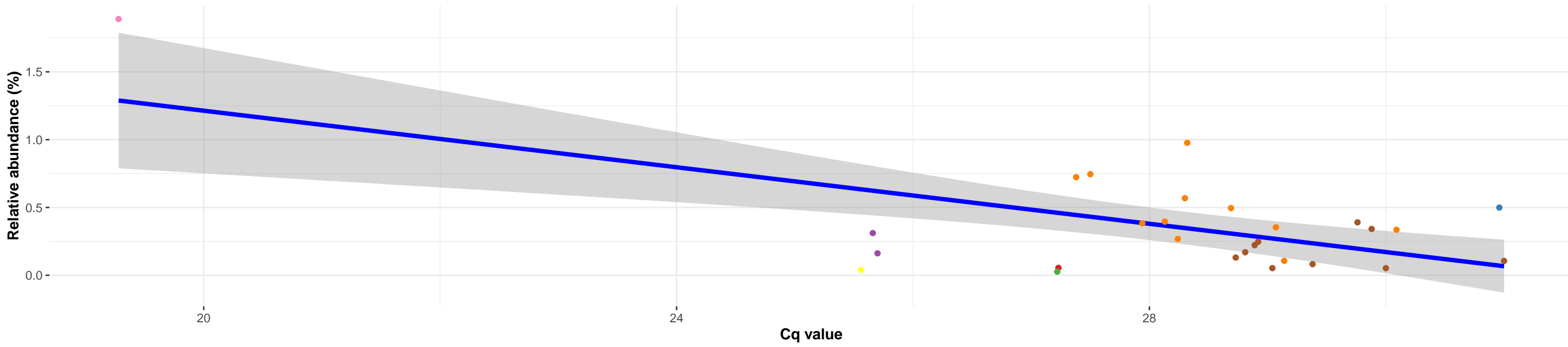
Correlation within: IM-DIM



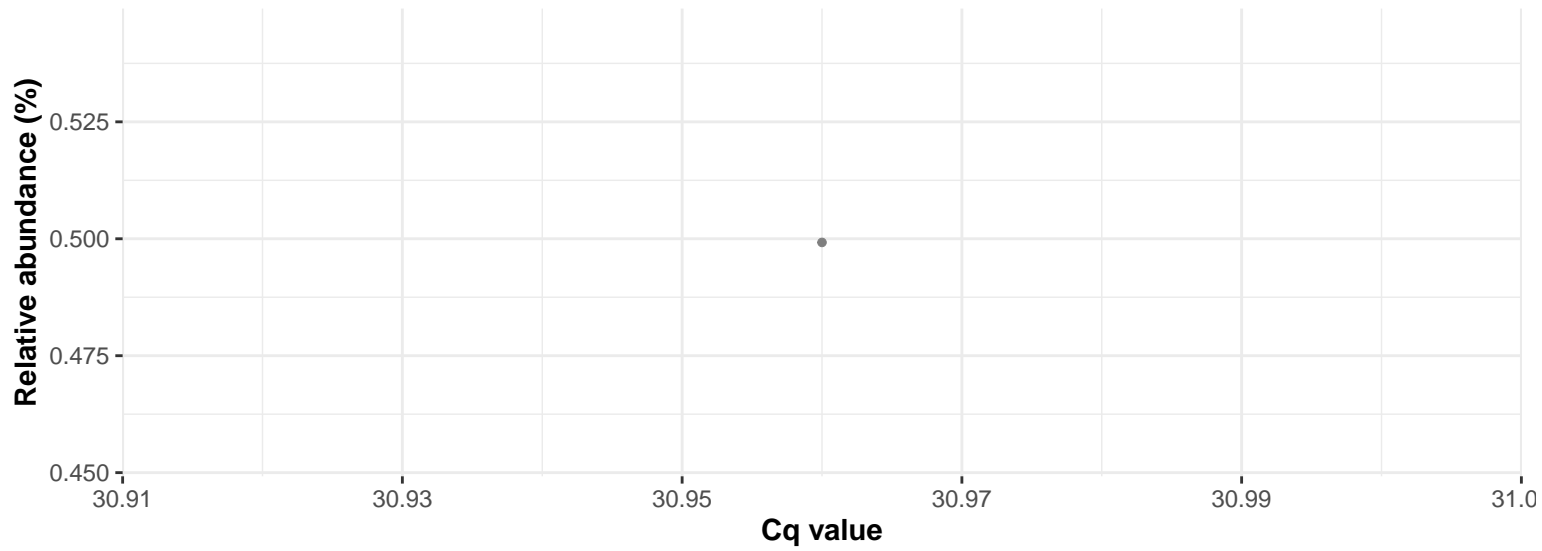
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Savagea; Ambiguous\_taxa

### Correlation with all samples

$\log_e(S) = 8.312$ ,  $p = 0.562$ ,  $\hat{\rho}_{\text{Spearman}} = -0.114$ ,  $\text{CI}_{95\%} [-0.477, 0.281]$ ,  $n_{\text{pairs}} = 28$

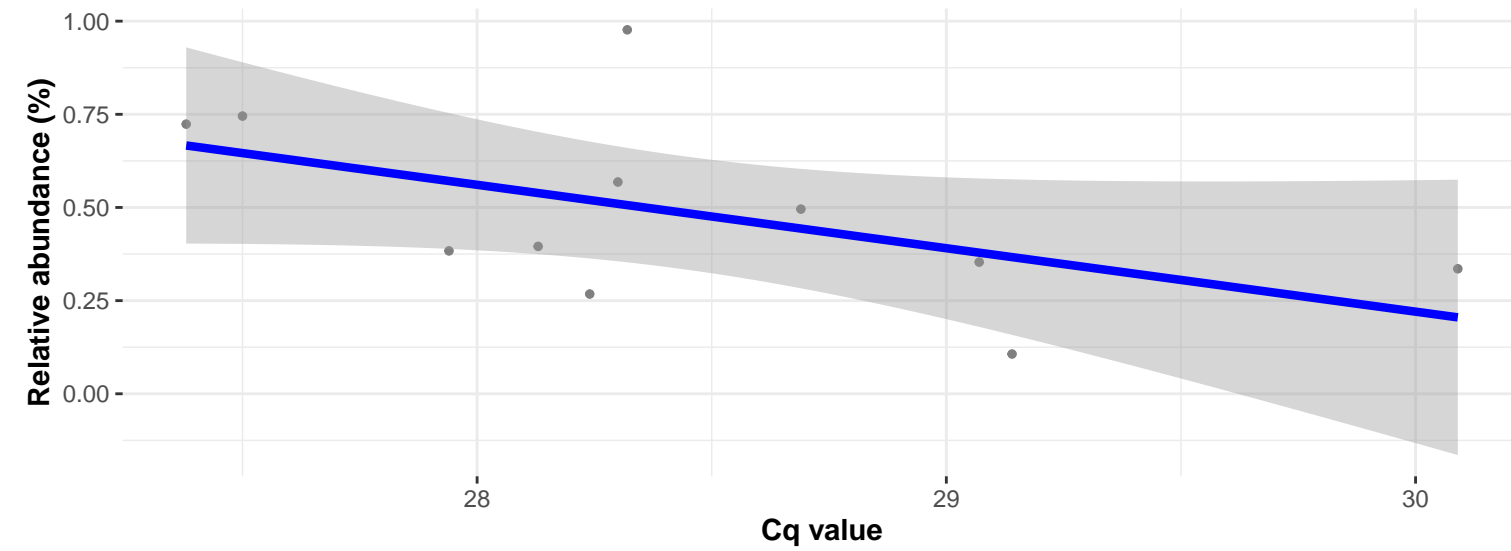


### Correlation within: REF-PIM



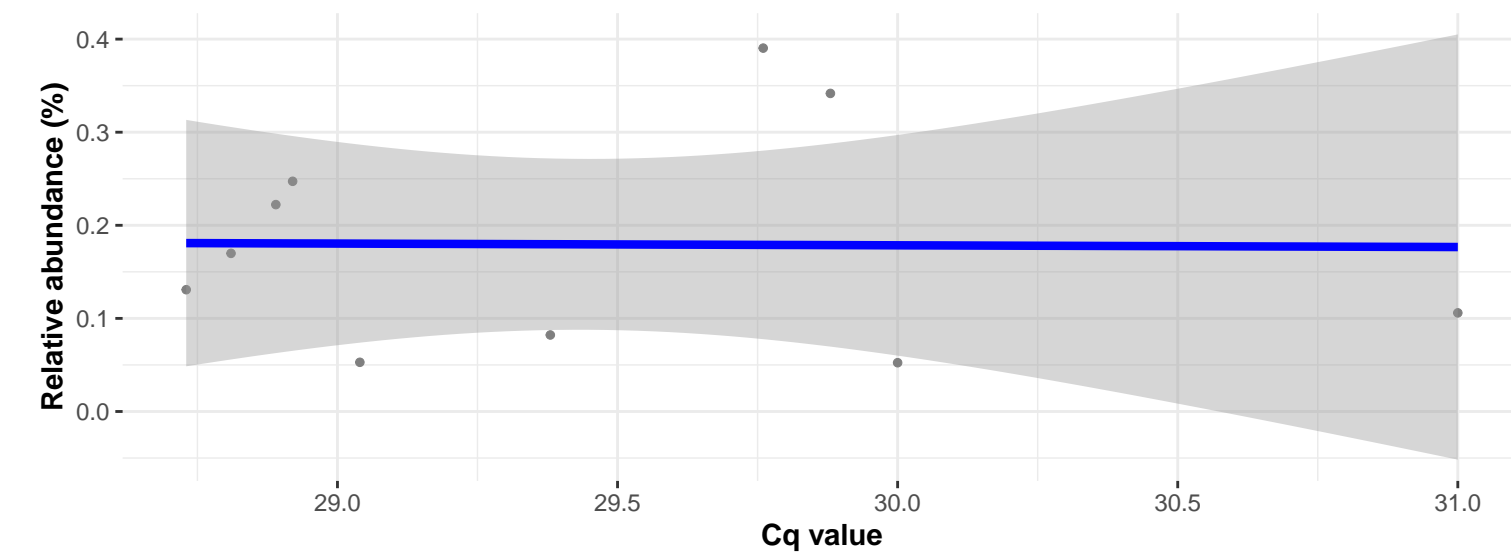
### Correlation within: IM-PIM

$\log_e(S) = 5.817$ ,  $p = 0.096$ ,  $\hat{\rho}_{\text{Spearman}} = -0.527$ ,  $\text{CI}_{95\%} [-0.862, 0.126]$ ,  $n_{\text{pairs}} = 11$

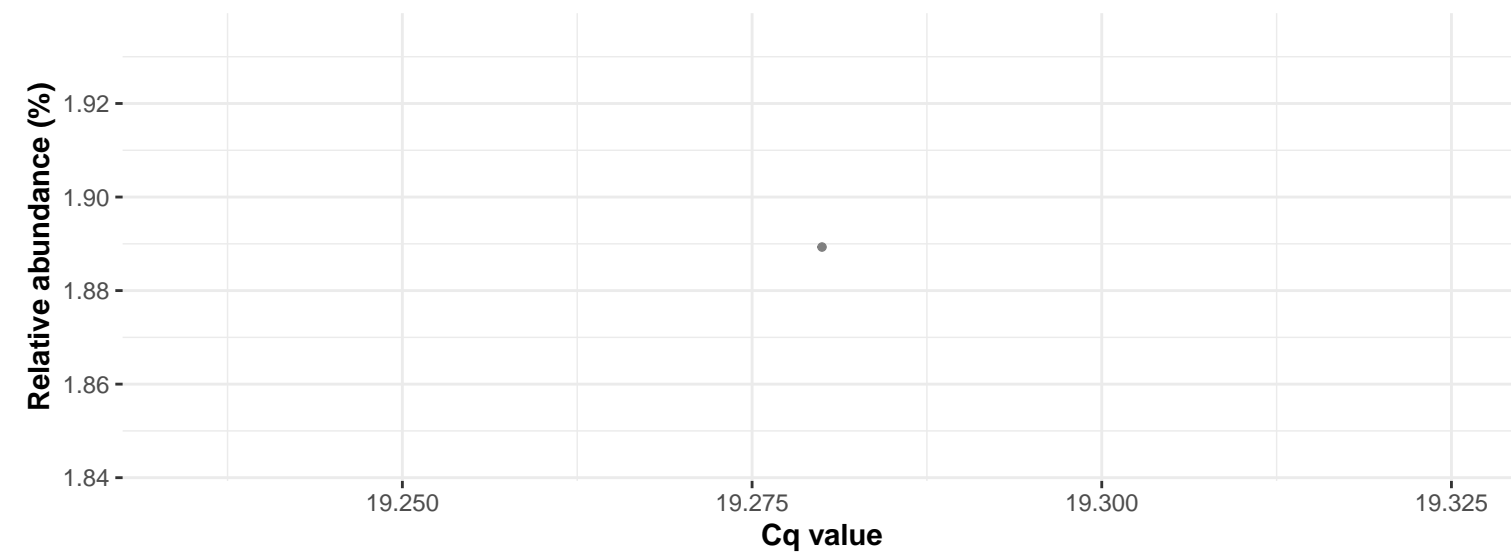


### Correlation within: IM-DIM

$\log_e(S) = 5.257$ ,  $p = 0.651$ ,  $\hat{\rho}_{\text{Spearman}} = -0.164$ ,  $\text{CI}_{95\%} [-0.730, 0.535]$ ,  $n_{\text{pairs}} = 10$



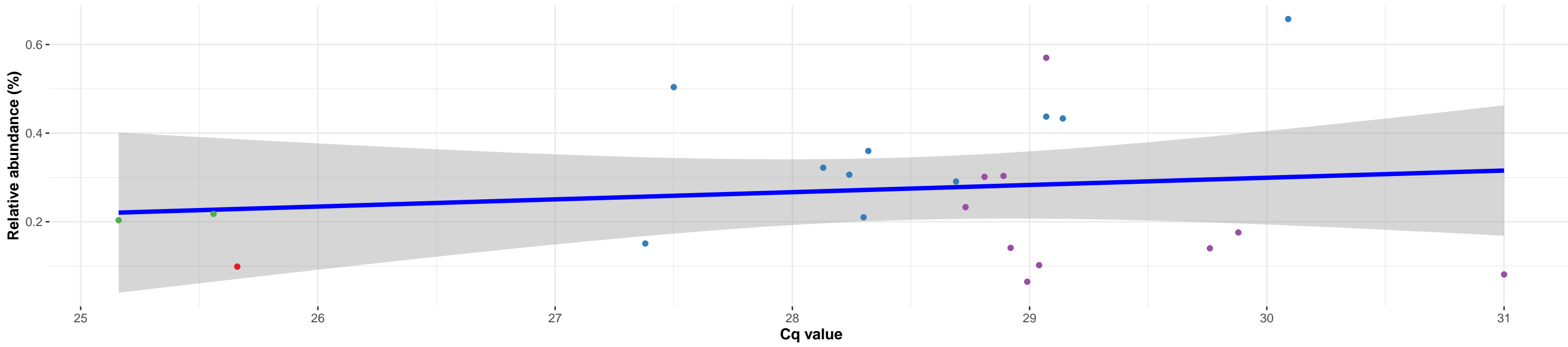
### Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Staphylococcaceae; g\_\_Staphylococcus; s\_\_Staphylococcus sciuri

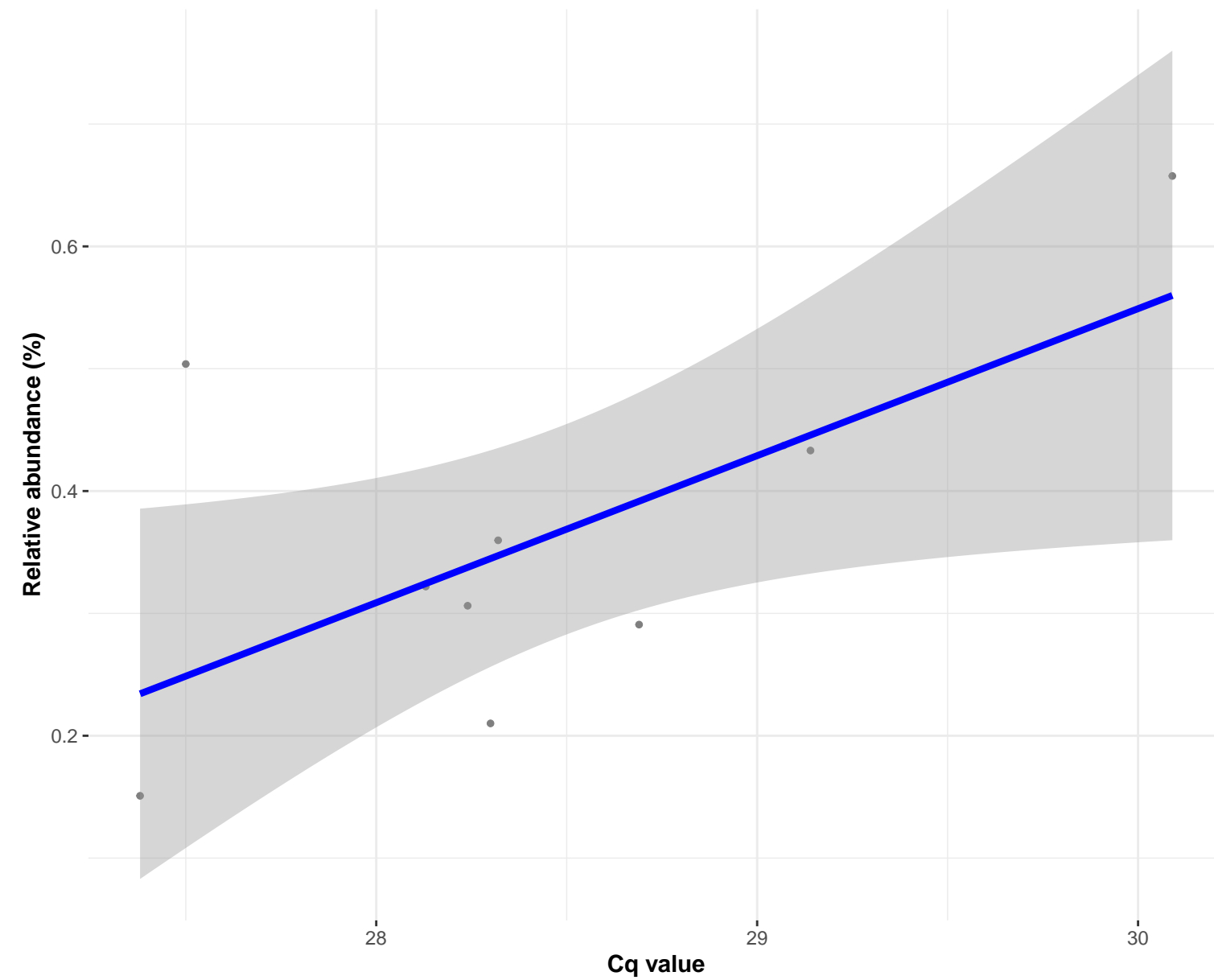
### Correlation with all samples

$\log_e(S) = 7.592$ ,  $p = 0.925$ ,  $\hat{\rho}_{\text{Spearman}} = 0.021$ ,  $CI_{95\%} [-0.406, 0.440]$ ,  $n_{\text{pairs}} = 23$



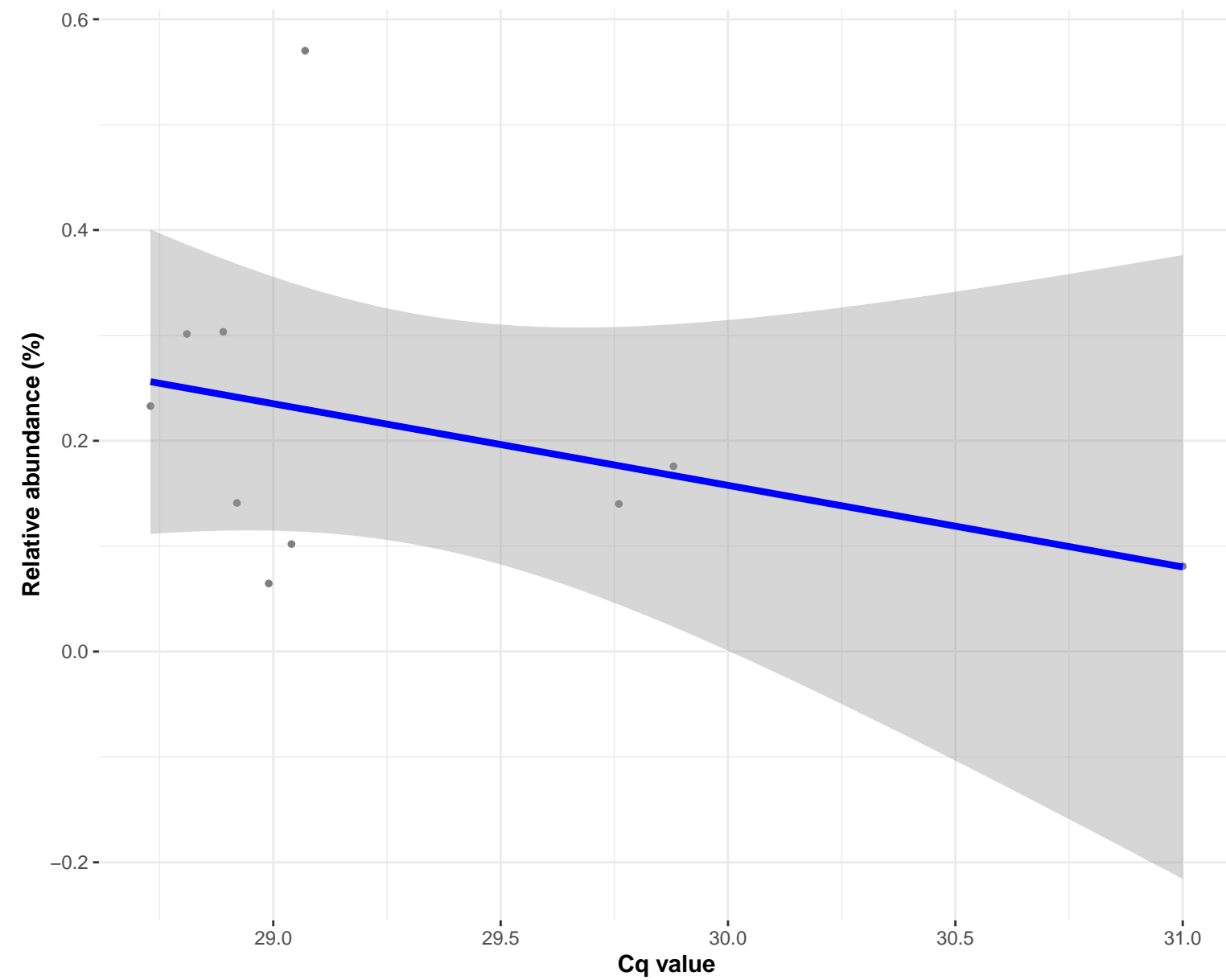
### Correlation within: IM-PIM

$\log_e(S) = 4.407$ ,  $p = 0.138$ ,  $\hat{\rho}_{\text{Spearman}} = 0.503$ ,  $CI_{95\%} [-0.206, 0.866]$ ,  $n_{\text{pairs}} = 10$

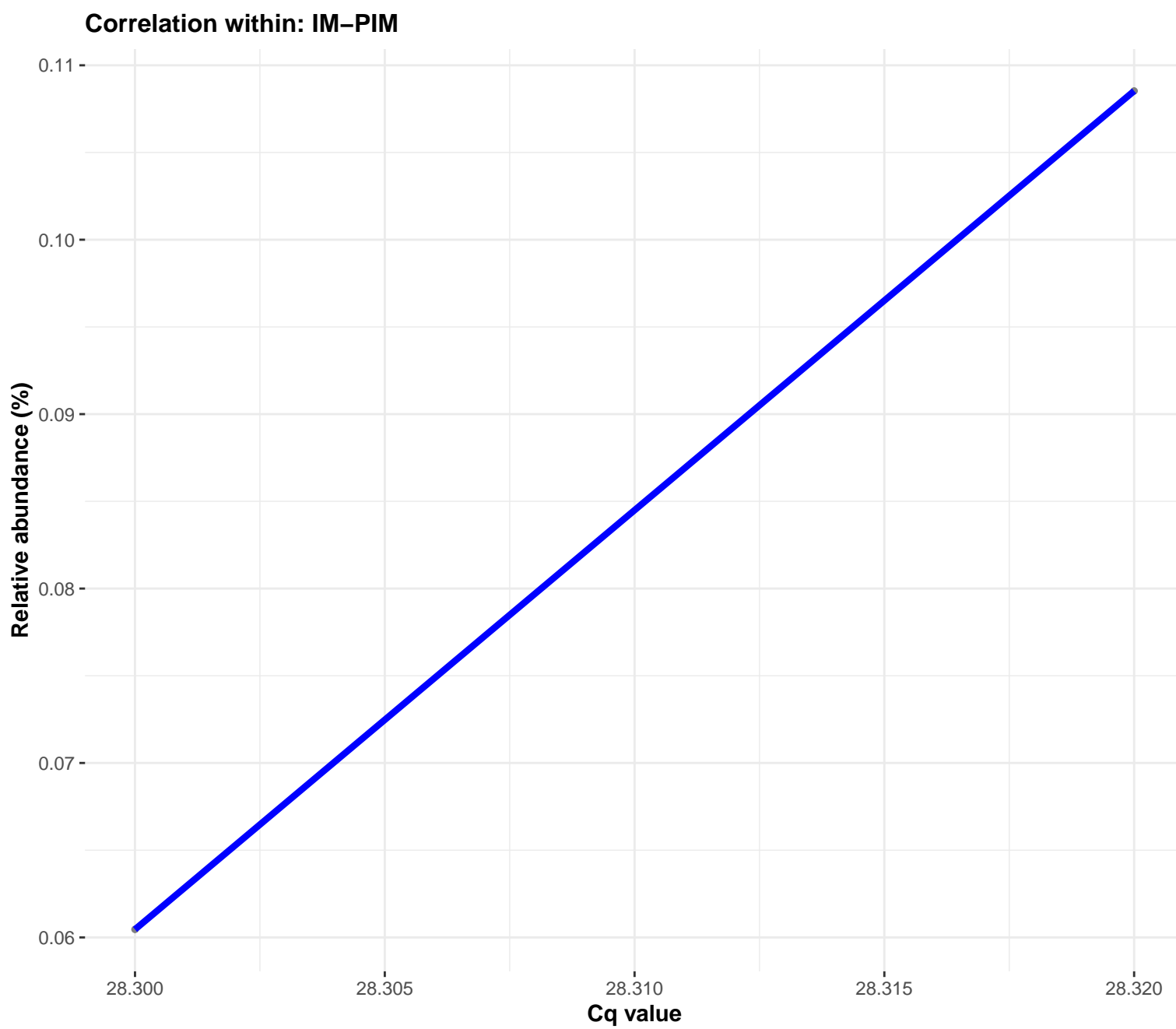
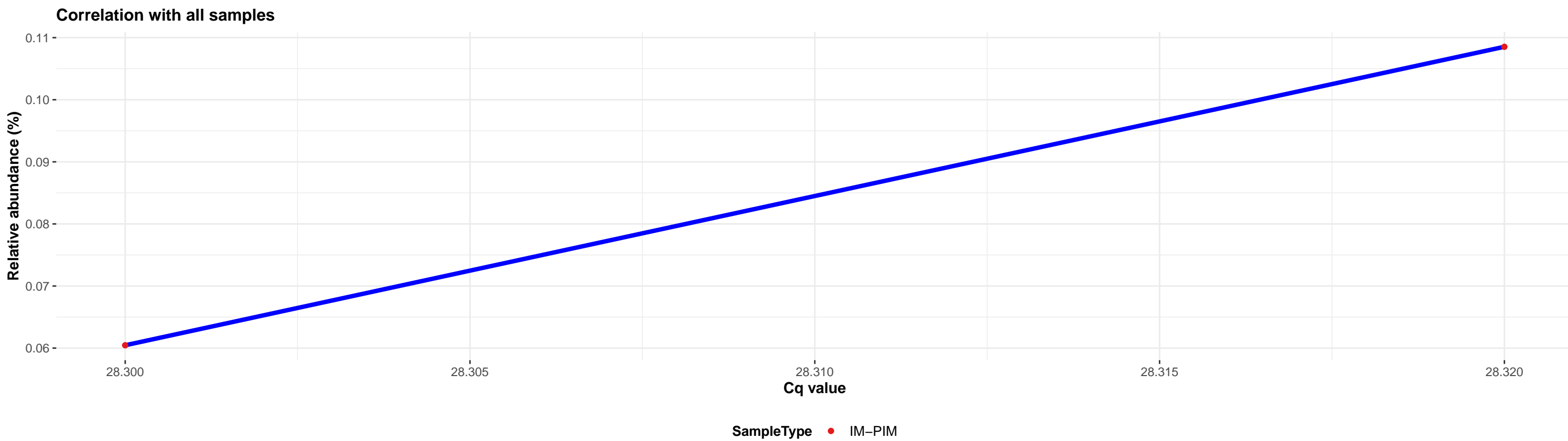


### Correlation within: IM-DIM

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



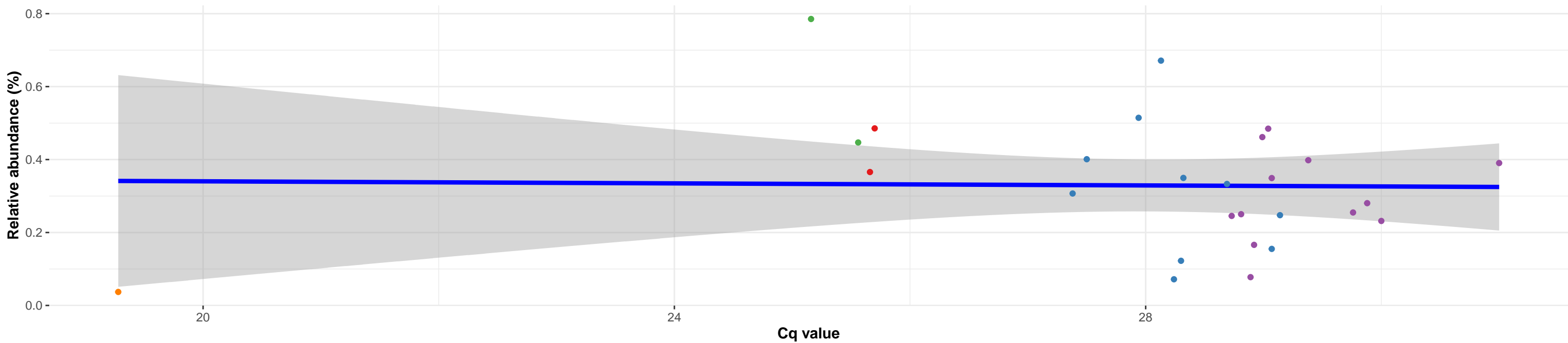
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; s\_\_Bacillus licheniformis



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

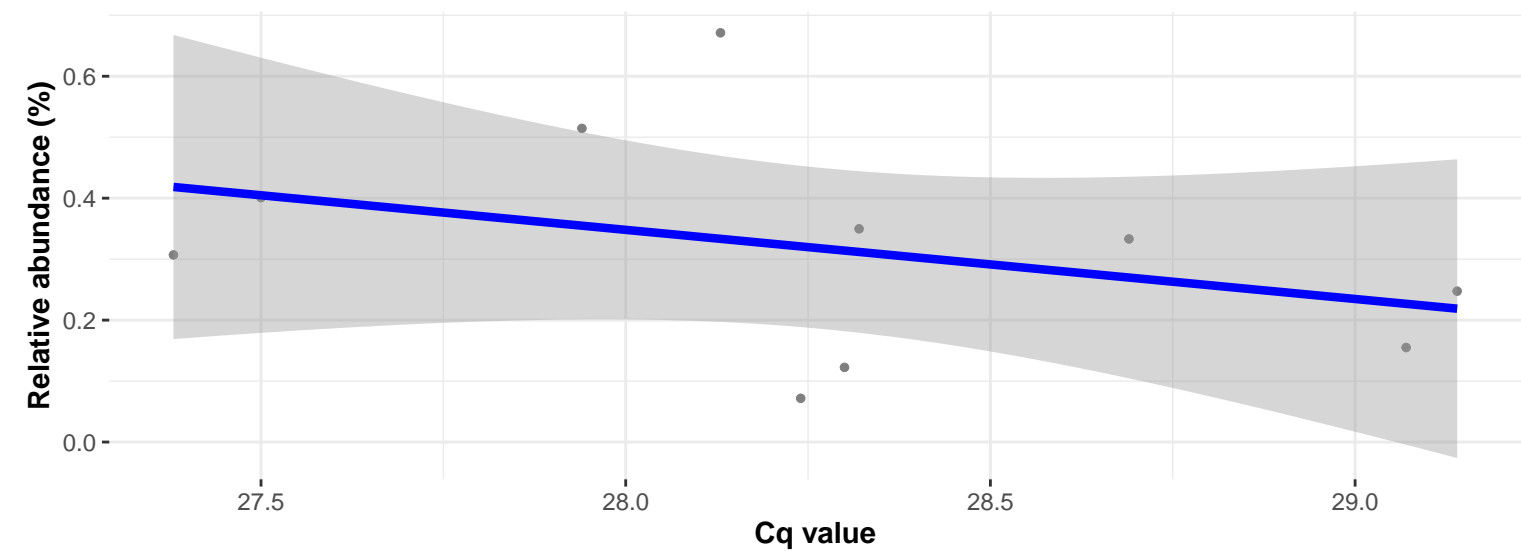
Correlation with all samples

$\log_e(S) = 8.300$ ,  $p = 0.252$ ,  $\hat{\rho}_{\text{Spearman}} = -0.228$ ,  $CI_{95\%} [-0.568, 0.178]$ ,  $n_{\text{pairs}} = 27$



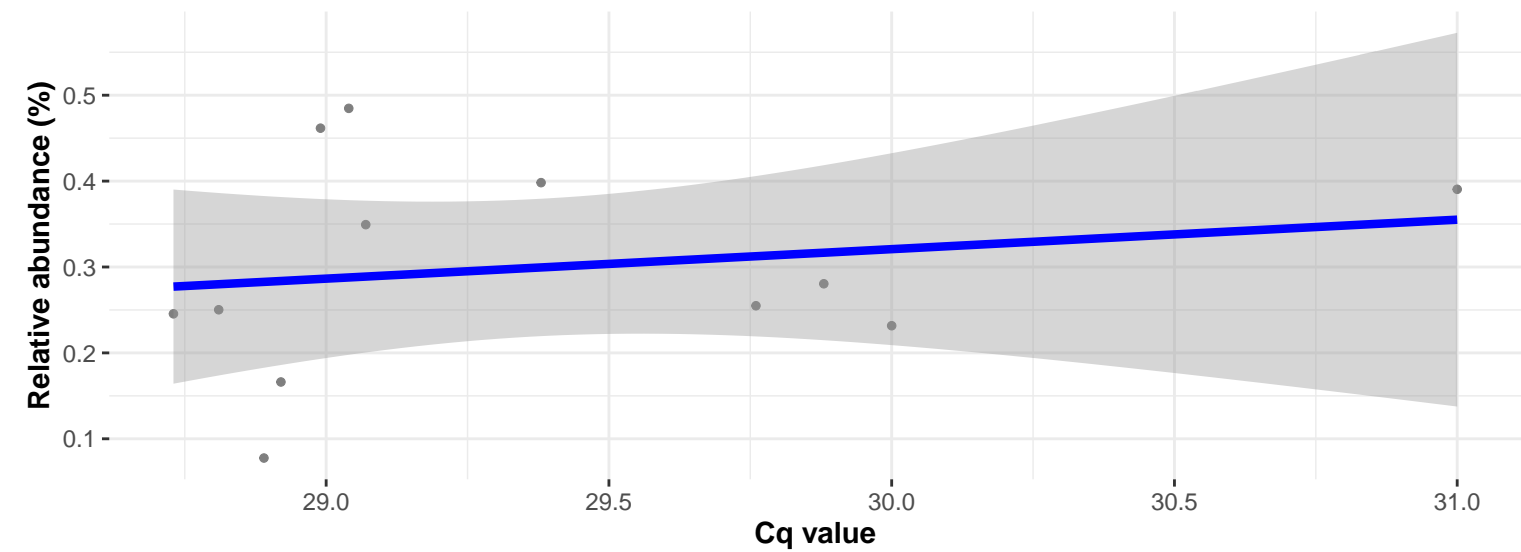
Correlation within: IM-PIM

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

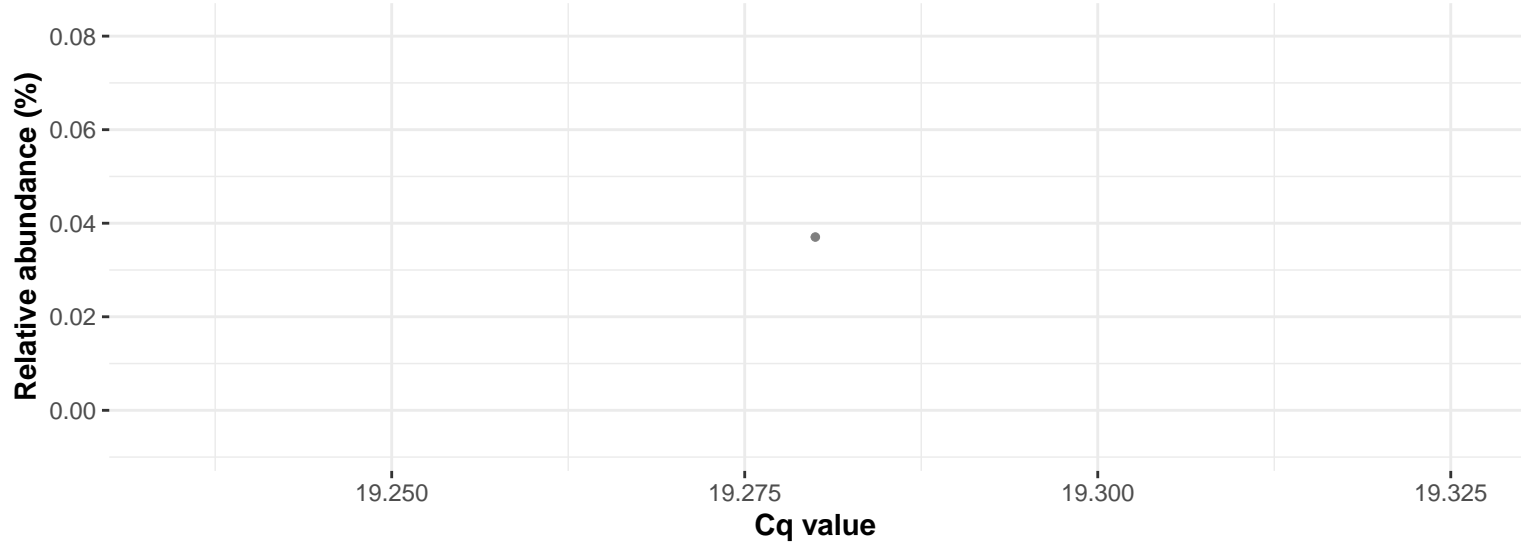


Correlation within: IM-DIM

$\log_e(S) = 5.268$ ,  $p = 0.308$ ,  $\hat{\rho}_{\text{Spearman}} = 0.322$ ,  $CI_{95\%} [-0.327, 0.764]$ ,  $n_{\text{pairs}} = 12$



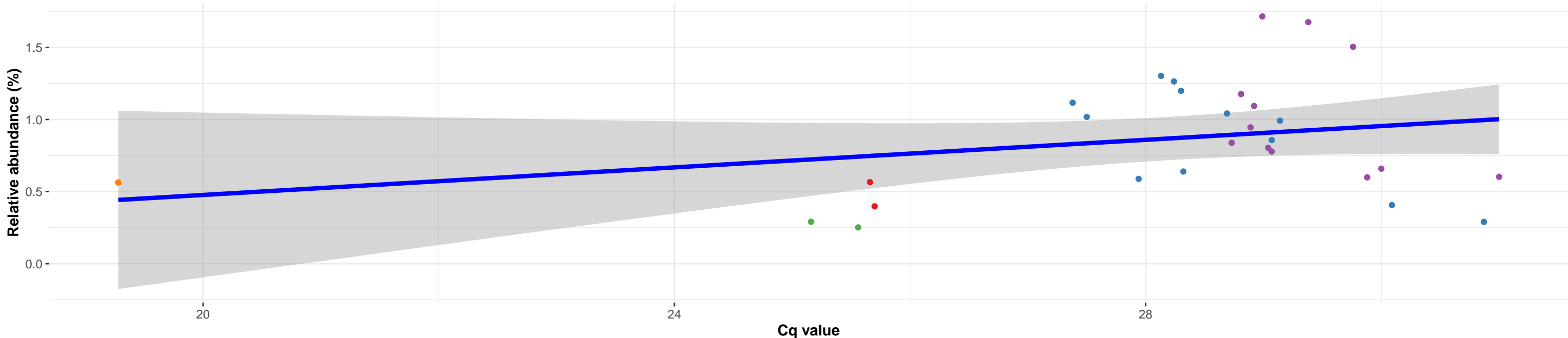
Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

Correlation with all samples

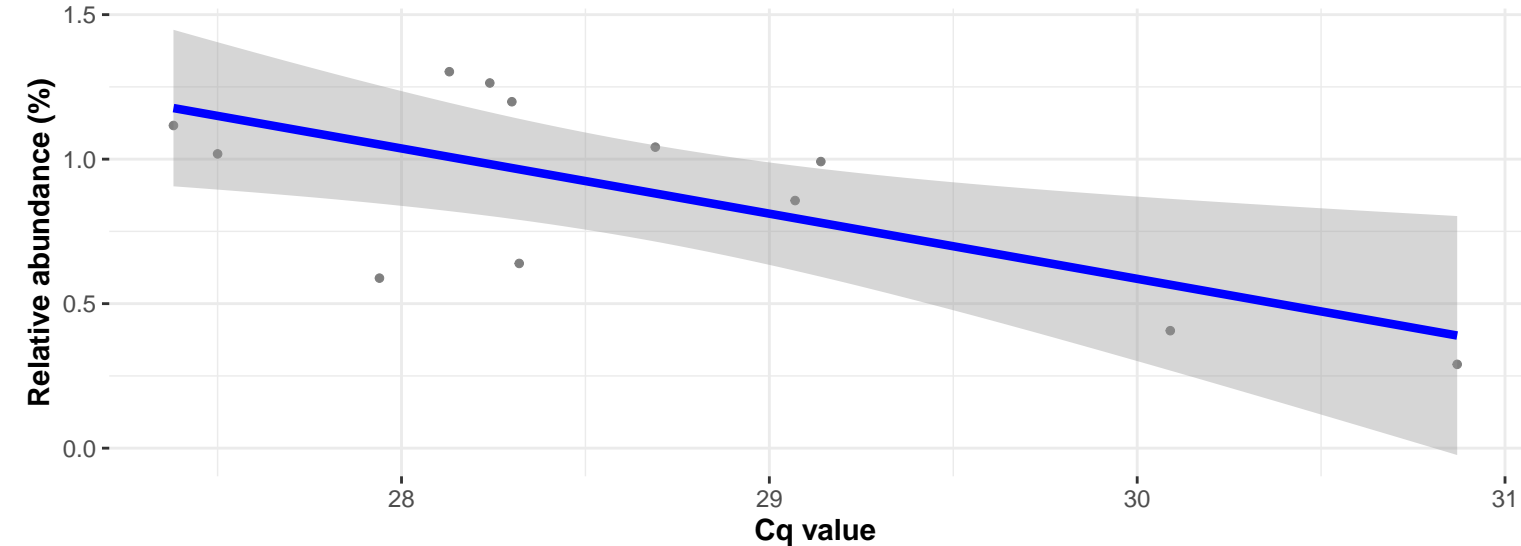
$\log_e(S) = 8.161$ ,  $p = 0.476$ ,  $\hat{\rho}_{\text{Spearman}} = 0.138$ ,  $CI_{95\%} [-0.252, 0.489]$ ,  $n_{\text{pairs}} = 29$



SampleType IM-PID IM-PIM IM-DID IM-DIM Feed

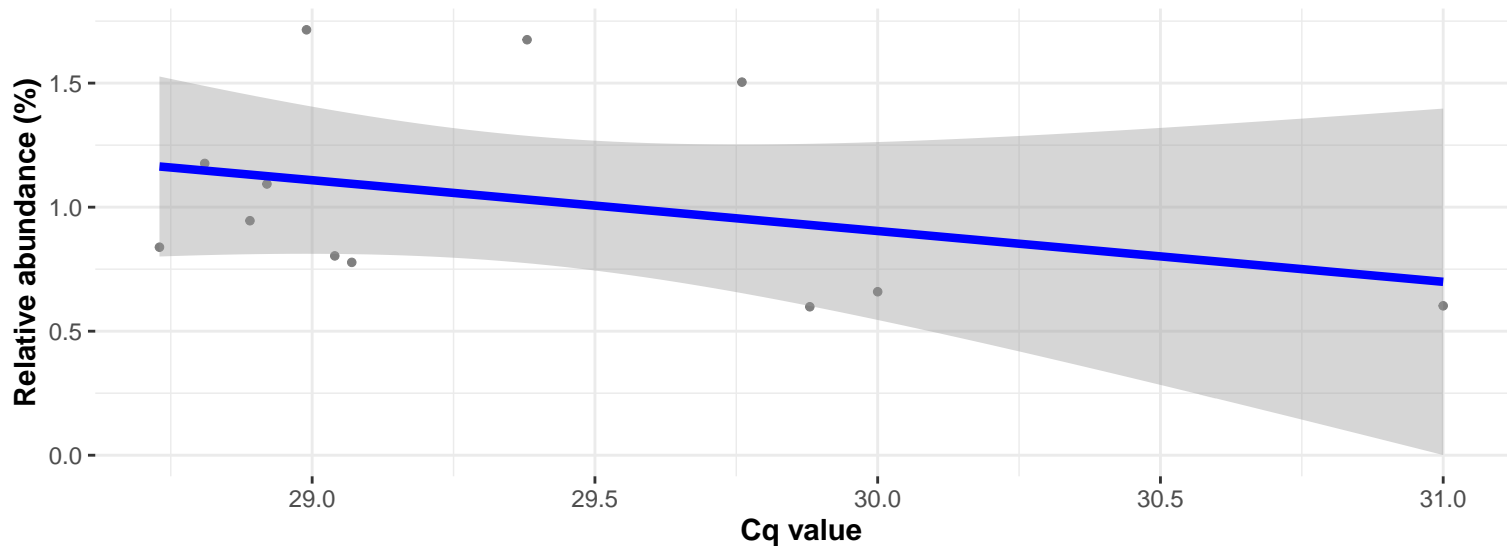
Correlation within: IM-PIM

$\log_e(S) = 6.105$ ,  $p = 0.055$ ,  $\hat{\rho}_{\text{Spearman}} = -0.566$ ,  $CI_{95\%} [-0.866, 0.030]$ ,  $n_{\text{pairs}} = 12$

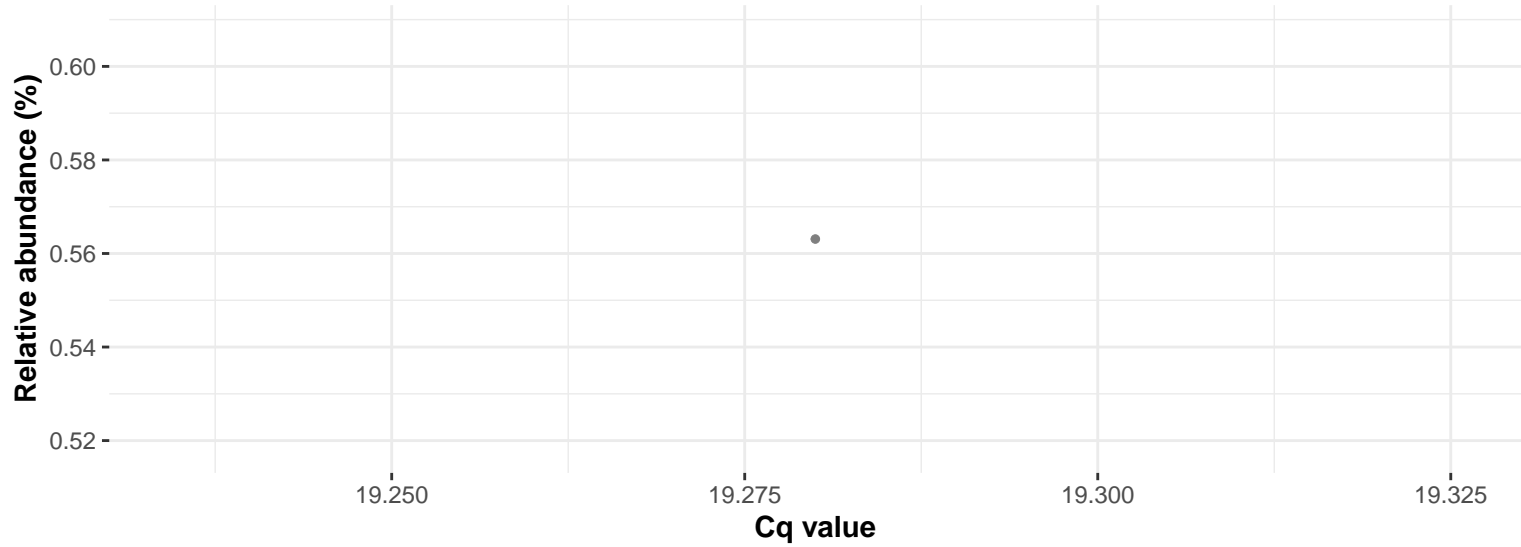


Correlation within: IM-DIM

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



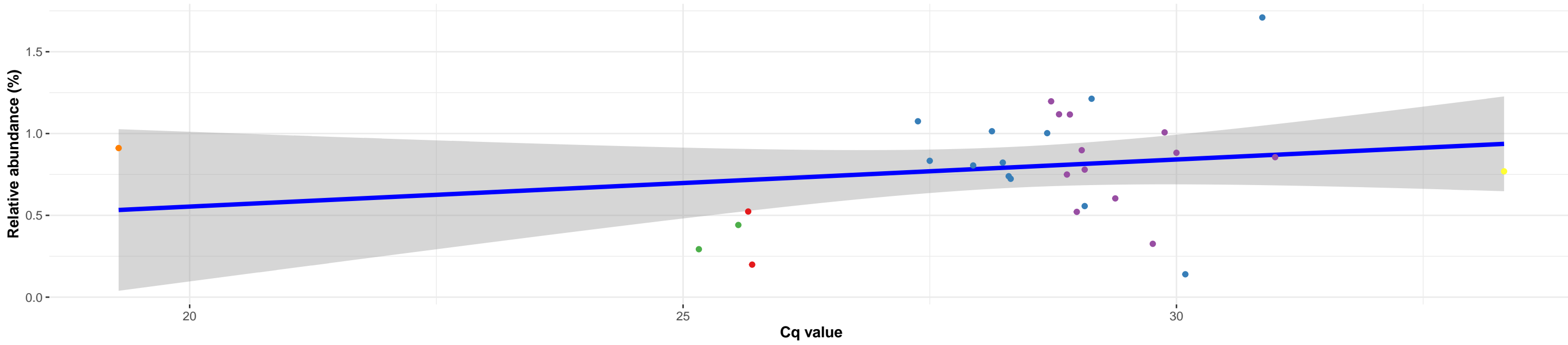
Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Micrococcales; f\_\_Microbacteriaceae; g\_\_Microbacterium; Ambiguous\_taxa

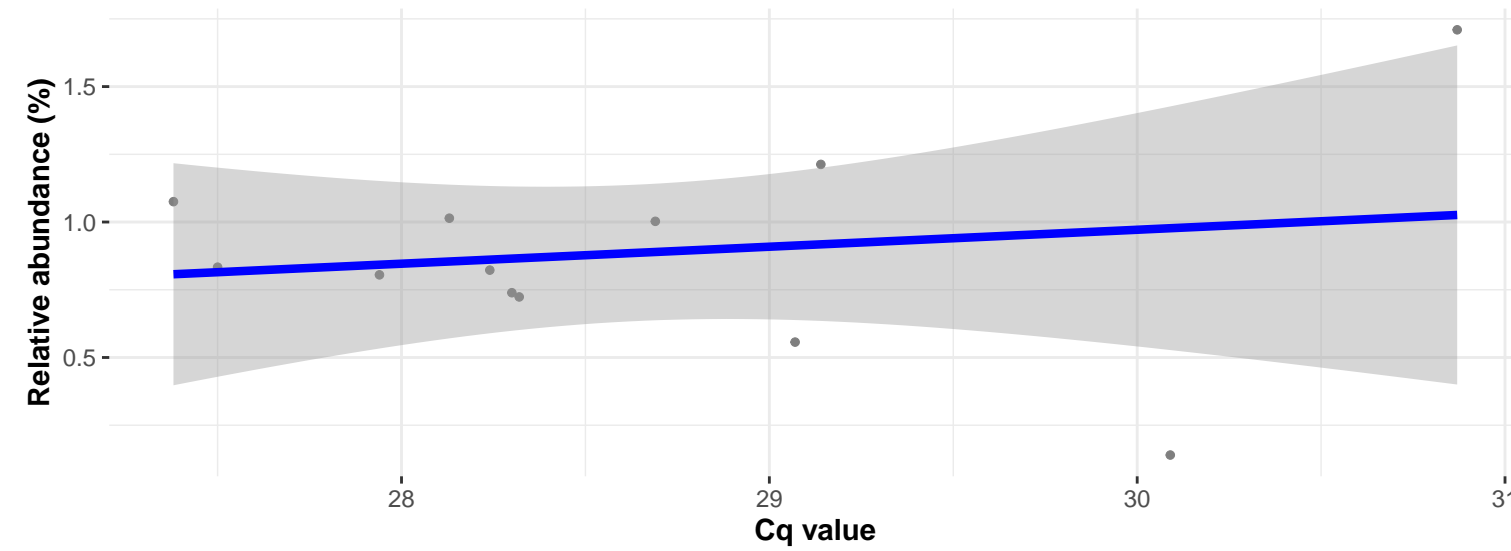
### Correlation with all samples

$\log_e(S) = 8.255$ ,  $p = 0.448$ ,  $\hat{\rho}_{\text{Spearman}} = 0.144$ ,  $CI_{95\%} [-0.239, 0.488]$ ,  $n_{\text{pairs}} = 30$



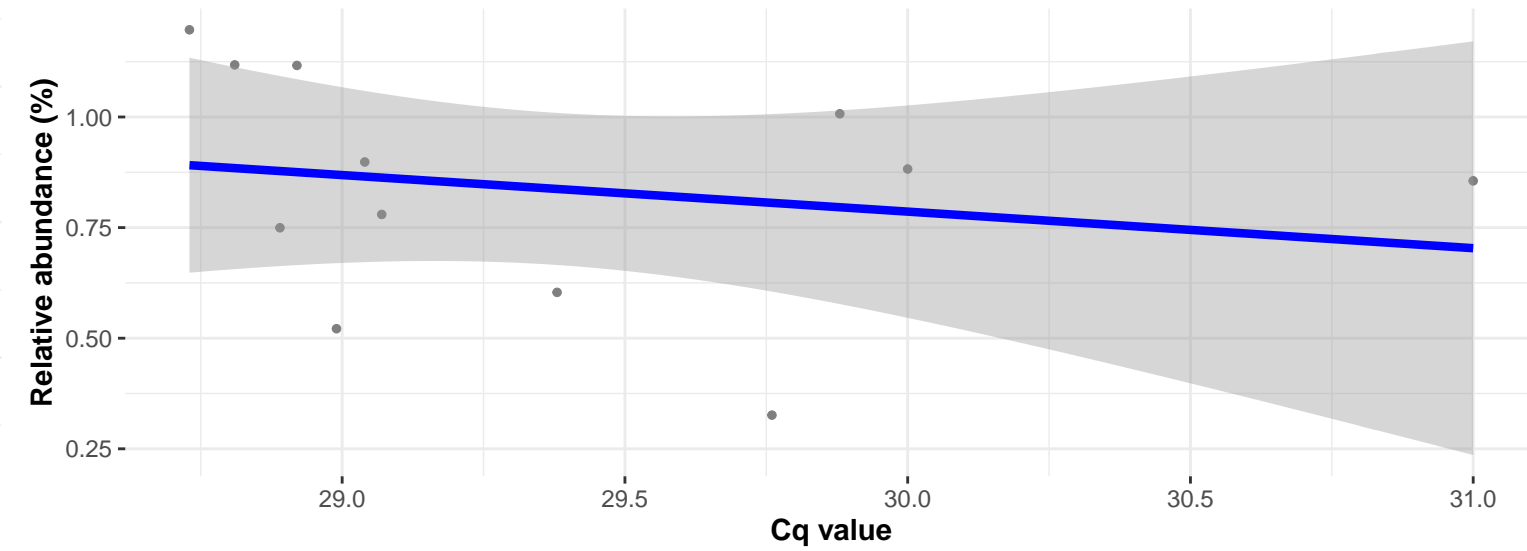
### Correlation within: IM-PIM

$\log_e(S) = 5.724$ ,  $p = 0.829$ ,  $\hat{\rho}_{\text{Spearman}} = -0.070$ ,  $CI_{95\%} [-0.631, 0.539]$ ,  $n_{\text{pairs}} = 12$

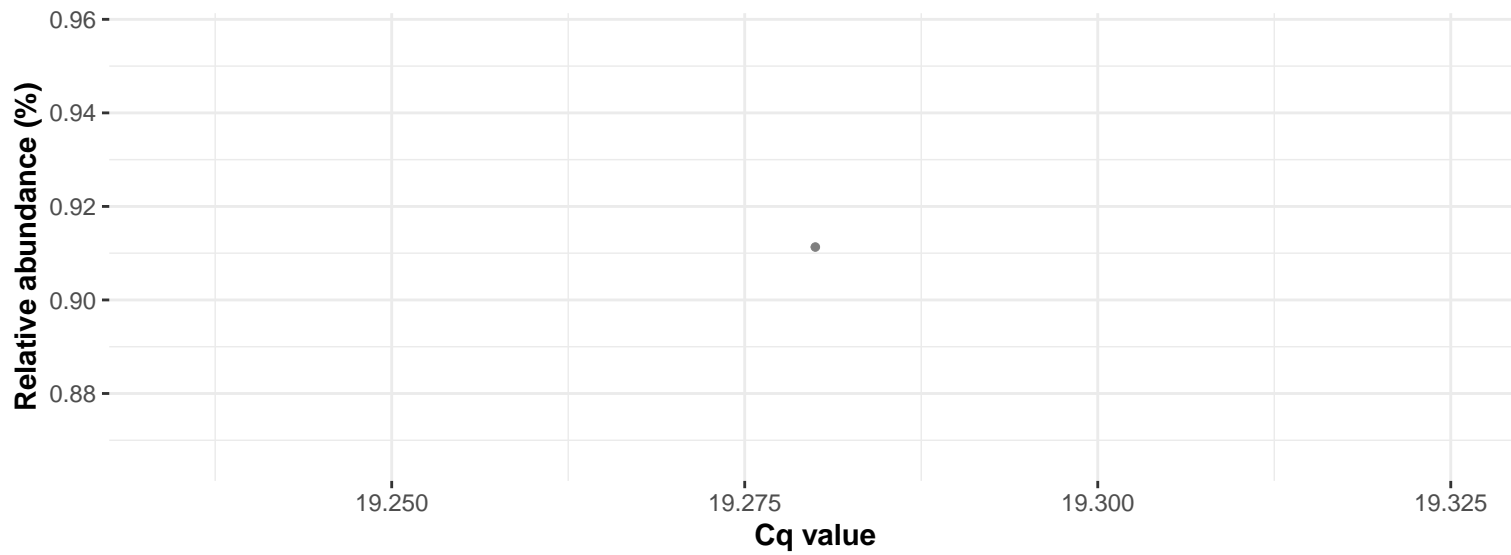


### Correlation within: IM-DIM

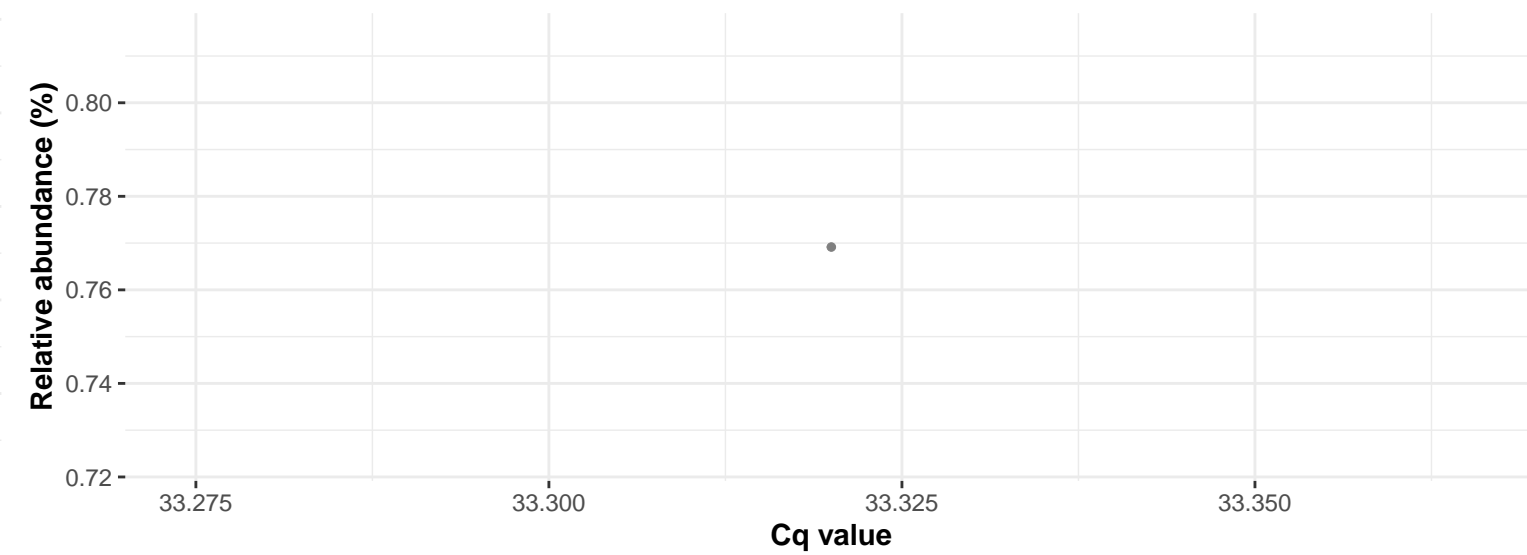
$\log_e(S) = 5.986$ ,  $p = 0.208$ ,  $\hat{\rho}_{\text{Spearman}} = -0.392$ ,  $CI_{95\%} [-0.796, 0.253]$ ,  $n_{\text{pairs}} = 12$



### Correlation within: Feed



### Correlation within: Water

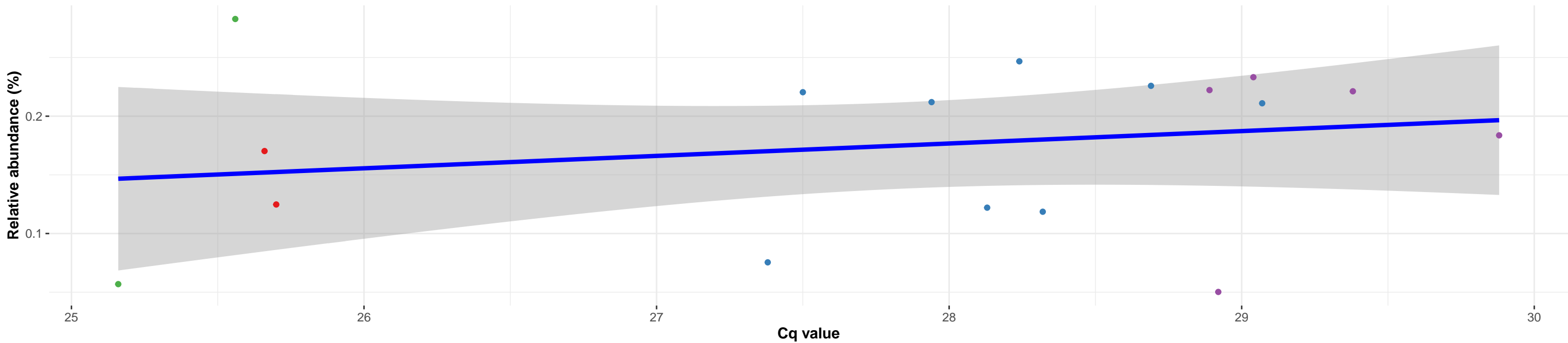




k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA

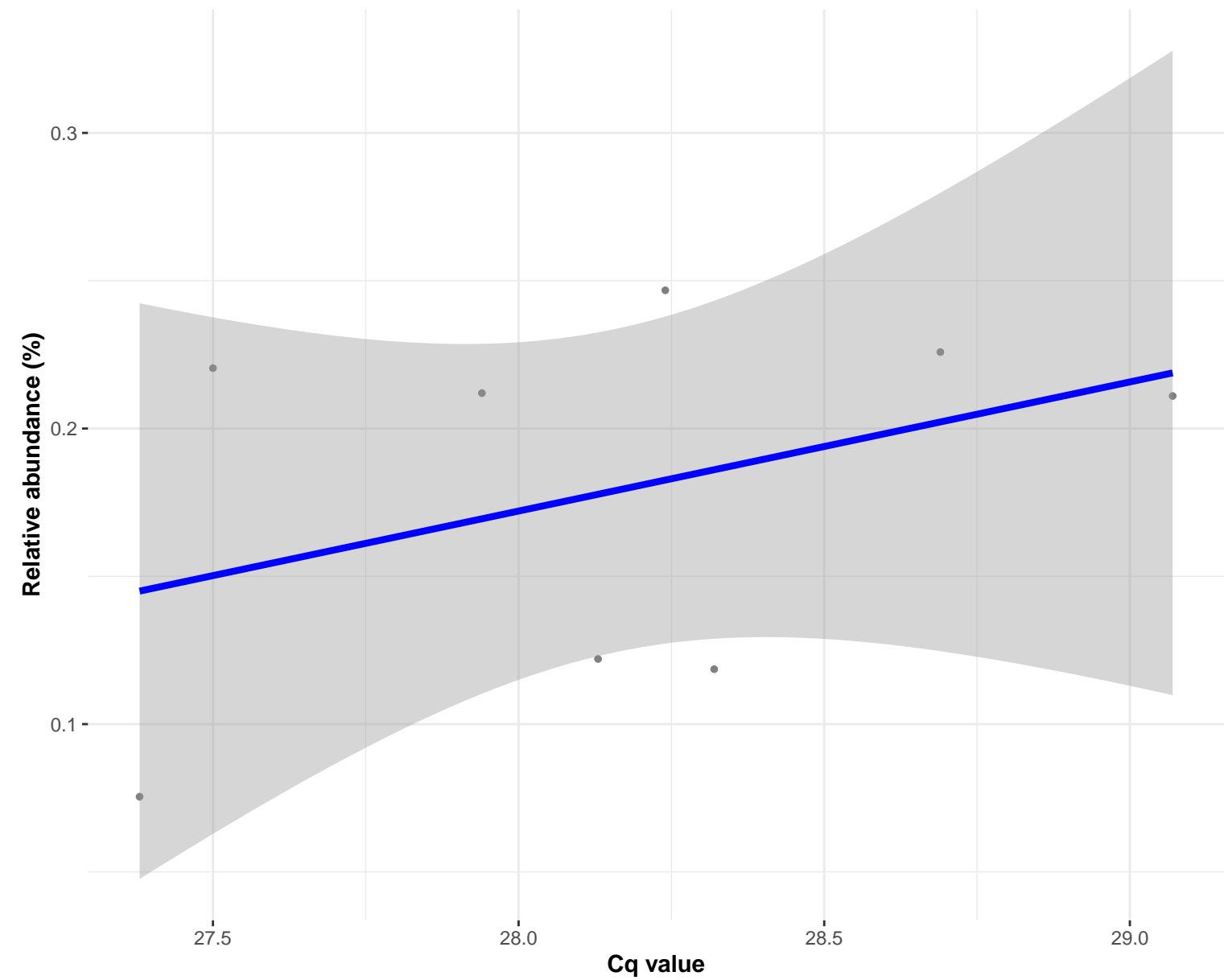
Correlation with all samples

$\log_e(S) = 6.501$ ,  $p = 0.480$ ,  $\hat{\rho}_{\text{Spearman}} = 0.184$ ,  $CI_{95\%} [-0.339, 0.620]$ ,  $n_{\text{pairs}} = 17$

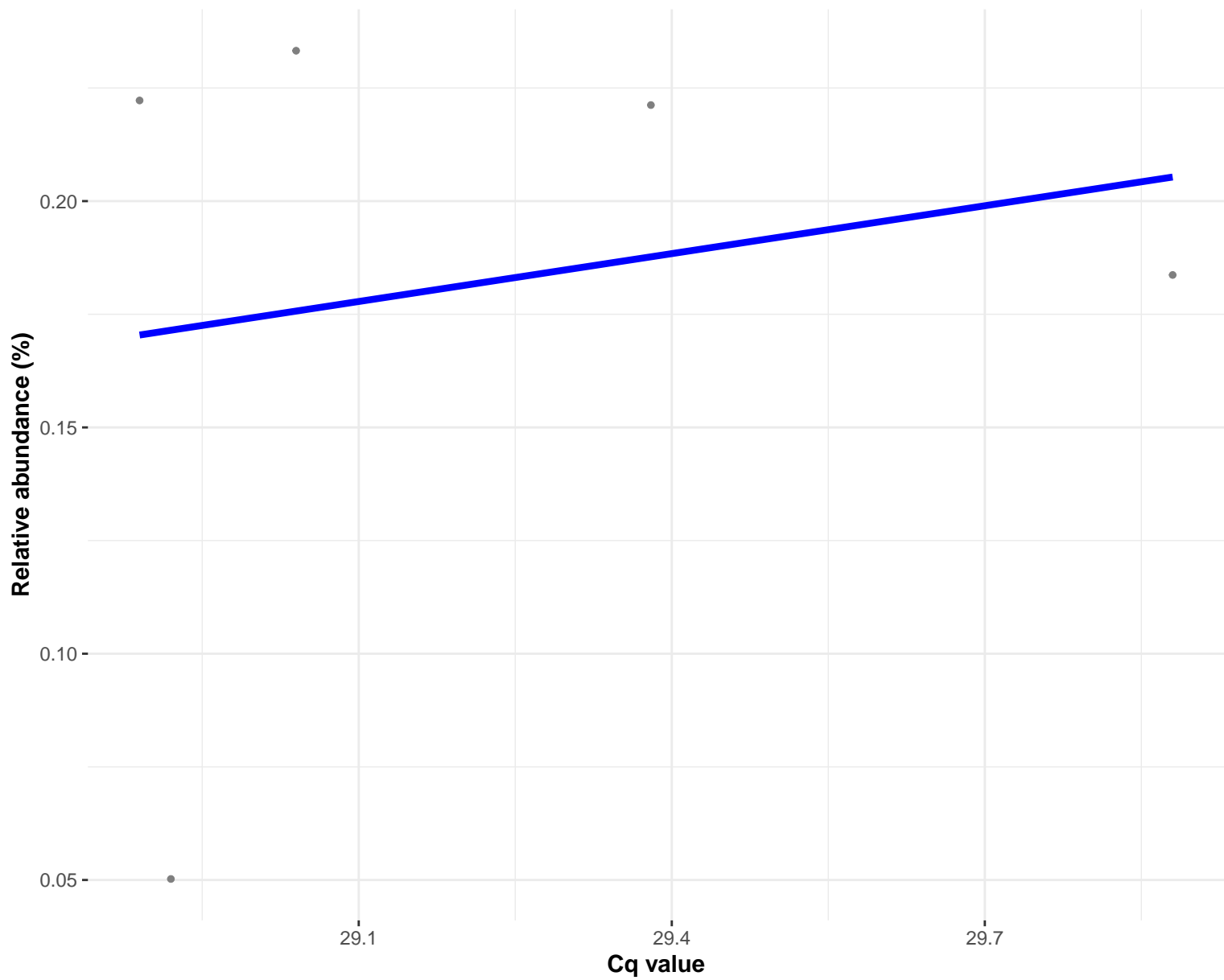


Correlation within: IM-PIM

$\log_e(S) = 4.127$ ,  $p = 0.531$ ,  $\hat{\rho}_{\text{Spearman}} = 0.262$ ,  $CI_{95\%} [-0.561, 0.824]$ ,  $n_{\text{pairs}} = 8$



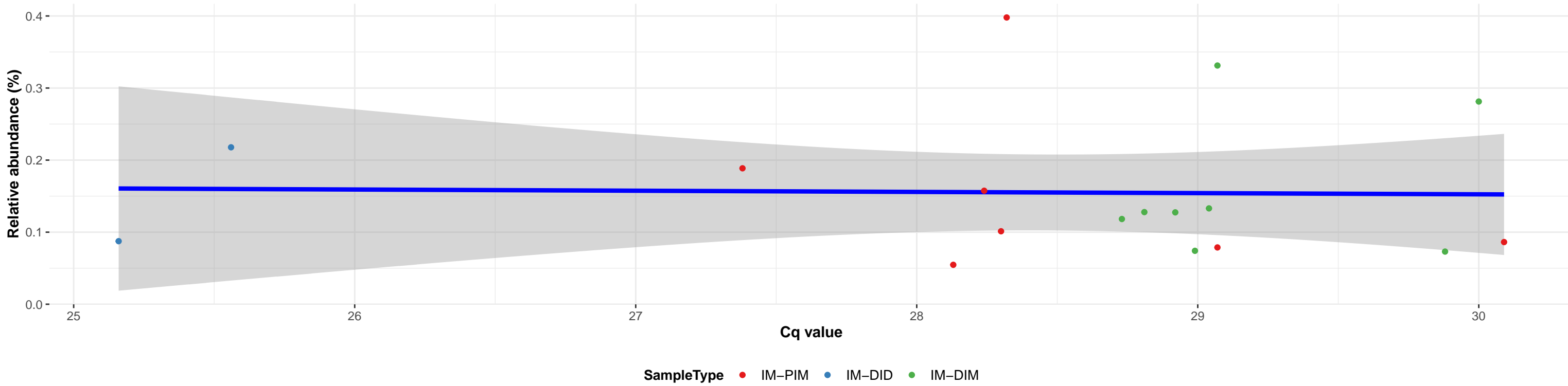
Correlation within: IM-DIM



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

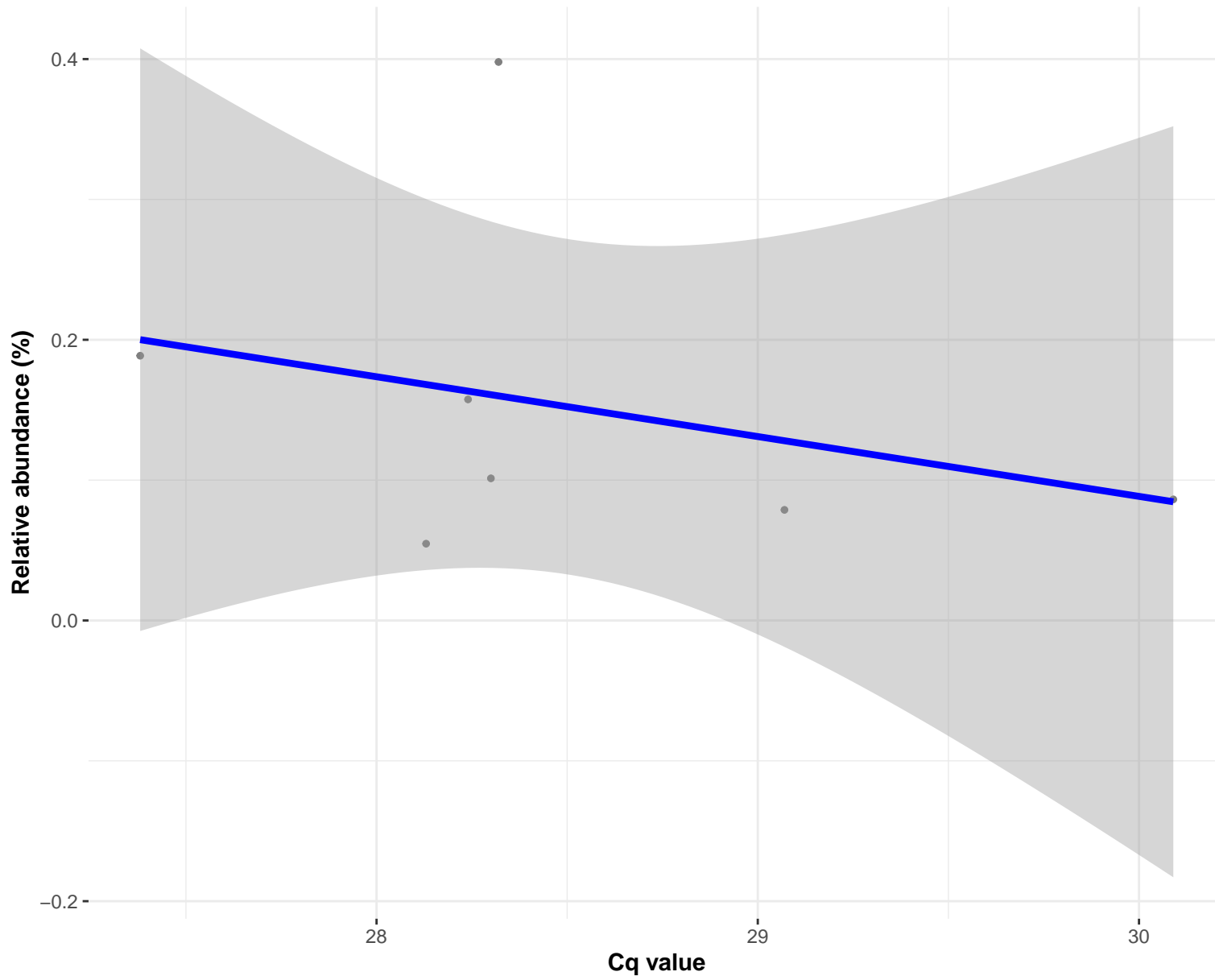
### Correlation with all samples

$\log_e(S) = 6.809$ ,  $p = 0.673$ ,  $\hat{\rho}_{\text{Spearman}} = -0.110$ ,  $CI_{95\%} [-0.572, 0.404]$ ,  $n_{\text{pairs}} = 17$



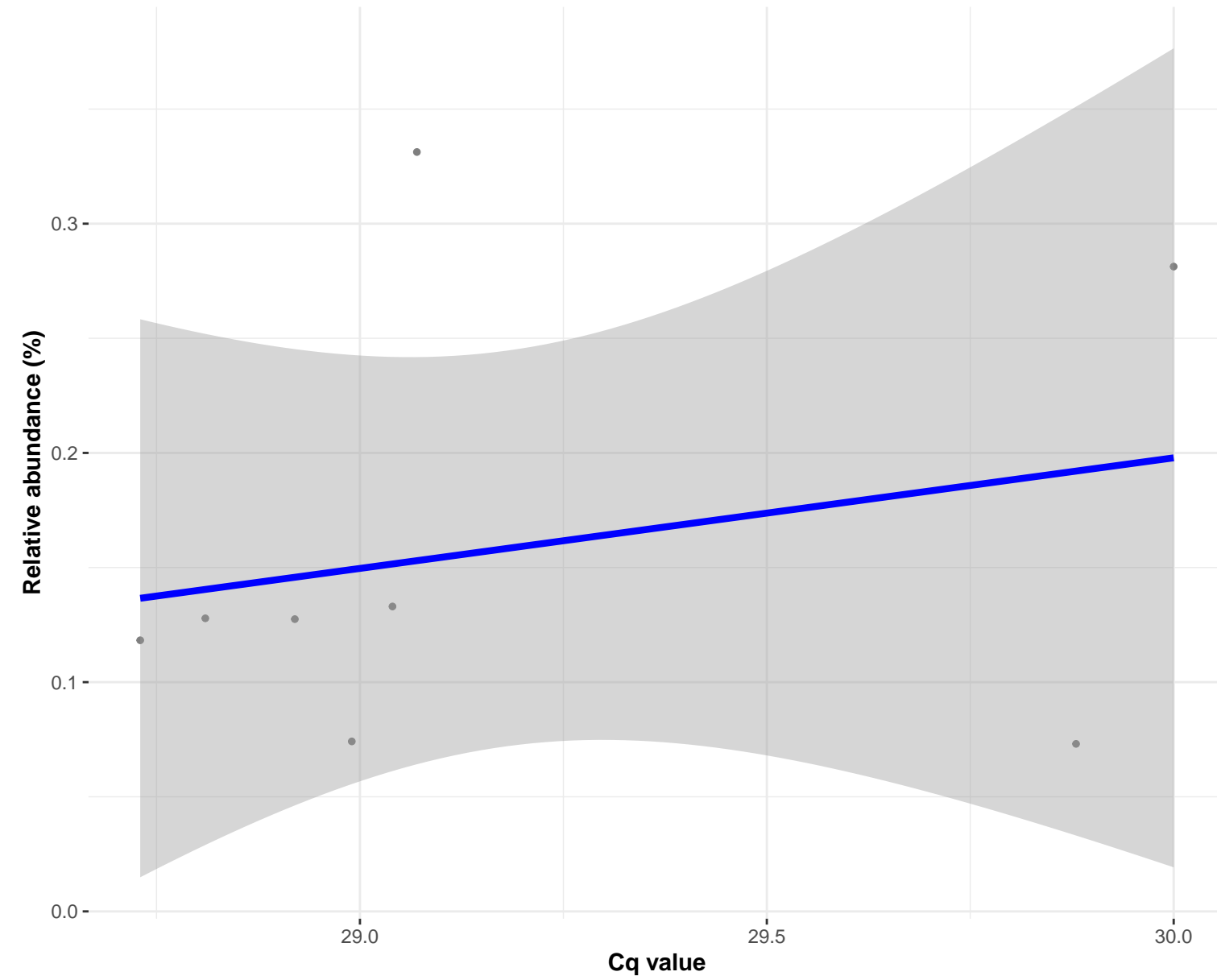
### Correlation within: IM-PIM

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



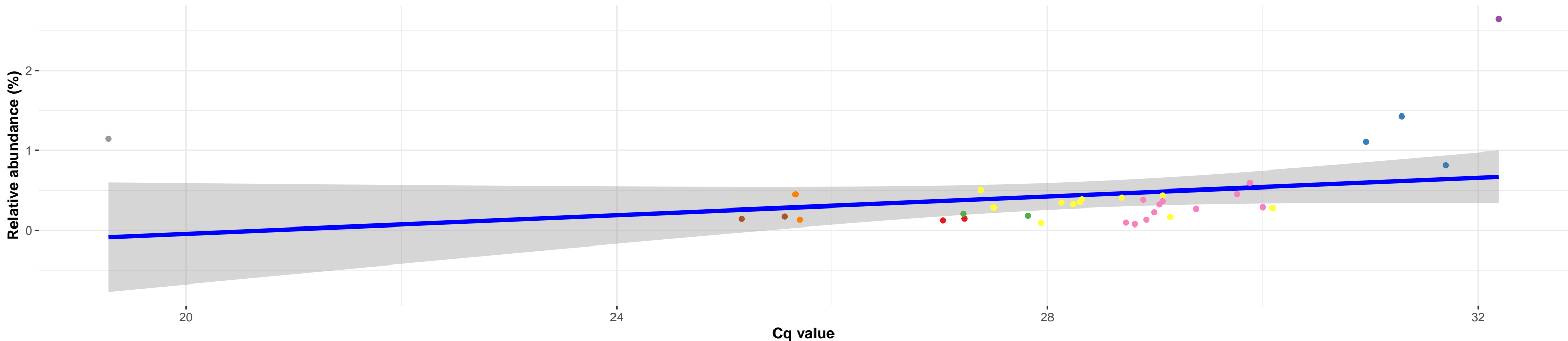
### Correlation within: IM-DIM

$\log_e(S) = 4.094$ ,  $p = 0.493$ ,  $\hat{\rho}_{\text{Spearman}} = 0.286$ ,  $CI_{95\%} [-0.543, 0.833]$ ,  $n_{\text{pairs}} = 8$

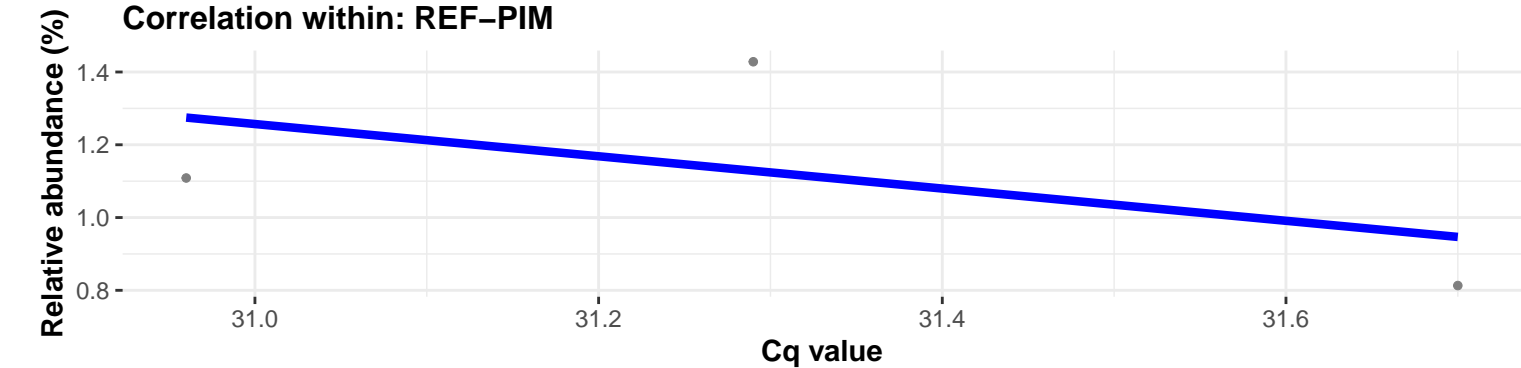


Correlation with all samples

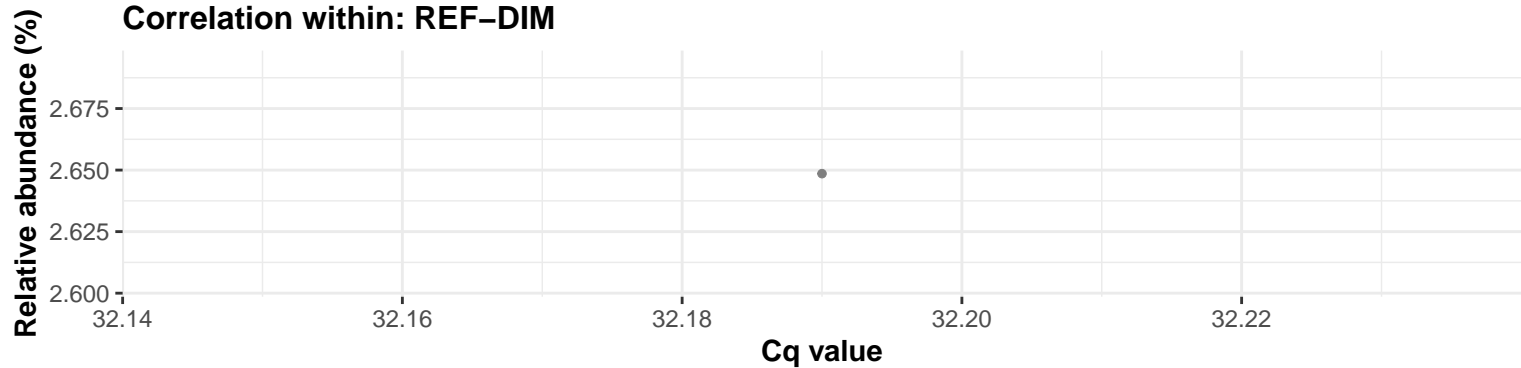
$\log_e(S) = 8.356$ ,  $p = 0.016$ ,  $\hat{\rho}_{\text{Spearman}} = 0.404$ ,  $CI_{95\%} [0.072, 0.656]$ ,  $n_{\text{pairs}} = 35$



Correlation within: REF-PIM

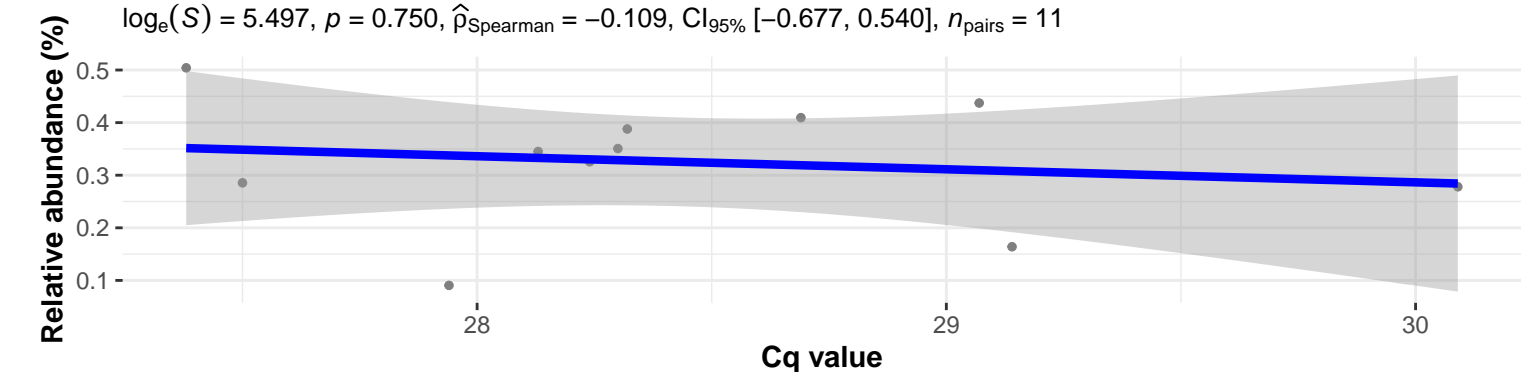


Correlation within: REF-DIM



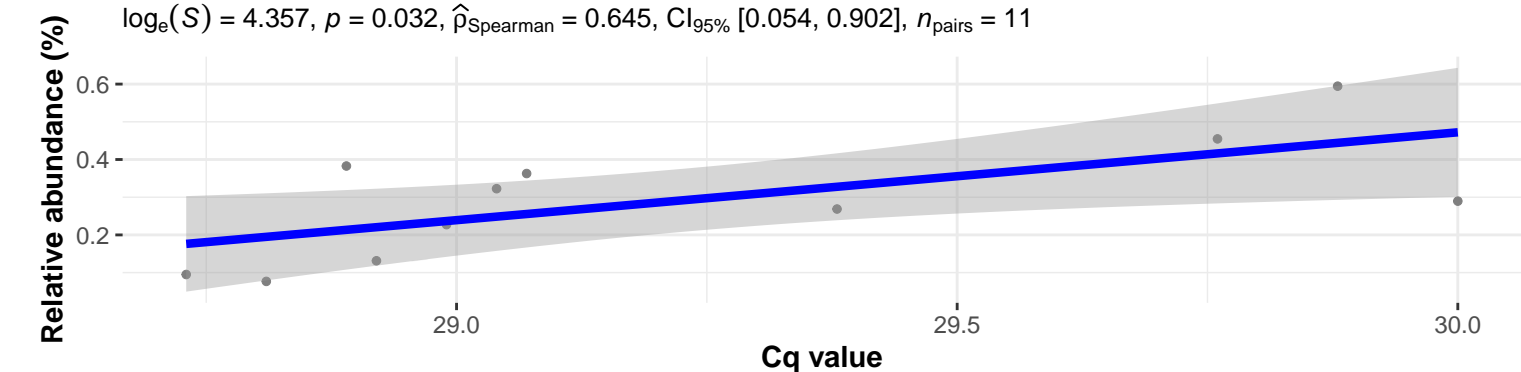
Correlation within: IM-PIM

$\log_e(S) = 5.497$ ,  $p = 0.750$ ,  $\hat{\rho}_{\text{Spearman}} = -0.109$ ,  $CI_{95\%} [-0.677, 0.540]$ ,  $n_{\text{pairs}} = 11$

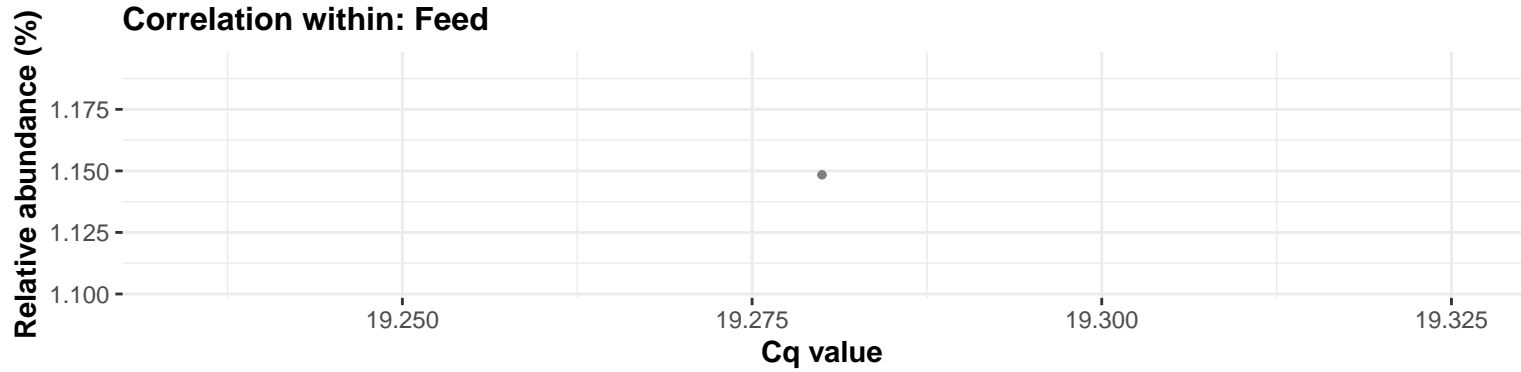


Correlation within: IM-DIM

$\log_e(S) = 4.357$ ,  $p = 0.032$ ,  $\hat{\rho}_{\text{Spearman}} = 0.645$ ,  $CI_{95\%} [0.054, 0.902]$ ,  $n_{\text{pairs}} = 11$



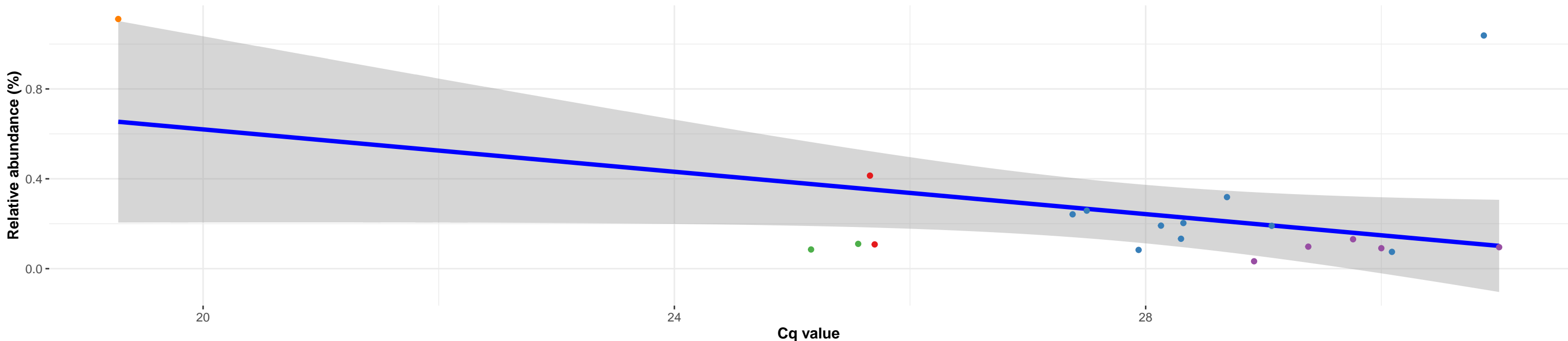
Correlation within: Feed



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

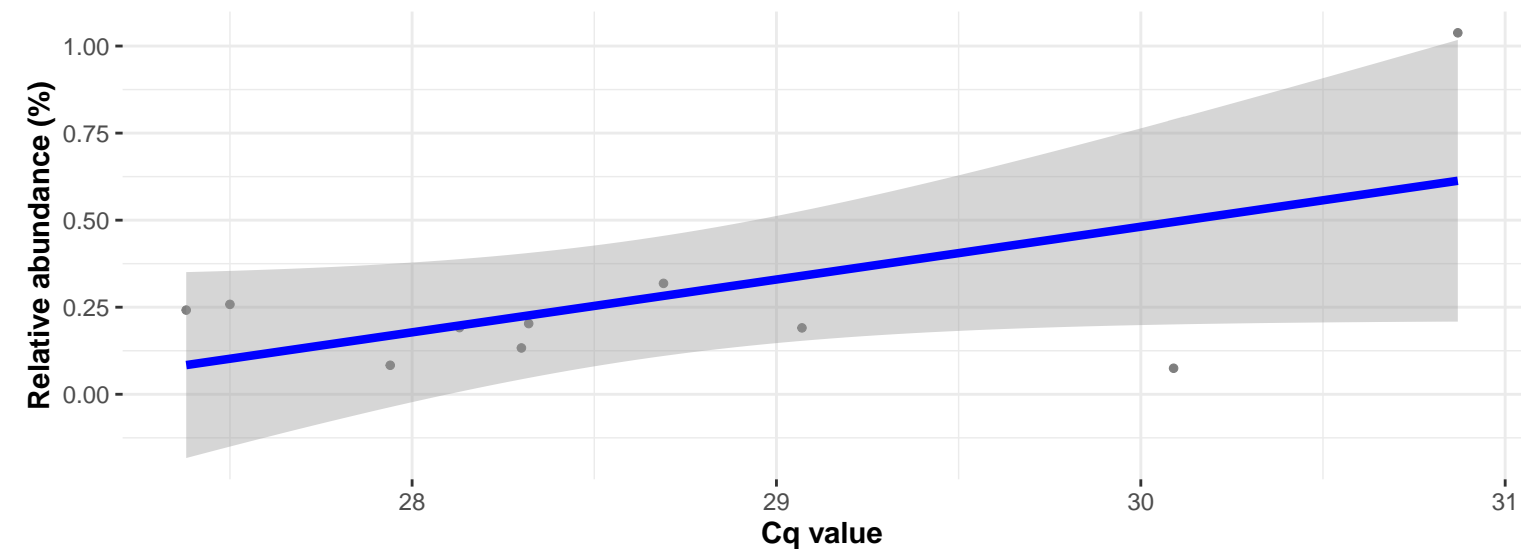
Correlation with all samples

$\log_e(S) = 7.431$ ,  $p = 0.251$ ,  $\hat{\rho}_{\text{Spearman}} = -0.269$ ,  $CI_{95\%} [-0.644, 0.210]$ ,  $n_{\text{pairs}} = 20$

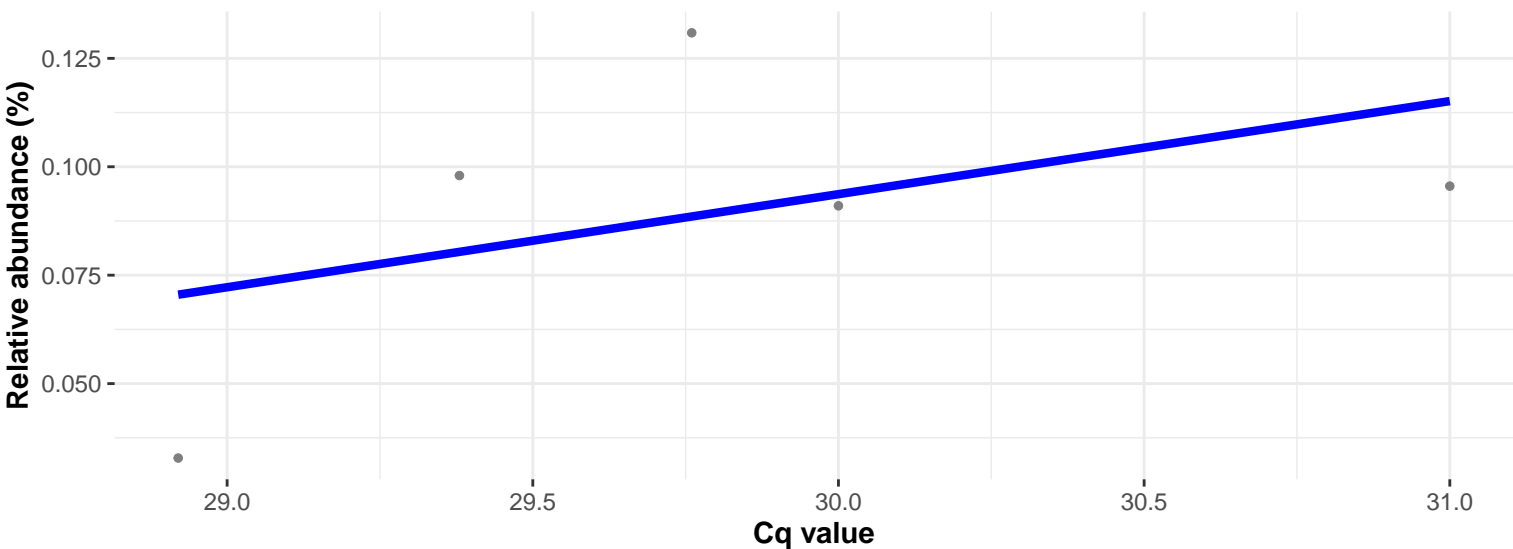


Correlation within: IM-PIM

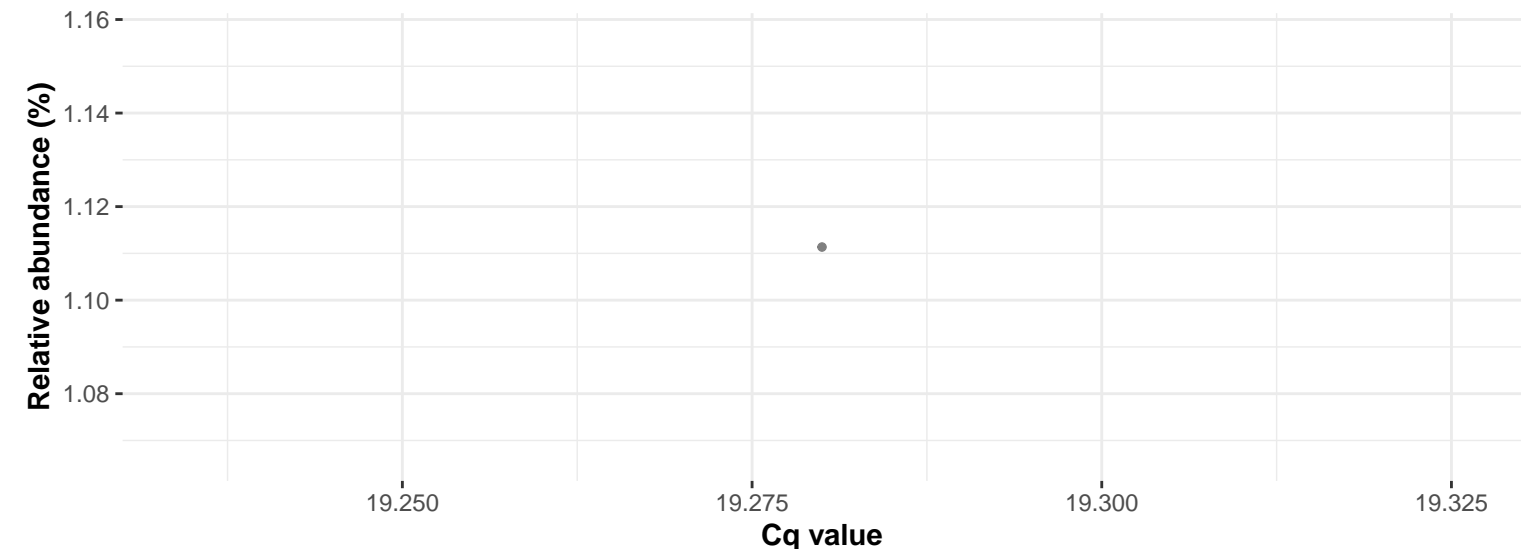
$\log_e(S) = 5.088$ ,  $p = 0.960$ ,  $\hat{\rho}_{\text{Spearman}} = 0.018$ ,  $CI_{95\%} [-0.632, 0.653]$ ,  $n_{\text{pairs}} = 10$



Correlation within: IM-DIM



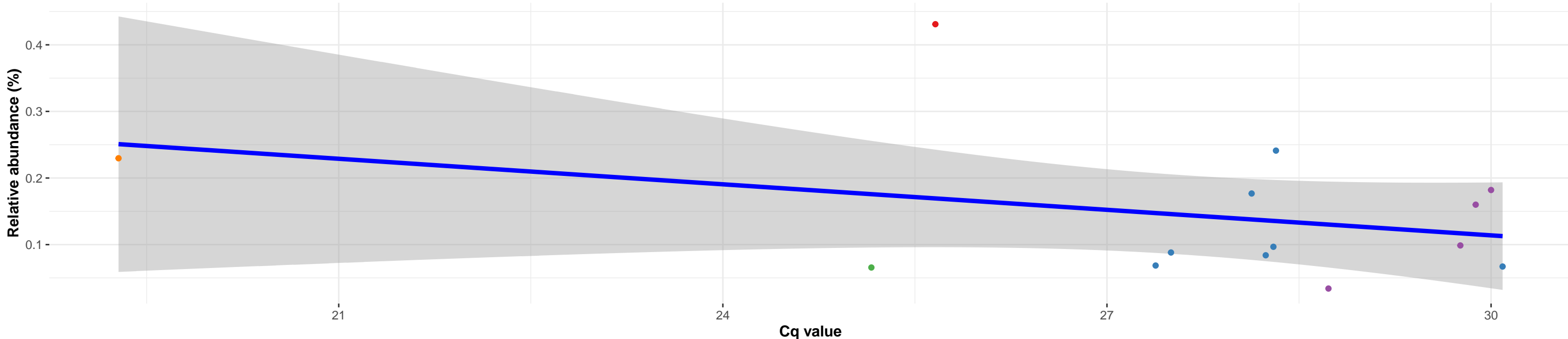
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; NA

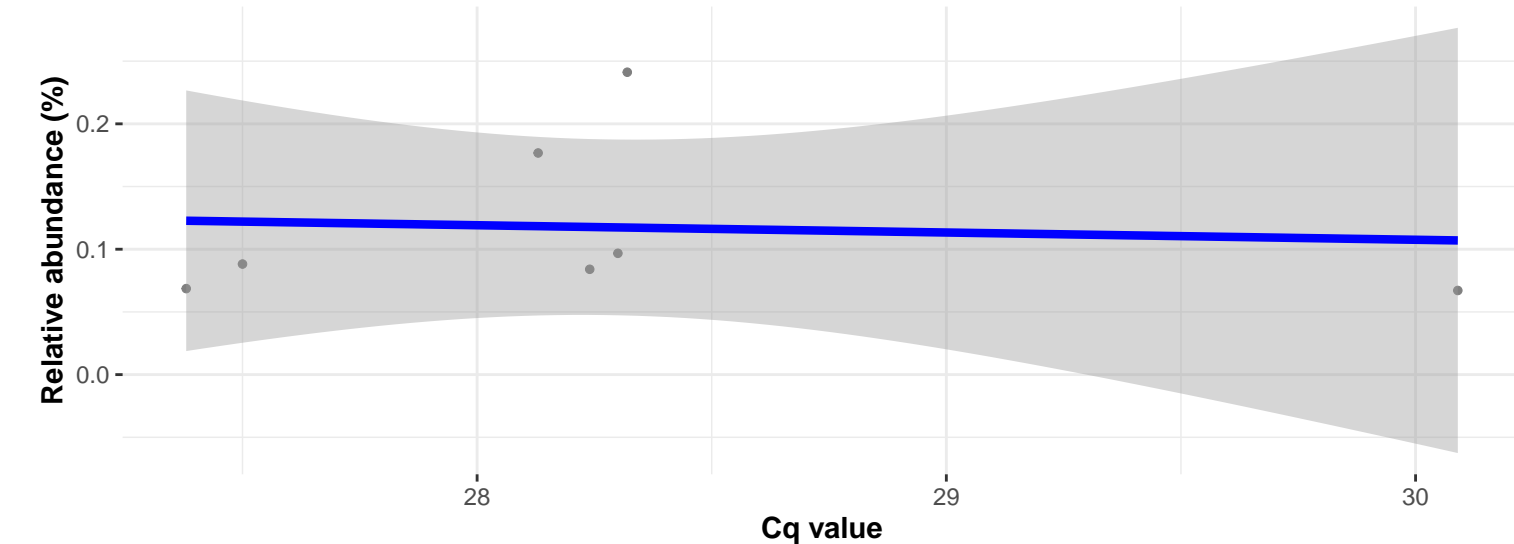
Correlation with all samples

$\log_e(S) = 6.223$ ,  $p = 0.714$ ,  $\hat{\rho}_{\text{Spearman}} = -0.108$ ,  $\text{CI}_{95\%} [-0.615, 0.462]$ ,  $n_{\text{pairs}} = 14$

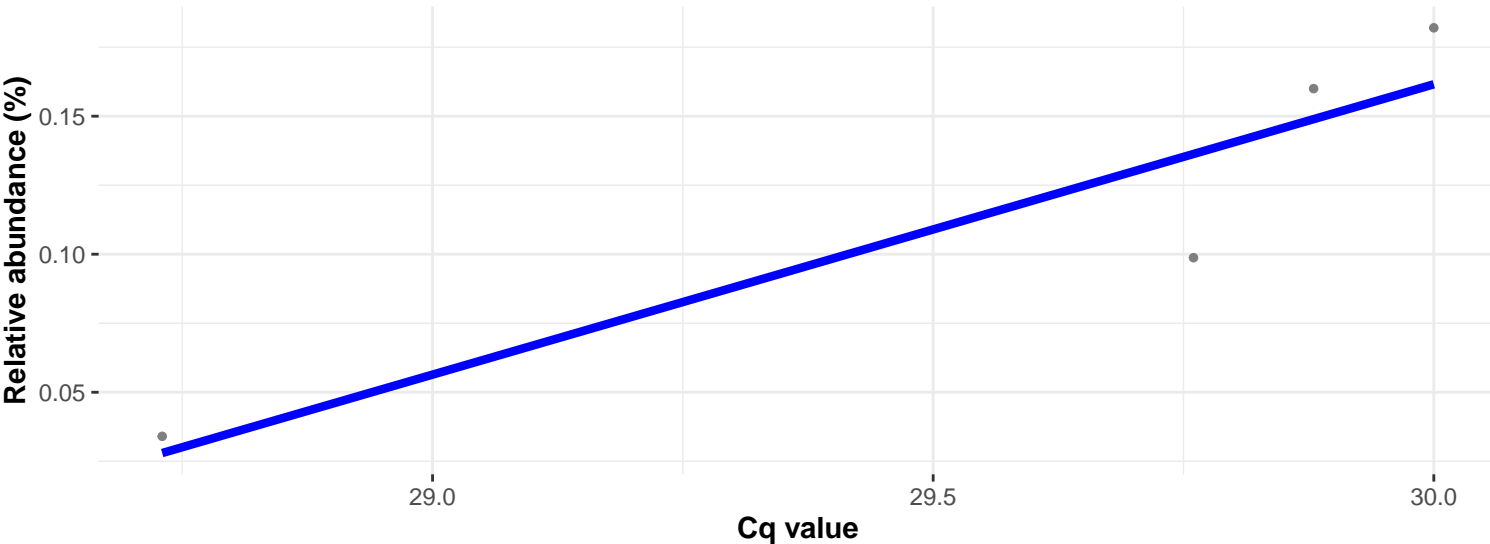


Correlation within: IM-PIM

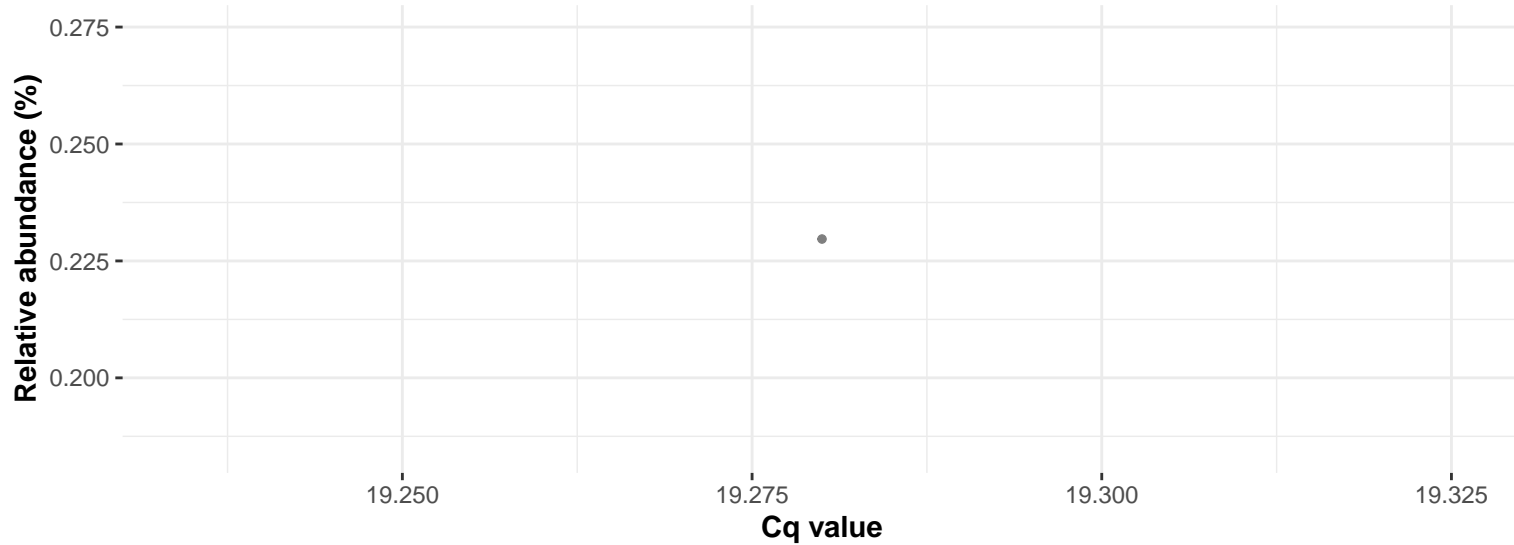
$\log_e(S) = 3.951$ ,  $p = 0.879$ ,  $\hat{\rho}_{\text{Spearman}} = 0.071$ ,  $\text{CI}_{95\%} [-0.734, 0.793]$ ,  $n_{\text{pairs}} = 7$



Correlation within: IM-DIM



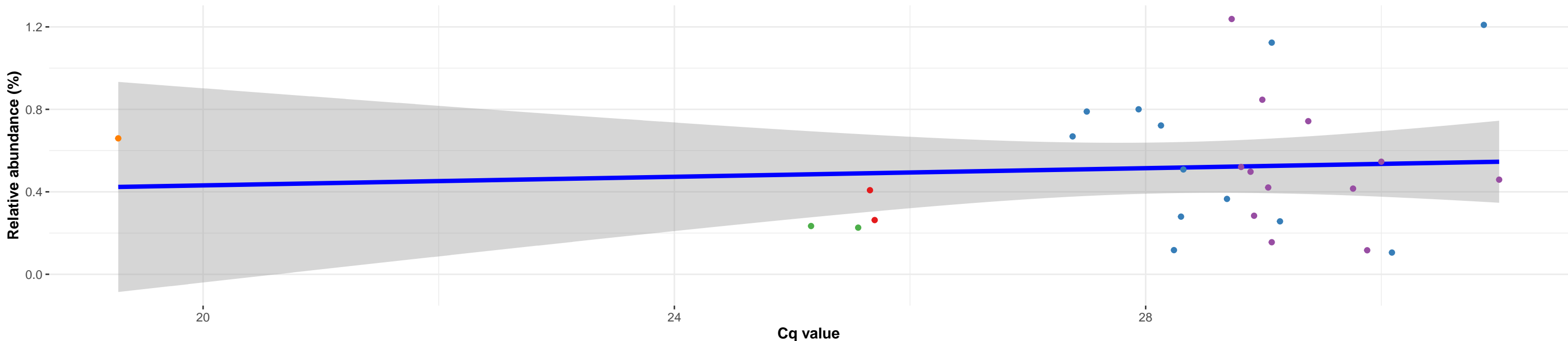
Correlation within: Feed



k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Actinomycetales; f\_\_Actinomycetaceae; g\_\_Actinomyces; s\_\_uncultured Actinomycetales bacterium

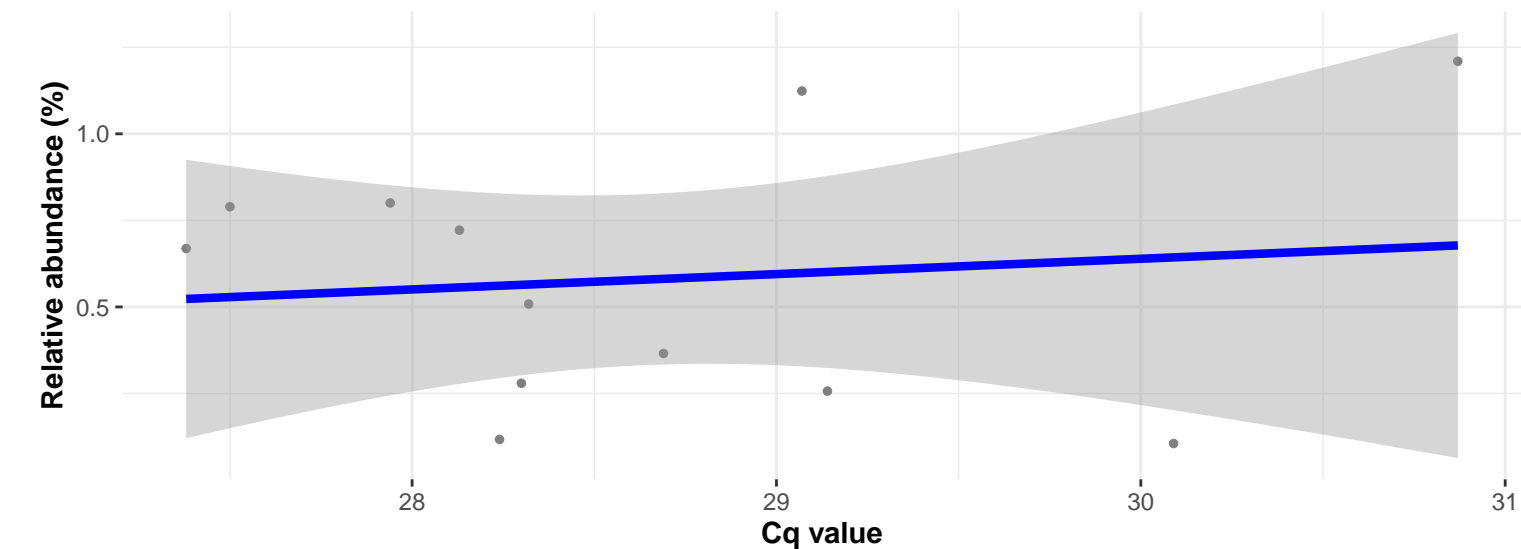
Correlation with all samples

$\log_e(S) = 8.292$ ,  $p = 0.930$ ,  $\hat{\rho}_{\text{Spearman}} = 0.017$ ,  $CI_{95\%} [-0.362, 0.391]$ ,  $n_{\text{pairs}} = 29$



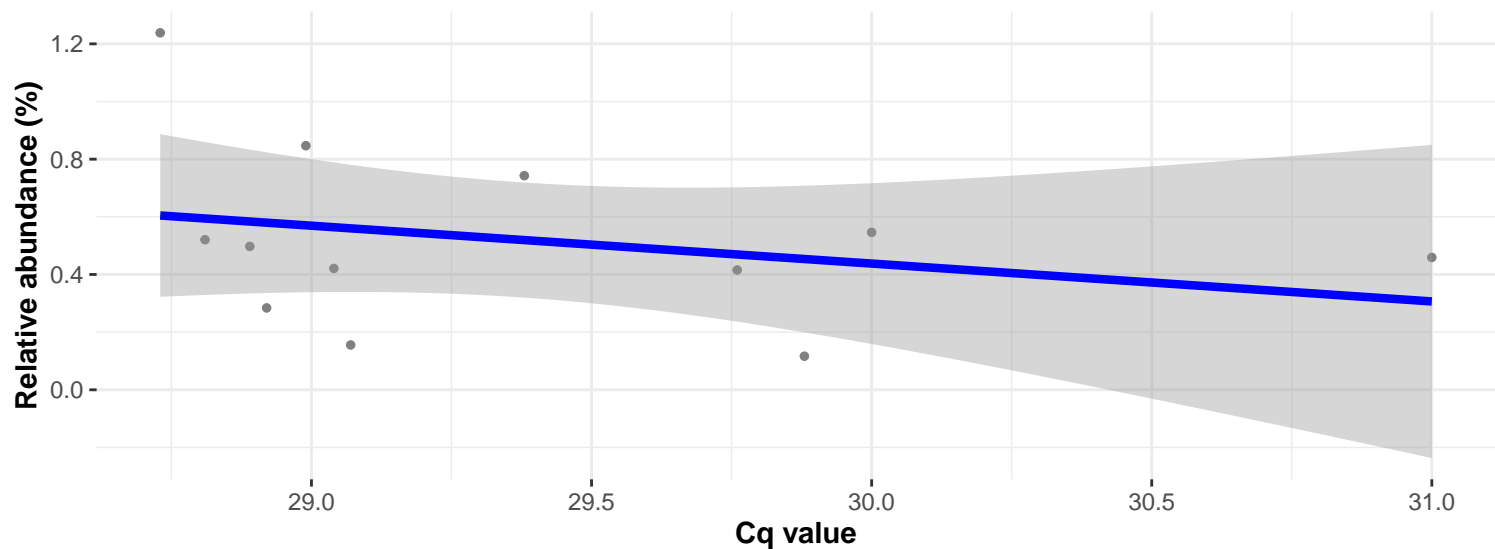
Correlation within: IM-PIM

$\log_e(S) = 5.787$ ,  $p = 0.665$ ,  $\hat{\rho}_{\text{Spearman}} = -0.140$ ,  $CI_{95\%} [-0.671, 0.487]$ ,  $n_{\text{pairs}} = 12$

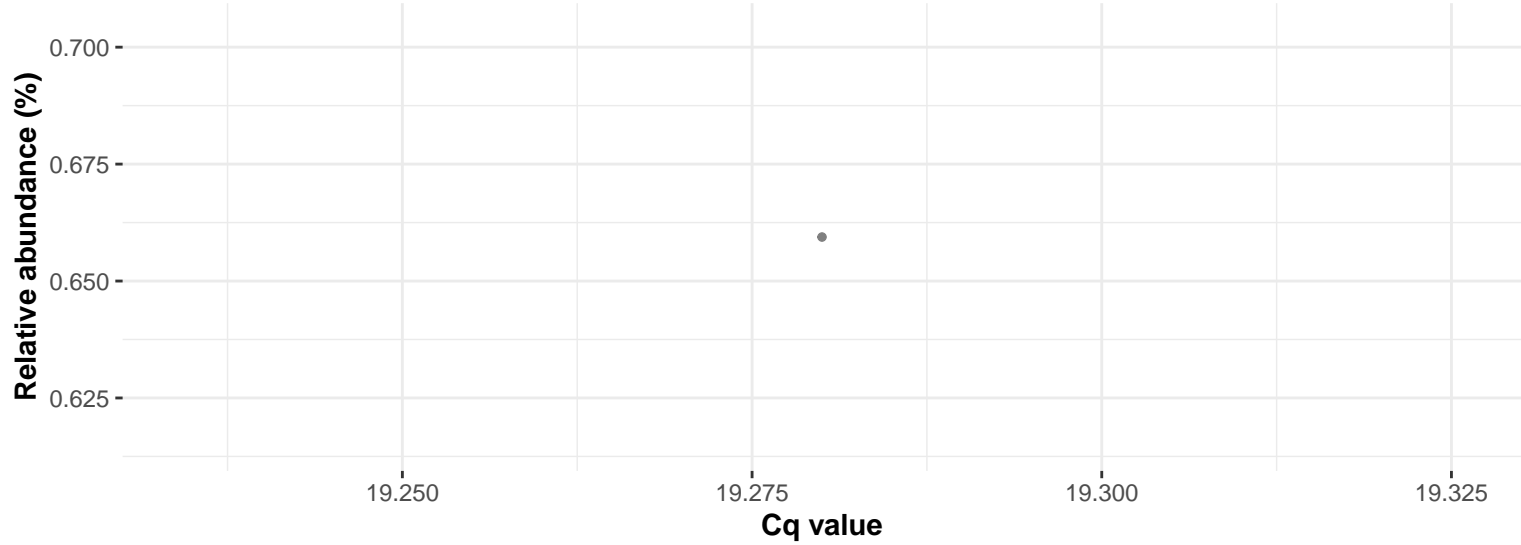


Correlation within: IM-DIM

$\log_e(S) = 5.956$ ,  $p = 0.265$ ,  $\hat{\rho}_{\text{Spearman}} = -0.350$ ,  $CI_{95\%} [-0.777, 0.298]$ ,  $n_{\text{pairs}} = 12$



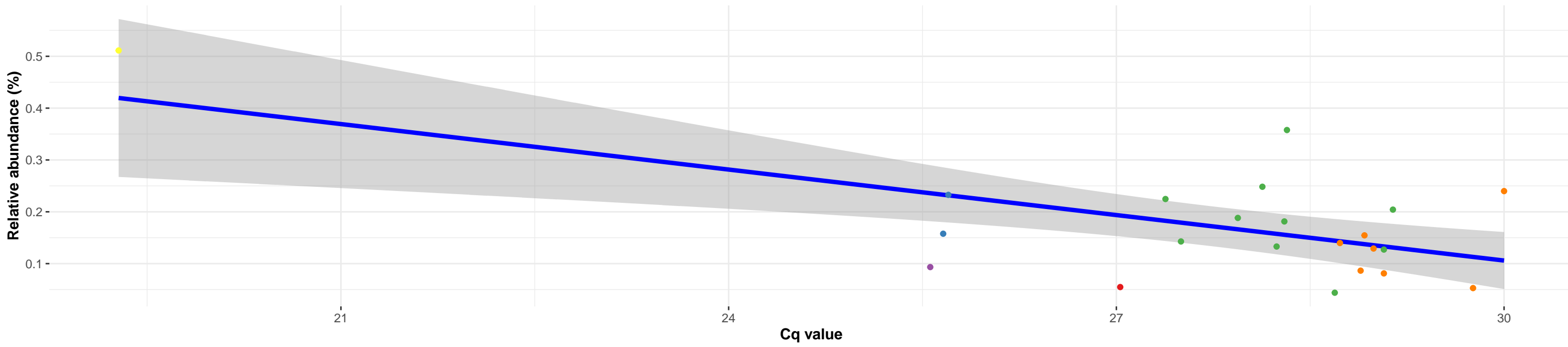
Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Vagococcus; Ambiguous\_taxa

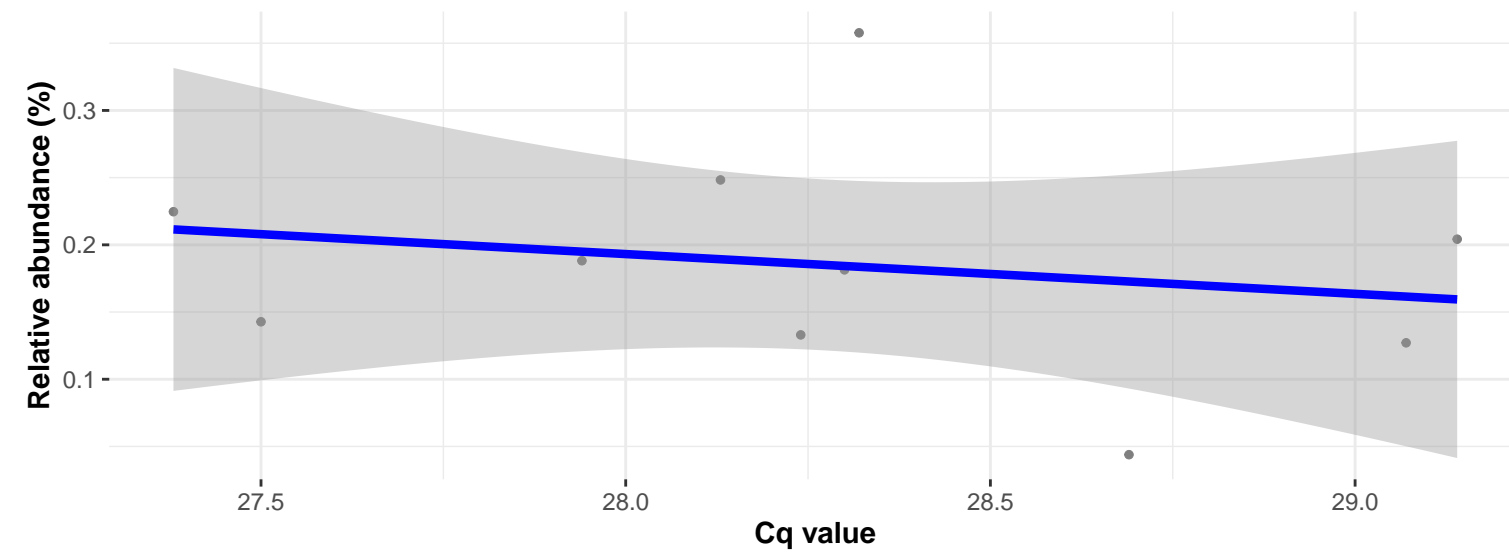
### Correlation with all samples

$\log_e(S) = 7.715$ ,  $p = 0.232$ ,  $\hat{\rho}_{\text{Spearman}} = -0.265$ ,  $CI_{95\%} [-0.626, 0.189]$ ,  $n_{\text{pairs}} = 22$



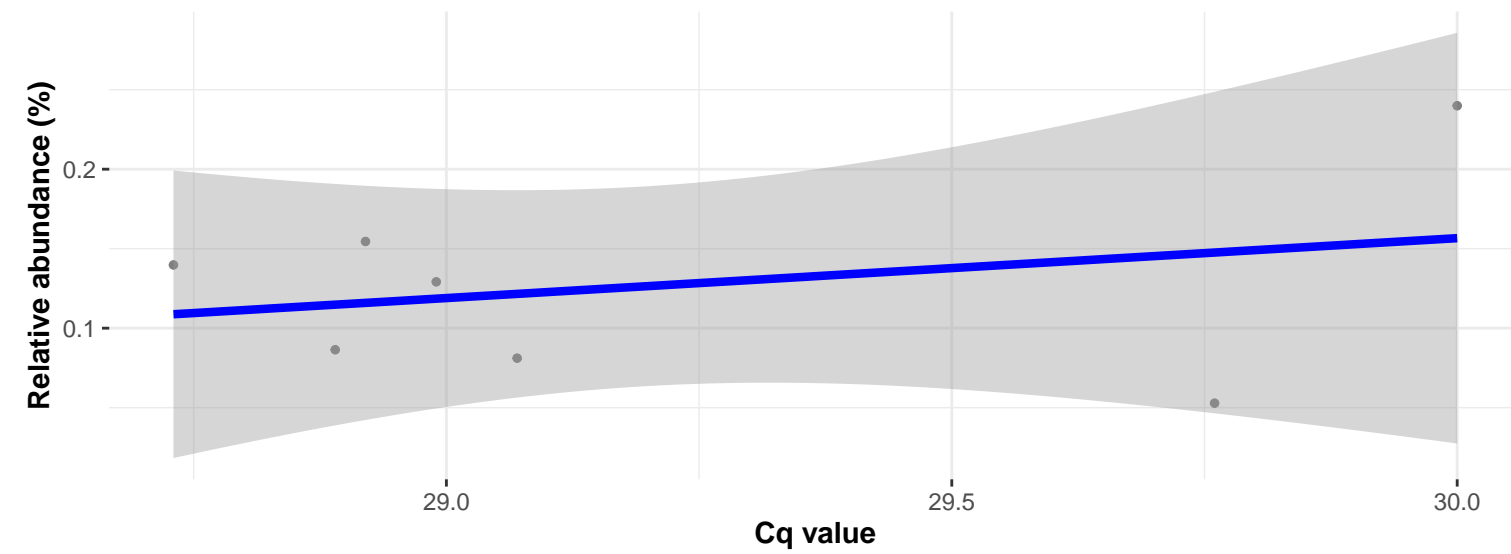
### Correlation within: IM-PIM

$\log_e(S) = 5.338$ ,  $p = 0.467$ ,  $\hat{\rho}_{\text{Spearman}} = -0.261$ ,  $CI_{95\%} [-0.774, 0.459]$ ,  $n_{\text{pairs}} = 10$

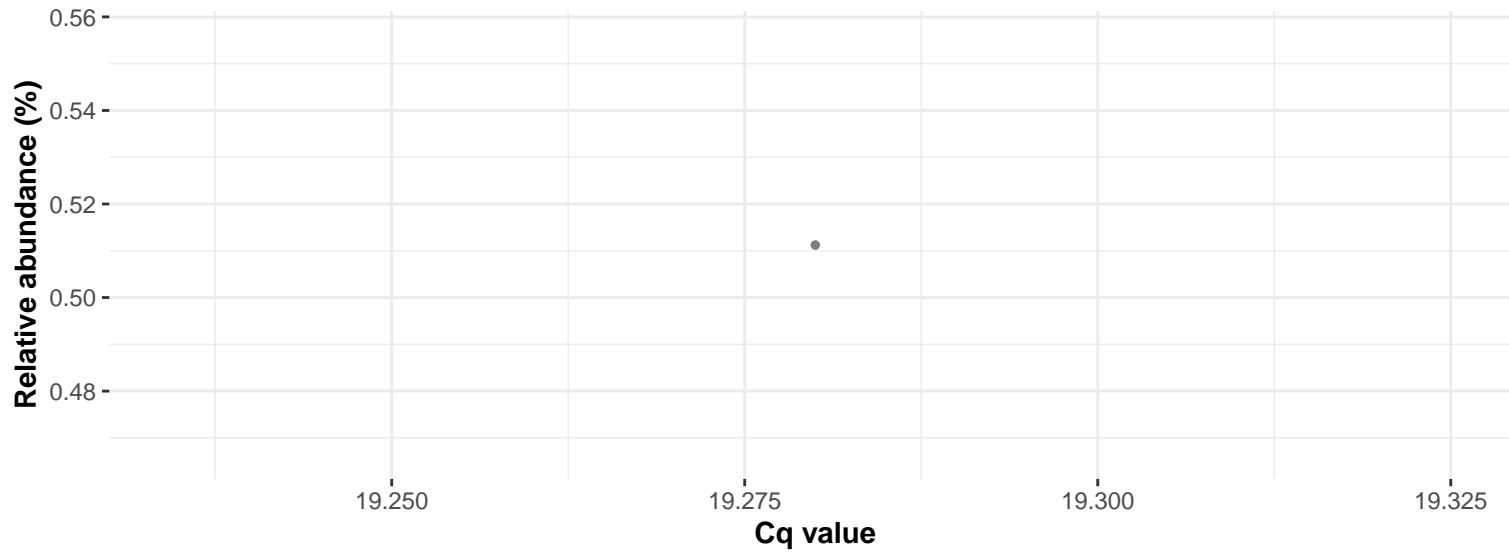


### Correlation within: IM-DIM

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



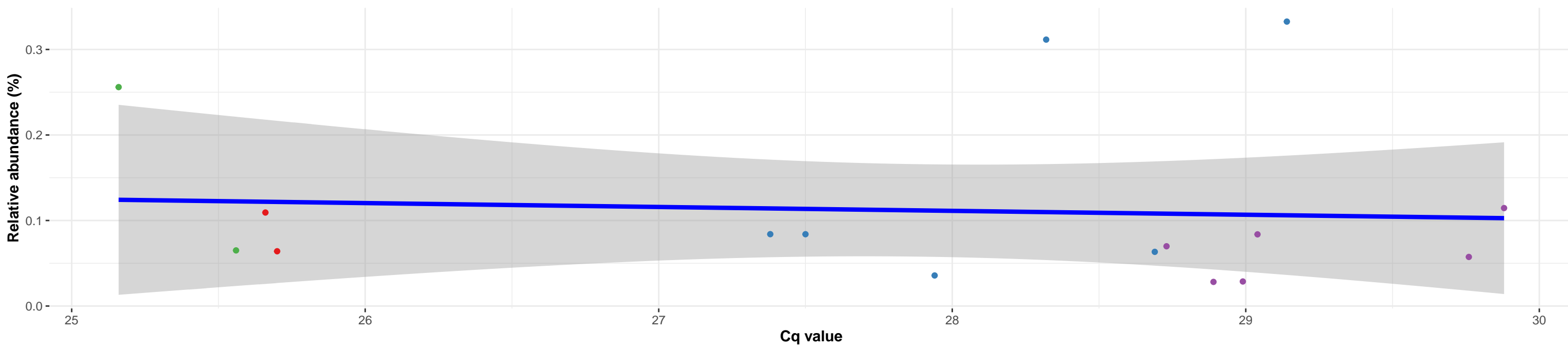
### Correlation within: Feed



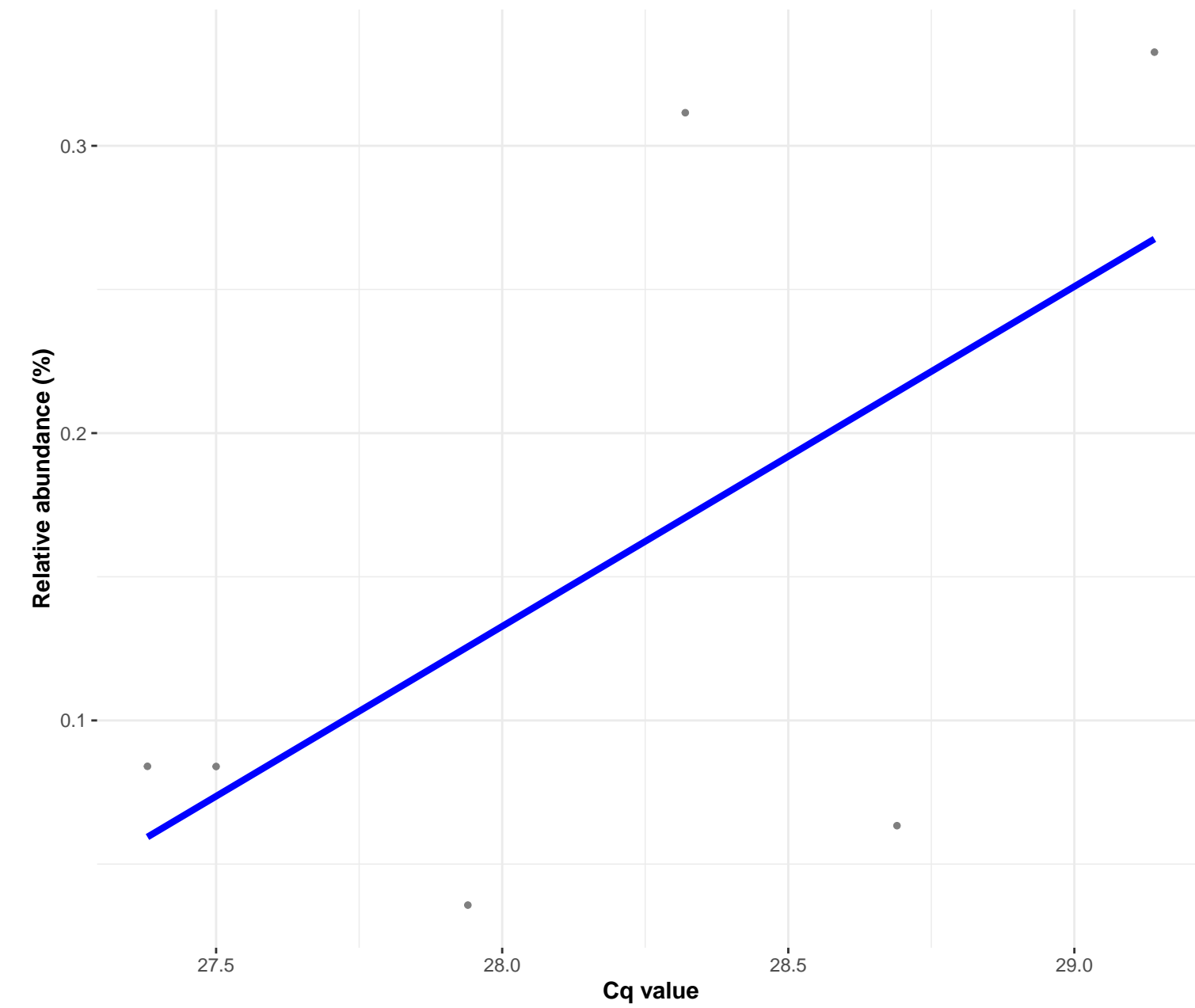
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Enterococcaceae; g\_\_Enterococcus; Ambiguous\_taxa

### Correlation with all samples

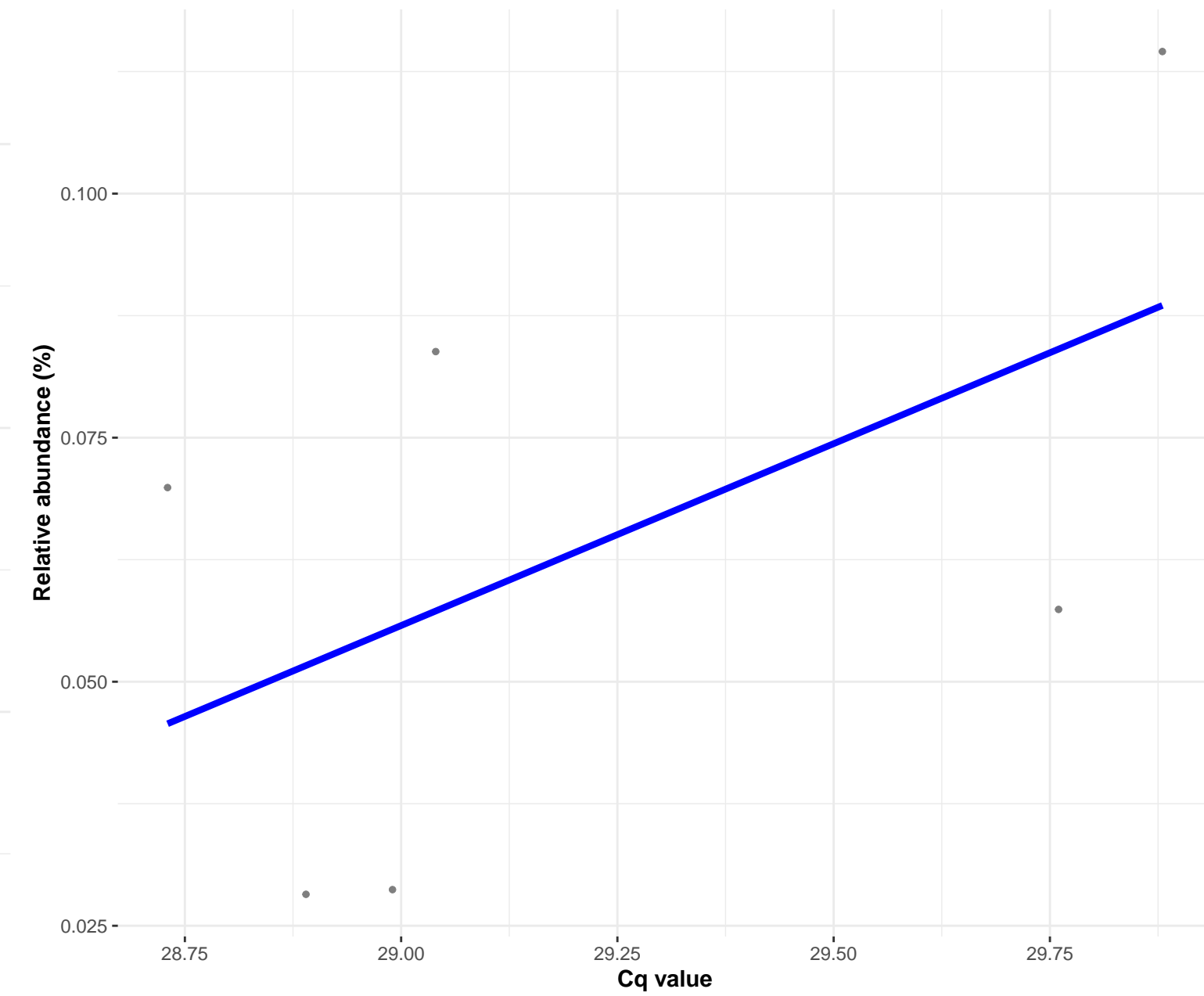
$\log_e(S) = 6.641$ ,  $p = 0.641$ ,  $\hat{\rho}_{\text{Spearman}} = -0.126$ ,  $\text{CI}_{95\%} [-0.596, 0.407]$ ,  $n_{\text{pairs}} = 16$



### Correlation within: IM-PIM



### Correlation within: IM-DIM

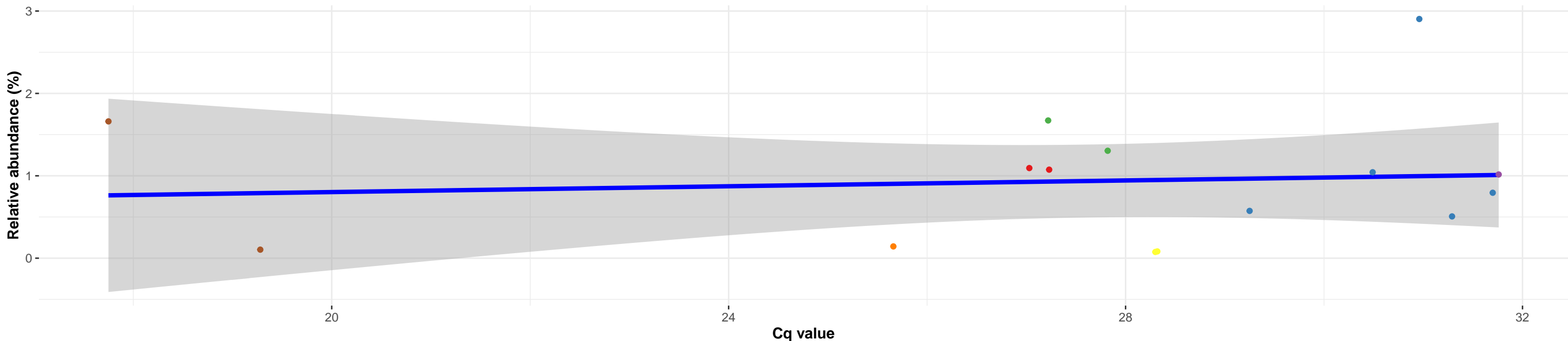




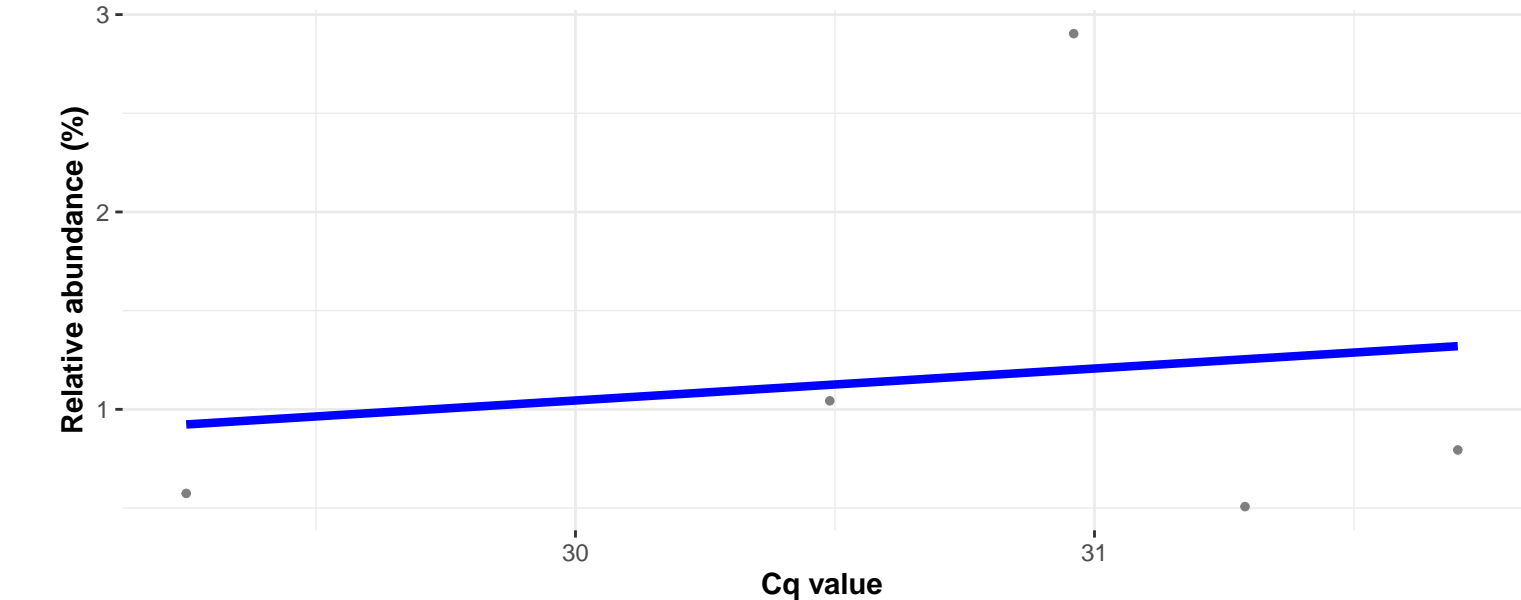
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus helveticus

Correlation with all samples

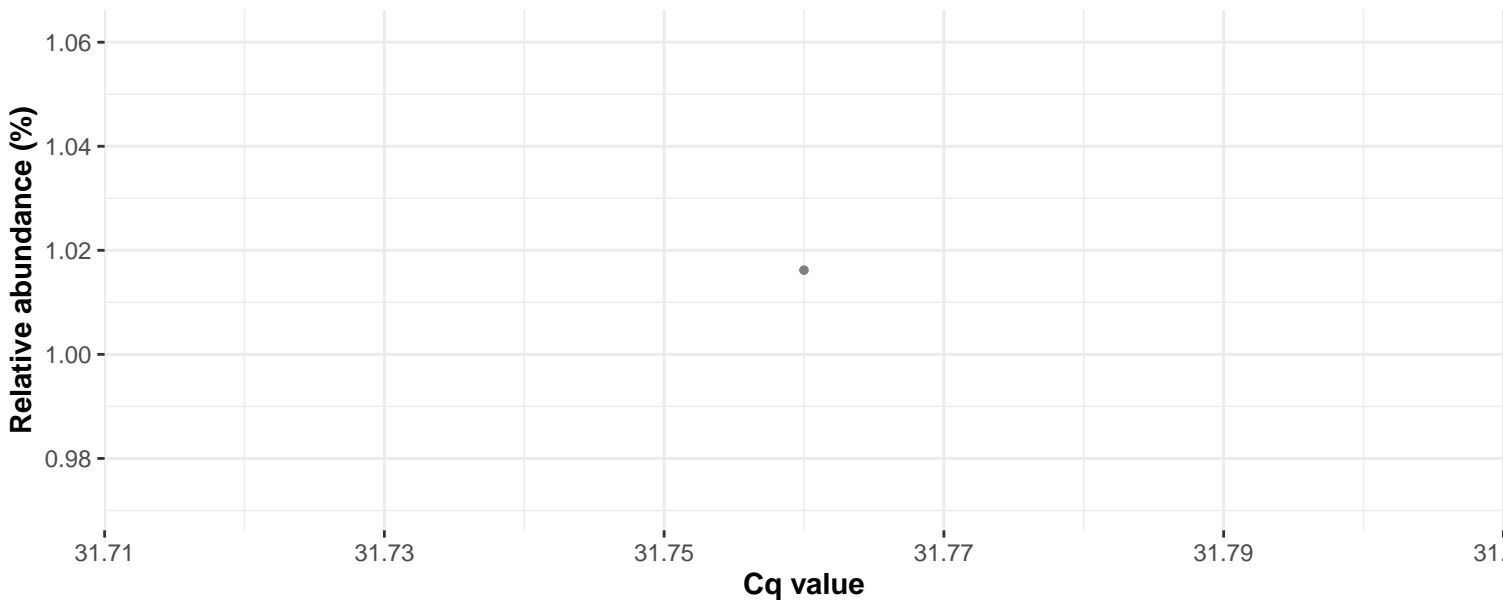
$\log_e(S) = 6.407$ ,  $p = 0.771$ ,  $\hat{\rho}_{\text{Spearman}} = -0.082$ ,  $CI_{95\%} [-0.582, 0.462]$ ,  $n_{\text{pairs}} = 15$



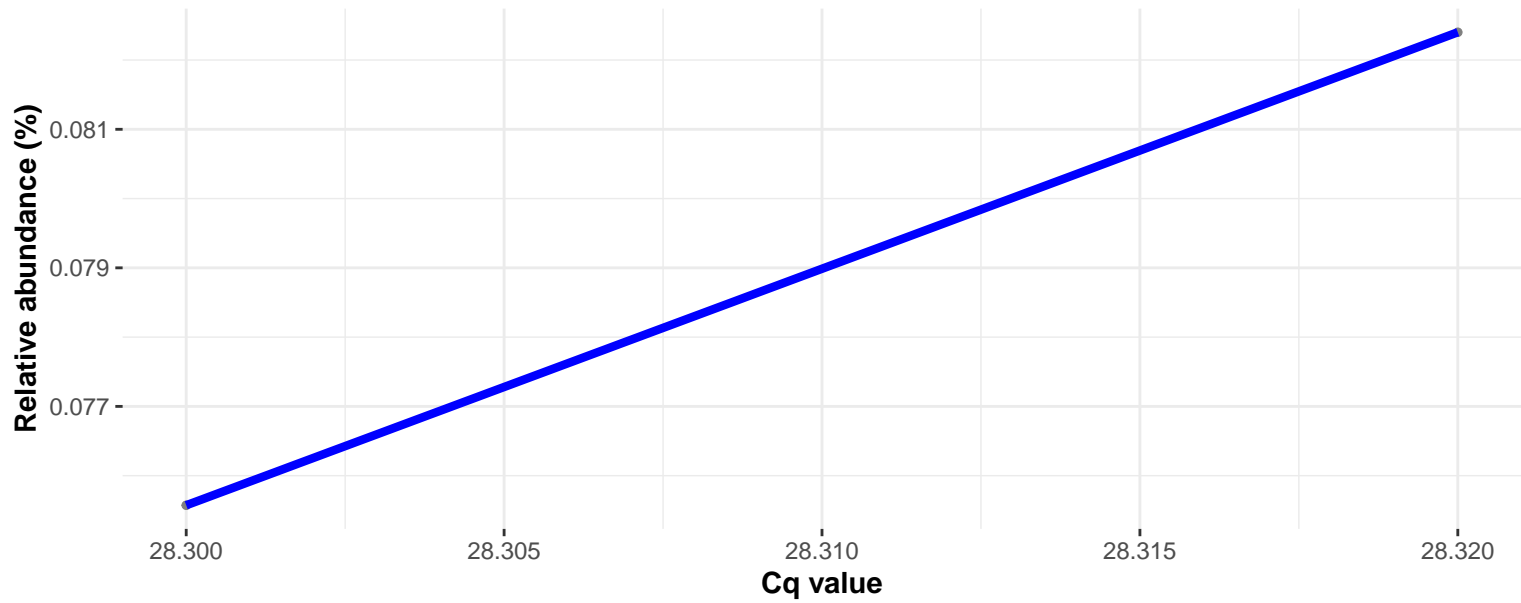
Correlation within: REF-PIM



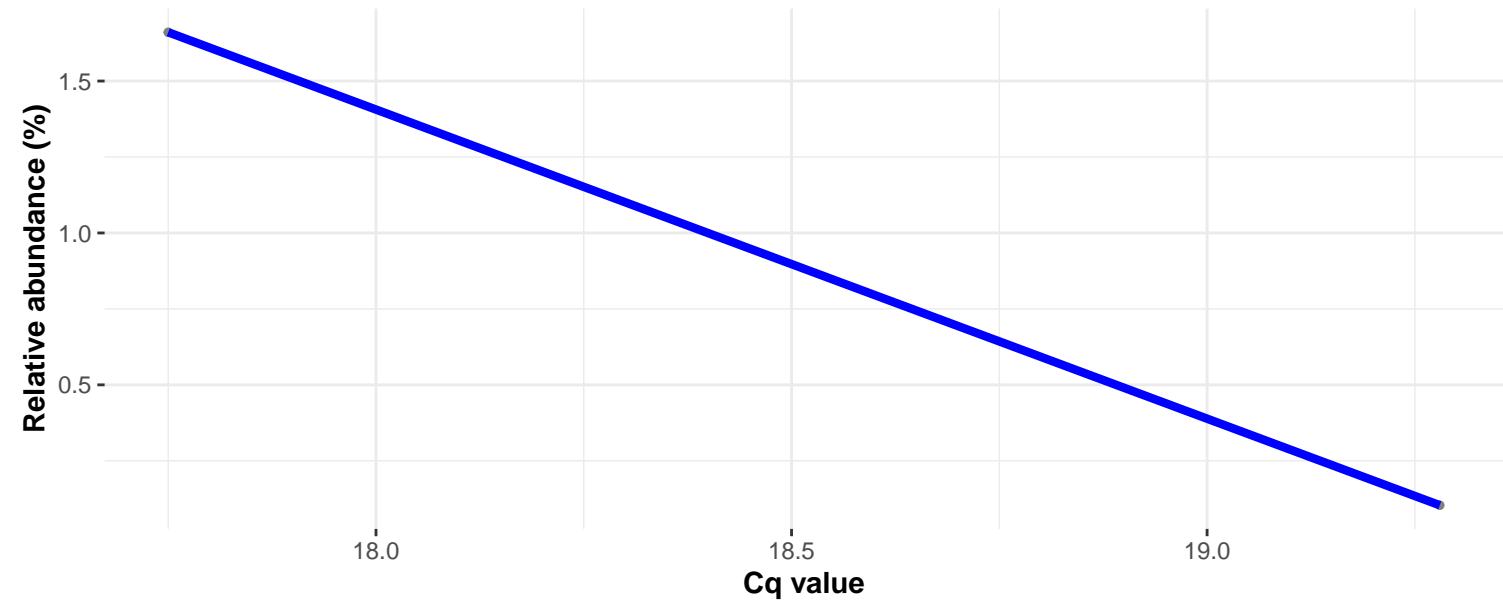
Correlation within: REF-DIM



Correlation within: IM-PIM



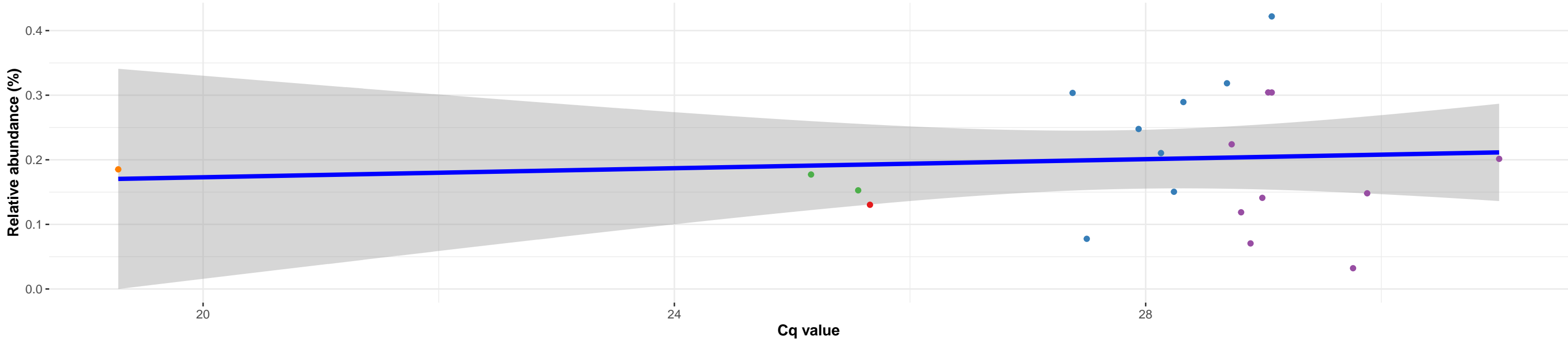
Correlation within: Feed



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

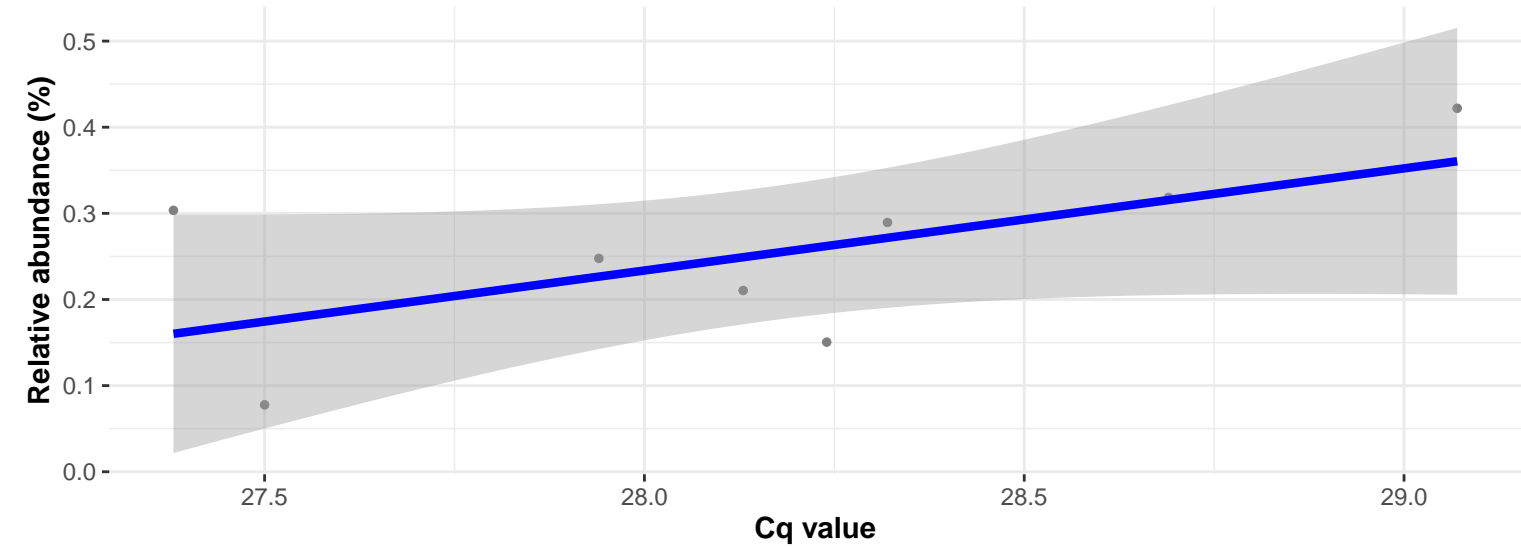
Correlation with all samples

$\log_e(S) = 7.291$ ,  $p = 0.838$ ,  $\hat{\rho}_{\text{Spearman}} = 0.047$ ,  $CI_{95\%} [-0.404, 0.480]$ ,  $n_{\text{pairs}} = 21$



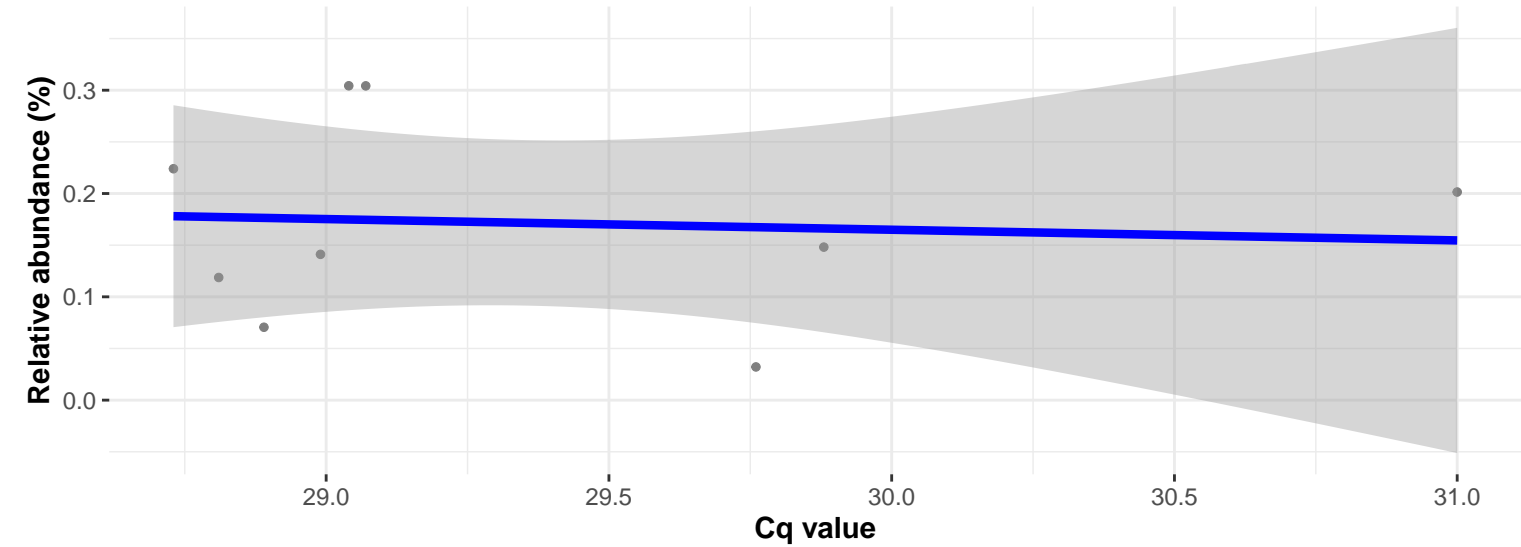
Correlation within: IM-PIM

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

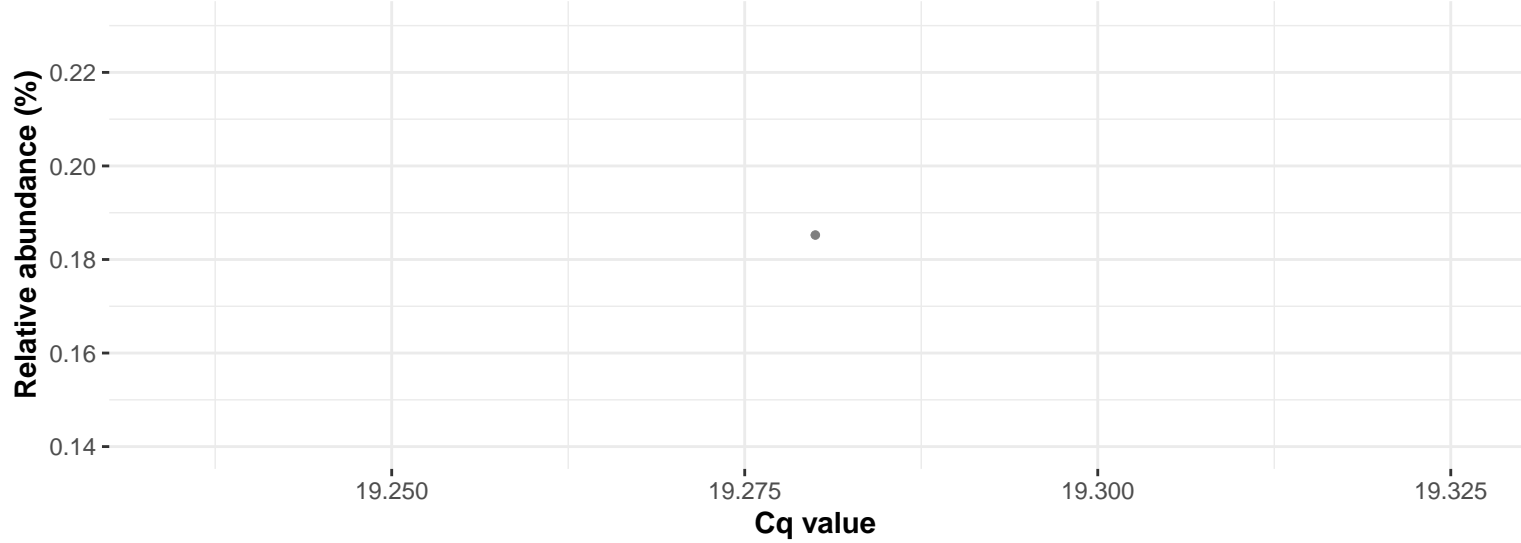


Correlation within: IM-DIM

$\log_e(S) = 4.718$ ,  $p = 0.865$ ,  $\hat{\rho}_{\text{Spearman}} = 0.067$ ,  $CI_{95\%} [-0.639, 0.712]$ ,  $n_{\text{pairs}} = 9$

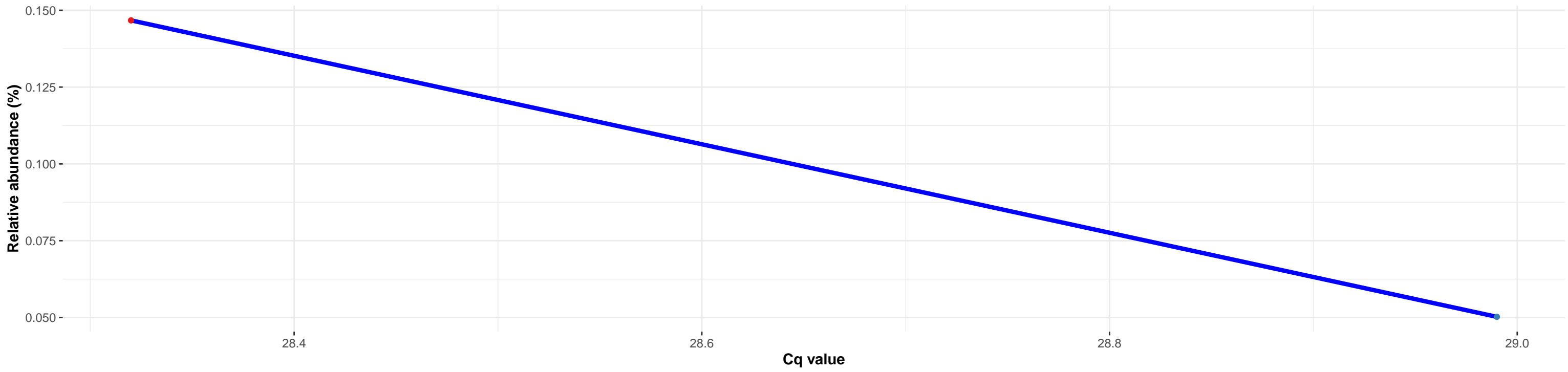


Correlation within: Feed



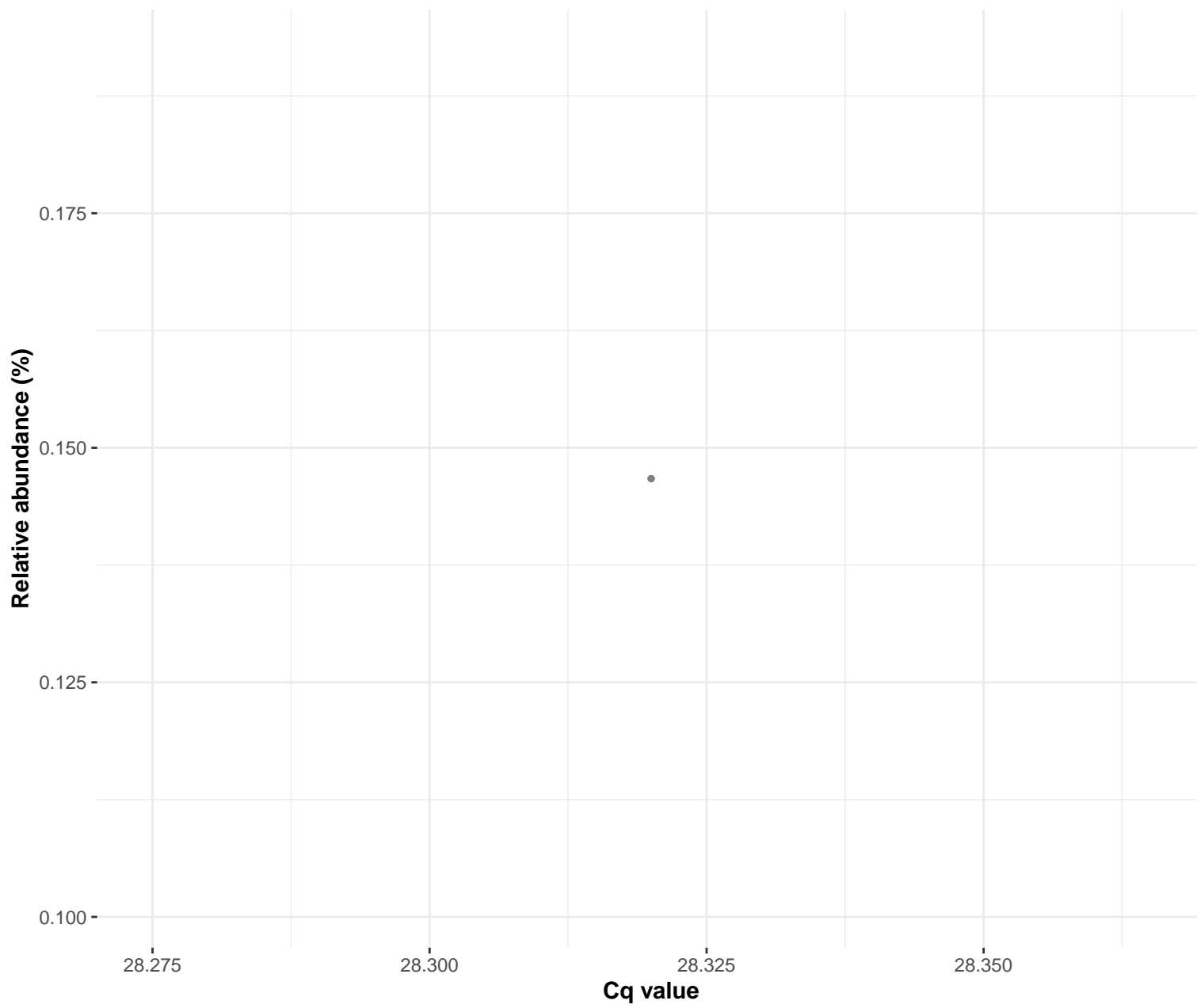
k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Alphaproteobacteria; o\_\_Sphingomonadales; f\_\_Sphingomonadaceae; g\_\_Sphingobium; s\_\_alpha proteobacterium PI\_GH4.1.H5

Correlation with all samples

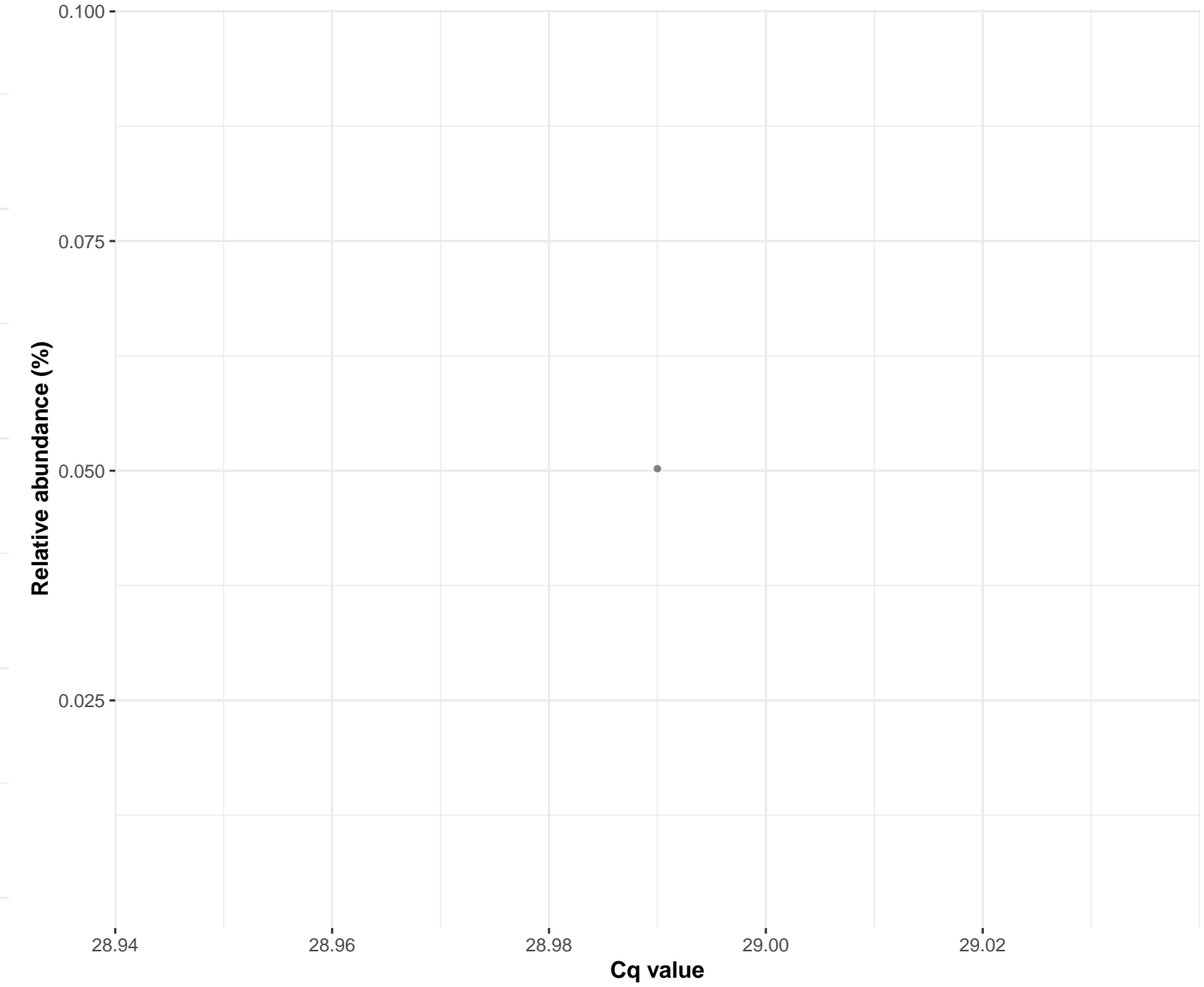


SampleType • IM-PIM • IM-DIM

Correlation within: IM-PIM



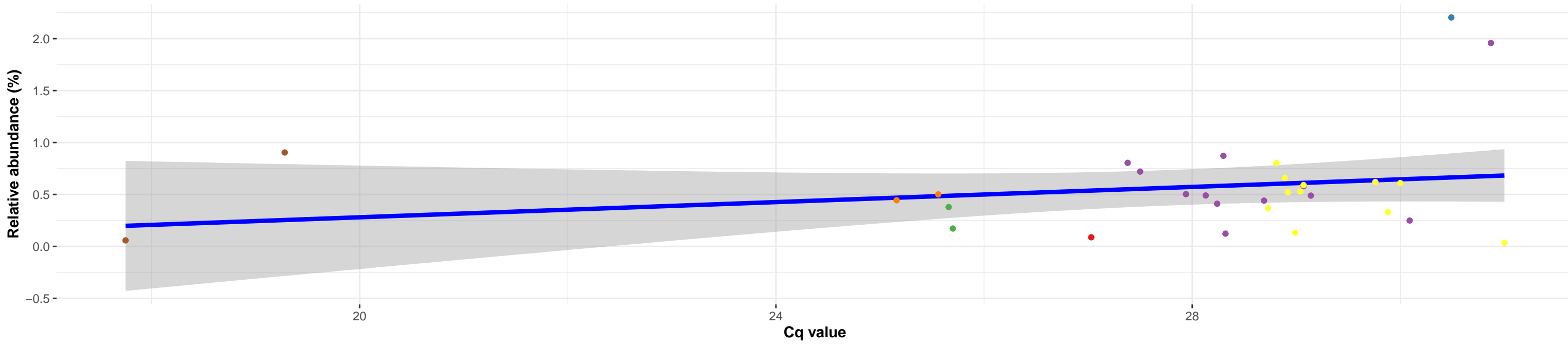
Correlation within: IM-DIM



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus sp. DJF\_WC57

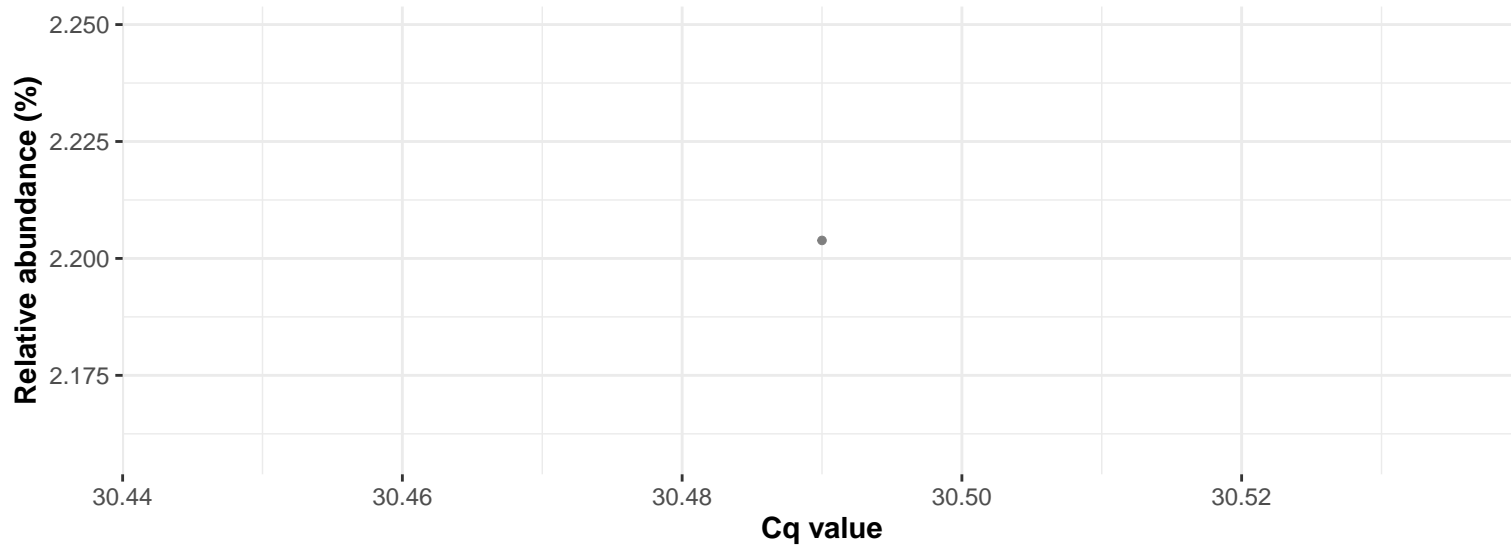
### Correlation with all samples

$\log_e(S) = 8.351$ ,  $p = 0.433$ ,  $\hat{\rho}_{\text{Spearman}} = 0.146$ ,  $\text{CI}_{95\%} [-0.230, 0.484]$ ,  $n_{\text{pairs}} = 31$



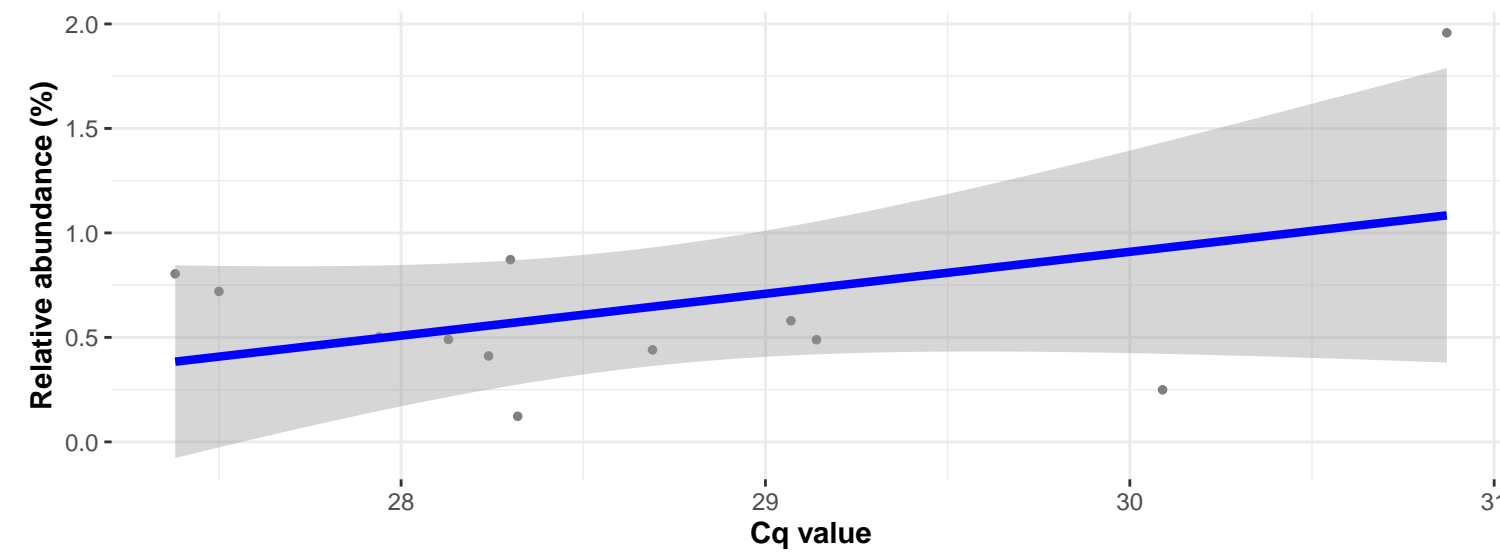
SampleType    ● REF-PID    ● REF-PIM    ● IM-PID    ● IM-PIM    ● IM-DID    ● IM-DIM    ● Feed

### Correlation within: REF-PIM



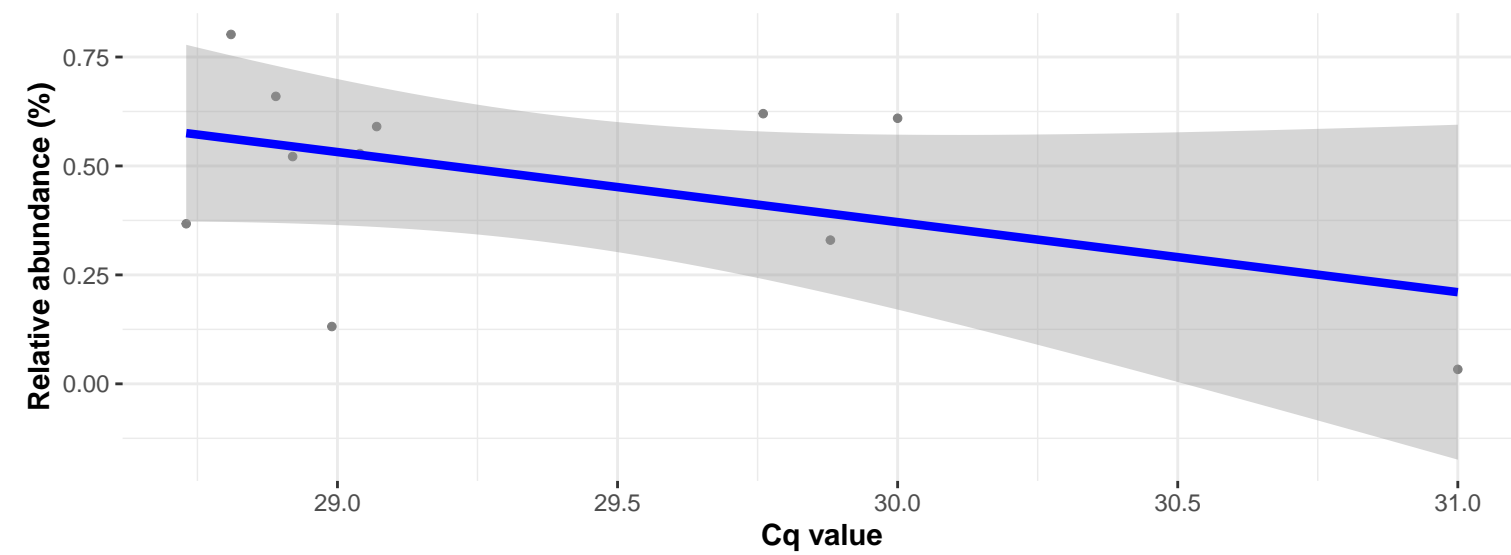
### Correlation within: IM-PIM

$\log_e(S) = 5.823$ ,  $p = 0.572$ ,  $\hat{\rho}_{\text{Spearman}} = -0.182$ ,  $\text{CI}_{95\%} [-0.694, 0.453]$ ,  $n_{\text{pairs}} = 12$

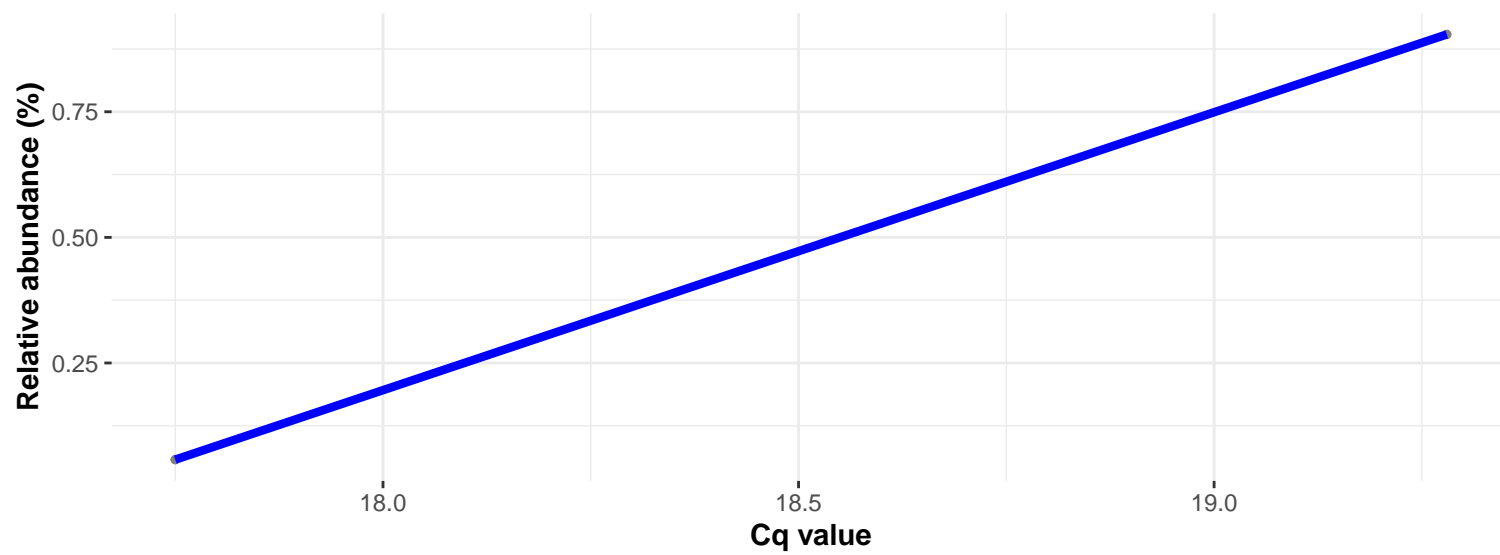


### Correlation within: IM-DIM

$\log_e(S) = 5.670$ ,  $p = 0.340$ ,  $\hat{\rho}_{\text{Spearman}} = -0.318$ ,  $\text{CI}_{95\%} [-0.779, 0.366]$ ,  $n_{\text{pairs}} = 11$



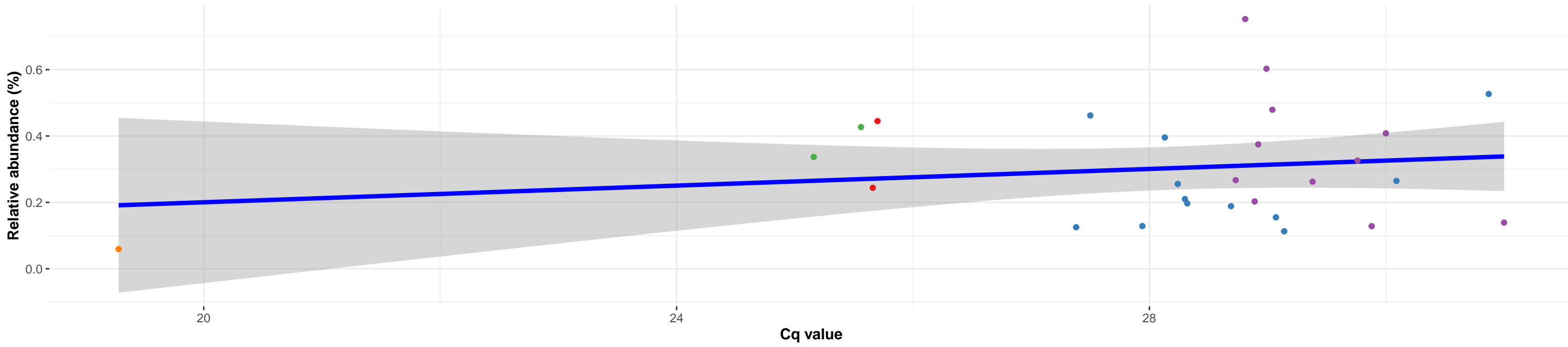
### Correlation within: Feed



k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

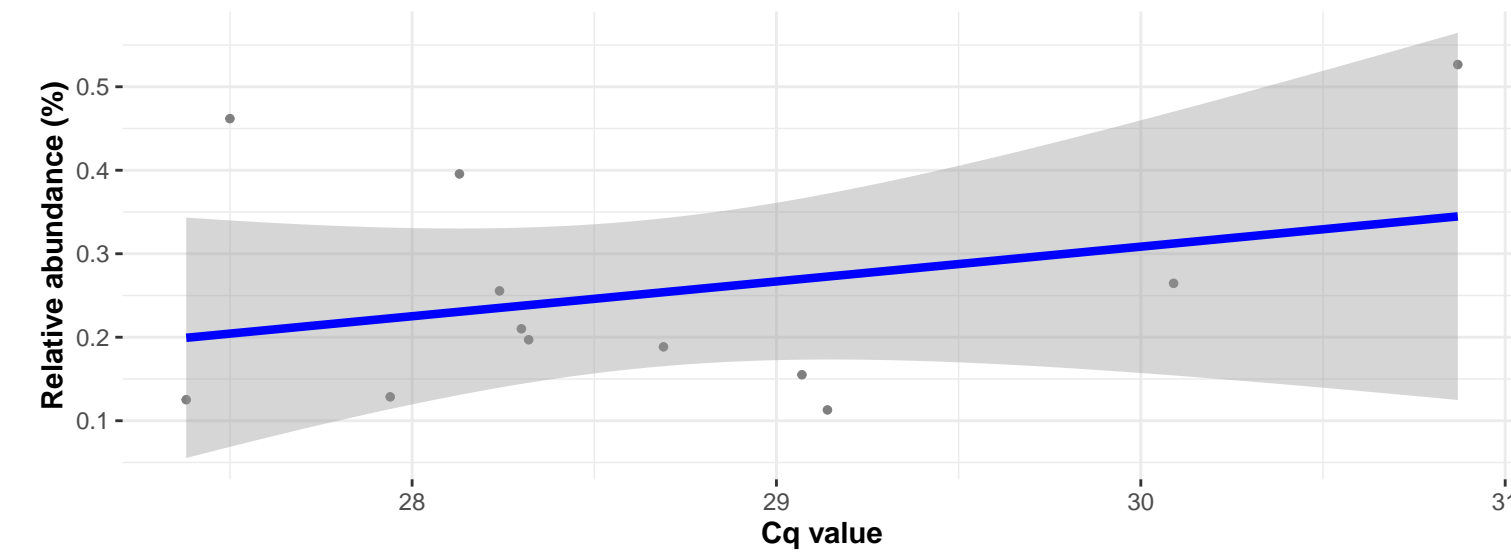
### Correlation with all samples

$\log_e(S) = 8.148$ ,  $p = 0.786$ ,  $\hat{\rho}_{\text{Spearman}} = 0.054$ ,  $CI_{95\%} [-0.336, 0.428]$ ,  $n_{\text{pairs}} = 28$



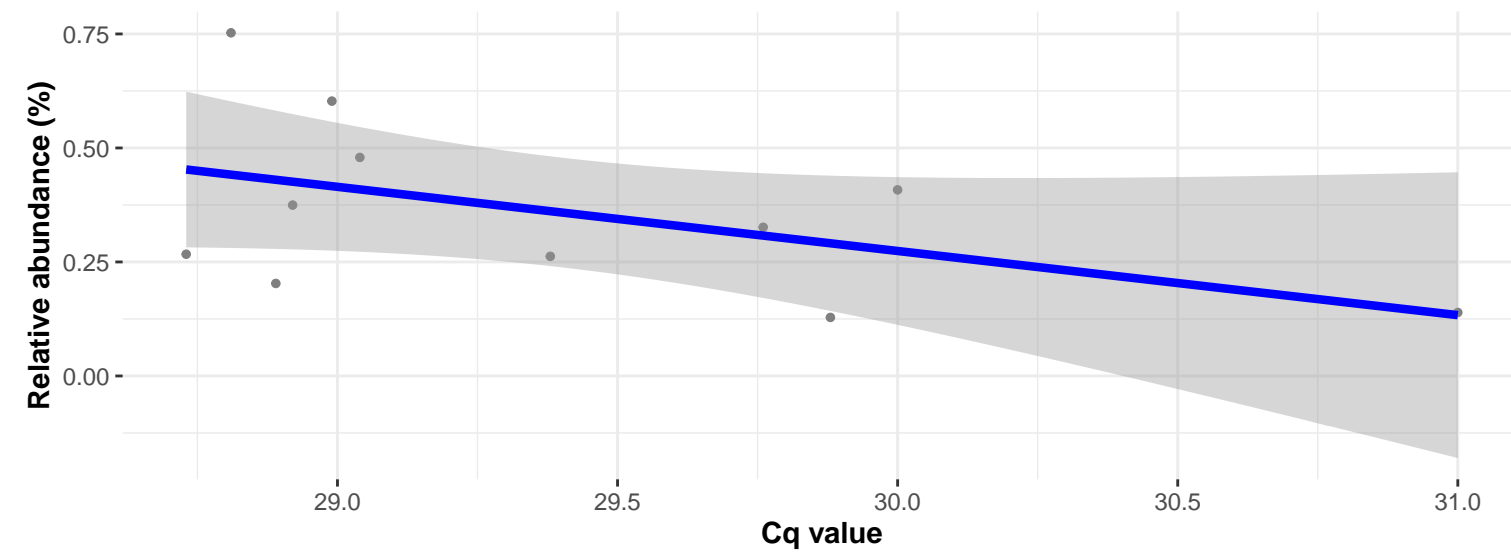
### Correlation within: IM-PIM

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

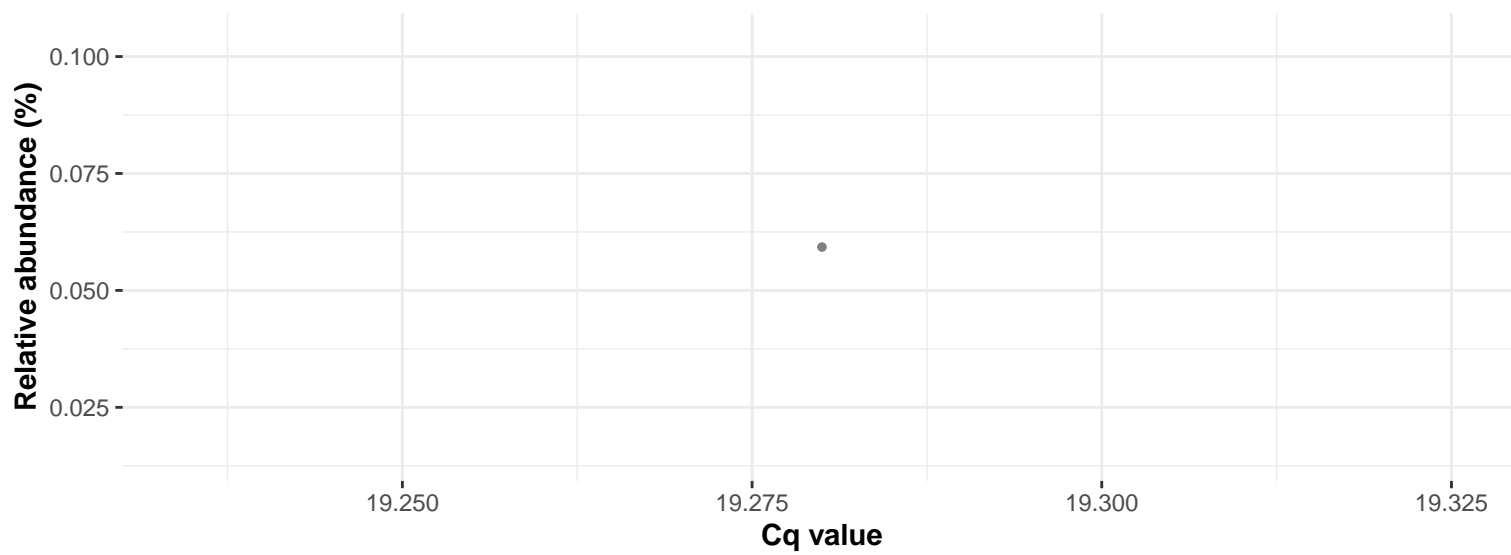


### Correlation within: IM-DIM

$\log_e(S) = 5.710$ ,  $p = 0.259$ ,  $\hat{\rho}_{\text{Spearman}} = -0.373$ ,  $CI_{95\%} [-0.802, 0.311]$ ,  $n_{\text{pairs}} = 11$



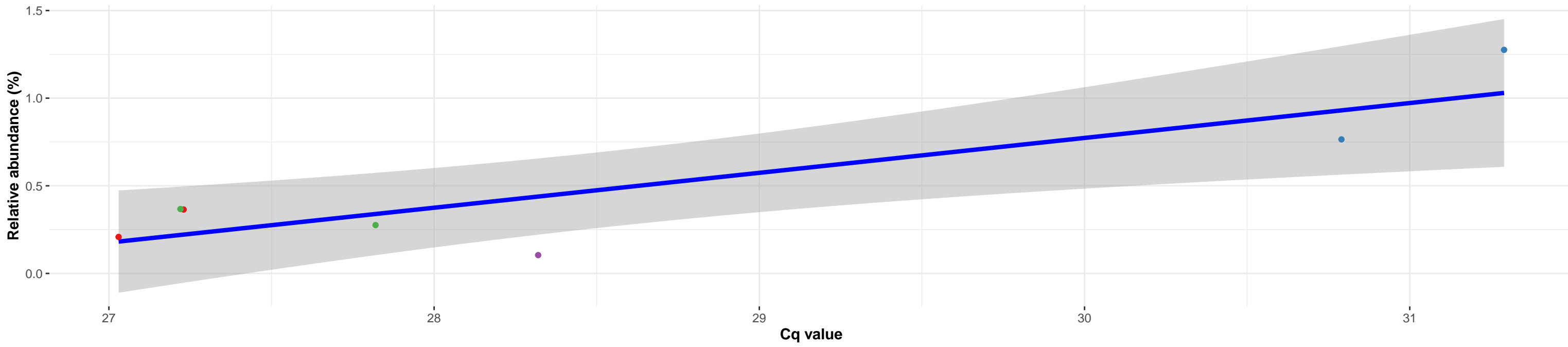
### Correlation within: Feed



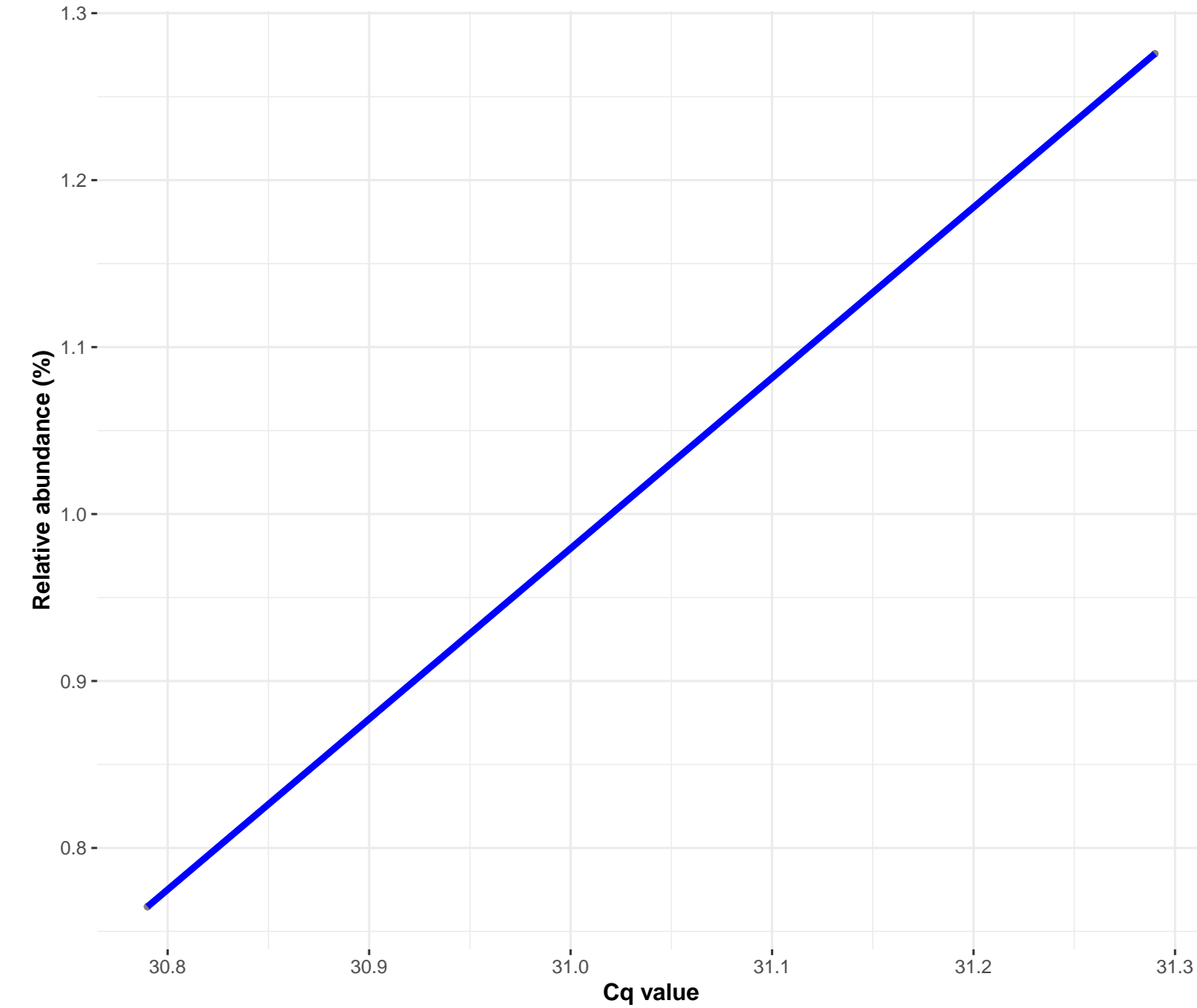
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Planococcaceae; g\_\_Kurthia; s\_\_uncultured bacterium

### Correlation with all samples

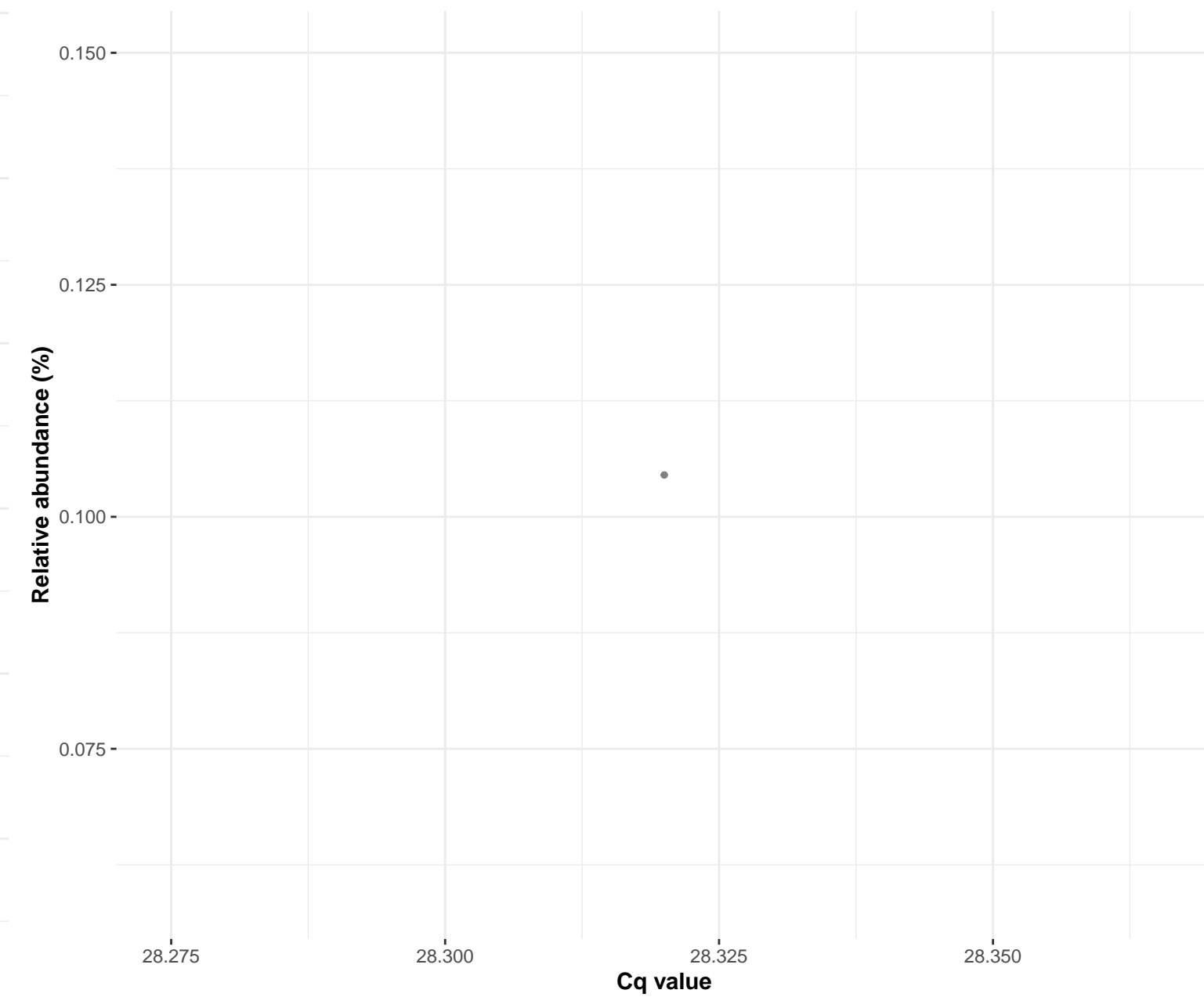
$\log_e(S) = 3.332$ ,  $p = 0.253$ ,  $\hat{\rho}_{\text{Spearman}} = 0.500$ ,  $CI_{95\%} [-0.430, 0.915]$ ,  $n_{\text{pairs}} = 7$



### Correlation within: REF-PIM



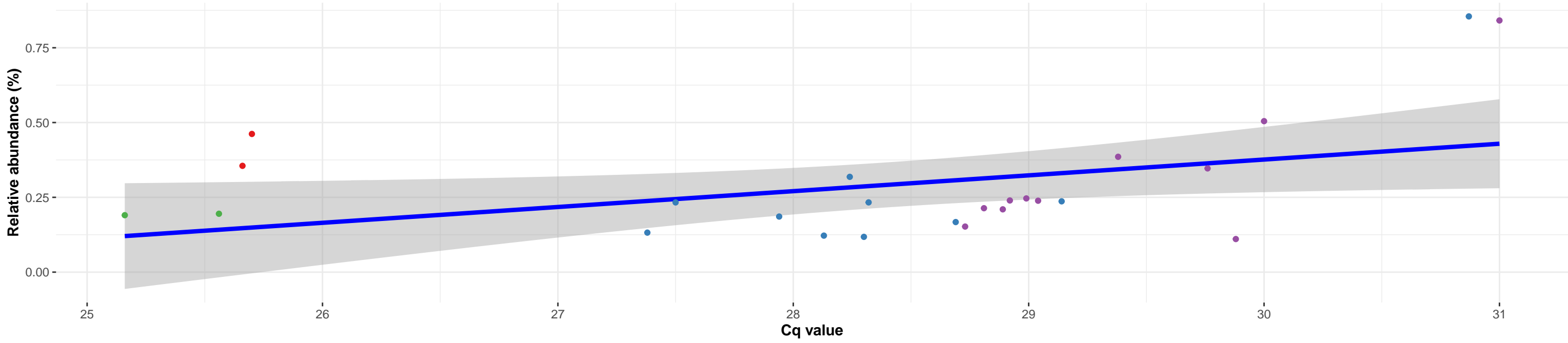
### Correlation within: IM-PIM



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

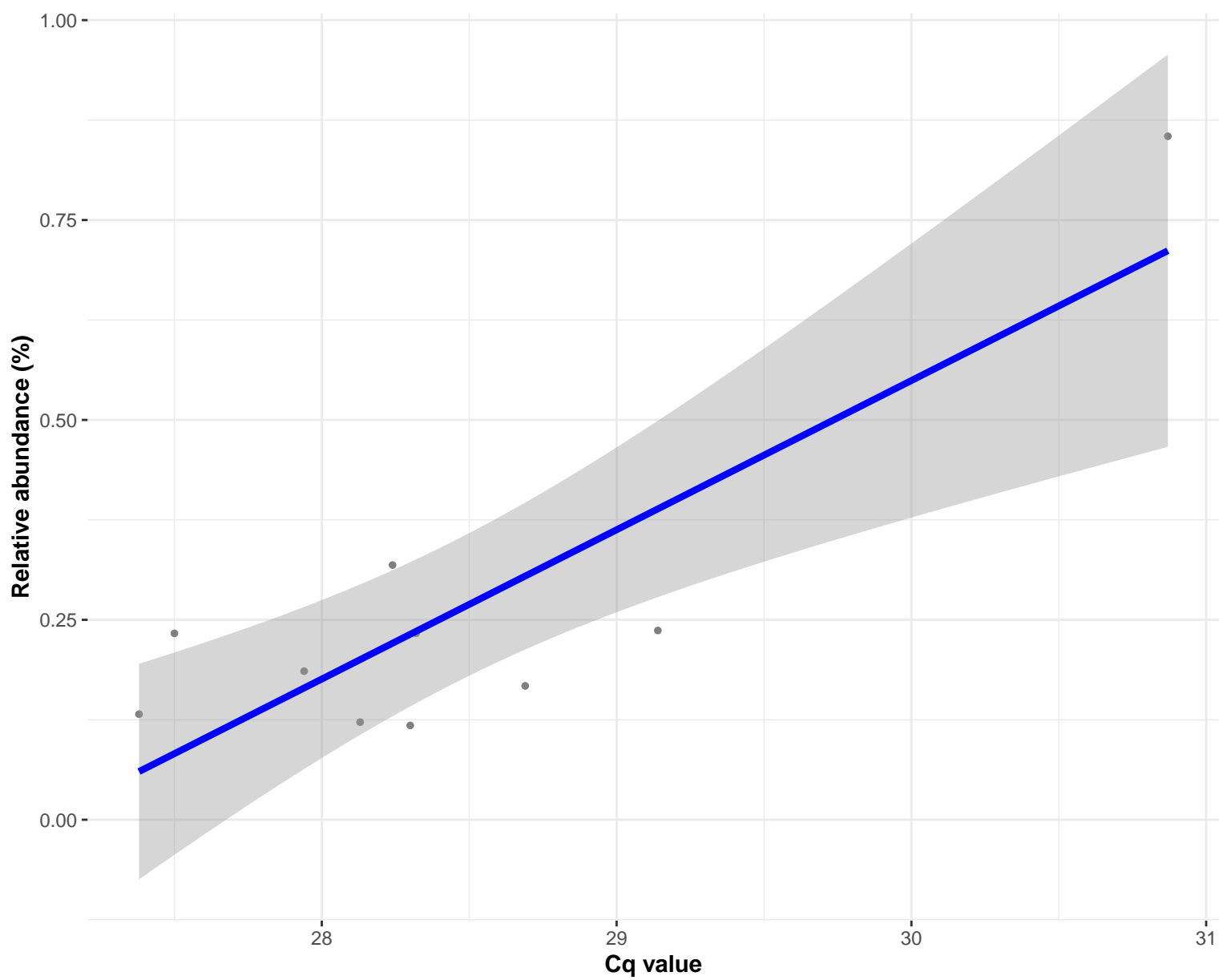
### Correlation with all samples

$\log_e(S) = 7.338$ ,  $p = 0.043$ ,  $\hat{\rho}_{\text{Spearman}} = 0.408$ ,  $CI_{95\%} [0.004, 0.698]$ ,  $n_{\text{pairs}} = 25$



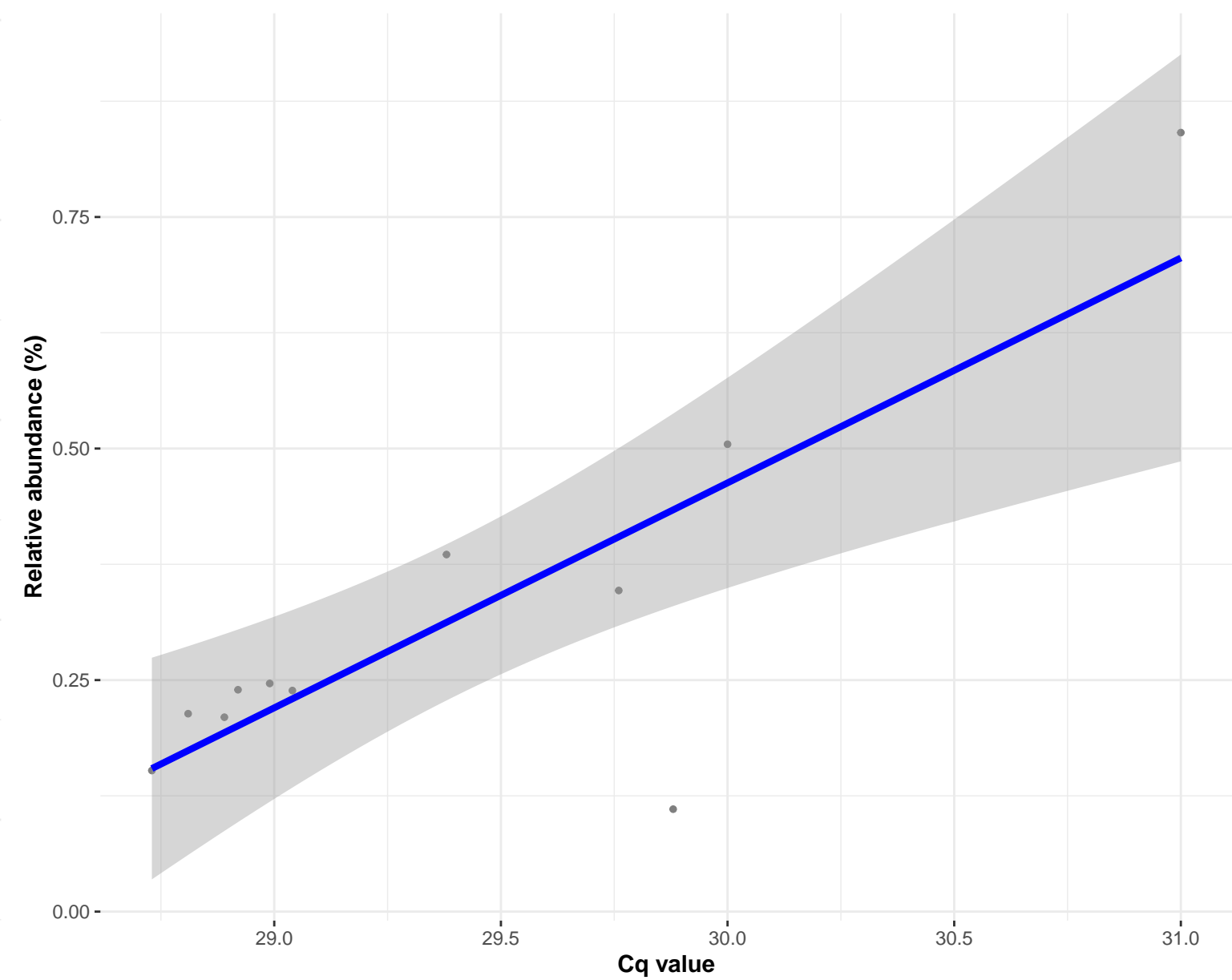
### Correlation within: IM-PIM

$\log_e(S) = 4.454$ ,  $p = 0.162$ ,  $\hat{\rho}_{\text{Spearman}} = 0.479$ ,  $CI_{95\%} [-0.237, 0.858]$ ,  $n_{\text{pairs}} = 10$

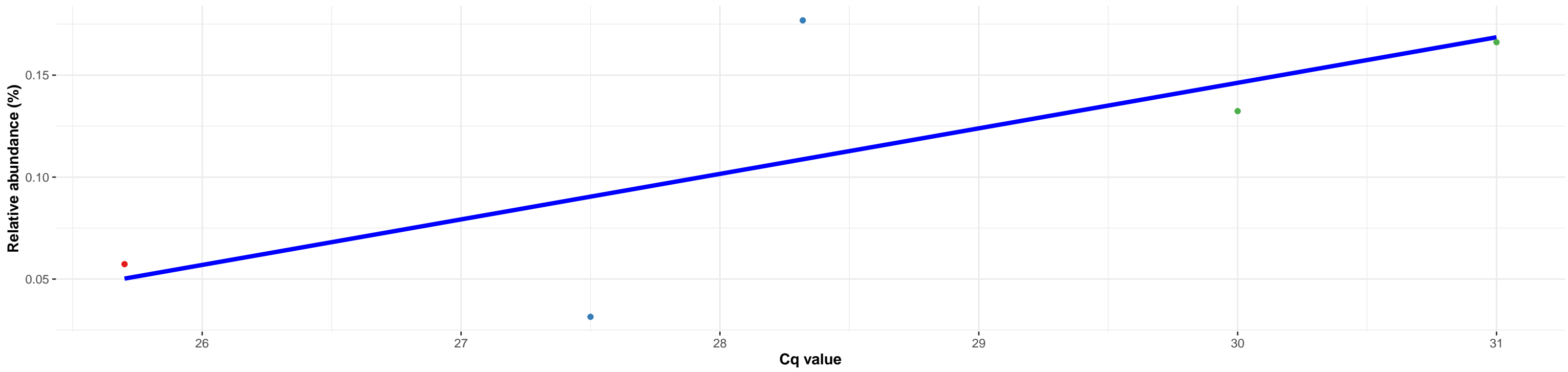


### Correlation within: IM-DIM

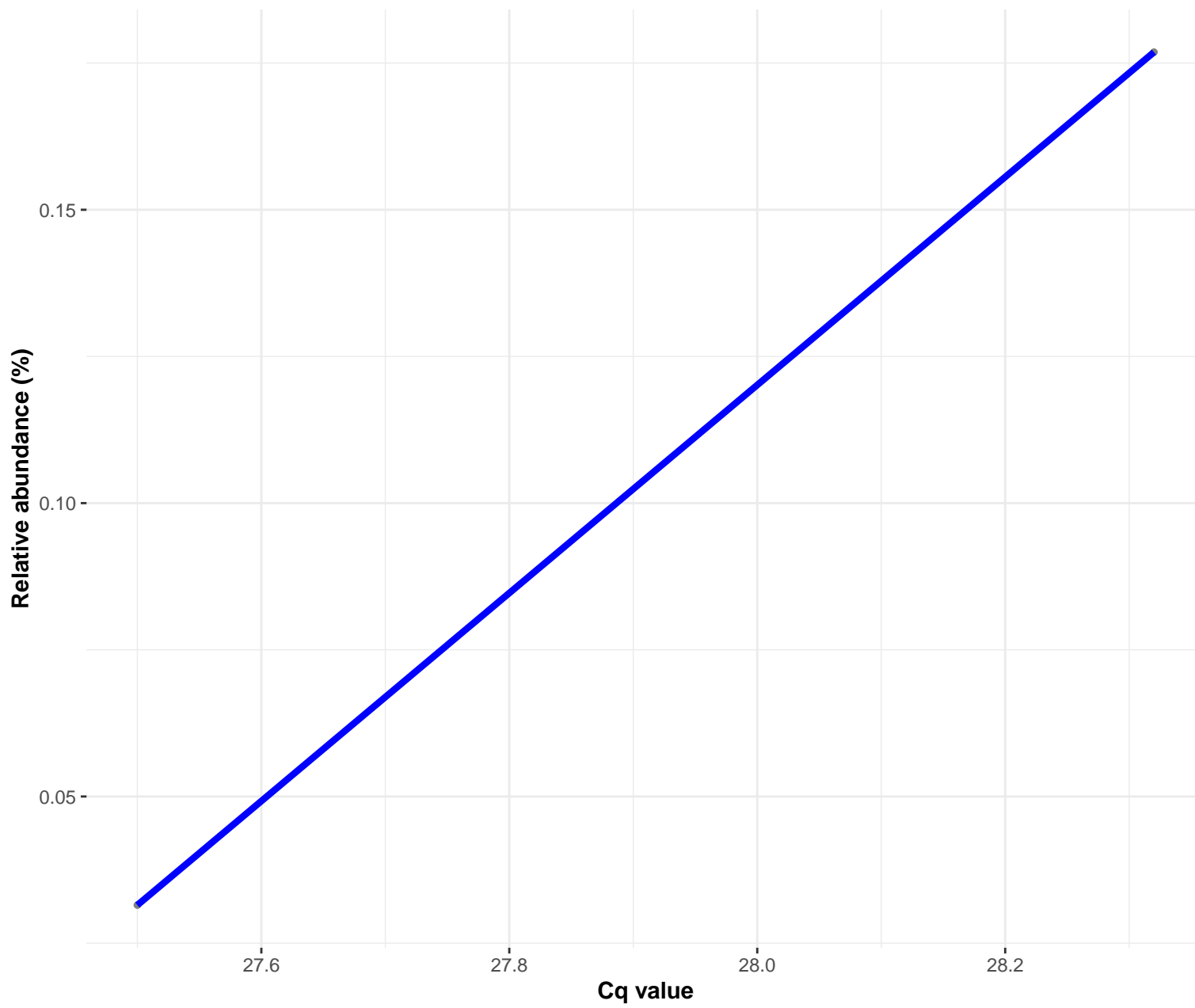
$\log_e(S) = 4.407$ ,  $p = 0.039$ ,  $\hat{\rho}_{\text{Spearman}} = 0.627$ ,  $CI_{95\%} [0.023, 0.896]$ ,  $n_{\text{pairs}} = 11$



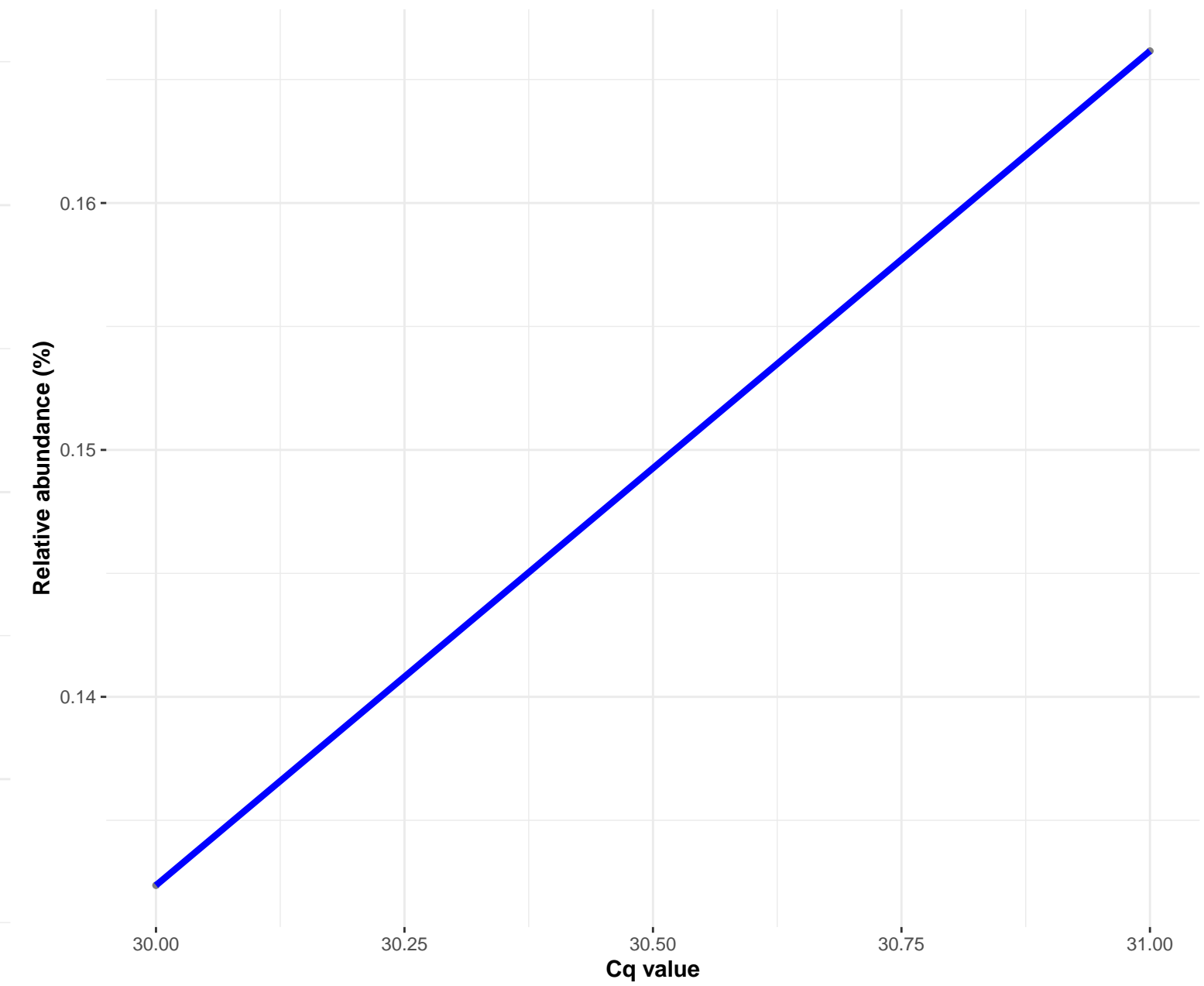
Correlation with all samples



Correlation within: IM-PIM



Correlation within: IM-DIM

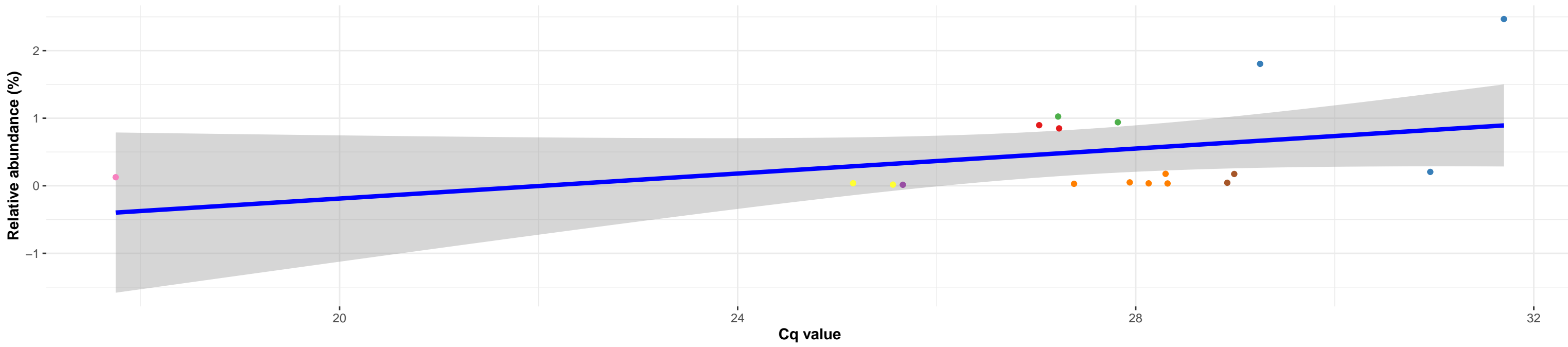




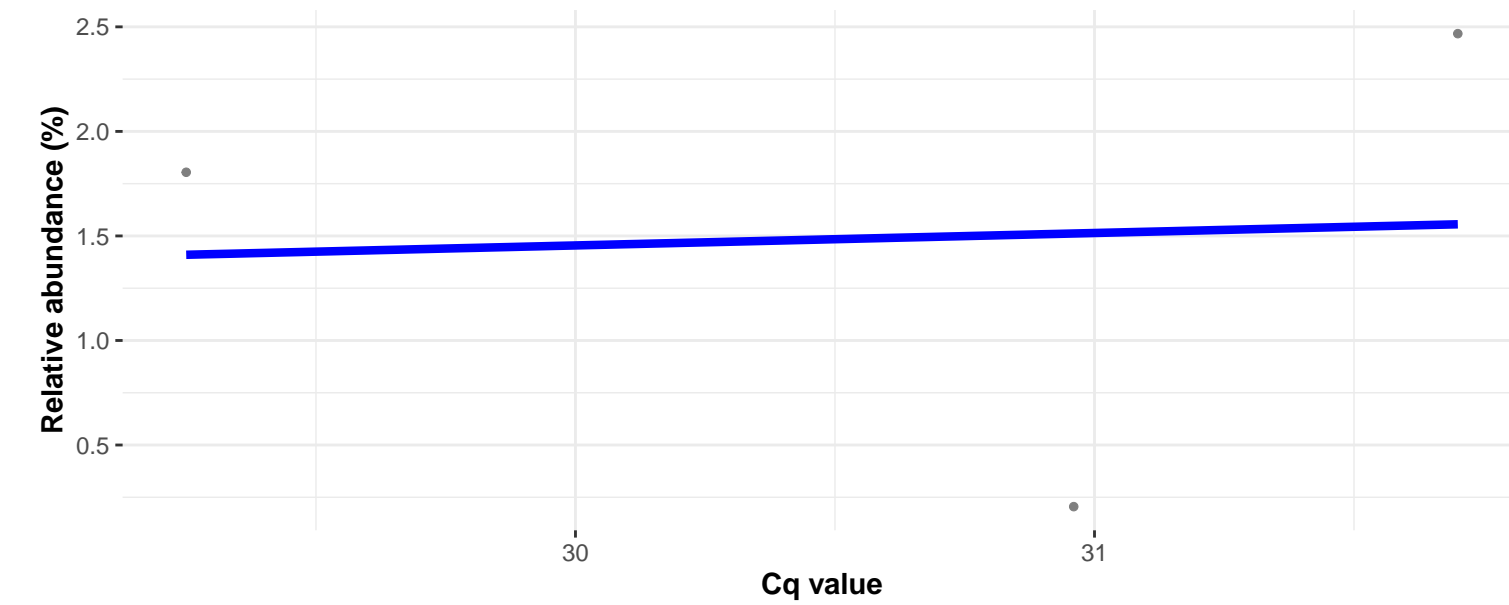
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Streptococcus; Ambiguous\_taxa

### Correlation with all samples

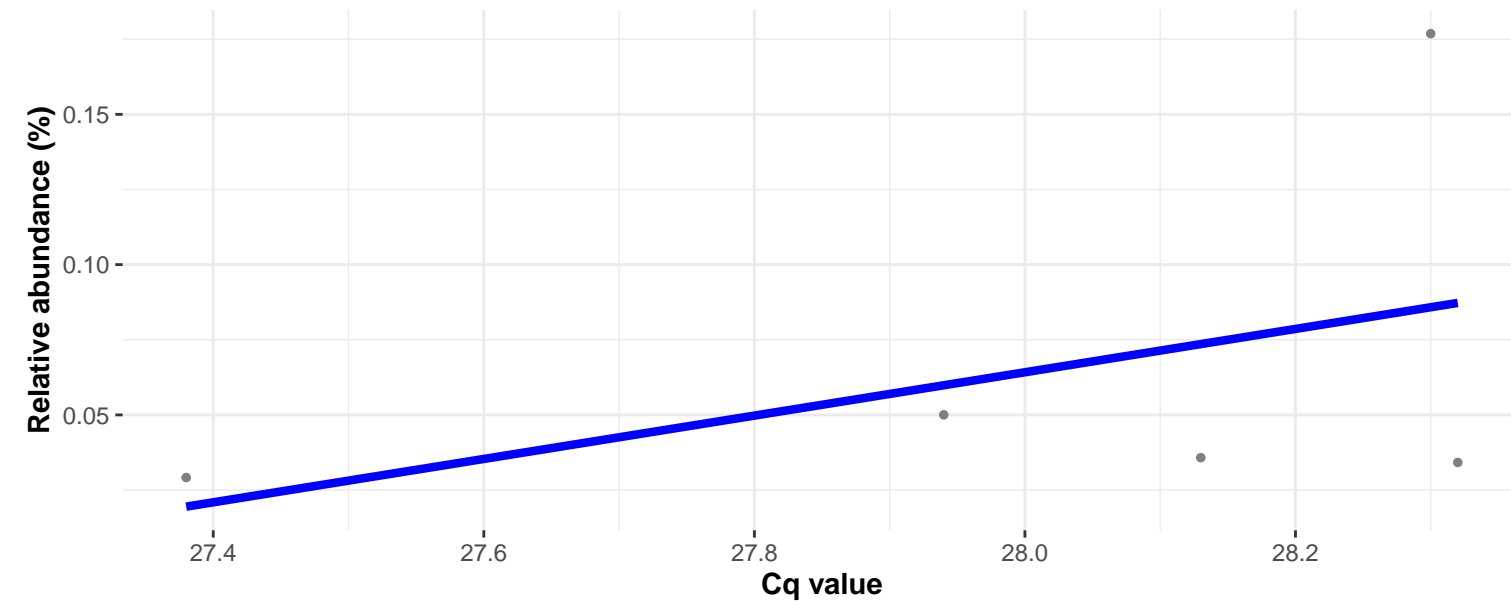
$\log_e(S) = 6.380$ ,  $p = 0.108$ ,  $\hat{\rho}_{\text{Spearman}} = 0.391$ ,  $CI_{95\%} [-0.107, 0.733]$ ,  $n_{\text{pairs}} = 18$



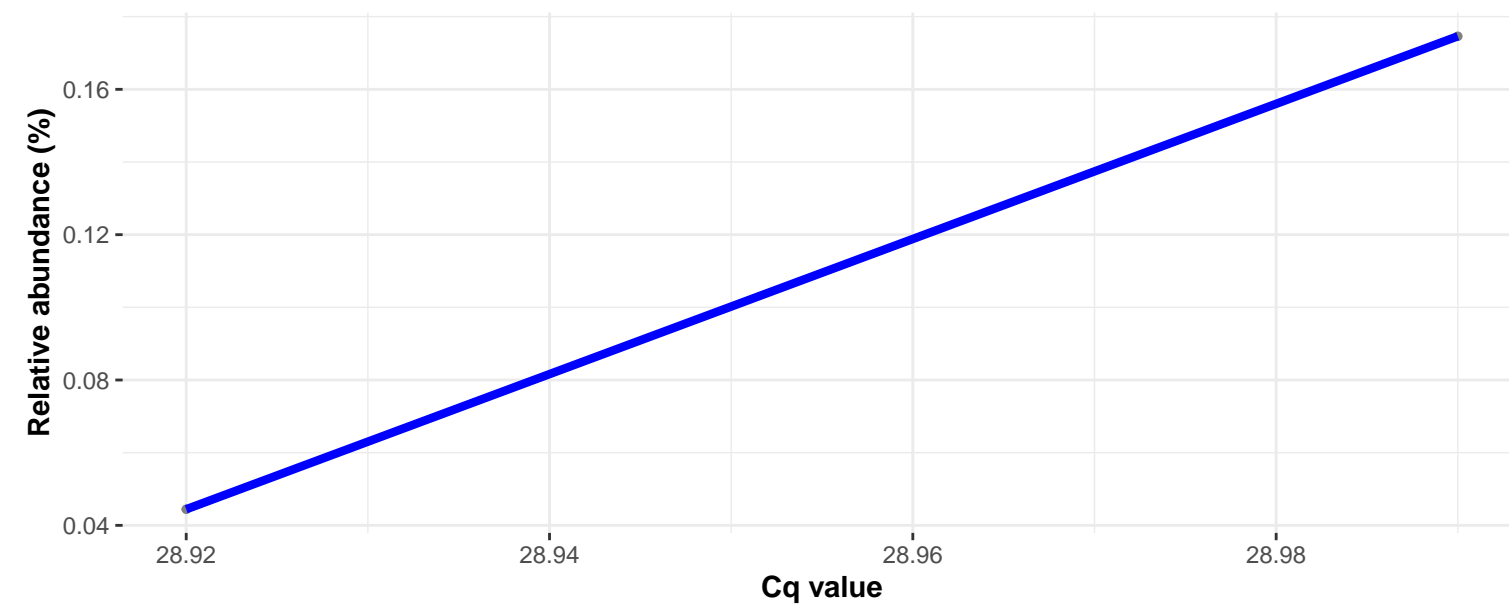
### Correlation within: REF-PIM



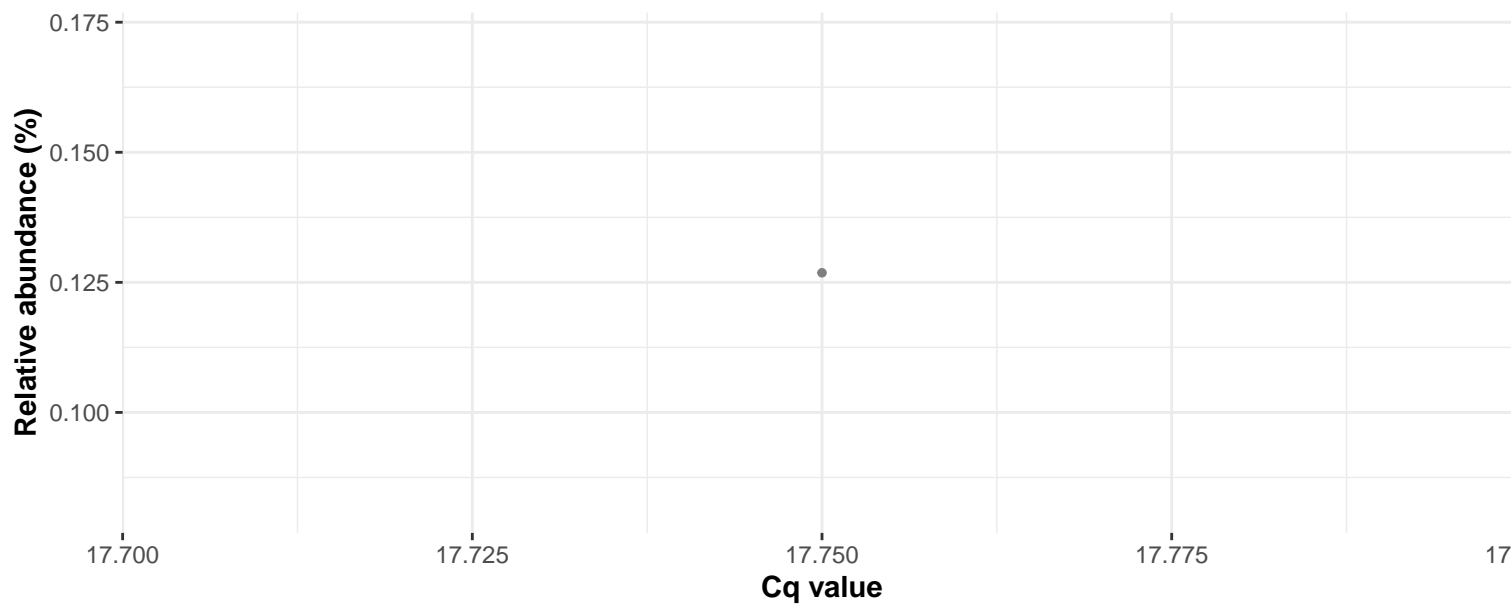
### Correlation within: IM-PIM



### Correlation within: IM-DIM



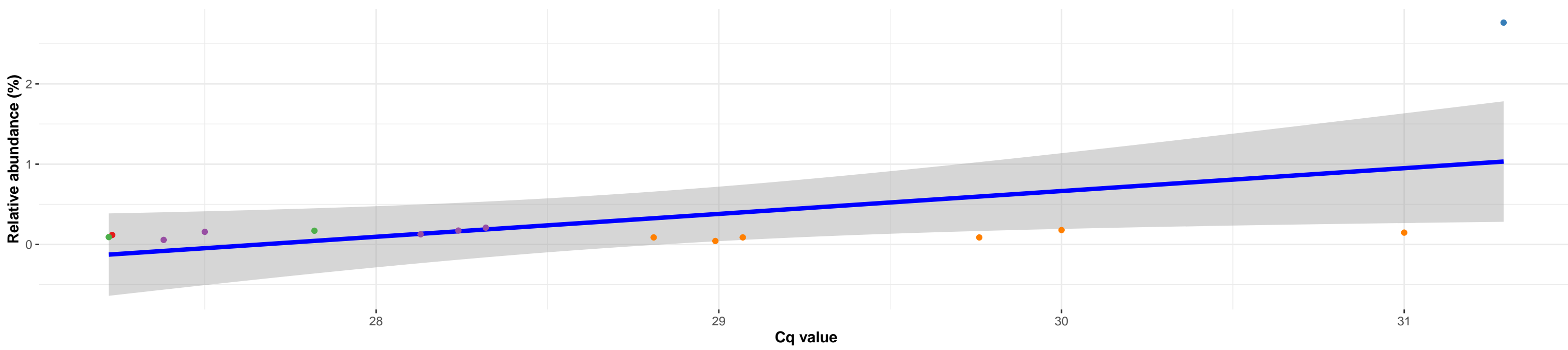
### Correlation within: Feed



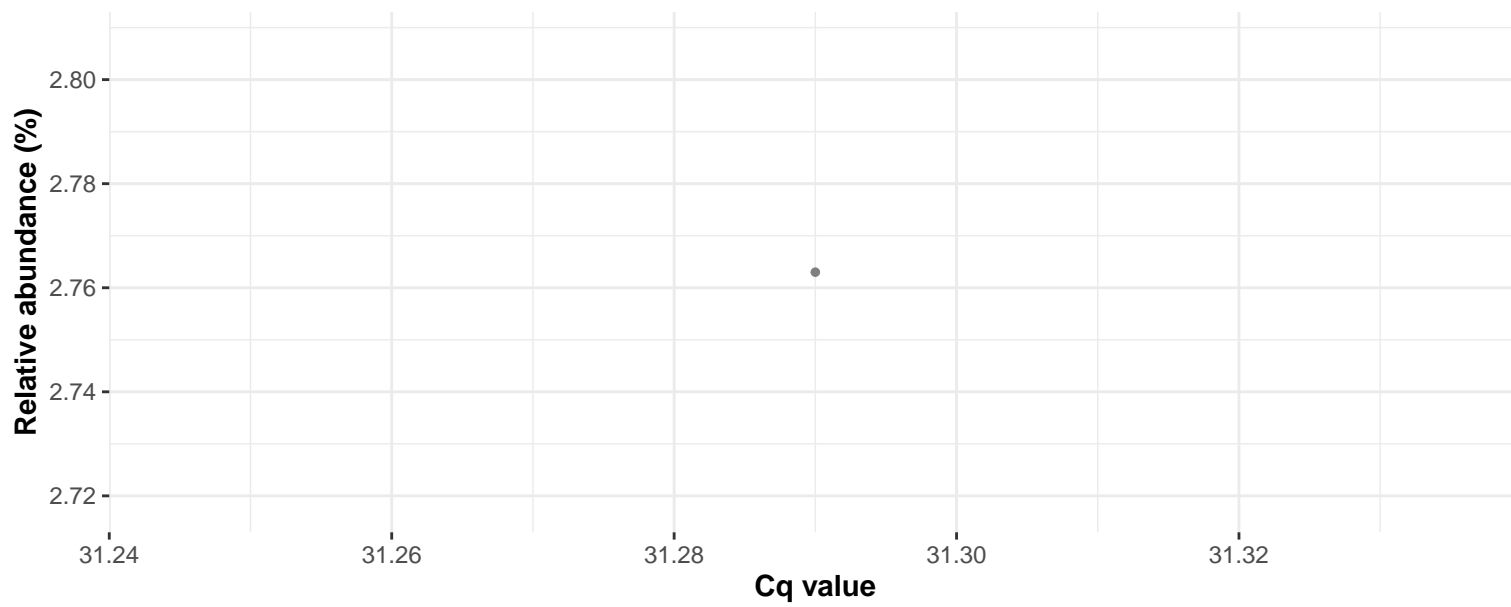
k\_\_Bacteria; p\_\_Actinobacteria; c\_\_Actinobacteria; o\_\_Corynebacteriales; f\_\_Corynebacteriaceae; g\_\_Corynebacterium 1; Ambiguous\_taxa

### Correlation with all samples

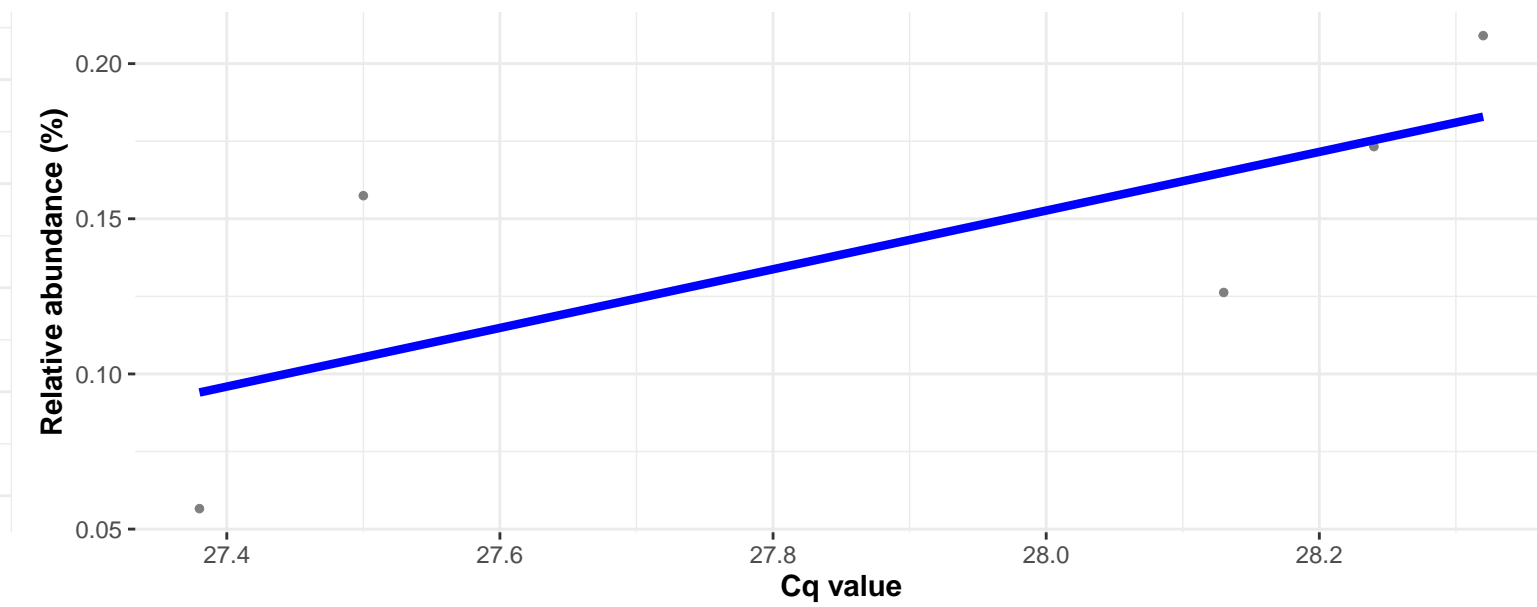
$\log_e(S) = 6.078$ ,  $p = 0.428$ ,  $\hat{\rho}_{\text{Spearman}} = 0.221$ ,  $\text{CI}_{95\%} [-0.343, 0.668]$ ,  $n_{\text{pairs}} = 15$



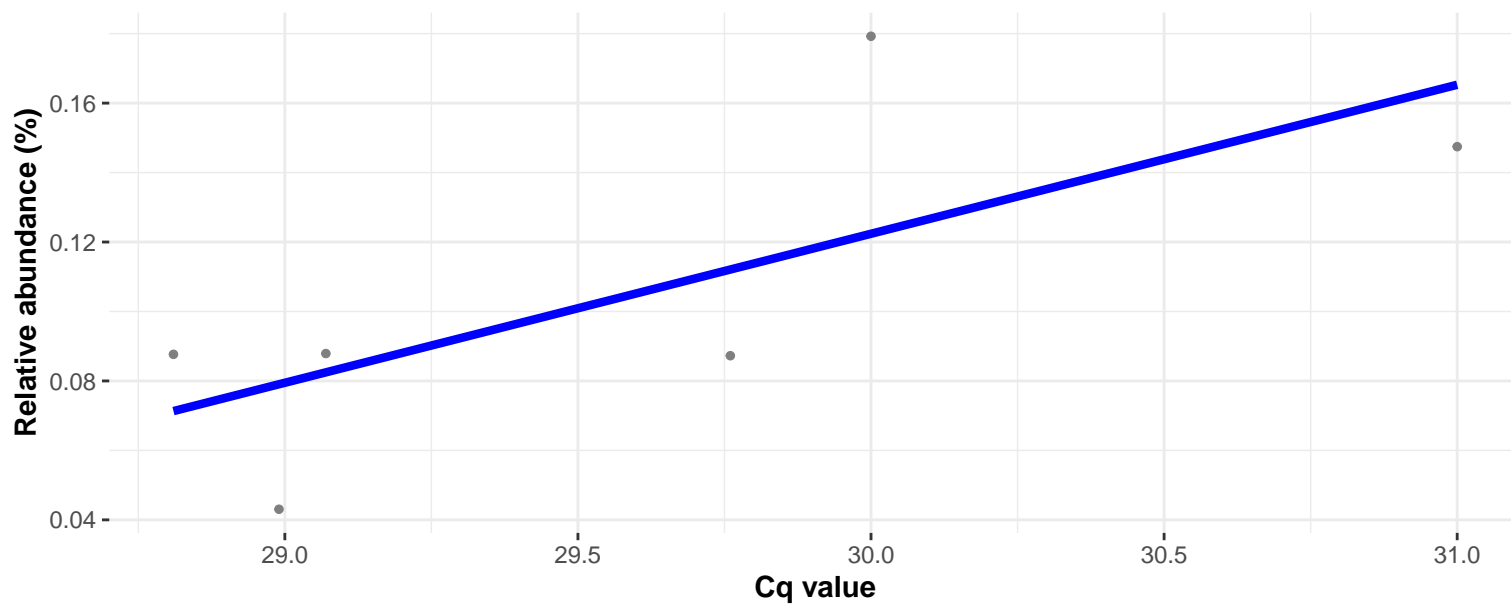
### Correlation within: REF-PIM



### Correlation within: IM-PIM



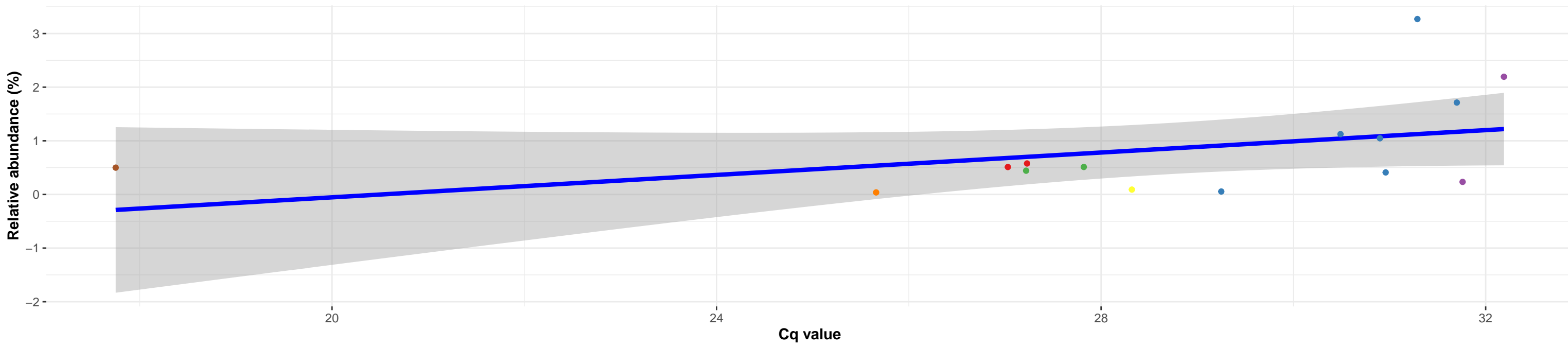
### Correlation within: IM-DIM



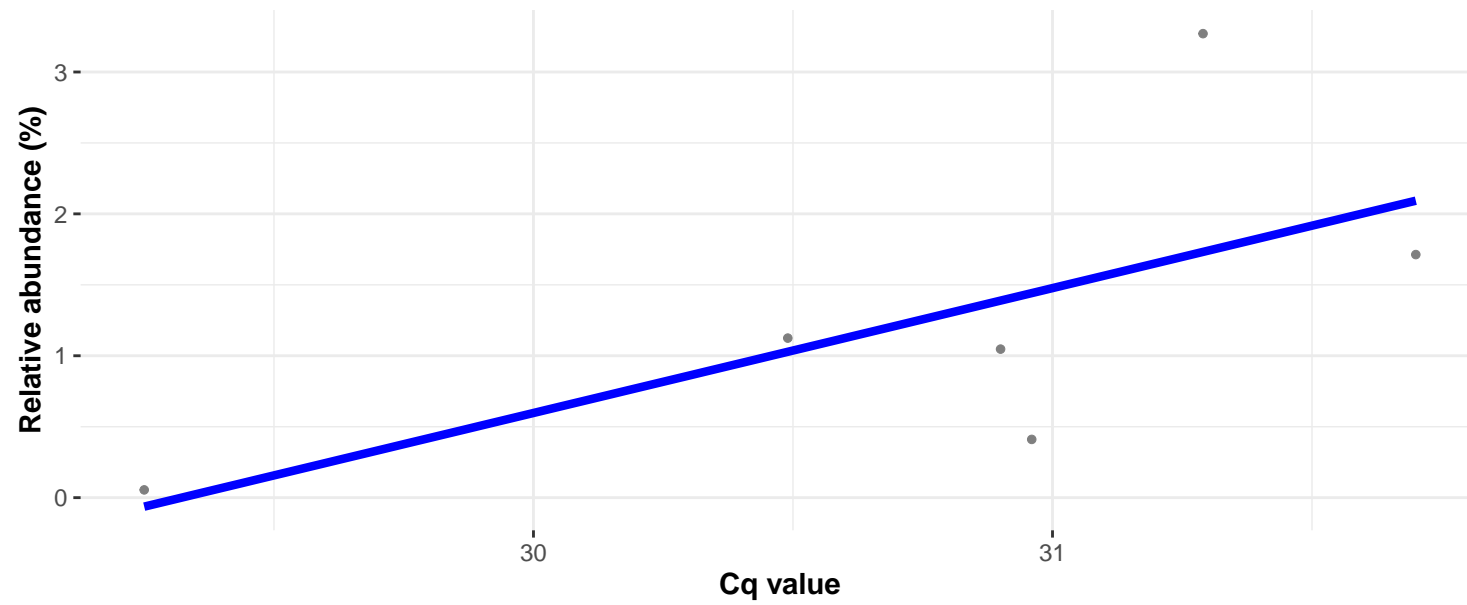
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Lactobacillaceae; g\_\_Lactobacillus; s\_\_Lactobacillus sp. LA-6

### Correlation with all samples

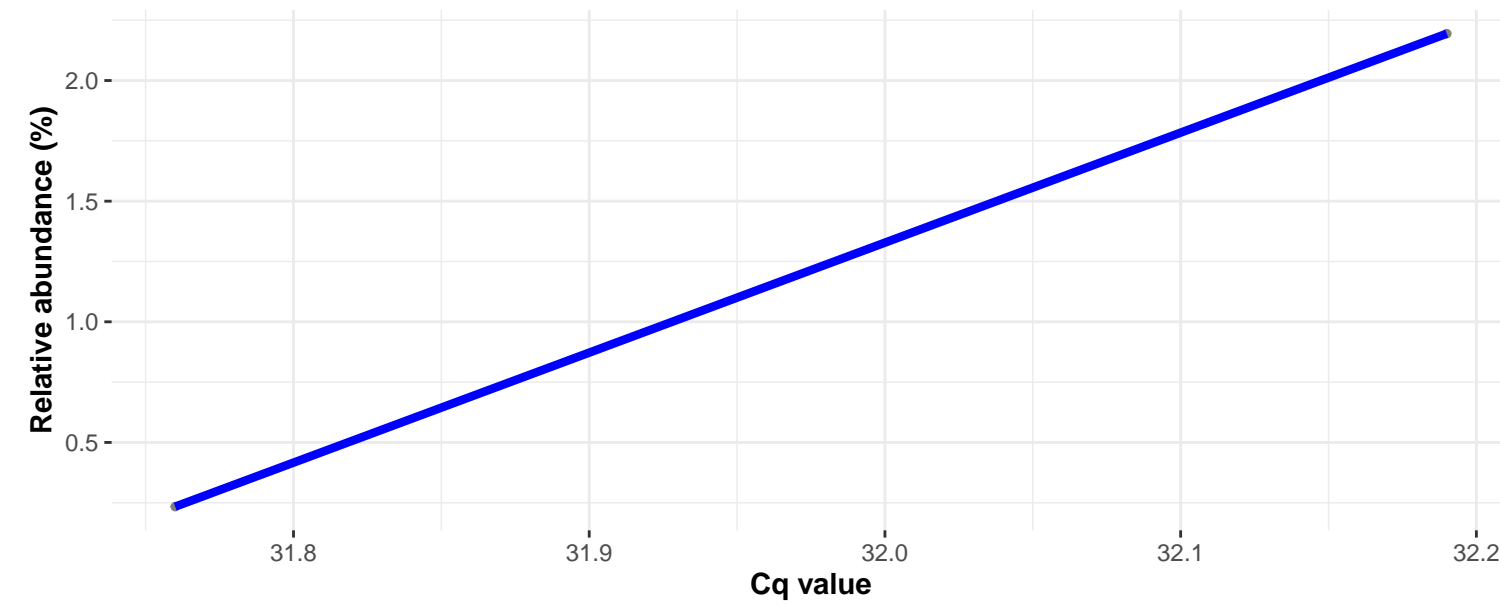
$\log_e(S) = 5.730$ ,  $p = 0.092$ ,  $\hat{\rho}_{\text{Spearman}} = 0.450$ ,  $CI_{95\%} [-0.098, 0.788]$ ,  $n_{\text{pairs}} = 15$



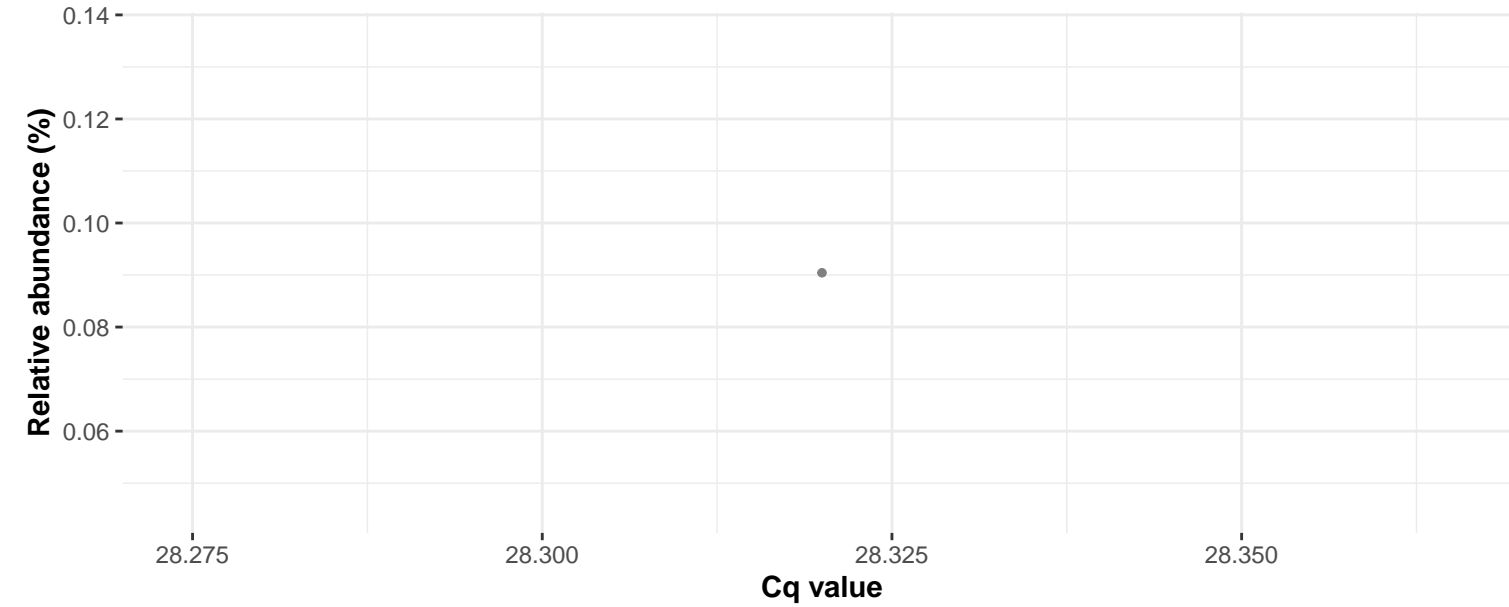
### Correlation within: REF-PIM



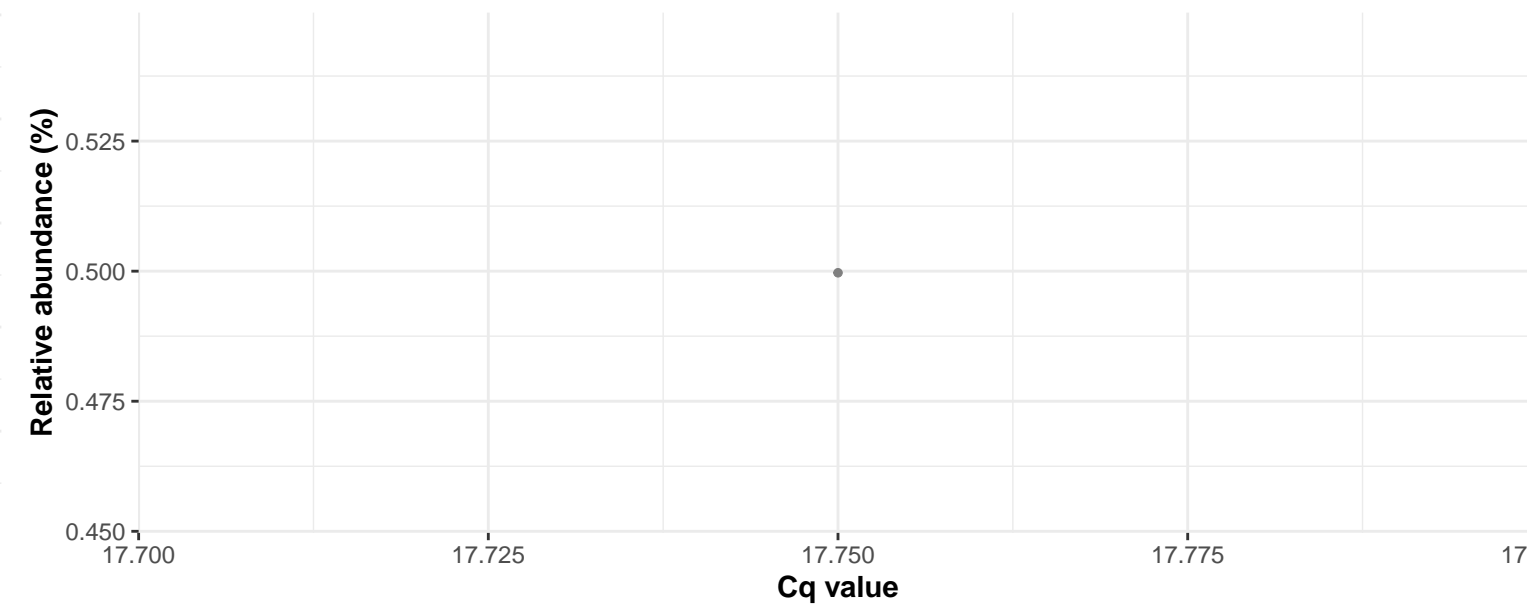
### Correlation within: REF-DIM



### Correlation within: IM-PIM

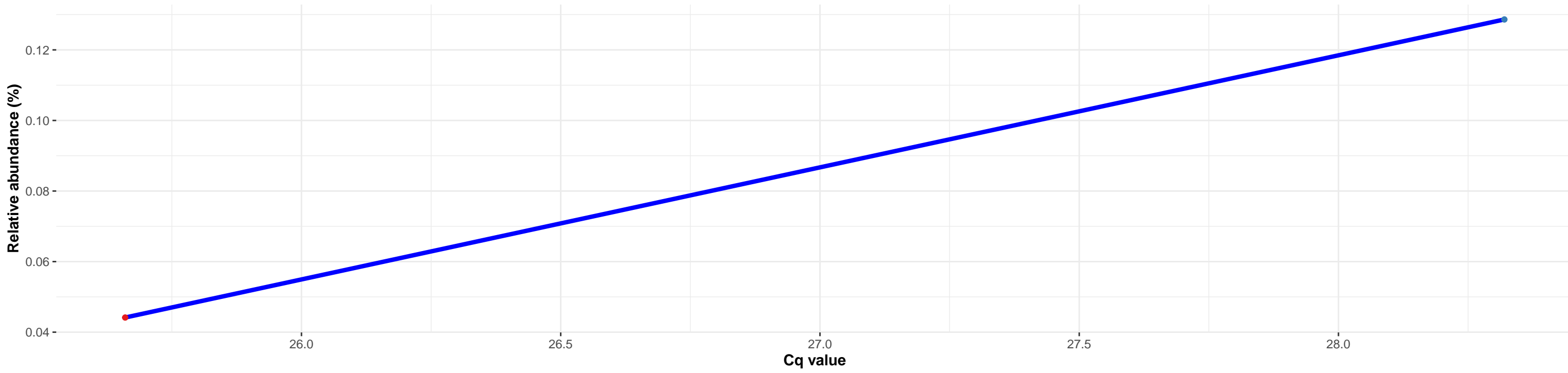


### Correlation within: Feed



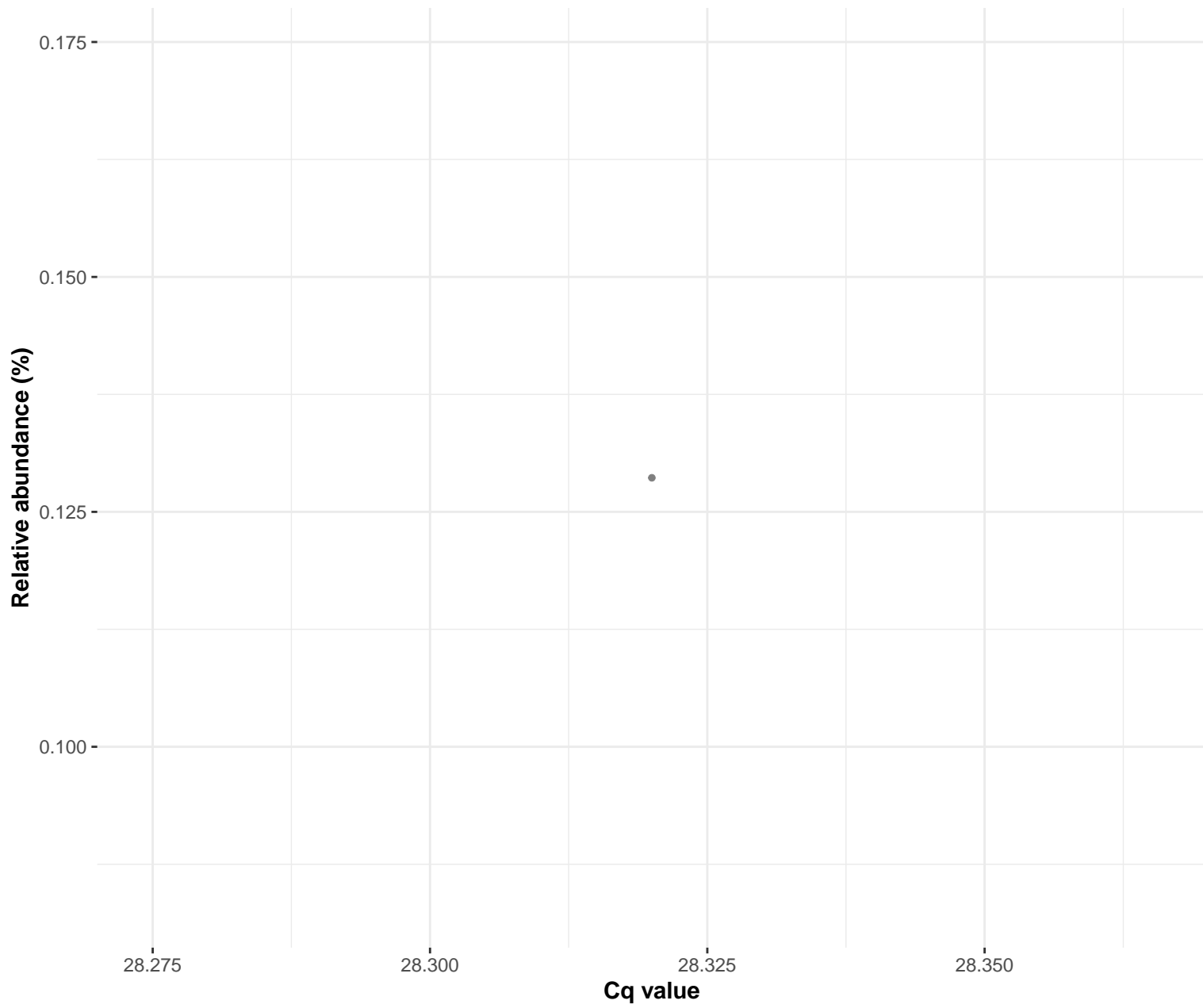
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Oceanobacillus; Ambiguous\_taxa

Correlation with all samples

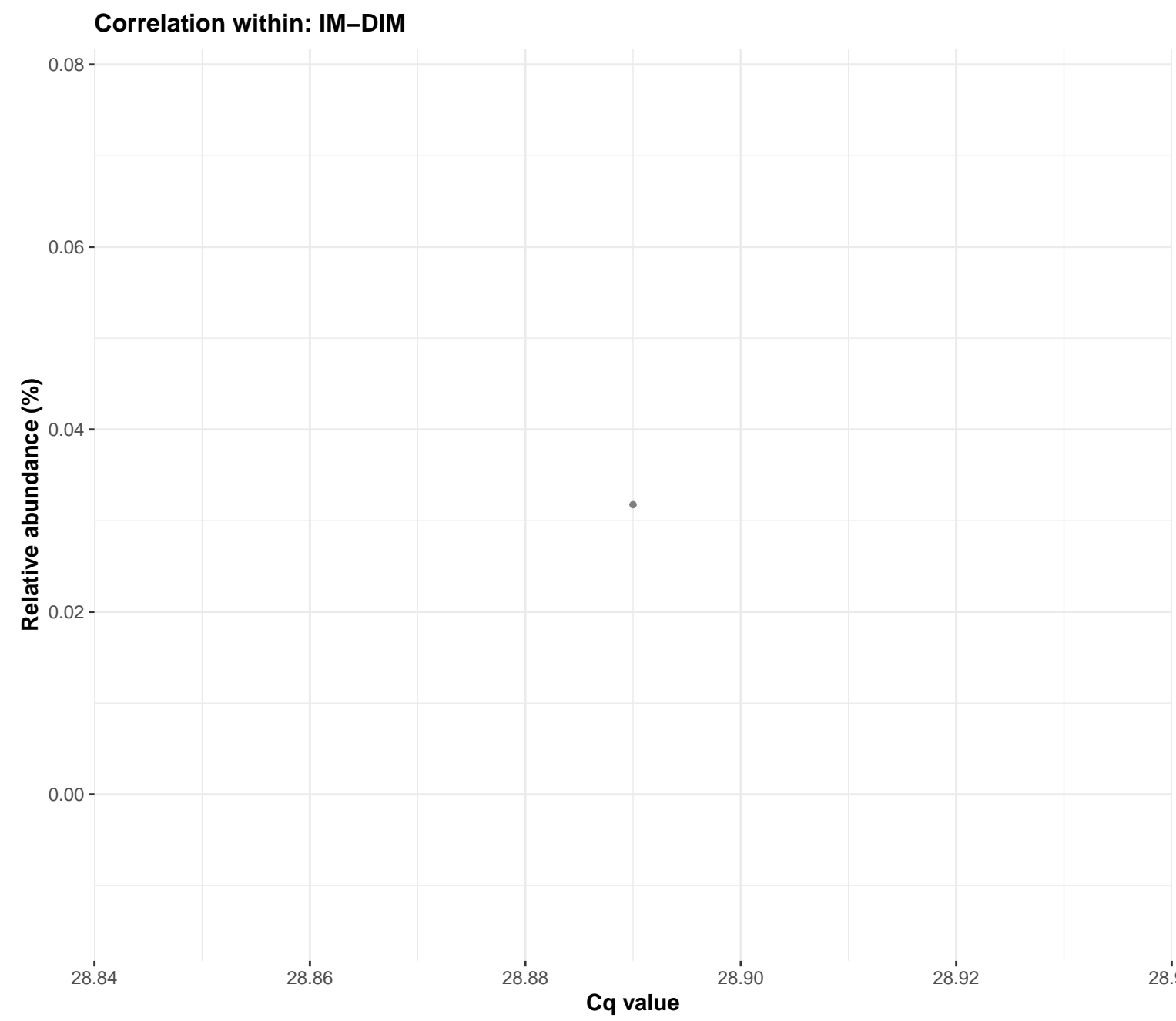
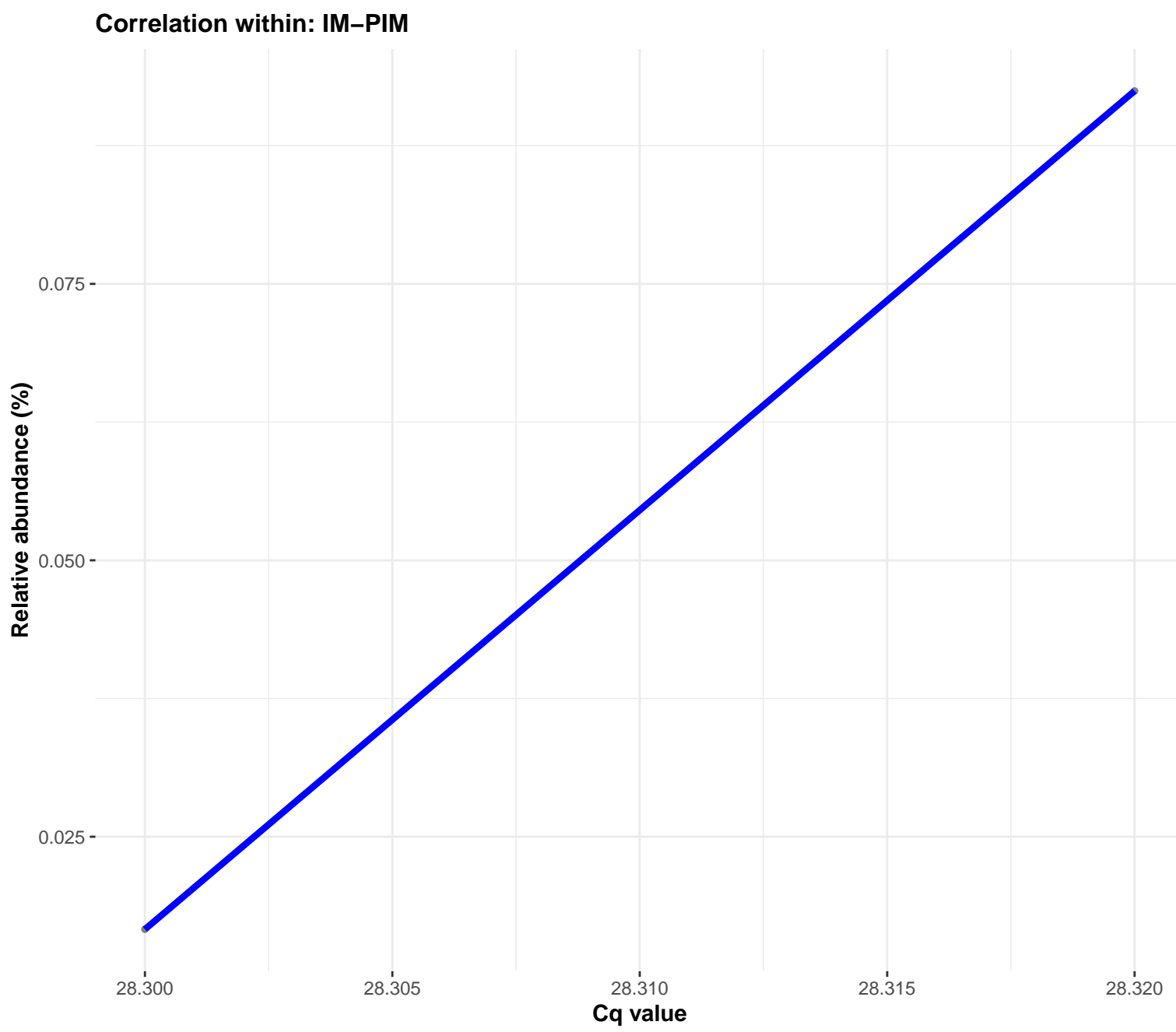
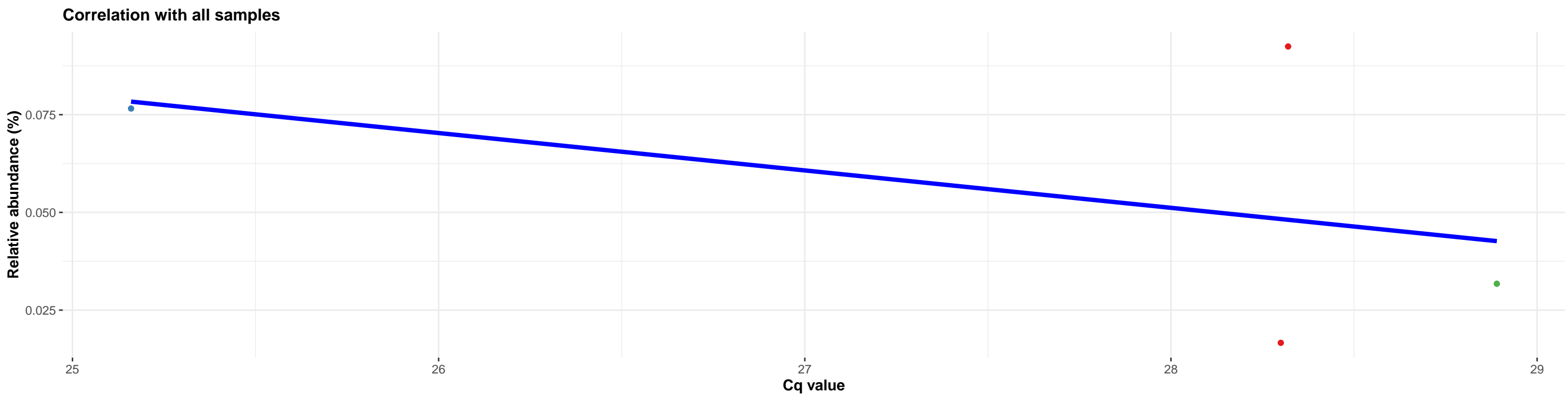


SampleType IM-PID IM-PIM

Correlation within: IM-PIM



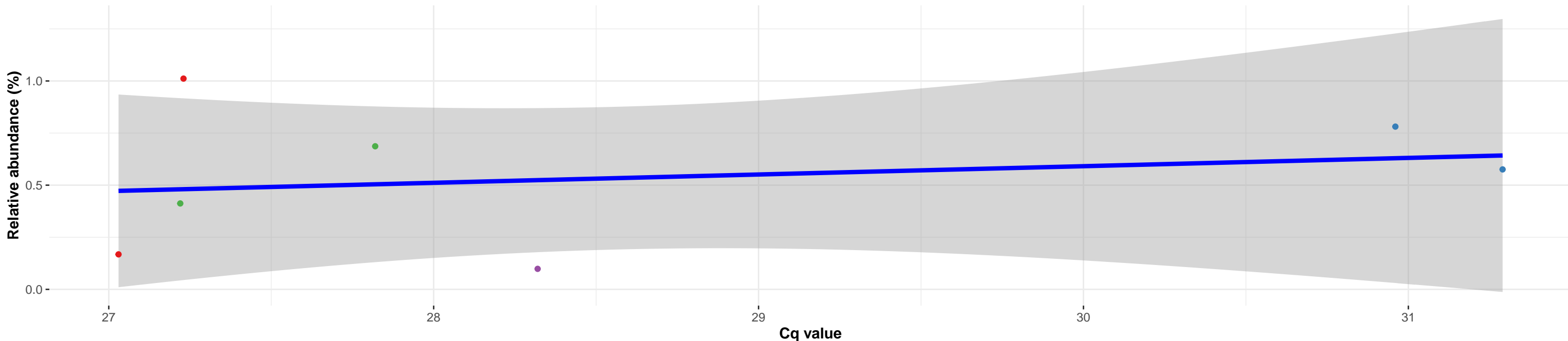
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Bacillales; f\_\_Bacillaceae; g\_\_Bacillus; NA



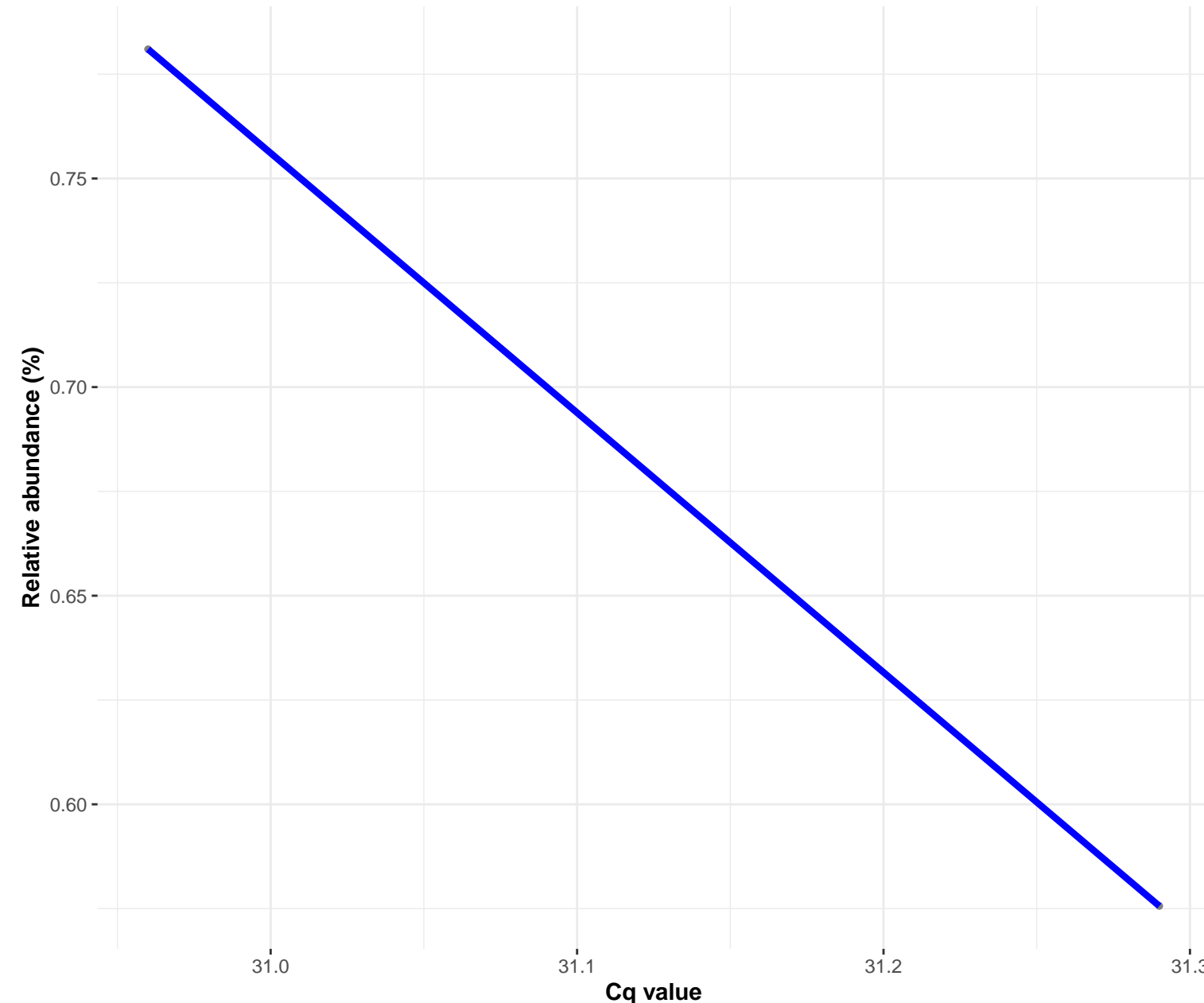
k\_\_Bacteria; p\_\_Firmicutes; c\_\_Bacilli; o\_\_Lactobacillales; f\_\_Streptococcaceae; g\_\_Lactococcus; NA

Correlation with all samples

$\log_e(S) = 3.784$ ,  $p = 0.645$ ,  $\hat{\rho}_{\text{Spearman}} = 0.214$ ,  $CI_{95\%} [-0.659, 0.842]$ ,  $n_{\text{pairs}} = 7$



Correlation within: REF-PIM



Correlation within: IM-PIM

