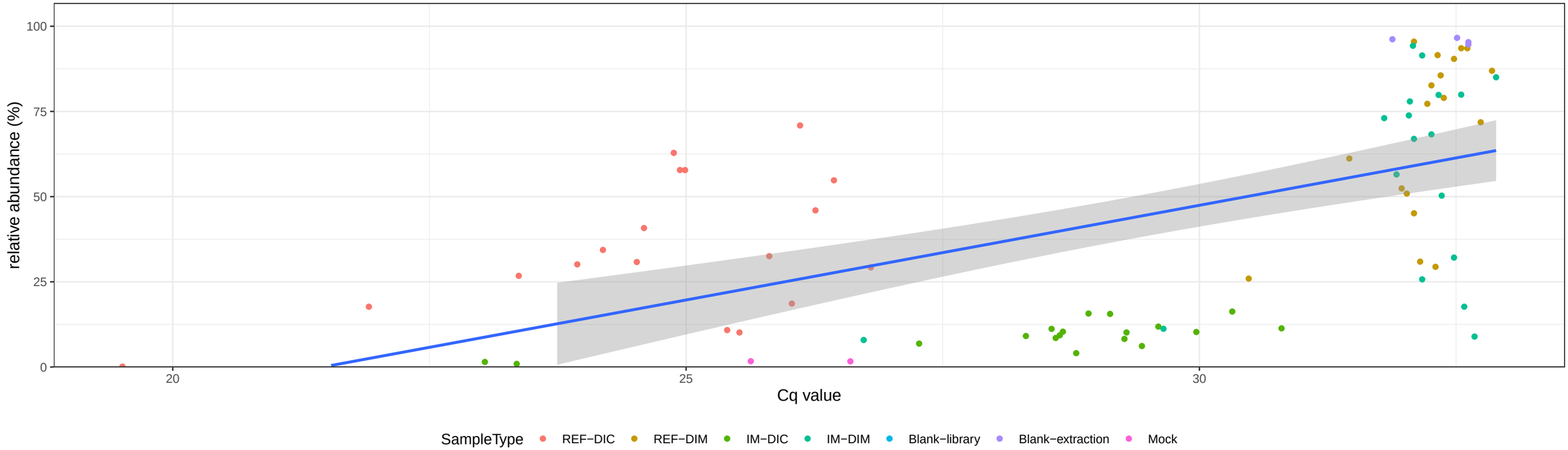
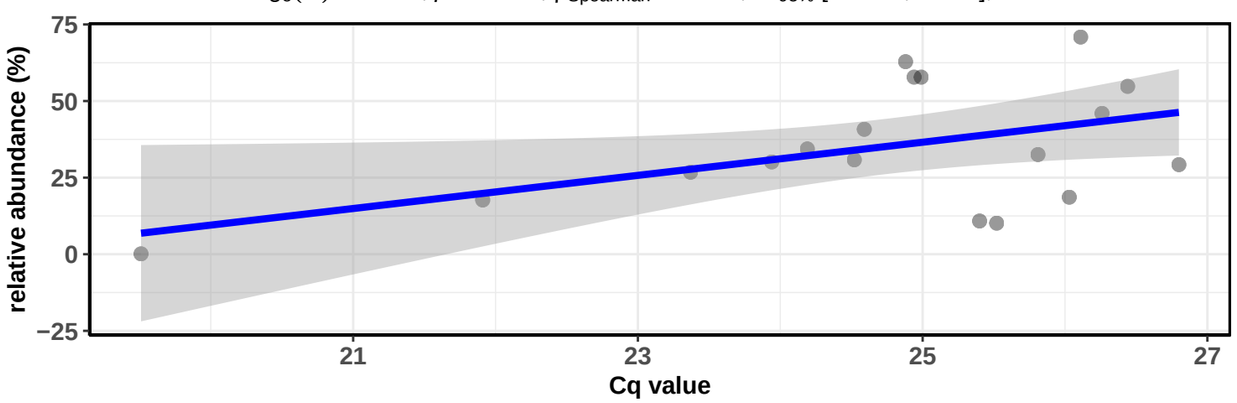
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



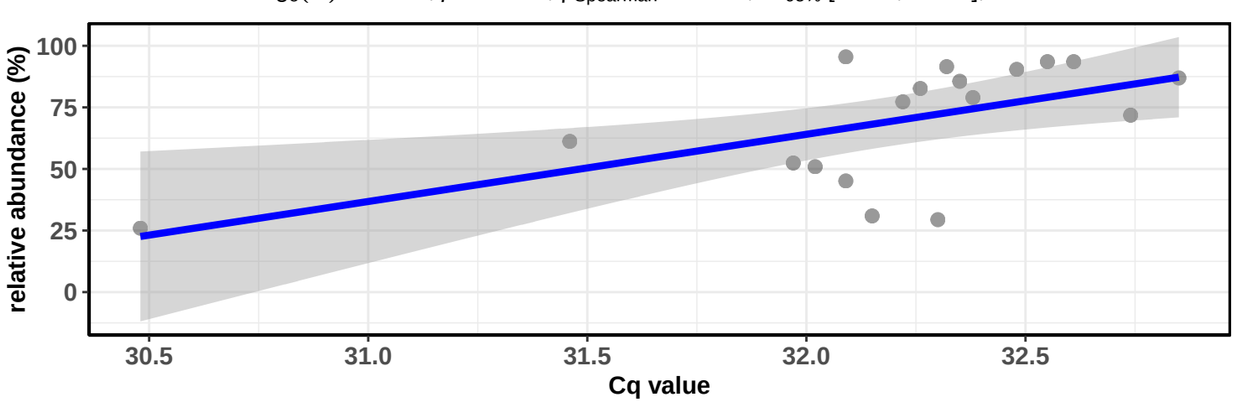
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.486, p = 0.191, $\rho_{Spearman}$ = 0.323, $CI_{95\%}$ [−0.169, 0.686], n = 18



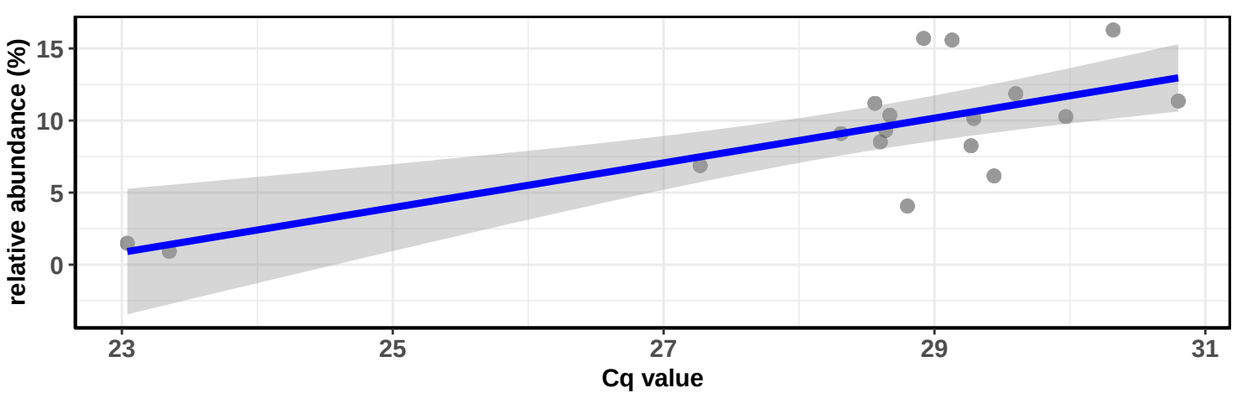
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.025, p = 0.013, $\rho_{Spearman}$ = 0.573, $CI_{95\%}$ [0.145, 0.820], n = 18



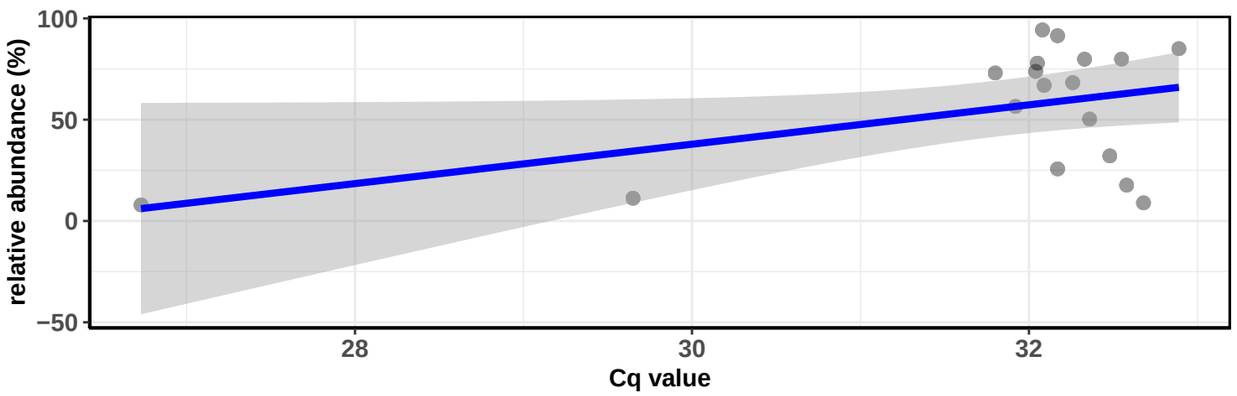
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.001, p = 0.011, $\rho_{Spearman}$ = 0.583, $CI_{95\%}$ [0.160, 0.825], n = 18



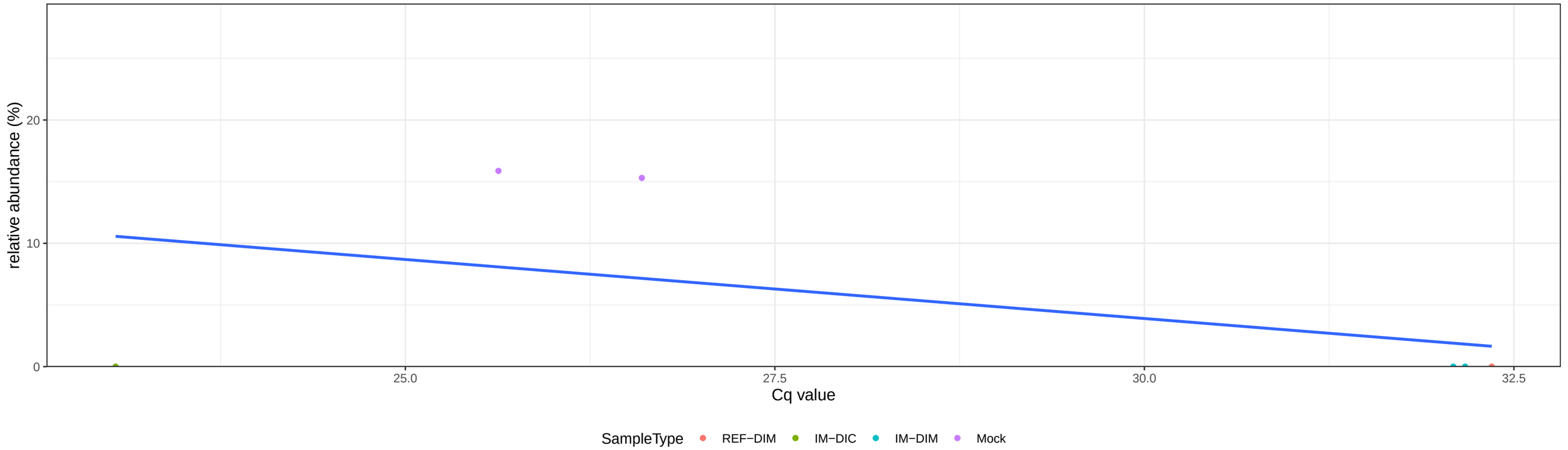
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.752, p = 0.645, $\rho_{Spearman}$ = 0.117, $CI_{95\%}$ [−0.370, 0.553], n = 18

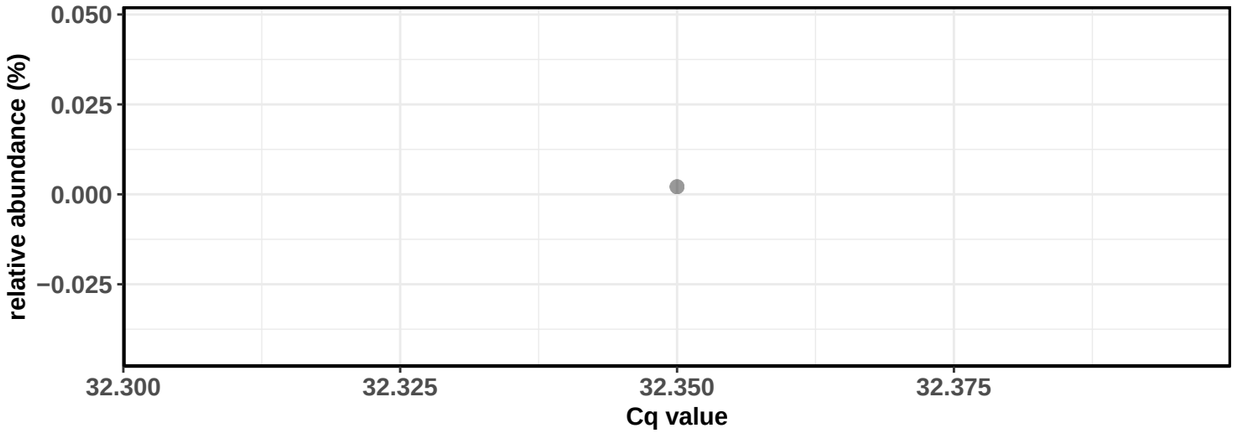


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Enterobacteriales; D_4__Enterobacteriaceae; D_5__Salmonella

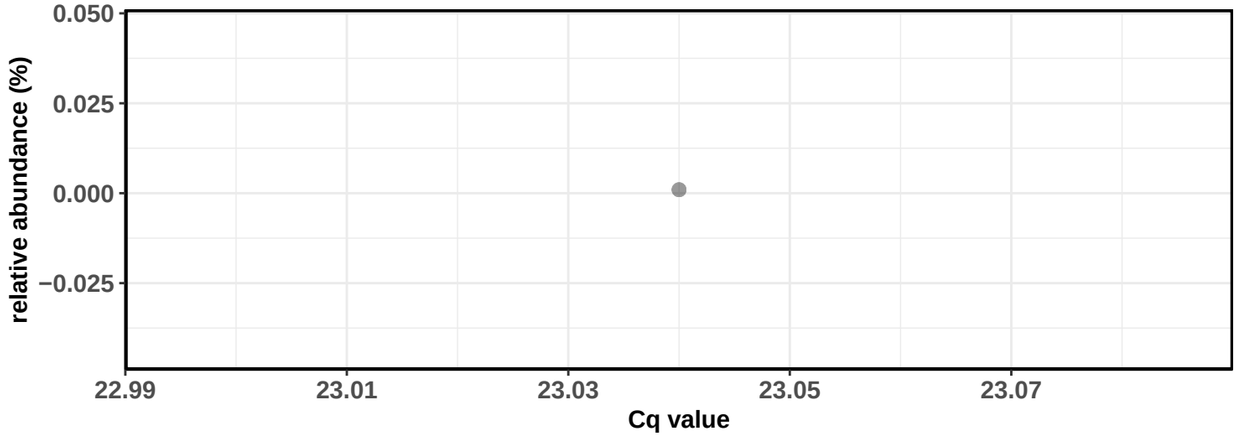
Correlation with all samples



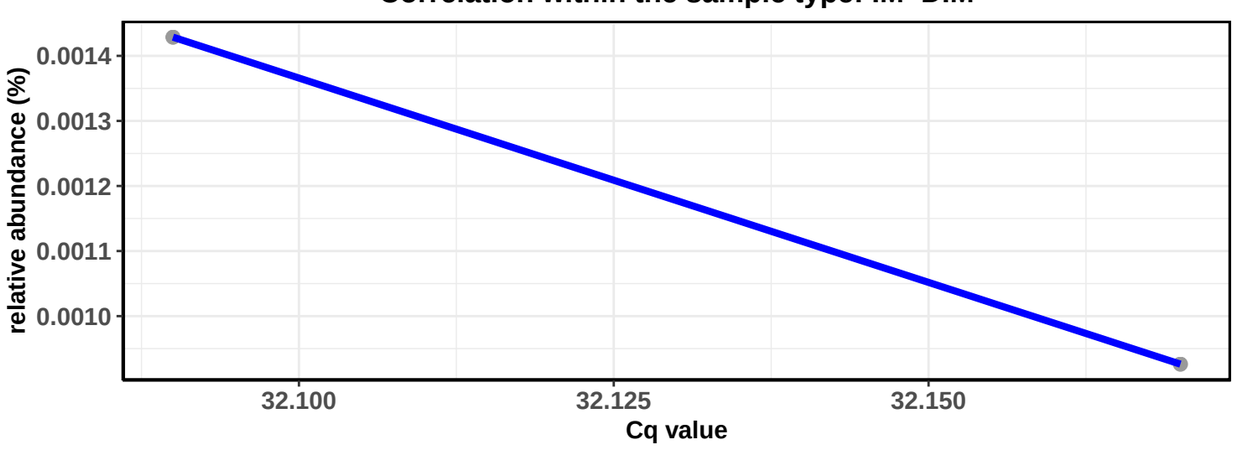
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

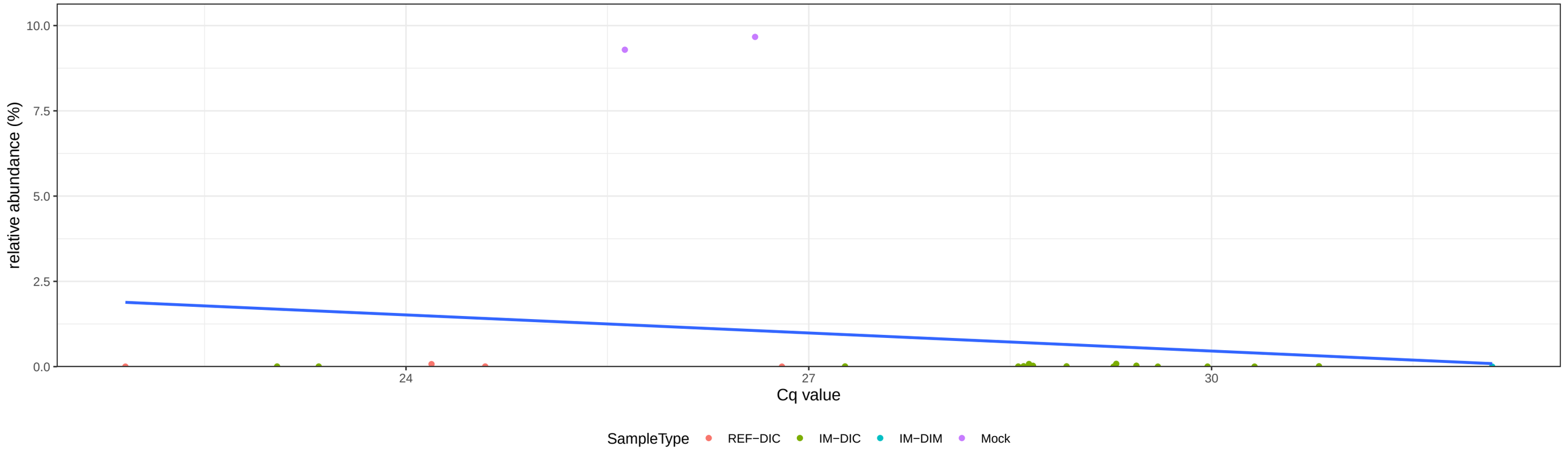


Correlation within the sample type: IM−DIM

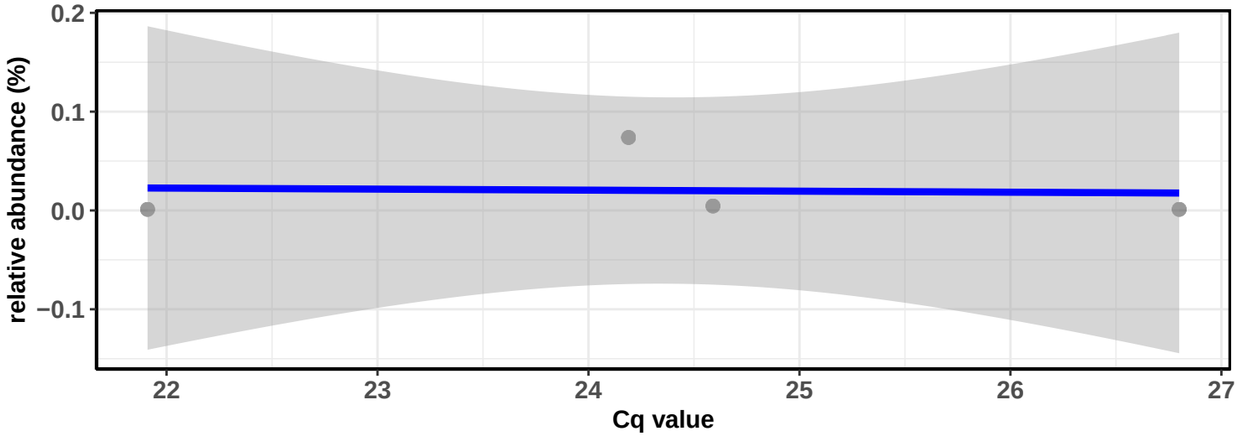


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Enterobacteriales; D_4__Enterobacteriaceae; D_5__Escherichia−Shigella

Correlation with all samples

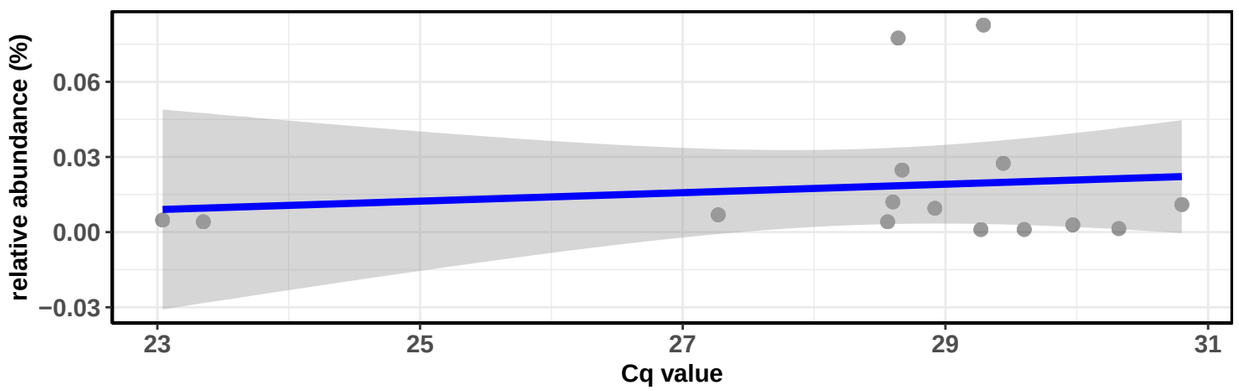


Correlation within the sample type: REF−DIC

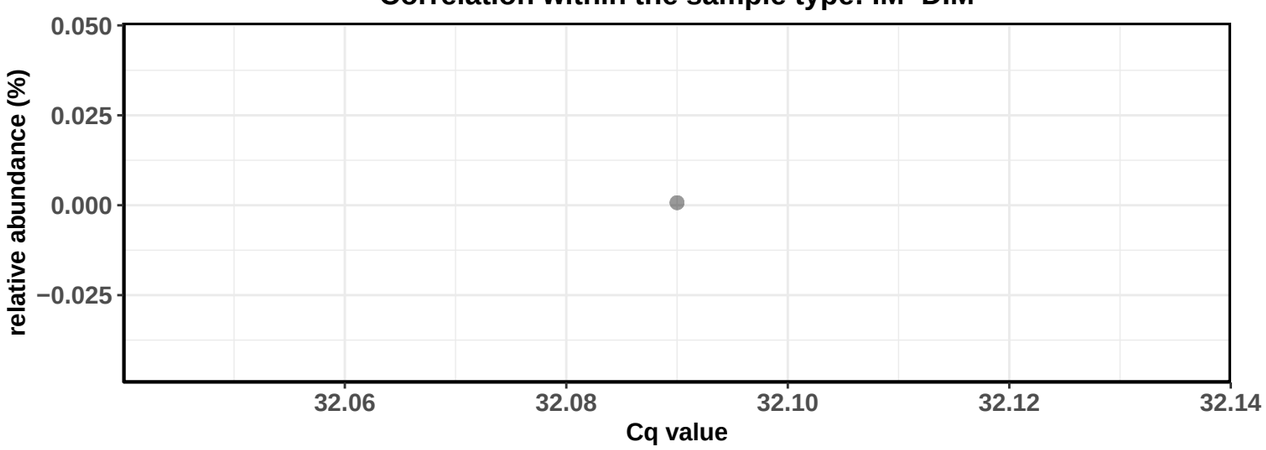


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.436, p = 0.685, $\rho_{Spearman}$ = −0.114, $CI_{95\%}$ [−0.592, 0.423], n = 15

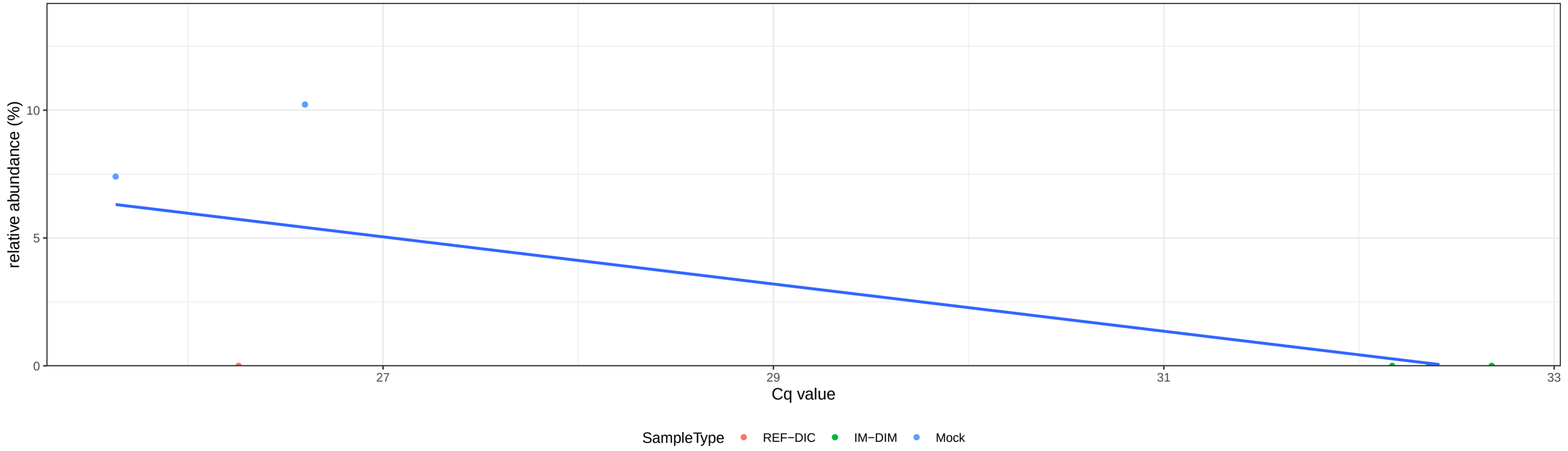


Correlation within the sample type: IM−DIM

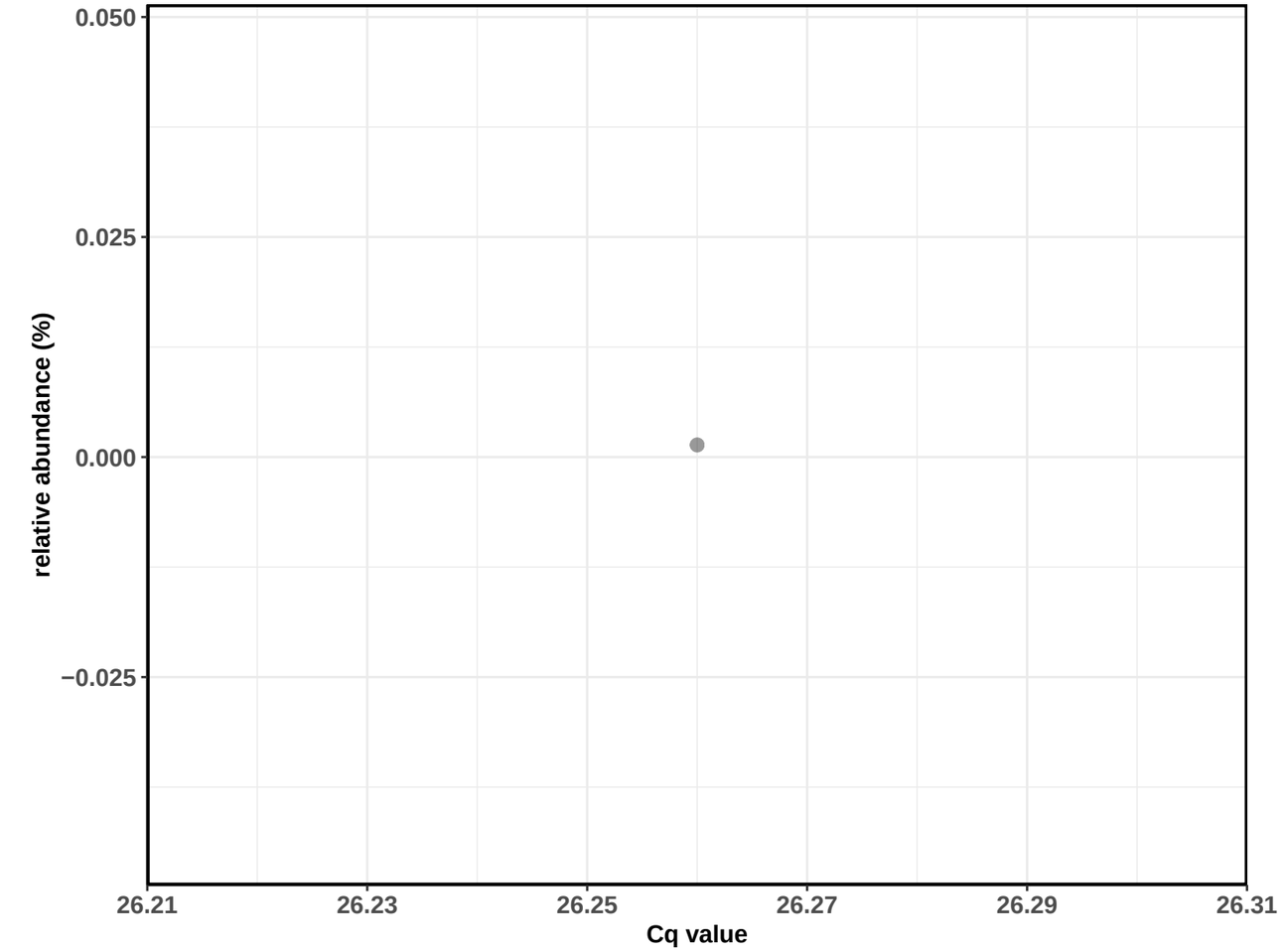


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Bacillus

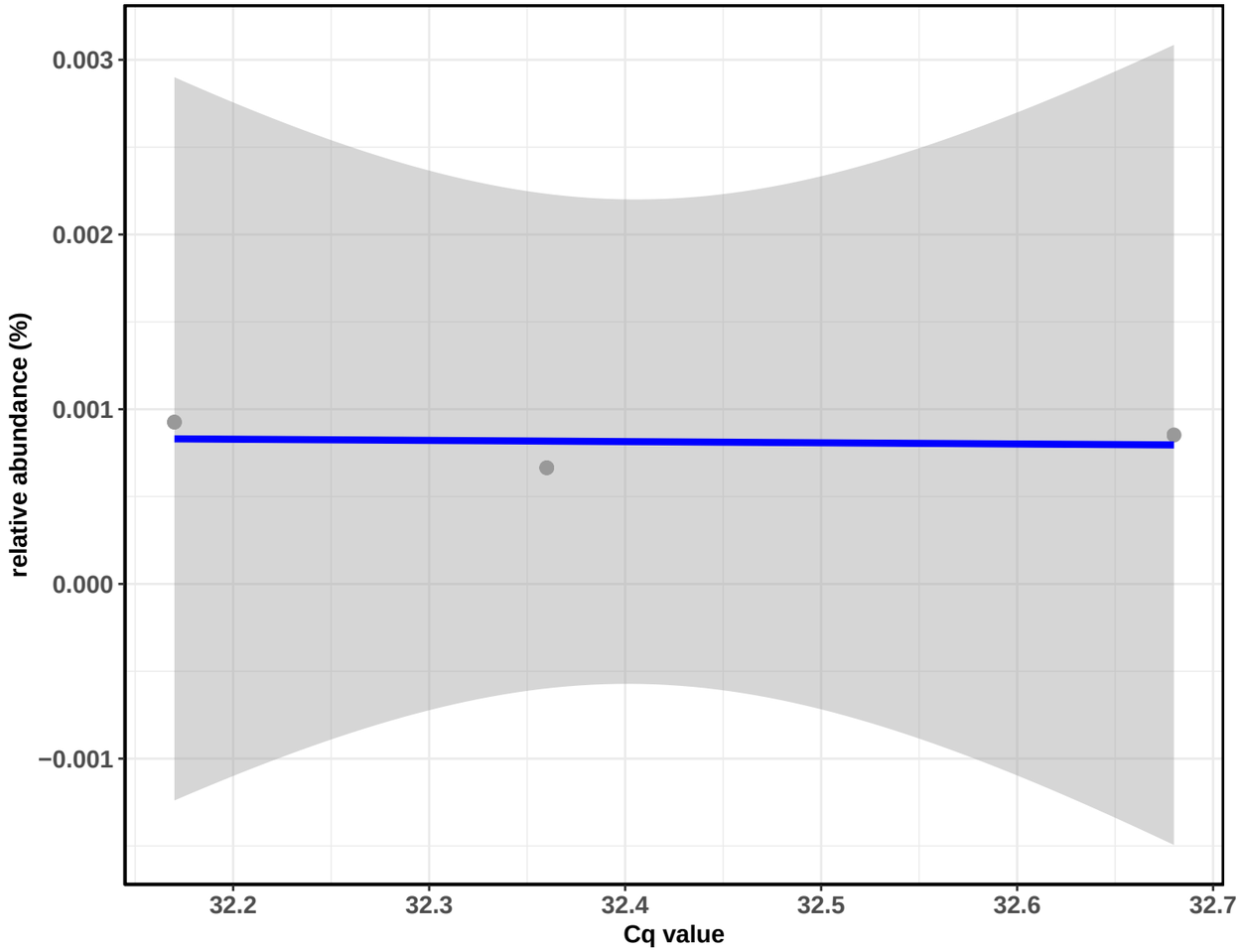
Correlation with all samples



Correlation within the sample type: REF−DIC

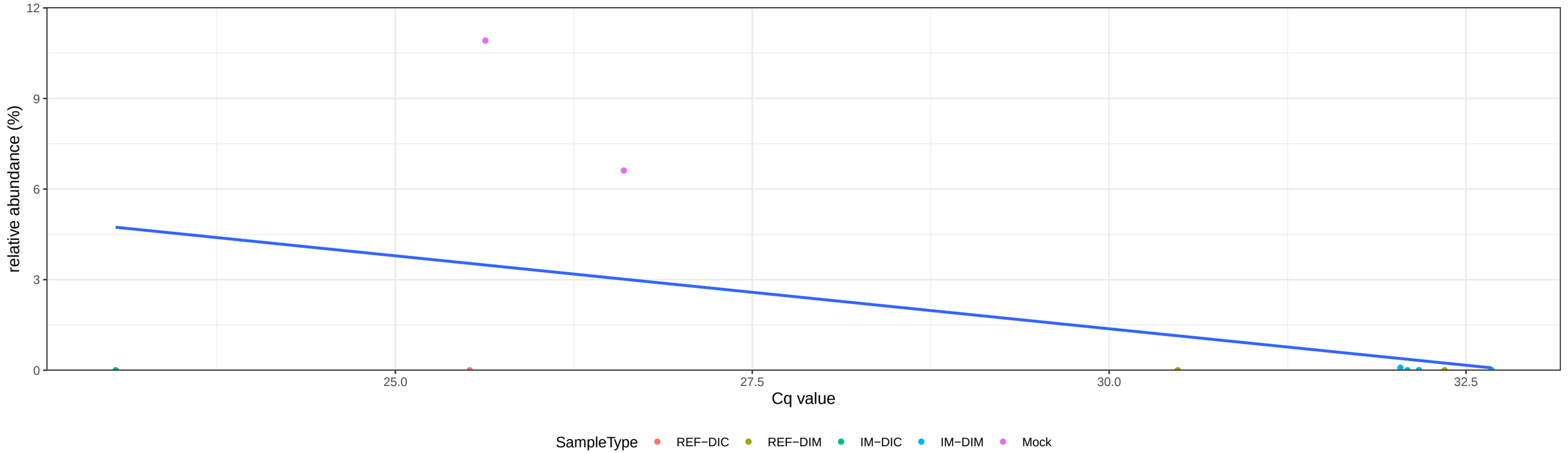


Correlation within the sample type: IM−DIM

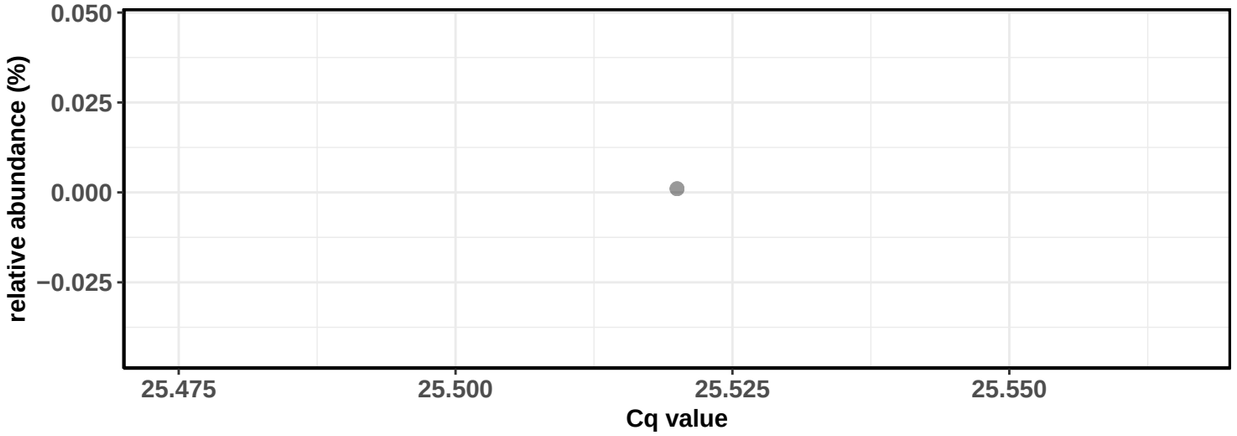


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

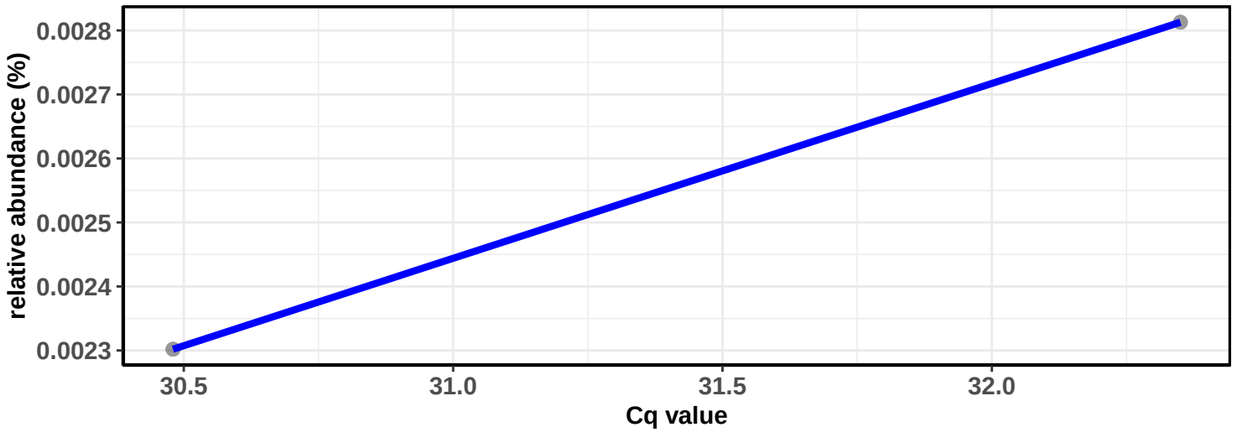
Correlation with all samples



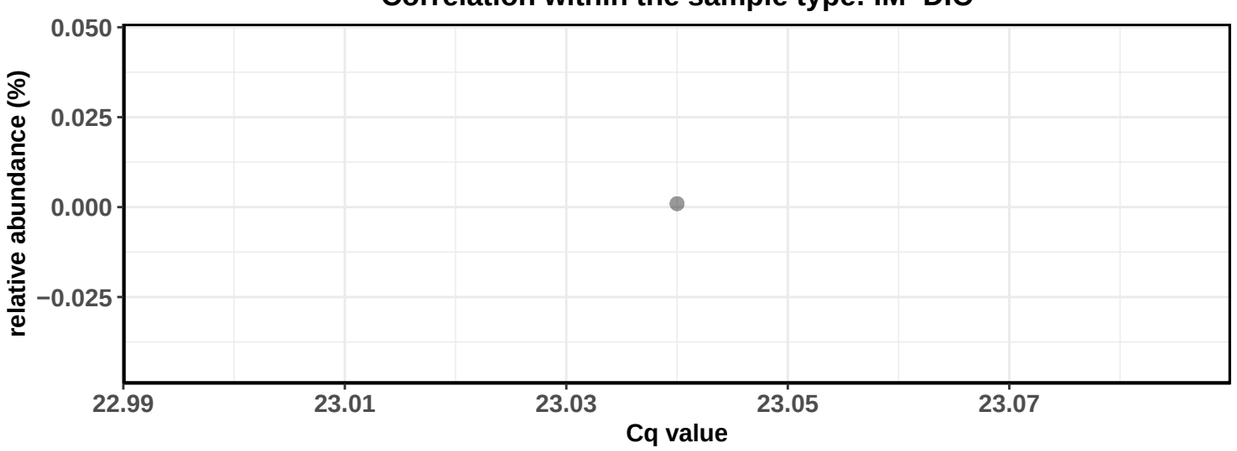
Correlation within the sample type: REF−DIC



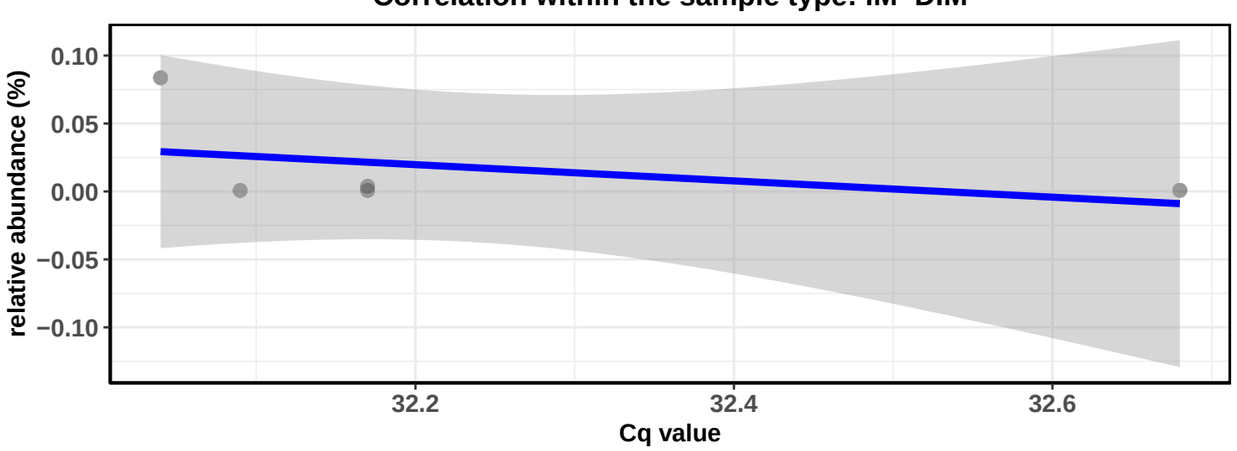
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

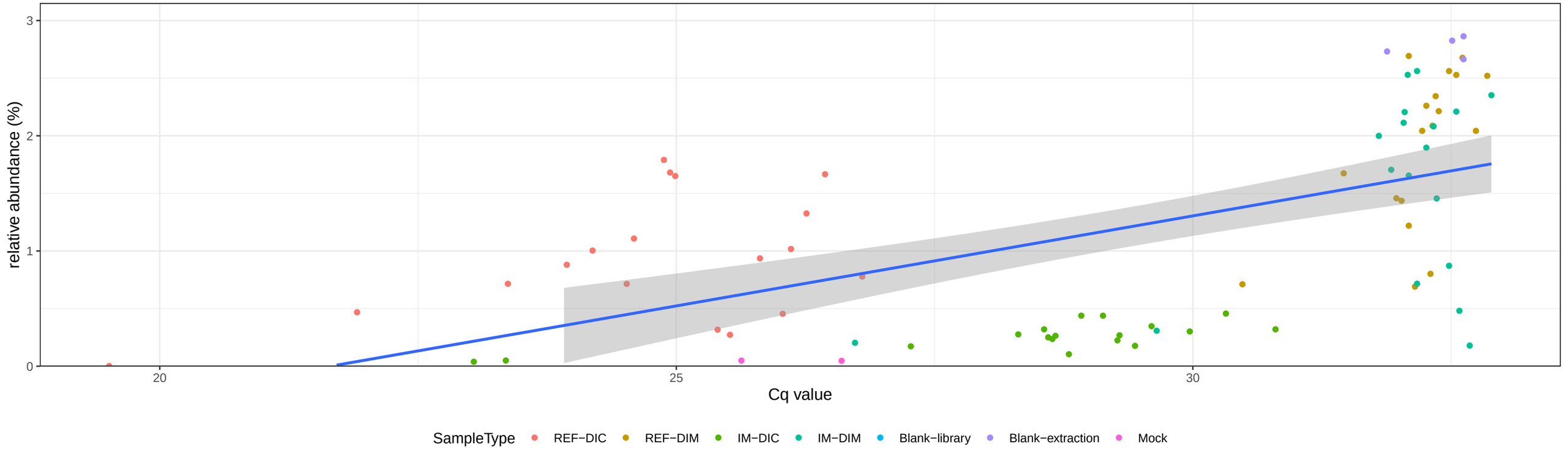


Correlation within the sample type: IM−DIM



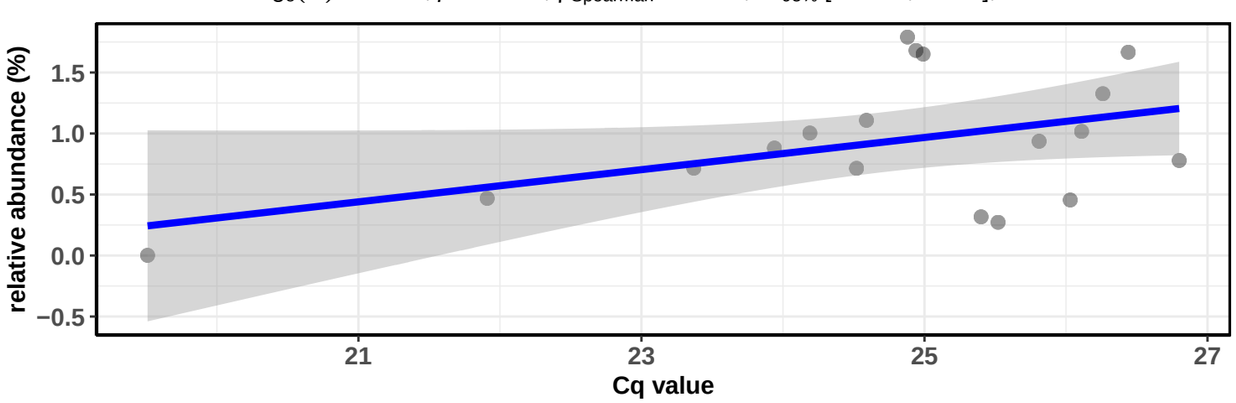
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



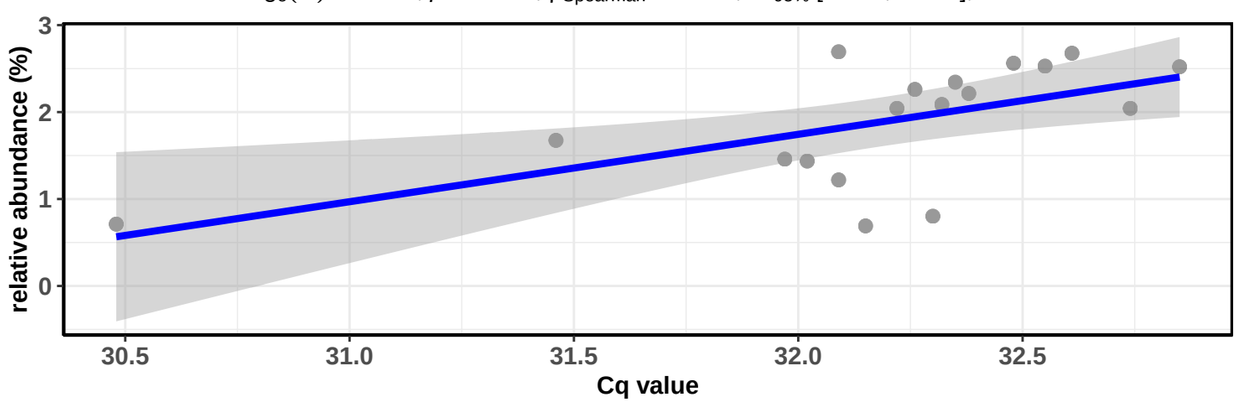
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.548, p = 0.261, $\rho_{Spearman}$ = 0.280, $CI_{95\%}$ [−0.215, 0.660], n = 18



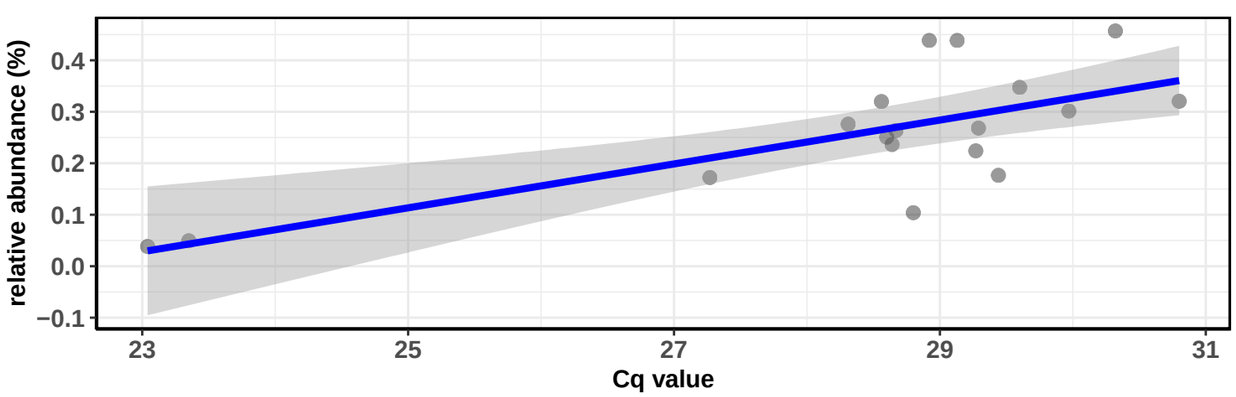
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.986, p = 0.010, $\rho_{Spearman}$ = 0.590, $CI_{95\%}$ [0.169, 0.828], n = 18



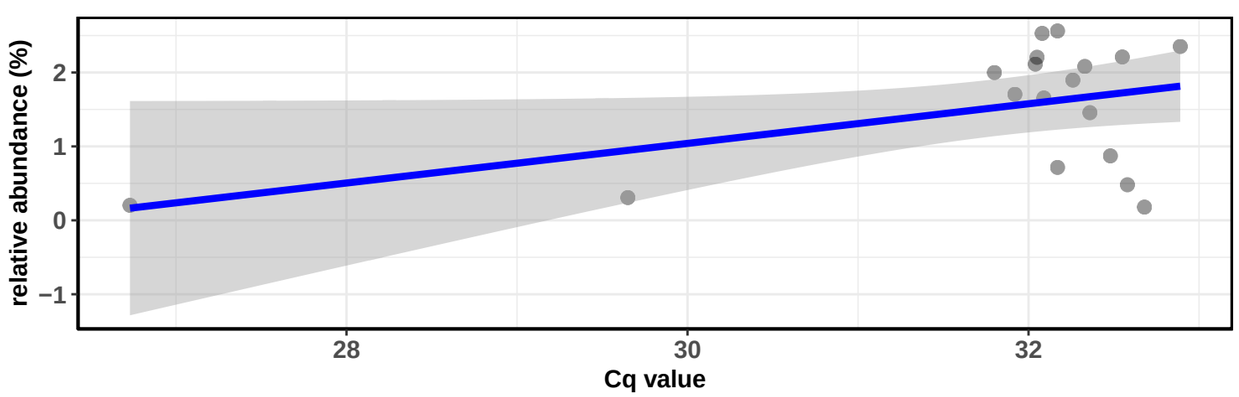
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.961, p = 0.009, $\rho_{Spearman}$ = 0.600, $CI_{95\%}$ [0.184, 0.833], n = 18



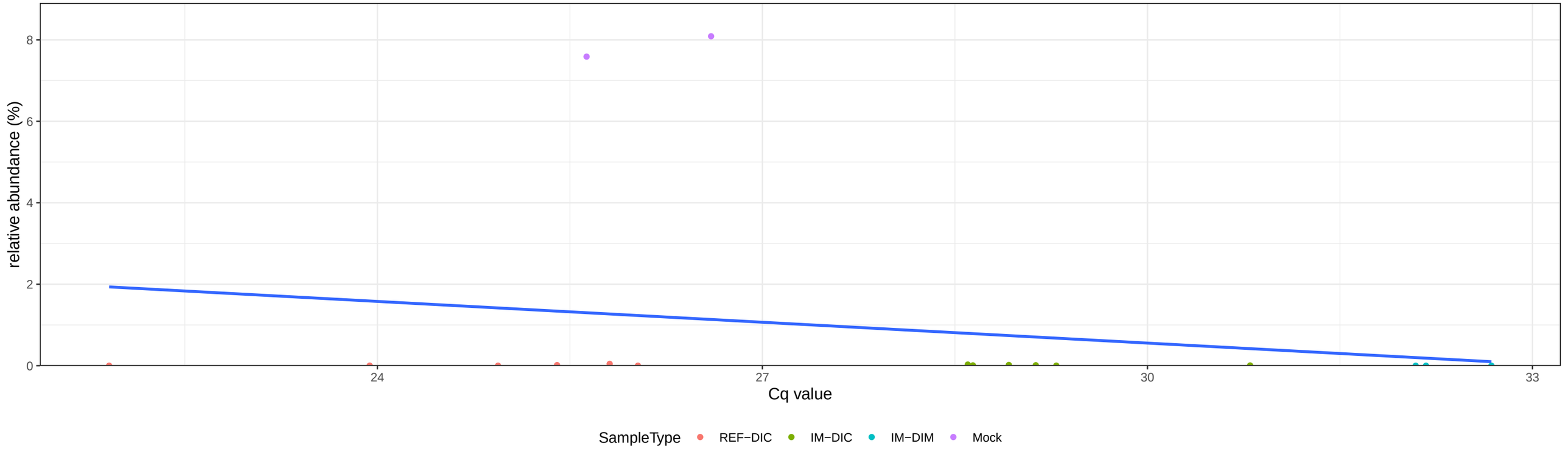
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.821, p = 0.832, $\rho_{Spearman}$ = 0.054, $CI_{95\%}$ [−0.424, 0.508], n = 18



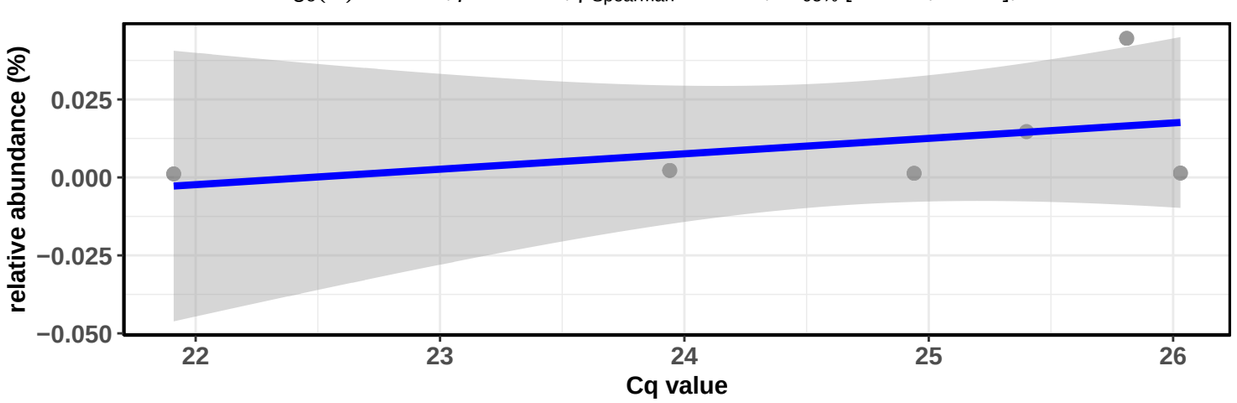
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples



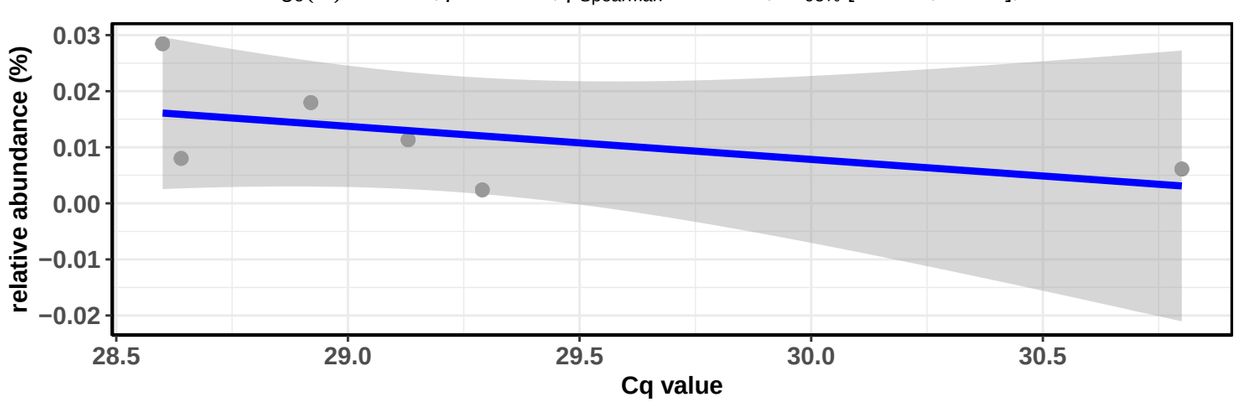
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 2.773, p = 0.266, $\rho_{Spearman}$ = 0.543, $CI_{95\%}$ [−0.480, 0.940], n = 6

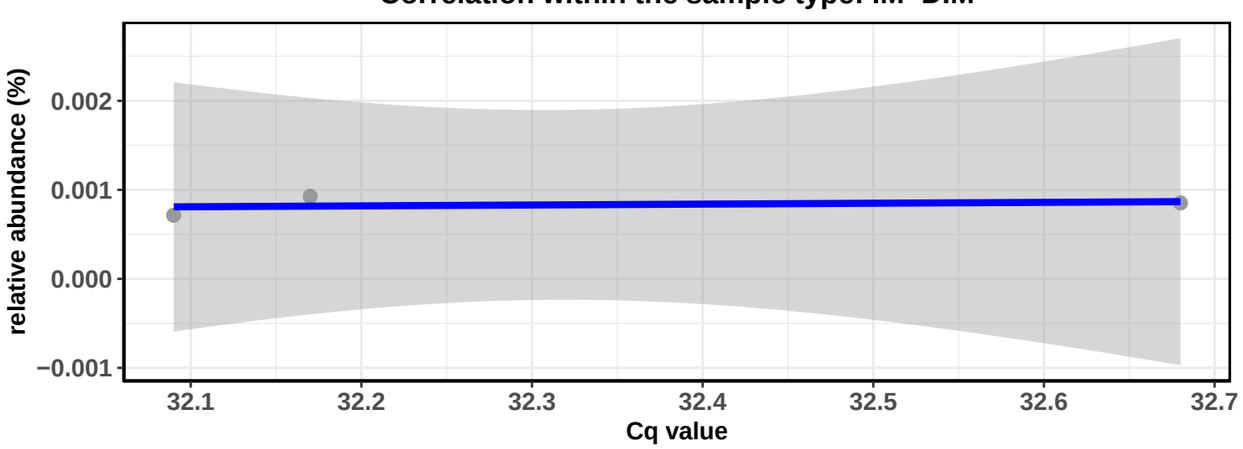


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 4.127, p = 0.072, $\rho_{Spearman}$ = −0.771, $CI_{95\%}$ [−0.974, 0.107], n = 6

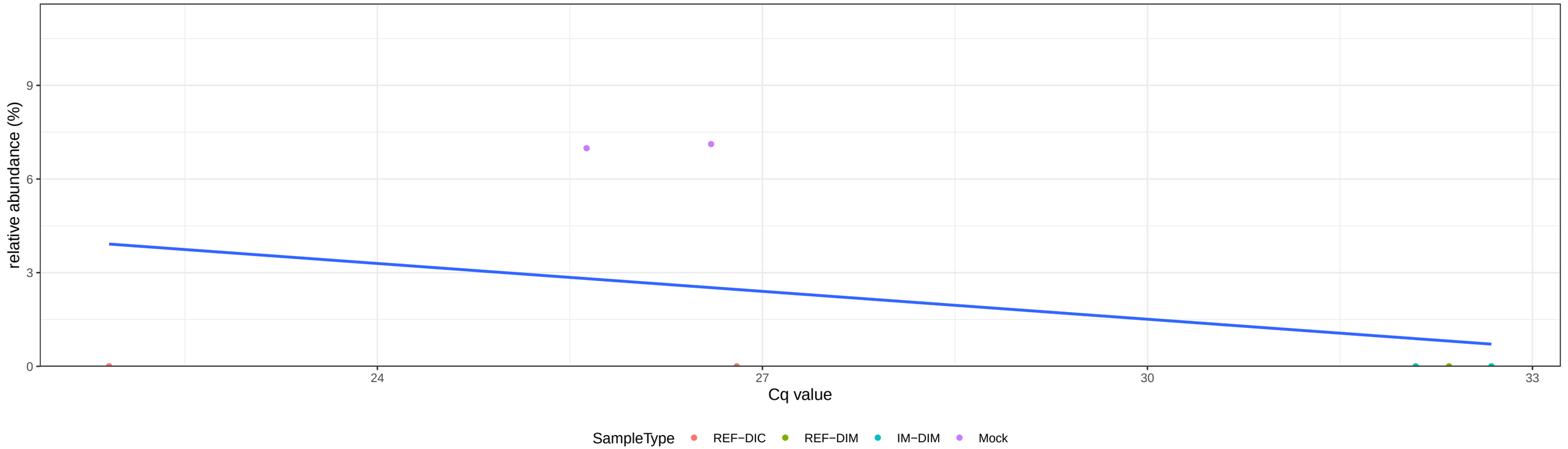


Correlation within the sample type: IM−DIM

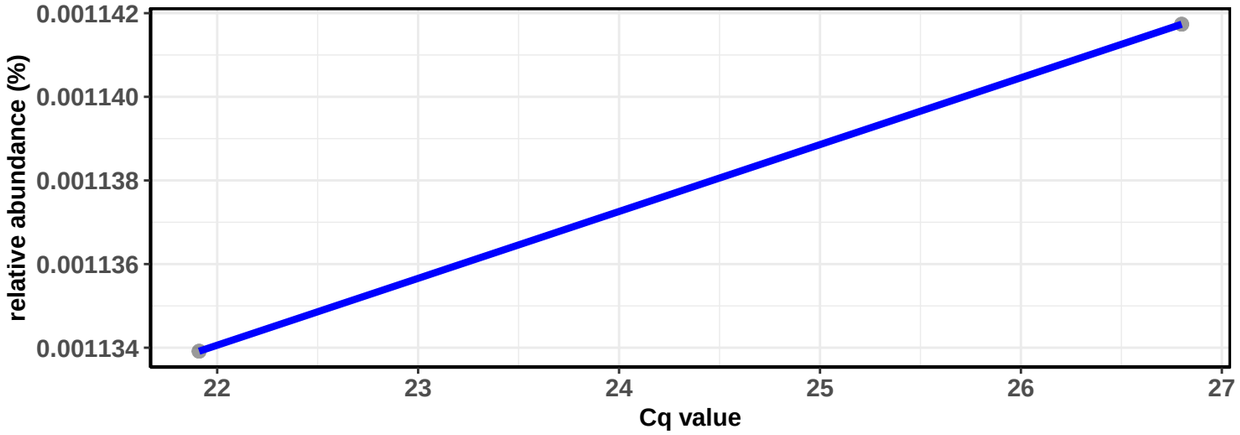


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Enterobacteriales; D_4__Enterobacteriaceae; D_5__Escherichia−Shigella

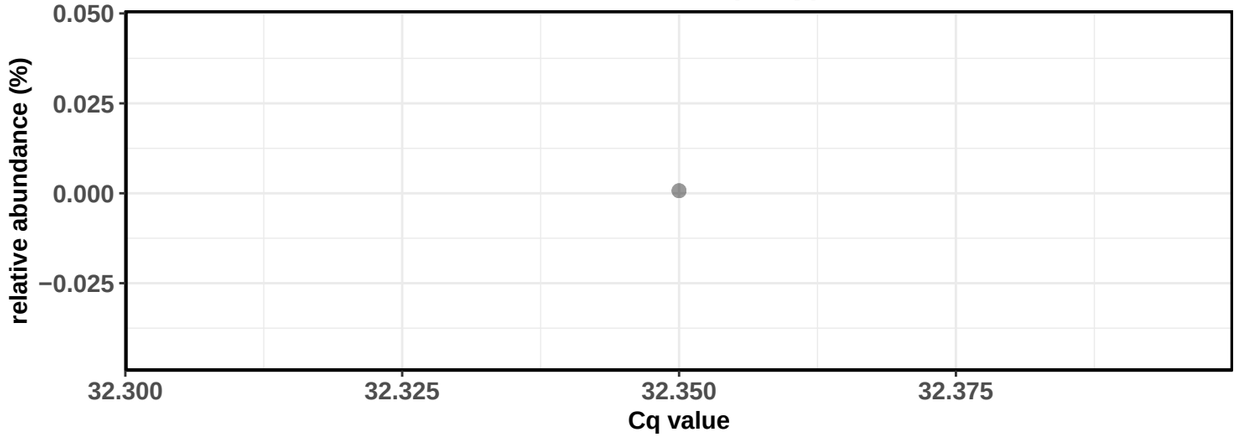
Correlation with all samples



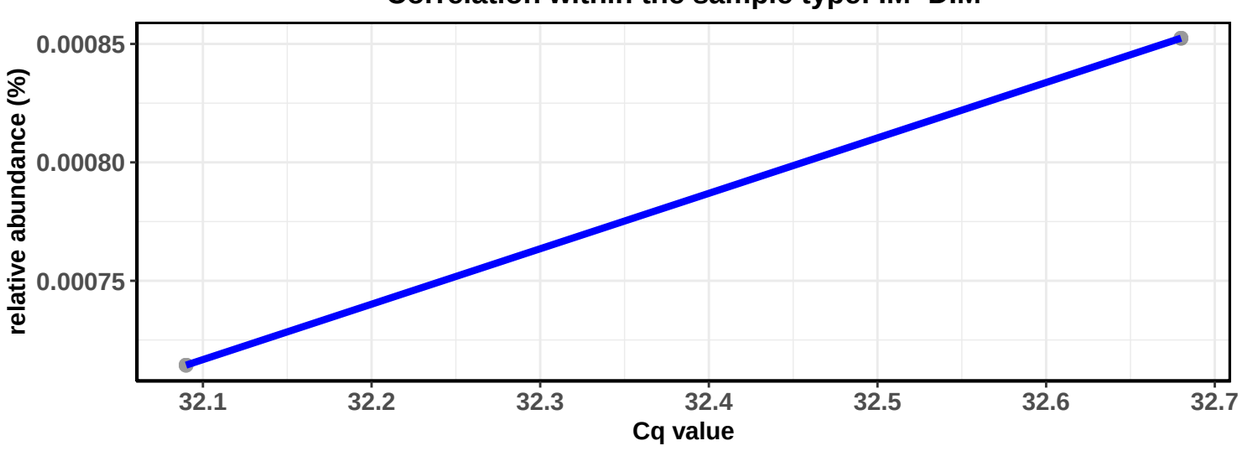
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

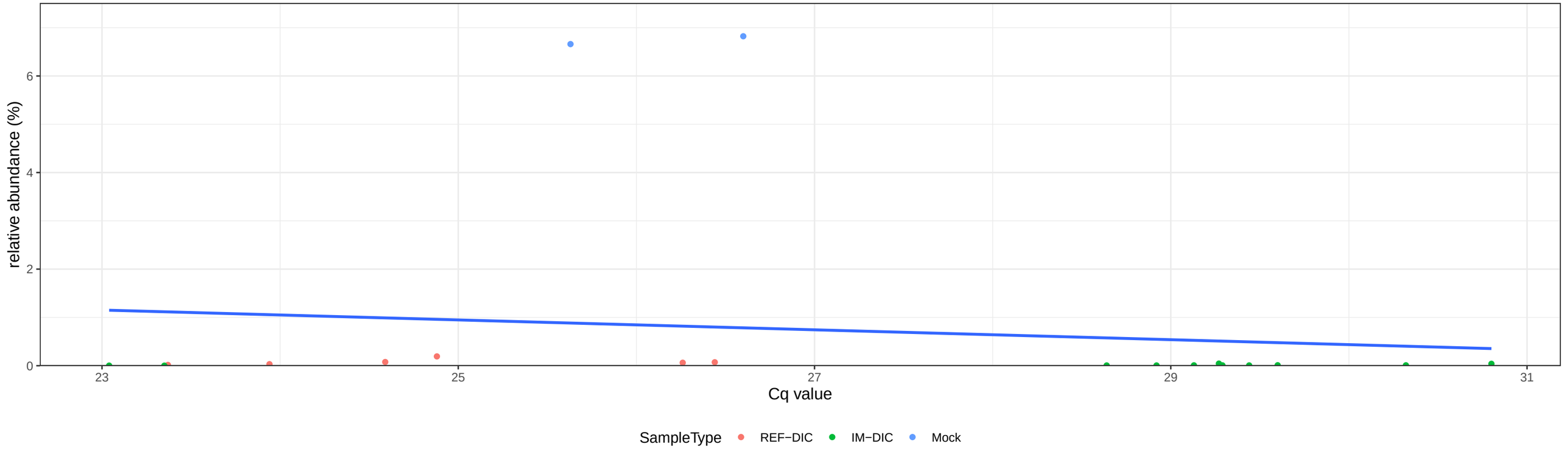


Correlation within the sample type: IM−DIM



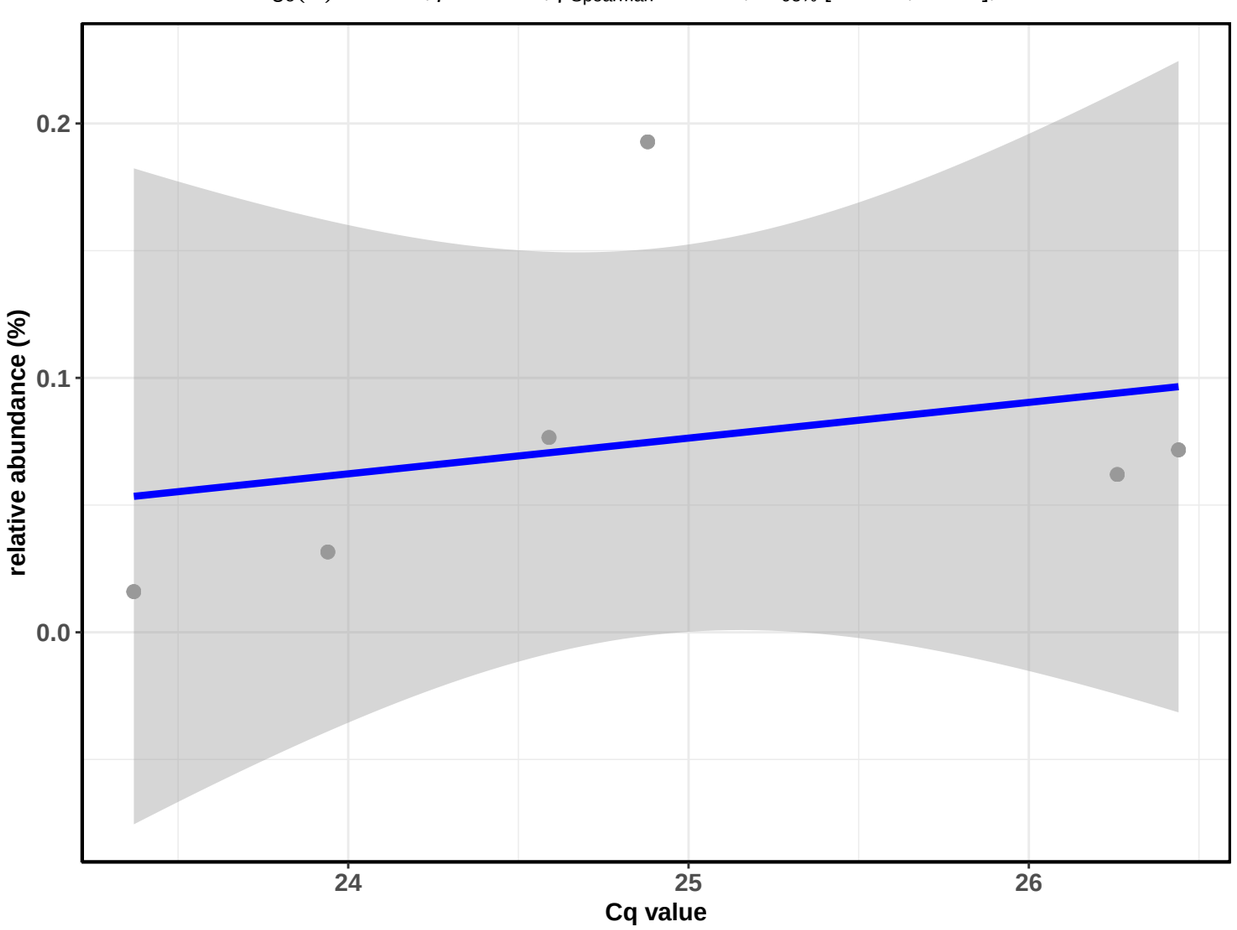
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples



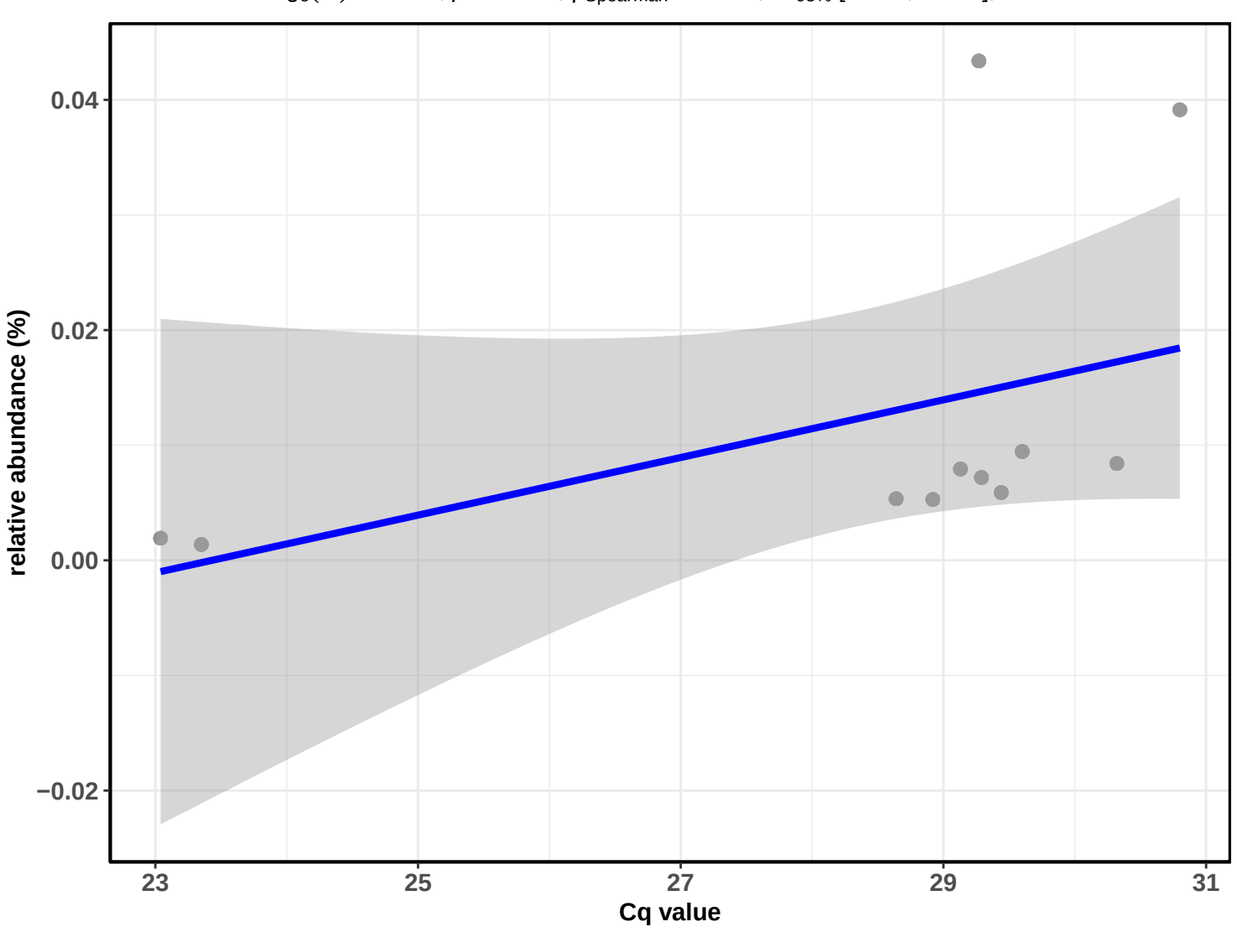
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 2.773, p = 0.266, $\rho_{Spearman}$ = 0.543, $CI_{95\%}$ [−0.480, 0.940], n = 6



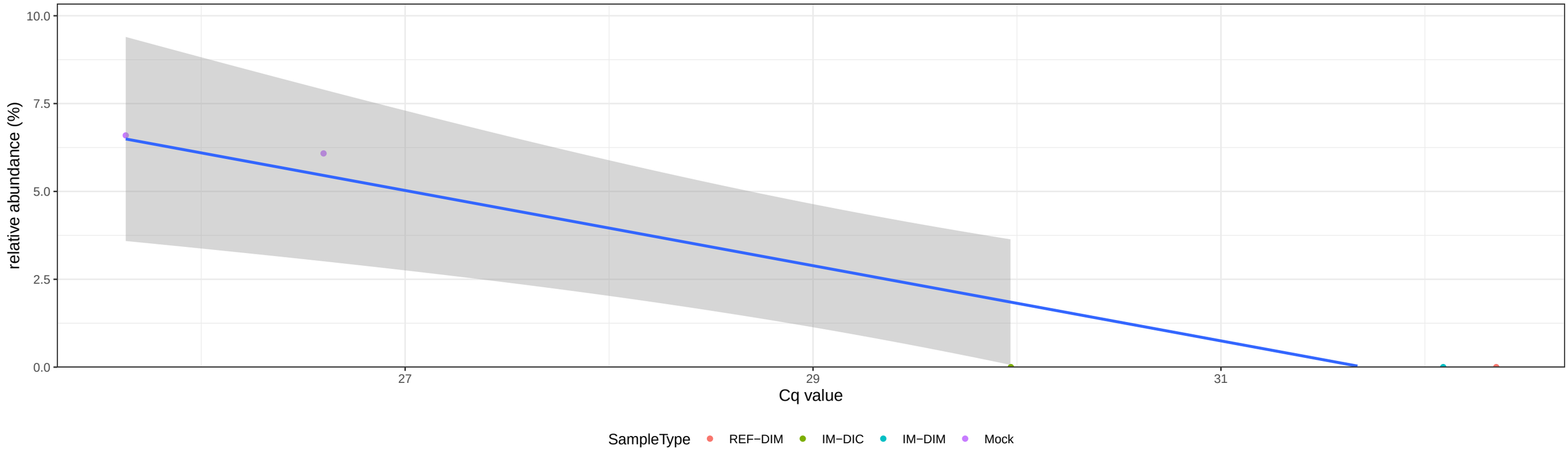
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 3.871, p = 0.004, $\rho_{Spearman}$ = 0.782, $CI_{95\%}$ [0.343, 0.941], n = 11

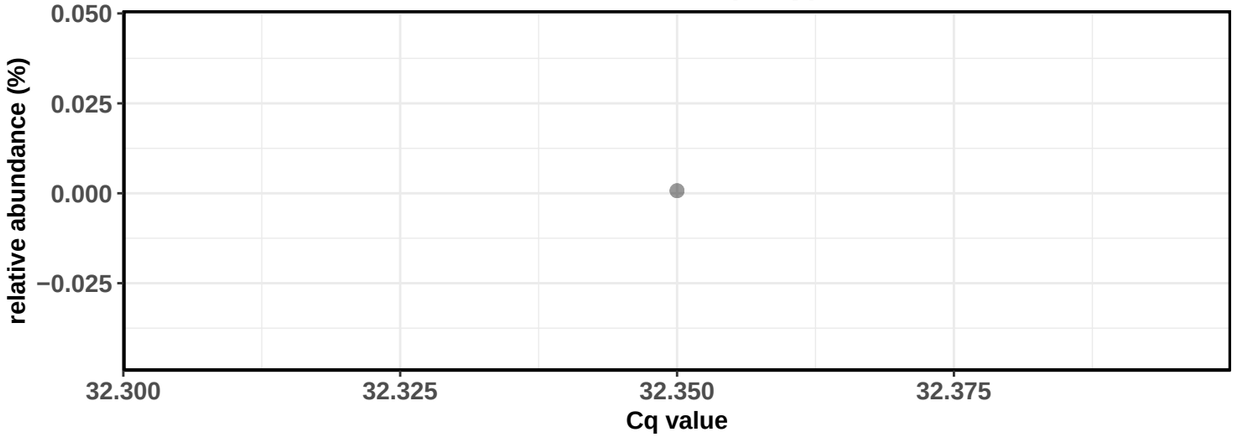


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

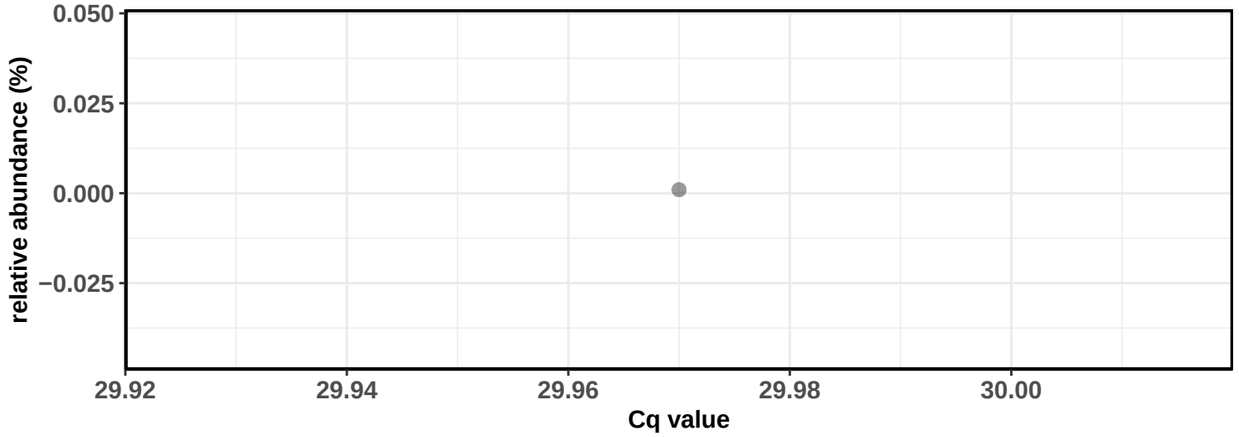
Correlation with all samples



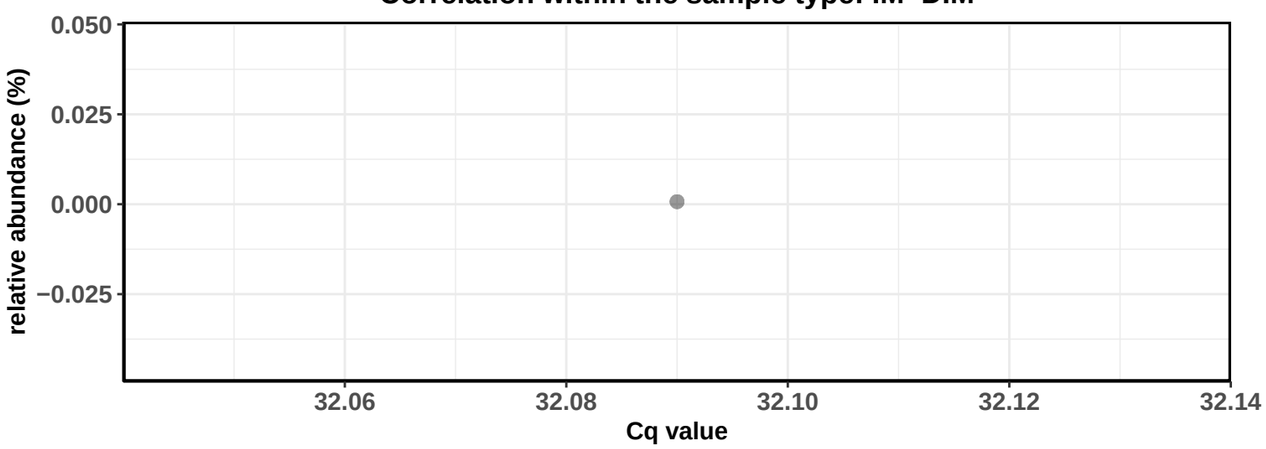
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

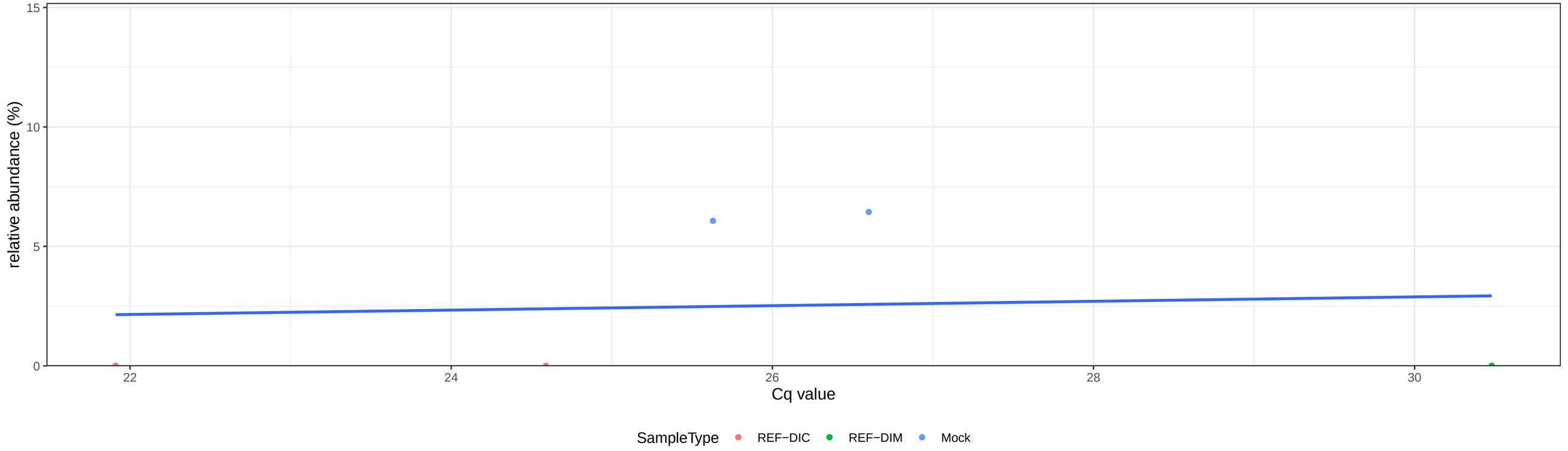


Correlation within the sample type: IM−DIM

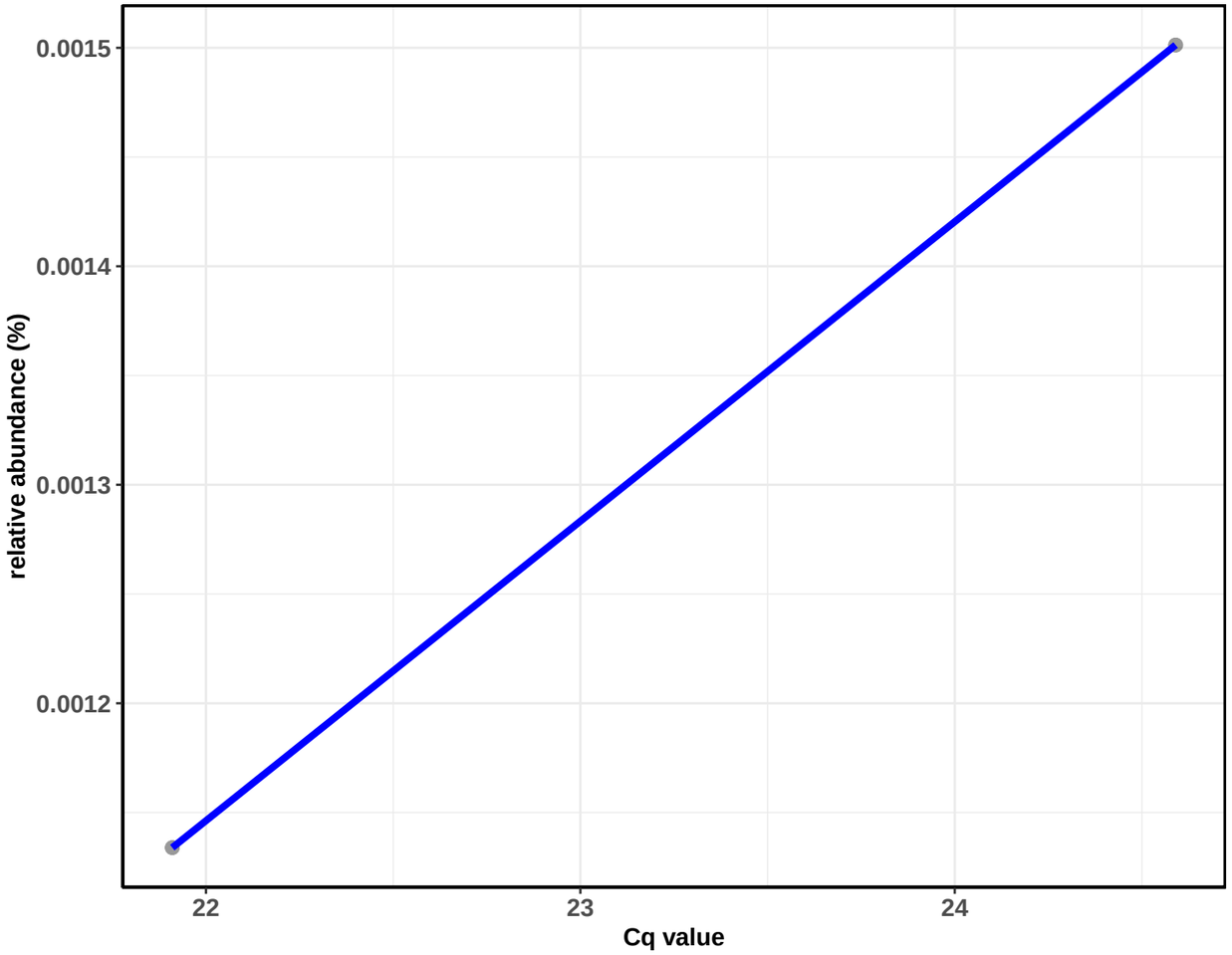


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Staphylococcaceae; D_5__Staphylococcus; D_6__Staphylococcus aureus

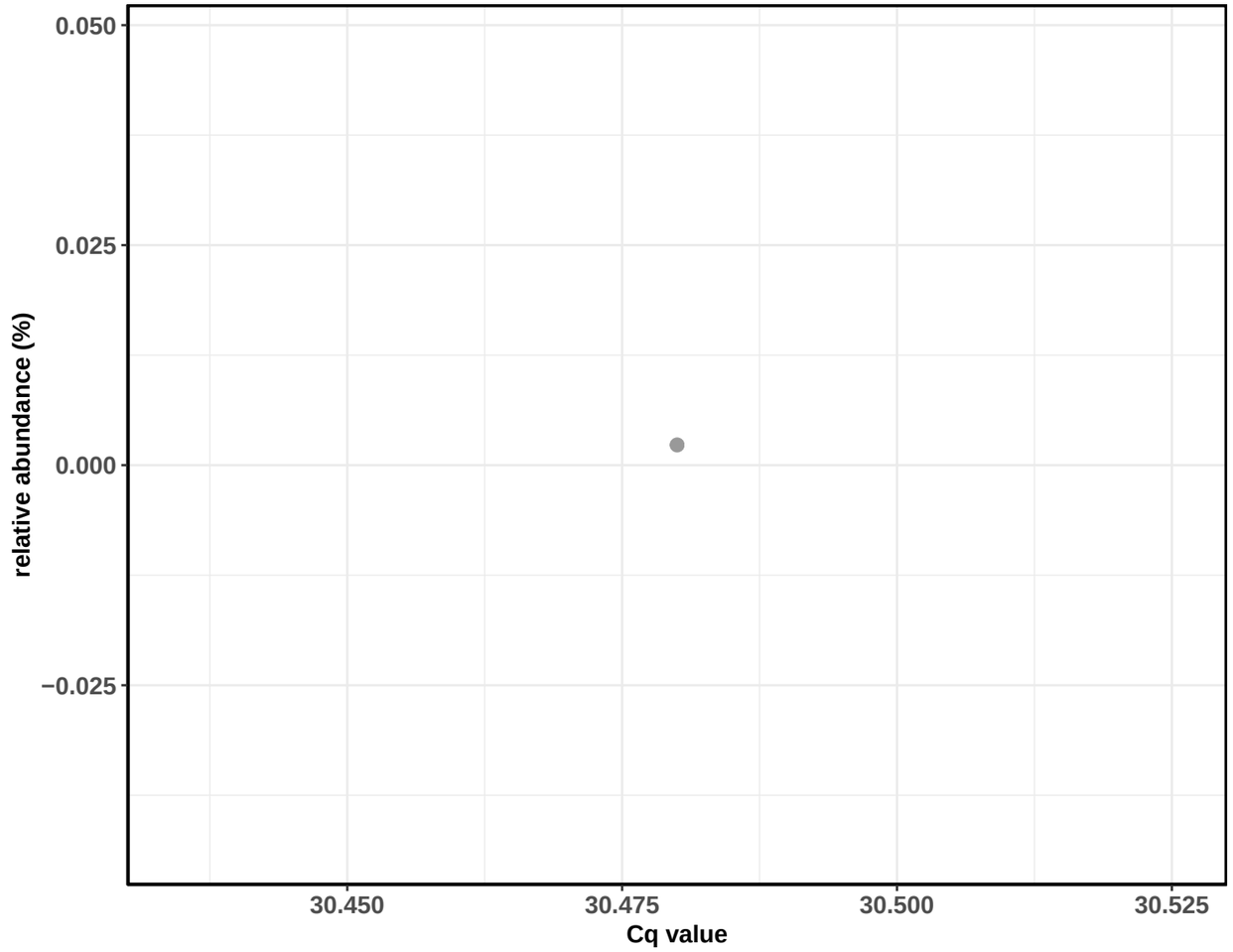
Correlation with all samples



Correlation within the sample type: REF−DIC

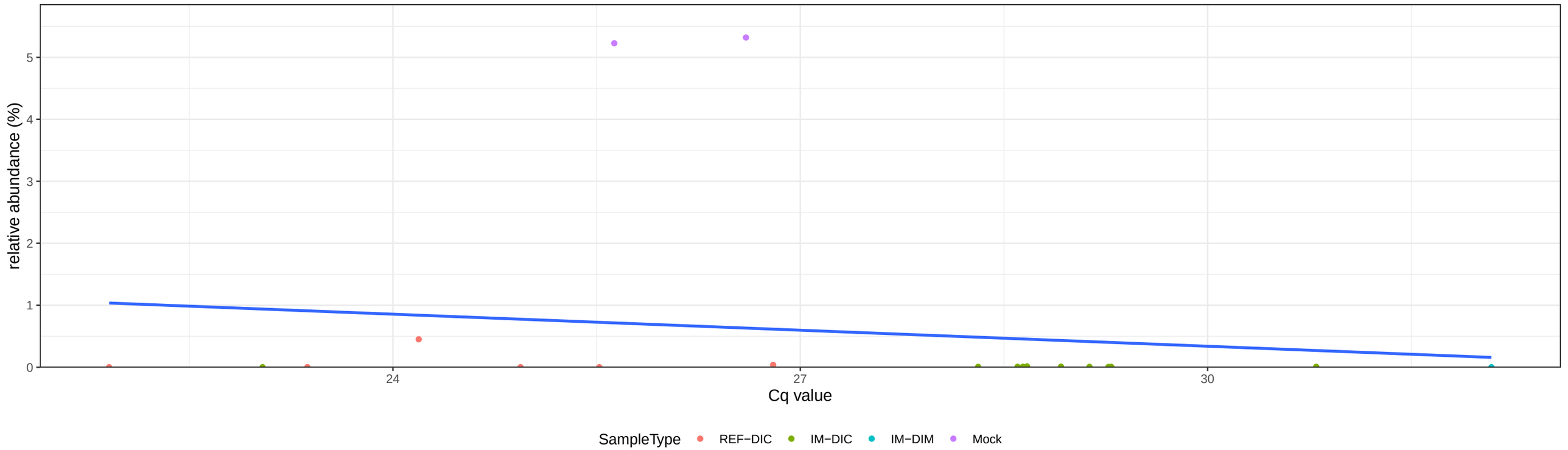


Correlation within the sample type: REF−DIM



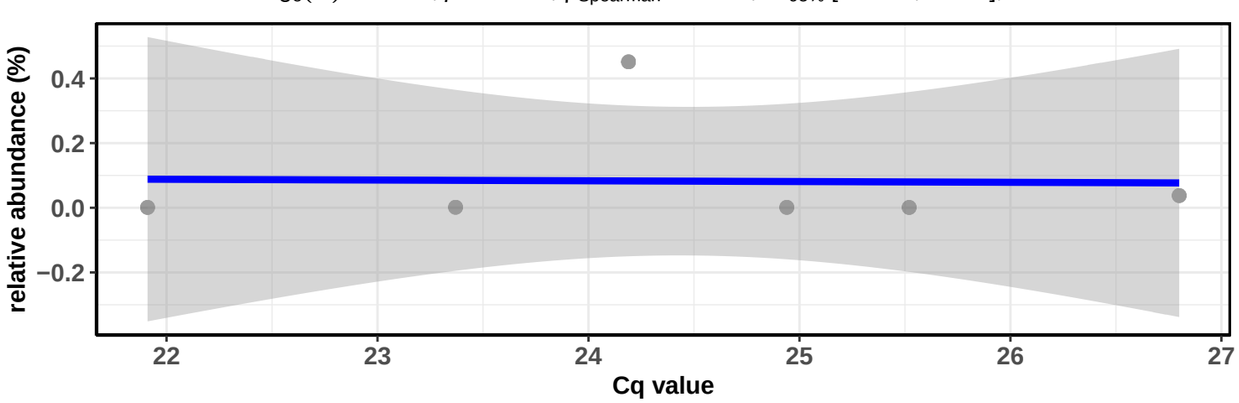
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples



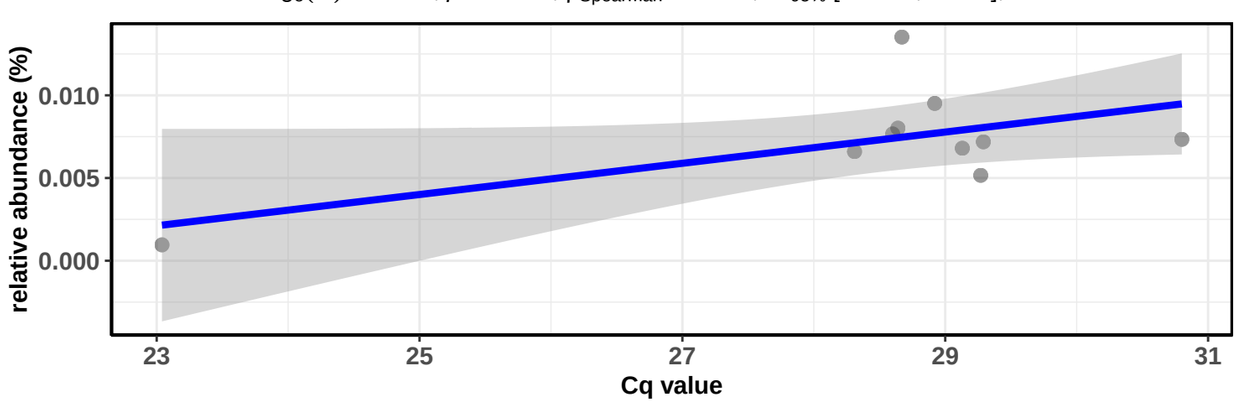
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 3.466, p = 0.872, $\rho_{Spearman}$ = 0.086, $CI_{95\%}$ [−0.780, 0.839], n = 6

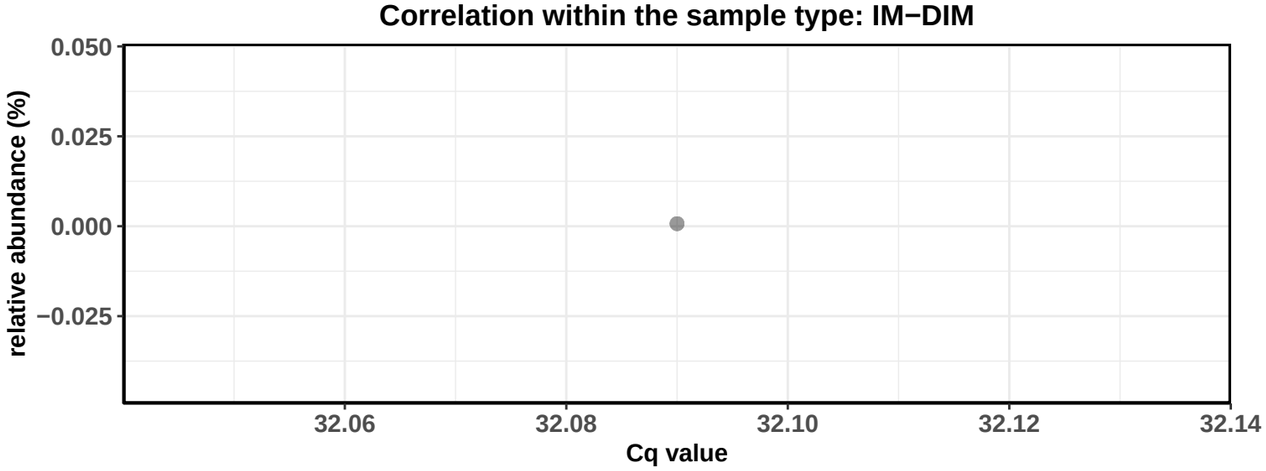


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 4.970, p = 0.726, $\rho_{Spearman}$ = 0.127, $CI_{95\%}$ [−0.546, 0.701], n = 10

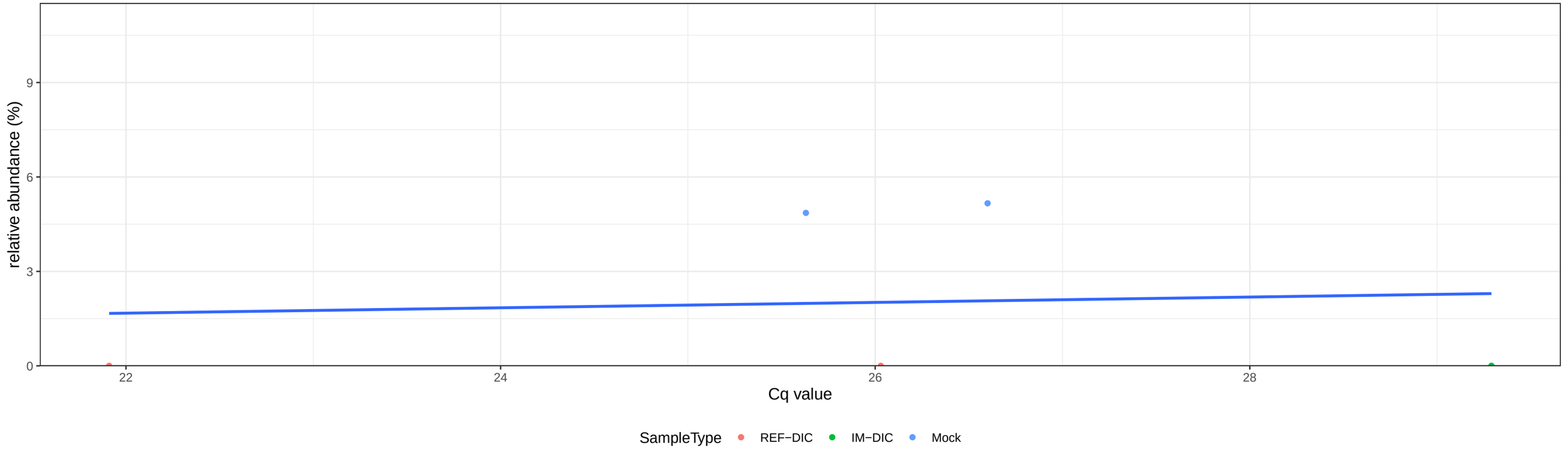


Correlation within the sample type: IM−DIM

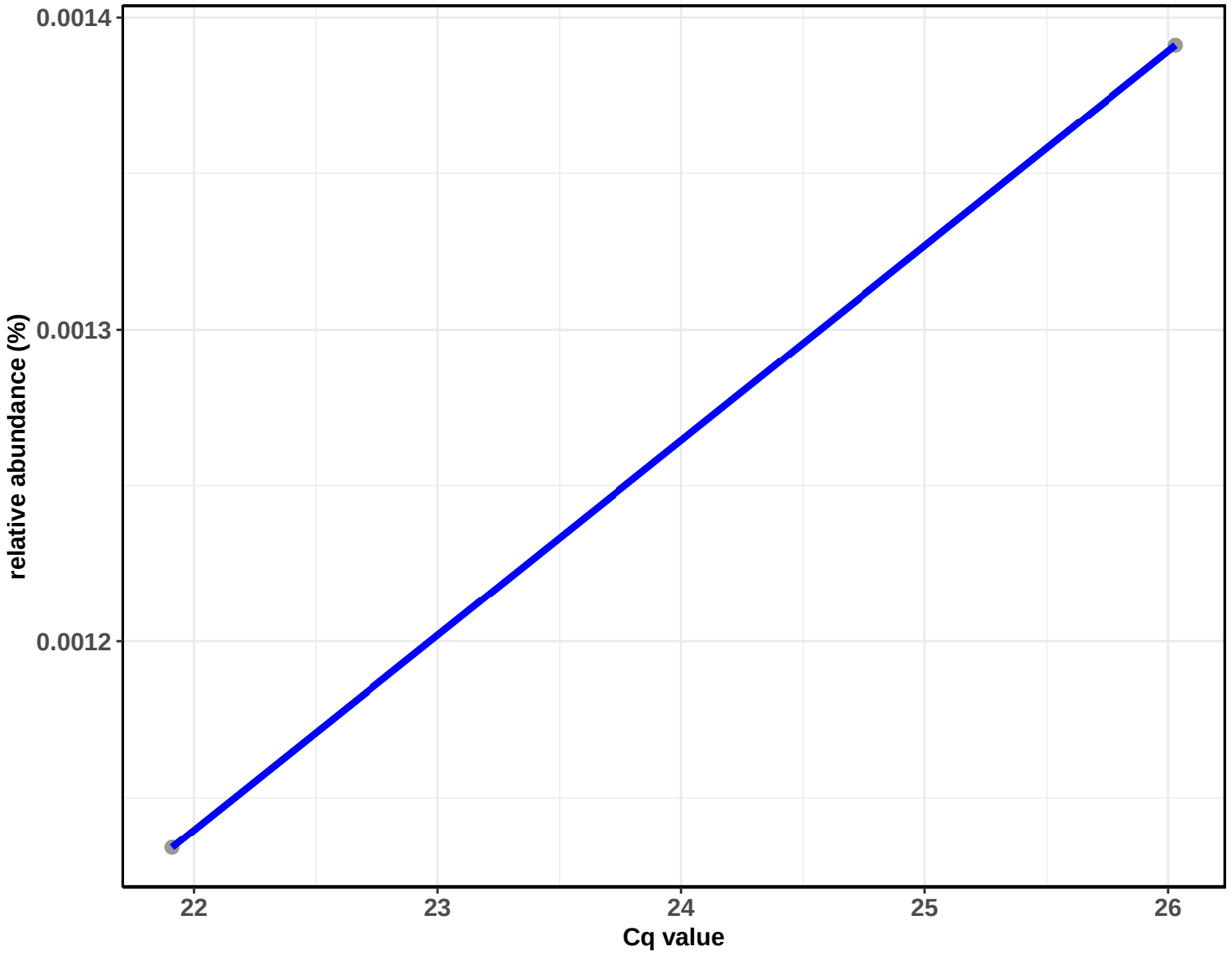


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

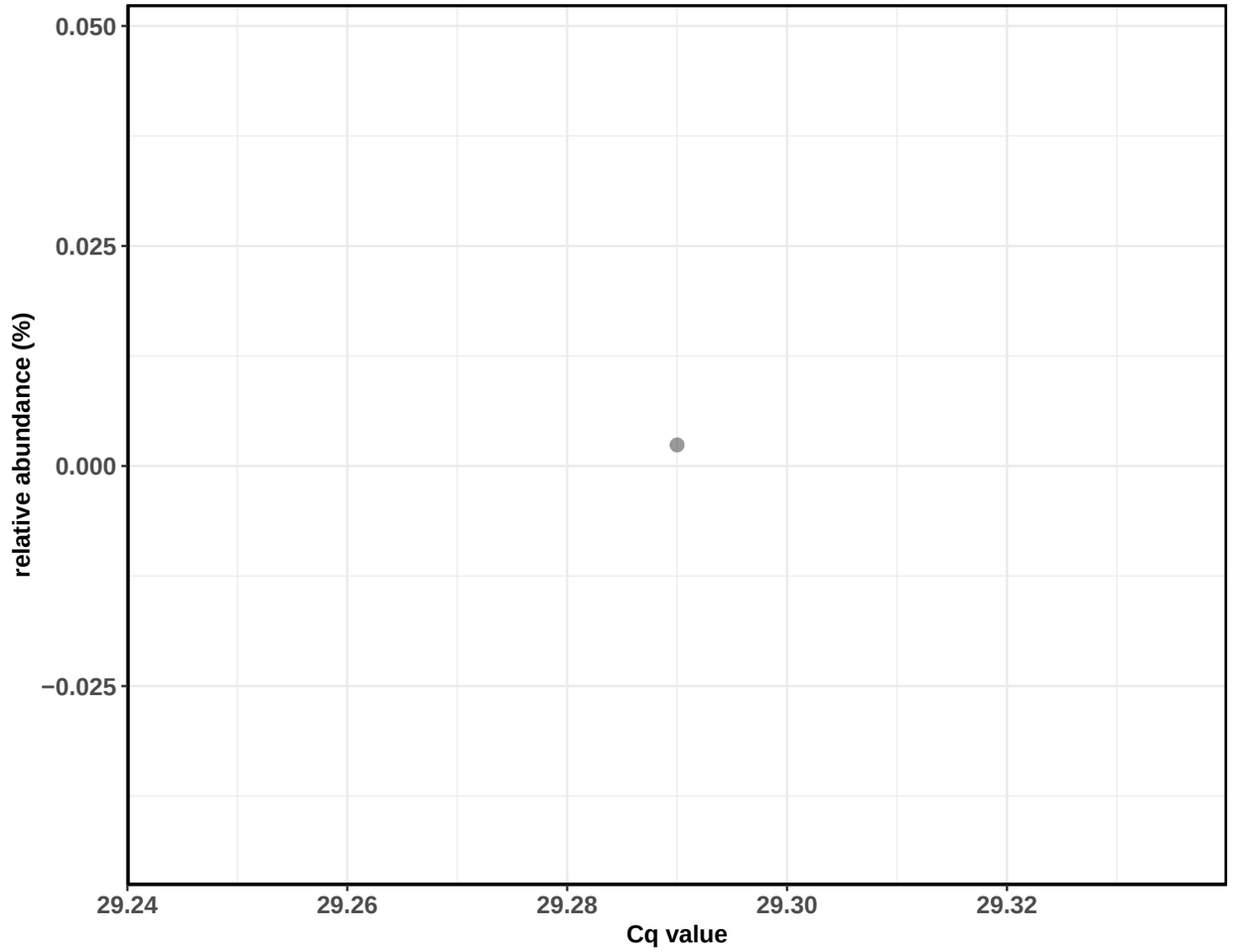
Correlation with all samples



Correlation within the sample type: REF−DIC

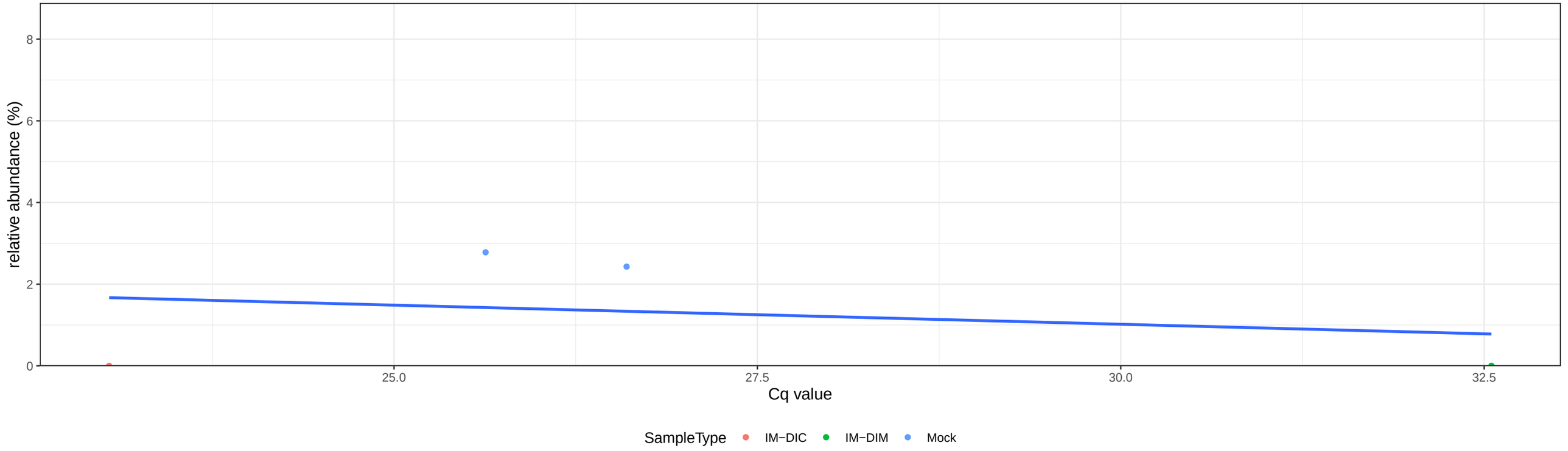


Correlation within the sample type: IM−DIC

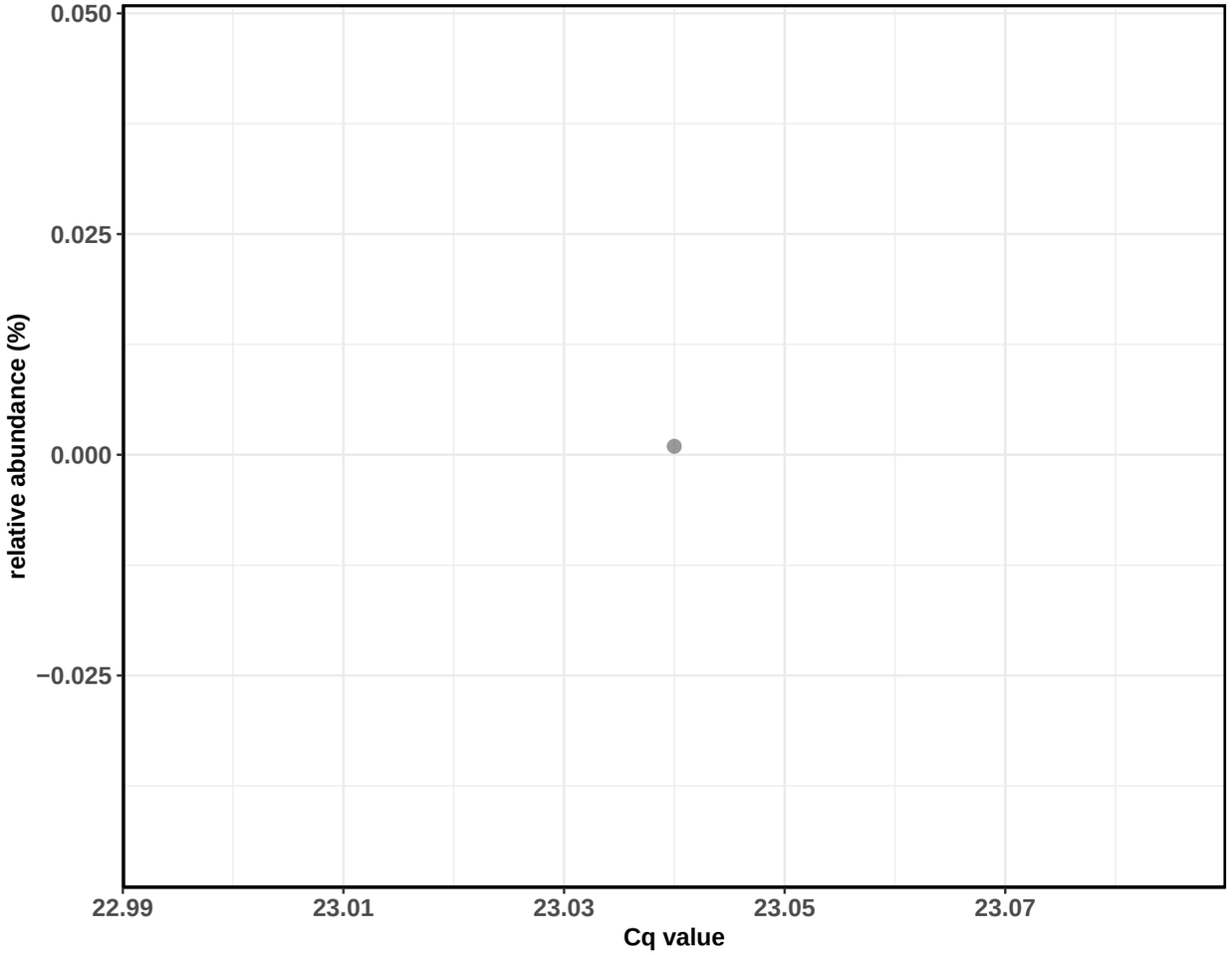


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Enterobacteriales; D_4__Enterobacteriaceae; D_5__Salmonella

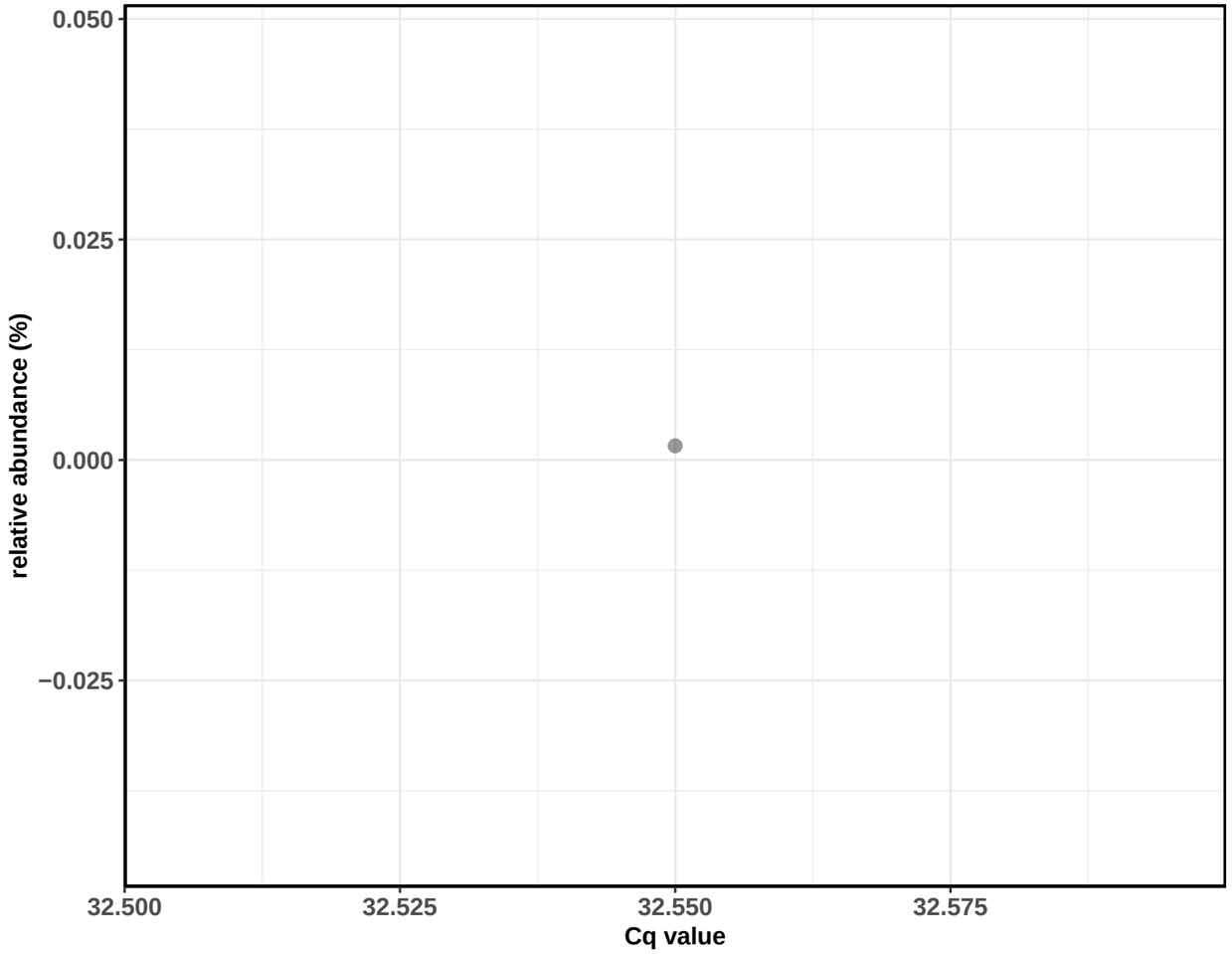
Correlation with all samples



Correlation within the sample type: IM−DIC

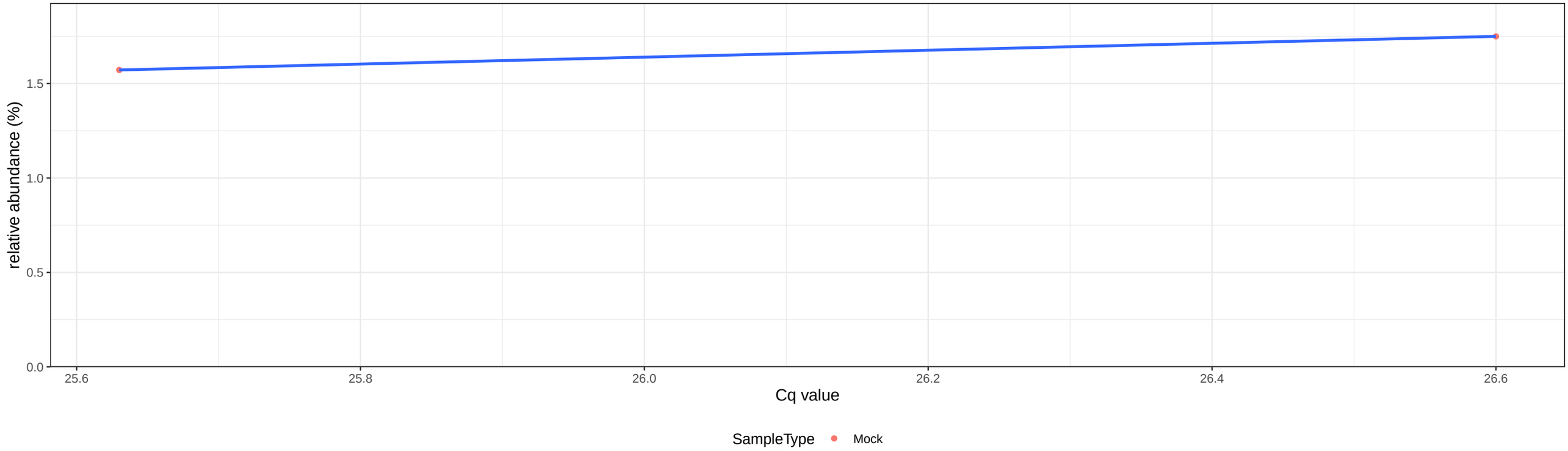


Correlation within the sample type: IM−DIM

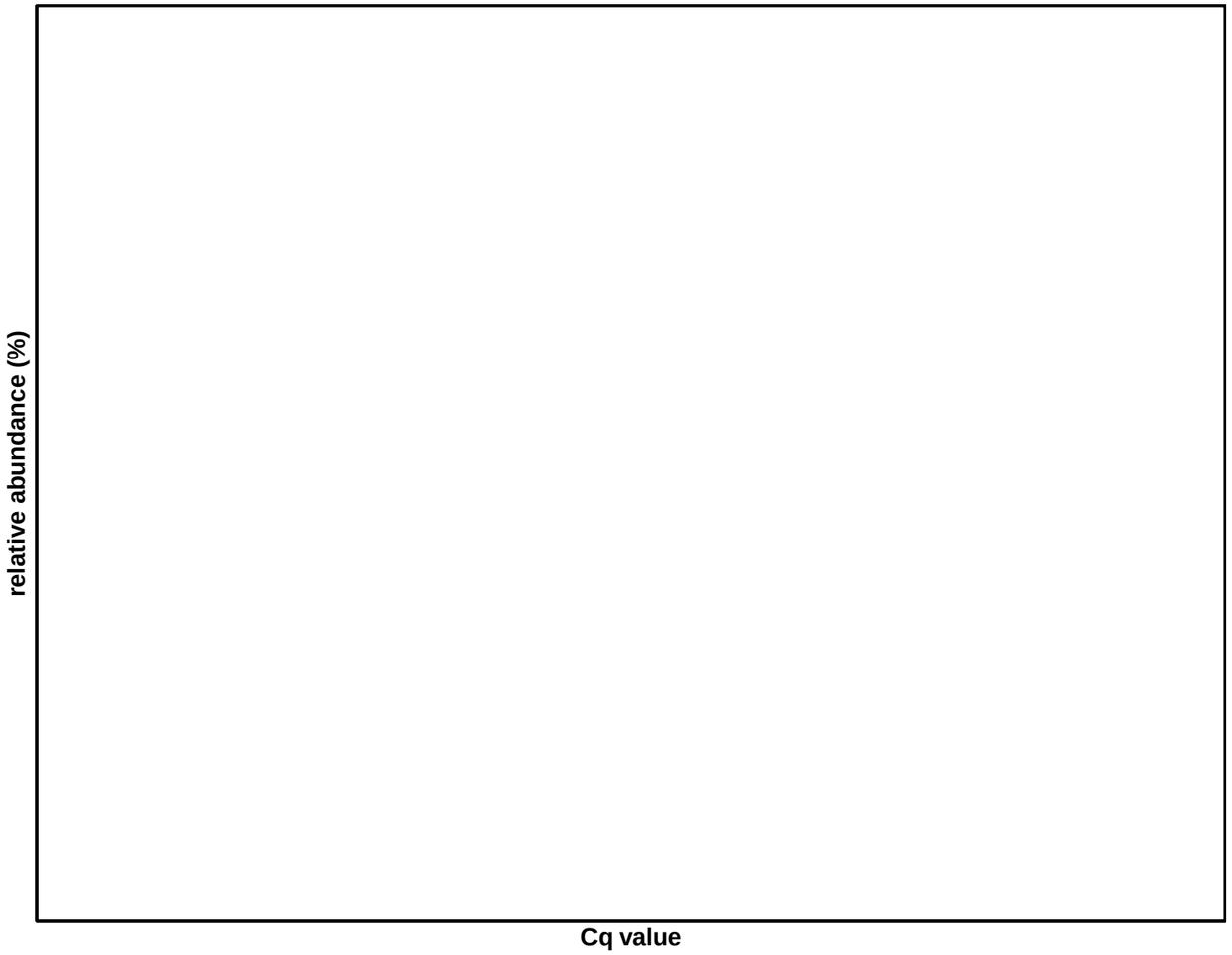


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Staphylococcaceae; D_5__Staphylococcus; D_6__Staphylococcus aureus

Correlation with all samples

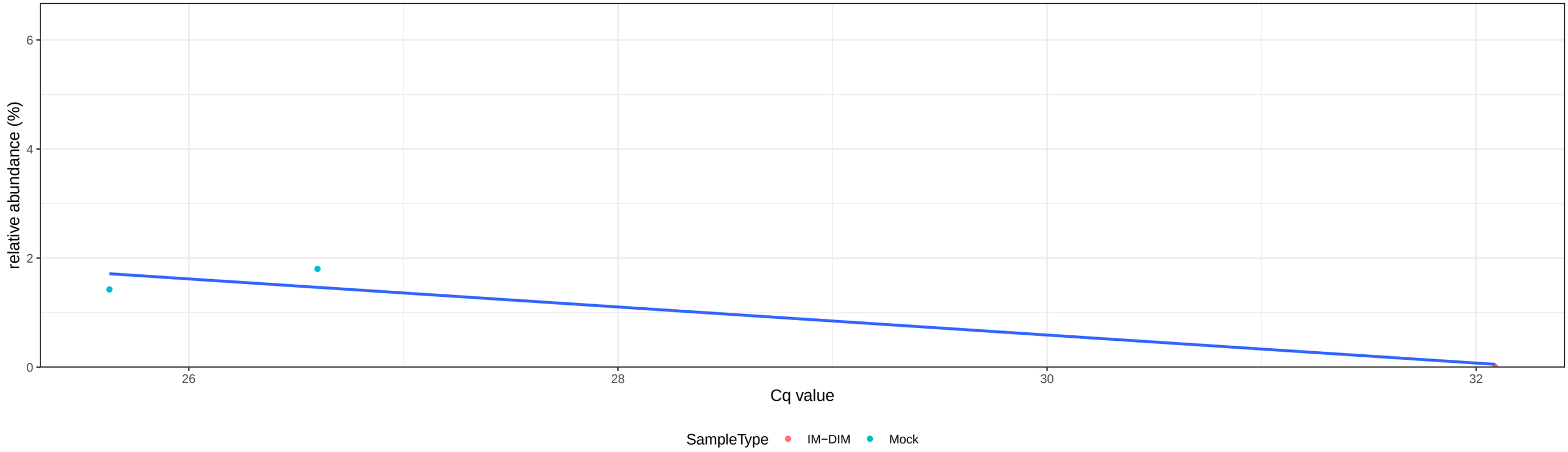


Correlation within the sample type:

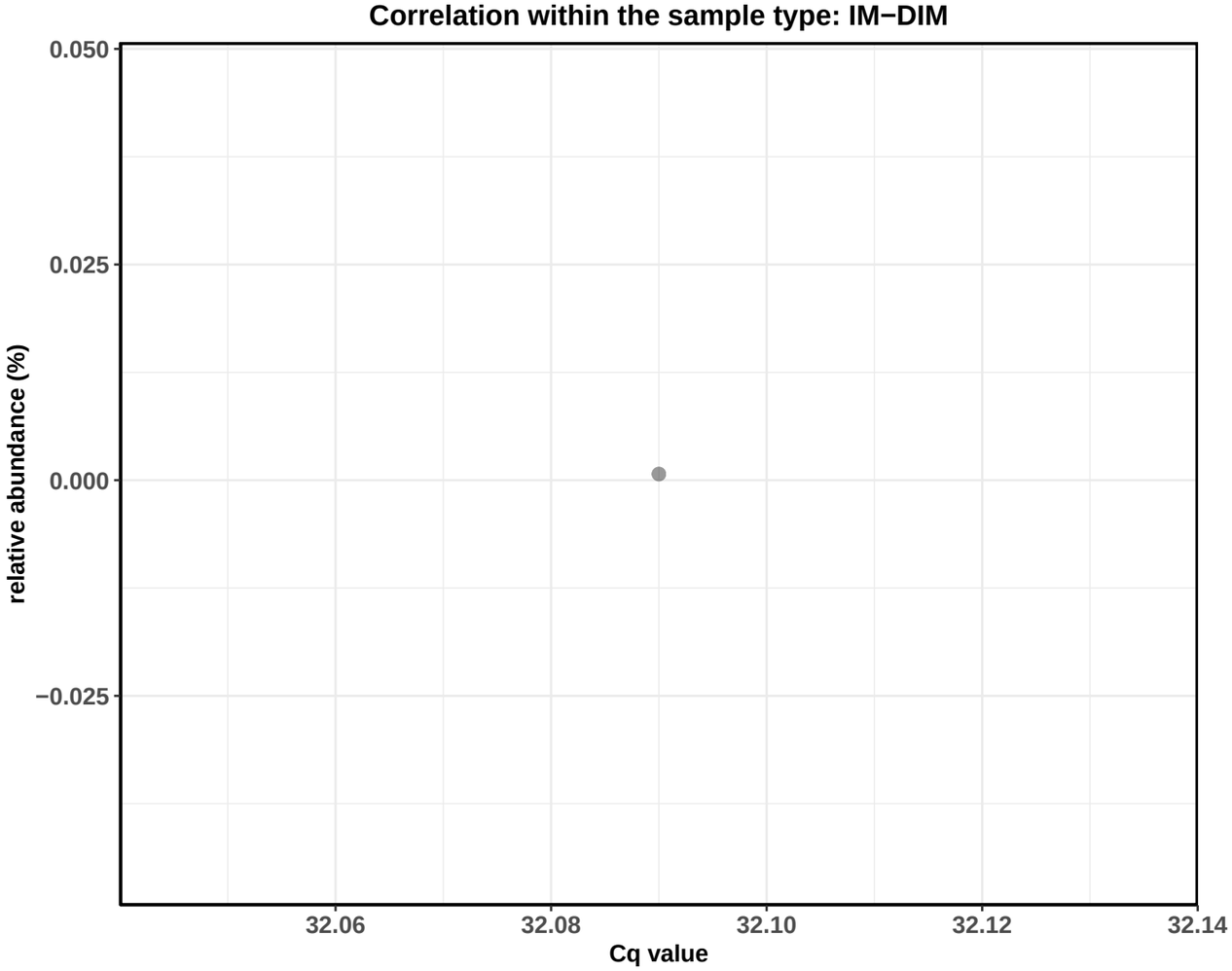


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Staphylococcaceae; D_5__Staphylococcus; D_6__Staphylococcus aureus

Correlation with all samples

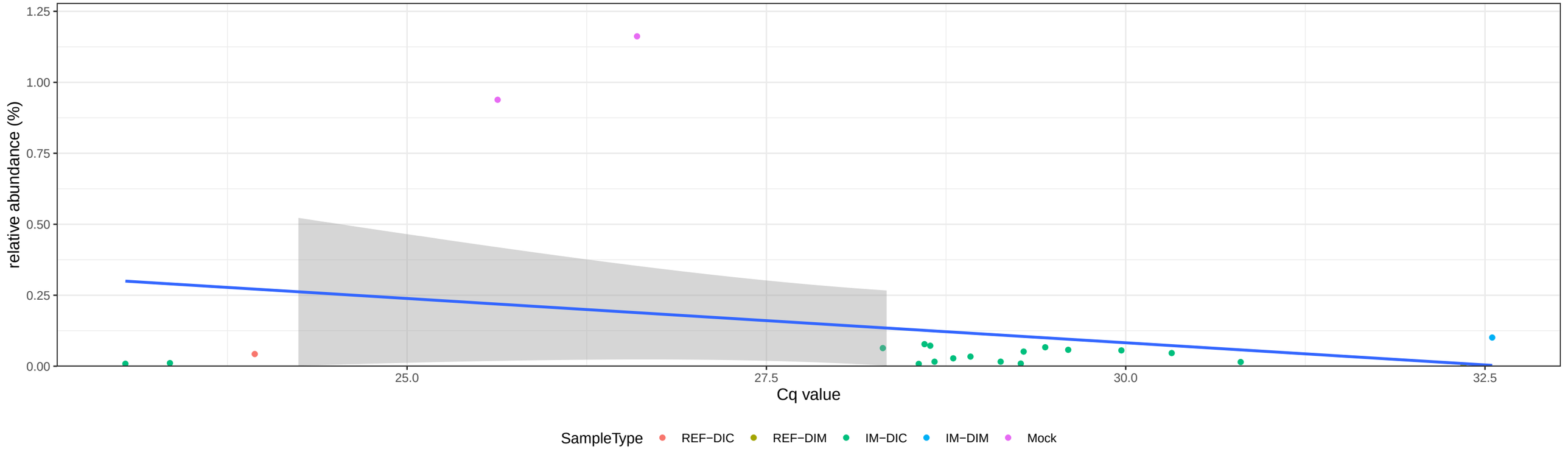


Correlation within the sample type: IM−DIM

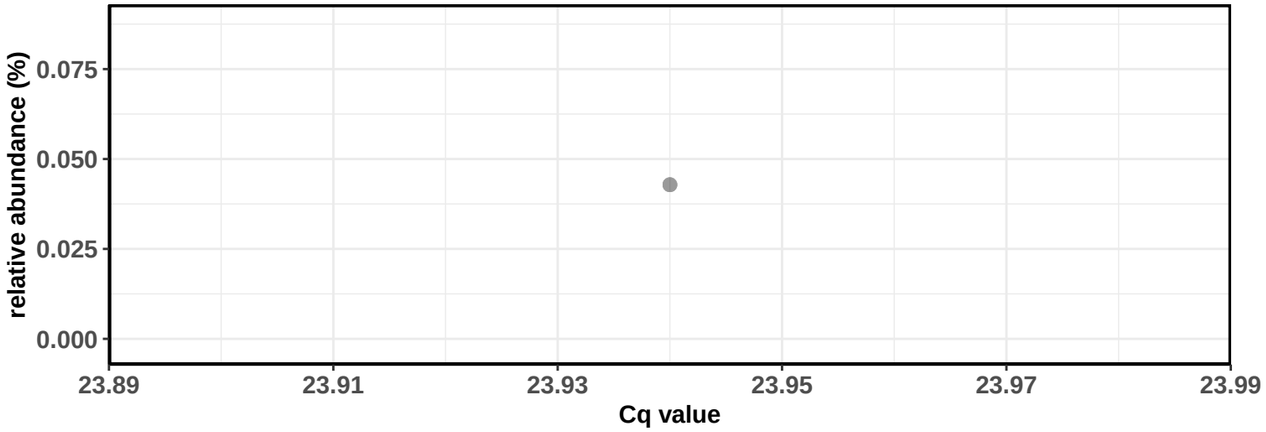


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Enterococcaceae; D_5__Enterococcus; D_6__Enterococcus faecalis

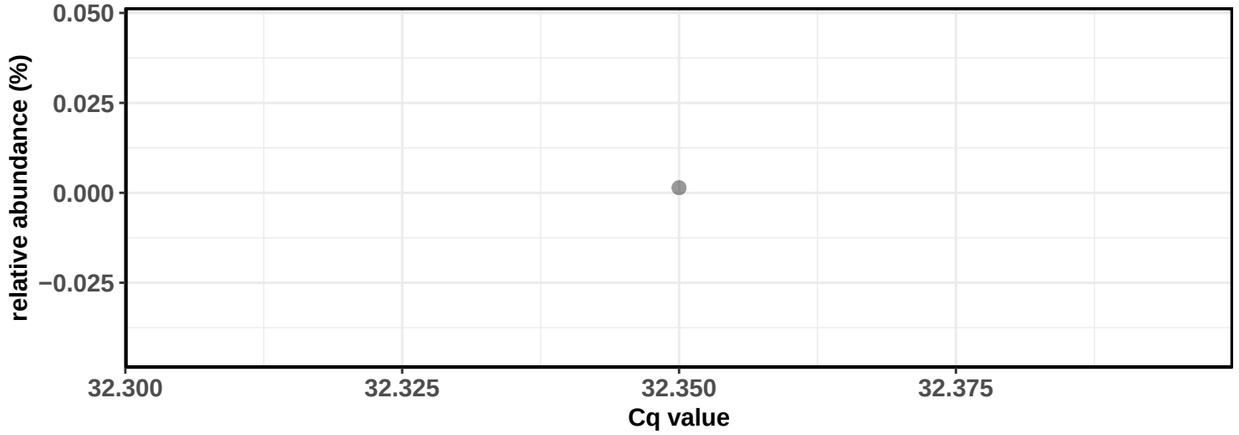
Correlation with all samples



Correlation within the sample type: REF−DIC

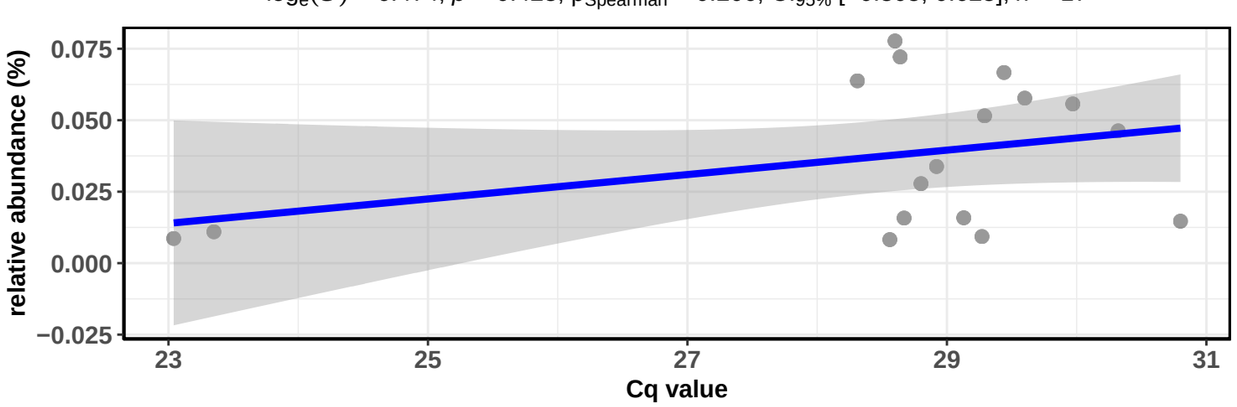


Correlation within the sample type: REF−DIM

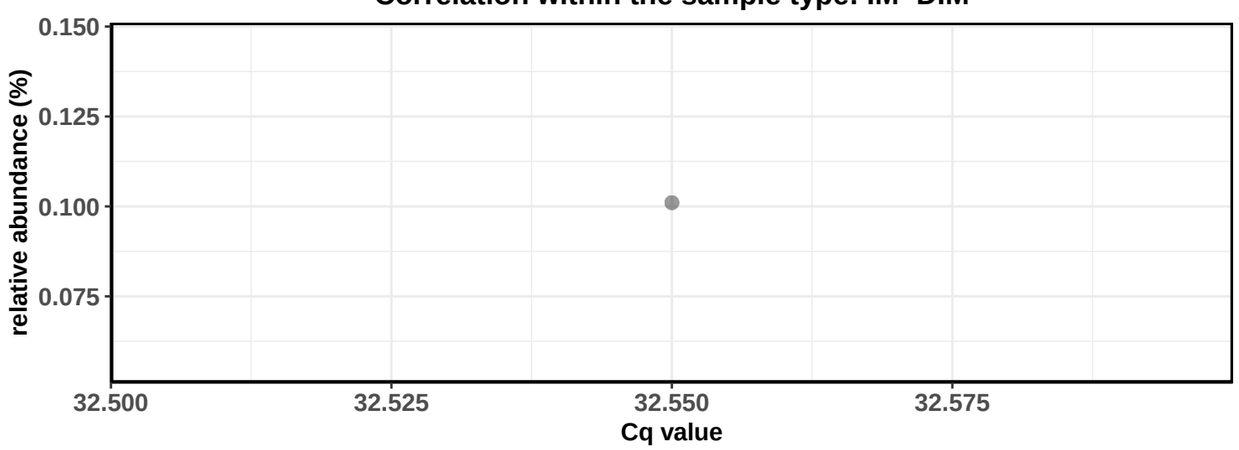


Correlation within the sample type: IM−DIC

$\log_e(S) = 6.474$, $p = 0.428$, $\rho_{Spearman} = 0.206$, $CI_{95\%}$ [−0.305, 0.625], $n = 17$

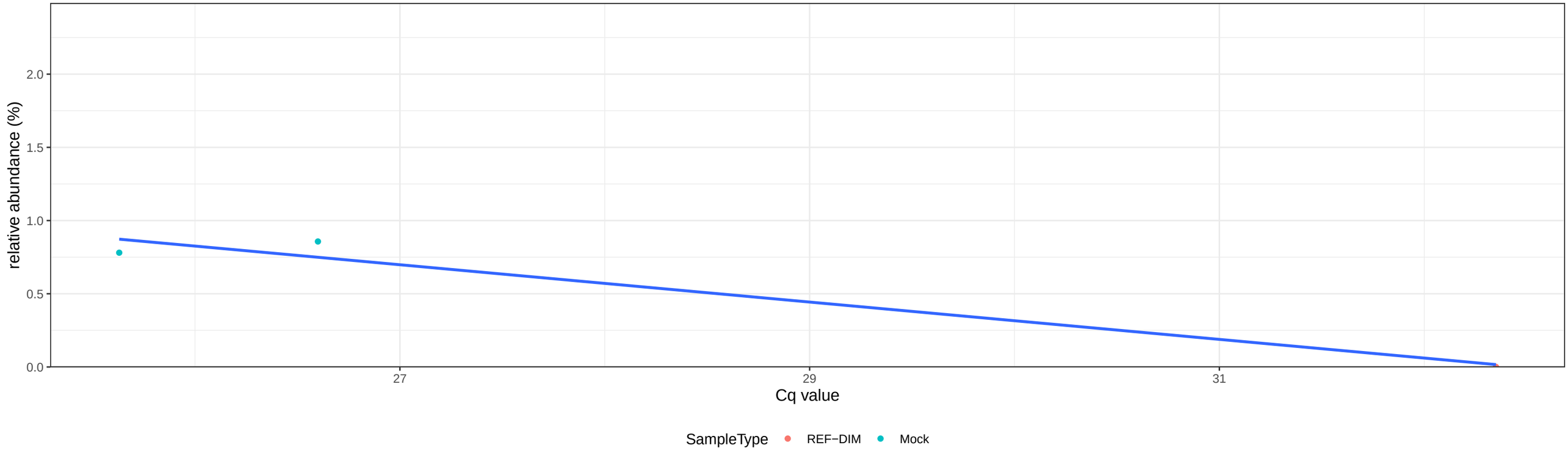


Correlation within the sample type: IM−DIM

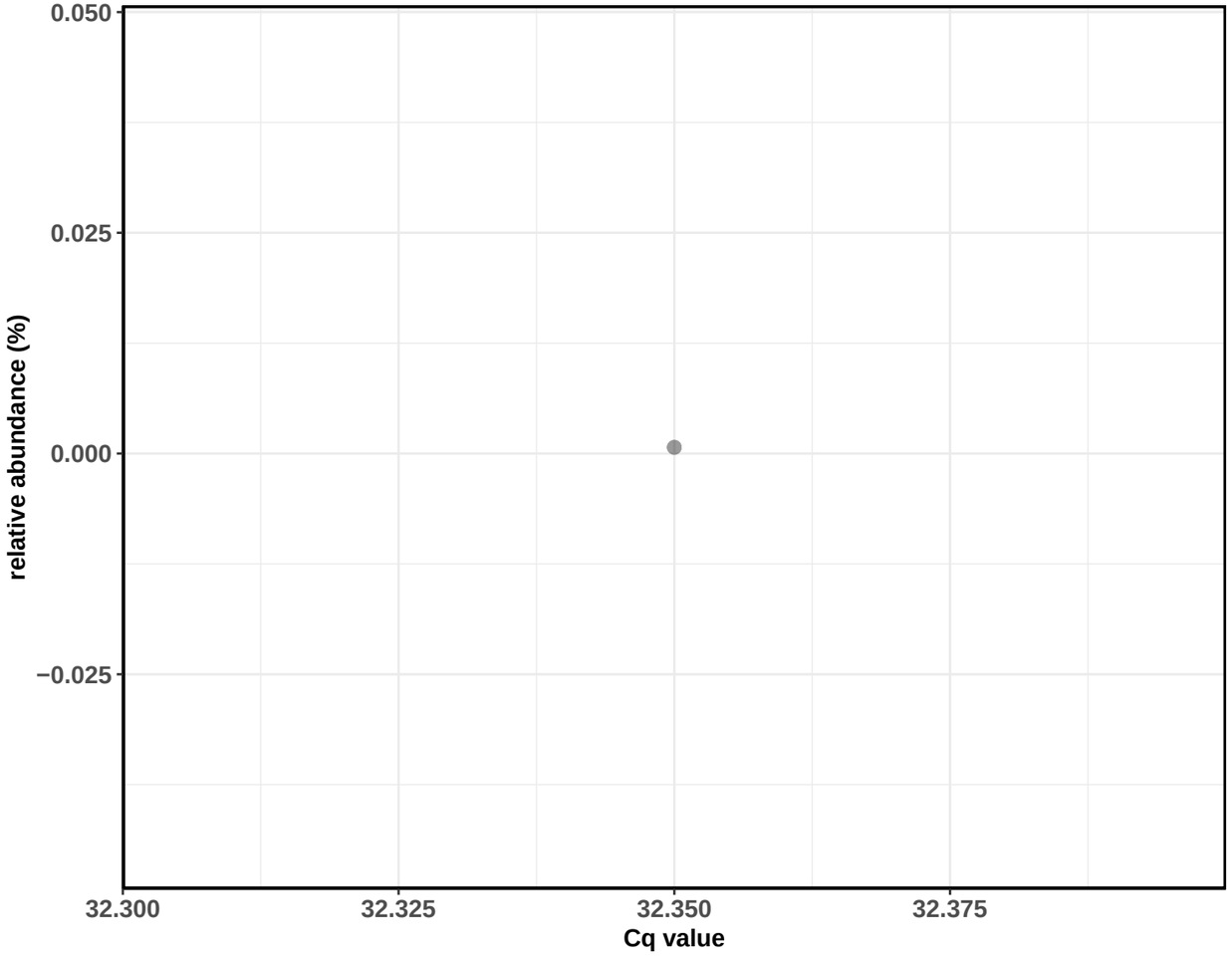


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Listeriaceae; D_5__Listeria; D_6__Listeria monocytogenes

Correlation with all samples

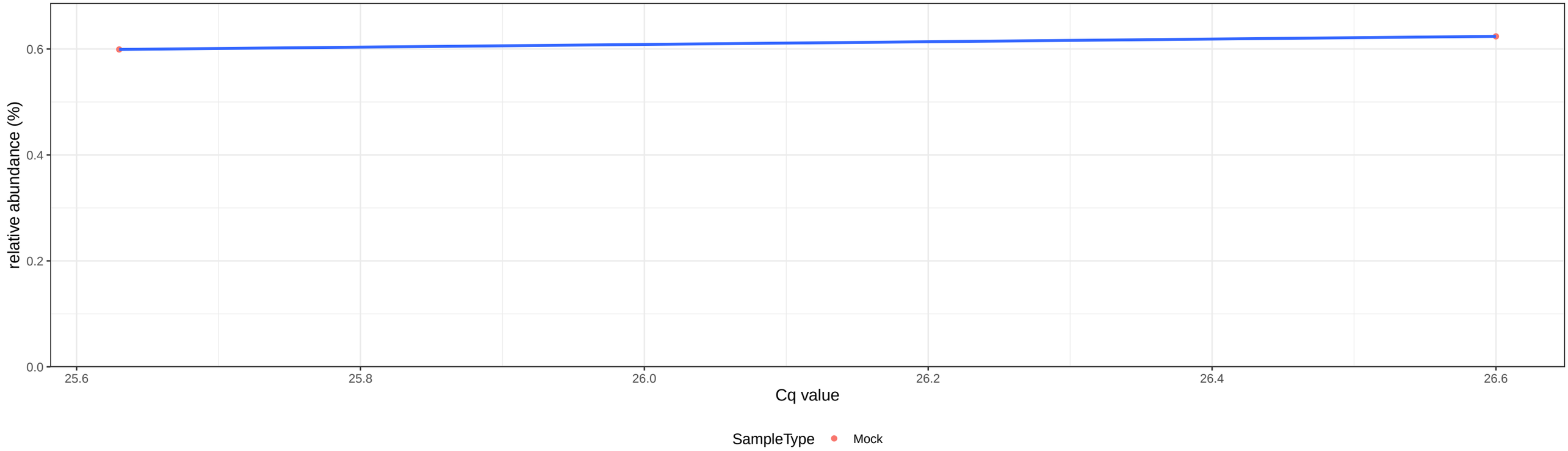


Correlation within the sample type: REF−DIM

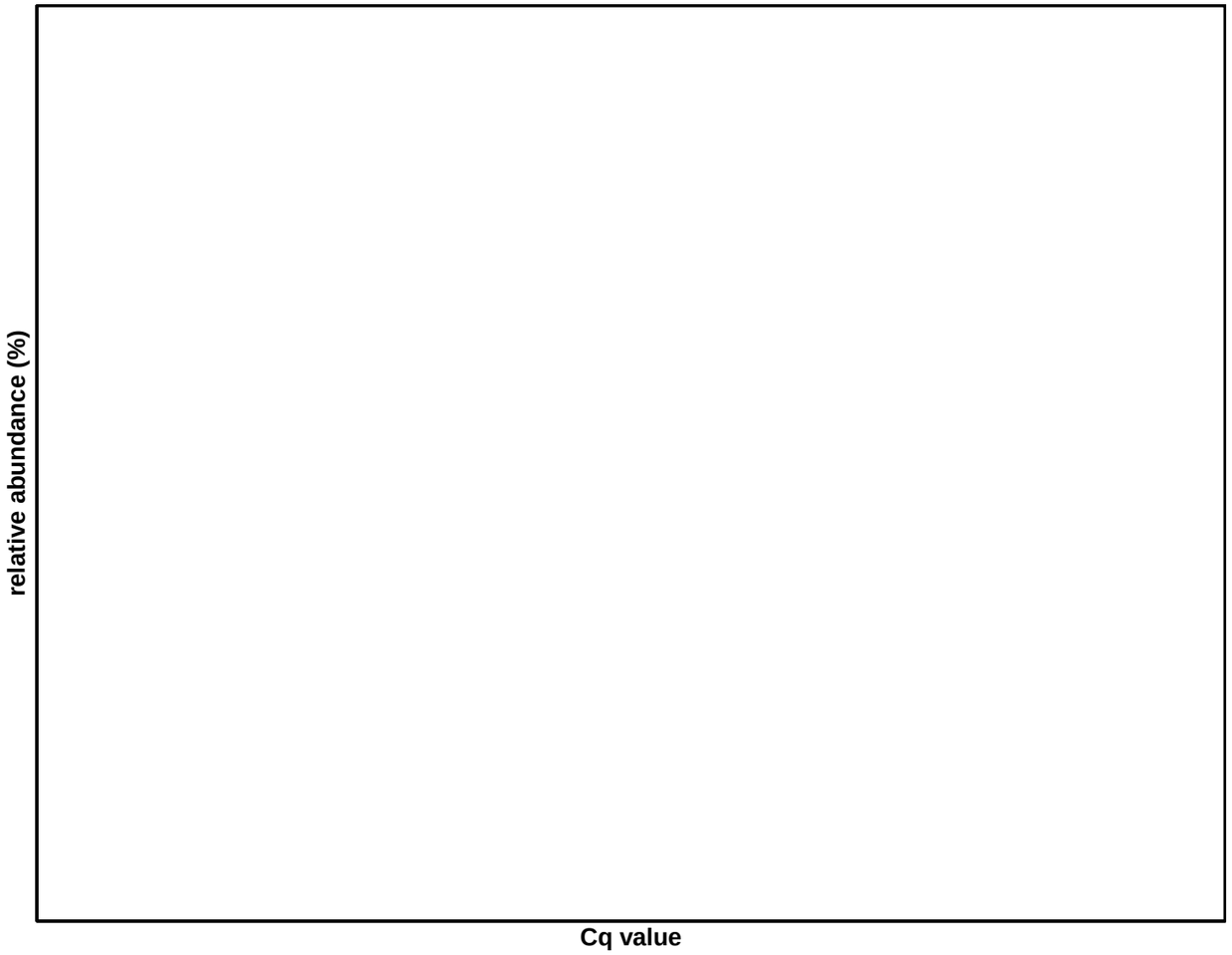


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Enterococcaceae; D_5__Enterococcus; D_6__Enterococcus faecalis

Correlation with all samples

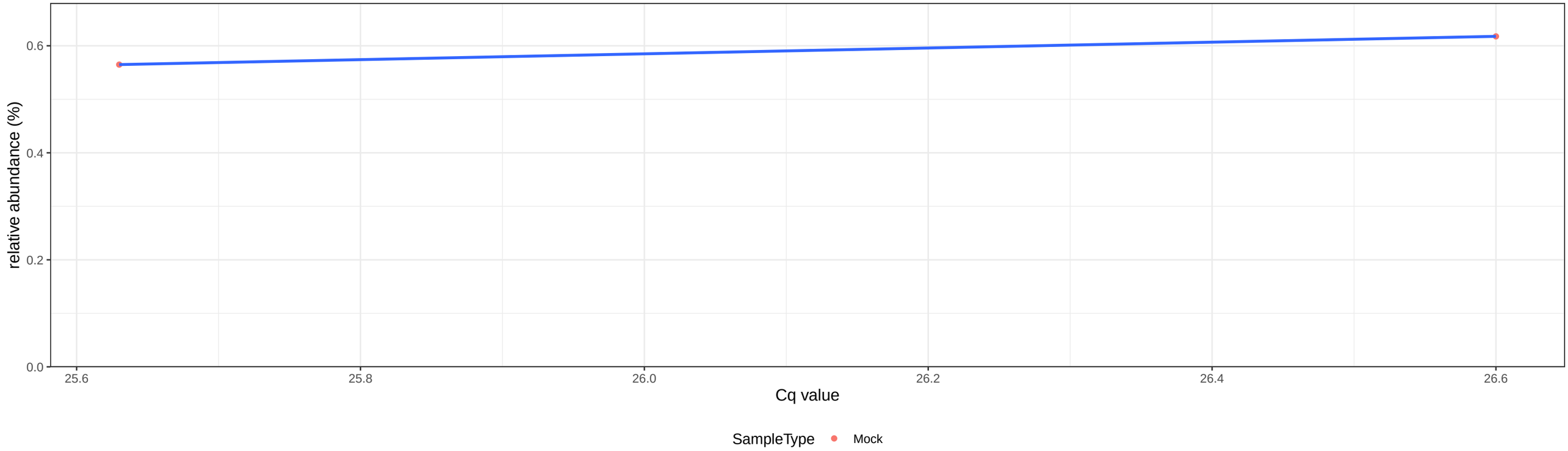


Correlation within the sample type:

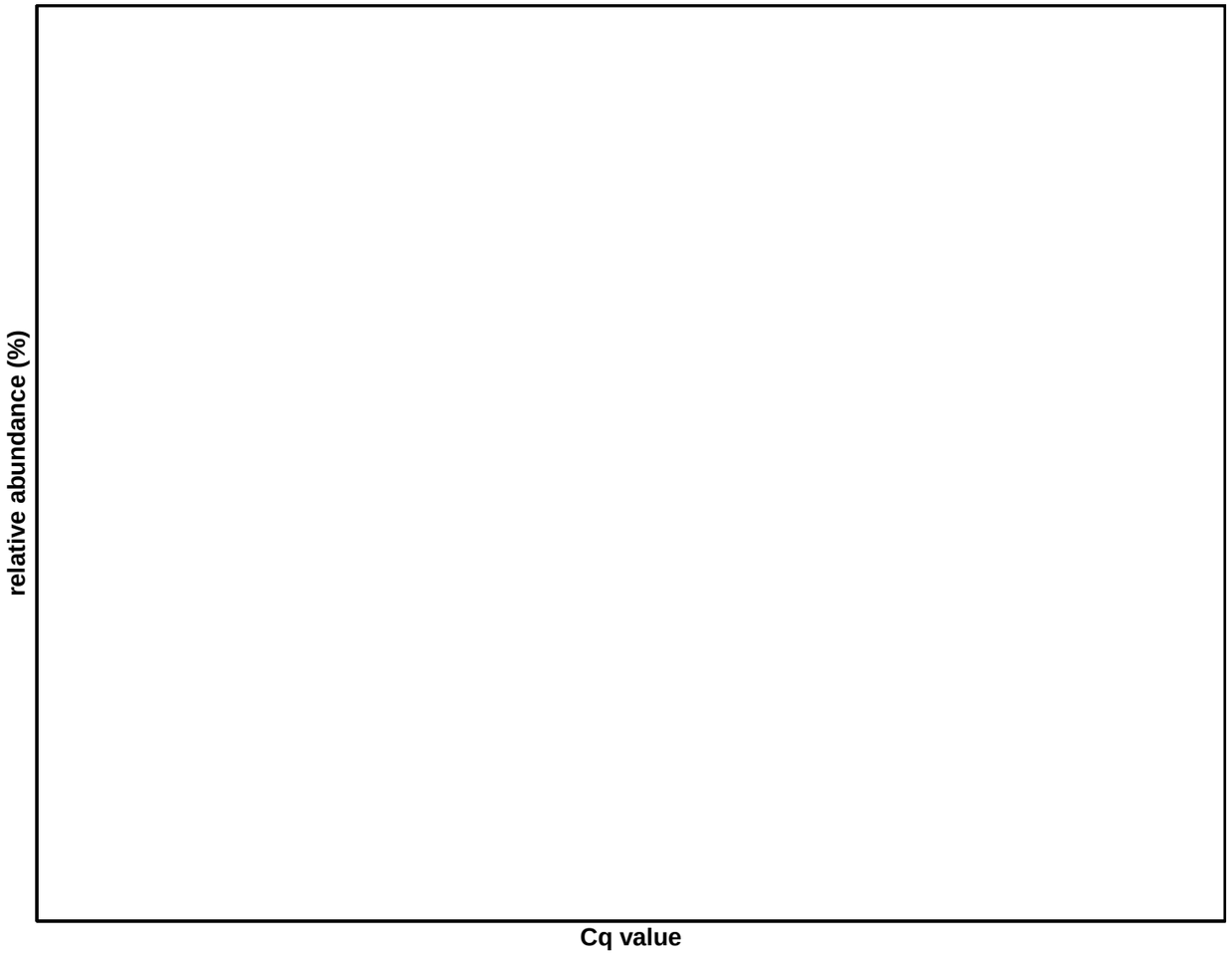


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Listeriaceae; D_5__Listeria; D_6__Listeria monocytogenes

Correlation with all samples

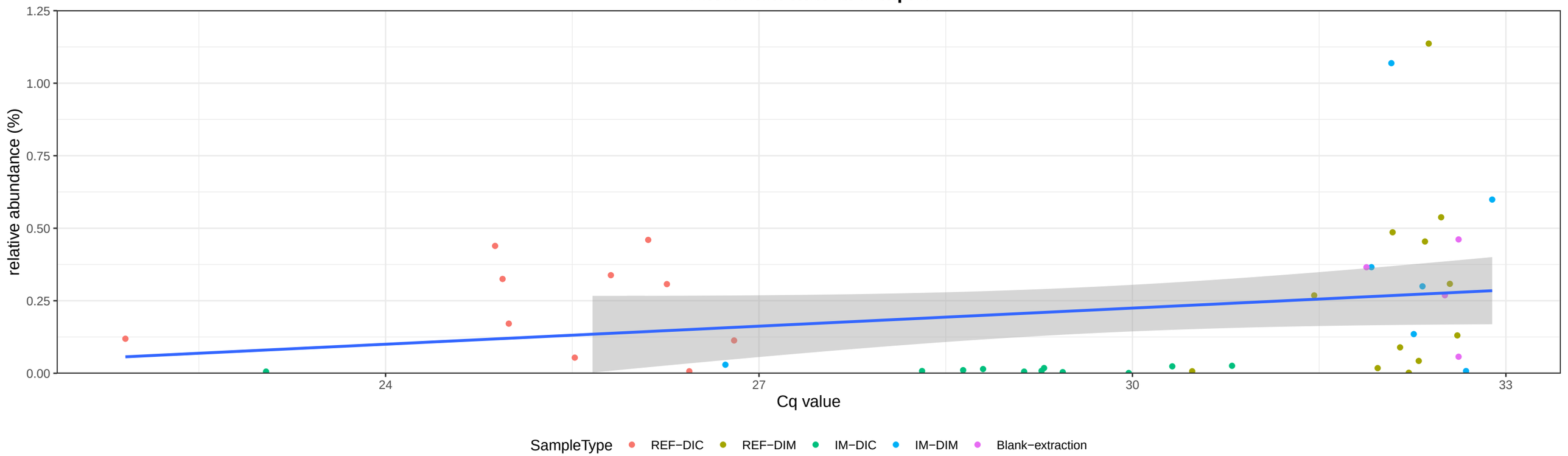


Correlation within the sample type:



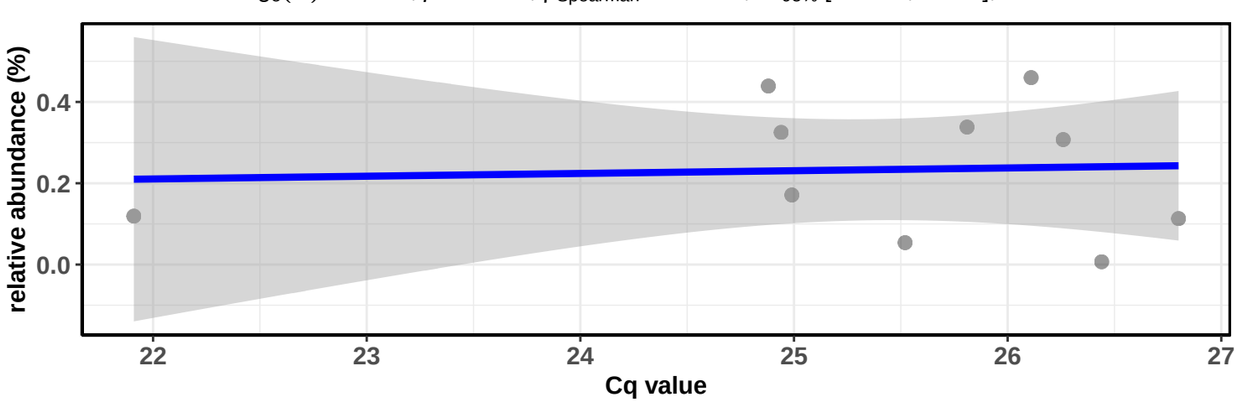
D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Propionibacteriales; D_4__Propionibacteriaceae; D_5__Cutibacterium

Correlation with all samples



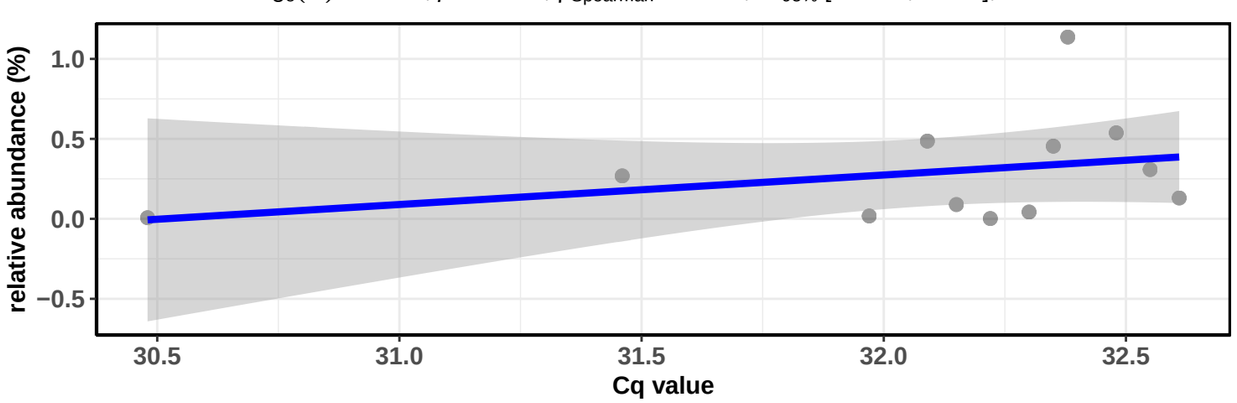
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.366, p = 0.405, $\rho_{Spearman}$ = −0.297, $CI_{95\%}$ [−0.781, 0.409], n = 10



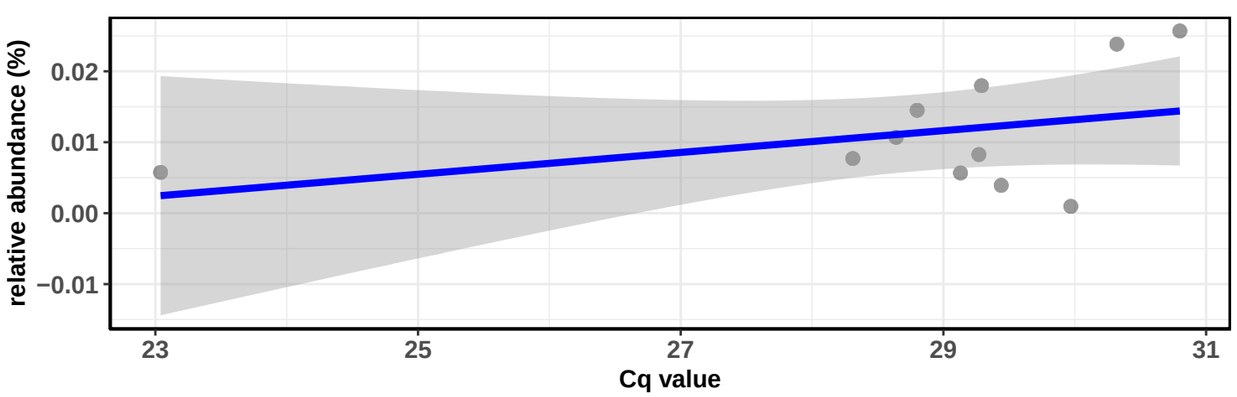
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.024, p = 0.124, $\rho_{Spearman}$ = 0.469, $CI_{95\%}$ [−0.144, 0.822], n = 12



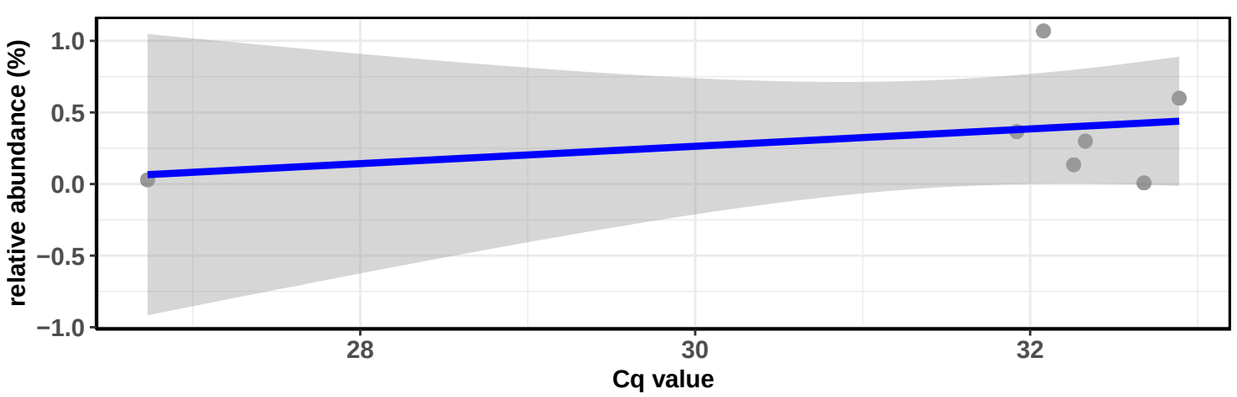
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.063, p = 0.401, $\rho_{Spearman}$ = 0.282, $CI_{95\%}$ [−0.383, 0.754], n = 11



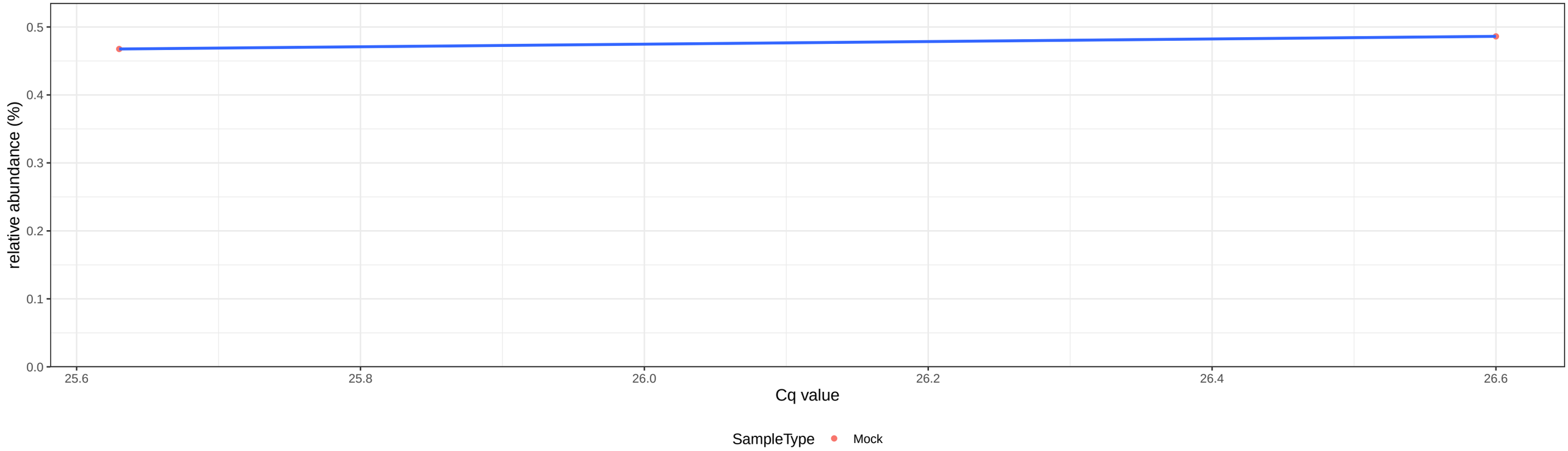
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 3.989, p = 0.939, $\rho_{Spearman}$ = 0.036, $CI_{95\%}$ [−0.737, 0.768], n = 7

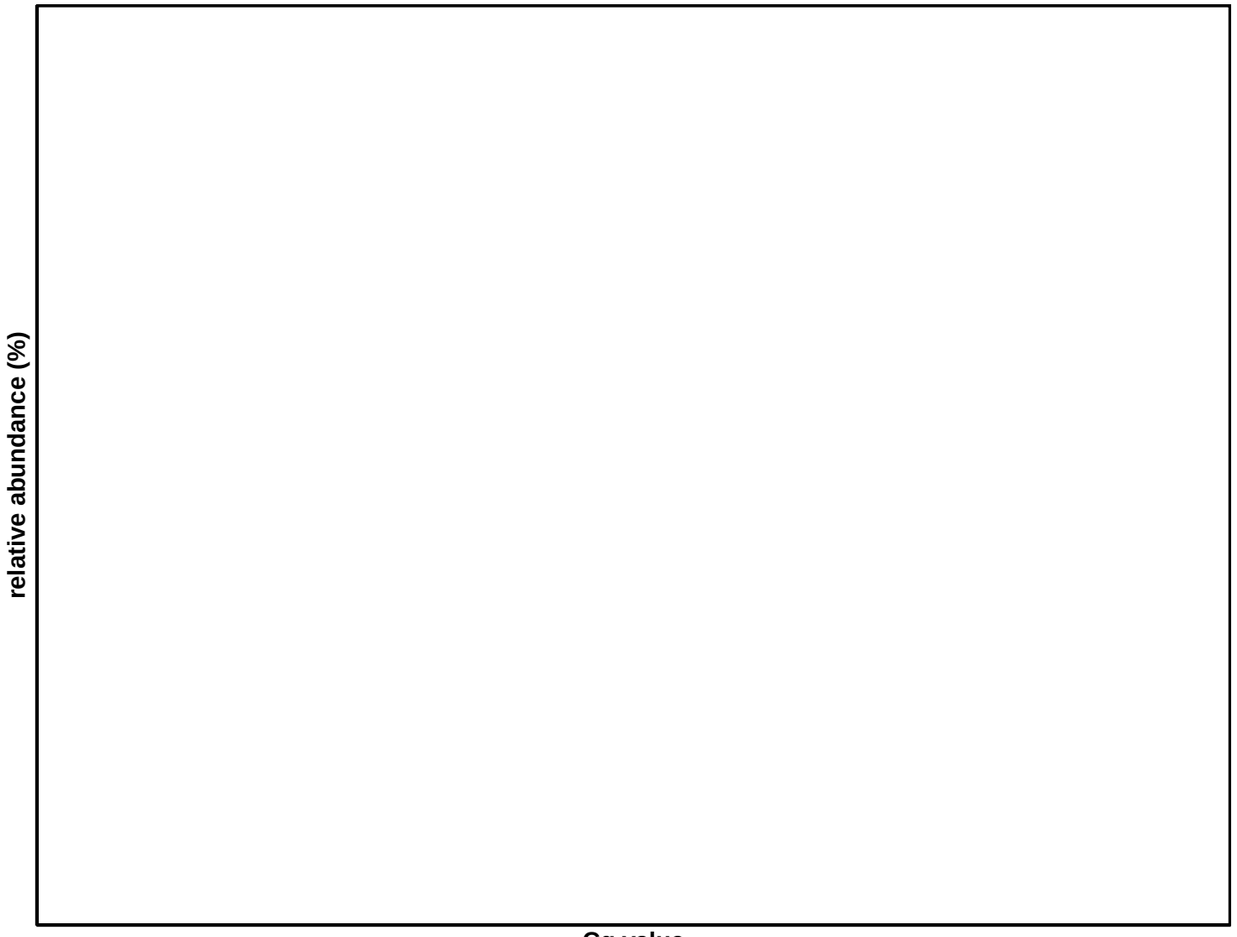


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Enterococcaceae; D_5__Enterococcus; D_6__Enterococcus faecalis

Correlation with all samples

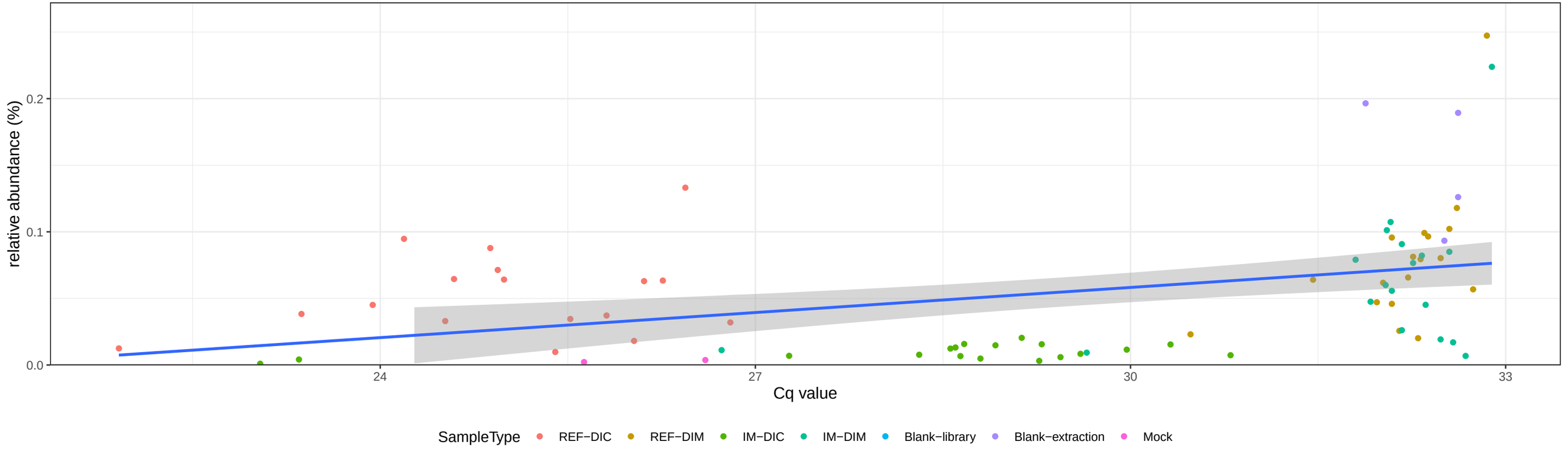


Correlation within the sample type:



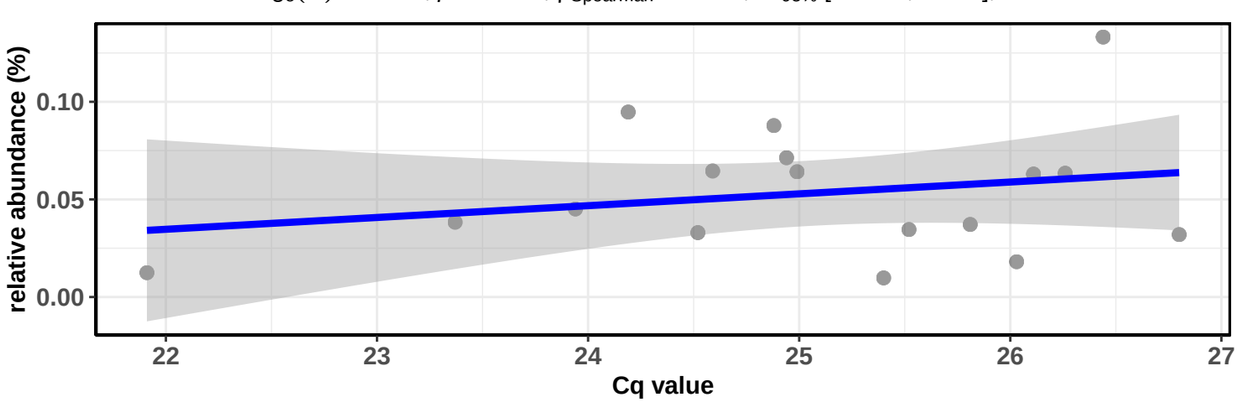
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



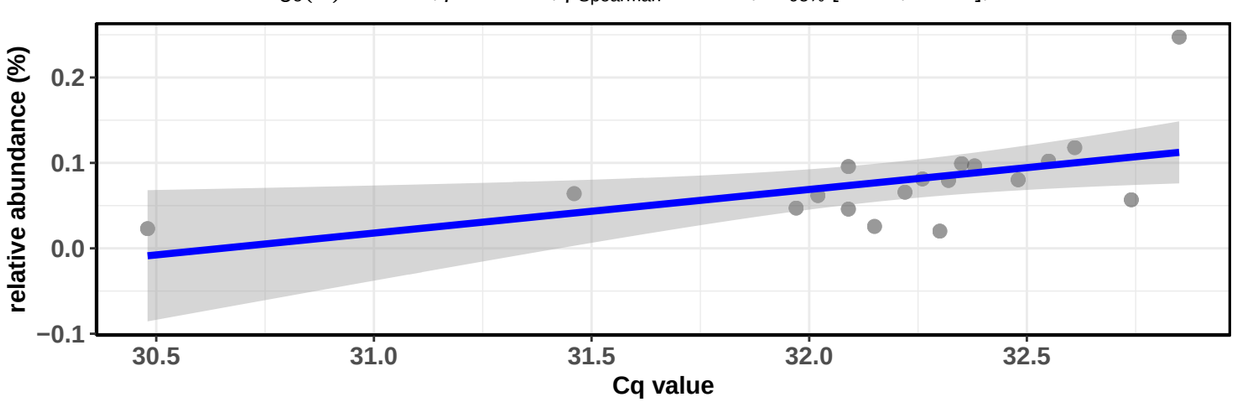
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.695, p = 0.970, $\rho_{Spearman}$ = 0.010, $CI_{95\%}$ [−0.473, 0.488], n = 17



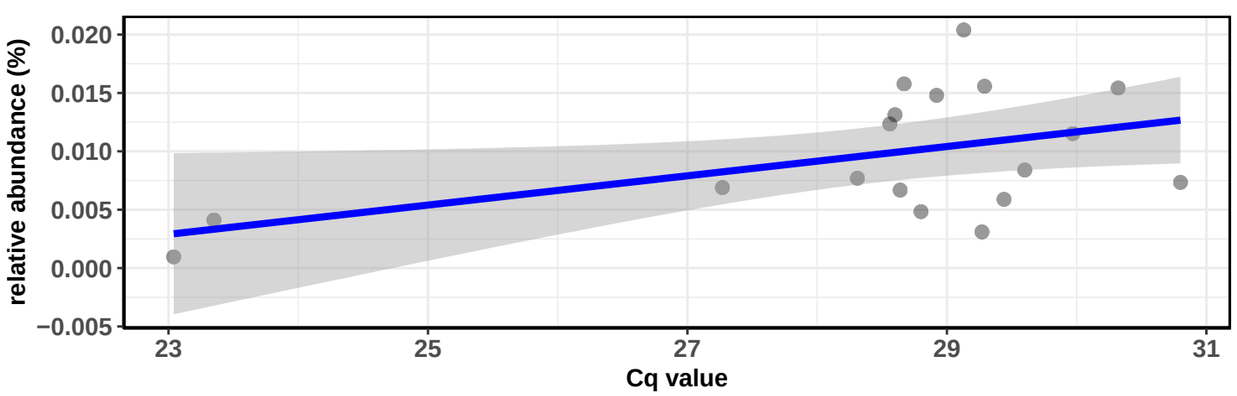
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.882, p = 0.005, $\rho_{Spearman}$ = 0.630, $CI_{95\%}$ [0.231, 0.847], n = 18



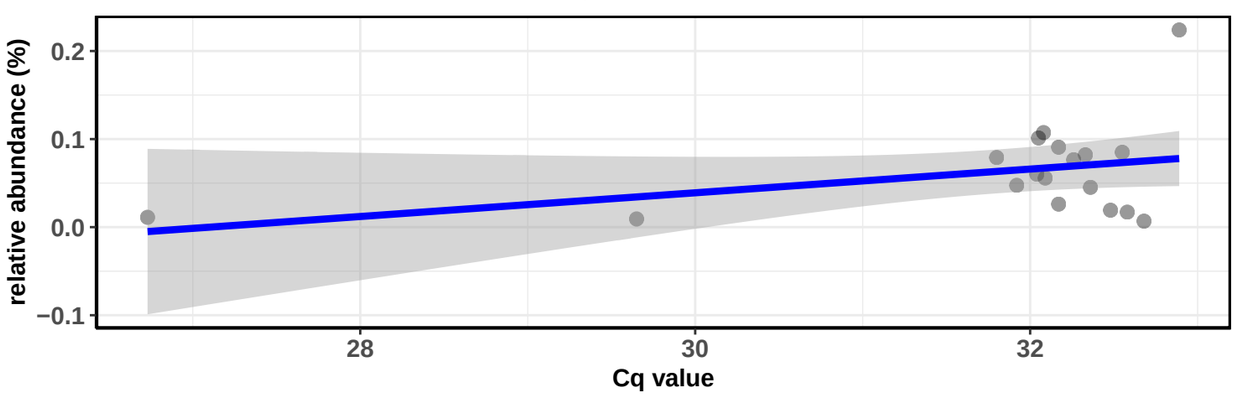
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.486, p = 0.191, $\rho_{Spearman}$ = 0.323, $CI_{95\%}$ [−0.169, 0.686], n = 18



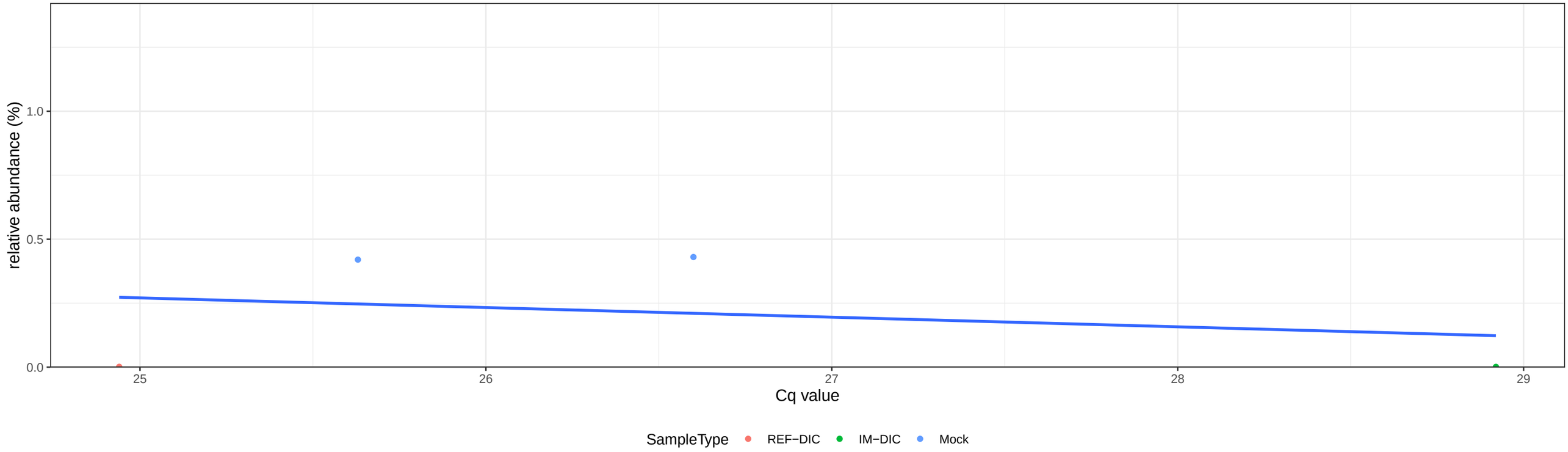
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.790, p = 0.745, $\rho_{Spearman}$ = 0.083, $CI_{95\%}$ [−0.400, 0.529], n = 18

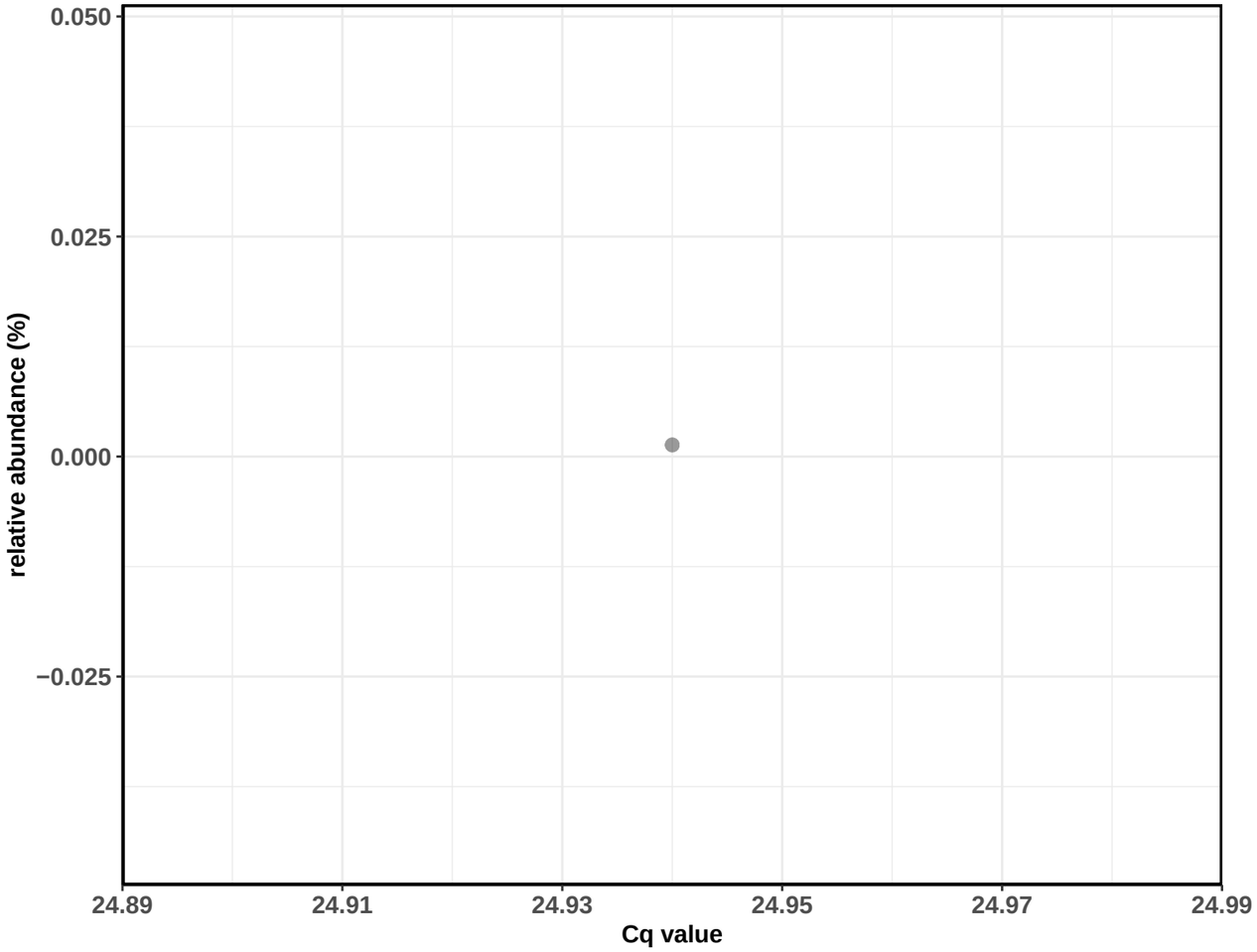


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

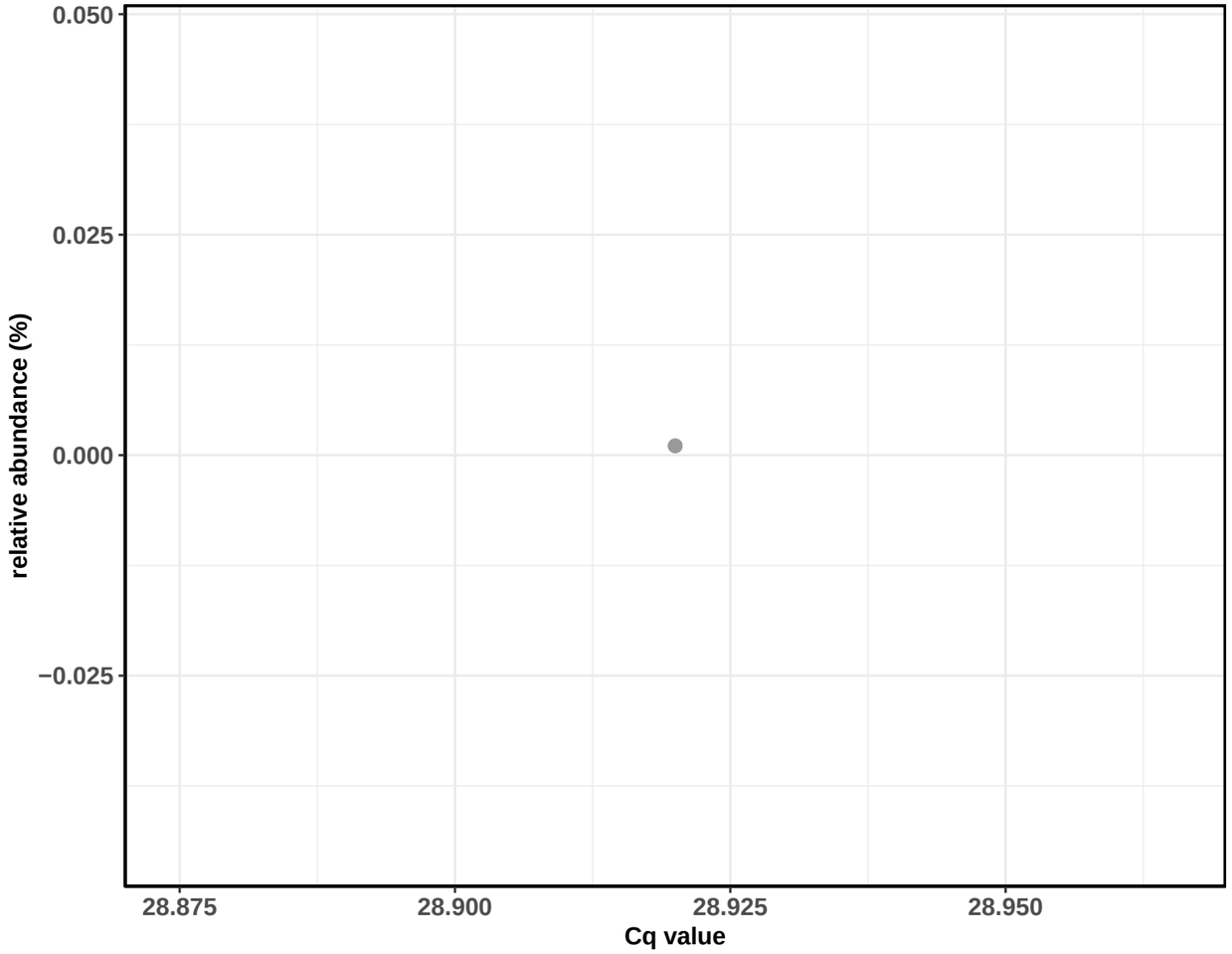
Correlation with all samples



Correlation within the sample type: REF−DIC

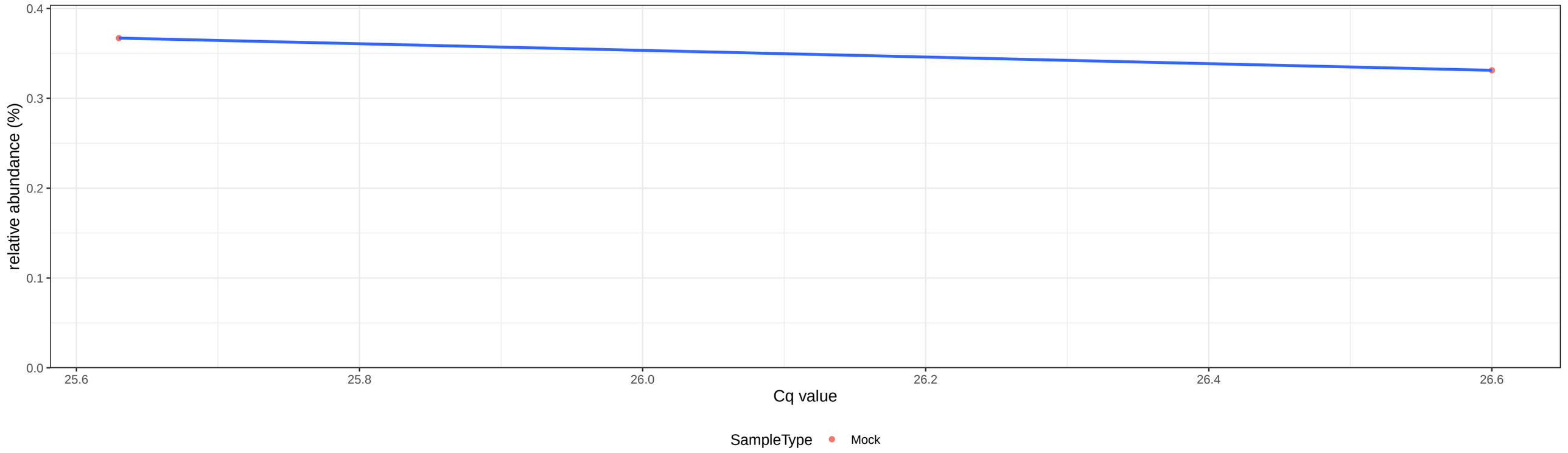


Correlation within the sample type: IM−DIC

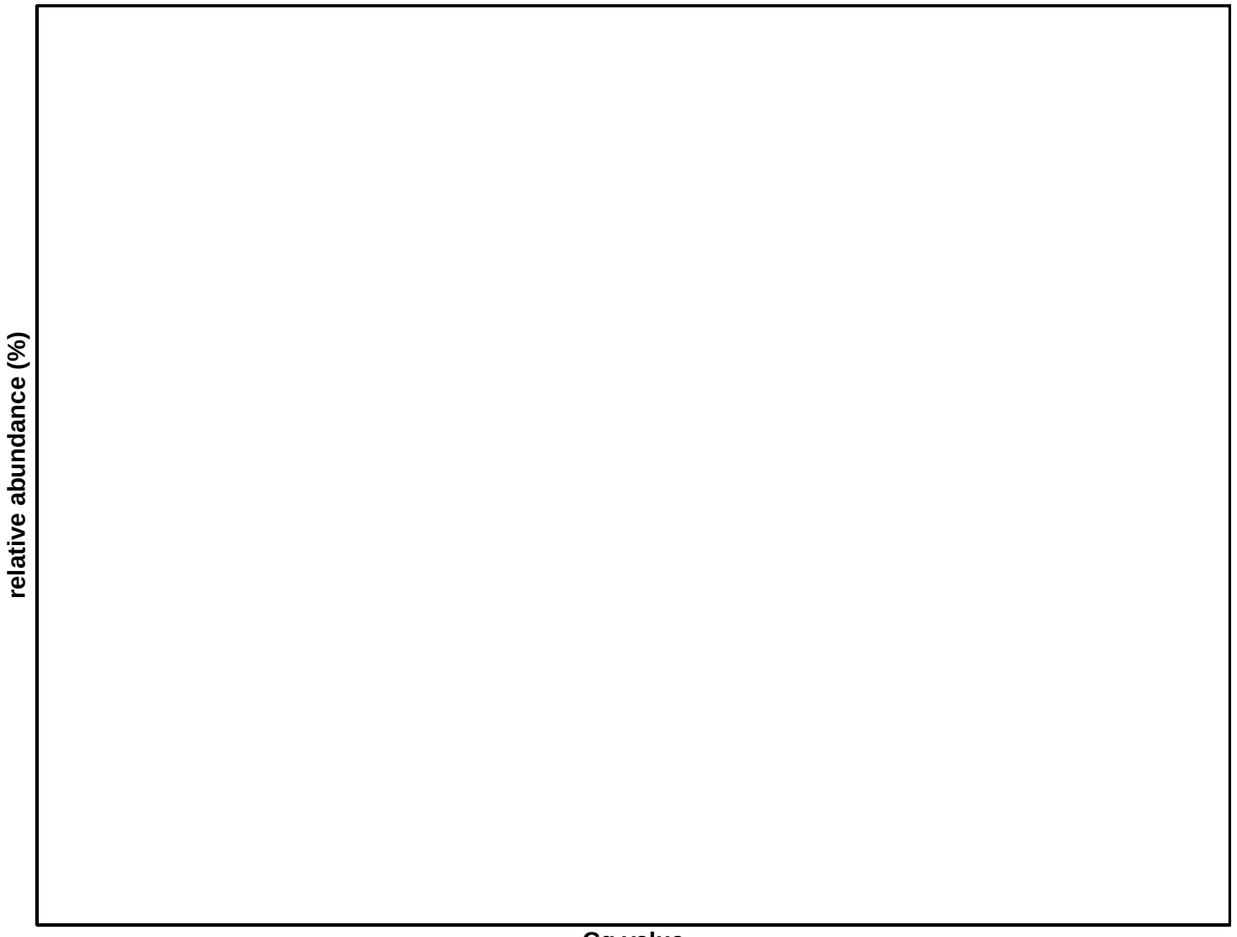


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples

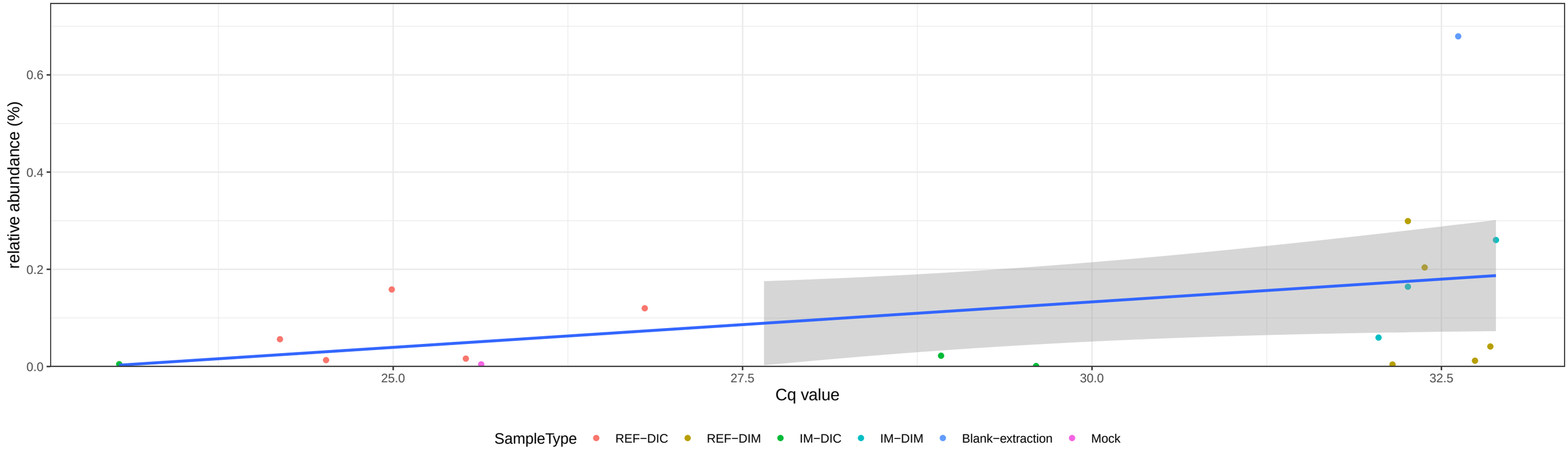


Correlation within the sample type:

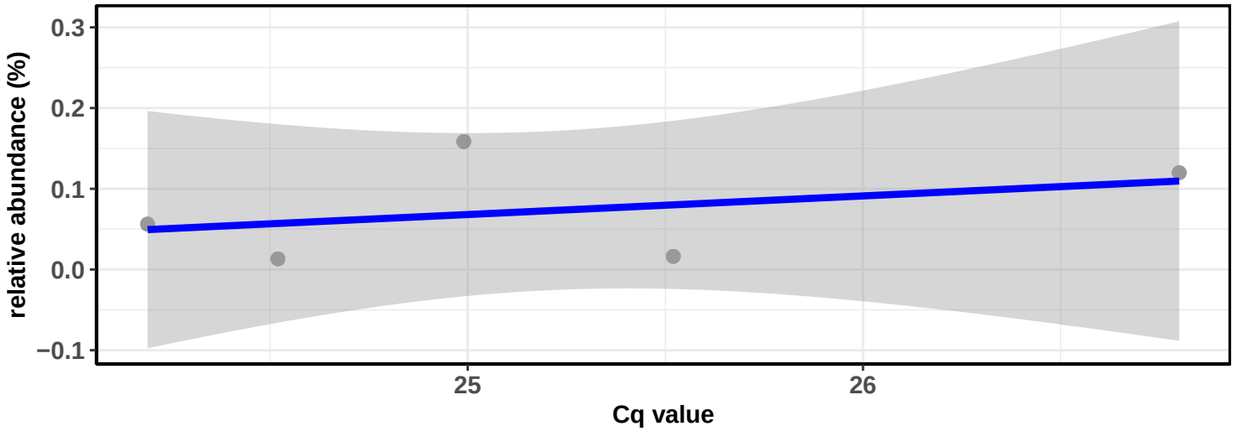


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Micrococcales; D_4__Microbacteriaceae; D_5__Curtobacterium; Ambiguous_taxa

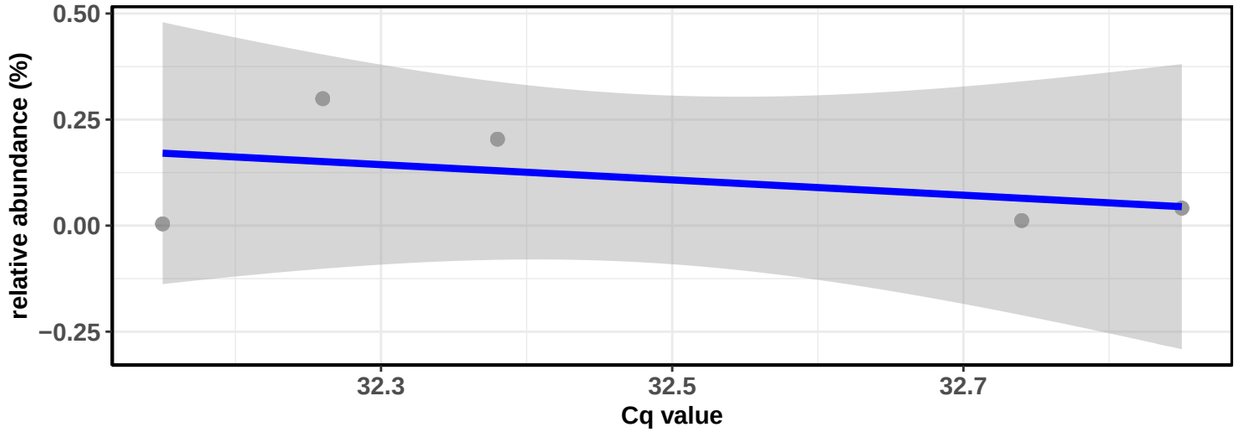
Correlation with all samples



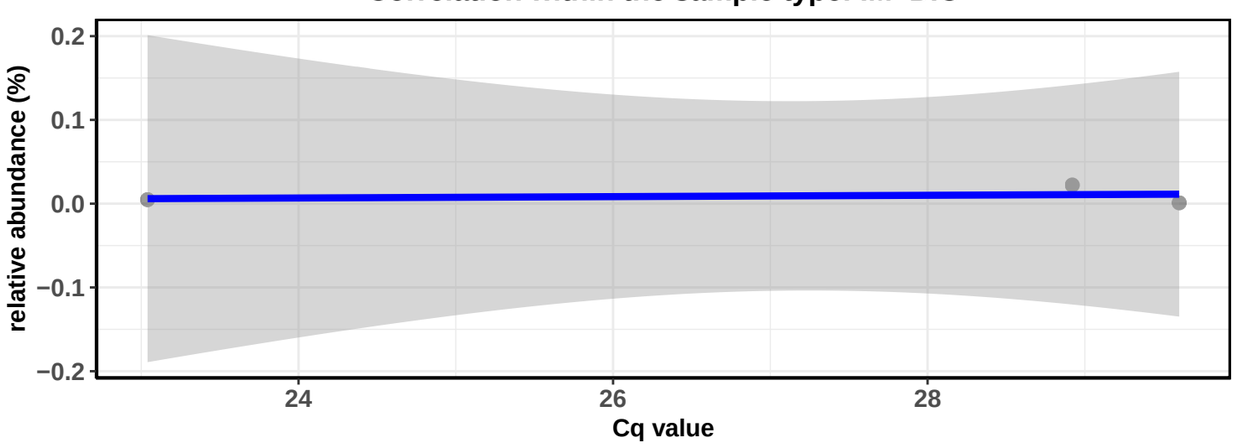
Correlation within the sample type: REF−DIC



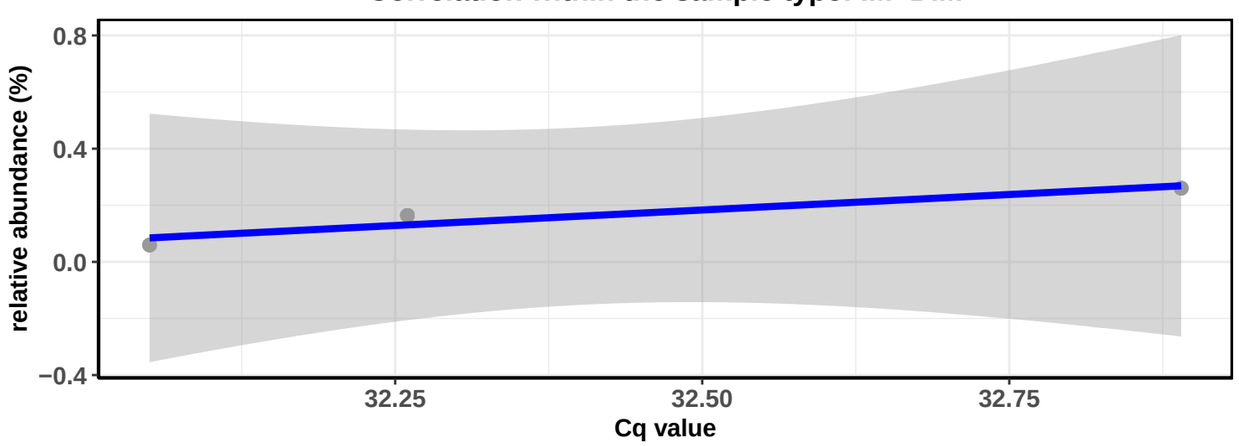
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

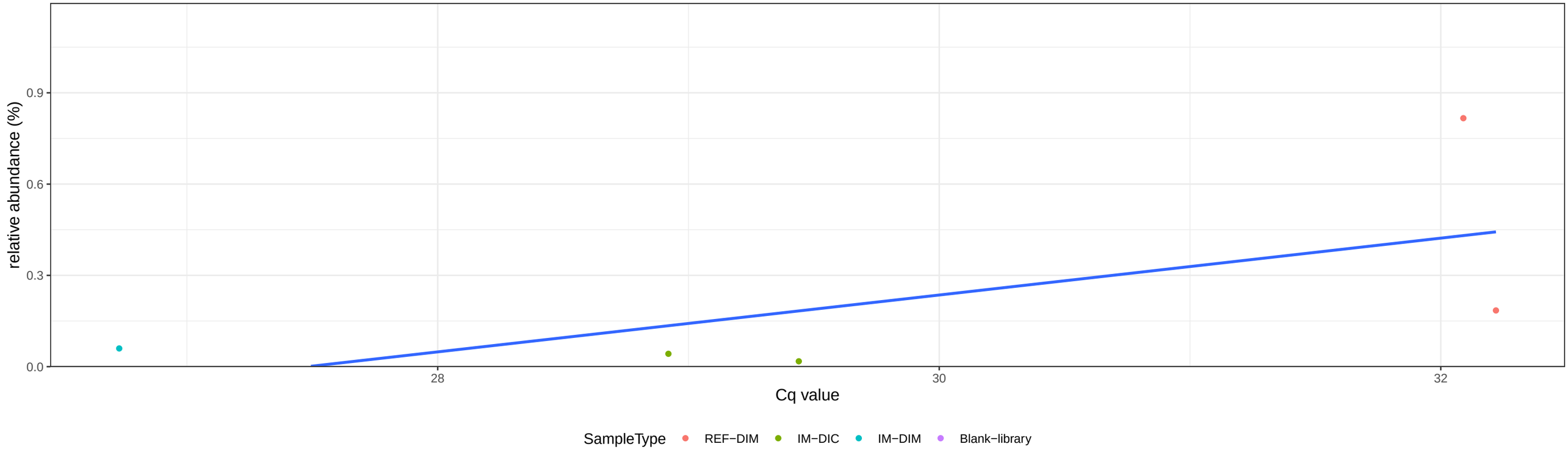


Correlation within the sample type: IM−DIM

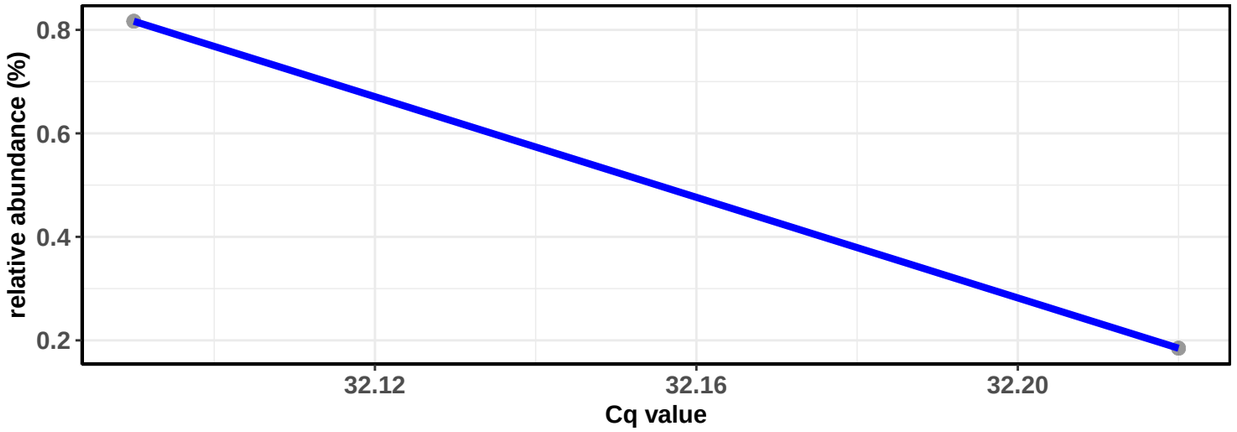


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Staphylococcaceae; D_5__Jeotgalicoccus; Ambiguous_taxa

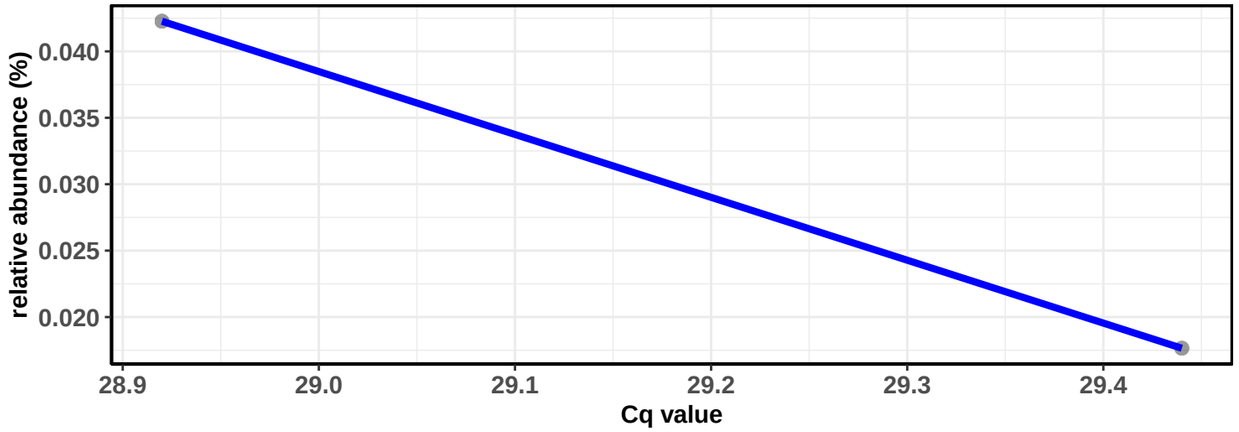
Correlation with all samples



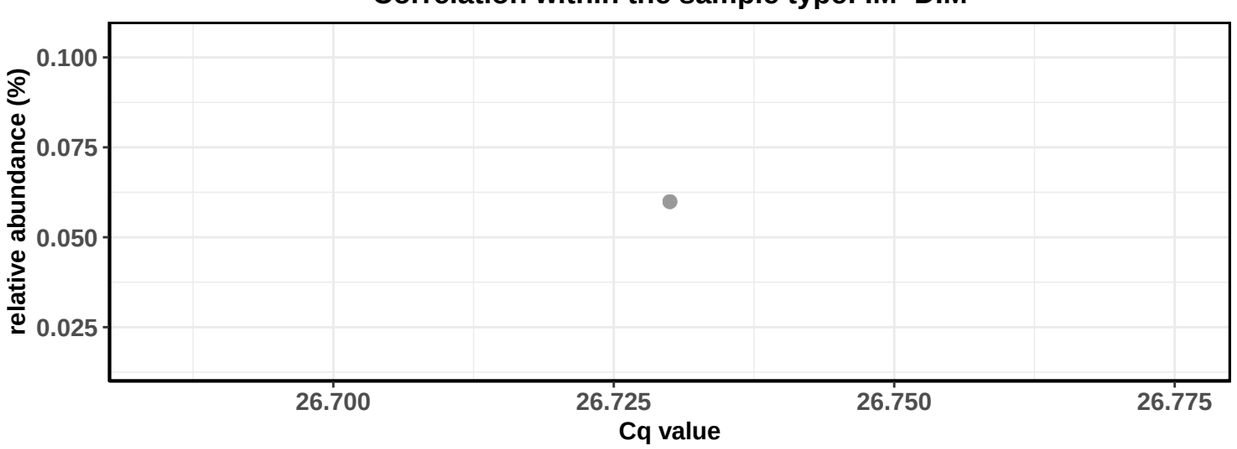
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

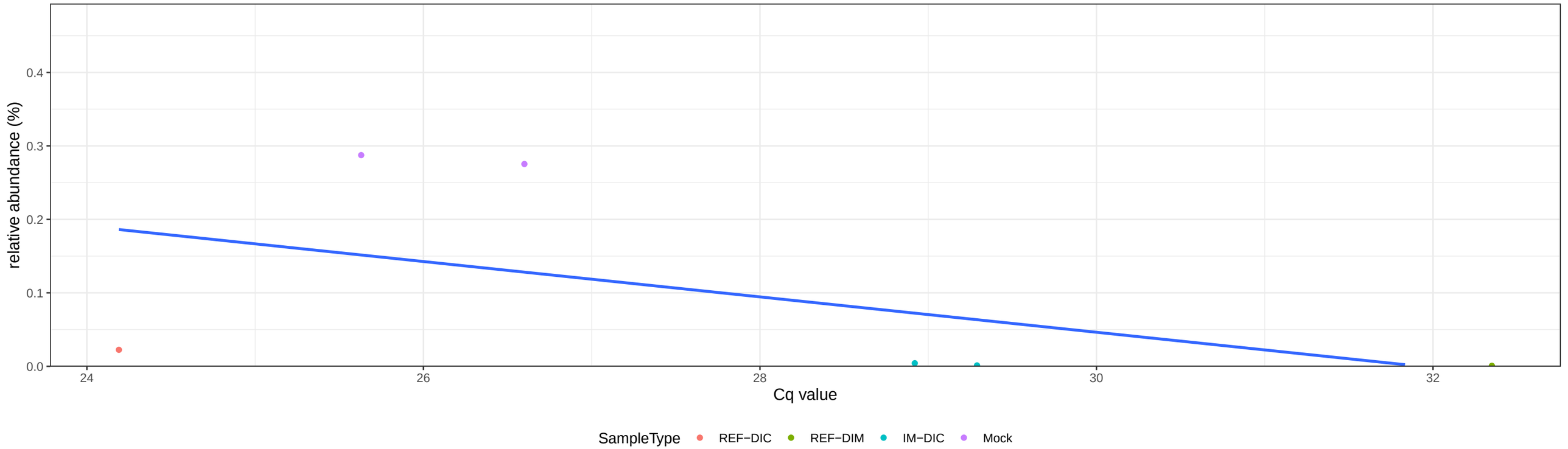


Correlation within the sample type: IM−DIM

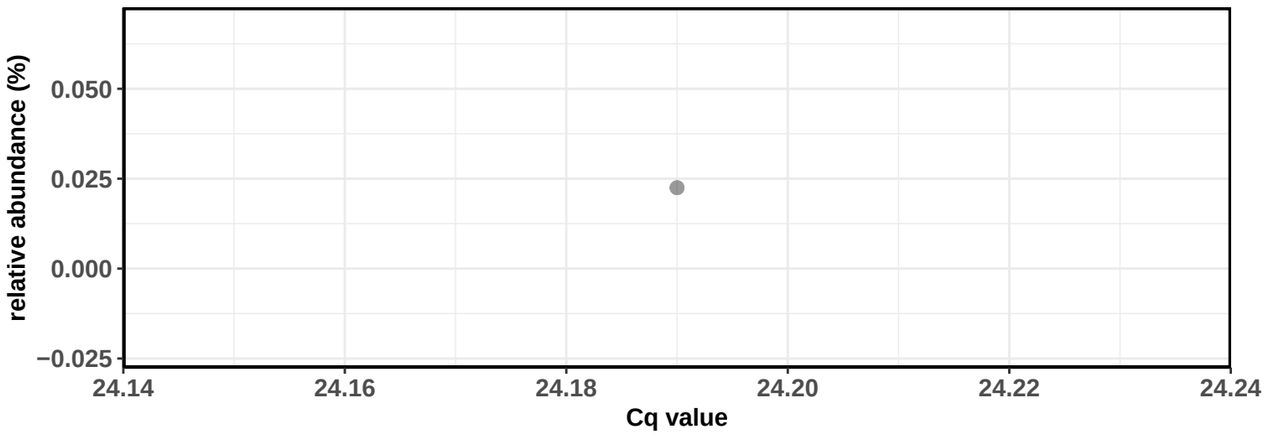


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

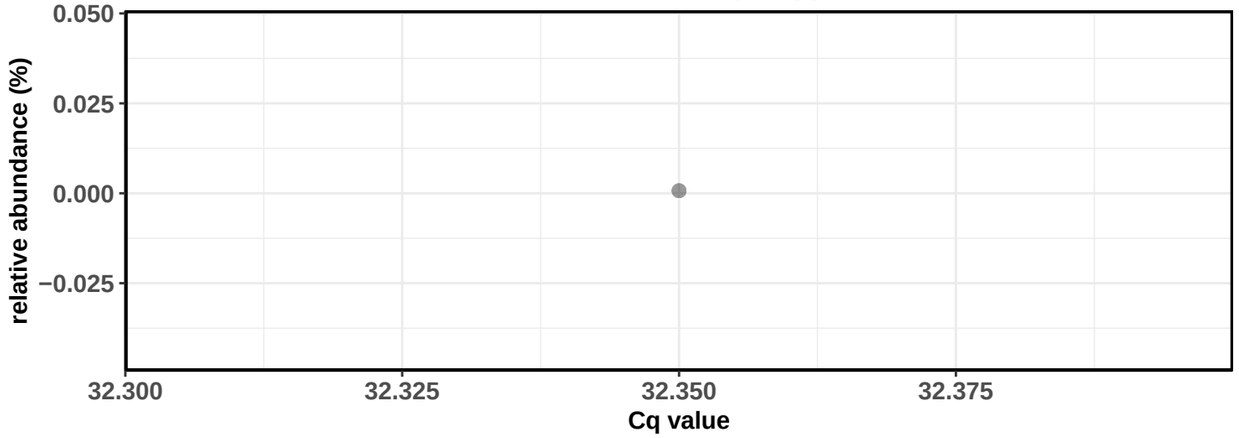
Correlation with all samples



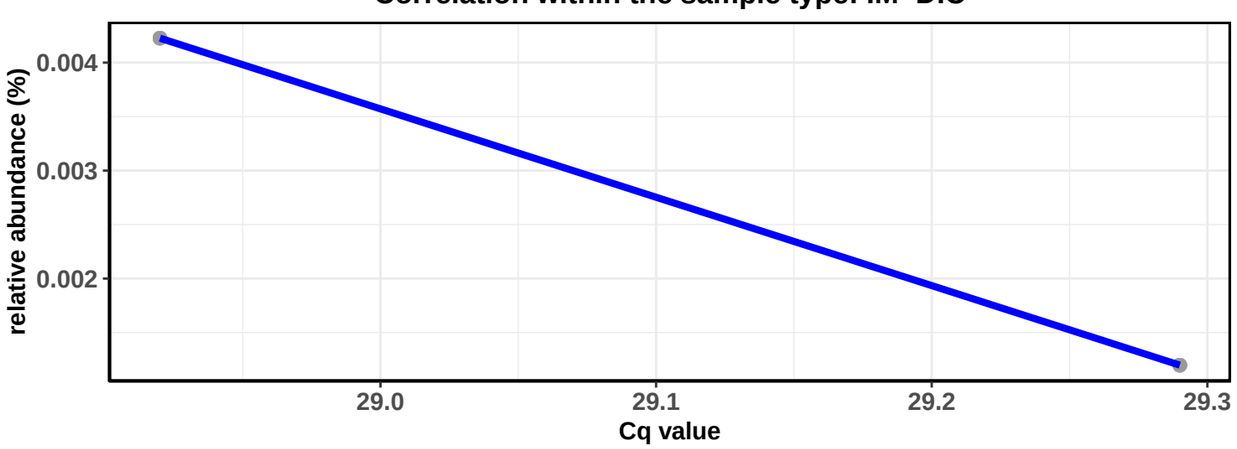
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

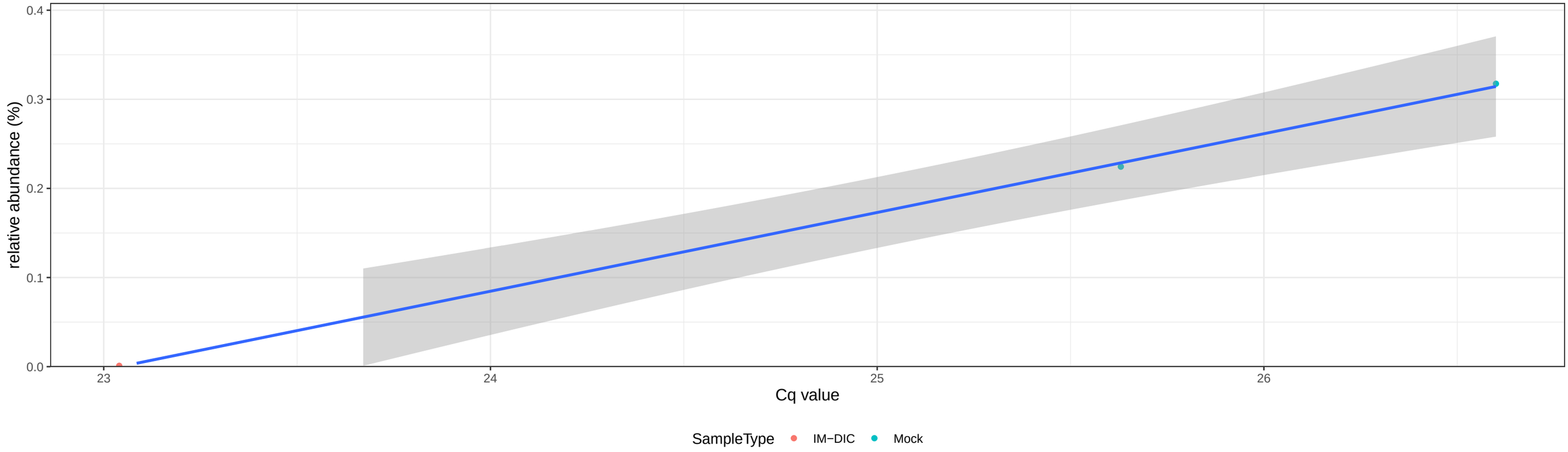


Correlation within the sample type: IM−DIC

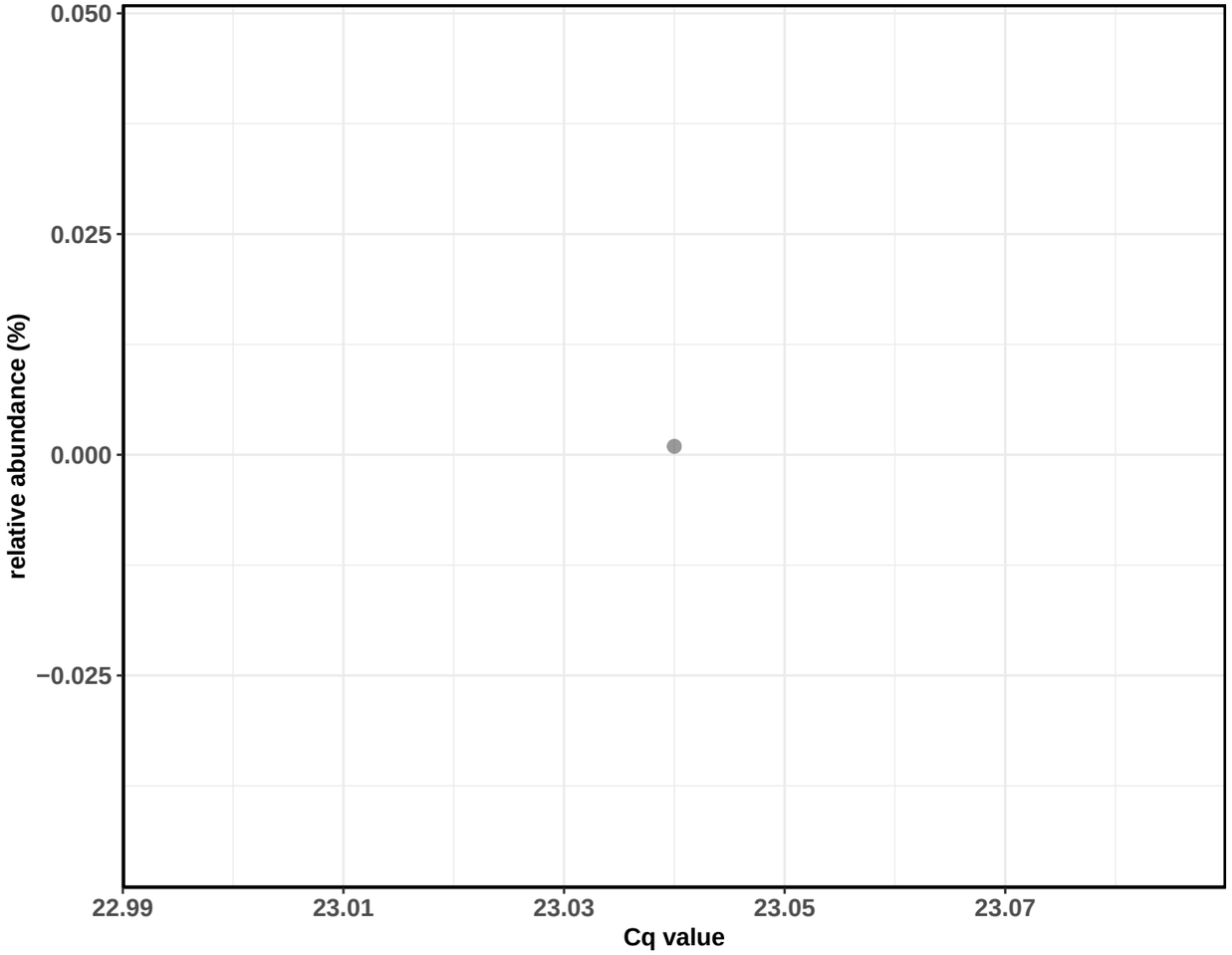


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Listeriaceae; D_5__Listeria; D_6__Listeria monocytogenes

Correlation with all samples

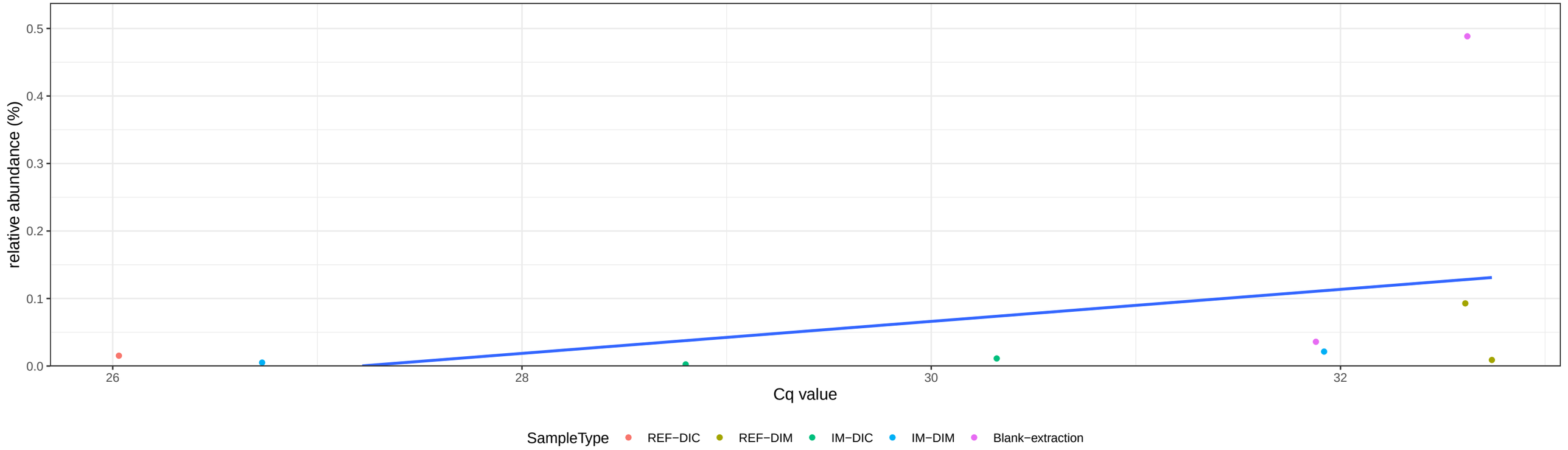


Correlation within the sample type: IM−DIC

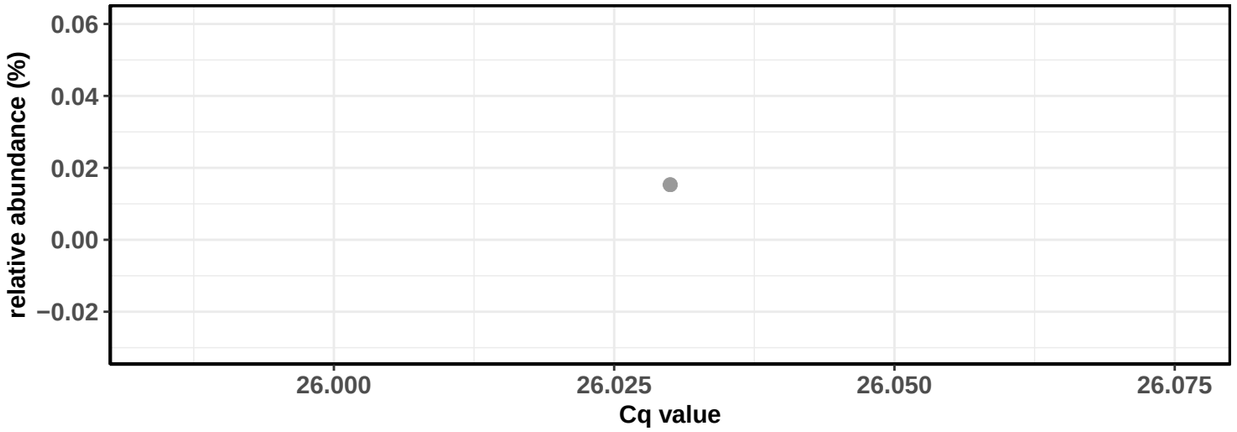


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Frankiales; D_4__Geodermatophilaceae; D_5__Modestobacter; Ambiguous_taxa

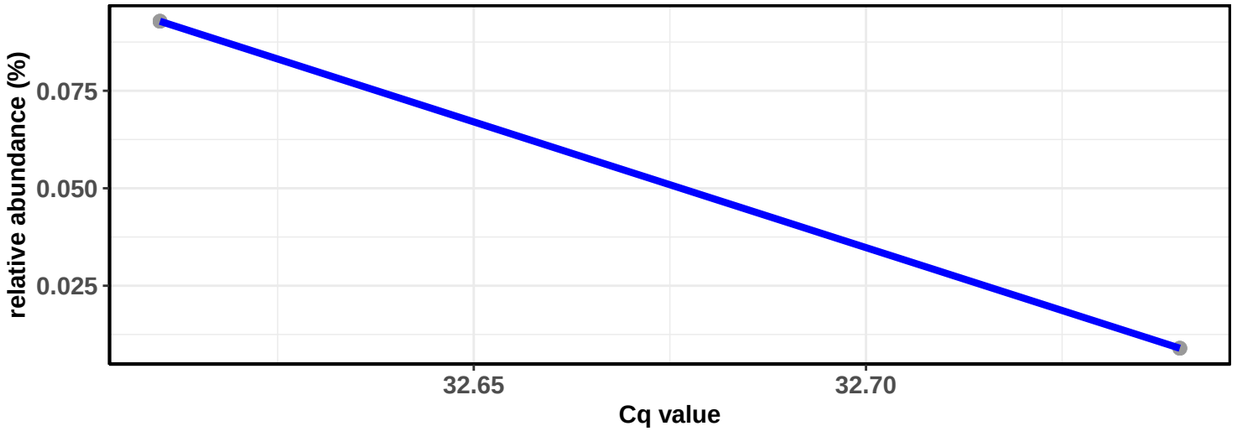
Correlation with all samples



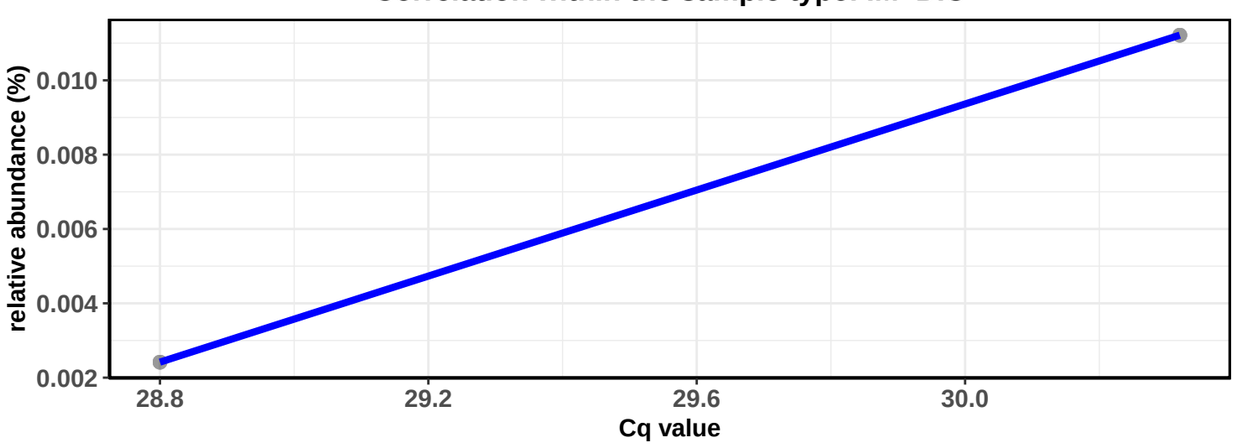
Correlation within the sample type: REF−DIC



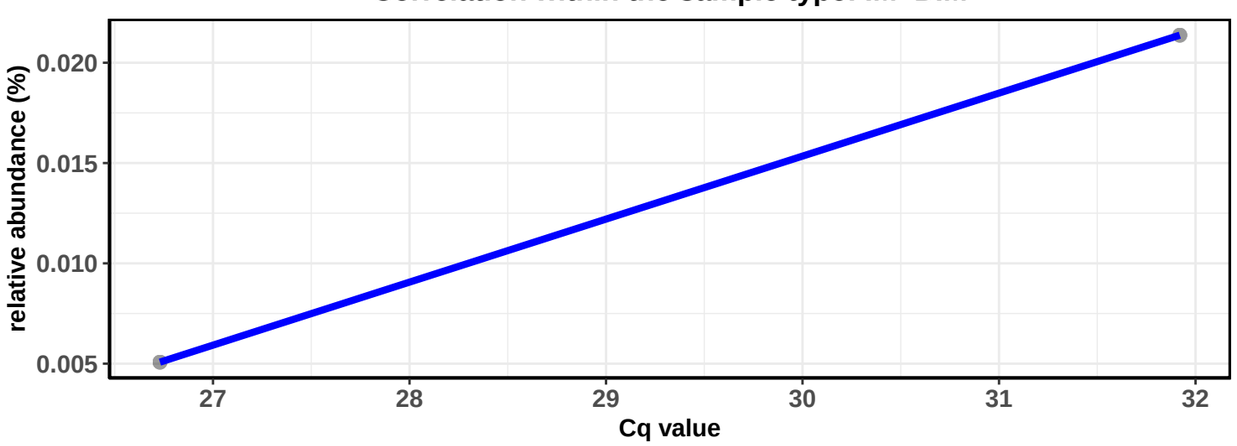
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

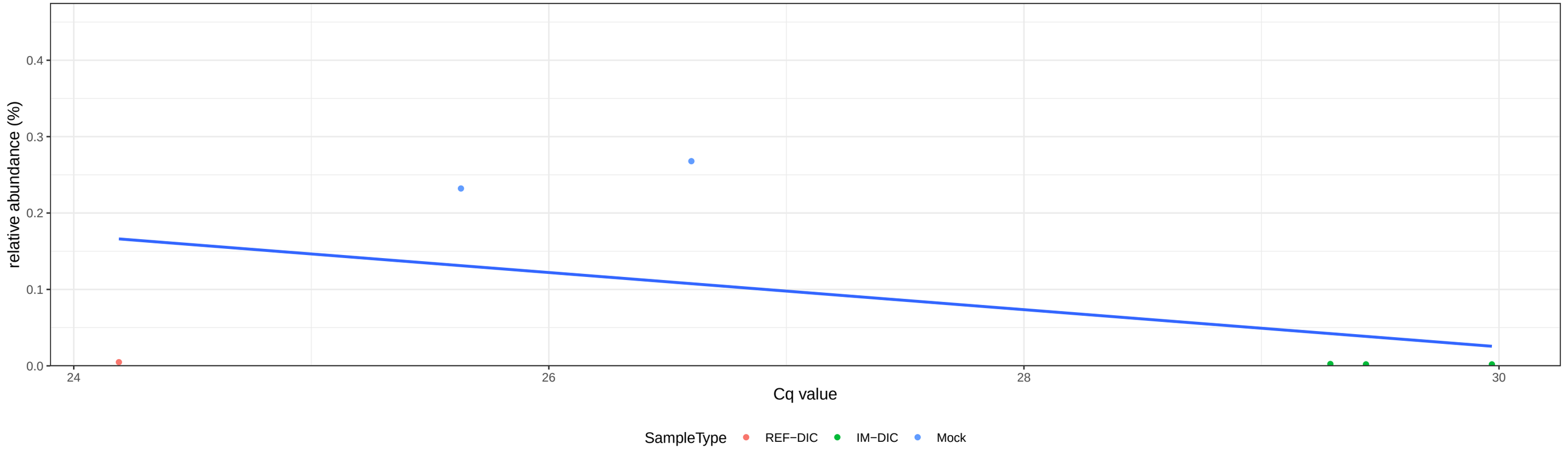


Correlation within the sample type: IM−DIM

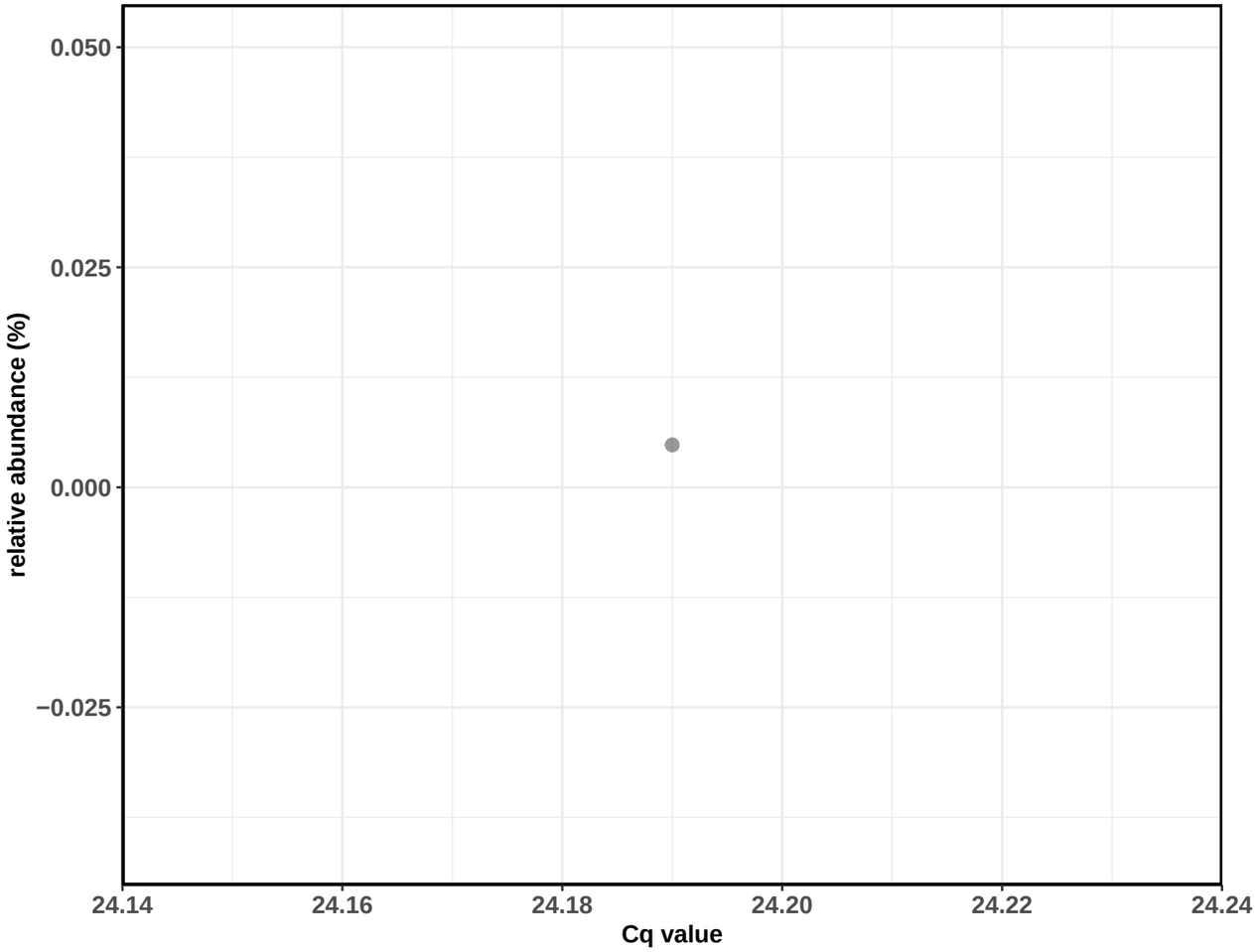


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

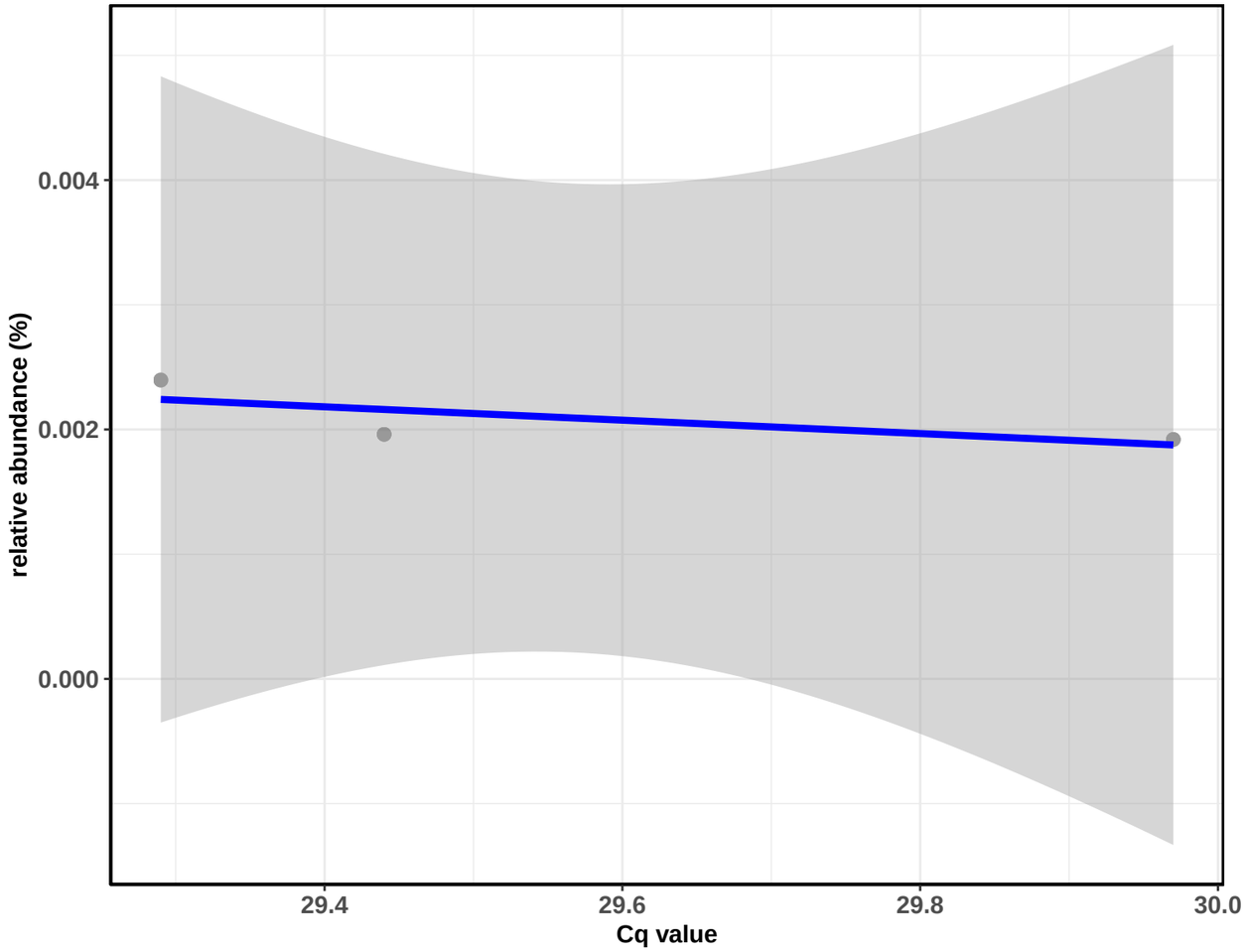
Correlation with all samples



Correlation within the sample type: REF−DIC

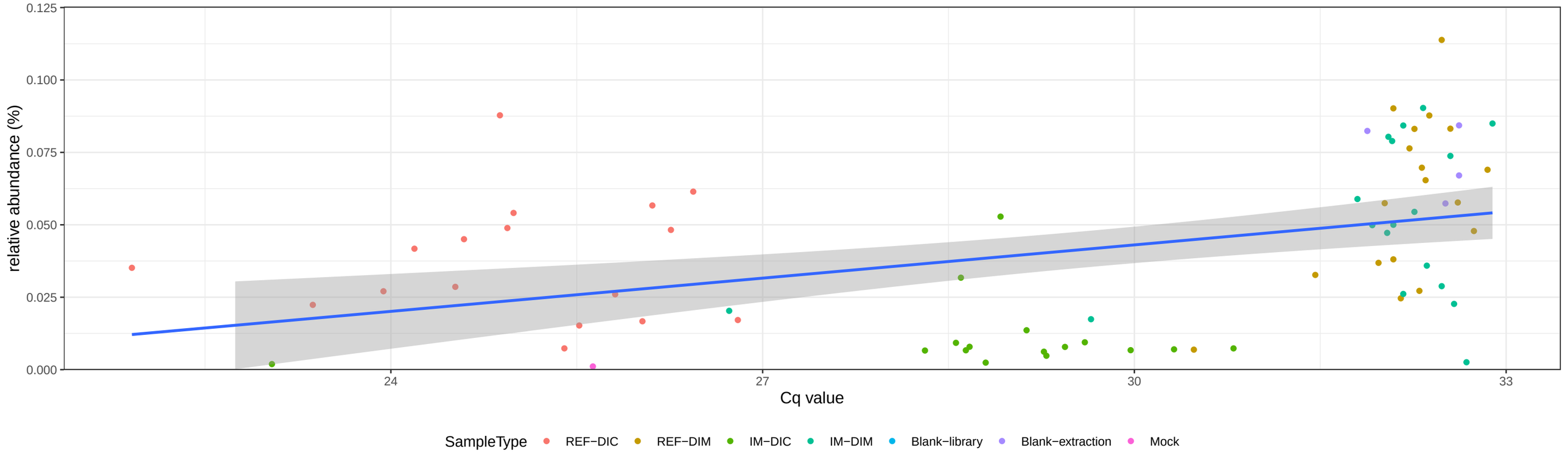


Correlation within the sample type: IM−DIC



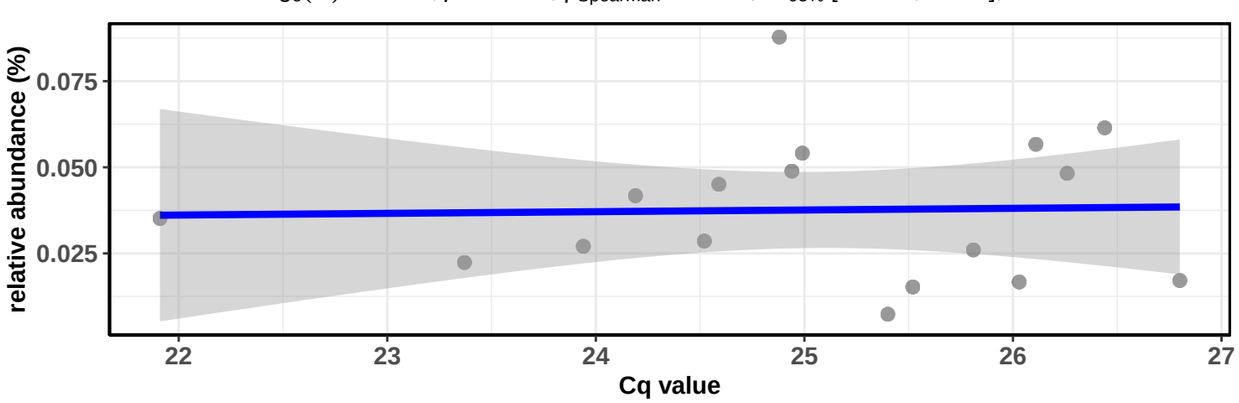
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



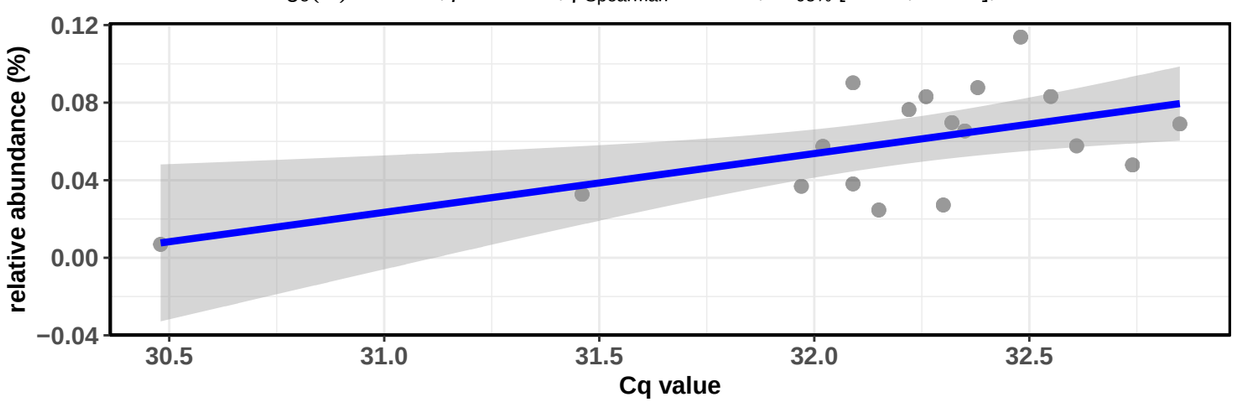
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.667, p = 0.889, $\rho_{Spearman}$ = 0.037, $CI_{95\%}$ [−0.452, 0.508], n = 17



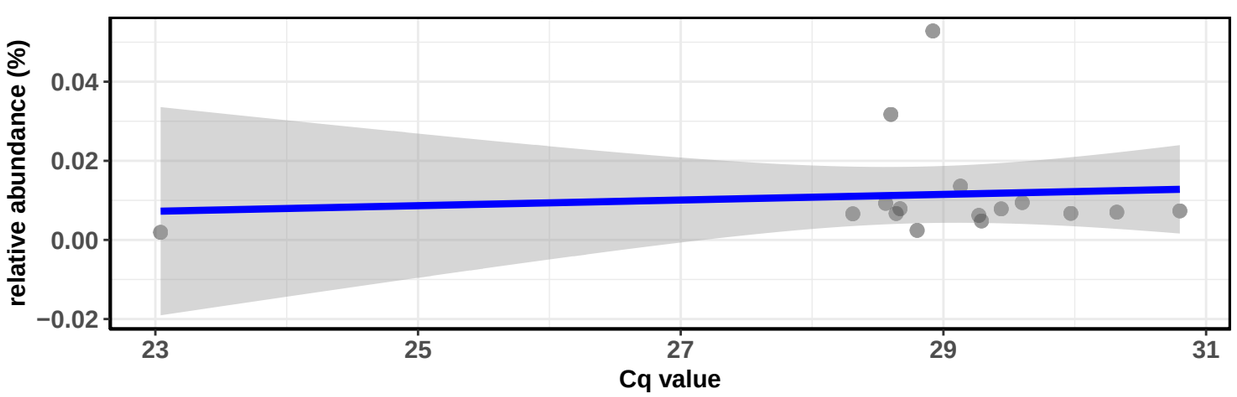
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.232, p = 0.046, $\rho_{Spearman}$ = 0.475, $CI_{95\%}$ [0.010, 0.771], n = 18



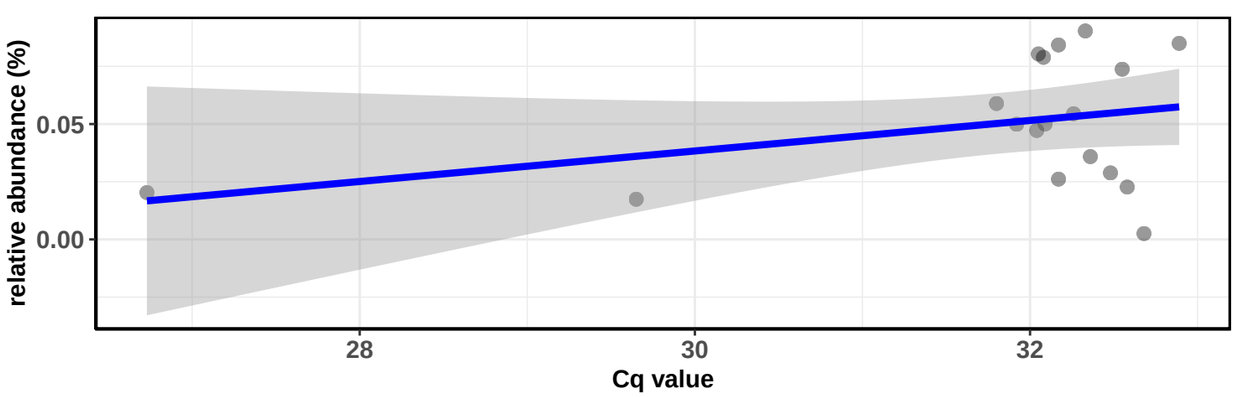
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.400, p = 0.672, $\rho_{Spearman}$ = 0.115, $CI_{95\%}$ [−0.404, 0.578], n = 16



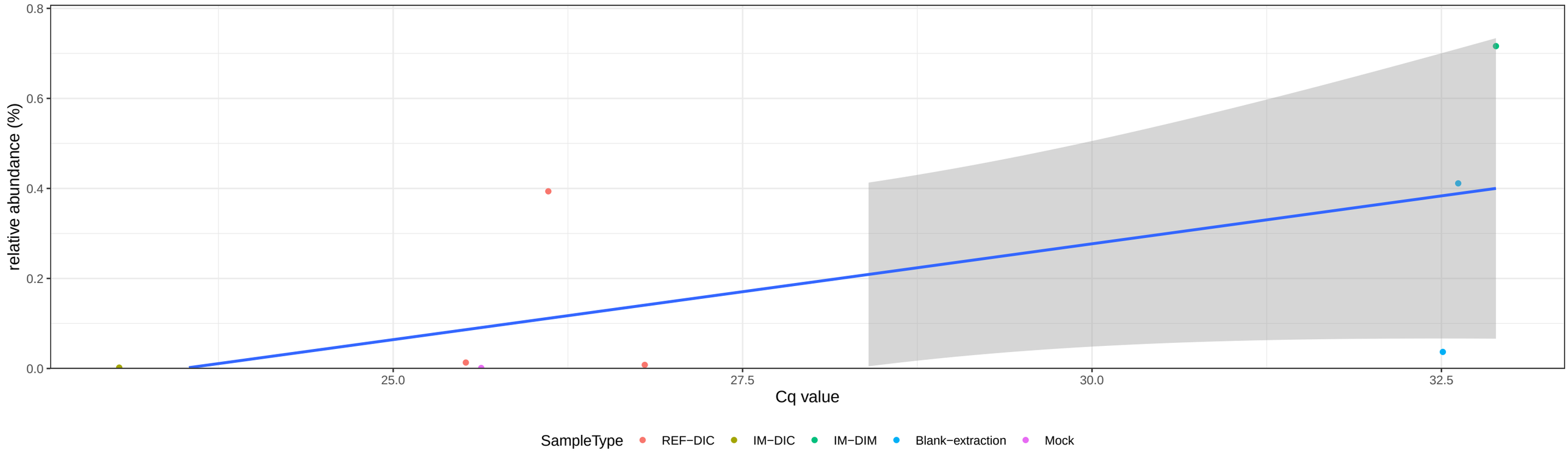
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.753, p = 0.648, $\rho_{Spearman}$ = 0.116, $CI_{95\%}$ [−0.371, 0.553], n = 18

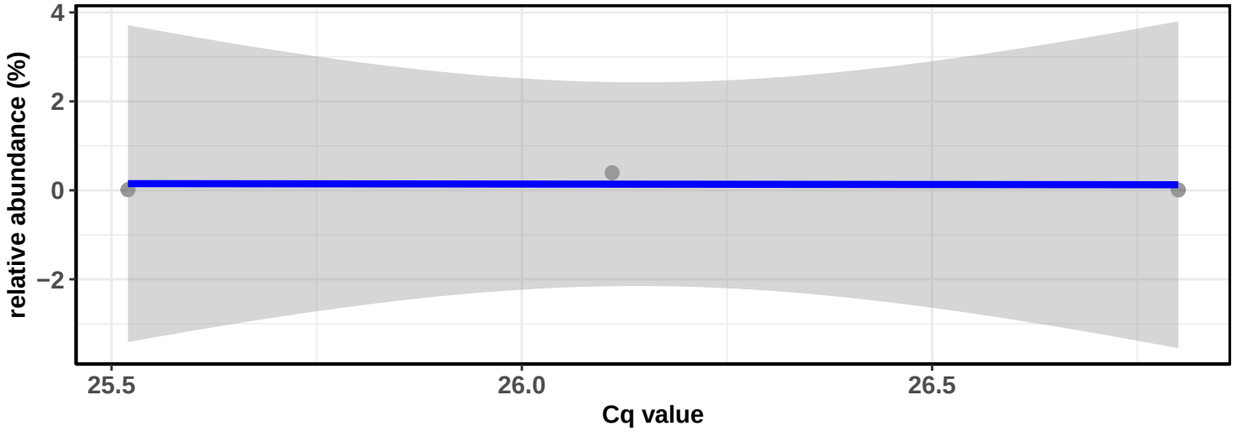


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

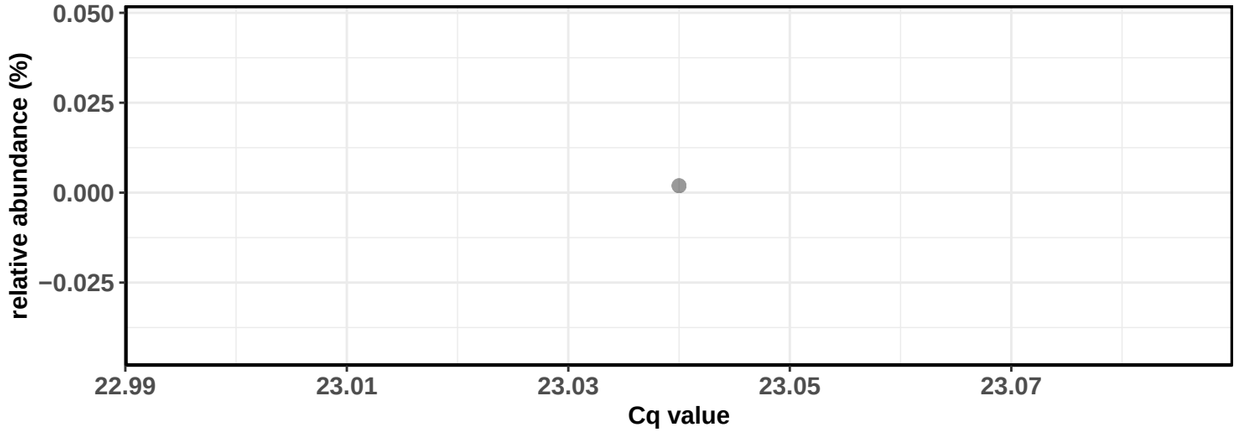
Correlation with all samples



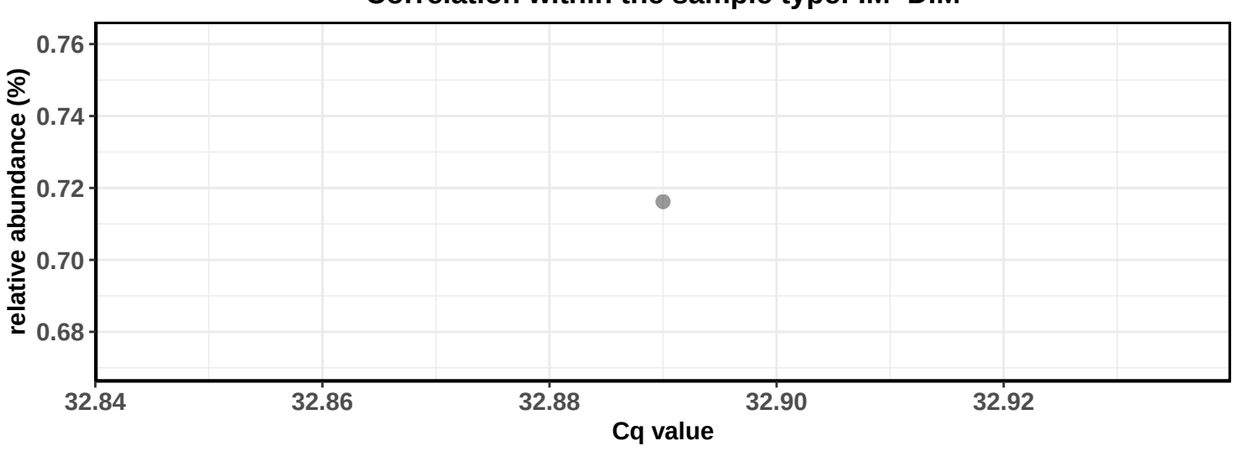
Correlation within the sample type: REF−DIC



Correlation within the sample type: IM−DIC

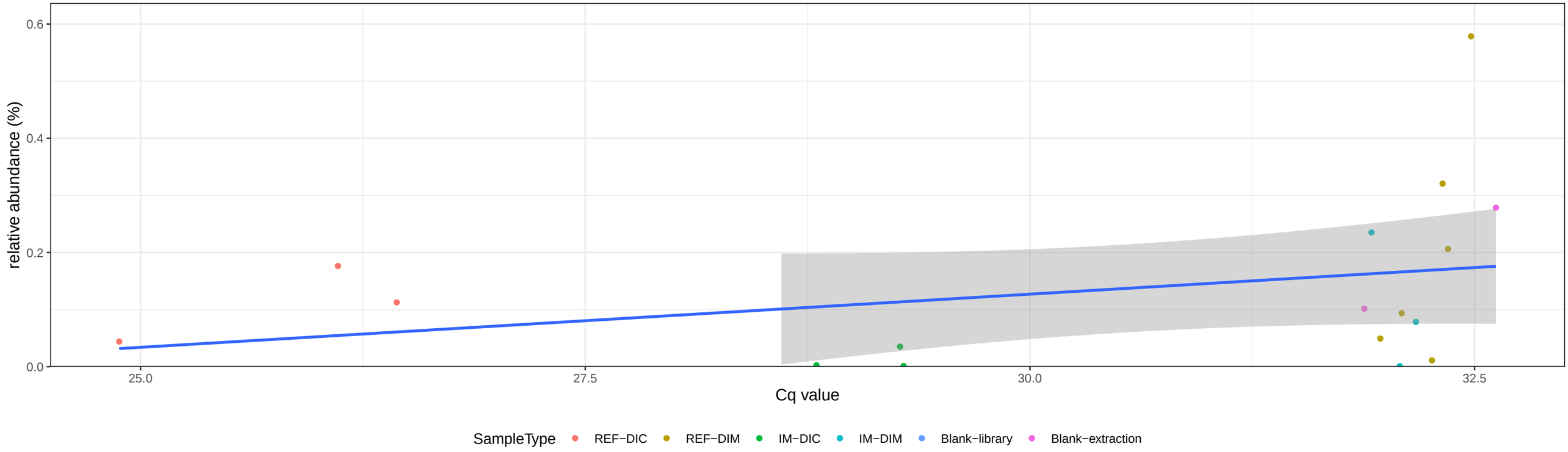


Correlation within the sample type: IM−DIM

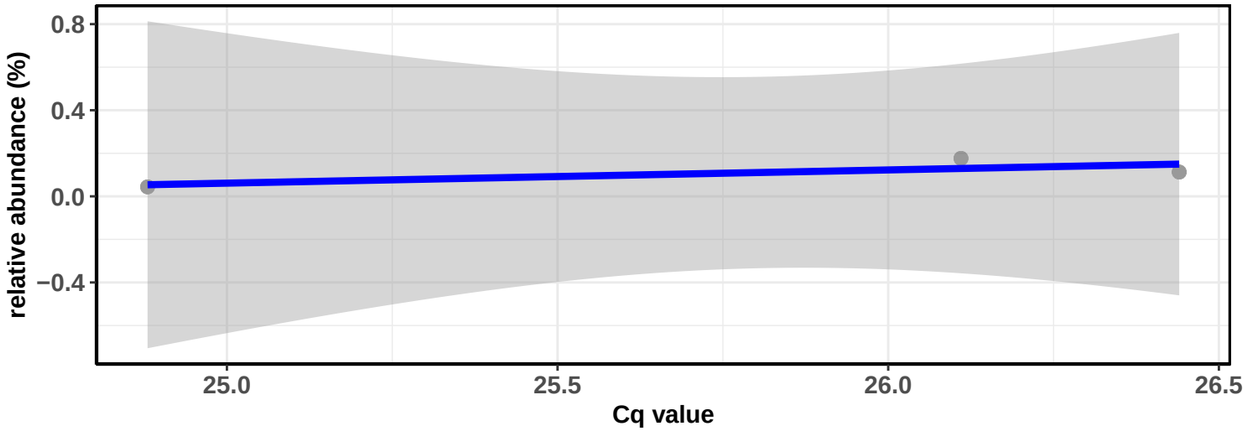


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Caulobacterales; D_4__Caulobacteraceae; D_5__Brevundimonas; Ambiguous_taxa

Correlation with all samples

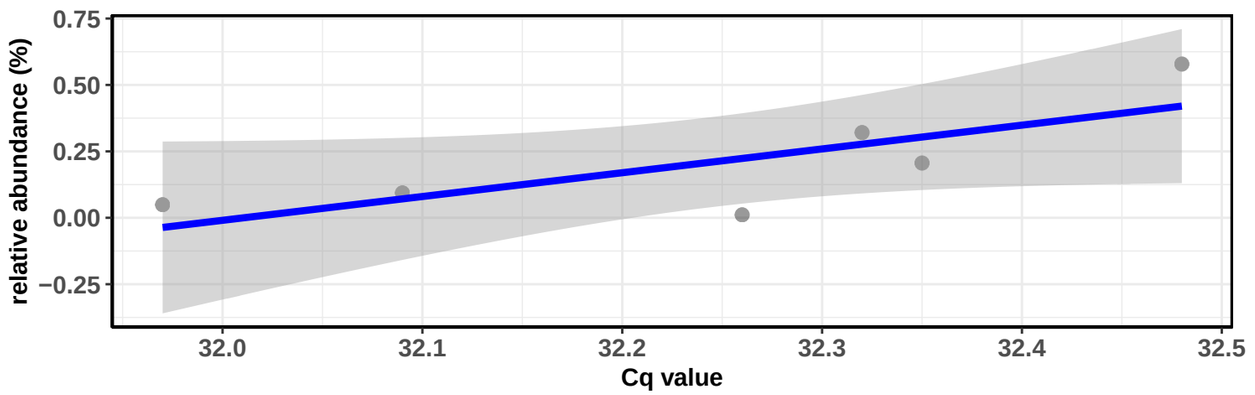


Correlation within the sample type: REF−DIC

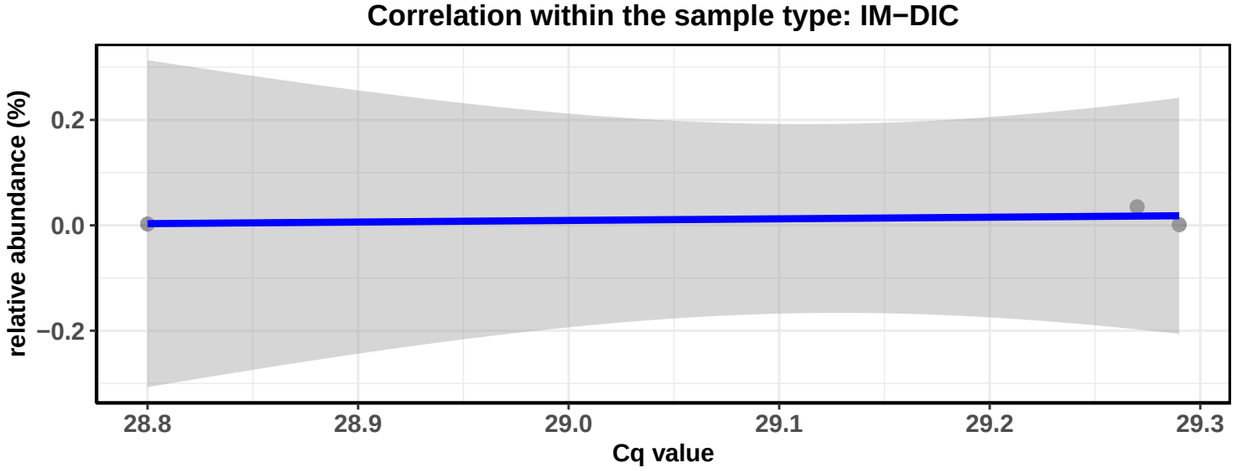


Correlation within the sample type: REF−DIM

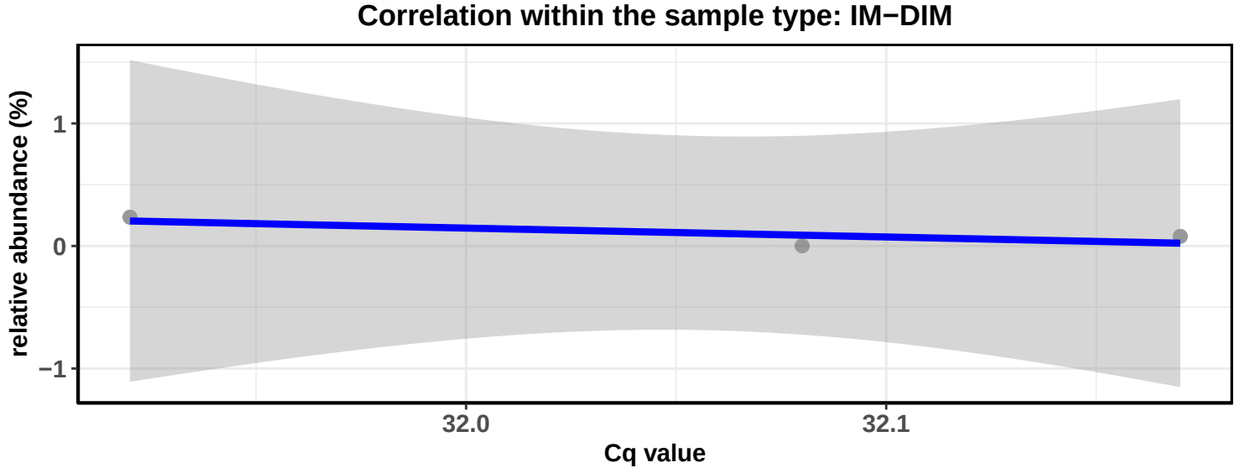
$\log_e(S)$ = 2.079, p = 0.072, $\rho_{Spearman}$ = 0.771, $CI_{95\%}$ [−0.107, 0.974], n = 6



Correlation within the sample type: IM−DIC

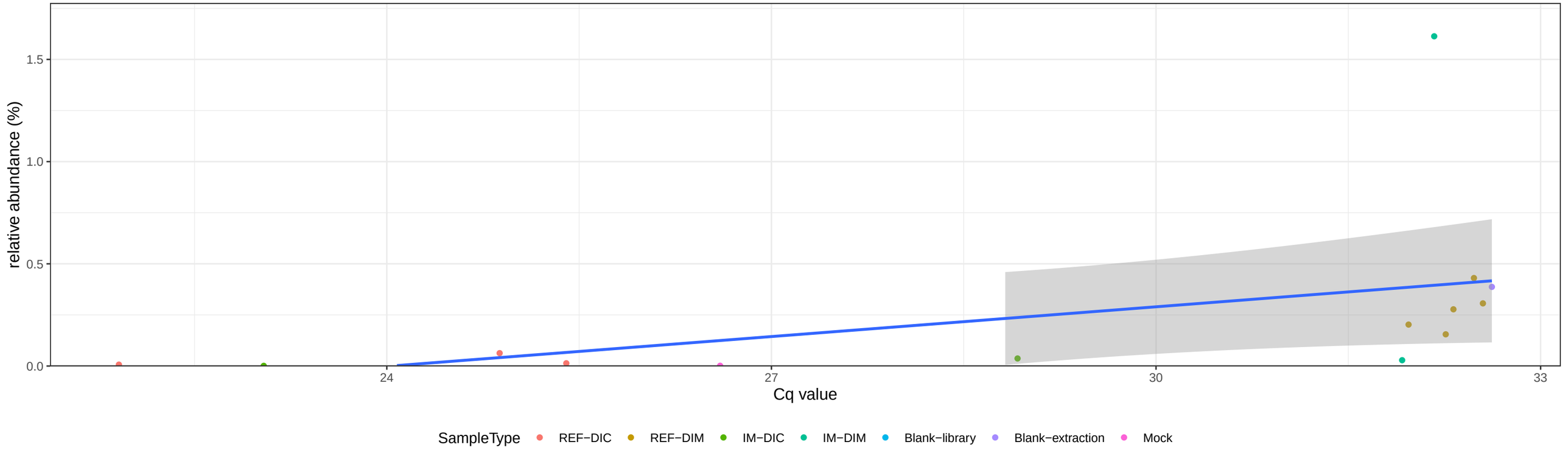


Correlation within the sample type: IM−DIM

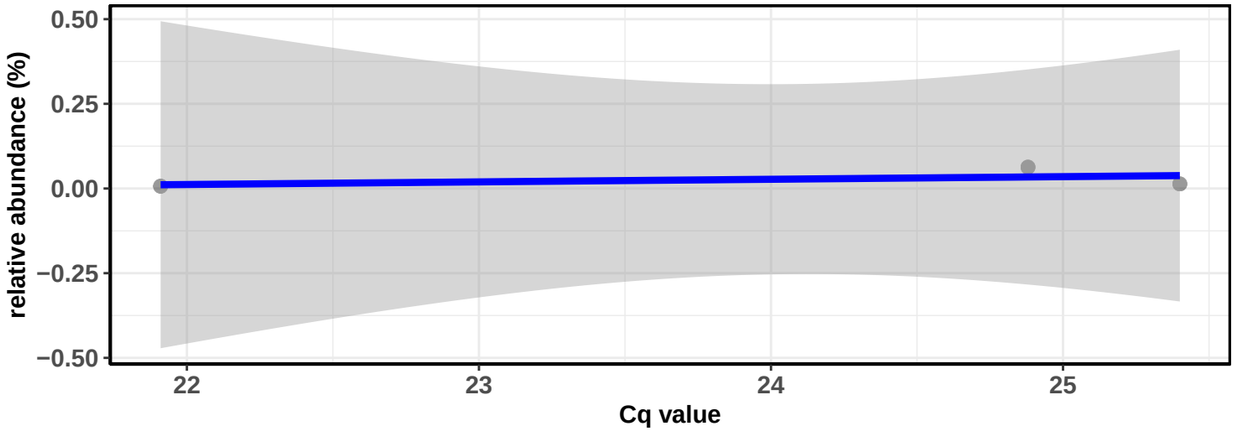


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Caulobacterales; D_4__Caulobacteraceae; D_5__Brevundimonas; Ambiguous_taxa

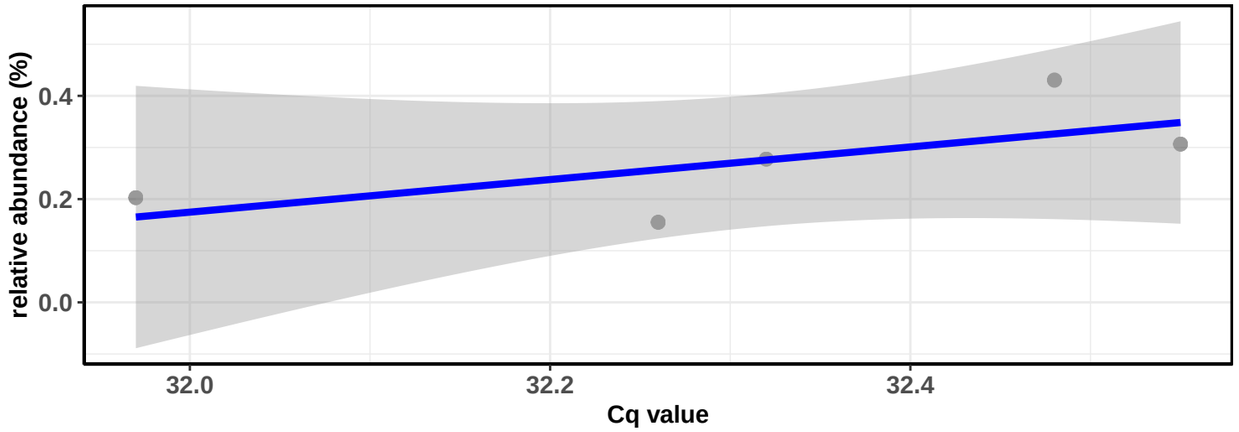
Correlation with all samples



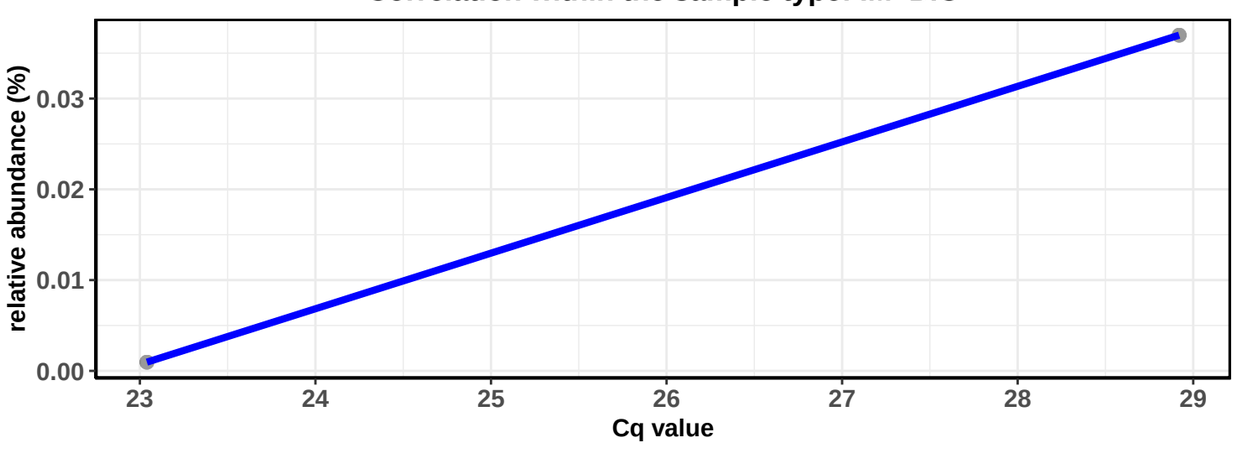
Correlation within the sample type: REF−DIC



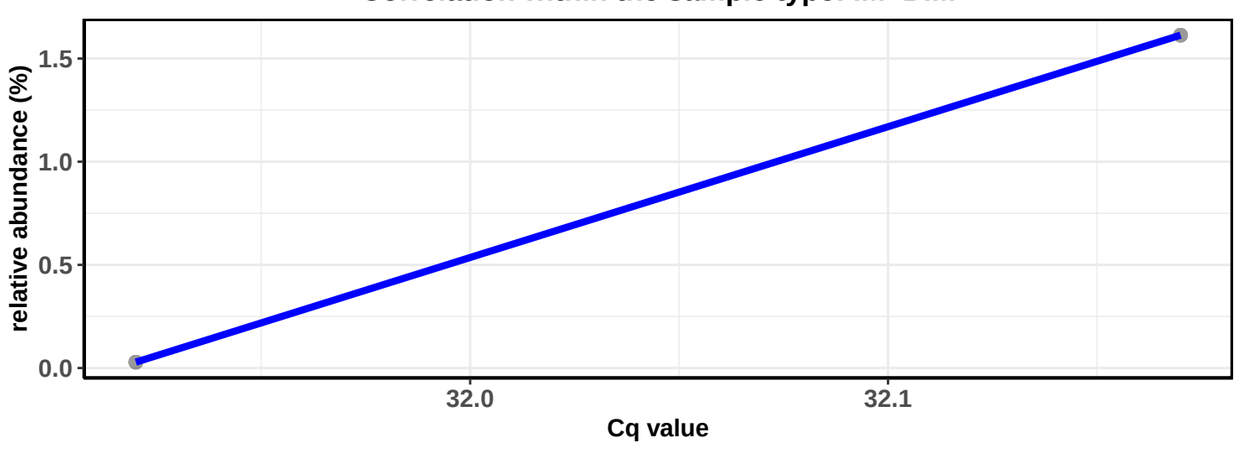
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

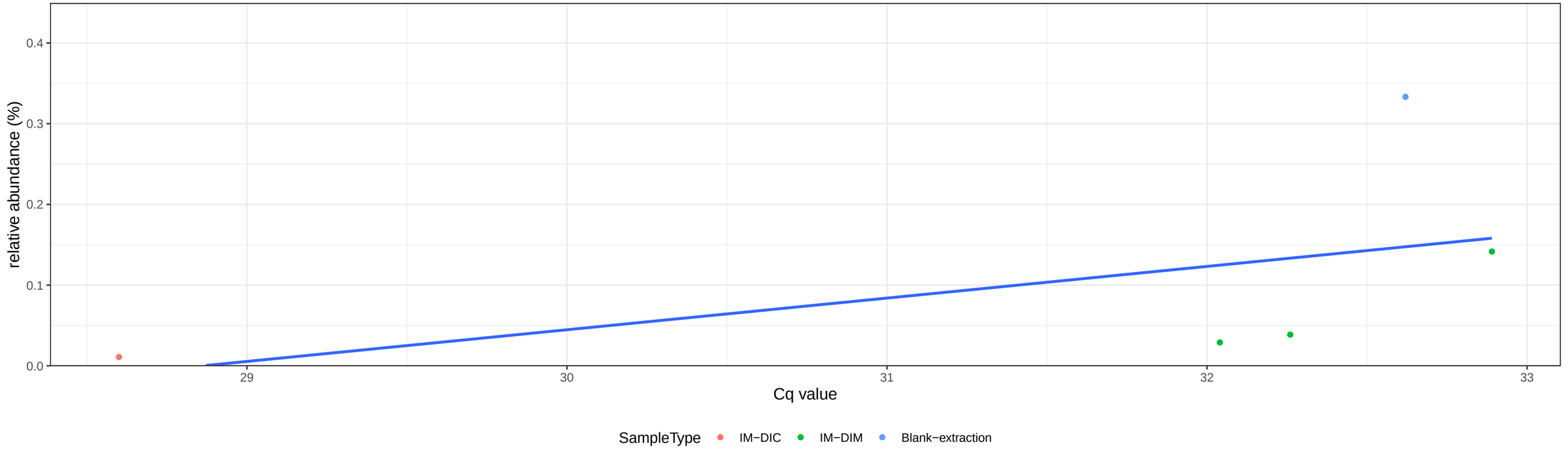


Correlation within the sample type: IM−DIM

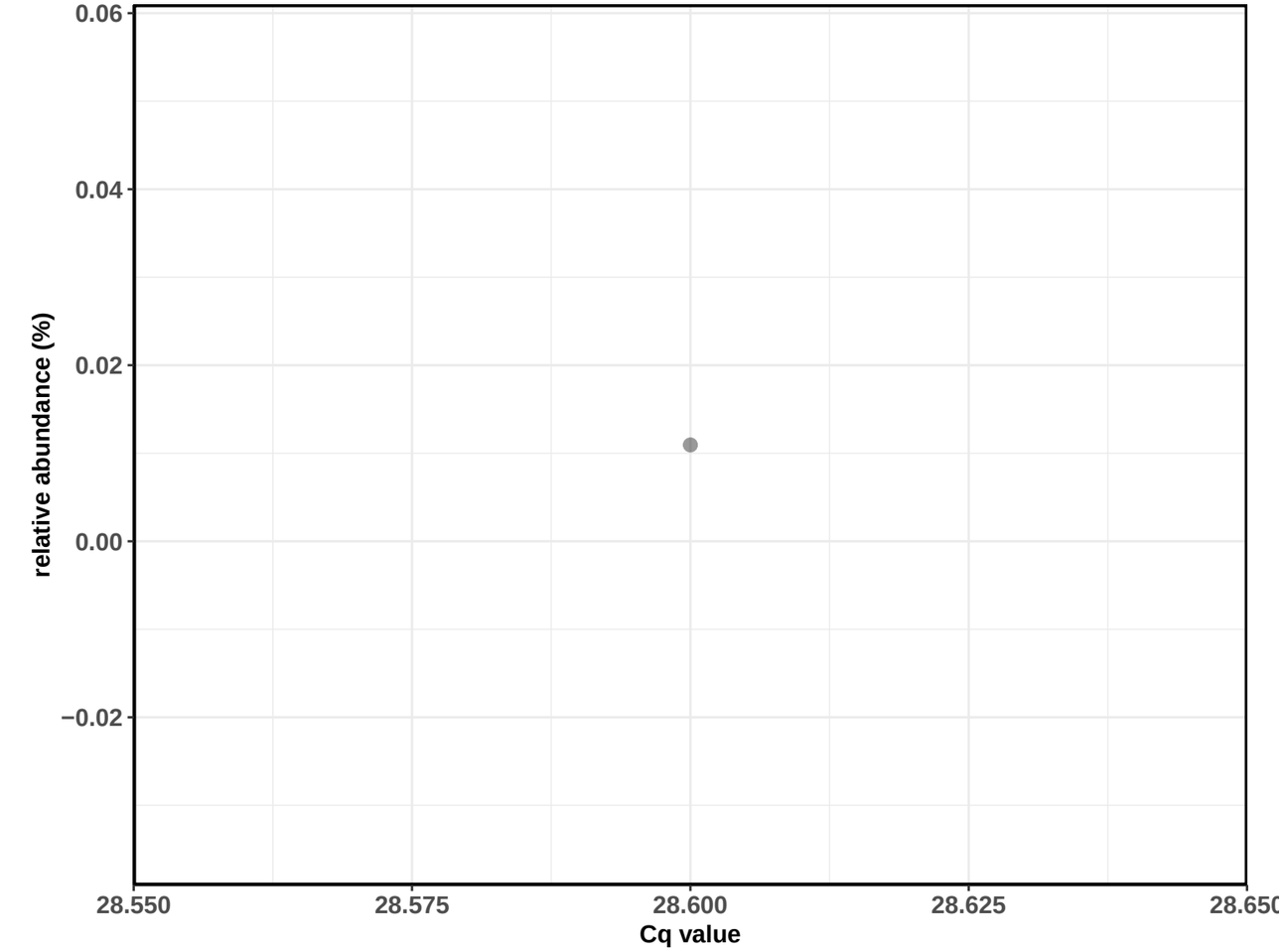


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

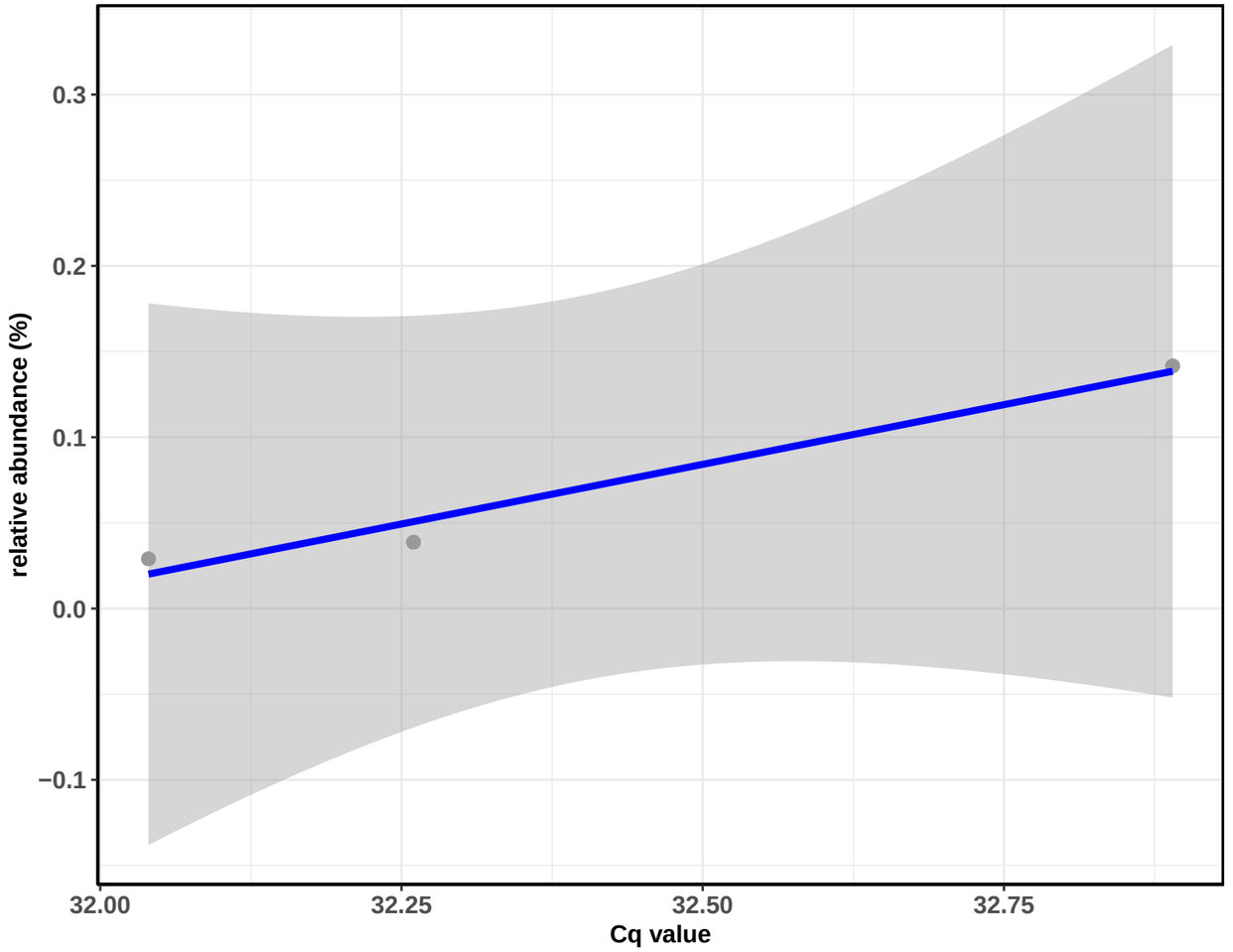
Correlation with all samples



Correlation within the sample type: IM−DIC

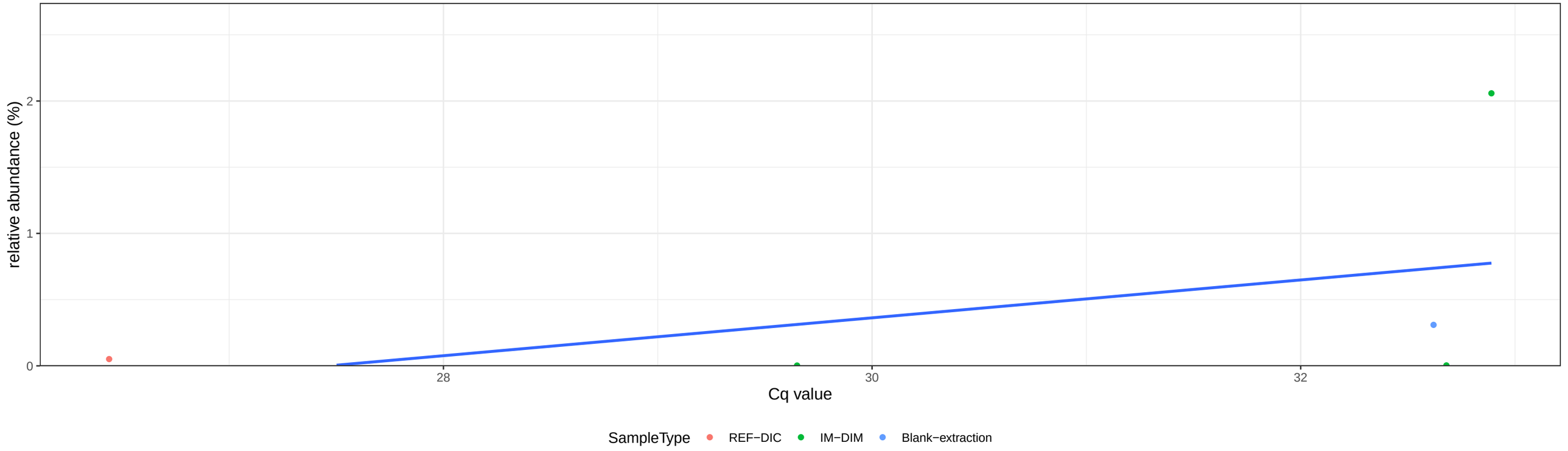


Correlation within the sample type: IM−DIM

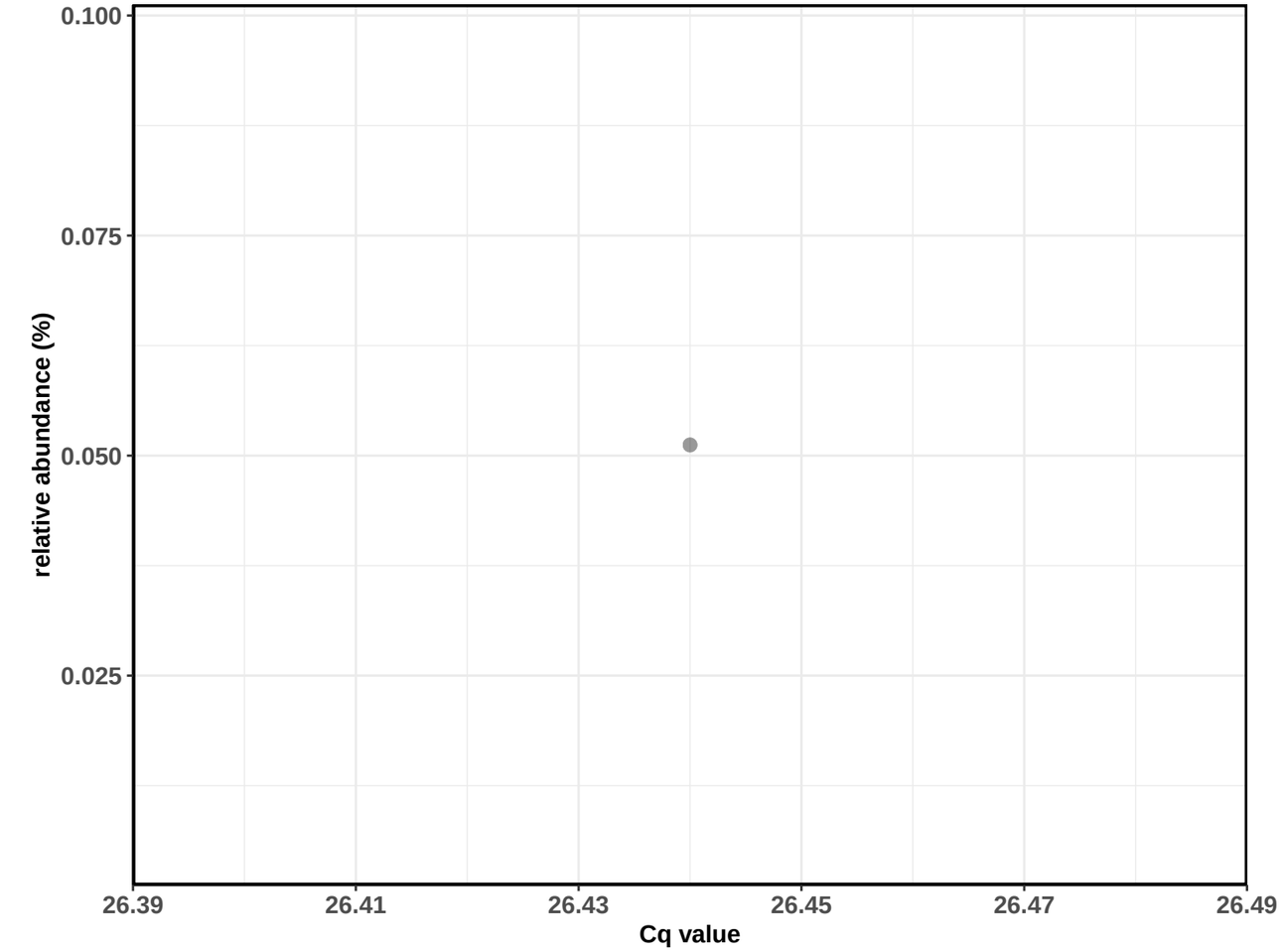


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

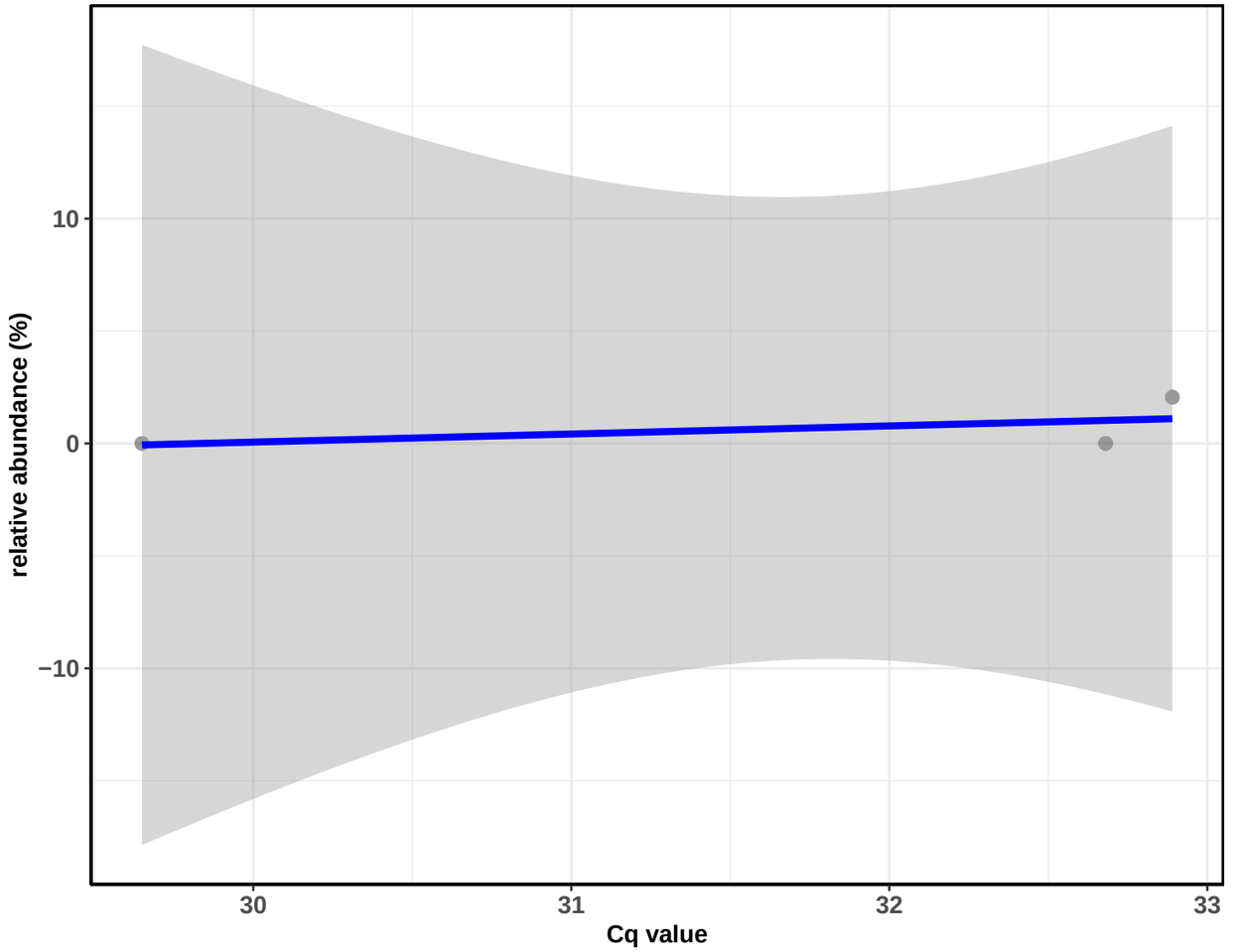
Correlation with all samples



Correlation within the sample type: REF−DIC

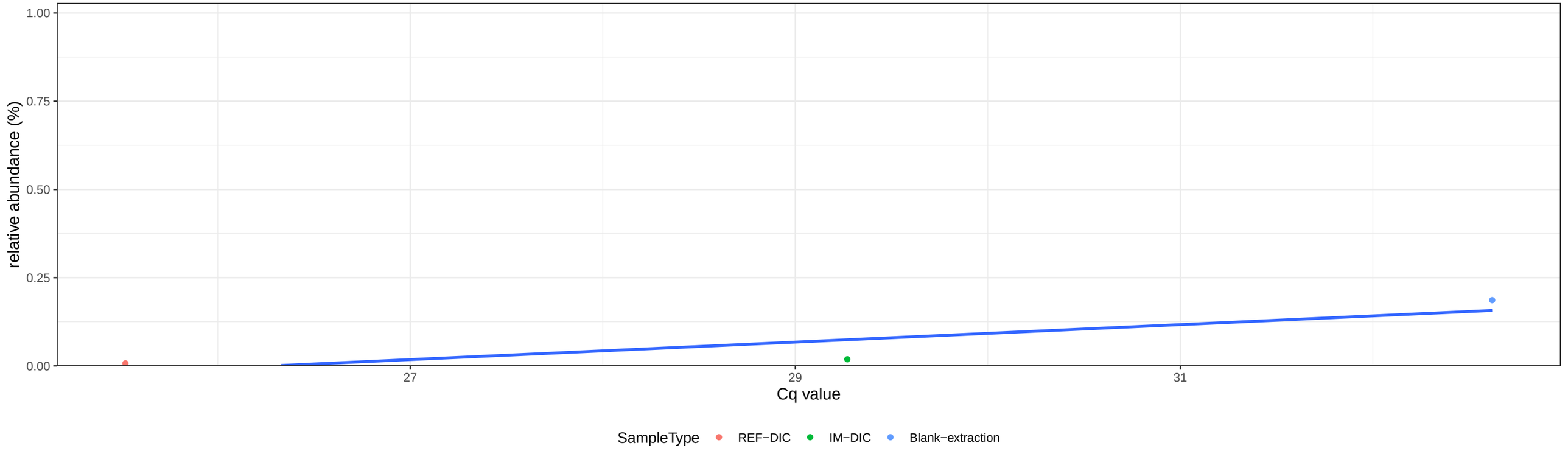


Correlation within the sample type: IM−DIM

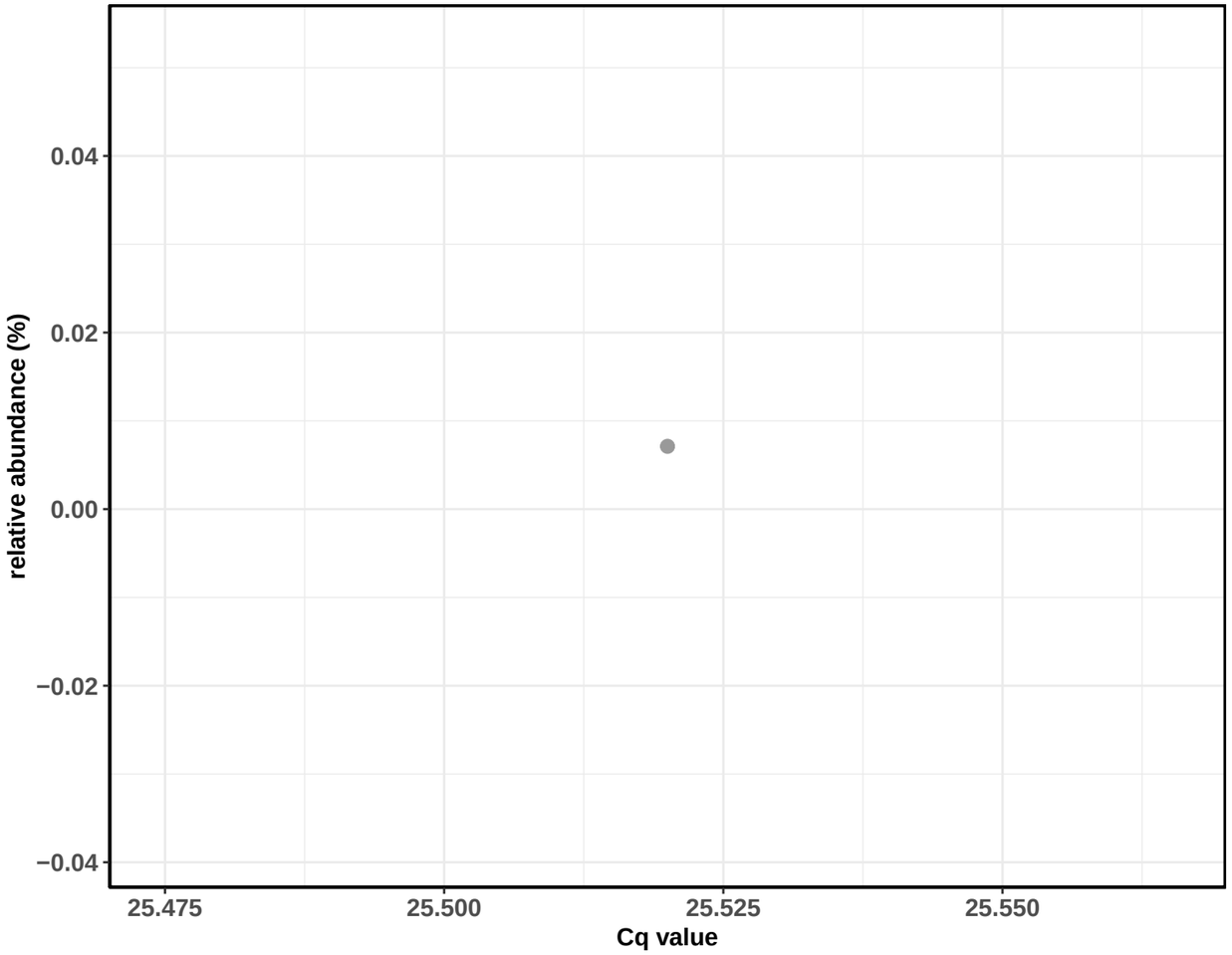


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Micrococcales; D_4__Micrococcaceae; D_5__Micrococcus; Ambiguous_taxa

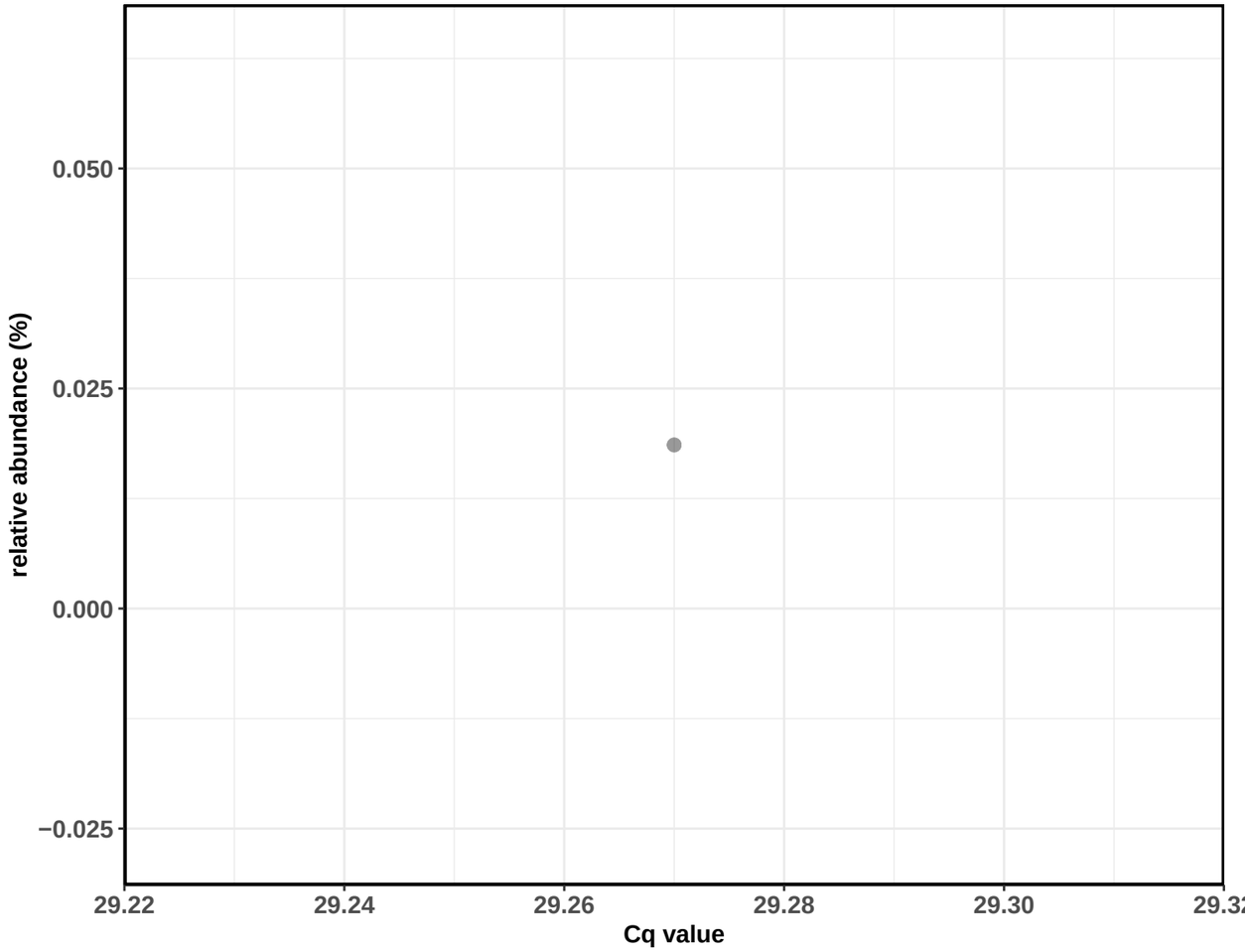
Correlation with all samples



Correlation within the sample type: REF−DIC

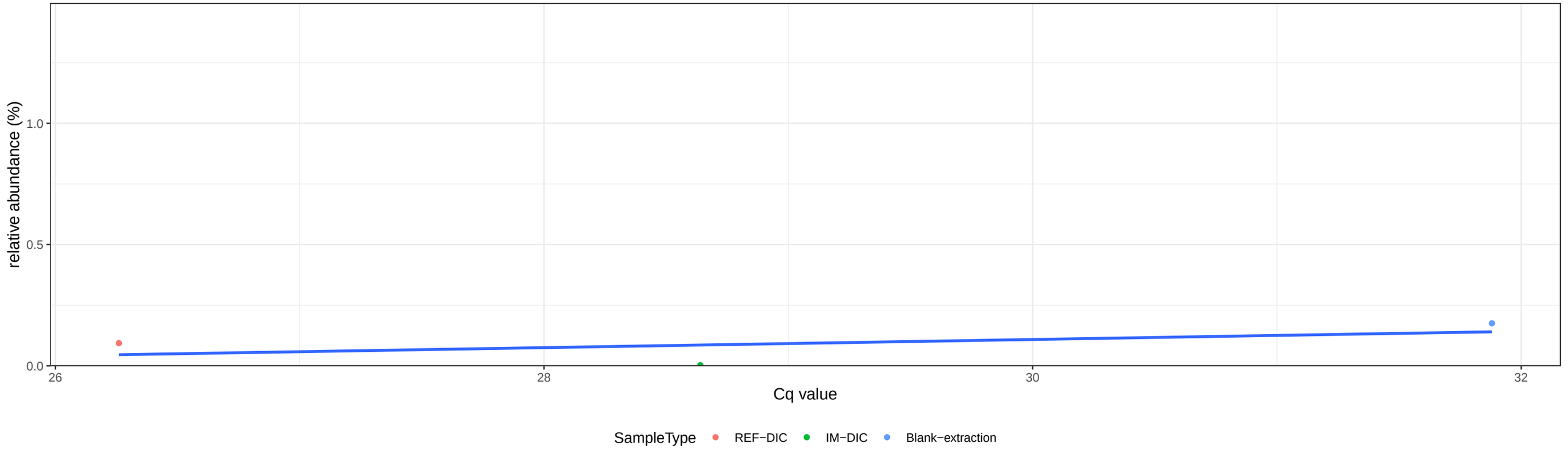


Correlation within the sample type: IM−DIC

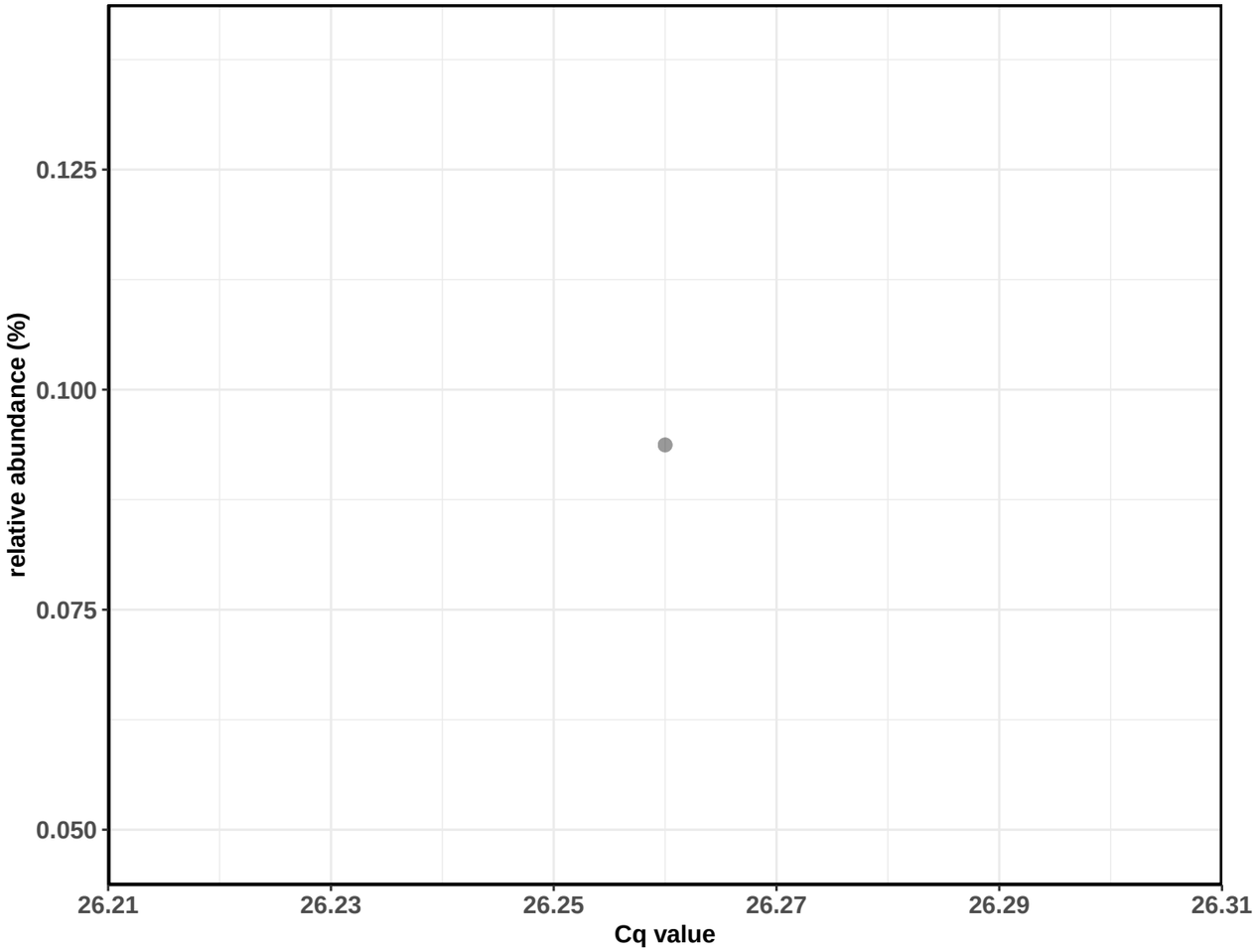


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

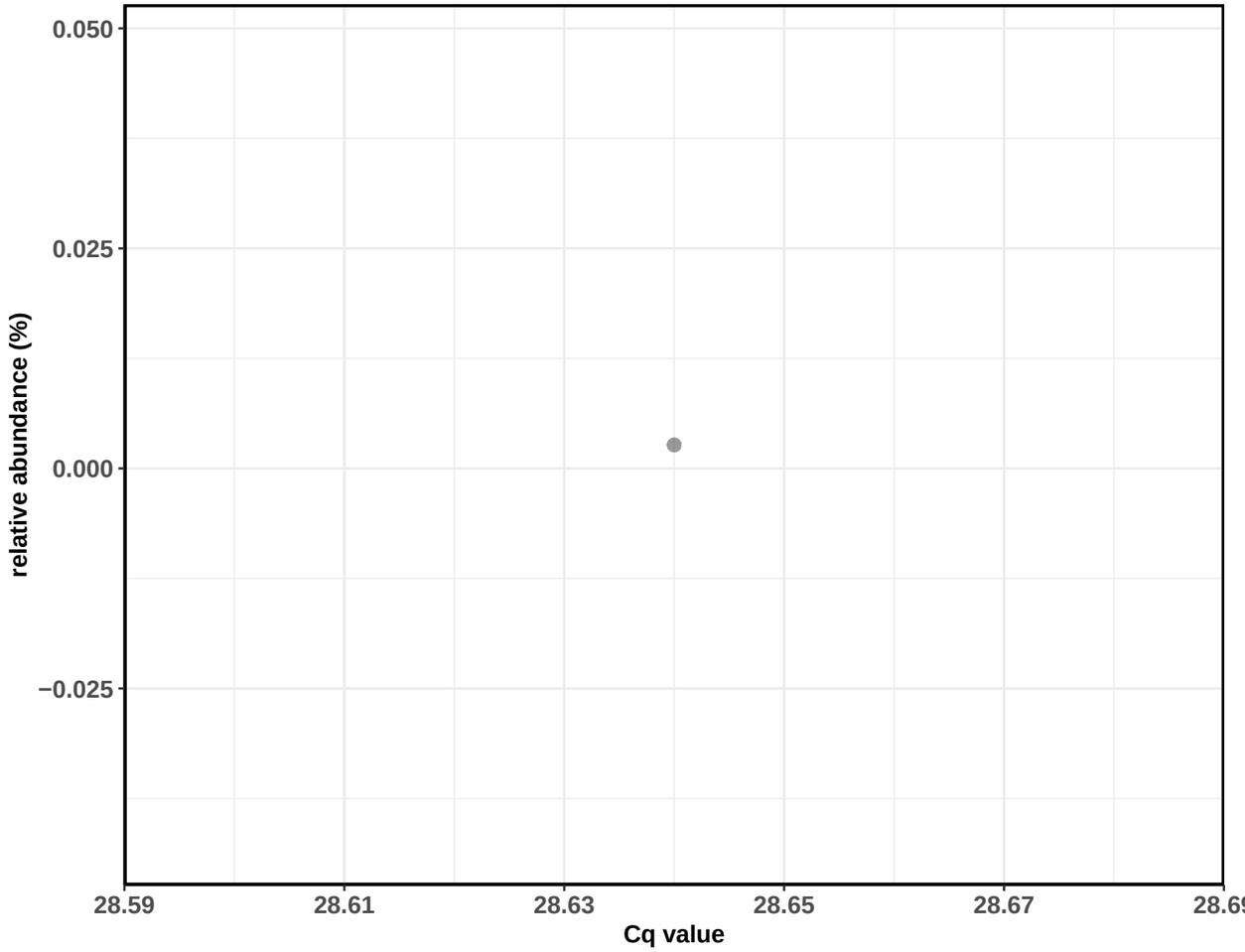
Correlation with all samples



Correlation within the sample type: REF−DIC

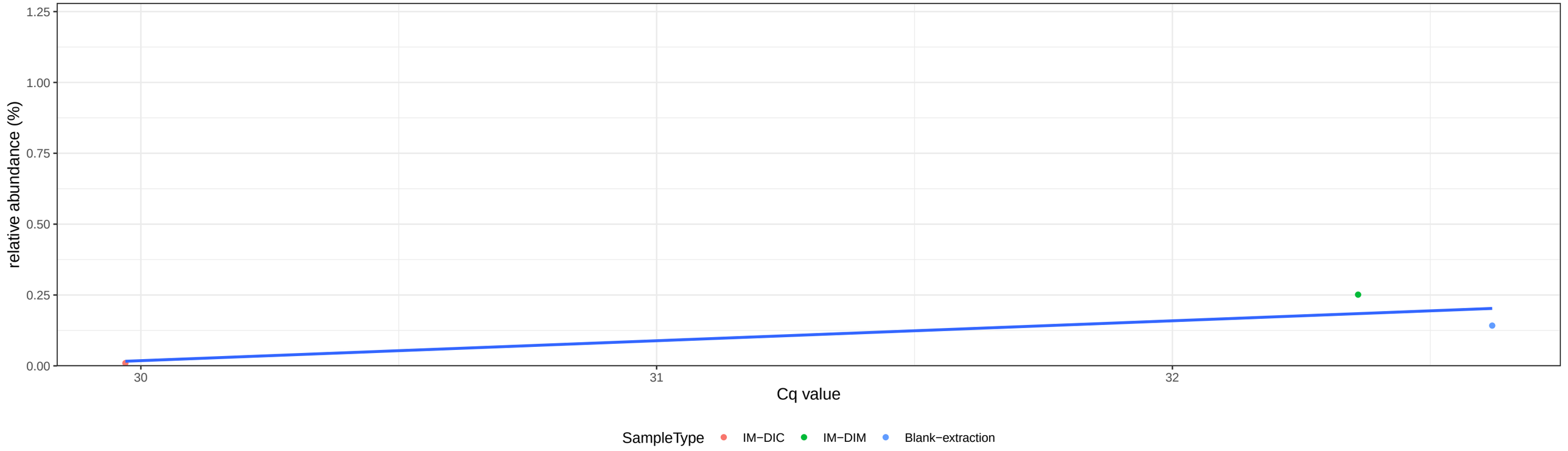


Correlation within the sample type: IM−DIC

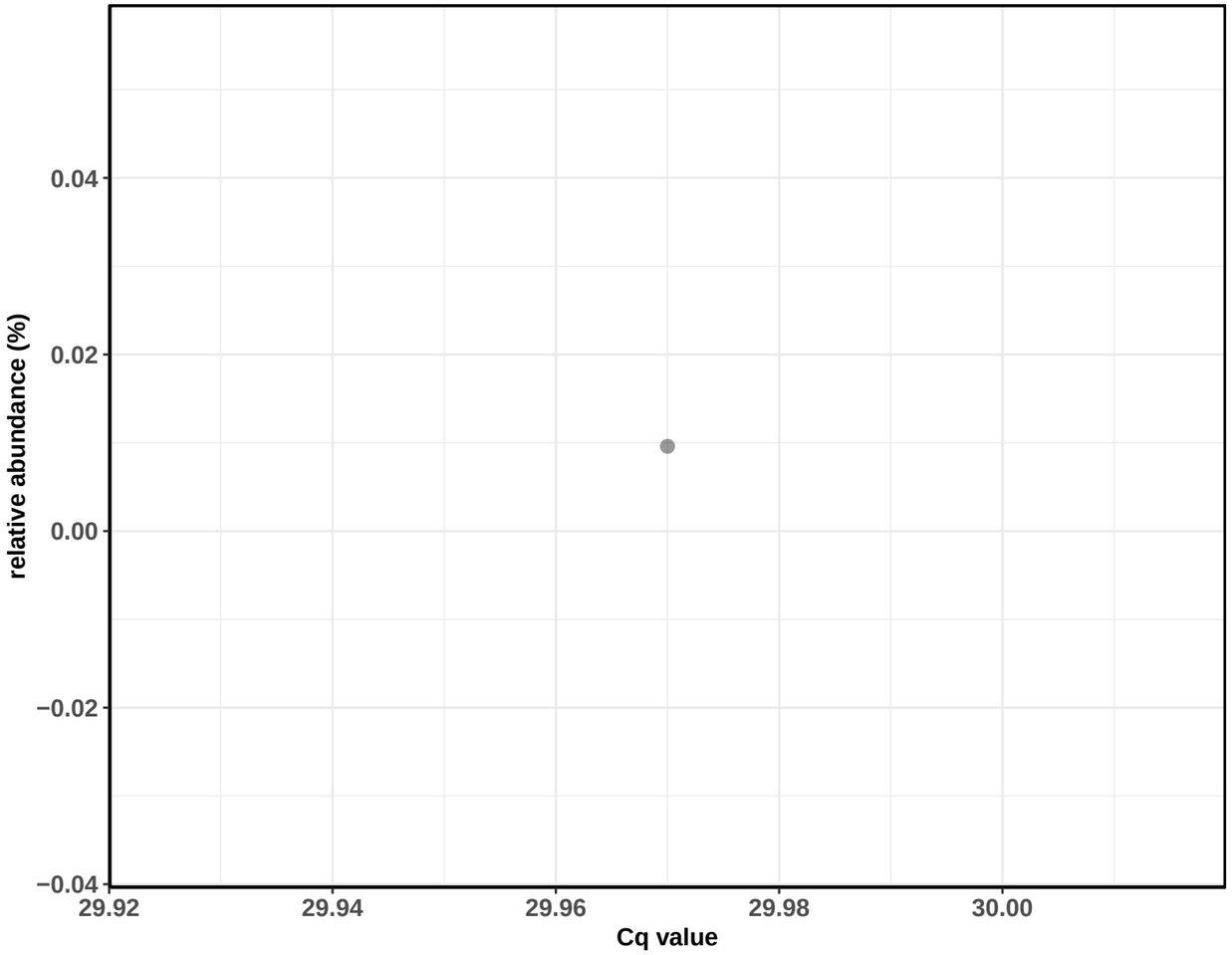


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Sphingomonadales; D_4__Sphingomonadaceae; D_5__Sphingomonas; Ambiguous_taxa

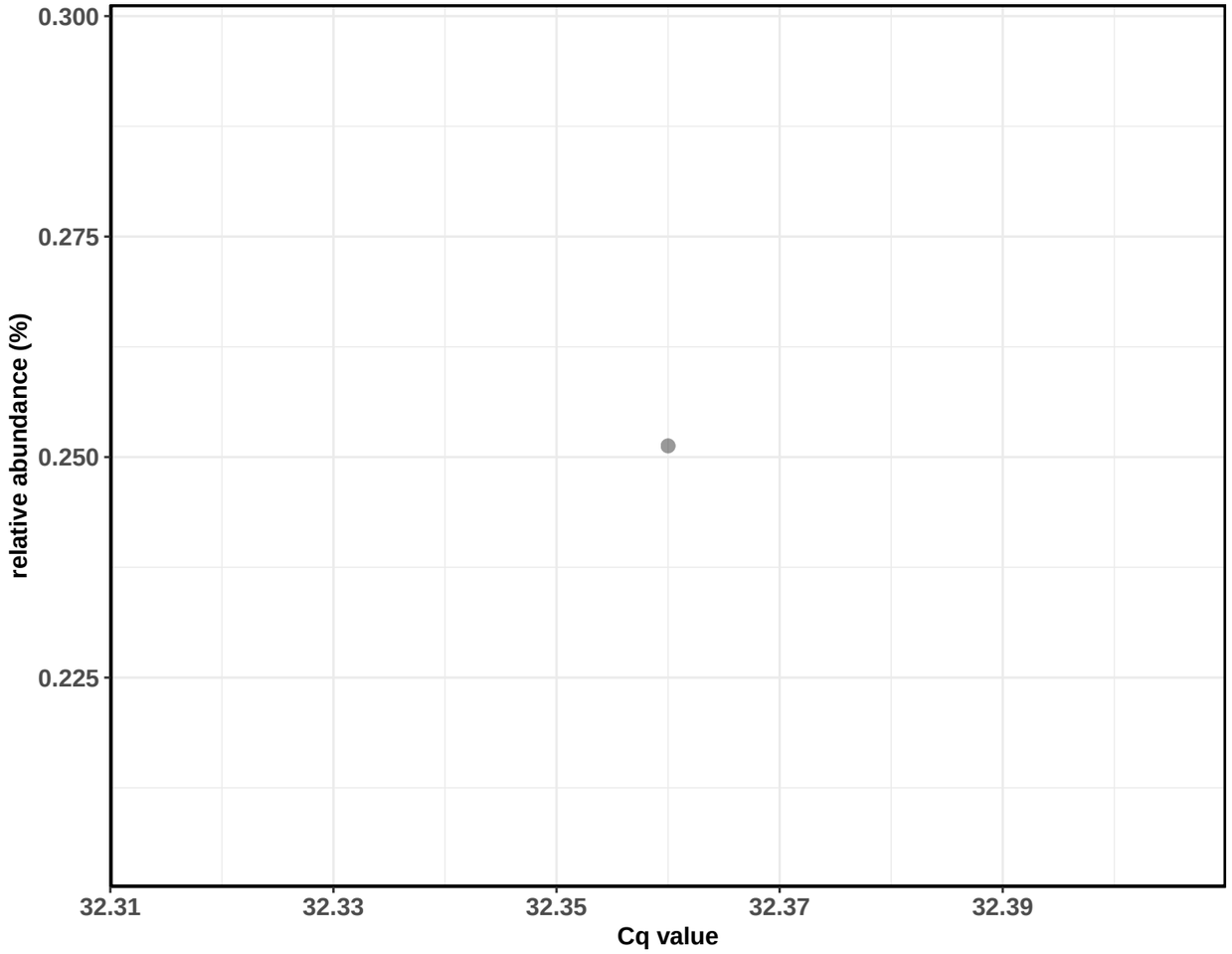
Correlation with all samples



Correlation within the sample type: IM−DIC

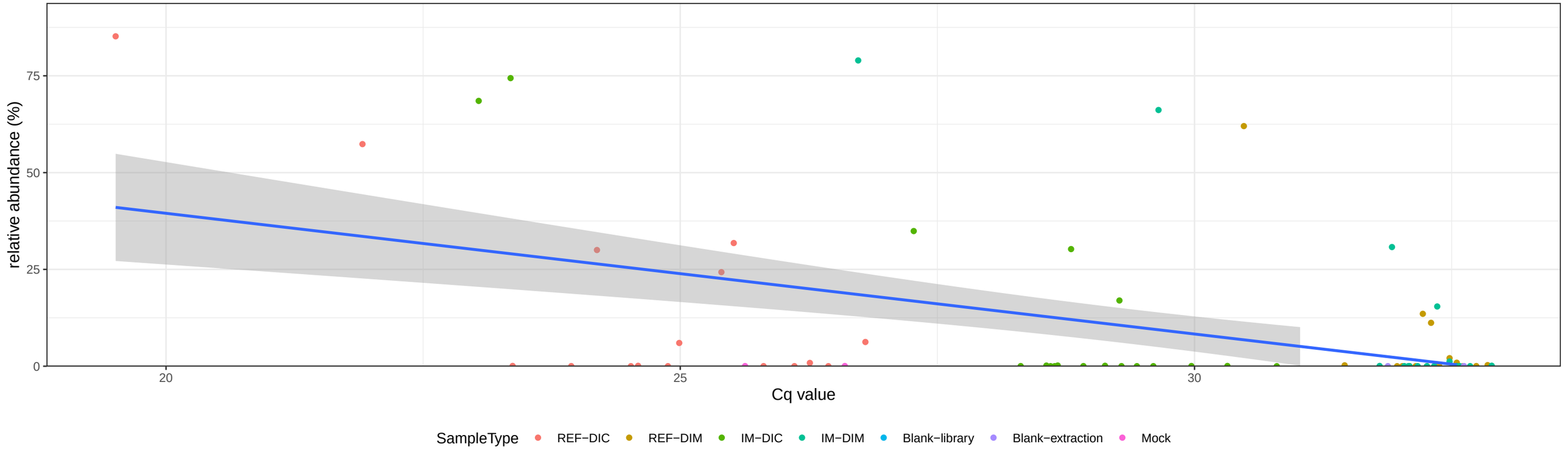


Correlation within the sample type: IM−DIM



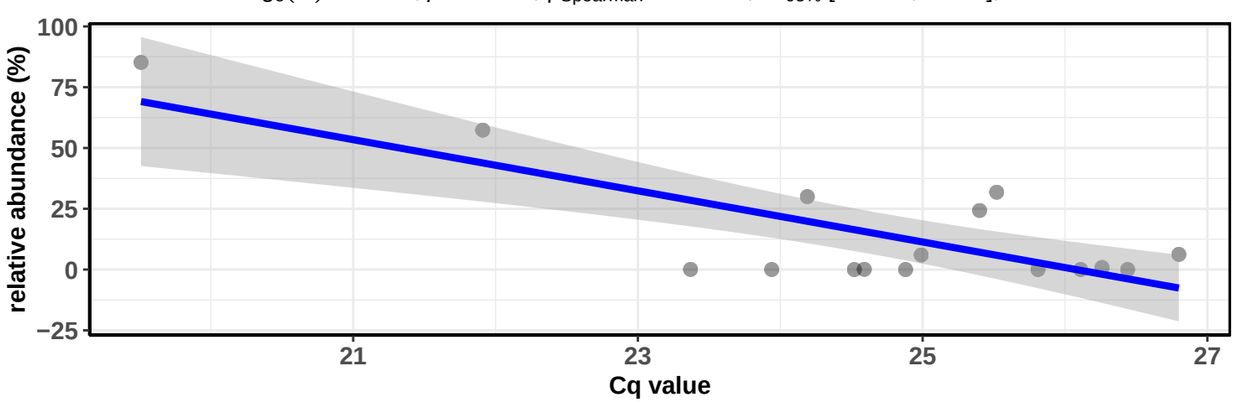
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Aliivibrio; D_6__uncultured bacterium

Correlation with all samples



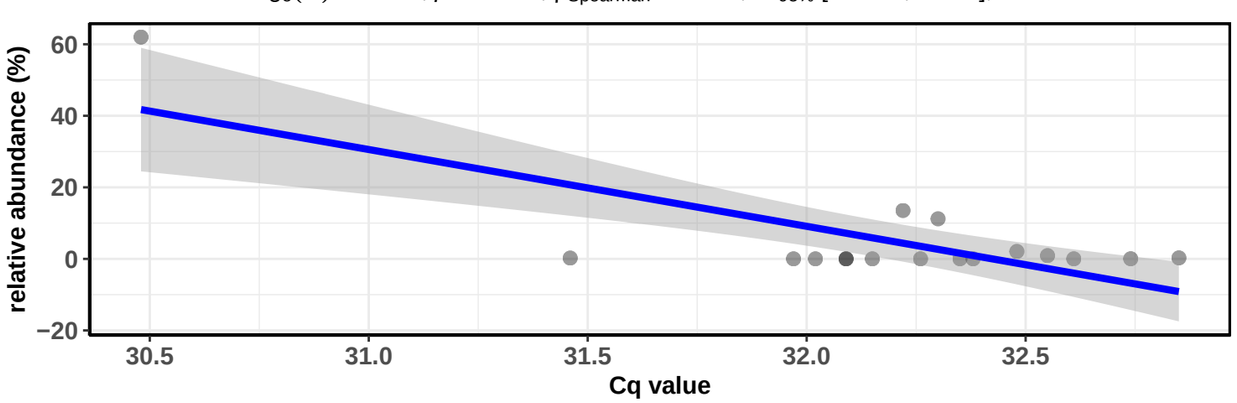
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.793, p = 0.240, $\rho_{Spearman}$ = −0.312, $CI_{95\%}$ [−0.699, 0.218], n = 16



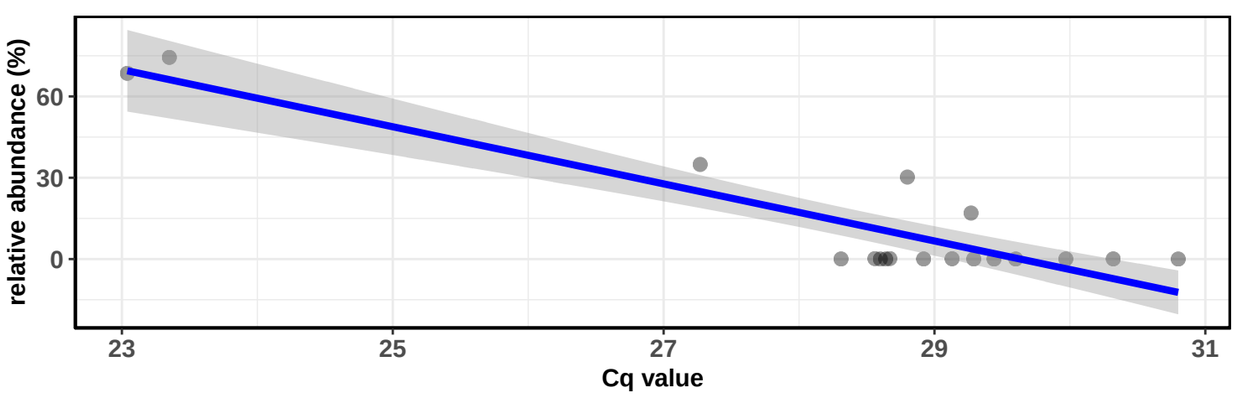
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.525, p = 0.529, $\rho_{Spearman}$ = 0.164, $CI_{95\%}$ [−0.343, 0.598], n = 17



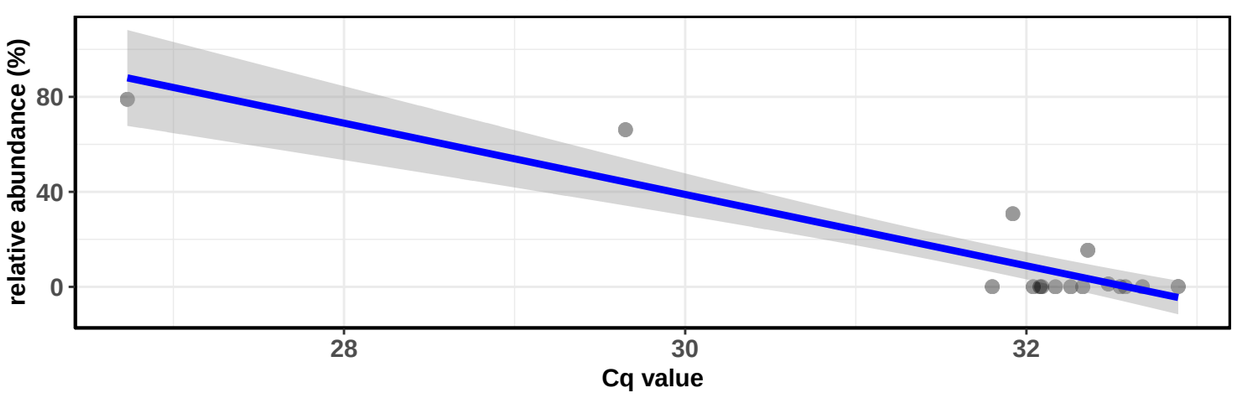
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 7.305, p = 0.022, $\rho_{Spearman}$ = −0.536, $CI_{95\%}$ [−0.802, −0.092], n = 18



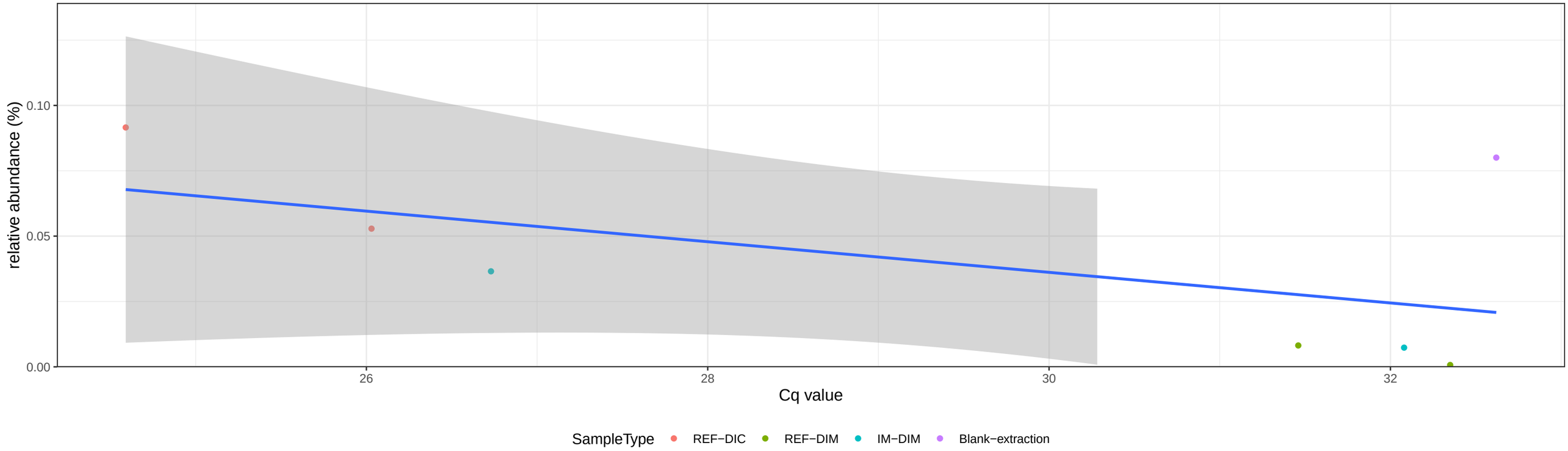
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.859, p = 0.125, $\rho_{Spearman}$ = −0.400, $CI_{95\%}$ [−0.747, 0.119], n = 16

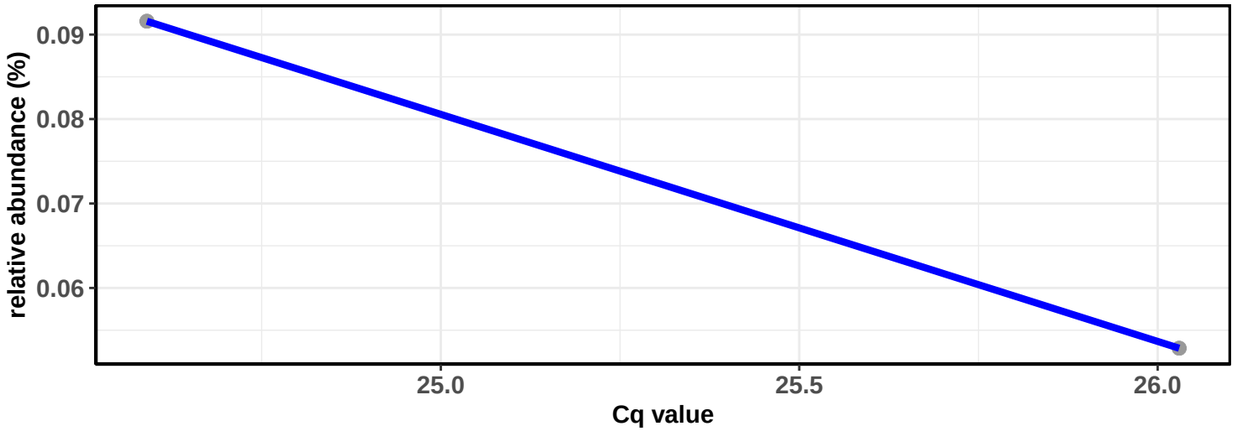


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Sphingomonadales; D_4__Sphingomonadaceae; D_5__Sphingomonas; Ambiguous_taxa

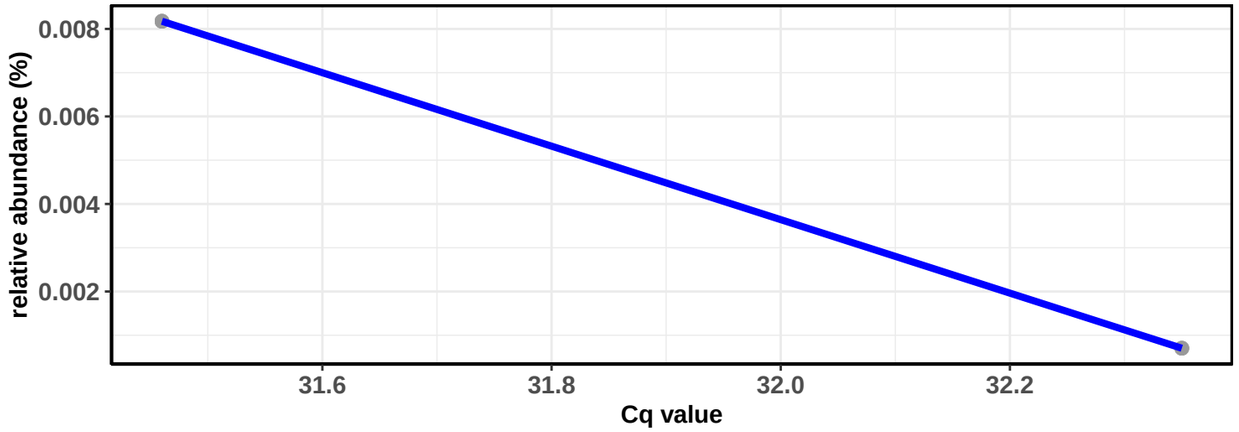
Correlation with all samples



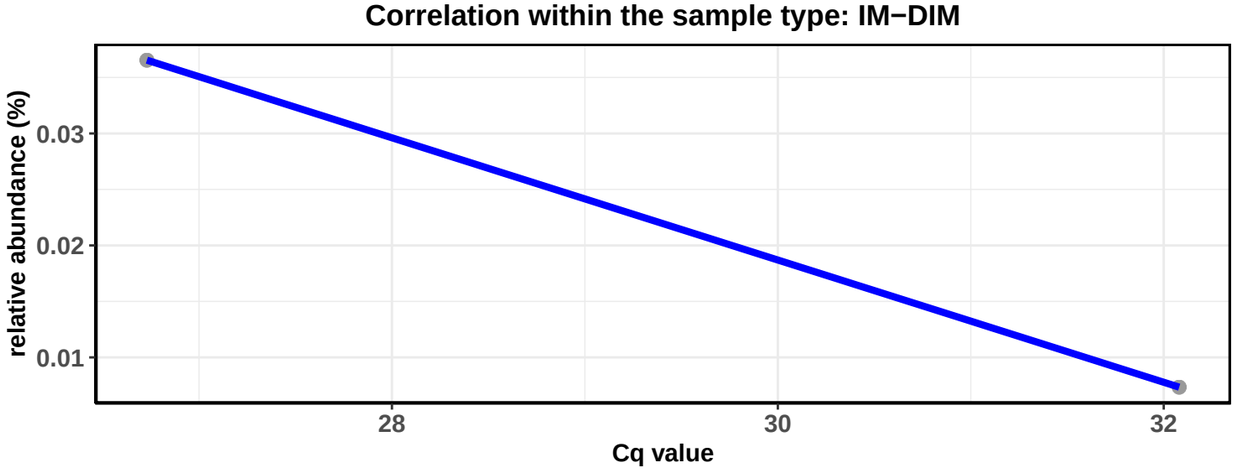
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

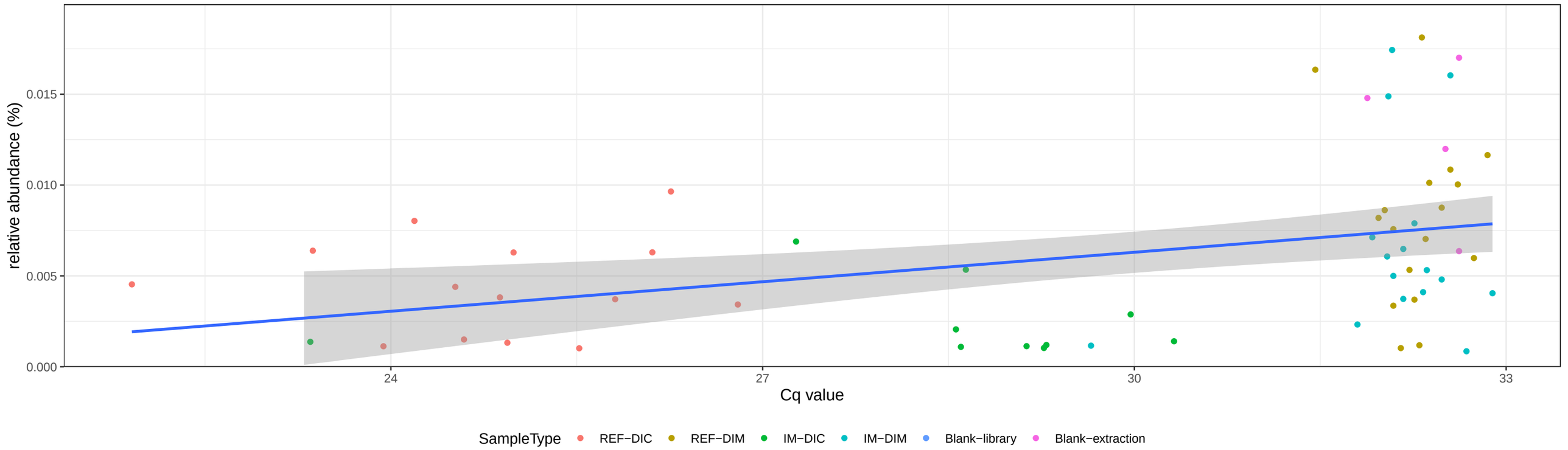


Correlation within the sample type: IM−DIM



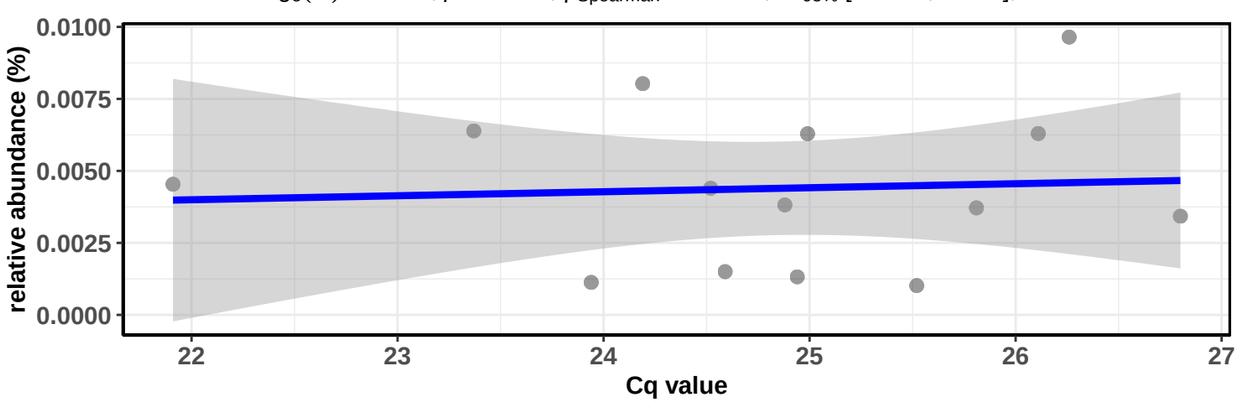
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



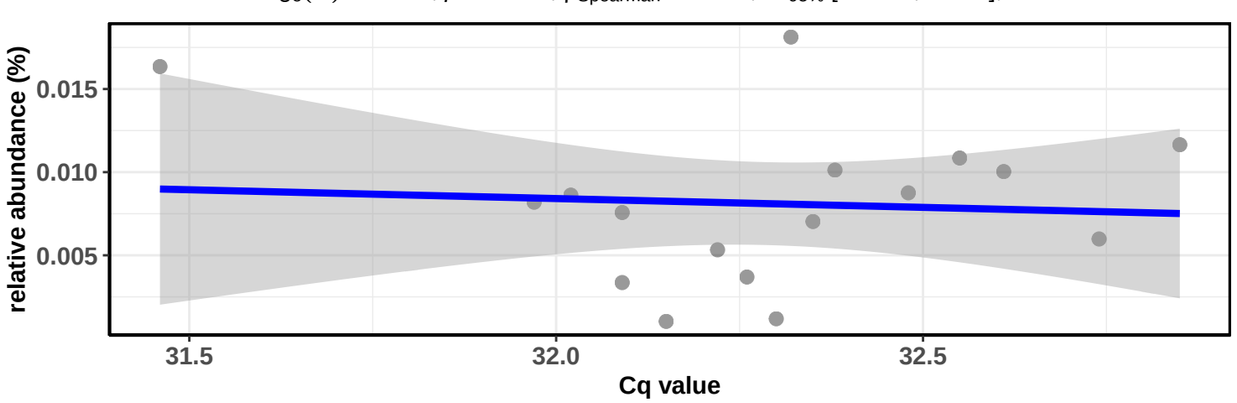
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.161, p = 0.887, $\rho_{Spearman}$ = −0.042, $CI_{95\%}$ [−0.560, 0.500], n = 14



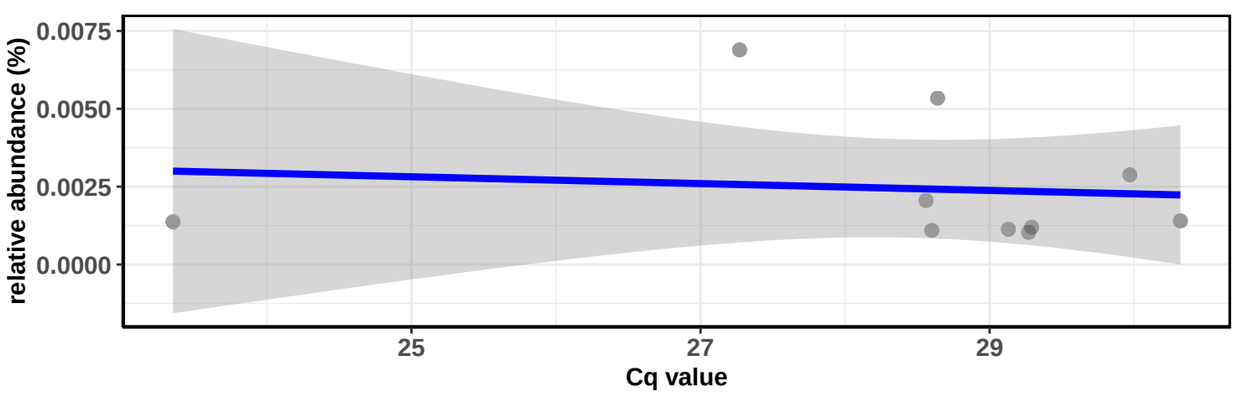
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.421, p = 0.340, $\rho_{Spearman}$ = 0.246, $CI_{95\%}$ [−0.266, 0.650], n = 17



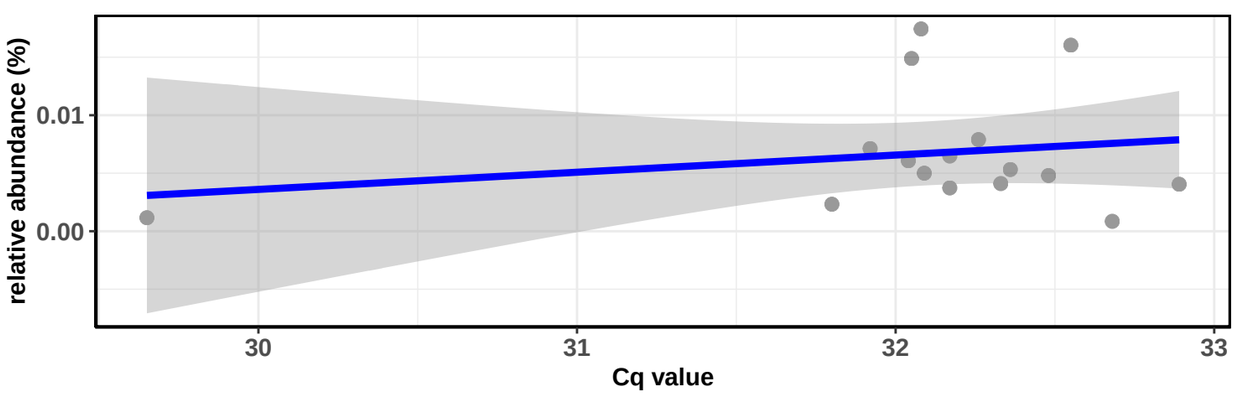
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.268, p = 0.627, $\rho_{Spearman}$ = −0.176, $CI_{95\%}$ [−0.725, 0.510], n = 10



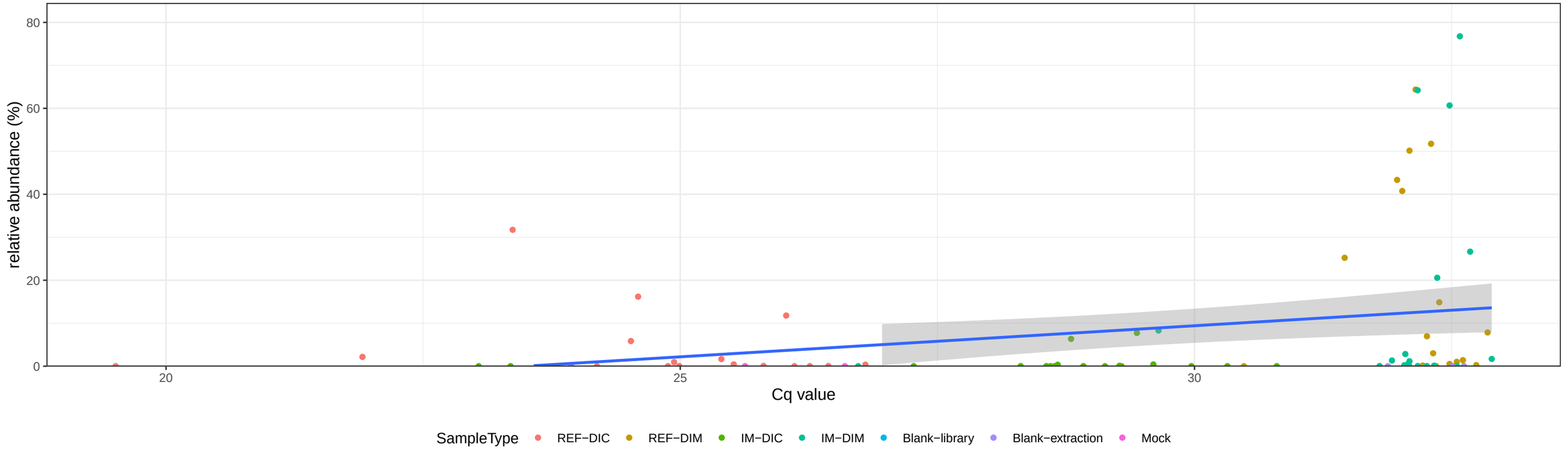
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.586, p = 0.807, $\rho_{Spearman}$ = −0.066, $CI_{95\%}$ [−0.544, 0.444], n = 16



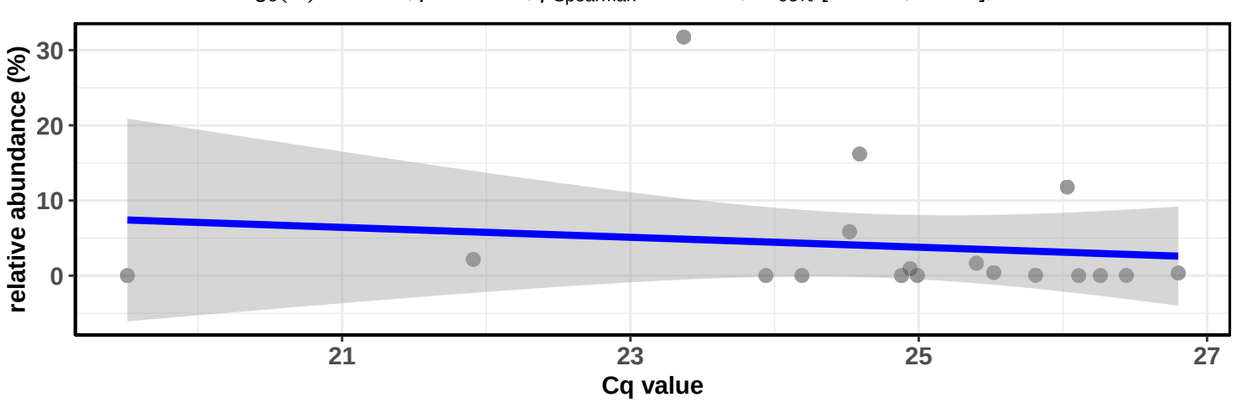
D_0__Bacteria; D_1__Spirochaetes; D_2__Spirochaetia; D_3__Brevinematales; D_4__Brevinemataceae; D_5__Brevinema; D_6__Brevinema andersonii

Correlation with all samples



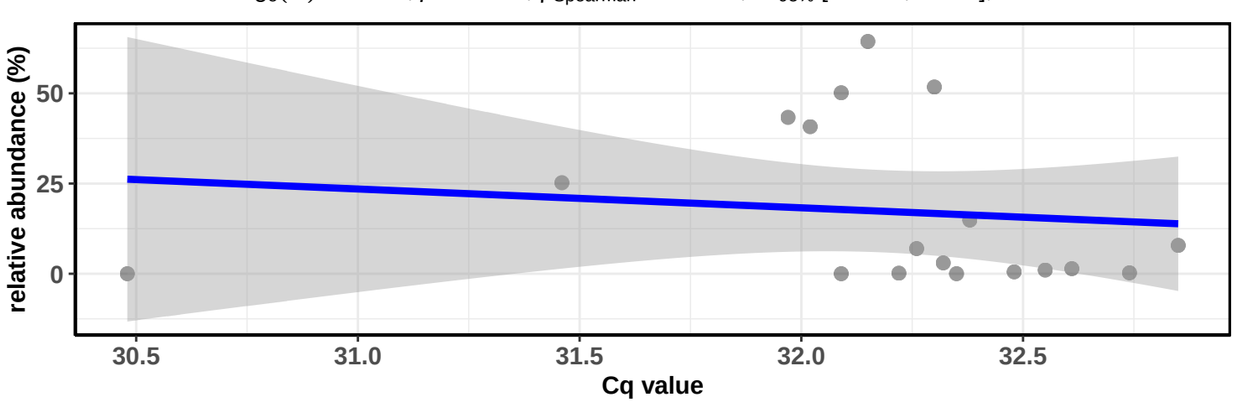
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 7.051, p = 0.448, $\rho_{Spearman}$ = −0.191, $CI_{95\%}$ [−0.604, 0.303], n = 18



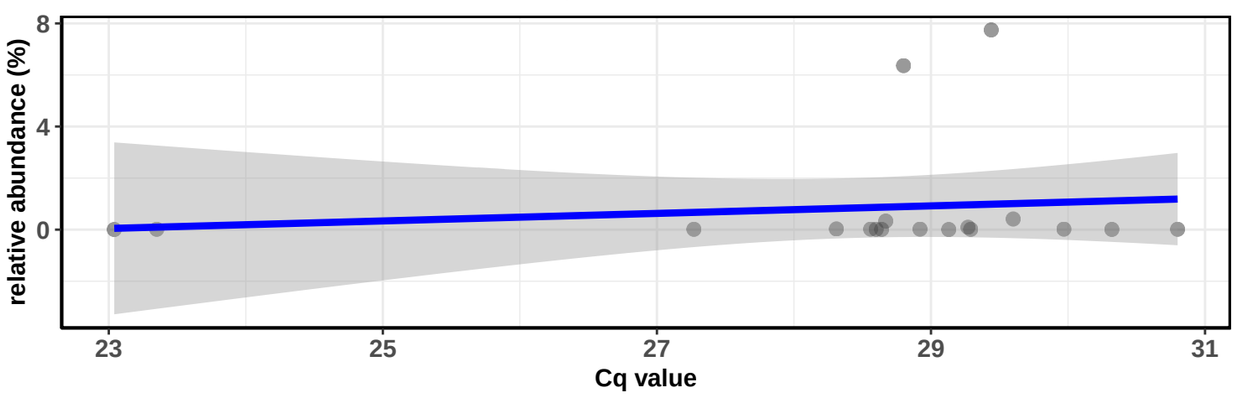
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 7.044, p = 0.468, $\rho_{Spearman}$ = −0.183, $CI_{95\%}$ [−0.599, 0.311], n = 18



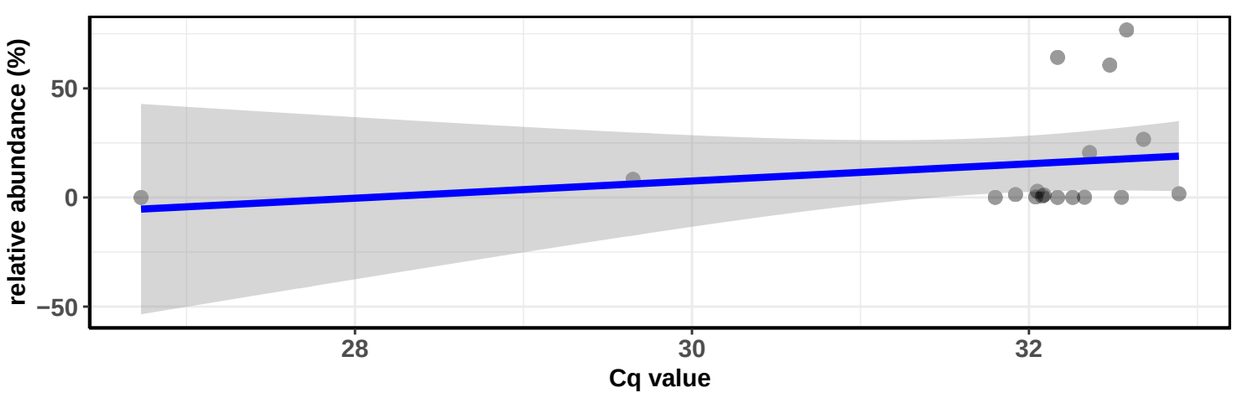
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.654, p = 0.428, $\rho_{Spearman}$ = 0.199, $CI_{95\%}$ [−0.295, 0.609], n = 18



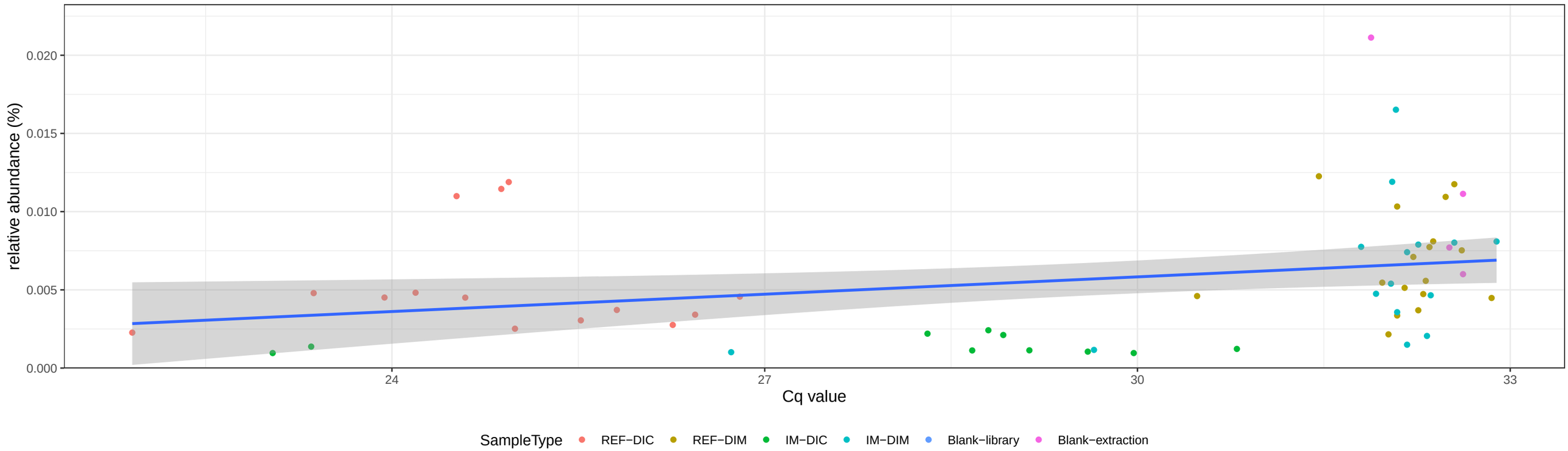
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.359, p = 0.097, $\rho_{Spearman}$ = 0.404, $CI_{95\%}$ [−0.078, 0.733], n = 18



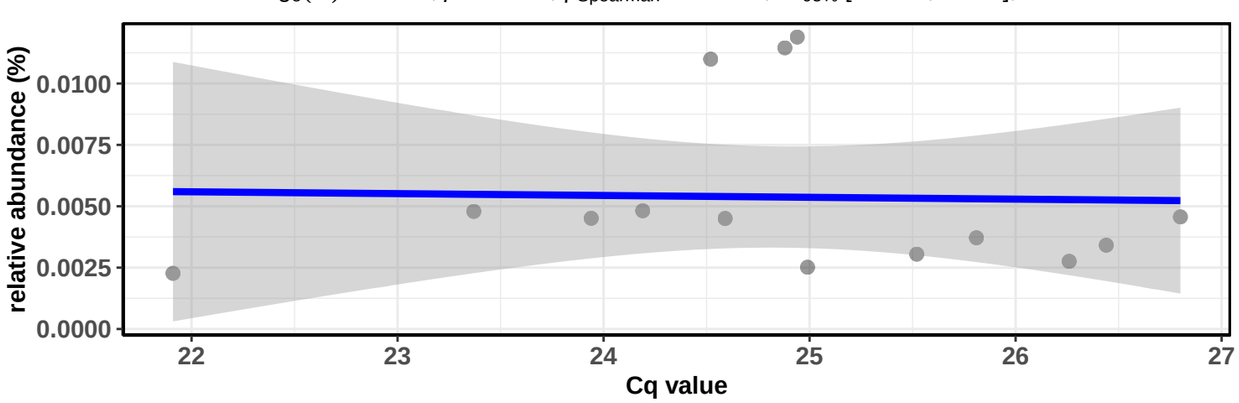
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



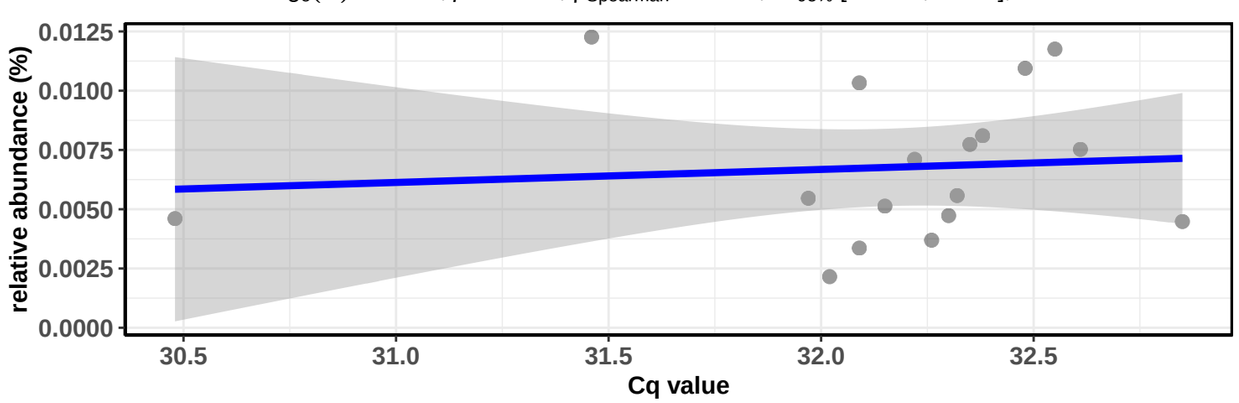
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.292, p = 0.523, $\rho_{Spearman}$ = −0.187, $CI_{95\%}$ [−0.653, 0.382], n = 14



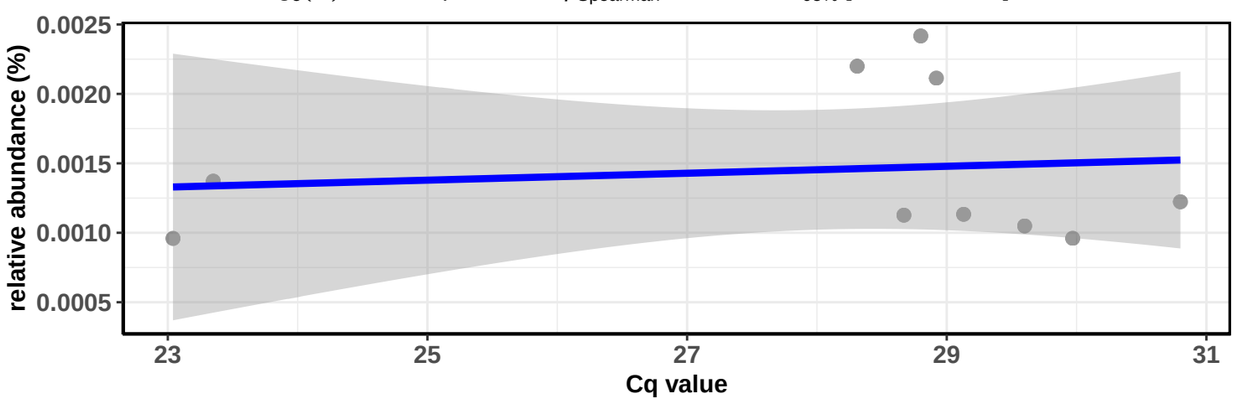
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.423, p = 0.343, $\rho_{Spearman}$ = 0.245, $CI_{95\%}$ [−0.267, 0.649], n = 17



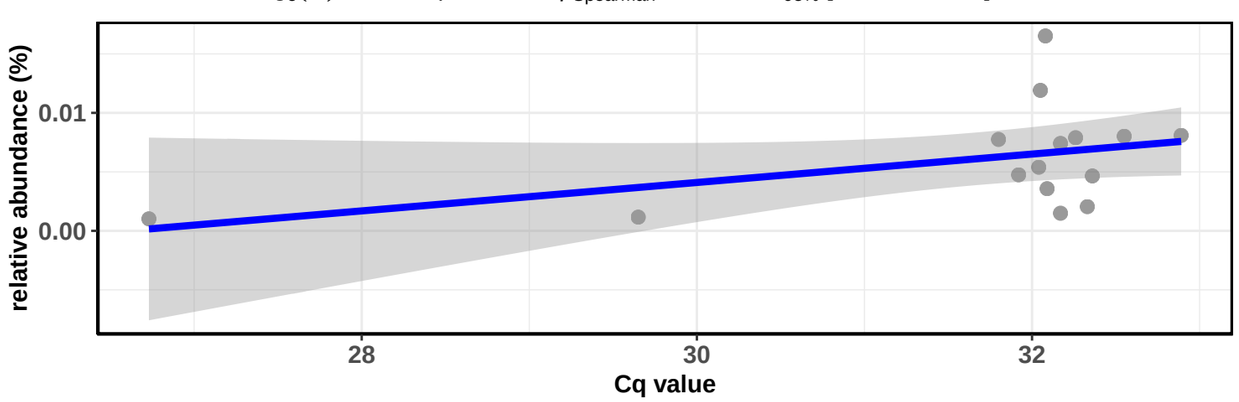
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.215, p = 0.751, $\rho_{Spearman}$ = −0.115, $CI_{95\%}$ [−0.694, 0.555], n = 10



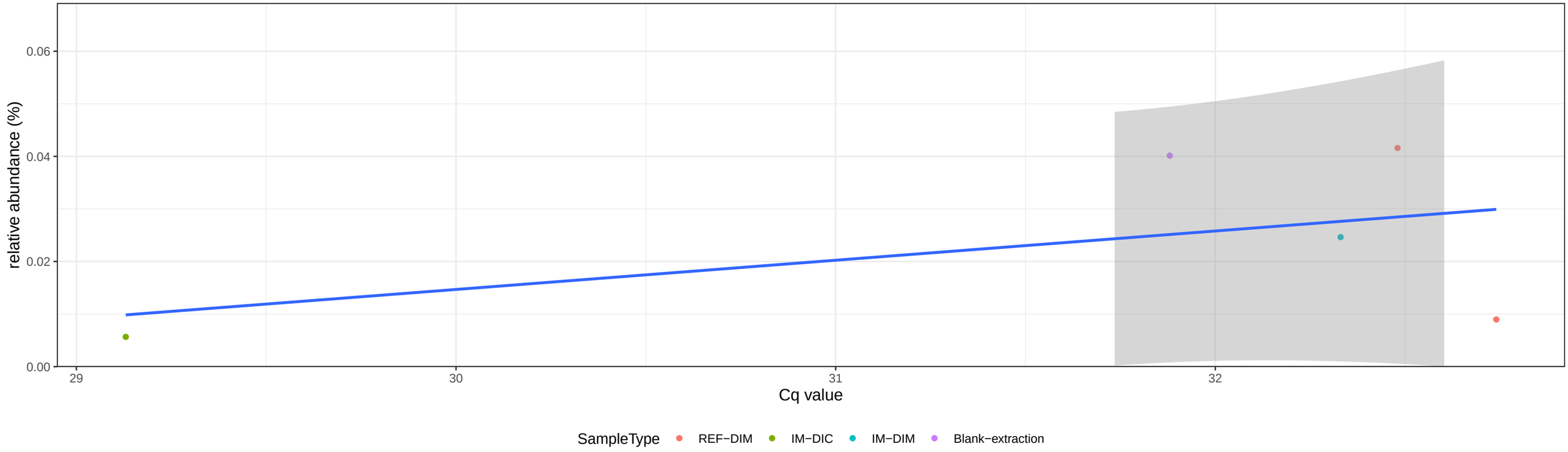
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.908, p = 0.210, $\rho_{Spearman}$ = 0.343, $CI_{95\%}$ [−0.205, 0.728], n = 15

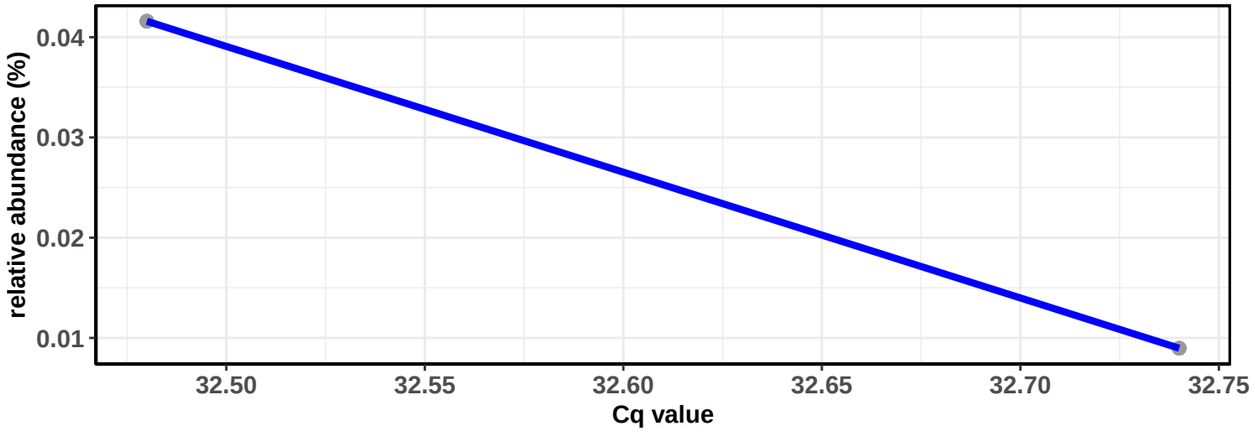


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Rhizobiales; D_4__Devosiaceae; D_5__Devosia

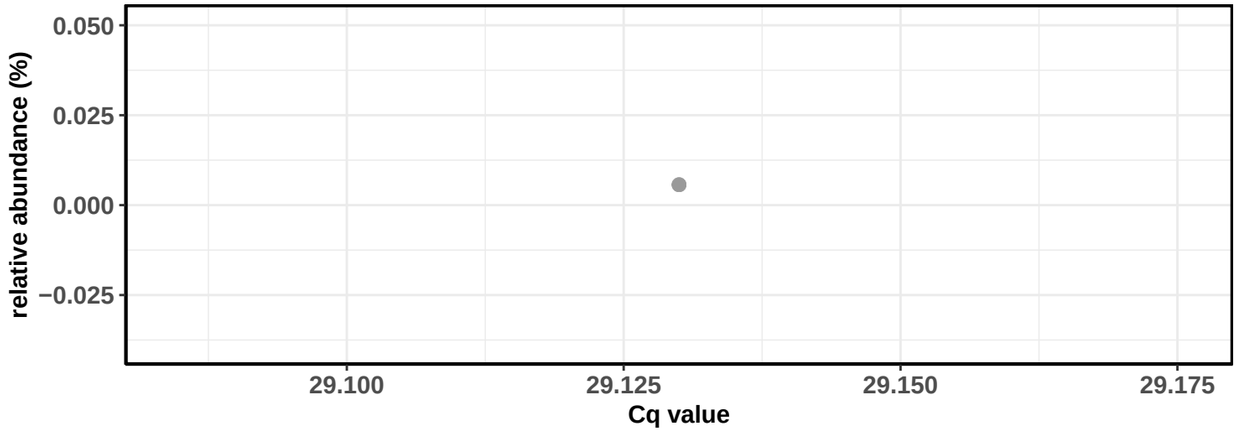
Correlation with all samples



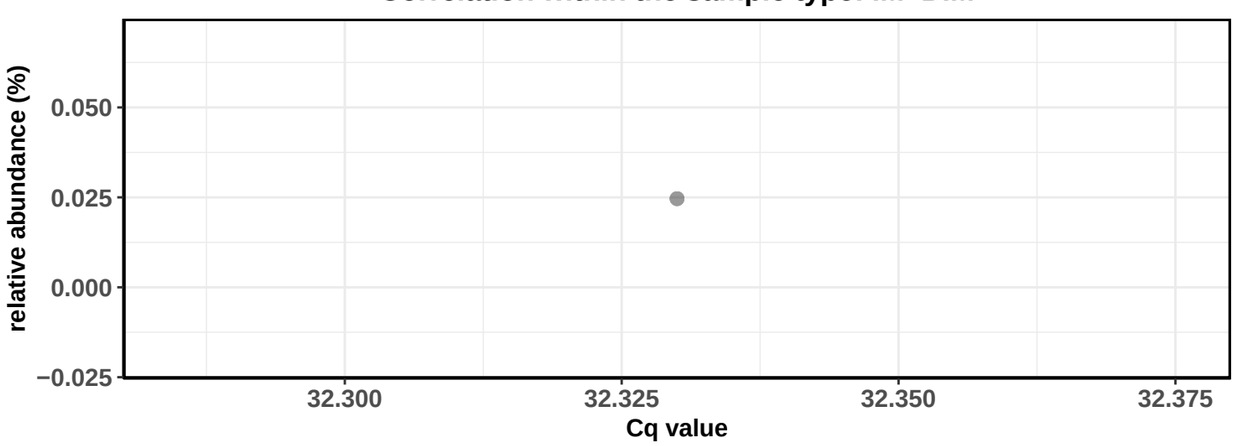
Correlation within the sample type: REF−DIM



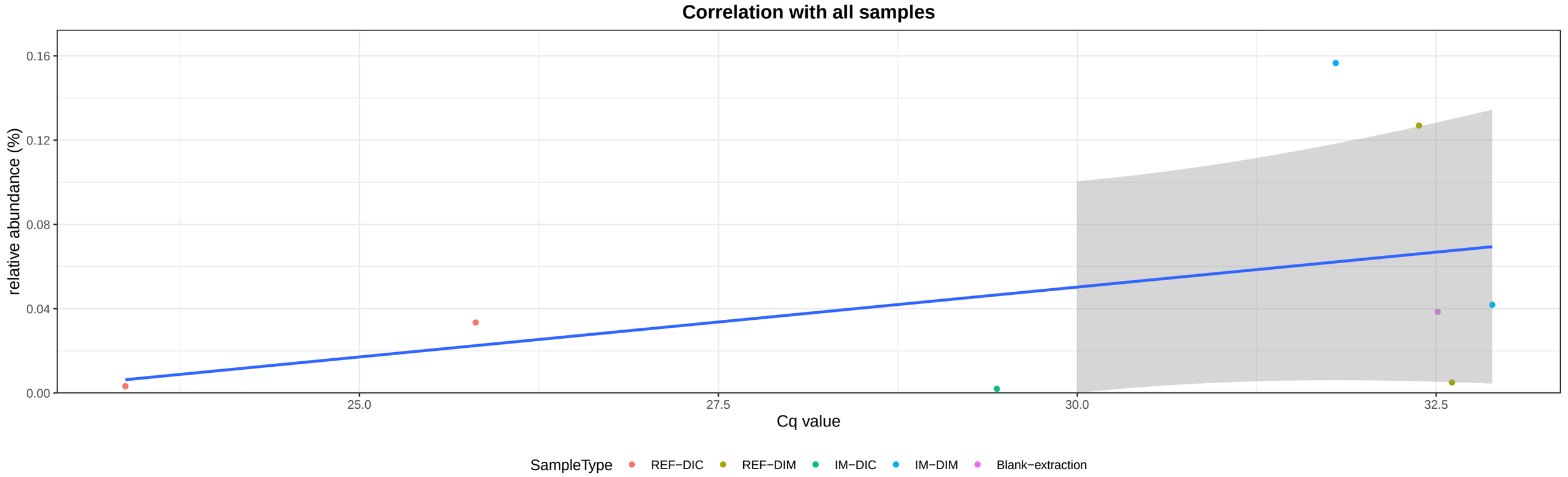
Correlation within the sample type: IM−DIC

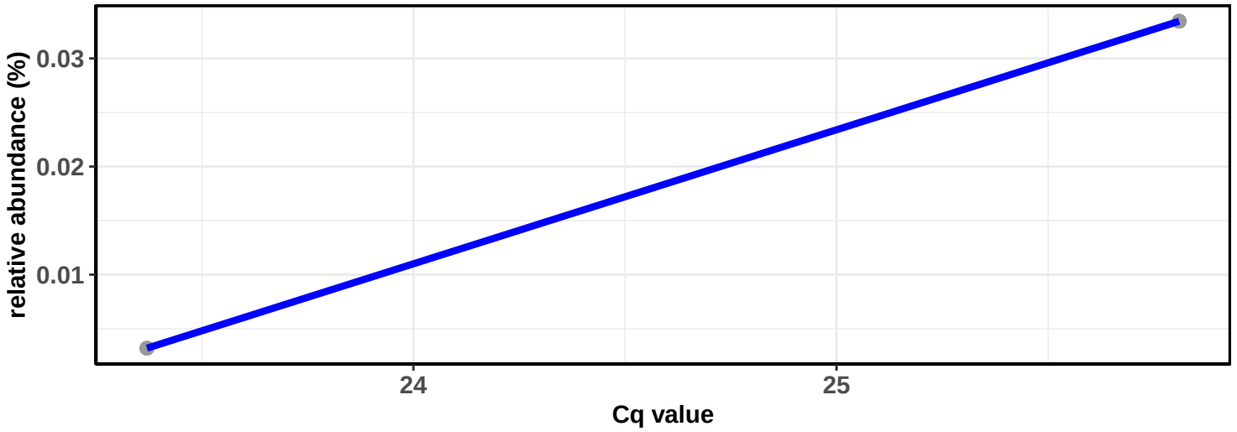


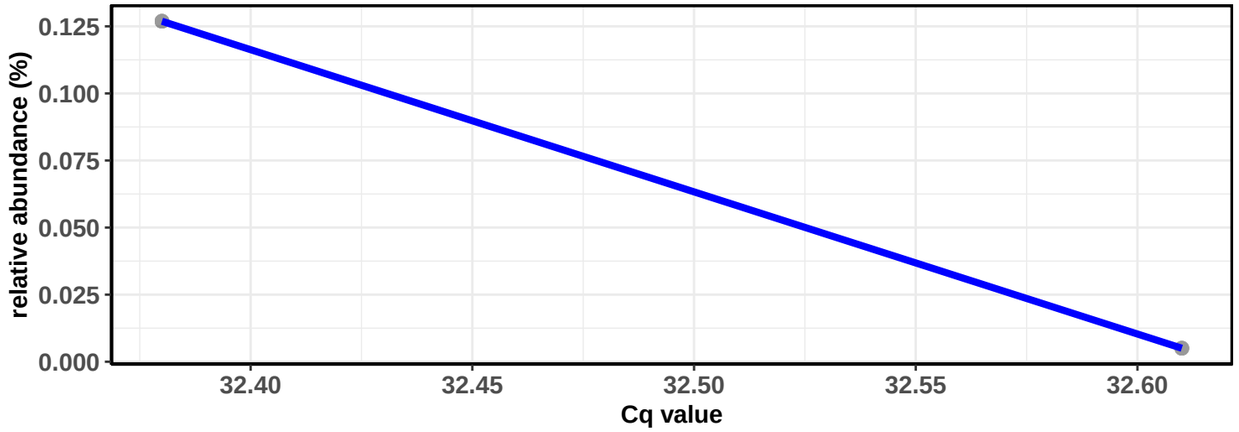
Correlation within the sample type: IM−DIM

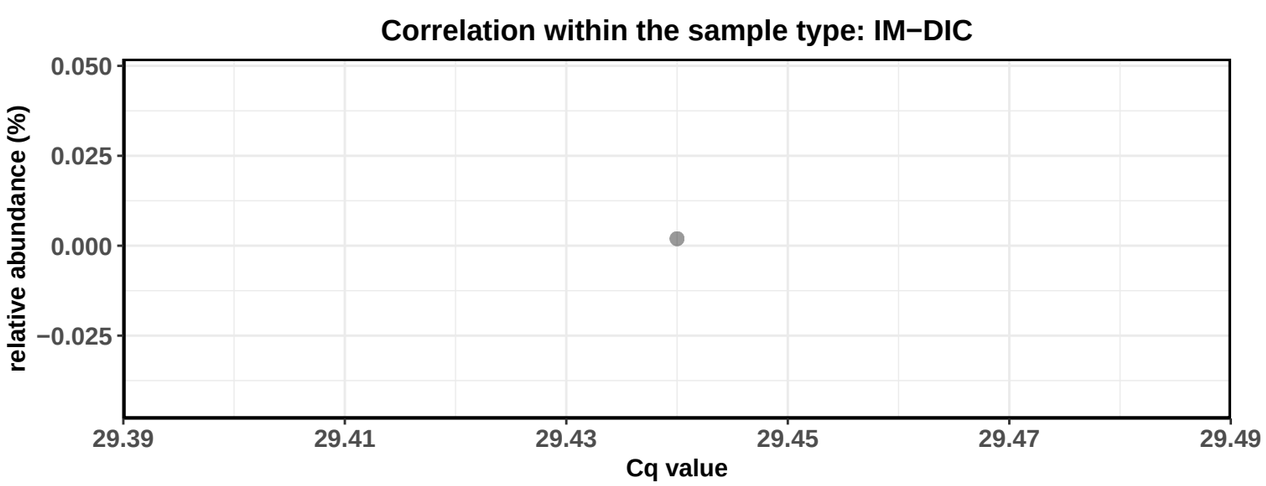


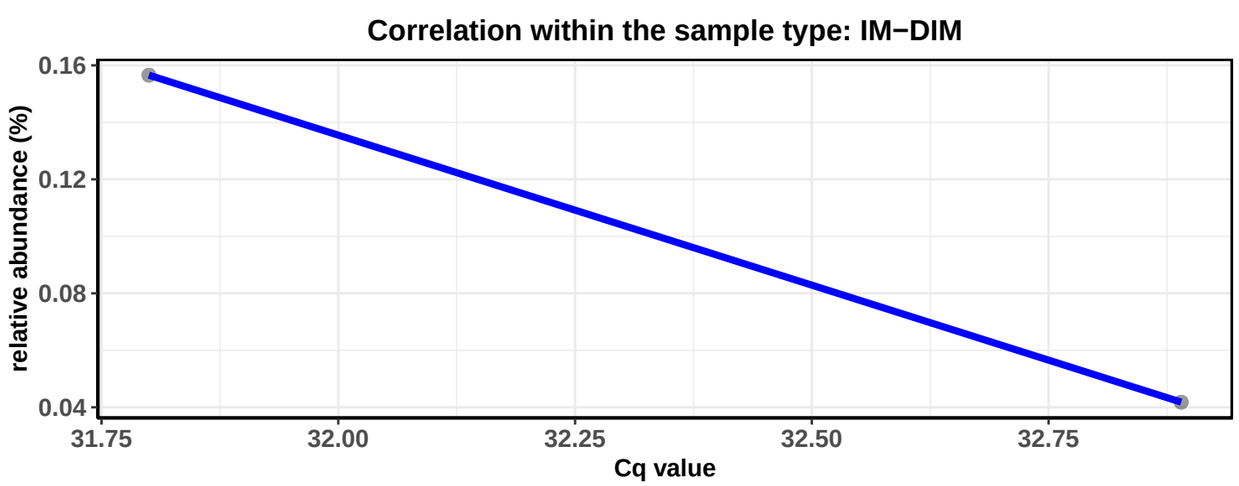
_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Sphingomonadales; D_4__Sphingomonadaceae; D_5__Sphingomonas; D_6__Sphingomonas aurantiac





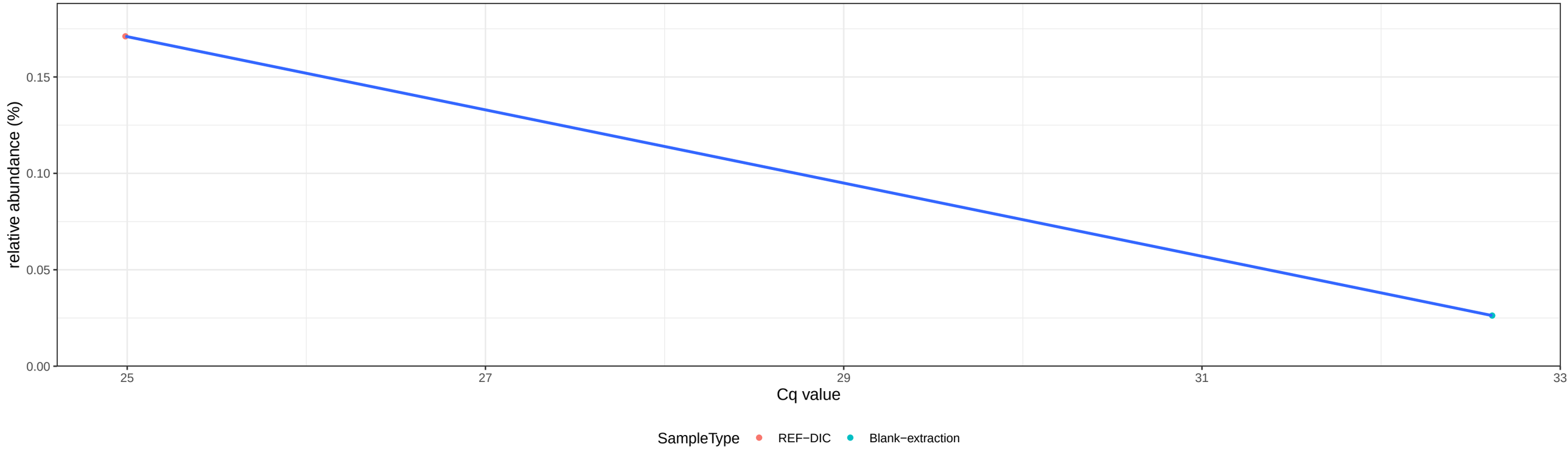




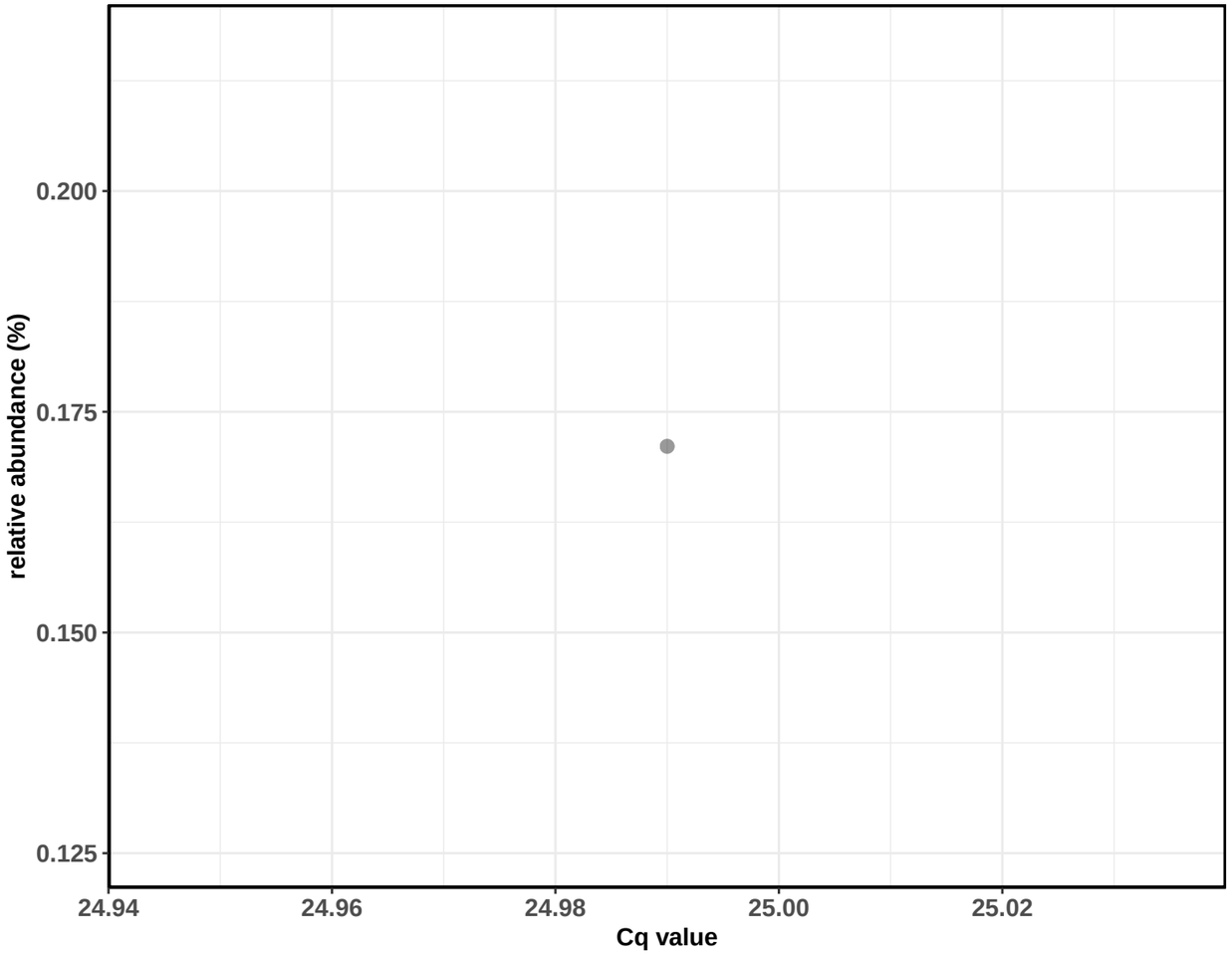


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured Hymenobacter sp.

Correlation with all samples

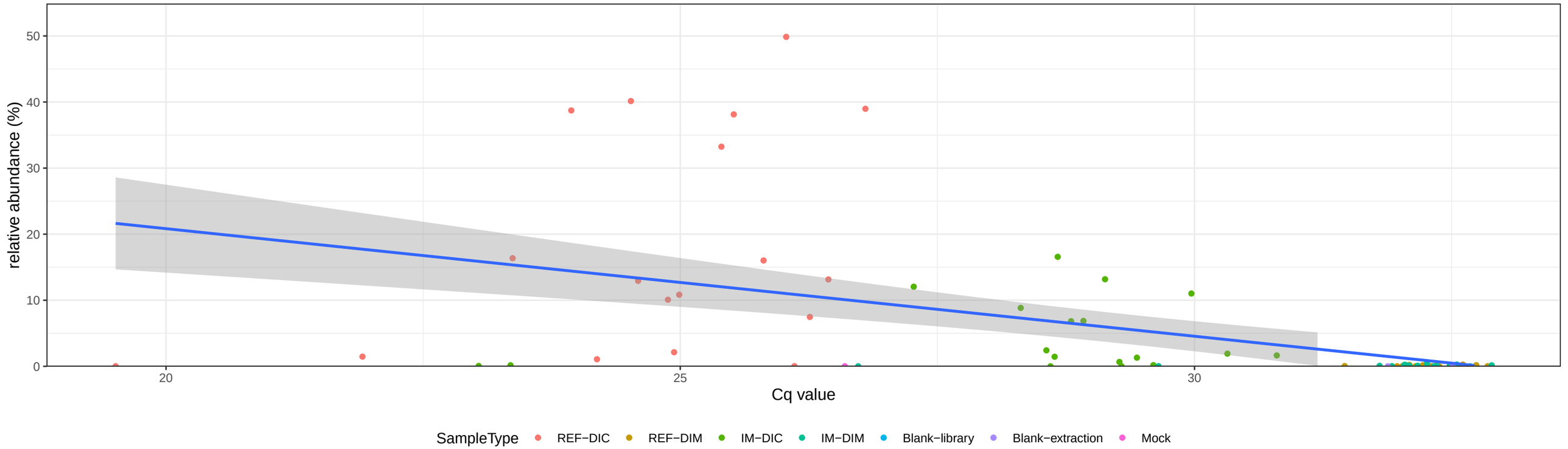


Correlation within the sample type: REF−DIC



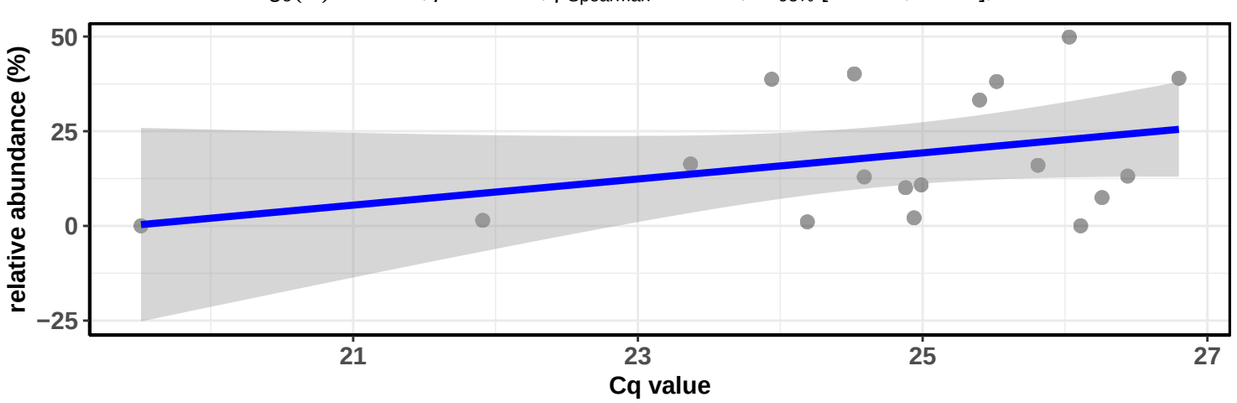
D_0__Bacteria; D_1__Tenericutes; D_2__Mollicutes; D_3__Mycoplasmatales; D_4__Mycoplasmataceae; D_5__Mycoplasma; D_6__uncultured bacterium

Correlation with all samples



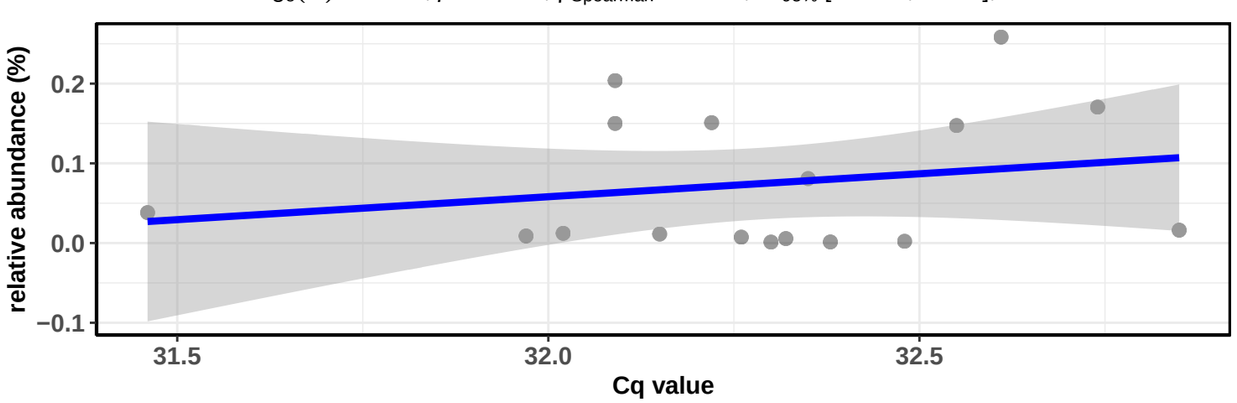
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.560, p = 0.276, $\rho_{Spearman}$ = 0.271, $CI_{95\%}$ [−0.224, 0.655], n = 18



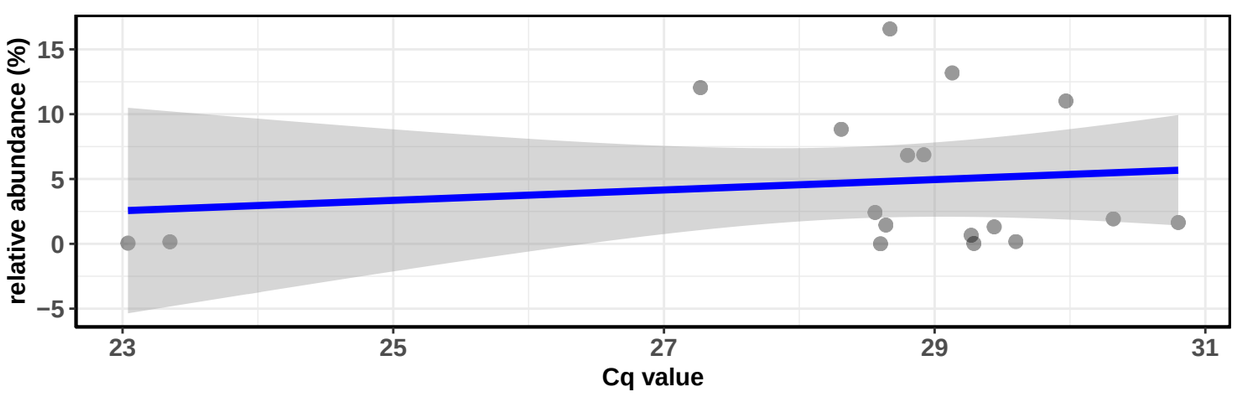
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.632, p = 0.790, $\rho_{Spearman}$ = 0.070, $CI_{95\%}$ [−0.425, 0.533], n = 17



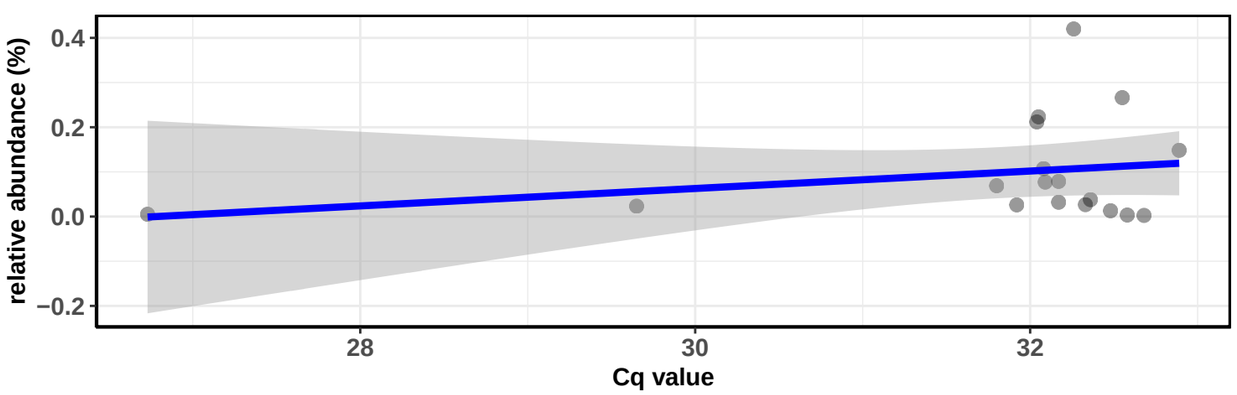
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.835, p = 0.874, $\rho_{Spearman}$ = 0.040, $CI_{95\%}$ [−0.435, 0.498], n = 18



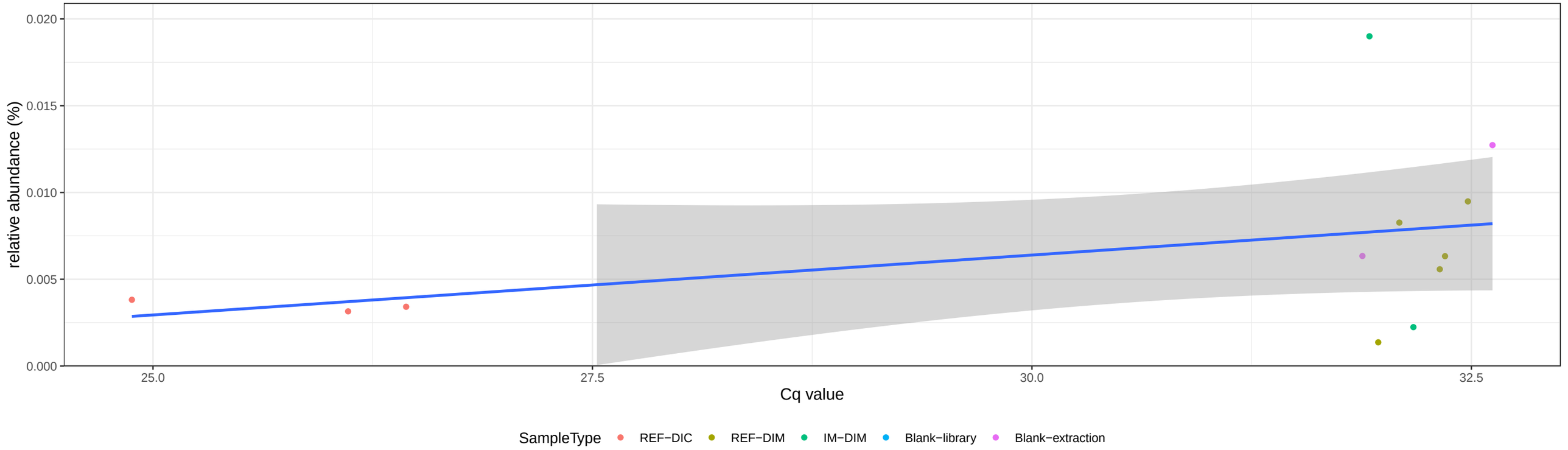
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.890, p = 0.958, $\rho_{Spearman}$ = −0.013, $CI_{95\%}$ [−0.477, 0.456], n = 18

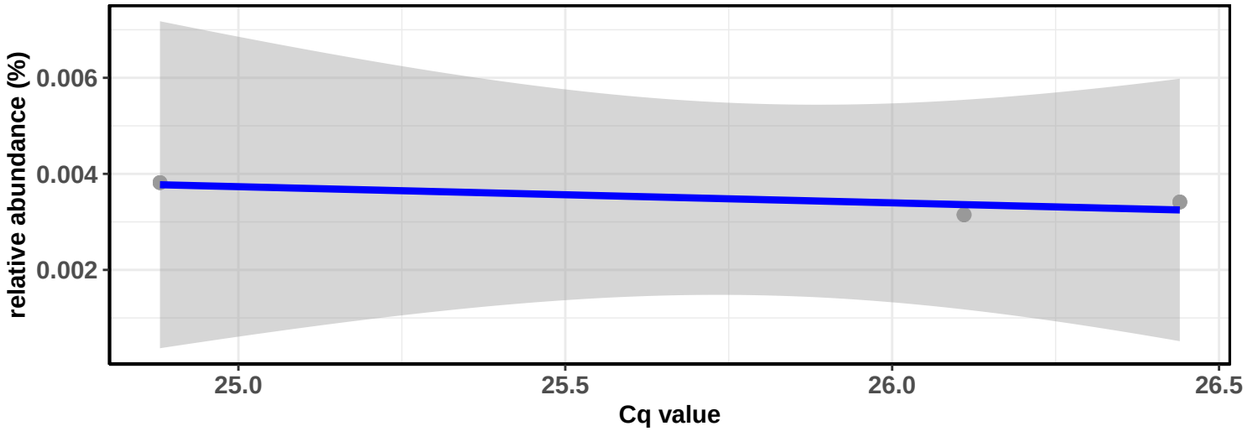


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Caulobacterales; D_4__Caulobacteraceae; D_5__Brevundimonas; Ambiguous_taxa

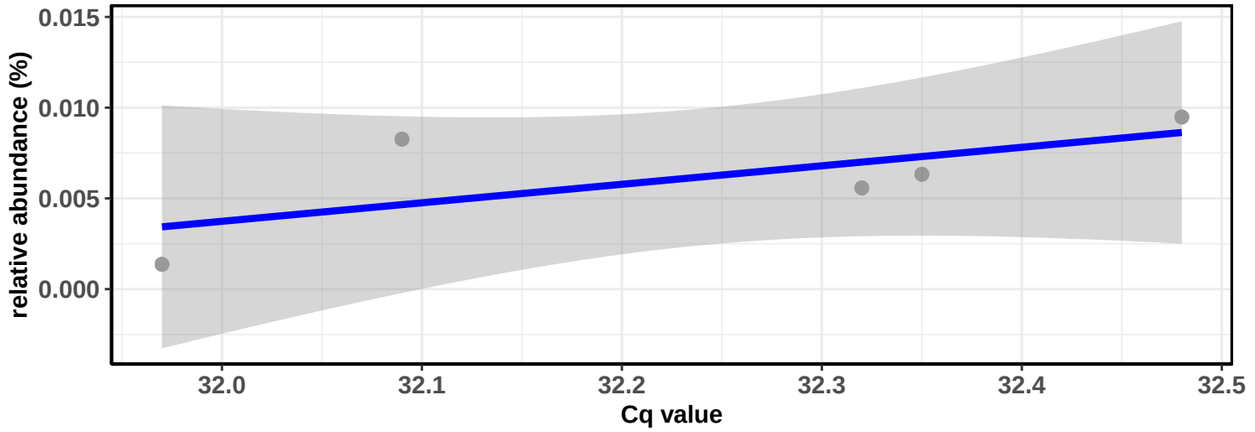
Correlation with all samples



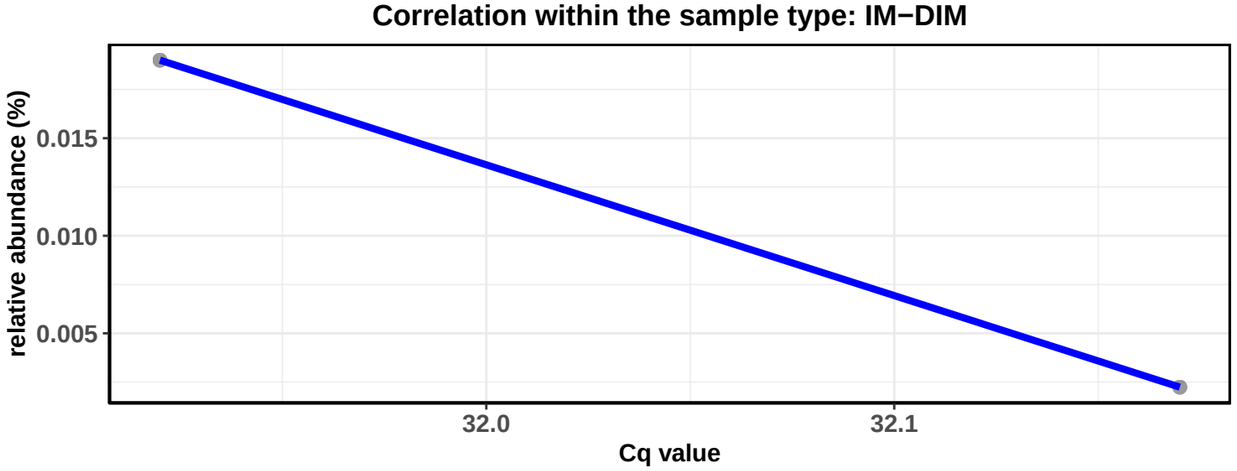
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

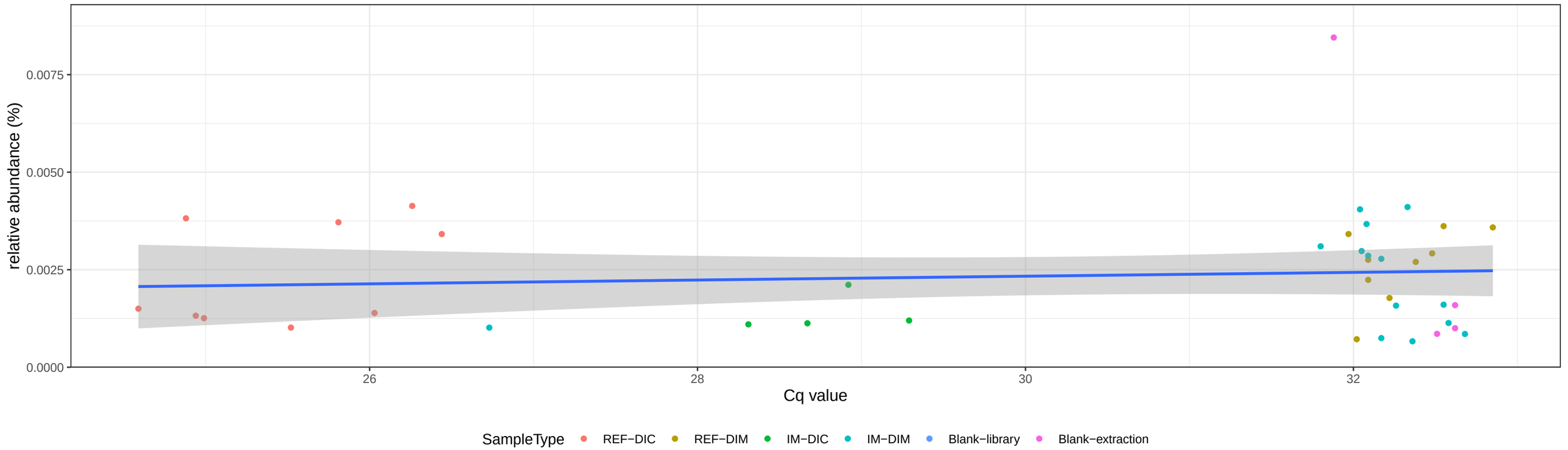


Correlation within the sample type: IM−DIM



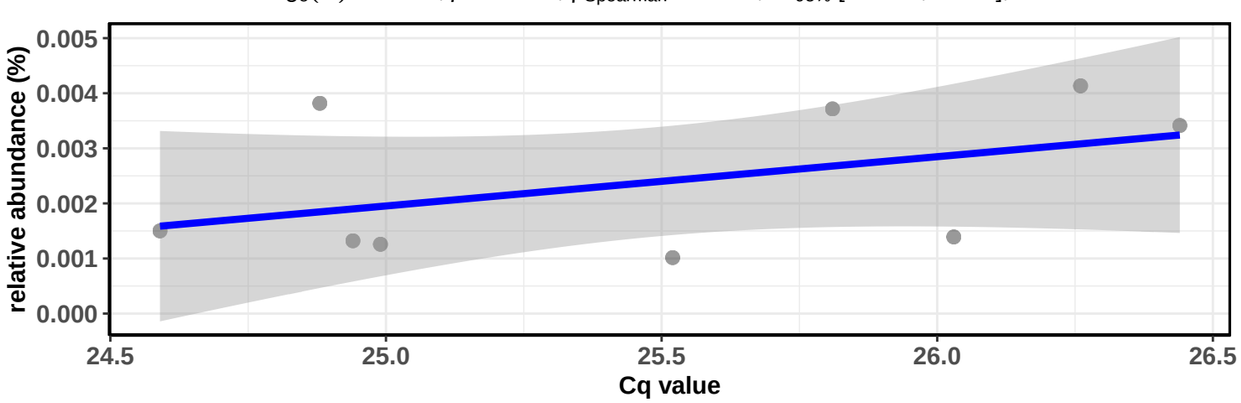
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



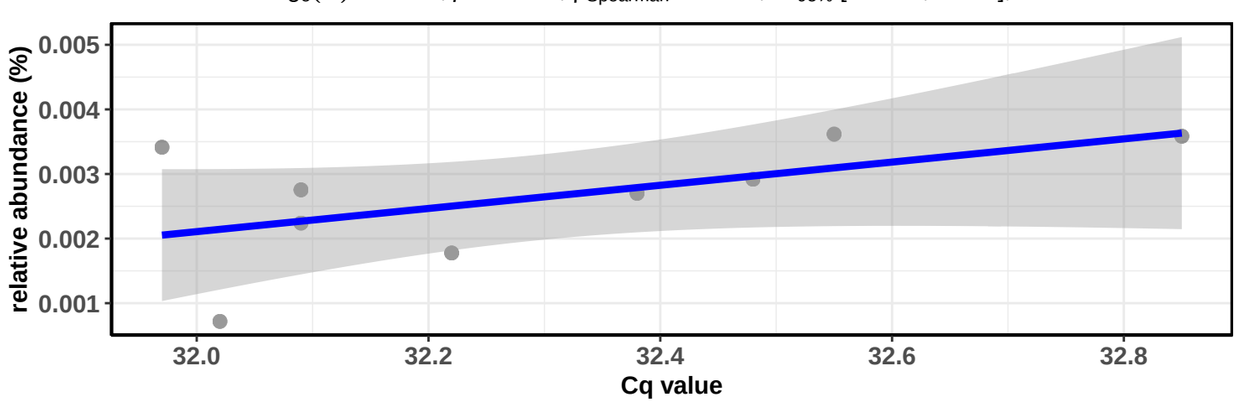
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 4.522, p = 0.546, $\rho_{Spearman}$ = 0.233, $CI_{95\%}$ [−0.510, 0.777], n = 9

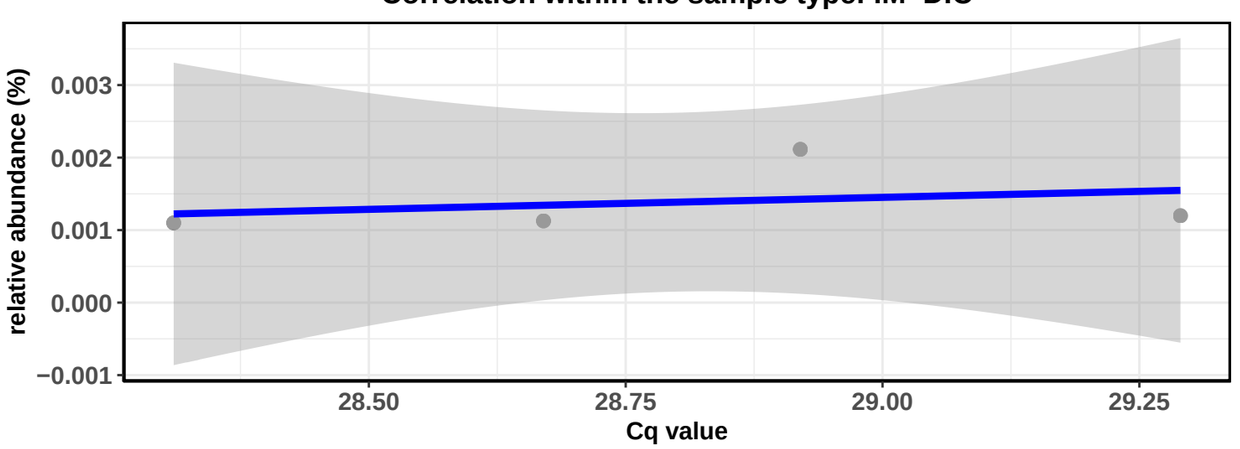


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 4.021, p = 0.137, $\rho_{Spearman}$ = 0.536, $CI_{95\%}$ [−0.200, 0.885], n = 9

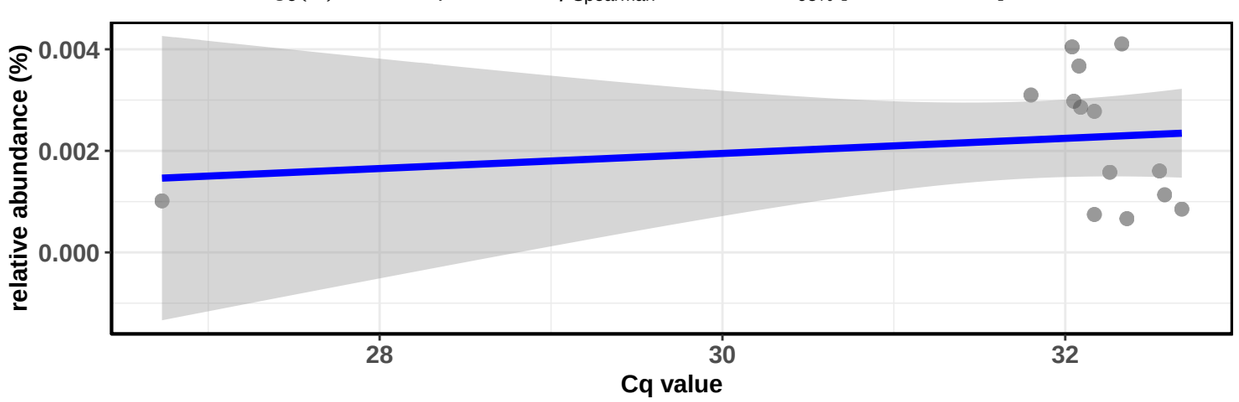


Correlation within the sample type: IM−DIC



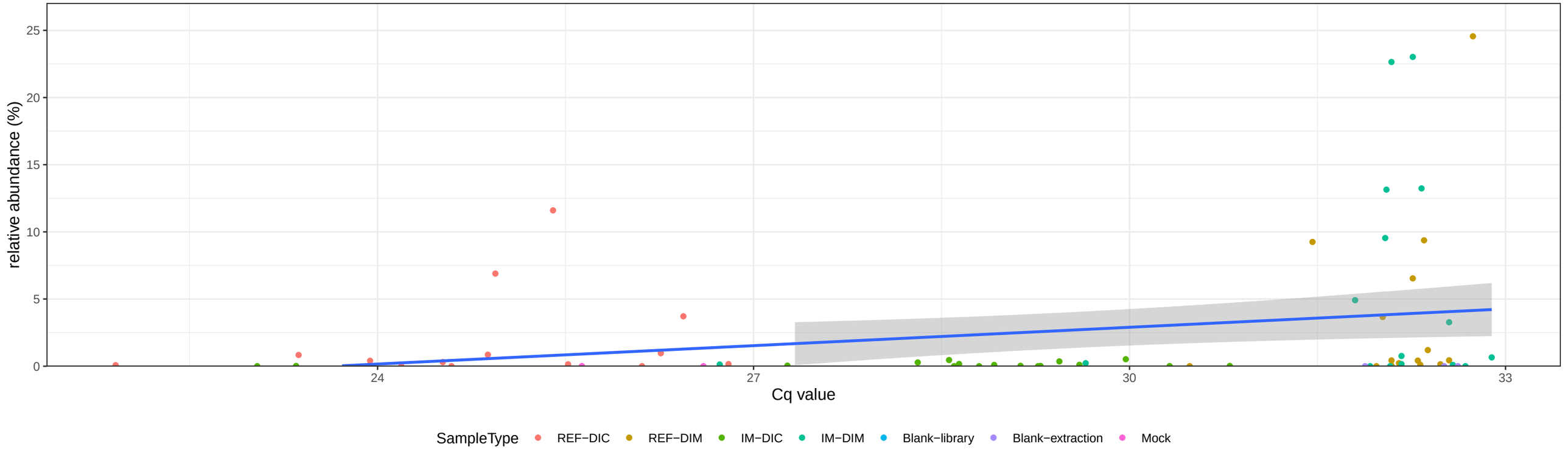
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.477, p = 0.126, $\rho_{Spearman}$ = −0.429, $CI_{95\%}$ [−0.782, 0.131], n = 14



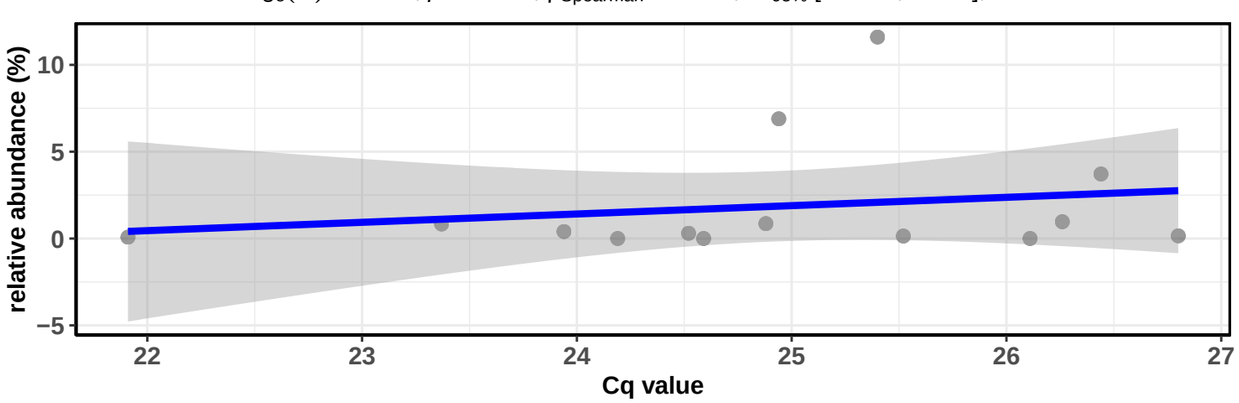
D_0__Bacteria; D_1__Spirochaetes; D_2__Spirochaetia; D_3__Spirochaetales; D_4__Spirochaetaceae

Correlation with all samples



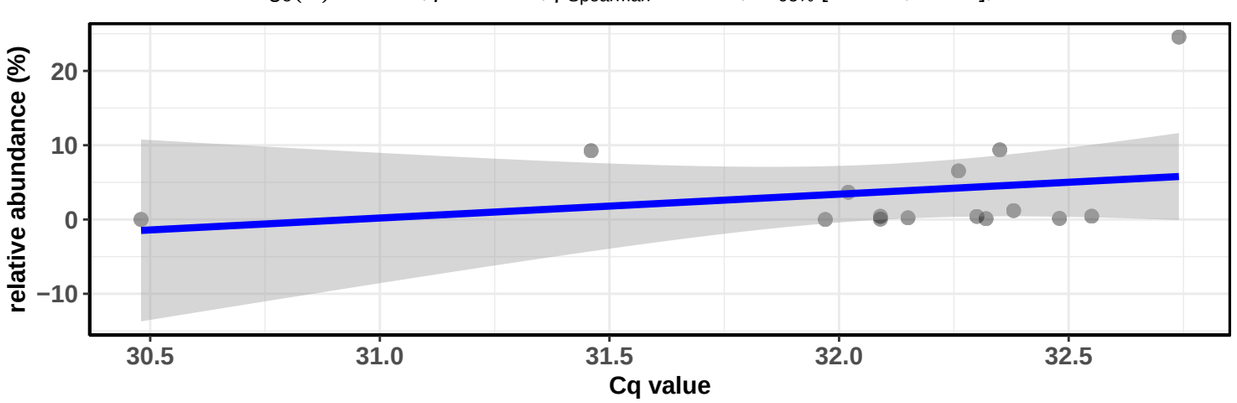
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.799, p = 0.342, $\rho_{Spearman}$ = 0.275, $CI_{95\%}$ [−0.300, 0.703], n = 14



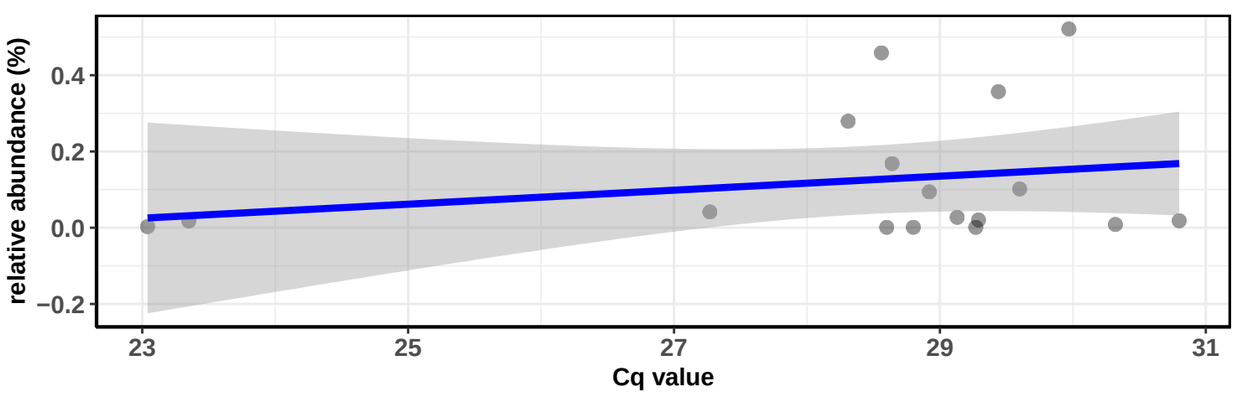
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.849, p = 0.162, $\rho_{Spearman}$ = 0.381, $CI_{95\%}$ [−0.163, 0.747], n = 15



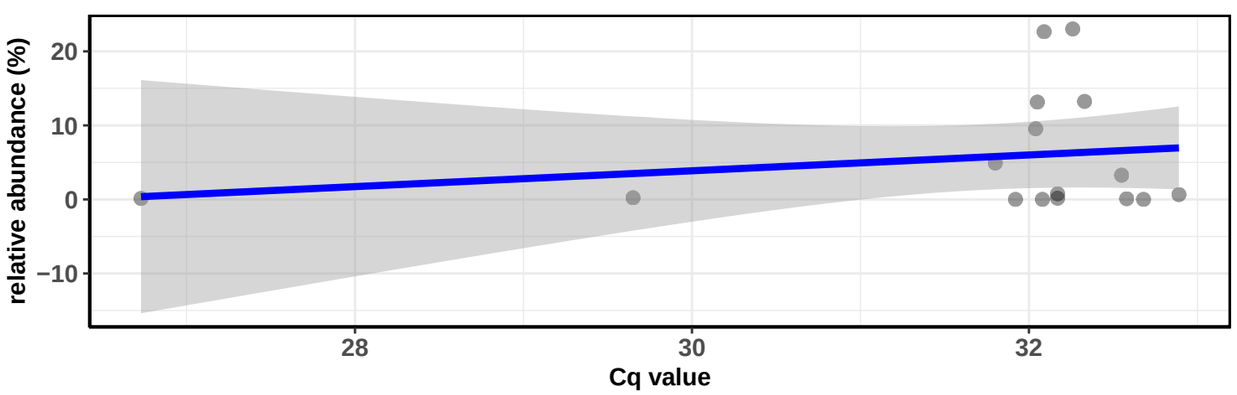
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.588, p = 0.673, $\rho_{Spearman}$ = 0.110, $CI_{95\%}$ [−0.391, 0.561], n = 17



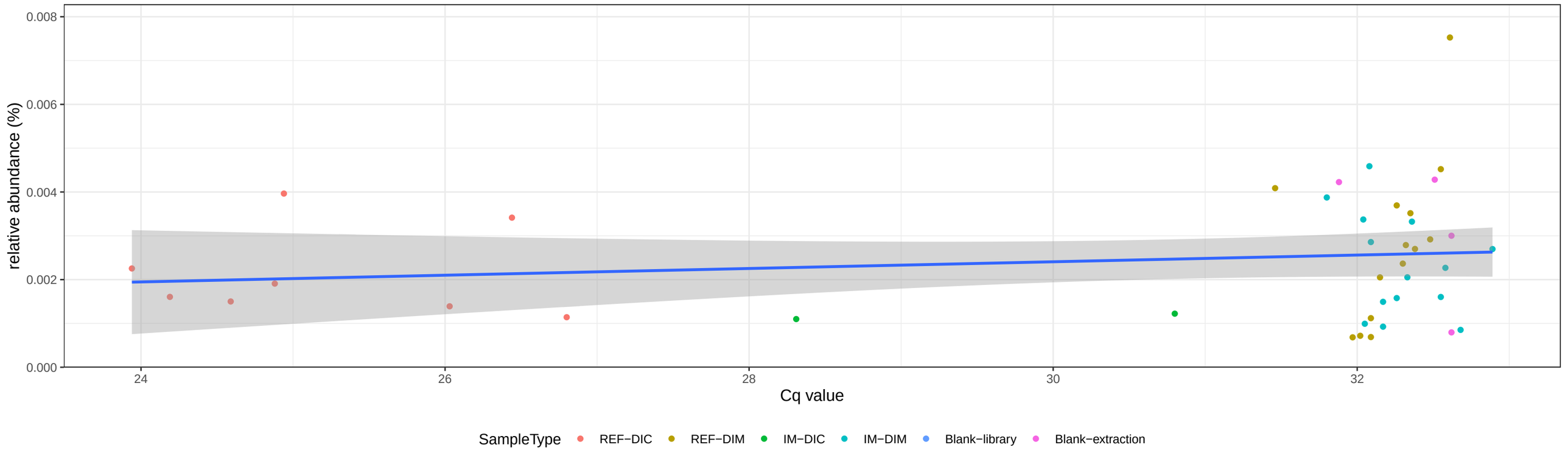
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.494, p = 0.918, $\rho_{Spearman}$ = 0.028, $CI_{95\%}$ [−0.474, 0.517], n = 16



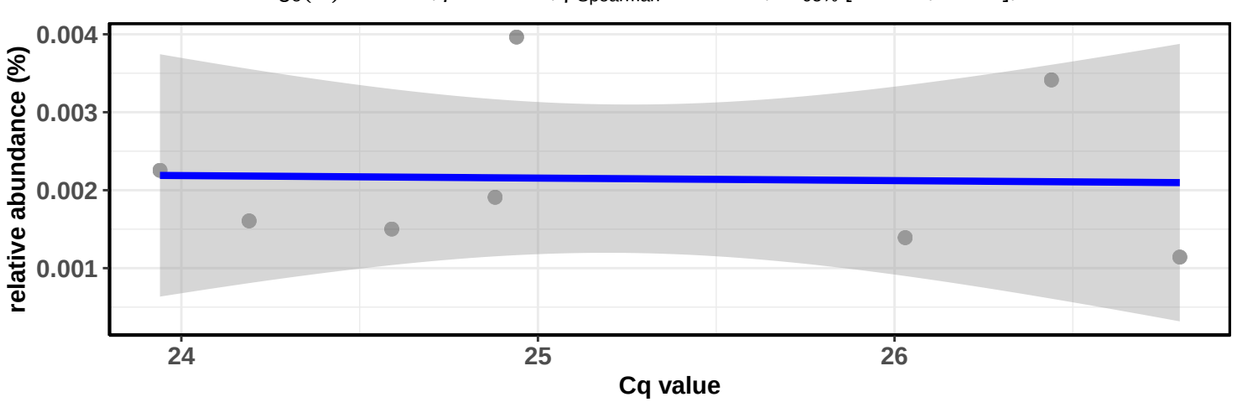
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



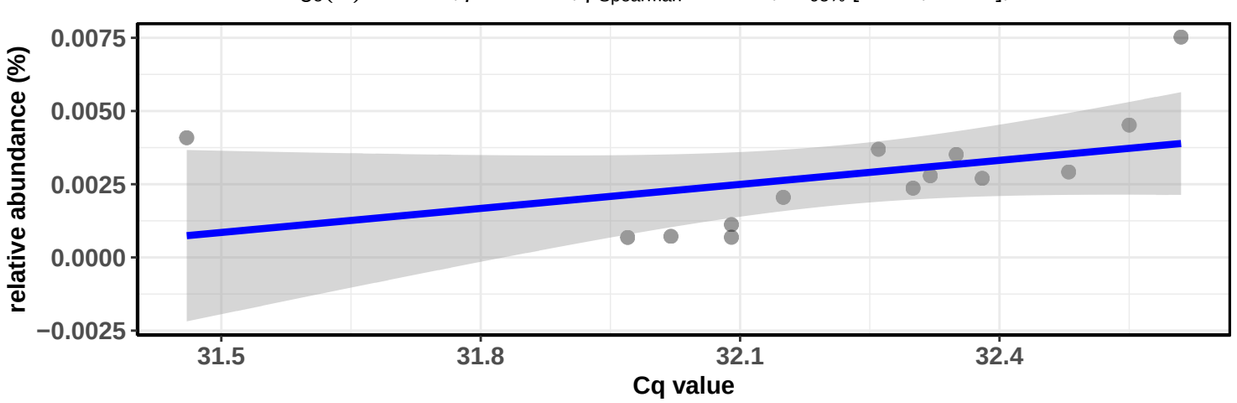
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 4.644, p = 0.570, $\rho_{Spearman}$ = −0.238, $CI_{95\%}$ [−0.807, 0.561], n = 8

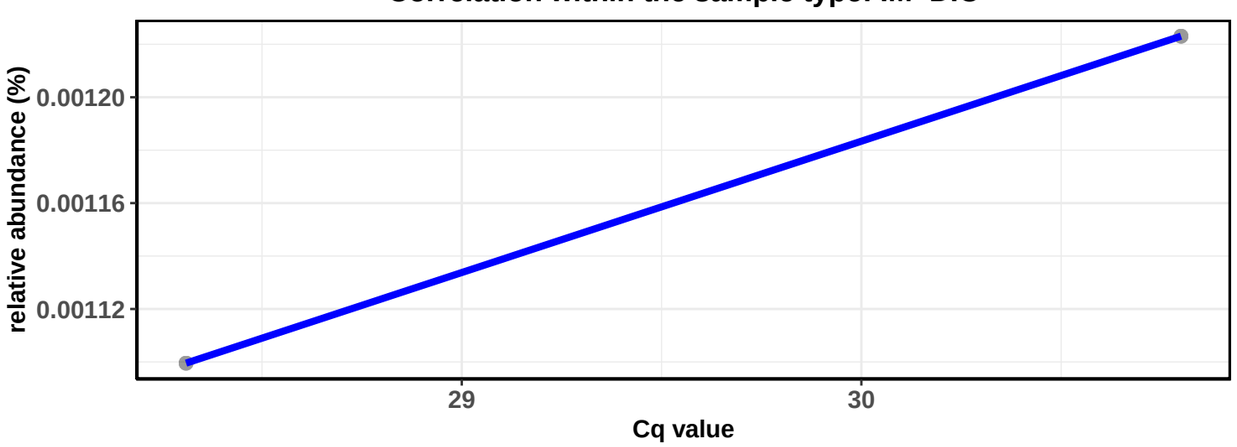


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.169, p = 0.020, $\rho_{Spearman}$ = 0.614, $CI_{95\%}$ [0.124, 0.863], n = 14

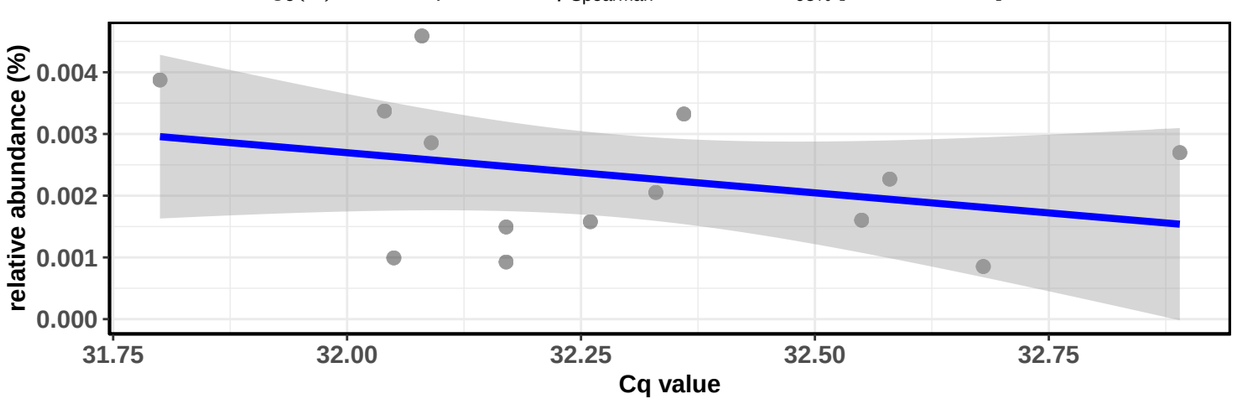


Correlation within the sample type: IM−DIC



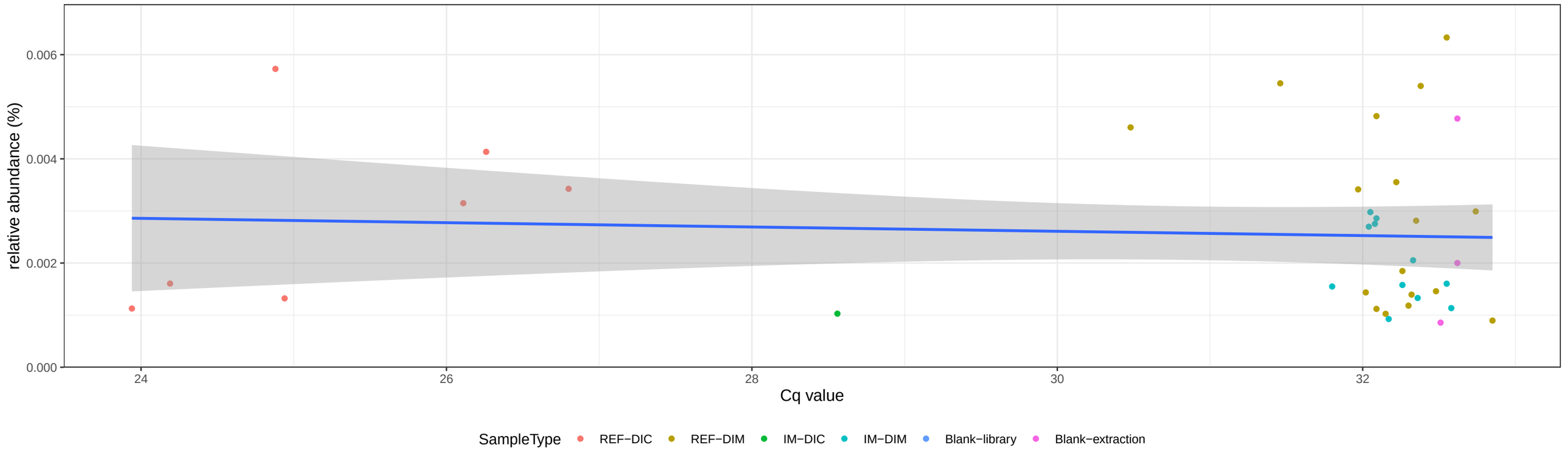
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.430, p = 0.202, $\rho_{Spearman}$ = −0.363, $CI_{95\%}$ [−0.749, 0.208], n = 14



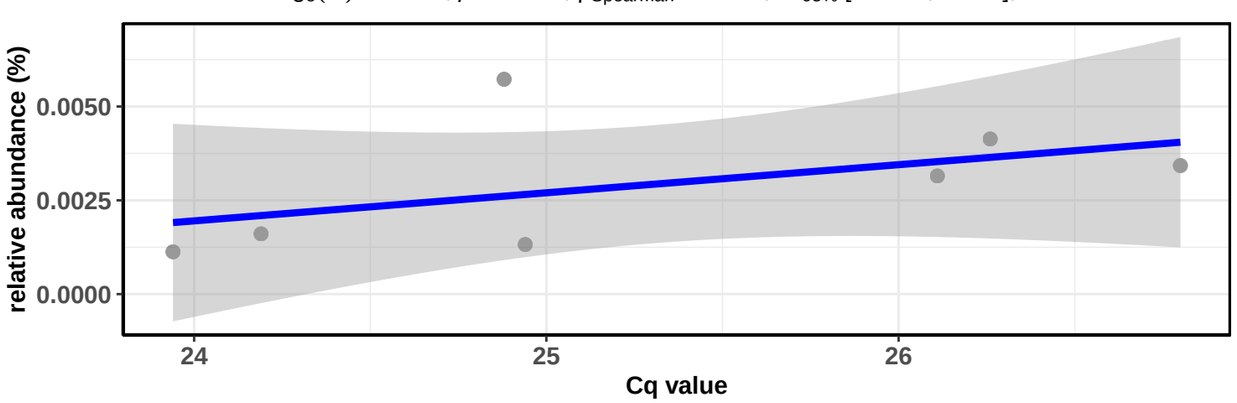
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



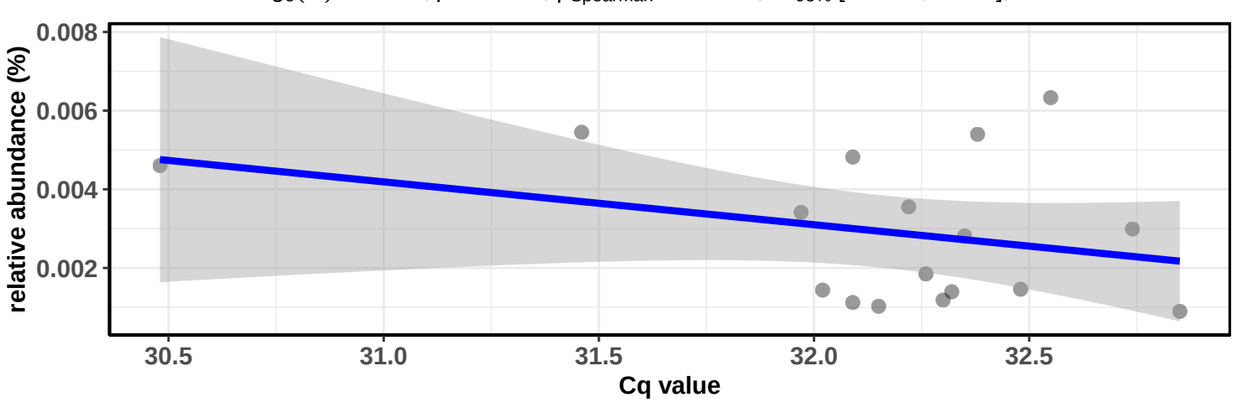
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 3.258, p = 0.215, $\rho_{Spearman}$ = 0.536, $CI_{95\%}$ [−0.364, 0.918], n = 7

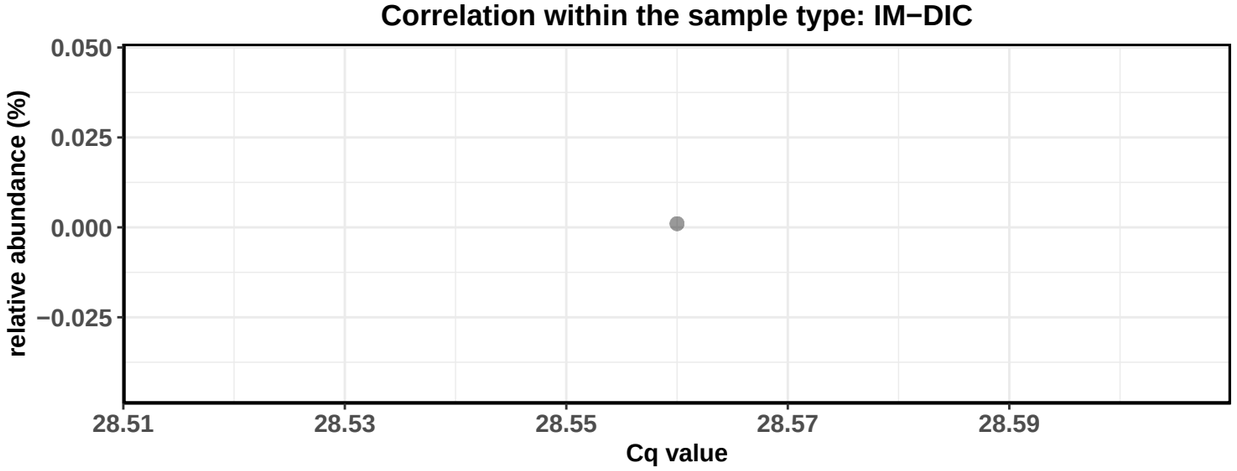


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.866, p = 0.501, $\rho_{Spearman}$ = −0.175, $CI_{95\%}$ [−0.605, 0.333], n = 17

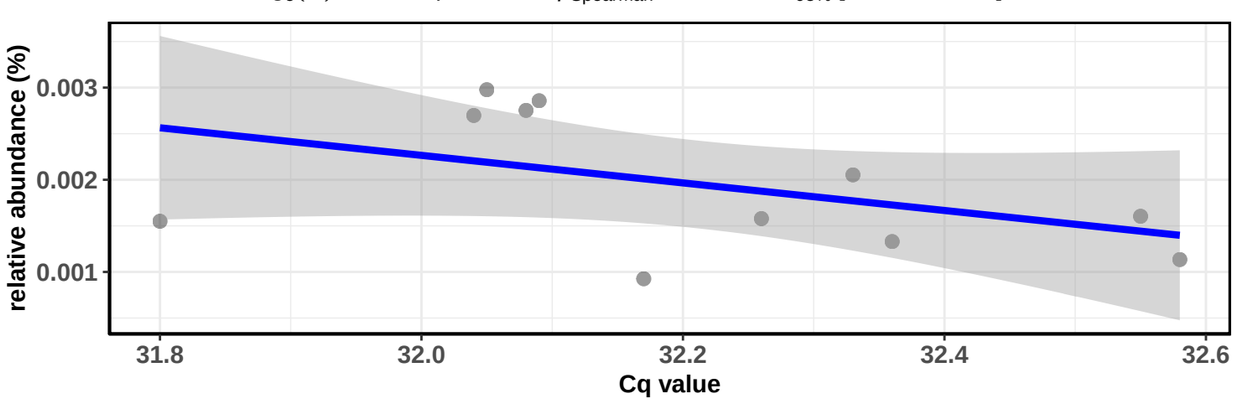


Correlation within the sample type: IM−DIC



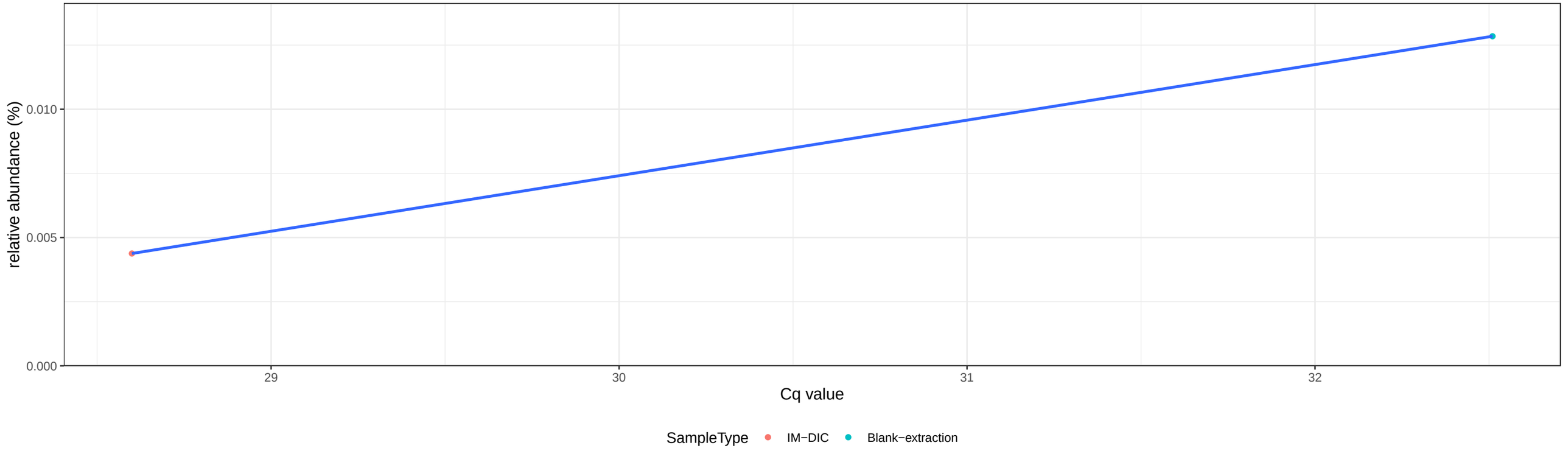
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.775, p = 0.151, $\rho_{Spearman}$ = −0.464, $CI_{95\%}$ [−0.832, 0.189], n = 11

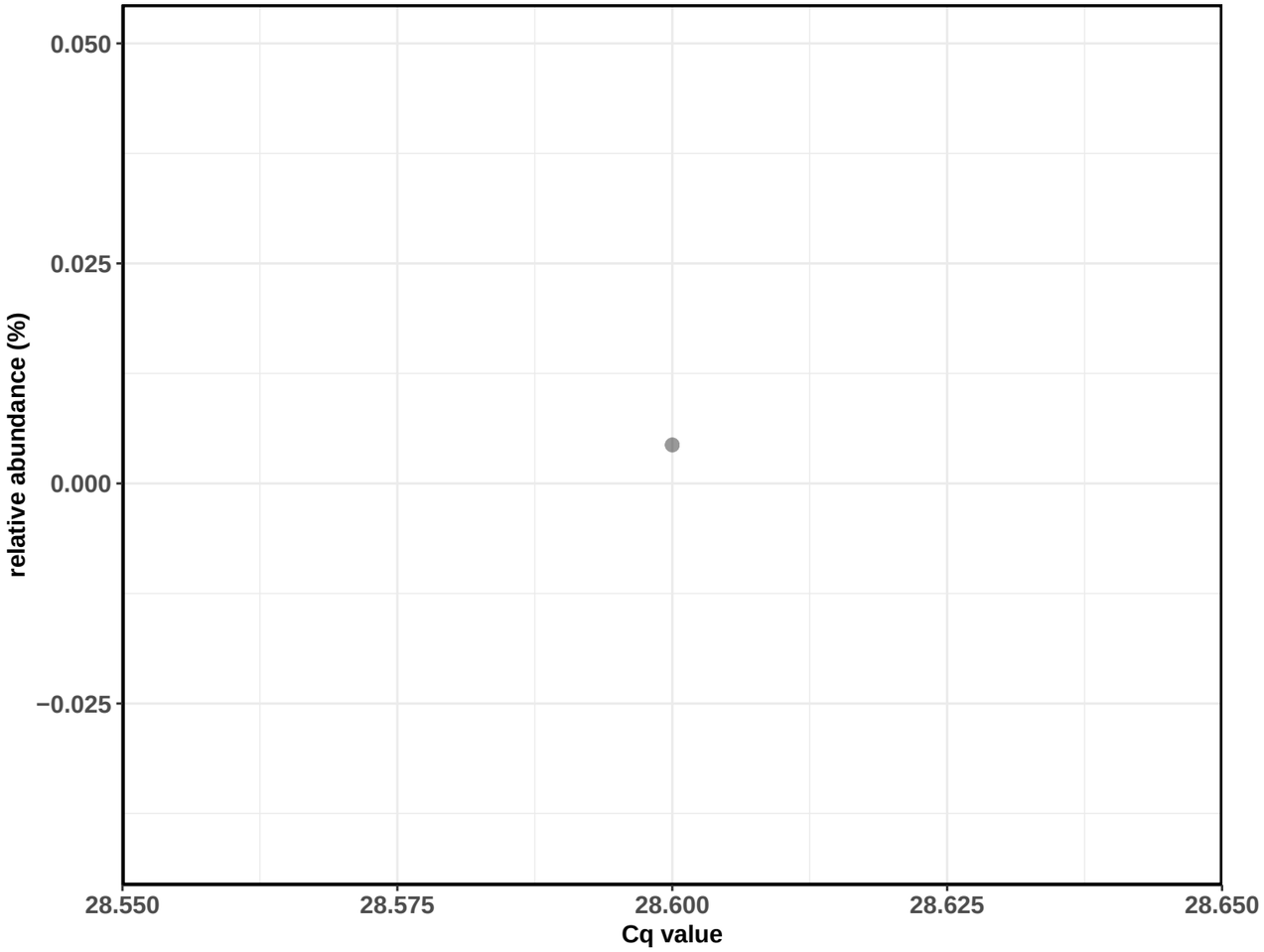


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Sphingobacteriales; D_4__Sphingobacteriaceae; D_5__Pedobacter

Correlation with all samples

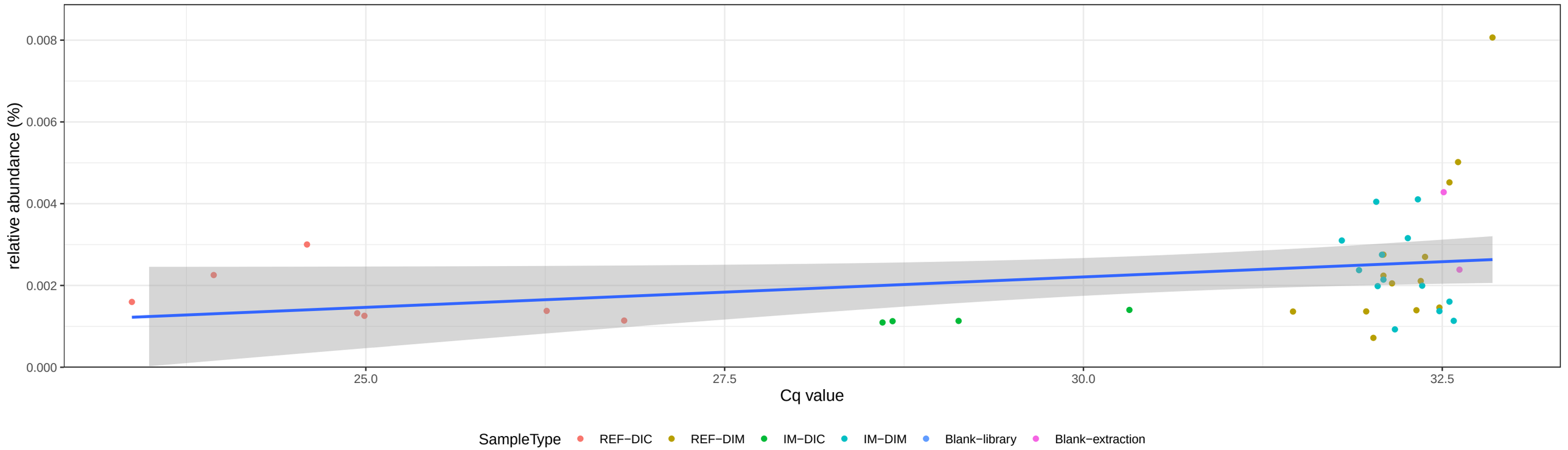


Correlation within the sample type: IM−DIC



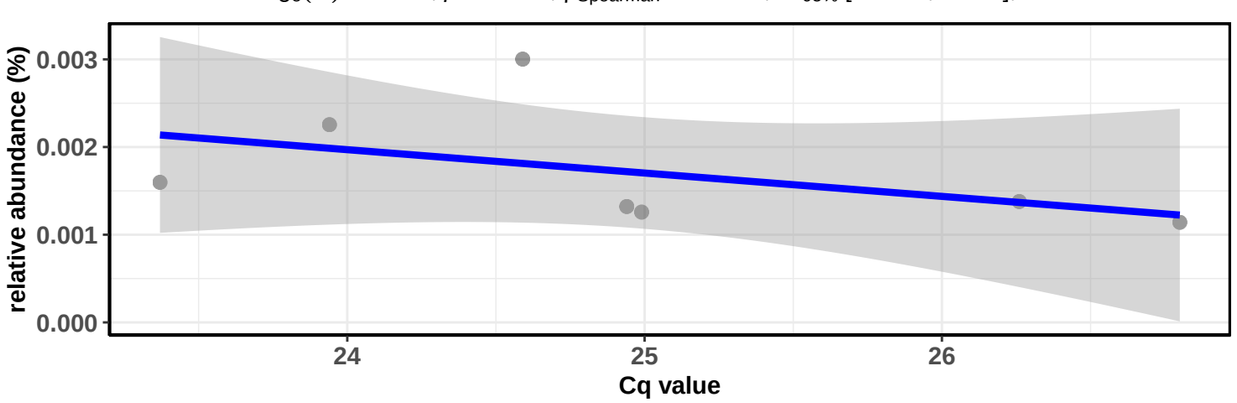
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



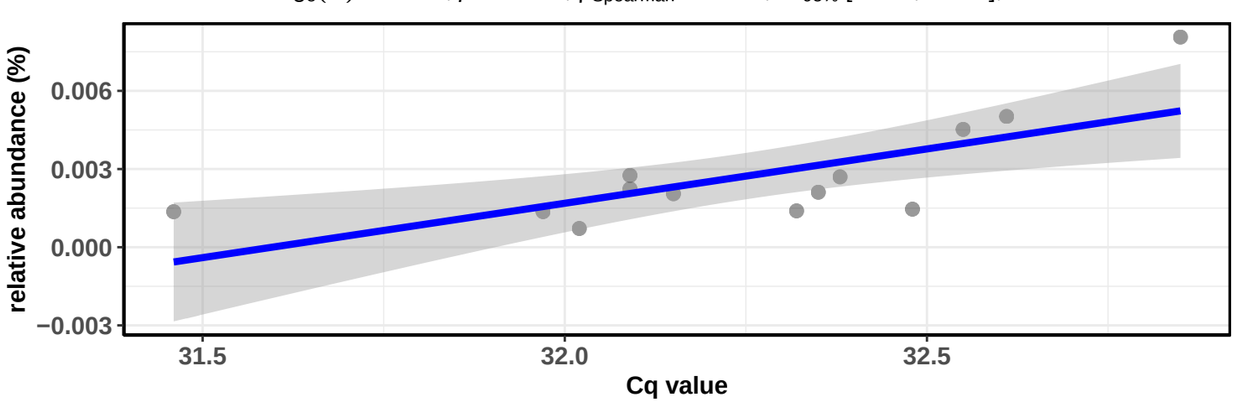
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 4.585, p = 0.052, $\rho_{Spearman}$ = −0.750, $CI_{95\%}$ [−0.961, 0.007], n = 7

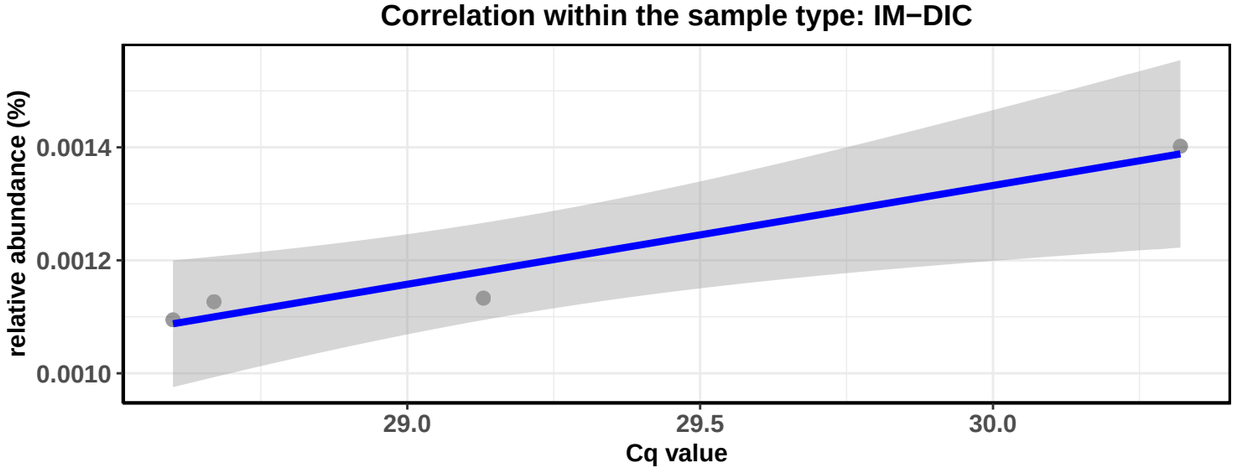


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 4.426, p = 0.002, $\rho_{Spearman}$ = 0.770, $CI_{95\%}$ [0.381, 0.928], n = 13

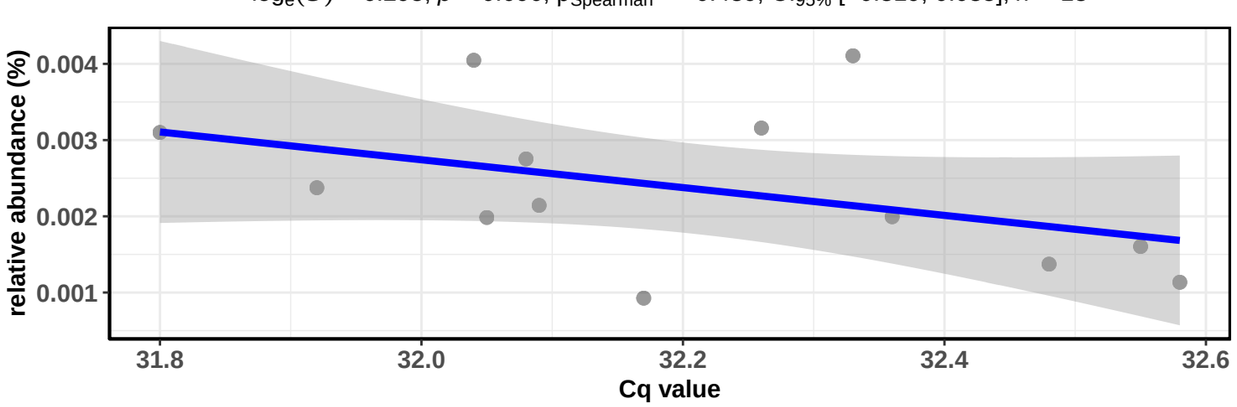


Correlation within the sample type: IM−DIC



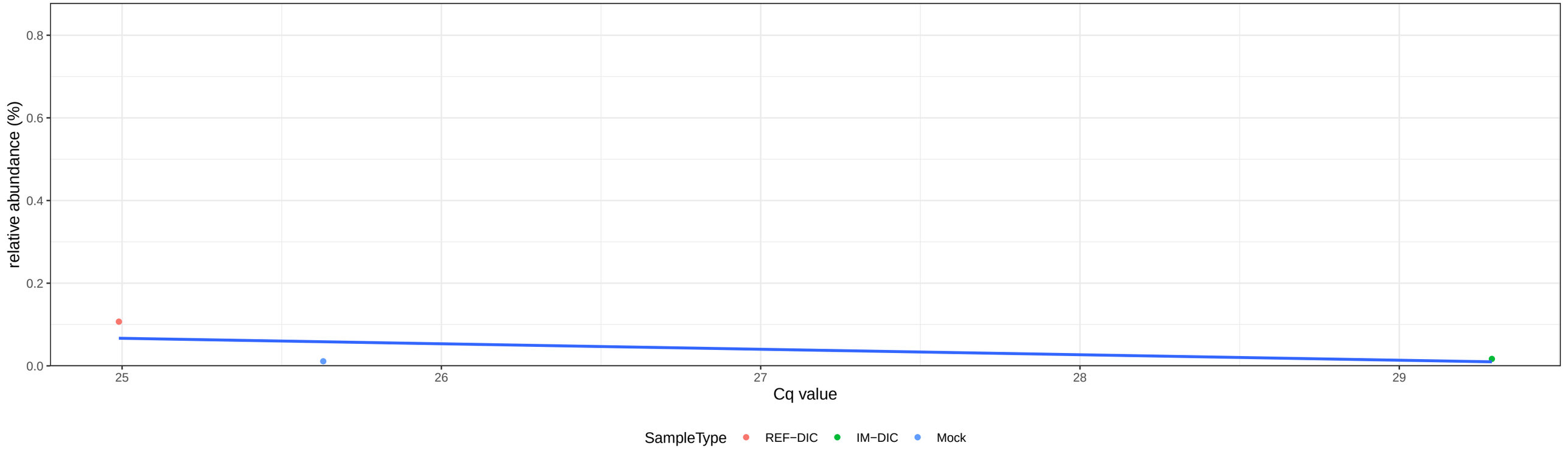
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.295, p = 0.090, $\rho_{Spearman}$ = −0.489, $CI_{95\%}$ [−0.819, 0.085], n = 13

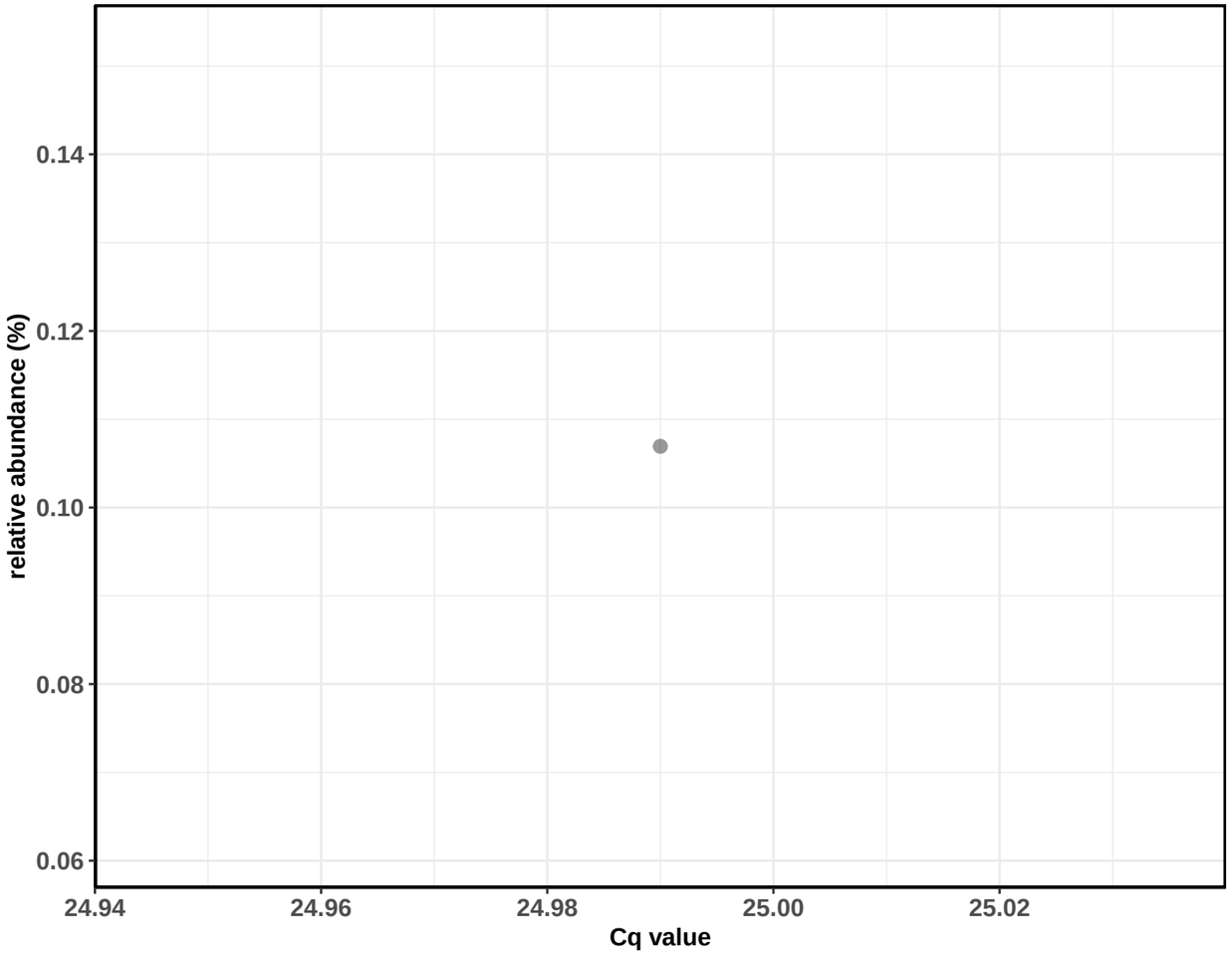


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

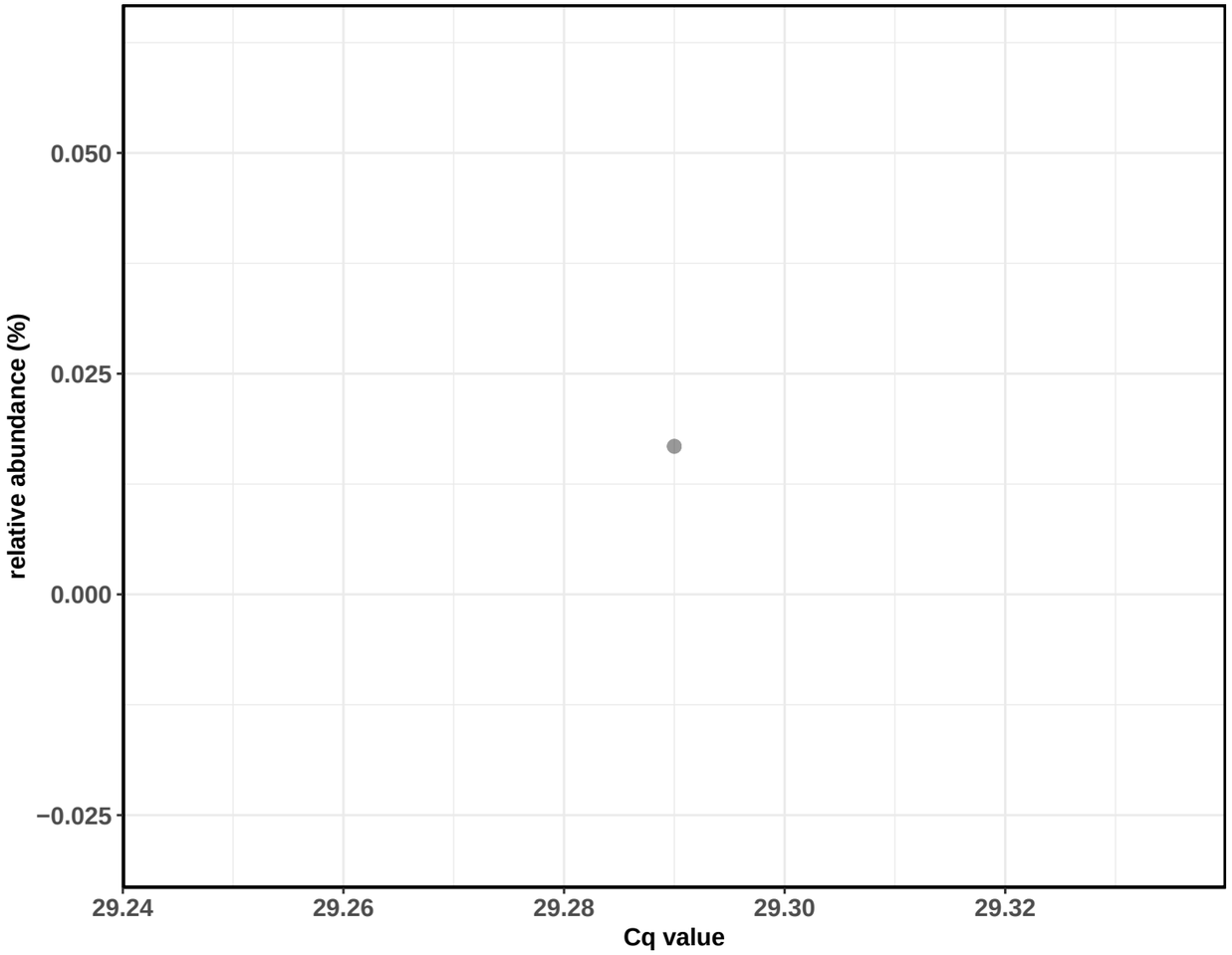
Correlation with all samples



Correlation within the sample type: REF−DIC

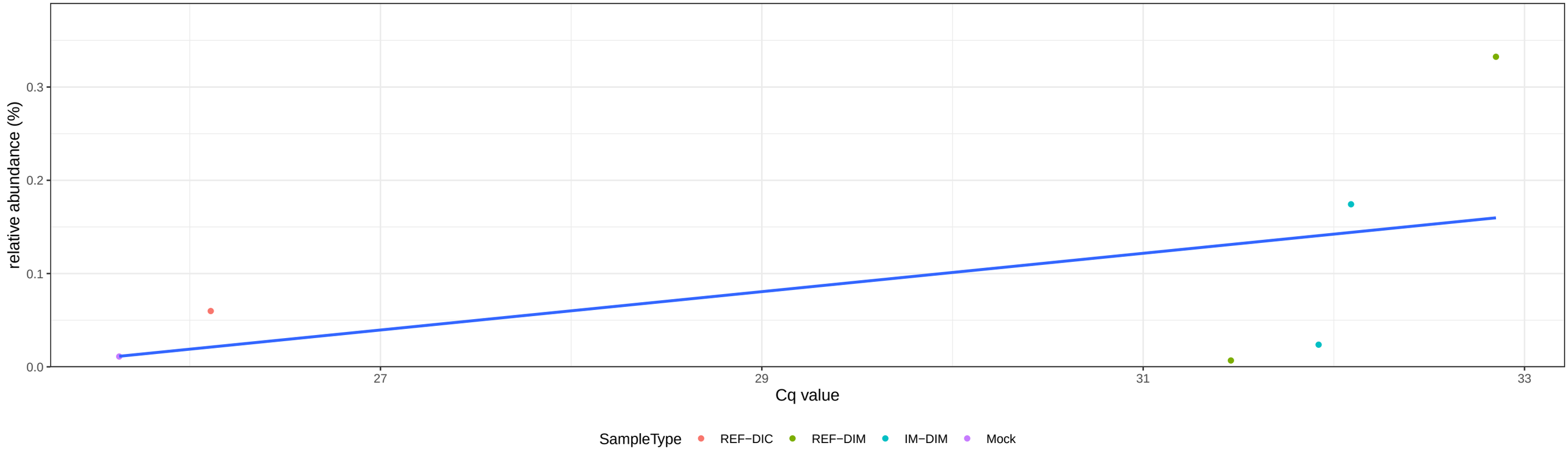


Correlation within the sample type: IM−DIC

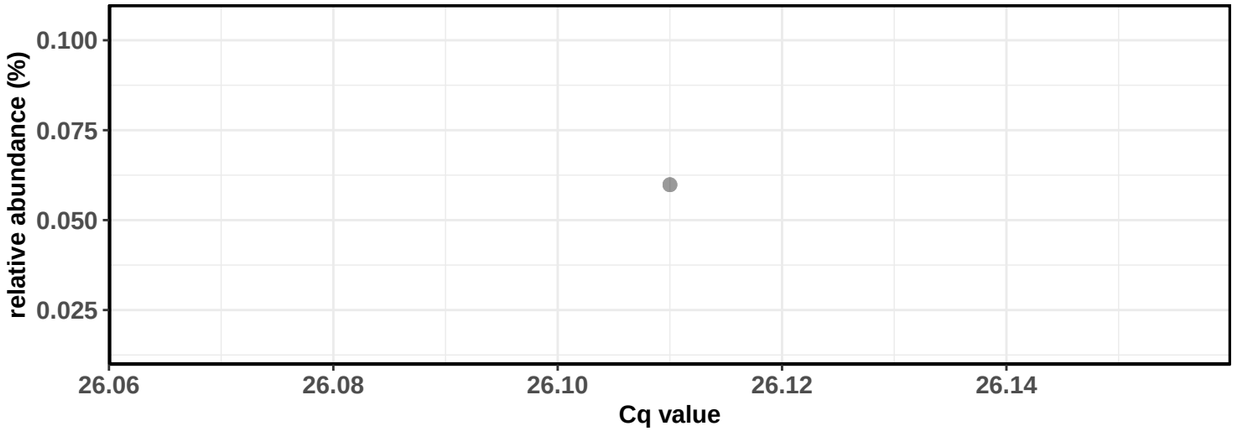


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Sphingomonadales; D_4__Sphingomonadaceae; D_5__Sphingomonas

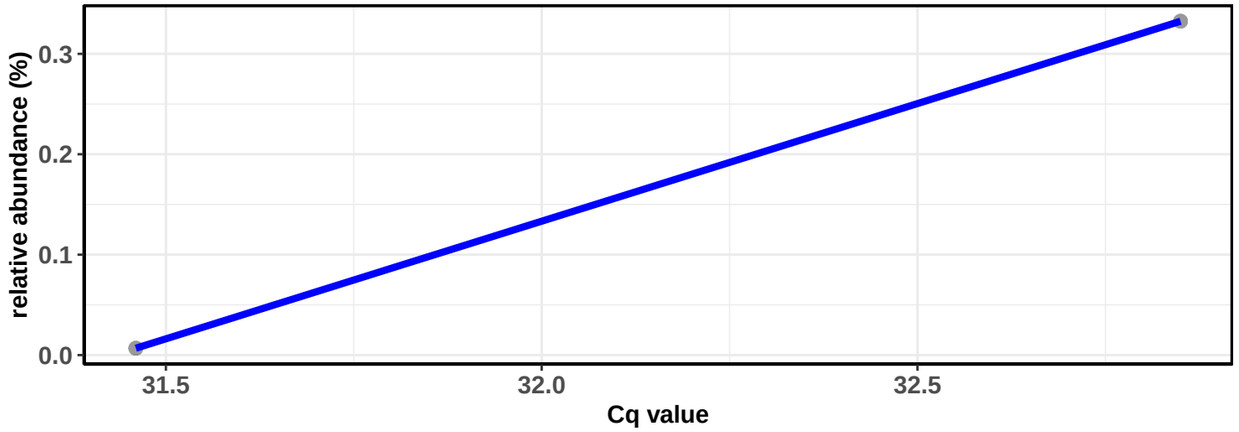
Correlation with all samples



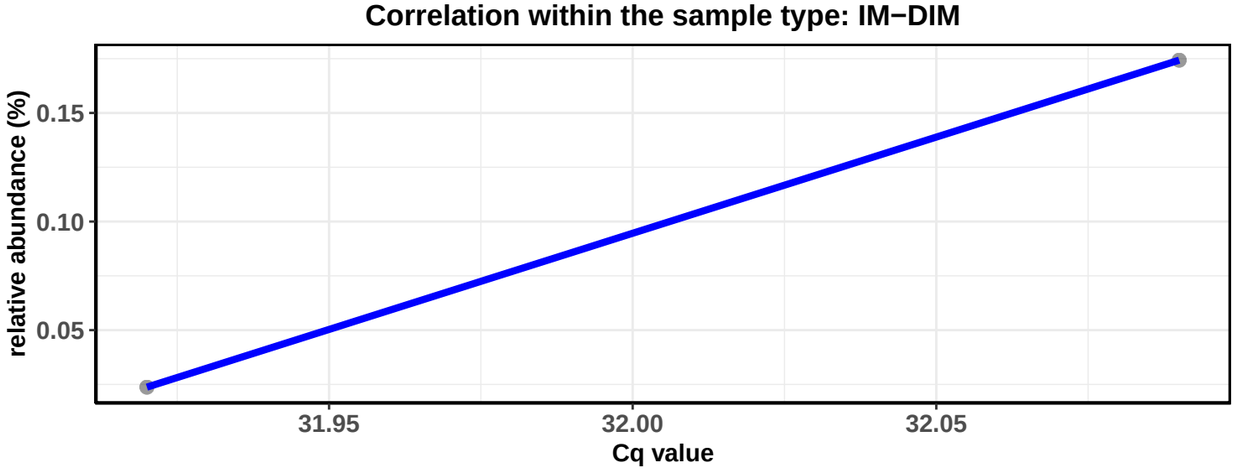
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

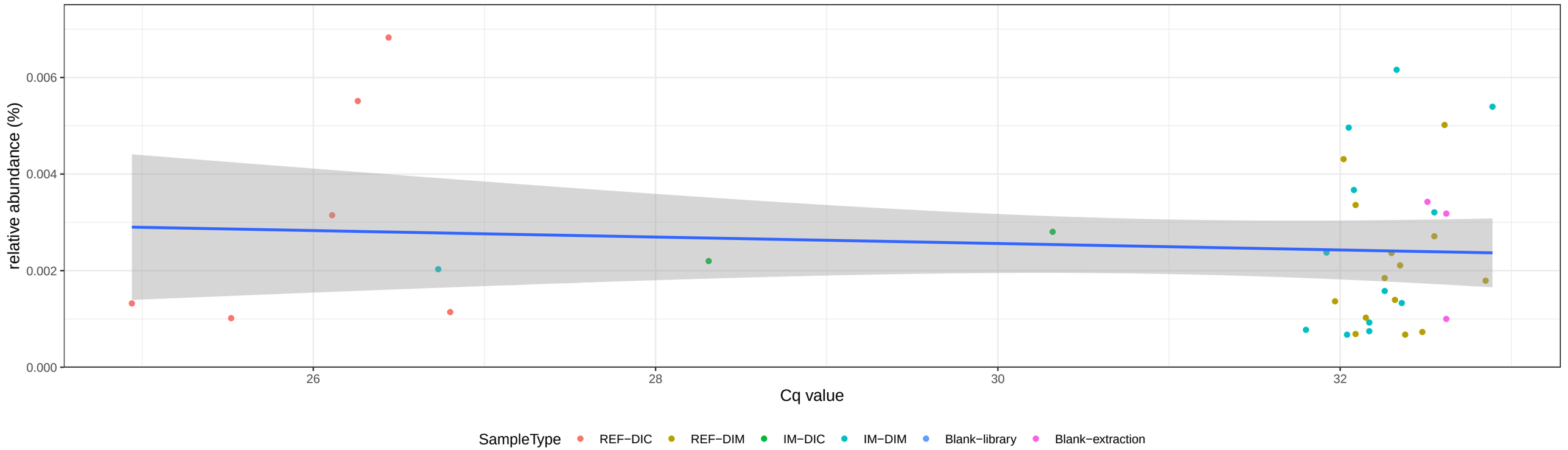


Correlation within the sample type: IM−DIM



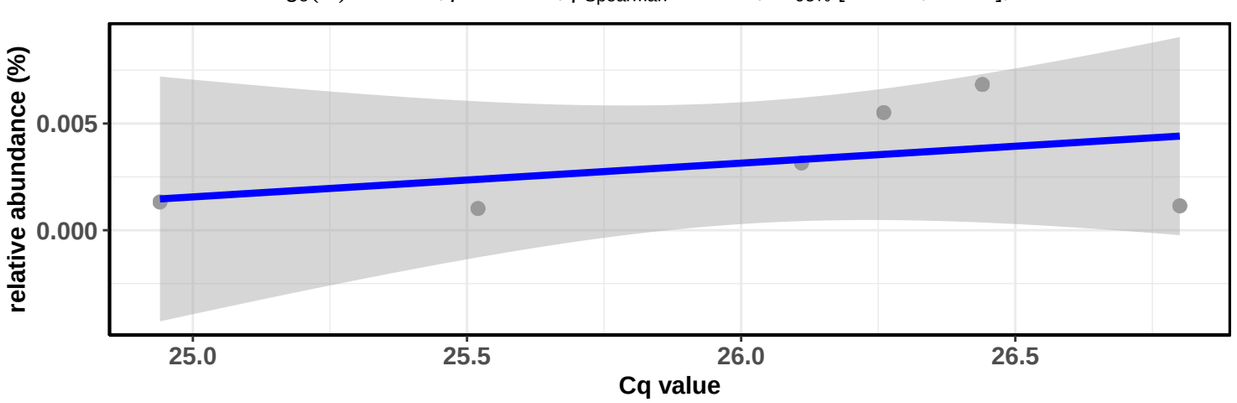
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



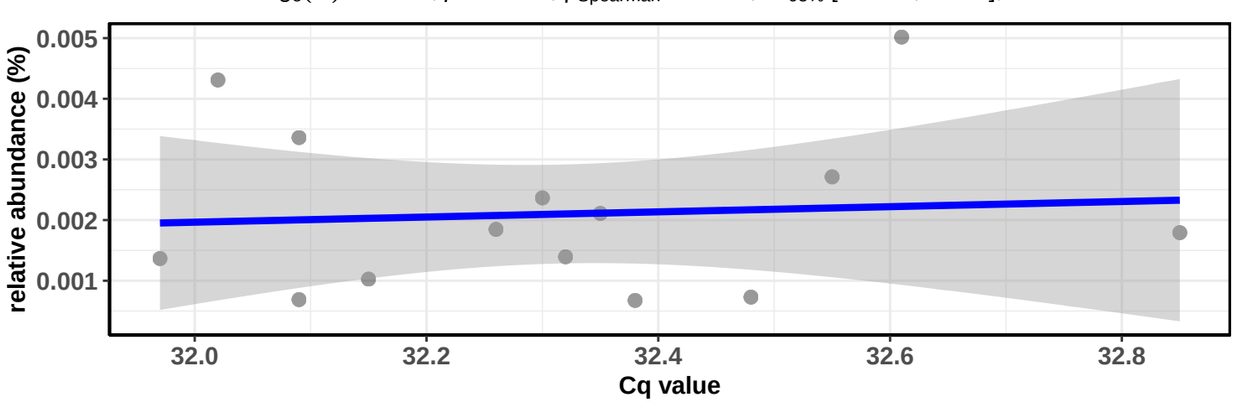
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 3.178, p = 0.544, $\rho_{Spearman}$ = 0.314, $CI_{95\%}$ [−0.668, 0.897], n = 6

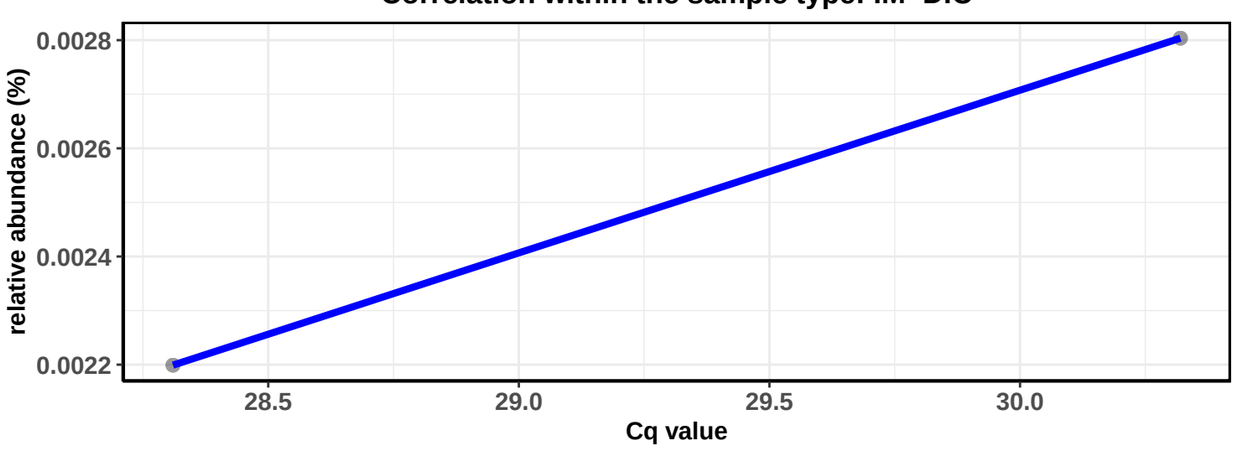


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.054, p = 0.828, $\rho_{Spearman}$ = 0.064, $CI_{95\%}$ [−0.483, 0.575], n = 14

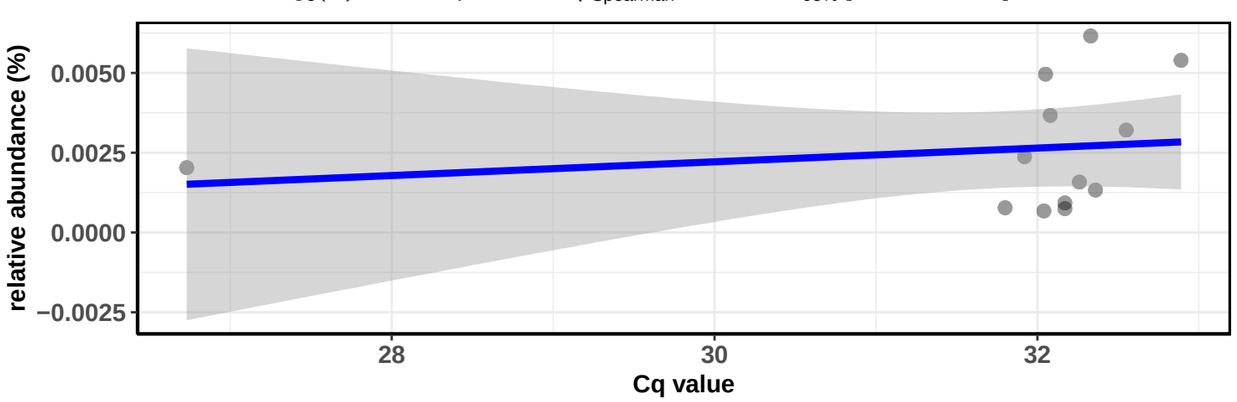


Correlation within the sample type: IM−DIC



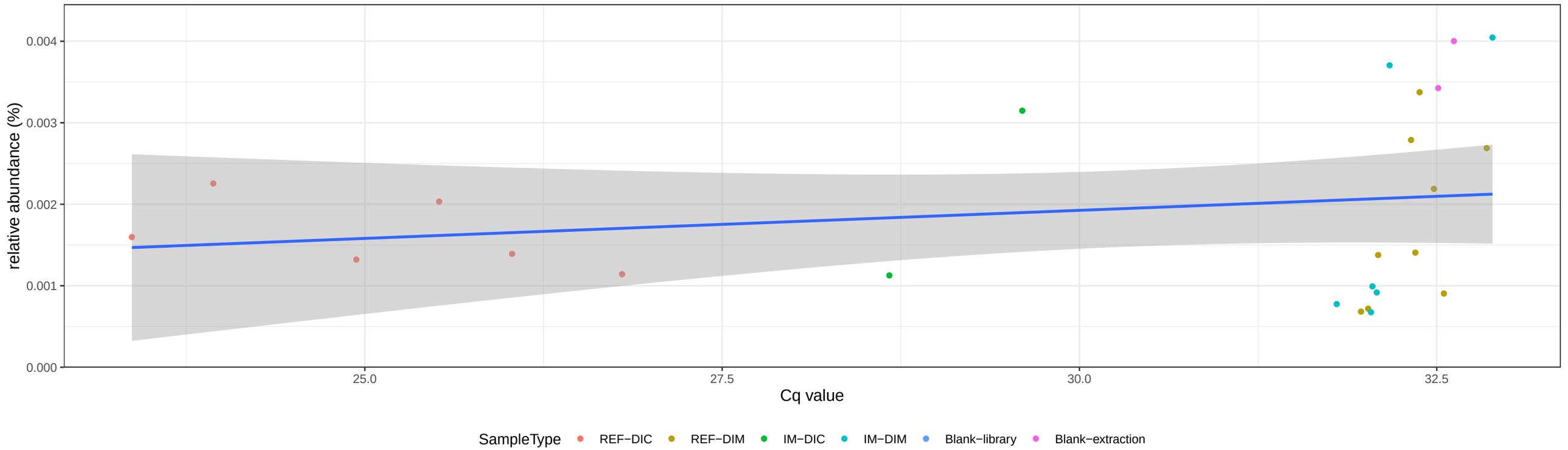
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.437, p = 0.215, $\rho_{Spearman}$ = 0.369, $CI_{95\%}$ [−0.229, 0.764], n = 13



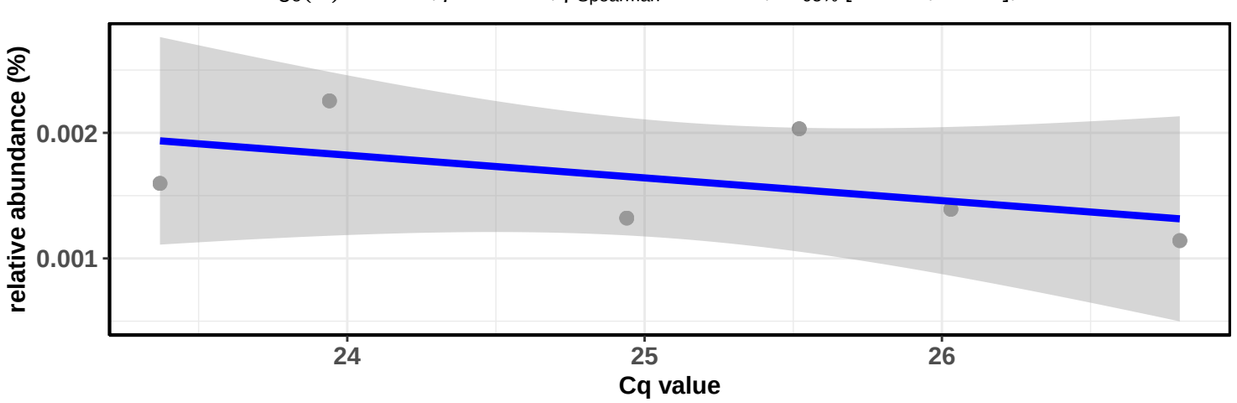
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



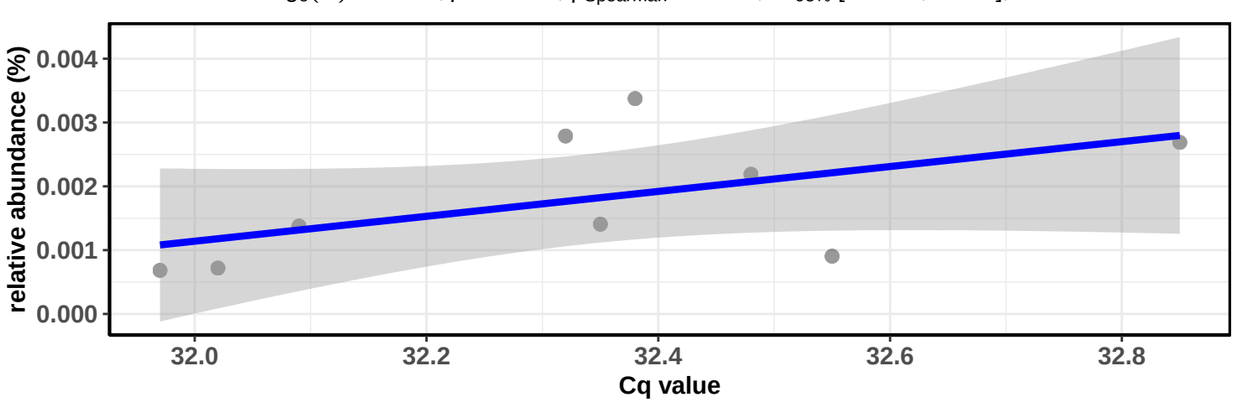
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 4.025, p = 0.208, $\rho_{Spearman}$ = −0.600, $CI_{95\%}$ [−0.949, 0.412], n = 6

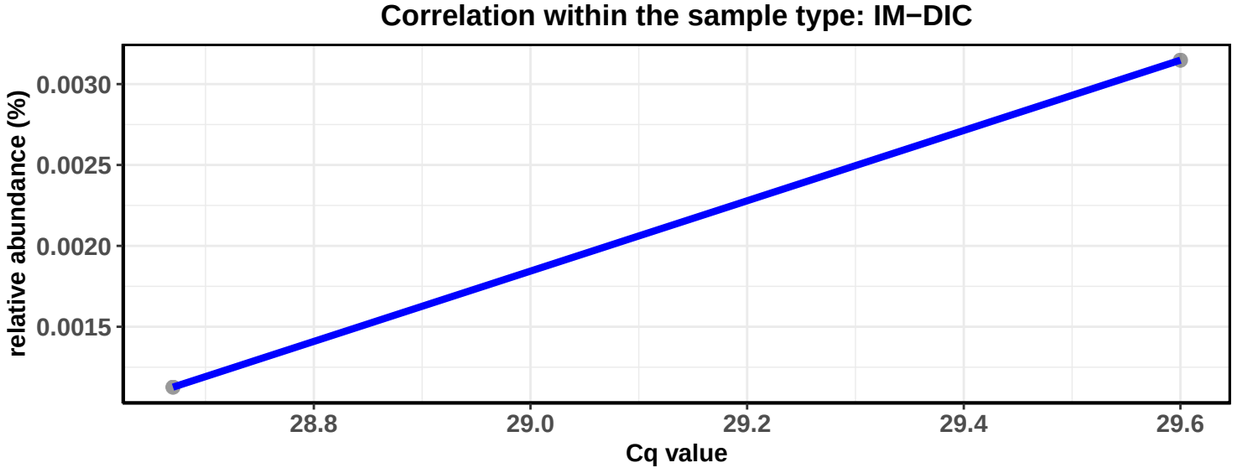


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 4.025, p = 0.139, $\rho_{Spearman}$ = 0.533, $CI_{95\%}$ [−0.203, 0.884], n = 9

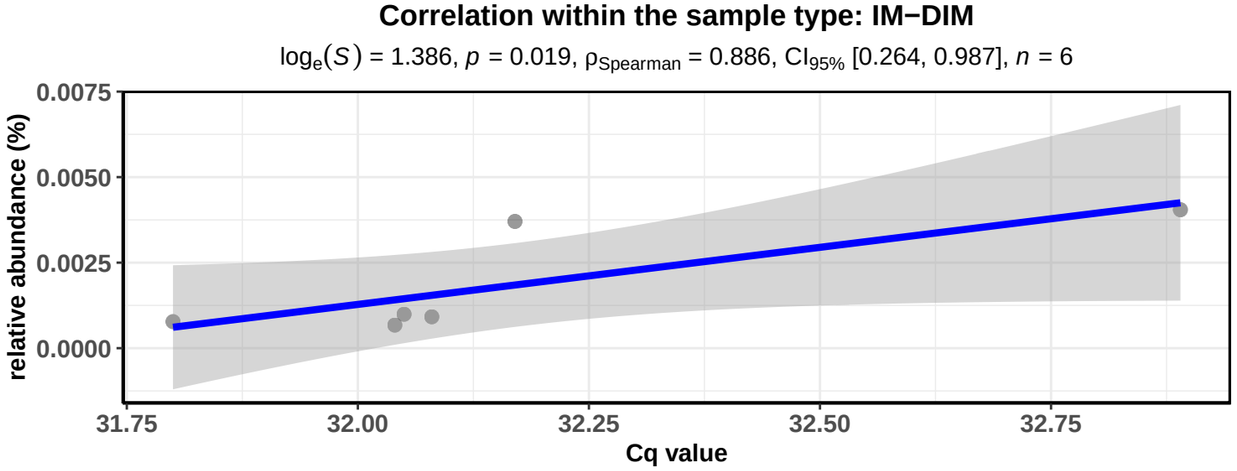


Correlation within the sample type: IM−DIC



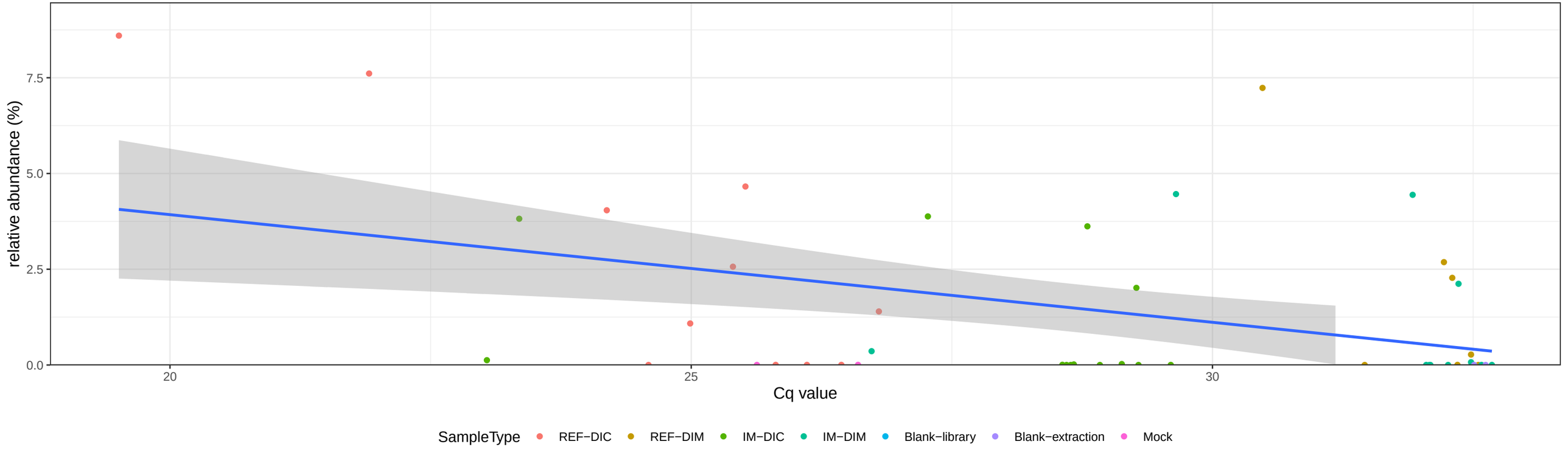
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 1.386, p = 0.019, $\rho_{Spearman}$ = 0.886, $CI_{95\%}$ [0.264, 0.987], n = 6



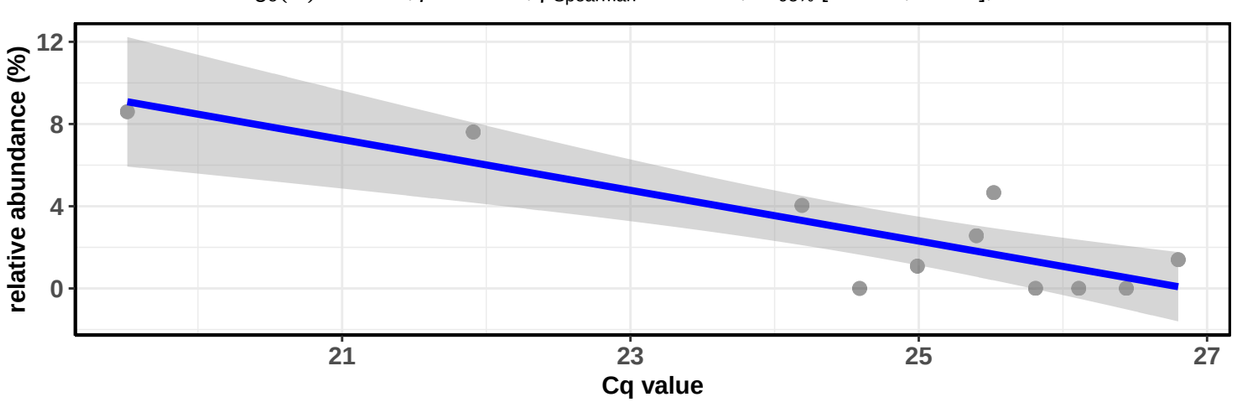
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Aliivibrio; Ambiguous_taxa

Correlation with all samples



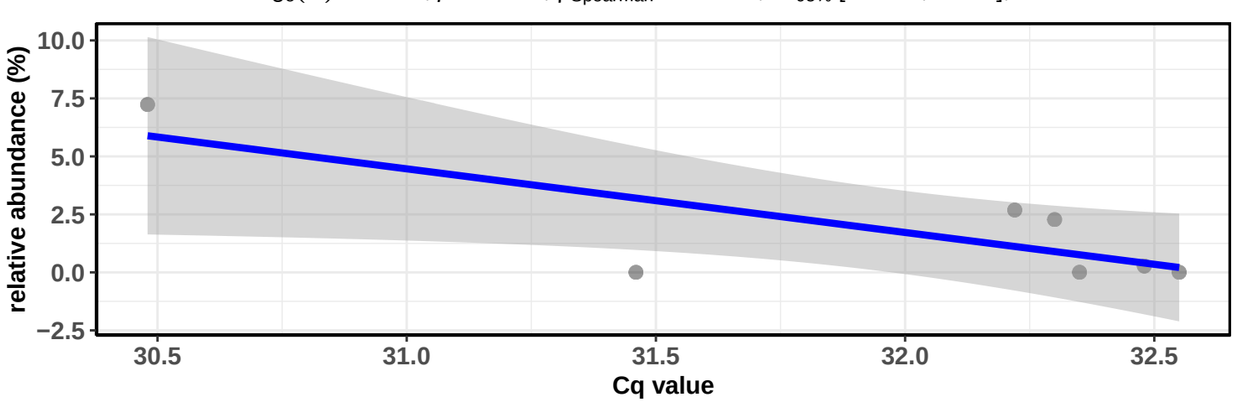
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.835, p = 0.077, $\rho_{Spearman}$ = −0.555, $CI_{95\%}$ [−0.866, 0.068], n = 11



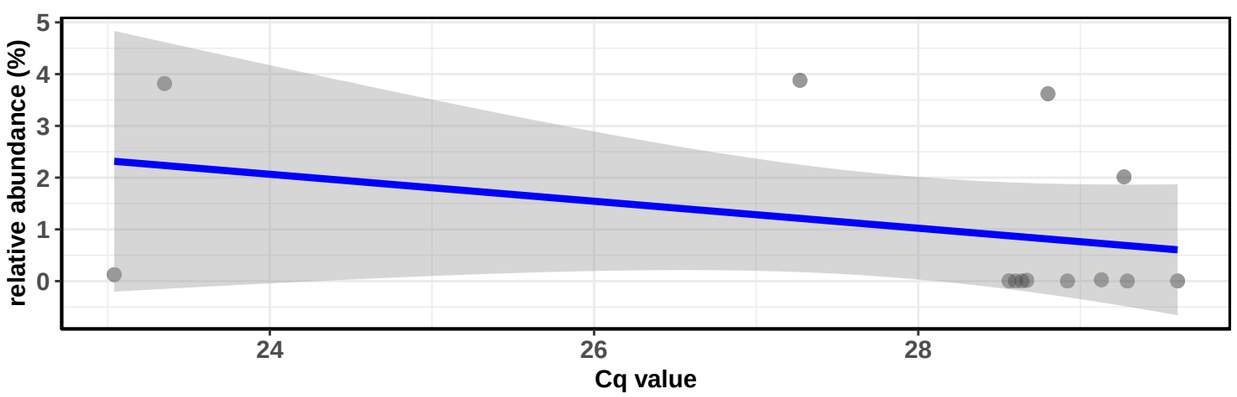
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 4.500, p = 0.148, $\rho_{Spearman}$ = −0.607, $CI_{95\%}$ [−0.933, 0.269], n = 7



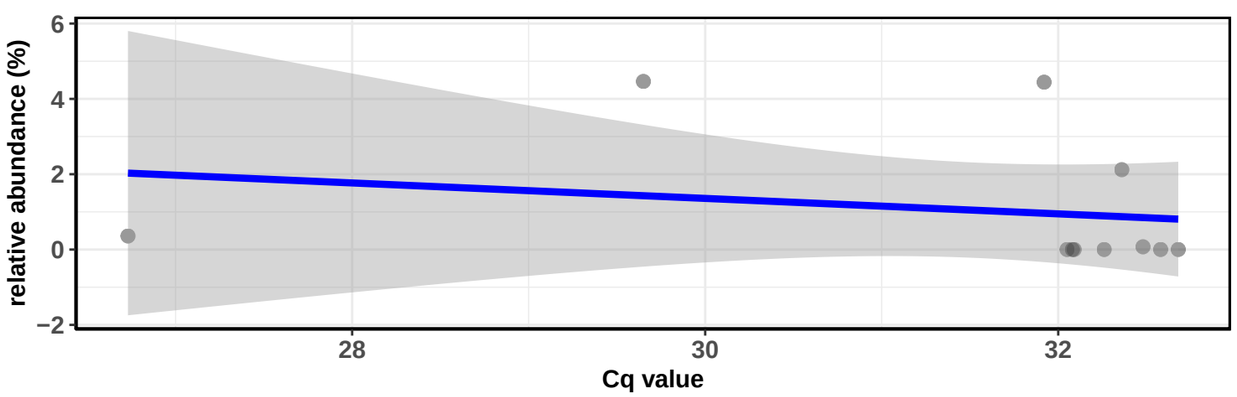
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.223, p = 0.194, $\rho_{Spearman}$ = −0.385, $CI_{95\%}$ [−0.772, 0.211], n = 13



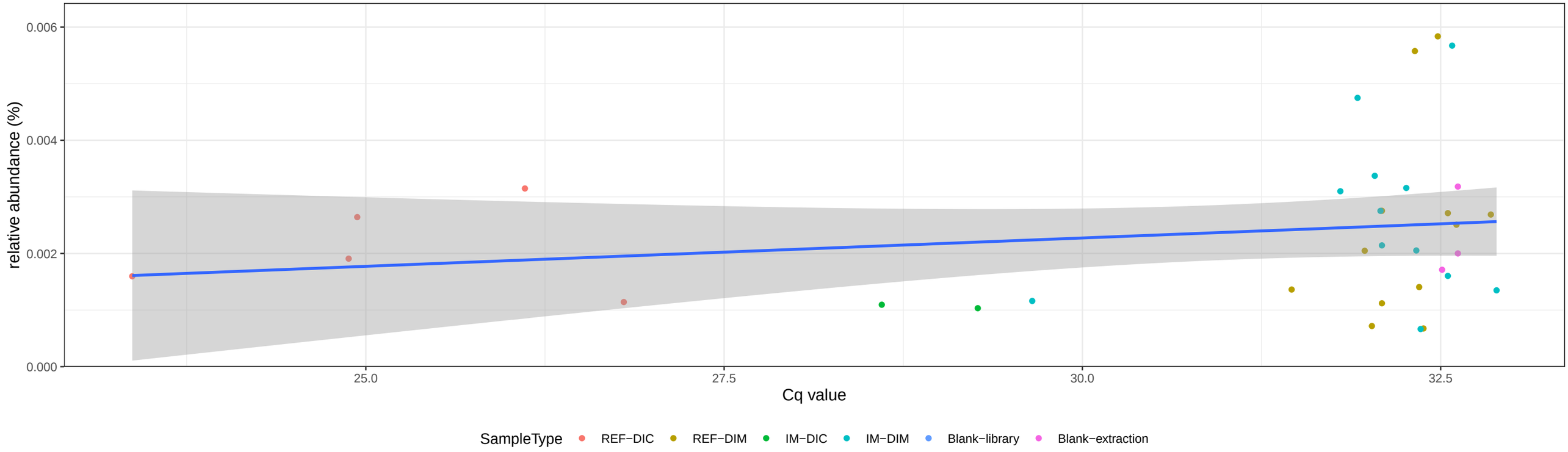
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.642, p = 0.401, $\rho_{Spearman}$ = −0.282, $CI_{95\%}$ [−0.754, 0.383], n = 11

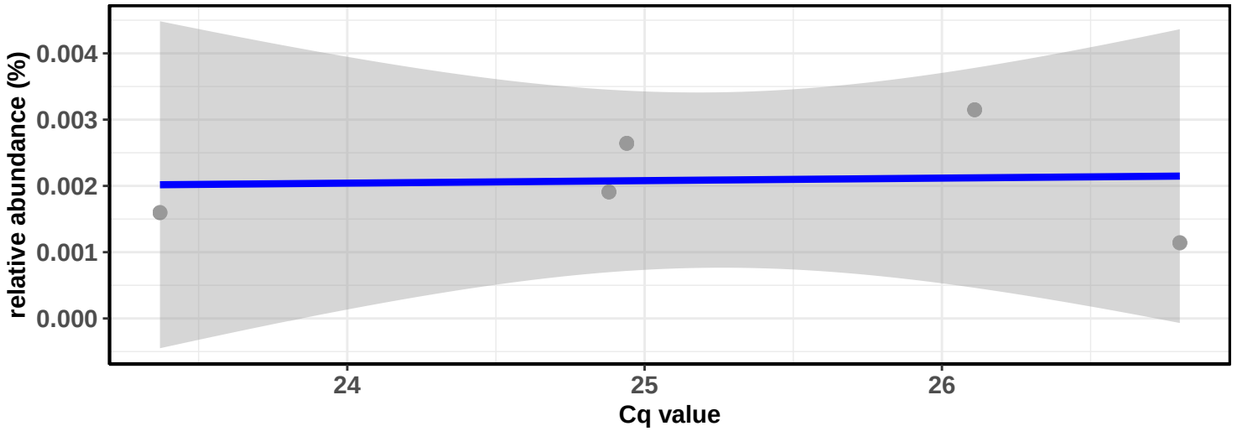


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples

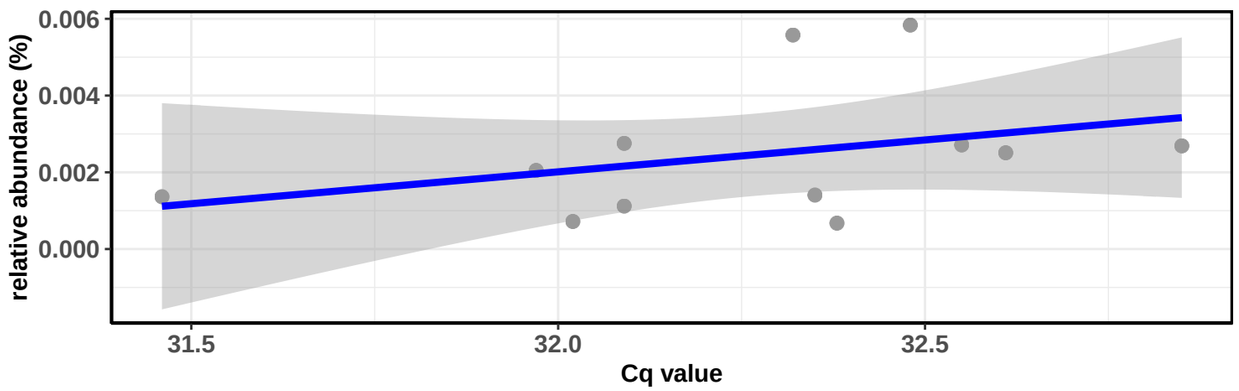


Correlation within the sample type: REF−DIC

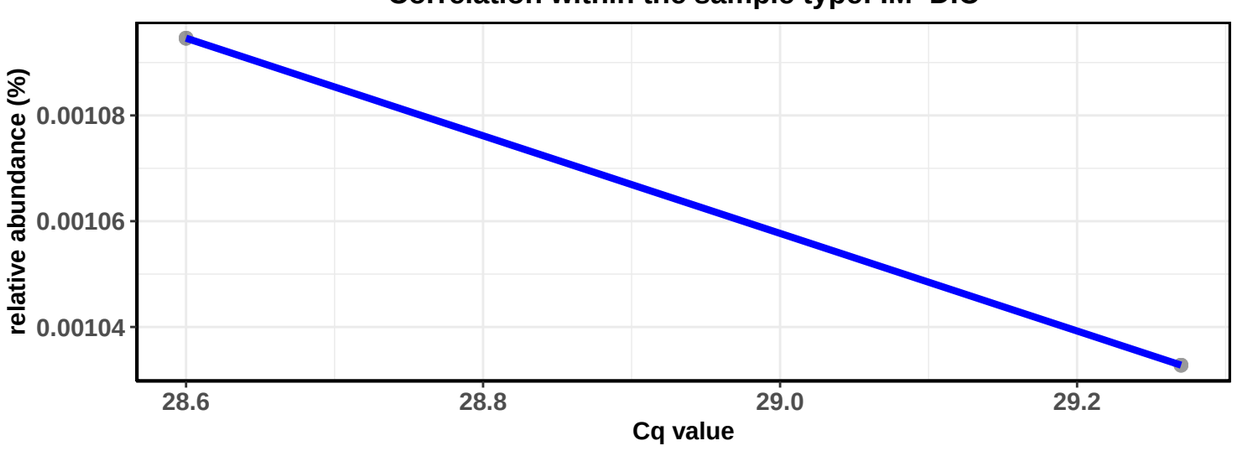


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.186, p = 0.230, $\rho_{Spearman}$ = 0.375, $CI_{95\%}$ [−0.254, 0.781], n = 12

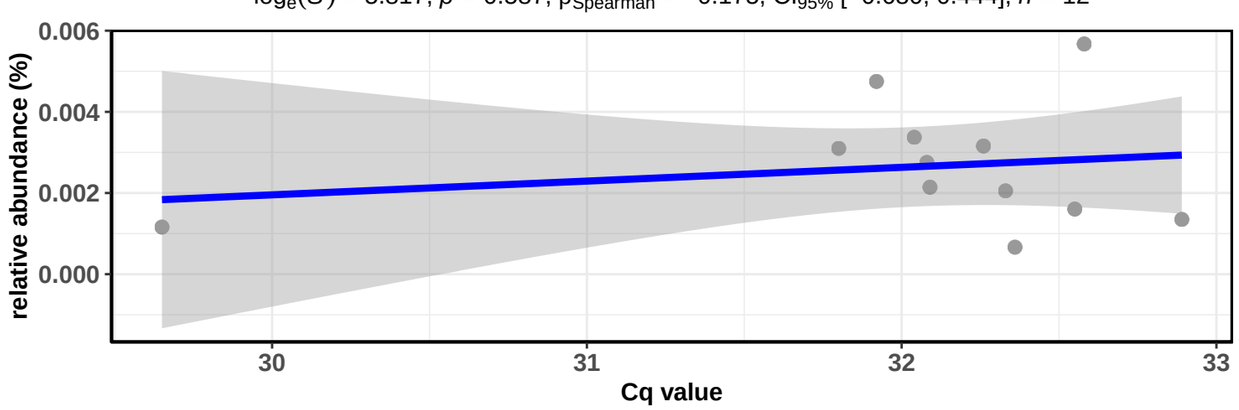


Correlation within the sample type: IM−DIC



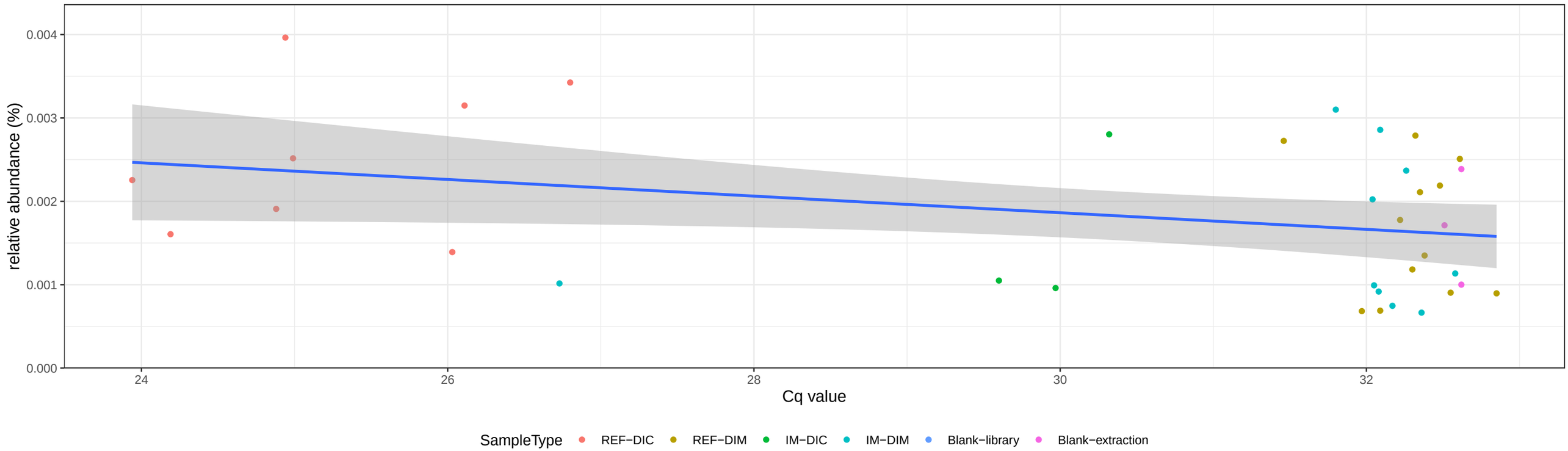
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.817, p = 0.587, $\rho_{Spearman}$ = −0.175, $CI_{95\%}$ [−0.680, 0.444], n = 12



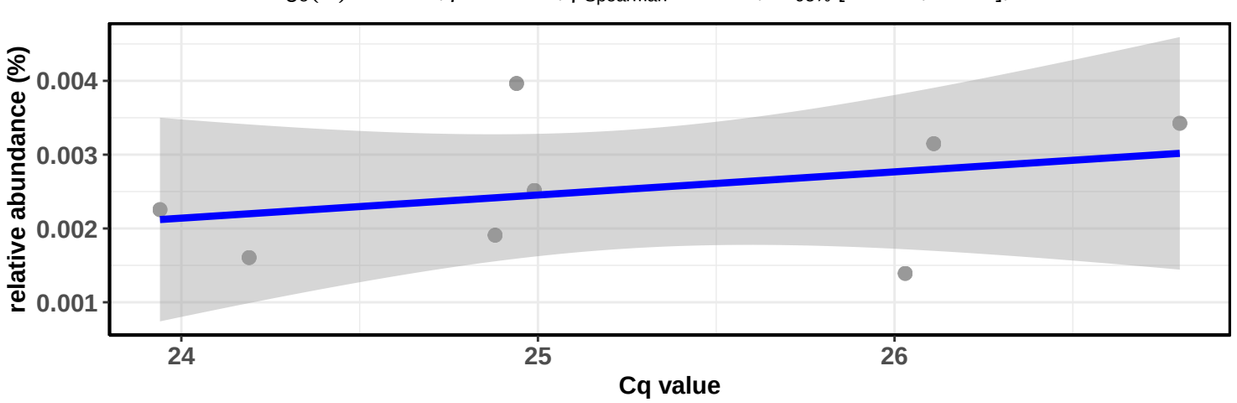
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas

Correlation with all samples



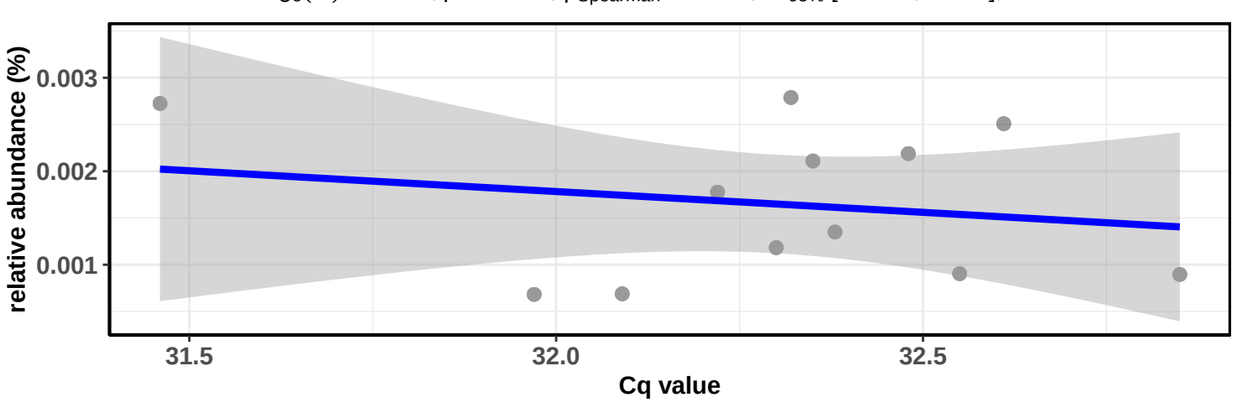
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 3.951, p = 0.352, $\rho_{Spearman}$ = 0.381, $CI_{95\%}$ [−0.443, 0.856], n = 8

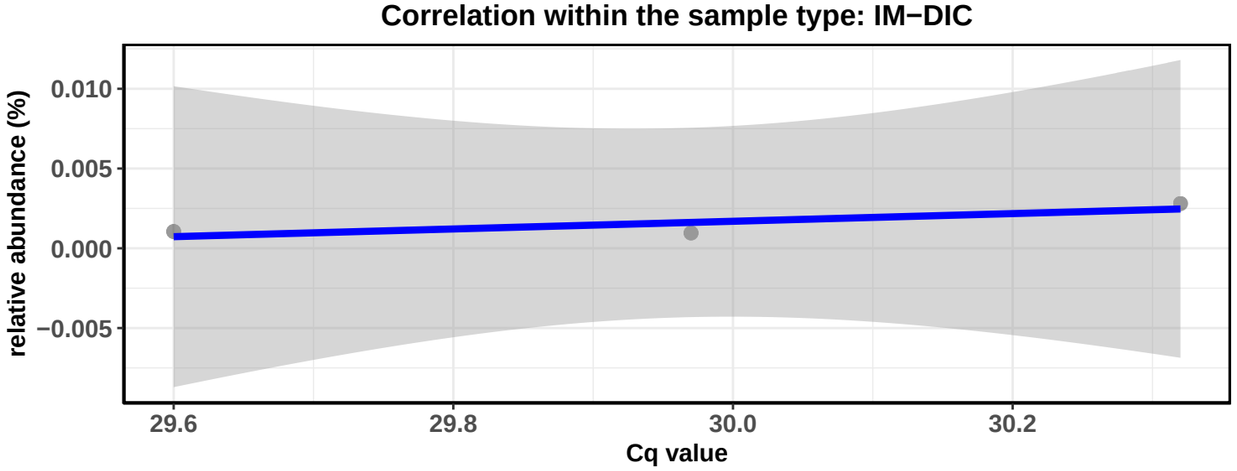


Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.598, p = 0.863, $\rho_{Spearman}$ = 0.056, $CI_{95\%}$ [−0.535, 0.610], n = 12

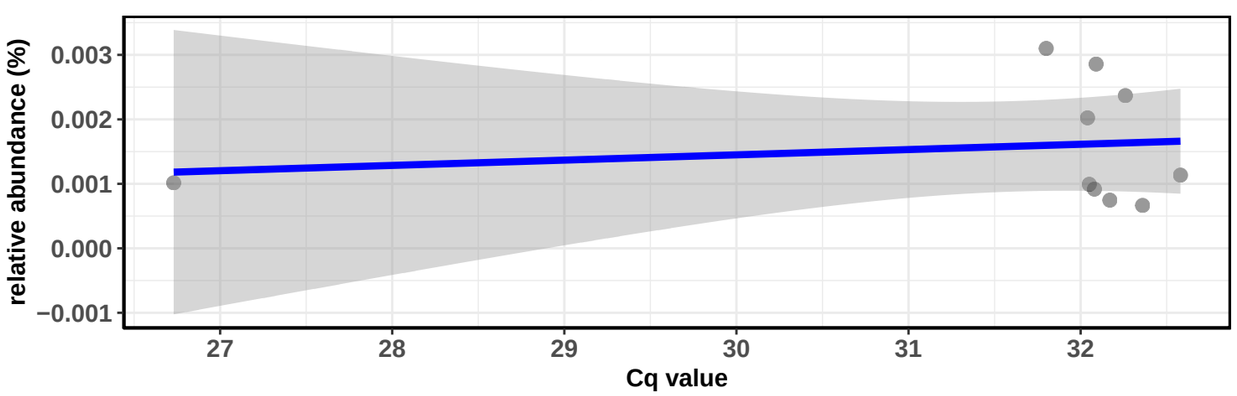


Correlation within the sample type: IM−DIC



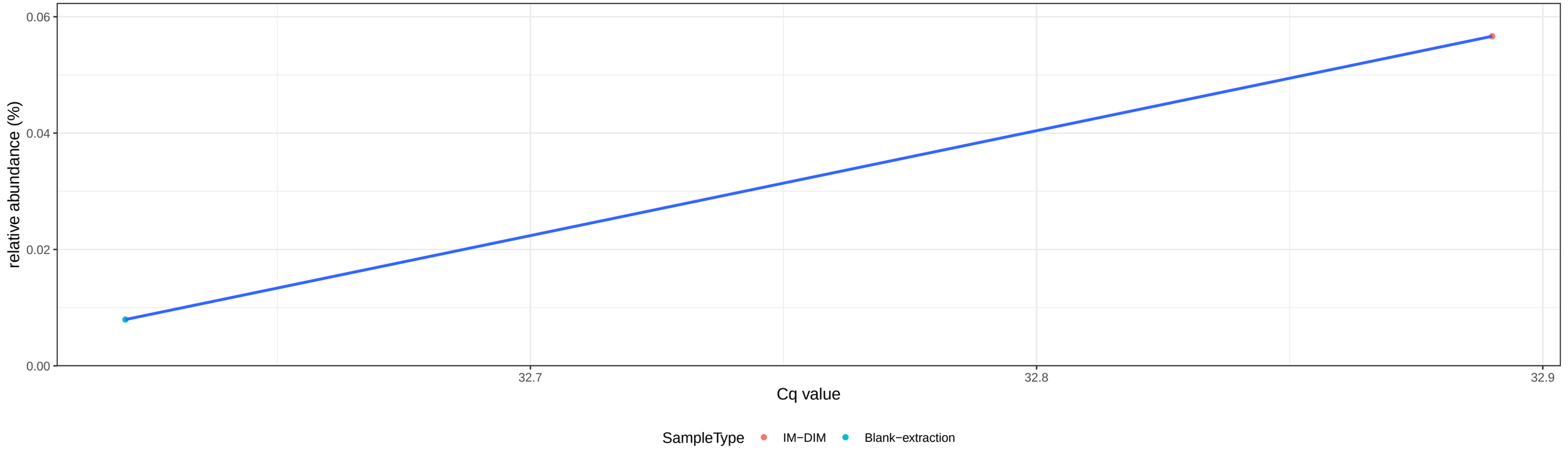
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.366, p = 0.405, $\rho_{Spearman}$ = −0.297, $CI_{95\%}$ [−0.781, 0.409], n = 10

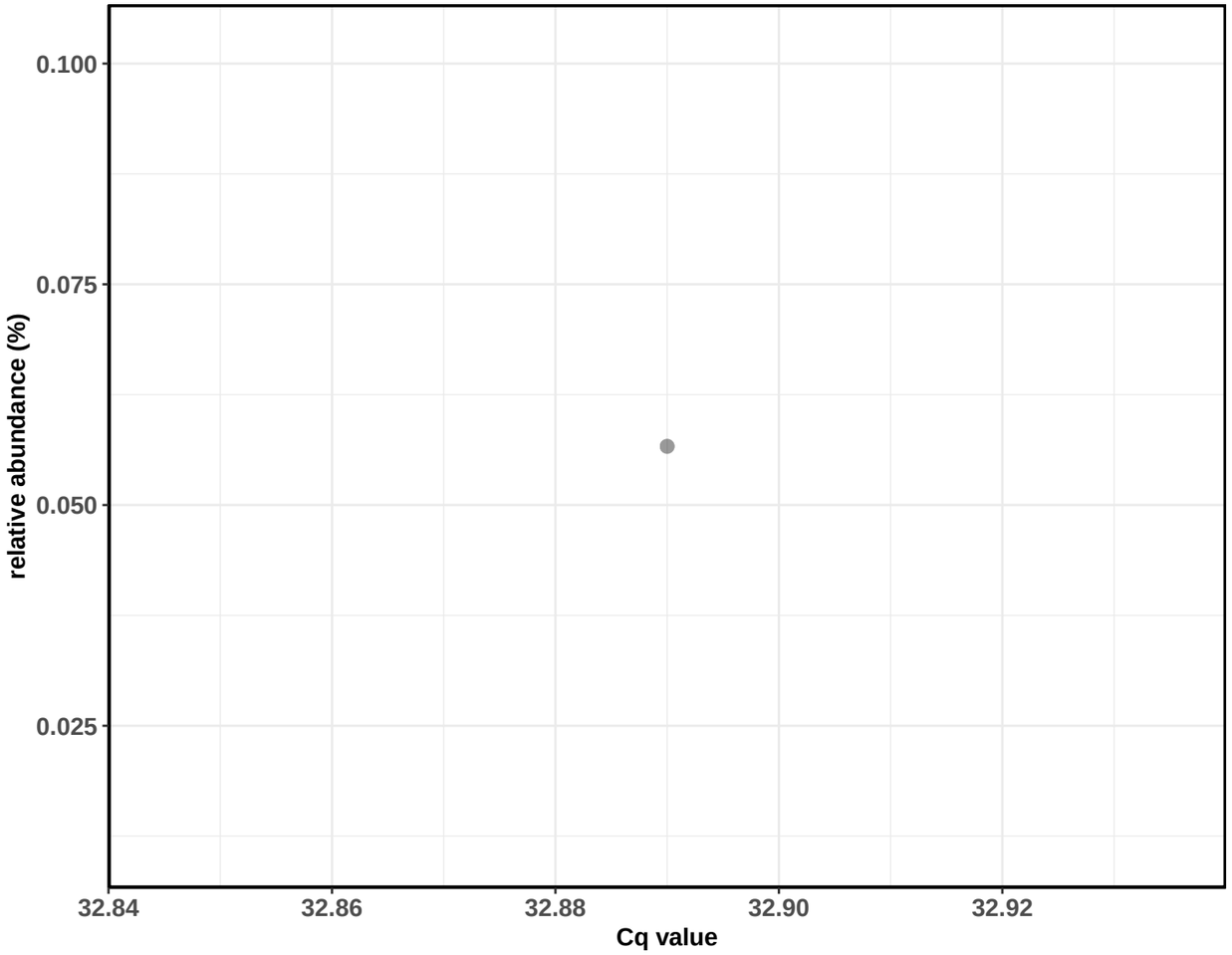


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

Correlation with all samples

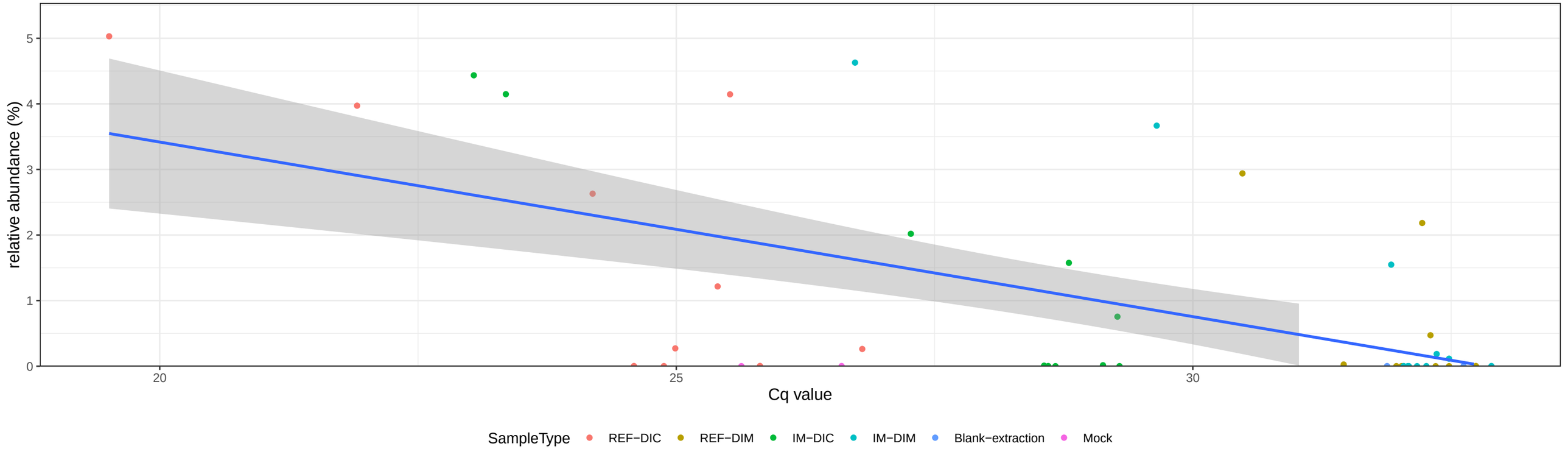


Correlation within the sample type: IM−DIM



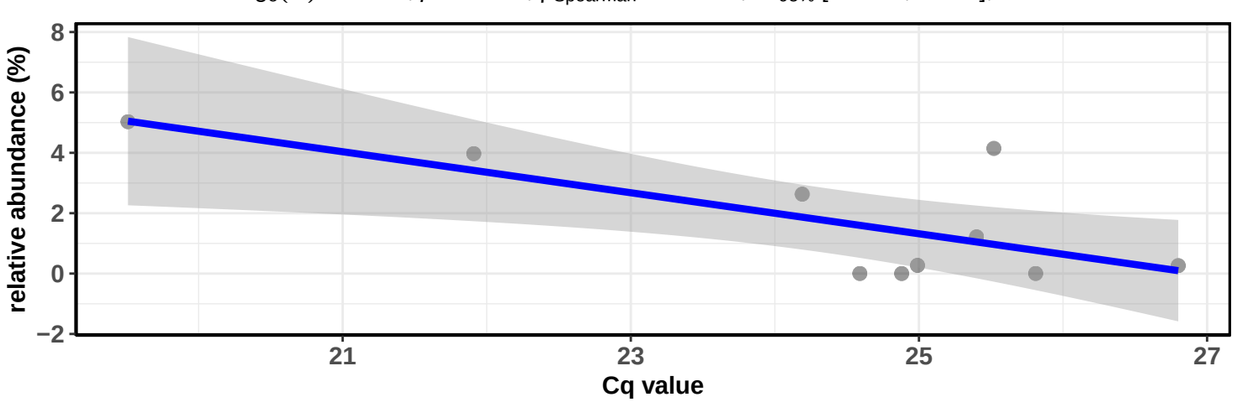
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Aliivibrio; D_6__uncultured bacterium

Correlation with all samples



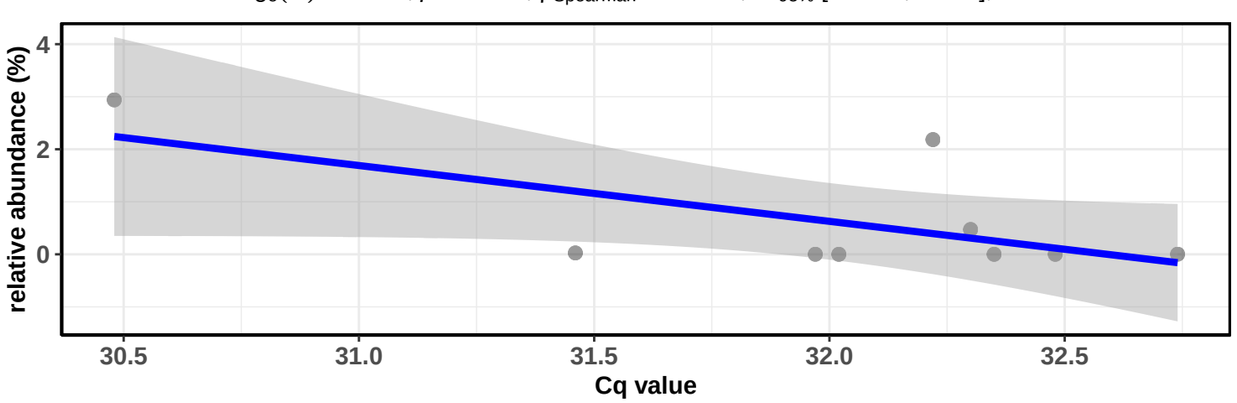
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.429, p = 0.276, $\rho_{Spearman}$ = −0.382, $CI_{95\%}$ [−0.815, 0.326], n = 10



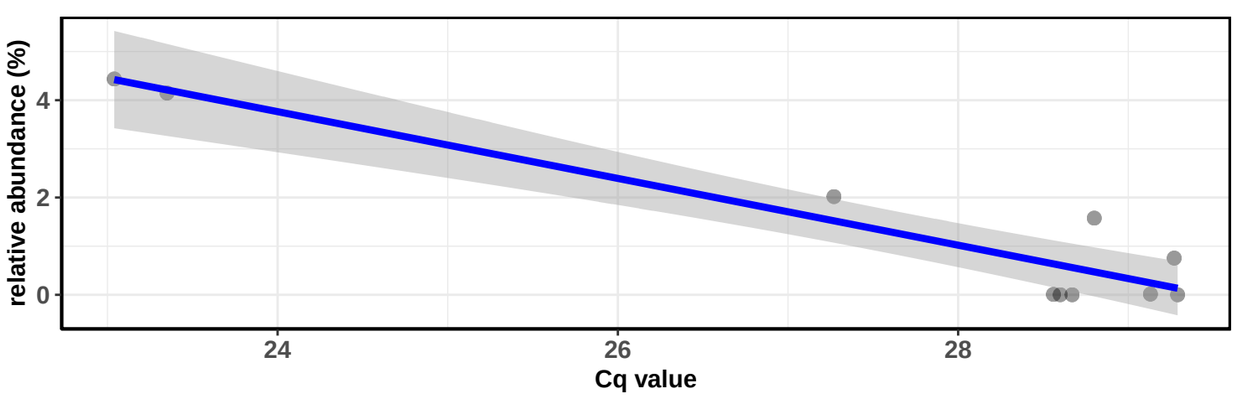
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.147, p = 0.244, $\rho_{Spearman}$ = −0.433, $CI_{95\%}$ [−0.852, 0.324], n = 9



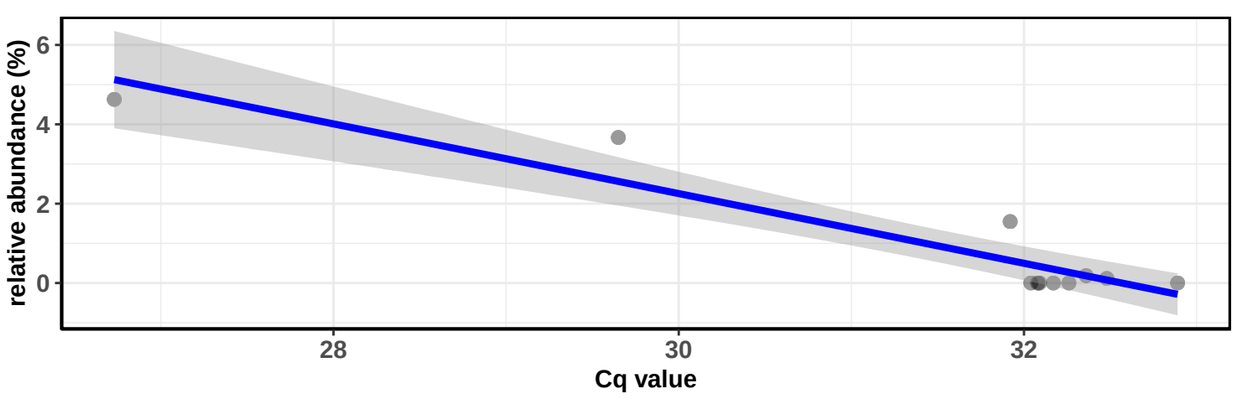
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.583, p = 0.060, $\rho_{Spearman}$ = −0.612, $CI_{95\%}$ [−0.896, 0.028], n = 10



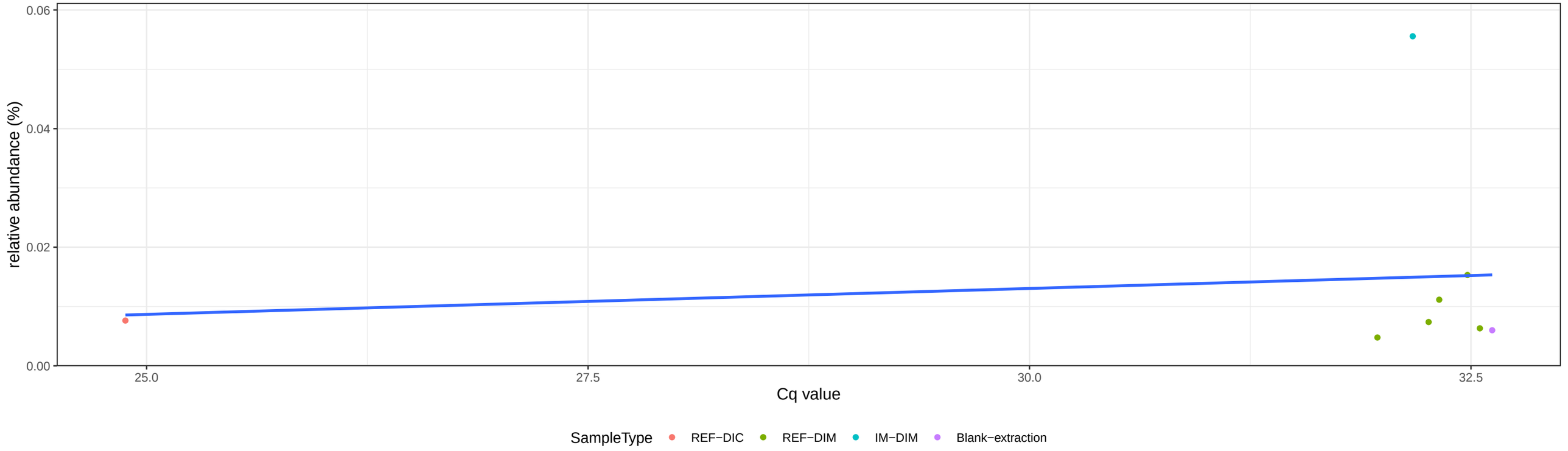
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 5.710, p = 0.259, $\rho_{Spearman}$ = −0.373, $CI_{95\%}$ [−0.795, 0.293], n = 11

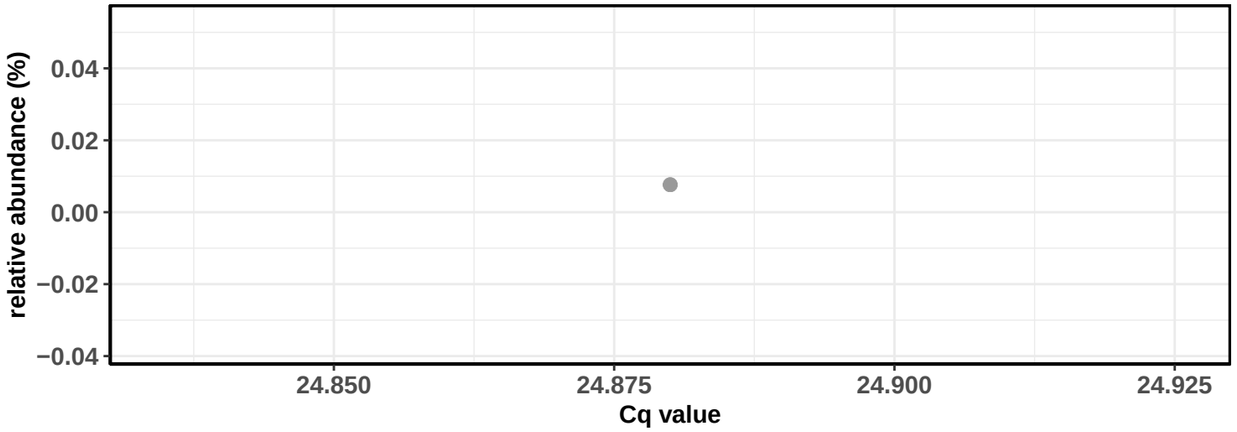


D_0__Bacteria; D_1__Proteobacteria; D_2__Alphaproteobacteria; D_3__Caulobacterales; D_4__Caulobacteraceae; D_5__Brevundimonas

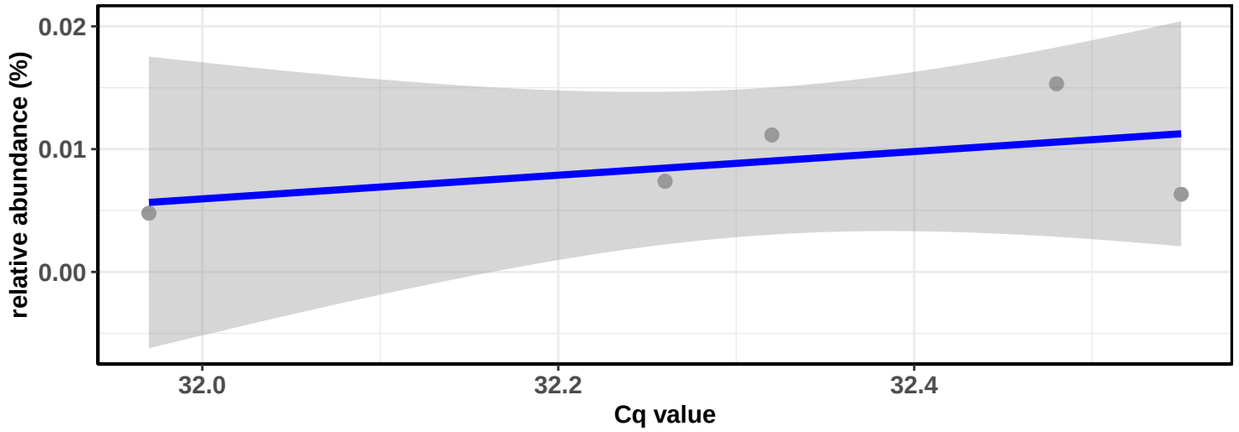
Correlation with all samples



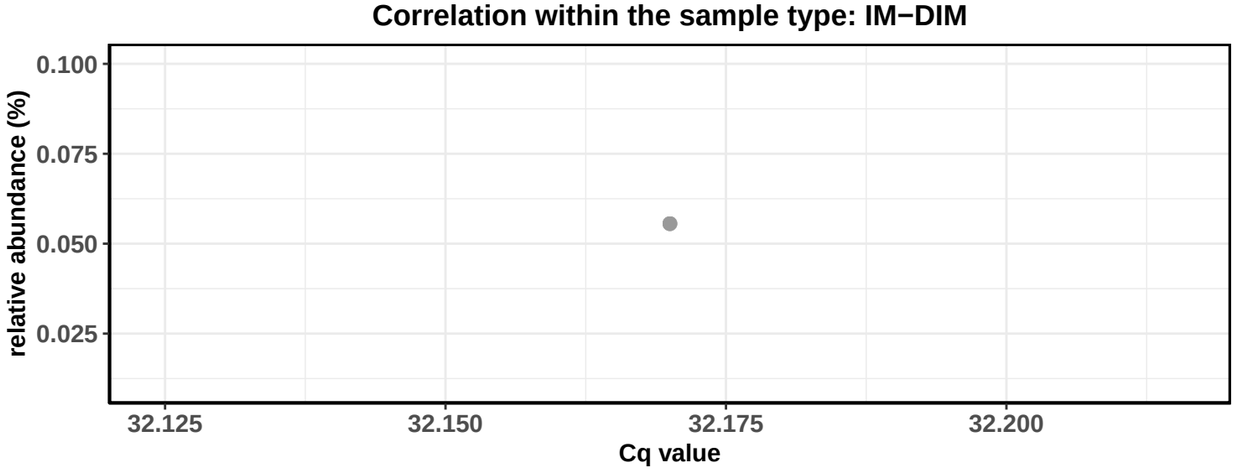
Correlation within the sample type: REF−DIC



Correlation within the sample type: REF−DIM

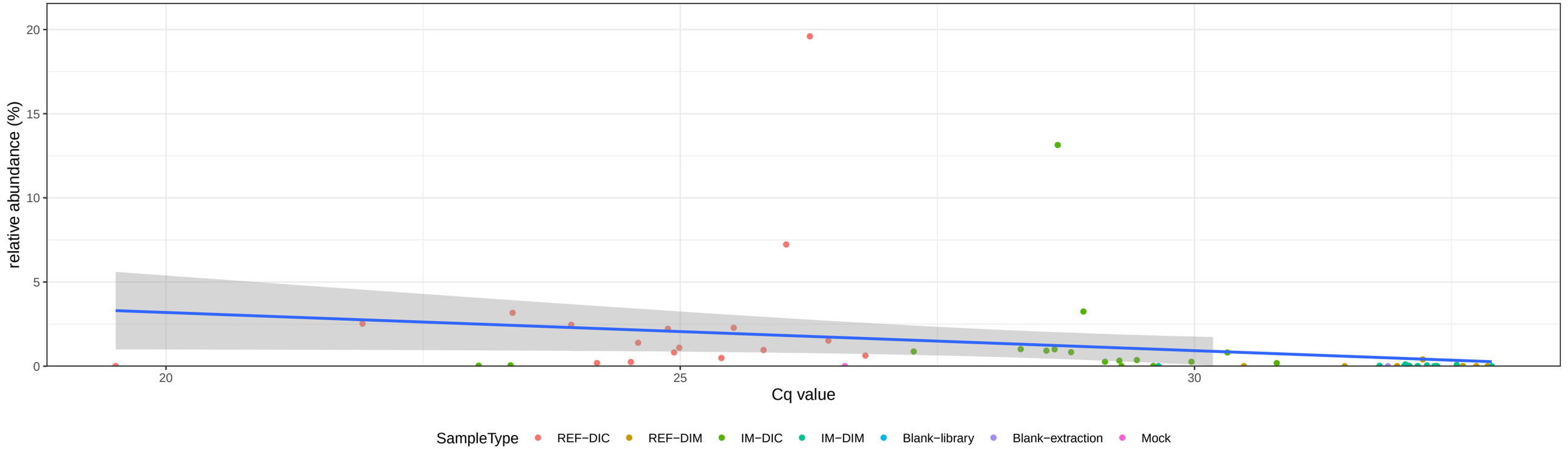


Correlation within the sample type: IM−DIM



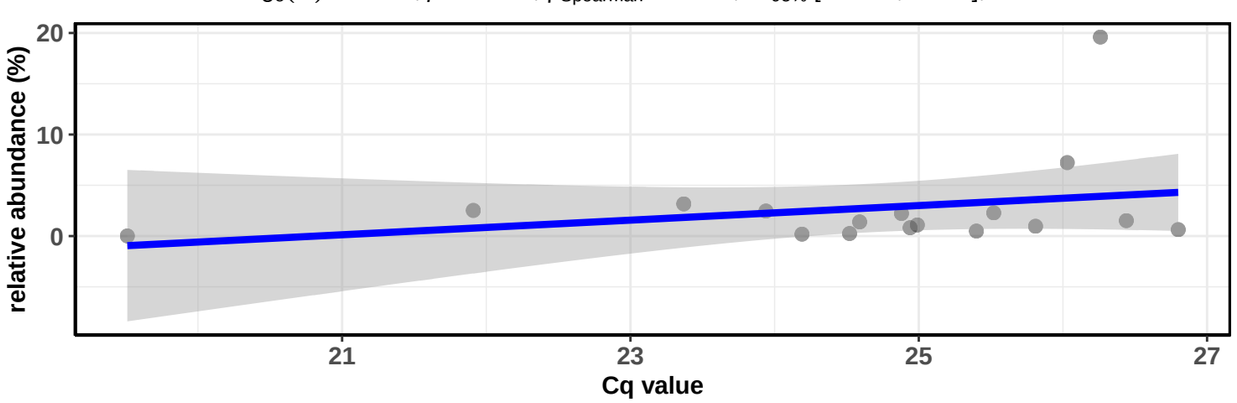
D_0__Bacteria; D_1__Tenericutes; D_2__Mollicutes; D_3__Mycoplasmatales; D_4__Mycoplasmataceae; D_5__Mycoplasma; D_6__uncultured bacterium

Correlation with all samples



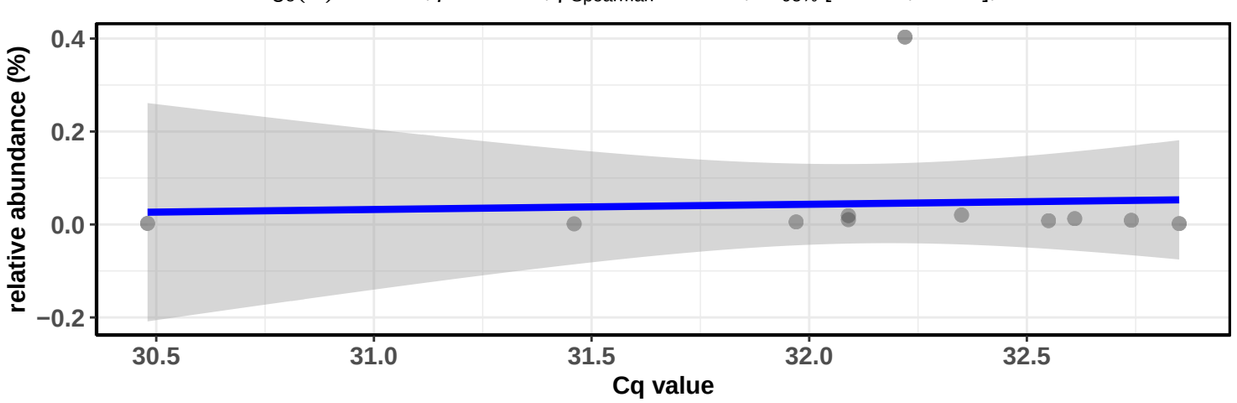
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.531, p = 0.541, $\rho_{Spearman}$ = 0.159, $CI_{95\%}$ [−0.348, 0.594], n = 17



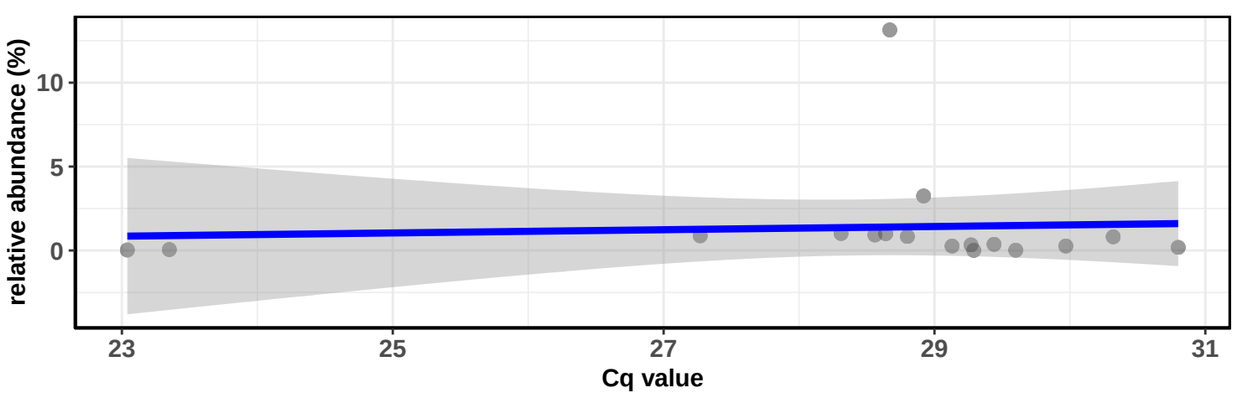
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 5.158, p = 0.536, $\rho_{Spearman}$ = 0.210, $CI_{95\%}$ [−0.446, 0.719], n = 11



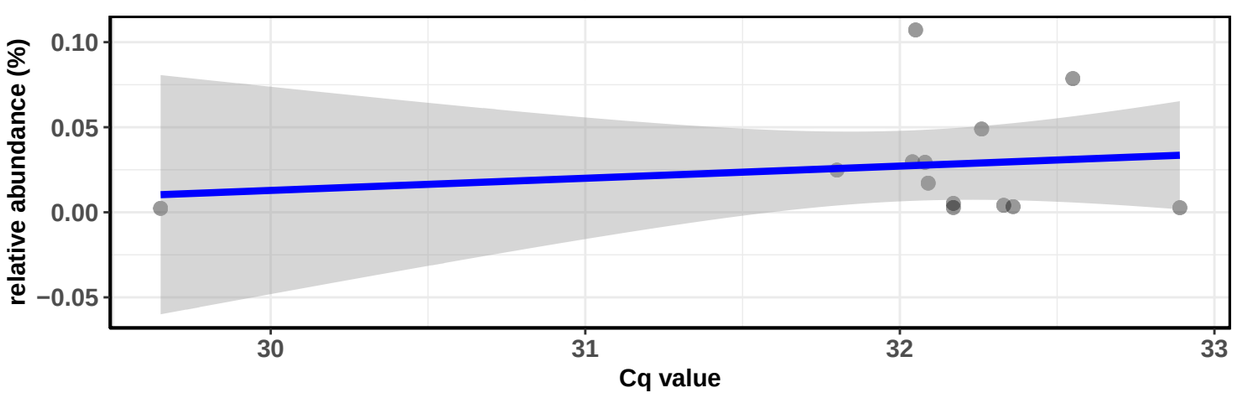
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.953, p = 0.273, $\rho_{Spearman}$ = −0.282, $CI_{95\%}$ [−0.672, 0.230], n = 17



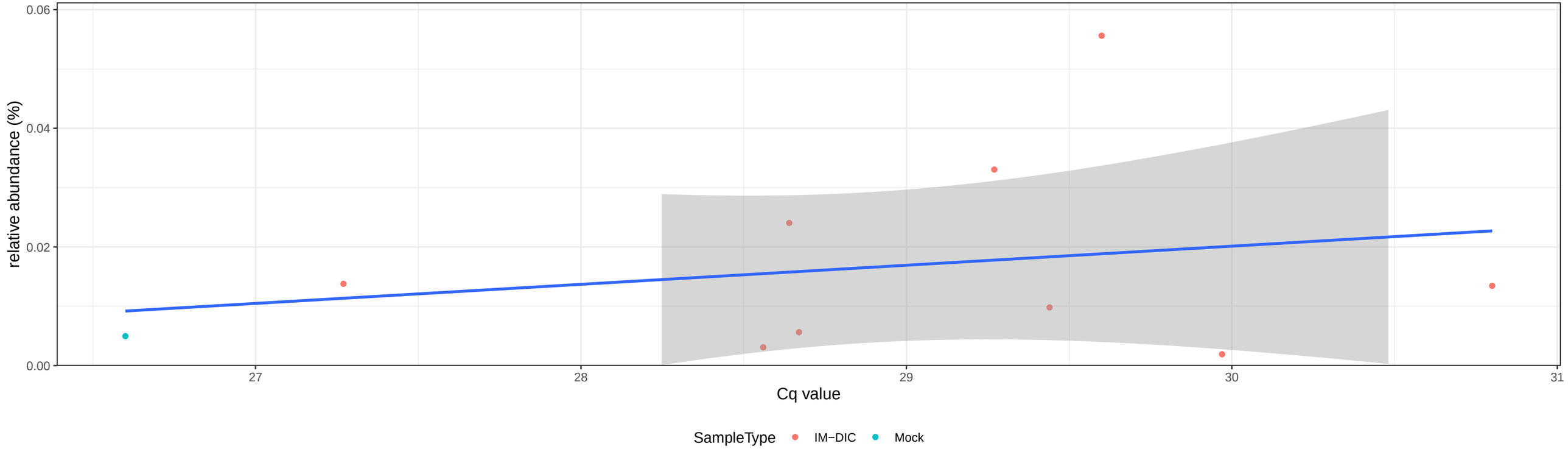
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.004, p = 0.714, $\rho_{Spearman}$ = −0.113, $CI_{95\%}$ [−0.625, 0.467], n = 13



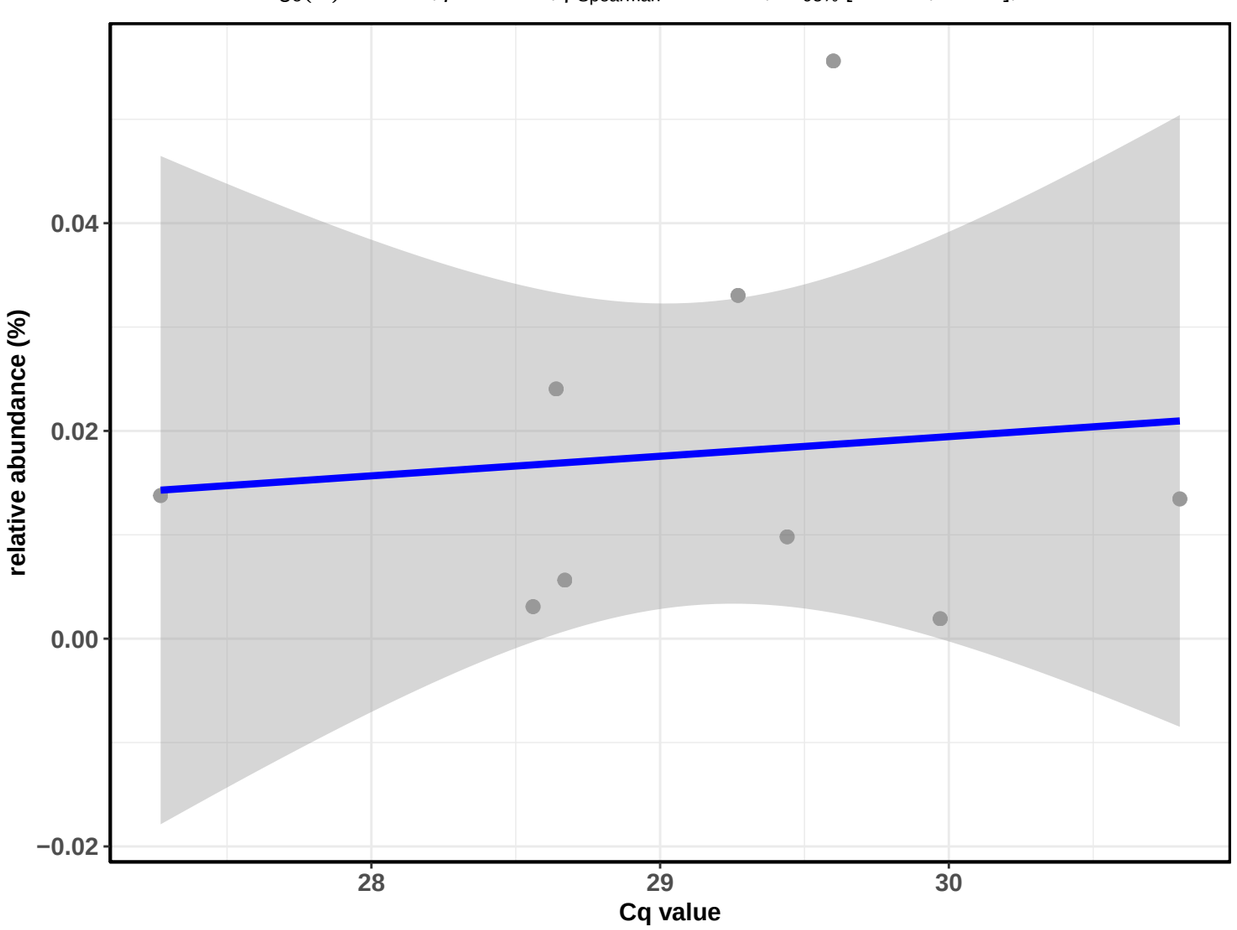
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Enterobacteriales; D_4__Enterobacteriaceae; D_5__Escherichia−Shigella

Correlation with all samples



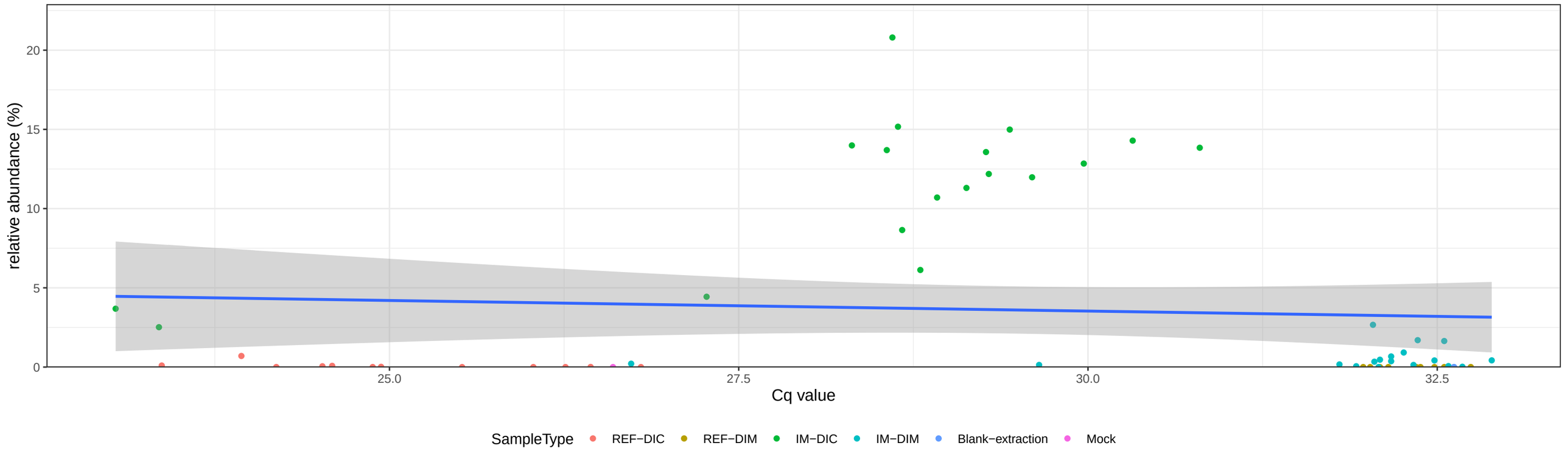
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 4.820, p = 0.932, $\rho_{Spearman}$ = −0.033, $CI_{95\%}$ [−0.682, 0.645], n = 9



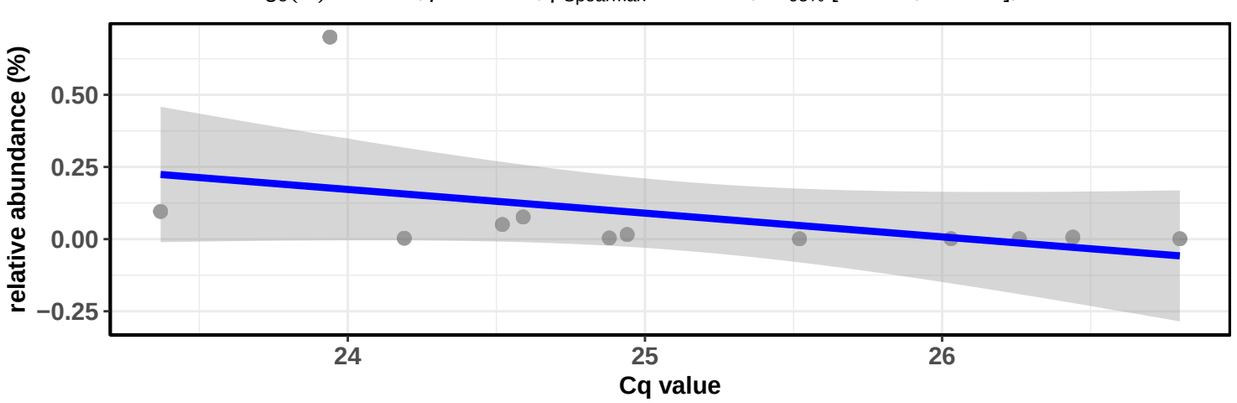
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales

Correlation with all samples



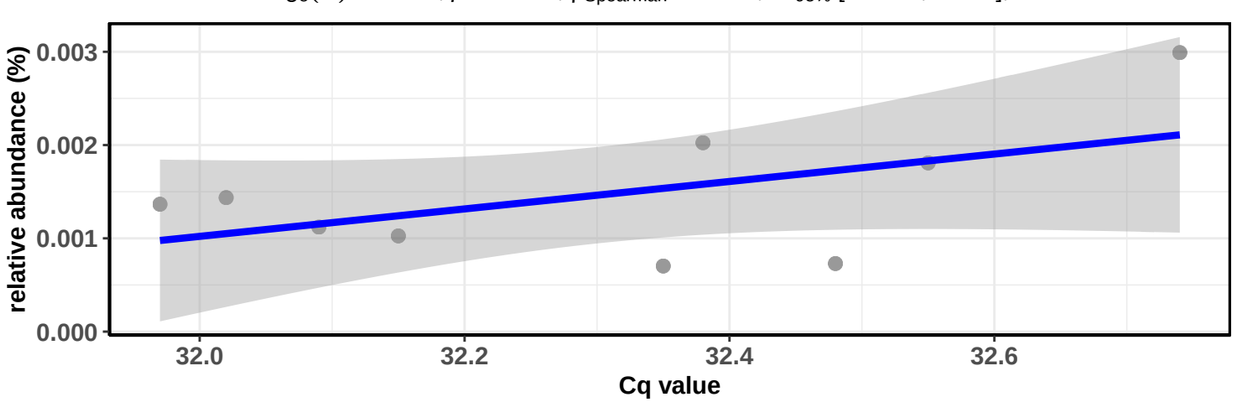
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.203, p = 0.007, $\rho_{Spearman}$ = −0.727, $CI_{95\%}$ [−0.918, −0.263], n = 12



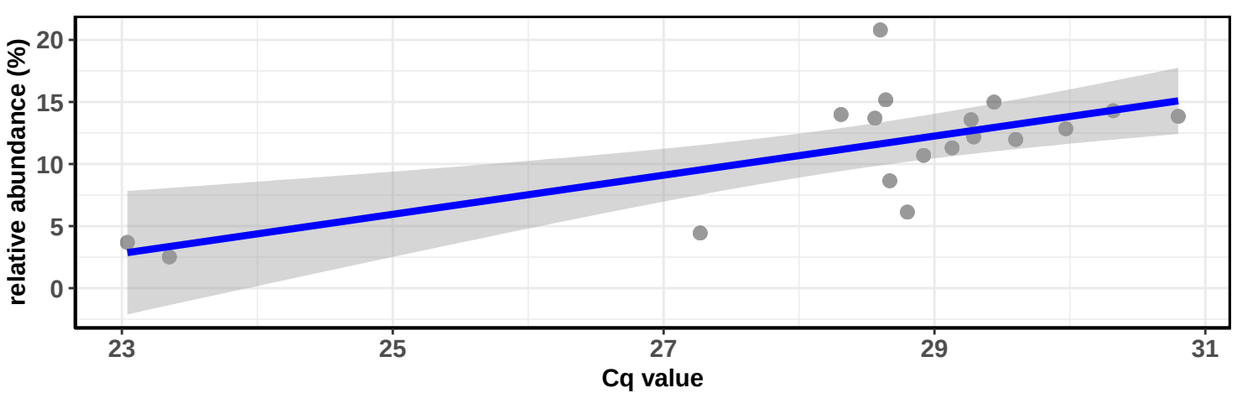
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 4.382, p = 0.381, $\rho_{Spearman}$ = 0.333, $CI_{95\%}$ [−0.425, 0.817], n = 9



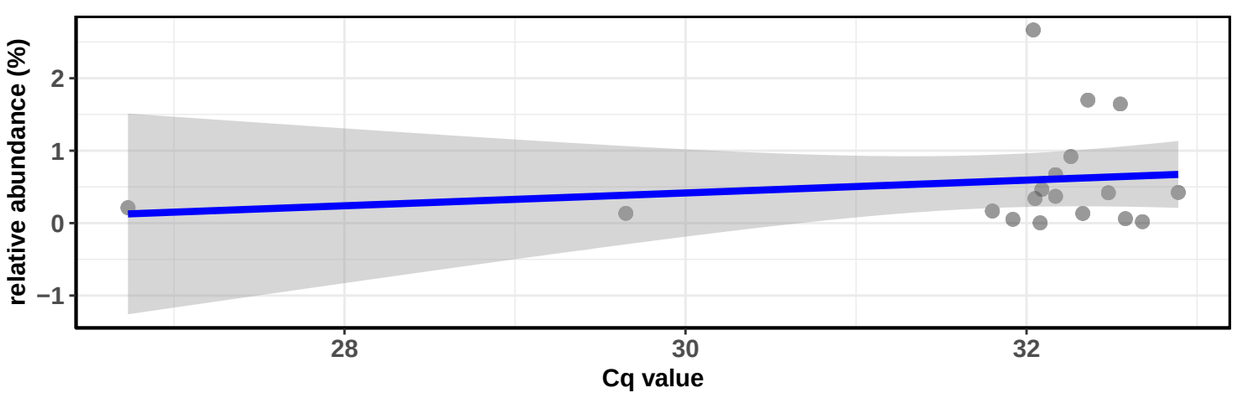
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.390, p = 0.115, $\rho_{Spearman}$ = 0.385, $CI_{95\%}$ [−0.100, 0.722], n = 18



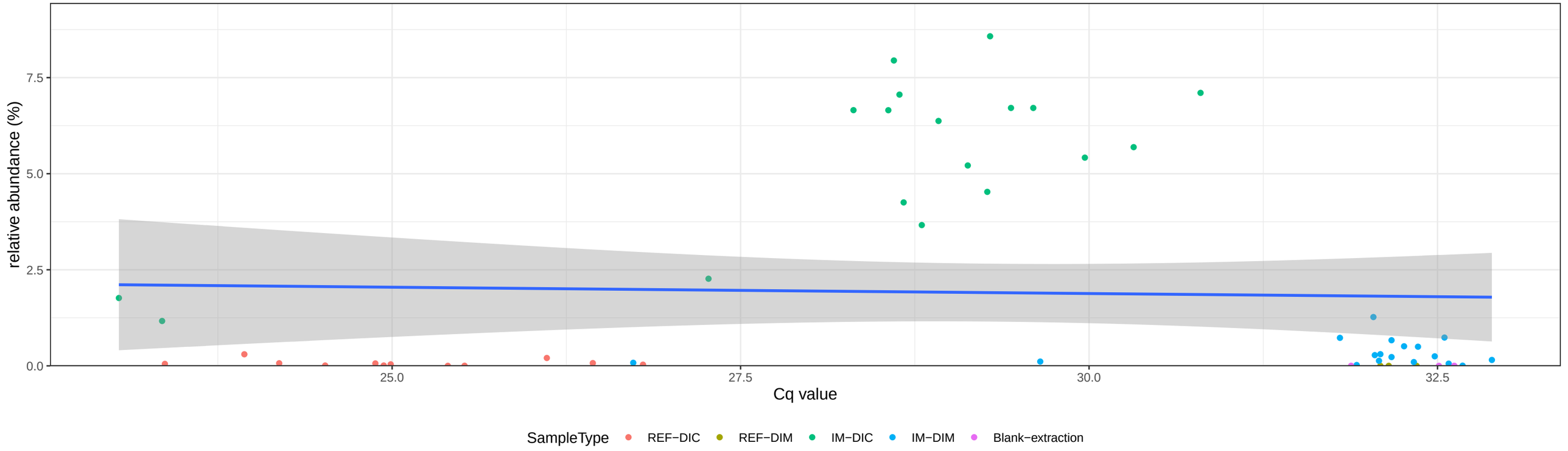
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.731, p = 0.593, $\rho_{Spearman}$ = 0.135, $CI_{95\%}$ [−0.354, 0.566], n = 18



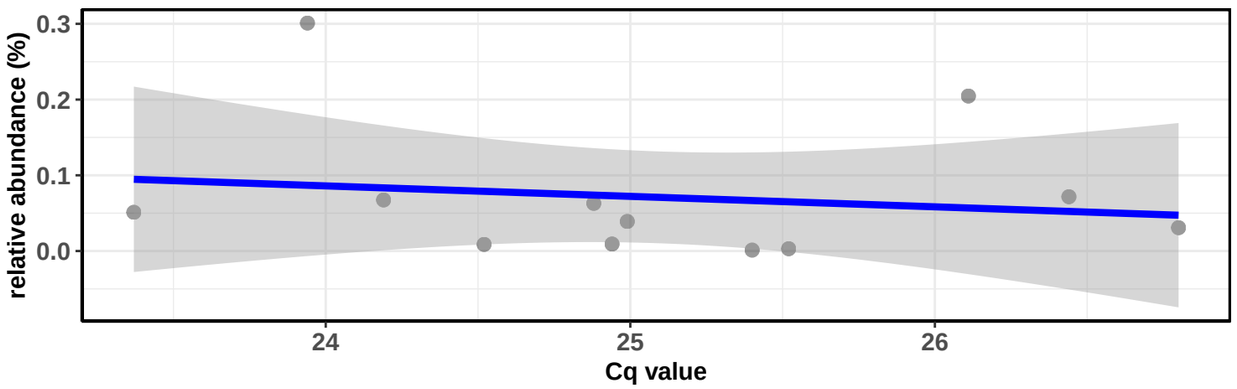
D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Corynebacteriales; D_4__Corynebacteriaceae; D_5__Corynebacterium 1; Ambiguous_taxa

Correlation with all samples

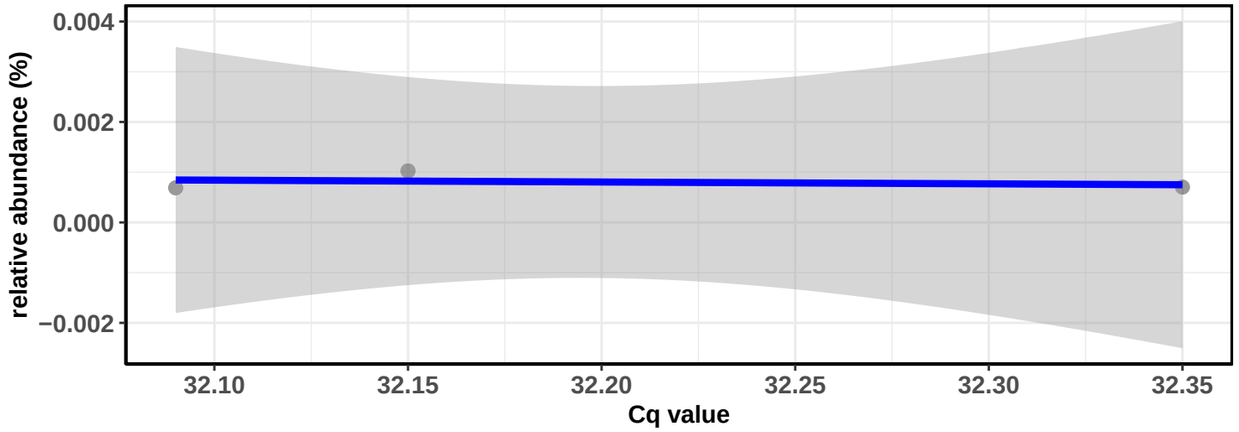


Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.817, p = 0.587, $\rho_{Spearman}$ = −0.175, $CI_{95\%}$ [−0.680, 0.444], n = 12

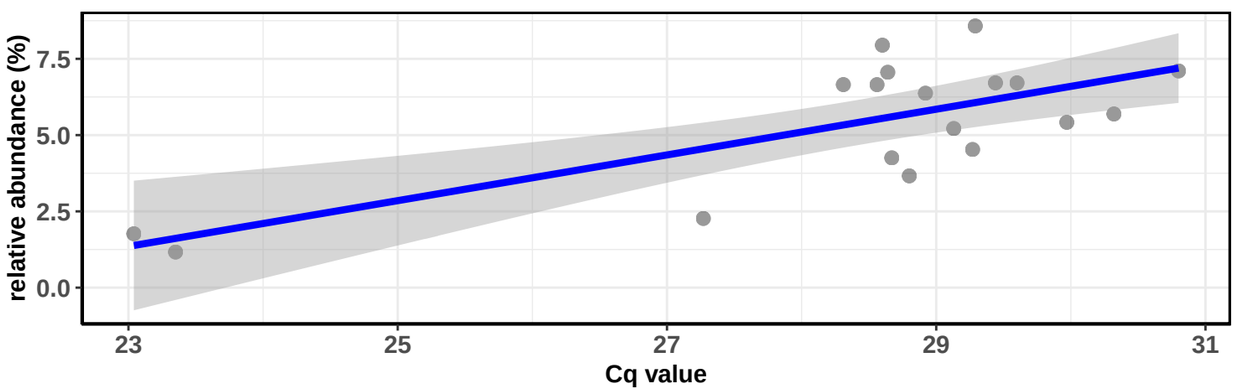


Correlation within the sample type: REF−DIM



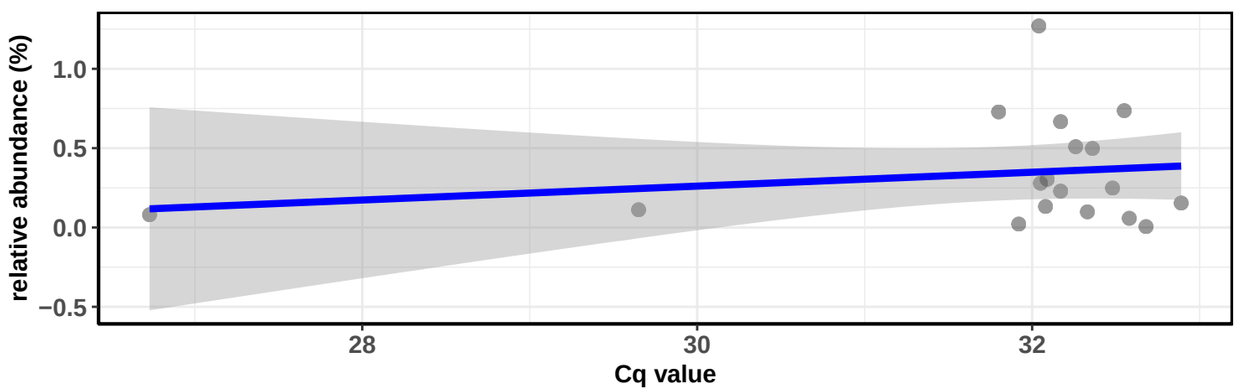
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.280, p = 0.062, $\rho_{Spearman}$ = 0.449, $CI_{95\%}$ [−0.023, 0.757], n = 18



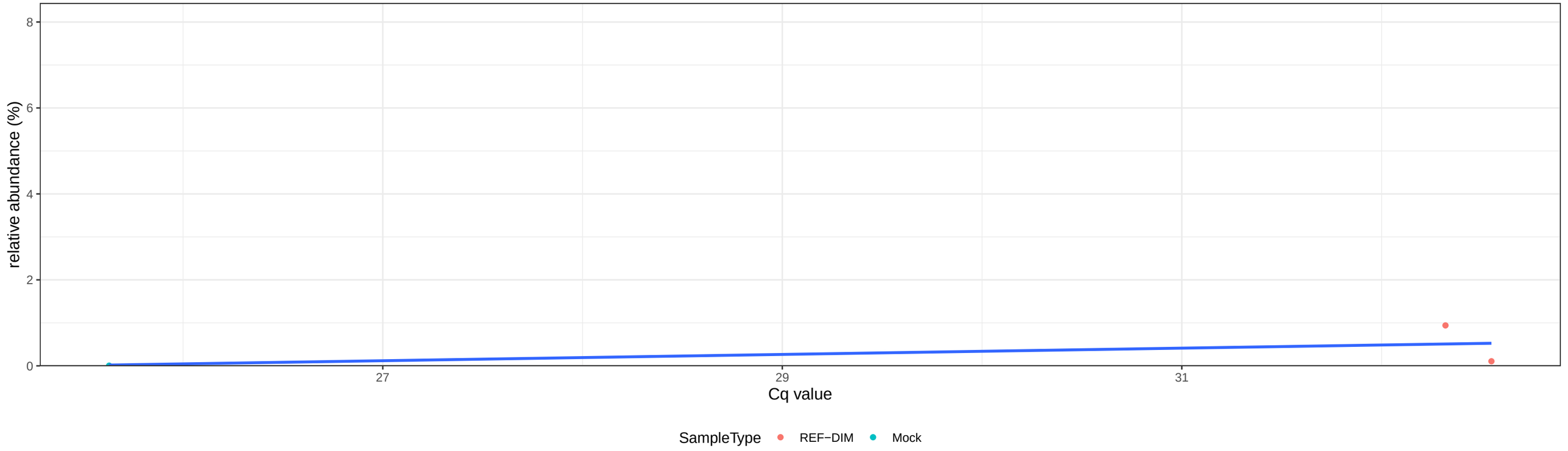
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.949, p = 0.766, $\rho_{Spearman}$ = −0.075, $CI_{95\%}$ [−0.524, 0.406], n = 18

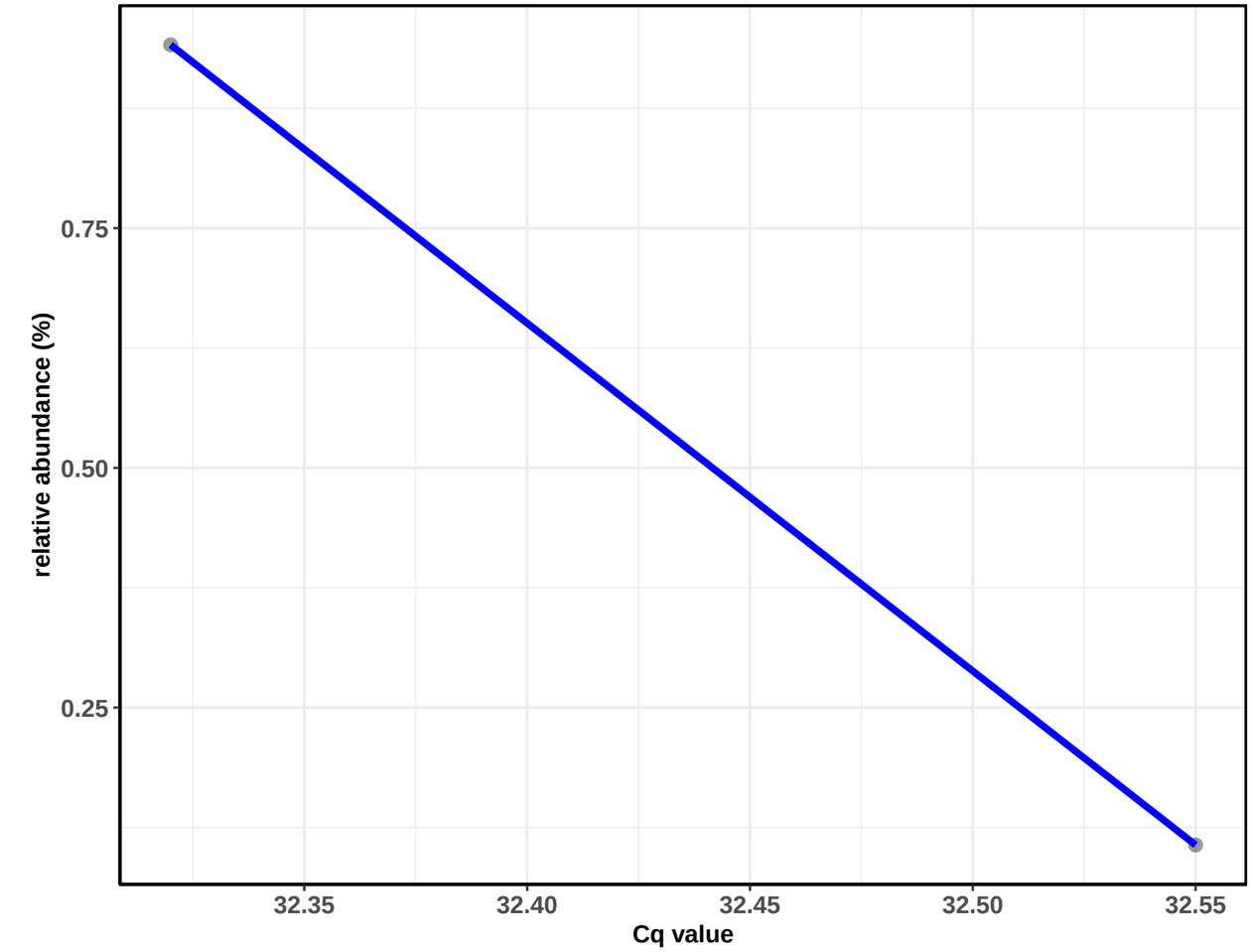


D_0__Bacteria; D_1__Cyanobacteria; D_2__Melainabacteria; D_3__Obscuribacterales; Ambiguous_taxa; Ambiguous_taxa; Ambiguous_taxa

Correlation with all samples

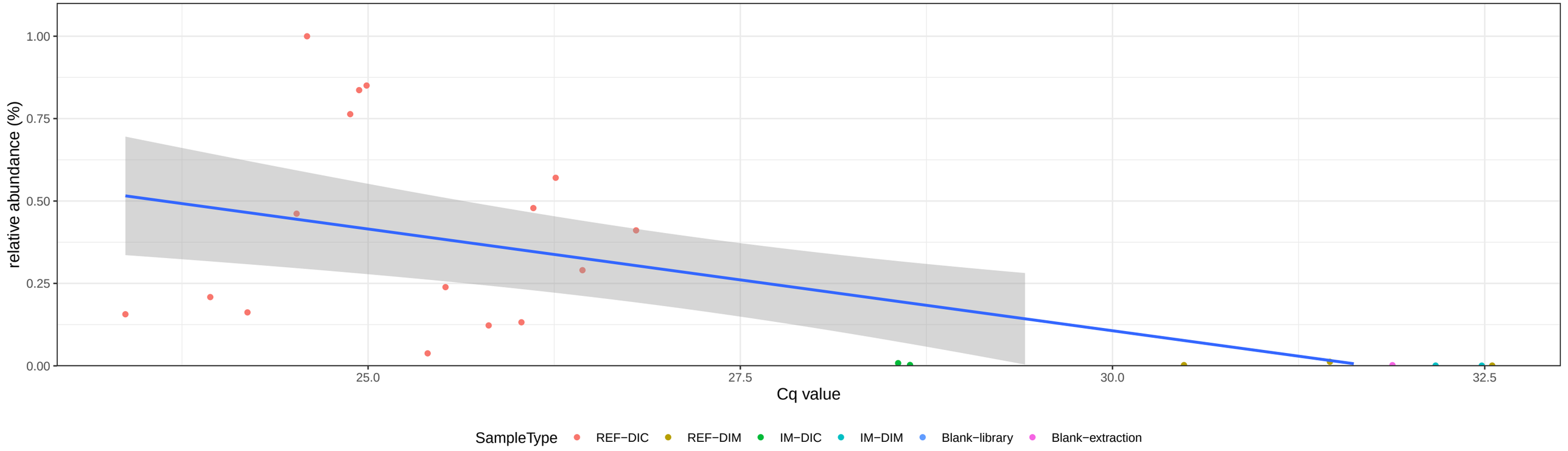


Correlation within the sample type: REF−DIM

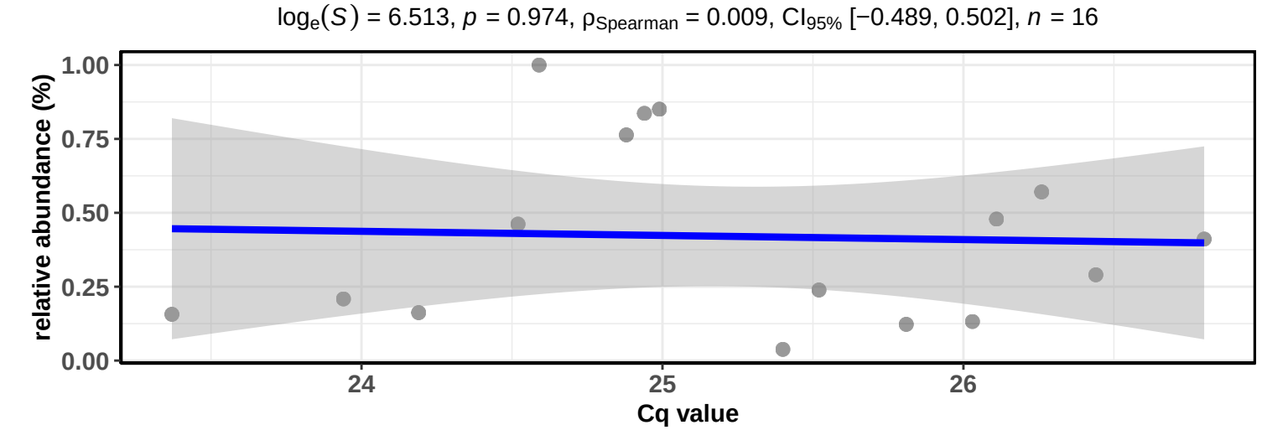


D_0__Bacteria; D_1__Firmicutes; D_2__Clostridia; D_3__Clostridiales; D_4__Family XI; D_5__Tepidimicrobium; D_6__Tepidimicrobium sp. GRC1

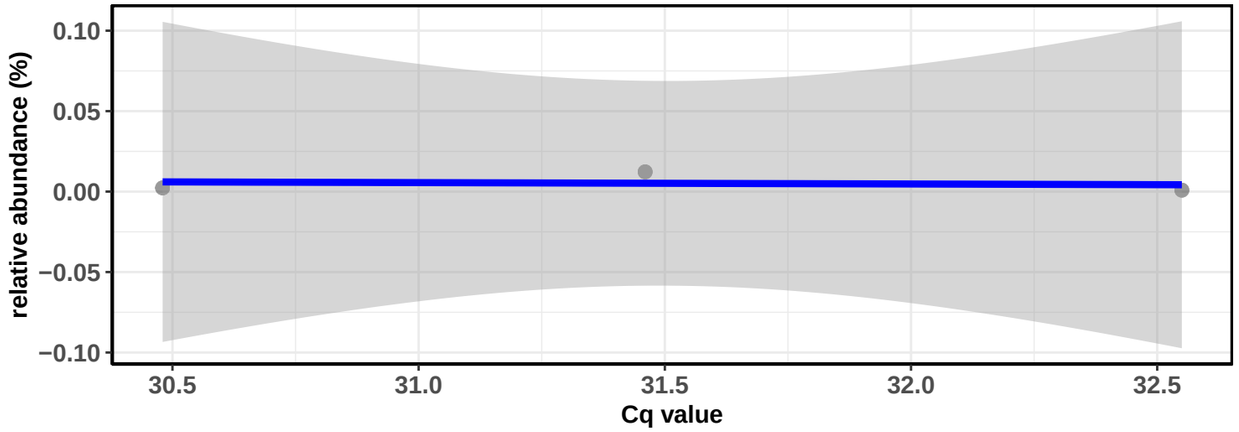
Correlation with all samples



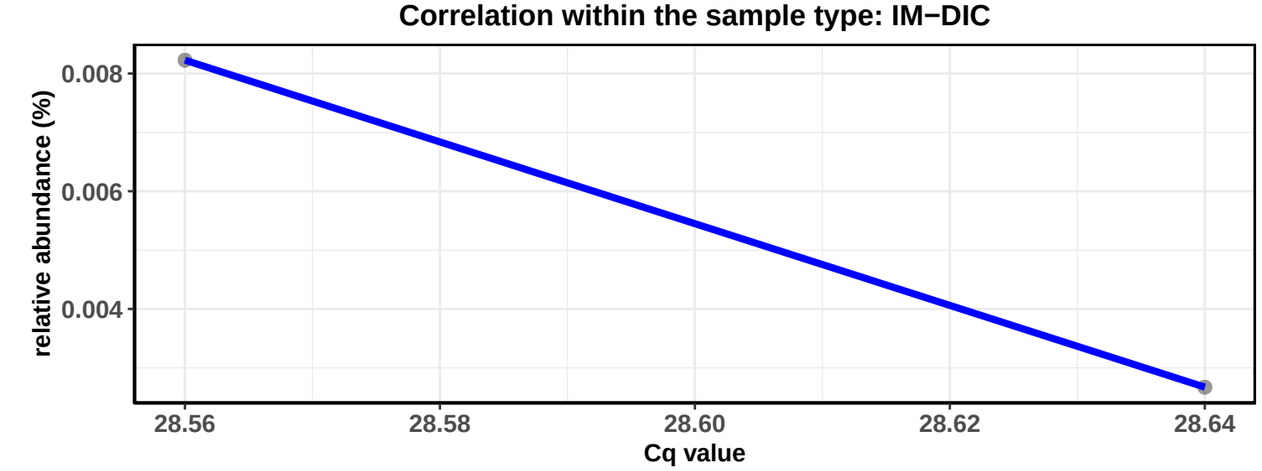
Correlation within the sample type: REF−DIC



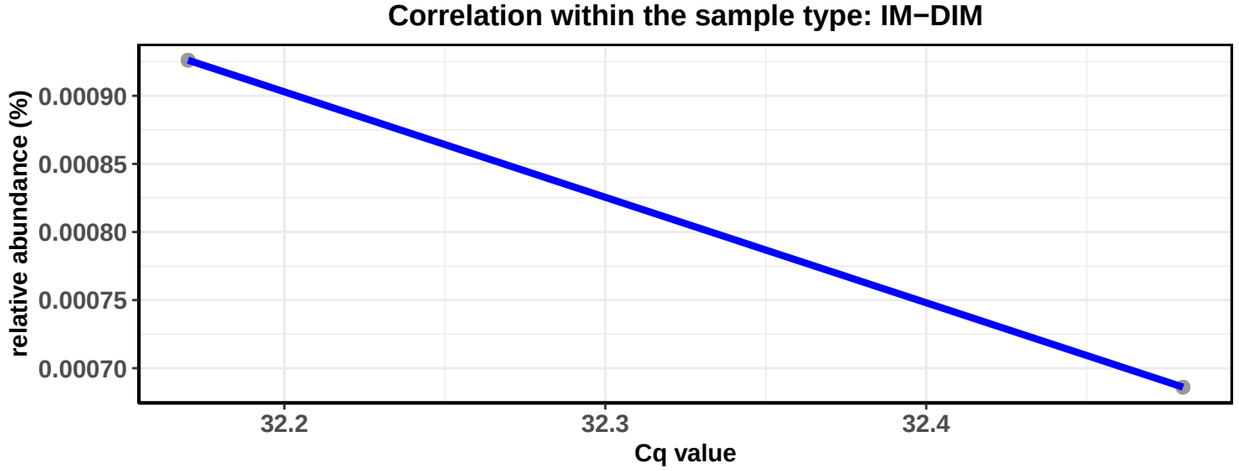
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

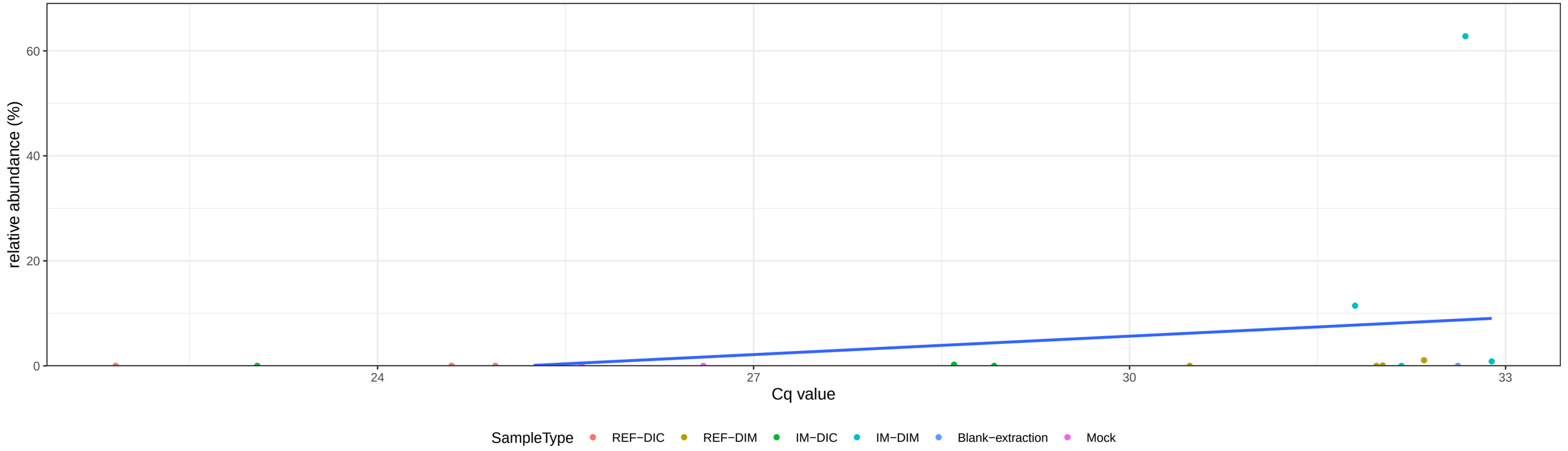


Correlation within the sample type: IM−DIM

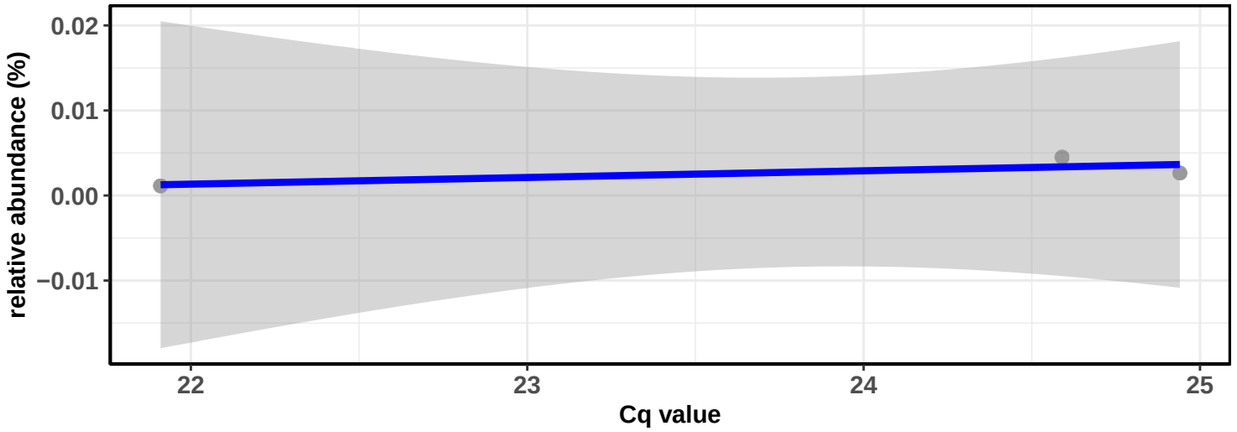


D_0__Bacteria; D_1__Tenericutes; D_2__Mollicutes; D_3__Mycoplasmatales; D_4__Mycoplasmataceae; D_5__Mycoplasma; D_6__uncultured Mycoplasma sp.

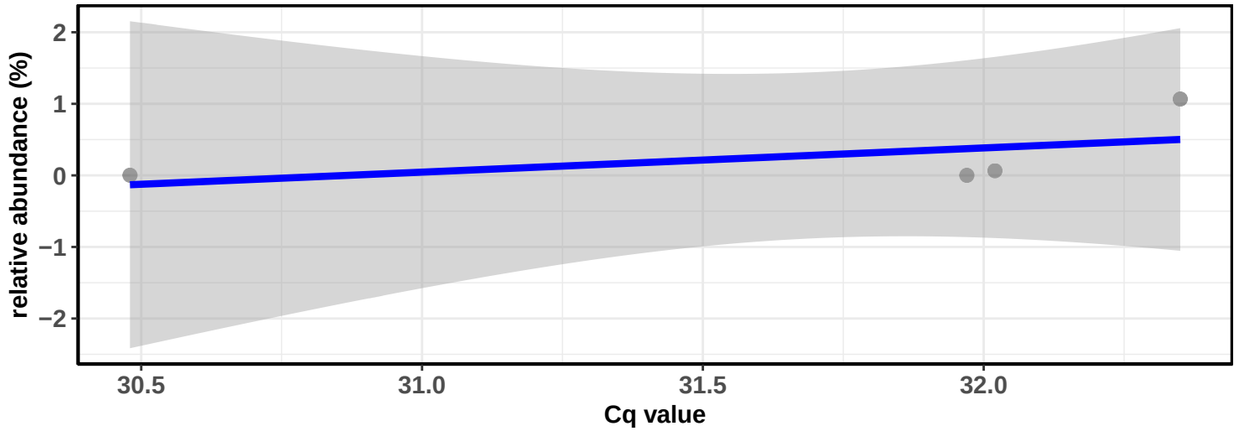
Correlation with all samples



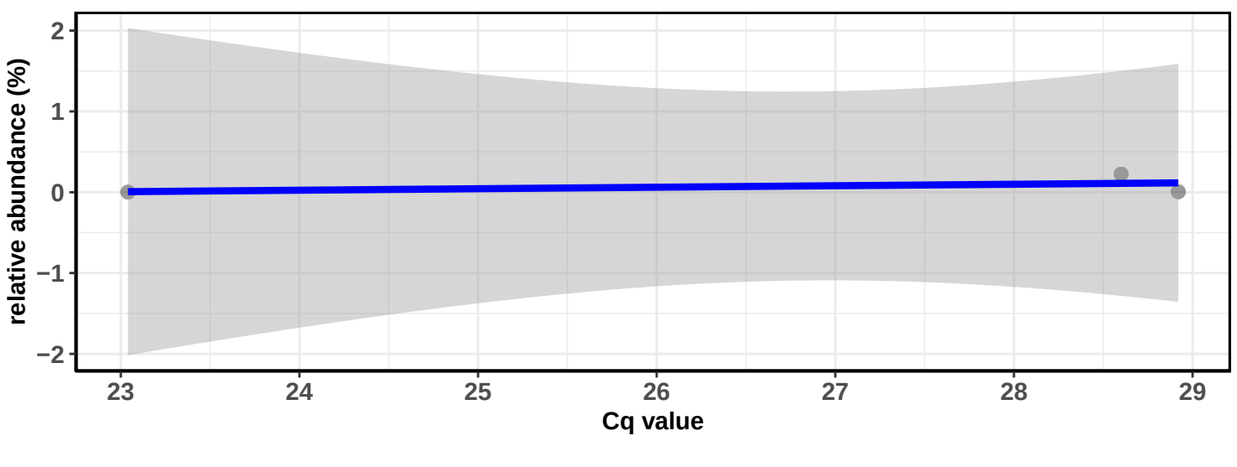
Correlation within the sample type: REF−DIC



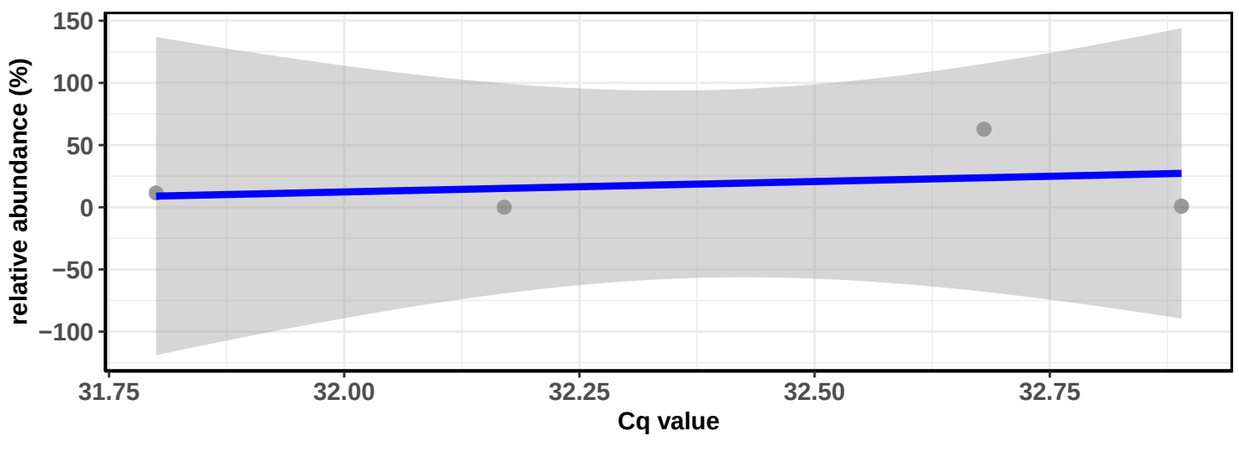
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

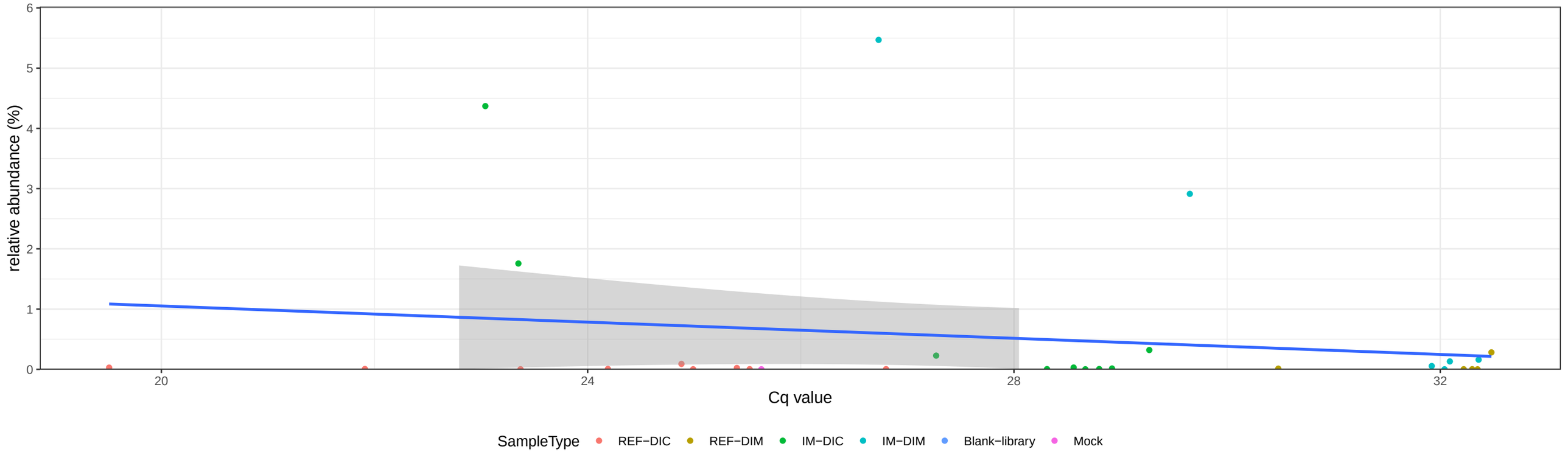


Correlation within the sample type: IM−DIM



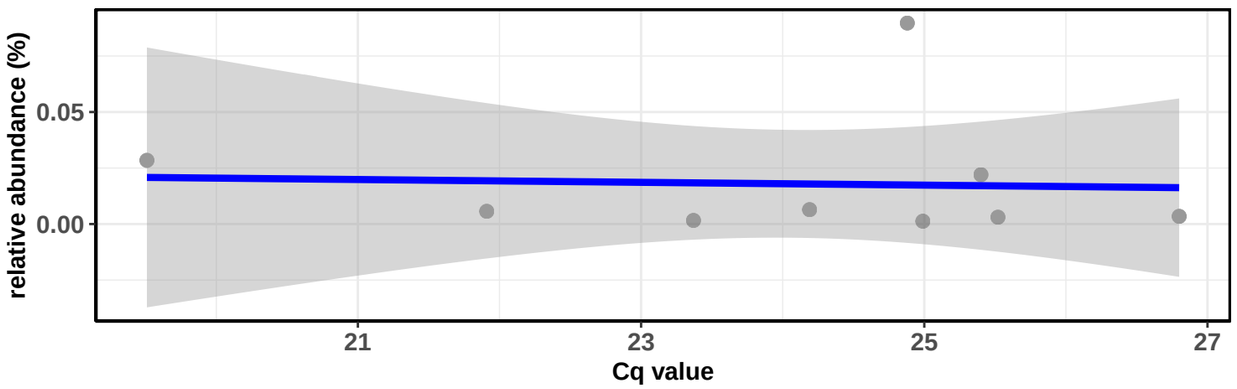
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Aliivibrio; D_6__uncultured bacterium

Correlation with all samples

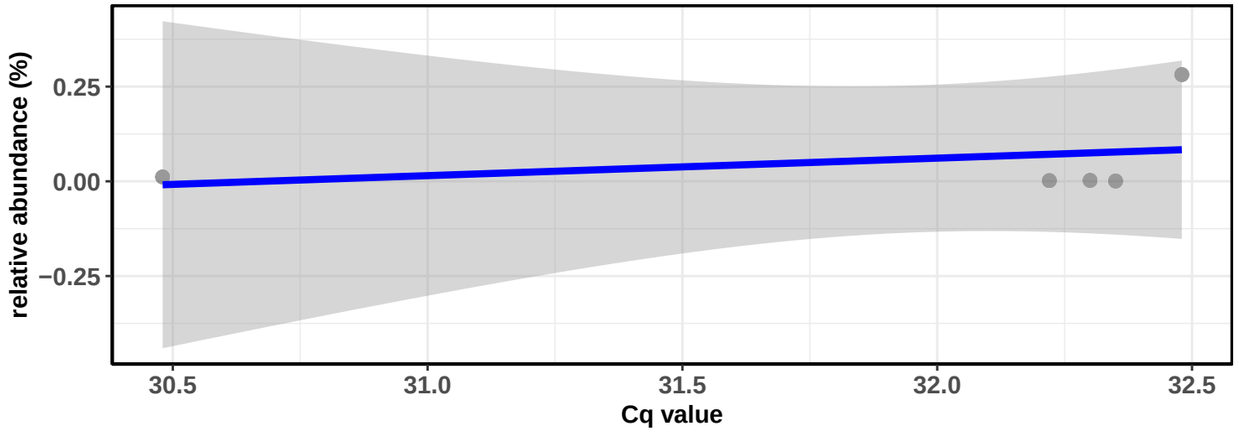


Correlation within the sample type: REF−DIC

$\log_e(S)$ = 5.037, p = 0.460, $\rho_{Spearman}$ = −0.283, $CI_{95\%}$ [−0.797, 0.469], n = 9

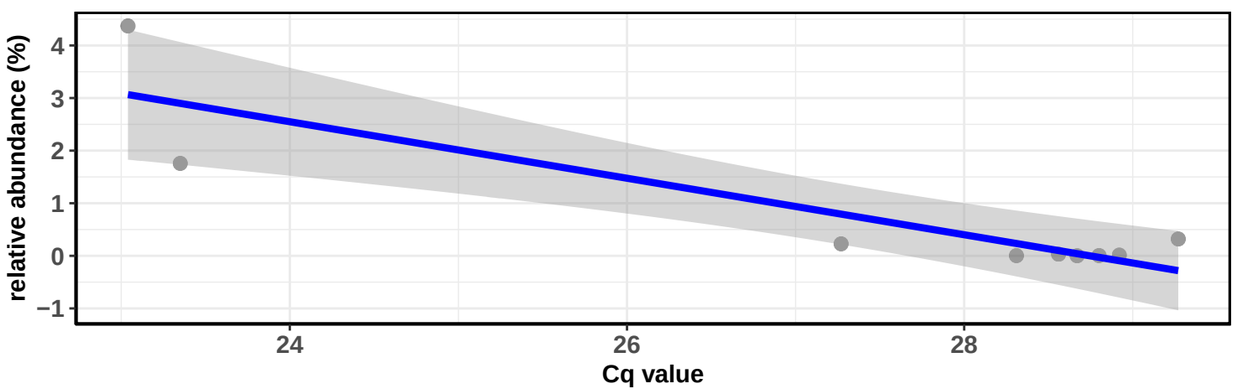


Correlation within the sample type: REF−DIM



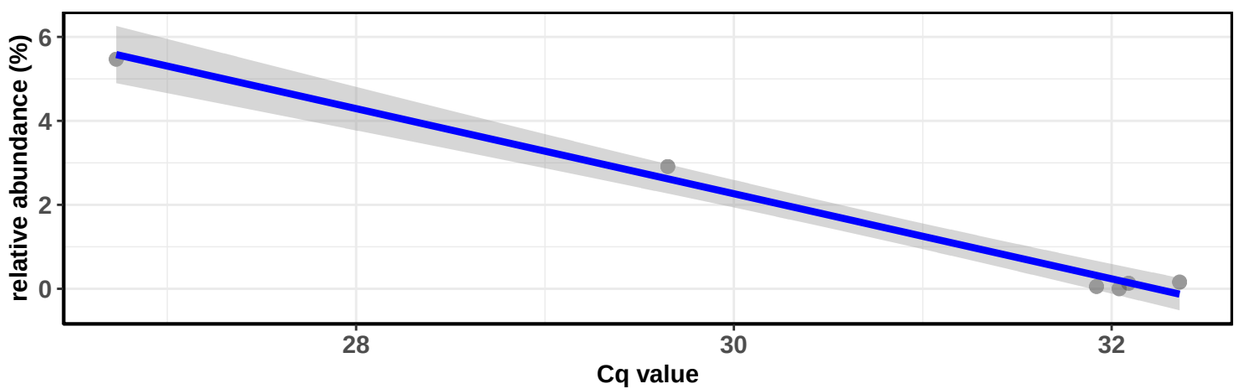
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 5.159, p = 0.224, $\rho_{Spearman}$ = −0.450, $CI_{95\%}$ [−0.858, 0.305], n = 9



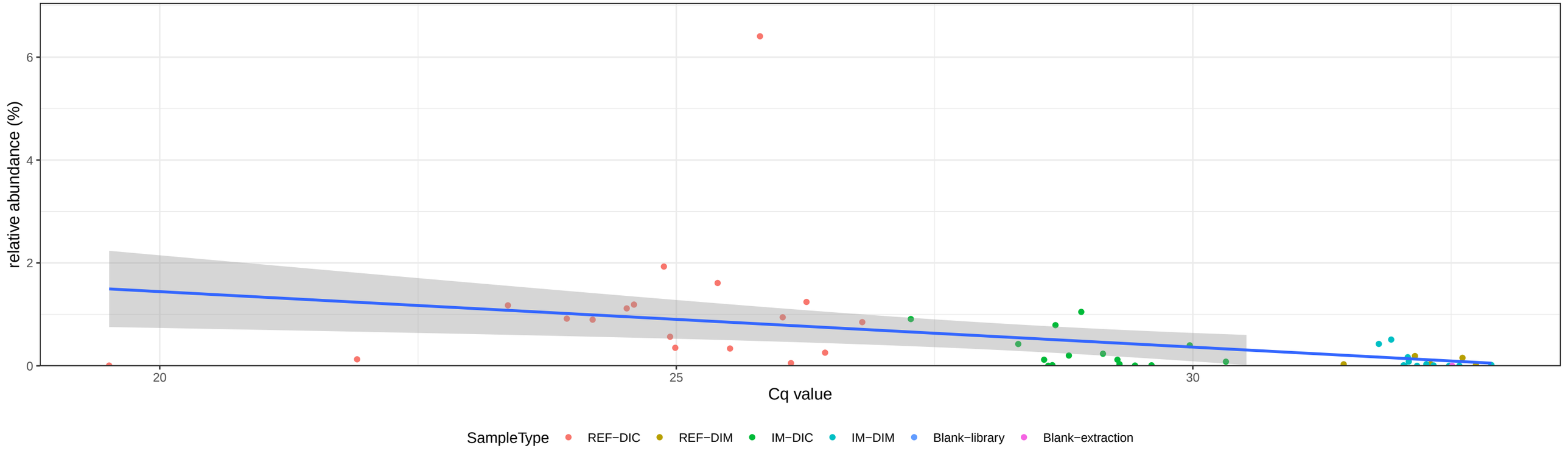
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 3.951, p = 0.329, $\rho_{Spearman}$ = −0.486, $CI_{95\%}$ [−0.930, 0.538], n = 6



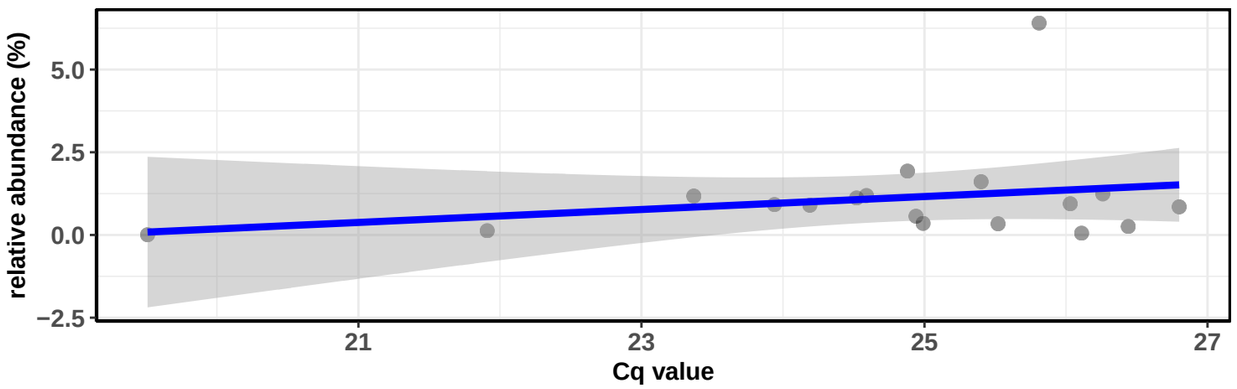
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Photobacterium

Correlation with all samples

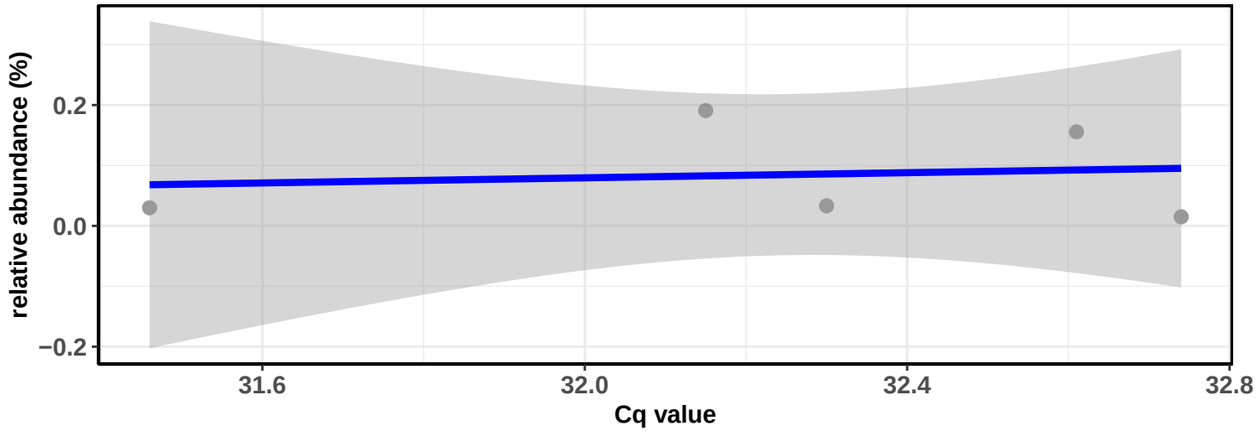


Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.787, p = 0.735, $\rho_{Spearman}$ = 0.086, $CI_{95\%}$ [−0.397, 0.531], n = 18

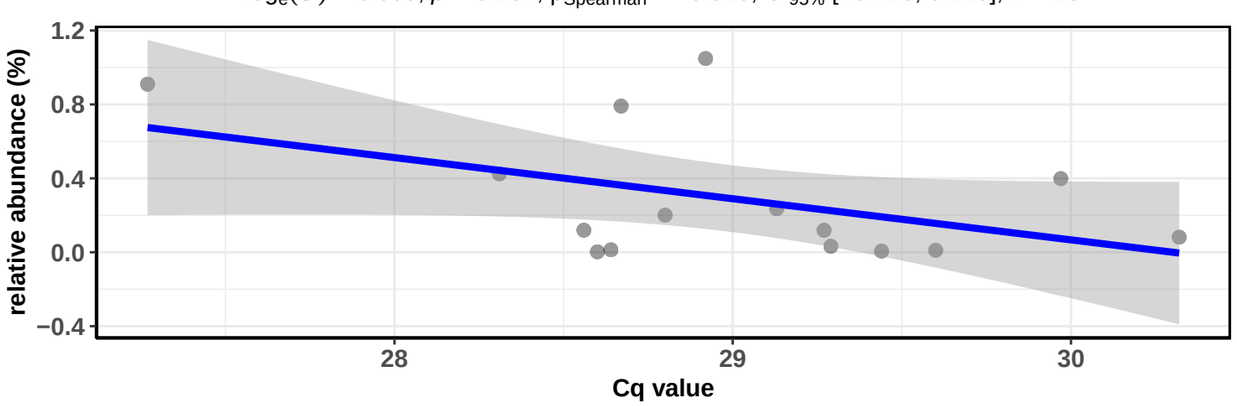


Correlation within the sample type: REF−DIM



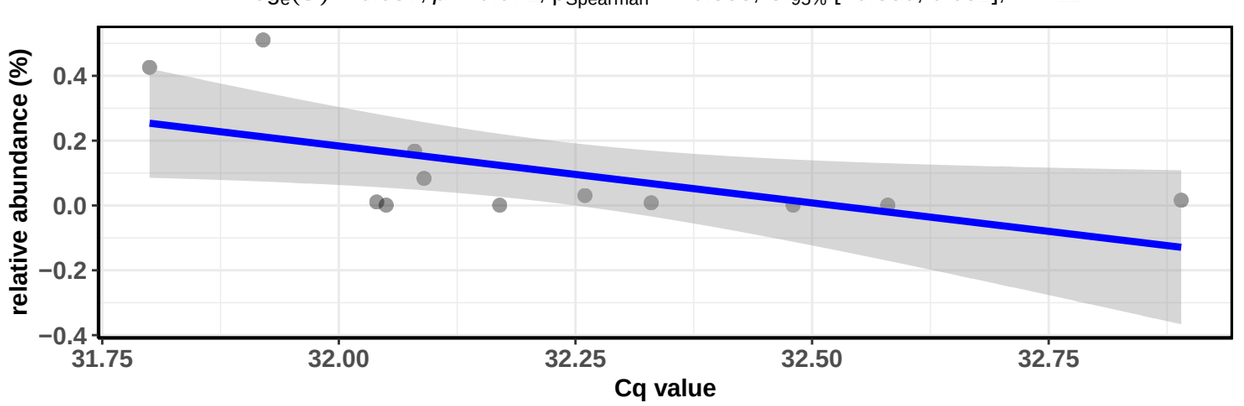
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.609, p = 0.237, $\rho_{Spearman}$ = −0.325, $CI_{95\%}$ [−0.718, 0.225], n = 15



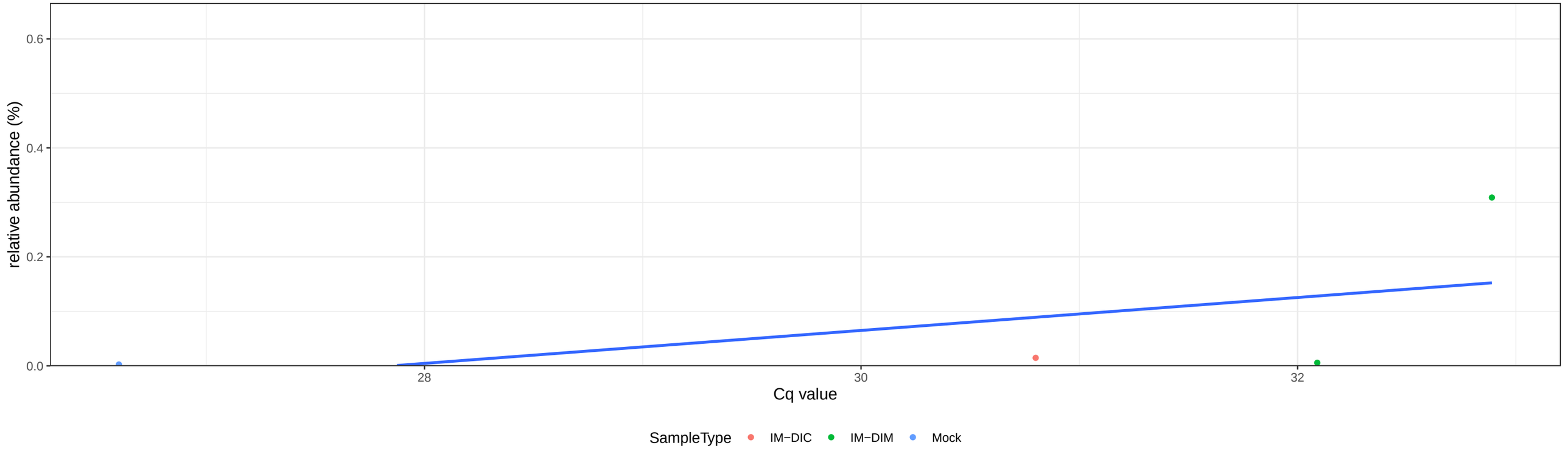
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.087, p = 0.071, $\rho_{Spearman}$ = −0.538, $CI_{95\%}$ [−0.850, 0.051], n = 12

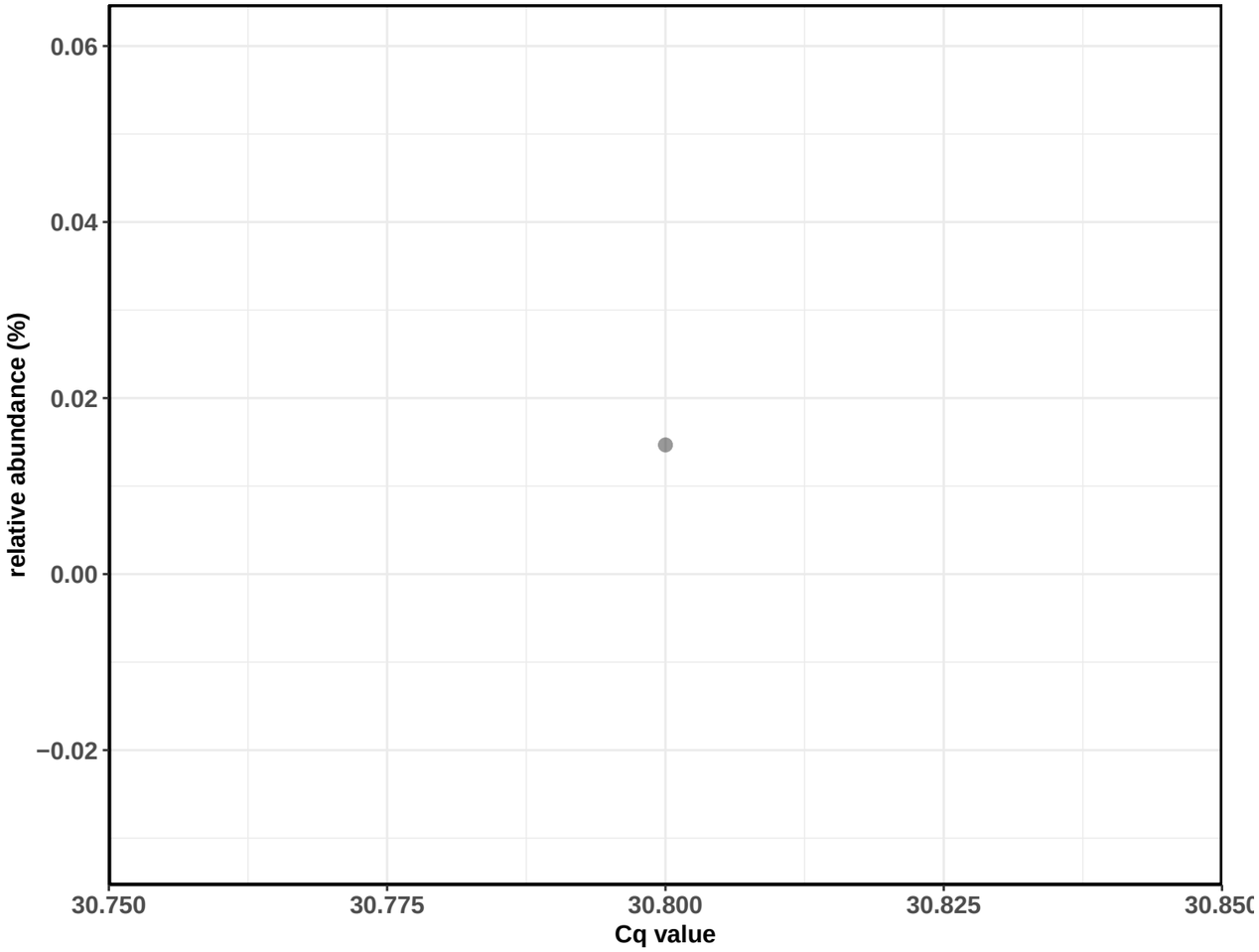


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Micrococcales; D_4__Micrococcaceae; D_5__Arthrobacter; Ambiguous_taxa

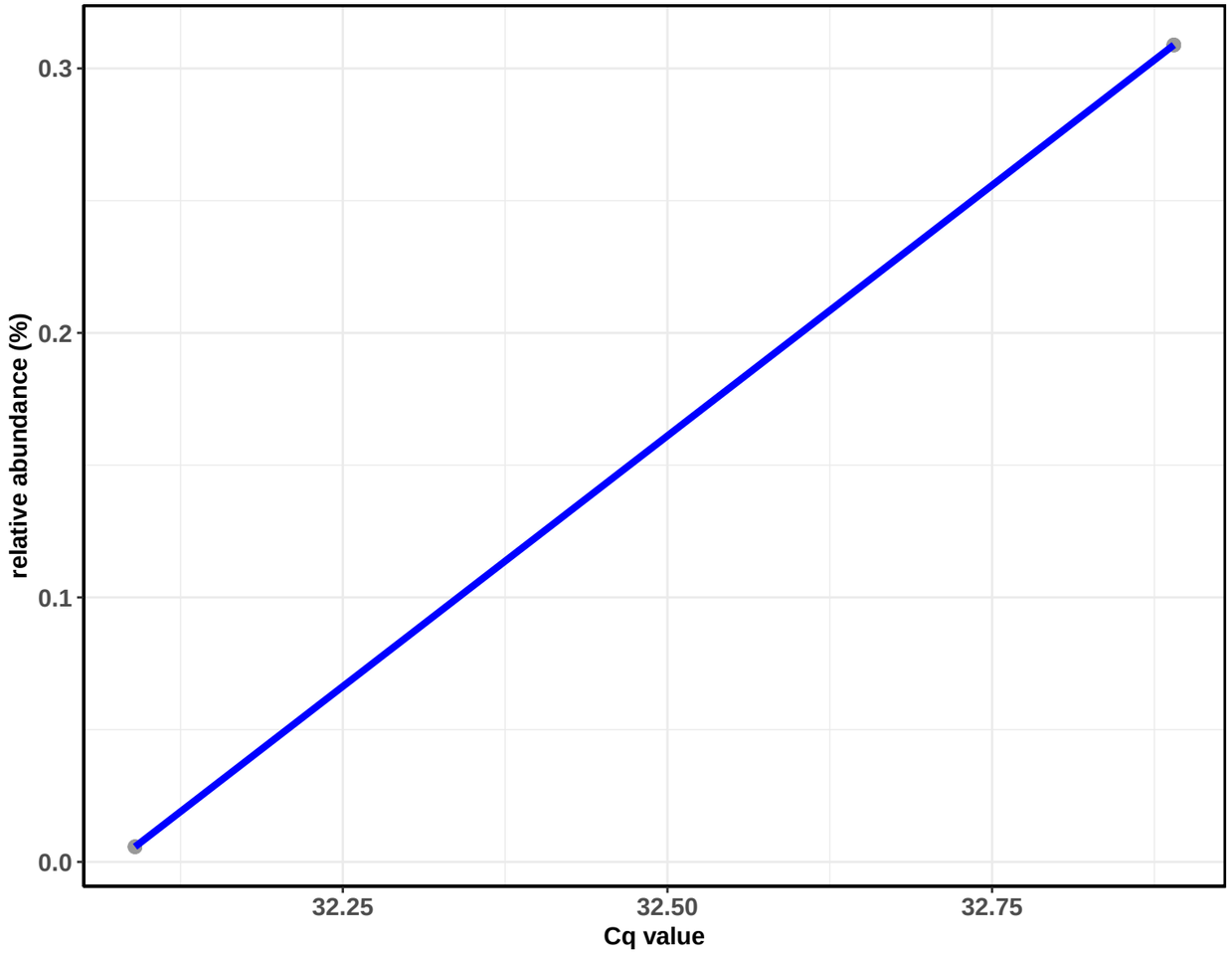
Correlation with all samples



Correlation within the sample type: IM−DIC

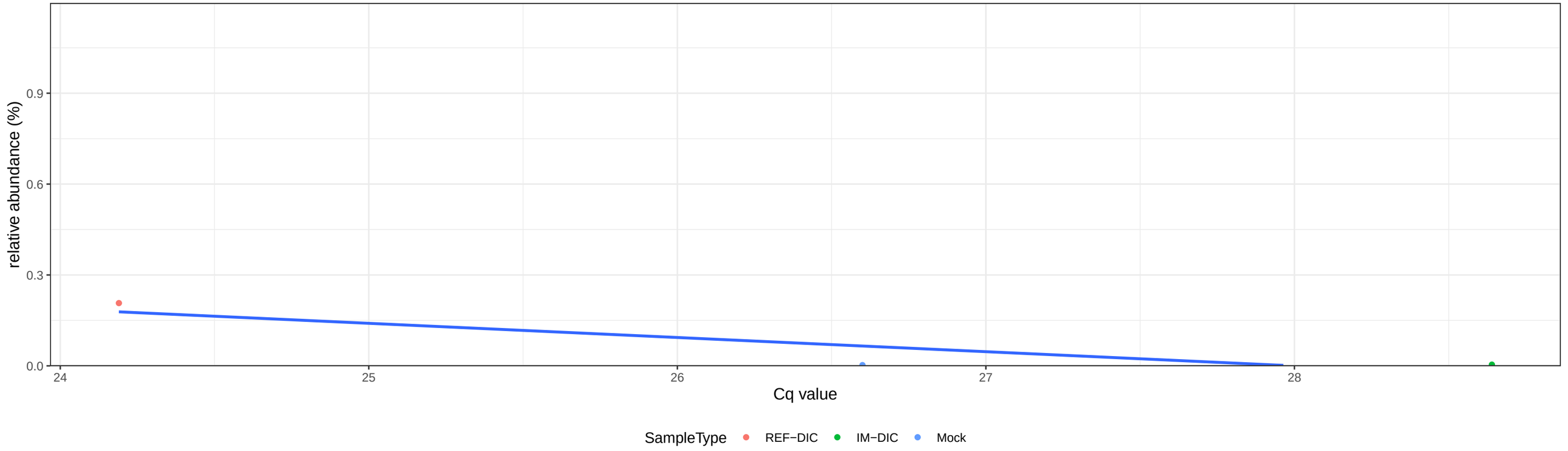


Correlation within the sample type: IM−DIM

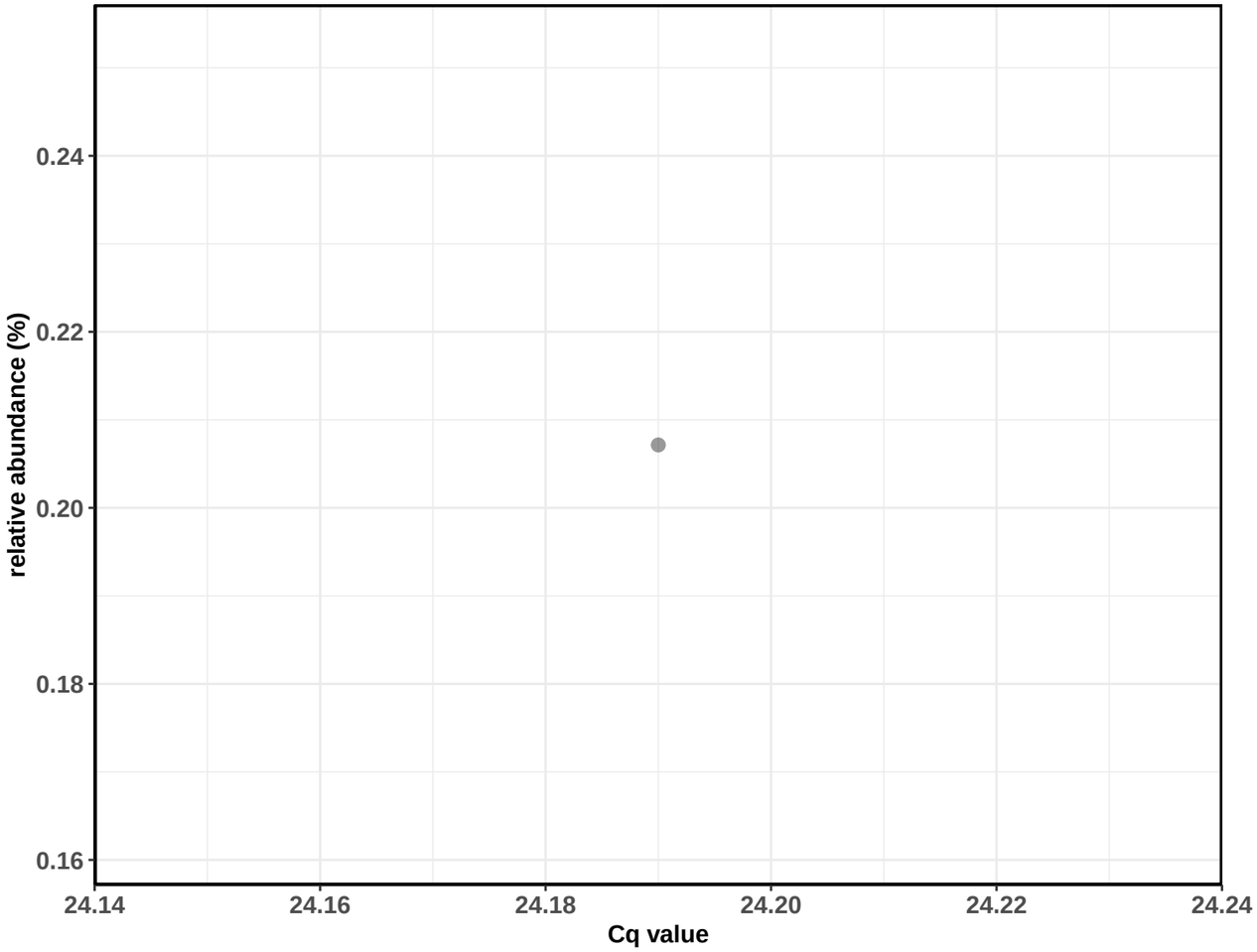


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

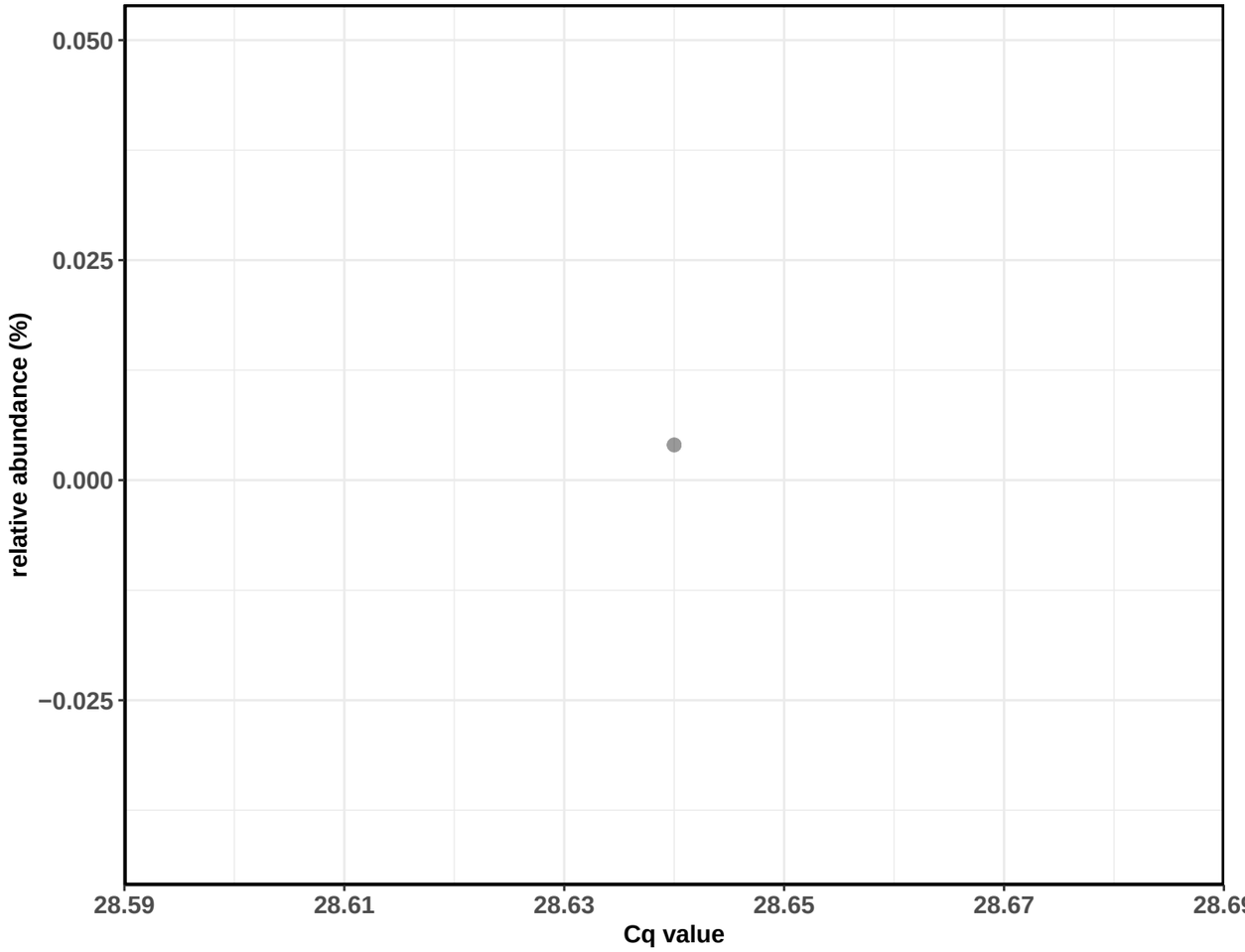
Correlation with all samples



Correlation within the sample type: REF−DIC

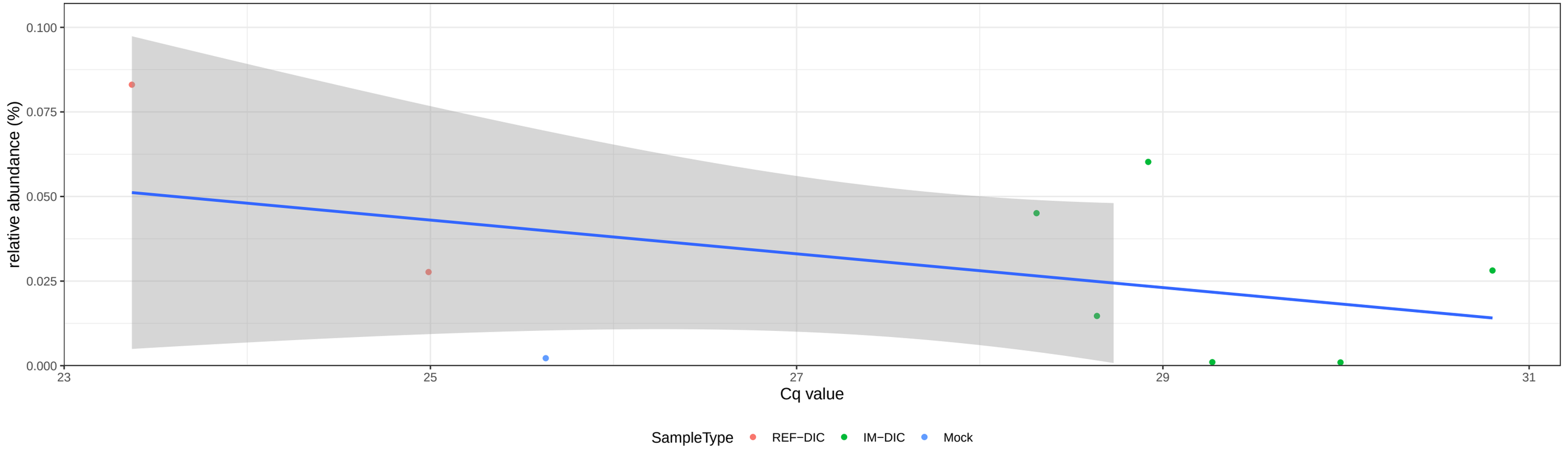


Correlation within the sample type: IM−DIC

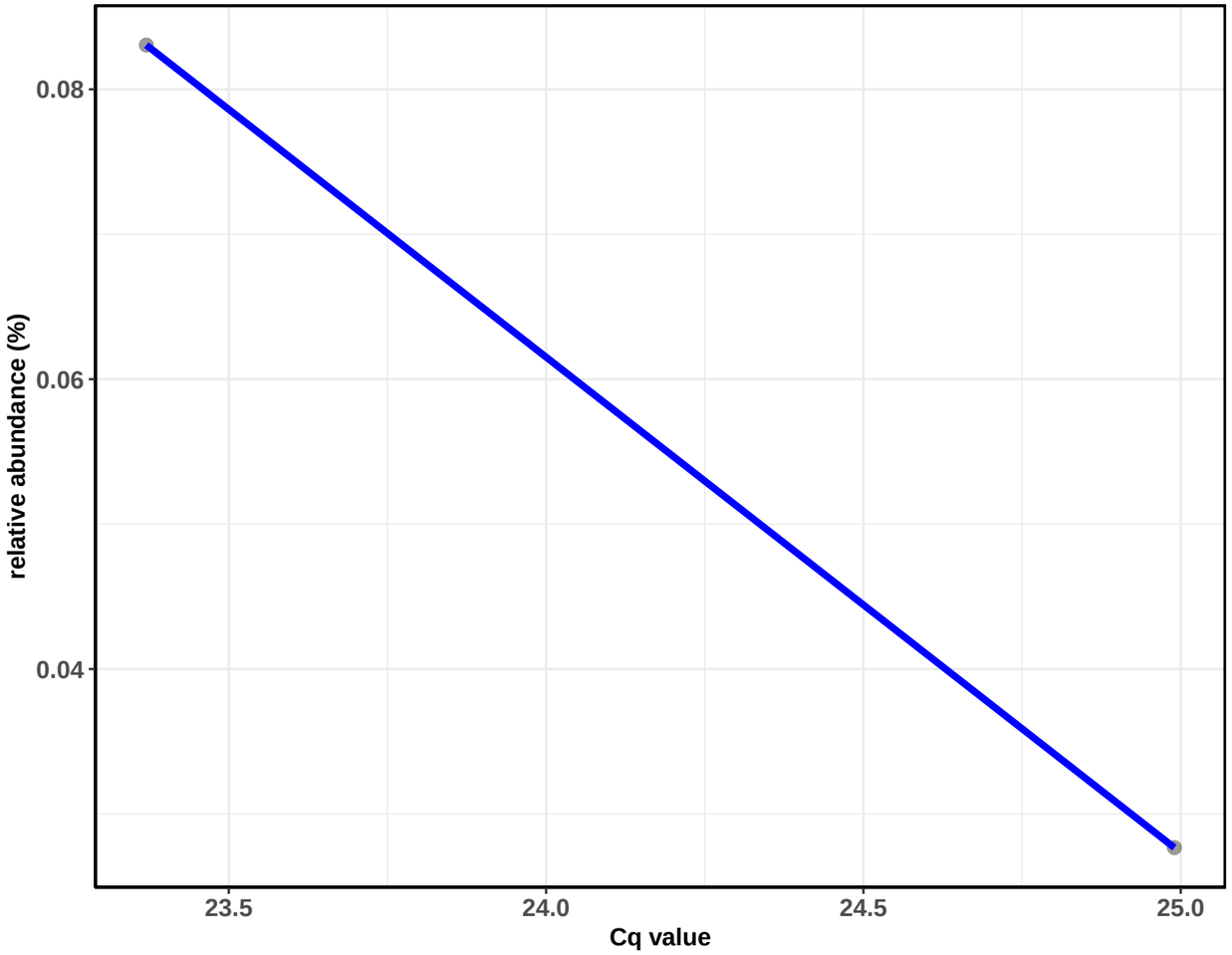


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples

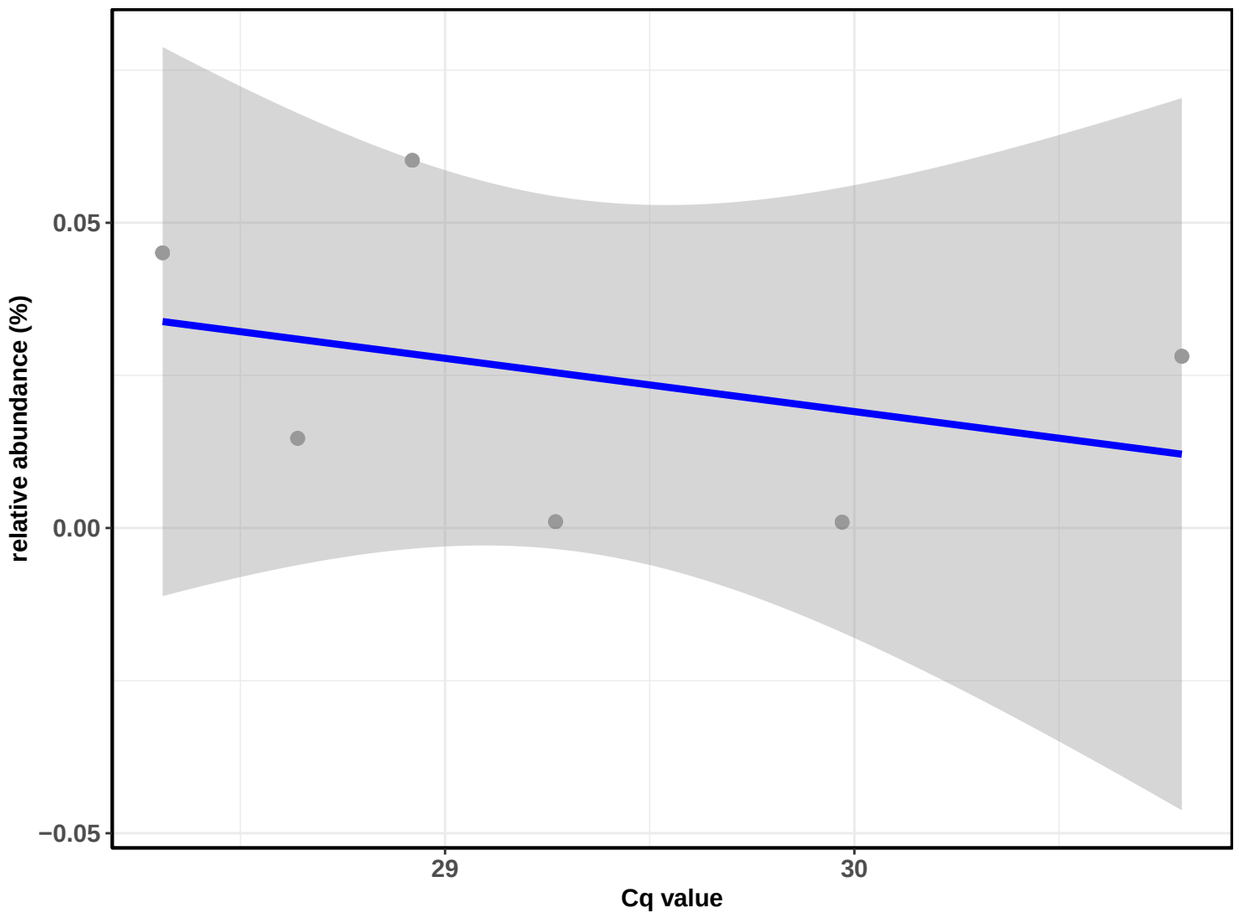


Correlation within the sample type: REF−DIC



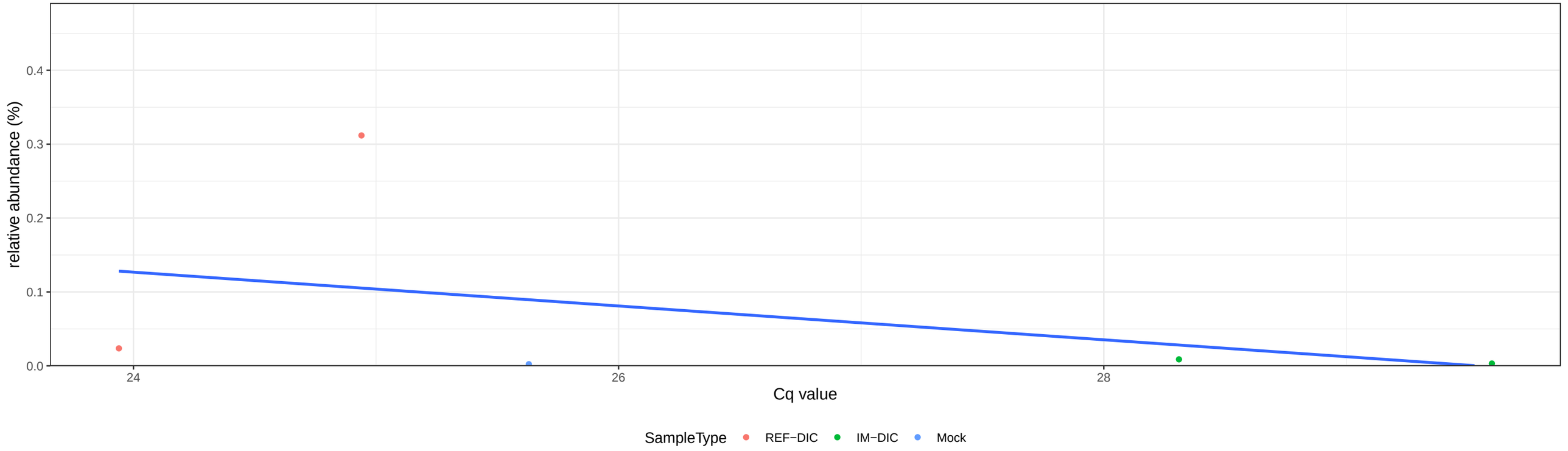
Correlation within the sample type: IM−DIC

$\log_e(S) = 3.912$, $p = 0.397$, $\rho_{Spearman} = -0.429$, $CI_{95\%}$ [−0.920, 0.587], $n = 6$

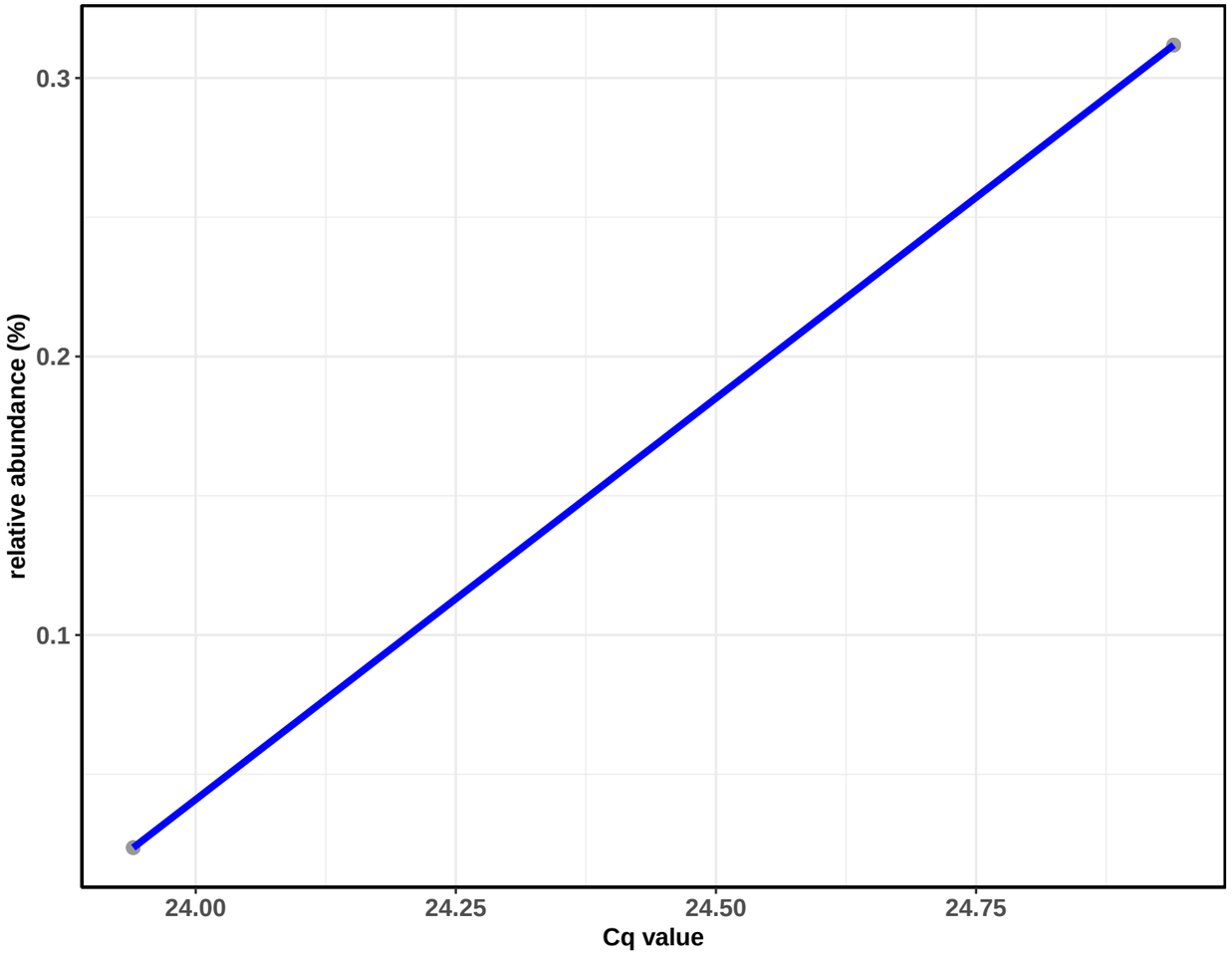


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

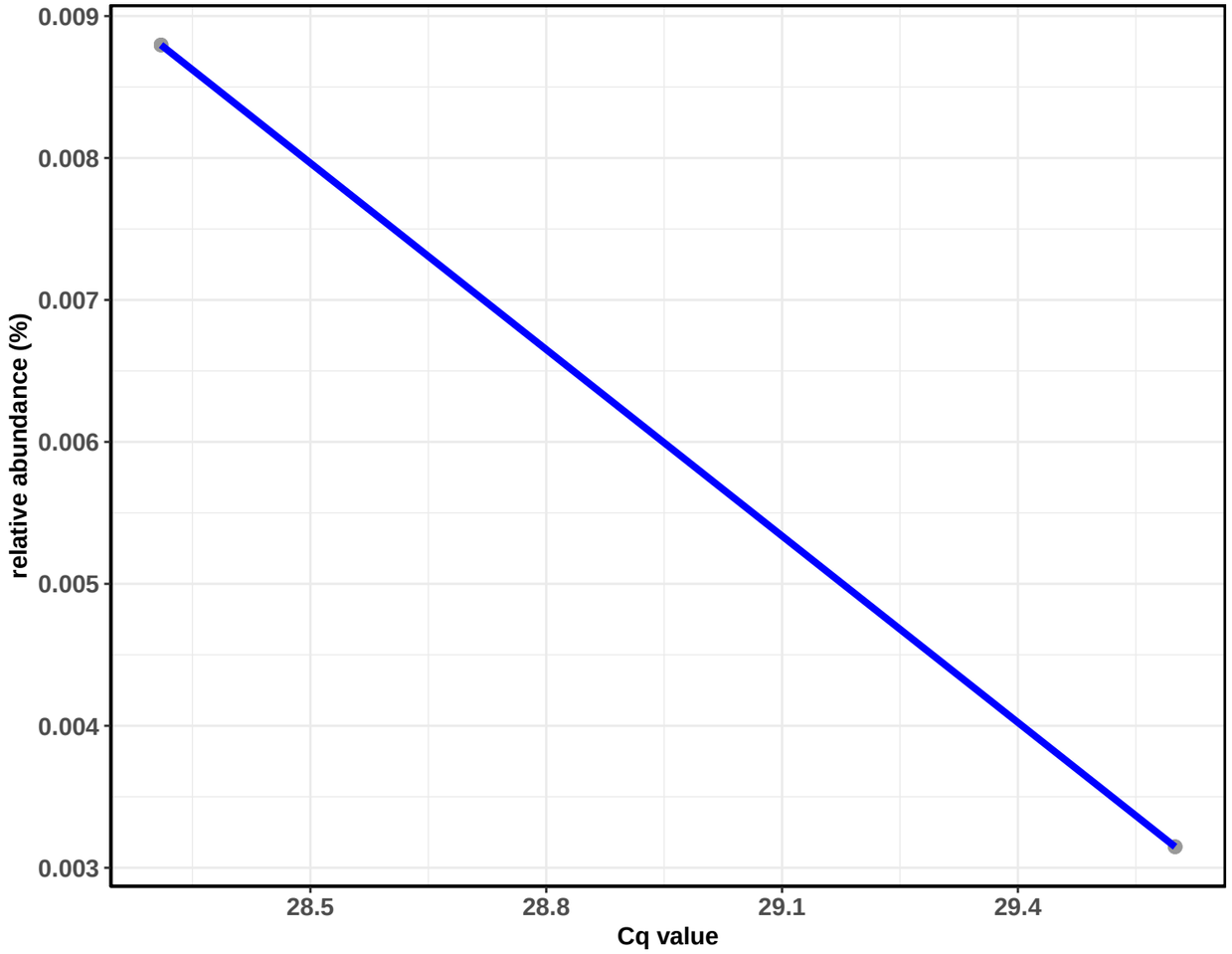
Correlation with all samples



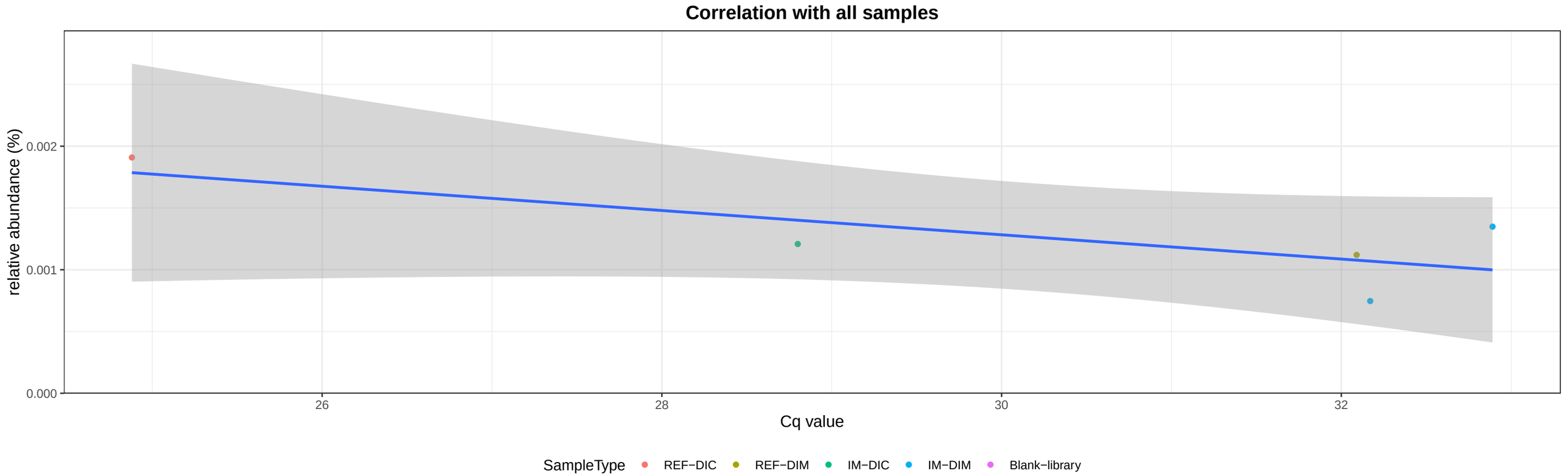
Correlation within the sample type: REF−DIC

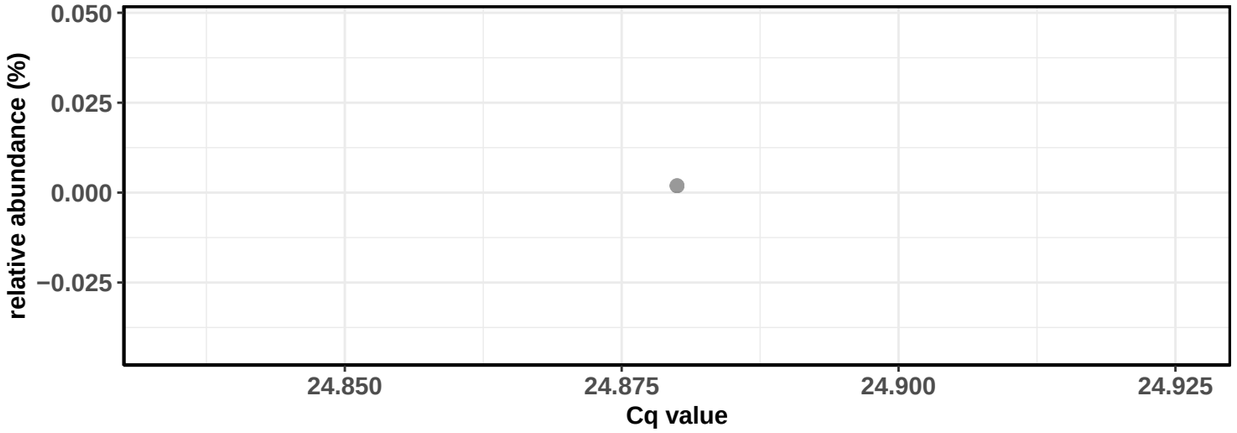


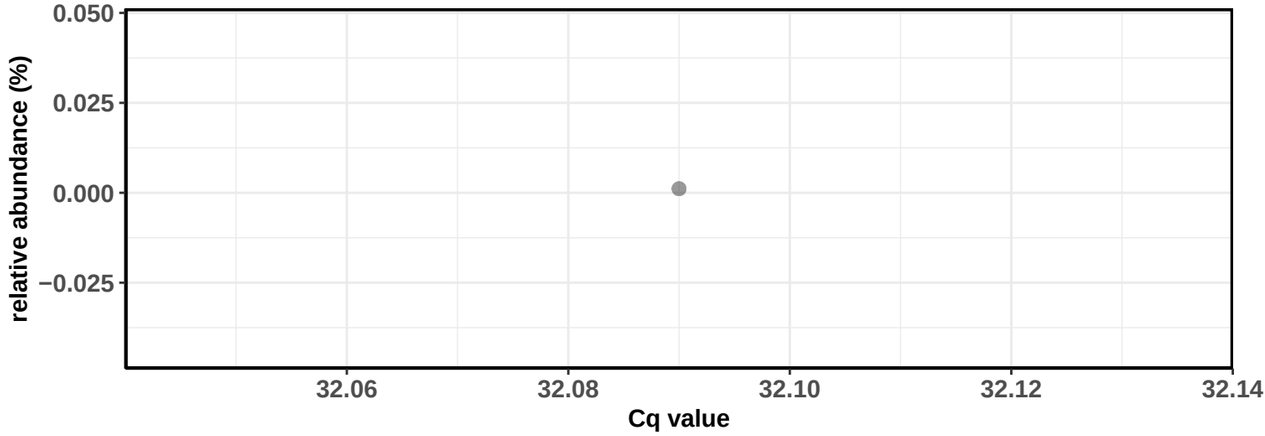
Correlation within the sample type: IM−DIC

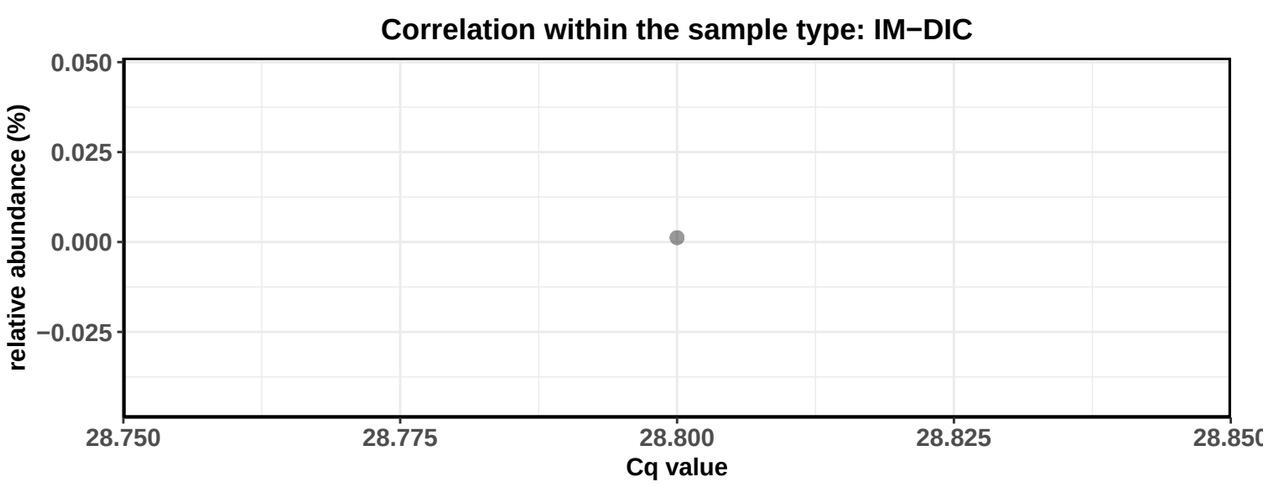


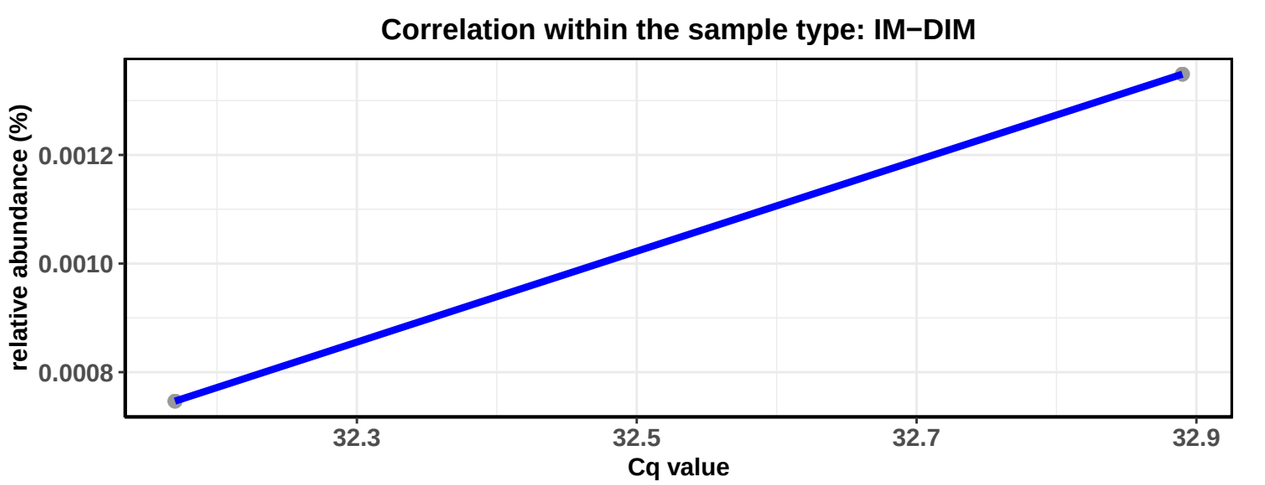
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Alteromonadales; D_4__Marinobacteraceae; D_5__Marinobacter; D_6__Marinobacter adhaerens





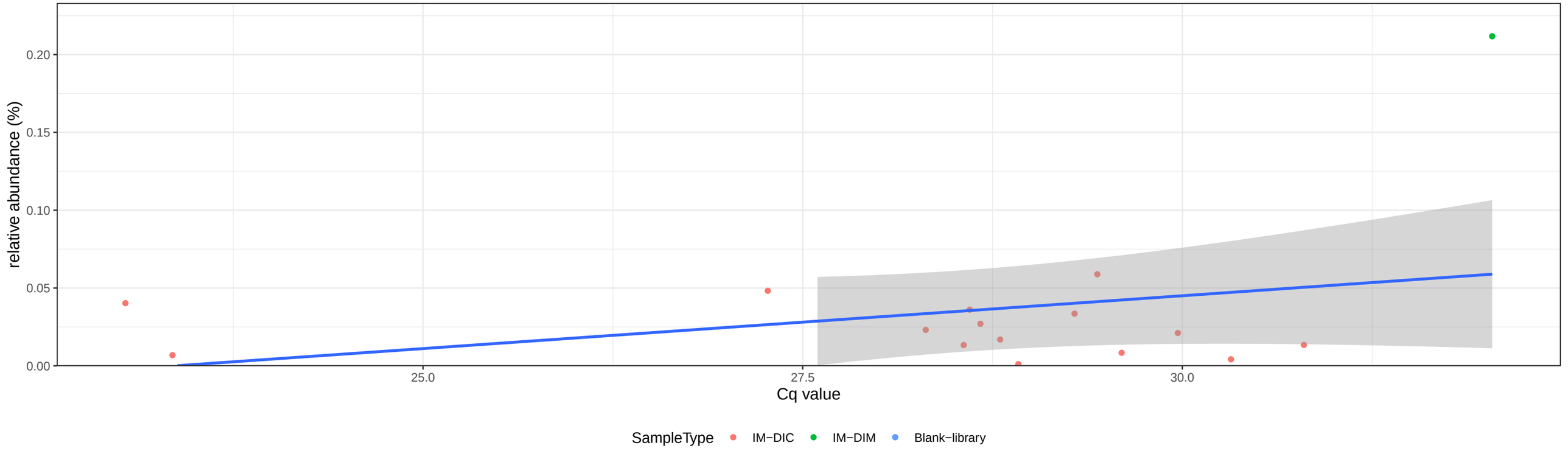






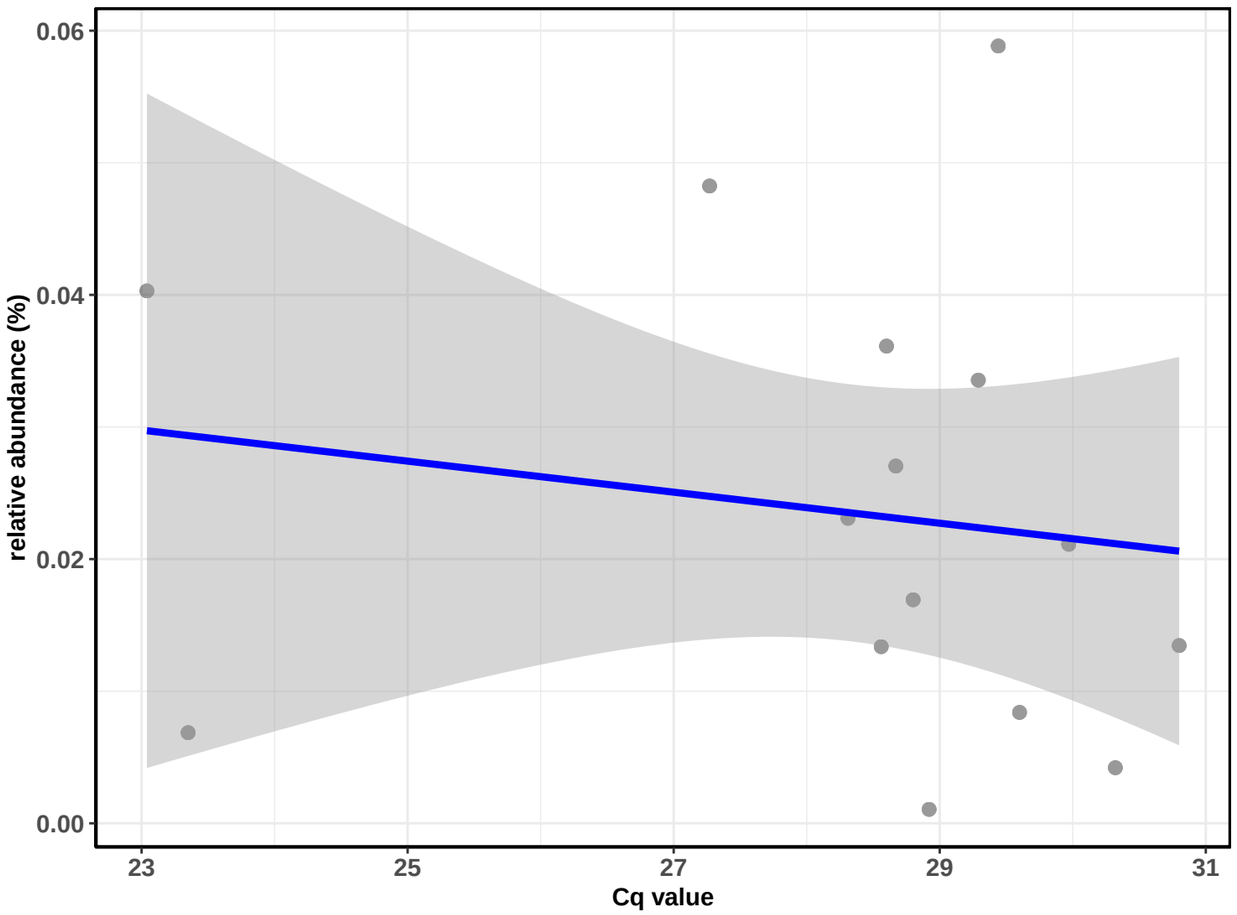
D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Actinomycetales; D_4__Actinomycetaceae; D_5__Actinomyces; D_6__uncultured Actinomycetales bacterium

Correlation with all samples

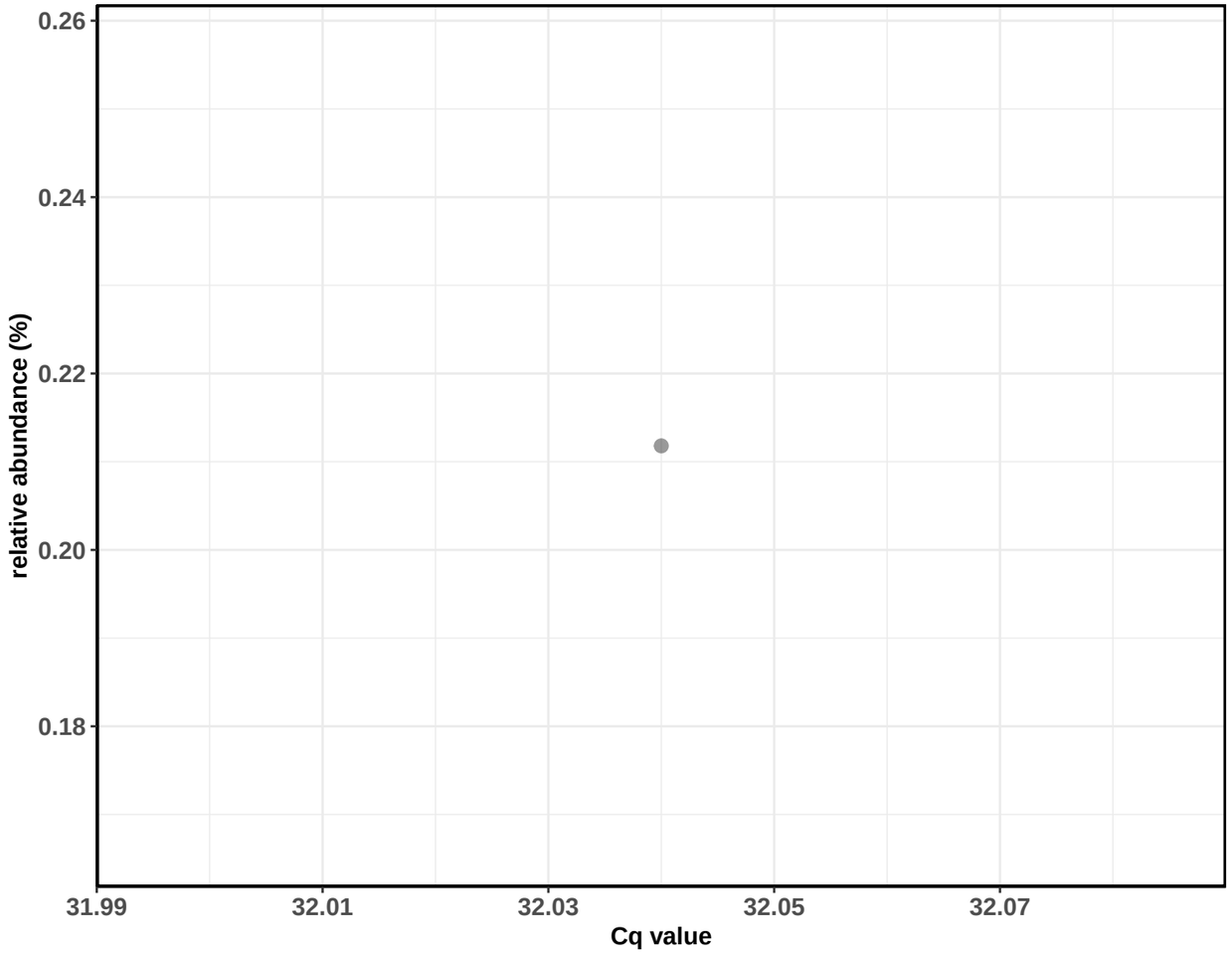


Correlation within the sample type: IM−DIC

$\log_e(S) = 6.596$, $p = 0.265$, $\rho_{Spearman} = -0.307$, $CI_{95\%}$ [−0.708, 0.243], $n = 15$

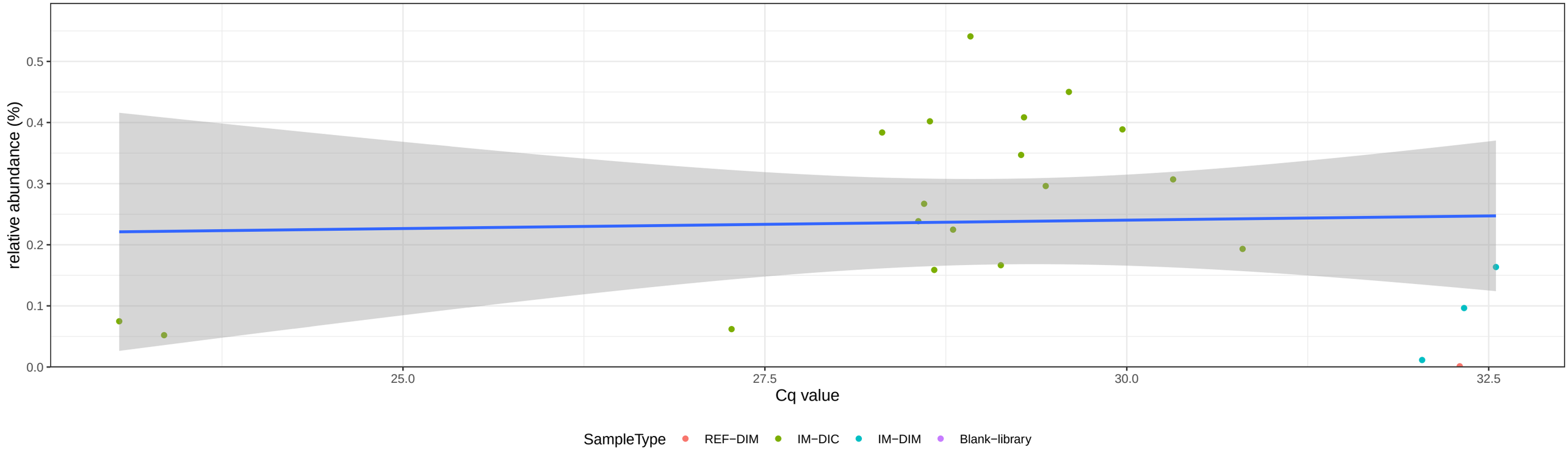


Correlation within the sample type: IM−DIM

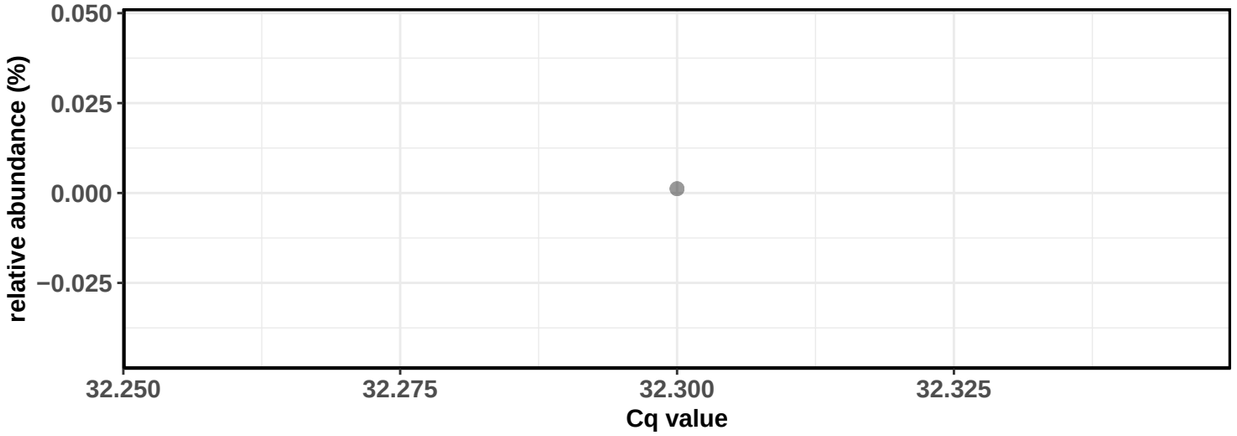


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Micrococcales; D_4__Brevibacteriaceae; D_5__Brevibacterium; D_6__Brevibacterium album

Correlation with all samples

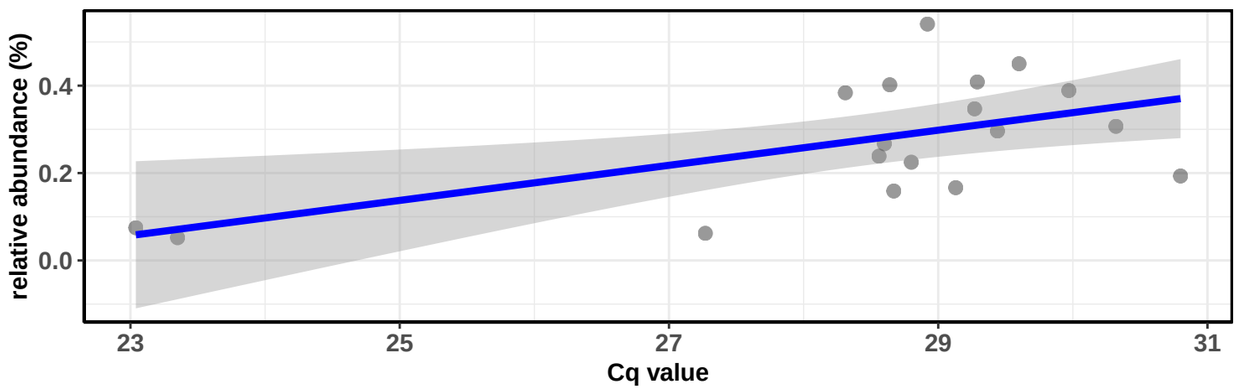


Correlation within the sample type: REF−DIM

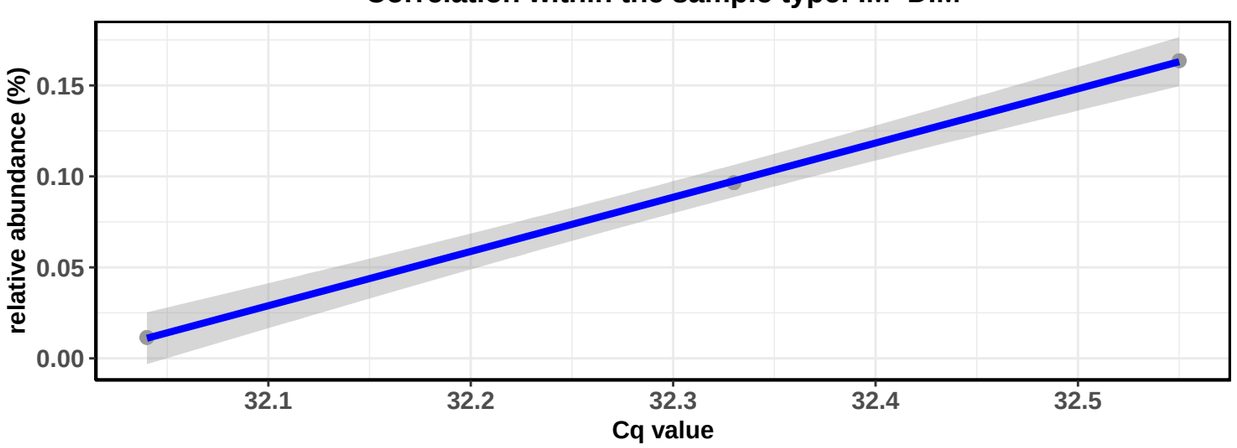


Correlation within the sample type: IM−DIC

$\log_e(S) = 6.219$, $p = 0.043$, $\rho_{Spearman} = 0.482$, $CI_{95\%}$ [0.019, 0.775], $n = 18$

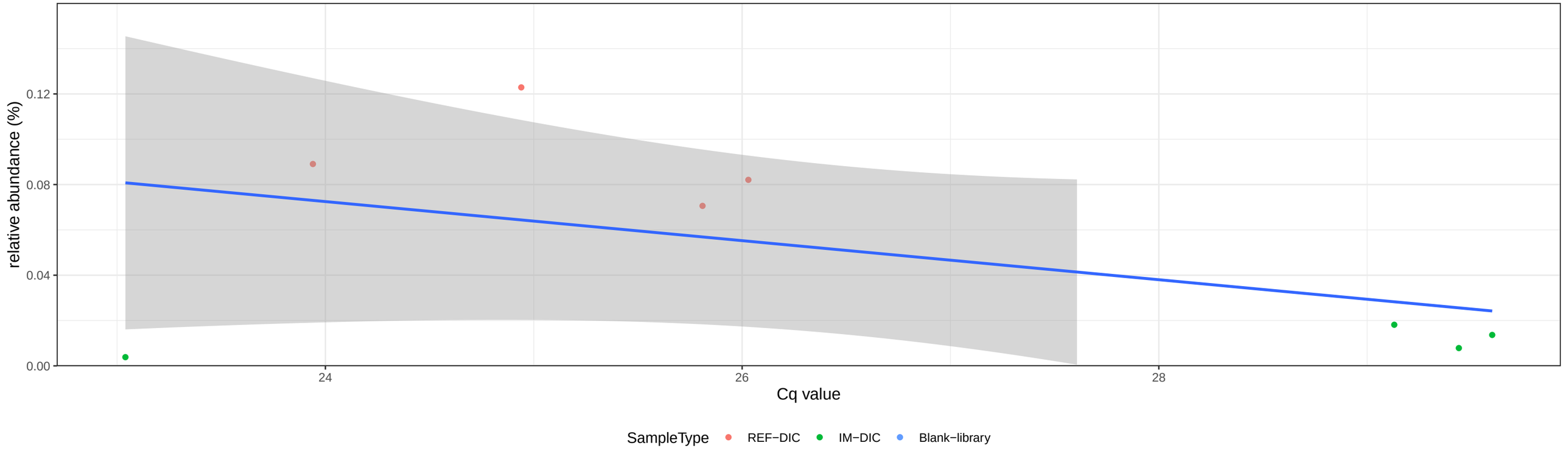


Correlation within the sample type: IM−DIM

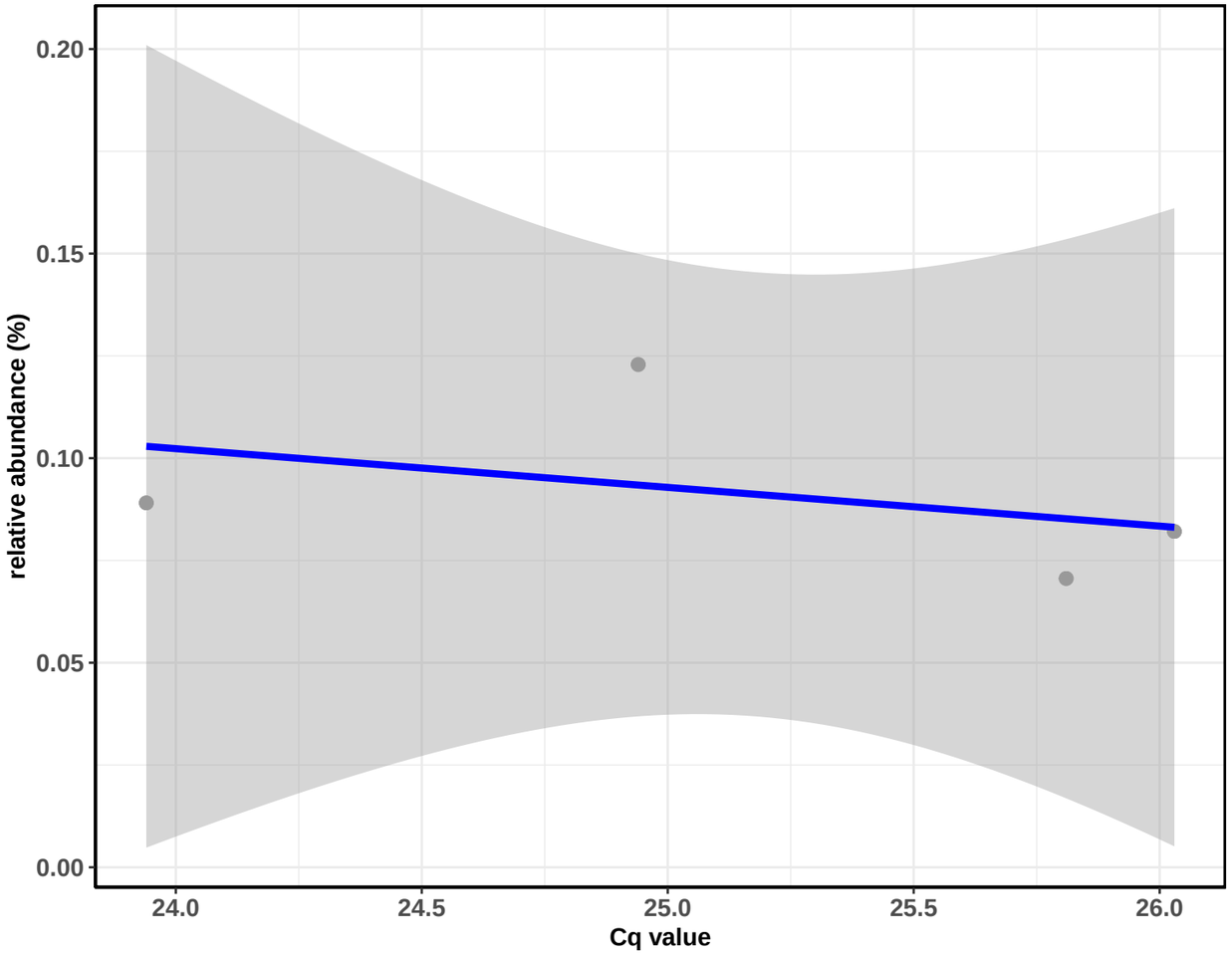


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Bacillus

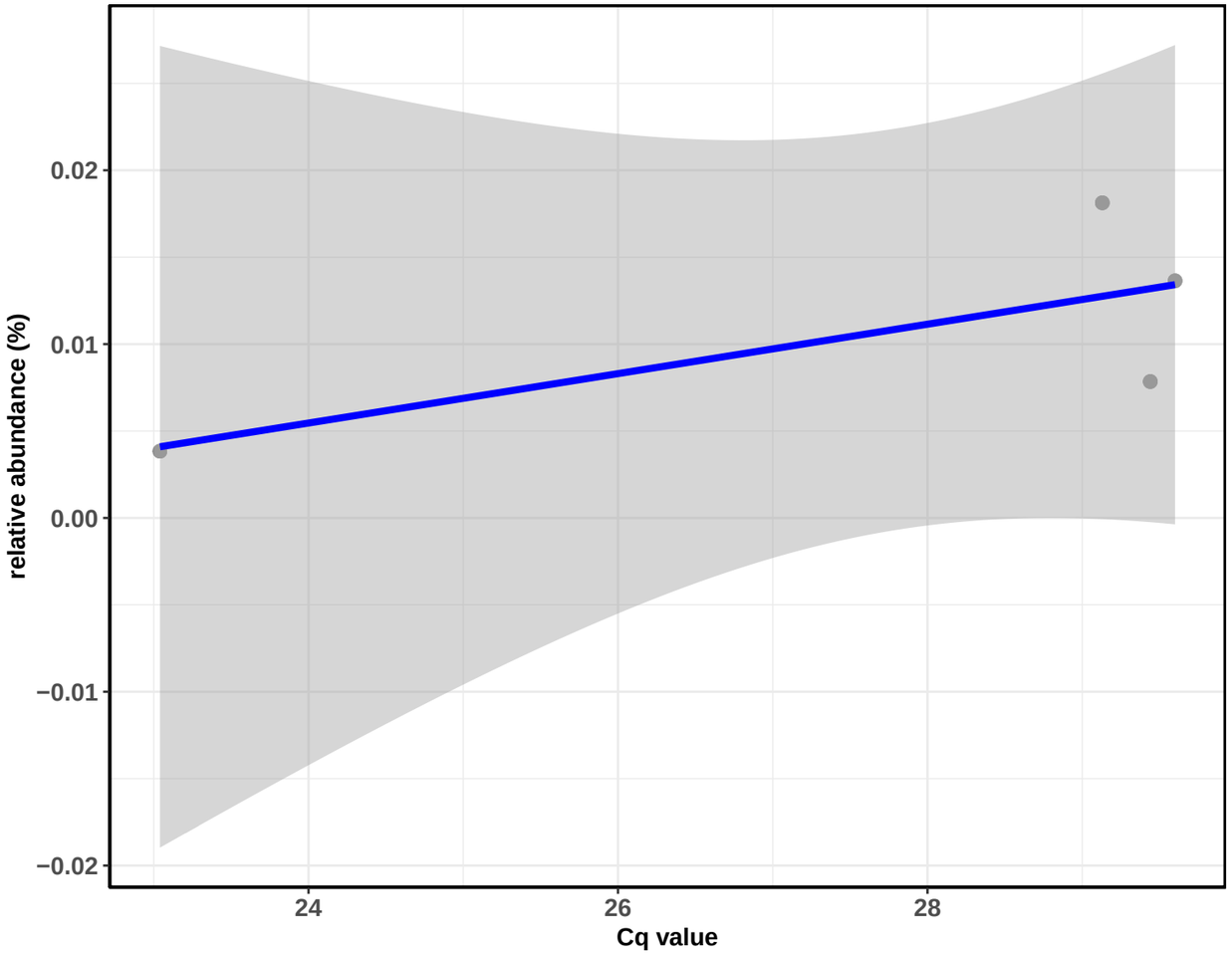
Correlation with all samples



Correlation within the sample type: REF−DIC

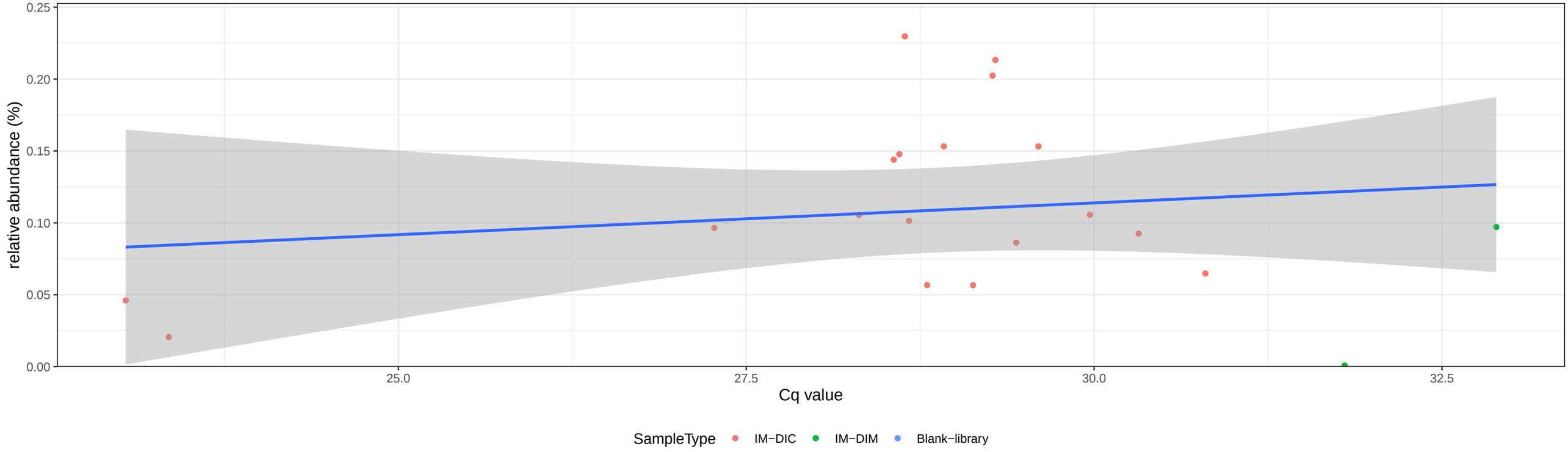


Correlation within the sample type: IM−DIC



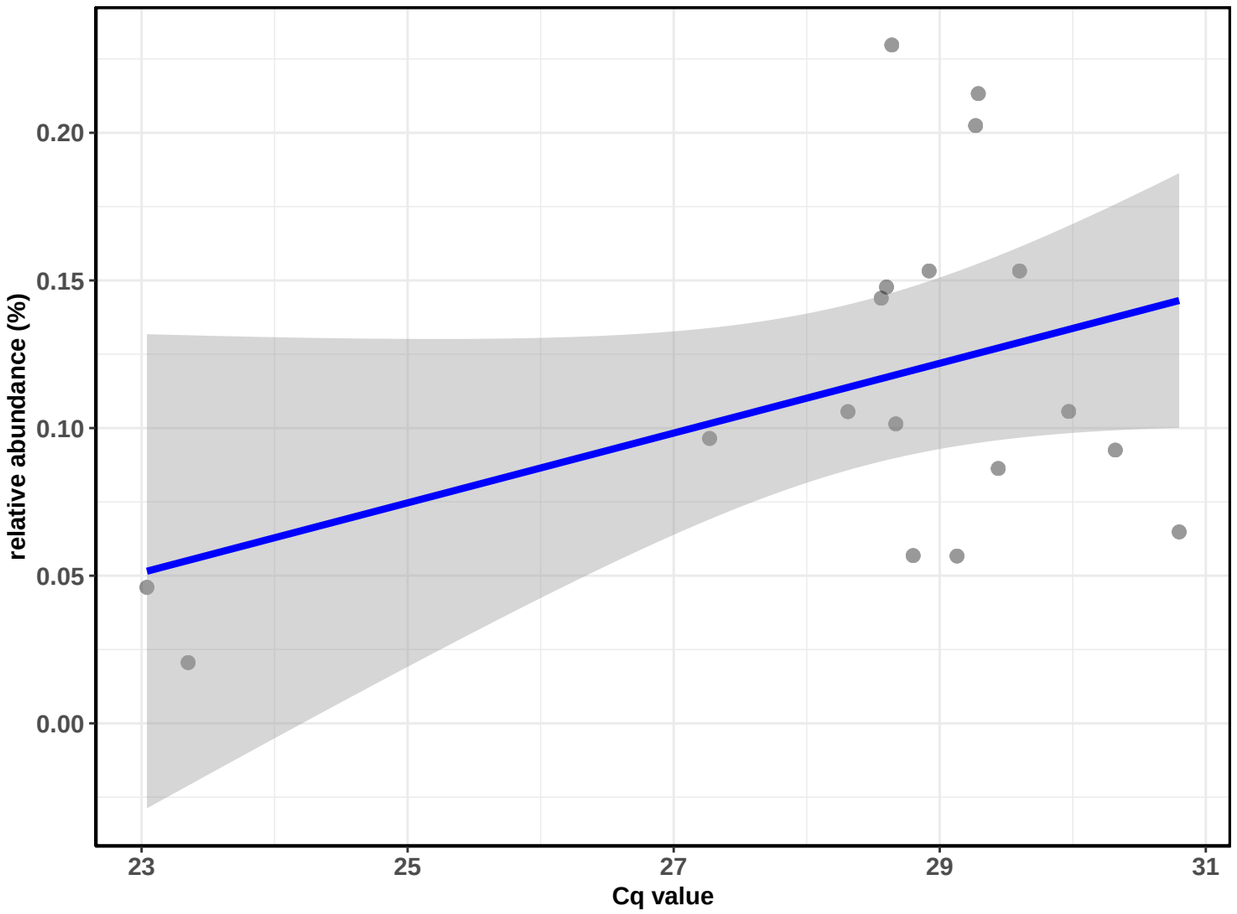
D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Micrococcales; D_4__Brevibacteriaceae; D_5__Brevibacterium

Correlation with all samples

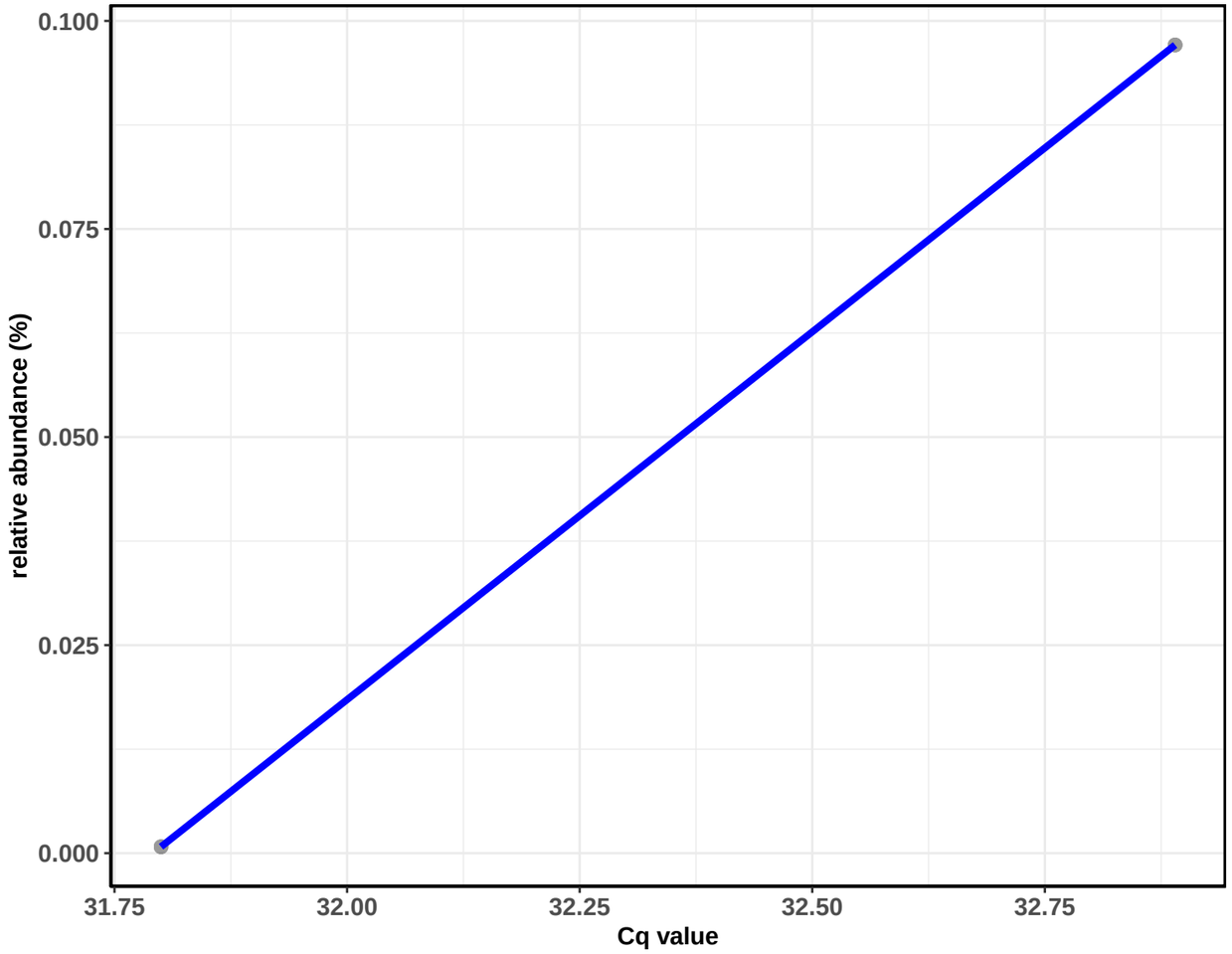


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.669, p = 0.458, $\rho_{Spearman}$ = 0.187, $CI_{95\%}$ [−0.307, 0.601], n = 18

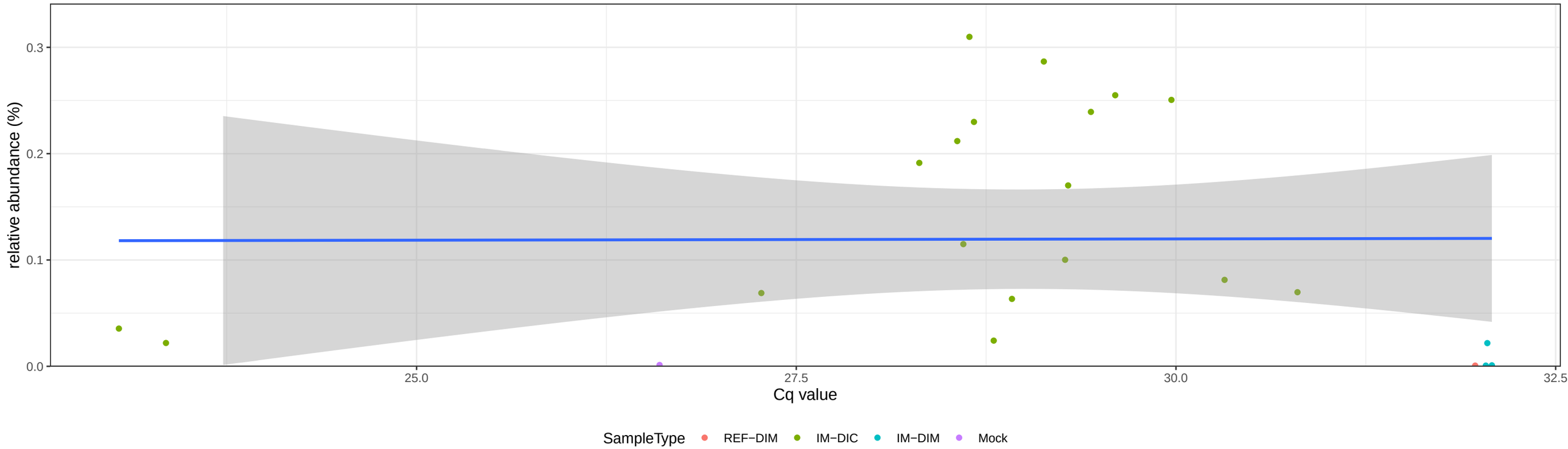


Correlation within the sample type: IM−DIM

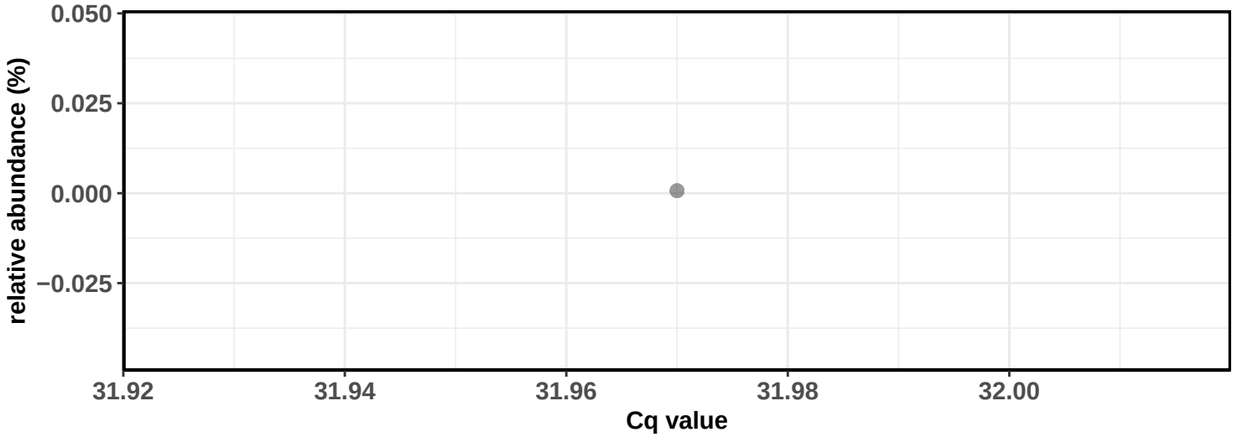


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Flavobacteriales; D_4__Flavobacteriaceae; D_5__Flavobacterium

Correlation with all samples

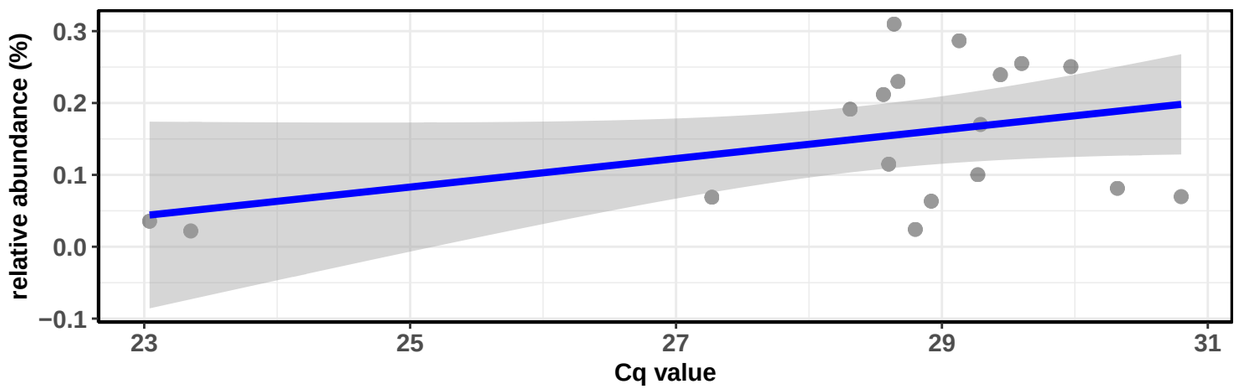


Correlation within the sample type: REF−DIM

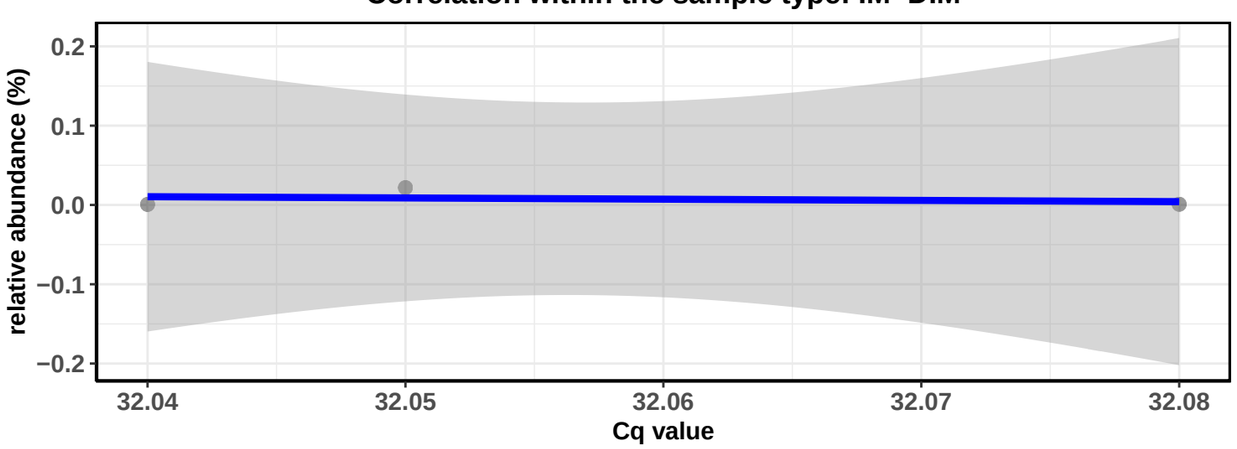


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.483, p = 0.188, $\rho_{Spearman}$ = 0.325, $CI_{95\%}$ [−0.167, 0.688], n = 18

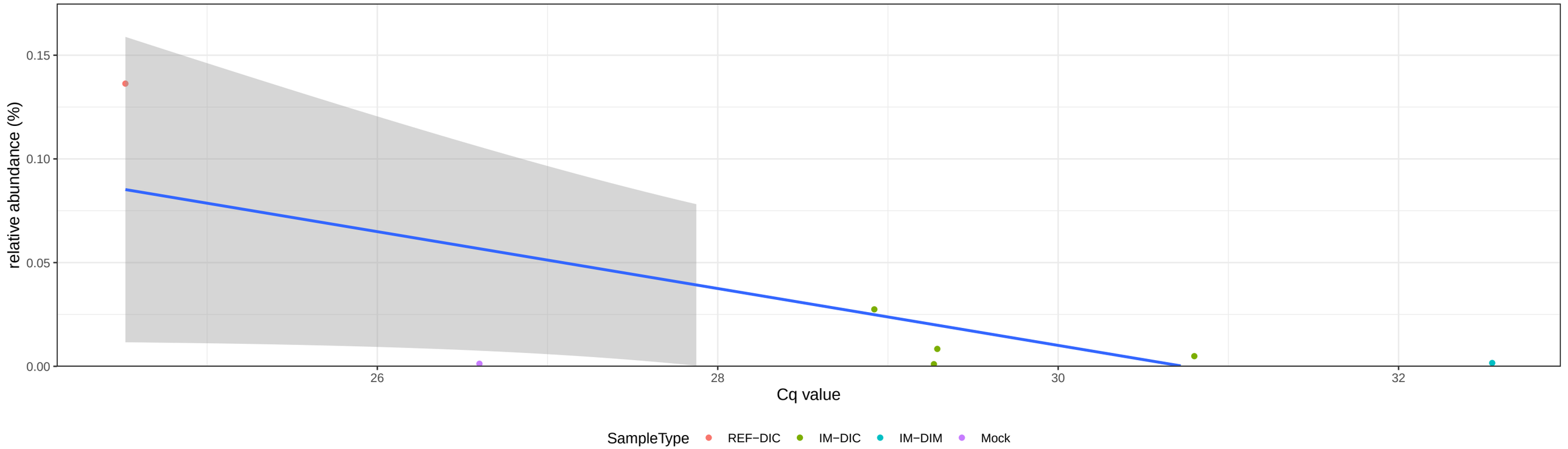


Correlation within the sample type: IM−DIM

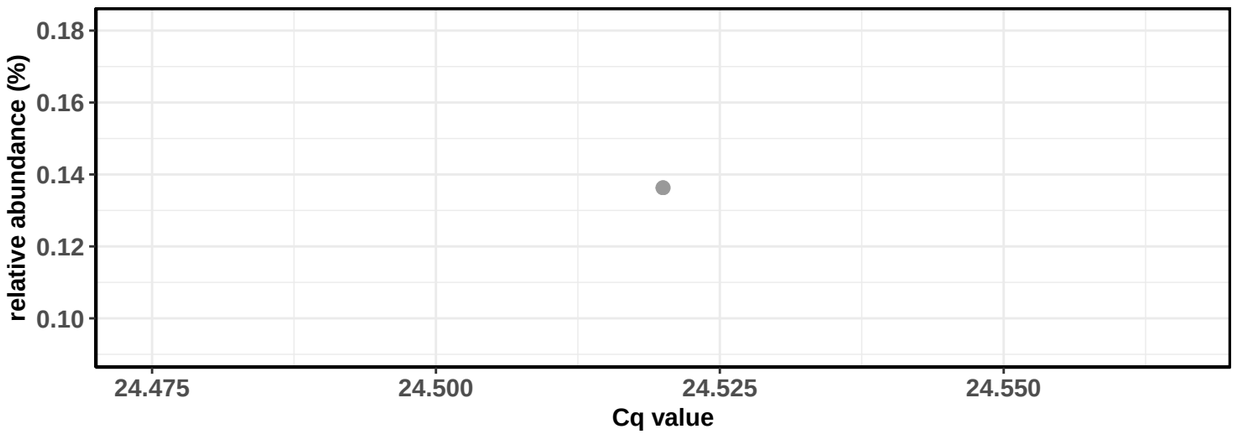


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

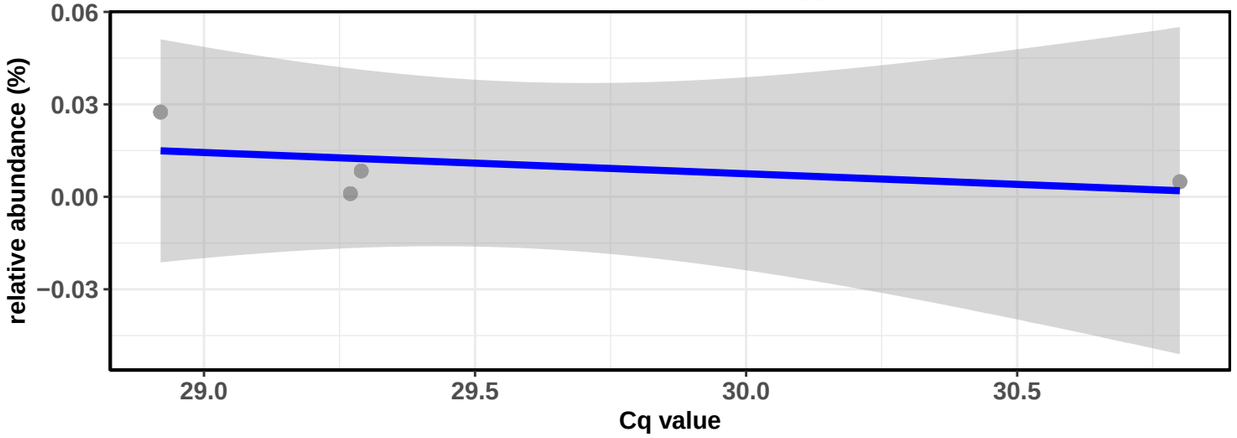
Correlation with all samples



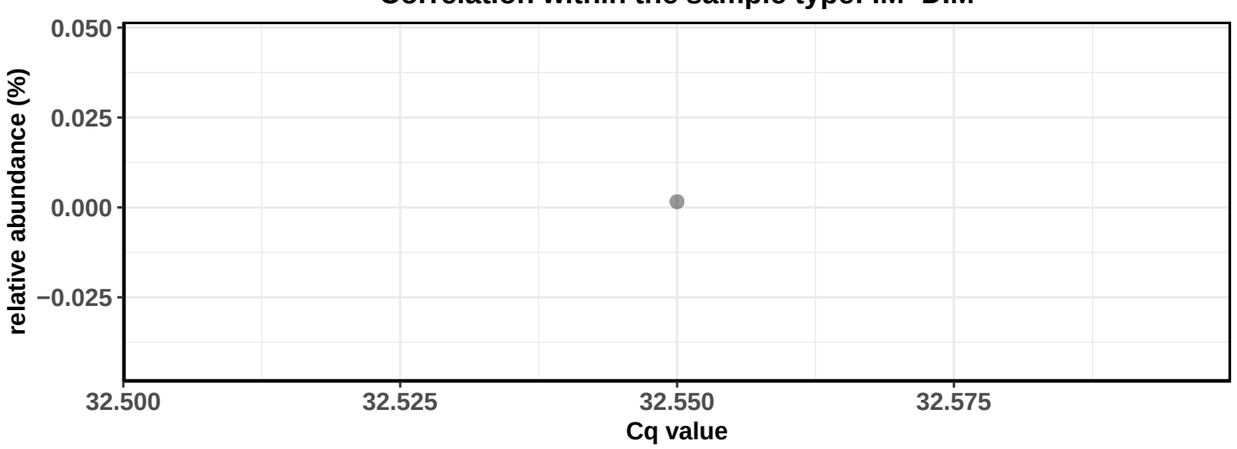
Correlation within the sample type: REF−DIC



Correlation within the sample type: IM−DIC

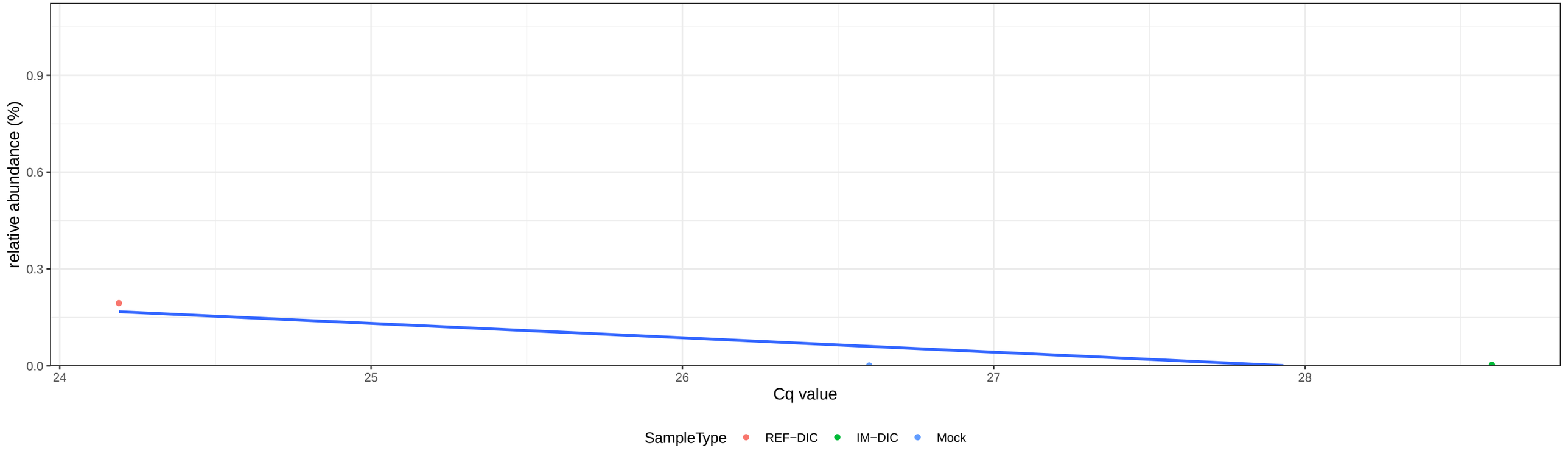


Correlation within the sample type: IM−DIM

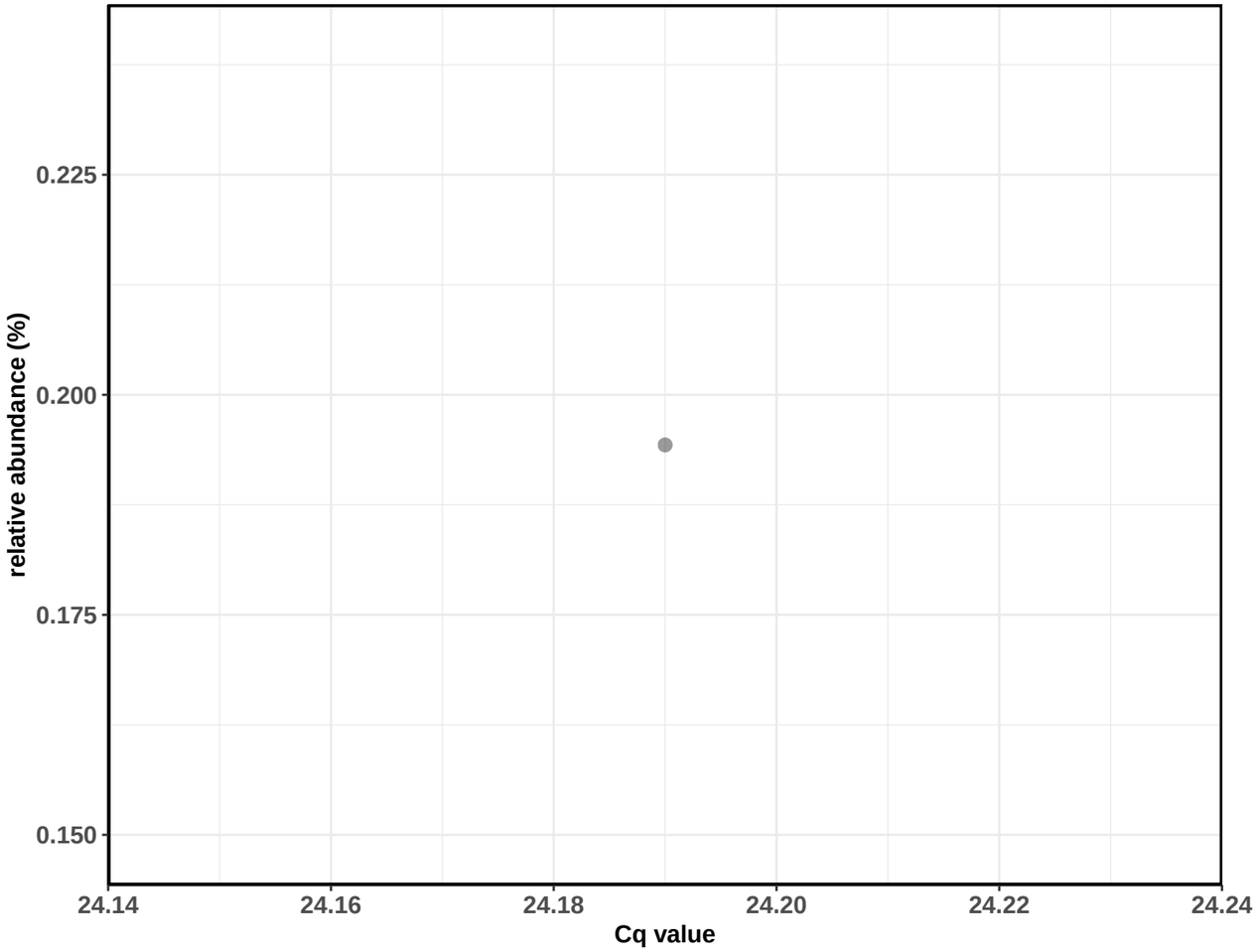


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

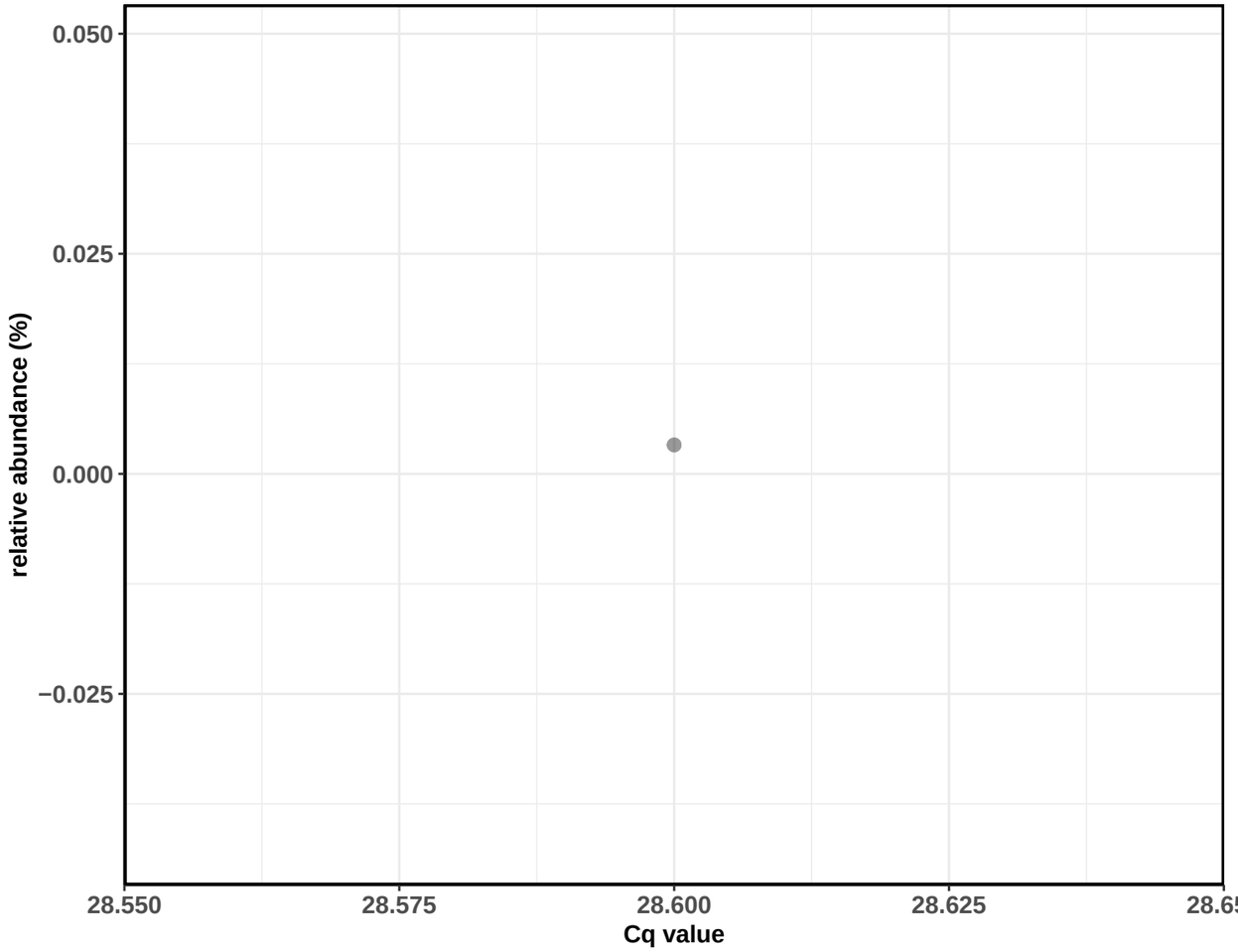
Correlation with all samples



Correlation within the sample type: REF−DIC

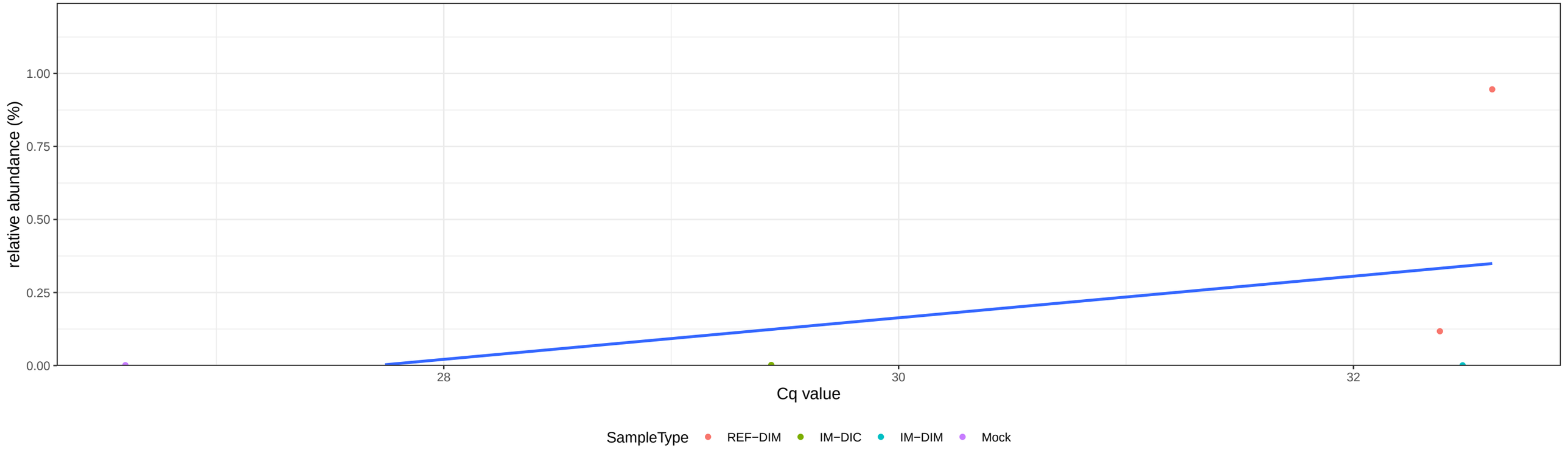


Correlation within the sample type: IM−DIC

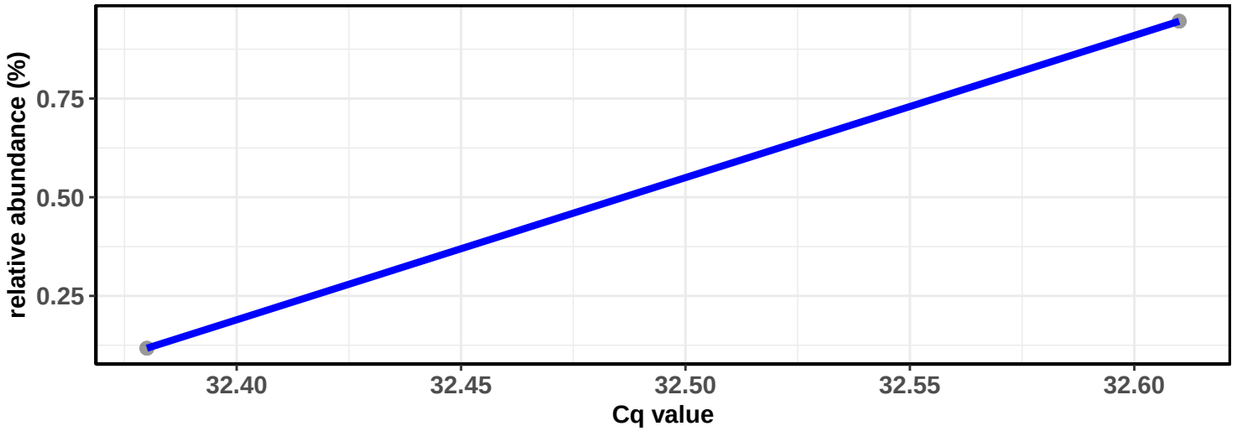


D_0__Bacteria; D_1__Bacteroidetes; D_2__Bacteroidia; D_3__Cytophagales; D_4__Hymenobacteraceae; D_5__Hymenobacter; D_6__uncultured bacterium

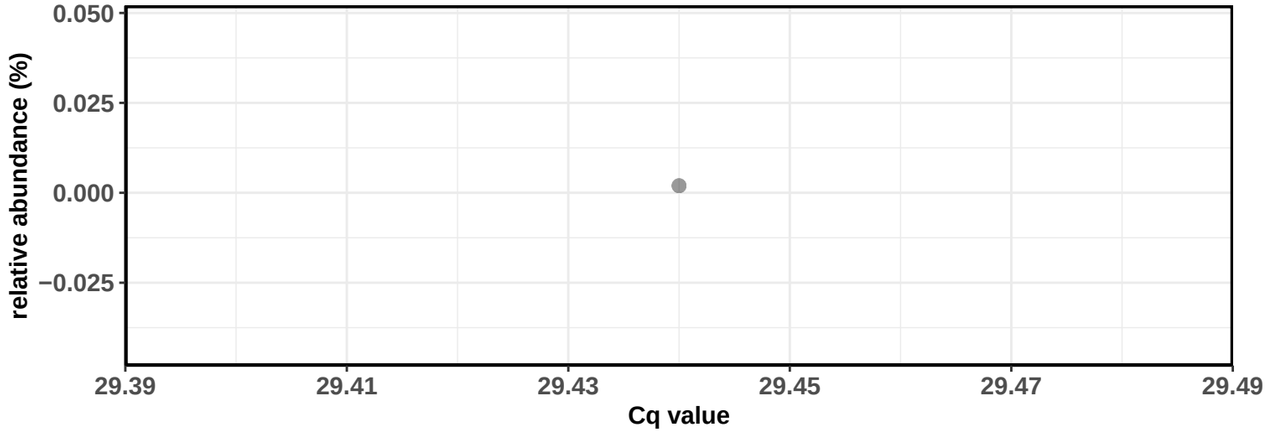
Correlation with all samples



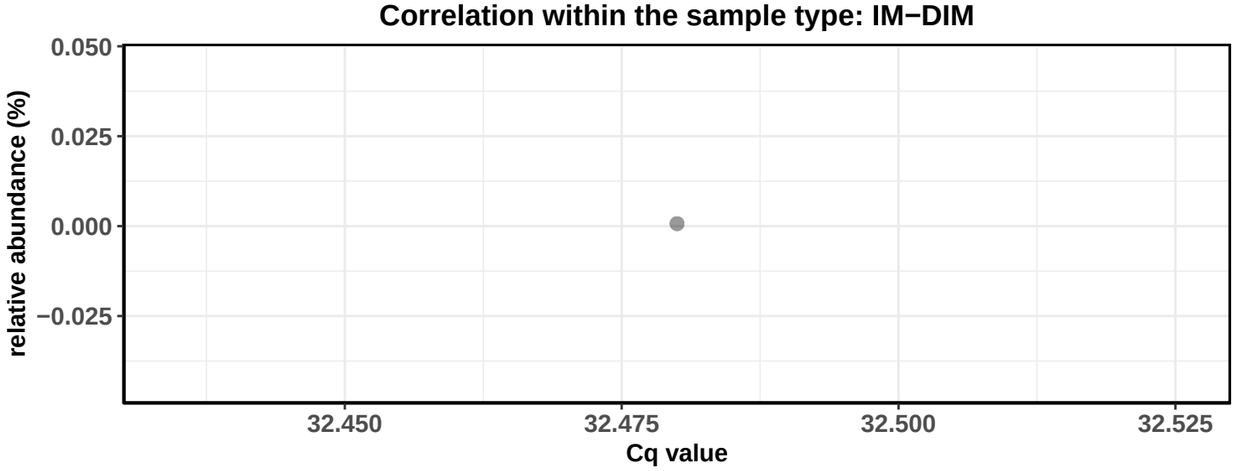
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

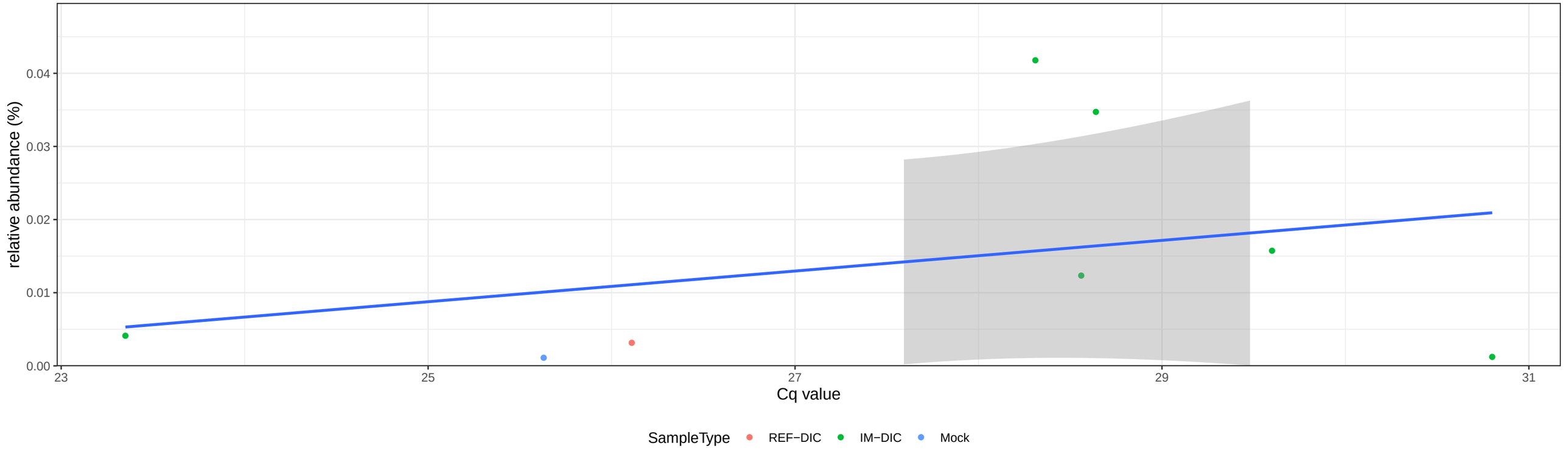


Correlation within the sample type: IM−DIM

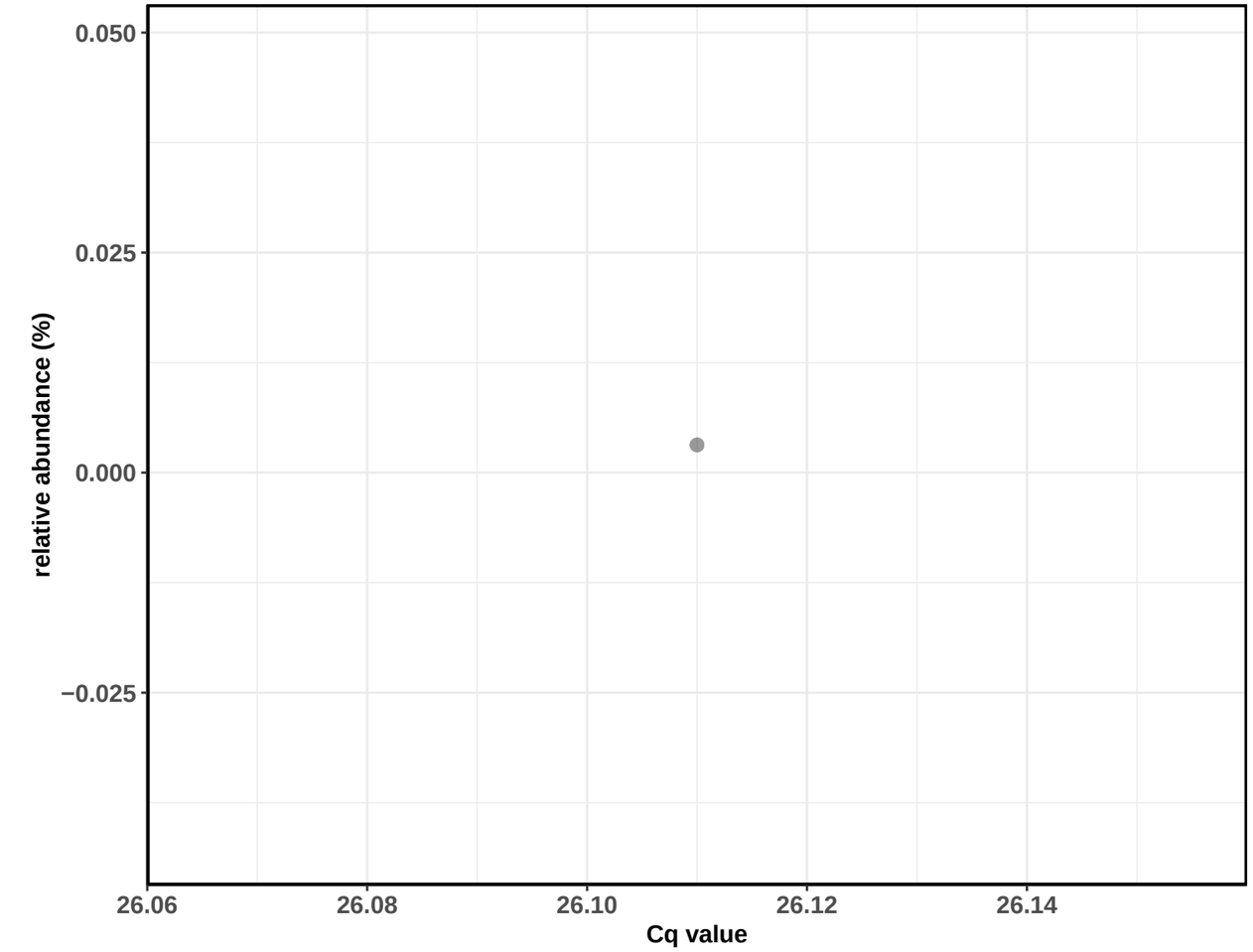


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; D_6__Lactobacillus fermentum

Correlation with all samples

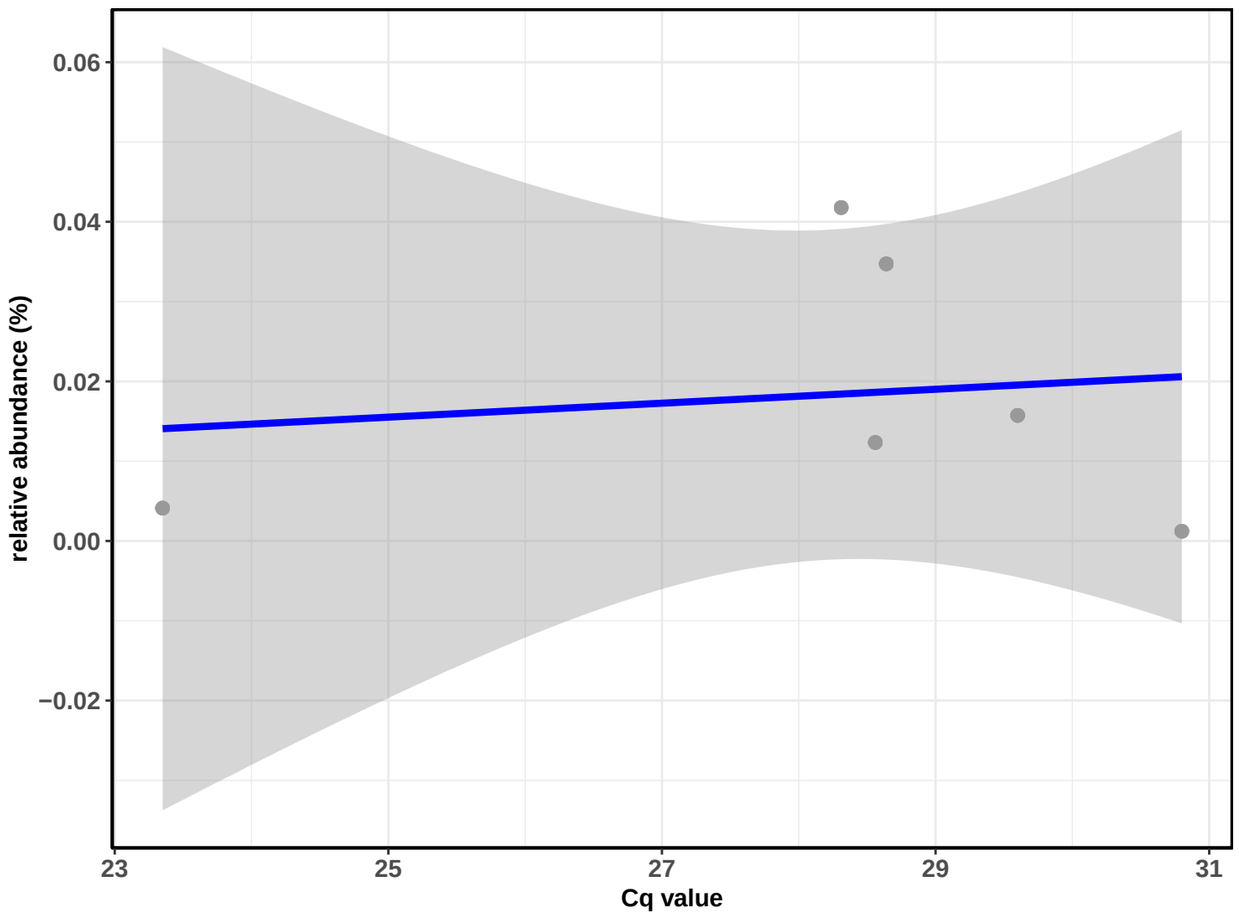


Correlation within the sample type: REF−DIC



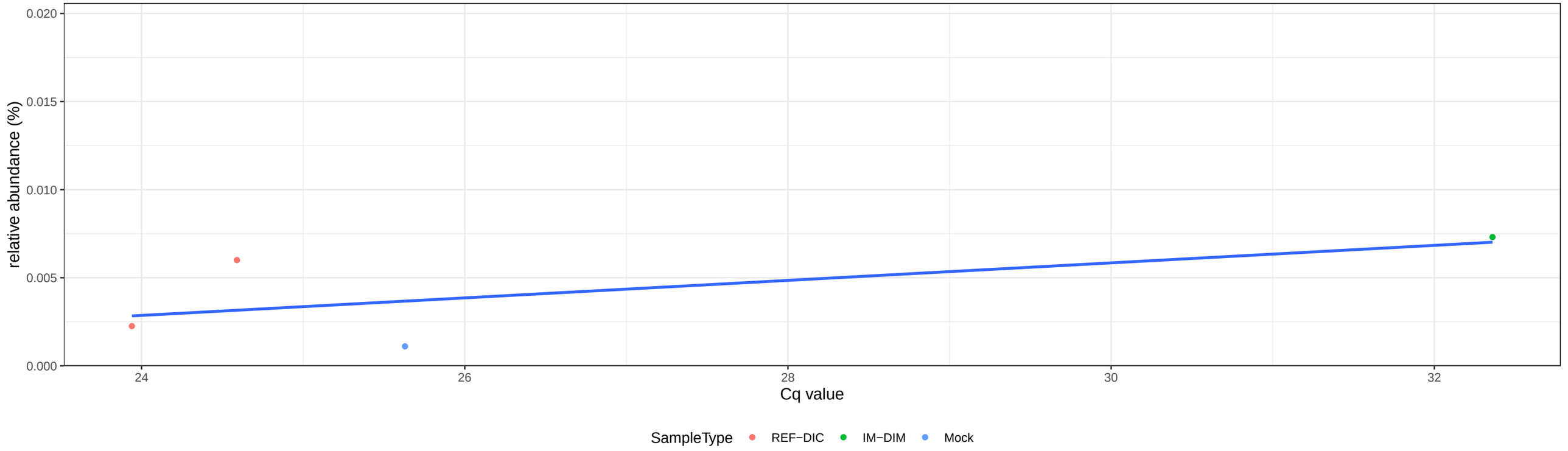
Correlation within the sample type: IM−DIC

$\log_e(S) = 3.784$, $p = 0.623$, $\rho_{Spearman} = -0.257$, $CI_{95\%}$ [−0.884, 0.701], $n = 6$

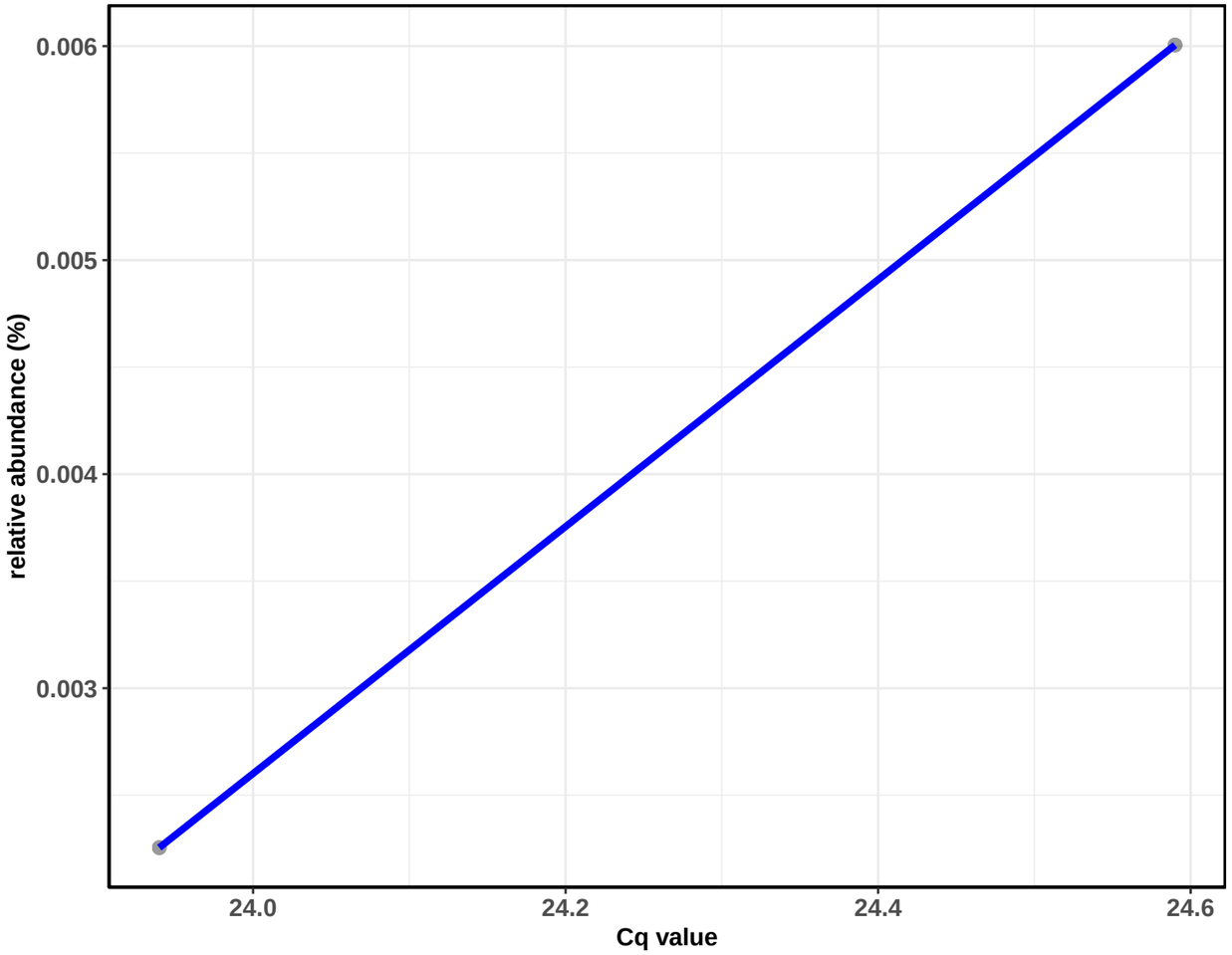


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Betaproteobacteriales; D_4__Burkholderiaceae; D_5__Acidovorax

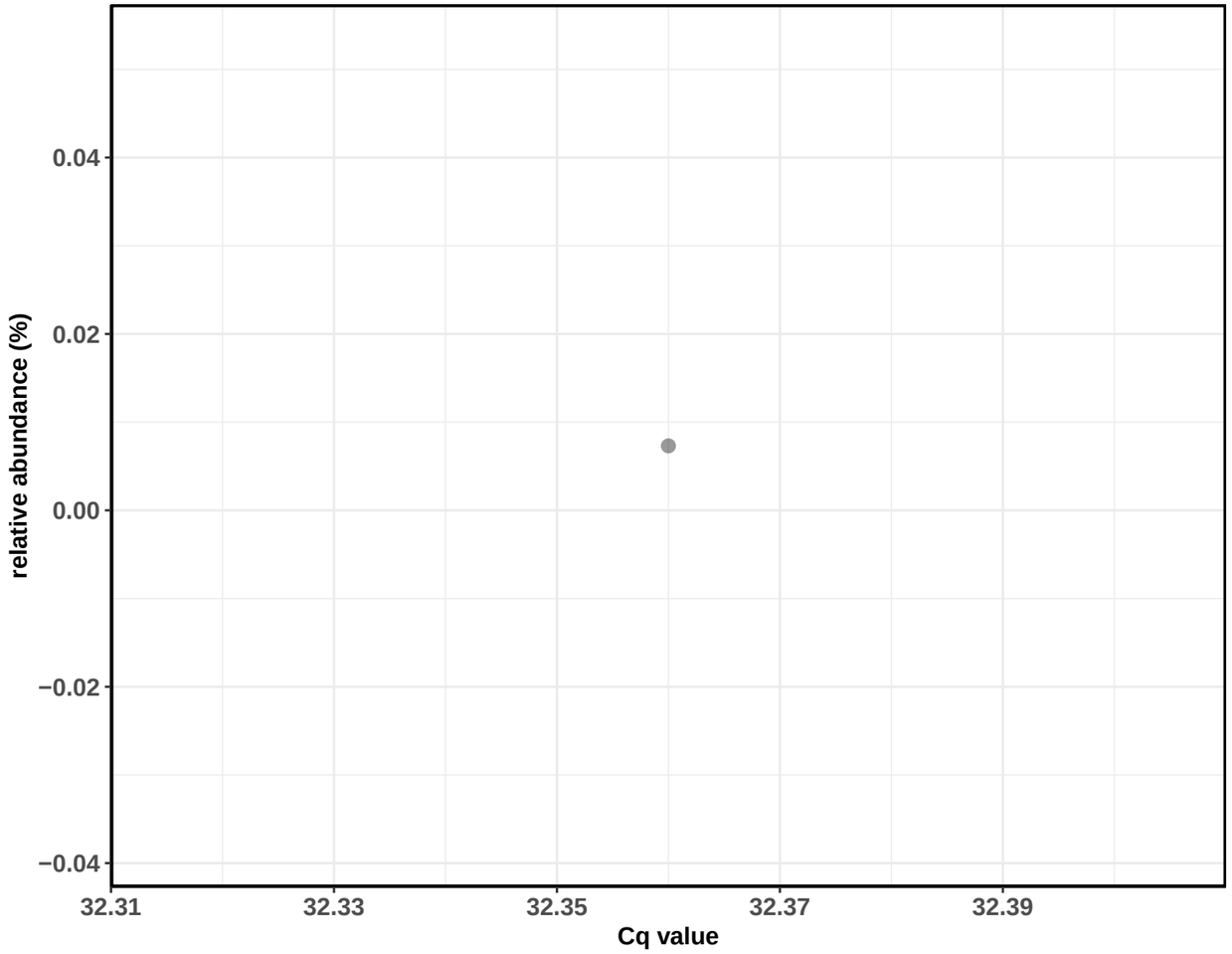
Correlation with all samples



Correlation within the sample type: REF−DIC

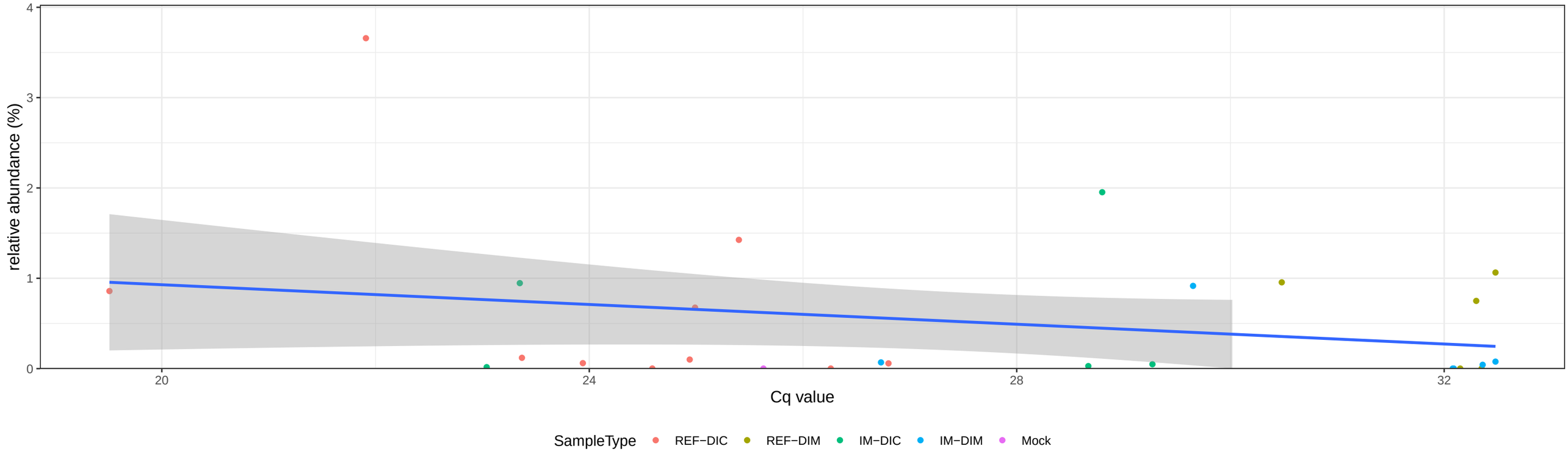


Correlation within the sample type: IM−DIM



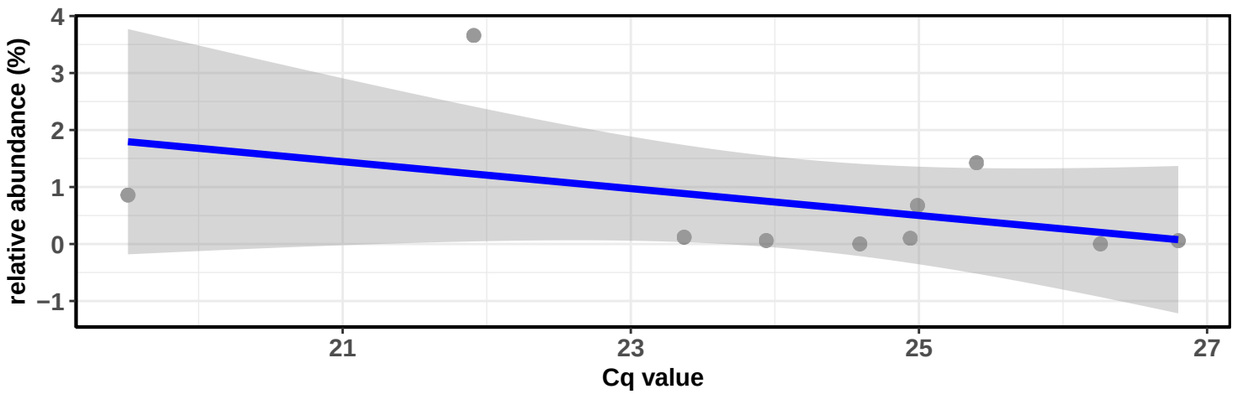
D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Vibrionales; D_4__Vibrionaceae; D_5__Aliivibrio; Ambiguous_taxa

Correlation with all samples

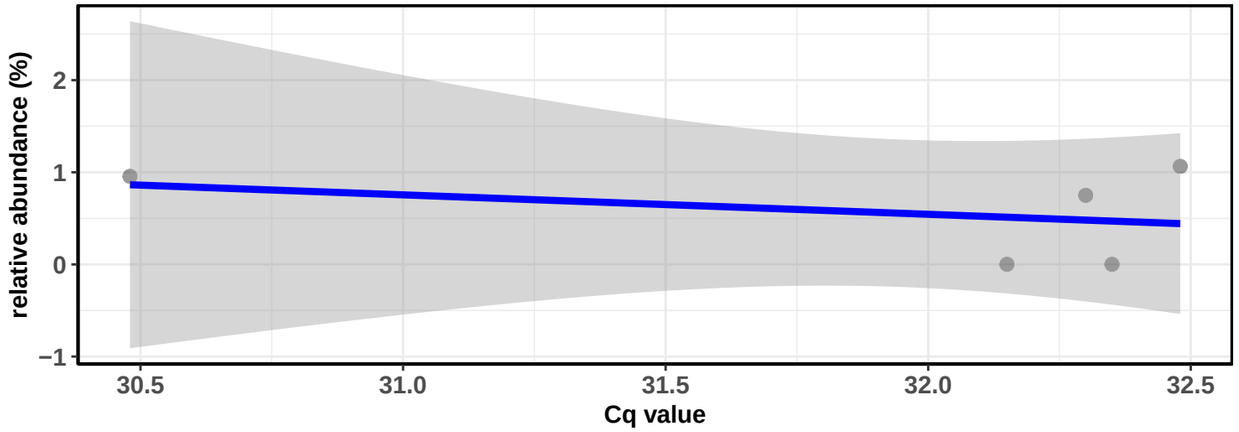


Correlation within the sample type: REF−DIC

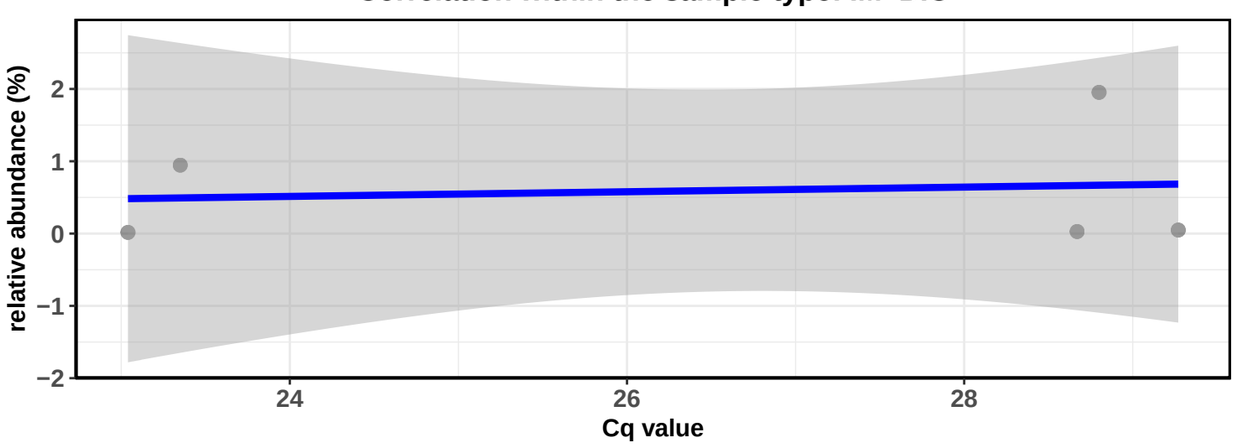
$\log_e(S)$ = 5.505, p = 0.150, $\rho_{Spearman}$ = −0.491, $CI_{95\%}$ [−0.856, 0.201], n = 10



Correlation within the sample type: REF−DIM

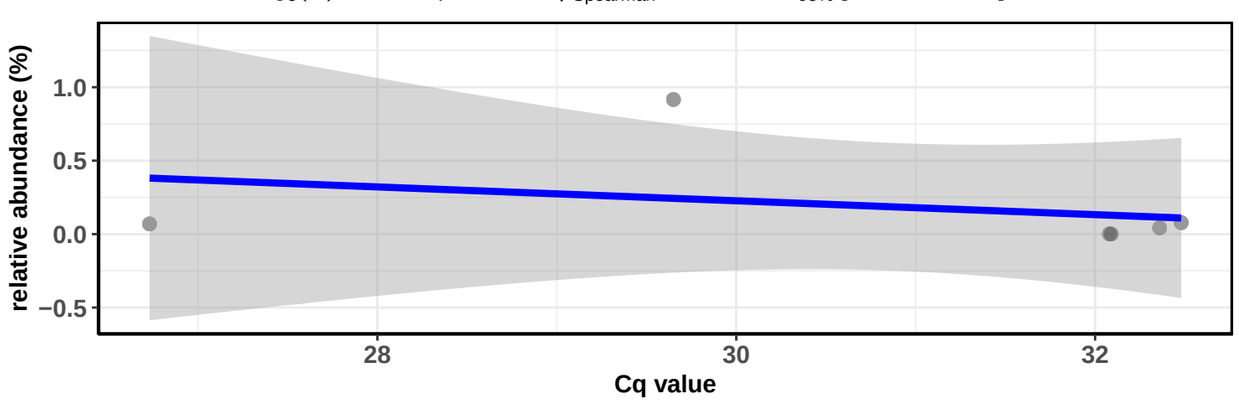


Correlation within the sample type: IM−DIC



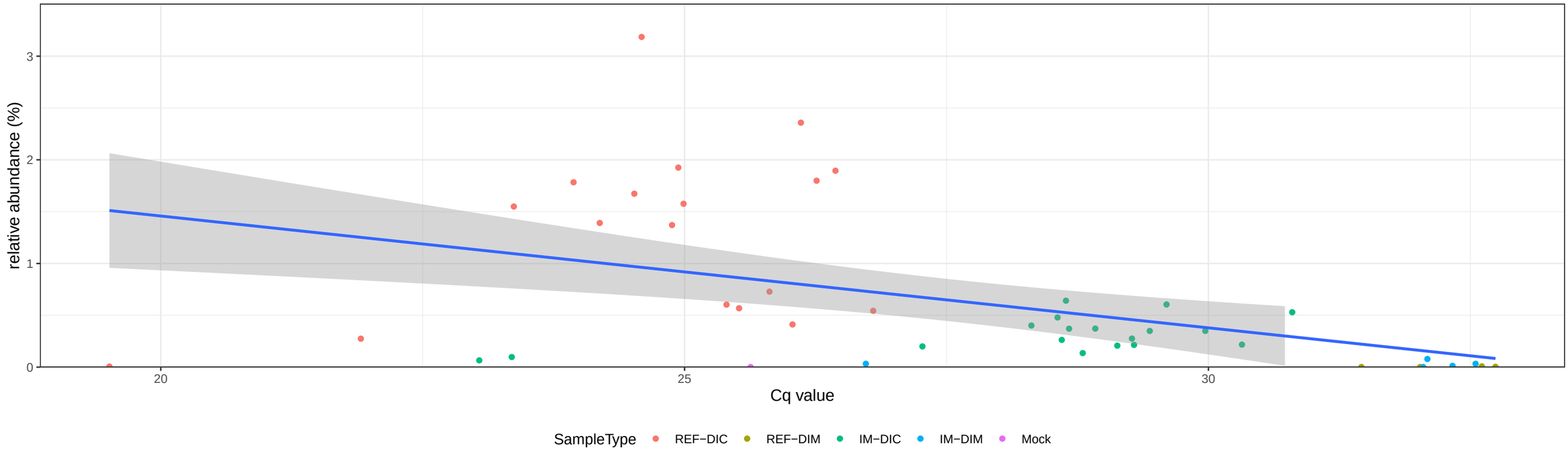
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 3.689, p = 0.787, $\rho_{Spearman}$ = −0.143, $CI_{95\%}$ [−0.855, 0.756], n = 6



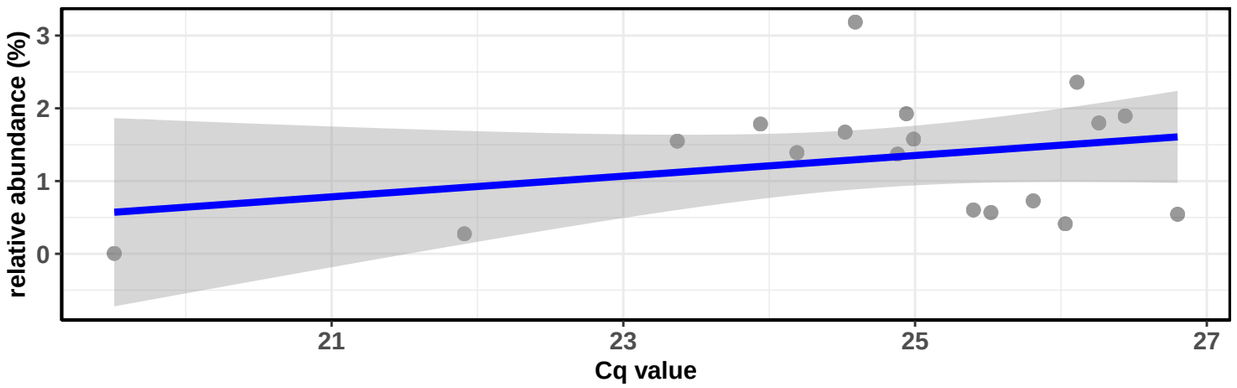
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Leuconostocaceae; D_5__Weissella; D_6__uncultured bacterium

Correlation with all samples

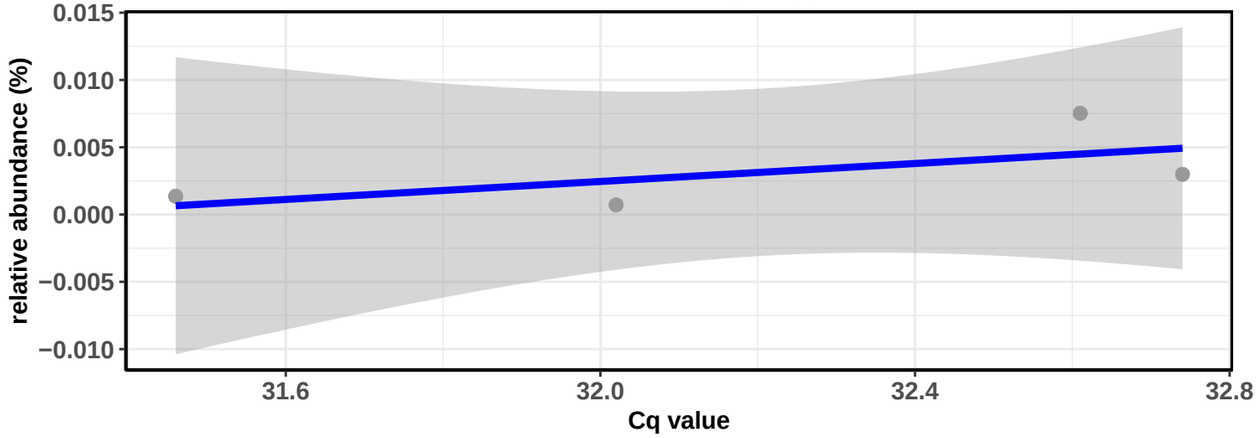


Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.675, p = 0.468, $\rho_{Spearman}$ = 0.183, $CI_{95\%}$ [−0.311, 0.598], n = 18

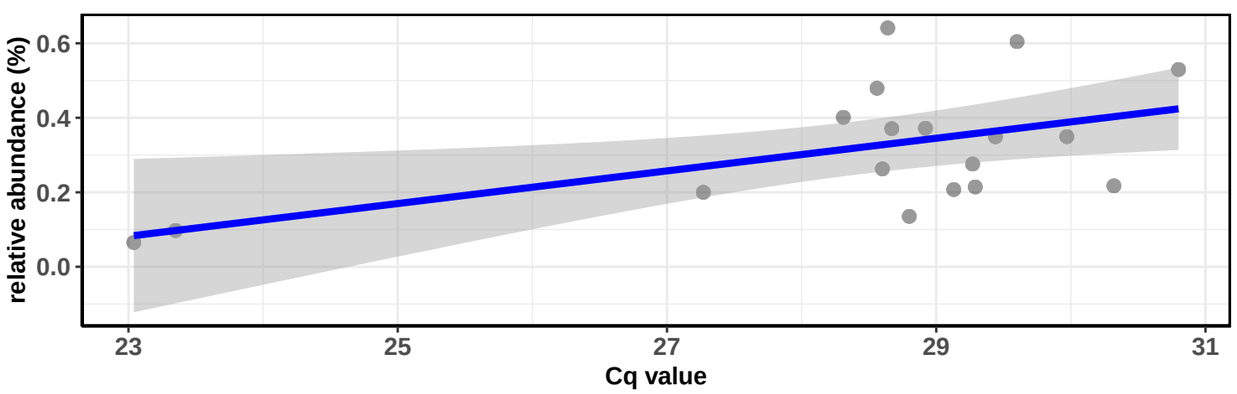


Correlation within the sample type: REF−DIM

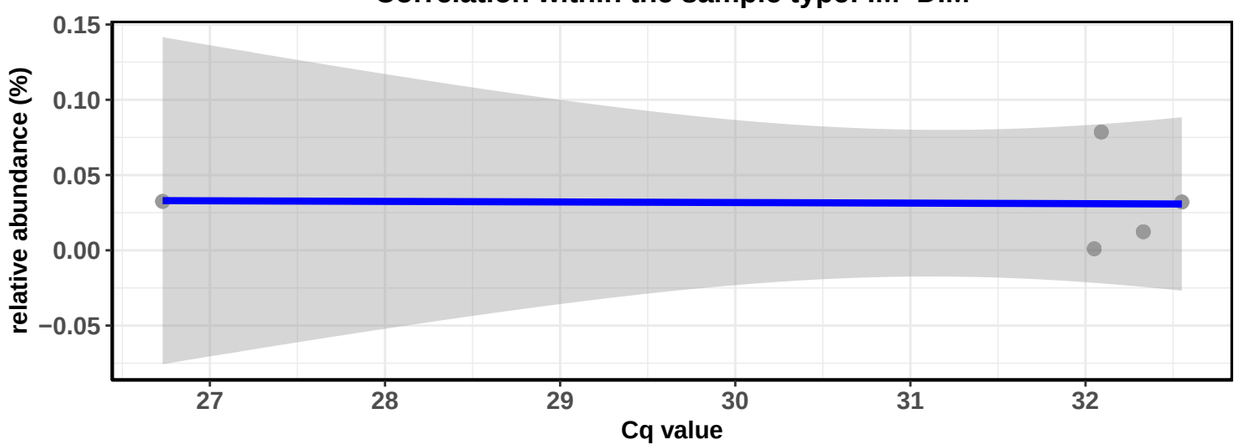


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.446, p = 0.155, $\rho_{Spearman}$ = 0.350, $CI_{95\%}$ [−0.140, 0.702], n = 18

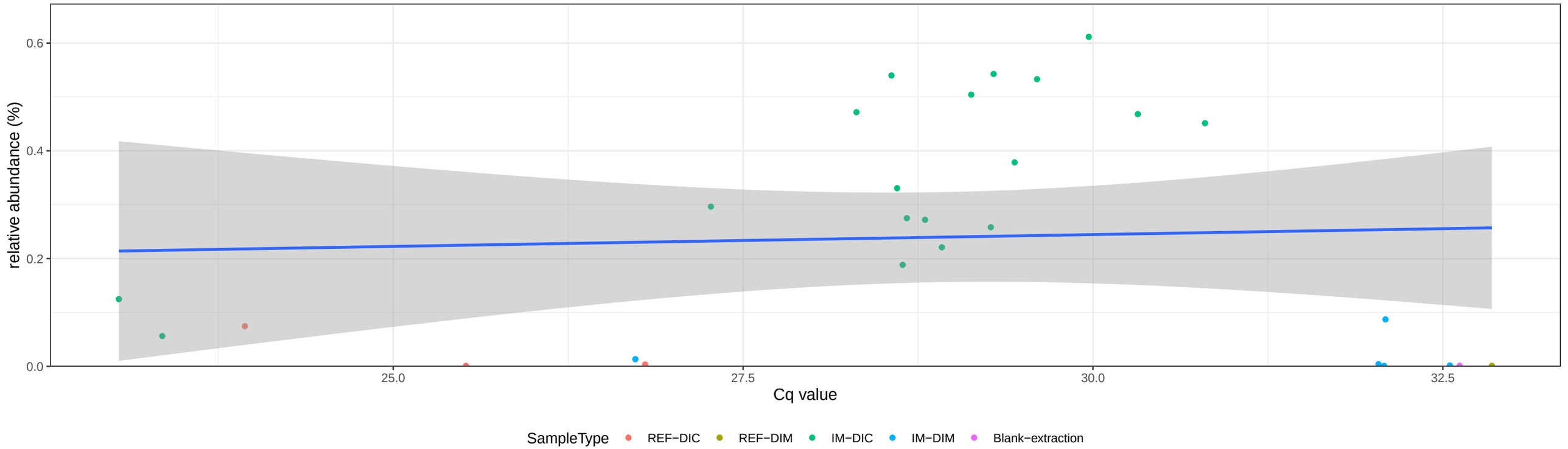


Correlation within the sample type: IM−DIM

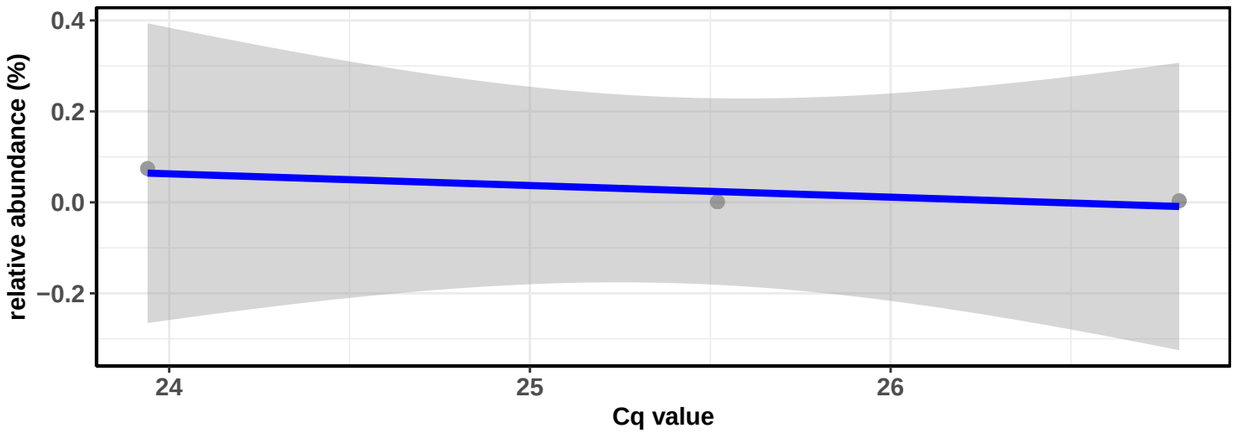


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Ornithinibacillus; Ambiguous_taxa

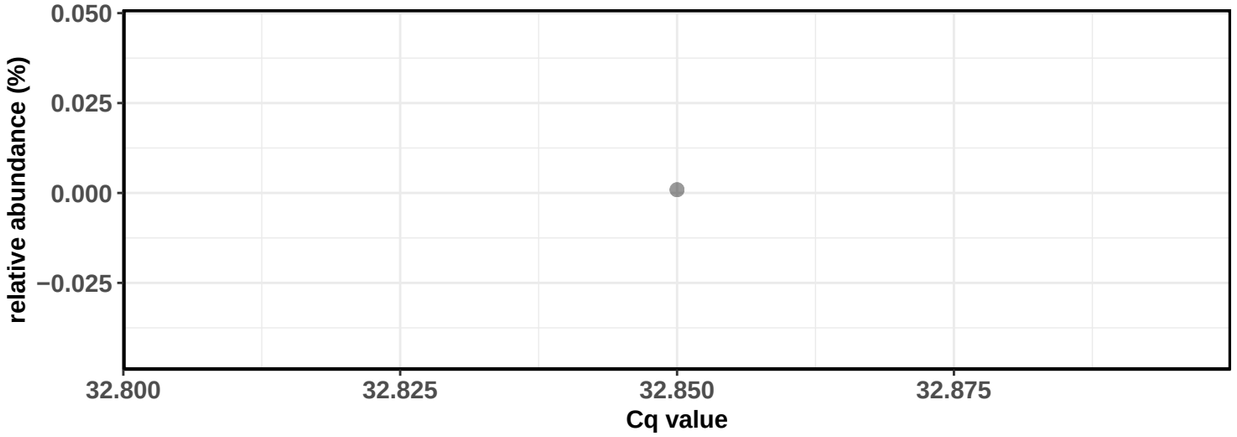
Correlation with all samples



Correlation within the sample type: REF−DIC

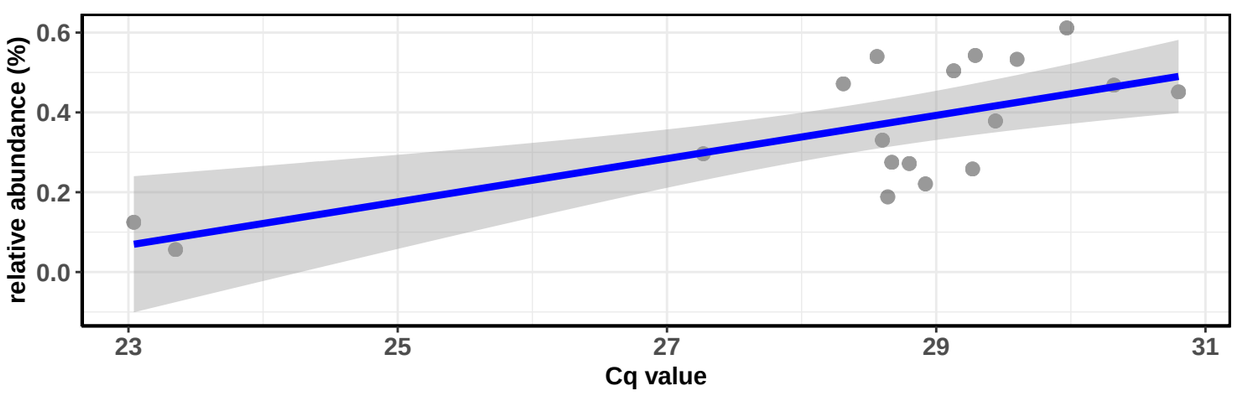


Correlation within the sample type: REF−DIM

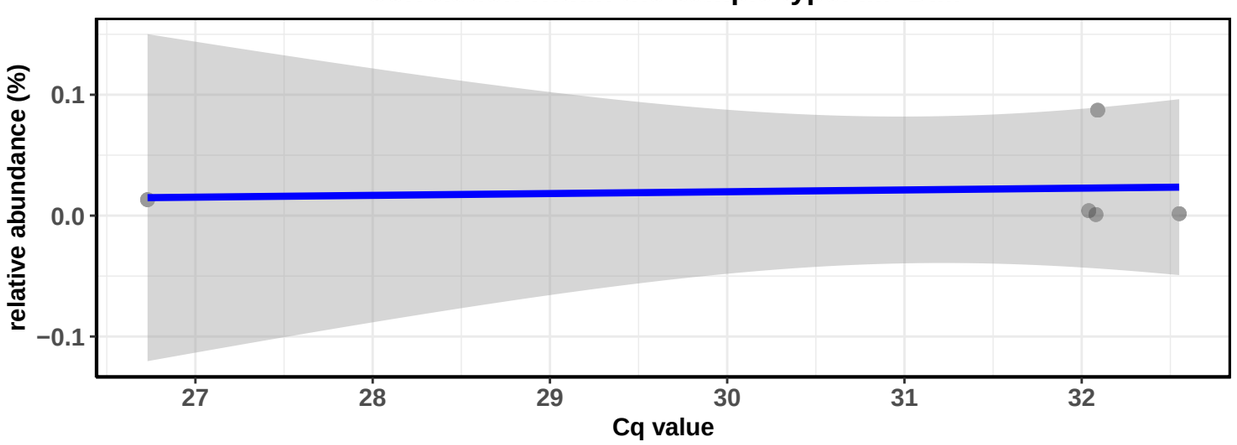


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.148, p = 0.028, $\rho_{Spearman}$ = 0.517, $CI_{95\%}$ [0.066, 0.793], n = 18

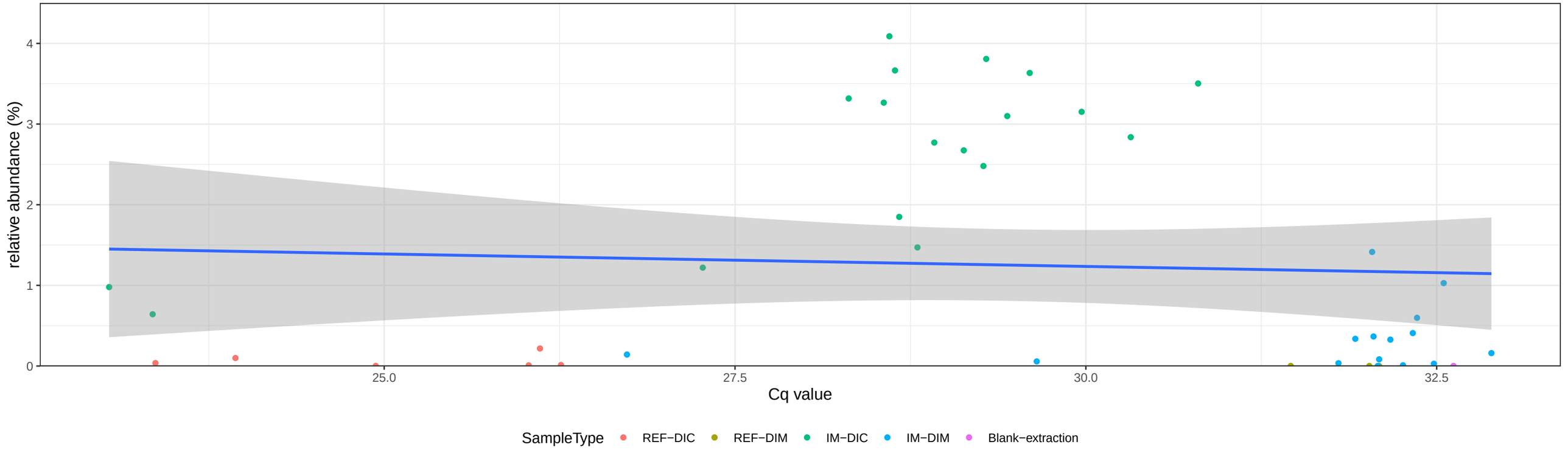


Correlation within the sample type: IM−DIM



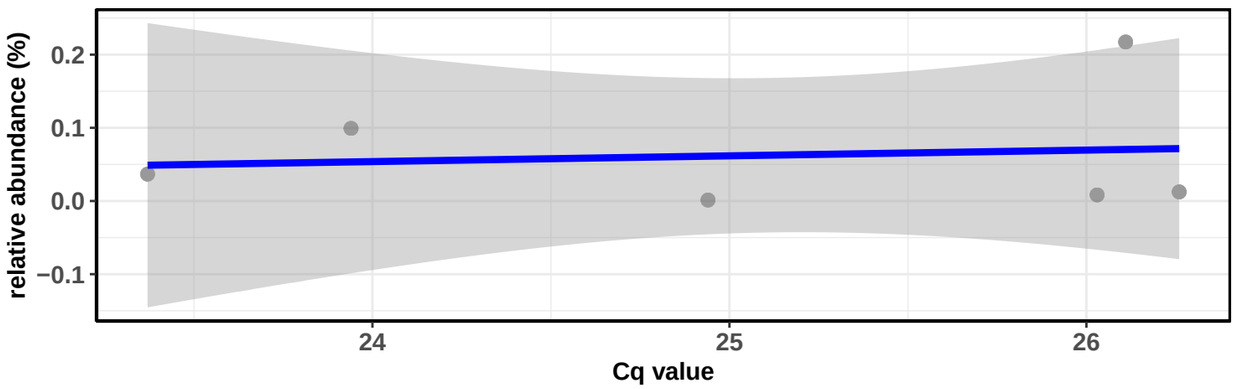
cteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Corynebacteriales; D_4__Corynebacteriaceae; D_5__Corynebacterium 1; D_6__Corynebacterium aurimucosum ATC

Correlation with all samples

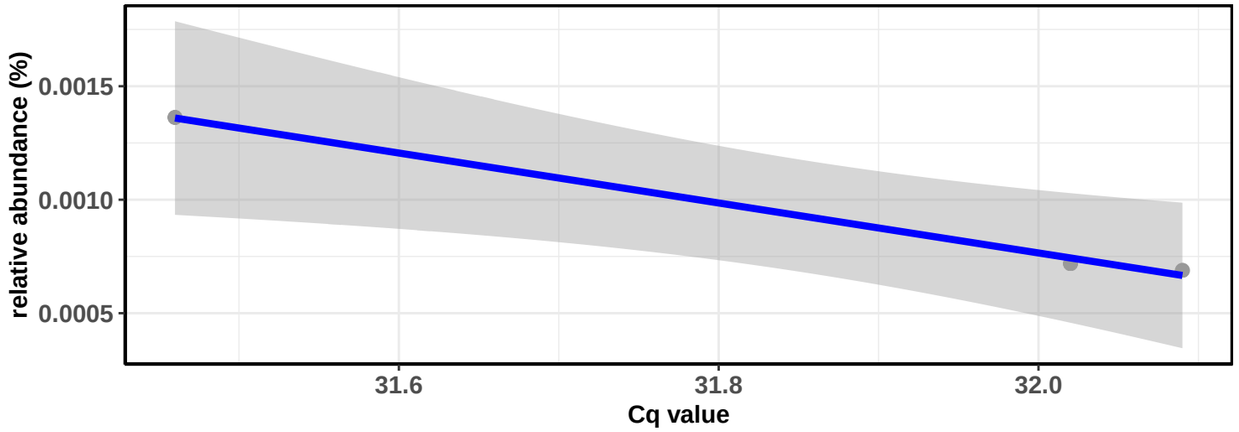


Correlation within the sample type: REF−DIC

$\log_e(S)$ = 3.584, p = 0.957, $\rho_{Spearman}$ = −0.029, $CI_{95\%}$ [−0.821, 0.802], n = 6

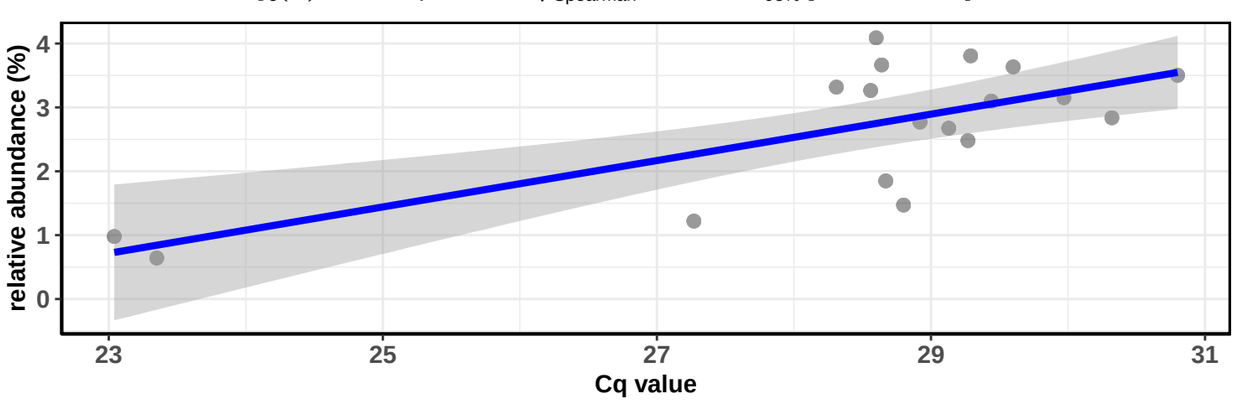


Correlation within the sample type: REF−DIM



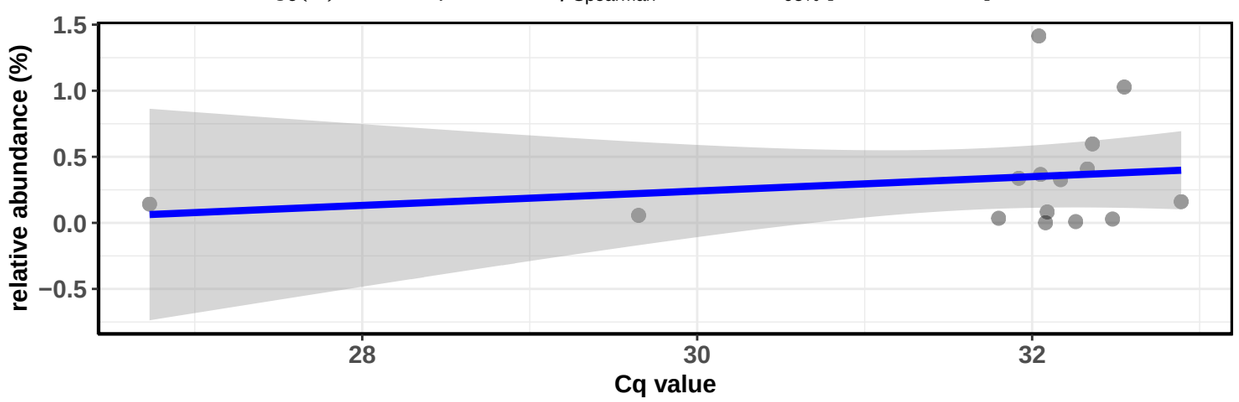
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.370, p = 0.103, $\rho_{Spearman}$ = 0.397, $CI_{95\%}$ [−0.085, 0.729], n = 18



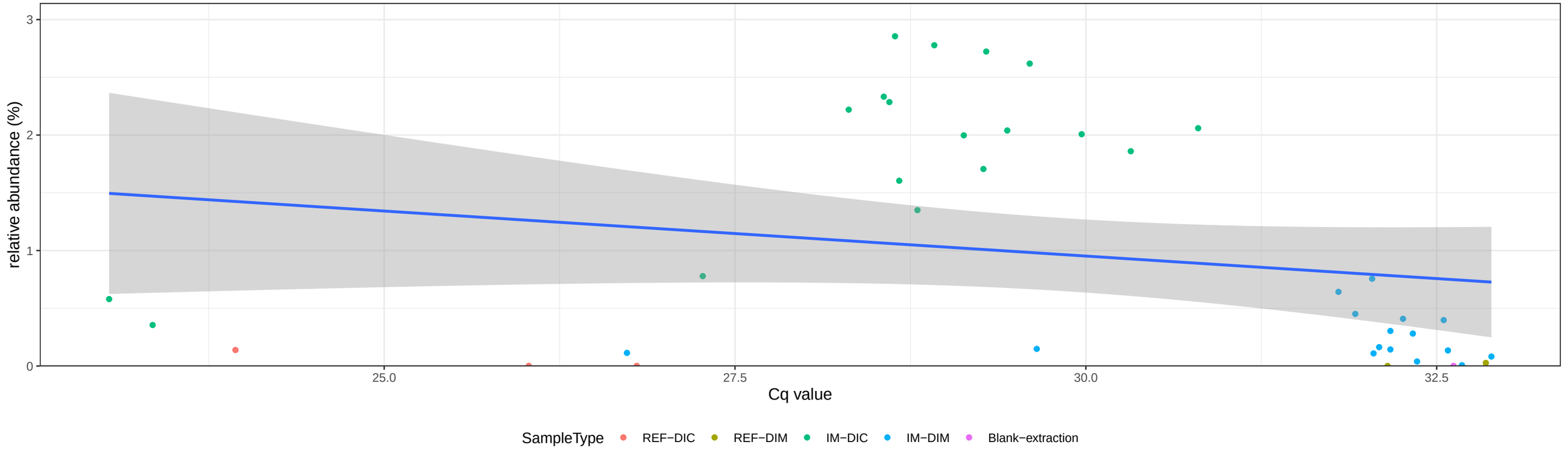
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.136, p = 0.533, $\rho_{Spearman}$ = 0.175, $CI_{95\%}$ [−0.370, 0.631], n = 15

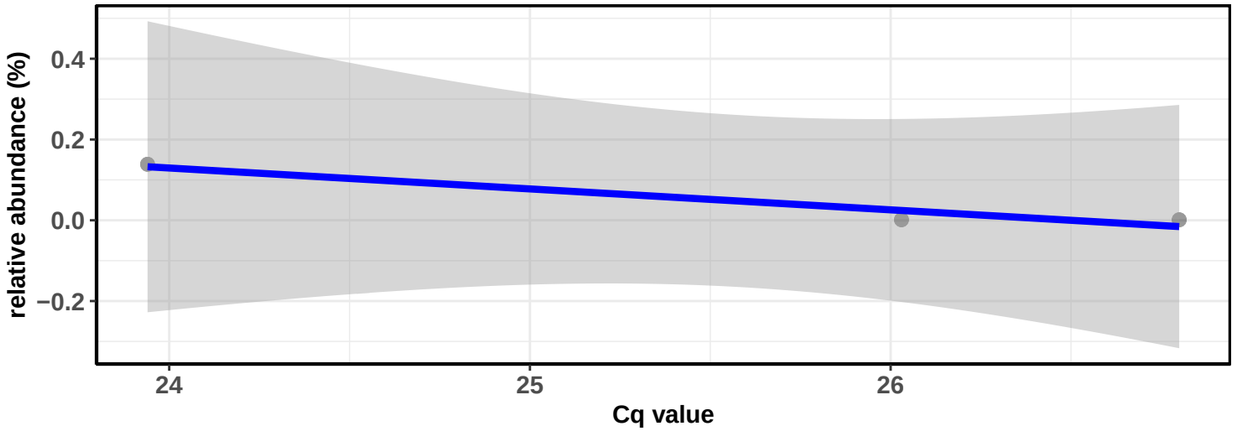


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Actinomycetales; D_4__Actinomycetaceae; D_5__Actinomyces; D_6__uncultured Actinomycetales bacterium

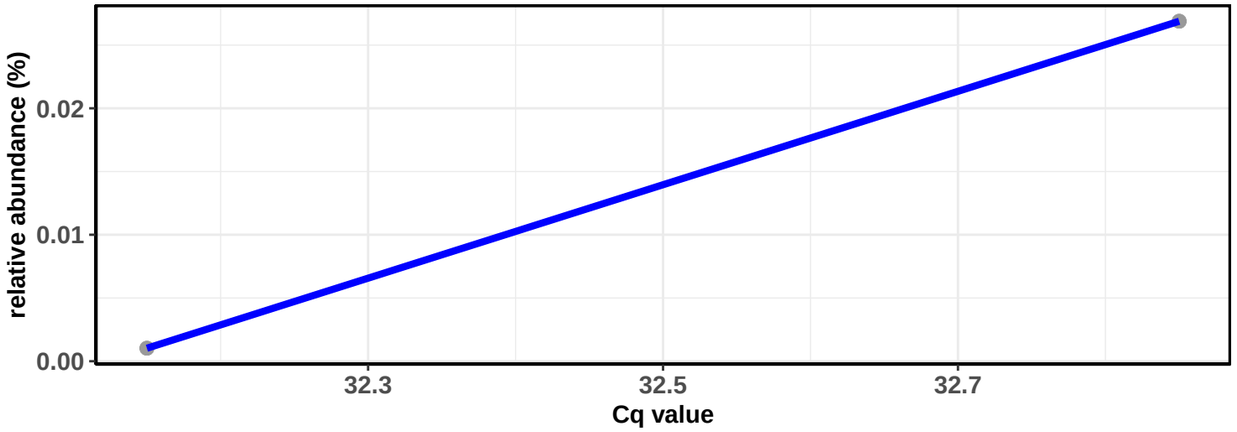
Correlation with all samples



Correlation within the sample type: REF−DIC

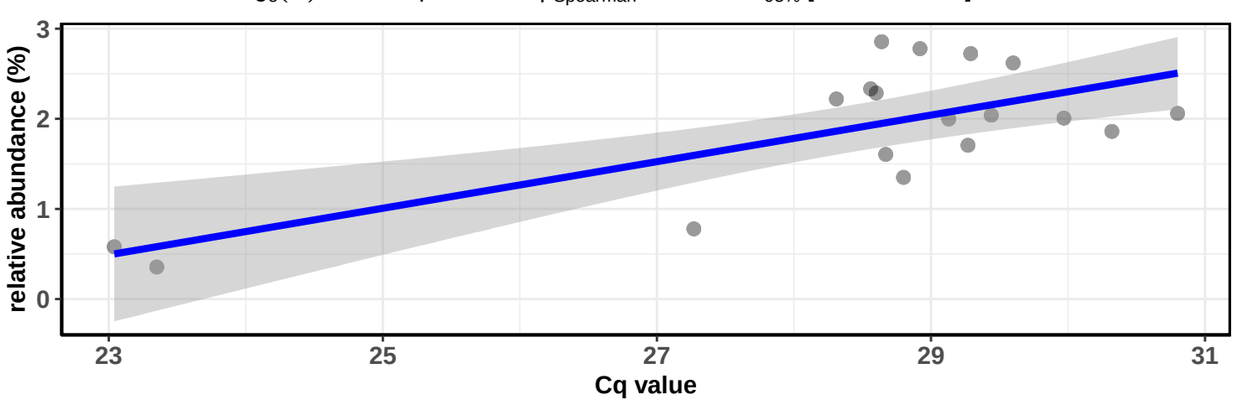


Correlation within the sample type: REF−DIM



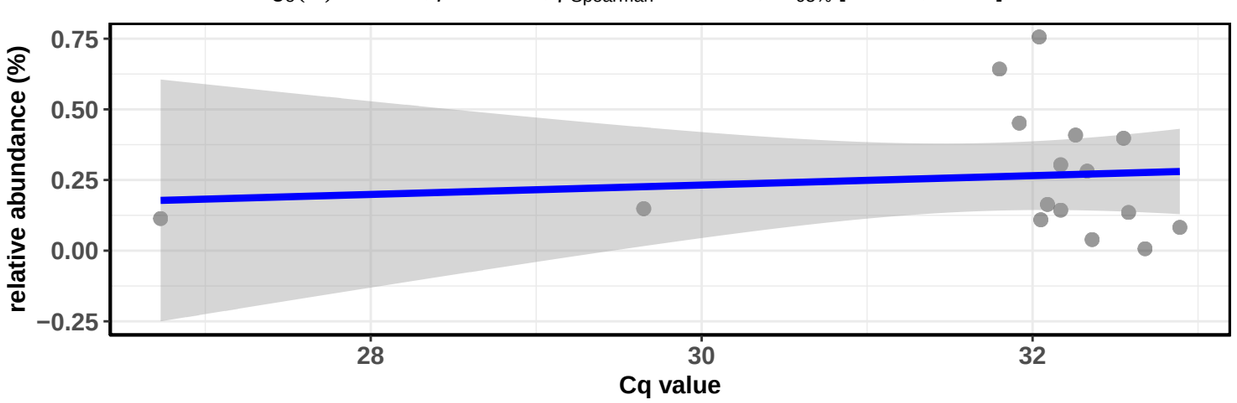
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.504, p = 0.210, $\rho_{Spearman}$ = 0.311, $CI_{95\%}$ [−0.183, 0.679], n = 18



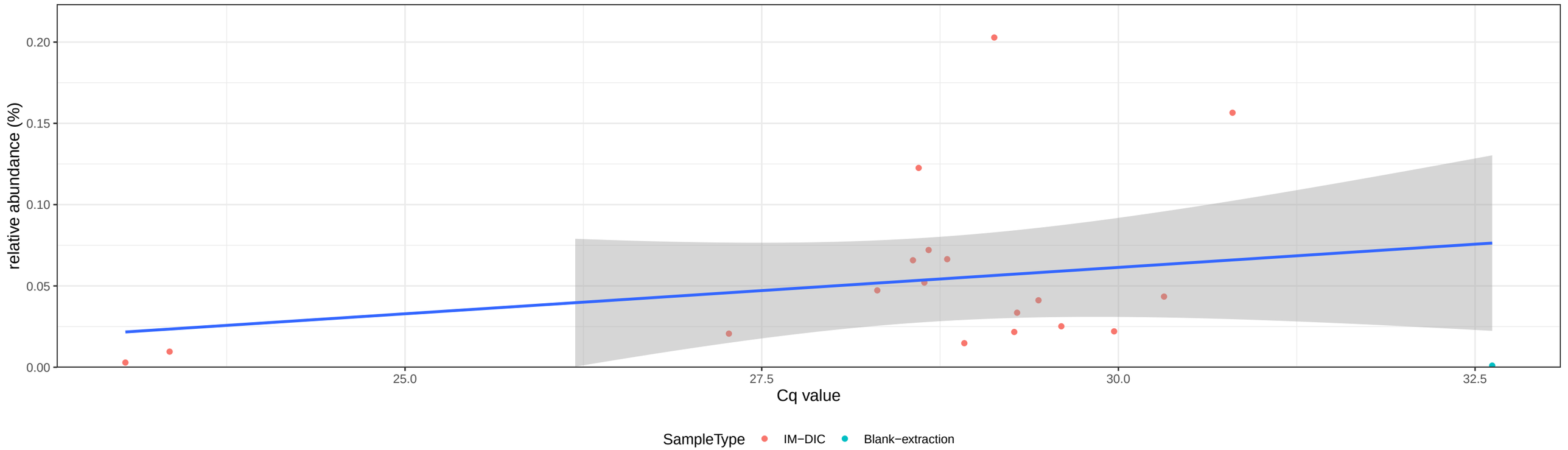
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.882, p = 0.094, $\rho_{Spearman}$ = −0.433, $CI_{95\%}$ [−0.764, 0.080], n = 16



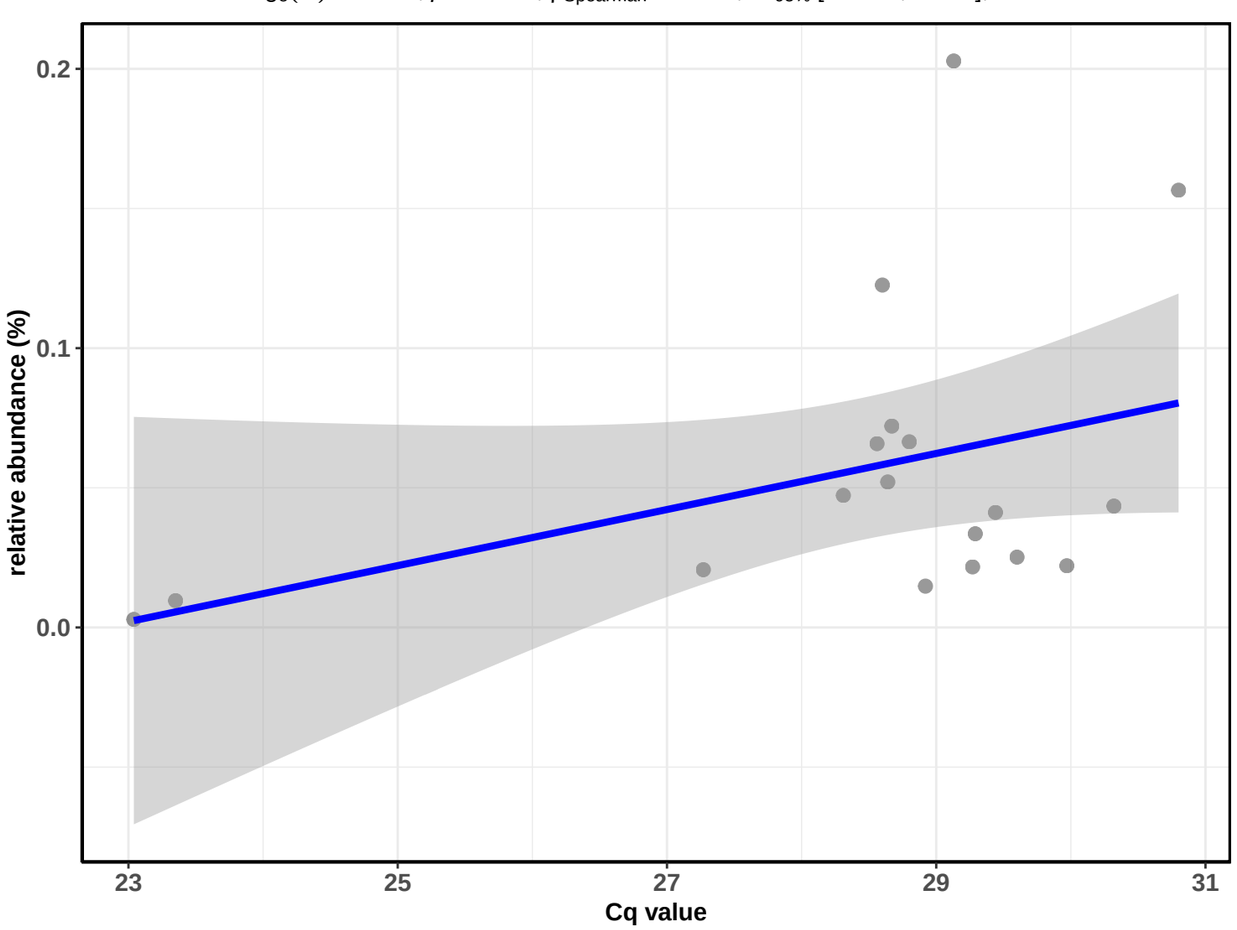
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Lactobacillales; D_4__Lactobacillaceae; D_5__Lactobacillus; Ambiguous_taxa

Correlation with all samples



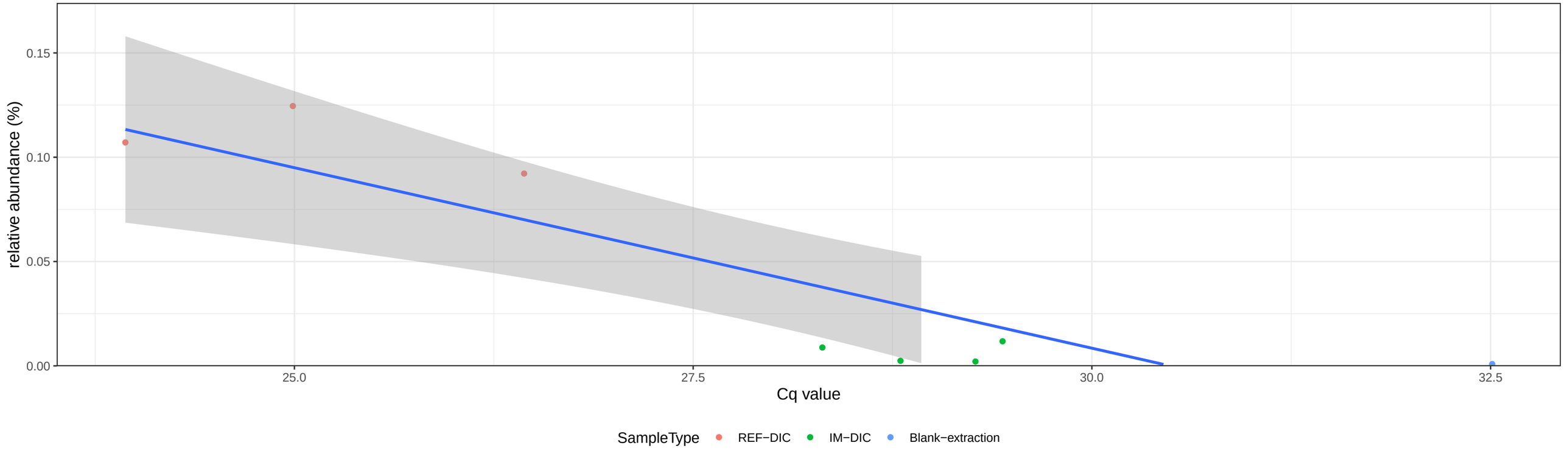
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.585, p = 0.311, $\rho_{Spearman}$ = 0.253, $CI_{95\%}$ [−0.243, 0.644], n = 18

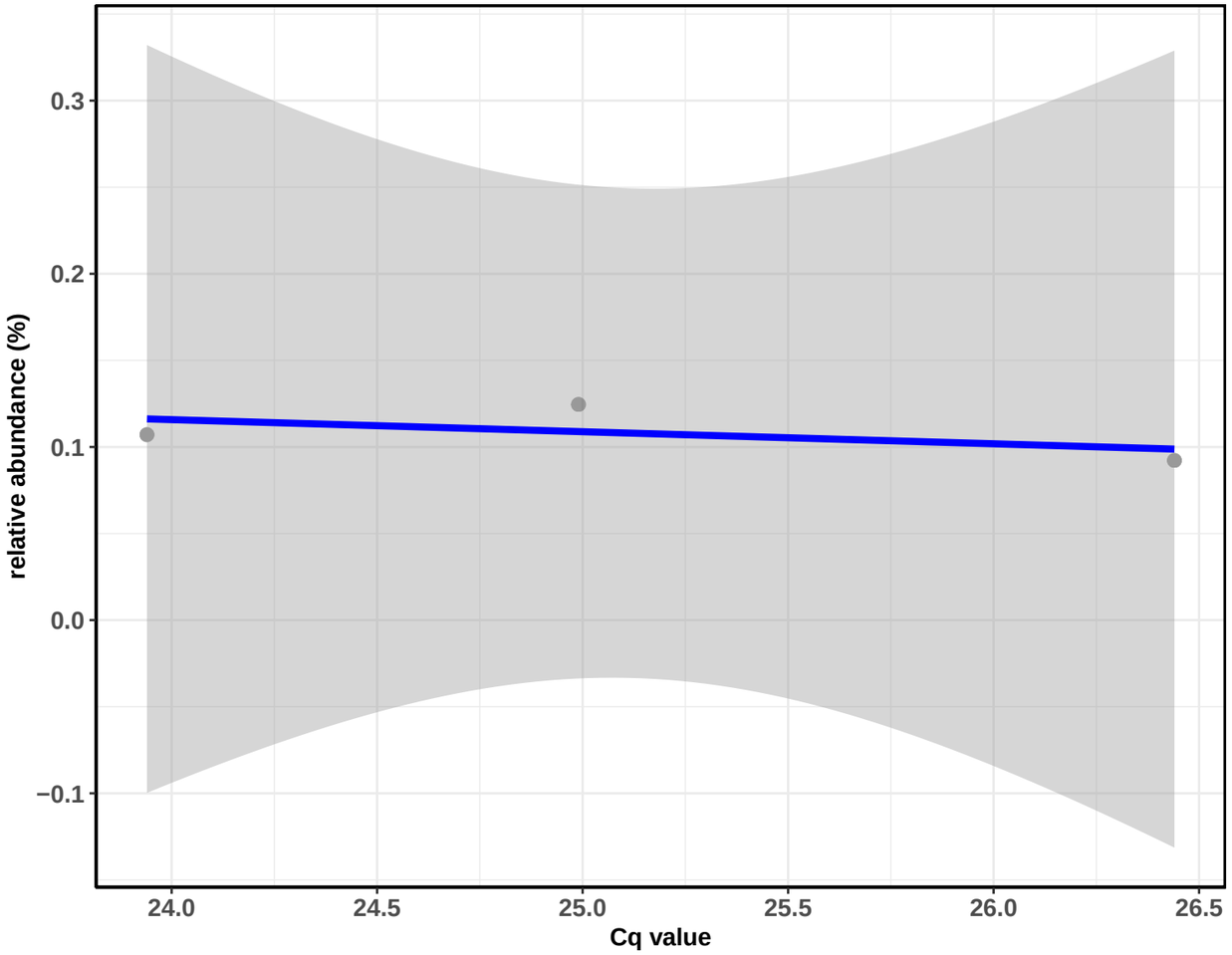


D_0__Bacteria; D_1__Firmicutes; D_2__Erysipelotrichia; D_3__Erysipelotrichales; D_4__Erysipelotrichaceae

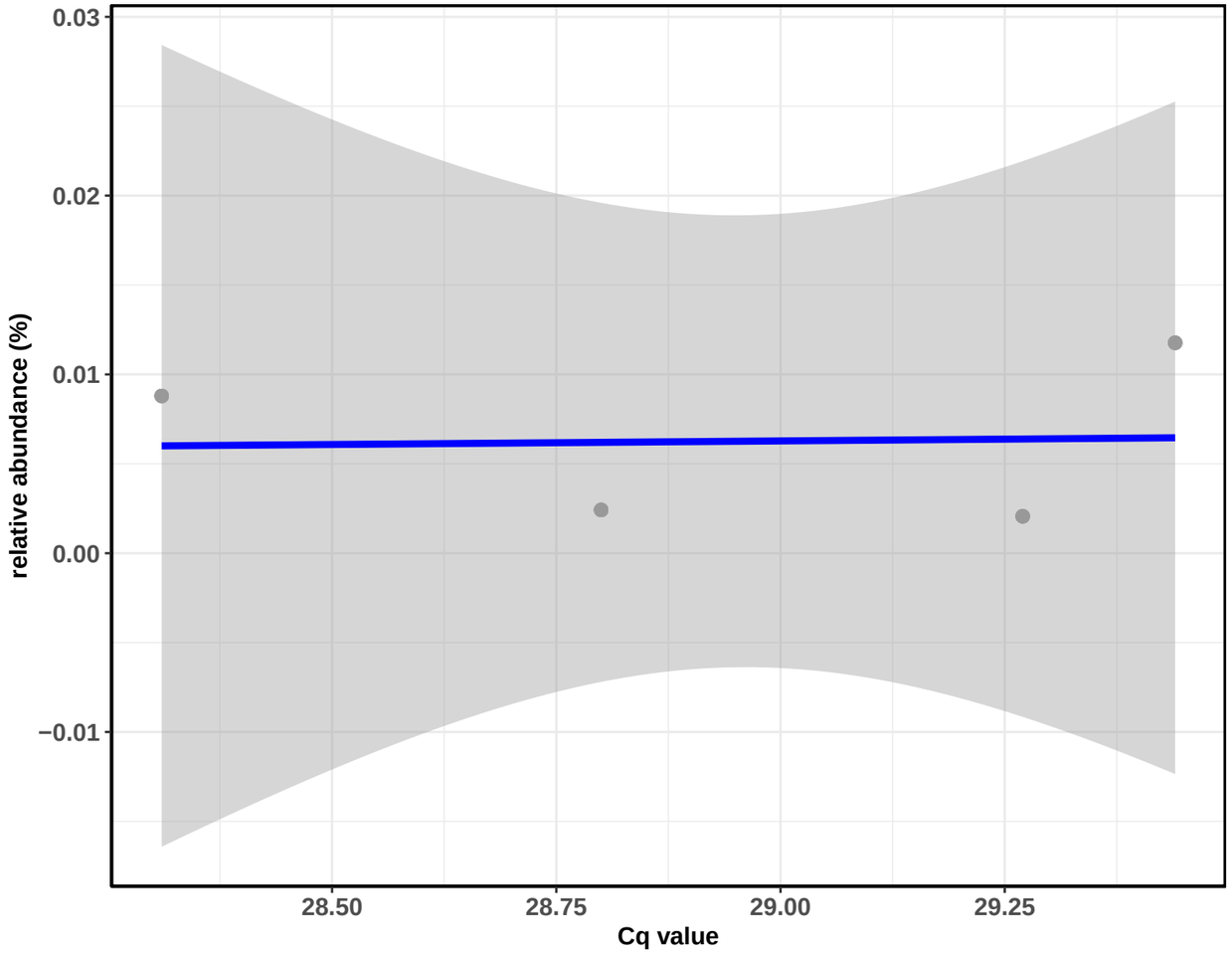
Correlation with all samples



Correlation within the sample type: REF−DIC

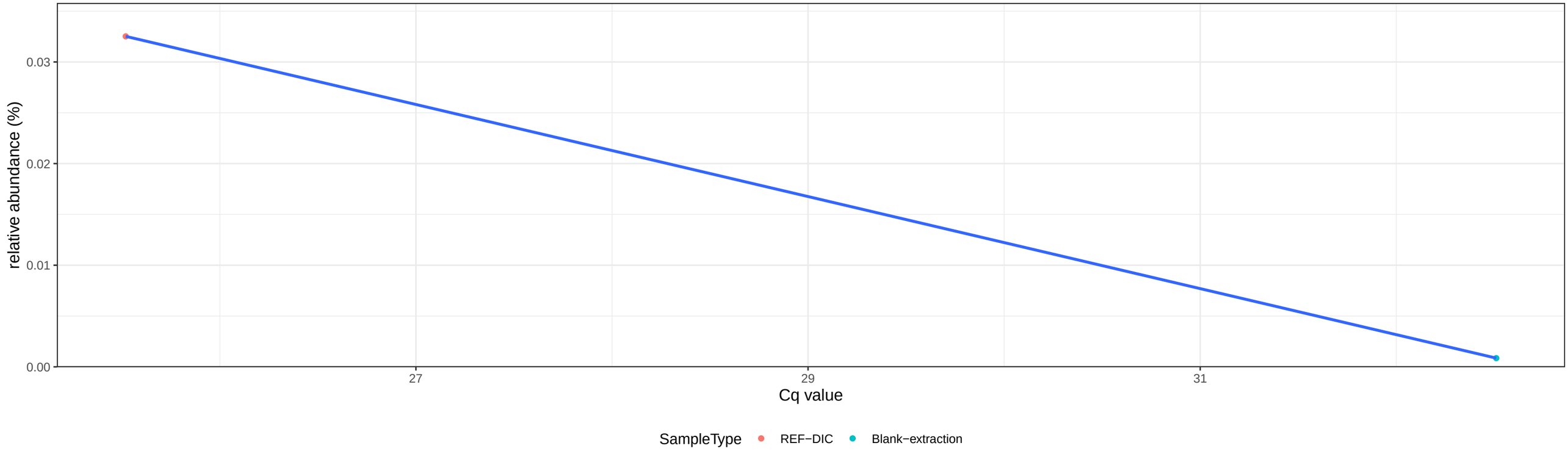


Correlation within the sample type: IM−DIC

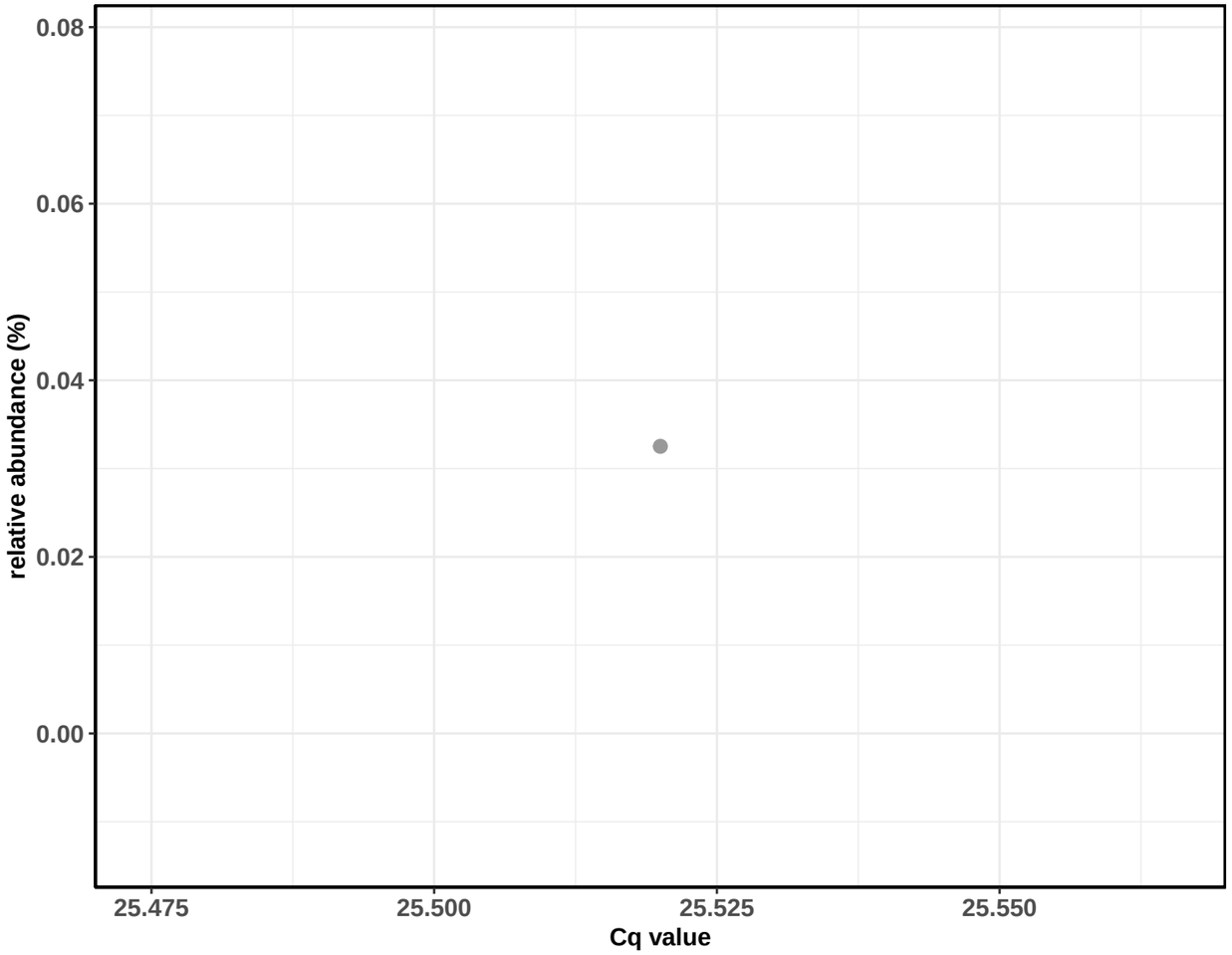


D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Corynebacteriales; D_4__Corynebacteriaceae; D_5__Corynebacterium 1; D_6__uncultured bacterium

Correlation with all samples

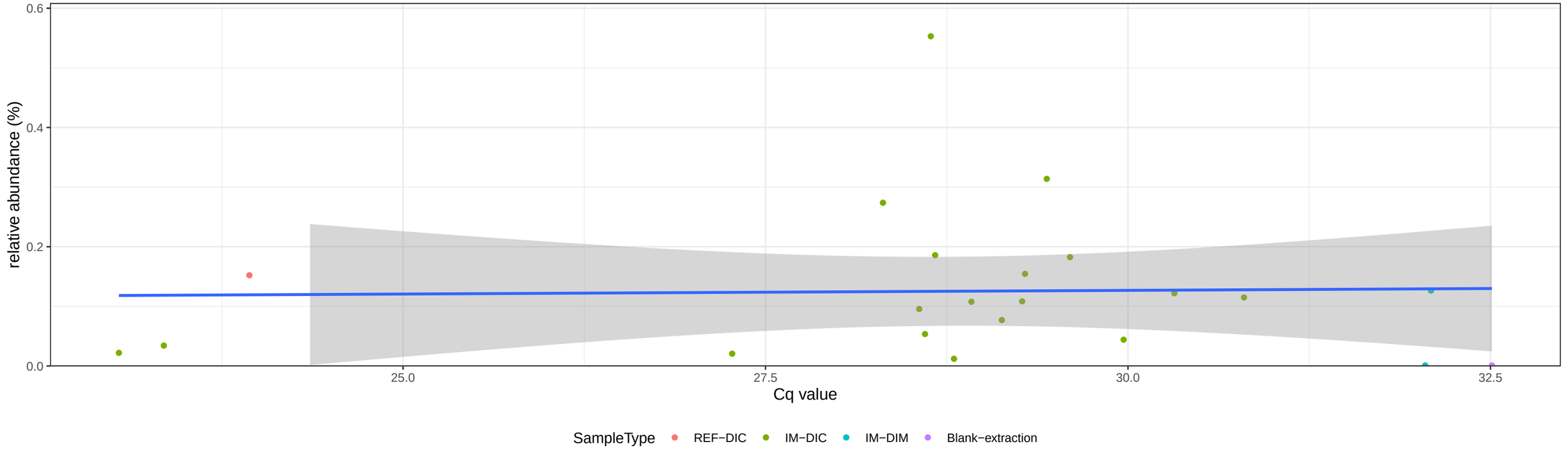


Correlation within the sample type: REF−DIC

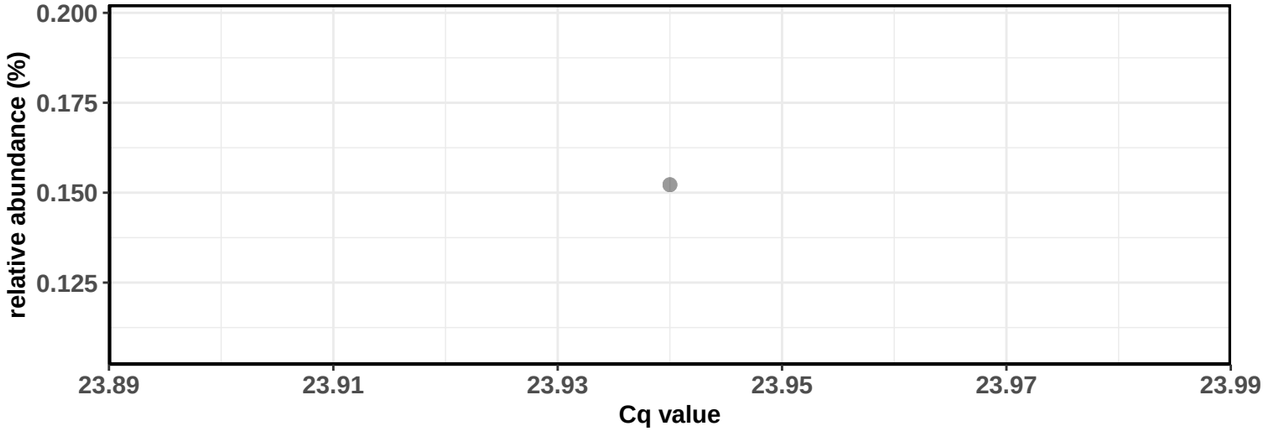


D_0__Bacteria; D_1__Proteobacteria; D_2__Gammaproteobacteria; D_3__Pseudomonadales; D_4__Pseudomonadaceae; D_5__Pseudomonas; D_6__uncultured bacterium

Correlation with all samples

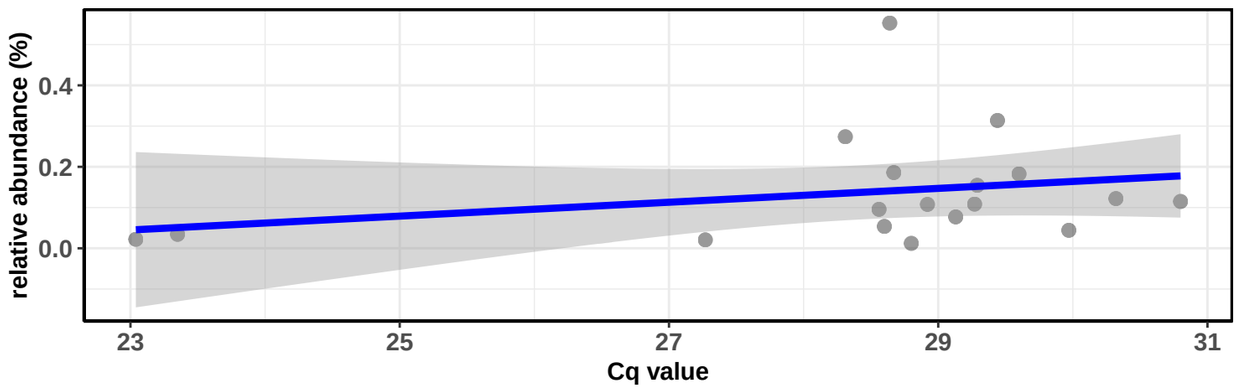


Correlation within the sample type: REF−DIC

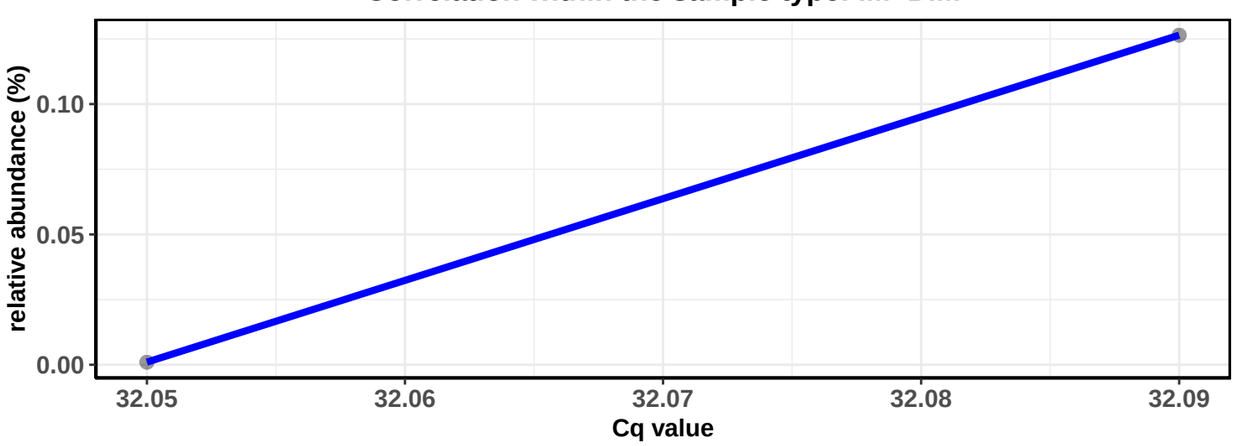


Correlation within the sample type: IM−DIC

$\log_e(S) = 6.433$, $p = 0.145$, $\rho_{Spearman} = 0.358$, $CI_{95\%}$ [−0.131, 0.707], $n = 18$

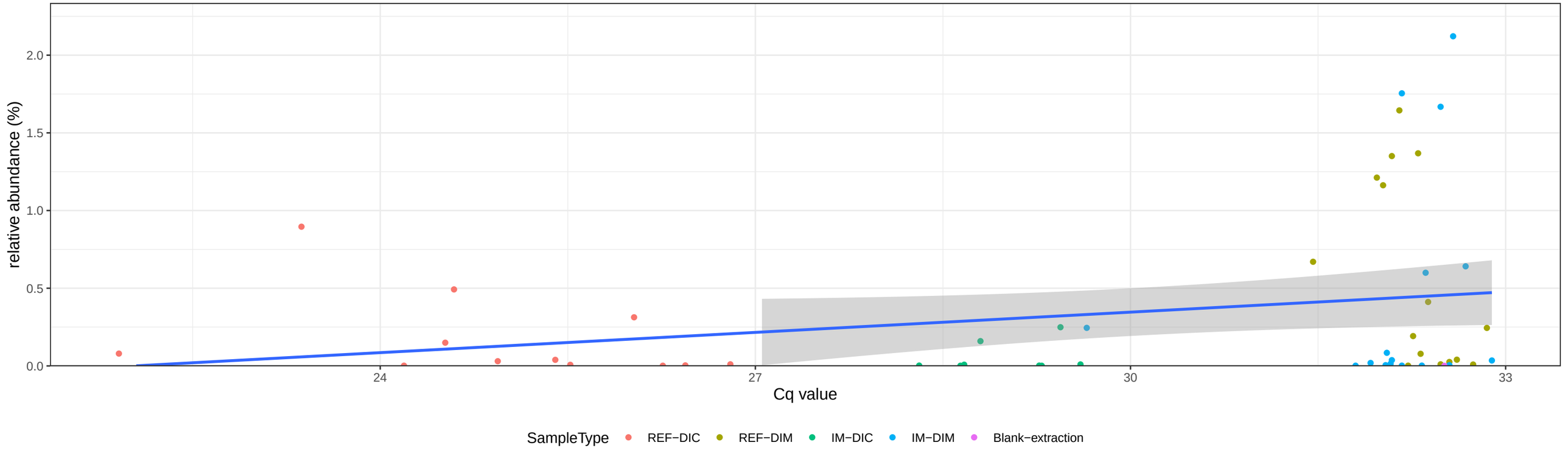


Correlation within the sample type: IM−DIM



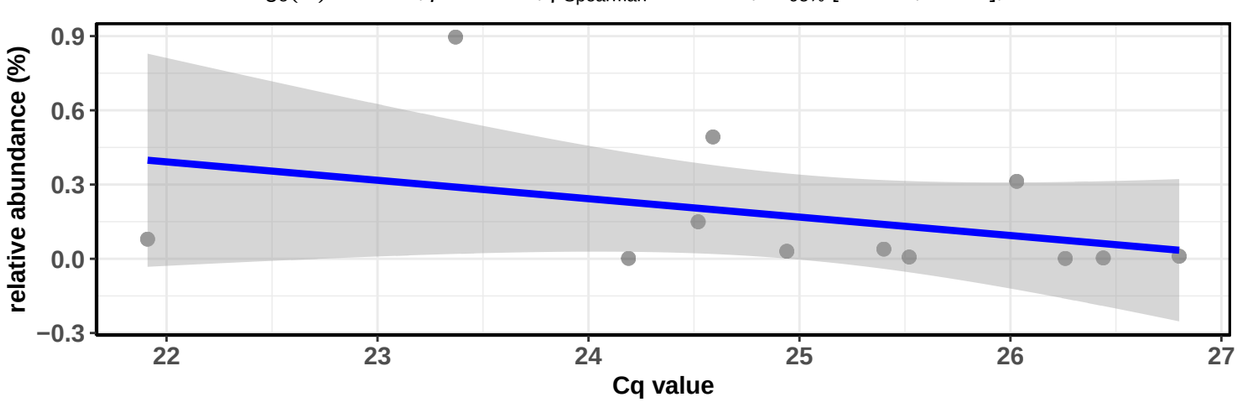
D_0__Bacteria; D_1__Spirochaetes; D_2__Spirochaetia; D_3__Brevinematales; D_4__Brevinemataceae; D_5__Brevinema; D_6__Brevinema andersonii

Correlation with all samples



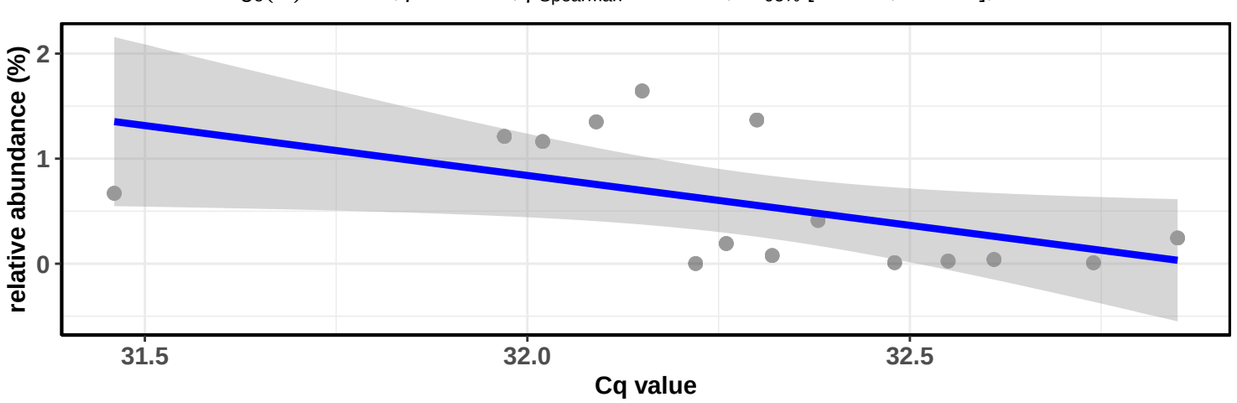
Correlation within the sample type: REF−DIC

$\log_e(S)$ = 6.045, p = 0.118, $\rho_{Spearman}$ = −0.476, $CI_{95\%}$ [−0.824, 0.135], n = 12



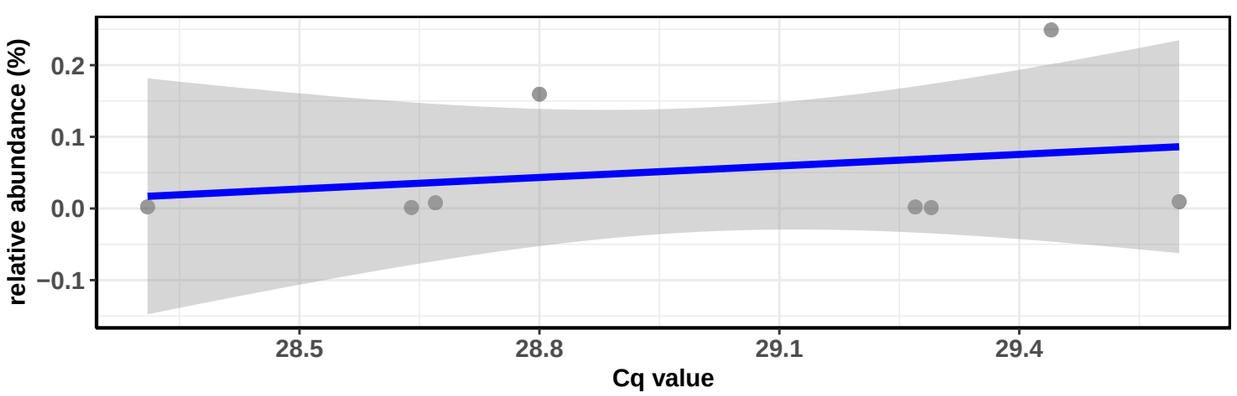
Correlation within the sample type: REF−DIM

$\log_e(S)$ = 6.782, p = 0.025, $\rho_{Spearman}$ = −0.575, $CI_{95\%}$ [−0.840, −0.089], n = 15



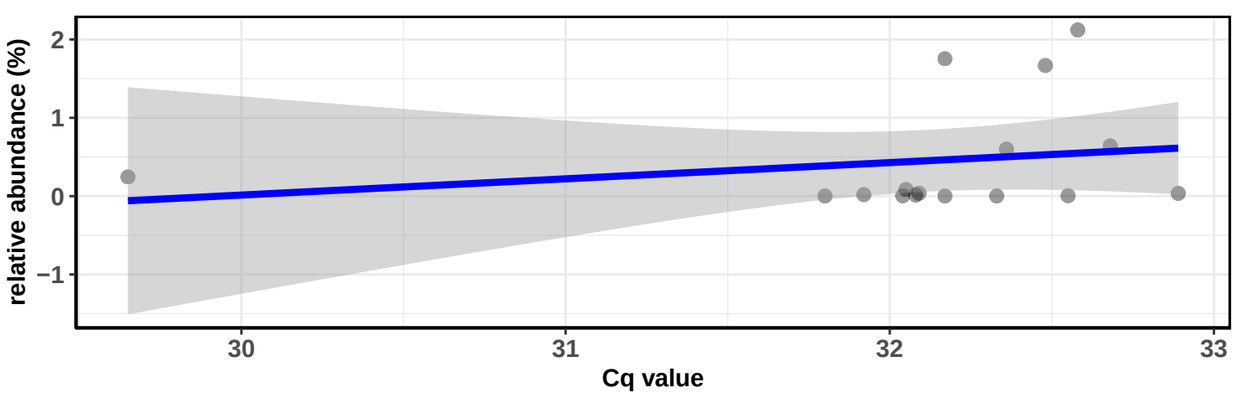
Correlation within the sample type: IM−DIC

$\log_e(S)$ = 4.025, p = 0.420, $\rho_{Spearman}$ = 0.333, $CI_{95\%}$ [−0.485, 0.841], n = 8



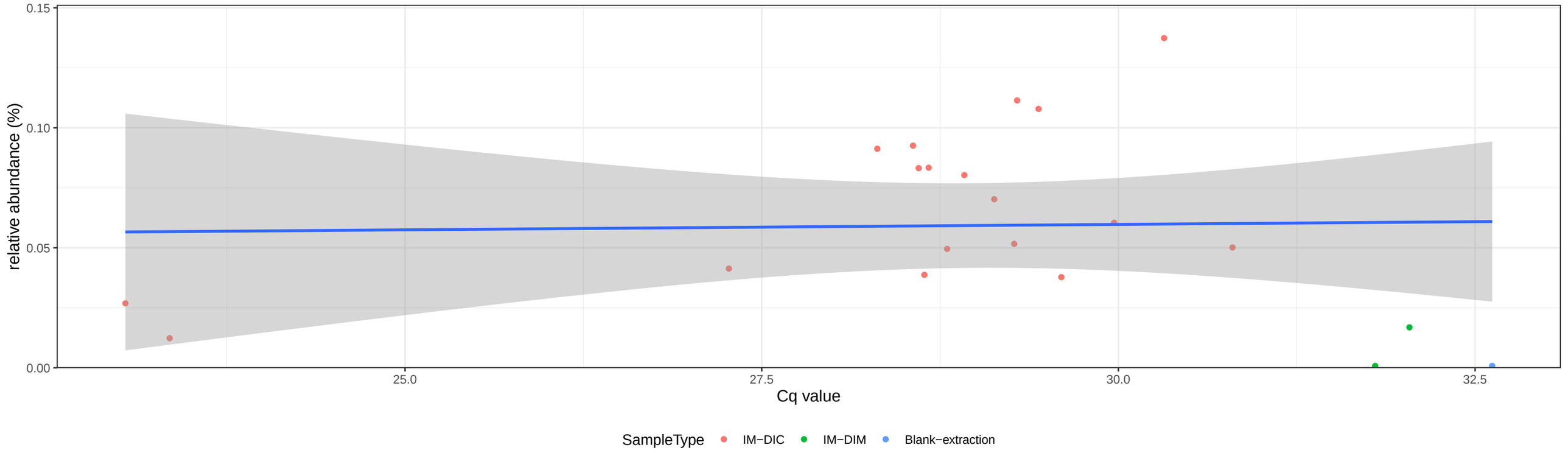
Correlation within the sample type: IM−DIM

$\log_e(S)$ = 6.042, p = 0.145, $\rho_{Spearman}$ = 0.381, $CI_{95\%}$ [−0.141, 0.738], n = 16



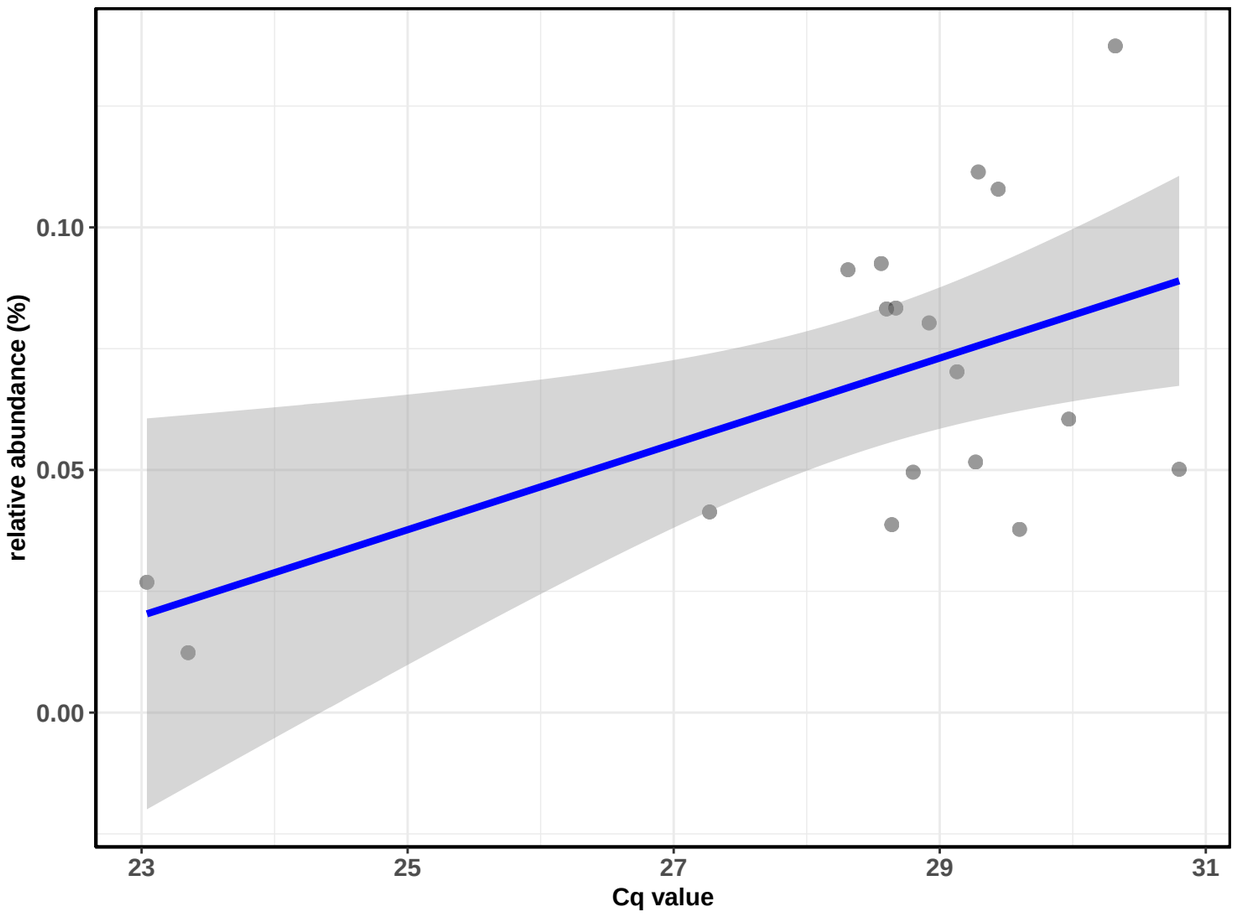
D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Gracilibacillus; Ambiguous_taxa

Correlation with all samples

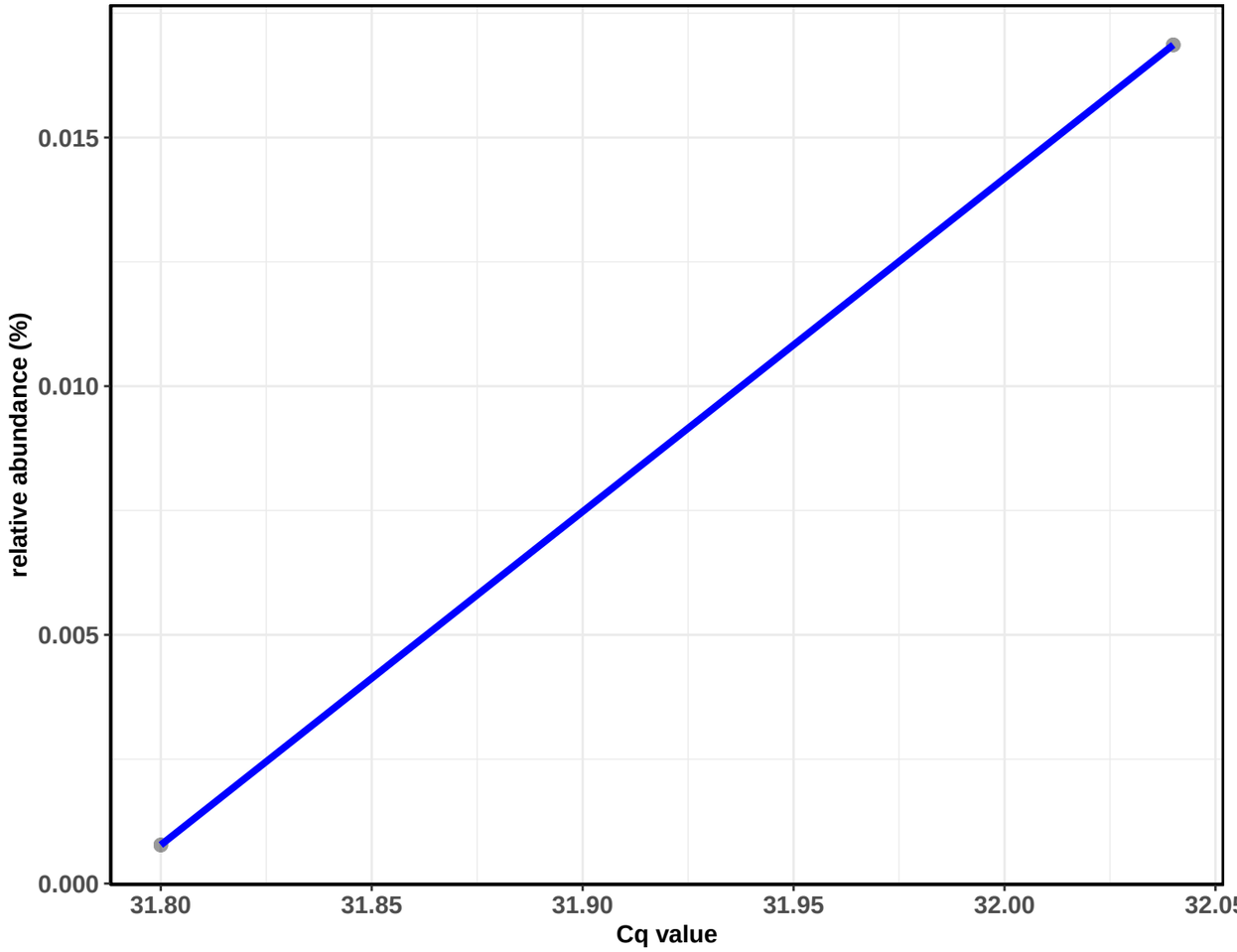


Correlation within the sample type: IM−DIC

$\log_e(S)$ = 6.458, p = 0.165, $\rho_{Spearman}$ = 0.342, $CI_{95\%}$ [−0.149, 0.697], n = 18

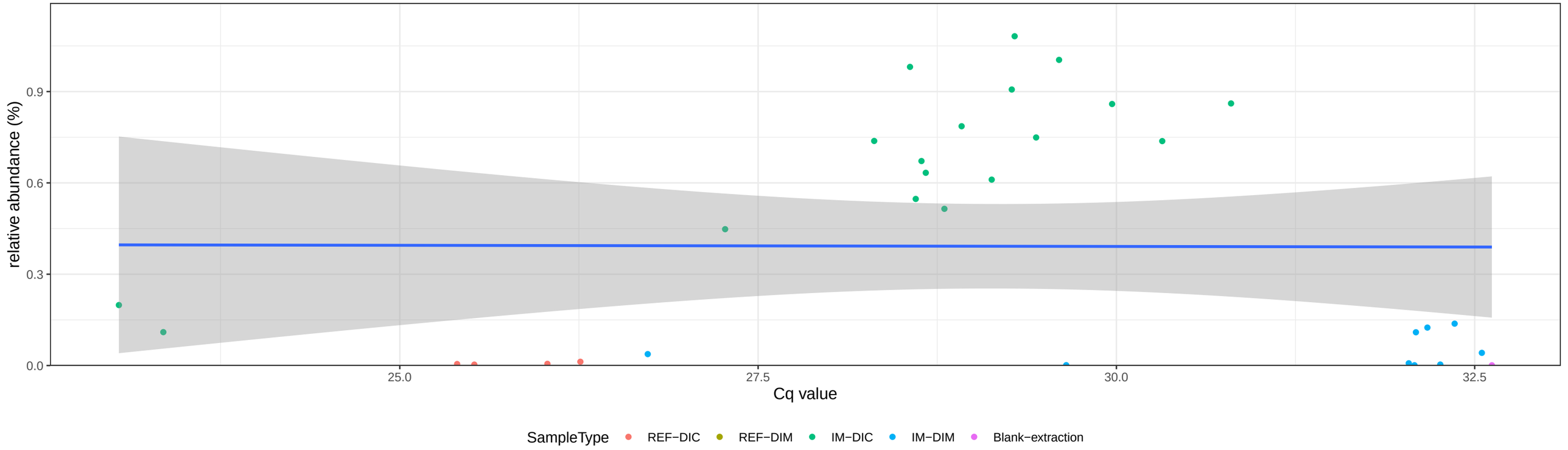


Correlation within the sample type: IM−DIM

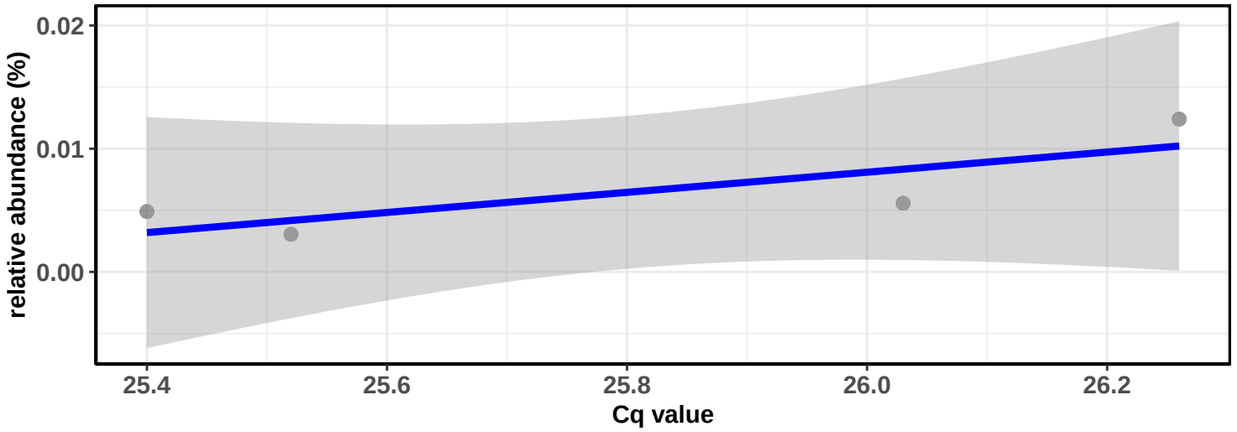


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Oceanobacillus; D_6__Oceanobacillus caeni

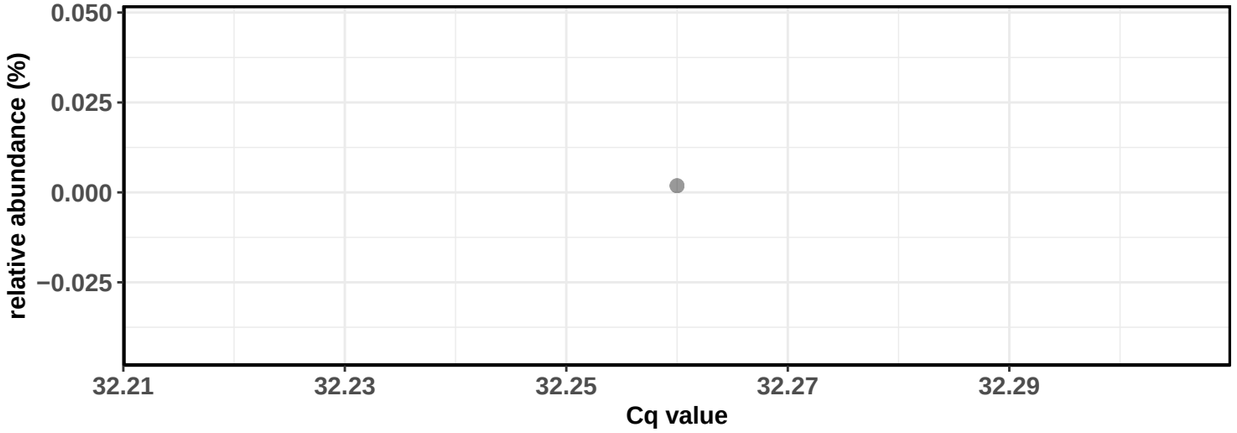
Correlation with all samples



Correlation within the sample type: REF−DIC

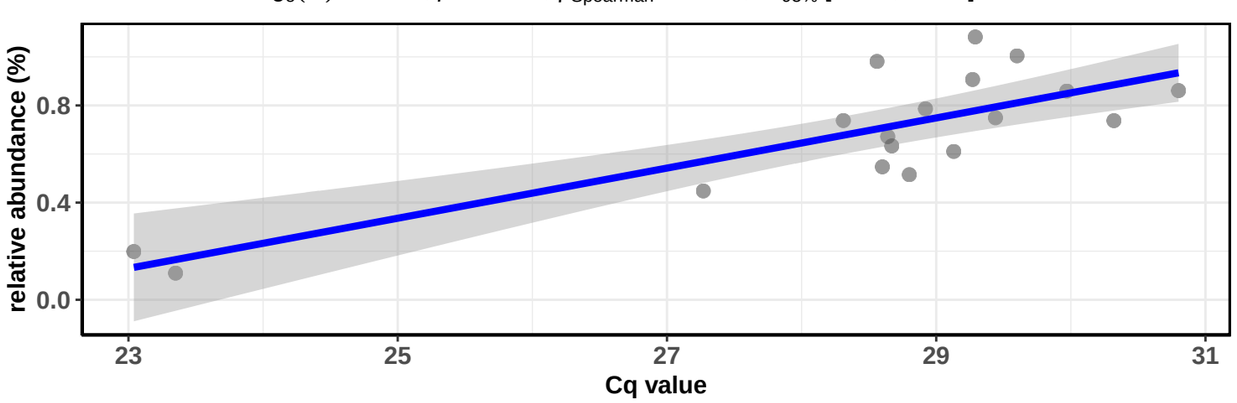


Correlation within the sample type: REF−DIM



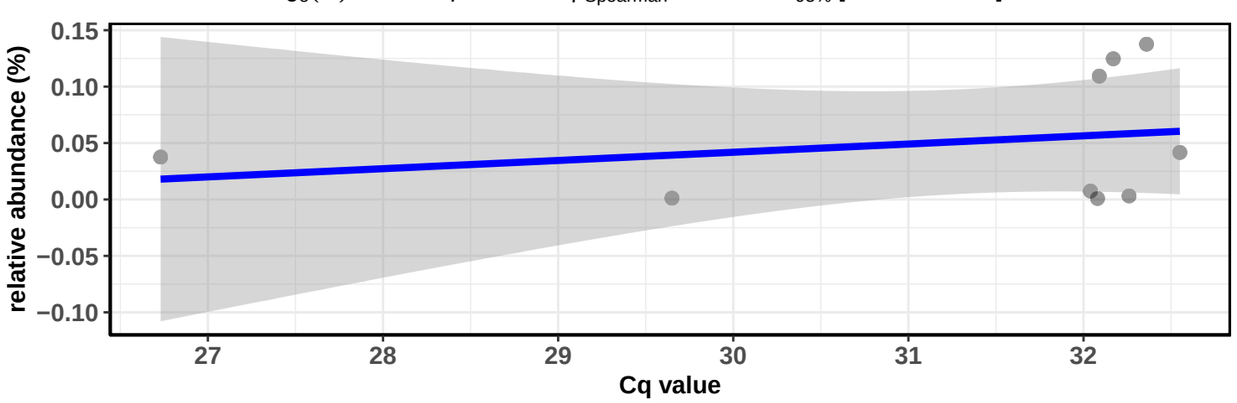
Correlation within the sample type: IM−DIC

$\log_e(S) = 5.864$, $p = 0.004$, $\rho_{Spearman} = 0.637$, $CI_{95\%}$ [0.242, 0.851], $n = 18$



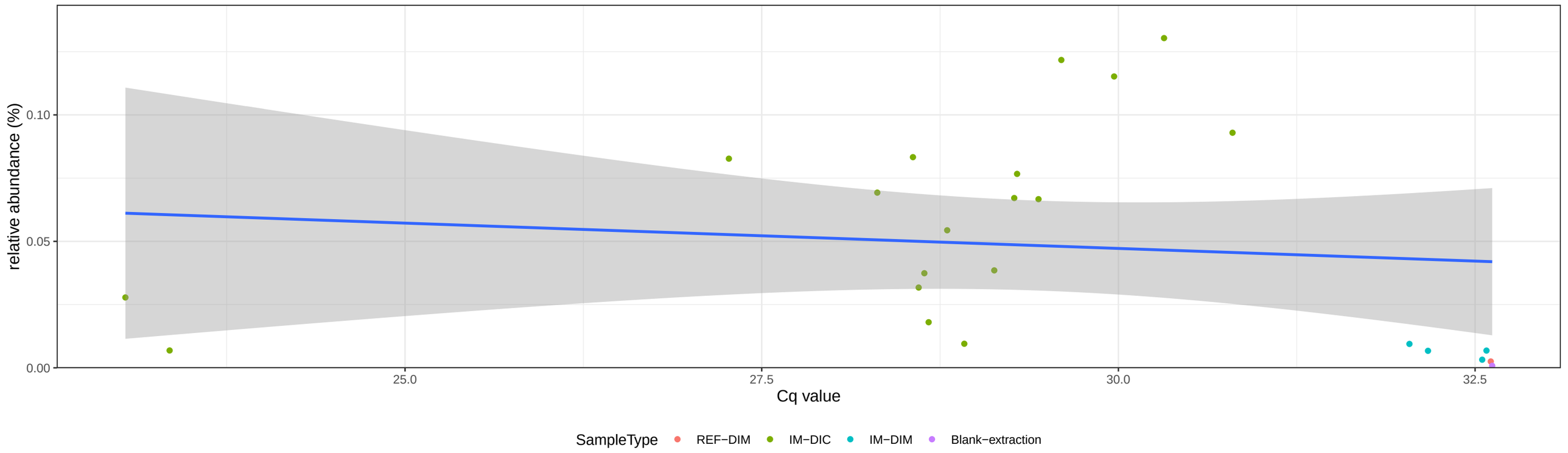
Correlation within the sample type: IM−DIM

$\log_e(S) = 4.094$, $p = 0.170$, $\rho_{Spearman} = 0.500$, $CI_{95\%}$ [−0.246, 0.874], $n = 9$

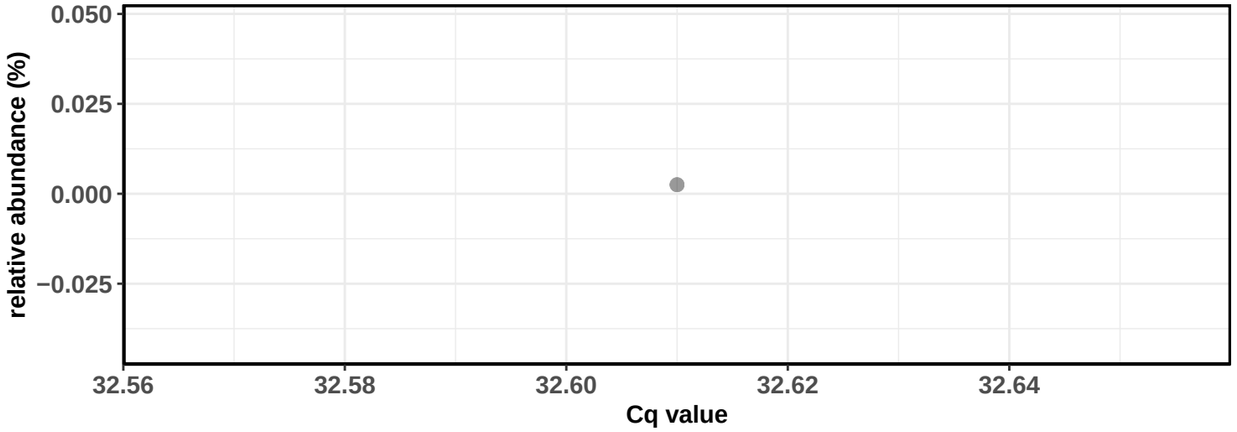


D_0__Bacteria; D_1__Firmicutes; D_2__Bacilli; D_3__Bacillales; D_4__Bacillaceae; D_5__Oceanobacillus; Ambiguous_taxa

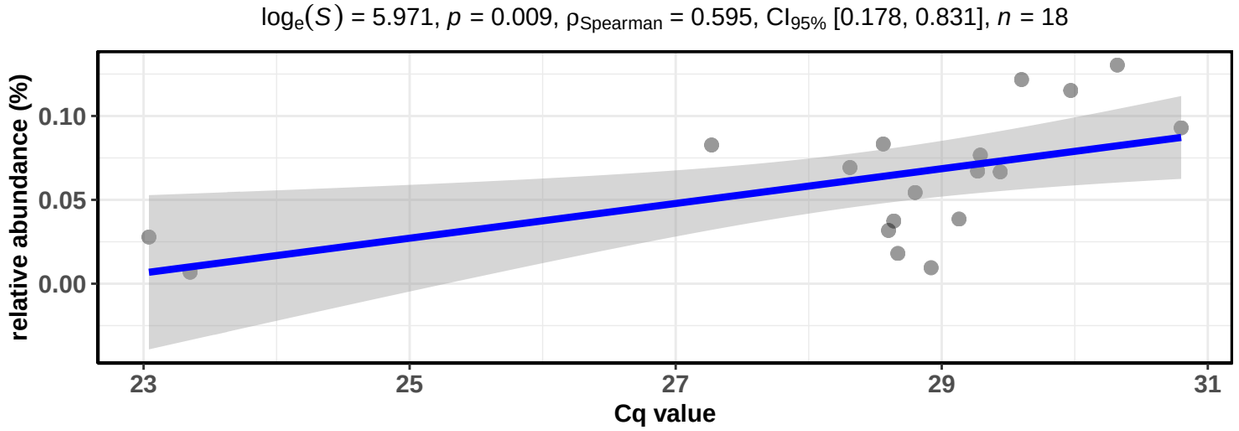
Correlation with all samples



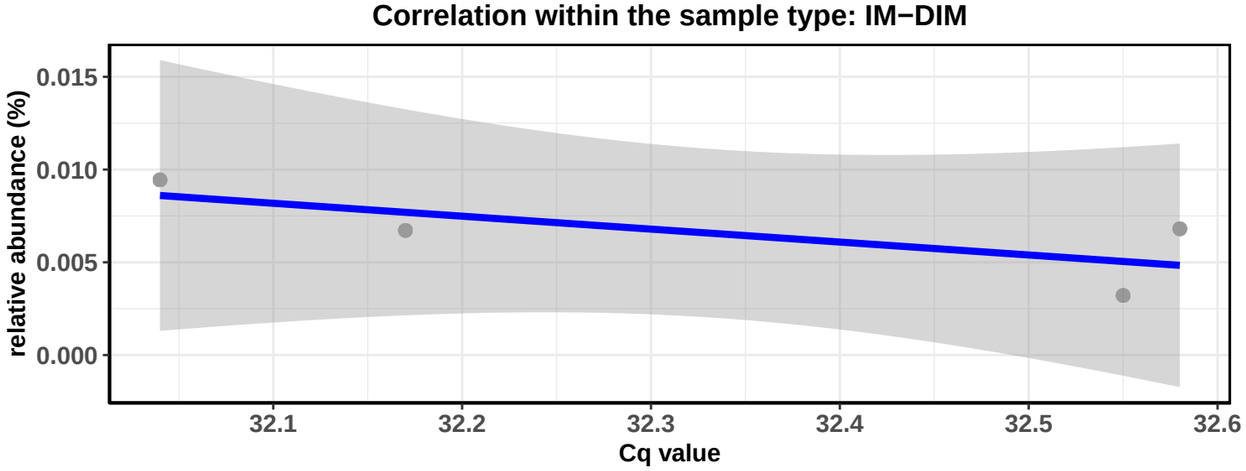
Correlation within the sample type: REF−DIM



Correlation within the sample type: IM−DIC

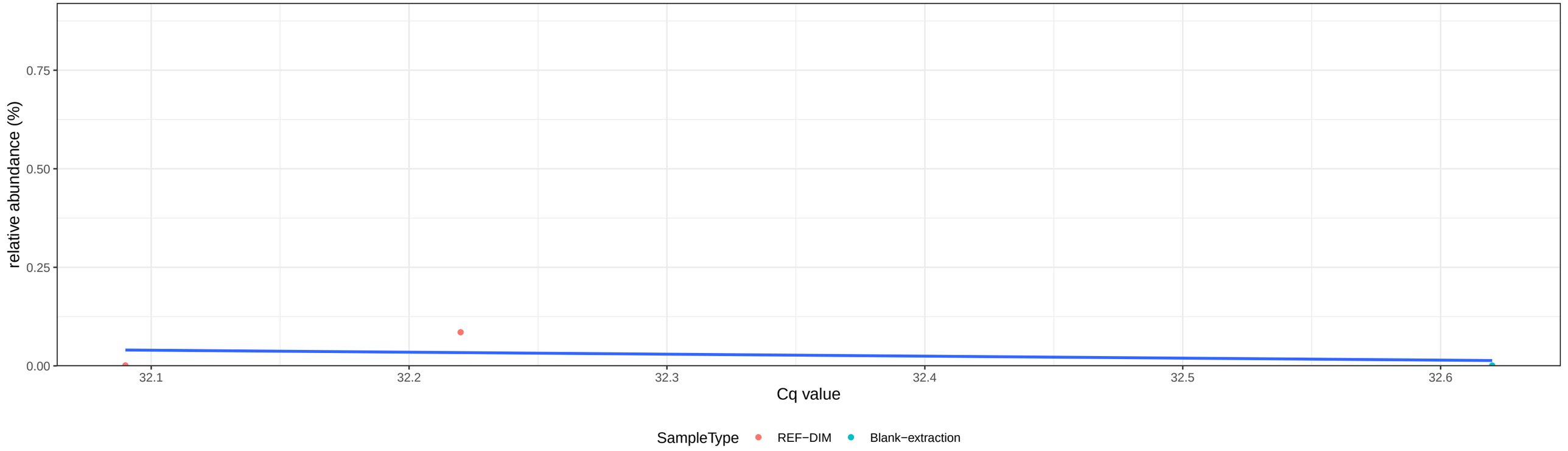


Correlation within the sample type: IM−DIM



D_0__Bacteria; D_1__Actinobacteria; D_2__Actinobacteria; D_3__Propionibacteriales; D_4__Propionibacteriaceae; D_5__Cutibacterium

Correlation with all samples



Correlation within the sample type: REF−DIM