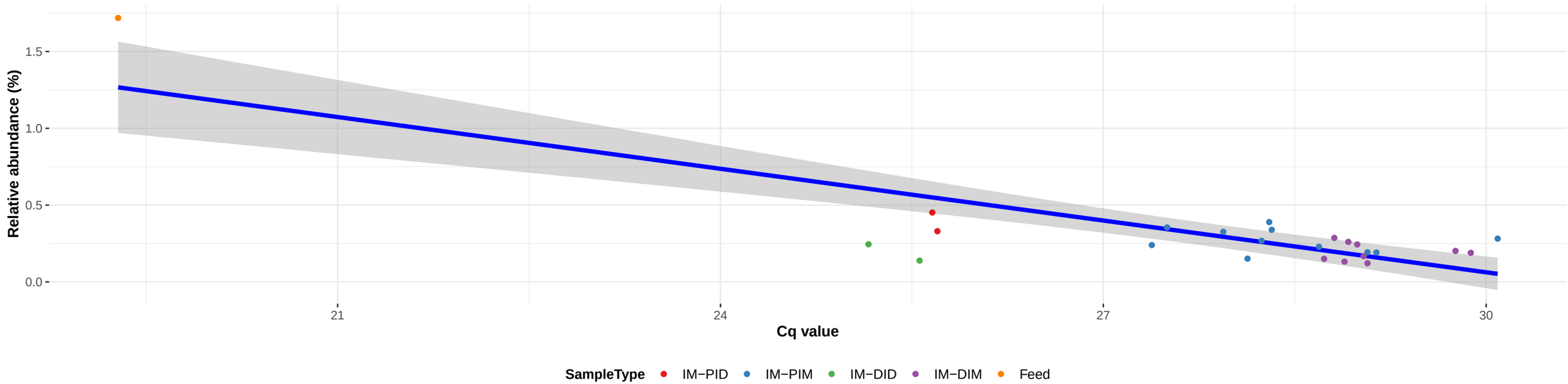
k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae 1; g__Clostridium sensu stricto 1; s__Clostridium perfringens

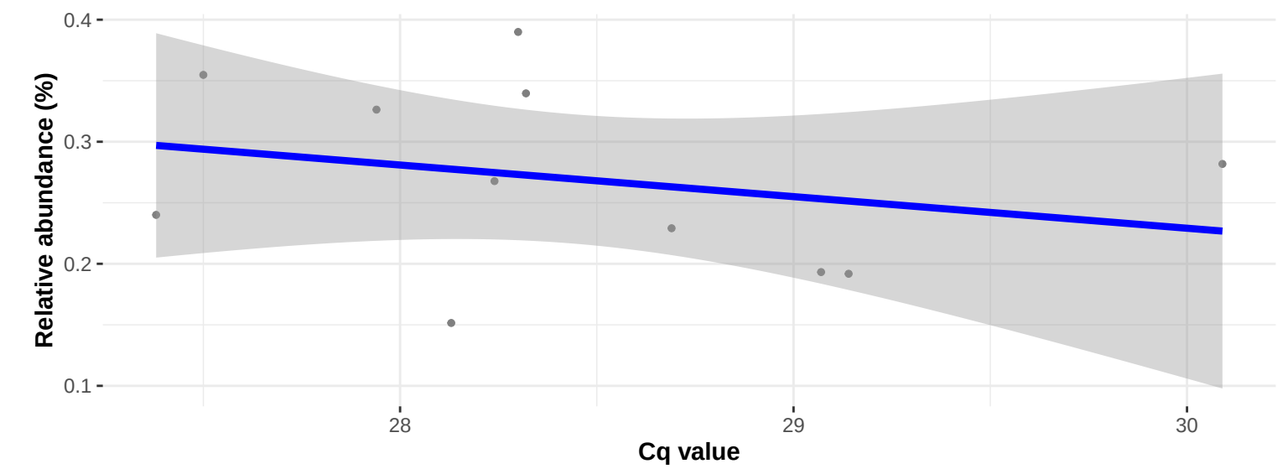
Correlation with all samples

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



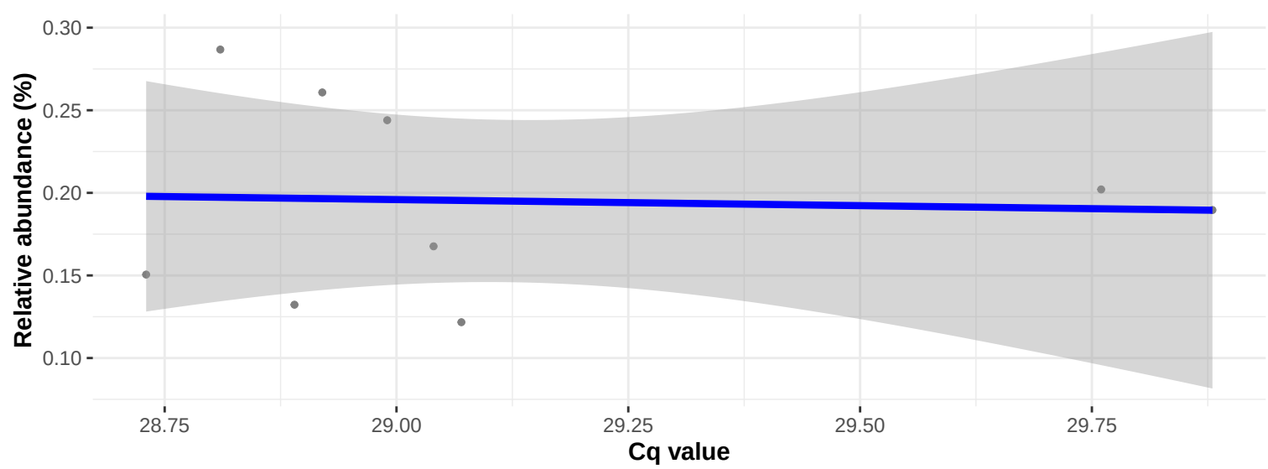
Correlation within: IM−PIM

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

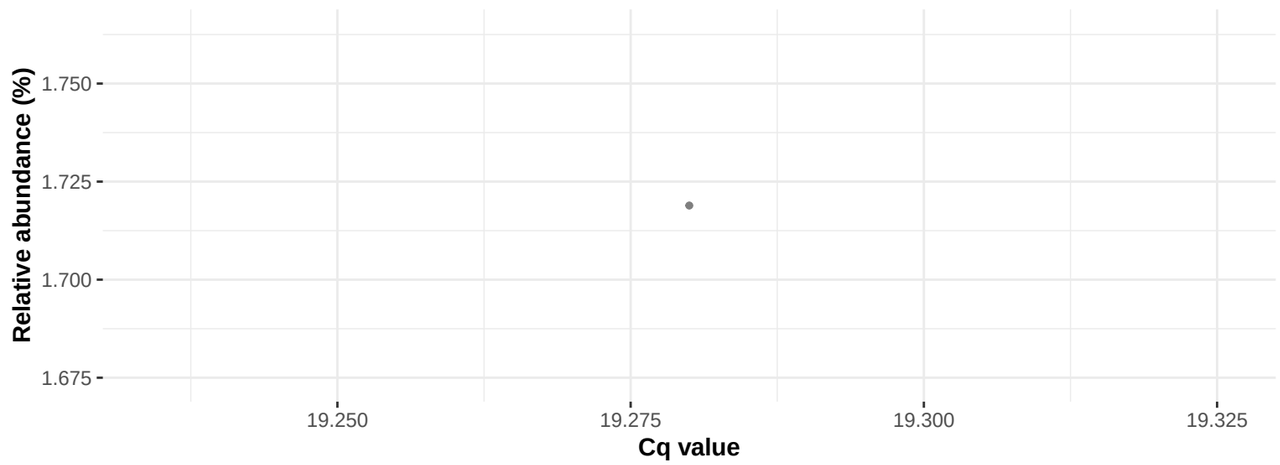


Correlation within: IM−DIM

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



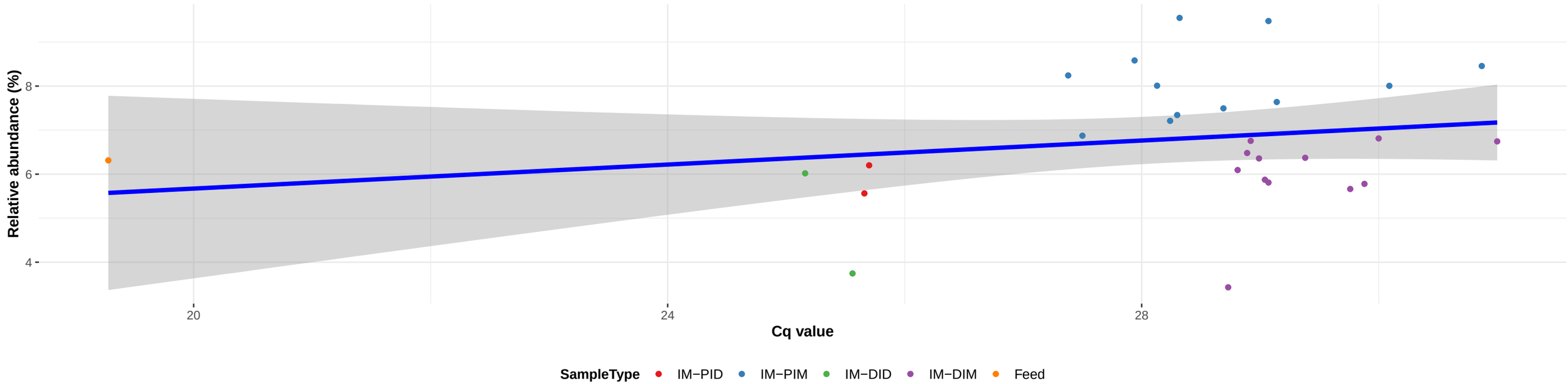
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; NA; NA; NA

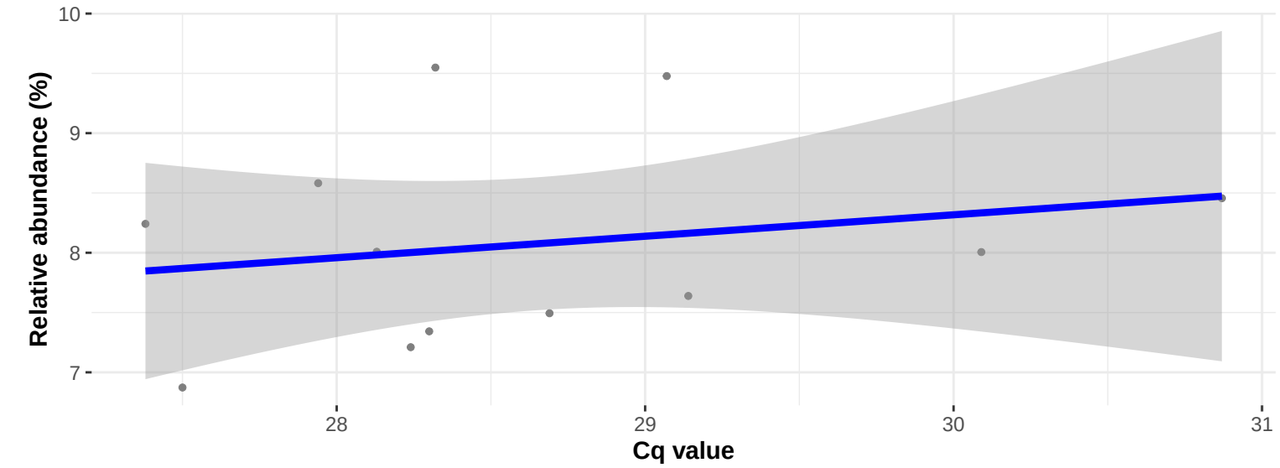
Correlation with all samples

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



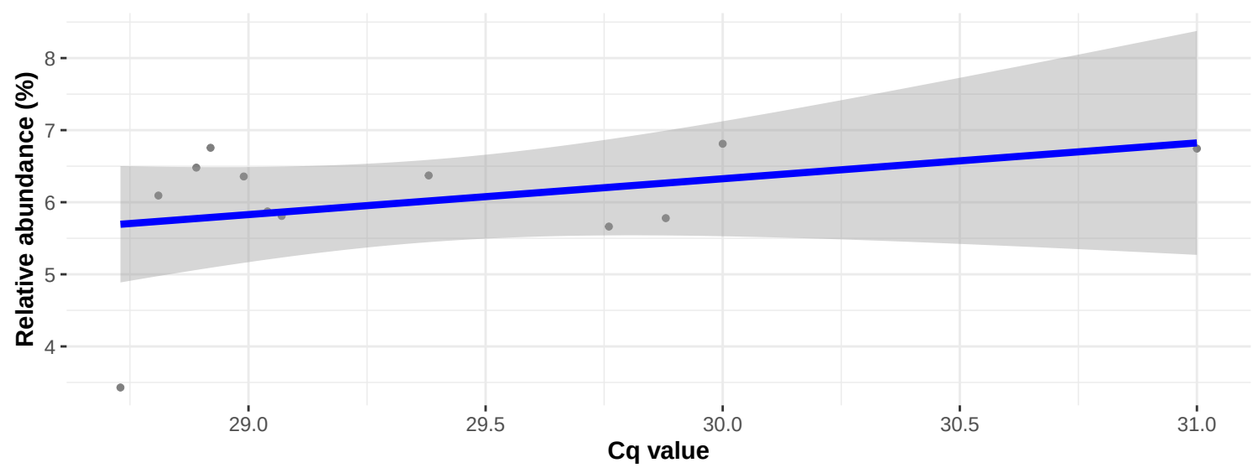
Correlation within: IM−PIM

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

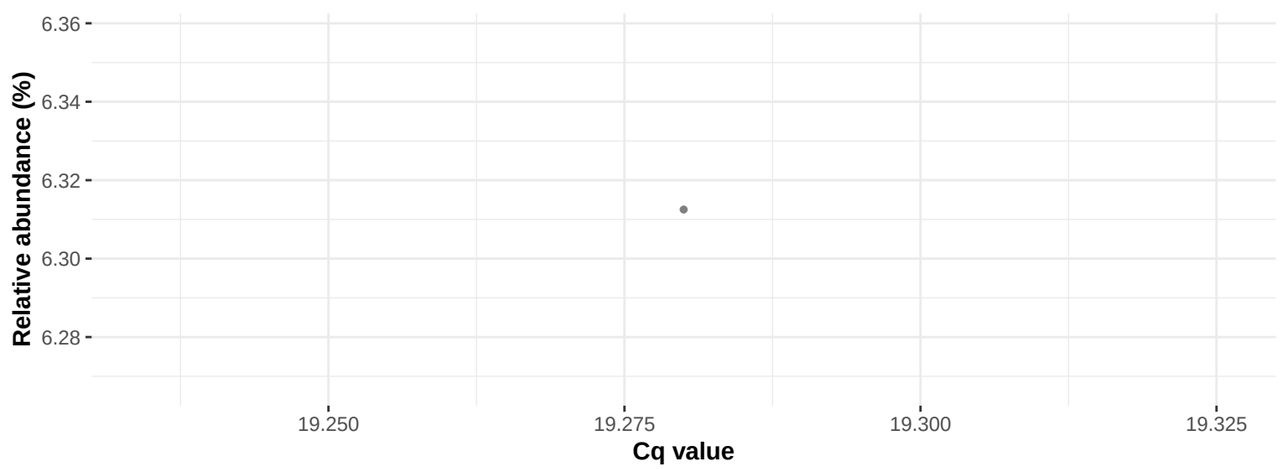


Correlation within: IM−DIM

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



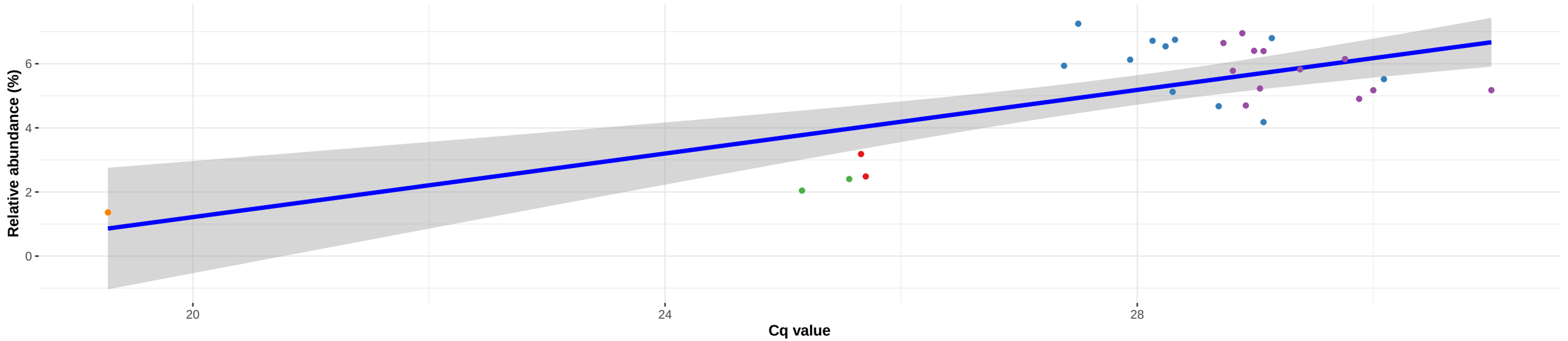
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium aurimucosum ATCC 700975

Correlation with all samples

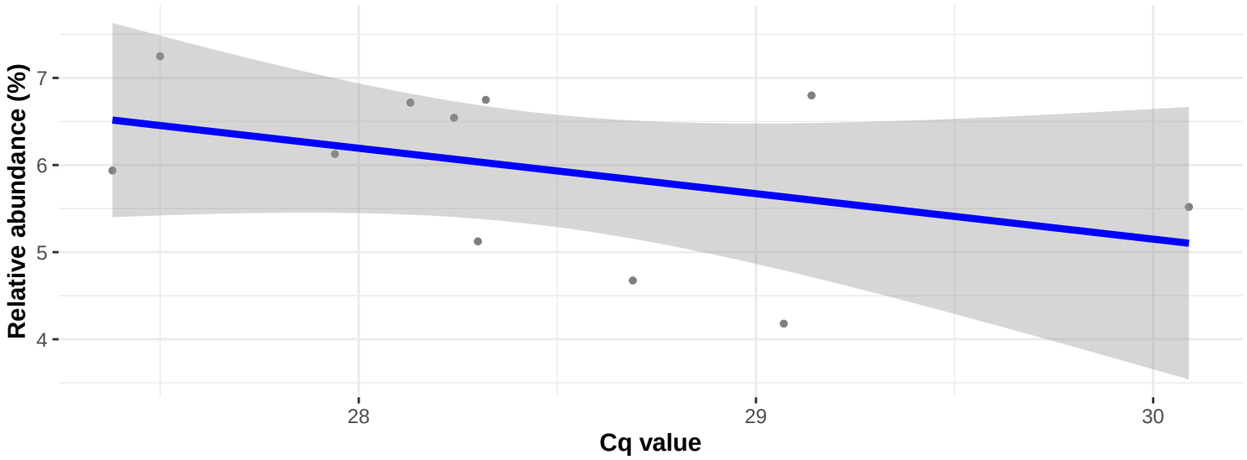
$\log_e(S)$ = 7.928, p = 0.217, $\hat{\rho}_{Spearman}$ = 0.241, $CI_{95\%}$ [−0.157, 0.571], n_{pairs} = 28



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

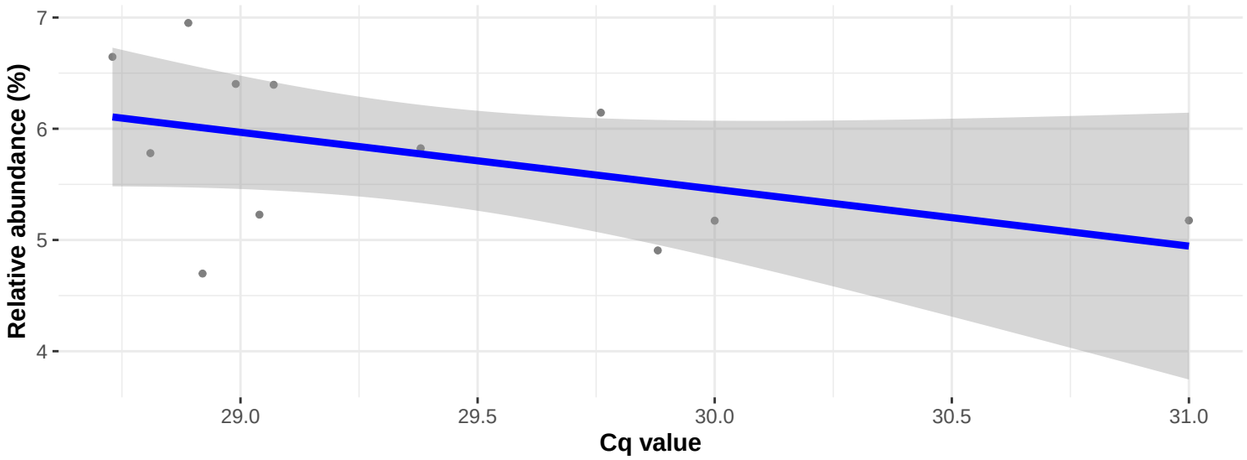
Correlation within: IM−PIM

$\log_e(S)$ = 5.663, p = 0.355, $\hat{\rho}_{Spearman}$ = −0.309, $CI_{95\%}$ [−0.775, 0.375], n_{pairs} = 11

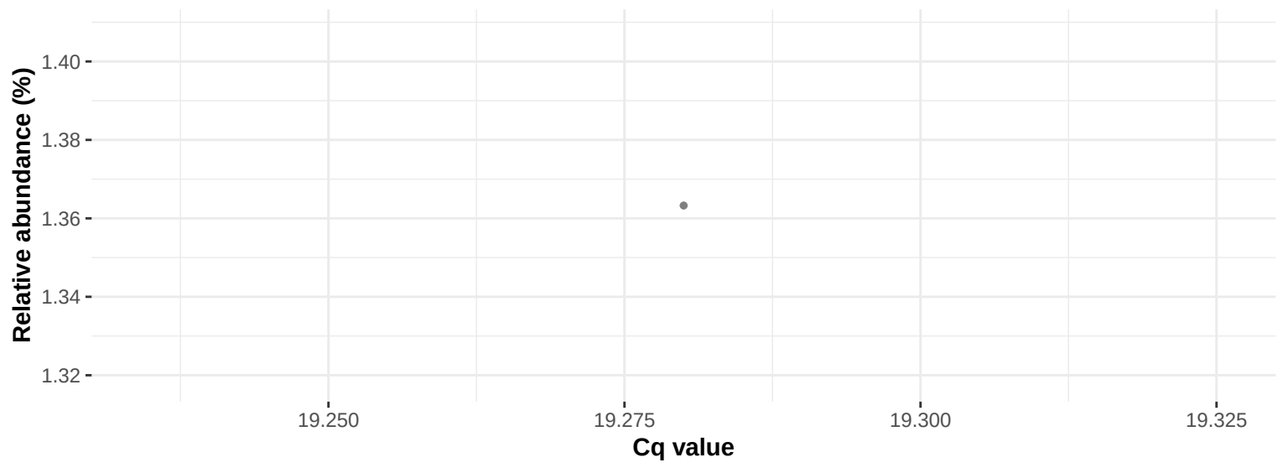


Correlation within: IM−DIM

$\log_e(S)$ = 6.064, p = 0.095, $\hat{\rho}_{Spearman}$ = −0.503, $CI_{95\%}$ [−0.842, 0.118], n_{pairs} = 12



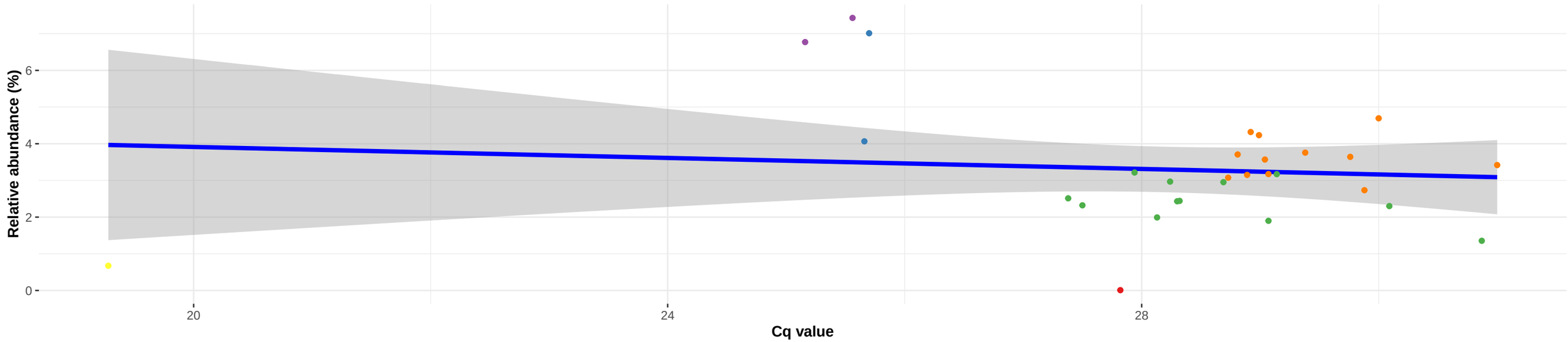
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

Correlation with all samples

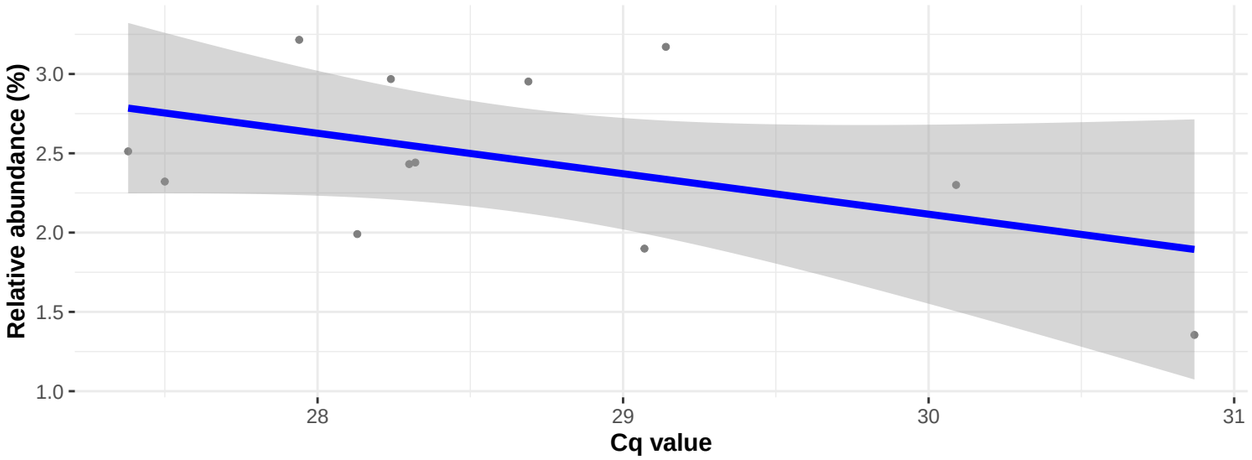
$\log_e(S)$ = 8.441, p = 0.872, $\hat{\rho}_{Spearman}$ = −0.031, $CI_{95\%}$ [−0.396, 0.343], n_{pairs} = 30



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

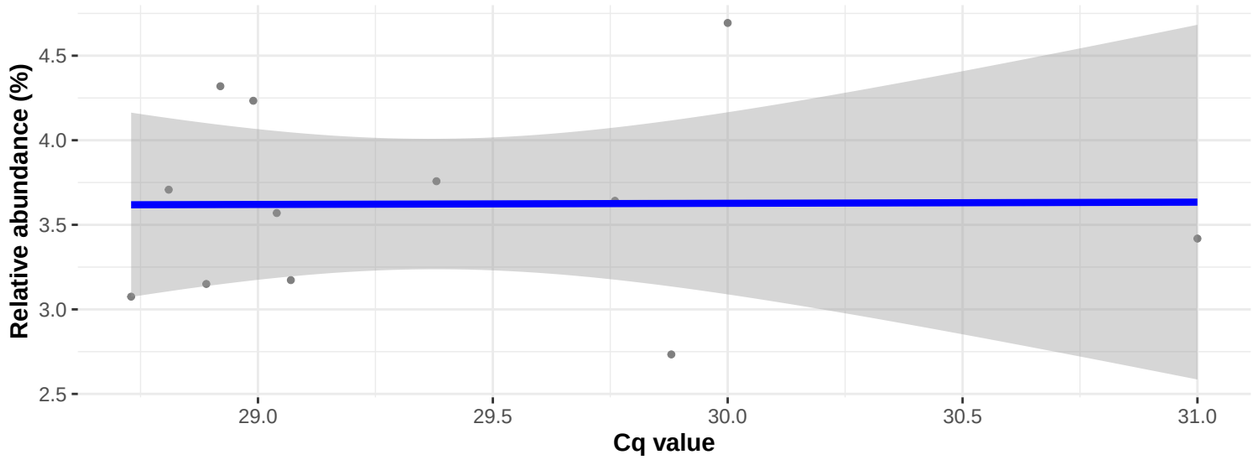
Correlation within: IM−PIM

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

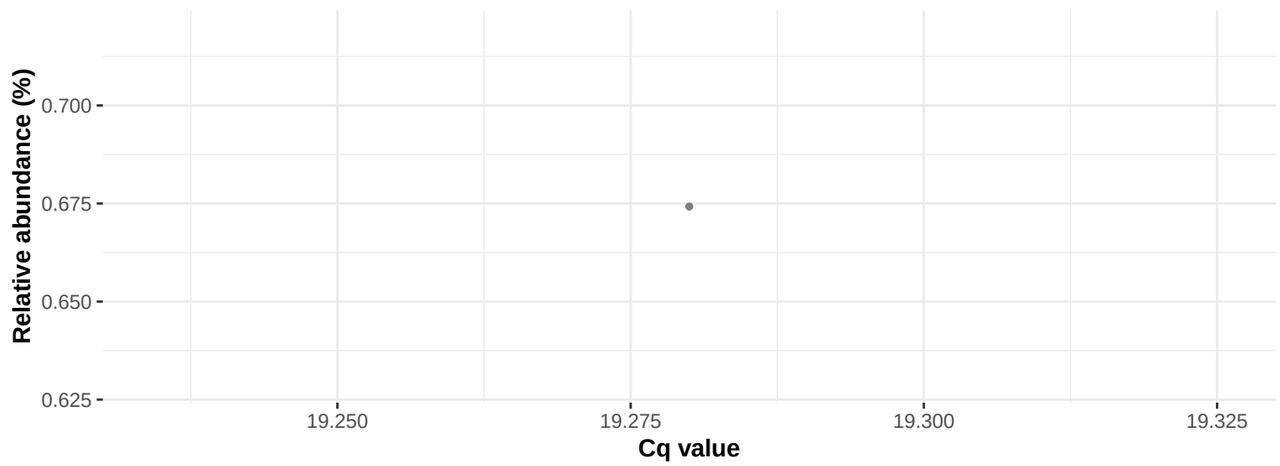


Correlation within: IM−DIM

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



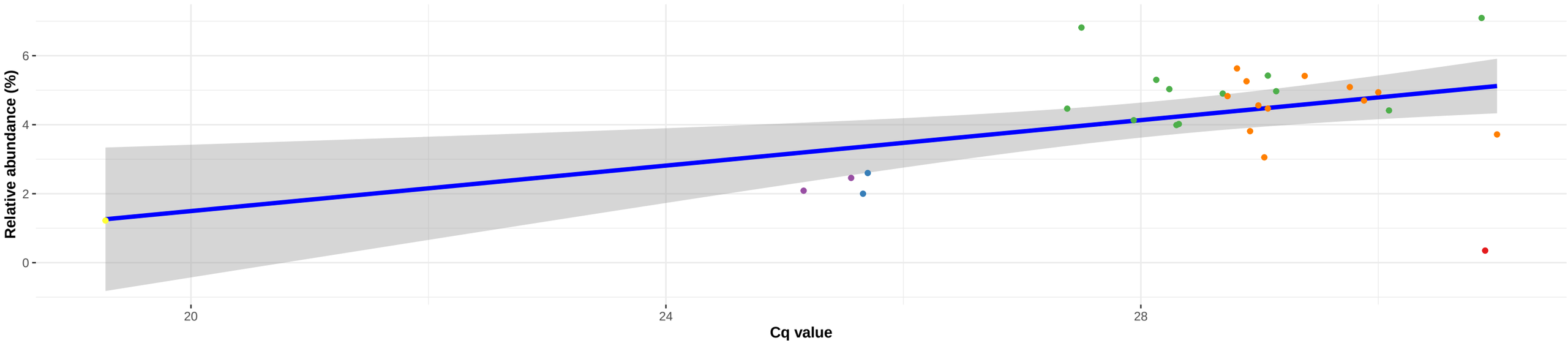
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

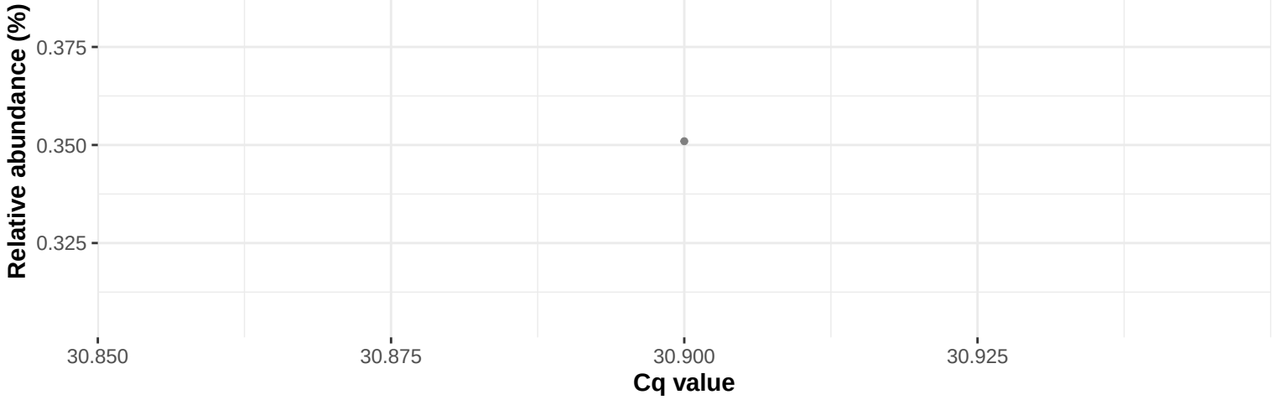
Correlation with all samples

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



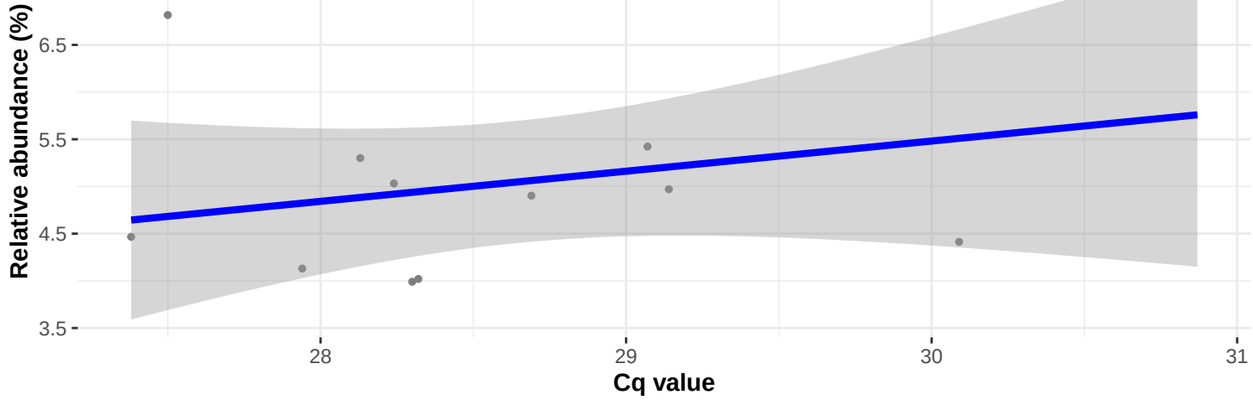
SampleType REF−PIM IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



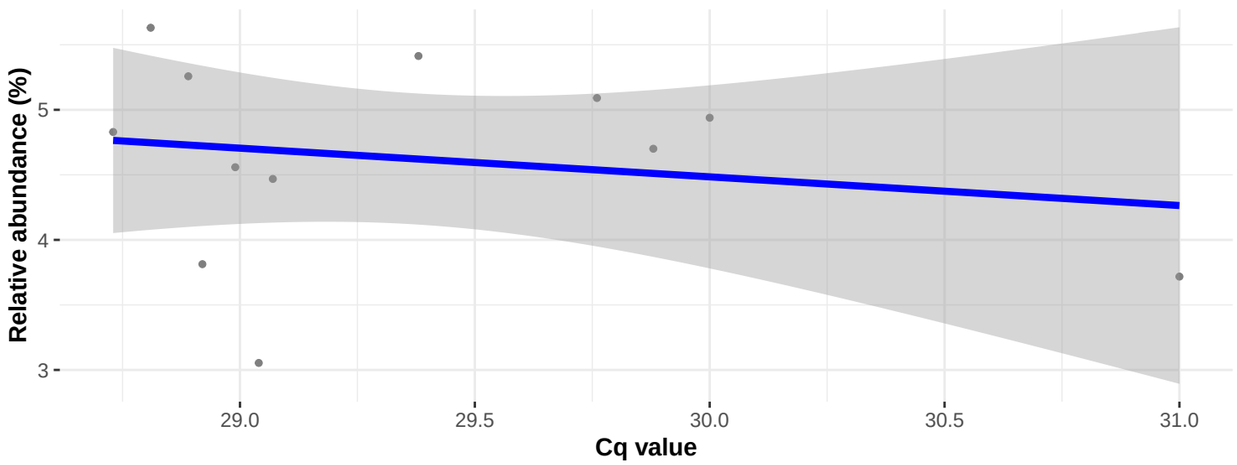
Correlation within: IM−PIM

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

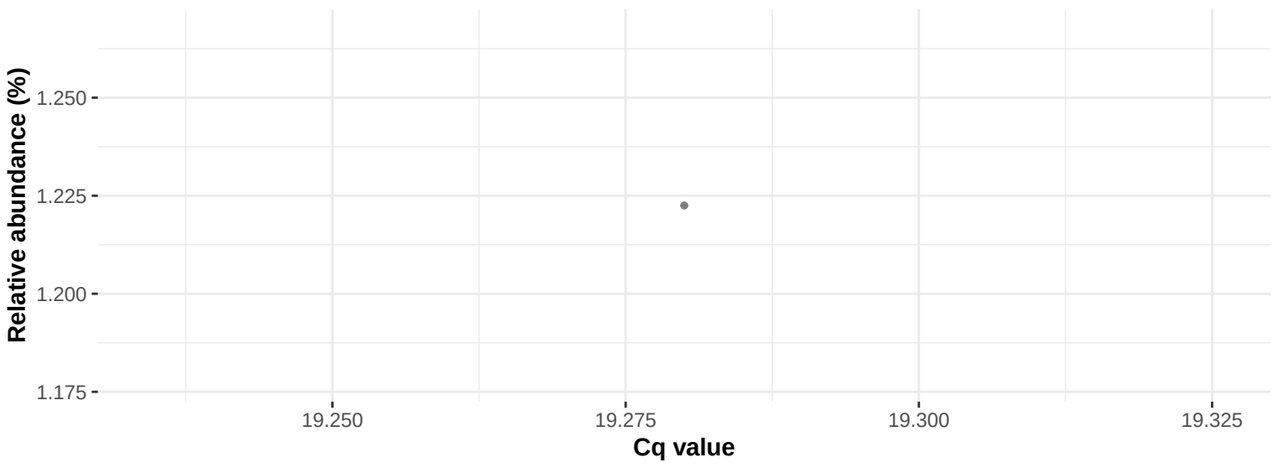


Correlation within: IM−DIM

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



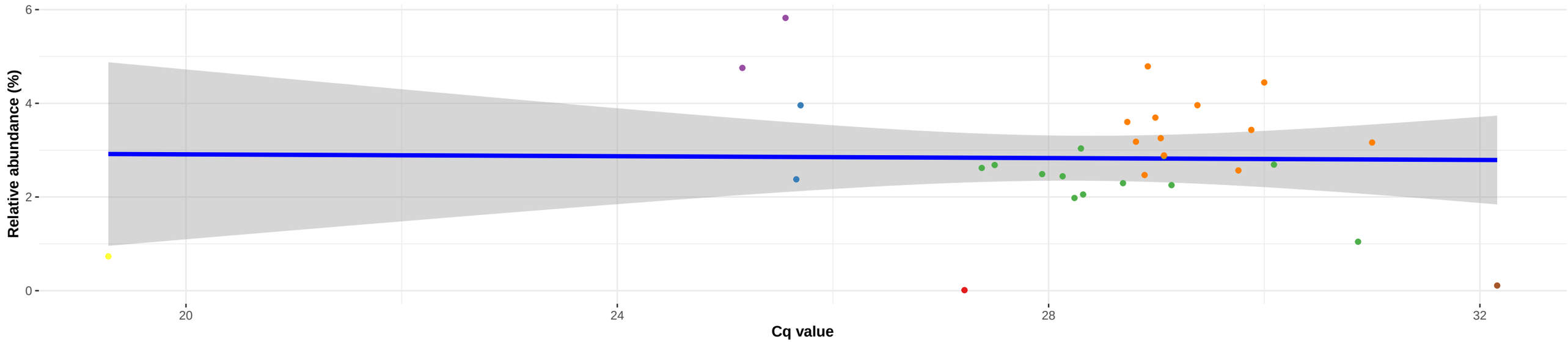
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa

Correlation with all samples

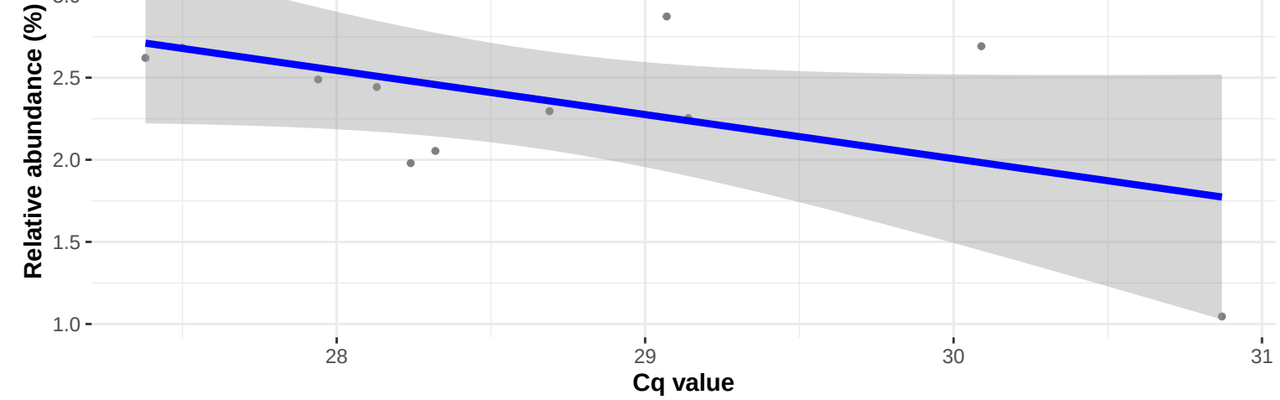
$\log_e(S)$ = 8.471, p = 0.840, $\hat{\rho}_{Spearman}$ = 0.038, $CI_{95\%}$ [−0.331, 0.396], n_{pairs} = 31



SampleType REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed Water

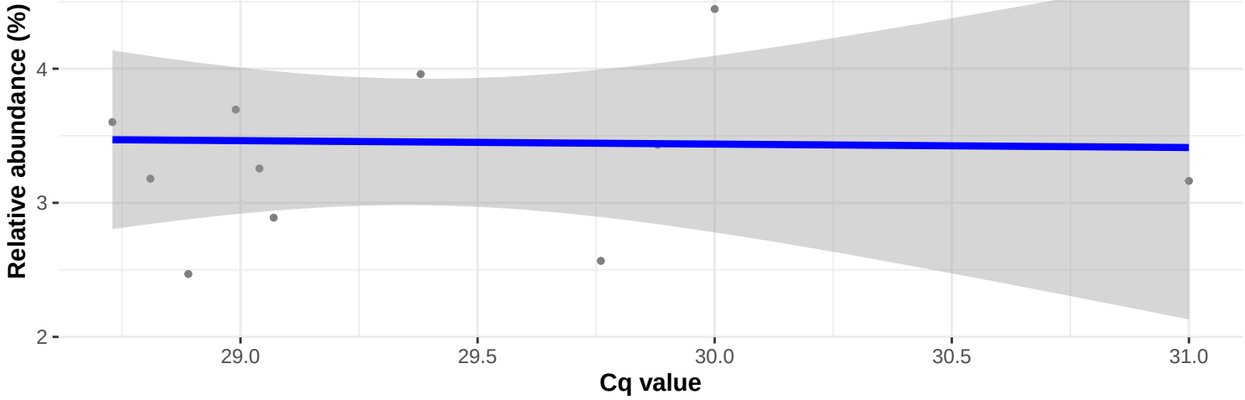
Correlation within: IM−PIM

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

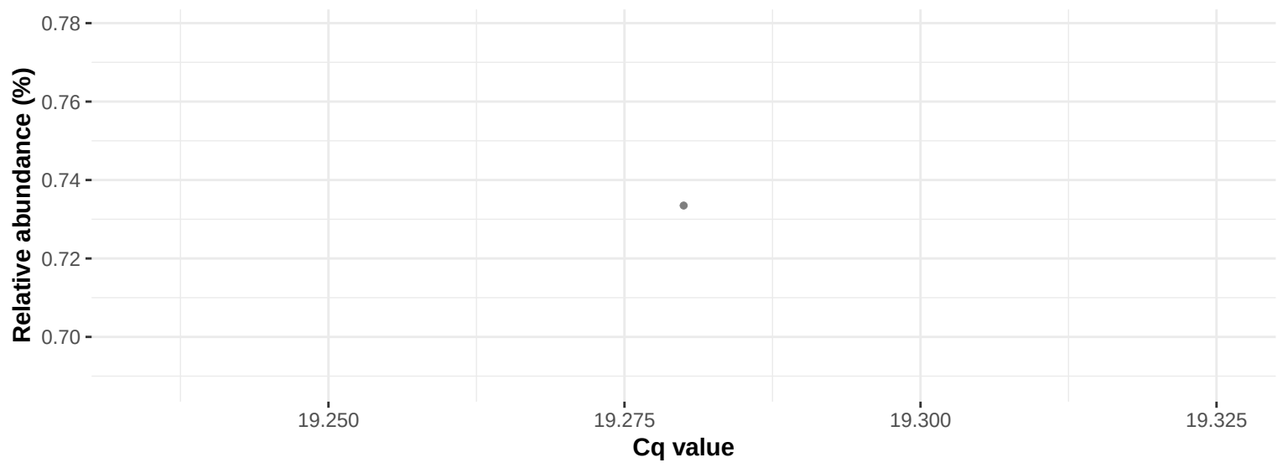


Correlation within: IM−DIM

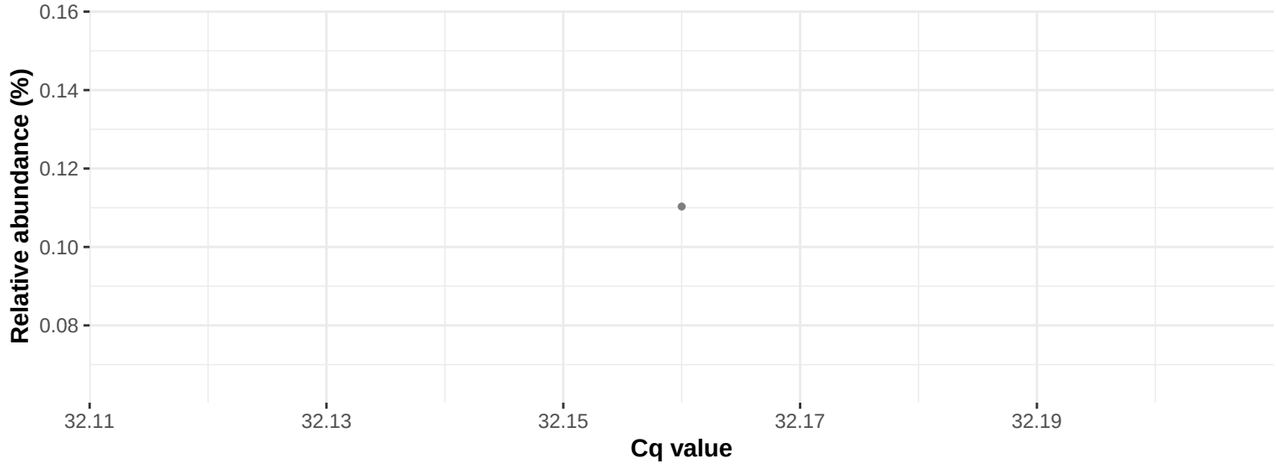
$\log_e(S)$ = 5.649, p = 0.983, $\hat{\rho}_{Spearman}$ = 0.007, $CI_{95\%}$ [−0.582, 0.591], n_{pairs} = 12



Correlation within: Feed



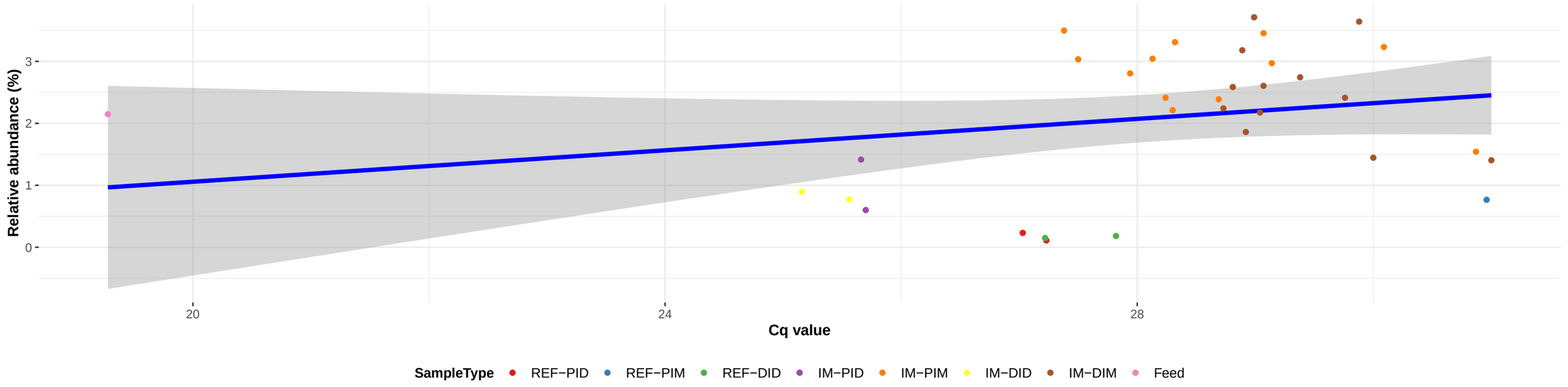
Correlation within: Water



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Brevibacteriaceae; g__Brevibacterium; NA

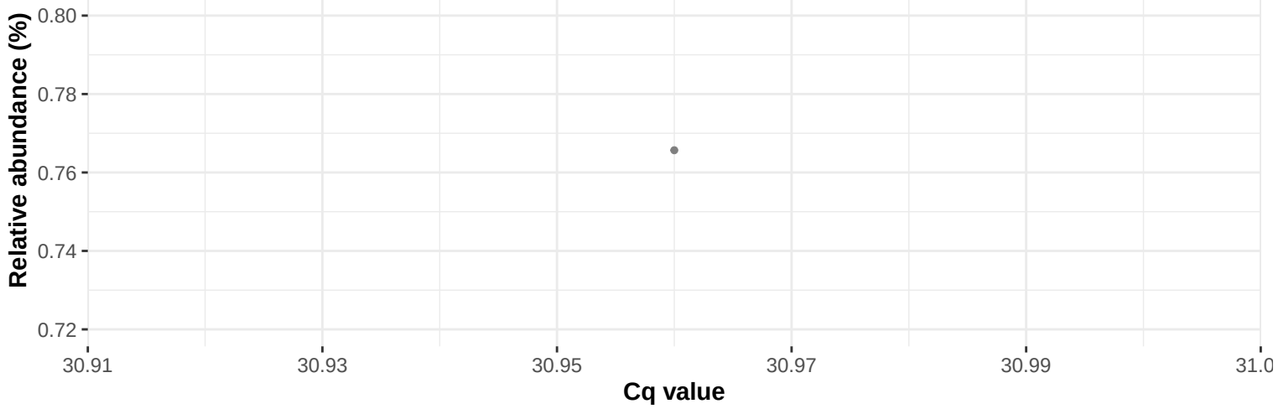
Correlation with all samples

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



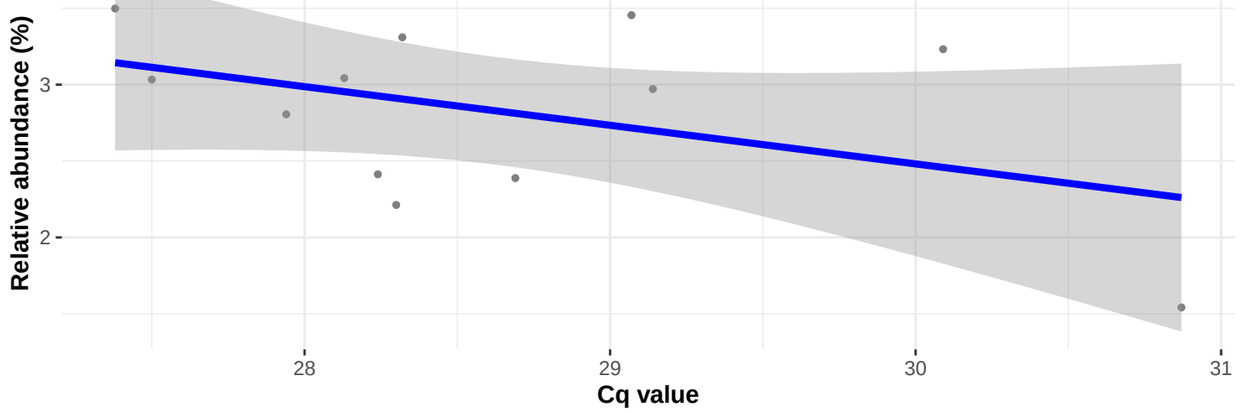
SampleType REF−PID REF−PIM REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



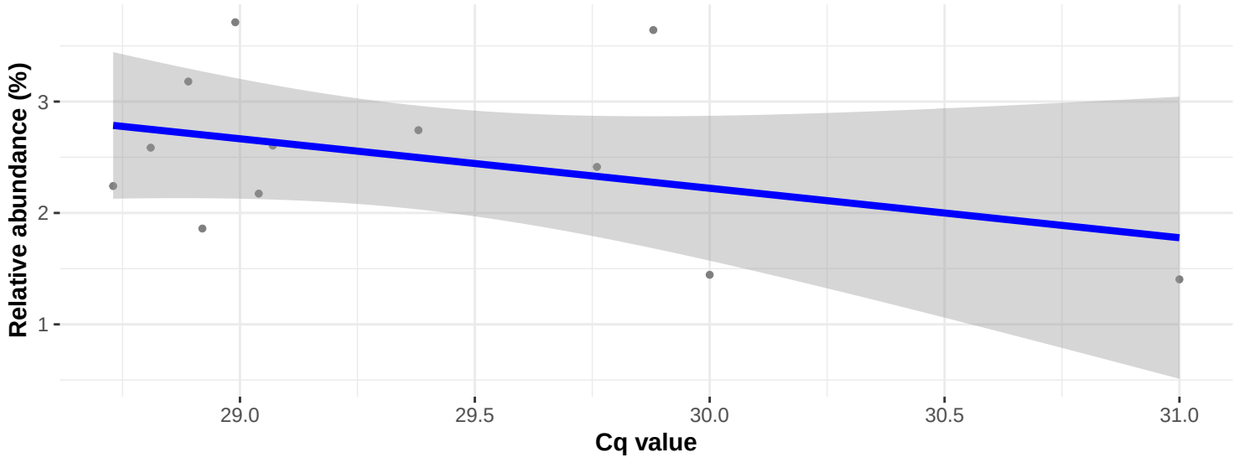
Correlation within: IM−PIM

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

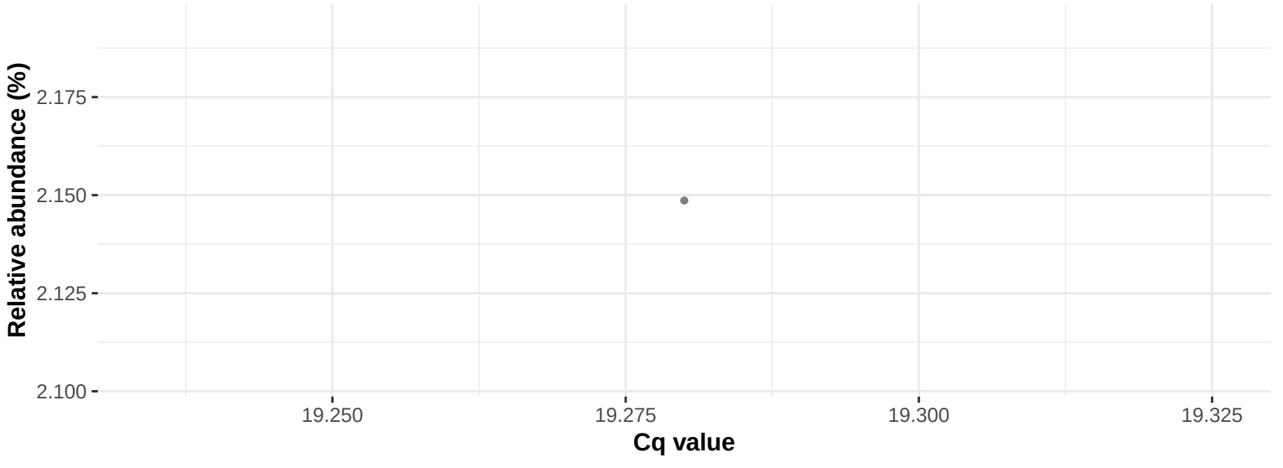


Correlation within: IM−DIM

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



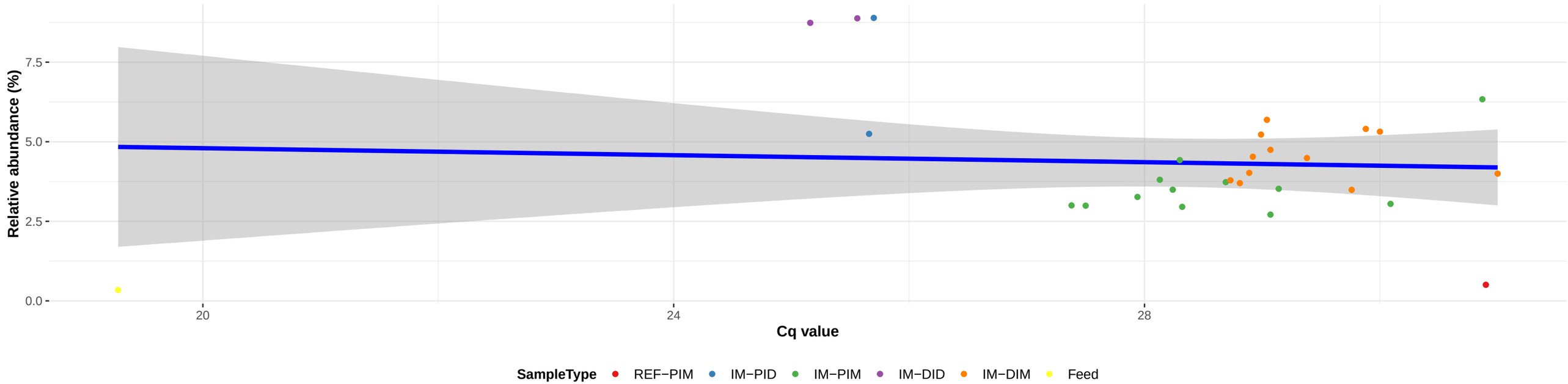
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus caeni

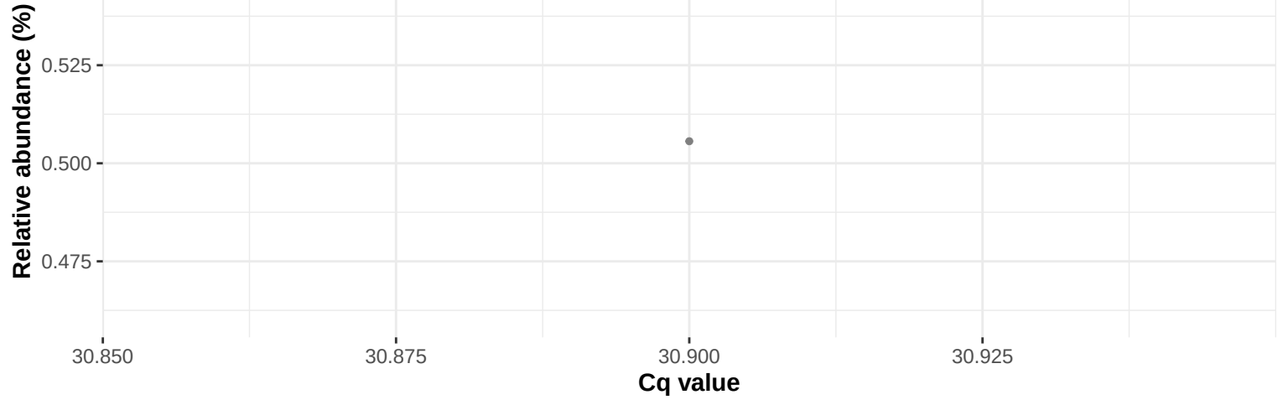
Correlation with all samples

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



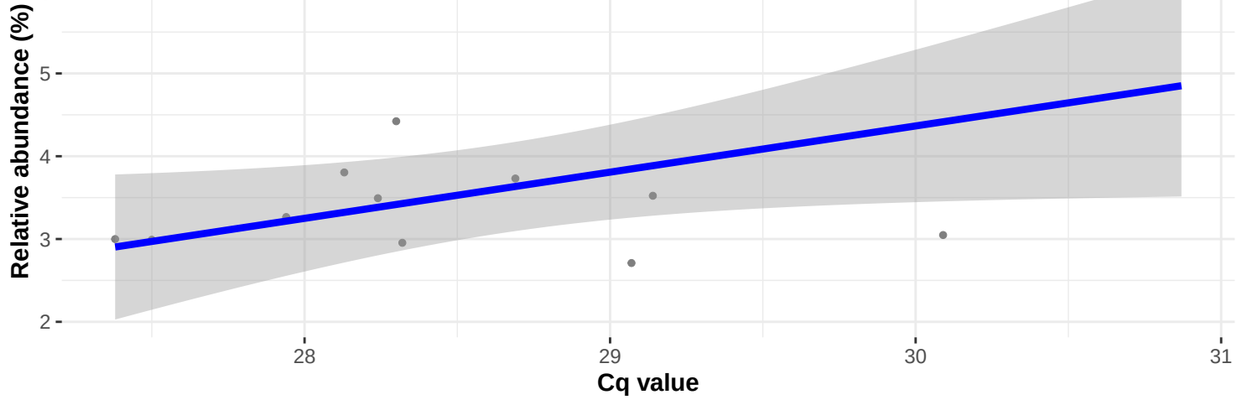
SampleType REF−PIM IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



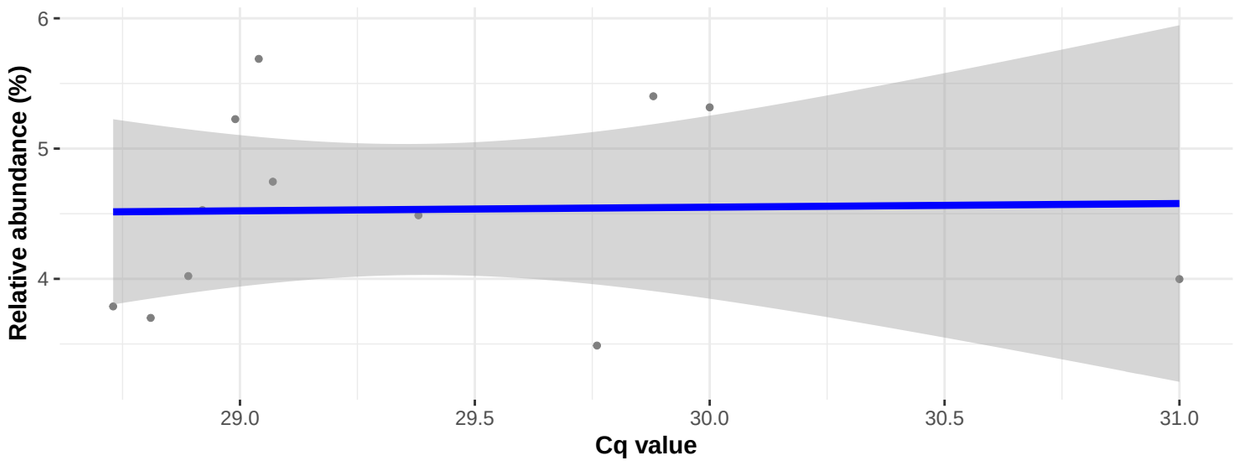
Correlation within: IM−PIM

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

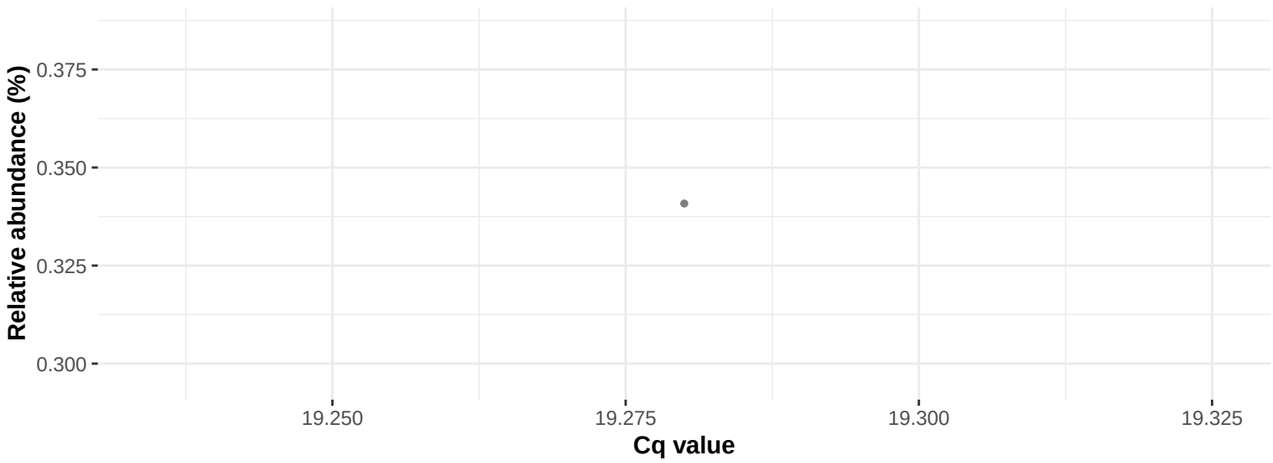


Correlation within: IM−DIM

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



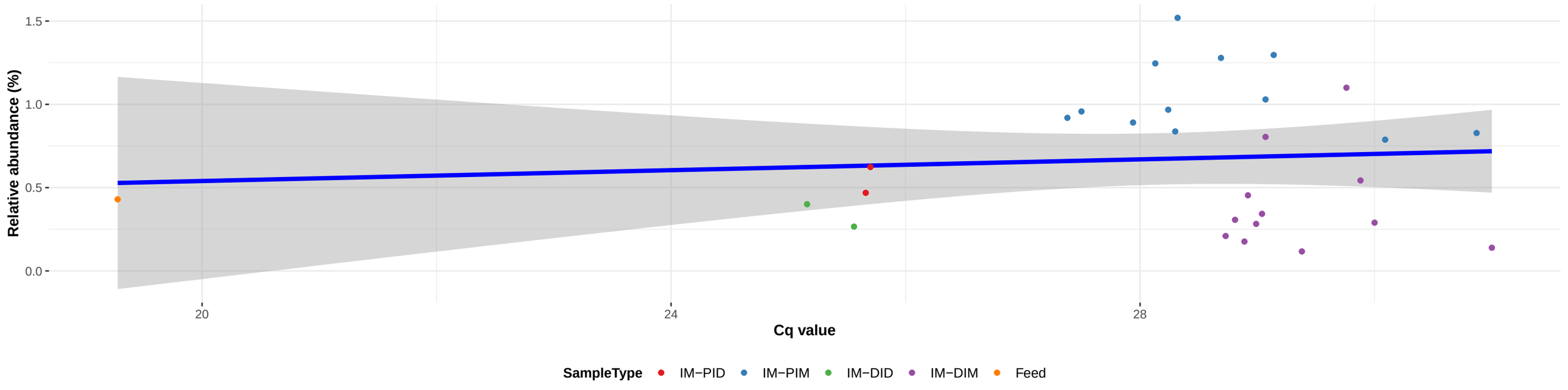
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA

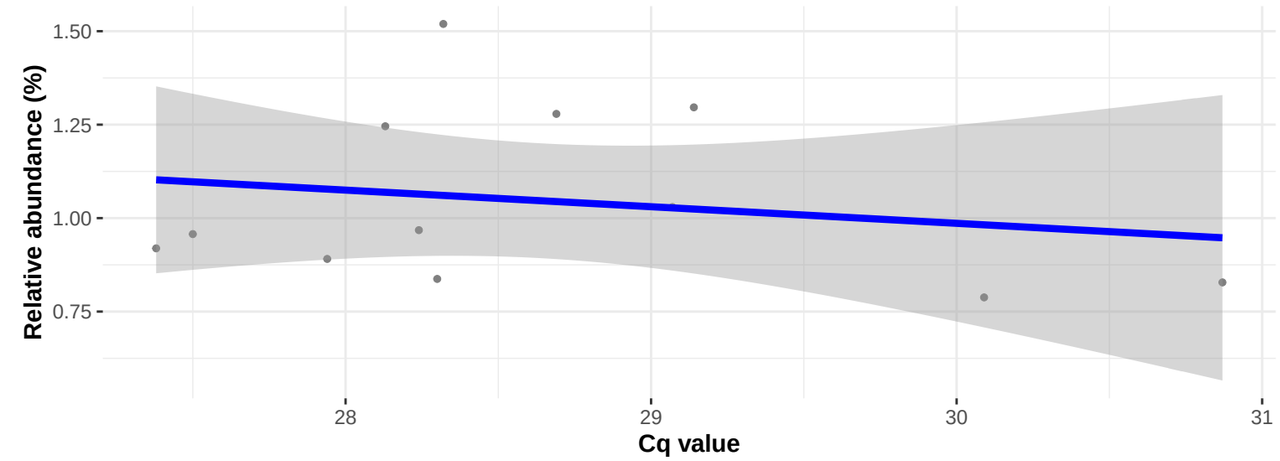
Correlation with all samples

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



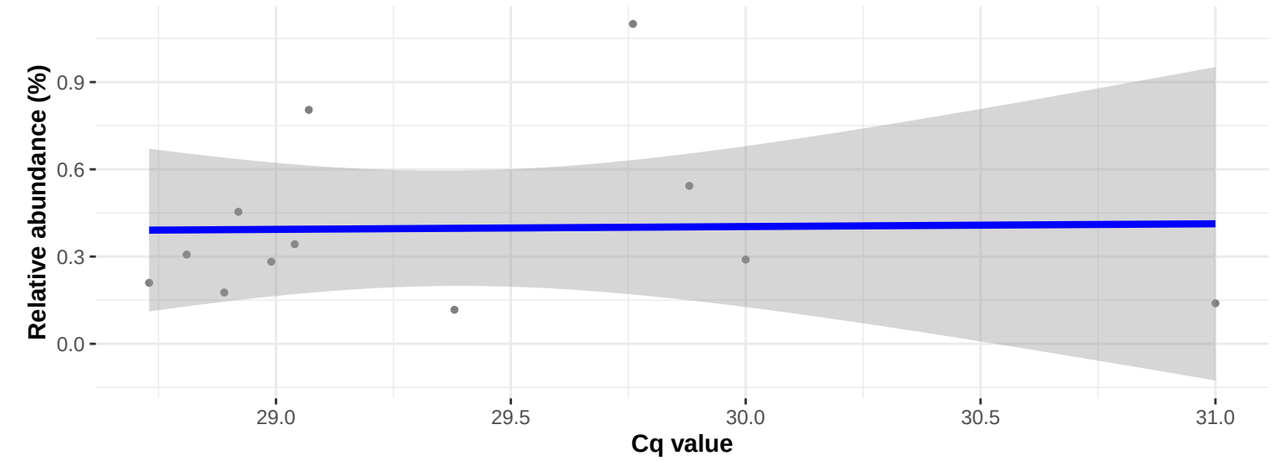
Correlation within: IM−PIM

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

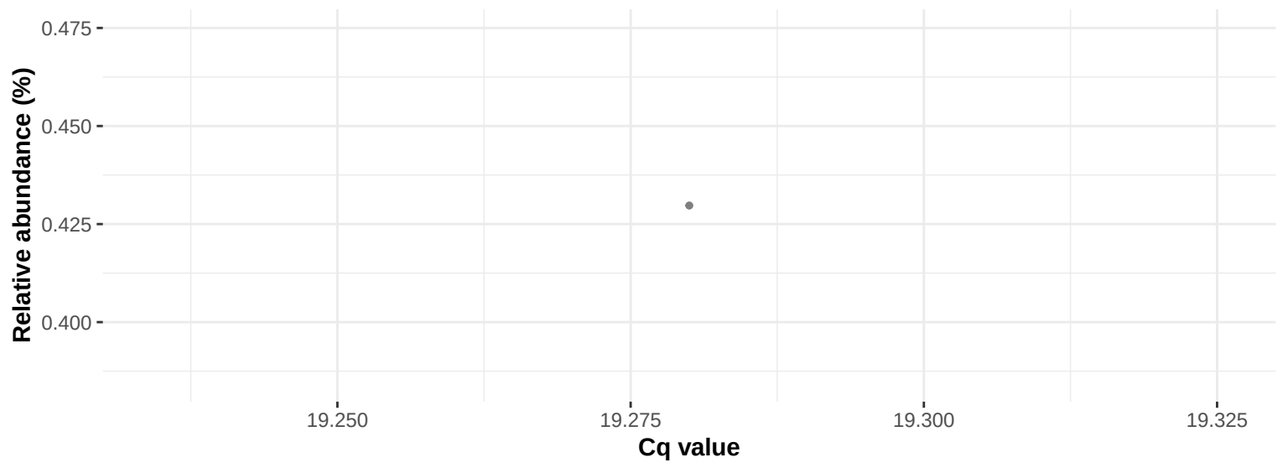


Correlation within: IM−DIM

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



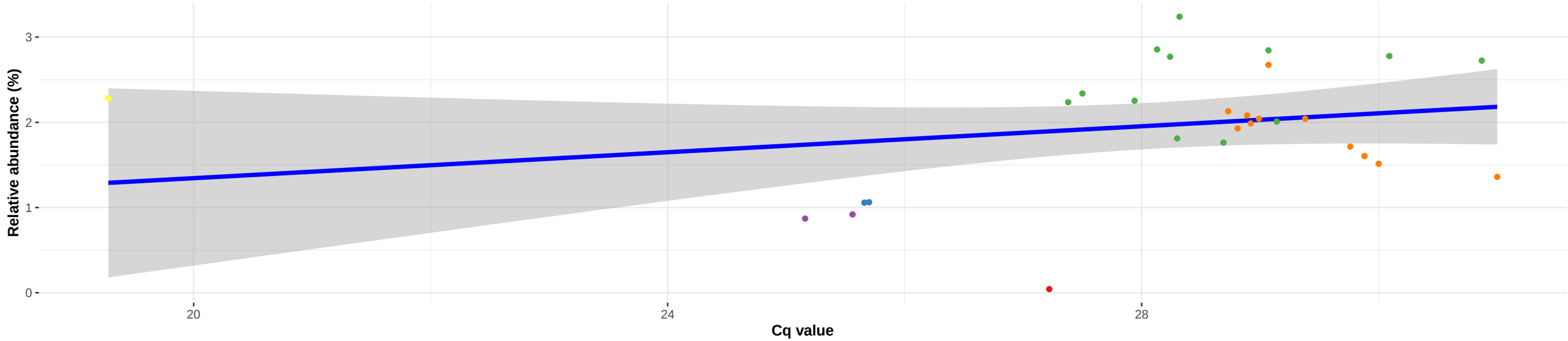
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Beutenbergiaceae; NA; NA

Correlation with all samples

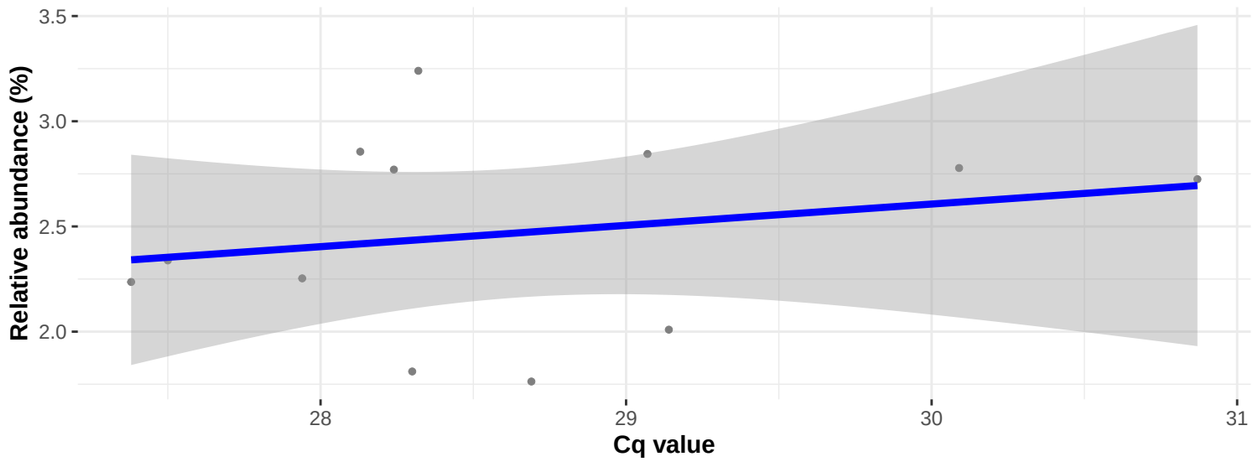
$\log_e(S)$ = 8.113, p = 0.355, $\hat{\rho}_{Spearman}$ = 0.178, $CI_{95\%}$ [−0.212, 0.520], n_{pairs} = 29



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

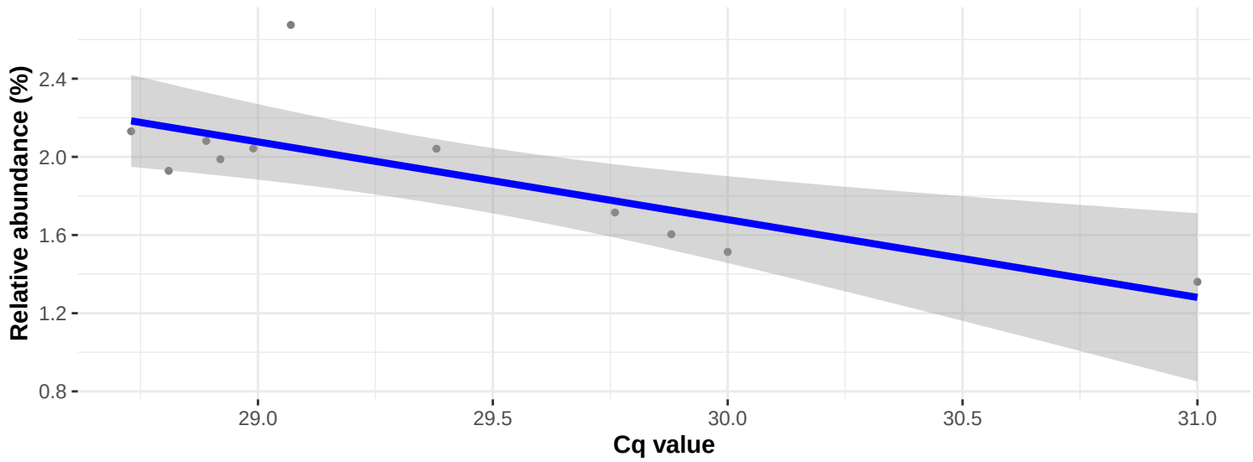
Correlation within: IM−PIM

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

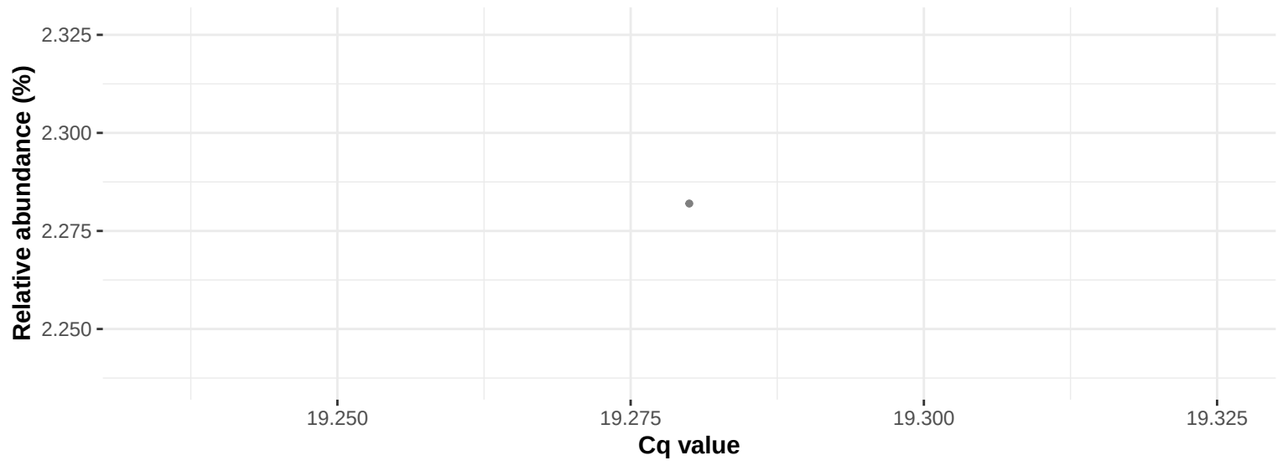


Correlation within: IM−DIM

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



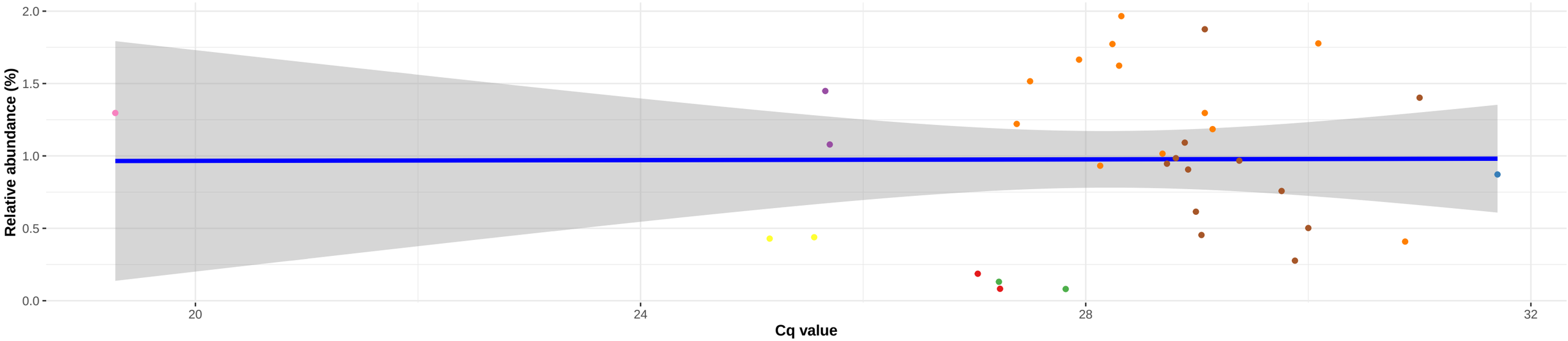
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa

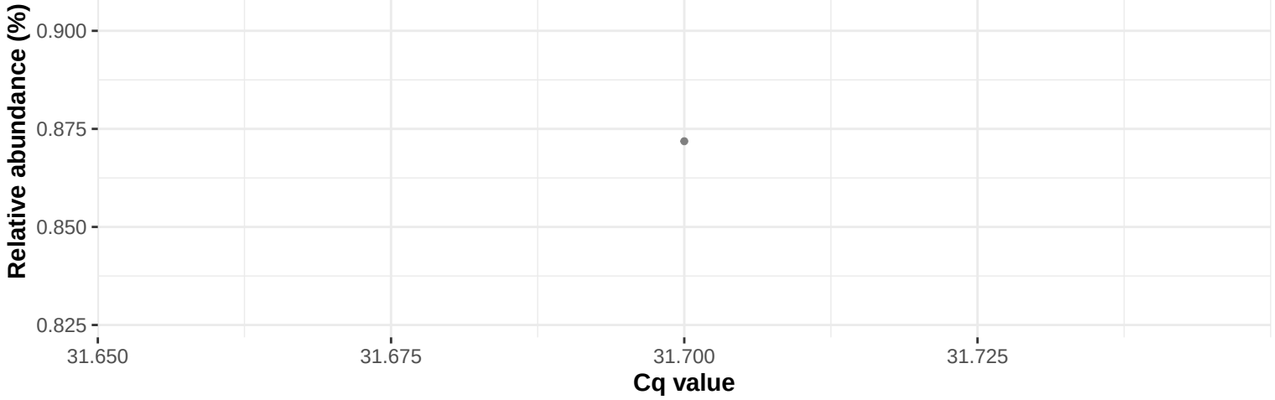
Correlation with all samples

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



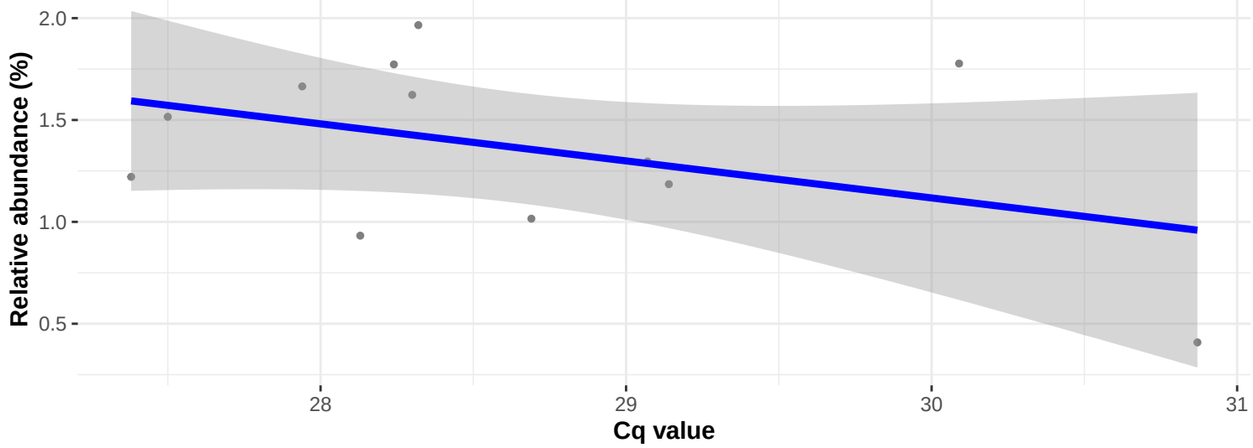
SampleType REF−PID REF−PIM REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



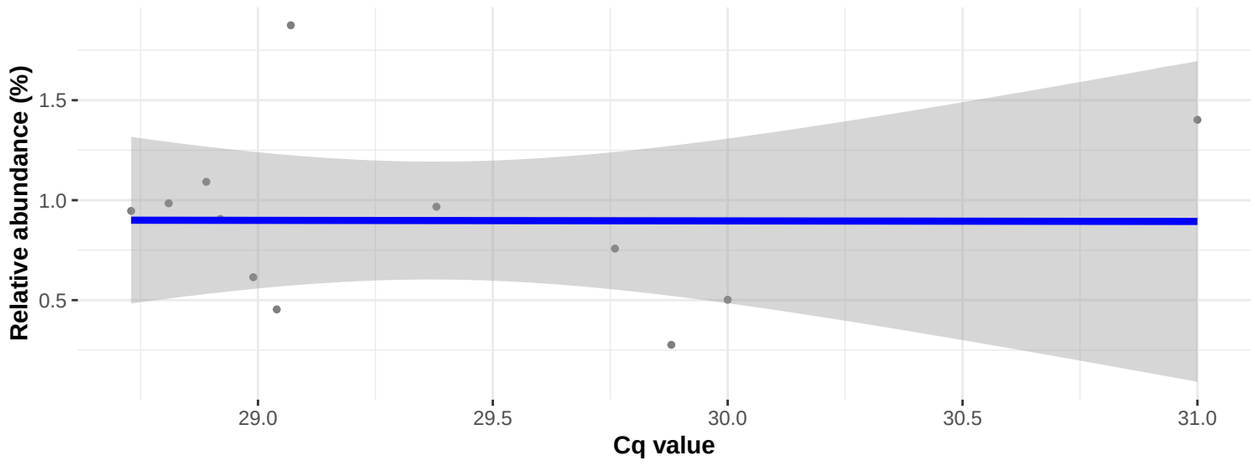
Correlation within: IM−PIM

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

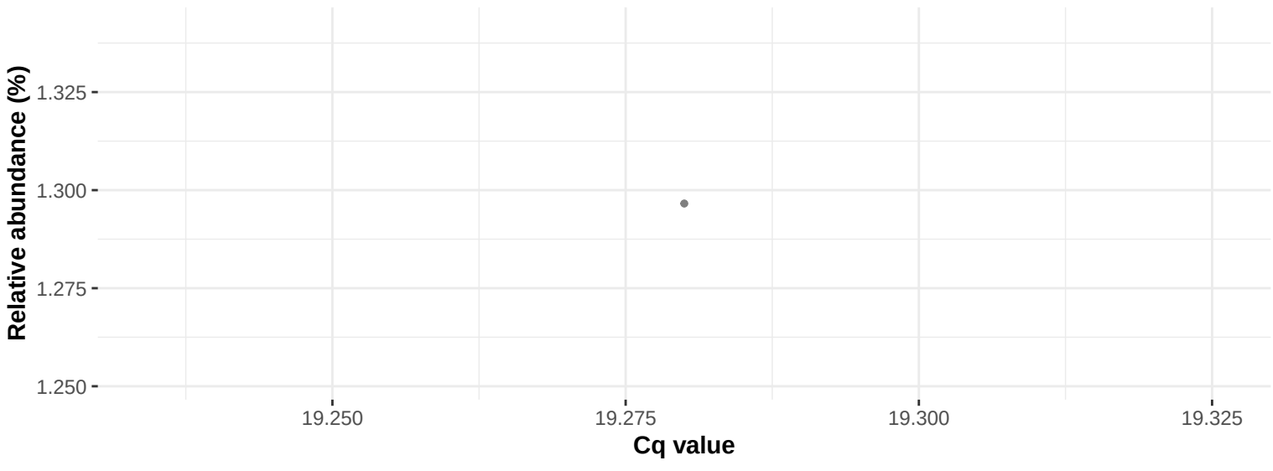


Correlation within: IM−DIM

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



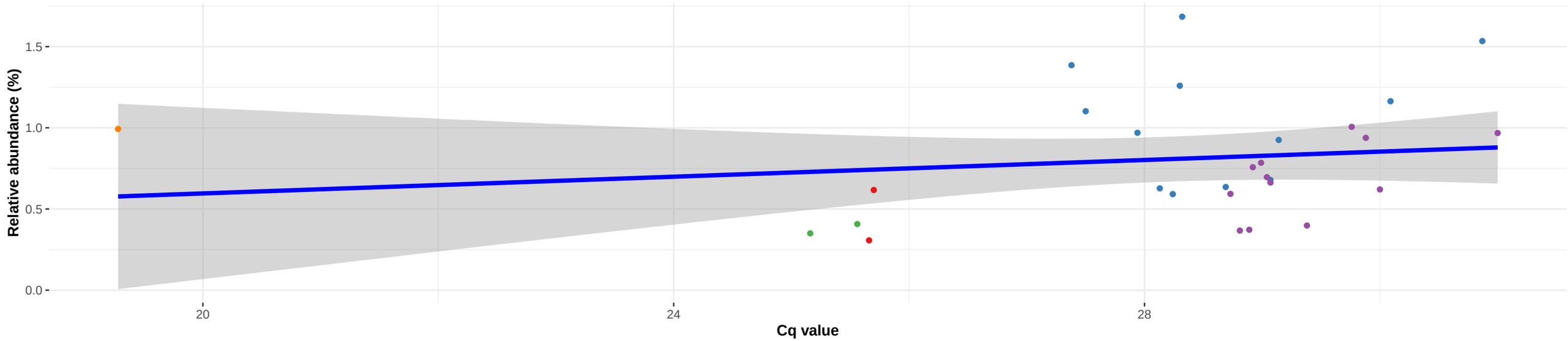
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; NA; NA

Correlation with all samples

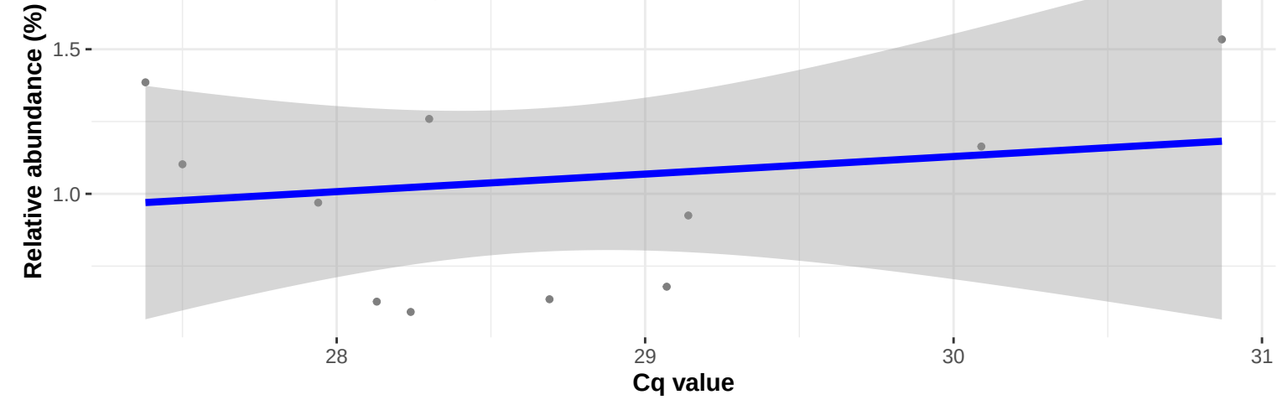
$\log_e(S)$ = 8.026, p = 0.198, $\hat{\rho}_{Spearman}$ = 0.246, $CI_{95\%}$ [−0.144, 0.570], n_{pairs} = 29



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed

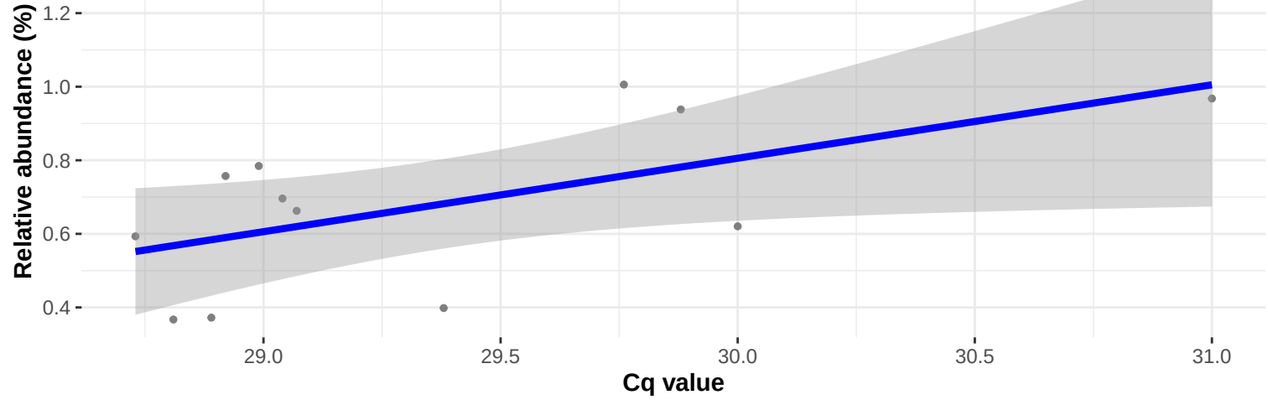
Correlation within: IM−PIM

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

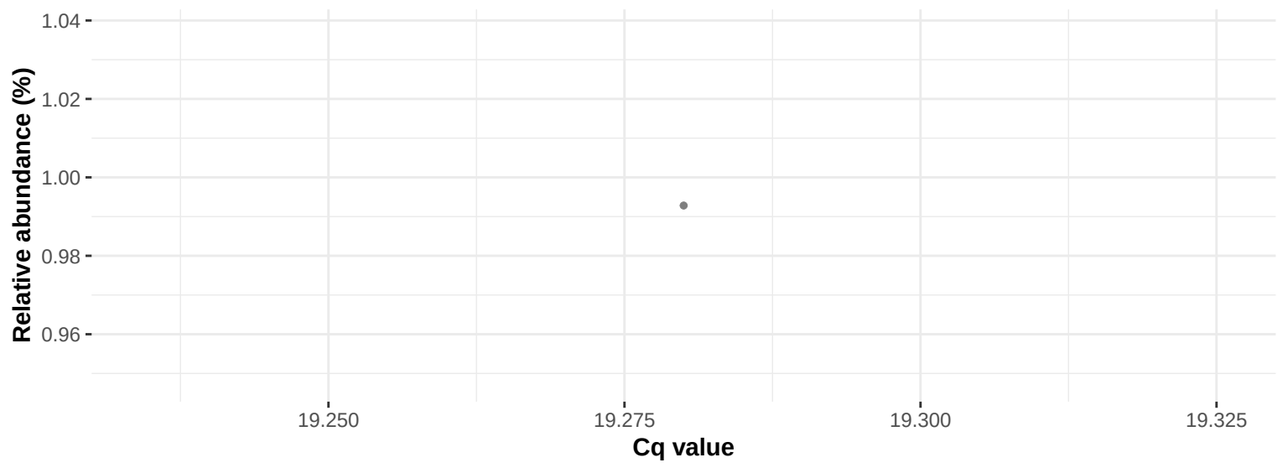


Correlation within: IM−DIM

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



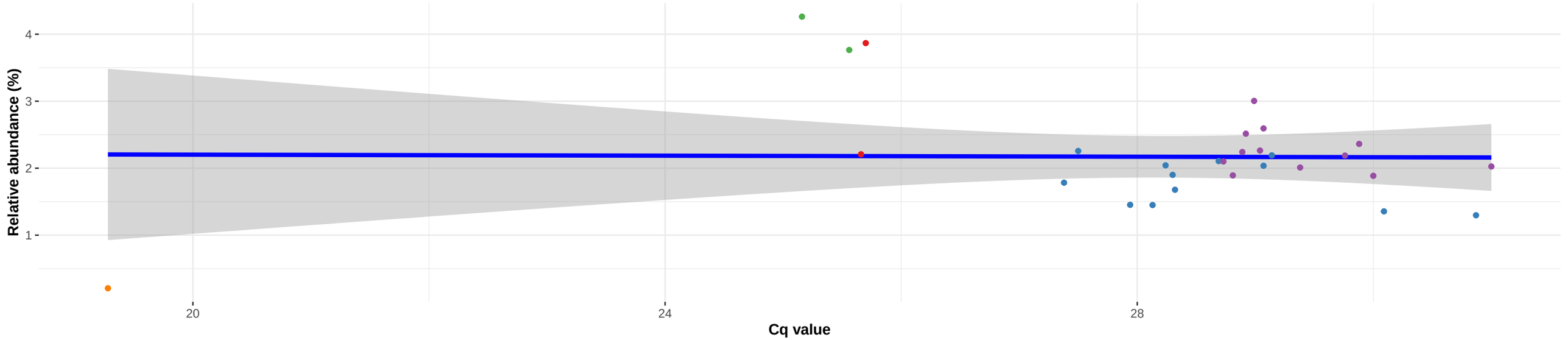
Correlation within: Feed



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

Correlation with all samples

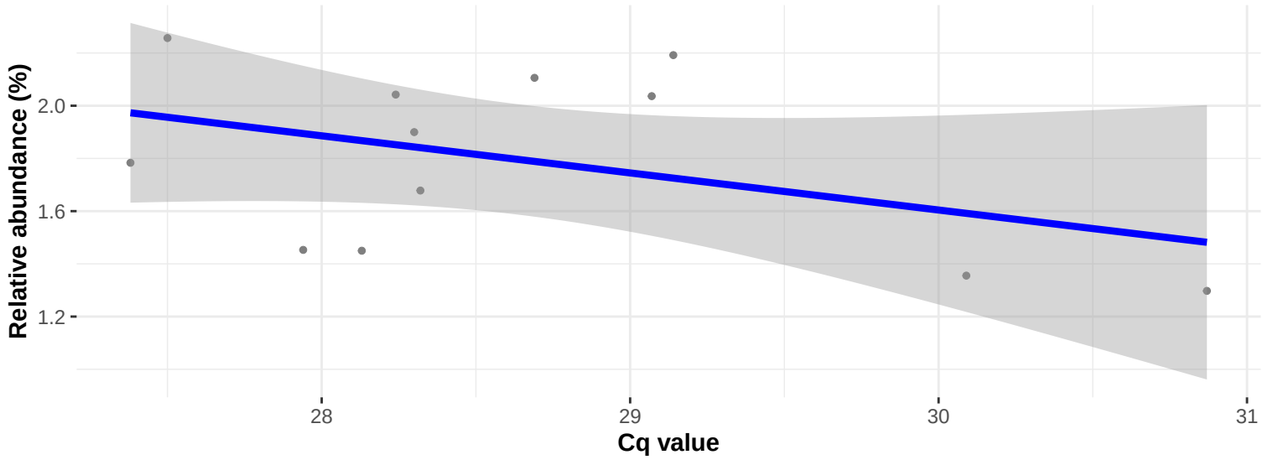
$\log_e(S)$ = 8.451, p = 0.427, $\hat{\rho}_{Spearman}$ = −0.153, $CI_{95\%}$ [−0.501, 0.237], n_{pairs} = 29



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

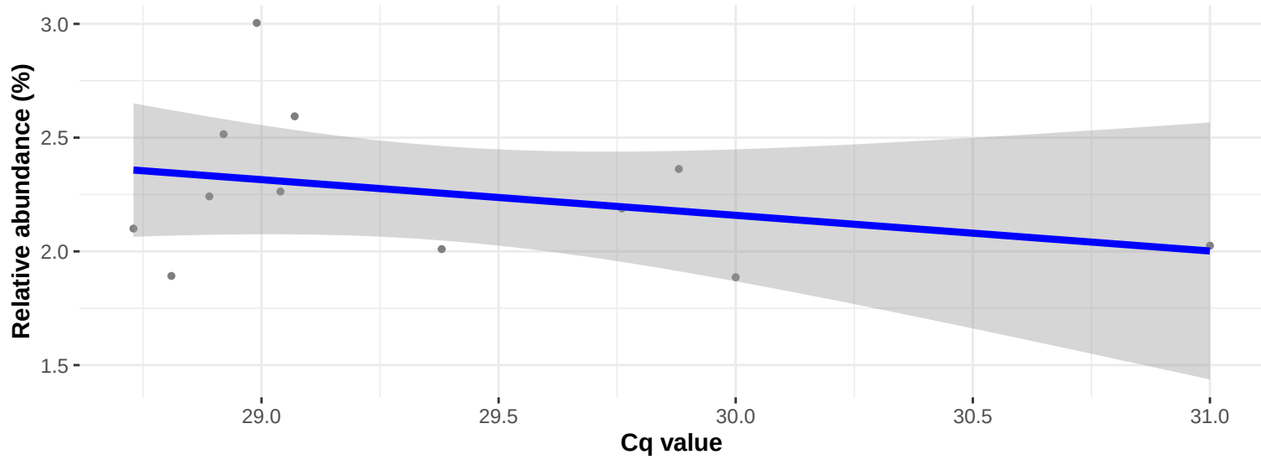
Correlation within: IM−PIM

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

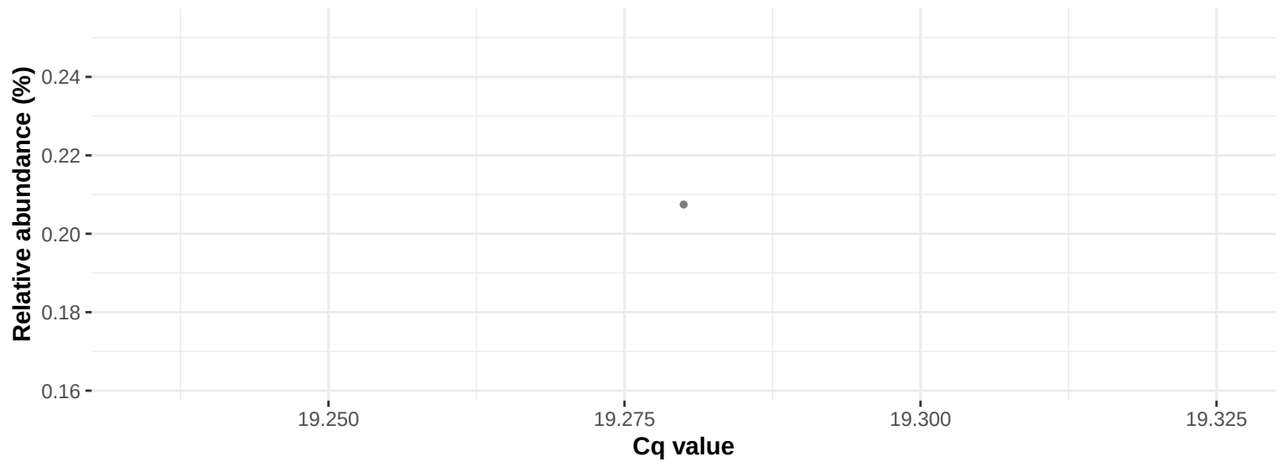


Correlation within: IM−DIM

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



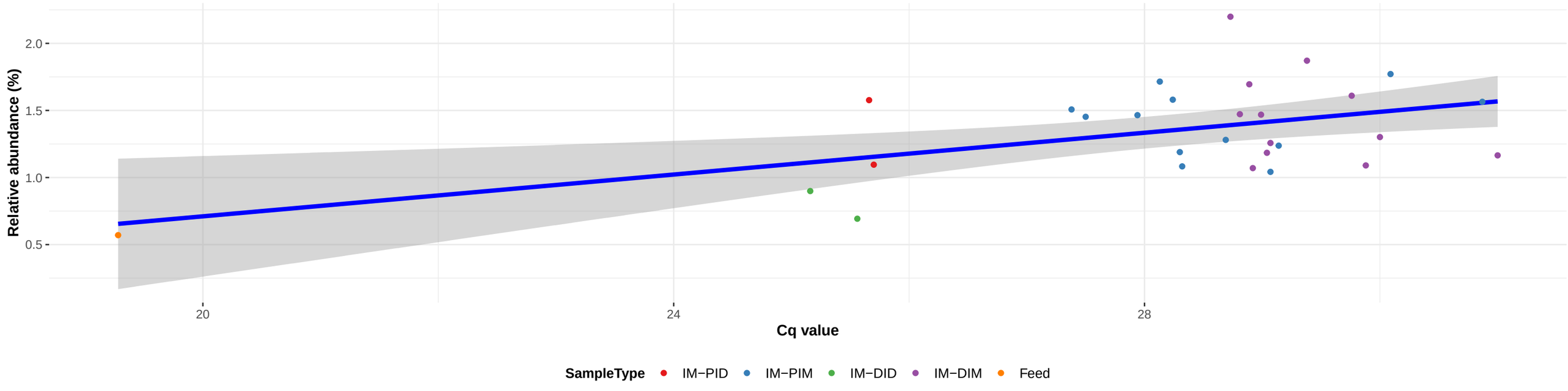
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; Ambiguous_taxa; Ambiguous_taxa

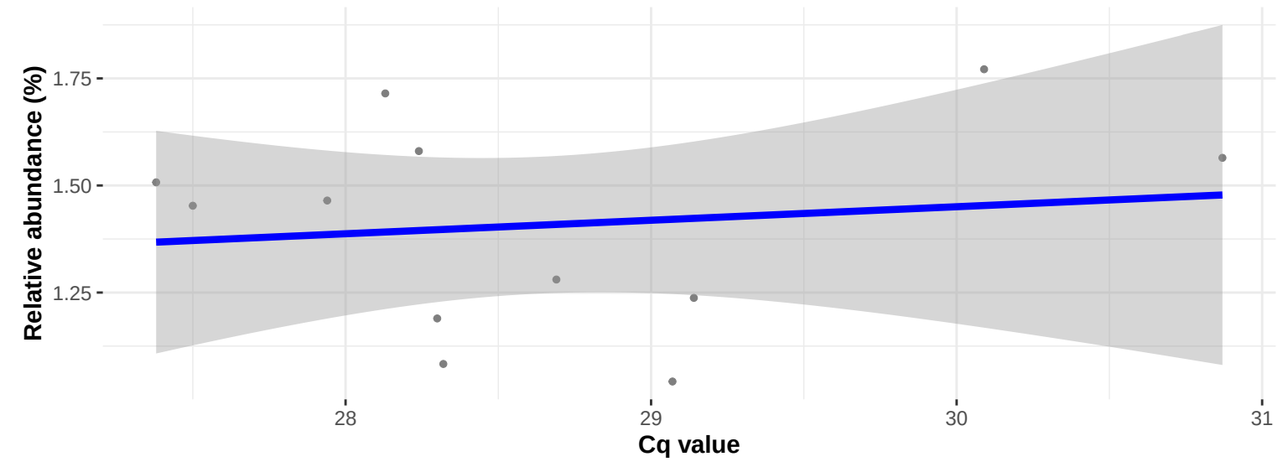
Correlation with all samples

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



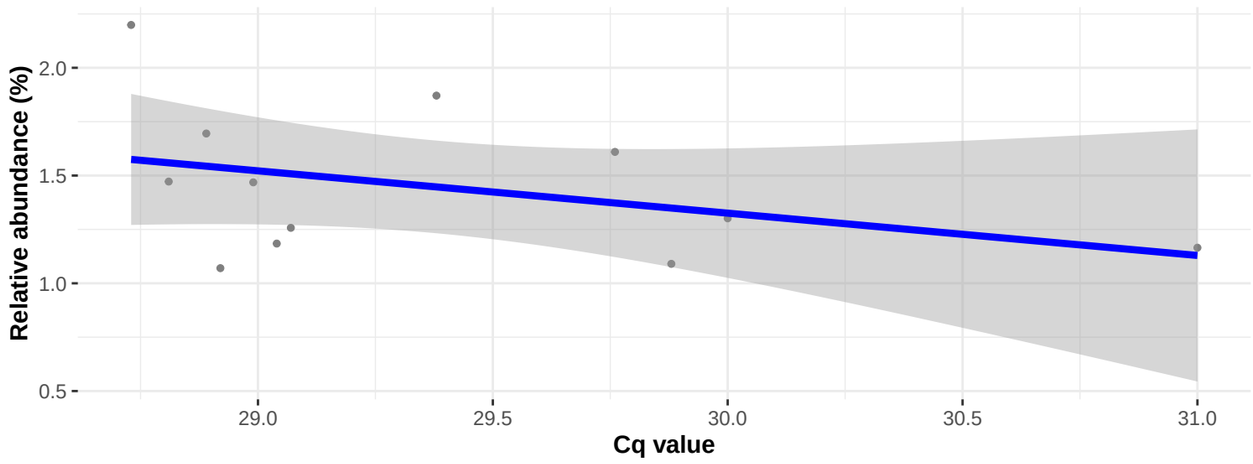
Correlation within: IM−PIM

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

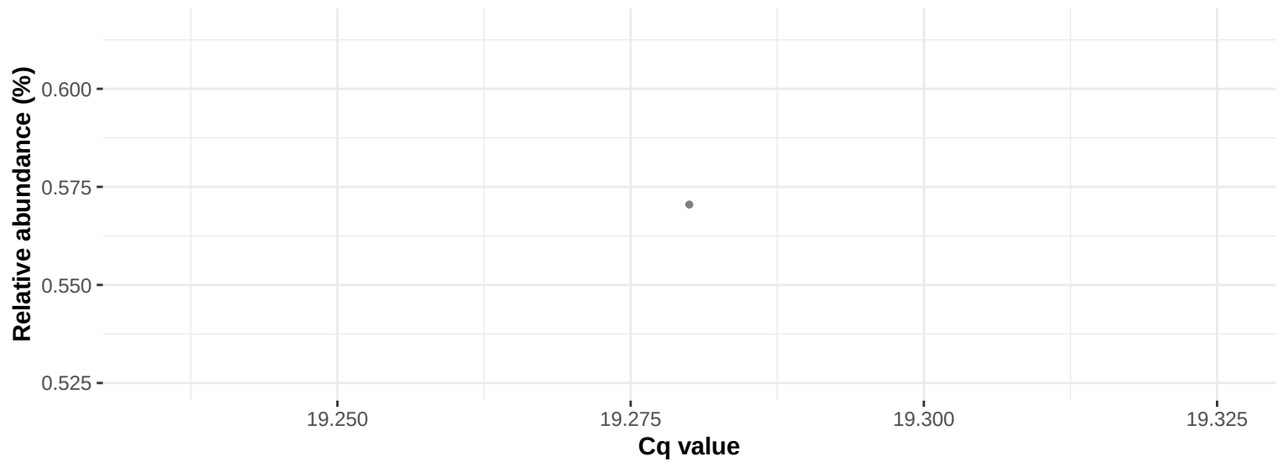


Correlation within: IM−DIM

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



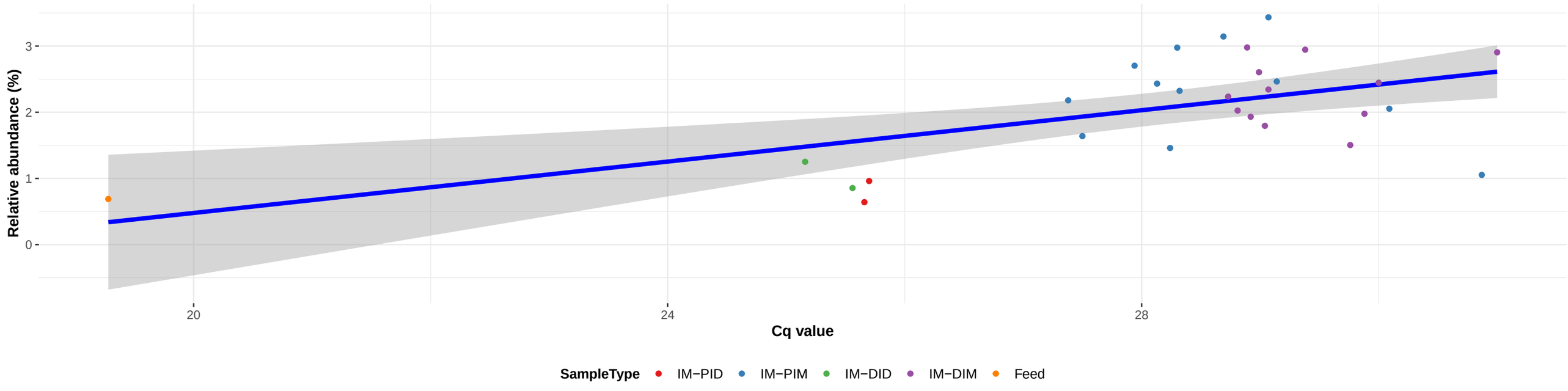
Correlation within: Feed



k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium

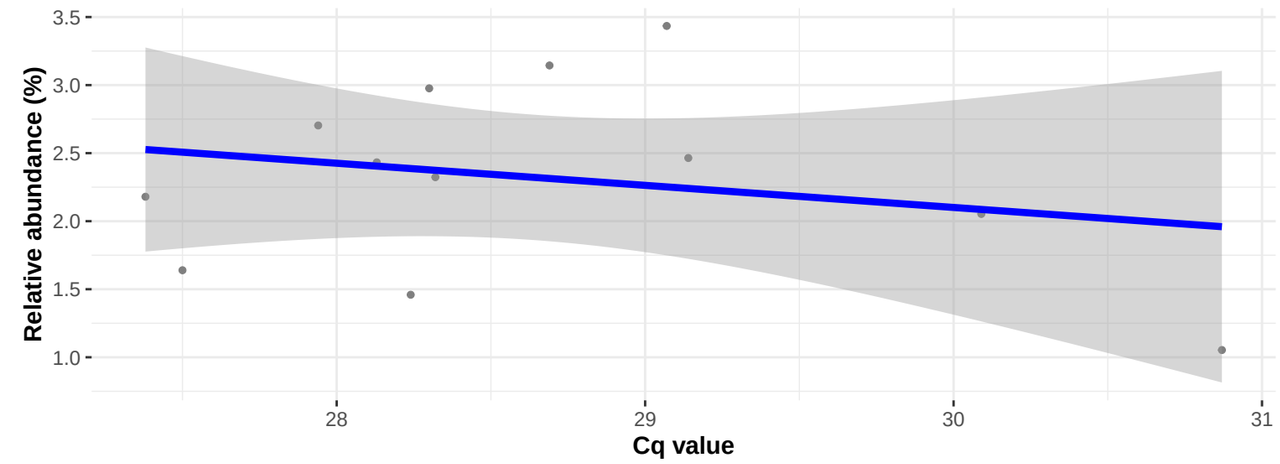
Correlation with all samples

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



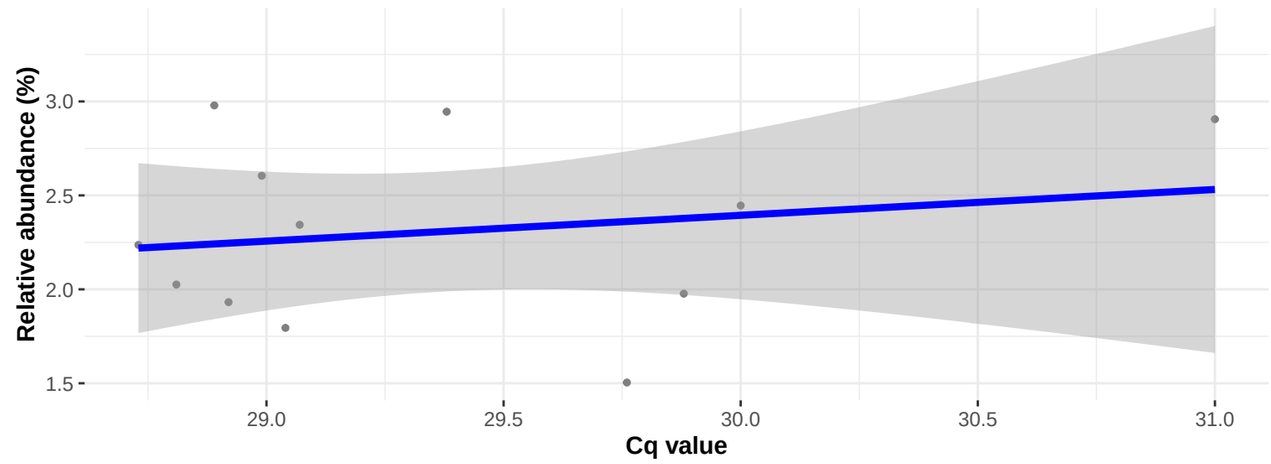
Correlation within: IM−PIM

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

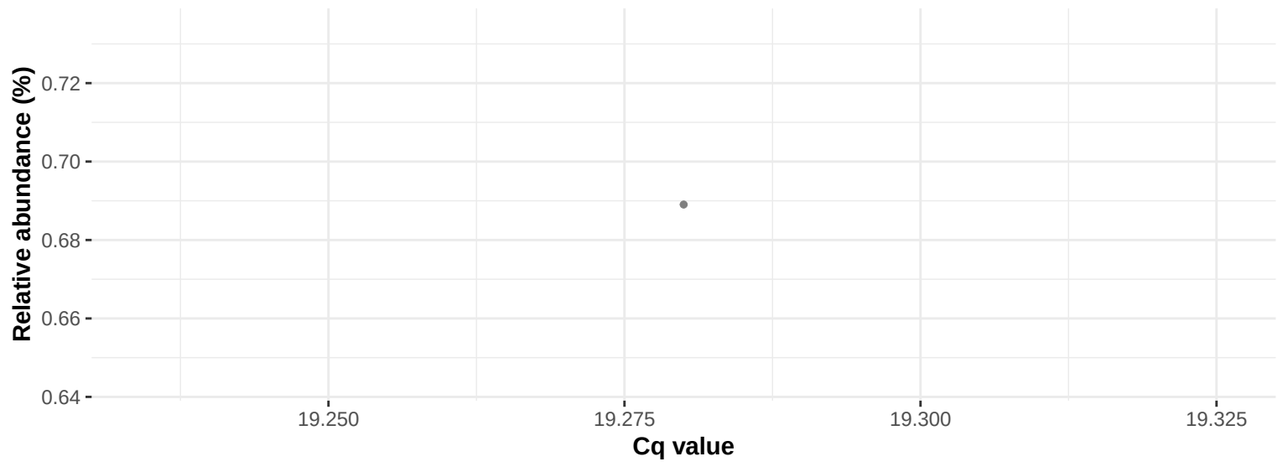


Correlation within: IM−DIM

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



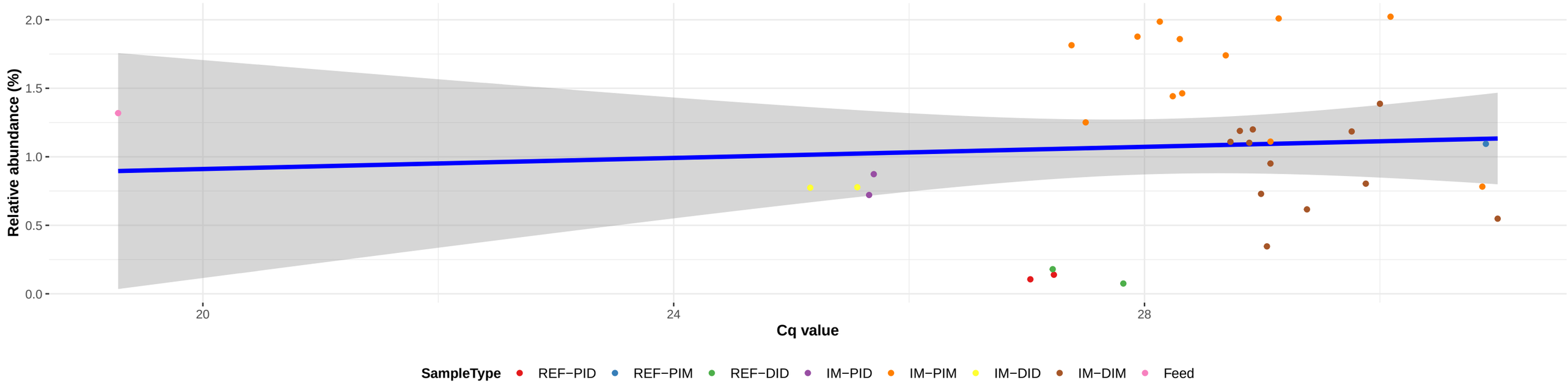
Correlation within: Feed



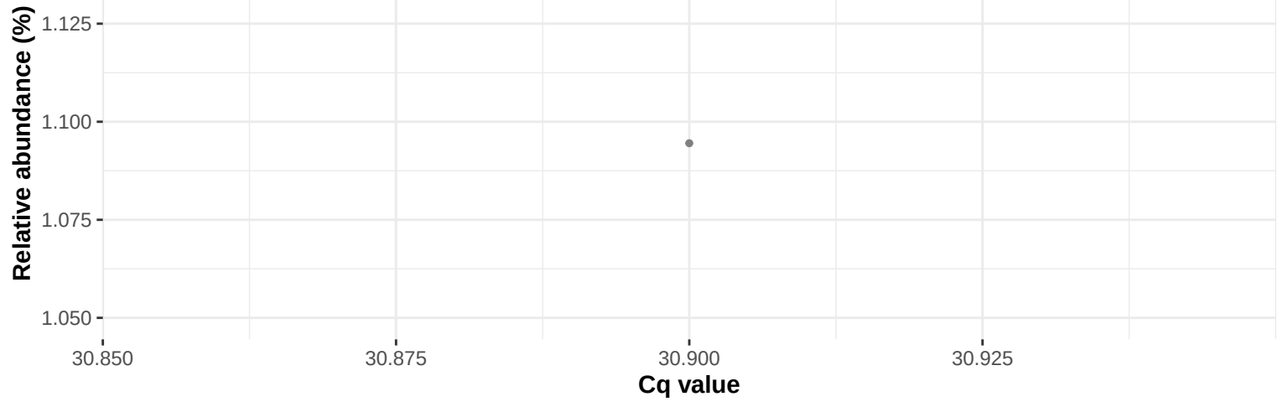
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Aerococcaceae; g__Globicatella; Ambiguous_taxa

Correlation with all samples

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

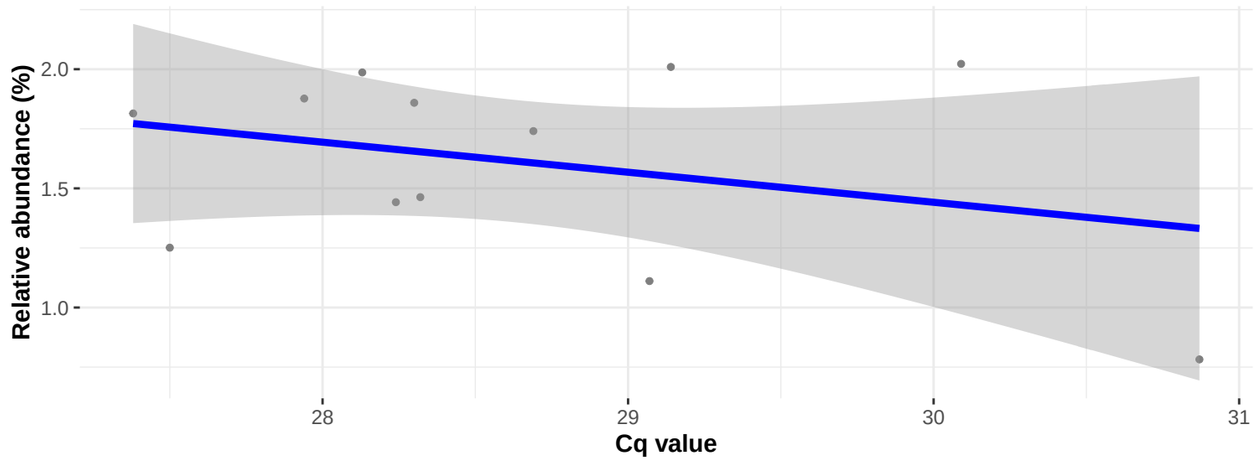


Correlation within: REF−PIM



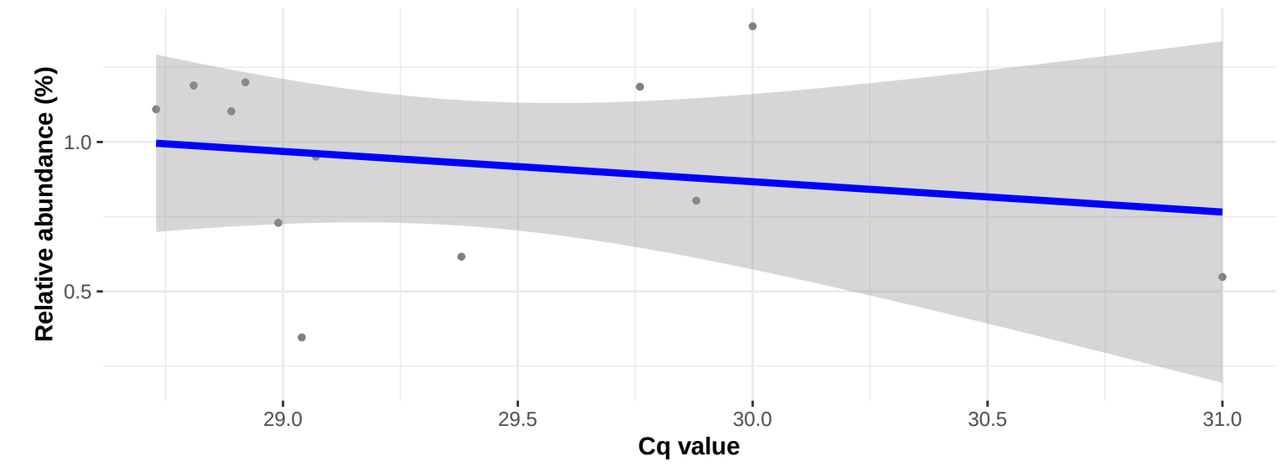
Correlation within: IM−PIM

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

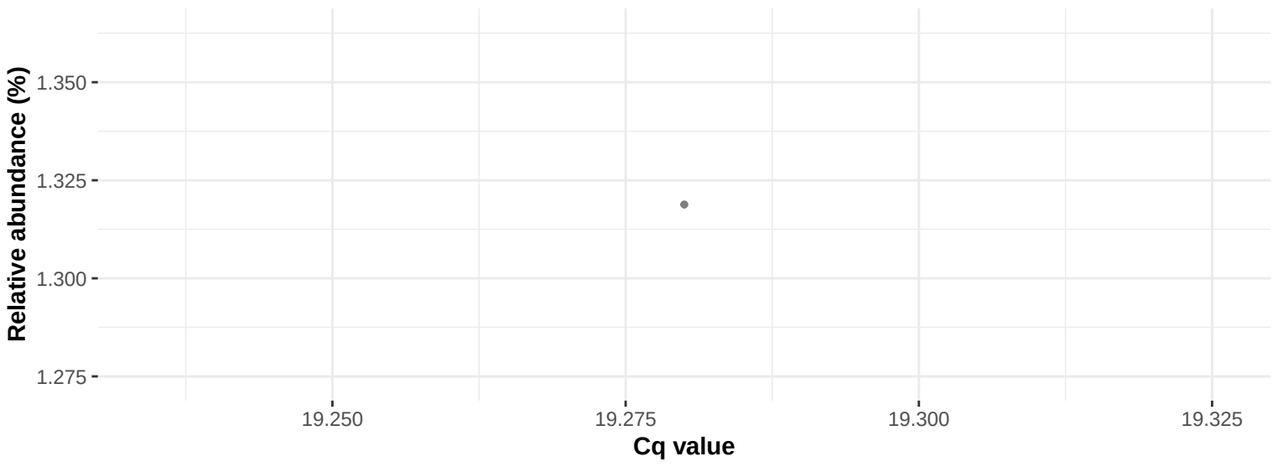


Correlation within: IM−DIM

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



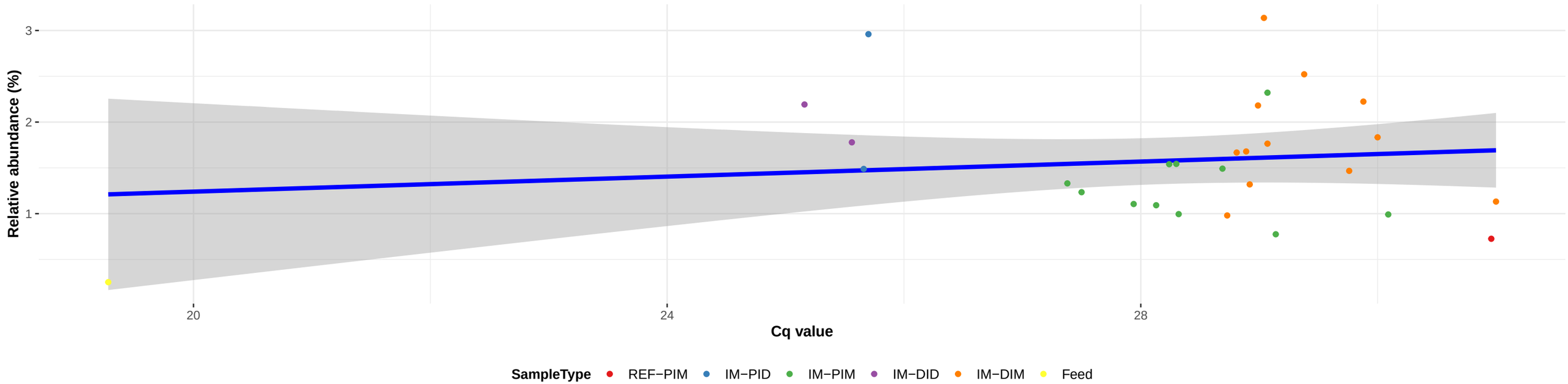
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Lysinibacillus; NA

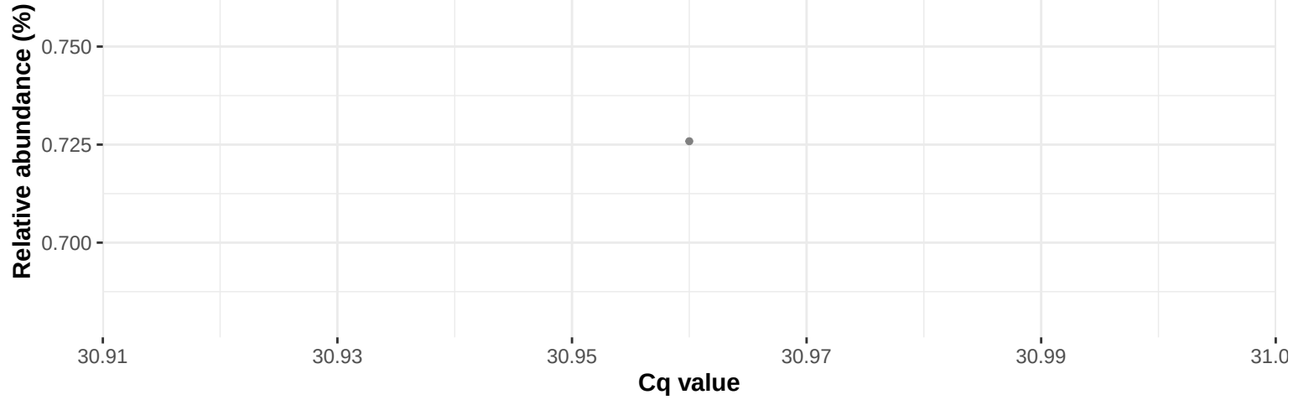
Correlation with all samples

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



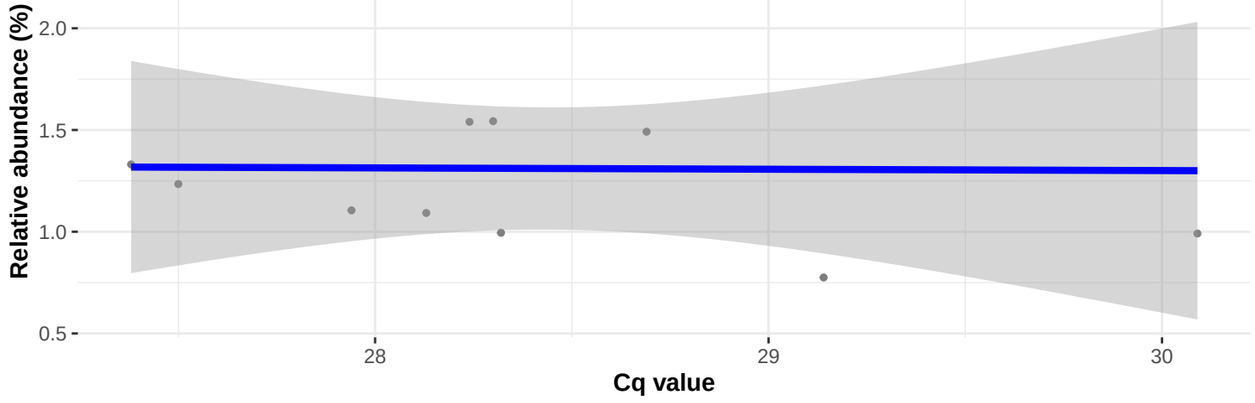
SampleType ● REF−PIM ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

Correlation within: REF−PIM



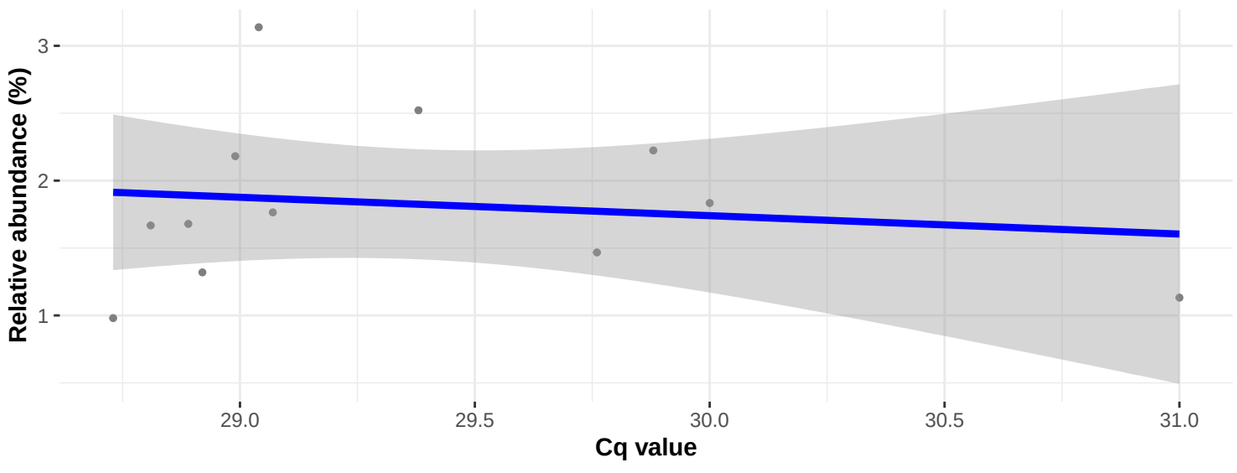
Correlation within: IM−PIM

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

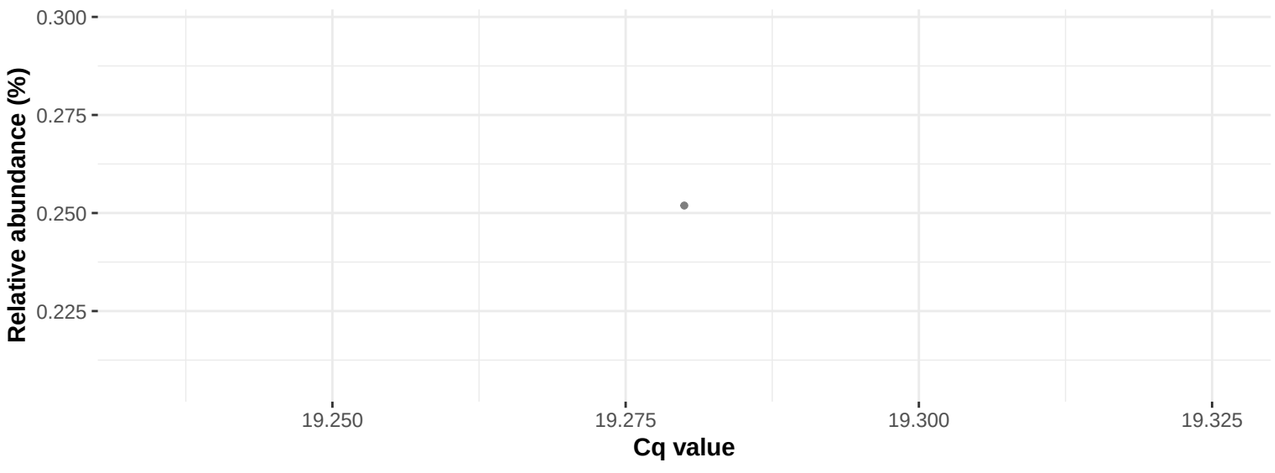


Correlation within: IM−DIM

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



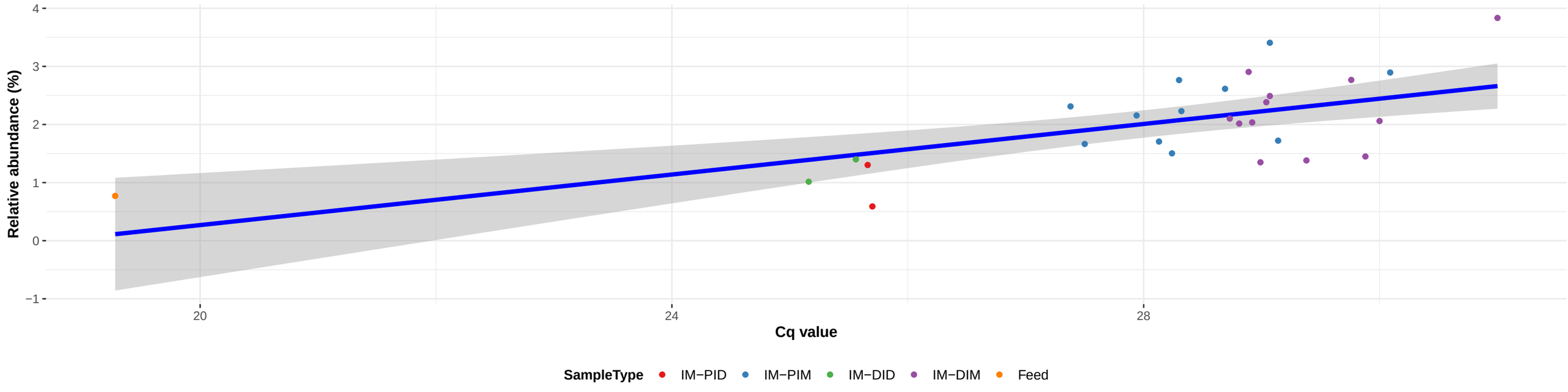
Correlation within: Feed



k__Bacteria; p__RsaHF231; c__uncultured bacterium; o__uncultured bacterium; f__uncultured bacterium; g__uncultured bacterium; s__uncultured bacterium

Correlation with all samples

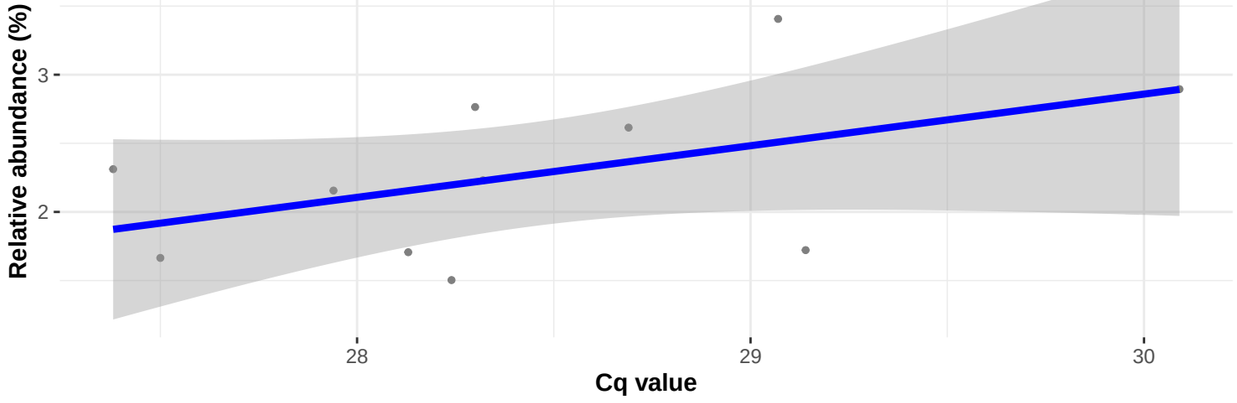
$\log_e(S)$ = 7.434, p = 0.003, $\hat{\rho}_{Spearman}$ = 0.537, $CI_{95\%}$ [0.194, 0.763], n_{pairs} = 28



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

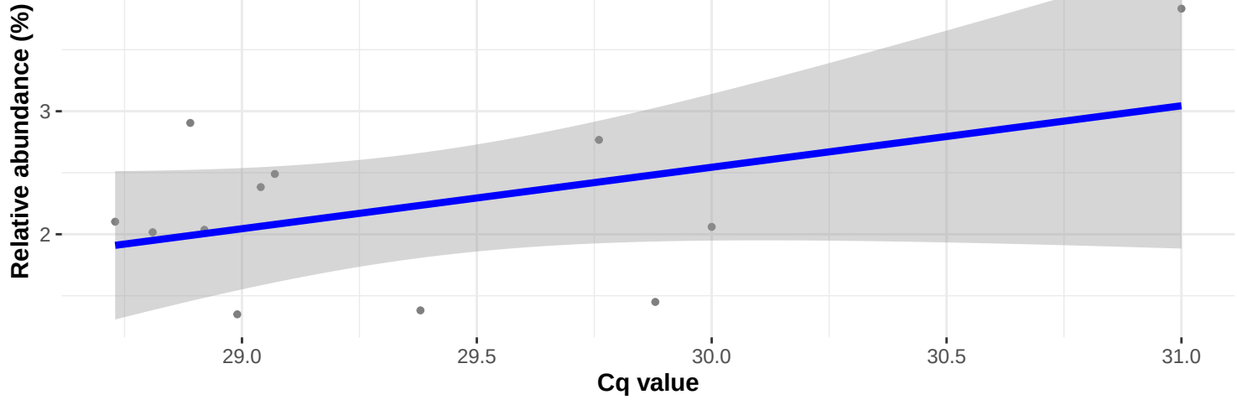
Correlation within: IM−PIM

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

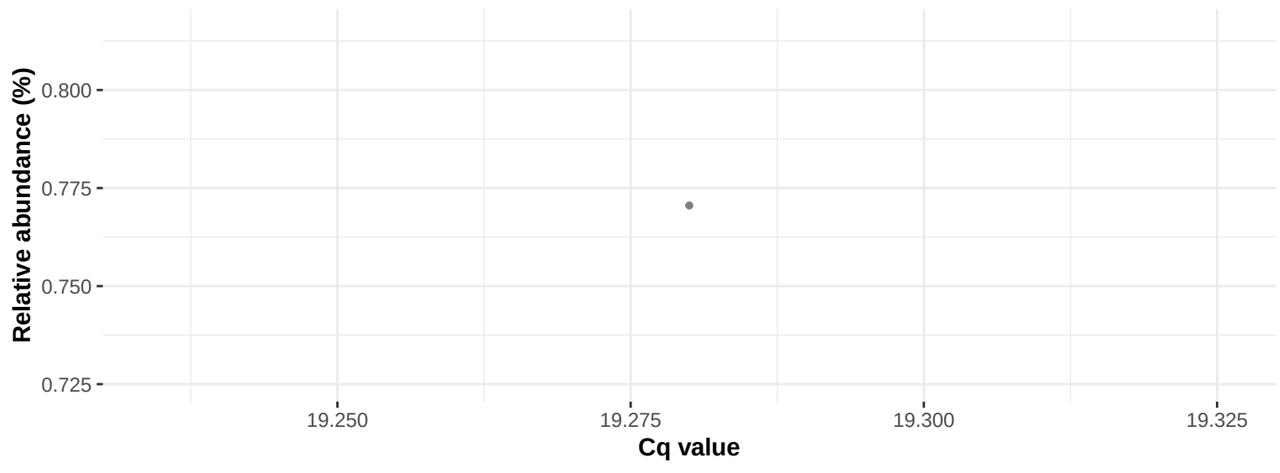


Correlation within: IM−DIM

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



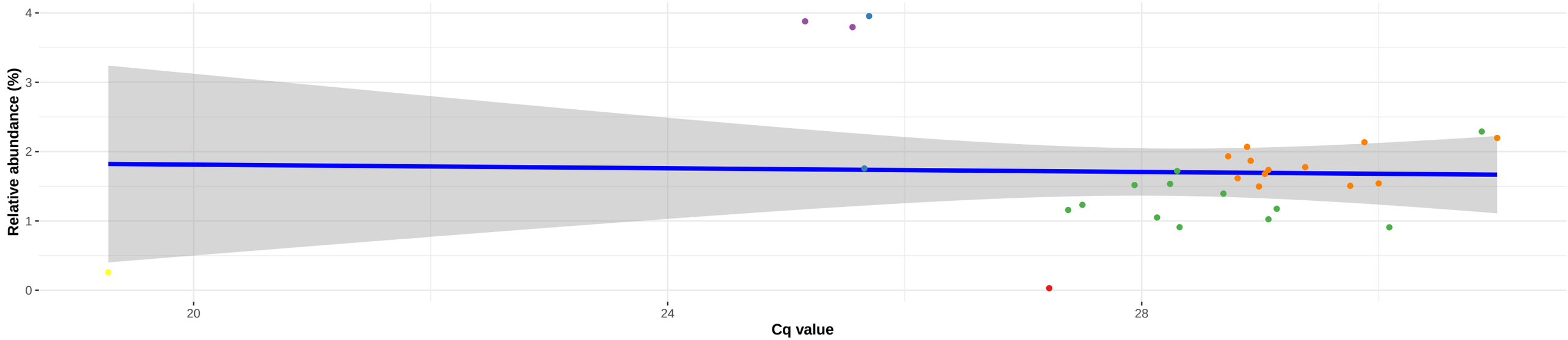
Correlation within: Feed



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

Correlation with all samples

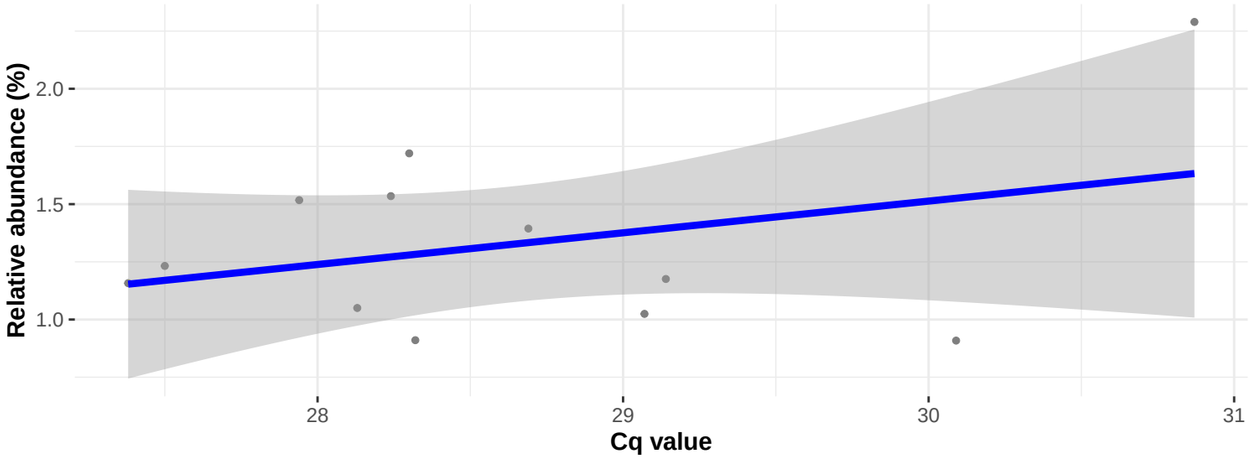
$\log_e(S)$ = 8.321, p = 0.653, $\hat{\rho}_{Spearman}$ = 0.086, $CI_{95\%}$ [−0.294, 0.442], n_{pairs} = 30



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

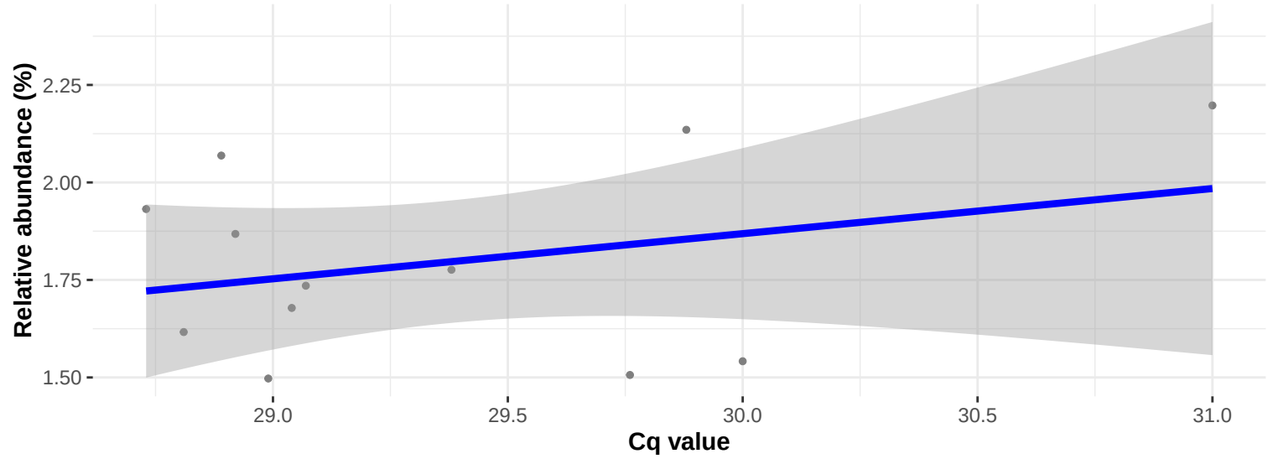
Correlation within: IM−PIM

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

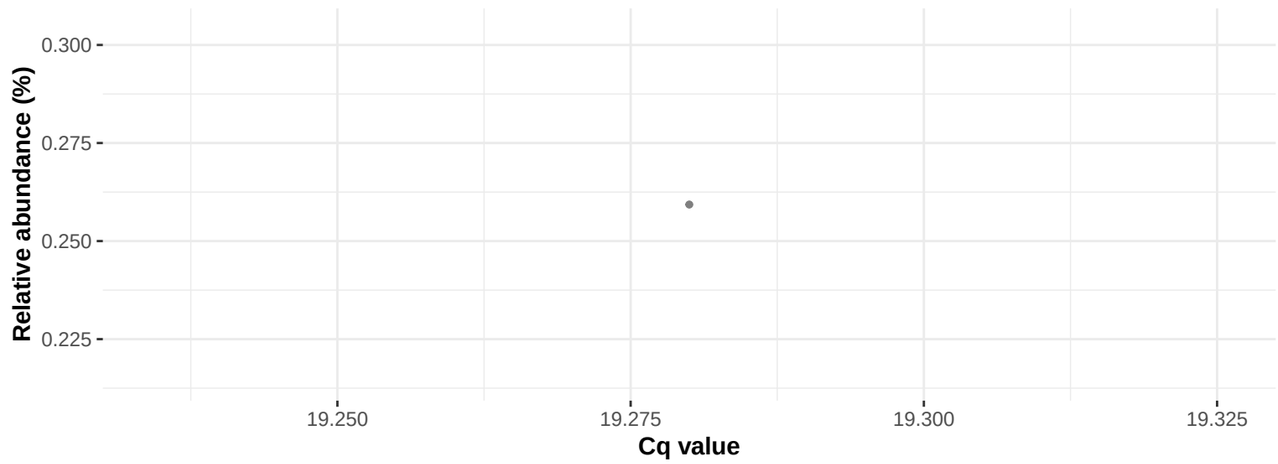


Correlation within: IM−DIM

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



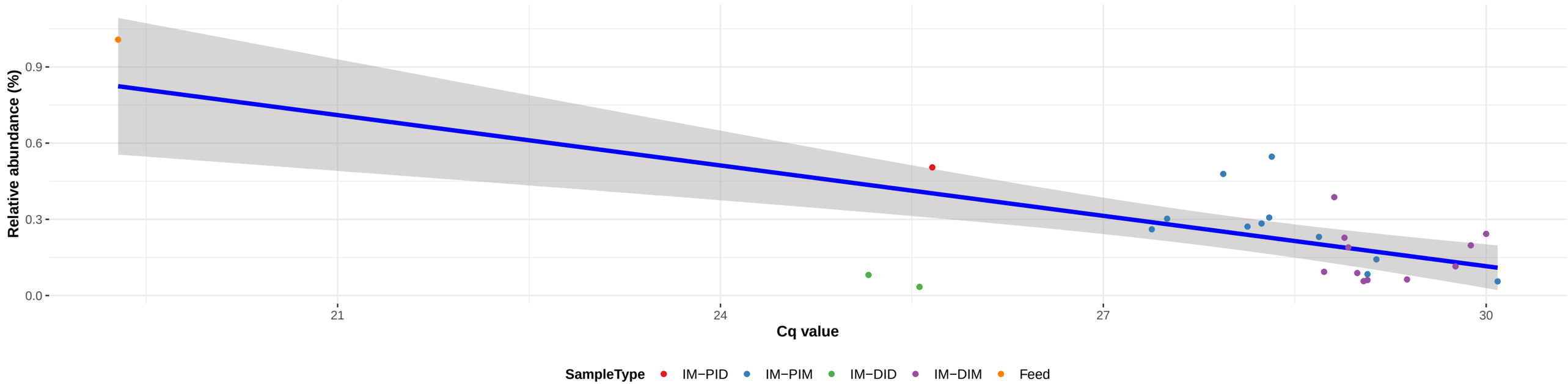
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus cecorum

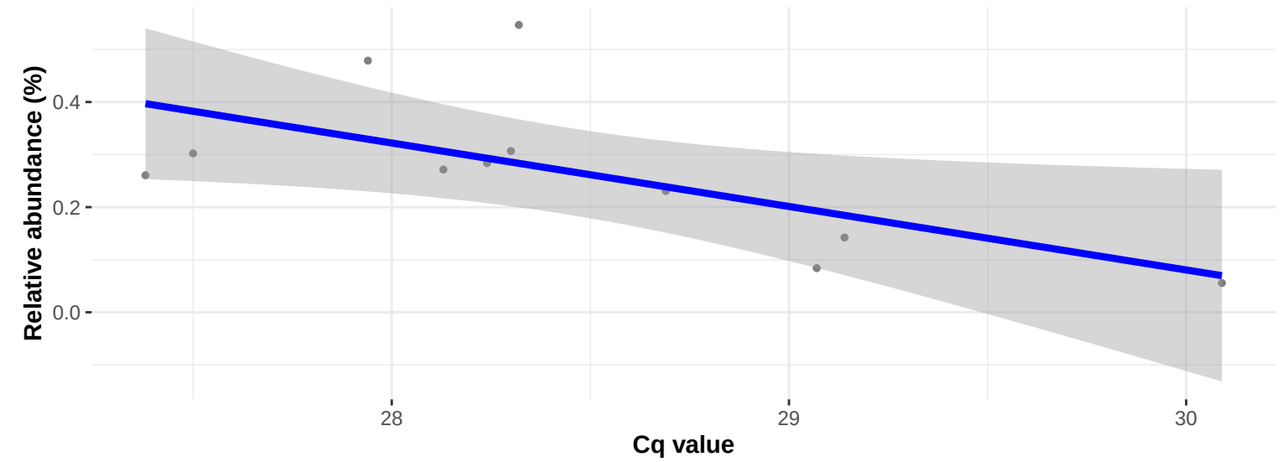
Correlation with all samples

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



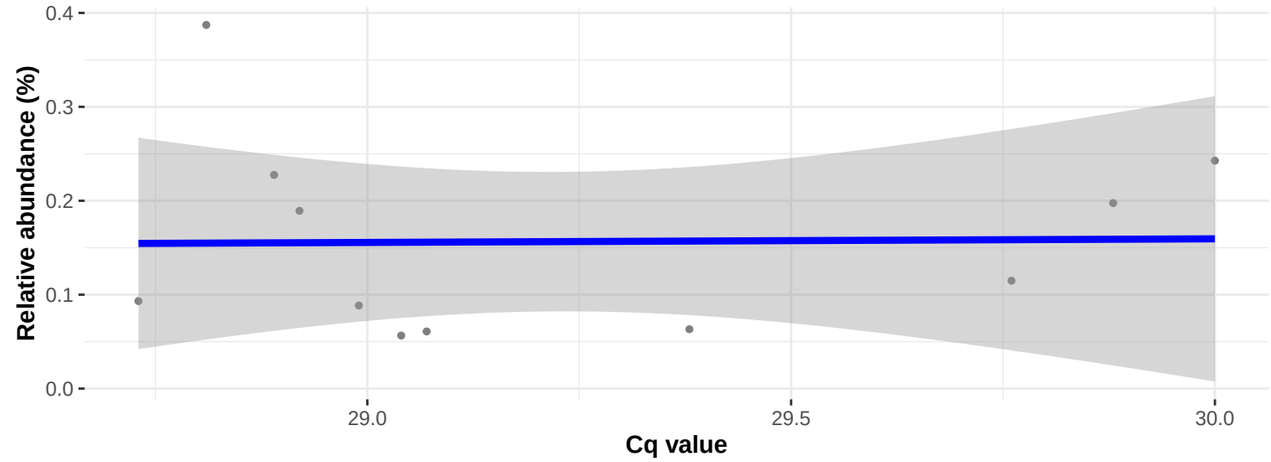
Correlation within: IM−PIM

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

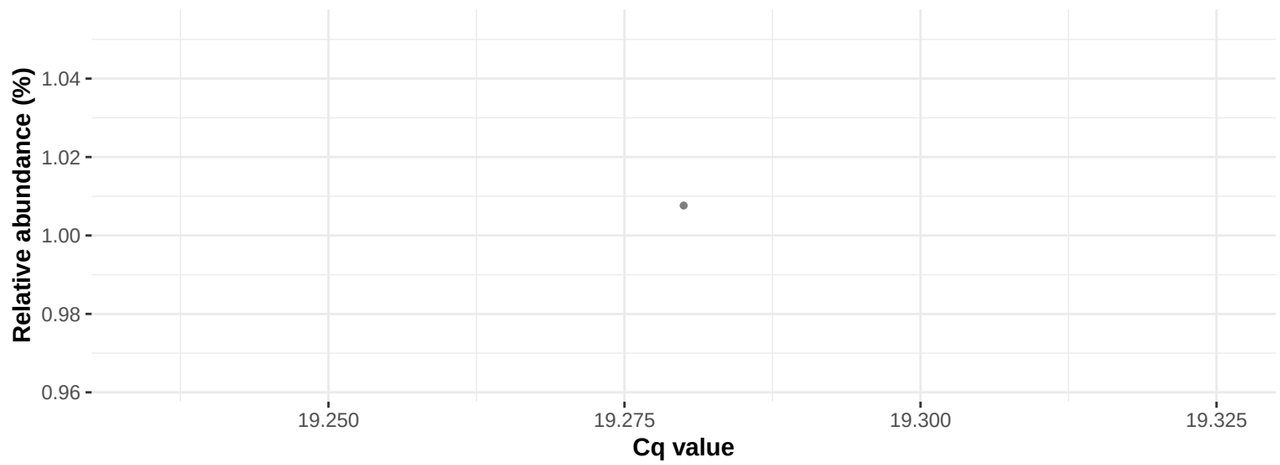


Correlation within: IM−DIM

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



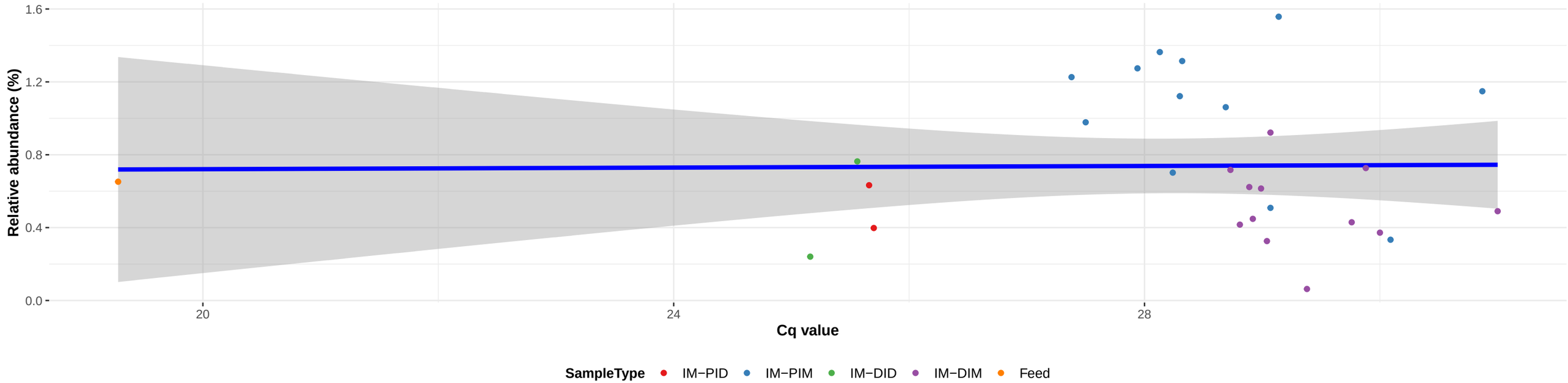
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA

Correlation with all samples

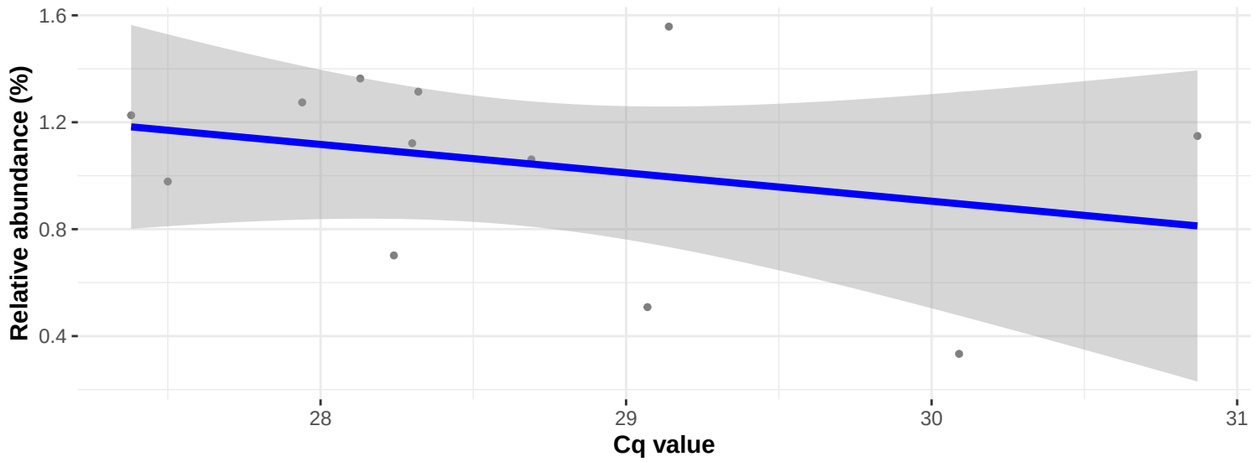
$\log_e(S)$ = 8.516, p = 0.229, $\hat{\rho}_{Spearman}$ = −0.230, $CI_{95\%}$ [−0.558, 0.160], n_{pairs} = 29



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed

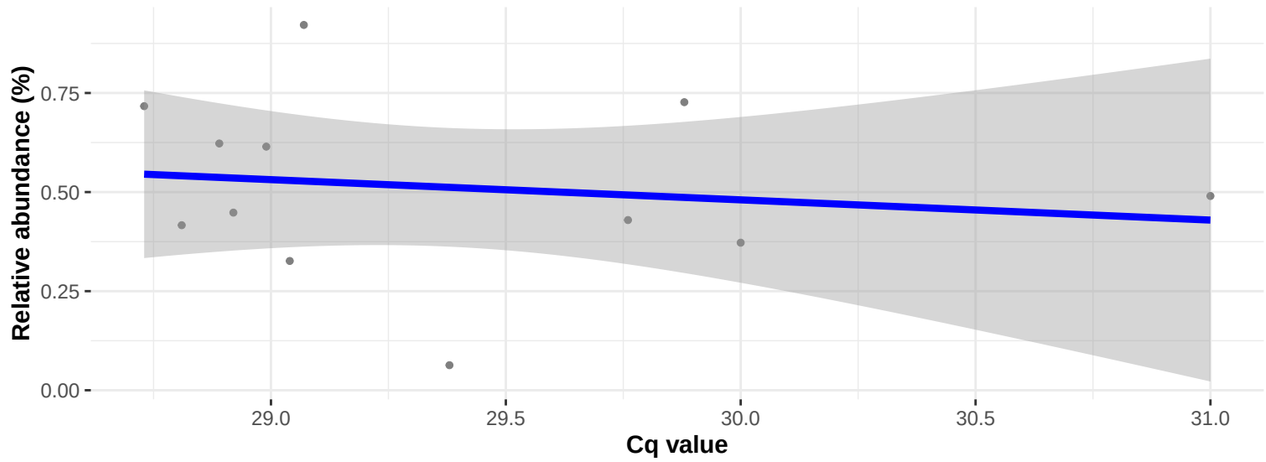
Correlation within: IM−PIM

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

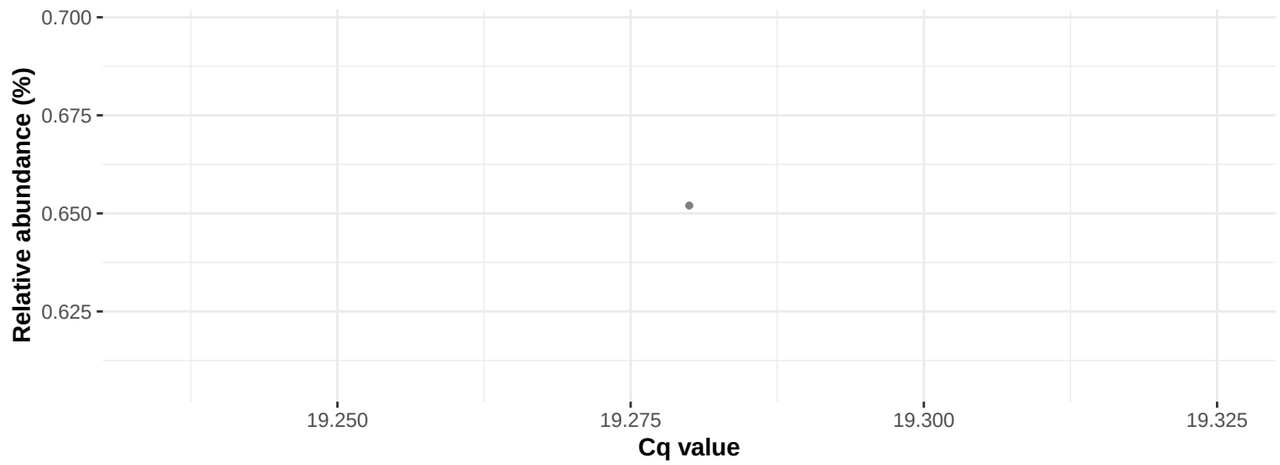


Correlation within: IM−DIM

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



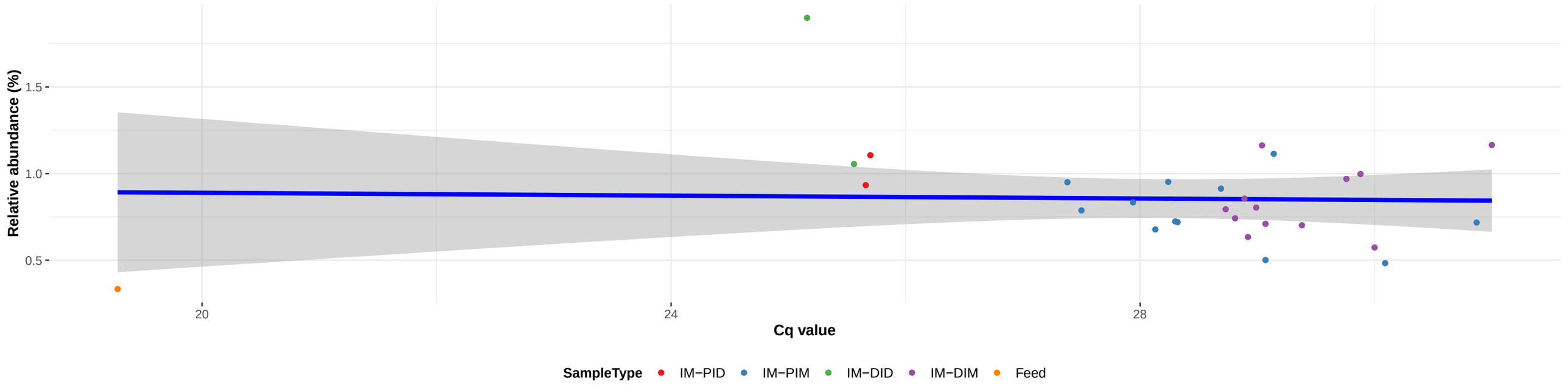
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__uncultured Virgibacillus sp.

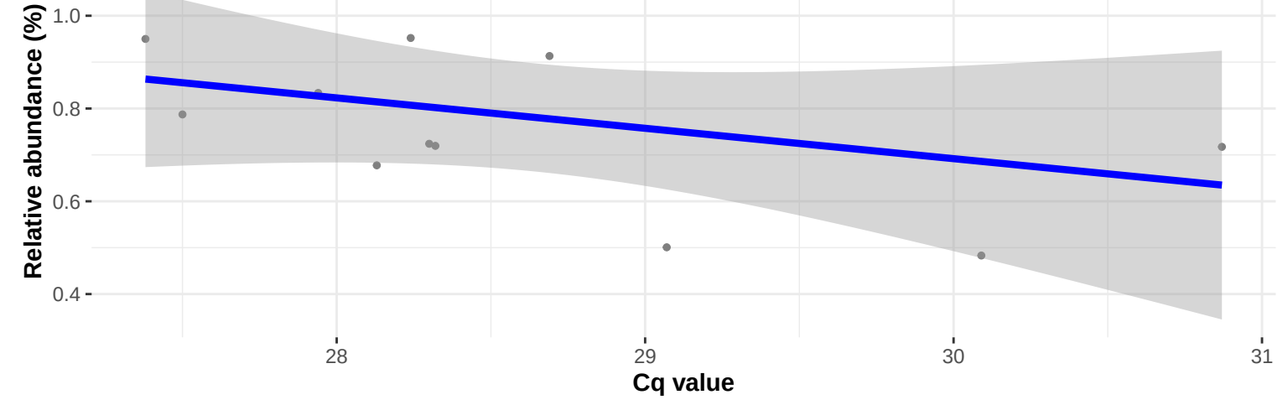
Correlation with all samples

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



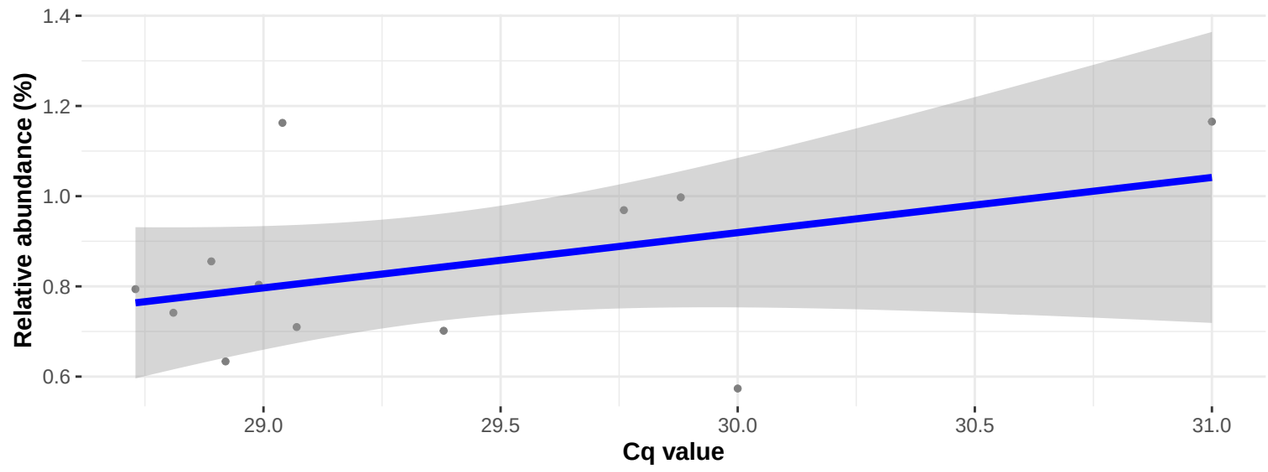
Correlation within: IM−PIM

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

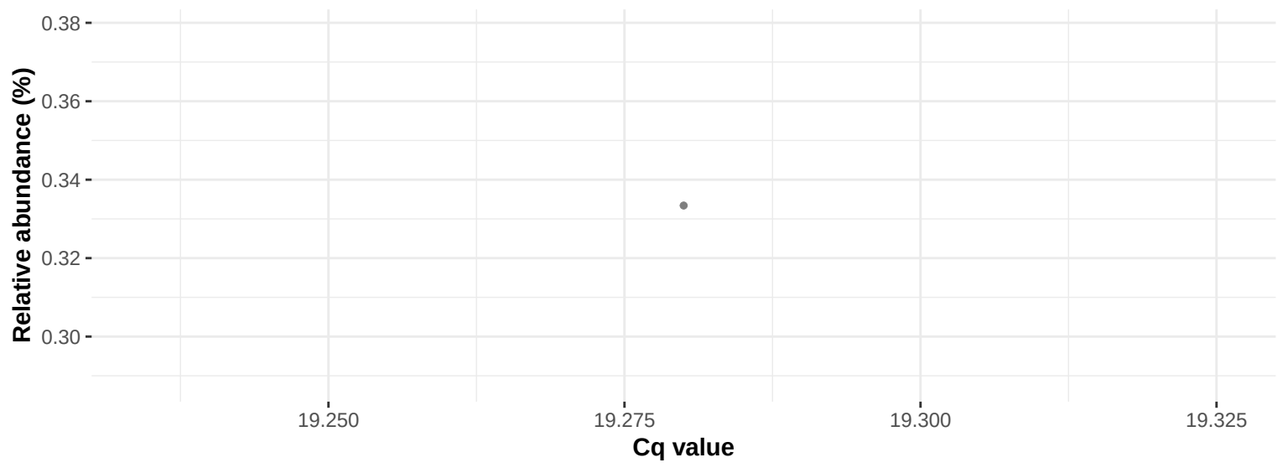


Correlation within: IM−DIM

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



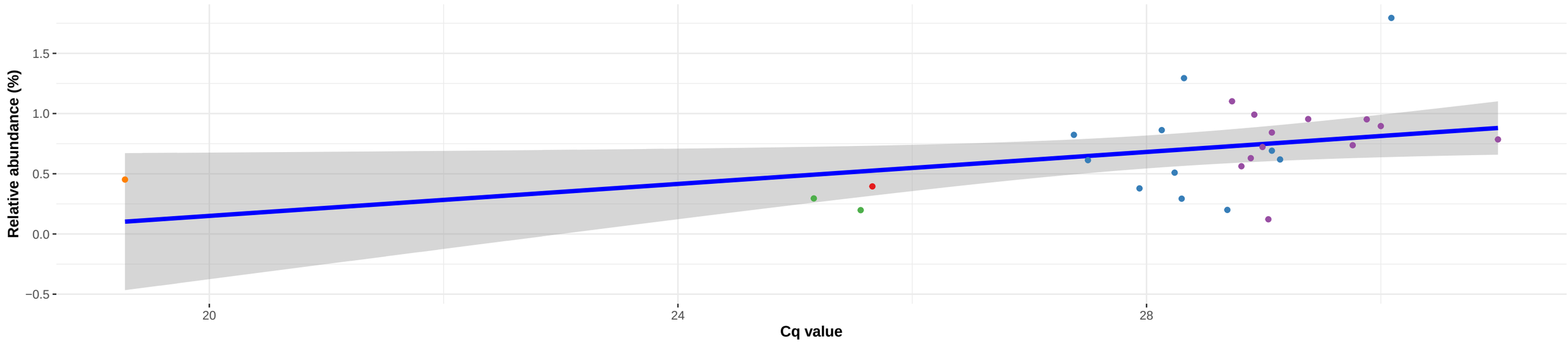
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; NA

Correlation with all samples

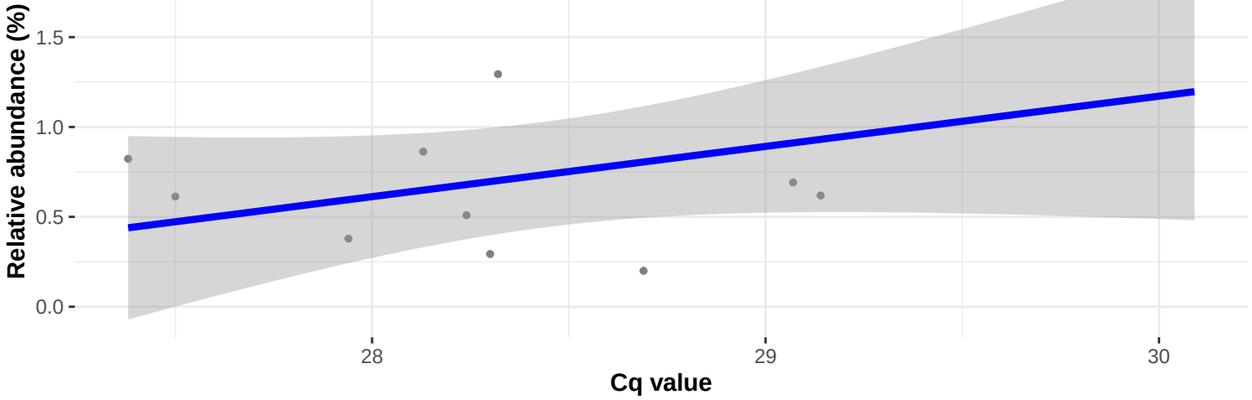
$\log_e(S)$ = 7.348, p = 0.005, $\hat{\rho}_{Spearman}$ = 0.526, $CI_{95\%}$ [0.171, 0.760], n_{pairs} = 27



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

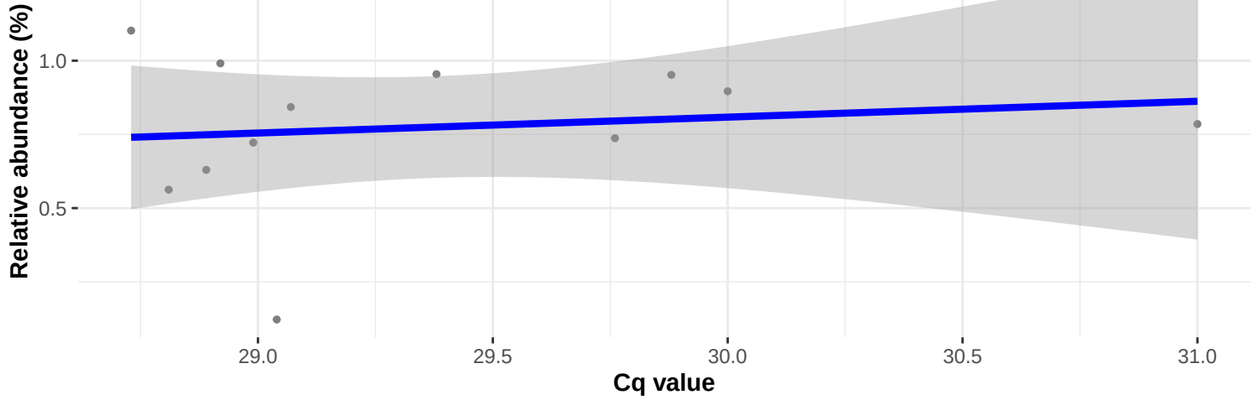
Correlation within: IM−PIM

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

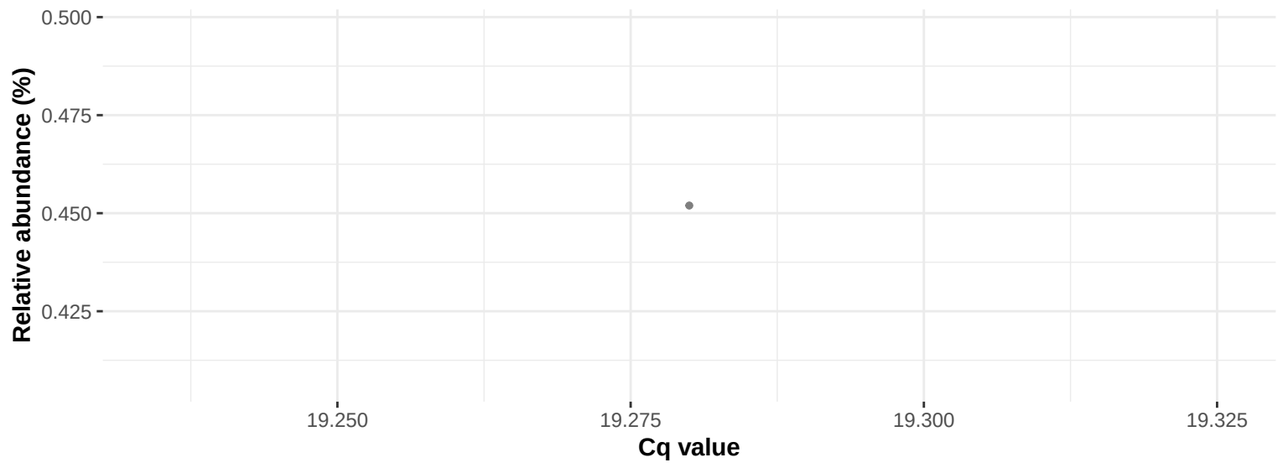


Correlation within: IM−DIM

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



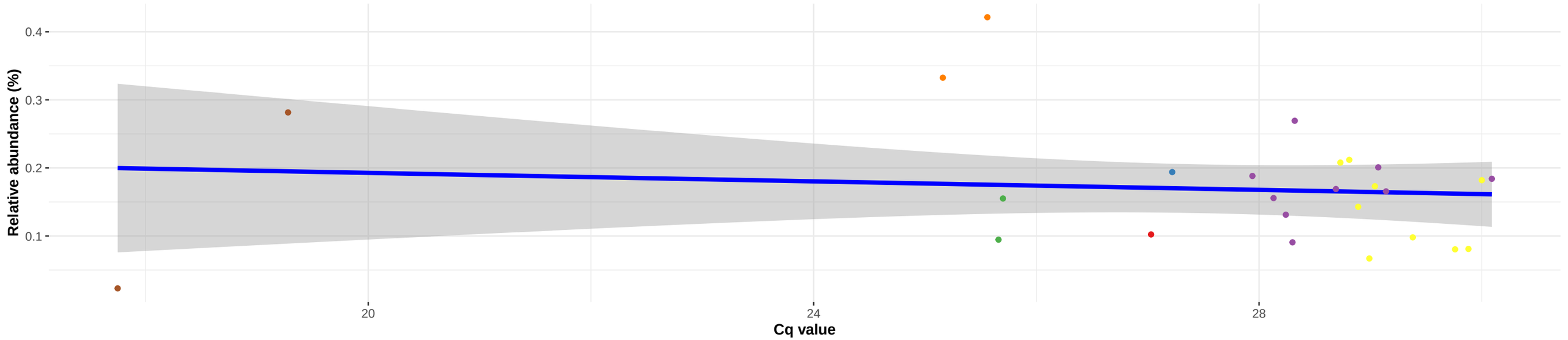
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus thermoamylovorans

Correlation with all samples

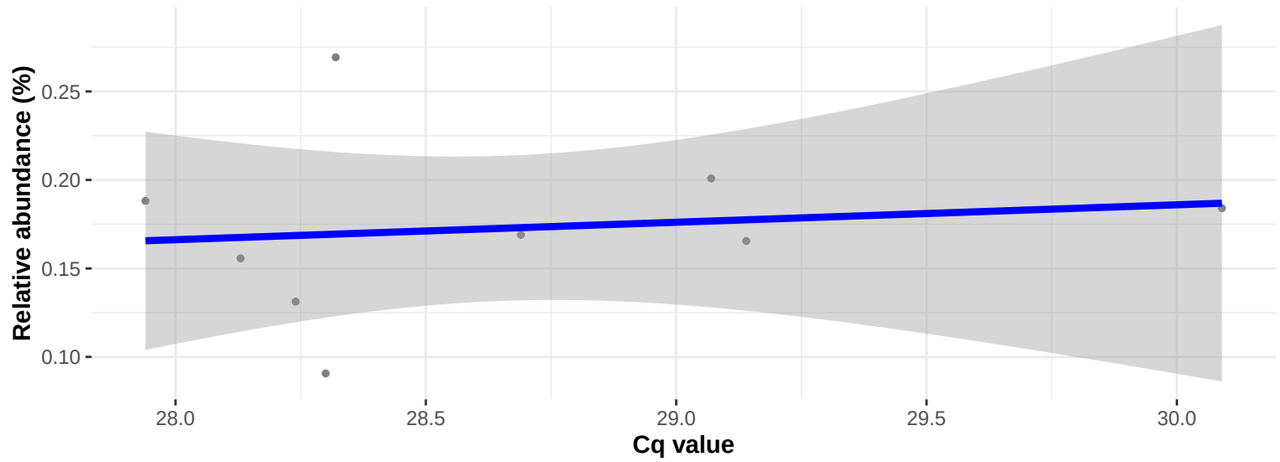
$\log_e(S)$ = 8.155, p = 0.351, $\hat{\rho}_{Spearman}$ = −0.190, $CI_{95\%}$ [−0.547, 0.224], n_{pairs} = 26



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

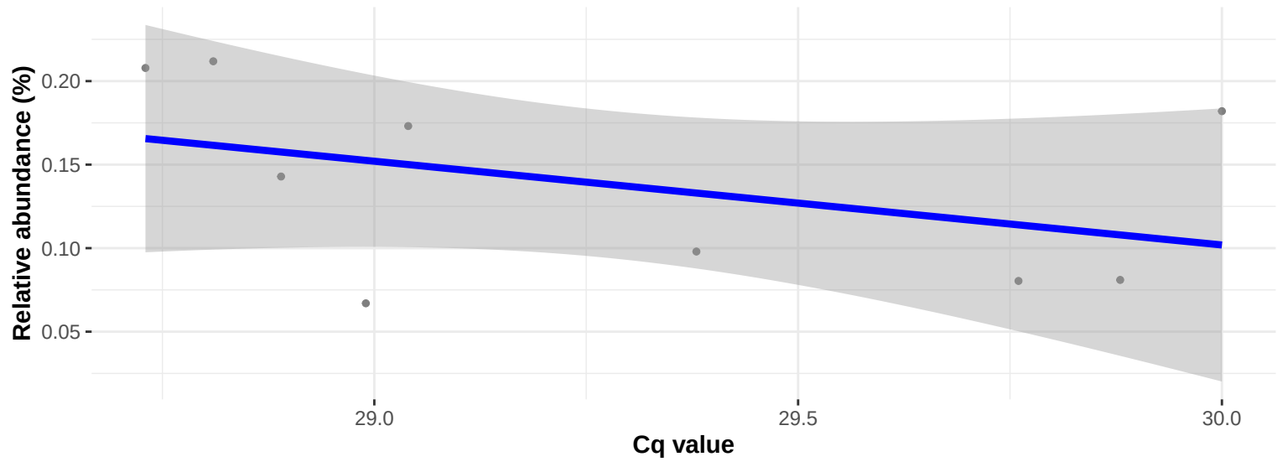
Correlation within: IM−PIM

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

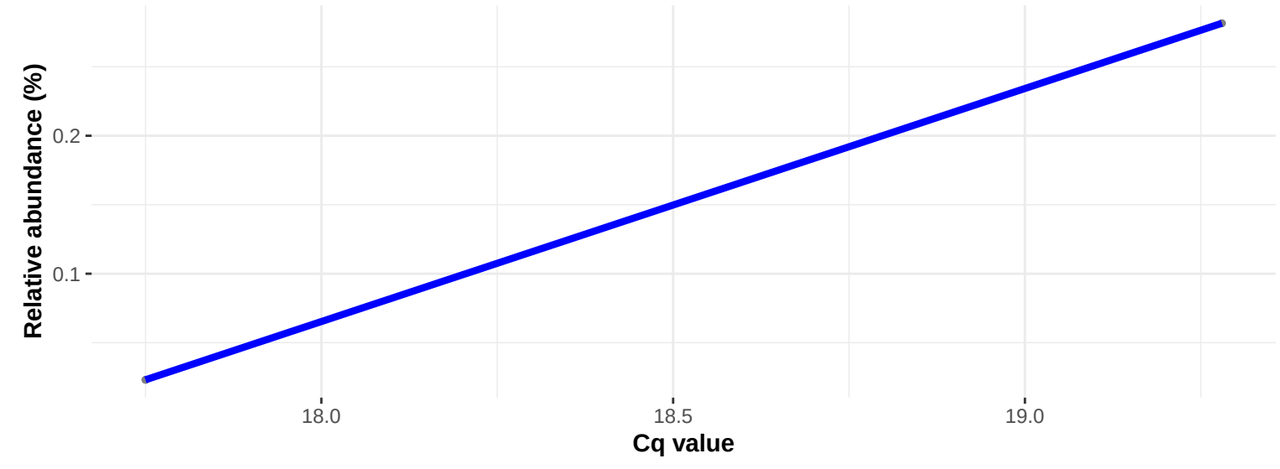


Correlation within: IM−DIM

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



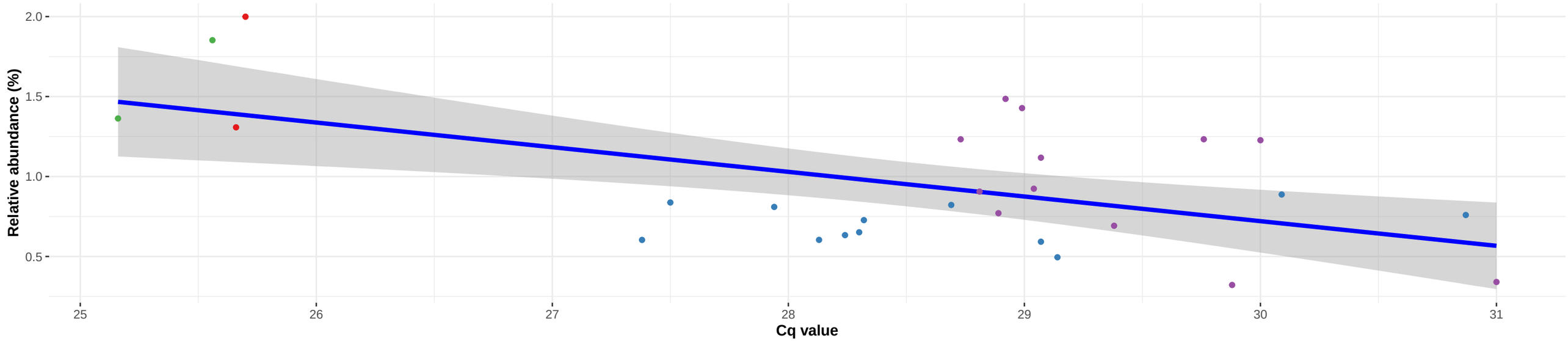
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples

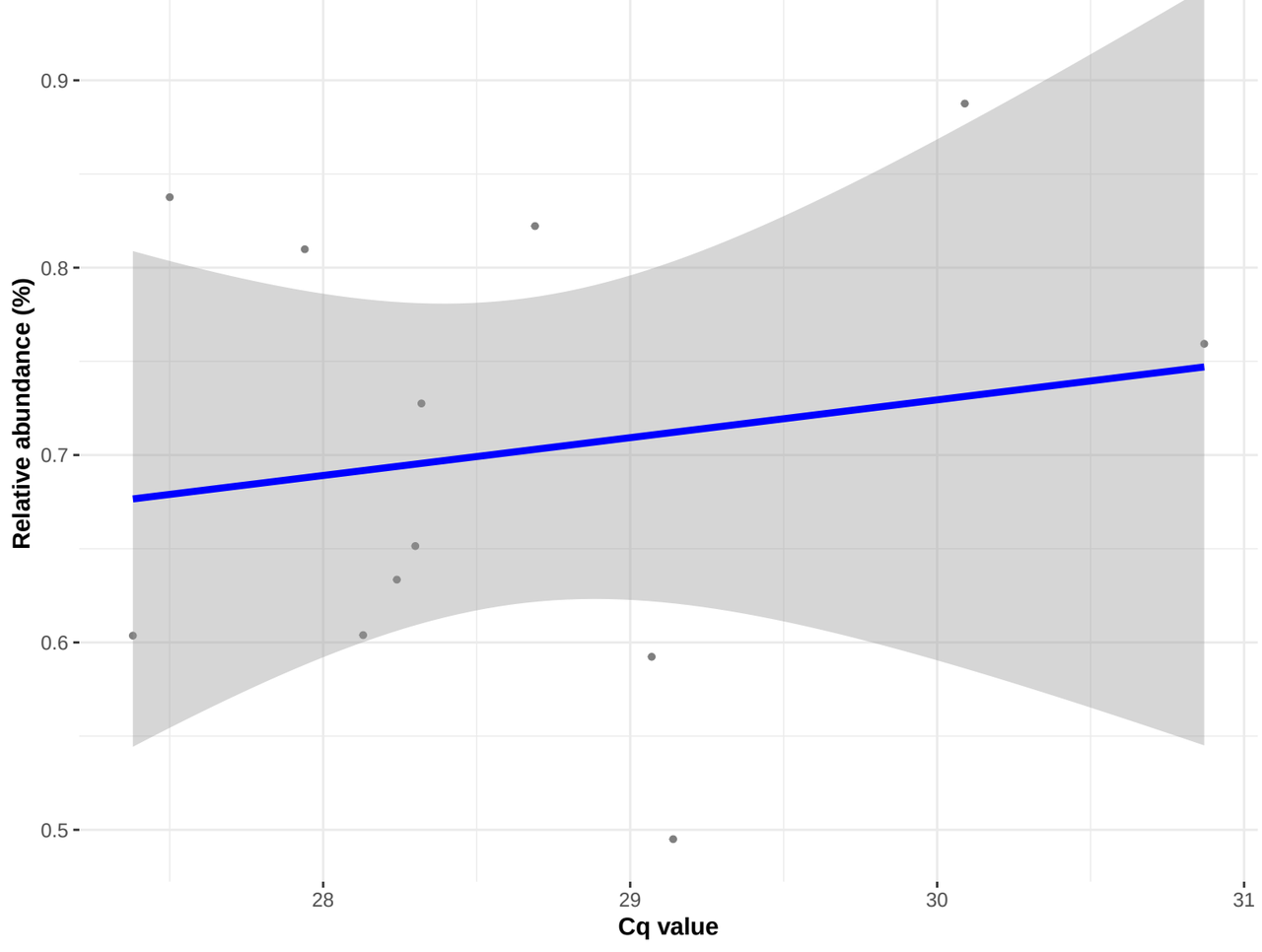
$\log_e(S)$ = 8.483, p = 0.095, $\hat{\rho}_{Spearman}$ = −0.322, $CI_{95\%}$ [−0.628, 0.069], n_{pairs} = 28



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM

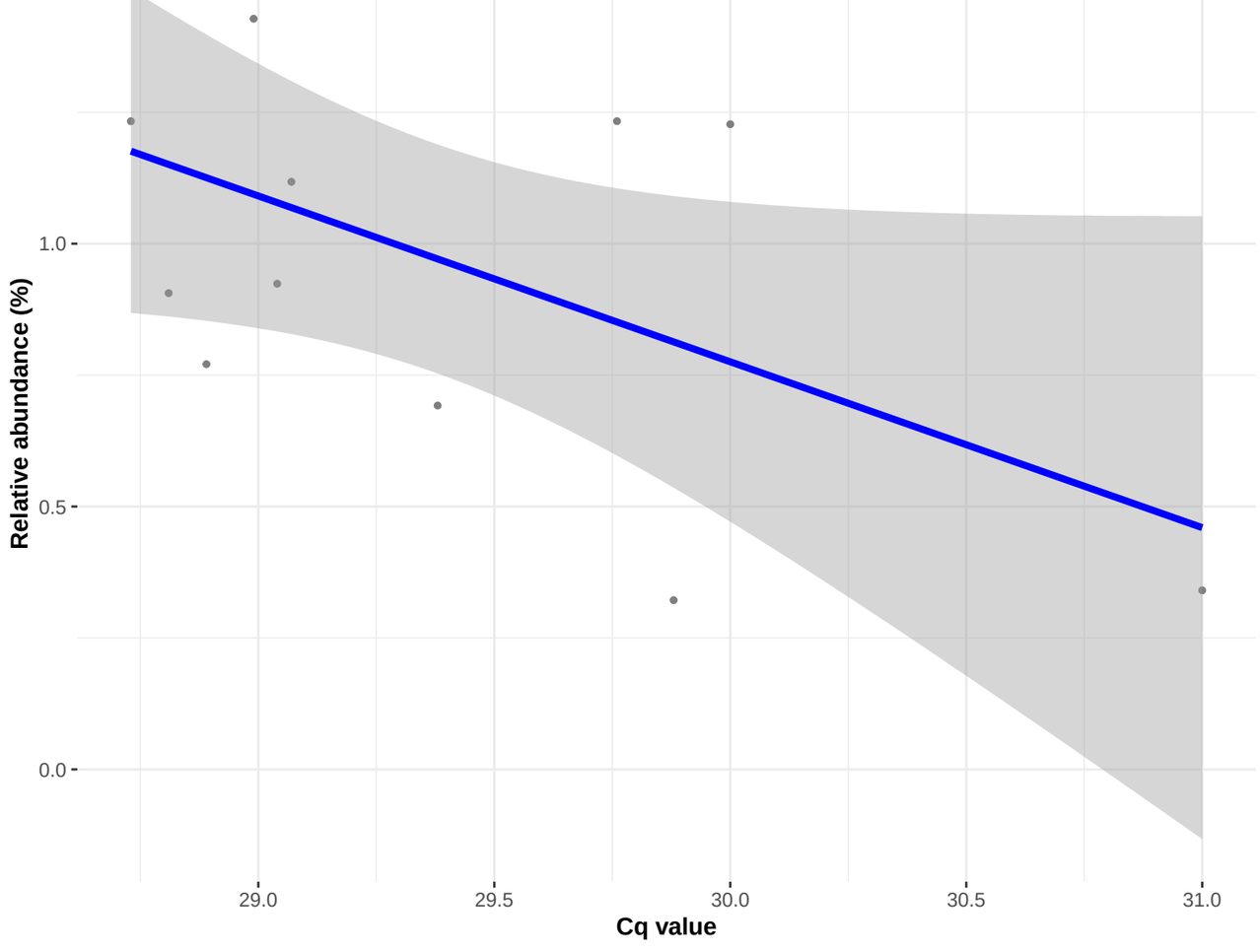
Correlation within: IM−PIM

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



Correlation within: IM−DIM

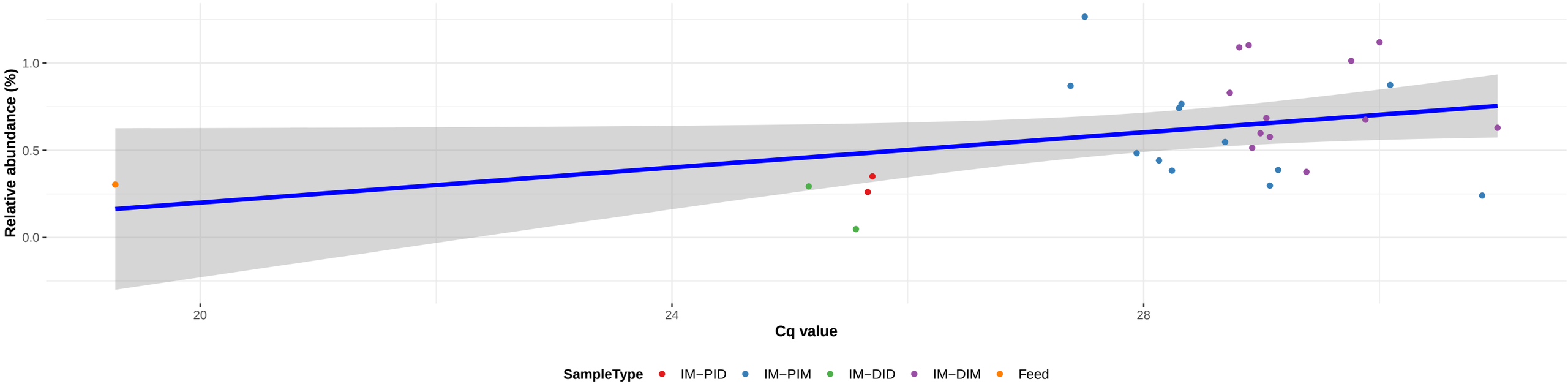
$\log_e(S)$ = 5.966, p = 0.245, $\hat{\rho}_{Spearman}$ = −0.364, $CI_{95\%}$ [−0.783, 0.284], n_{pairs} = 12



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; s__Corynebacterium xerosis

Correlation with all samples

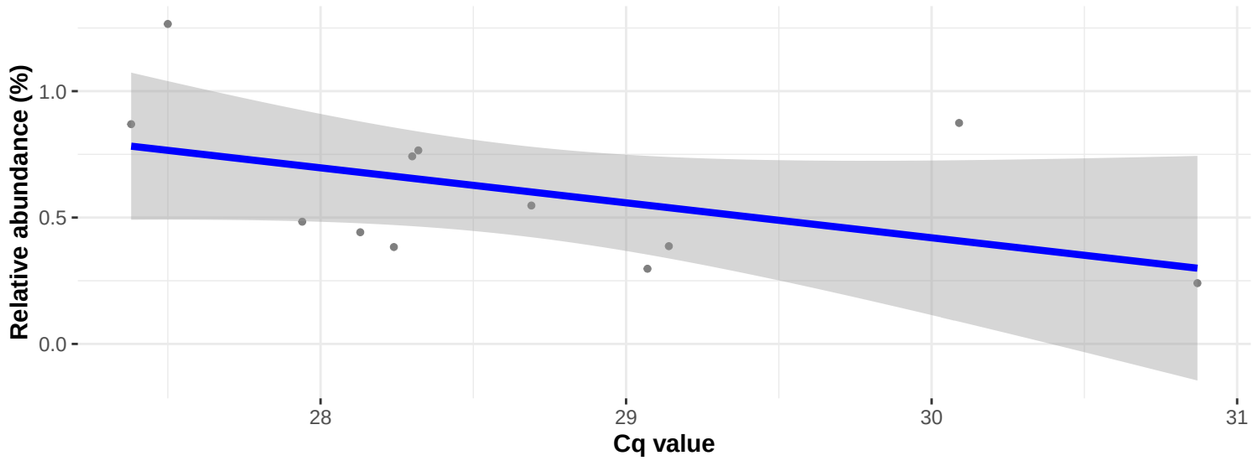
$\log_e(S)$ = 7.953, p = 0.114, $\hat{\rho}_{Spearman}$ = 0.300, $CI_{95\%}$ [−0.087, 0.607], n_{pairs} = 29



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed

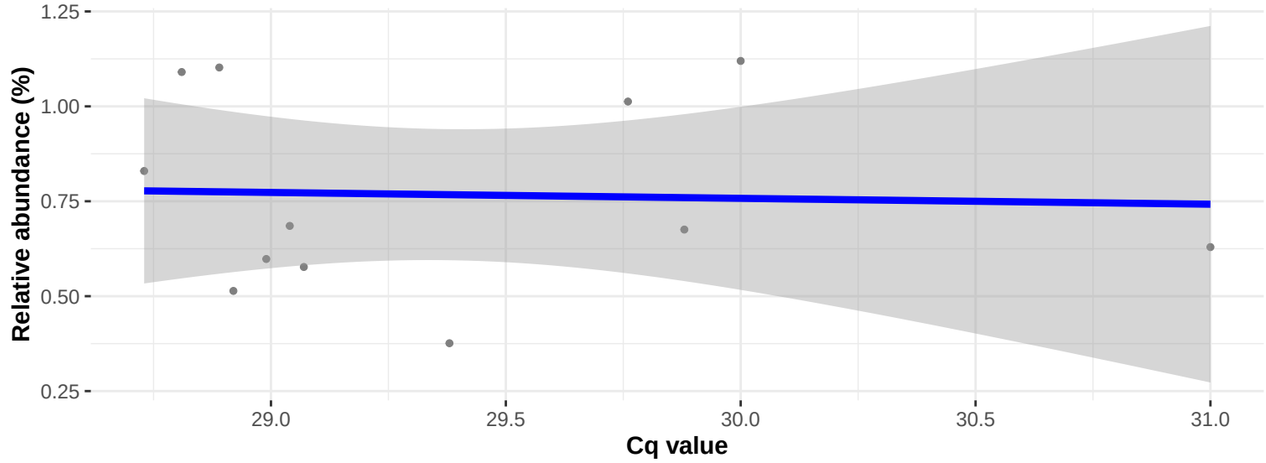
Correlation within: IM−PIM

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

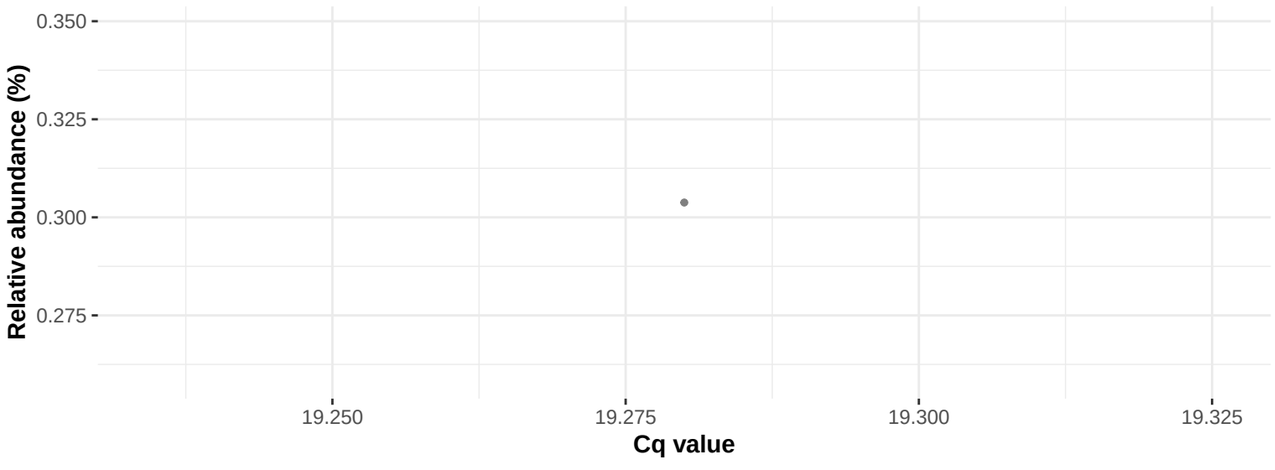


Correlation within: IM−DIM

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



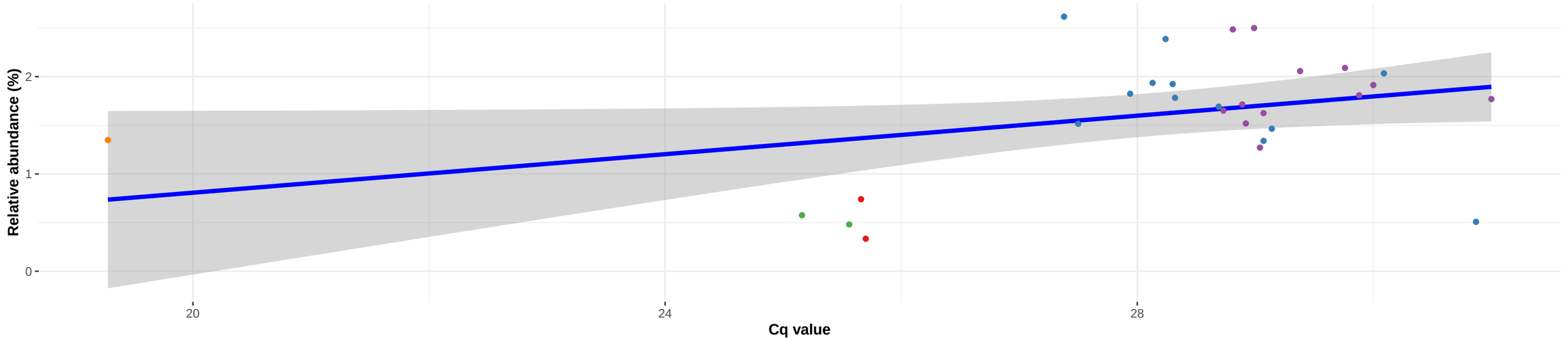
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

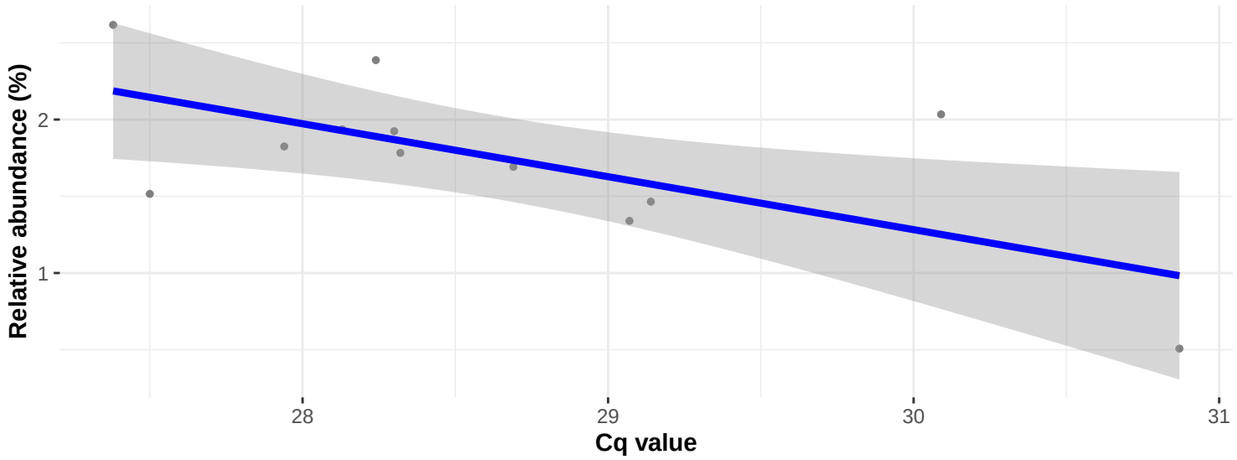
$\log_e(S)$ = 8.024, p = 0.194, $\hat{\rho}_{Spearman}$ = 0.248, $CI_{95\%}$ [−0.141, 0.571], n_{pairs} = 29



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed

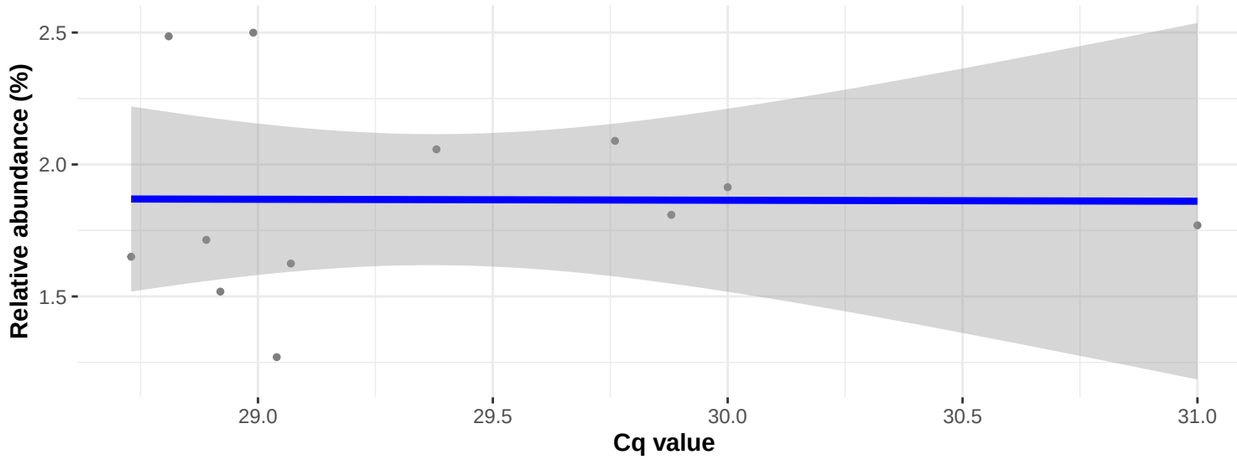
Correlation within: IM−PIM

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

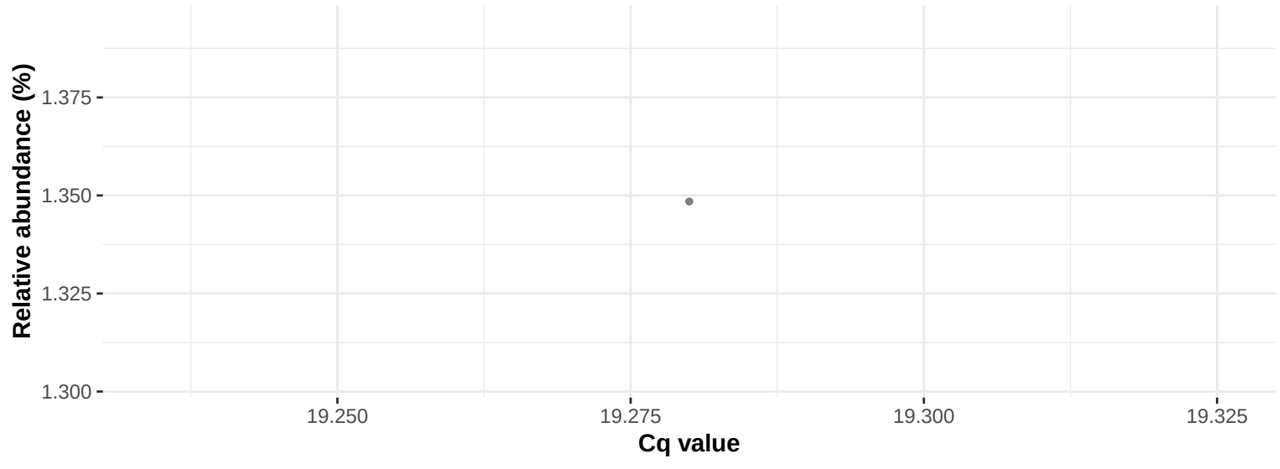


Correlation within: IM−DIM

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



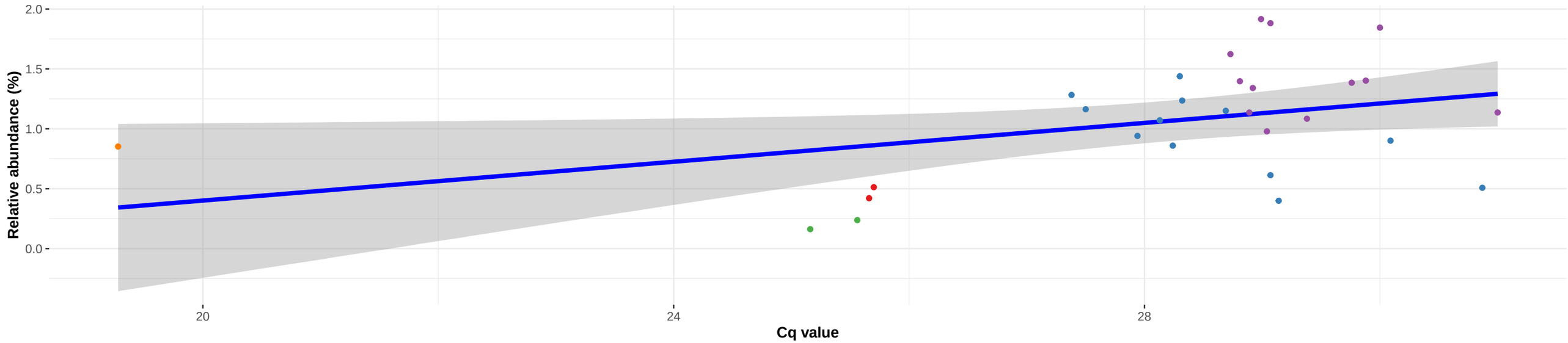
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Microbacterium; Ambiguous_taxa

Correlation with all samples

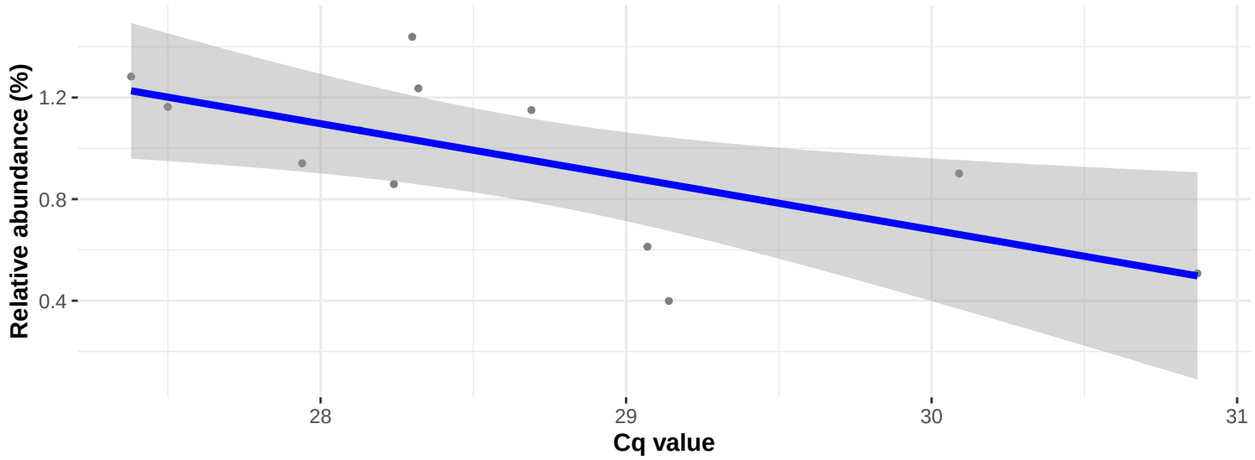
$\log_e(S)$ = 7.910, p = 0.082, $\hat{\rho}_{Spearman}$ = 0.329, $CI_{95\%}$ [−0.054, 0.628], n_{pairs} = 29



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

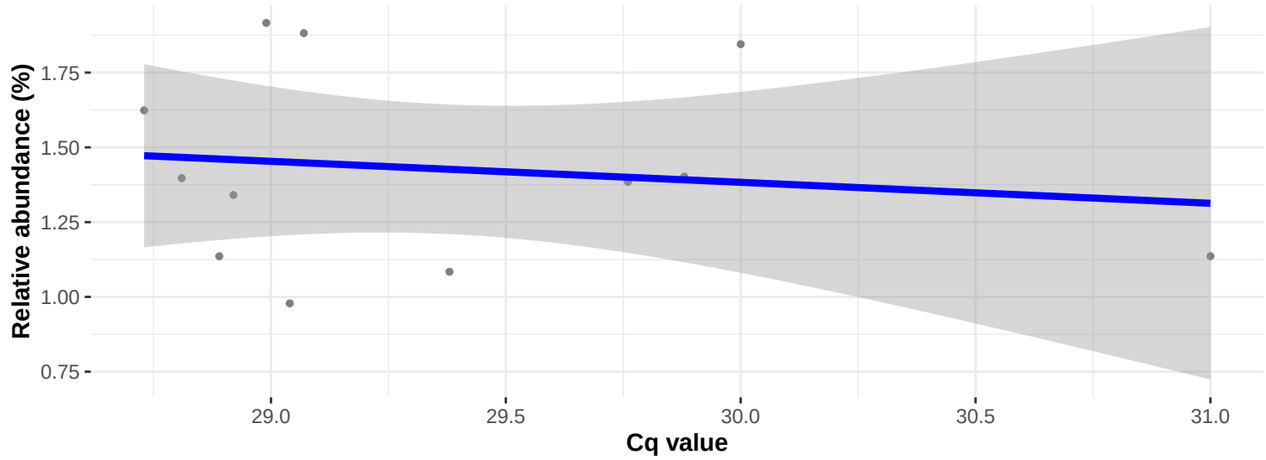
Correlation within: IM−PIM

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

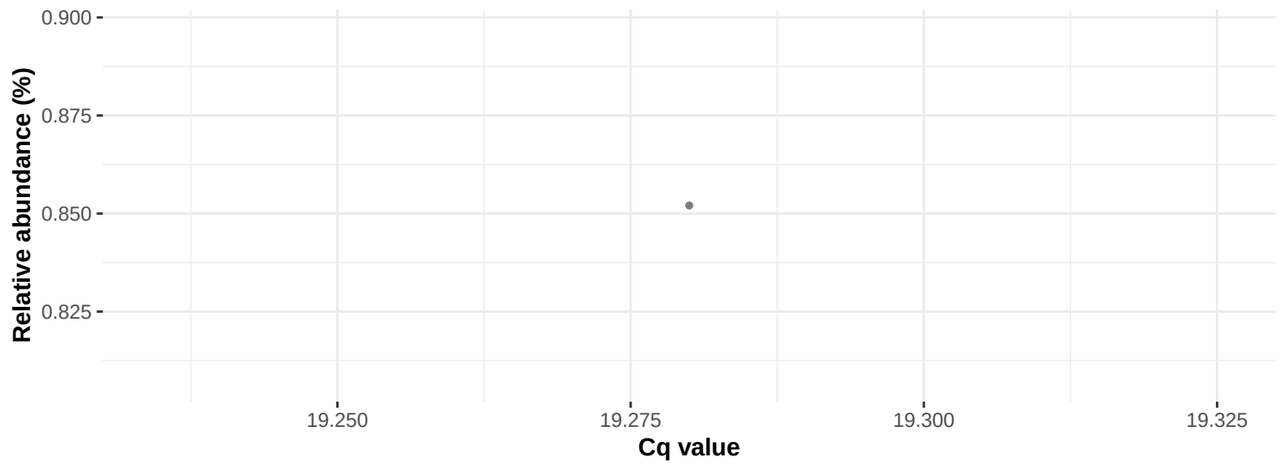


Correlation within: IM−DIM

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



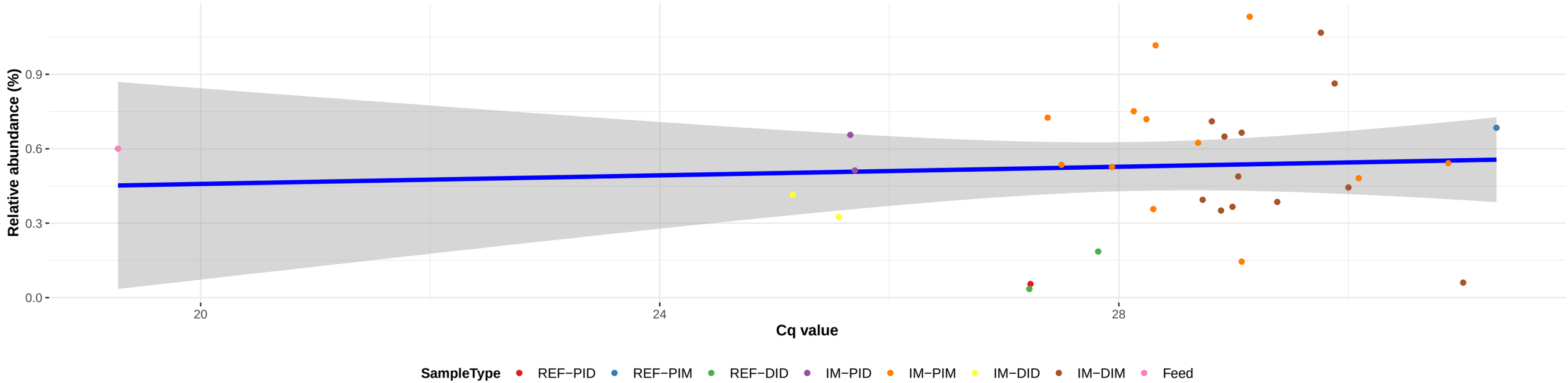
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Macrococcus; Ambiguous_taxa

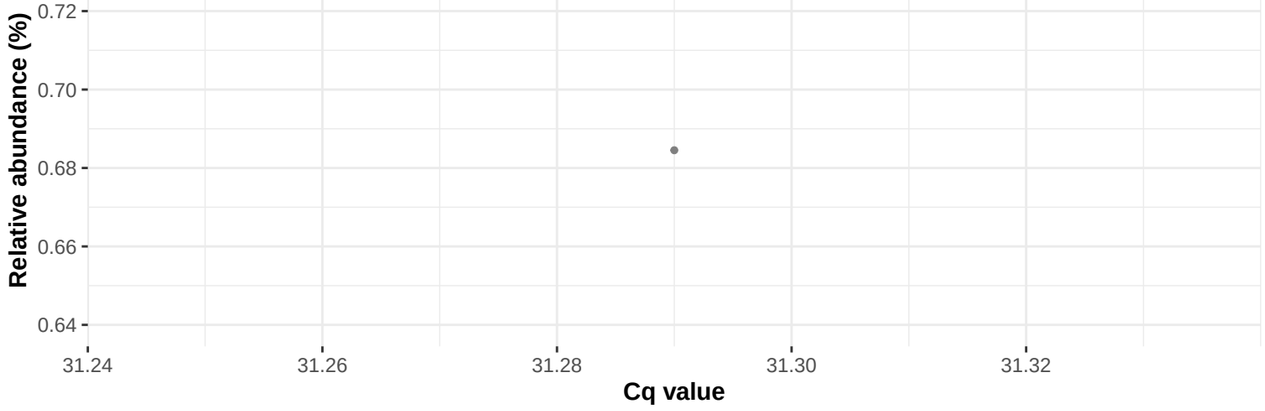
Correlation with all samples

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



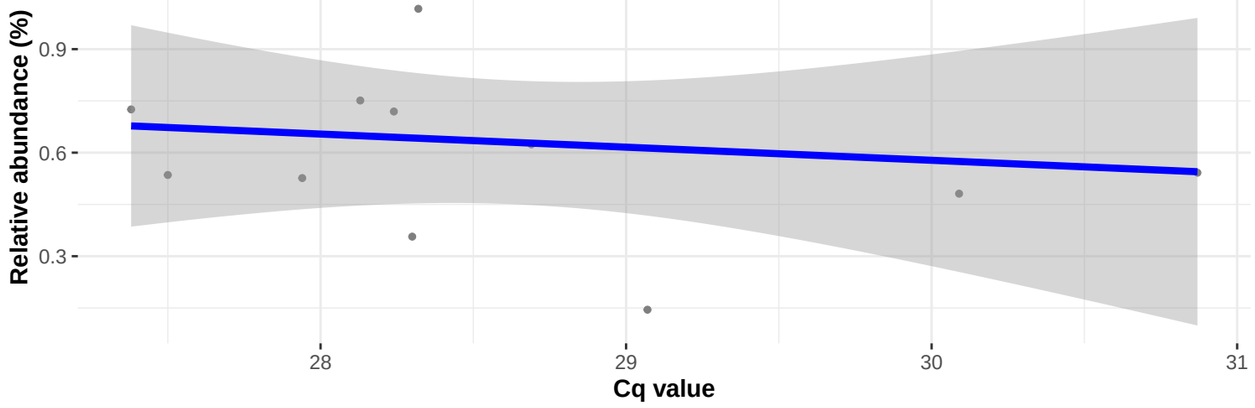
SampleType REF−PID REF−PIM REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



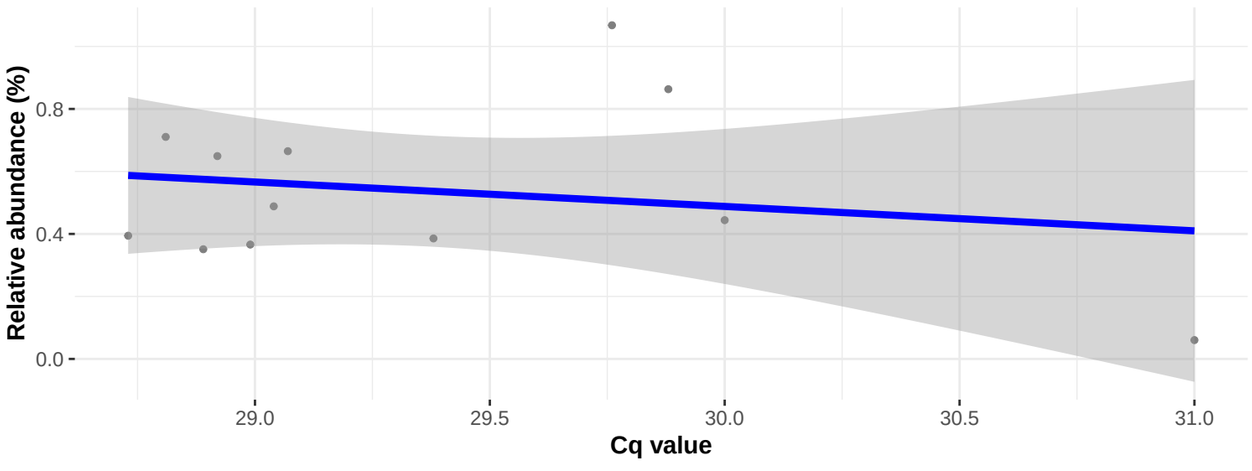
Correlation within: IM−PIM

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

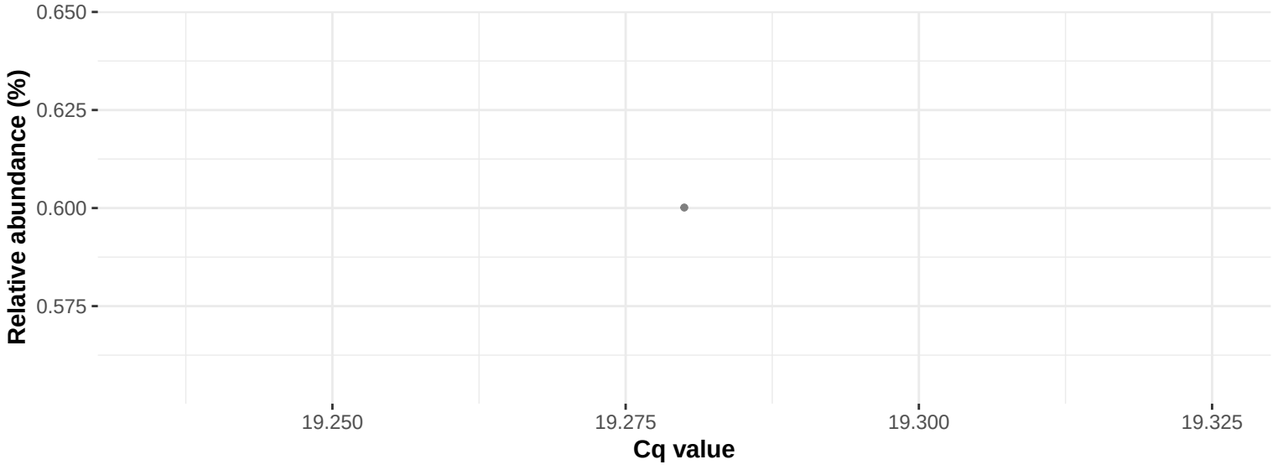


Correlation within: IM−DIM

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



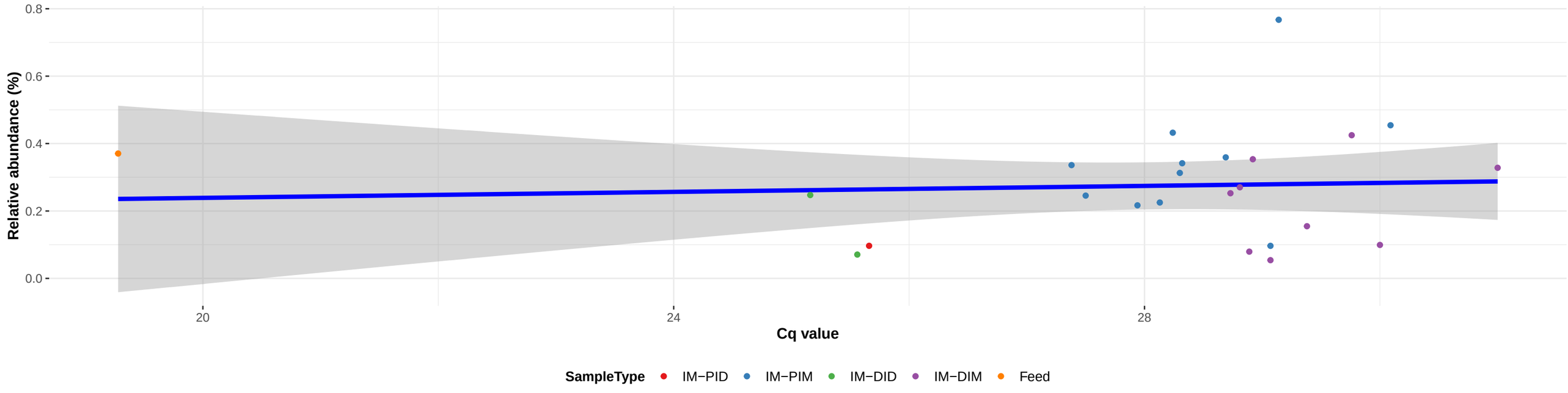
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA

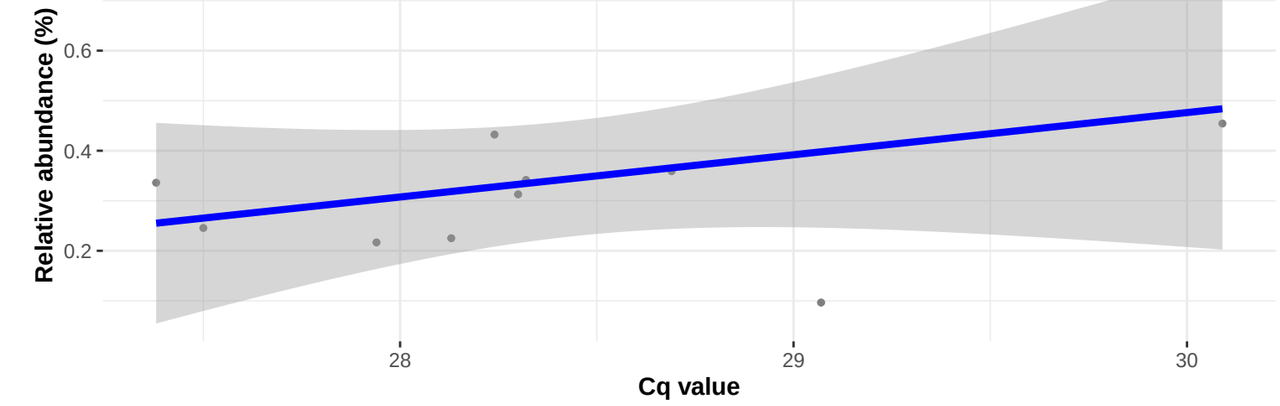
Correlation with all samples

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



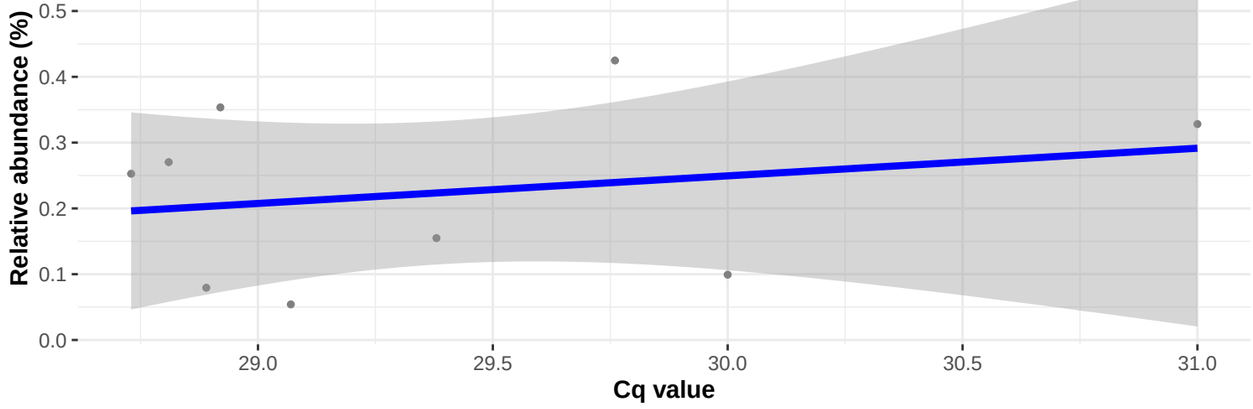
Correlation within: IM−PIM

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

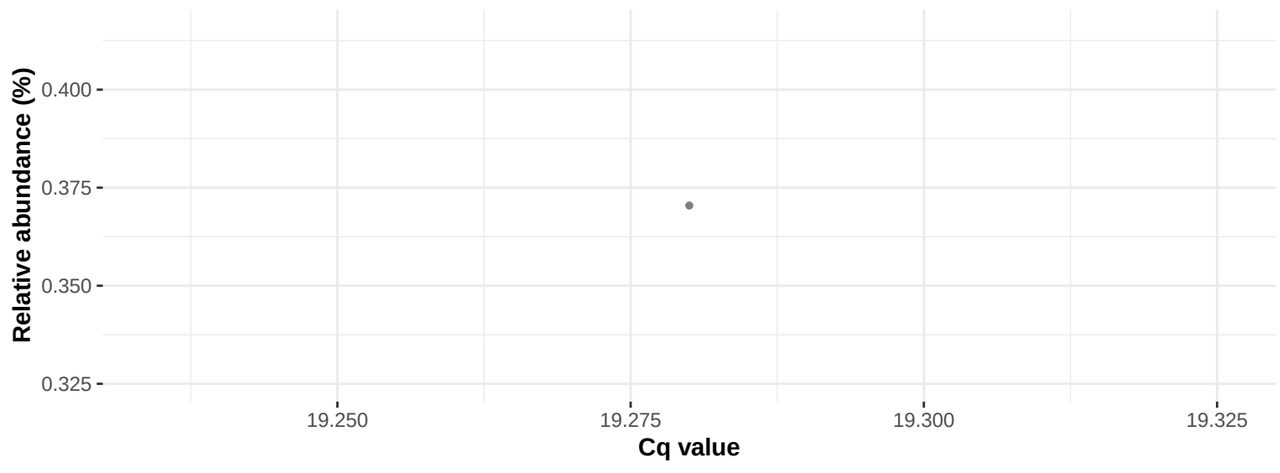


Correlation within: IM−DIM

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



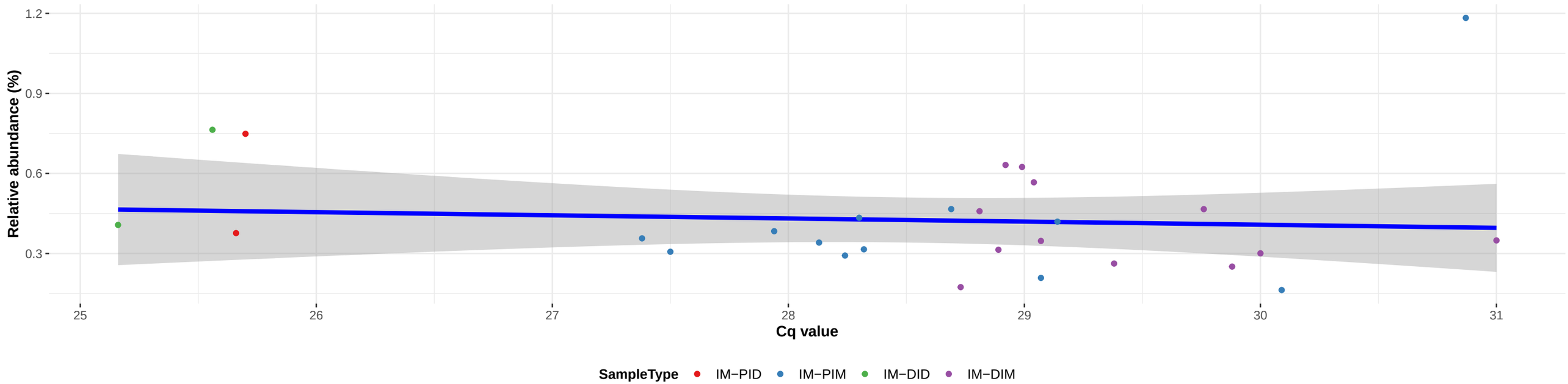
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Ornithinibacillus; Ambiguous_taxa

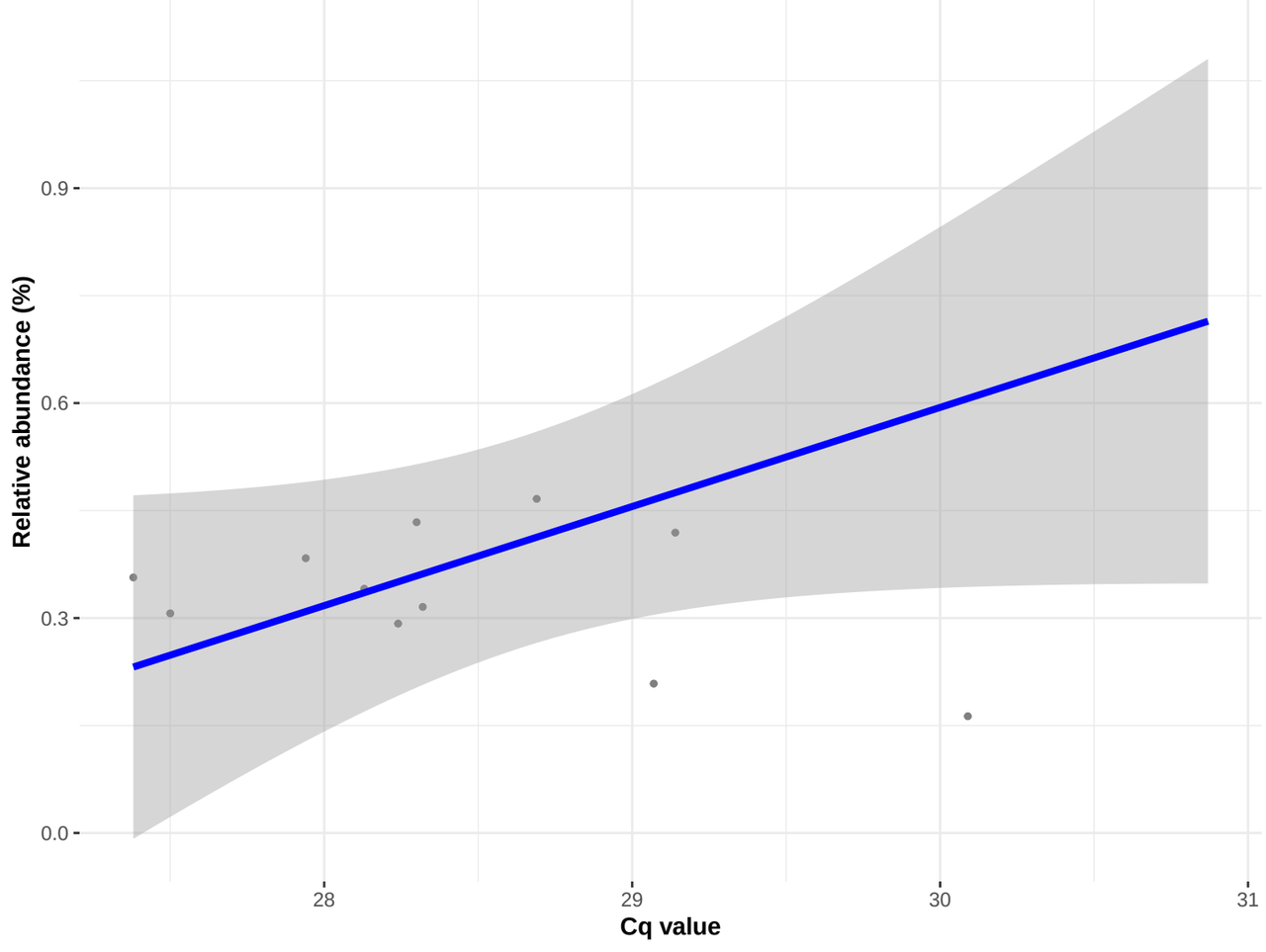
Correlation with all samples

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



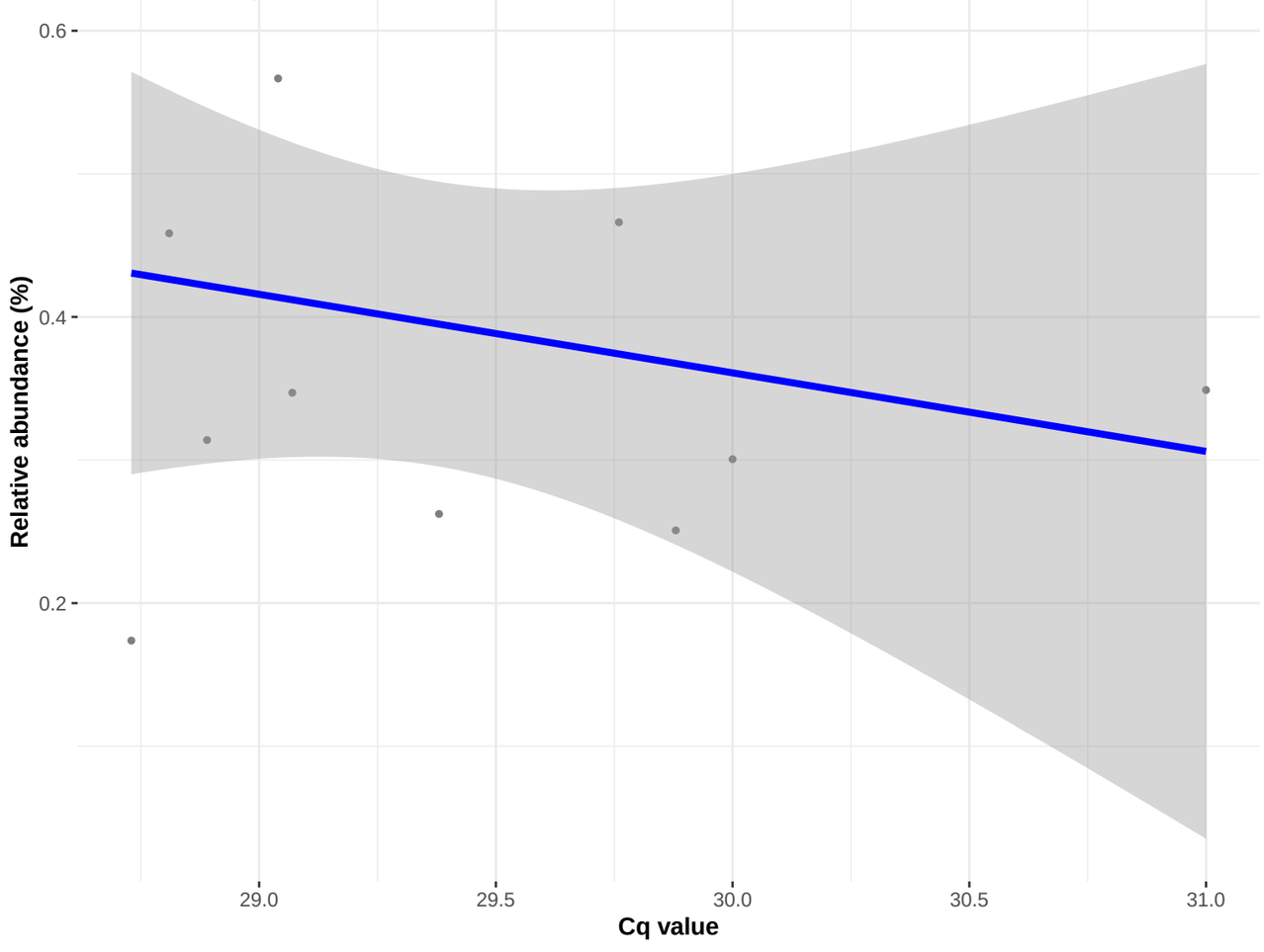
Correlation within: IM−PIM

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



Correlation within: IM−DIM

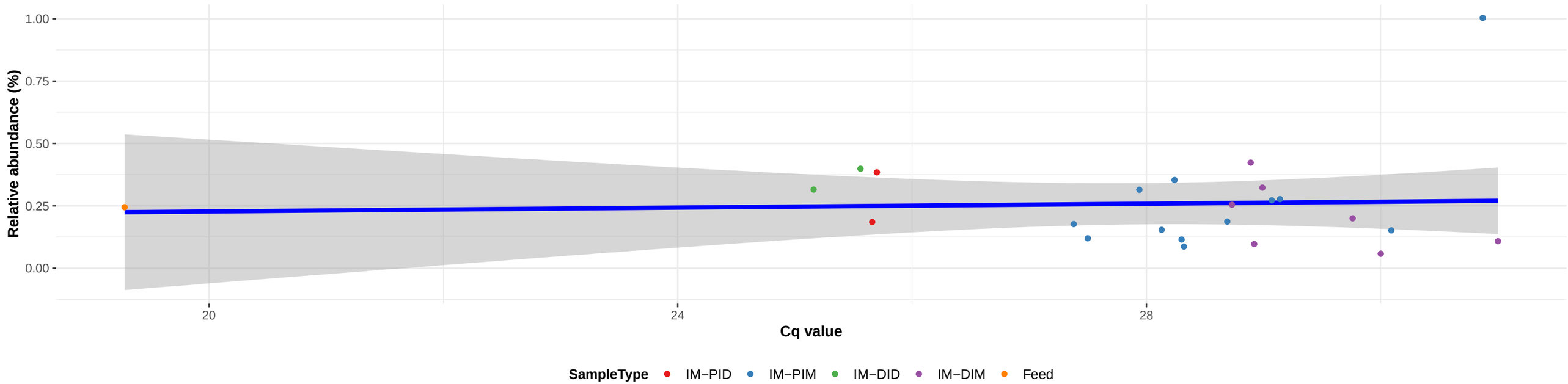
$\log_e(S)$ = 5.768, p = 0.713, $\hat{\rho}_{Spearman}$ = −0.119, $CI_{95\%}$ [−0.660, 0.503], n_{pairs} = 12



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

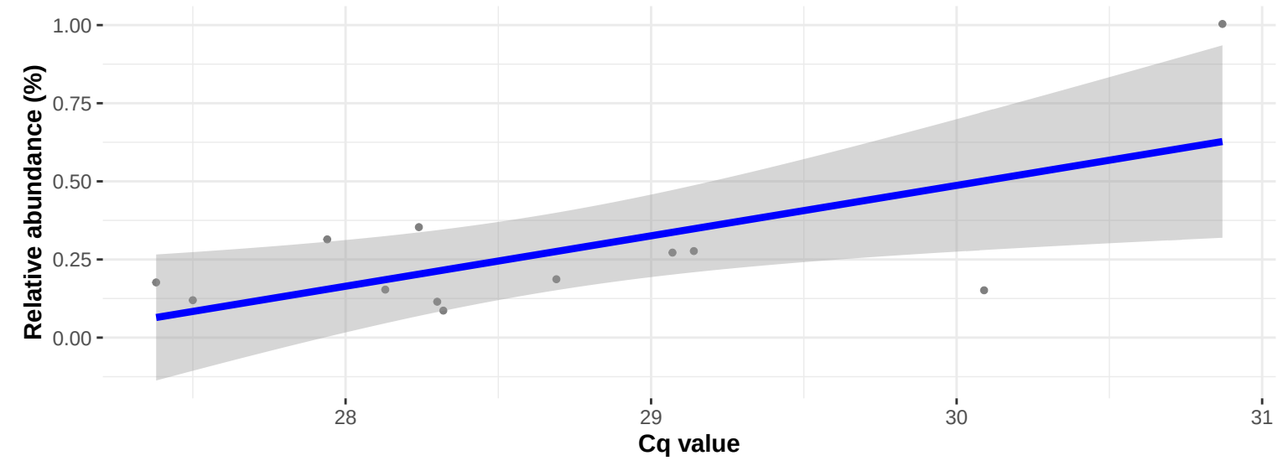
Correlation with all samples

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



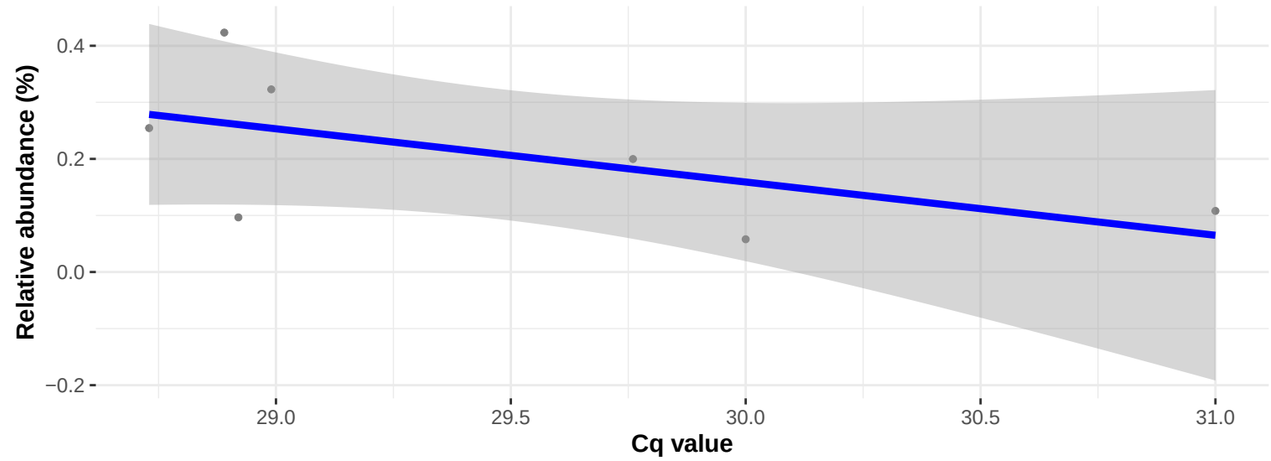
Correlation within: IM−PIM

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

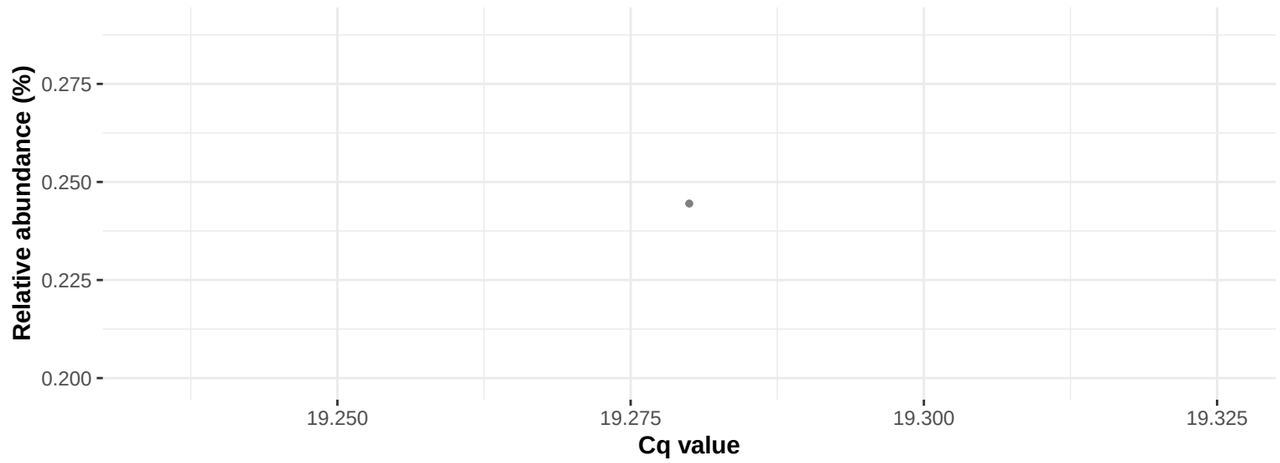


Correlation within: IM−DIM

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



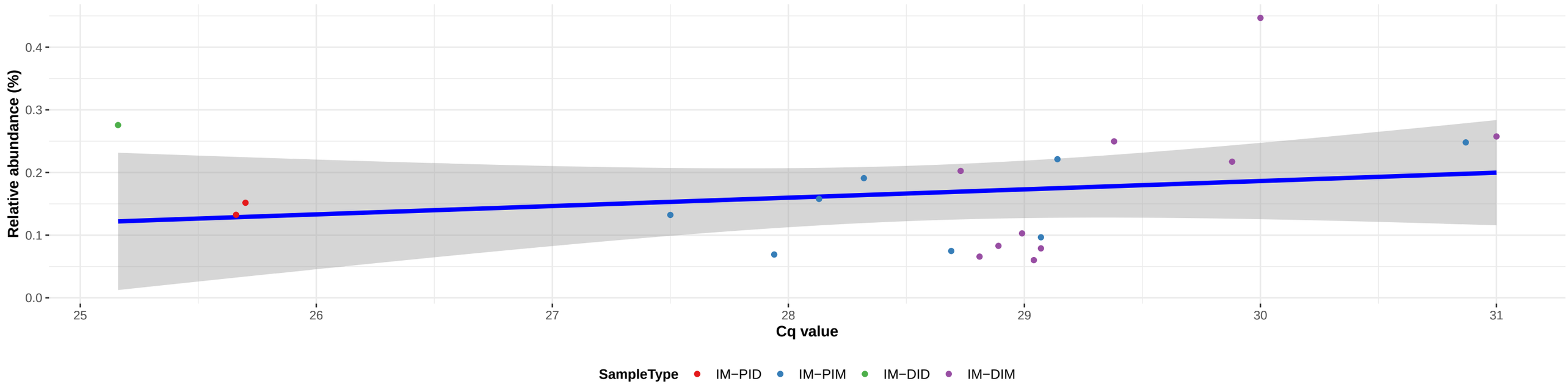
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Gracilibacillus; Ambiguous_taxa

Correlation with all samples

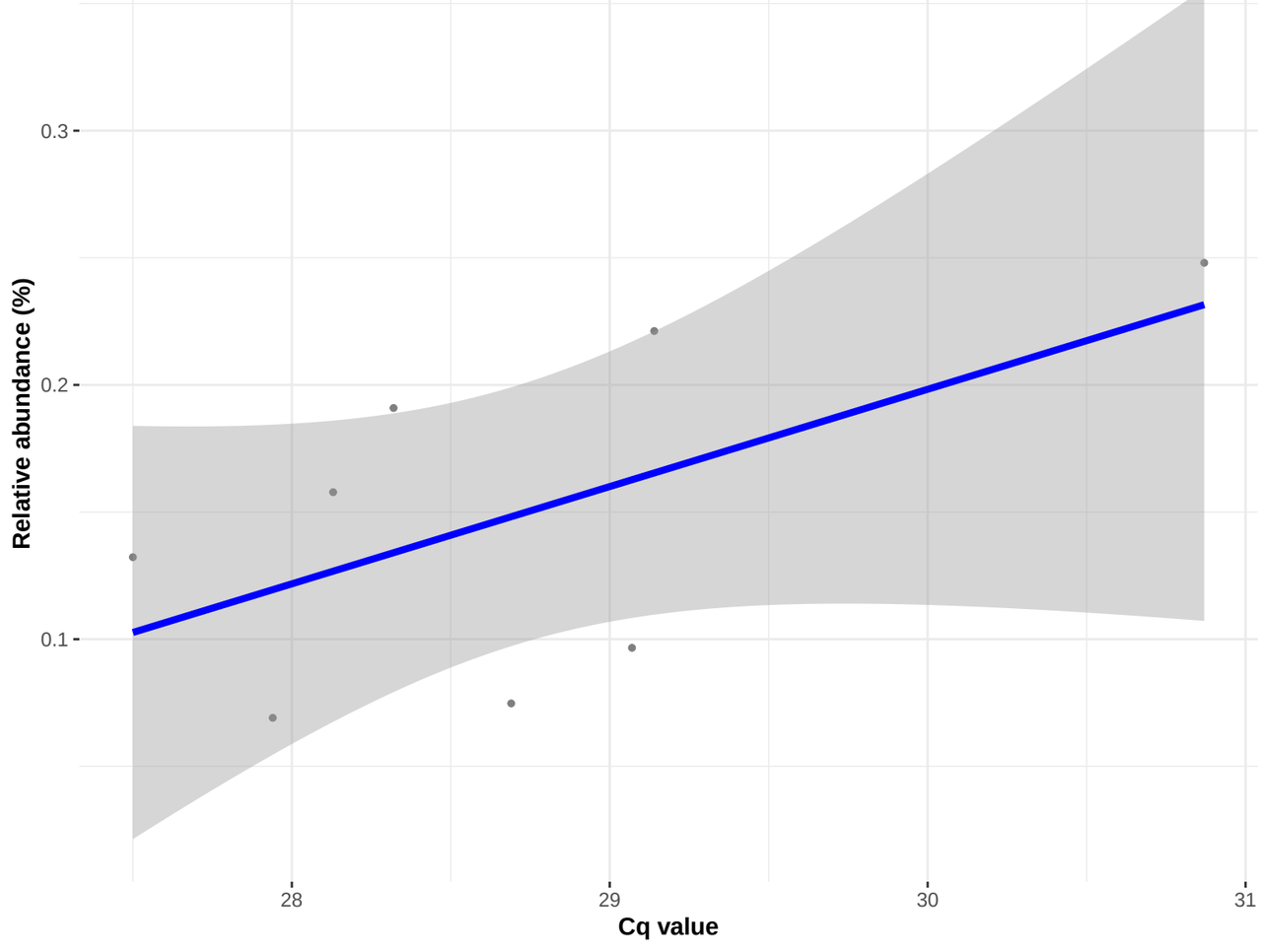
$\log_e(S)$ = 6.960, p = 0.163, $\hat{\rho}_{Spearman}$ = 0.316, $CI_{95\%}$ [−0.148, 0.665], n_{pairs} = 21



SampleType IM−PID IM−PIM IM−DID IM−DIM

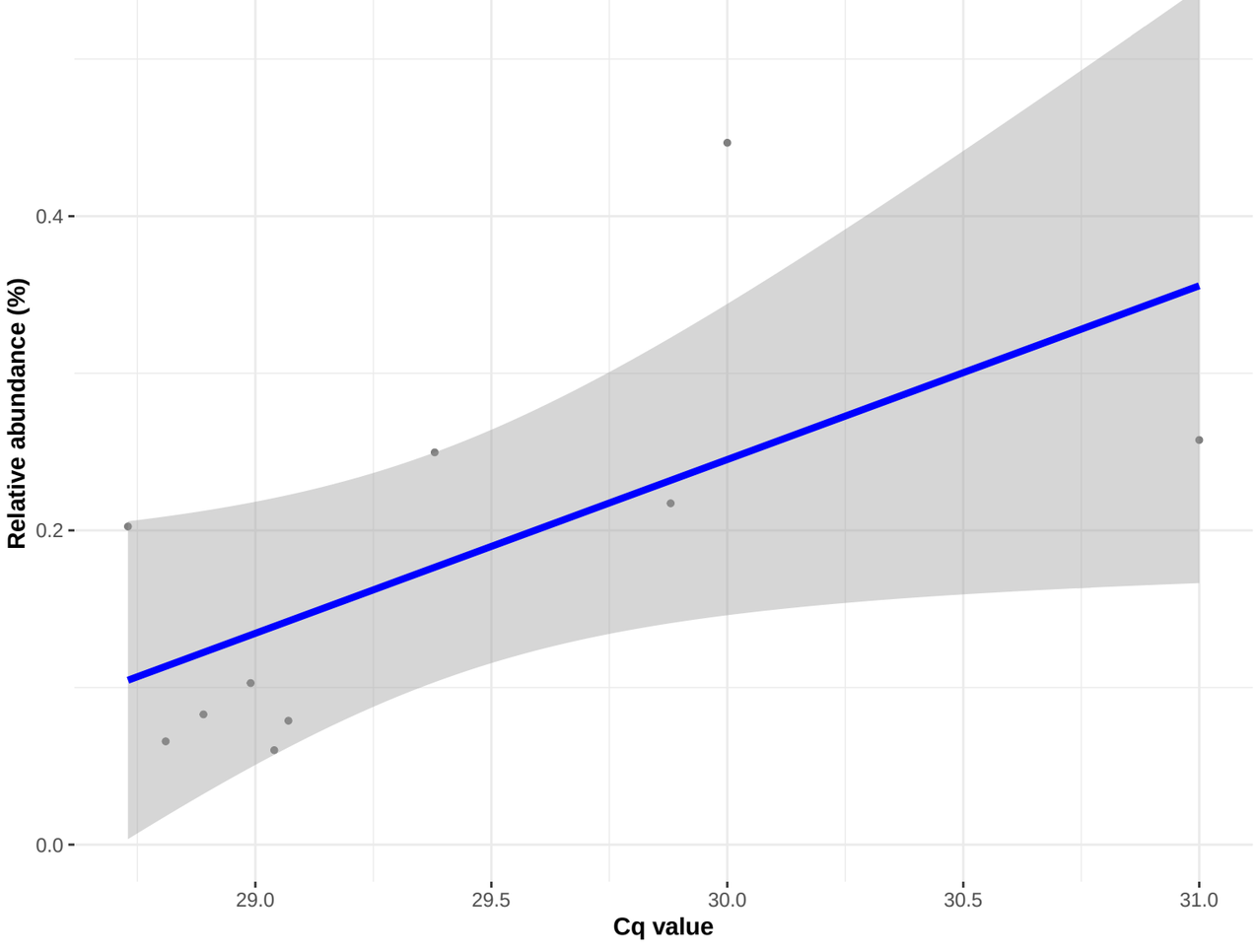
Correlation within: IM−PIM

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



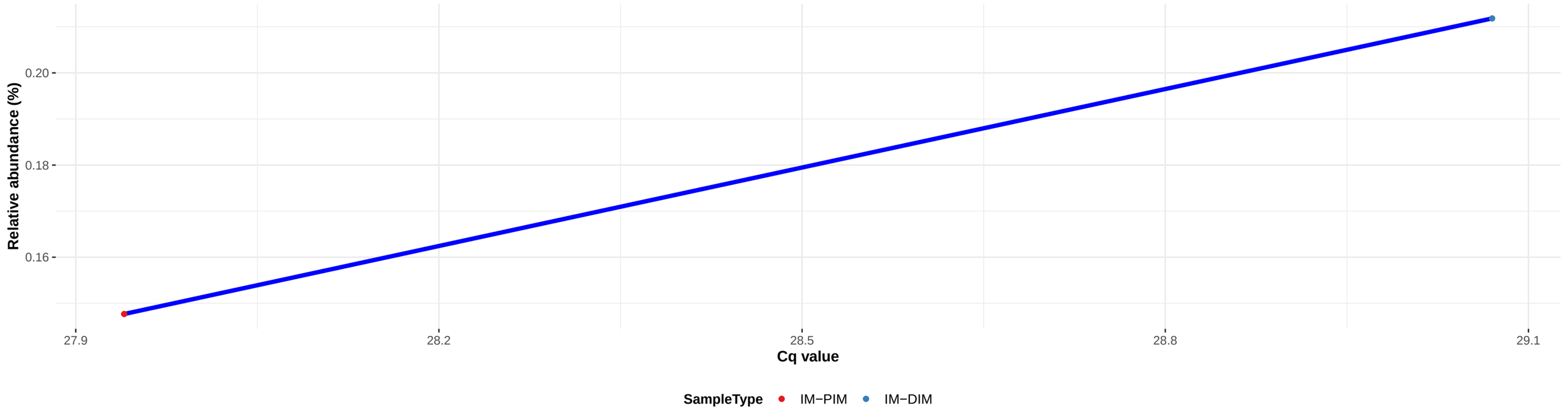
Correlation within: IM−DIM

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

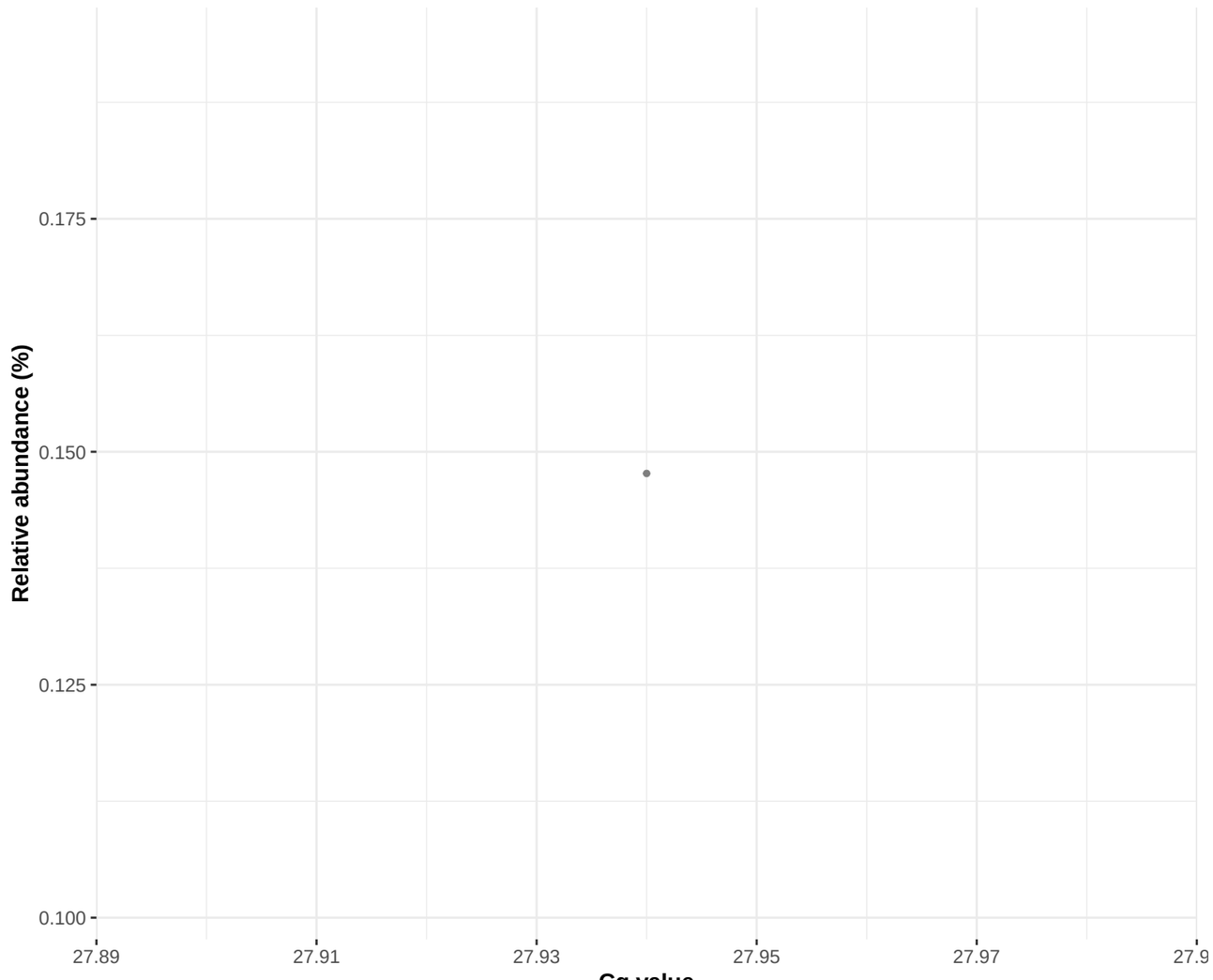


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Xanthobacteraceae; g__Bradyrhizobium; NA

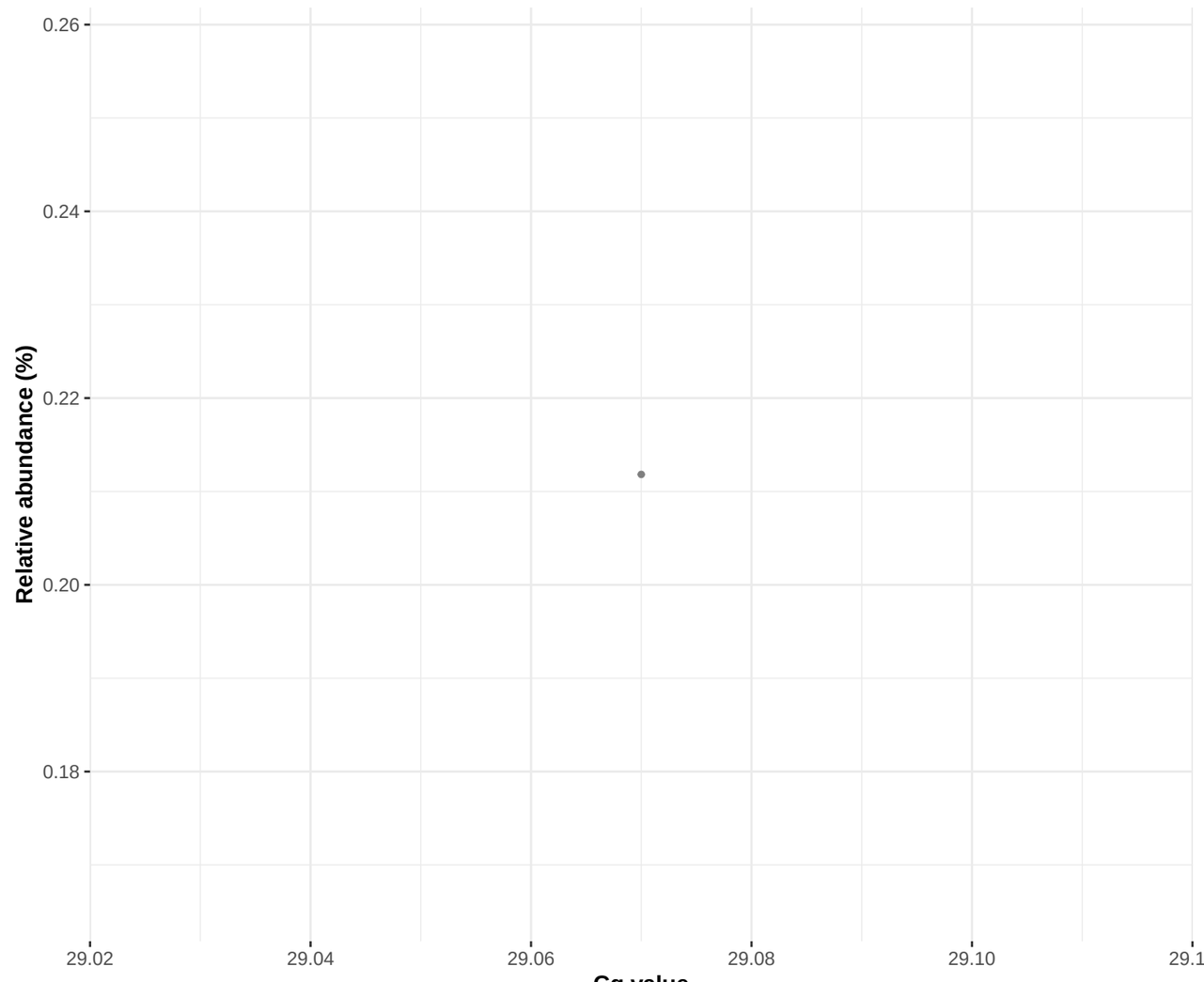
Correlation with all samples



Correlation within: IM−PIM



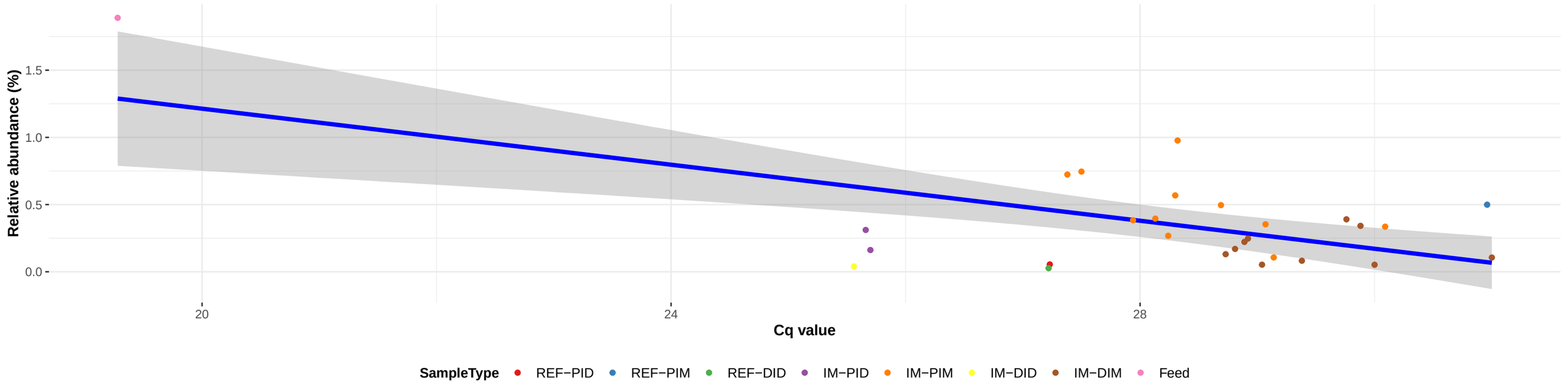
Correlation within: IM−DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Savagea; Ambiguous_taxa

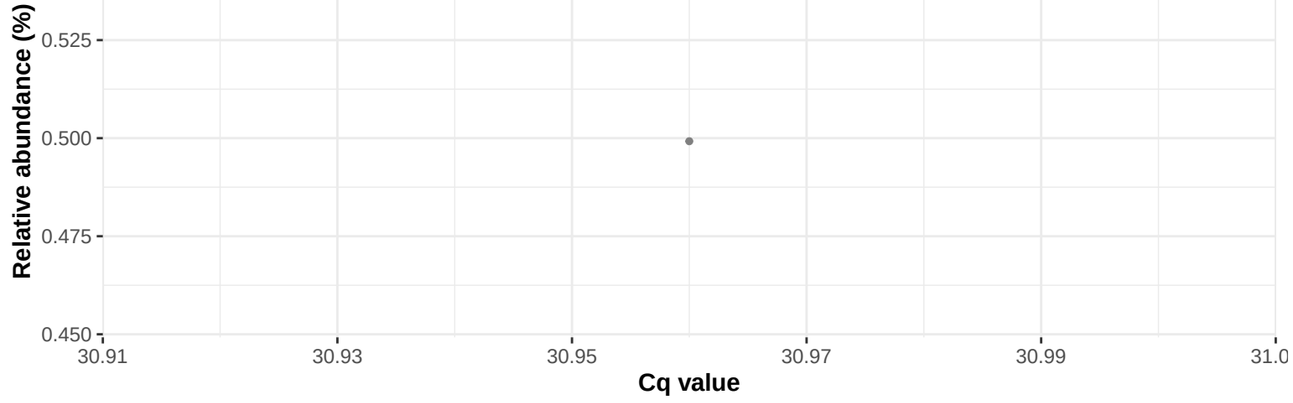
Correlation with all samples

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



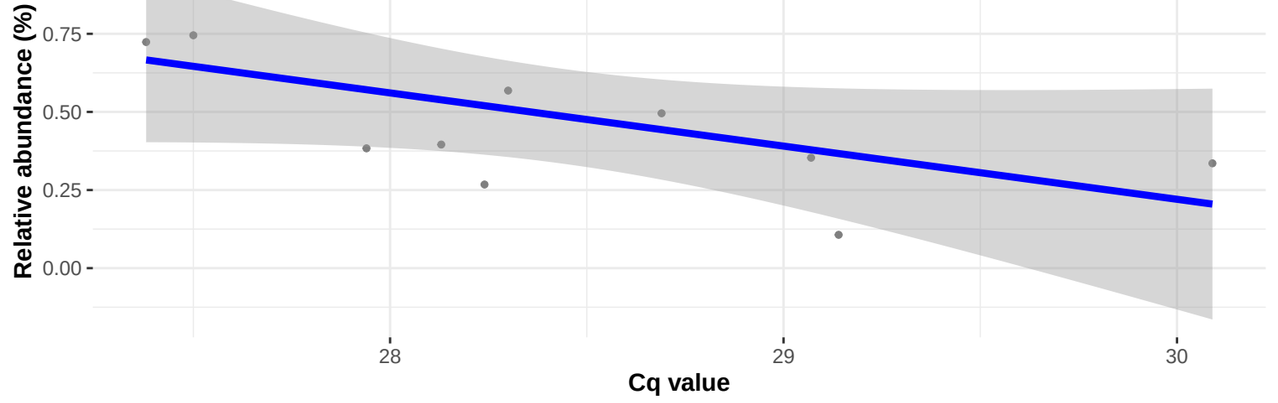
SampleType REF−PID REF−PIM REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed

Correlation within: REF−PIM



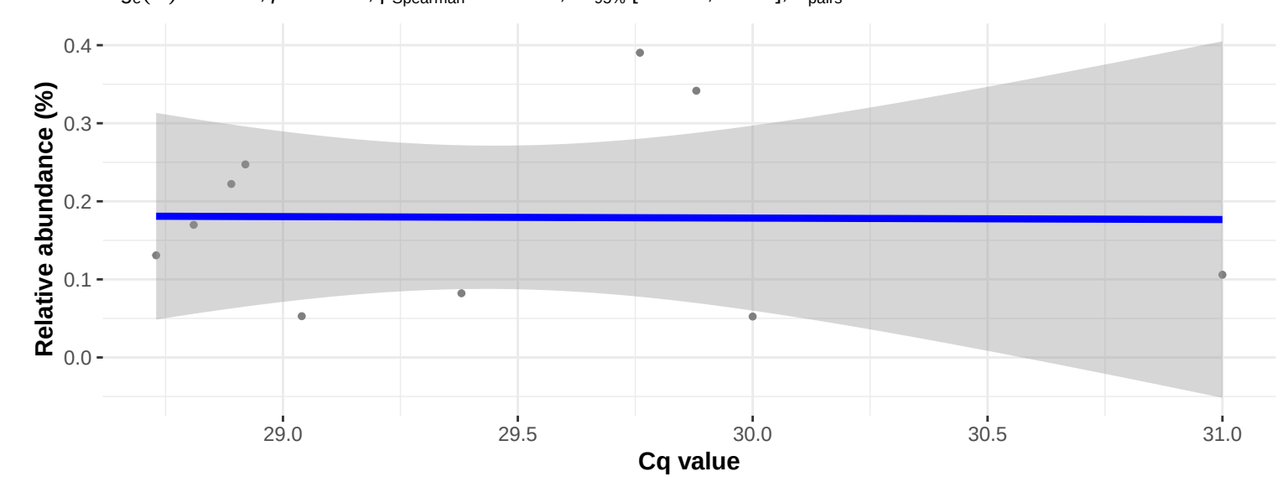
Correlation within: IM−PIM

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

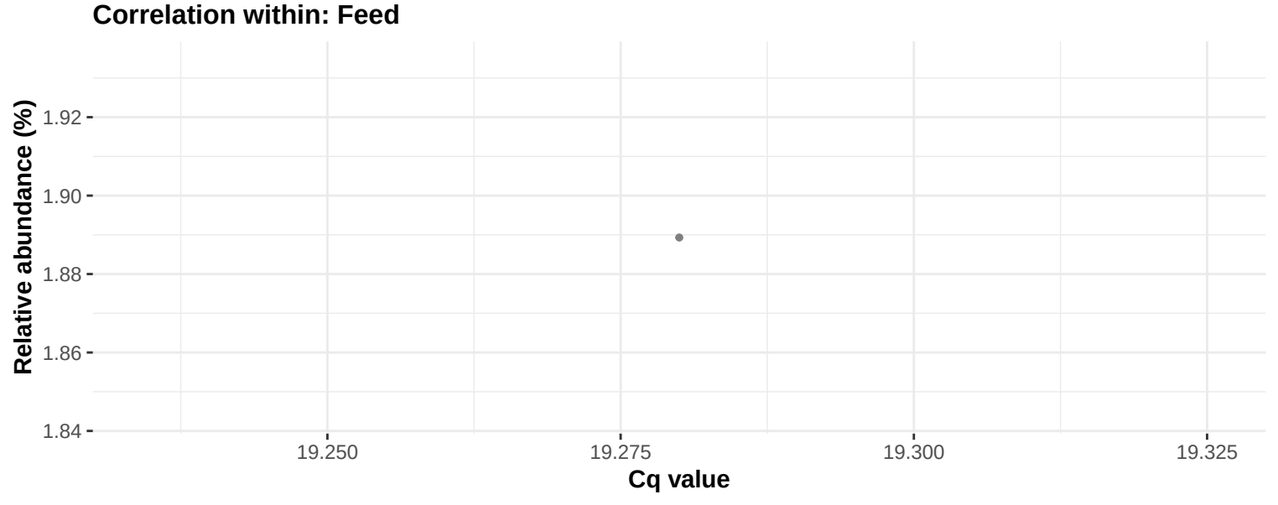


Correlation within: IM−DIM

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



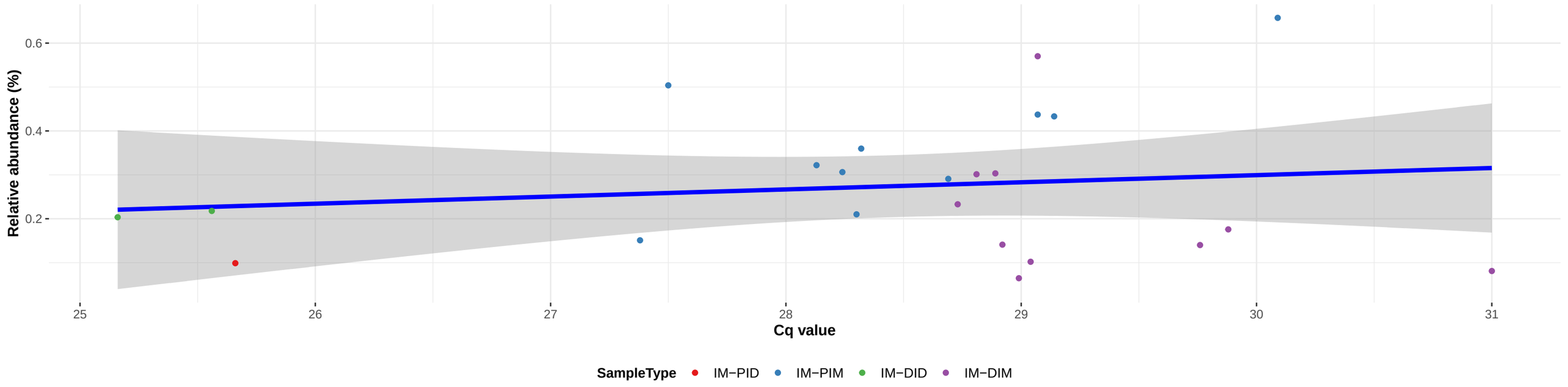
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus sciuri

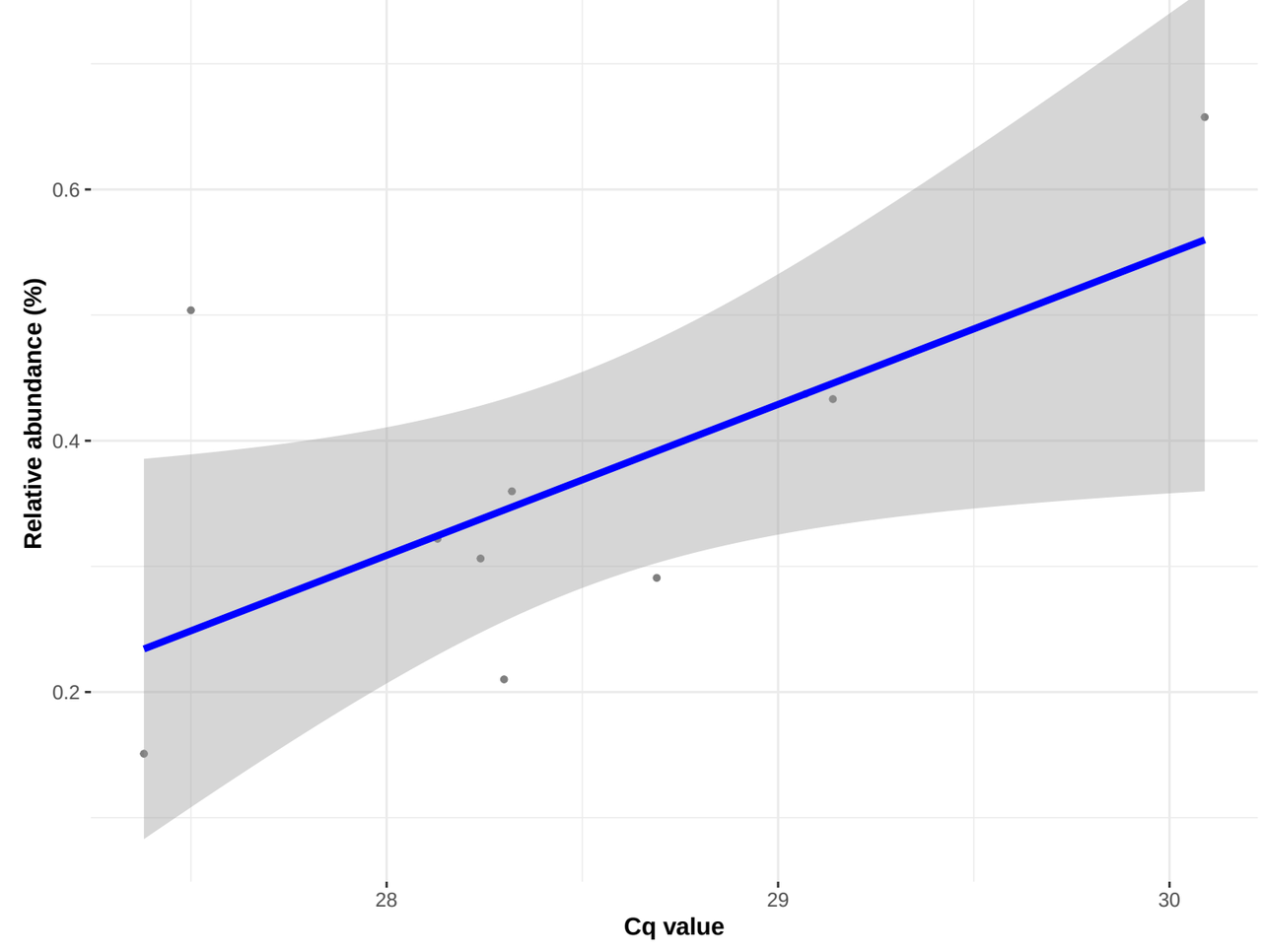
Correlation with all samples

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



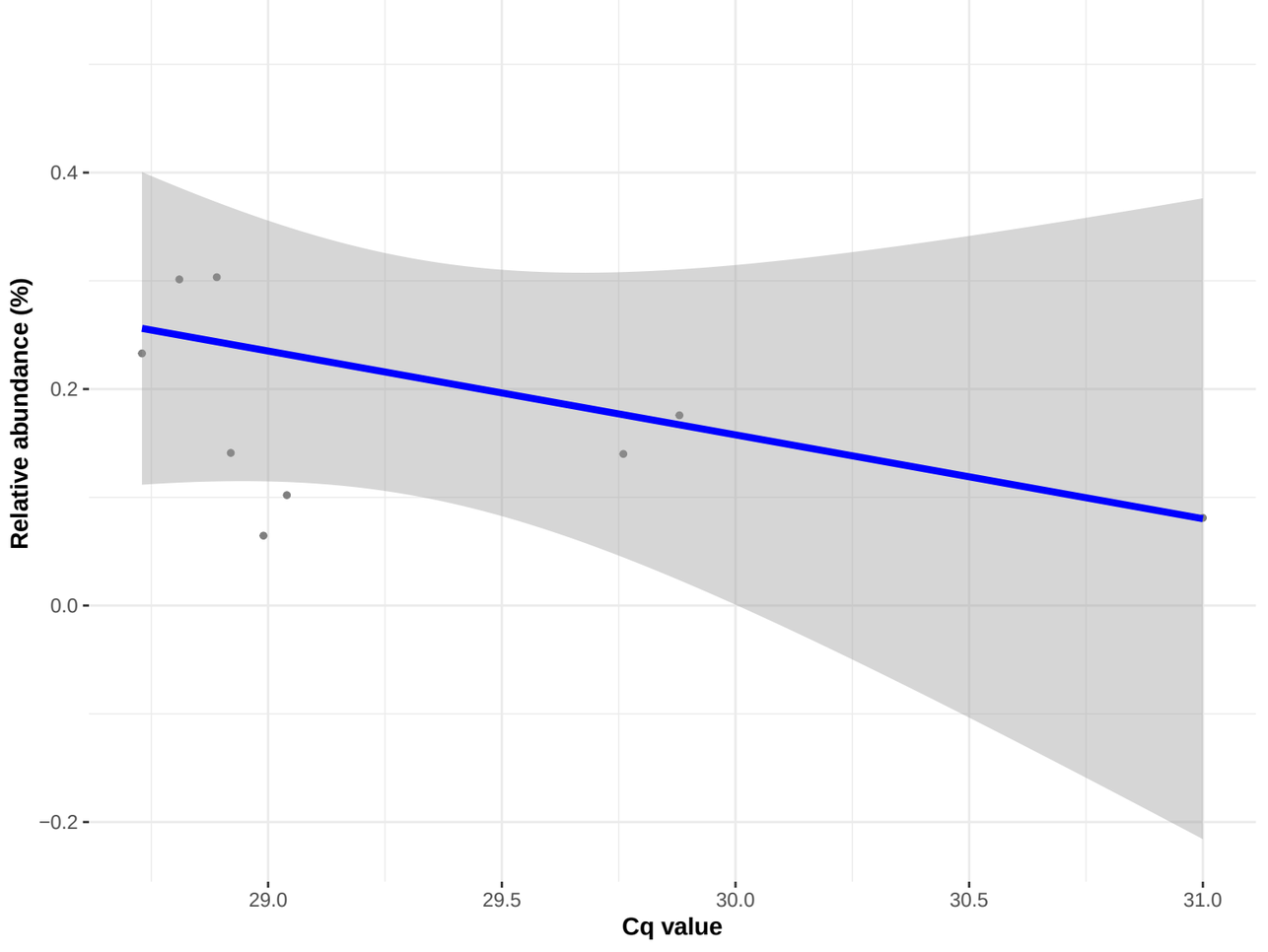
Correlation within: IM−PIM

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



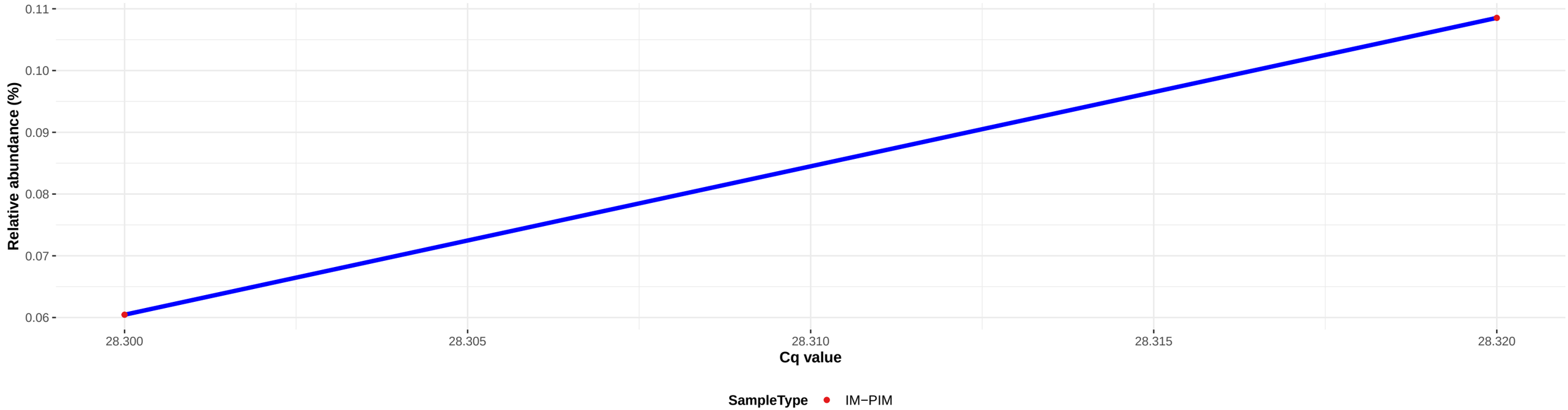
Correlation within: IM−DIM

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

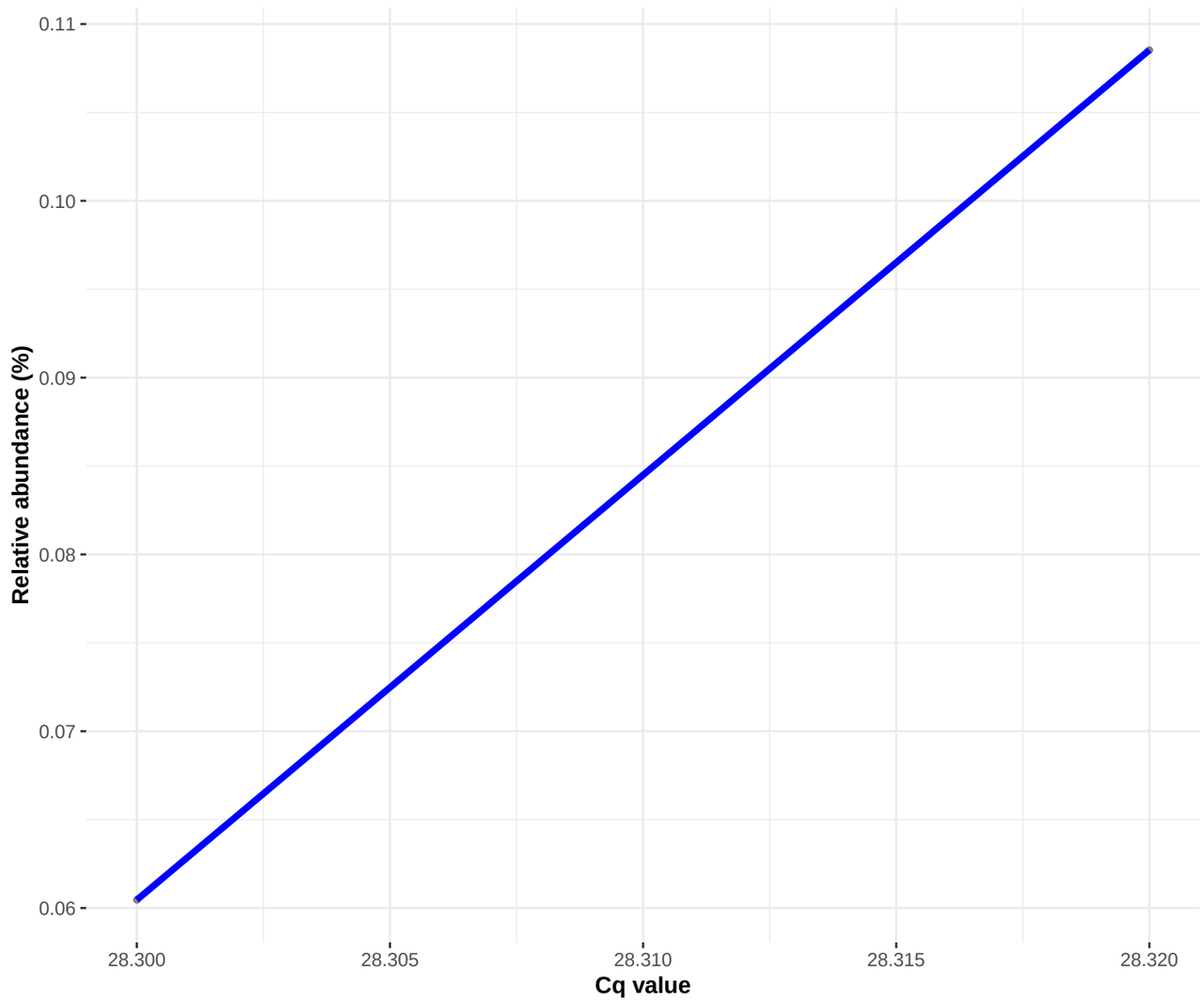


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus licheniformis

Correlation with all samples



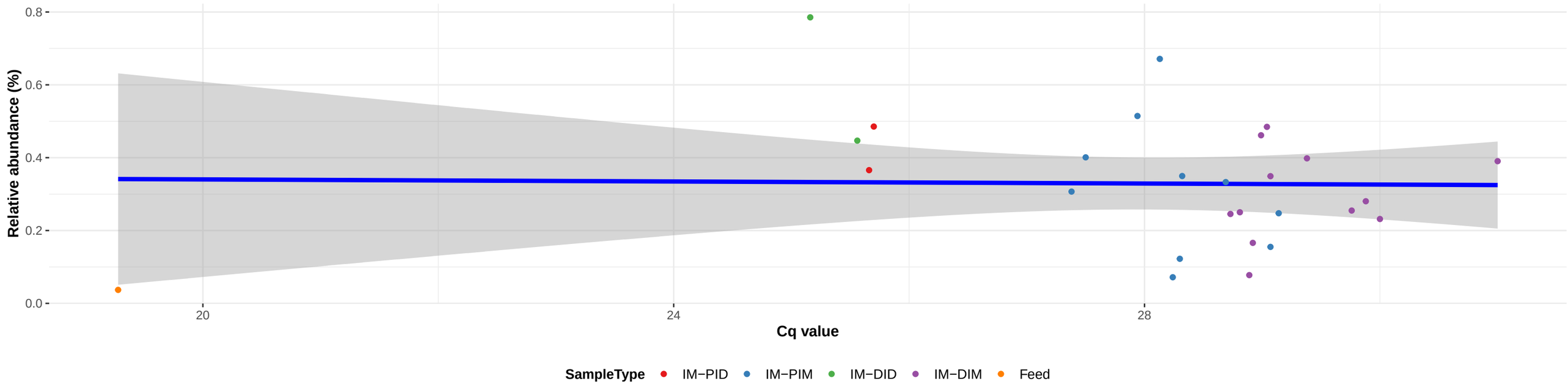
Correlation within: IM−PIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus andreraoultii

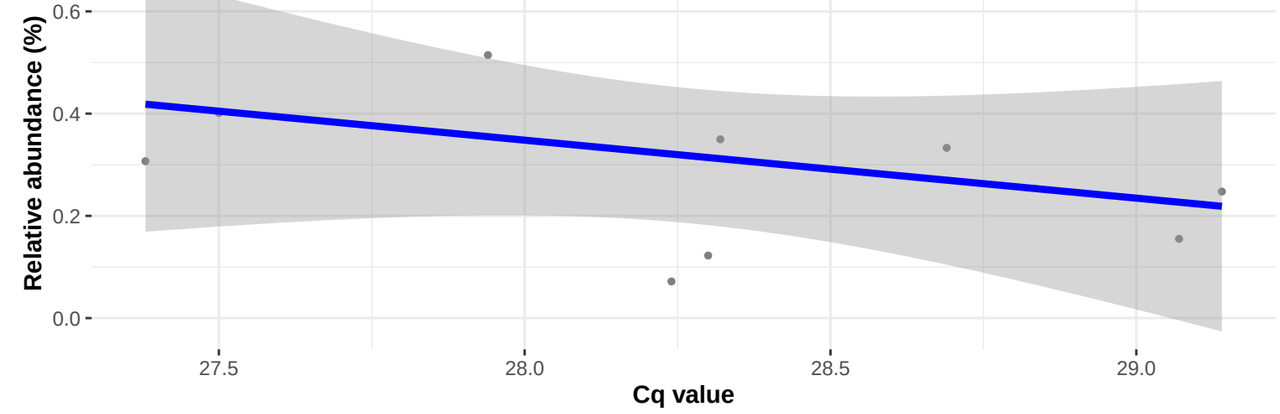
Correlation with all samples

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



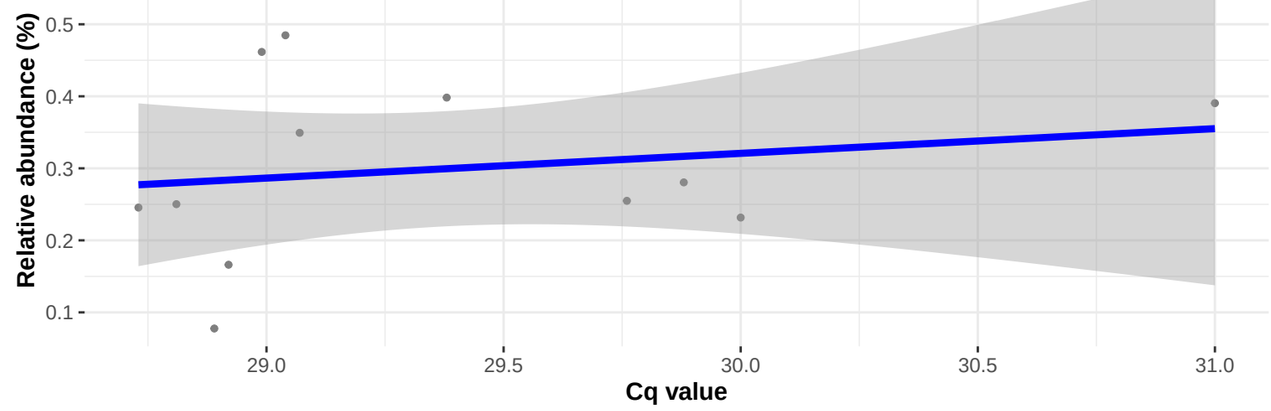
Correlation within: IM−PIM

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

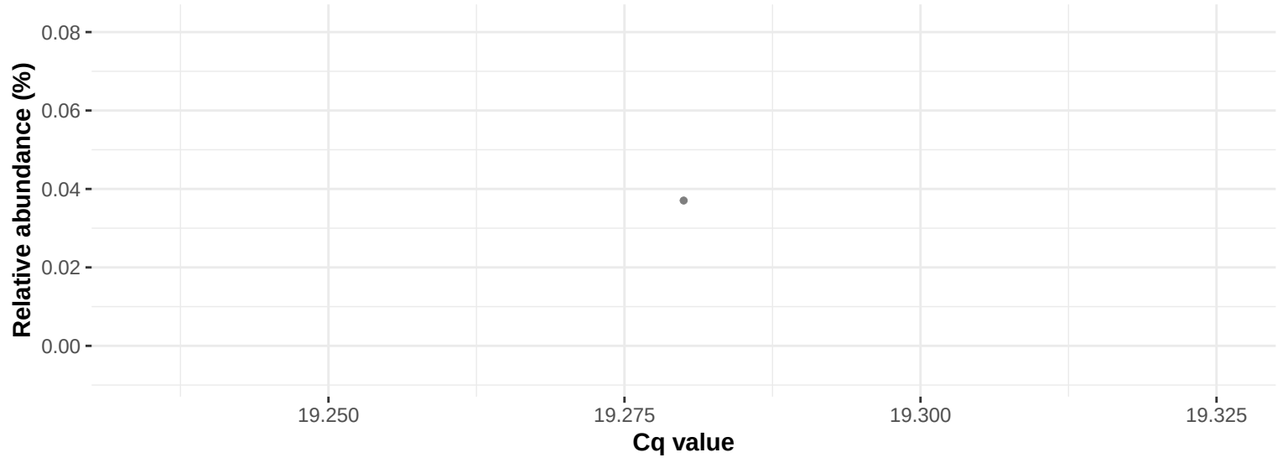


Correlation within: IM−DIM

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



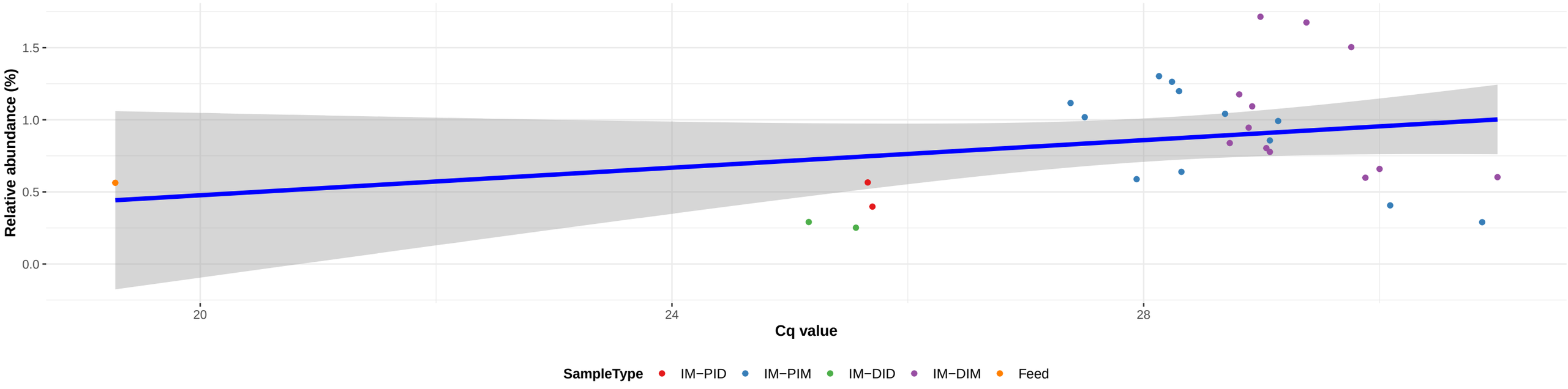
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

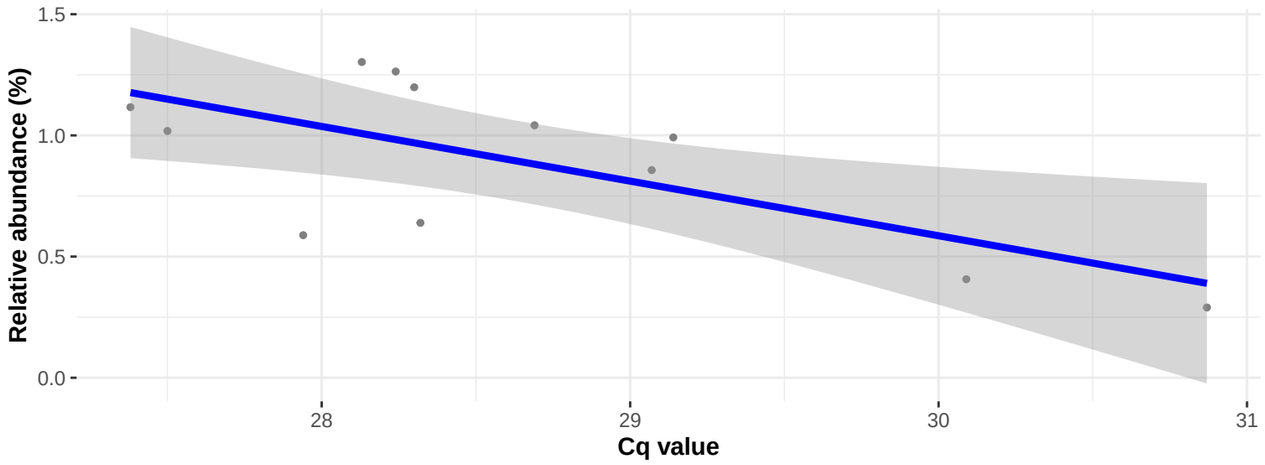
Correlation with all samples

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



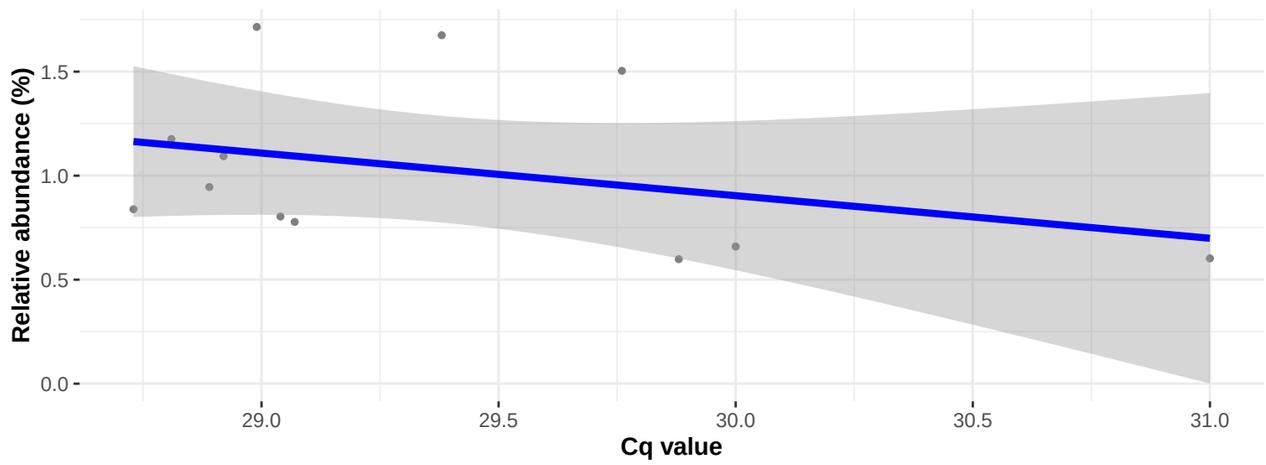
Correlation within: IM−PIM

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

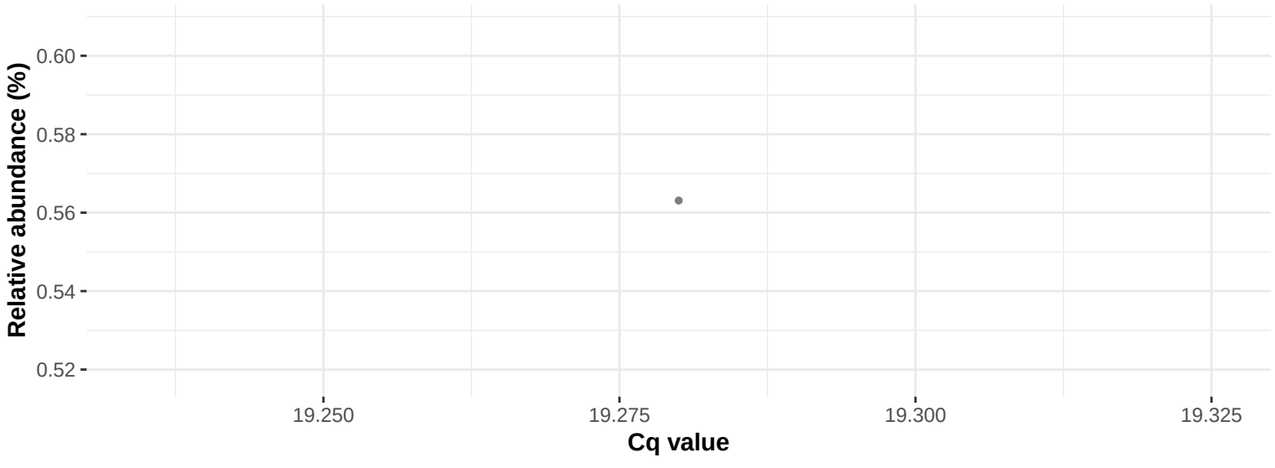


Correlation within: IM−DIM

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



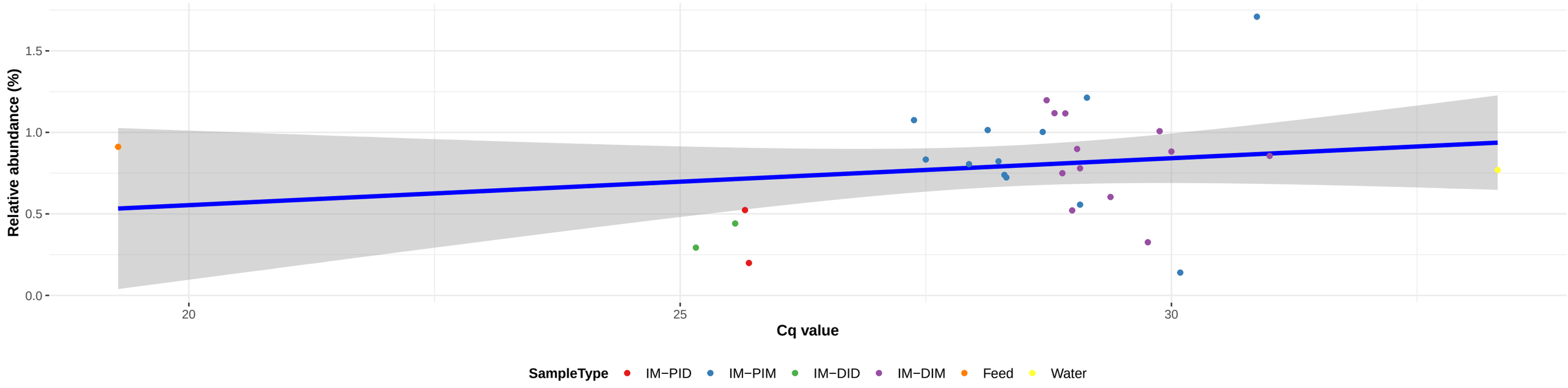
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Micrococcales; f__Microbacteriaceae; g__Microbacterium; Ambiguous_taxa

Correlation with all samples

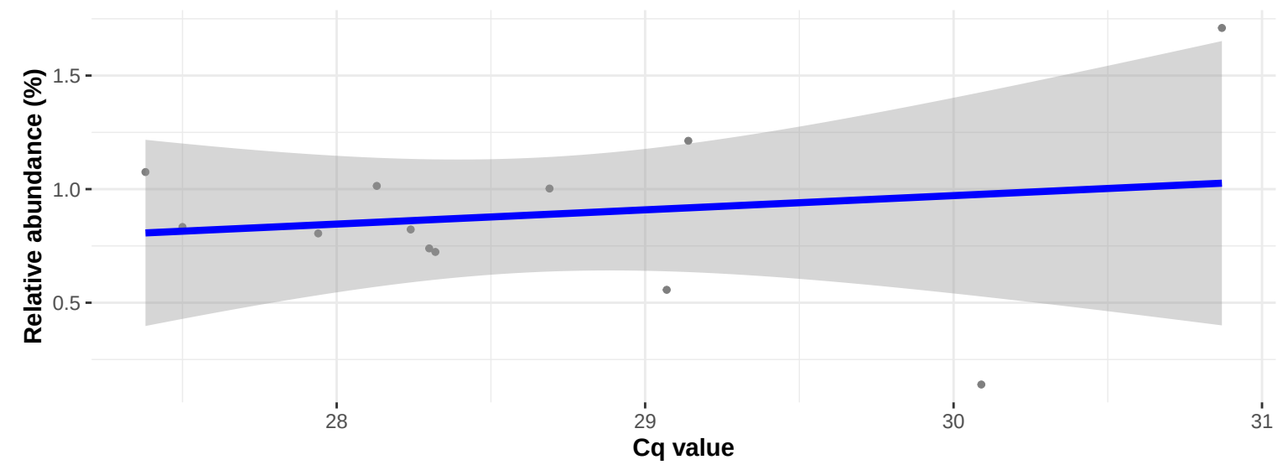
$\log_e(S)$ = 8.255, p = 0.448, $\hat{\rho}_{Spearman}$ = 0.144, $CI_{95\%}$ [−0.239, 0.488], n_{pairs} = 30



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed Water

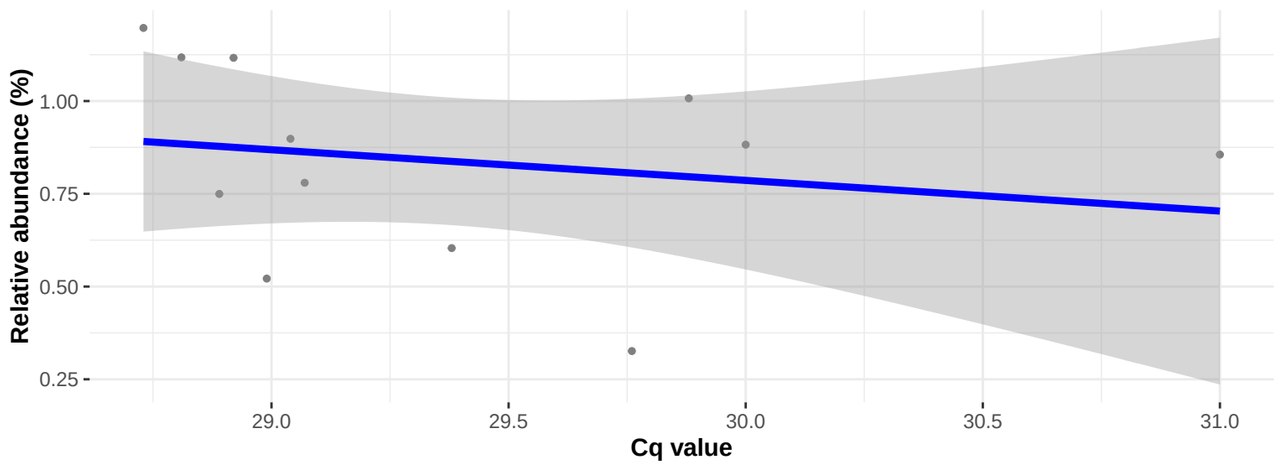
Correlation within: IM−PIM

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

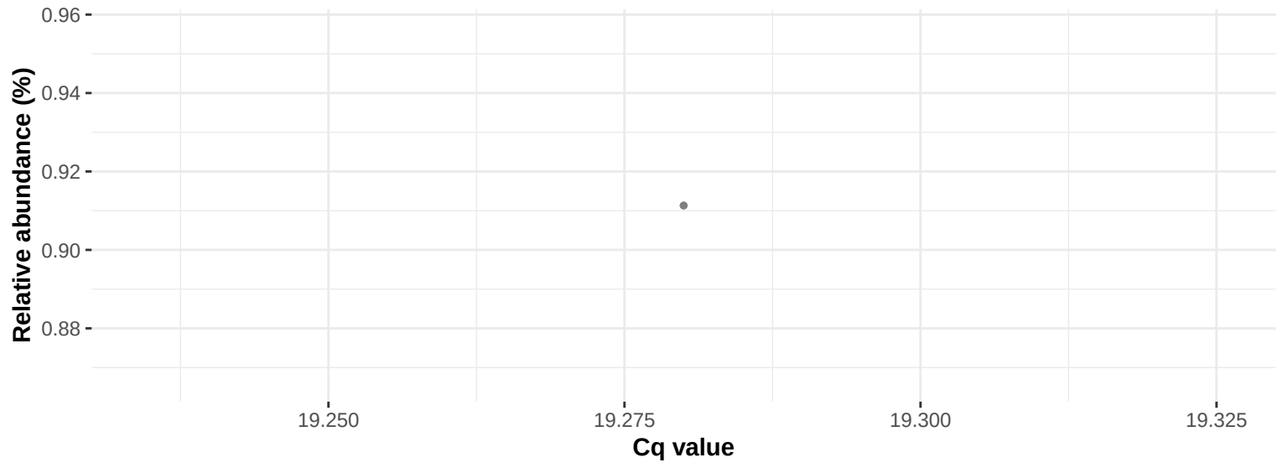


Correlation within: IM−DIM

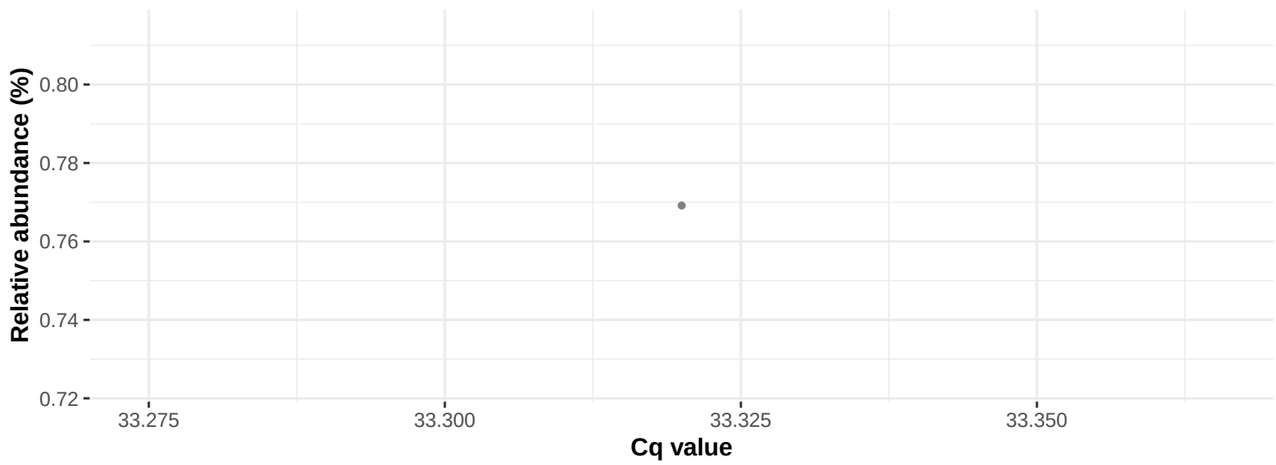
$\log_e(S)$ = 5.986, p = 0.208, $\hat{\rho}_{Spearman}$ = −0.392, $CI_{95\%}$ [−0.796, 0.253], n_{pairs} = 12



Correlation within: Feed



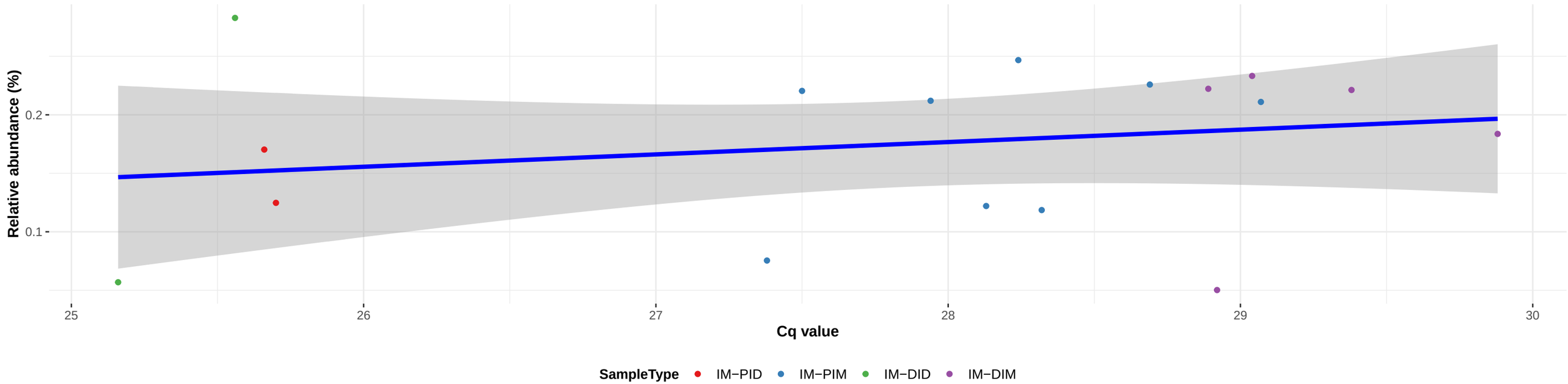
Correlation within: Water



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

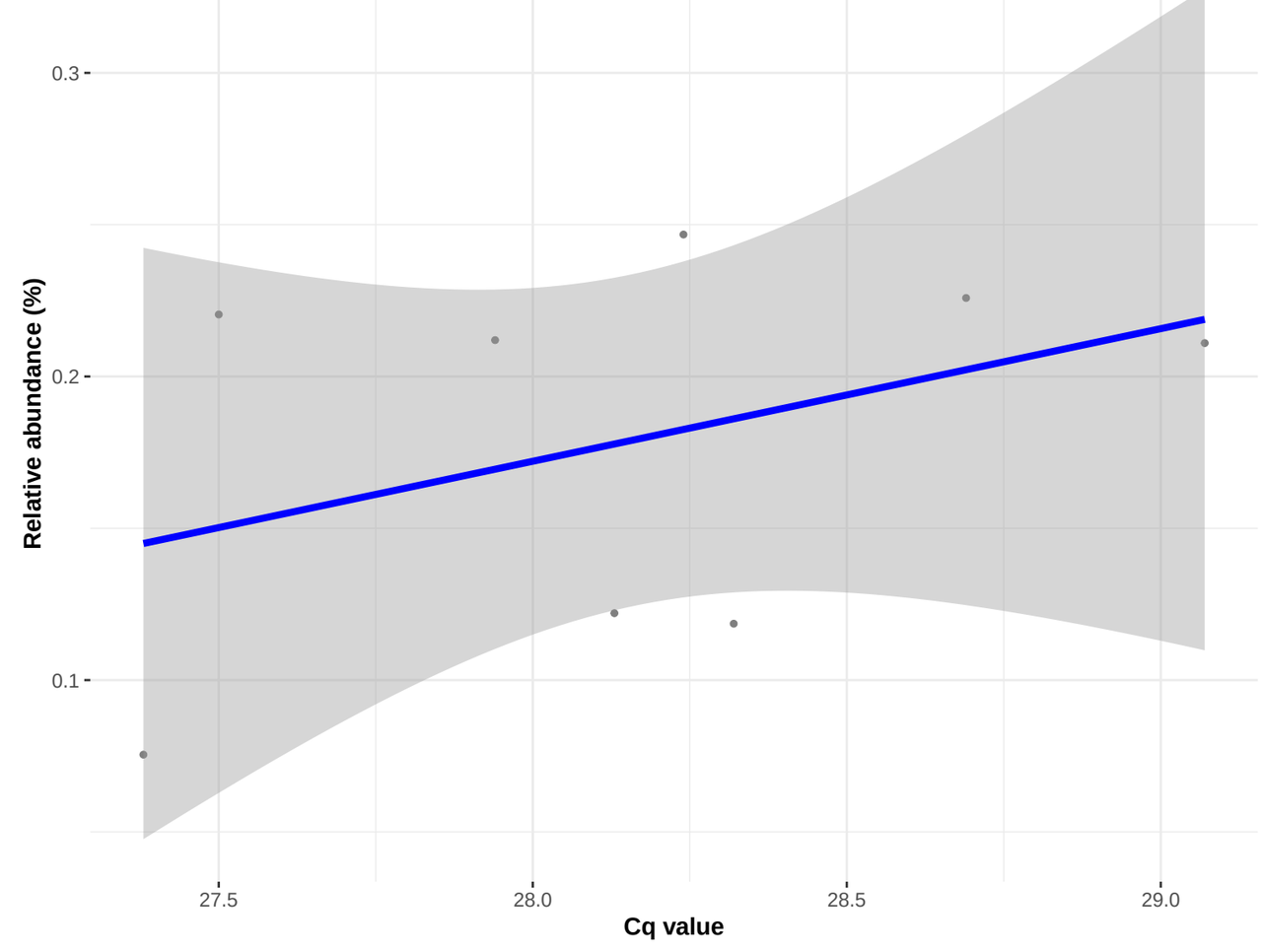
Correlation with all samples

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

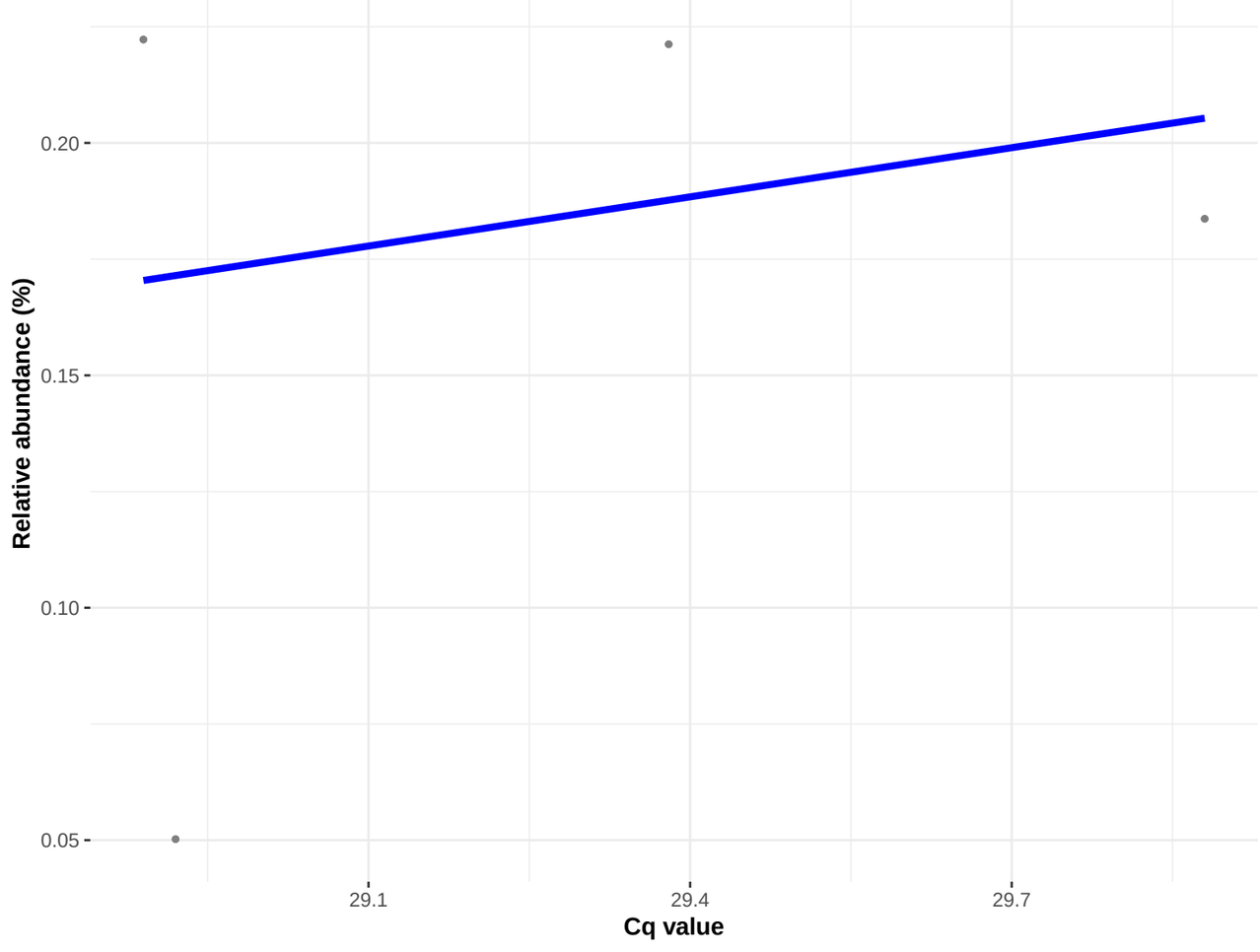


Correlation within: IM−PIM

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



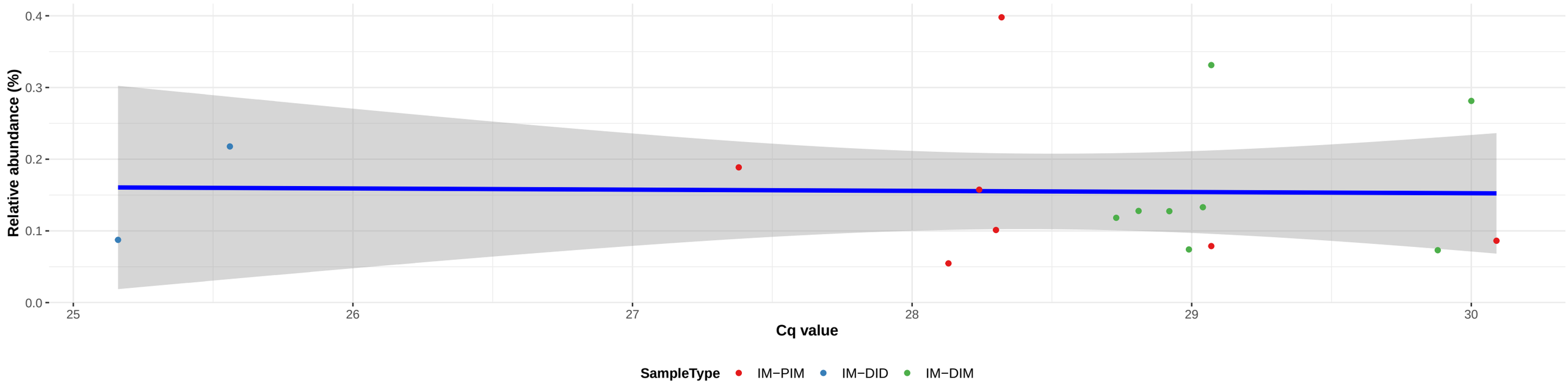
Correlation within: IM−DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus niabensis

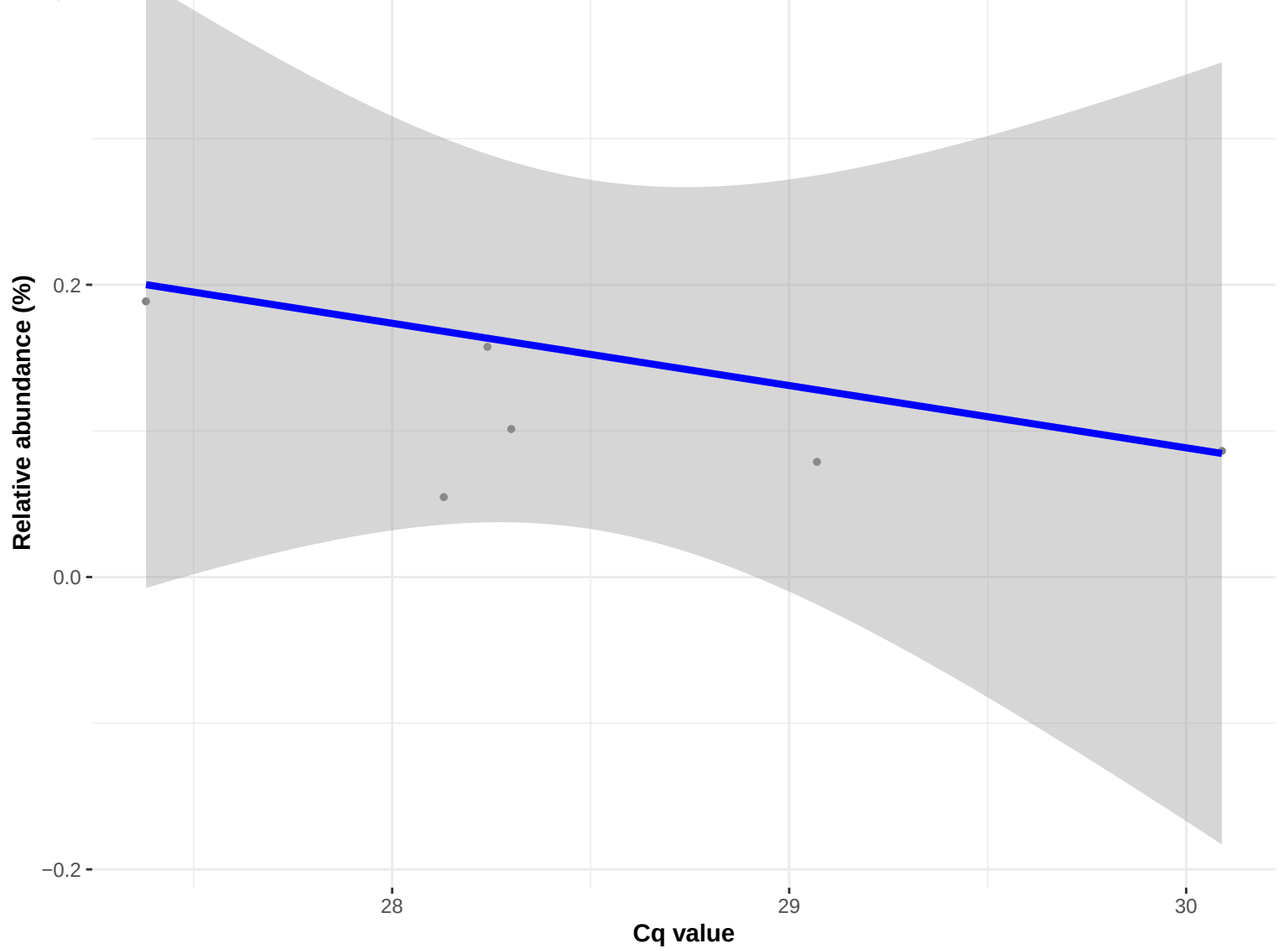
Correlation with all samples

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



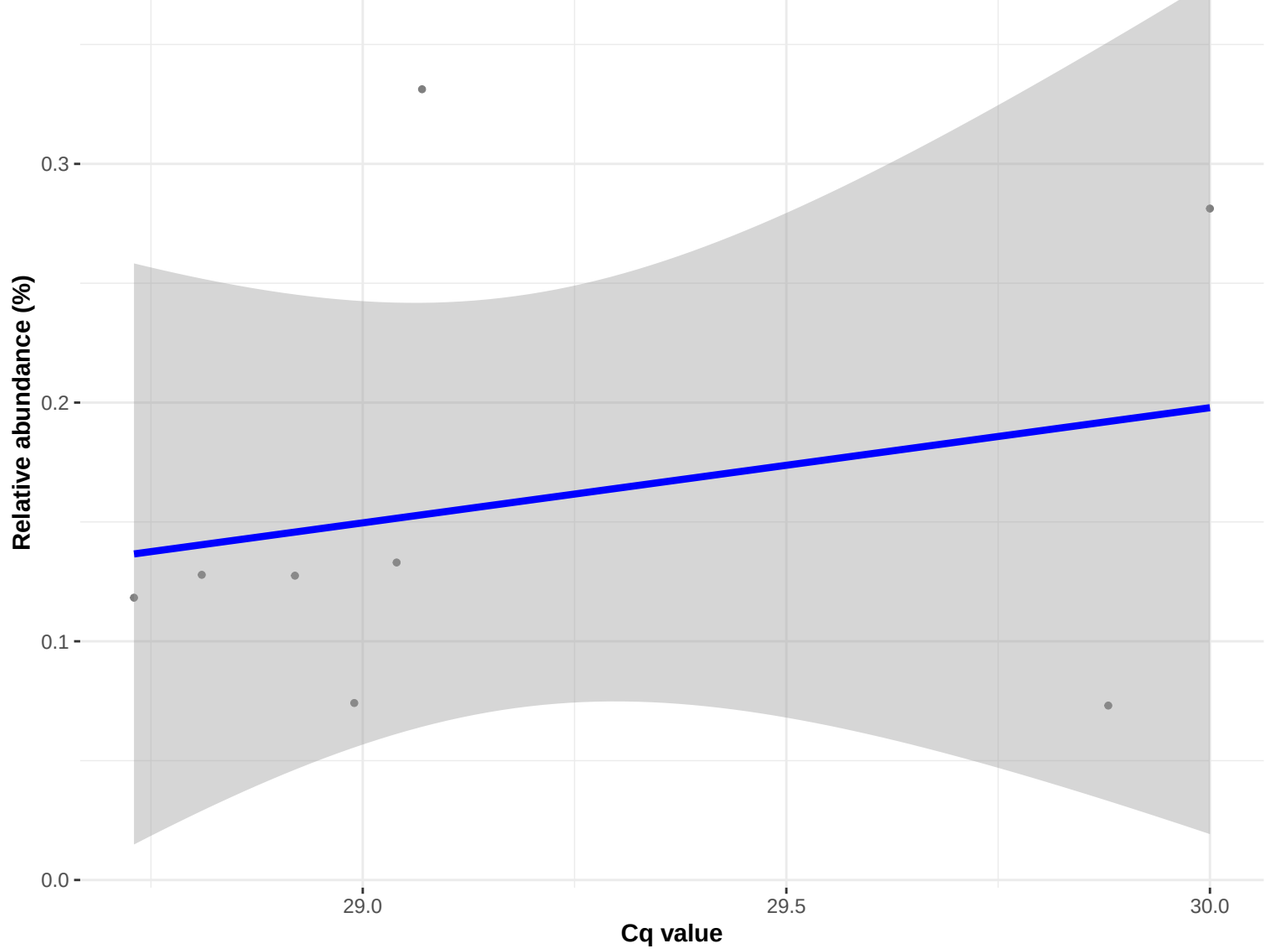
Correlation within: IM−PIM

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



Correlation within: IM−DIM

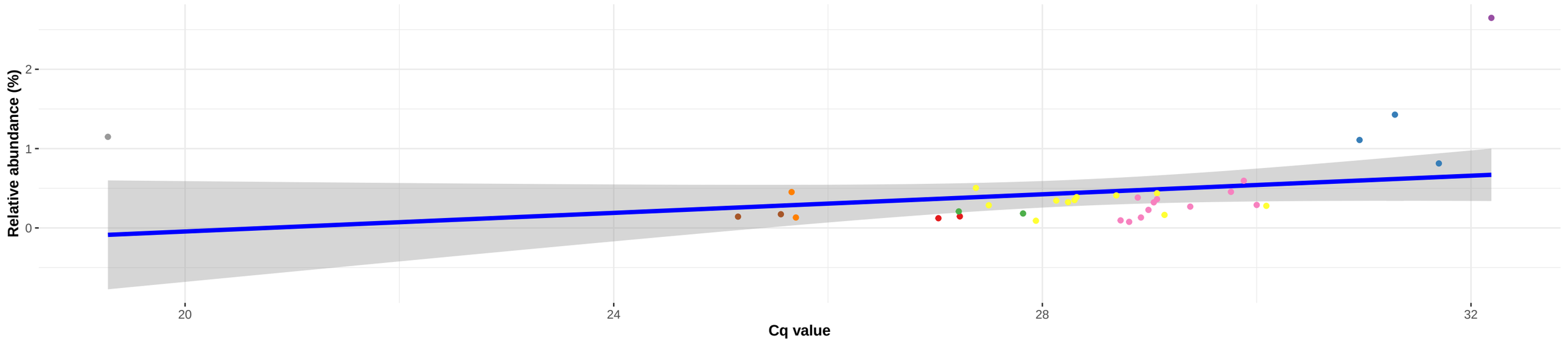
$\log_e(S)$ = 4.094, p = 0.493, $\hat{\rho}_{Spearman}$ = 0.286, $CI_{95\%}$ [−0.543, 0.833], n_{pairs} = 8



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Kurthia; s__Kurthia sp. PAOGL173

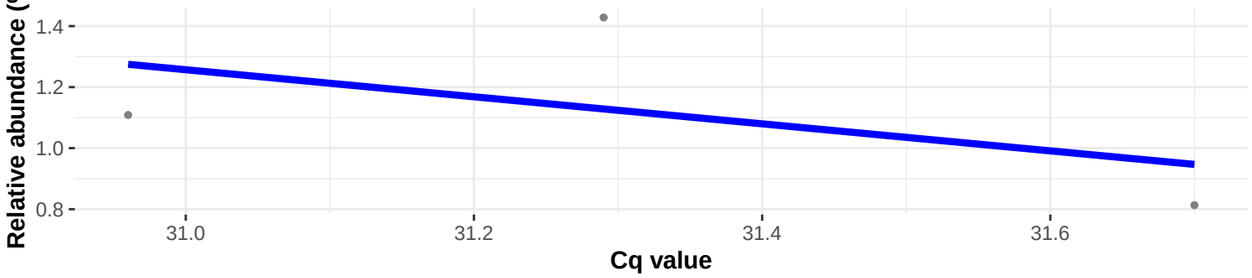
Correlation with all samples

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

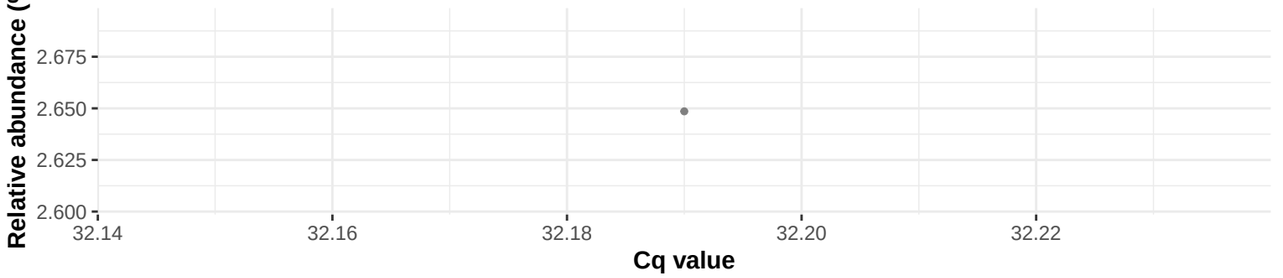


SampleType ● REF−PID ● REF−PIM ● REF−DID ● REF−DIM ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

Correlation within: REF−PIM

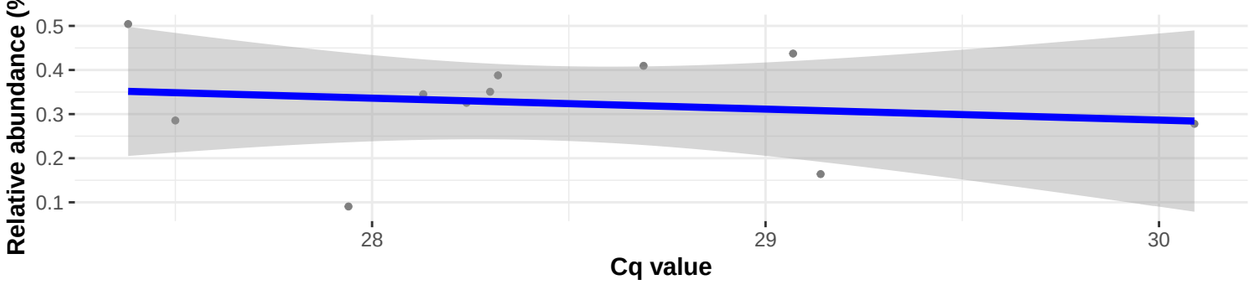


Correlation within: REF−DIM



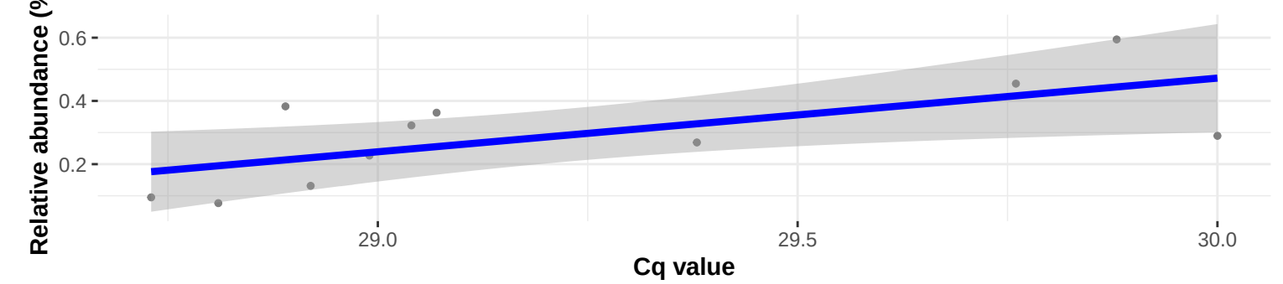
Correlation within: IM−PIM

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

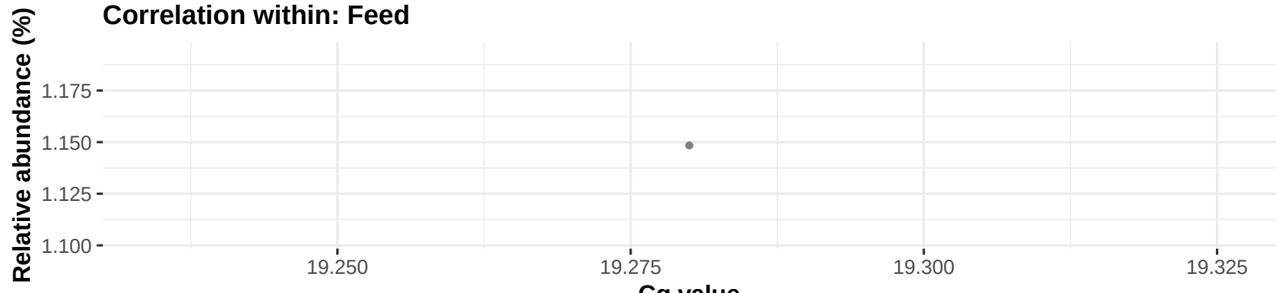


Correlation within: IM−DIM

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



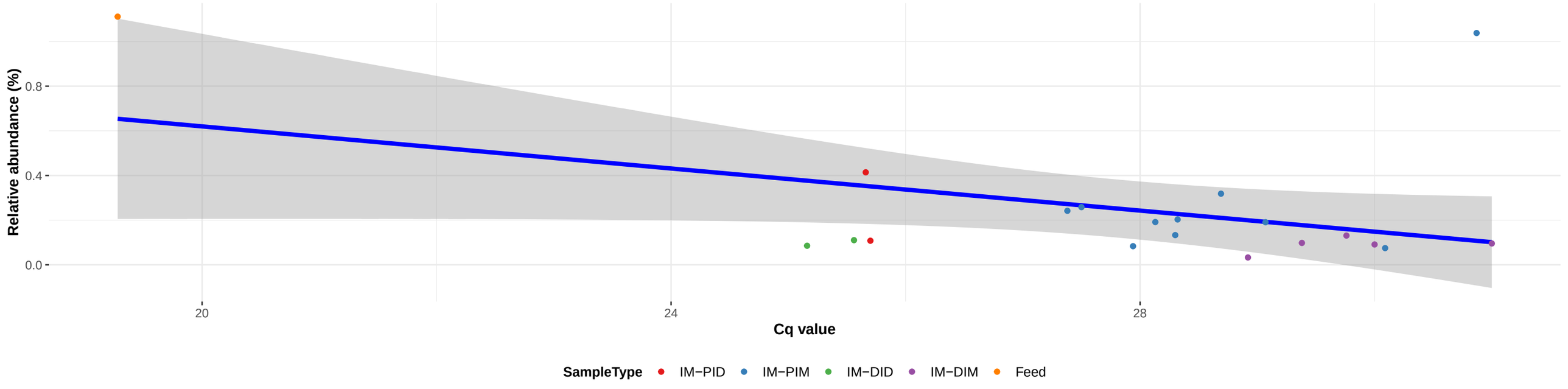
Correlation within: Feed



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

Correlation with all samples

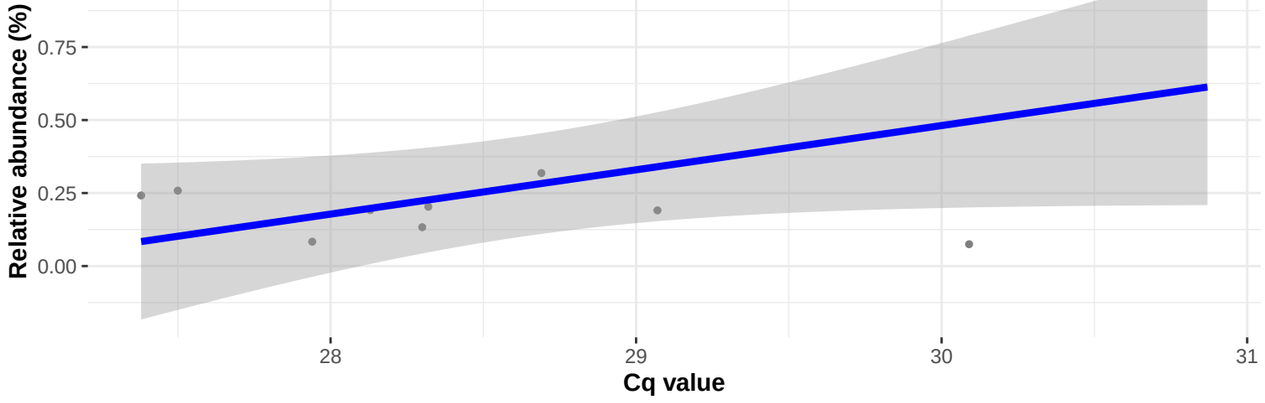
$\log_e(S)$ = 7.431, p = 0.251, $\hat{\rho}_{Spearman}$ = −0.269, $CI_{95\%}$ [−0.644, 0.210], n_{pairs} = 20



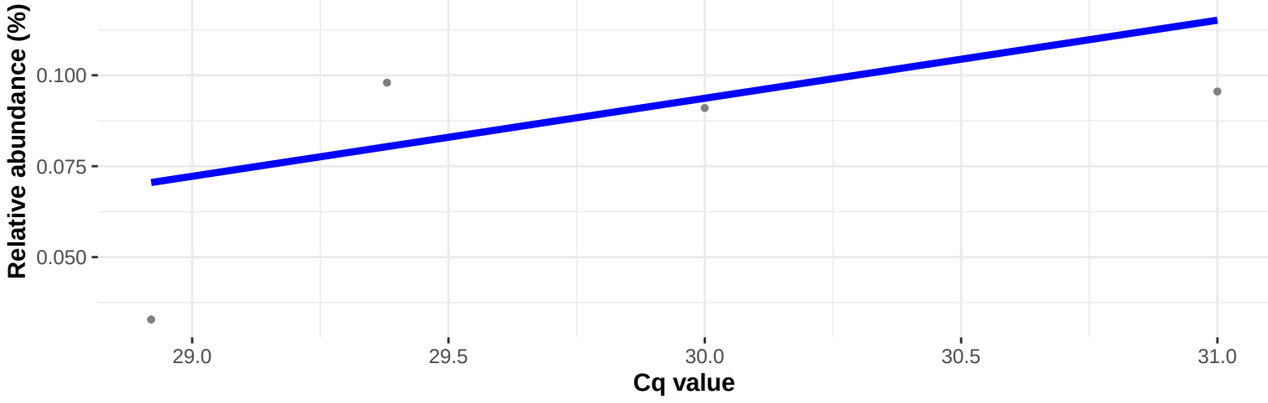
SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

Correlation within: IM−PIM

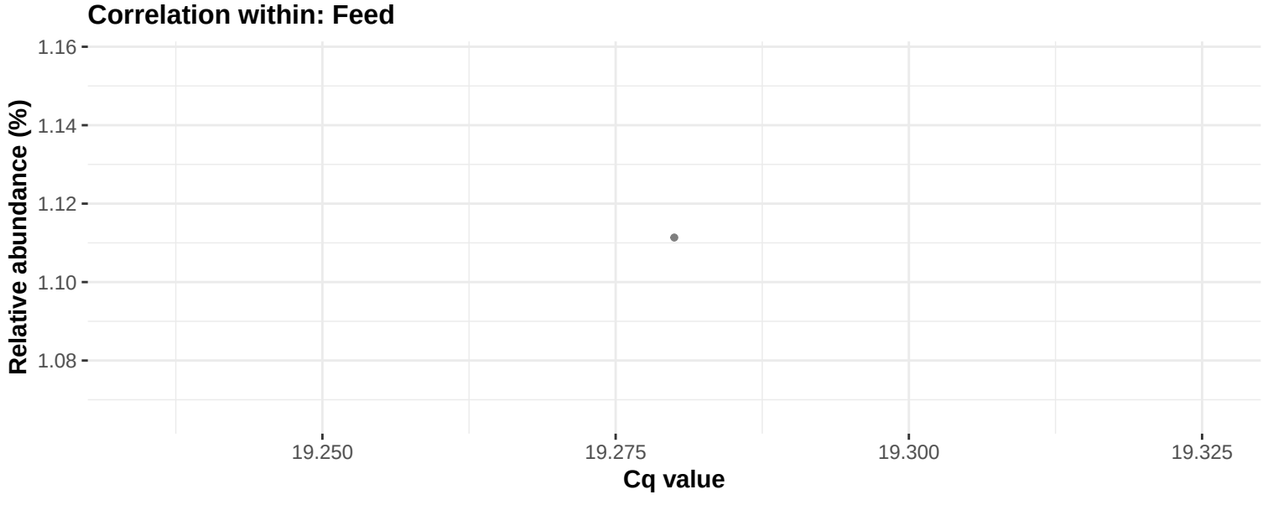
$\log_e(S)$ = 5.088, p = 0.960, $\hat{\rho}_{Spearman}$ = 0.018, $CI_{95\%}$ [−0.632, 0.653], n_{pairs} = 10



Correlation within: IM−DIM



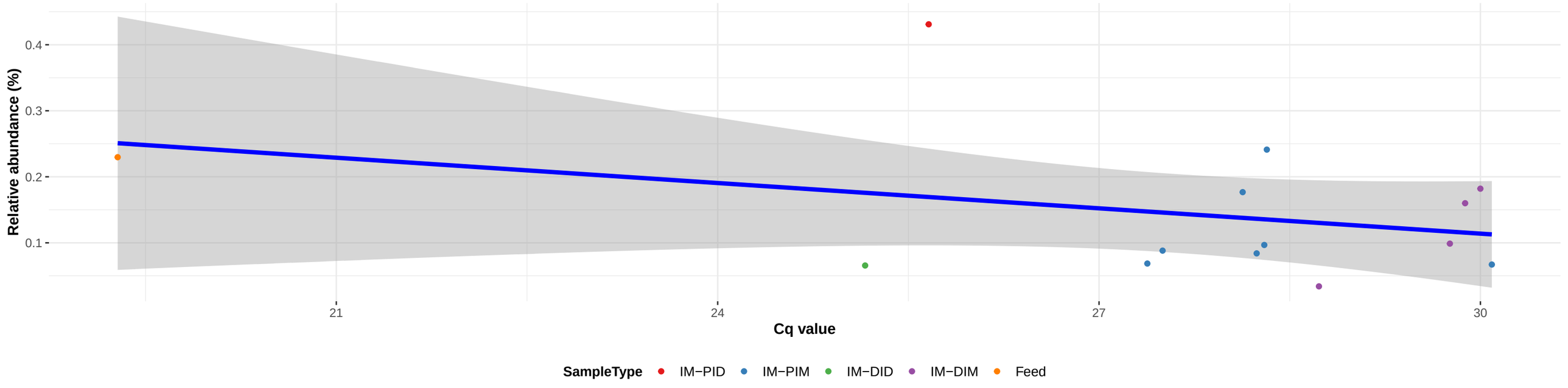
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; NA

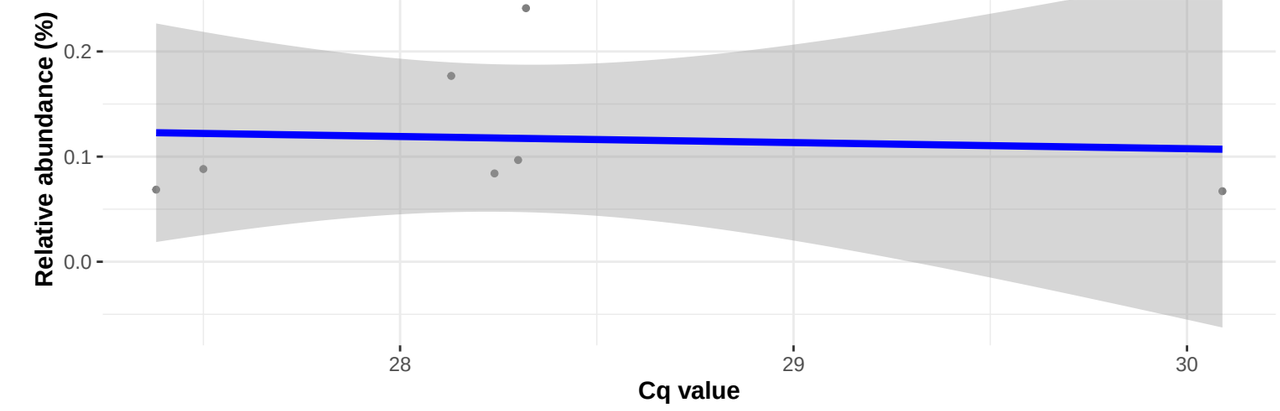
Correlation with all samples

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

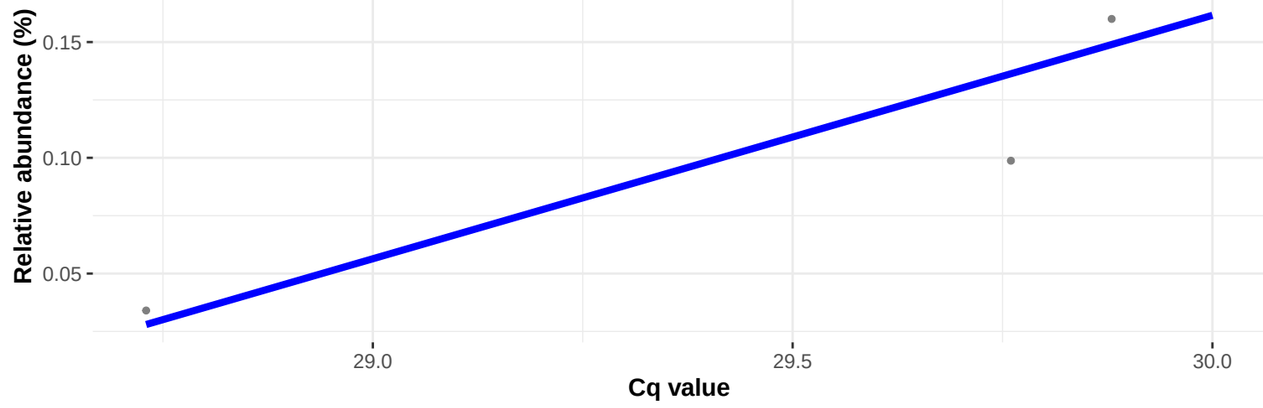


Correlation within: IM−PIM

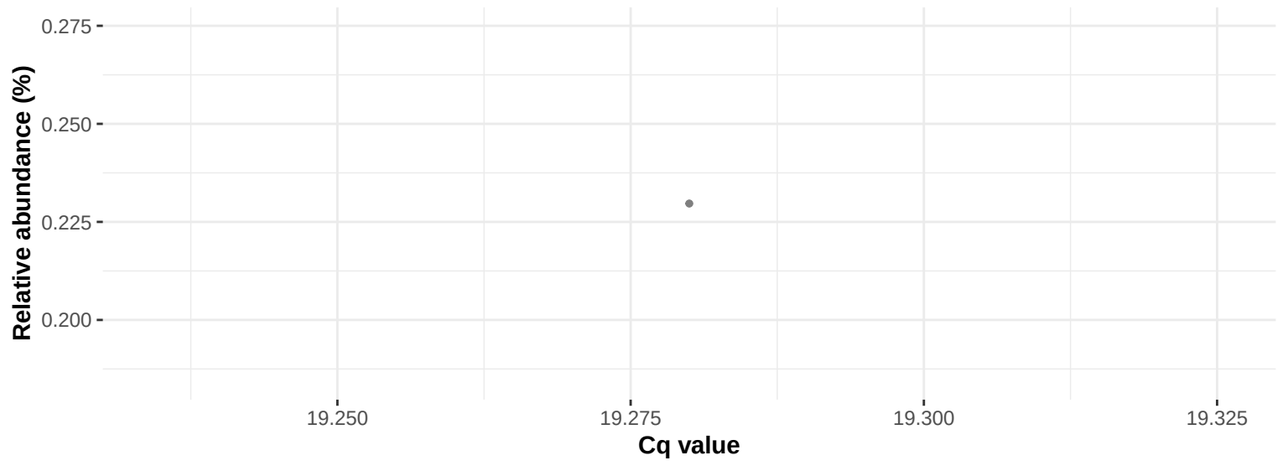
$\log_e(S)$ = 3.951, p = 0.879, $\hat{\rho}_{Spearman}$ = 0.071, $CI_{95\%}$ [−0.734, 0.793], n_{pairs} = 7



Correlation within: IM−DIM



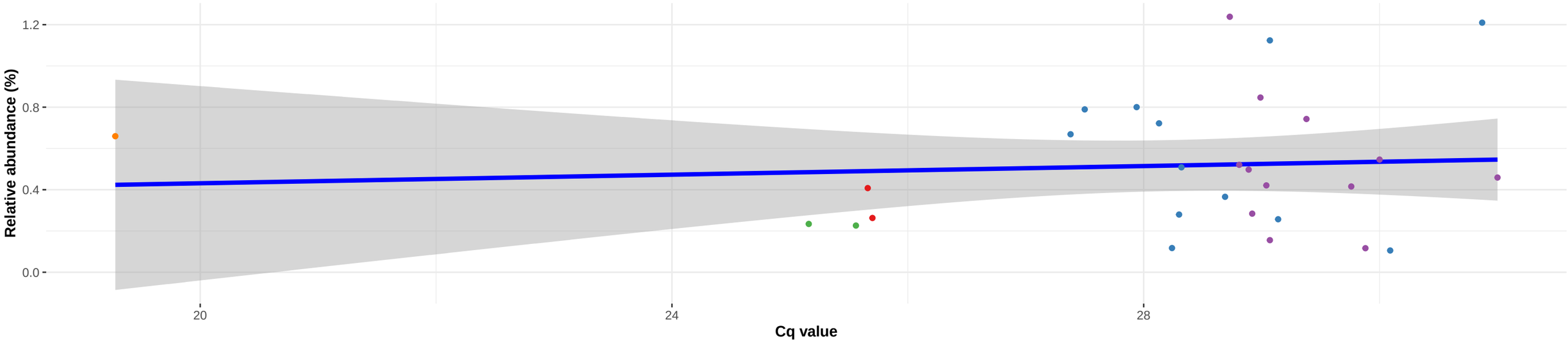
Correlation within: Feed



k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Actinomycetaceae; g__Actinomyces; s__uncultured Actinomycetales bacterium

Correlation with all samples

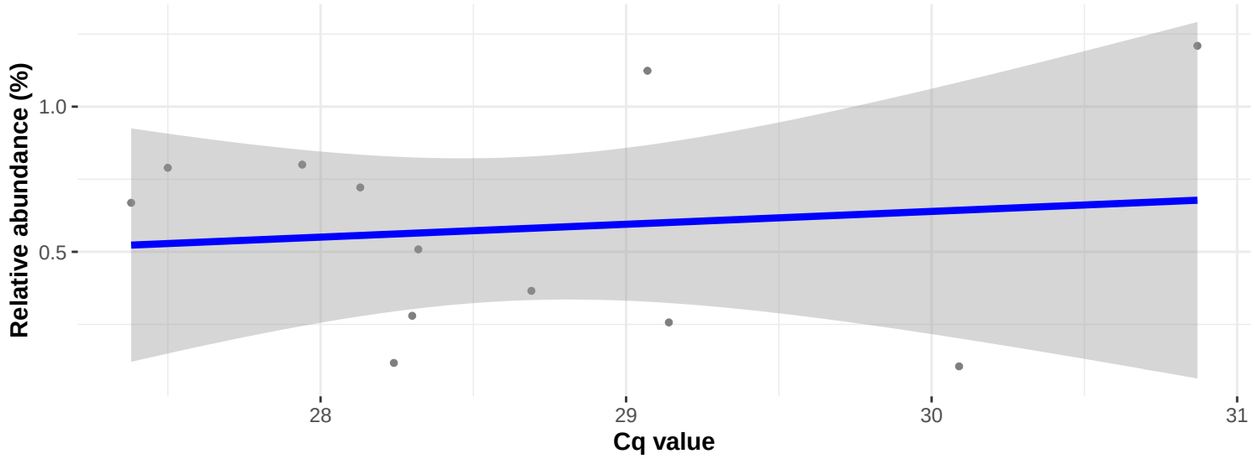
$\log_e(S)$ = 8.292, p = 0.930, $\hat{\rho}_{Spearman}$ = 0.017, $CI_{95\%}$ [−0.362, 0.391], n_{pairs} = 29



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

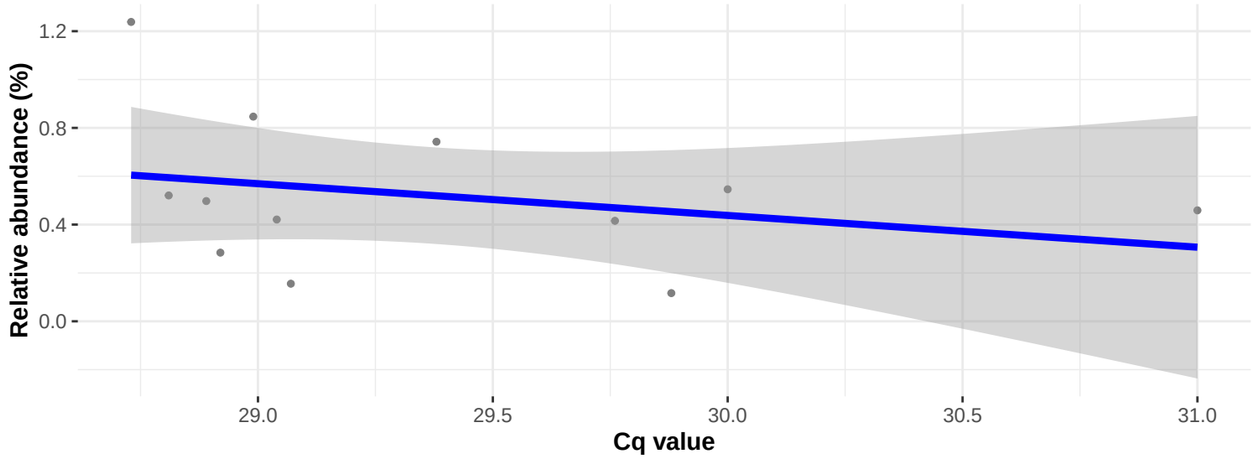
Correlation within: IM−PIM

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

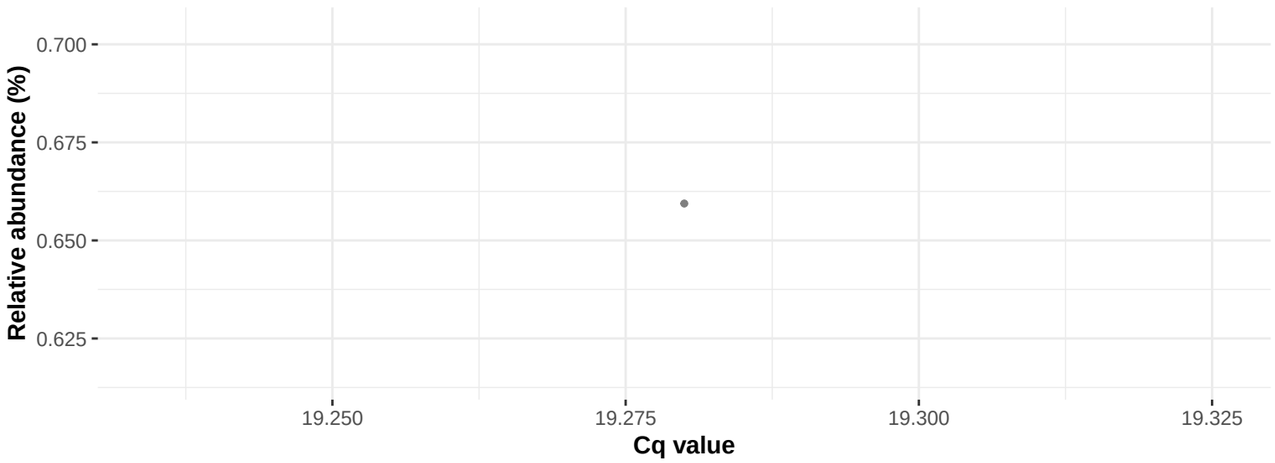


Correlation within: IM−DIM

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



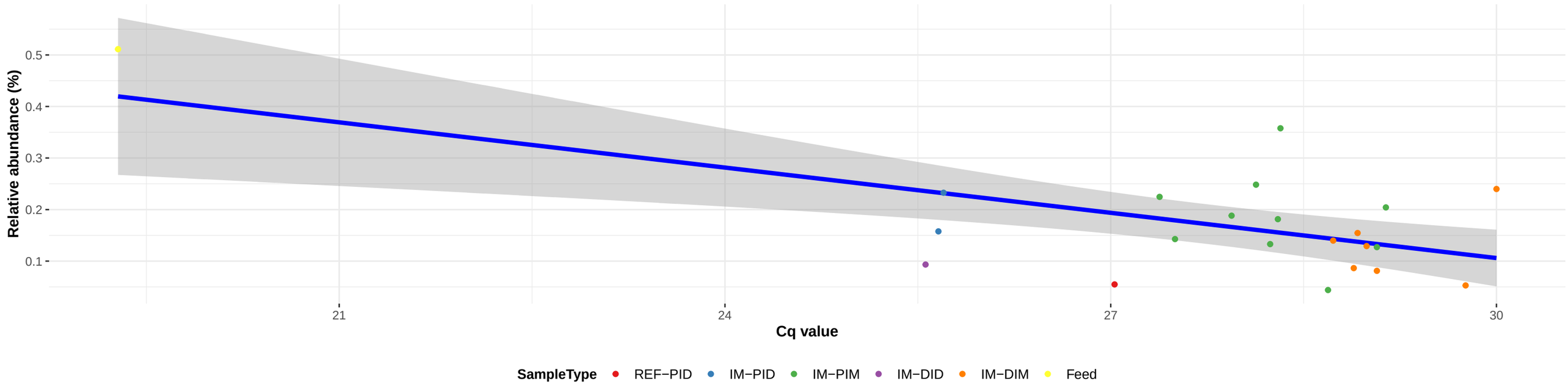
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Vagococcus; Ambiguous_taxa

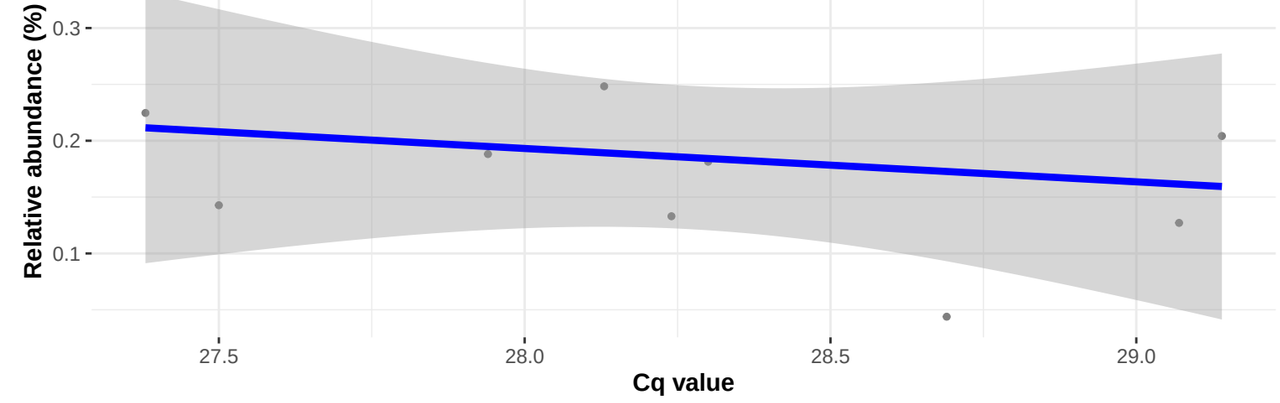
Correlation with all samples

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



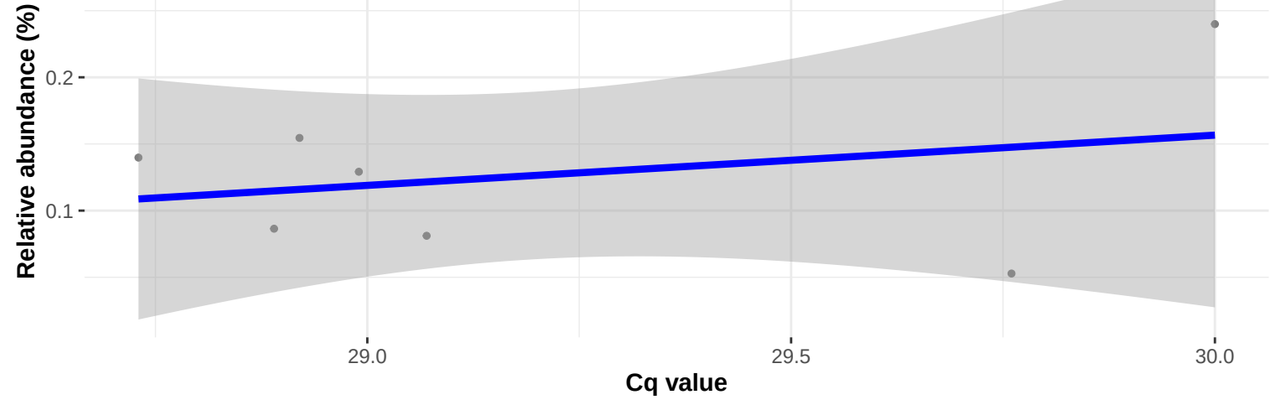
Correlation within: IM−PIM

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

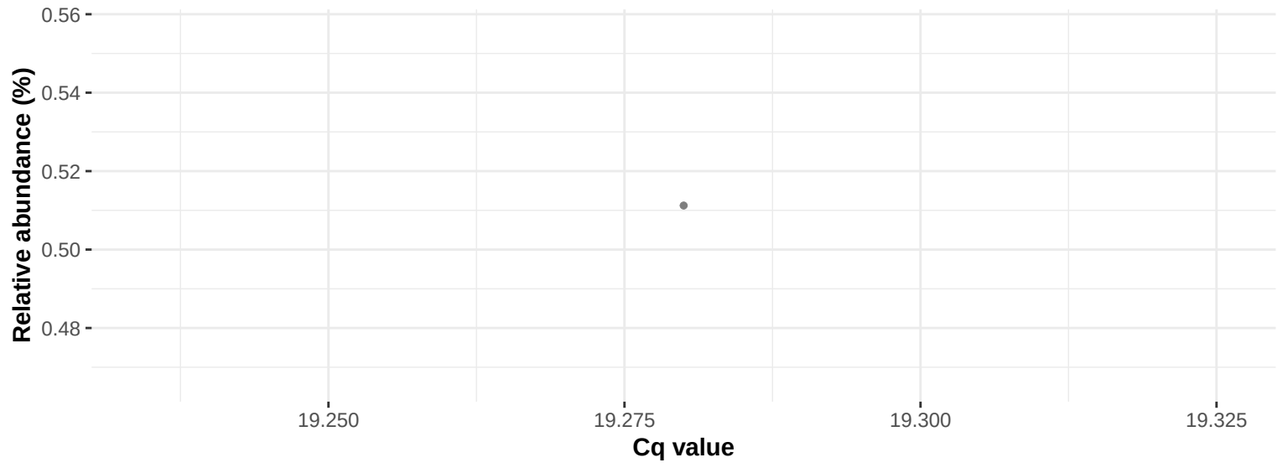


Correlation within: IM−DIM

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



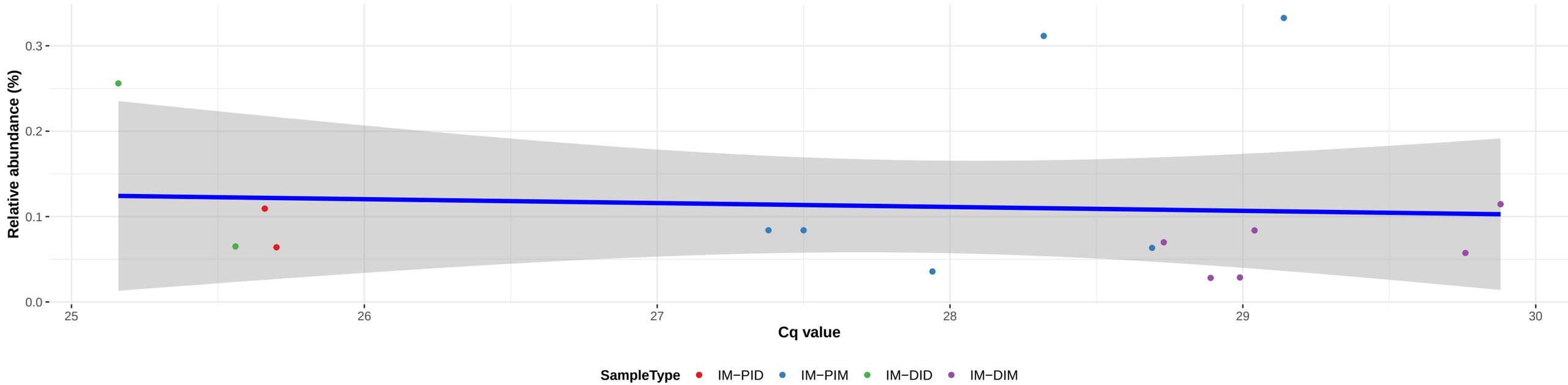
Correlation within: Feed



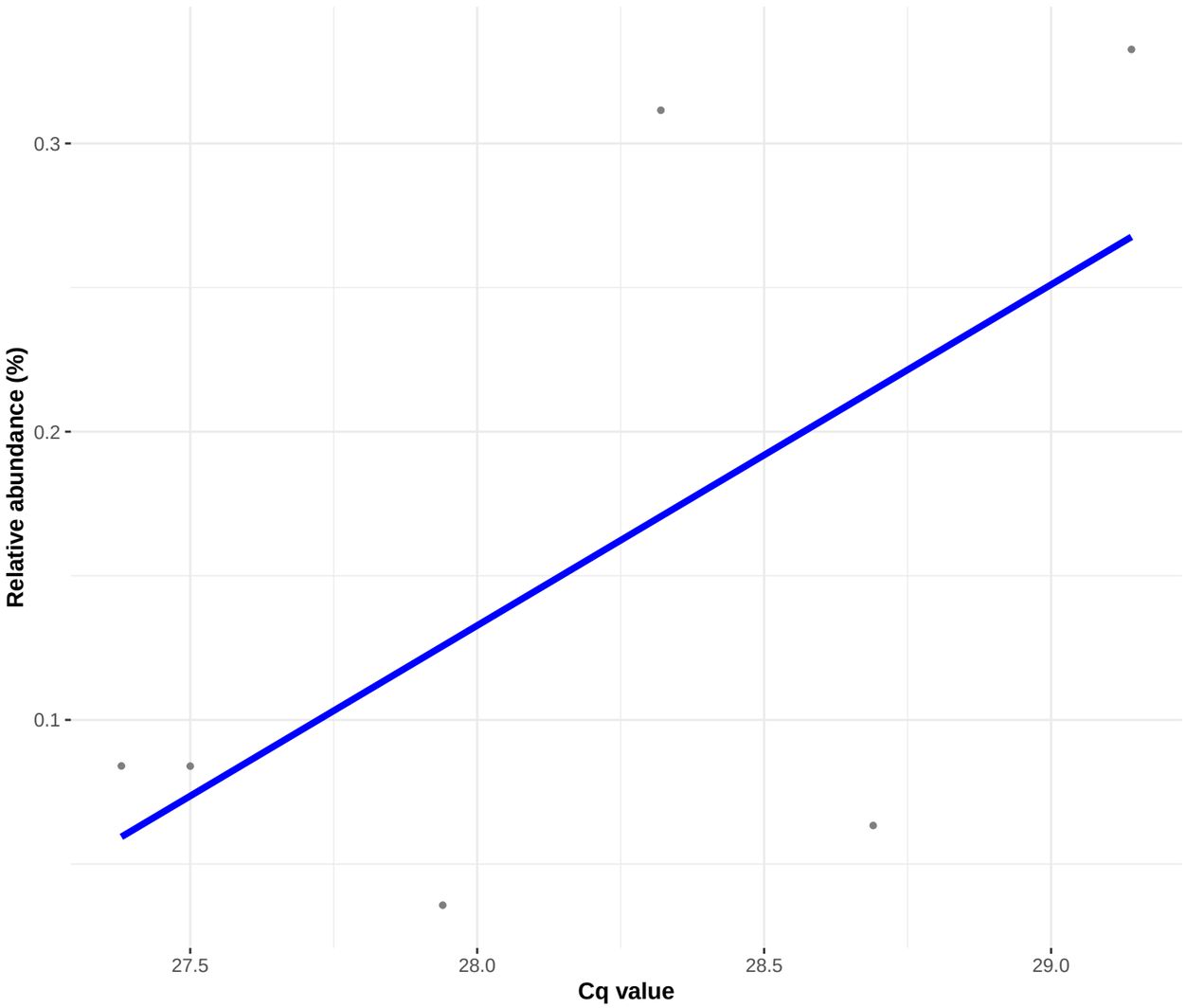
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; Ambiguous_taxa

Correlation with all samples

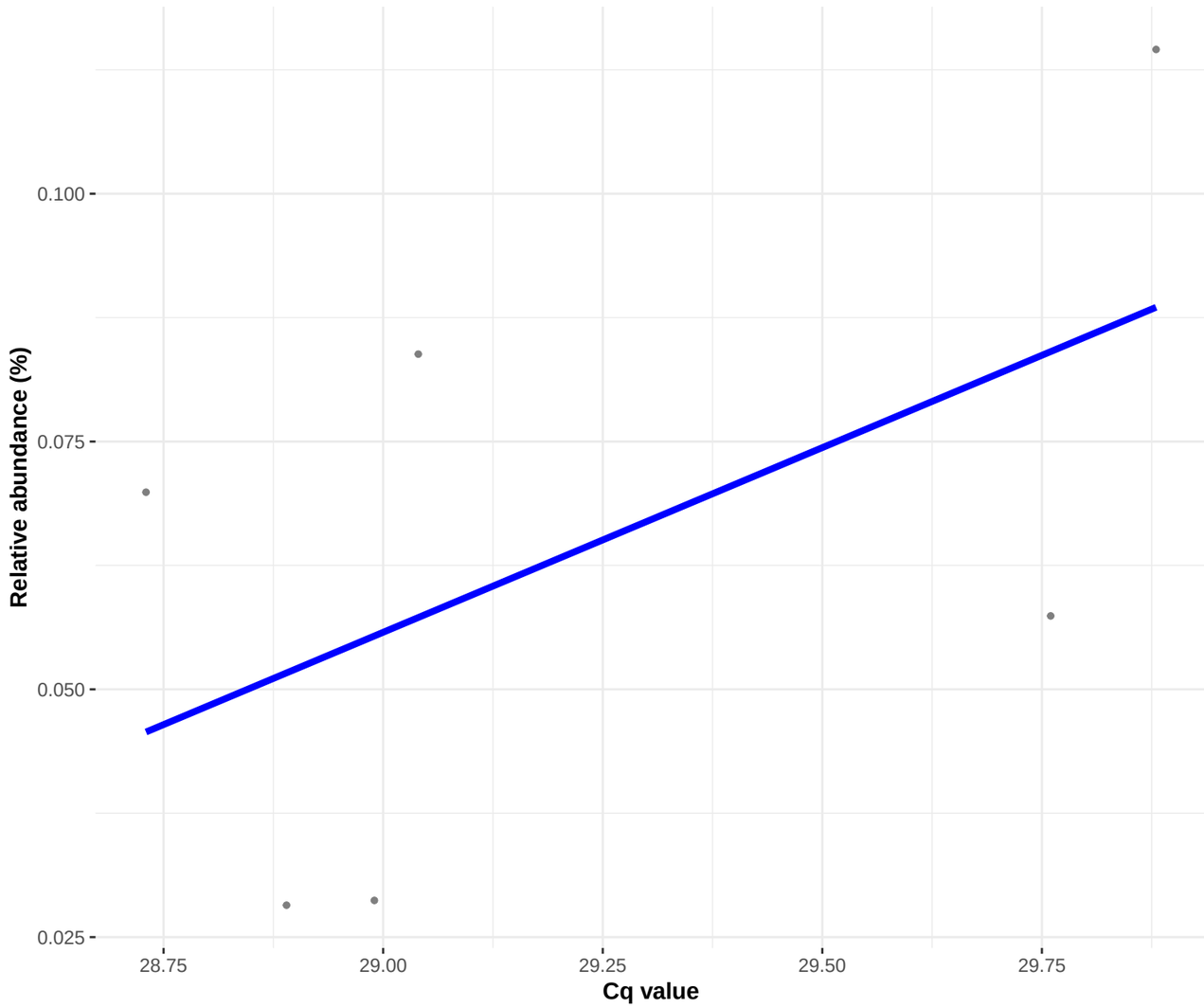
$\log_e(S) = 6.641$, $p = 0.641$, $\hat{\rho}_{Spearman} = -0.126$, $CI_{95\%}$ [−0.596, 0.407], $n_{pairs} = 16$



Correlation within: IM−PIM



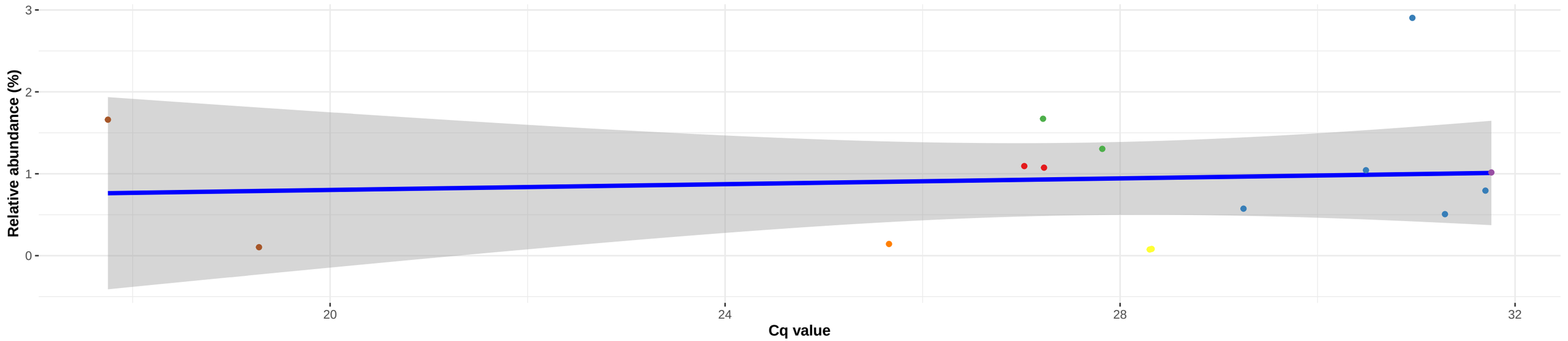
Correlation within: IM−DIM

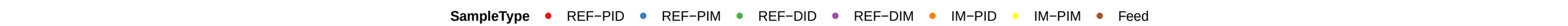


k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus helveticus

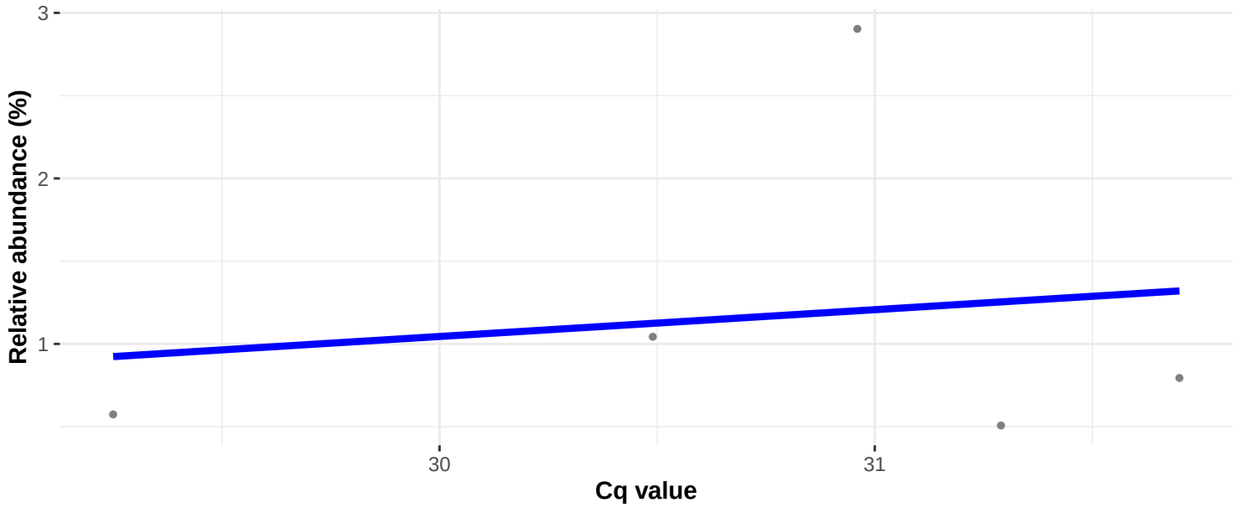
Correlation with all samples

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

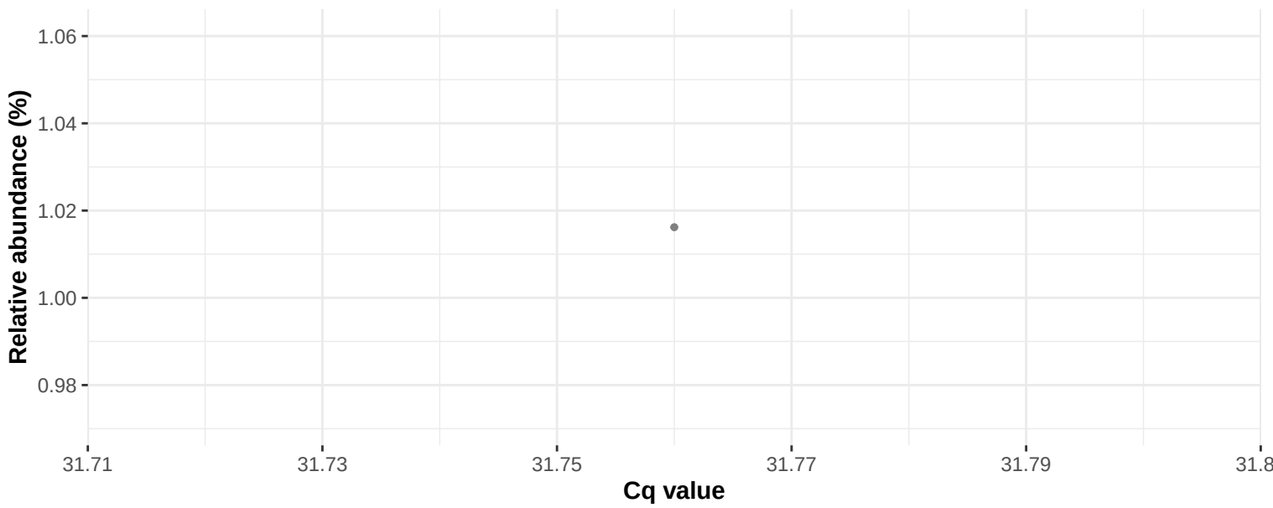




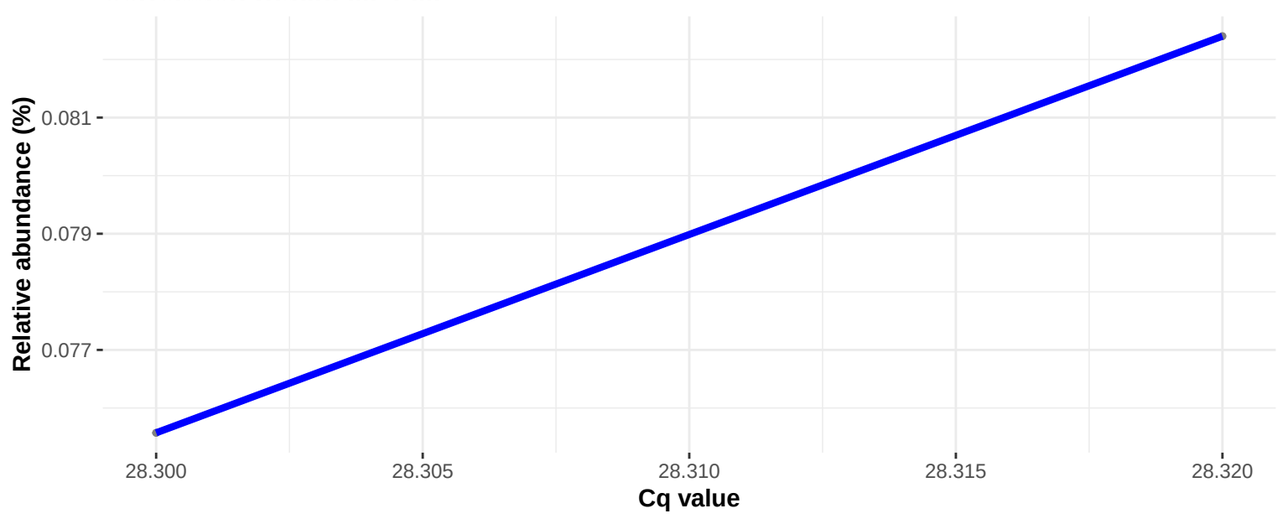
Correlation within: REF−PIM



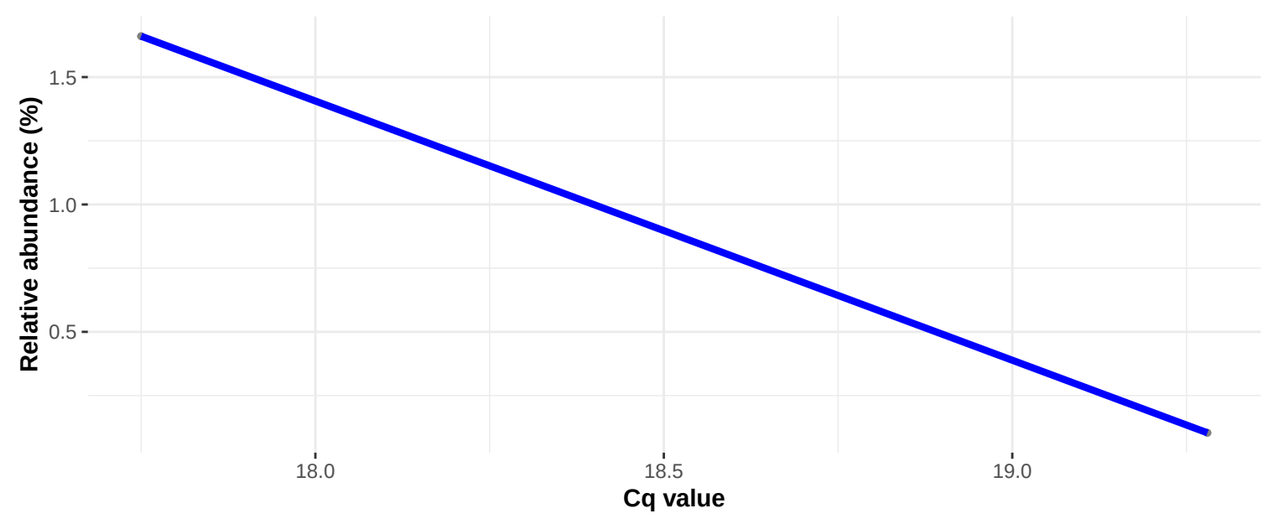
Correlation within: REF−DIM



Correlation within: IM−PIM



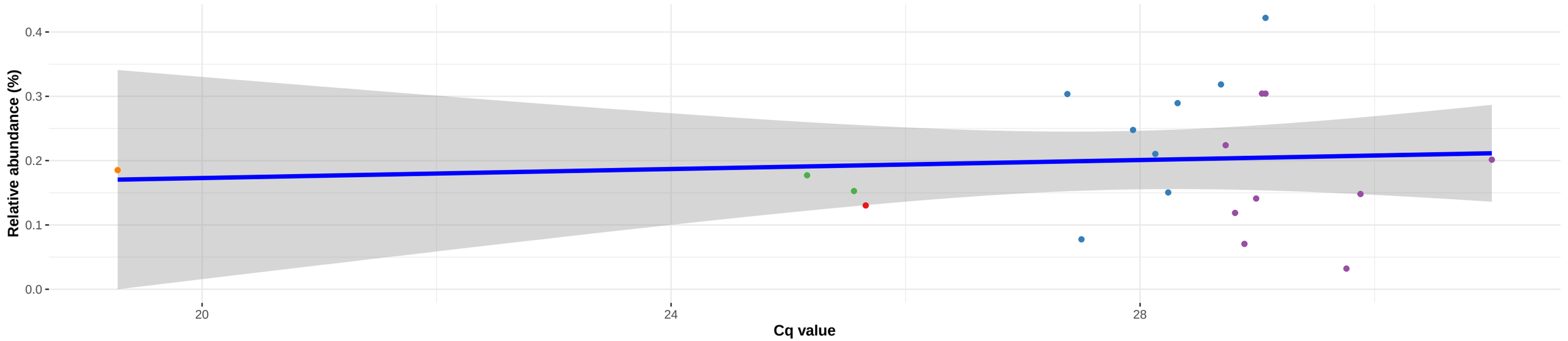
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; NA

Correlation with all samples

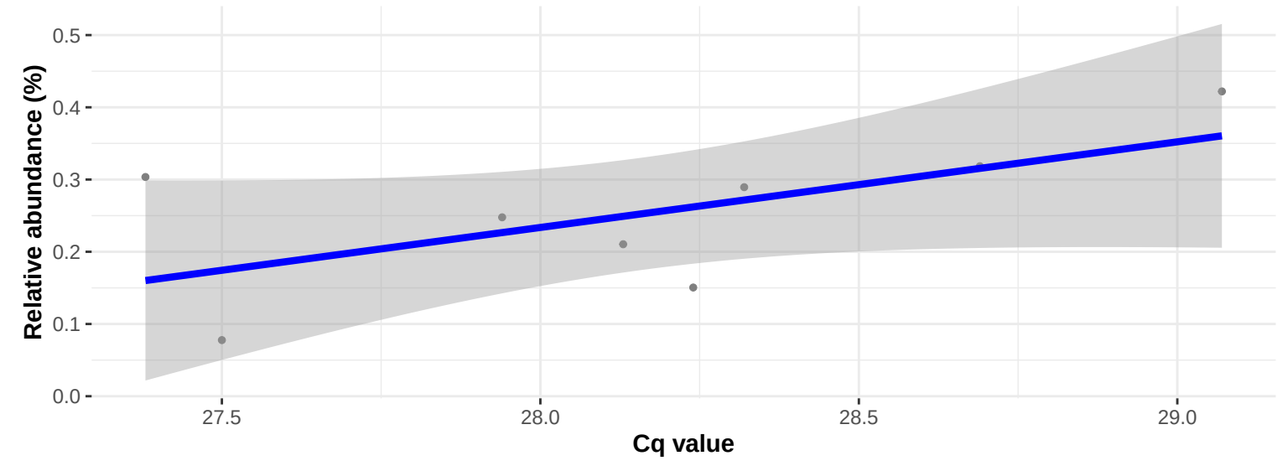
$\log_e(S)$ = 7.291, p = 0.838, $\hat{\rho}_{Spearman}$ = 0.047, $CI_{95\%}$ [−0.404, 0.480], n_{pairs} = 21



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

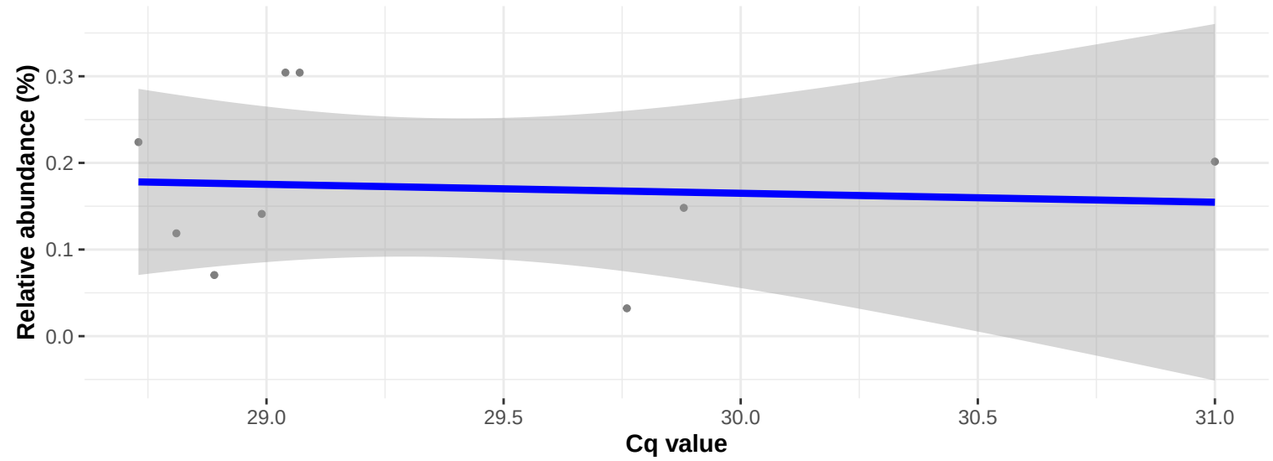
Correlation within: IM−PIM

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

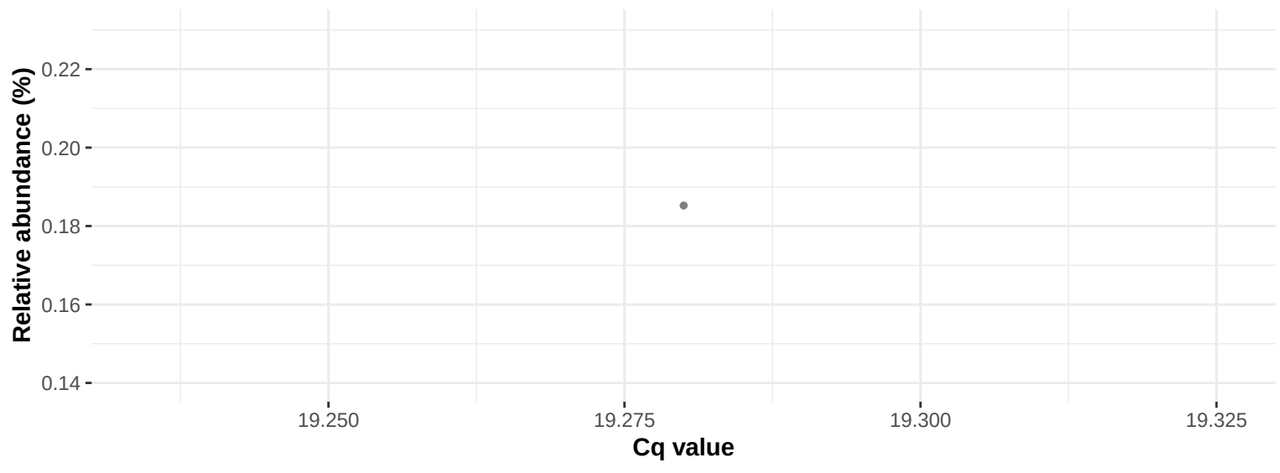


Correlation within: IM−DIM

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

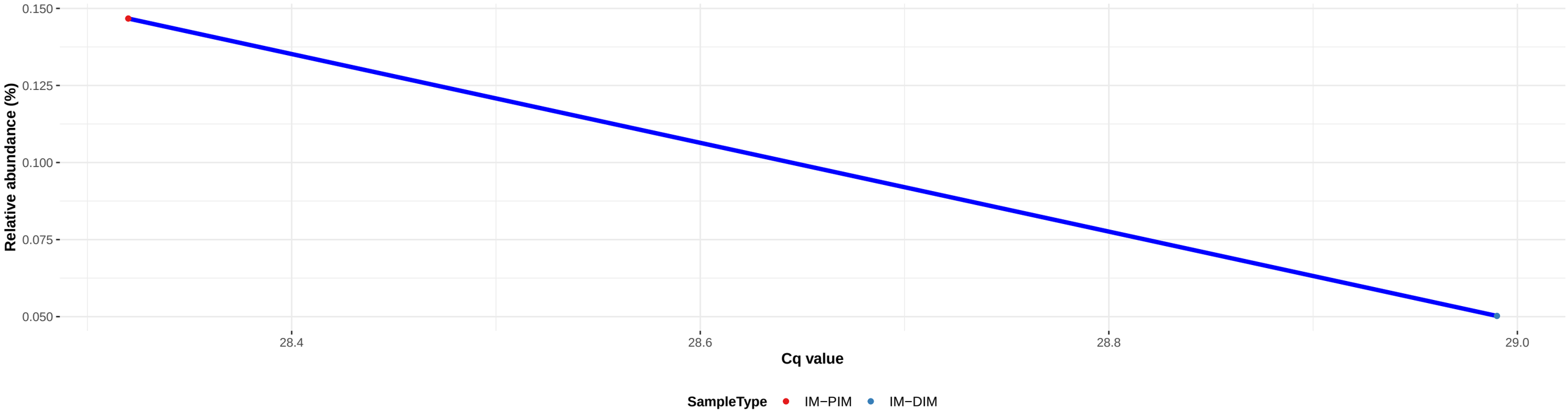


Correlation within: Feed

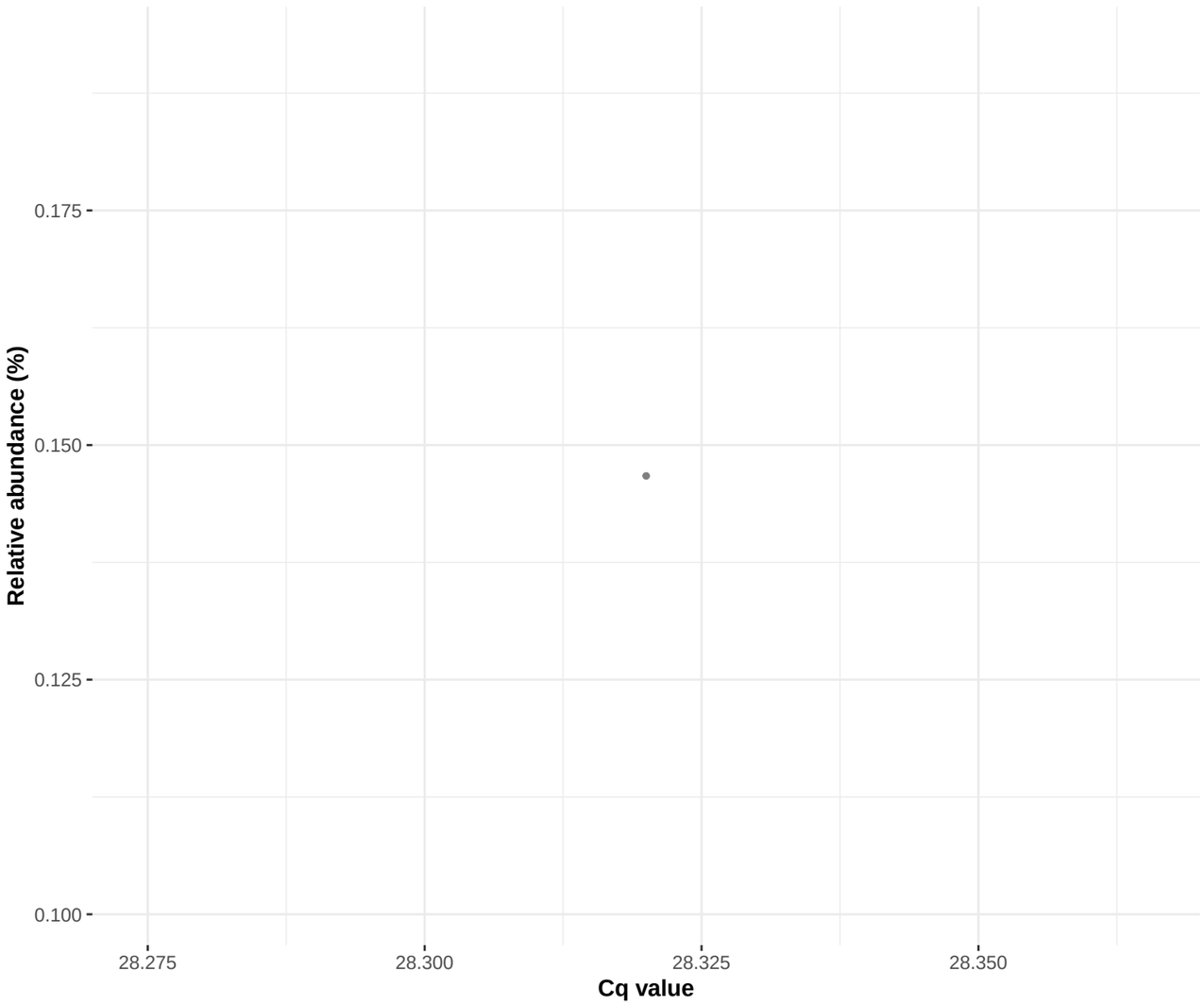


k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingobium; s__alpha proteobacterium PI_GH4.1.H5

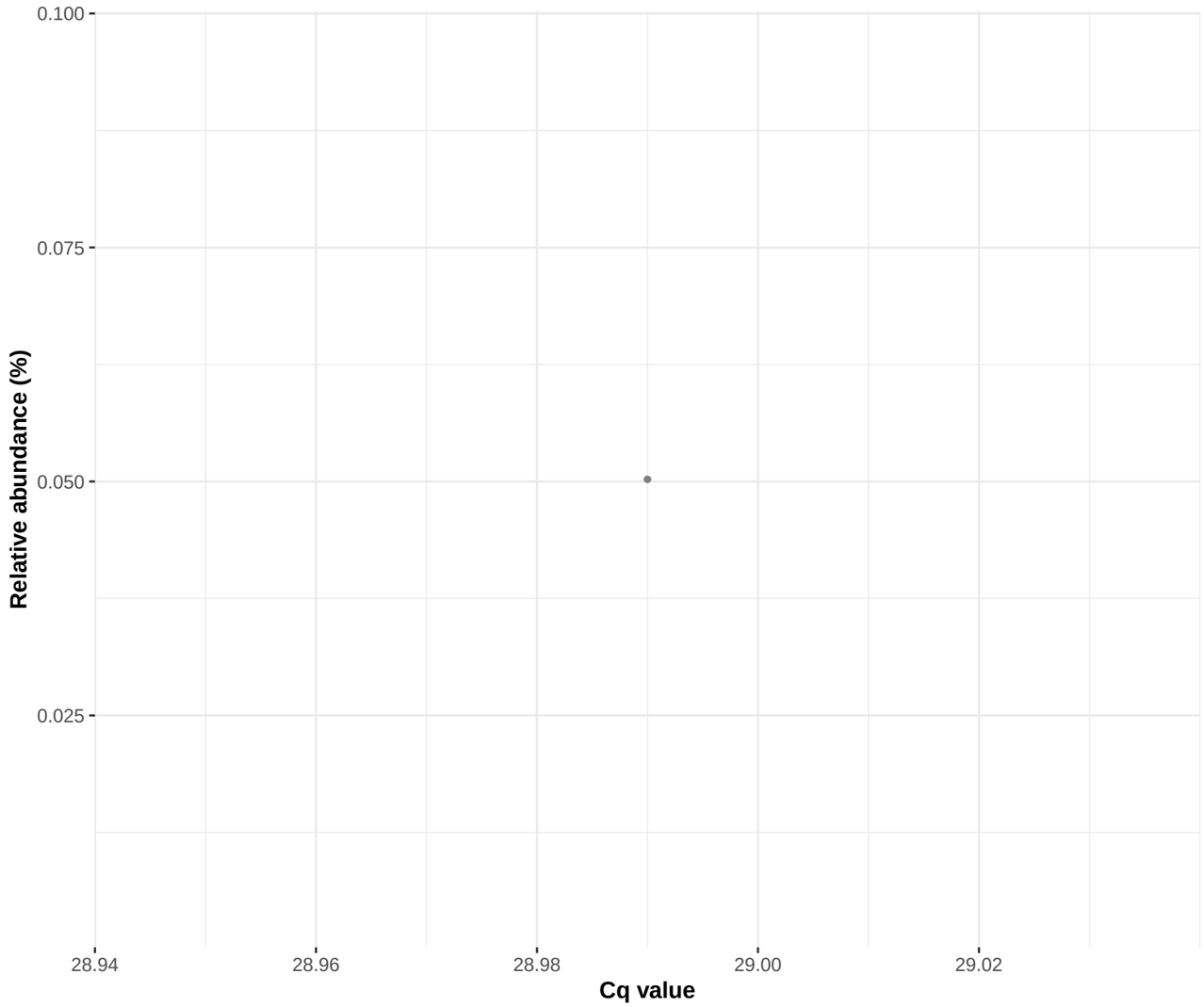
Correlation with all samples



Correlation within: IM−PIM



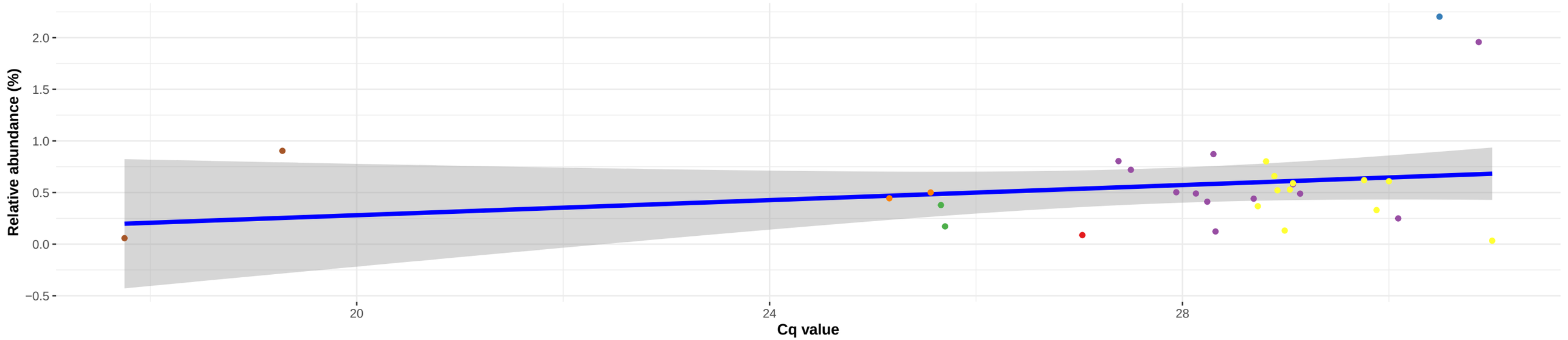
Correlation within: IM−DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. DJF_WC57

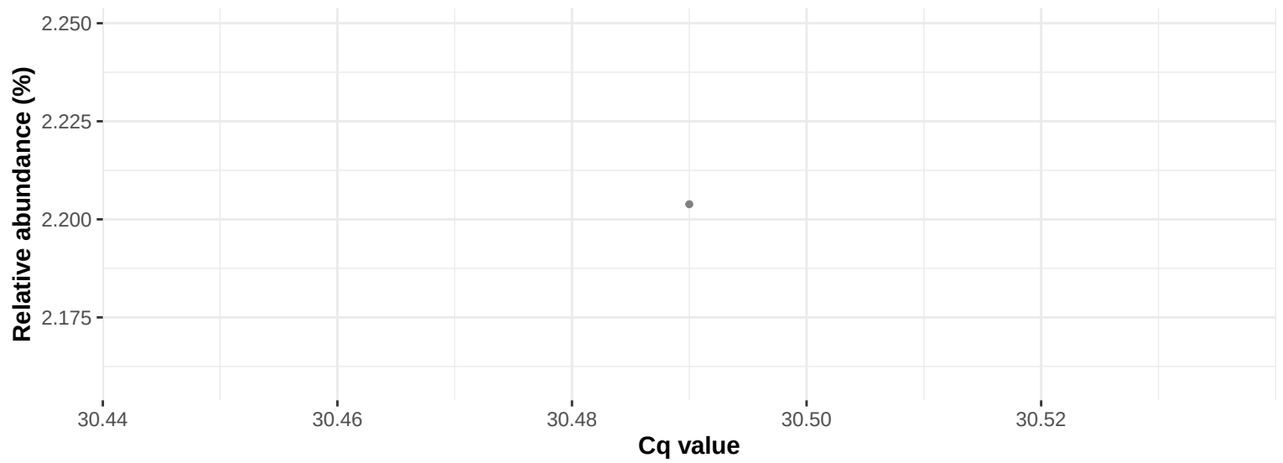
Correlation with all samples

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



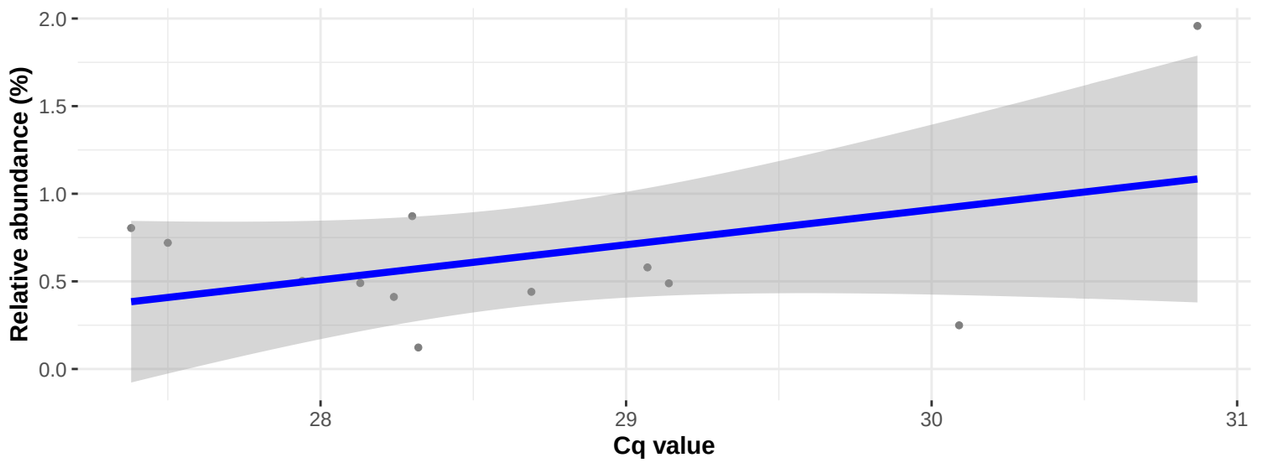
SampleType ● REF−PID ● REF−PIM ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM ● Feed

Correlation within: REF−PIM



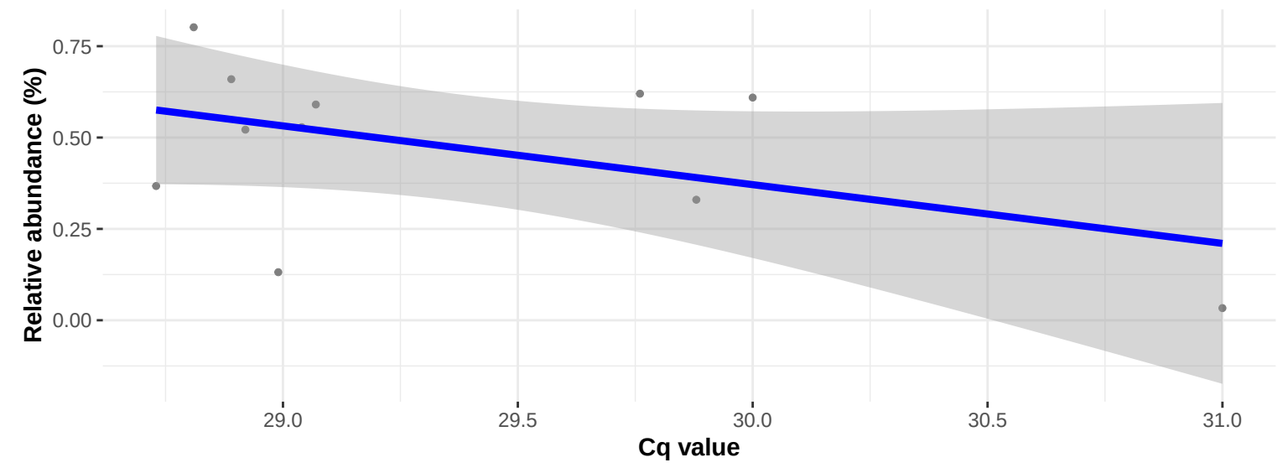
Correlation within: IM−PIM

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

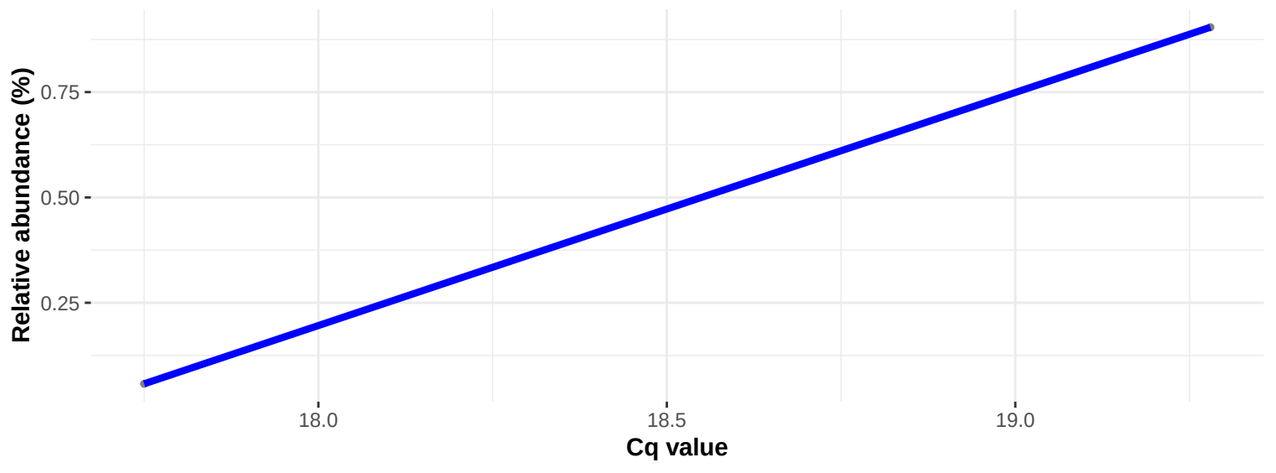


Correlation within: IM−DIM

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



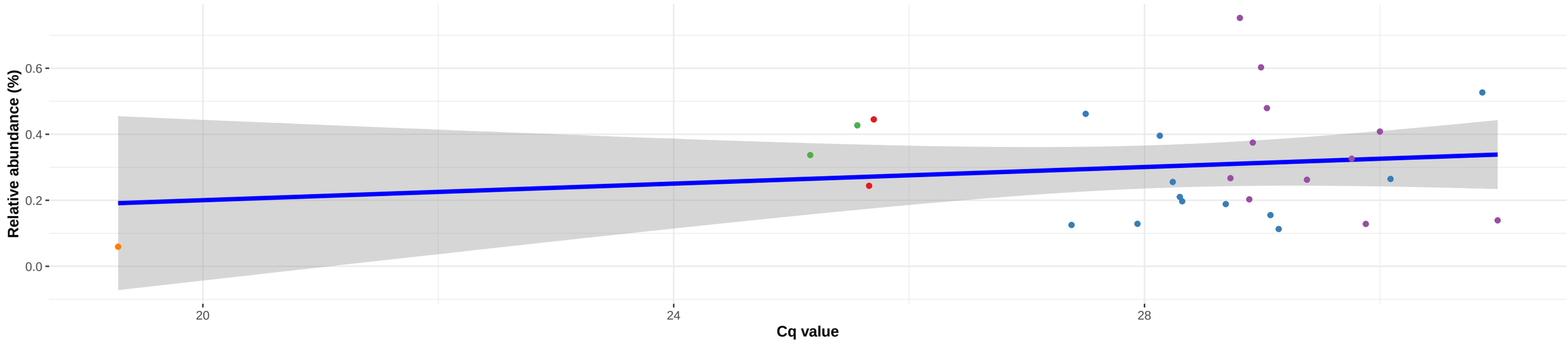
Correlation within: Feed



k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples

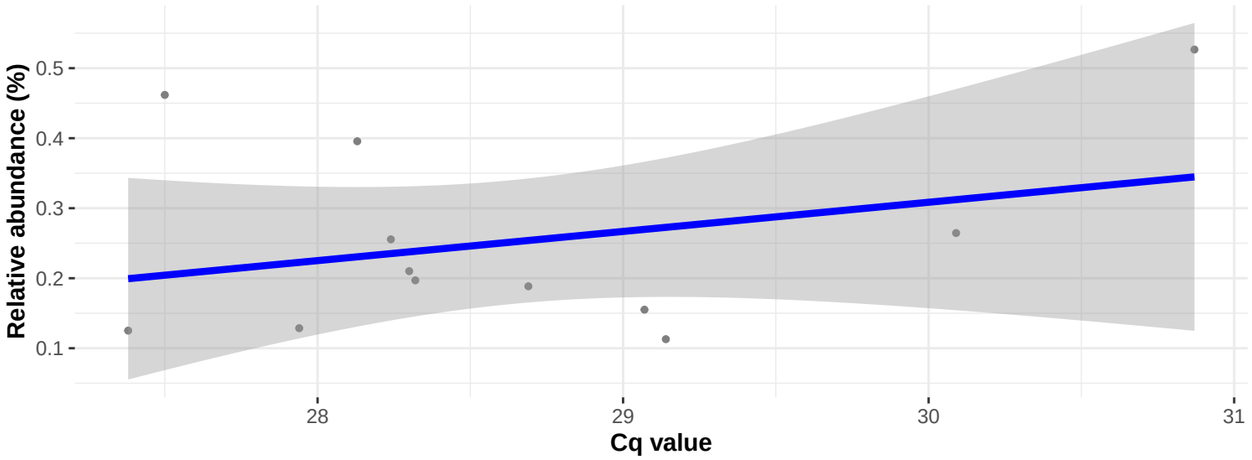
$\log_e(S)$ = 8.148, p = 0.786, $\hat{\rho}_{Spearman}$ = 0.054, $CI_{95\%}$ [−0.336, 0.428], n_{pairs} = 28



SampleType IM−PID IM−PIM IM−DID IM−DIM Feed

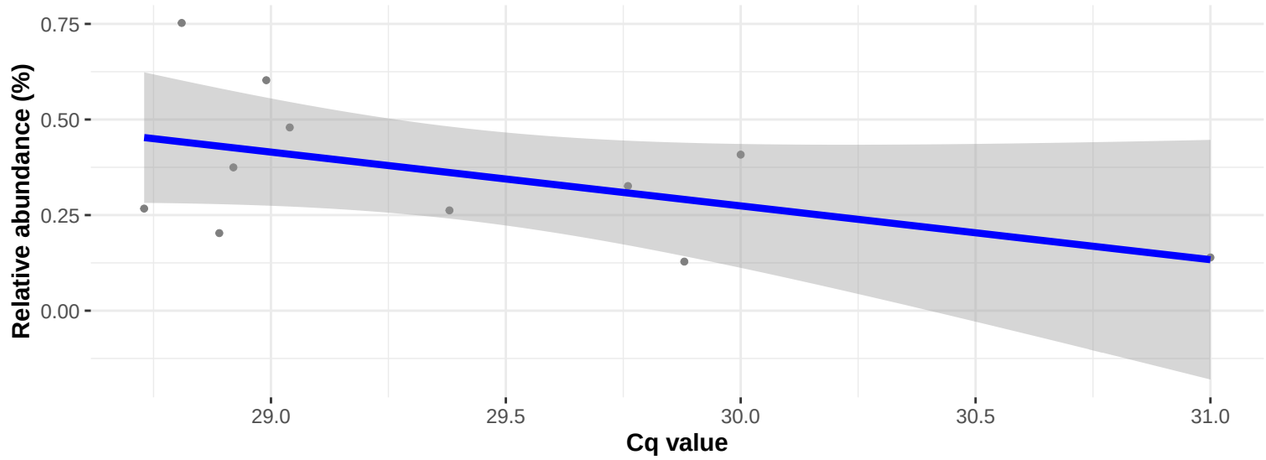
Correlation within: IM−PIM

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

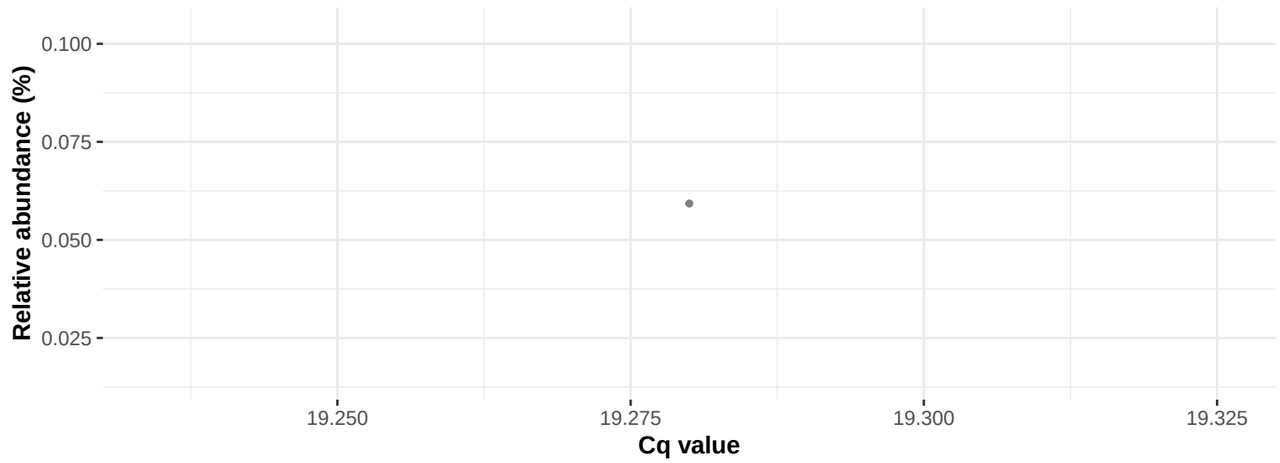


Correlation within: IM−DIM

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



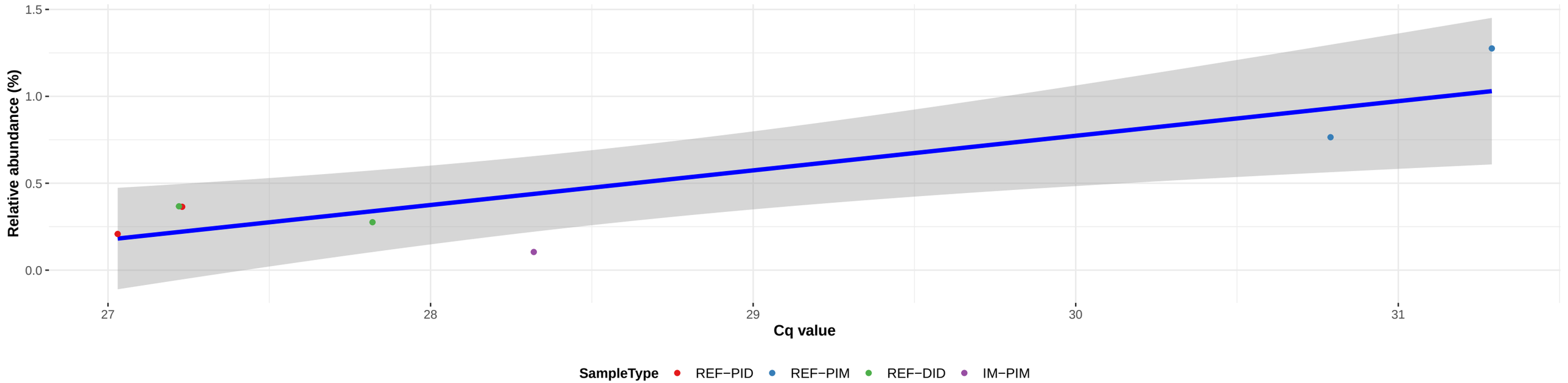
Correlation within: Feed



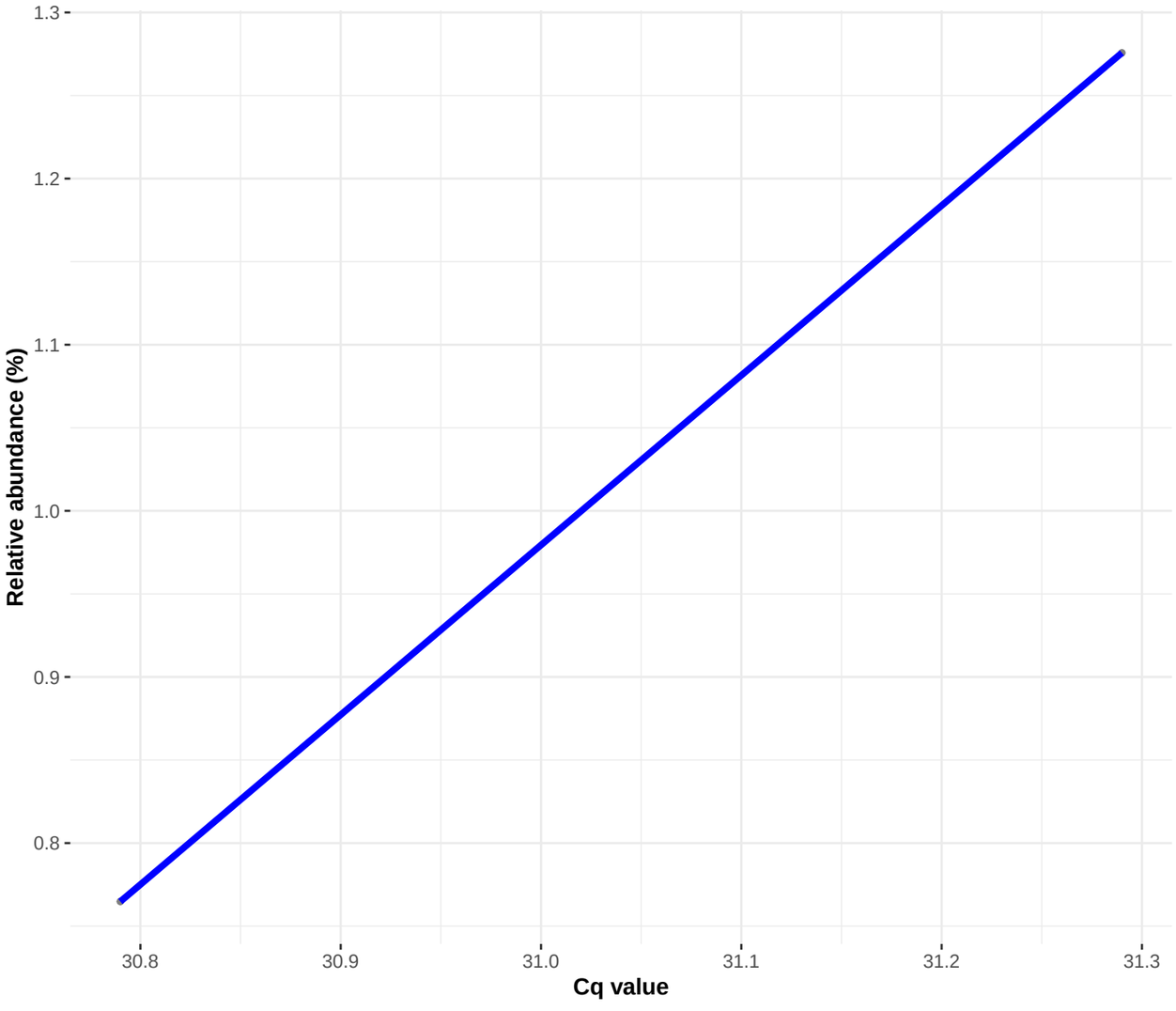
k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Kurthia; s__uncultured bacterium

Correlation with all samples

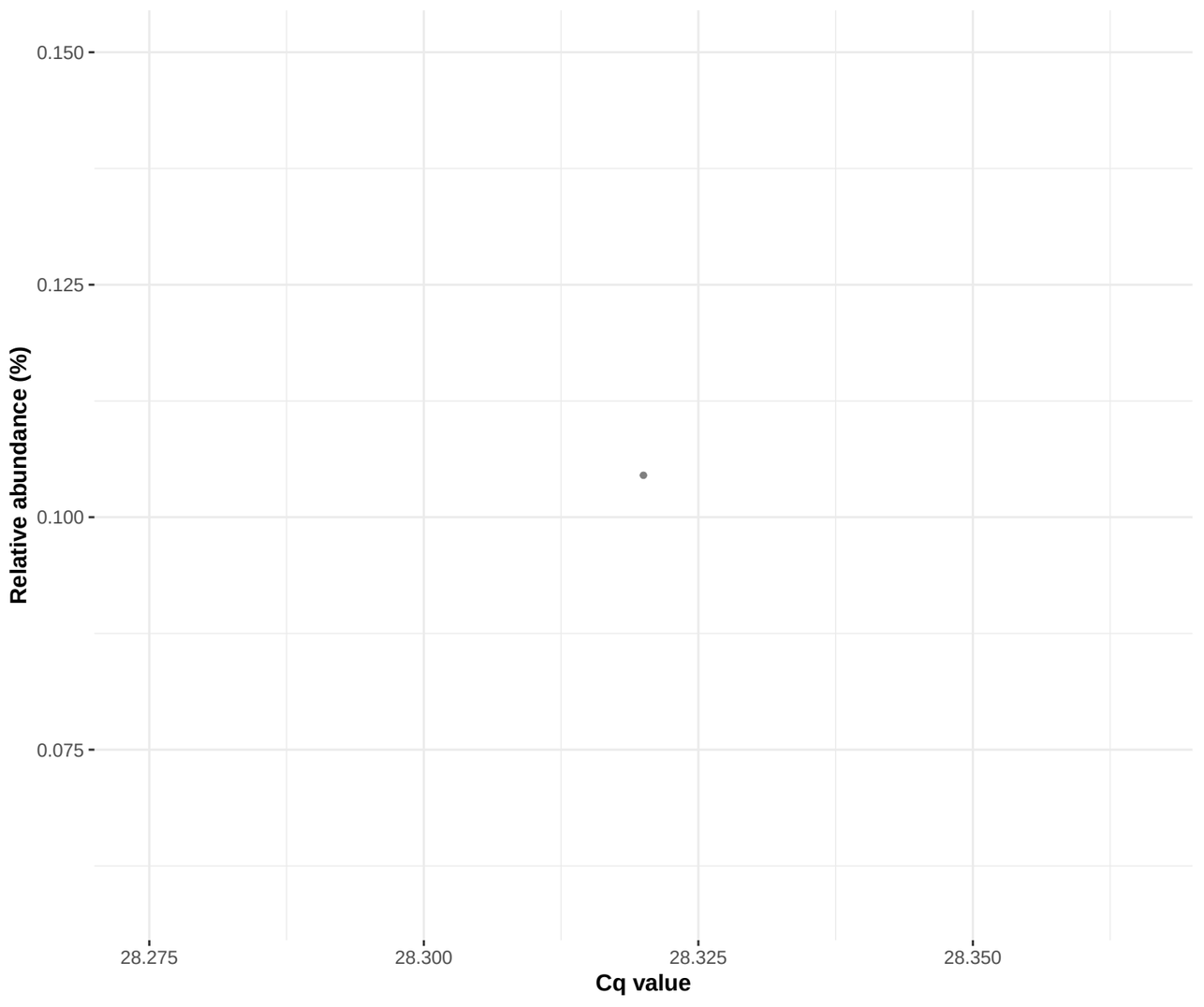
$\log_e(S) = 3.332$, $p = 0.253$, $\hat{\rho}_{Spearman} = 0.500$, $CI_{95\%}$ [−0.430, 0.915], $n_{pairs} = 7$



Correlation within: REF−PIM



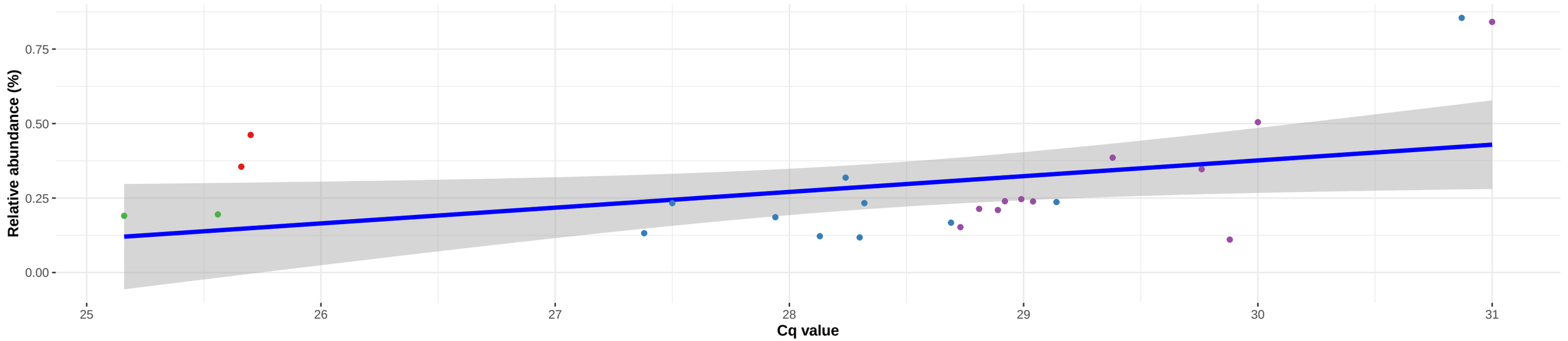
Correlation within: IM−PIM



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

Correlation with all samples

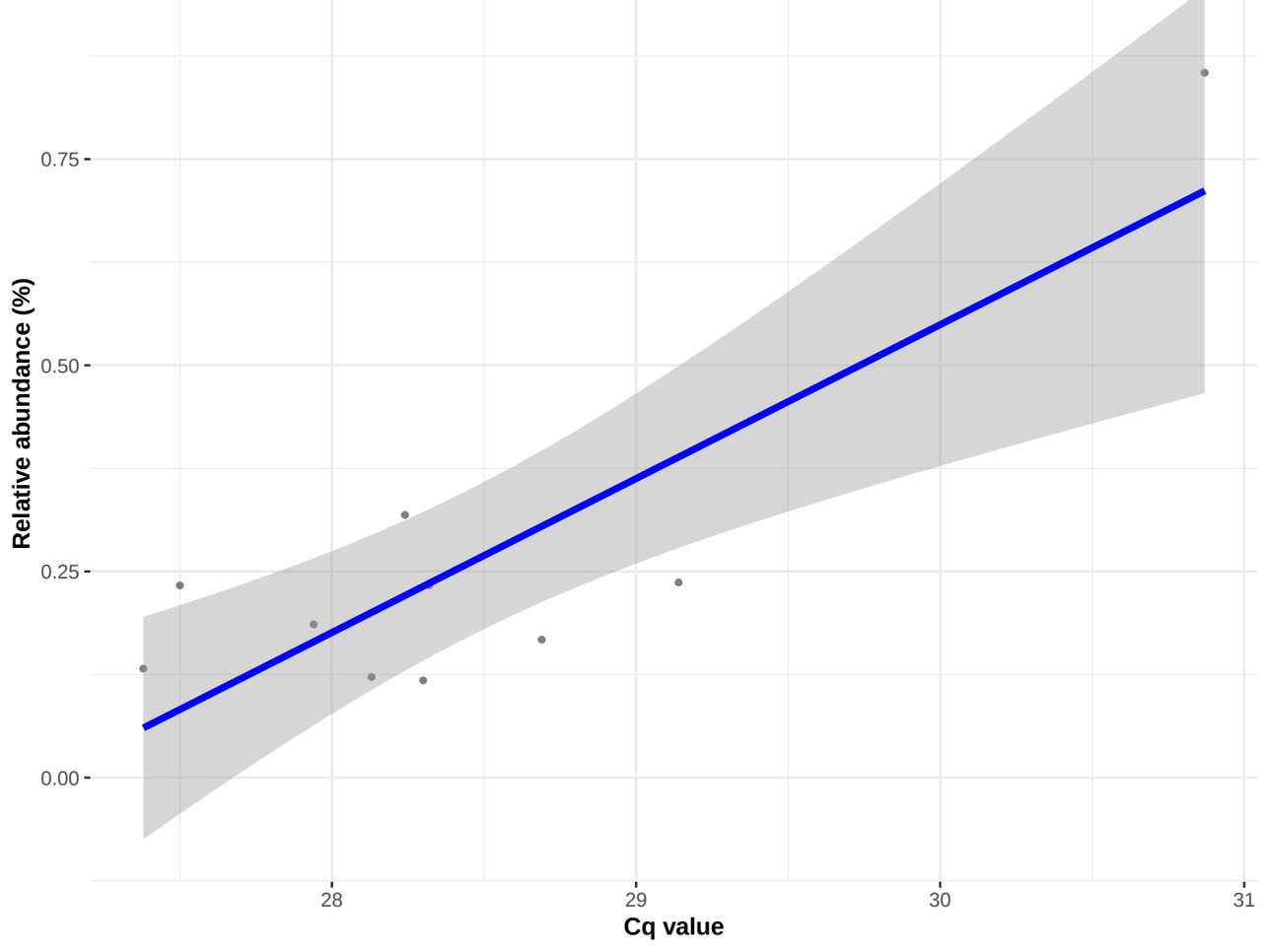
$\log_e(S)$ = 7.338, p = 0.043, $\hat{\rho}_{Spearman}$ = 0.408, $CI_{95\%}$ [0.004, 0.698], n_{pairs} = 25



SampleType ● IM−PID ● IM−PIM ● IM−DID ● IM−DIM

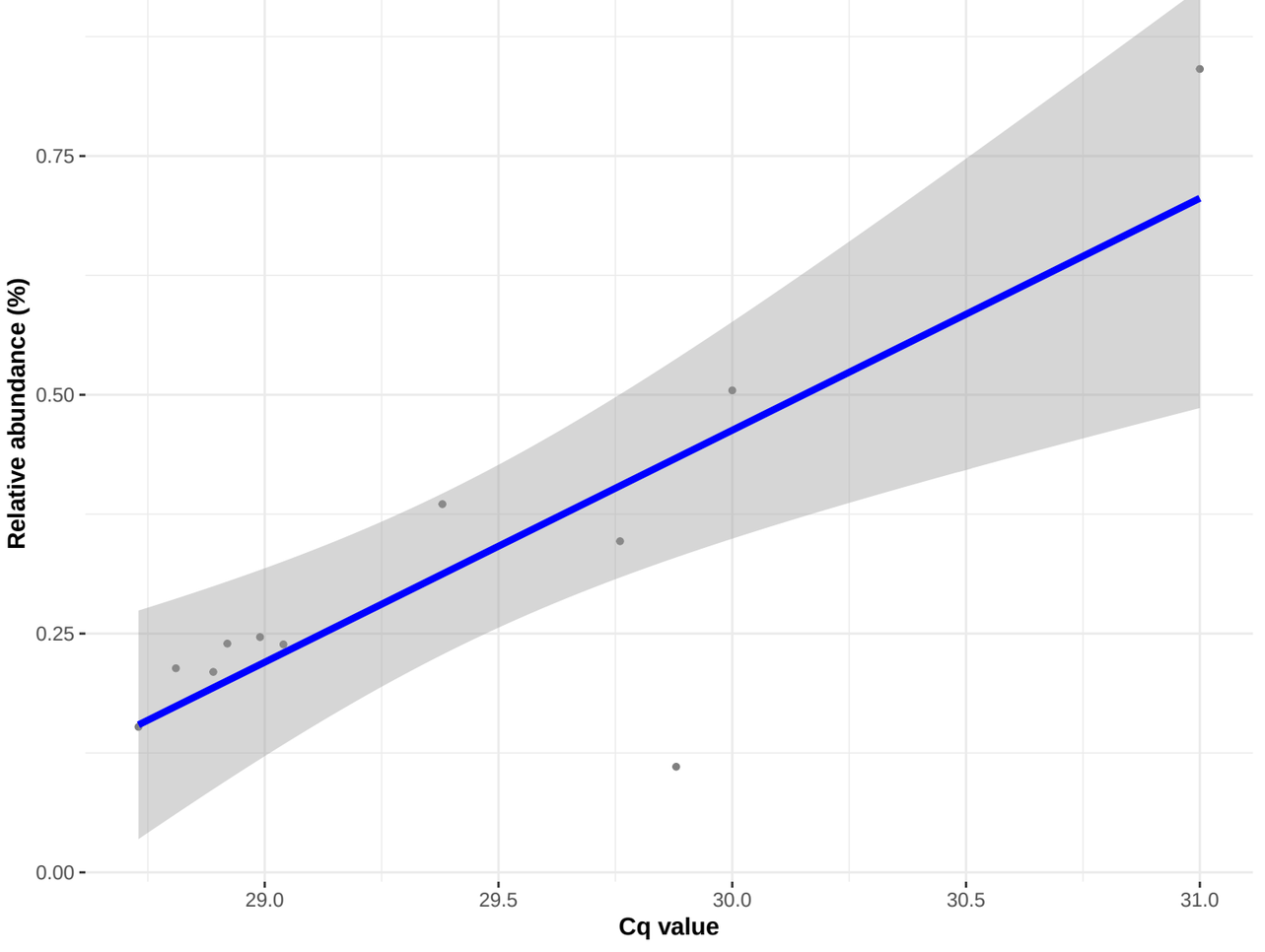
Correlation within: IM−PIM

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



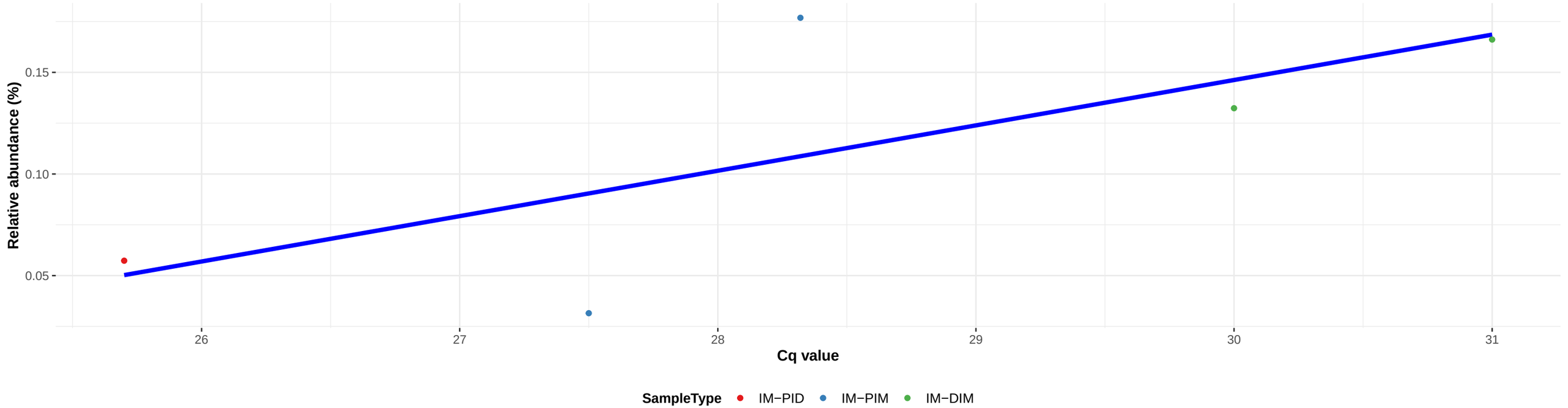
Correlation within: IM−DIM

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

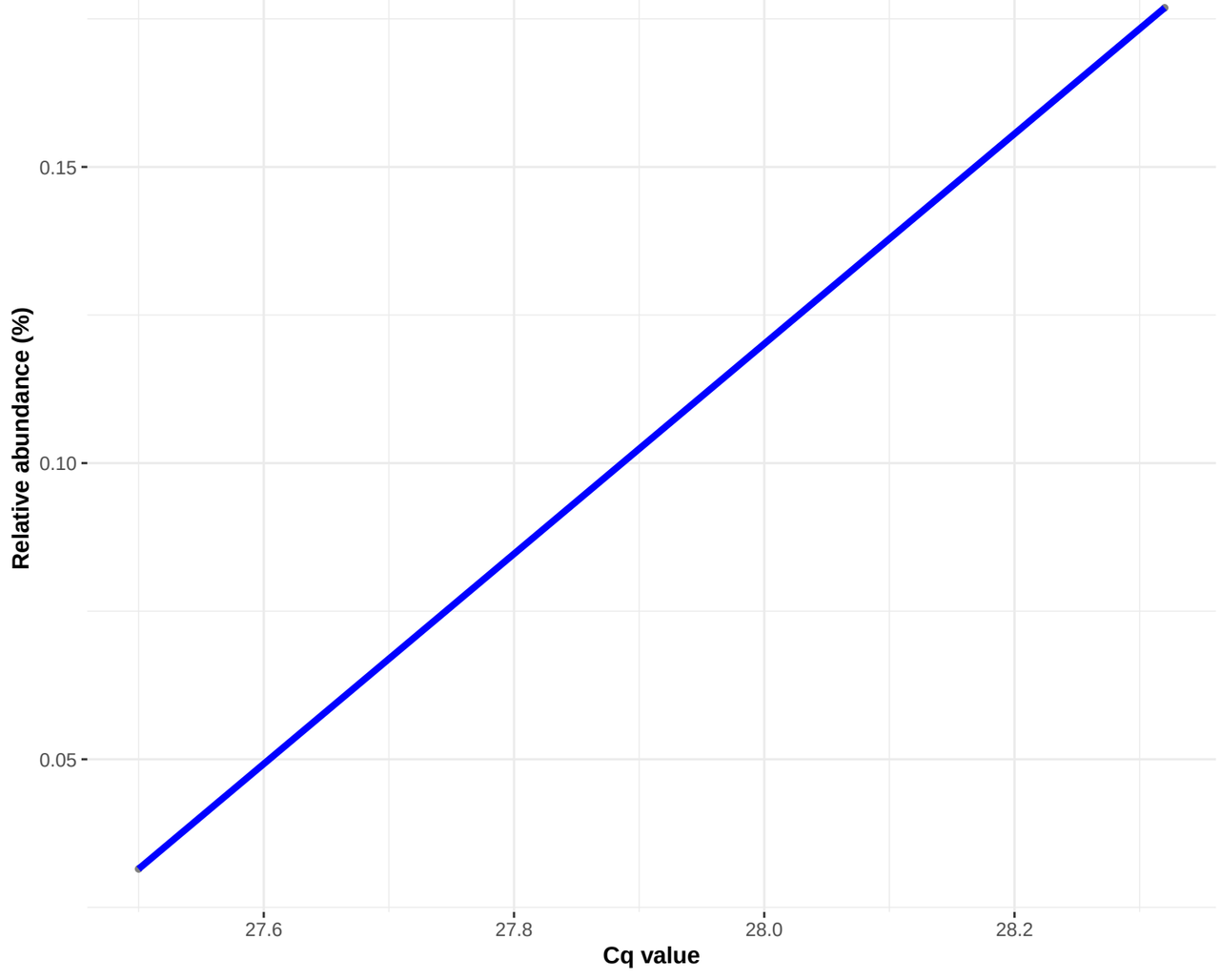


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Paenibacillaceae; g__Paenibacillus; NA

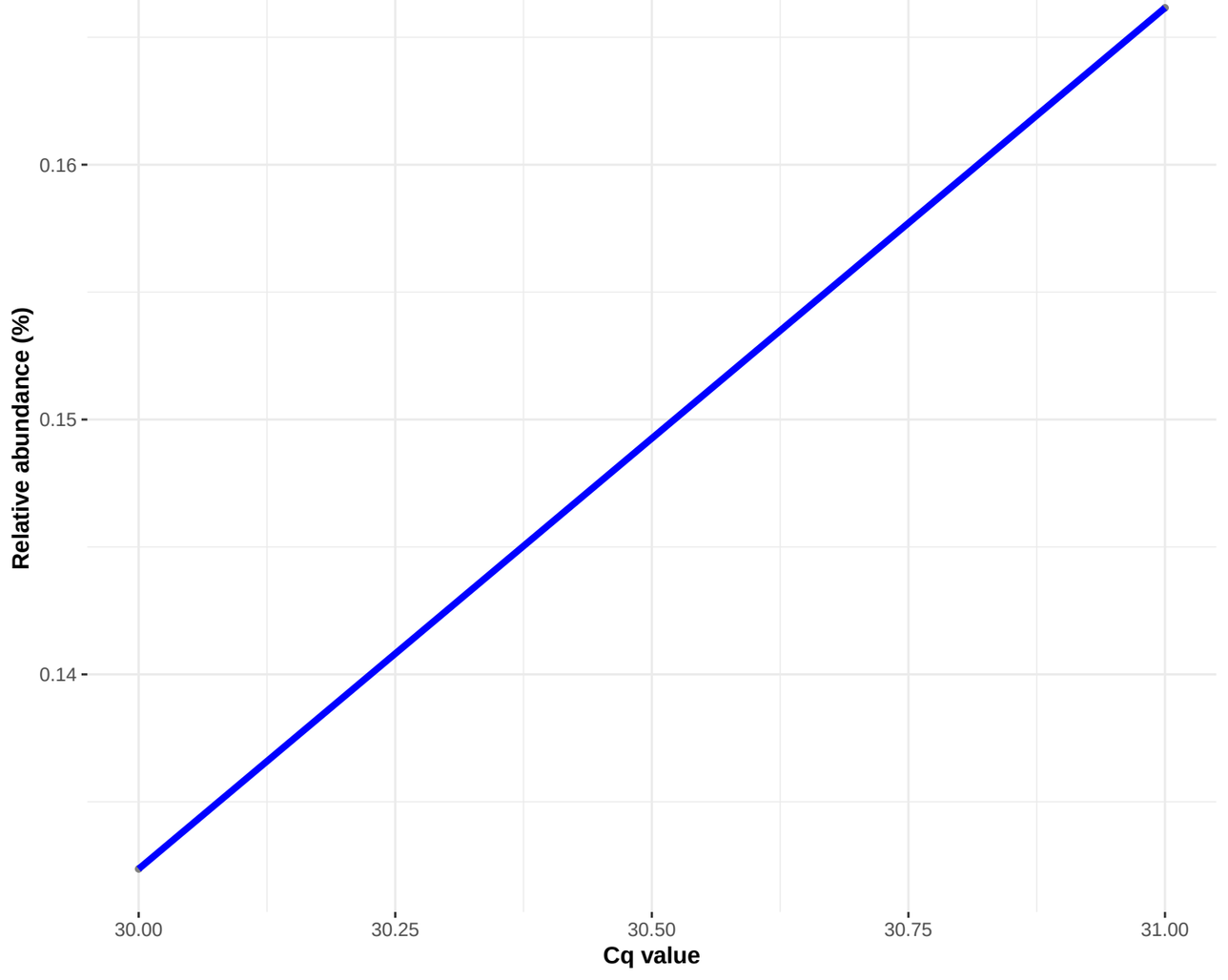
Correlation with all samples



Correlation within: IM−PIM



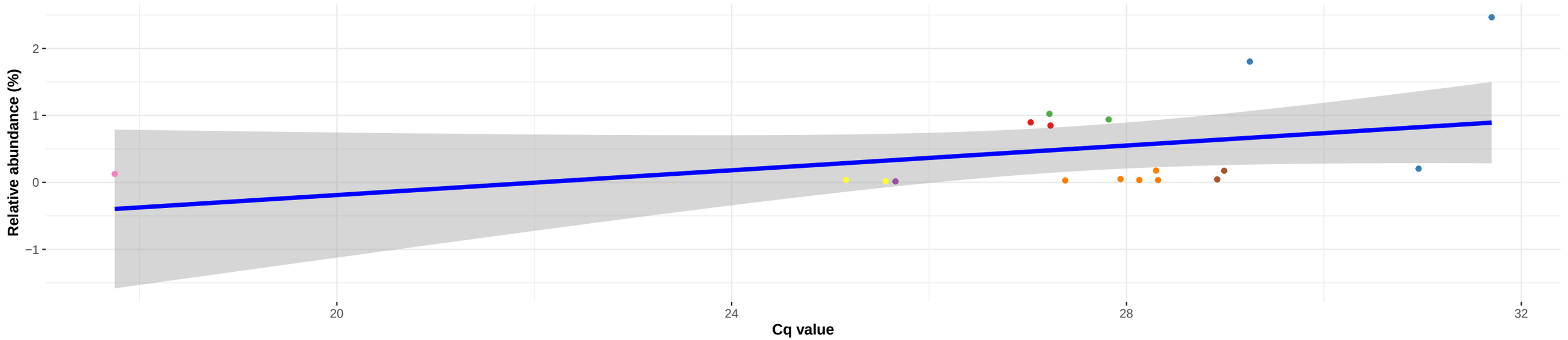
Correlation within: IM−DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; Ambiguous_taxa

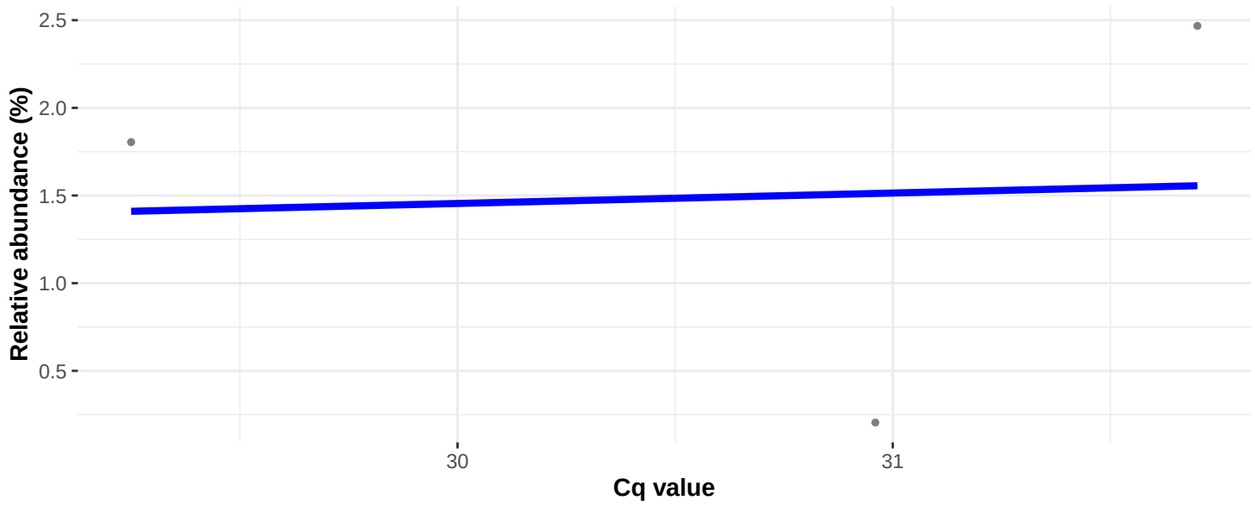
Correlation with all samples

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

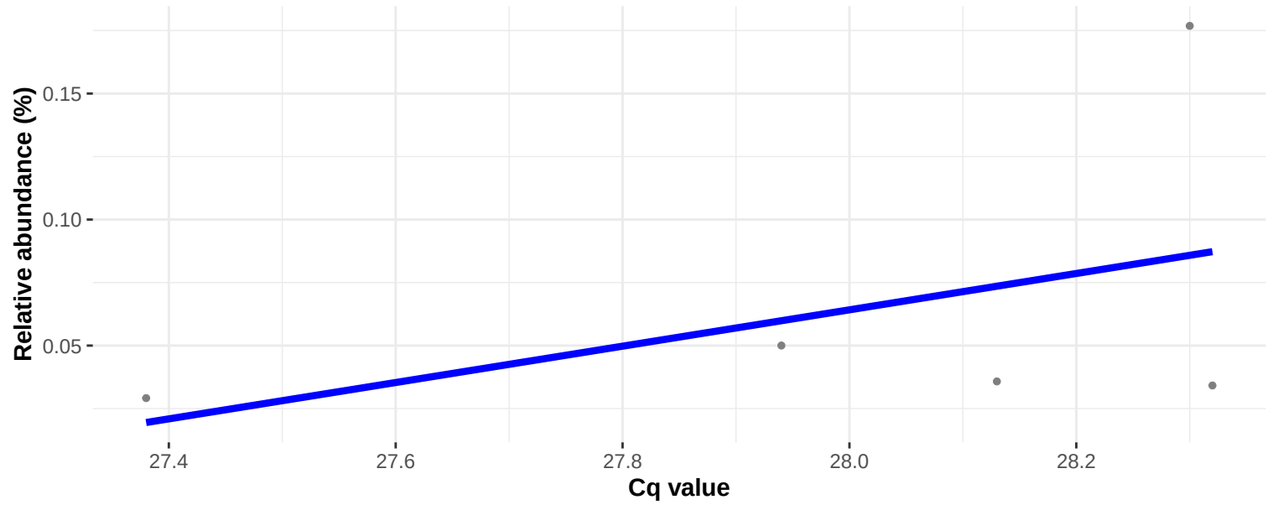


SampleType REF−PID REF−PIM REF−DID IM−PID IM−PIM IM−DID IM−DIM Feed

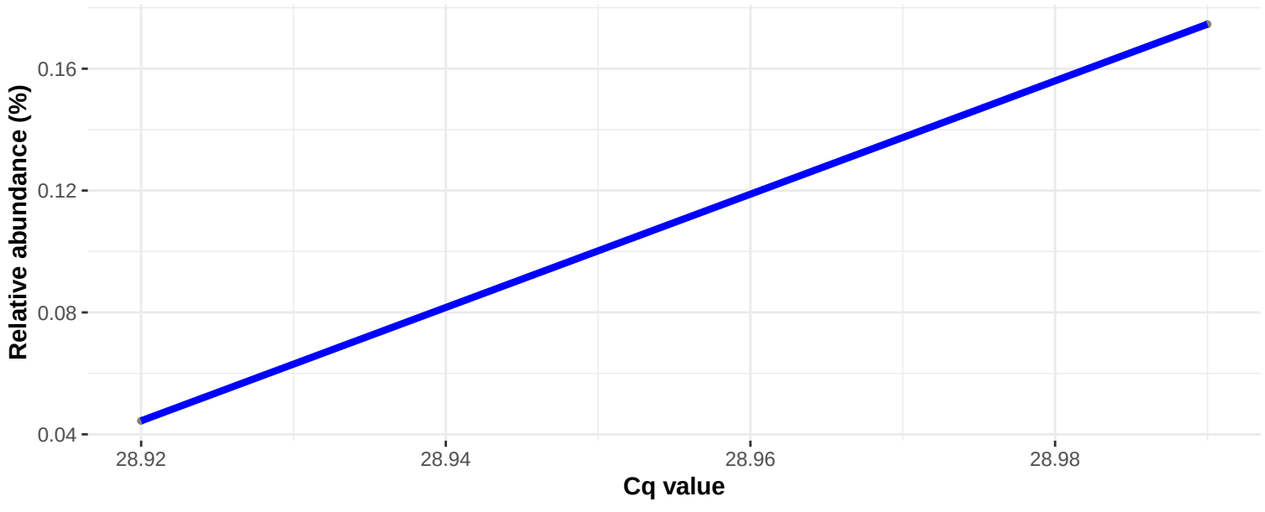
Correlation within: REF−PIM



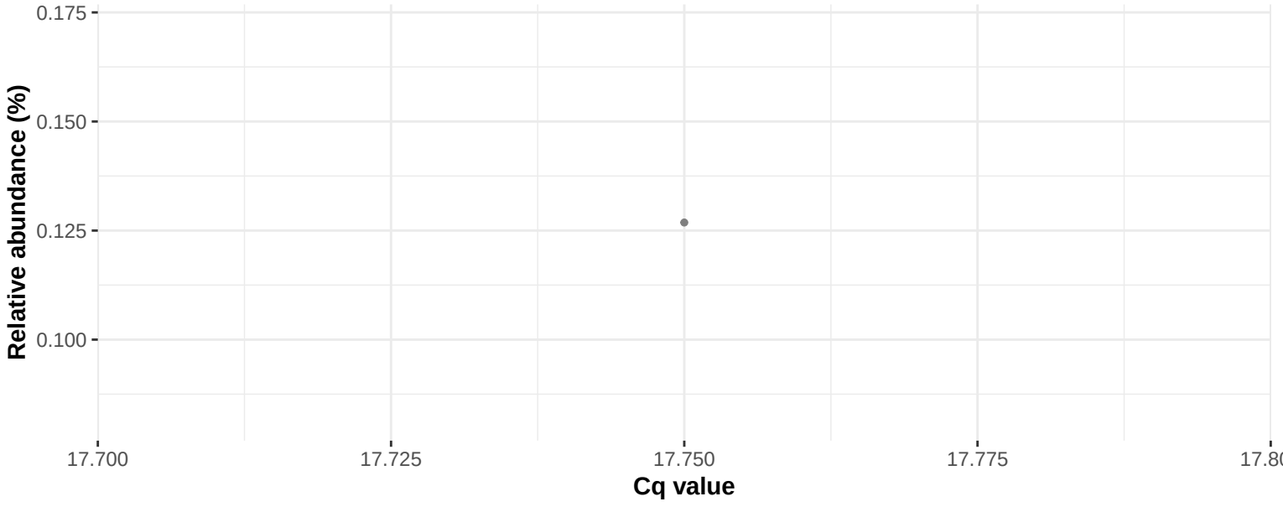
Correlation within: IM−PIM



Correlation within: IM−DIM



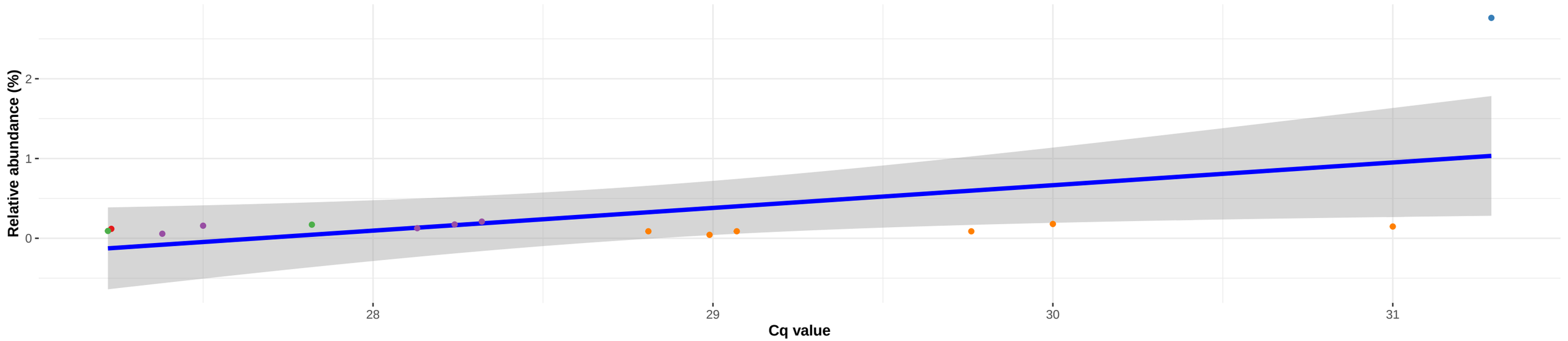
Correlation within: Feed



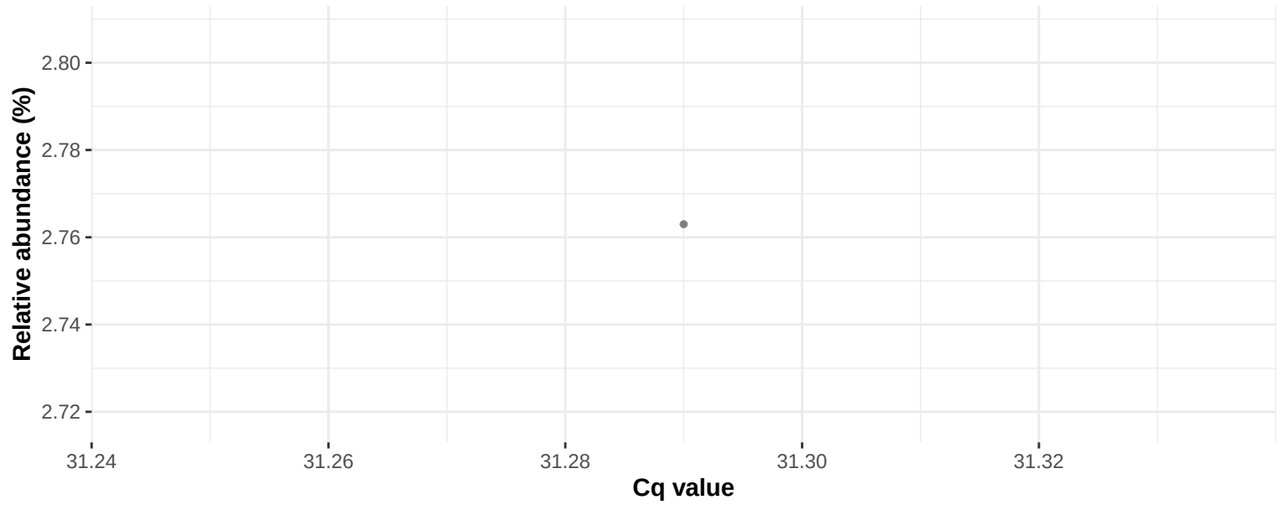
k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium 1; Ambiguous_taxa

Correlation with all samples

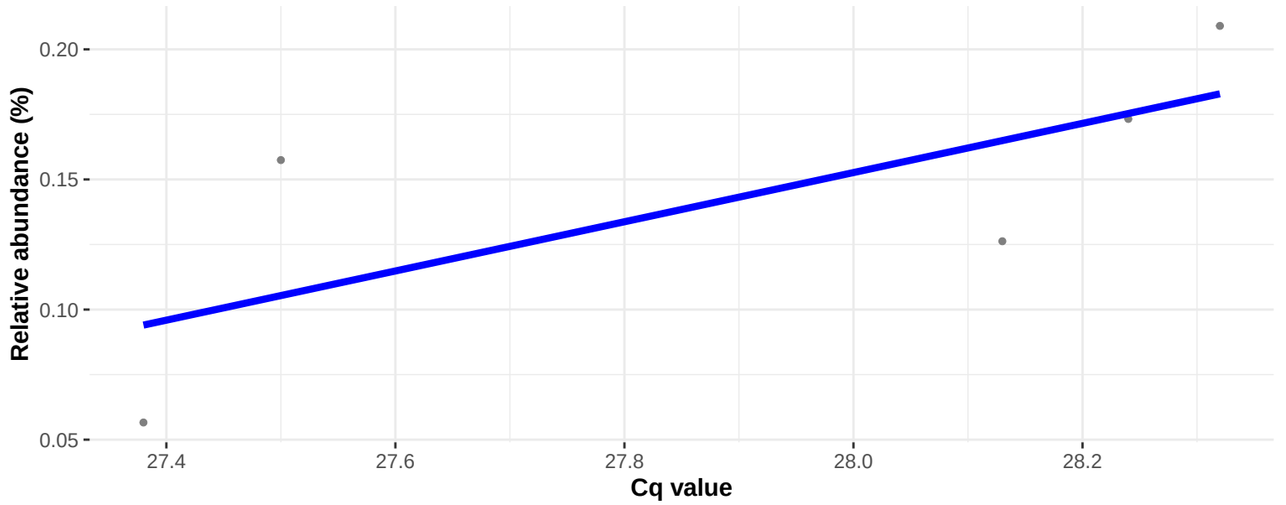
$\log_e(S)$ = 6.078, p = 0.428, $\hat{\rho}_{Spearman}$ = 0.221, $CI_{95\%}$ [−0.343, 0.668], n_{pairs} = 15



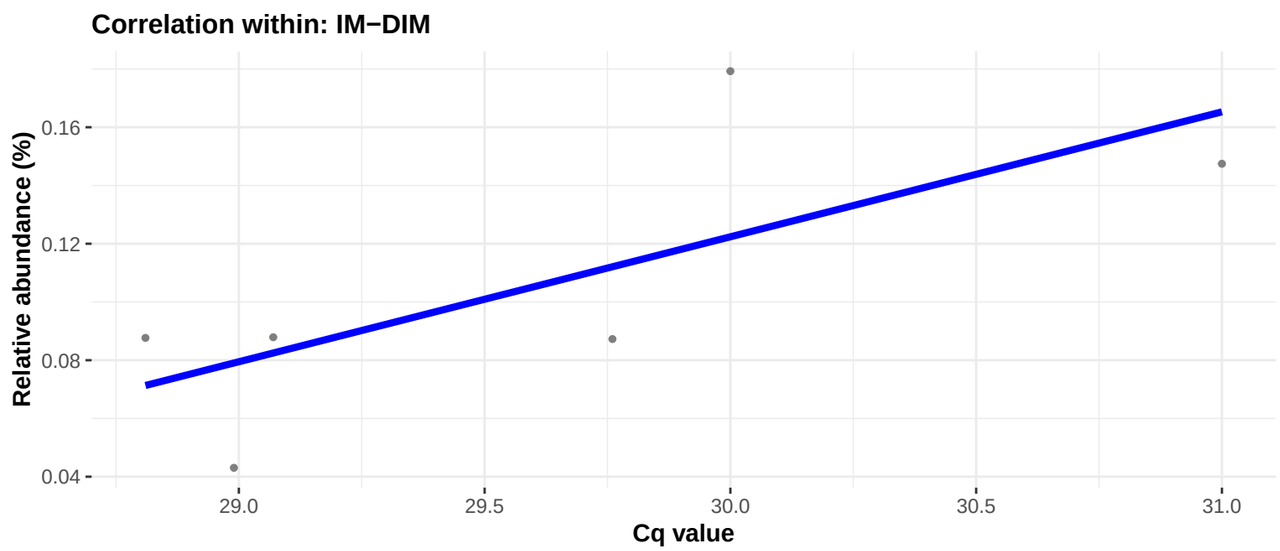
Correlation within: REF−PIM



Correlation within: IM−PIM



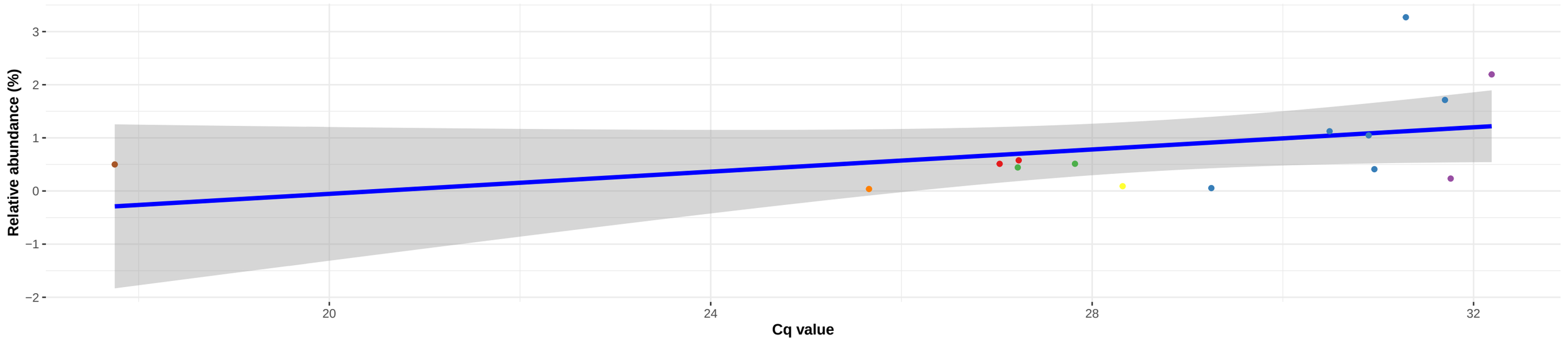
Correlation within: IM−DIM



k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus; s__Lactobacillus sp. LA−6

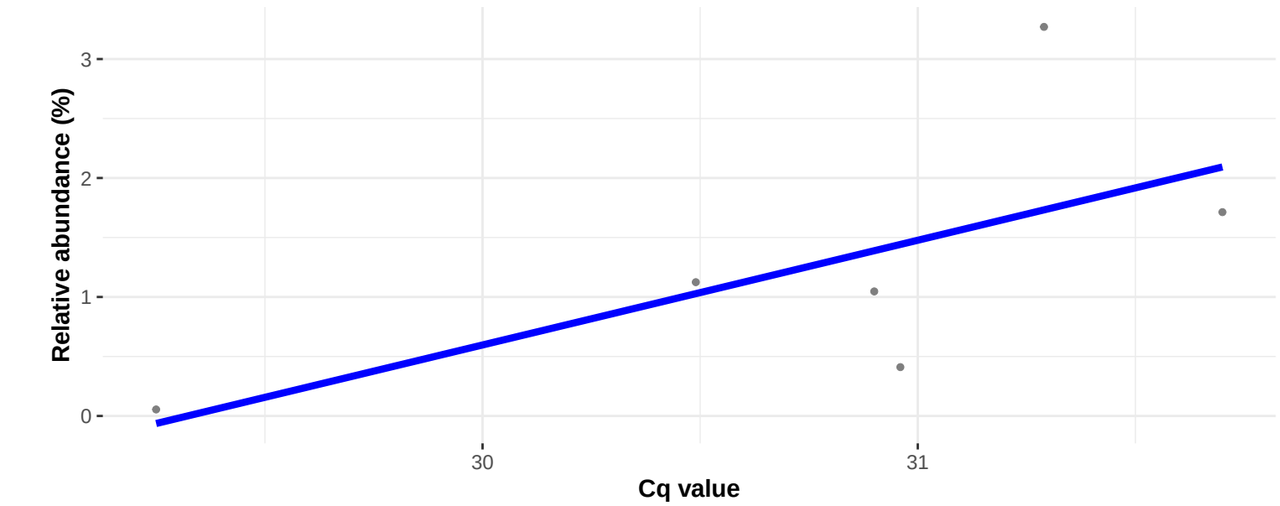
Correlation with all samples

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

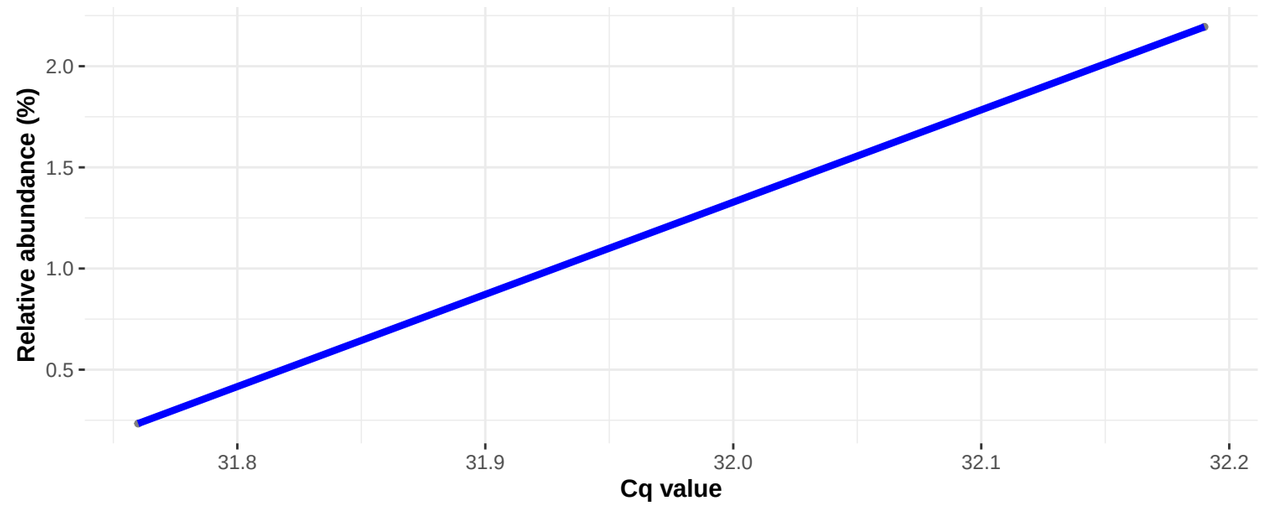


SampleType REF−PID REF−PIM REF−DID REF−DIM IM−PID IM−PIM Feed

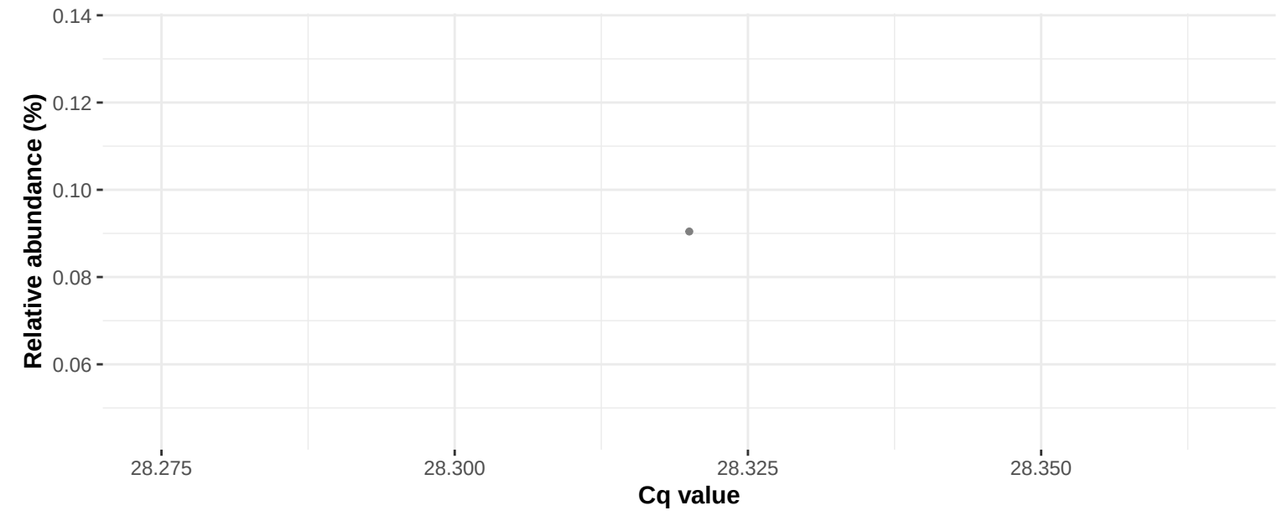
Correlation within: REF−PIM



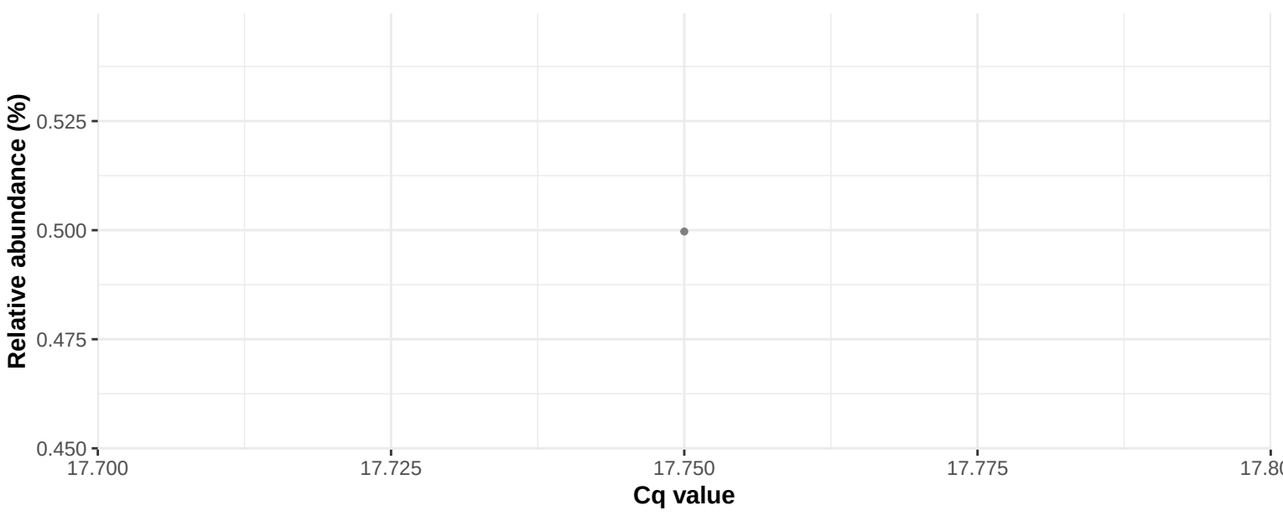
Correlation within: REF−DIM



Correlation within: IM−PIM

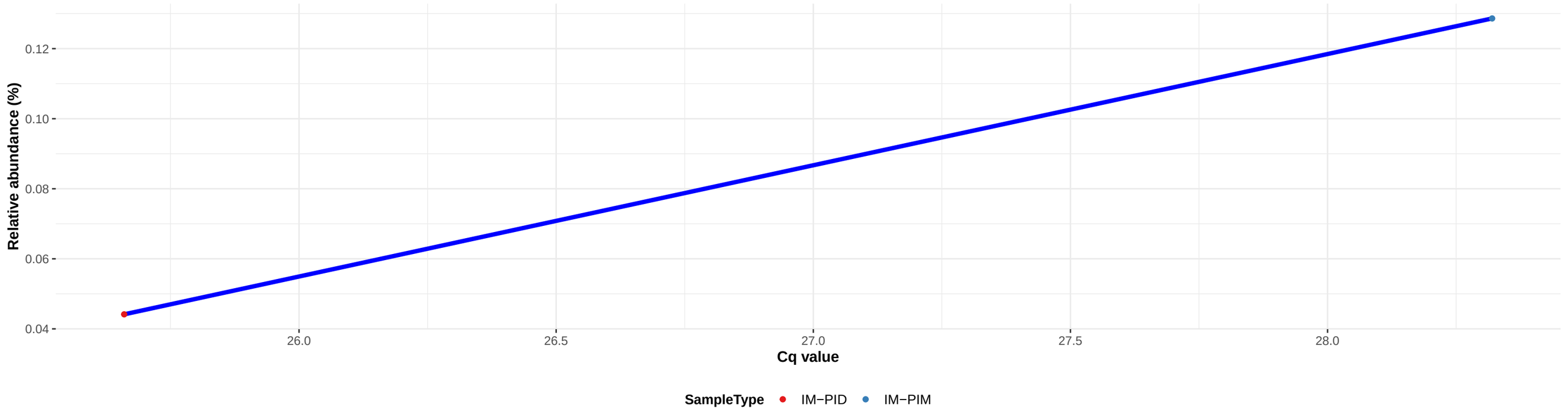


Correlation within: Feed

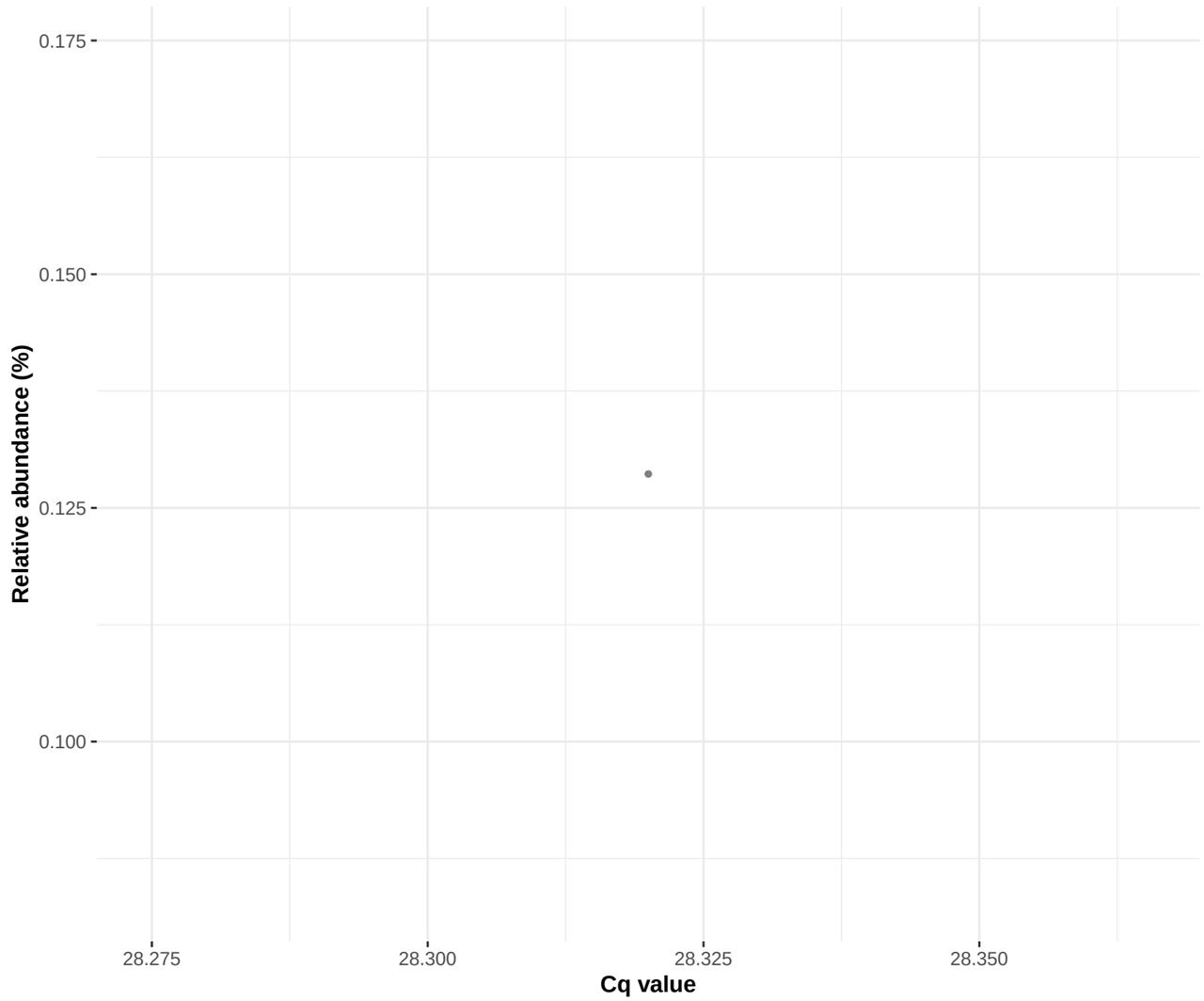


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; Ambiguous_taxa

Correlation with all samples

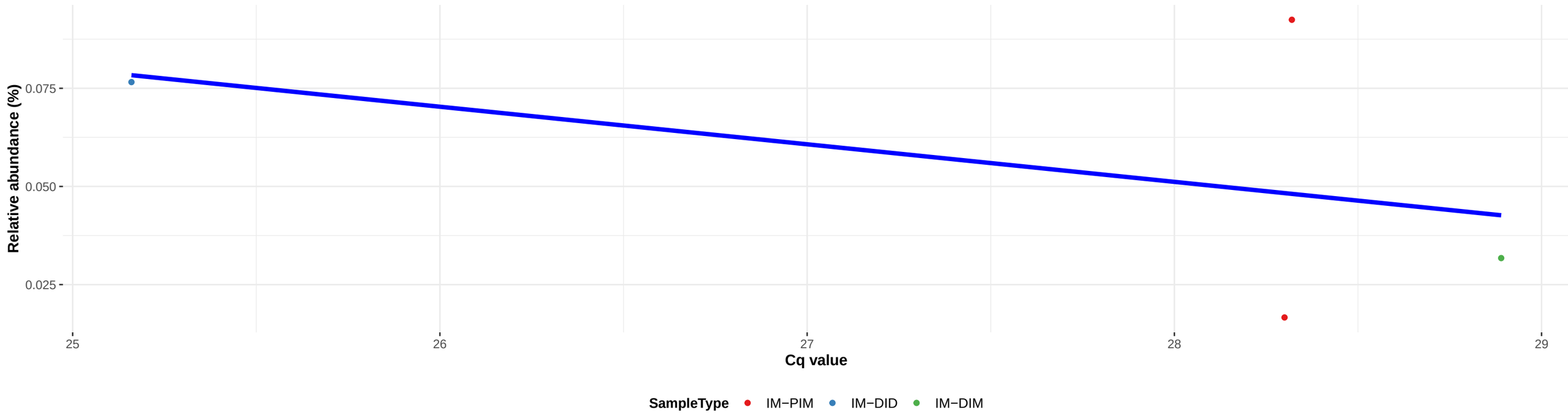


Correlation within: IM−PIM

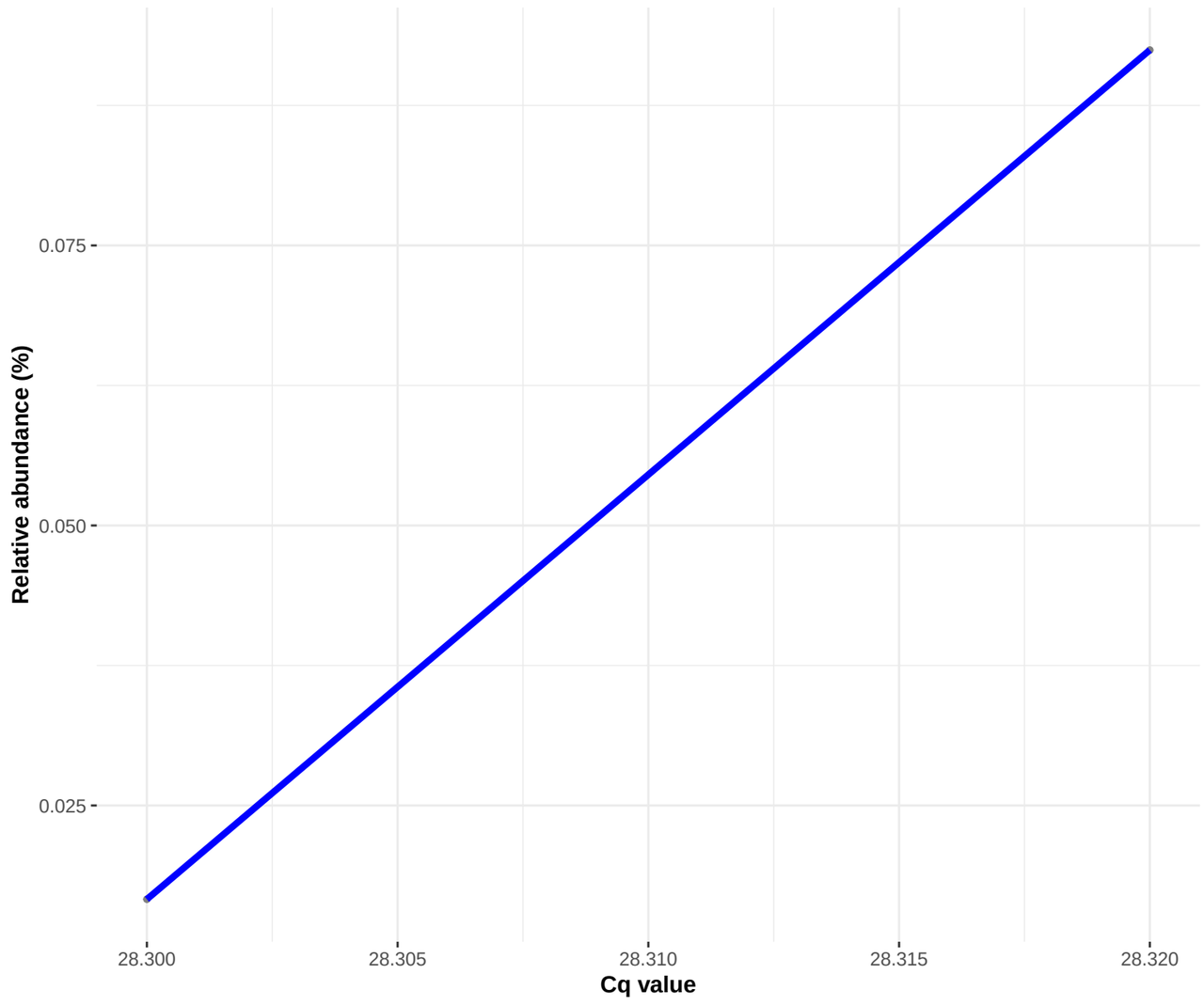


k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; NA

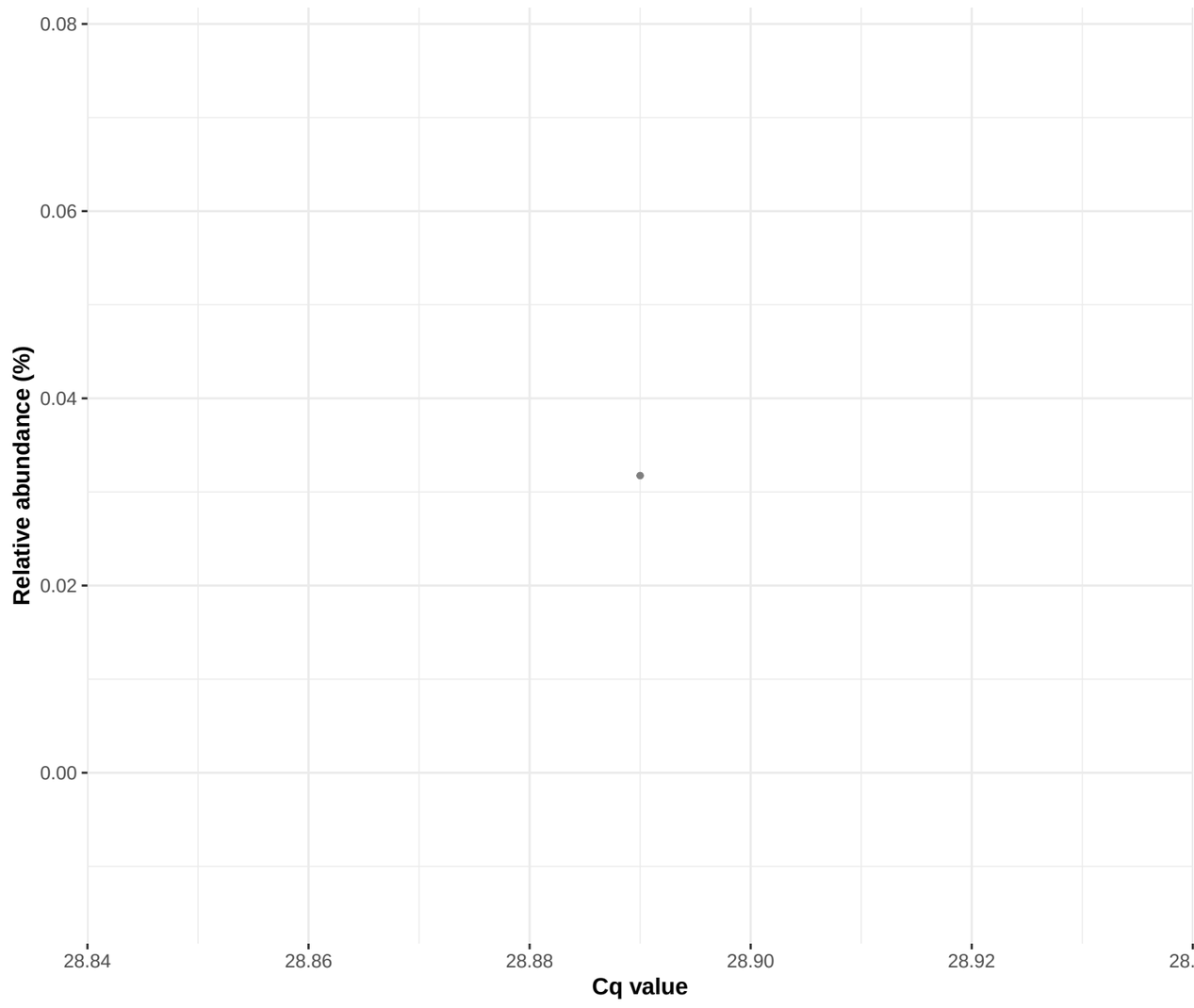
Correlation with all samples



Correlation within: IM−PIM



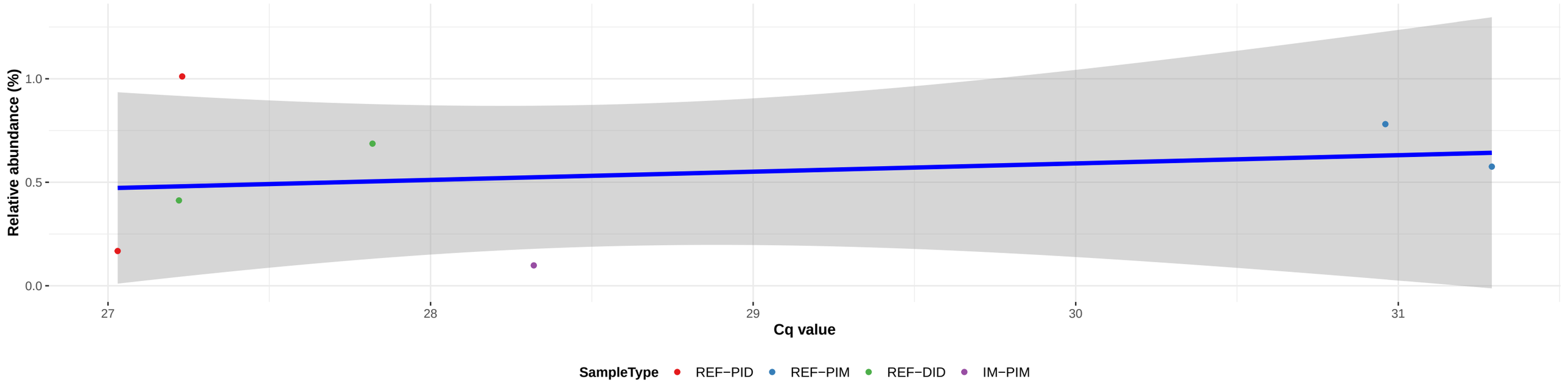
Correlation within: IM−DIM



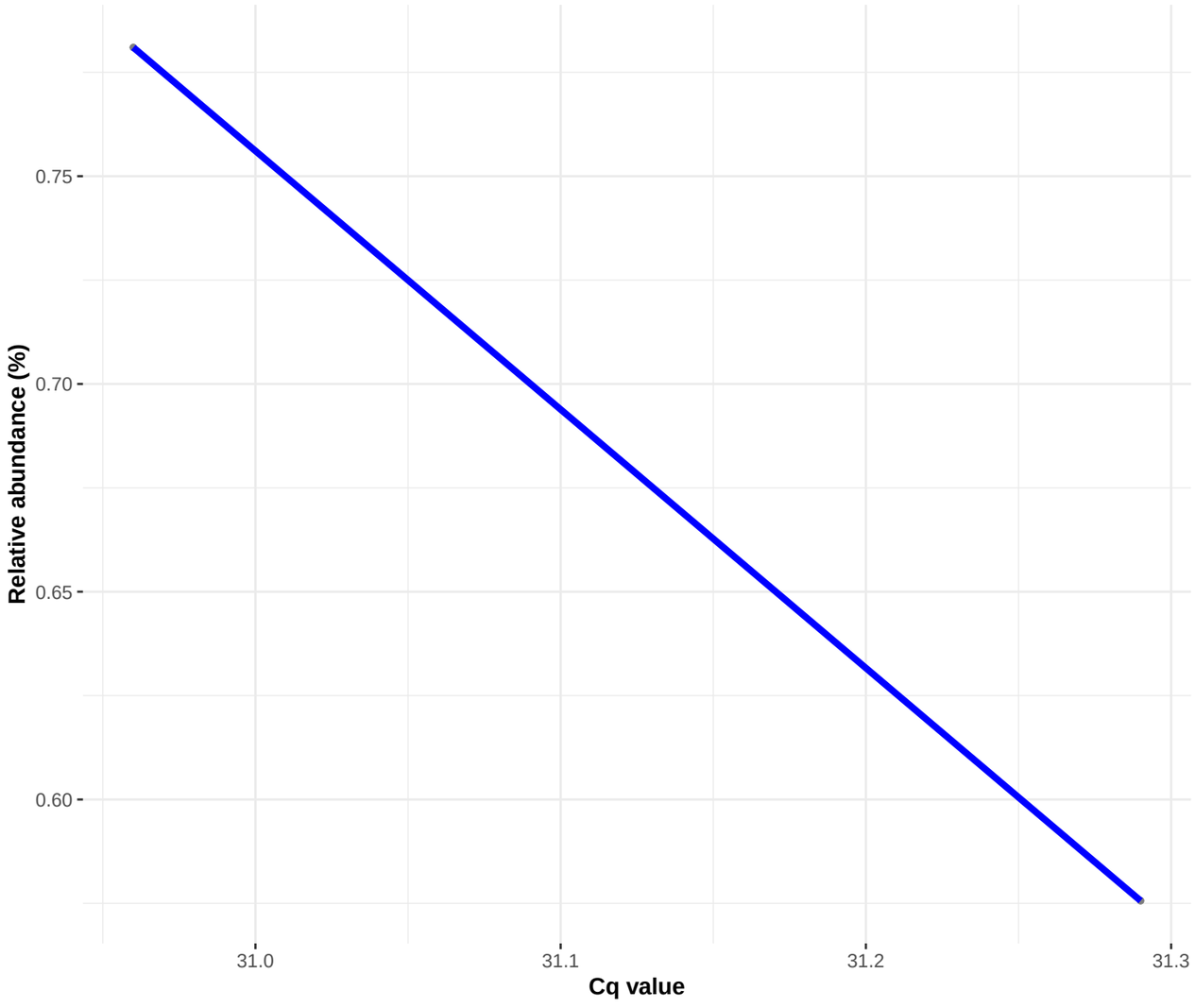
k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; NA

Correlation with all samples

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



Correlation within: REF−PIM



Correlation within: IM−PIM