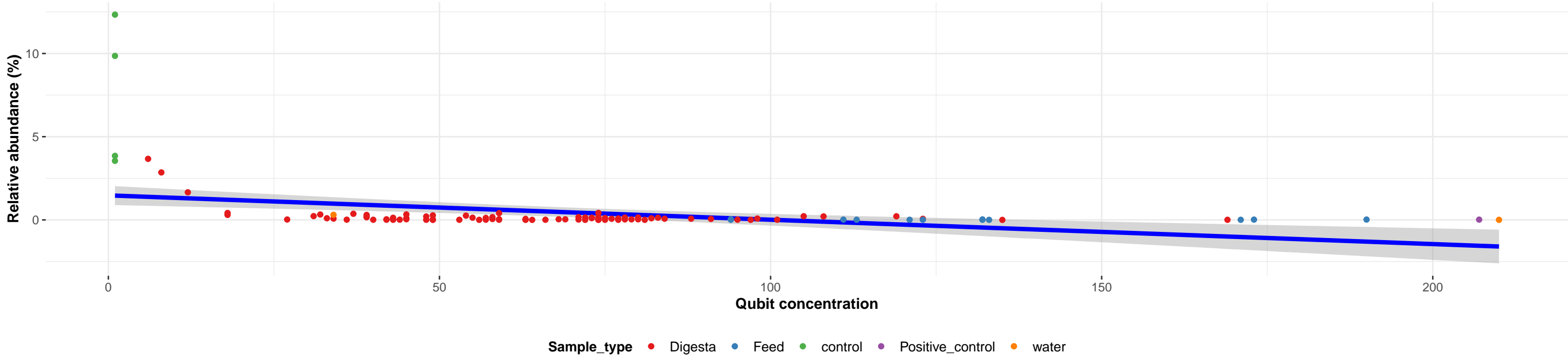


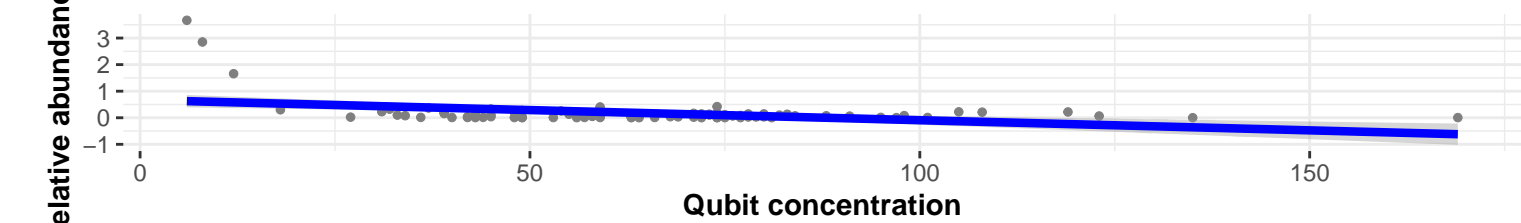
Correlation with all samples

$\log_e(S) = 12.635$, $p = 4.66\text{e-}07$, $\hat{\rho}_{\text{Spearman}} = -0.463$, $\text{CI}_{95\%} [-0.603, -0.295]$, $n_{\text{pairs}} = 108$



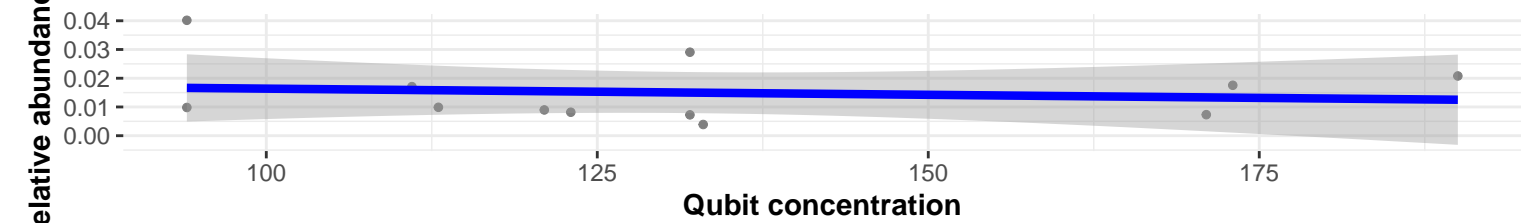
Correlation within: Digesta

$\log_e(S) = 11.912$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.269$, $\text{CI}_{95\%} [-0.457, -0.058]$, $n_{\text{pairs}} = 89$

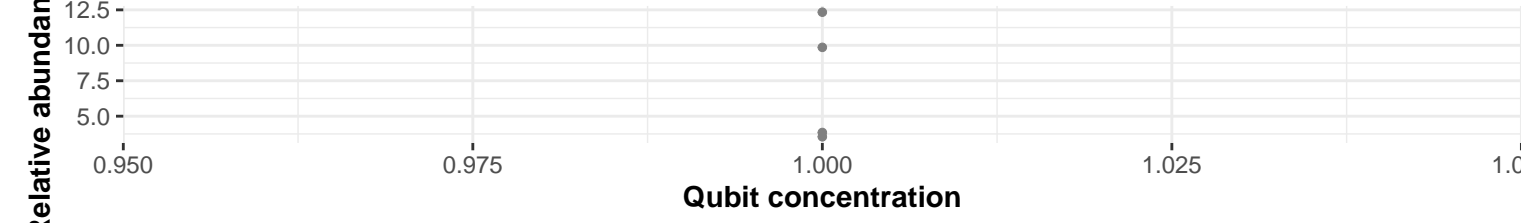


Correlation within: Feed

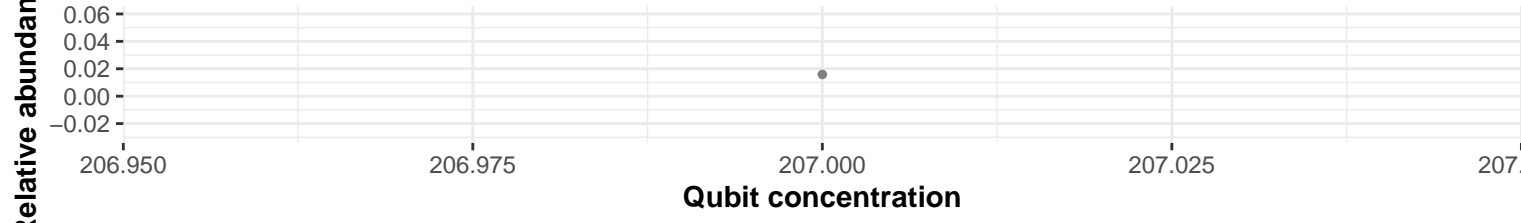
$\log_e(S) = 5.809$, $p = 0.609$, $\hat{\rho}_{\text{Spearman}} = -0.165$, $\text{CI}_{95\%} [-0.685, 0.467]$, $n_{\text{pairs}} = 12$



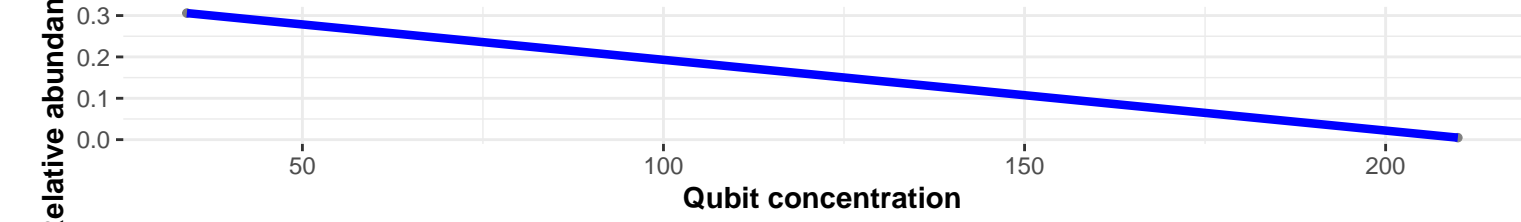
Correlation within: control



Correlation within: Positive_control



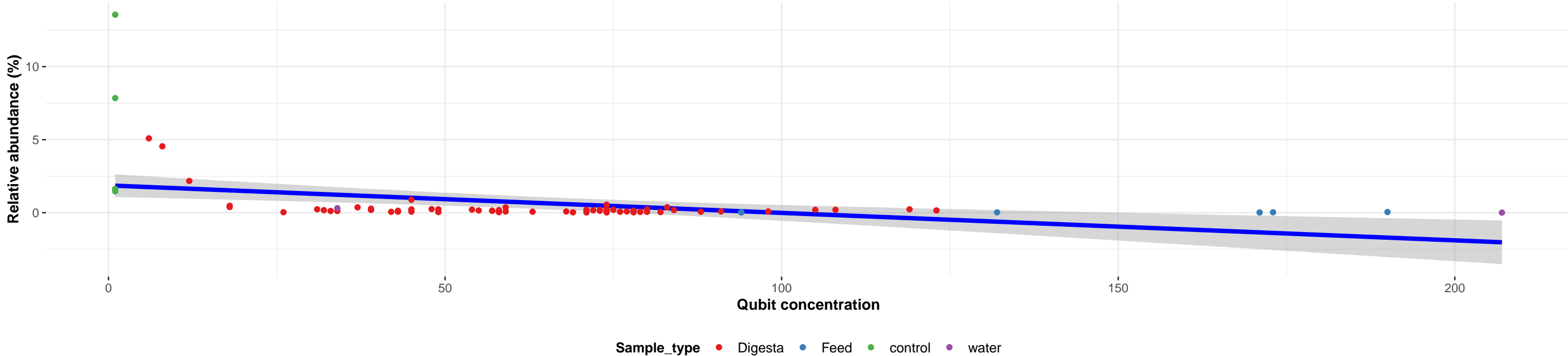
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

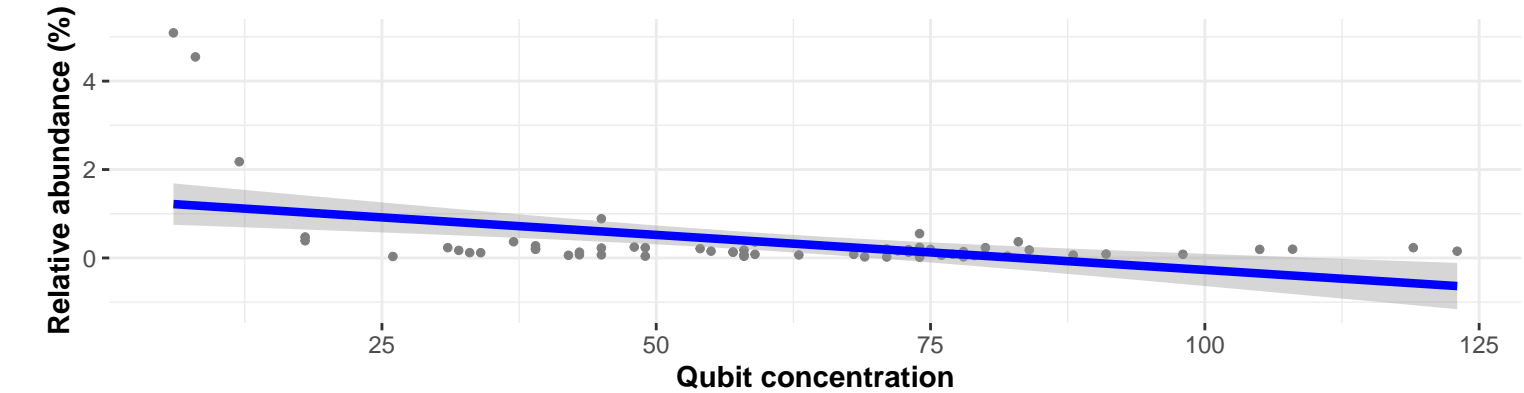
Correlation with all samples

$\log_e(S) = 11.561$, $p = 3.08e-07$, $\hat{\rho}_{\text{Spearman}} = -0.554$, $CI_{95\%} [-0.698, -0.367]$, $n_{\text{pairs}} = 74$



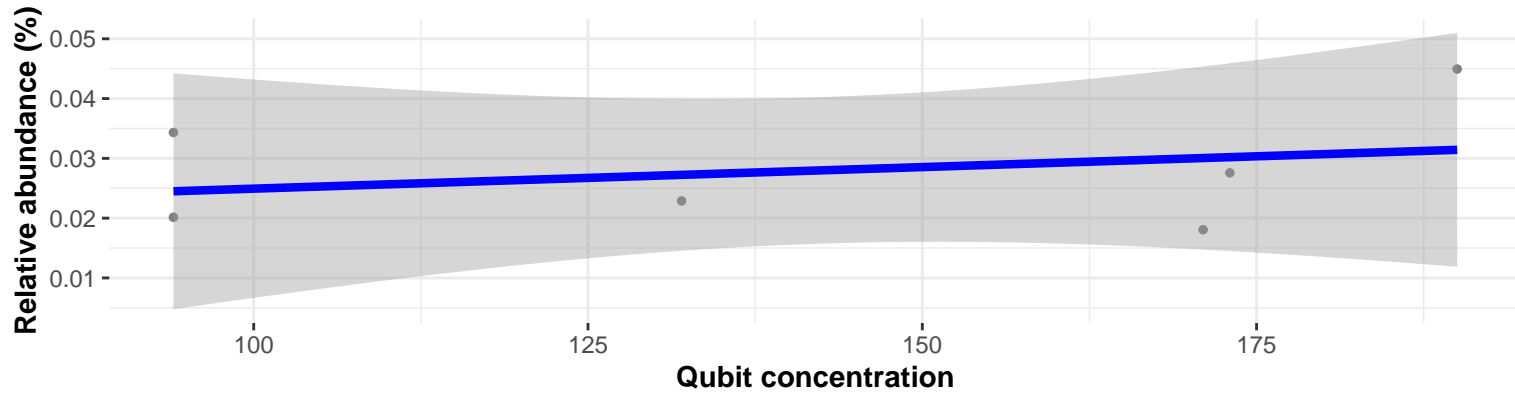
Correlation within: Digesta

$\log_e(S) = 10.857$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = -0.307$, $CI_{95\%} [-0.522, -0.054]$, $n_{\text{pairs}} = 62$

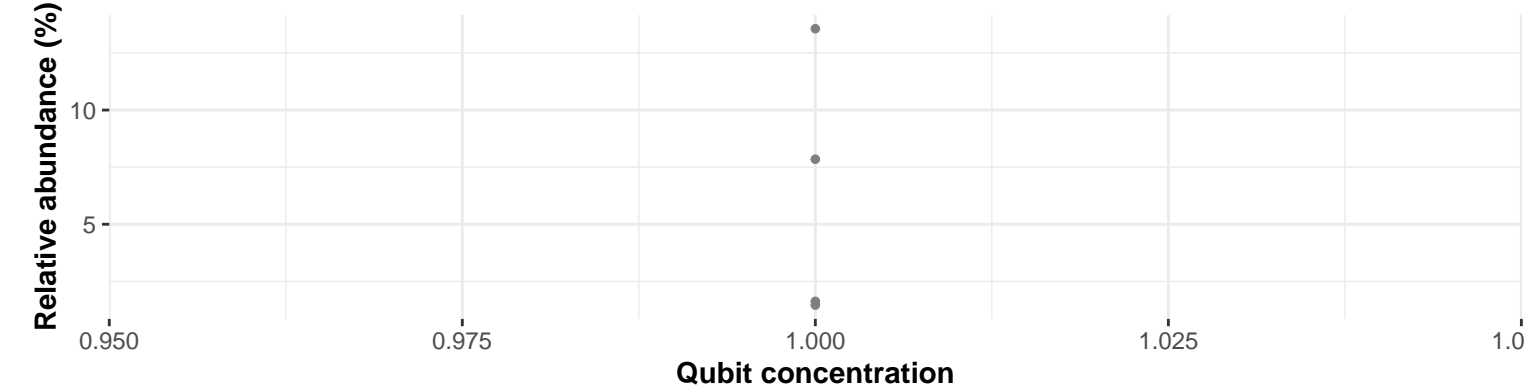


Correlation within: Feed

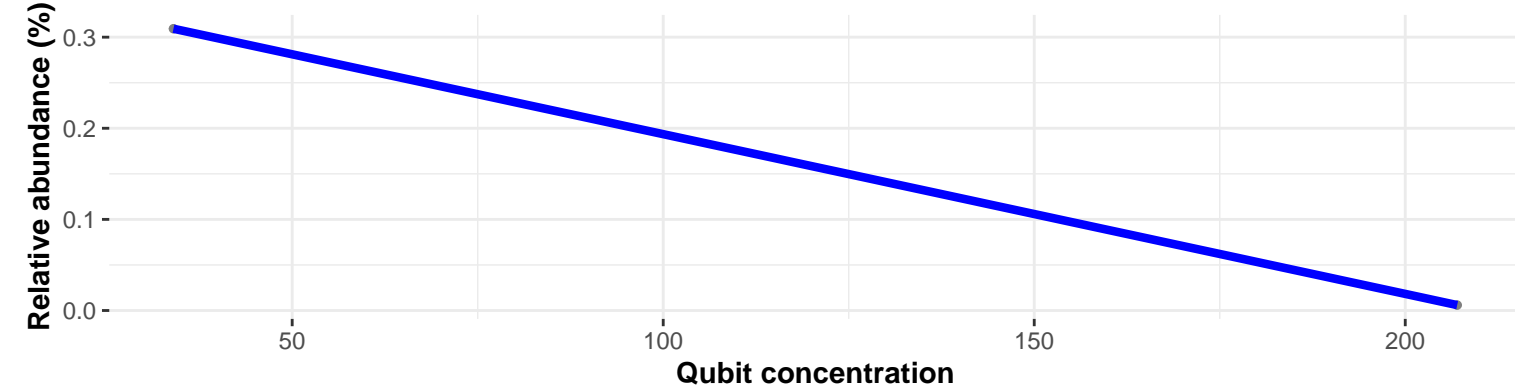
$\log_e(S) = 3.128$, $p = 0.499$, $\hat{\rho}_{\text{Spearman}} = 0.348$, $CI_{95\%} [-0.665, 0.910]$, $n_{\text{pairs}} = 6$



Correlation within: control



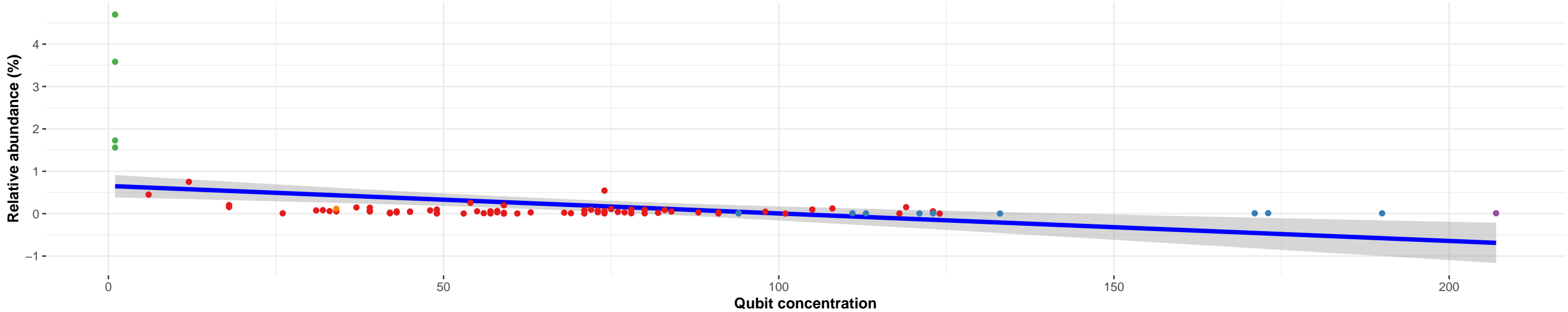
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; NA

Correlation with all samples

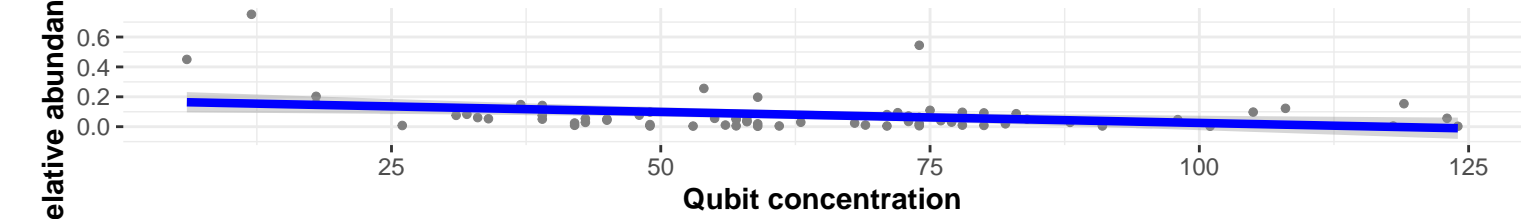
$\log_e(S) = 11.965$, $p = 2.56e-06$, $\hat{\rho}_{\text{Spearman}} = -0.482$, $CI_{95\%} [-0.634, -0.296]$, $n_{\text{pairs}} = 86$



Sample_type ● Digesta ● Feed ● control ● Positive_control ● water

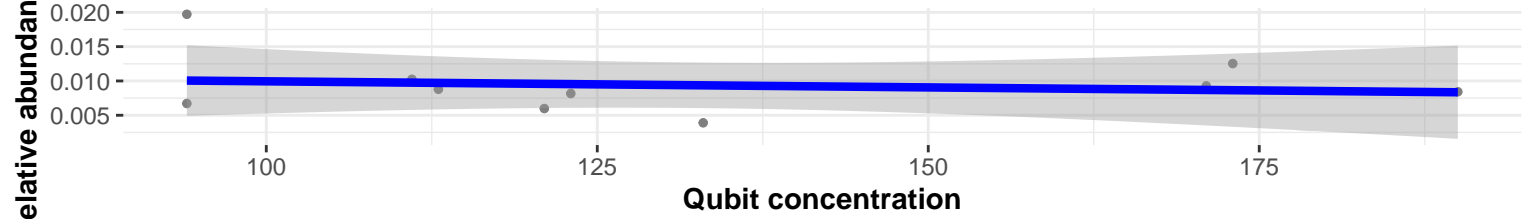
Correlation within: Digesta

$\log_e(S) = 11.165$, $p = 0.049$, $\hat{\rho}_{\text{Spearman}} = -0.236$, $CI_{95\%} [-0.452, 0.006]$, $n_{\text{pairs}} = 70$

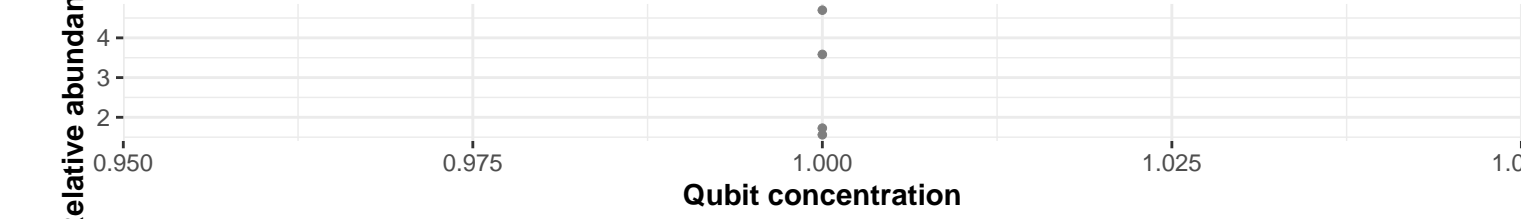


Correlation within: Feed

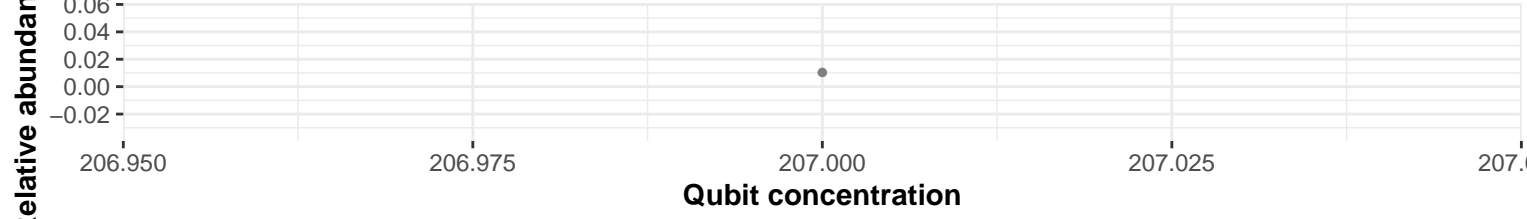
$\log_e(S) = 5.188$, $p = 0.815$, $\hat{\rho}_{\text{Spearman}} = -0.085$, $CI_{95\%} [-0.690, 0.590]$, $n_{\text{pairs}} = 10$



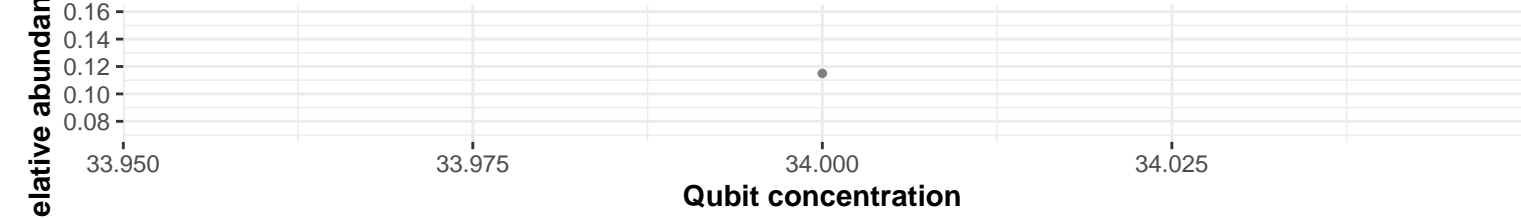
Correlation within: control



Correlation within: Positive_control



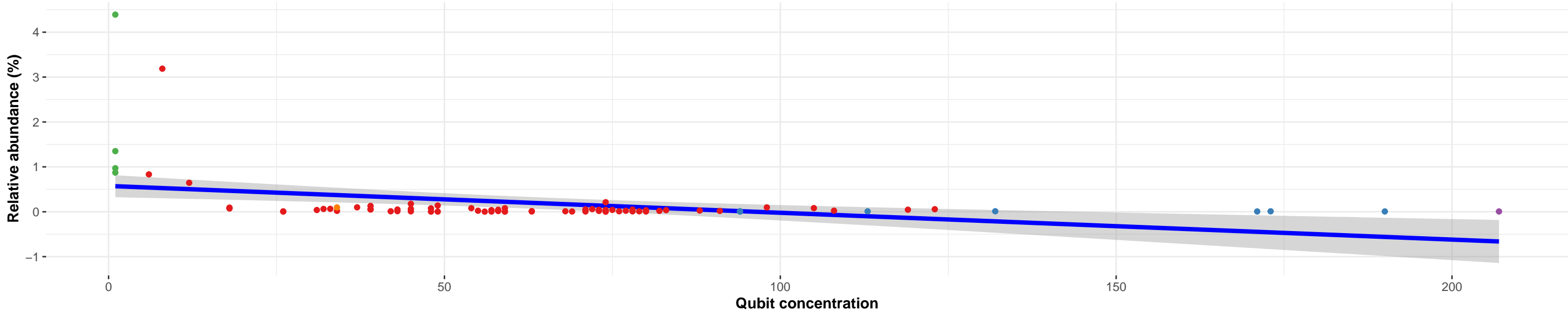
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; NA

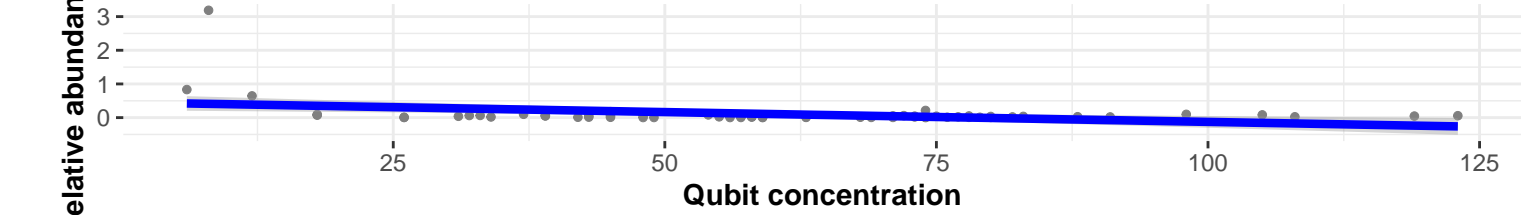
Correlation with all samples

$\log_e(S) = 11.752$, $p = 5.2e-05$, $\hat{\rho}_{\text{Spearman}} = -0.434$, $CI_{95\%} [-0.600, -0.232]$, $n_{\text{pairs}} = 81$



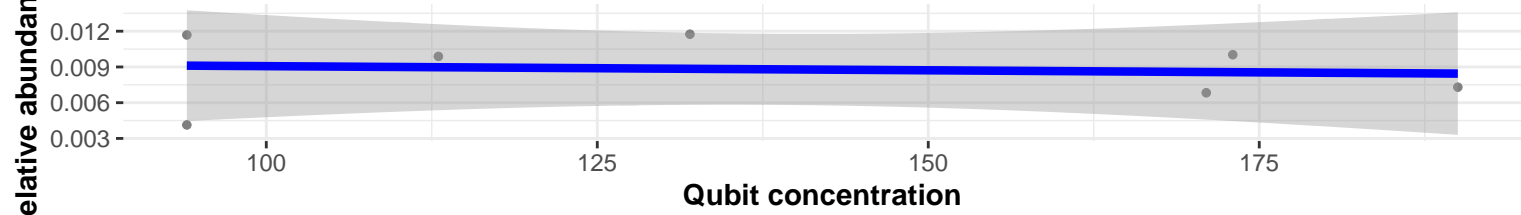
Correlation within: Digesta

$\log_e(S) = 11.072$, $p = 0.062$, $\hat{\rho}_{\text{Spearman}} = -0.228$, $CI_{95\%} [-0.448, 0.018]$, $n_{\text{pairs}} = 68$

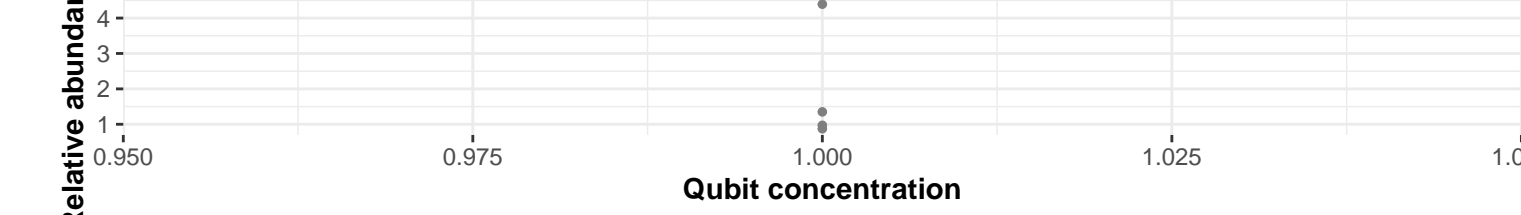


Correlation within: Feed

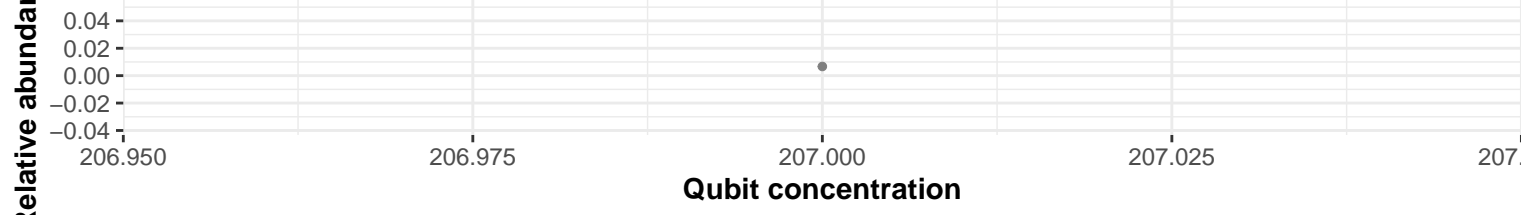
$\log_e(S) = 4.043$, $p = 0.969$, $\hat{\rho}_{\text{Spearman}} = -0.018$, $CI_{95\%} [-0.773, 0.758]$, $n_{\text{pairs}} = 7$



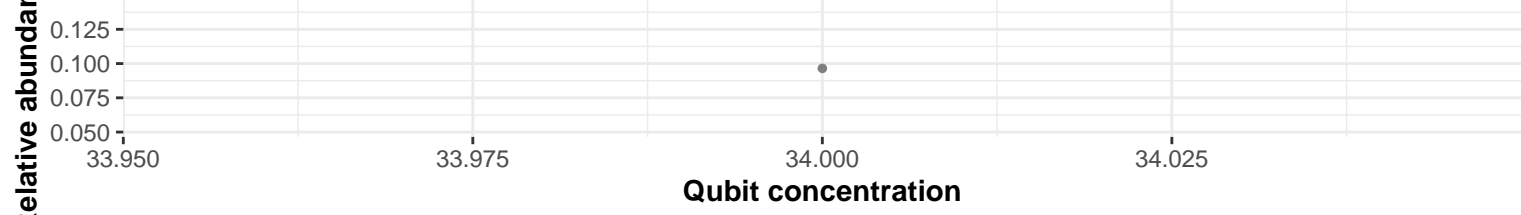
Correlation within: control



Correlation within: Positive_control



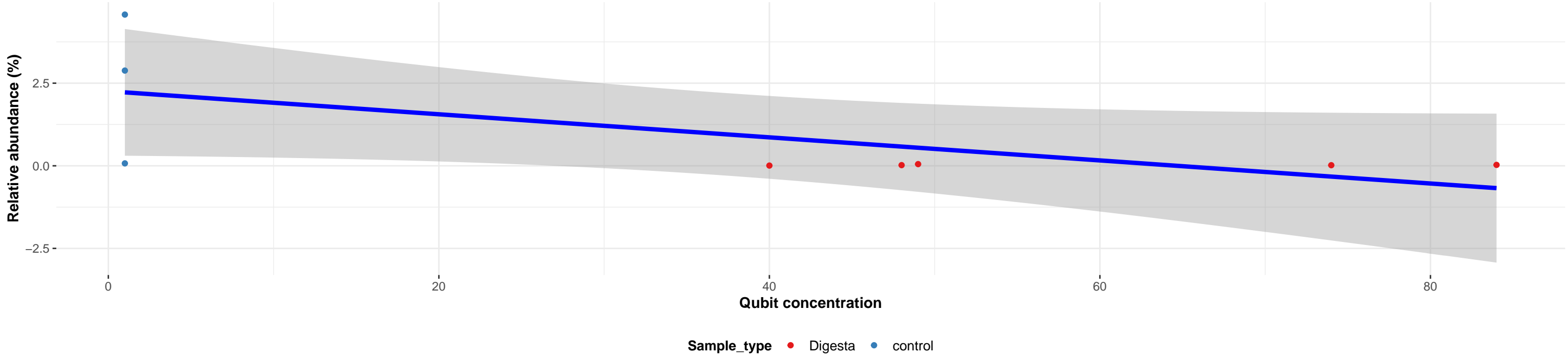
Correlation within: water



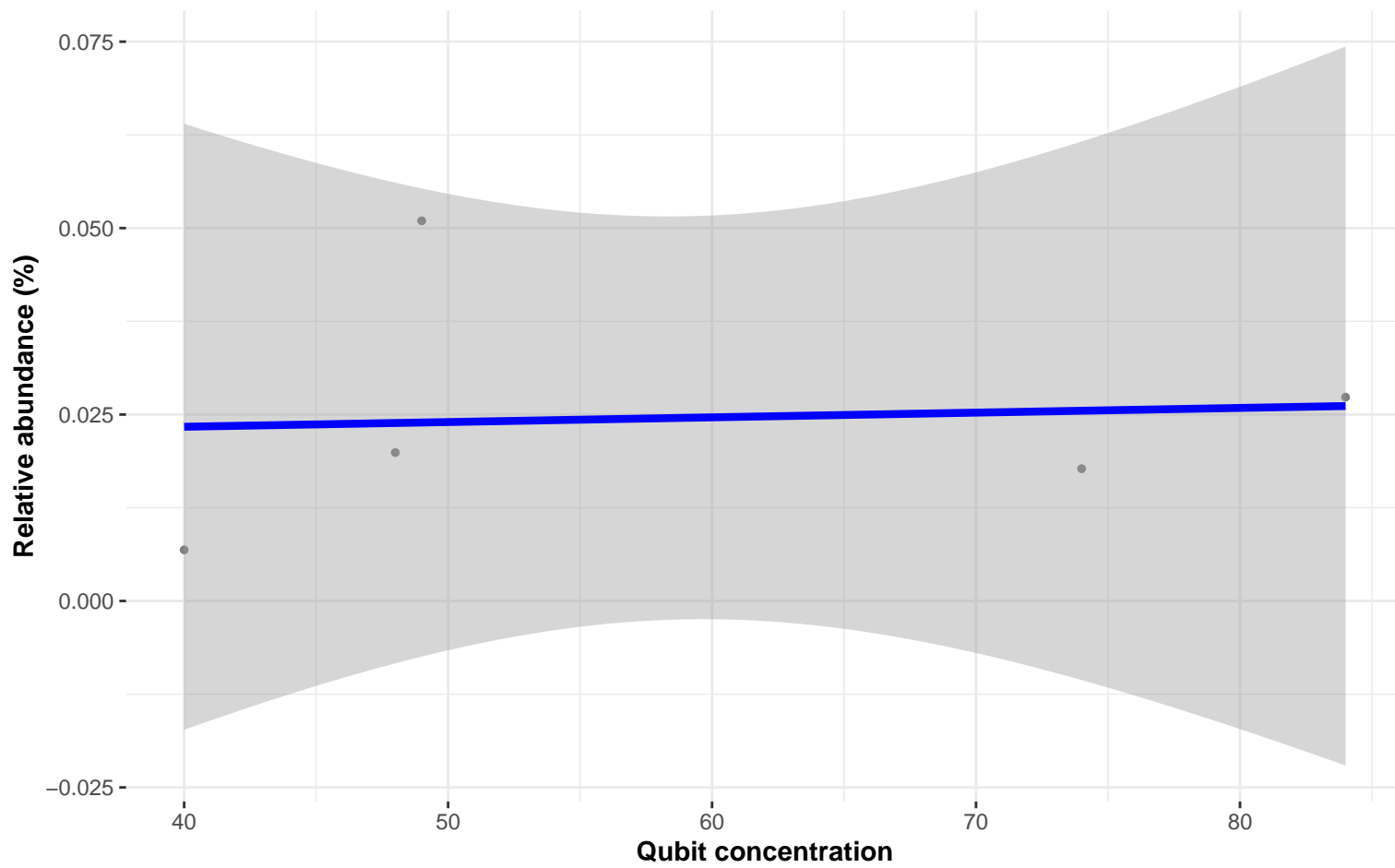
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus; NA

Correlation with all samples

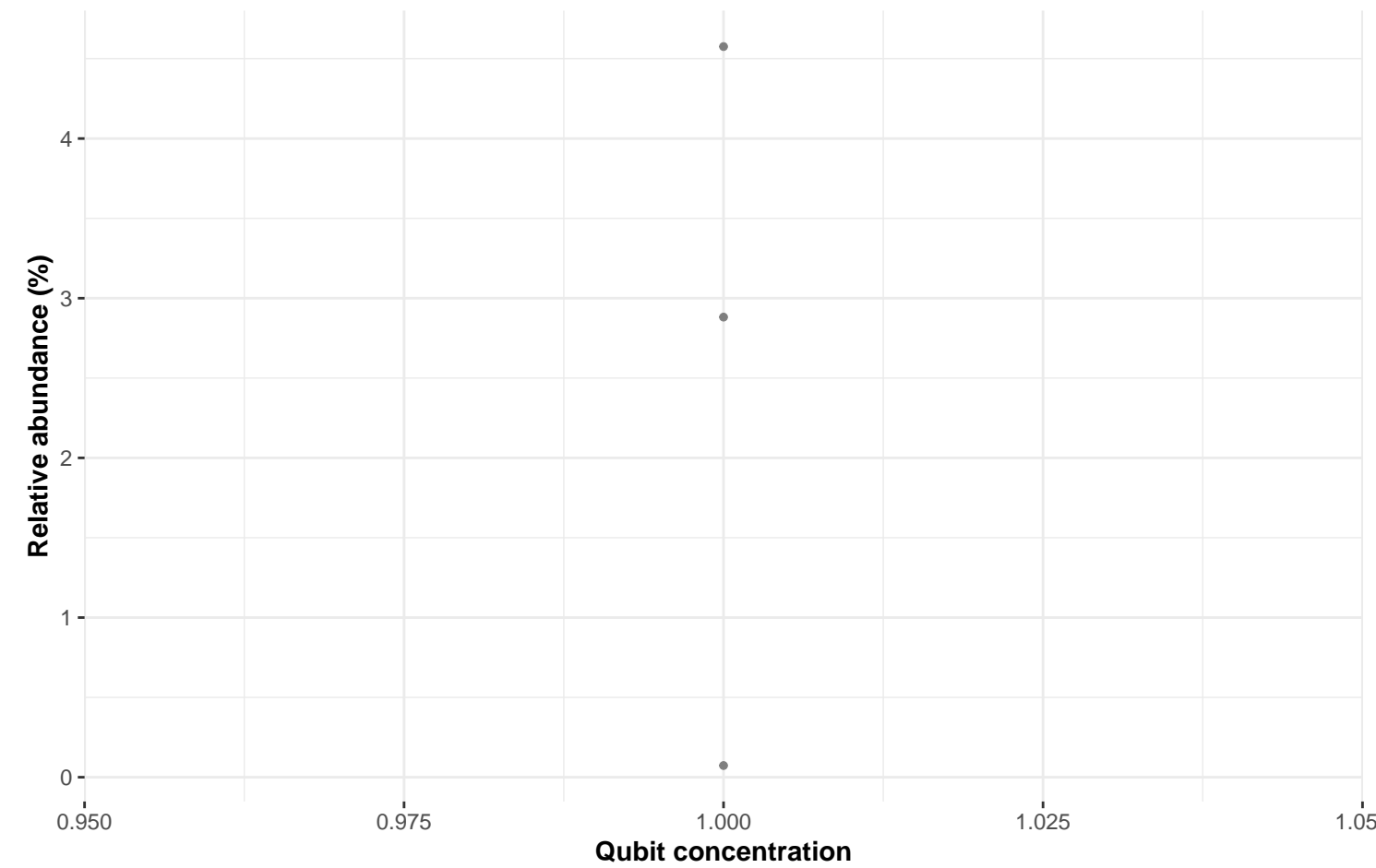
$\log_e(S) = 4.907$, $p = 0.108$, $\hat{\rho}_{\text{Spearman}} = -0.610$, $\text{CI}_{95\%} [-0.923, 0.191]$, $n_{\text{pairs}} = 8$



Correlation within: Digesta



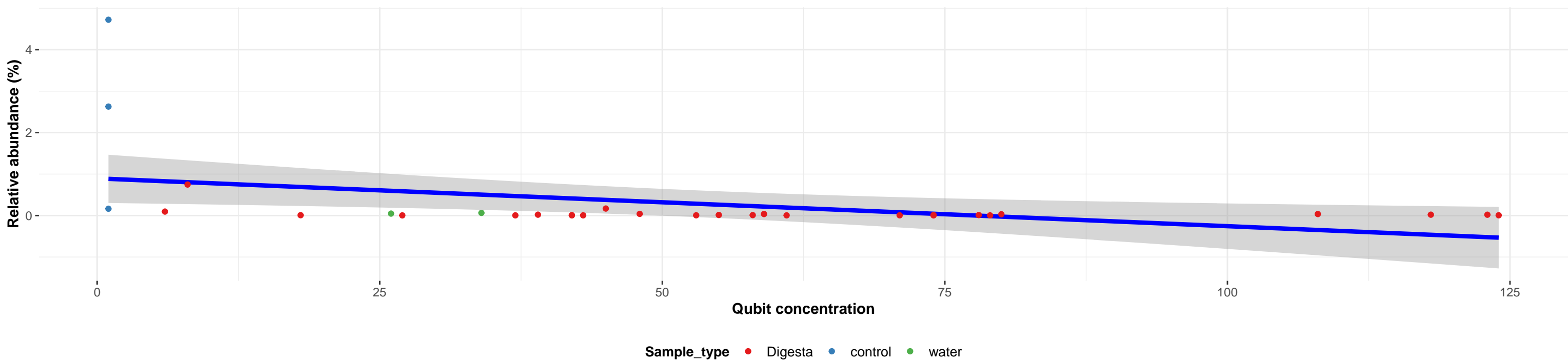
Correlation within: control



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Micrococcaceae; Micrococcus; NA

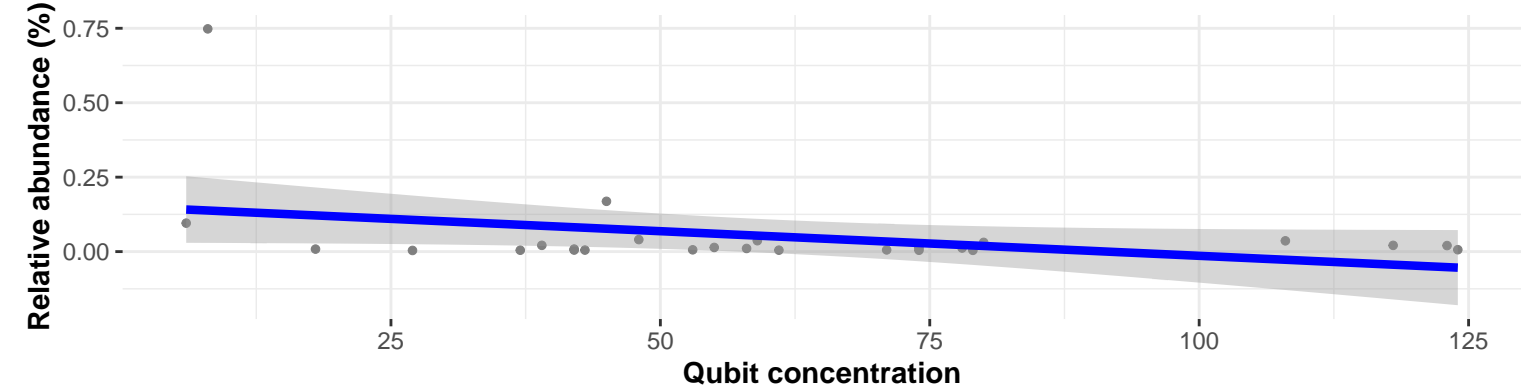
Correlation with all samples

$\log_e(S) = 8.843$, $p = 0.027$, $\hat{\rho}_{\text{Spearman}} = -0.396$, $\text{CI}_{95\%} [-0.664, -0.038]$, $n_{\text{pairs}} = 31$

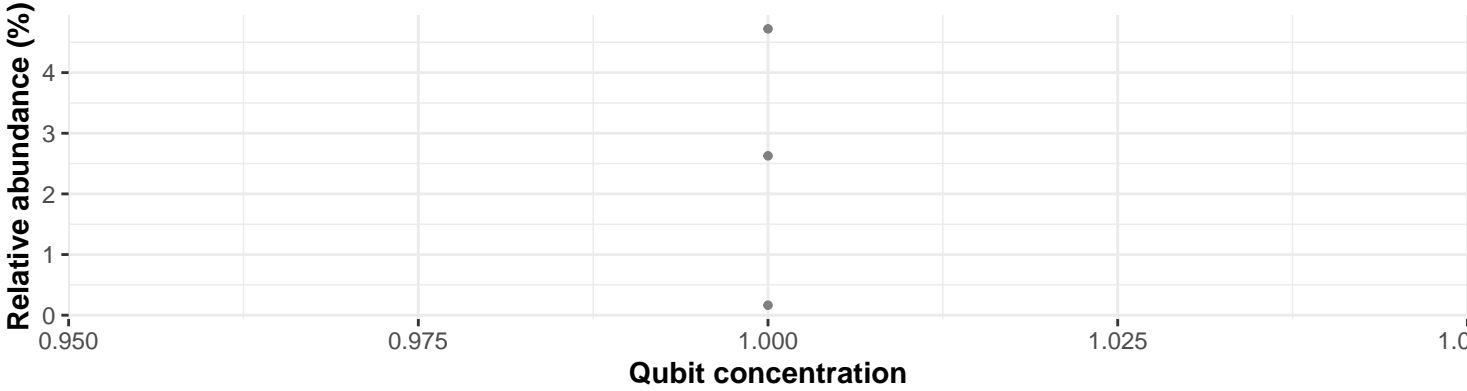


Correlation within: Digesta

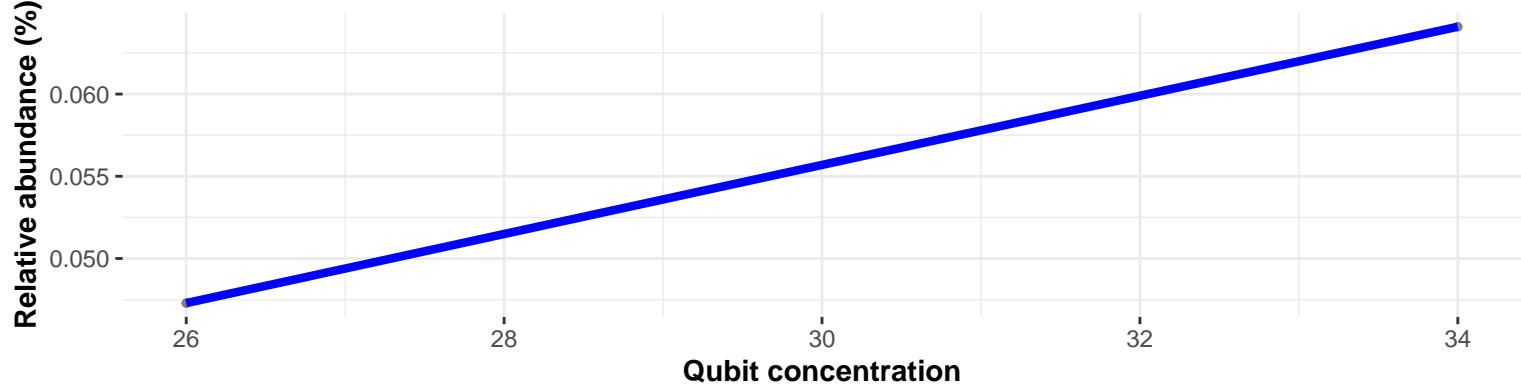
$\log_e(S) = 8.017$, $p = 0.860$, $\hat{\rho}_{\text{Spearman}} = -0.036$, $\text{CI}_{95\%} [-0.428, 0.367]$, $n_{\text{pairs}} = 26$



Correlation within: control



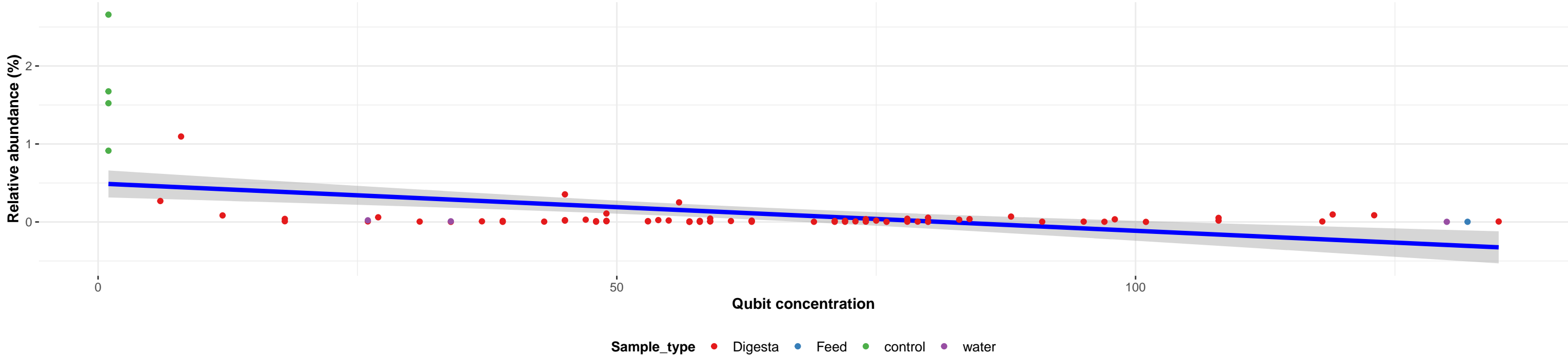
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Propionibacteriales; Propionibacteriaceae; Cutibacterium; NA

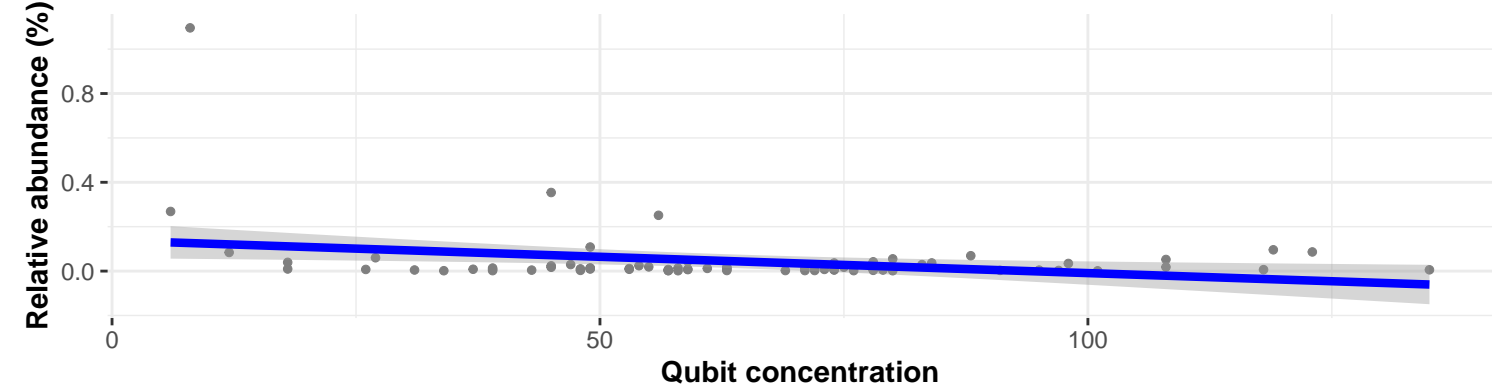
Correlation with all samples

$\log_e(S) = 11.672$, $p = 0.012$, $\hat{\rho}_{\text{Spearman}} = -0.277$, $\text{CI}_{95\%} [-0.471, -0.057]$, $n_{\text{pairs}} = 82$

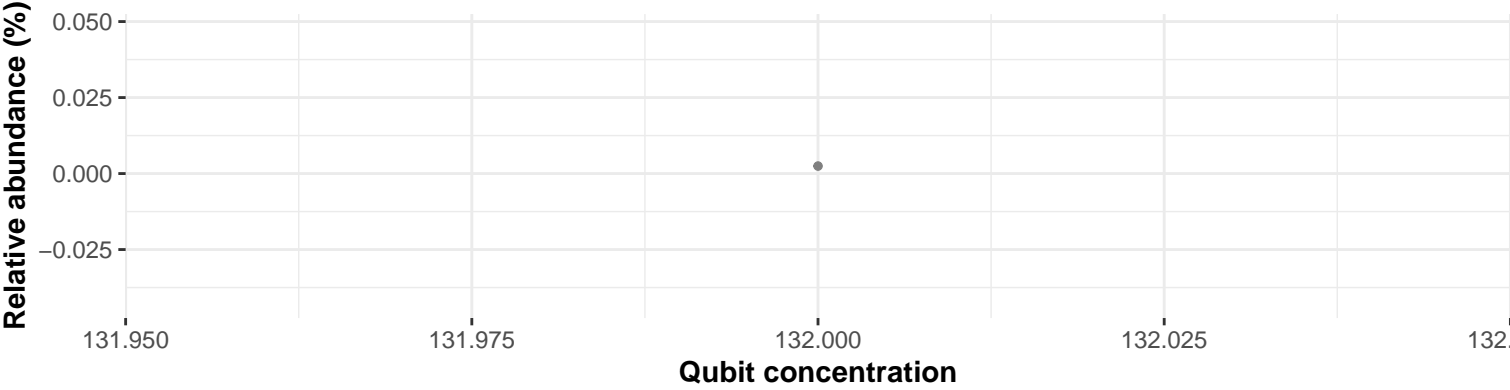


Correlation within: Digesta

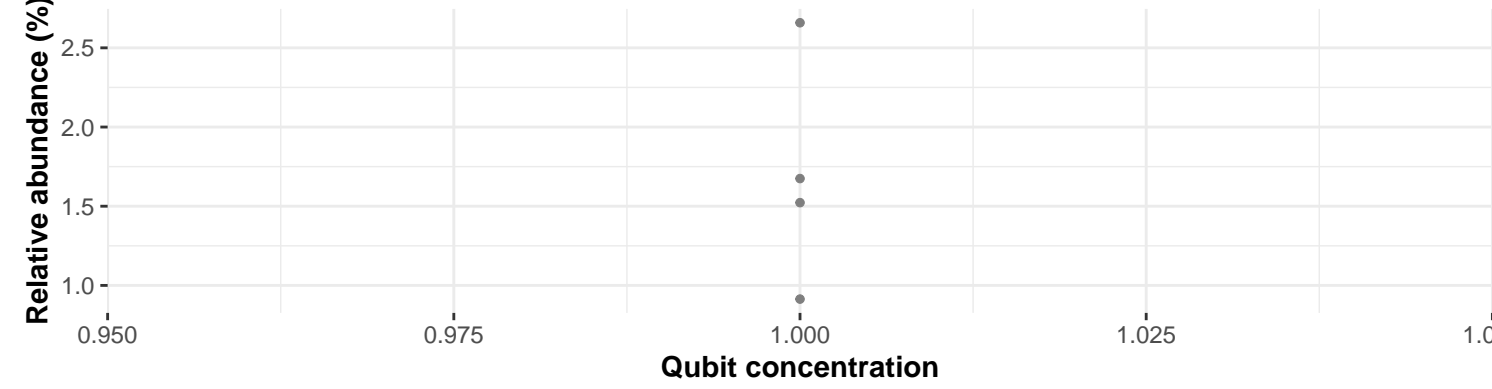
$\log_e(S) = 11.213$, $p = 0.409$, $\hat{\rho}_{\text{Spearman}} = -0.097$, $\text{CI}_{95\%} [-0.325, 0.141]$, $n_{\text{pairs}} = 74$



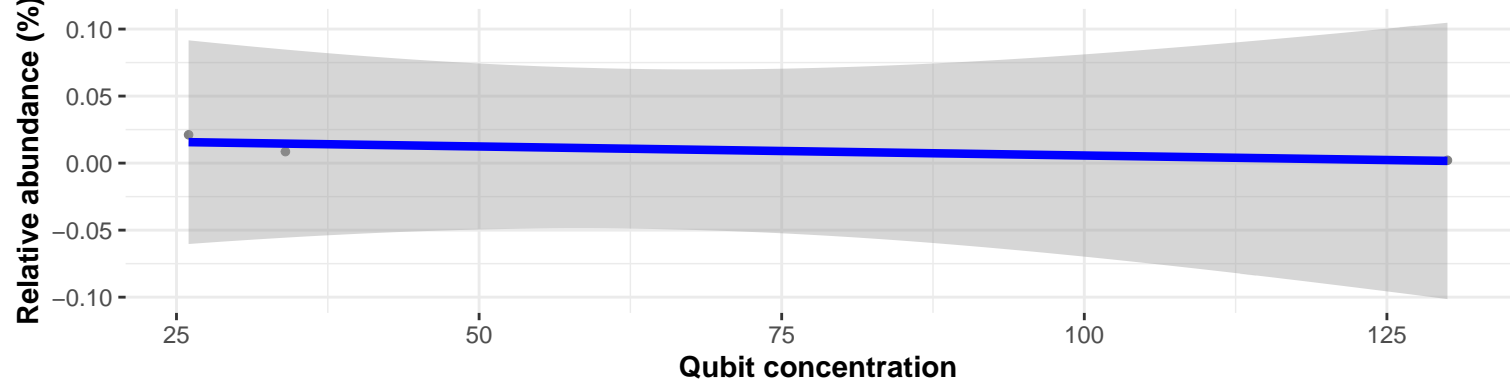
Correlation within: Feed



Correlation within: control



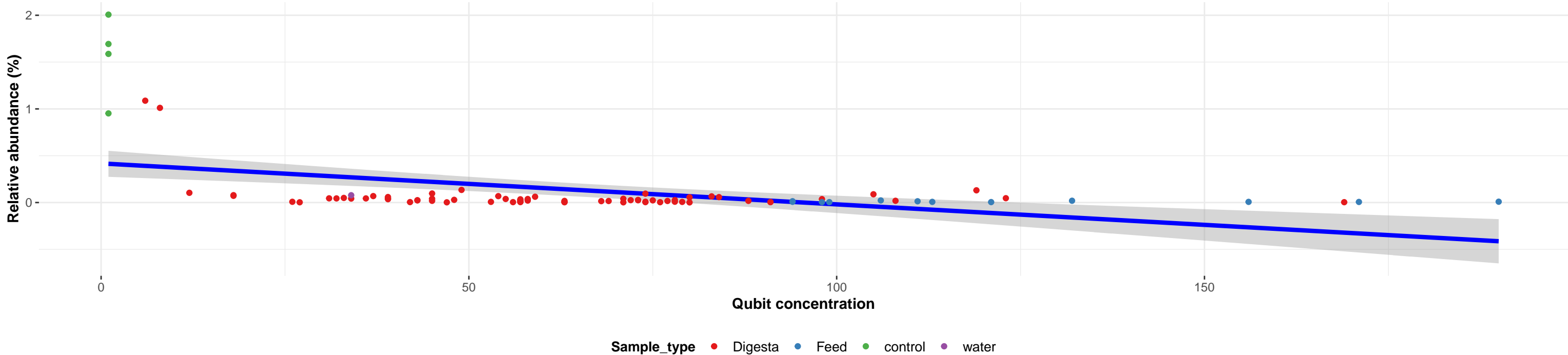
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Oceanobacillus; caeni

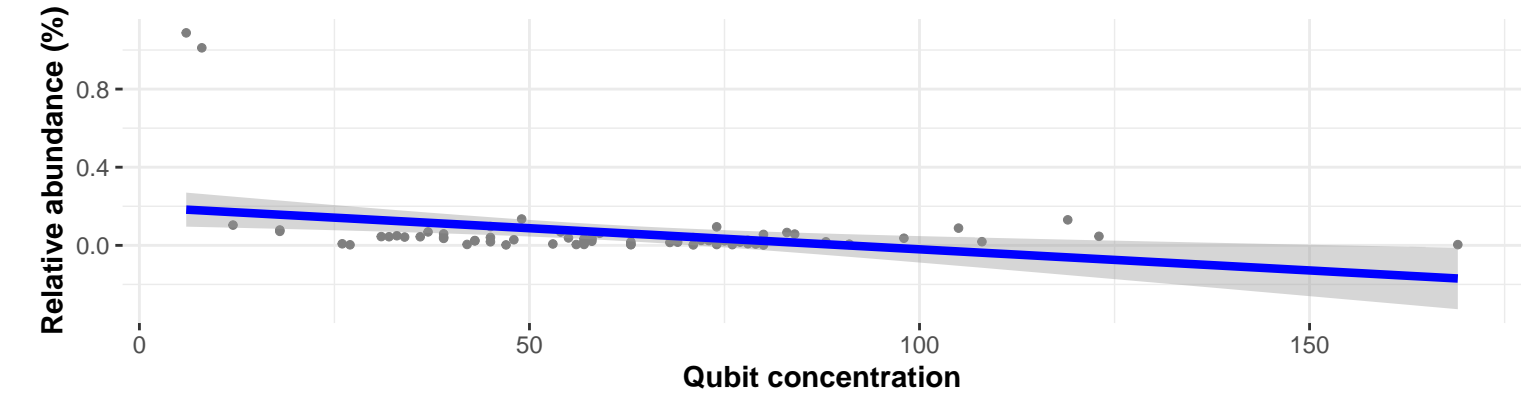
Correlation with all samples

$\log_e(S) = 11.960$, $p = 3.86e-06$, $\hat{\rho}_{\text{Spearman}} = -0.475$, $CI_{95\%} [-0.628, -0.286]$, $n_{\text{pairs}} = 86$



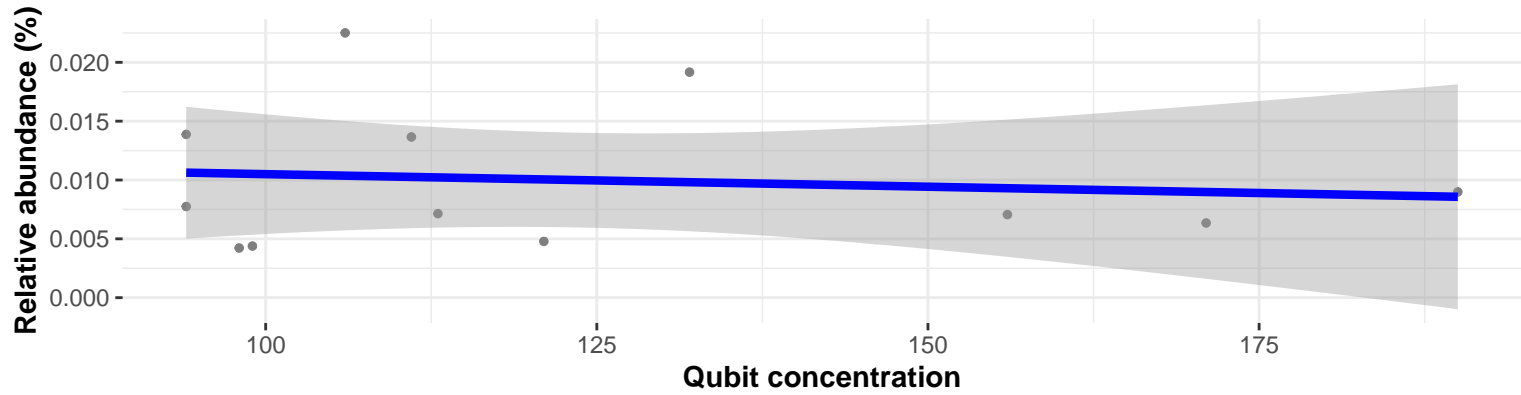
Correlation within: Digesta

$\log_e(S) = 11.166$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = -0.292$, $CI_{95\%} [-0.500, -0.052]$, $n_{\text{pairs}} = 69$

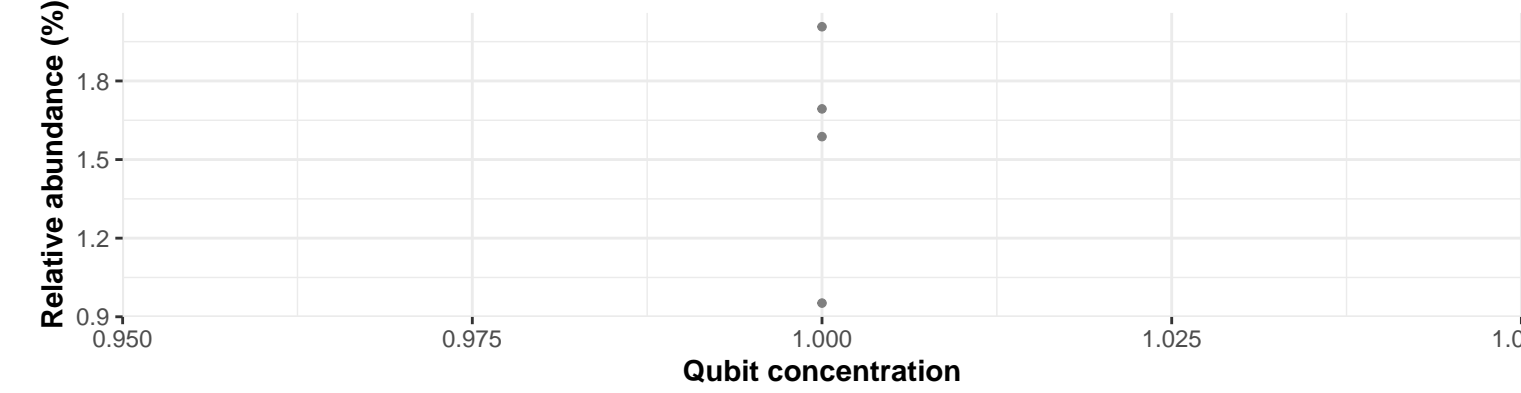


Correlation within: Feed

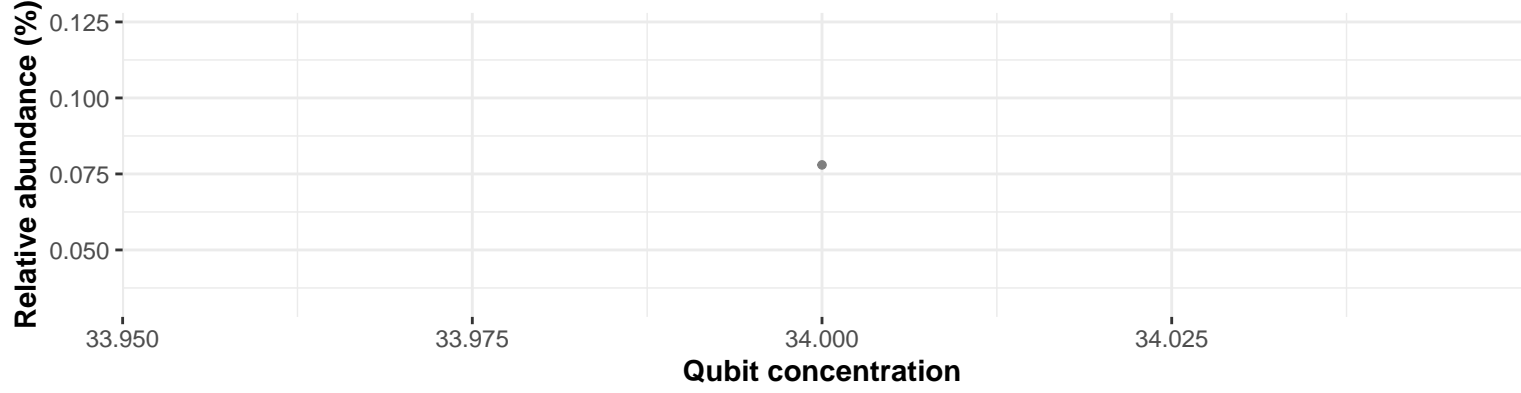
$\log_e(S) = 5.666$, $p = 0.974$, $\hat{\rho}_{\text{Spearman}} = -0.011$, $CI_{95\%} [-0.594, 0.580]$, $n_{\text{pairs}} = 12$



Correlation within: control



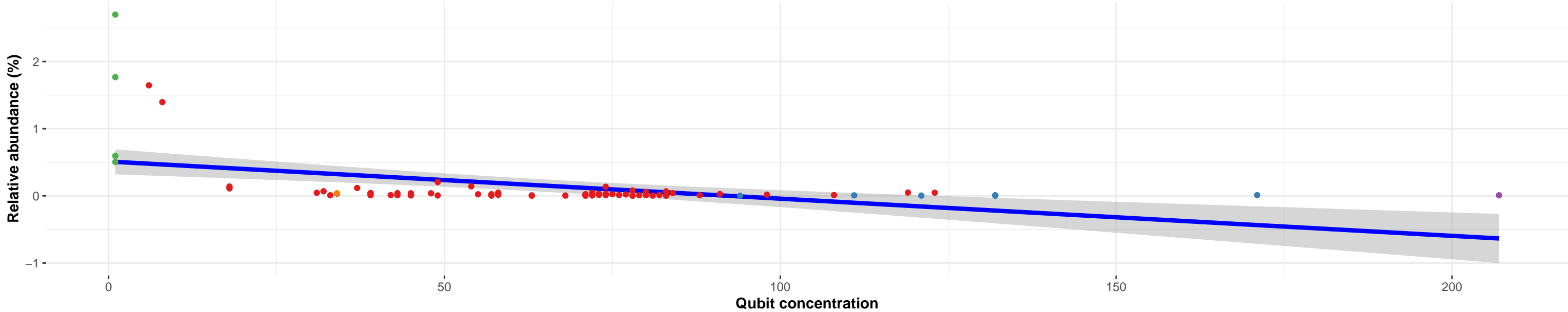
Correlation within: water



Bacteria; Firmicutes; Clostridia; Lachnospirales; Lachnospiraceae; NA; NA

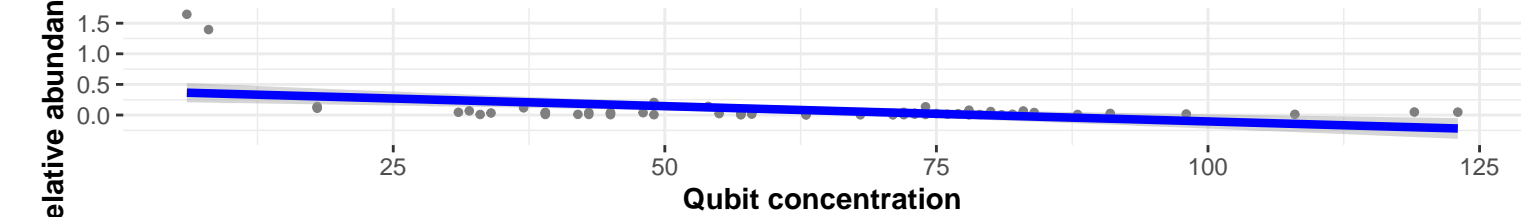
Correlation with all samples

$\log_e(S) = 11.476$, $p = 1.27\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = -0.487$, $\text{CI}_{95\%} [-0.649, -0.283]$, $n_{\text{pairs}} = 73$



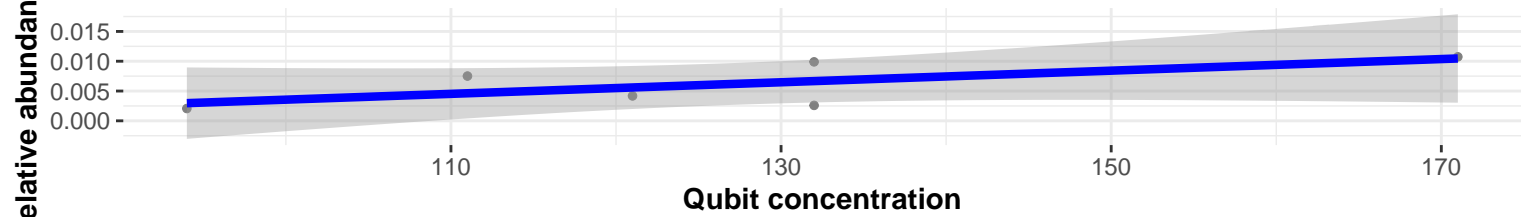
Correlation within: Digesta

$\log_e(S) = 10.782$, $p = 0.034$, $\hat{\rho}_{\text{Spearman}} = -0.272$, $\text{CI}_{95\%} [-0.496, -0.015]$, $n_{\text{pairs}} = 61$

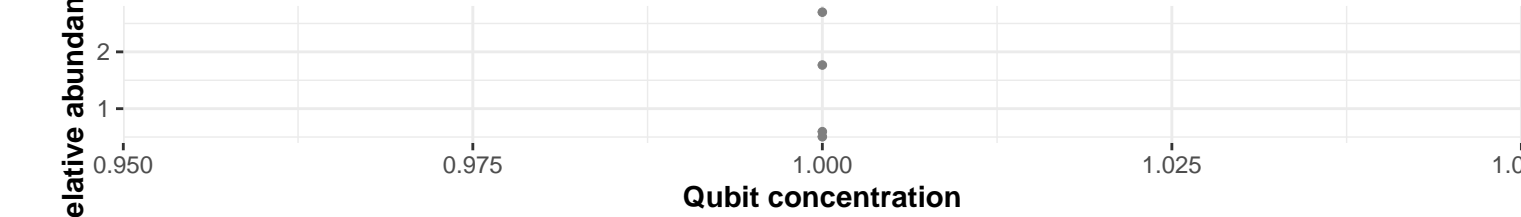


Correlation within: Feed

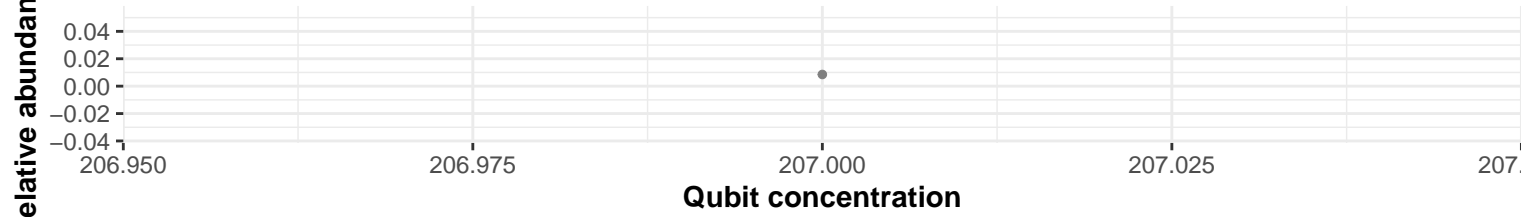
$\log_e(S) = 2.366$, $p = 0.125$, $\hat{\rho}_{\text{Spearman}} = 0.696$, $\text{CI}_{95\%} [-0.297, 0.966]$, $n_{\text{pairs}} = 6$



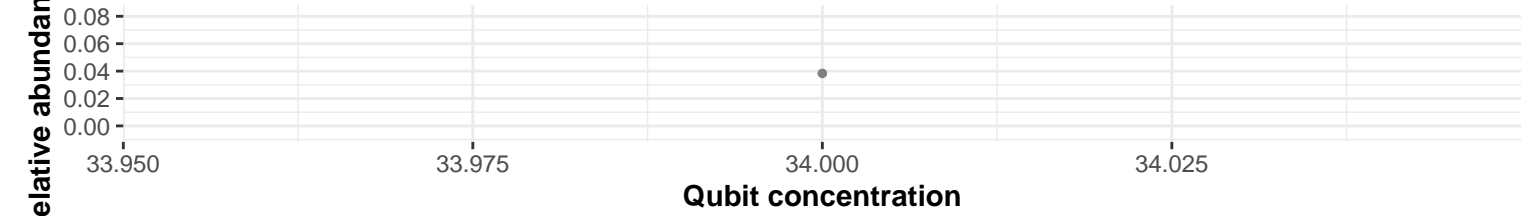
Correlation within: control



Correlation within: Positive_control



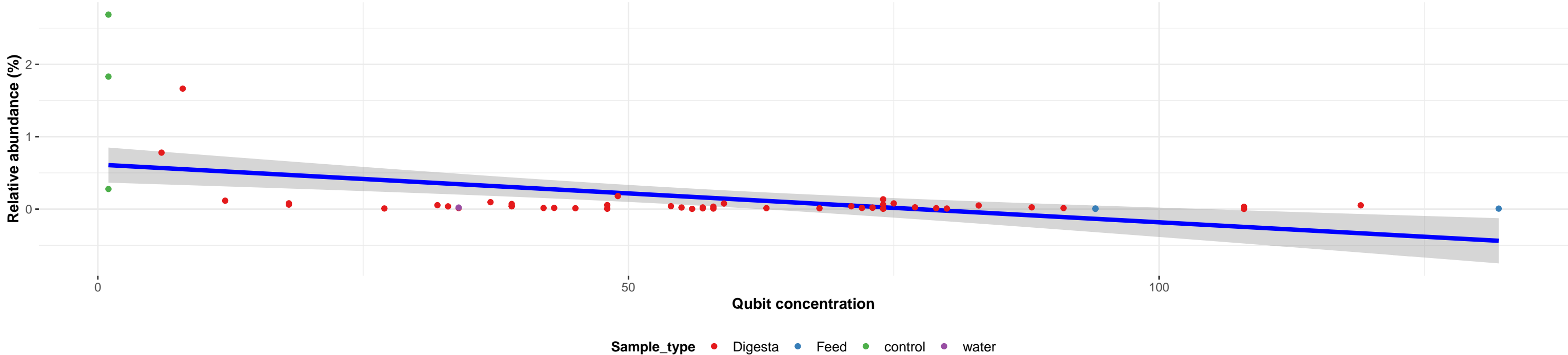
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Beutenbergiaceae; Salana; NA

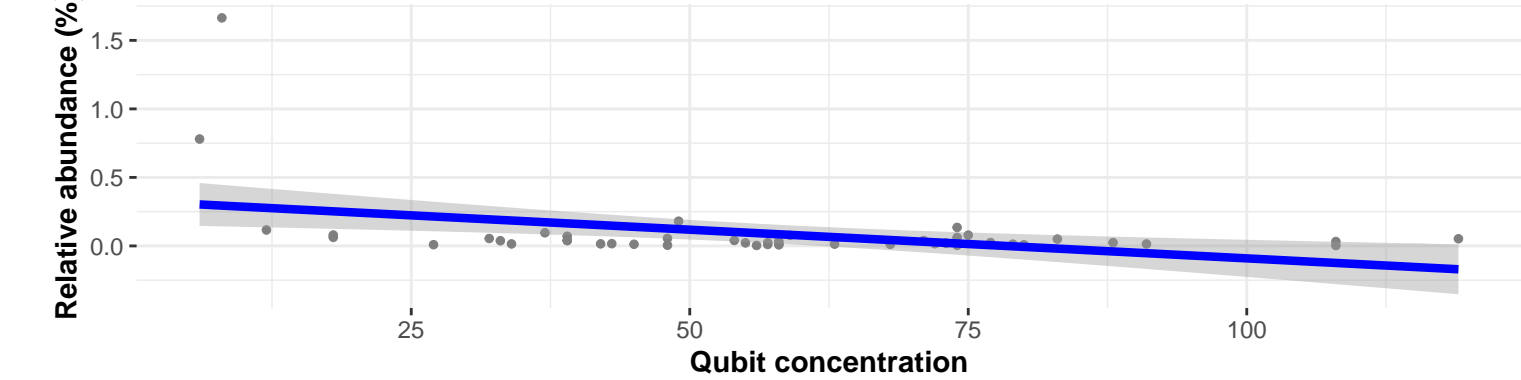
Correlation with all samples

$\log_e(S) = 10.636$, $p = 9.8e-05$, $\hat{\rho}_{\text{Spearman}} = -0.501$, $CI_{95\%} [-0.681, -0.264]$, $n_{\text{pairs}} = 55$

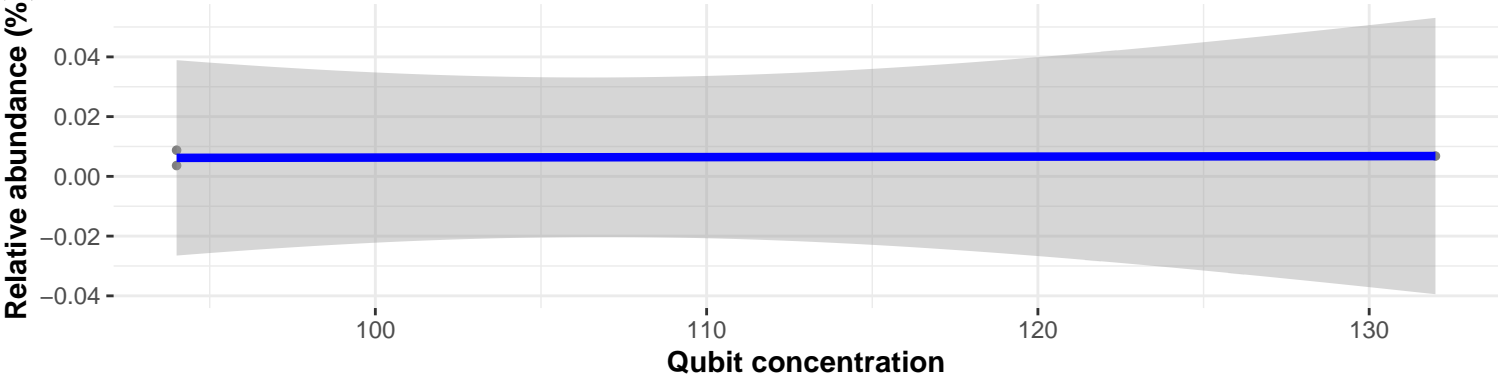


Correlation within: Digesta

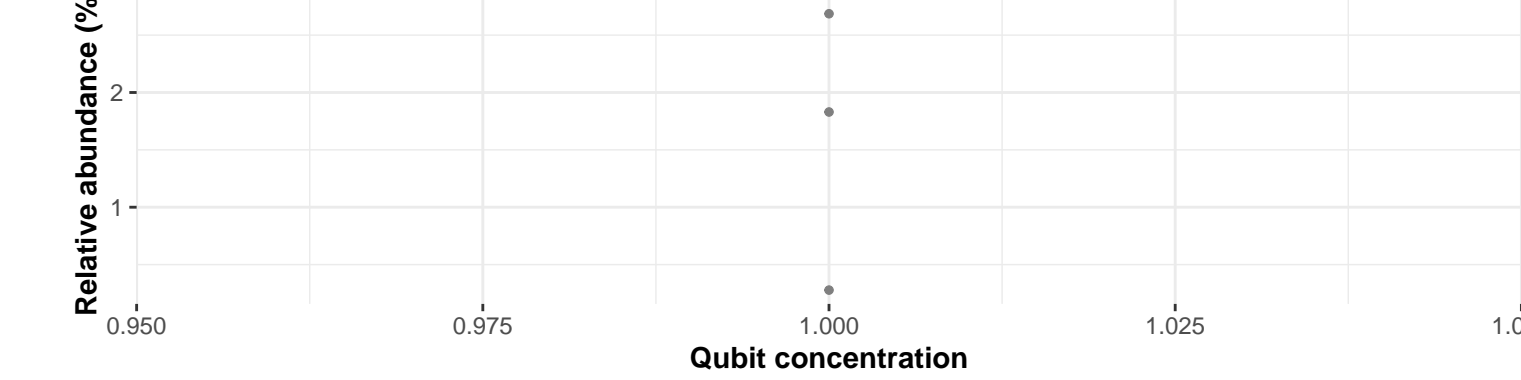
$\log_e(S) = 10.116$, $p = 0.017$, $\hat{\rho}_{\text{Spearman}} = -0.342$, $CI_{95\%} [-0.576, -0.055]$, $n_{\text{pairs}} = 48$



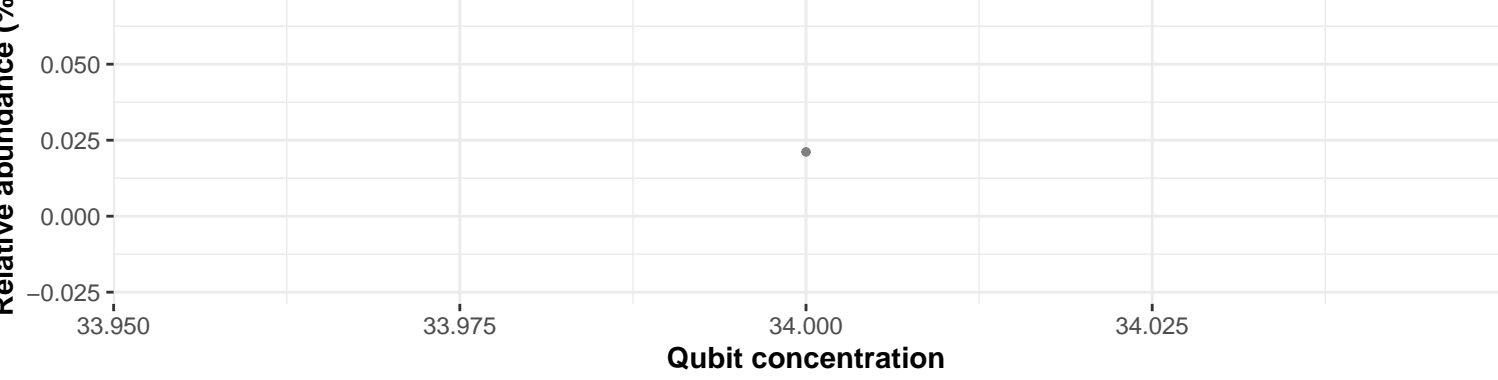
Correlation within: Feed



Correlation within: control



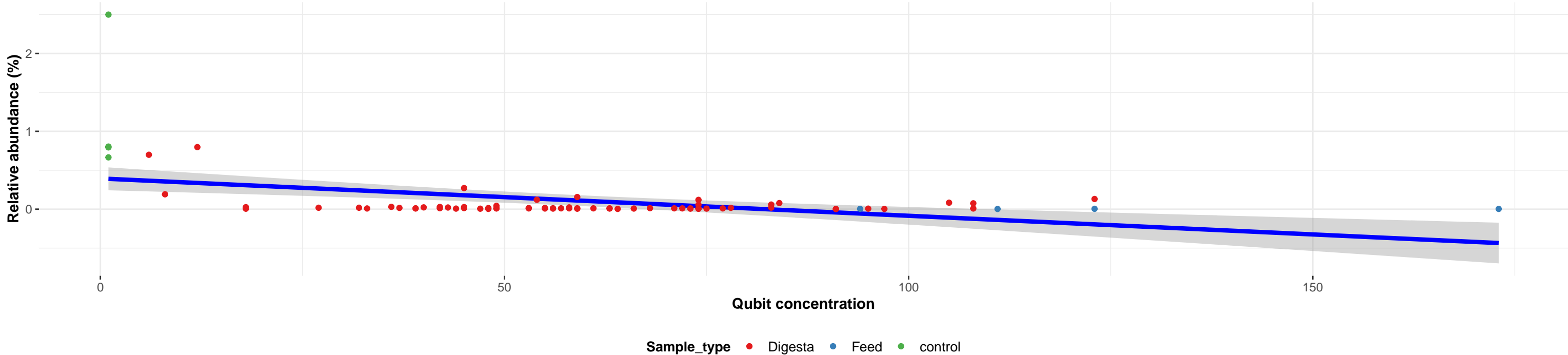
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Halomonadaceae; Halomonas; NA

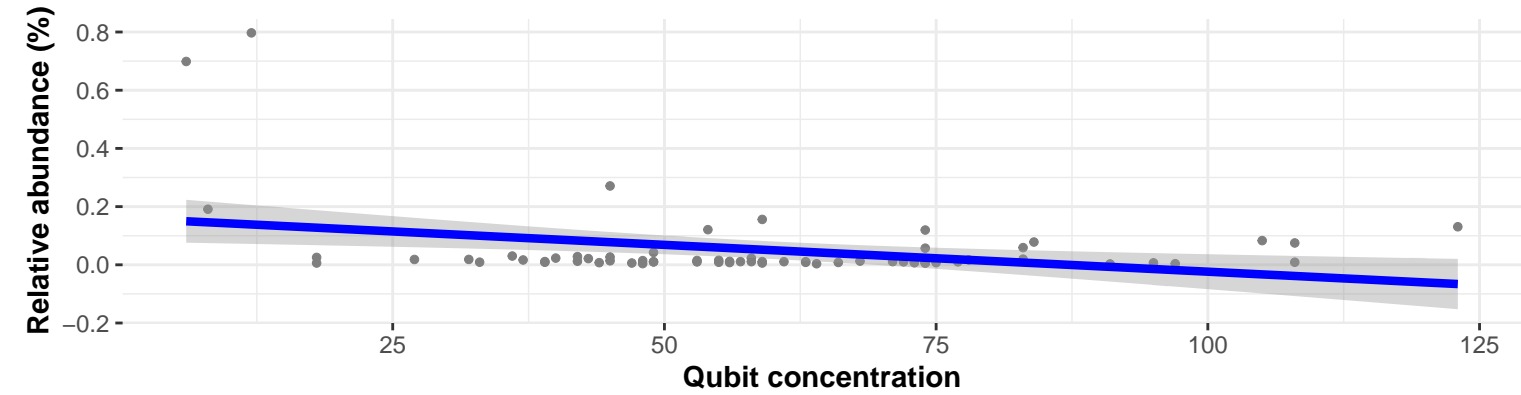
Correlation with all samples

$\log_e(S) = 11.560$, $p = 9.12e-05$, $\hat{\rho}_{\text{Spearman}} = -0.434$, $CI_{95\%} [-0.605, -0.224]$, $n_{\text{pairs}} = 76$

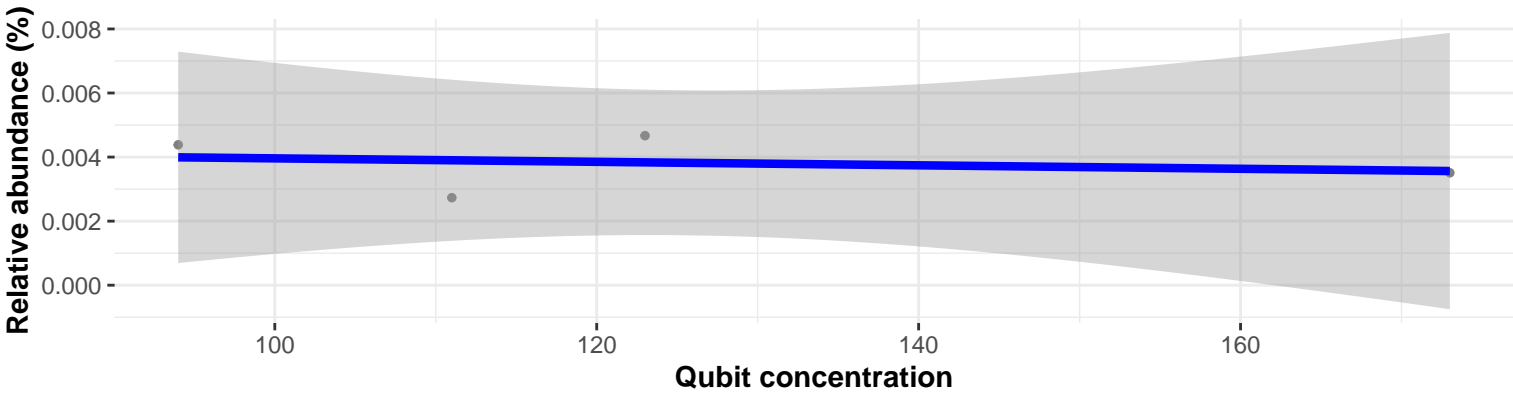


Correlation within: Digesta

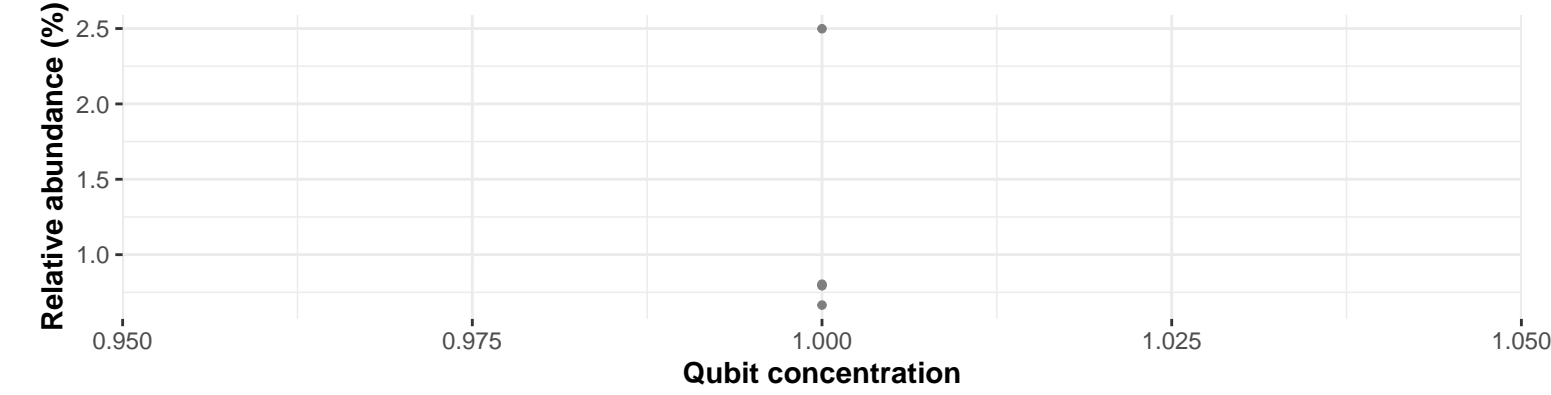
$\log_e(S) = 11.073$, $p = 0.060$, $\hat{\rho}_{\text{Spearman}} = -0.230$, $CI_{95\%} [-0.449, 0.017]$, $n_{\text{pairs}} = 68$



Correlation within: Feed



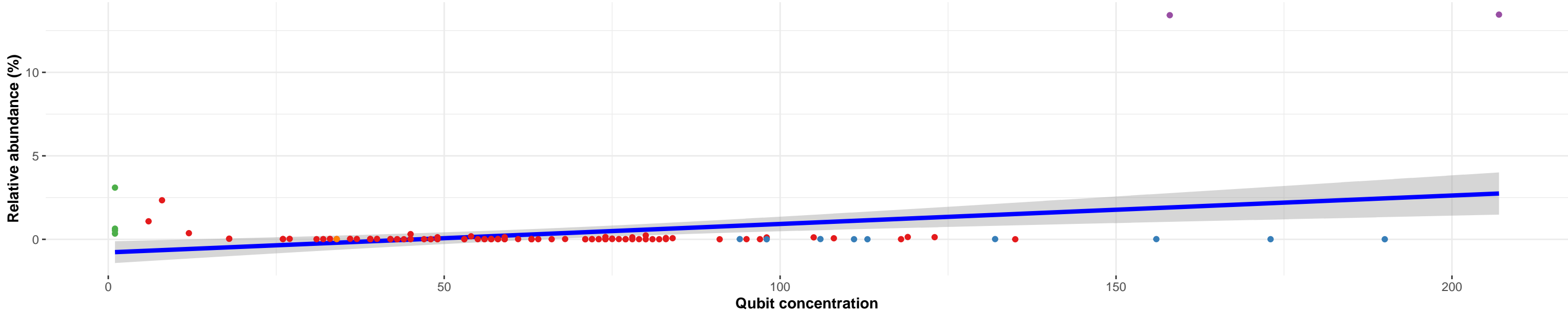
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia–Shigella; NA

Correlation with all samples

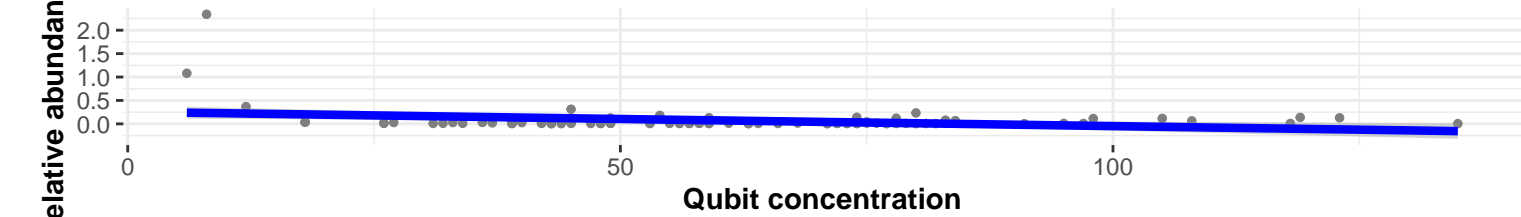
$\log_e(S) = 12.553$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.242$, $\text{CI}_{95\%} [-0.414, -0.052]$, $n_{\text{pairs}} = 111$



Sample_type • Digesta • Feed • control • Positive_control • water

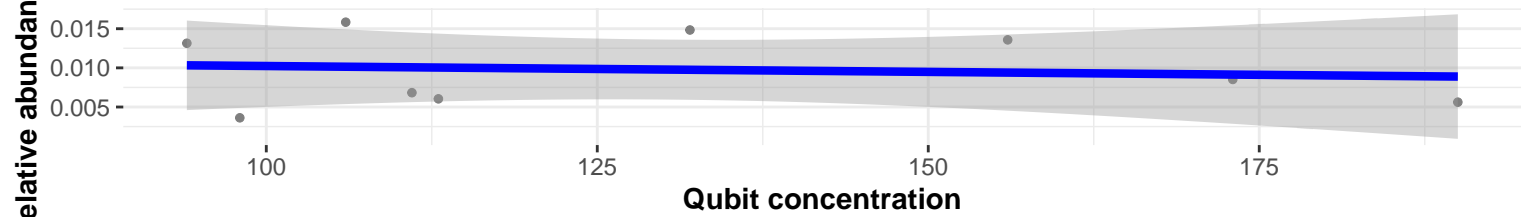
Correlation within: Digesta

$\log_e(S) = 12.025$, $p = 0.104$, $\hat{\rho}_{\text{Spearman}} = -0.168$, $\text{CI}_{95\%} [-0.363, 0.041]$, $n_{\text{pairs}} = 95$

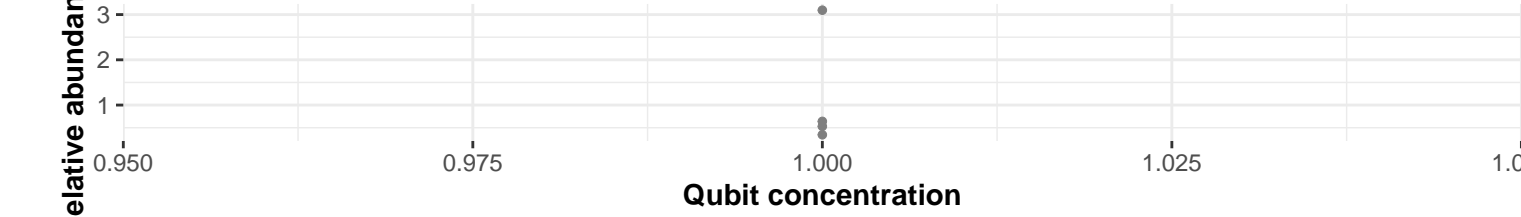


Correlation within: Feed

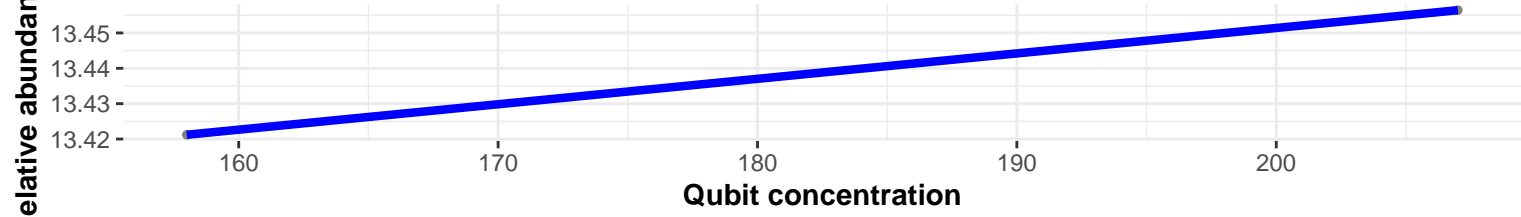
$\log_e(S) = 4.852$, $p = 0.865$, $\hat{\rho}_{\text{Spearman}} = -0.067$, $\text{CI}_{95\%} [-0.712, 0.639]$, $n_{\text{pairs}} = 9$



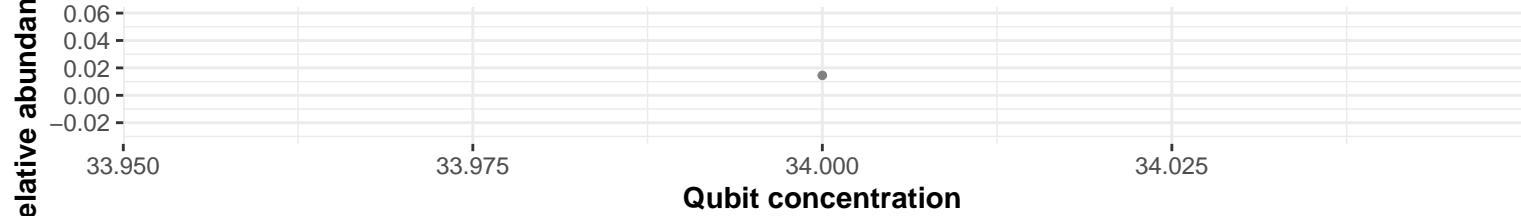
Correlation within: control



Correlation within: Positive_control



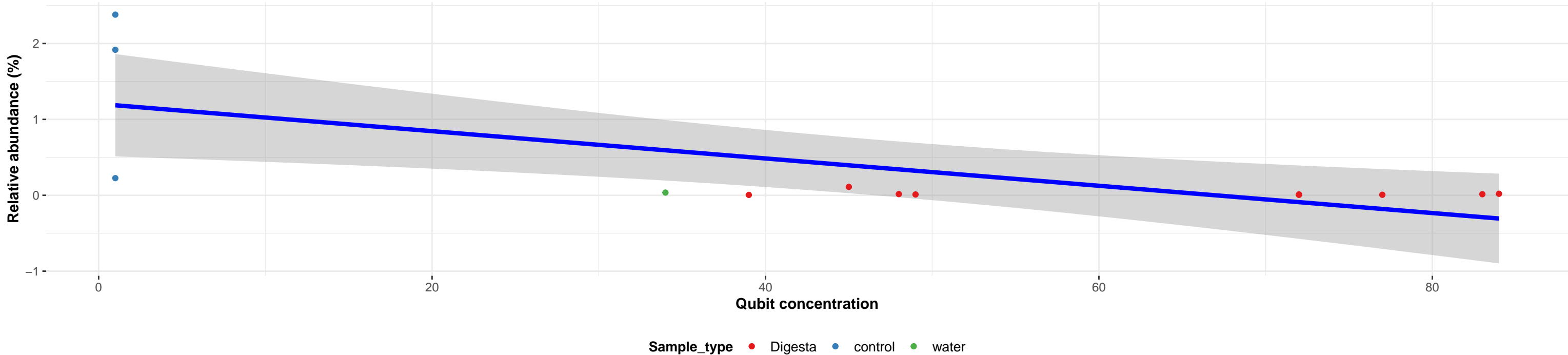
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Micrococcaceae; Citricoccus; NA

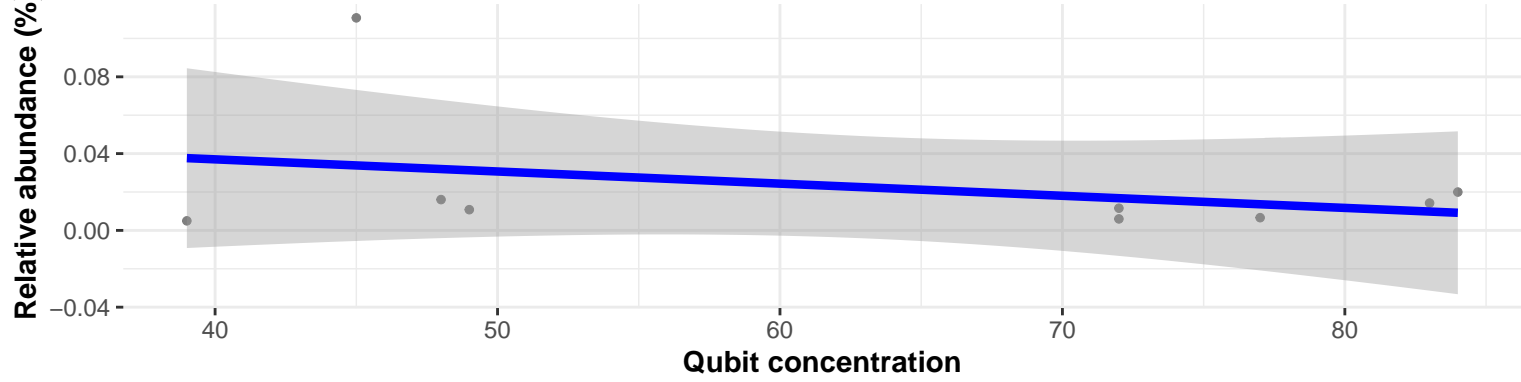
Correlation with all samples

$\log_e(S) = 6.364$, $p = 0.032$, $\hat{\rho}_{\text{Spearman}} = -0.595$, $CI_{95\%} [-0.868, -0.047]$, $n_{\text{pairs}} = 13$

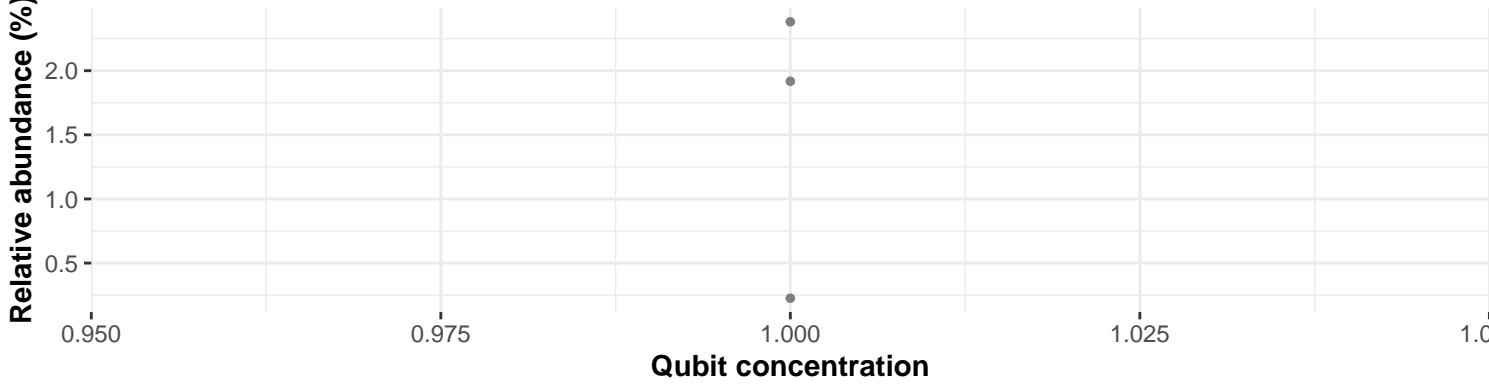


Correlation within: Digesta

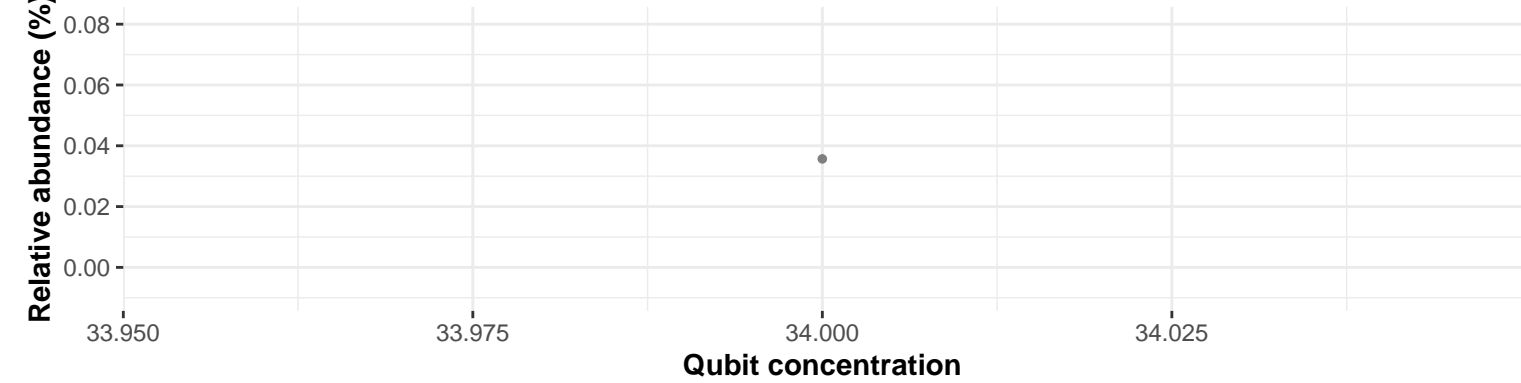
$\log_e(S) = 4.594$, $p = 0.651$, $\hat{\rho}_{\text{Spearman}} = 0.176$, $CI_{95\%} [-0.569, 0.762]$, $n_{\text{pairs}} = 9$



Correlation within: control



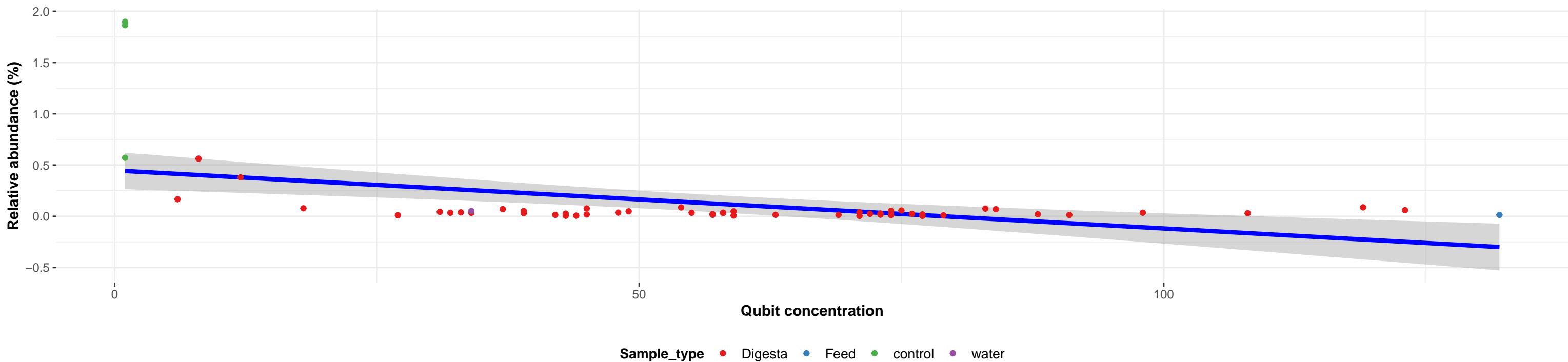
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; NA

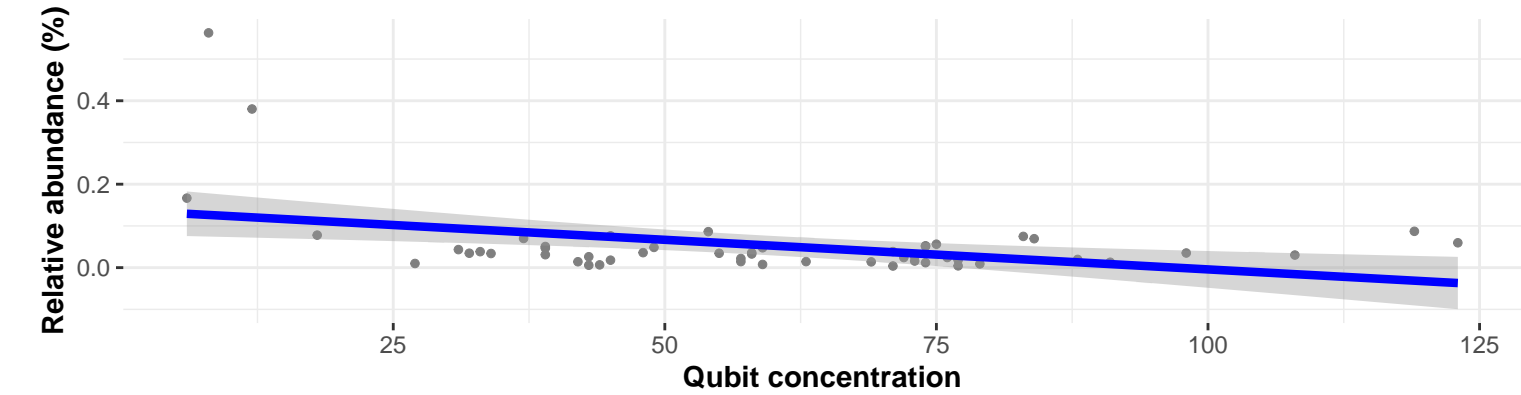
Correlation with all samples

$\log_e(S) = 10.641$, $p = 0.007$, $\hat{\rho}_{\text{Spearman}} = -0.355$, $\text{CI}_{95\%} [-0.569, -0.097]$, $n_{\text{pairs}} = 57$

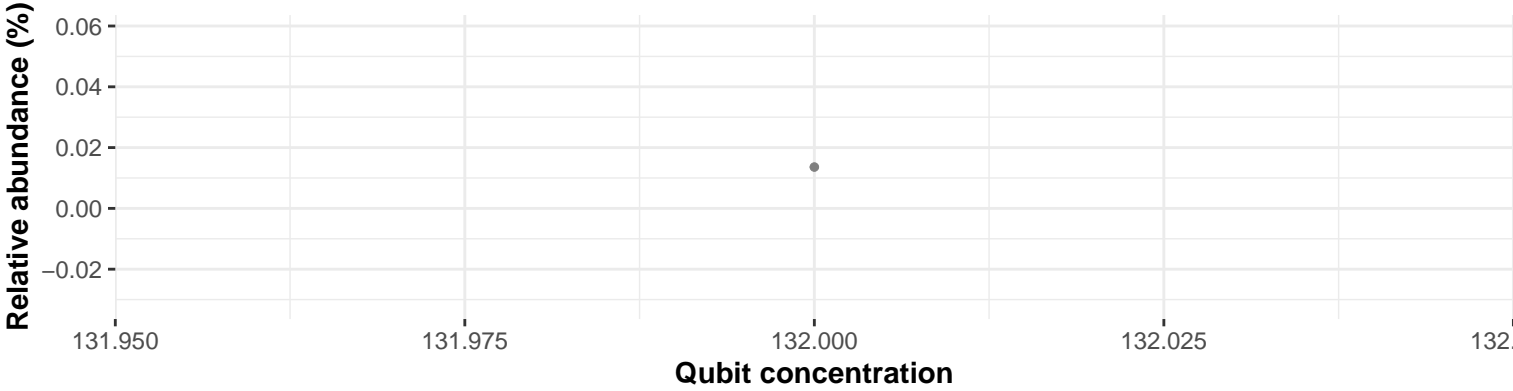


Correlation within: Digesta

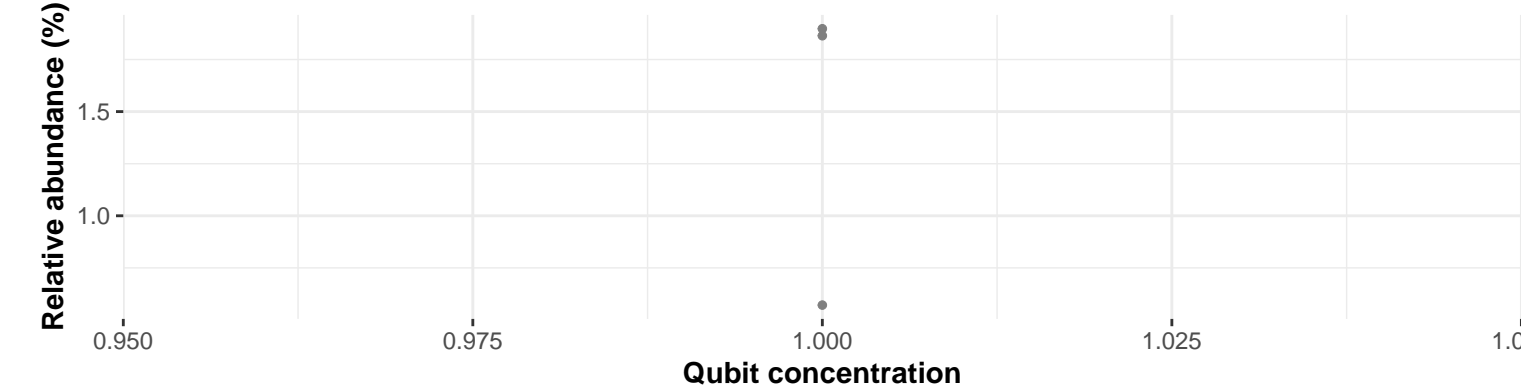
$\log_e(S) = 10.243$, $p = 0.157$, $\hat{\rho}_{\text{Spearman}} = -0.199$, $\text{CI}_{95\%} [-0.454, 0.086]$, $n_{\text{pairs}} = 52$



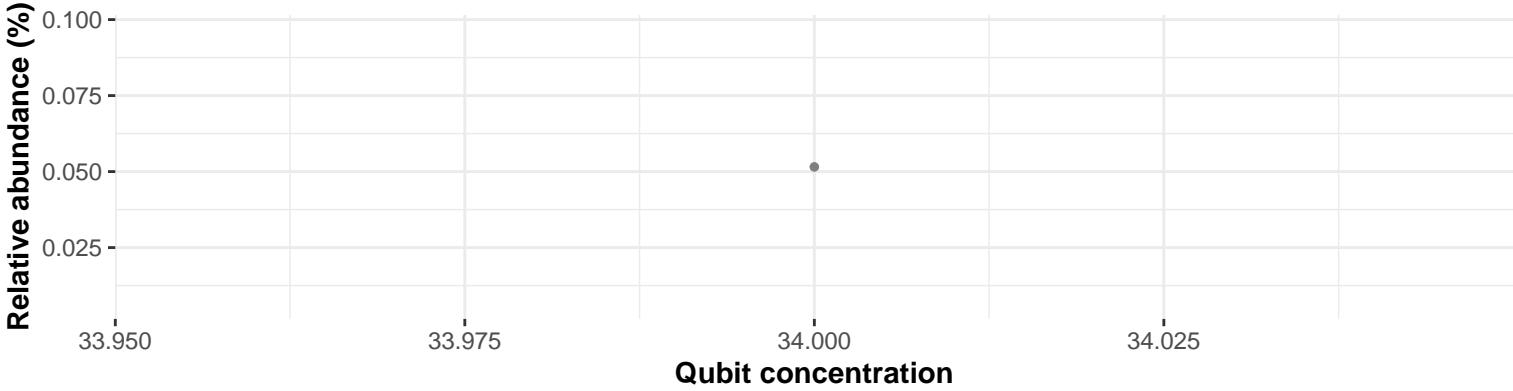
Correlation within: Feed



Correlation within: control



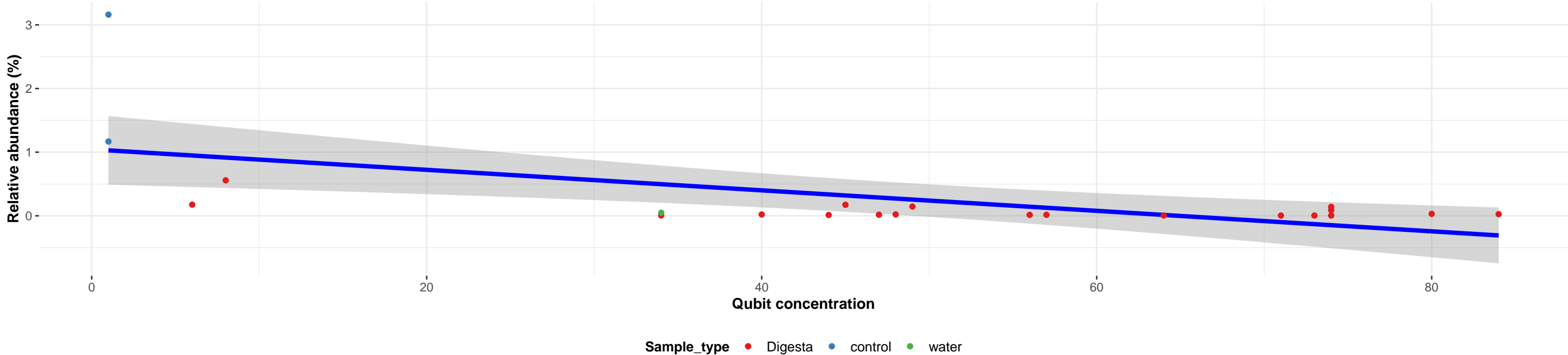
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Micrococcaceae; Micrococcus; NA

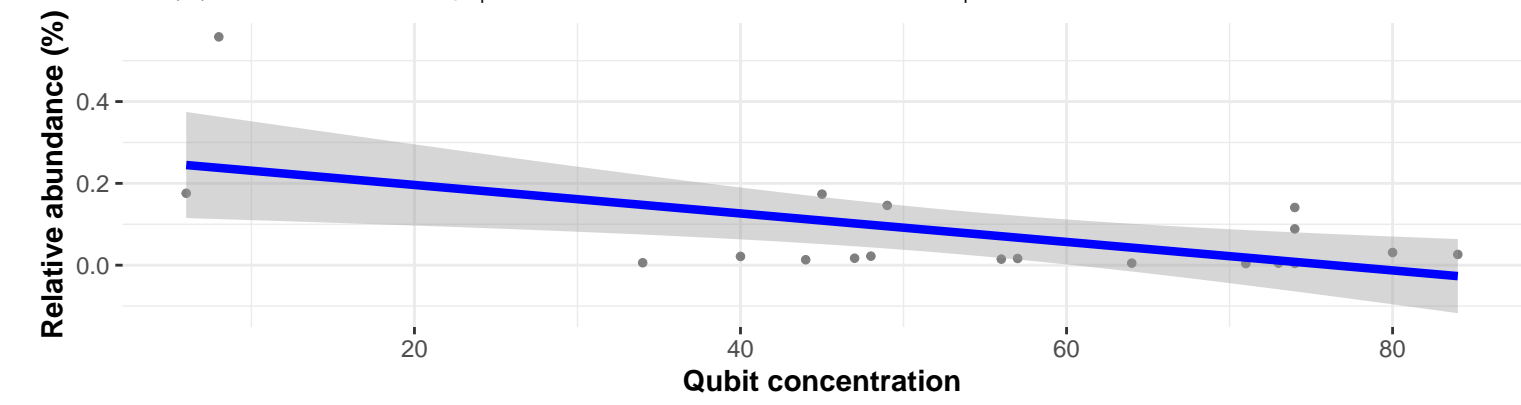
Correlation with all samples

$\log_e(S) = 7.864$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = -0.469$, $\text{CI}_{95\%} [-0.749, -0.046]$, $n_{\text{pairs}} = 22$

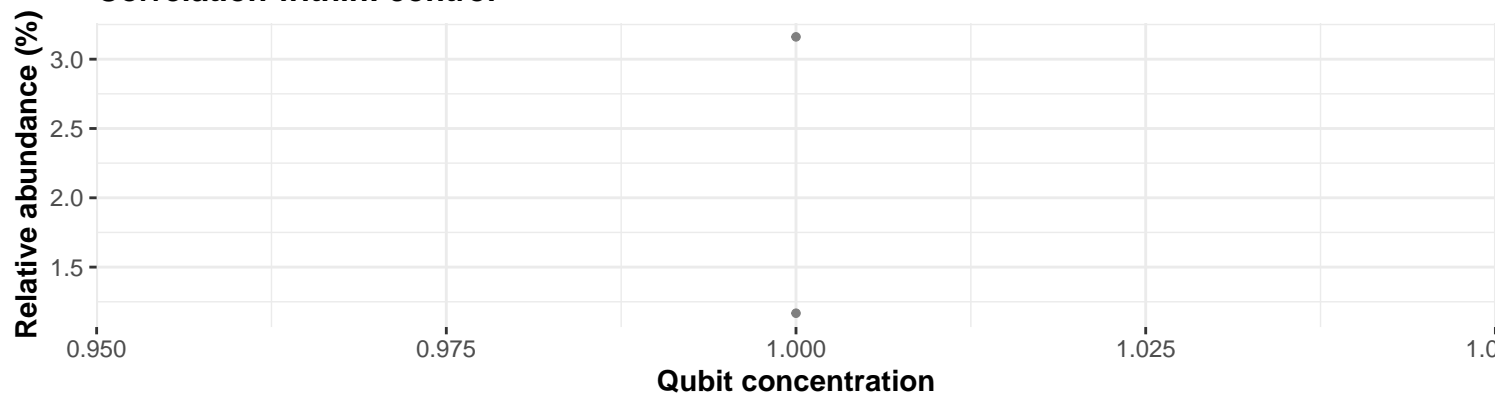


Correlation within: Digesta

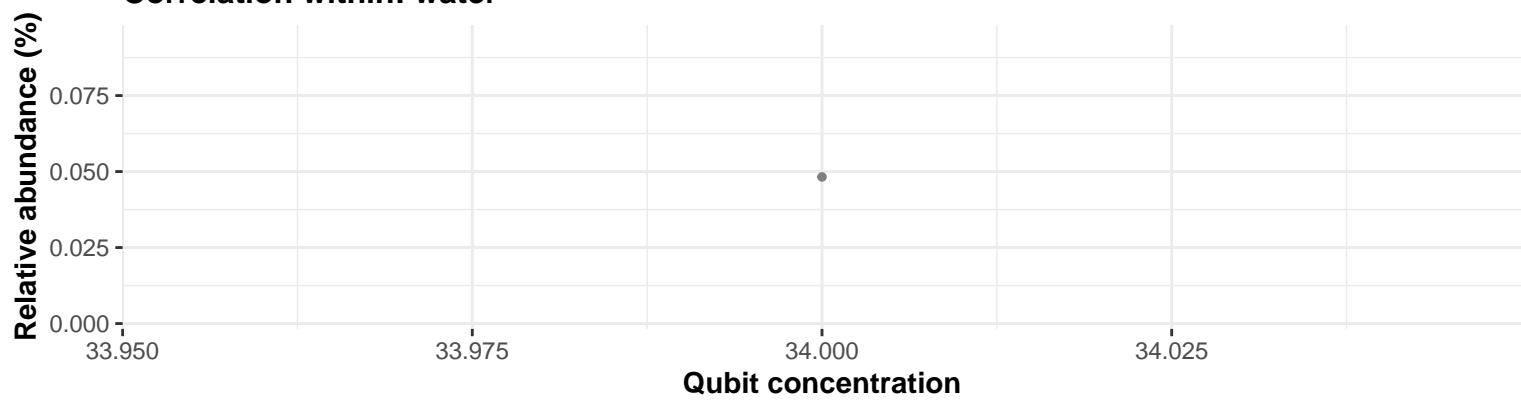
$\log_e(S) = 7.263$, $p = 0.299$, $\hat{\rho}_{\text{Spearman}} = -0.251$, $\text{CI}_{95\%} [-0.642, 0.243]$, $n_{\text{pairs}} = 19$



Correlation within: control



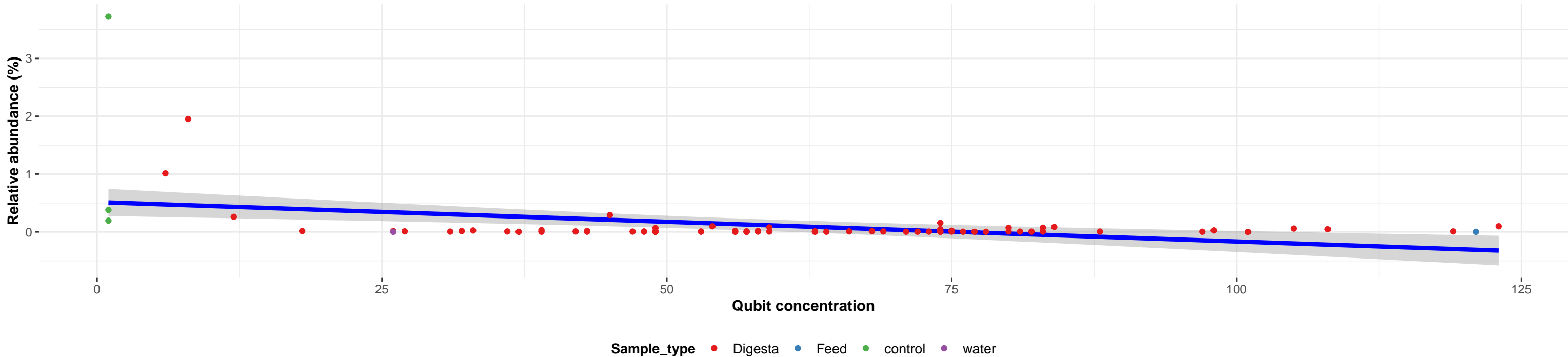
Correlation within: water



Bacteria; Firmicutes; Bacilli; Erysipelotrichales; Erysipelotrichaceae; Erysipelothrix; NA

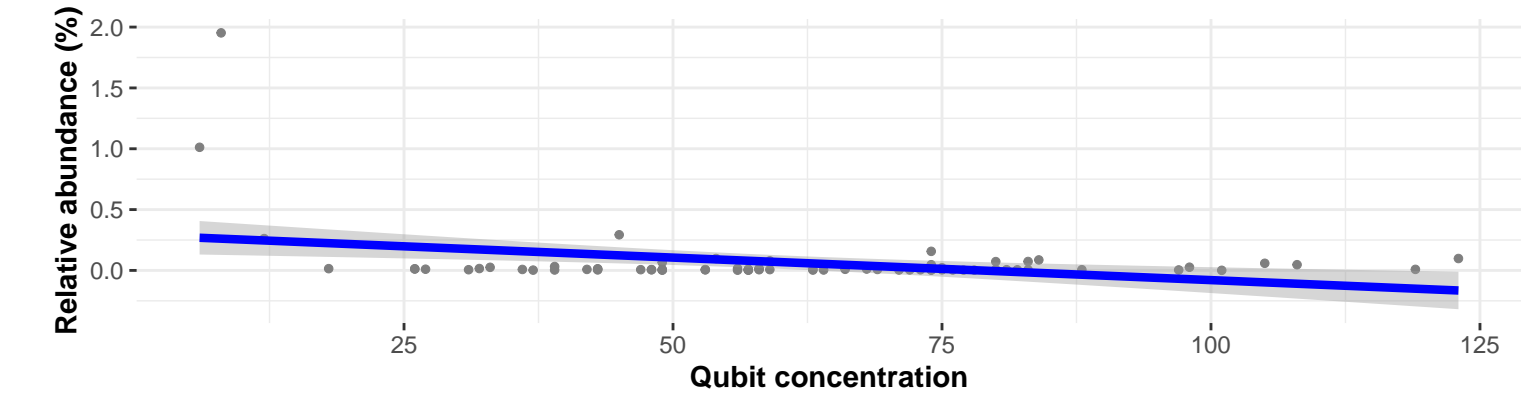
Correlation with all samples

$\log_e(S) = 11.521$, $p = 0.045$, $\hat{\rho}_{\text{Spearman}} = -0.227$, $CI_{95\%} [-0.432, 9.069e-04]$, $n_{\text{pairs}} = 79$

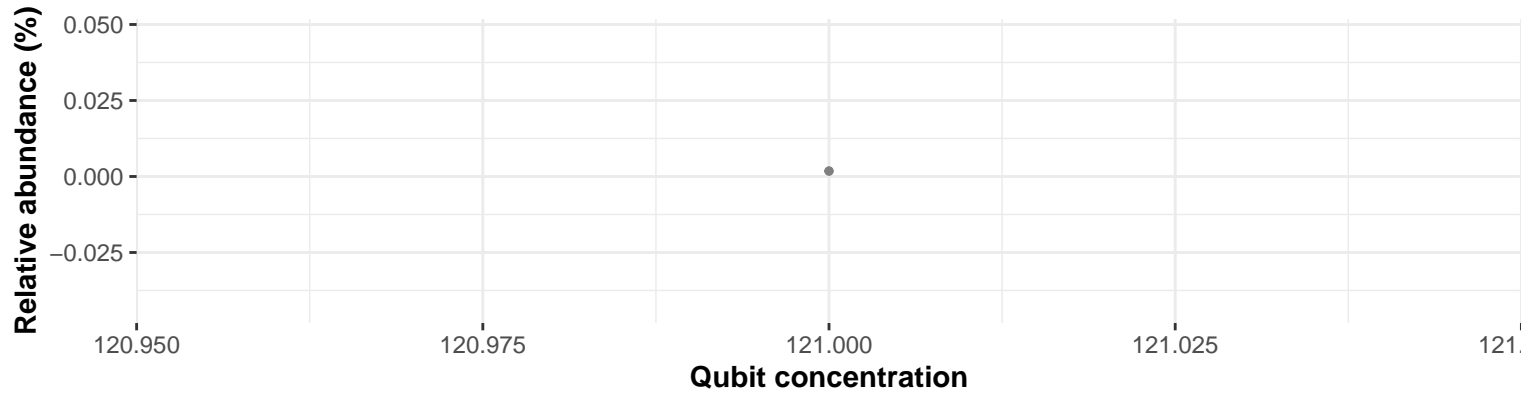


Correlation within: Digesta

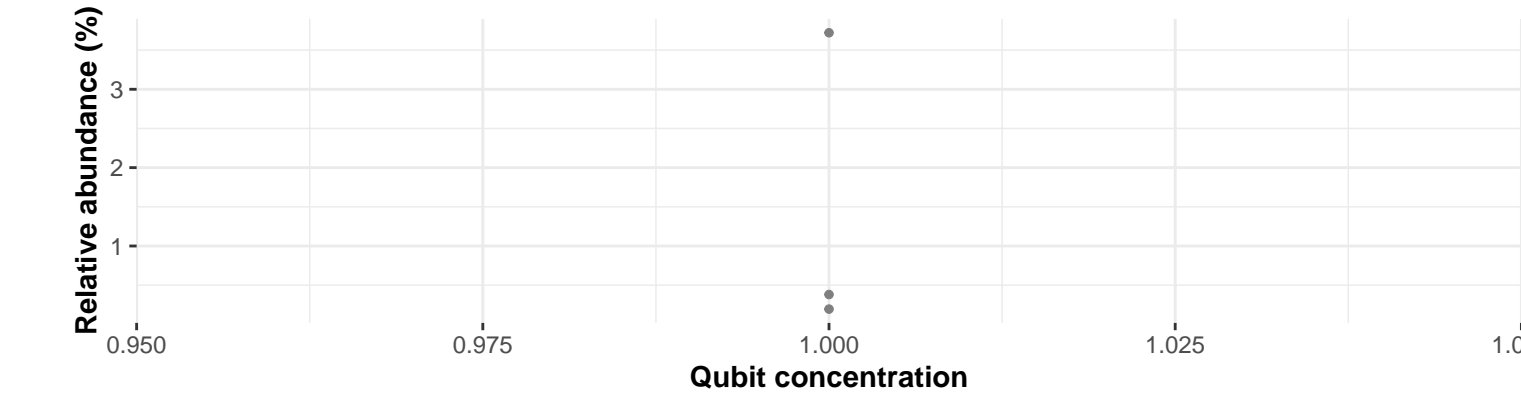
$\log_e(S) = 11.245$, $p = 0.259$, $\hat{\rho}_{\text{Spearman}} = -0.133$, $CI_{95\%} [-0.357, 0.105]$, $n_{\text{pairs}} = 74$



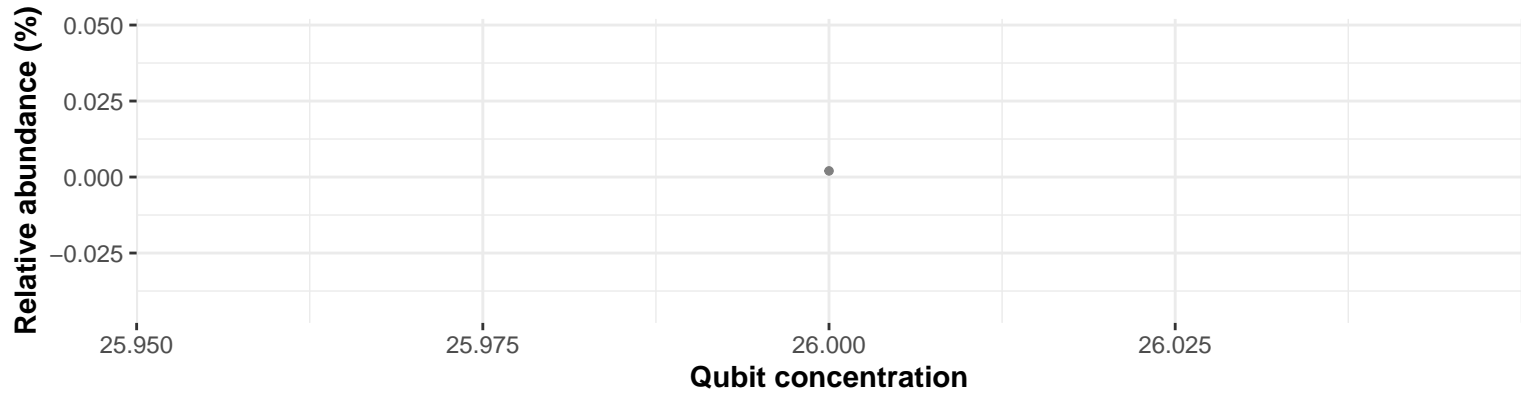
Correlation within: Feed



Correlation within: control



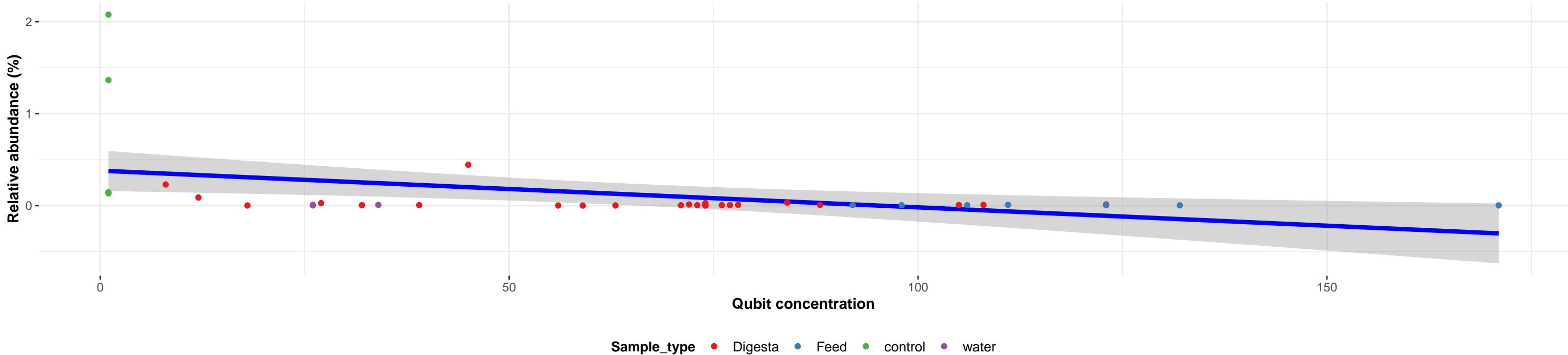
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Enhydrobacter; aerosaccus

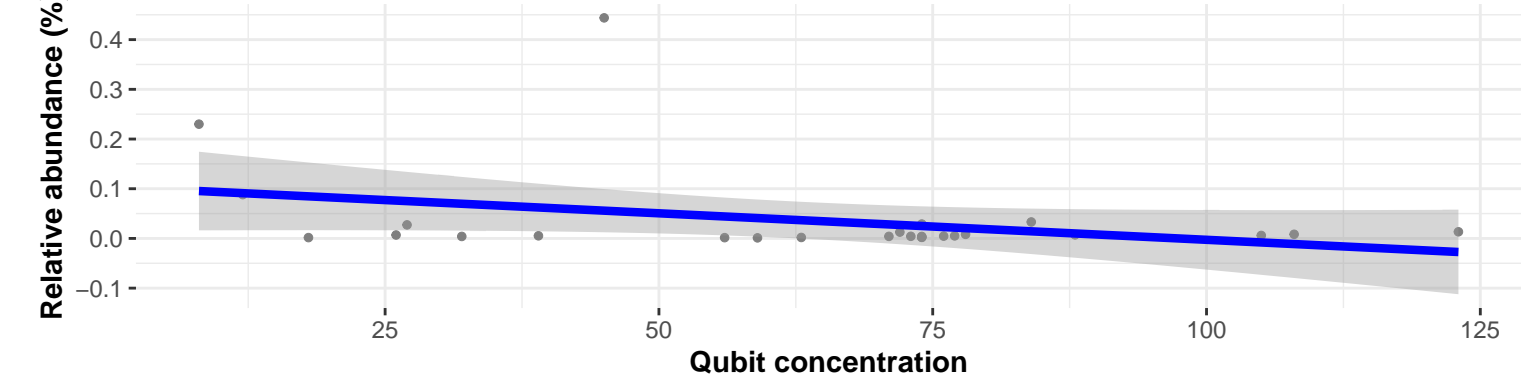
Correlation with all samples

$\log_e(S) = 9.467$, $p = 0.056$, $\hat{\rho}_{\text{Spearman}} = -0.308$, $CI_{95\%} [-0.575, 0.017]$, $n_{\text{pairs}} = 39$



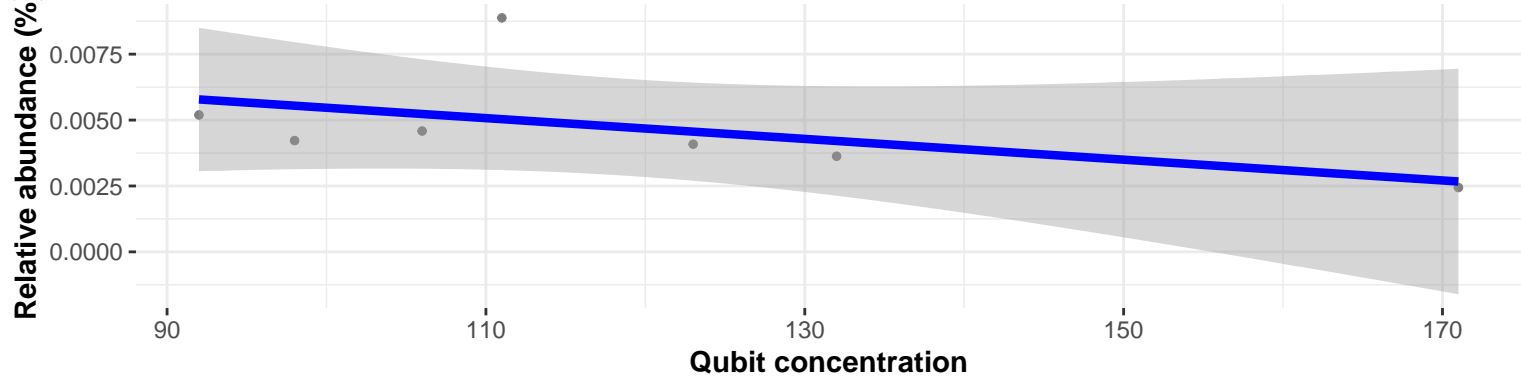
Correlation within: Digesta

$\log_e(S) = 7.933$, $p = 0.820$, $\hat{\rho}_{\text{Spearman}} = 0.047$, $CI_{95\%} [-0.357, 0.436]$, $n_{\text{pairs}} = 26$

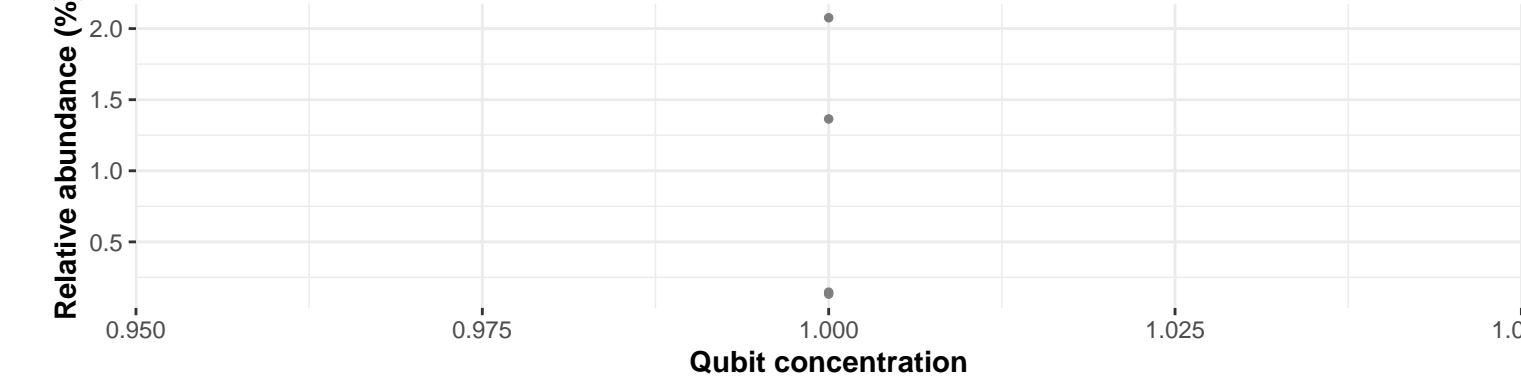


Correlation within: Feed

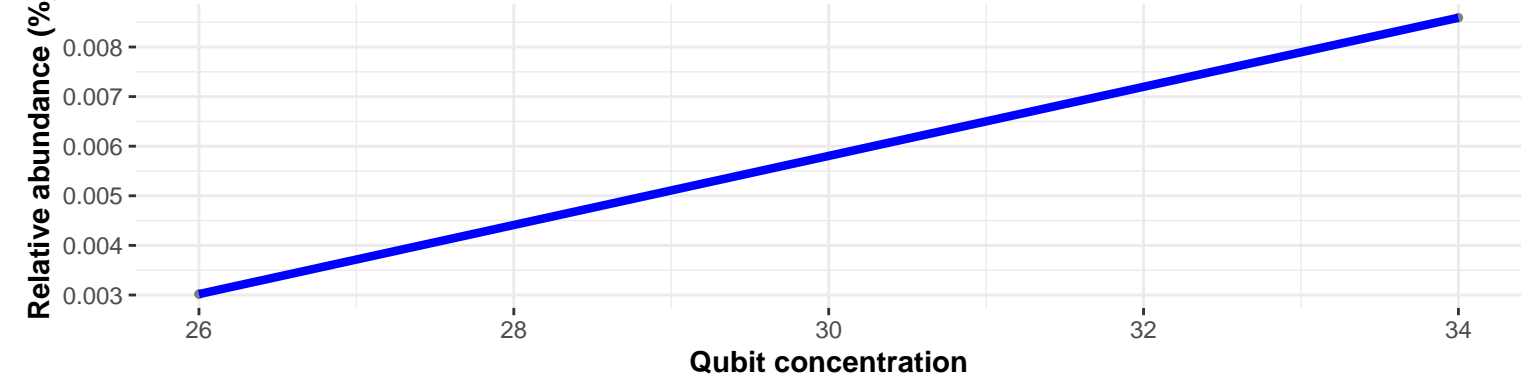
$\log_e(S) = 4.585$, $p = 0.052$, $\hat{\rho}_{\text{Spearman}} = -0.750$, $CI_{95\%} [-0.963, 0.036]$, $n_{\text{pairs}} = 7$



Correlation within: control



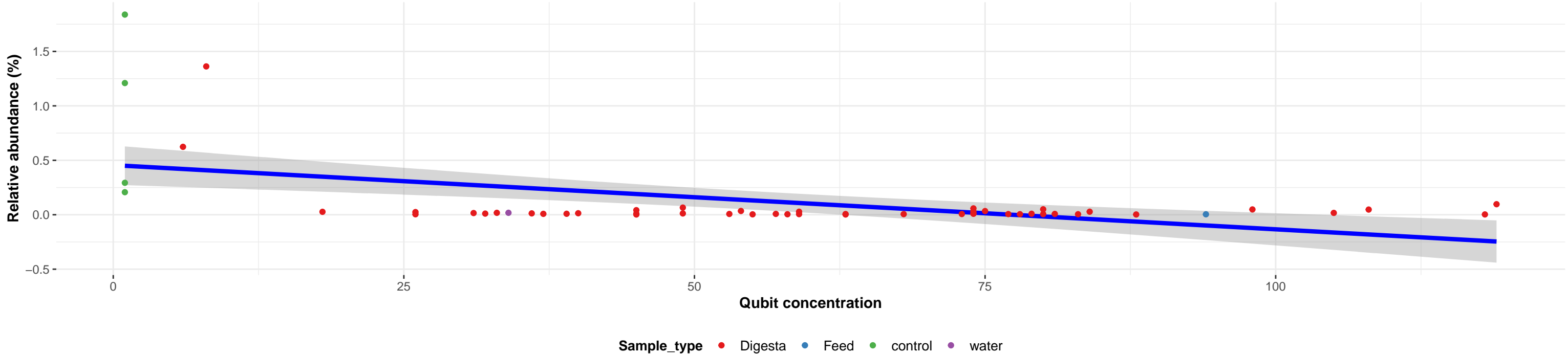
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anaerobacillus; NA

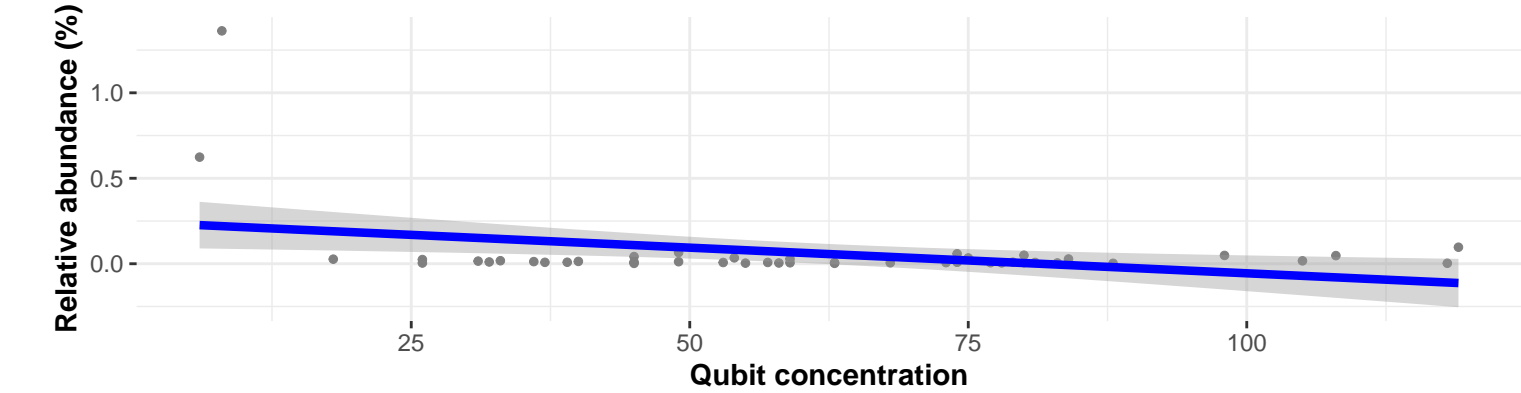
Correlation with all samples

$\log_e(S) = 10.403$, $p = 0.016$, $\hat{\rho}_{\text{Spearman}} = -0.328$, $\text{CI}_{95\%} [-0.555, -0.055]$, $n_{\text{pairs}} = 53$

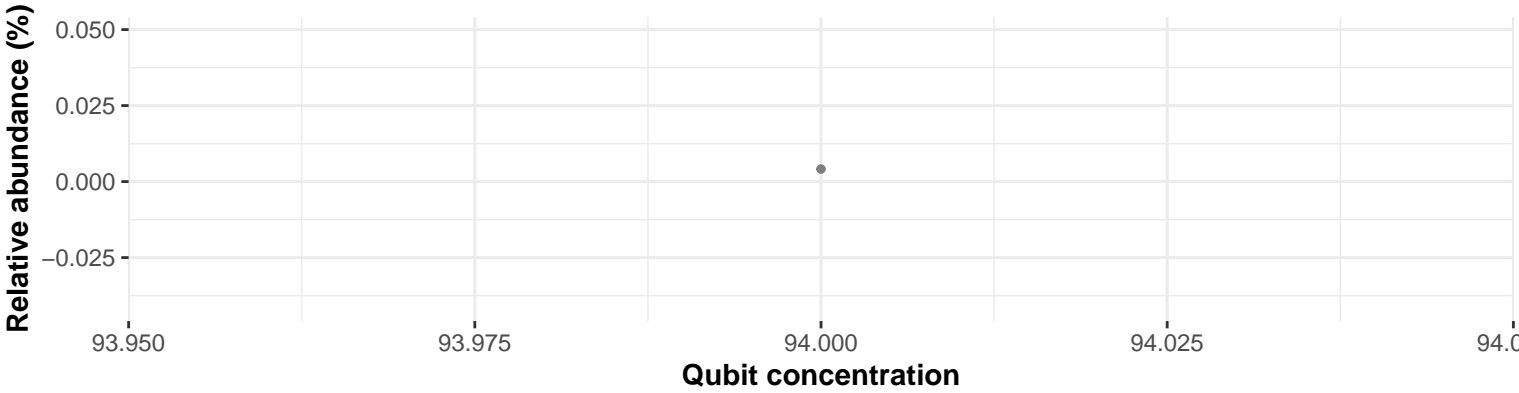


Correlation within: Digesta

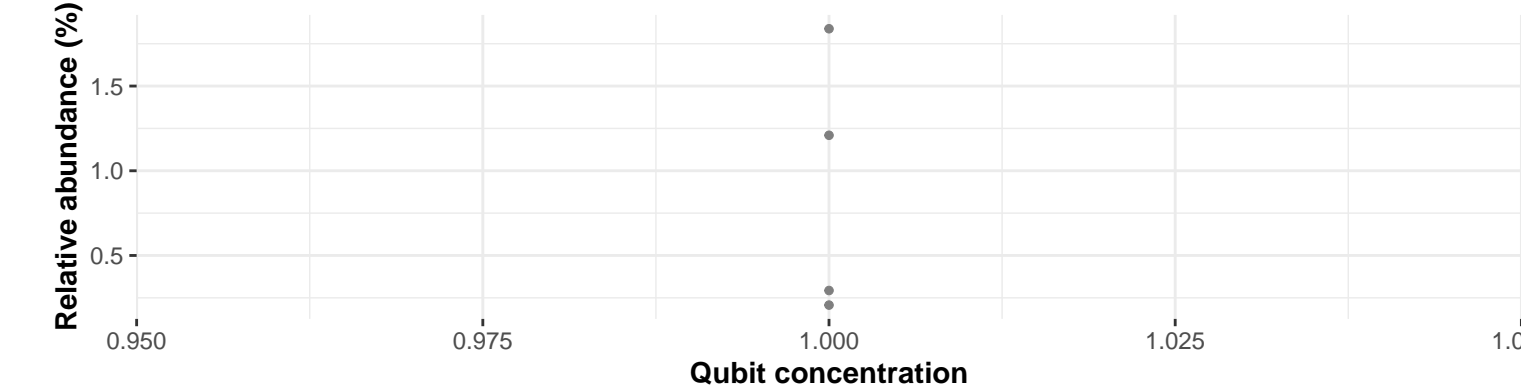
$\log_e(S) = 9.863$, $p = 0.459$, $\hat{\rho}_{\text{Spearman}} = -0.111$, $\text{CI}_{95\%} [-0.393, 0.191]$, $n_{\text{pairs}} = 47$



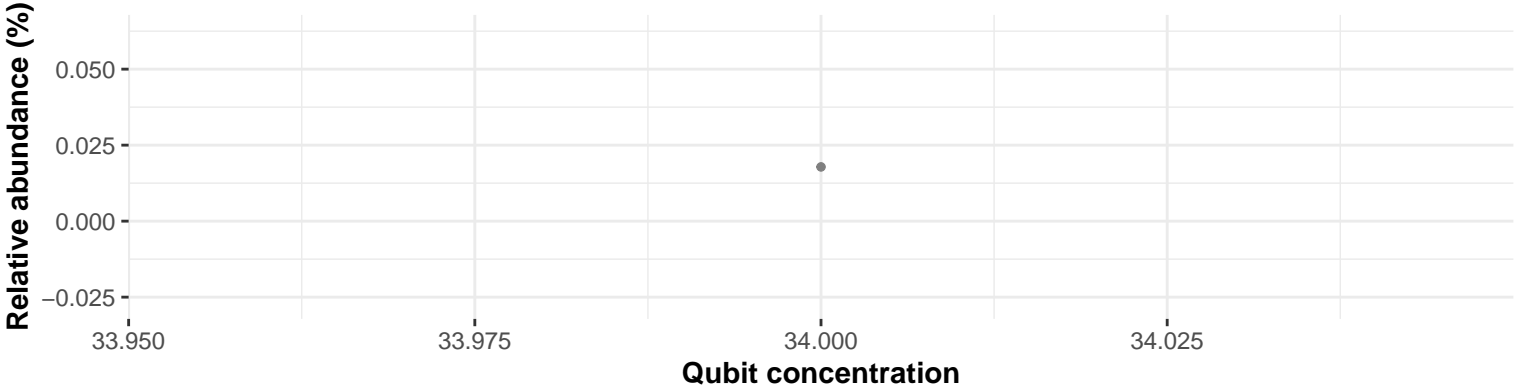
Correlation within: Feed



Correlation within: control



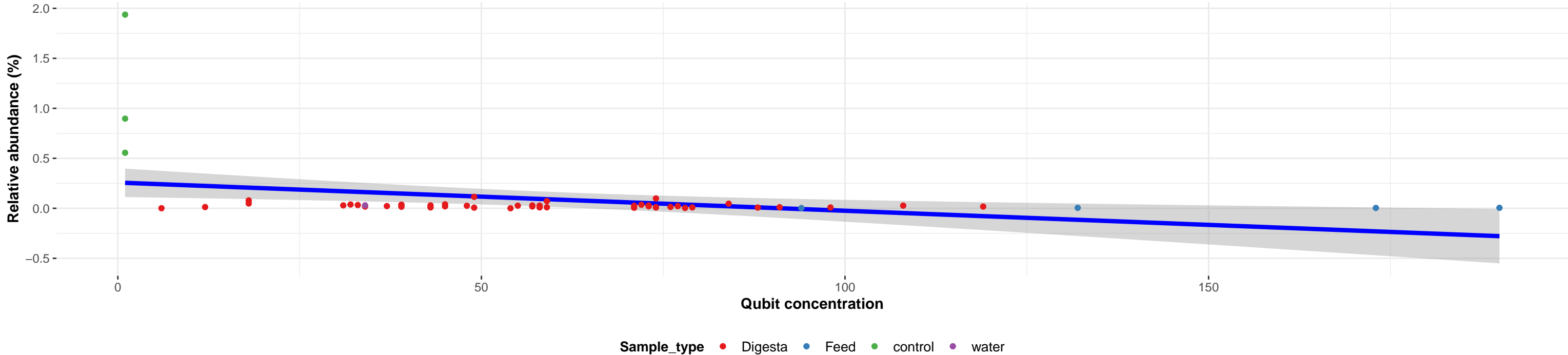
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

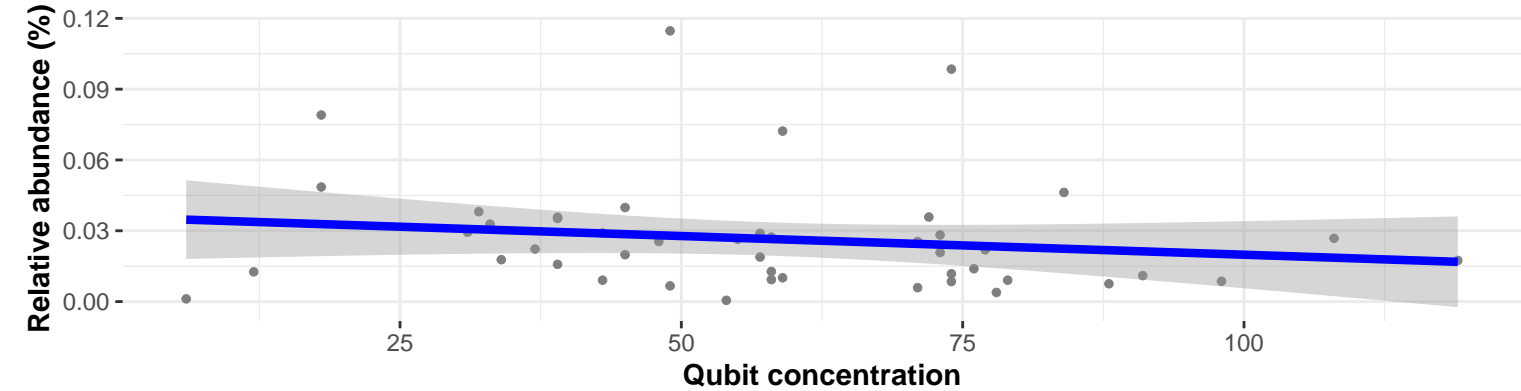
Correlation with all samples

$\log_e(S) = 10.577$, $p = 1.38e-04$, $\hat{\rho}_{\text{Spearman}} = -0.496$, $CI_{95\%} [-0.678, -0.255]$, $n_{\text{pairs}} = 54$

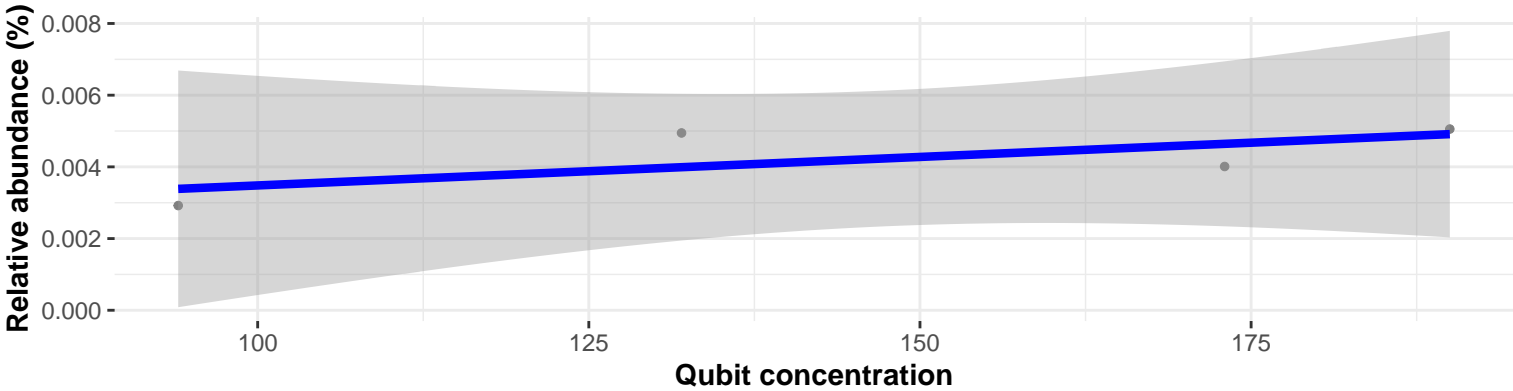


Correlation within: Digesta

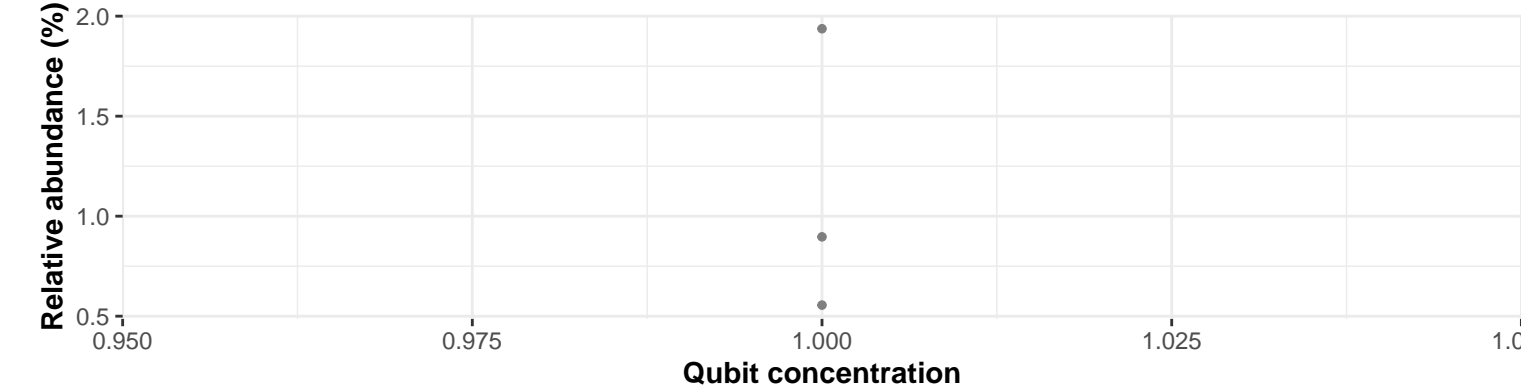
$\log_e(S) = 9.929$, $p = 0.075$, $\hat{\rho}_{\text{Spearman}} = -0.265$, $CI_{95\%} [-0.522, 0.036]$, $n_{\text{pairs}} = 46$



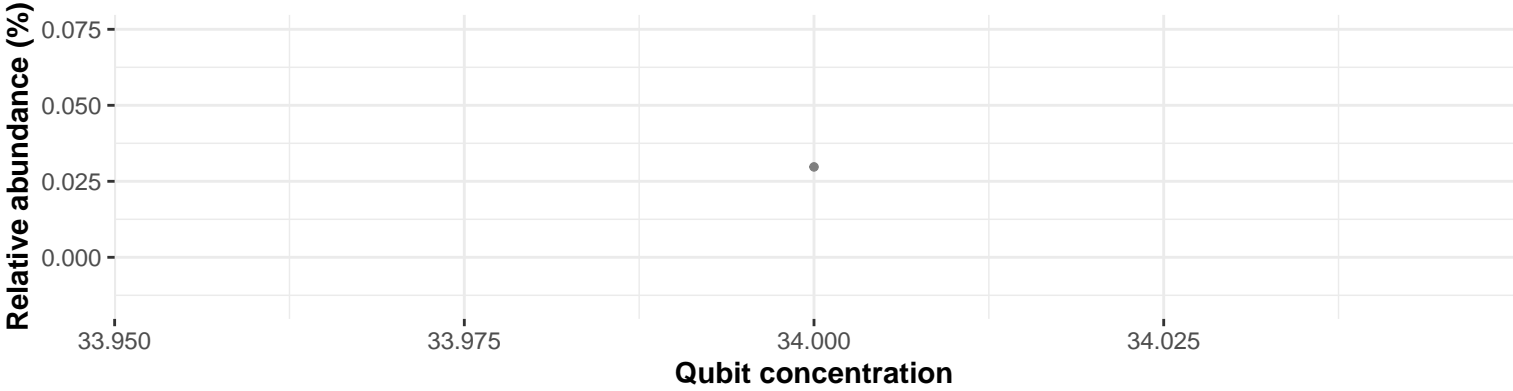
Correlation within: Feed



Correlation within: control



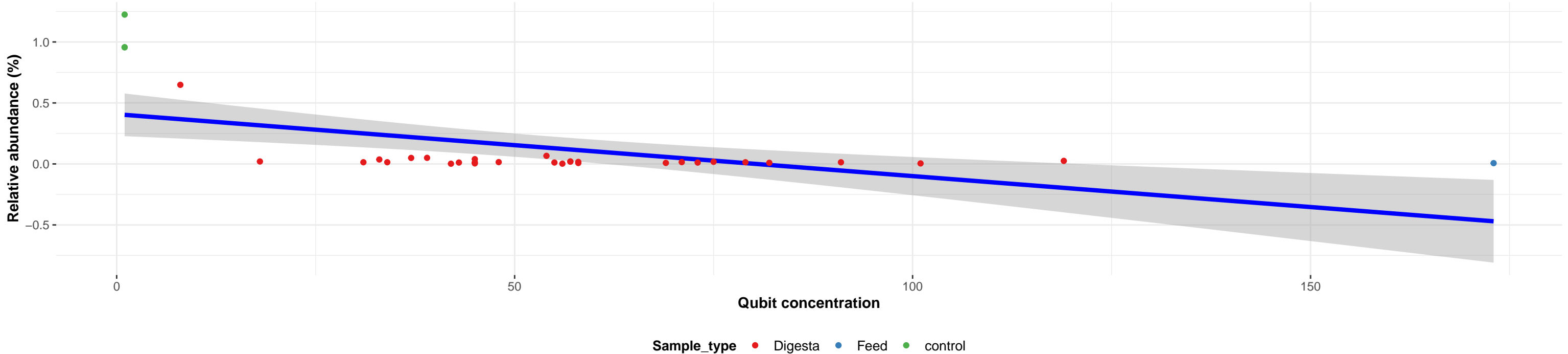
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium; ravenspurgense

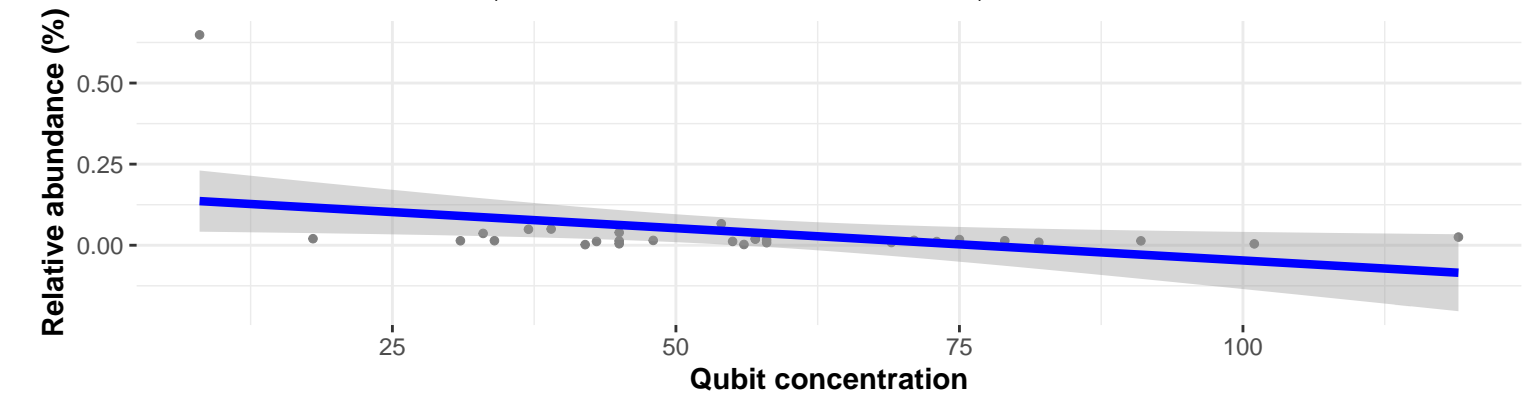
Correlation with all samples

$\log_e(S) = 9.122$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.529$, $\text{CI}_{95\%} [-0.743, -0.217]$, $n_{\text{pairs}} = 33$

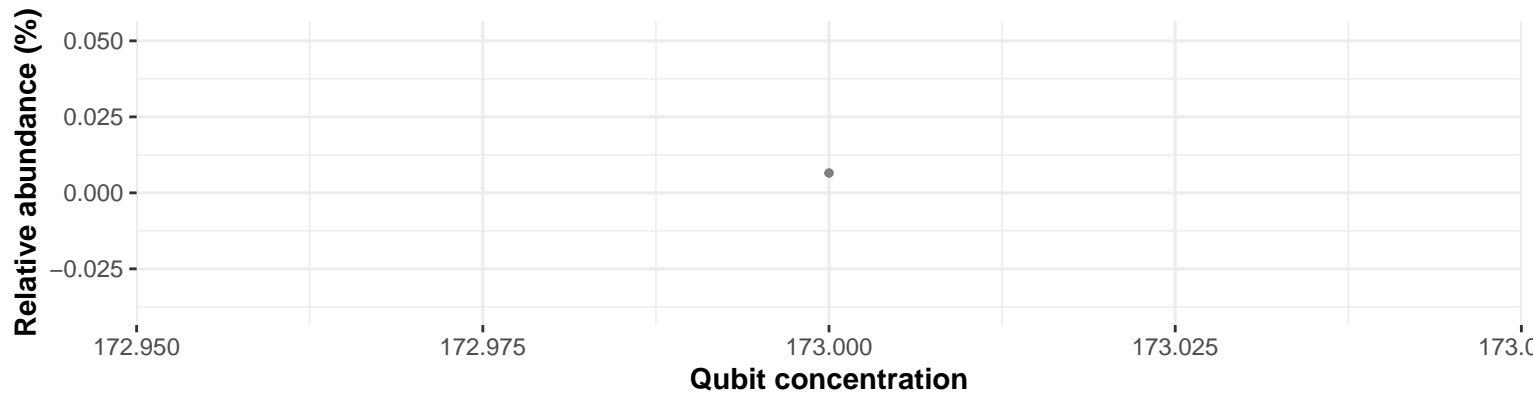


Correlation within: Digesta

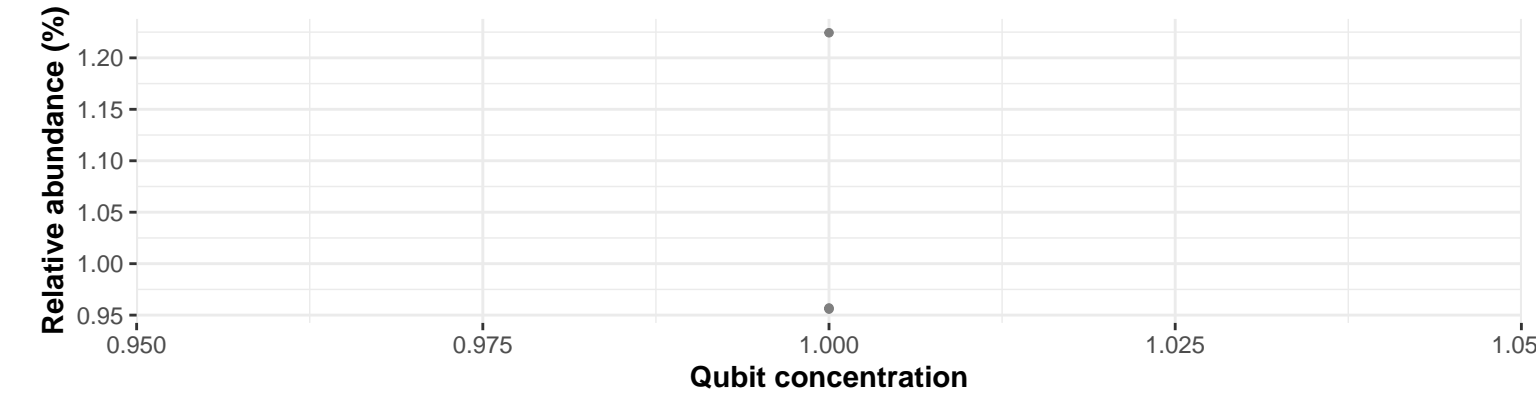
$\log_e(S) = 8.598$, $p = 0.076$, $\hat{\rho}_{\text{Spearman}} = -0.335$, $\text{CI}_{95\%} [-0.632, 0.047]$, $n_{\text{pairs}} = 29$



Correlation within: Feed



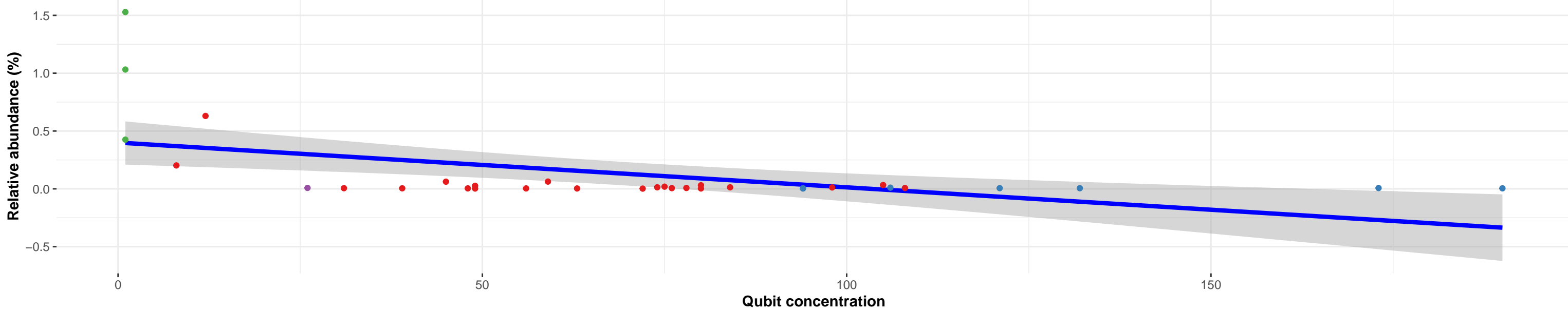
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Lactococcus; NA

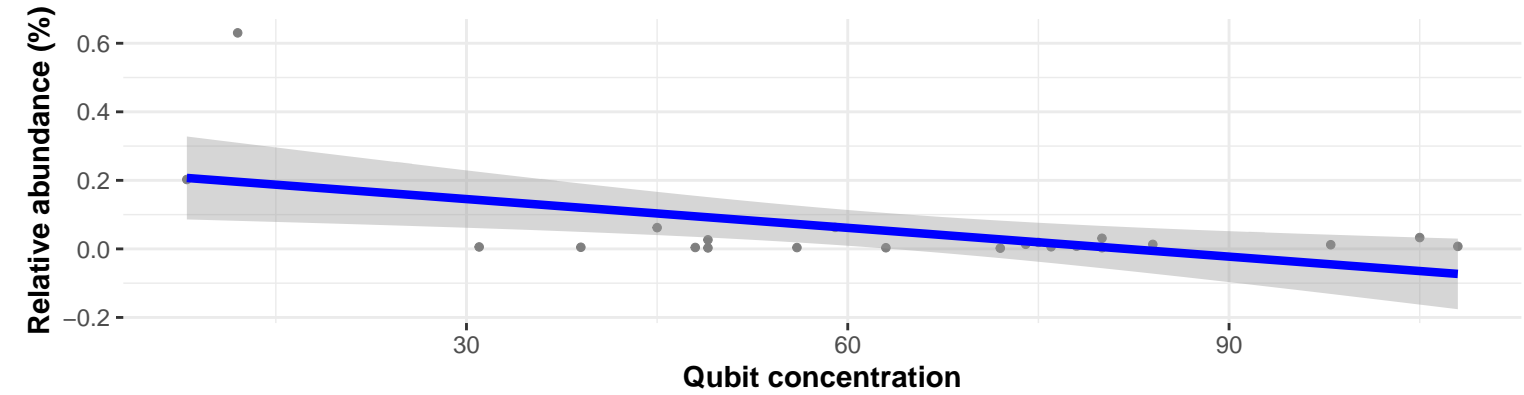
Correlation with all samples

$\log_e(S) = 9.016$, $p = 0.031$, $\hat{\rho}_{\text{Spearman}} = -0.375$, $\text{CI}_{95\%} [-0.643, -0.026]$, $n_{\text{pairs}} = 33$



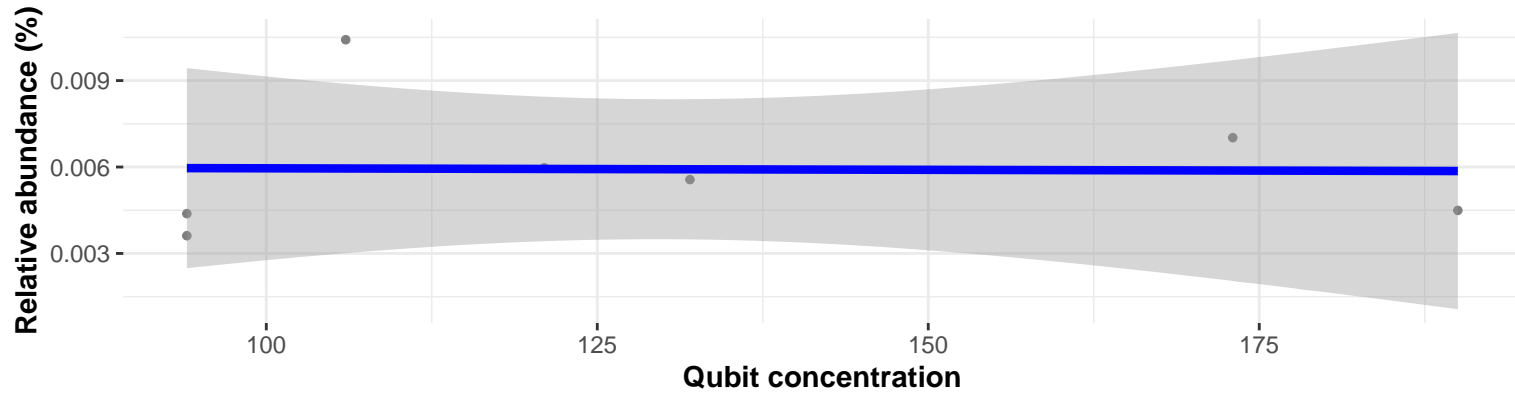
Correlation within: Digesta

$\log_e(S) = 7.574$, $p = 0.662$, $\hat{\rho}_{\text{Spearman}} = -0.099$, $\text{CI}_{95\%} [-0.510, 0.349]$, $n_{\text{pairs}} = 22$

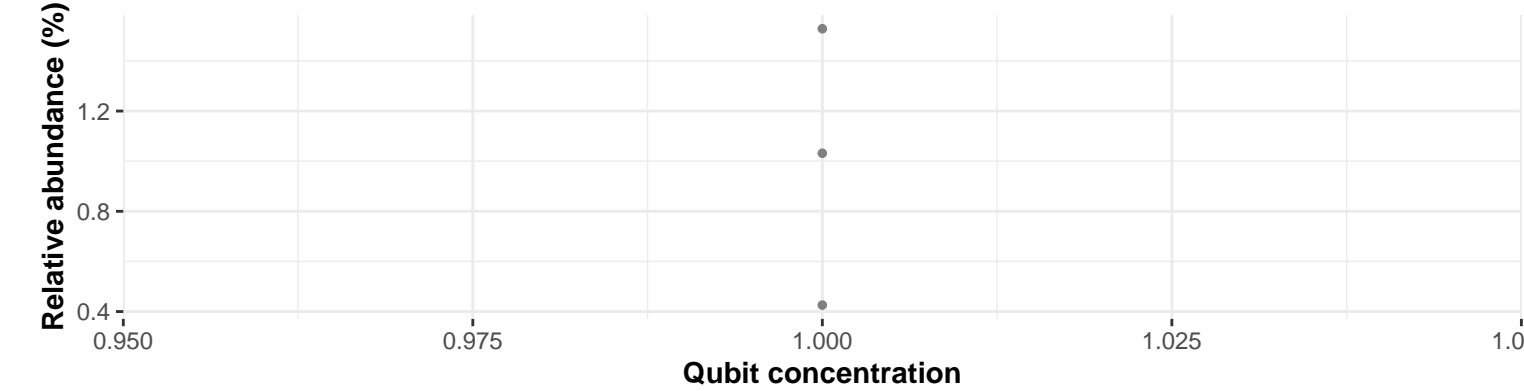


Correlation within: Feed

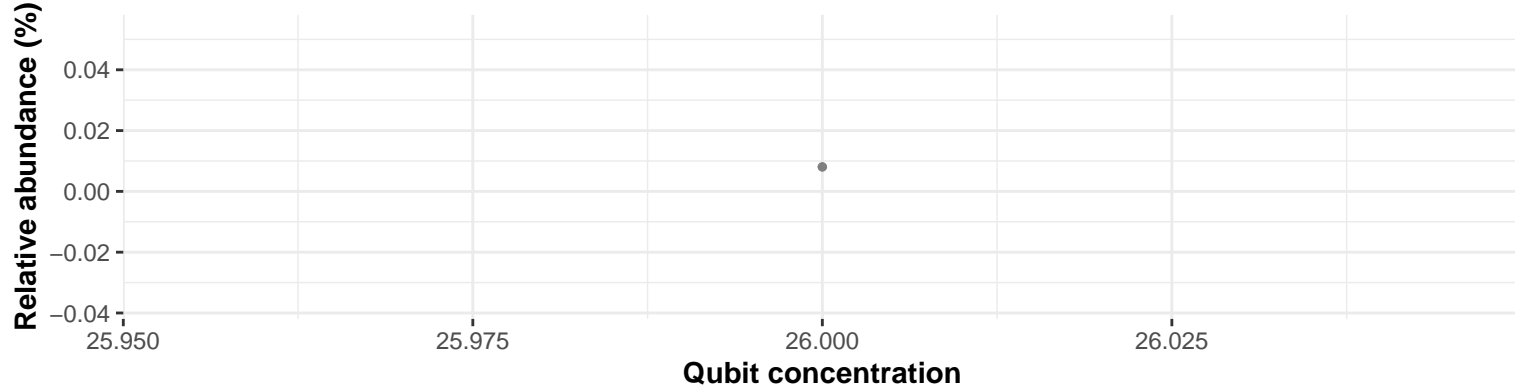
$\log_e(S) = 3.550$, $p = 0.403$, $\hat{\rho}_{\text{Spearman}} = 0.378$, $\text{CI}_{95\%} [-0.545, 0.887]$, $n_{\text{pairs}} = 7$



Correlation within: control



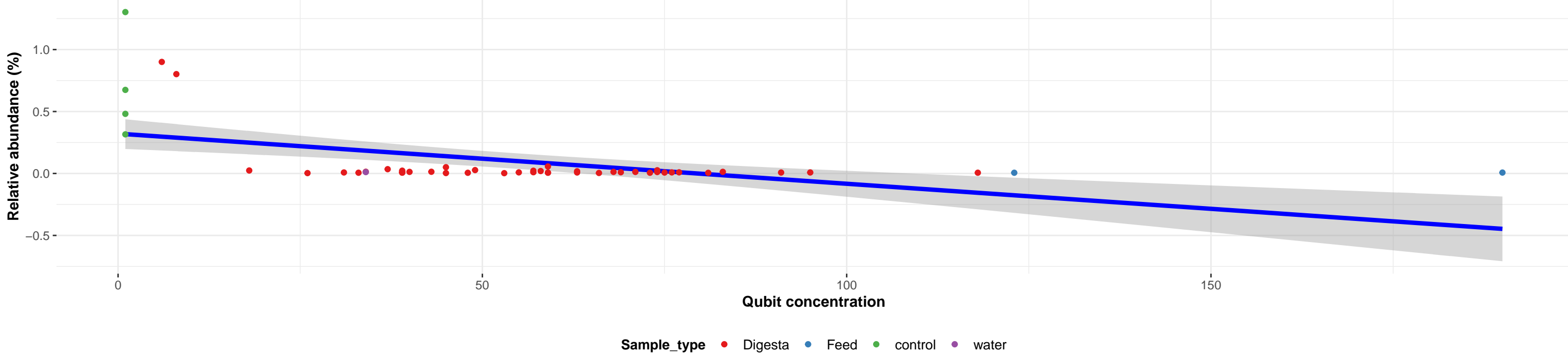
Correlation within: water



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; NA; NA

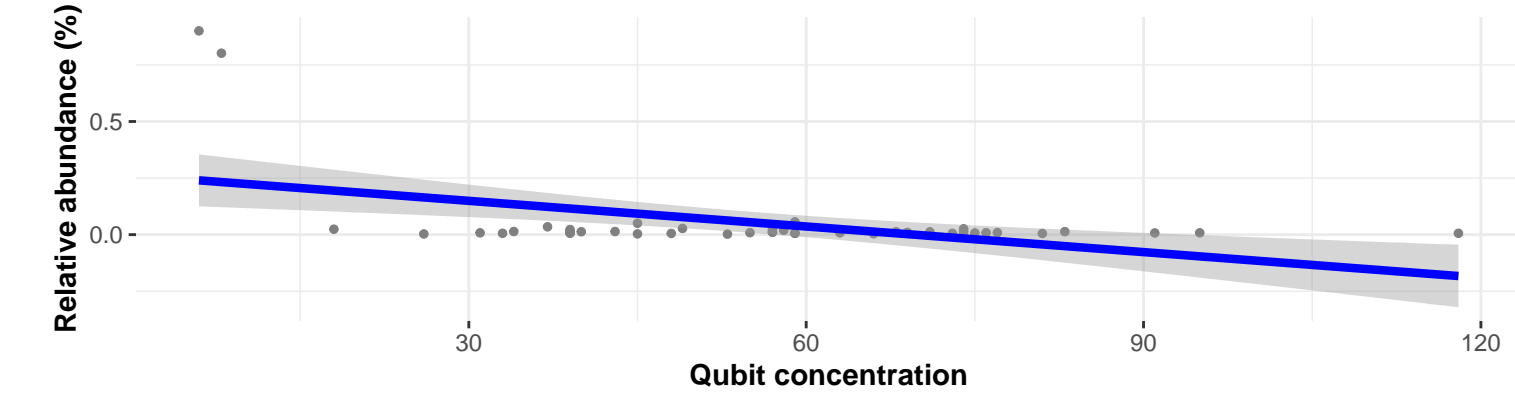
Correlation with all samples

$\log_e(S) = 10.417$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.427$, $\text{CI}_{95\%} [-0.632, -0.166]$, $n_{\text{pairs}} = 52$

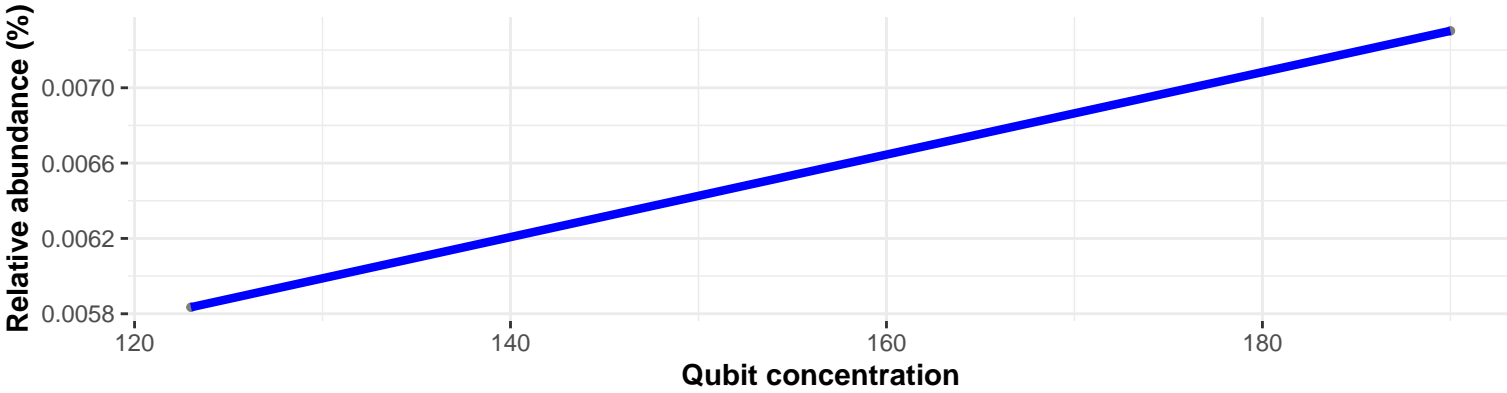


Correlation within: Digesta

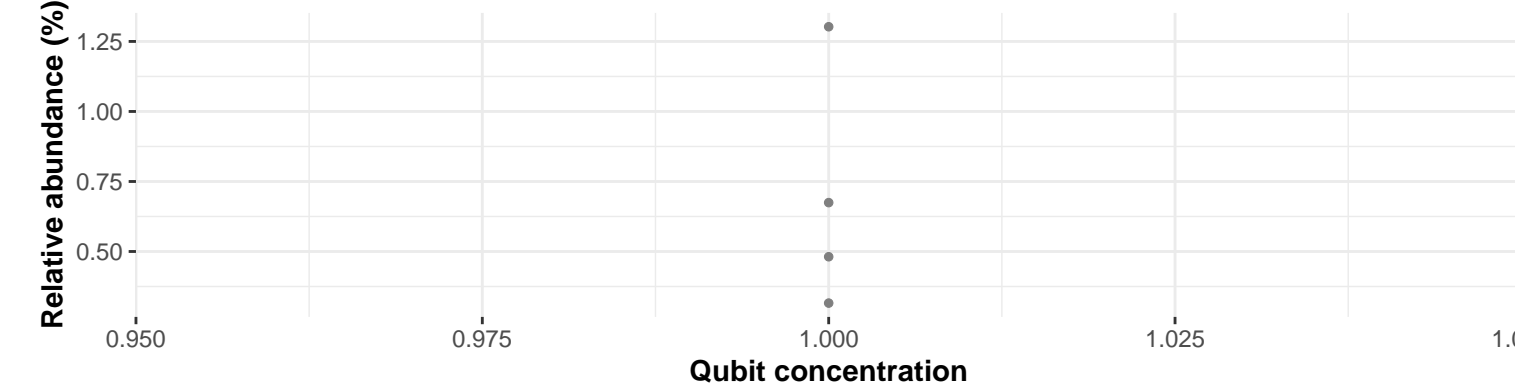
$\log_e(S) = 9.840$, $p = 0.117$, $\hat{\rho}_{\text{Spearman}} = -0.237$, $\text{CI}_{95\%} [-0.503, 0.070]$, $n_{\text{pairs}} = 45$



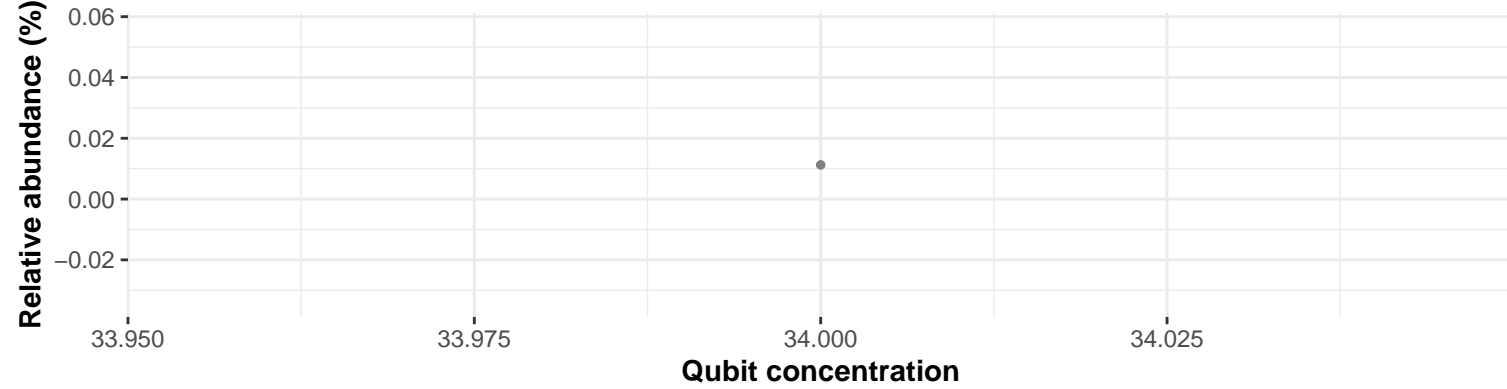
Correlation within: Feed



Correlation within: control



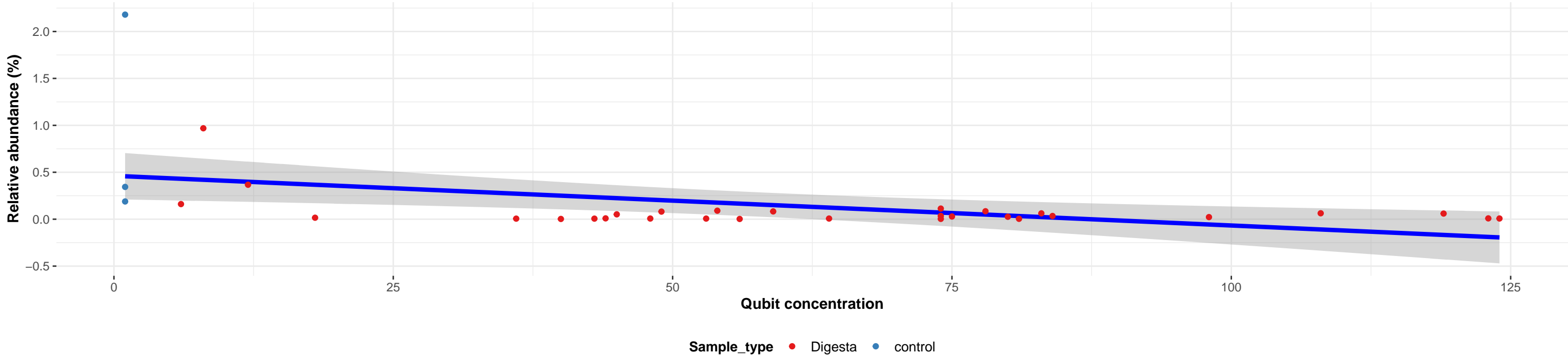
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; NA

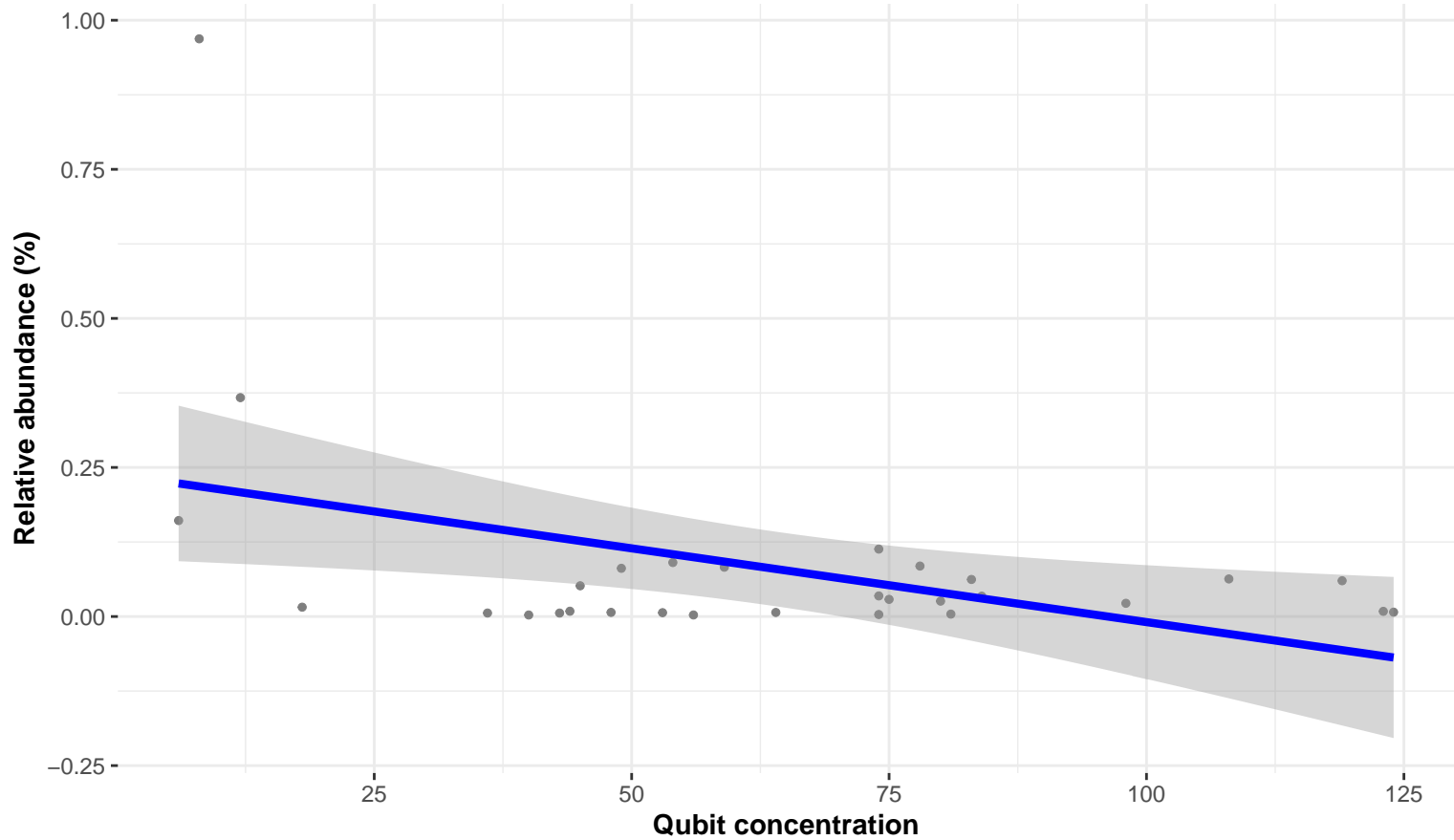
Correlation with all samples

$\log_e(S) = 8.958$, $p = 0.091$, $\hat{\rho}_{\text{Spearman}} = -0.299$, $\text{CI}_{95\%} [-0.589, 0.060]$, $n_{\text{pairs}} = 33$

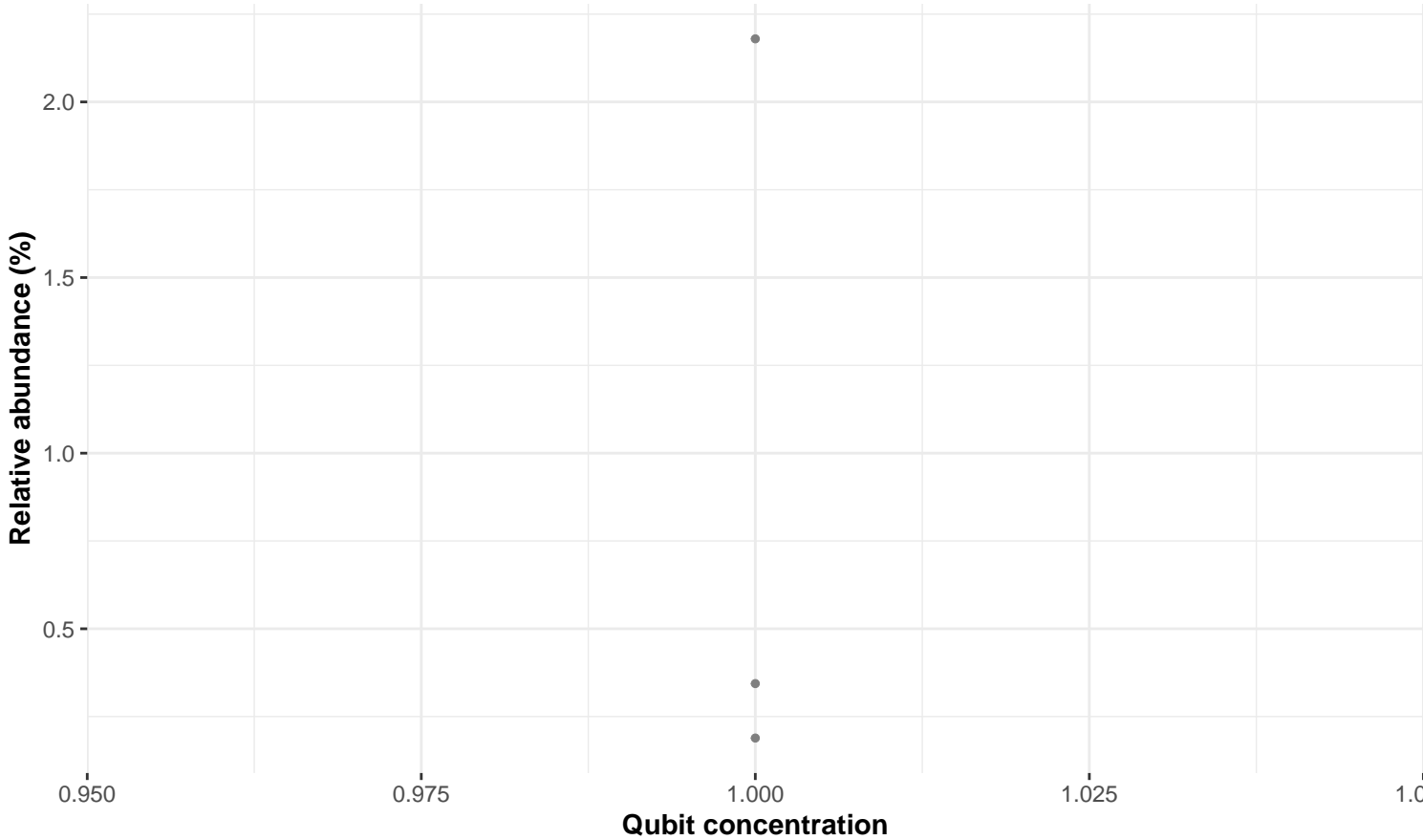


Correlation within: Digesta

$\log_e(S) = 8.481$, $p = 0.701$, $\hat{\rho}_{\text{Spearman}} = -0.073$, $\text{CI}_{95\%} [-0.431, 0.305]$, $n_{\text{pairs}} = 30$



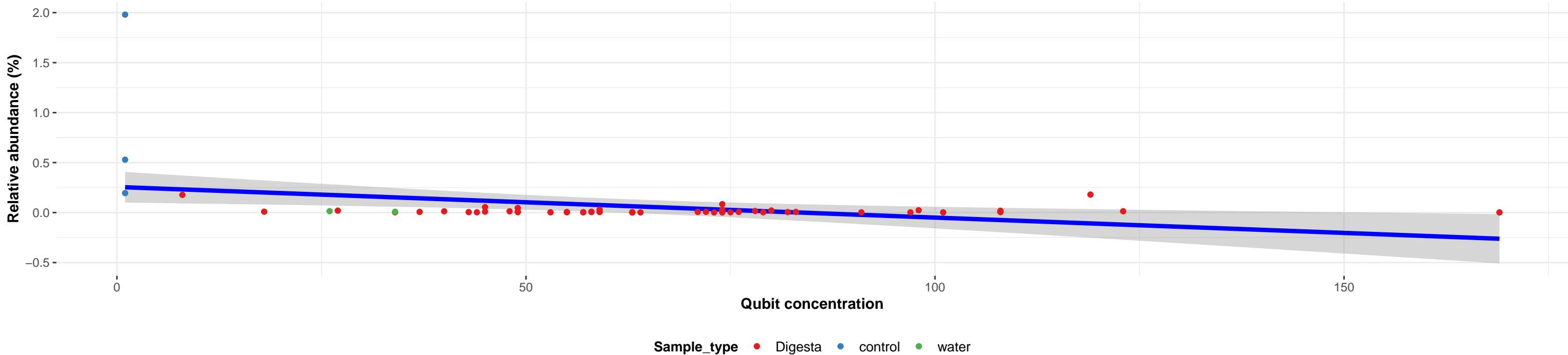
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA

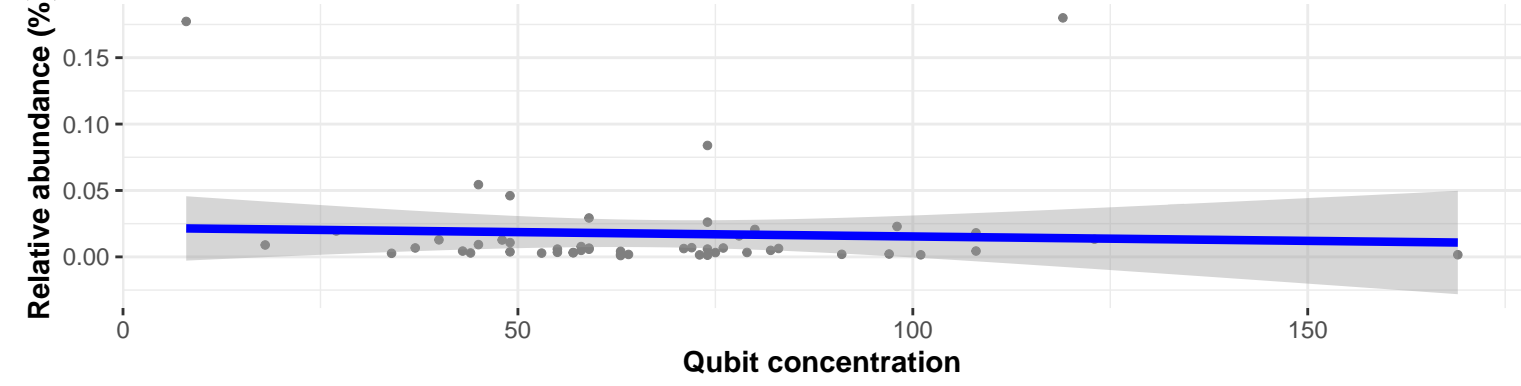
Correlation with all samples

$\log_e(S) = 10.535$, $p = 0.033$, $\hat{\rho}_{\text{Spearman}} = -0.285$, $\text{CI}_{95\%} [-0.515, -0.016]$, $n_{\text{pairs}} = 56$

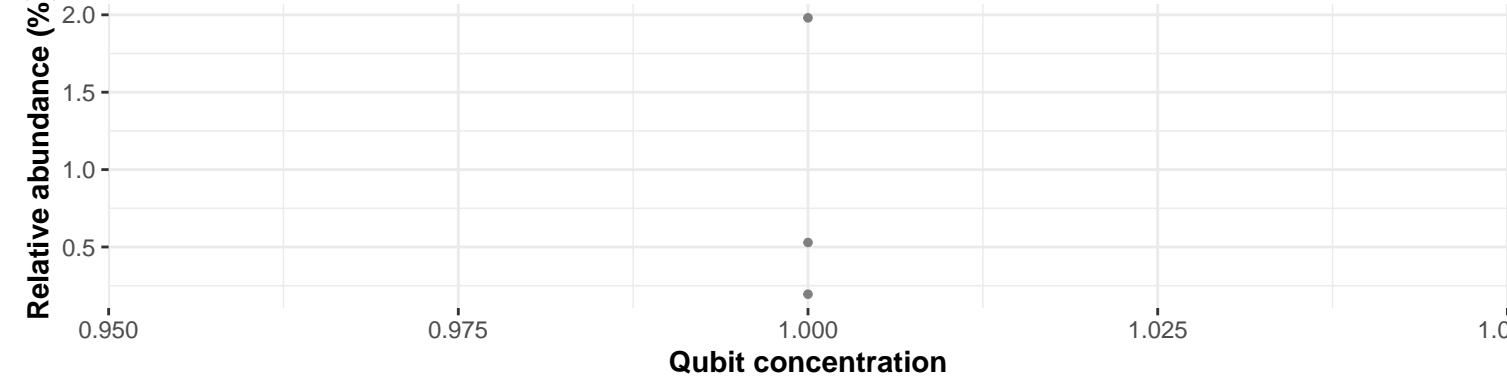


Correlation within: Digesta

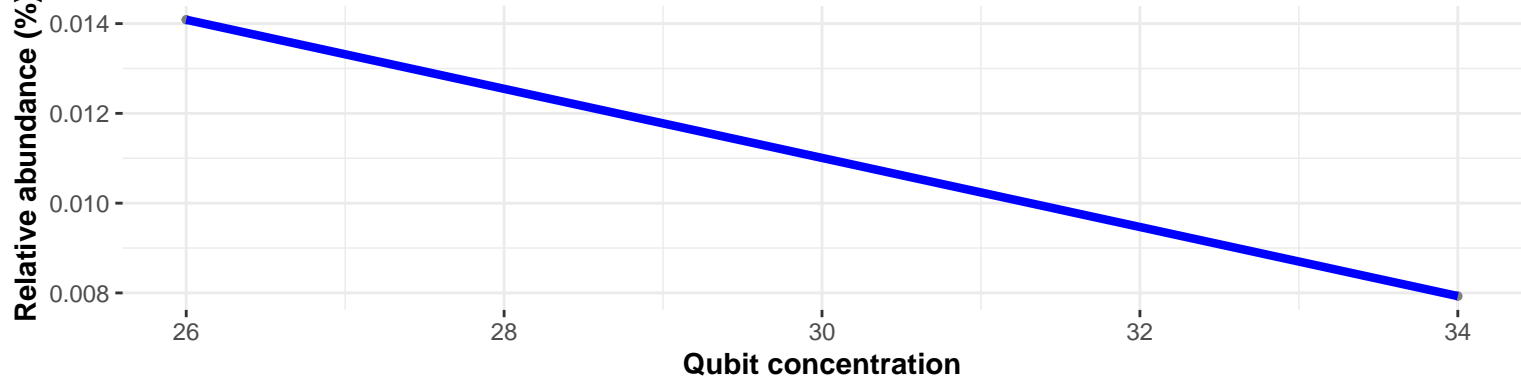
$\log_e(S) = 10.118$, $p = 0.396$, $\hat{\rho}_{\text{Spearman}} = -0.121$, $\text{CI}_{95\%} [-0.391, 0.168]$, $n_{\text{pairs}} = 51$



Correlation within: control



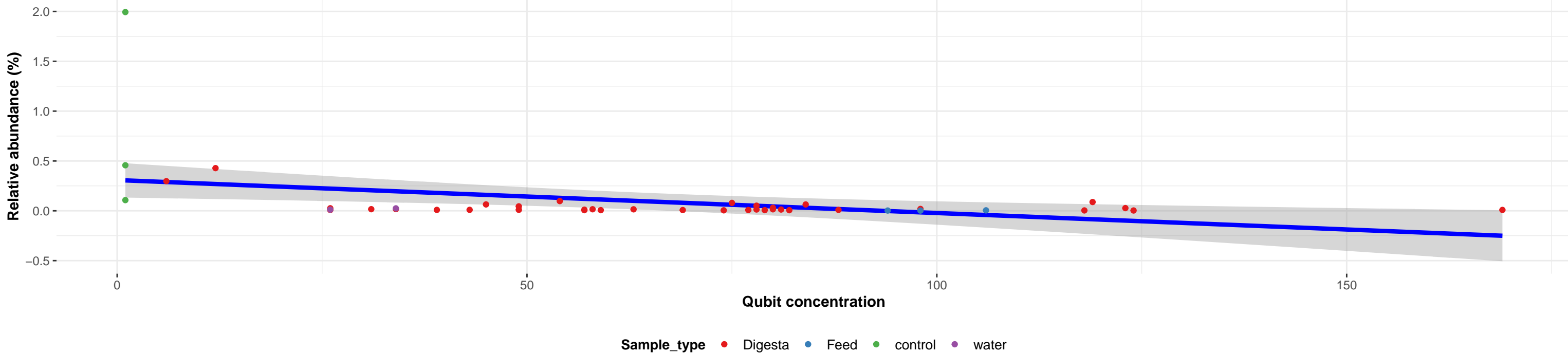
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Halomonadaceae; Halomonas; NA

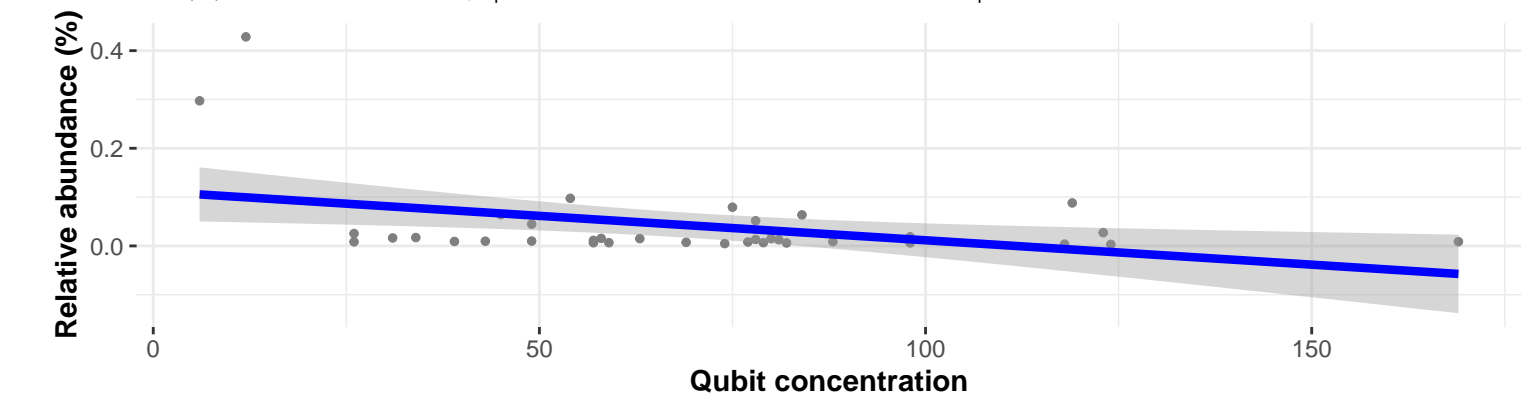
Correlation with all samples

$\log_e(S) = 10.033$, $p = 4.85e-04$, $\hat{\rho}_{\text{Spearman}} = -0.499$, $CI_{95\%} [-0.696, -0.232]$, $n_{\text{pairs}} = 45$

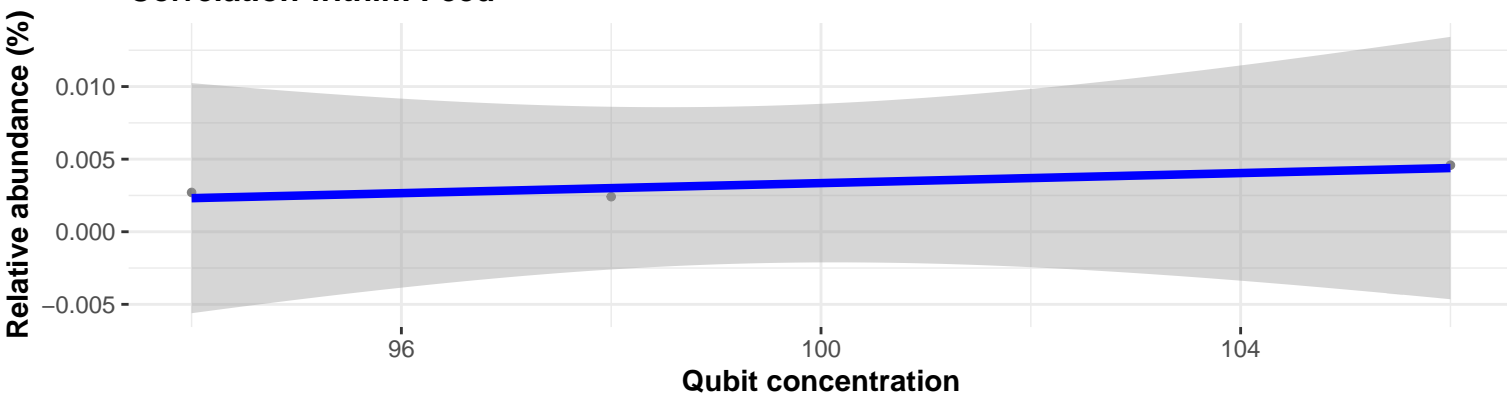


Correlation within: Digesta

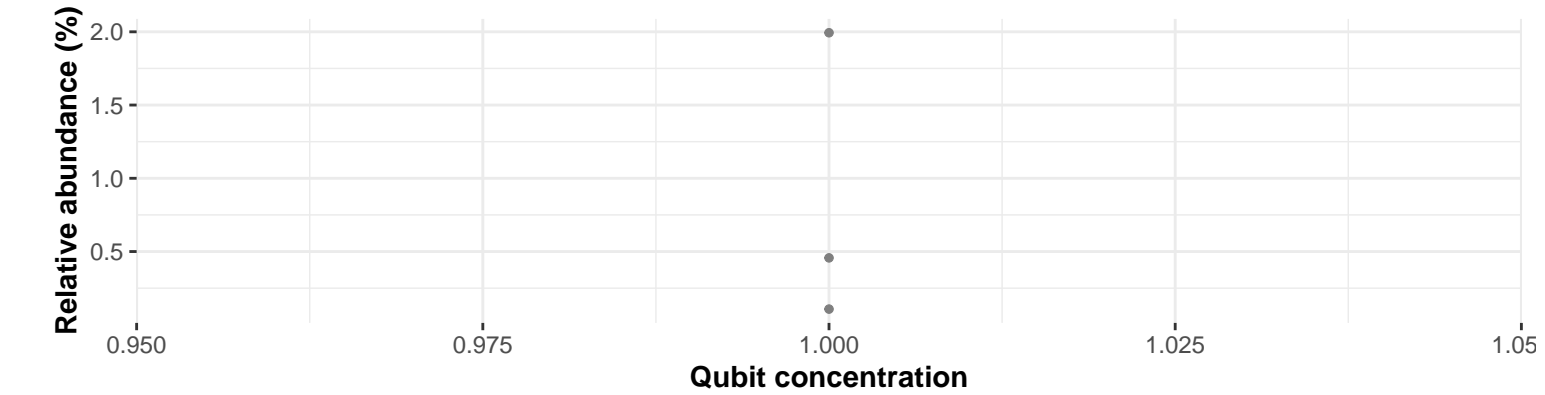
$\log_e(S) = 9.301$, $p = 0.073$, $\hat{\rho}_{\text{Spearman}} = -0.298$, $CI_{95\%} [-0.574, 0.039]$, $n_{\text{pairs}} = 37$



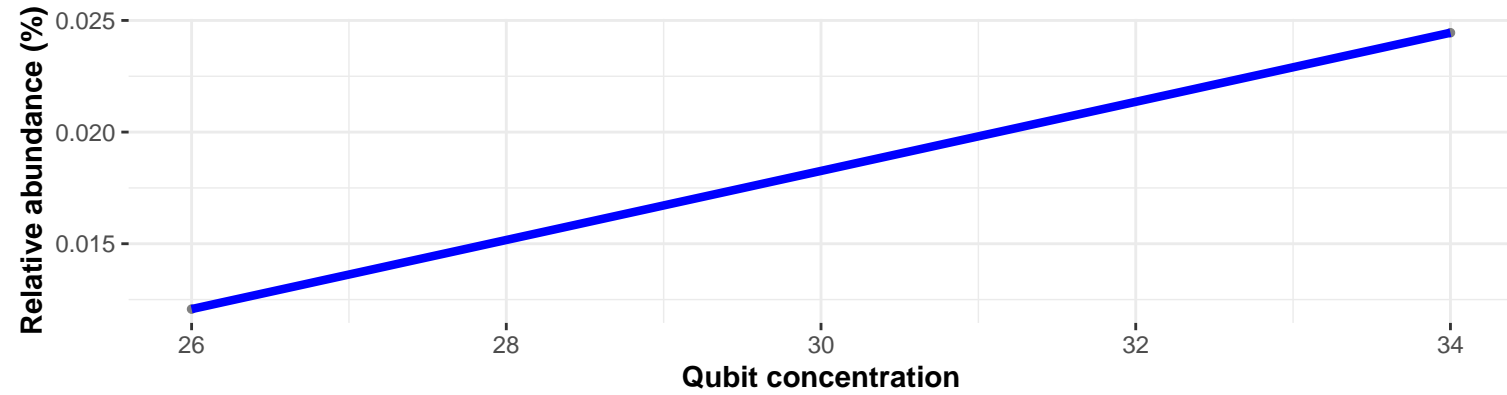
Correlation within: Feed



Correlation within: control



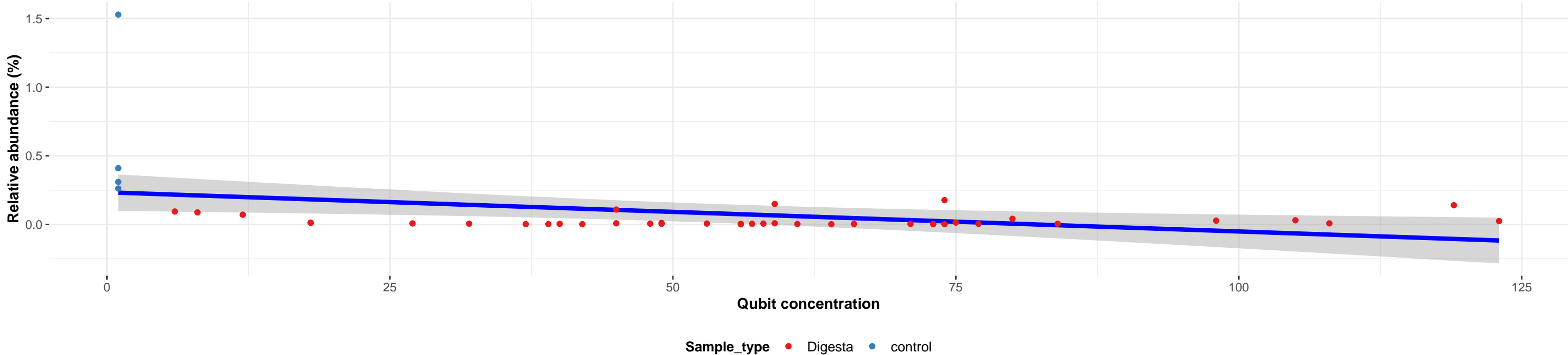
Correlation within: water



Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA

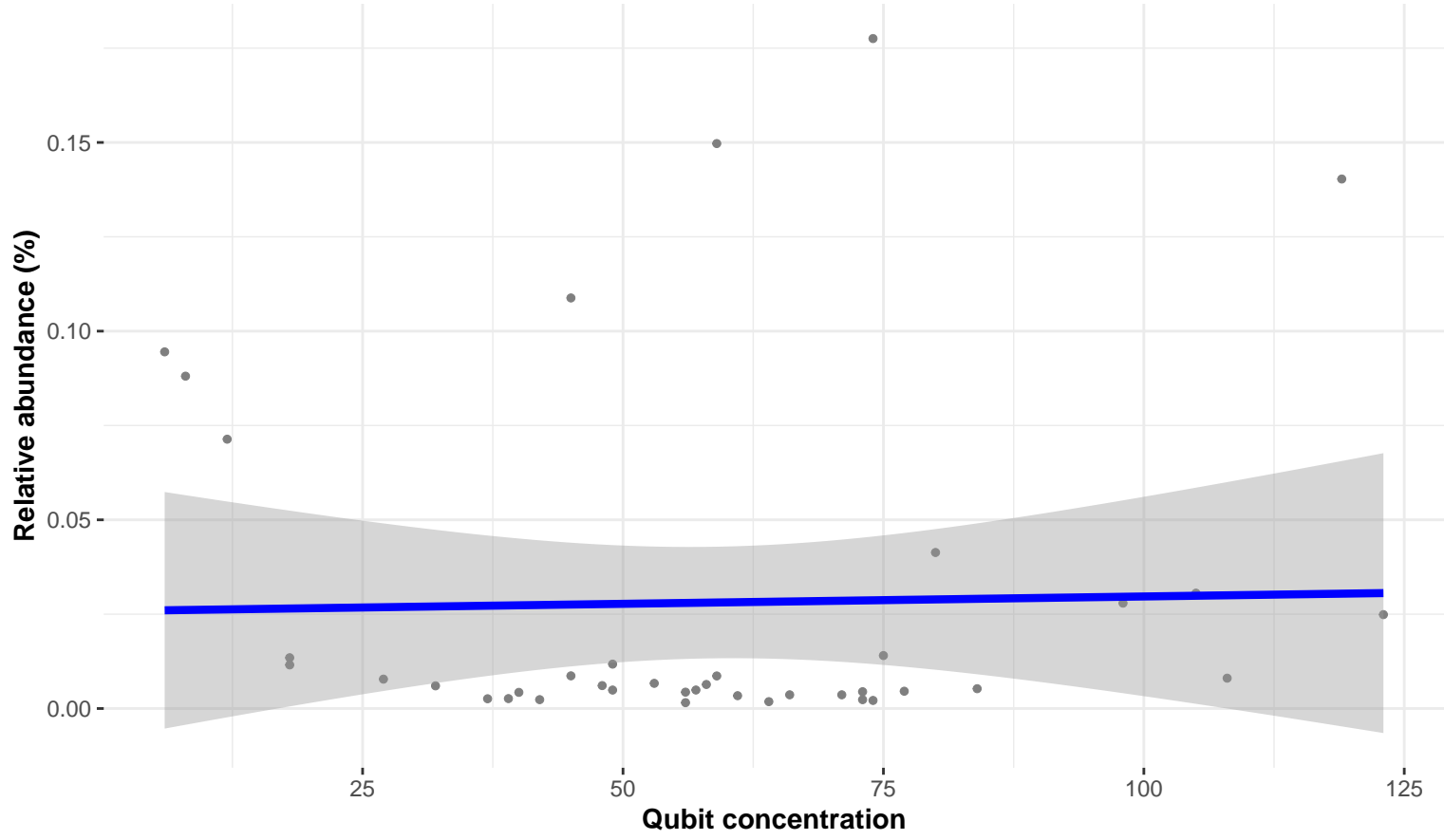
Correlation with all samples

$\log_e(S) = 9.768$, $p = 0.132$, $\hat{\rho}_{\text{Spearman}} = -0.230$, $\text{CI}_{95\%} [-0.500, 0.080]$, $n_{\text{pairs}} = 44$

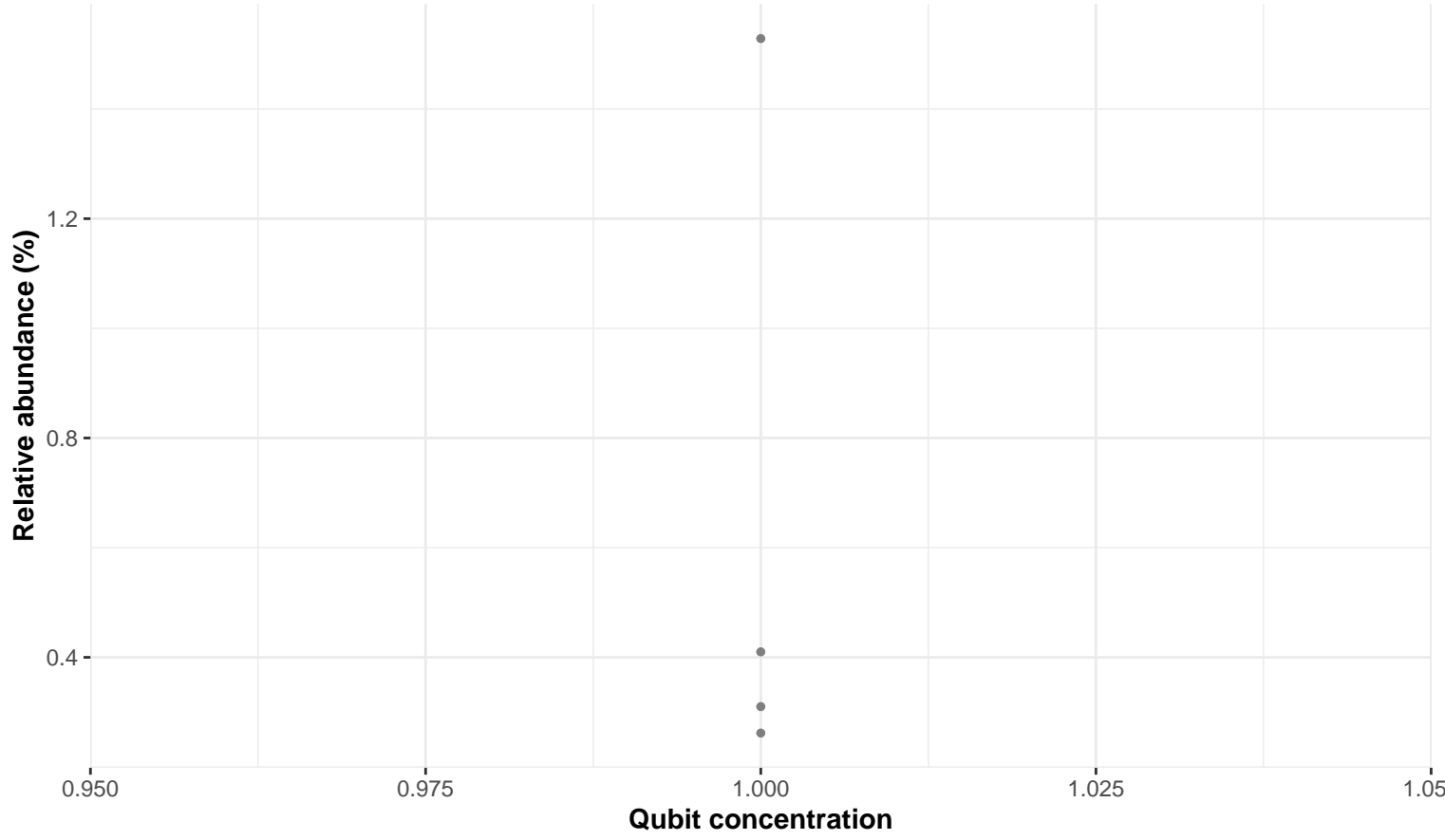


Correlation within: Digesta

$\log_e(S) = 9.250$, $p = 0.885$, $\hat{\rho}_{\text{Spearman}} = 0.024$, $\text{CI}_{95\%} [-0.299, 0.341]$, $n_{\text{pairs}} = 40$



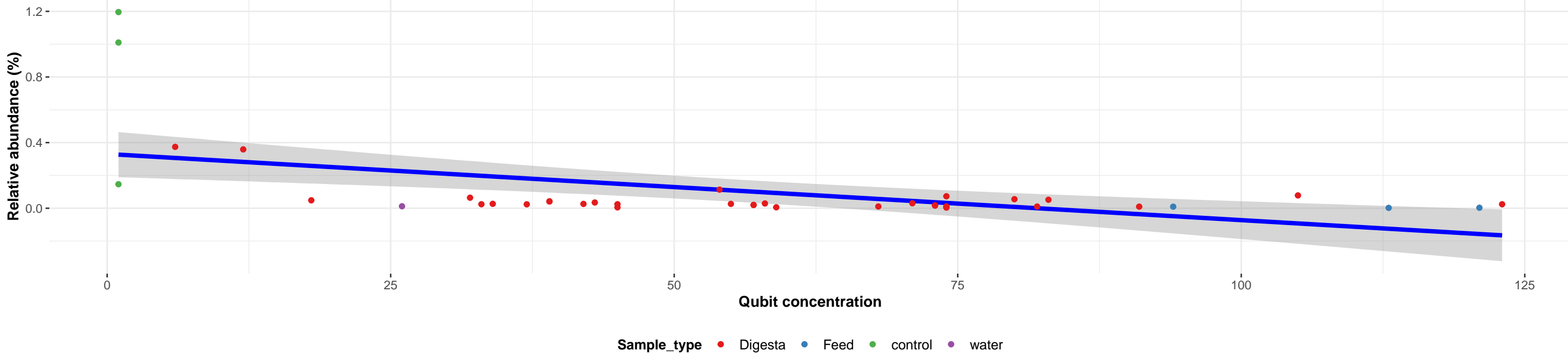
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

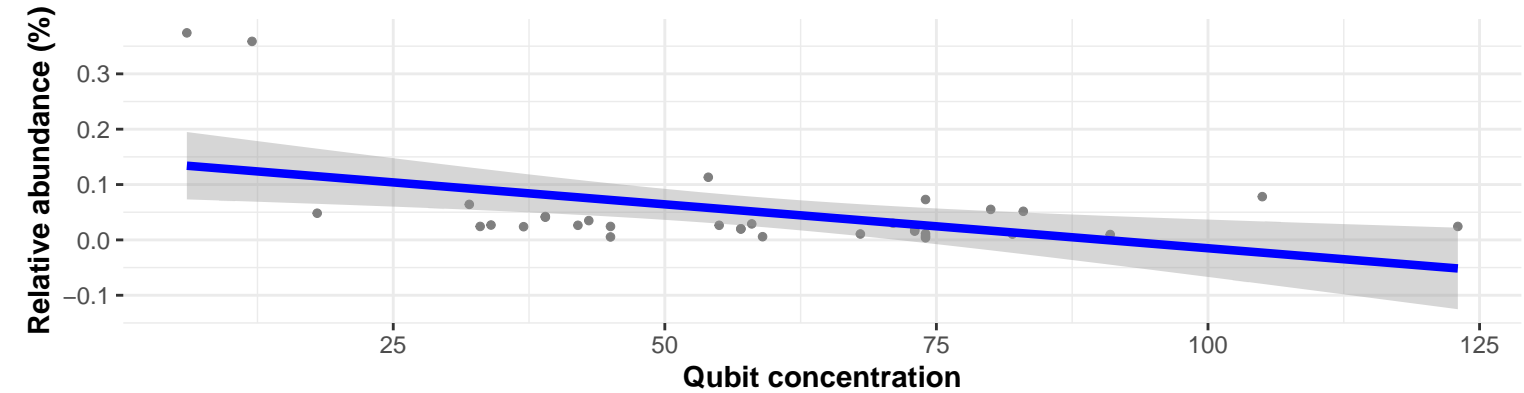
Correlation with all samples

$\log_e(S) = 9.715$, $p = 2.06e-04$, $\hat{\rho}_{\text{Spearman}} = -0.554$, $CI_{95\%} [-0.743, -0.285]$, $n_{\text{pairs}} = 40$

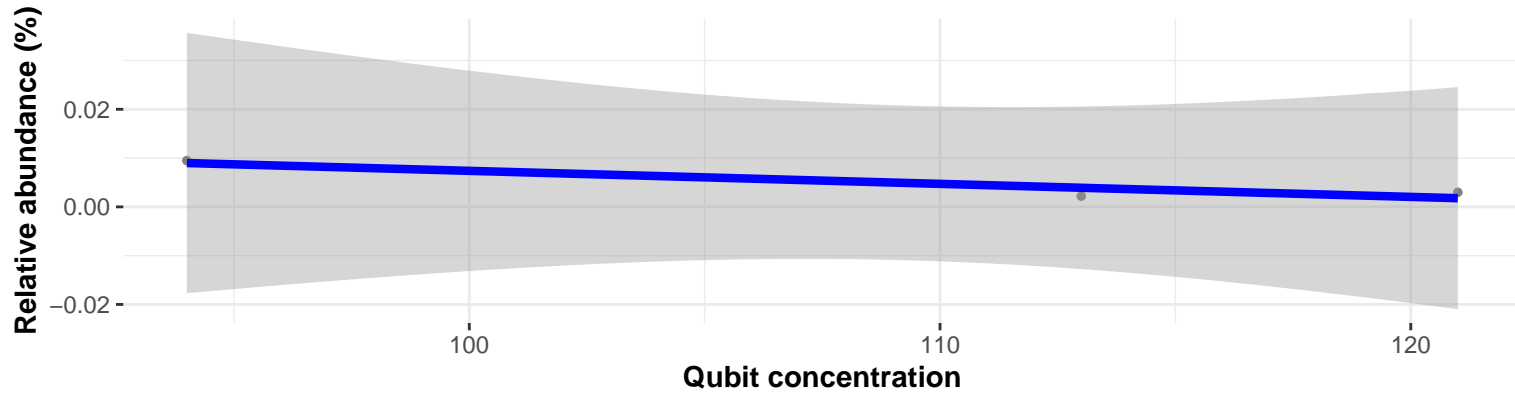


Correlation within: Digesta

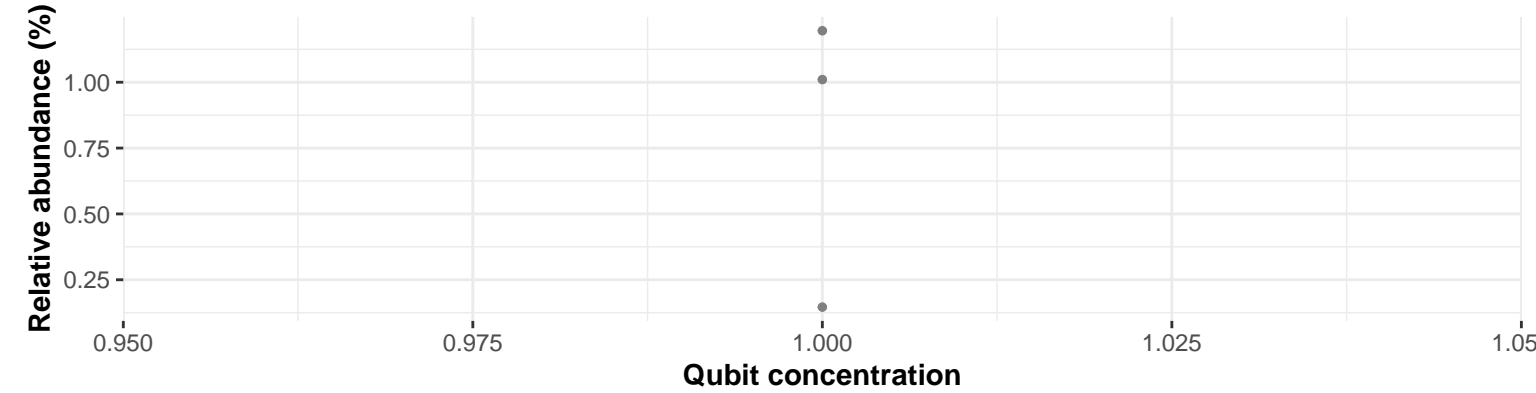
$\log_e(S) = 9.000$, $p = 0.044$, $\hat{\rho}_{\text{Spearman}} = -0.354$, $CI_{95\%} [-0.628, -0.001]$, $n_{\text{pairs}} = 33$



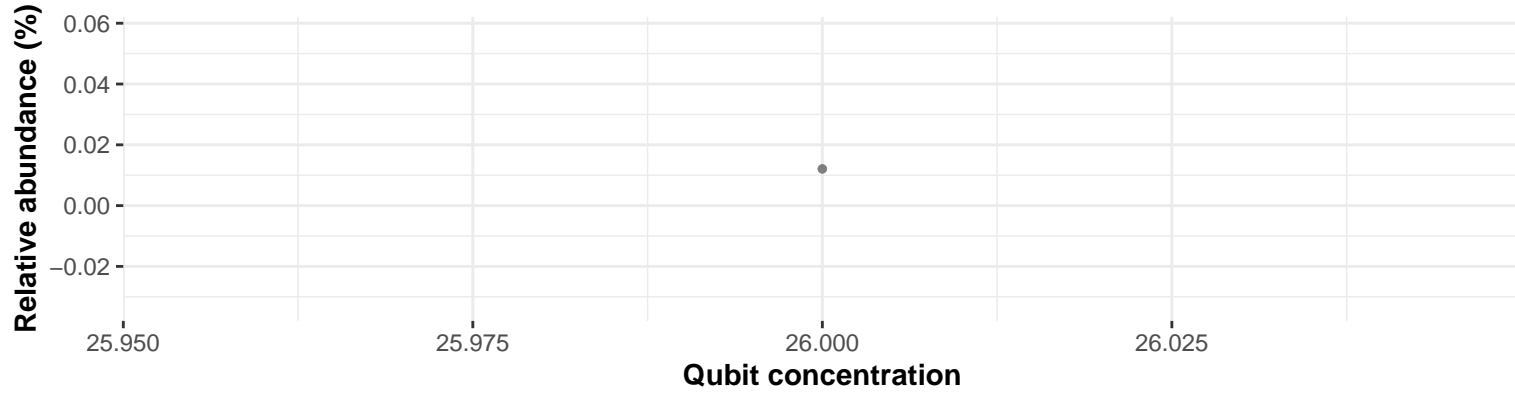
Correlation within: Feed



Correlation within: control



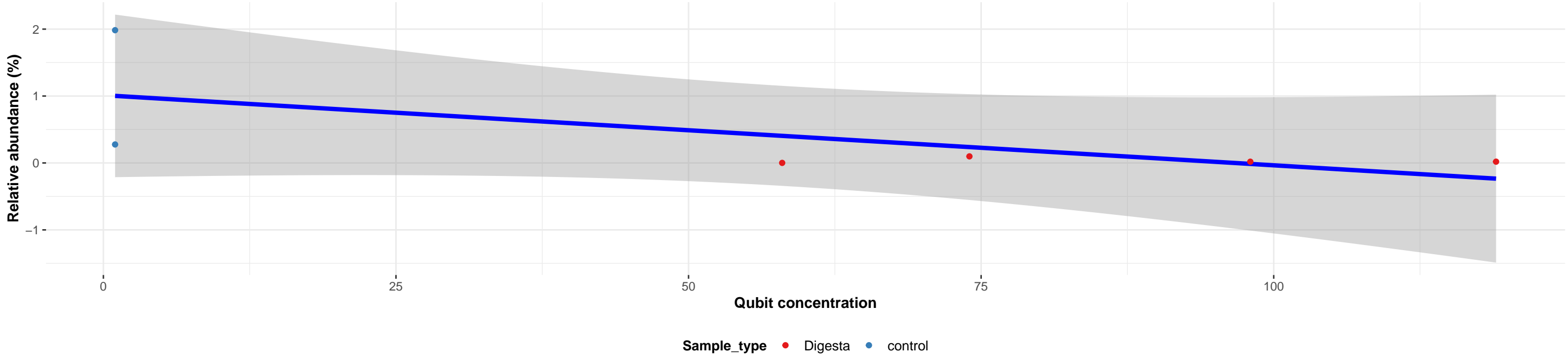
Correlation within: water



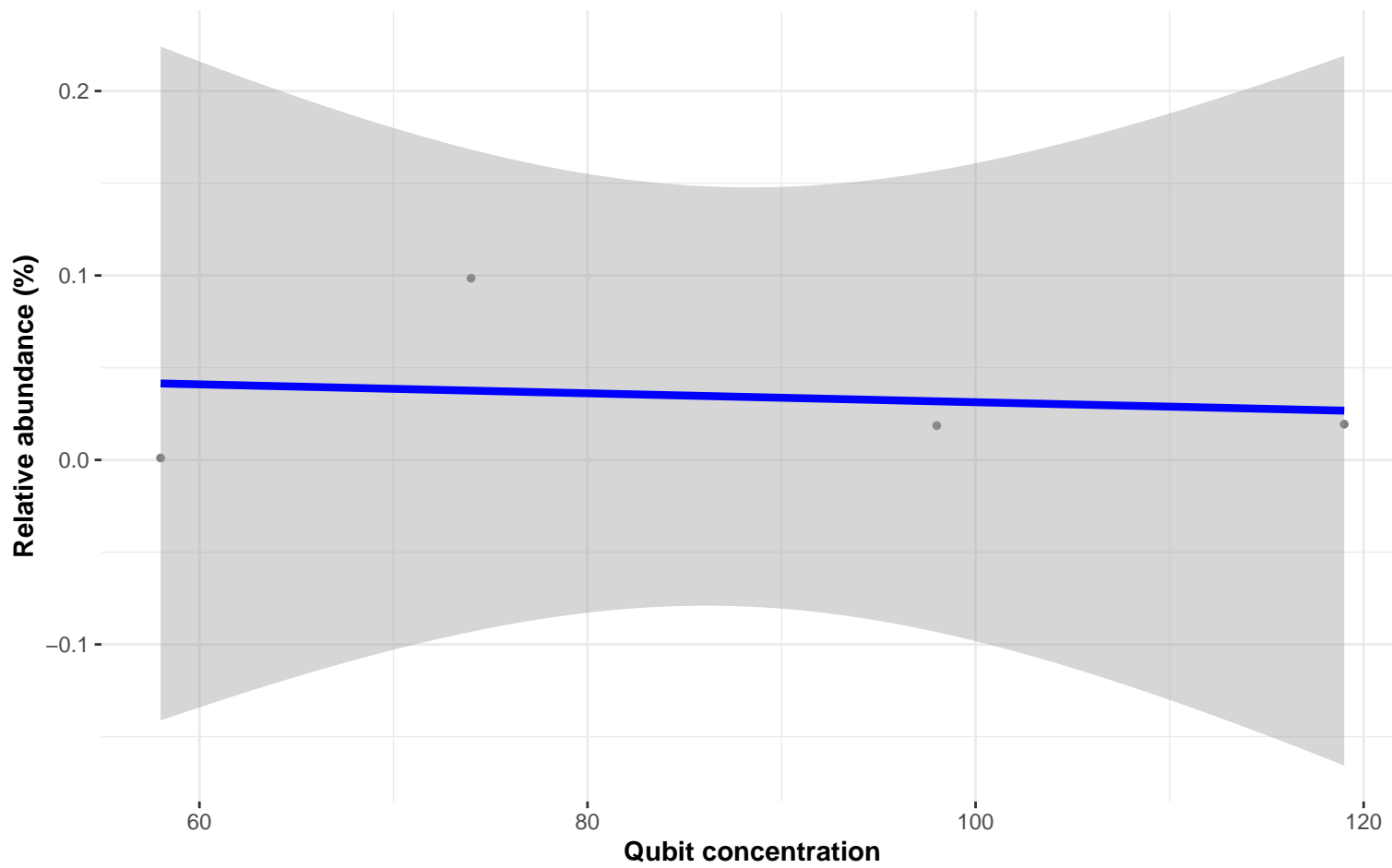
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Enhydrobacter; NA

Correlation with all samples

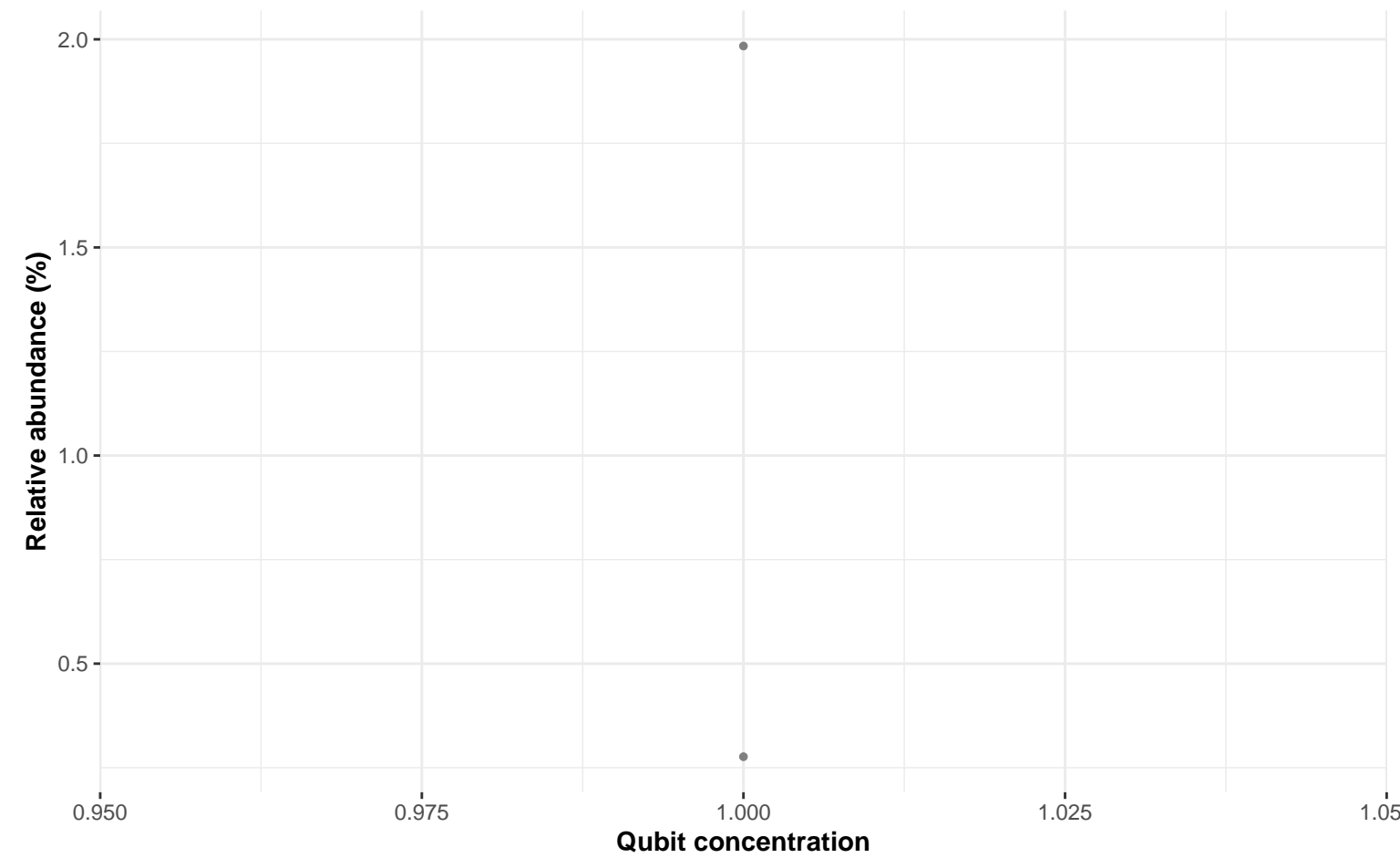
$\log_e(S) = 4.013$, $p = 0.228$, $\hat{\rho}_{\text{Spearman}} = -0.580$, $CI_{95\%} [-0.950, 0.464]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



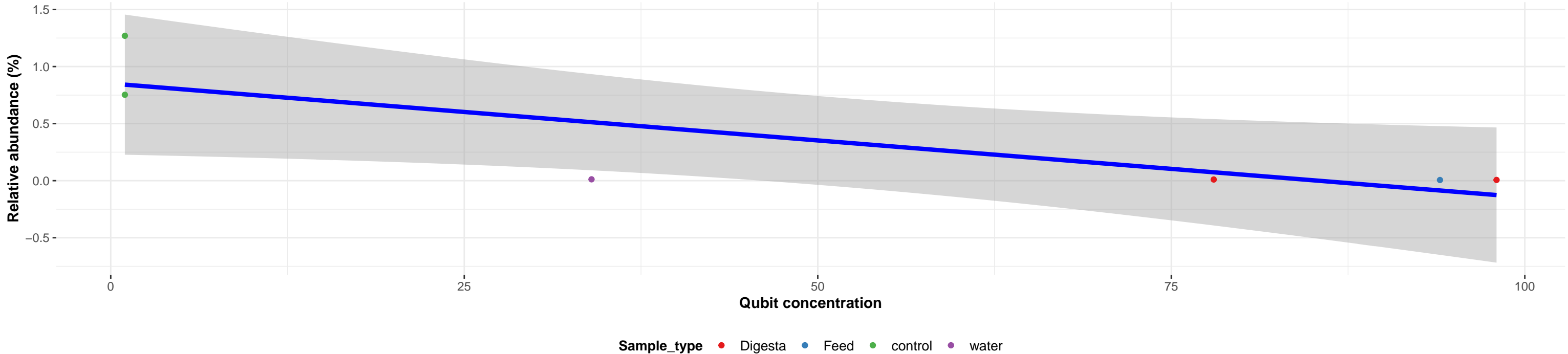
Correlation within: control



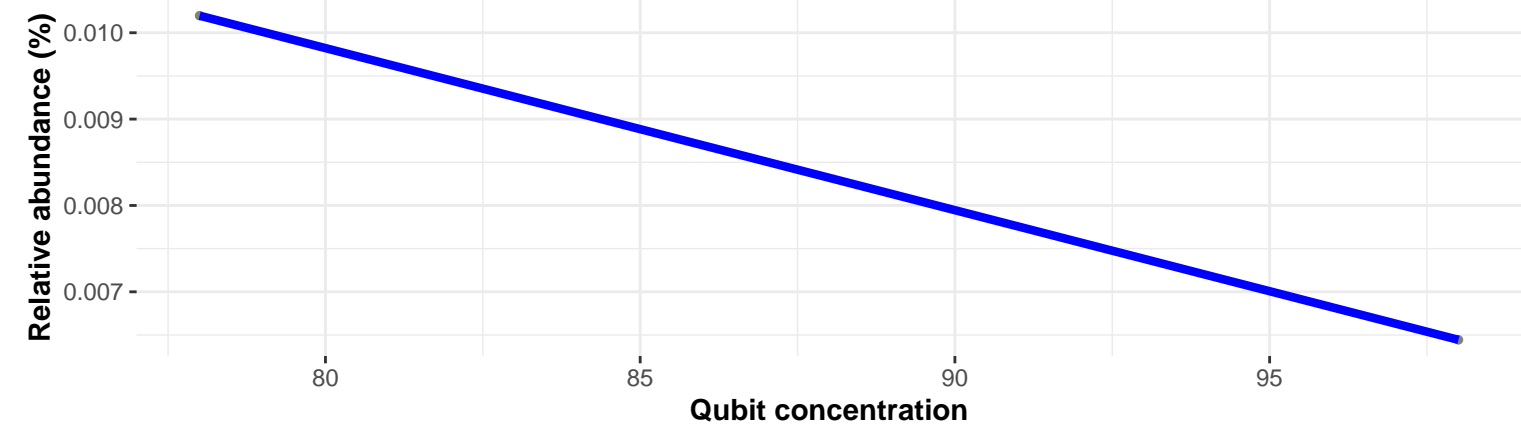
Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Acidovorax; NA

Correlation with all samples

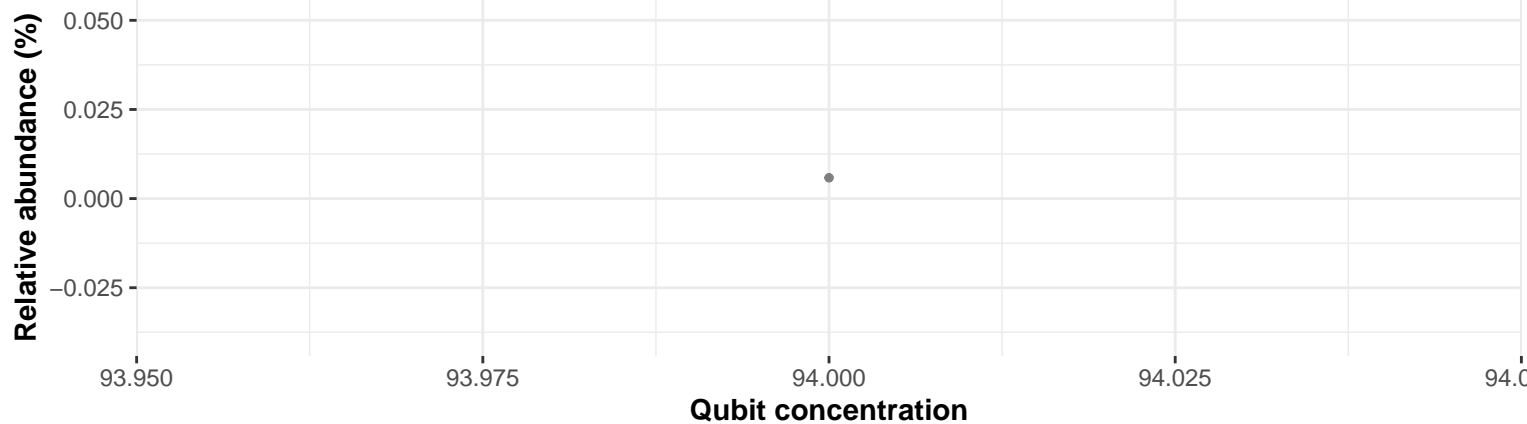
$\log_e(S) = 4.212$, $p = 0.008$, $\hat{\rho}_{\text{Spearman}} = -0.928$, $CI_{95\%} [-0.993, -0.443]$, $n_{\text{pairs}} = 6$



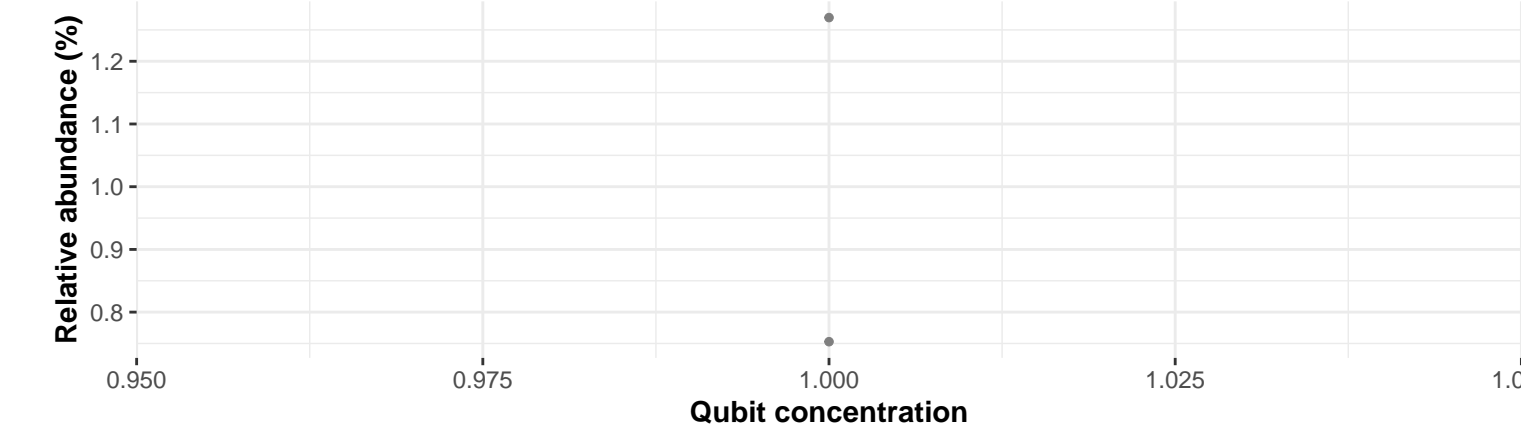
Correlation within: Digesta



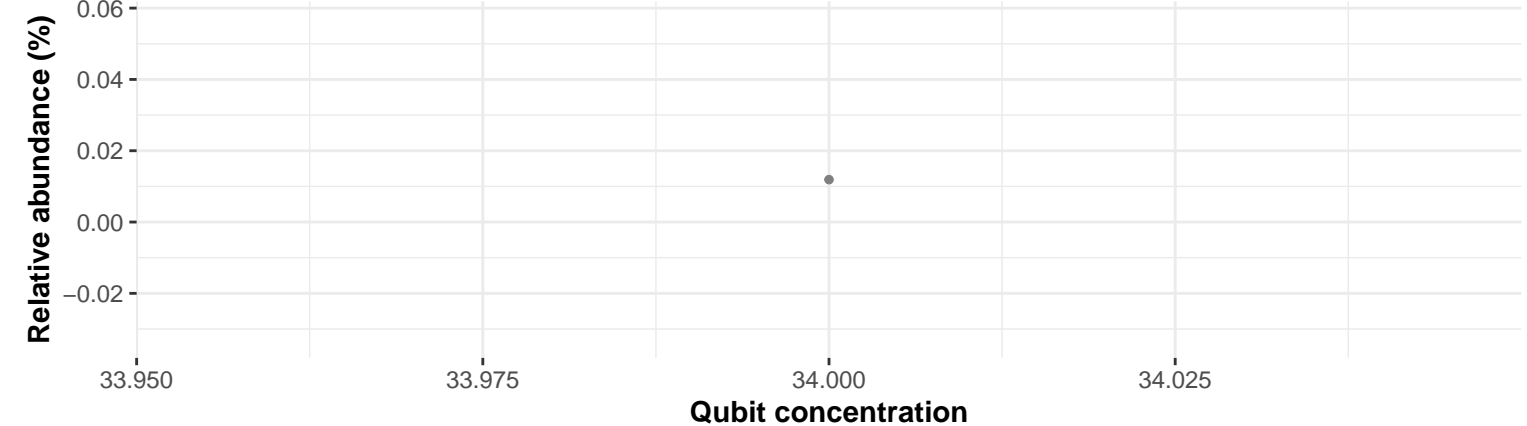
Correlation within: Feed



Correlation within: control



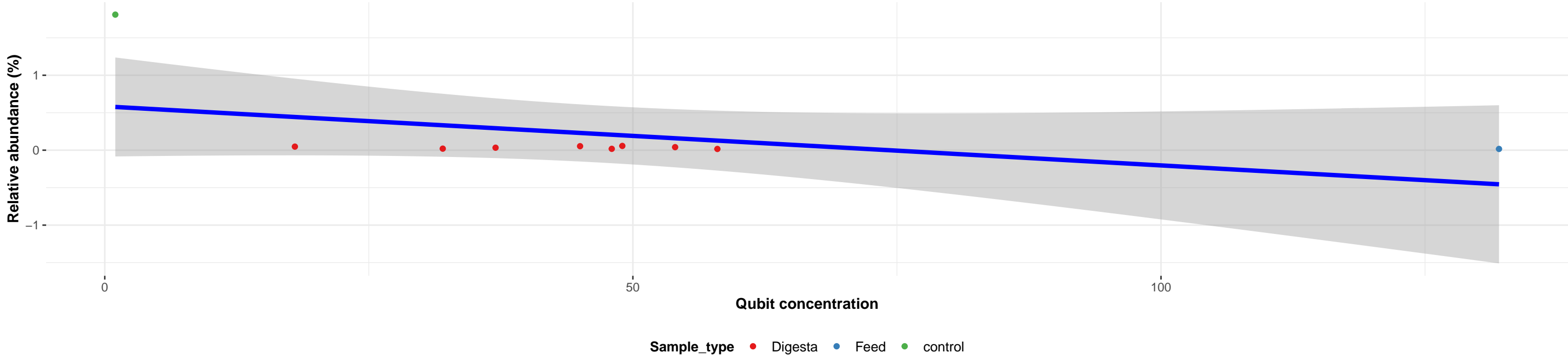
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces; NA

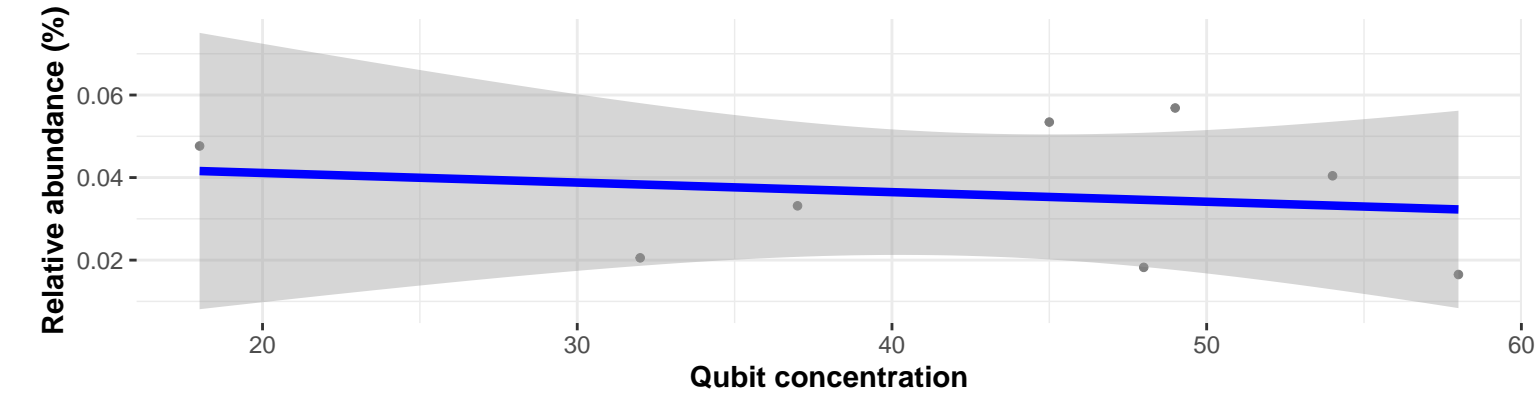
Correlation with all samples

$\log_e(S) = 5.568$, $p = 0.074$, $\hat{\rho}_{\text{Spearman}} = -0.588$, $CI_{95\%} [-0.893, 0.088]$, $n_{\text{pairs}} = 10$

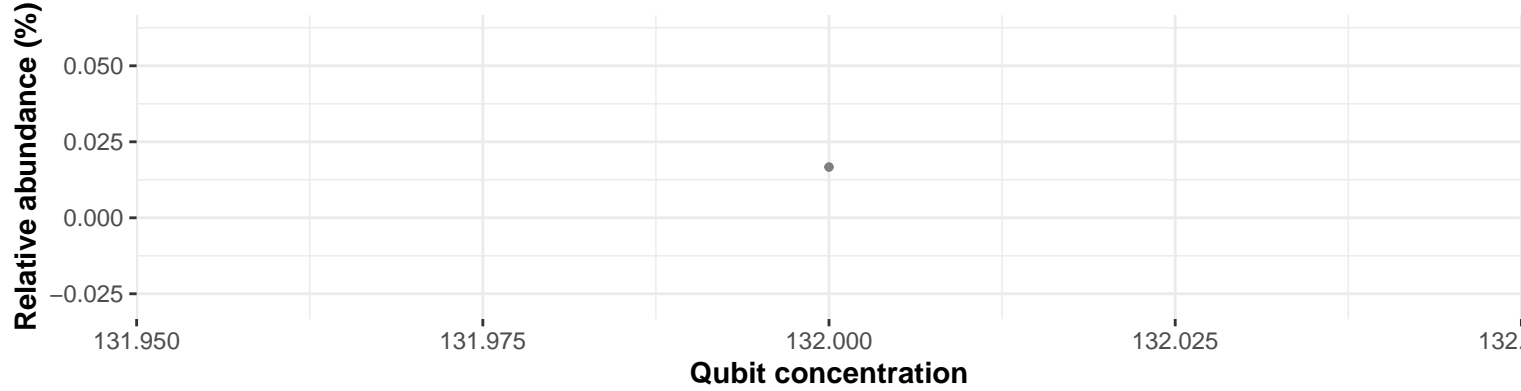


Correlation within: Digesta

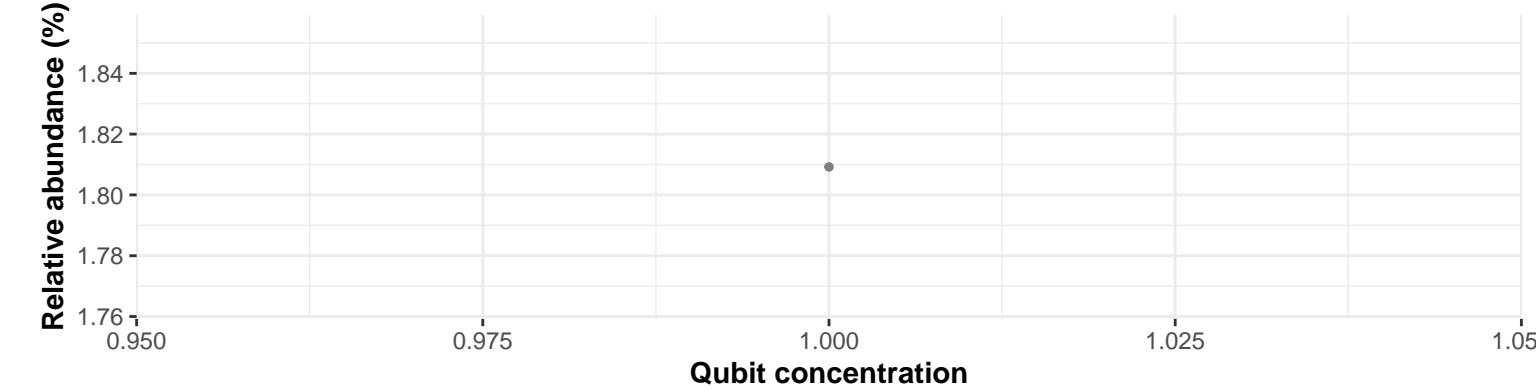
$\log_e(S) = 4.625$, $p = 0.610$, $\hat{\rho}_{\text{Spearman}} = -0.214$, $CI_{95\%} [-0.808, 0.595]$, $n_{\text{pairs}} = 8$



Correlation within: Feed



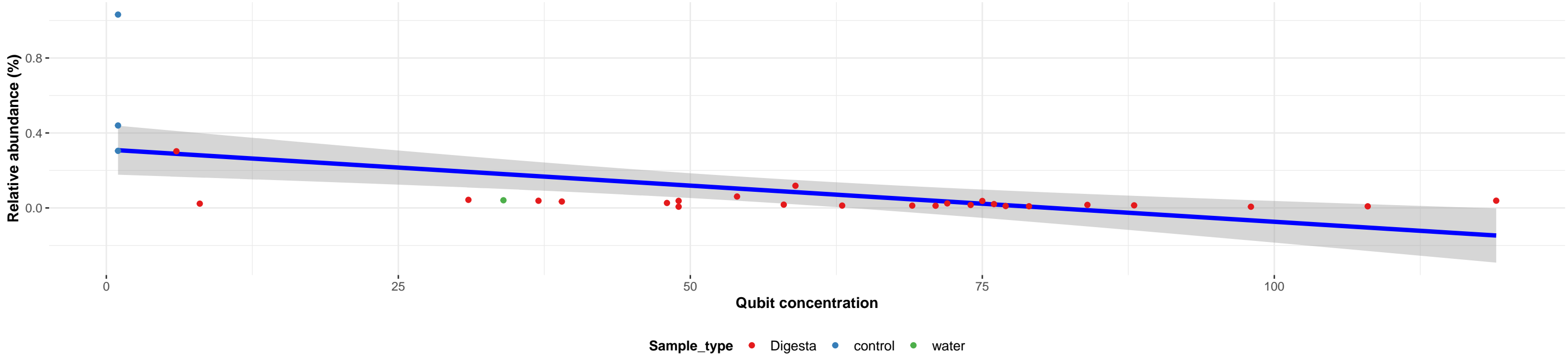
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

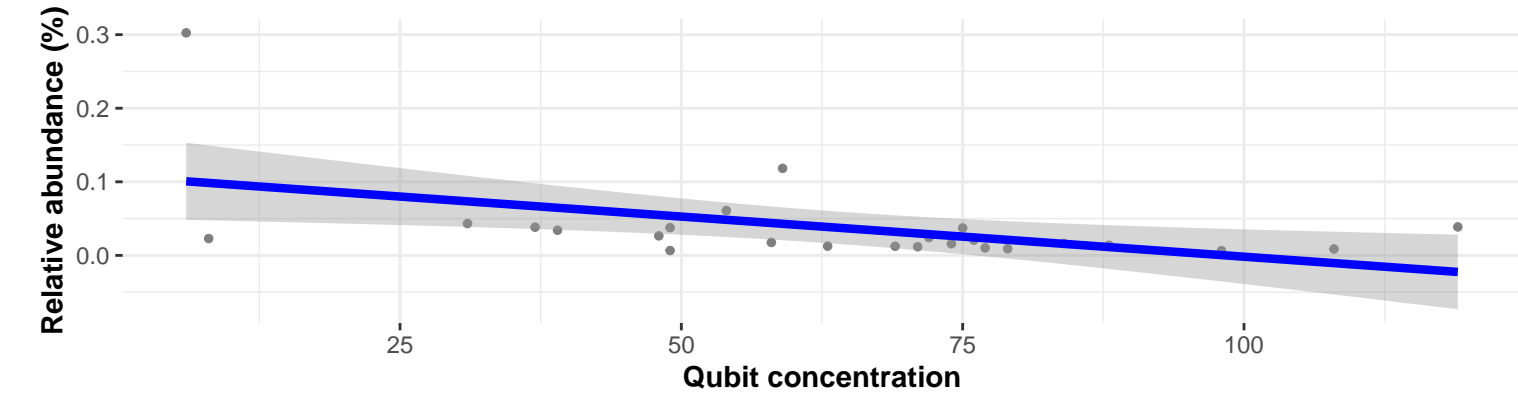
Correlation with all samples

$\log_e(S) = 8.827$, $p = 5.13\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = -0.679$, $\text{CI}_{95\%} [-0.841, -0.407]$, $n_{\text{pairs}} = 29$

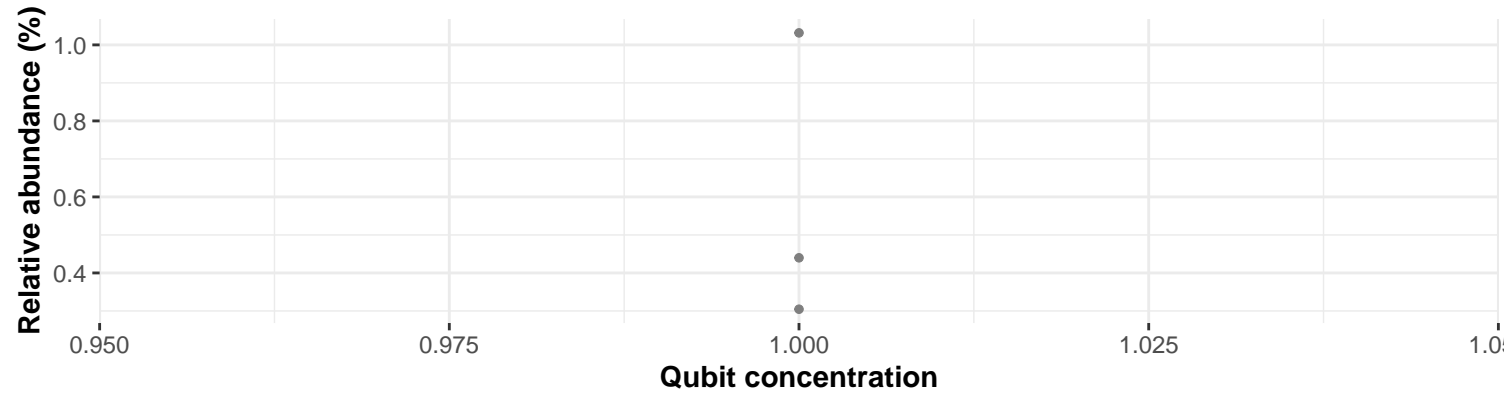


Correlation within: Digesta

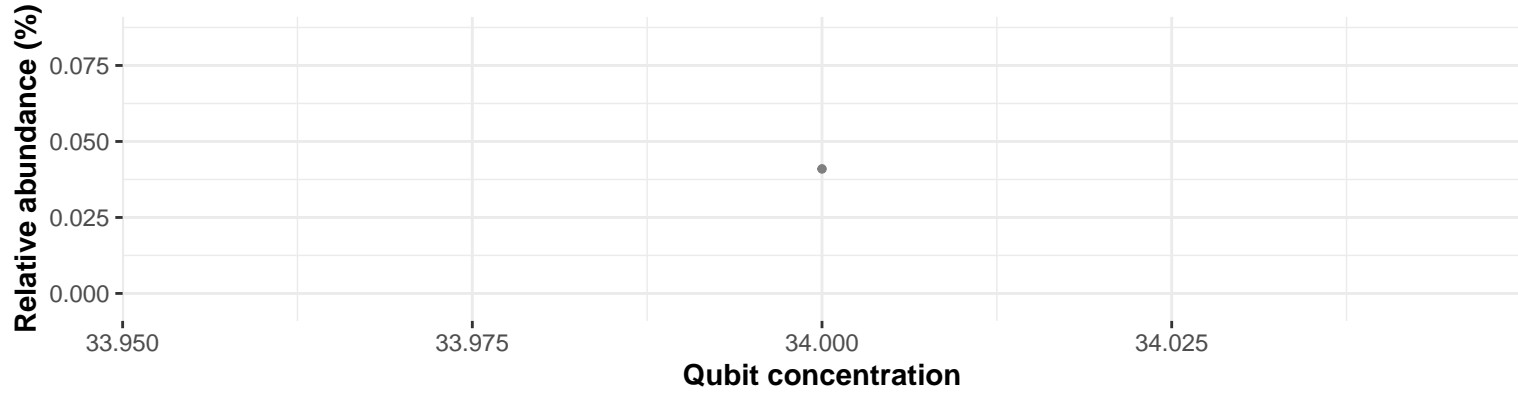
$\log_e(S) = 8.282$, $p = 0.008$, $\hat{\rho}_{\text{Spearman}} = -0.520$, $\text{CI}_{95\%} [-0.765, -0.146]$, $n_{\text{pairs}} = 25$



Correlation within: control



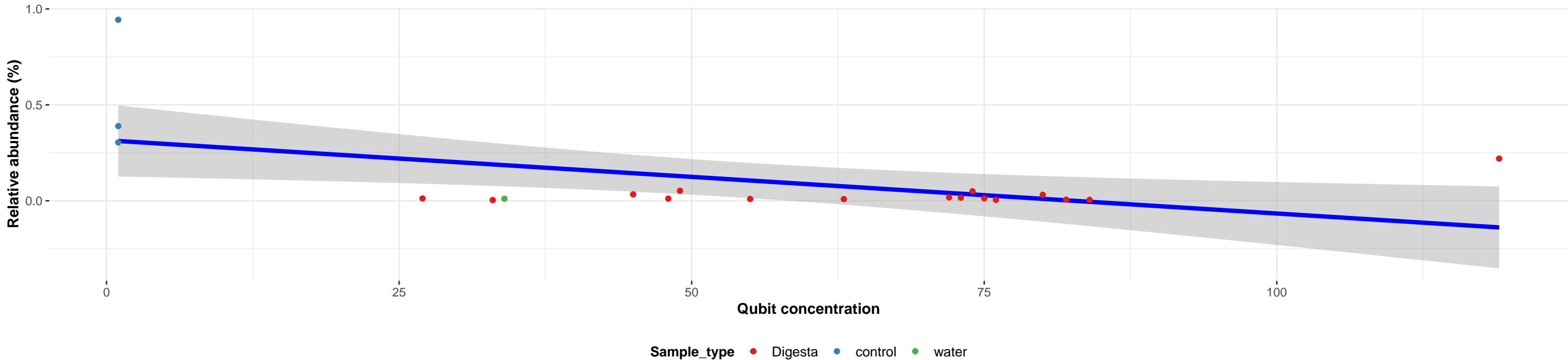
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; NA

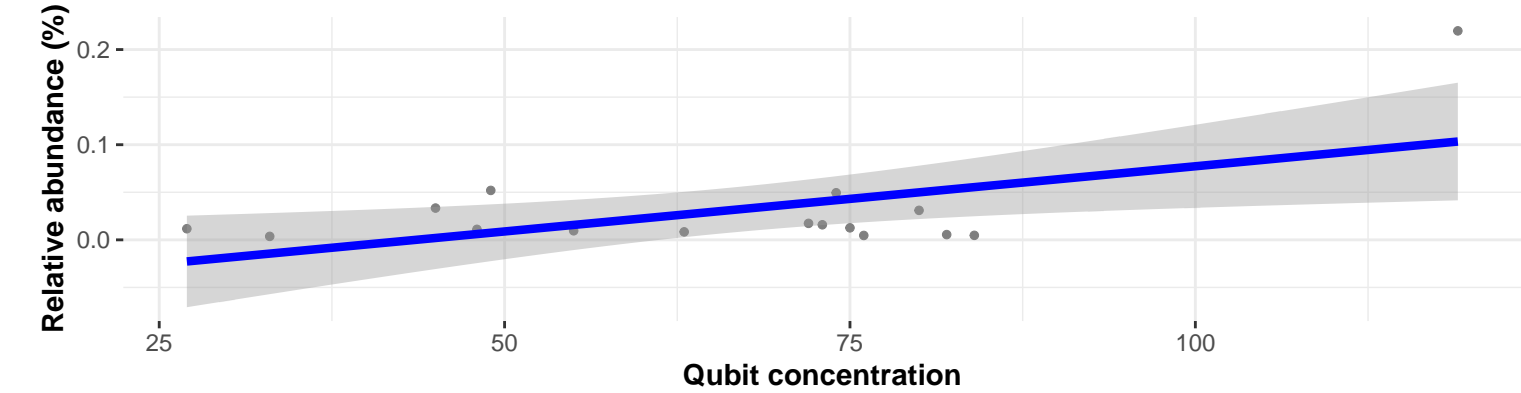
Correlation with all samples

$\log_e(S) = 7.477$, $p = 0.158$, $\hat{\rho}_{\text{Spearman}} = -0.328$, $\text{CI}_{95\%} [-0.681, 0.147]$, $n_{\text{pairs}} = 20$

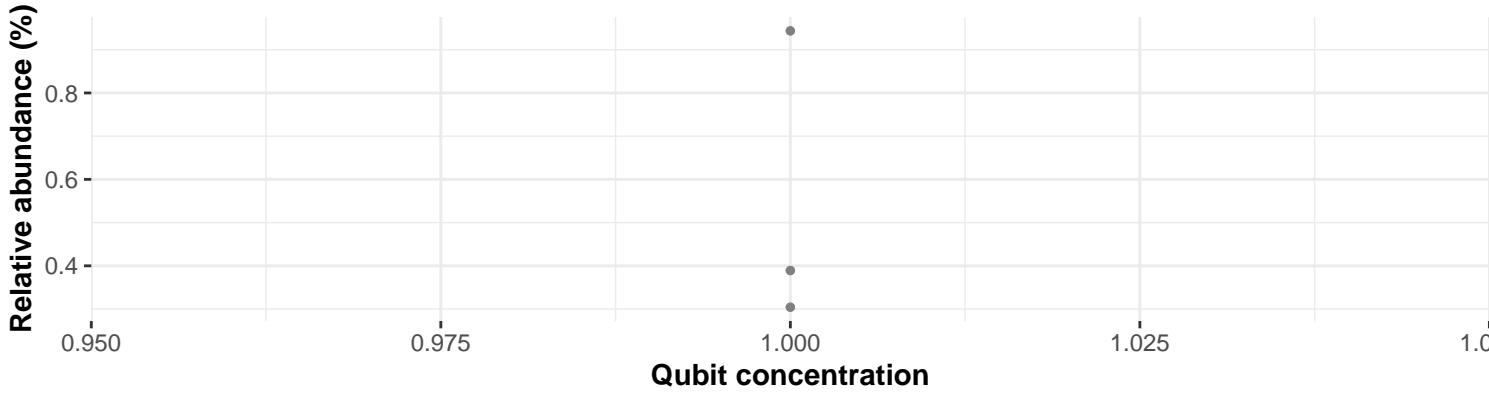


Correlation within: Digesta

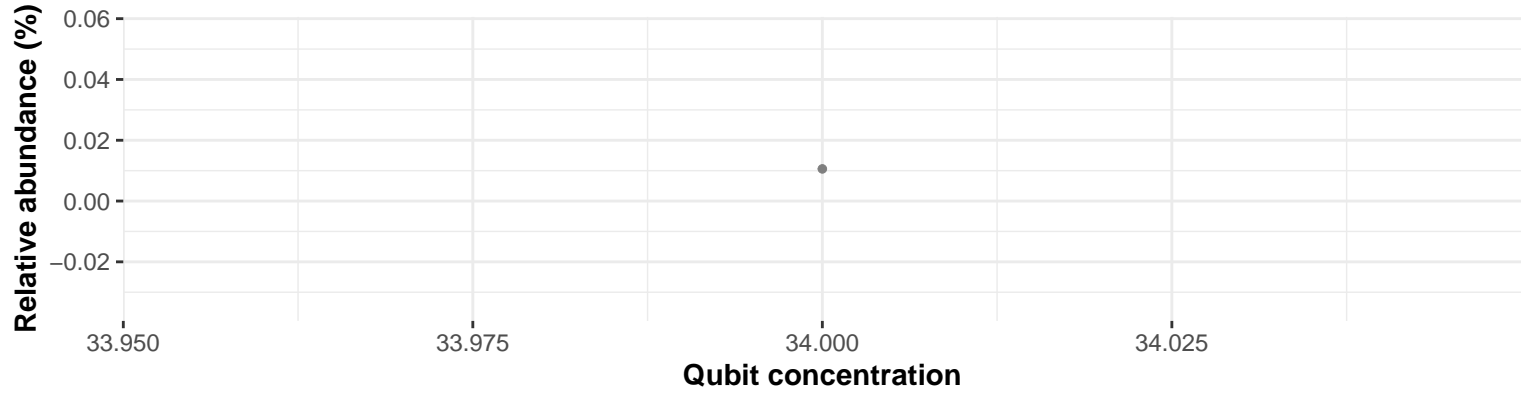
$\log_e(S) = 6.458$, $p = 0.820$, $\hat{\rho}_{\text{Spearman}} = 0.062$, $\text{CI}_{95\%} [-0.460, 0.552]$, $n_{\text{pairs}} = 16$



Correlation within: control



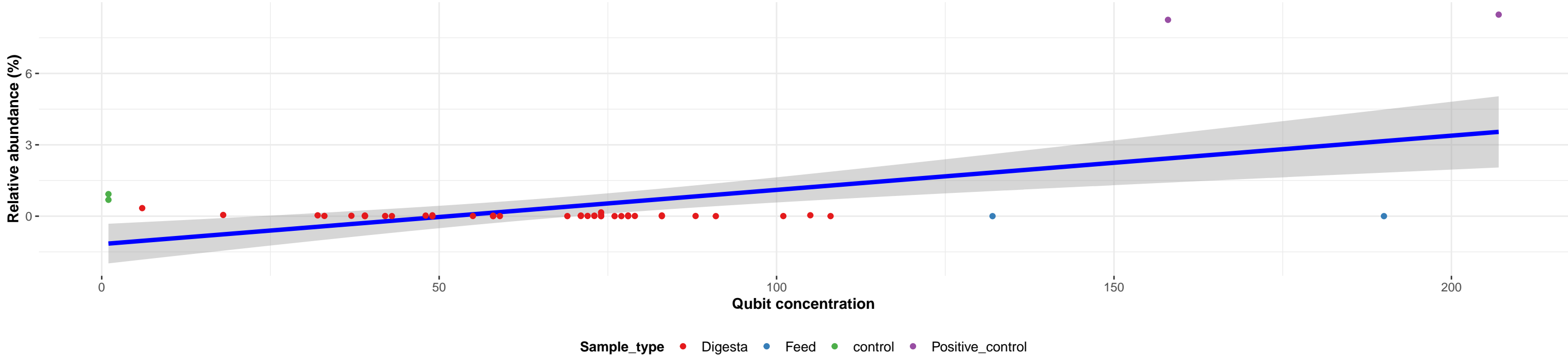
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

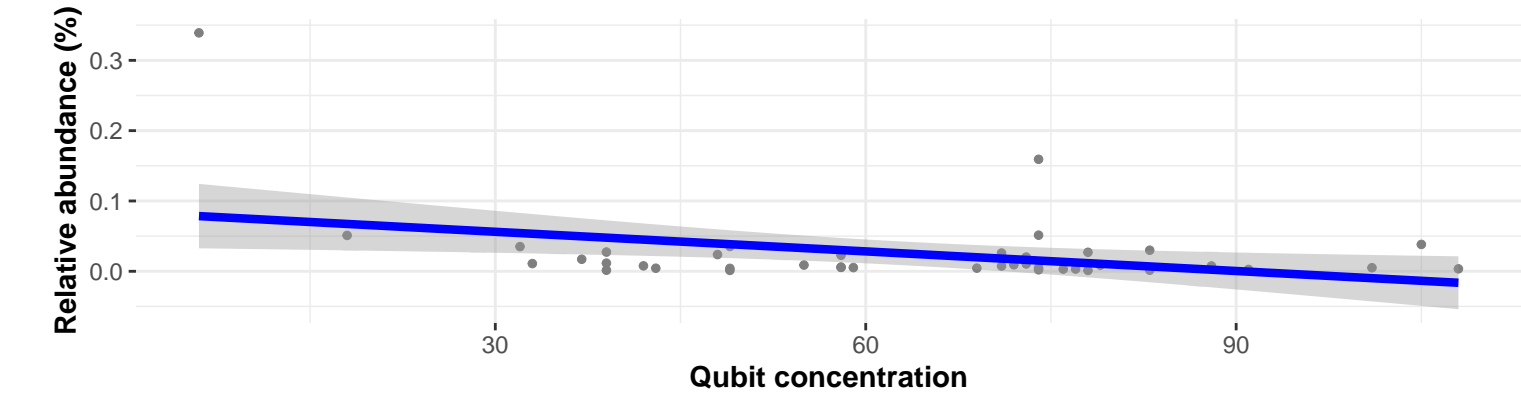
Correlation with all samples

$\log_e(S) = 9.989$, $p = 0.078$, $\hat{\rho}_{\text{Spearman}} = -0.260$, $CI_{95\%} [-0.515, 0.039]$, $n_{\text{pairs}} = 47$

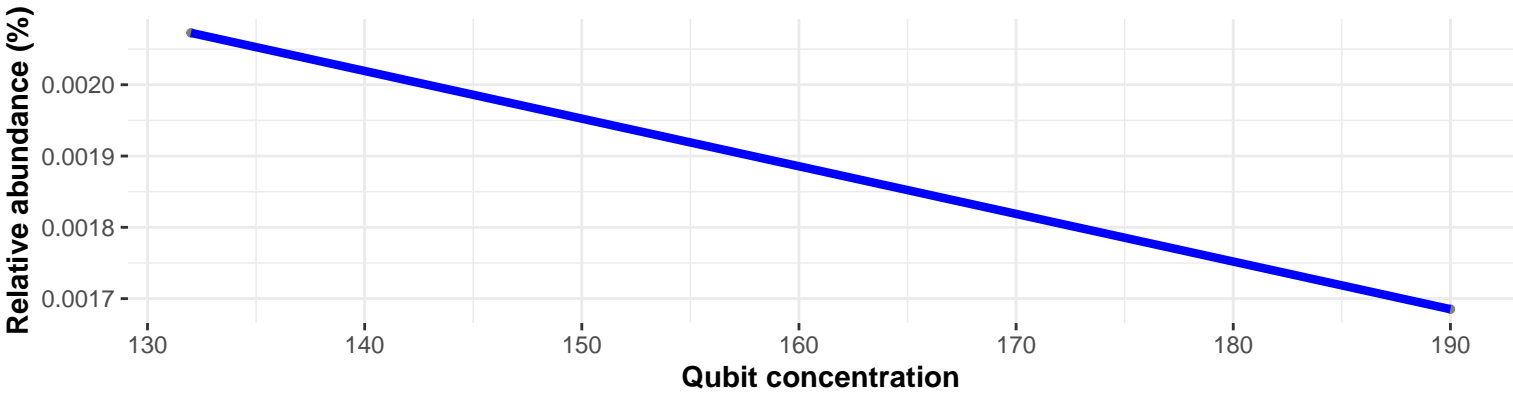


Correlation within: Digesta

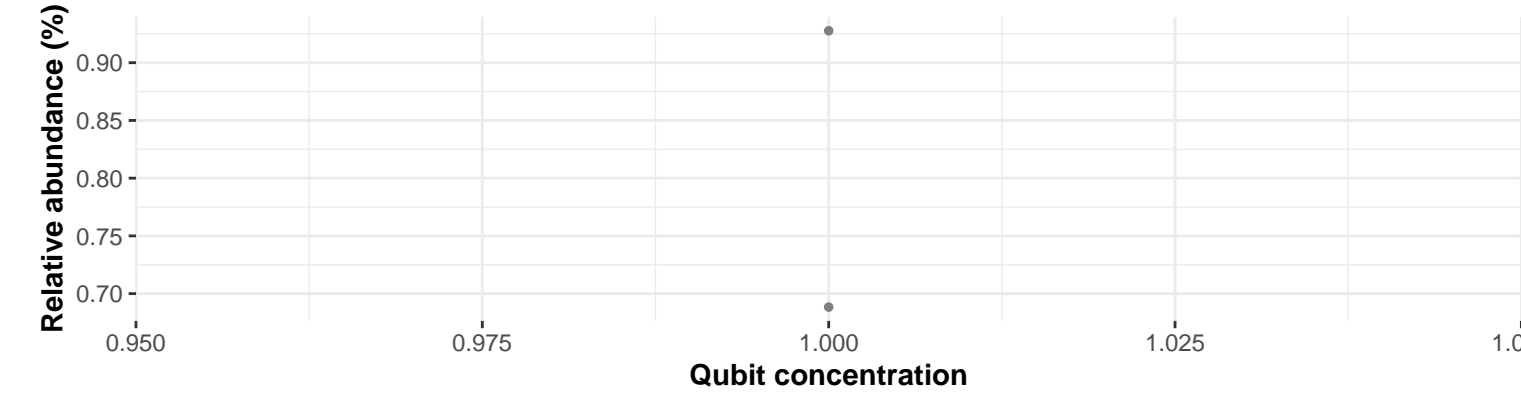
$\log_e(S) = 9.591$, $p = 0.082$, $\hat{\rho}_{\text{Spearman}} = -0.275$, $CI_{95\%} [-0.543, 0.046]$, $n_{\text{pairs}} = 41$



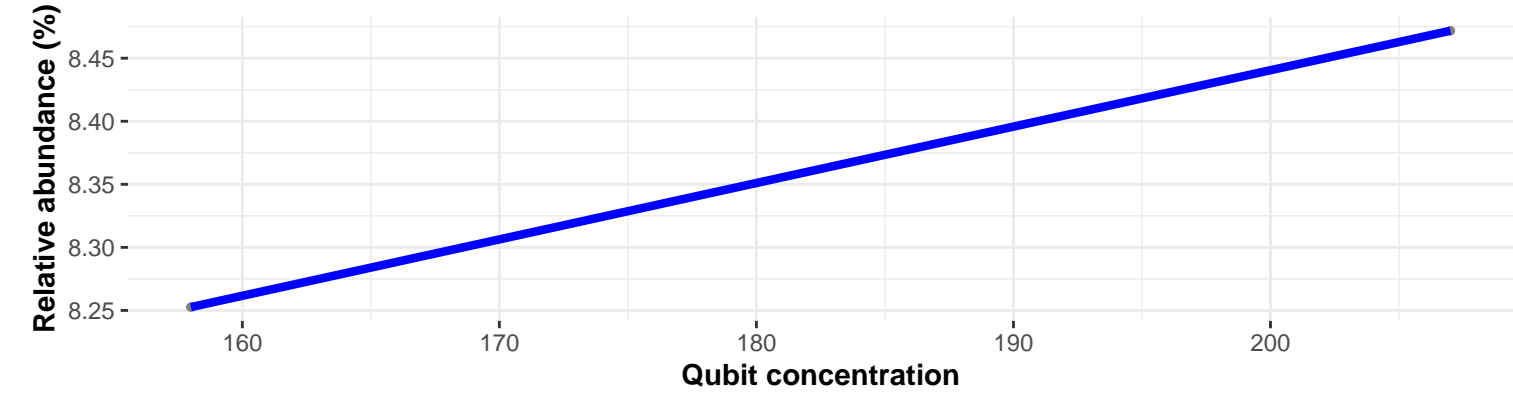
Correlation within: Feed



Correlation within: control



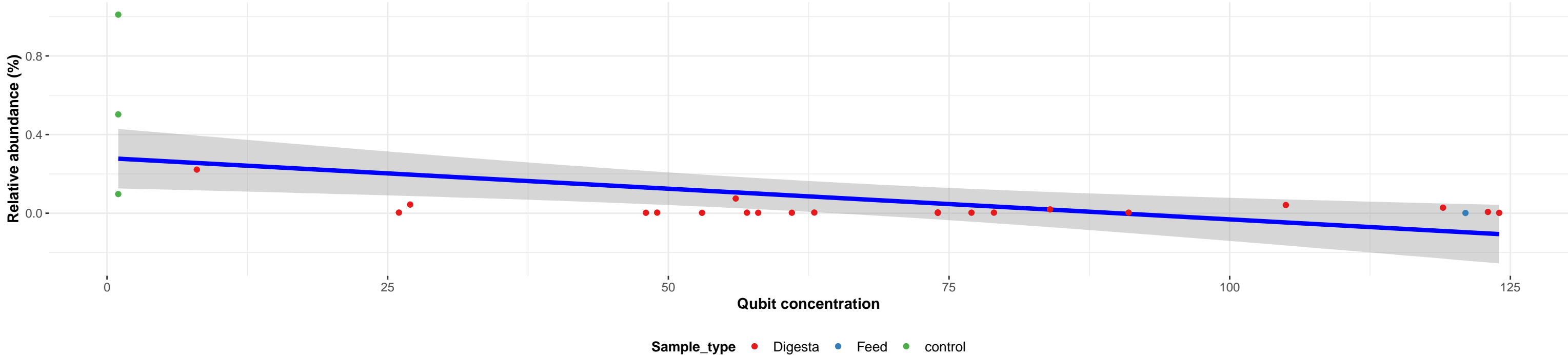
Correlation within: Positive_control



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Lawsonella; NA

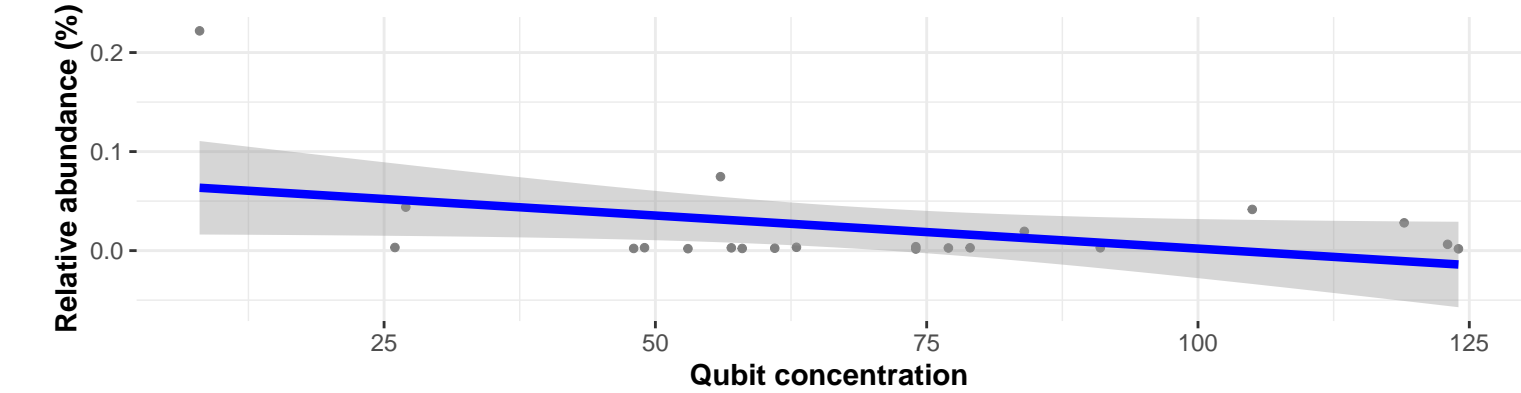
Correlation with all samples

$\log_e(S) = 8.228$, $p = 0.028$, $\hat{\rho}_{\text{Spearman}} = -0.440$, $CI_{95\%} [-0.718, -0.042]$, $n_{\text{pairs}} = 25$

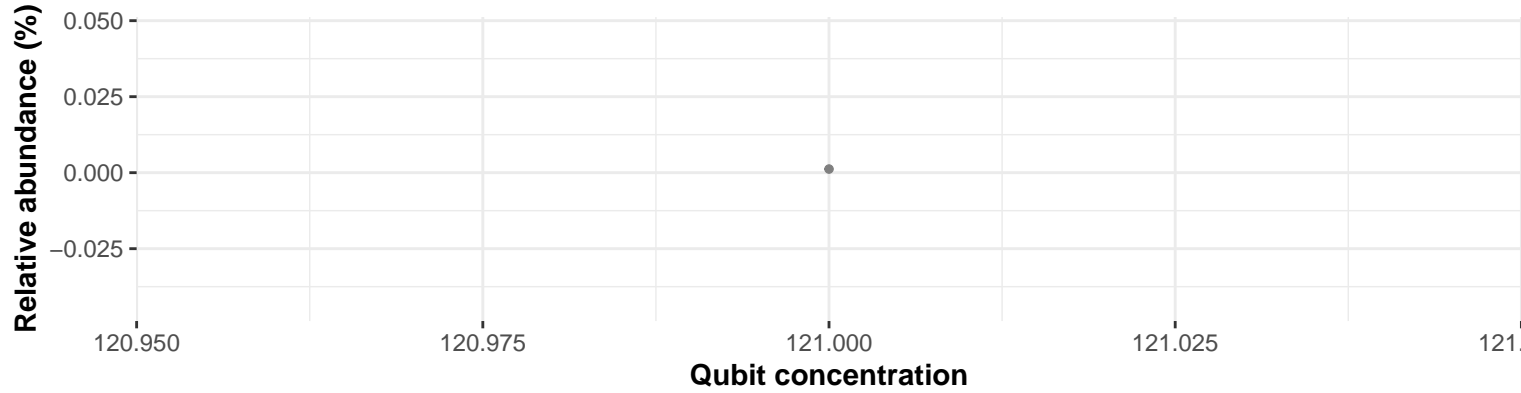


Correlation within: Digesta

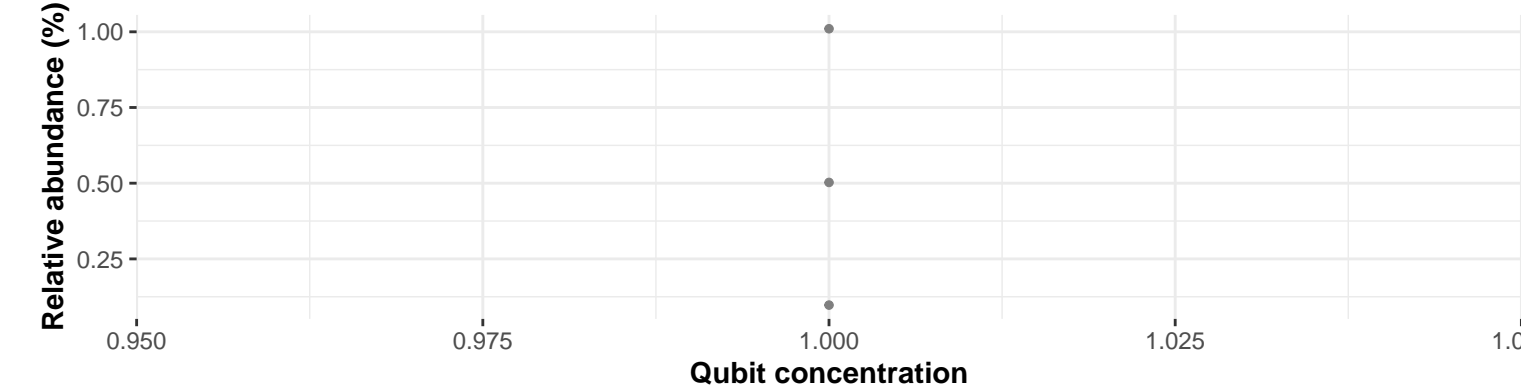
$\log_e(S) = 7.418$, $p = 0.726$, $\hat{\rho}_{\text{Spearman}} = -0.081$, $CI_{95\%} [-0.506, 0.375]$, $n_{\text{pairs}} = 21$



Correlation within: Feed



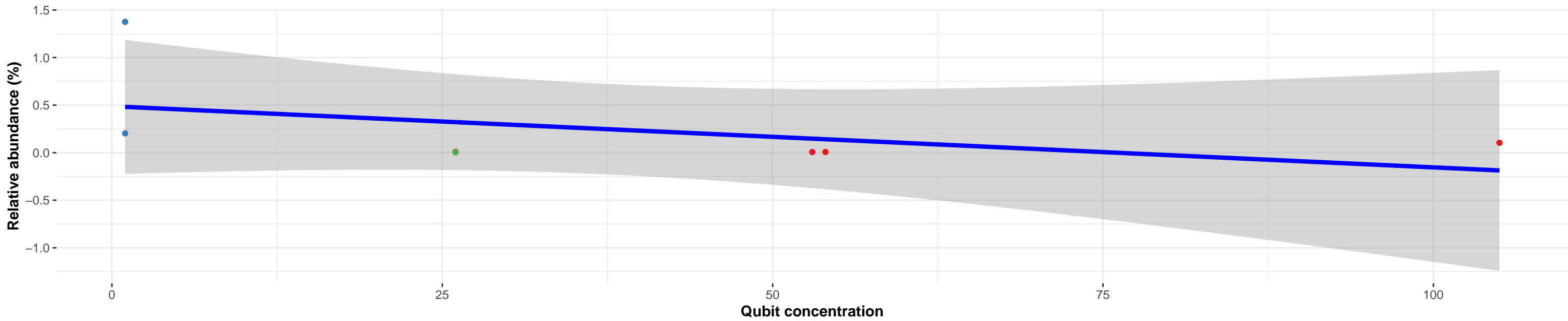
Correlation within: control



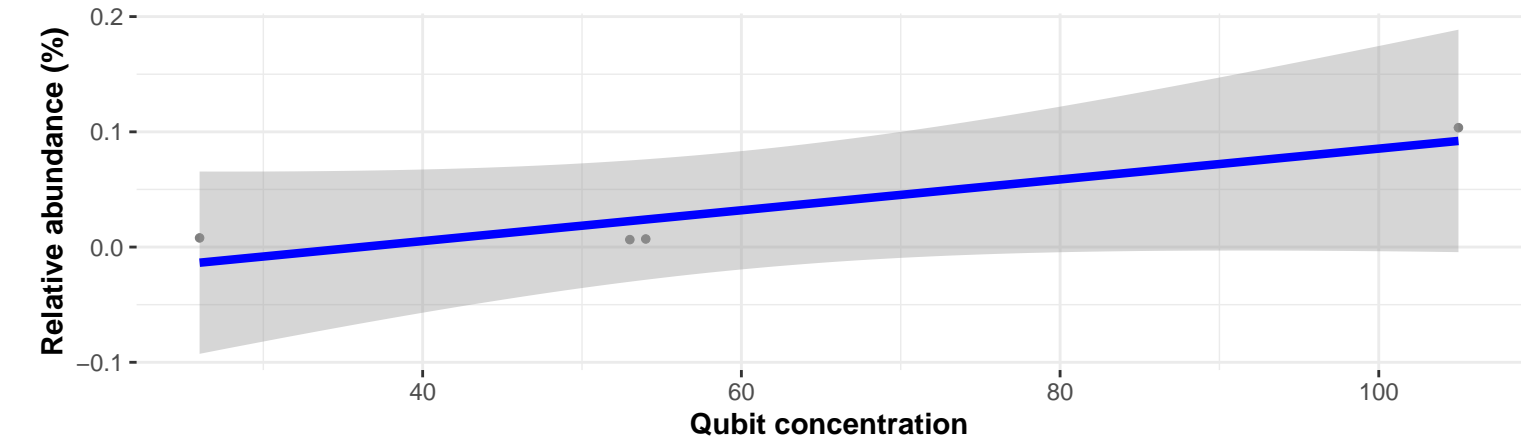
Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Staphylococcus; NA

Correlation with all samples

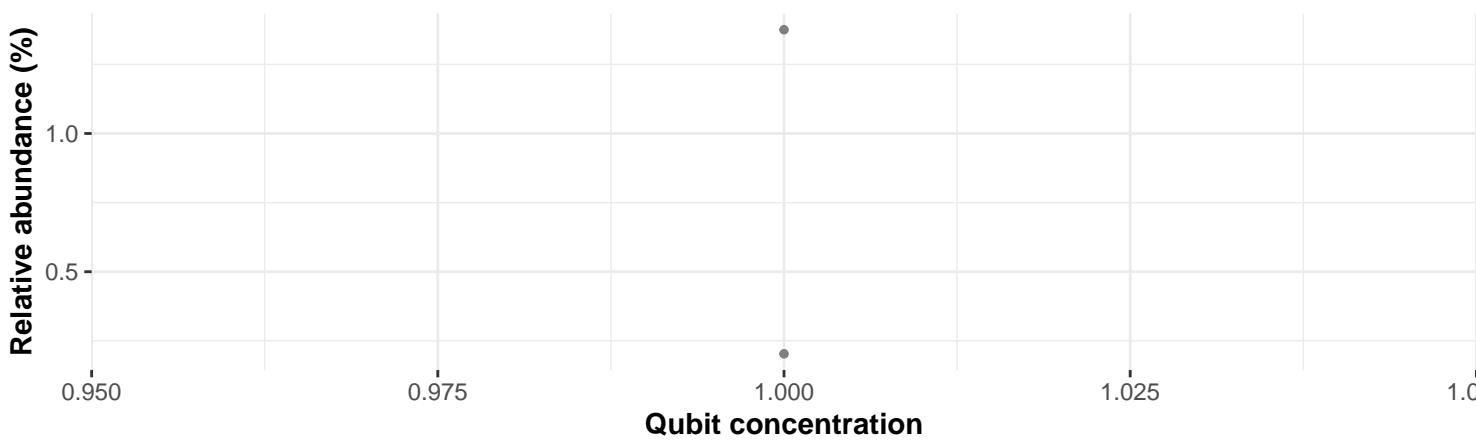
$\log_e(S) = 4.388$, $p = 0.328$, $\hat{\rho}_{\text{Spearman}} = -0.436$, $\text{CI}_{95\%} [-0.901, 0.494]$, $n_{\text{pairs}} = 7$



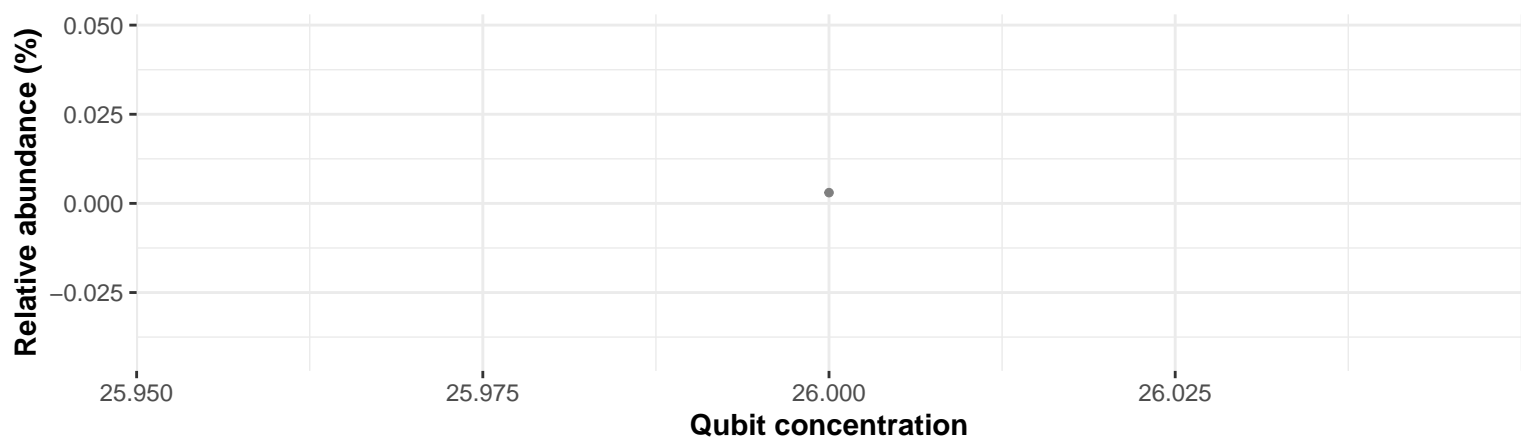
Correlation within: Digesta



Correlation within: control



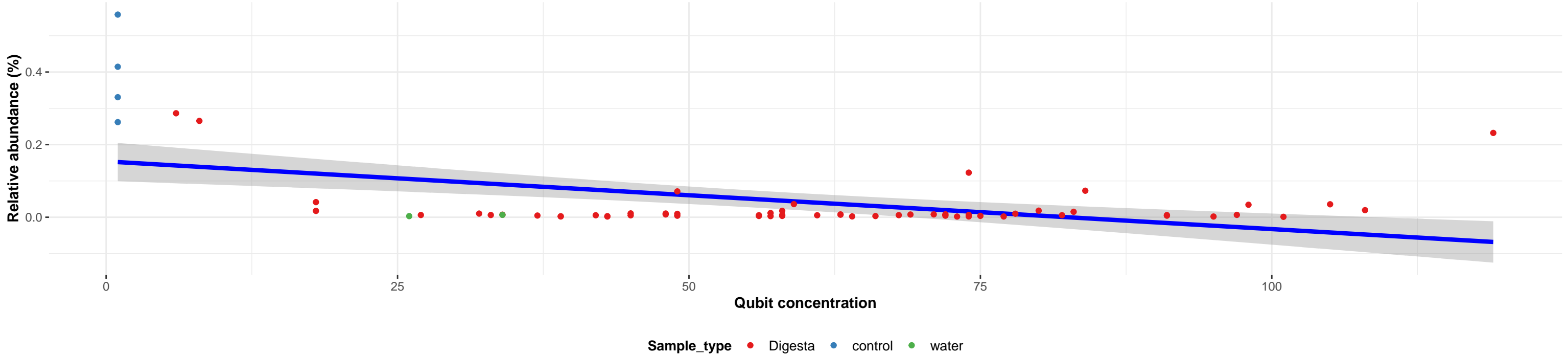
Correlation within: water



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

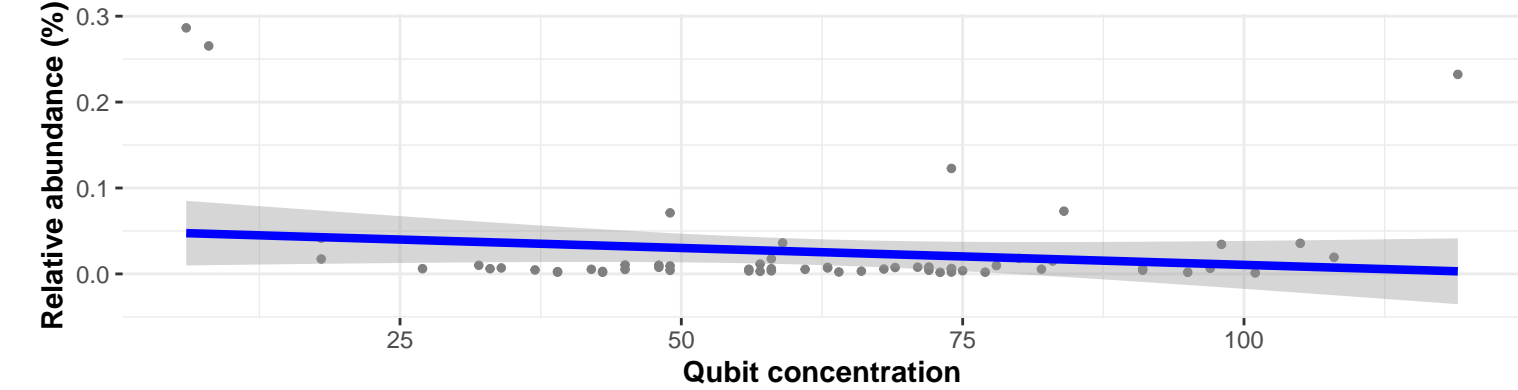
Correlation with all samples

$\log_e(S) = 10.938$, $p = 0.161$, $\hat{\rho}_{\text{Spearman}} = -0.175$, $CI_{95\%} [-0.406, 0.078]$, $n_{\text{pairs}} = 66$

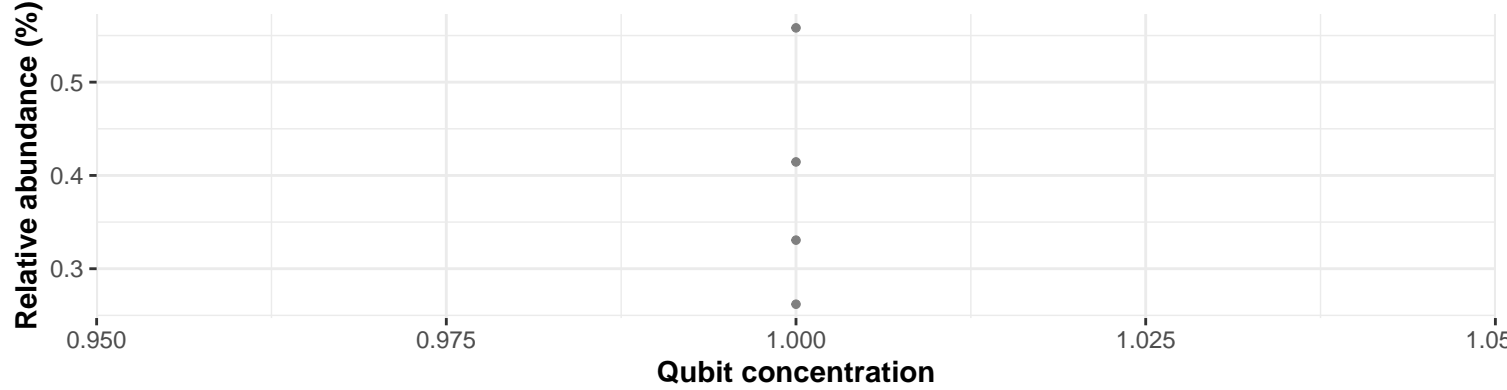


Correlation within: Digesta

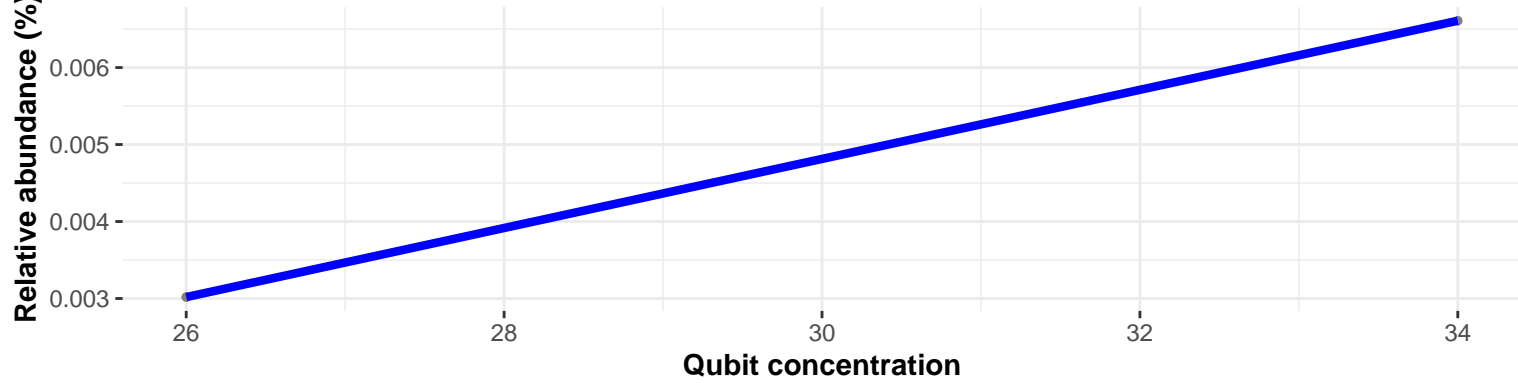
$\log_e(S) = 10.511$, $p = 0.880$, $\hat{\rho}_{\text{Spearman}} = -0.020$, $CI_{95\%} [-0.279, 0.243]$, $n_{\text{pairs}} = 60$



Correlation within: control



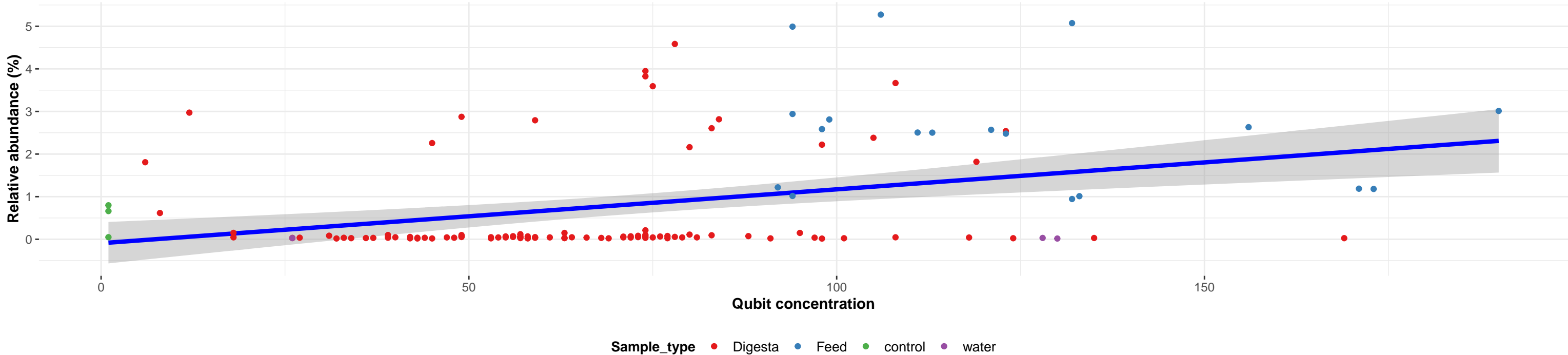
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Limosilactobacillus; NA

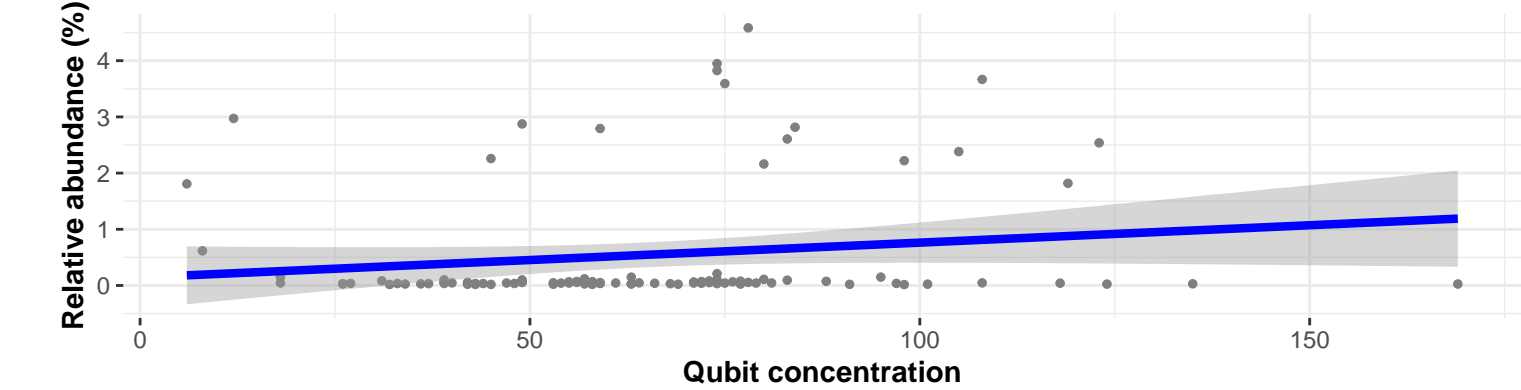
Correlation with all samples

$\log_e(S) = 12.271$, $p = 4.46e-04$, $\hat{\rho}_{\text{Spearman}} = 0.312$, $CI_{95\%} [0.138, 0.467]$, $n_{\text{pairs}} = 123$



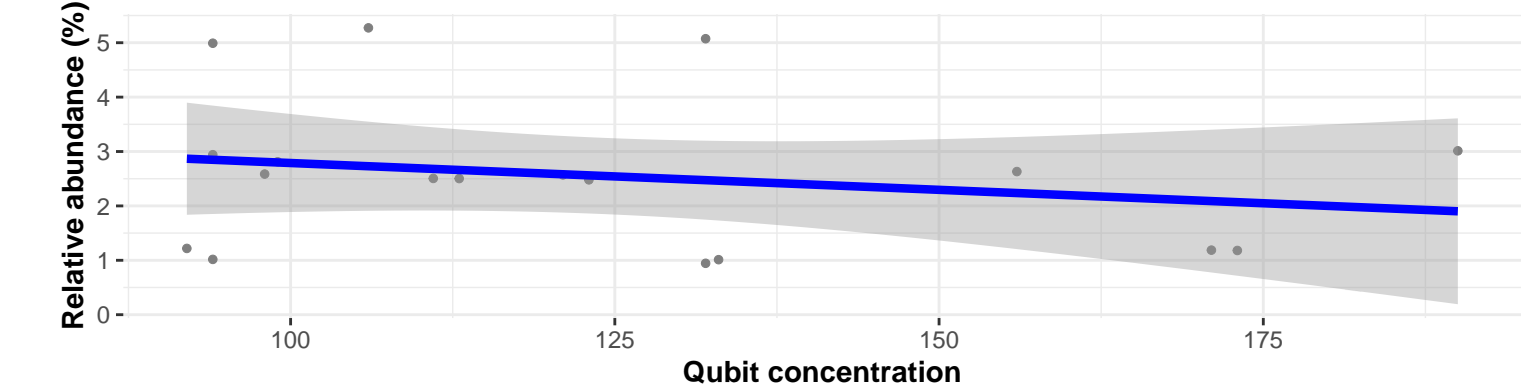
Correlation within: Digesta

$\log_e(S) = 11.822$, $p = 0.119$, $\hat{\rho}_{\text{Spearman}} = 0.158$, $CI_{95\%} [-0.047, 0.350]$, $n_{\text{pairs}} = 99$

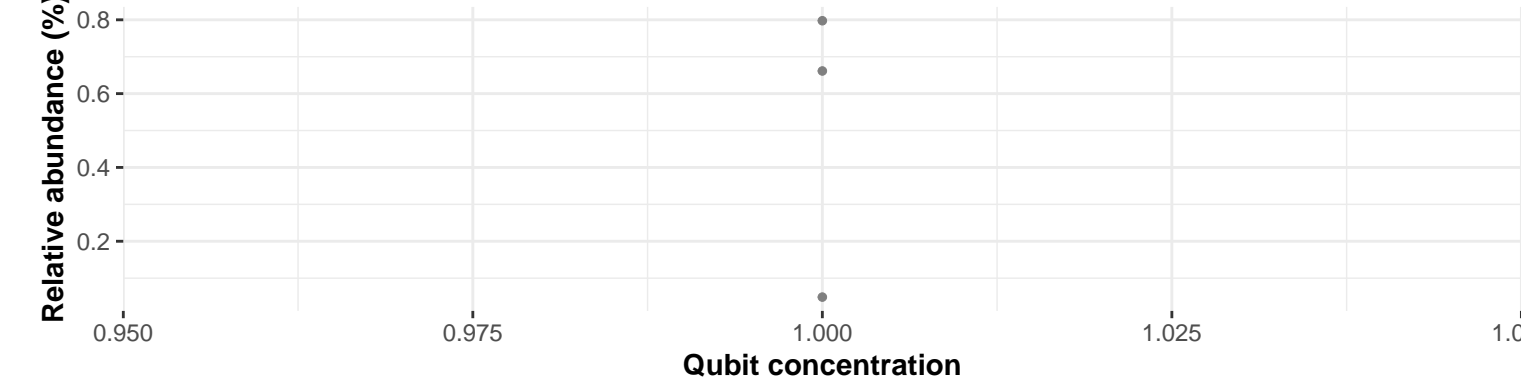


Correlation within: Feed

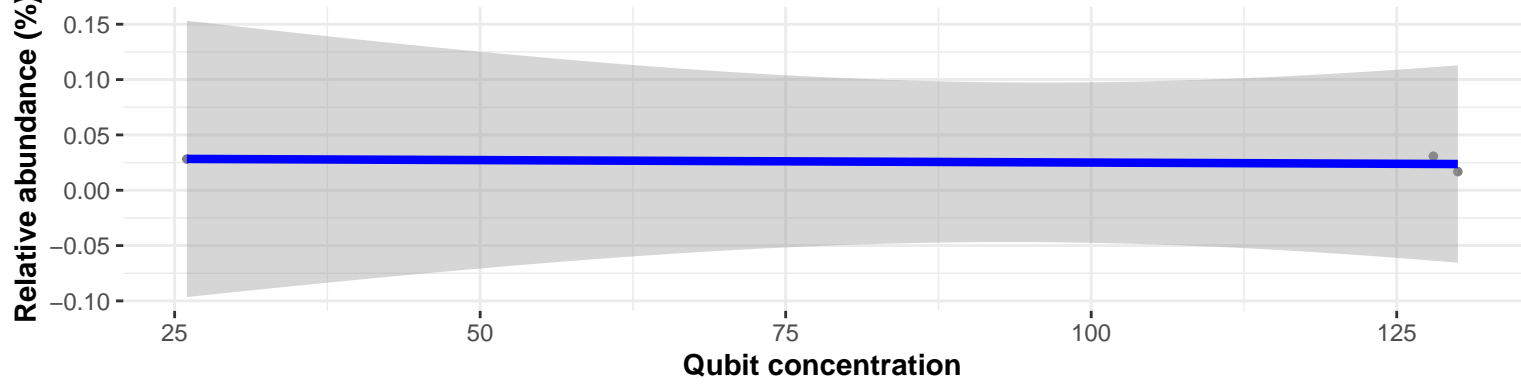
$\log_e(S) = 7.044$, $p = 0.467$, $\hat{\rho}_{\text{Spearman}} = -0.183$, $CI_{95\%} [-0.608, 0.324]$, $n_{\text{pairs}} = 18$



Correlation within: control



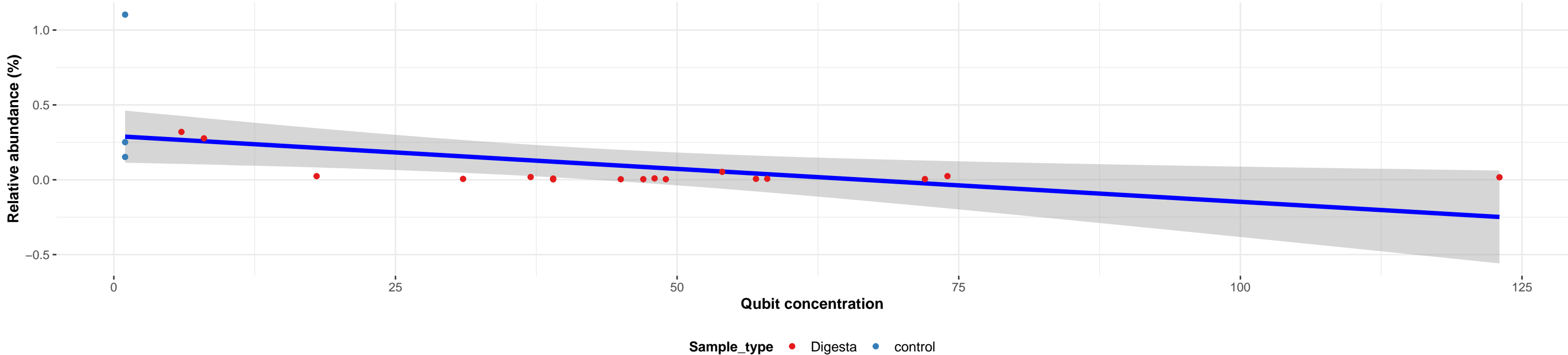
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium; senegalense

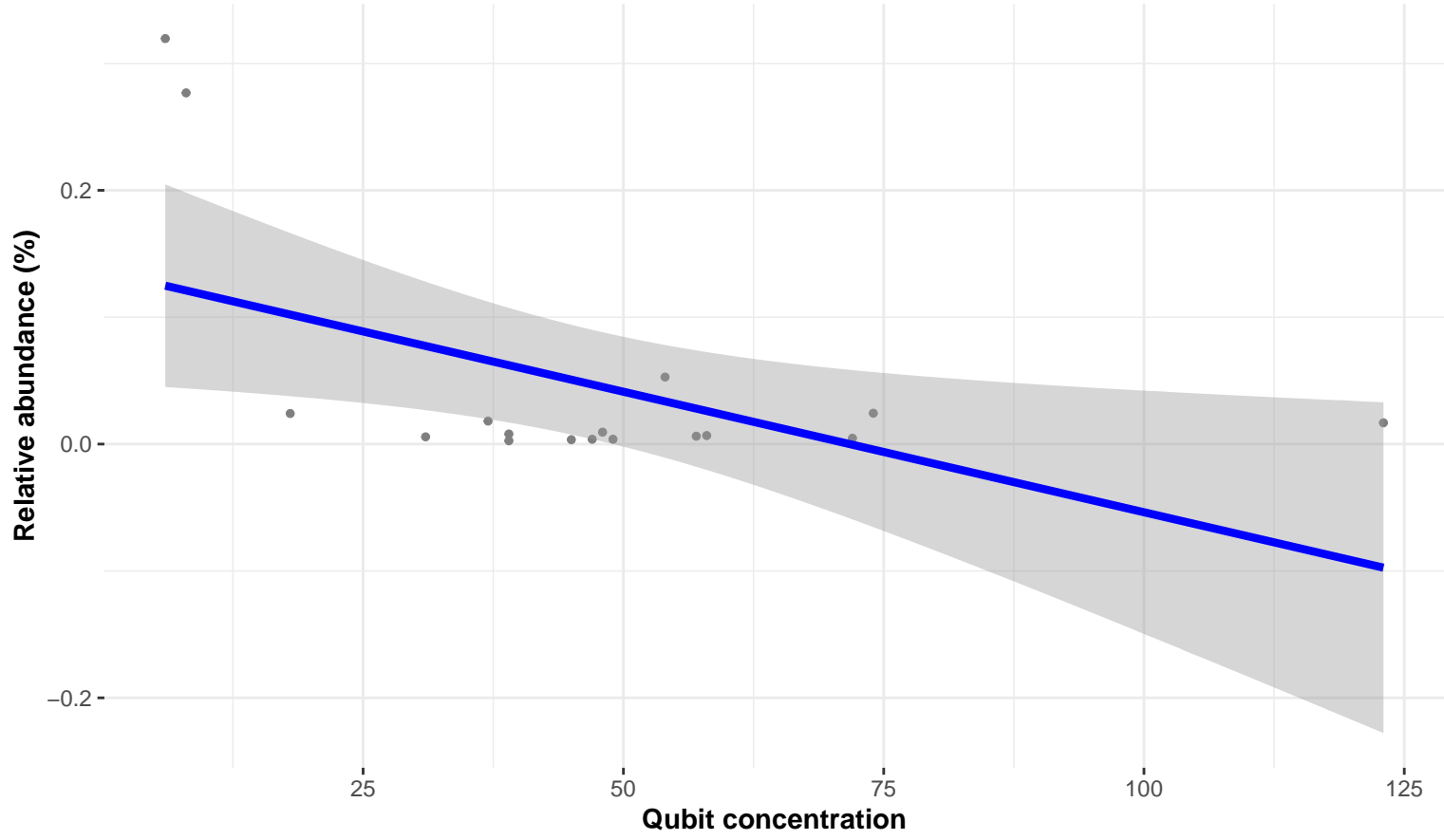
Correlation with all samples

$\log_e(S) = 7.596$, $p = 0.026$, $\hat{\rho}_{\text{Spearman}} = -0.496$, $\text{CI}_{95\%} [-0.775, -0.054]$, $n_{\text{pairs}} = 20$

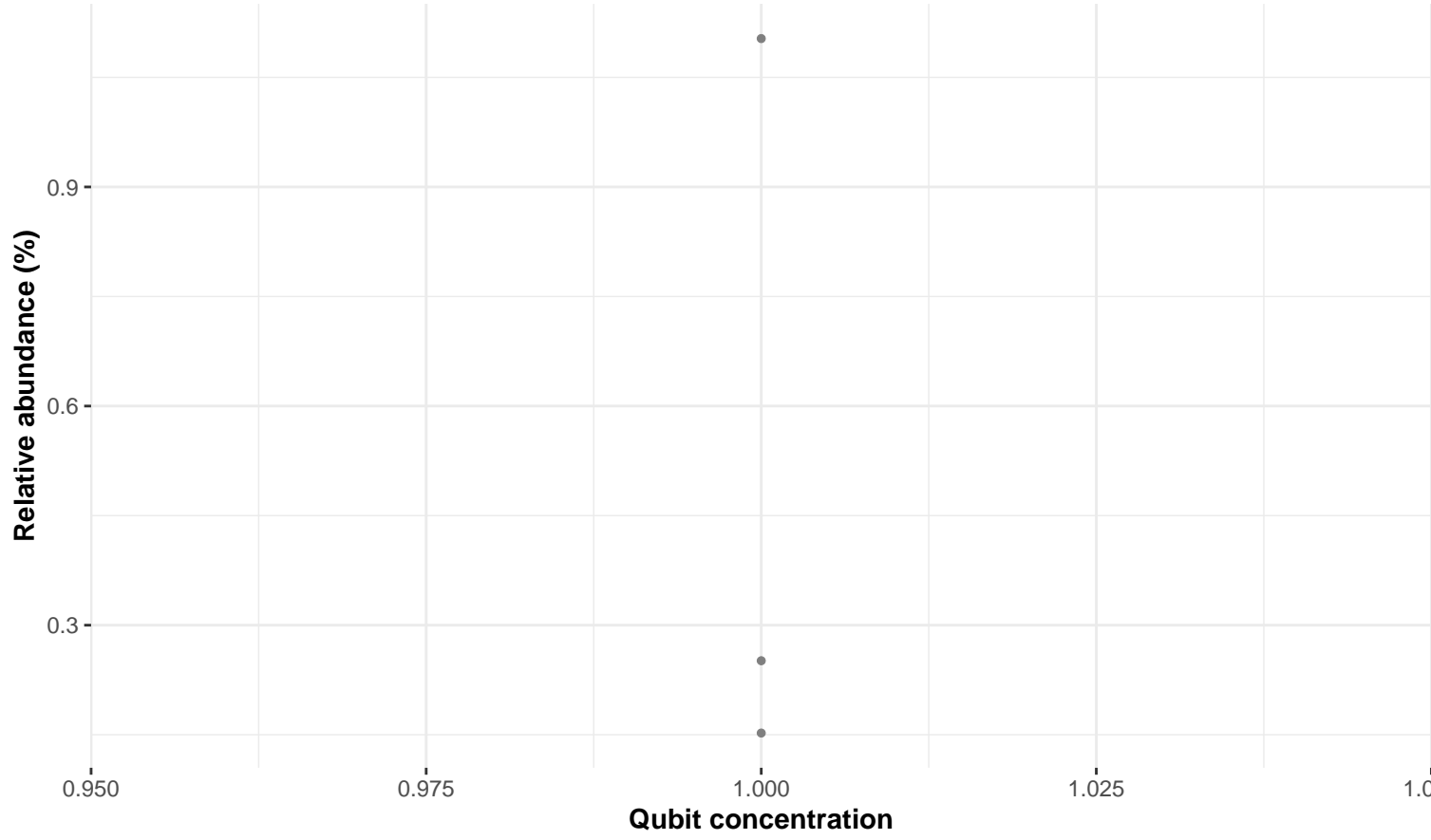


Correlation within: Digesta

$\log_e(S) = 6.892$, $p = 0.428$, $\hat{\rho}_{\text{Spearman}} = -0.206$, $\text{CI}_{95\%} [-0.634, 0.319]$, $n_{\text{pairs}} = 17$



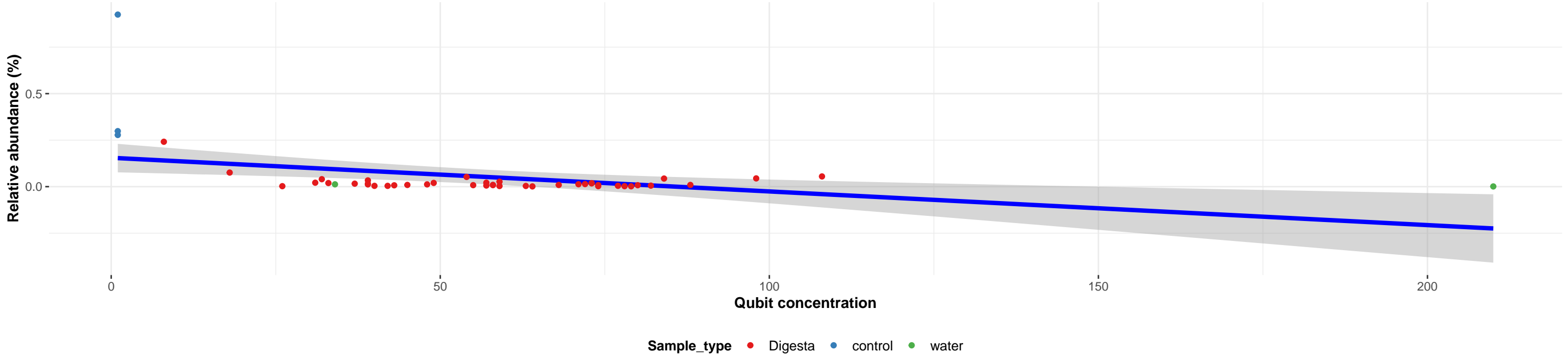
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Pseudogracilibacillus; NA

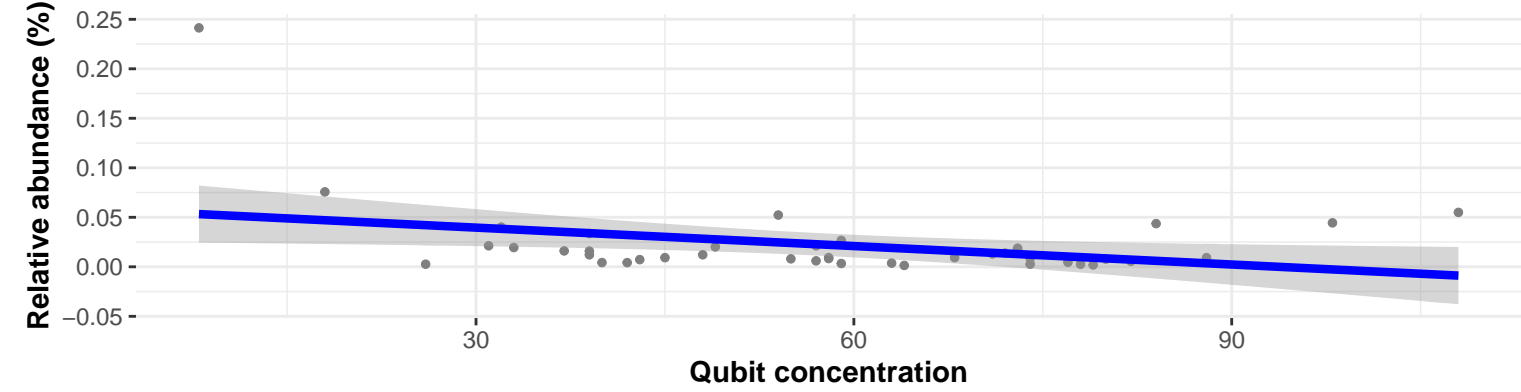
Correlation with all samples

$\log_e(S) = 10.104$, $p = 0.004$, $\hat{\rho}_{\text{Spearman}} = -0.413$, $CI_{95\%} [-0.631, -0.134]$, $n_{\text{pairs}} = 47$

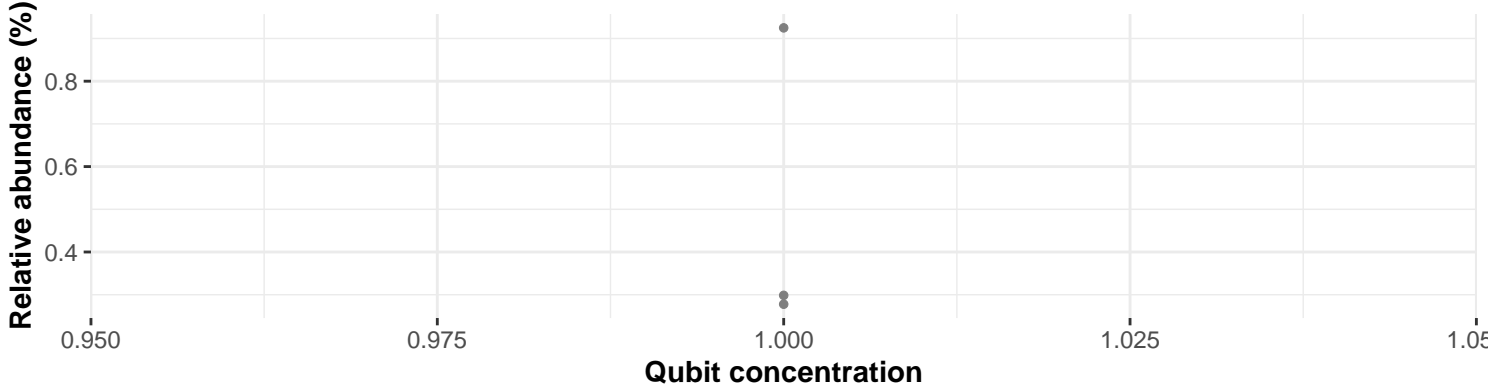


Correlation within: Digesta

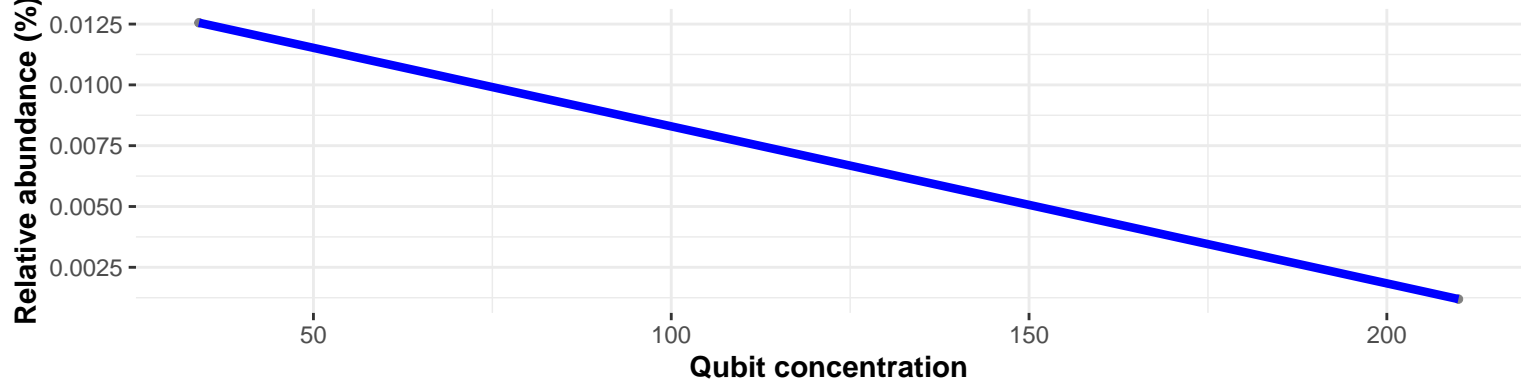
$\log_e(S) = 9.626$, $p = 0.146$, $\hat{\rho}_{\text{Spearman}} = -0.228$, $CI_{95\%} [-0.505, 0.091]$, $n_{\text{pairs}} = 42$



Correlation within: control



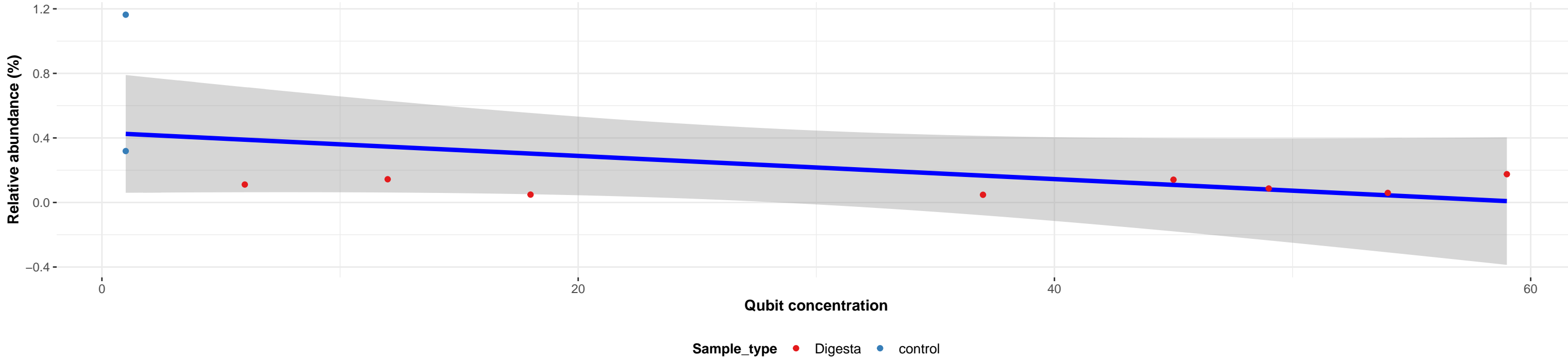
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

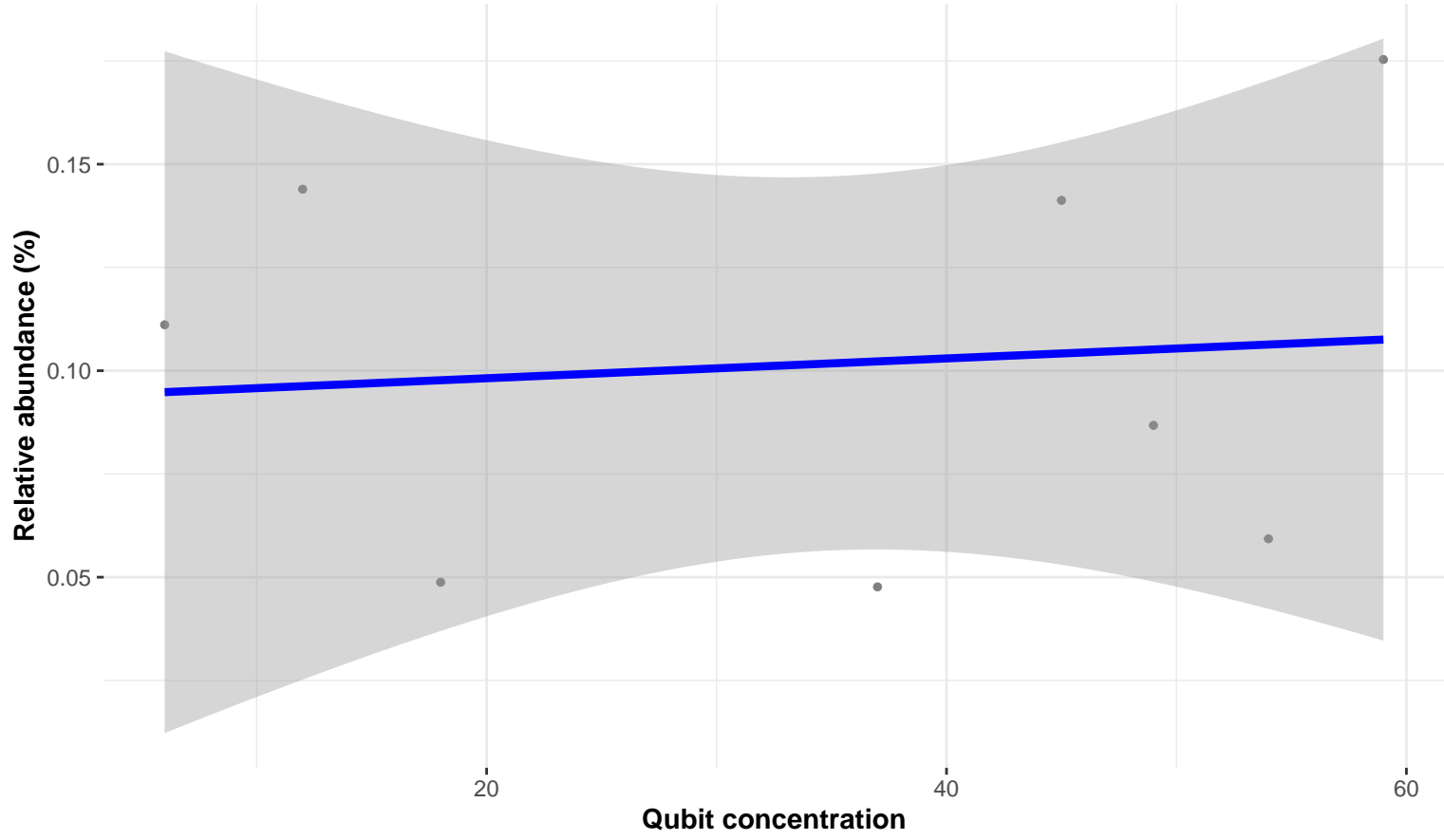
Correlation with all samples

$\log_e(S) = 5.452$, $p = 0.235$, $\hat{\rho}_{\text{Spearman}} = -0.413$, $\text{CI}_{95\%} [-0.834, 0.312]$, $n_{\text{pairs}} = 10$

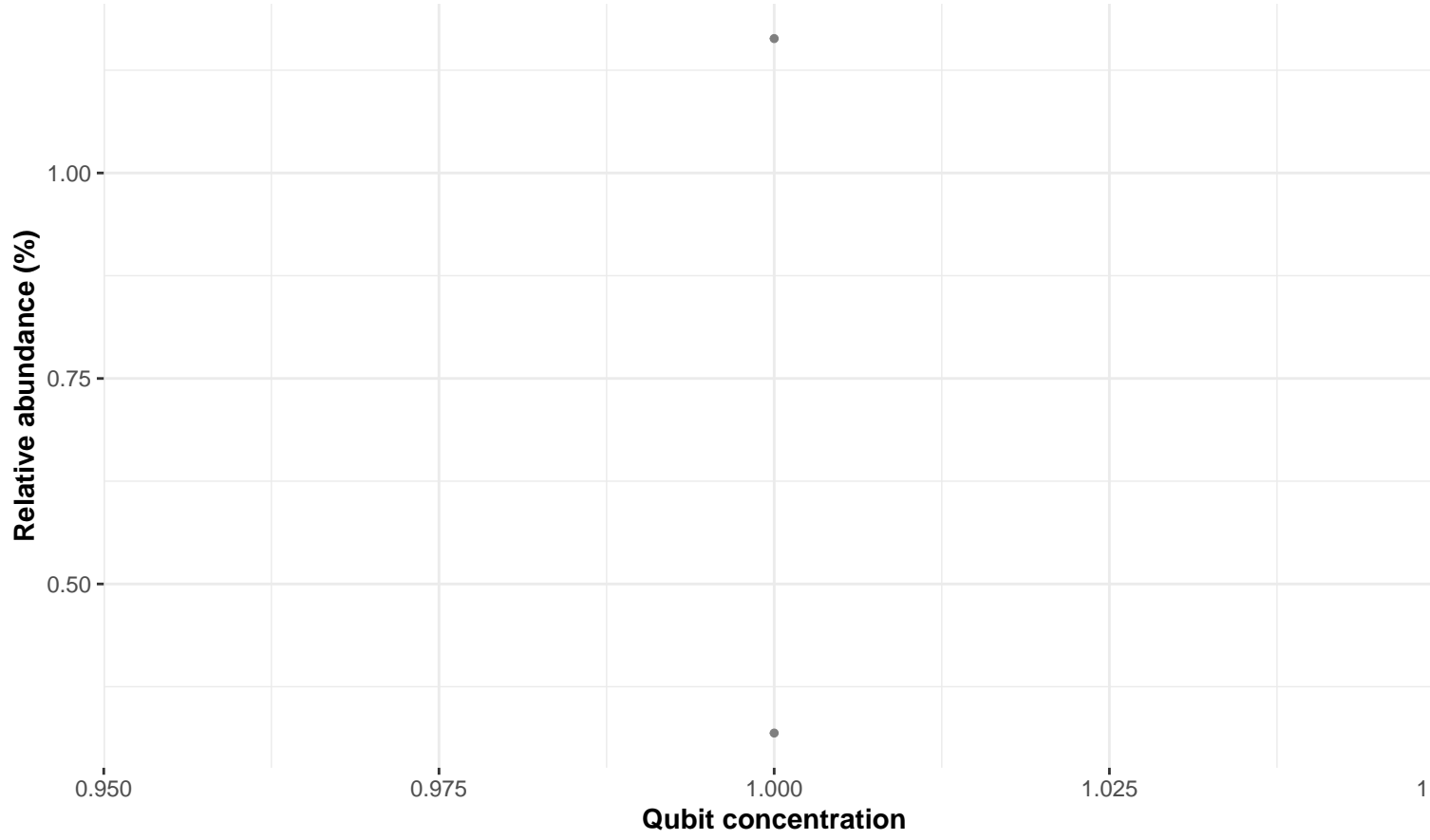


Correlation within: Digesta

$\log_e(S) = 4.277$, $p = 0.736$, $\hat{\rho}_{\text{Spearman}} = 0.143$, $\text{CI}_{95\%} [-0.640, 0.780]$, $n_{\text{pairs}} = 8$



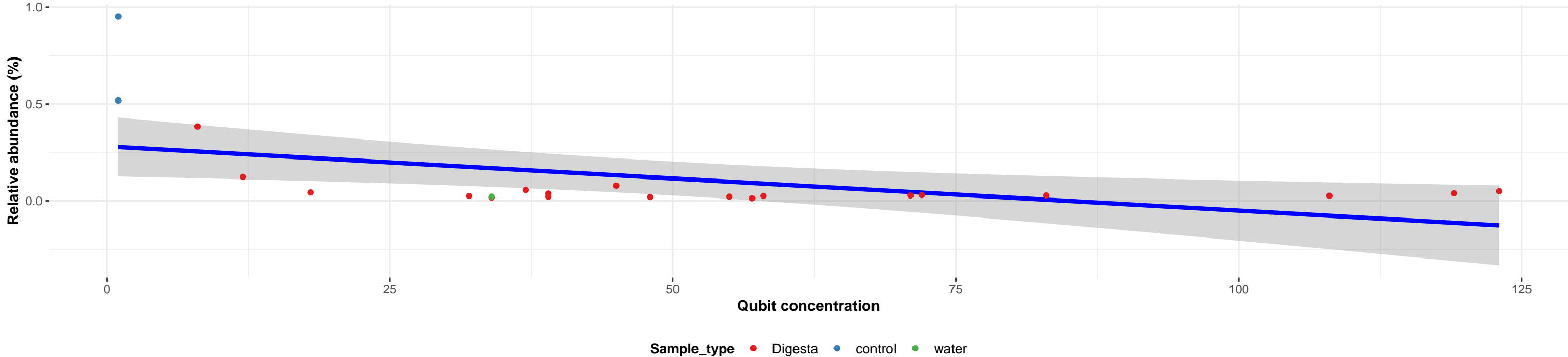
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

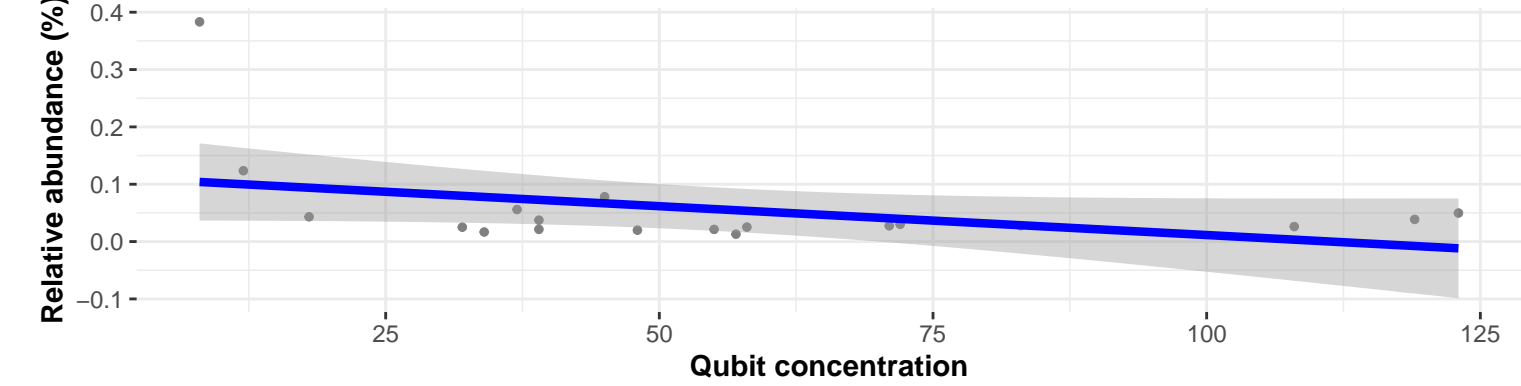
Correlation with all samples

$\log_e(S) = 7.784$, $p = 0.104$, $\hat{\rho}_{\text{Spearman}} = -0.356$, $CI_{95\%} [-0.683, 0.090]$, $n_{\text{pairs}} = 22$

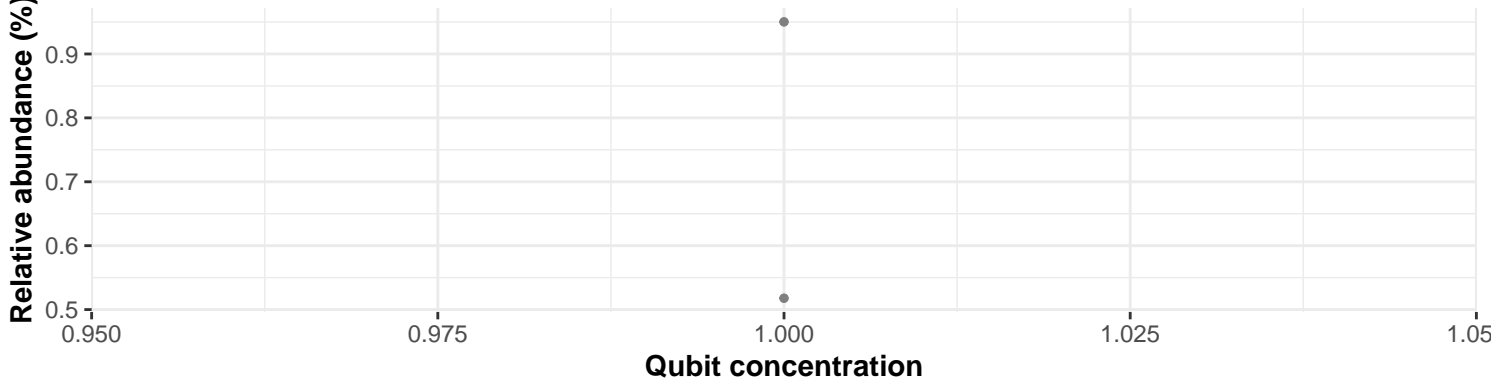


Correlation within: Digesta

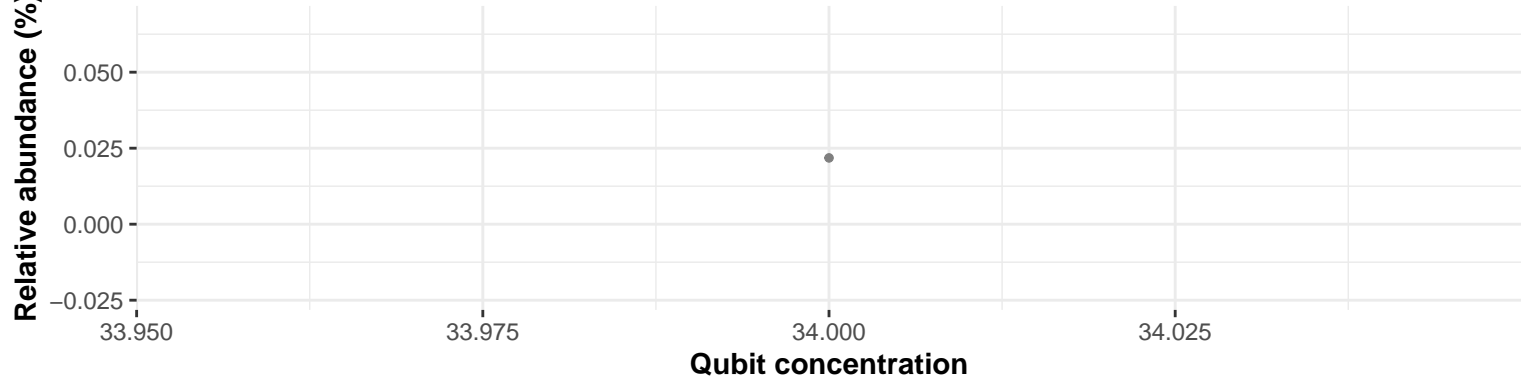
$\log_e(S) = 7.215$, $p = 0.431$, $\hat{\rho}_{\text{Spearman}} = -0.192$, $CI_{95\%} [-0.604, 0.300]$, $n_{\text{pairs}} = 19$



Correlation within: control



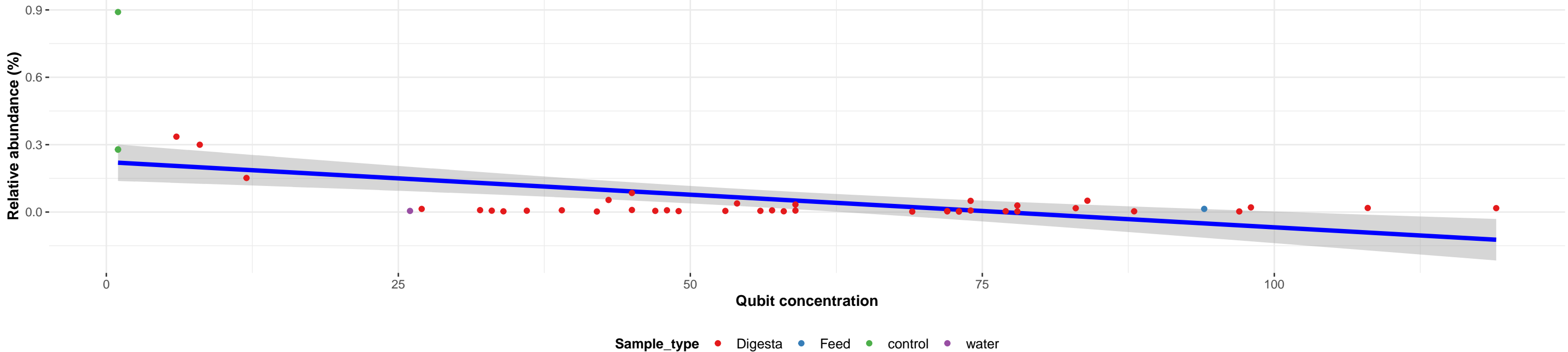
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; NA

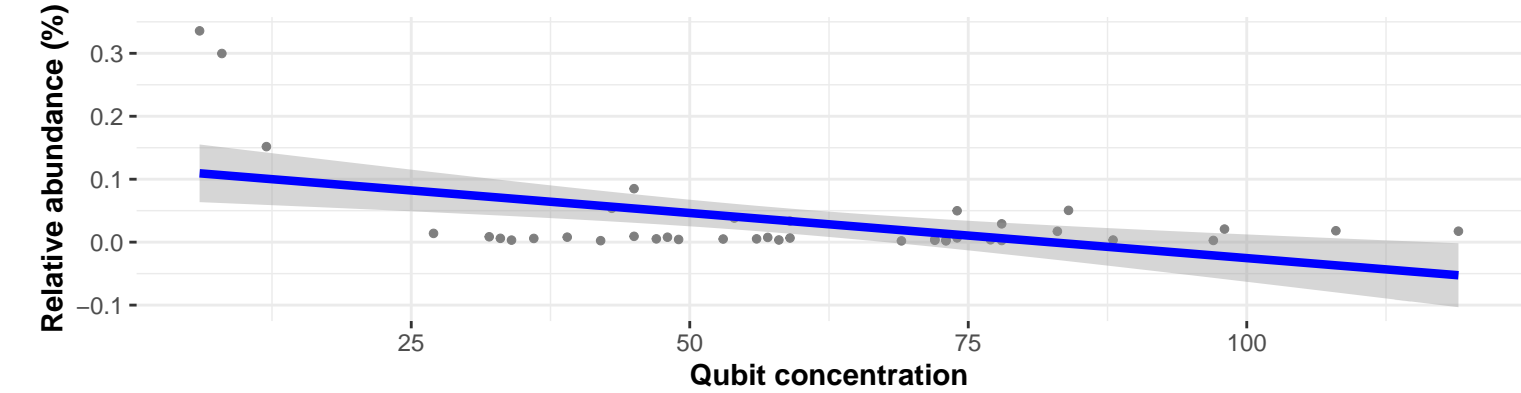
Correlation with all samples

$\log_e(S) = 9.900$, $p = 0.036$, $\hat{\rho}_{\text{Spearman}} = -0.313$, $CI_{95\%} [-0.562, -0.013]$, $n_{\text{pairs}} = 45$

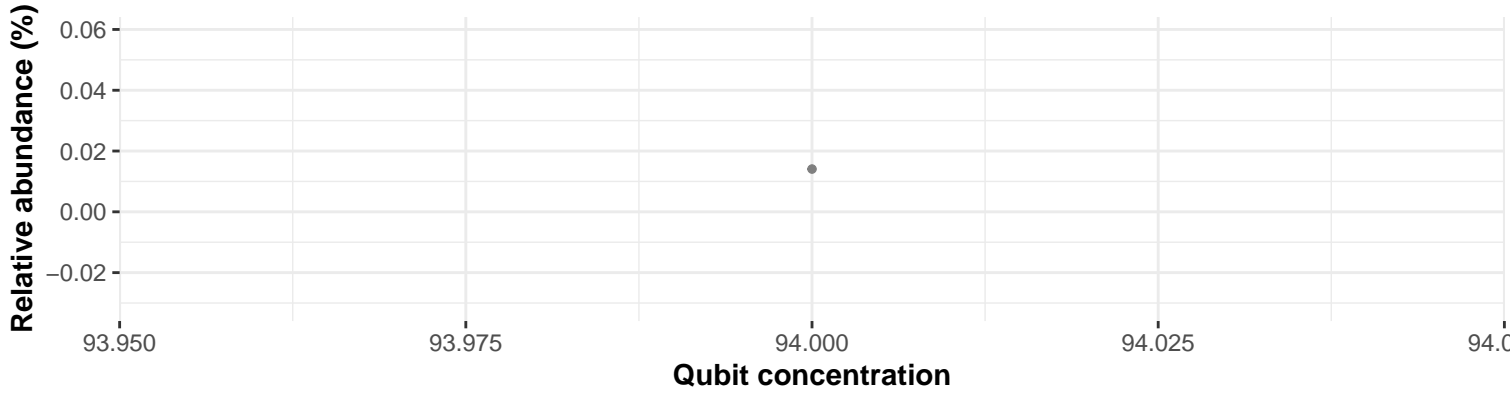


Correlation within: Digesta

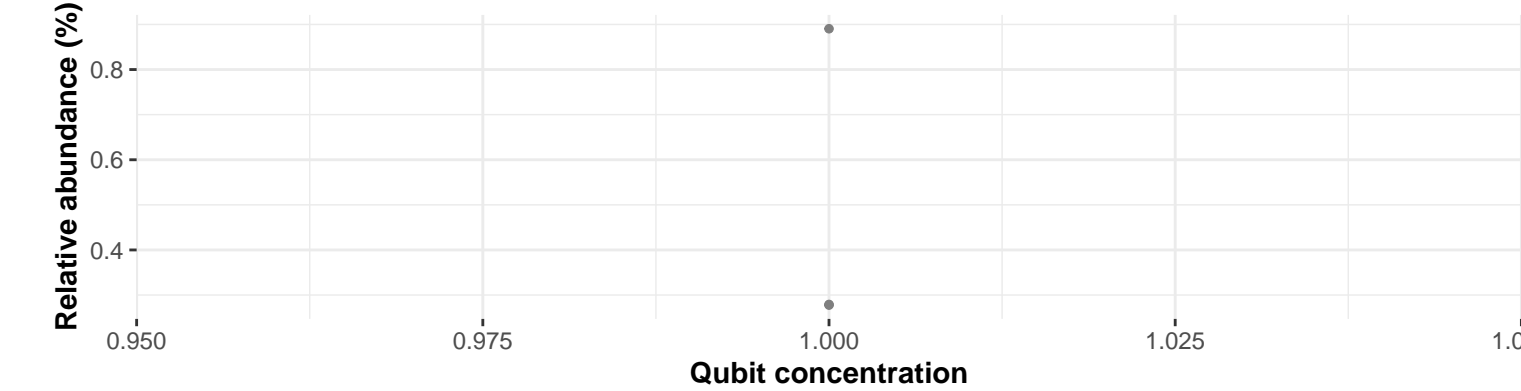
$\log_e(S) = 9.466$, $p = 0.192$, $\hat{\rho}_{\text{Spearman}} = -0.211$, $CI_{95\%} [-0.497, 0.117]$, $n_{\text{pairs}} = 40$



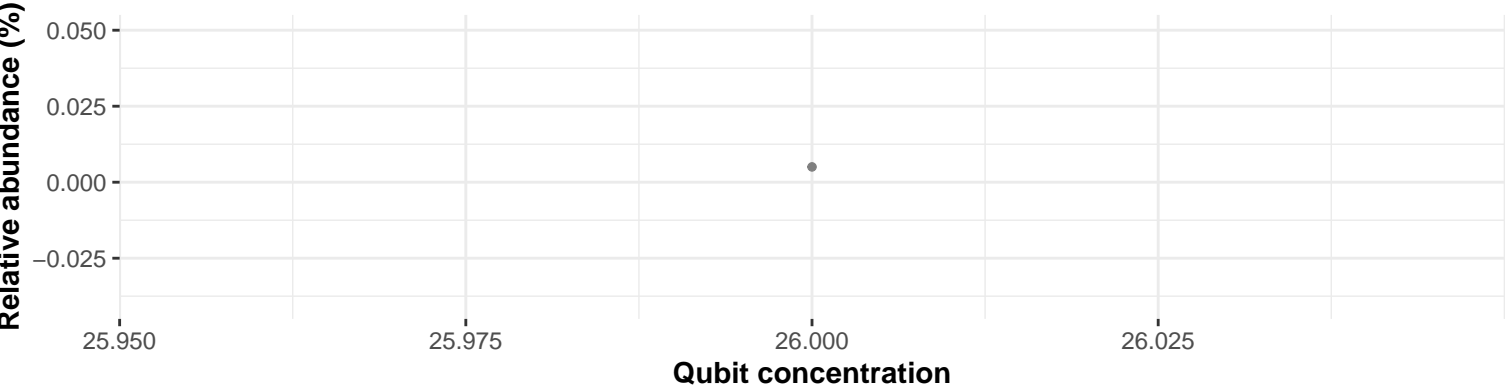
Correlation within: Feed



Correlation within: control



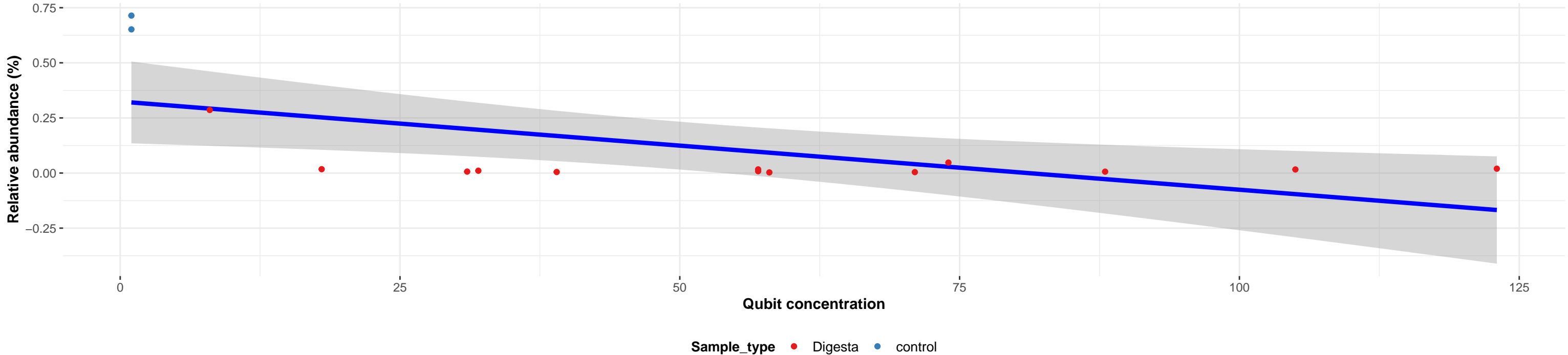
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

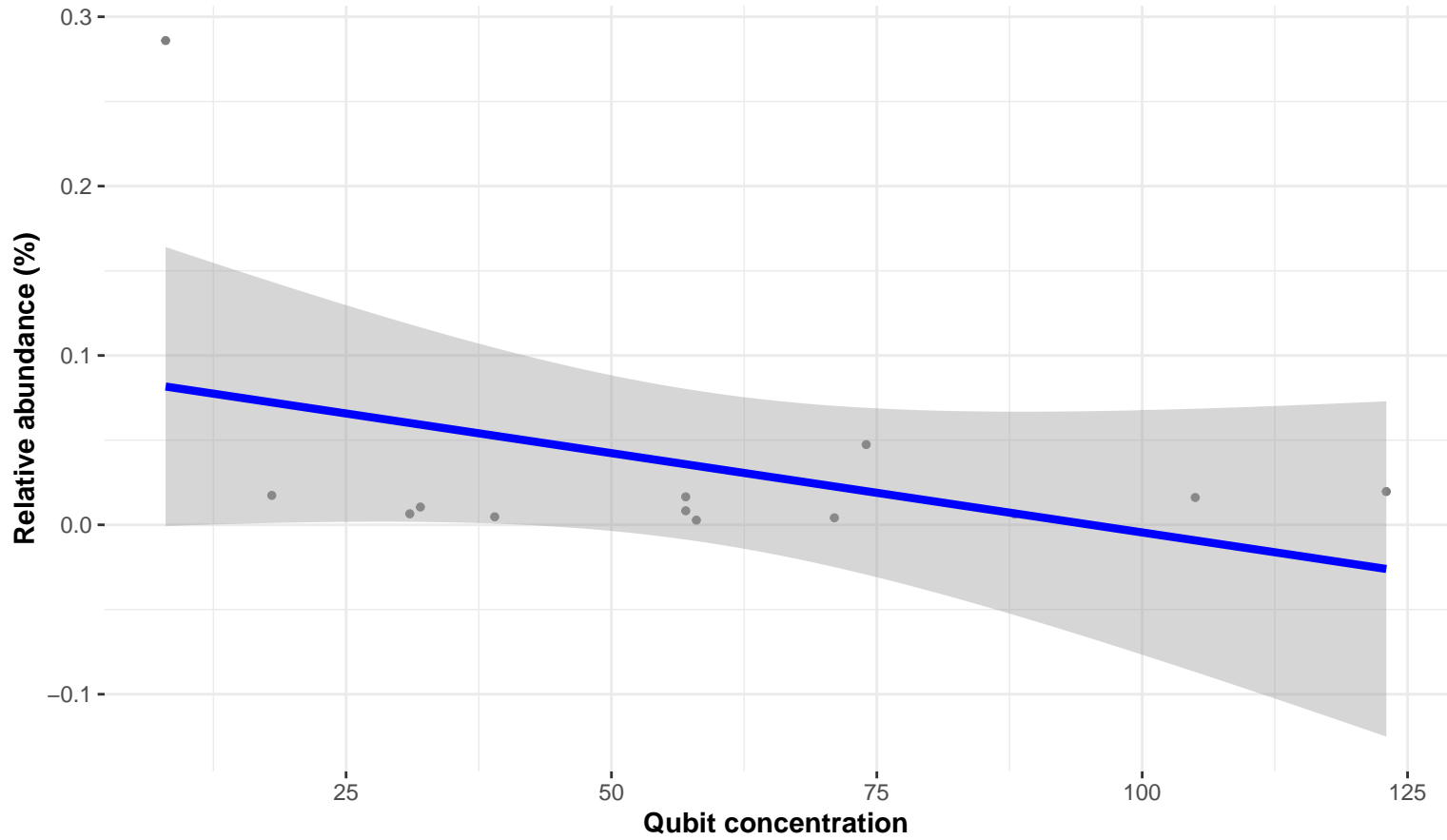
Correlation with all samples

$\log_e(S) = 6.678$, $p = 0.120$, $\hat{\rho}_{\text{Spearman}} = -0.419$, $\text{CI}_{95\%} [-0.773, 0.136]$, $n_{\text{pairs}} = 15$

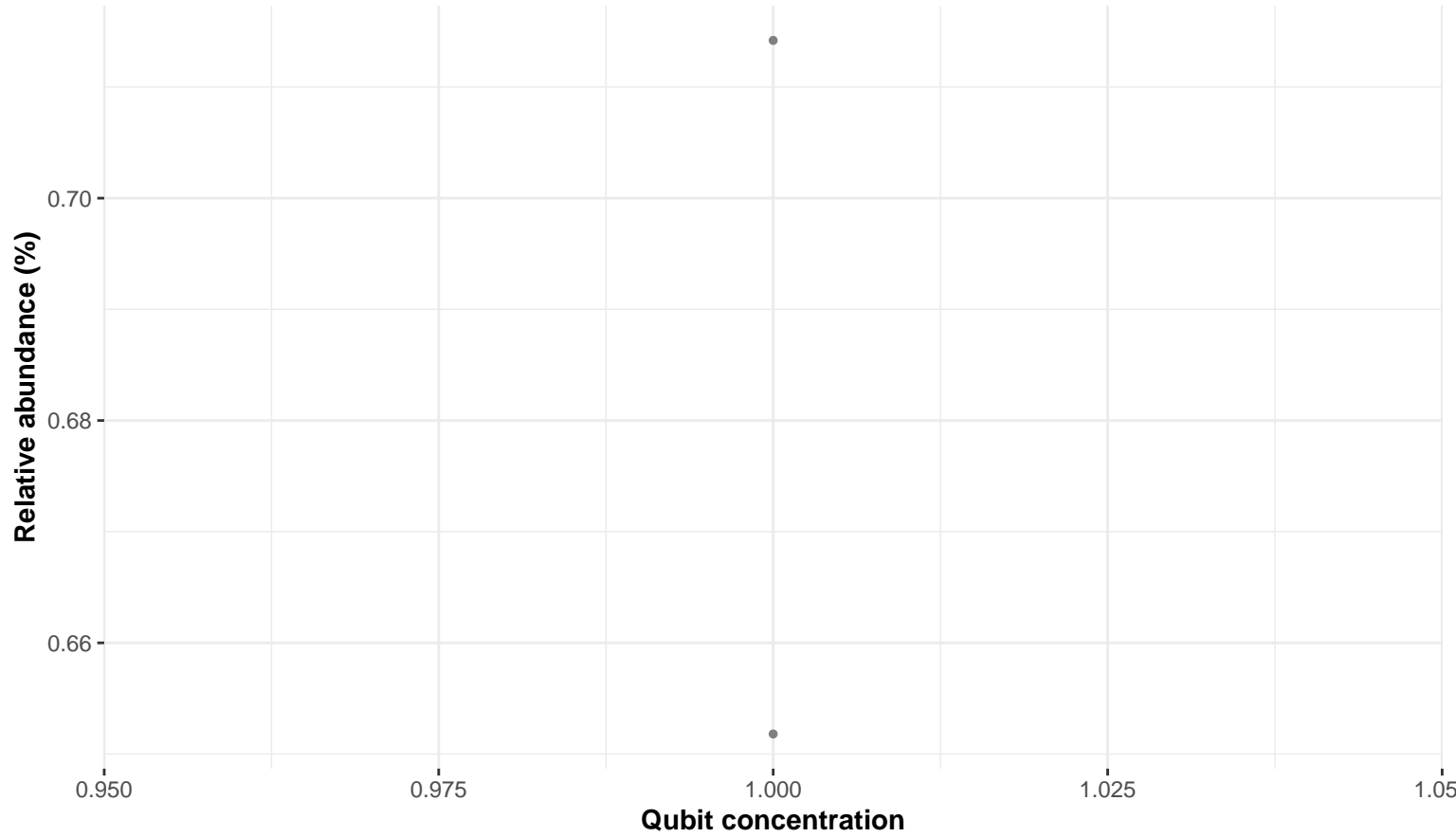


Correlation within: Digesta

$\log_e(S) = 5.999$, $p = 0.727$, $\hat{\rho}_{\text{Spearman}} = -0.107$, $\text{CI}_{95\%} [-0.633, 0.486]$, $n_{\text{pairs}} = 13$



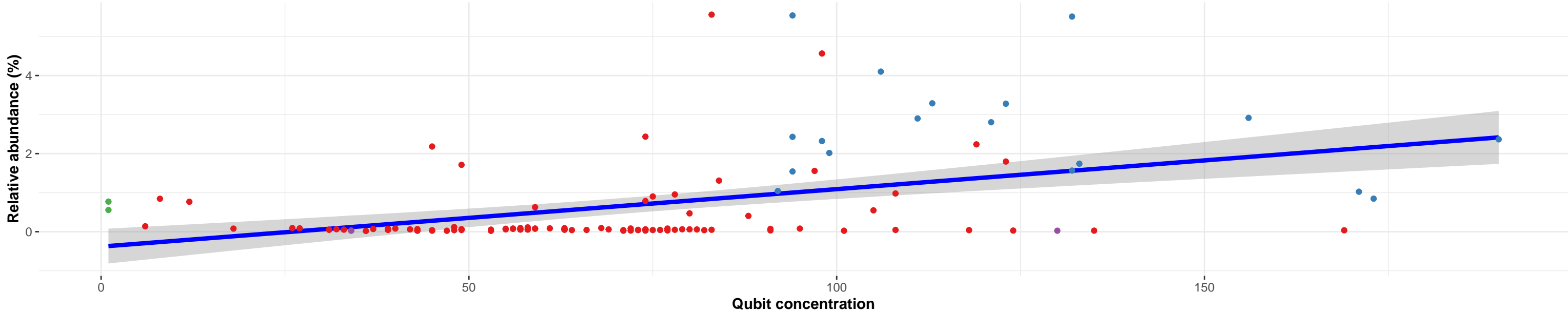
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Vibrionaceae; Photobacterium; phosphoreum

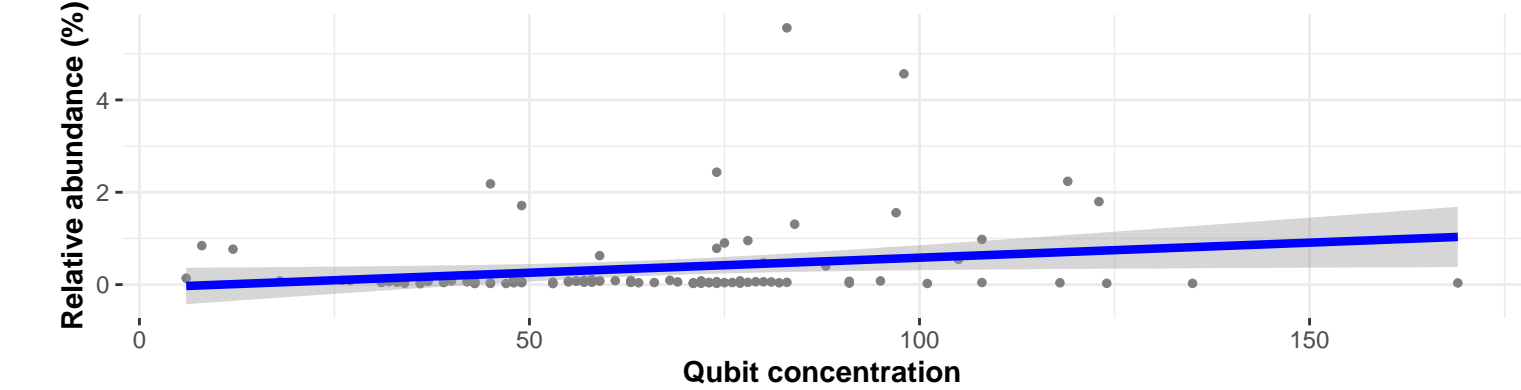
Correlation with all samples

$\log_e(S) = 12.228$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.307$, $\text{CI}_{95\%} [0.131, 0.465]$, $n_{\text{pairs}} = 121$



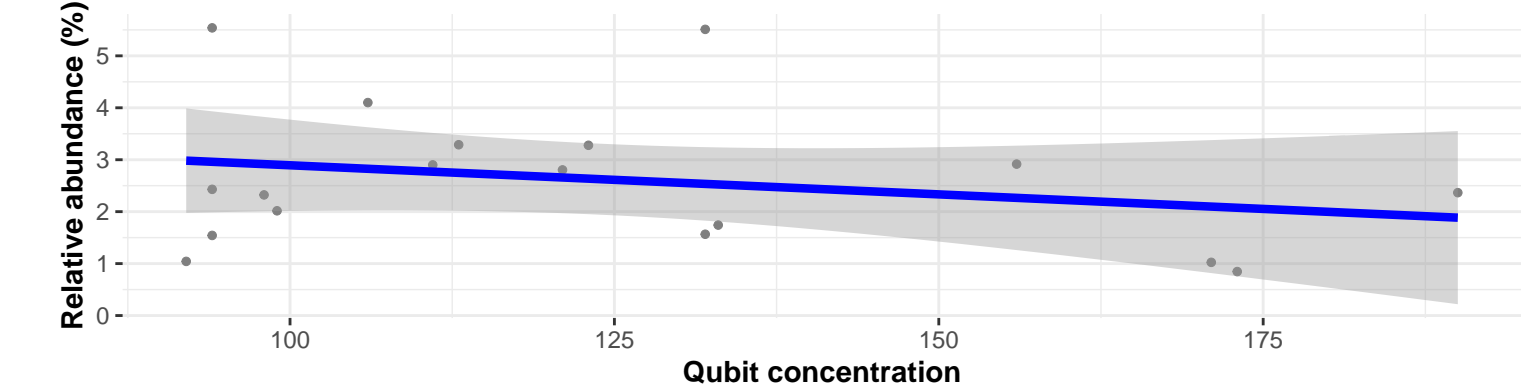
Correlation within: Digesta

$\log_e(S) = 11.950$, $p = 0.676$, $\hat{\rho}_{\text{Spearman}} = 0.043$, $\text{CI}_{95\%} [-0.162, 0.243]$, $n_{\text{pairs}} = 99$

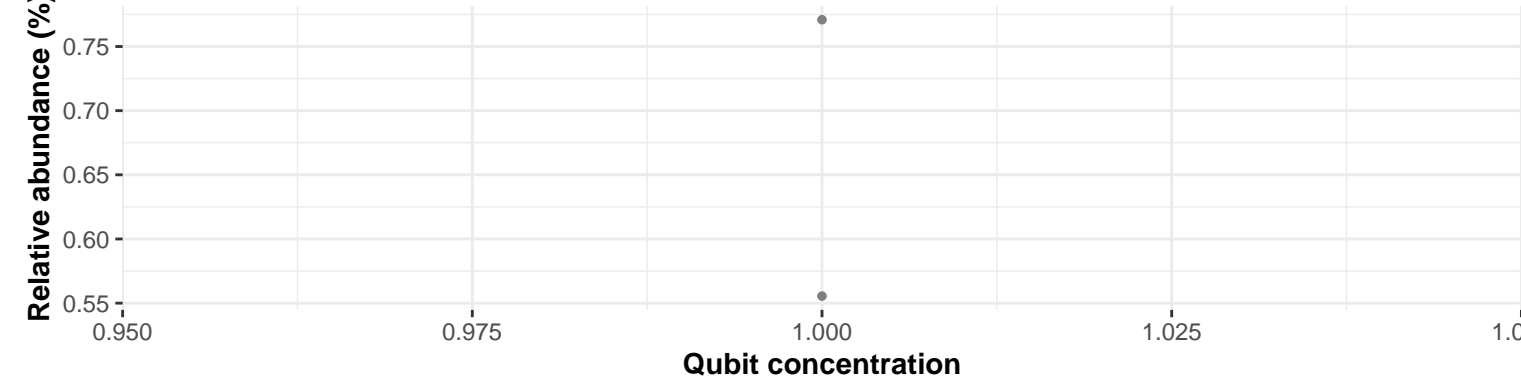


Correlation within: Feed

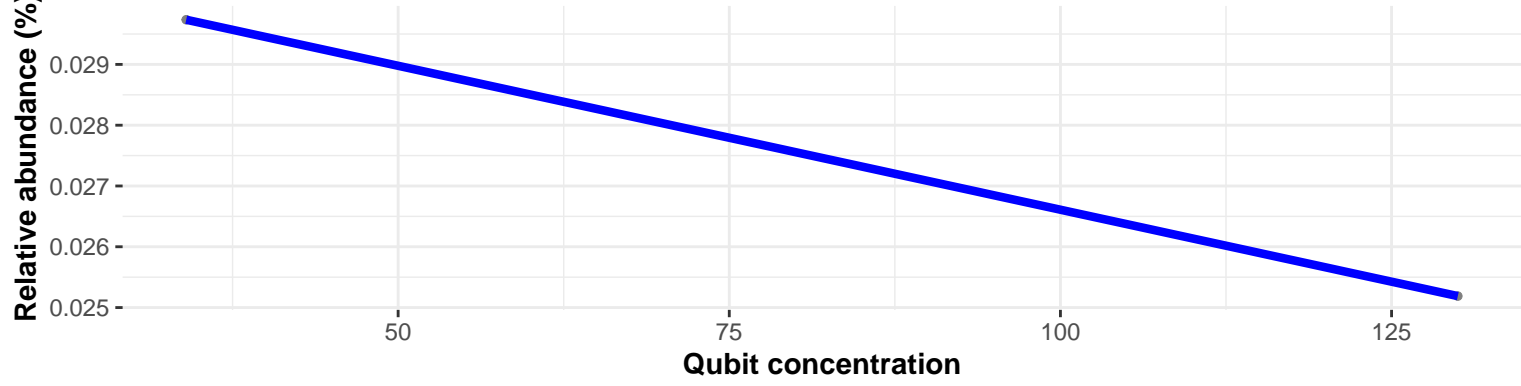
$\log_e(S) = 7.014$, $p = 0.558$, $\hat{\rho}_{\text{Spearman}} = -0.148$, $\text{CI}_{95\%} [-0.585, 0.356]$, $n_{\text{pairs}} = 18$



Correlation within: control



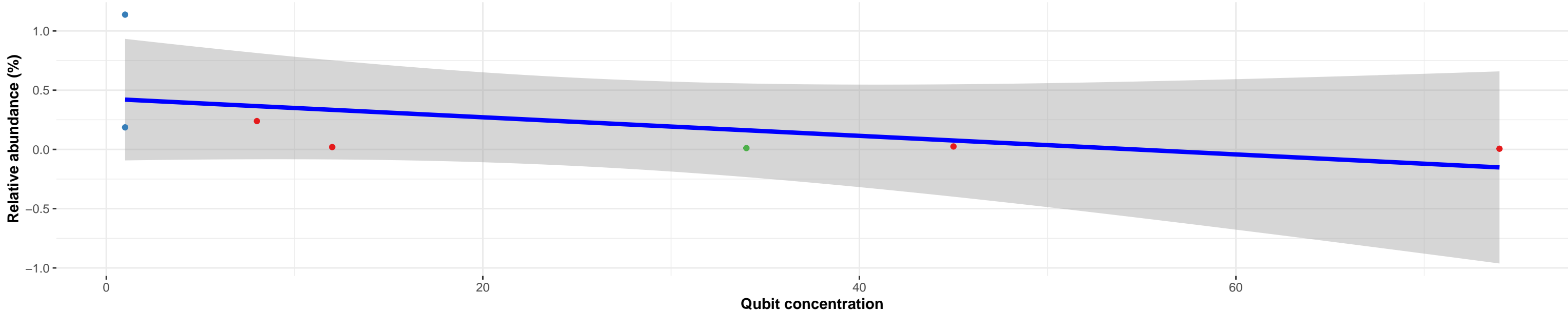
Correlation within: water



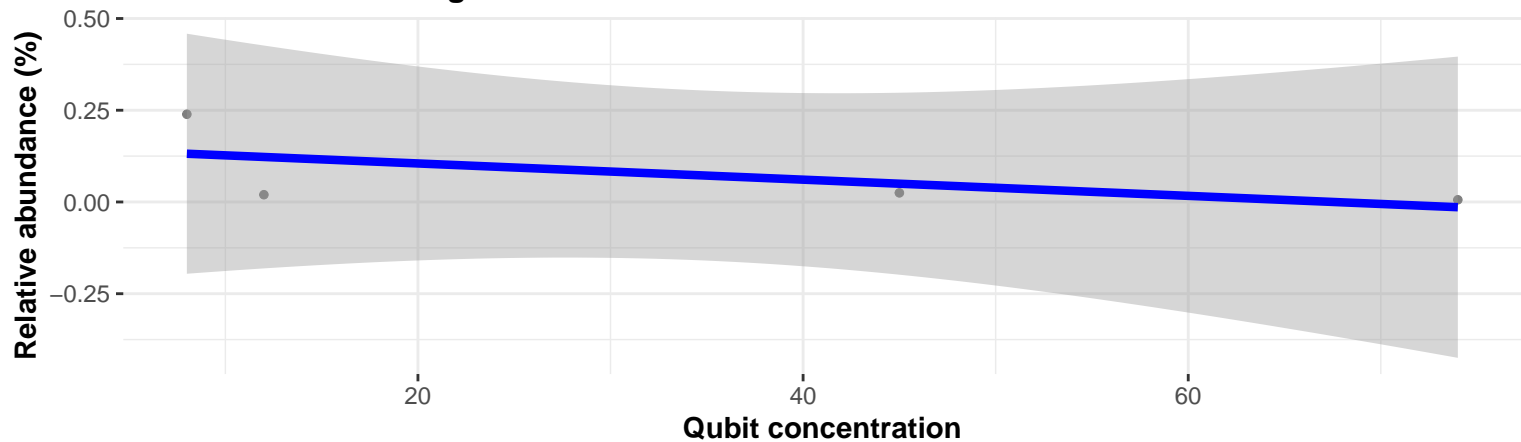
Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Dermabacteraceae; Brachybacterium; muris

Correlation with all samples

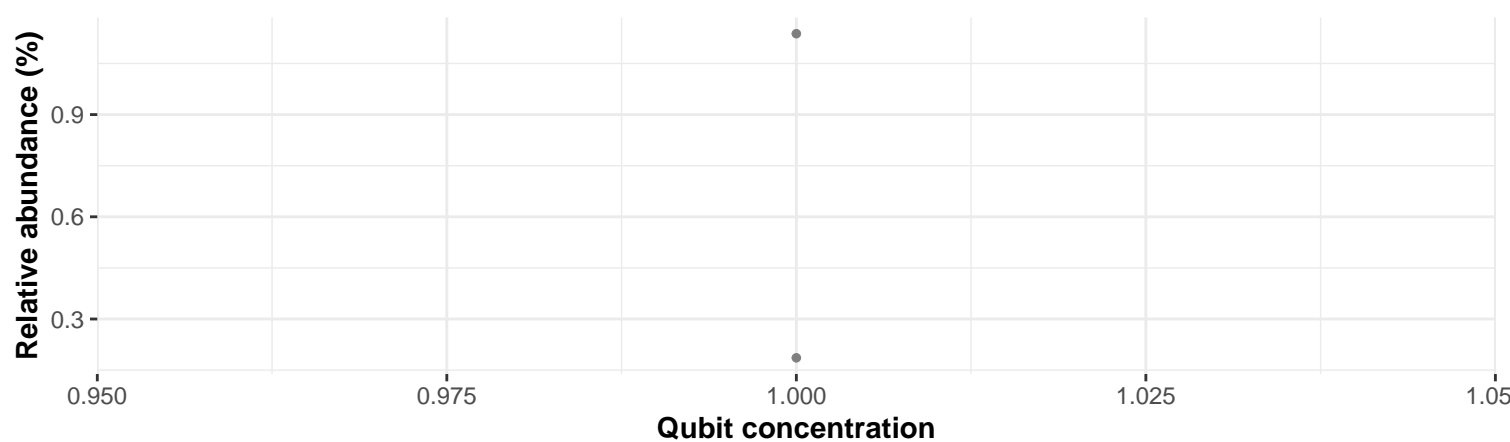
$\log_e(S) = 4.629$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = -0.829$, $CI_{95\%} [-0.975, -0.174]$, $n_{\text{pairs}} = 7$



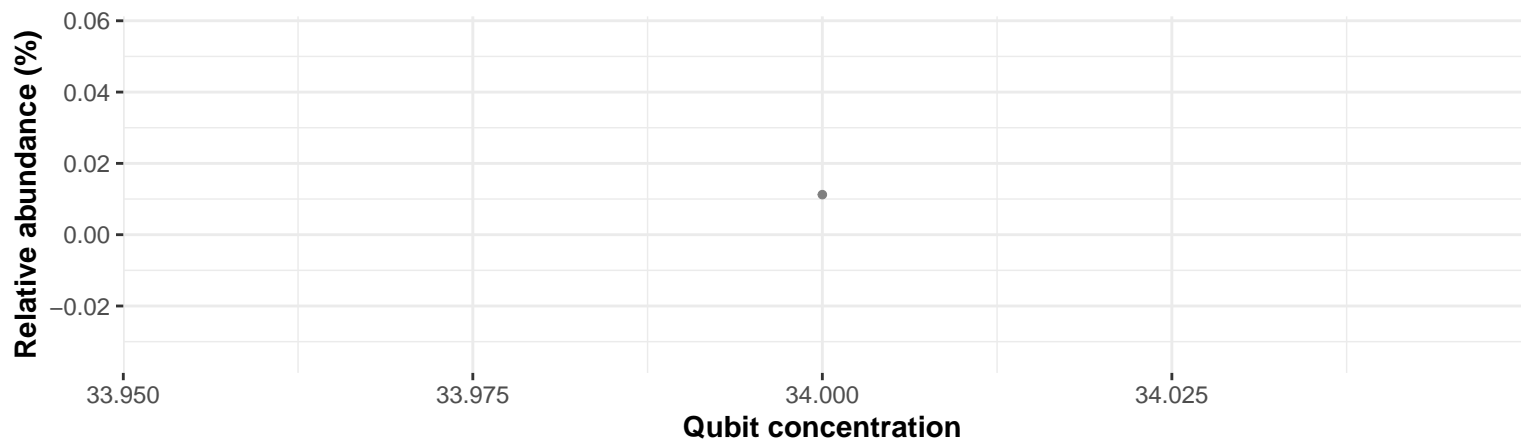
Correlation within: Digesta



Correlation within: control



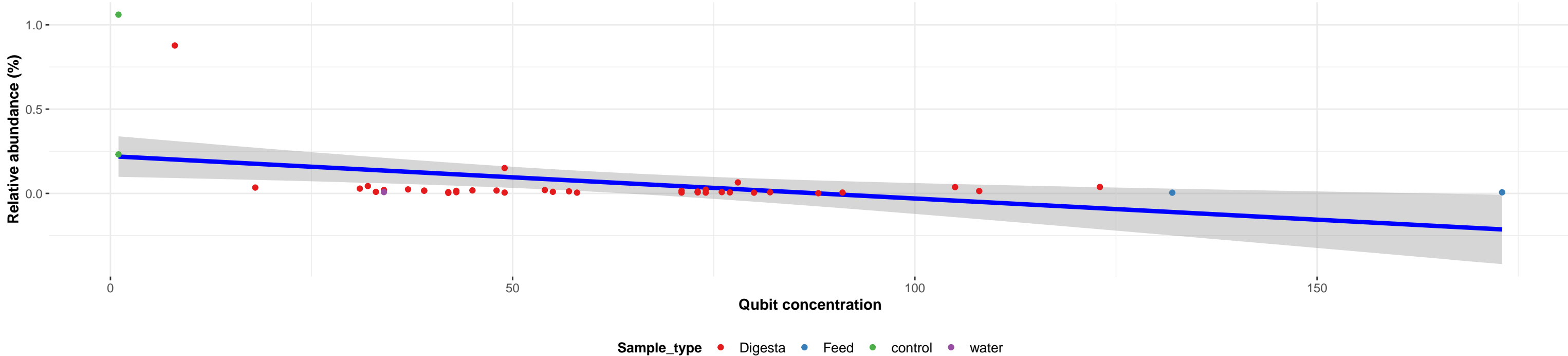
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Micrococcaceae; Pseudoglutamicibacter; NA

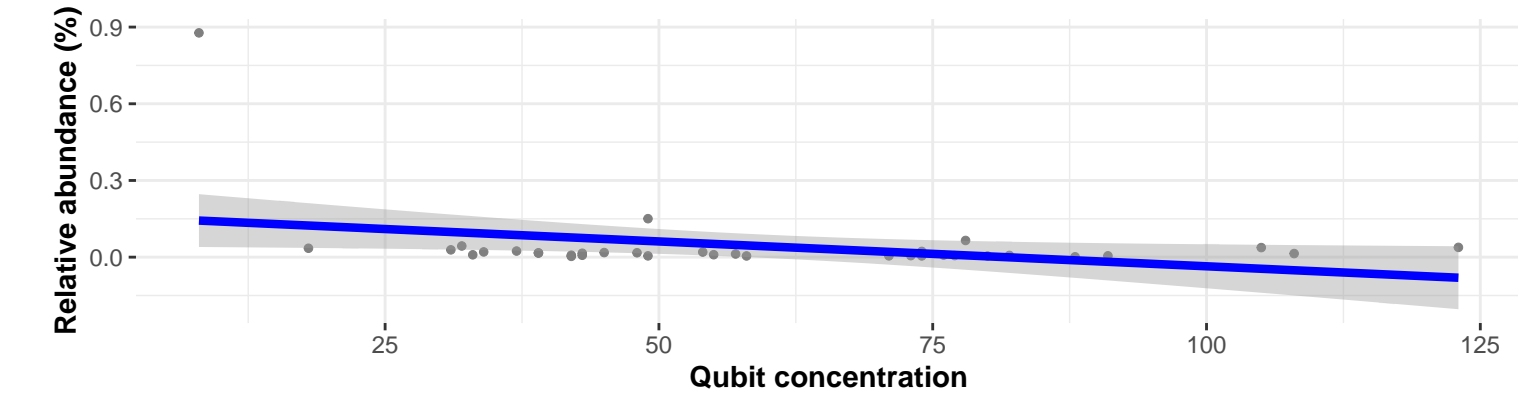
Correlation with all samples

$\log_e(S) = 9.803$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.466$, $CI_{95\%} [-0.679, -0.179]$, $n_{\text{pairs}} = 42$

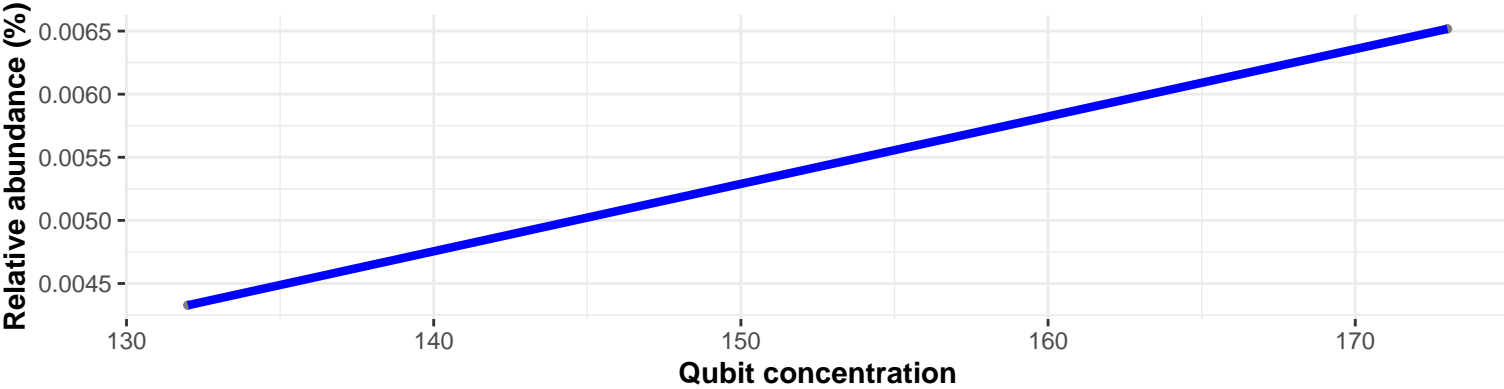


Correlation within: Digesta

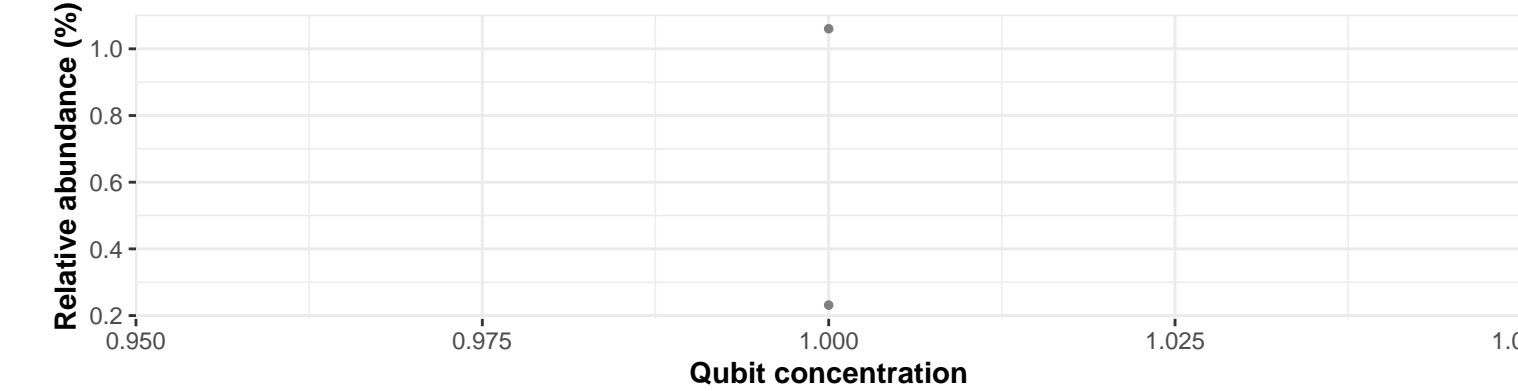
$\log_e(S) = 9.324$, $p = 0.047$, $\hat{\rho}_{\text{Spearman}} = -0.328$, $CI_{95\%} [-0.596, 0.005]$, $n_{\text{pairs}} = 37$



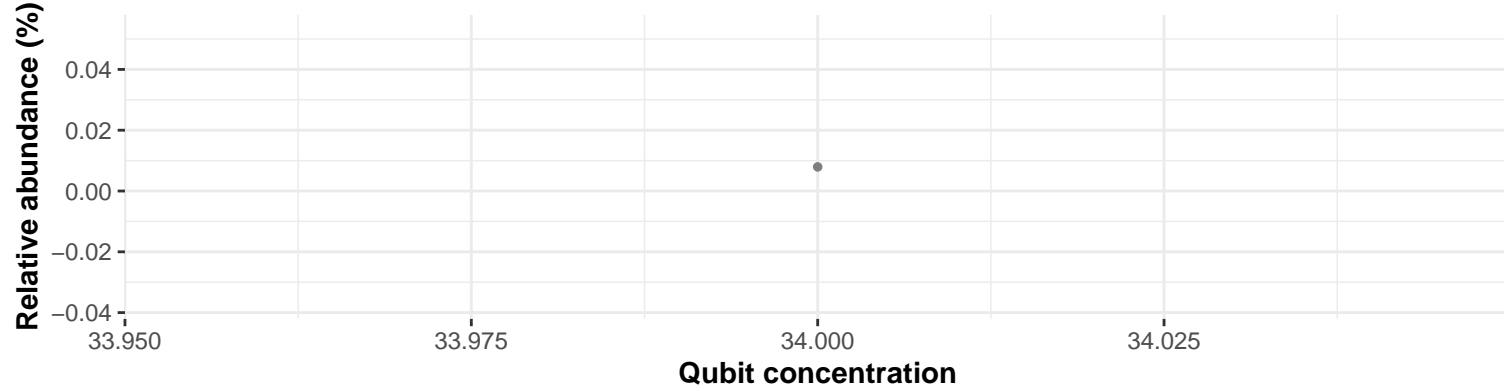
Correlation within: Feed



Correlation within: control



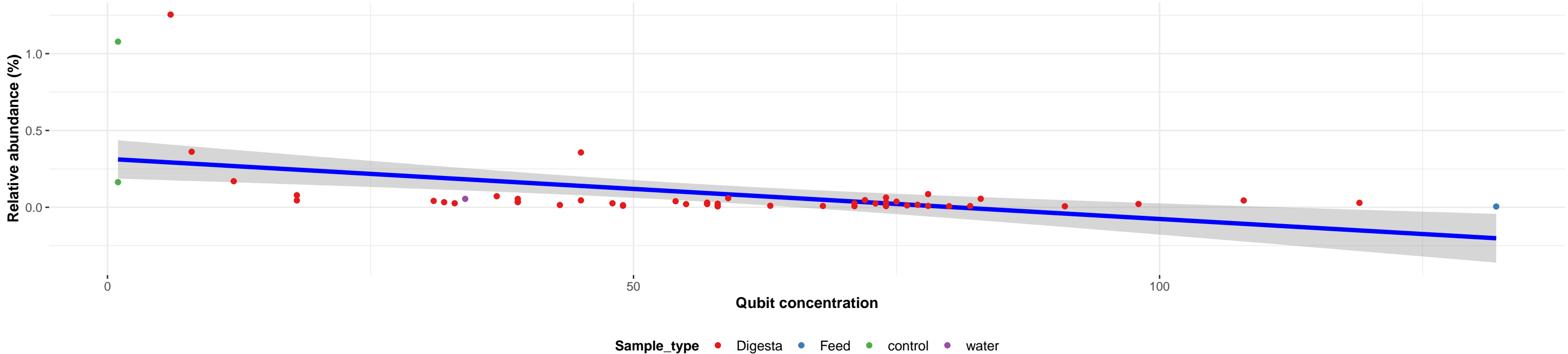
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

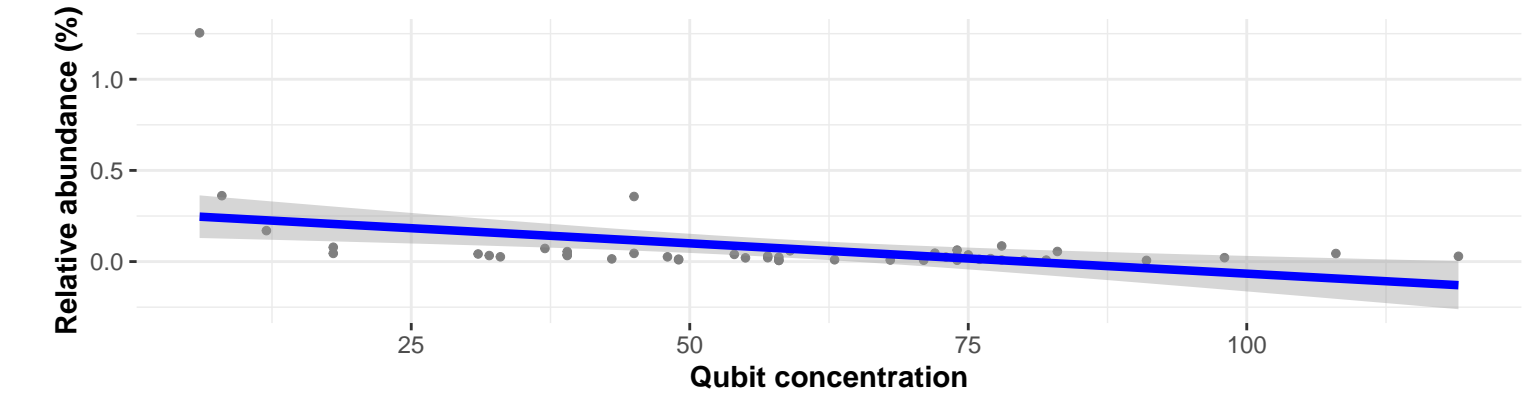
Correlation with all samples

$\log_e(S) = 10.492$, $p = 3.88e-05$, $\hat{\rho}_{\text{Spearman}} = -0.538$, $CI_{95\%} [-0.711, -0.303]$, $n_{\text{pairs}} = 52$

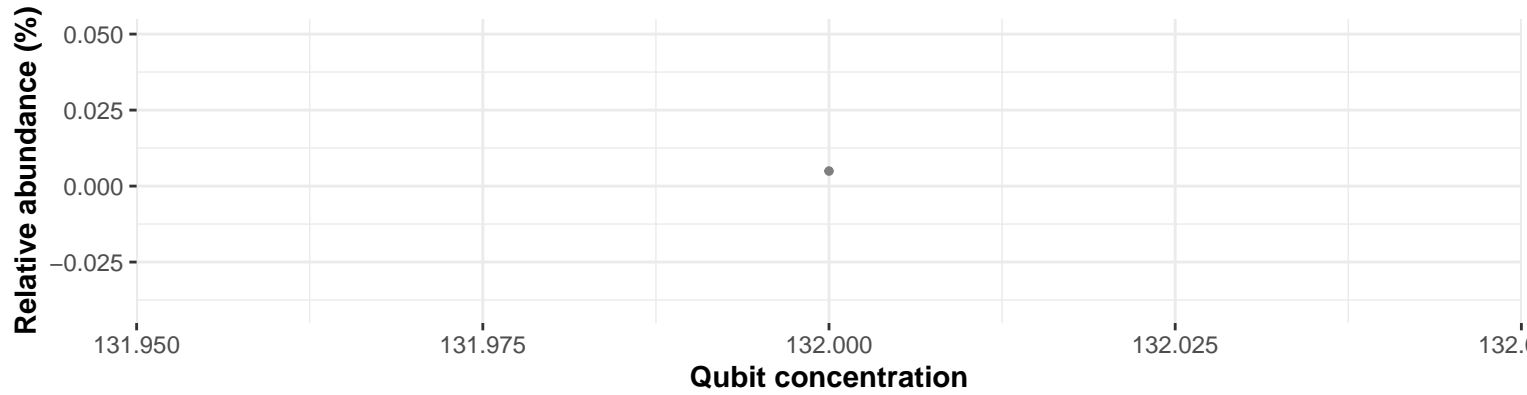


Correlation within: Digesta

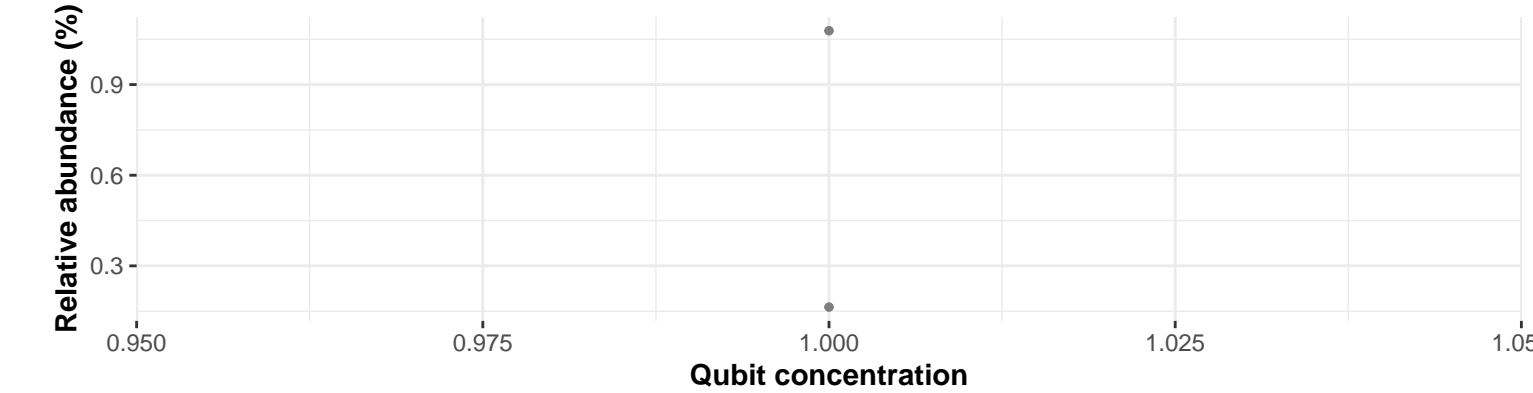
$\log_e(S) = 10.183$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.436$, $CI_{95\%} [-0.645, -0.164]$, $n_{\text{pairs}} = 48$



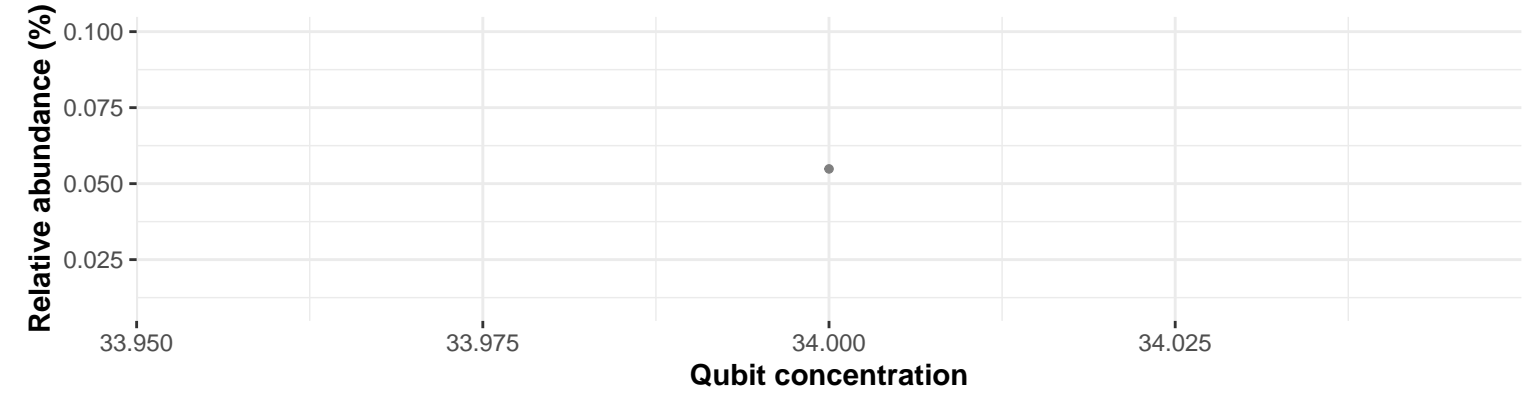
Correlation within: Feed



Correlation within: control



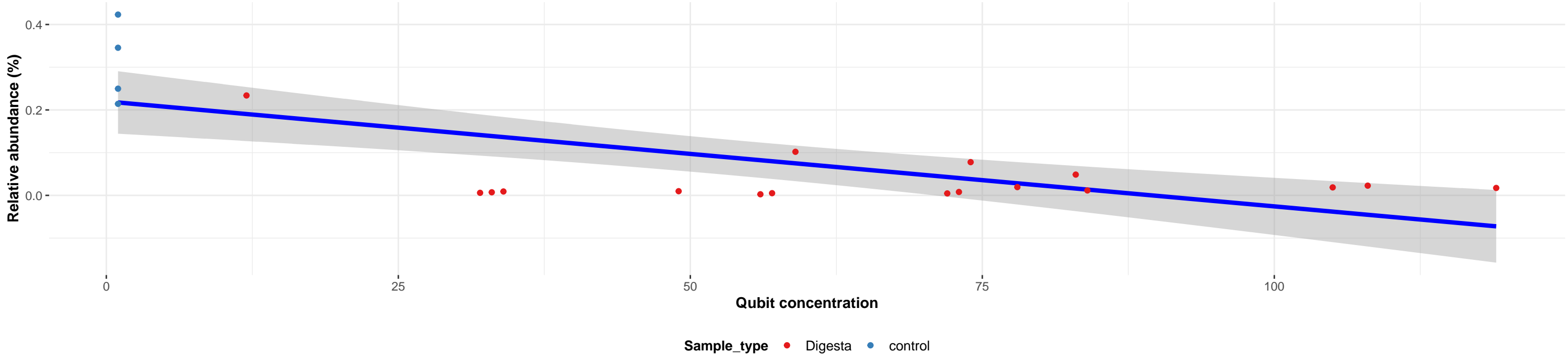
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

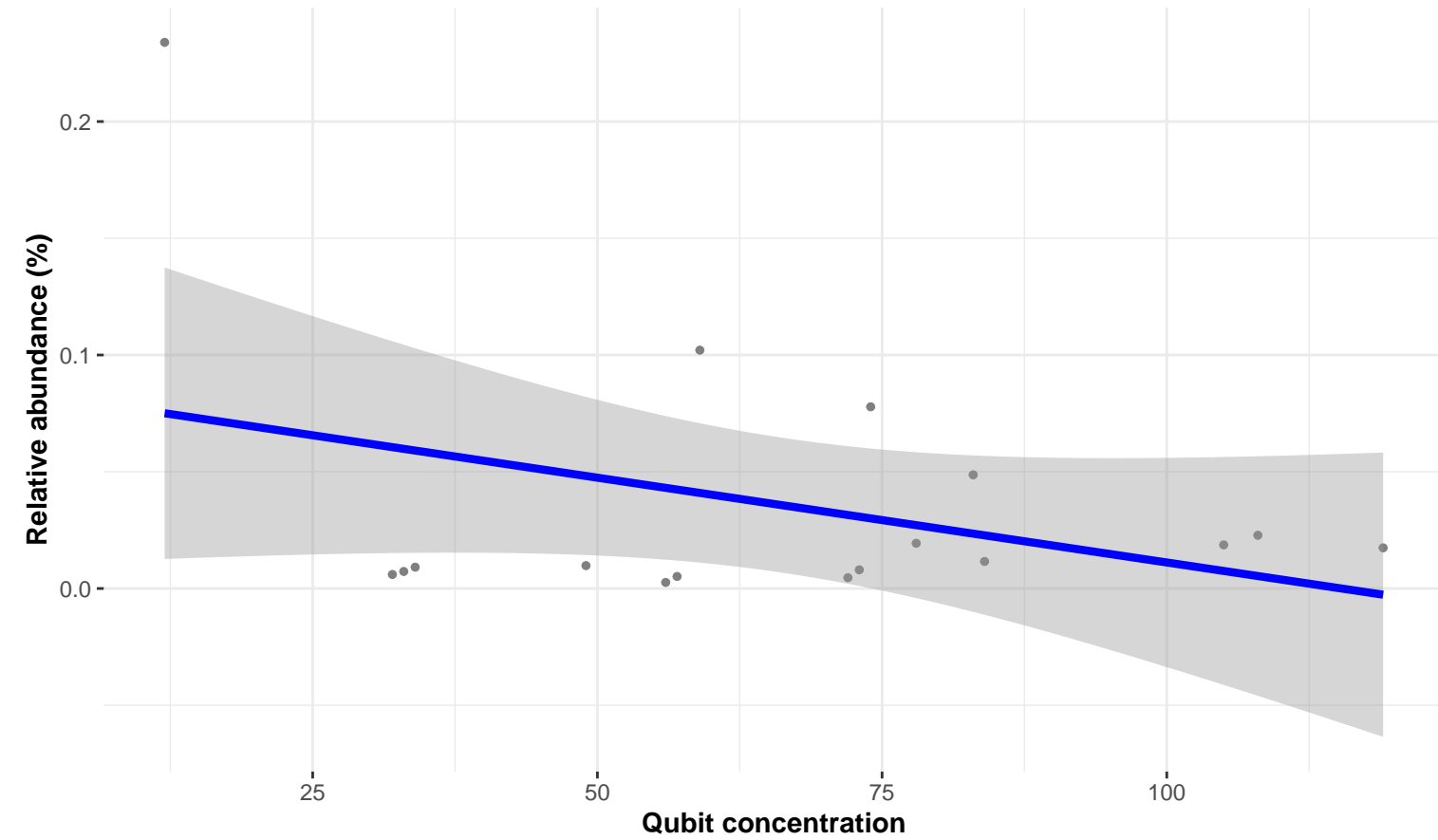
Correlation with all samples

$\log_e(S) = 7.602$, $p = 0.186$, $\hat{\rho}_{\text{Spearman}} = -0.300$, $CI_{95\%} [-0.656, 0.164]$, $n_{\text{pairs}} = 21$

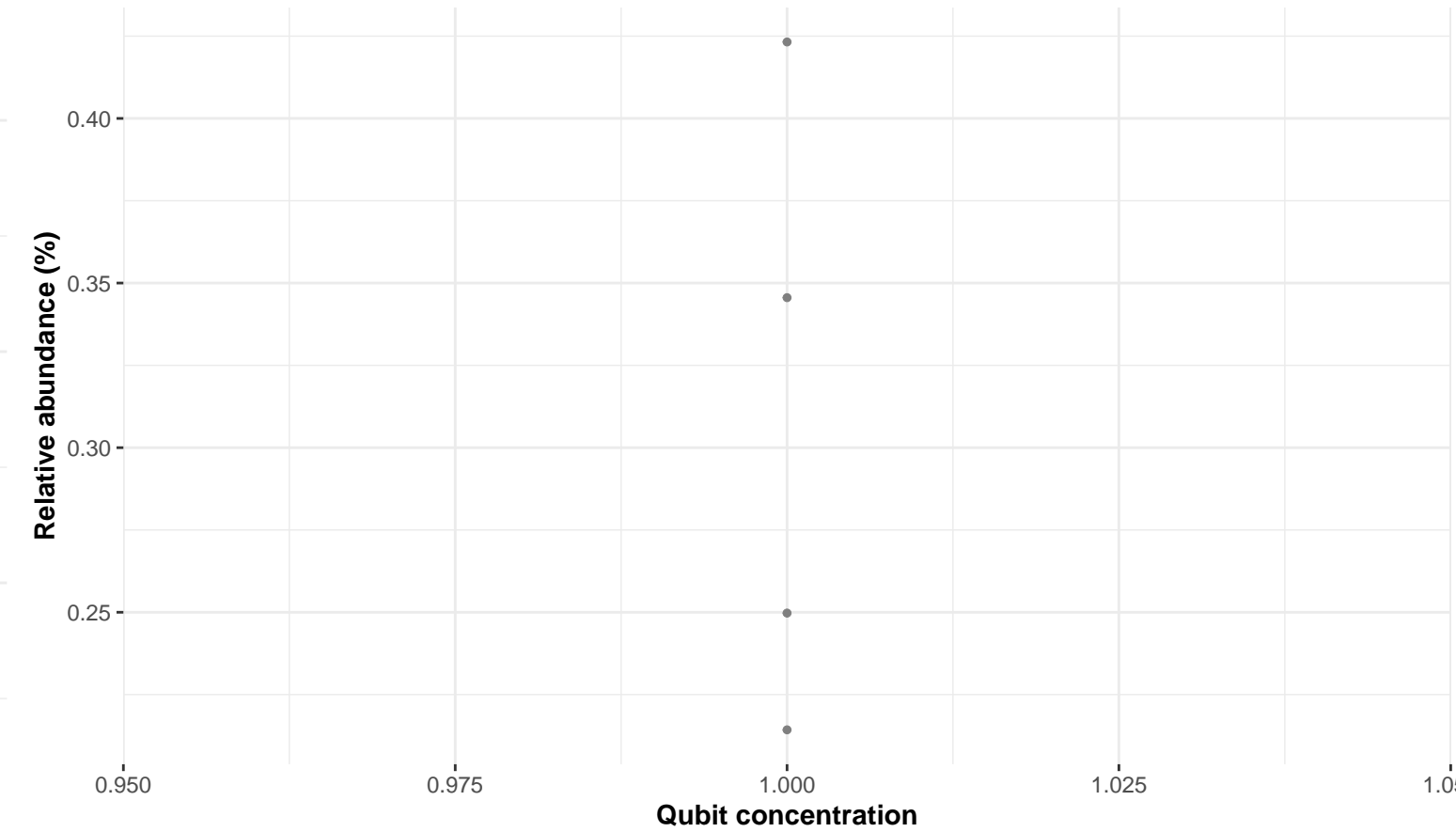


Correlation within: Digesta

$\log_e(S) = 6.342$, $p = 0.236$, $\hat{\rho}_{\text{Spearman}} = 0.304$, $CI_{95\%} [-0.222, 0.693]$, $n_{\text{pairs}} = 17$



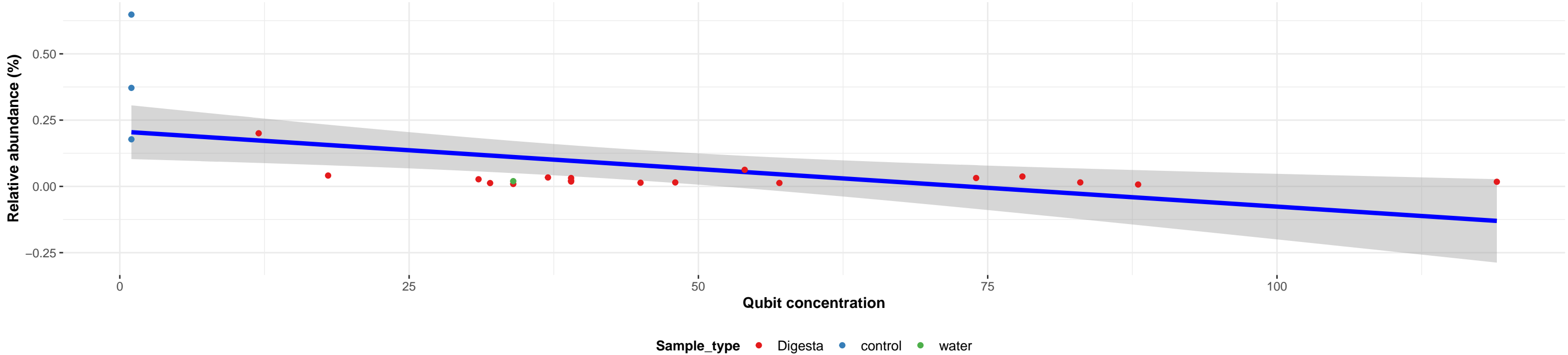
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

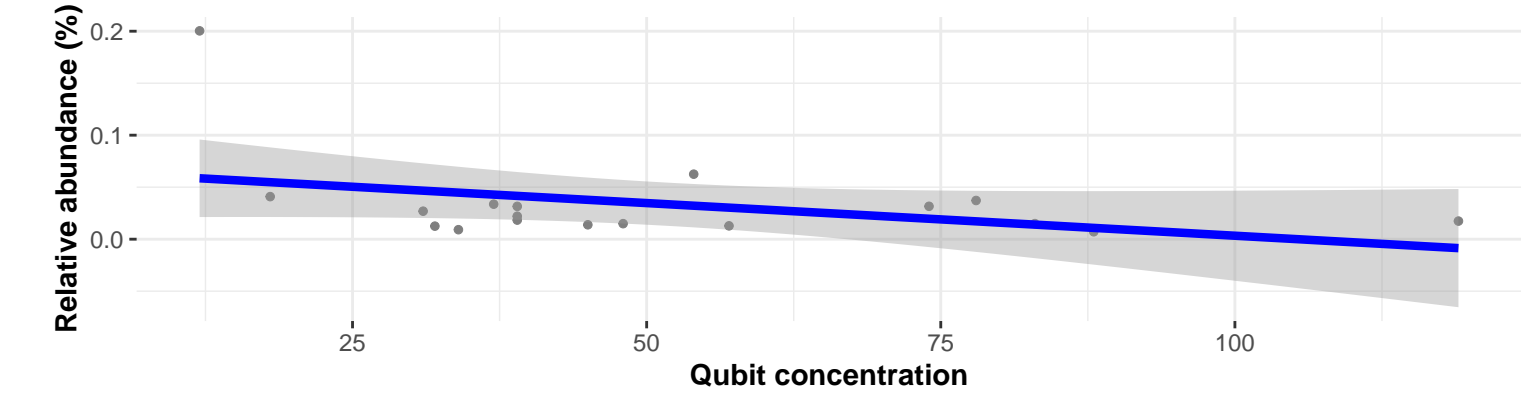
Correlation with all samples

$\log_e(S) = 7.906$, $p = 0.011$, $\hat{\rho}_{\text{Spearman}} = -0.533$, $\text{CI}_{95\%} [-0.784, -0.130]$, $n_{\text{pairs}} = 22$

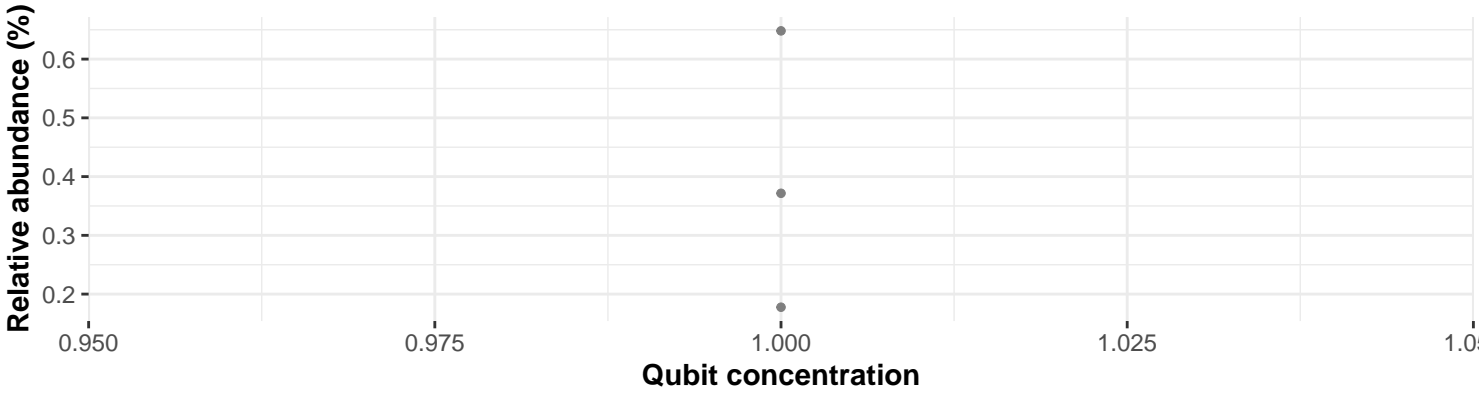


Correlation within: Digesta

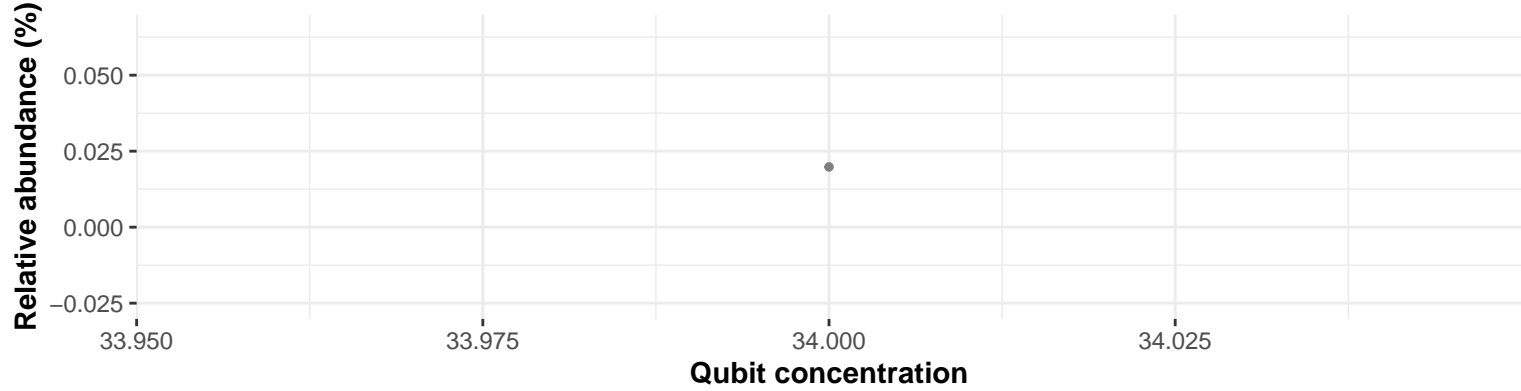
$\log_e(S) = 7.123$, $p = 0.260$, $\hat{\rho}_{\text{Spearman}} = -0.280$, $\text{CI}_{95\%} [-0.669, 0.229]$, $n_{\text{pairs}} = 18$



Correlation within: control



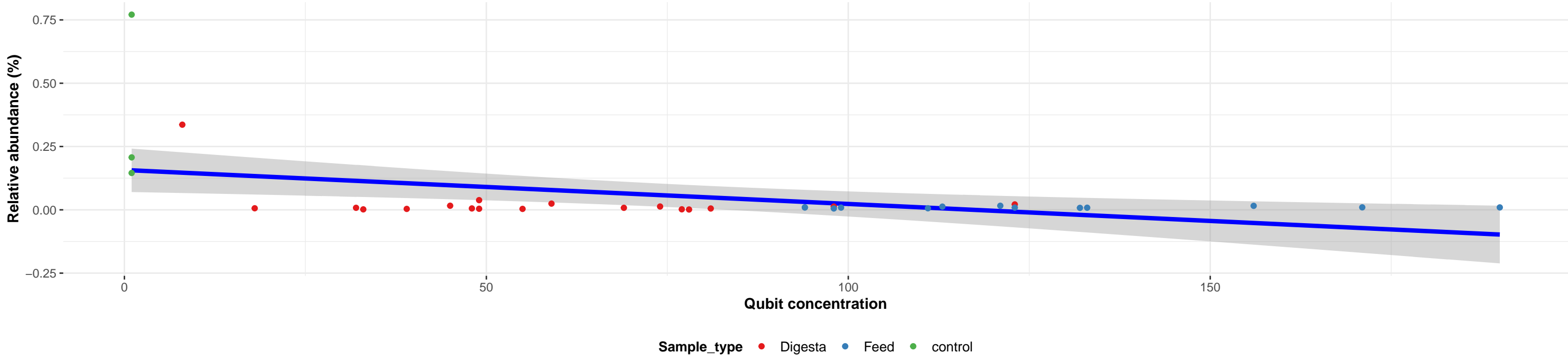
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; NA

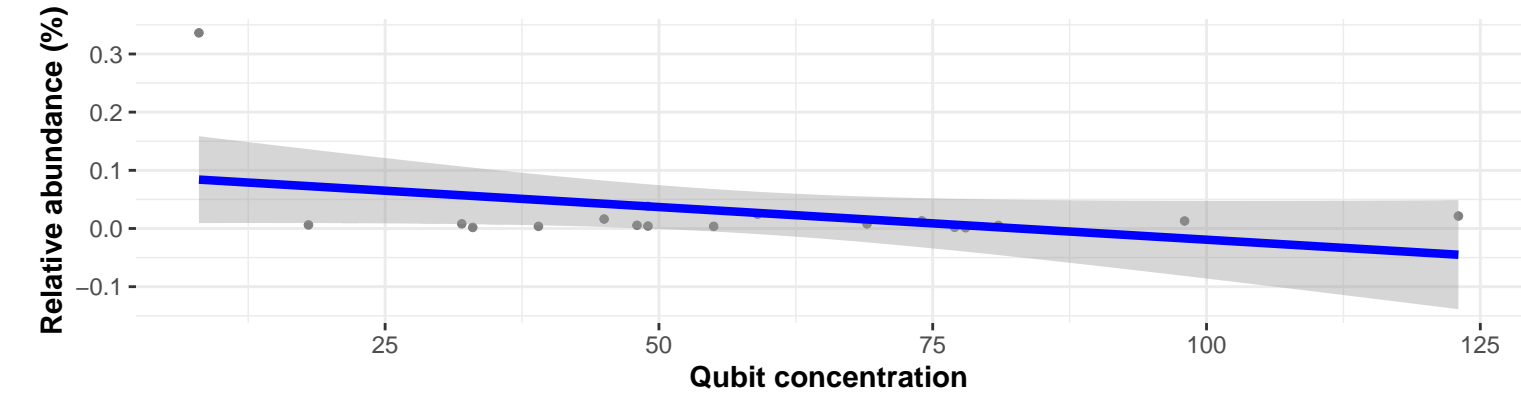
Correlation with all samples

$\log_e(S) = 8.869$, $p = 0.629$, $\hat{\rho}_{\text{Spearman}} = -0.086$, $\text{CI}_{95\%} [-0.421, 0.269]$, $n_{\text{pairs}} = 34$



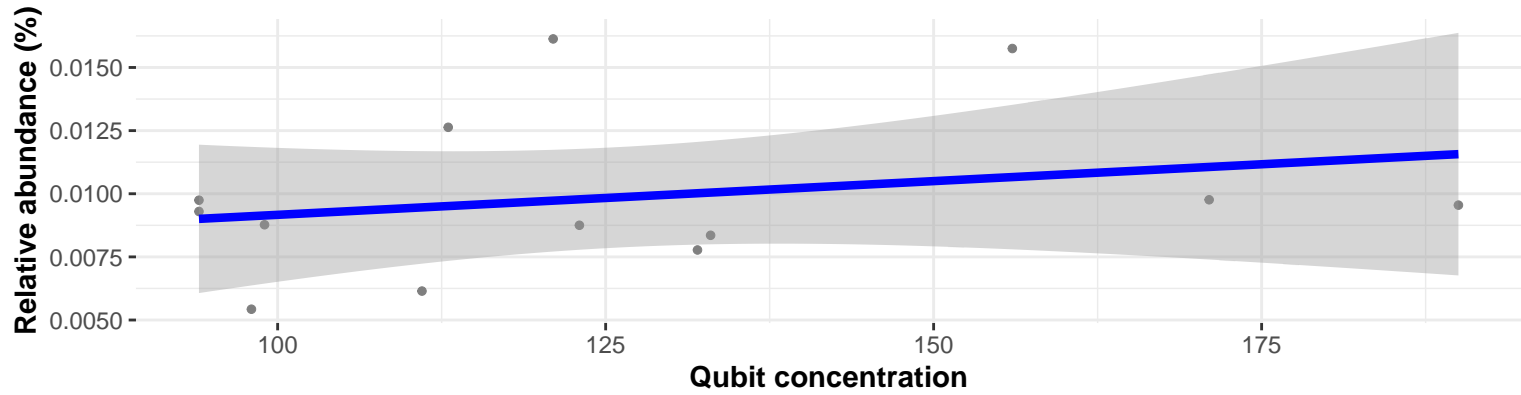
Correlation within: Digesta

$\log_e(S) = 6.954$, $p = 0.751$, $\hat{\rho}_{\text{Spearman}} = -0.081$, $\text{CI}_{95\%} [-0.538, 0.414]$, $n_{\text{pairs}} = 18$

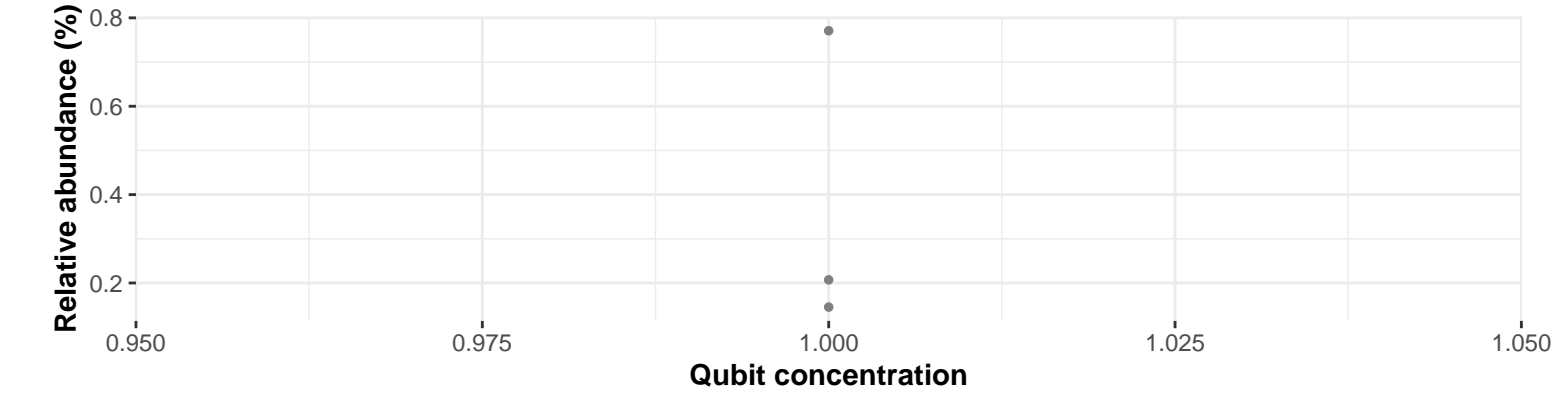


Correlation within: Feed

$\log_e(S) = 5.620$, $p = 0.426$, $\hat{\rho}_{\text{Spearman}} = 0.242$, $\text{CI}_{95\%} [-0.372, 0.709]$, $n_{\text{pairs}} = 13$



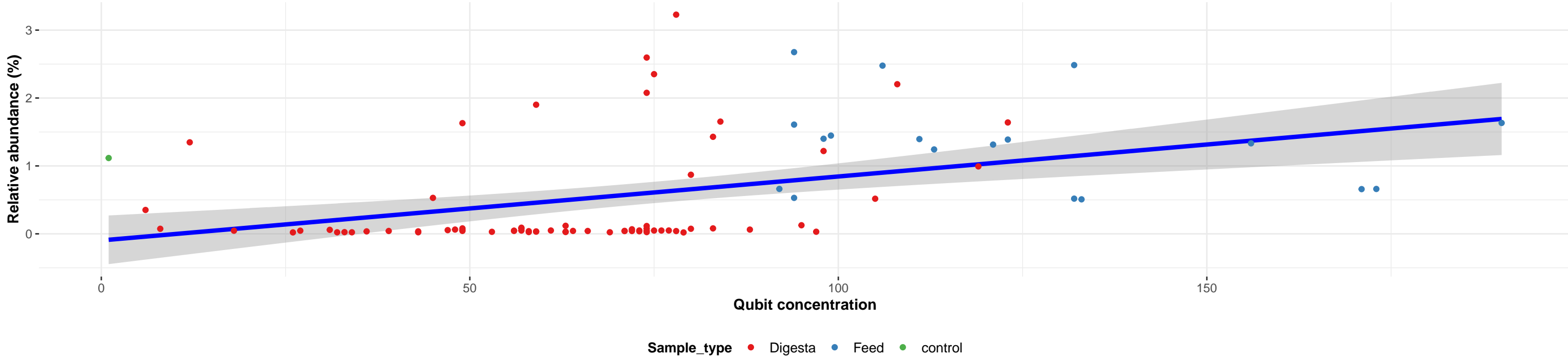
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; HT002; NA

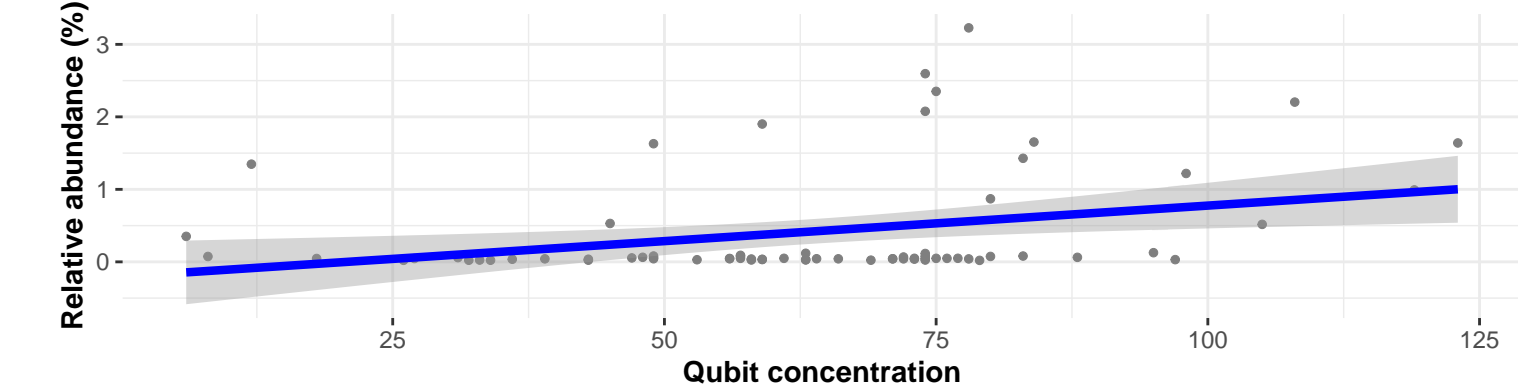
Correlation with all samples

$\log_e(S) = 10.941$, $p = 5.5e-08$, $\hat{\rho}_{\text{Spearman}} = 0.535$, $CI_{95\%} [0.364, 0.672]$, $n_{\text{pairs}} = 90$



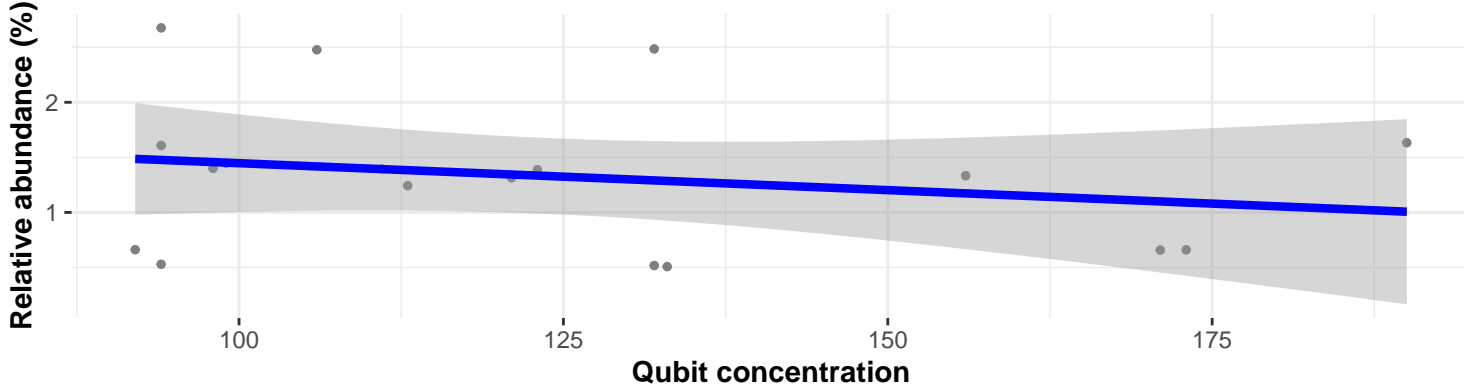
Correlation within: Digesta

$\log_e(S) = 10.559$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.354$, $CI_{95\%} [0.125, 0.547]$, $n_{\text{pairs}} = 71$

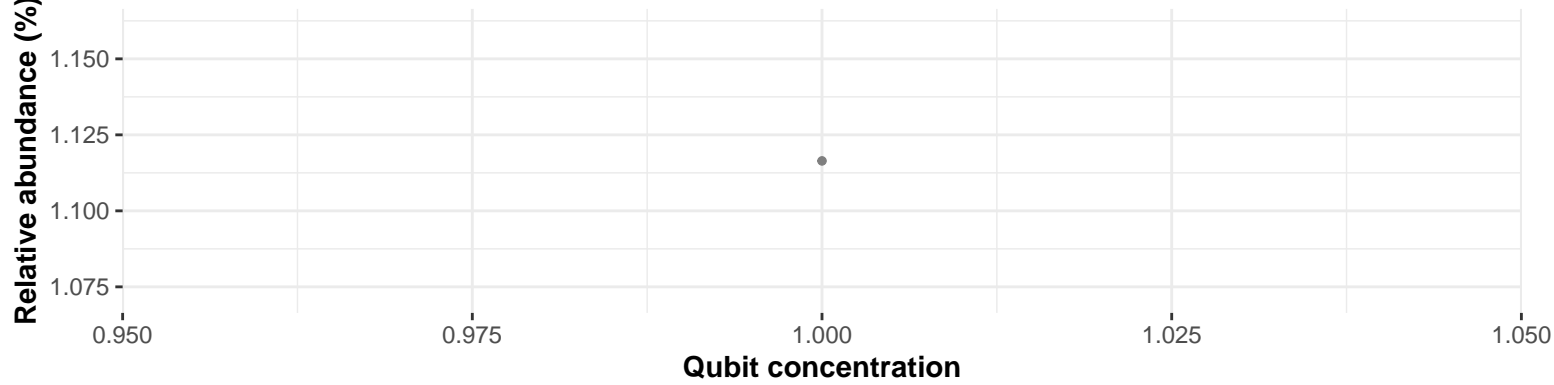


Correlation within: Feed

$\log_e(S) = 7.093$, $p = 0.333$, $\hat{\rho}_{\text{Spearman}} = -0.242$, $CI_{95\%} [-0.646, 0.267]$, $n_{\text{pairs}} = 18$



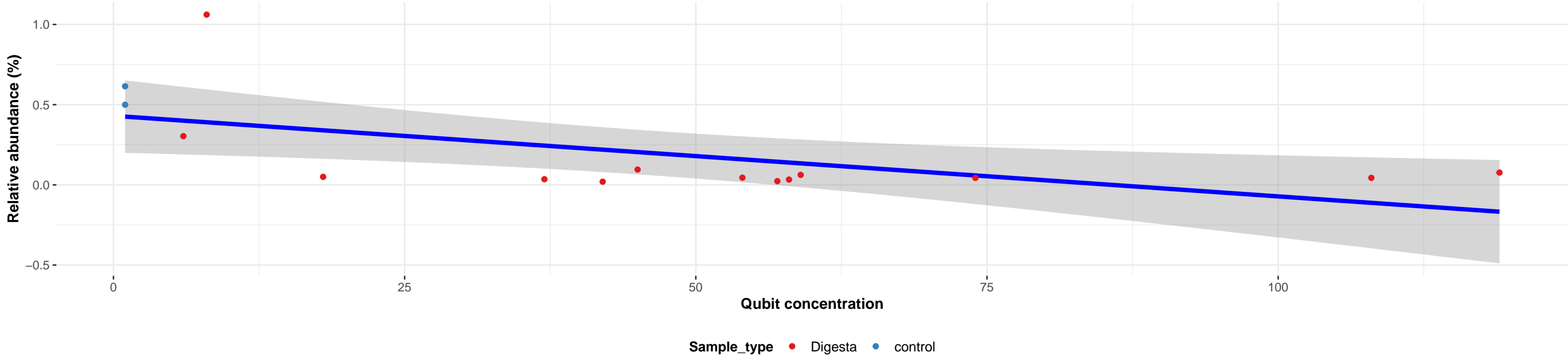
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

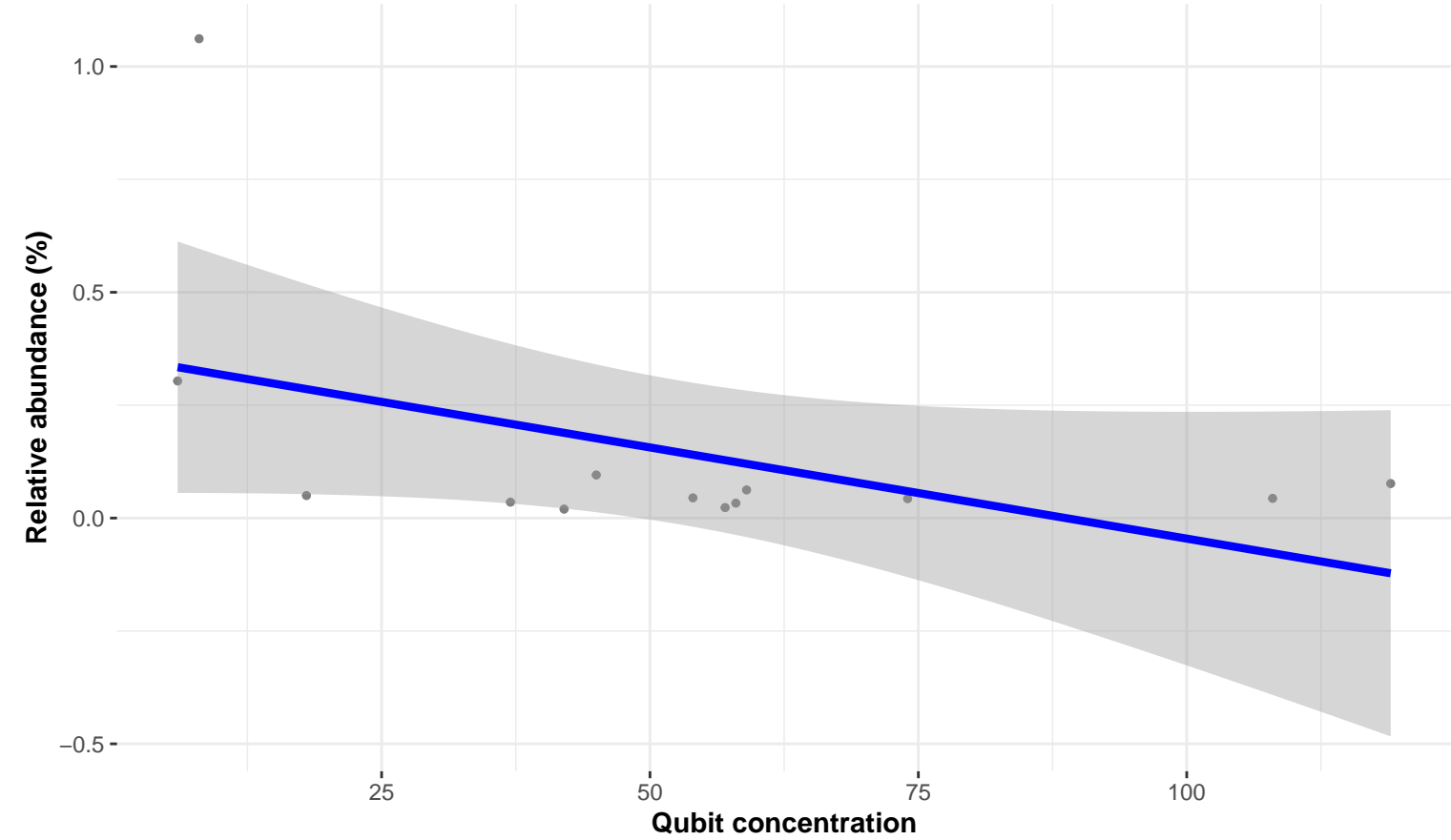
Correlation with all samples

$\log_e(S) = 6.737$, $p = 0.054$, $\hat{\rho}_{\text{Spearman}} = -0.506$, $\text{CI}_{95\%} [-0.814, 0.025]$, $n_{\text{pairs}} = 15$

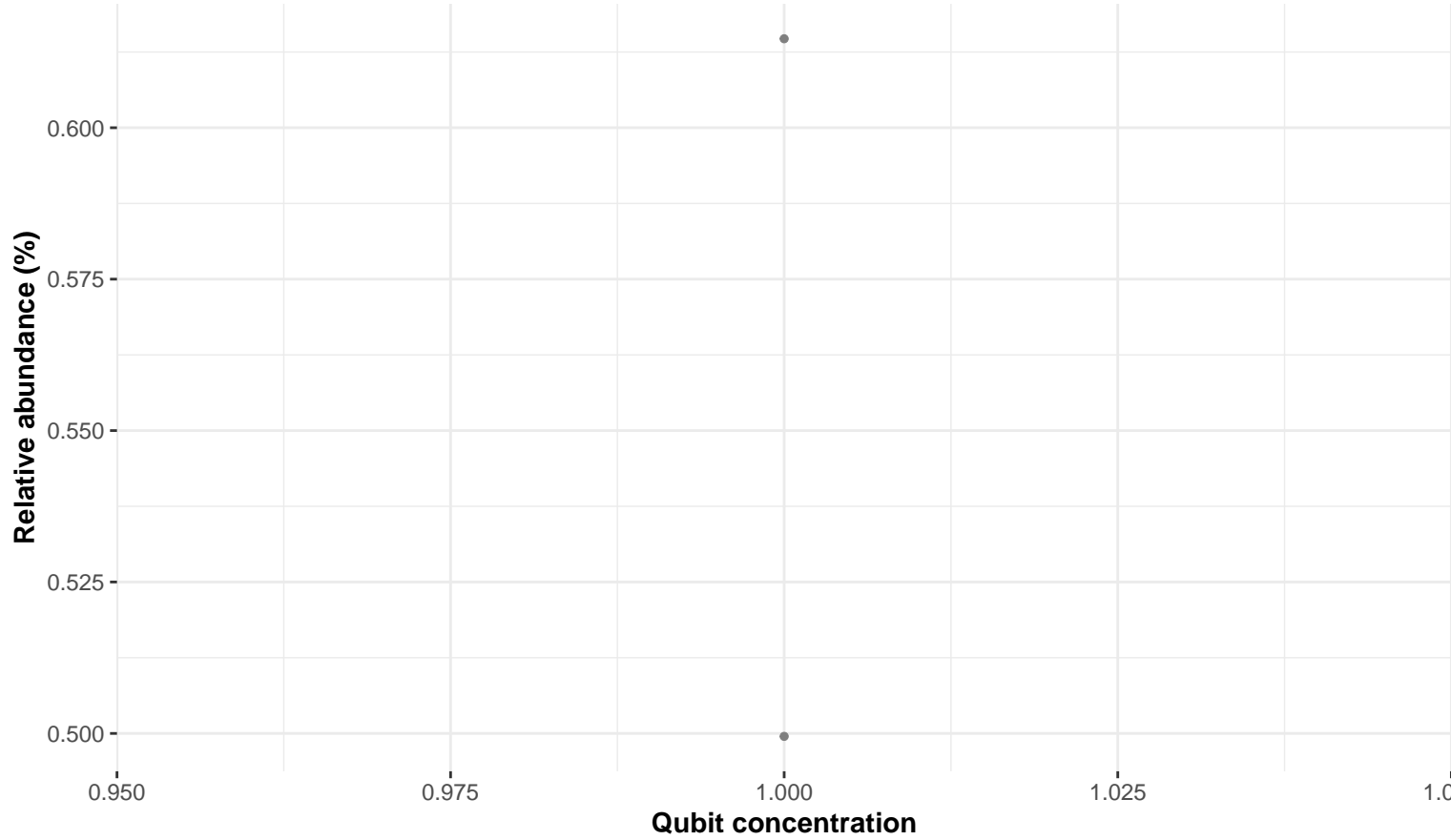


Correlation within: Digesta

$\log_e(S) = 6.136$, $p = 0.374$, $\hat{\rho}_{\text{Spearman}} = -0.269$, $\text{CI}_{95\%} [-0.723, 0.347]$, $n_{\text{pairs}} = 13$



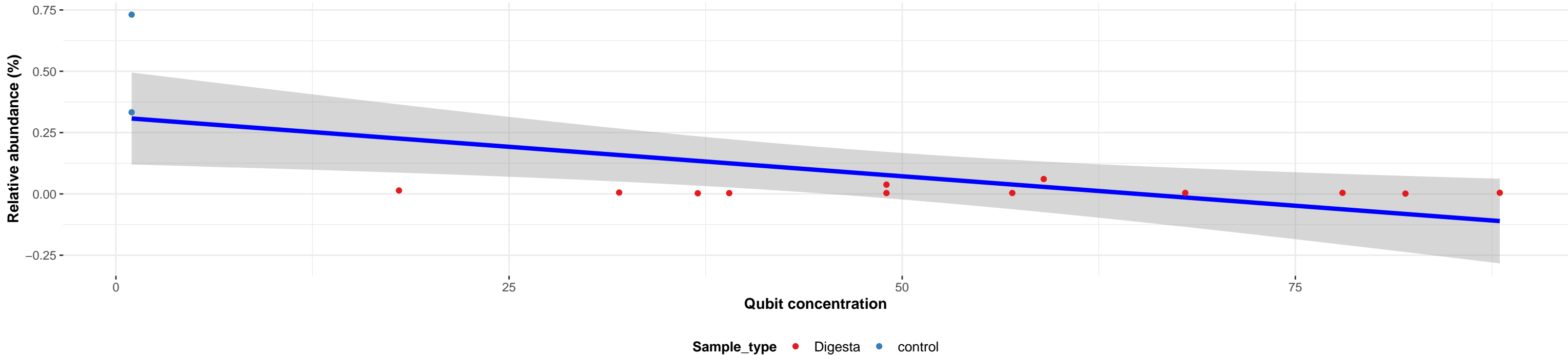
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Aerococcaceae; Globicatella; NA

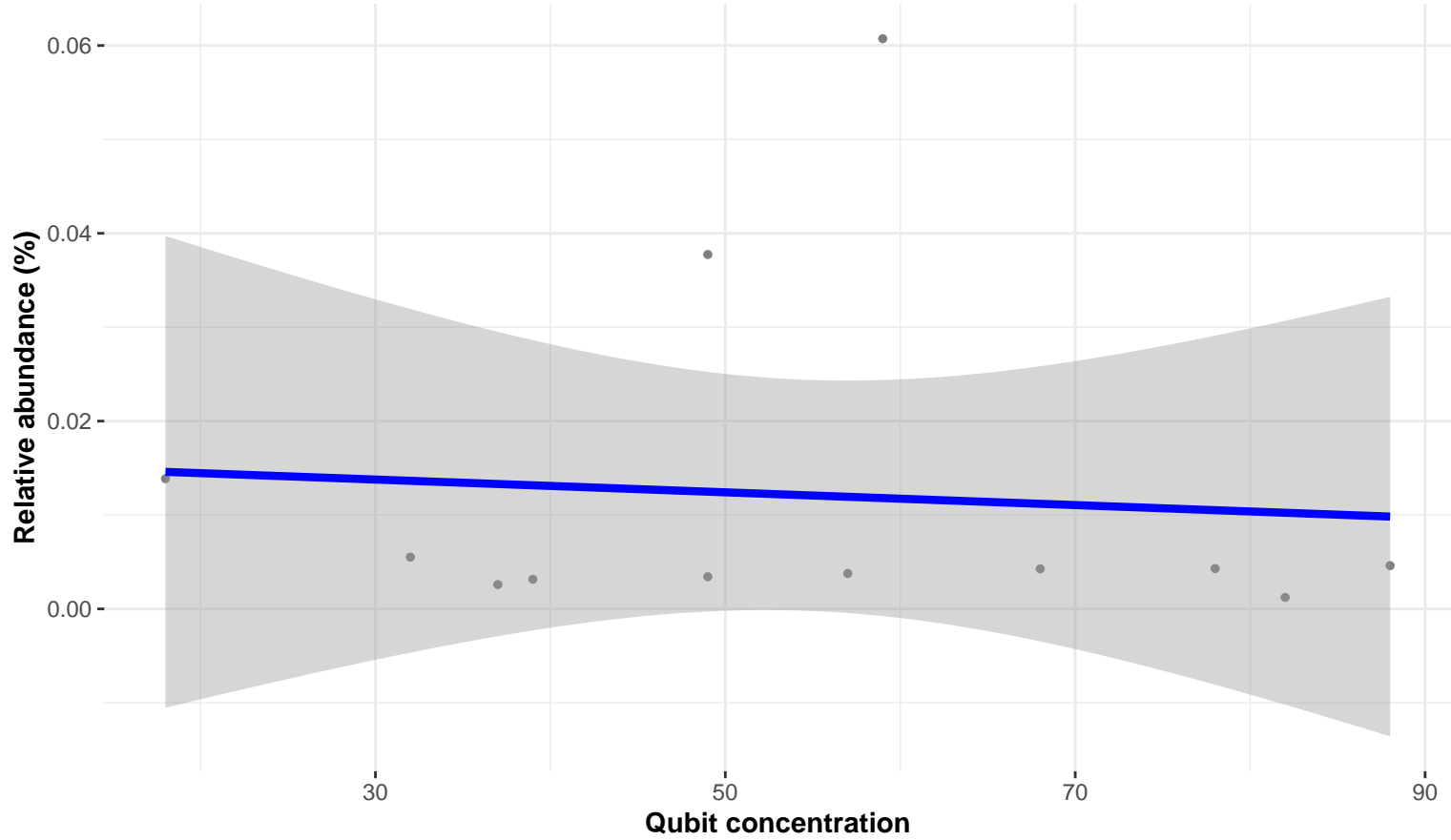
Correlation with all samples

$\log_e(S) = 6.487$, $p = 0.113$, $\hat{\rho}_{\text{Spearman}} = -0.443$, $\text{CI}_{95\%} [-0.795, 0.132]$, $n_{\text{pairs}} = 14$

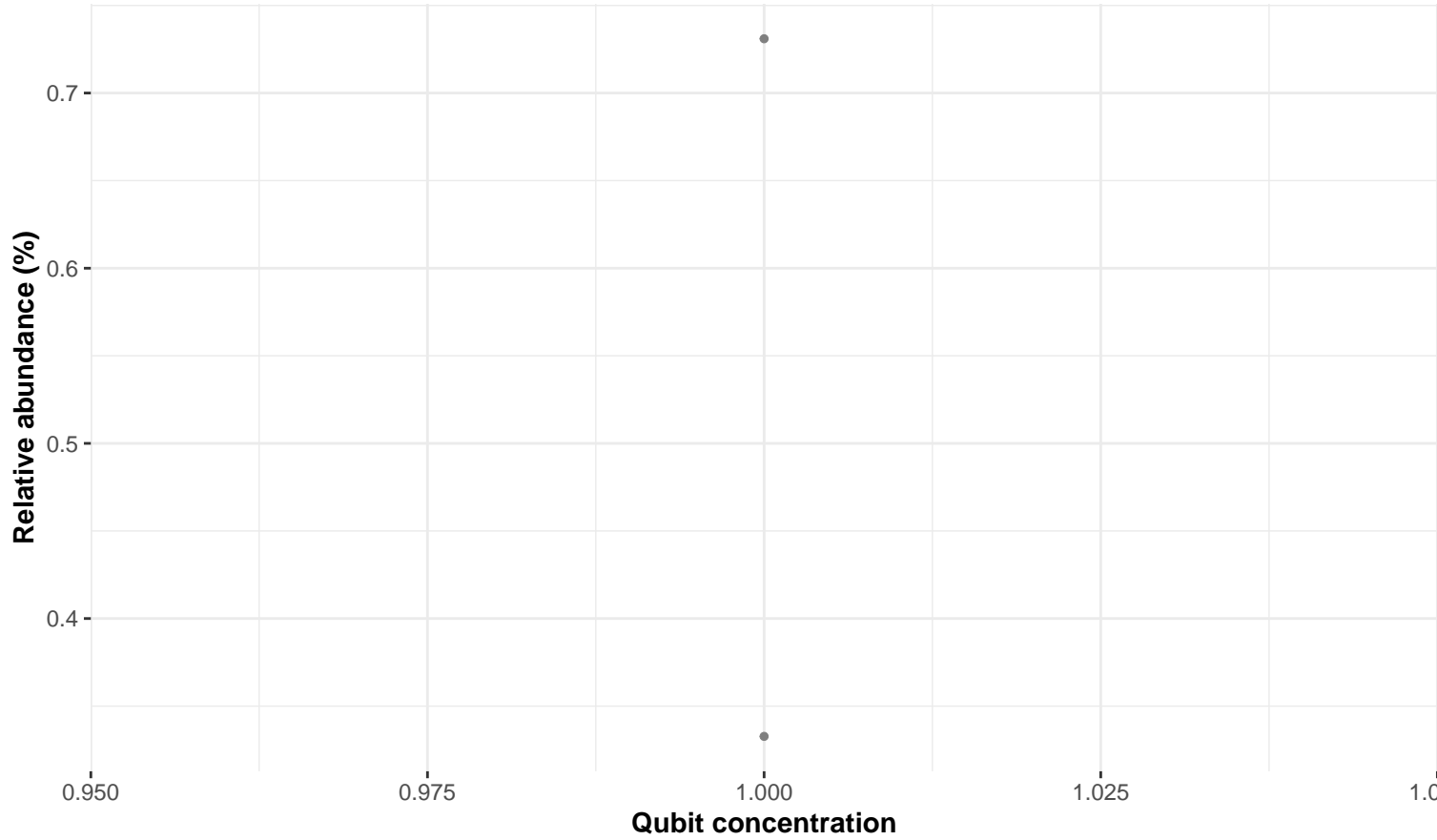


Correlation within: Digesta

$\log_e(S) = 5.765$, $p = 0.721$, $\hat{\rho}_{\text{Spearman}} = -0.116$, $\text{CI}_{95\%} [-0.658, 0.505]$, $n_{\text{pairs}} = 12$



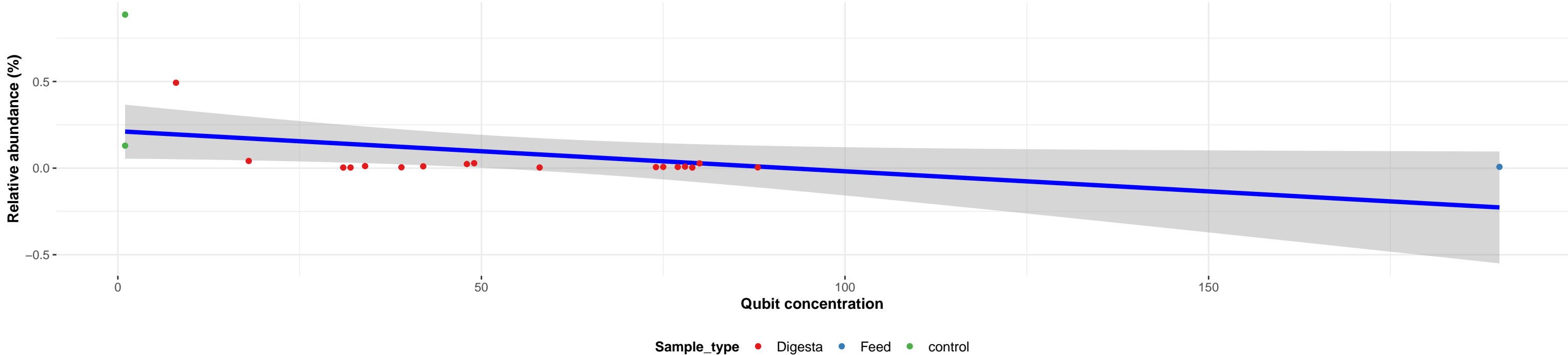
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

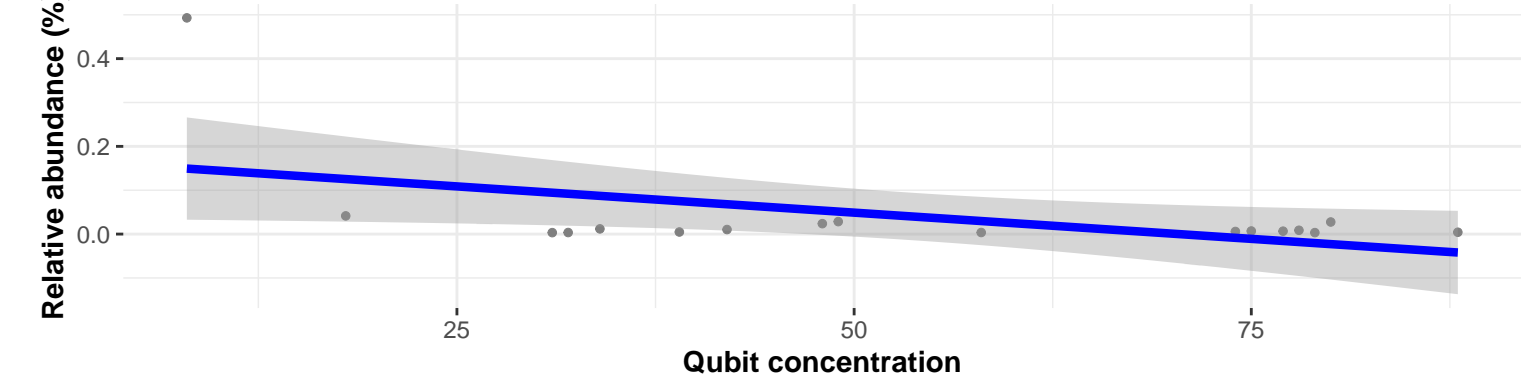
Correlation with all samples

$\log_e(S) = 7.541$, $p = 0.068$, $\hat{\rho}_{\text{Spearman}} = -0.417$, $\text{CI}_{95\%} [-0.732, 0.046]$, $n_{\text{pairs}} = 20$

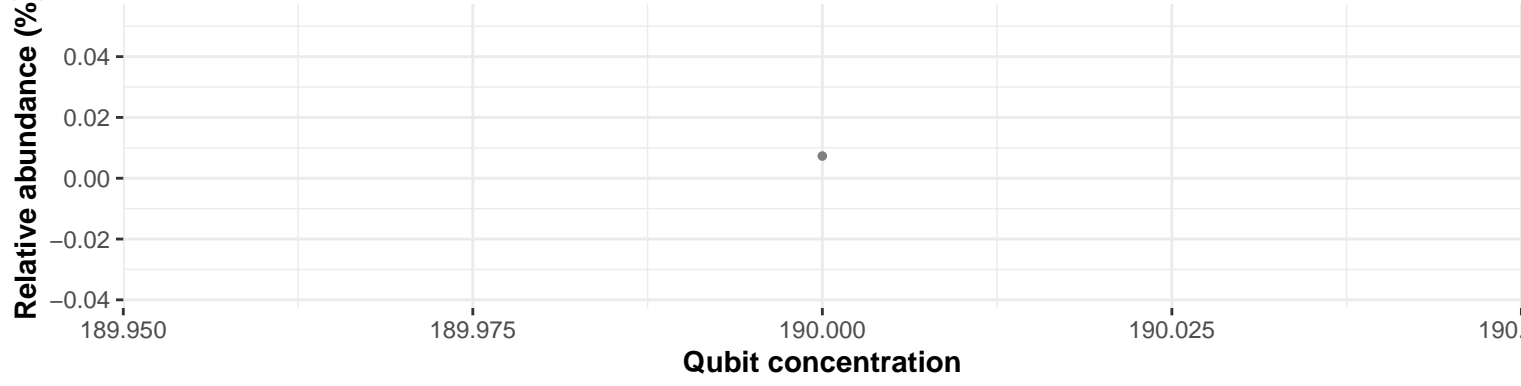


Correlation within: Digesta

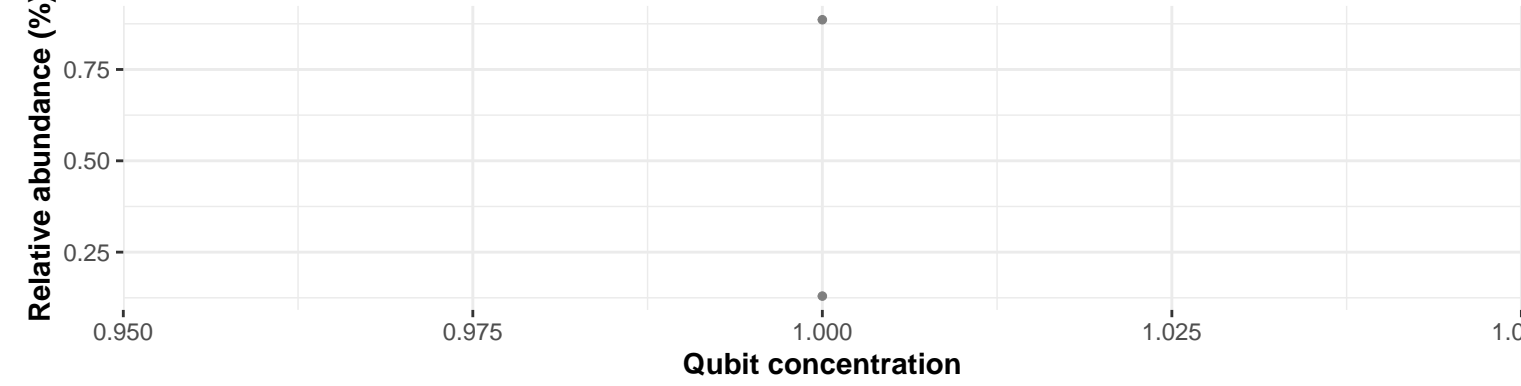
$\log_e(S) = 6.910$, $p = 0.379$, $\hat{\rho}_{\text{Spearman}} = -0.228$, $\text{CI}_{95\%} [-0.648, 0.298]$, $n_{\text{pairs}} = 17$



Correlation within: Feed

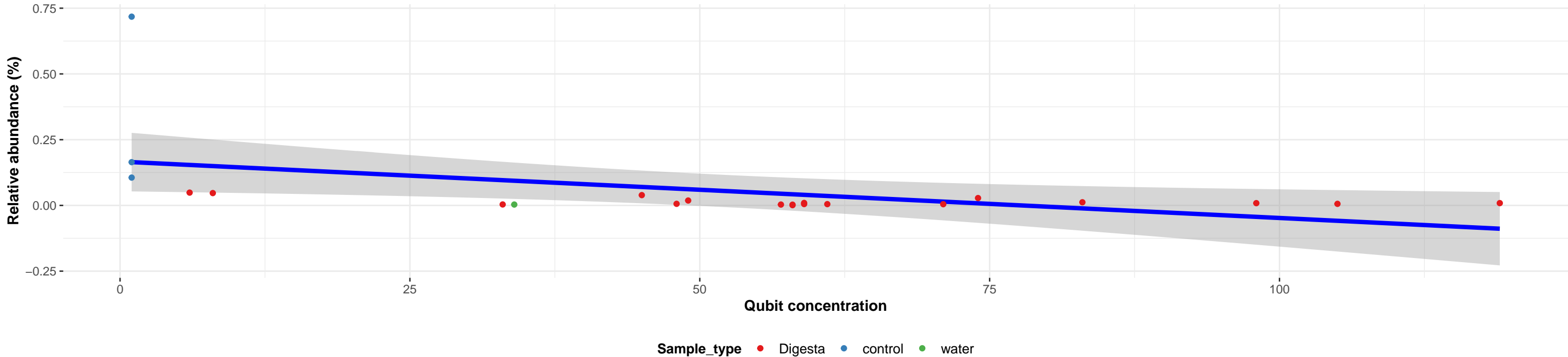


Correlation within: control



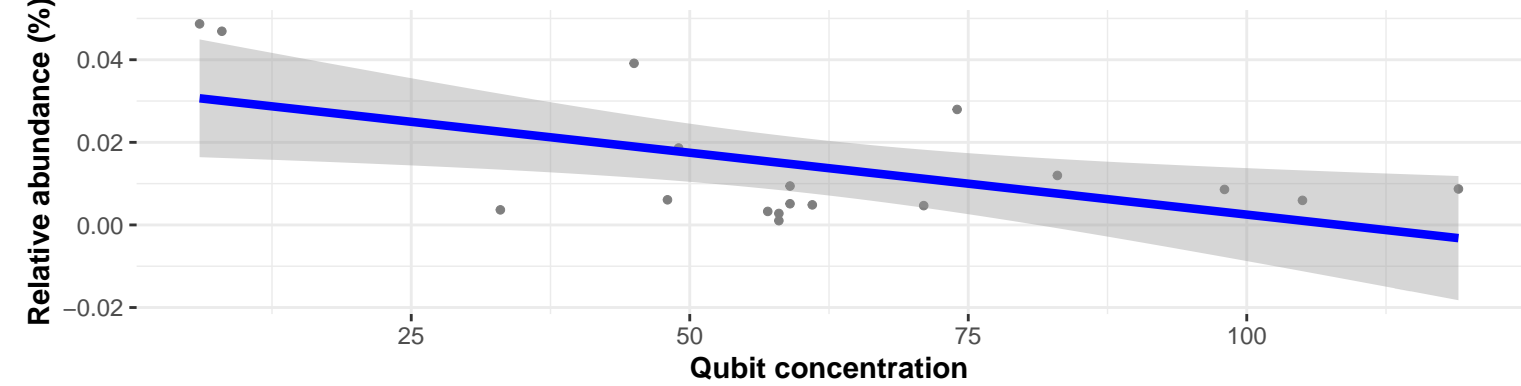
Correlation with all samples

$\log_e(S) = 7.827$, $p = 0.054$, $\hat{\rho}_{\text{Spearman}} = -0.416$, $\text{CI}_{95\%} [-0.719, 0.020]$, $n_{\text{pairs}} = 22$

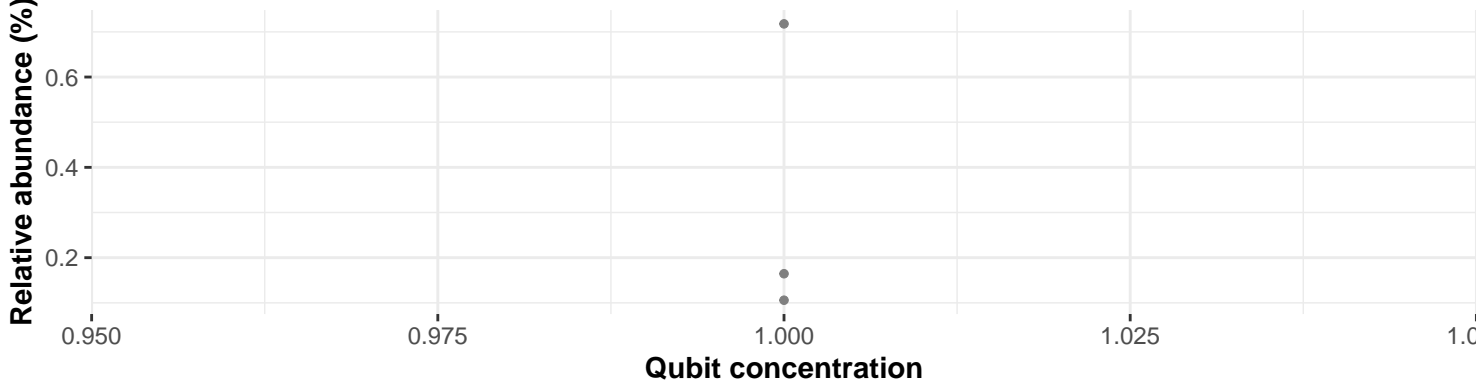


Correlation within: Digesta

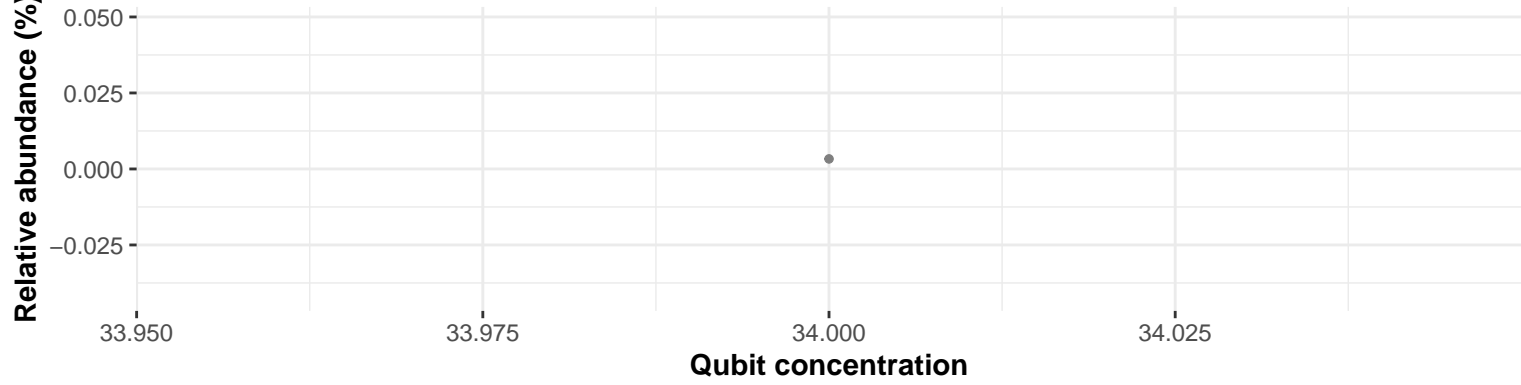
$\log_e(S) = 7.039$, $p = 0.483$, $\hat{\rho}_{\text{Spearman}} = -0.177$, $\text{CI}_{95\%} [-0.604, 0.330]$, $n_{\text{pairs}} = 18$



Correlation within: control



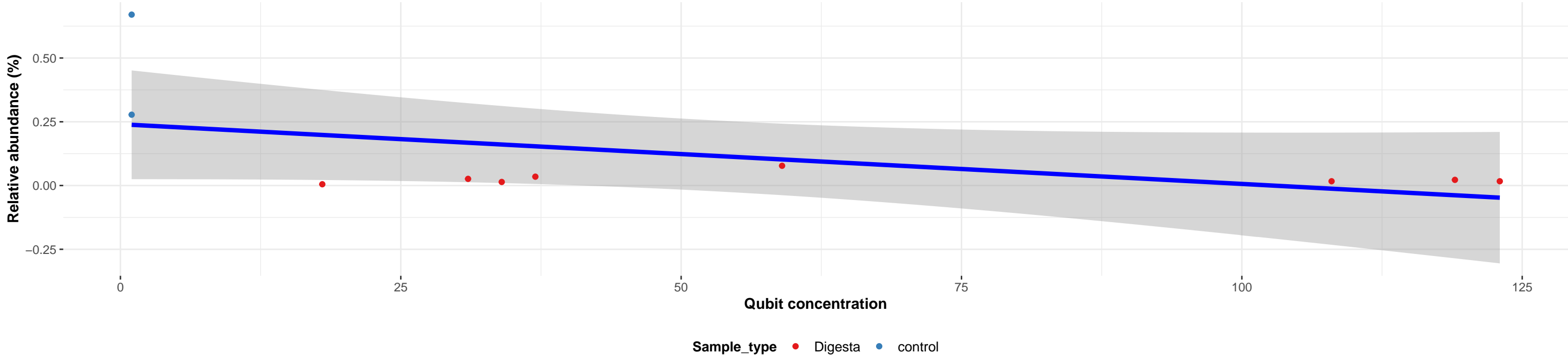
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

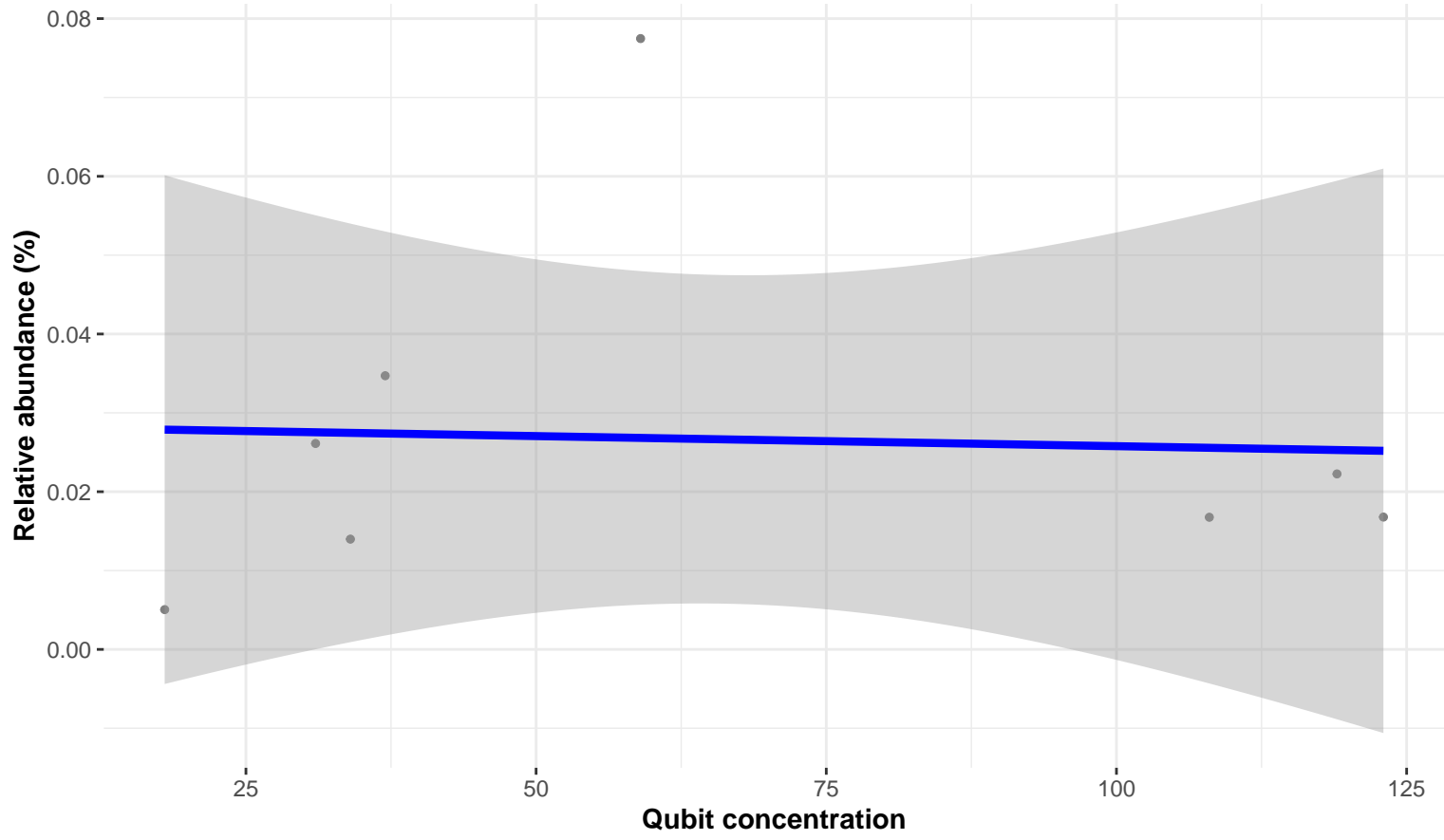
Correlation with all samples

$\log_e(S) = 5.417$, $p = 0.300$, $\hat{\rho}_{\text{Spearman}} = -0.365$, $\text{CI}_{95\%} [-0.816, 0.363]$, $n_{\text{pairs}} = 10$

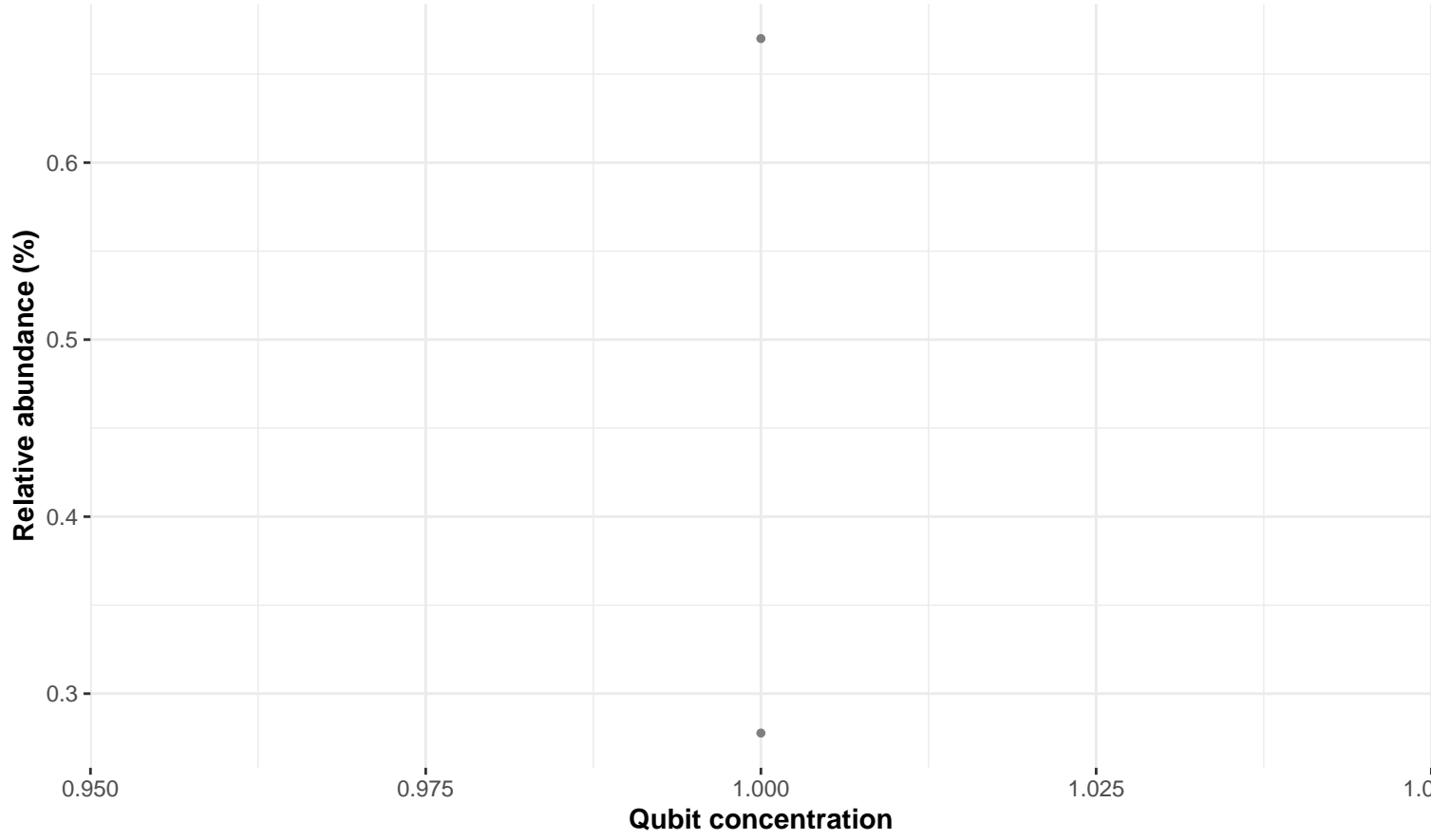


Correlation within: Digesta

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



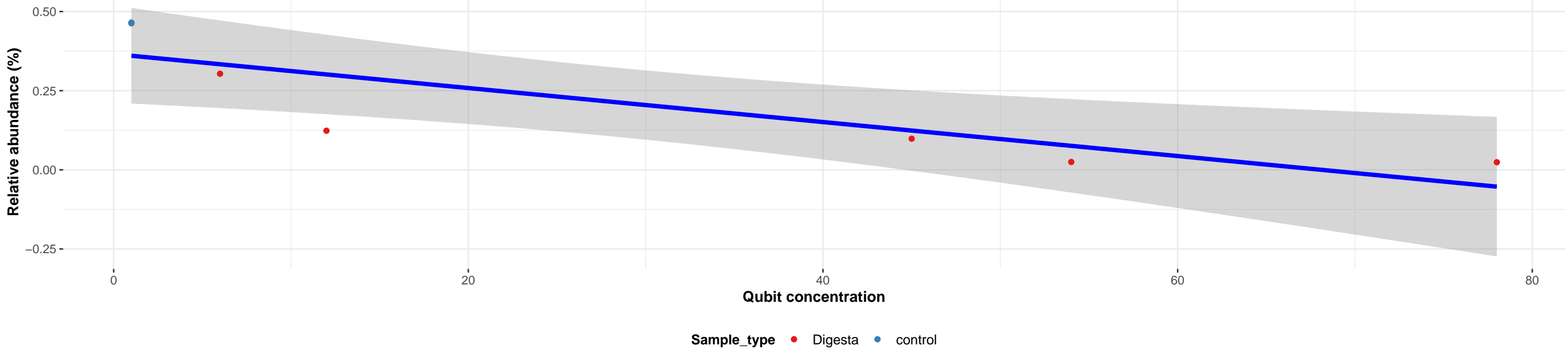
Correlation within: control



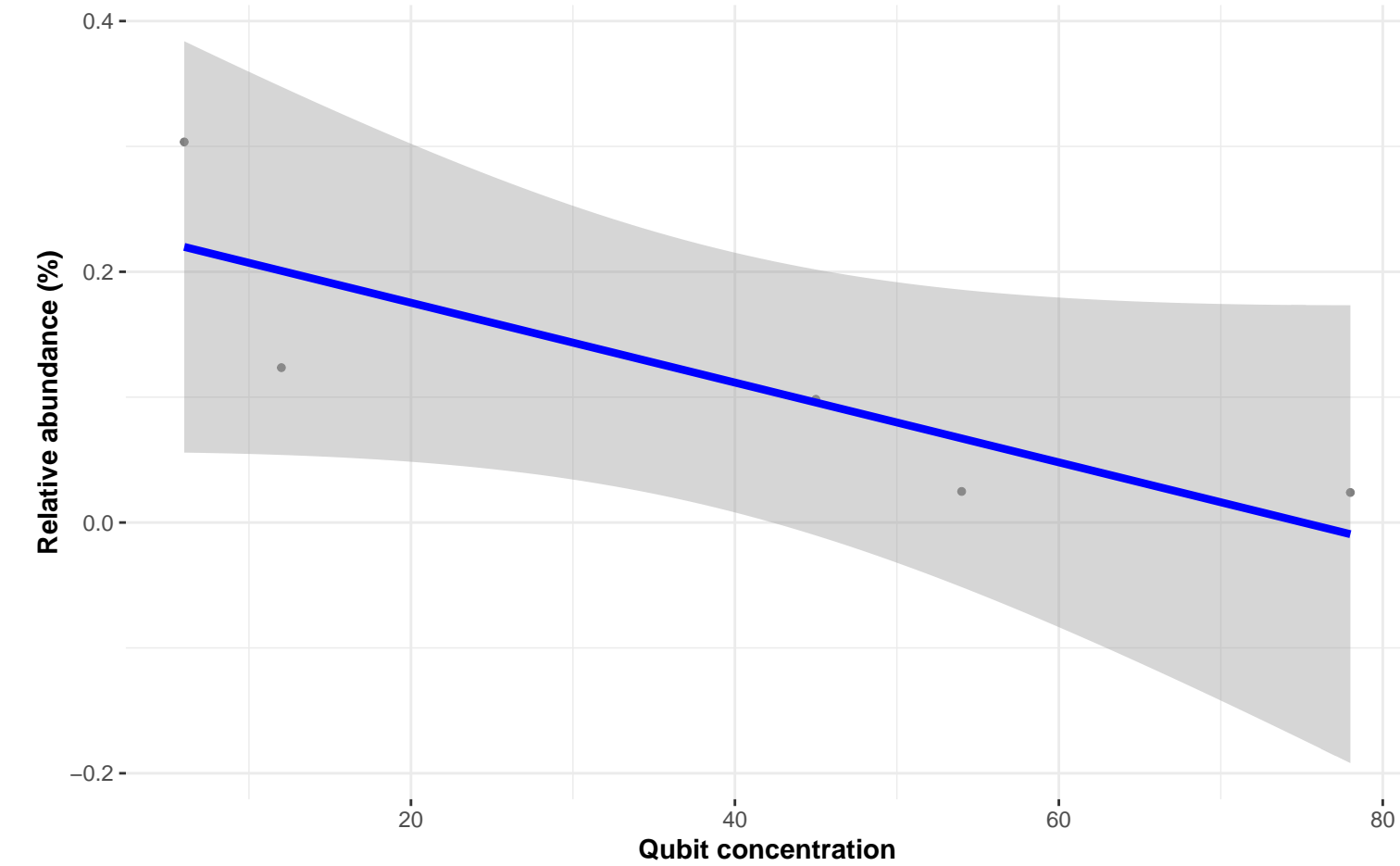
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia–Shigella; NA

Correlation with all samples

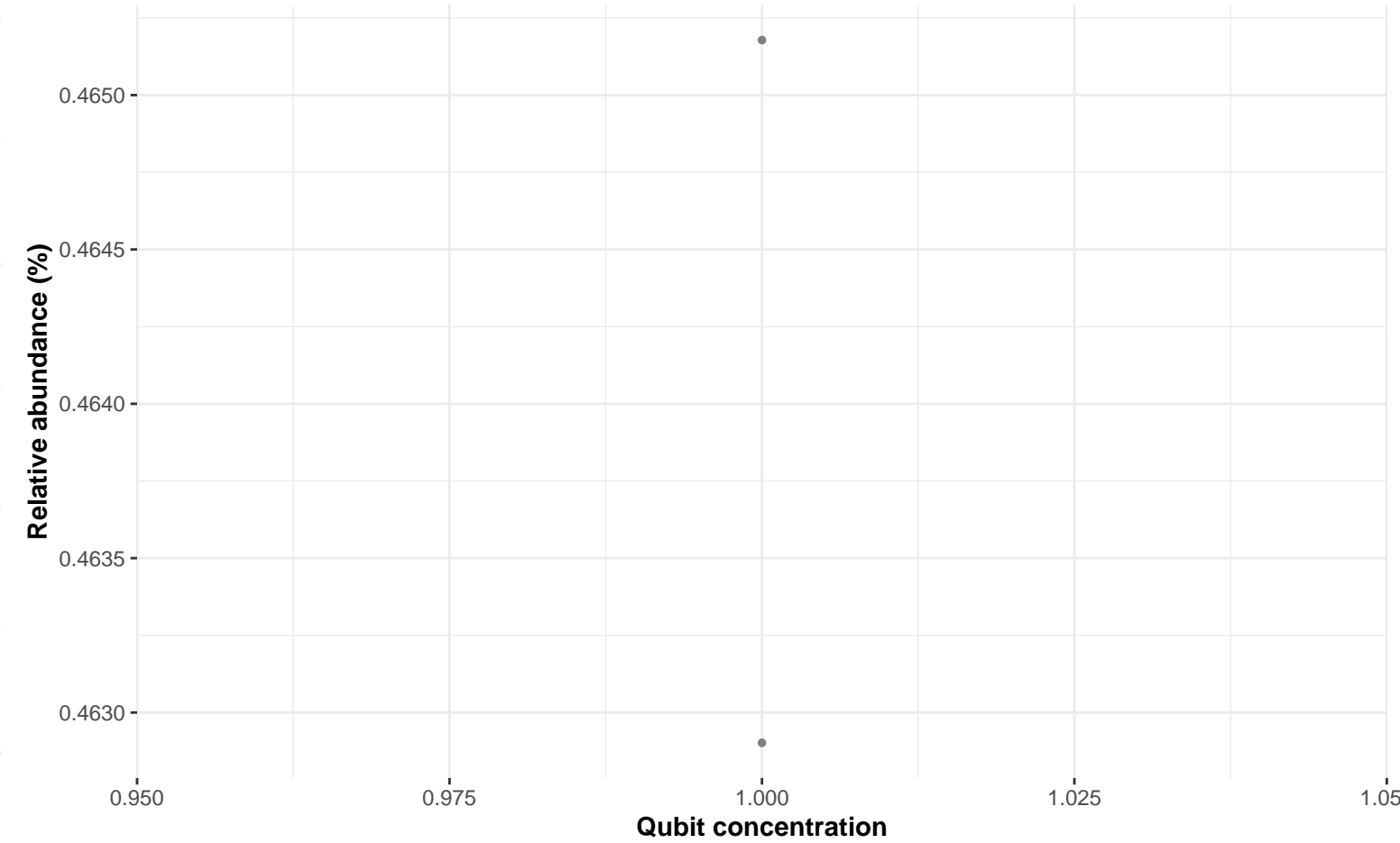
$\log_e(S) = 4.714$, $p = 1.46e-05$, $\hat{\rho}_{\text{Spearman}} = -0.991$, $CI_{95\%} [-0.999, -0.934]$, $n_{\text{pairs}} = 7$



Correlation within: Digesta



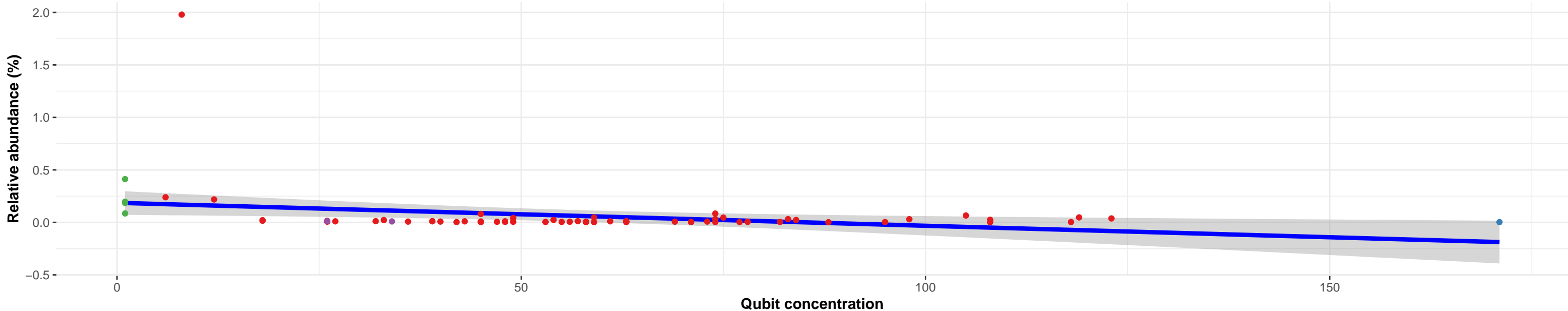
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Halomonadaceae; Halomonas; nitritophilus

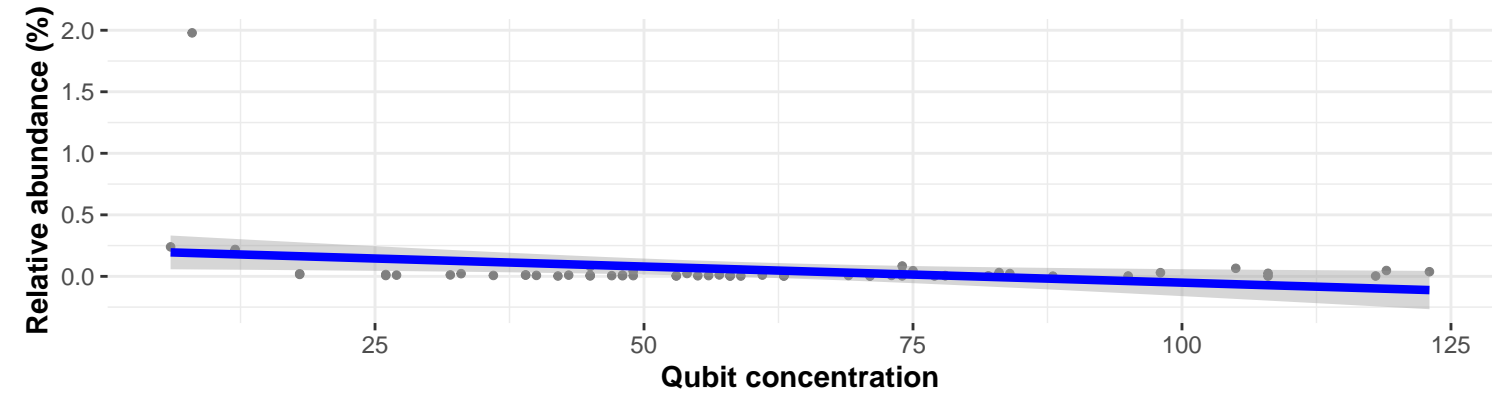
Correlation with all samples

$\log_e(S) = 11.260$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.359$, $\text{CI}_{95\%} [-0.553, -0.128]$, $n_{\text{pairs}} = 70$

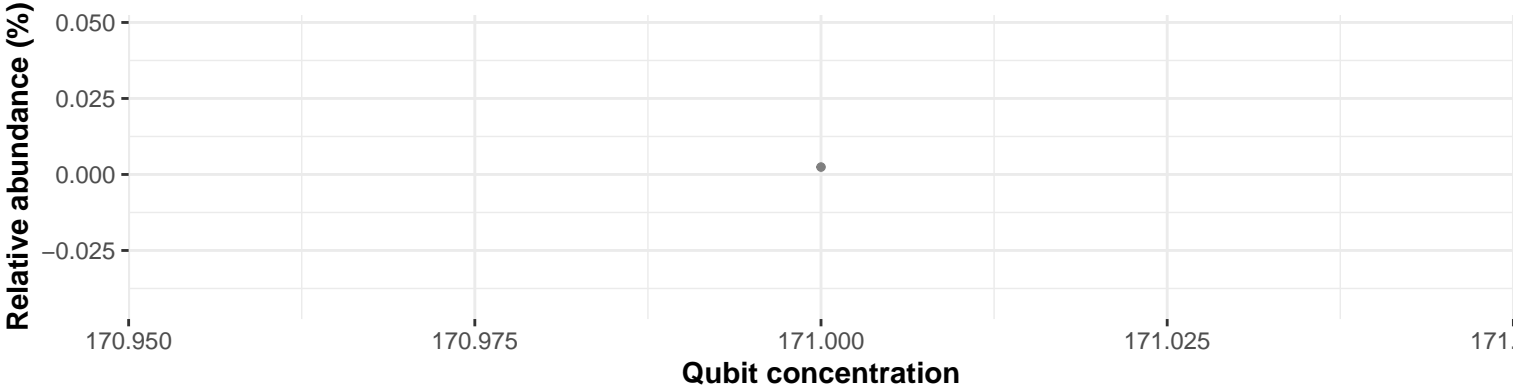


Correlation within: Digesta

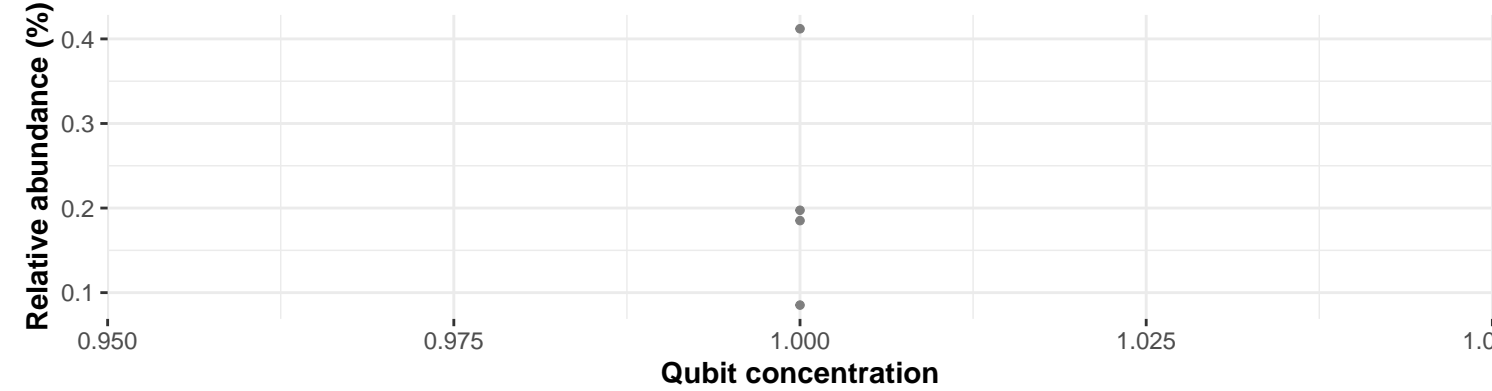
$\log_e(S) = 10.814$, $p = 0.130$, $\hat{\rho}_{\text{Spearman}} = -0.193$, $\text{CI}_{95\%} [-0.427, 0.065]$, $n_{\text{pairs}} = 63$



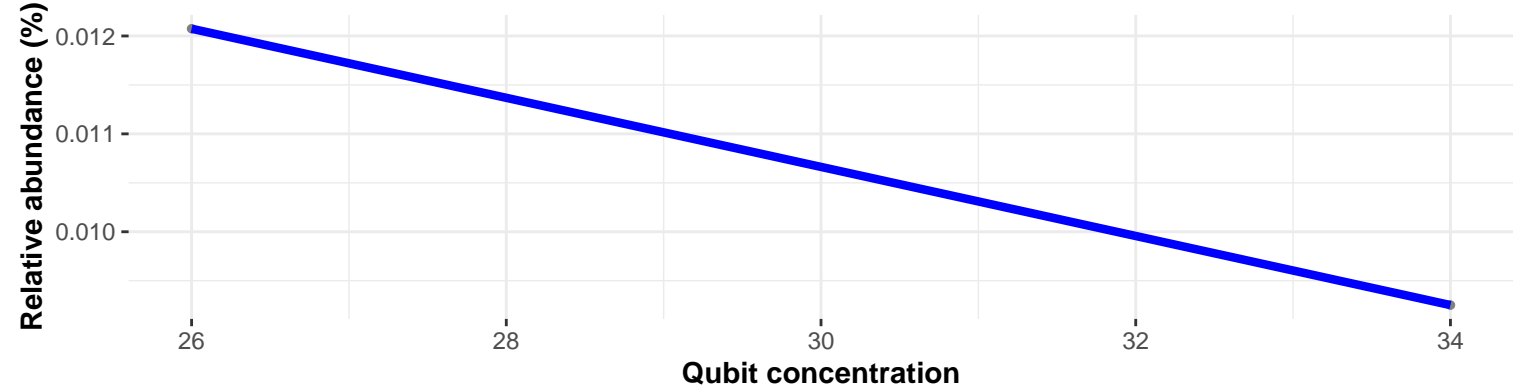
Correlation within: Feed



Correlation within: control



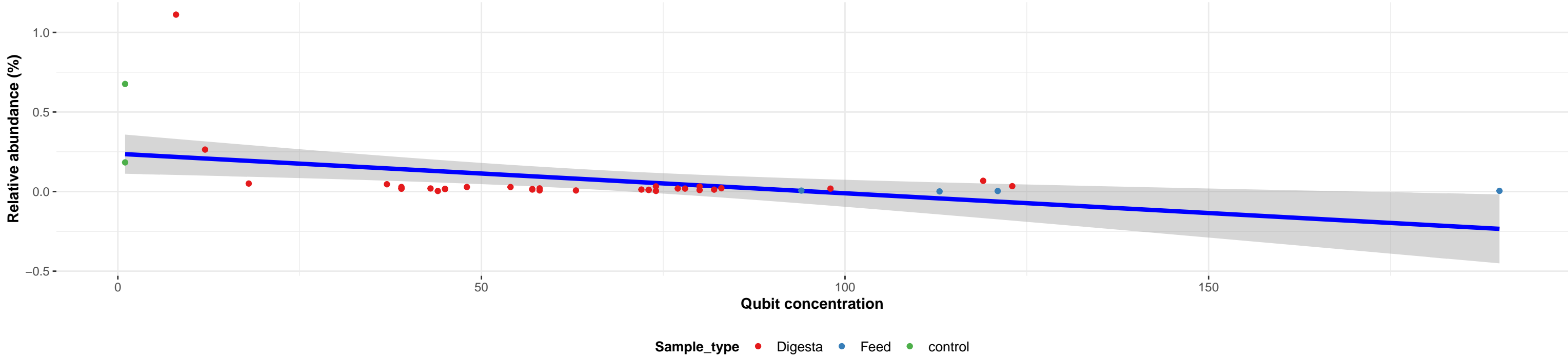
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; urealyticum

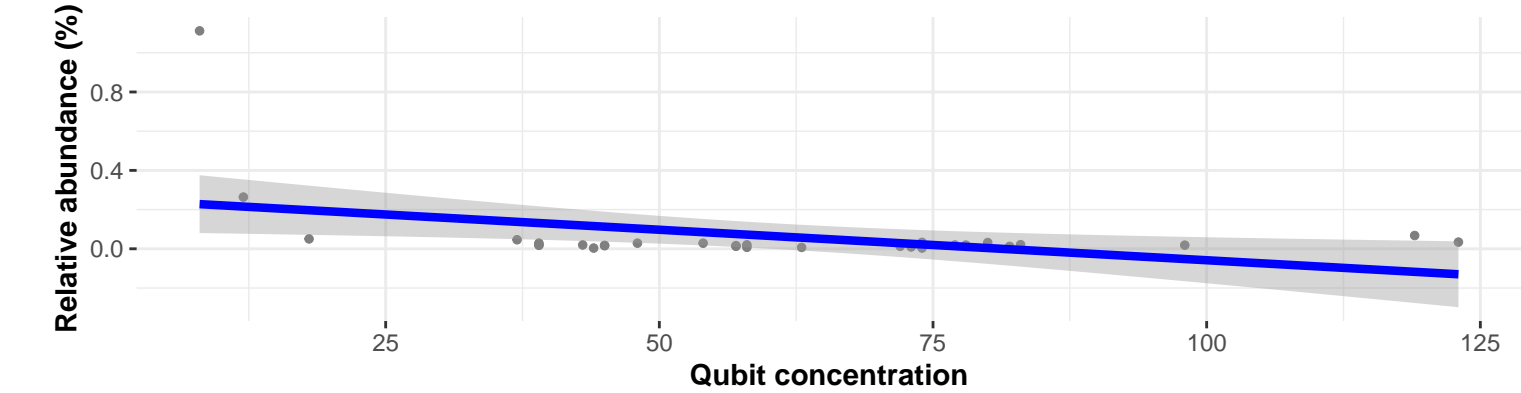
Correlation with all samples

$\log_e(S) = 9.513$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = -0.481$, $\text{CI}_{95\%} [-0.699, -0.181]$, $n_{\text{pairs}} = 38$

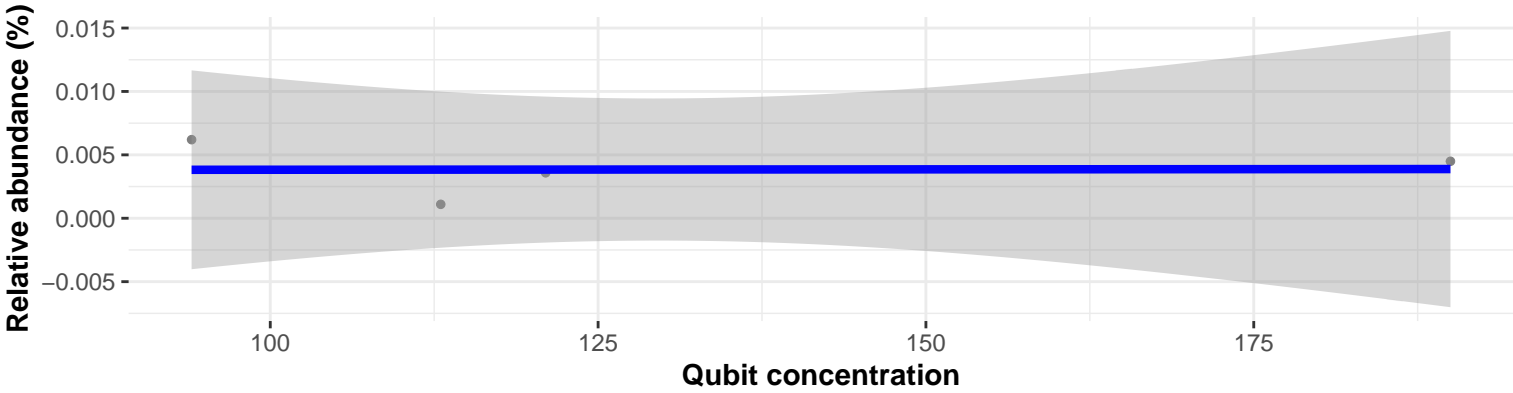


Correlation within: Digesta

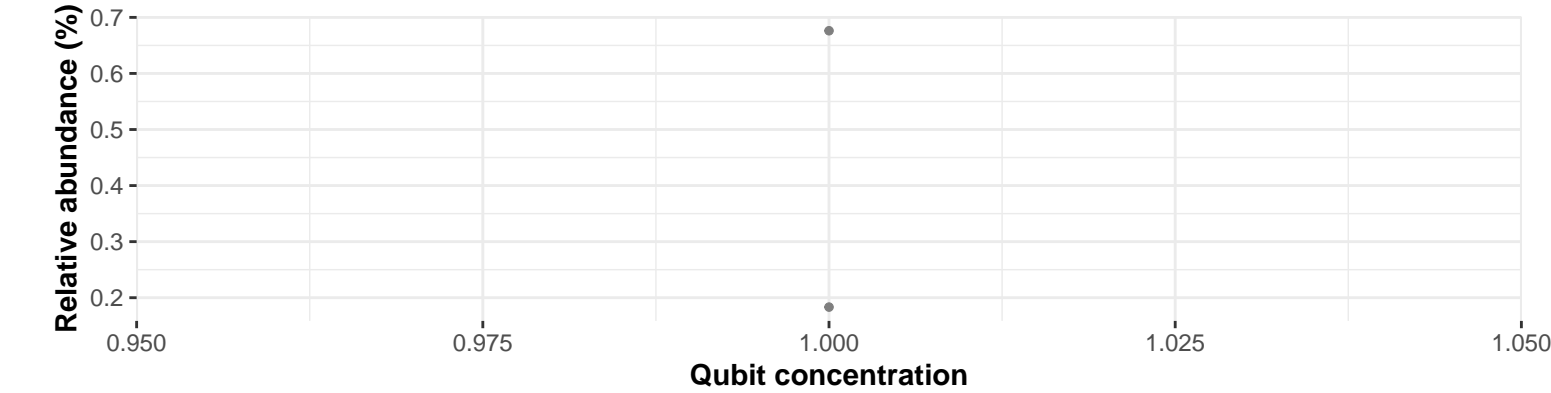
$\log_e(S) = 8.803$, $p = 0.228$, $\hat{\rho}_{\text{Spearman}} = -0.219$, $\text{CI}_{95\%} [-0.535, 0.151]$, $n_{\text{pairs}} = 32$



Correlation within: Feed



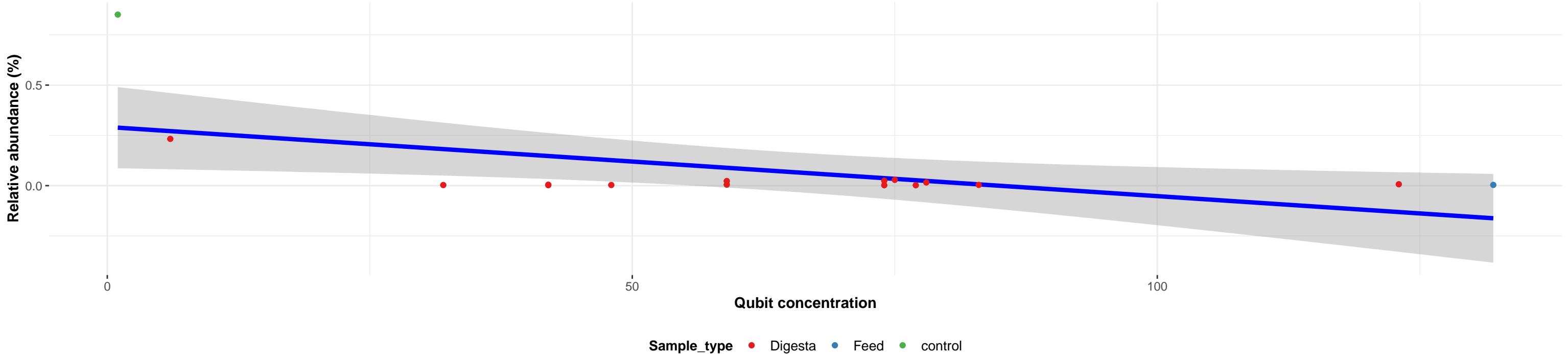
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Providencia; NA

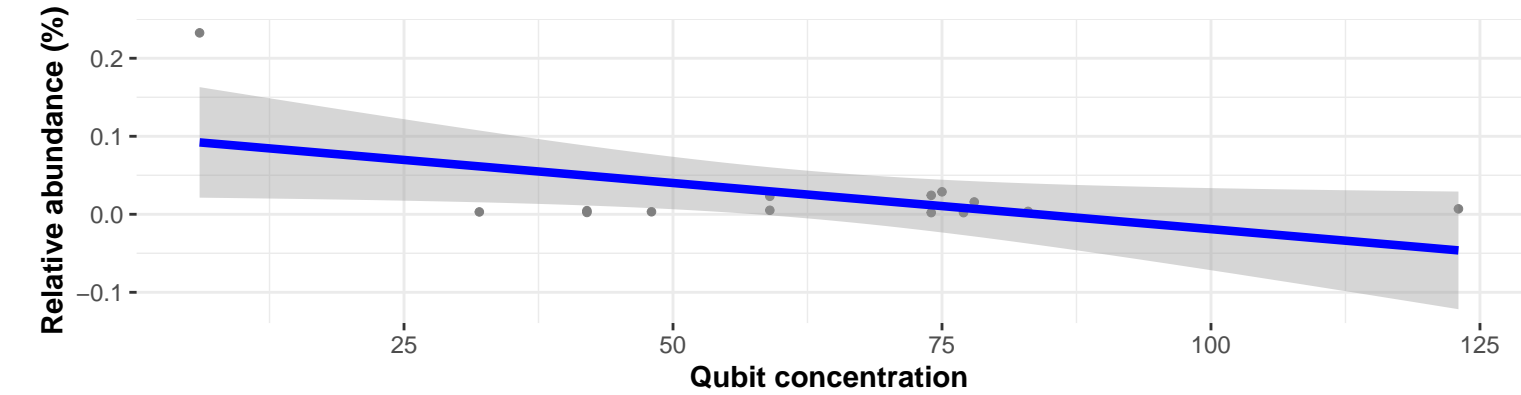
Correlation with all samples

$\log_e(S) = 6.687$, $p = 0.505$, $\hat{\rho}_{\text{Spearman}} = -0.180$, $CI_{95\%} [-0.630, 0.361]$, $n_{\text{pairs}} = 16$

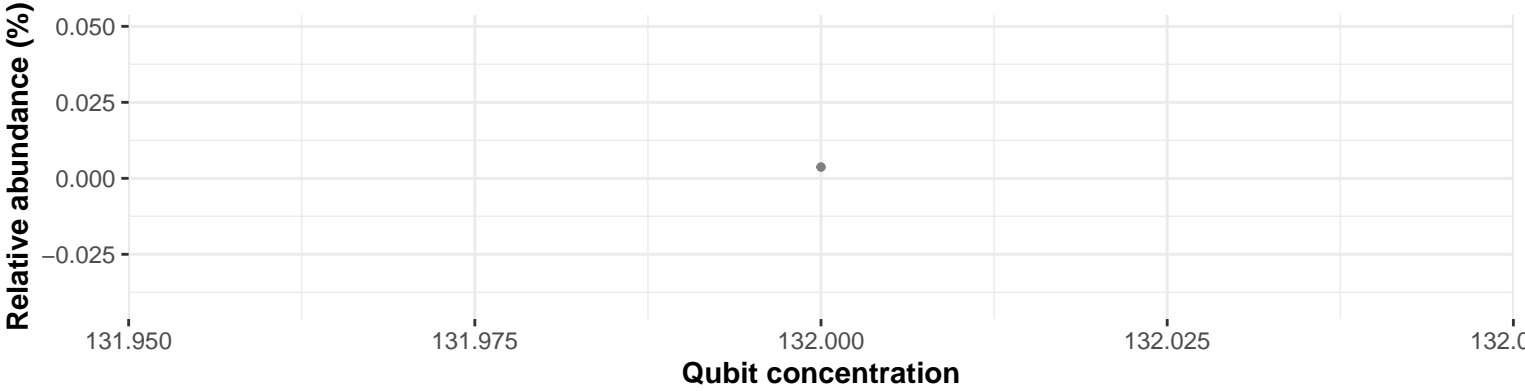


Correlation within: Digesta

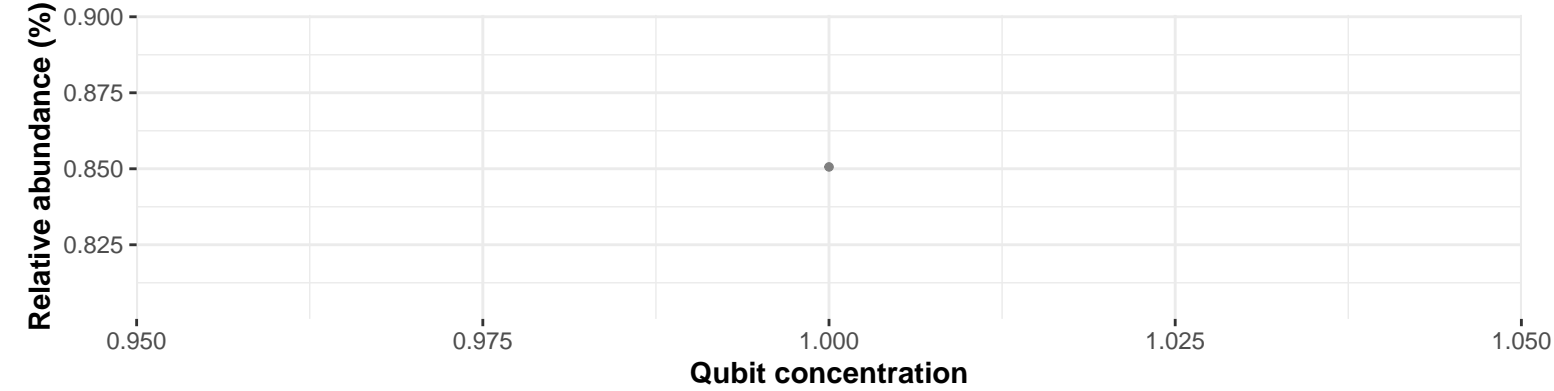
$\log_e(S) = 6.100$, $p = 0.946$, $\hat{\rho}_{\text{Spearman}} = 0.020$, $CI_{95\%} [-0.529, 0.557]$, $n_{\text{pairs}} = 14$



Correlation within: Feed



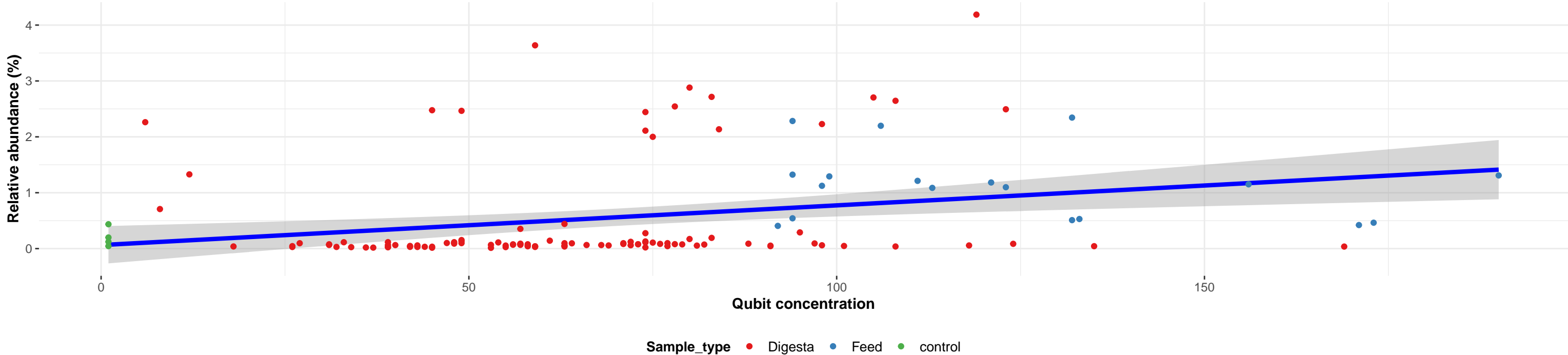
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Ligilactobacillus; NA

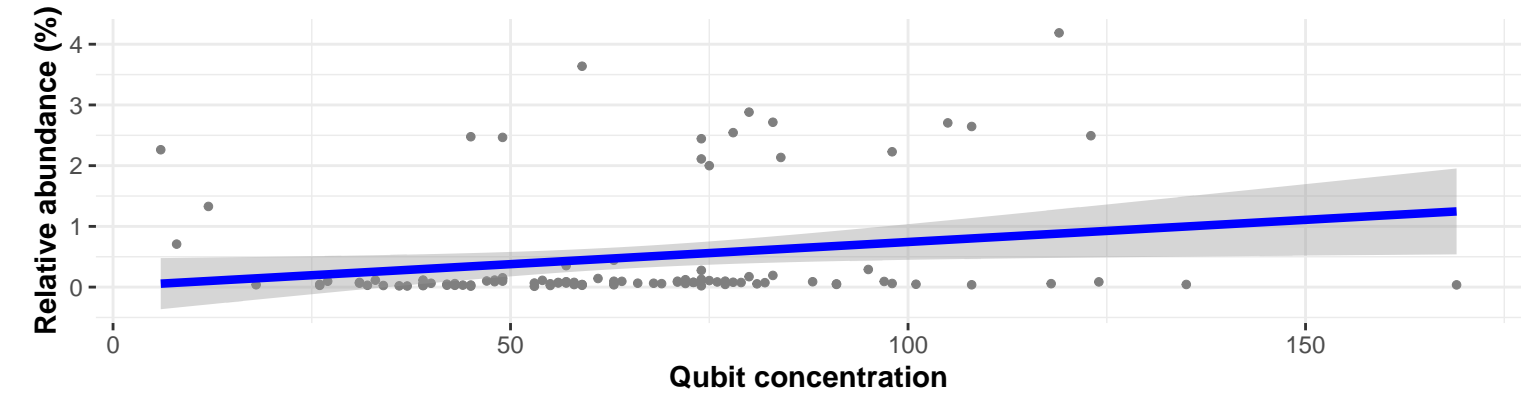
Correlation with all samples

$\log_e(S) = 12.247$, $p = 2.27\text{e-}06$, $\hat{\rho}_{\text{Spearman}} = 0.404$, $\text{CI}_{95\%} [0.243, 0.543]$, $n_{\text{pairs}} = 128$



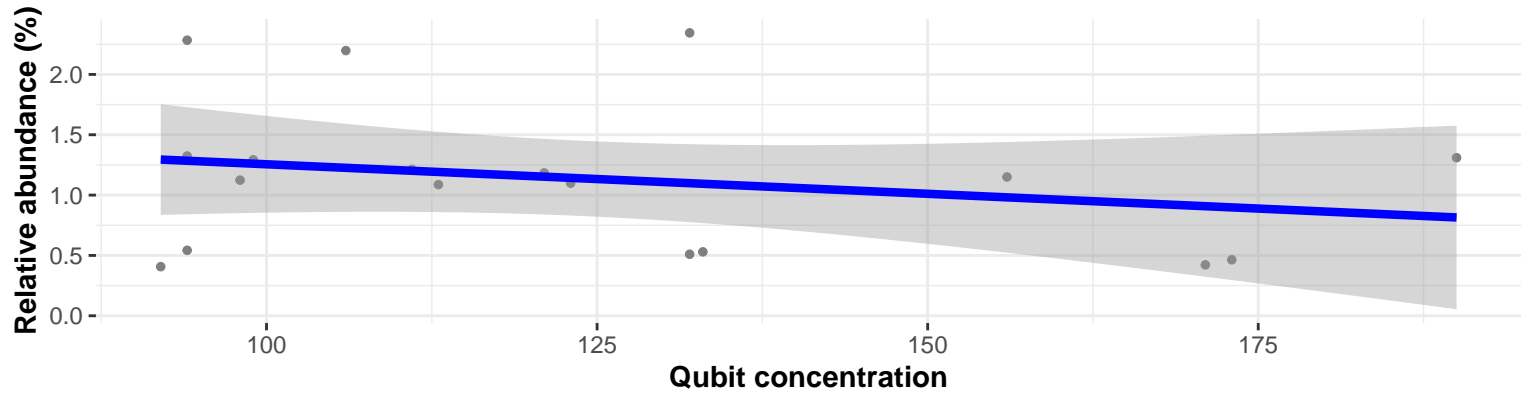
Correlation within: Digesta

$\log_e(S) = 11.862$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.286$, $\text{CI}_{95\%} [0.095, 0.456]$, $n_{\text{pairs}} = 106$

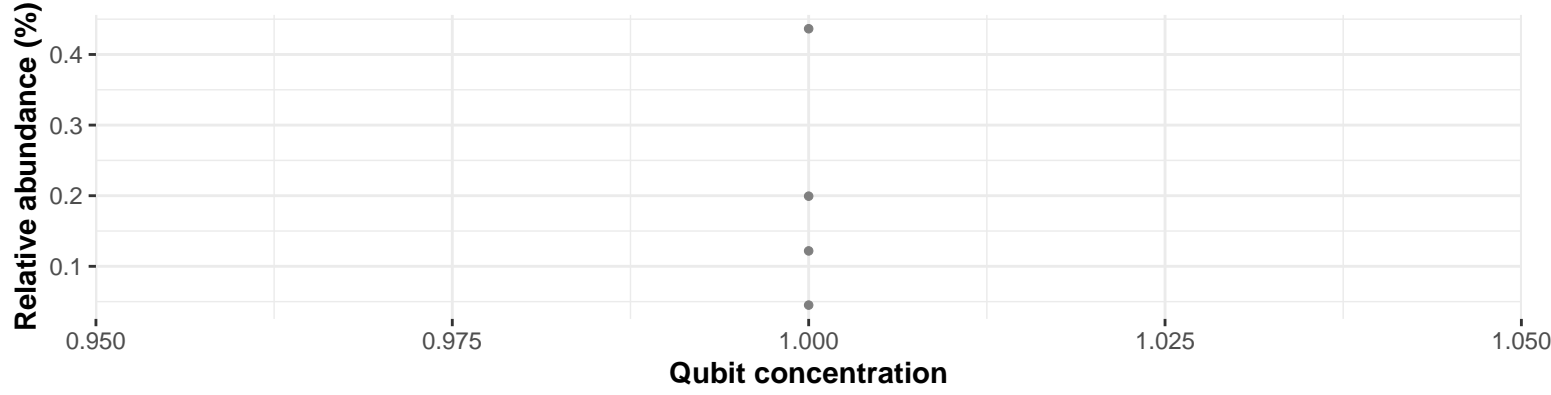


Correlation within: Feed

$\log_e(S) = 7.043$, $p = 0.472$, $\hat{\rho}_{\text{Spearman}} = -0.181$, $\text{CI}_{95\%} [-0.607, 0.326]$, $n_{\text{pairs}} = 18$



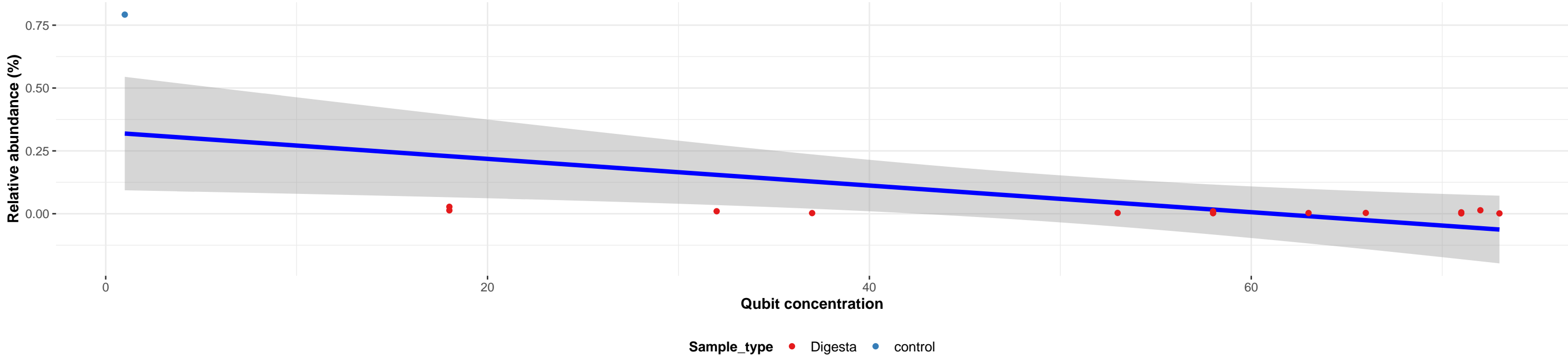
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Carnobacteriaceae; Atopostipes; suicloacalis

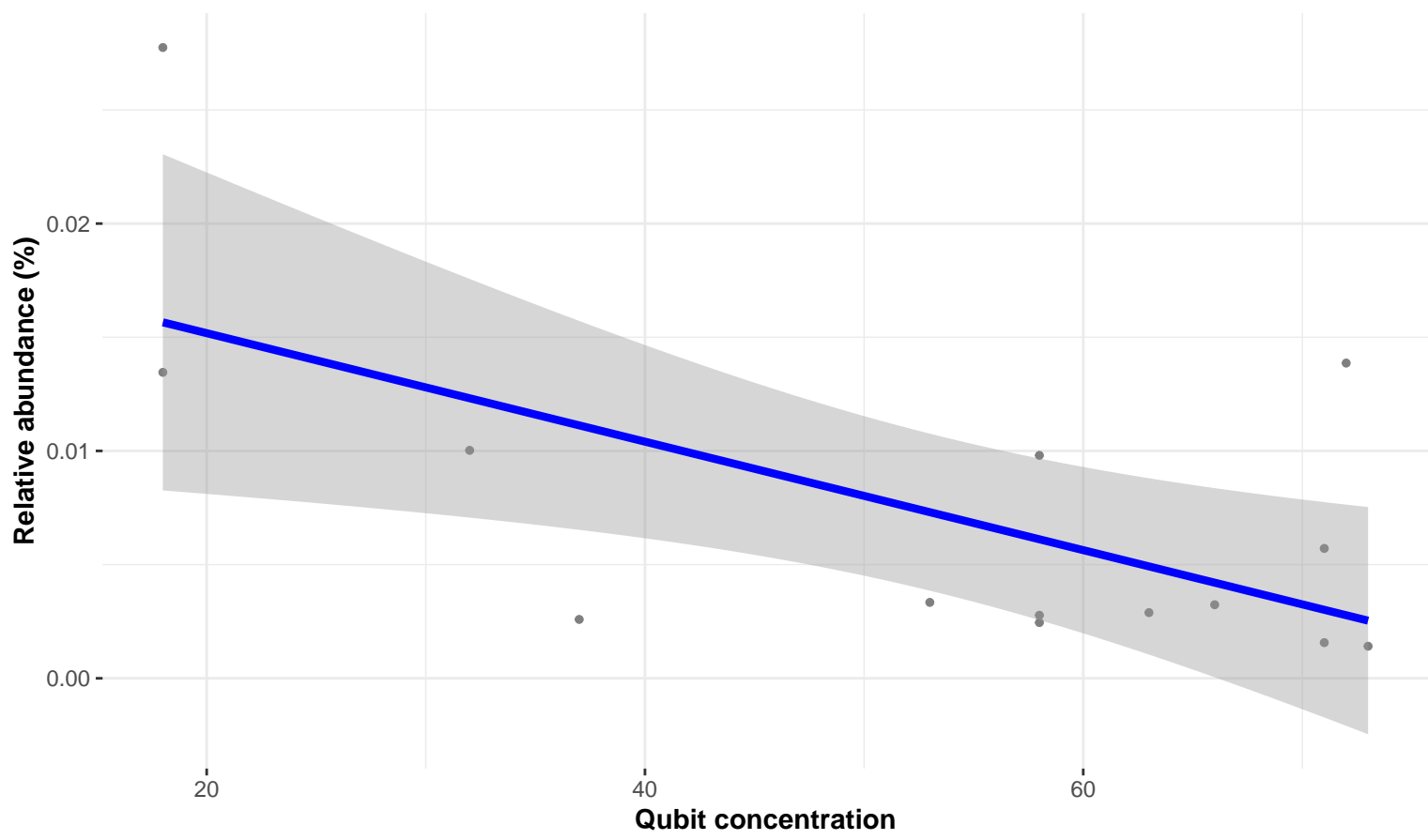
Correlation with all samples

$\log_e(S) = 6.765$, $p = 0.035$, $\hat{\rho}_{\text{Spearman}} = -0.548$, $\text{CI}_{95\%} [-0.833, -0.032]$, $n_{\text{pairs}} = 15$

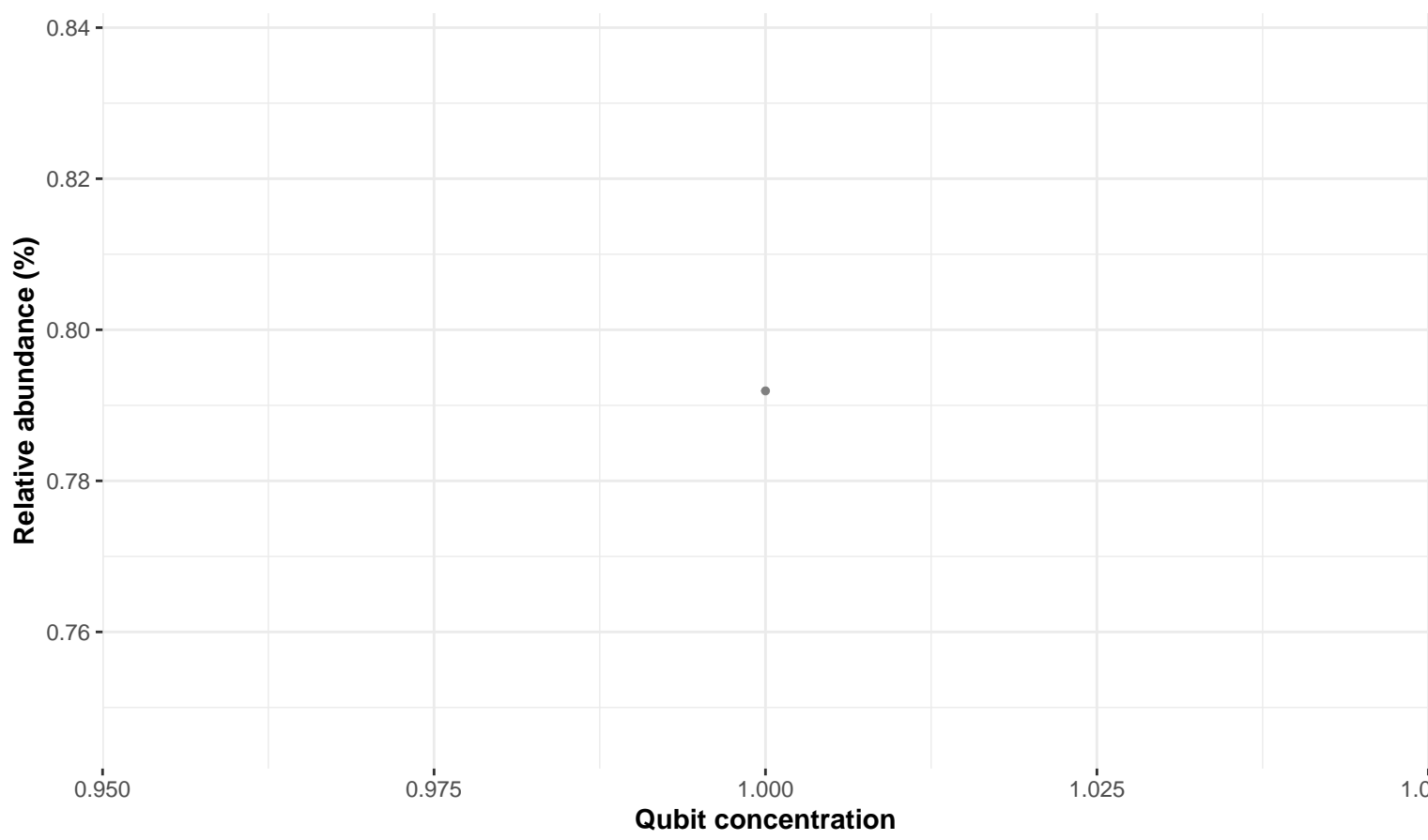


Correlation within: Digesta

$\log_e(S) = 6.487$, $p = 0.113$, $\hat{\rho}_{\text{Spearman}} = -0.442$, $\text{CI}_{95\%} [-0.795, 0.132]$, $n_{\text{pairs}} = 14$



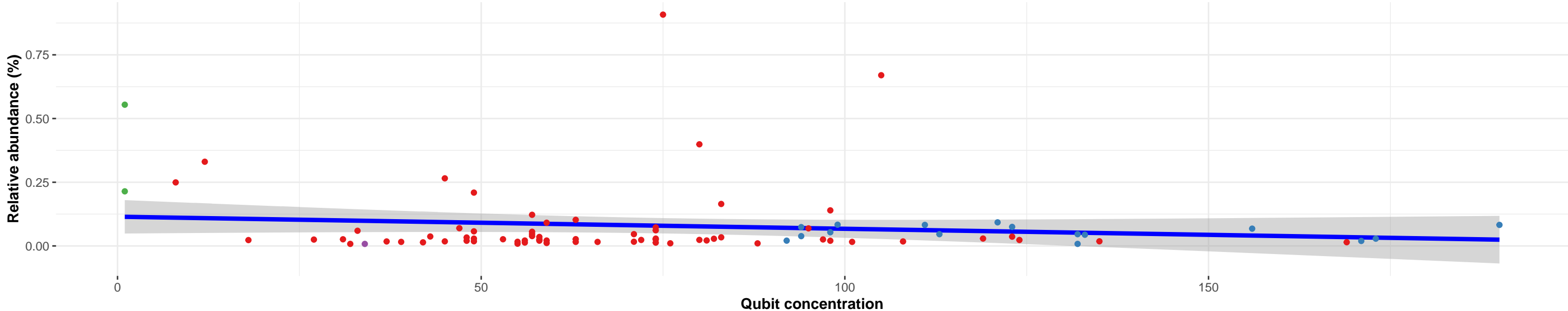
Correlation within: control



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Staphylococcus; NA

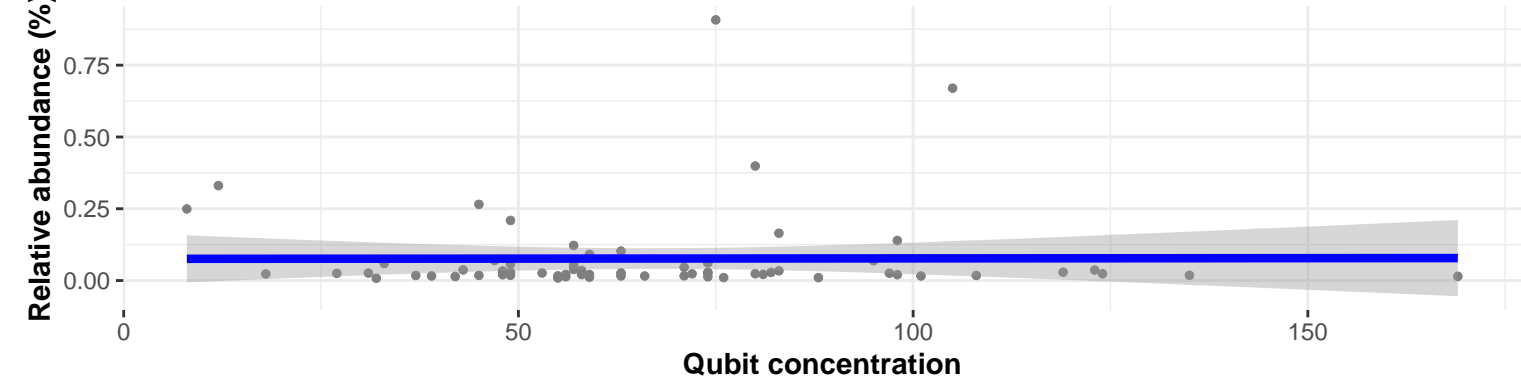
Correlation with all samples

$\log_e(S) = 11.560$, $p = 0.678$, $\hat{\rho}_{\text{Spearman}} = 0.045$, $\text{CI}_{95\%} [-0.173, 0.259]$, $n_{\text{pairs}} = 87$



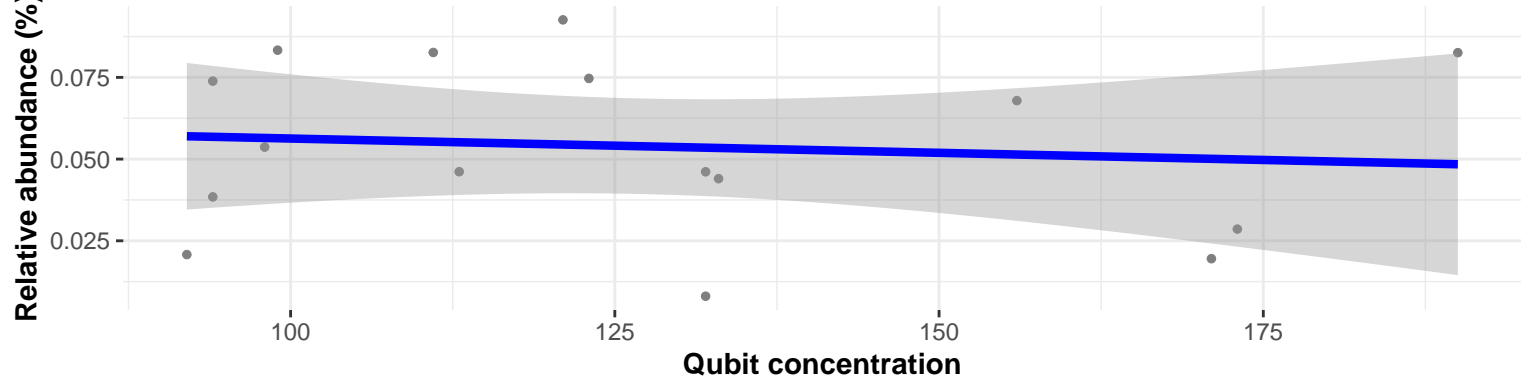
Correlation within: Digesta

$\log_e(S) = 10.883$, $p = 0.892$, $\hat{\rho}_{\text{Spearman}} = -0.017$, $\text{CI}_{95\%} [-0.261, 0.229]$, $n_{\text{pairs}} = 68$

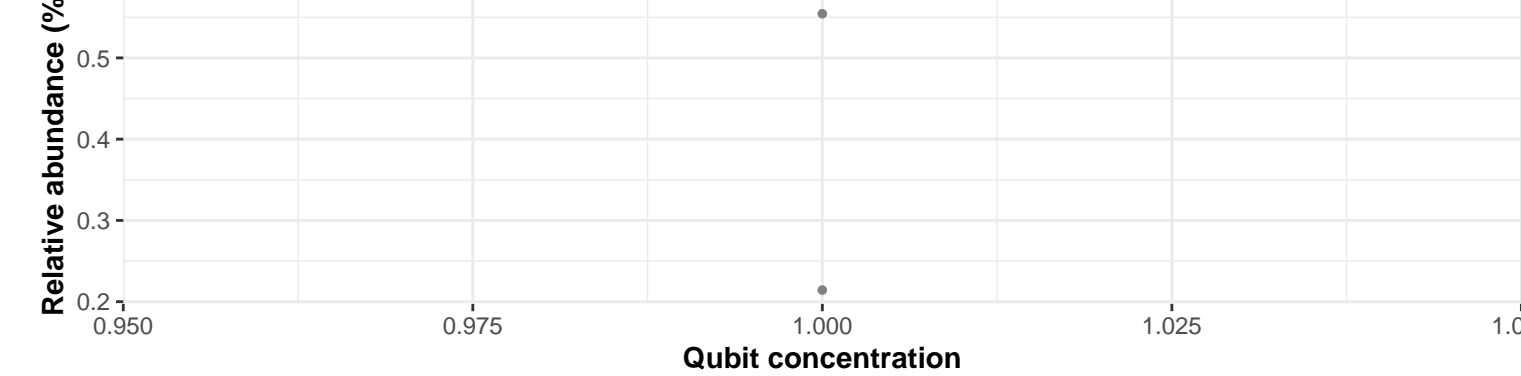


Correlation within: Feed

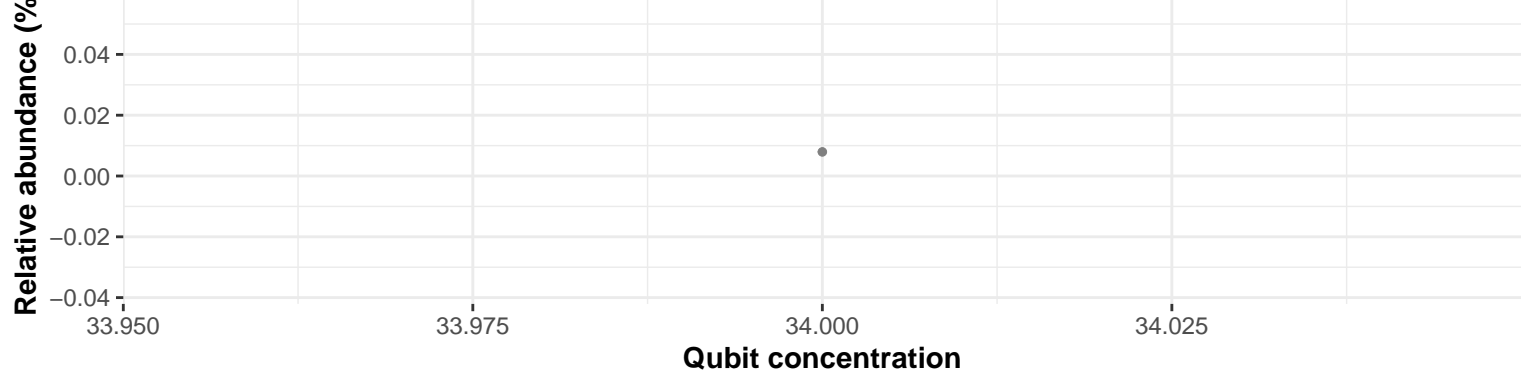
$\log_e(S) = 6.644$, $p = 0.632$, $\hat{\rho}_{\text{Spearman}} = -0.130$, $\text{CI}_{95\%} [-0.598, 0.405]$, $n_{\text{pairs}} = 16$



Correlation within: control



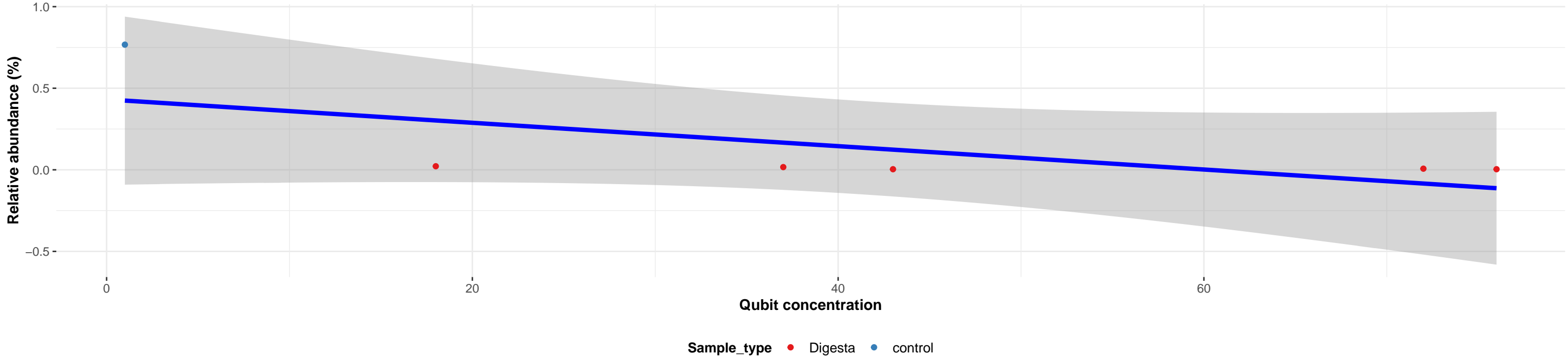
Correlation within: water



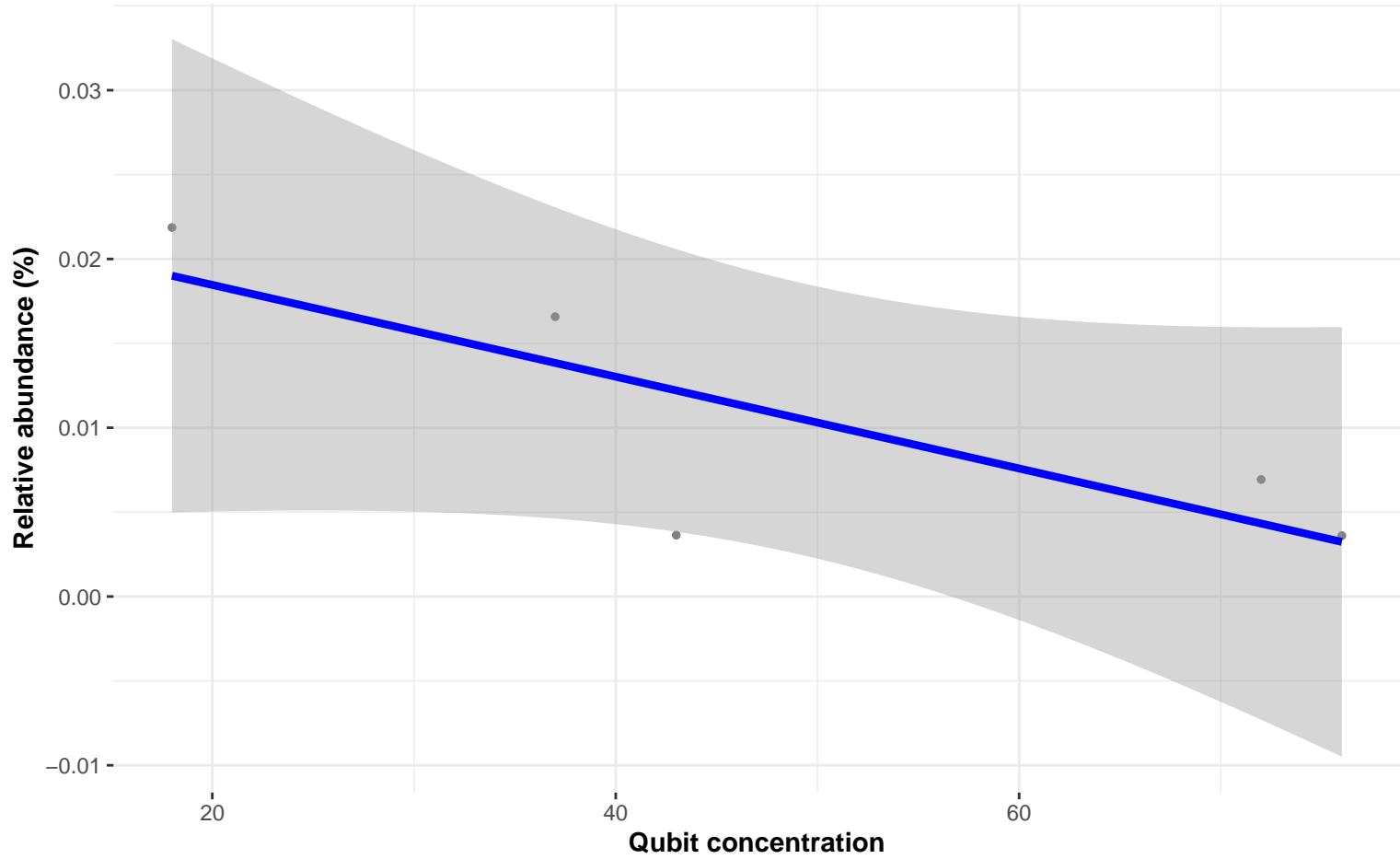
Bacteria; Firmicutes; Bacilli; Bacillales; Planococcaceae; NA; NA

Correlation with all samples

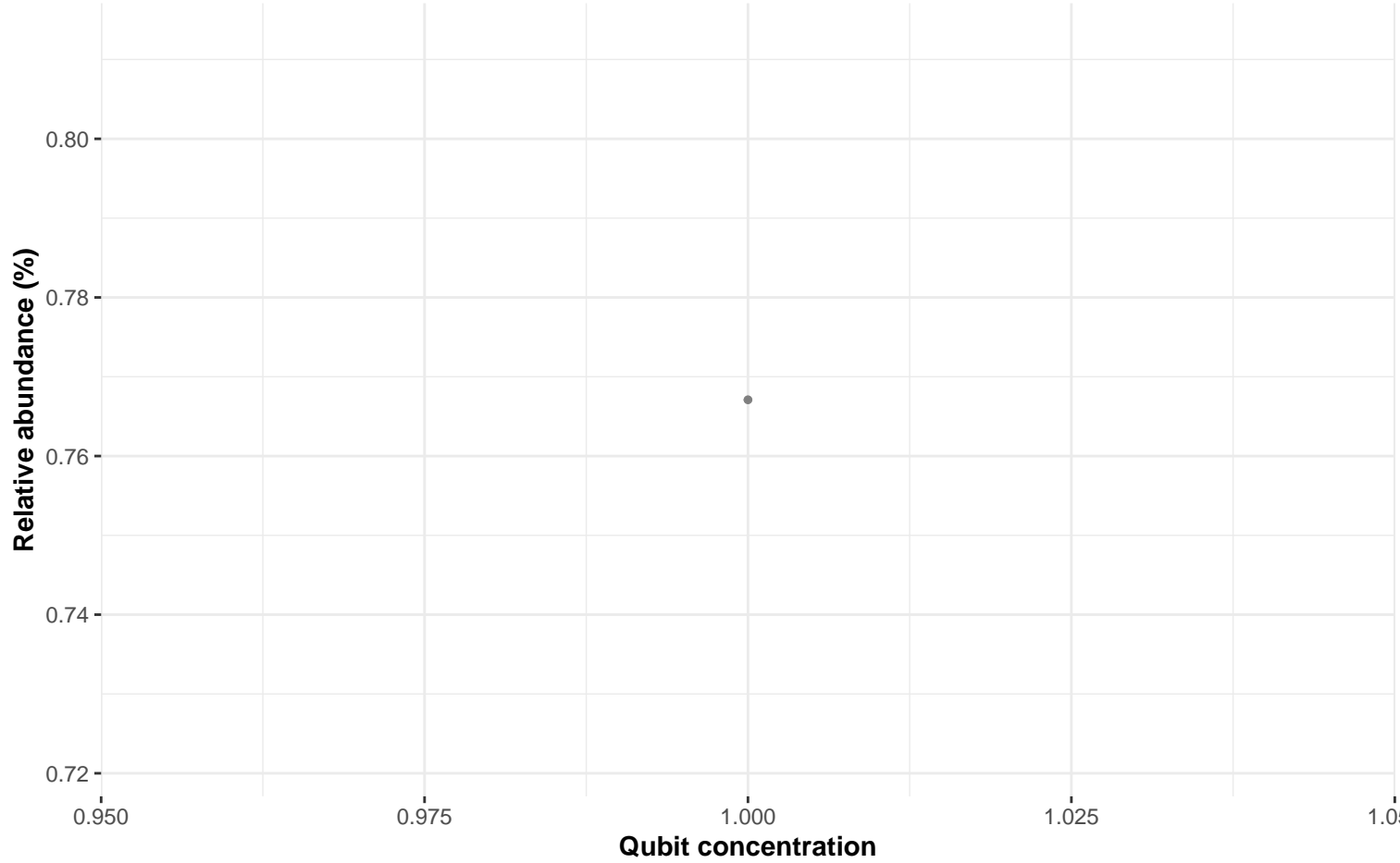
$\log_e(S) = 4.220$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = -0.943$, $\text{CI}_{95\%} [-0.994, -0.536]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



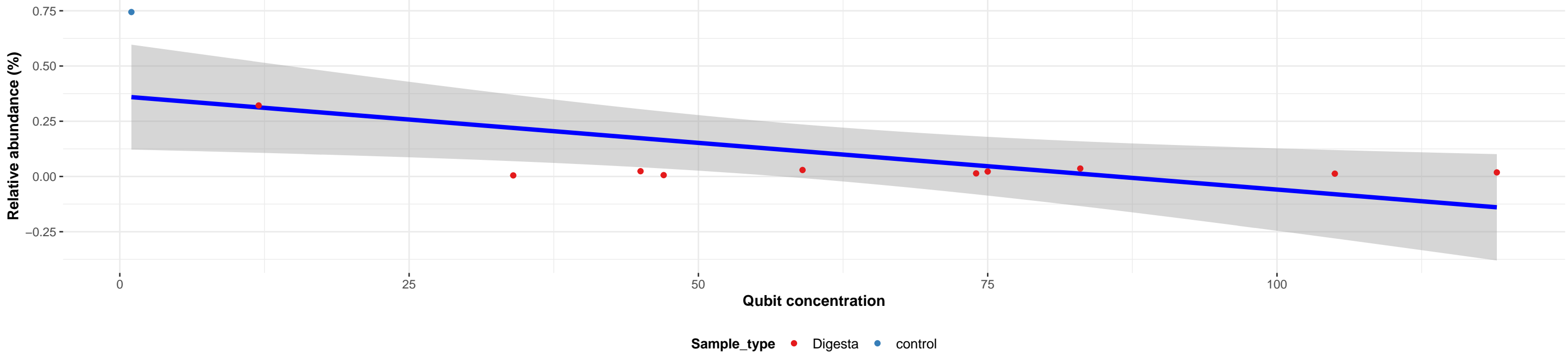
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; NA

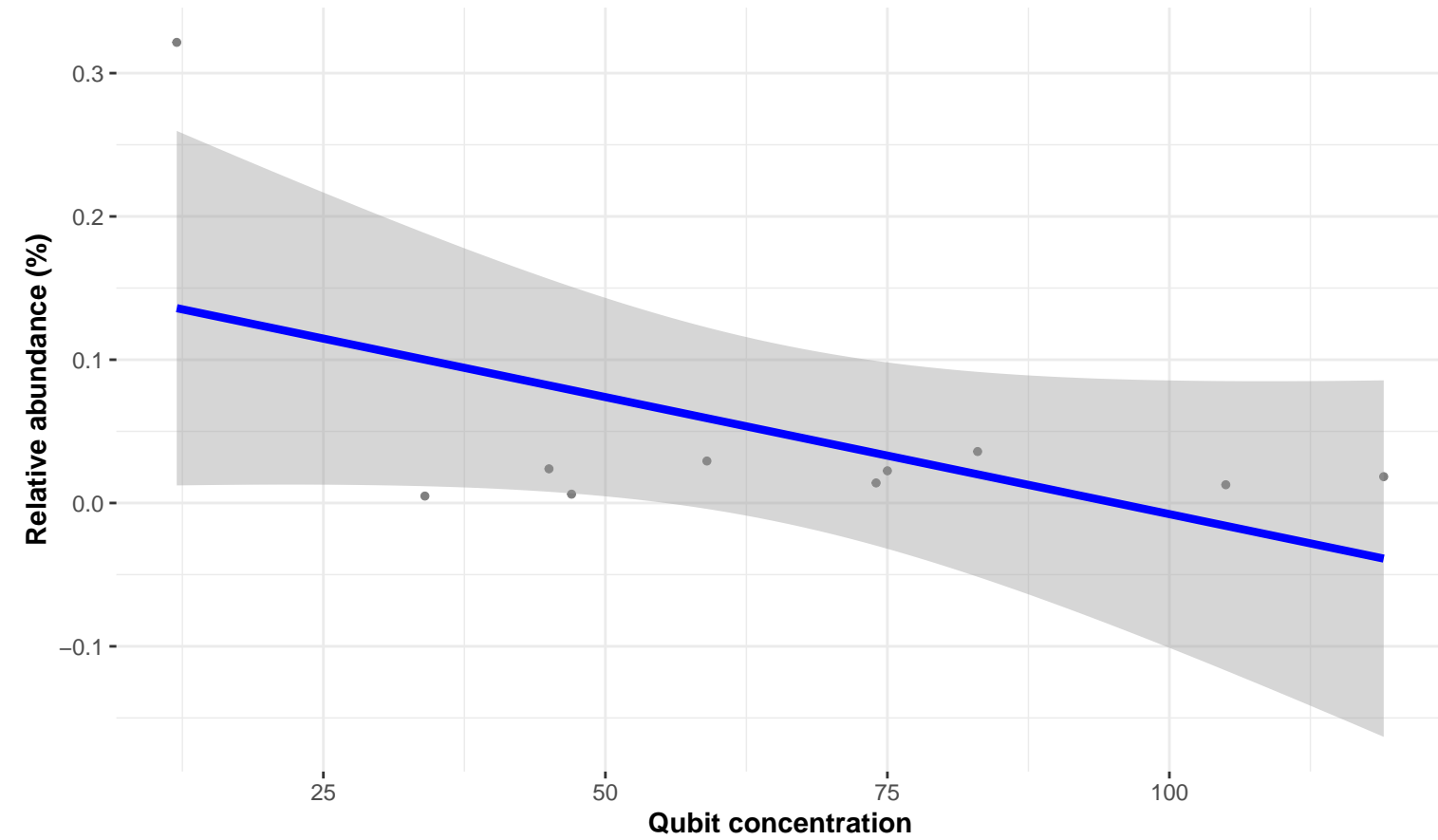
Correlation with all samples

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

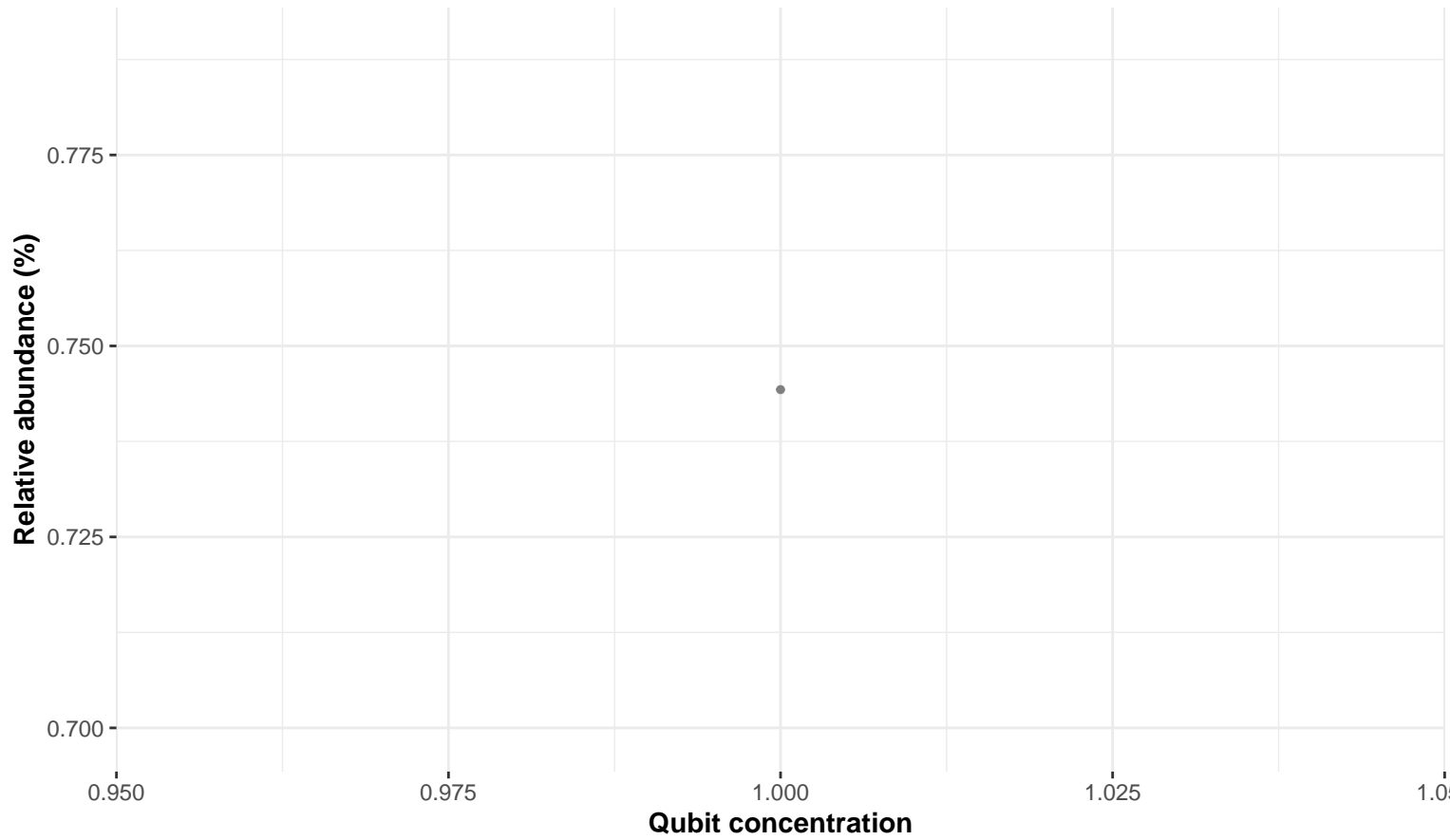


Correlation within: Digesta

$\log_e(S) = 5.182$, $p = 0.829$, $\hat{\rho}_{\text{Spearman}} = -0.079$, $\text{CI}_{95\%} [-0.687, 0.594]$, $n_{\text{pairs}} = 10$



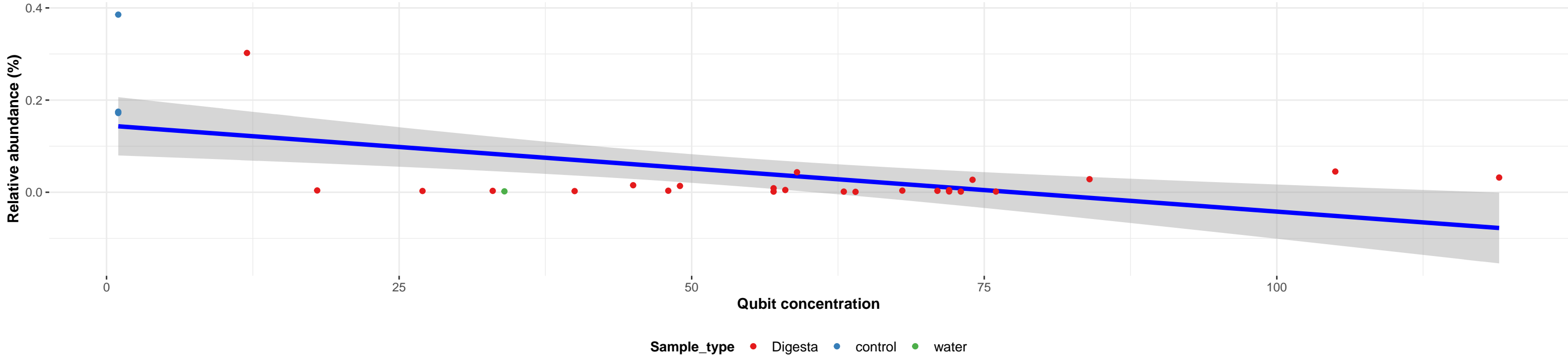
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Adlerbacteria; NA; NA; NA

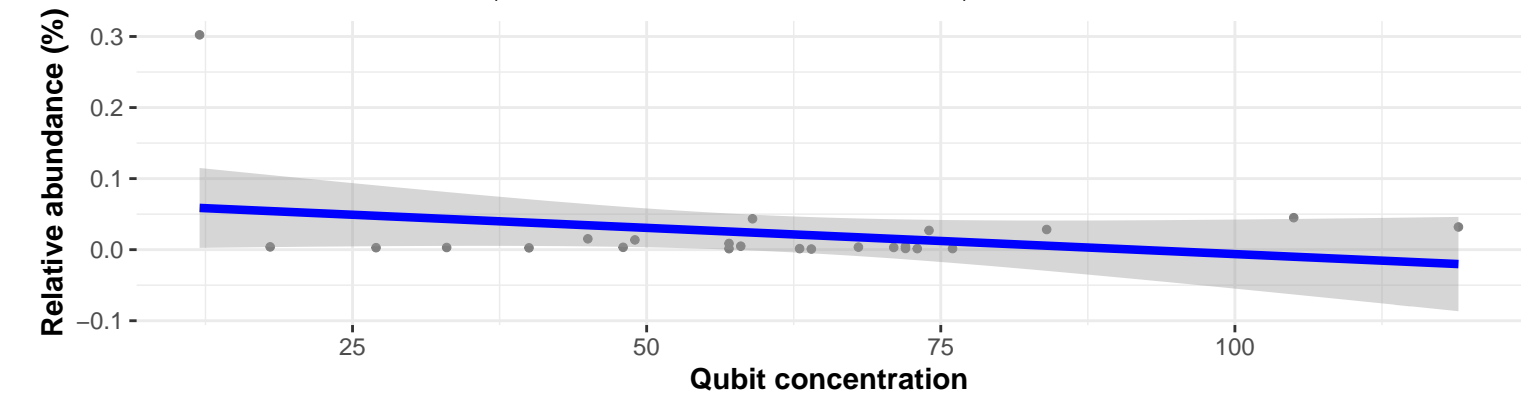
Correlation with all samples

$\log_e(S) = 8.403$, $p = 0.260$, $\hat{\rho}_{\text{Spearman}} = -0.220$, $\text{CI}_{95\%} [-0.556, 0.178]$, $n_{\text{pairs}} = 28$

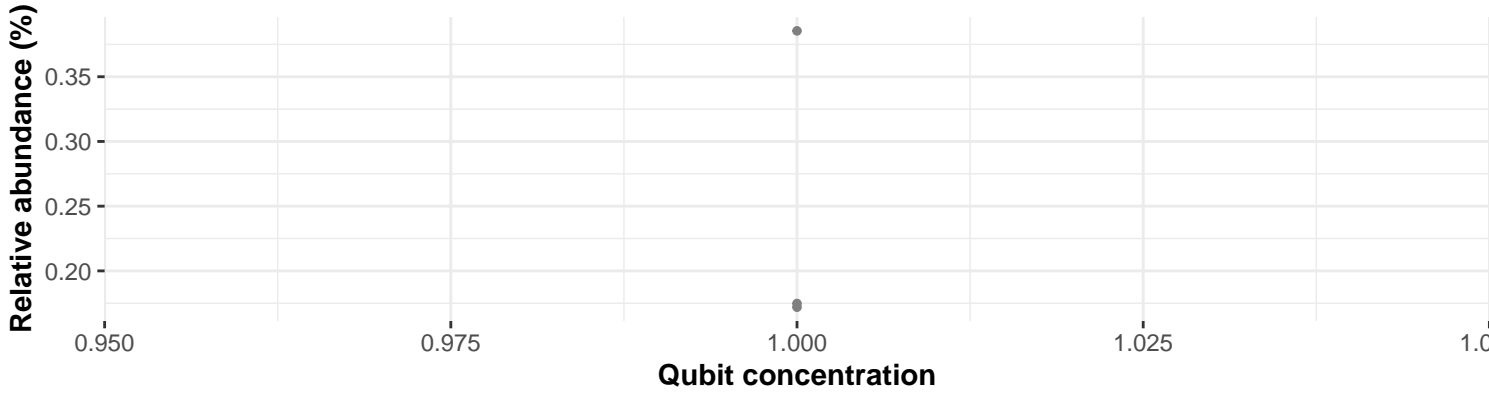


Correlation within: Digesta

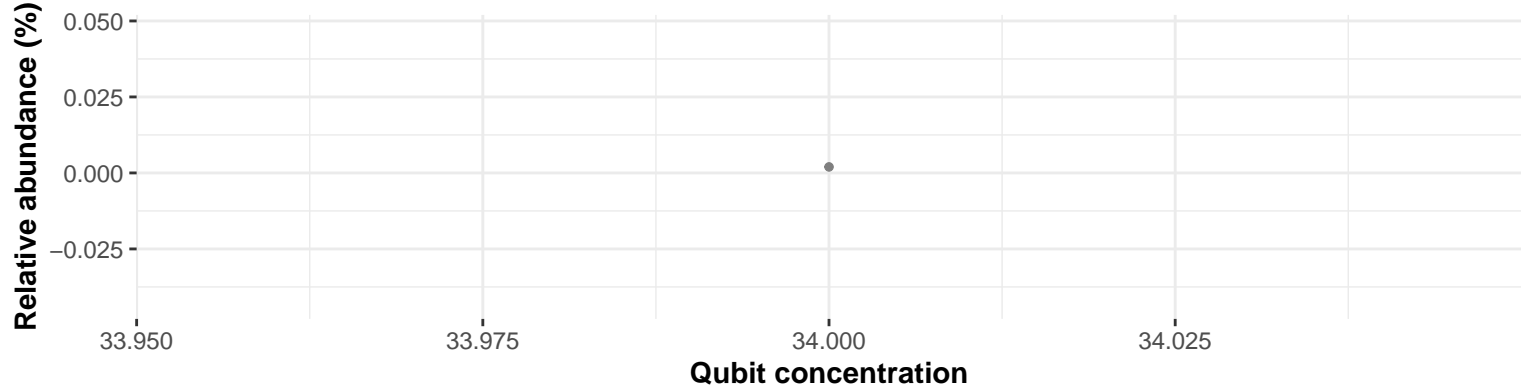
$\log_e(S) = 7.656$, $p = 0.707$, $\hat{\rho}_{\text{Spearman}} = 0.081$, $\text{CI}_{95\%} [-0.345, 0.479]$, $n_{\text{pairs}} = 24$



Correlation within: control



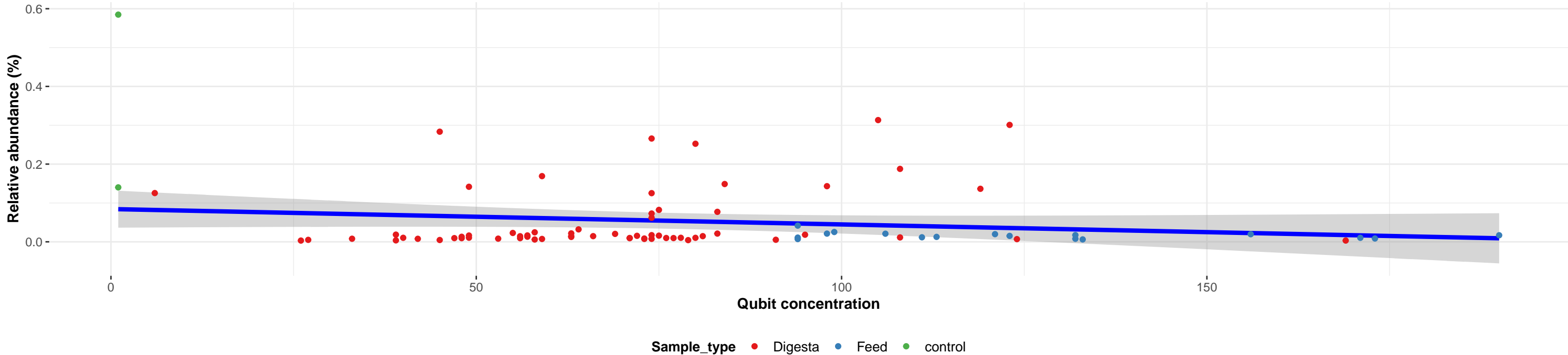
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; cecorum

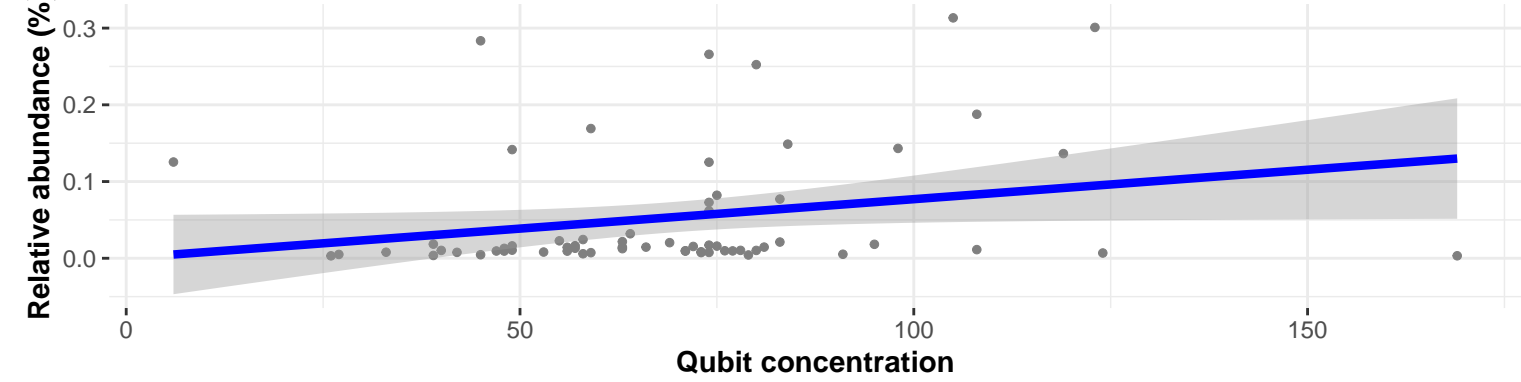
Correlation with all samples

$\log_e(S) = 11.416$, $p = 0.466$, $\hat{\rho}_{\text{Spearman}} = 0.081$, $CI_{95\%} [-0.142, 0.296]$, $n_{\text{pairs}} = 84$



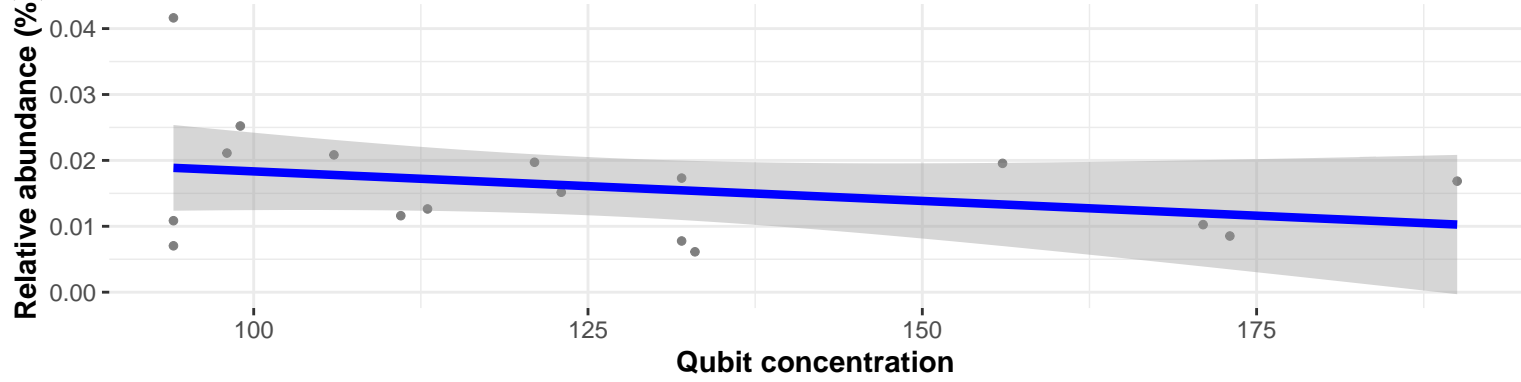
Correlation within: Digesta

$\log_e(S) = 10.419$, $p = 0.031$, $\hat{\rho}_{\text{Spearman}} = 0.268$, $CI_{95\%} [0.018, 0.486]$, $n_{\text{pairs}} = 65$

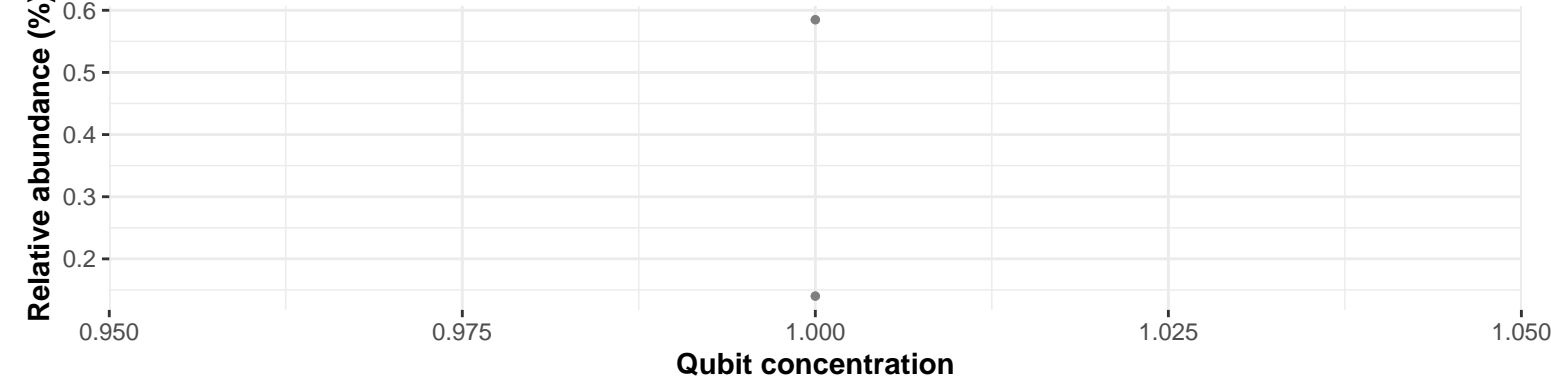


Correlation within: Feed

$\log_e(S) = 6.985$, $p = 0.204$, $\hat{\rho}_{\text{Spearman}} = -0.325$, $CI_{95\%} [-0.704, 0.200]$, $n_{\text{pairs}} = 17$



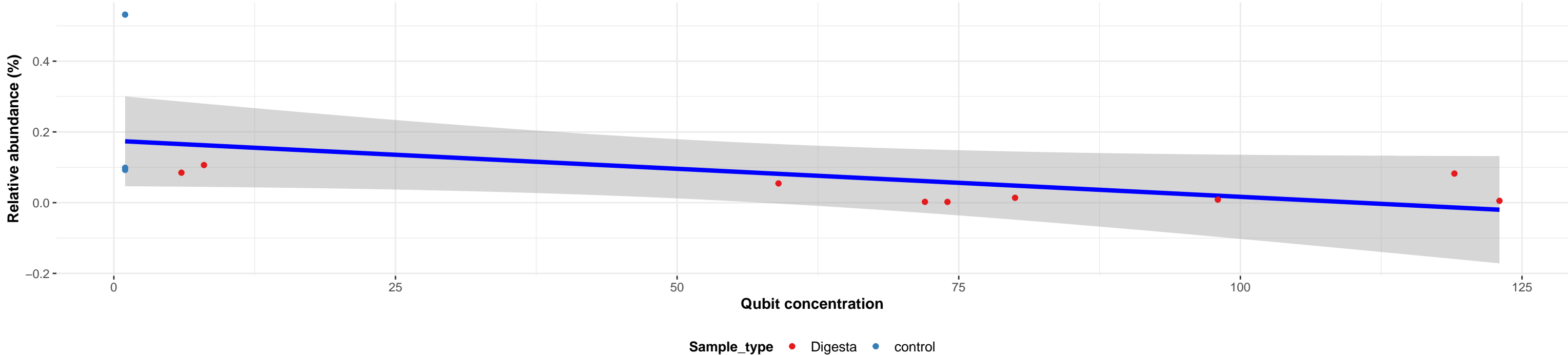
Correlation within: control



Bacteria; Verrucomicrobiota; Verrucomicrobiae; Verrucomicrobiales; Rubritaleaceae; Luteolibacter; NA

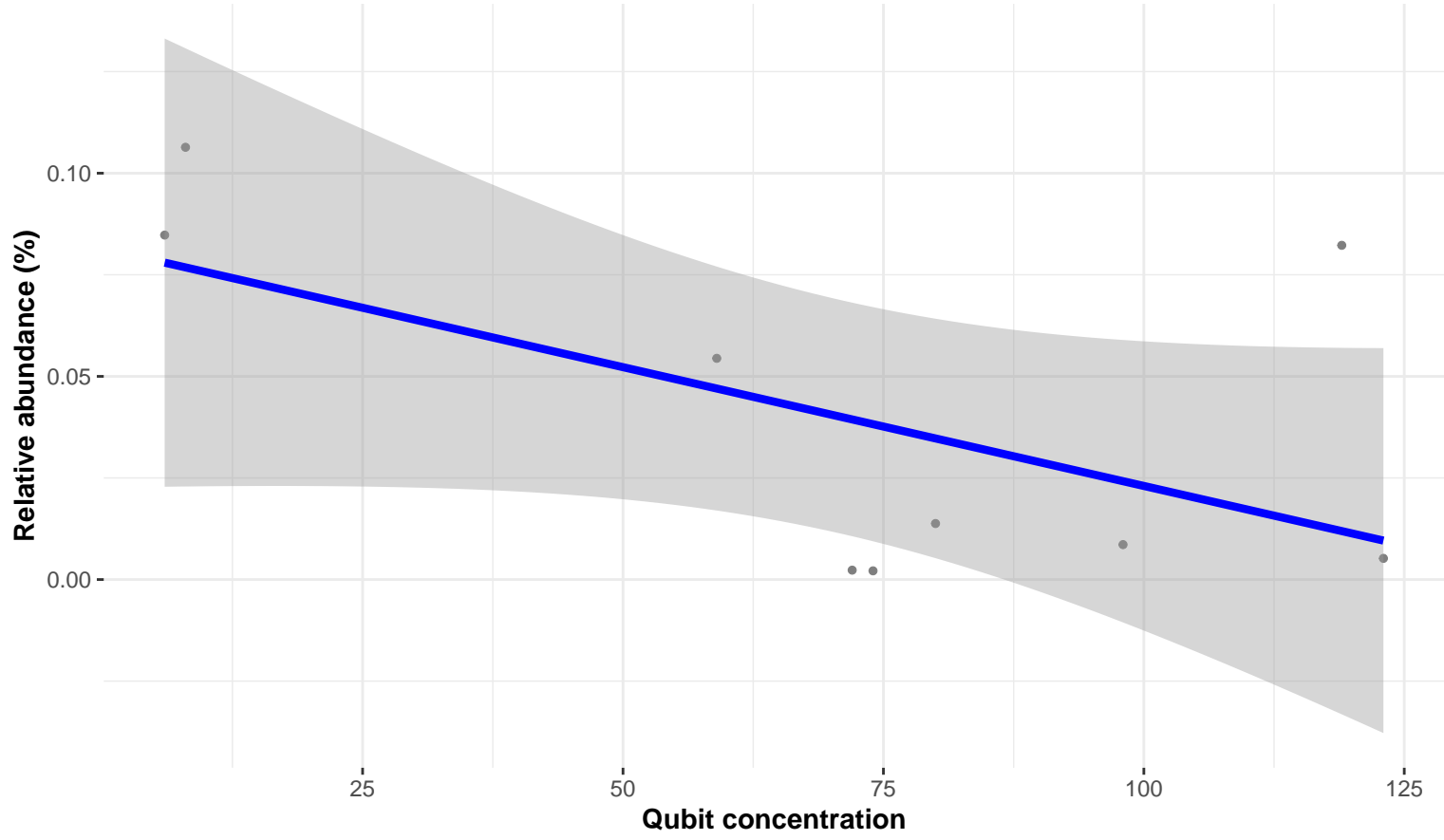
Correlation with all samples

$\log_e(S) = 6.197$, $p = 0.009$, $\hat{\rho}_{\text{Spearman}} = -0.718$, $\text{CI}_{95\%} [-0.918, -0.227]$, $n_{\text{pairs}} = 12$

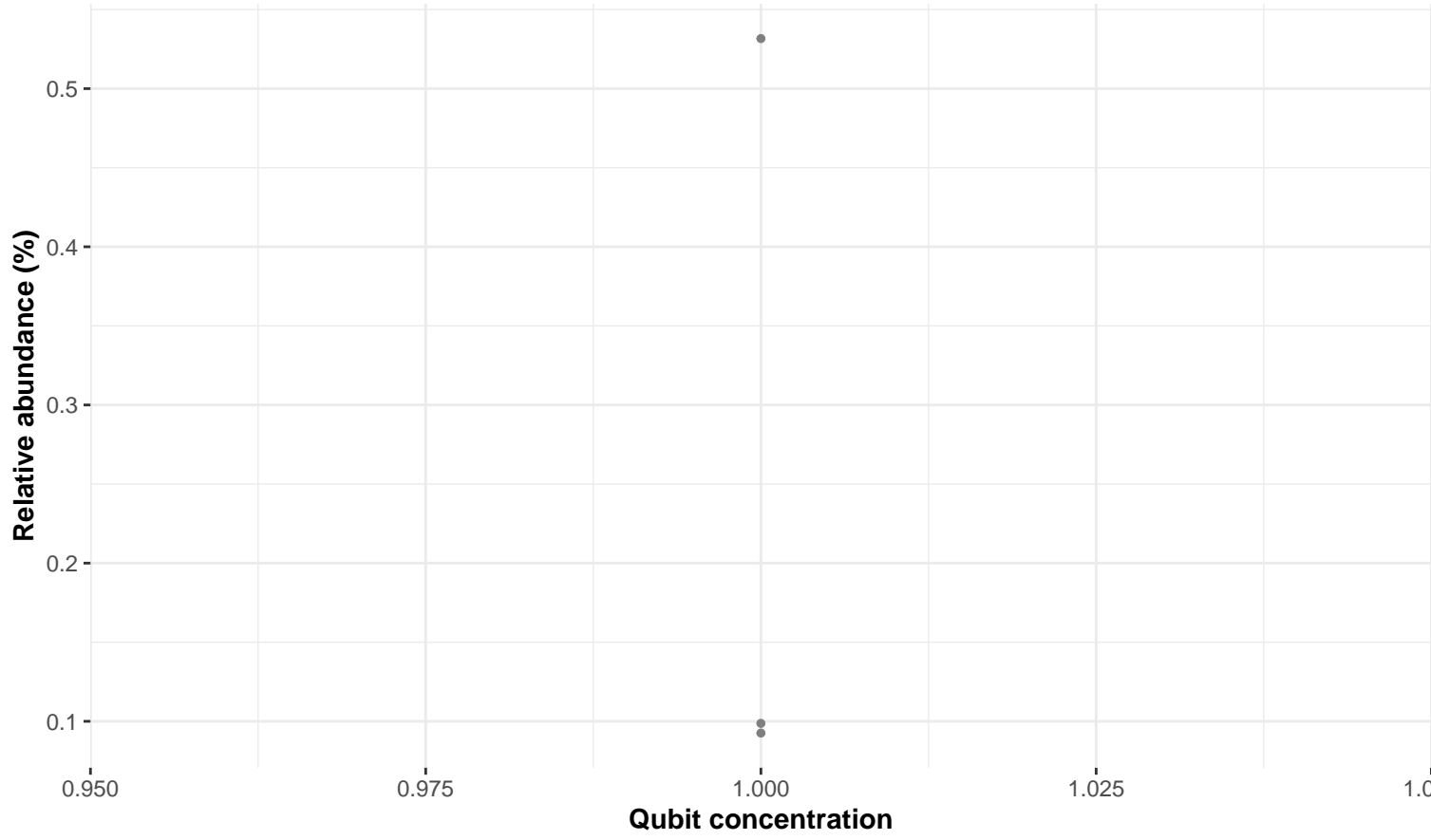


Correlation within: Digesta

$\log_e(S) = 5.159$, $p = 0.224$, $\hat{\rho}_{\text{Spearman}} = -0.450$, $\text{CI}_{95\%} [-0.864, 0.327]$, $n_{\text{pairs}} = 9$



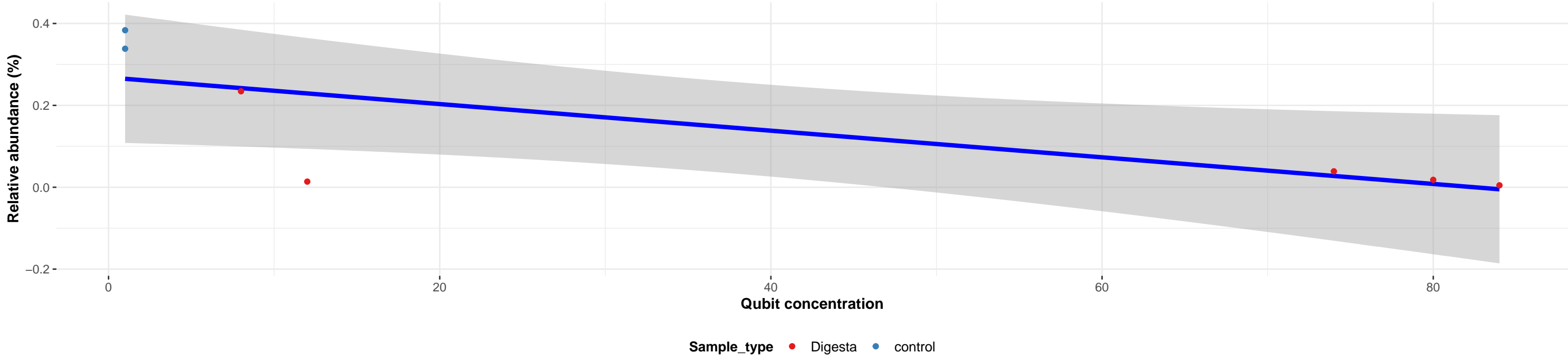
Correlation within: control



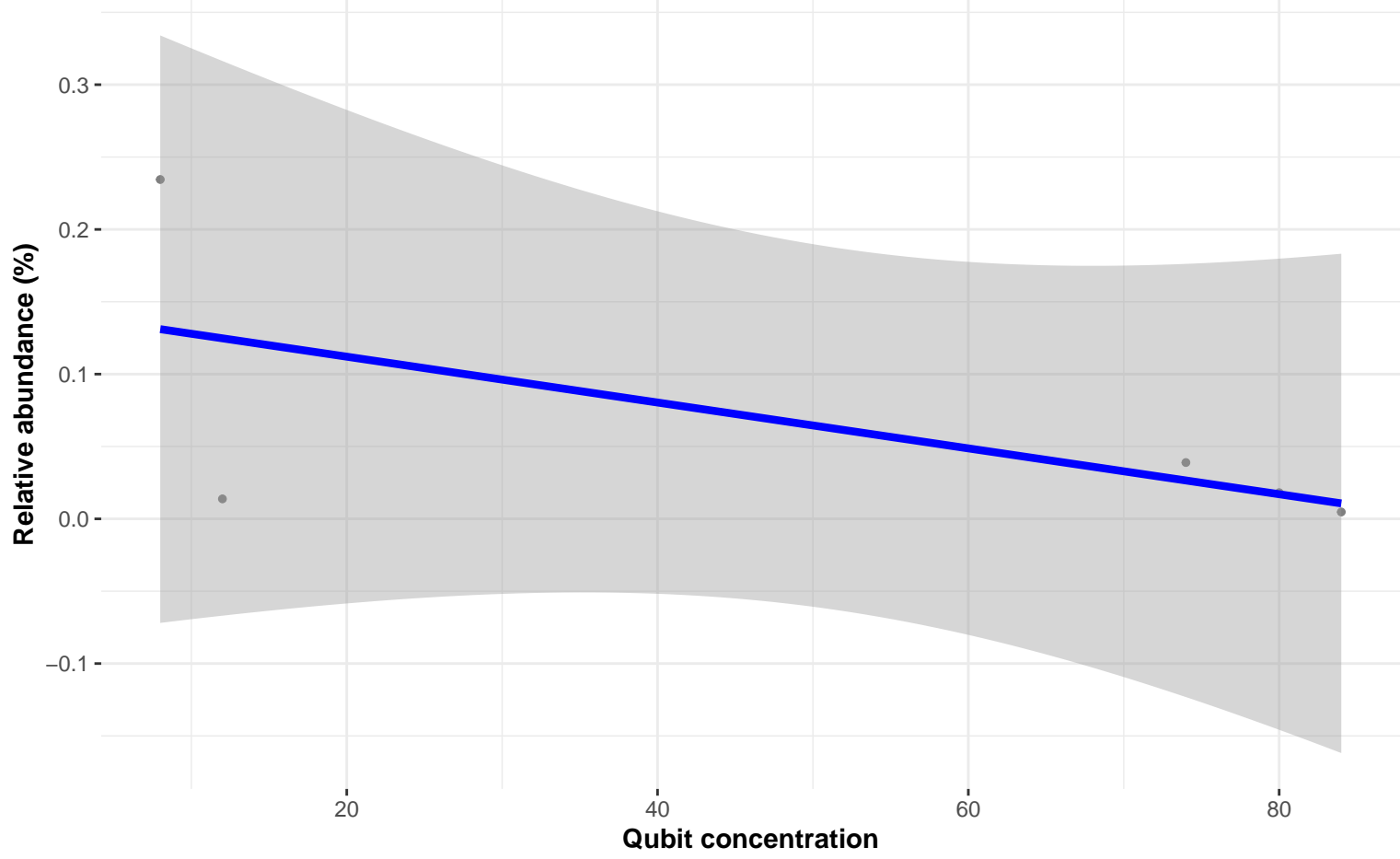
Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; lipophiloflavum

Correlation with all samples

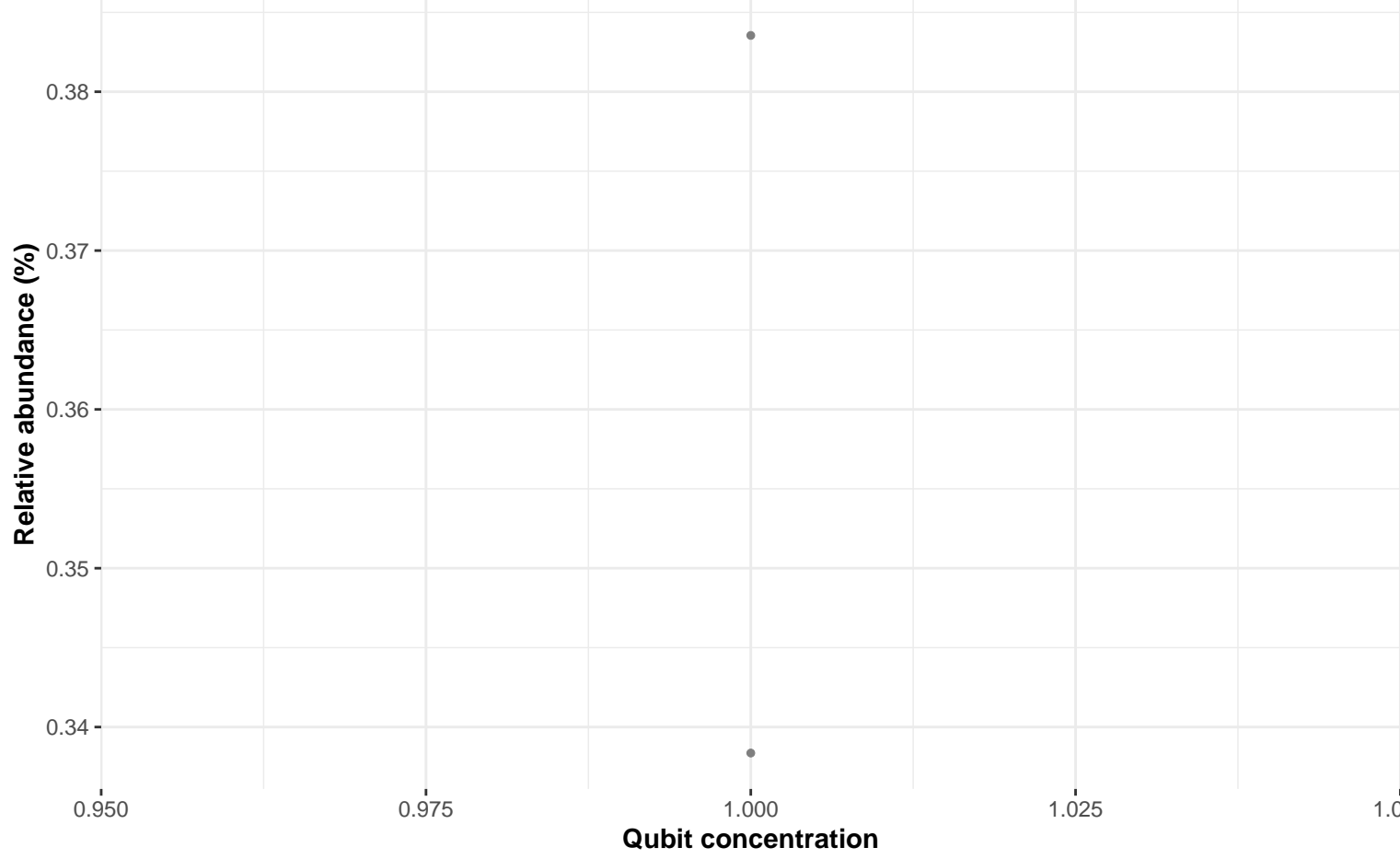
$\log_e(S) = 4.658$, $p = 0.008$, $\hat{\rho}_{\text{Spearman}} = -0.883$, $CI_{95\%} [-0.984, -0.363]$, $n_{\text{pairs}} = 7$



Correlation within: Digesta



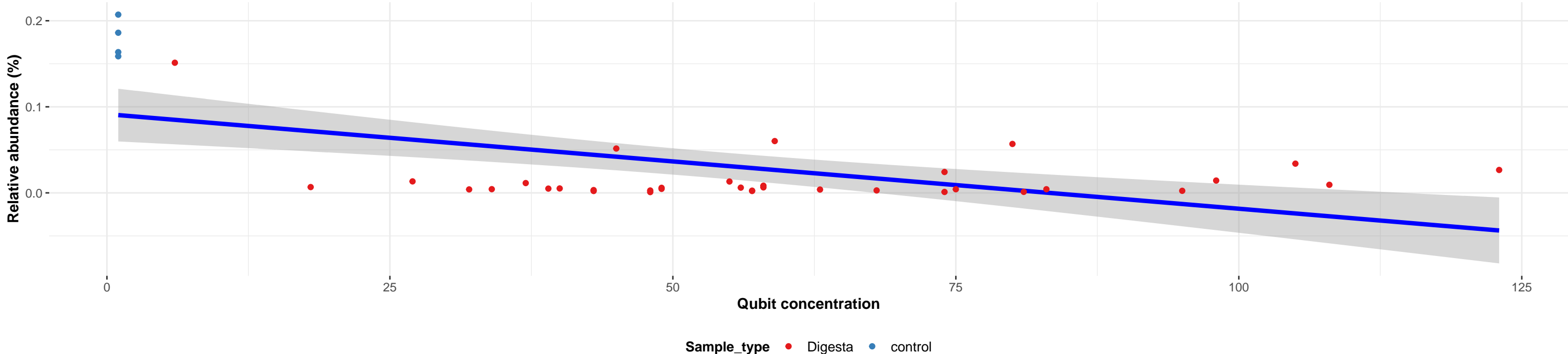
Correlation within: control



Bacteria; Dependuntiae; Babeliae; Babeliales; NA; NA; NA

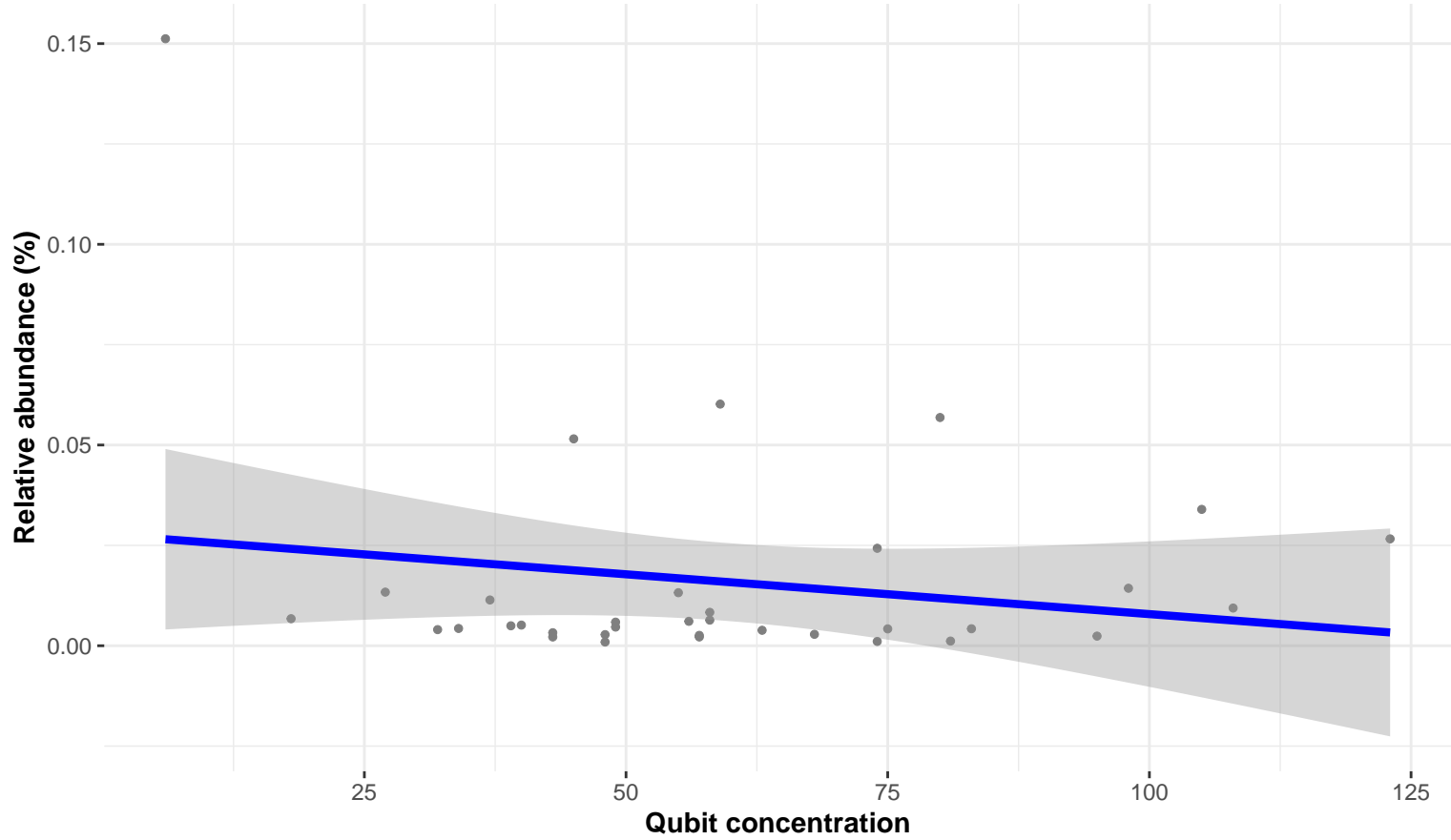
Correlation with all samples

$\log_e(S) = 9.426$, $p = 0.116$, $\hat{\rho}_{\text{Spearman}} = -0.256$, $\text{CI}_{95\%} [-0.536, 0.074]$, $n_{\text{pairs}} = 39$

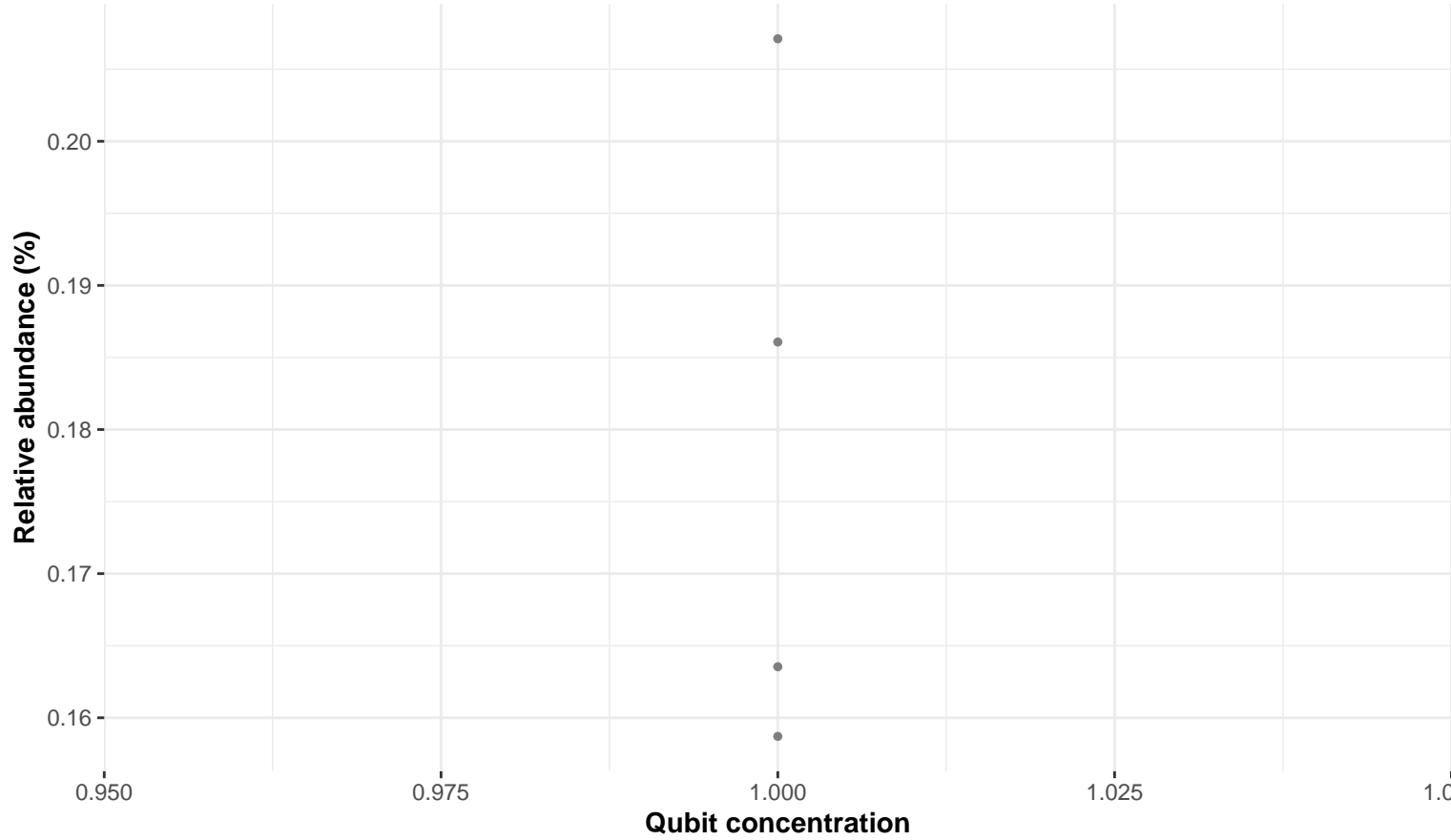


Correlation within: Digesta

$\log_e(S) = 8.845$, $p = 0.871$, $\hat{\rho}_{\text{Spearman}} = 0.028$, $\text{CI}_{95\%} [-0.317, 0.367]$, $n_{\text{pairs}} = 35$



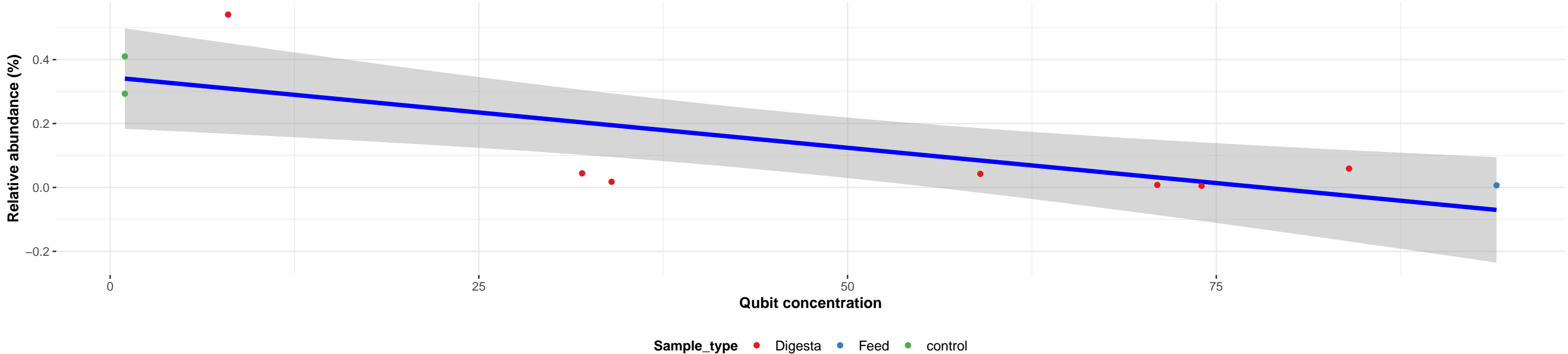
Correlation within: control



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; NA

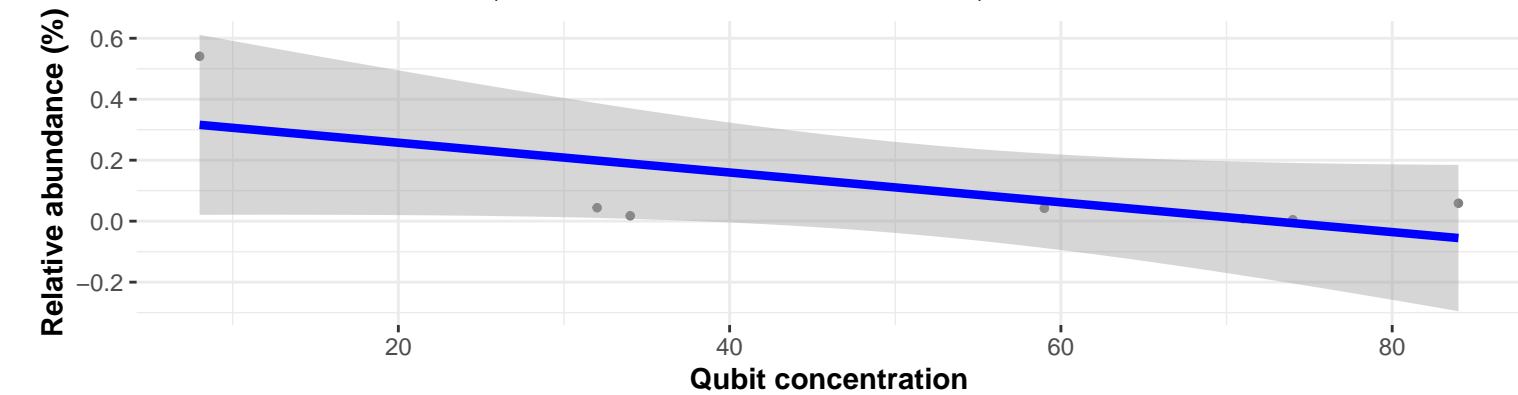
Correlation with all samples

$\log_e(S) = 5.661$, $p = 0.014$, $\hat{\rho}_{\text{Spearman}} = -0.742$, $CI_{95\%} [-0.937, -0.189]$, $n_{\text{pairs}} = 10$

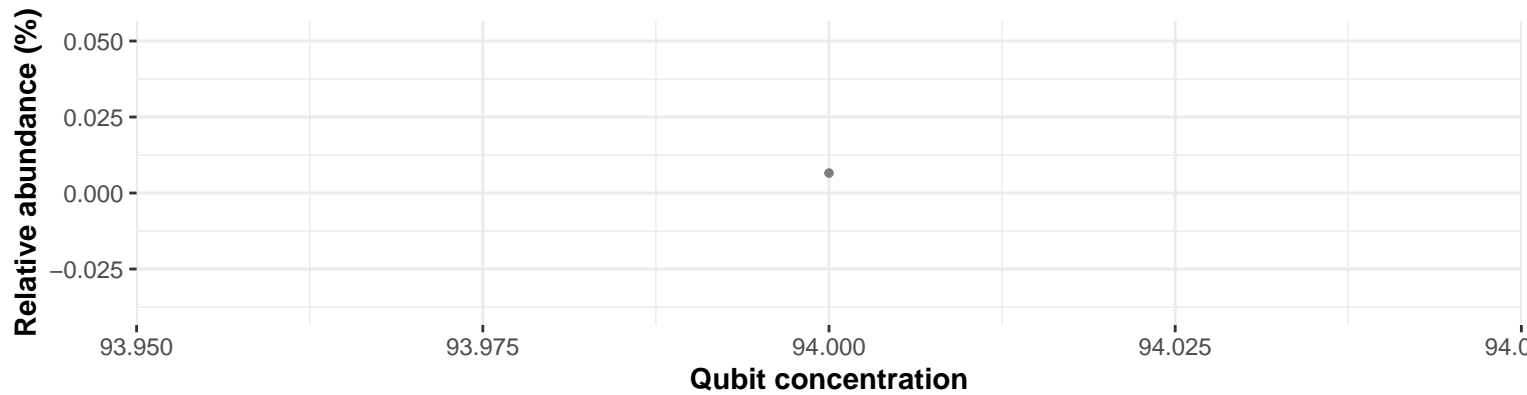


Correlation within: Digesta

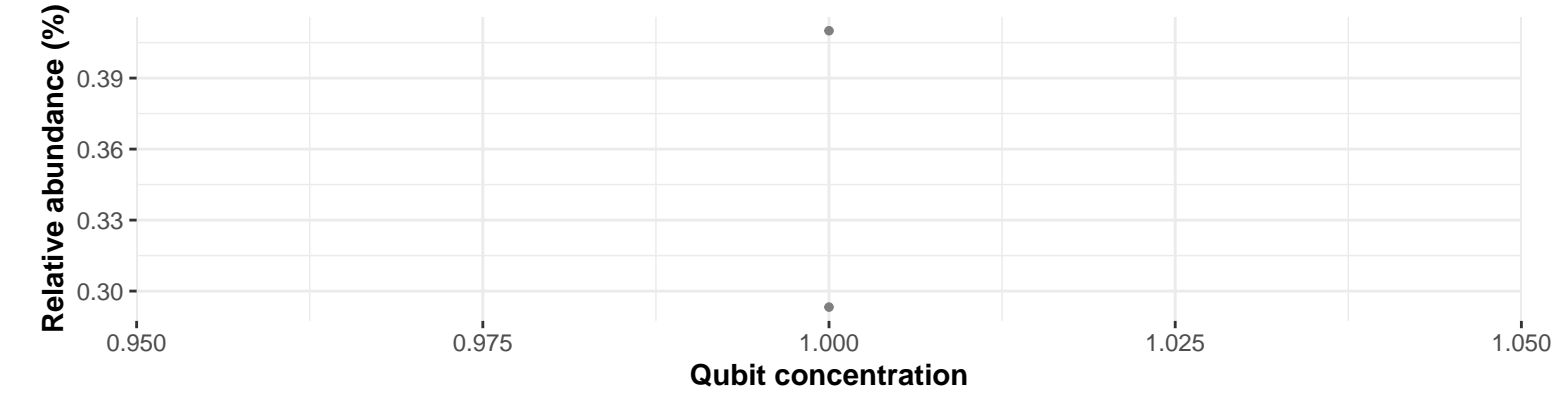
$\log_e(S) = 4.382$, $p = 0.337$, $\hat{\rho}_{\text{Spearman}} = -0.429$, $CI_{95\%} [-0.899, 0.501]$, $n_{\text{pairs}} = 7$



Correlation within: Feed



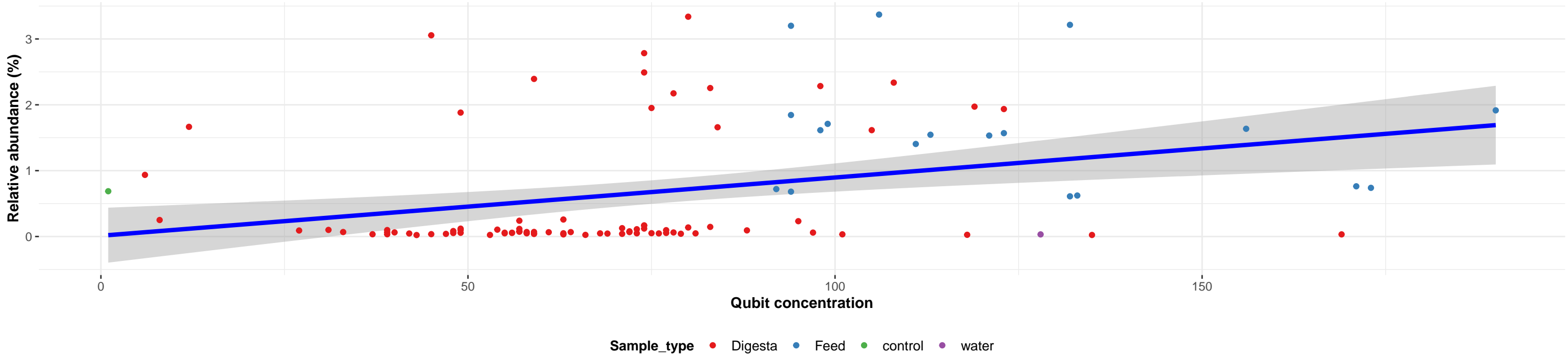
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; HT002; NA

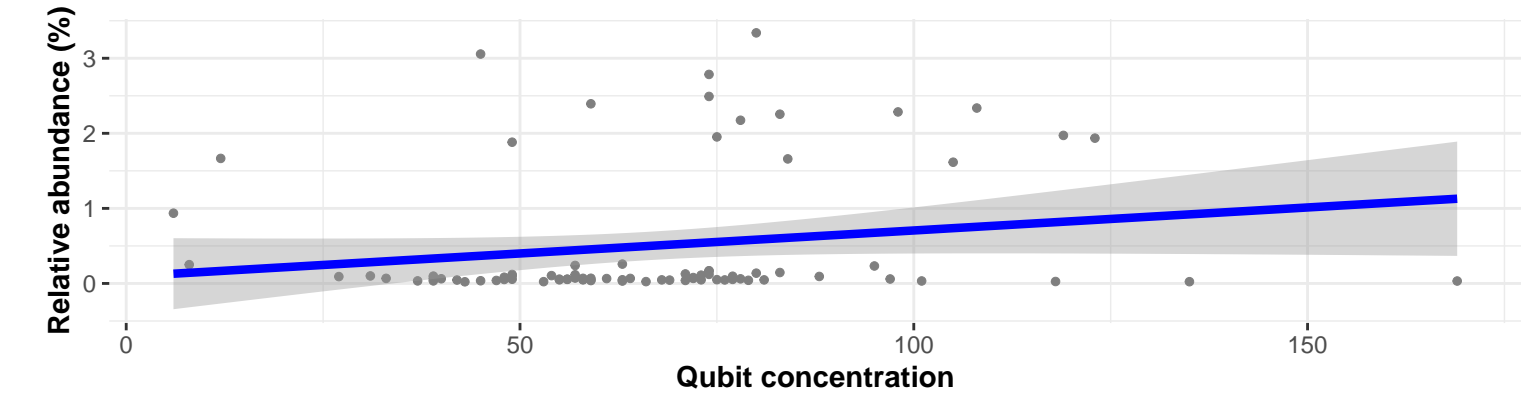
Correlation with all samples

$\log_e(S) = 11.742$, $p = 0.001$, $\hat{\rho}_{\text{Spearman}} = 0.329$, $\text{CI}_{95\%} [0.140, 0.495]$, $n_{\text{pairs}} = 104$



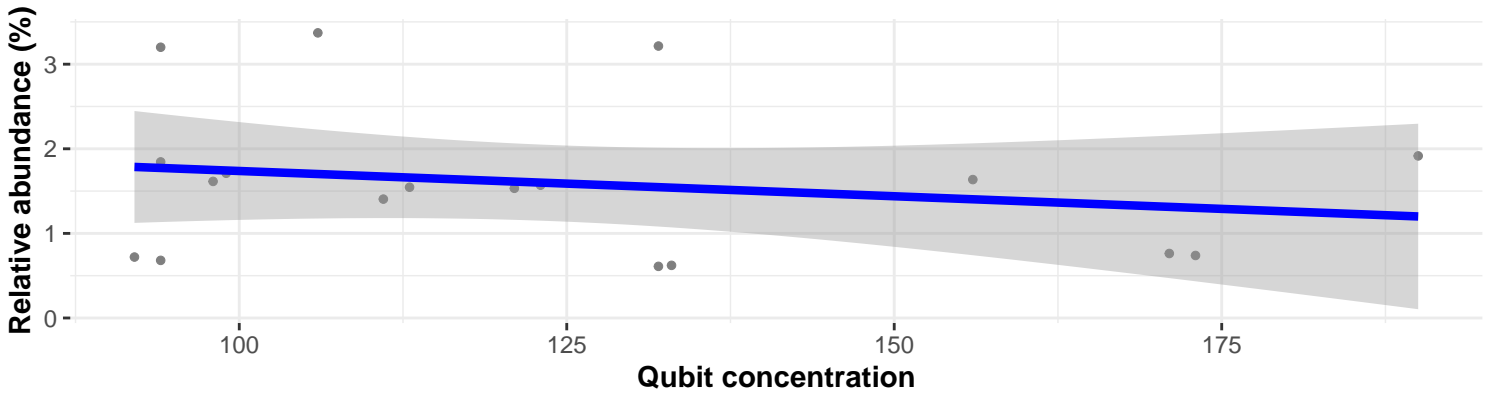
Correlation within: Digesta

$\log_e(S) = 11.351$, $p = 0.208$, $\hat{\rho}_{\text{Spearman}} = 0.139$, $\text{CI}_{95\%} [-0.084, 0.349]$, $n_{\text{pairs}} = 84$

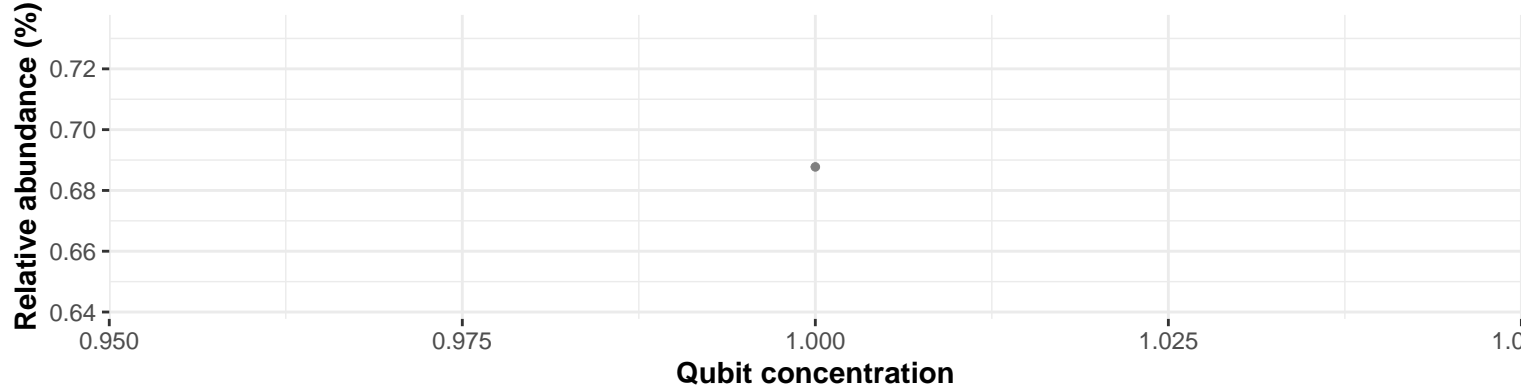


Correlation within: Feed

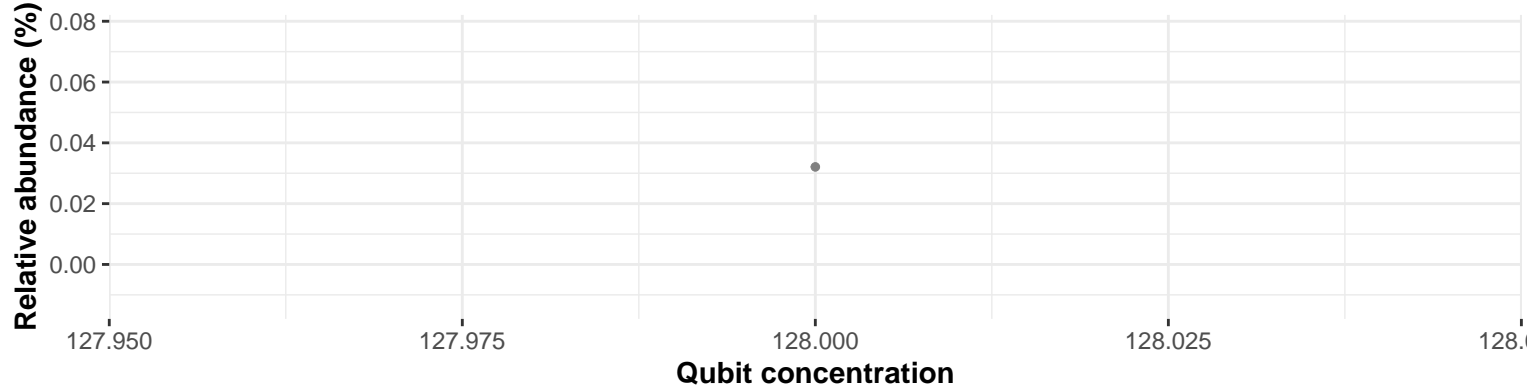
$\log_e(S) = 6.978$, $p = 0.674$, $\hat{\rho}_{\text{Spearman}} = -0.107$, $\text{CI}_{95\%} [-0.557, 0.392]$, $n_{\text{pairs}} = 18$



Correlation within: control



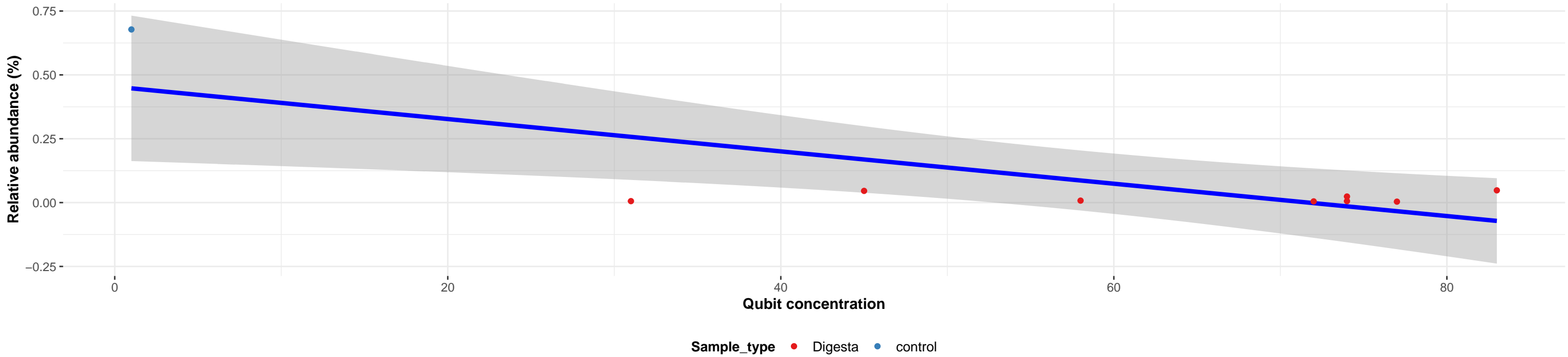
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Planococcaceae; Chungangia; NA

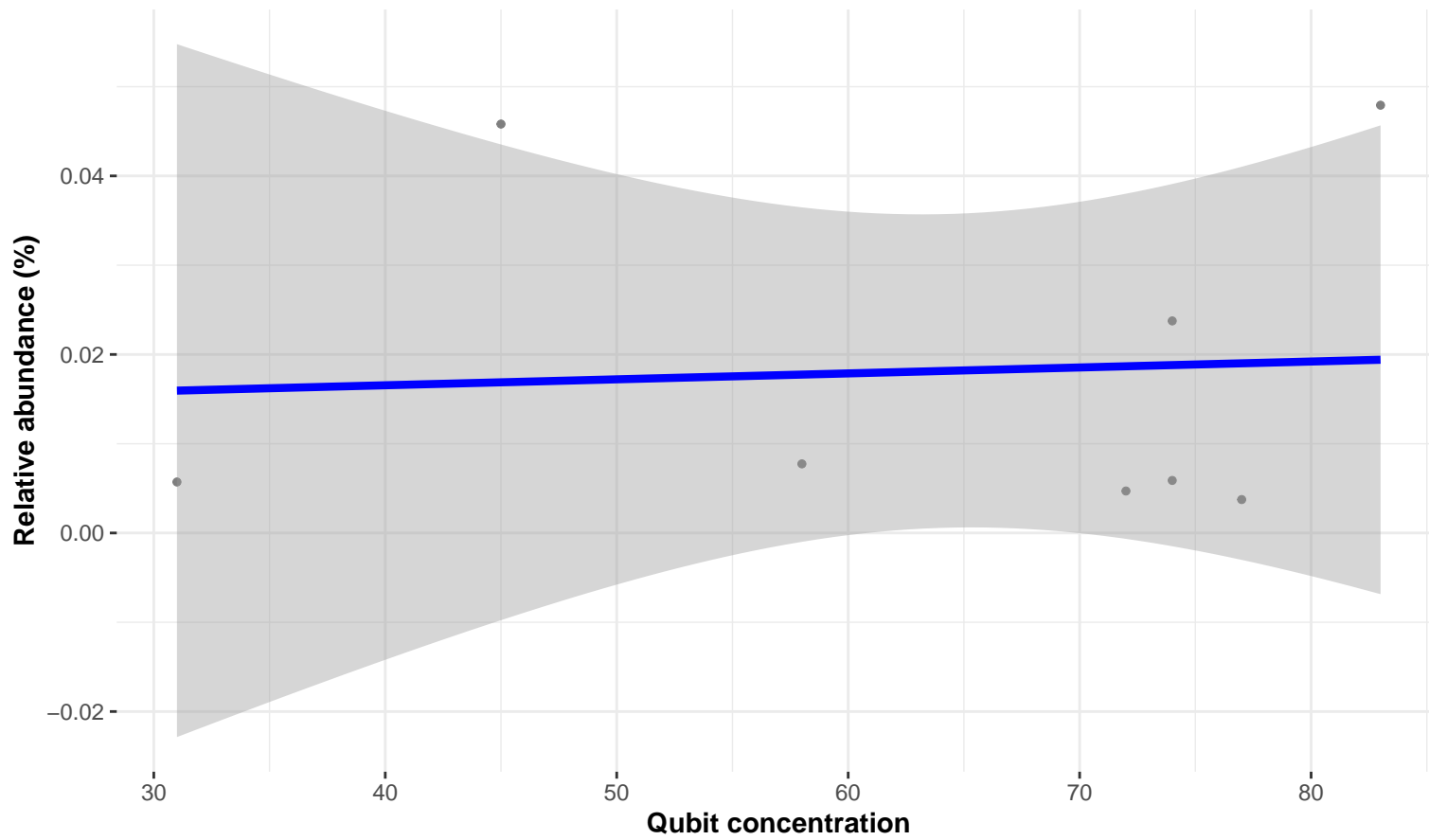
Correlation with all samples

$\log_e(S) = 4.998$, $p = 0.544$, $\hat{\rho}_{\text{Spearman}} = -0.234$, $\text{CI}_{95\%} [-0.787, 0.526]$, $n_{\text{pairs}} = 9$

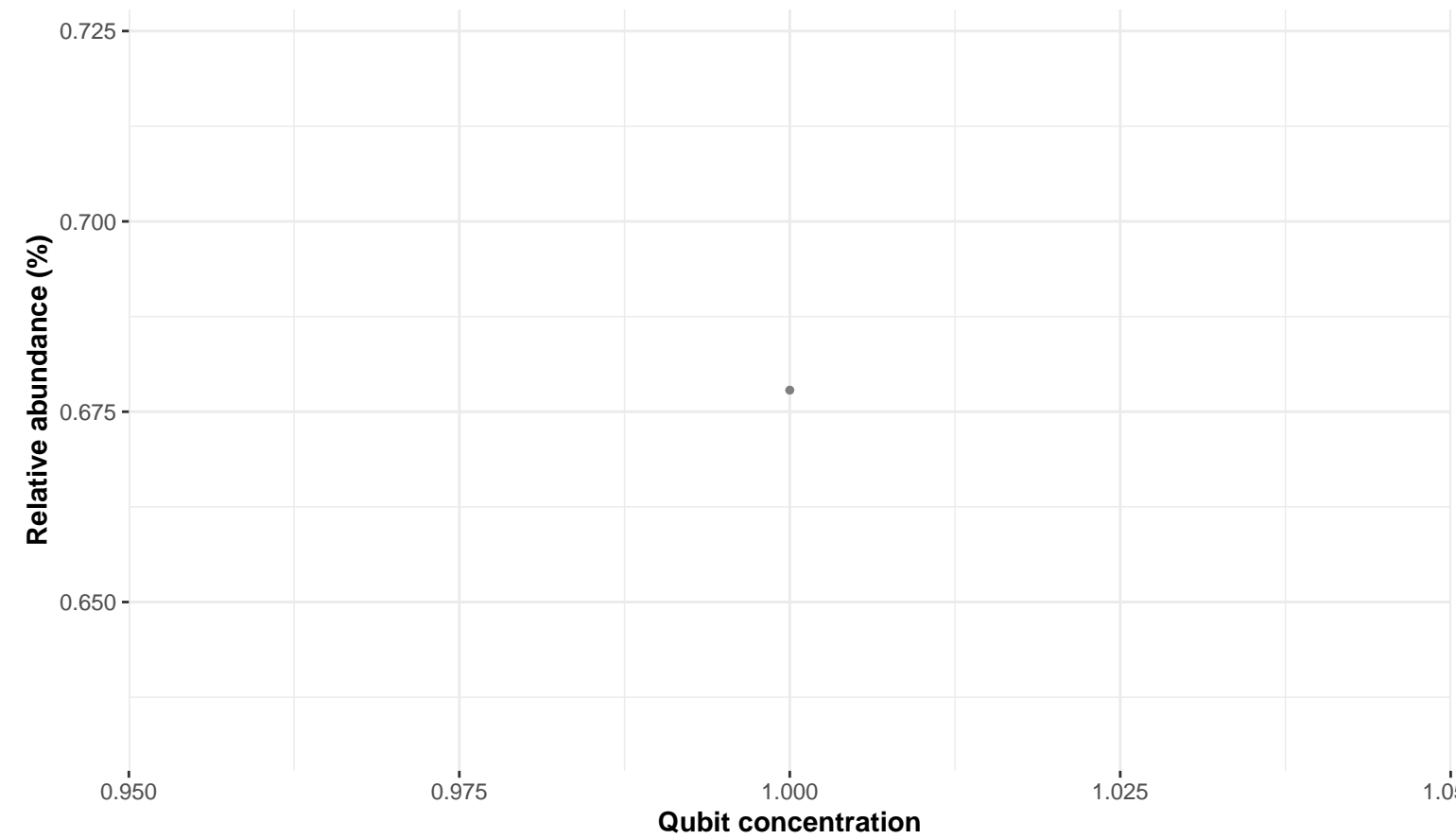


Correlation within: Digesta

$\log_e(S) = 4.330$, $p = 0.821$, $\hat{\rho}_{\text{Spearman}} = 0.096$, $\text{CI}_{95\%} [-0.668, 0.761]$, $n_{\text{pairs}} = 8$



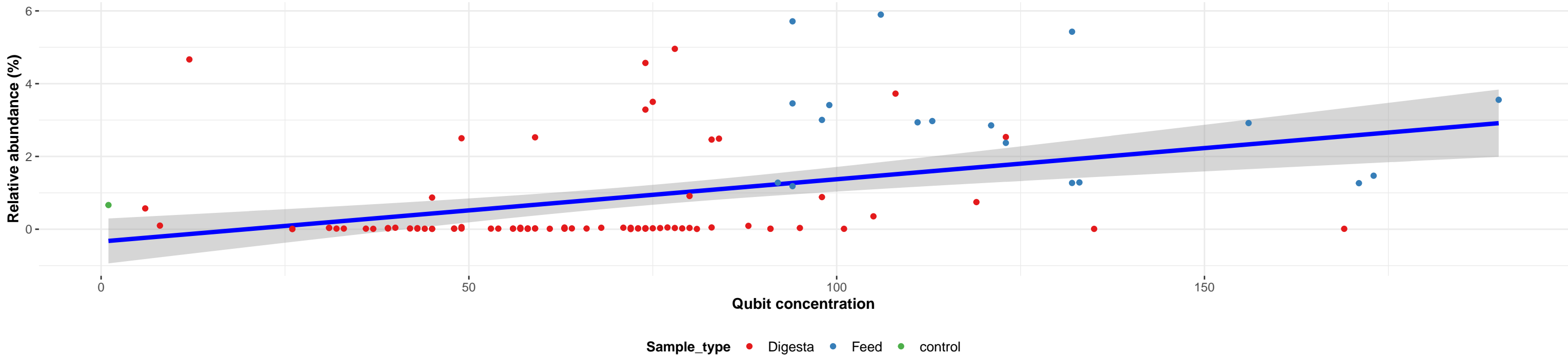
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; NA

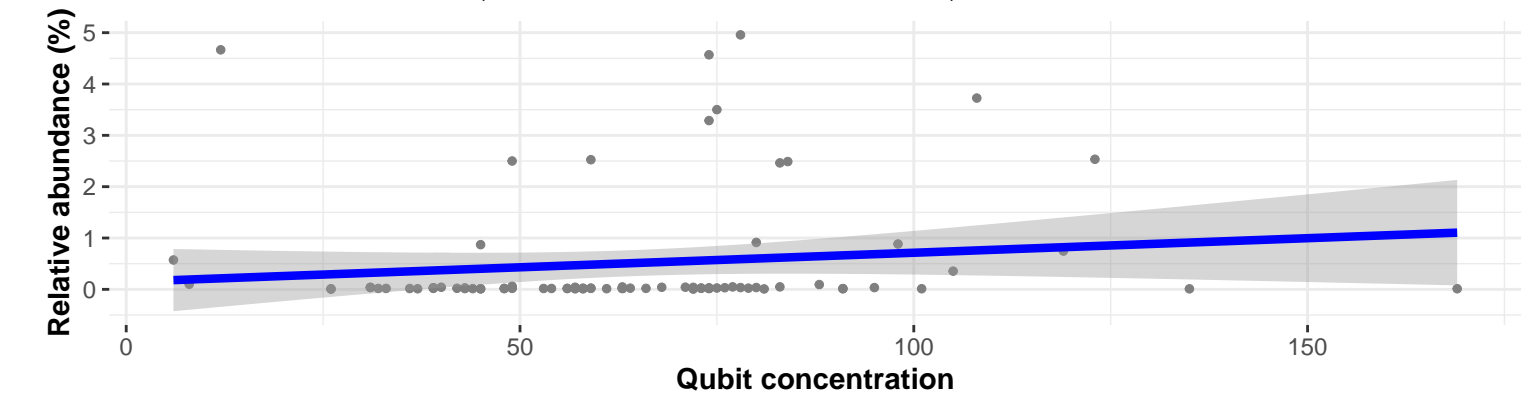
Correlation with all samples

$\log_e(S) = 11.544$, $p = 1.67e-06$, $\hat{\rho}_{\text{Spearman}} = 0.450$, $CI_{95\%} [0.276, 0.595]$, $n_{\text{pairs}} = 104$



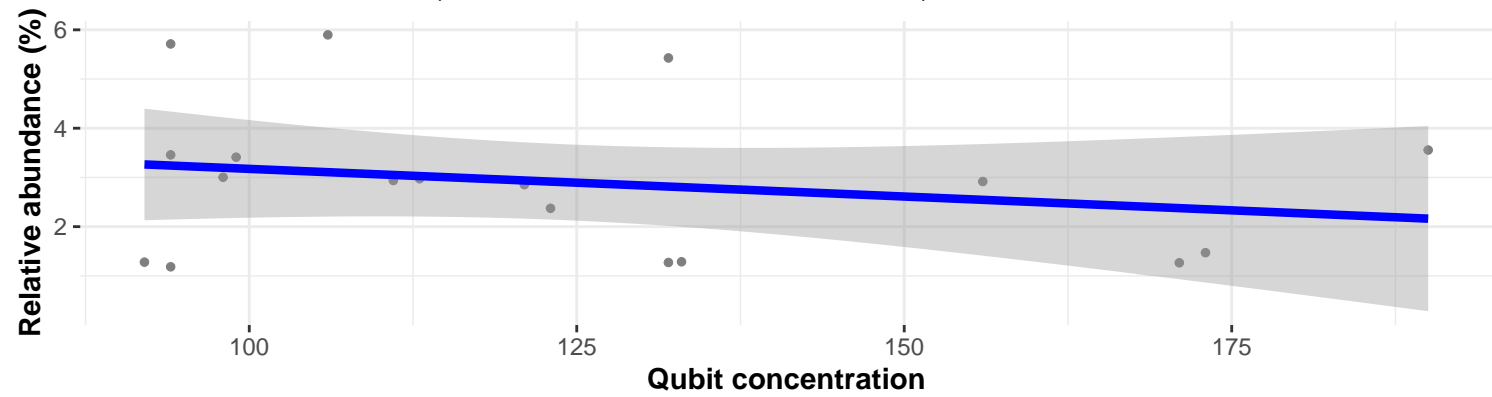
Correlation within: Digesta

$\log_e(S) = 11.292$, $p = 0.047$, $\hat{\rho}_{\text{Spearman}} = 0.216$, $CI_{95\%} [-0.003, 0.416]$, $n_{\text{pairs}} = 85$

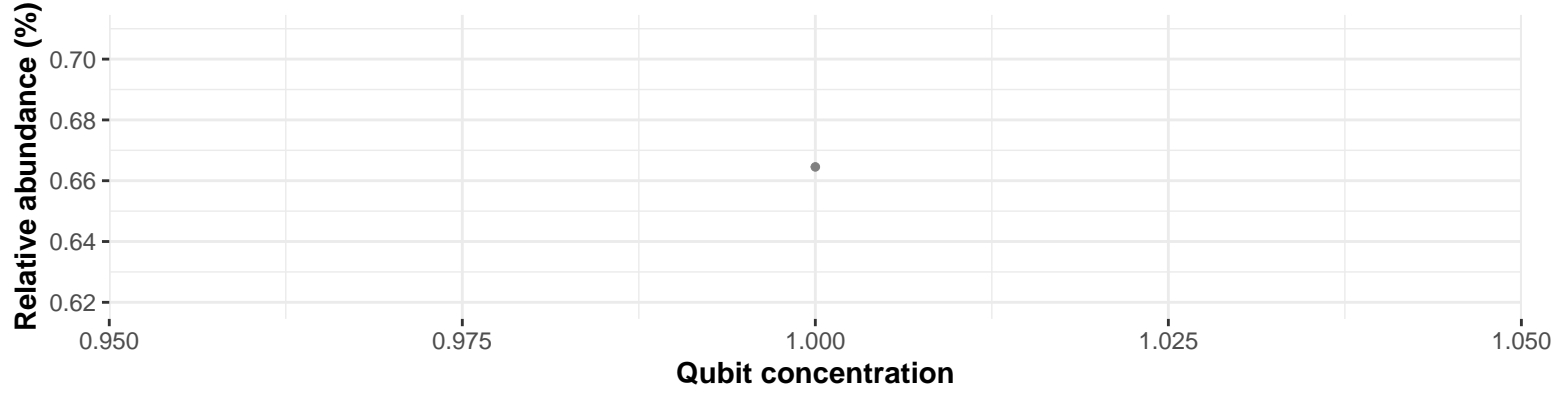


Correlation within: Feed

$\log_e(S) = 7.026$, $p = 0.522$, $\hat{\rho}_{\text{Spearman}} = -0.161$, $CI_{95\%} [-0.594, 0.344]$, $n_{\text{pairs}} = 18$



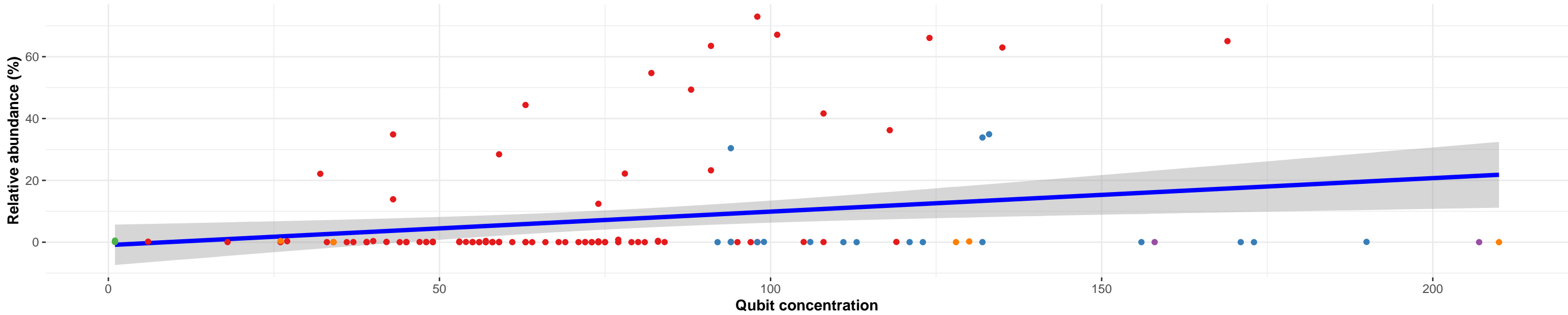
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Pediococcus; NA

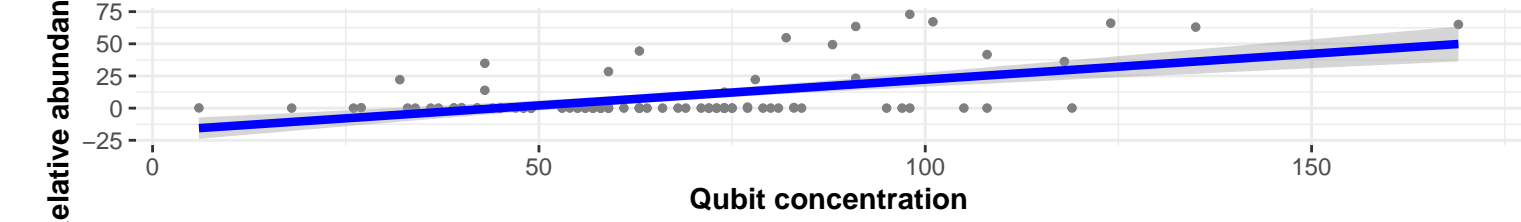
Correlation with all samples

$\log_e(S) = 12.546$, $p = 0.597$, $\hat{\rho}_{\text{Spearman}} = 0.049$, $CI_{95\%} [-0.136, 0.230]$, $n_{\text{pairs}} = 121$



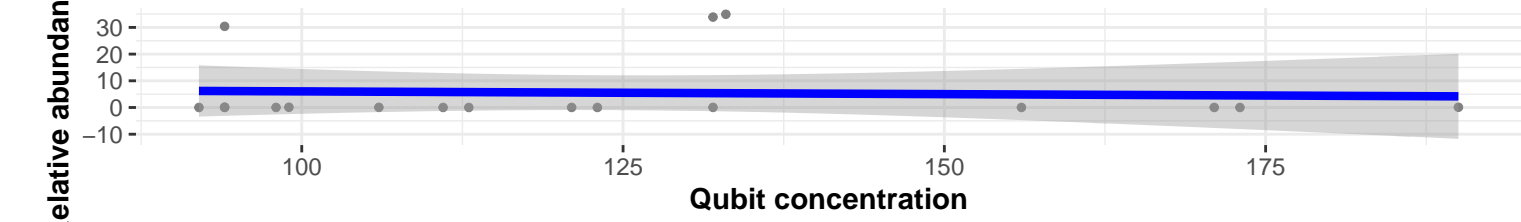
Correlation within: Digesta

$\log_e(S) = 11.564$, $p = 0.039$, $\hat{\rho}_{\text{Spearman}} = 0.214$, $CI_{95\%} [0.005, 0.406]$, $n_{\text{pairs}} = 93$

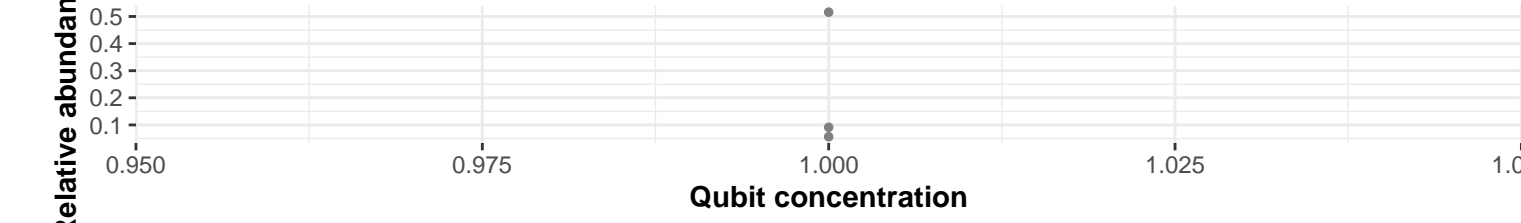


Correlation within: Feed

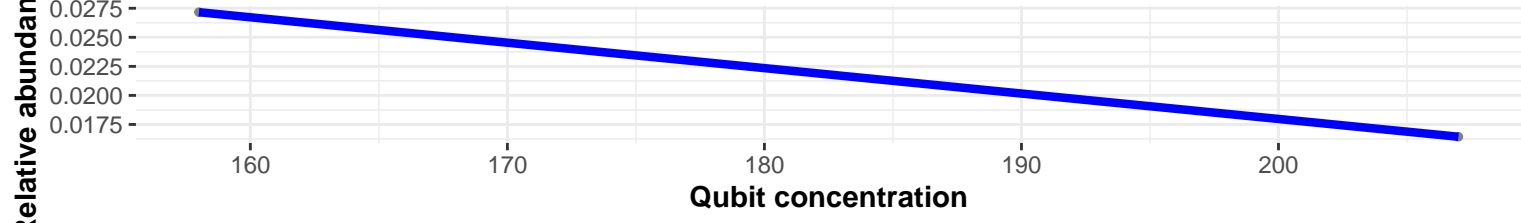
$\log_e(S) = 6.896$, $p = 0.938$, $\hat{\rho}_{\text{Spearman}} = -0.020$, $CI_{95\%} [-0.494, 0.463]$, $n_{\text{pairs}} = 18$



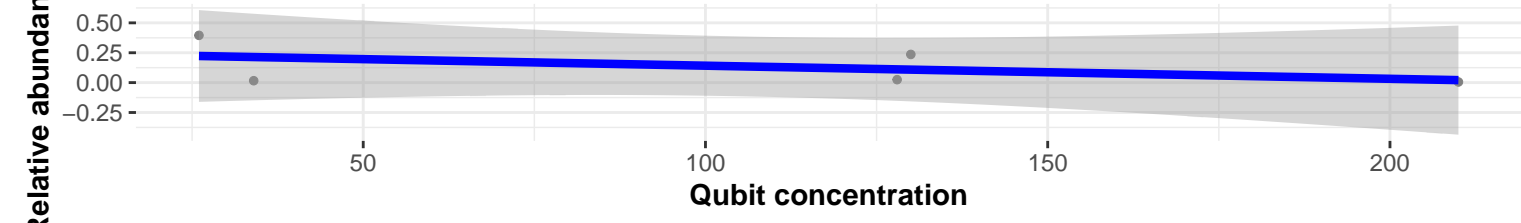
Correlation within: control



Correlation within: Positive_control



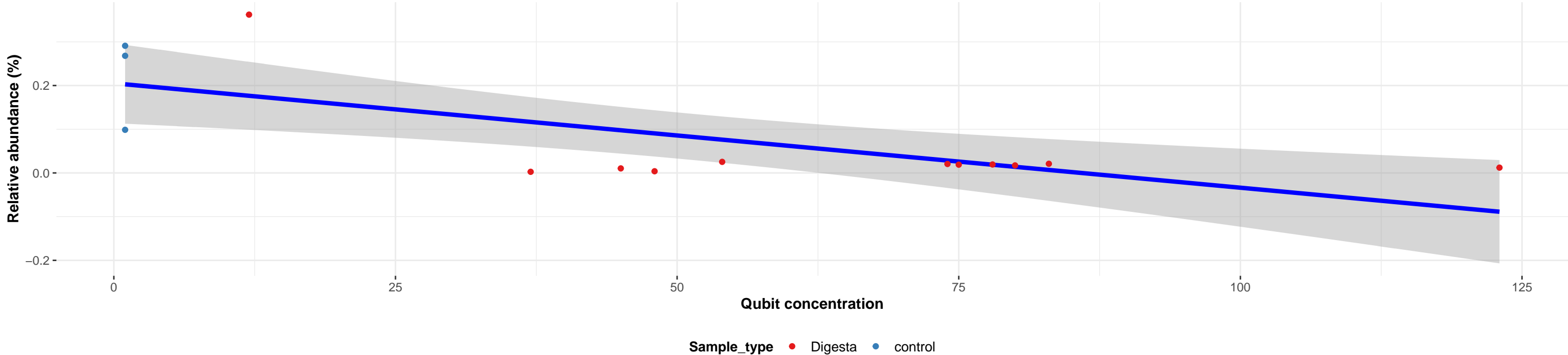
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anaerobacillus; NA

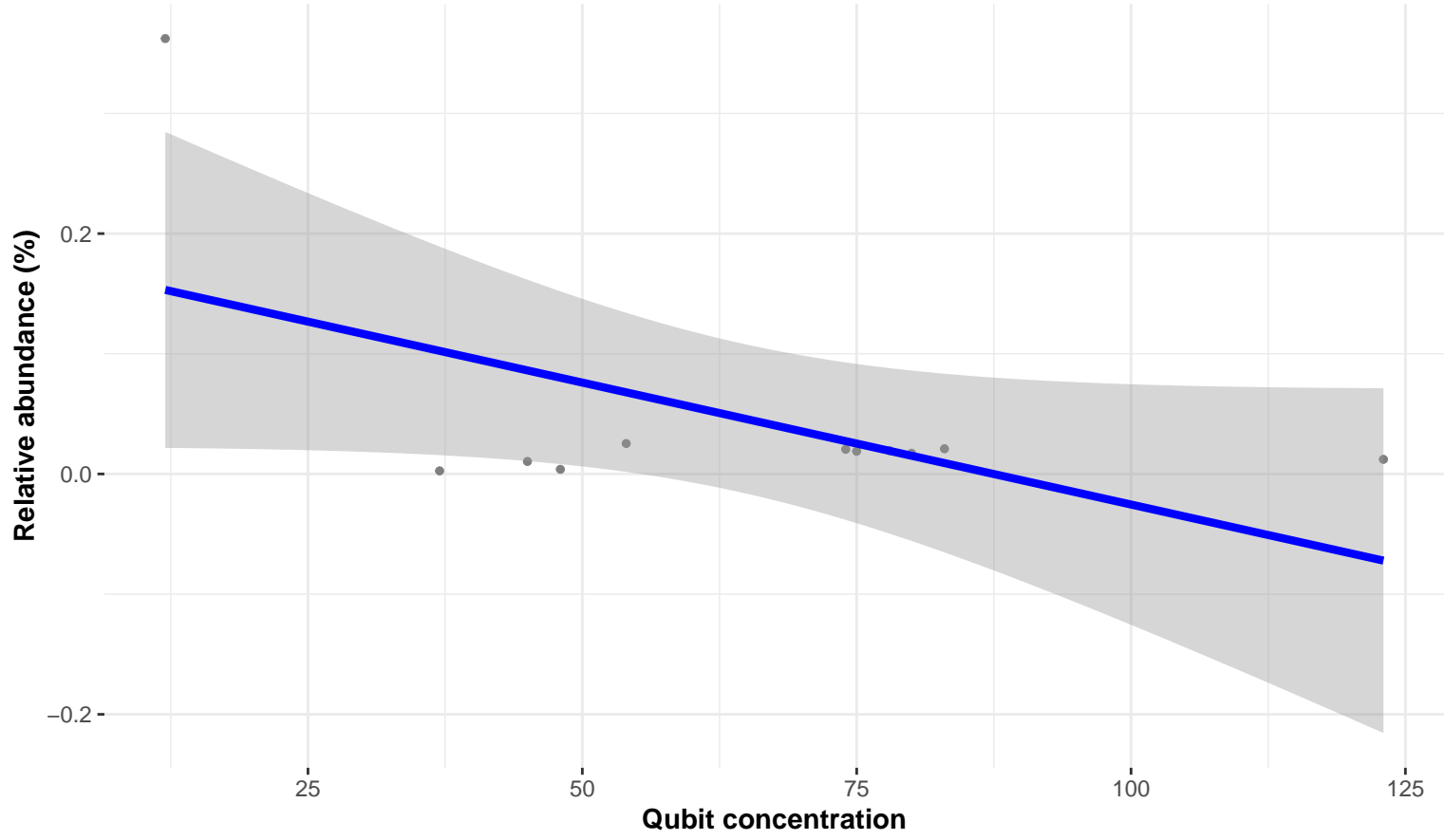
Correlation with all samples

$\log_e(S) = 6.488$, $p = 0.112$, $\hat{\rho}_{\text{Spearman}} = -0.444$, $\text{CI}_{95\%} [-0.795, 0.131]$, $n_{\text{pairs}} = 14$

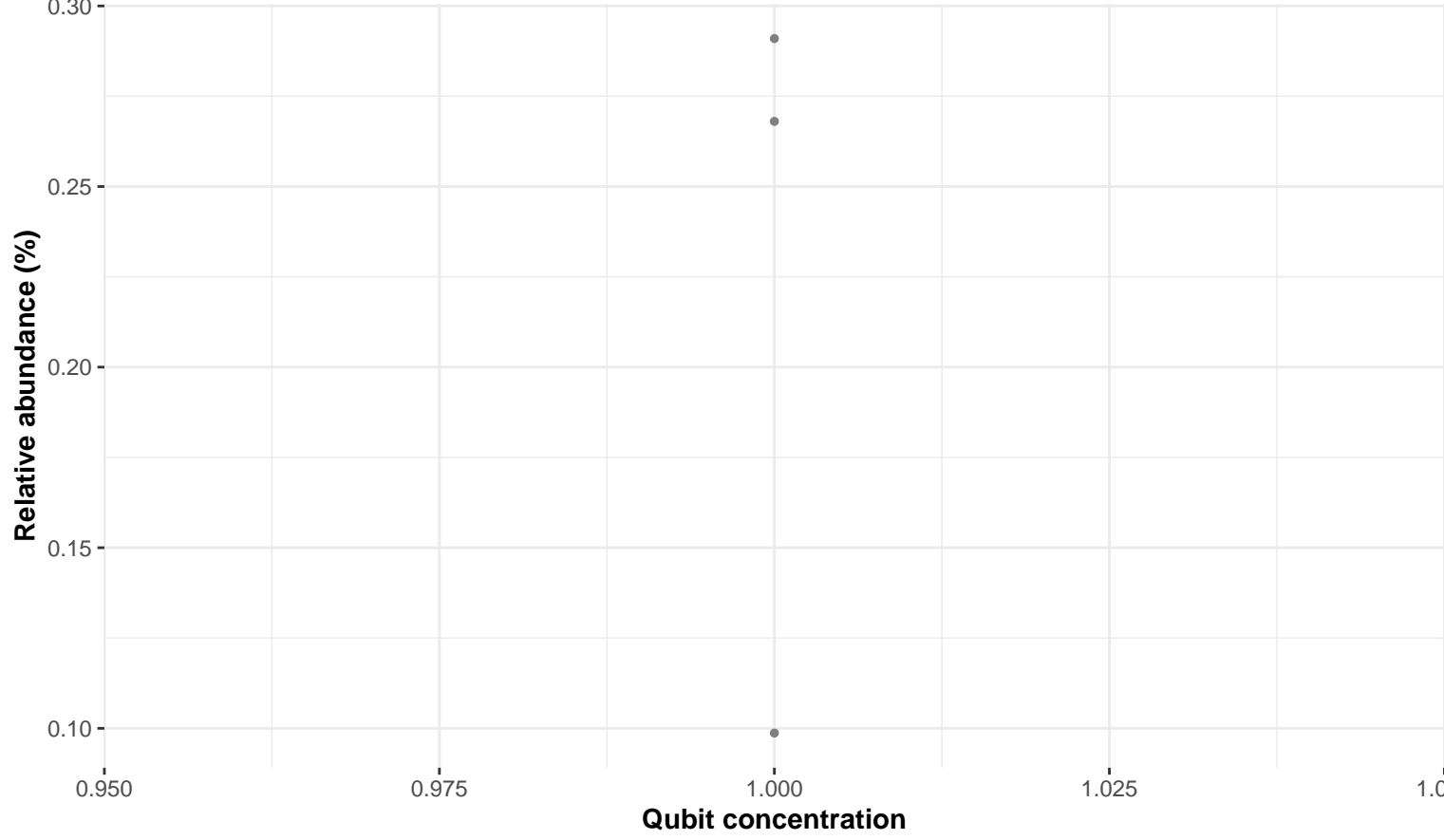


Correlation within: Digesta

$\log_e(S) = 5.308$, $p = 0.811$, $\hat{\rho}_{\text{Spearman}} = 0.082$, $\text{CI}_{95\%} [-0.559, 0.661]$, $n_{\text{pairs}} = 11$



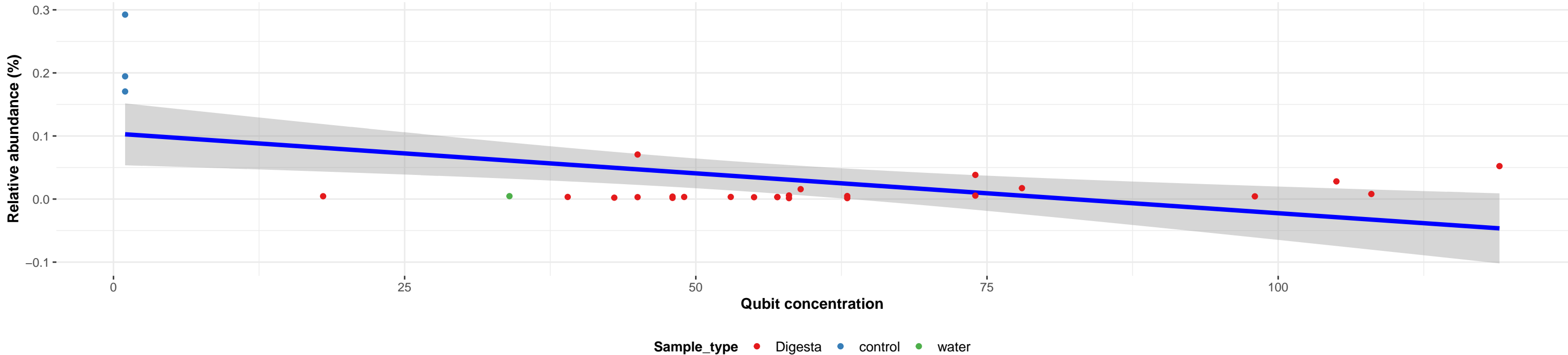
Correlation within: control



Bacteria; Bacteroidota; Bacteroidia; Sphingobacteriales; Sphingobacteriaceae; Pedobacter; NA

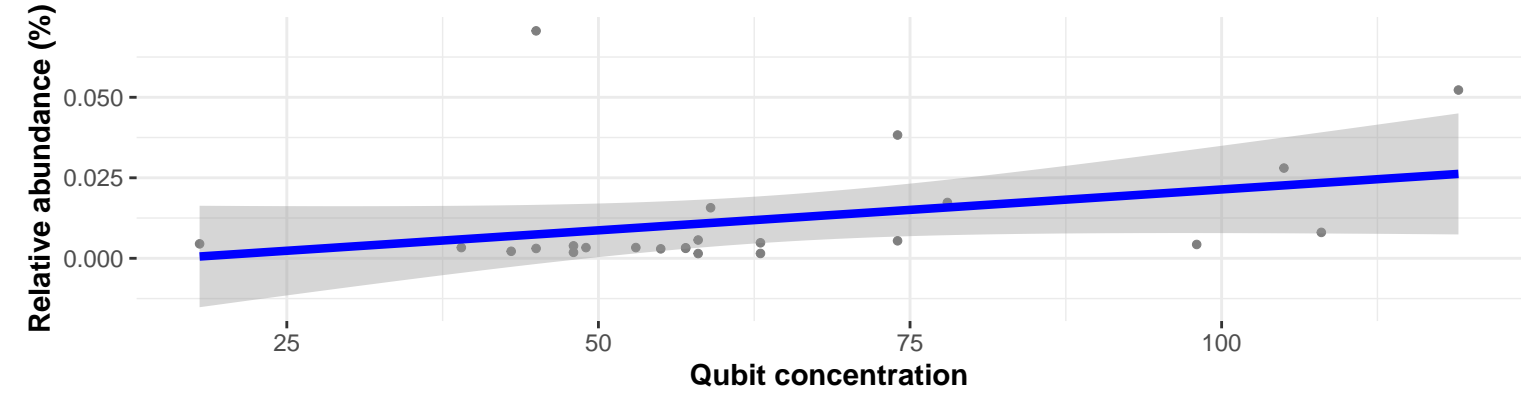
Correlation with all samples

$\log_e(S) = 8.184$, $p = 0.921$, $\hat{\rho}_{\text{Spearman}} = 0.020$, $CI_{95\%} [-0.366, 0.400]$, $n_{\text{pairs}} = 28$

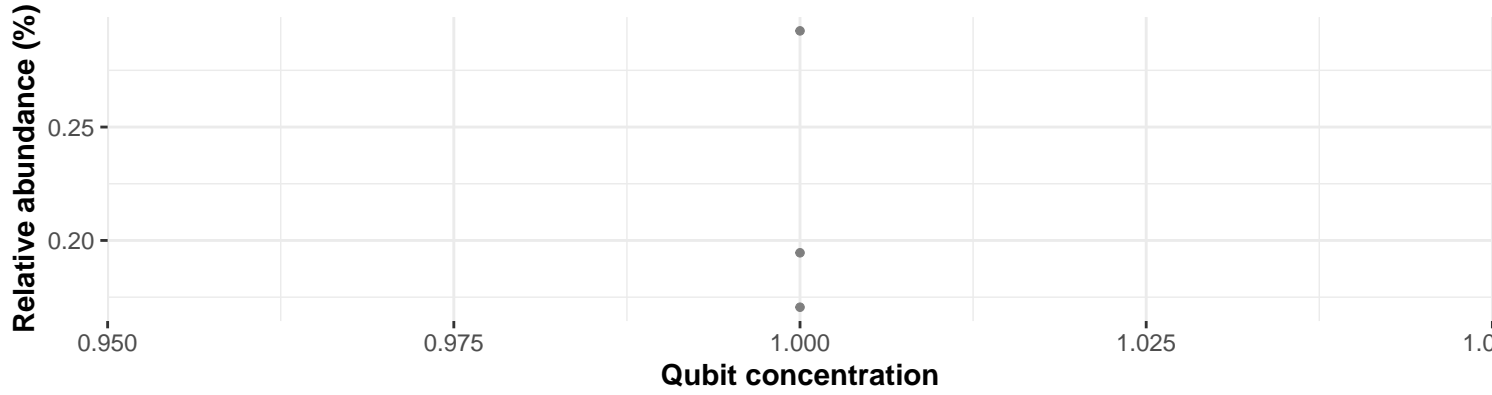


Correlation within: Digesta

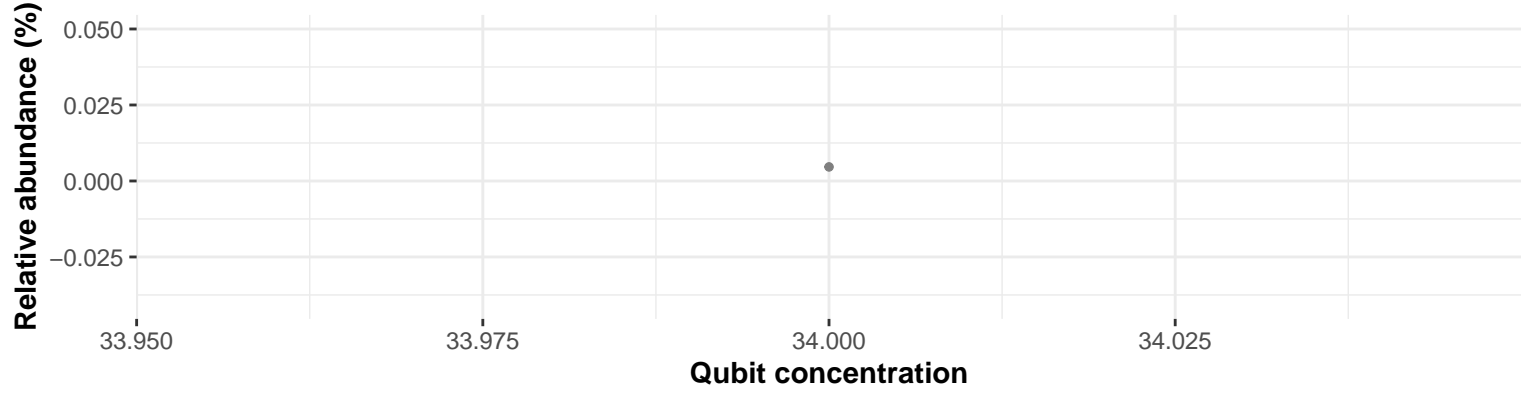
$\log_e(S) = 7.114$, $p = 0.022$, $\hat{\rho}_{\text{Spearman}} = 0.465$, $CI_{95\%} [0.064, 0.737]$, $n_{\text{pairs}} = 24$



Correlation within: control



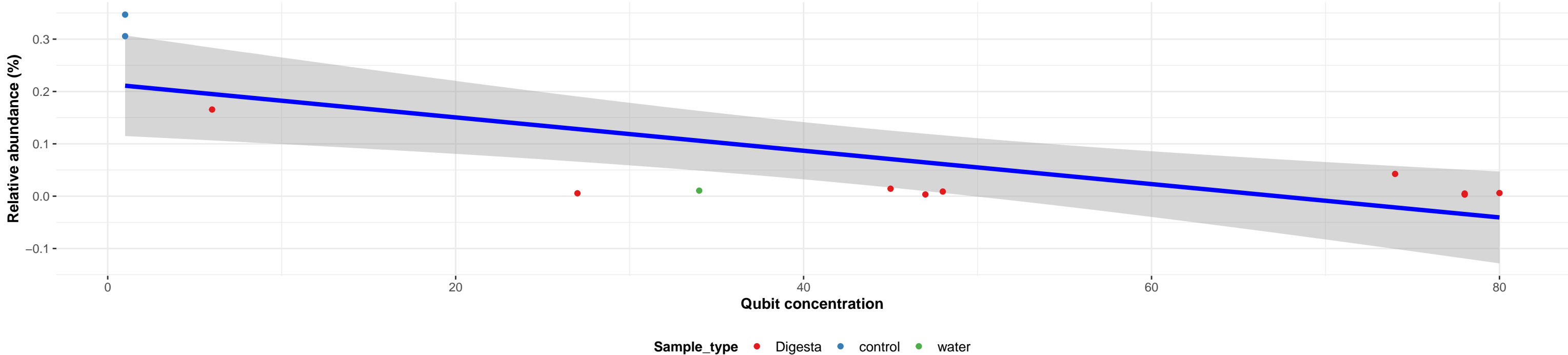
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Dietziaceae; Dietzia; NA

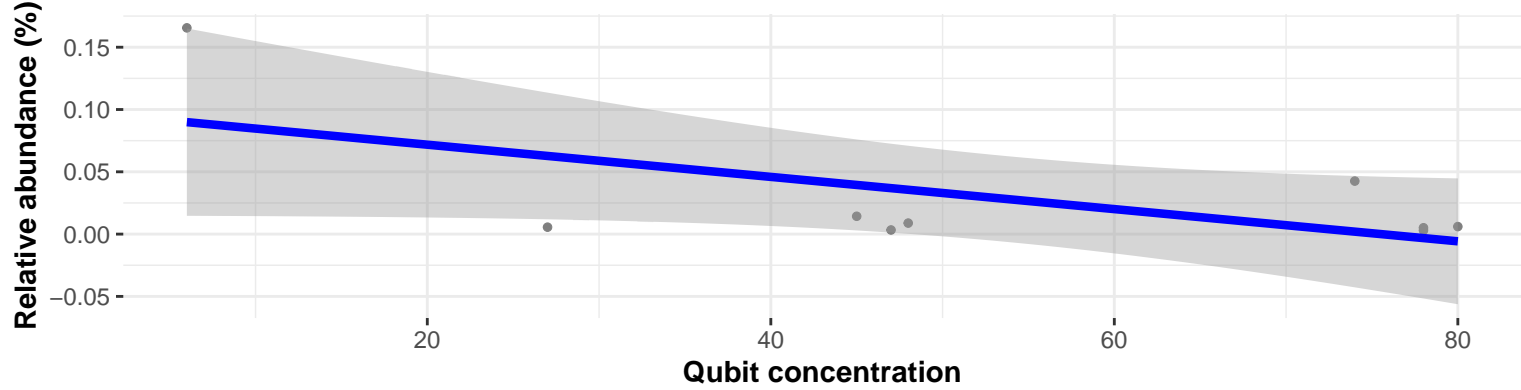
Correlation with all samples

$\log_e(S) = 6.181$, $p = 0.013$, $\hat{\rho}_{\text{Spearman}} = -0.691$, $\text{CI}_{95\%} [-0.909, -0.176]$, $n_{\text{pairs}} = 12$

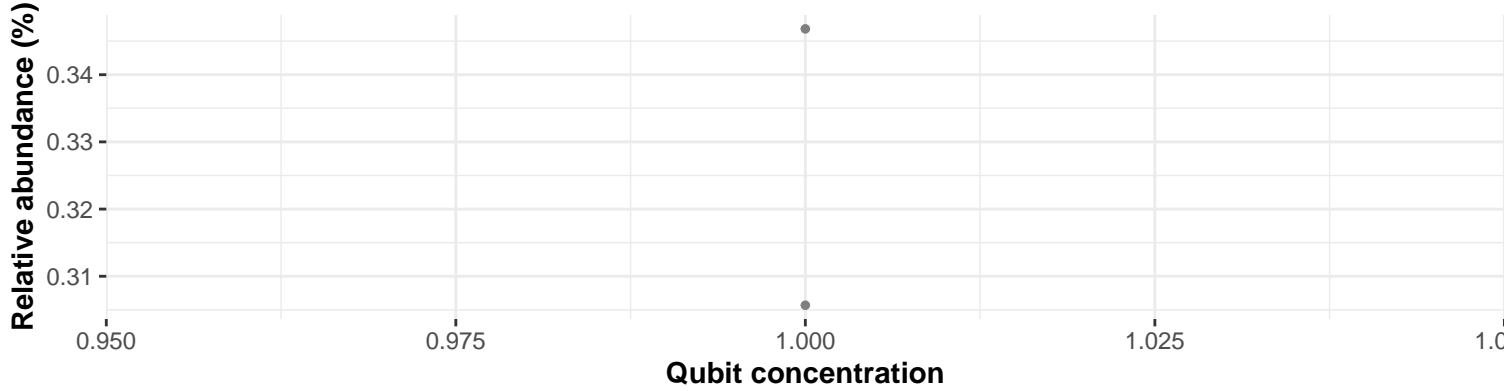


Correlation within: Digesta

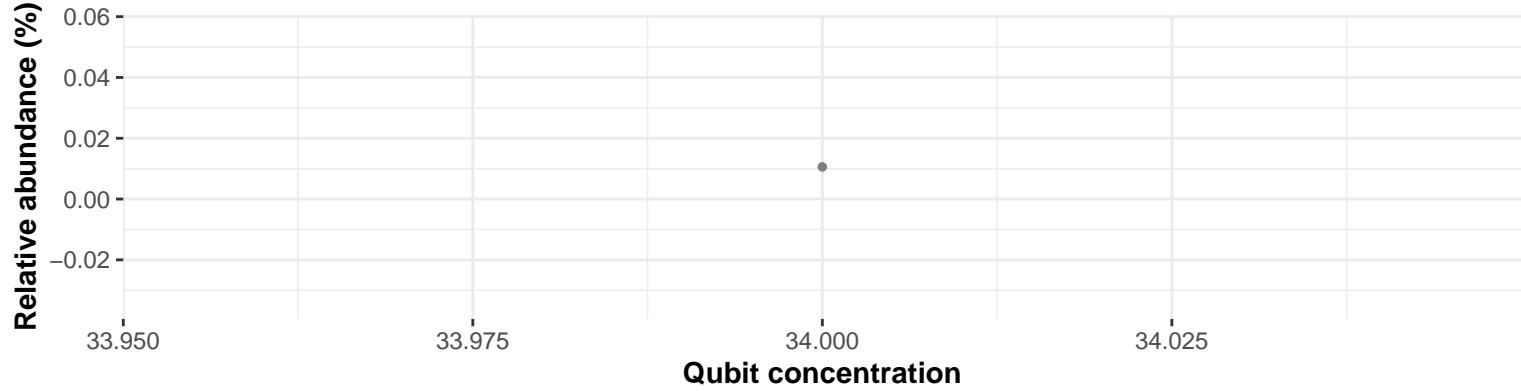
$\log_e(S) = 5.149$, $p = 0.242$, $\hat{\rho}_{\text{Spearman}} = -0.435$, $\text{CI}_{95\%} [-0.859, 0.343]$, $n_{\text{pairs}} = 9$



Correlation within: control



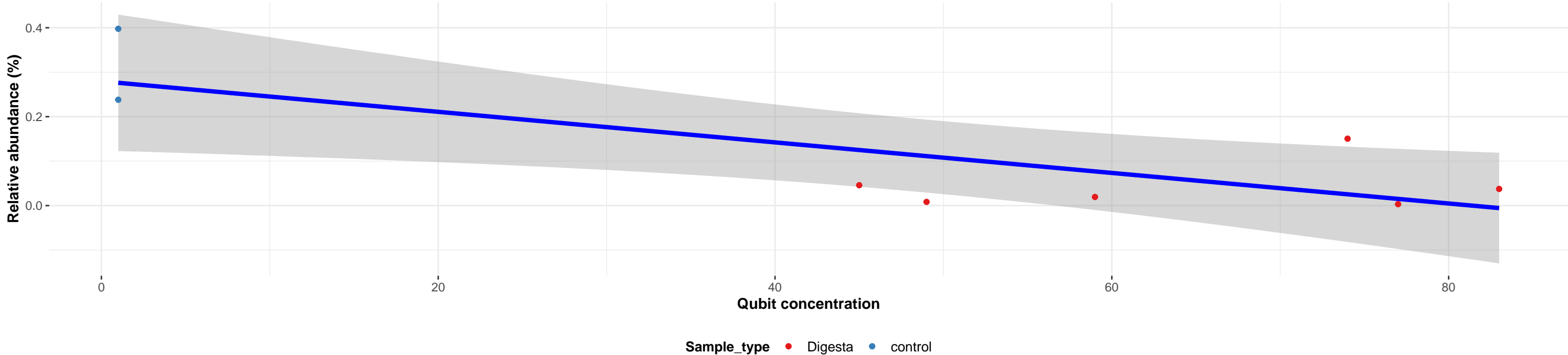
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Tepidimonas; NA

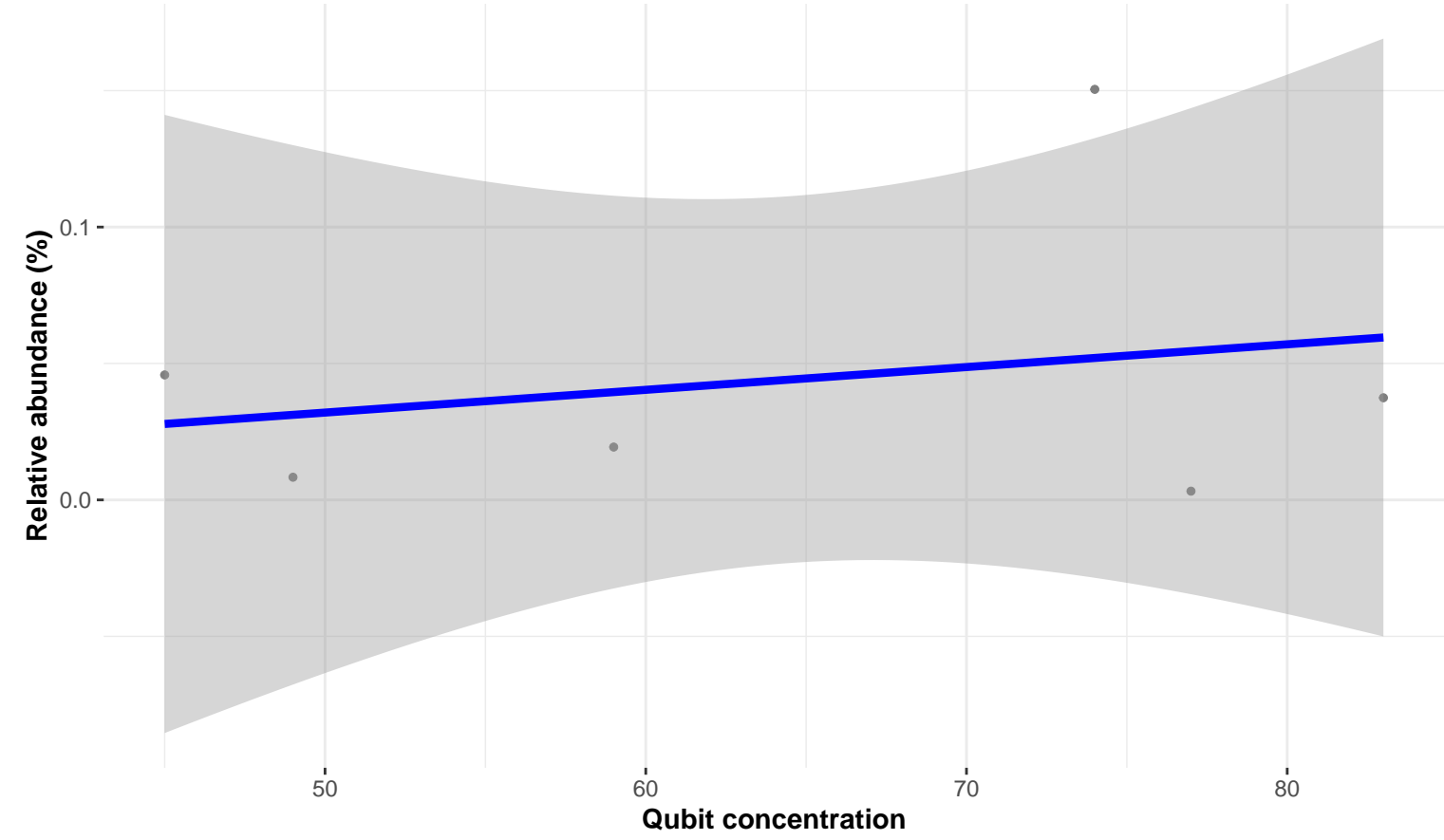
Correlation with all samples

$\log_e(S) = 4.922$, $p = 0.091$, $\hat{\rho}_{\text{Spearman}} = -0.635$, $CI_{95\%} [-0.929, 0.152]$, $n_{\text{pairs}} = 8$

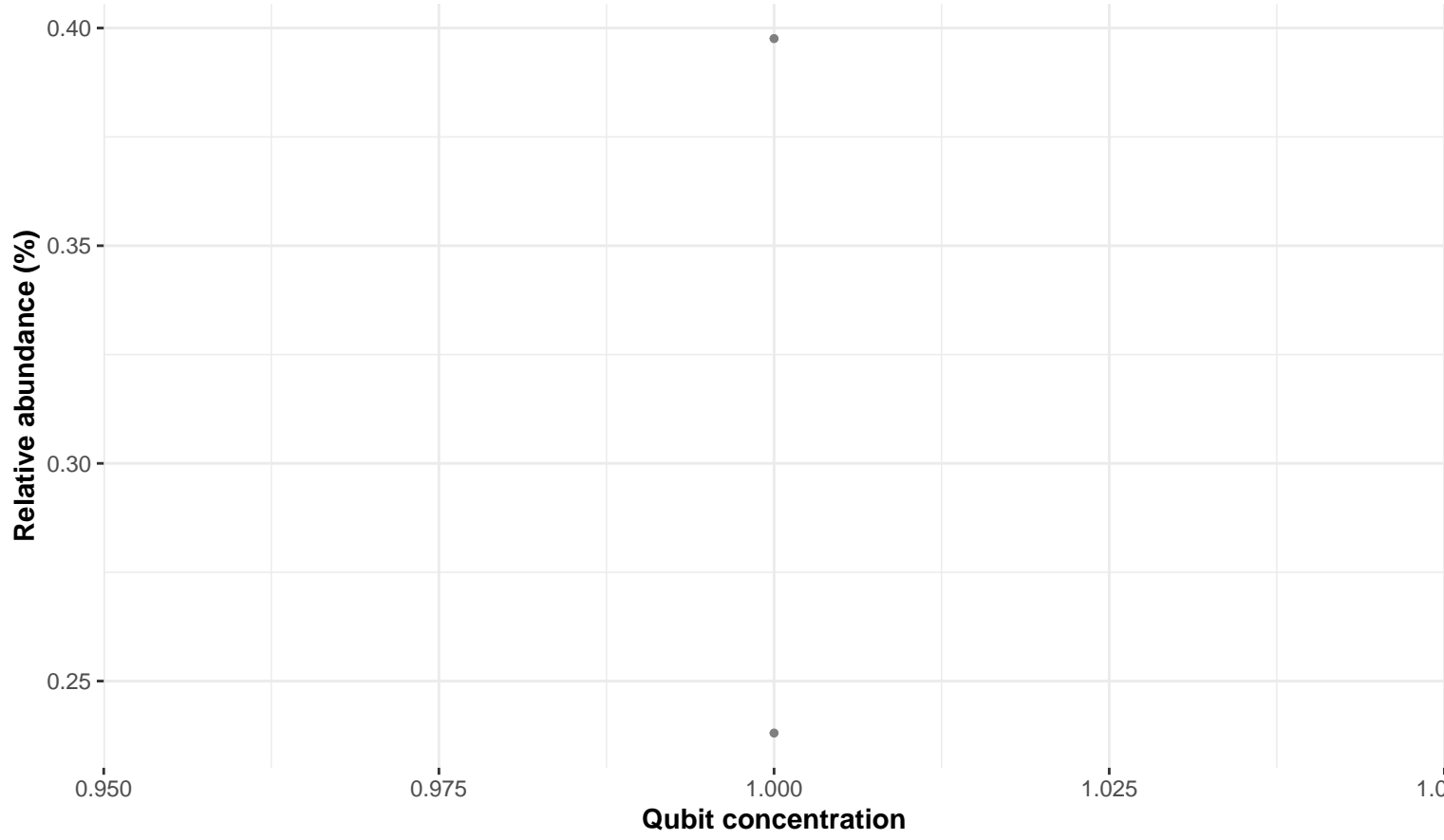


Correlation within: Digesta

$\log_e(S) = 3.689$, $p = 0.787$, $\hat{\rho}_{\text{Spearman}} = -0.143$, $CI_{95\%} [-0.864, 0.770]$, $n_{\text{pairs}} = 6$



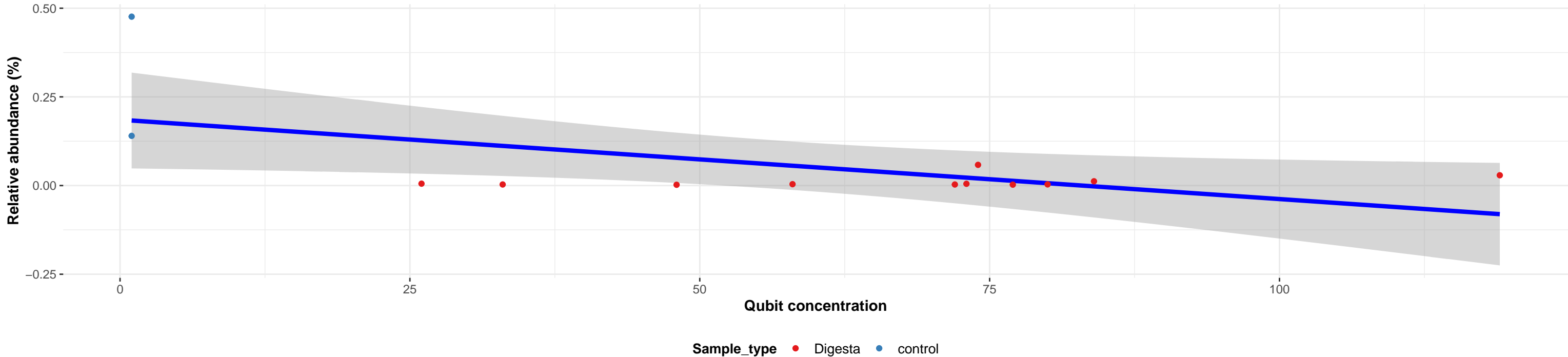
Correlation within: control



Bacteria; Verrucomicrobiota; Verrucomicrobiae; Verrucomicrobiales; Verrucomicrobiaceae; Prosthecobacter; NA

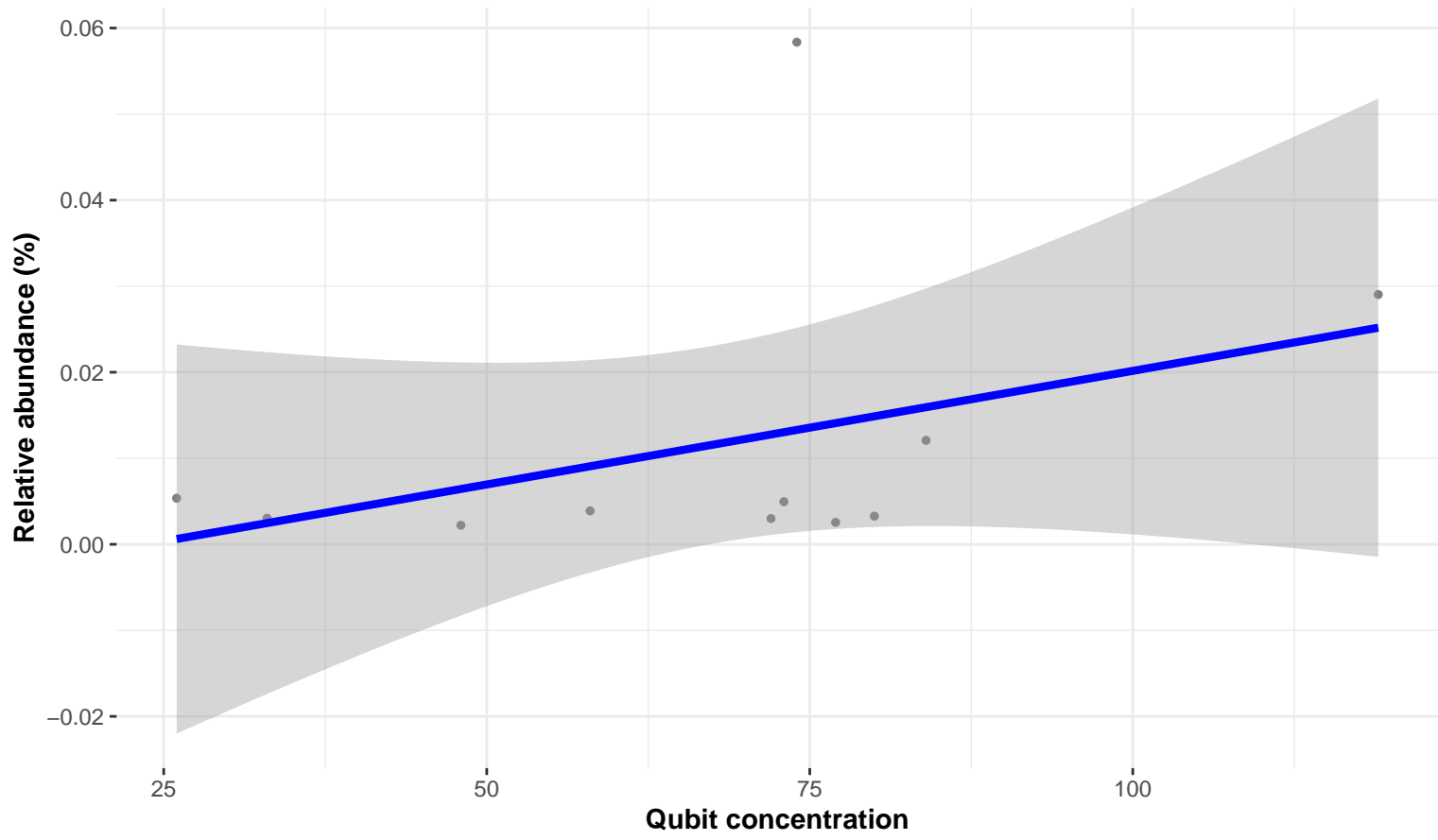
Correlation with all samples

$\log_e(S) = 6.048$, $p = 0.596$, $\hat{\rho}_{\text{Spearman}} = -0.162$, $\text{CI}_{95\%} [-0.665, 0.442]$, $n_{\text{pairs}} = 13$

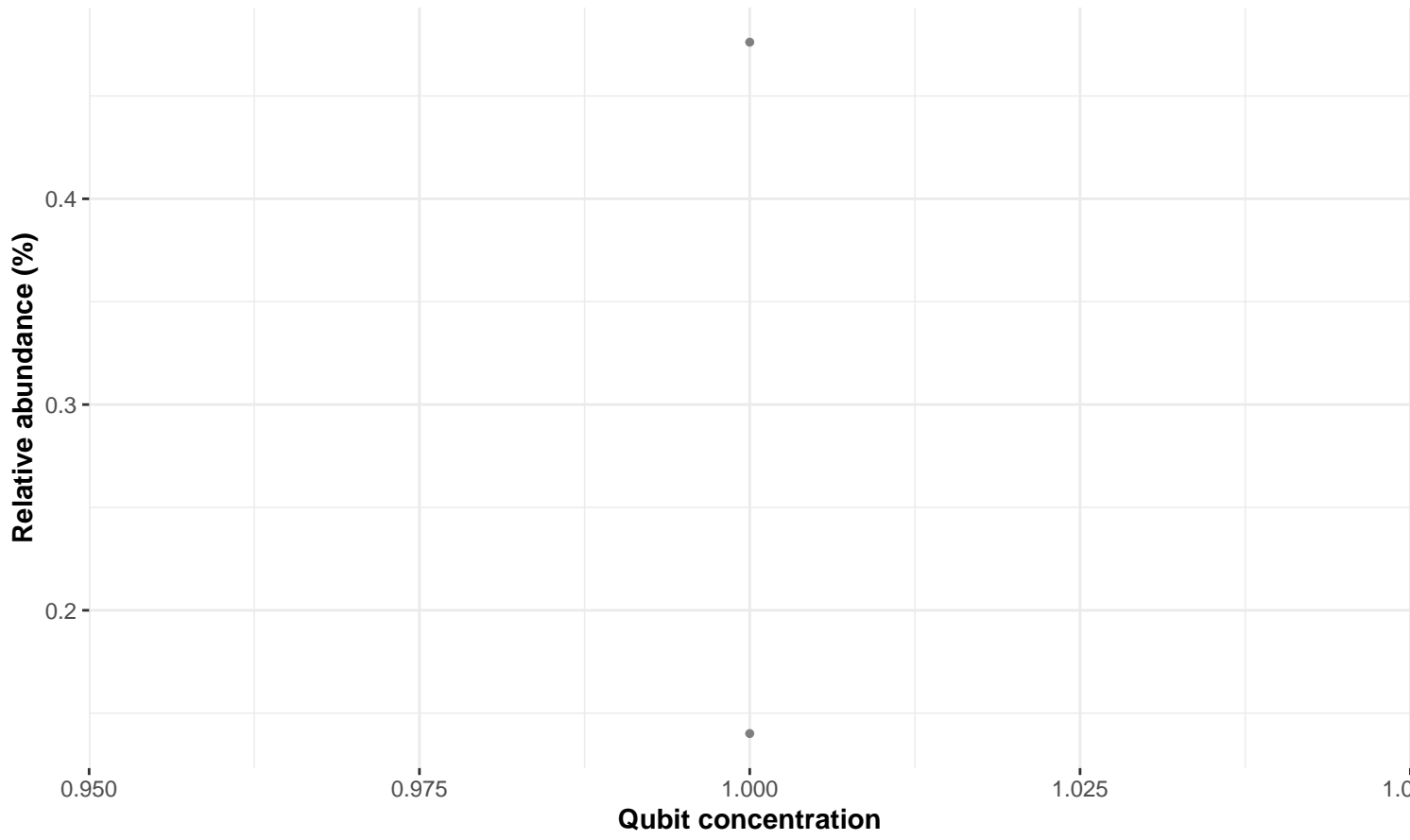


Correlation within: Digesta

$\log_e(S) = 4.913$, $p = 0.247$, $\hat{\rho}_{\text{Spearman}} = 0.382$, $\text{CI}_{95\%} [-0.302, 0.806]$, $n_{\text{pairs}} = 11$



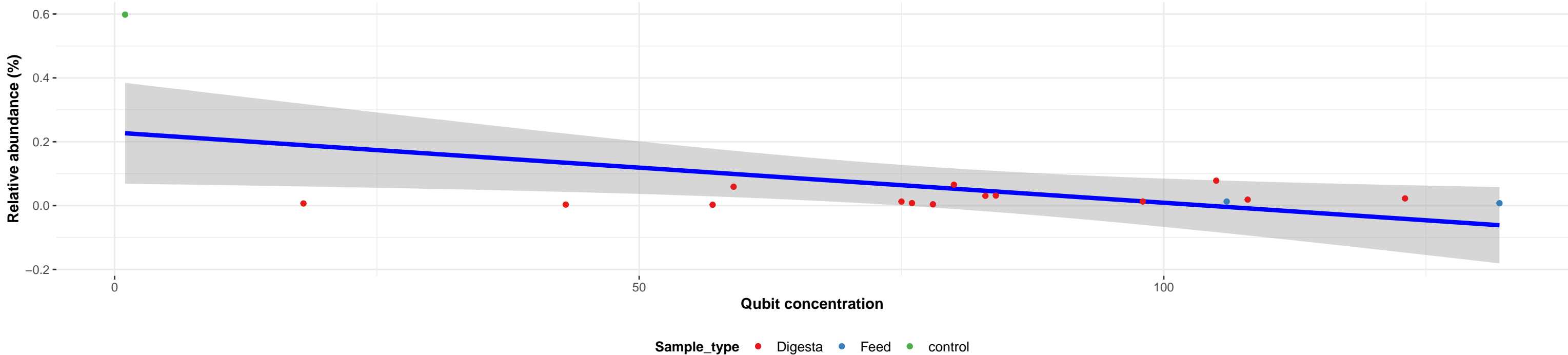
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Planococcaceae; Lysinibacillus; sphaericus

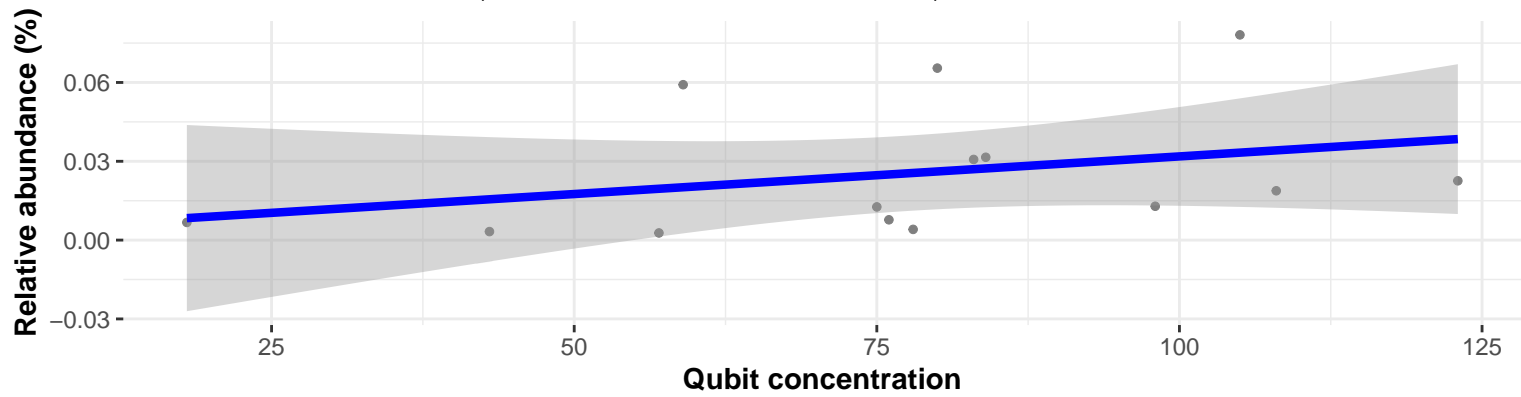
Correlation with all samples

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

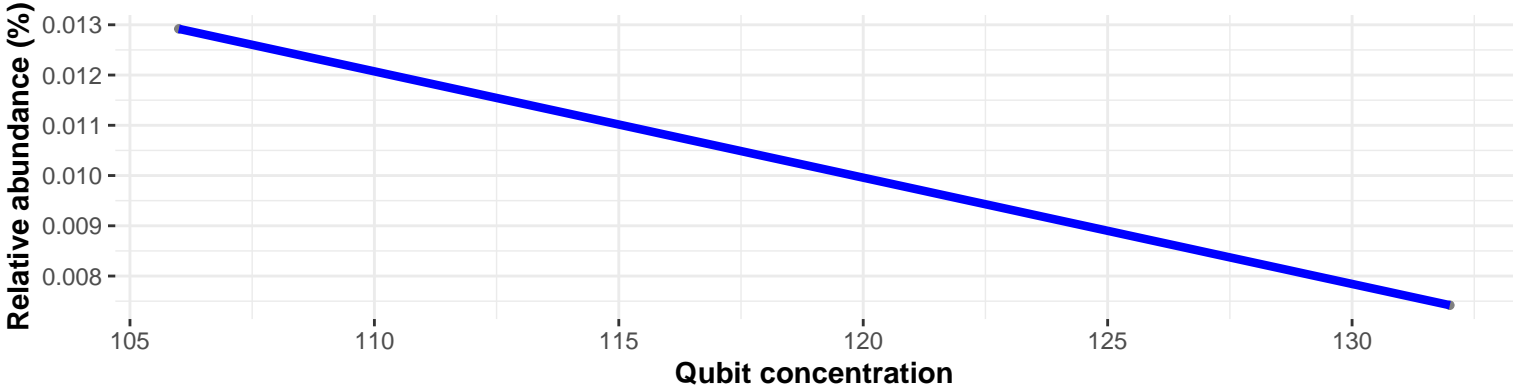


Correlation within: Digesta

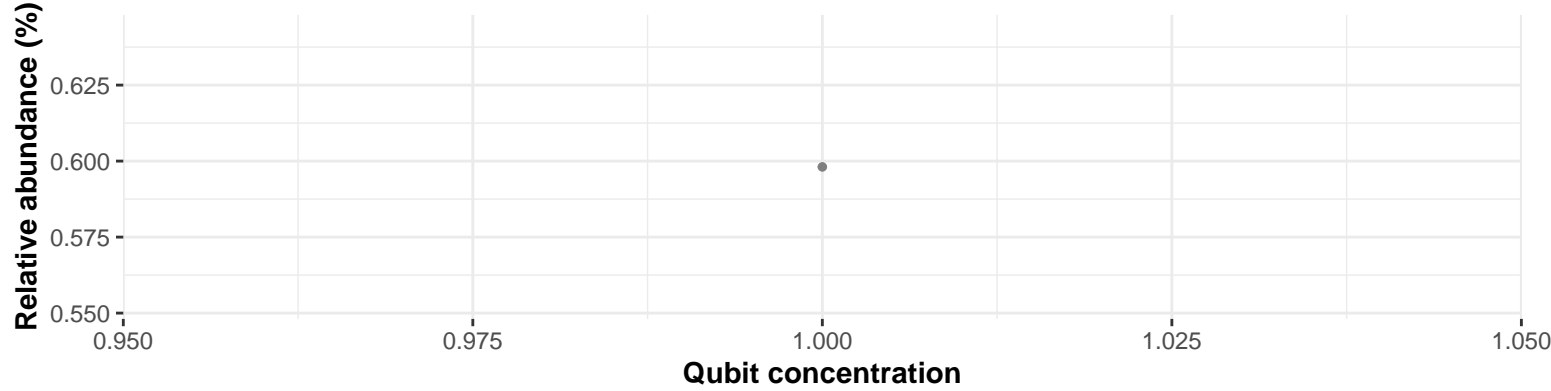
$\log_e(S) = 5.257$, $p = 0.030$, $\hat{\rho}_{\text{Spearman}} = 0.578$, $CI_{95\%} [0.051, 0.853]$, $n_{\text{pairs}} = 14$



Correlation within: Feed



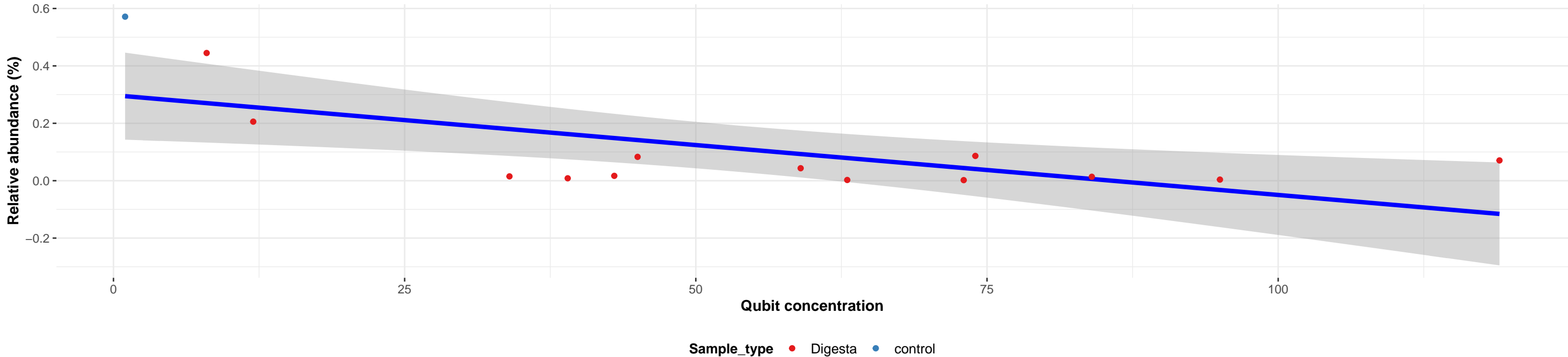
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anaerobacillus; NA

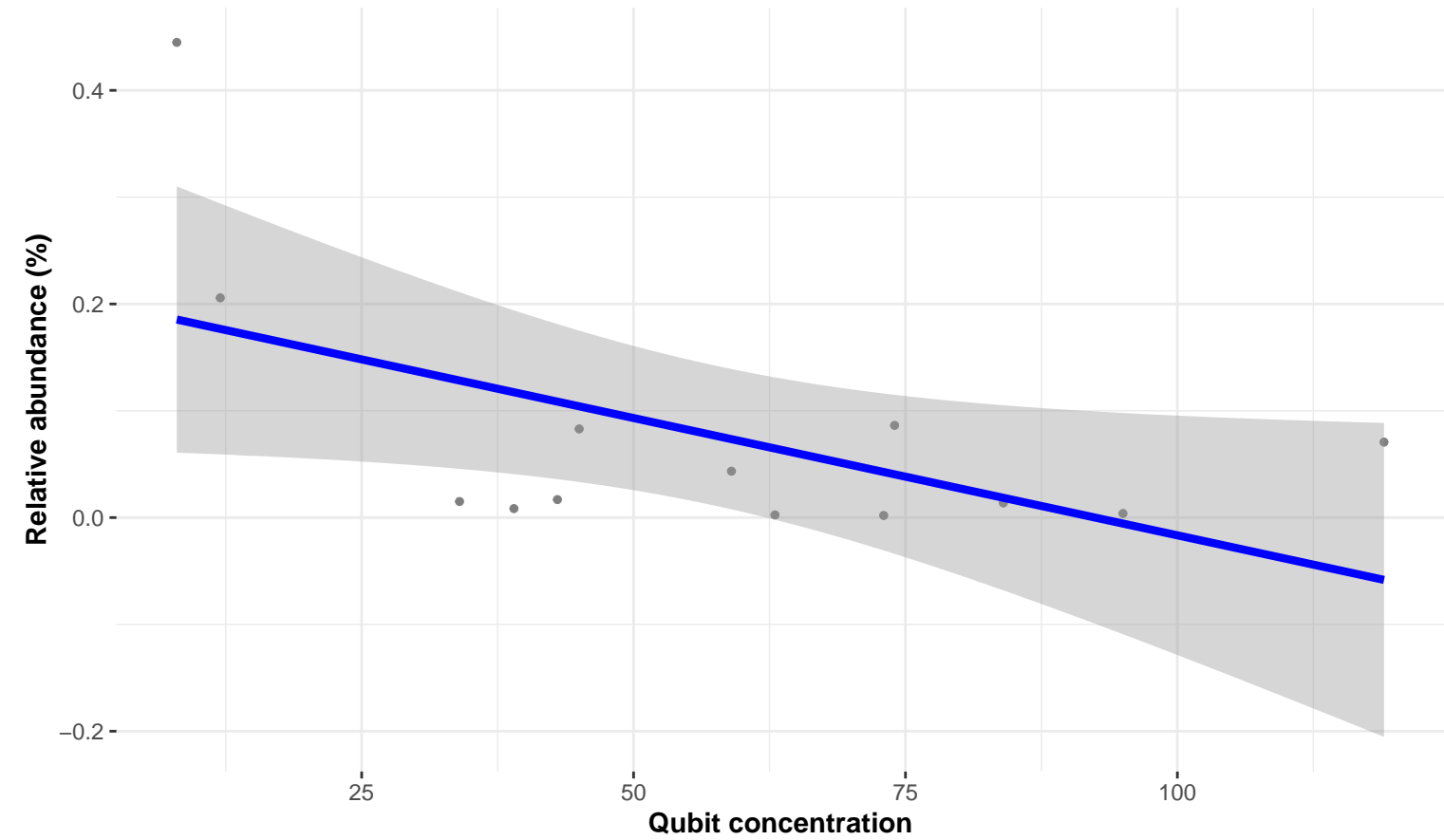
Correlation with all samples

$\log_e(S) = 6.537$, $p = 0.059$, $\hat{\rho}_{\text{Spearman}} = -0.516$, $\text{CI}_{95\%} [-0.827, 0.037]$, $n_{\text{pairs}} = 14$

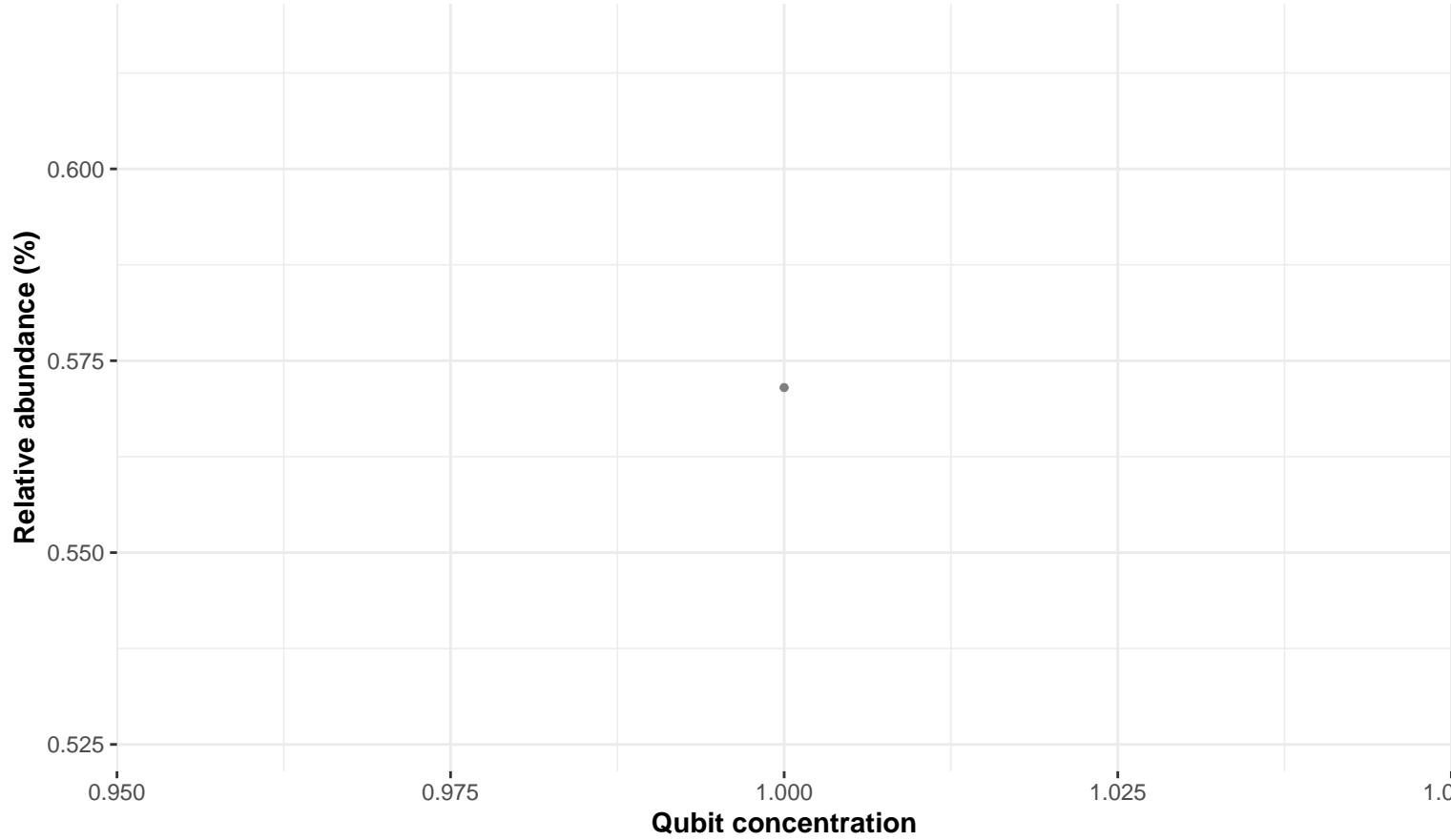


Correlation within: Digesta

$\log_e(S) = 6.230$, $p = 0.181$, $\hat{\rho}_{\text{Spearman}} = -0.396$, $\text{CI}_{95\%} [-0.784, 0.216]$, $n_{\text{pairs}} = 13$



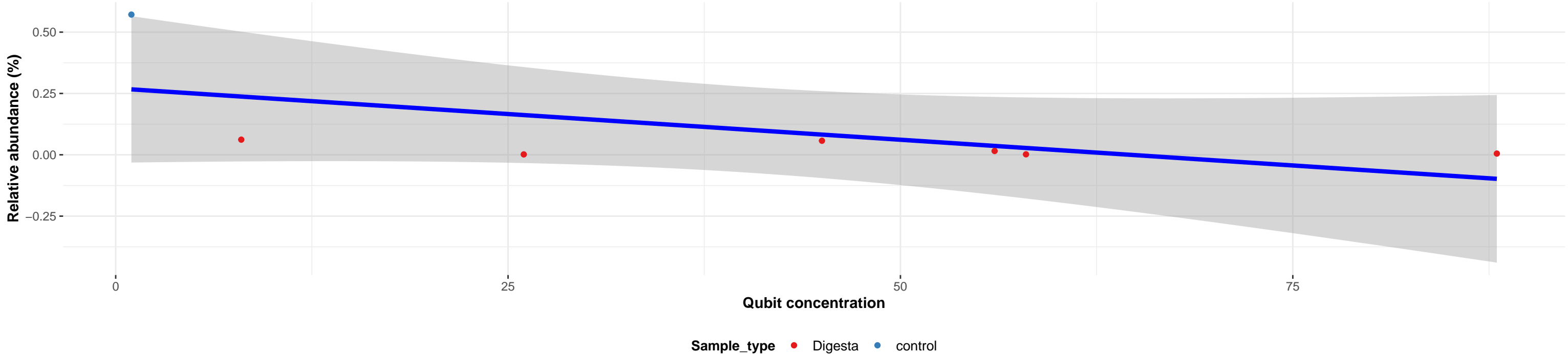
Correlation within: control



Bacteria; Firmicutes; Clostridia; Peptostreptococcales–Tissierellales; Family XI; Anaerococcus; NA

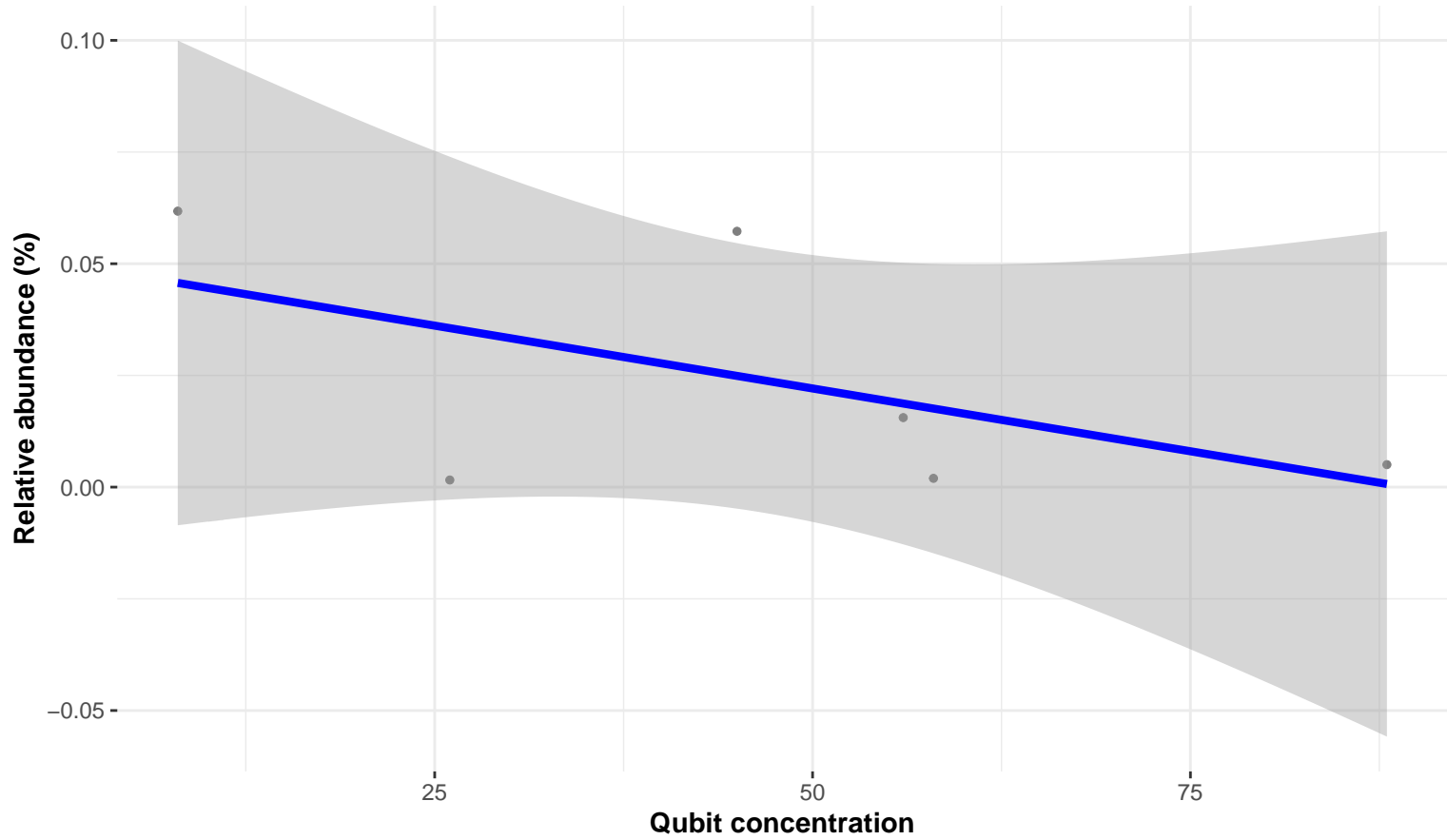
Correlation with all samples

$\log_e(S) = 4.500$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = -0.607$, $\text{CI}_{95\%} [-0.937, 0.295]$, $n_{\text{pairs}} = 7$

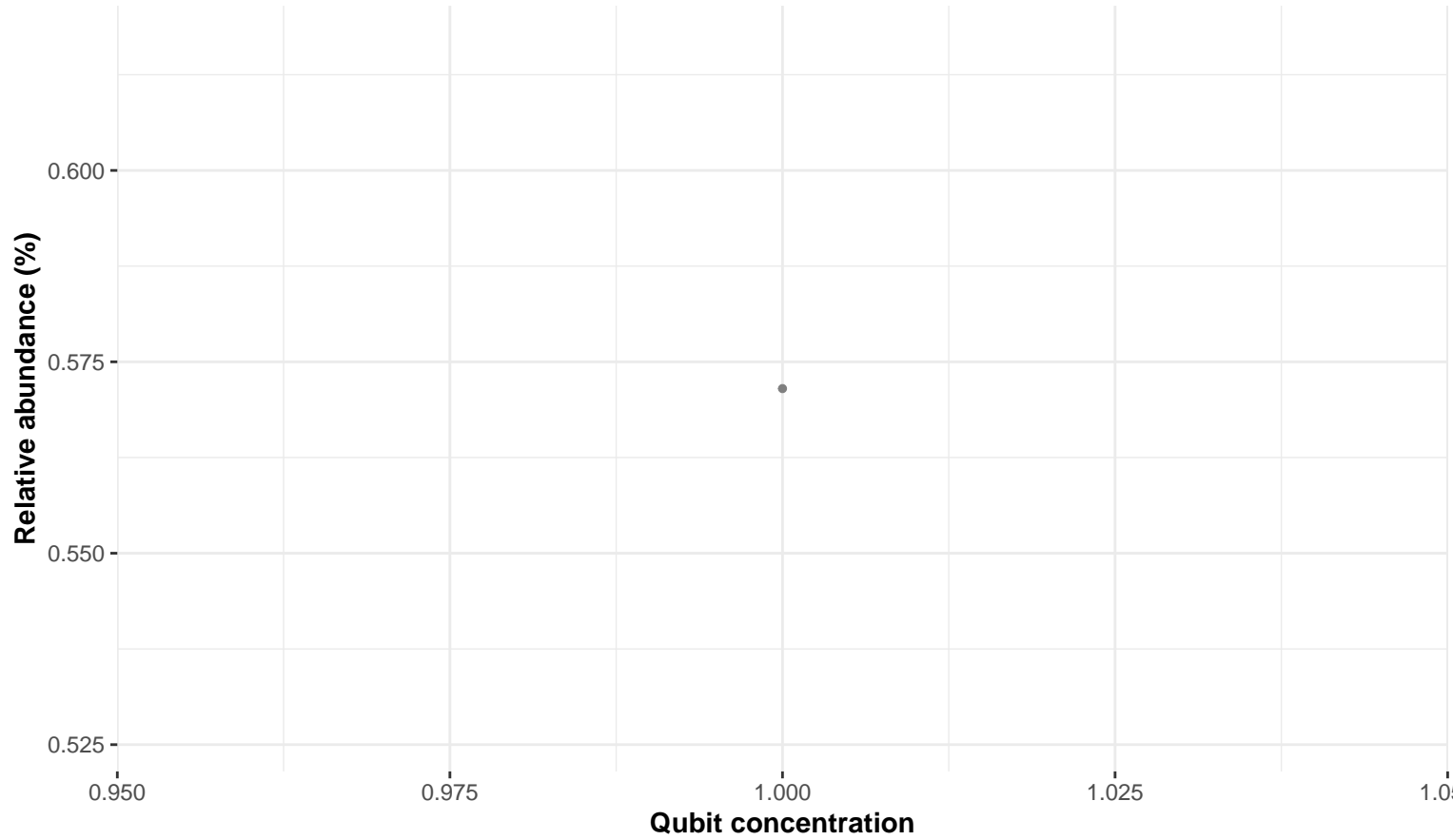


Correlation within: Digesta

$\log_e(S) = 3.871$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = -0.371$, $\text{CI}_{95\%} [-0.915, 0.650]$, $n_{\text{pairs}} = 6$



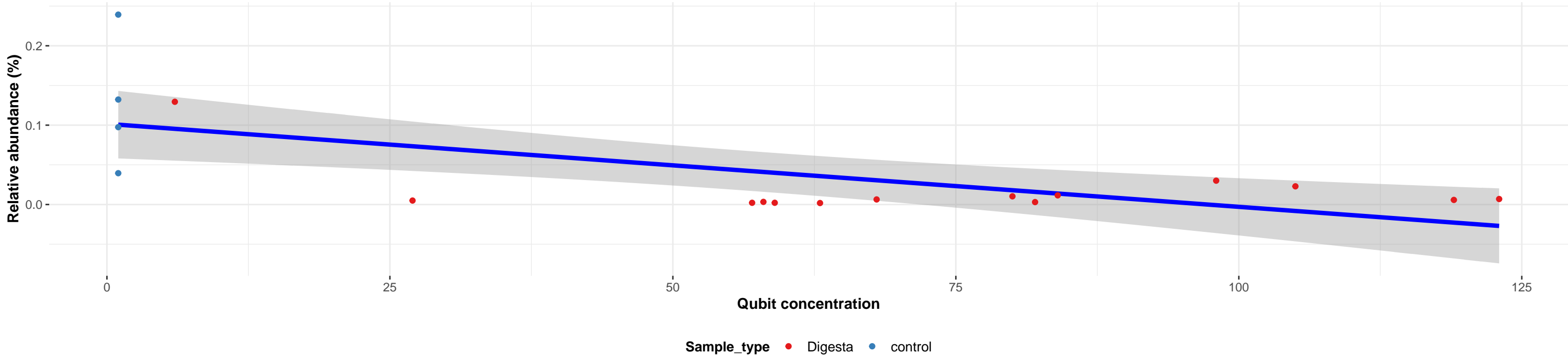
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Paucibacter; NA

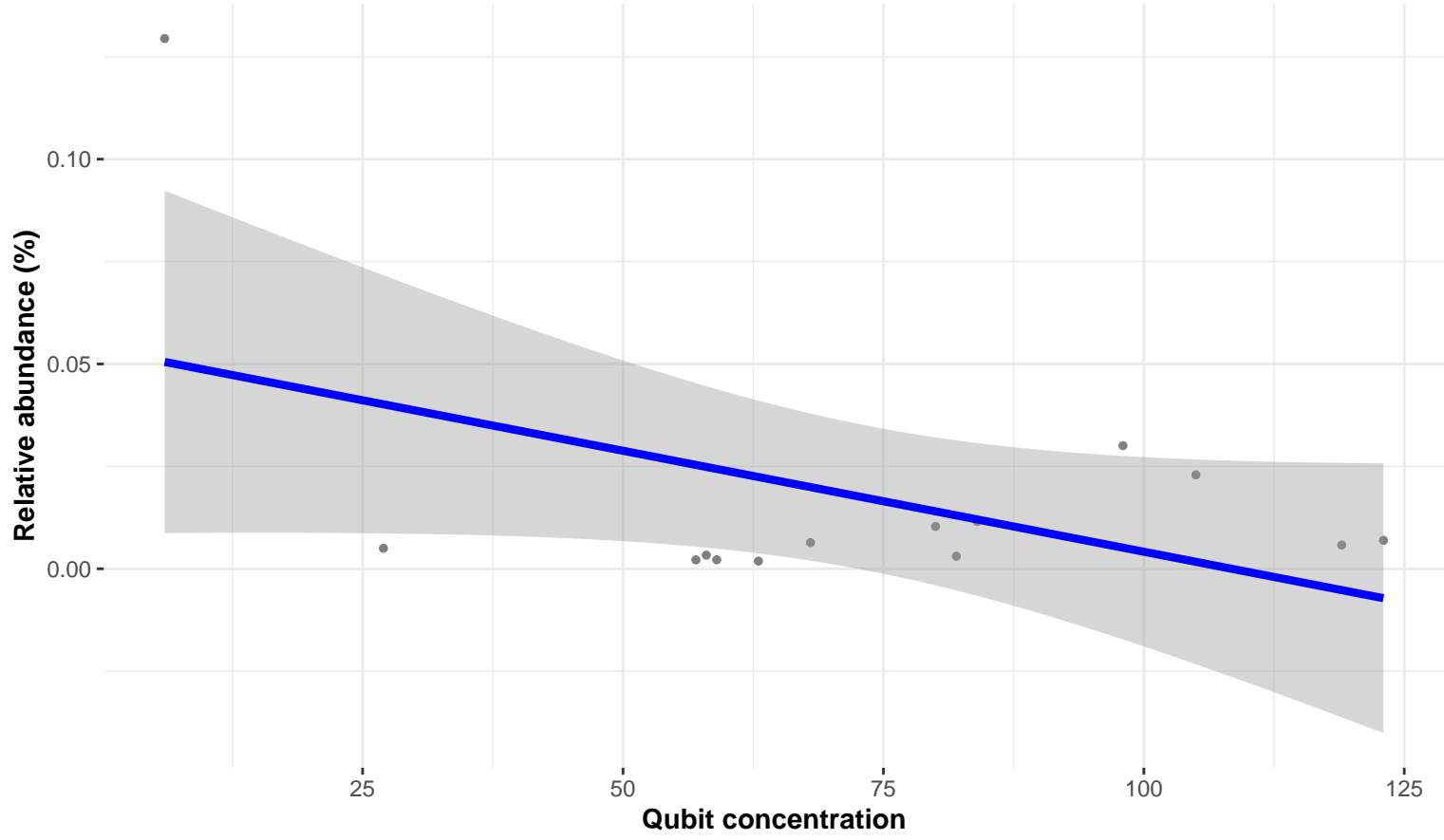
Correlation with all samples

$\log_e(S) = 7.187$, $p = 0.137$, $\hat{\rho}_{\text{Spearman}} = -0.364$, $\text{CI}_{95\%} [-0.718, 0.139]$, $n_{\text{pairs}} = 18$

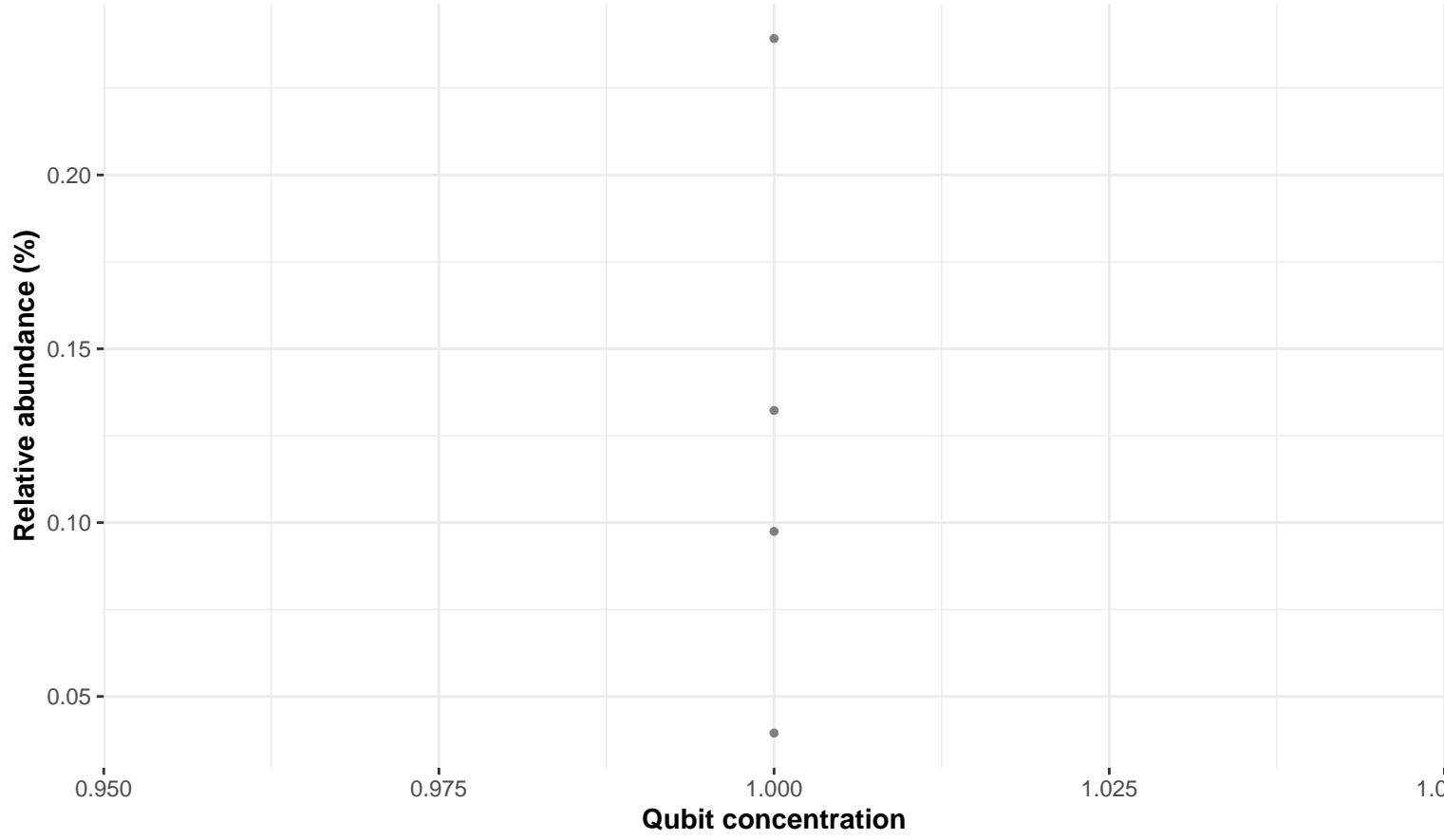


Correlation within: Digesta

$\log_e(S) = 5.743$, $p = 0.274$, $\hat{\rho}_{\text{Spearman}} = 0.314$, $\text{CI}_{95\%} [-0.276, 0.732]$, $n_{\text{pairs}} = 14$



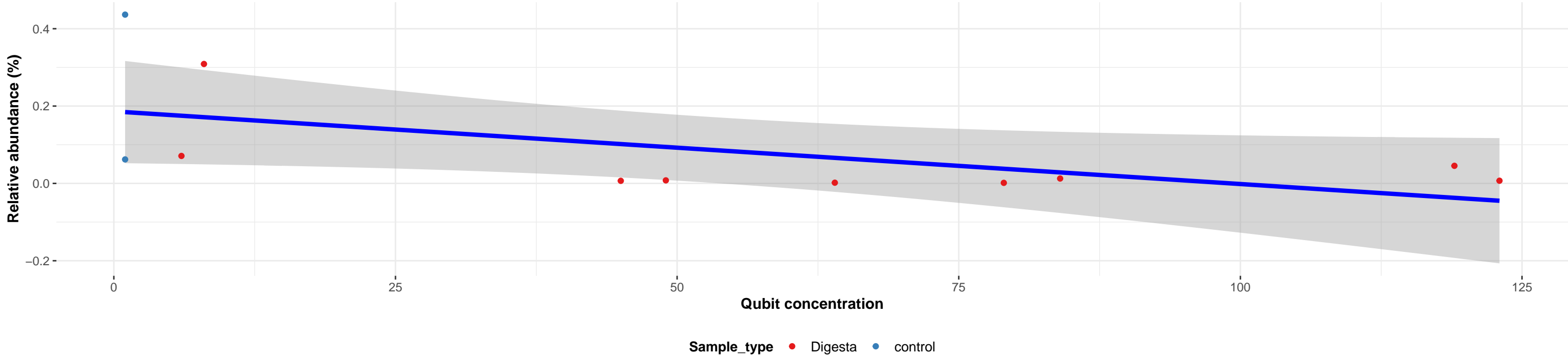
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Acidovorax; NA

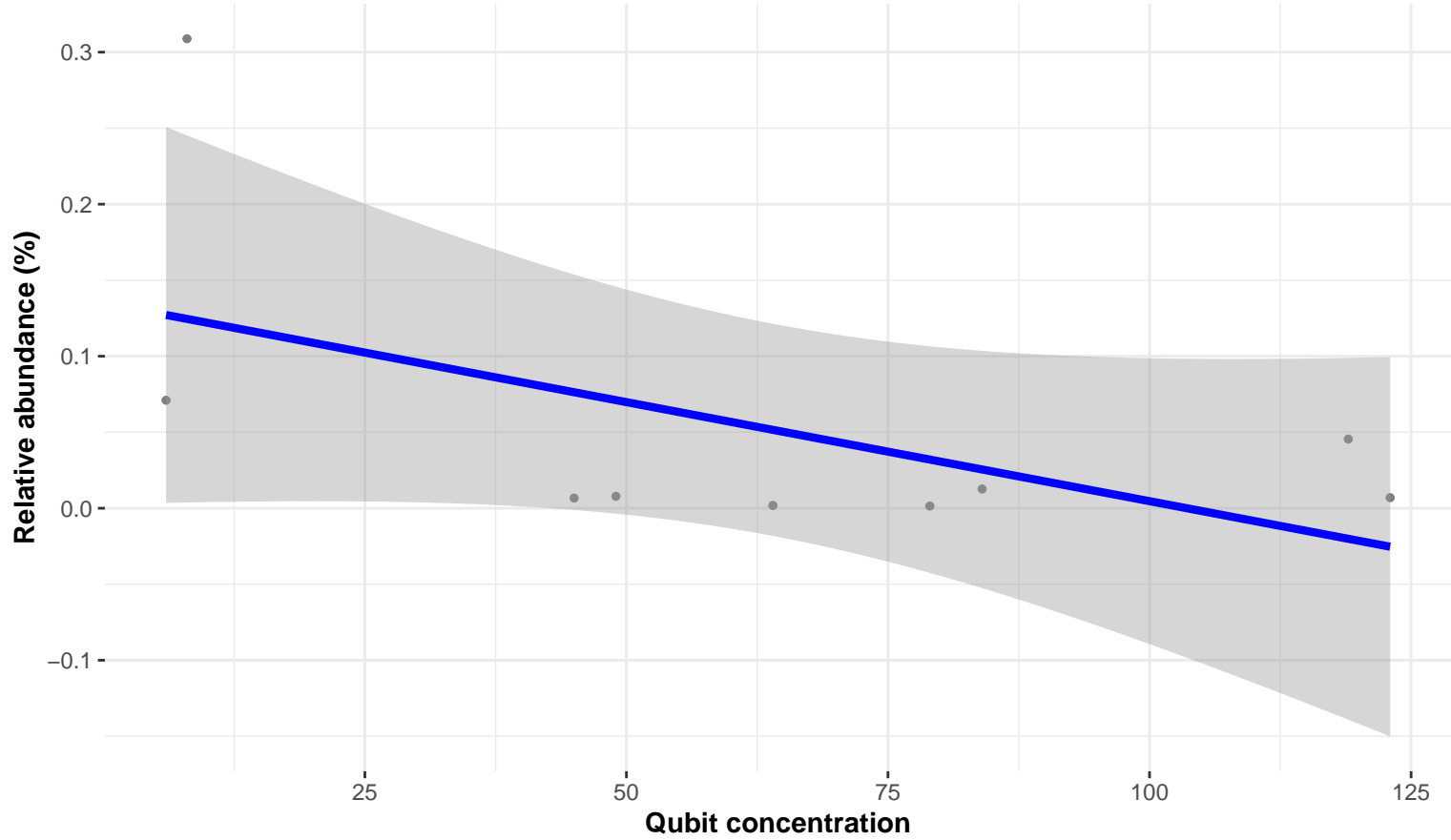
Correlation with all samples

$\log_e(S) = 5.862$, $p = 0.053$, $\hat{\rho}_{\text{Spearman}} = -0.597$, $\text{CI}_{95\%} [-0.886, 0.025]$, $n_{\text{pairs}} = 11$

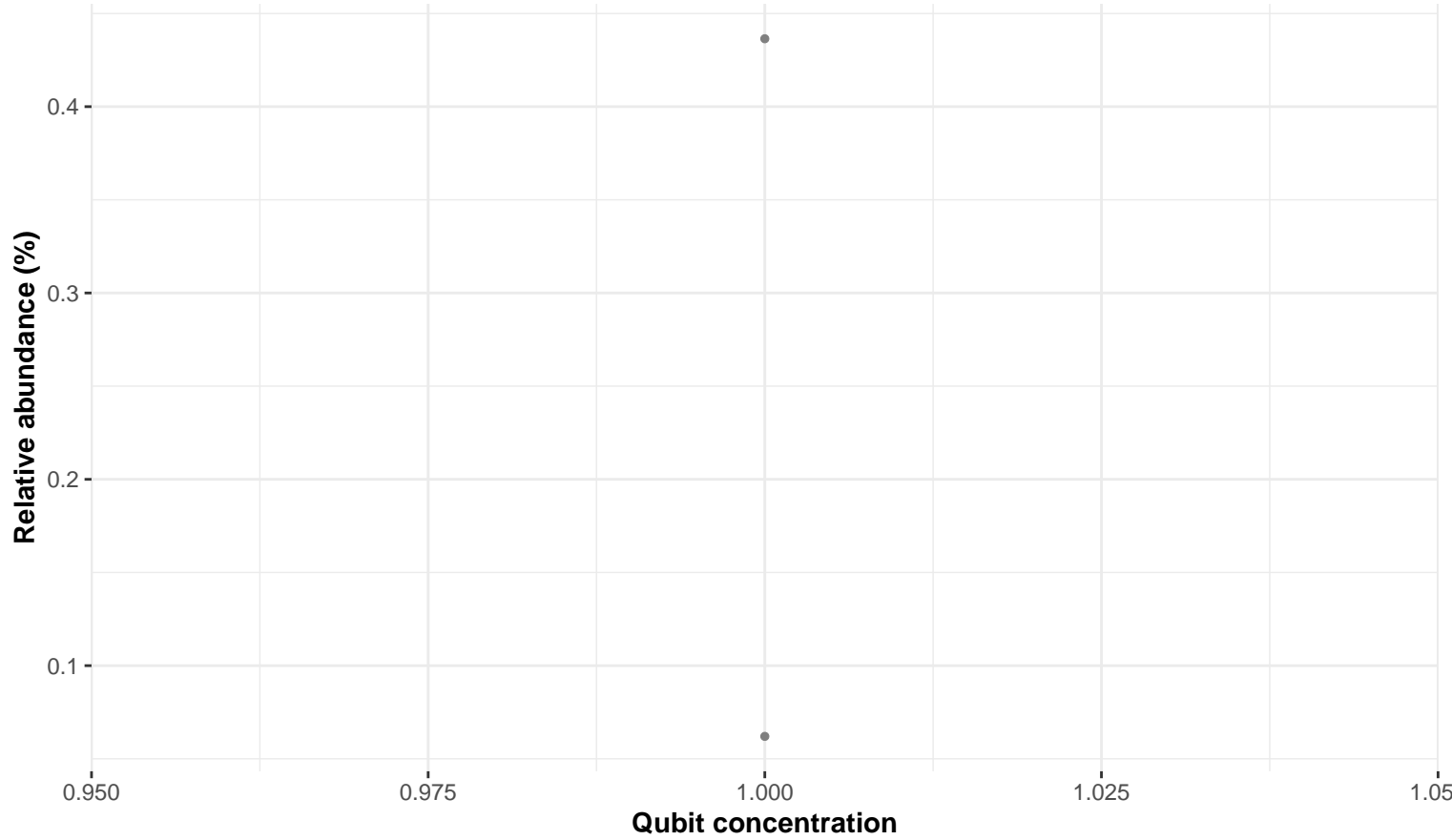


Correlation within: Digesta

$\log_e(S) = 5.075$, $p = 0.381$, $\hat{\rho}_{\text{Spearman}} = -0.333$, $\text{CI}_{95\%} [-0.824, 0.444]$, $n_{\text{pairs}} = 9$



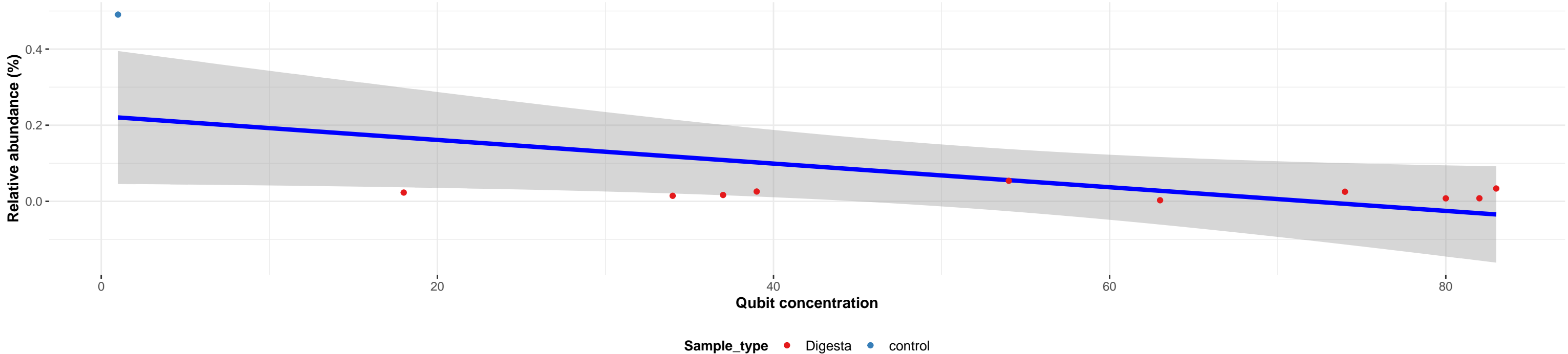
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

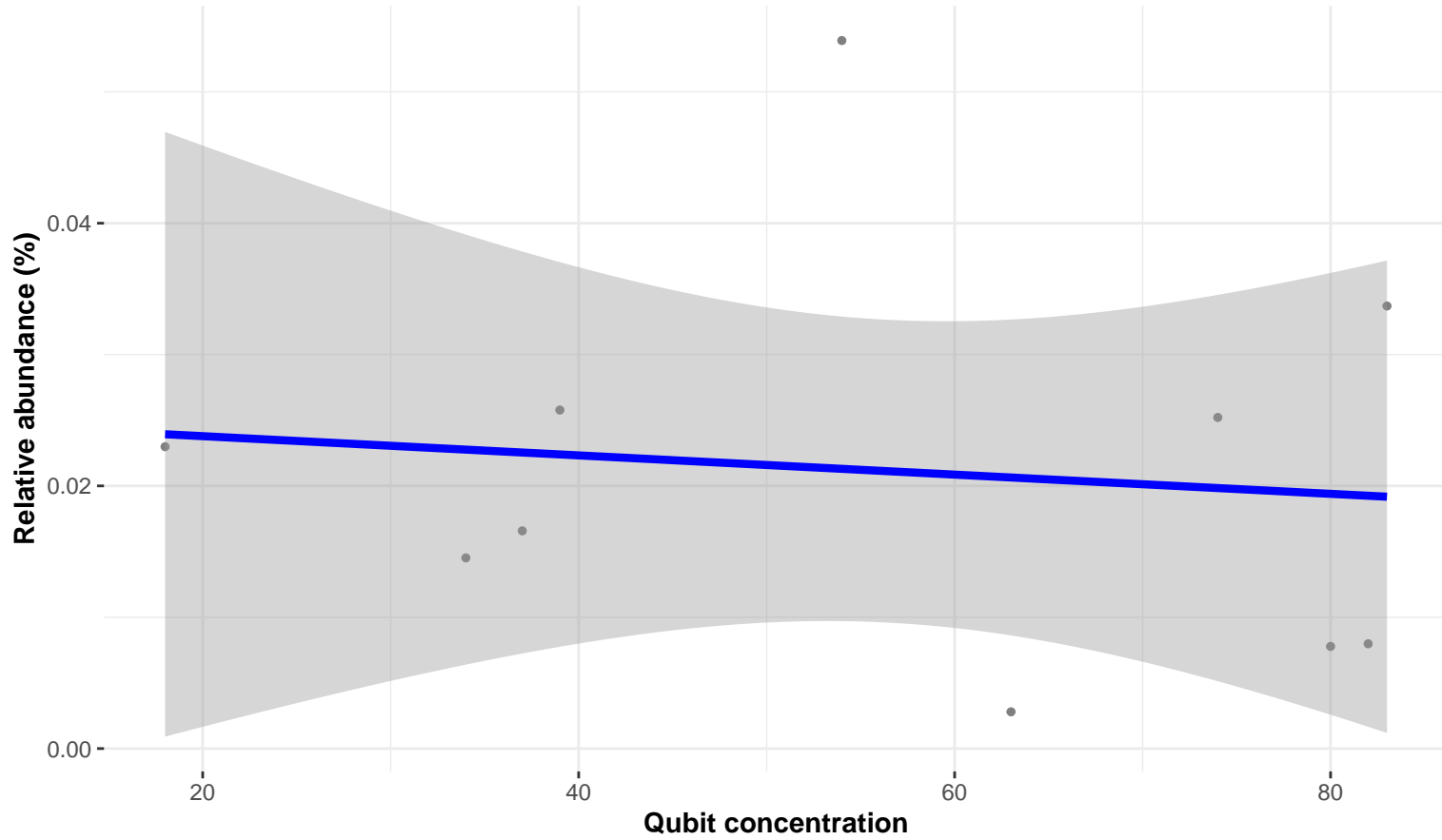
Correlation with all samples

$\log_e(S) = 5.642$, $p = 0.401$, $\hat{\rho}_{\text{Spearman}} = -0.282$, $\text{CI}_{95\%} [-0.763, 0.400]$, $n_{\text{pairs}} = 11$

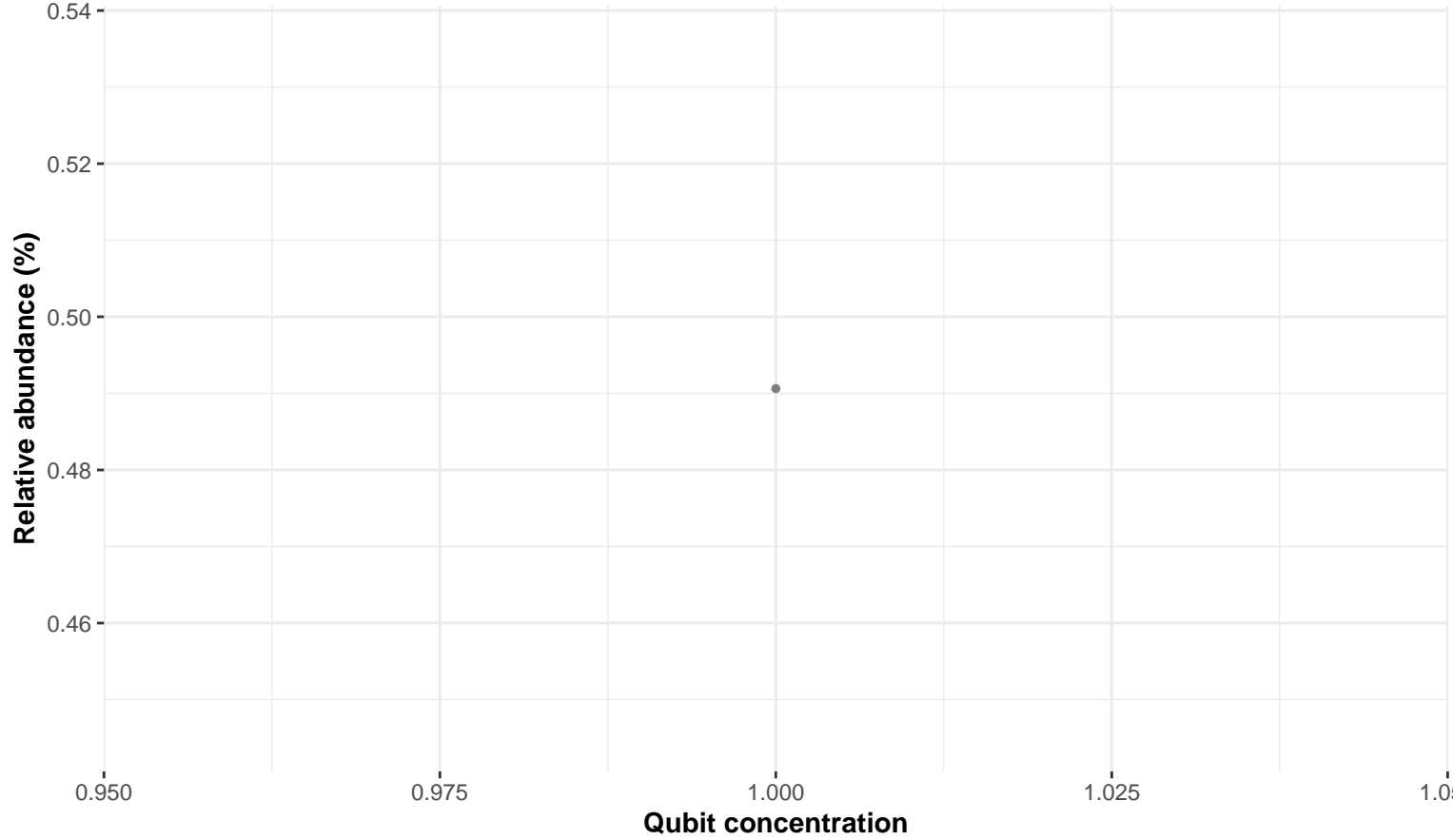


Correlation within: Digesta

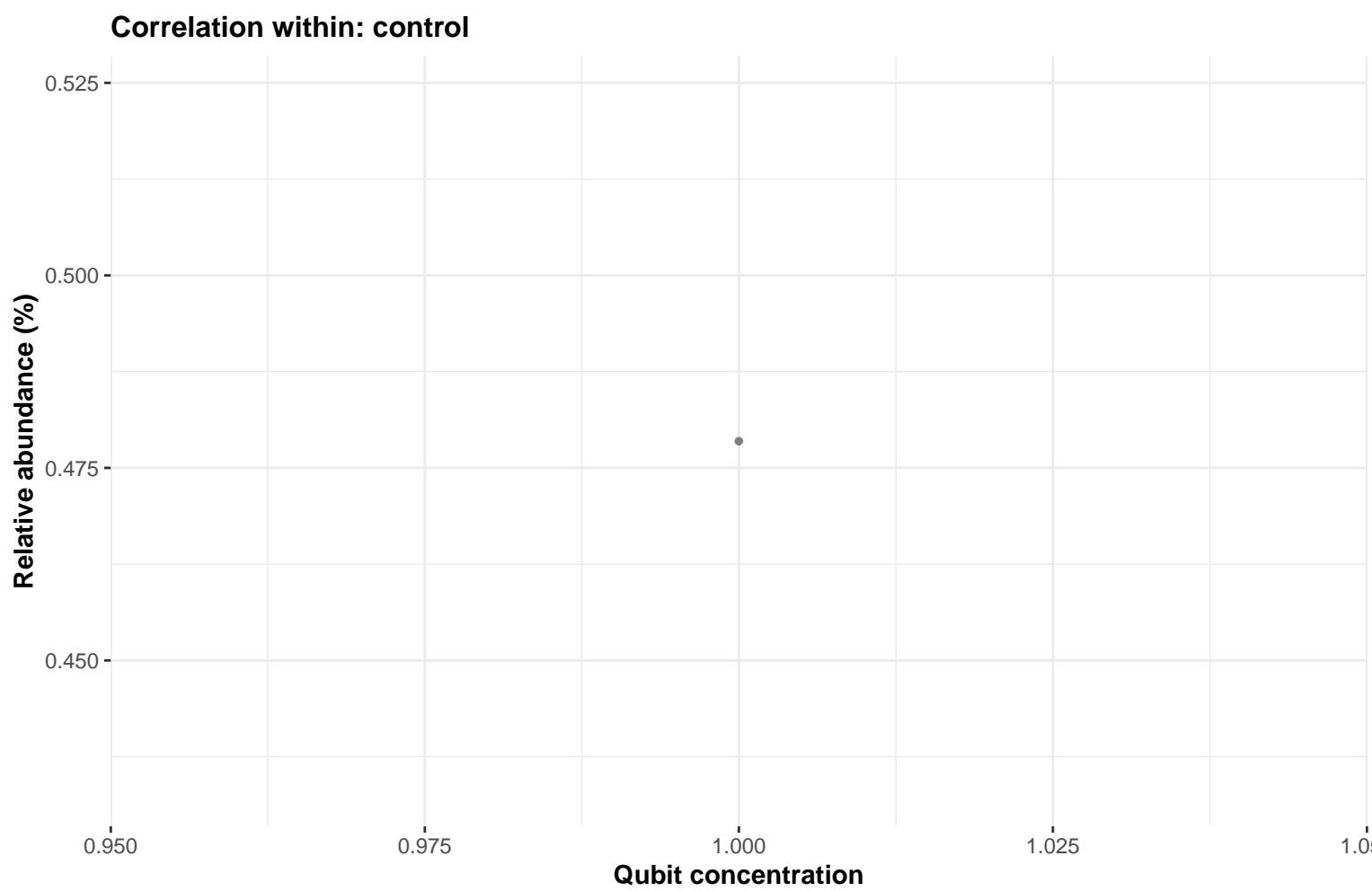
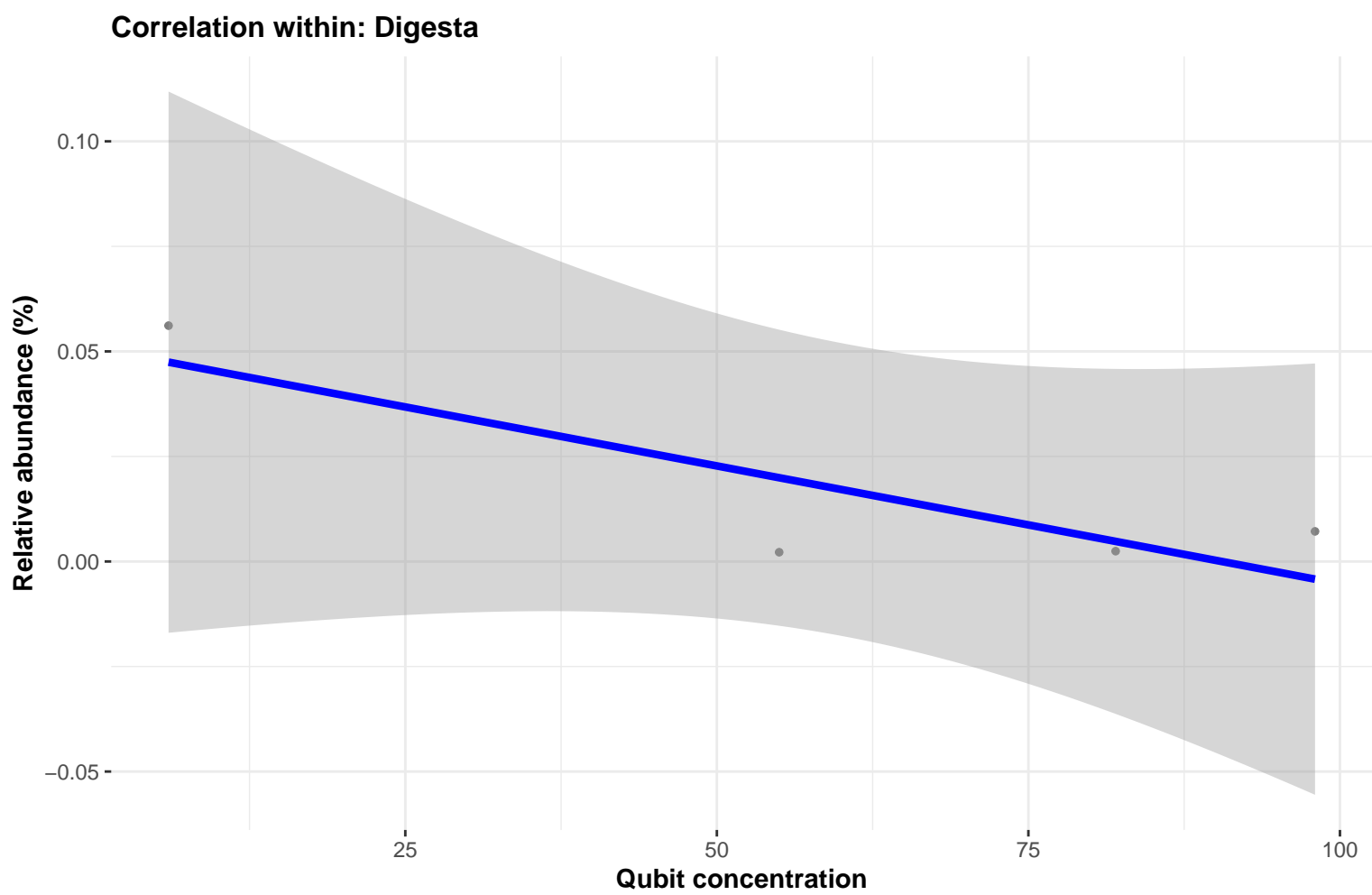
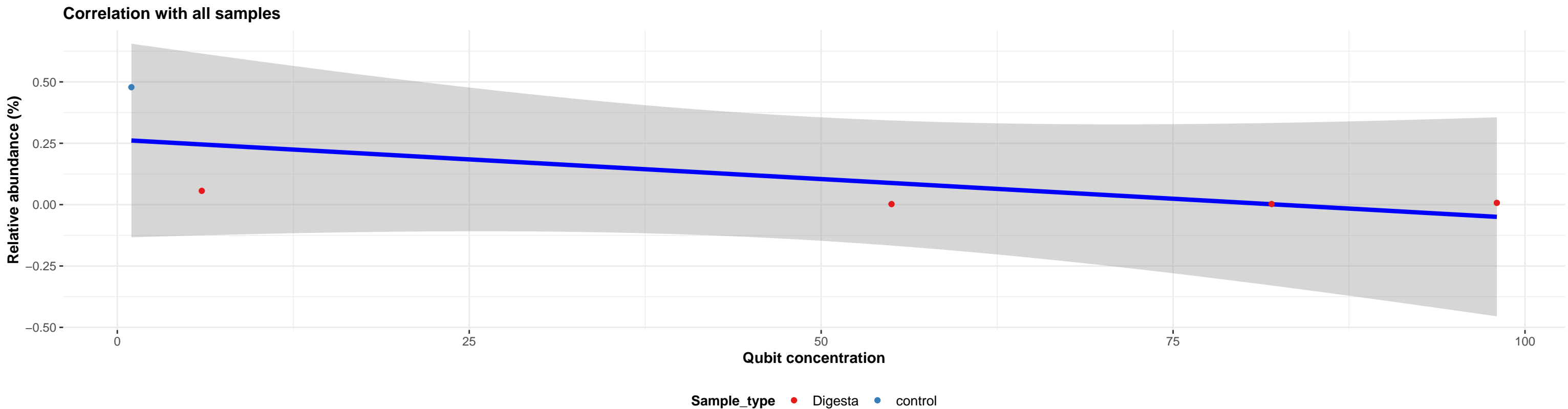
$\log_e(S) = 5.147$, $p = 0.907$, $\hat{\rho}_{\text{Spearman}} = -0.042$, $\text{CI}_{95\%} [-0.667, 0.617]$, $n_{\text{pairs}} = 10$



Correlation within: control



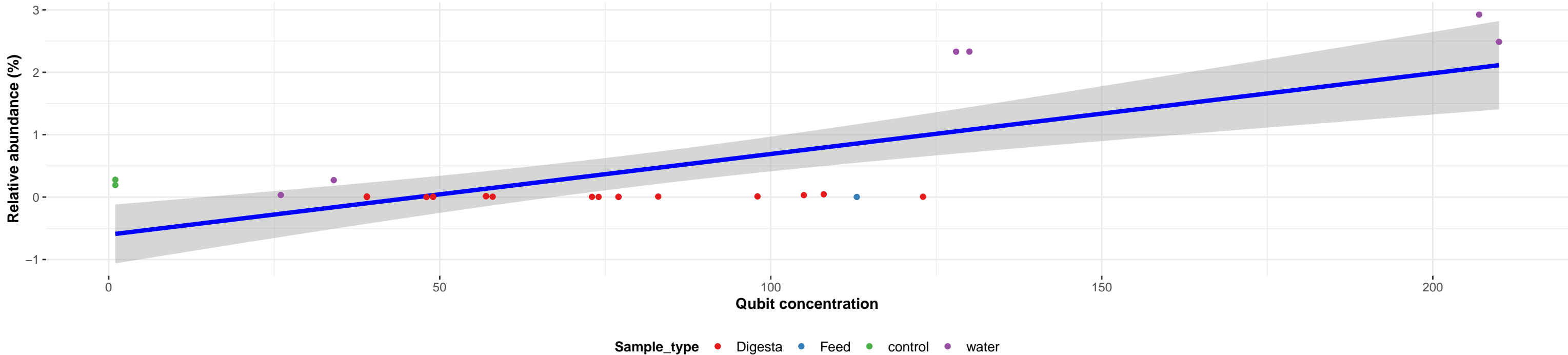
Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA



Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Pseudahrensia; NA

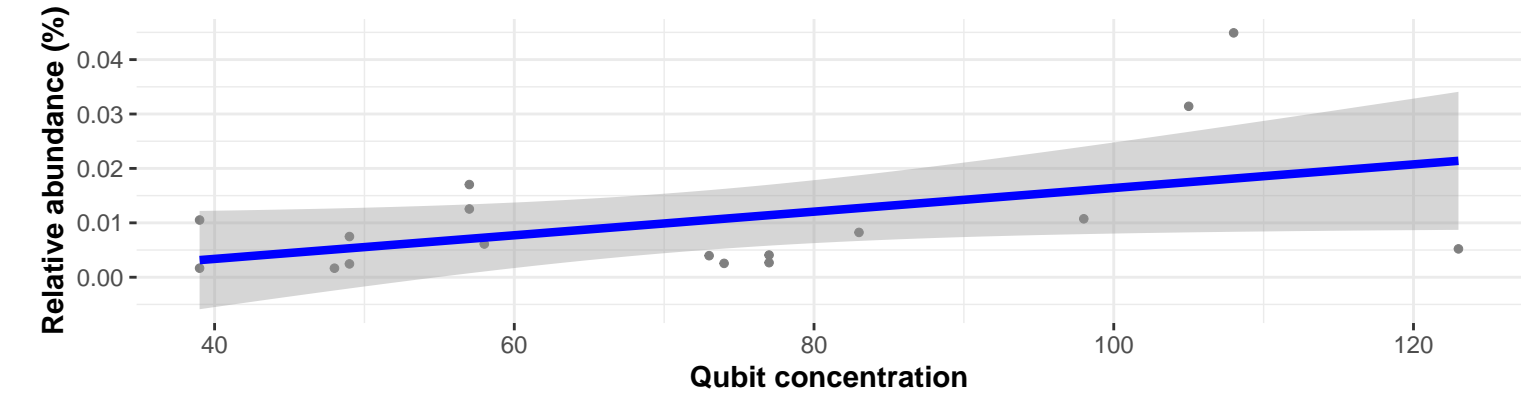
Correlation with all samples

$\log_e(S) = 7.727$, $p = 0.270$, $\hat{\rho}_{\text{Spearman}} = 0.224$, $CI_{95\%} [-0.190, 0.571]$, $n_{\text{pairs}} = 26$

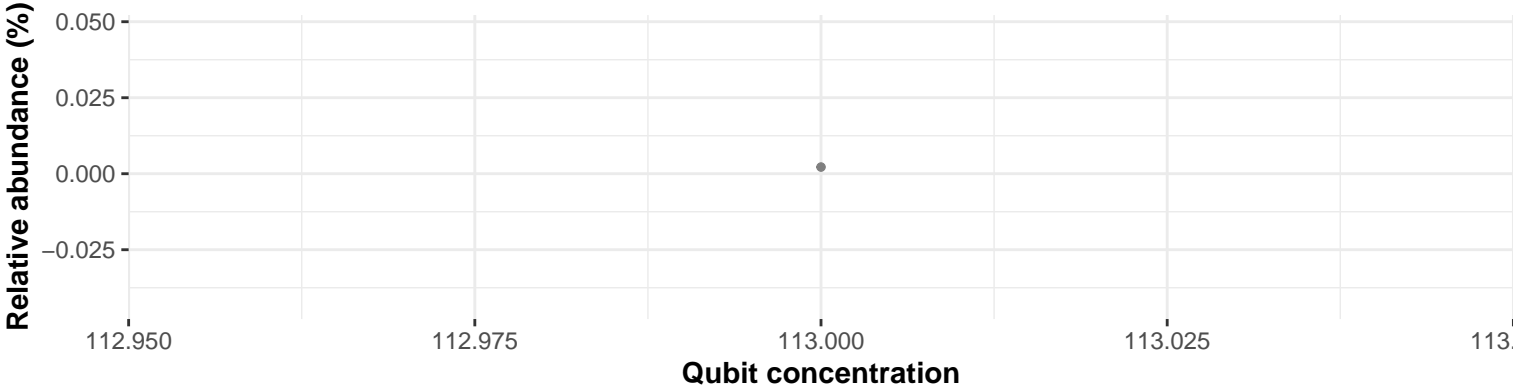


Correlation within: Digesta

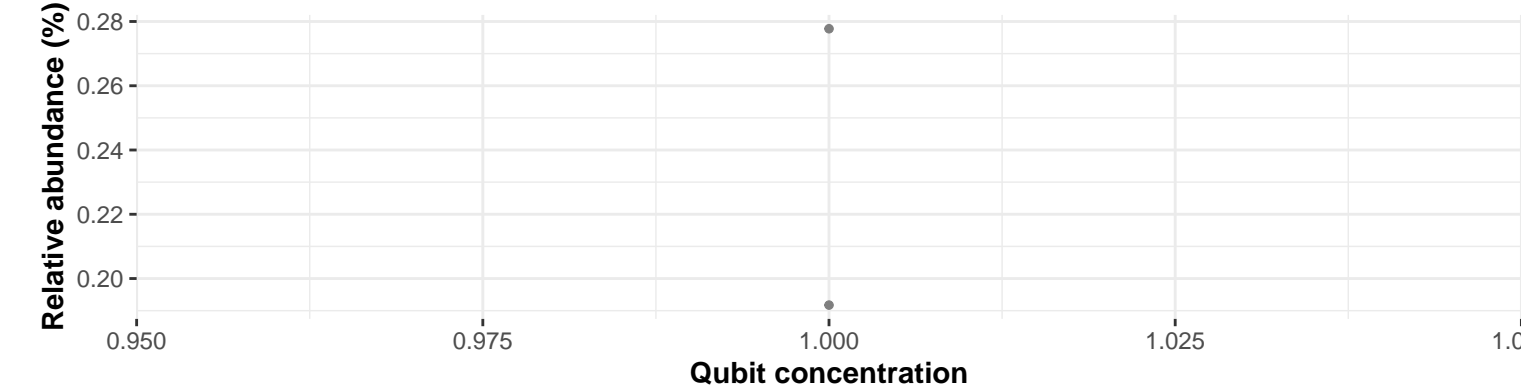
$\log_e(S) = 6.159$, $p = 0.093$, $\hat{\rho}_{\text{Spearman}} = 0.420$, $CI_{95\%} [-0.091, 0.756]$, $n_{\text{pairs}} = 17$



Correlation within: Feed

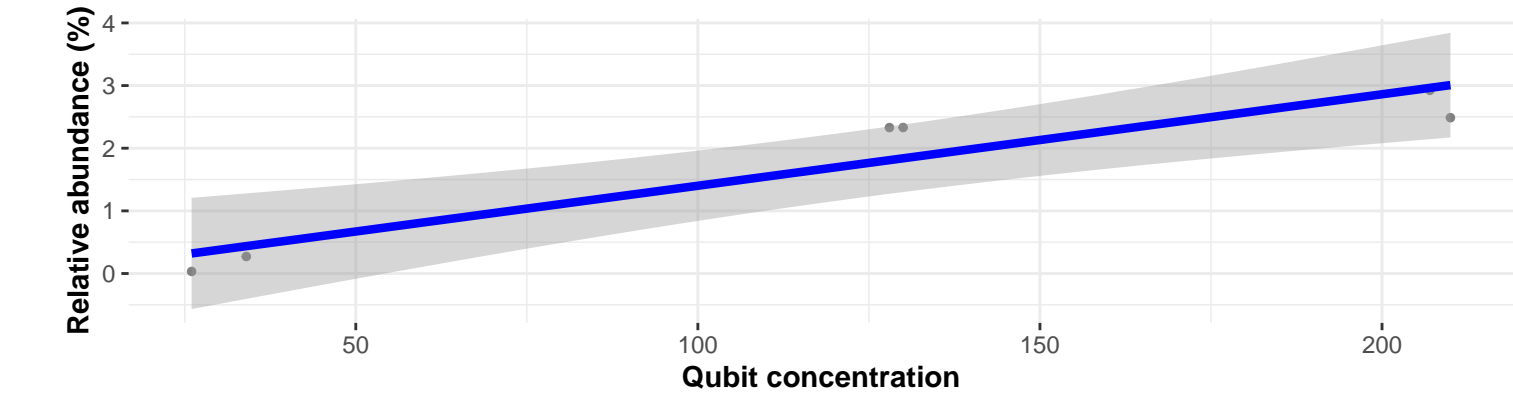


Correlation within: control



Correlation within: water

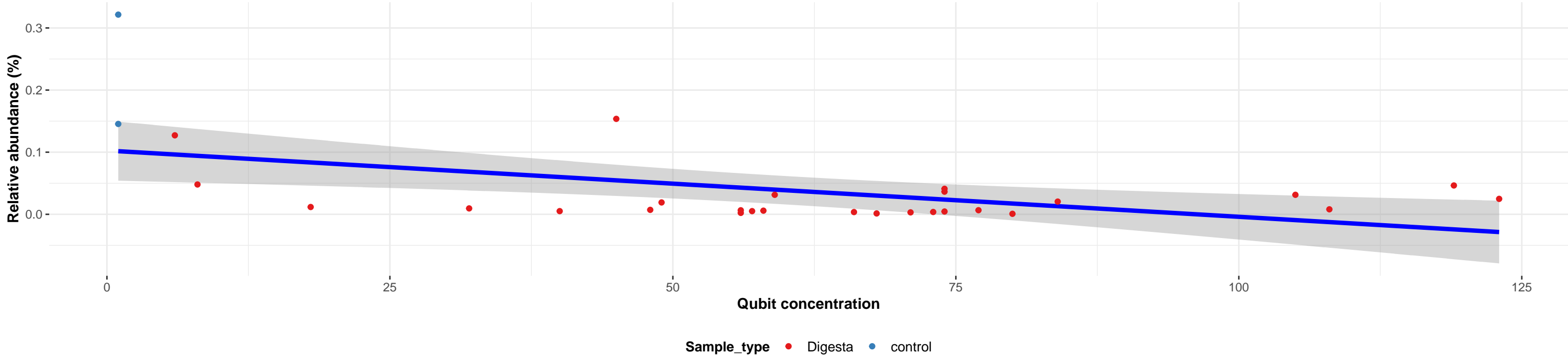
$\log_e(S) = 0.693$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.943$, $CI_{95\%} [0.536, 0.994]$, $n_{\text{pairs}} = 6$



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

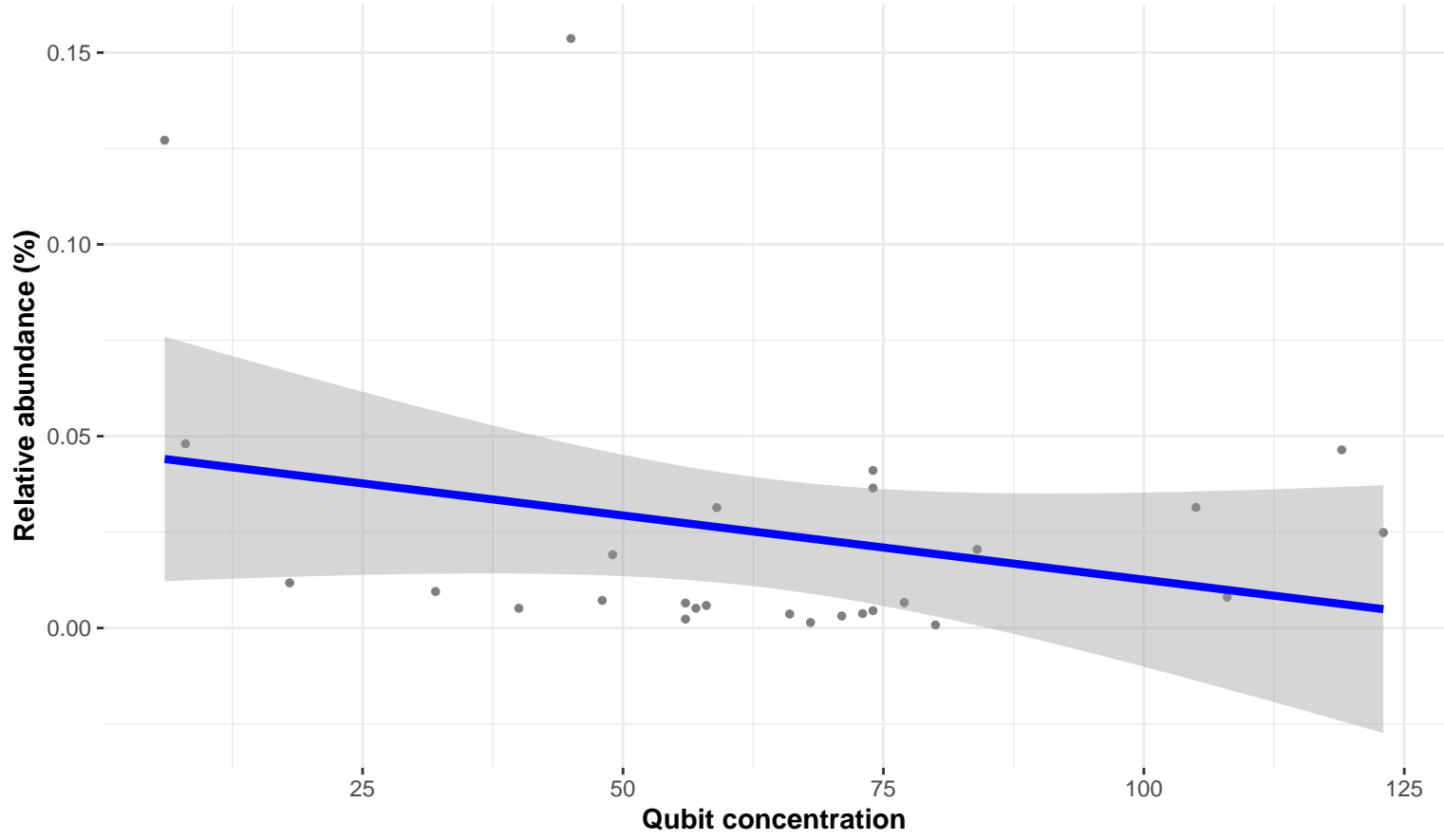
Correlation with all samples

$\log_e(S) = 8.537$, $p = 0.180$, $\hat{\rho}_{\text{Spearman}} = -0.256$, $\text{CI}_{95\%} [-0.577, 0.133]$, $n_{\text{pairs}} = 29$

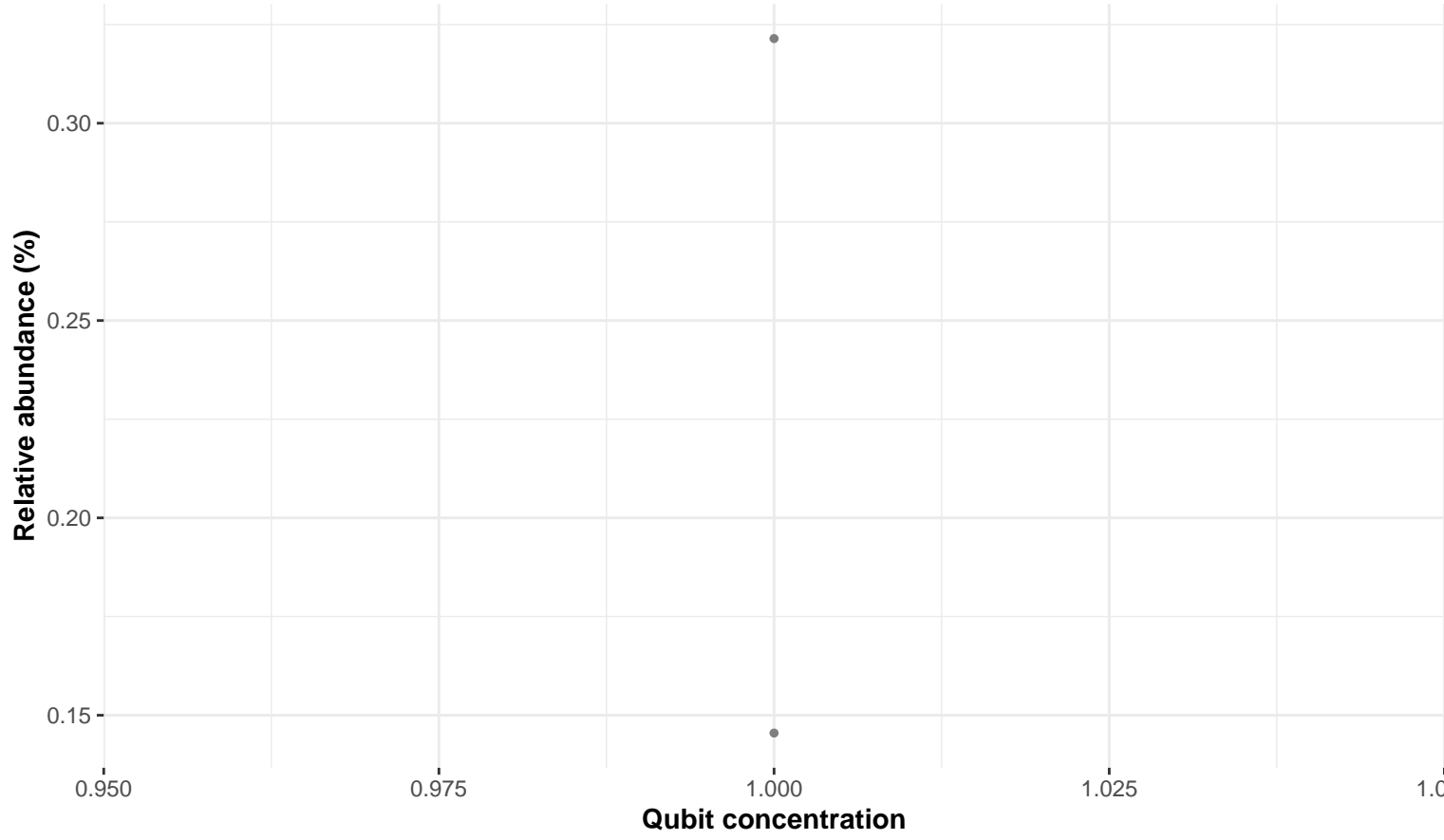


Correlation within: Digesta

$\log_e(S) = 8.173$, $p = 0.685$, $\hat{\rho}_{\text{Spearman}} = -0.082$, $\text{CI}_{95\%} [-0.457, 0.318]$, $n_{\text{pairs}} = 27$



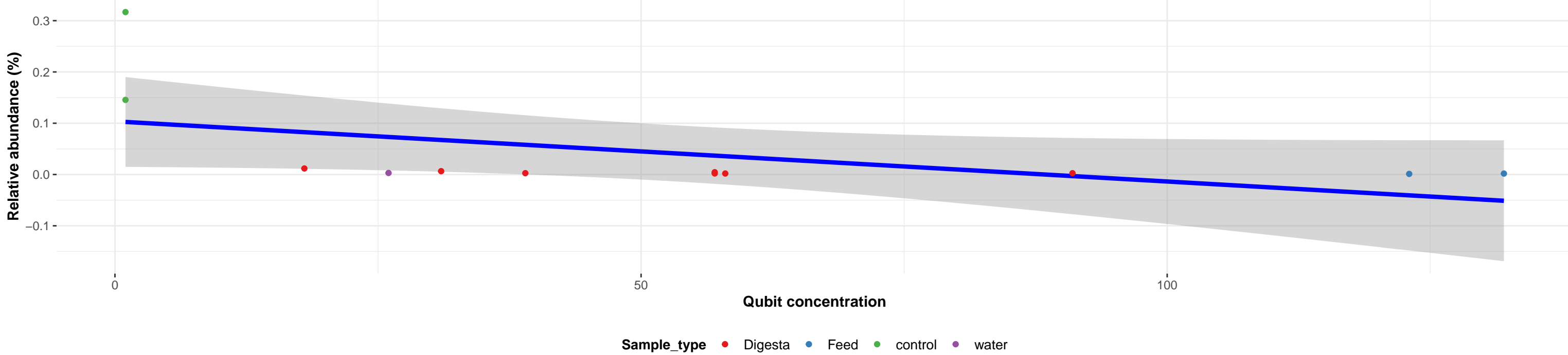
Correlation within: control



Bacteria; Patescibacteria; Saccharimonadia; Saccharimonadales; NA; NA; NA

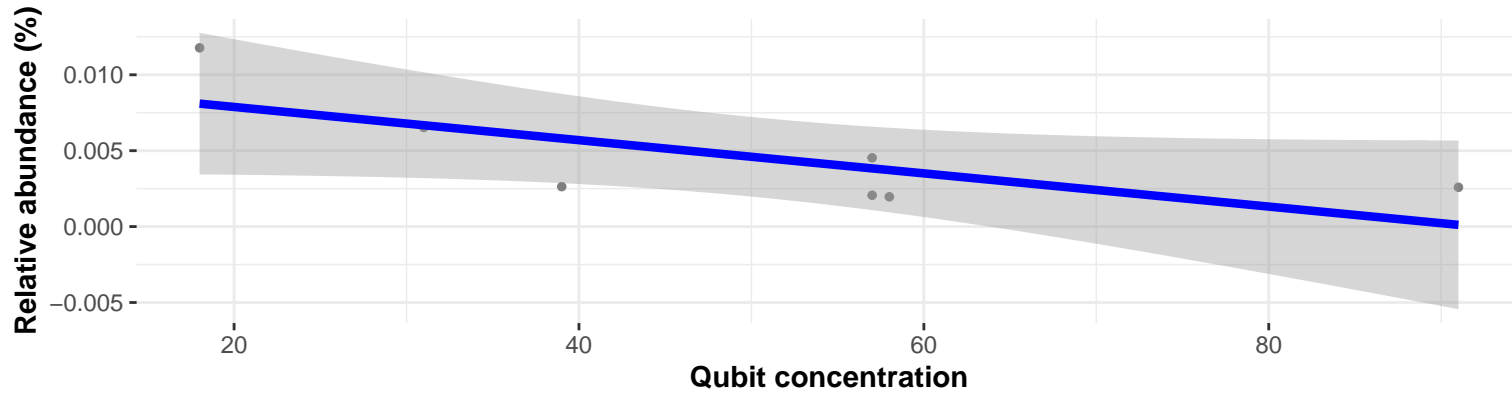
Correlation with all samples

$\log_e(S) = 6.310$, $p = 1.89e-05$, $\hat{\rho}_{\text{Spearman}} = -0.923$, $CI_{95\%} [-0.979, -0.733]$, $n_{\text{pairs}} = 12$

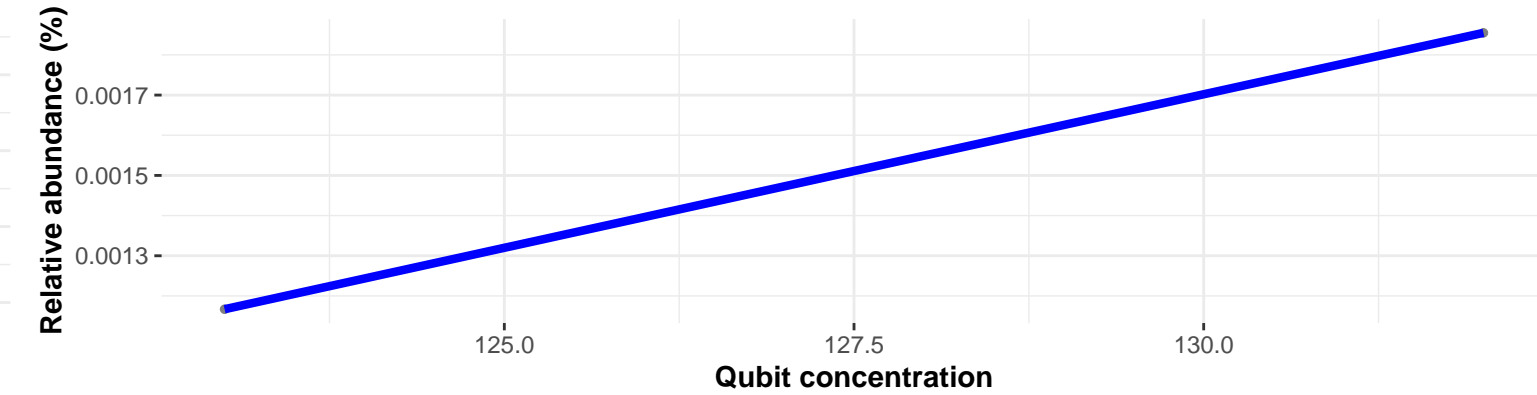


Correlation within: Digesta

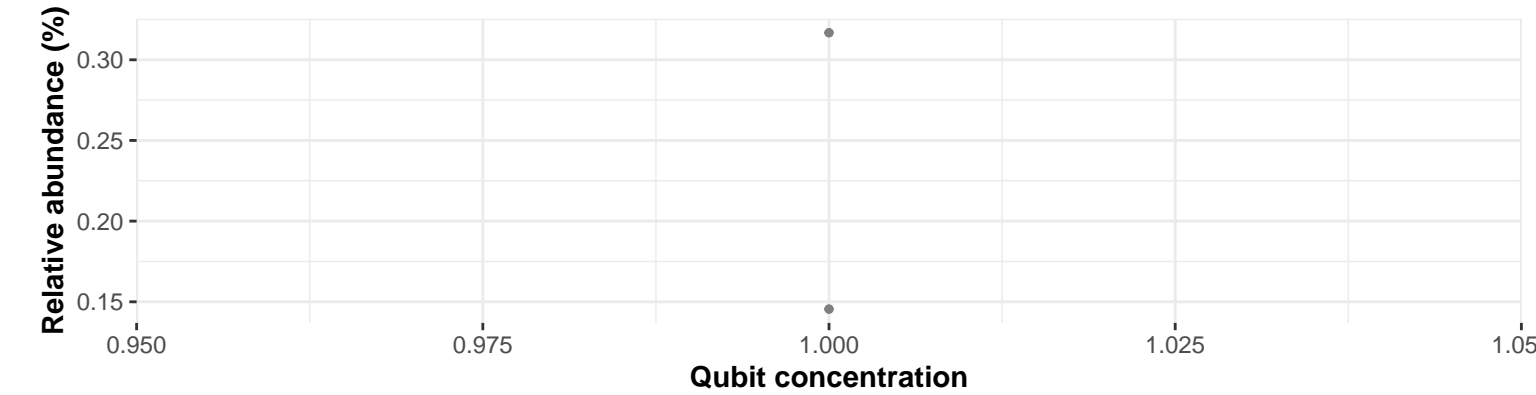
$\log_e(S) = 4.619$, $p = 0.027$, $\hat{\rho}_{\text{Spearman}} = -0.811$, $CI_{95\%} [-0.973, -0.120]$, $n_{\text{pairs}} = 7$



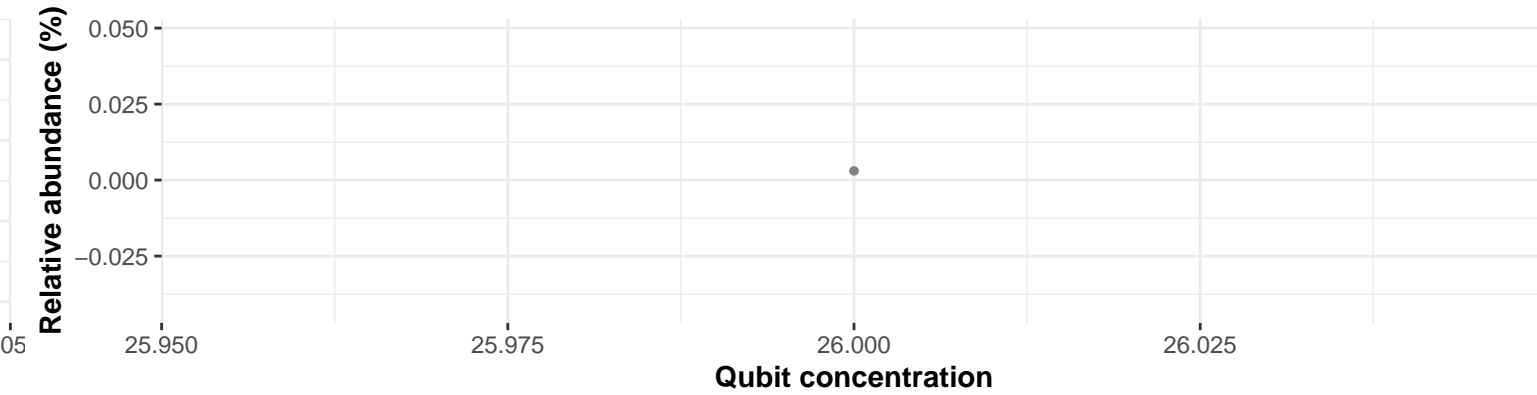
Correlation within: Feed



Correlation within: control



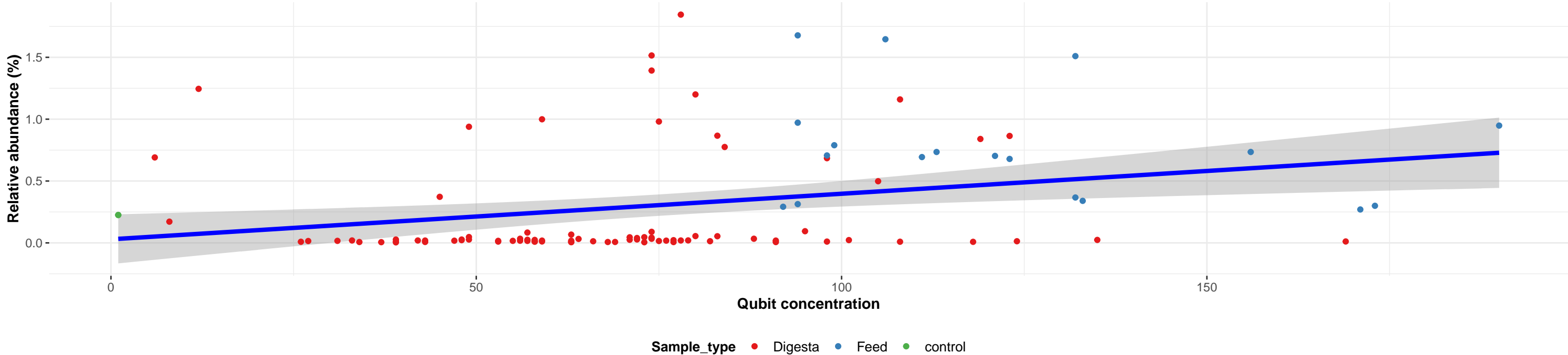
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Ligilactobacillus; NA

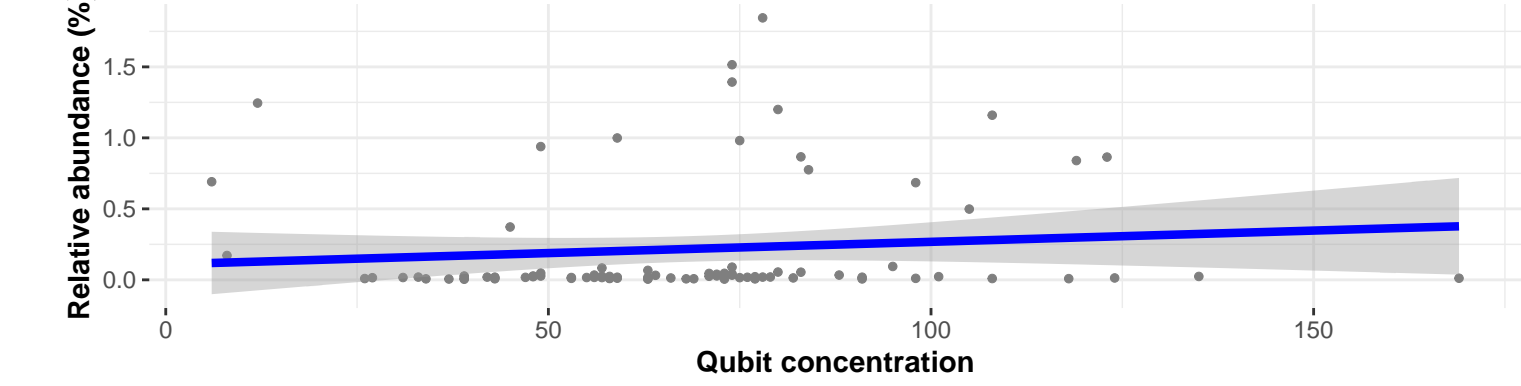
Correlation with all samples

$\log_e(S) = 11.735$, $p = 9\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = 0.371$, $\text{CI}_{95\%} [0.189, 0.529]$, $n_{\text{pairs}} = 106$



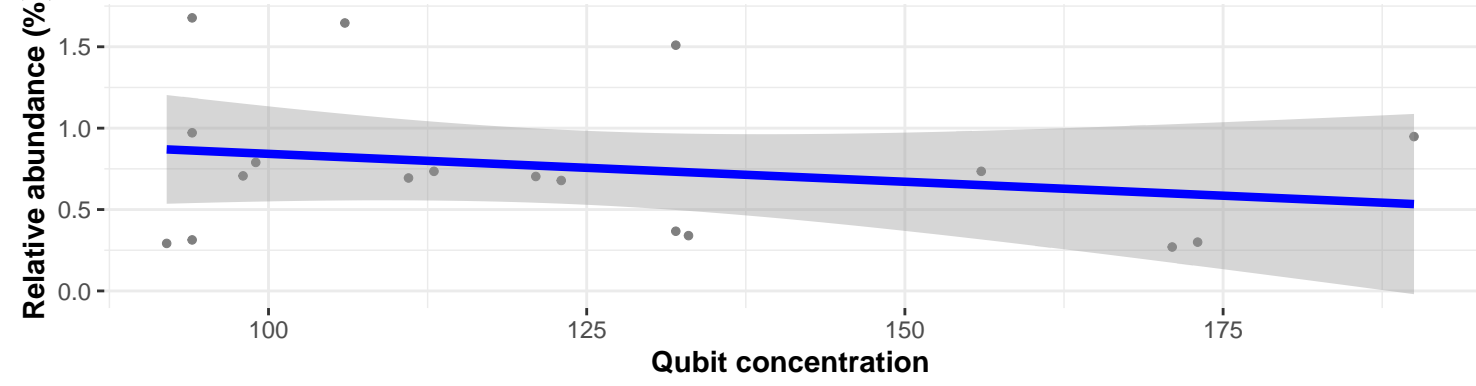
Correlation within: Digesta

$\log_e(S) = 11.366$, $p = 0.087$, $\hat{\rho}_{\text{Spearman}} = 0.186$, $\text{CI}_{95\%} [-0.034, 0.388]$, $n_{\text{pairs}} = 86$

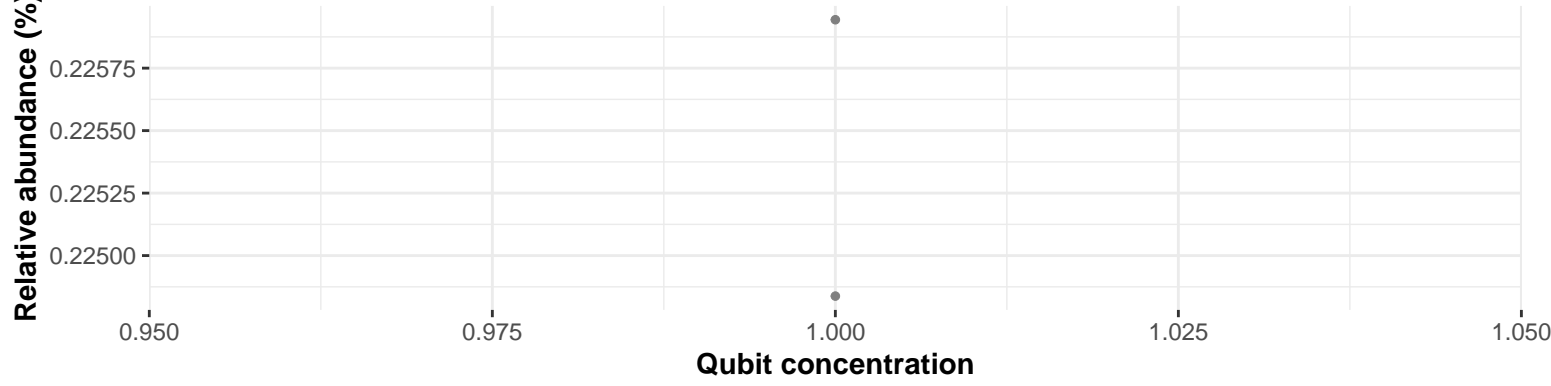


Correlation within: Feed

$\log_e(S) = 7.048$, $p = 0.457$, $\hat{\rho}_{\text{Spearman}} = -0.187$, $\text{CI}_{95\%} [-0.611, 0.320]$, $n_{\text{pairs}} = 18$



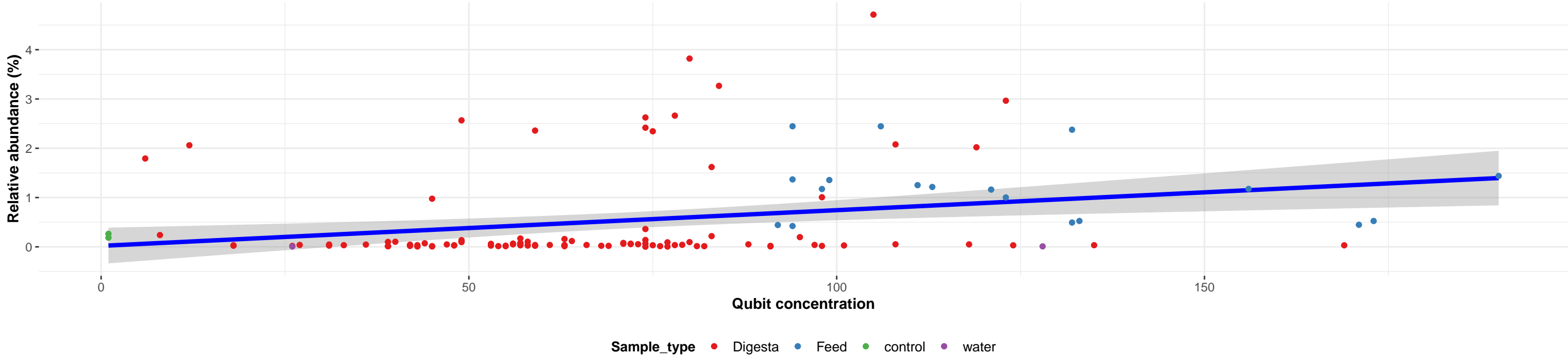
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; delbrueckii

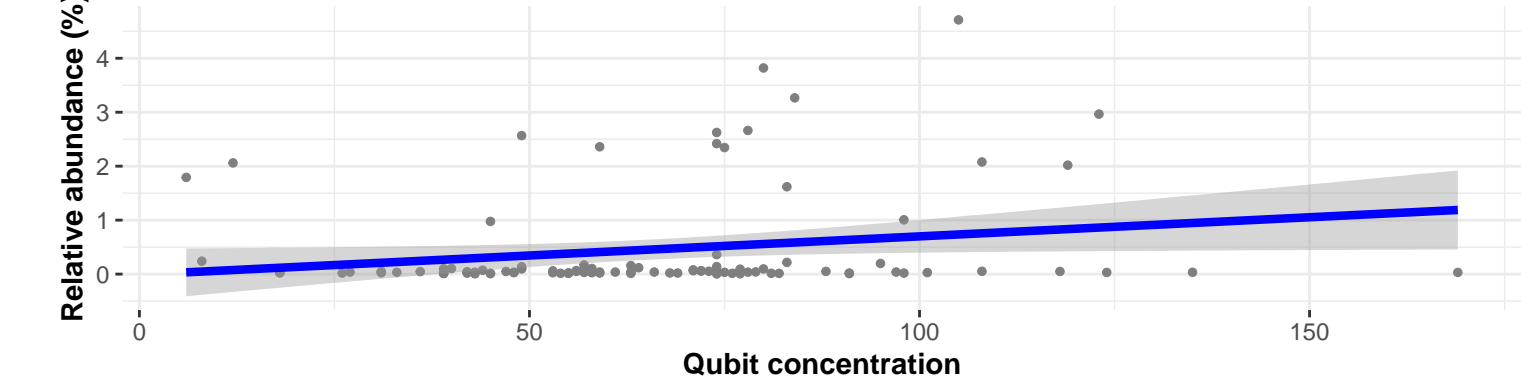
Correlation with all samples

$\log_e(S) = 12.234$, $p = 5.82e-05$, $\hat{\rho}_{\text{Spearman}} = 0.353$, $CI_{95\%} [0.183, 0.502]$, $n_{\text{pairs}} = 124$



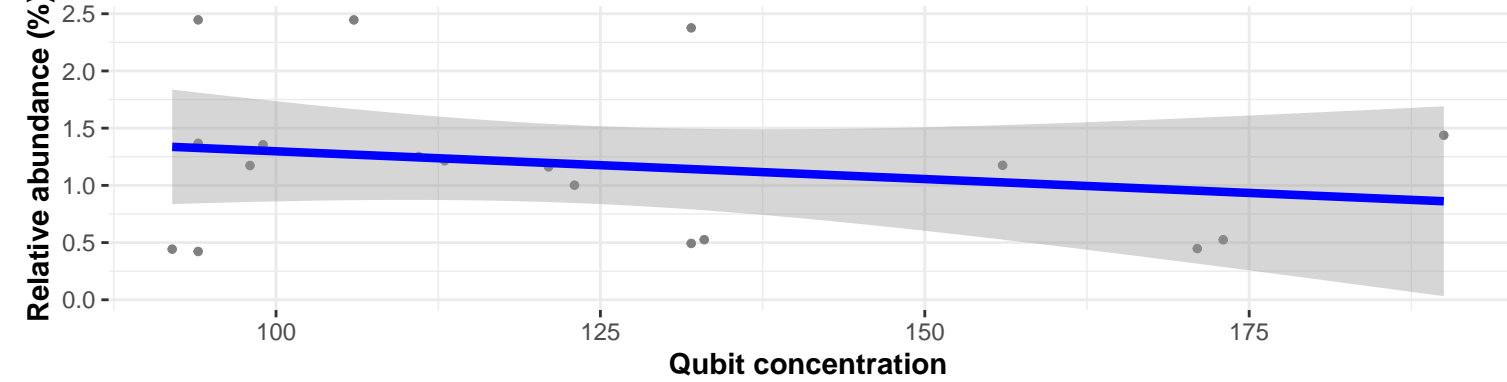
Correlation within: Digesta

$\log_e(S) = 11.872$, $p = 0.056$, $\hat{\rho}_{\text{Spearman}} = 0.190$, $CI_{95\%} [-0.010, 0.376]$, $n_{\text{pairs}} = 102$

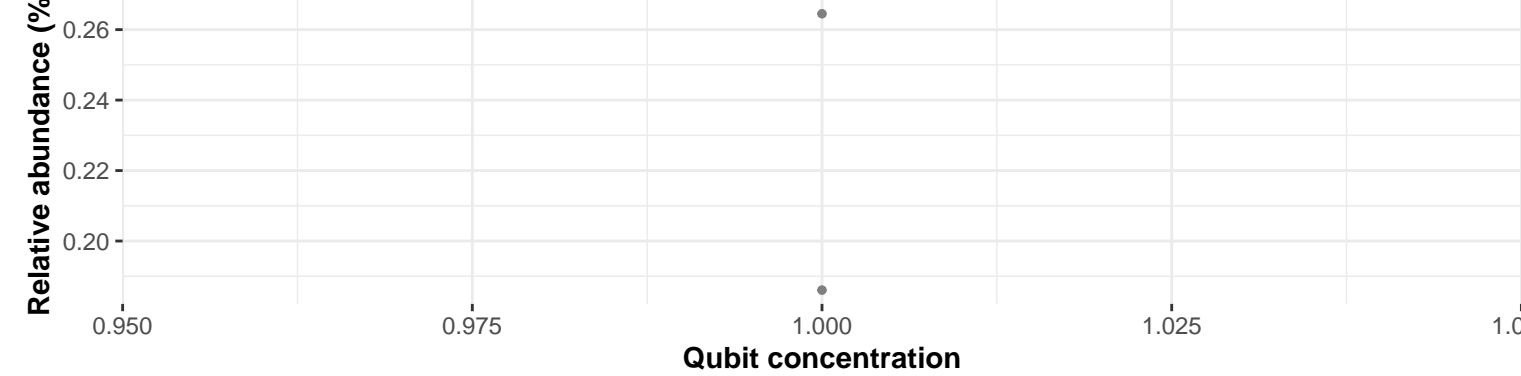


Correlation within: Feed

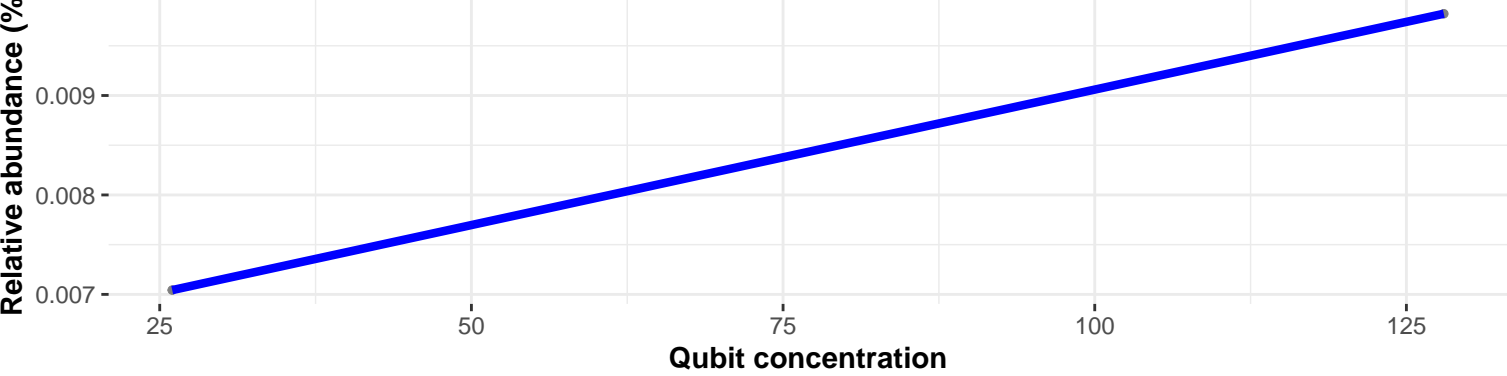
$\log_e(S) = 6.961$, $p = 0.729$, $\hat{\rho}_{\text{Spearman}} = -0.088$, $CI_{95\%} [-0.544, 0.408]$, $n_{\text{pairs}} = 18$



Correlation within: control



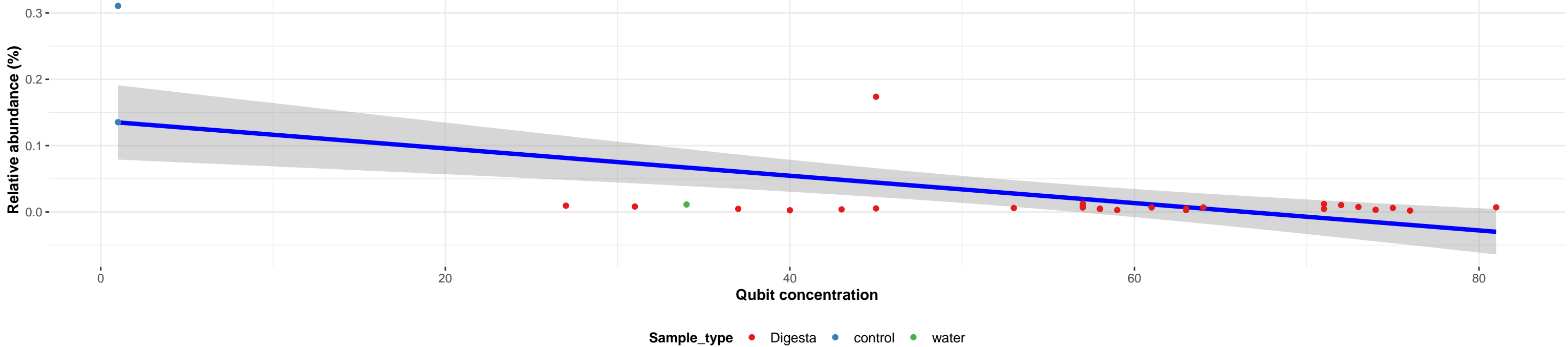
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Oceanobacillus; indicireducens

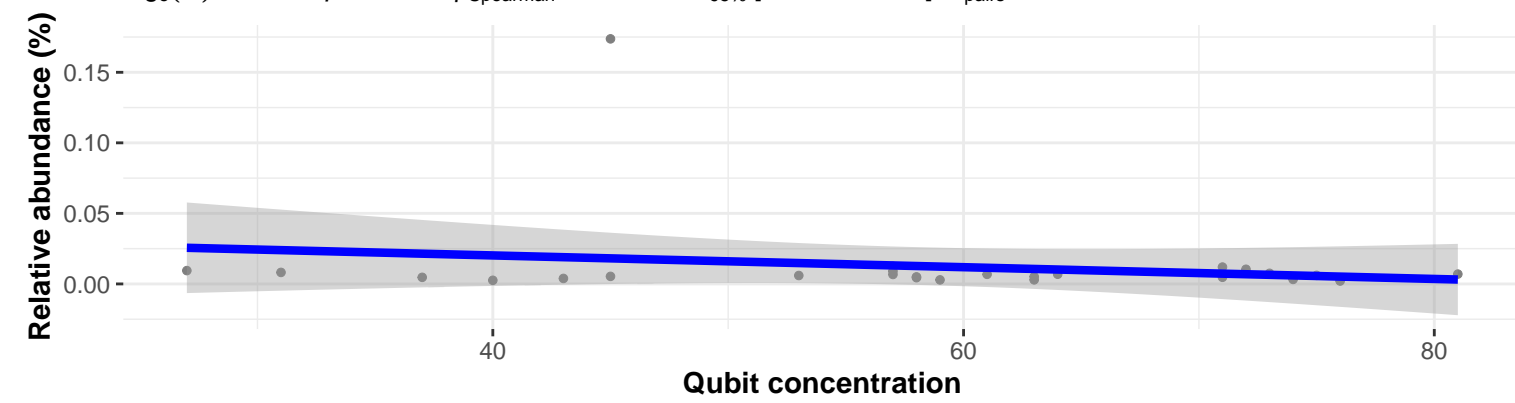
Correlation with all samples

$\log_e(S) = 8.581$, $p = 0.099$, $\hat{\rho}_{\text{Spearman}} = -0.313$, $CI_{95\%} [-0.616, 0.072]$, $n_{\text{pairs}} = 29$

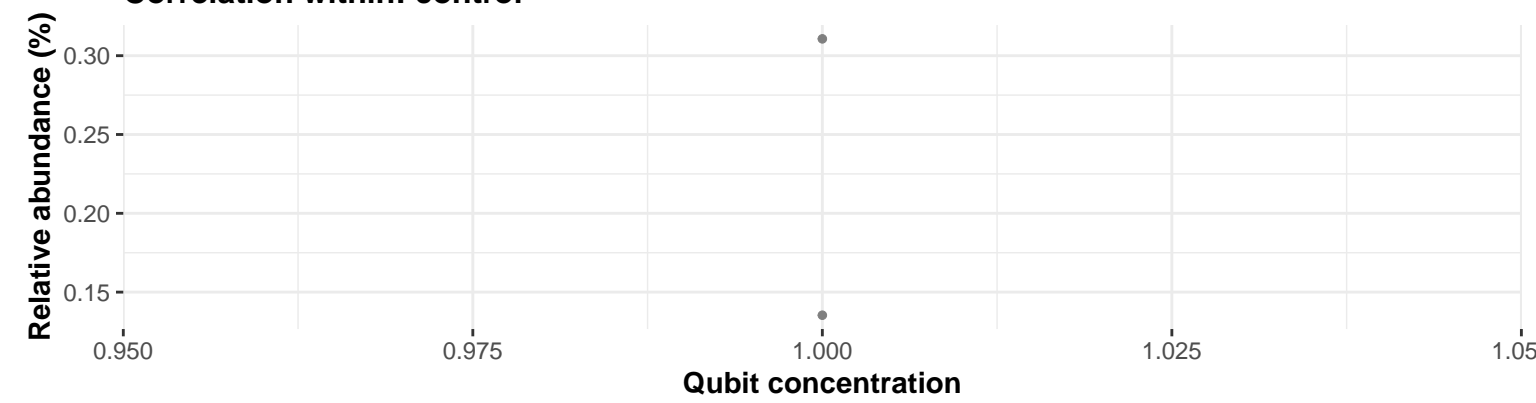


Correlation within: Digesta

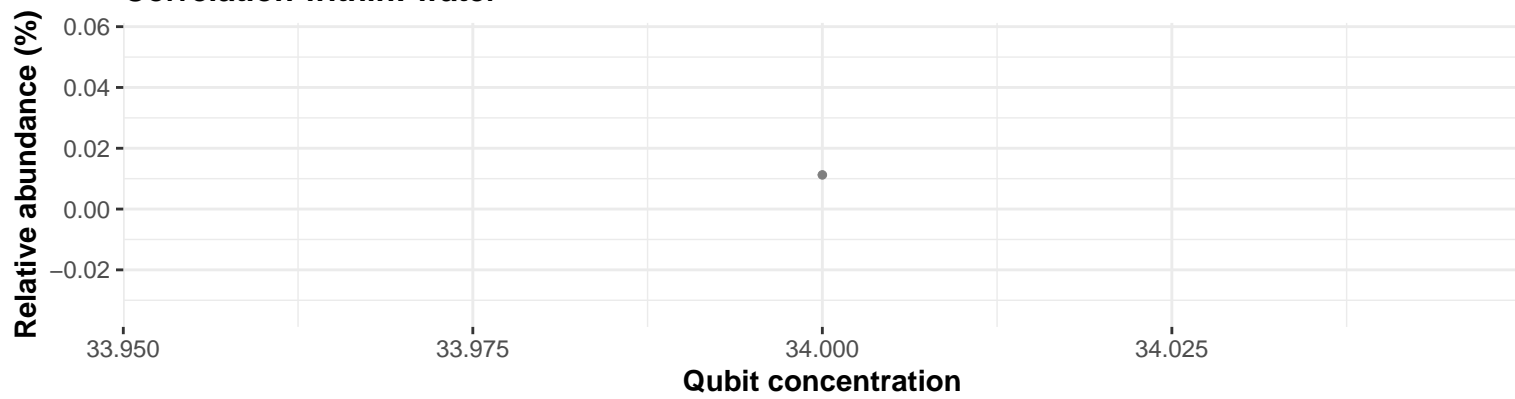
$\log_e(S) = 8.058$, $p = 0.697$, $\hat{\rho}_{\text{Spearman}} = -0.080$, $CI_{95\%} [-0.463, 0.328]$, $n_{\text{pairs}} = 26$



Correlation within: control



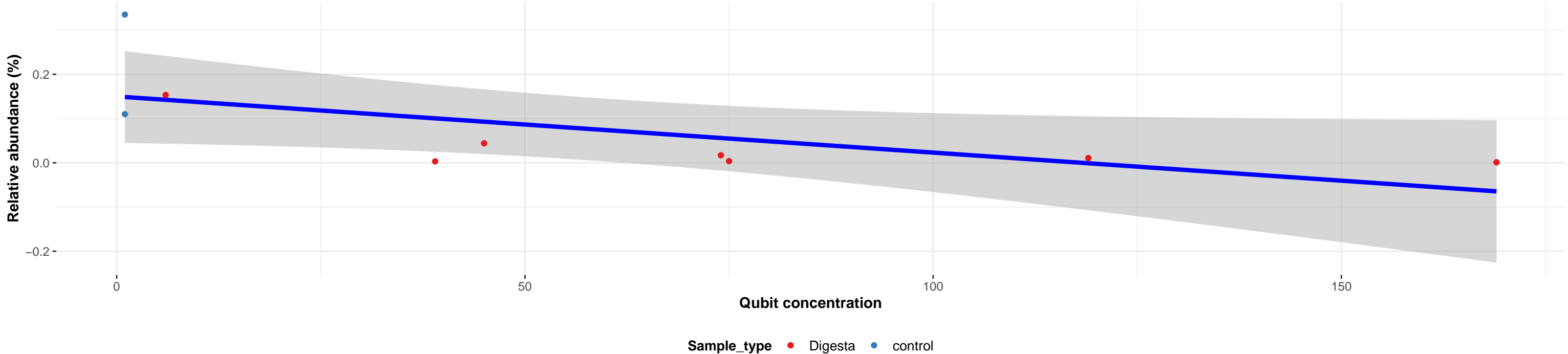
Correlation within: water



Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Pelomonas; saccharophila

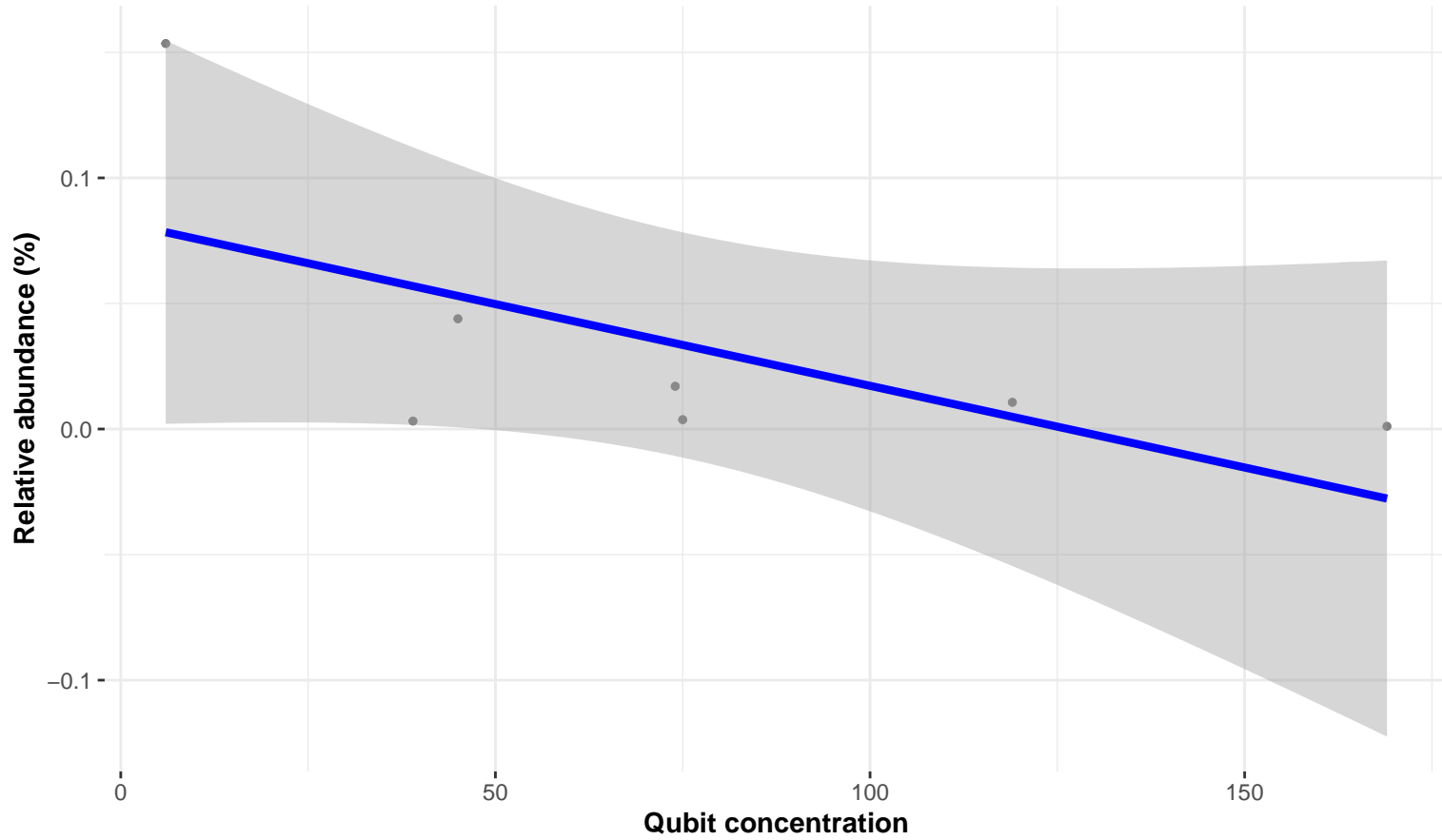
Correlation with all samples

$\log_e(S) = 5.368$, $p = 0.012$, $\hat{\rho}_{\text{Spearman}} = -0.787$, $\text{CI}_{95\%} [-0.955, -0.234]$, $n_{\text{pairs}} = 9$

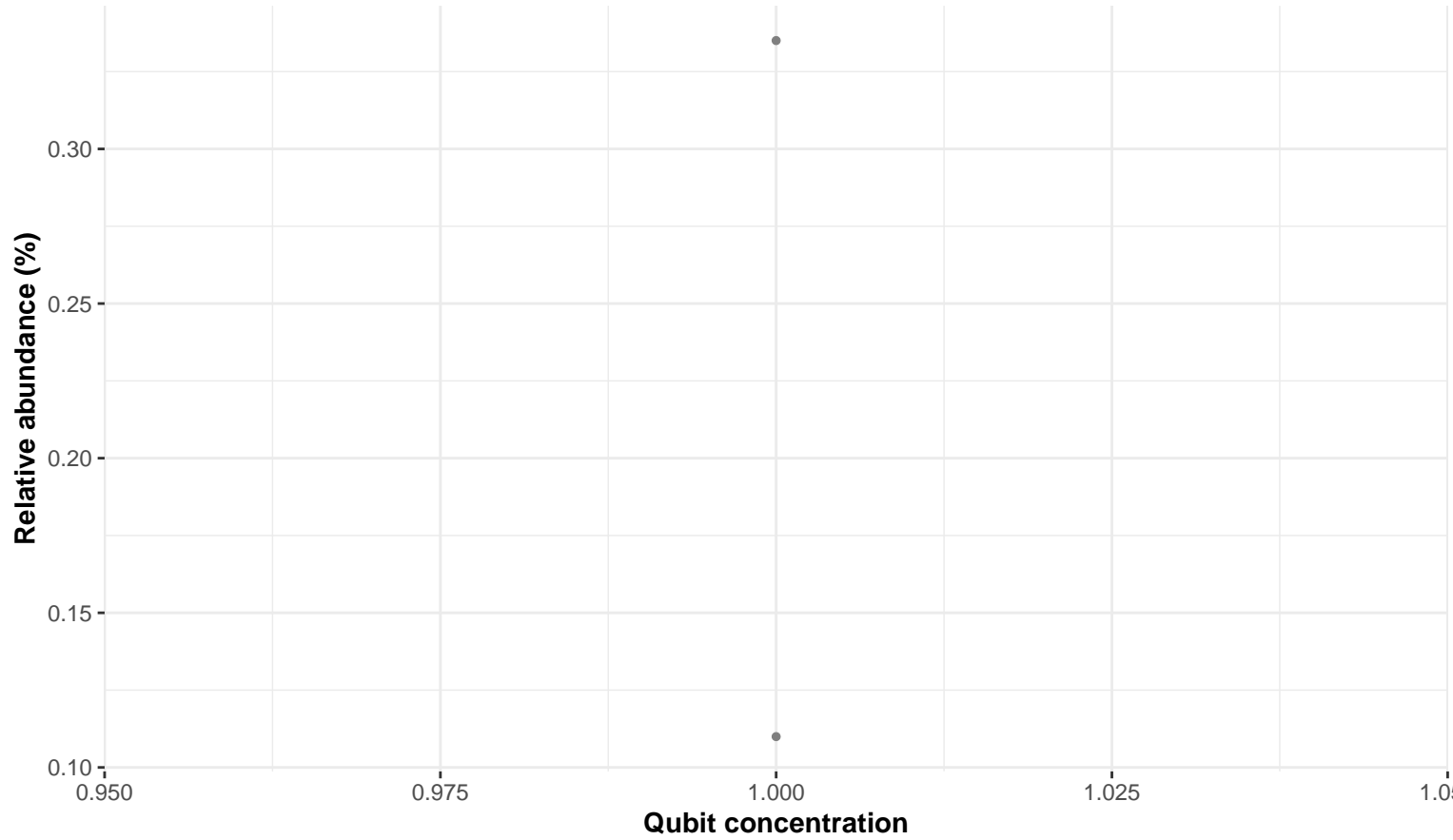


Correlation within: Digesta

$\log_e(S) = 4.500$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = -0.607$, $\text{CI}_{95\%} [-0.937, 0.295]$, $n_{\text{pairs}} = 7$

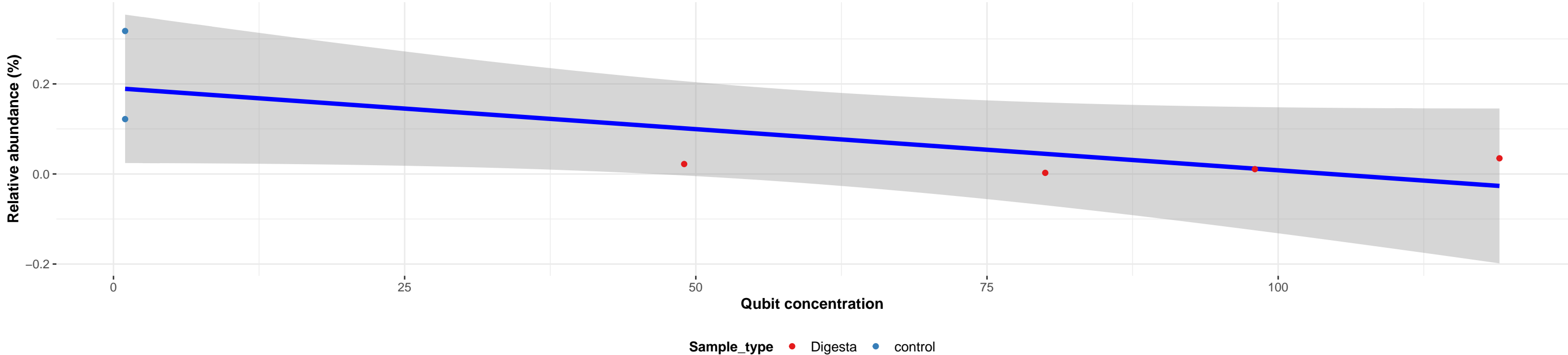


Correlation within: control

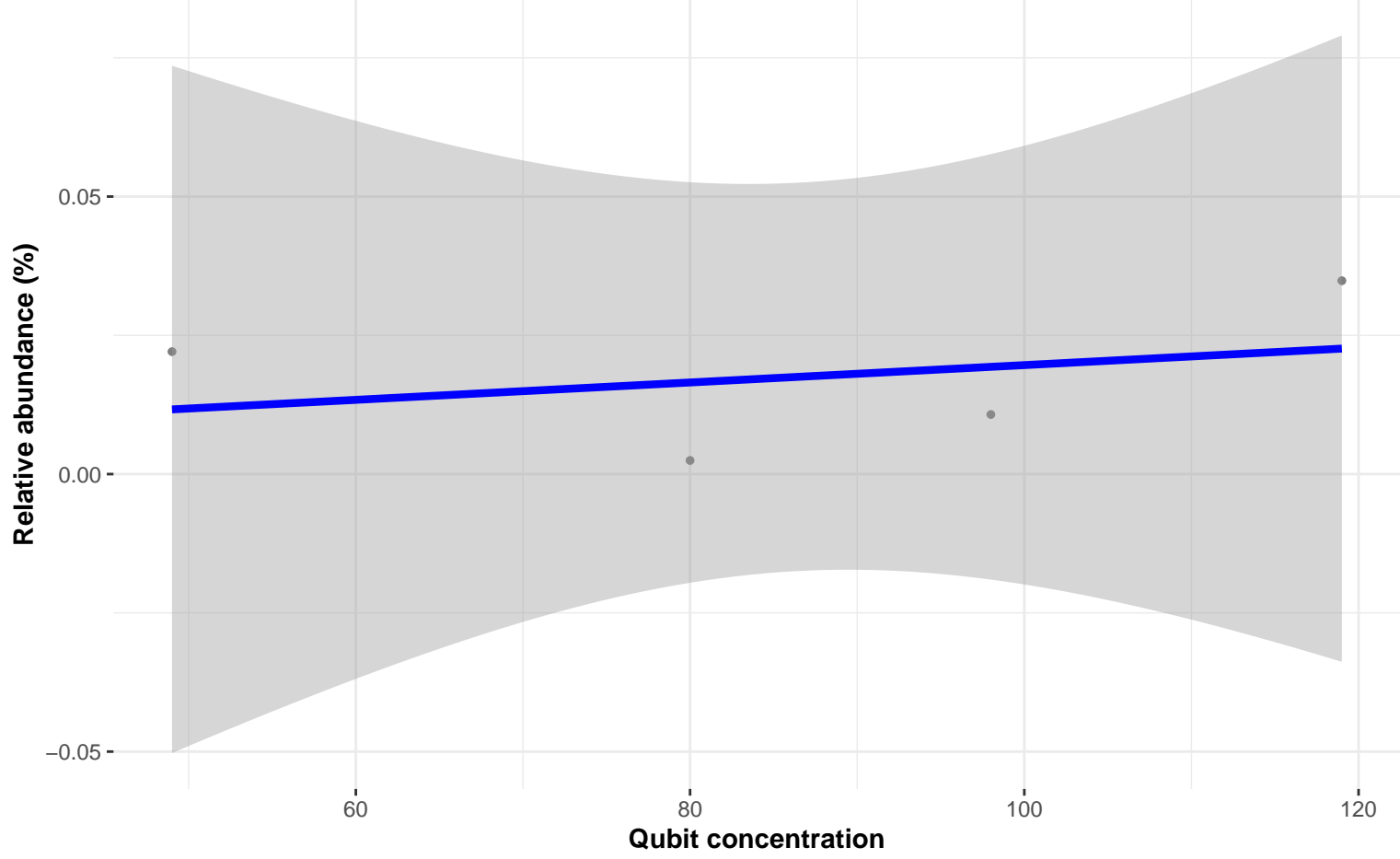


Correlation with all samples

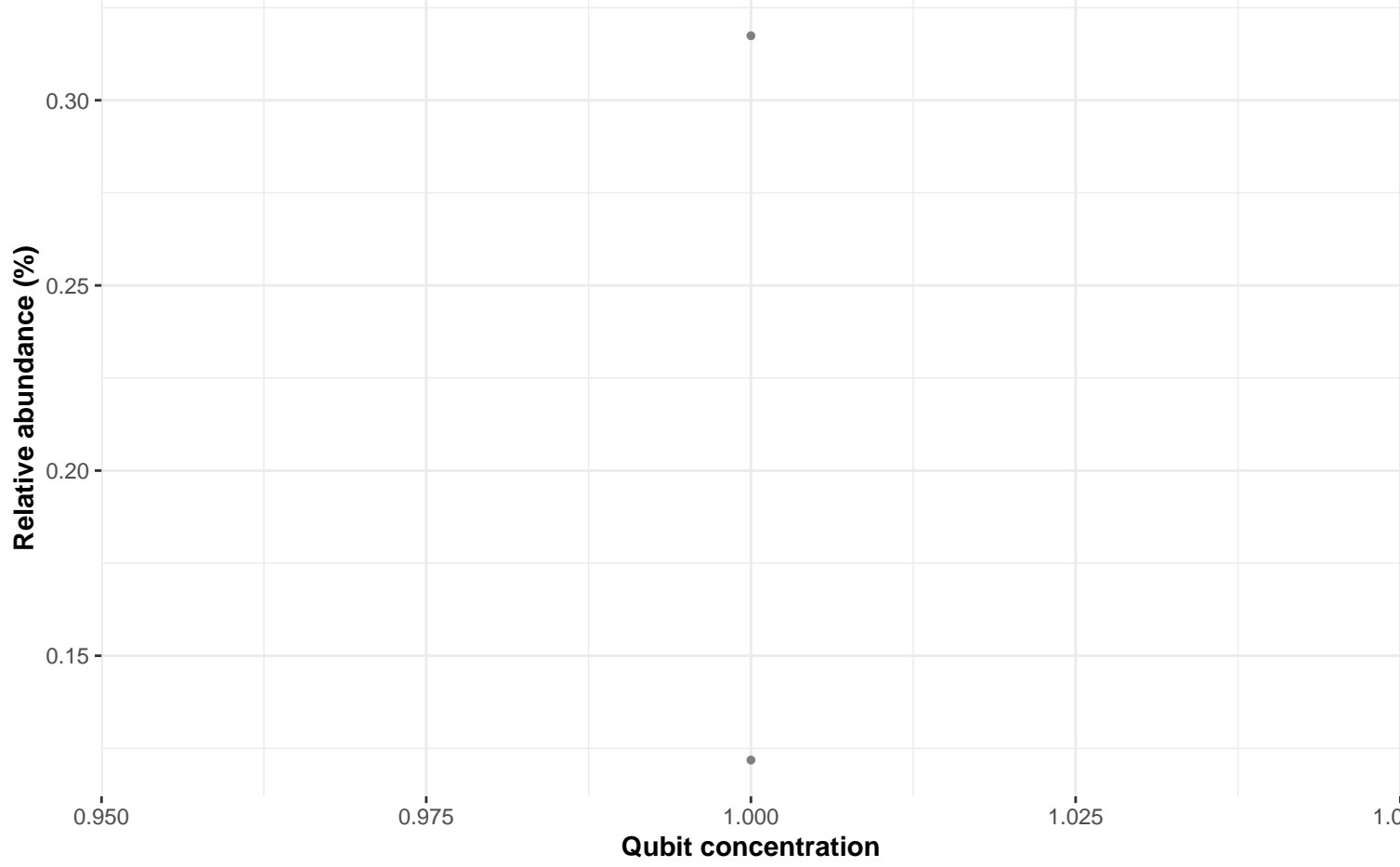
$\log_e(S) = 4.013$, $p = 0.228$, $\hat{\rho}_{\text{Spearman}} = -0.580$, $\text{CI}_{95\%} [-0.950, 0.464]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



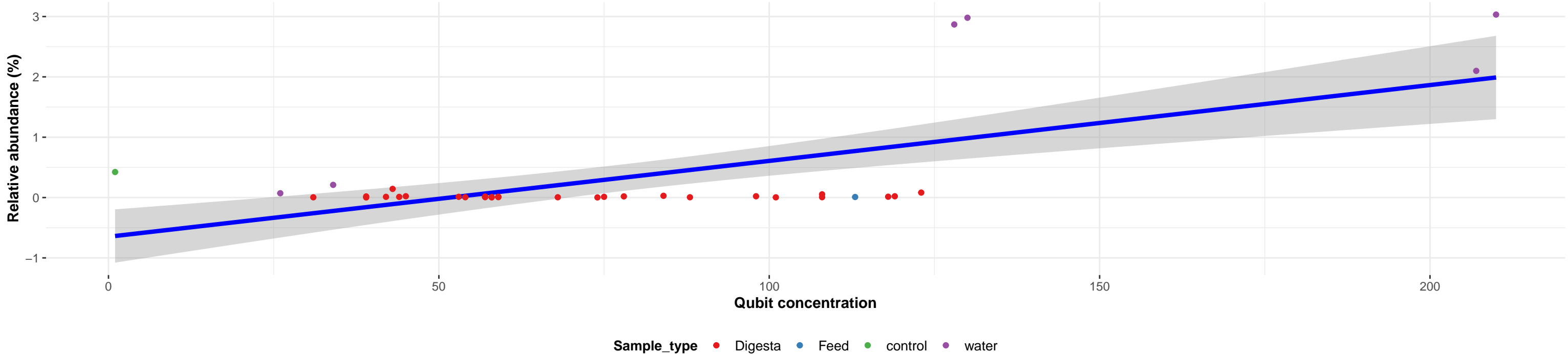
Correlation within: control



Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Sulfitobacter; NA

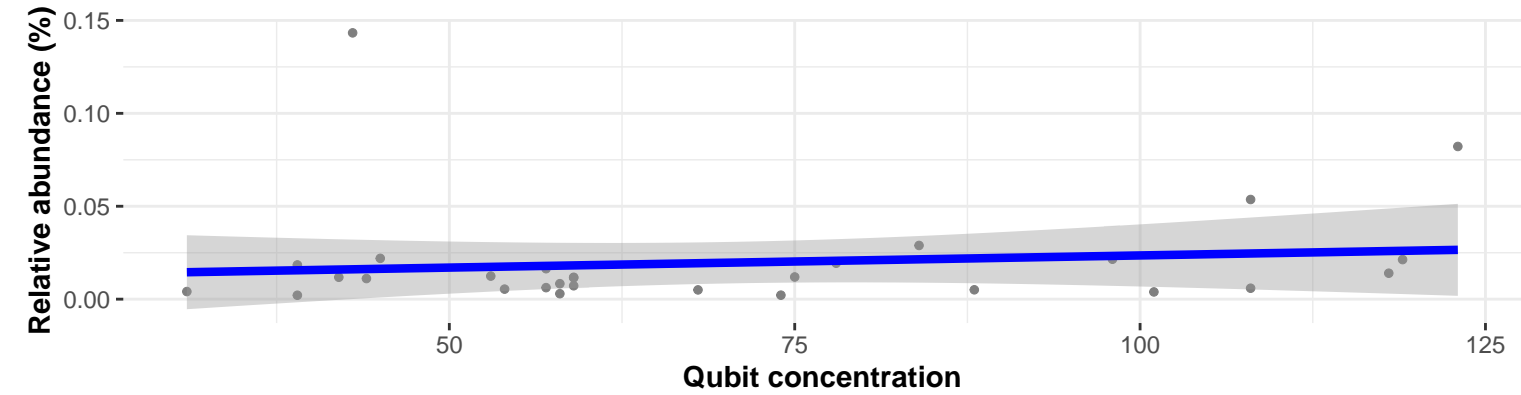
Correlation with all samples

$\log_e(S) = 8.769$, $p = 0.157$, $\hat{\rho}_{\text{Spearman}} = 0.238$, $\text{CI}_{95\%} [-0.103, 0.529]$, $n_{\text{pairs}} = 37$

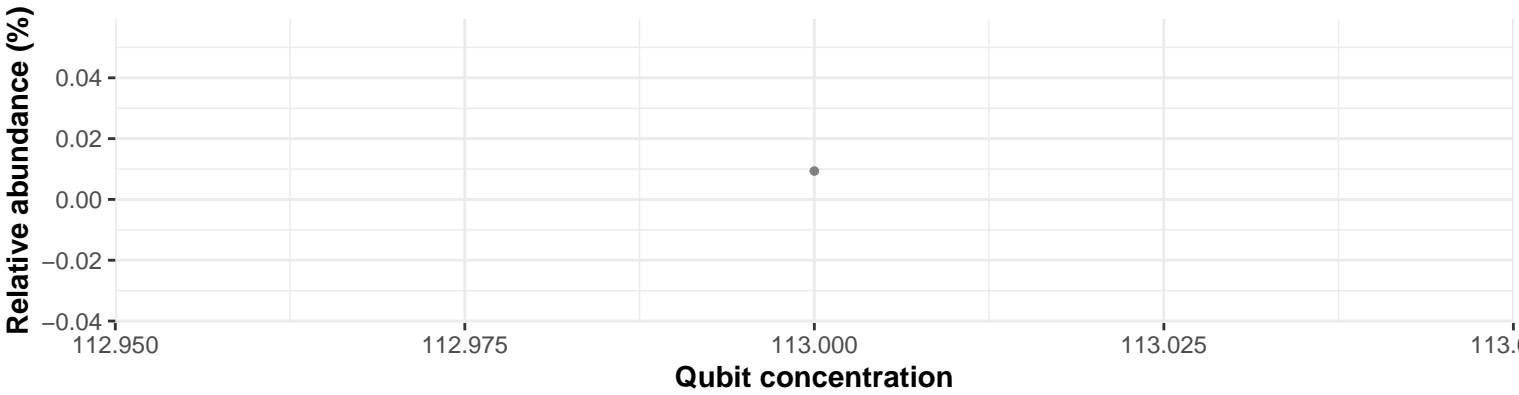


Correlation within: Digesta

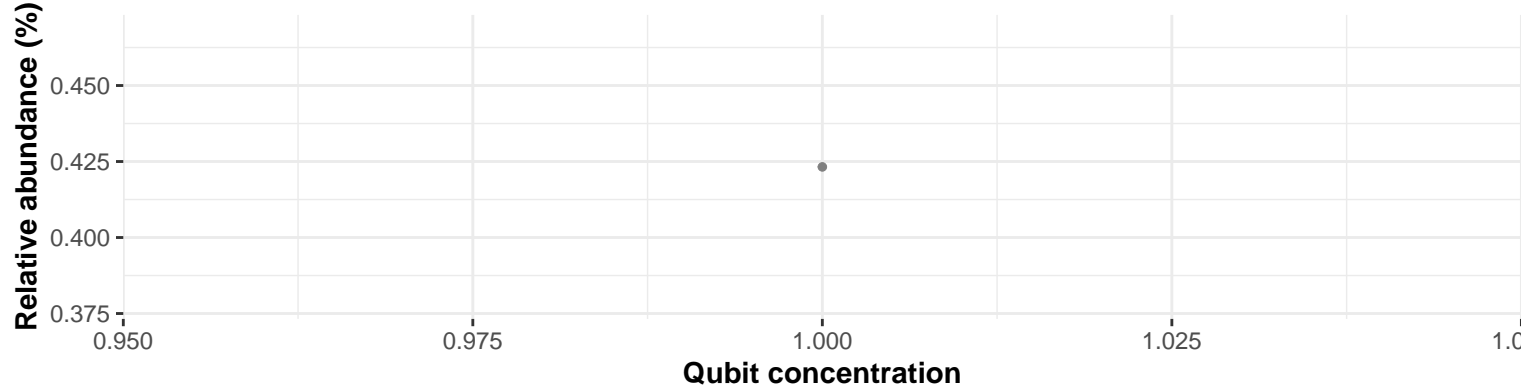
$\log_e(S) = 8.057$, $p = 0.246$, $\hat{\rho}_{\text{Spearman}} = 0.223$, $\text{CI}_{95\%} [-0.168, 0.553]$, $n_{\text{pairs}} = 29$



Correlation within: Feed

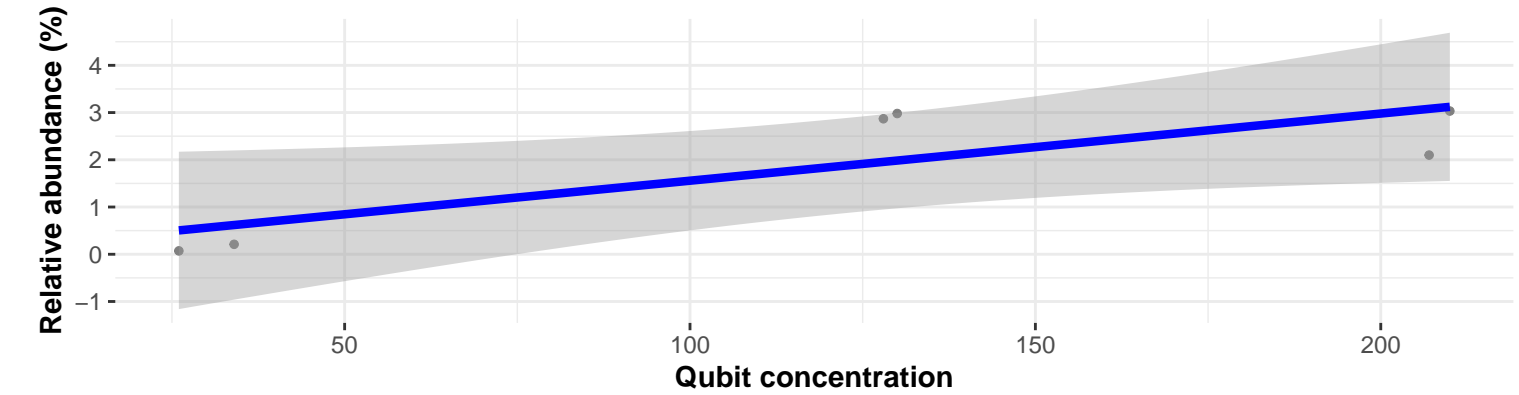


Correlation within: control



Correlation within: water

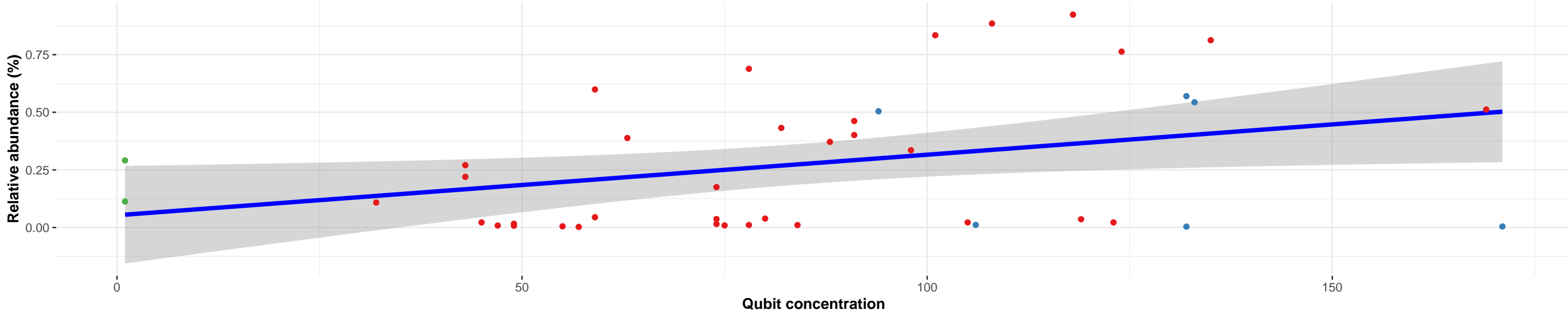
$\log_e(S) = 1.792$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.829$, $\text{CI}_{95\%} [0.019, 0.982]$, $n_{\text{pairs}} = 6$



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; coagulans

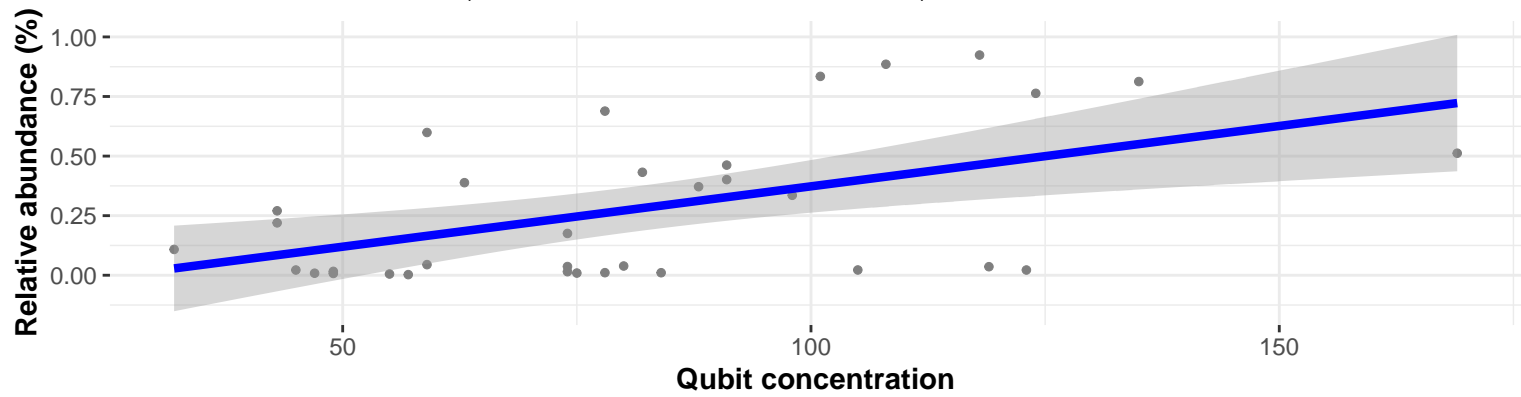
Correlation with all samples

$\log_e(S) = 9.050$, $p = 0.046$, $\hat{\rho}_{\text{Spearman}} = 0.309$, $\text{CI}_{95\%} [-0.003, 0.567]$, $n_{\text{pairs}} = 42$



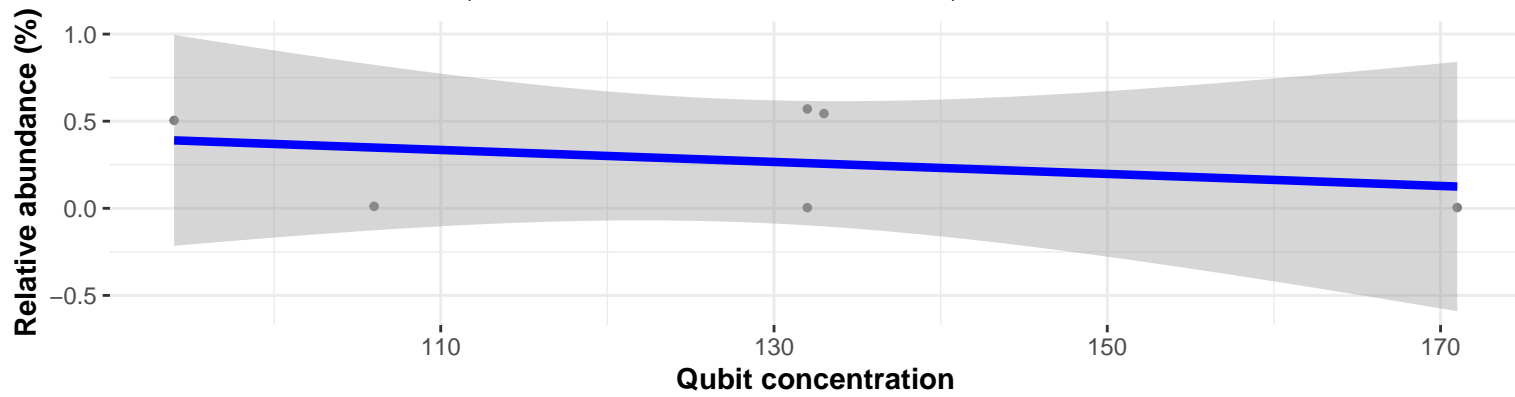
Correlation within: Digesta

$\log_e(S) = 8.074$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.509$, $\text{CI}_{95\%} [0.197, 0.728]$, $n_{\text{pairs}} = 34$

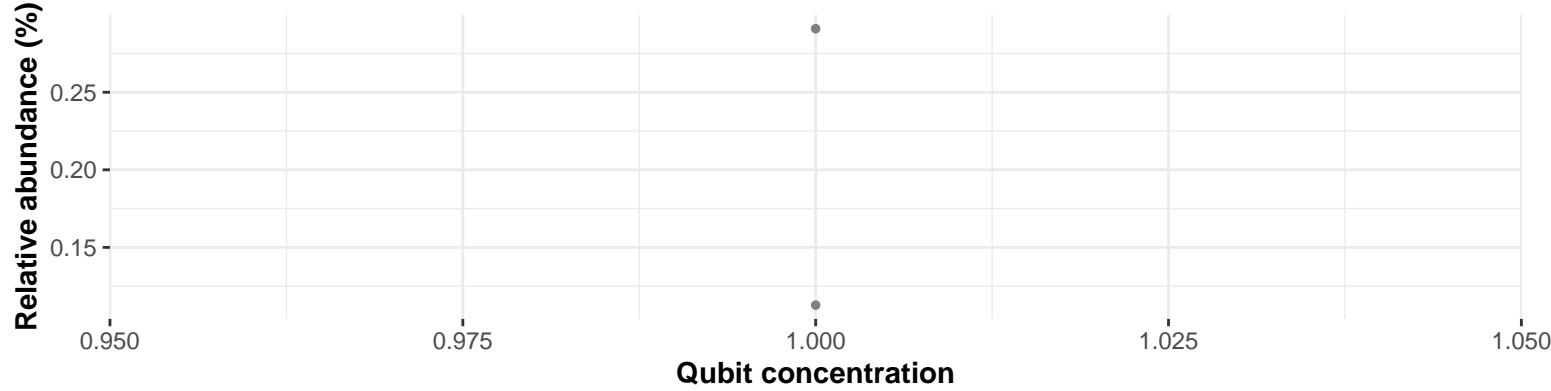


Correlation within: Feed

$\log_e(S) = 3.665$, $p = 0.827$, $\hat{\rho}_{\text{Spearman}} = -0.116$, $\text{CI}_{95\%} [-0.857, 0.781]$, $n_{\text{pairs}} = 6$



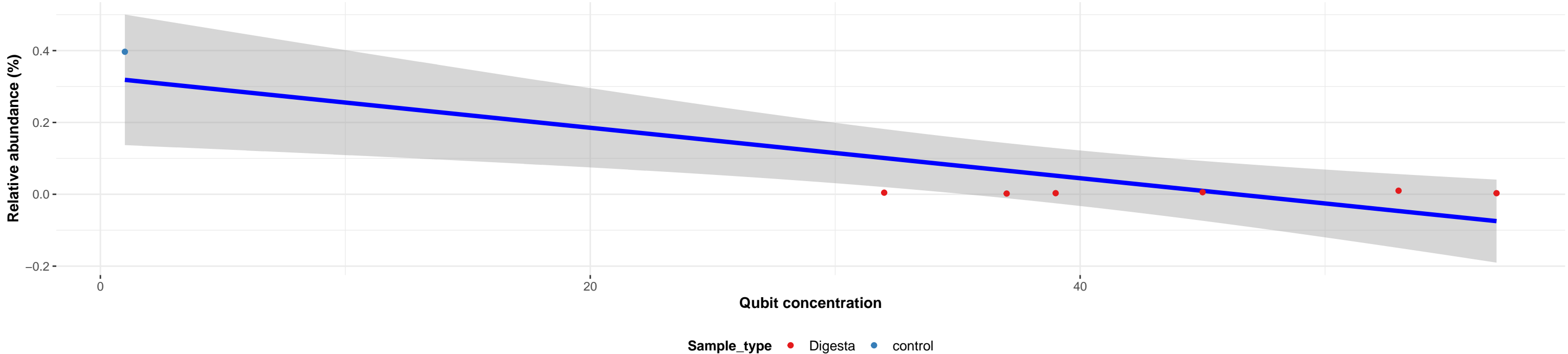
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

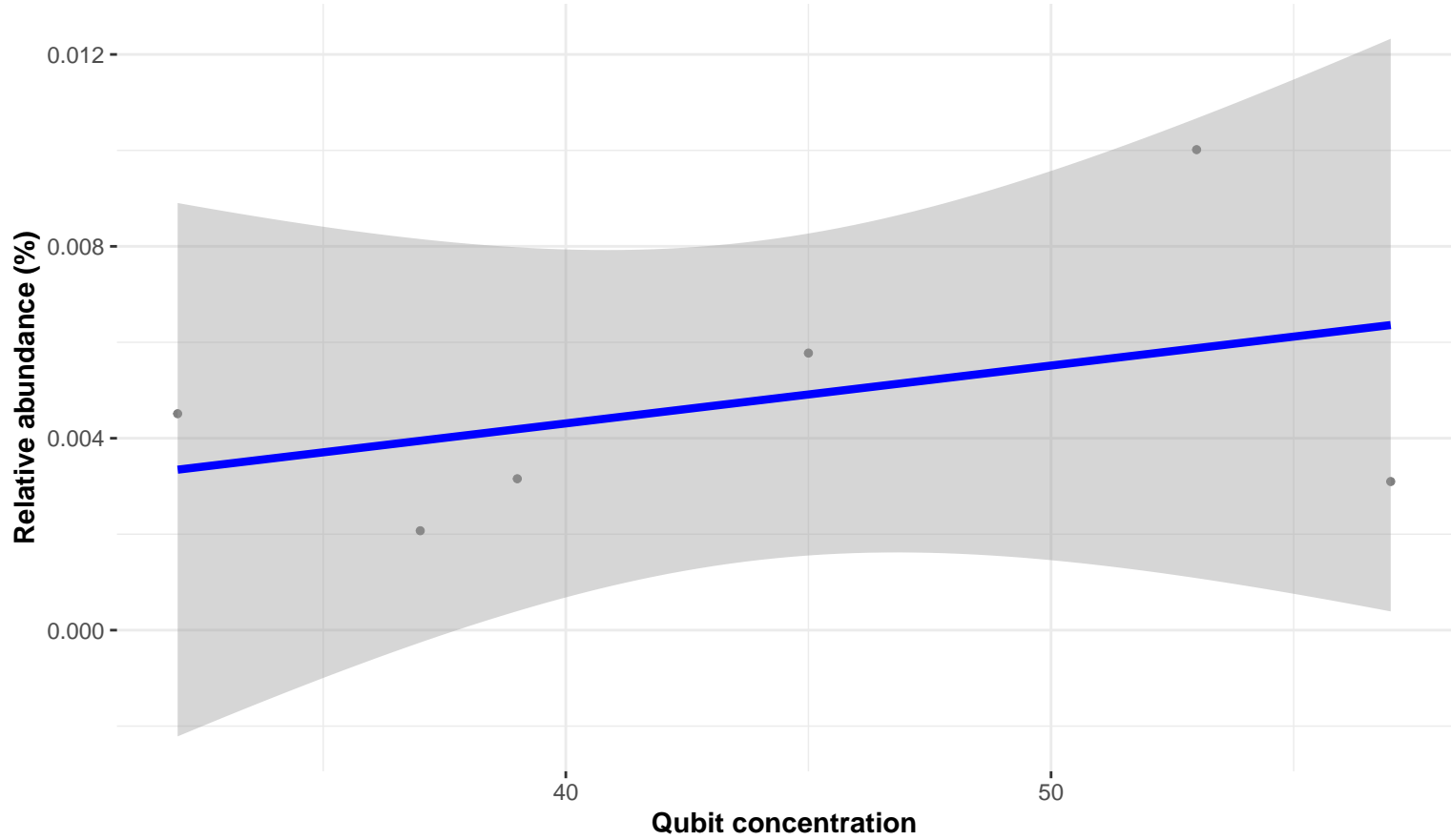
Correlation with all samples

$\log_e(S) = 4.248$, $p = 0.589$, $\hat{\rho}_{\text{Spearman}} = -0.250$, $\text{CI}_{95\%} [-0.852, 0.637]$, $n_{\text{pairs}} = 7$

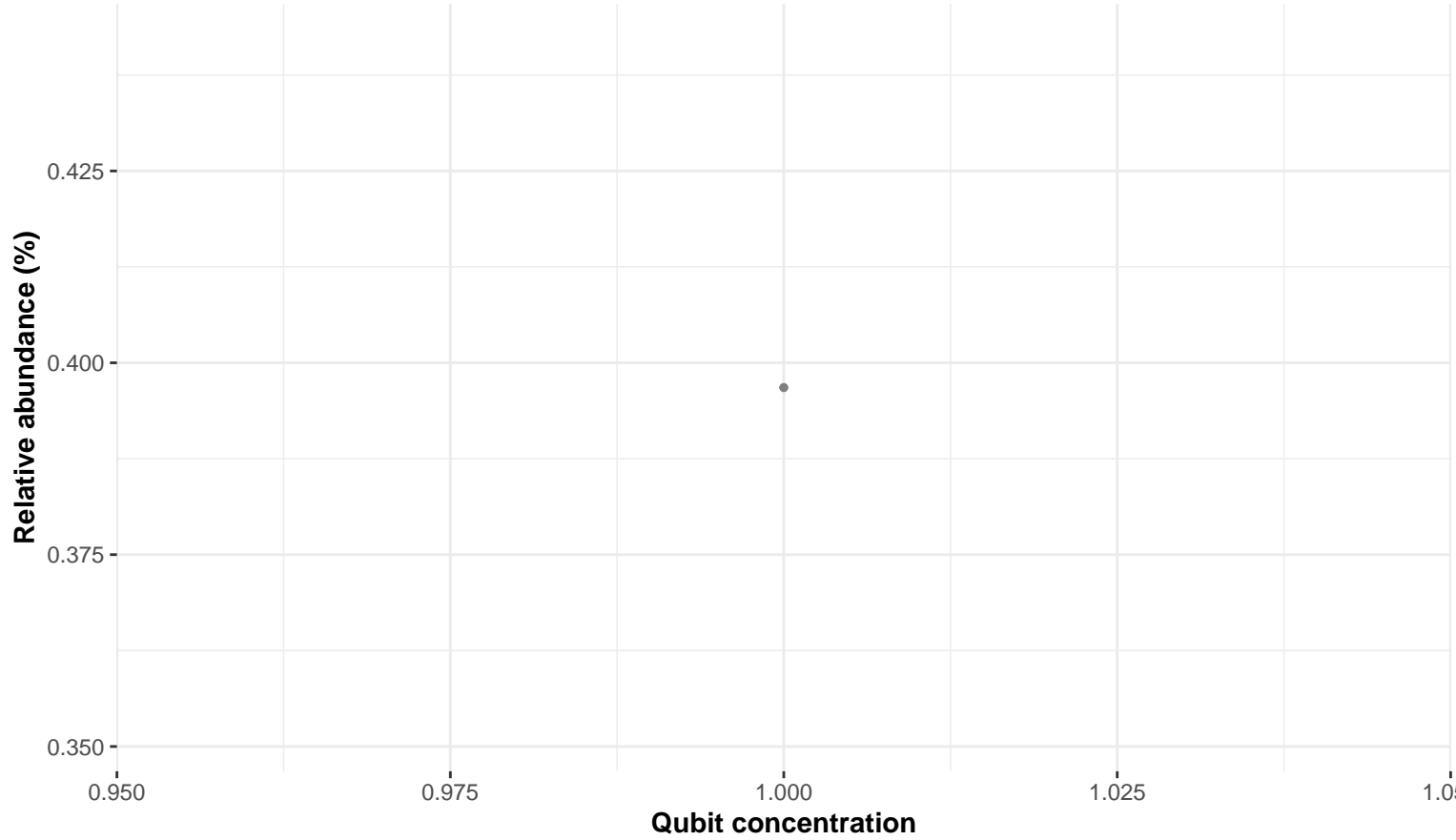


Correlation within: Digesta

$\log_e(S) = 3.332$, $p = 0.704$, $\hat{\rho}_{\text{Spearman}} = 0.200$, $\text{CI}_{95\%} [-0.745, 0.878]$, $n_{\text{pairs}} = 6$



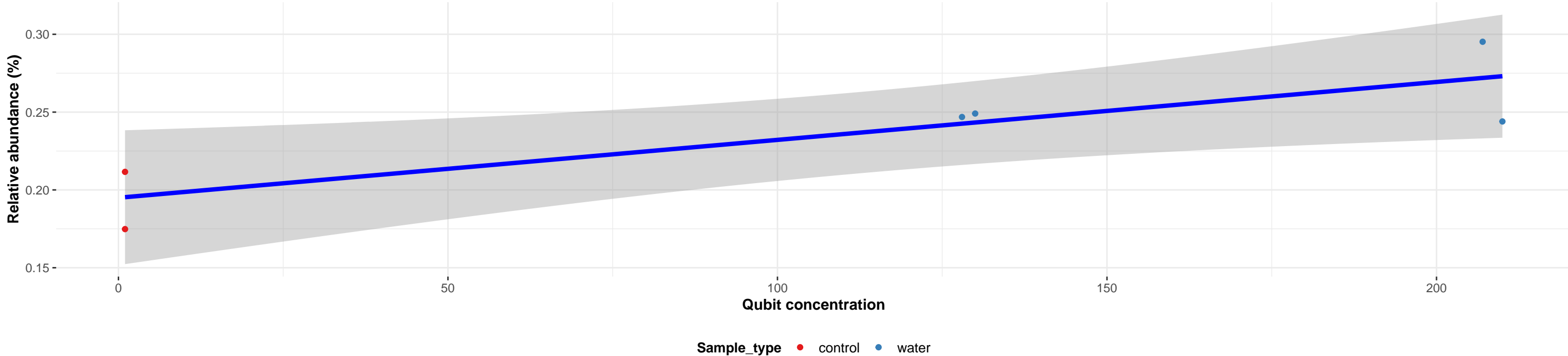
Correlation within: control



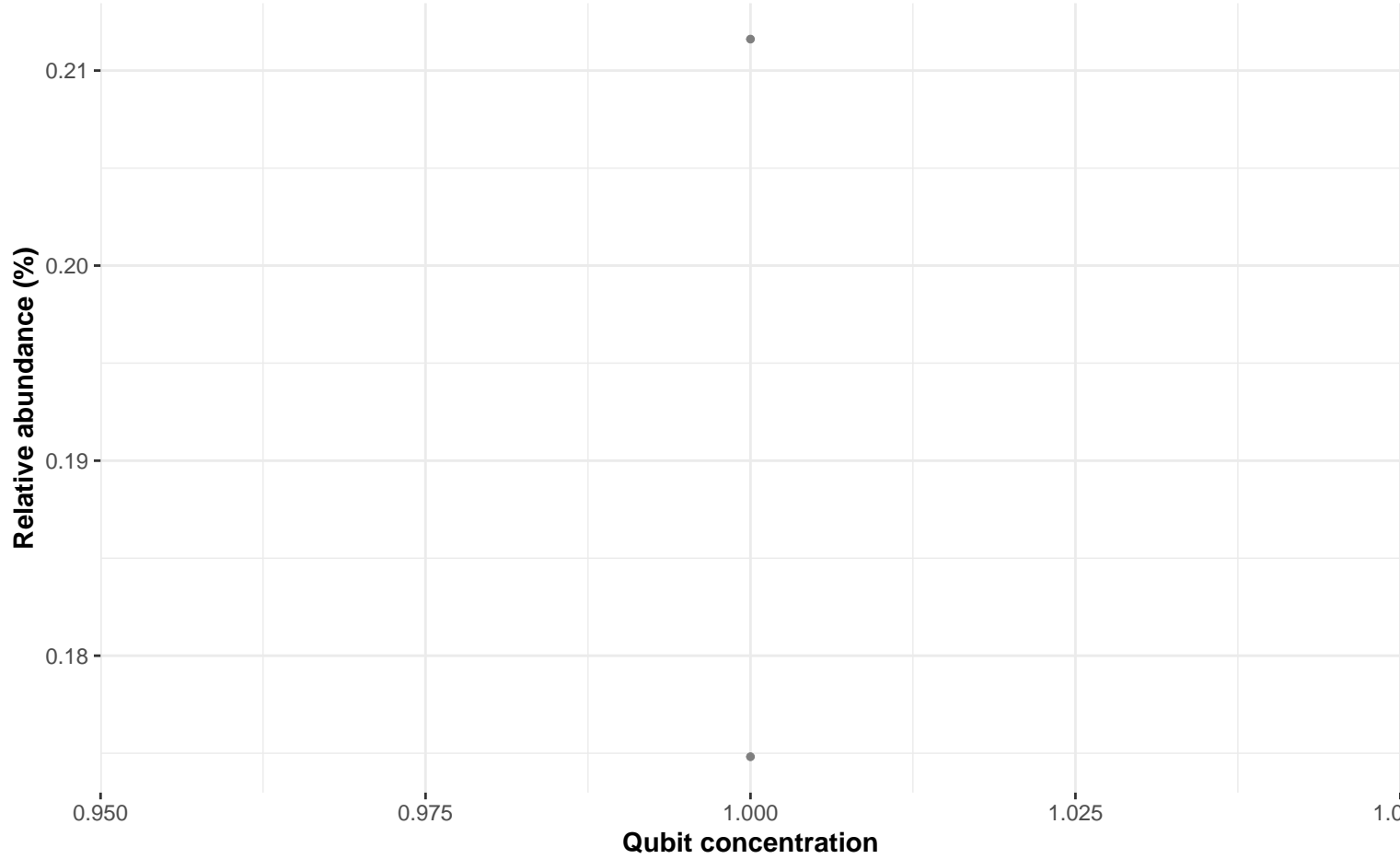
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Yoonia–Loktanelle; NA

Correlation with all samples

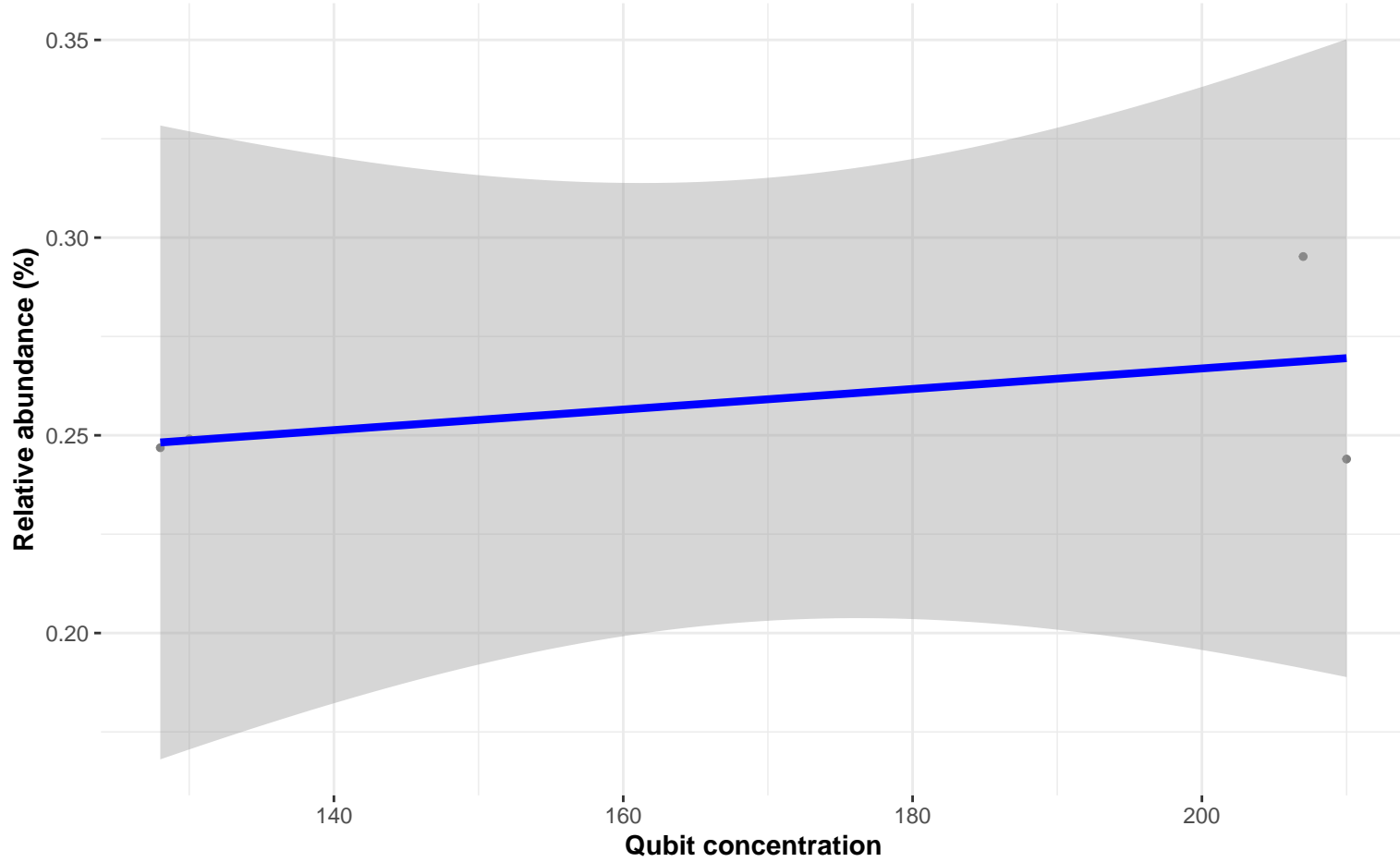
$\log_e(S) = 2.540$, $p = 0.173$, $\hat{\rho}_{\text{Spearman}} = 0.638$, $CI_{95\%} [-0.389, 0.958]$, $n_{\text{pairs}} = 6$



Correlation within: control



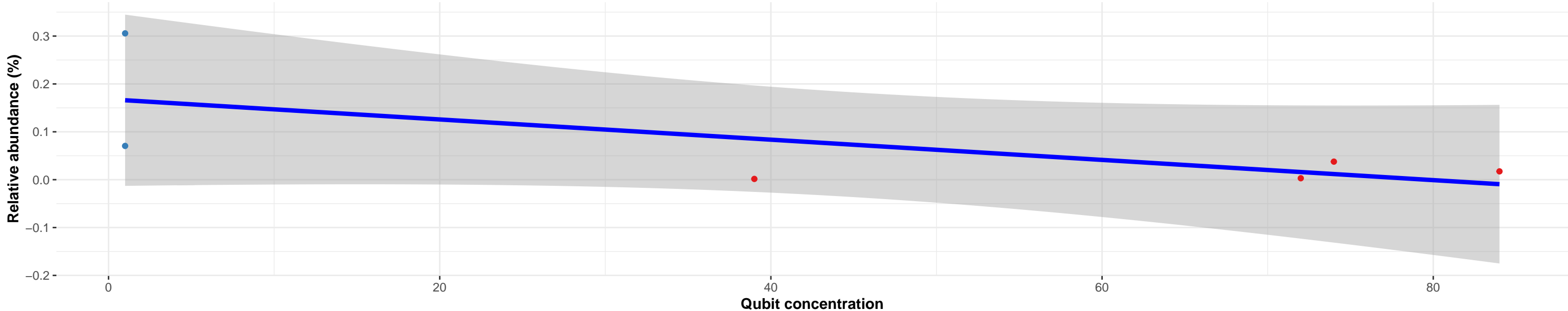
Correlation within: water



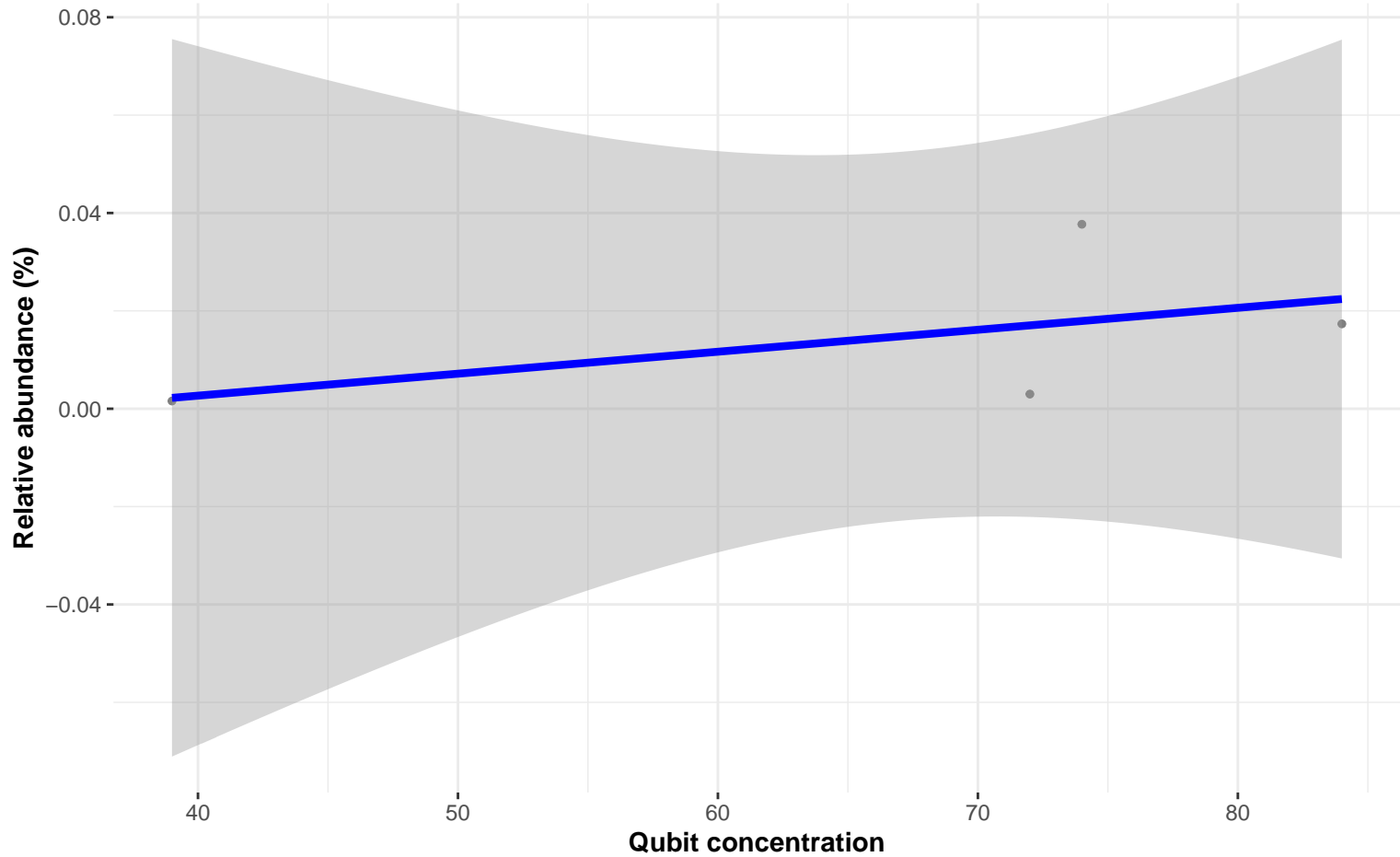
Bacteria; Bacteroidota; Bacteroidia; Sphingobacteriales; Sphingobacteriaceae; Pedobacter; NA

Correlation with all samples

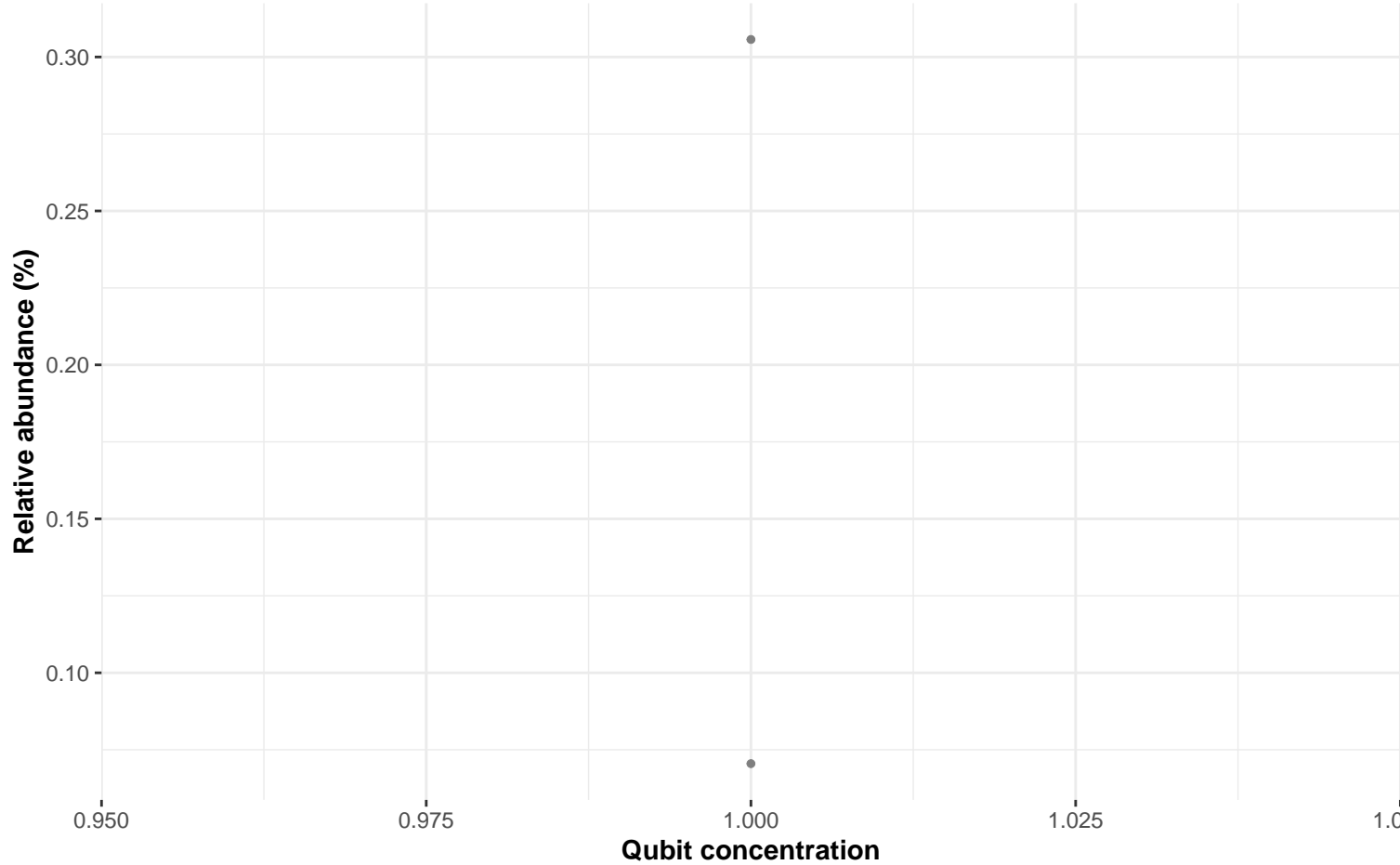
$\log_e(S) = 3.936$, $p = 0.354$, $\hat{\rho}_{\text{Spearman}} = -0.464$, $\text{CI}_{95\%} [-0.931, 0.580]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



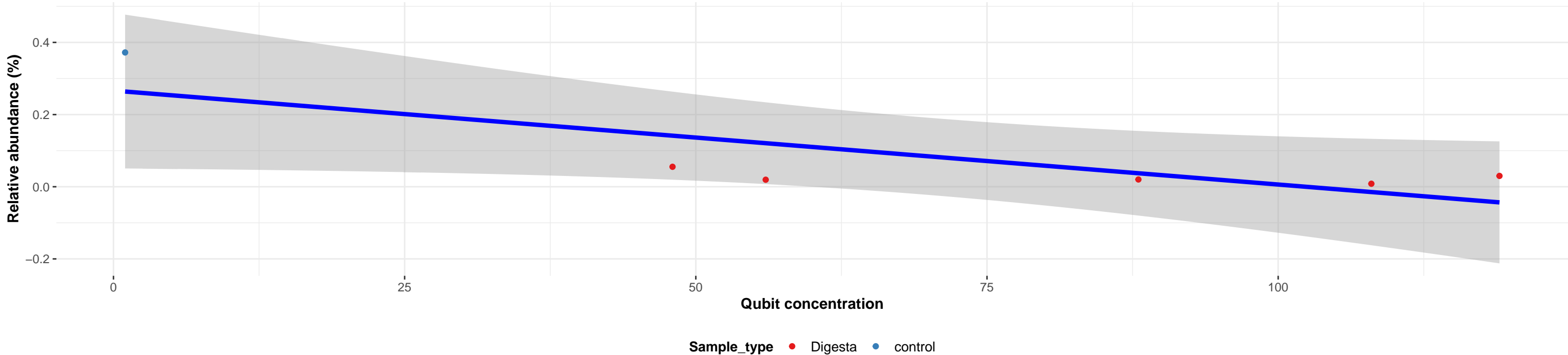
Correlation within: control



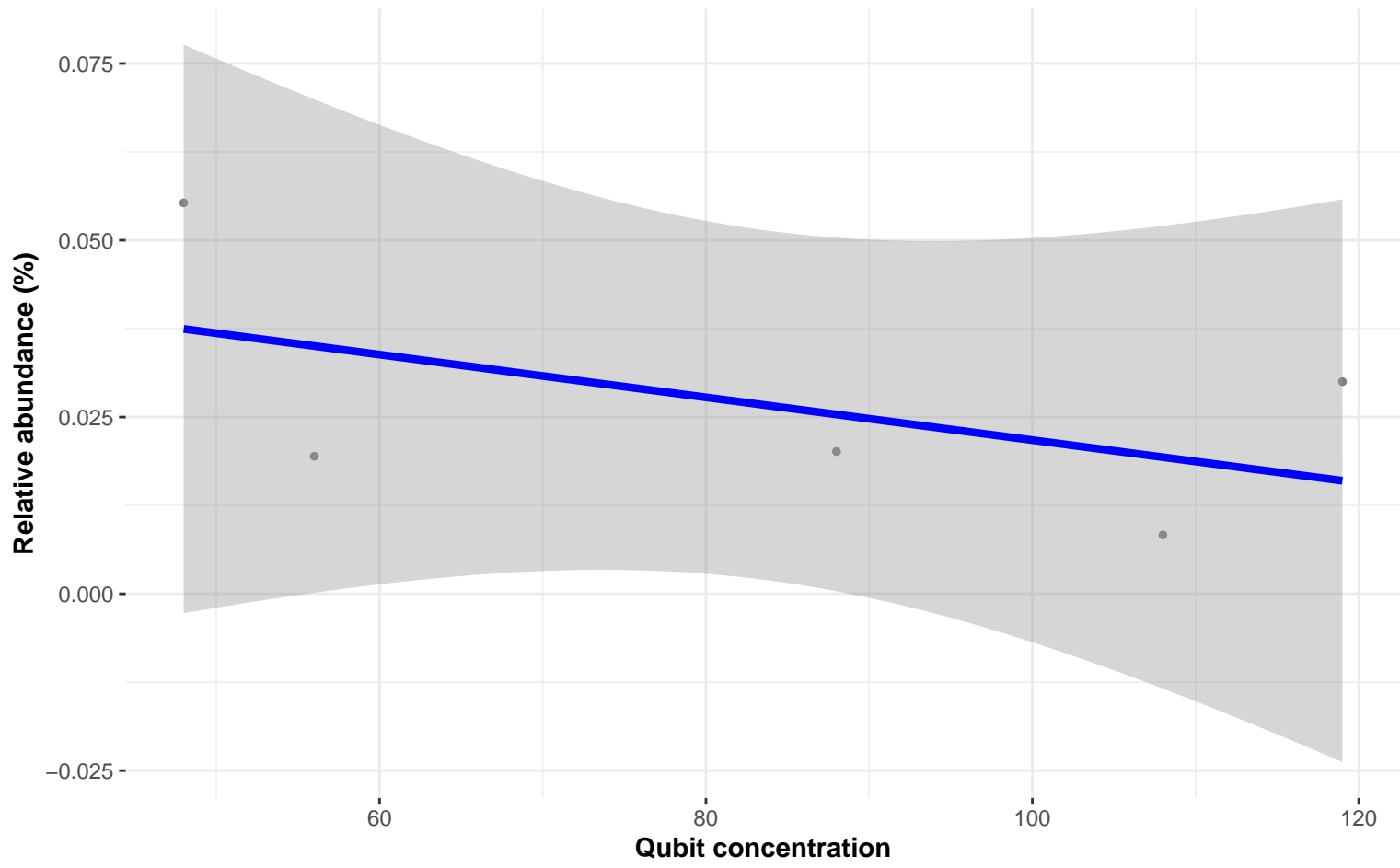
Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Staphylococcus; NA

Correlation with all samples

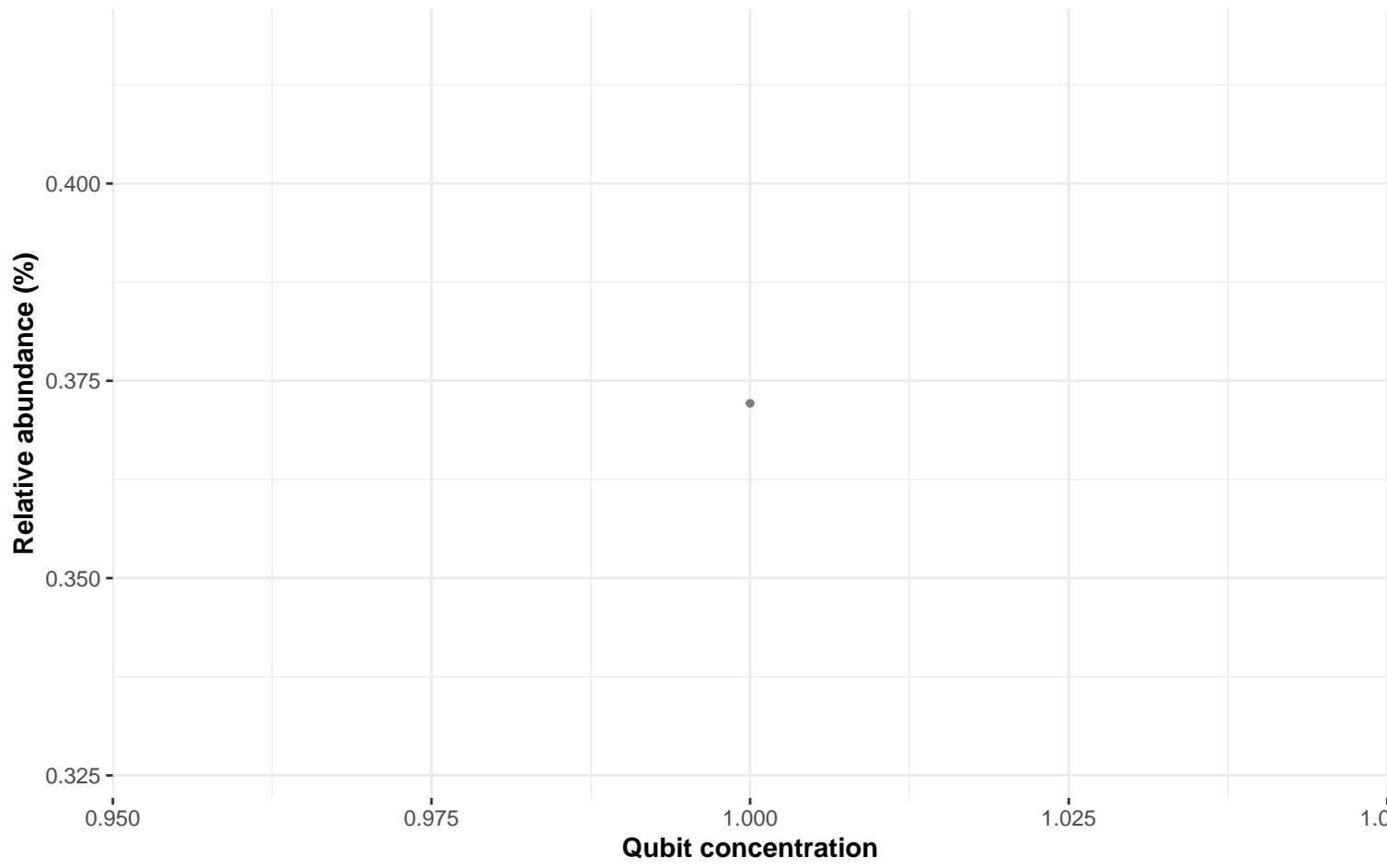
$\log_e(S) = 4.025$, $p = 0.208$, $\hat{\rho}_{\text{Spearman}} = -0.600$, $CI_{95\%} [-0.953, 0.440]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



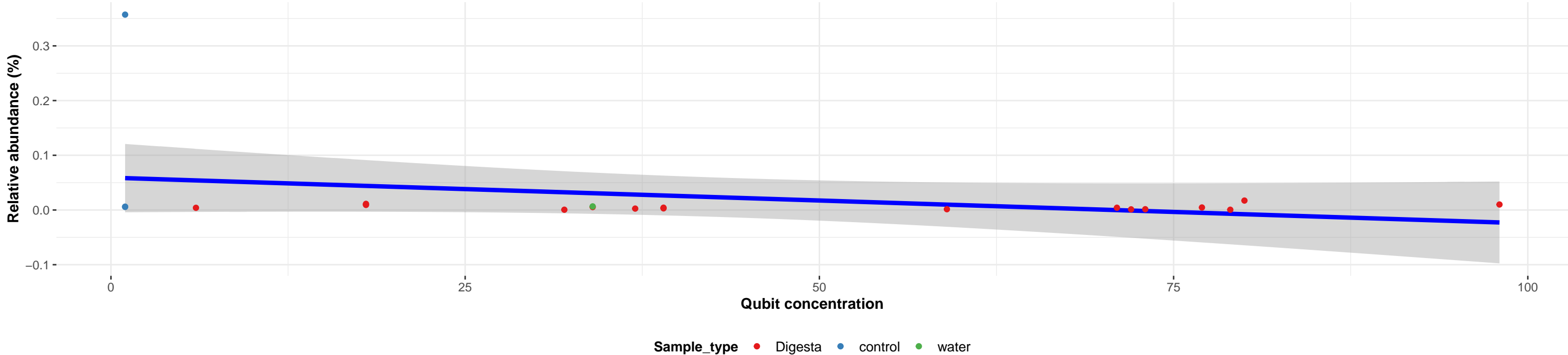
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; faecalis

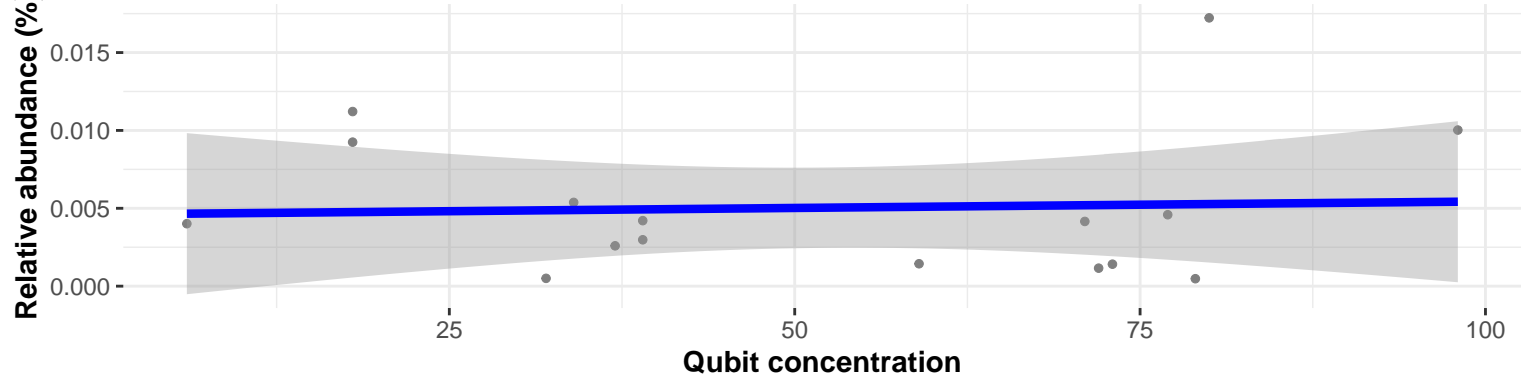
Correlation with all samples

$\log_e(S) = 7.441$, $p = 0.228$, $\hat{\rho}_{\text{Spearman}} = -0.282$, $\text{CI}_{95\%} [-0.652, 0.197]$, $n_{\text{pairs}} = 20$

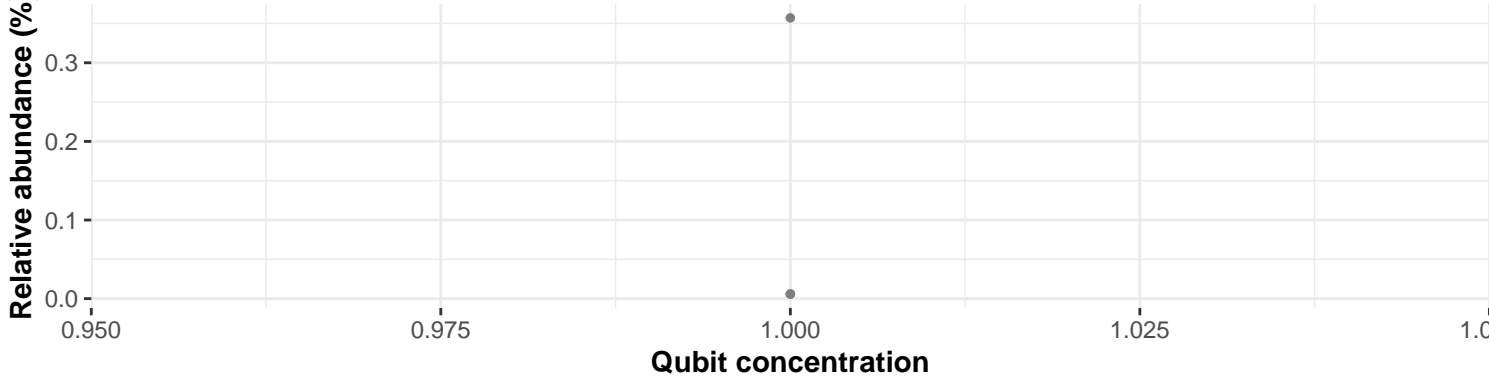


Correlation within: Digesta

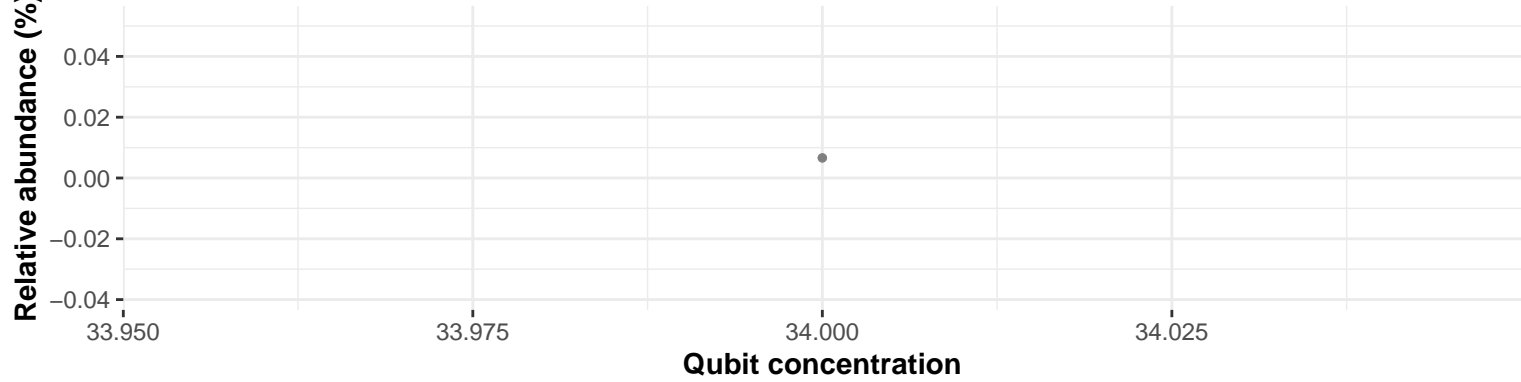
$\log_e(S) = 6.550$, $p = 0.918$, $\hat{\rho}_{\text{Spearman}} = -0.028$, $\text{CI}_{95\%} [-0.528, 0.487]$, $n_{\text{pairs}} = 16$



Correlation within: control



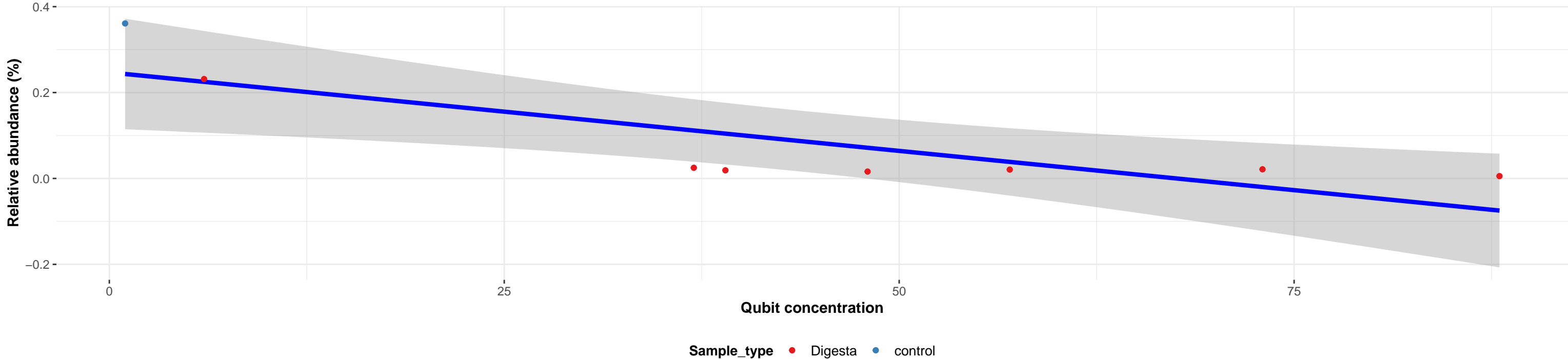
Correlation within: water



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Staphylococcus; NA

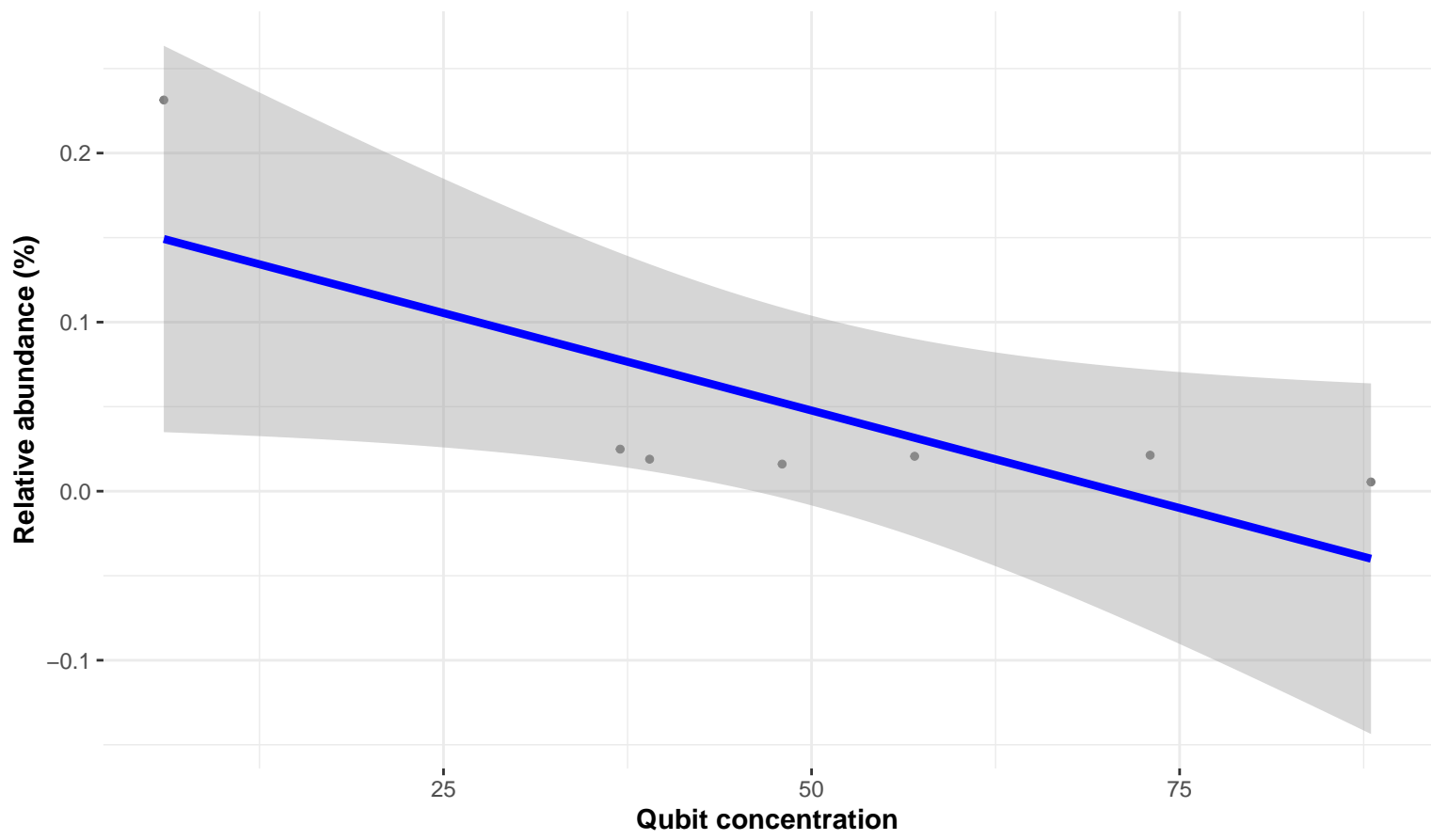
Correlation with all samples

$\log_e(S) = 5.011$, $p = 0.021$, $\hat{\rho}_{\text{Spearman}} = -0.786$, $\text{CI}_{95\%} [-0.961, -0.156]$, $n_{\text{pairs}} = 8$

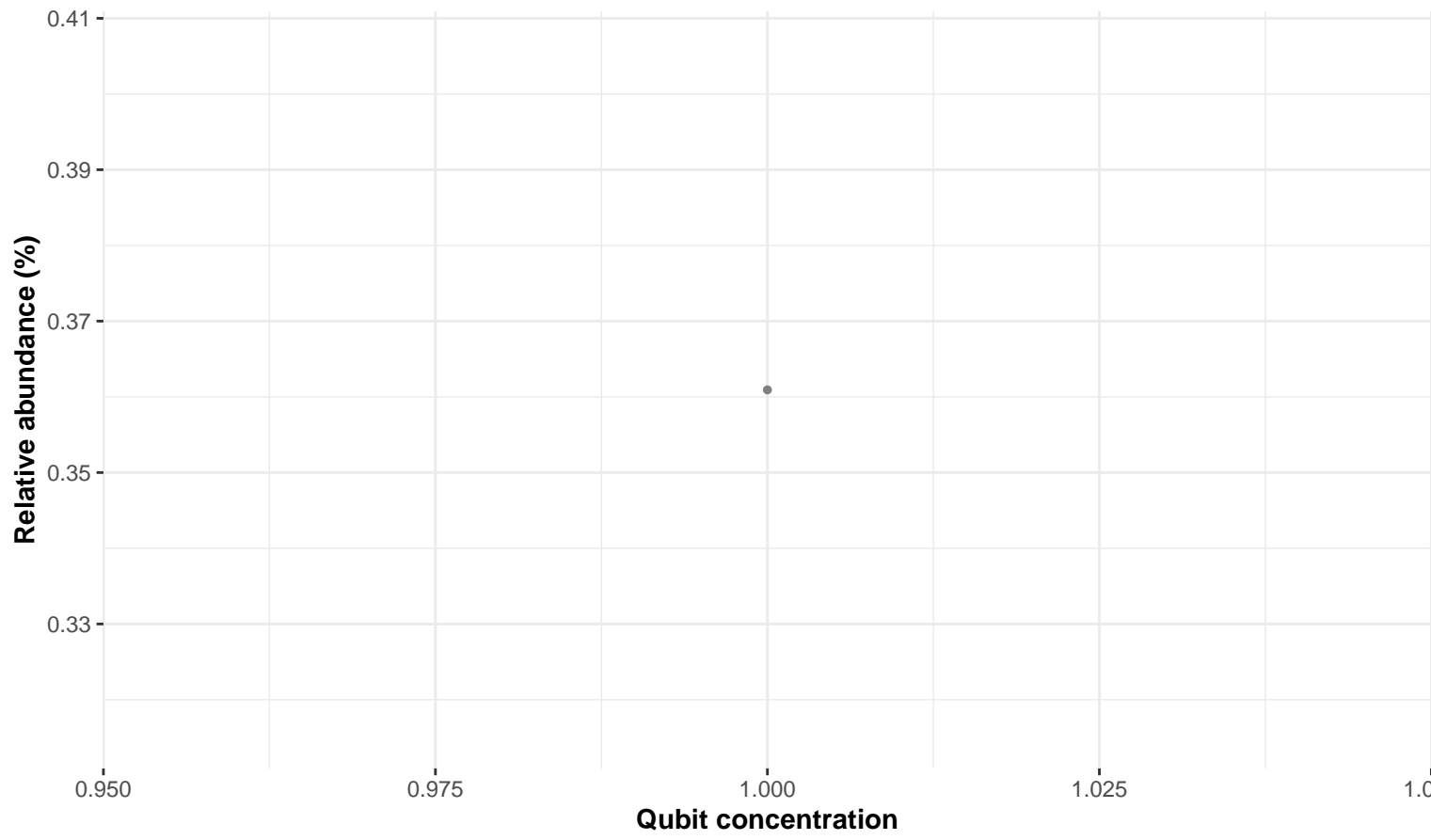


Correlation within: Digesta

$\log_e(S) = 4.543$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = -0.679$, $\text{CI}_{95\%} [-0.950, 0.180]$, $n_{\text{pairs}} = 7$



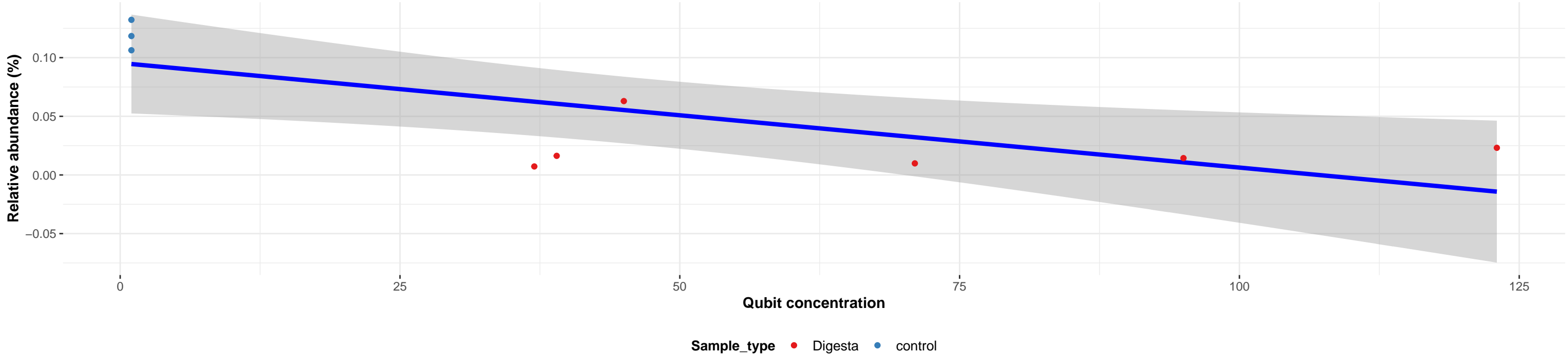
Correlation within: control



Bacteria; Firmicutes; Bacilli; Thermicanales; Thermicanaceae; Thermicanus; NA

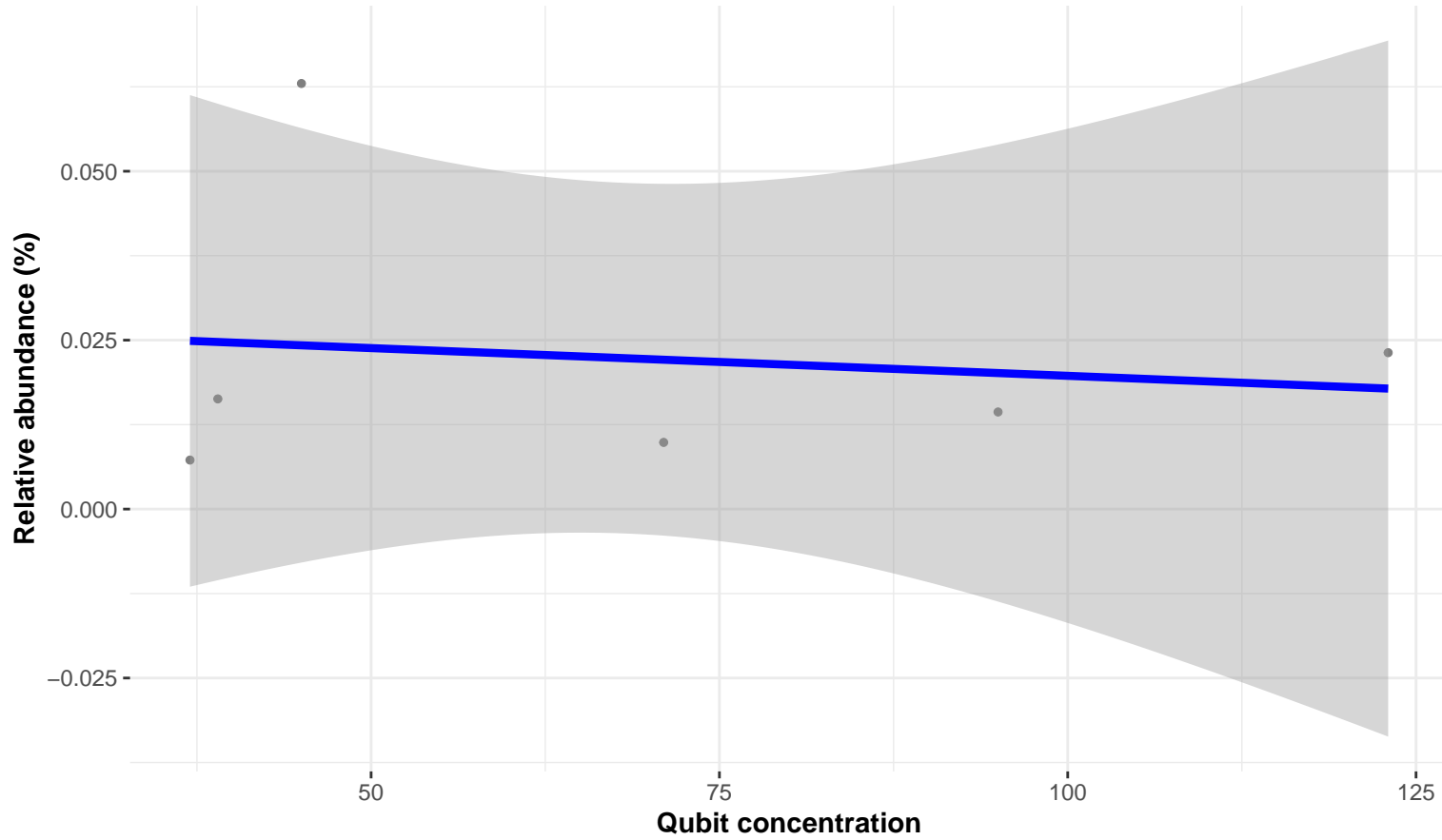
Correlation with all samples

$\log_e(S) = 5.243$, $p = 0.104$, $\hat{\rho}_{\text{Spearman}} = -0.576$, $\text{CI}_{95\%} [-0.902, 0.165]$, $n_{\text{pairs}} = 9$

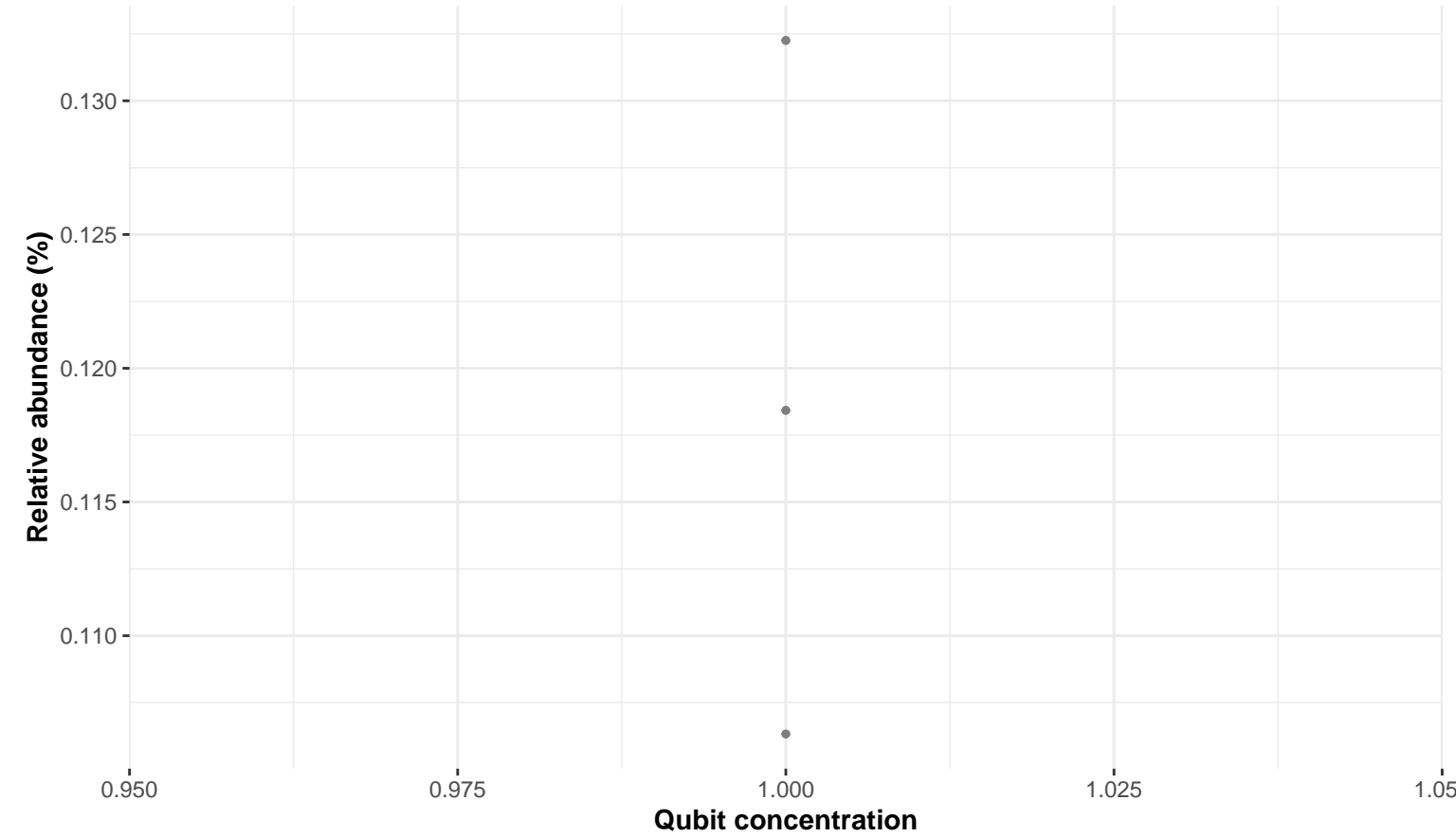


Correlation within: Digesta

$\log_e(S) = 3.091$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = 0.371$, $\text{CI}_{95\%} [-0.650, 0.915]$, $n_{\text{pairs}} = 6$



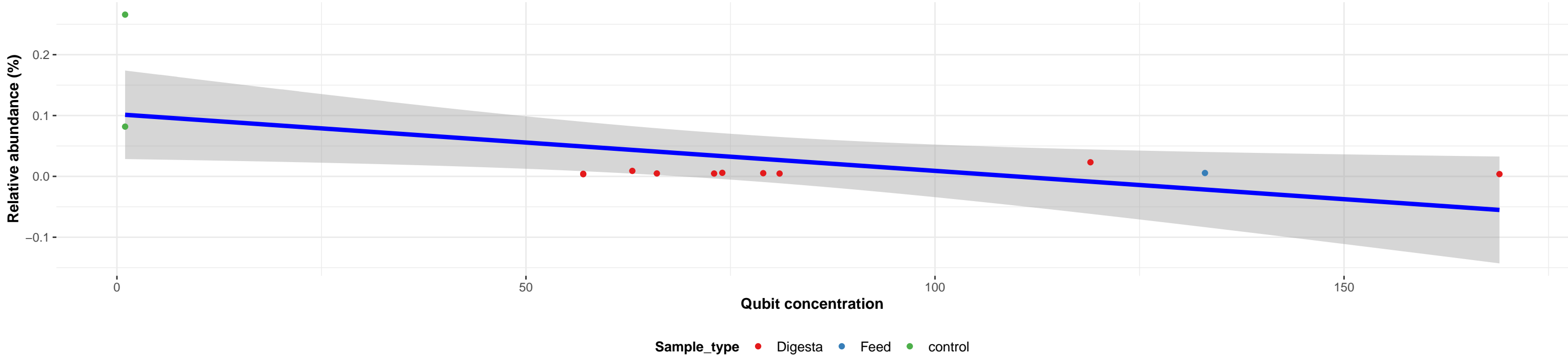
Correlation within: control



Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Beijerinckiaceae; Methylobacterium–Methylorubrum; NA

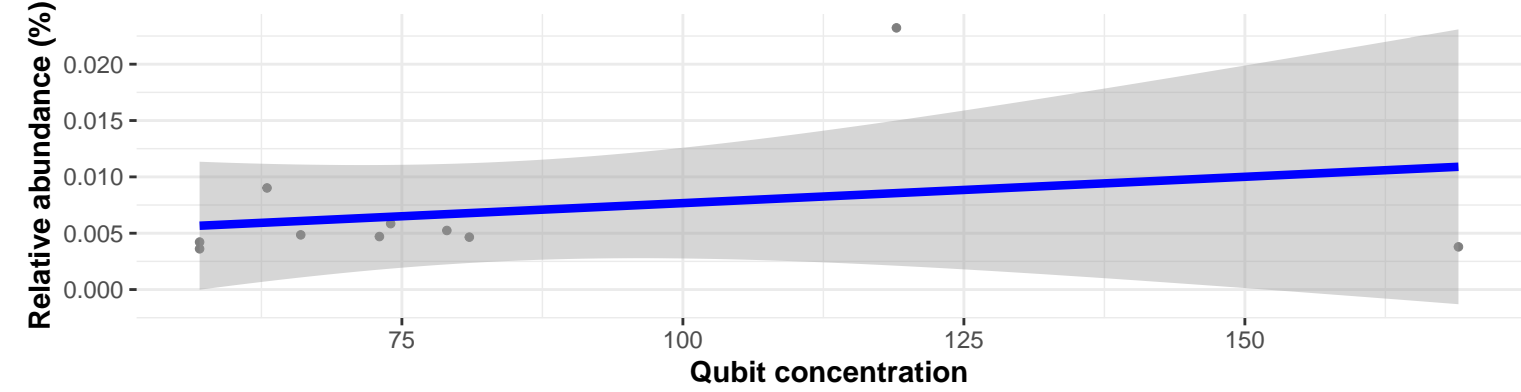
Correlation with all samples

$\log_e(S) = 6.125$, $p = 0.398$, $\hat{\rho}_{\text{Spearman}} = -0.256$, $\text{CI}_{95\%} [-0.716, 0.359]$, $n_{\text{pairs}} = 13$

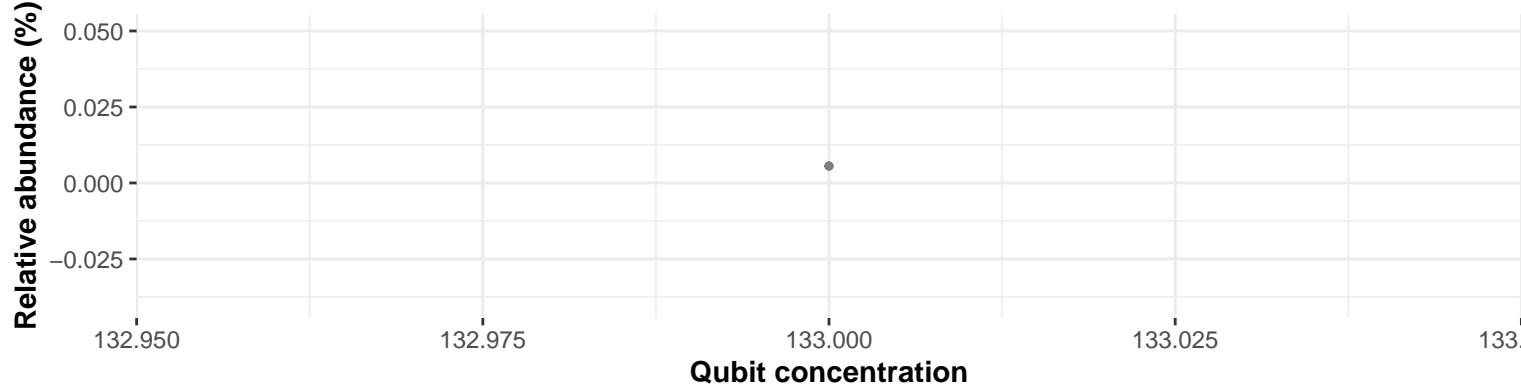


Correlation within: Digesta

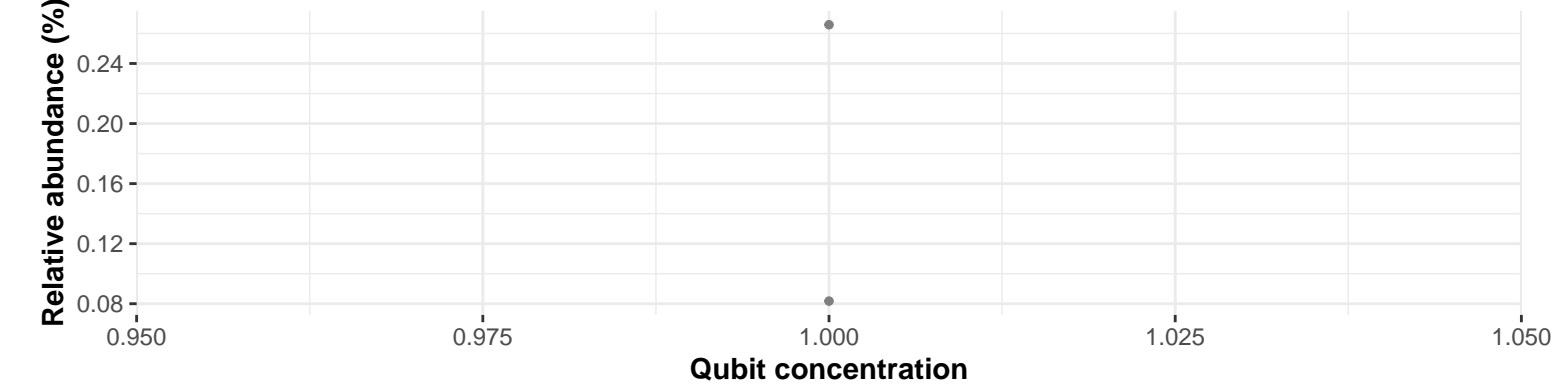
$\log_e(S) = 4.851$, $p = 0.532$, $\hat{\rho}_{\text{Spearman}} = 0.225$, $\text{CI}_{95\%} [-0.488, 0.758]$, $n_{\text{pairs}} = 10$



Correlation within: Feed



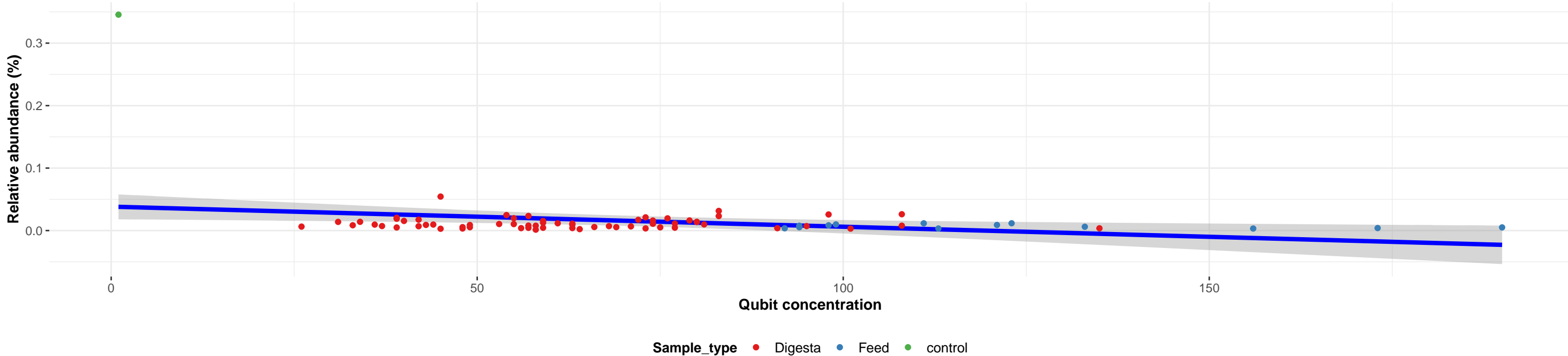
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; NA

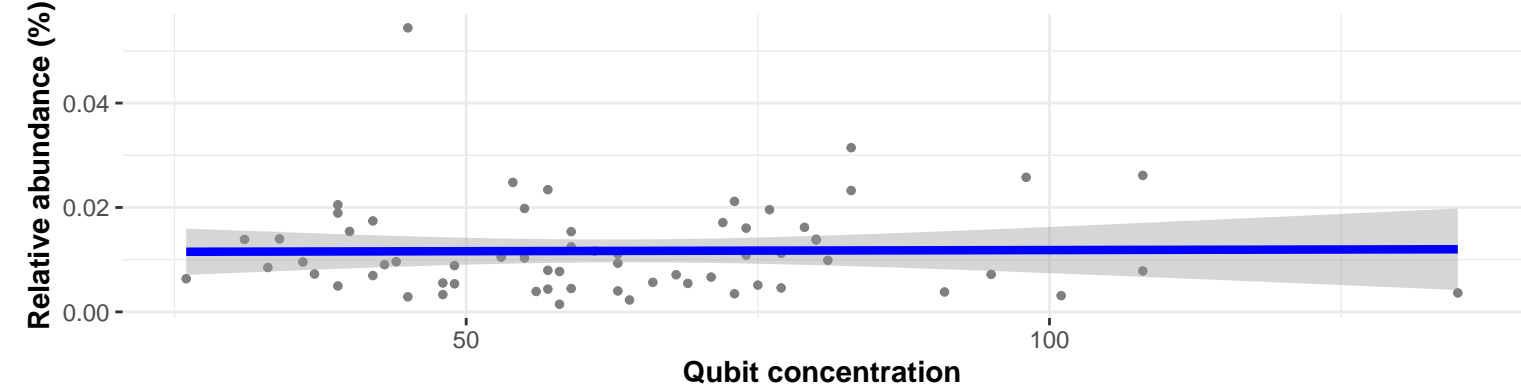
Correlation with all samples

$\log_e(S) = 11.517$, $p = 0.116$, $\hat{\rho}_{\text{Spearman}} = -0.177$, $\text{CI}_{95\%} [-0.387, 0.051]$, $n_{\text{pairs}} = 80$



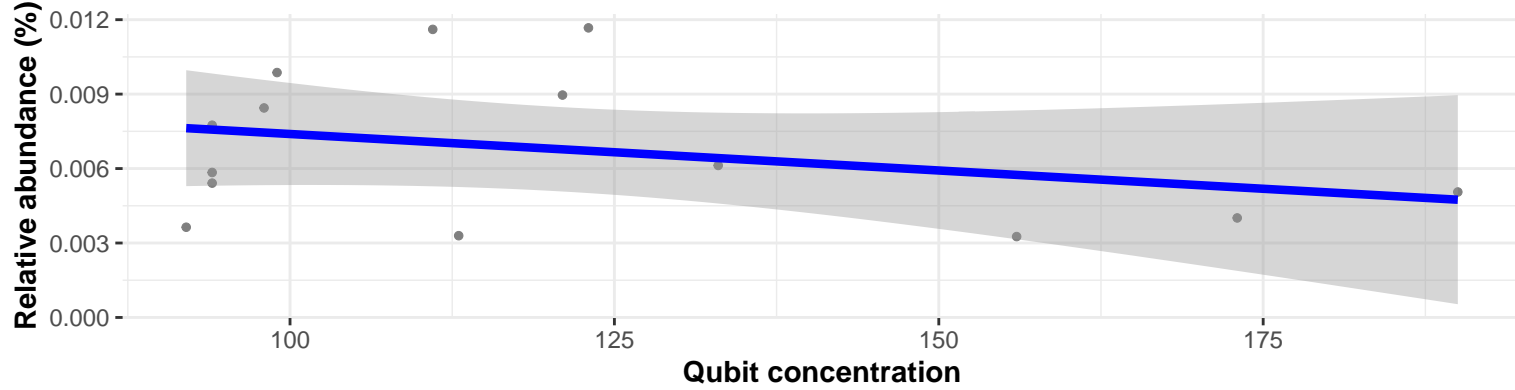
Correlation within: Digesta

$\log_e(S) = 10.707$, $p = 0.850$, $\hat{\rho}_{\text{Spearman}} = 0.024$, $\text{CI}_{95\%} [-0.228, 0.273]$, $n_{\text{pairs}} = 65$

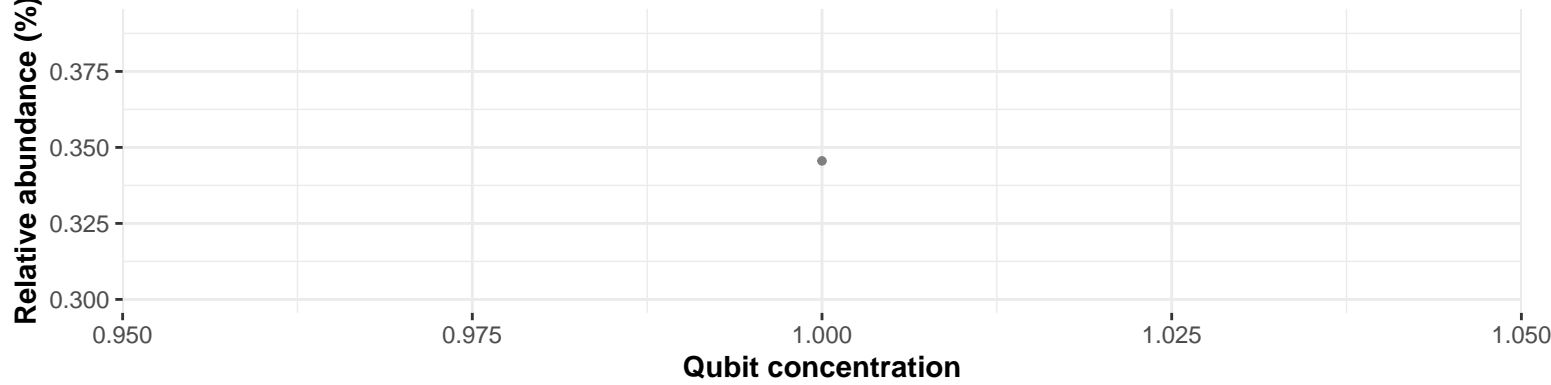


Correlation within: Feed

$\log_e(S) = 6.239$, $p = 0.668$, $\hat{\rho}_{\text{Spearman}} = -0.126$, $\text{CI}_{95\%} [-0.626, 0.448]$, $n_{\text{pairs}} = 14$



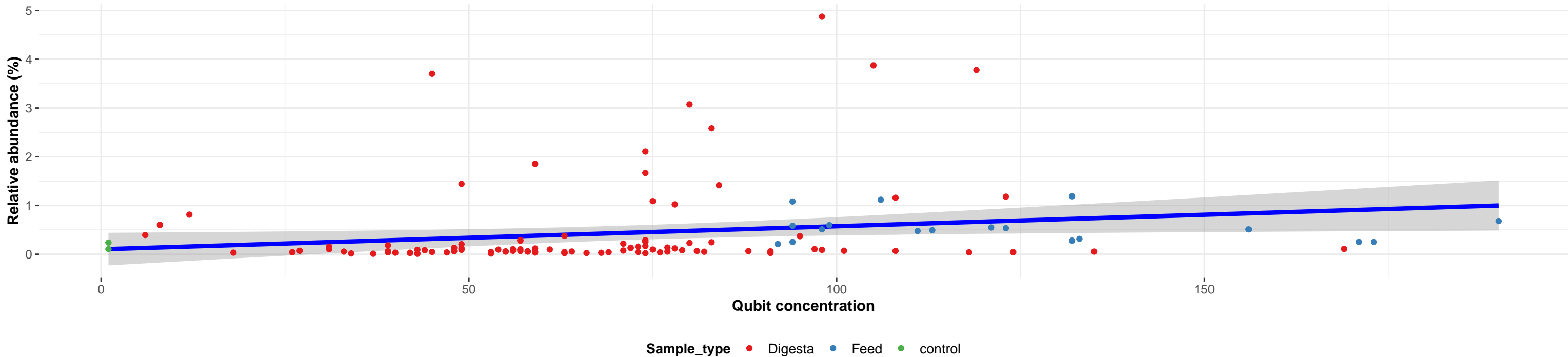
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; NA

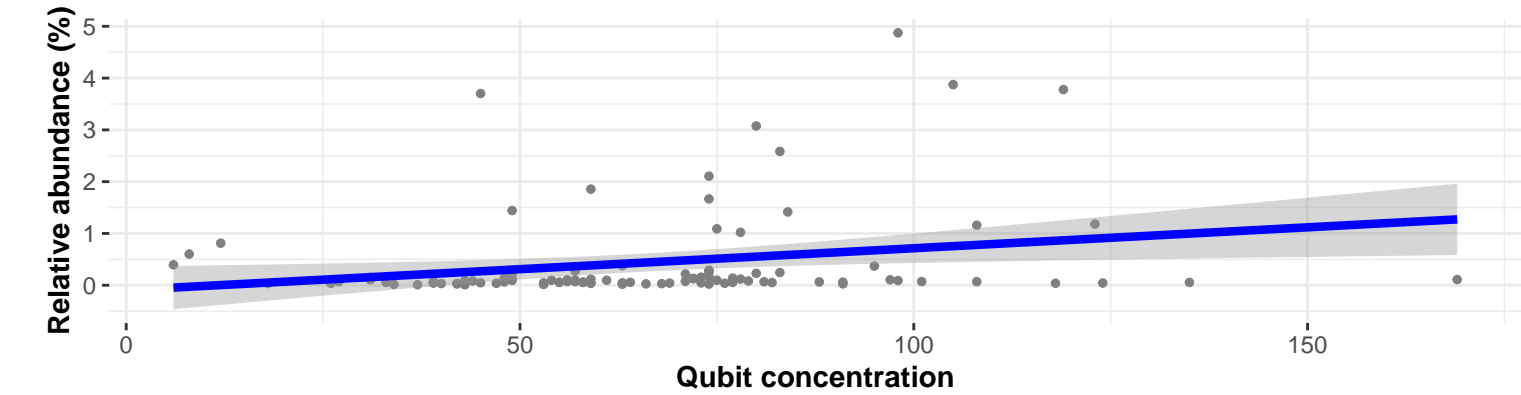
Correlation with all samples

$\log_e(S) = 12.123$, $p = 3.09\text{e-}06$, $\hat{\rho}_{\text{Spearman}} = 0.406$, $\text{CI}_{95\%} [0.242, 0.548]$, $n_{\text{pairs}} = 123$



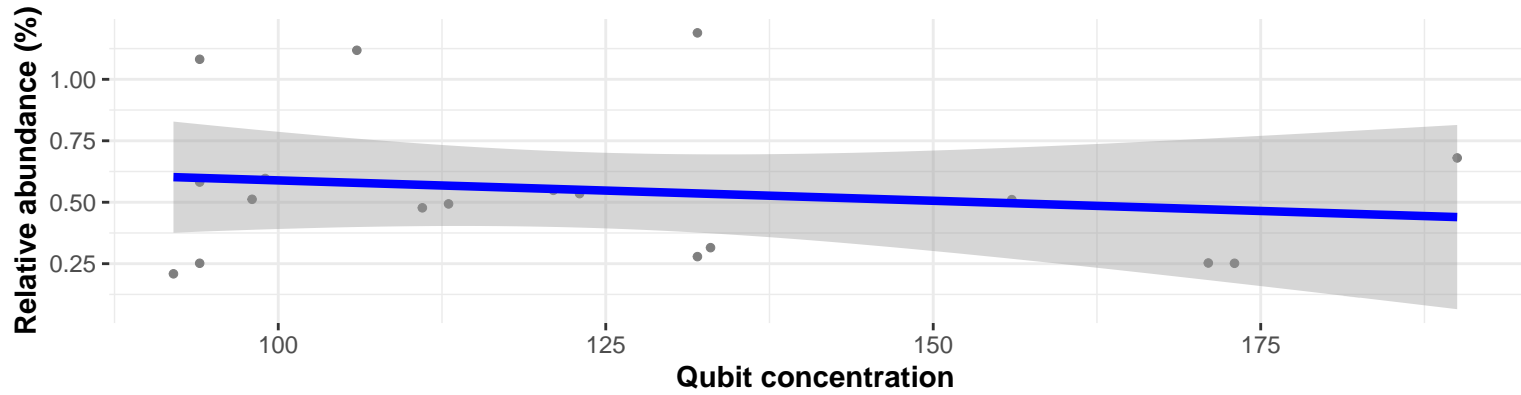
Correlation within: Digesta

$\log_e(S) = 11.793$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.274$, $\text{CI}_{95\%} [0.079, 0.448]$, $n_{\text{pairs}} = 103$

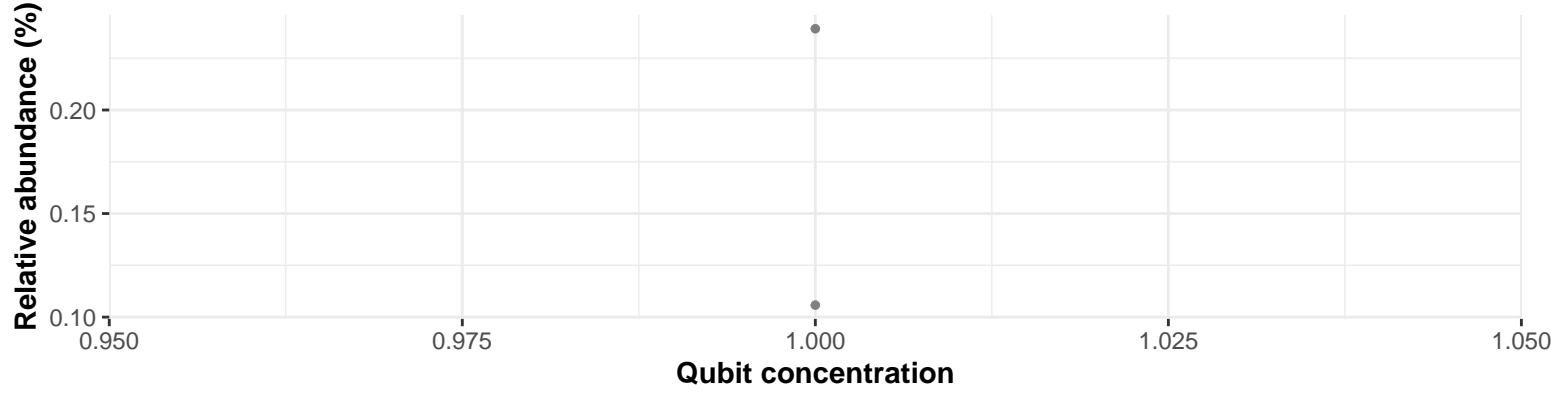


Correlation within: Feed

$\log_e(S) = 6.938$, $p = 0.800$, $\hat{\rho}_{\text{Spearman}} = -0.064$, $\text{CI}_{95\%} [-0.526, 0.427]$, $n_{\text{pairs}} = 18$



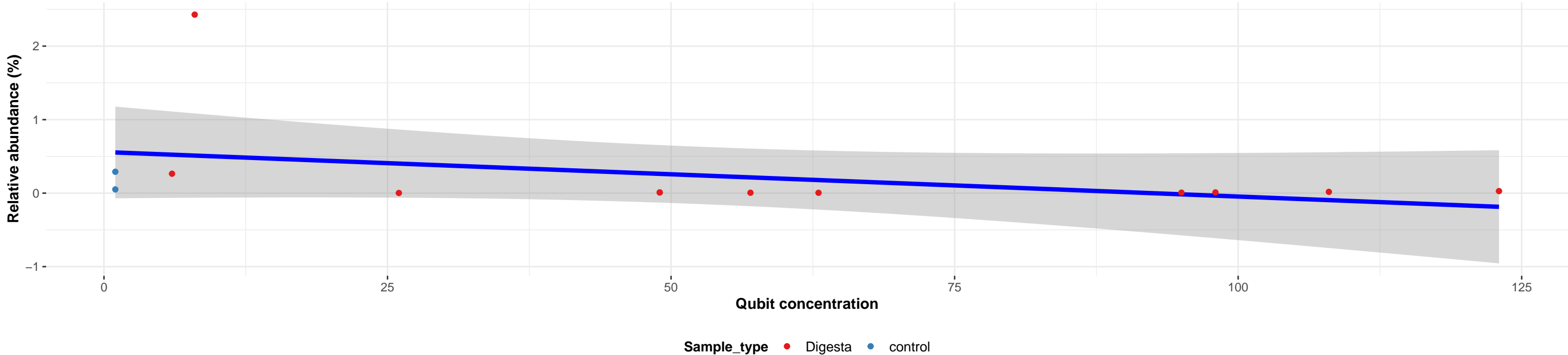
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Streptococcaceae; Streptococcus; NA

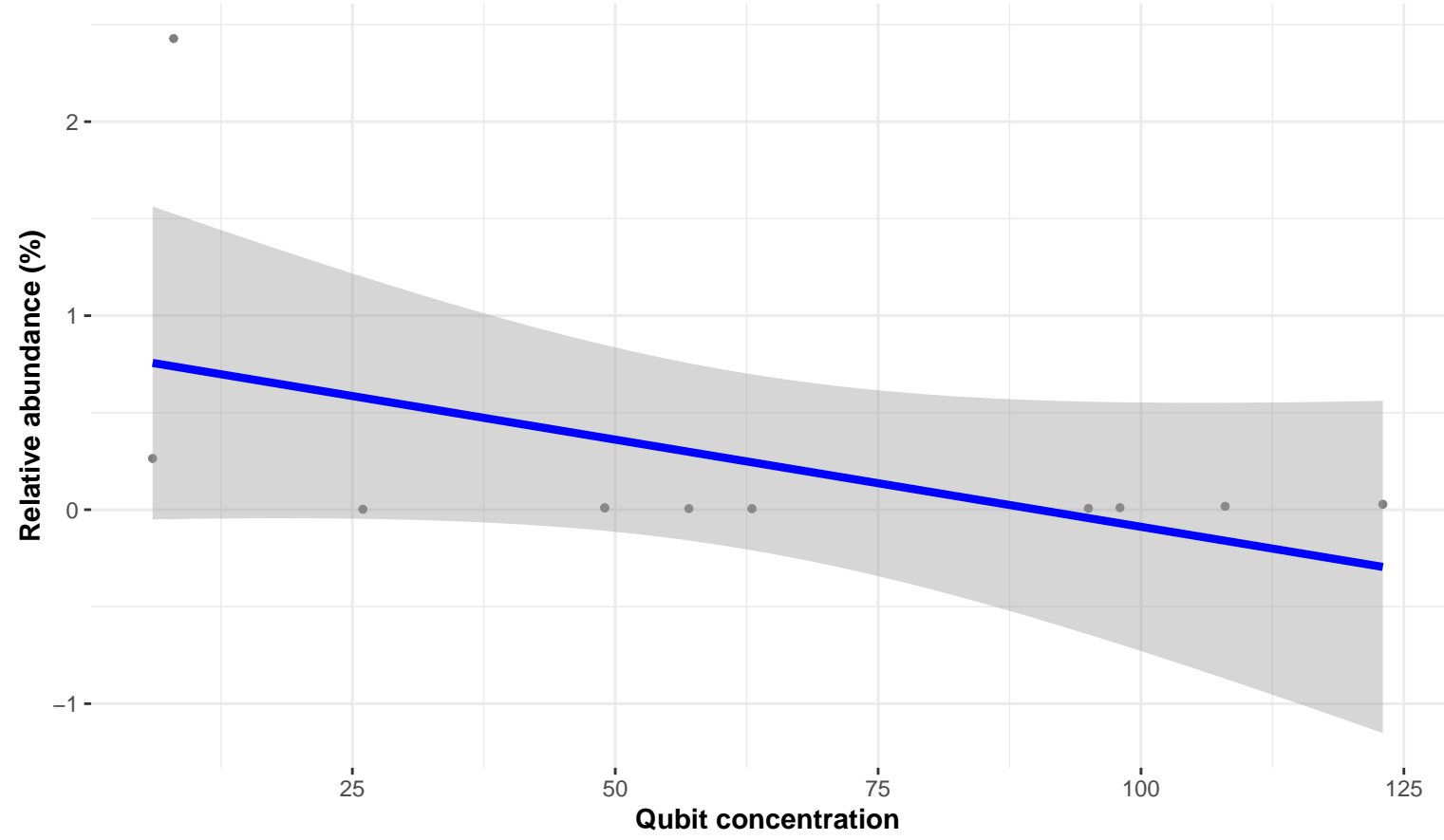
Correlation with all samples

$\log_e(S) = 6.225$, $p = 0.190$, $\hat{\rho}_{\text{Spearman}} = -0.388$, $\text{CI}_{95\%} [-0.781, 0.224]$, $n_{\text{pairs}} = 13$

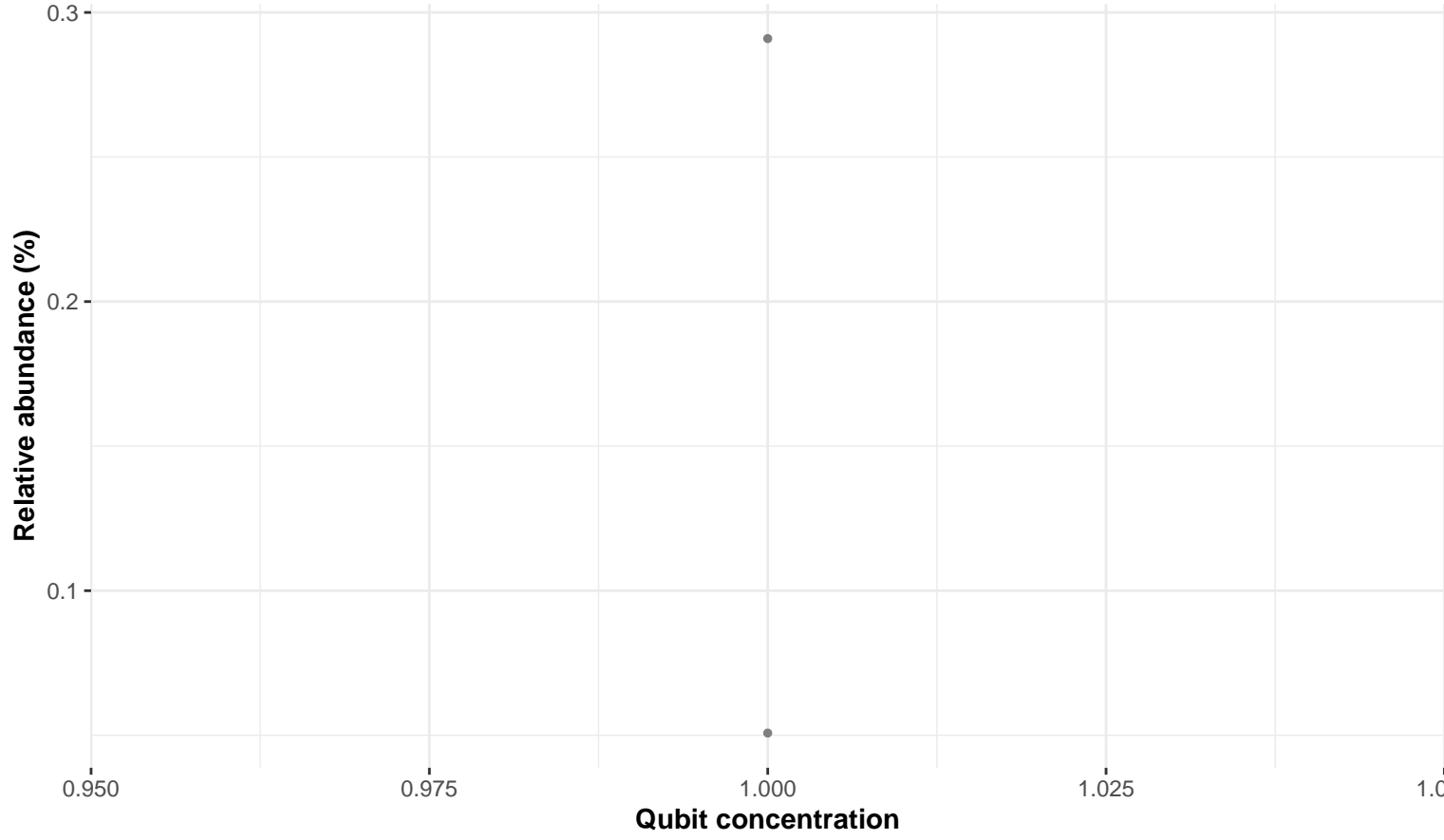


Correlation within: Digesta

$\log_e(S) = 5.443$, $p = 0.884$, $\hat{\rho}_{\text{Spearman}} = -0.050$, $\text{CI}_{95\%} [-0.643, 0.581]$, $n_{\text{pairs}} = 11$



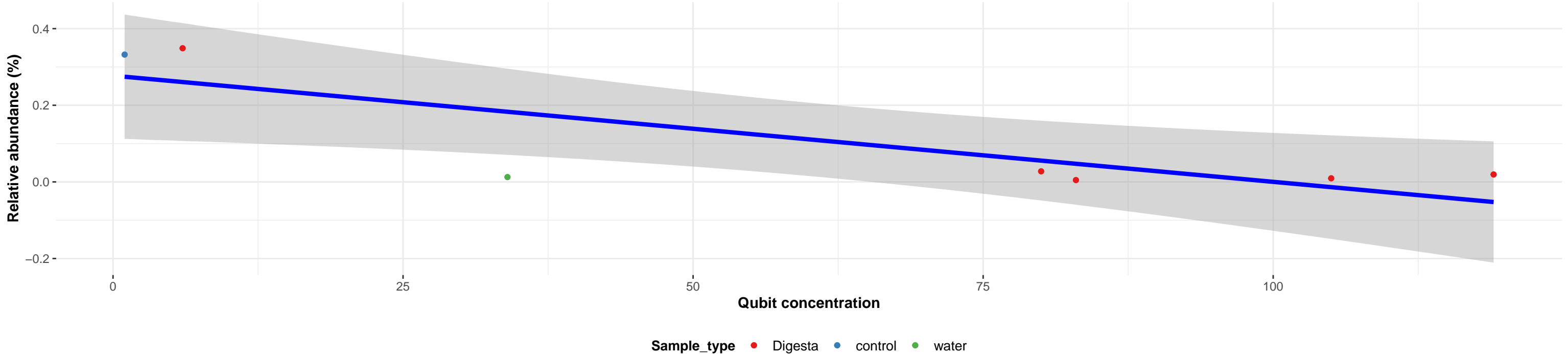
Correlation within: control



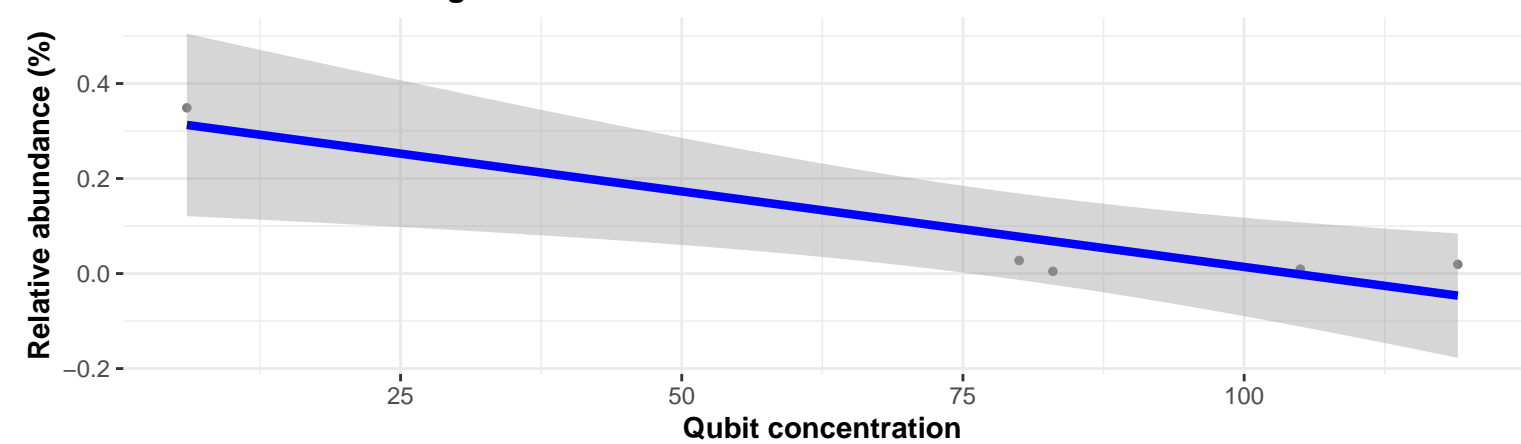
Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Variovorax; NA

Correlation with all samples

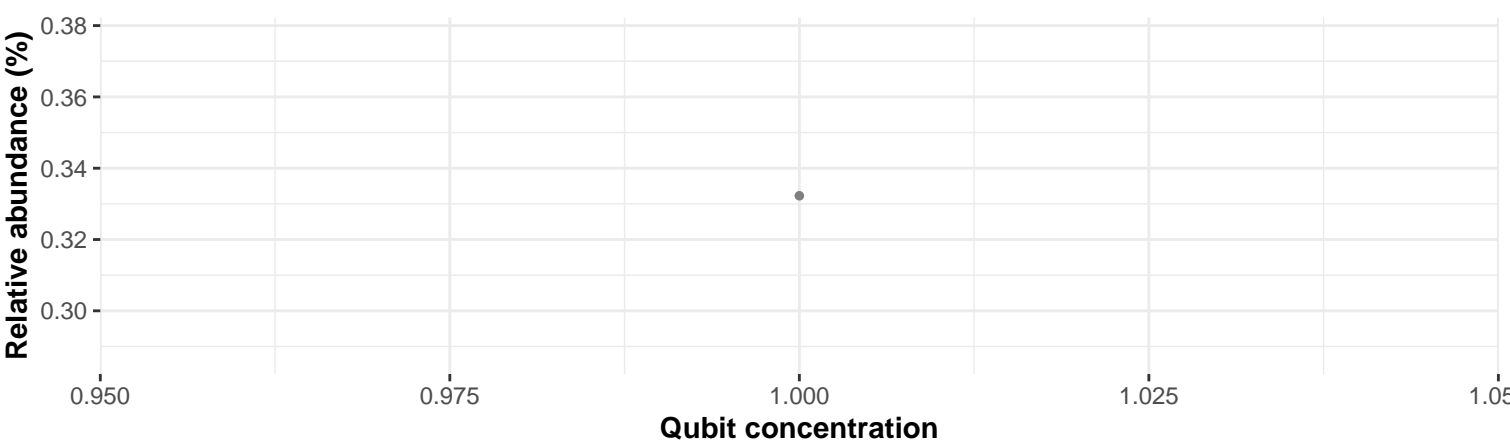
$\log_e(S) = 4.522$, $p = 0.119$, $\hat{\rho}_{\text{Spearman}} = -0.643$, $\text{CI}_{95\%} [-0.944, 0.241]$, $n_{\text{pairs}} = 7$



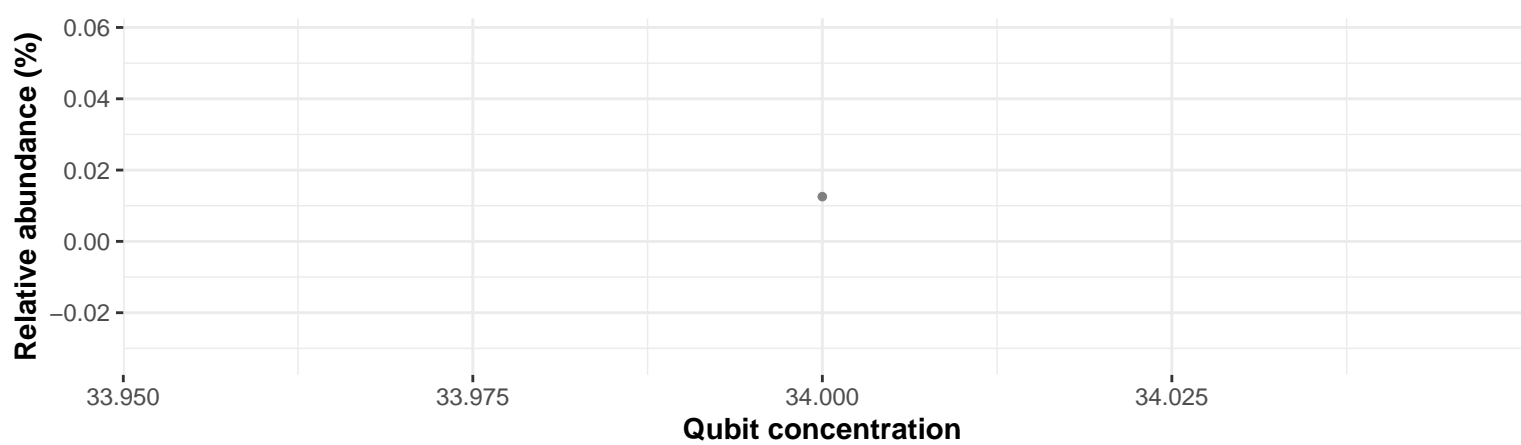
Correlation within: Digesta



Correlation within: control



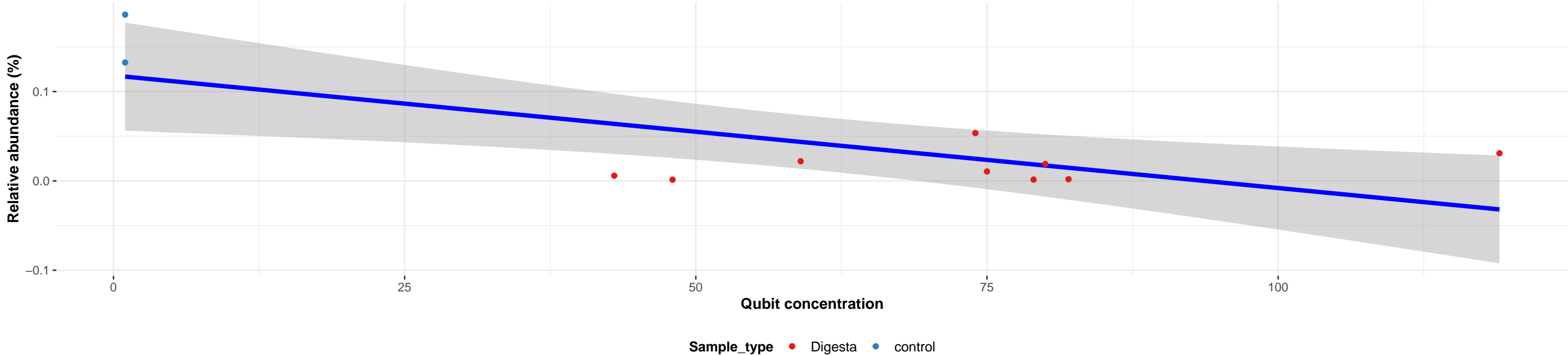
Correlation within: water



Bacteria; Verrucomicrobiota; Chlamydiae; Chlamydiales; Simkaniaceae; NA; NA

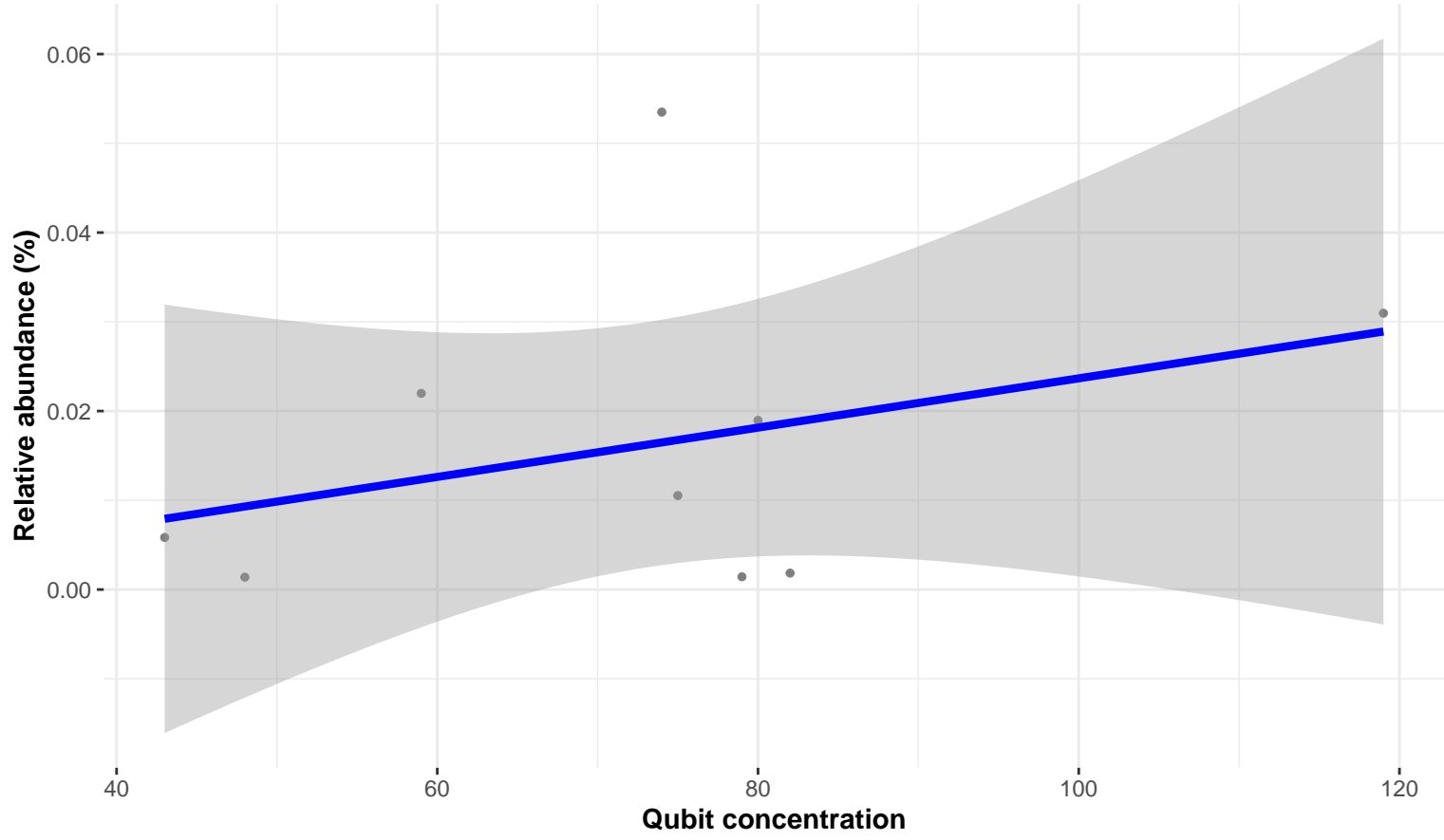
Correlation with all samples

$\log_e(S) = 5.681$, $p = 0.318$, $\hat{\rho}_{\text{Spearman}} = -0.333$, $\text{CI}_{95\%} [-0.785, 0.352]$, $n_{\text{pairs}} = 11$

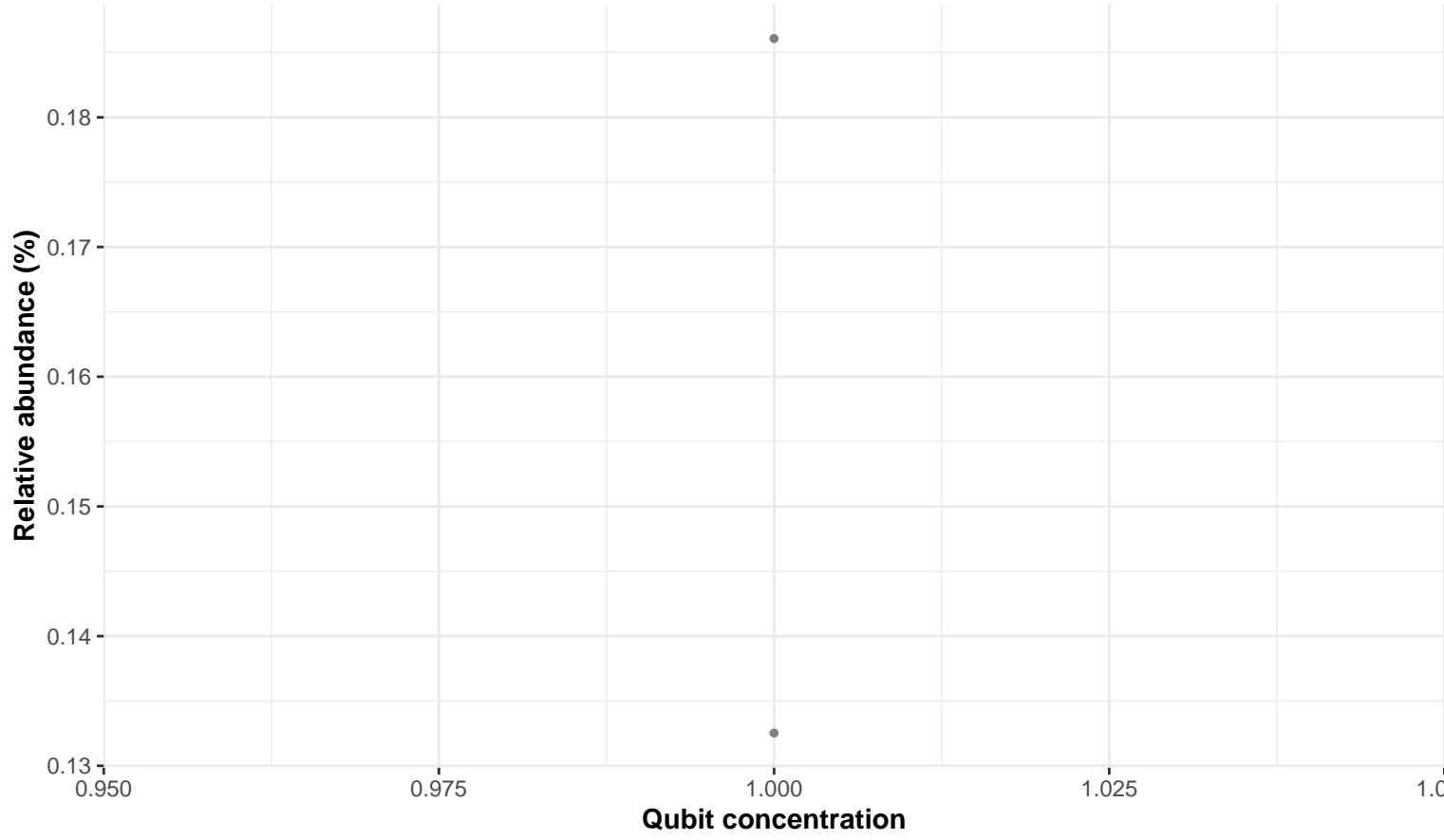


Correlation within: Digesta

$\log_e(S) = 4.543$, $p = 0.576$, $\hat{\rho}_{\text{Spearman}} = 0.217$, $\text{CI}_{95\%} [-0.540, 0.779]$, $n_{\text{pairs}} = 9$



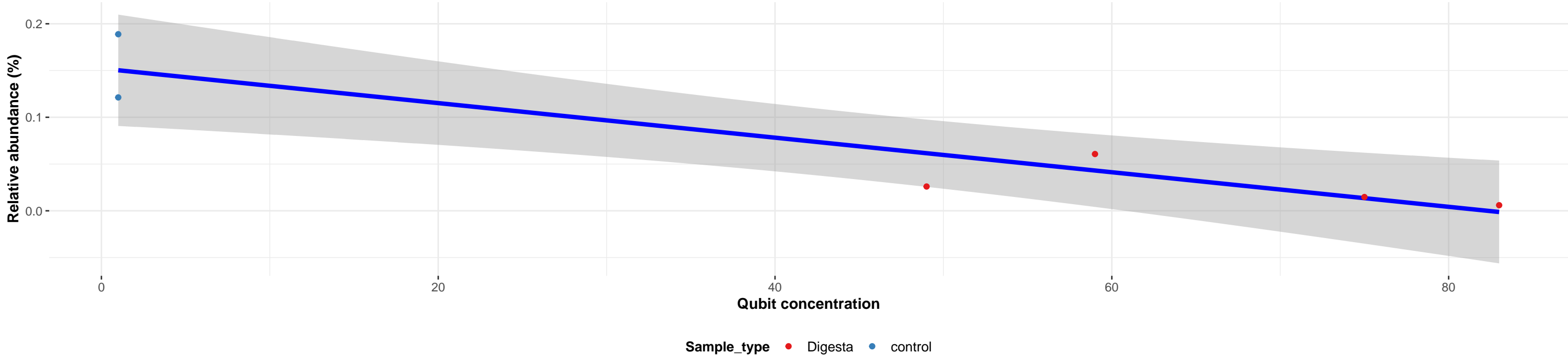
Correlation within: control



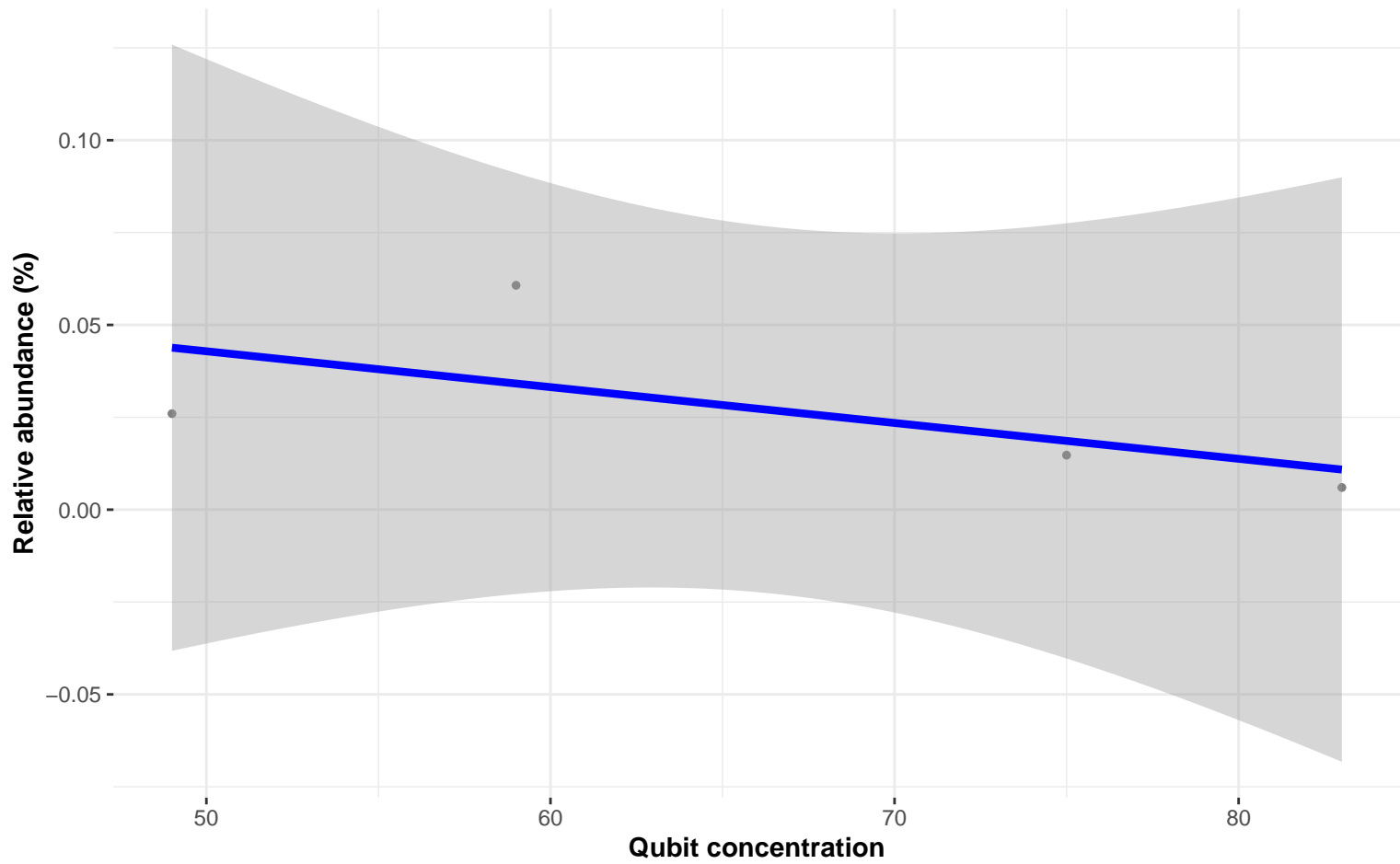
Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Pseudogracilibacillus; NA

Correlation with all samples

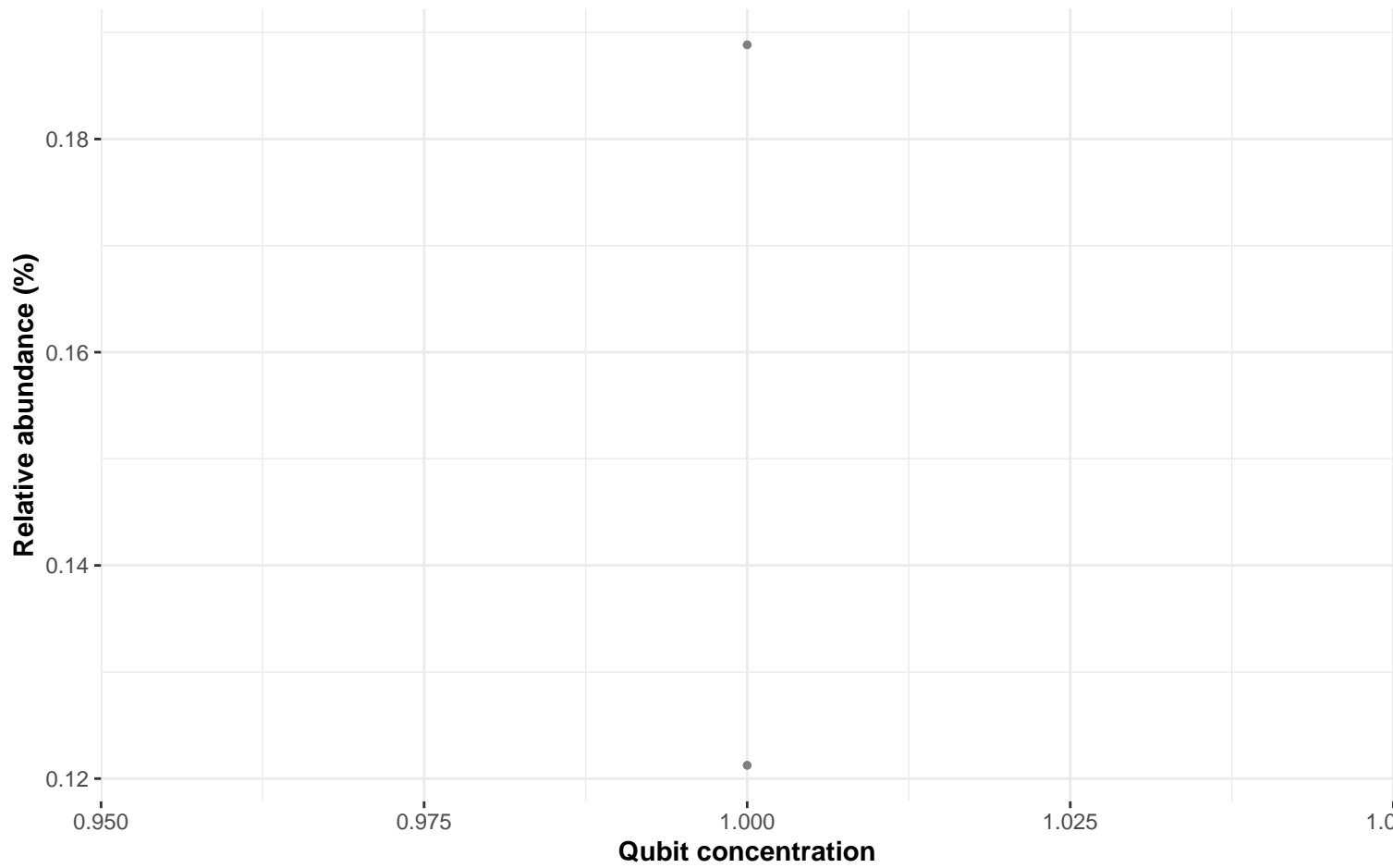
$\log_e(S) = 4.212$, $p = 0.008$, $\hat{\rho}_{\text{Spearman}} = -0.928$, $CI_{95\%} [-0.993, -0.443]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



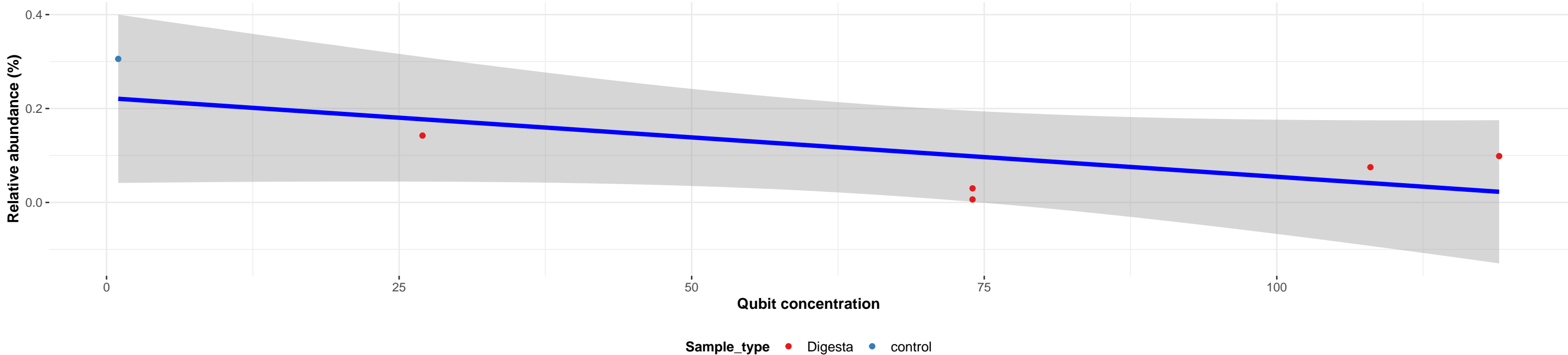
Correlation within: control



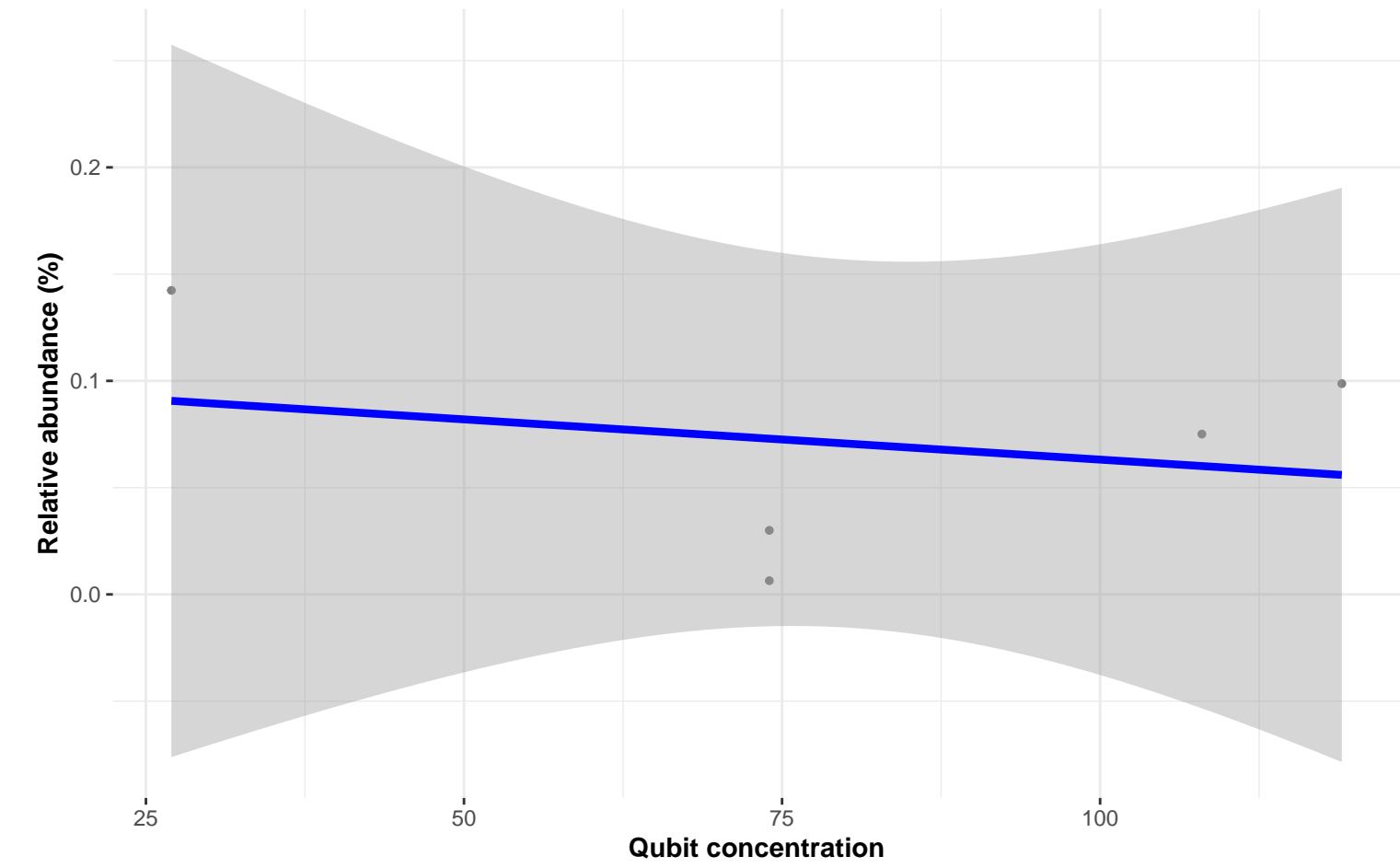
Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Microbacteriaceae; NA; NA

Correlation with all samples

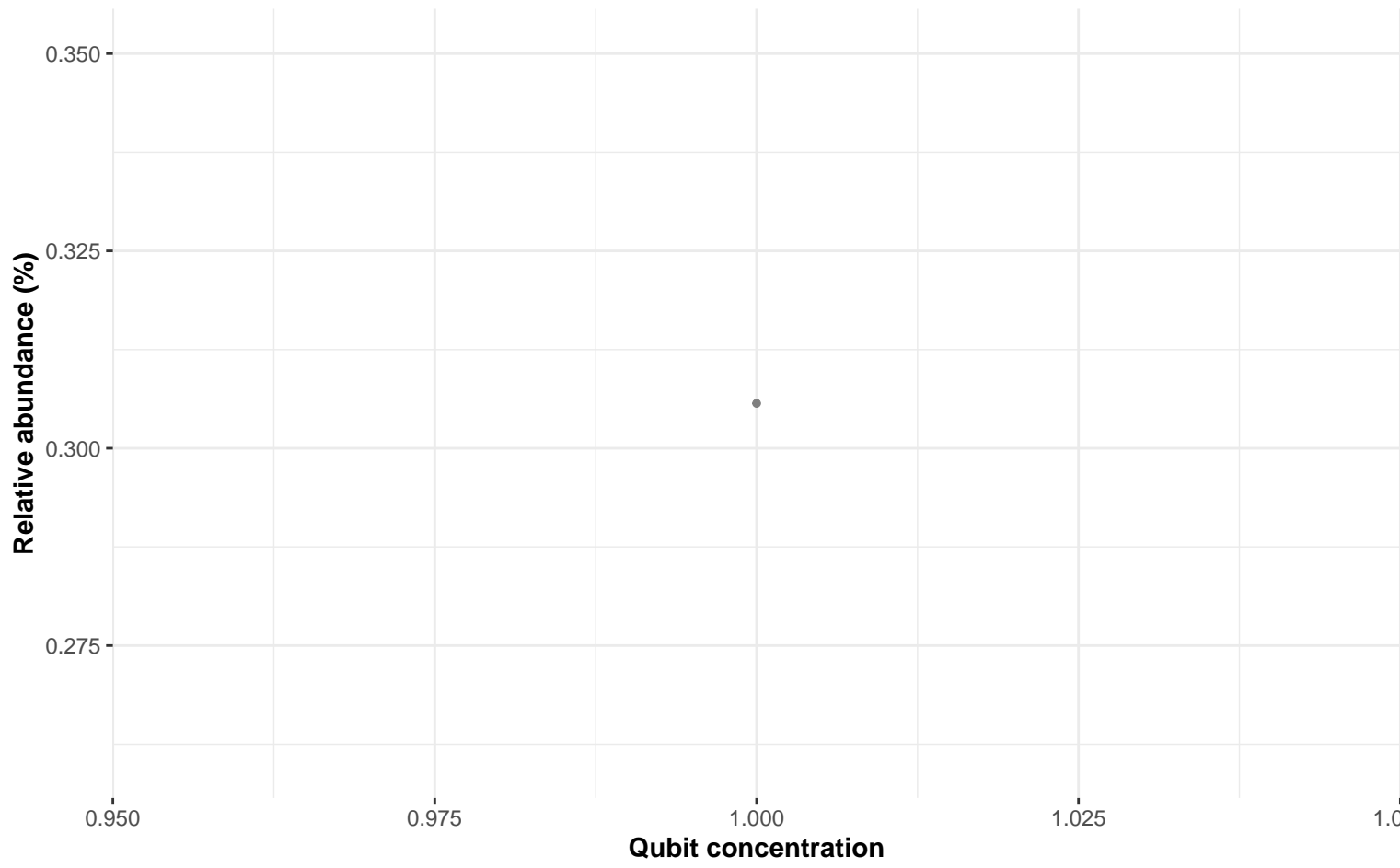
$\log_e(S) = 3.936$, $p = 0.354$, $\hat{\rho}_{\text{Spearman}} = -0.464$, $CI_{95\%} [-0.931, 0.580]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



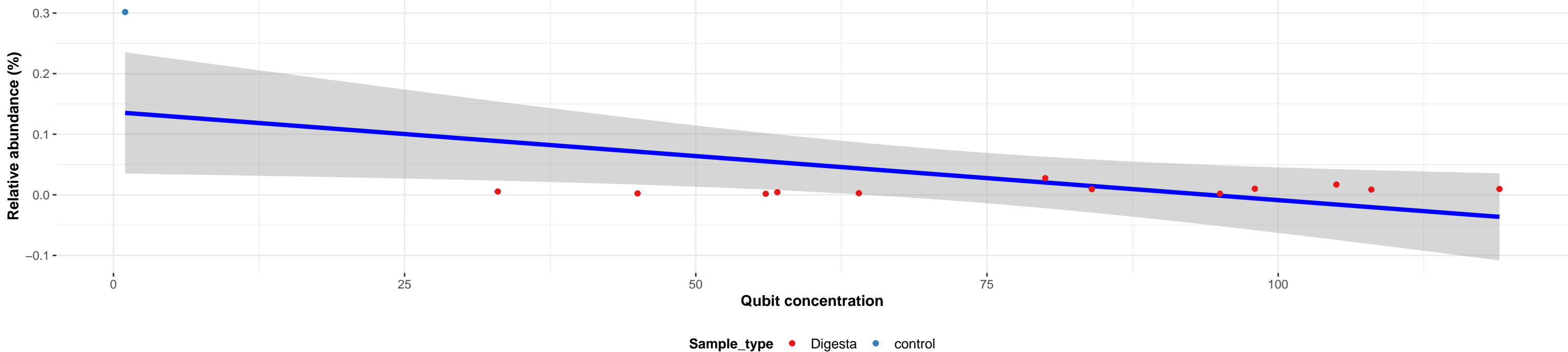
Correlation within: control



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Macrococcus; NA

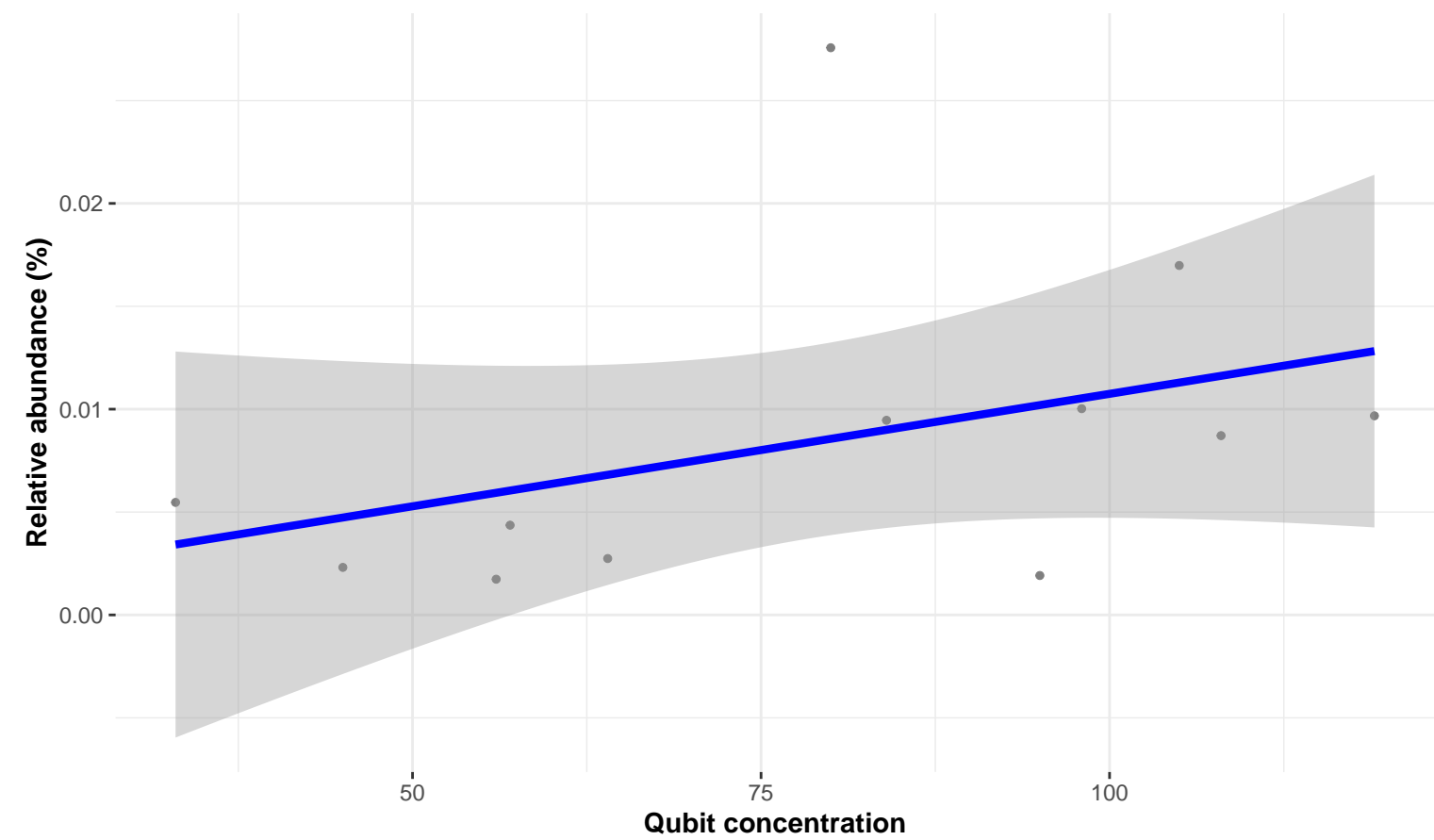
Correlation with all samples

$\log_e(S) = 5.663$, $p = 0.494$, $\hat{\rho}_{\text{Spearman}} = 0.209$, $CI_{95\%} [-0.402, 0.691]$, $n_{\text{pairs}} = 13$

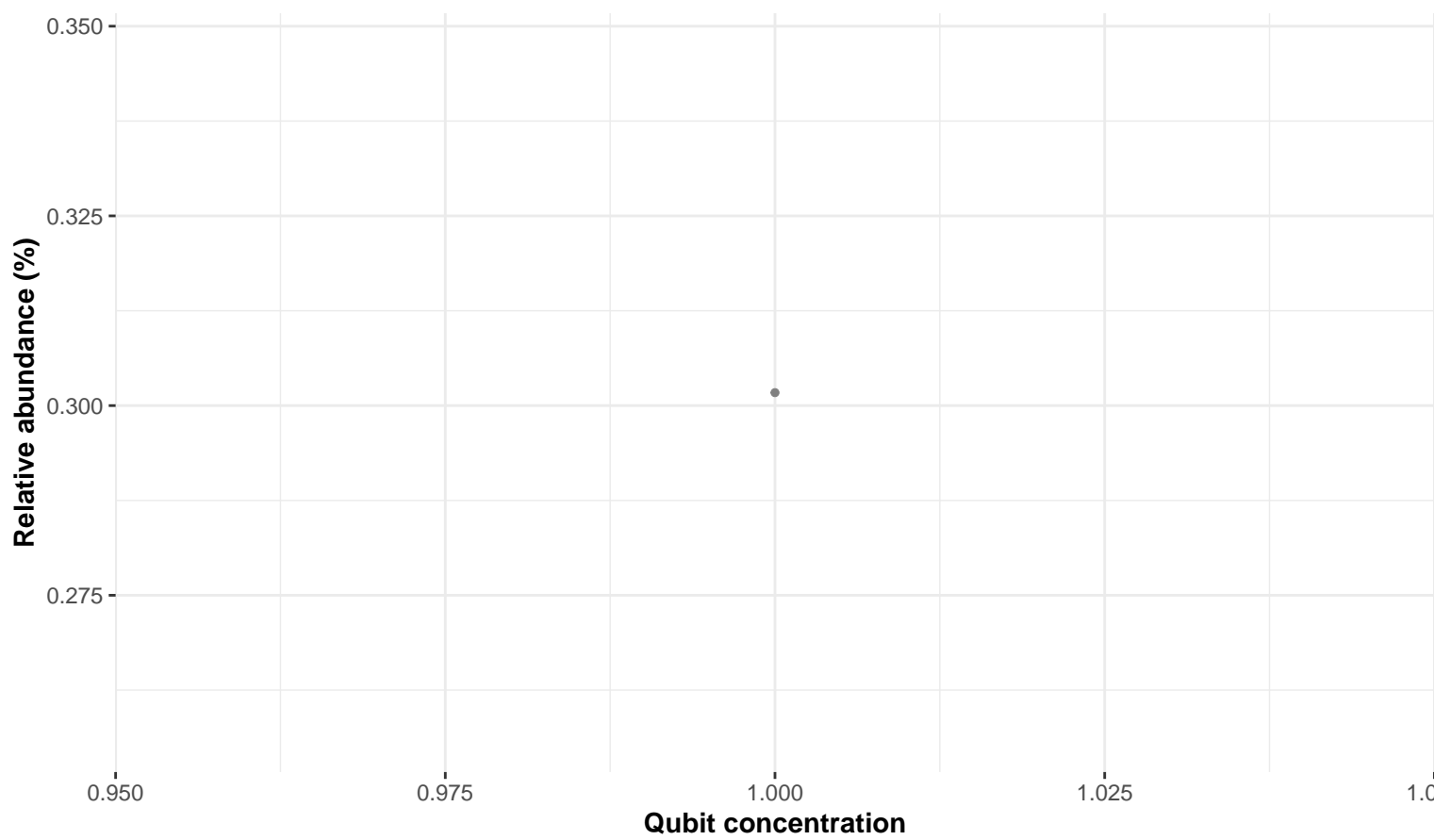


Correlation within: Digesta

$\log_e(S) = 4.883$, $p = 0.071$, $\hat{\rho}_{\text{Spearman}} = 0.538$, $CI_{95\%} [-0.071, 0.855]$, $n_{\text{pairs}} = 12$



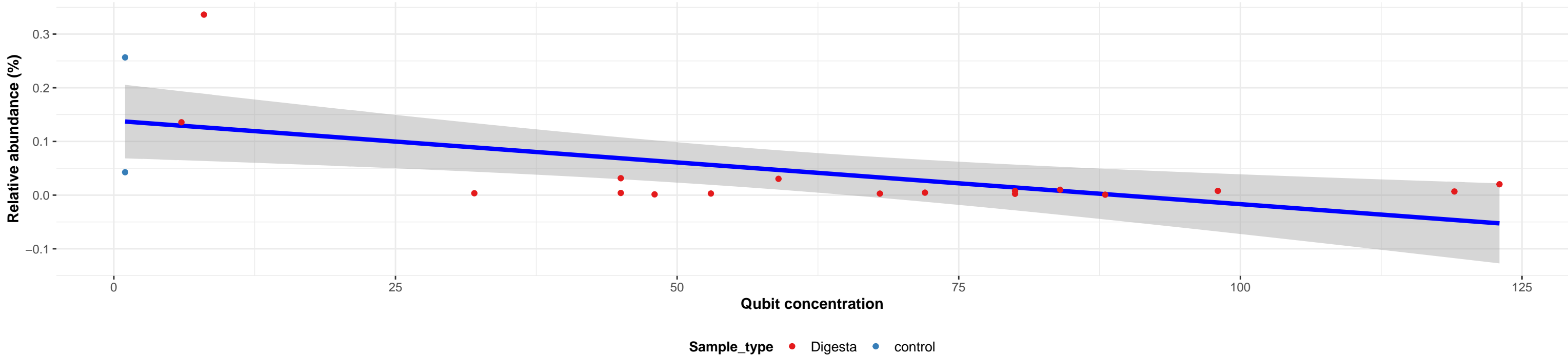
Correlation within: control



Bacteria; Verrucomicrobiota; Chlamydiae; Chlamydiales; Chlamydiaceae; NA; NA

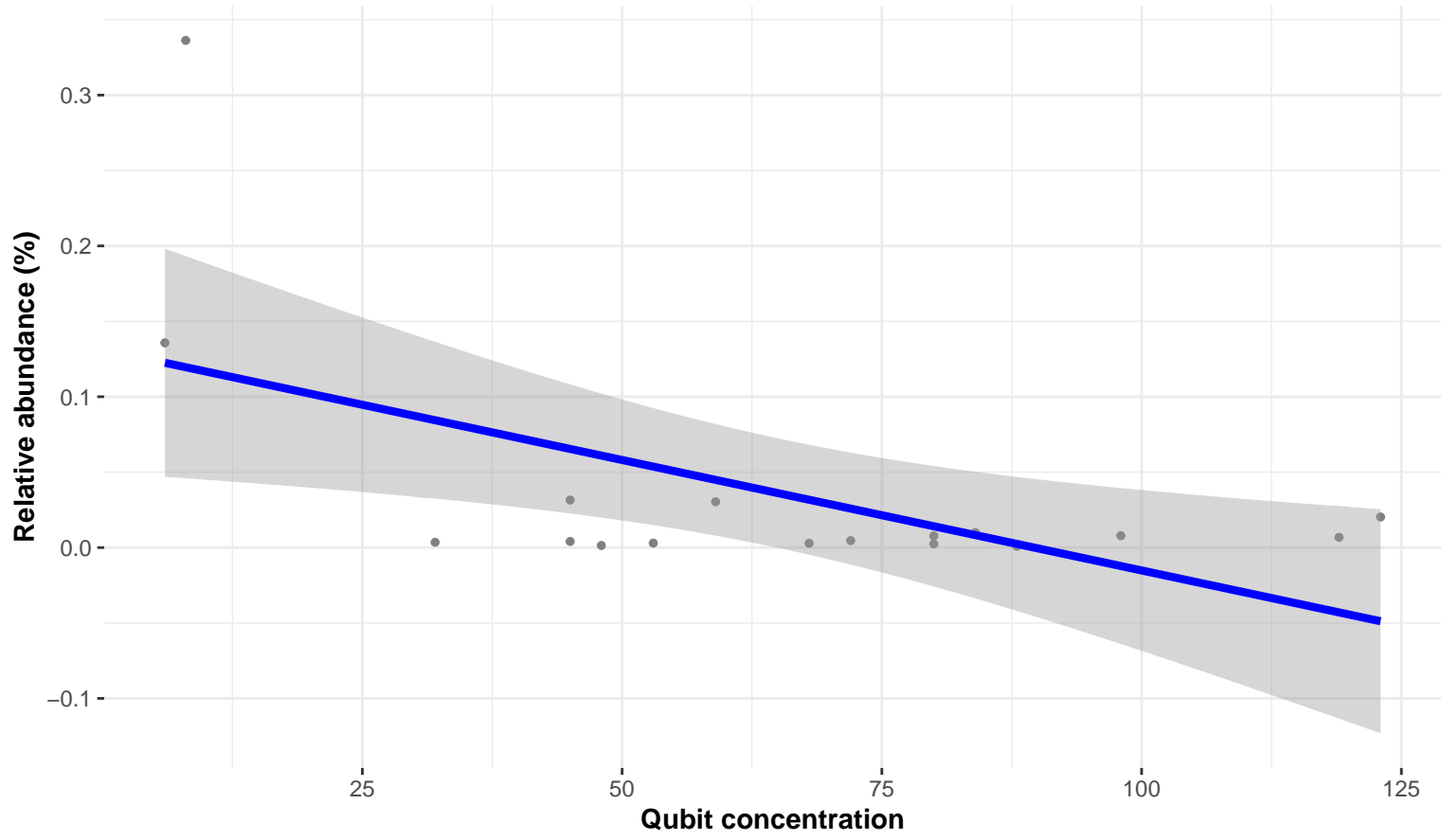
Correlation with all samples

$\log_e(S) = 7.391$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = -0.422$, $\text{CI}_{95\%} [-0.742, 0.054]$, $n_{\text{pairs}} = 19$

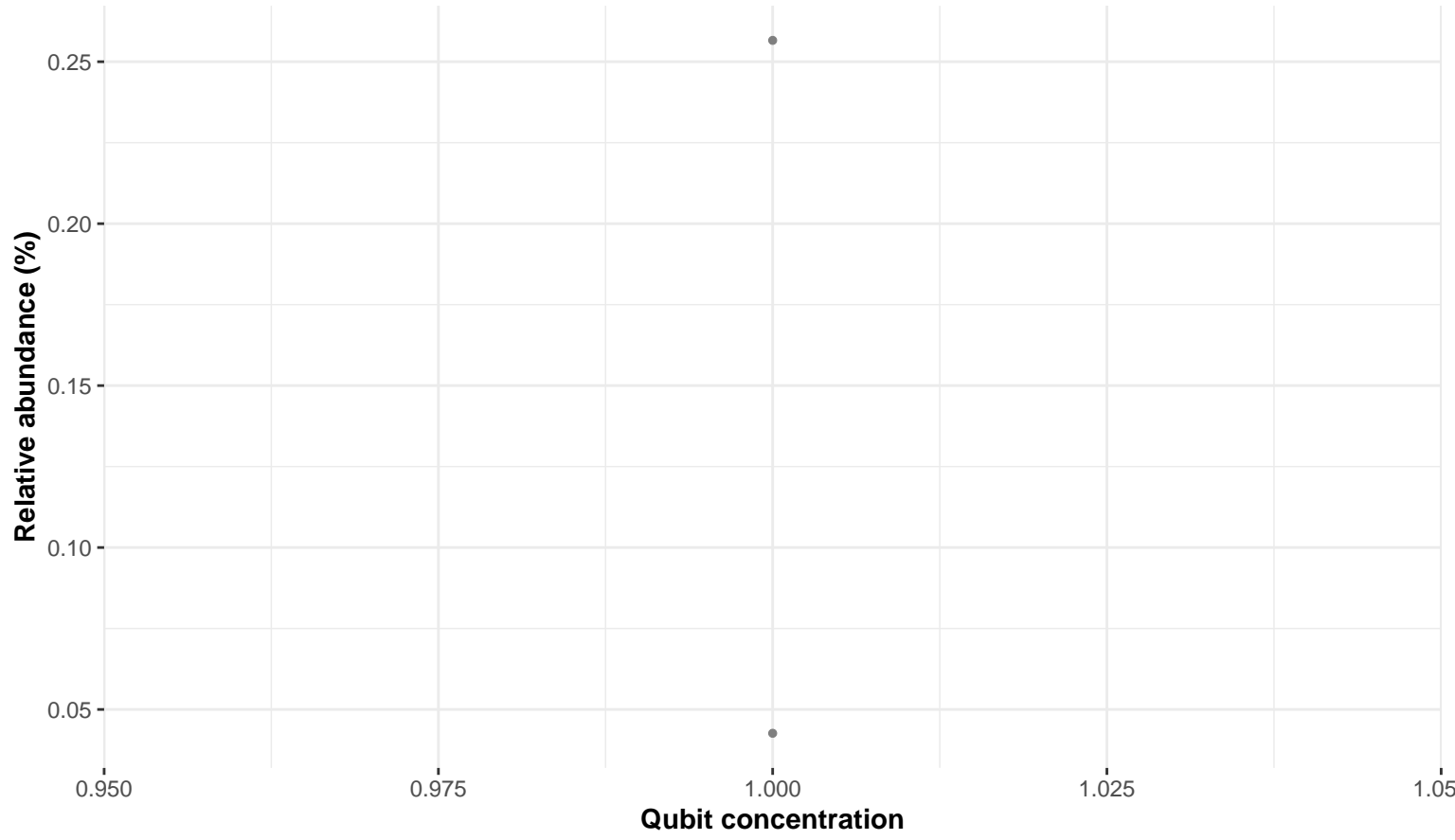


Correlation within: Digesta

$\log_e(S) = 6.895$, $p = 0.419$, $\hat{\rho}_{\text{Spearman}} = -0.210$, $\text{CI}_{95\%} [-0.637, 0.315]$, $n_{\text{pairs}} = 17$



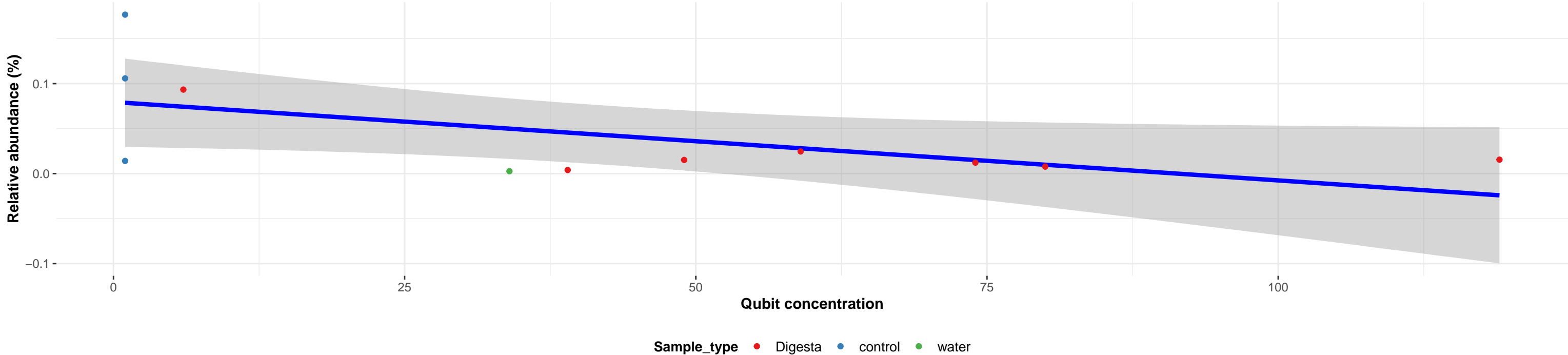
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

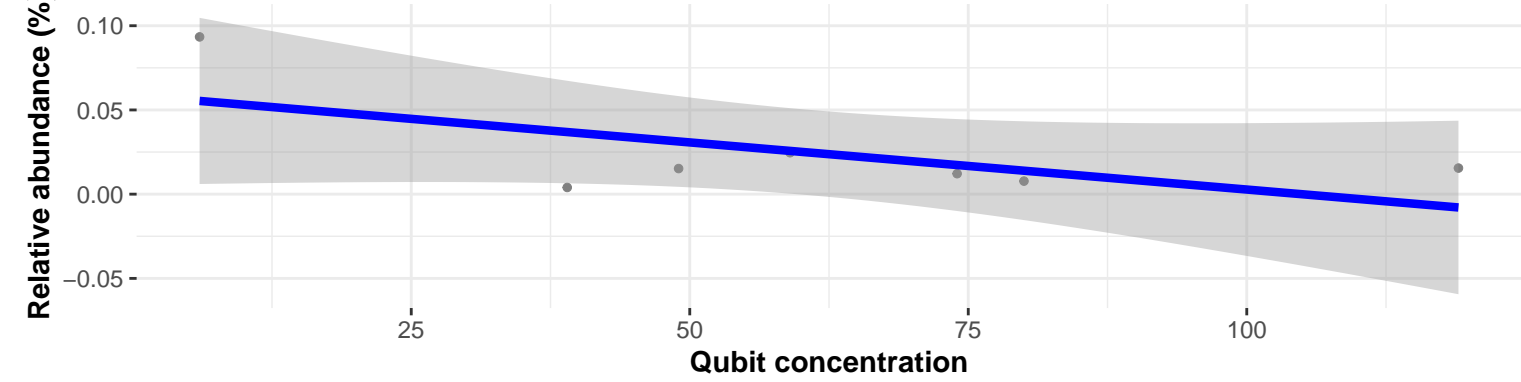
Correlation with all samples

$\log_e(S) = 5.720$, $p = 0.242$, $\hat{\rho}_{\text{Spearman}} = -0.385$, $\text{CI}_{95\%} [-0.807, 0.298]$, $n_{\text{pairs}} = 11$

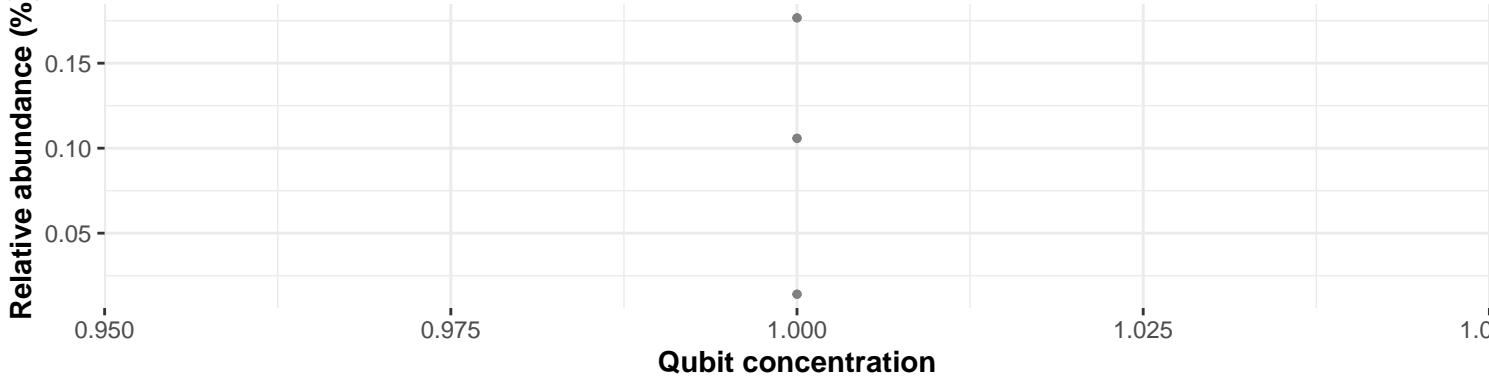


Correlation within: Digesta

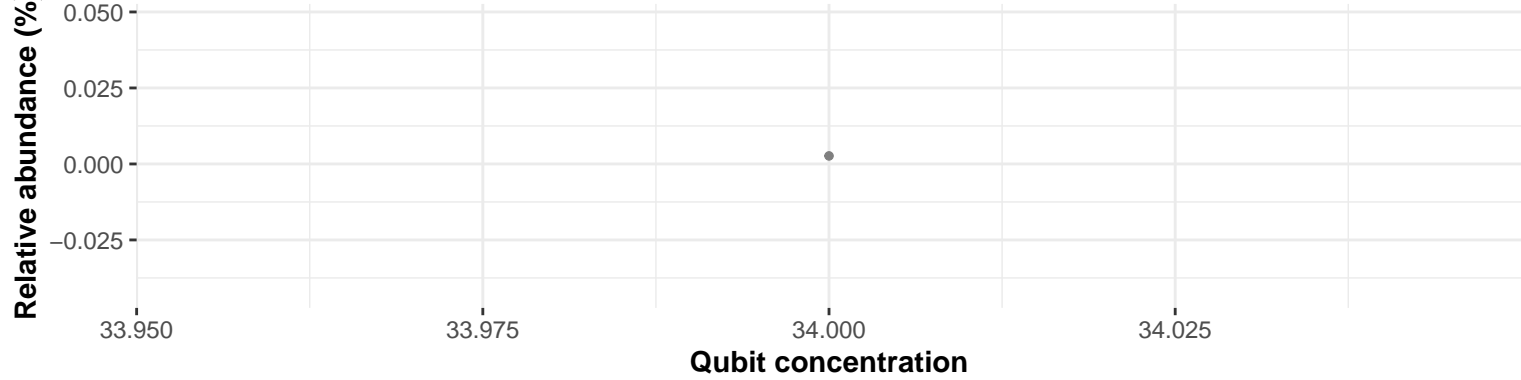
$\log_e(S) = 4.190$, $p = 0.702$, $\hat{\rho}_{\text{Spearman}} = -0.179$, $\text{CI}_{95\%} [-0.830, 0.680]$, $n_{\text{pairs}} = 7$



Correlation within: control



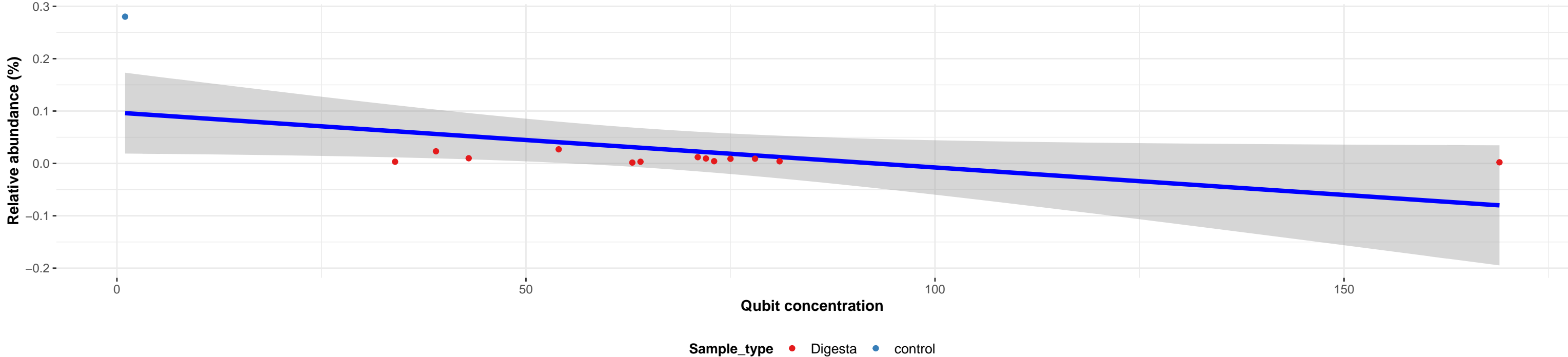
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Dermabacteraceae; Brachybacterium; NA

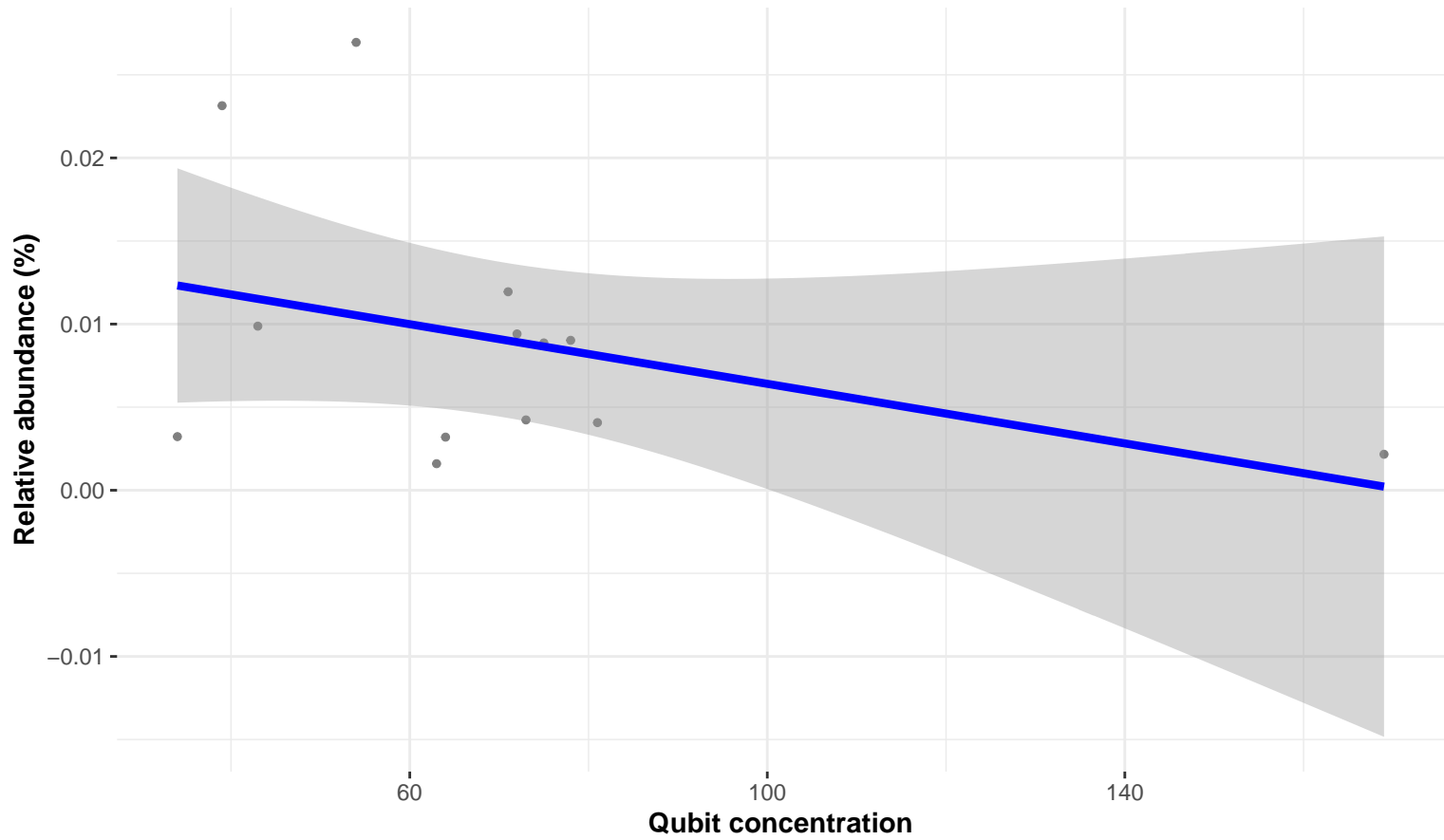
Correlation with all samples

$\log_e(S) = 6.492$, $p = 0.106$, $\hat{\rho}_{\text{Spearman}} = -0.451$, $\text{CI}_{95\%} [-0.798, 0.122]$, $n_{\text{pairs}} = 14$

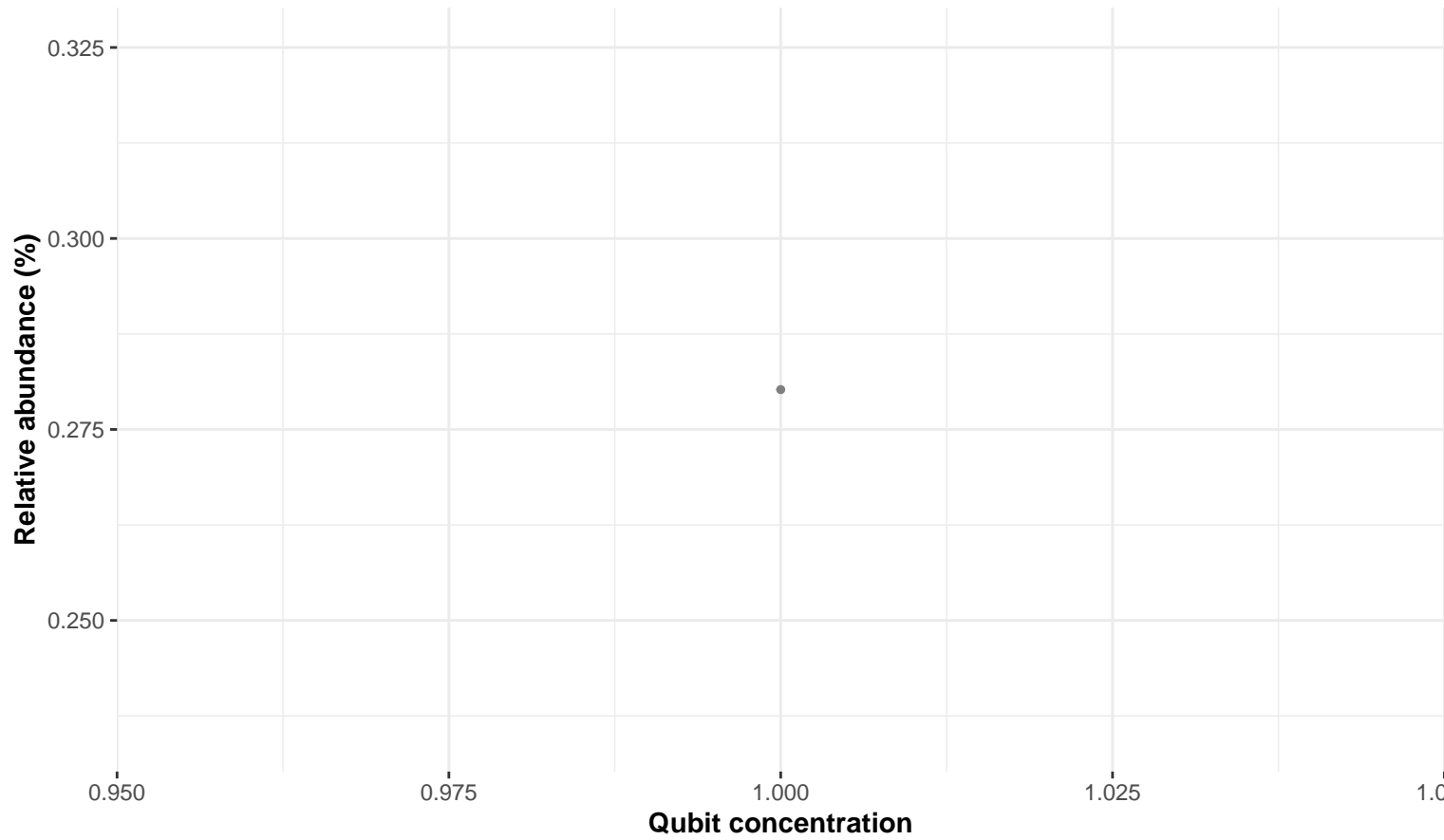


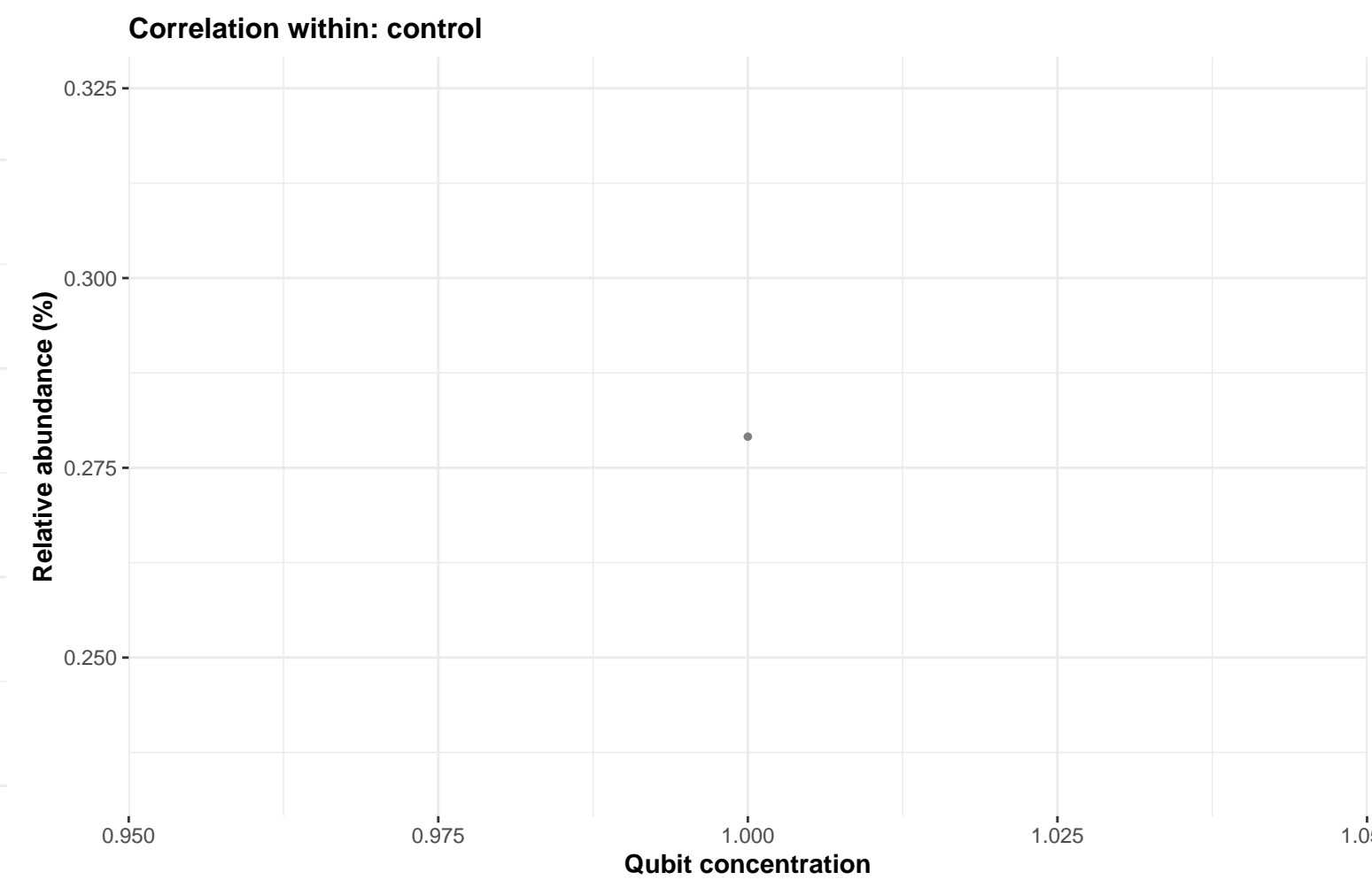
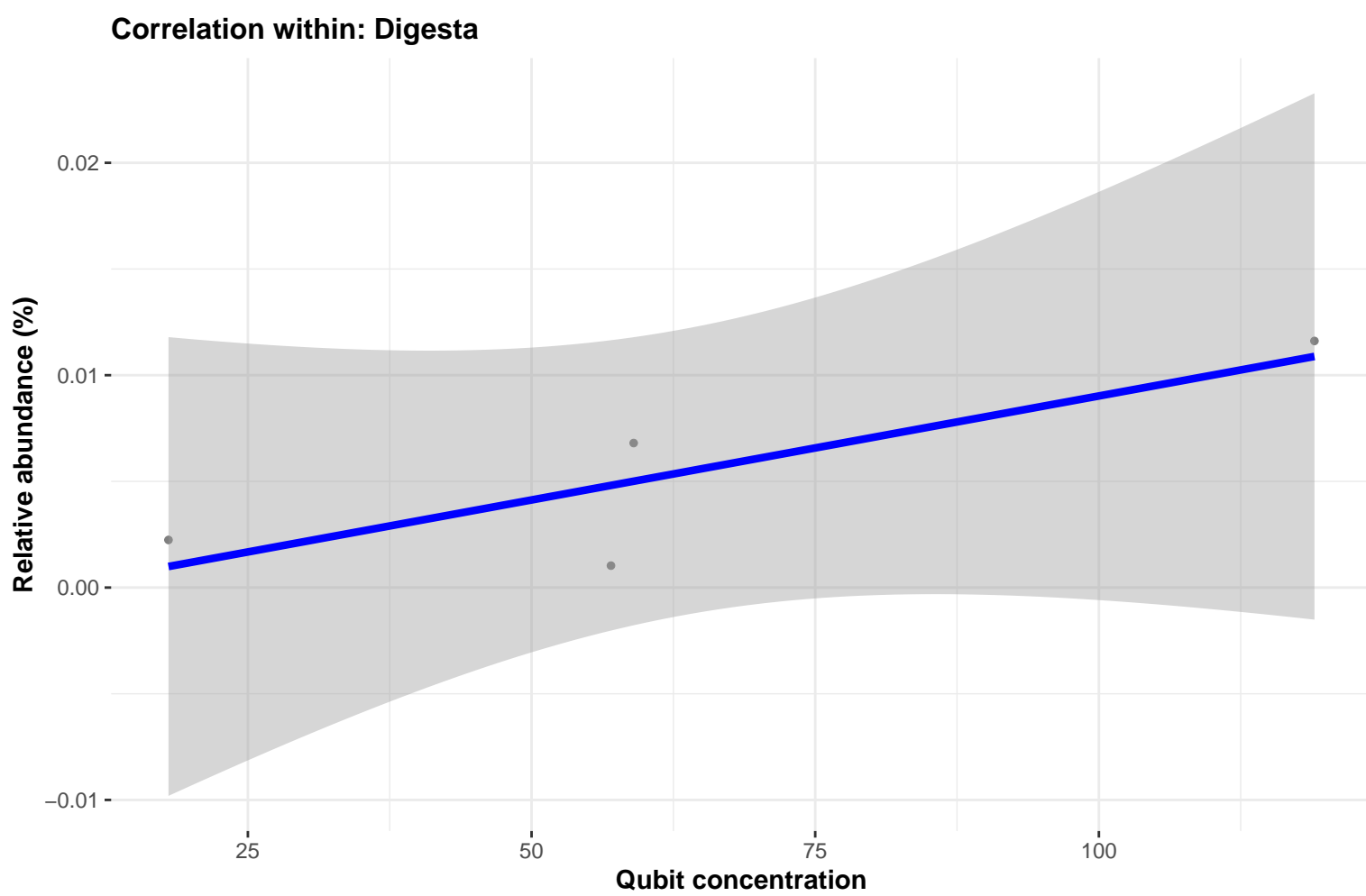
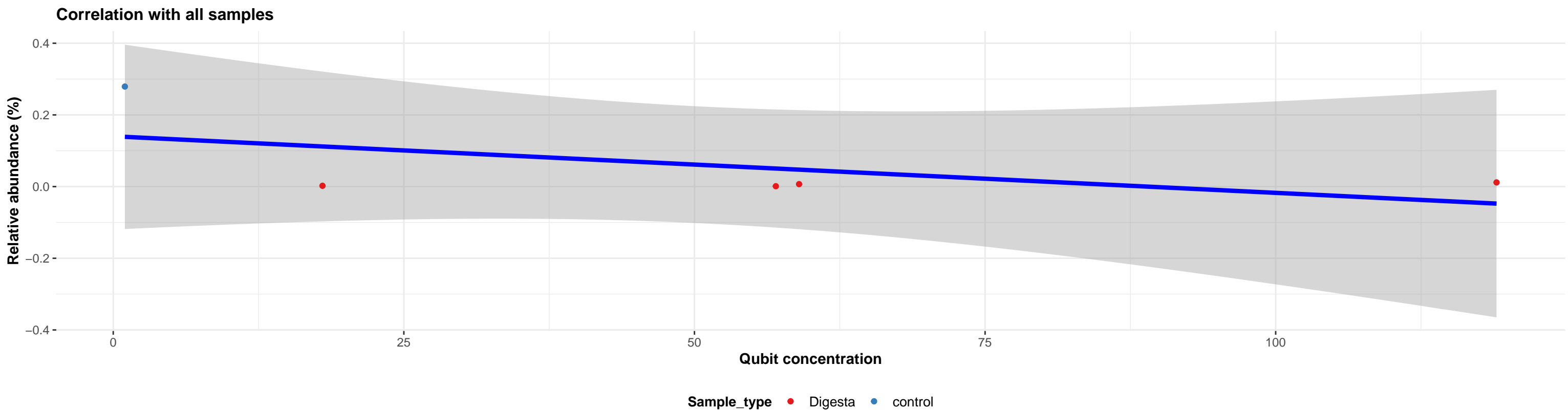
Correlation within: Digesta

$\log_e(S) = 6.170$, $p = 0.297$, $\hat{\rho}_{\text{Spearman}} = -0.313$, $\text{CI}_{95\%} [-0.745, 0.304]$, $n_{\text{pairs}} = 13$

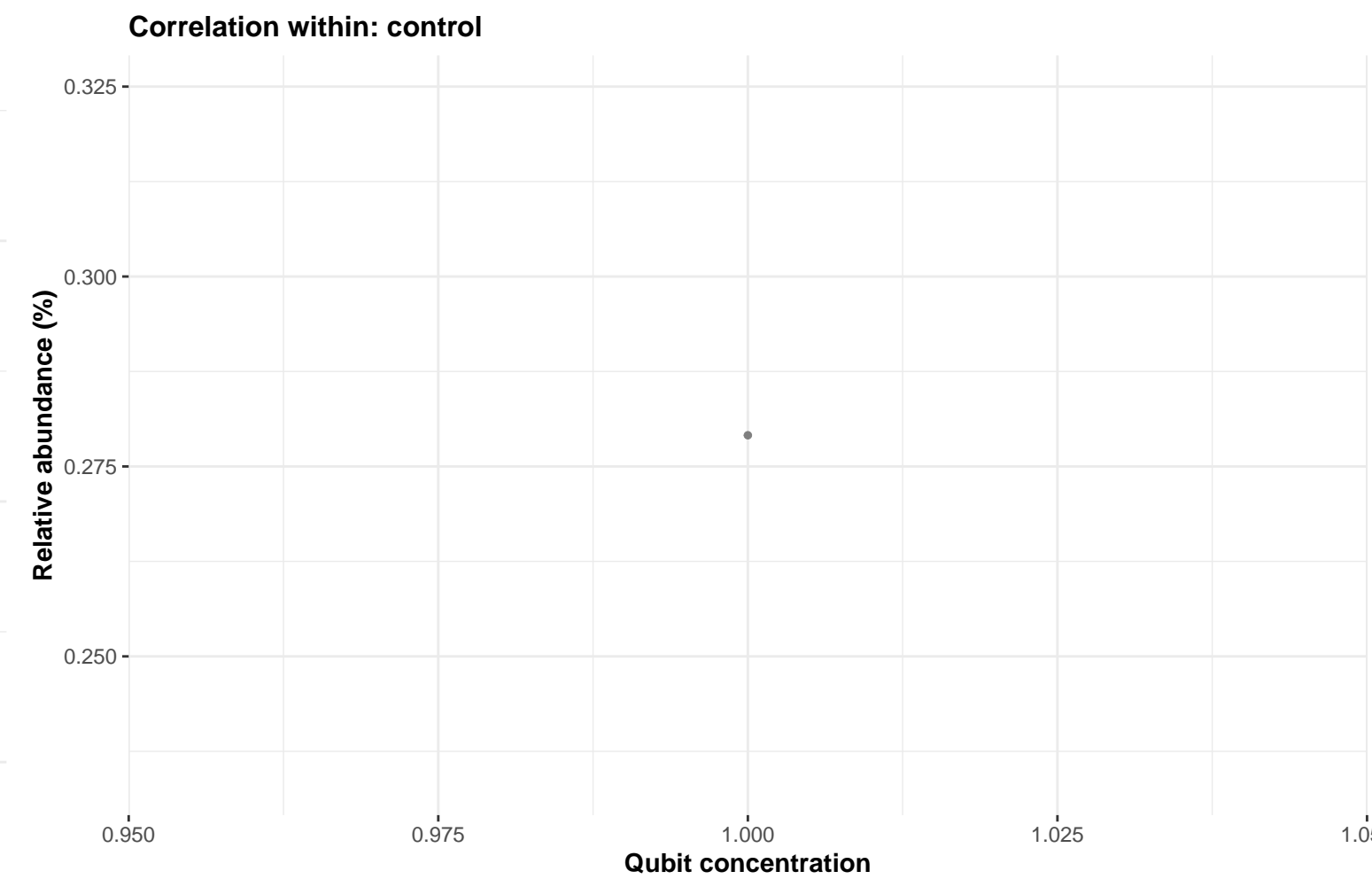
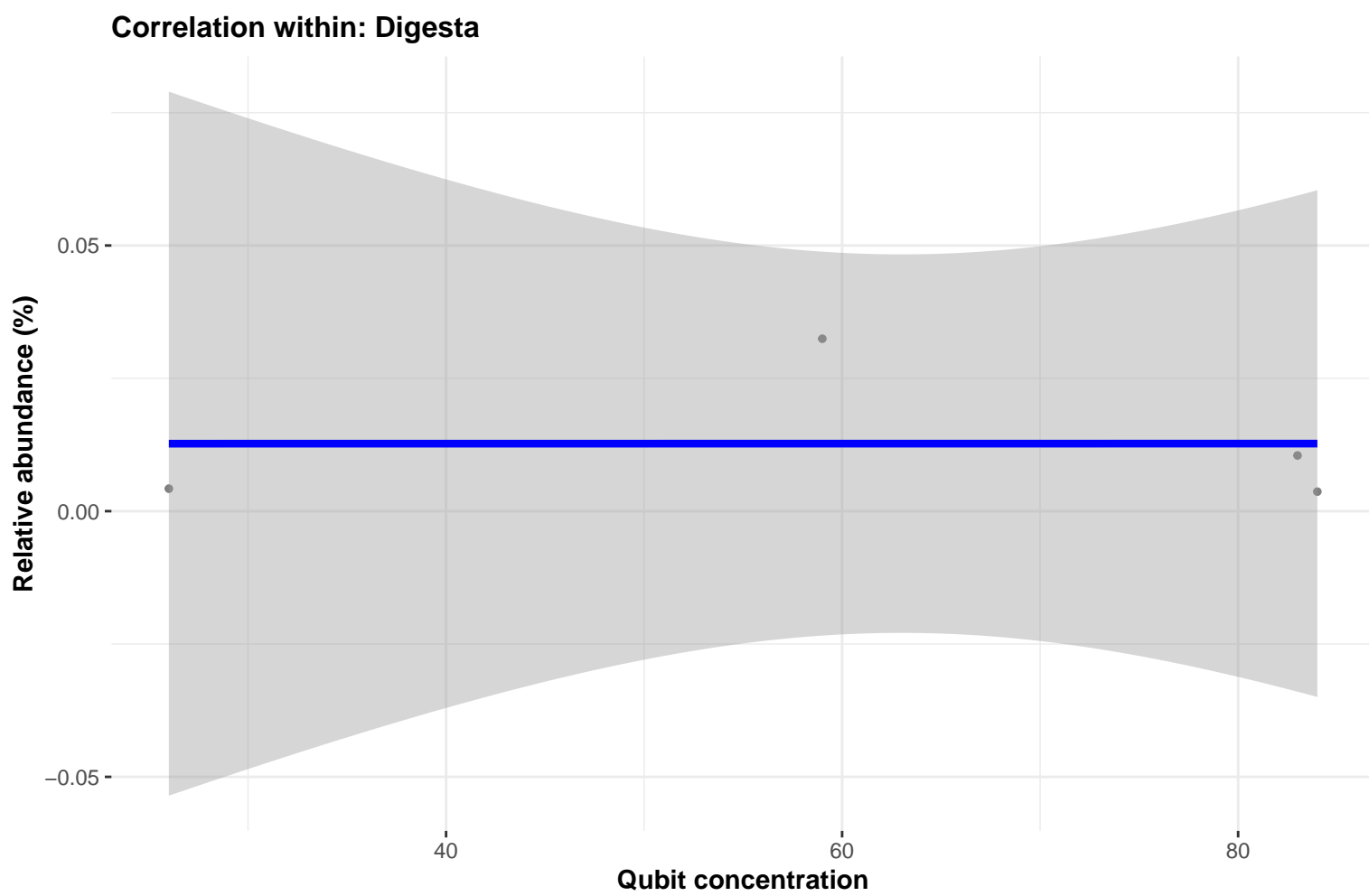
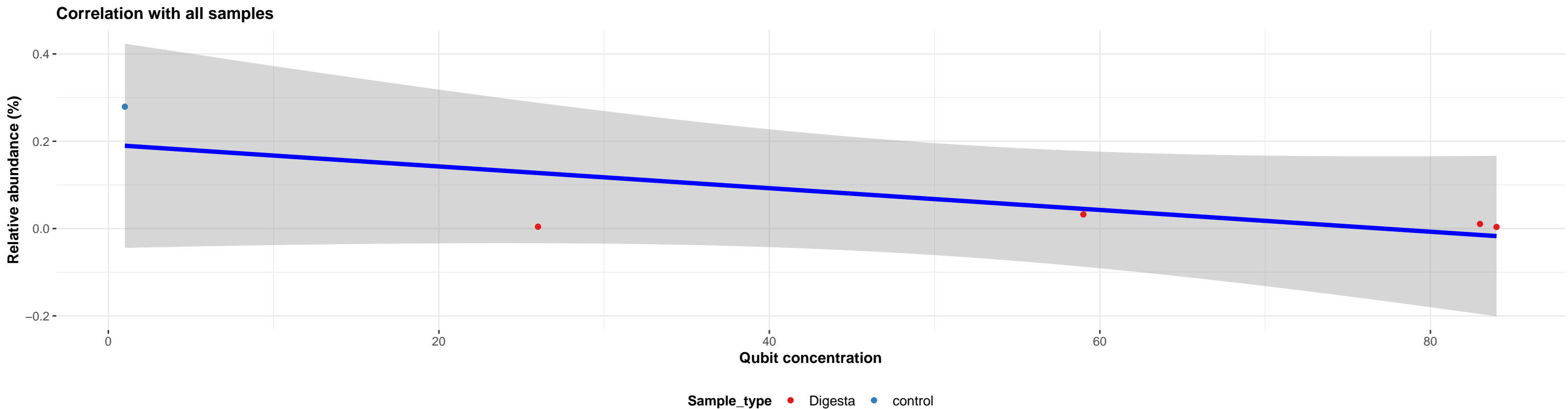


Correlation within: control





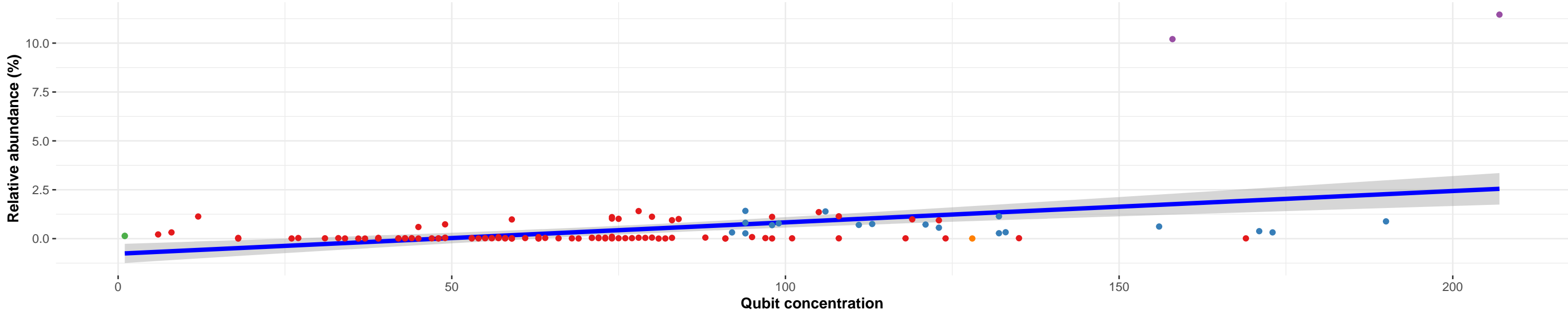
Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Rhizobacter; NA



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Limosilactobacillus; NA

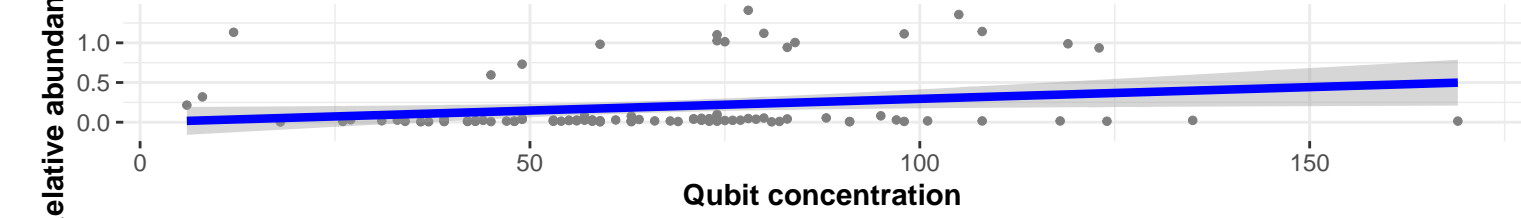
Correlation with all samples

$\log_e(S) = 12.130$, $p = 3.99e-06$, $\hat{\rho}_{\text{Spearman}} = 0.402$, $CI_{95\%} [0.237, 0.544]$, $n_{\text{pairs}} = 123$



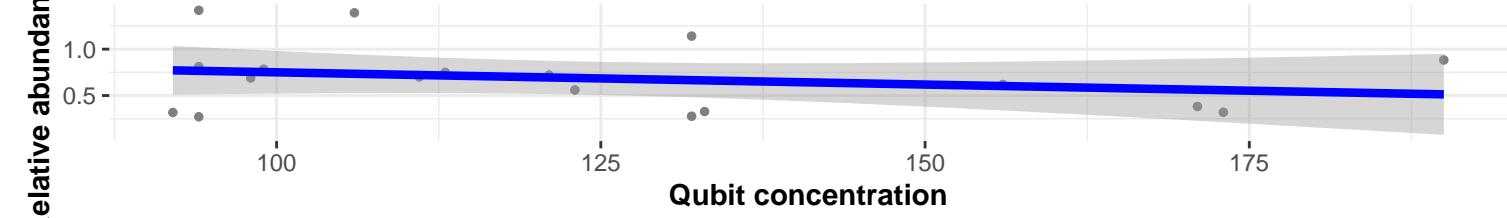
Correlation within: Digesta

$\log_e(S) = 11.764$, $p = 0.022$, $\hat{\rho}_{\text{Spearman}} = 0.228$, $CI_{95\%} [0.028, 0.412]$, $n_{\text{pairs}} = 100$

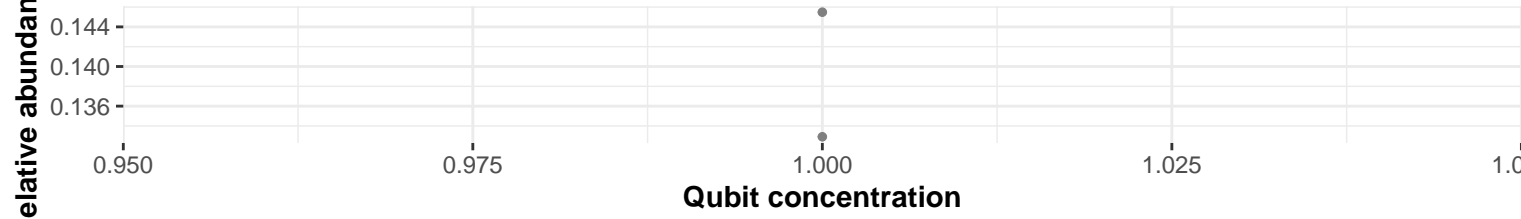


Correlation within: Feed

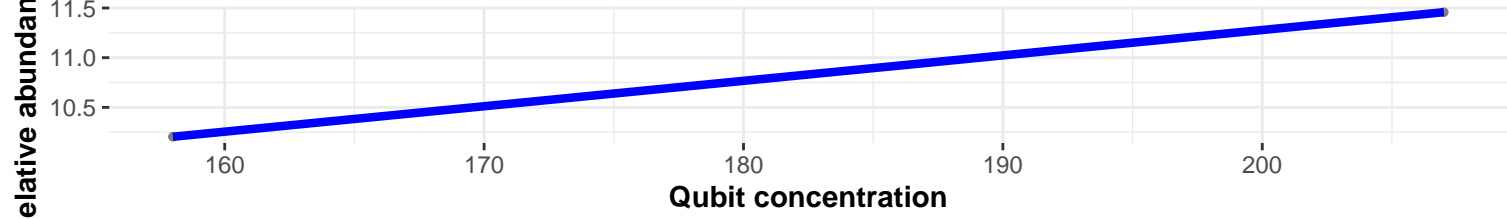
$\log_e(S) = 6.987$, $p = 0.644$, $\hat{\rho}_{\text{Spearman}} = -0.117$, $CI_{95\%} [-0.564, 0.383]$, $n_{\text{pairs}} = 18$



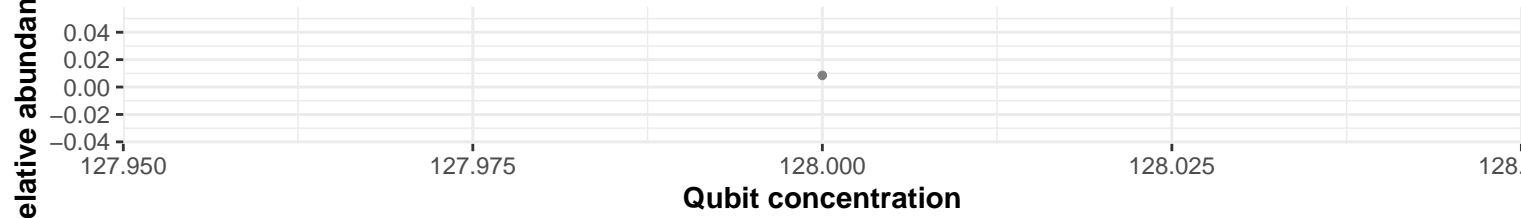
Correlation within: control



Correlation within: Positive_control



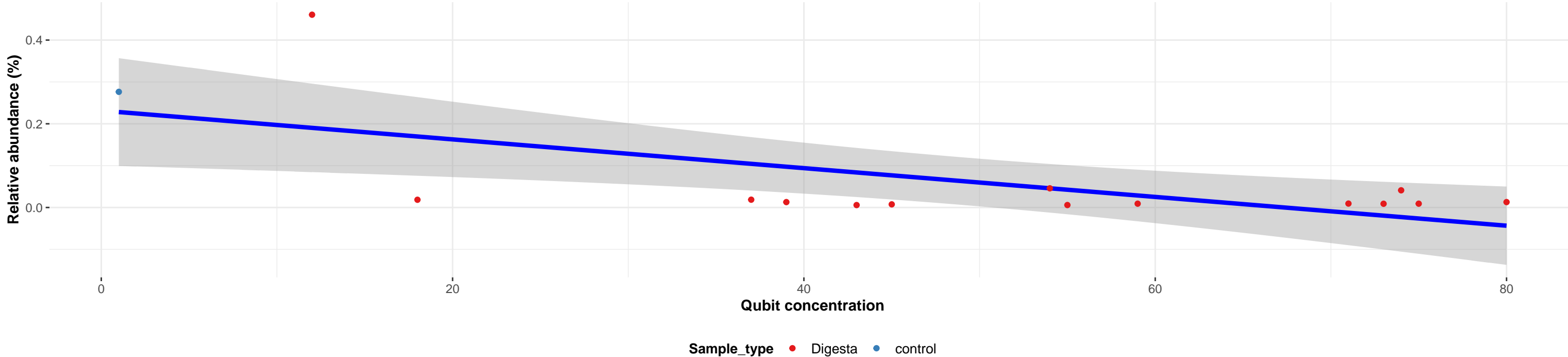
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; stationis

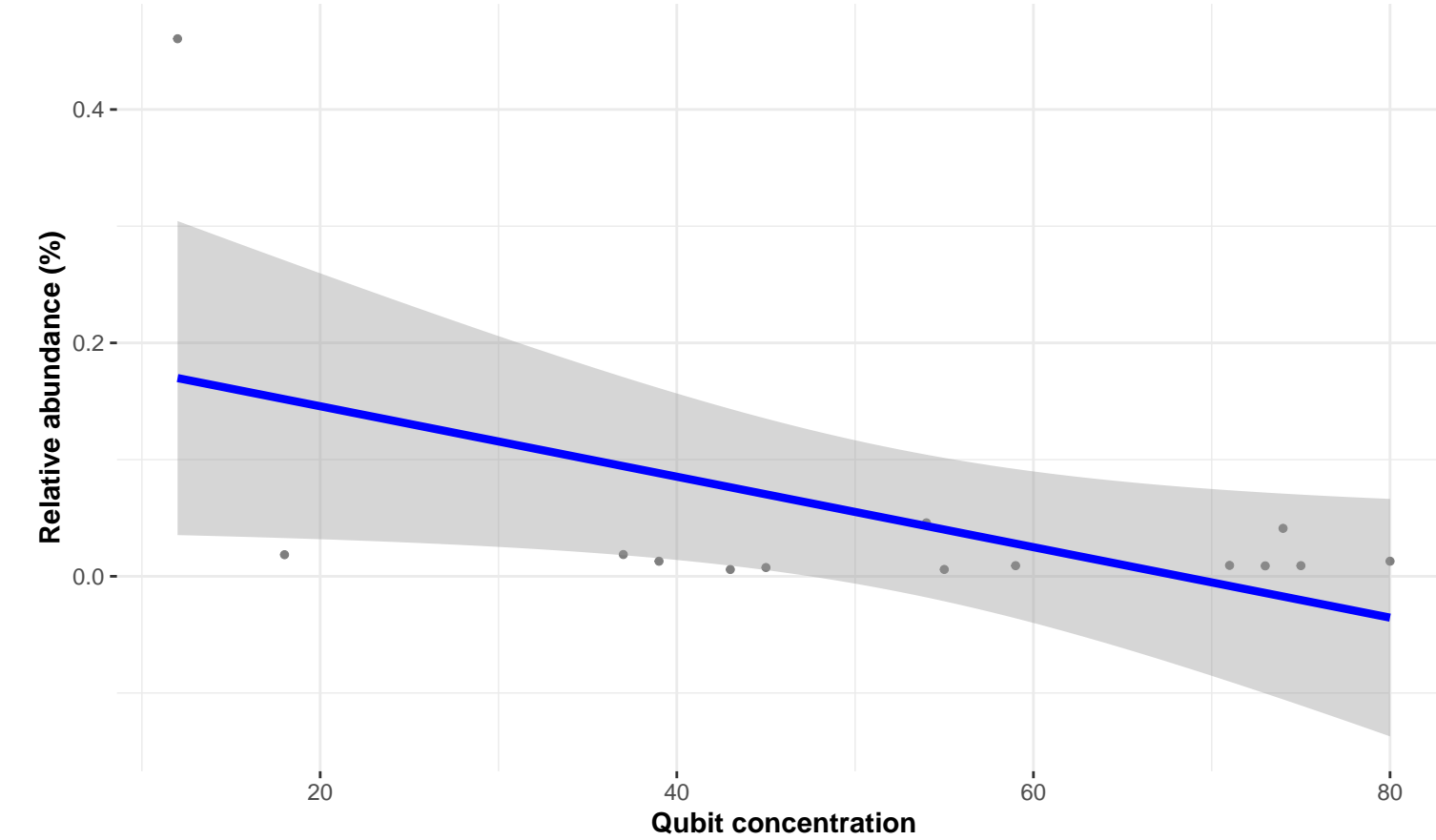
Correlation with all samples

$\log_e(S) = 6.641$, $p = 0.177$, $\hat{\rho}_{\text{Spearman}} = -0.368$, $CI_{95\%} [-0.748, 0.194]$, $n_{\text{pairs}} = 15$

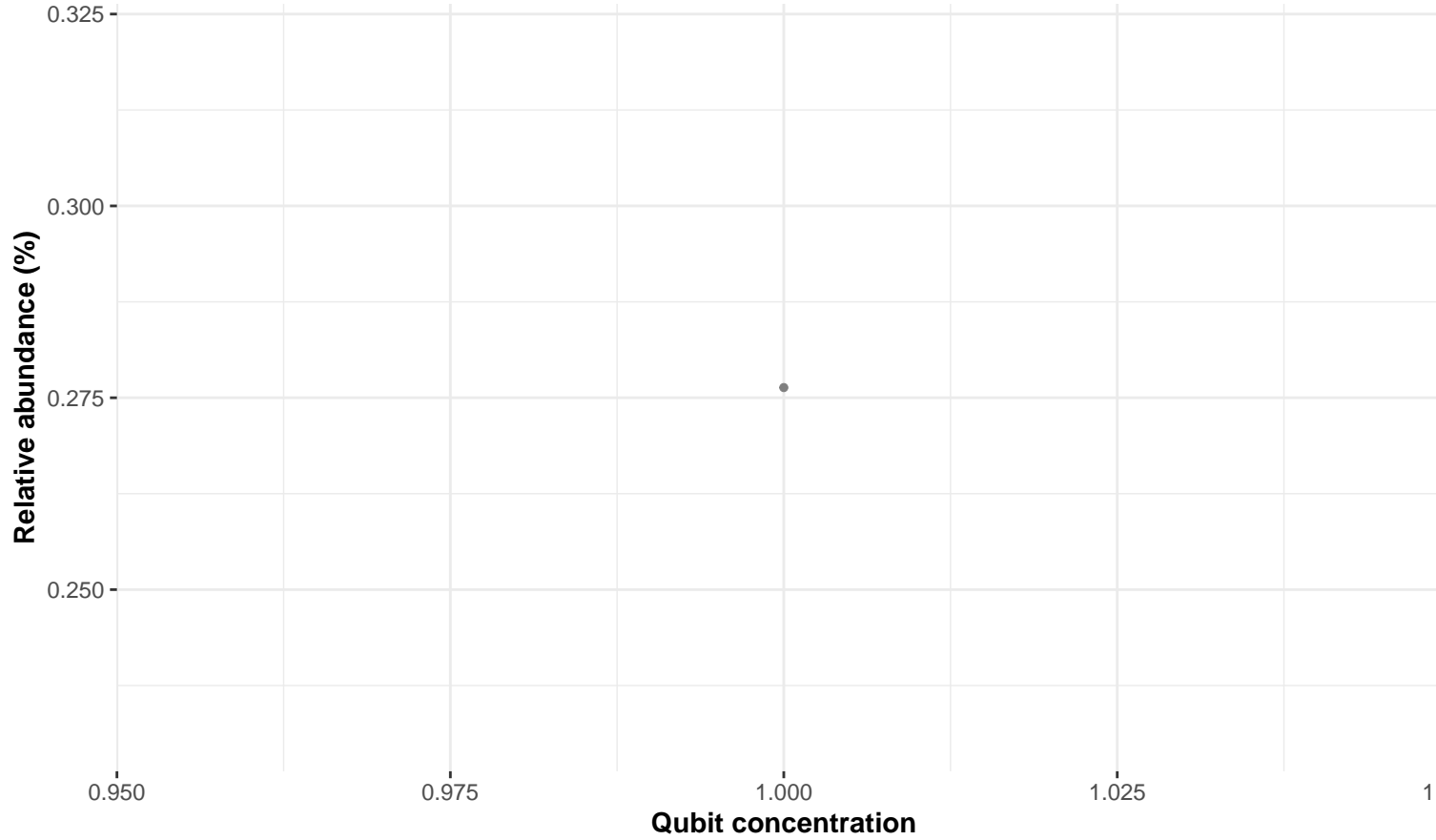


Correlation within: Digesta

$\log_e(S) = 6.324$, $p = 0.436$, $\hat{\rho}_{\text{Spearman}} = -0.226$, $CI_{95\%} [-0.685, 0.361]$, $n_{\text{pairs}} = 14$



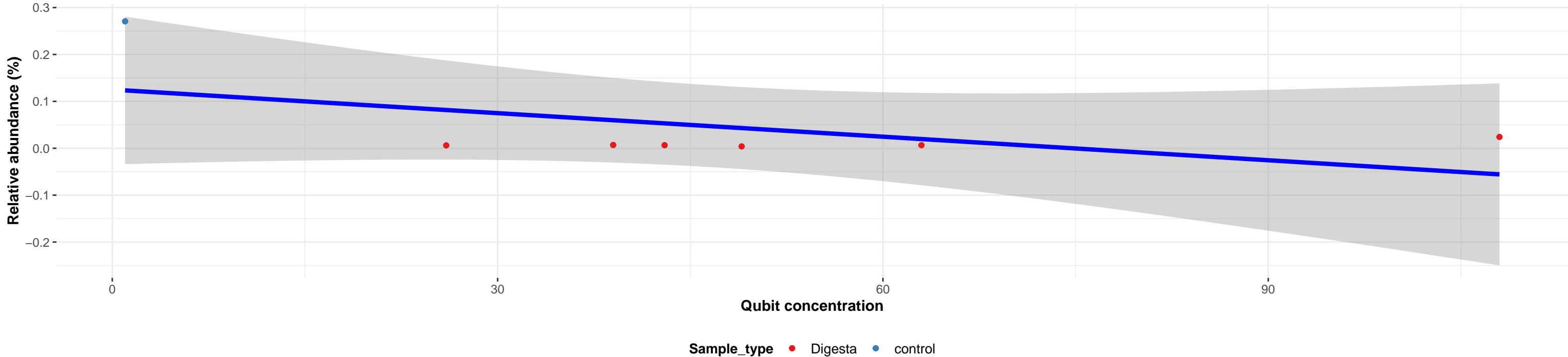
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Anaerobacillus; NA

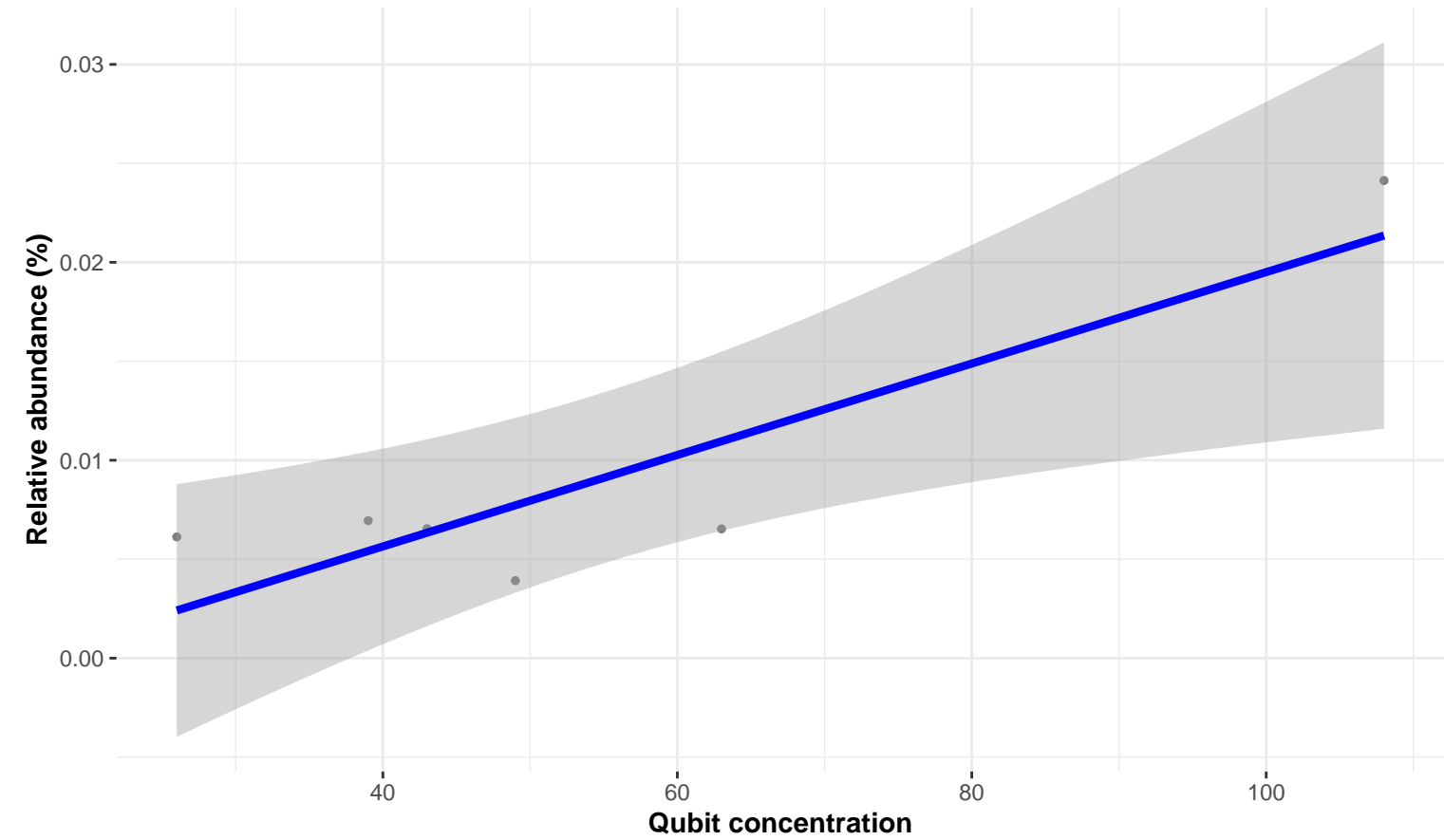
Correlation with all samples

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

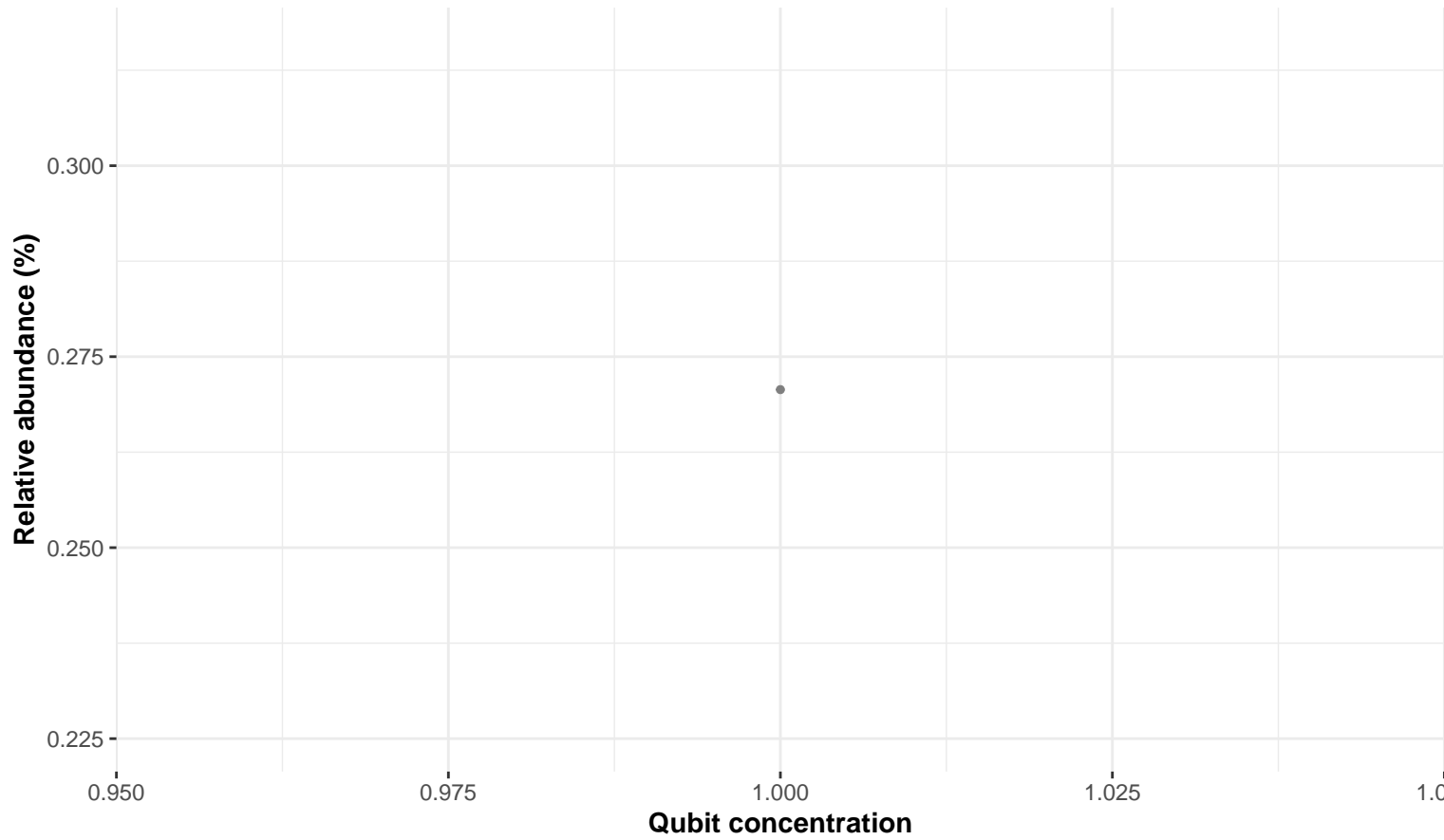


Correlation within: Digesta

$\log_e(S) = 3.178$, $p = 0.544$, $\hat{\rho}_{\text{Spearman}} = 0.314$, $\text{CI}_{95\%} [-0.686, 0.903]$, $n_{\text{pairs}} = 6$



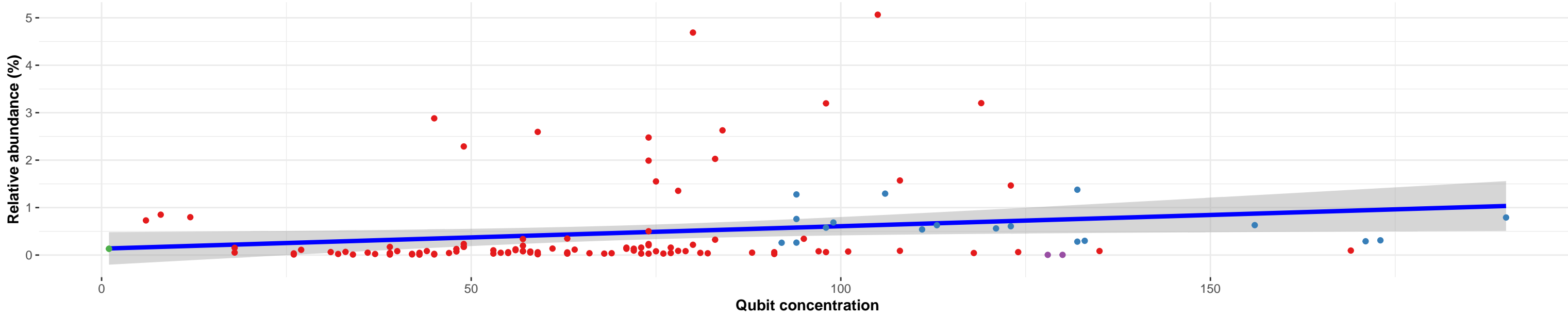
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Weissella; NA

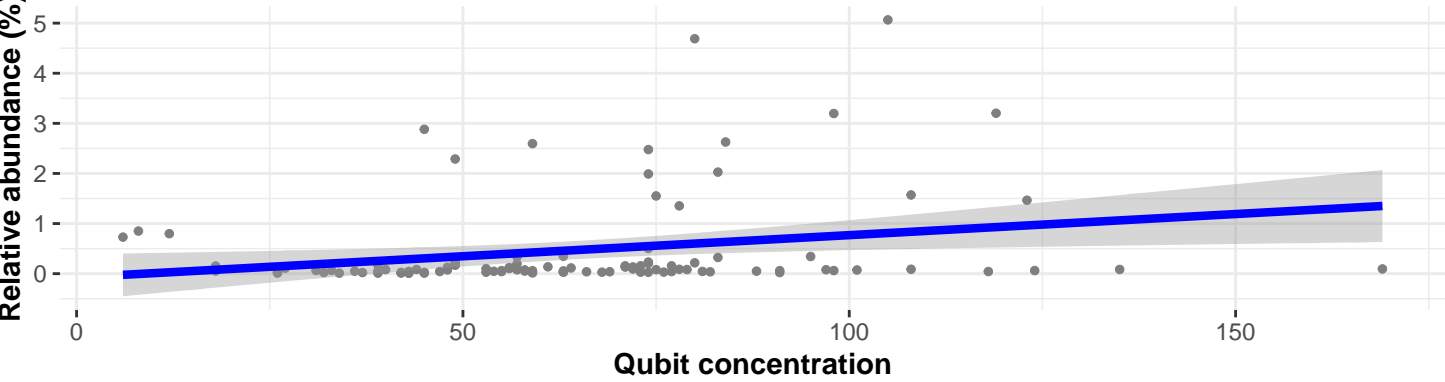
Correlation with all samples

$\log_e(S) = 12.302$, $p = 1.7\text{e-}05$, $\hat{\rho}_{\text{Spearman}} = 0.370$, $\text{CI}_{95\%} [0.205, 0.515]$, $n_{\text{pairs}} = 128$



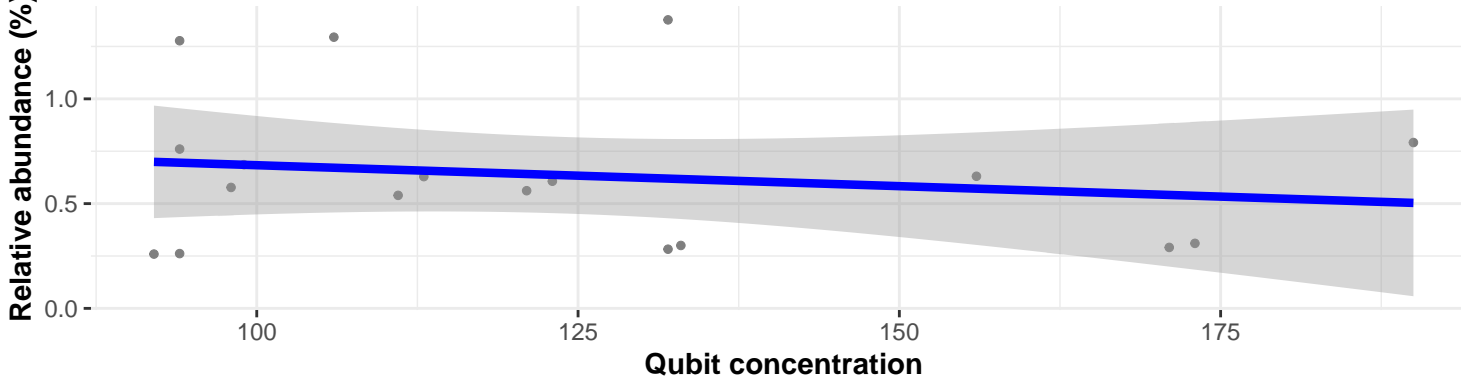
Correlation within: Digesta

$\log_e(S) = 11.838$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.303$, $\text{CI}_{95\%} [0.113, 0.471]$, $n_{\text{pairs}} = 106$

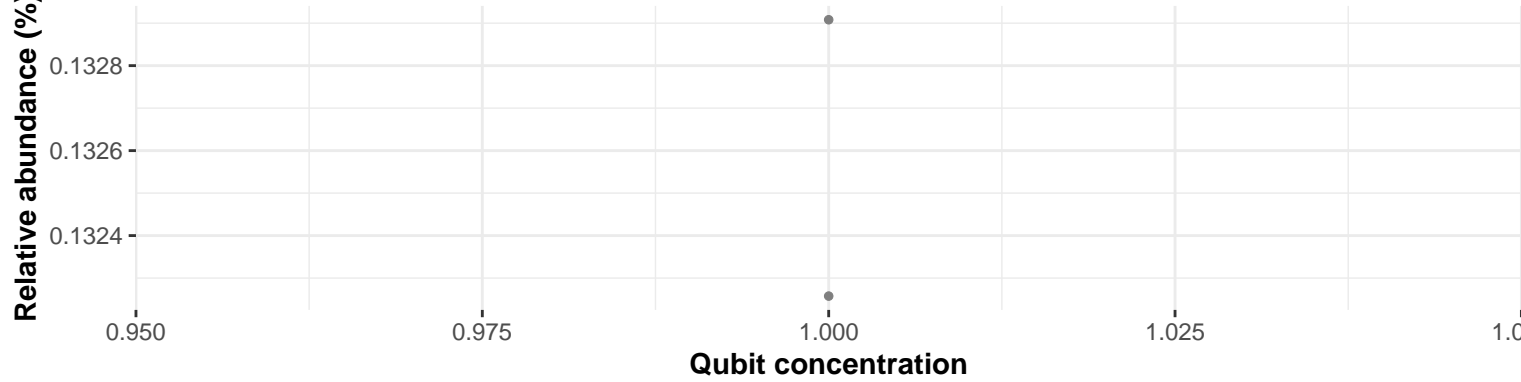


Correlation within: Feed

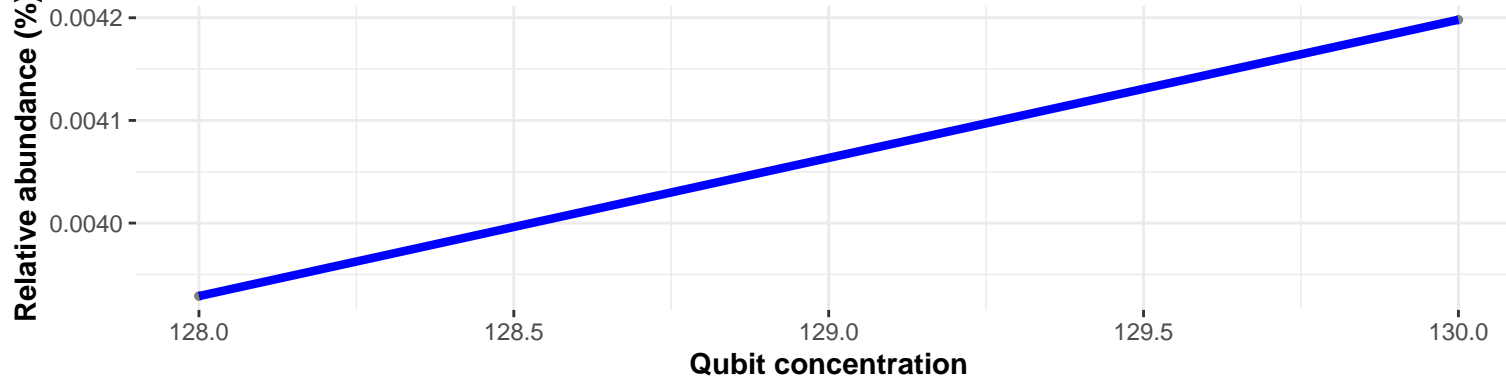
$\log_e(S) = 6.860$, $p = 0.948$, $\hat{\rho}_{\text{Spearman}} = 0.017$, $\text{CI}_{95\%} [-0.466, 0.491]$, $n_{\text{pairs}} = 18$



Correlation within: control



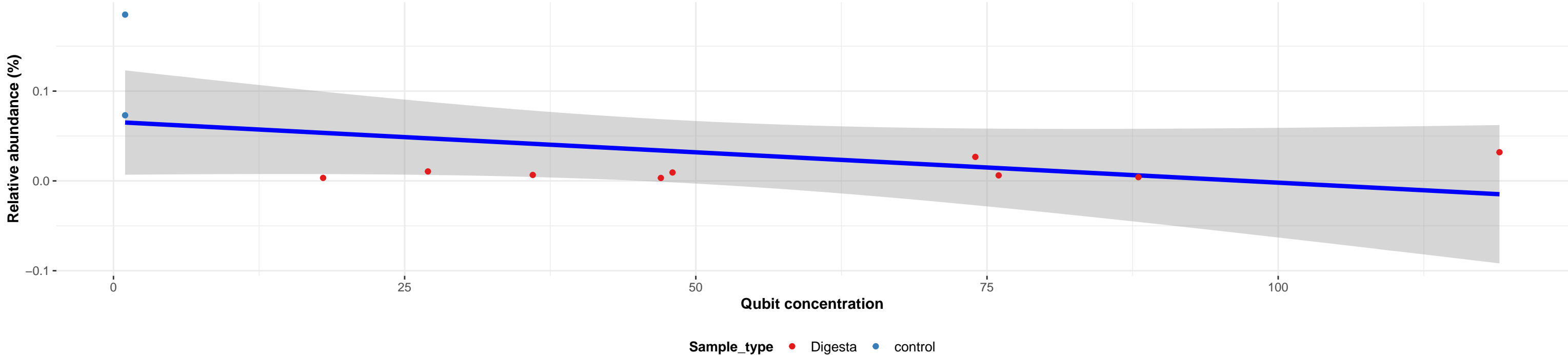
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; NA

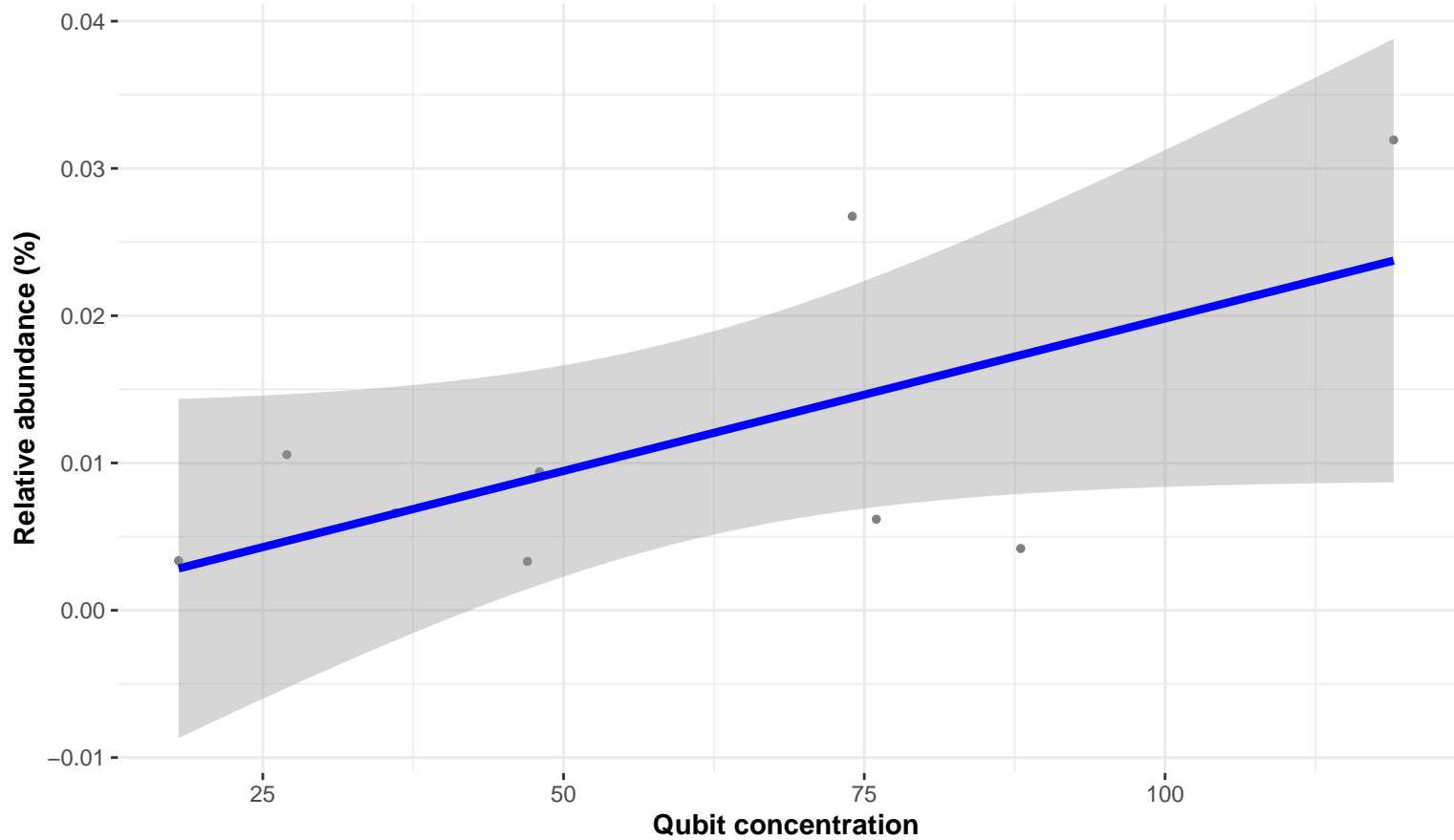
Correlation with all samples

$\log_e(S) = 5.624$, $p = 0.441$, $\hat{\rho}_{\text{Spearman}} = -0.260$, $\text{CI}_{95\%} [-0.753, 0.420]$, $n_{\text{pairs}} = 11$

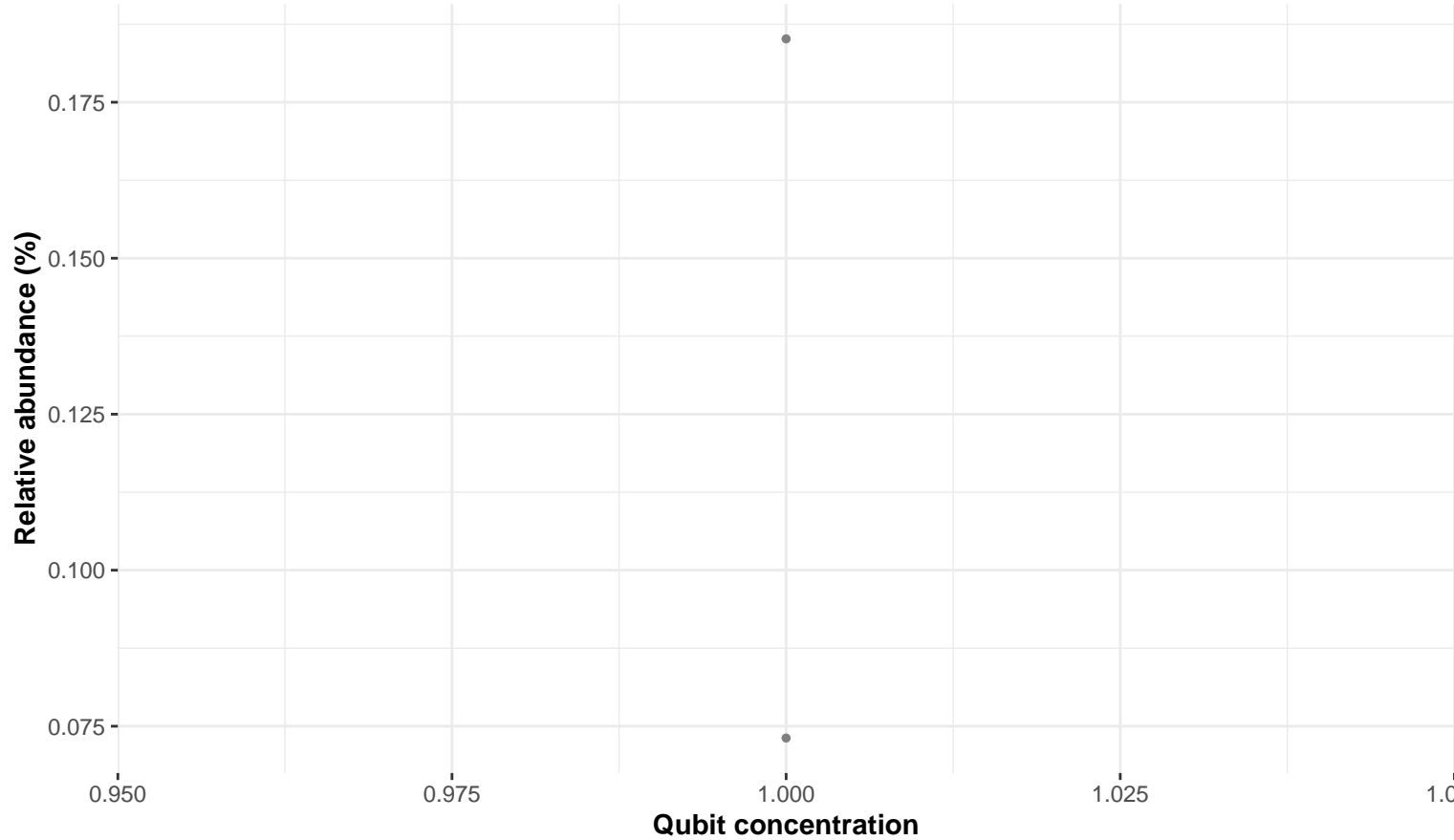


Correlation within: Digesta

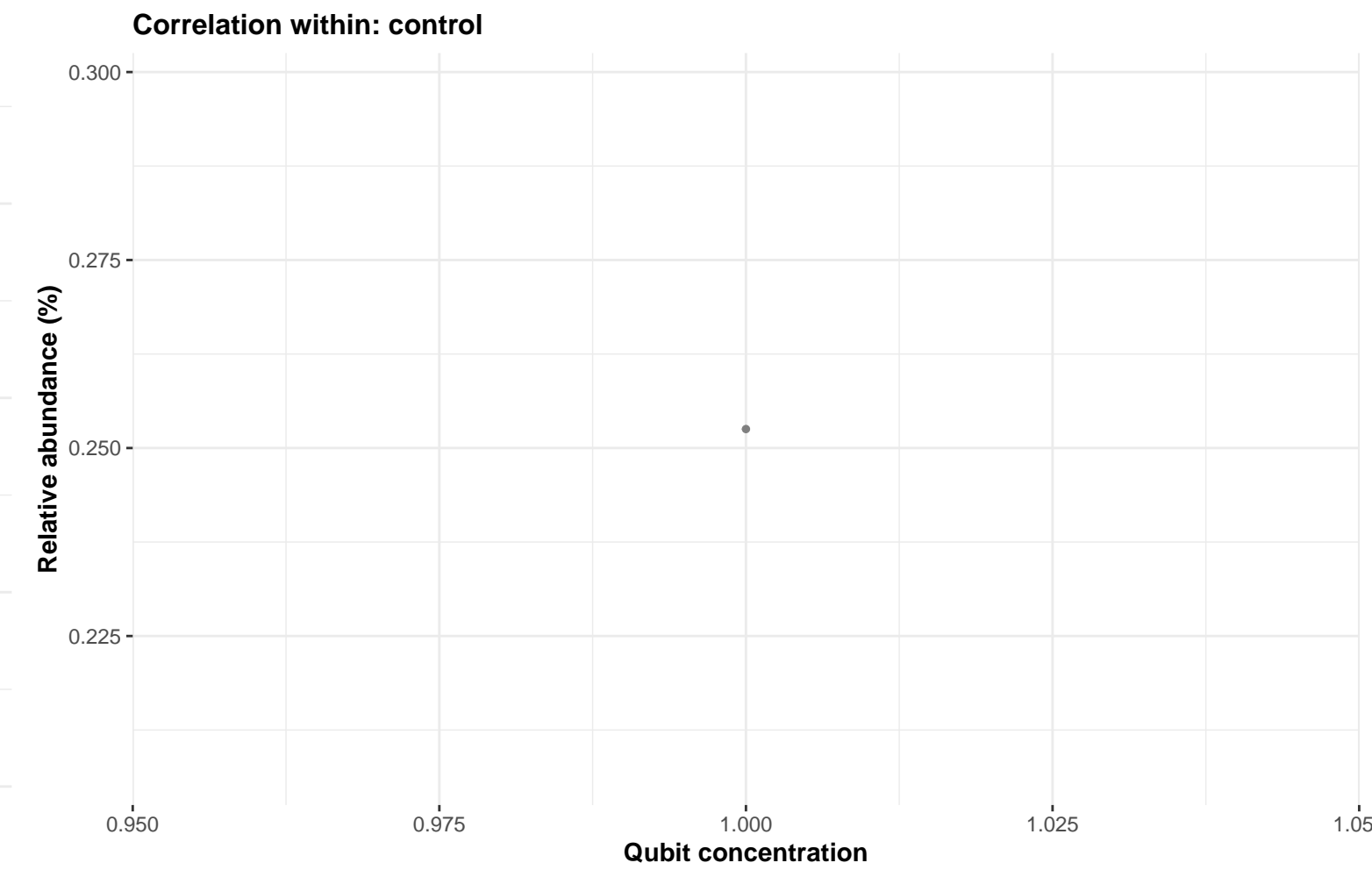
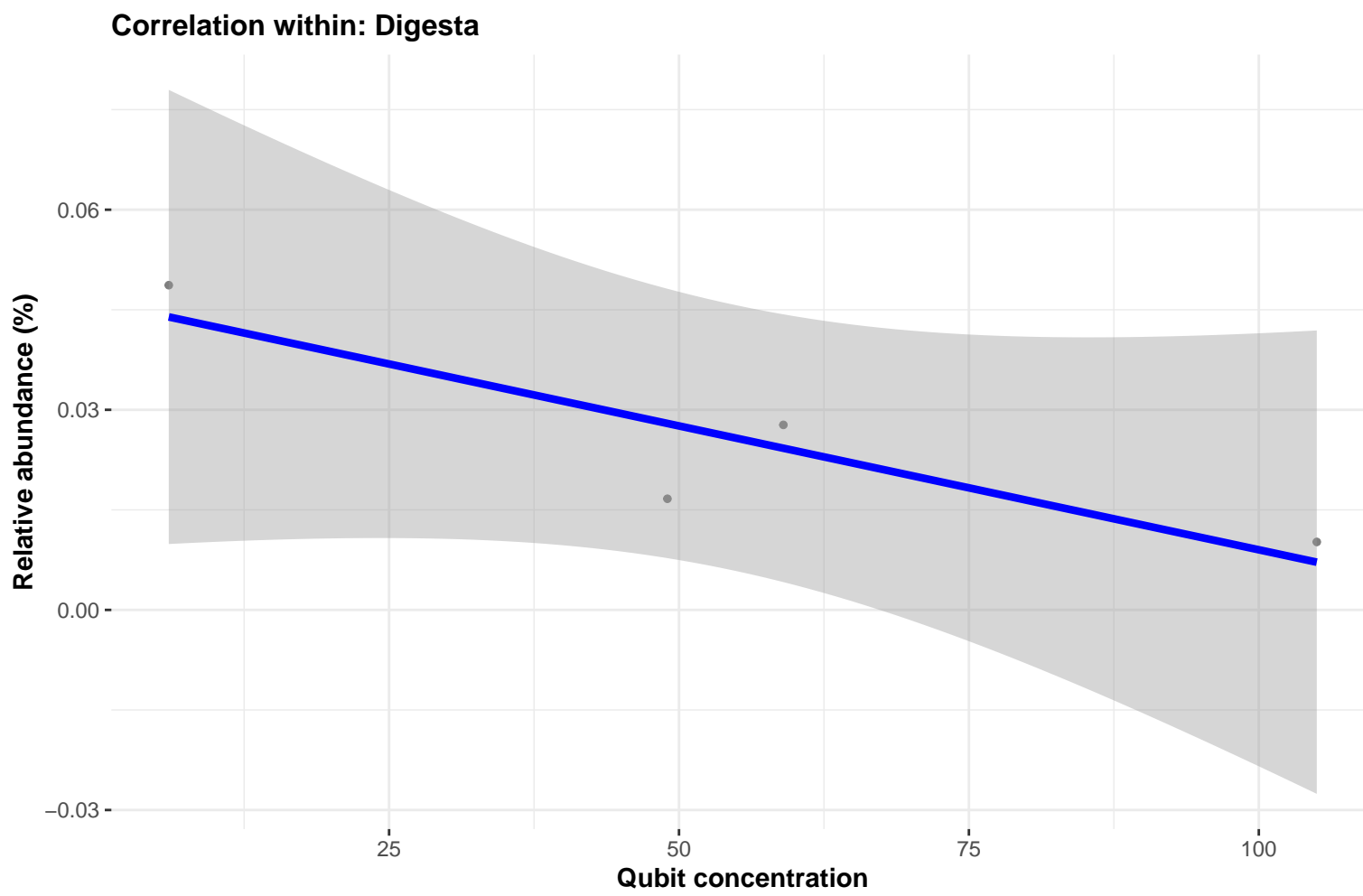
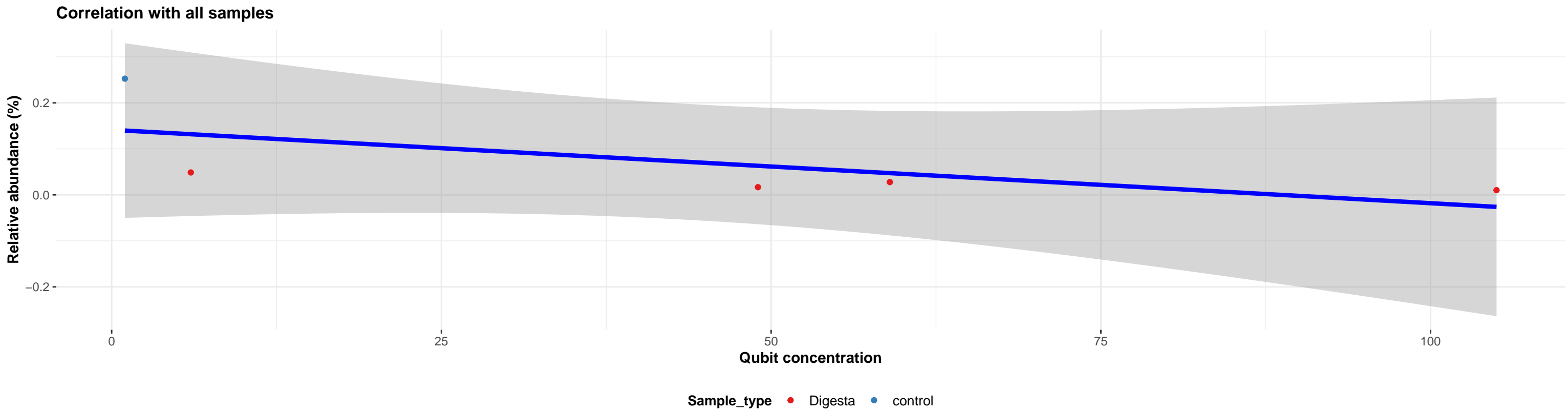
$\log_e(S) = 4.357$, $p = 0.356$, $\hat{\rho}_{\text{Spearman}} = 0.350$, $\text{CI}_{95\%} [-0.429, 0.830]$, $n_{\text{pairs}} = 9$



Correlation within: control



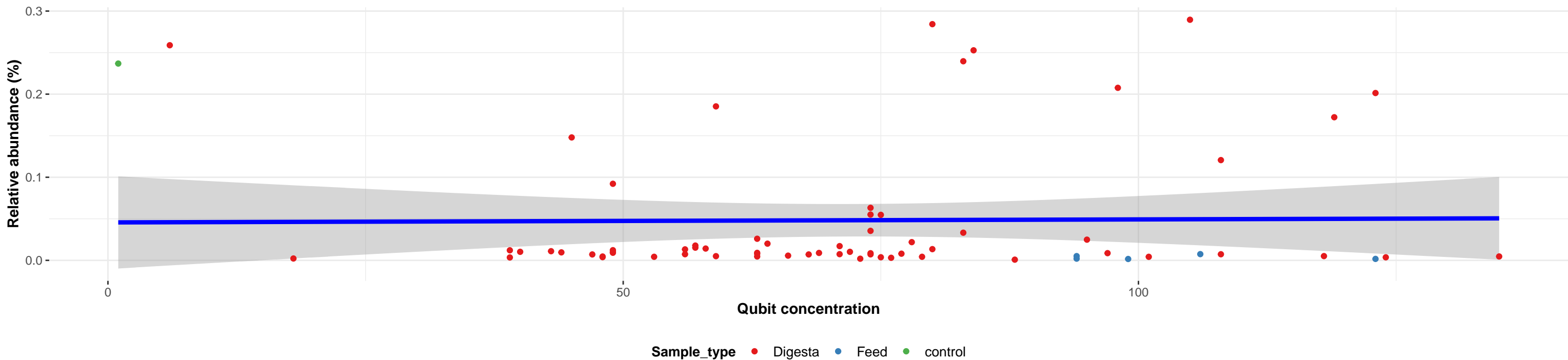
Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Microbacteriaceae; Rhodoluna; limnophila



Bacteria; Firmicutes; Clostridia; Peptococcales; Peptococcaceae; Peptococcus; NA

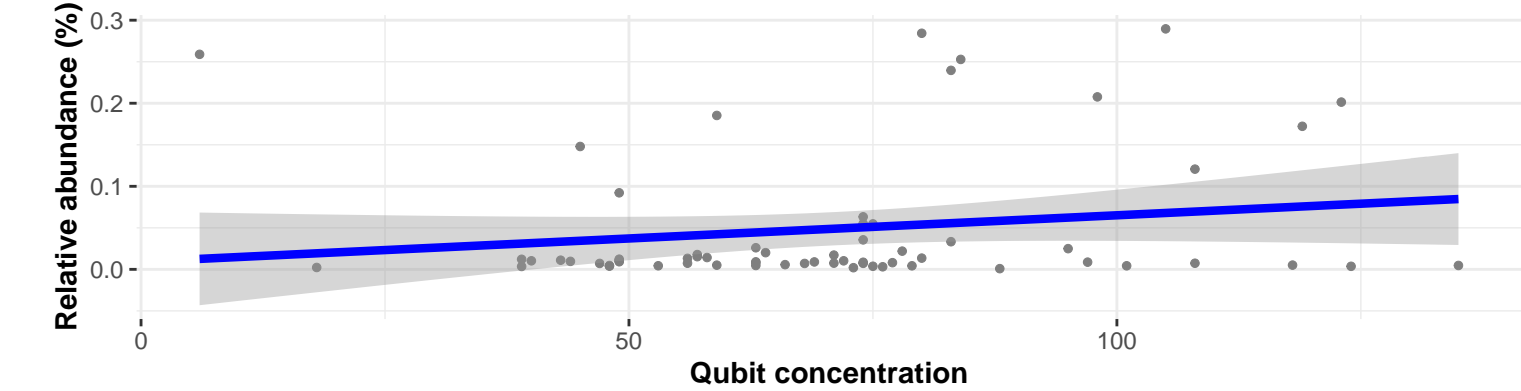
Correlation with all samples

$\log_e(S) = 11.001$, $p = 0.687$, $\hat{\rho}_{\text{Spearman}} = -0.049$, $CI_{95\%} [-0.287, 0.195]$, $n_{\text{pairs}} = 70$

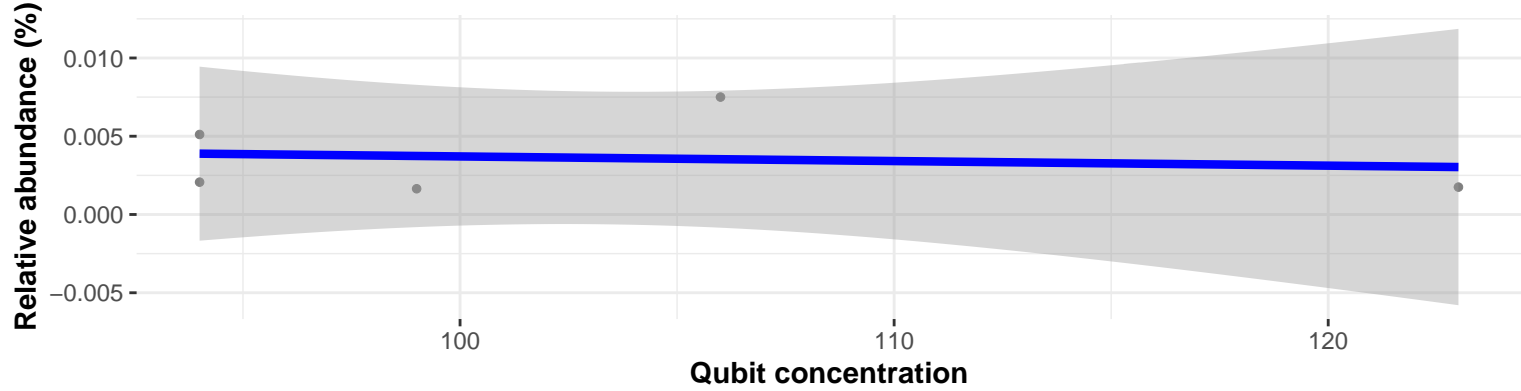


Correlation within: Digesta

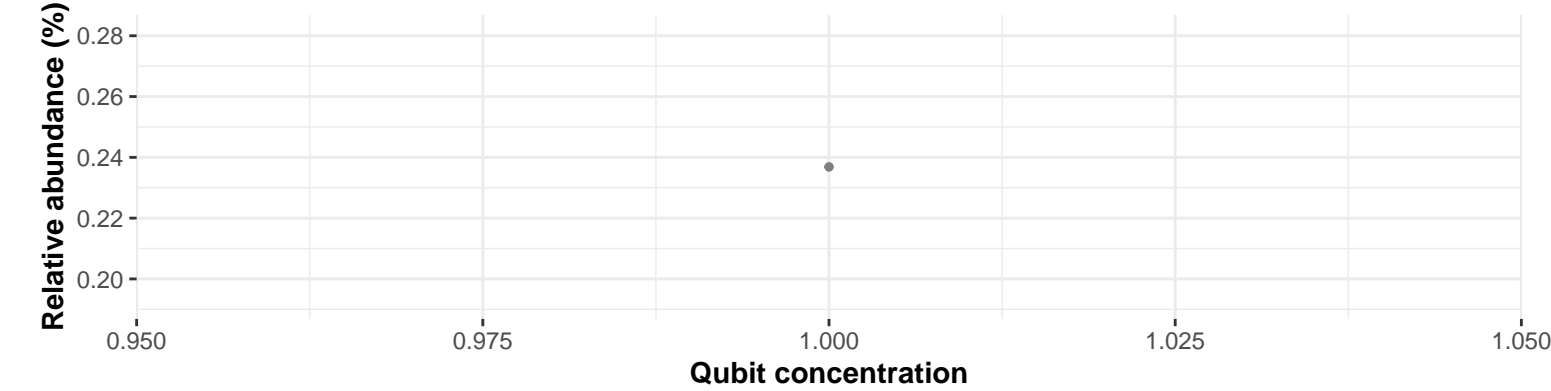
$\log_e(S) = 10.555$, $p = 0.339$, $\hat{\rho}_{\text{Spearman}} = 0.121$, $CI_{95\%} [-0.135, 0.363]$, $n_{\text{pairs}} = 64$



Correlation within: Feed



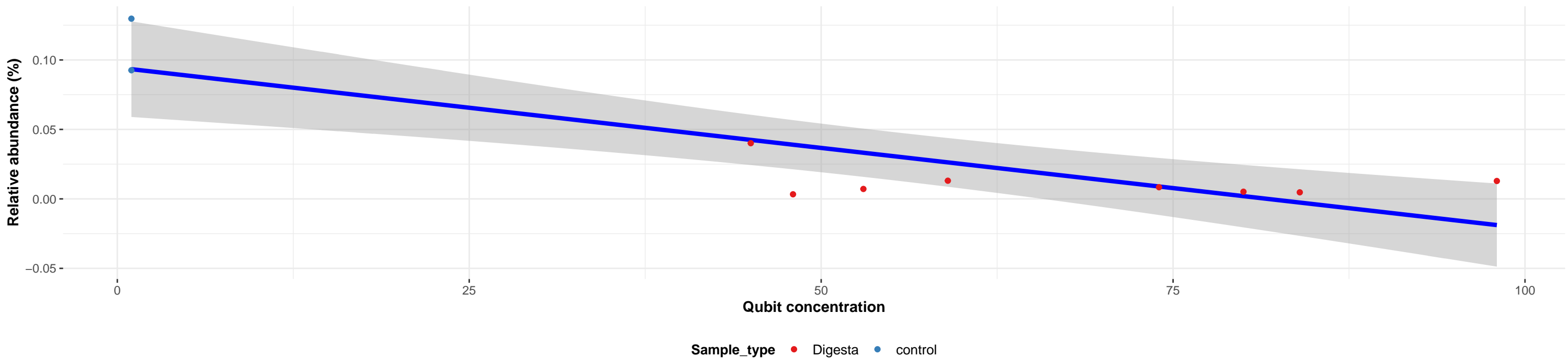
Correlation within: control



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Micrococcaceae; Paenarthrobacter; NA

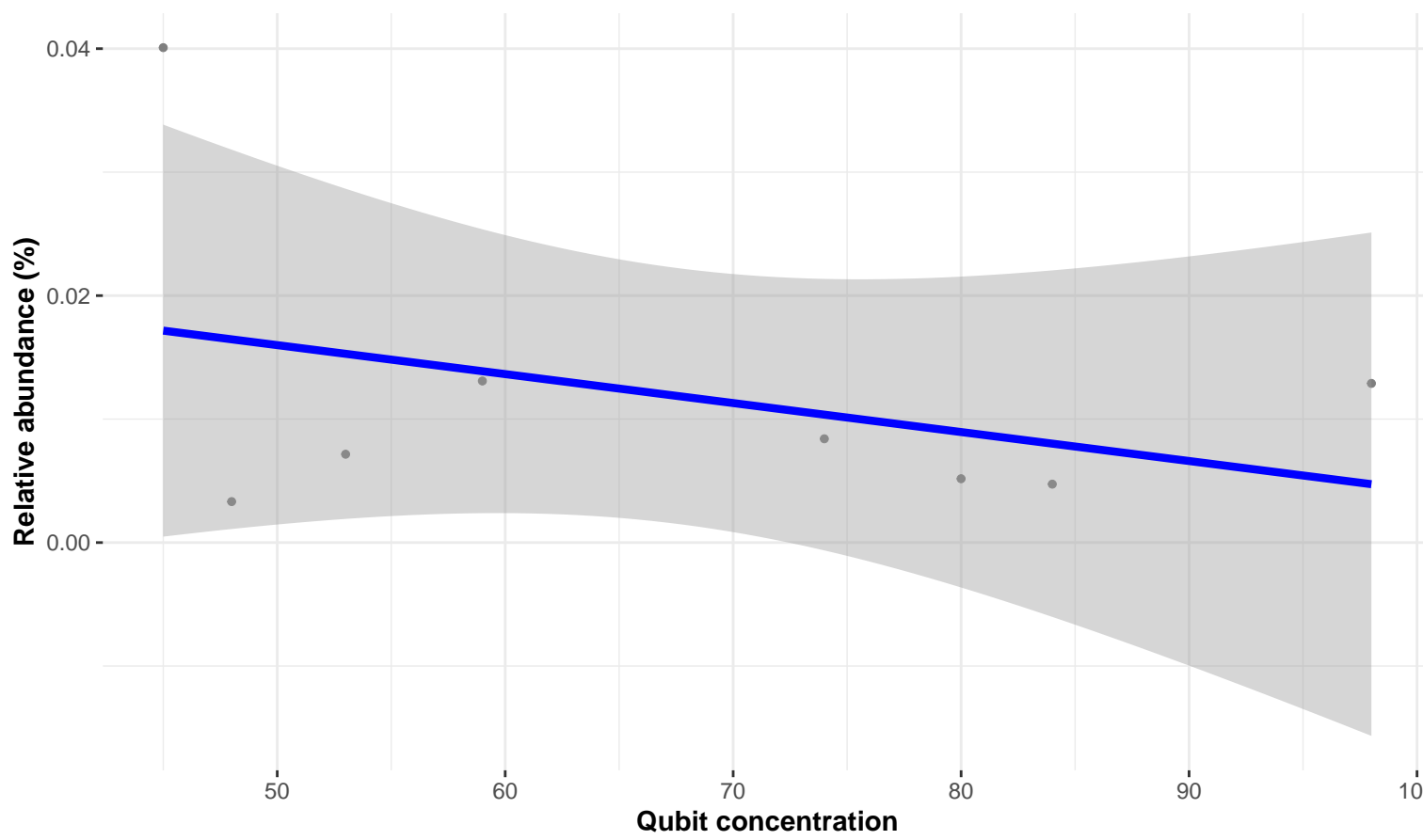
Correlation with all samples

$\log_e(S) = 5.558$, $p = 0.084$, $\hat{\rho}_{\text{Spearman}} = -0.571$, $\text{CI}_{95\%} [-0.888, 0.113]$, $n_{\text{pairs}} = 10$

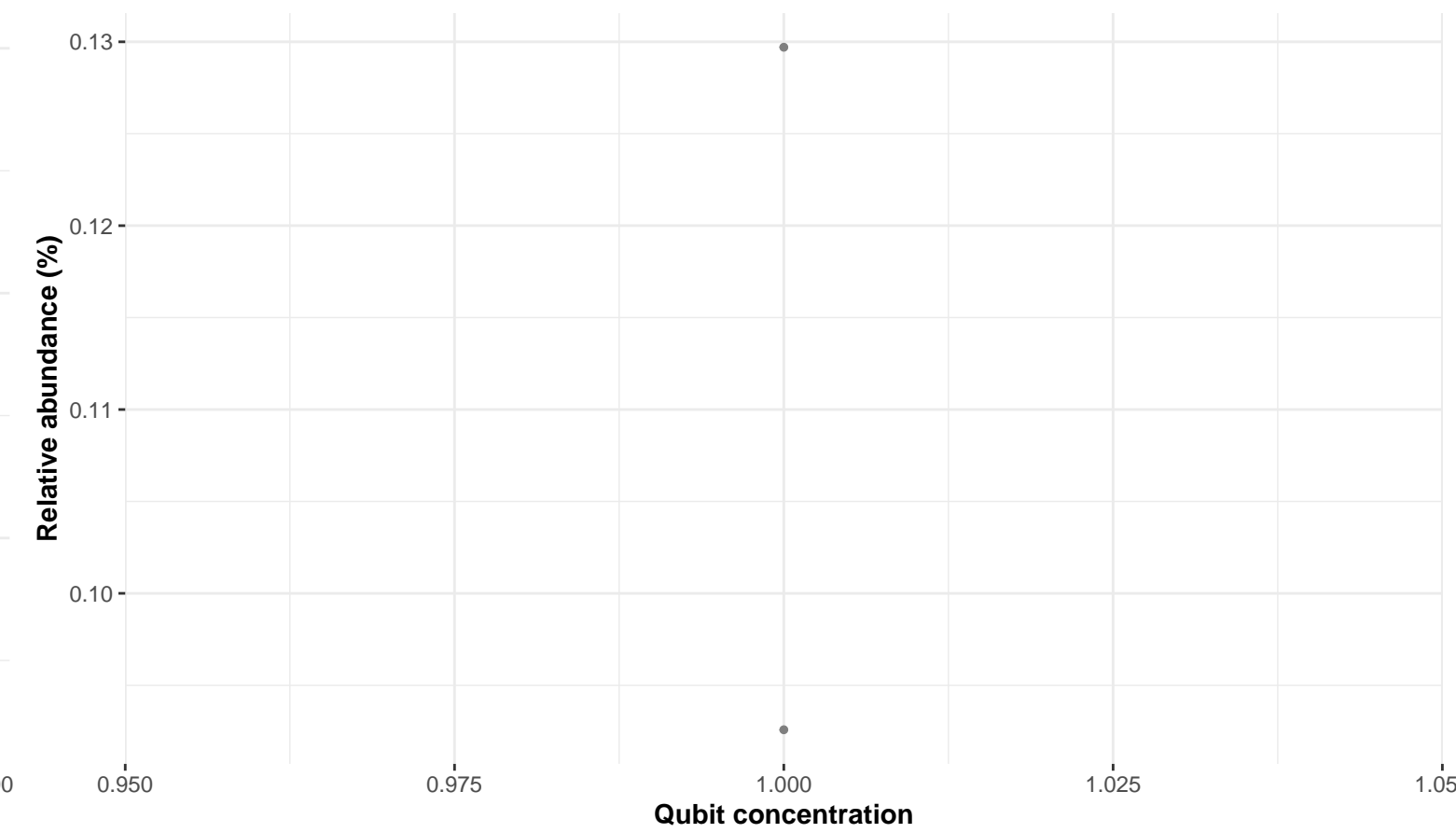


Correlation within: Digesta

$\log_e(S) = 4.585$, $p = 0.693$, $\hat{\rho}_{\text{Spearman}} = -0.167$, $\text{CI}_{95\%} [-0.790, 0.626]$, $n_{\text{pairs}} = 8$



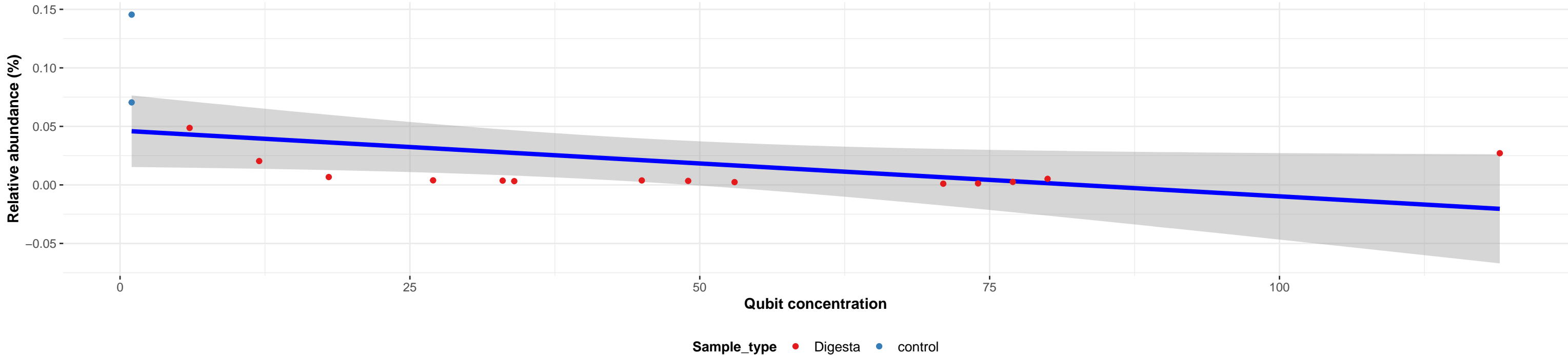
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

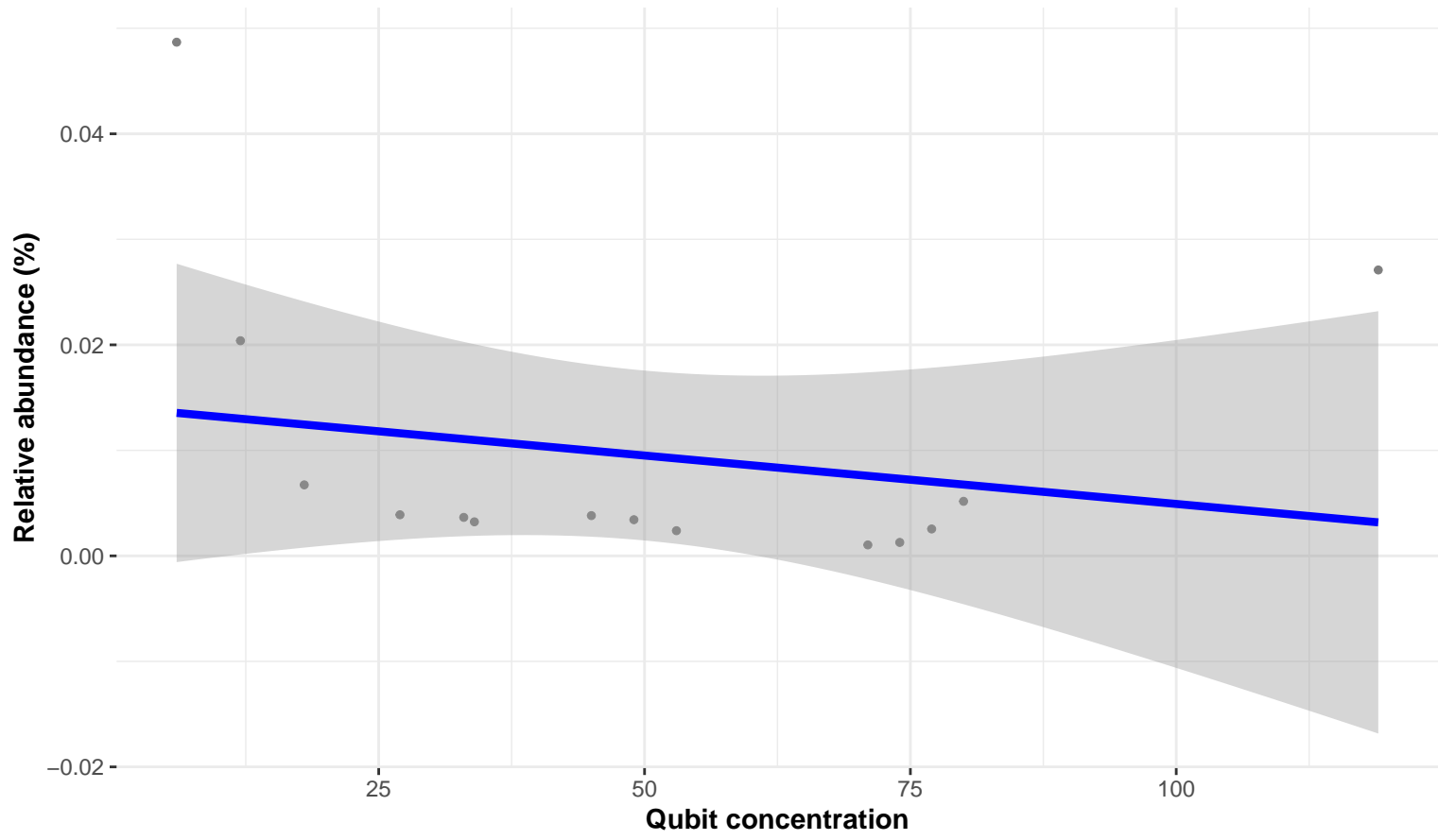
Correlation with all samples

$\log_e(S) = 6.993$, $p = 0.014$, $\hat{\rho}_{\text{Spearman}} = -0.602$, $\text{CI}_{95\%} [-0.850, -0.136]$, $n_{\text{pairs}} = 16$

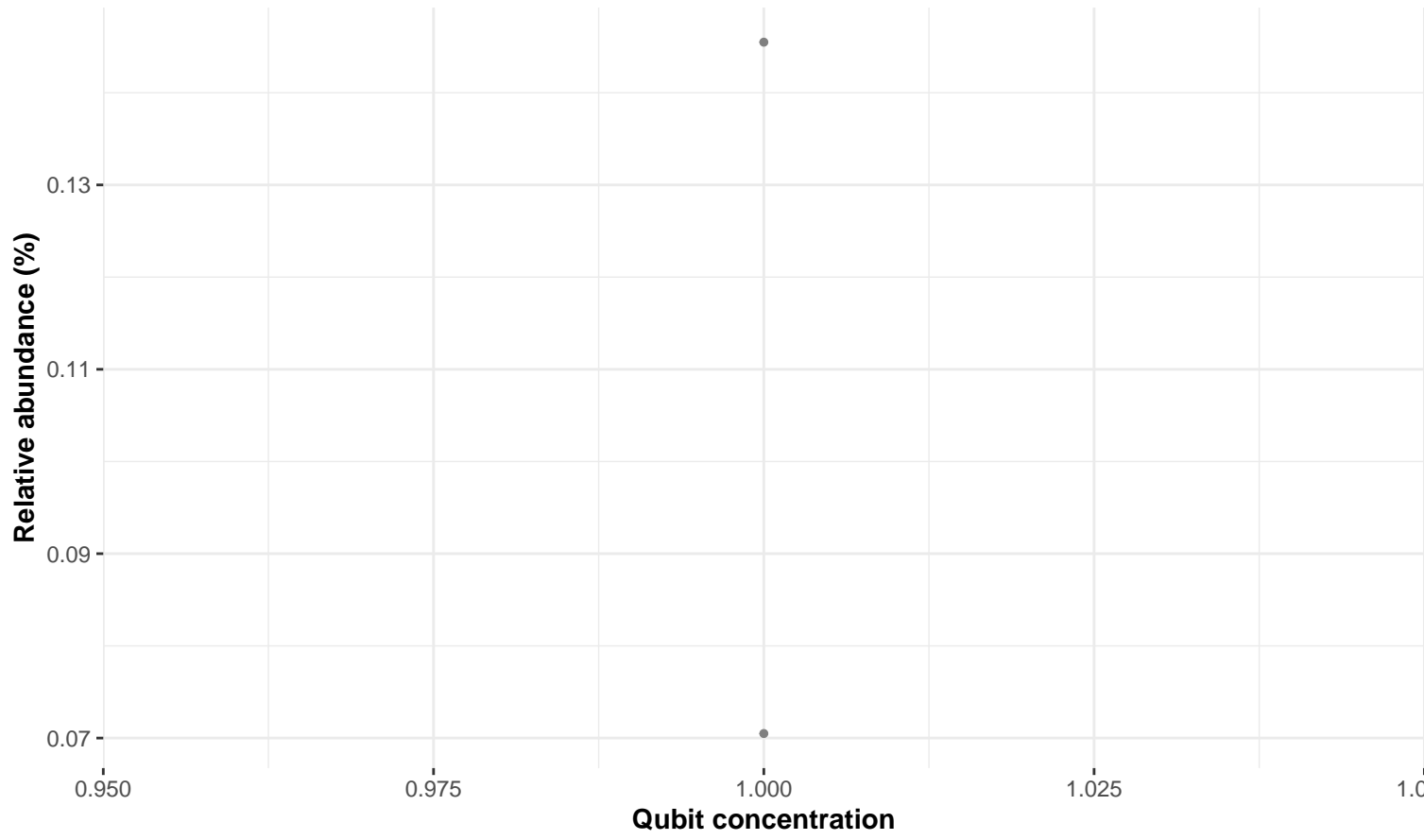


Correlation within: Digesta

$\log_e(S) = 6.461$, $p = 0.149$, $\hat{\rho}_{\text{Spearman}} = -0.407$, $\text{CI}_{95\%} [-0.778, 0.175]$, $n_{\text{pairs}} = 14$



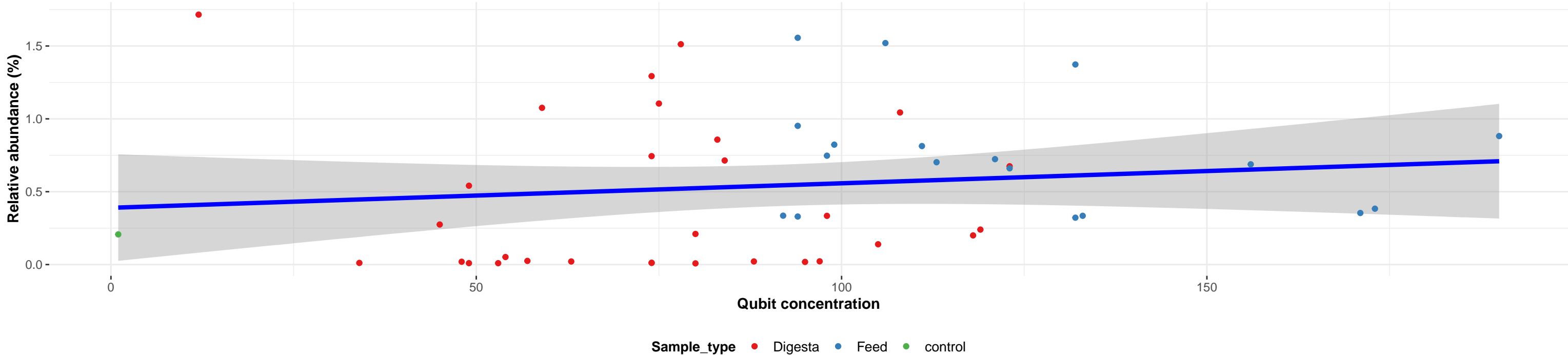
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; NA

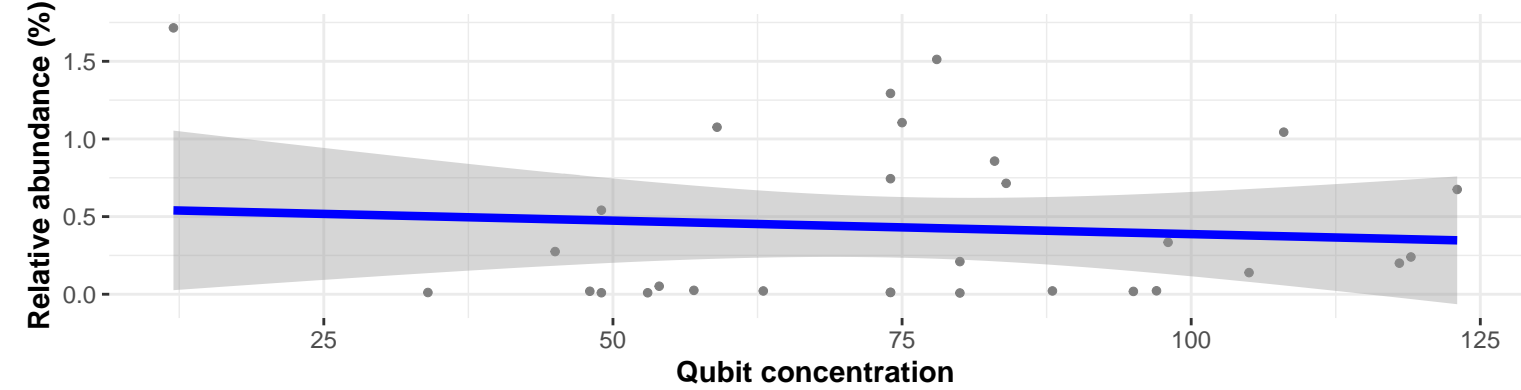
Correlation with all samples

$\log_e(S) = 9.534$, $p = 0.040$, $\hat{\rho}_{\text{Spearman}} = 0.295$, $CI_{95\%} [0.006, 0.538]$, $n_{\text{pairs}} = 49$



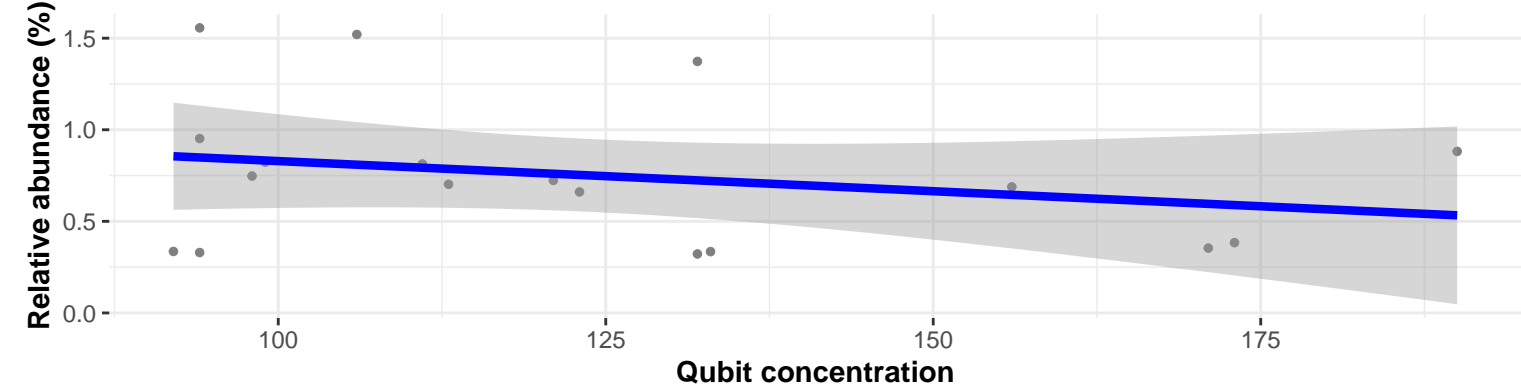
Correlation within: Digesta

$\log_e(S) = 8.242$, $p = 0.413$, $\hat{\rho}_{\text{Spearman}} = 0.155$, $CI_{95\%} [-0.228, 0.497]$, $n_{\text{pairs}} = 30$

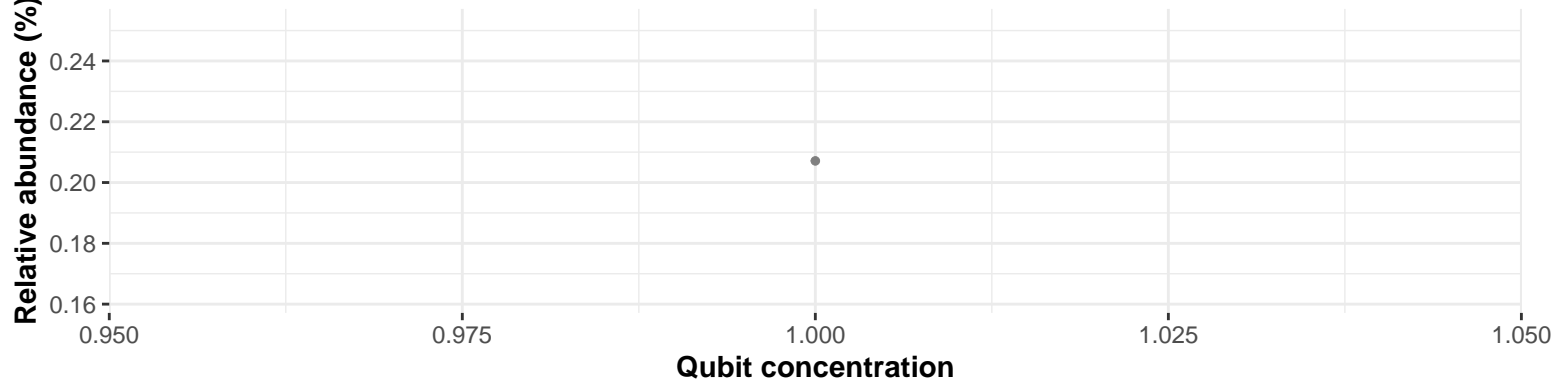


Correlation within: Feed

$\log_e(S) = 7.066$, $p = 0.405$, $\hat{\rho}_{\text{Spearman}} = -0.209$, $CI_{95\%} [-0.625, 0.299]$, $n_{\text{pairs}} = 18$



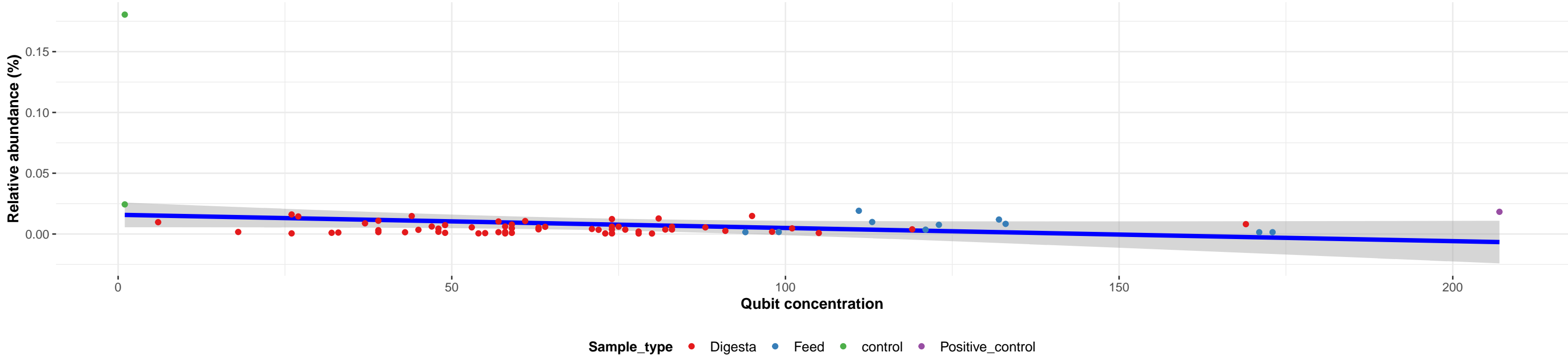
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

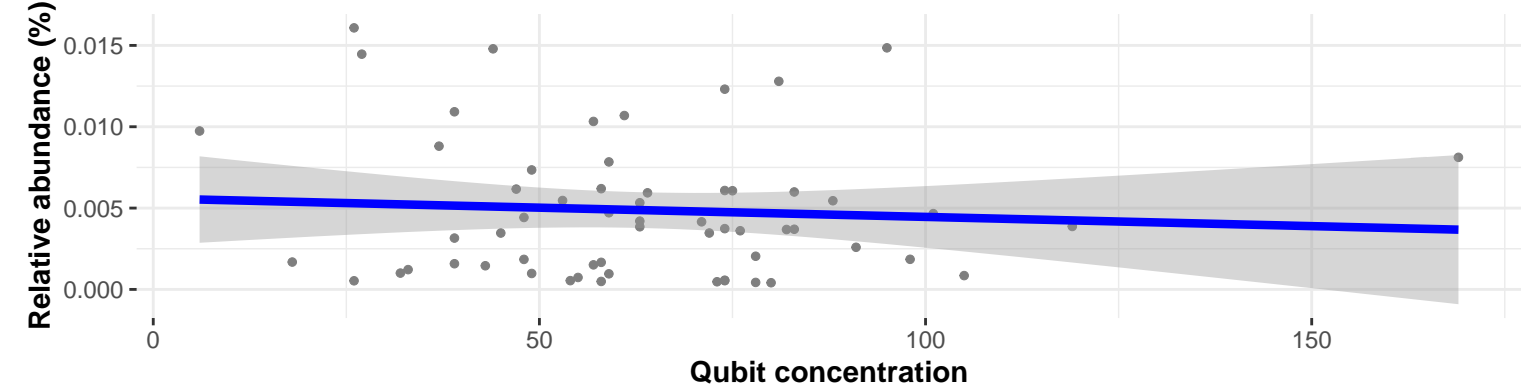
Correlation with all samples

$\log_e(S) = 11.081$, $p = 0.990$, $\hat{\rho}_{\text{Spearman}} = -0.001$, $\text{CI}_{95\%} [-0.238, 0.235]$, $n_{\text{pairs}} = 73$



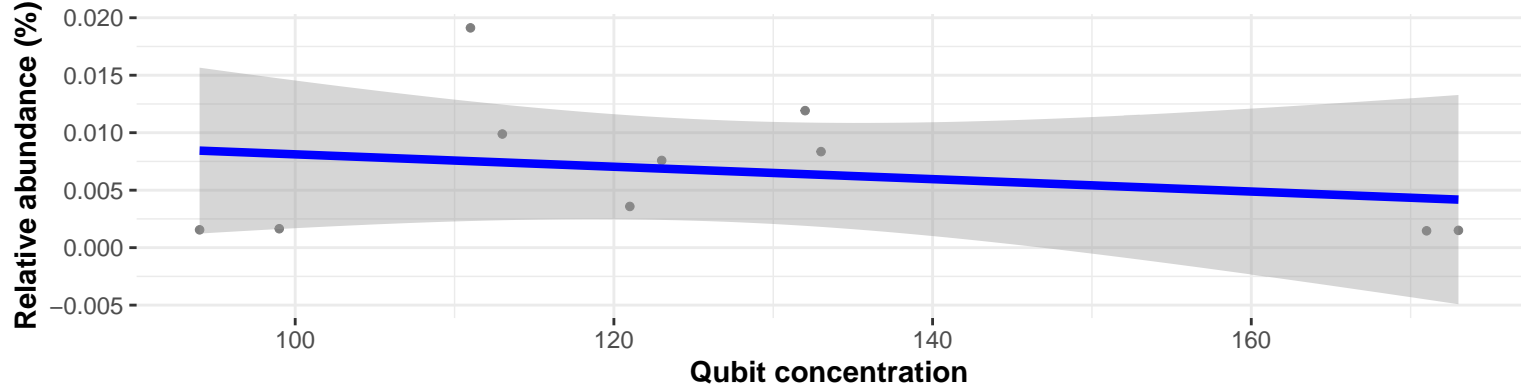
Correlation within: Digesta

$\log_e(S) = 10.522$, $p = 0.810$, $\hat{\rho}_{\text{Spearman}} = -0.032$, $\text{CI}_{95\%} [-0.290, 0.231]$, $n_{\text{pairs}} = 60$

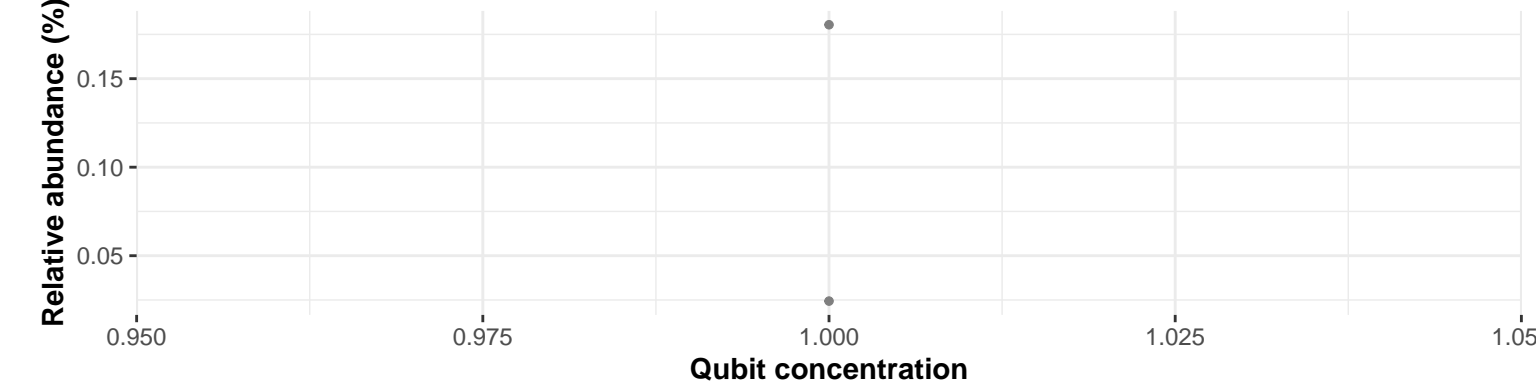


Correlation within: Feed

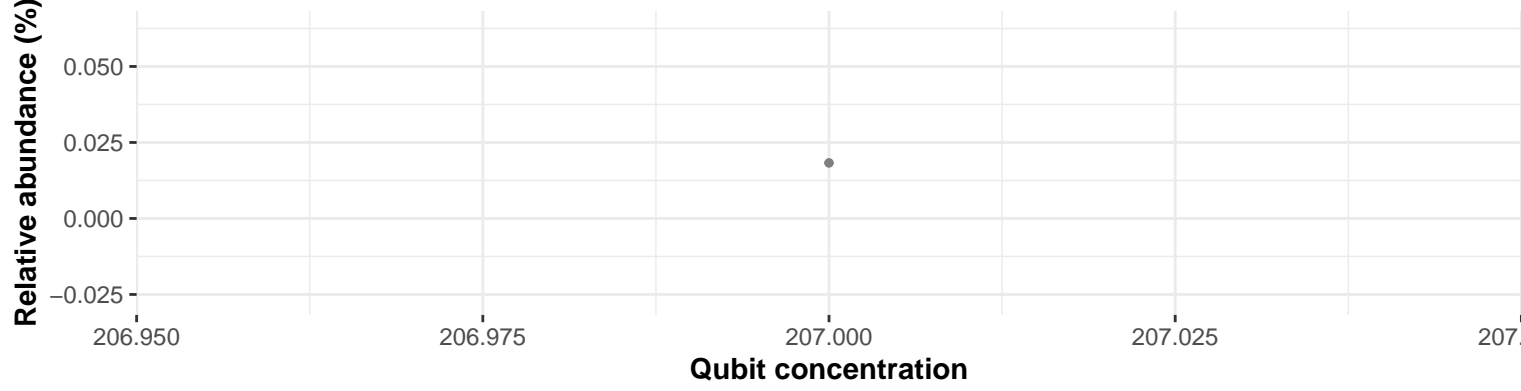
$\log_e(S) = 5.328$, $p = 0.489$, $\hat{\rho}_{\text{Spearman}} = -0.248$, $\text{CI}_{95\%} [-0.768, 0.469]$, $n_{\text{pairs}} = 10$



Correlation within: control



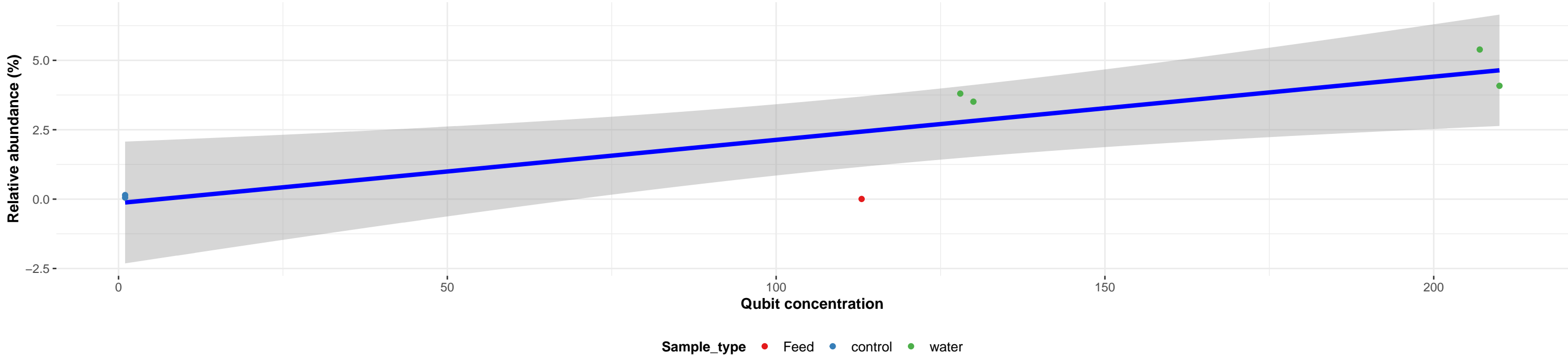
Correlation within: Positive_control



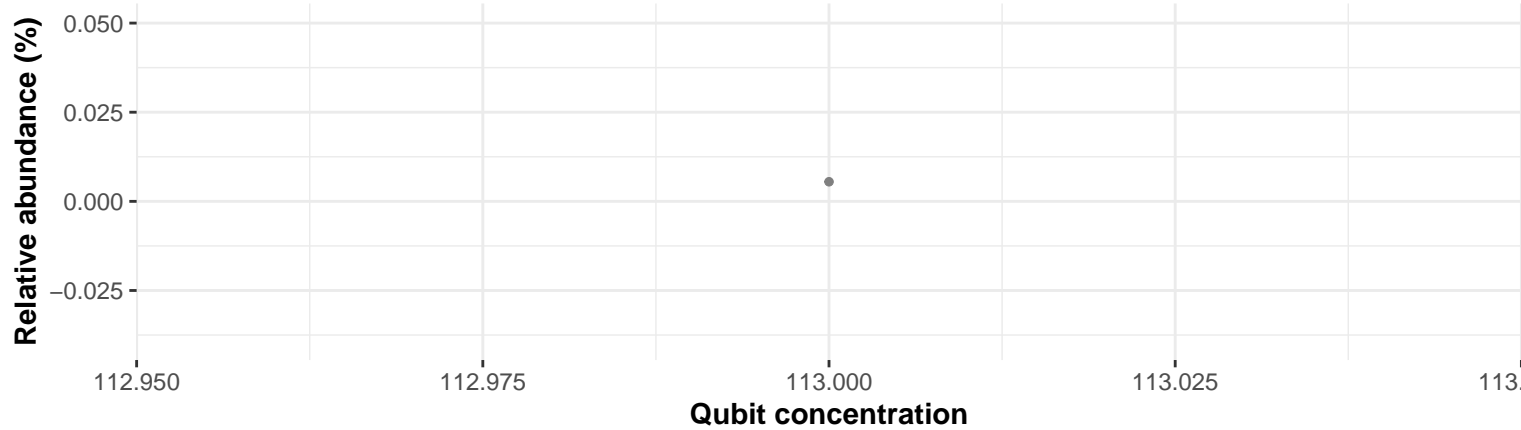
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Hyphomonadaceae; Hellea; NA

Correlation with all samples

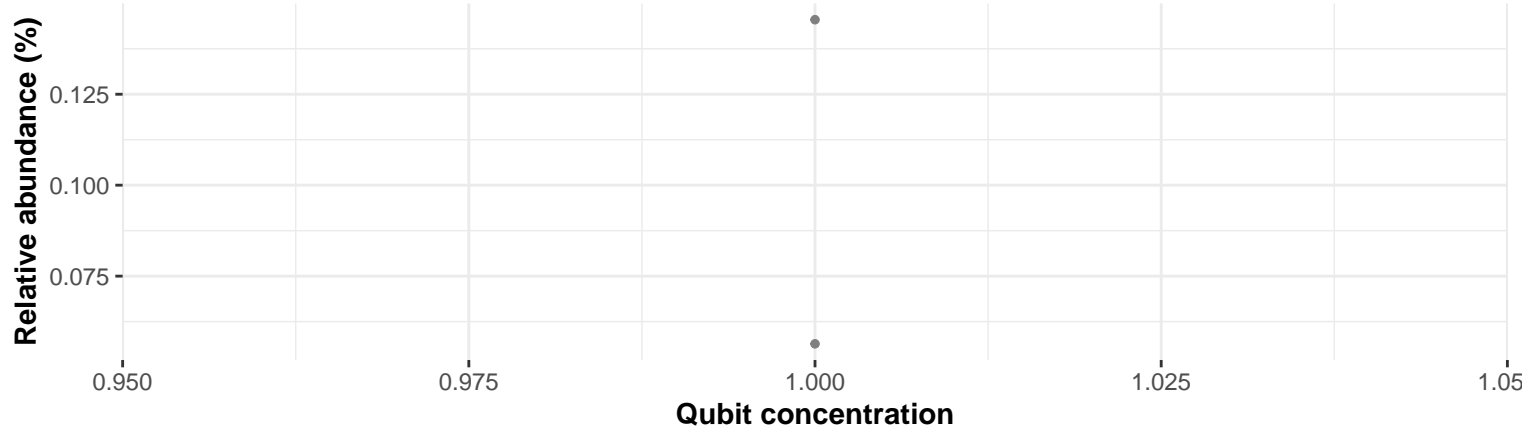
$\log_e(S) = 2.360$, $p = 0.027$, $\hat{\rho}_{\text{Spearman}} = 0.811$, $CI_{95\%} [0.120, 0.973]$, $n_{\text{pairs}} = 7$



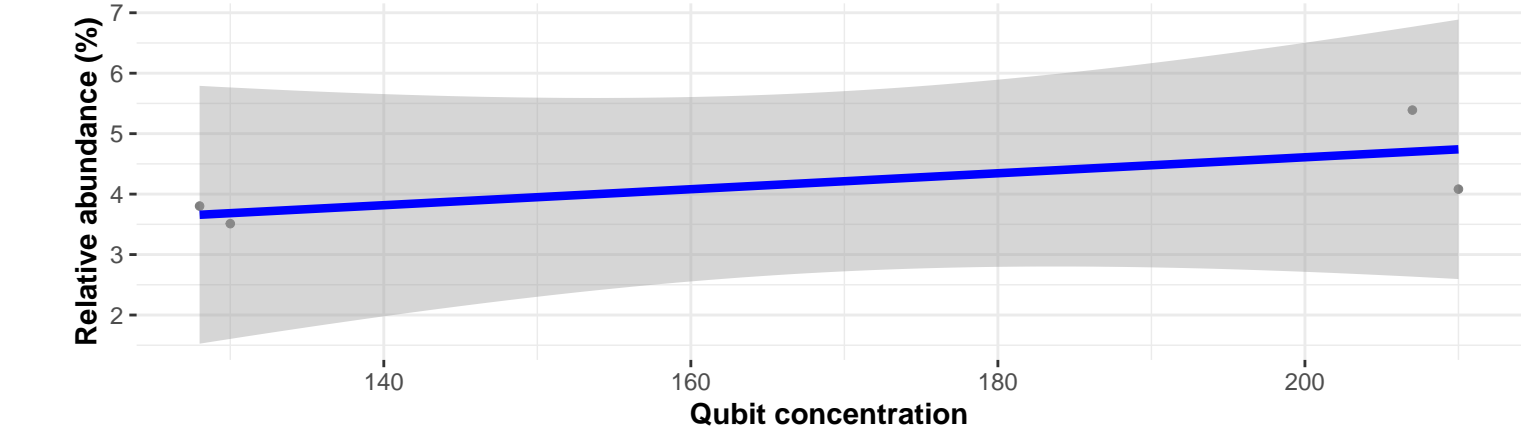
Correlation within: Feed



Correlation within: control



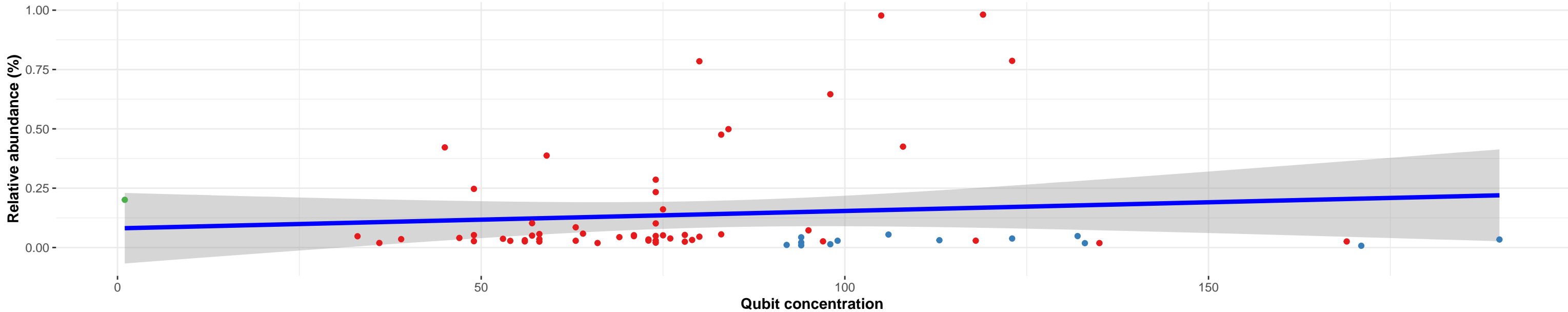
Correlation within: water



Bacteria; Firmicutes; Clostridia; Peptostreptococcales–Tissierellales; Peptostreptococcaceae; Peptostreptococcus; NA

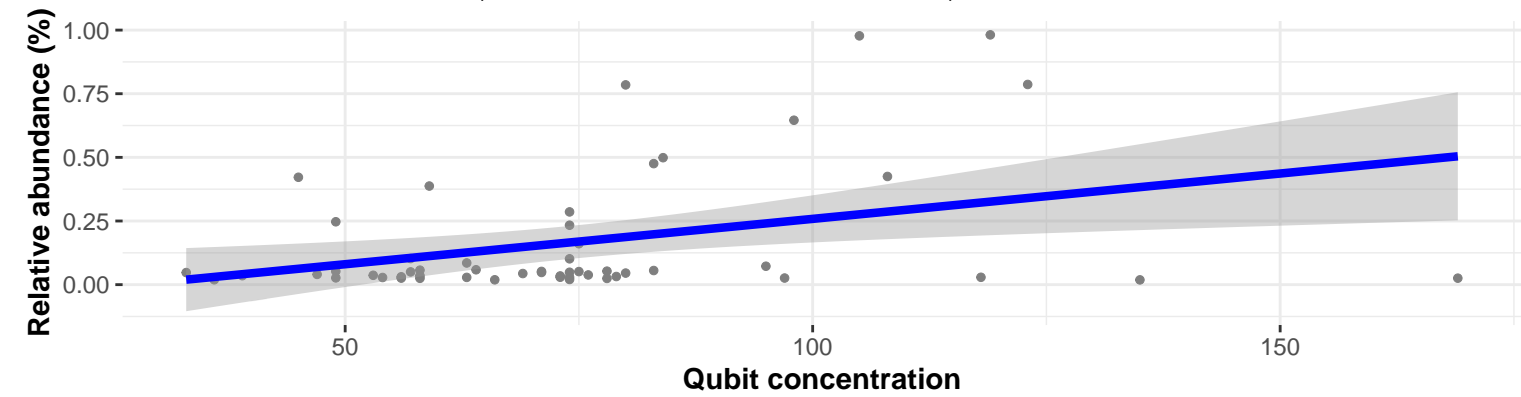
Correlation with all samples

$\log_e(S) = 10.943$, $p = 0.521$, $\hat{\rho}_{\text{Spearman}} = -0.079$, $\text{CI}_{95\%} [-0.318, 0.169]$, $n_{\text{pairs}} = 68$



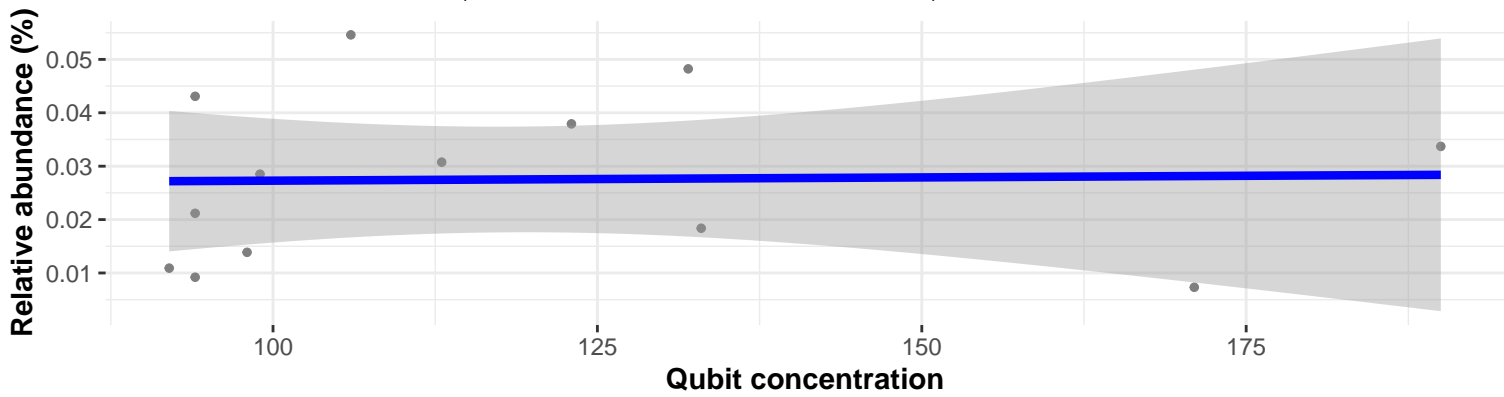
Correlation within: Digesta

$\log_e(S) = 9.902$, $p = 0.082$, $\hat{\rho}_{\text{Spearman}} = 0.239$, $\text{CI}_{95\%} [-0.039, 0.482]$, $n_{\text{pairs}} = 54$

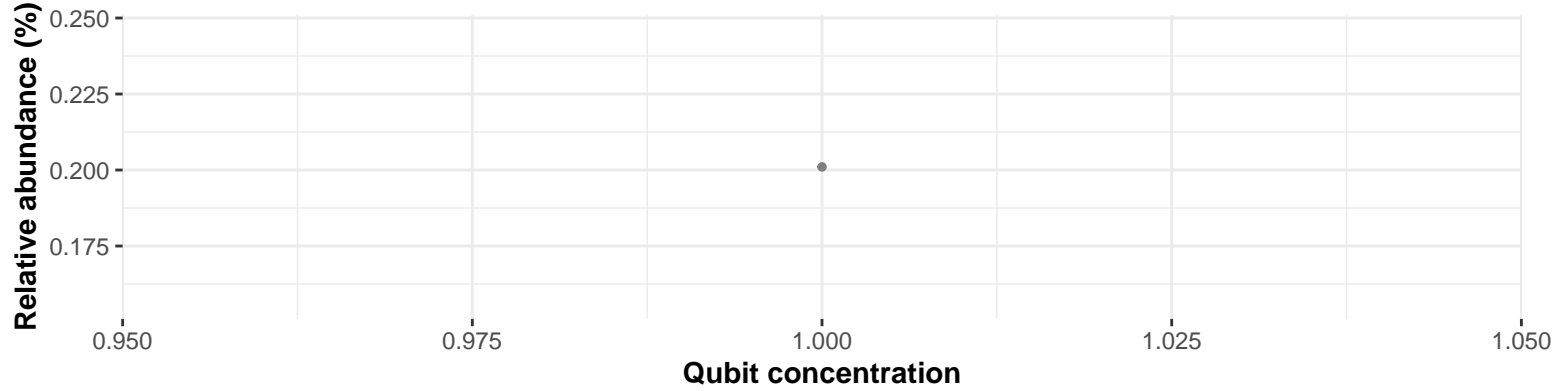


Correlation within: Feed

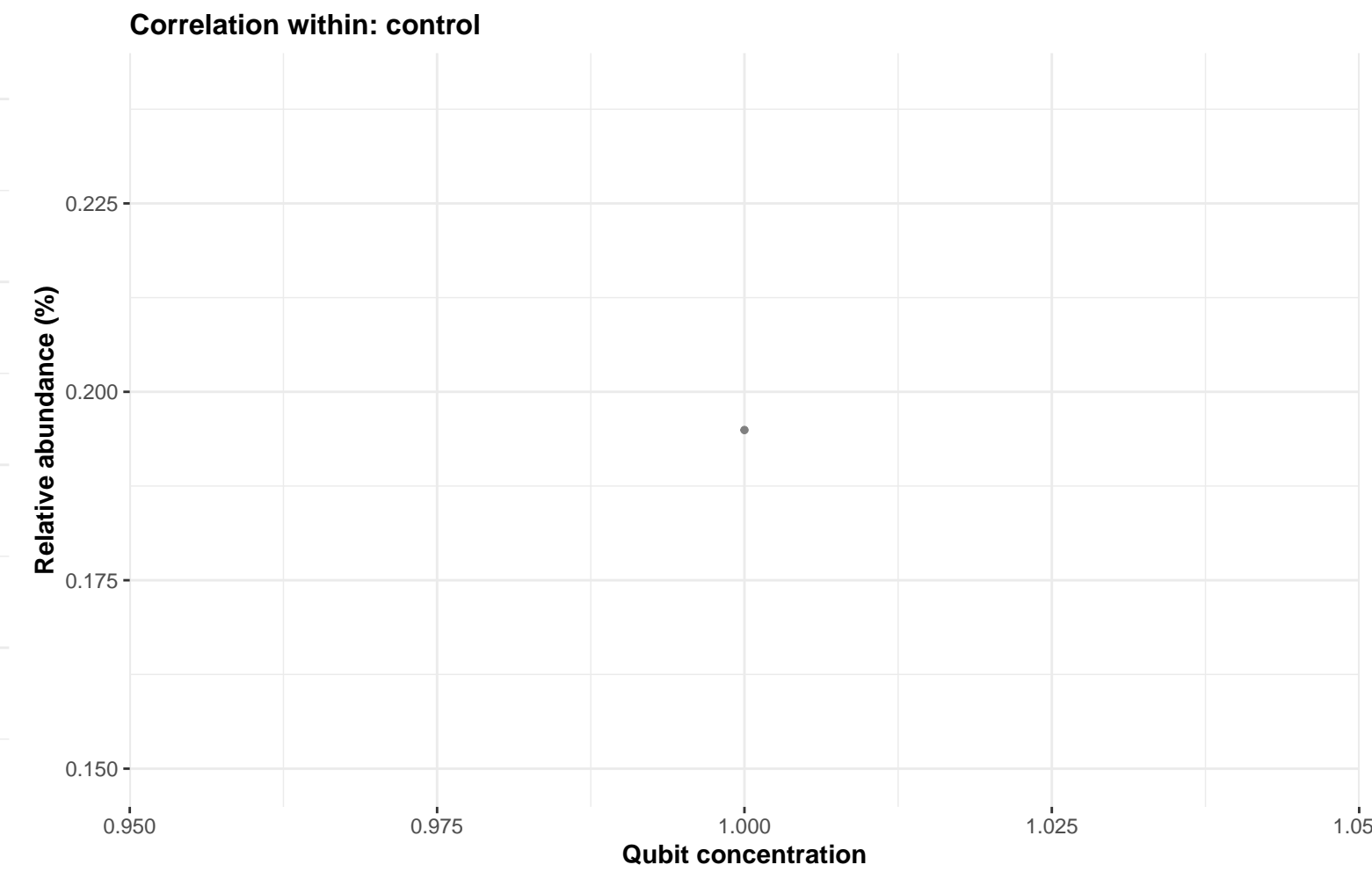
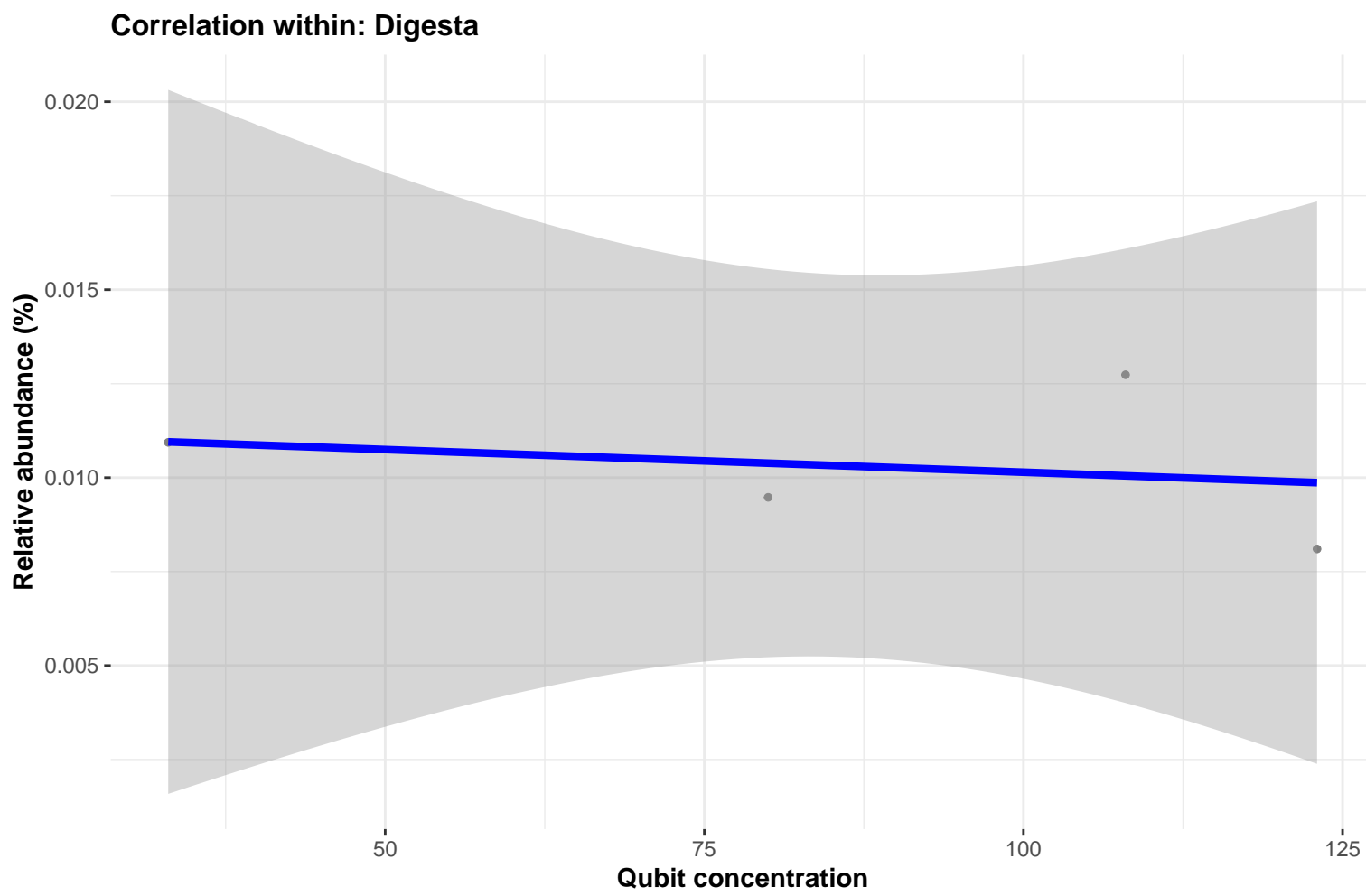
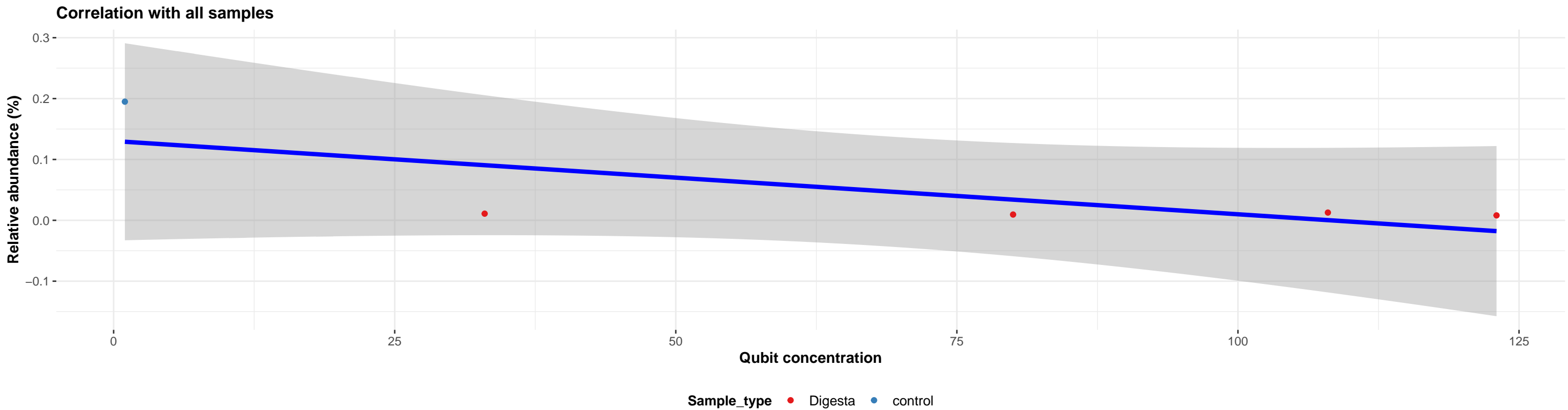
$\log_e(S) = 5.689$, $p = 0.539$, $\hat{\rho}_{\text{Spearman}} = 0.188$, $\text{CI}_{95\%} [-0.420, 0.680]$, $n_{\text{pairs}} = 13$



Correlation within: control



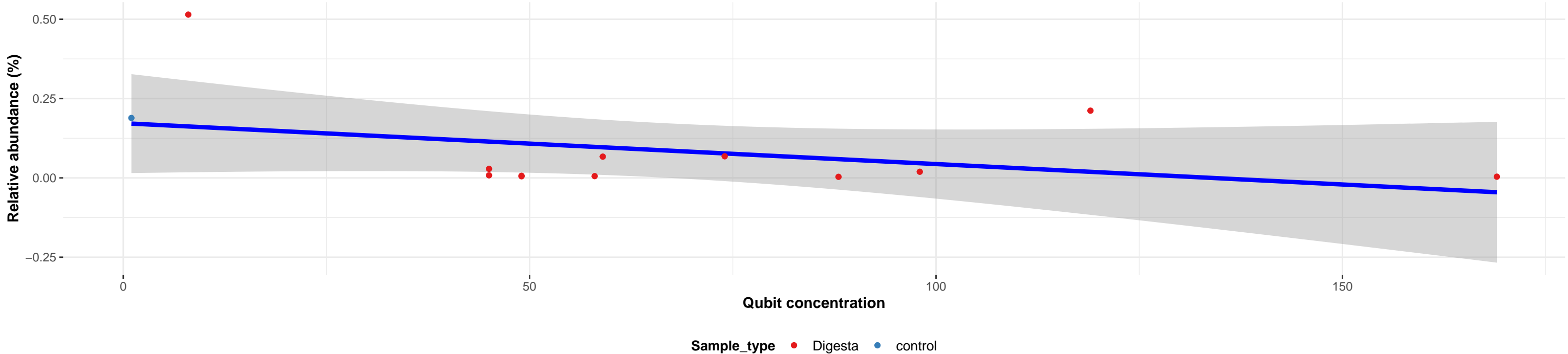
Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Alcaligenaceae; Achromobacter; NA



Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; junii

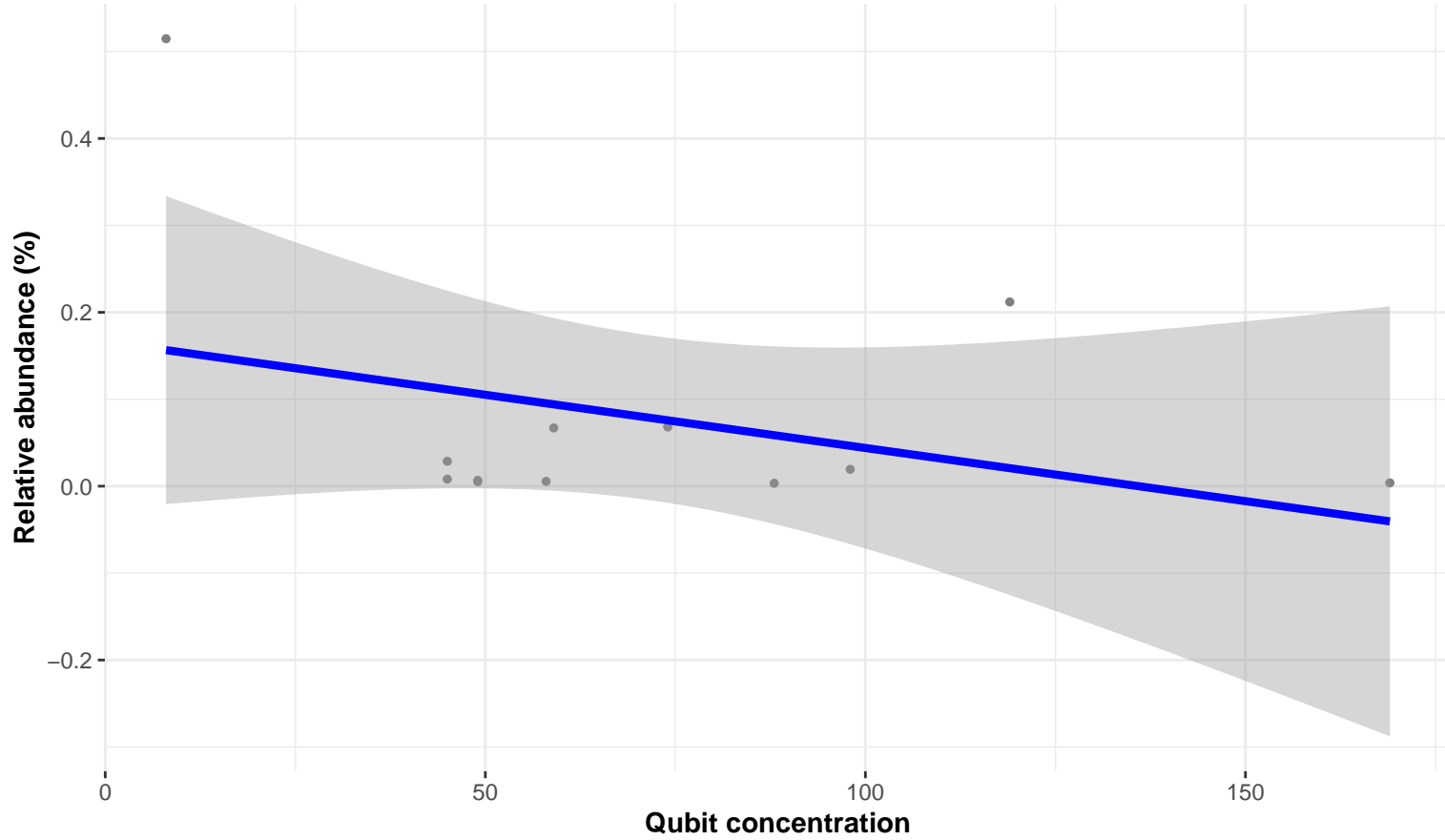
Correlation with all samples

$\log_e(S) = 6.183$, $p = 0.270$, $\hat{\rho}_{\text{Spearman}} = -0.331$, $\text{CI}_{95\%} [-0.754, 0.286]$, $n_{\text{pairs}} = 13$

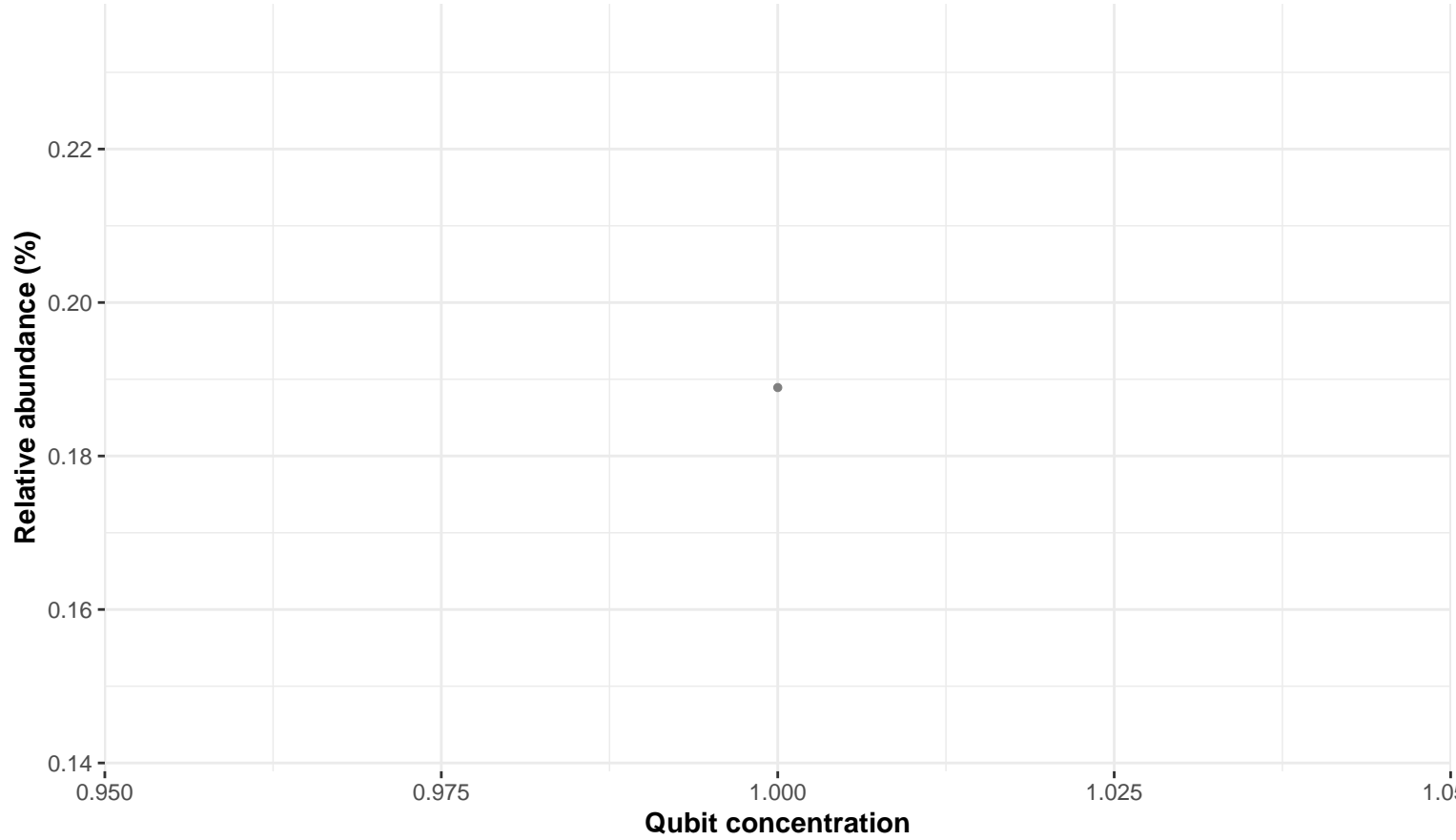


Correlation within: Digesta

$\log_e(S) = 5.864$, $p = 0.469$, $\hat{\rho}_{\text{Spearman}} = -0.232$, $\text{CI}_{95\%} [-0.720, 0.411]$, $n_{\text{pairs}} = 12$



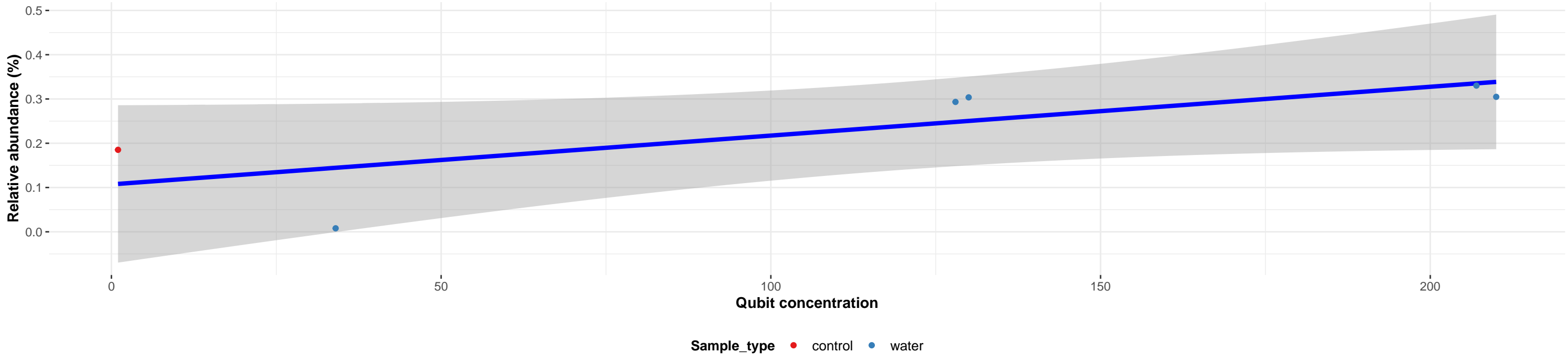
Correlation within: control



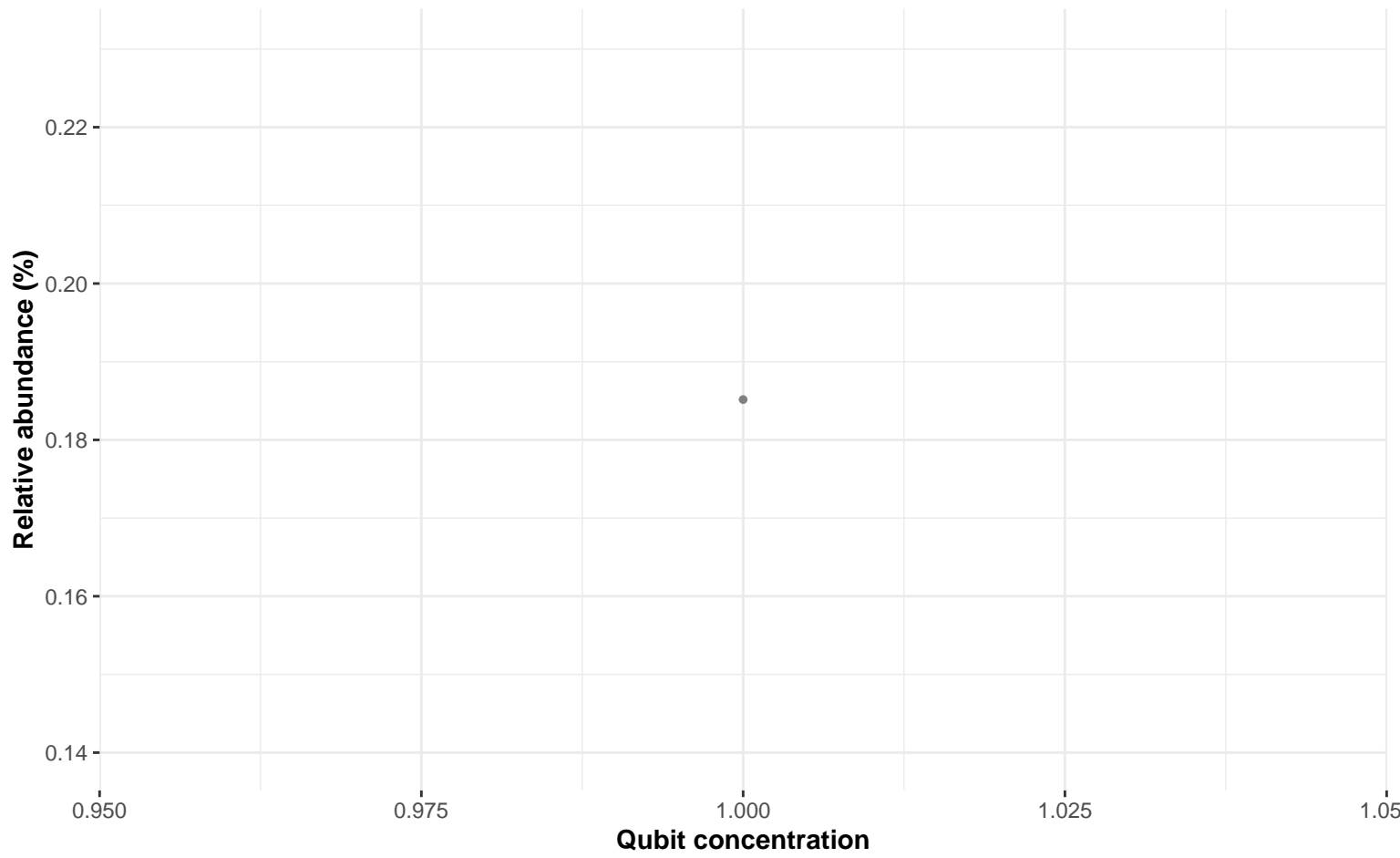
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Sphingobacteriaceae; BD1-7 clade; NA

Correlation with all samples

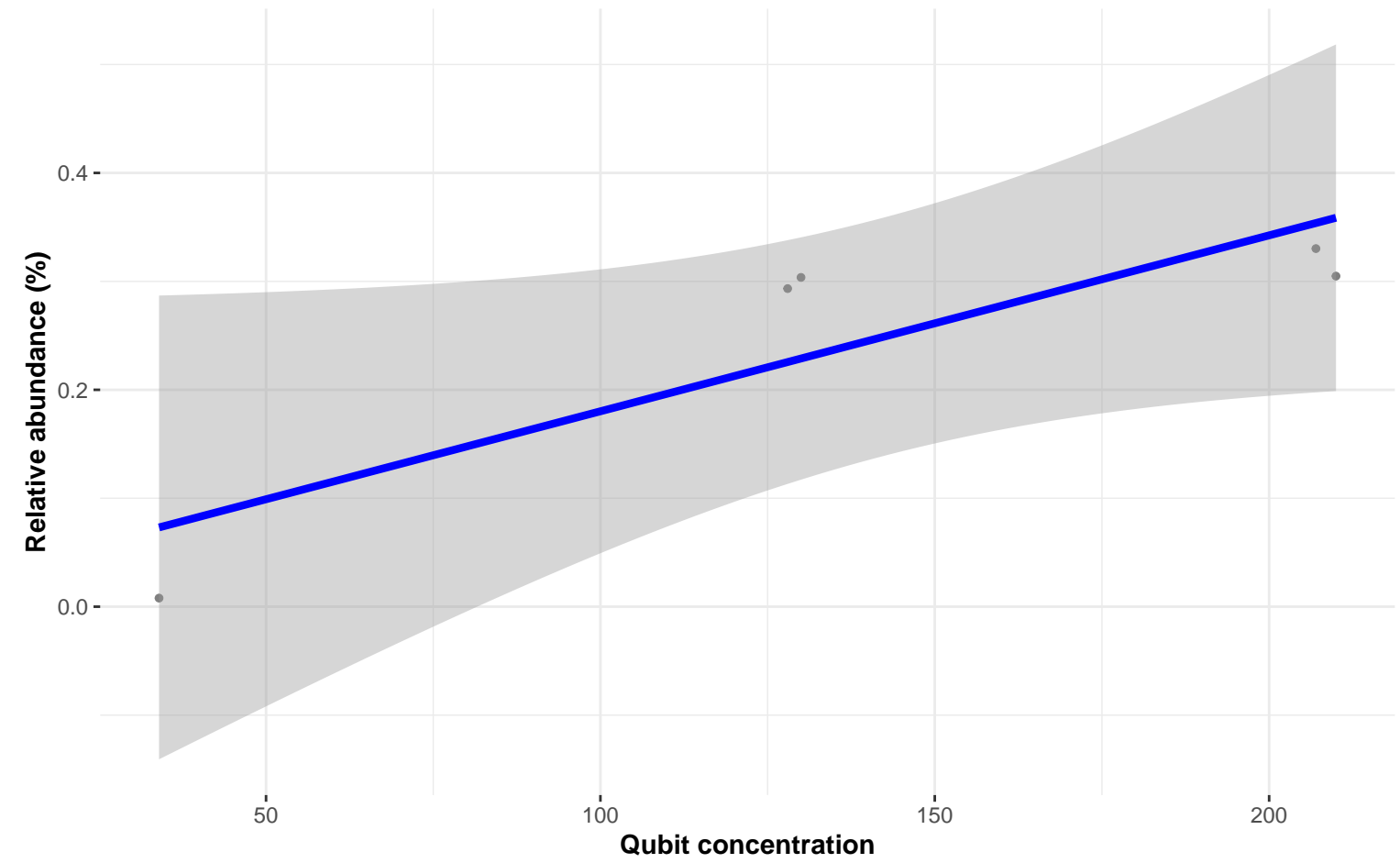
$\log_e(S) = 1.386$, $p = 0.019$, $\hat{\rho}_{\text{Spearman}} = 0.886$, $CI_{95\%} [0.232, 0.988]$, $n_{\text{pairs}} = 6$



Correlation within: control



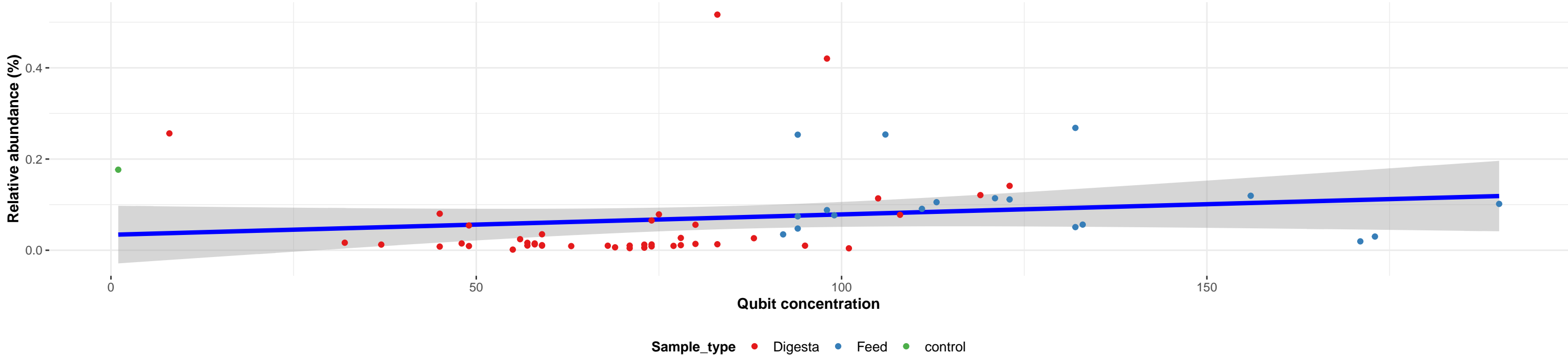
Correlation within: water



Bacteria; Fusobacteriota; Fusobacteriia; Fusobacteriales; Fusobacteriaceae; Fusobacterium; NA

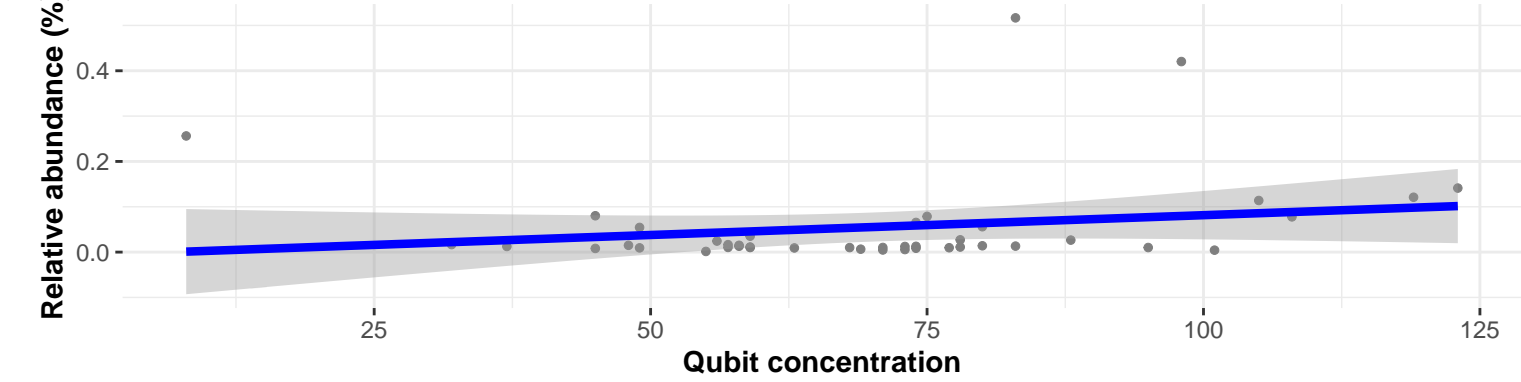
Correlation with all samples

$\log_e(S) = 9.966$, $p = 1.47e-04$, $\hat{\rho}_{\text{Spearman}} = 0.464$, $CI_{95\%} [0.235, 0.644]$, $n_{\text{pairs}} = 62$



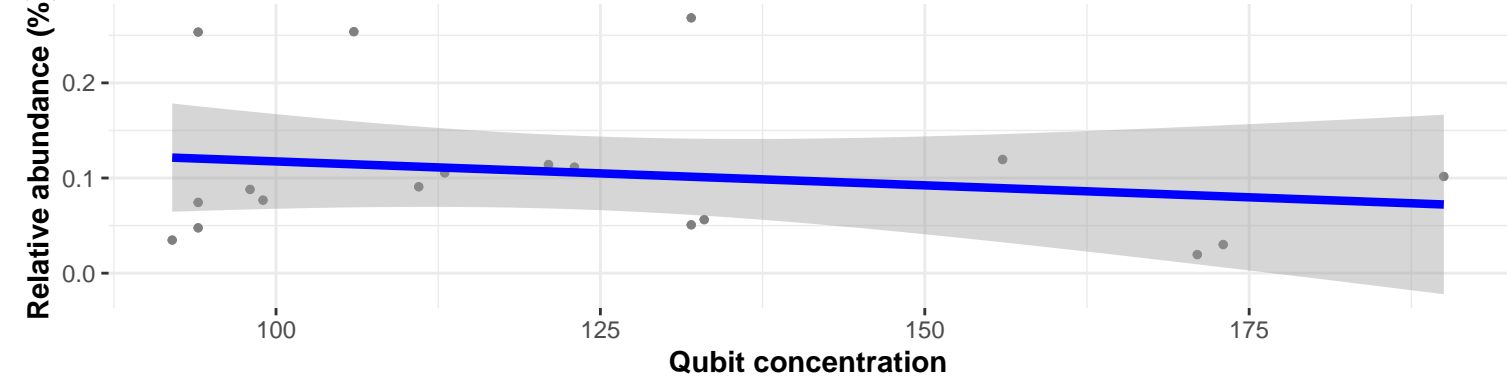
Correlation within: Digesta

$\log_e(S) = 9.234$, $p = 0.143$, $\hat{\rho}_{\text{Spearman}} = 0.227$, $CI_{95\%} [-0.088, 0.501]$, $n_{\text{pairs}} = 43$

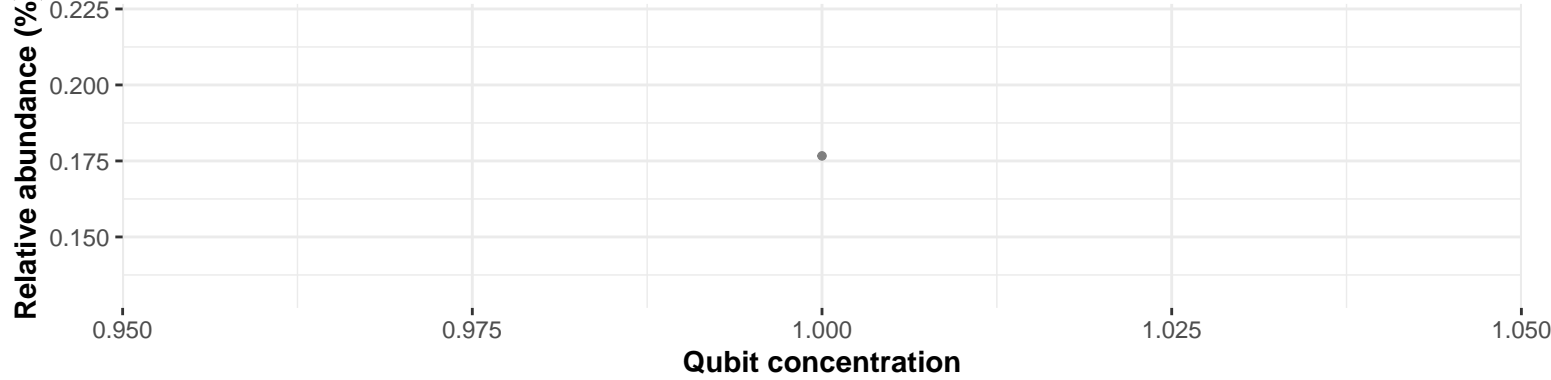


Correlation within: Feed

$\log_e(S) = 6.903$, $p = 0.916$, $\hat{\rho}_{\text{Spearman}} = -0.027$, $CI_{95\%} [-0.499, 0.457]$, $n_{\text{pairs}} = 18$



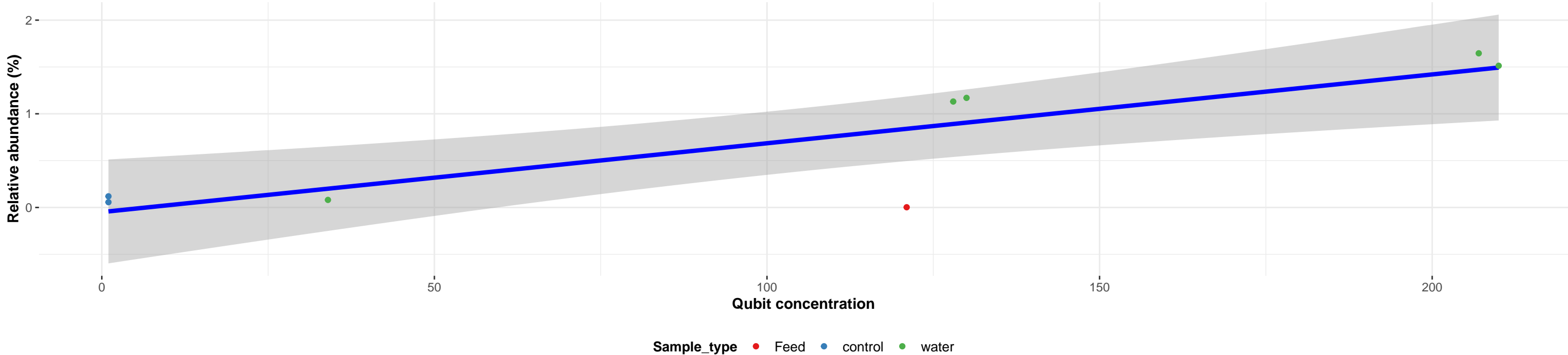
Correlation within: control



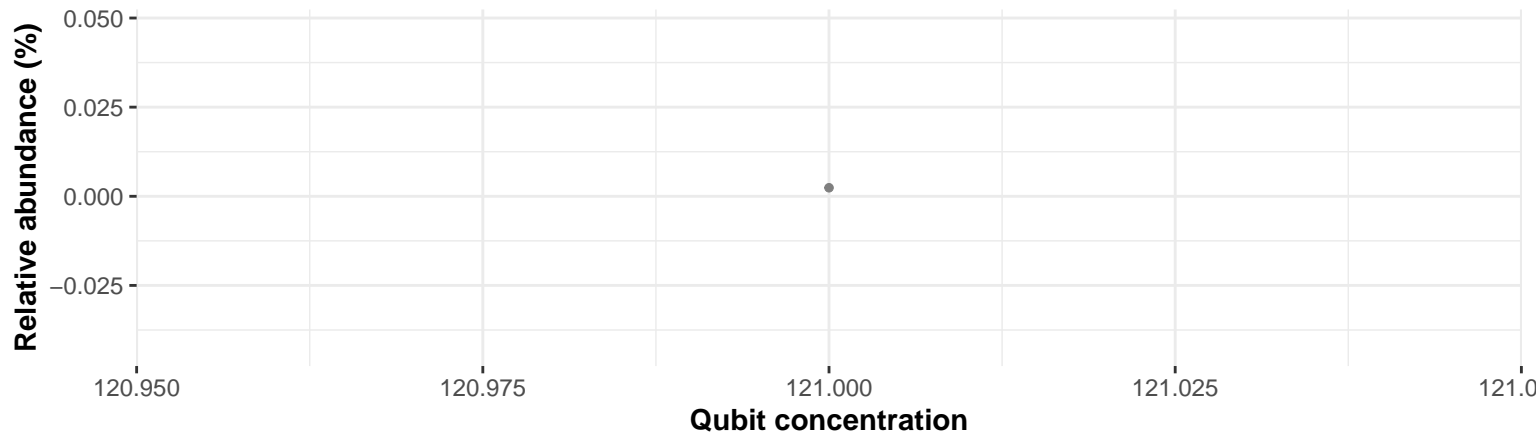
Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA

Correlation with all samples

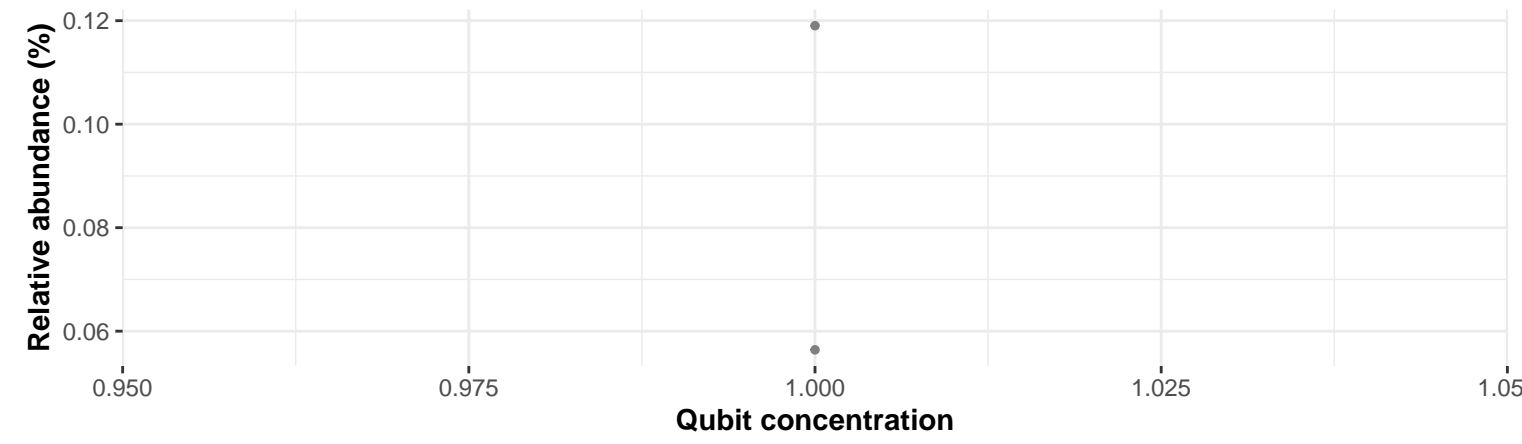
$\log_e(S) = 2.868$, $p = 0.020$, $\hat{\rho}_{\text{Spearman}} = 0.790$, $\text{CI}_{95\%} [0.169, 0.962]$, $n_{\text{pairs}} = 8$



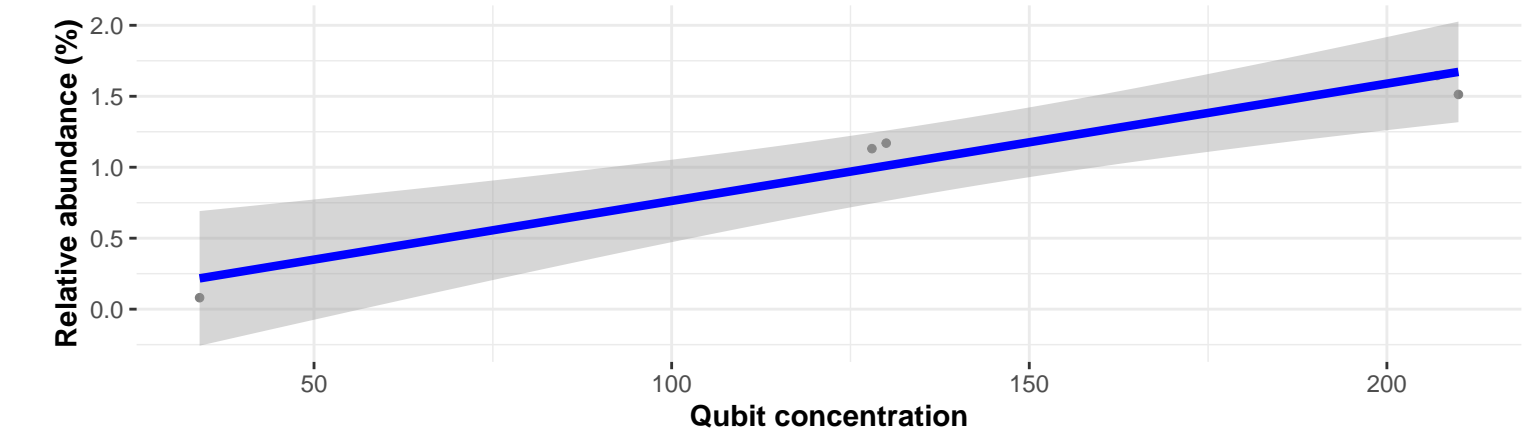
Correlation within: Feed



Correlation within: control



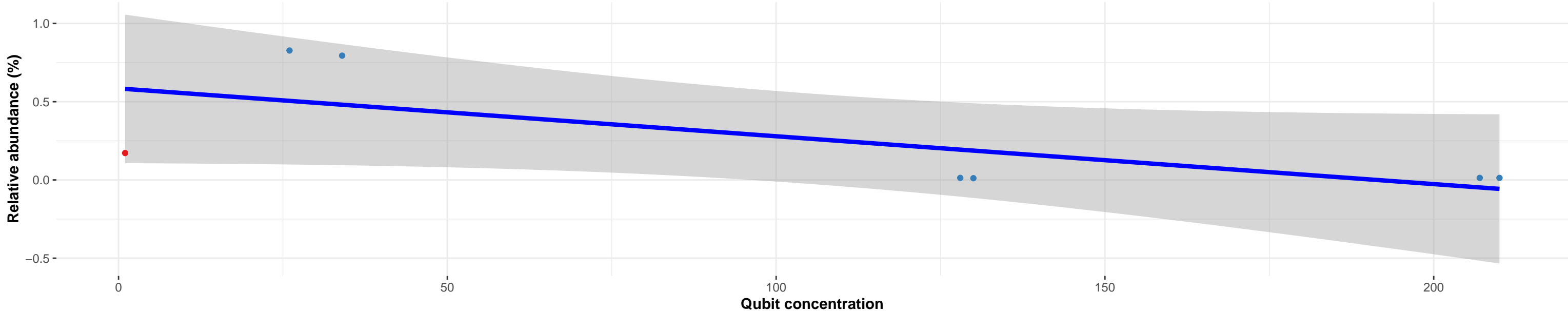
Correlation within: water



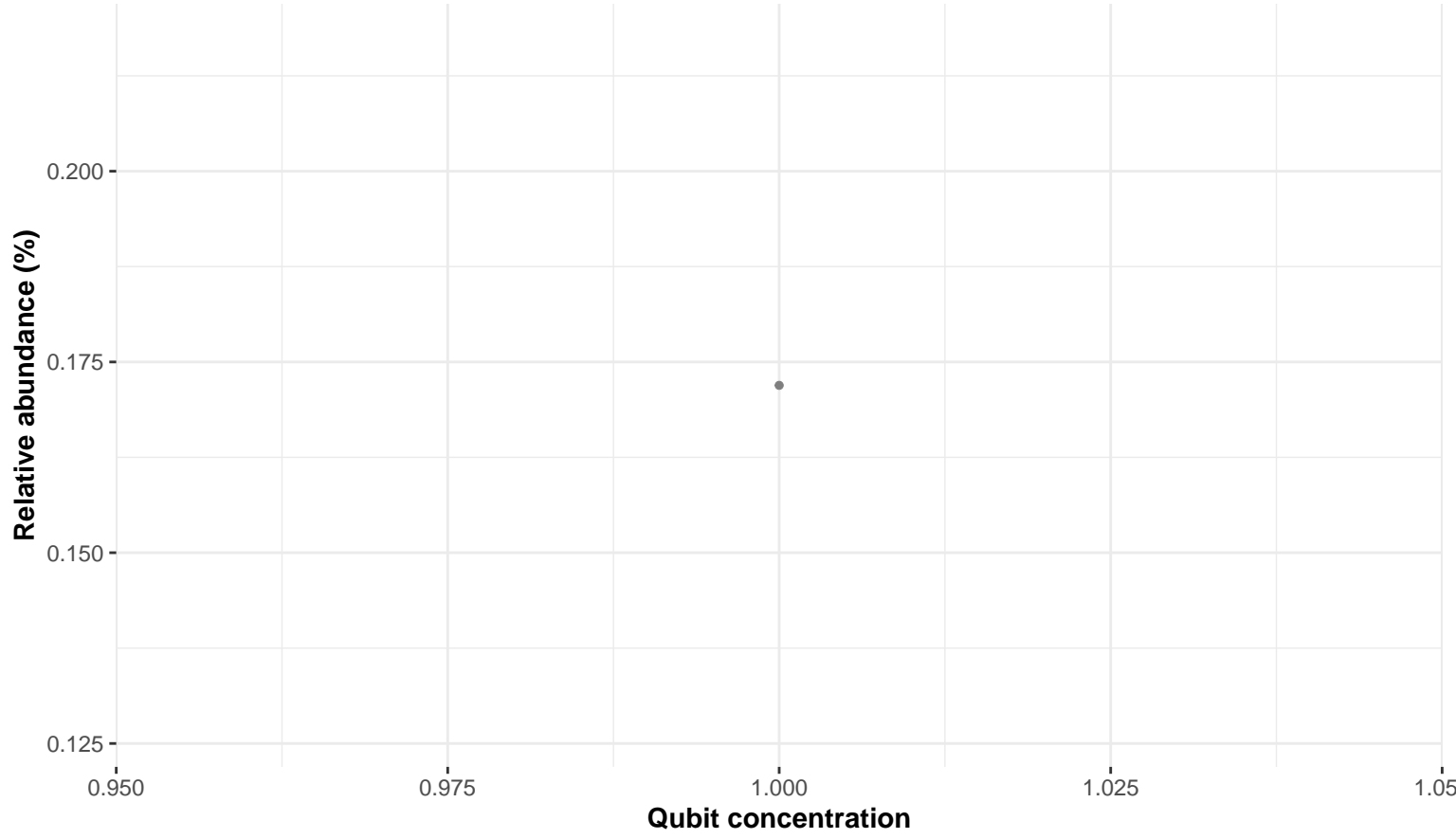
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Vibrionaceae; Aliivibrio; NA

Correlation with all samples

$\log_e(S) = 4.500$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = -0.607$, $\text{CI}_{95\%} [-0.937, 0.295]$, $n_{\text{pairs}} = 7$

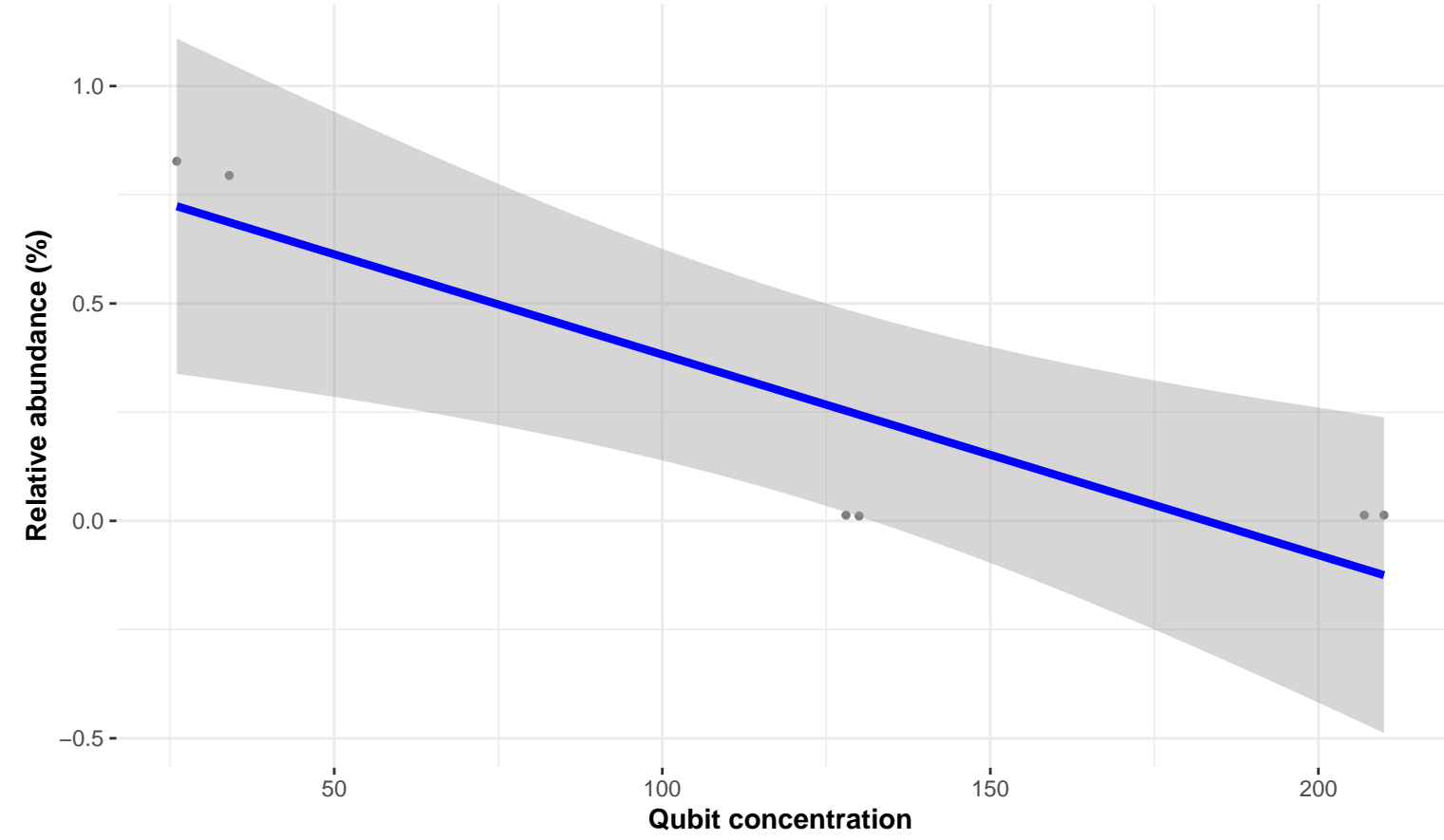


Correlation within: control



Correlation within: water

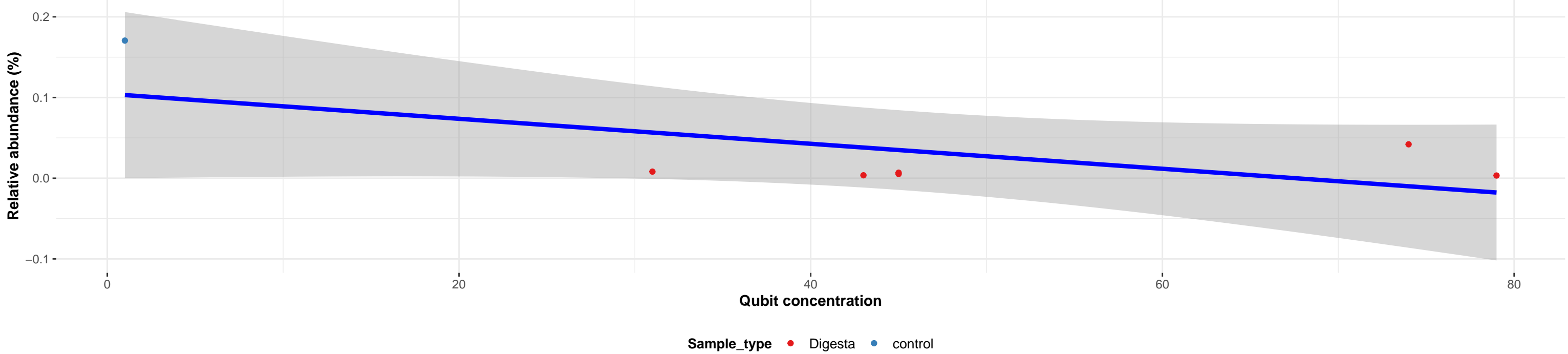
$\log_e(S) = 3.989$, $p = 0.266$, $\hat{\rho}_{\text{Spearman}} = -0.543$, $\text{CI}_{95\%} [-0.944, 0.506]$, $n_{\text{pairs}} = 6$



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Oceanobacillus; NA

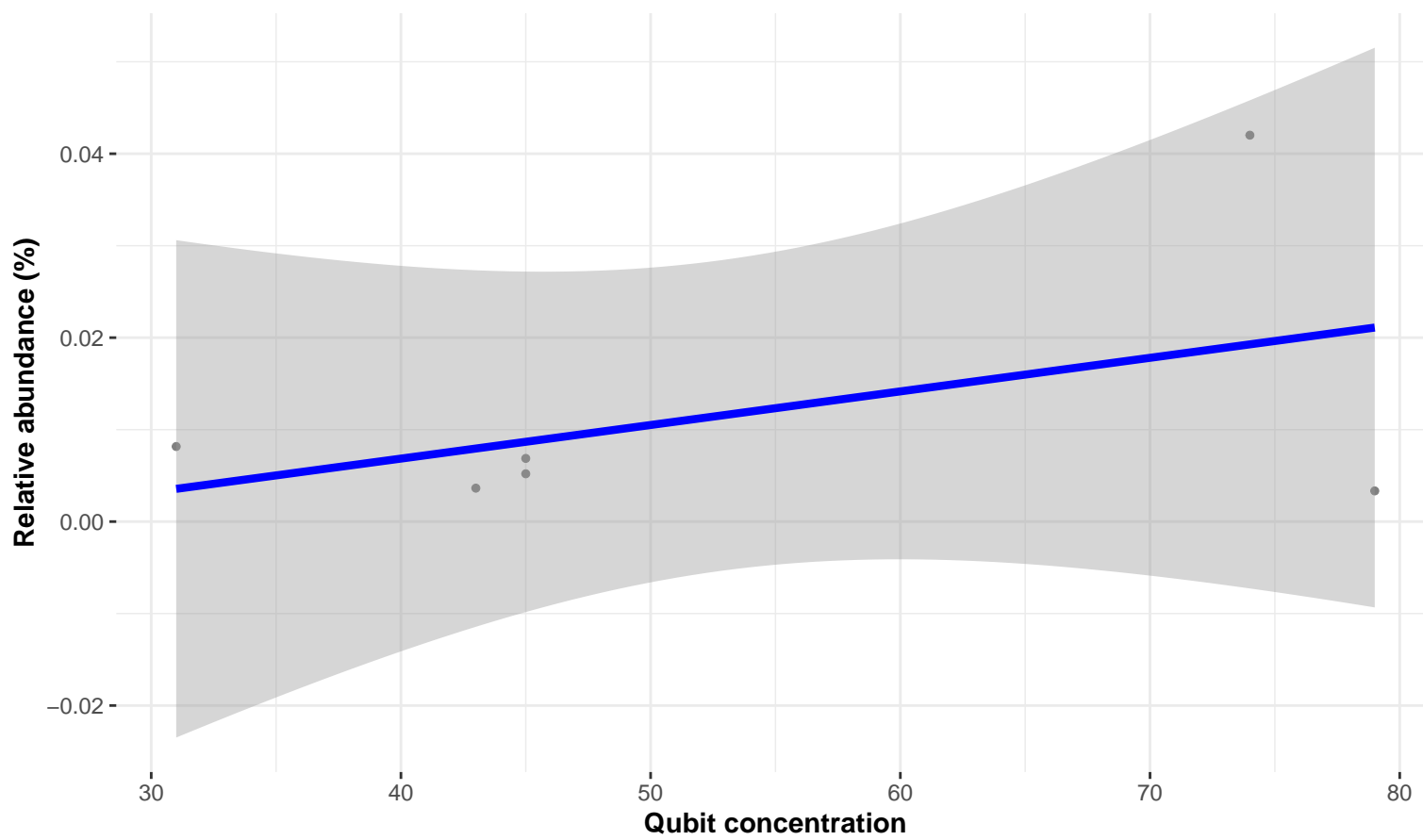
Correlation with all samples

$\log_e(S) = 4.446$, $p = 0.229$, $\hat{\rho}_{\text{Spearman}} = -0.523$, $\text{CI}_{95\%} [-0.920, 0.405]$, $n_{\text{pairs}} = 7$

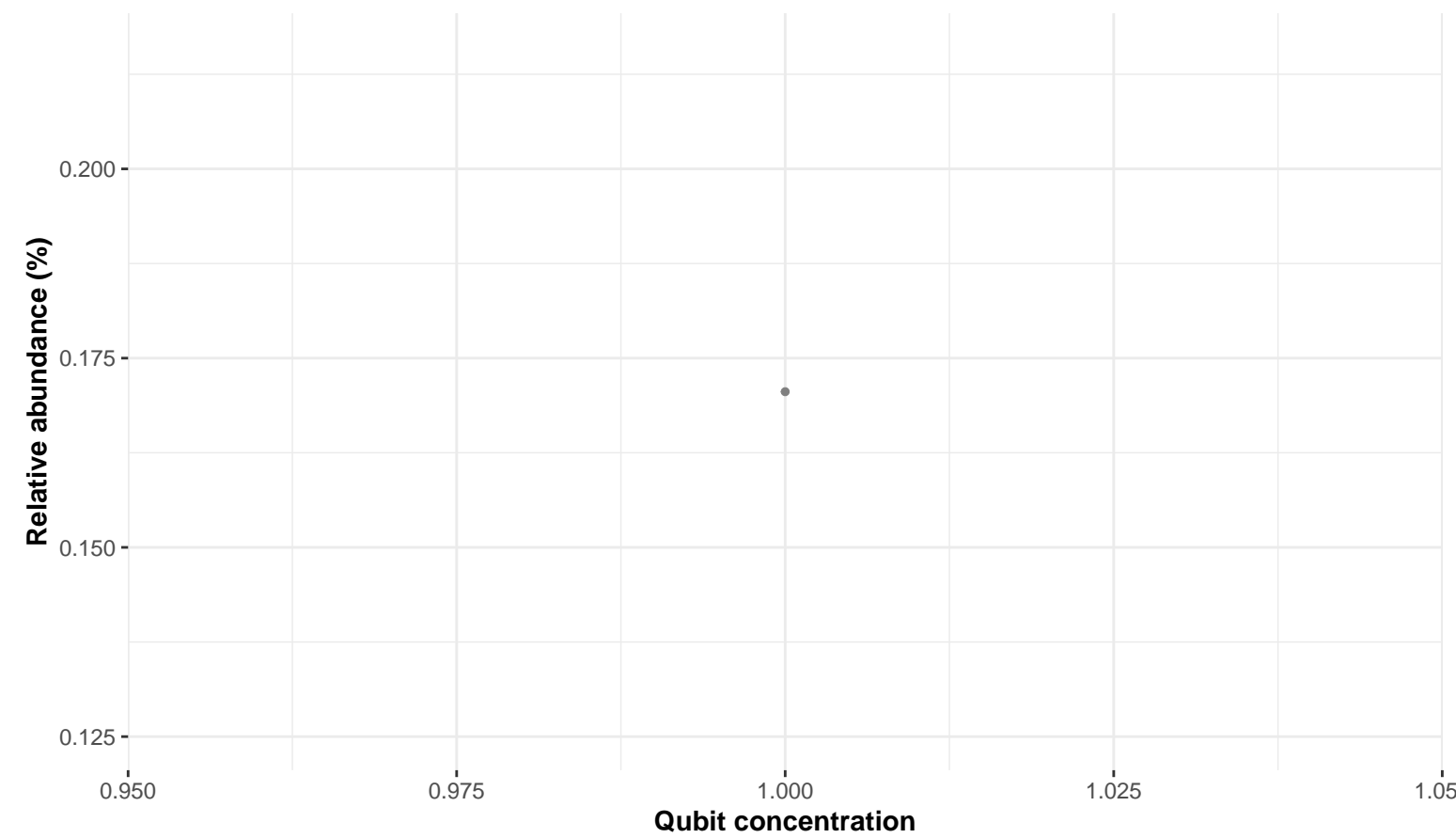


Correlation within: Digesta

$\log_e(S) = 3.764$, $p = 0.658$, $\hat{\rho}_{\text{Spearman}} = -0.232$, $\text{CI}_{95\%} [-0.886, 0.730]$, $n_{\text{pairs}} = 6$



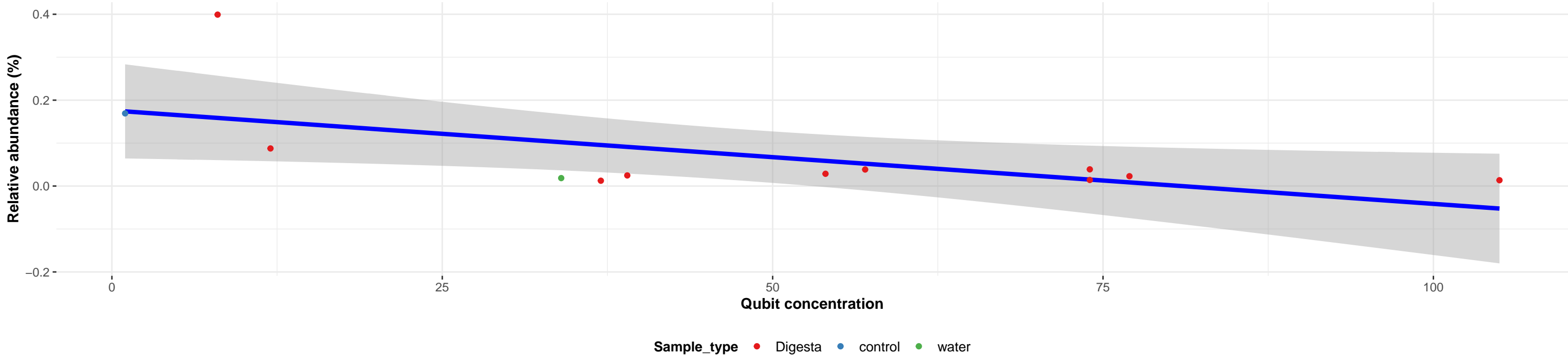
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

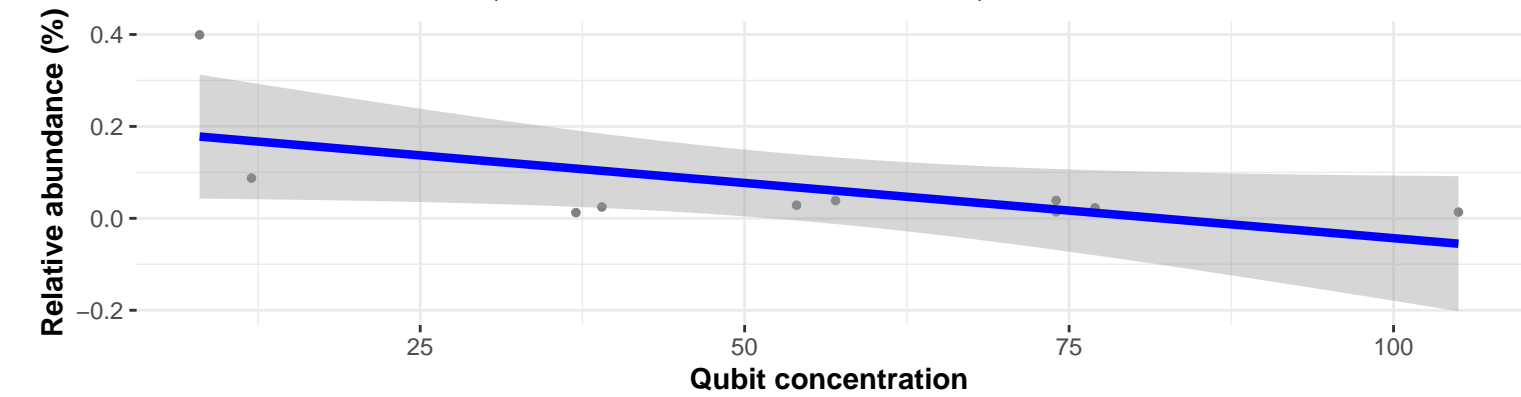
Correlation with all samples

$\log_e(S) = 6.096$, $p = 0.062$, $\hat{\rho}_{\text{Spearman}} = -0.553$, $CI_{95\%} [-0.861, 0.049]$, $n_{\text{pairs}} = 12$

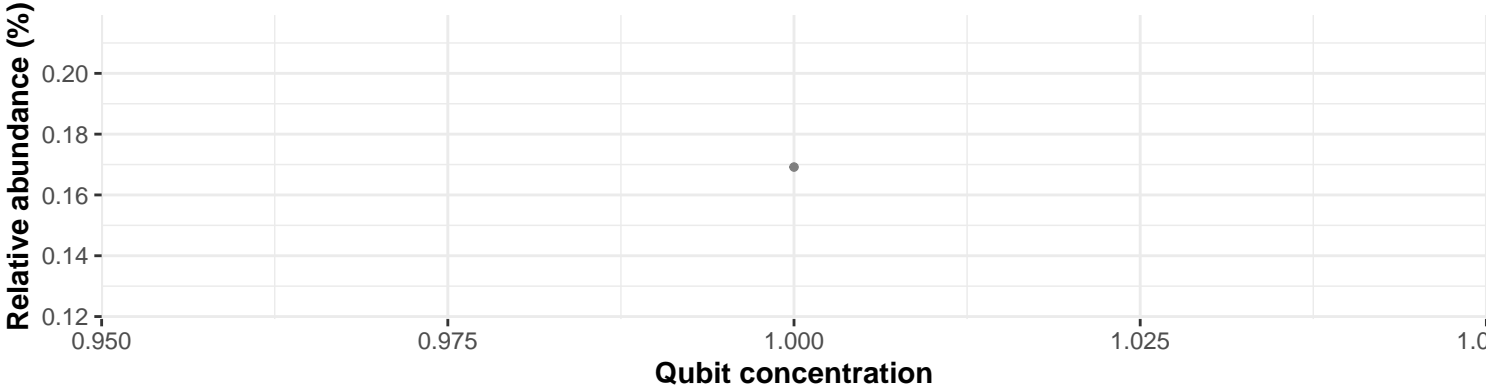


Correlation within: Digesta

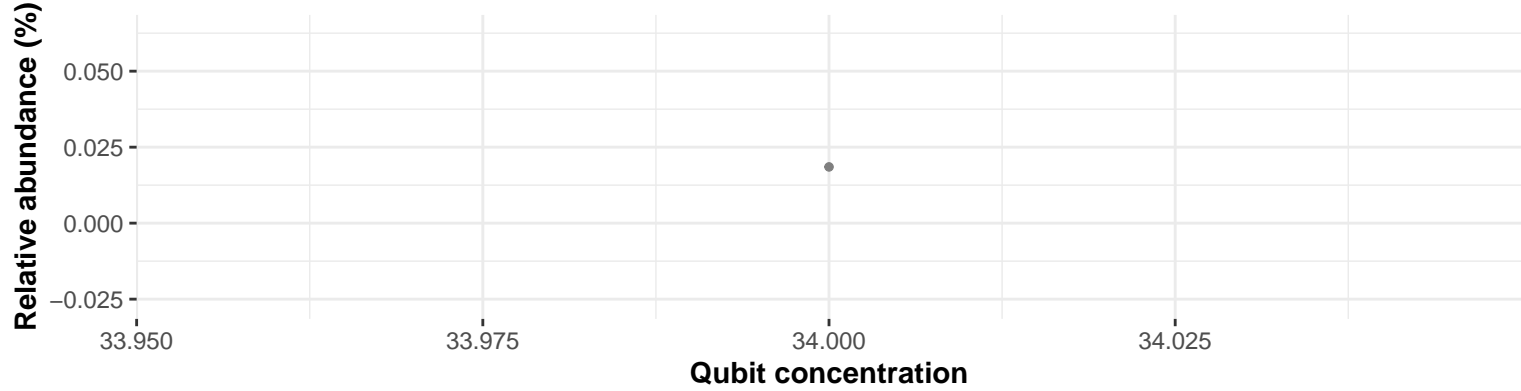
$\log_e(S) = 5.510$, $p = 0.143$, $\hat{\rho}_{\text{Spearman}} = -0.498$, $CI_{95\%} [-0.864, 0.212]$, $n_{\text{pairs}} = 10$



Correlation within: control



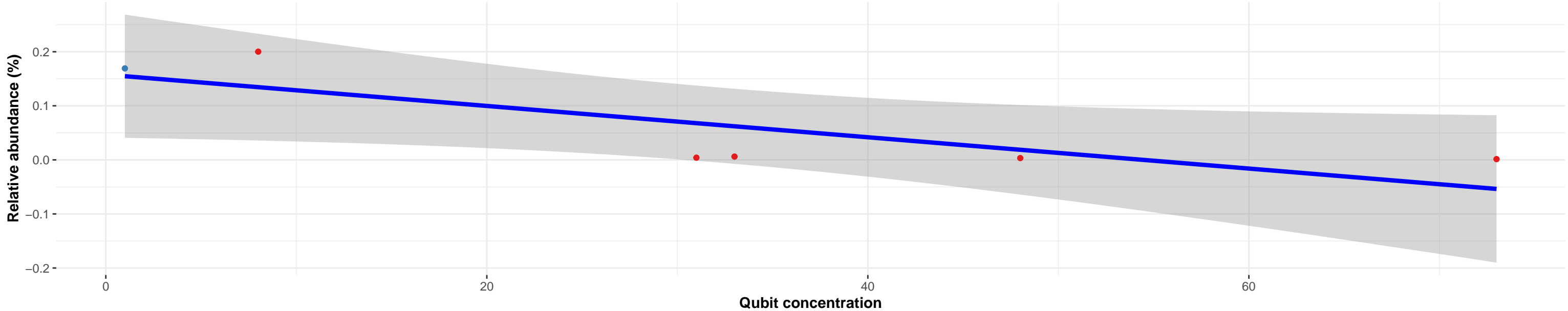
Correlation within: water



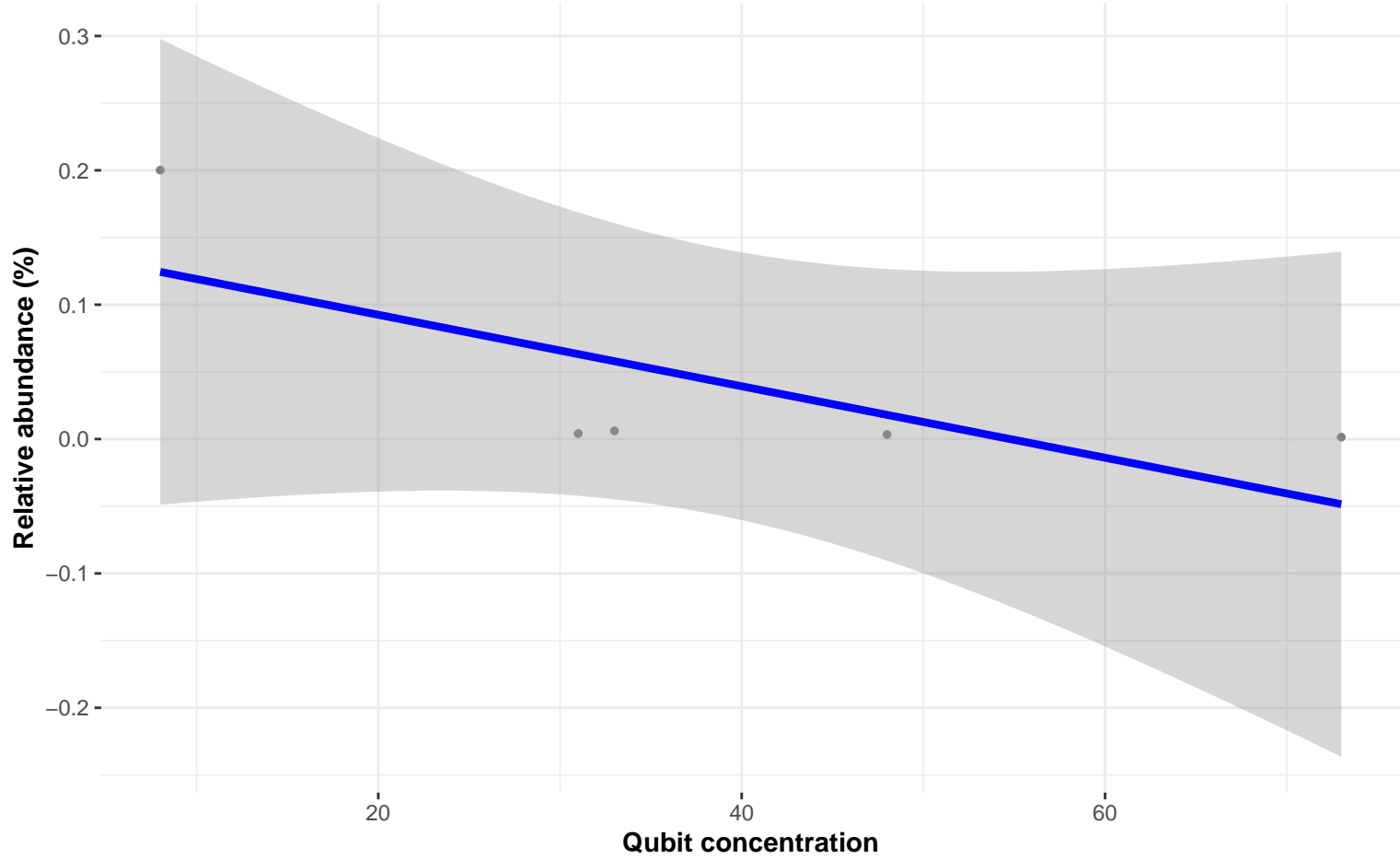
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; NA; NA

Correlation with all samples

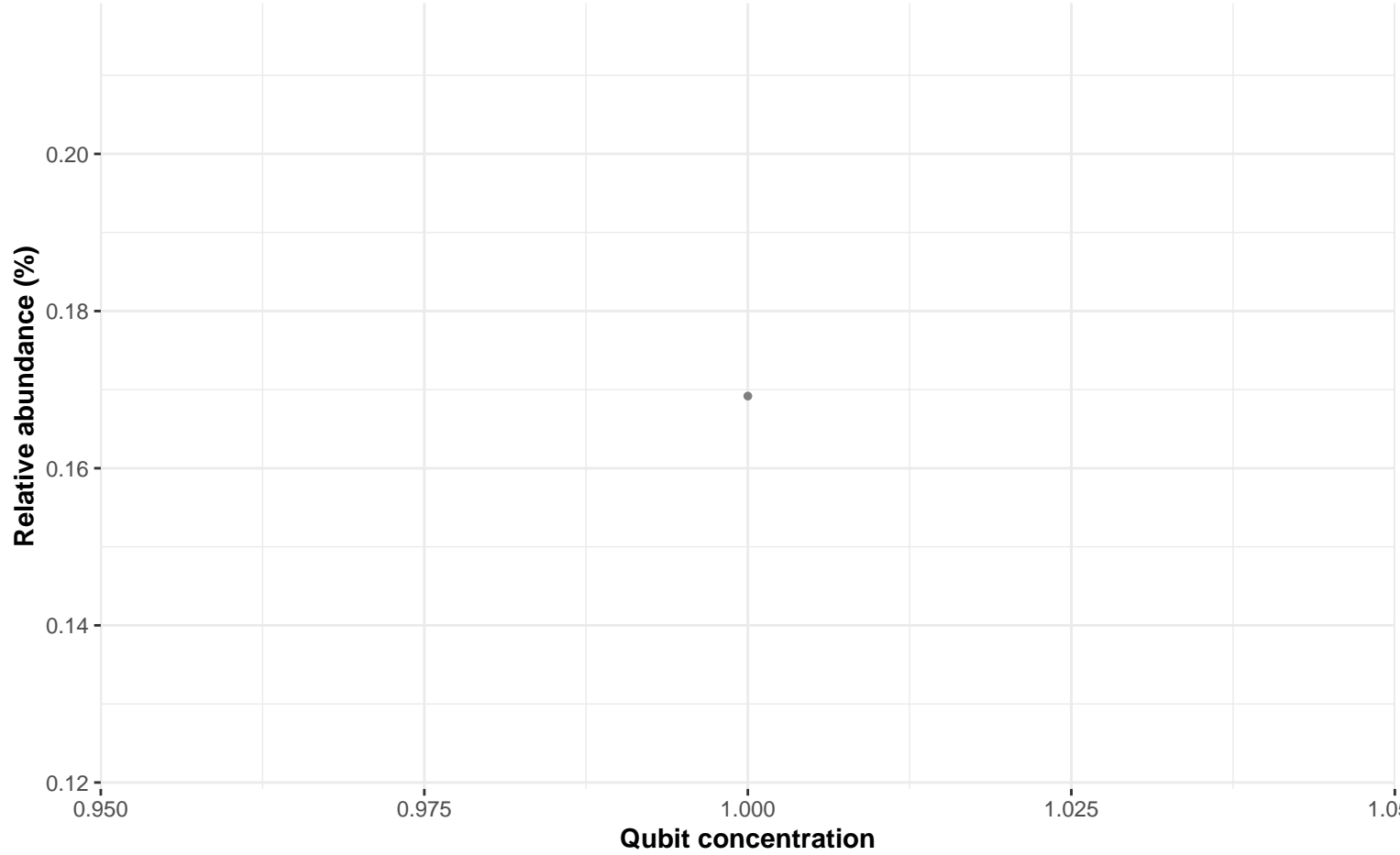
$\log_e(S) = 4.190$, $p = 0.019$, $\hat{\rho}_{\text{Spearman}} = -0.886$, $CI_{95\%} [-0.988, -0.232]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



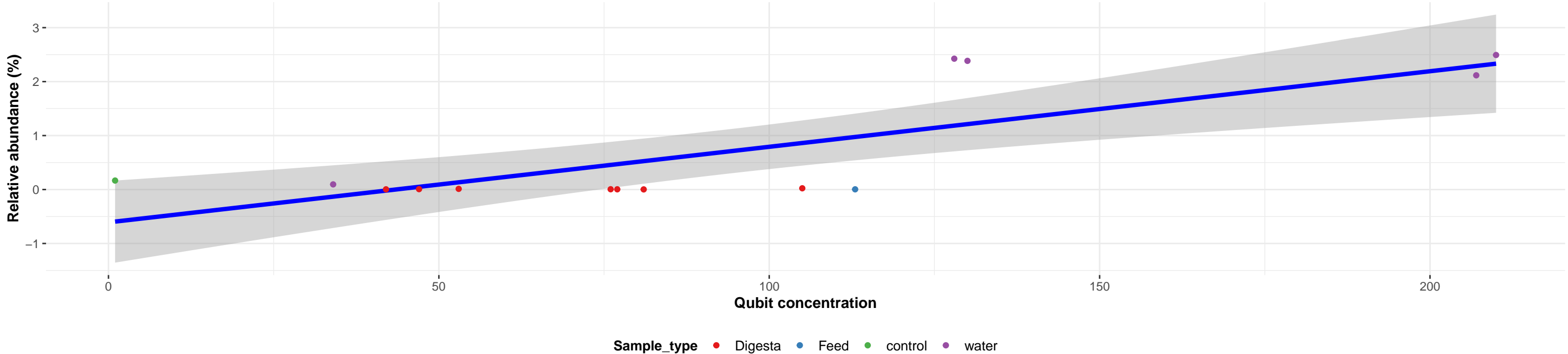
Correlation within: control



Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Sulfitobacter; NA

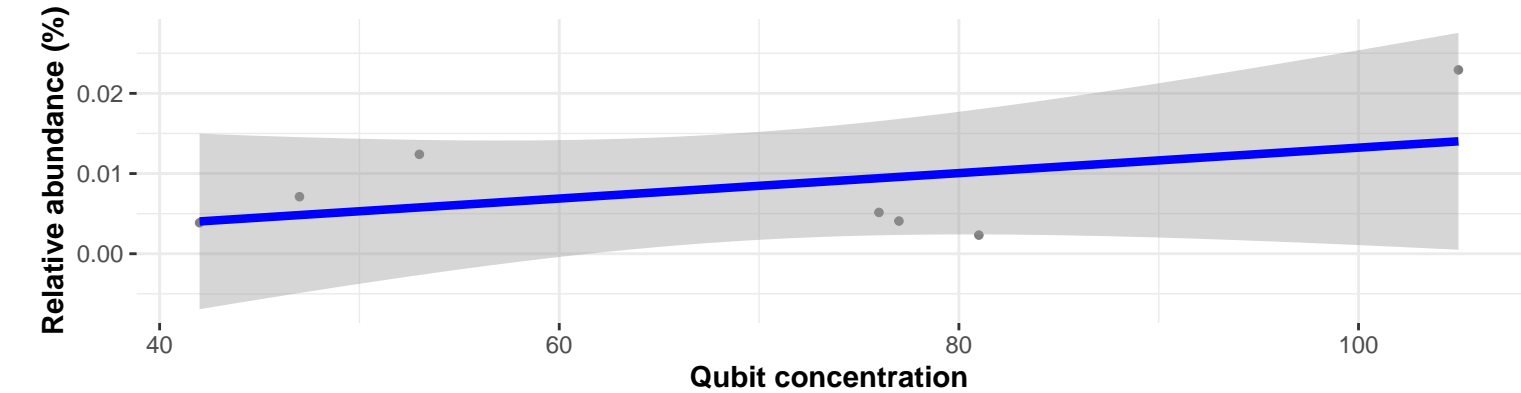
Correlation with all samples

$\log_e(S) = 5.598$, $p = 0.149$, $\hat{\rho}_{\text{Spearman}} = 0.407$, $CI_{95\%} [-0.175, 0.778]$, $n_{\text{pairs}} = 14$

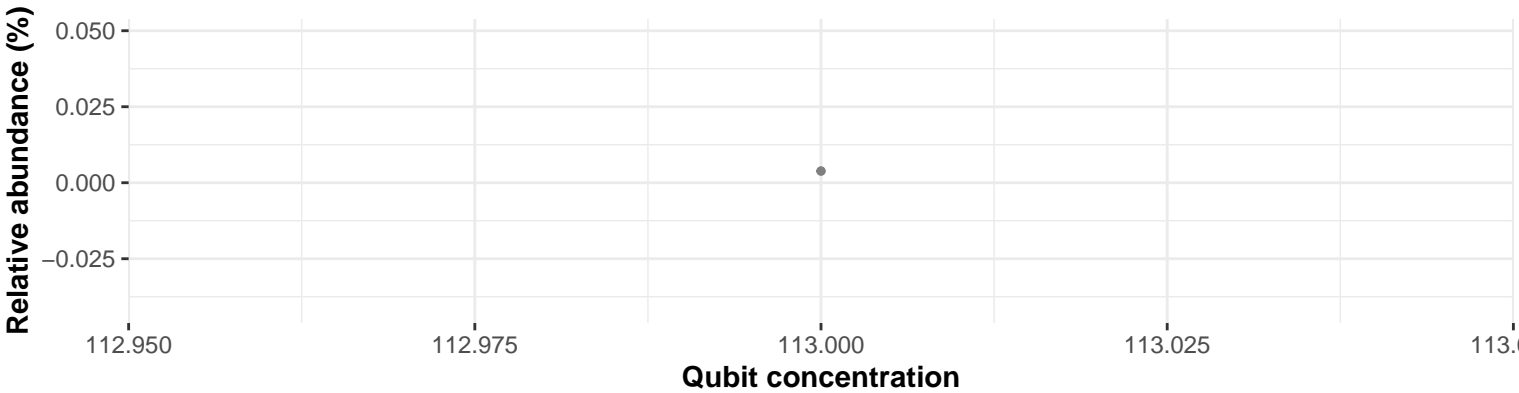


Correlation within: Digesta

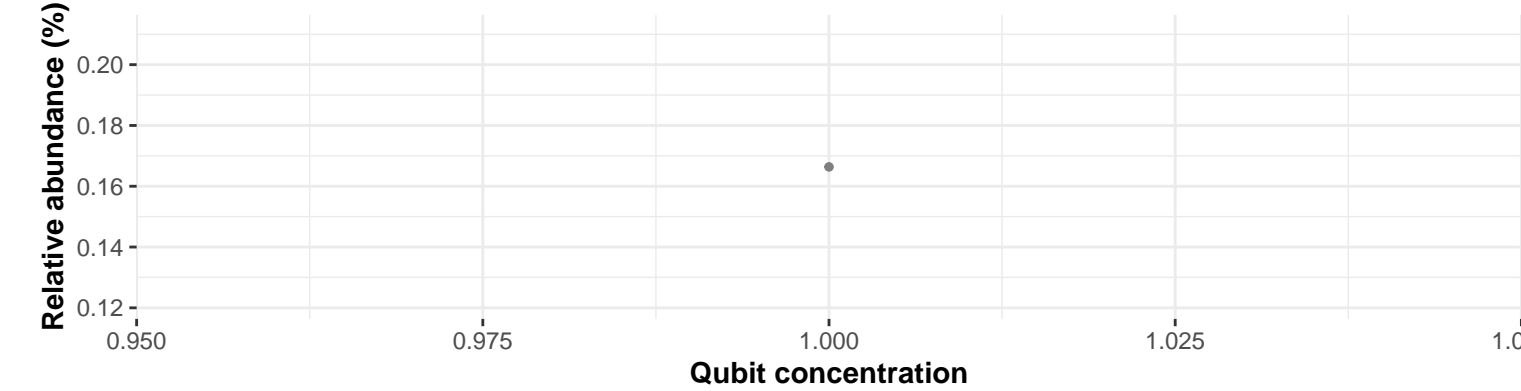
$\log_e(S) = 3.871$, $p = 0.760$, $\hat{\rho}_{\text{Spearman}} = 0.143$, $CI_{95\%} [-0.699, 0.819]$, $n_{\text{pairs}} = 7$



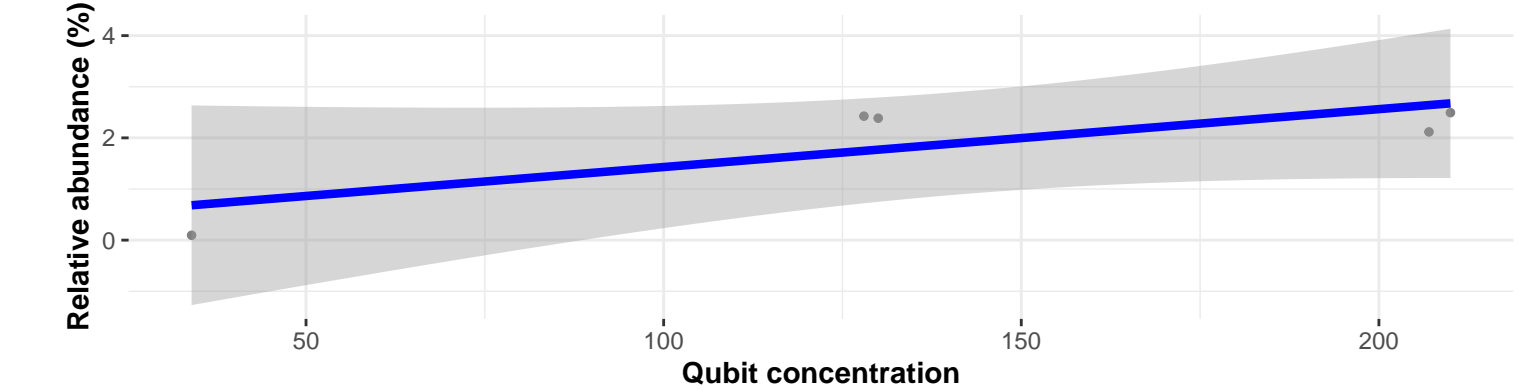
Correlation within: Feed



Correlation within: control



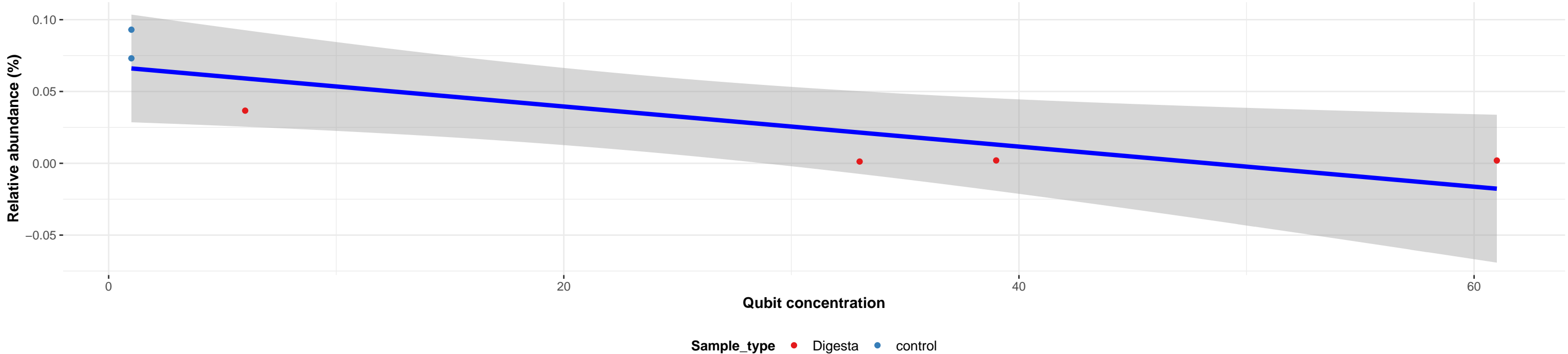
Correlation within: water



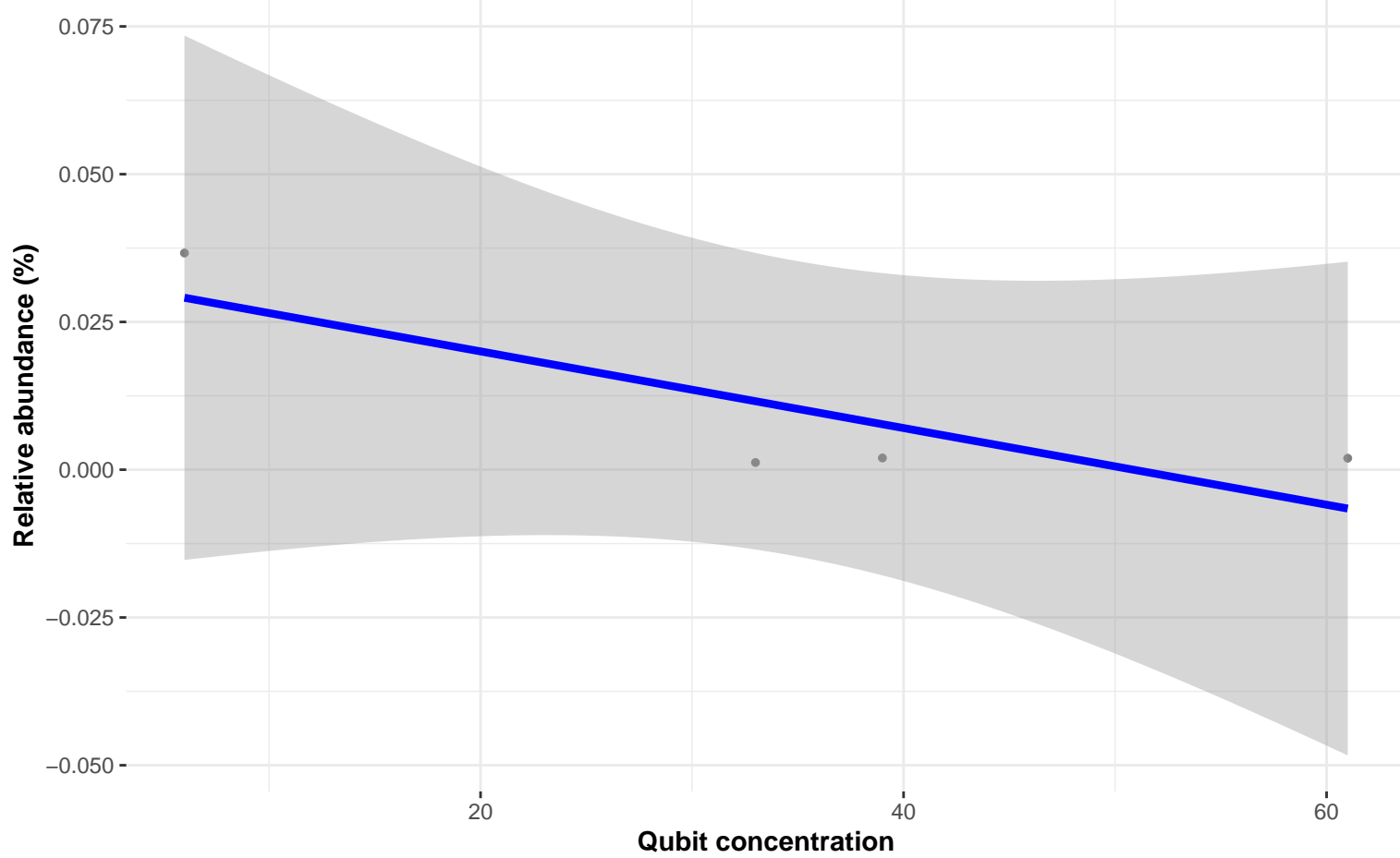
Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

Correlation with all samples

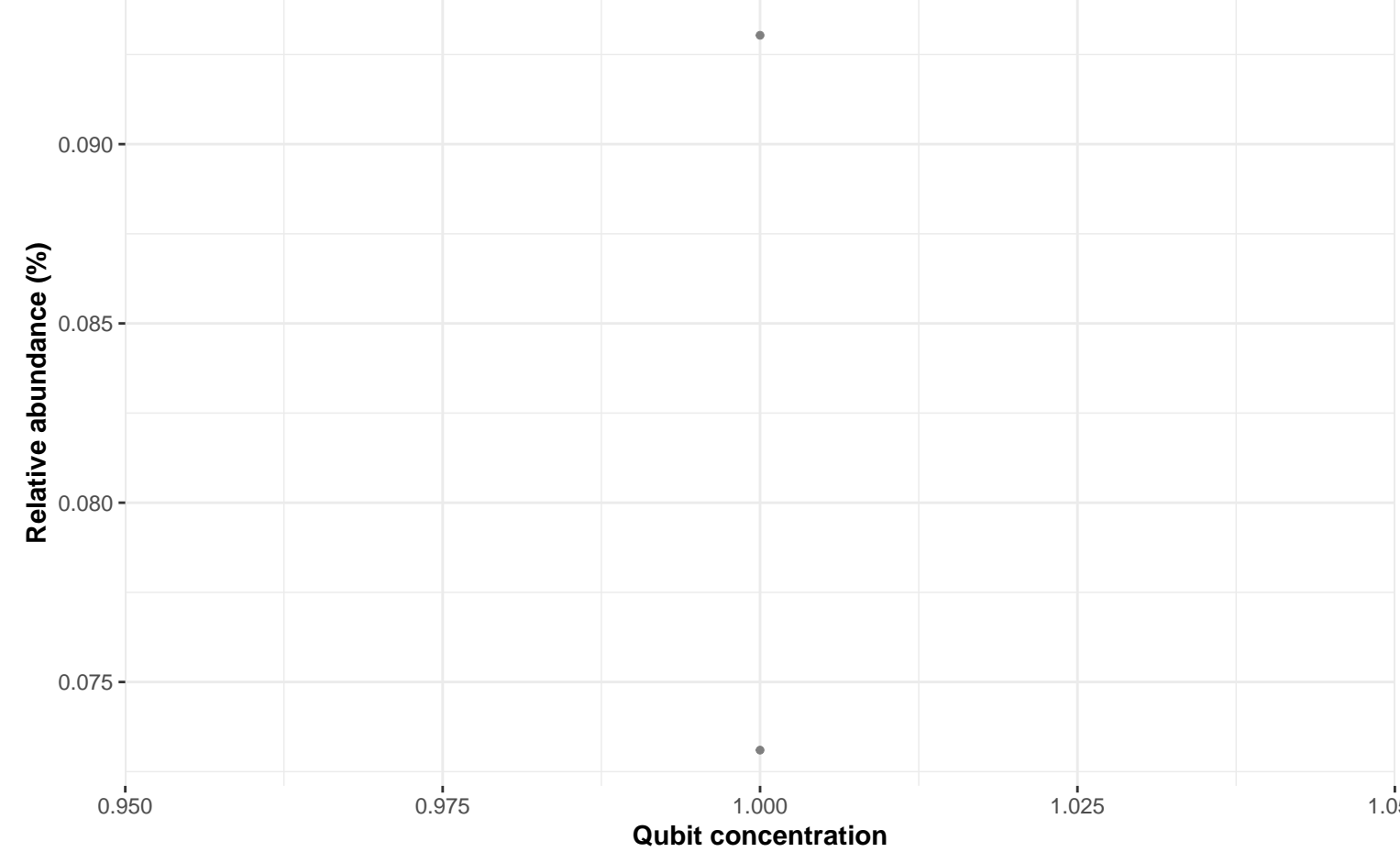
$\log_e(S) = 4.150$, $p = 0.050$, $\hat{\rho}_{\text{Spearman}} = -0.812$, $\text{CI}_{95\%} [-0.980, 0.033]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



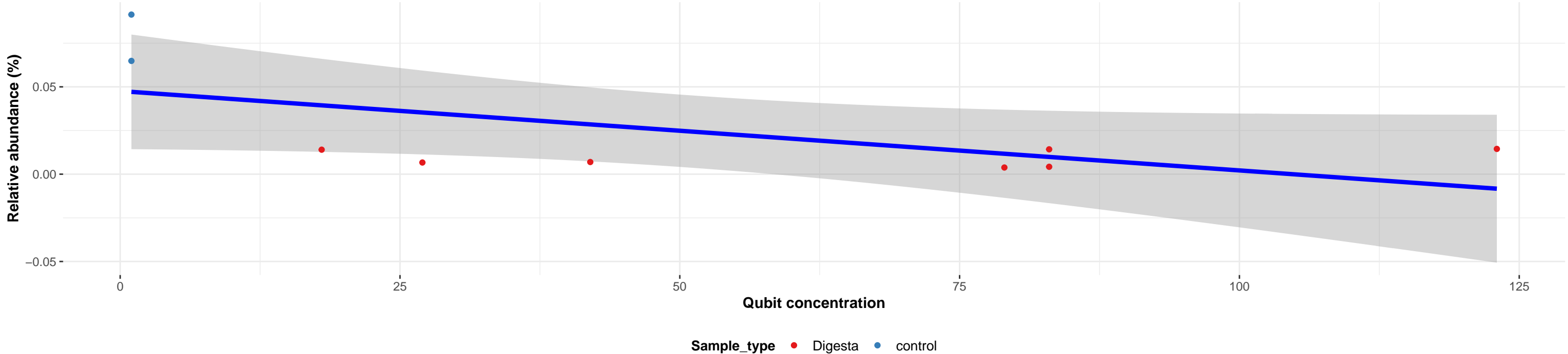
Correlation within: control



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; NA

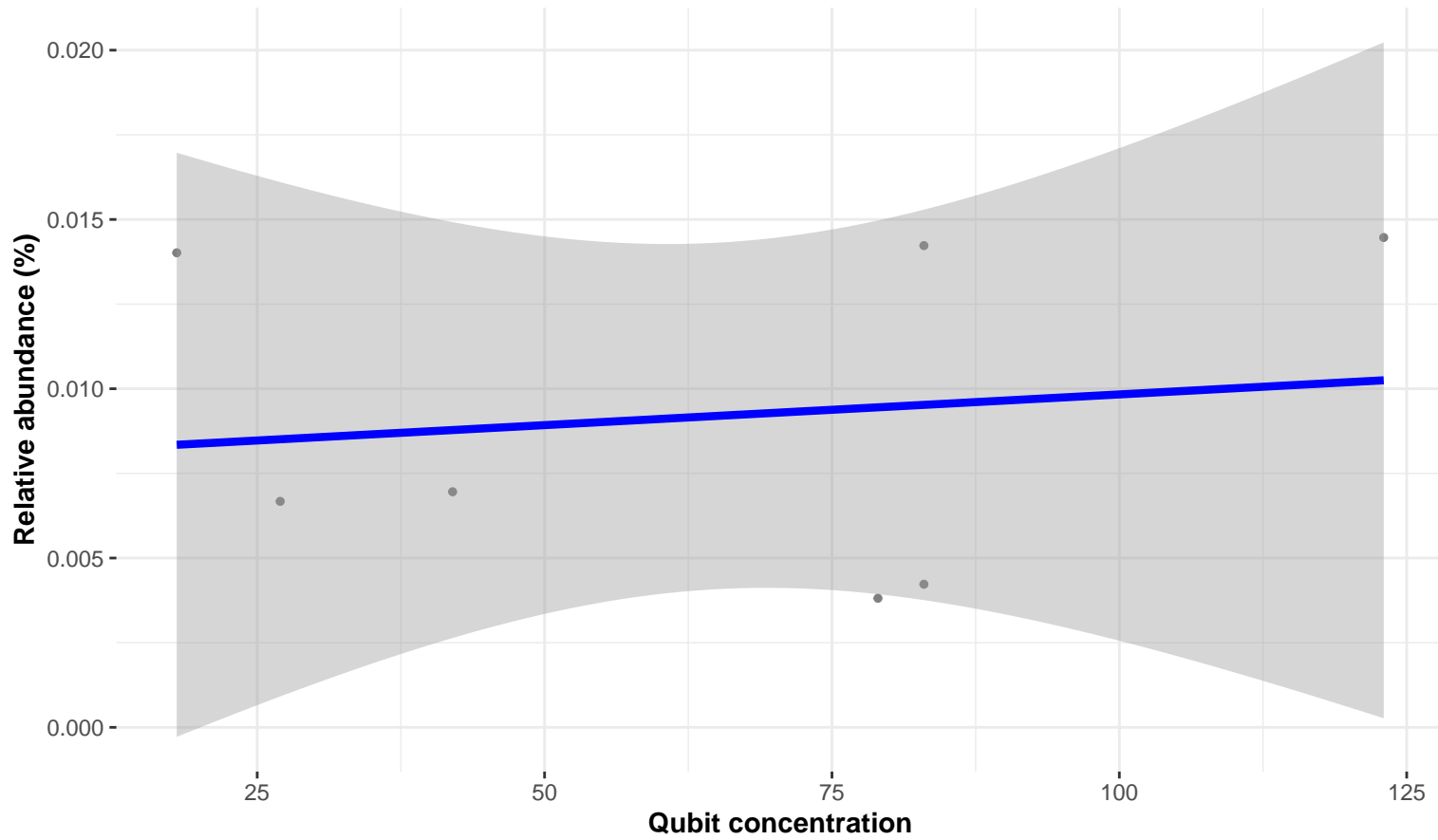
Correlation with all samples

$\log_e(S) = 5.120$, $p = 0.293$, $\hat{\rho}_{\text{Spearman}} = -0.395$, $\text{CI}_{95\%} [-0.846, 0.385]$, $n_{\text{pairs}} = 9$

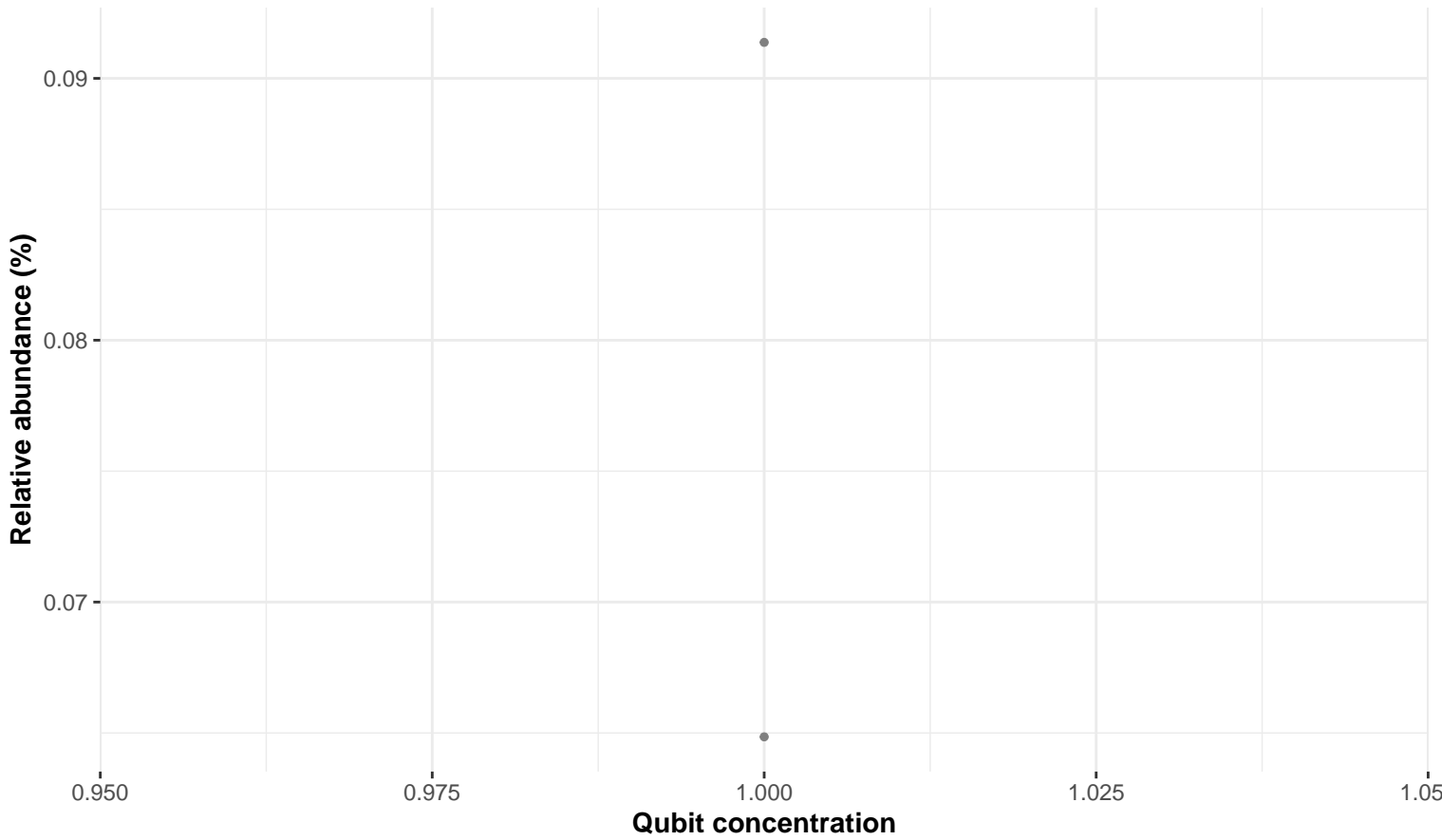


Correlation within: Digesta

$\log_e(S) = 3.685$, $p = 0.531$, $\hat{\rho}_{\text{Spearman}} = 0.288$, $\text{CI}_{95\%} [-0.612, 0.863]$, $n_{\text{pairs}} = 7$



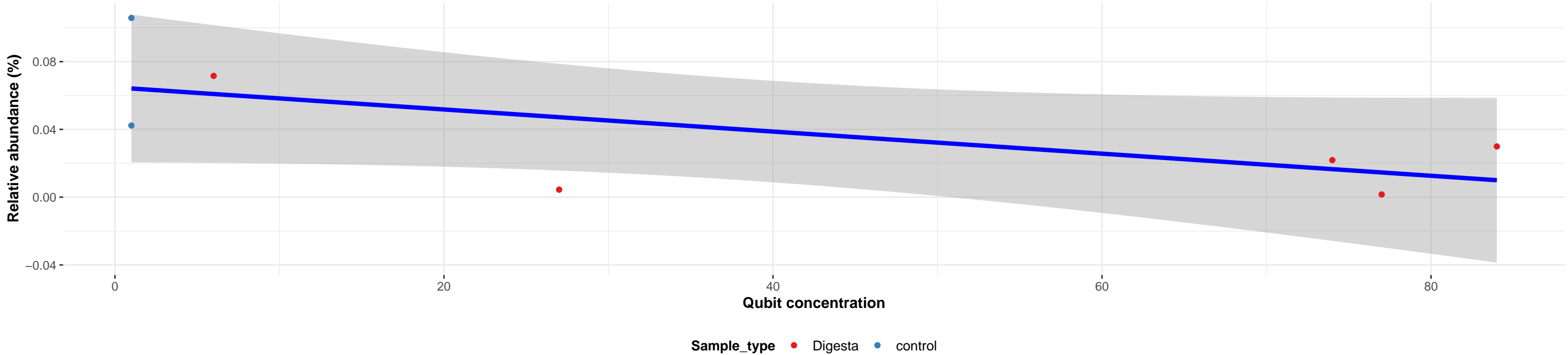
Correlation within: control



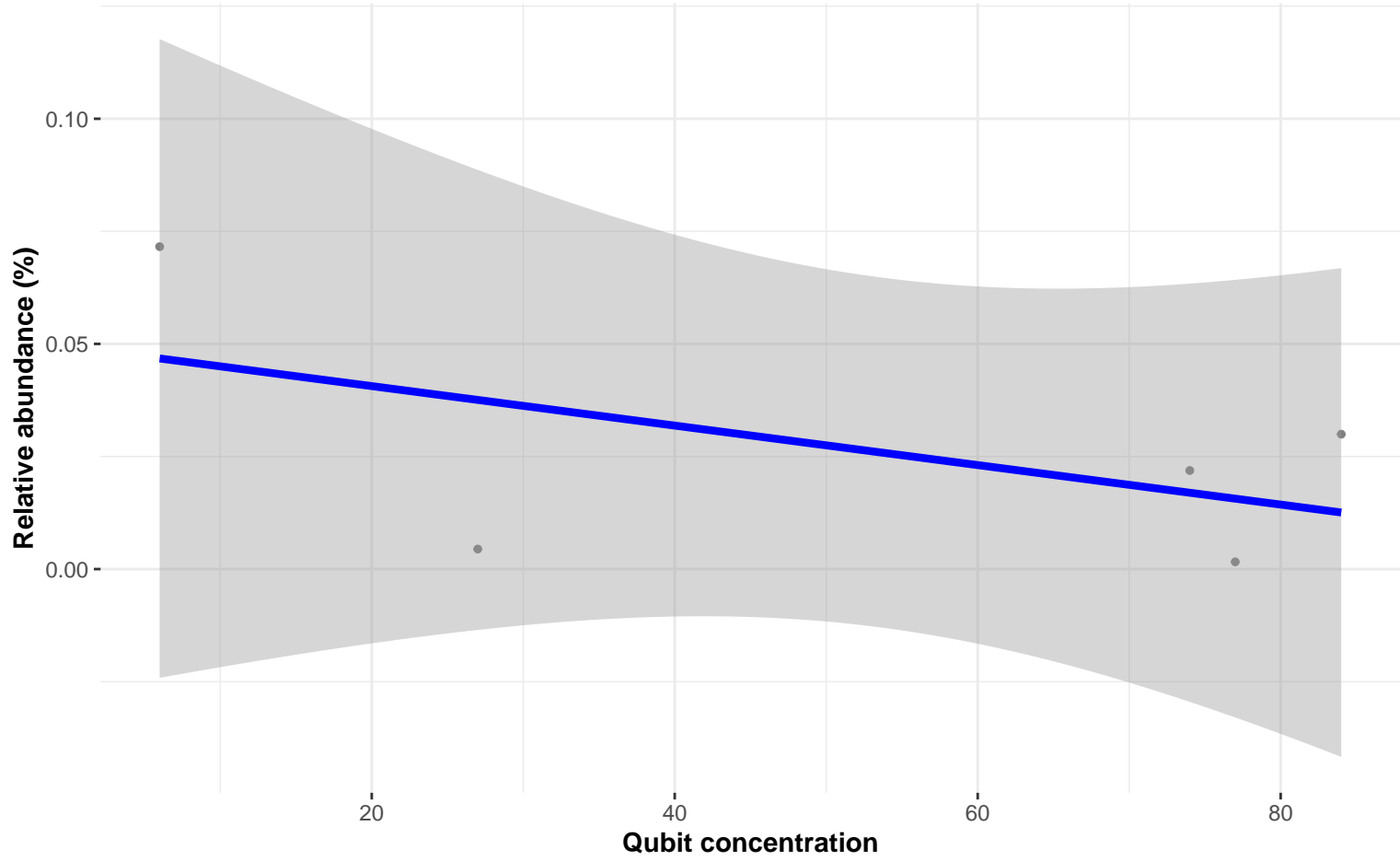
Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA

Correlation with all samples

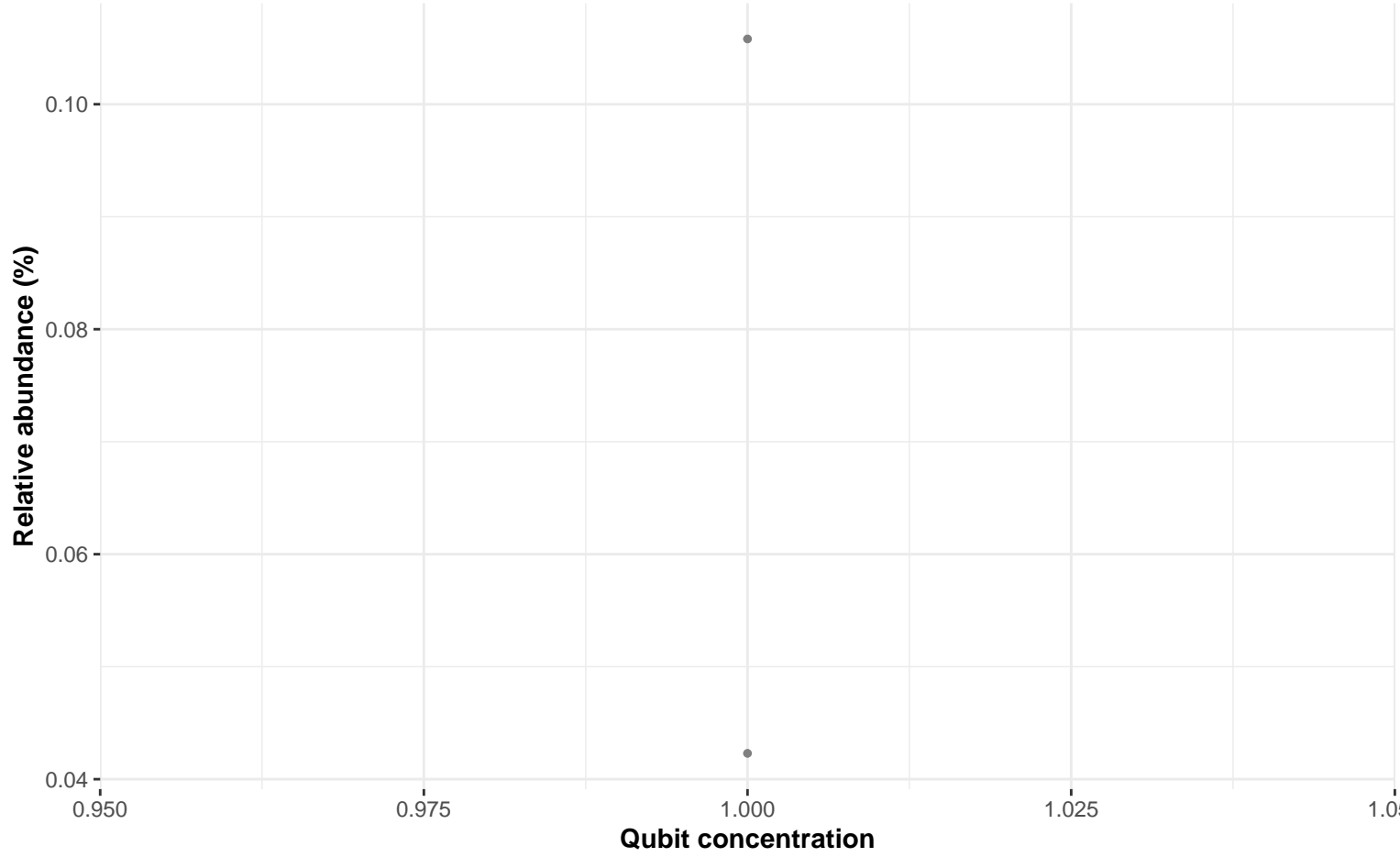
$\log_e(S) = 4.547$, $p = 0.090$, $\hat{\rho}_{\text{Spearman}} = -0.685$, $\text{CI}_{95\%} [-0.951, 0.169]$, $n_{\text{pairs}} = 7$



Correlation within: Digesta



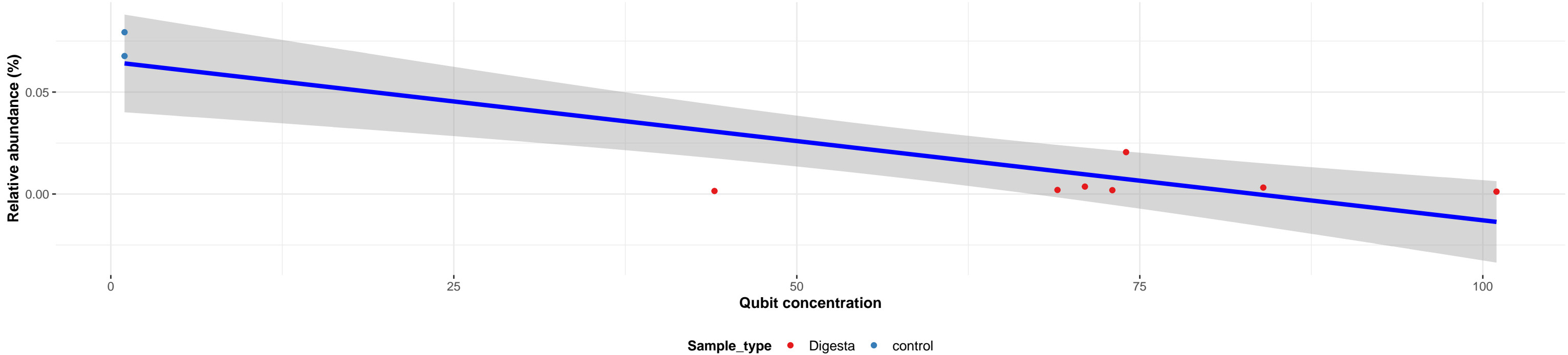
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Kaiserbacteria; NA; NA; NA

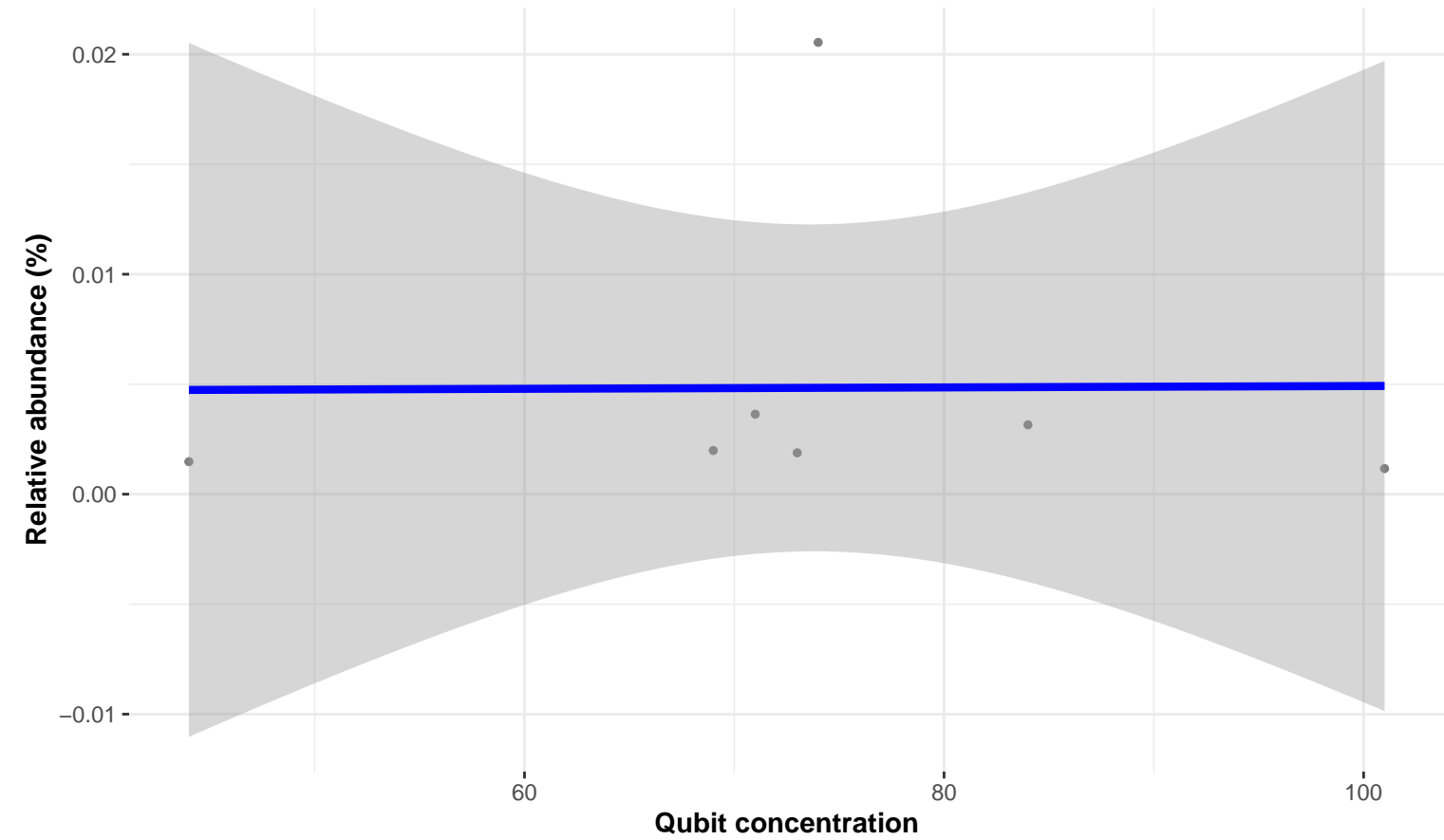
Correlation with all samples

$\log_e(S) = 5.211$, $p = 0.145$, $\hat{\rho}_{\text{Spearman}} = -0.527$, $\text{CI}_{95\%} [-0.888, 0.233]$, $n_{\text{pairs}} = 9$

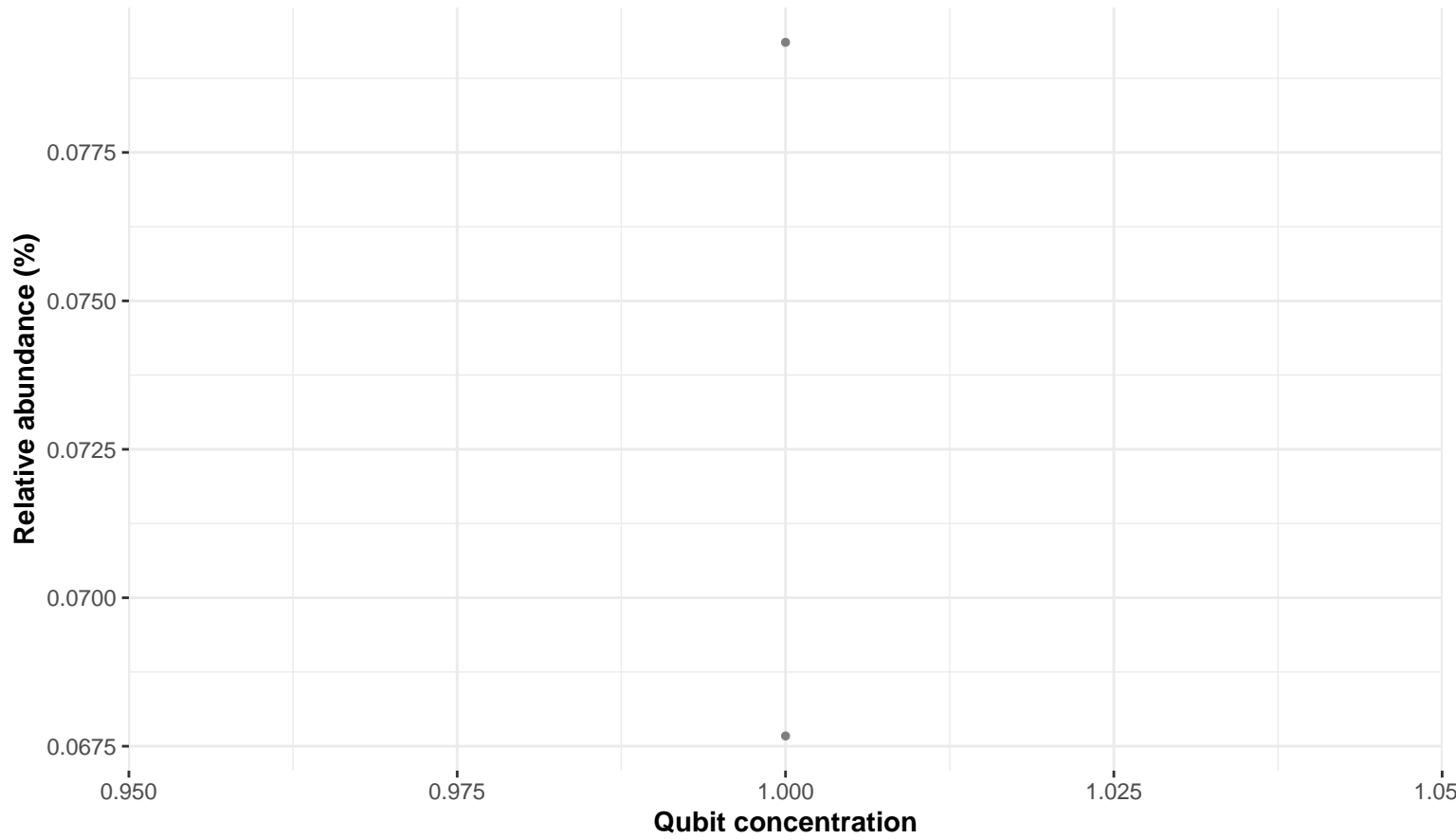


Correlation within: Digesta

$\log_e(S) = 4.025$, $p = 1.000$, $\hat{\rho}_{\text{Spearman}} = 0.000$, $\text{CI}_{95\%} [-0.765, 0.765]$, $n_{\text{pairs}} = 7$



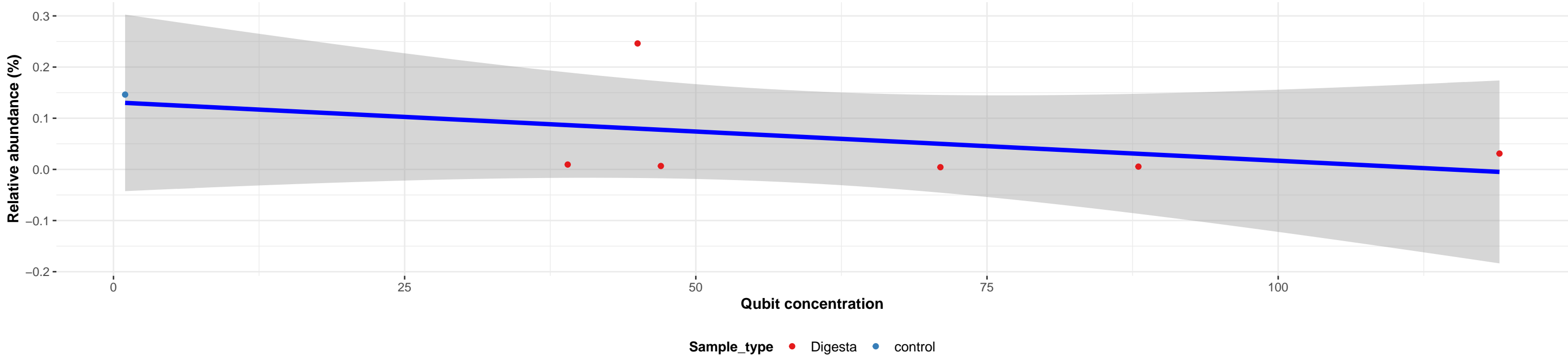
Correlation within: control



Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Oxalobacteraceae; Massilia; NA

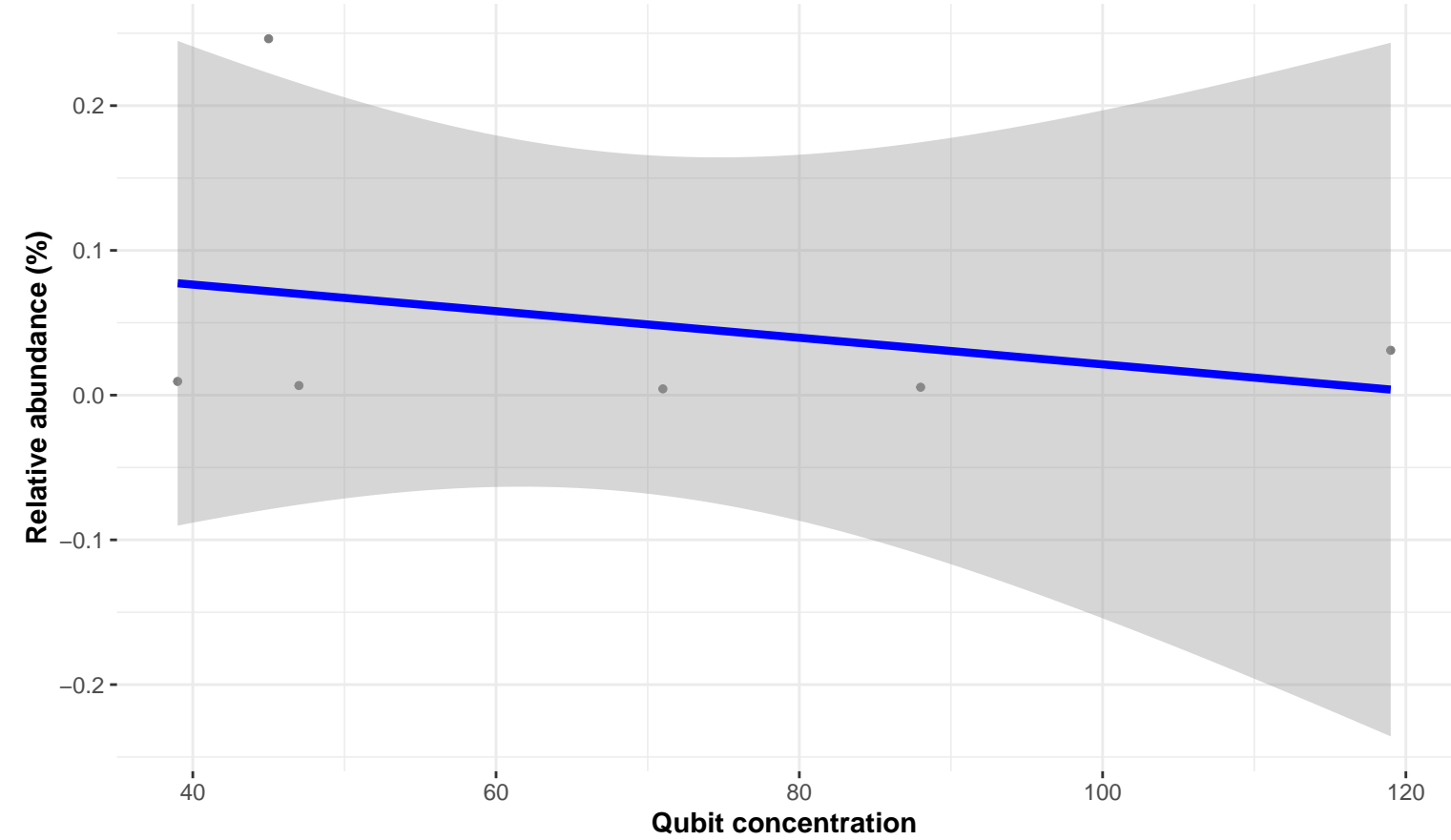
Correlation with all samples

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

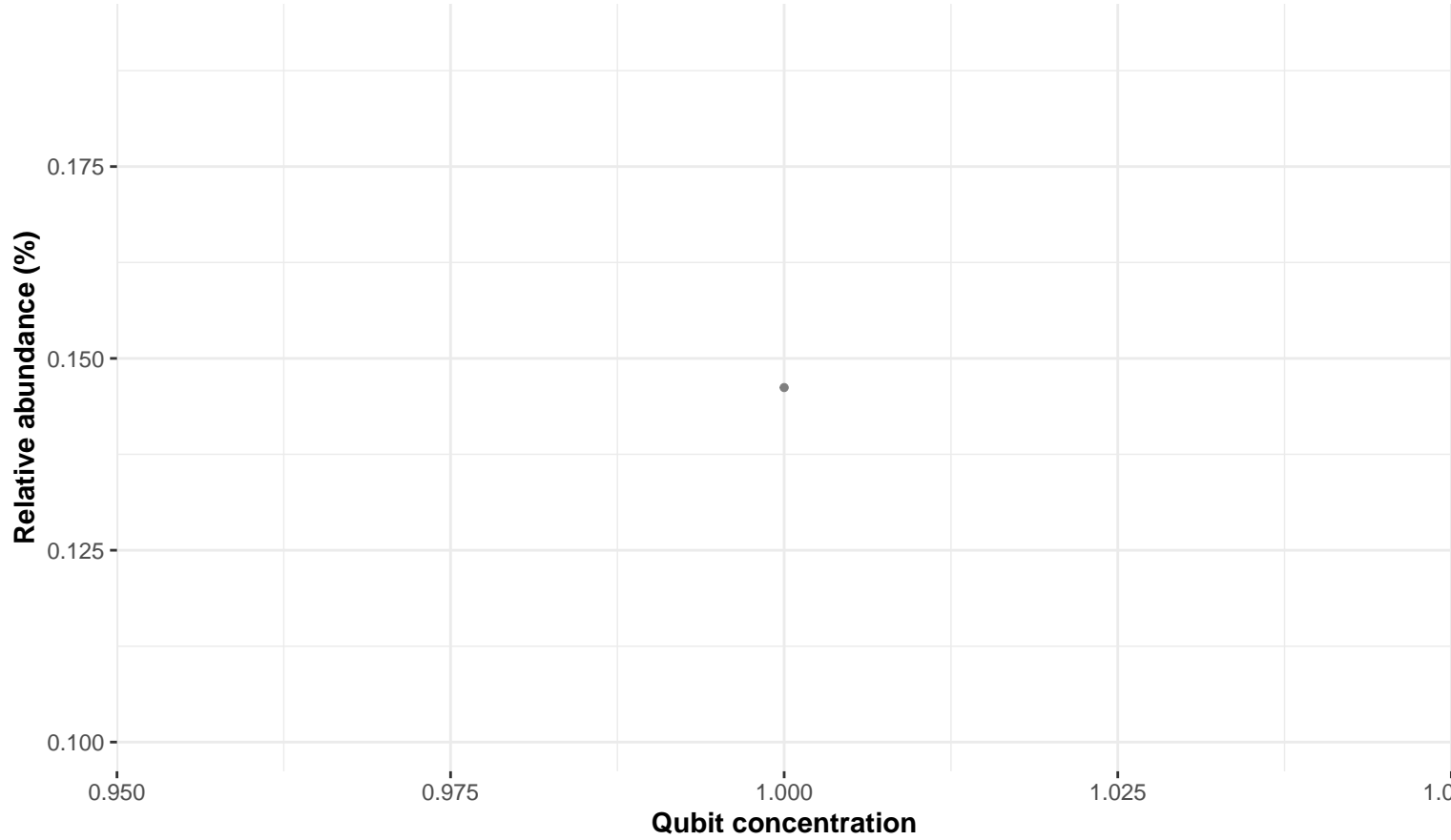


Correlation within: Digesta

$\log_e(S) = 3.784$, $p = 0.623$, $\hat{\rho}_{\text{Spearman}} = -0.257$, $\text{CI}_{95\%} [-0.891, 0.717]$, $n_{\text{pairs}} = 6$



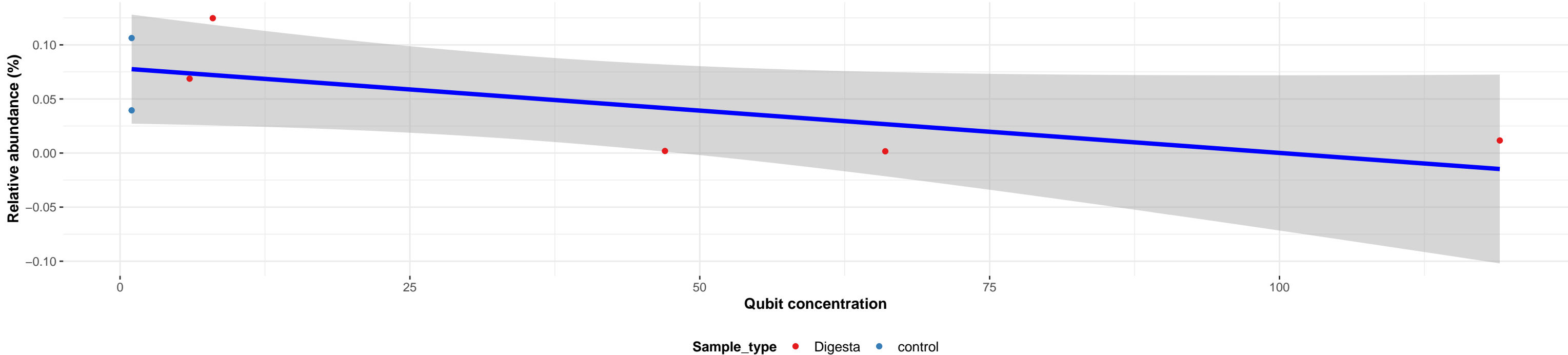
Correlation within: control



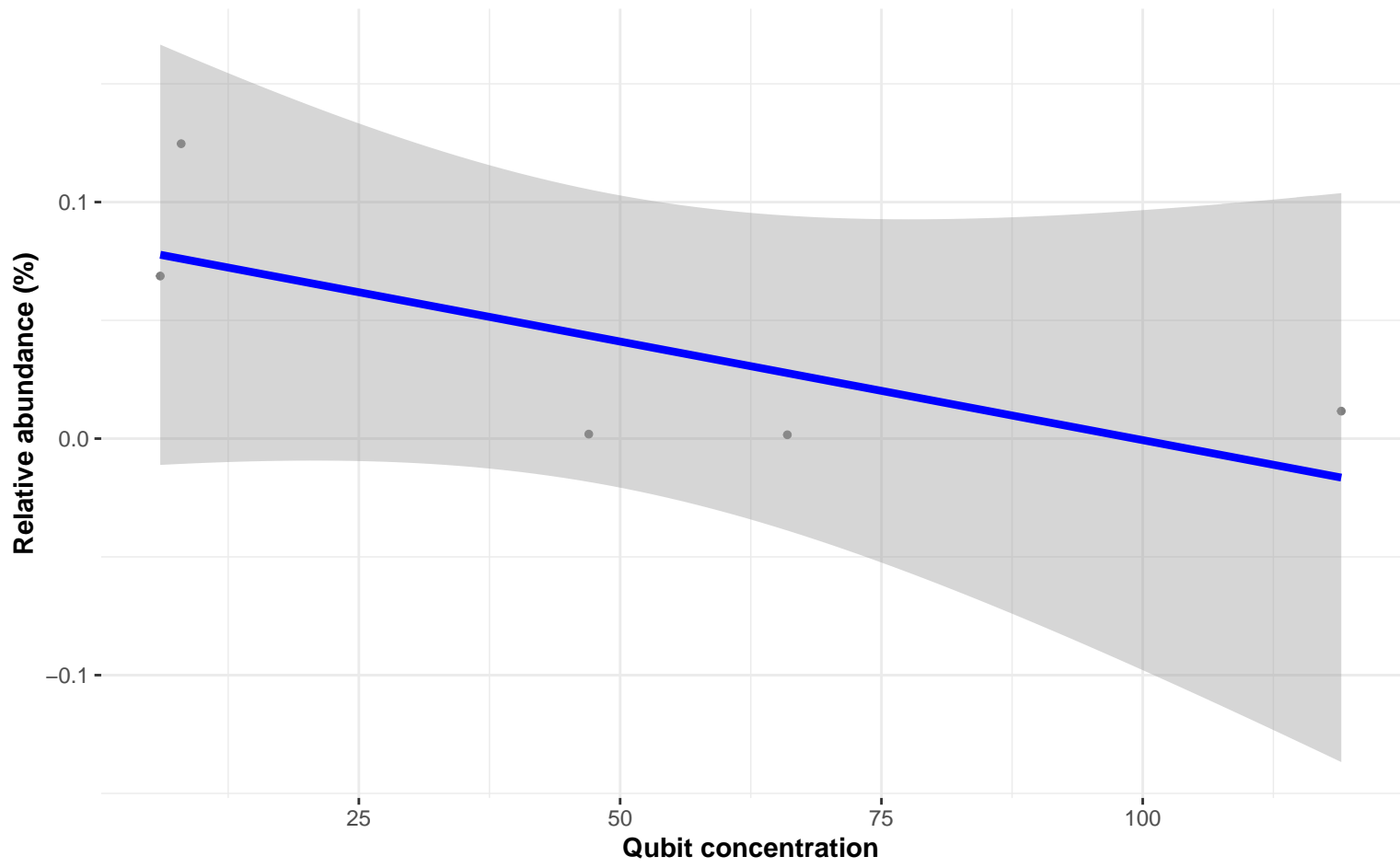
Bacteria; Patescibacteria; Parcubacteria; NA; NA; NA; NA

Correlation with all samples

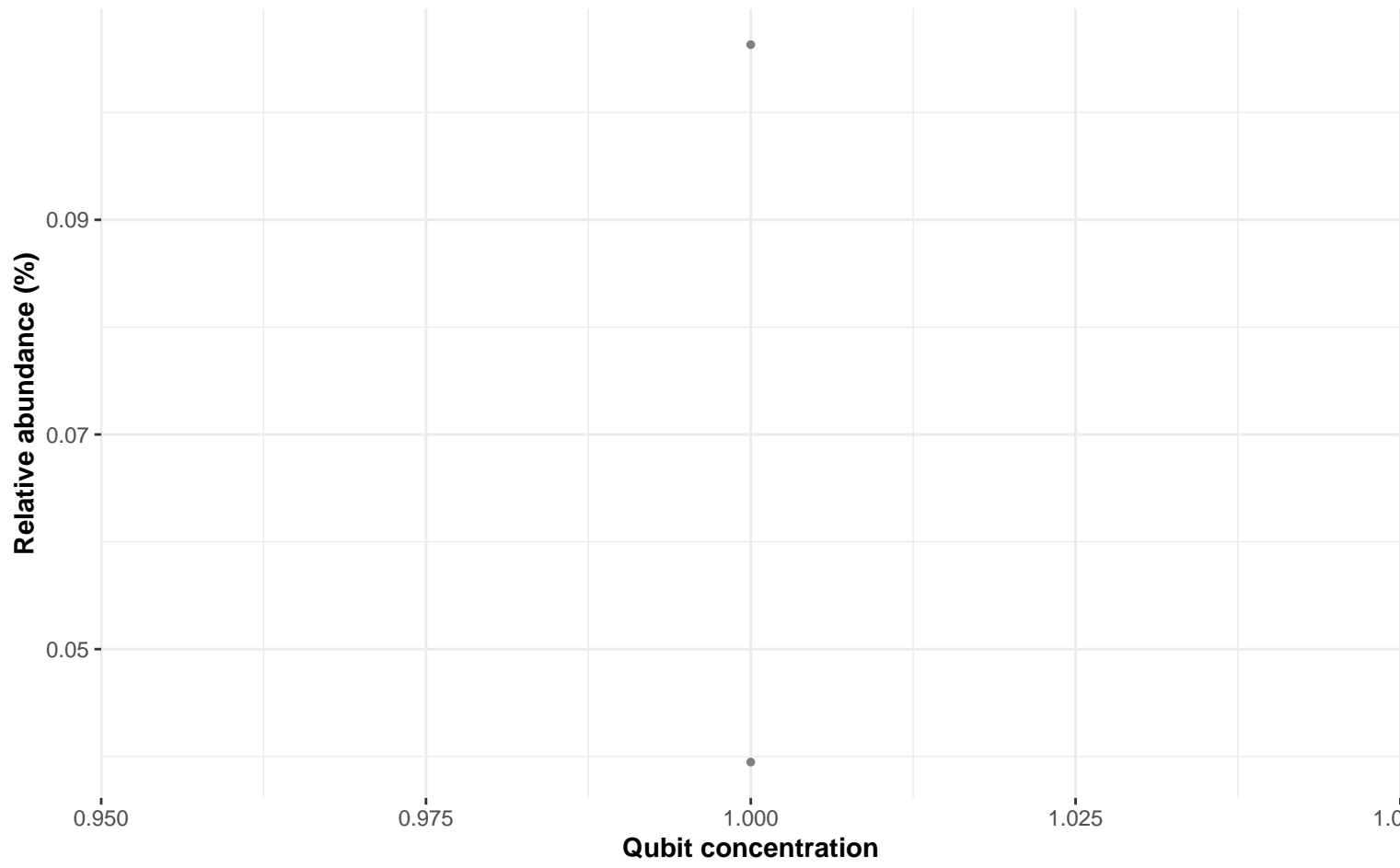
$\log_e(S) = 4.503$, $p = 0.144$, $\hat{\rho}_{\text{Spearman}} = -0.613$, $\text{CI}_{95\%} [-0.938, 0.287]$, $n_{\text{pairs}} = 7$



Correlation within: Digesta



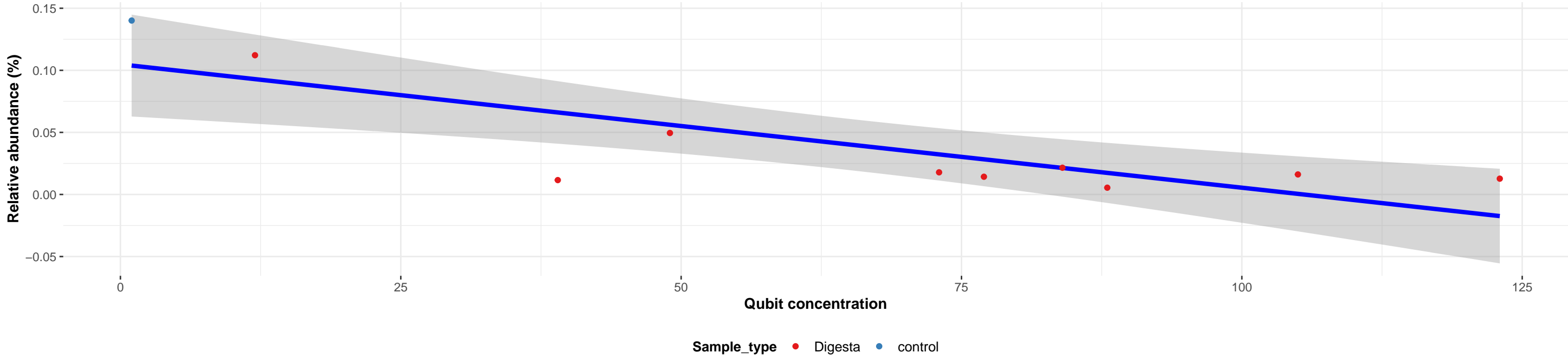
Correlation within: control



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Brevibacteriaceae; Brevibacterium; NA

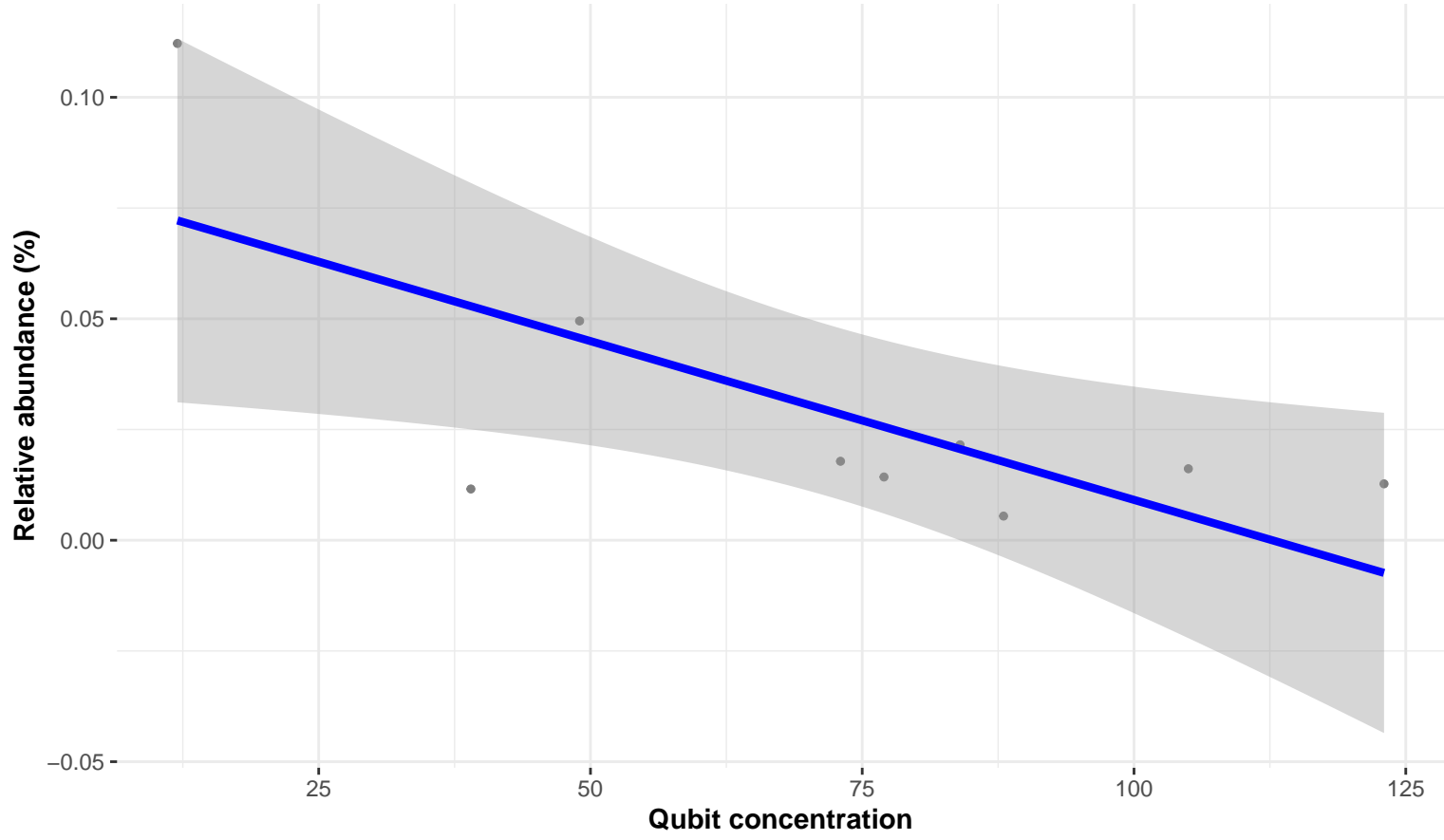
Correlation with all samples

$\log_e(S) = 5.583$, $p = 0.060$, $\hat{\rho}_{\text{Spearman}} = -0.612$, $\text{CI}_{95\%} [-0.901, 0.050]$, $n_{\text{pairs}} = 10$

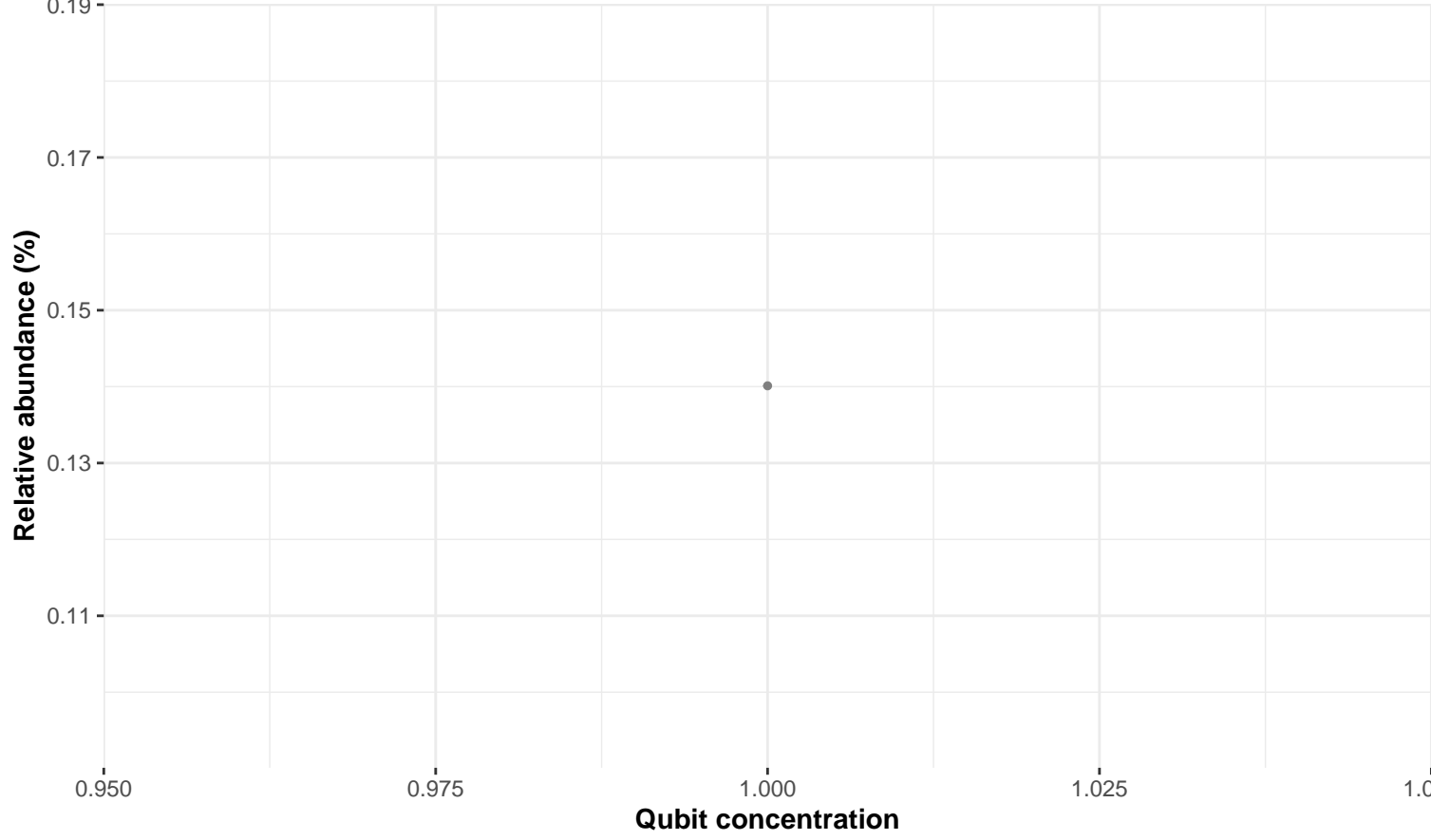


Correlation within: Digesta

$\log_e(S) = 5.170$, $p = 0.205$, $\hat{\rho}_{\text{Spearman}} = -0.467$, $\text{CI}_{95\%} [-0.869, 0.308]$, $n_{\text{pairs}} = 9$



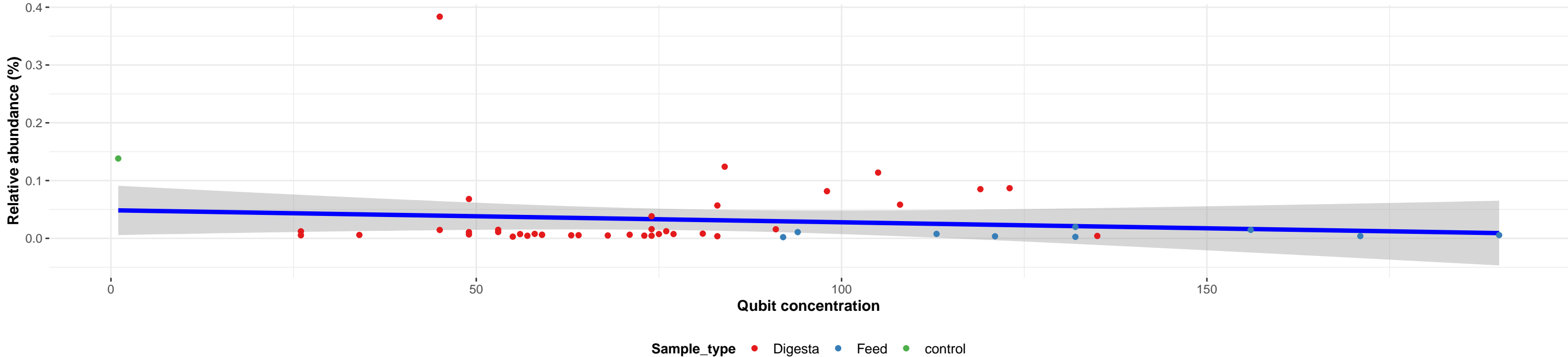
Correlation within: control



Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium sensu stricto 7; novyi

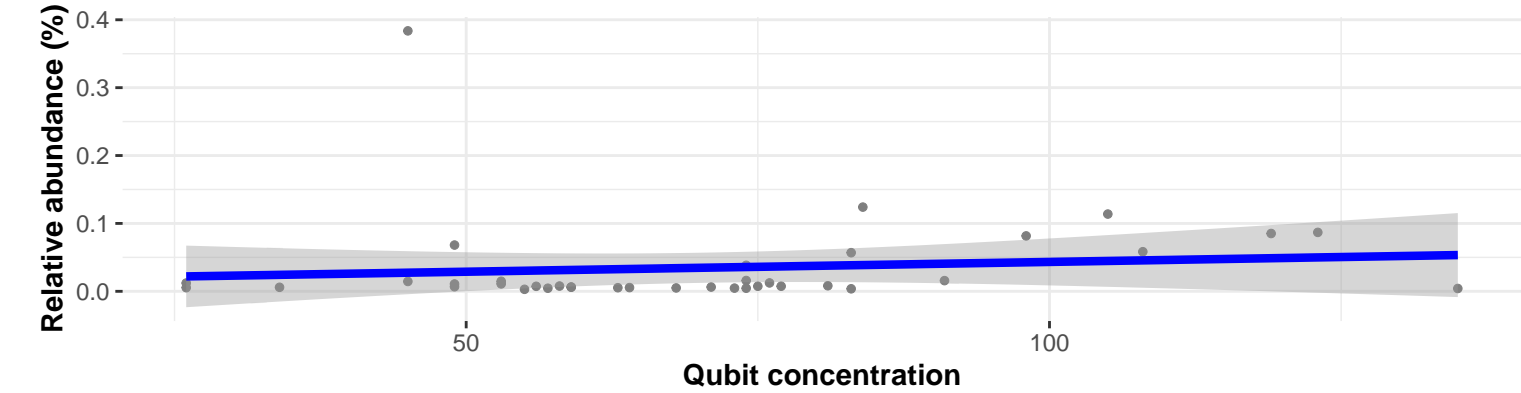
Correlation with all samples

$\log_e(S) = 9.867$, $p = 0.755$, $\hat{\rho}_{\text{Spearman}} = -0.046$, $CI_{95\%} [-0.334, 0.249]$, $n_{\text{pairs}} = 48$



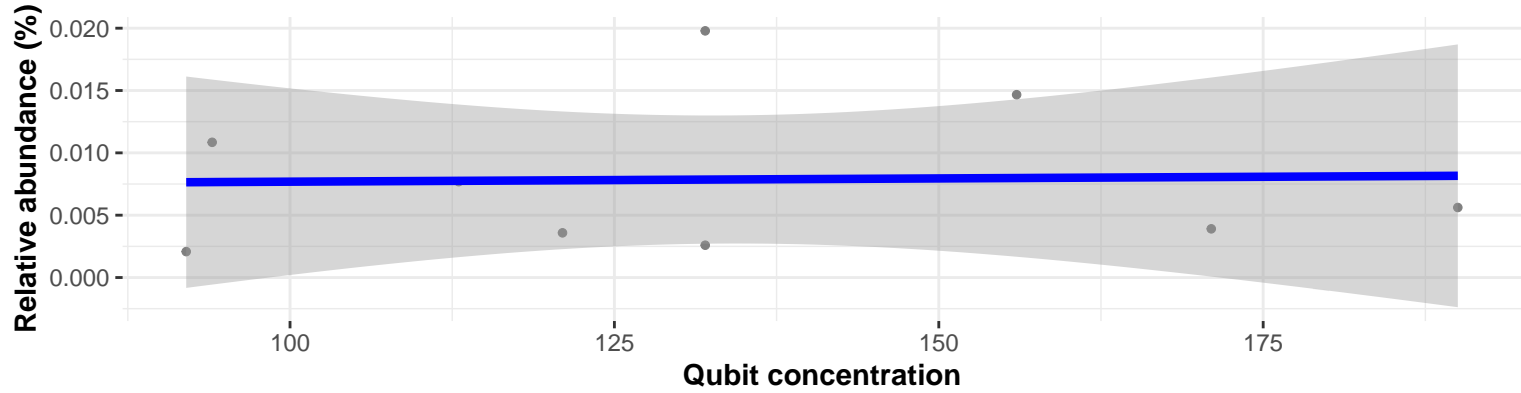
Correlation within: Digesta

$\log_e(S) = 8.843$, $p = 0.142$, $\hat{\rho}_{\text{Spearman}} = 0.243$, $CI_{95\%} [-0.093, 0.529]$, $n_{\text{pairs}} = 38$

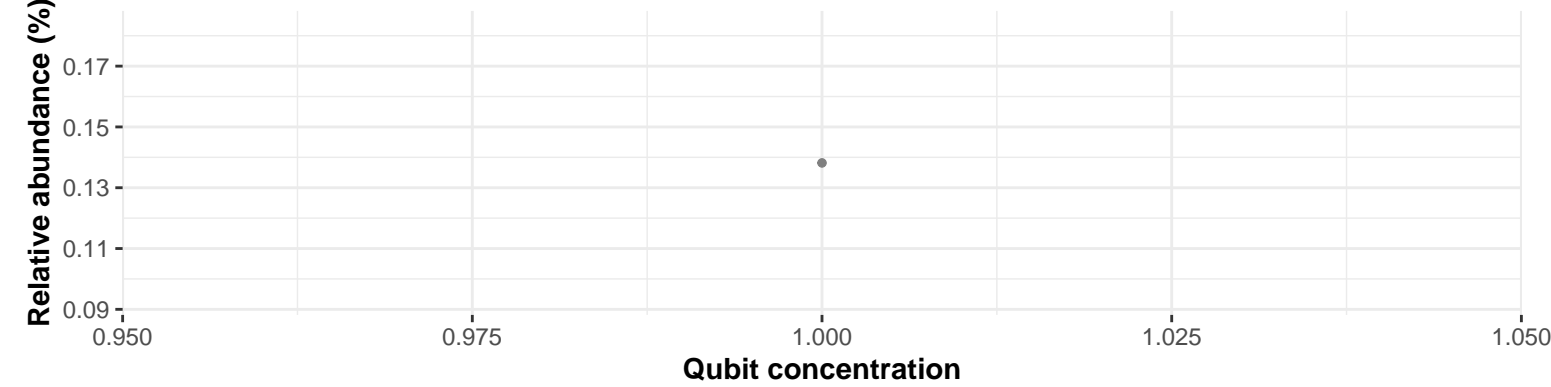


Correlation within: Feed

$\log_e(S) = 4.531$, $p = 0.559$, $\hat{\rho}_{\text{Spearman}} = 0.226$, $CI_{95\%} [-0.533, 0.783]$, $n_{\text{pairs}} = 9$



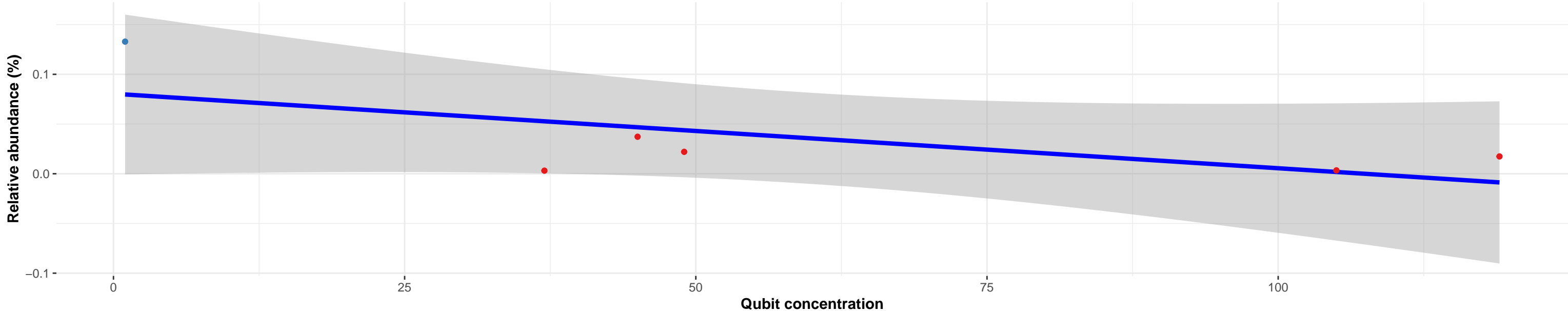
Correlation within: control



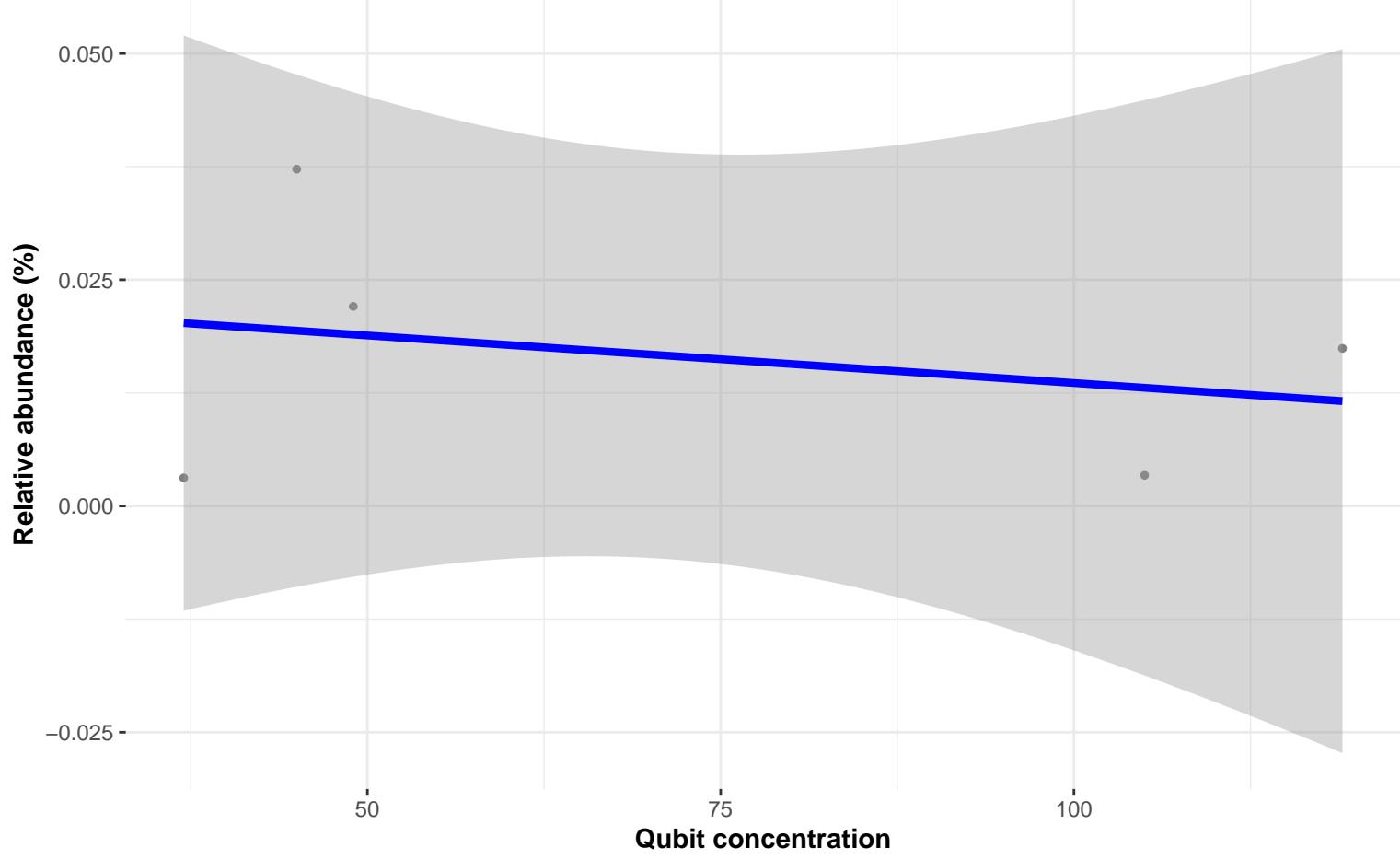
Bacteria; Patescibacteria; Parcubacteria; Candidatus Kaiserbacteria; NA; NA; NA

Correlation with all samples

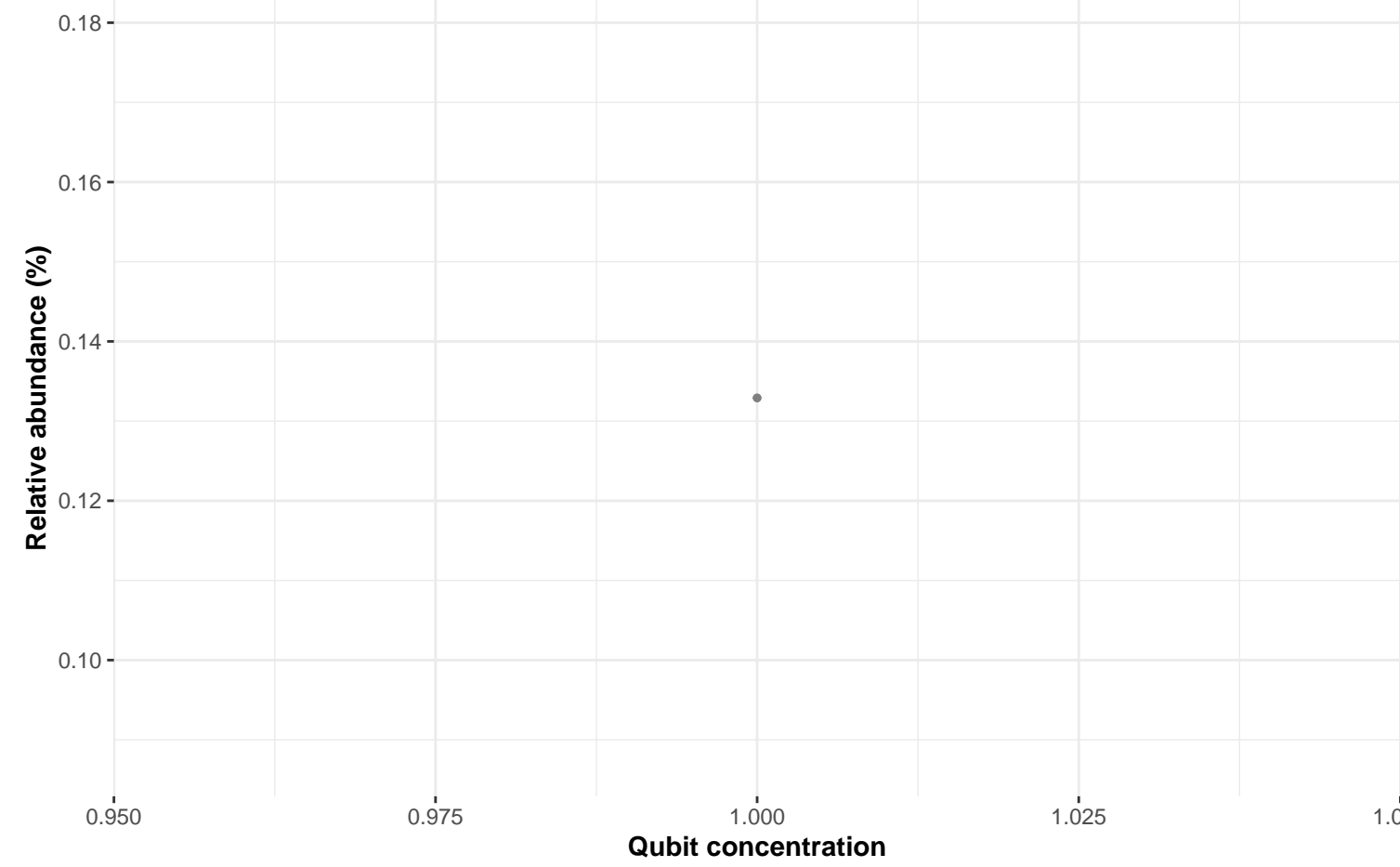
$\log_e(S) = 3.871$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = -0.371$, $\text{CI}_{95\%} [-0.915, 0.650]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



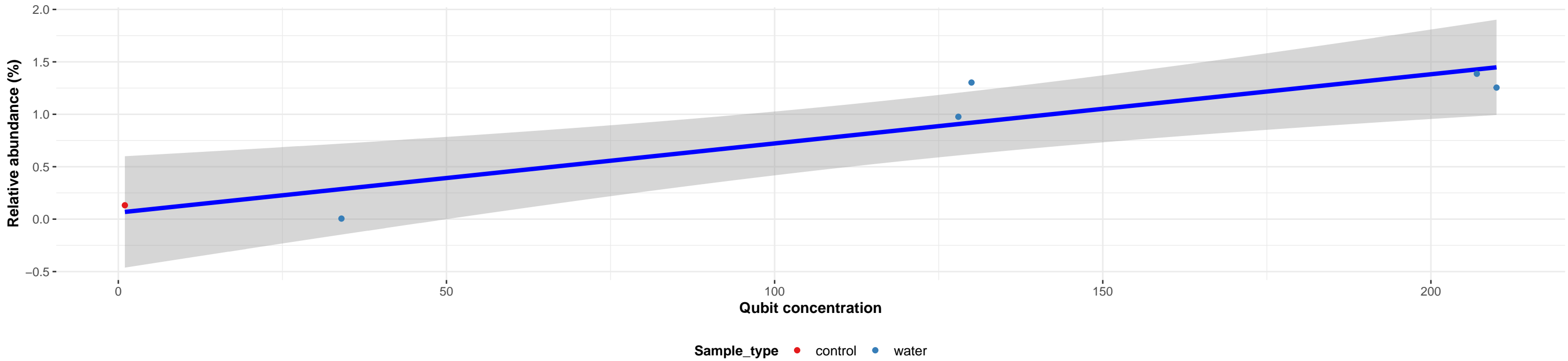
Correlation within: control



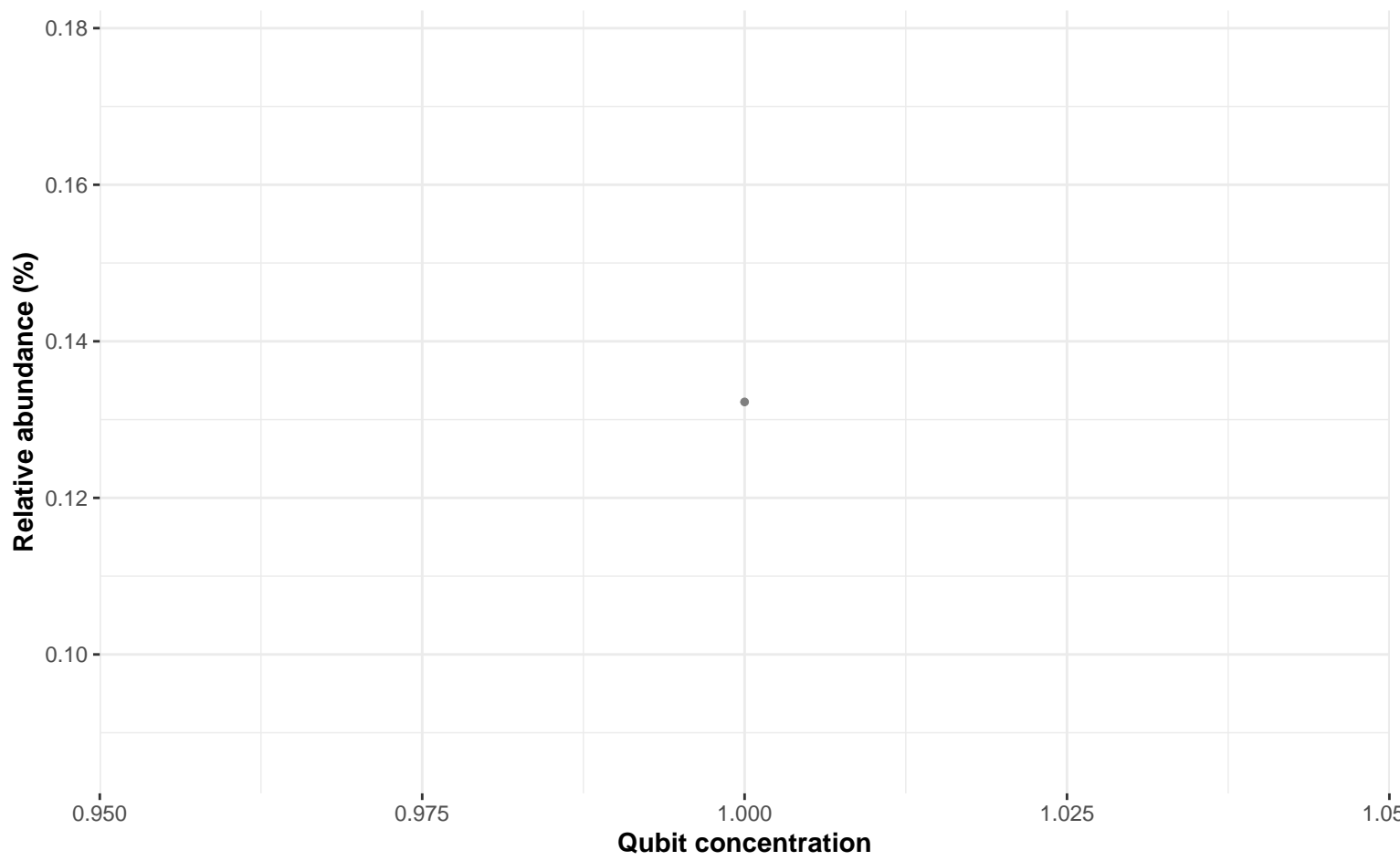
Bacteria; Bacteroidota; Bacteroidia; Chitinophagales; NA; NA; NA

Correlation with all samples

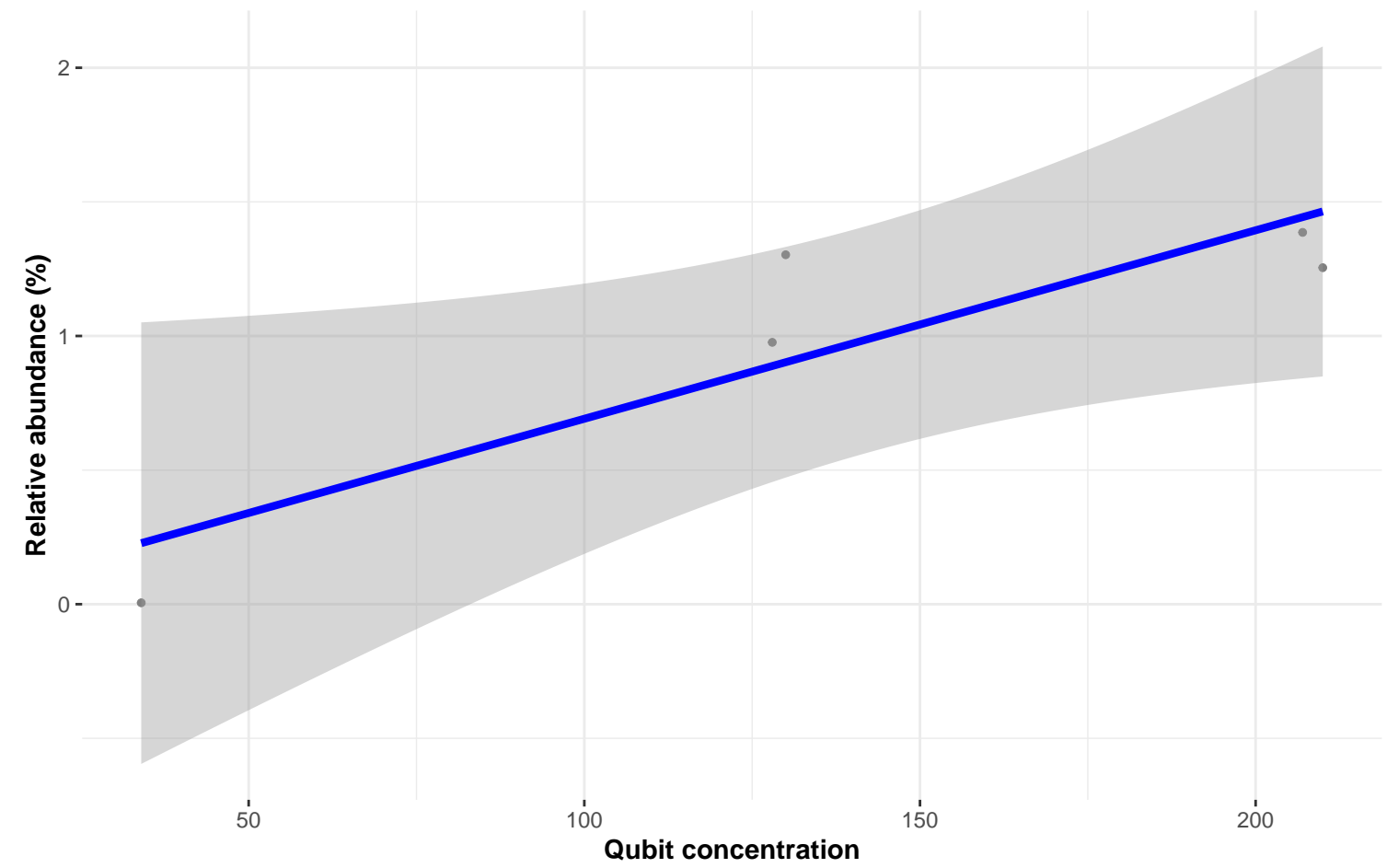
$\log_e(S) = 2.079$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = 0.771$, $CI_{95\%} [-0.140, 0.975]$, $n_{\text{pairs}} = 6$



Correlation within: control



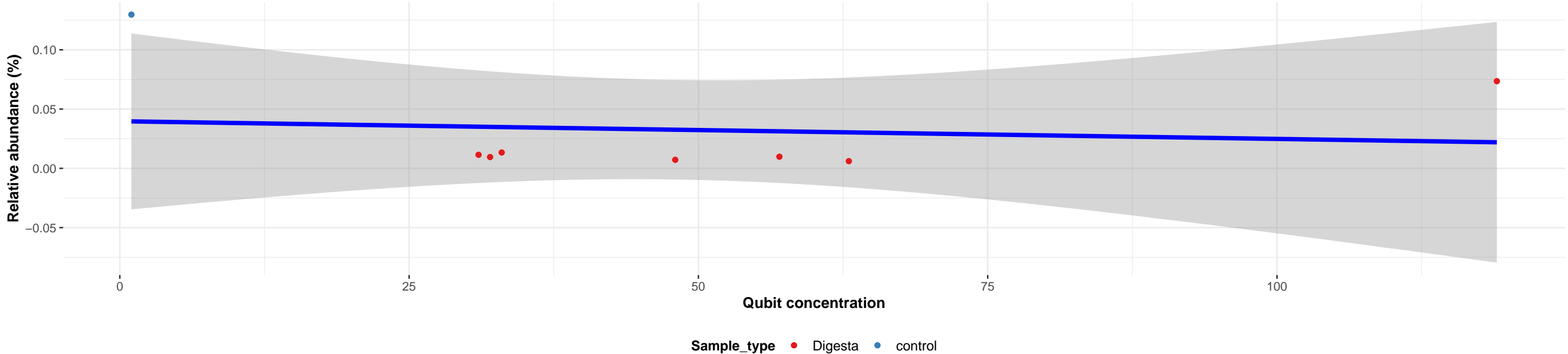
Correlation within: water



Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; NA; NA

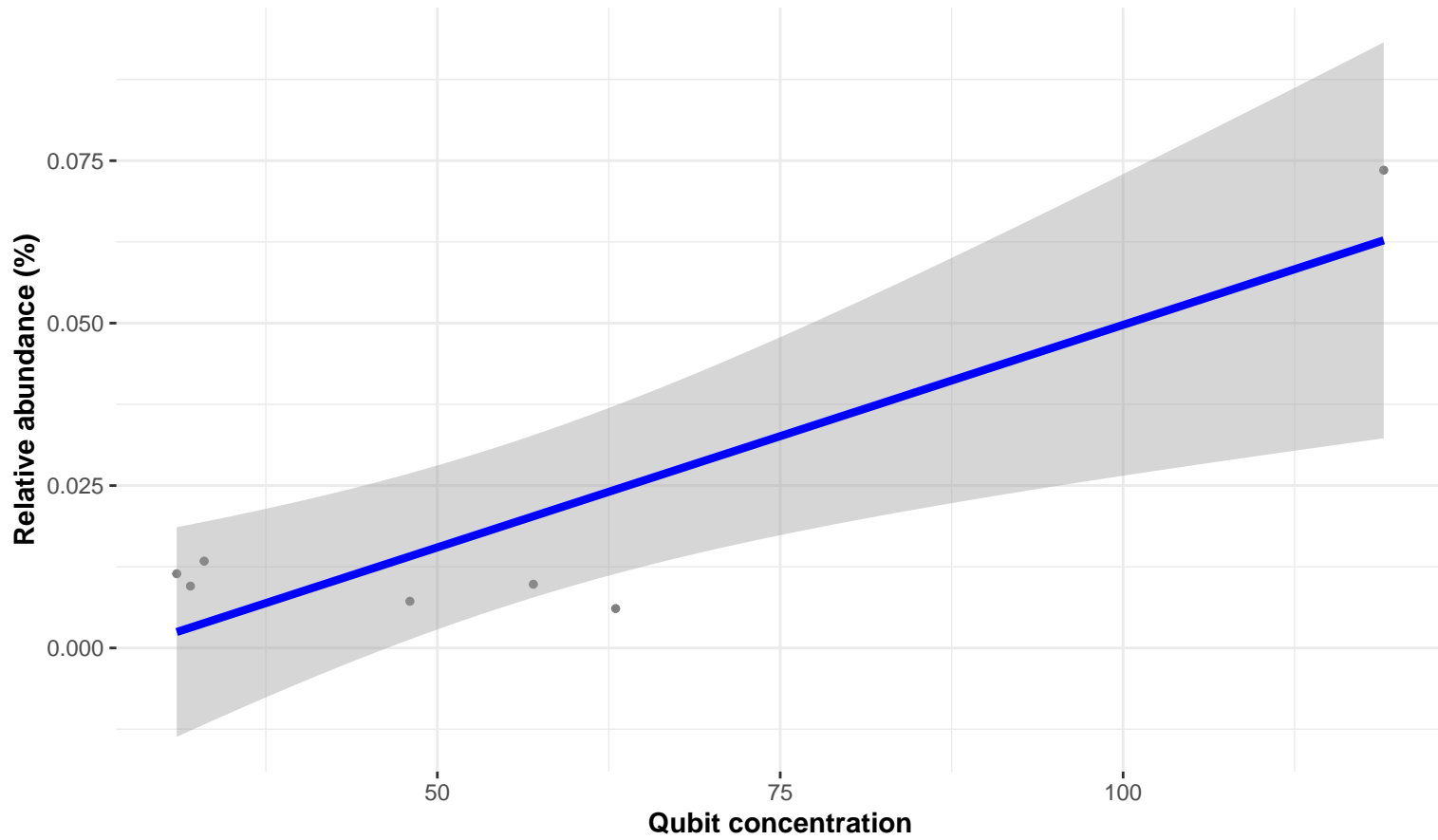
Correlation with all samples

$\log_e(S) = 4.718$, $p = 0.420$, $\hat{\rho}_{\text{Spearman}} = -0.333$, $\text{CI}_{95\%} [-0.848, 0.505]$, $n_{\text{pairs}} = 8$

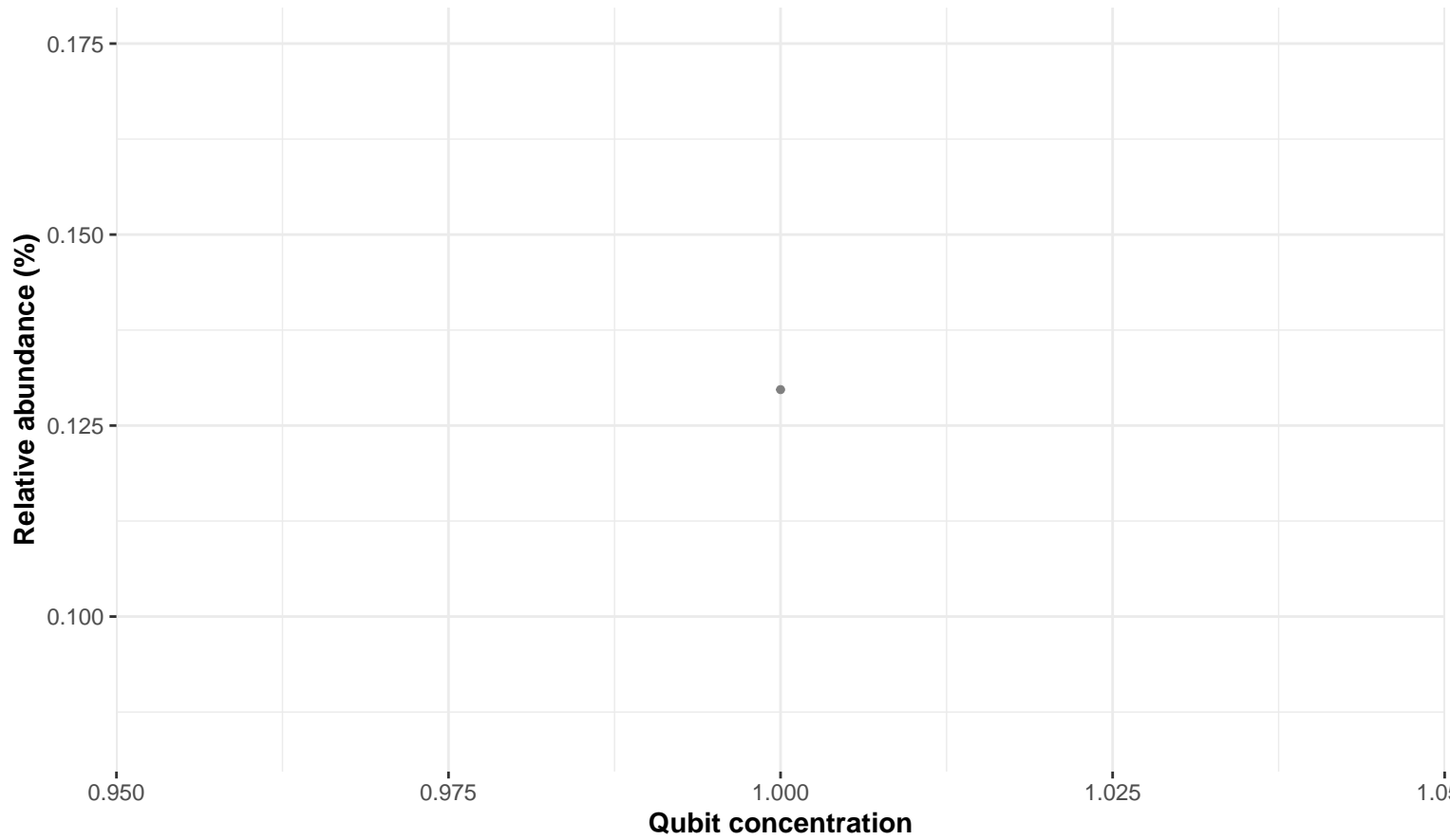


Correlation within: Digesta

$\log_e(S) = 4.025$, $p = 1.000$, $\hat{\rho}_{\text{Spearman}} = 0.000$, $\text{CI}_{95\%} [-0.765, 0.765]$, $n_{\text{pairs}} = 7$



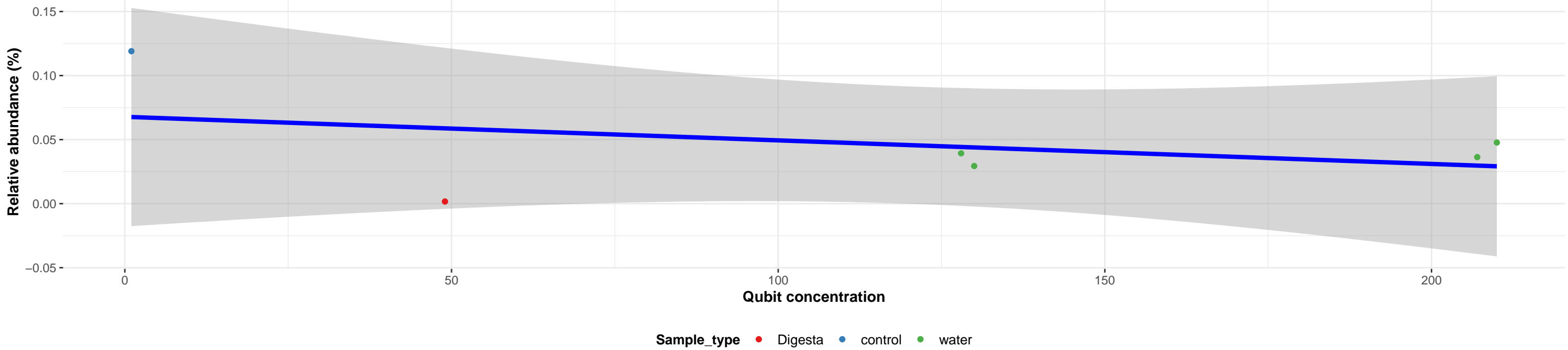
Correlation within: control



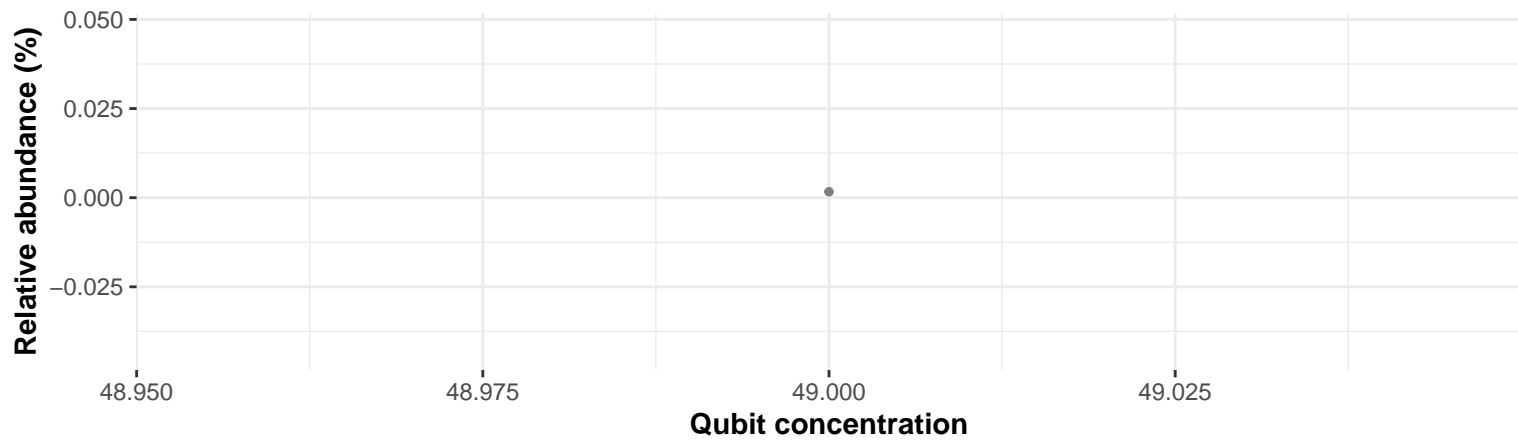
Bacteria; Verrucomicrobiota; Verrucomicrobiae; Verrucomicrobiales; Rubritaleaceae; Rubritalea; NA

Correlation with all samples

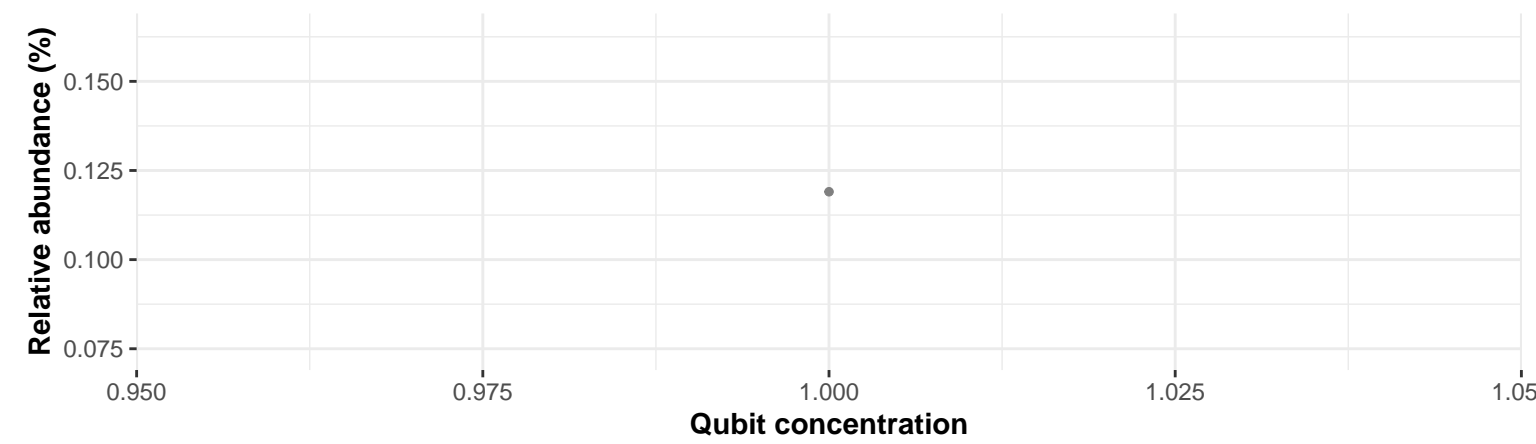
$\log_e(S) = 3.584$, $p = 0.957$, $\hat{\rho}_{\text{Spearman}} = -0.029$, $\text{CI}_{95\%} [-0.832, 0.813]$, $n_{\text{pairs}} = 6$



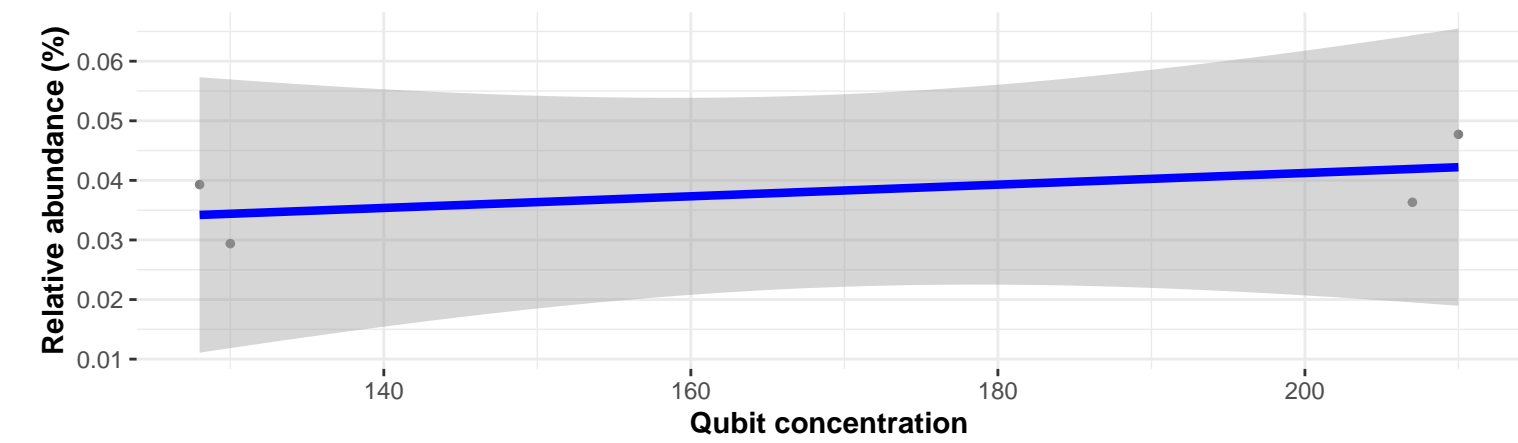
Correlation within: Digesta



Correlation within: control



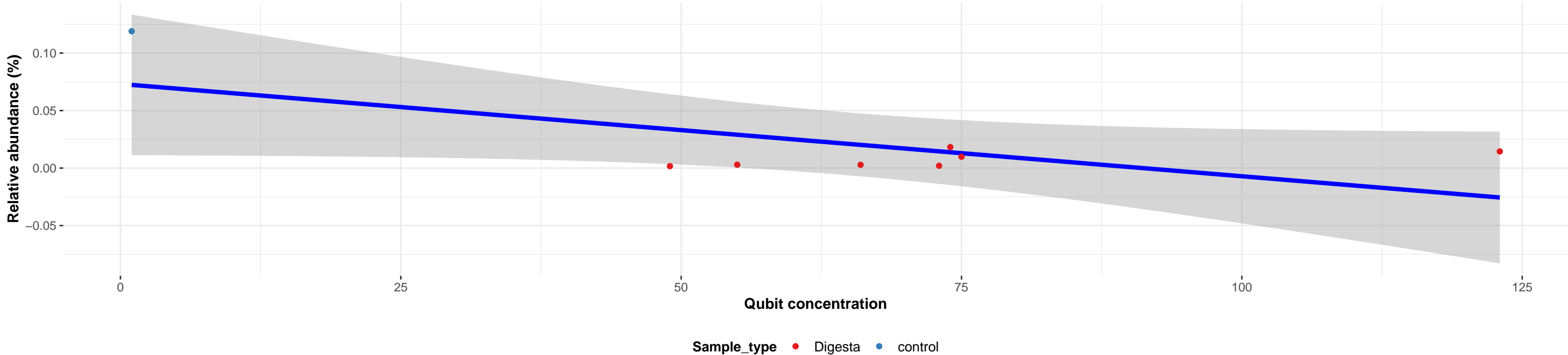
Correlation within: water



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

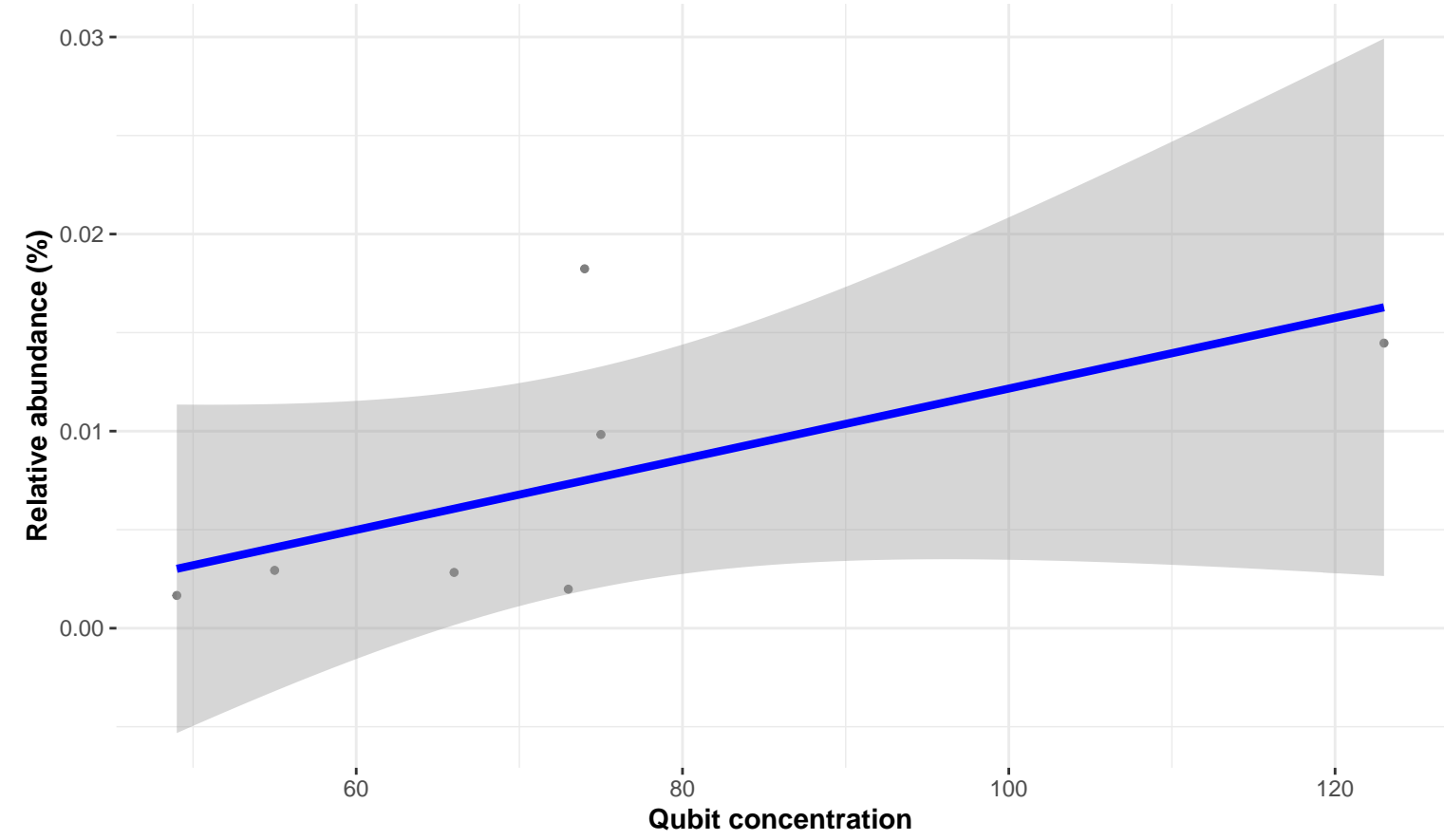
Correlation with all samples

$\log_e(S) = 4.248$, $p = 0.693$, $\hat{\rho}_{\text{Spearman}} = 0.167$, $\text{CI}_{95\%} [-0.626, 0.790]$, $n_{\text{pairs}} = 8$

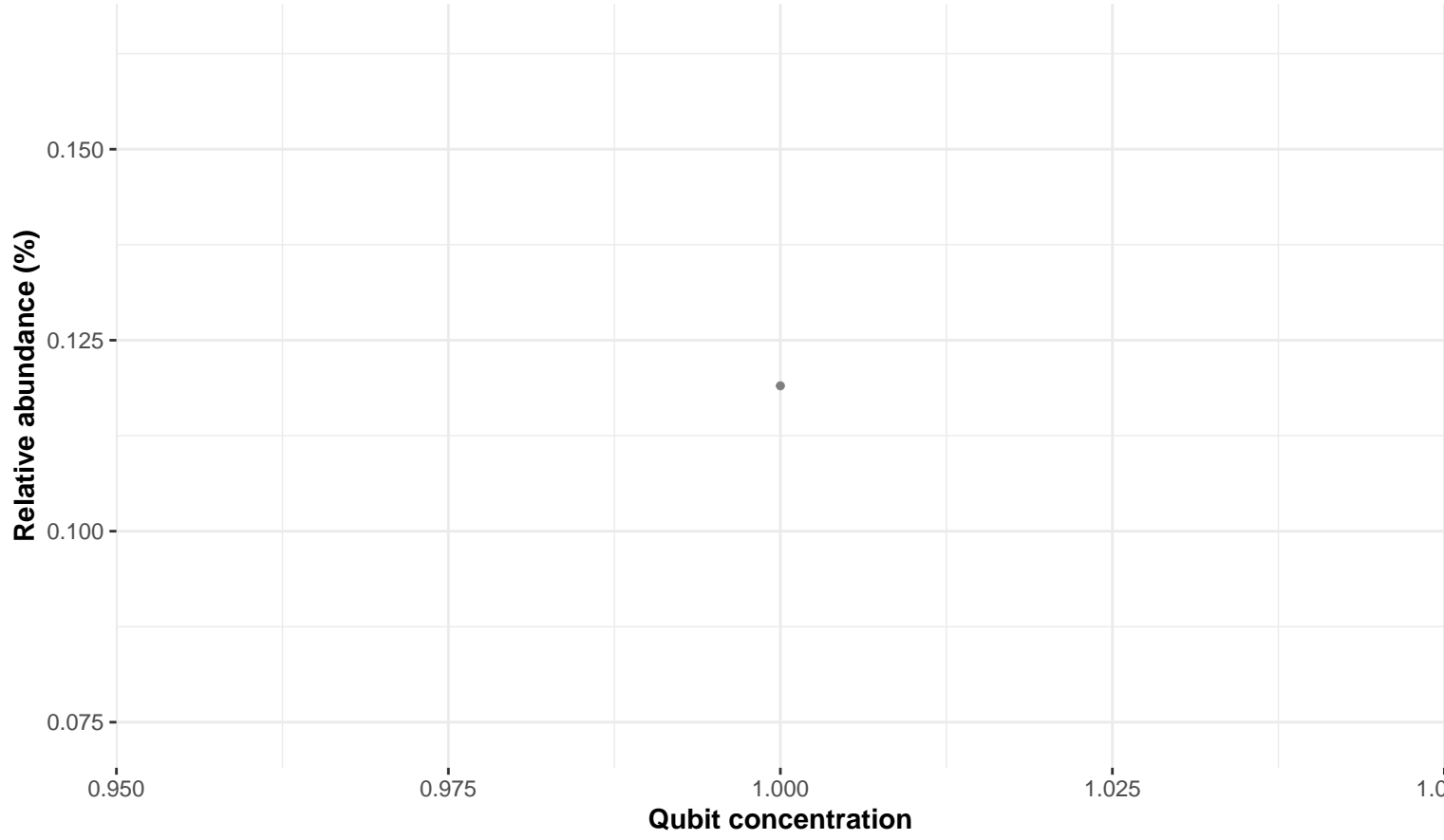


Correlation within: Digesta

$\log_e(S) = 2.639$, $p = 0.052$, $\hat{\rho}_{\text{Spearman}} = 0.750$, $\text{CI}_{95\%} [-0.036, 0.963]$, $n_{\text{pairs}} = 7$



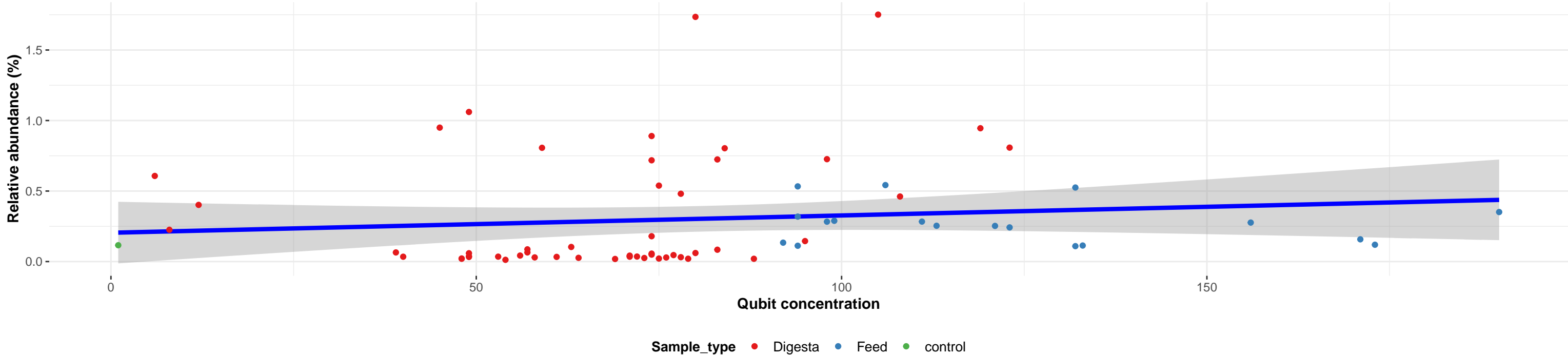
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Limosilactobacillus; NA

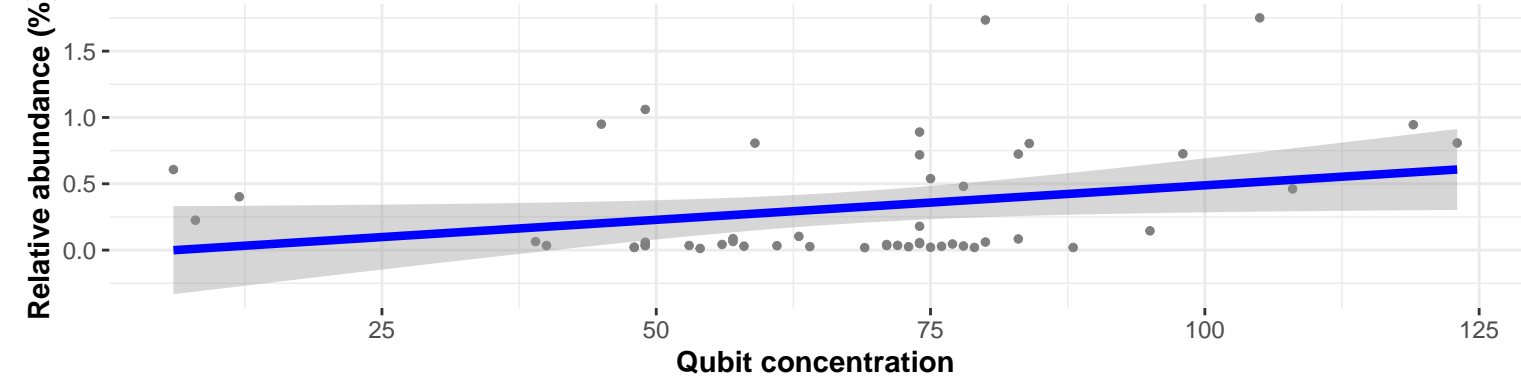
Correlation with all samples

$\log_e(S) = 10.507$, $p = 0.002$, $\hat{\rho}_{\text{Spearman}} = 0.360$, $CI_{95\%} [0.130, 0.554]$, $n_{\text{pairs}} = 70$



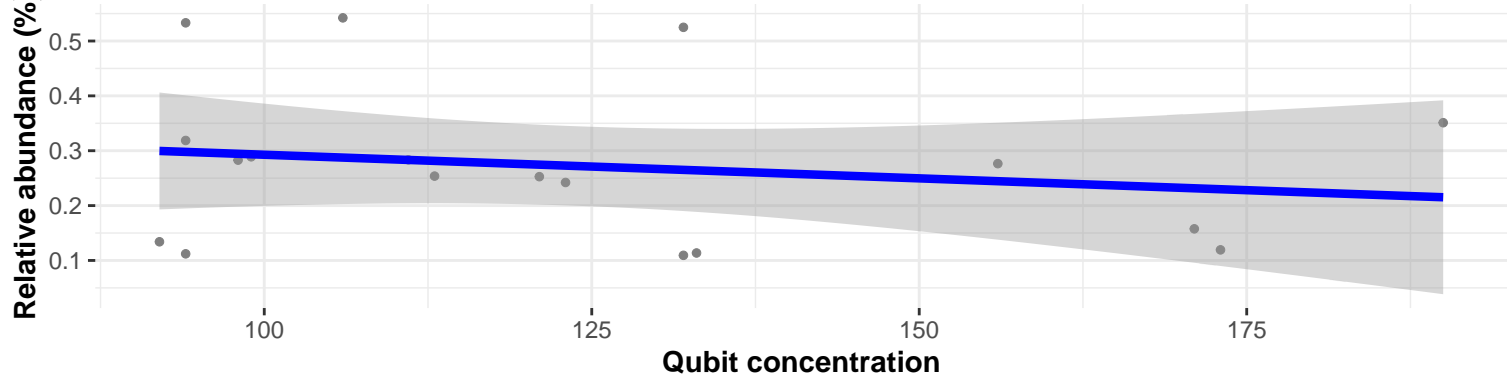
Correlation within: Digesta

$\log_e(S) = 9.723$, $p = 0.084$, $\hat{\rho}_{\text{Spearman}} = 0.244$, $CI_{95\%} [-0.042, 0.493]$, $n_{\text{pairs}} = 51$

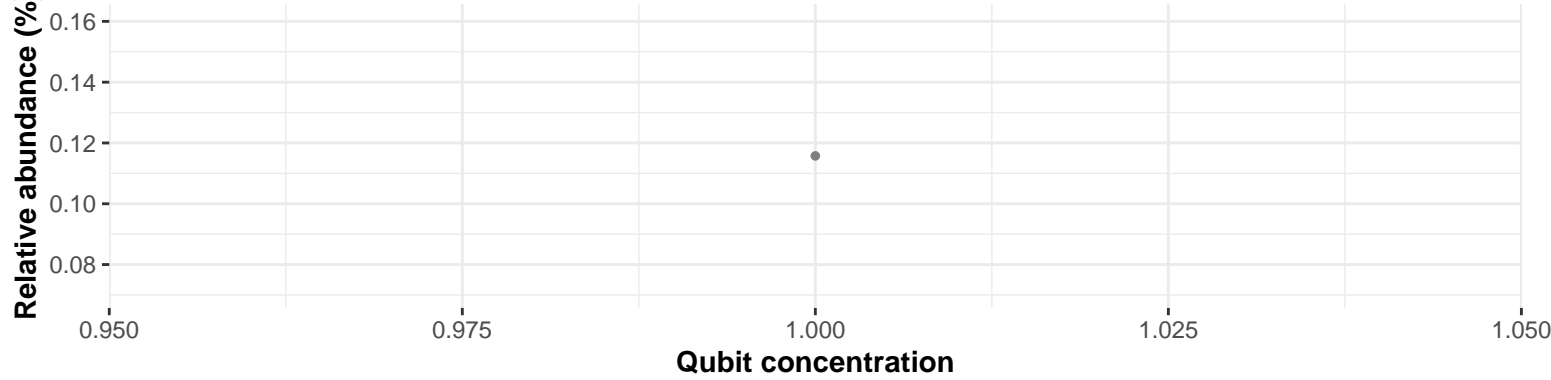


Correlation within: Feed

$\log_e(S) = 7.045$, $p = 0.464$, $\hat{\rho}_{\text{Spearman}} = -0.184$, $CI_{95\%} [-0.609, 0.323]$, $n_{\text{pairs}} = 18$



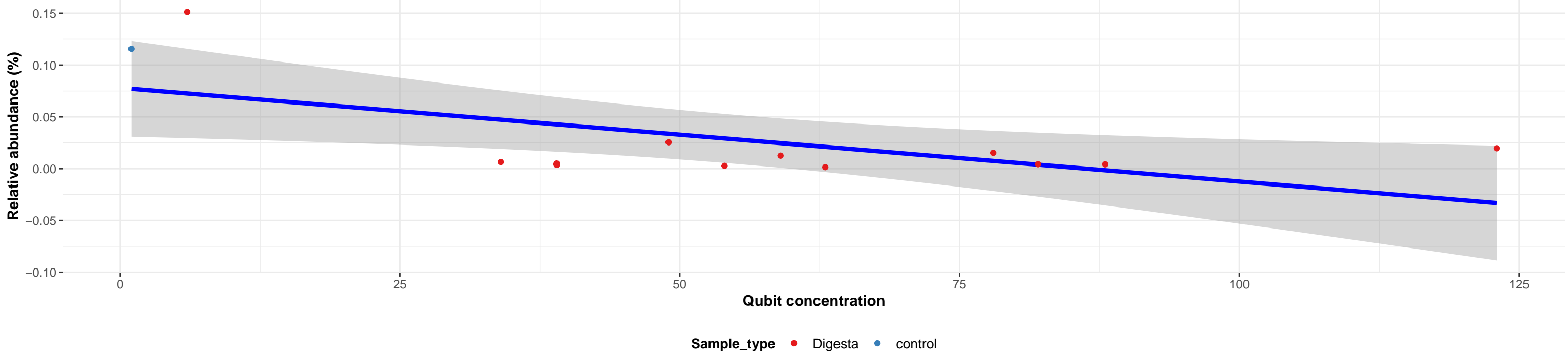
Correlation within: control



Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; NA

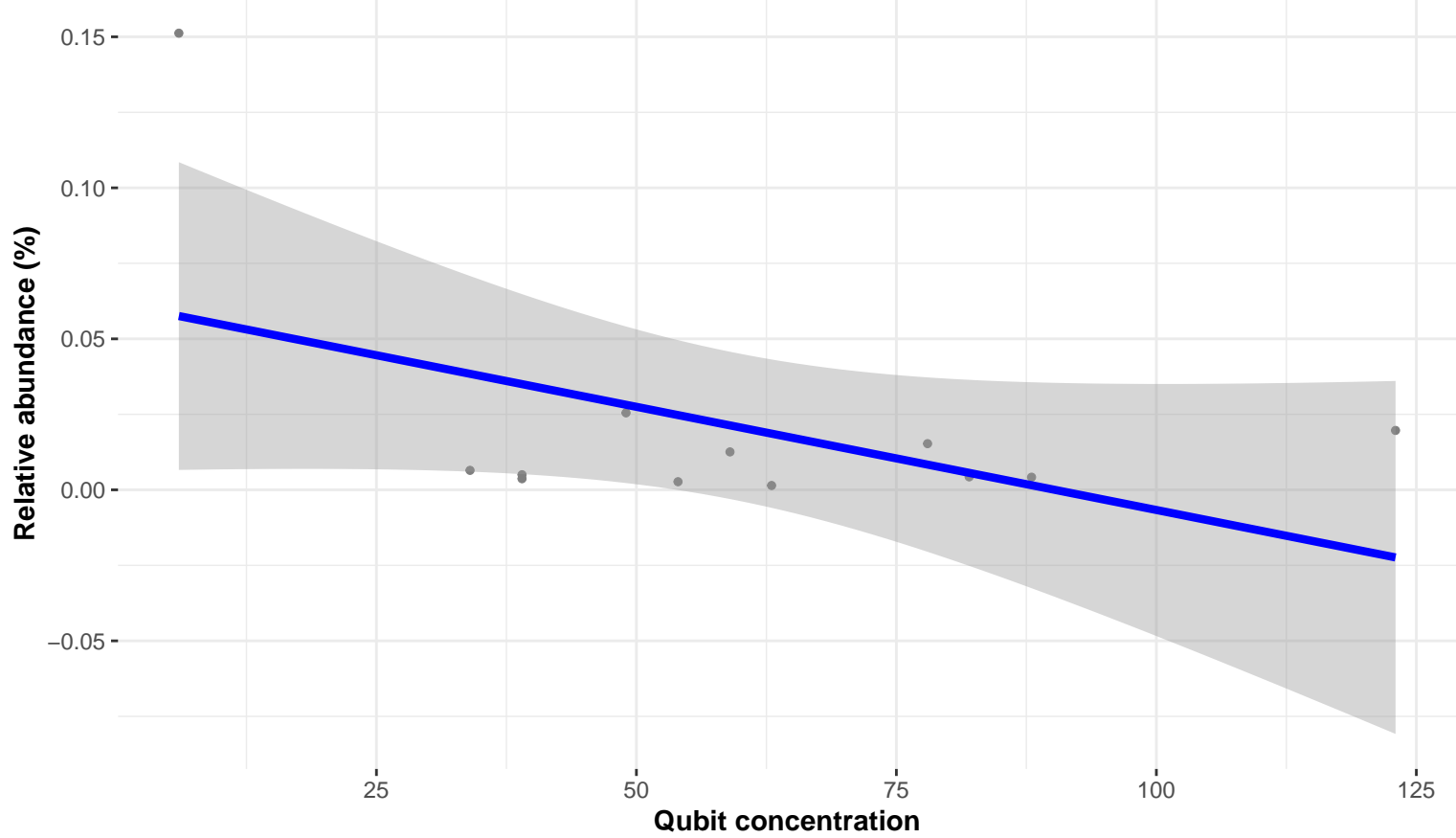
Correlation with all samples

$\log_e(S) = 6.189$, $p = 0.258$, $\hat{\rho}_{\text{Spearman}} = -0.338$, $\text{CI}_{95\%} [-0.758, 0.278]$, $n_{\text{pairs}} = 13$

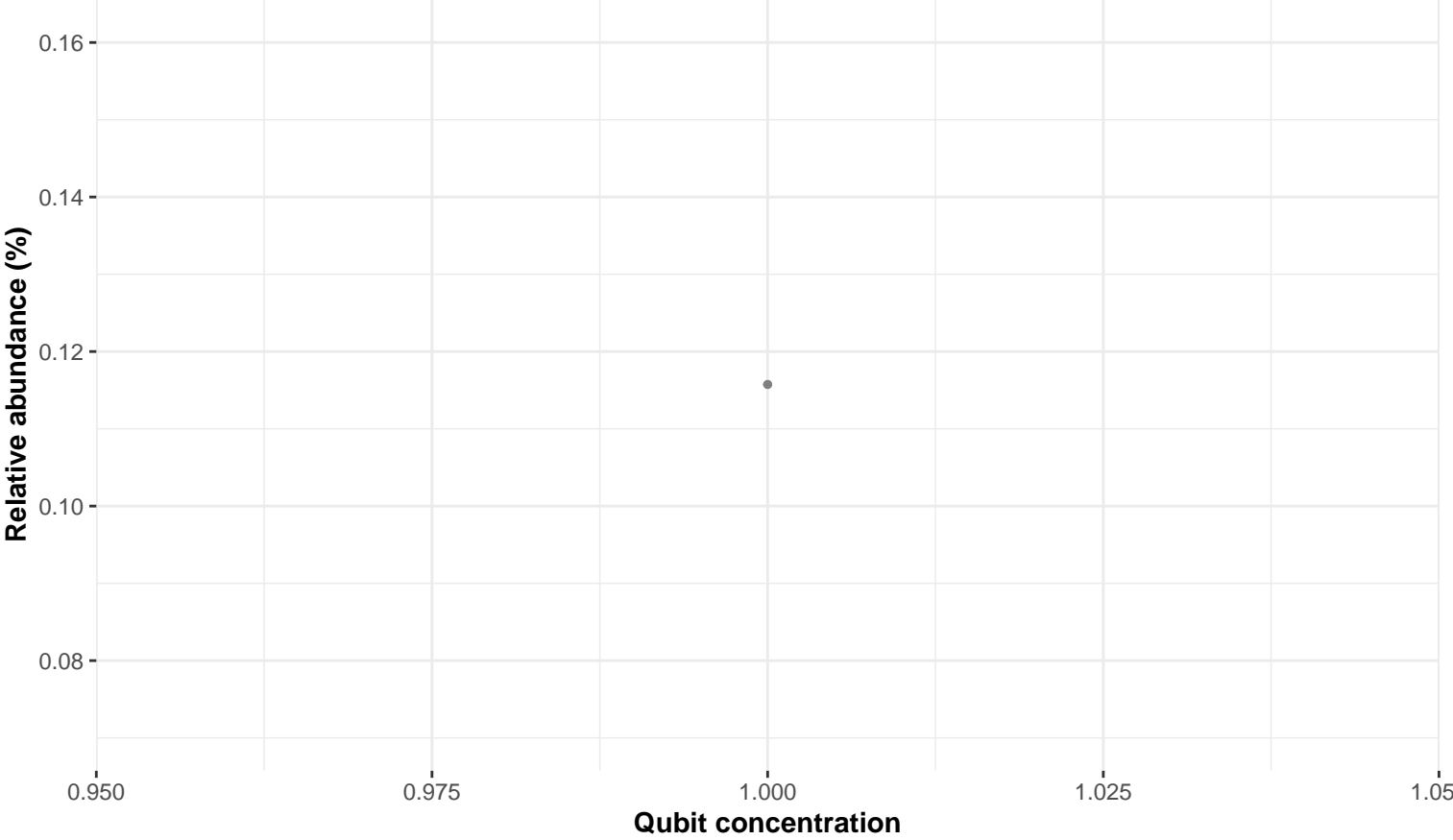


Correlation within: Digesta

$\log_e(S) = 5.808$, $p = 0.609$, $\hat{\rho}_{\text{Spearman}} = -0.165$, $\text{CI}_{95\%} [-0.685, 0.467]$, $n_{\text{pairs}} = 12$



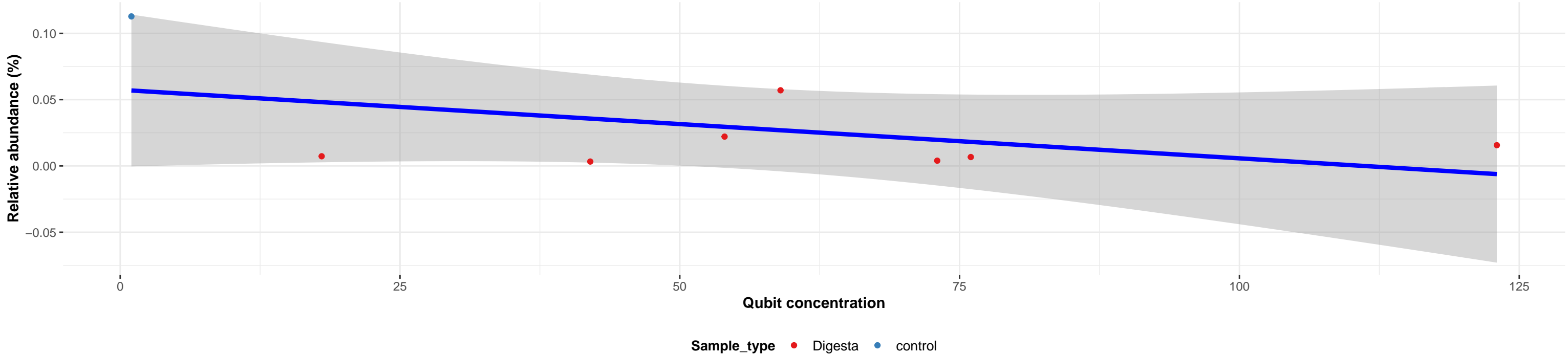
Correlation within: control



Bacteria; Actinobacteriota; Actinobacteria; Micrococcales; Microbacteriaceae; Leucobacter; NA

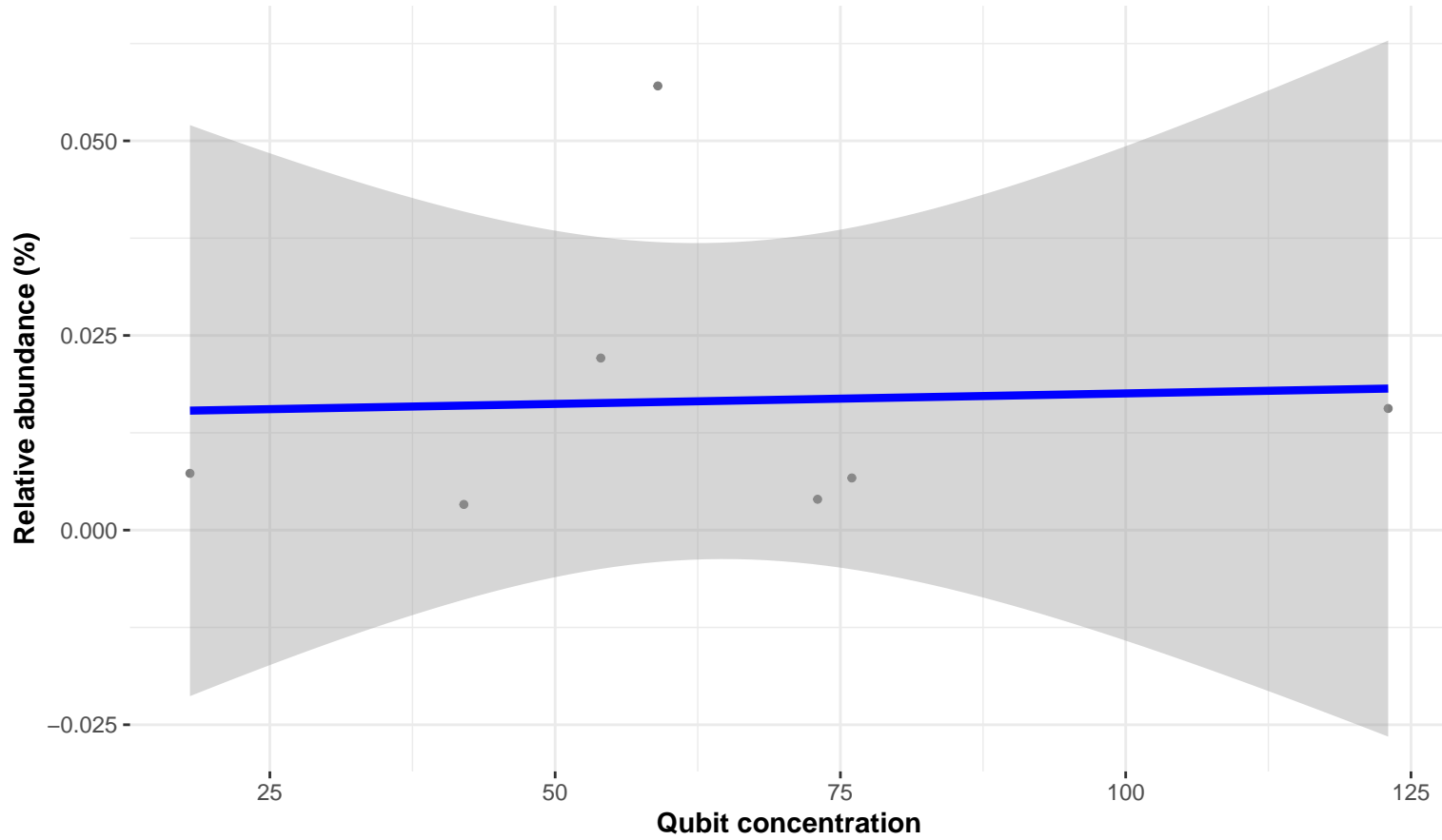
Correlation with all samples

$\log_e(S) = 4.663$, $p = 0.531$, $\hat{\rho}_{\text{Spearman}} = -0.262$, $\text{CI}_{95\%} [-0.824, 0.561]$, $n_{\text{pairs}} = 8$

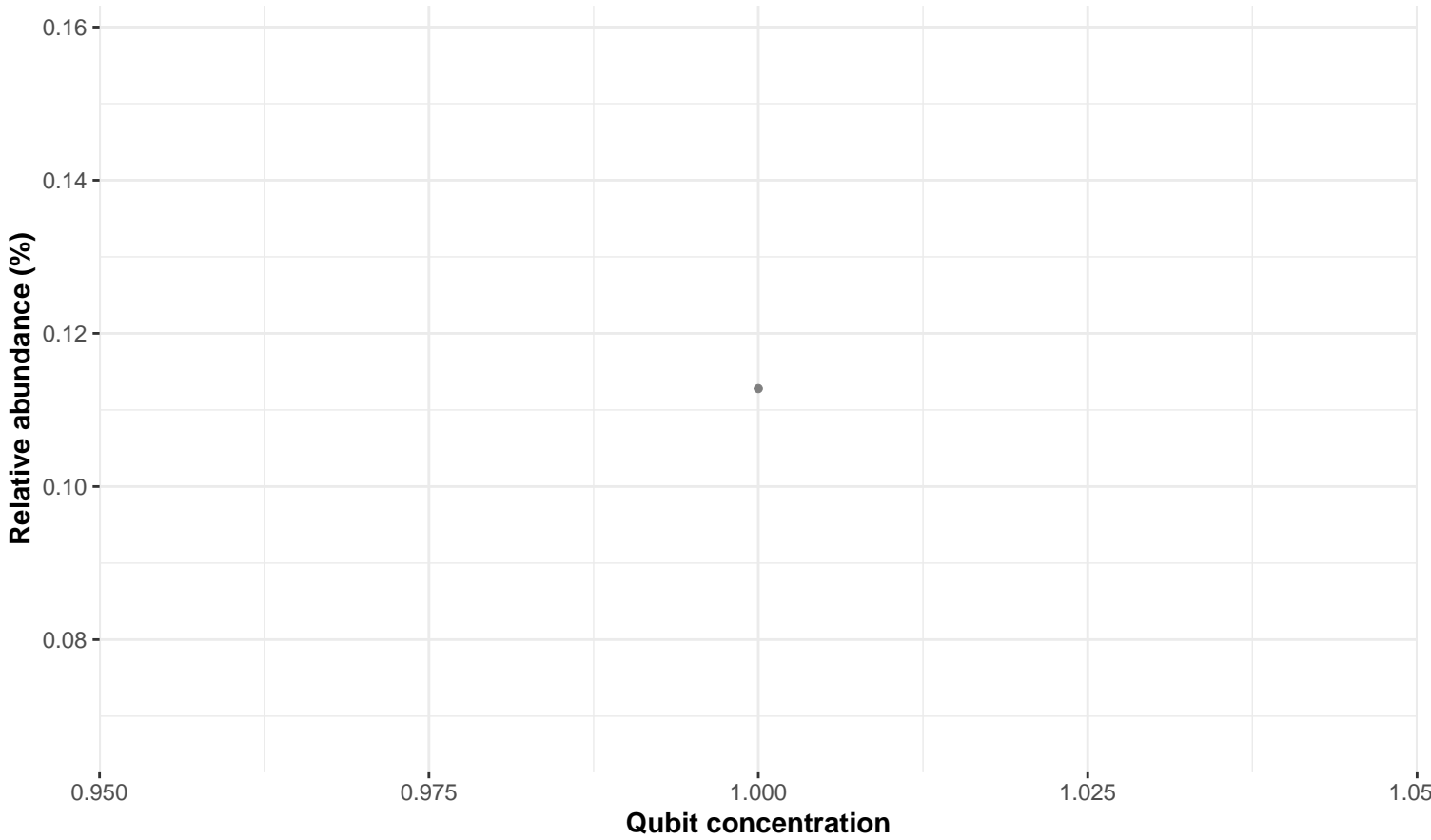


Correlation within: Digesta

$\log_e(S) = 3.912$, $p = 0.819$, $\hat{\rho}_{\text{Spearman}} = 0.107$, $\text{CI}_{95\%} [-0.717, 0.806]$, $n_{\text{pairs}} = 7$



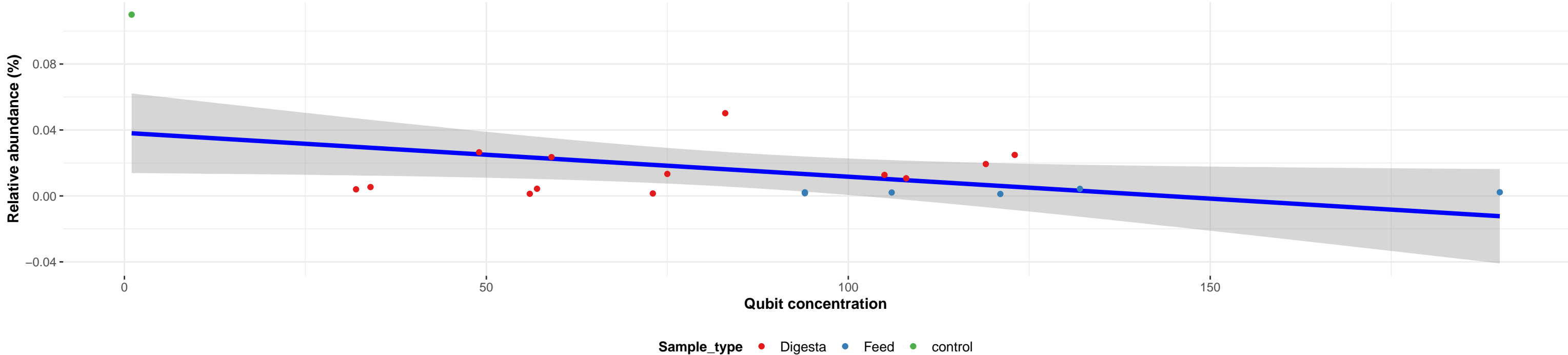
Correlation within: control



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Nosocomiicoccus; NA

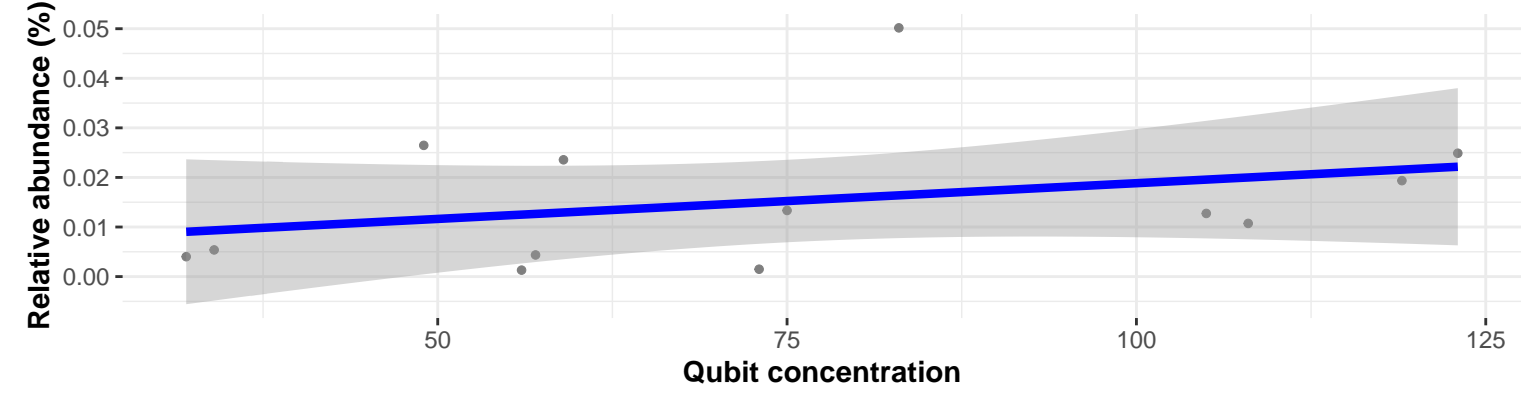
Correlation with all samples

$\log_e(S) = 7.518$, $p = 0.397$, $\hat{\rho}_{\text{Spearman}} = -0.195$, $\text{CI}_{95\%} [-0.587, 0.271]$, $n_{\text{pairs}} = 21$



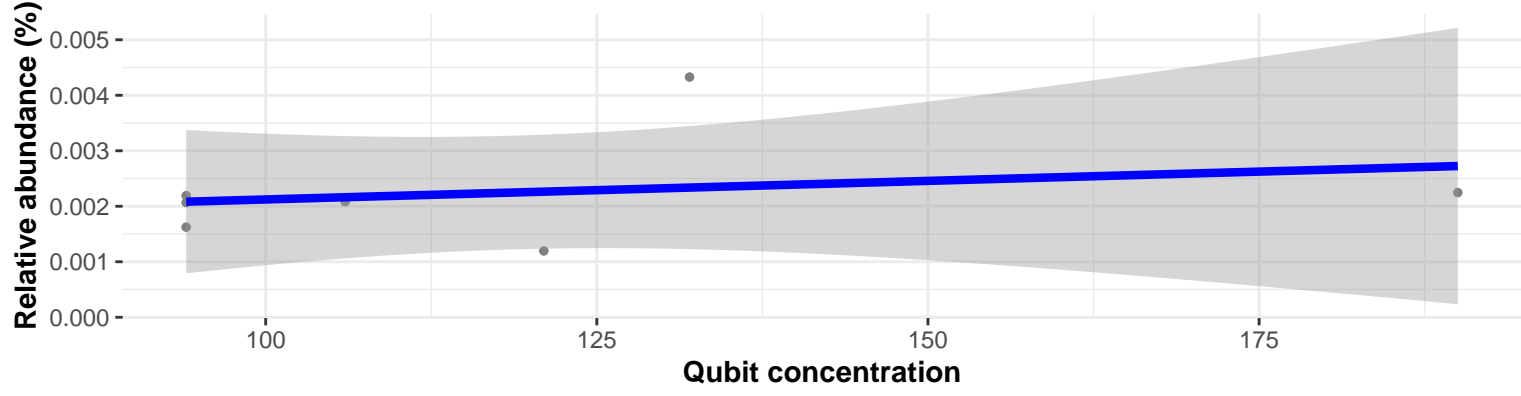
Correlation within: Digesta

$\log_e(S) = 5.338$, $p = 0.144$, $\hat{\rho}_{\text{Spearman}} = 0.429$, $\text{CI}_{95\%} [-0.178, 0.799]$, $n_{\text{pairs}} = 13$

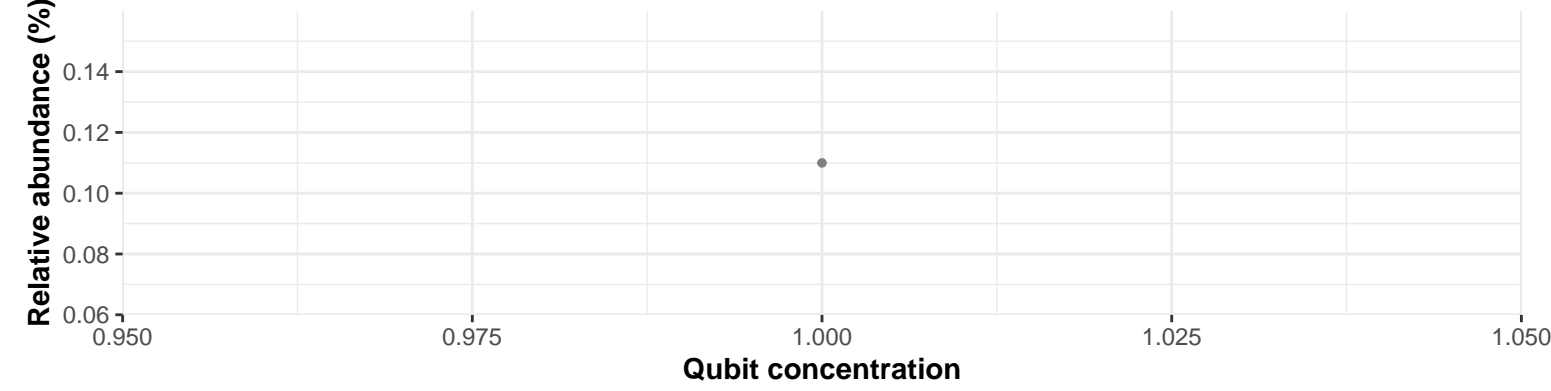


Correlation within: Feed

$\log_e(S) = 3.368$, $p = 0.274$, $\hat{\rho}_{\text{Spearman}} = 0.482$, $\text{CI}_{95\%} [-0.449, 0.911]$, $n_{\text{pairs}} = 7$



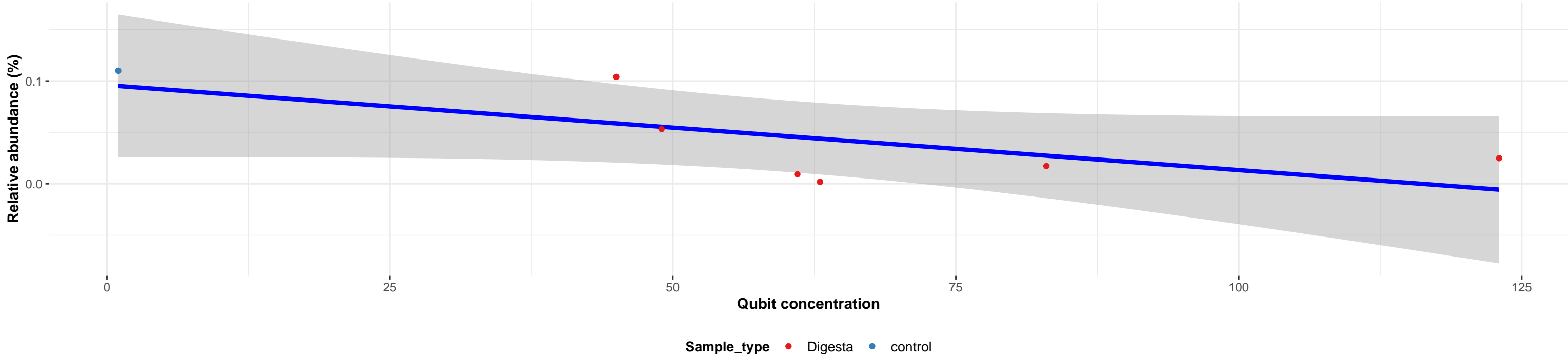
Correlation within: control



Bacteria; Firmicutes; Bacilli; Thermicanales; Thermicanaceae; Thermicanus; NA

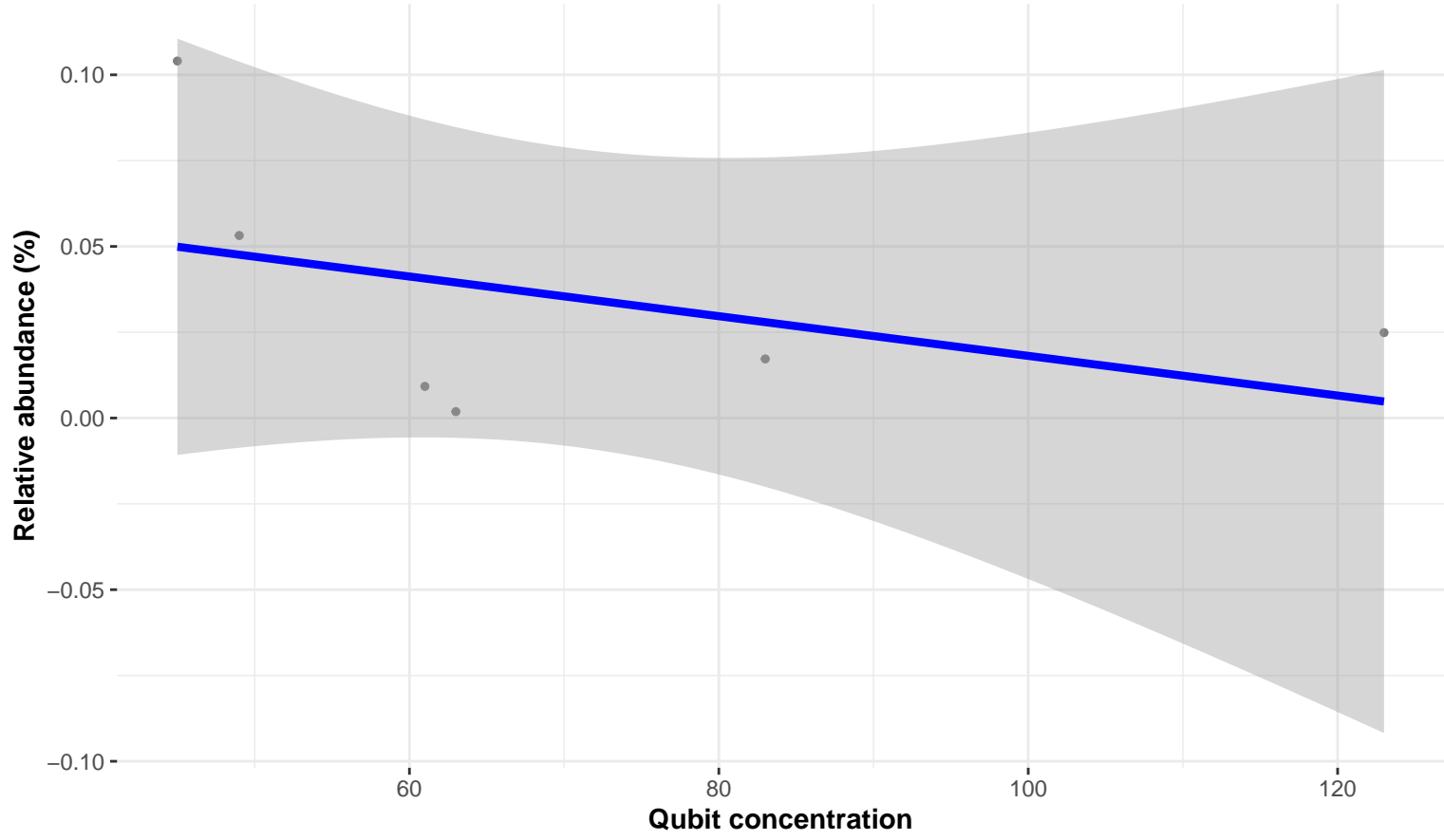
Correlation with all samples

$\log_e(S) = 4.543$, $p = 0.094$, $\hat{\rho}_{\text{Spearman}} = -0.679$, $\text{CI}_{95\%} [-0.950, 0.180]$, $n_{\text{pairs}} = 7$

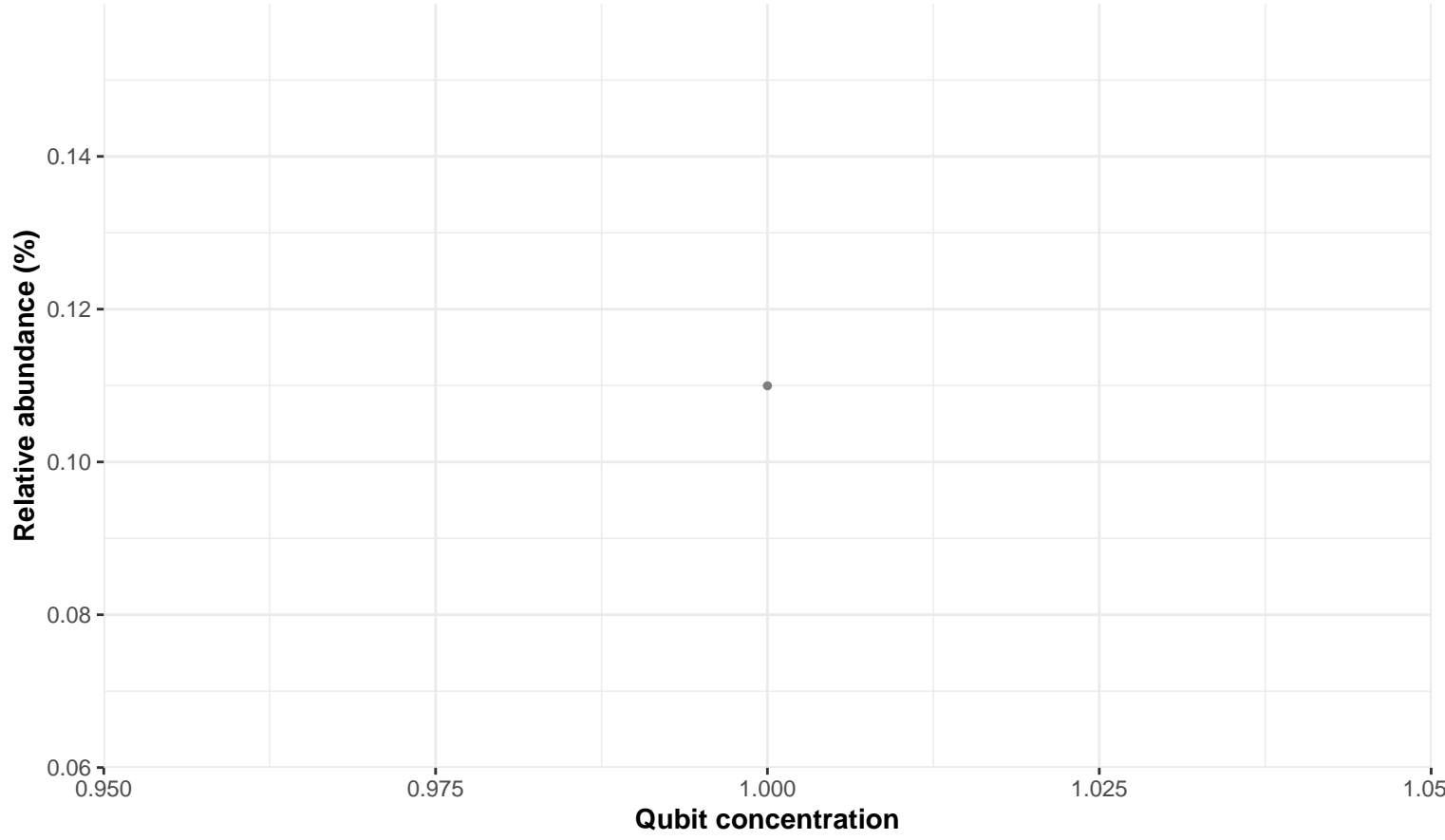


Correlation within: Digesta

$\log_e(S) = 3.951$, $p = 0.329$, $\hat{\rho}_{\text{Spearman}} = -0.486$, $\text{CI}_{95\%} [-0.935, 0.561]$, $n_{\text{pairs}} = 6$



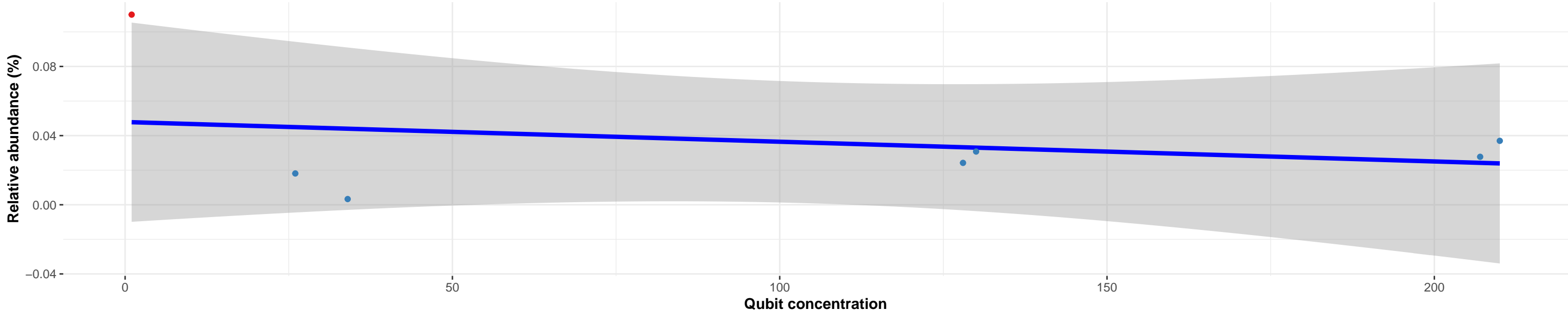
Correlation within: control



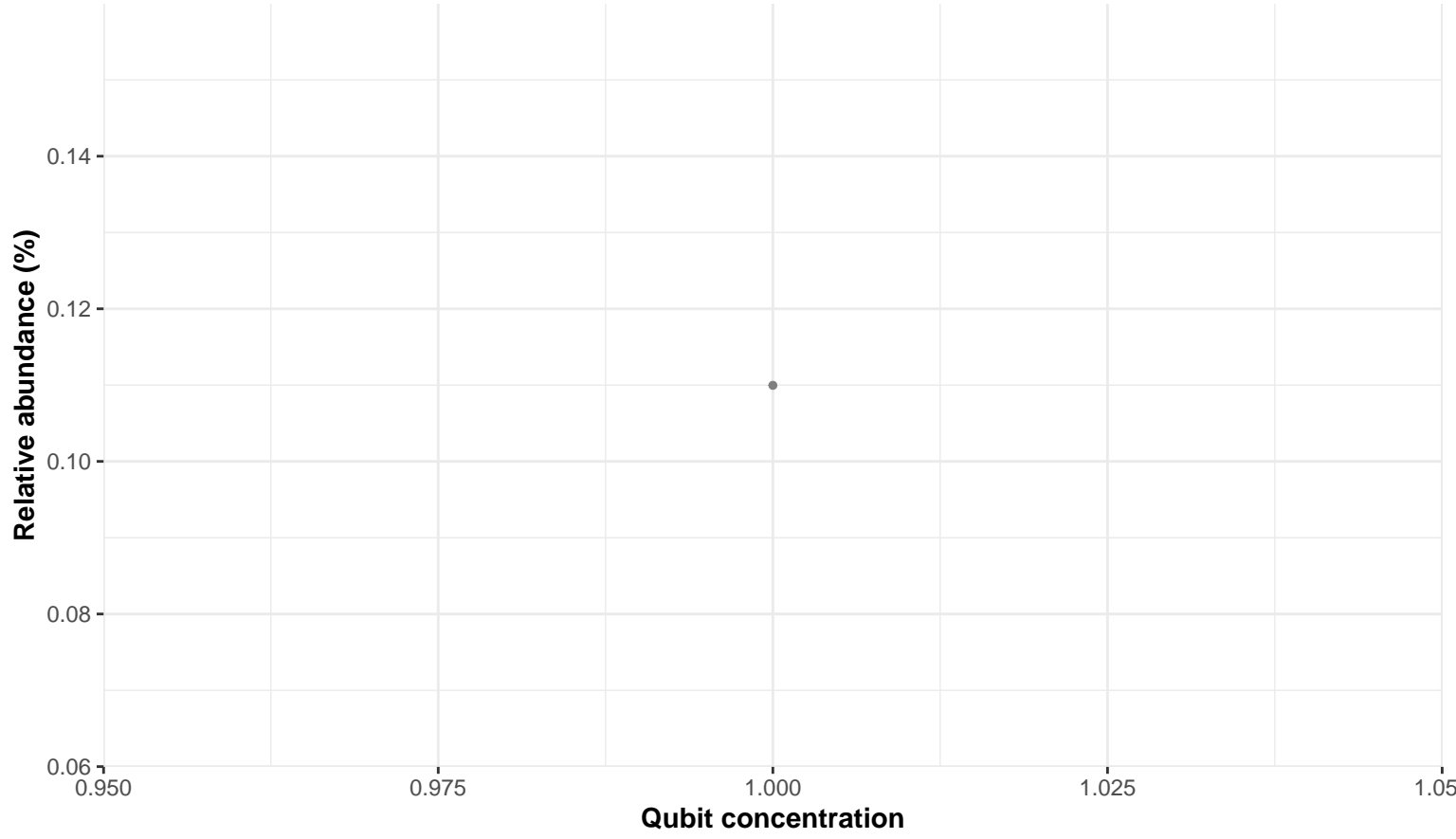
Bacteria; Proteobacteria; Alphaproteobacteria; Micavibrionales; Micavibrionaceae; NA; NA

Correlation with all samples

$\log_e(S) = 3.829$, $p = 0.702$, $\hat{\rho}_{\text{Spearman}} = 0.179$, $\text{CI}_{95\%} [-0.680, 0.830]$, $n_{\text{pairs}} = 7$

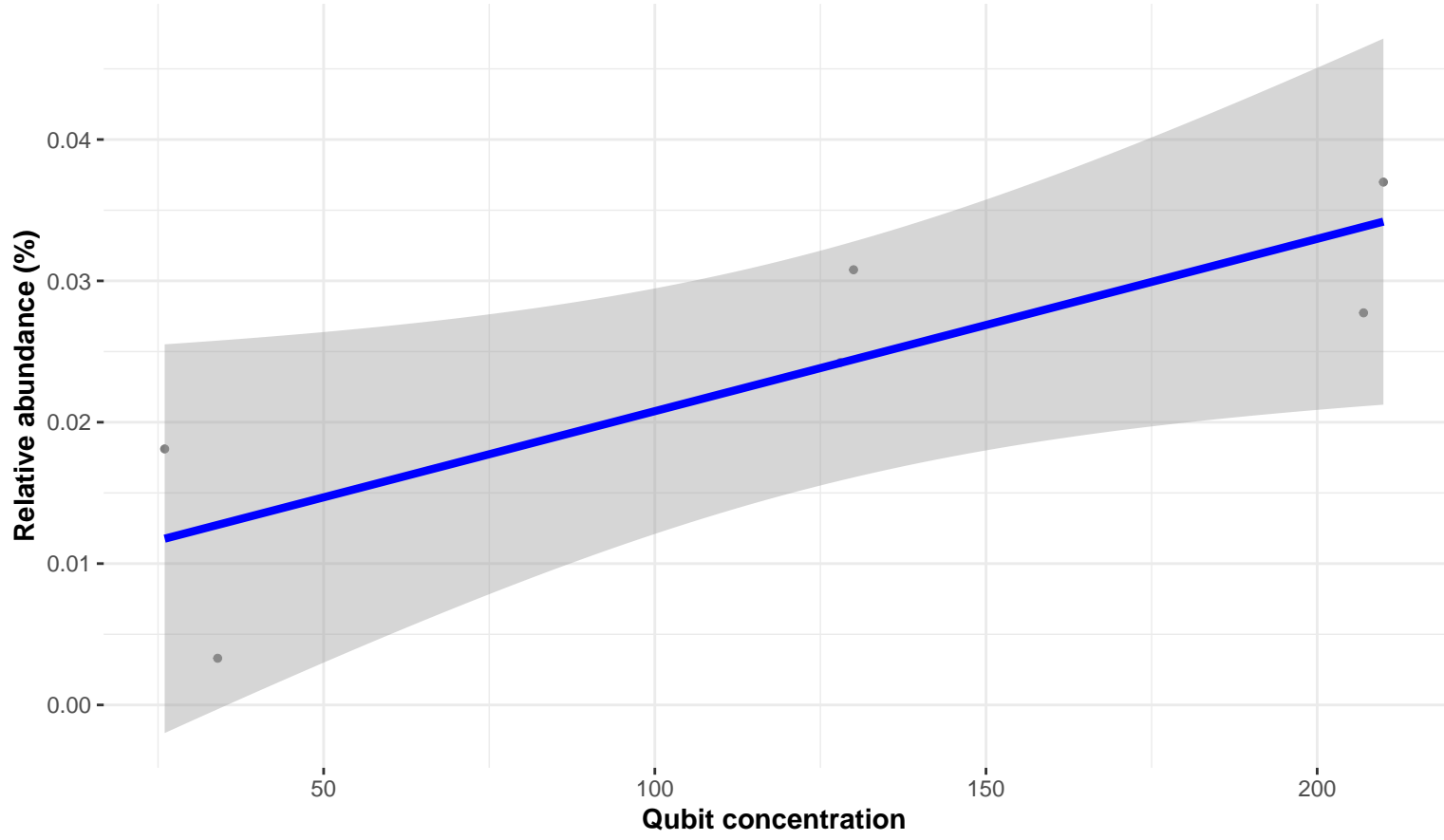


Correlation within: control



Correlation within: water

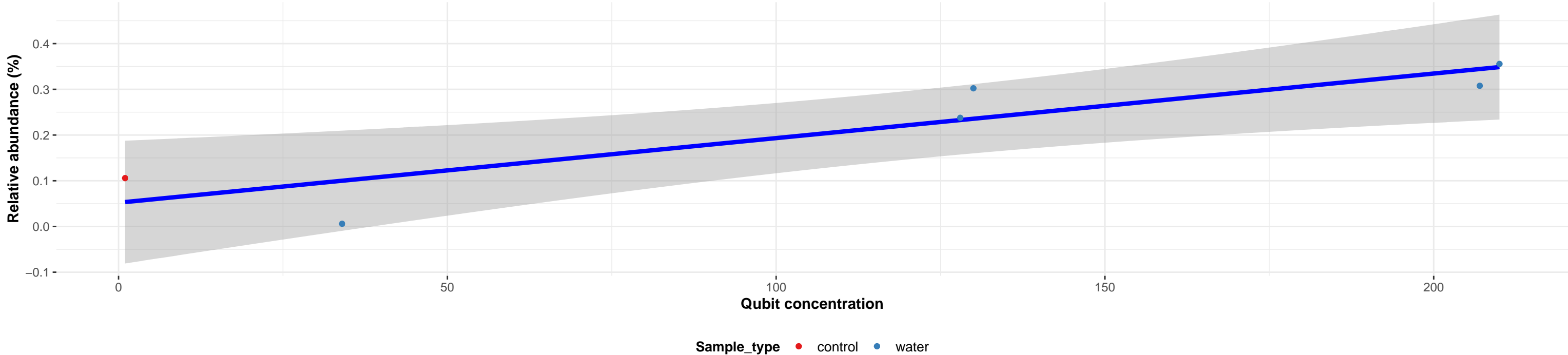
$\log_e(S) = 1.386$, $p = 0.019$, $\hat{\rho}_{\text{Spearman}} = 0.886$, $\text{CI}_{95\%} [0.232, 0.988]$, $n_{\text{pairs}} = 6$



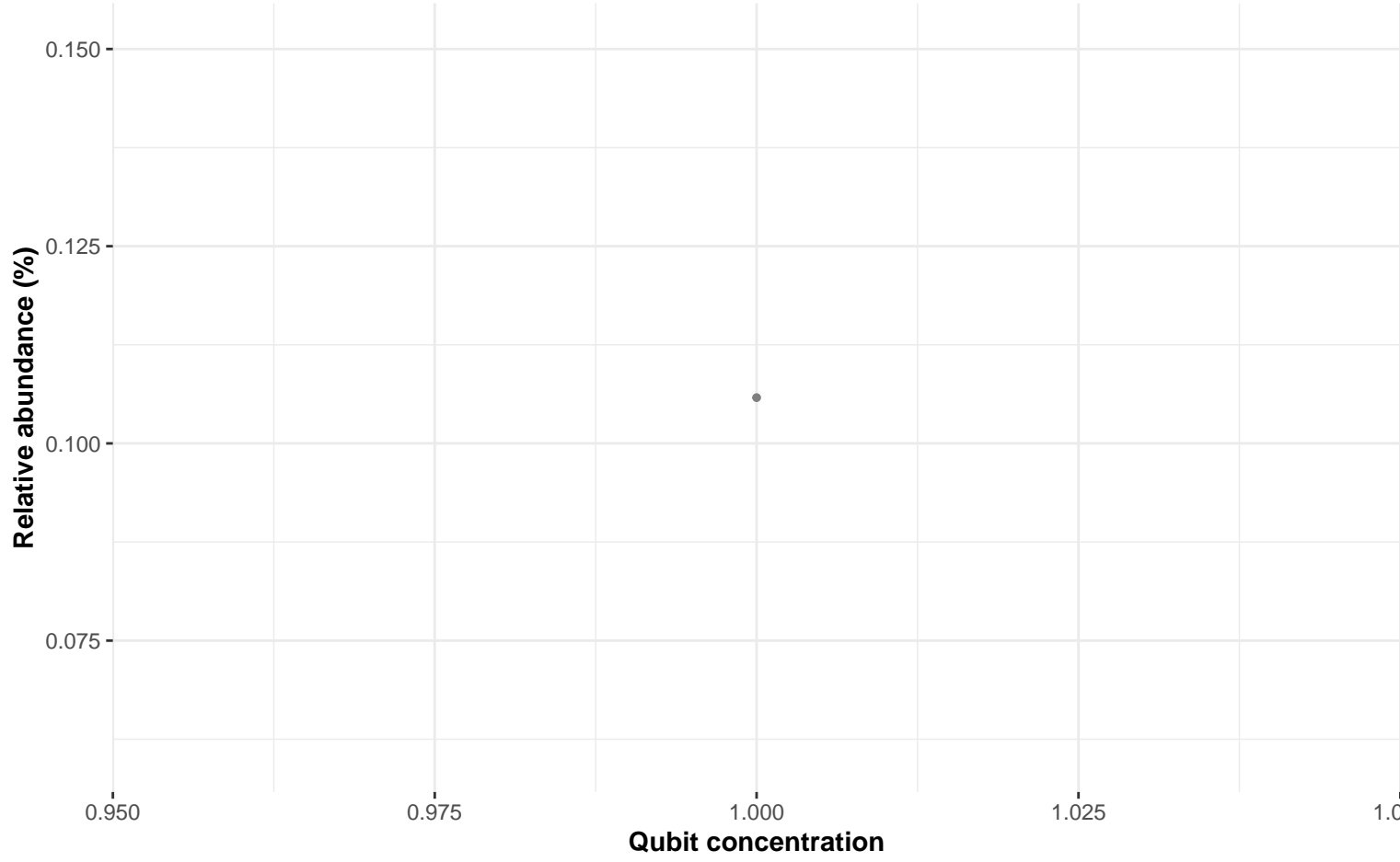
Bacteria; Bacteroidota; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Maribacter; NA

Correlation with all samples

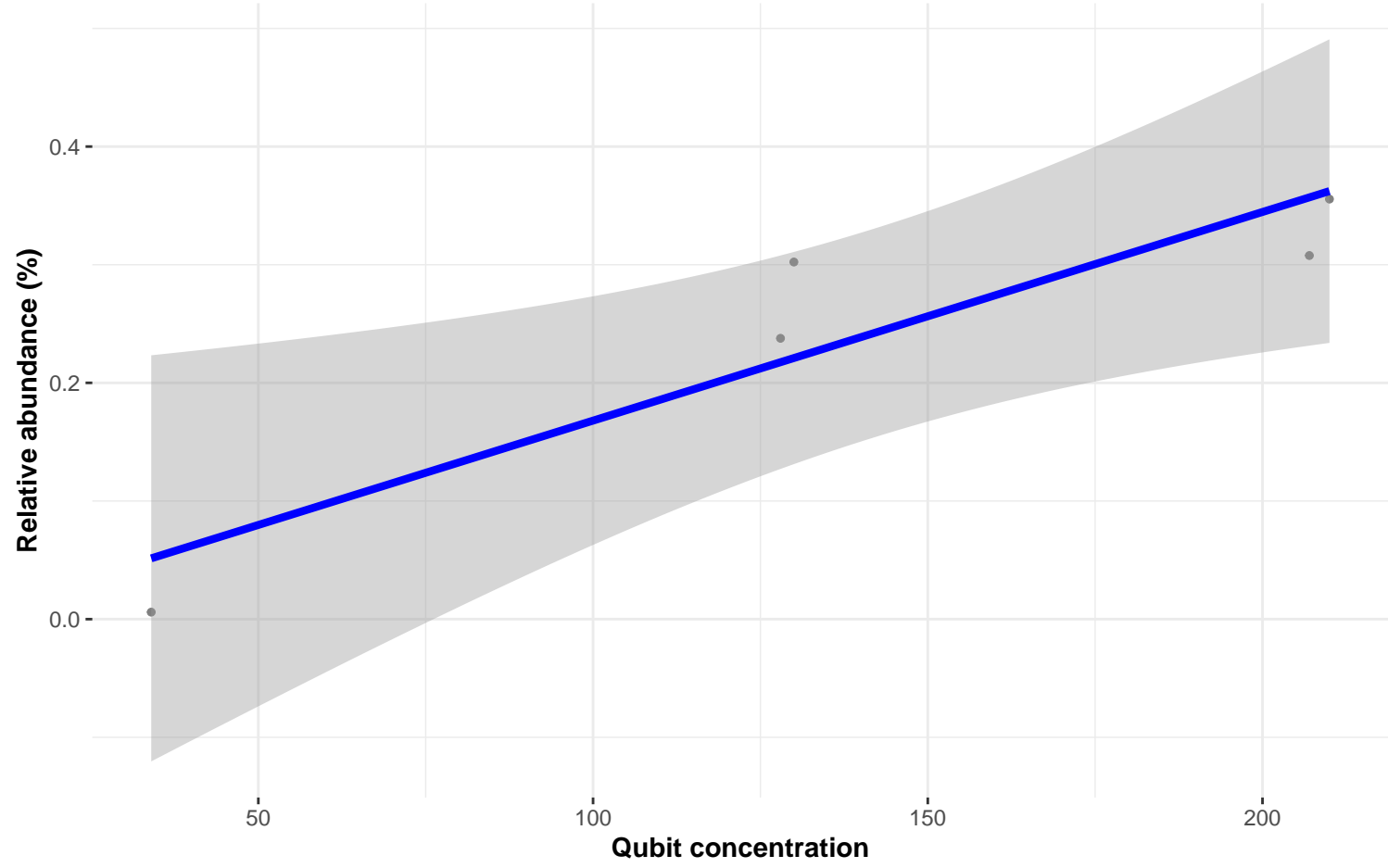
$\log_e(S) = 0.693$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.943$, $CI_{95\%} [0.536, 0.994]$, $n_{\text{pairs}} = 6$



Correlation within: control



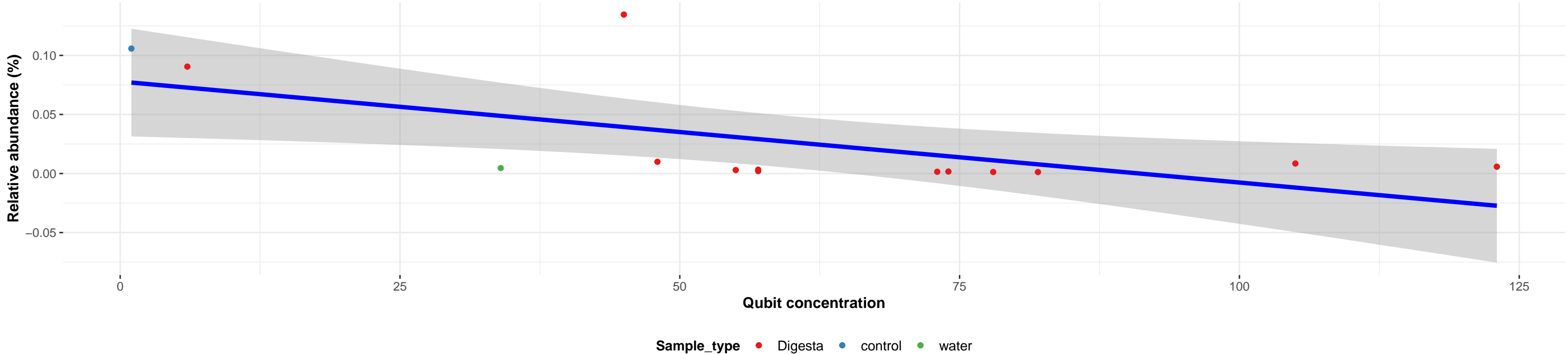
Correlation within: water



Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas; NA

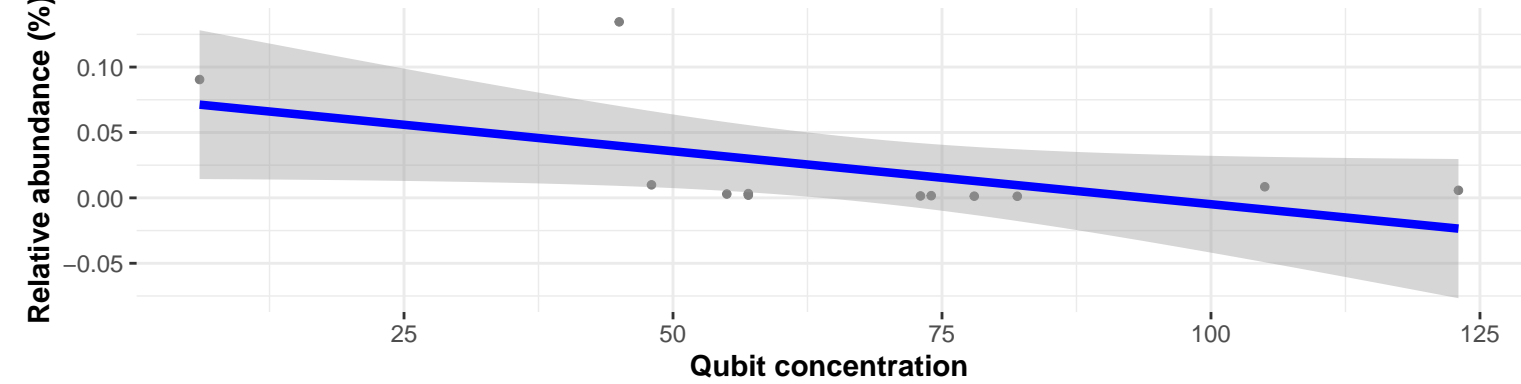
Correlation with all samples

$\log_e(S) = 6.580$, $p = 0.029$, $\hat{\rho}_{\text{Spearman}} = -0.583$, $\text{CI}_{95\%} [-0.855, -0.059]$, $n_{\text{pairs}} = 14$

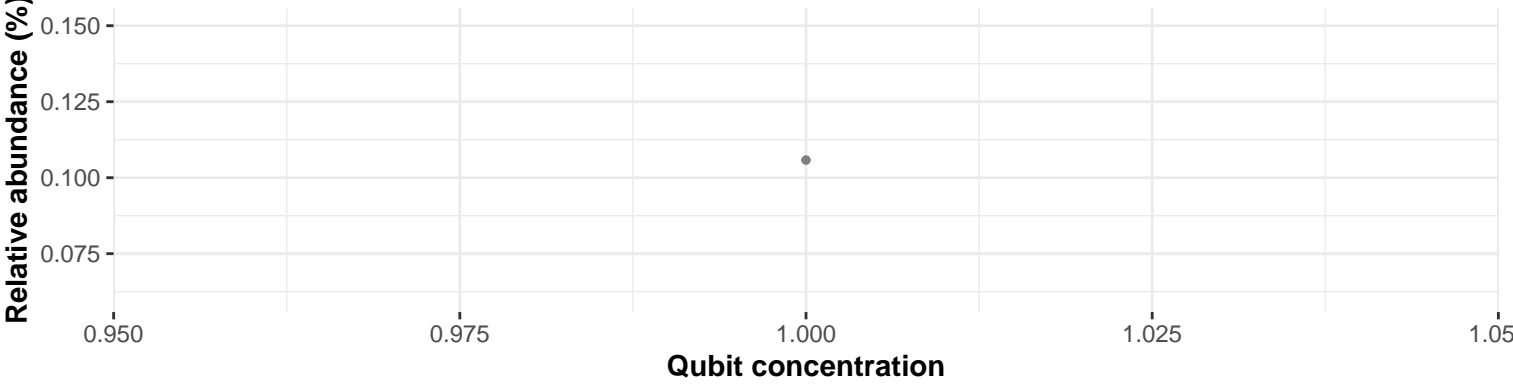


Correlation within: Digesta

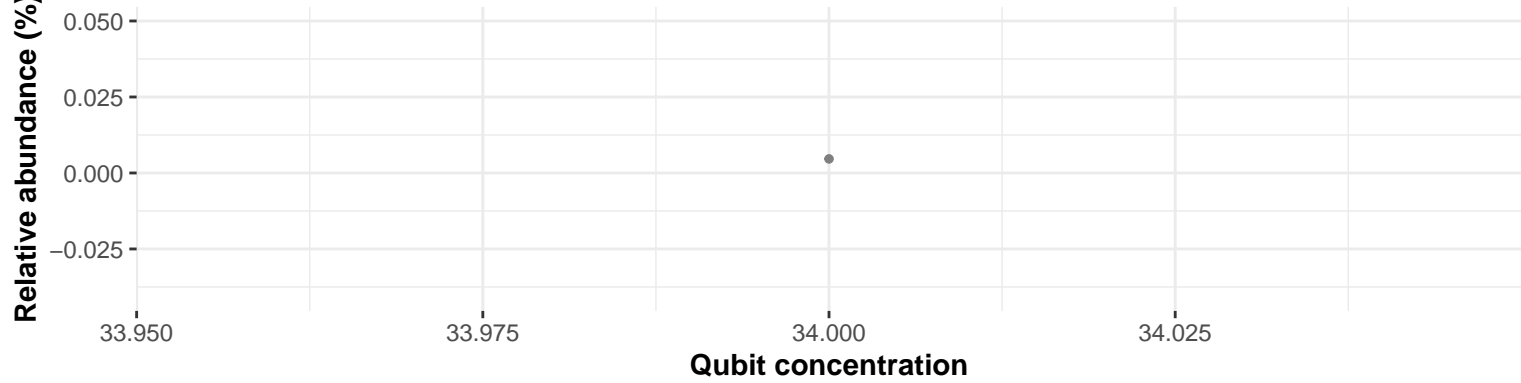
$\log_e(S) = 6.083$, $p = 0.075$, $\hat{\rho}_{\text{Spearman}} = -0.532$, $\text{CI}_{95\%} [-0.853, 0.079]$, $n_{\text{pairs}} = 12$



Correlation within: control



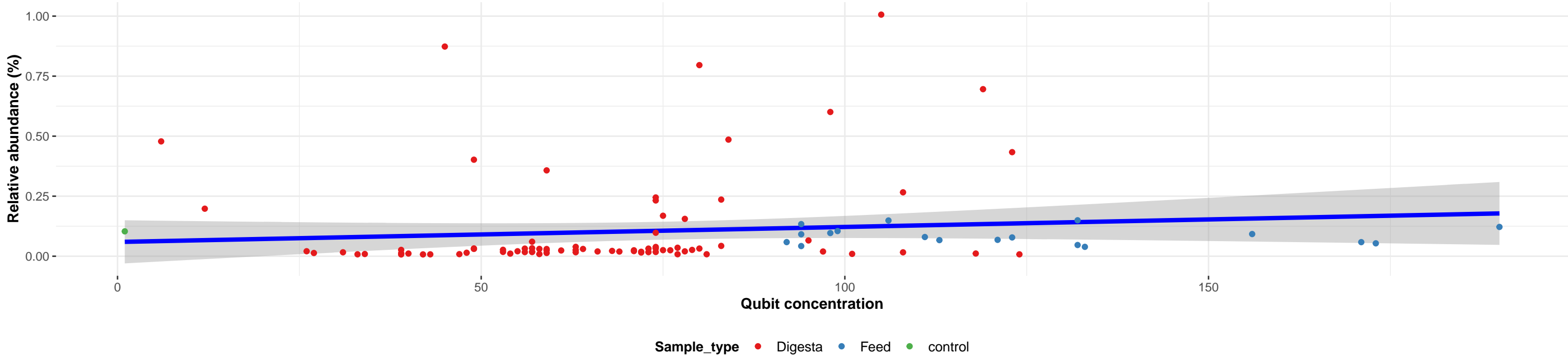
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Limosilactobacillus; NA

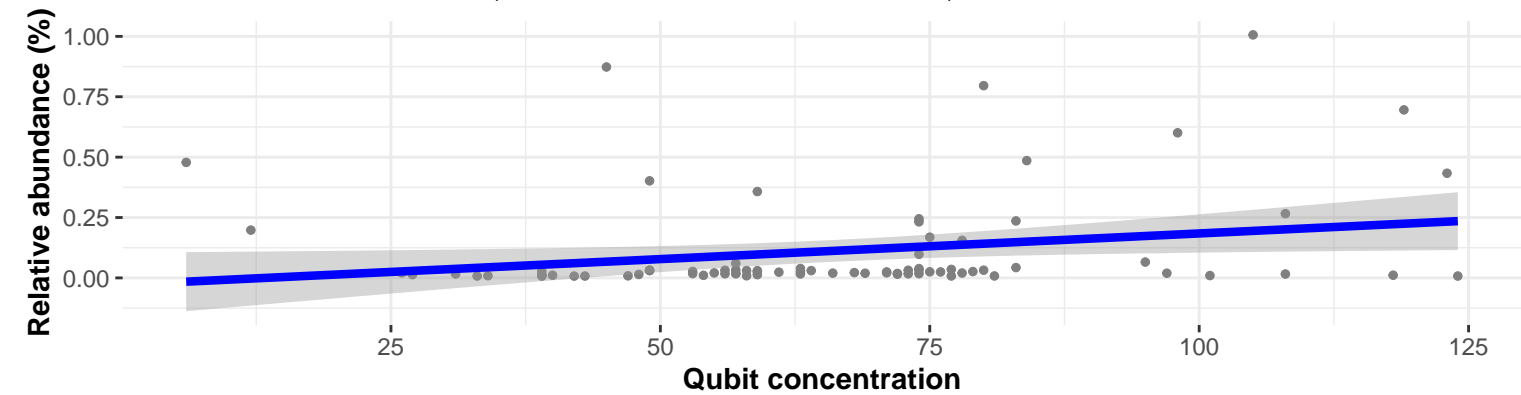
Correlation with all samples

$\log_e(S) = 11.520$, $p = 1.73e-05$, $\hat{\rho}_{\text{Spearman}} = 0.413$, $CI_{95\%} [0.232, 0.567]$, $n_{\text{pairs}} = 101$



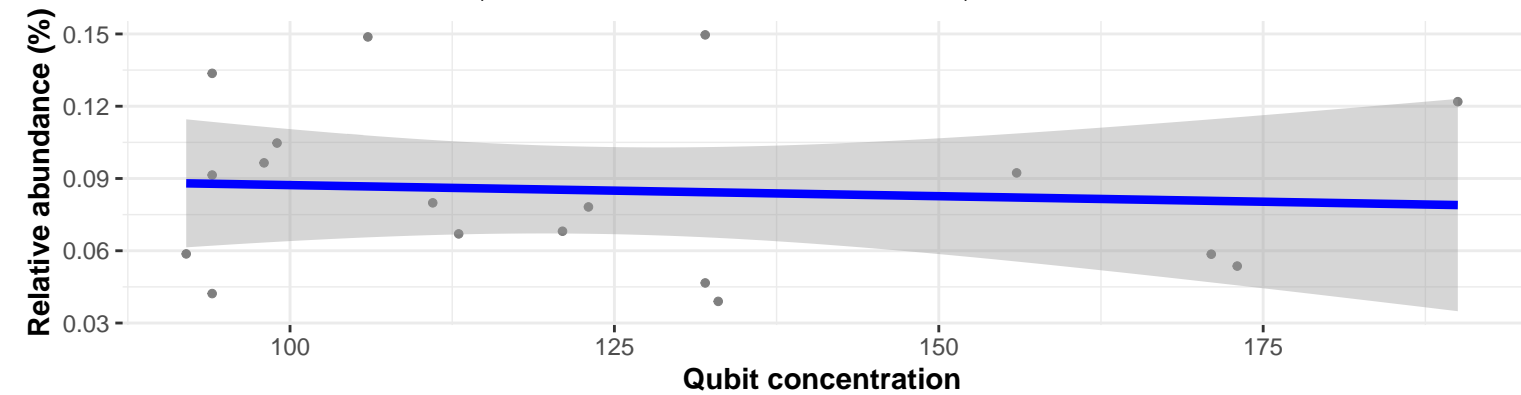
Correlation within: Digesta

$\log_e(S) = 11.059$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.308$, $CI_{95\%} [0.092, 0.497]$, $n_{\text{pairs}} = 82$

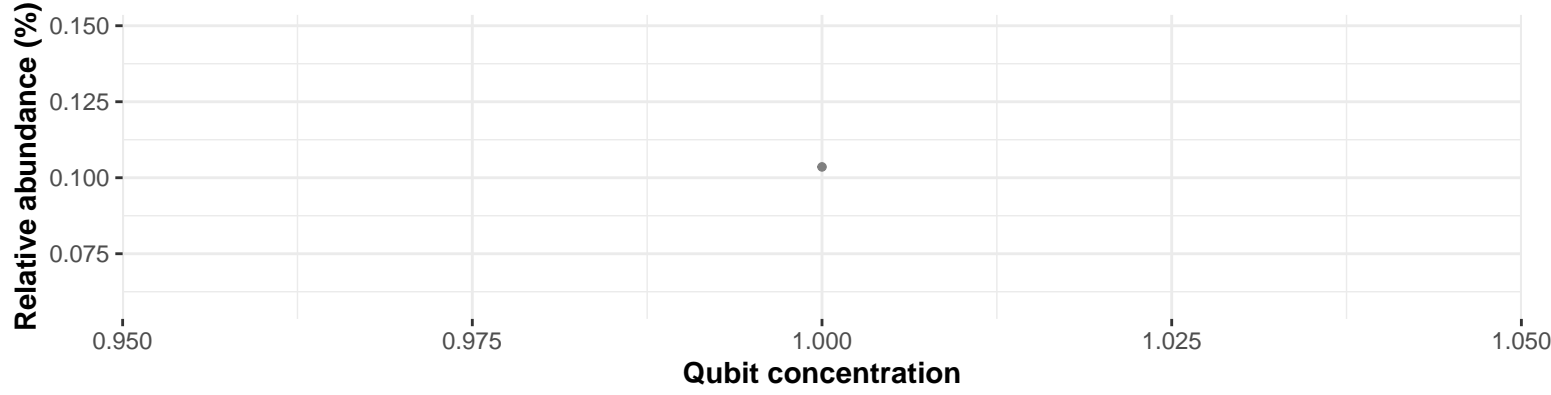


Correlation within: Feed

$\log_e(S) = 7.006$, $p = 0.583$, $\hat{\rho}_{\text{Spearman}} = -0.139$, $CI_{95\%} [-0.579, 0.364]$, $n_{\text{pairs}} = 18$



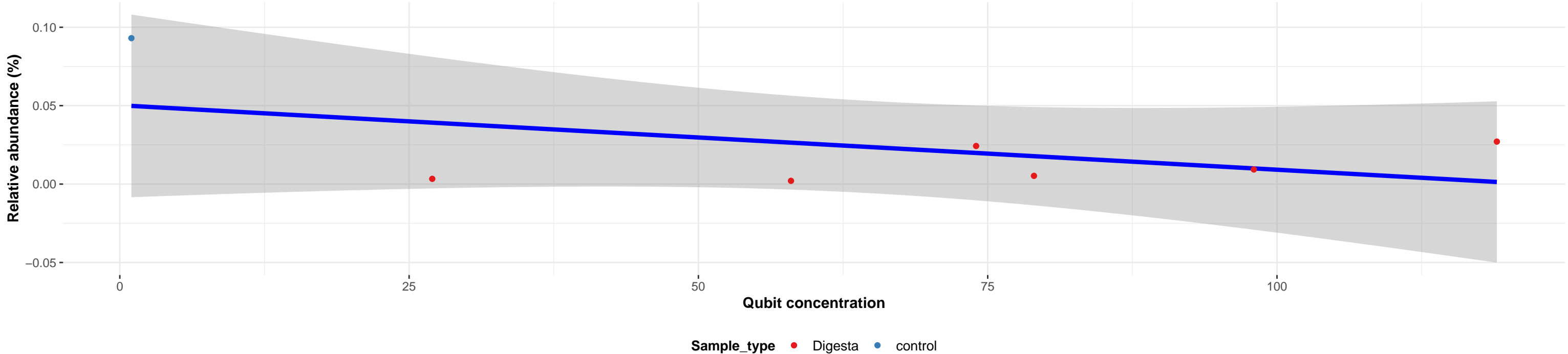
Correlation within: control



Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium sensu stricto 13; NA

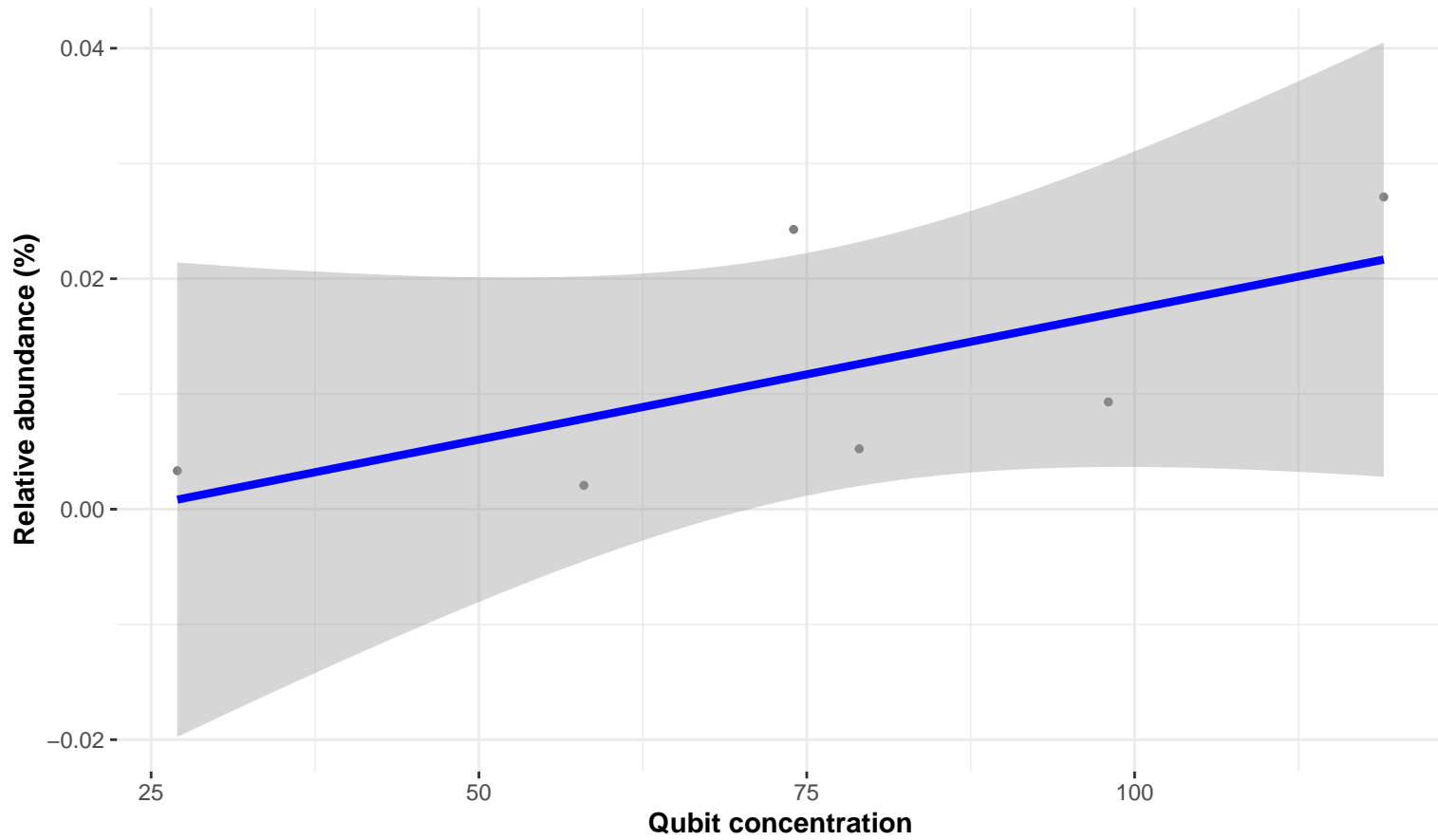
Correlation with all samples

$\log_e(S) = 3.912$, $p = 0.819$, $\hat{\rho}_{\text{Spearman}} = 0.107$, $\text{CI}_{95\%} [-0.717, 0.806]$, $n_{\text{pairs}} = 7$

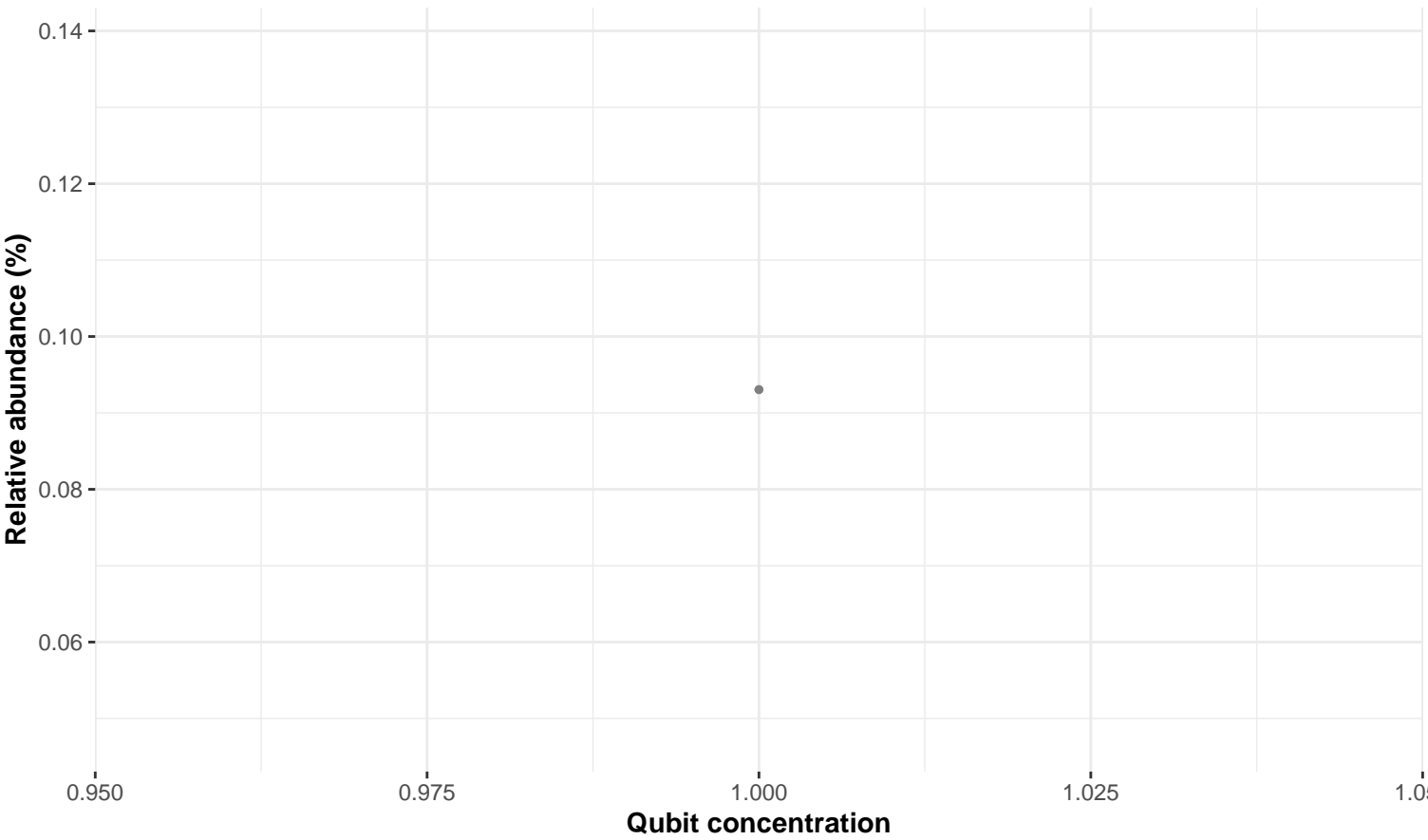


Correlation within: Digesta

$\log_e(S) = 2.079$, $p = 0.072$, $\hat{\rho}_{\text{Spearman}} = 0.771$, $\text{CI}_{95\%} [-0.140, 0.975]$, $n_{\text{pairs}} = 6$



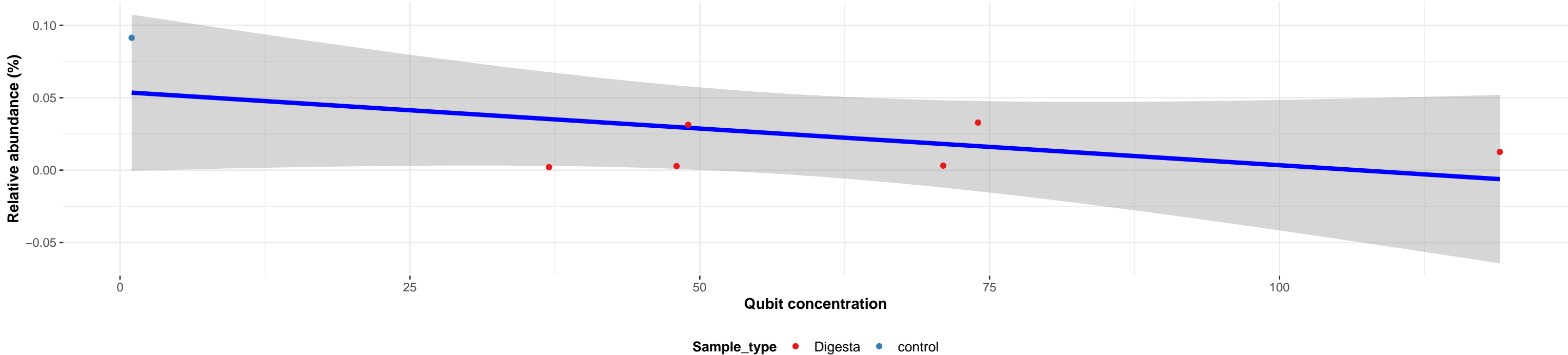
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

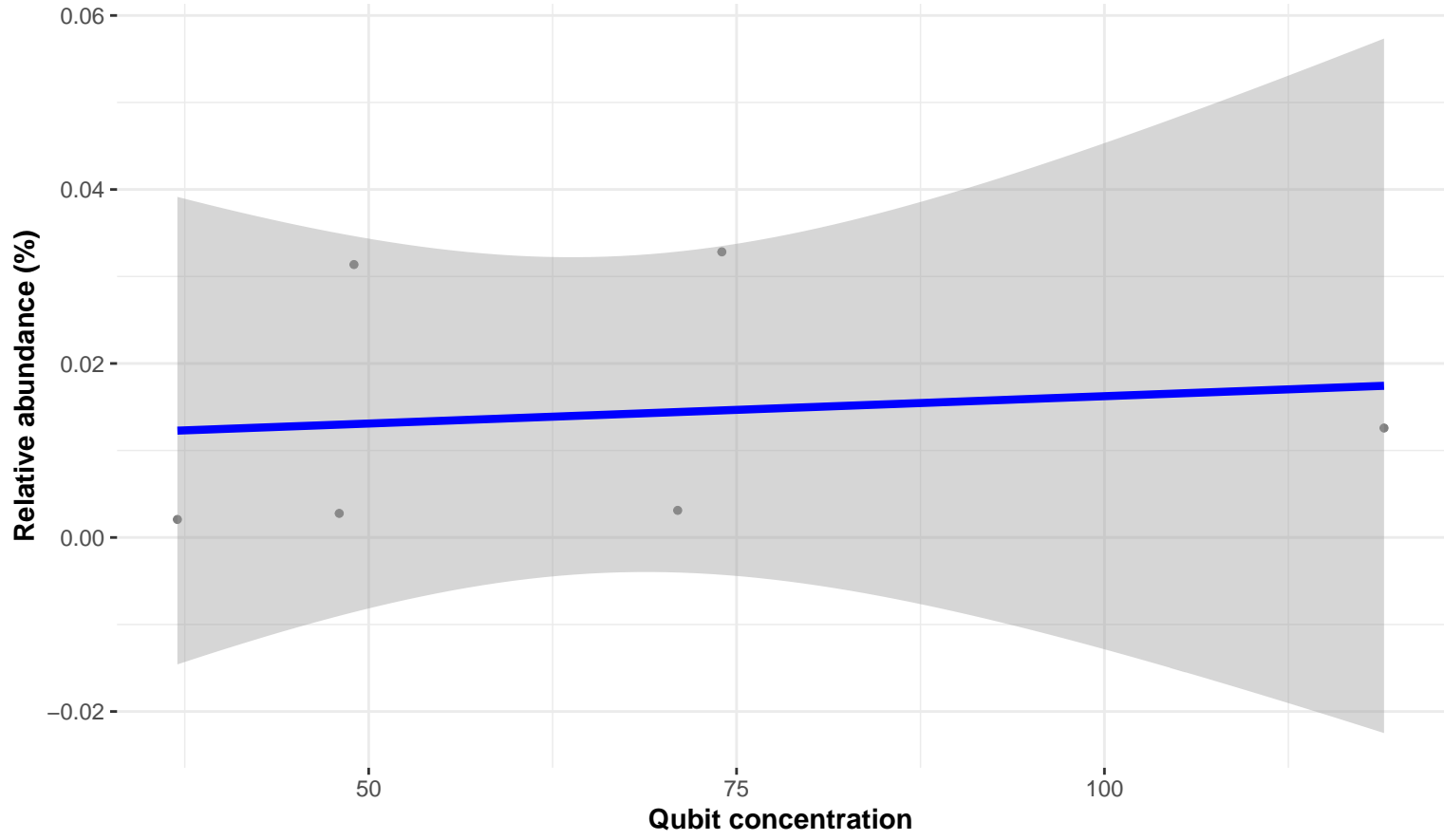
Correlation with all samples

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

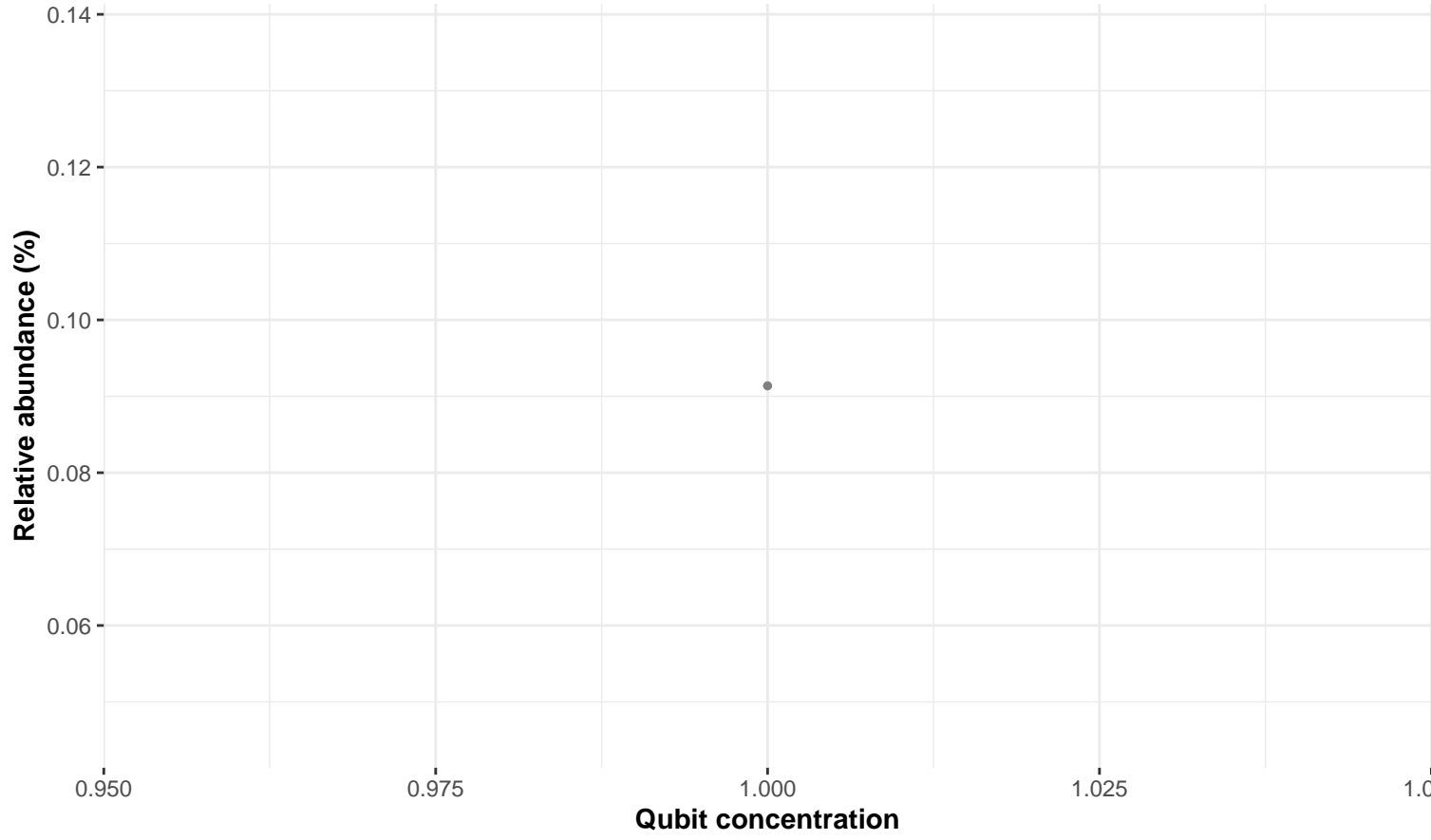


Correlation within: Digesta

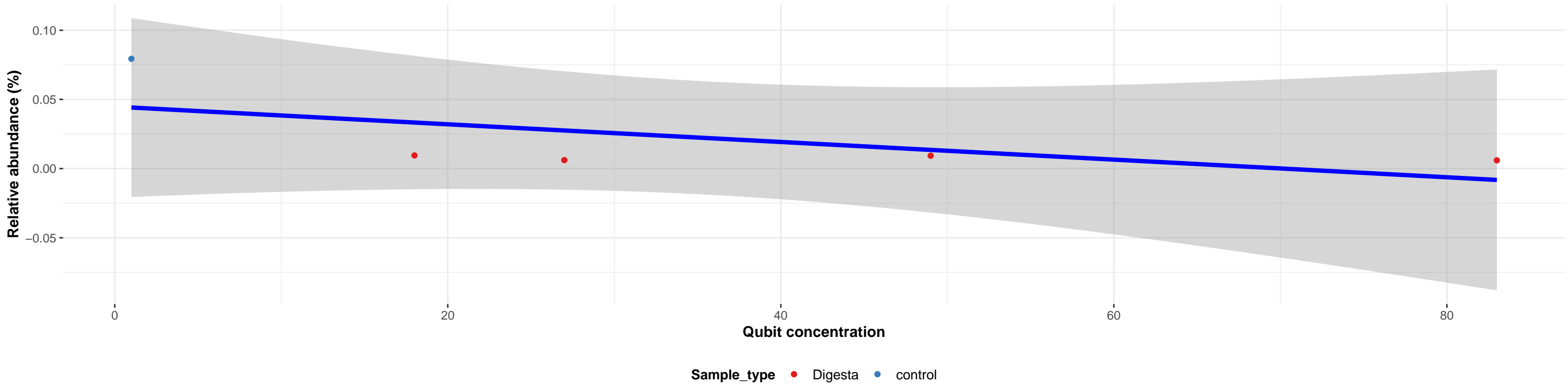
$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $\text{CI}_{95\%} [-0.263, 0.968]$, $n_{\text{pairs}} = 6$



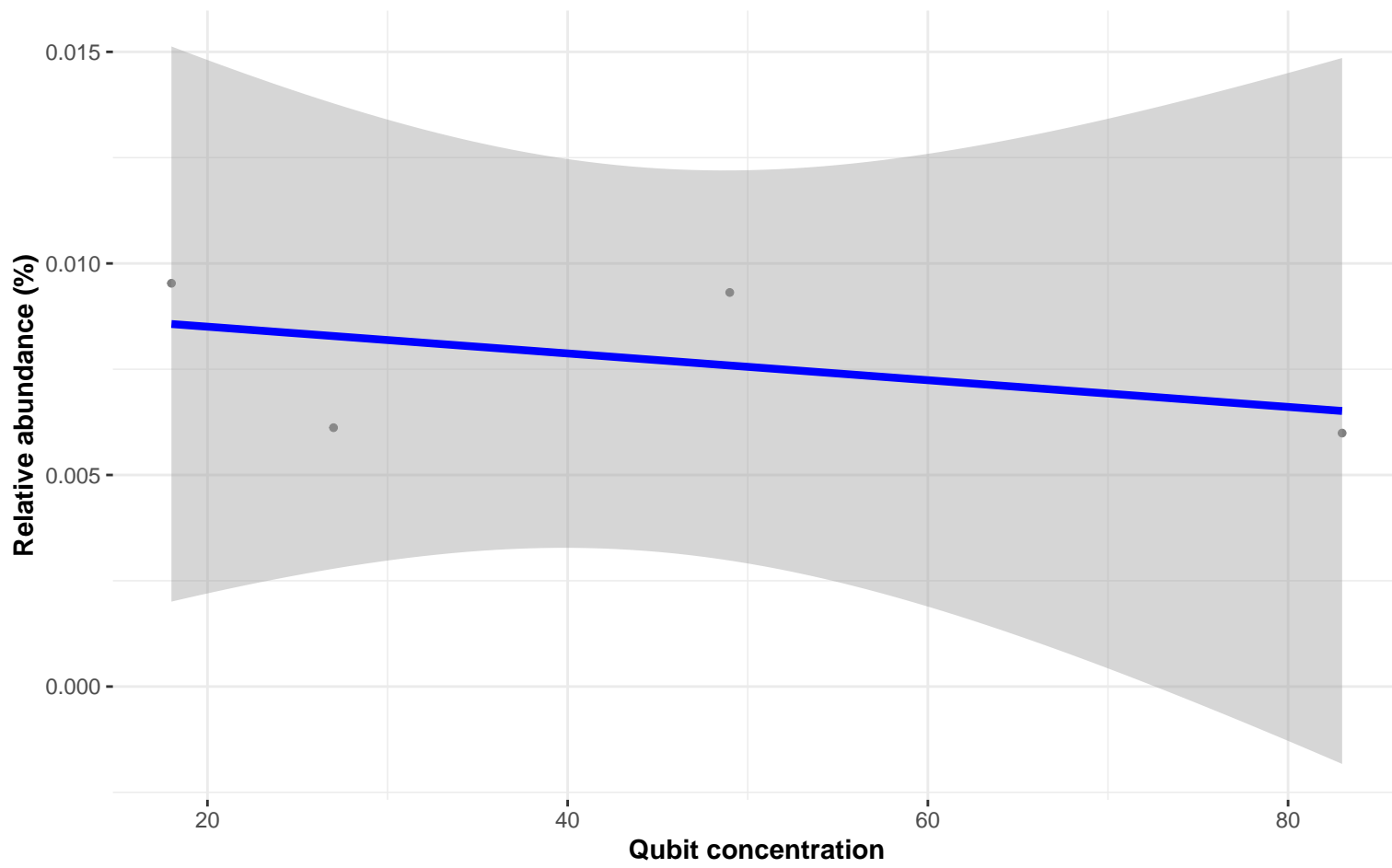
Correlation within: control



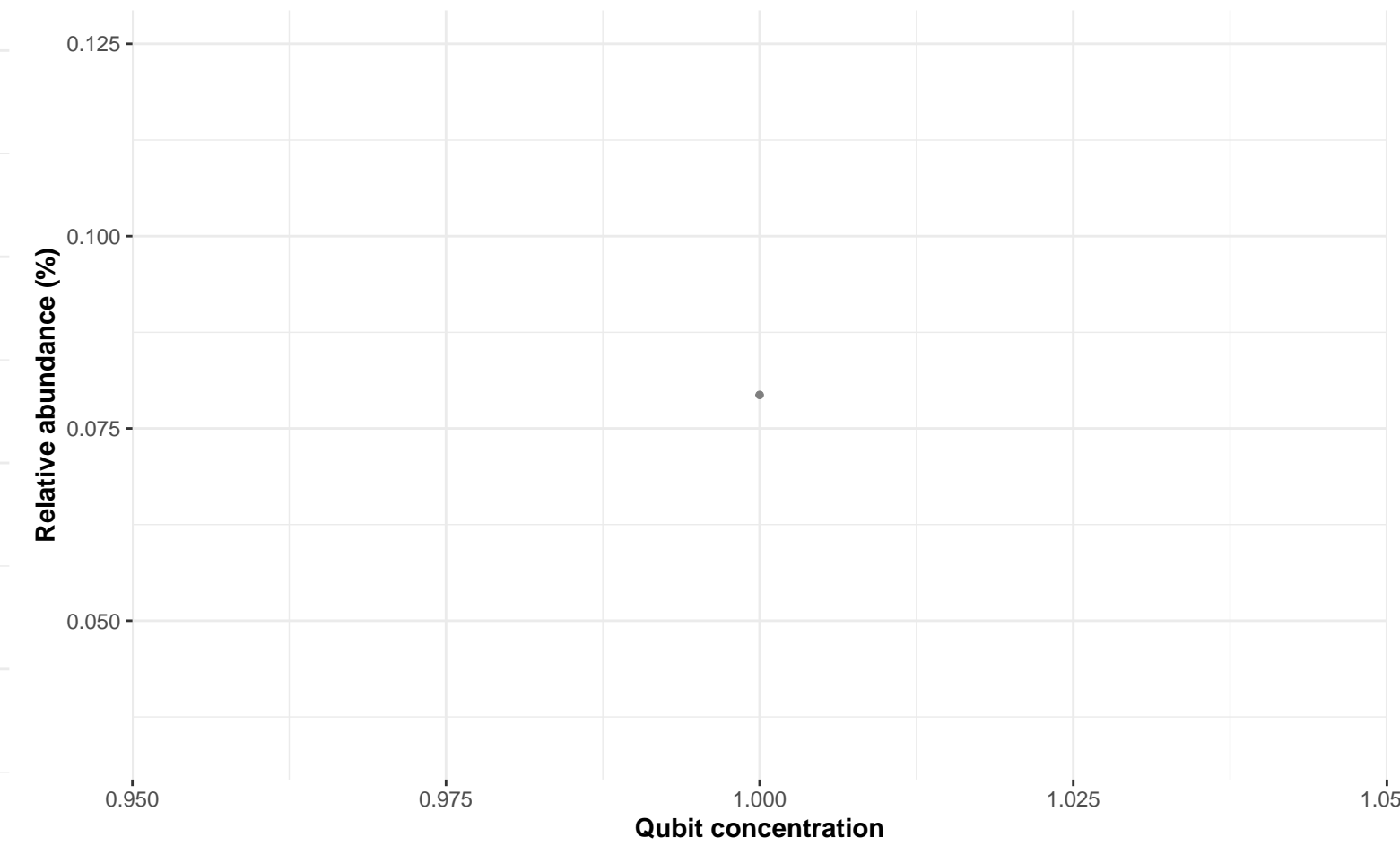
Correlation with all samples



Correlation within: Digesta



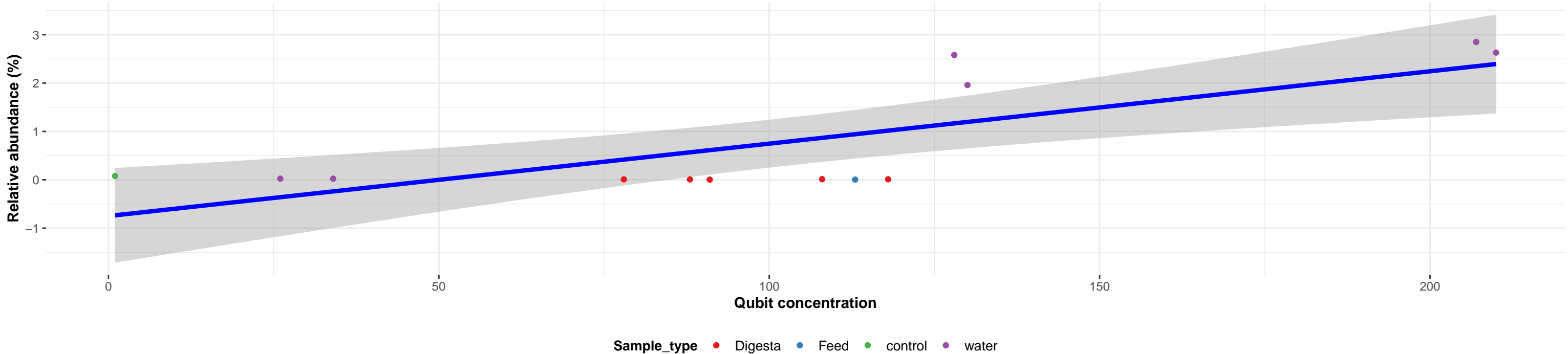
Correlation within: control



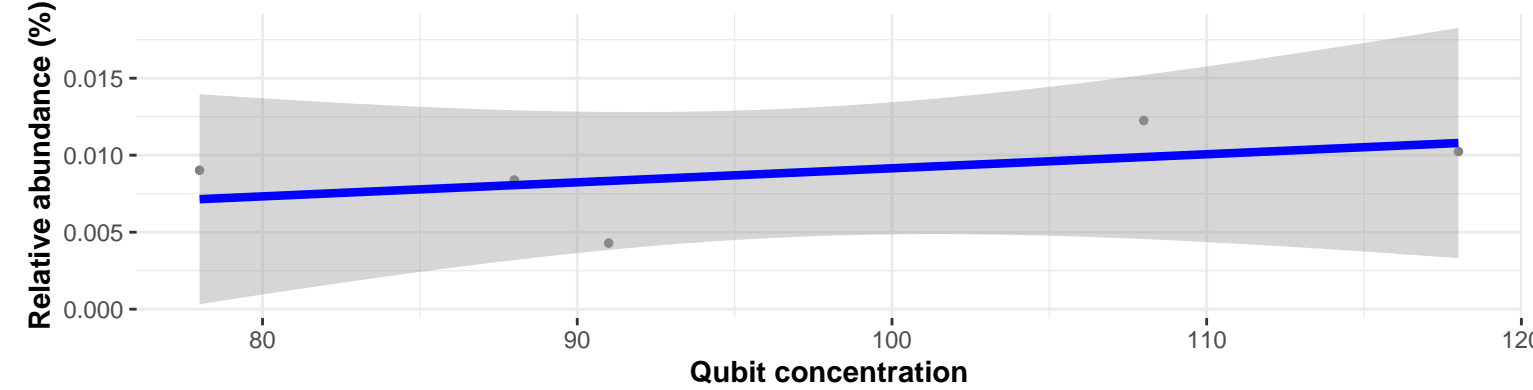
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Octadecabacter; NA

Correlation with all samples

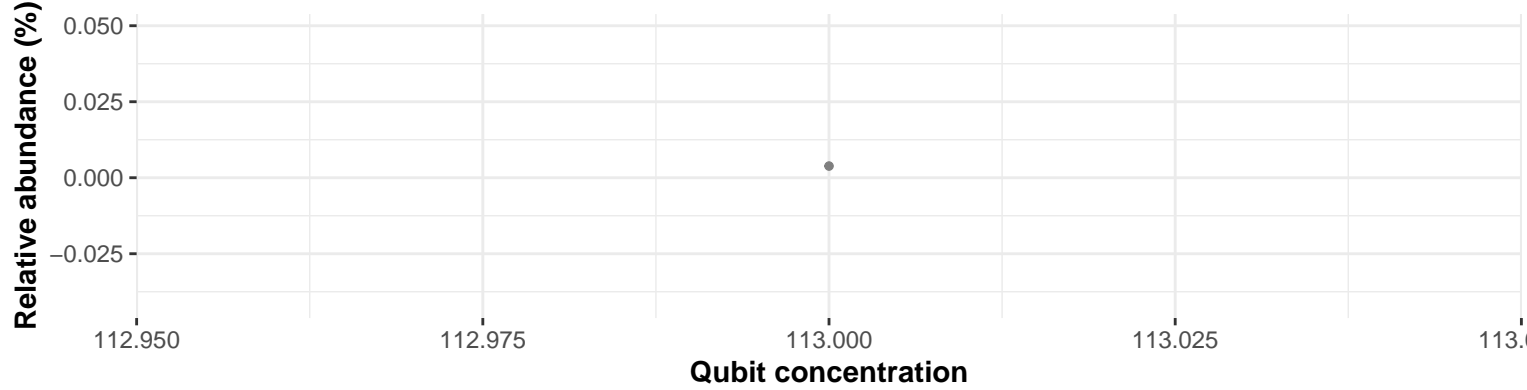
$\log_e(S) = 5.328$, $p = 0.138$, $\hat{\rho}_{\text{Spearman}} = 0.434$, $\text{CI}_{95\%} [-0.172, 0.802]$, $n_{\text{pairs}} = 13$



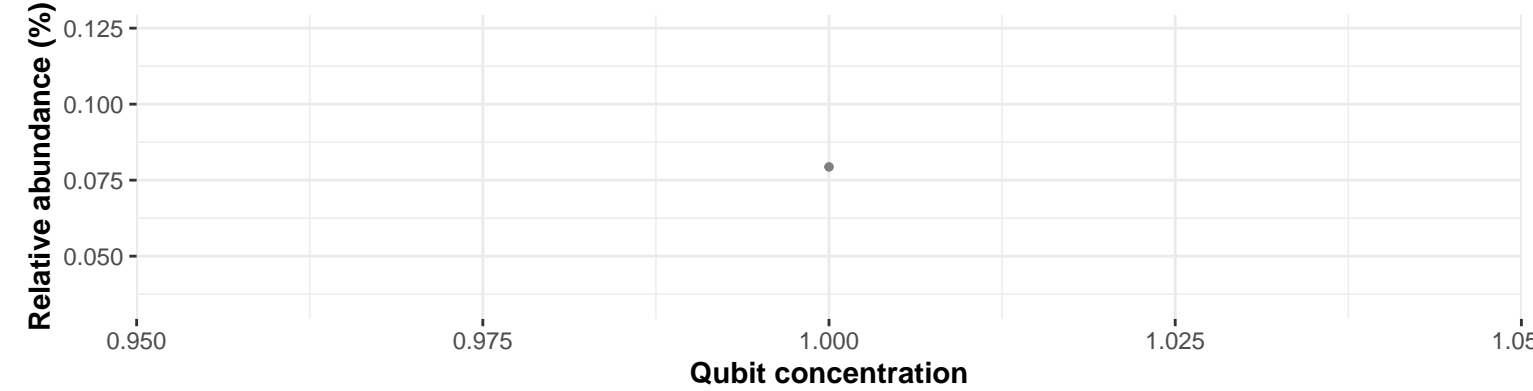
Correlation within: Digesta



Correlation within: Feed

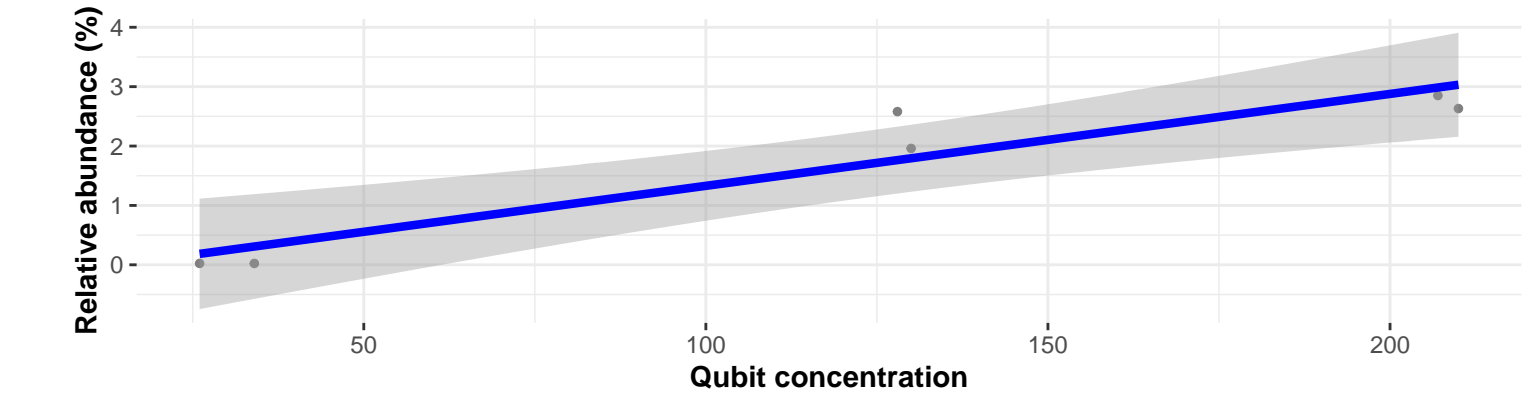


Correlation within: control



Correlation within: water

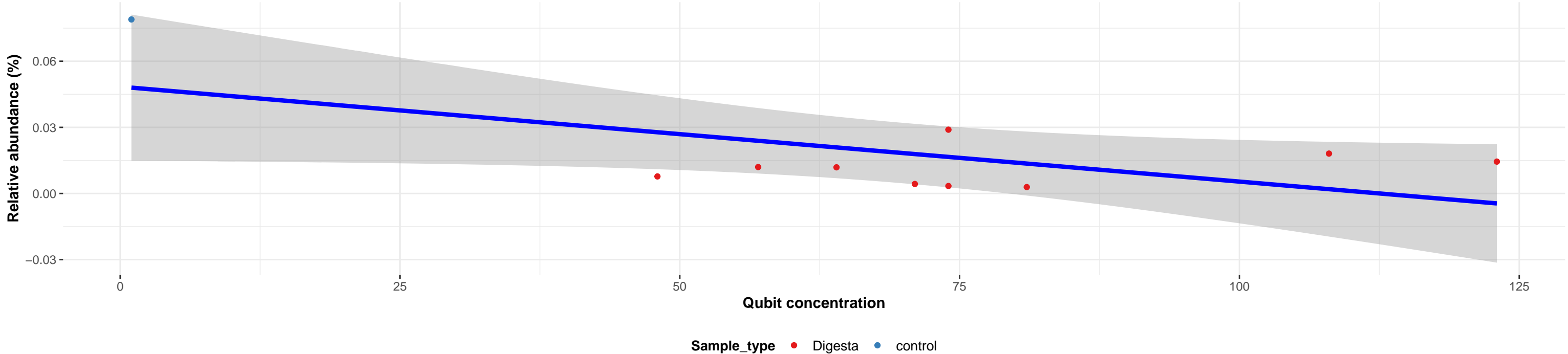
$\log_e(S) = 1.792$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.829$, $\text{CI}_{95\%} [0.019, 0.982]$, $n_{\text{pairs}} = 6$



Bacteria; Firmicutes; Bacilli; Bacillales; Planococcaceae; Chungangia; NA

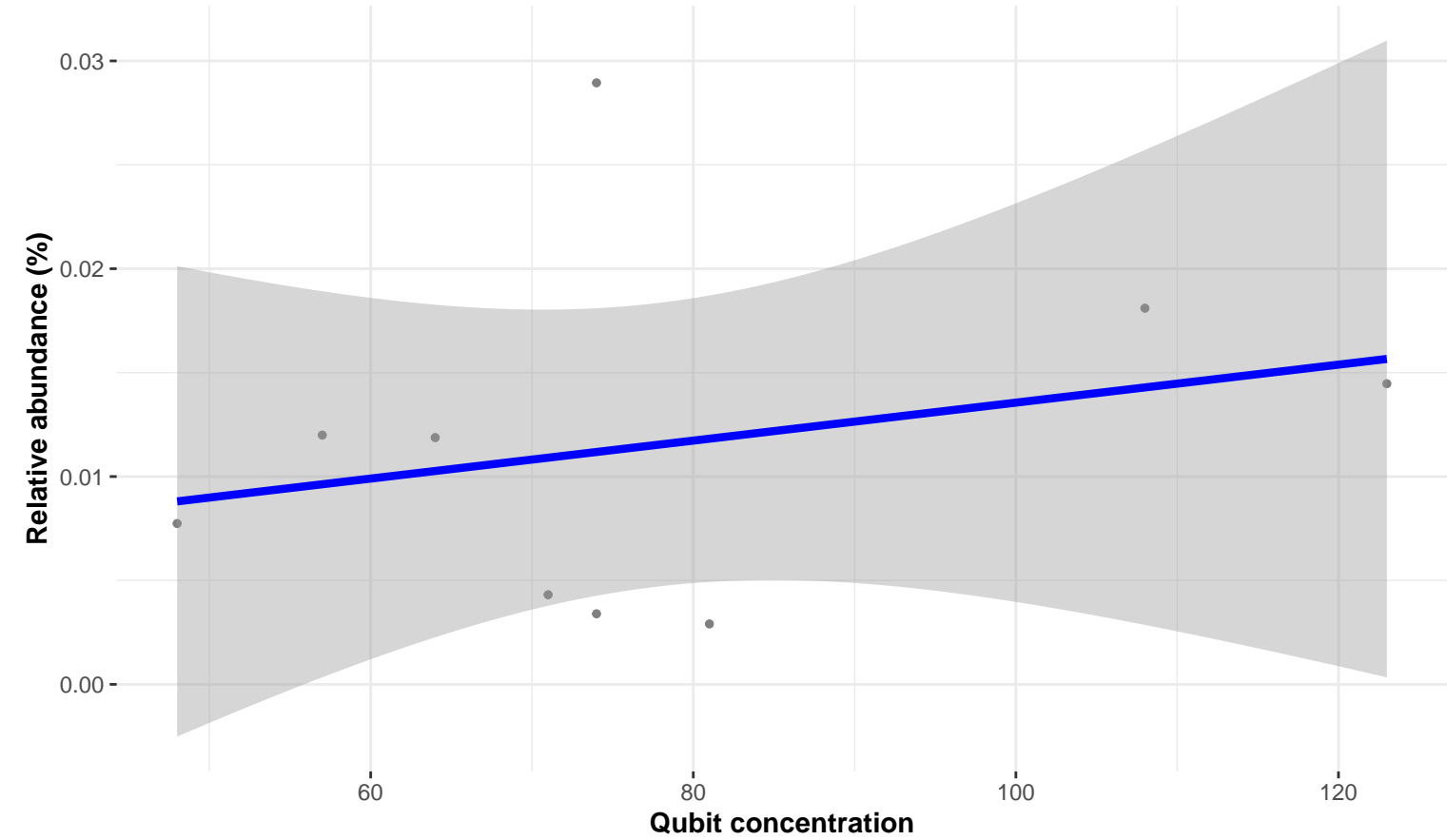
Correlation with all samples

$\log_e(S) = 5.221$, $p = 0.738$, $\hat{\rho}_{\text{Spearman}} = -0.122$, $\text{CI}_{95\%} [-0.709, 0.565]$, $n_{\text{pairs}} = 10$

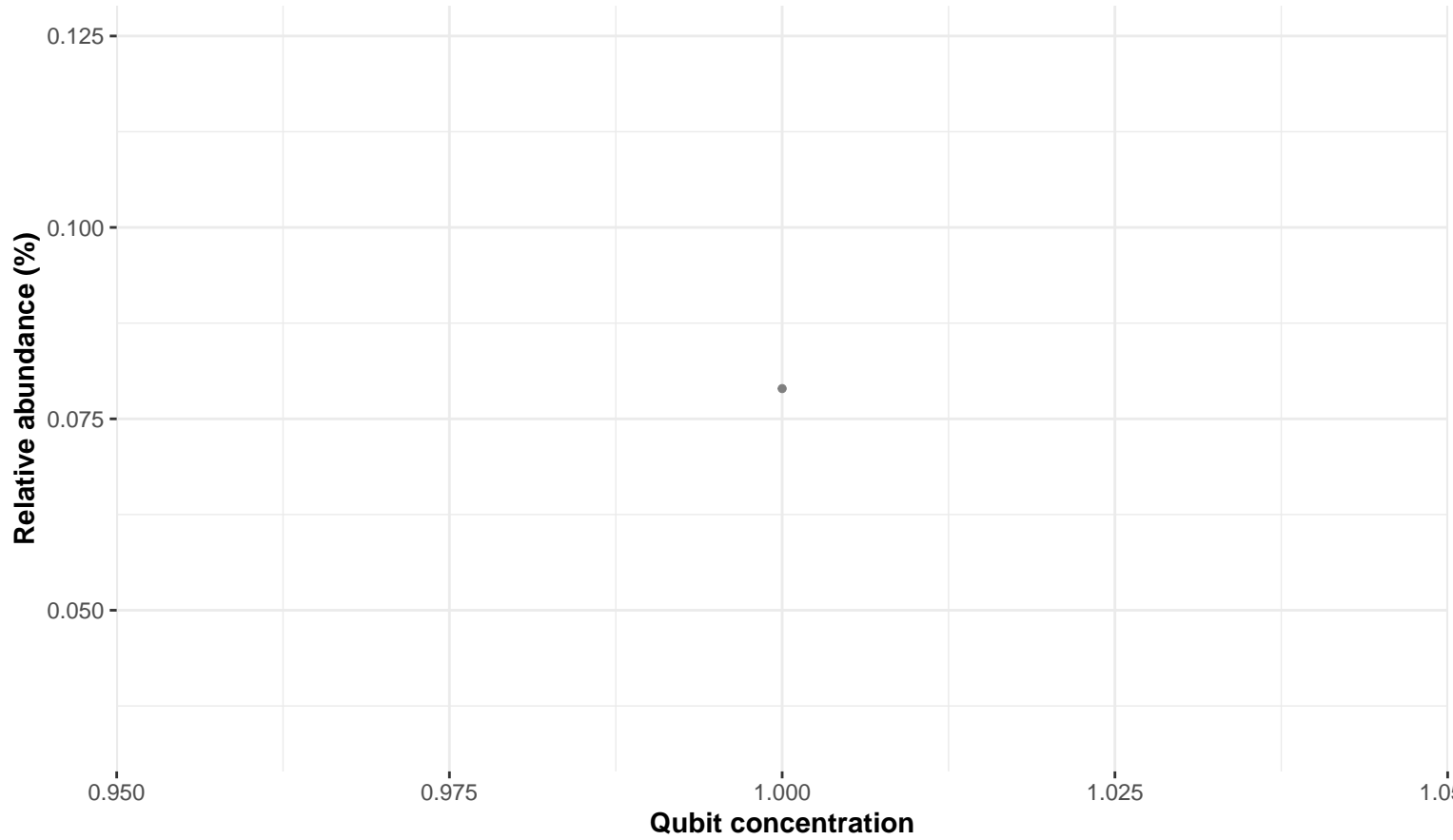


Correlation within: Digesta

$\log_e(S) = 4.553$, $p = 0.589$, $\hat{\rho}_{\text{Spearman}} = 0.209$, $\text{CI}_{95\%} [-0.545, 0.776]$, $n_{\text{pairs}} = 9$



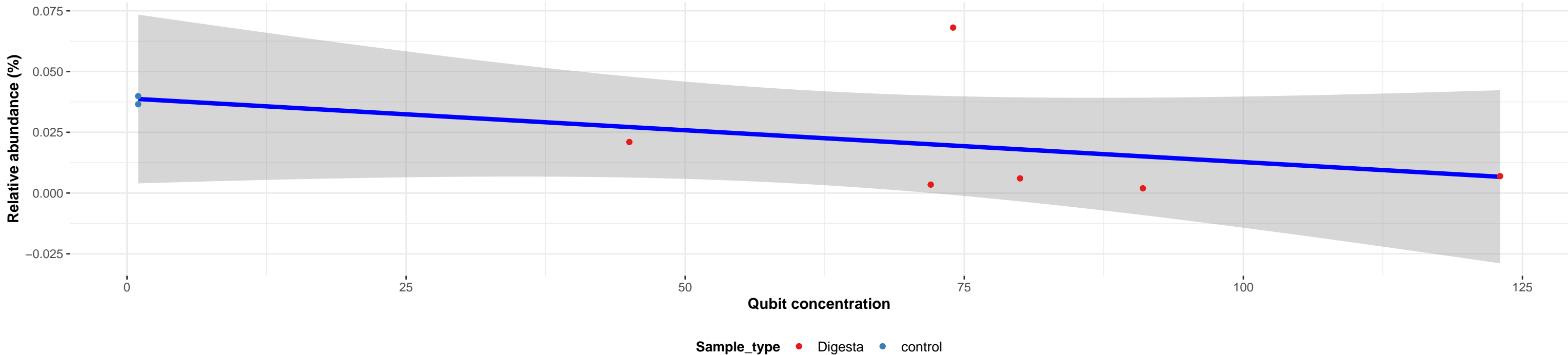
Correlation within: control



Bacteria; Verrucomicrobiota; Verrucomicrobiae; Chthoniobacterales; Chthoniobacteraceae; Chthoniobacter; NA

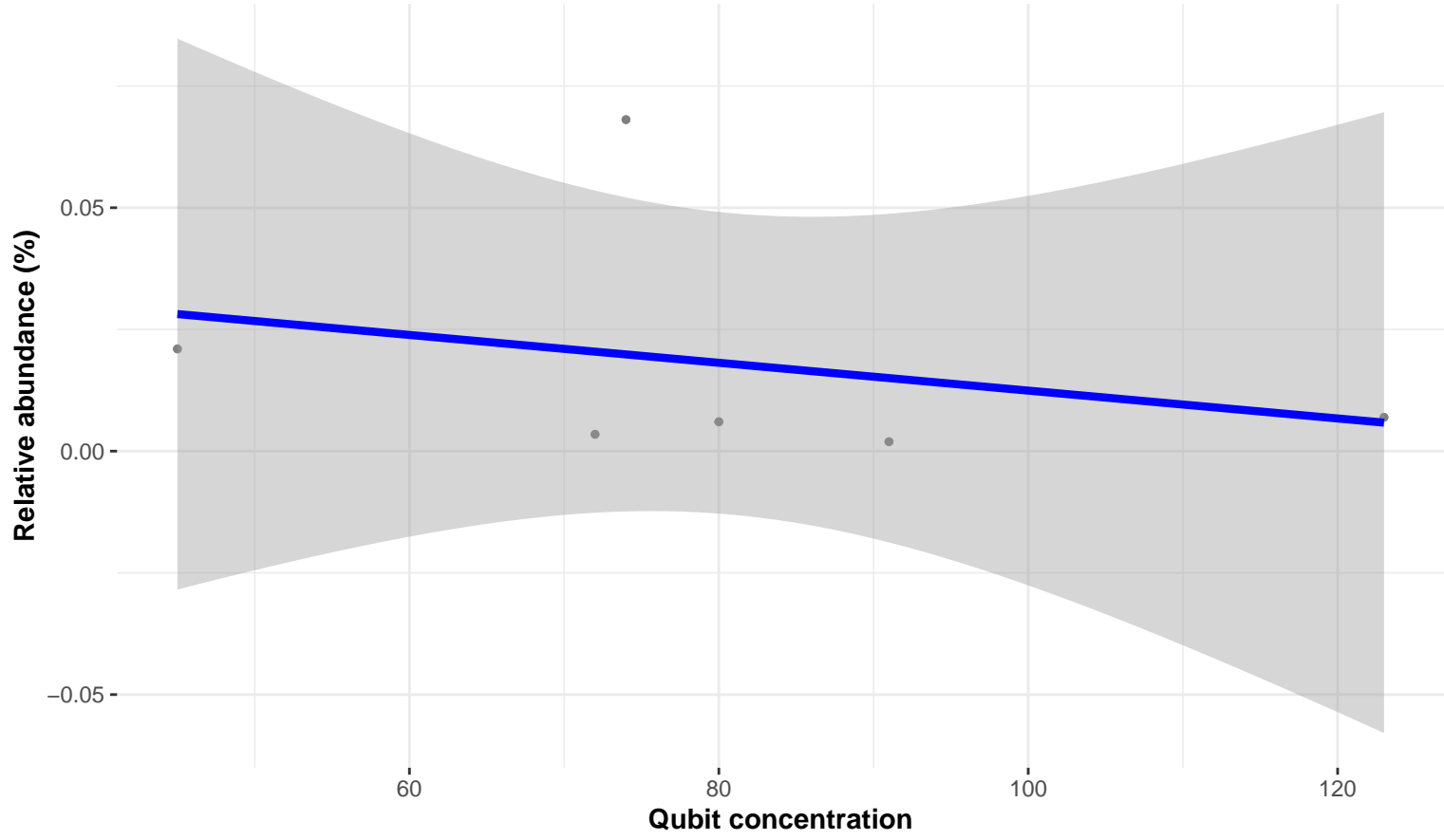
Correlation with all samples

$\log_e(S) = 4.862$, $p = 0.168$, $\hat{\rho}_{\text{Spearman}} = -0.539$, $\text{CI}_{95\%} [-0.906, 0.291]$, $n_{\text{pairs}} = 8$

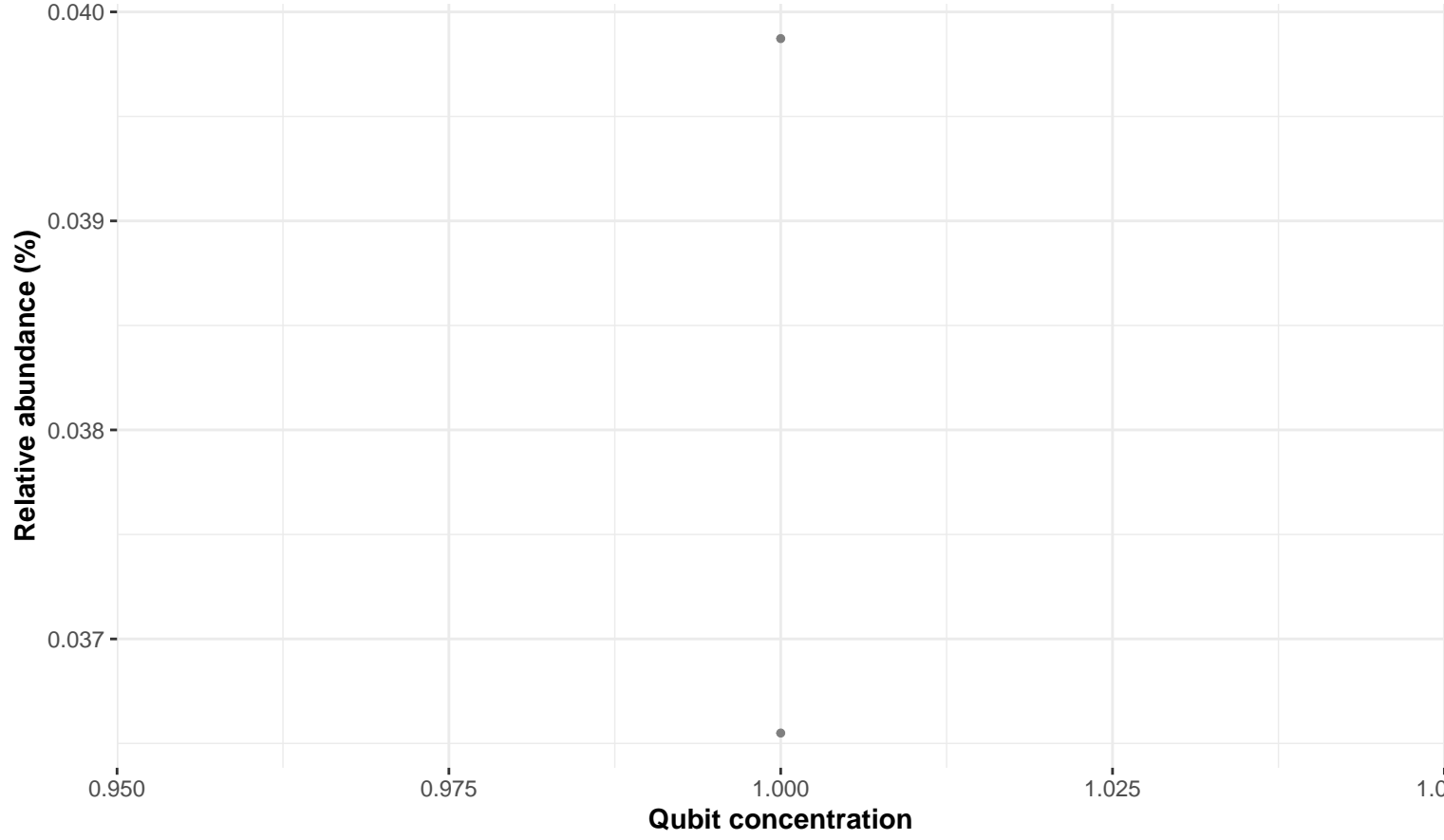


Correlation within: Digesta

$\log_e(S) = 3.829$, $p = 0.544$, $\hat{\rho}_{\text{Spearman}} = -0.314$, $\text{CI}_{95\%} [-0.903, 0.686]$, $n_{\text{pairs}} = 6$



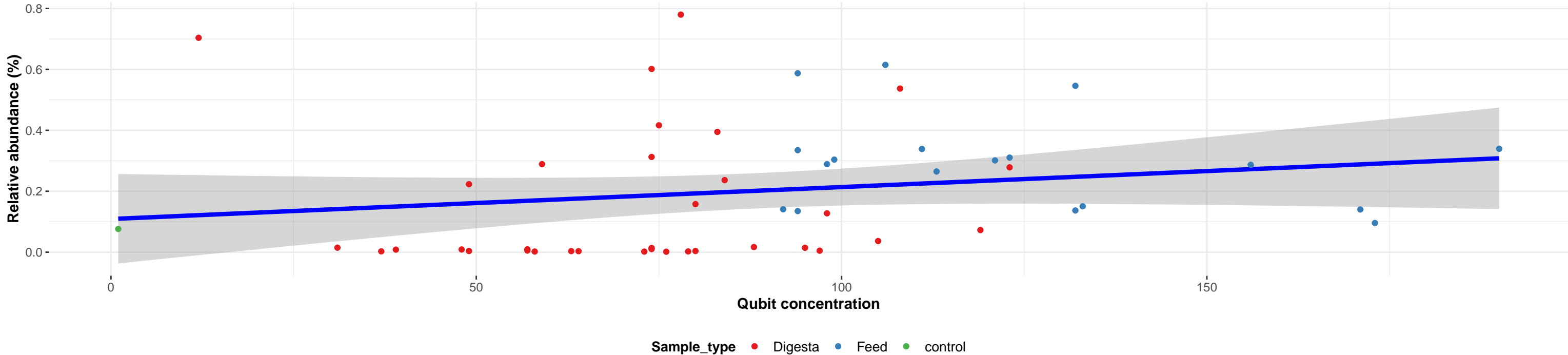
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus; NA

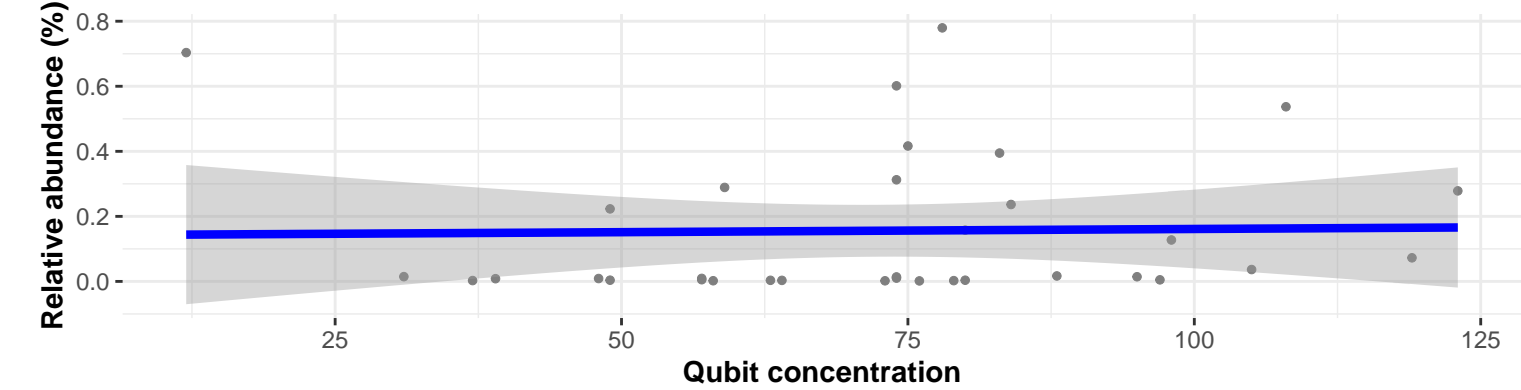
Correlation with all samples

$\log_e(S) = 9.610$, $p = 0.003$, $\hat{\rho}_{\text{Spearman}} = 0.399$, $CI_{95\%} [0.136, 0.609]$, $n_{\text{pairs}} = 53$



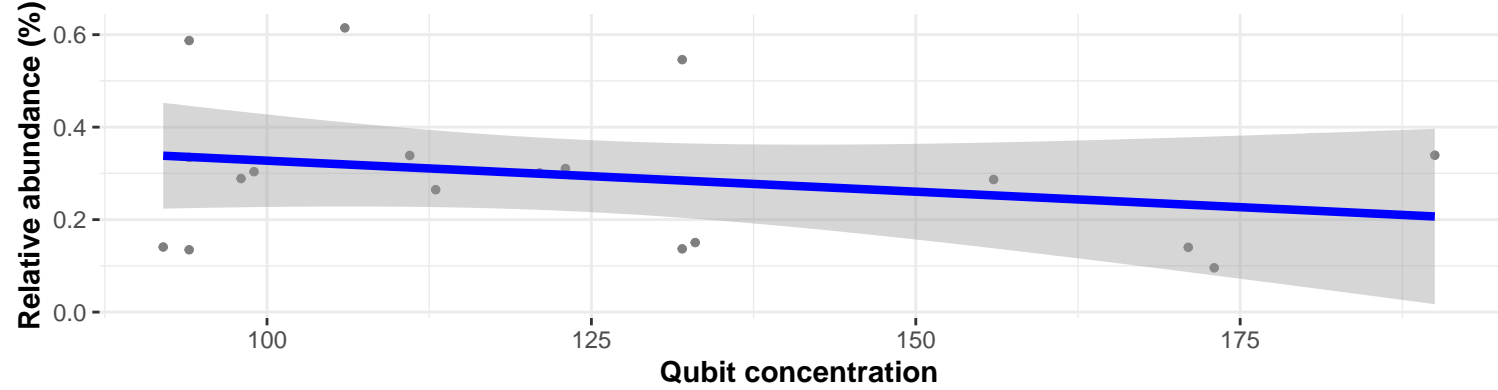
Correlation within: Digesta

$\log_e(S) = 8.484$, $p = 0.136$, $\hat{\rho}_{\text{Spearman}} = 0.261$, $CI_{95\%} [-0.095, 0.558]$, $n_{\text{pairs}} = 34$

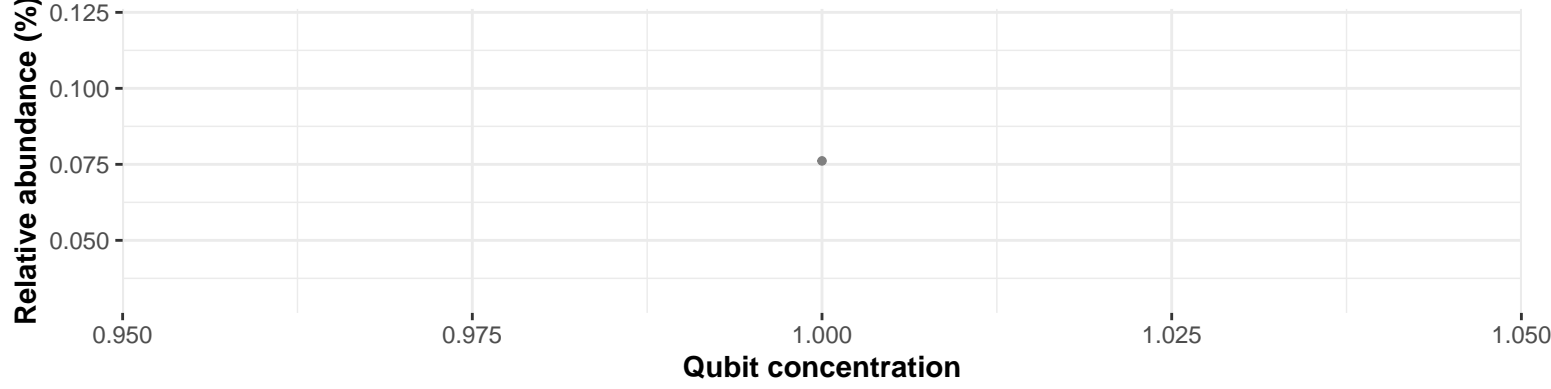


Correlation within: Feed

$\log_e(S) = 7.042$, $p = 0.475$, $\hat{\rho}_{\text{Spearman}} = -0.180$, $CI_{95\%} [-0.606, 0.327]$, $n_{\text{pairs}} = 18$



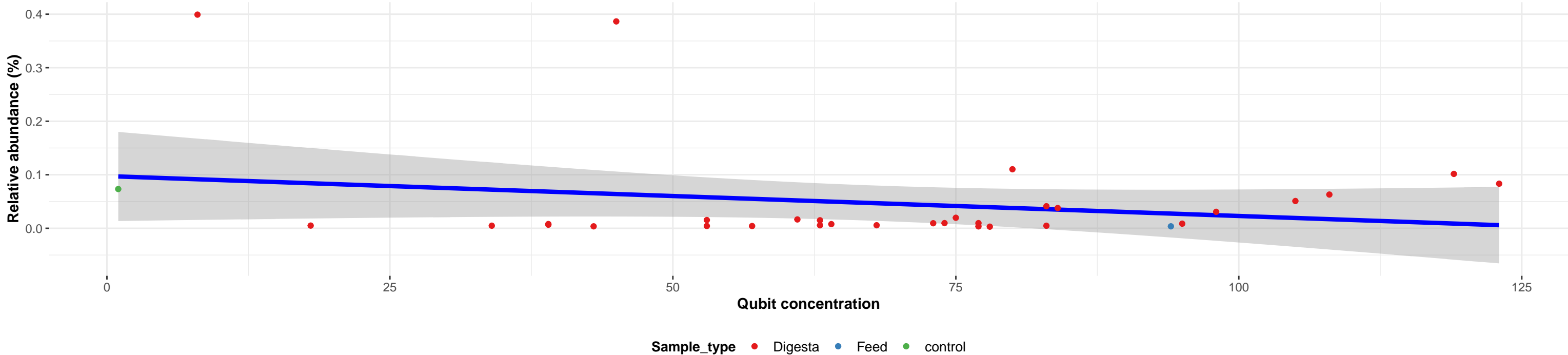
Correlation within: control



Bacteria; Firmicutes; Clostridia; Peptostreptococcales–Tissierellales; Peptostreptococcaceae; Paraclostridium; NA

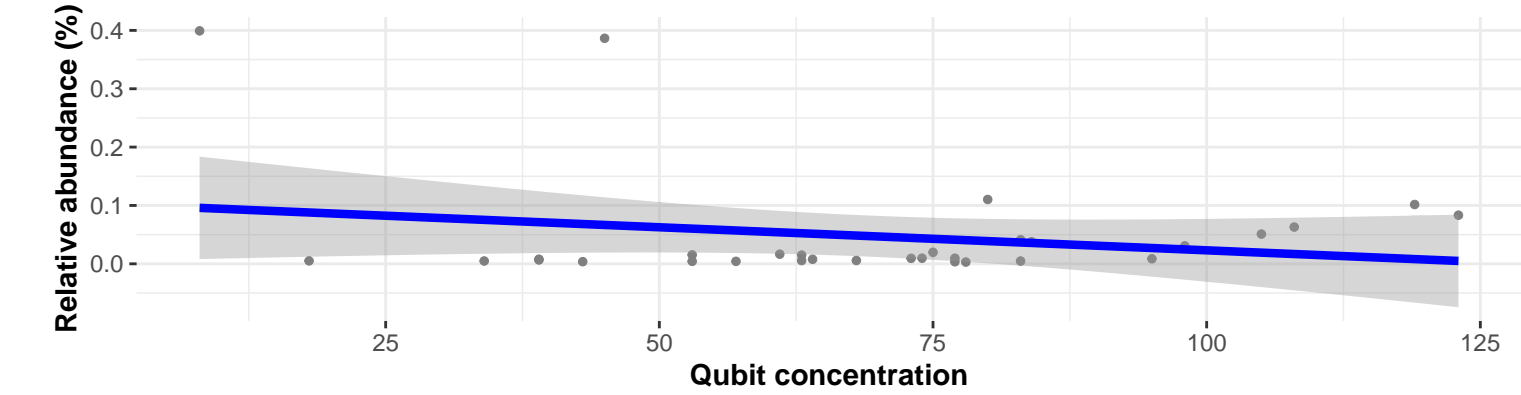
Correlation with all samples

$\log_e(S) = 8.461$, $p = 0.241$, $\hat{\rho}_{\text{Spearman}} = 0.210$, $CI_{95\%} [-0.154, 0.524]$, $n_{\text{pairs}} = 33$

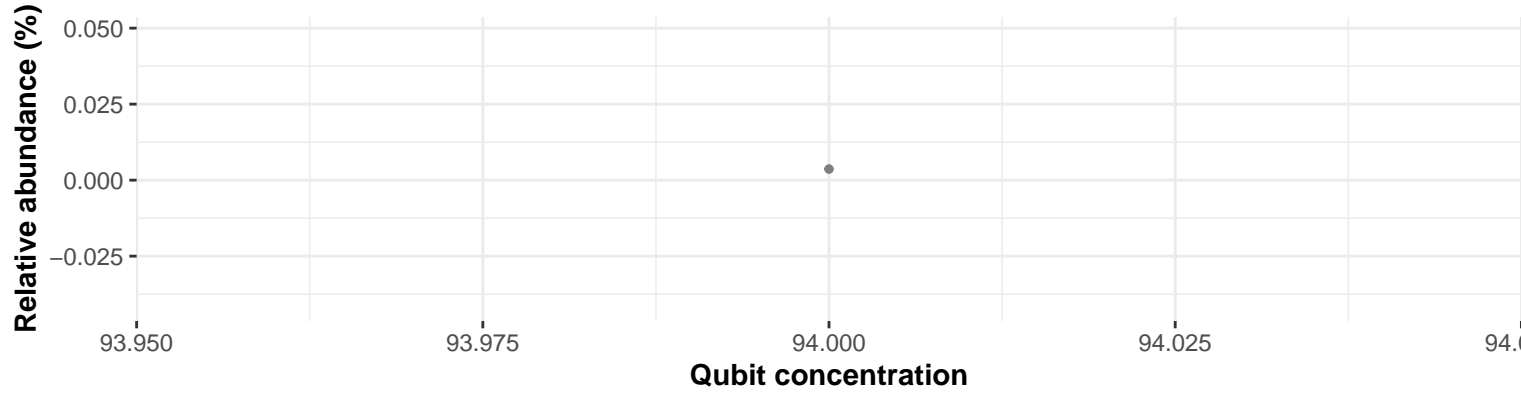


Correlation within: Digesta

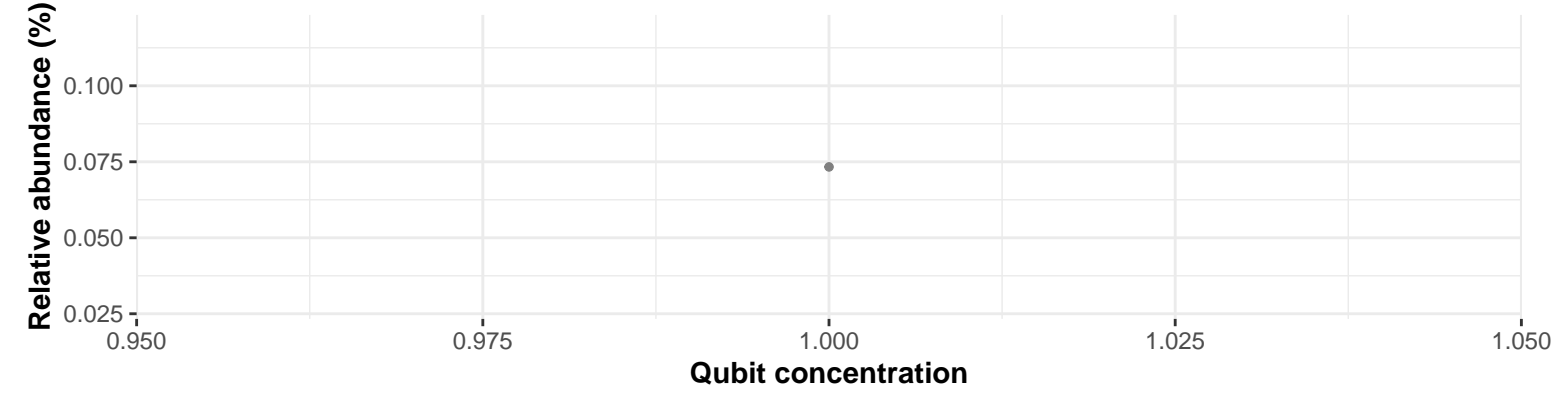
$\log_e(S) = 8.075$, $p = 0.052$, $\hat{\rho}_{\text{Spearman}} = 0.352$, $CI_{95\%} [-0.013, 0.635]$, $n_{\text{pairs}} = 31$



Correlation within: Feed



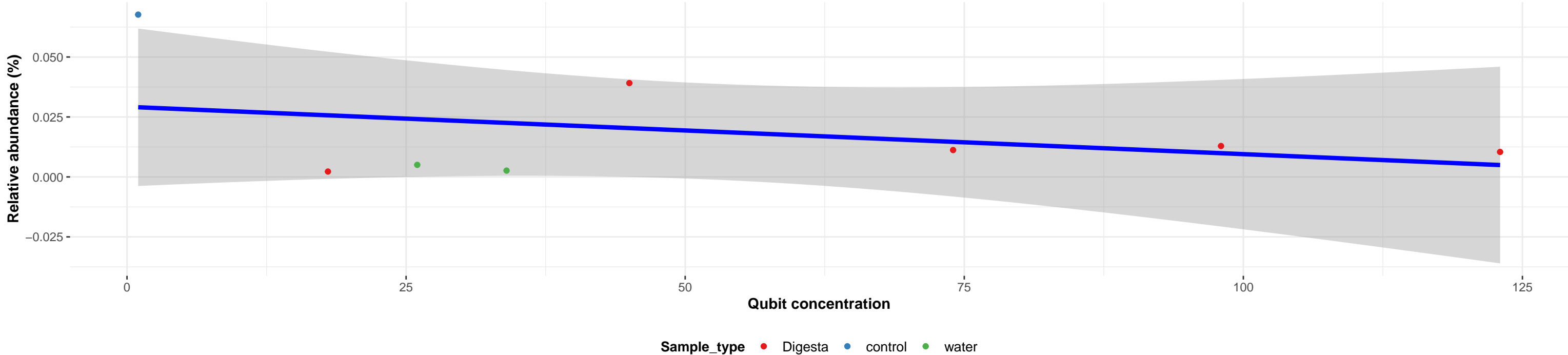
Correlation within: control



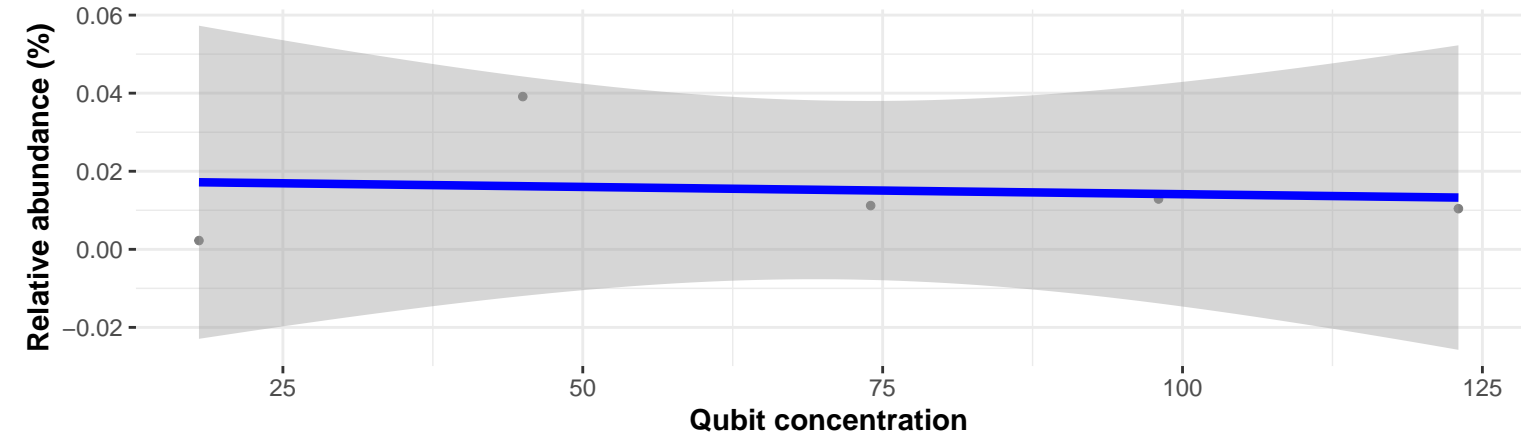
Bacteria; Bacteroidota; Bacteroidia; Chitinophagales; Chitinophagaceae; Parasediminibacterium; NA

Correlation with all samples

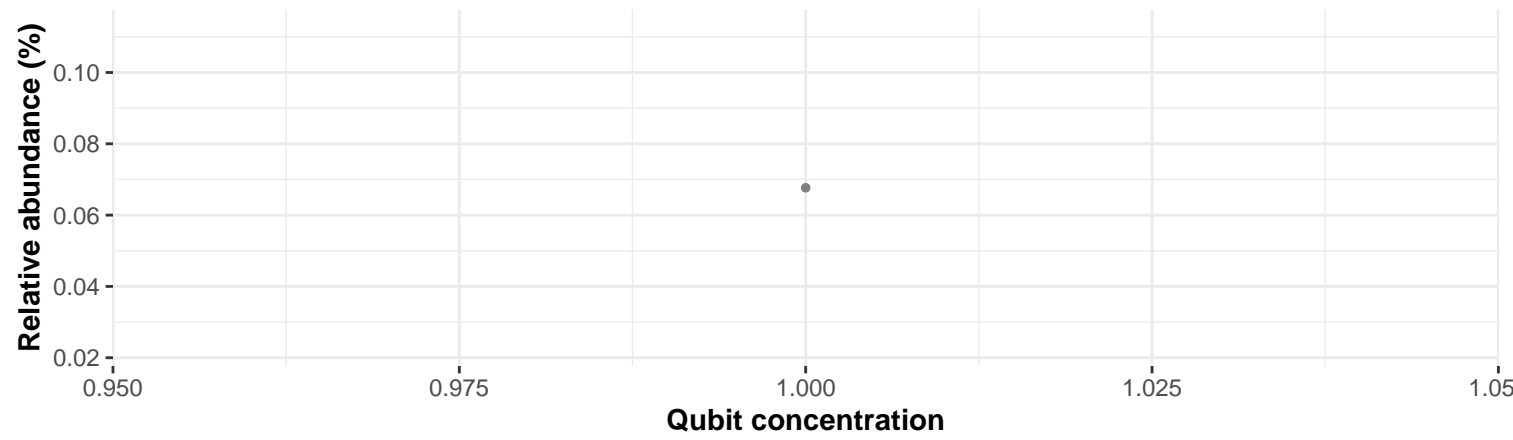
$\log_e(S) = 4.331$, $p = 0.823$, $\hat{\rho}_{\text{Spearman}} = 0.095$, $CI_{95\%} [-0.668, 0.761]$, $n_{\text{pairs}} = 8$



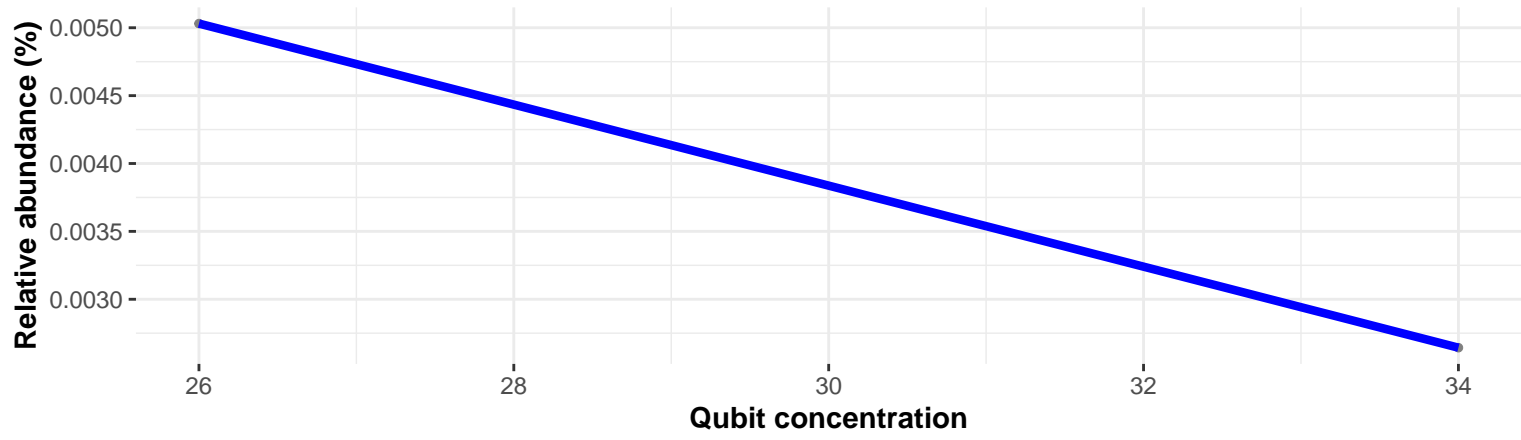
Correlation within: Digesta



Correlation within: control



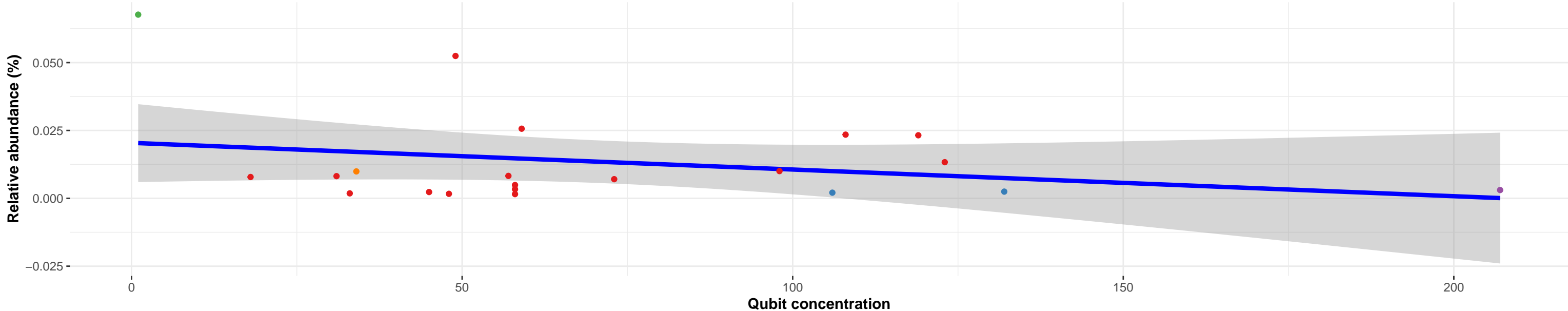
Correlation within: water



Bacteria; Firmicutes; Bacilli; Paenibacillales; Paenibacillaceae; Paenibacillus; NA

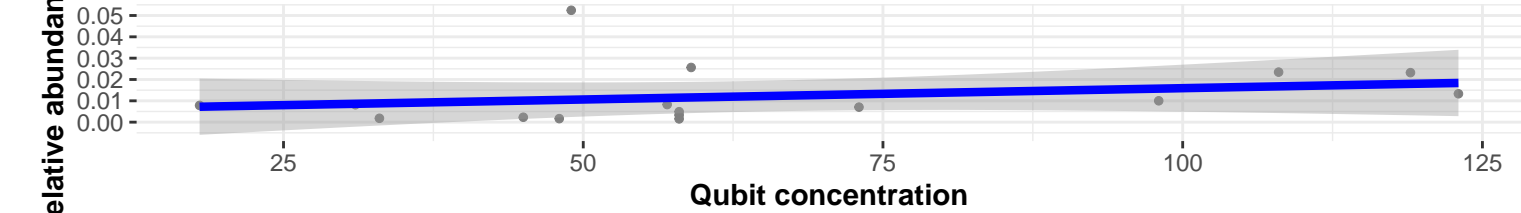
Correlation with all samples

$\log_e(S) = 7.342$, $p = 0.991$, $\hat{\rho}_{\text{Spearman}} = -0.003$, $CI_{95\%} [-0.445, 0.441]$, $n_{\text{pairs}} = 21$

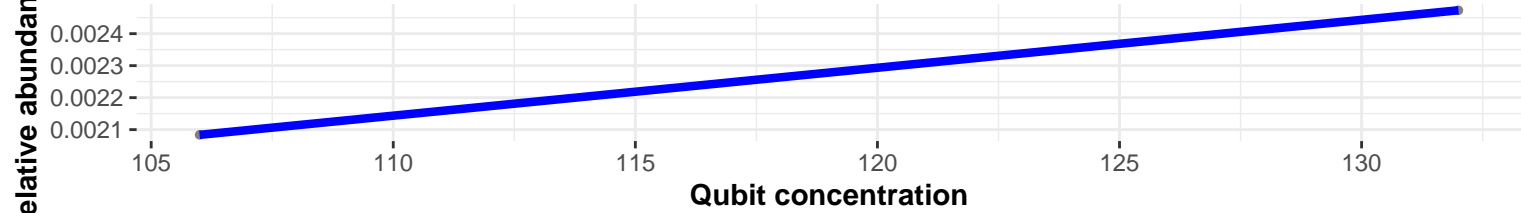


Correlation within: Digesta

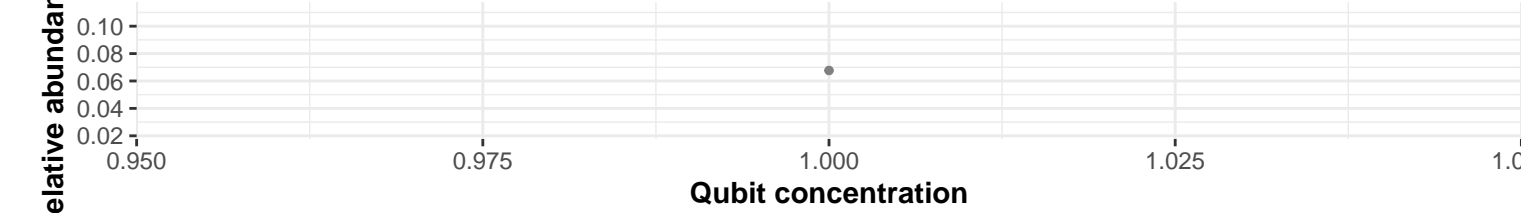
$\log_e(S) = 5.916$, $p = 0.077$, $\hat{\rho}_{\text{Spearman}} = 0.454$, $CI_{95\%} [-0.069, 0.782]$, $n_{\text{pairs}} = 16$



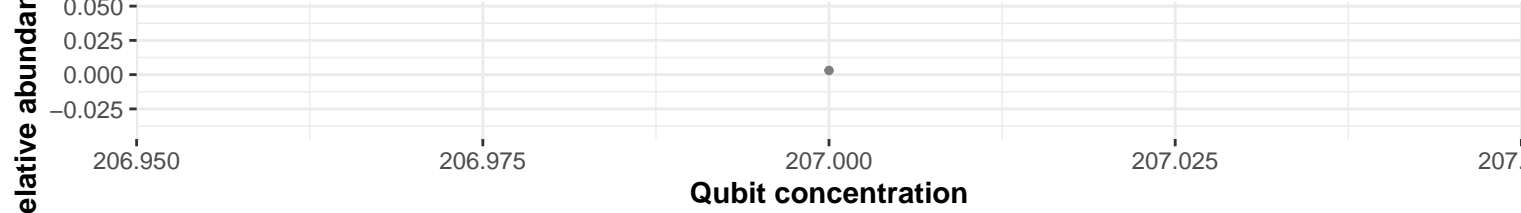
Correlation within: Feed



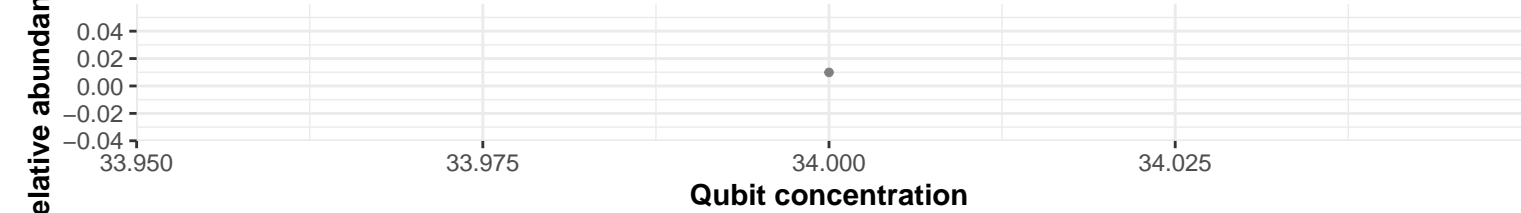
Correlation within: control



Correlation within: Positive_control



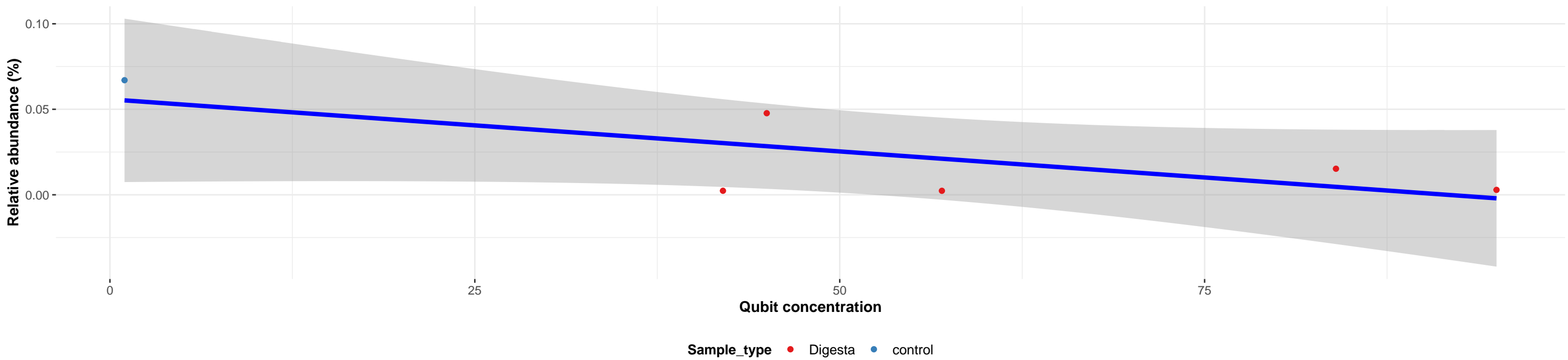
Correlation within: water



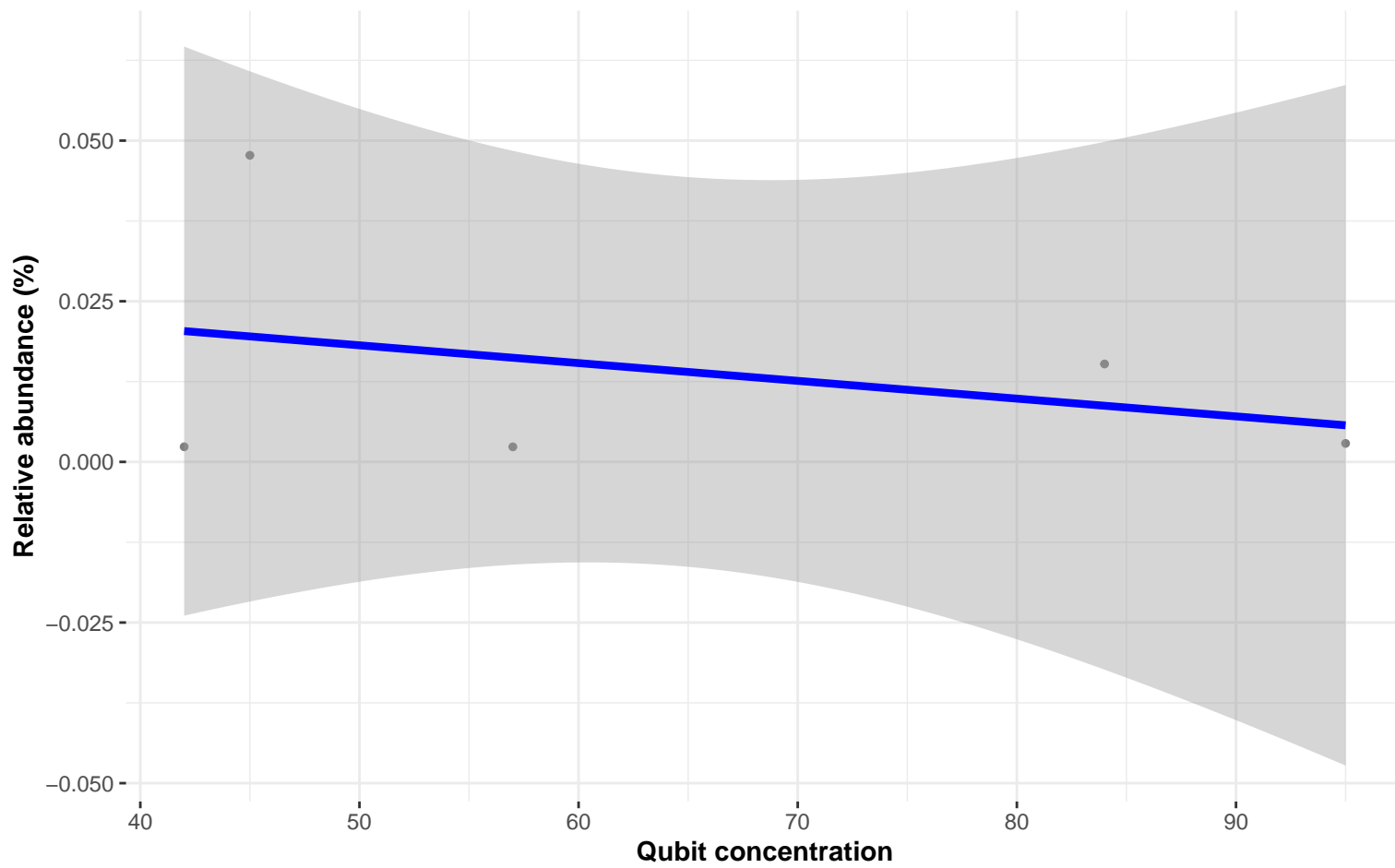
Bacteria; Bacteroidota; Bacteroidia; Chitinophagales; Chitinophagaceae; Sediminibacterium; NA

Correlation with all samples

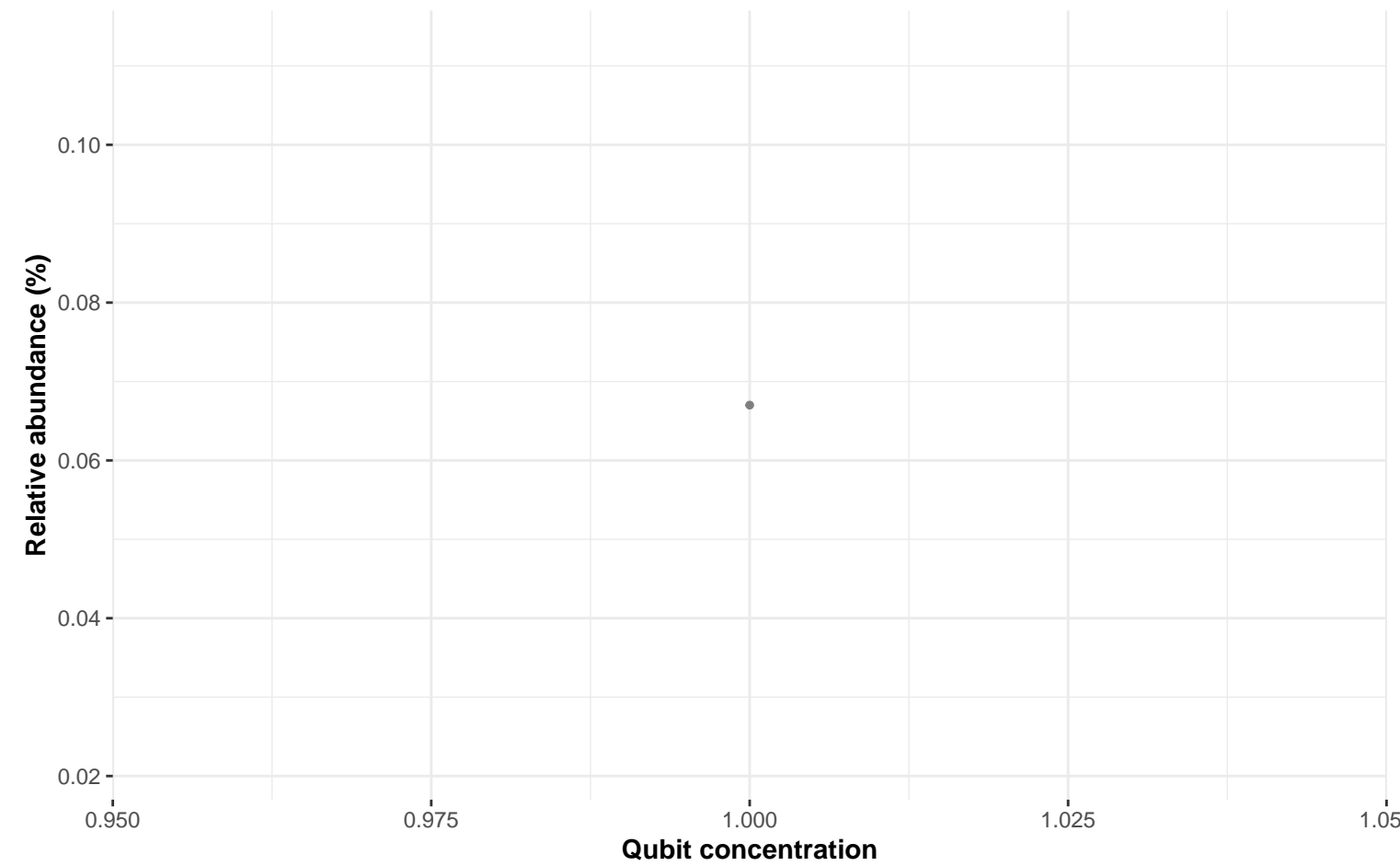
$\log_e(S) = 3.871$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = -0.371$, $\text{CI}_{95\%} [-0.915, 0.650]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



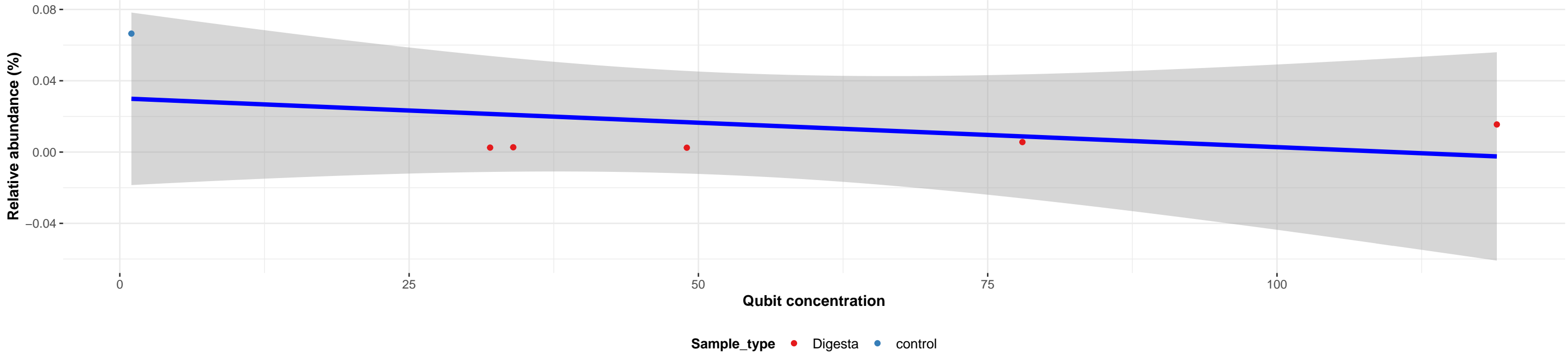
Correlation within: control



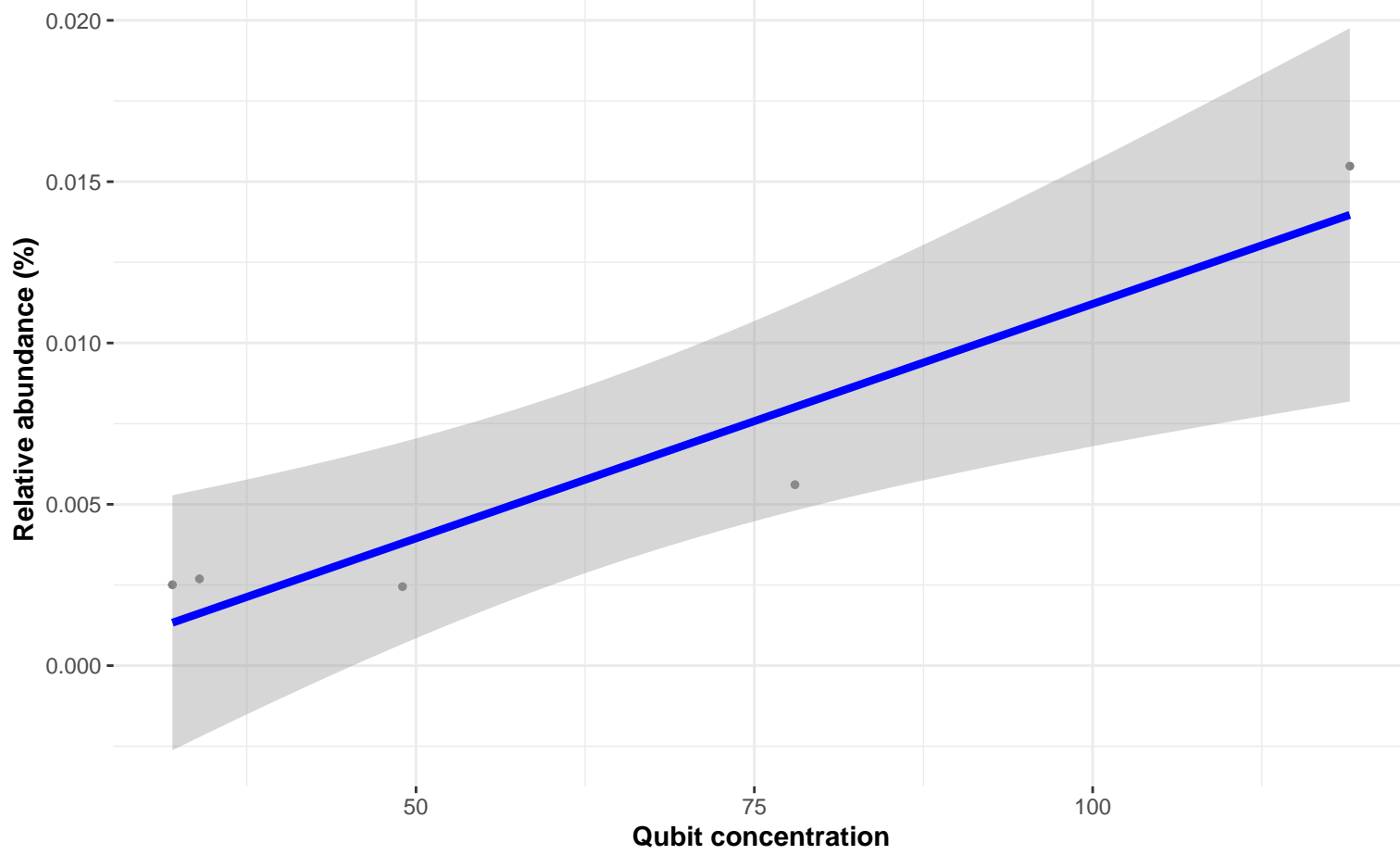
Bacteria; Bacteroidota; Bacteroidia; Cytophagales; Spirosomaceae; Rudanella; NA

Correlation with all samples

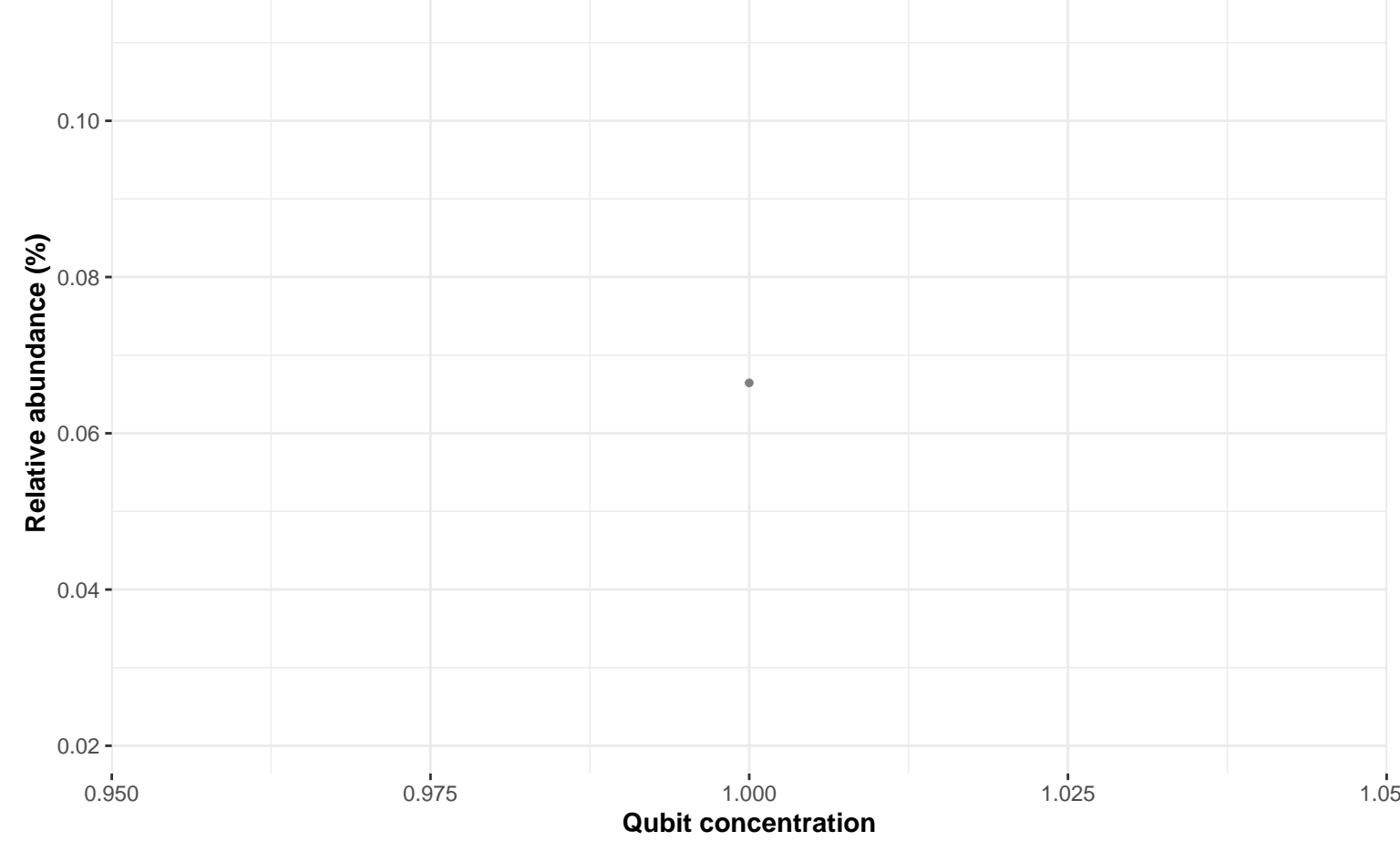
$\log_e(S) = 3.584$, $p = 0.957$, $\hat{\rho}_{\text{Spearman}} = -0.029$, $\text{CI}_{95\%} [-0.832, 0.813]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



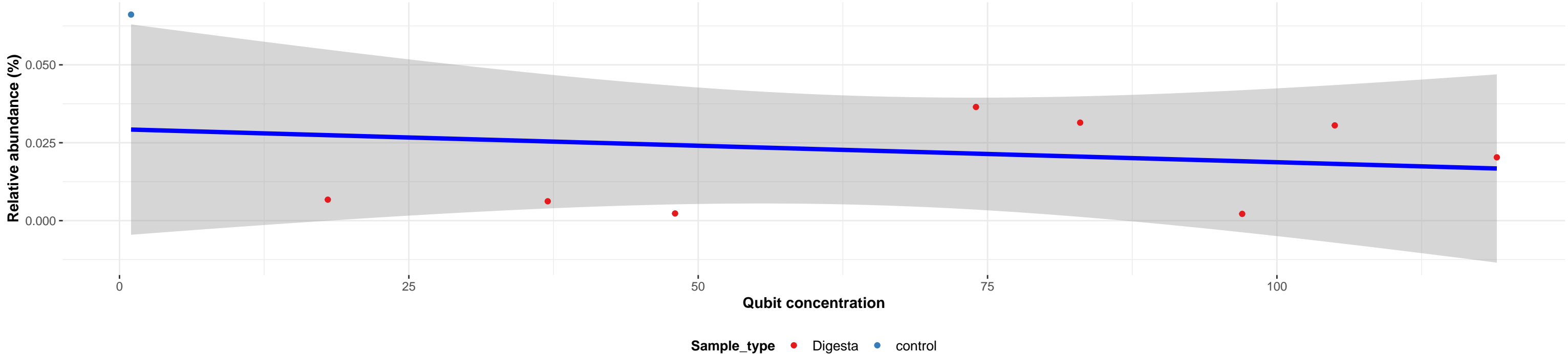
Correlation within: control



Bacteria; Dependientiae; Babeliae; Babeliales; NA; NA; NA

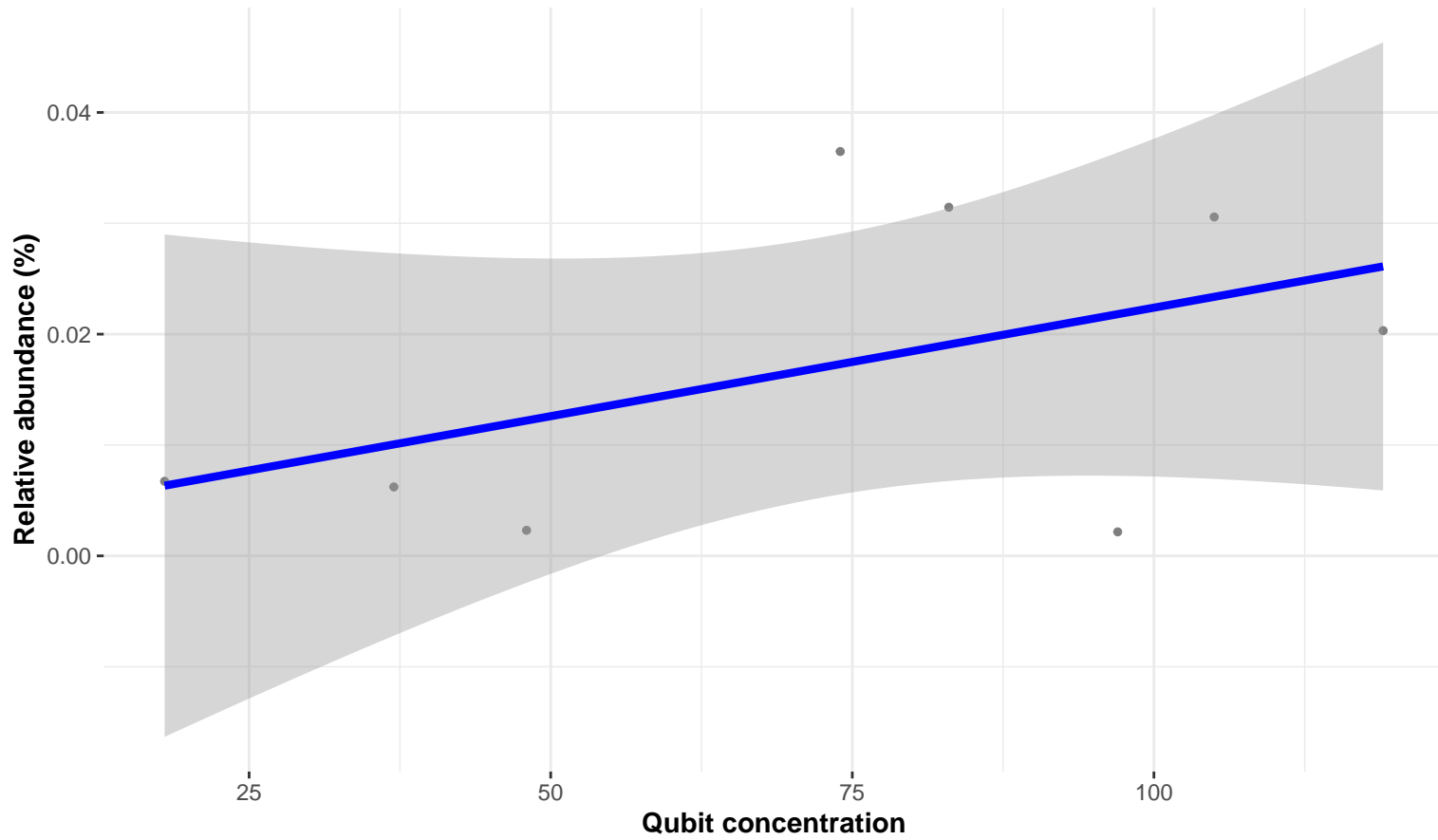
Correlation with all samples

$\log_e(S) = 4.927$, $p = 0.700$, $\hat{\rho}_{\text{Spearman}} = -0.150$, $\text{CI}_{95\%} [-0.751, 0.587]$, $n_{\text{pairs}} = 9$

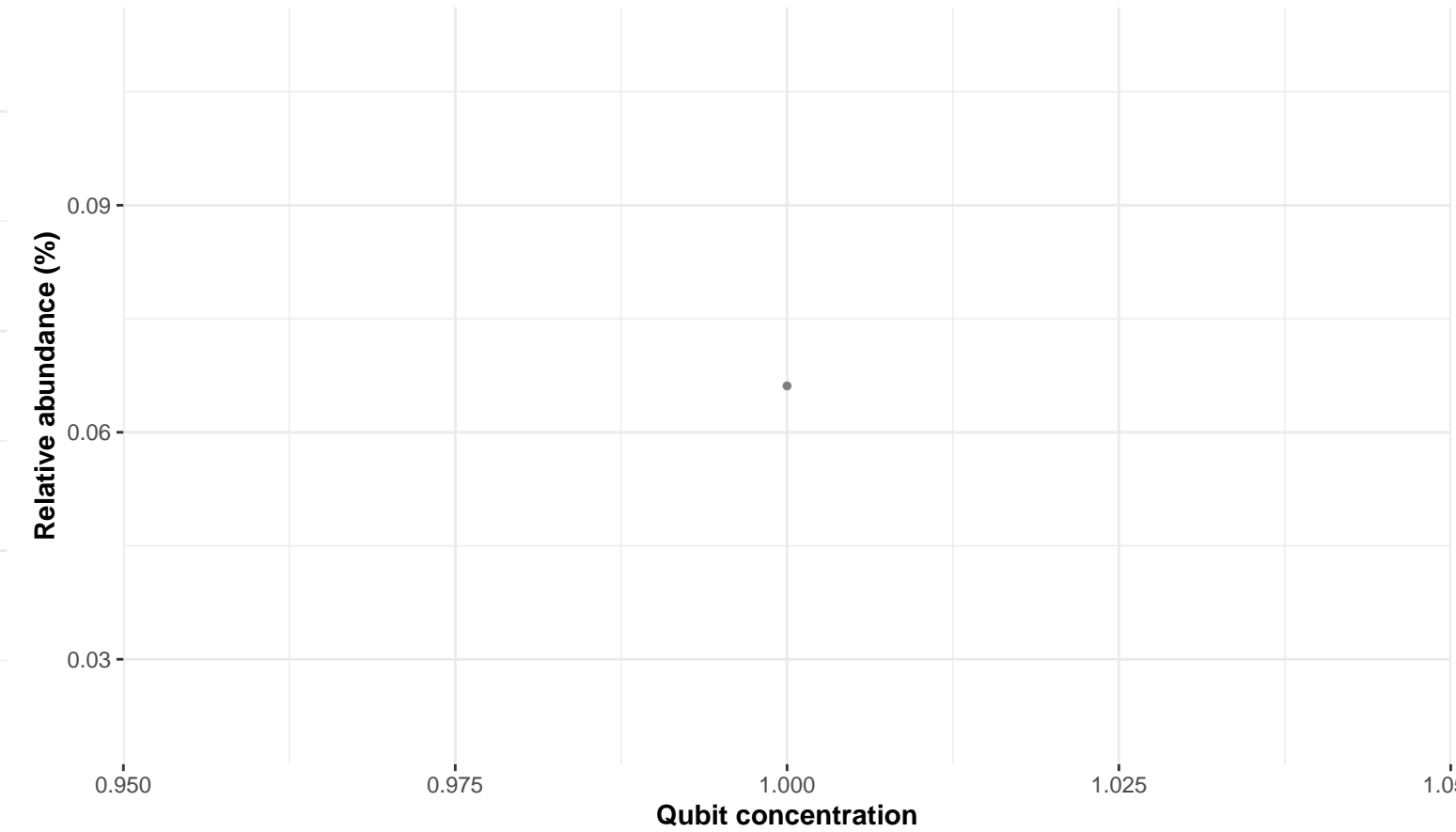


Correlation within: Digesta

$\log_e(S) = 4.190$, $p = 0.610$, $\hat{\rho}_{\text{Spearman}} = 0.214$, $\text{CI}_{95\%} [-0.595, 0.808]$, $n_{\text{pairs}} = 8$



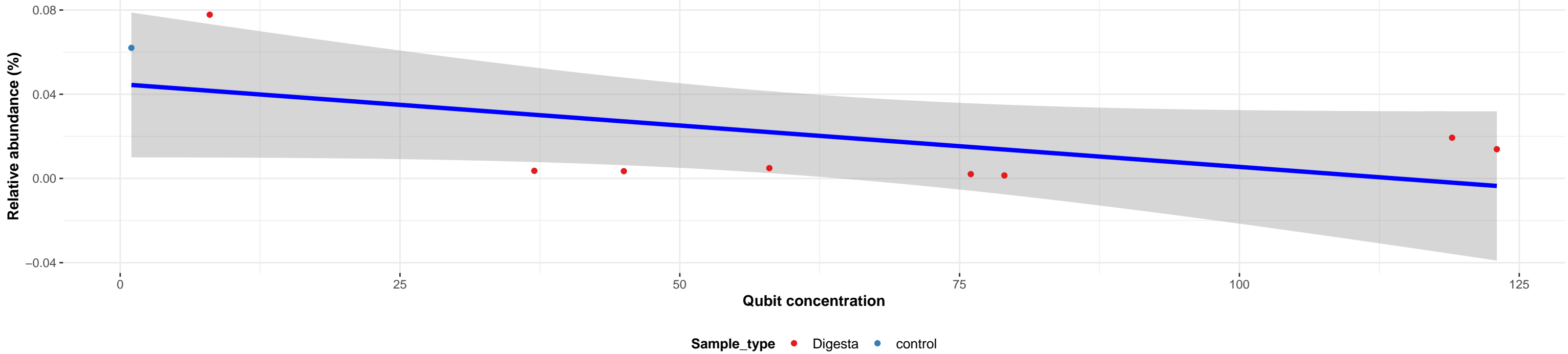
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Adlerbacteria; NA; NA; NA

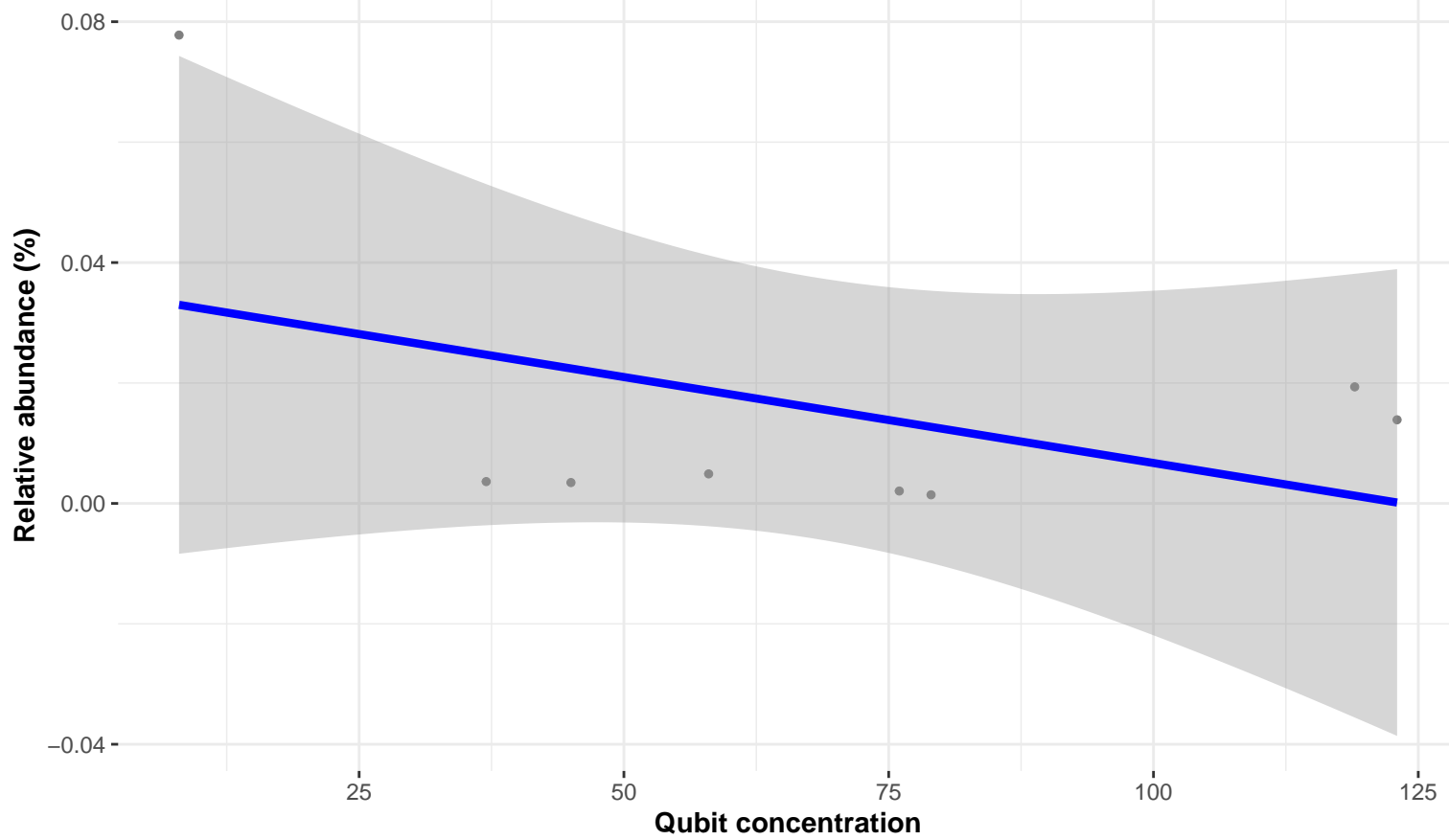
Correlation with all samples

$\log_e(S) = 5.088$, $p = 0.356$, $\hat{\rho}_{\text{Spearman}} = -0.350$, $\text{CI}_{95\%} [-0.830, 0.429]$, $n_{\text{pairs}} = 9$

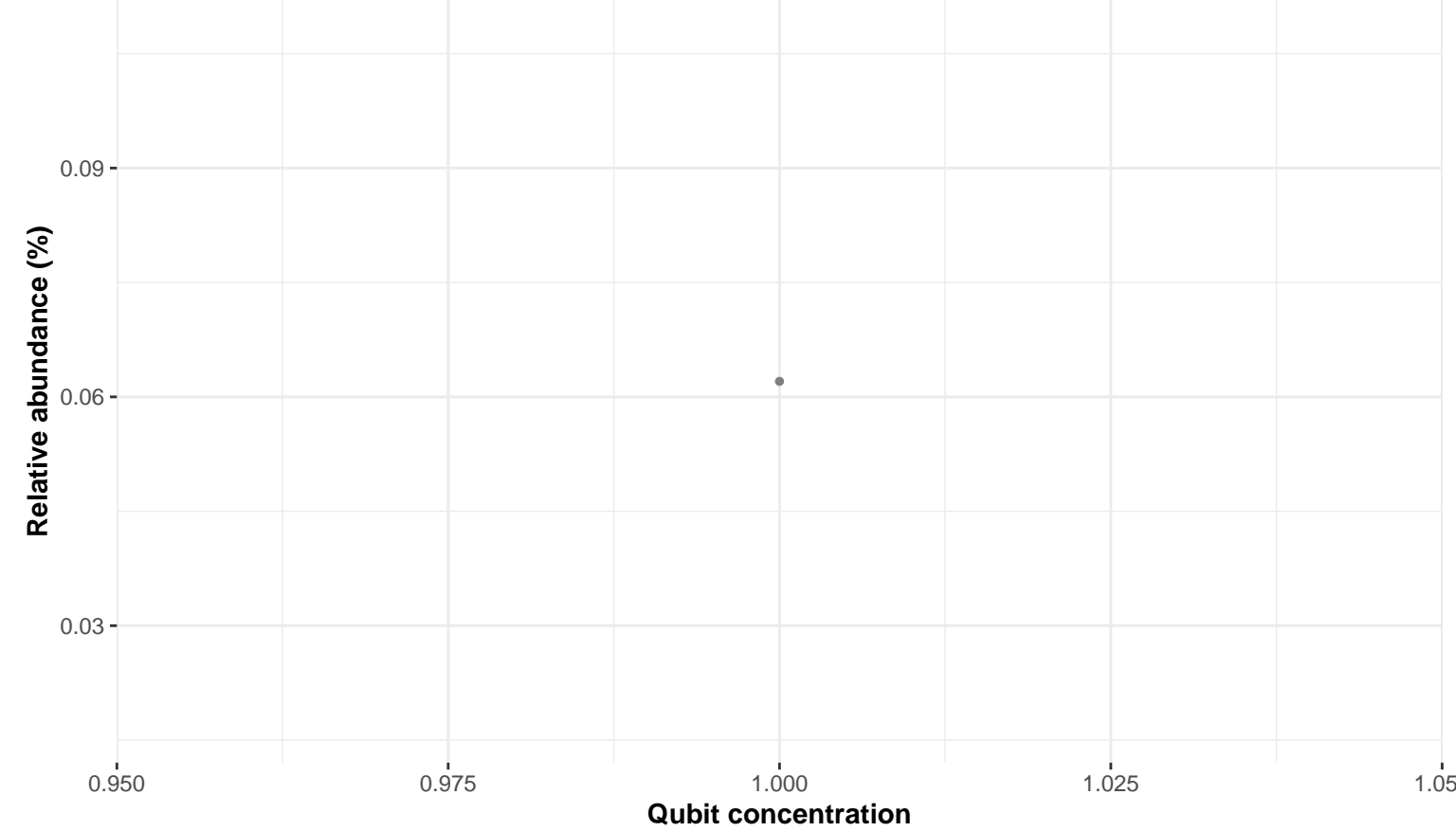


Correlation within: Digesta

$\log_e(S) = 4.522$, $p = 0.823$, $\hat{\rho}_{\text{Spearman}} = -0.095$, $\text{CI}_{95\%} [-0.761, 0.668]$, $n_{\text{pairs}} = 8$



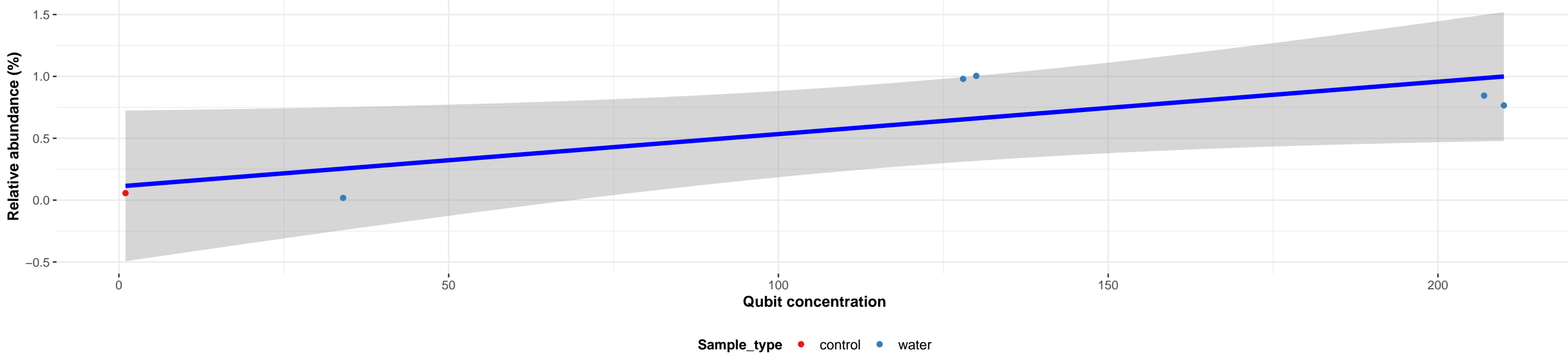
Correlation within: control



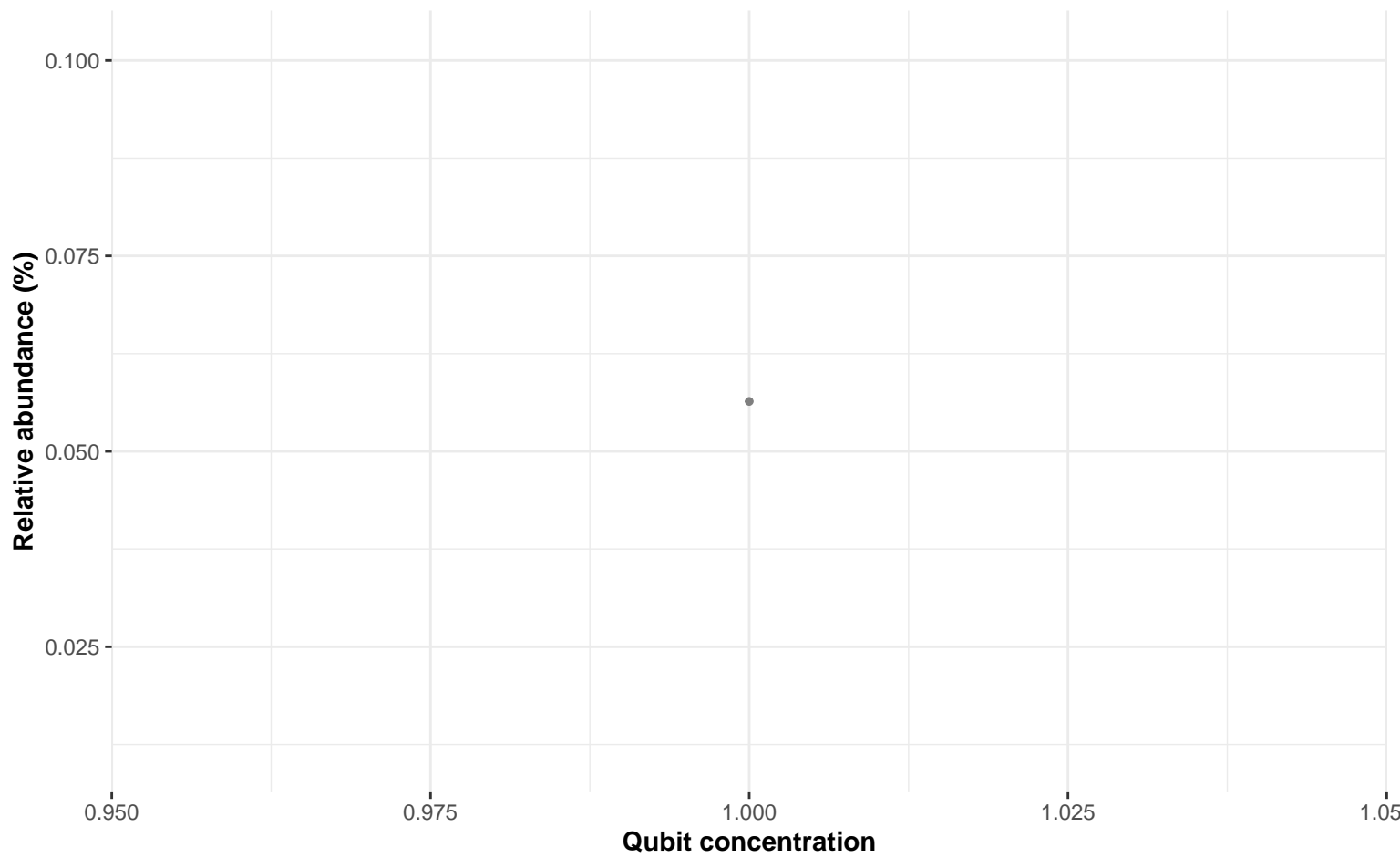
Bacteria; Bacteroidota; Bacteroidia; Chitinophagales; Saprospiraceae; Lewinella; NA

Correlation with all samples

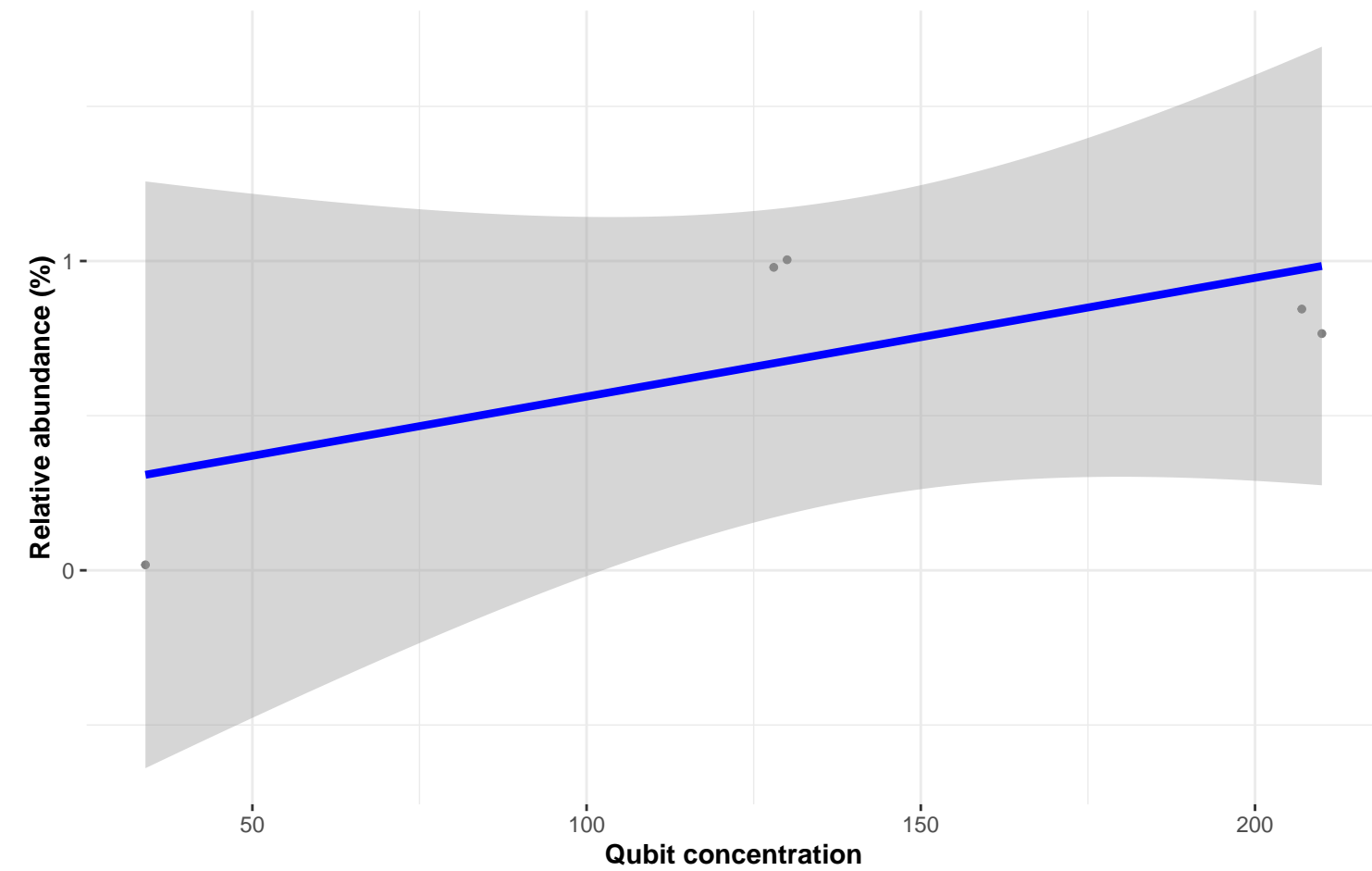
$\log_e(S) = 2.996$, $p = 0.397$, $\hat{\rho}_{\text{Spearman}} = 0.429$, $CI_{95\%} [-0.609, 0.925]$, $n_{\text{pairs}} = 6$



Correlation within: control



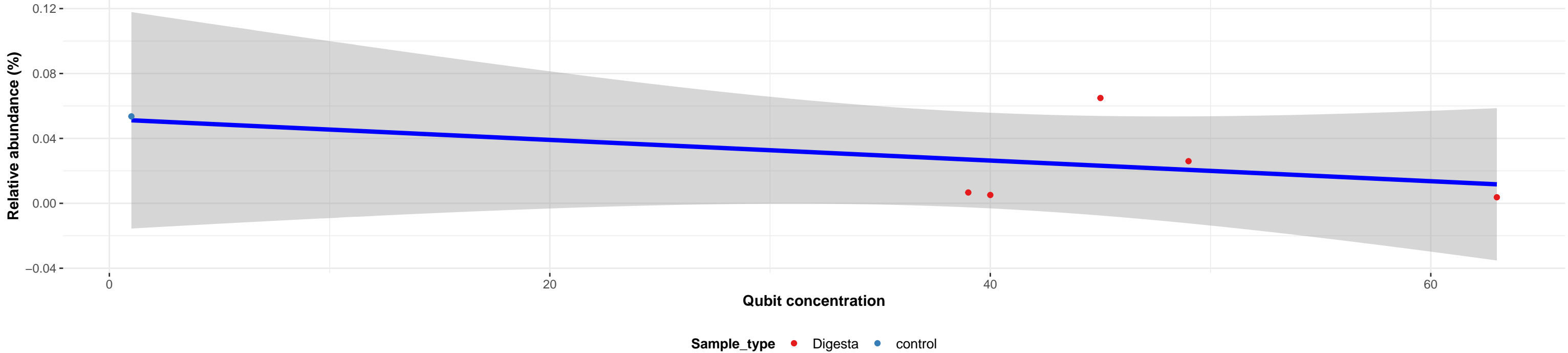
Correlation within: water



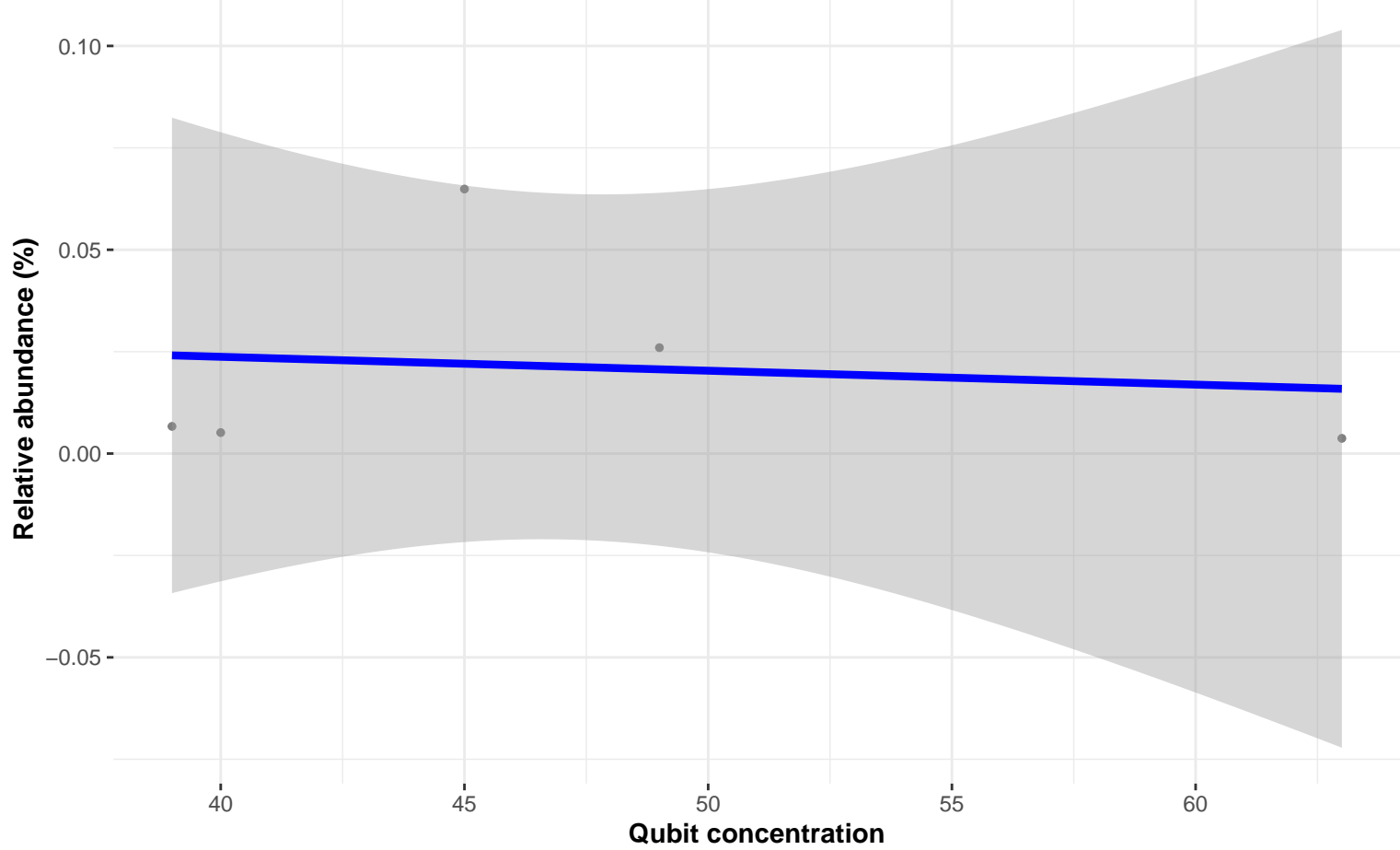
Bacteria; Proteobacteria; Gammaproteobacteria; Burkholderiales; Comamonadaceae; Comamonas; odontotermitis

Correlation with all samples

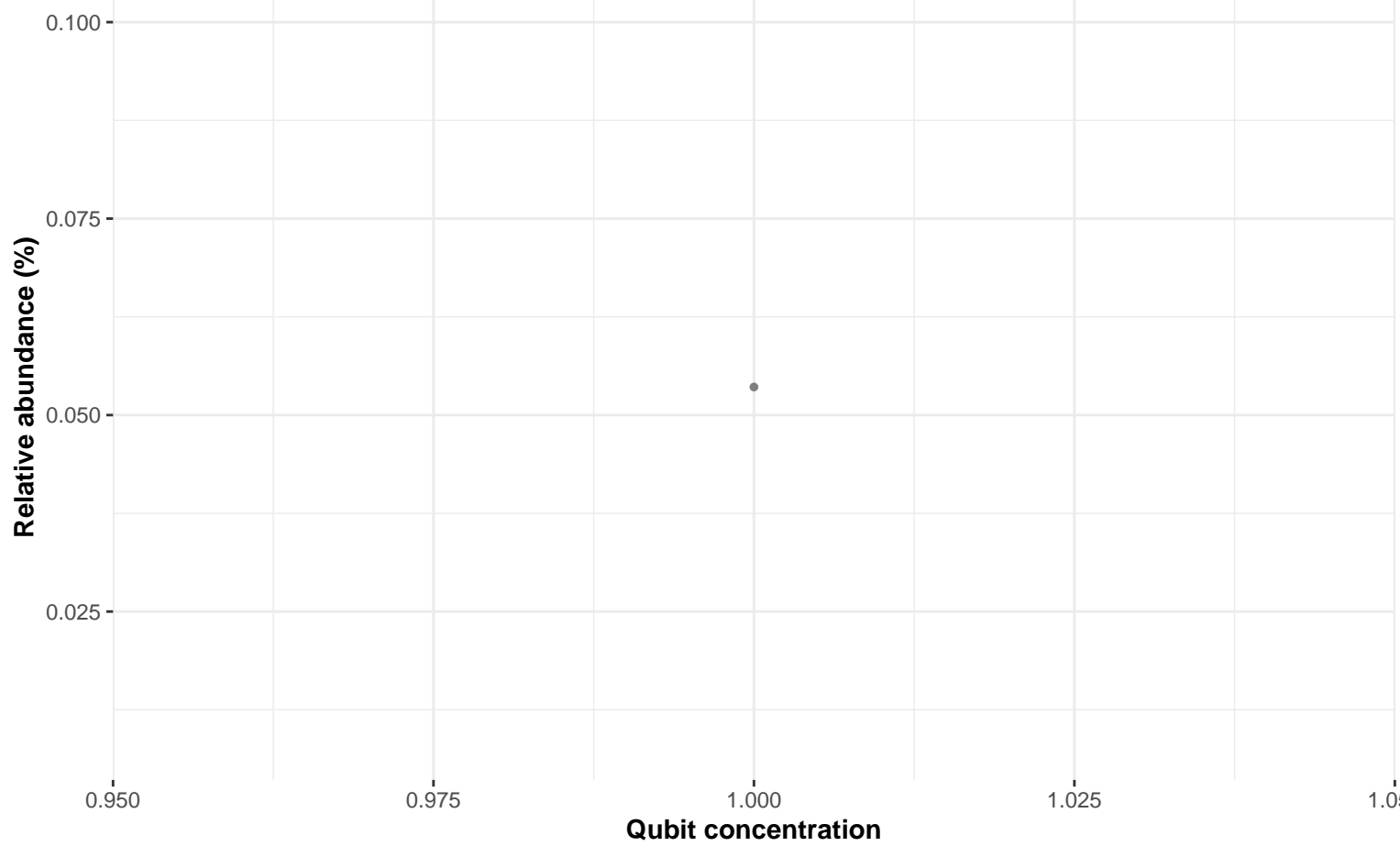
$\log_e(S) = 3.871$, $p = 0.468$, $\hat{\rho}_{\text{Spearman}} = -0.371$, $\text{CI}_{95\%} [-0.915, 0.650]$, $n_{\text{pairs}} = 6$



Correlation within: Digesta



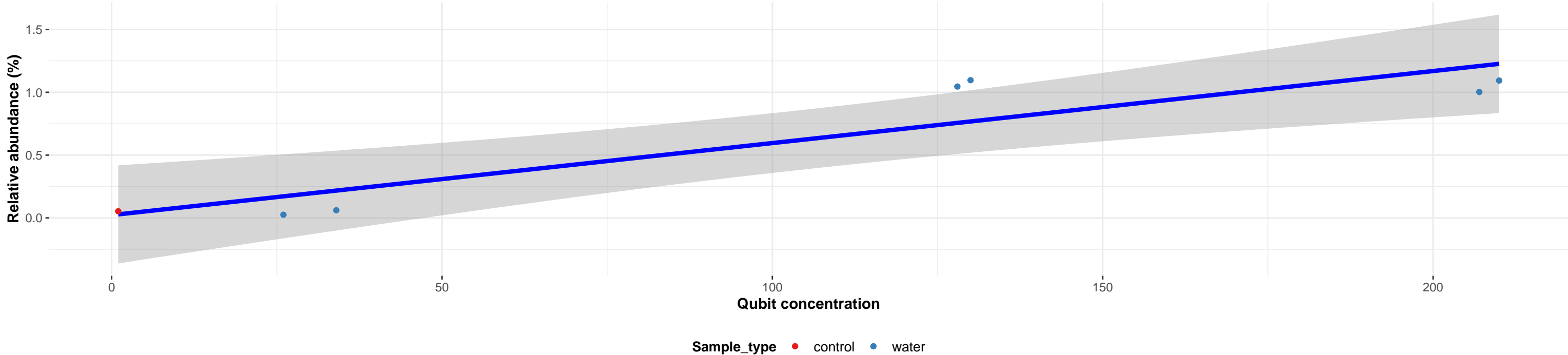
Correlation within: control



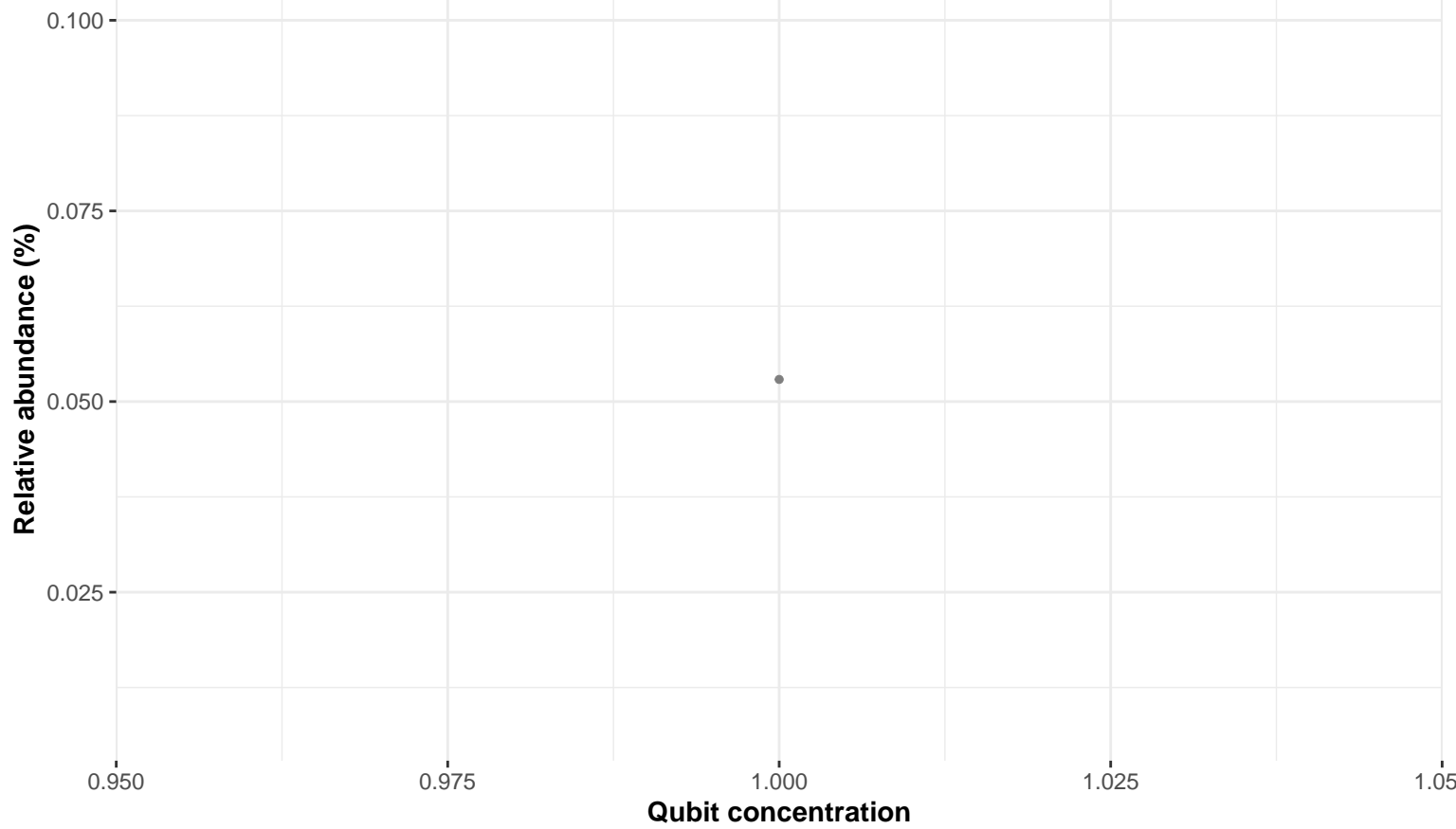
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Colwelliaceae; Colwellia; NA

Correlation with all samples

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

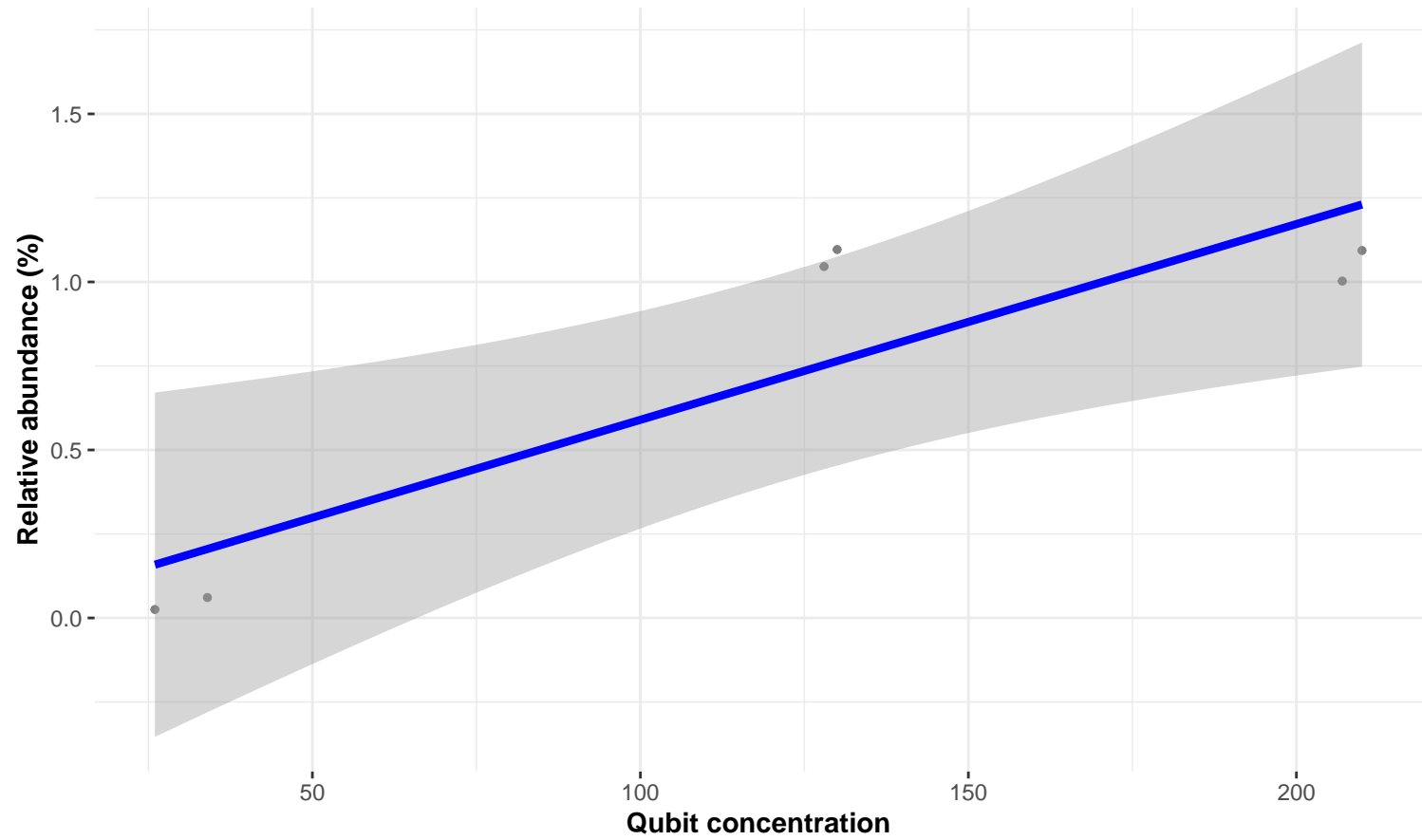


Correlation within: control



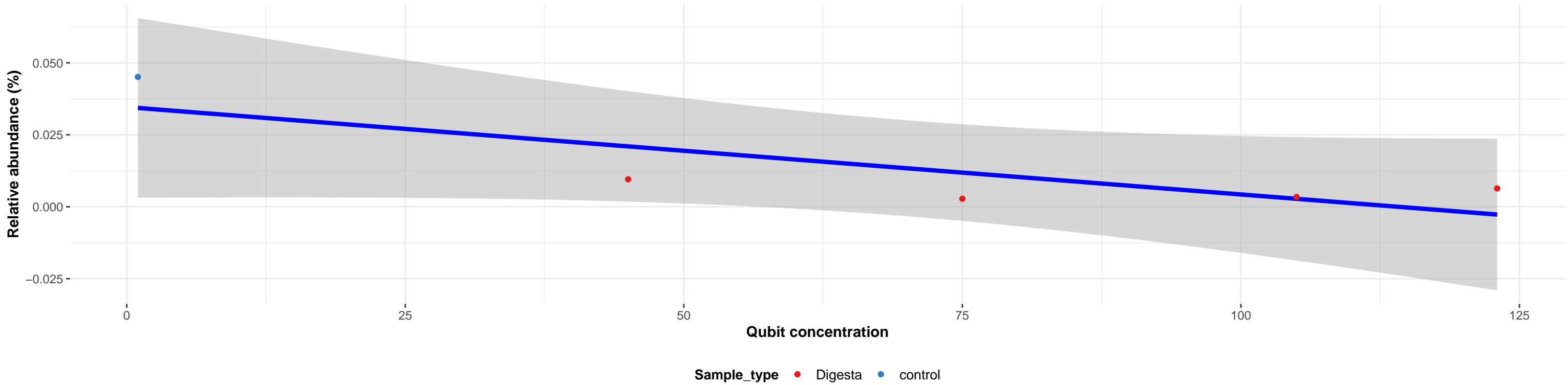
Correlation within: water

$\log_e(S) = 2.303$, $p = 0.111$, $\hat{\rho}_{\text{Spearman}} = 0.714$, $CI_{95\%} [-0.263, 0.968]$, $n_{\text{pairs}} = 6$

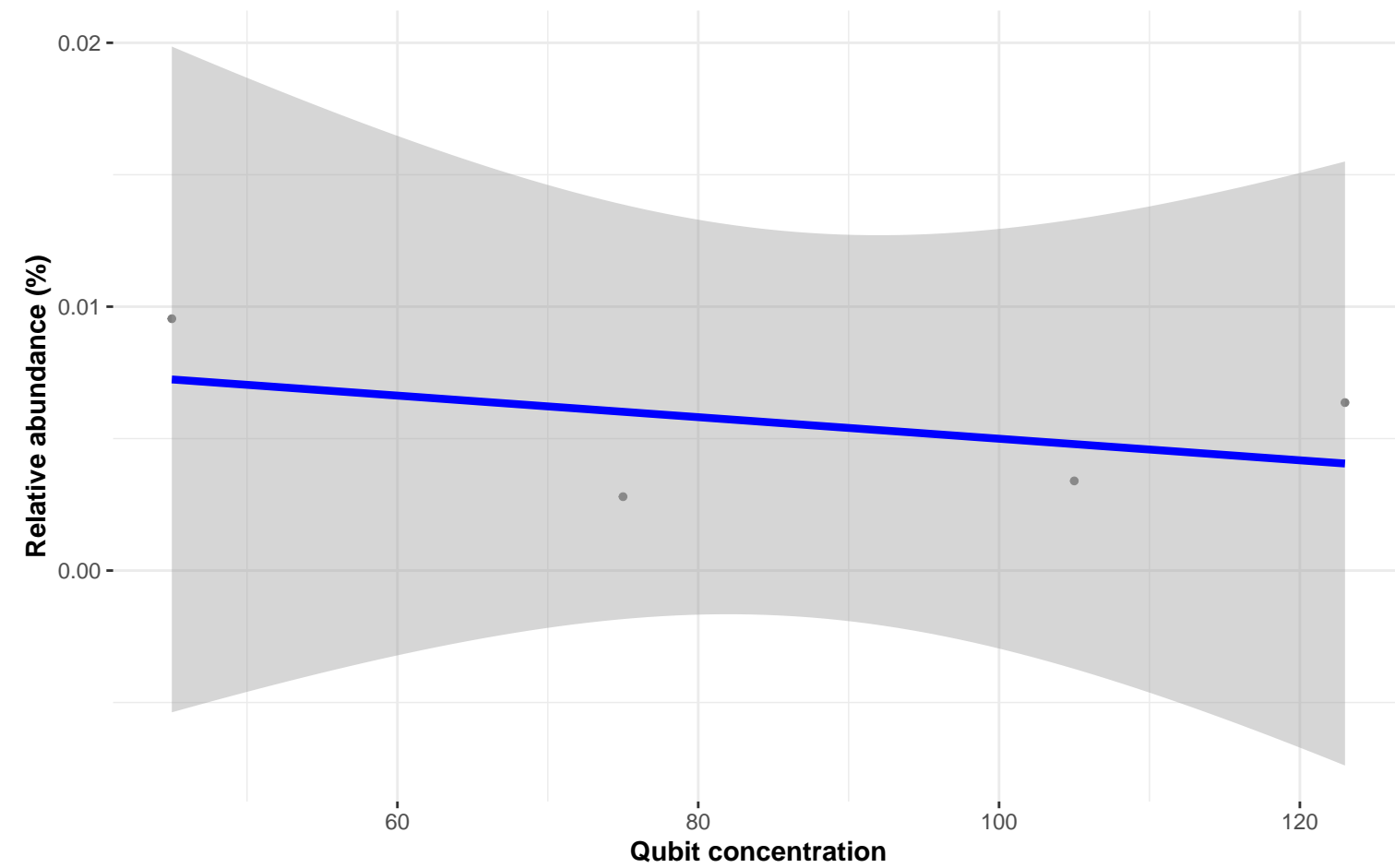


Bacteria; Patescibacteria; Gracilibacteria; NA; NA; NA; NA

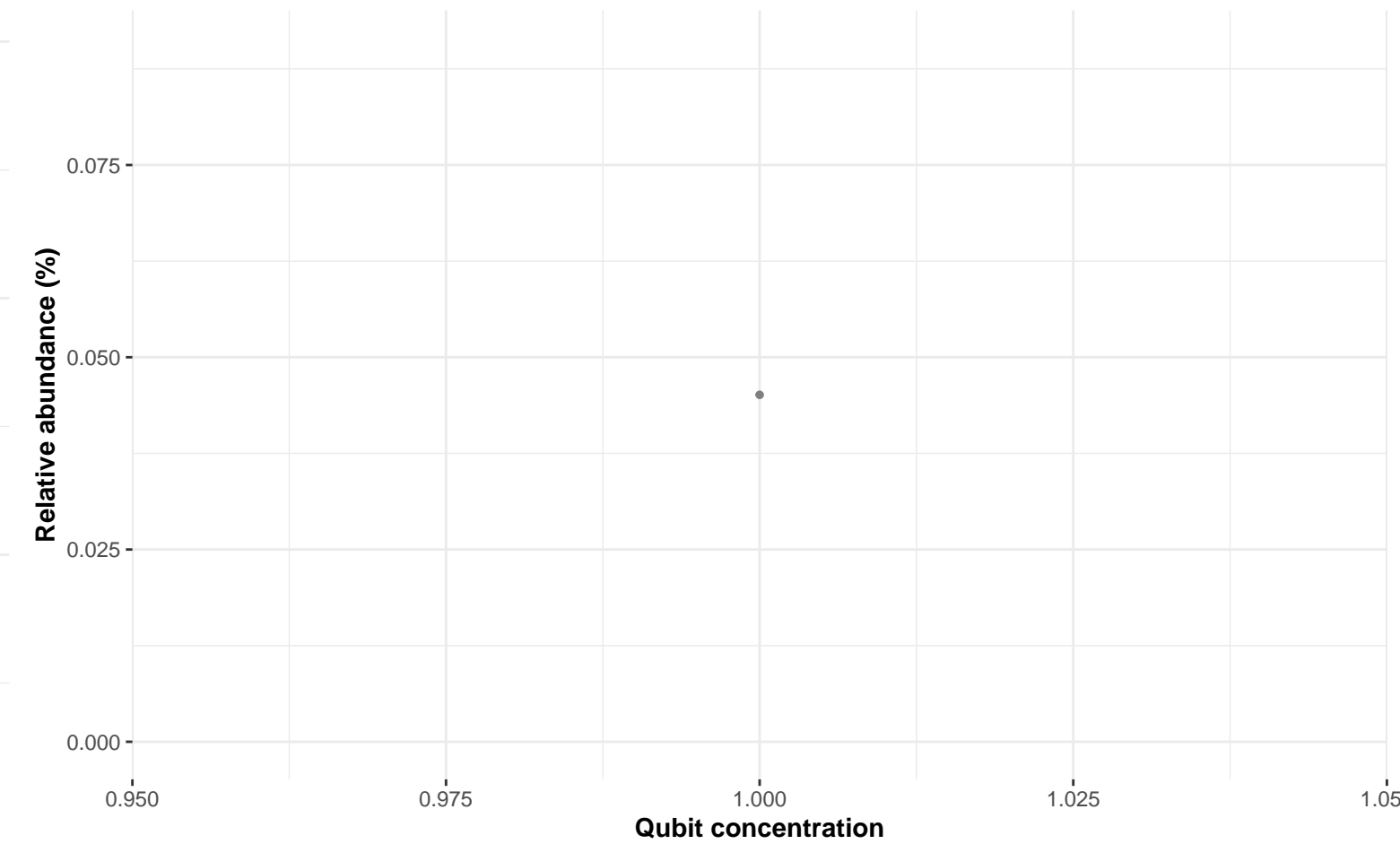
Correlation with all samples



Correlation within: Digesta



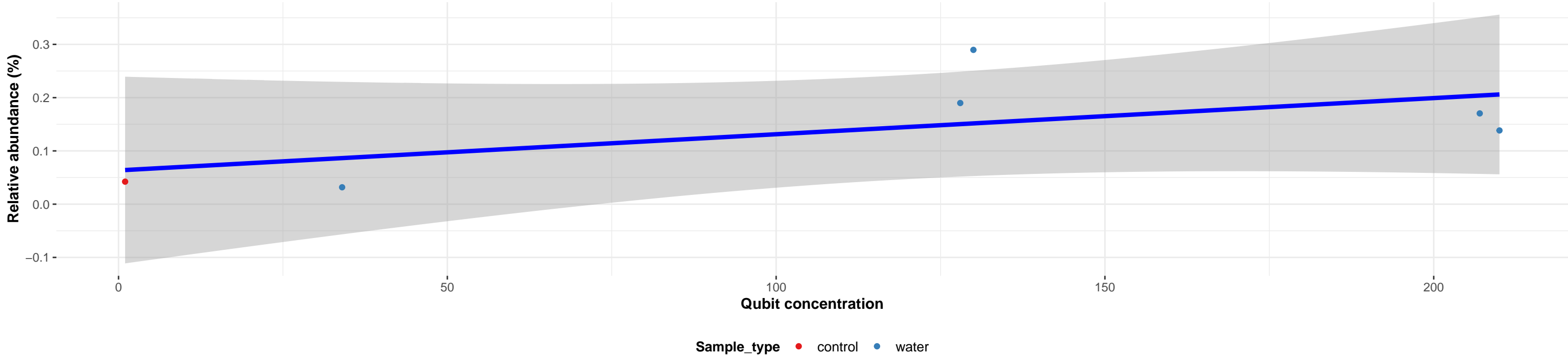
Correlation within: control



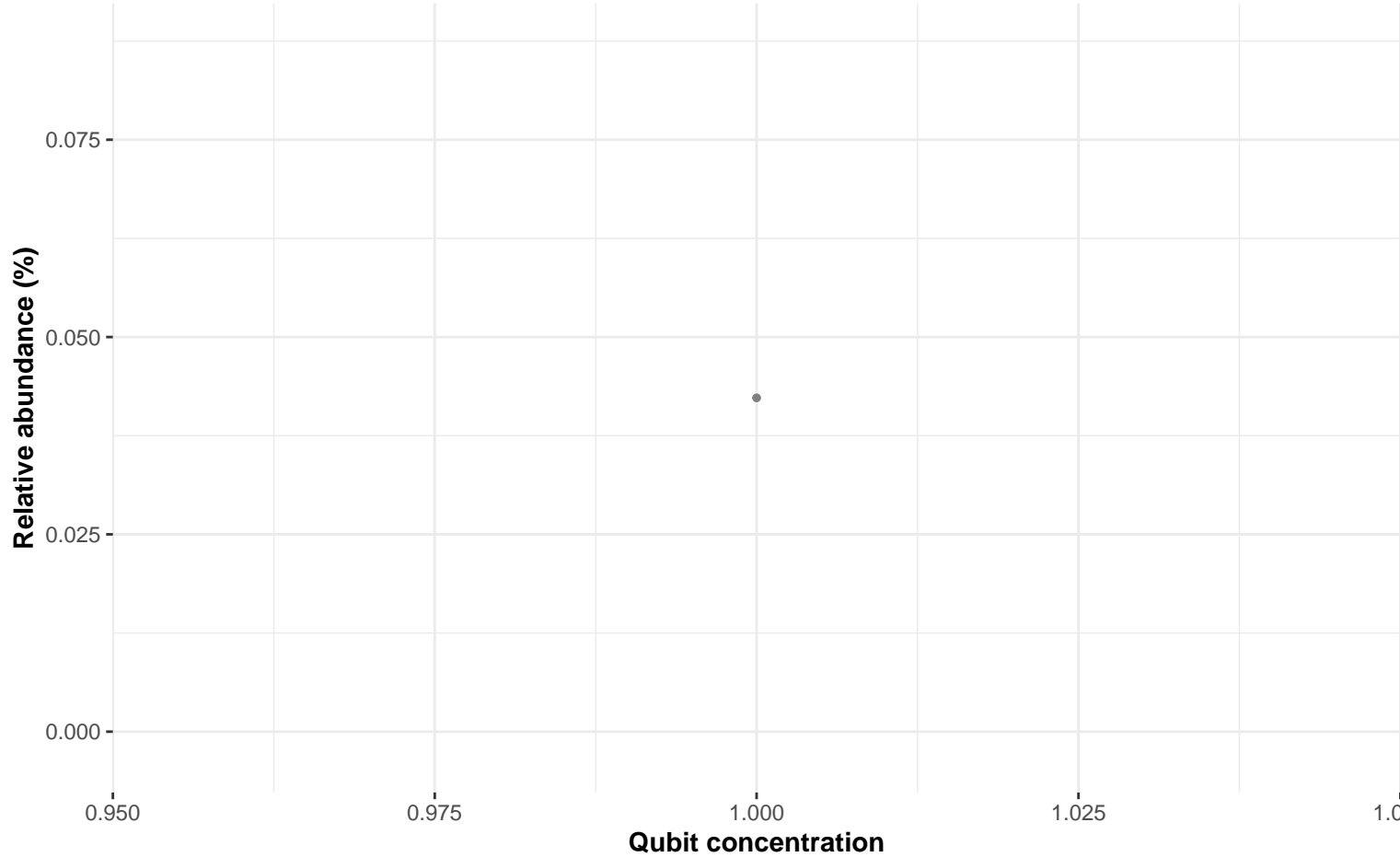
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Colwelliaceae; Colwellia; NA

Correlation with all samples

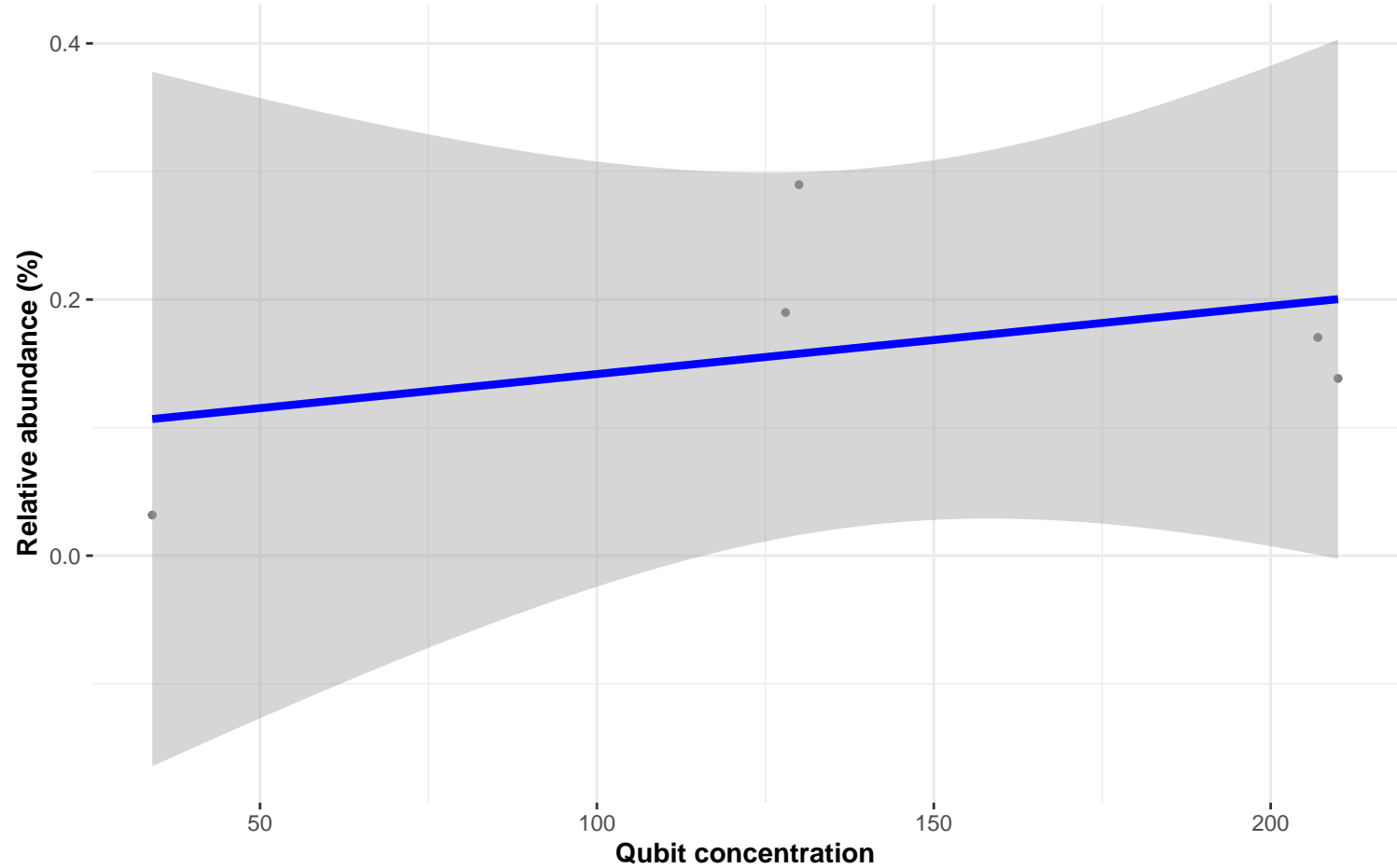
$\log_e(S) = 2.996$, $p = 0.397$, $\hat{\rho}_{\text{Spearman}} = 0.429$, $CI_{95\%} [-0.609, 0.925]$, $n_{\text{pairs}} = 6$



Correlation within: control



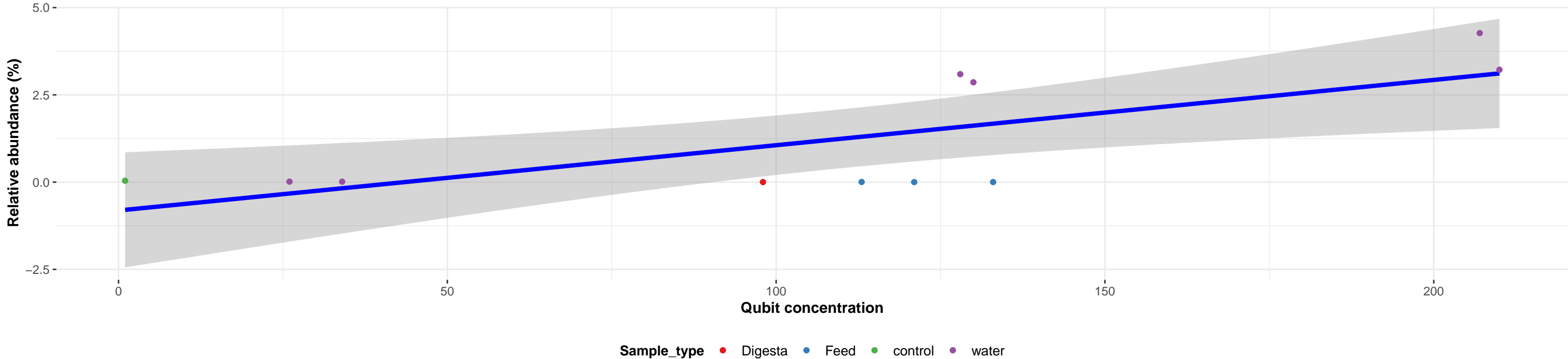
Correlation within: water



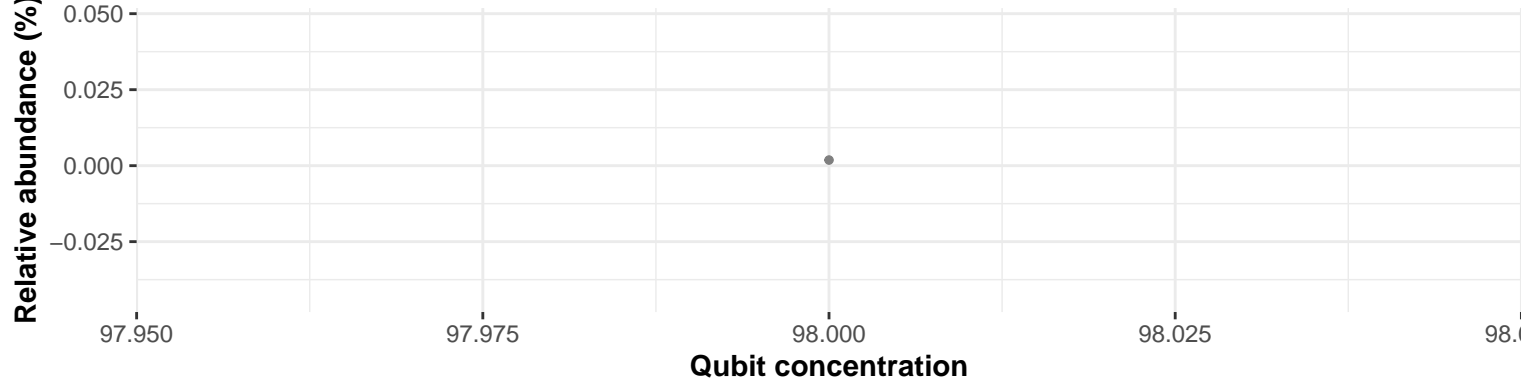
Bacteria; Bacteroidota; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Lacinutrix; NA

Correlation with all samples

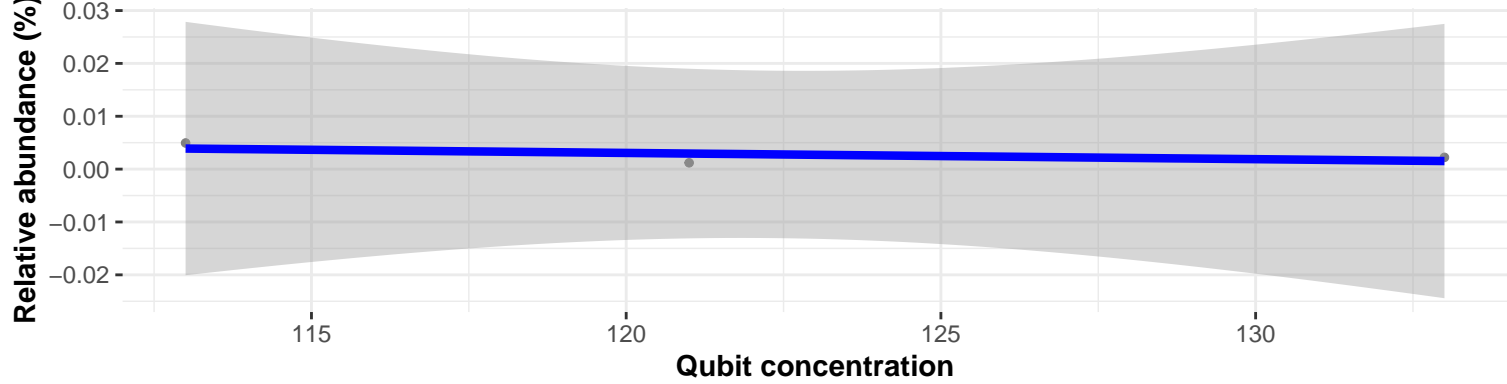
$\log_e(S) = 4.852$, $p = 0.201$, $\hat{\rho}_{\text{Spearman}} = 0.418$, $\text{CI}_{95\%} [-0.262, 0.821]$, $n_{\text{pairs}} = 11$



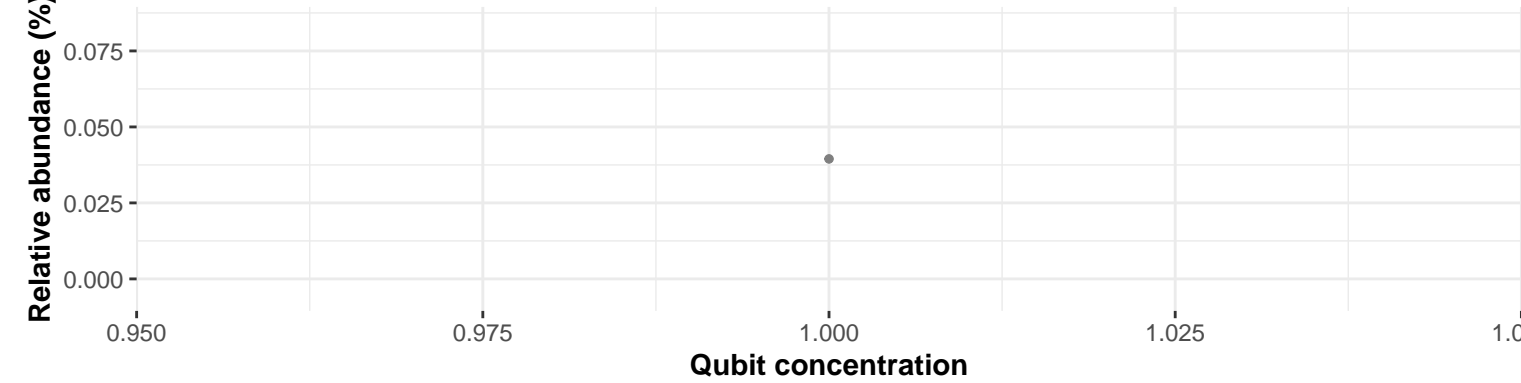
Correlation within: Digesta



Correlation within: Feed

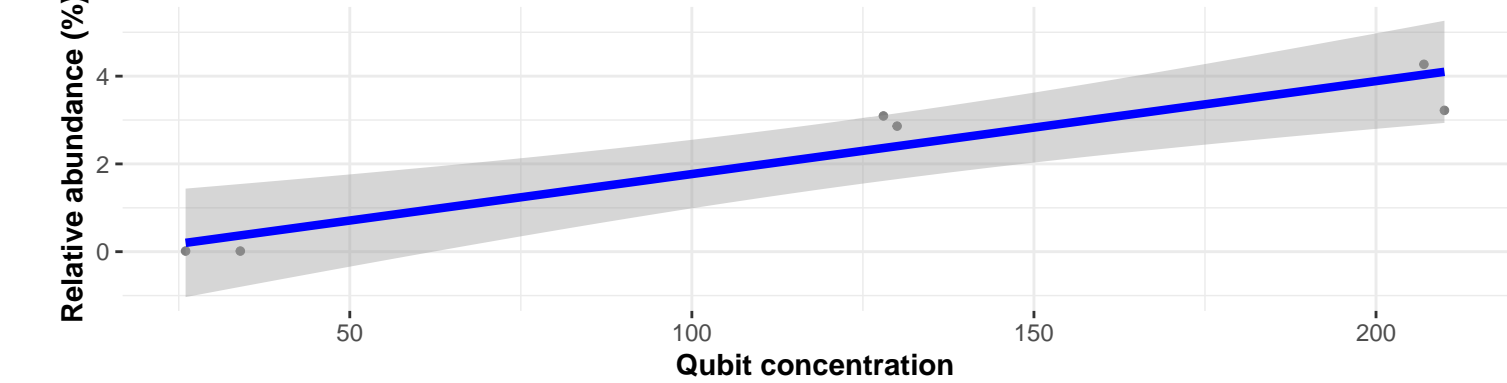


Correlation within: control



Correlation within: water

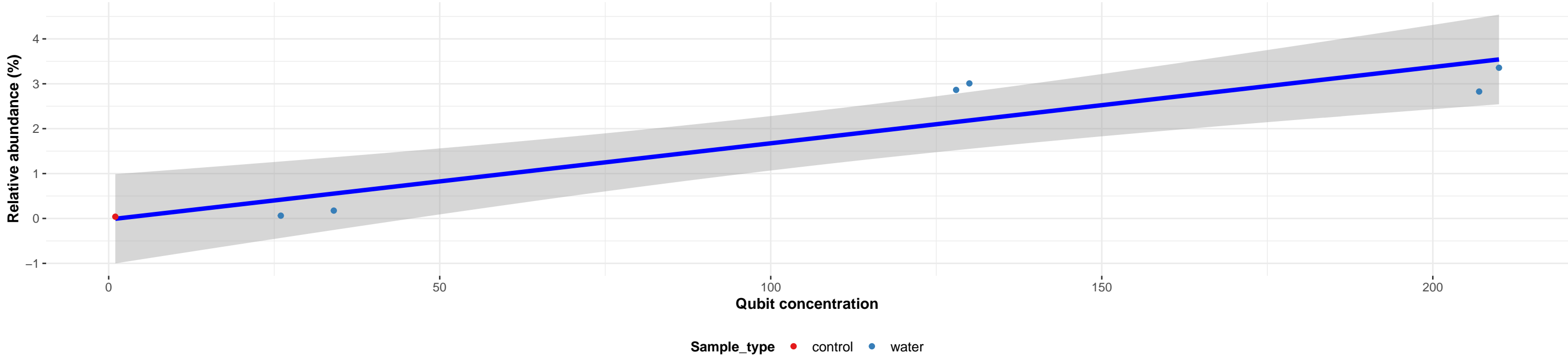
$\log_e(S) = 1.792$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.829$, $\text{CI}_{95\%} [0.019, 0.982]$, $n_{\text{pairs}} = 6$



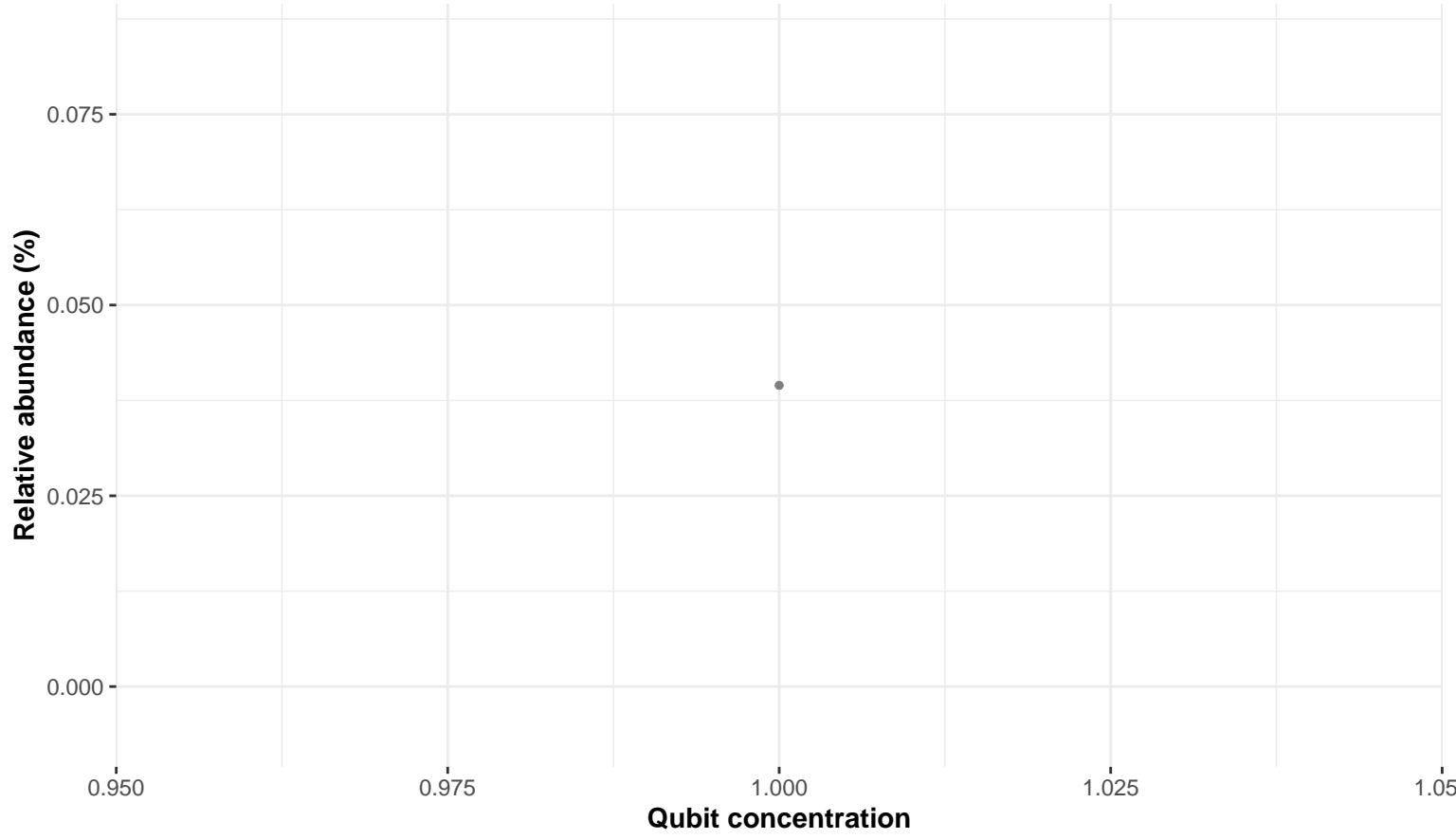
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Colwelliaceae; Colwellia; polaris

Correlation with all samples

$\log_e(S) = 1.792$, $p = 0.007$, $\hat{\rho}_{\text{Spearman}} = 0.893$, $CI_{95\%} [0.403, 0.985]$, $n_{\text{pairs}} = 7$

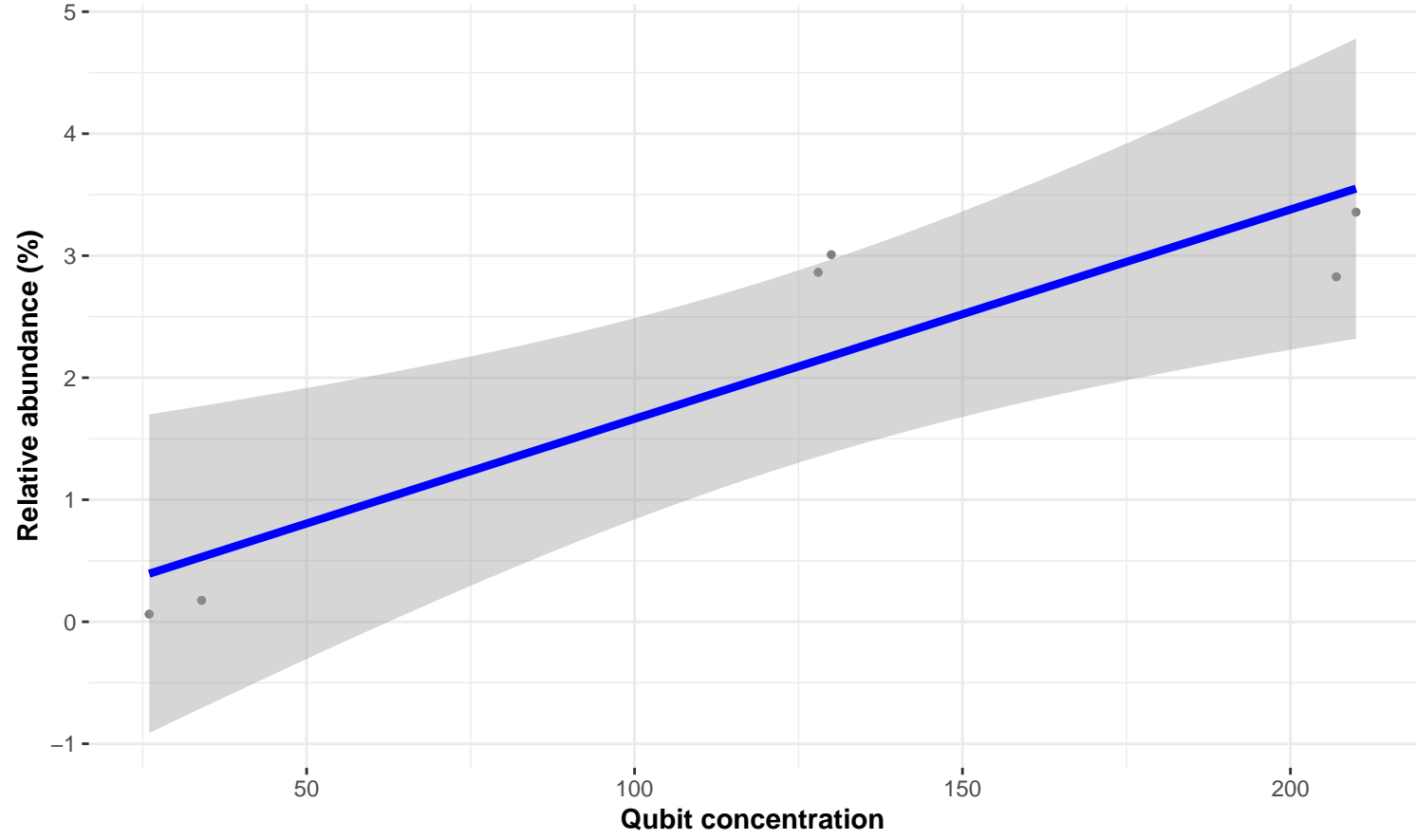


Correlation within: control



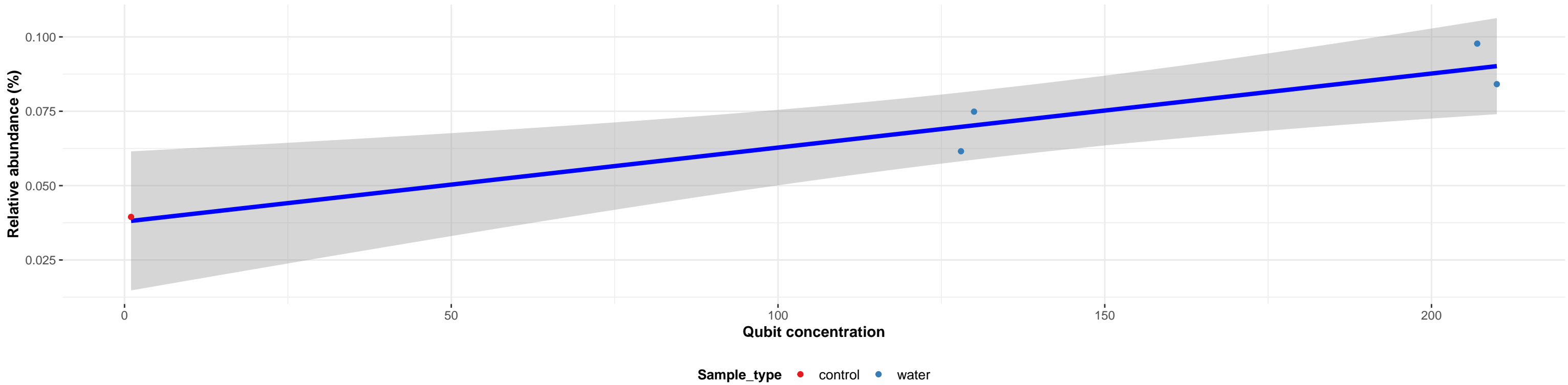
Correlation within: water

$\log_e(S) = 1.792$, $p = 0.042$, $\hat{\rho}_{\text{Spearman}} = 0.829$, $CI_{95\%} [0.019, 0.982]$, $n_{\text{pairs}} = 6$

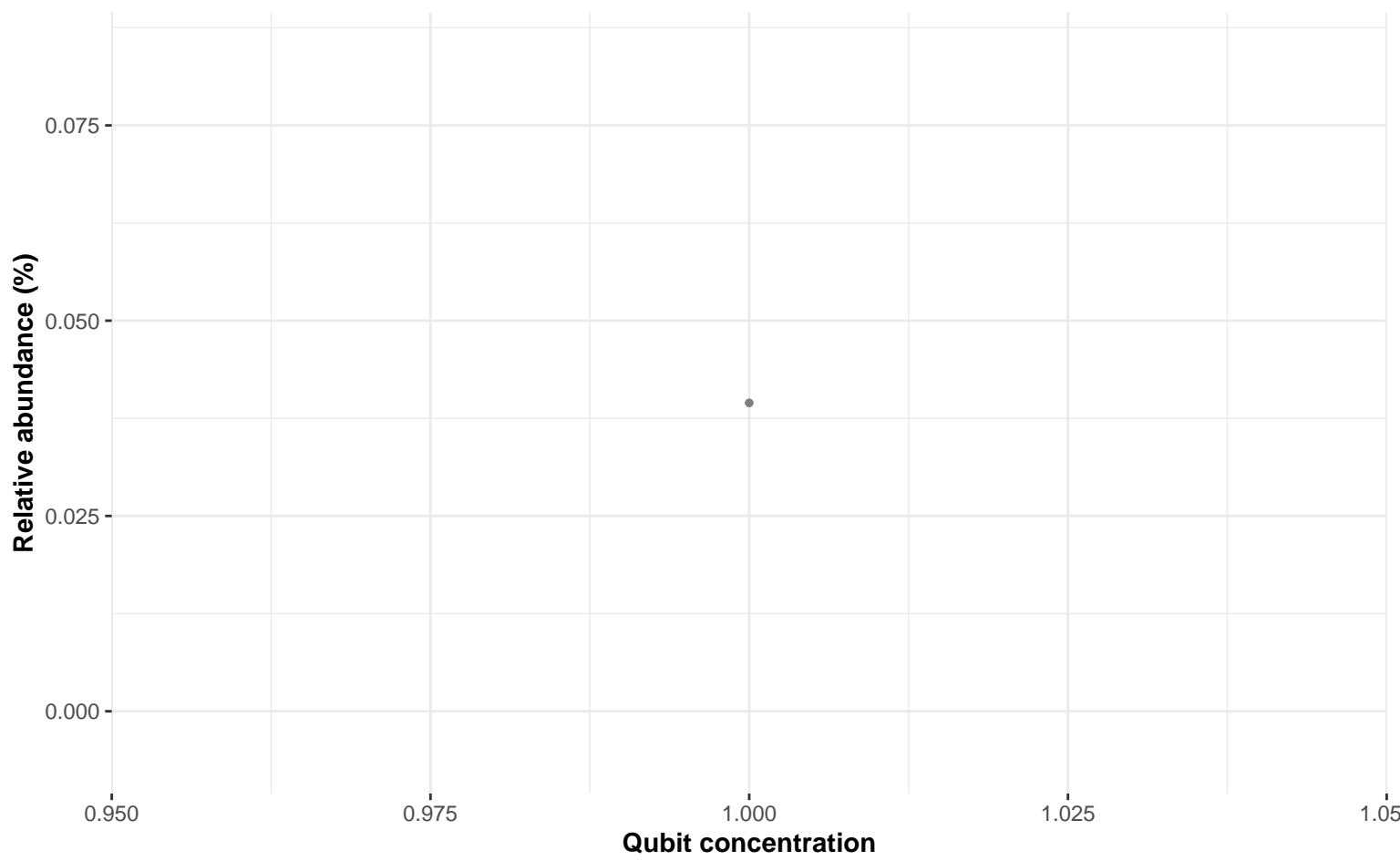


Bacteria; Desulfobacterota; Desulfuromonadia; PB19; NA; NA; NA

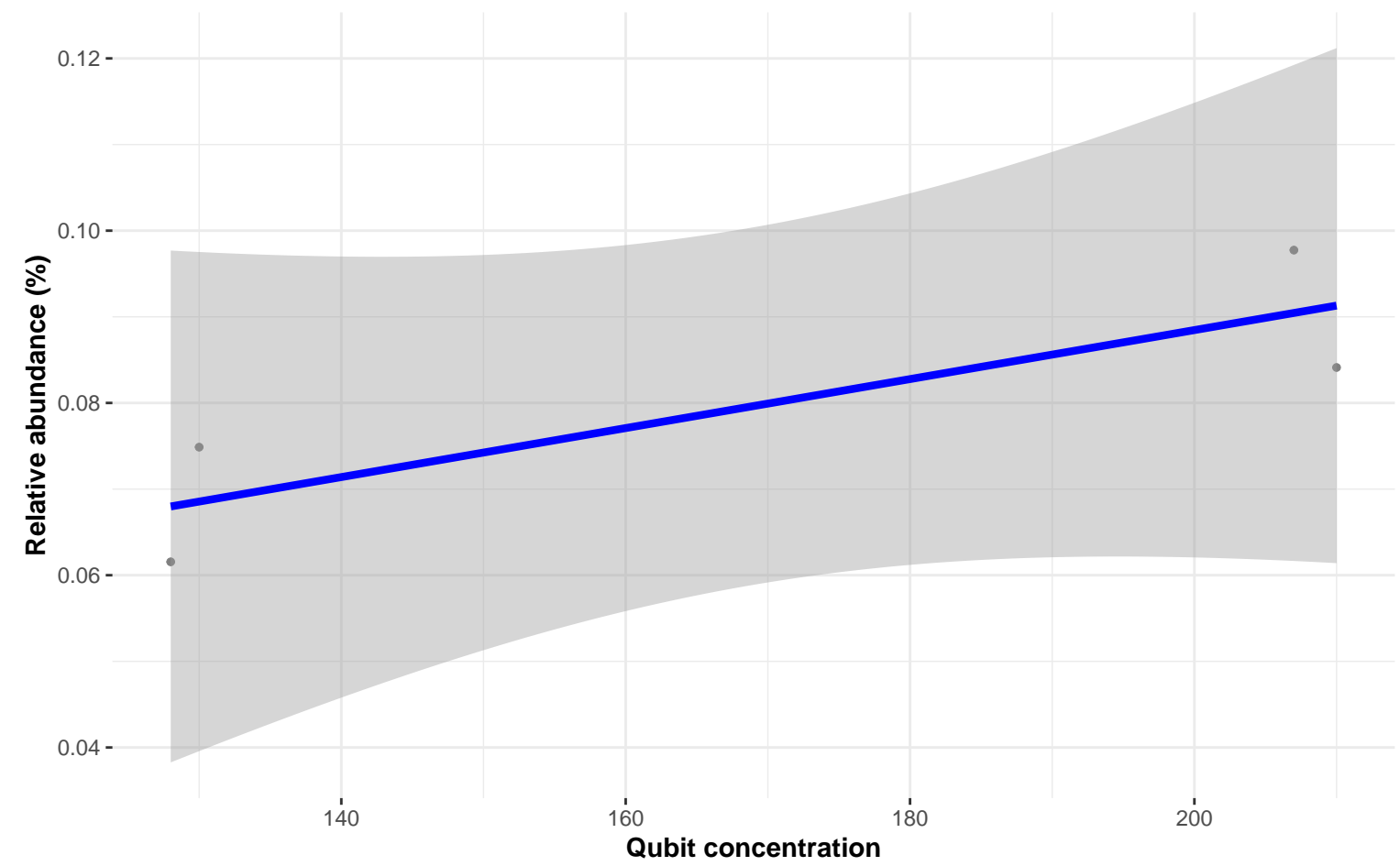
Correlation with all samples



Correlation within: control



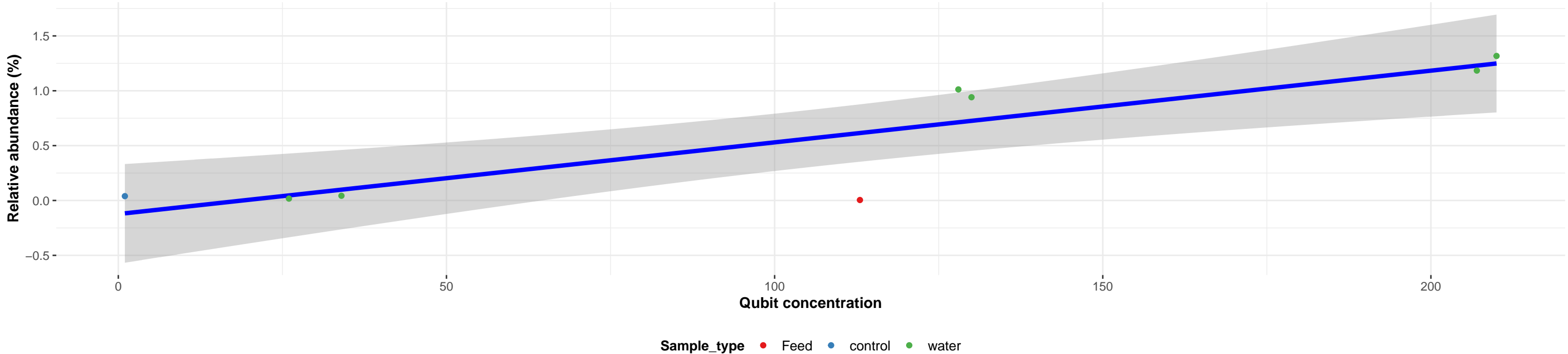
Correlation within: water



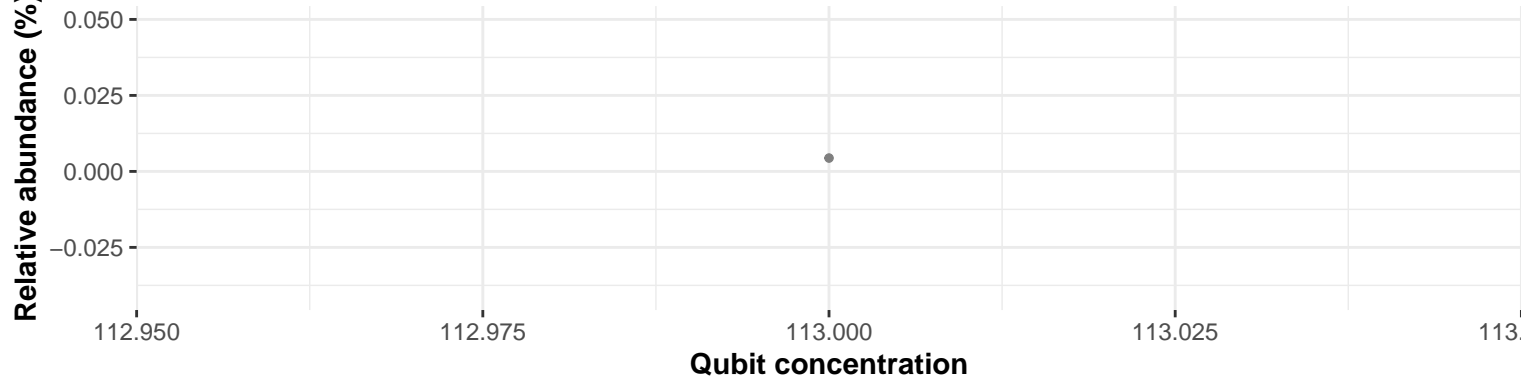
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Yoonia–Loktanella; NA

Correlation with all samples

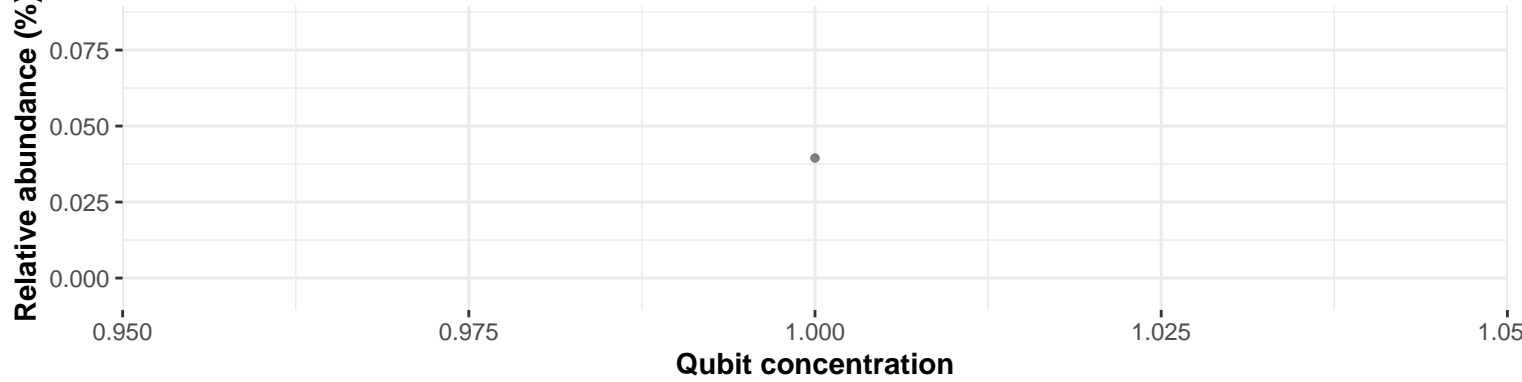
$\log_e(S) = 2.773$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = 0.810$, $\text{CI}_{95\%} [0.220, 0.966]$, $n_{\text{pairs}} = 8$



Correlation within: Feed

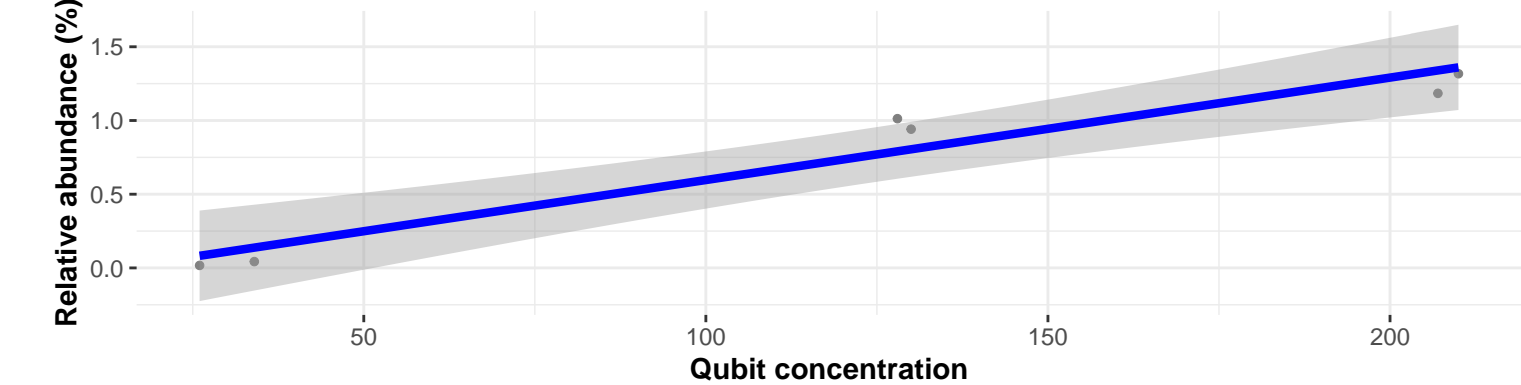


Correlation within: control



Correlation within: water

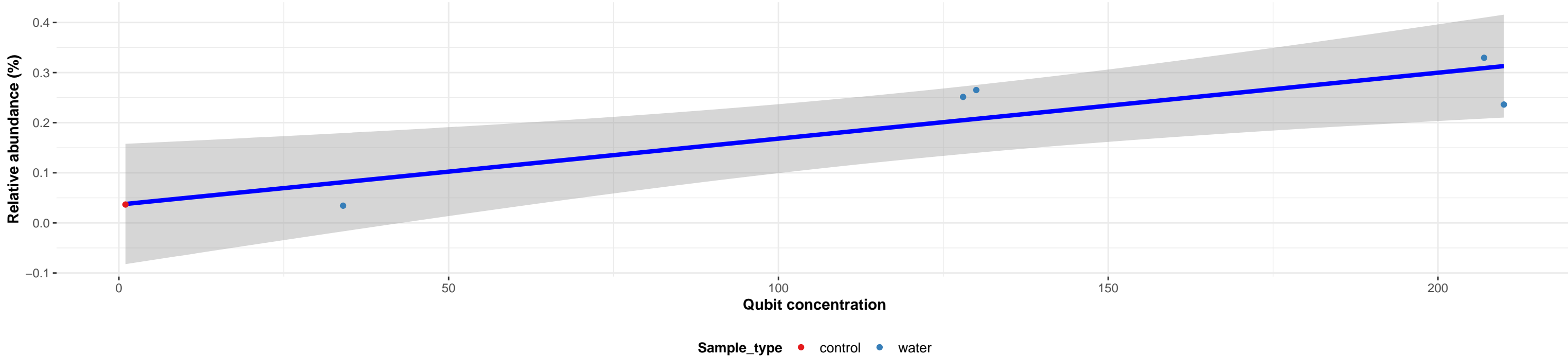
$\log_e(S) = 0.693$, $p = 0.005$, $\hat{\rho}_{\text{Spearman}} = 0.943$, $\text{CI}_{95\%} [0.536, 0.994]$, $n_{\text{pairs}} = 6$



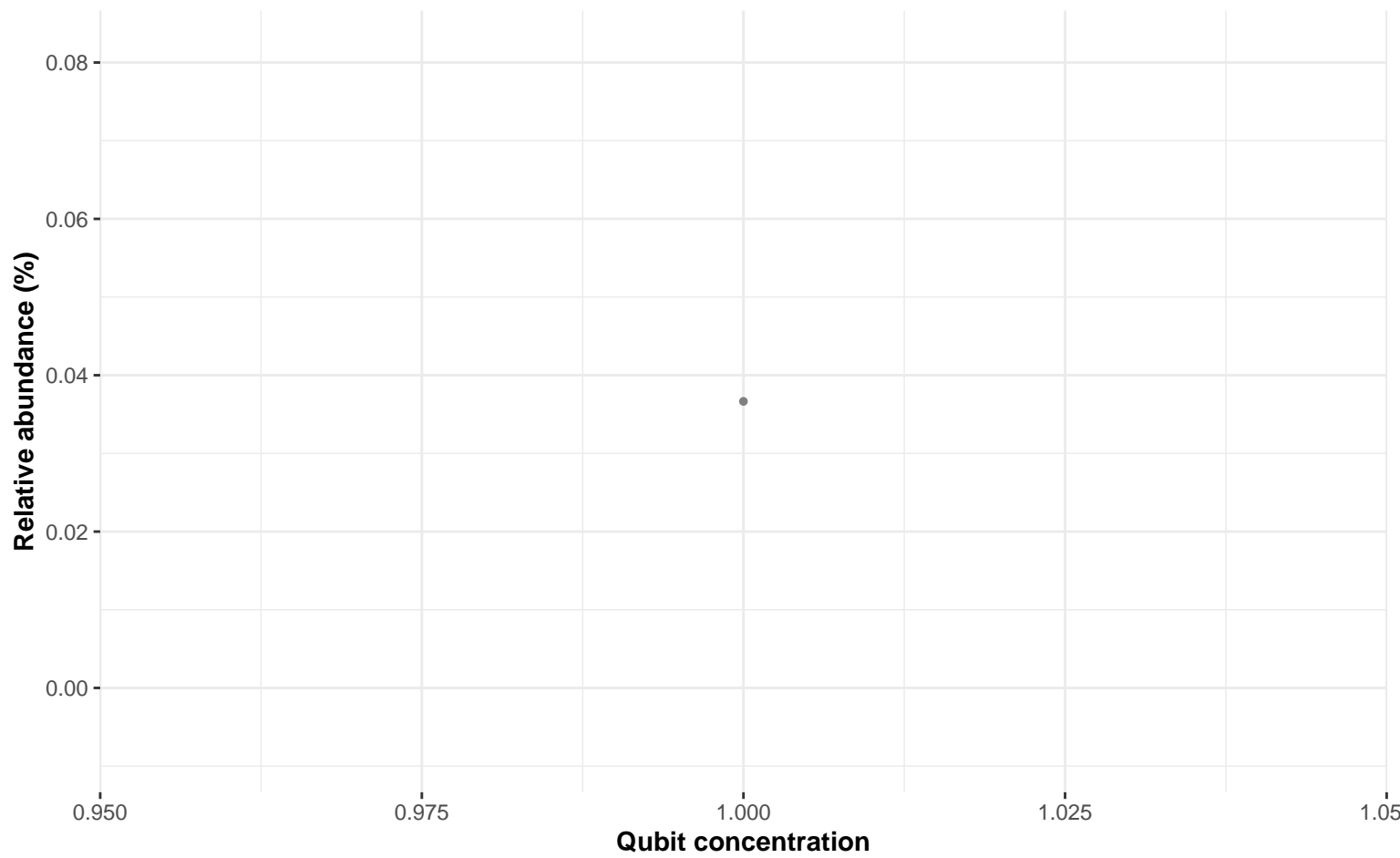
Bacteria; Bacteroidota; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Jejudonia; NA

Correlation with all samples

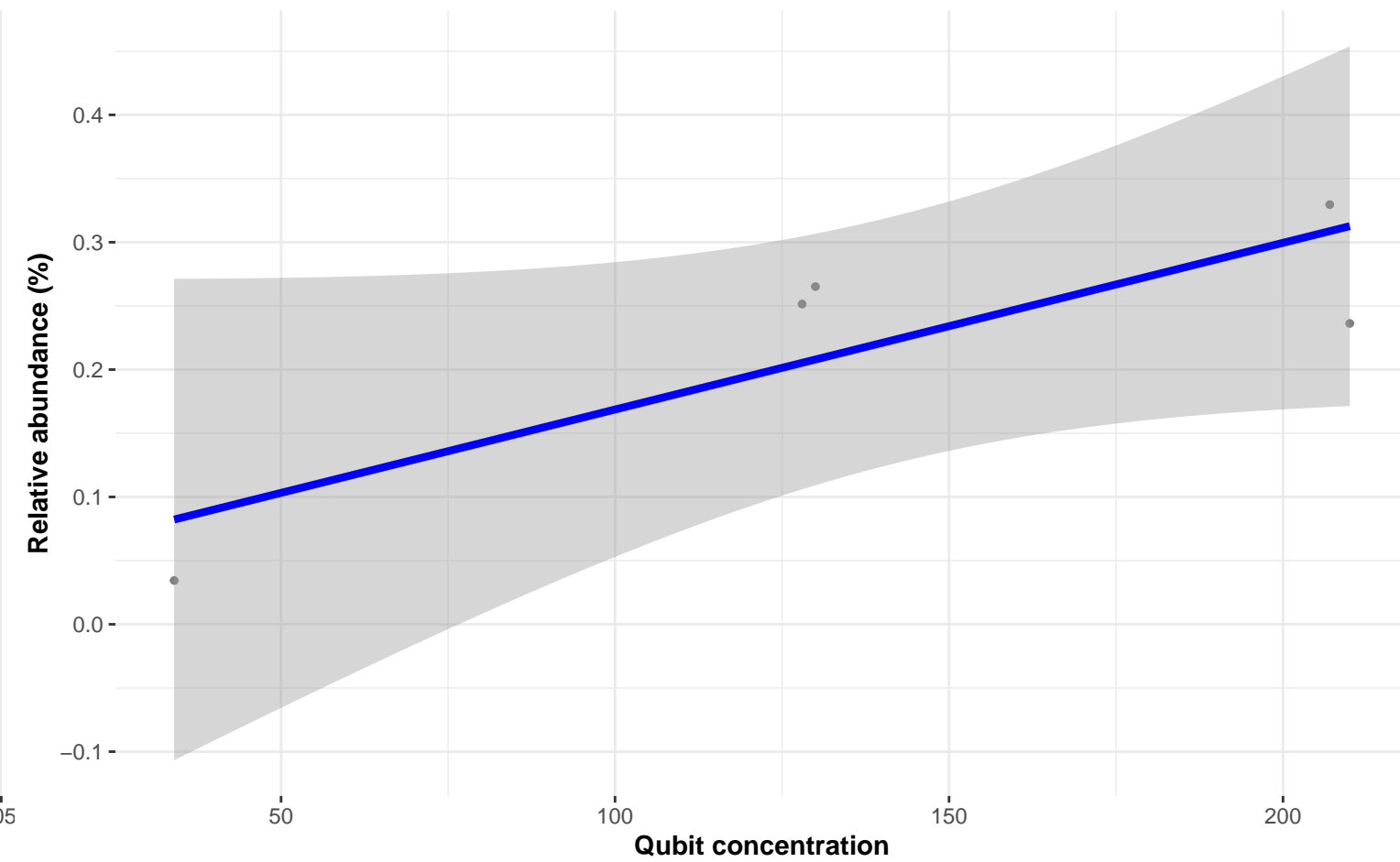
$\log_e(S) = 2.639$, $p = 0.208$, $\hat{\rho}_{\text{Spearman}} = 0.600$, $CI_{95\%} [-0.440, 0.953]$, $n_{\text{pairs}} = 6$



Correlation within: control



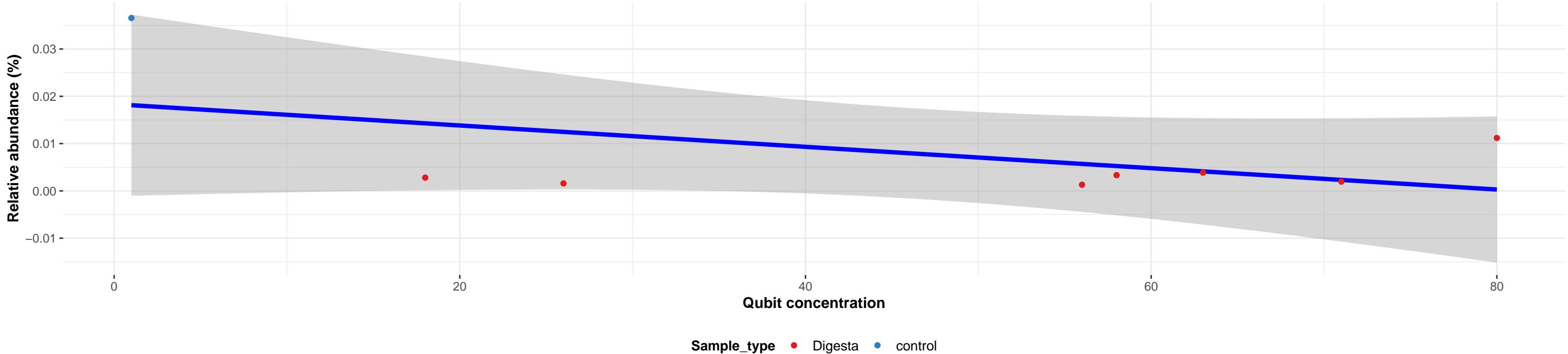
Correlation within: water



Bacteria; Patescibacteria; Parcubacteria; Candidatus Kaiserbacteria; NA; NA; NA

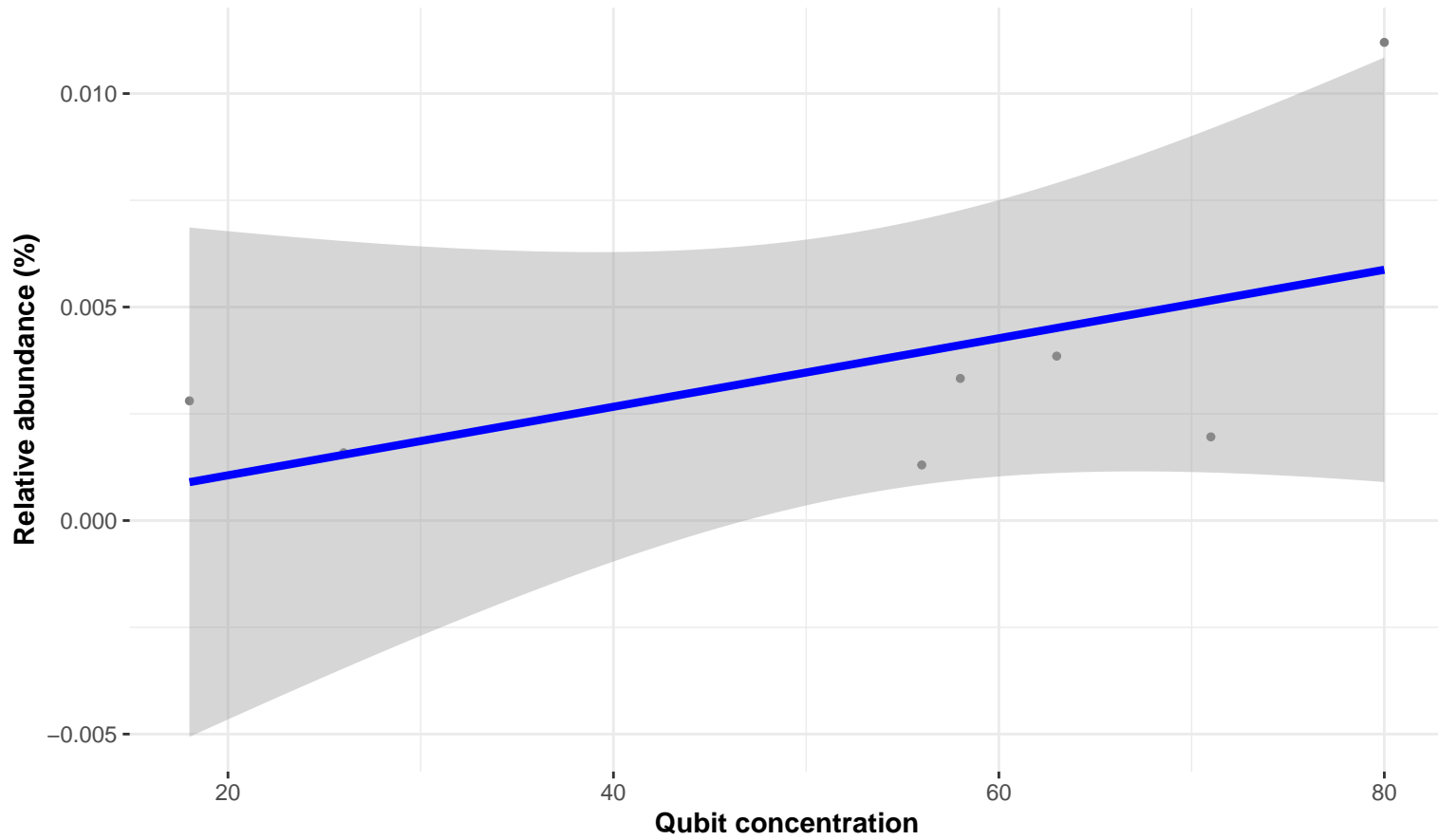
Correlation with all samples

$\log_e(S) = 4.382$, $p = 0.911$, $\hat{\rho}_{\text{Spearman}} = 0.048$, $\text{CI}_{95\%} [-0.694, 0.740]$, $n_{\text{pairs}} = 8$

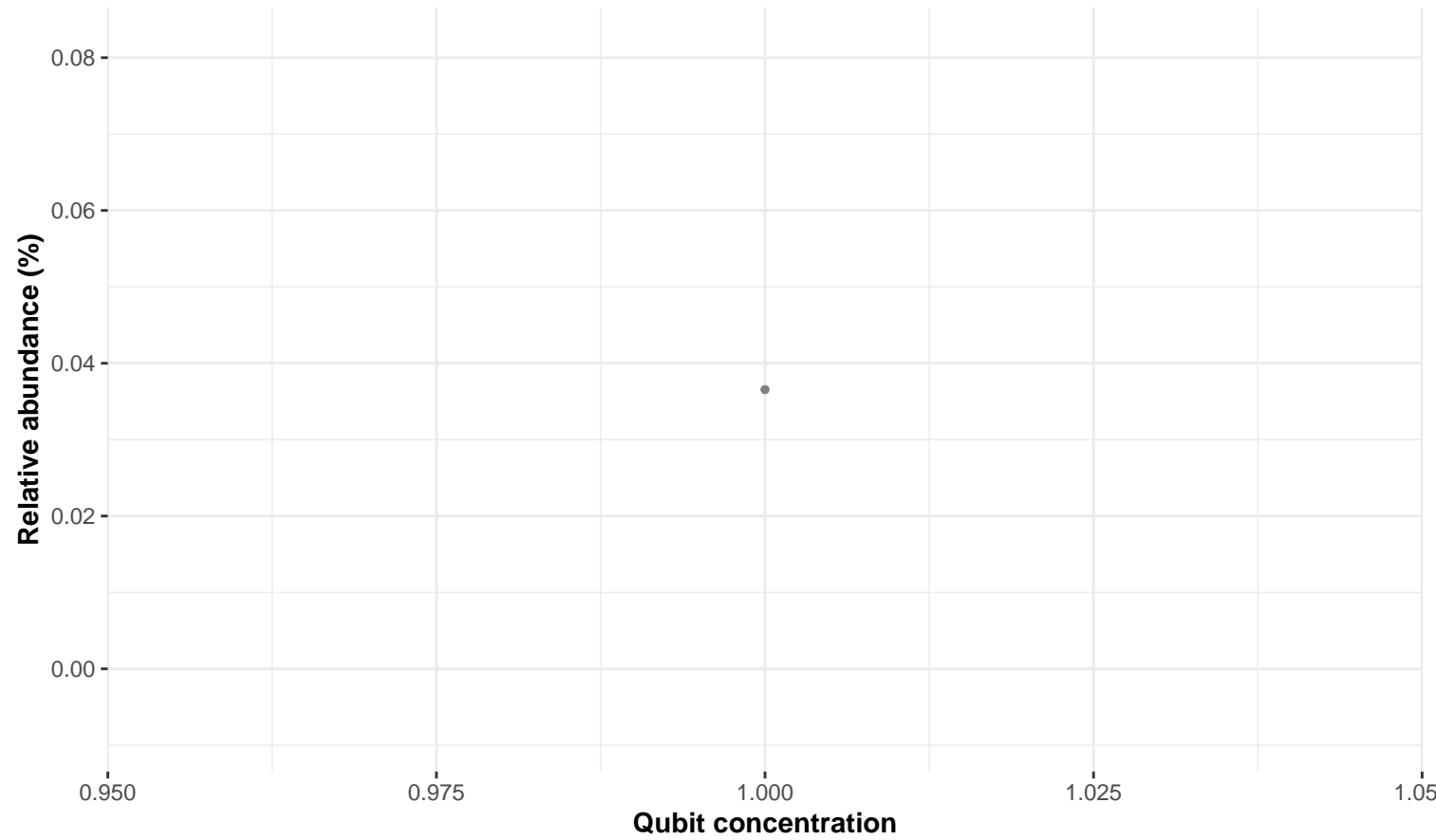


Correlation within: Digesta

$\log_e(S) = 3.178$, $p = 0.180$, $\hat{\rho}_{\text{Spearman}} = 0.571$, $\text{CI}_{95\%} [-0.345, 0.930]$, $n_{\text{pairs}} = 7$



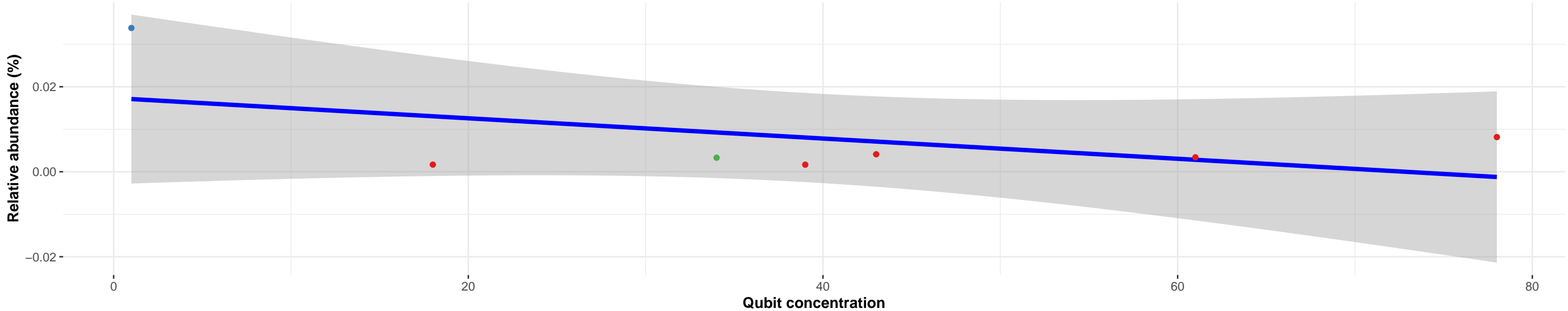
Correlation within: control



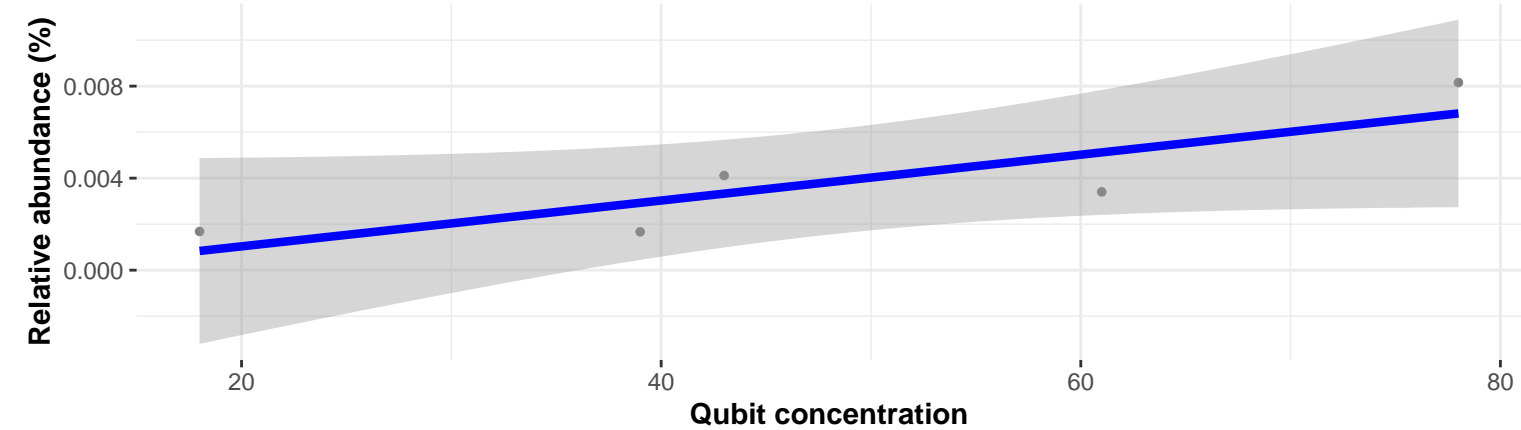
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Beijerinckiaceae; Methylosorula; NA

Correlation with all samples

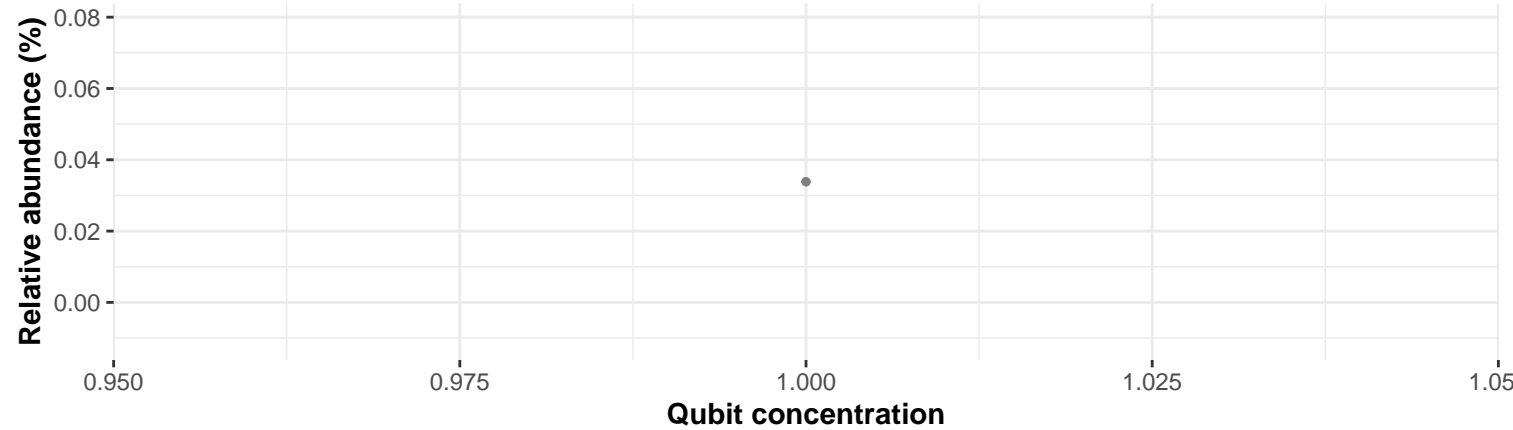
$\log_e(S) = 3.912$, $\rho = 0.819$, $\hat{\rho}_{\text{Spearman}} = 0.107$, $\text{CI}_{95\%} [-0.717, 0.806]$, $n_{\text{pairs}} = 7$



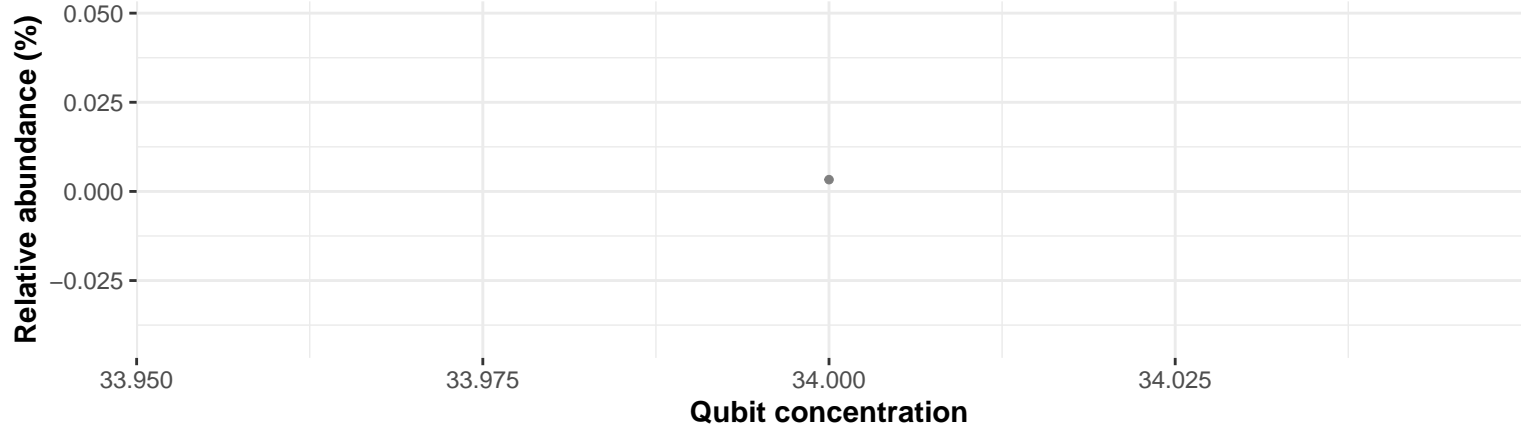
Correlation within: Digesta



Correlation within: control



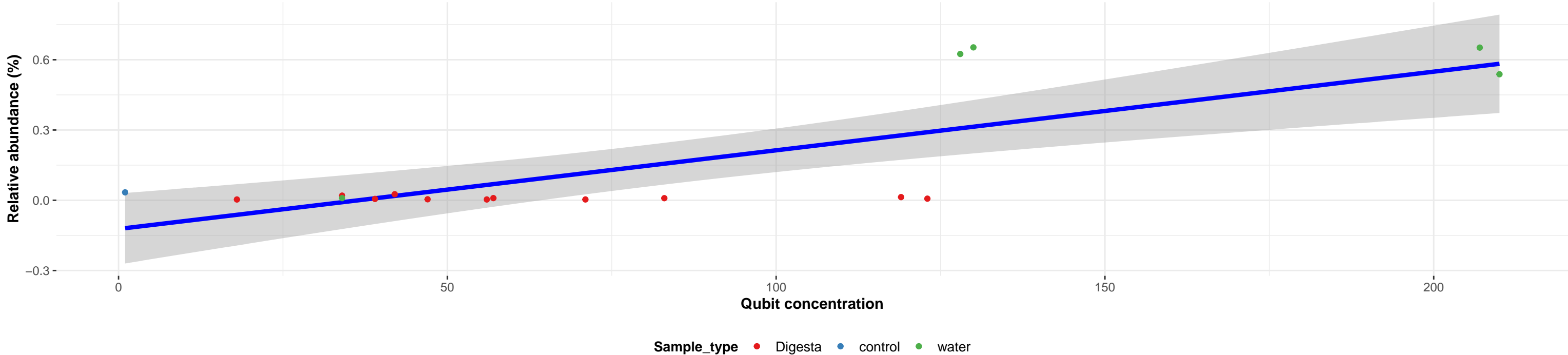
Correlation within: water



Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; NA; NA

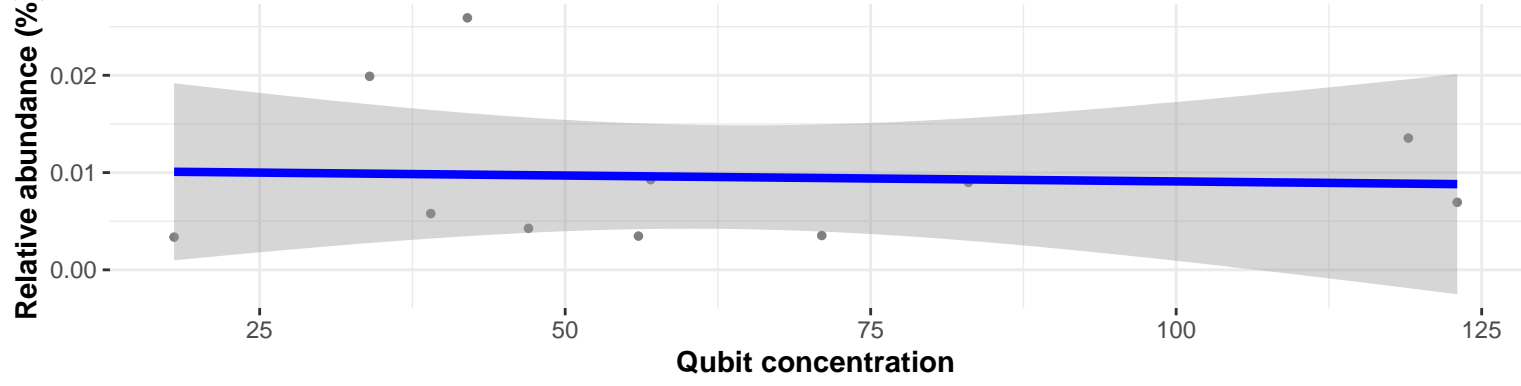
Correlation with all samples

$\log_e(S) = 6.075$, $p = 0.059$, $\hat{\rho}_{\text{Spearman}} = 0.467$, $CI_{95\%} [-0.033, 0.780]$, $n_{\text{pairs}} = 17$

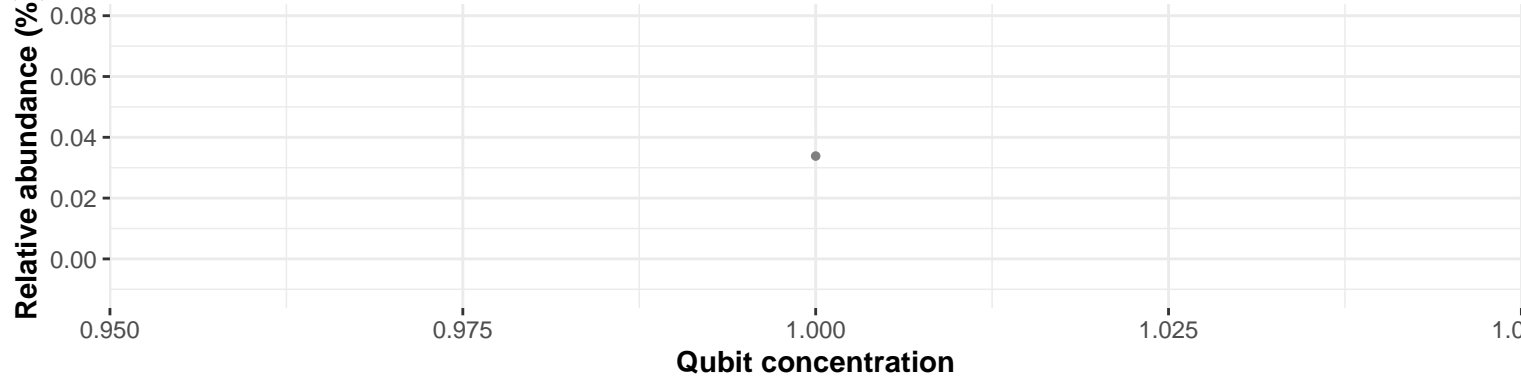


Correlation within: Digesta

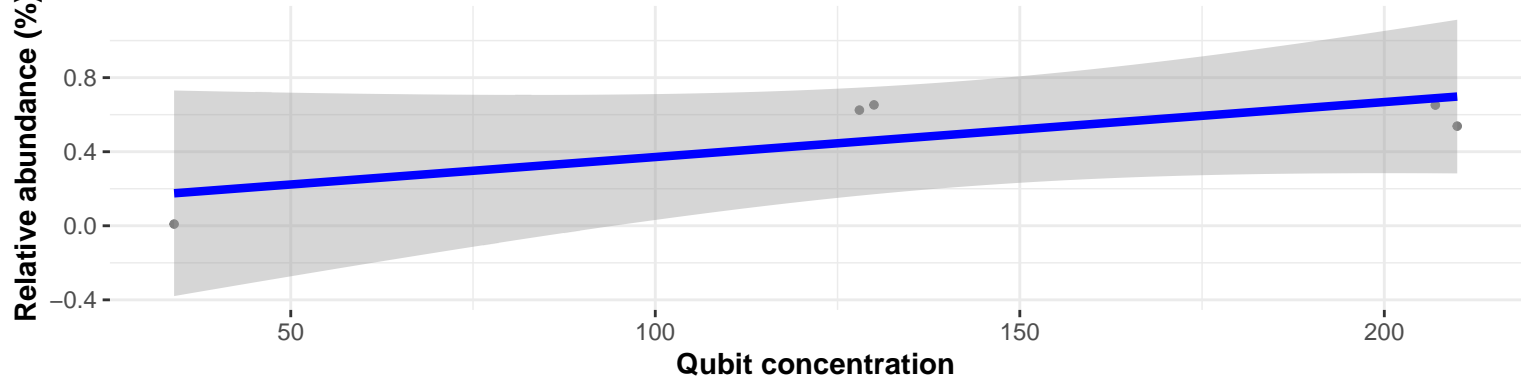
$\log_e(S) = 5.247$, $p = 0.689$, $\hat{\rho}_{\text{Spearman}} = 0.136$, $CI_{95\%} [-0.520, 0.691]$, $n_{\text{pairs}} = 11$



Correlation within: control



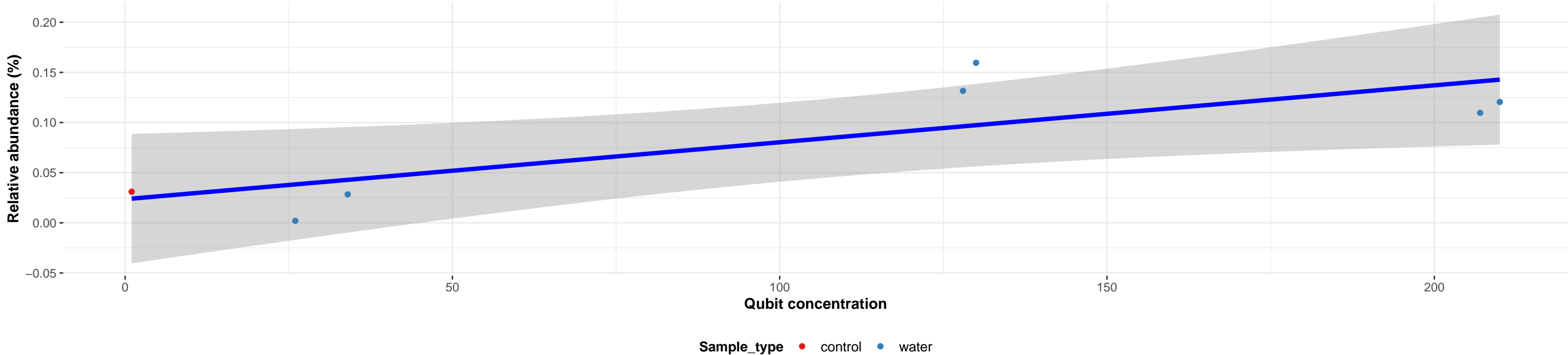
Correlation within: water



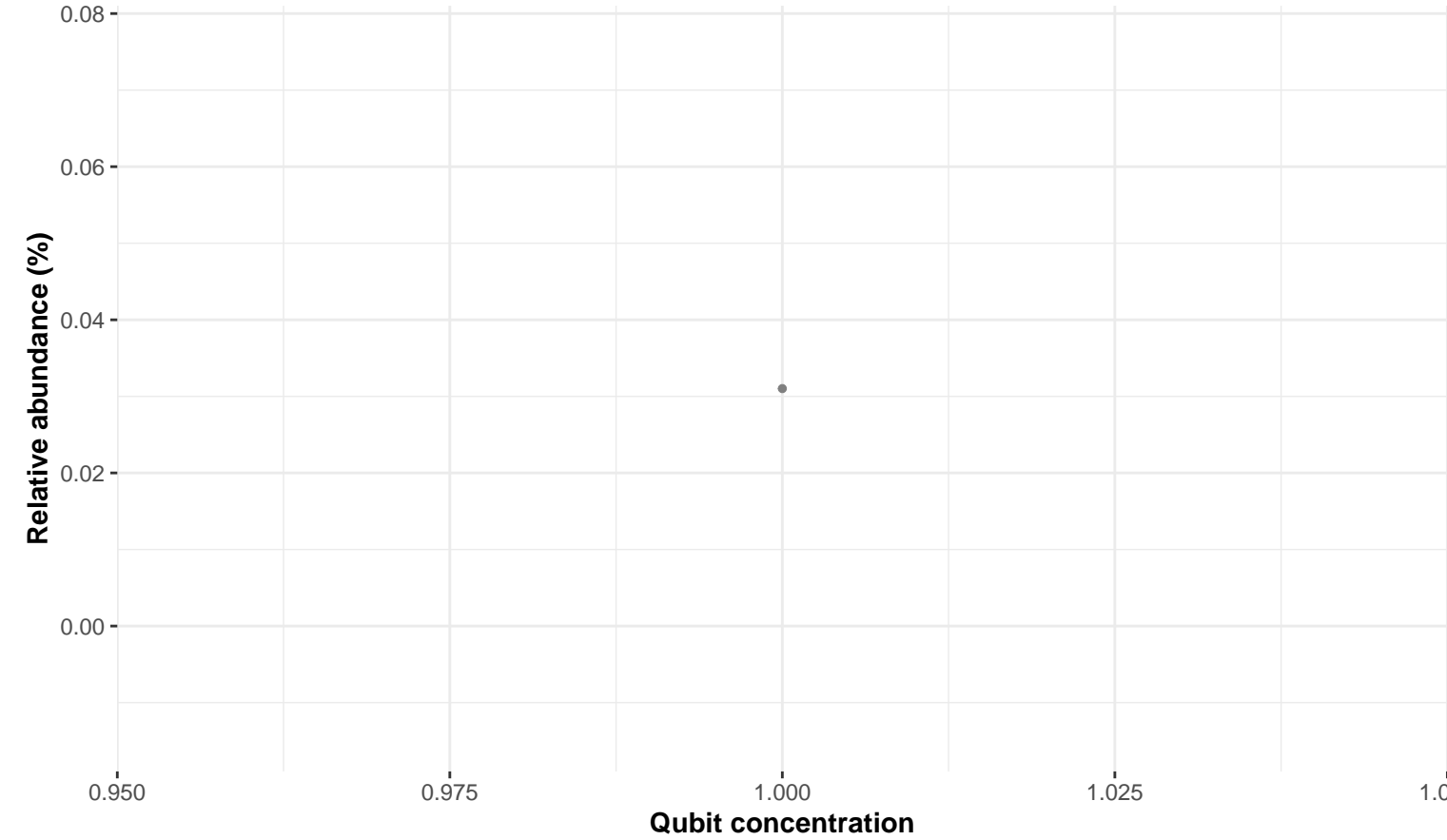
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Colwelliaceae; Colwellia; NA

Correlation with all samples

$\log_e(S) = 3.091$, $p = 0.148$, $\hat{\rho}_{\text{Spearman}} = 0.607$, $\text{CI}_{95\%} [-0.295, 0.937]$, $n_{\text{pairs}} = 7$

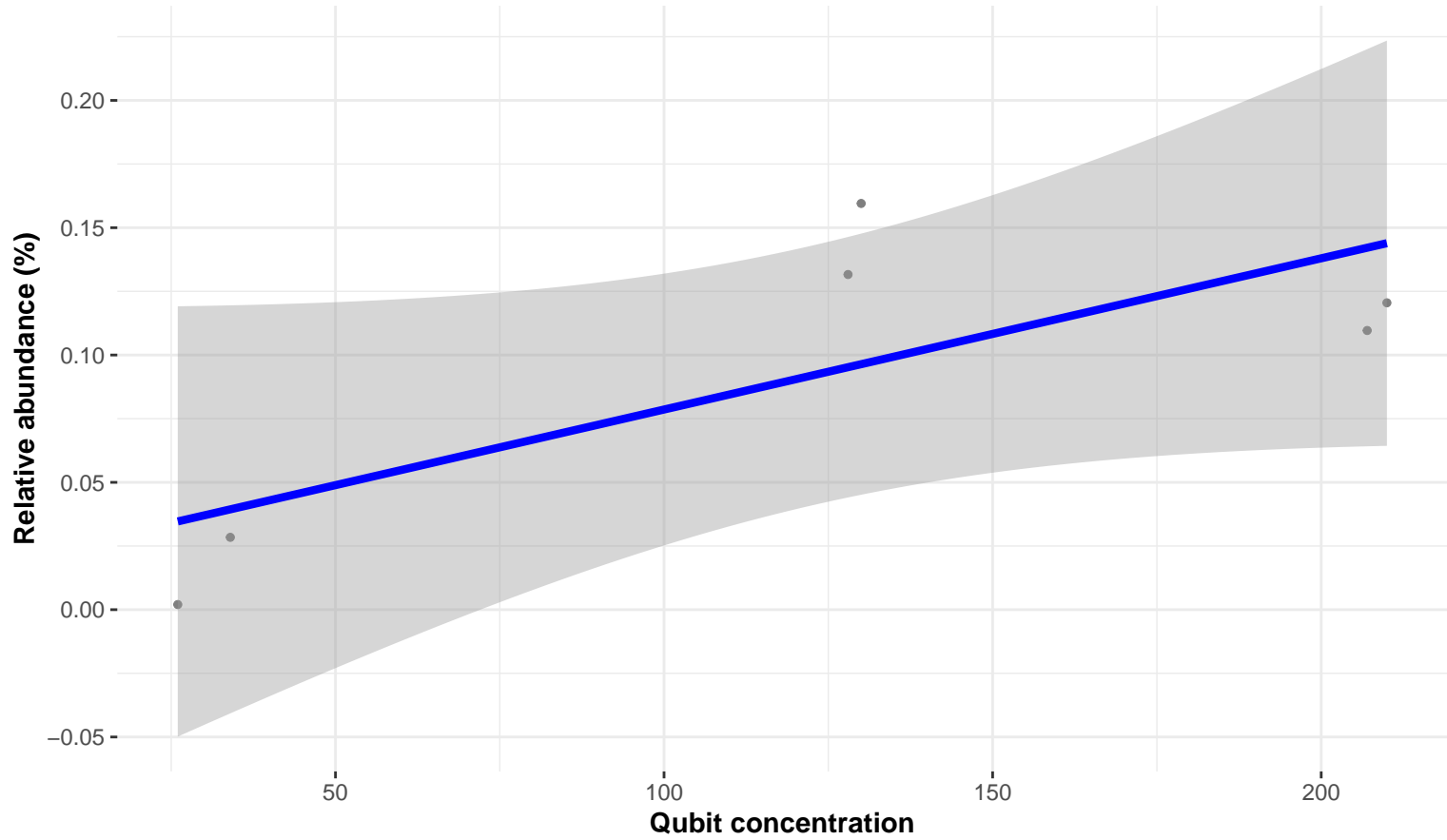


Correlation within: control



Correlation within: water

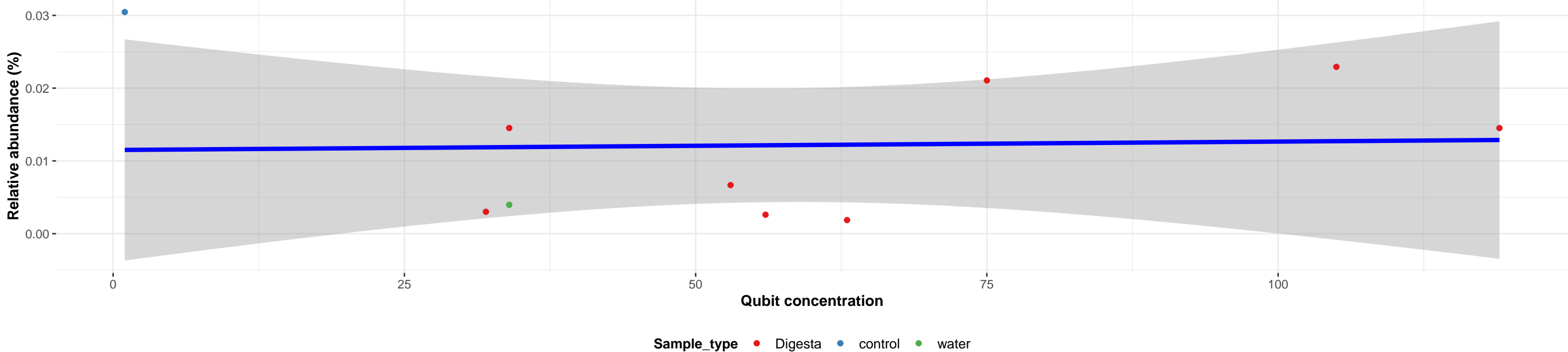
$\log_e(S) = 2.773$, $p = 0.266$, $\hat{\rho}_{\text{Spearman}} = 0.543$, $\text{CI}_{95\%} [-0.506, 0.944]$, $n_{\text{pairs}} = 6$



Bacteria; Firmicutes; Clostridia; Peptostreptococcales–Tissierellales; Peptostreptococcaceae; Romboutsia; NA

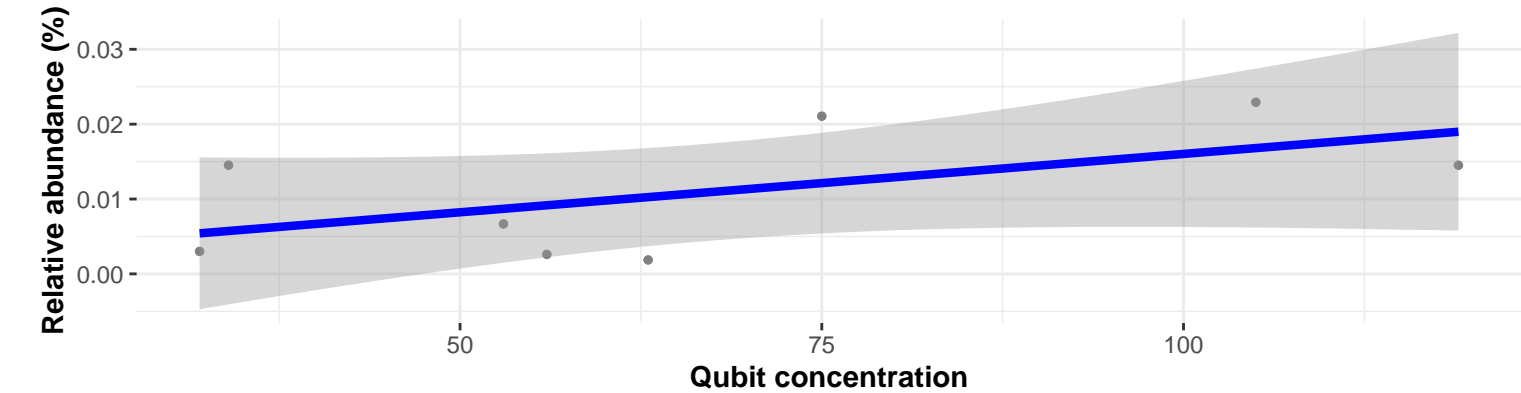
Correlation with all samples

$\log_e(S) = 5.094$, $p = 0.973$, $\hat{\rho}_{\text{Spearman}} = 0.012$, $CI_{95\%} [-0.635, 0.650]$, $n_{\text{pairs}} = 10$



Correlation within: Digesta

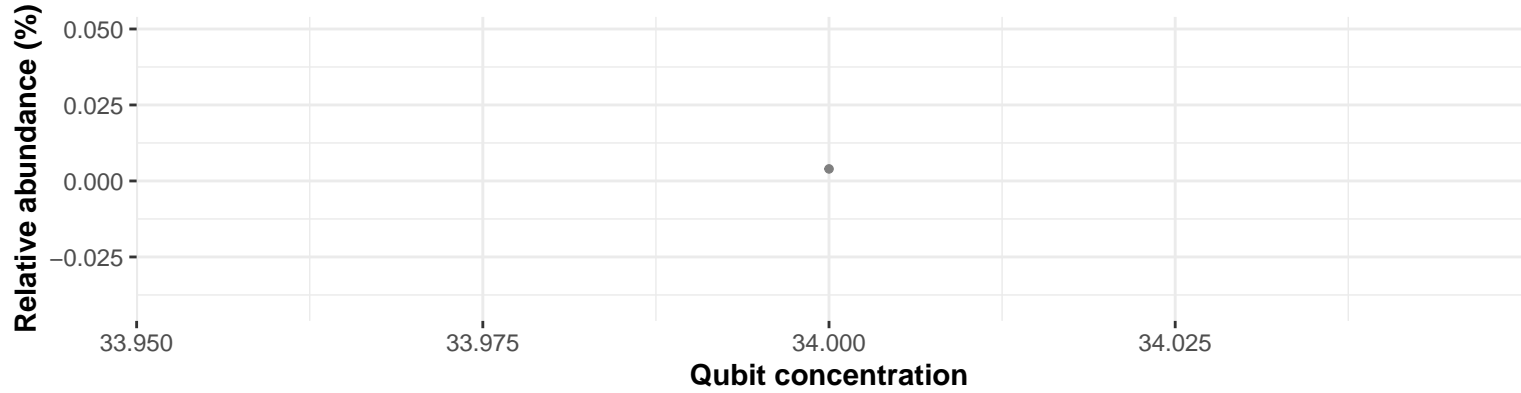
$\log_e(S) = 3.951$, $p = 0.352$, $\hat{\rho}_{\text{Spearman}} = 0.381$, $CI_{95\%} [-0.463, 0.863]$, $n_{\text{pairs}} = 8$



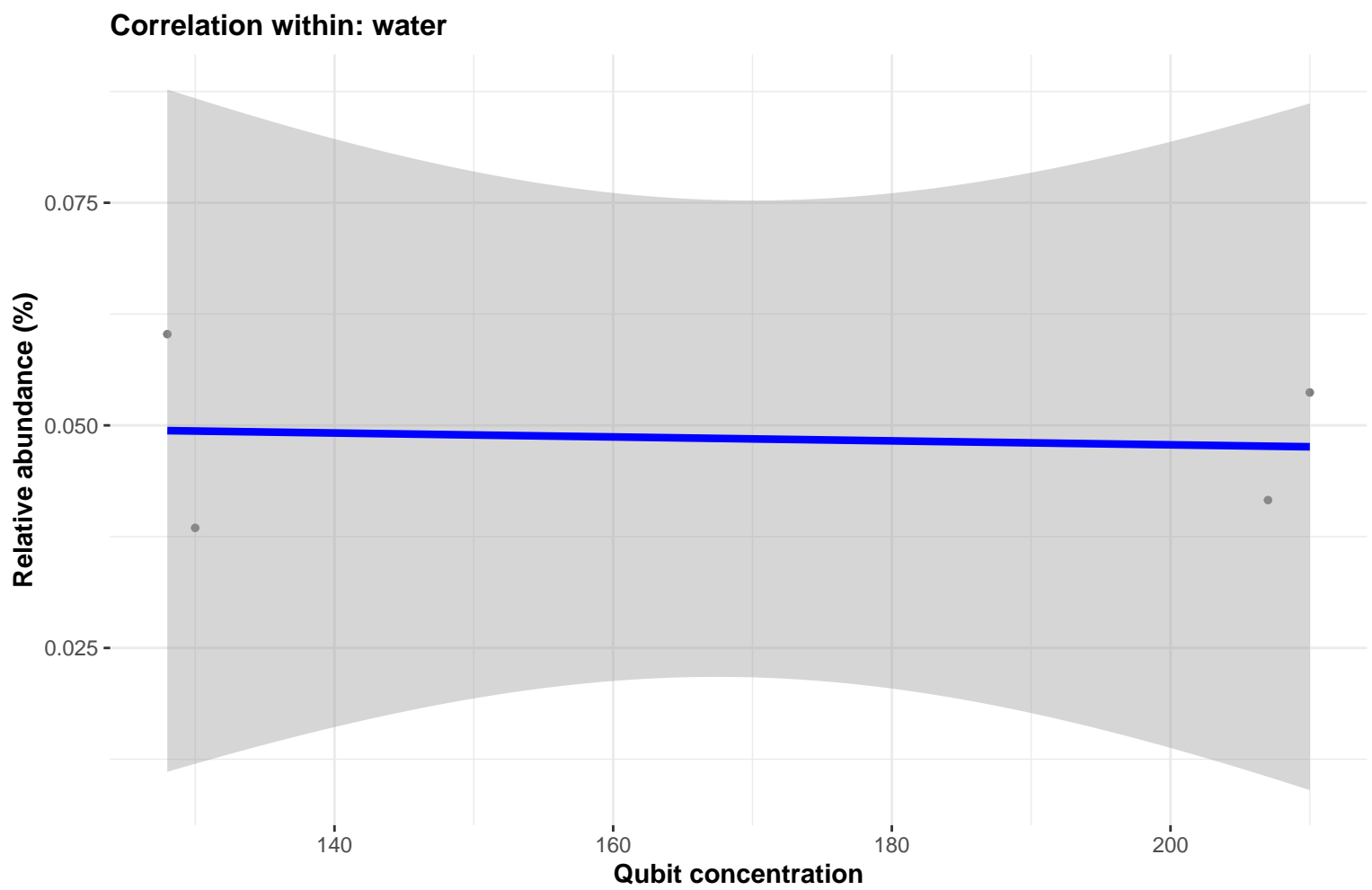
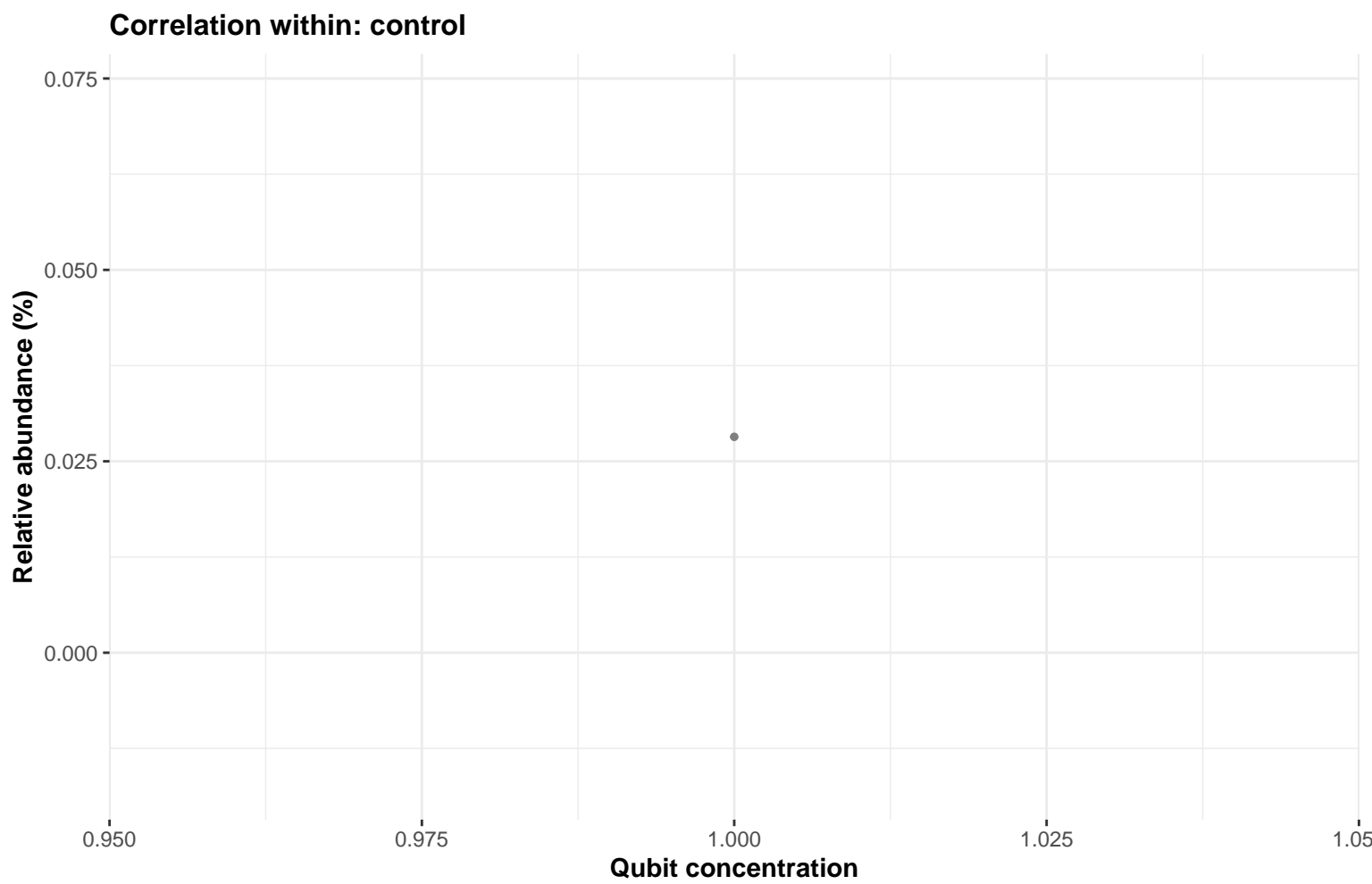
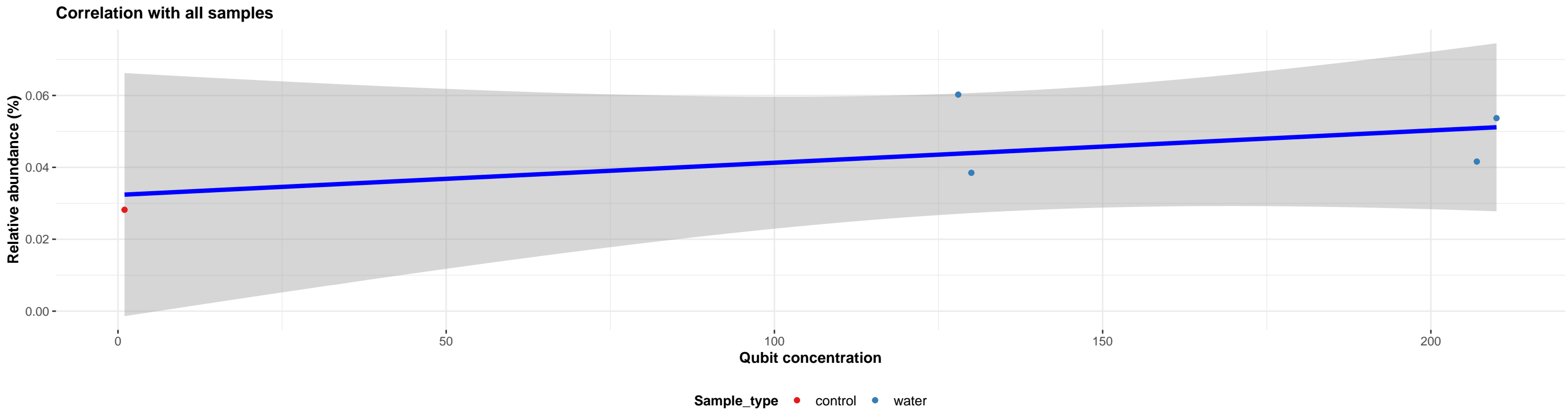
Correlation within: control



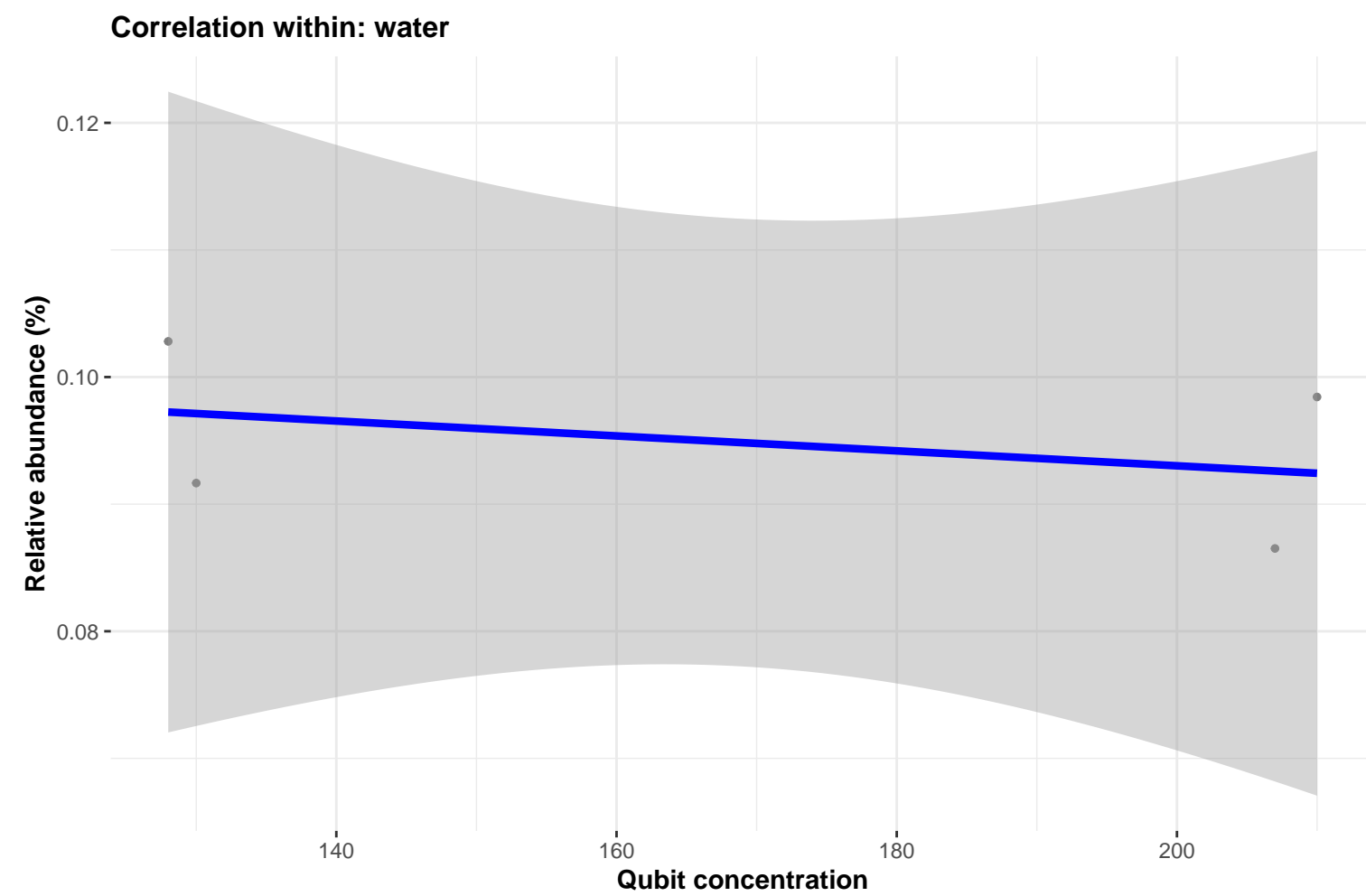
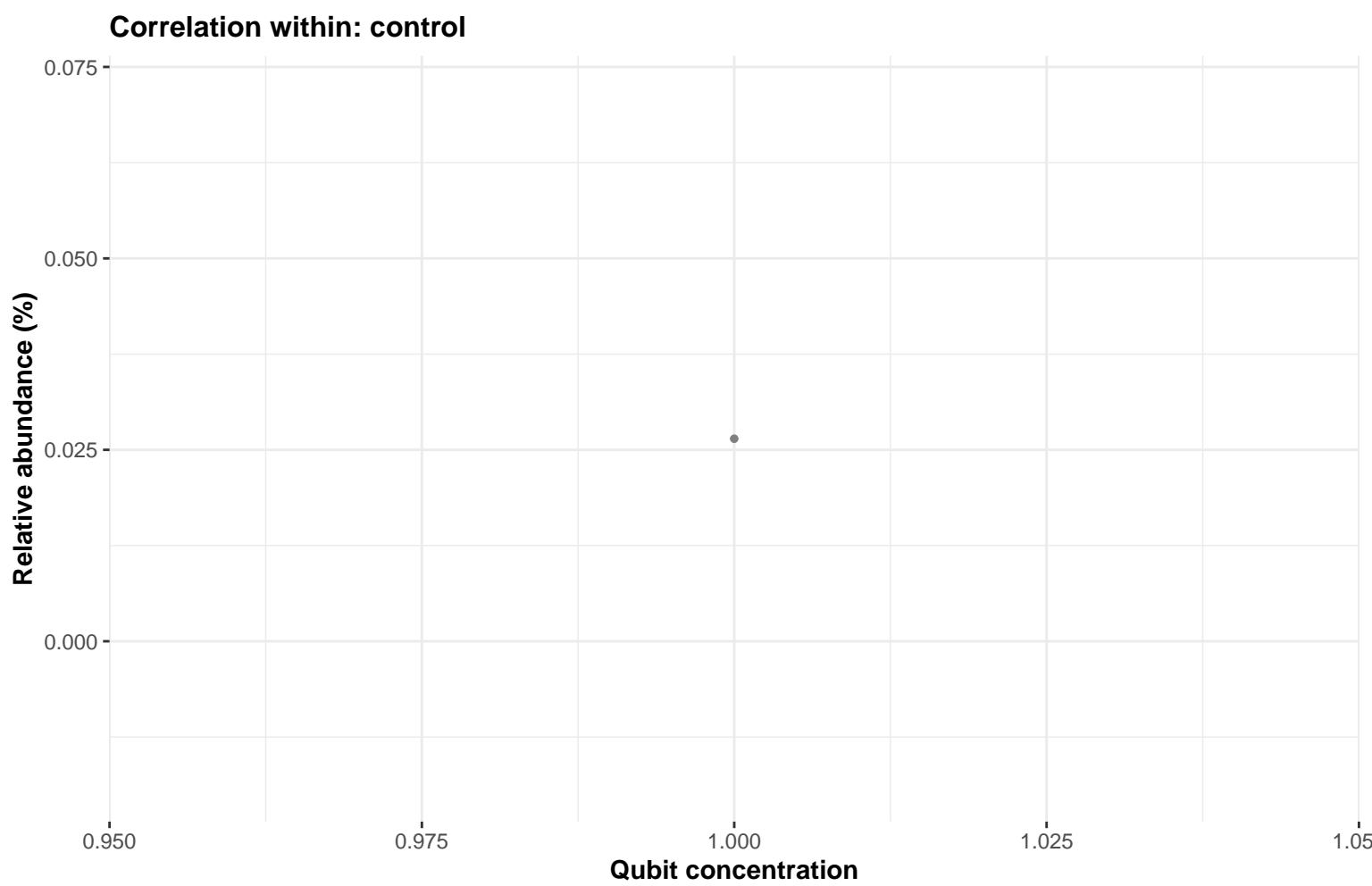
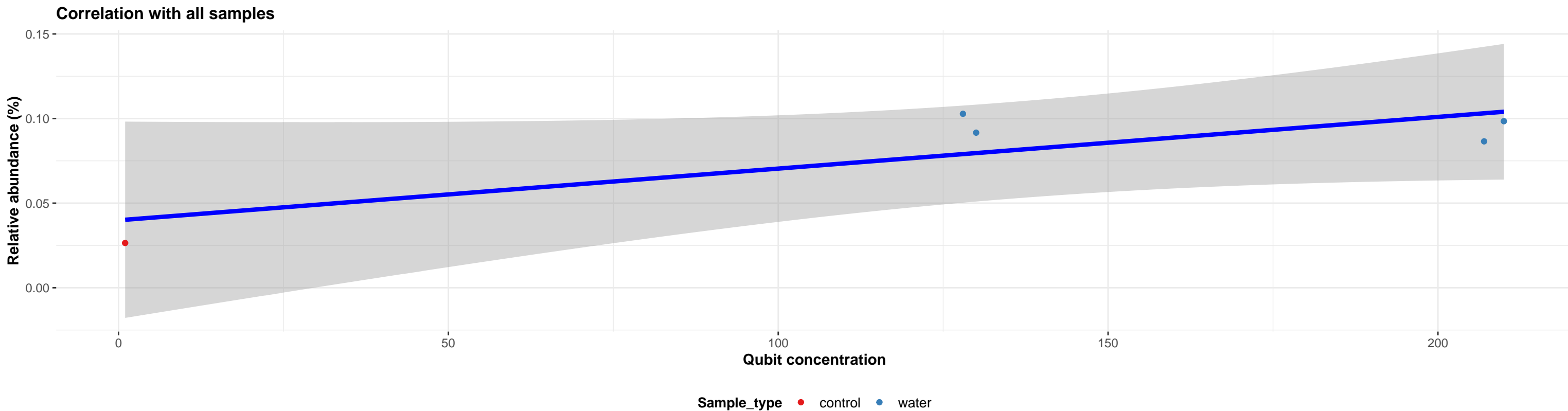
Correlation within: water



Bacteria; Bacteroidota; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Dokdonia; NA



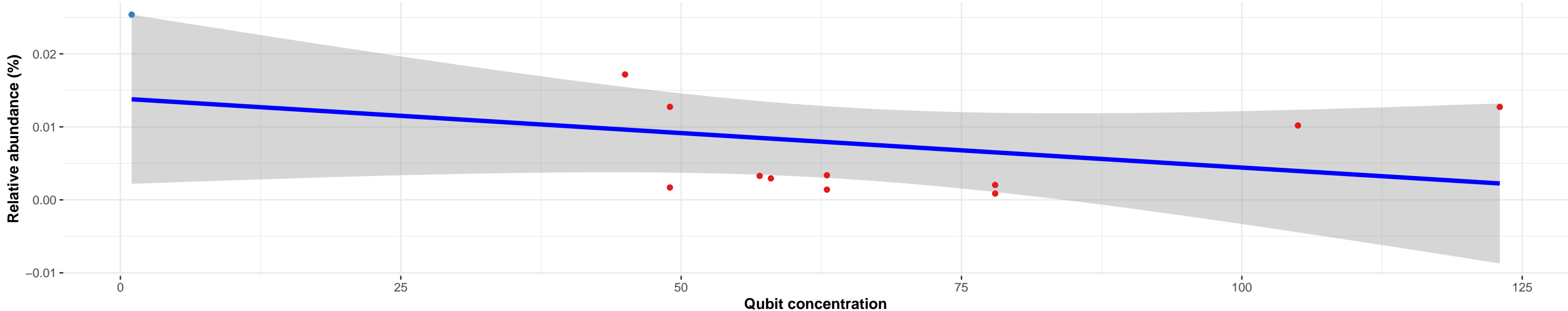
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellaceae; NA; NA



Bacteria; Dependientiae; Babeliae; Babeliales; Babeliaceae; NA; NA

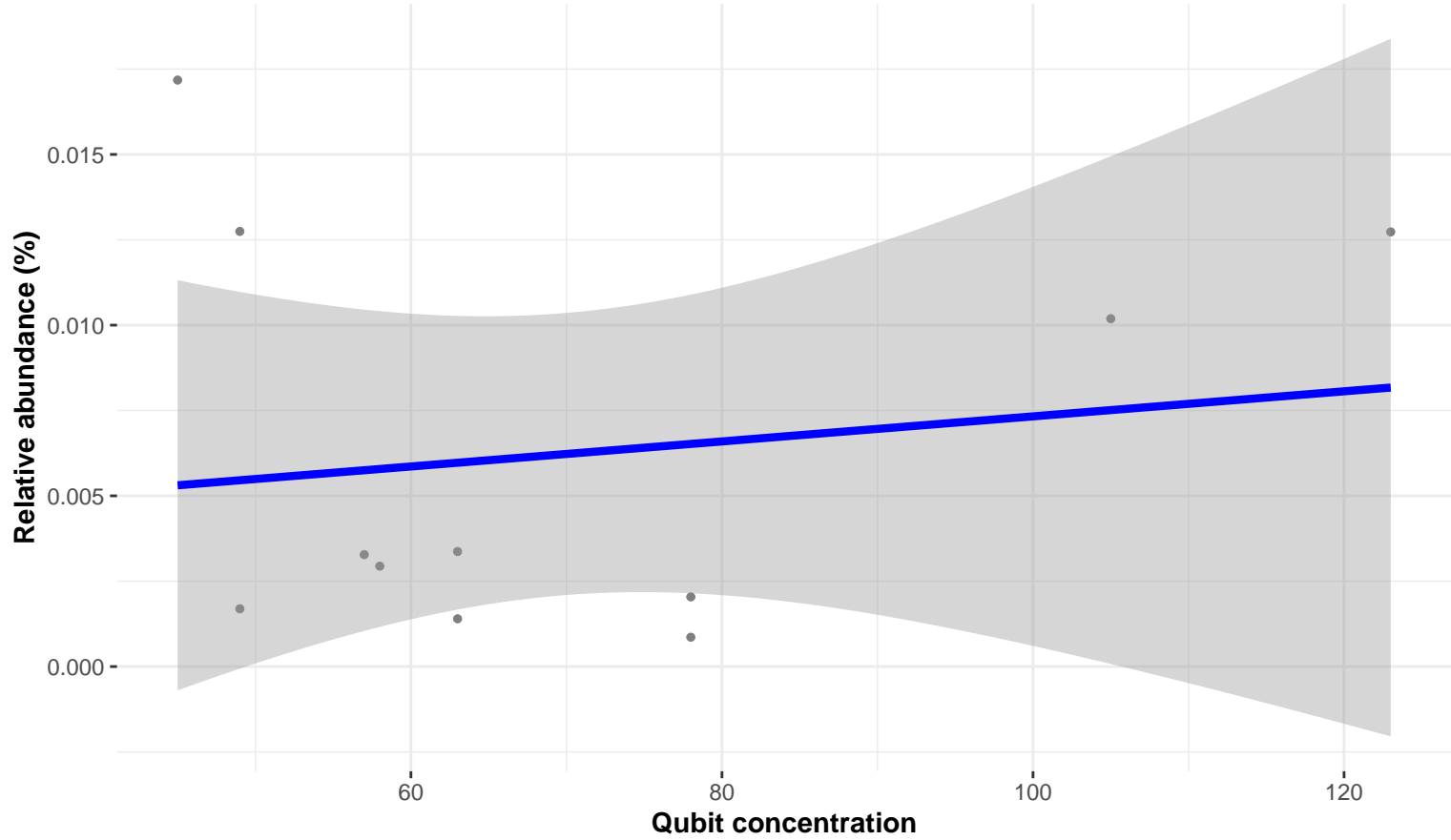
Correlation with all samples

$\log_e(S) = 5.990$, $p = 0.201$, $\hat{\rho}_{\text{Spearman}} = -0.397$, $\text{CI}_{95\%} [-0.798, 0.247]$, $n_{\text{pairs}} = 12$

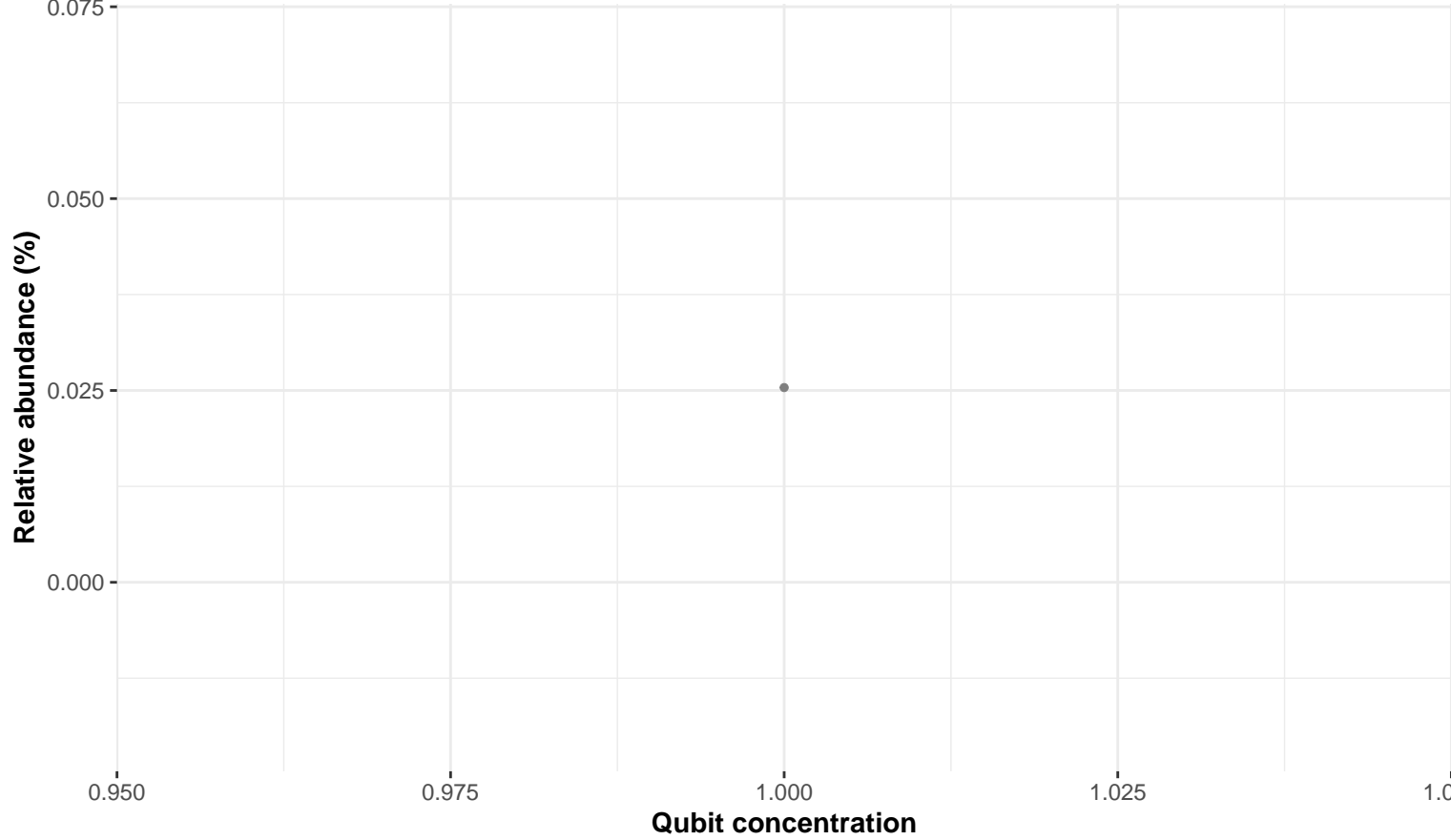


Correlation within: Digesta

$\log_e(S) = 5.588$, $p = 0.525$, $\hat{\rho}_{\text{Spearman}} = -0.215$, $\text{CI}_{95\%} [-0.732, 0.458]$, $n_{\text{pairs}} = 11$

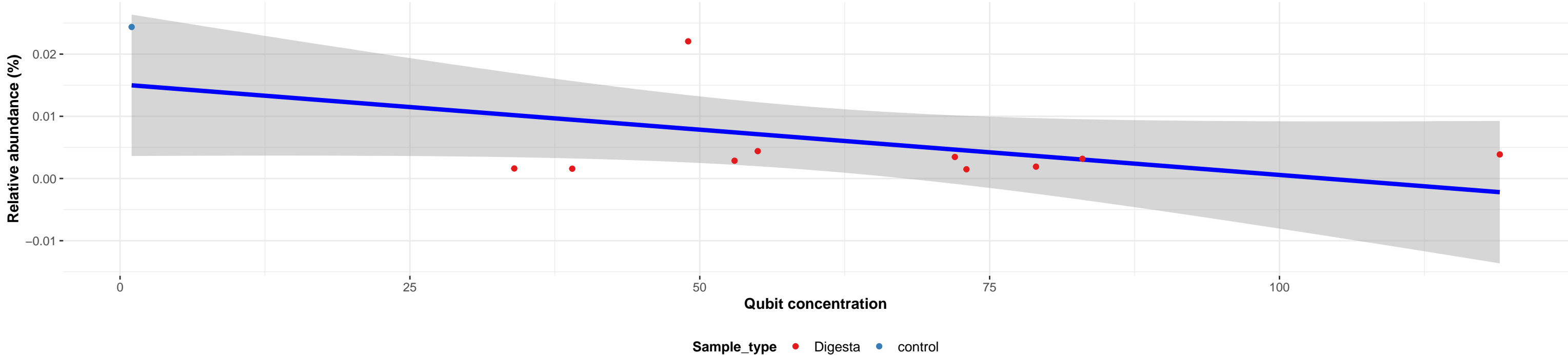


Correlation within: control



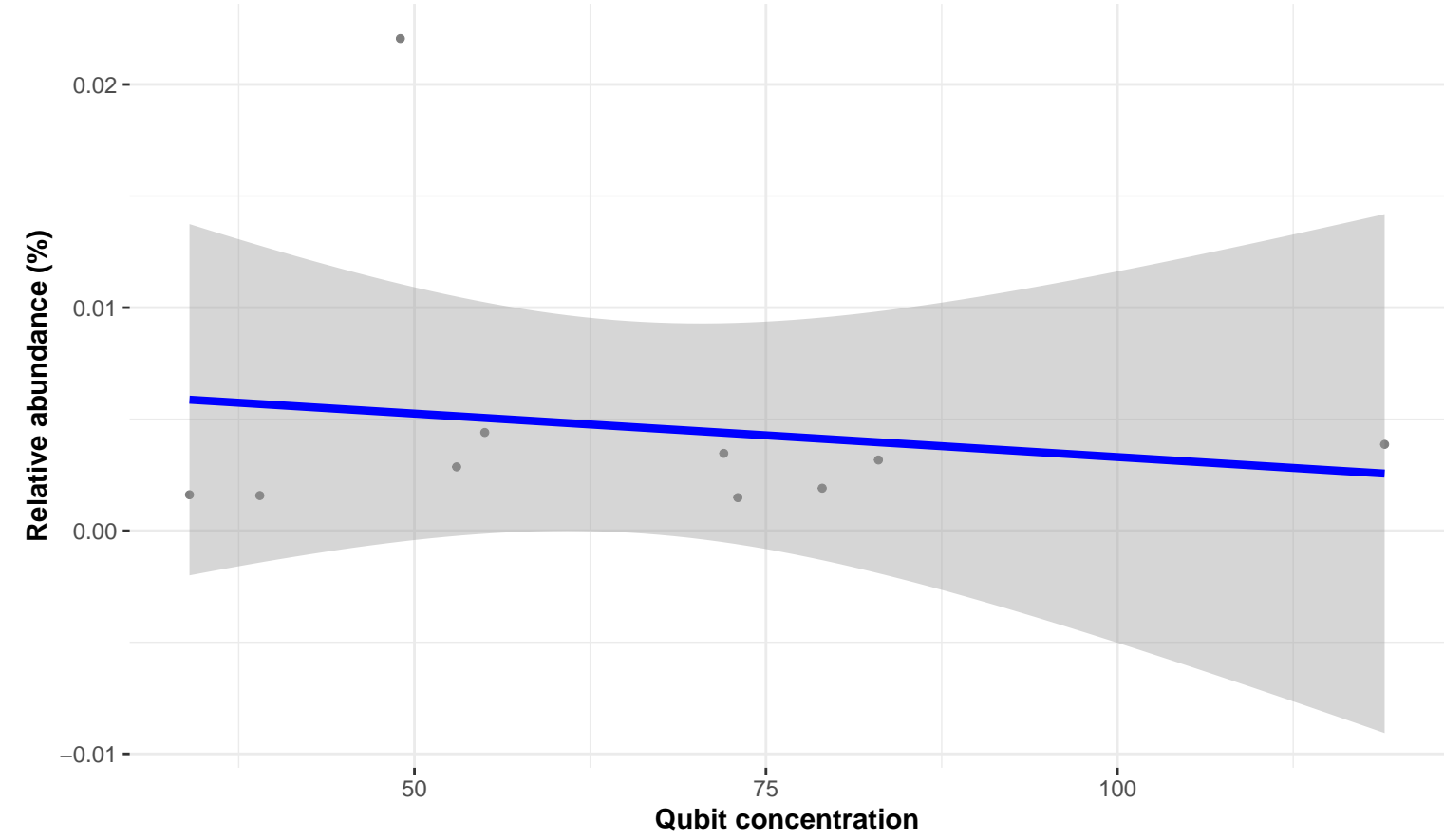
Correlation with all samples

$\log_e(S) = 5.505$, $p = 0.729$, $\hat{\rho}_{\text{Spearman}} = -0.118$, $\text{CI}_{95\%} [-0.682, 0.533]$, $n_{\text{pairs}} = 11$

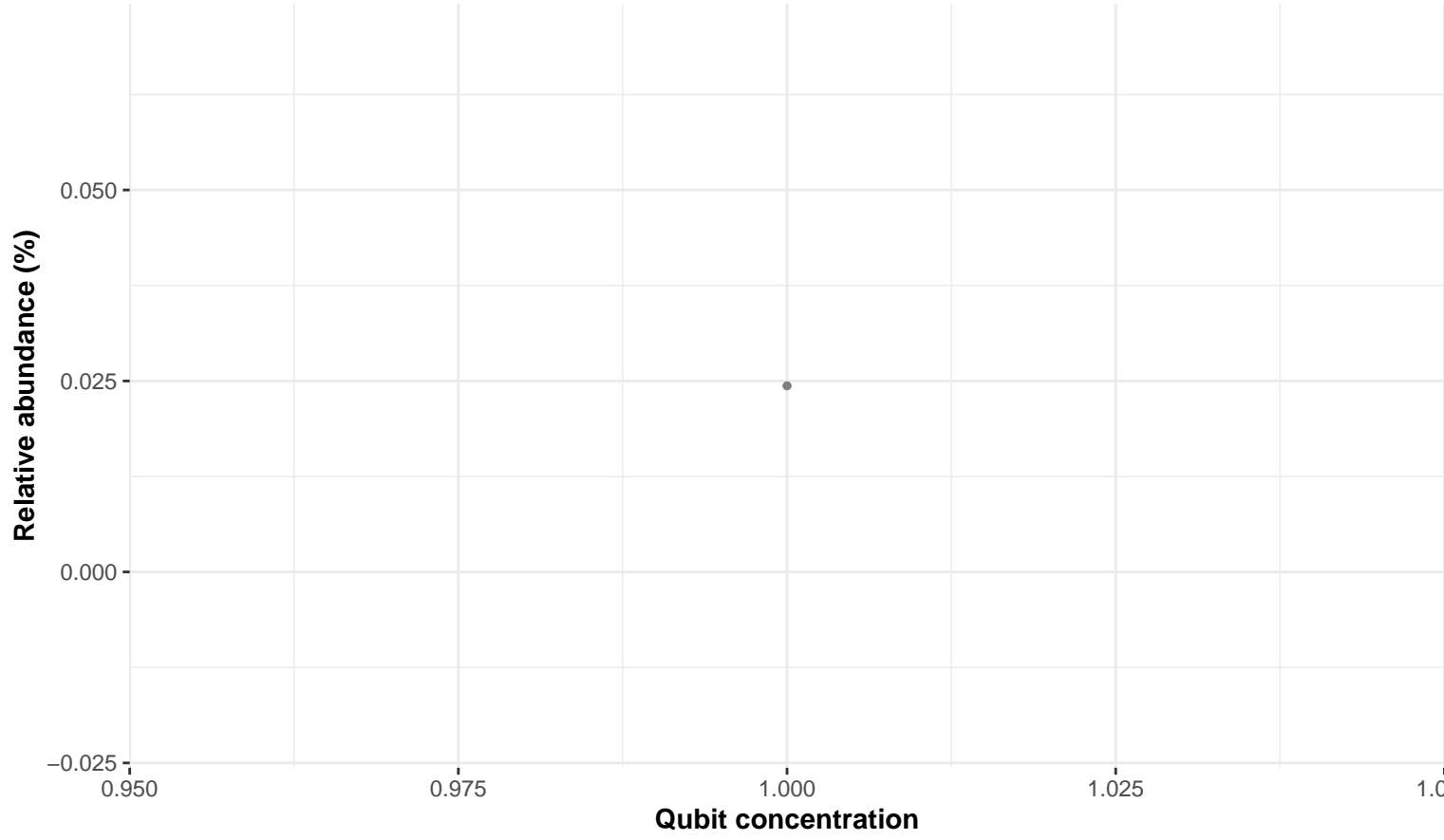


Correlation within: Digesta

$\log_e(S) = 4.913$, $p = 0.627$, $\hat{\rho}_{\text{Spearman}} = 0.176$, $\text{CI}_{95\%} [-0.526, 0.735]$, $n_{\text{pairs}} = 10$



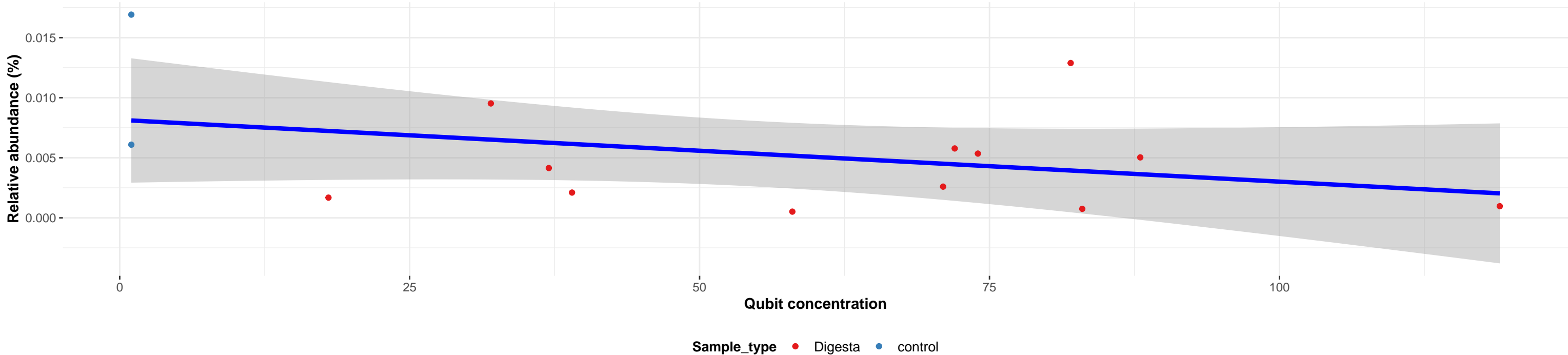
Correlation within: control



Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus; NA

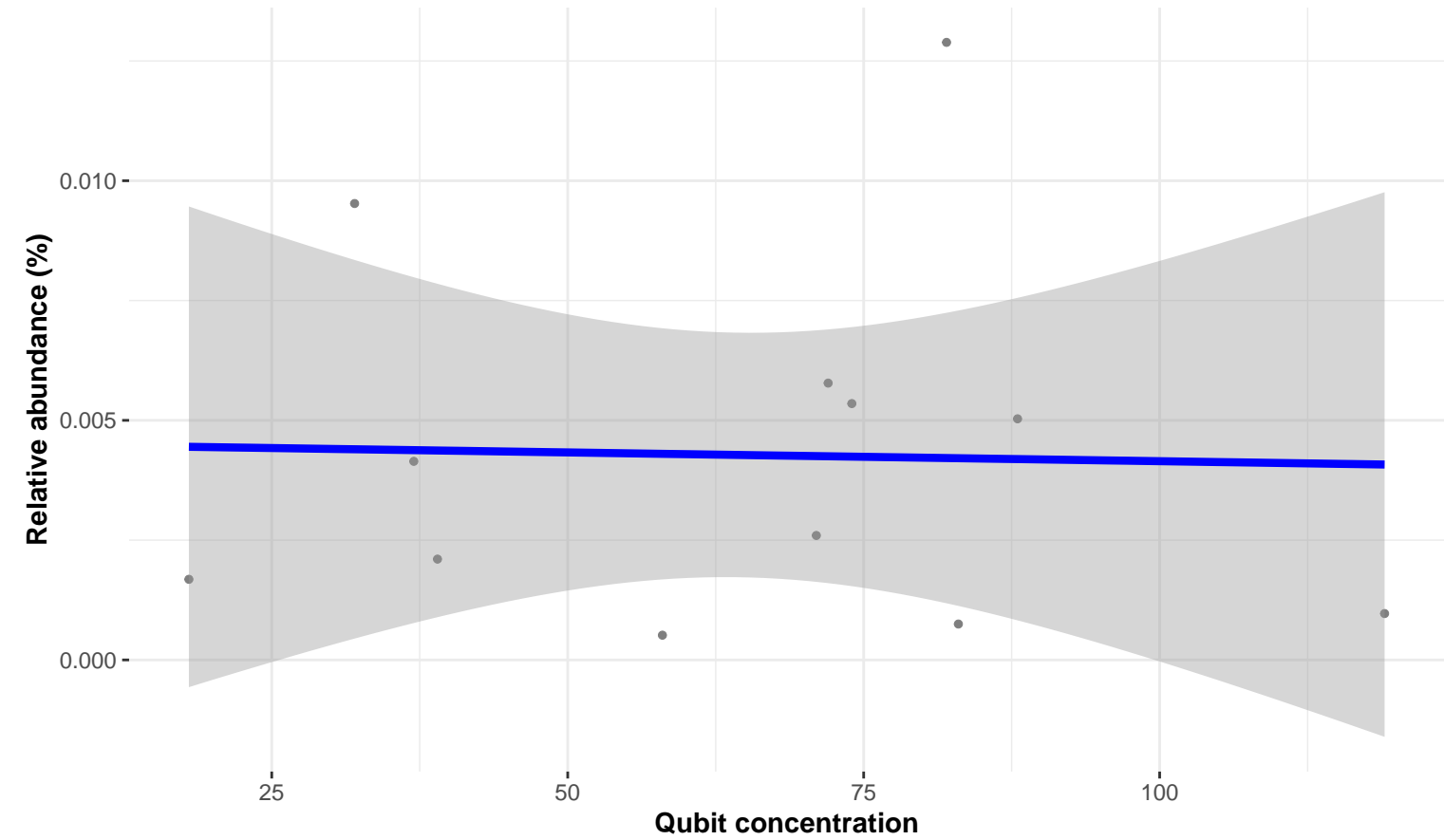
Correlation with all samples

$\log_e(S) = 6.412$, $p = 0.236$, $\hat{\rho}_{\text{Spearman}} = -0.339$, $CI_{95\%} [-0.745, 0.250]$, $n_{\text{pairs}} = 14$

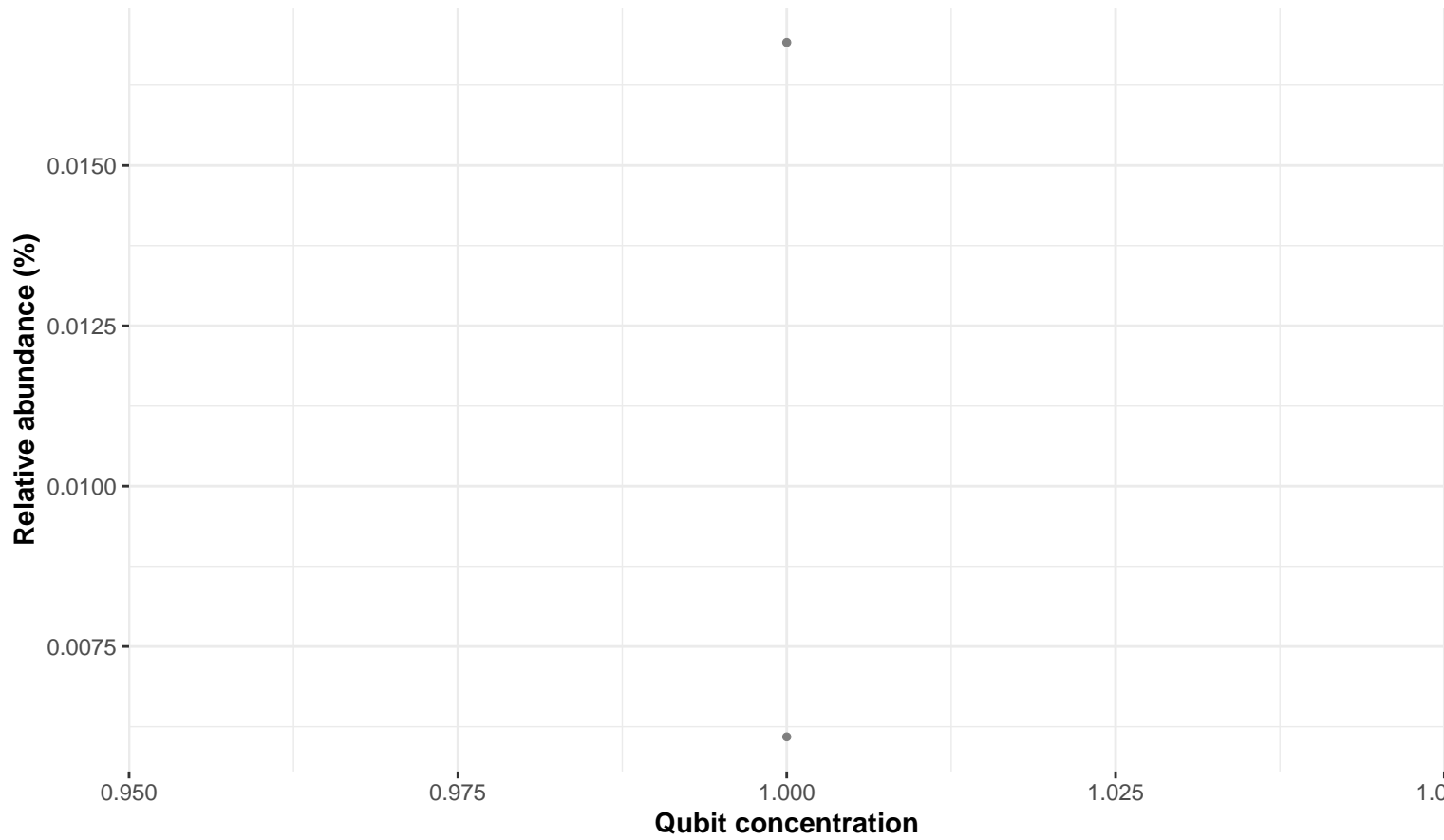


Correlation within: Digesta

$\log_e(S) = 5.690$, $p = 0.914$, $\hat{\rho}_{\text{Spearman}} = -0.035$, $CI_{95\%} [-0.609, 0.563]$, $n_{\text{pairs}} = 12$



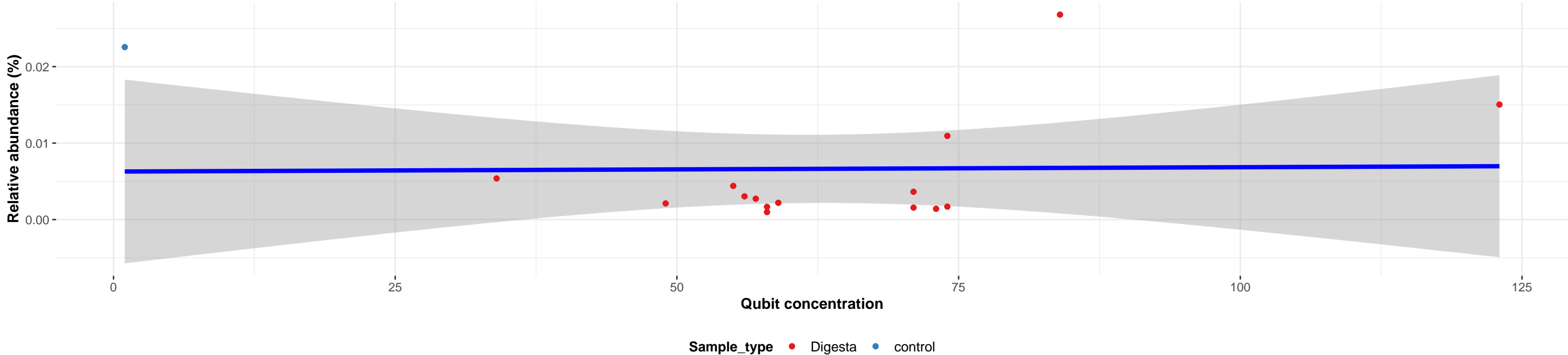
Correlation within: control



Bacteria; Patescibacteria; Parcubacteria; Candidatus Nomurabacteria; NA; NA; NA

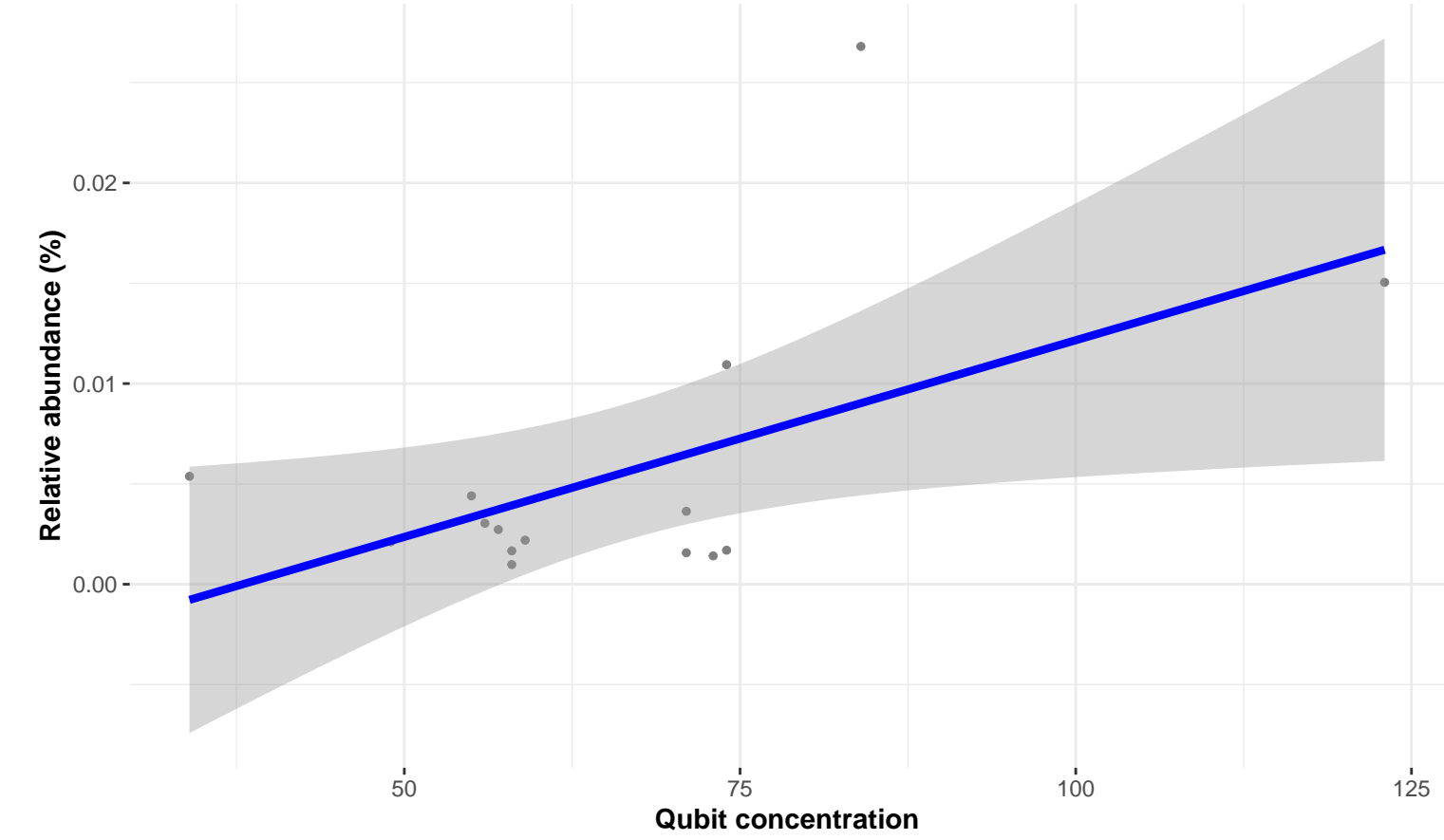
Correlation with all samples

$\log_e(S) = 6.504$, $p = 0.948$, $\hat{\rho}_{\text{Spearman}} = 0.018$, $\text{CI}_{95\%} [-0.494, 0.521]$, $n_{\text{pairs}} = 16$

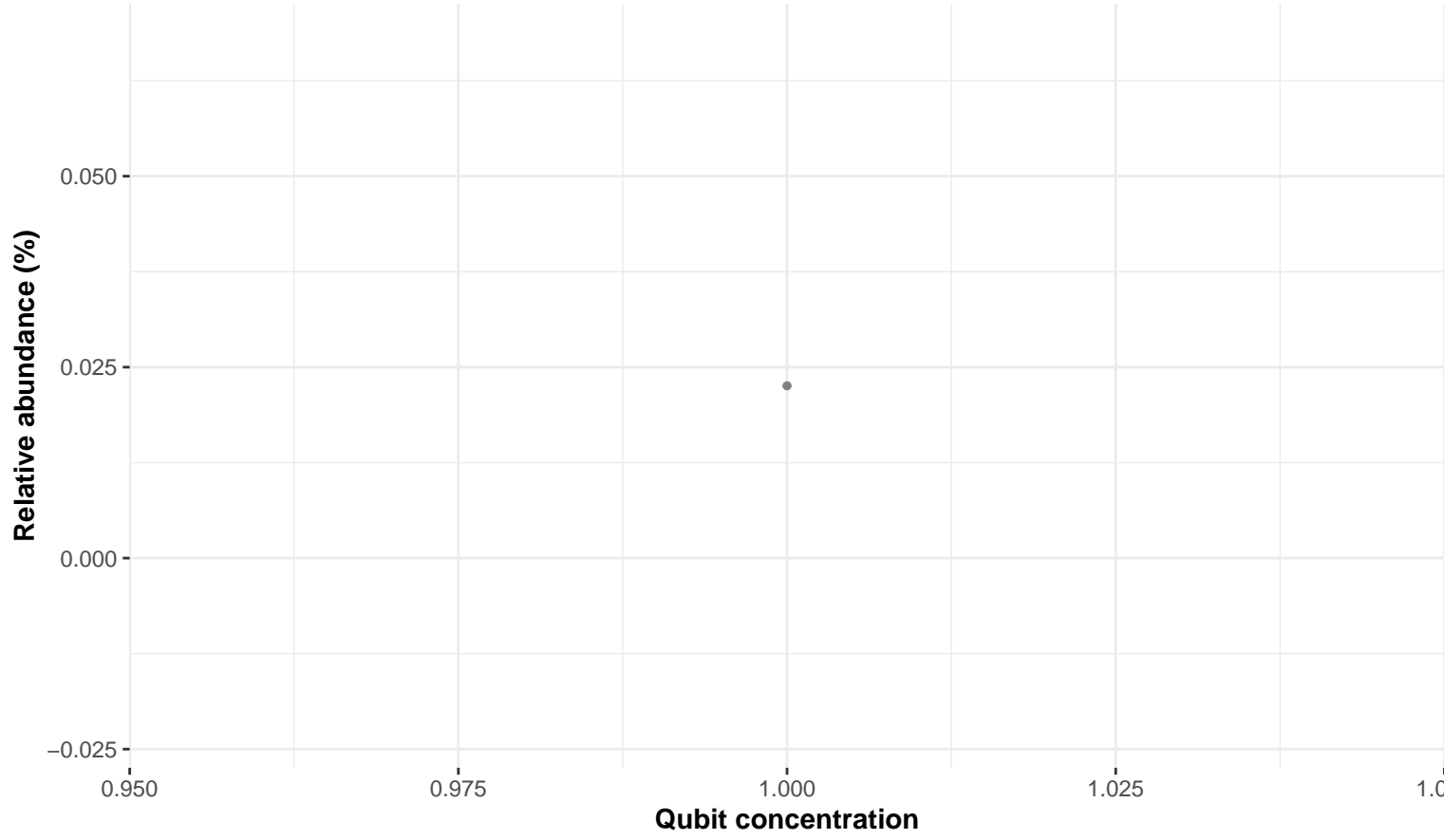


Correlation within: Digesta

$\log_e(S) = 6.122$, $p = 0.506$, $\hat{\rho}_{\text{Spearman}} = 0.186$, $\text{CI}_{95\%} [-0.375, 0.647]$, $n_{\text{pairs}} = 15$



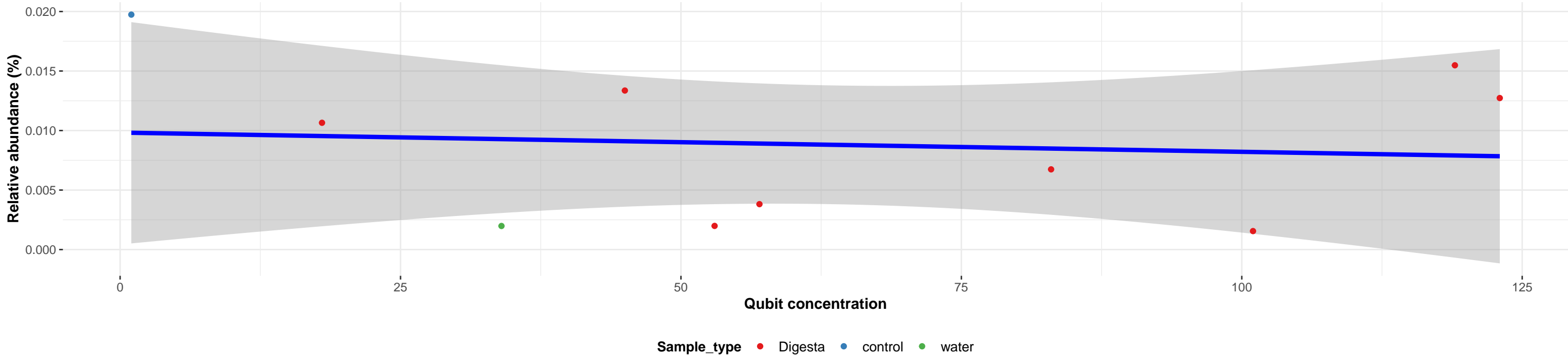
Correlation within: control



Bacteria; Verrucomicrobiota; Chlamydiae; Chlamydiales; Parachlamydiaceae; Neochlamydia; NA

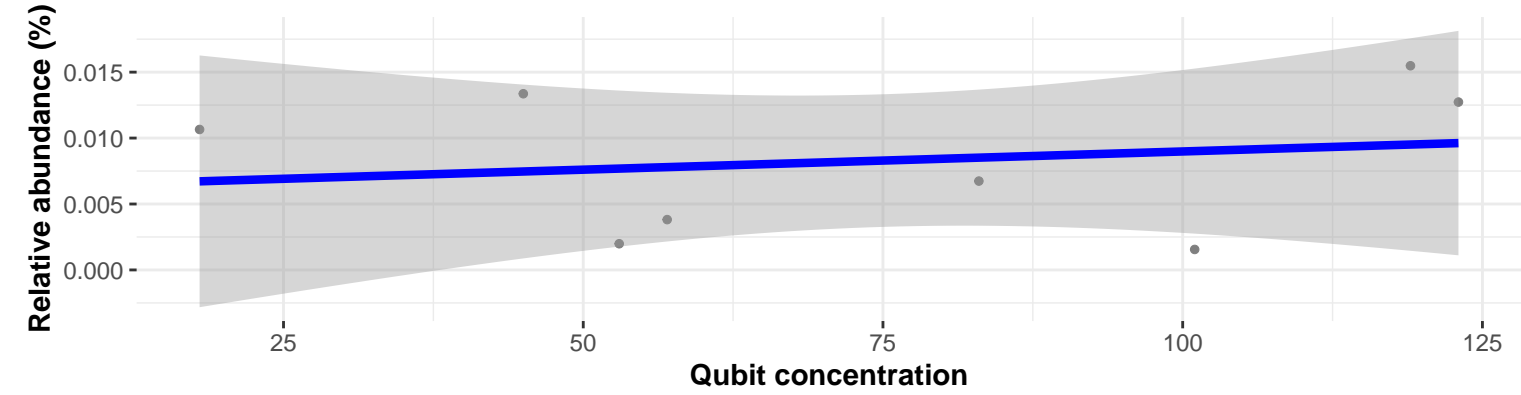
Correlation with all samples

$\log_e(S) = 5.215$, $p = 0.751$, $\hat{\rho}_{\text{Spearman}} = -0.115$, $\text{CI}_{95\%} [-0.706, 0.570]$, $n_{\text{pairs}} = 10$

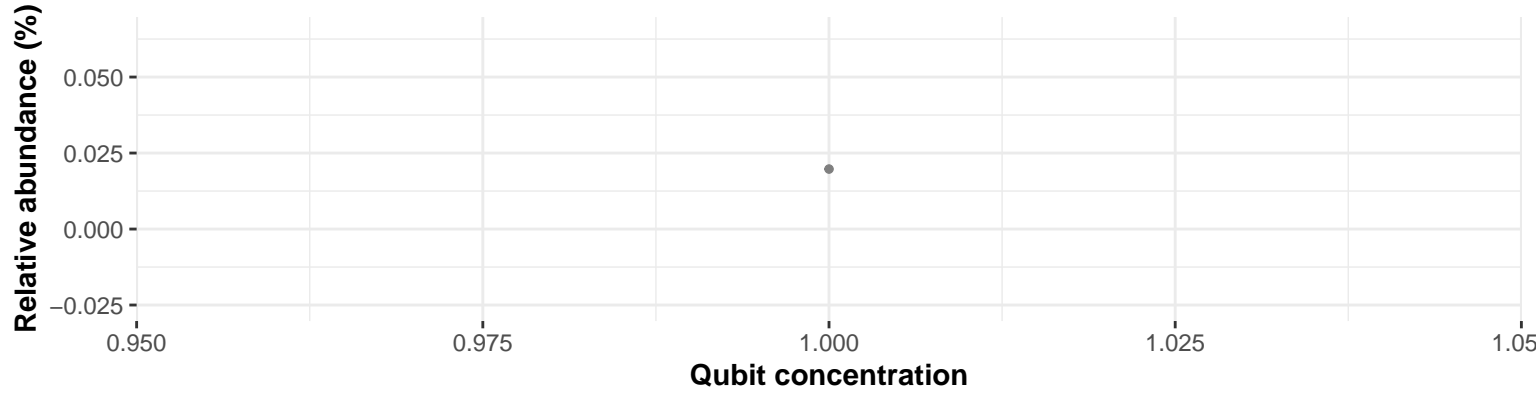


Correlation within: Digesta

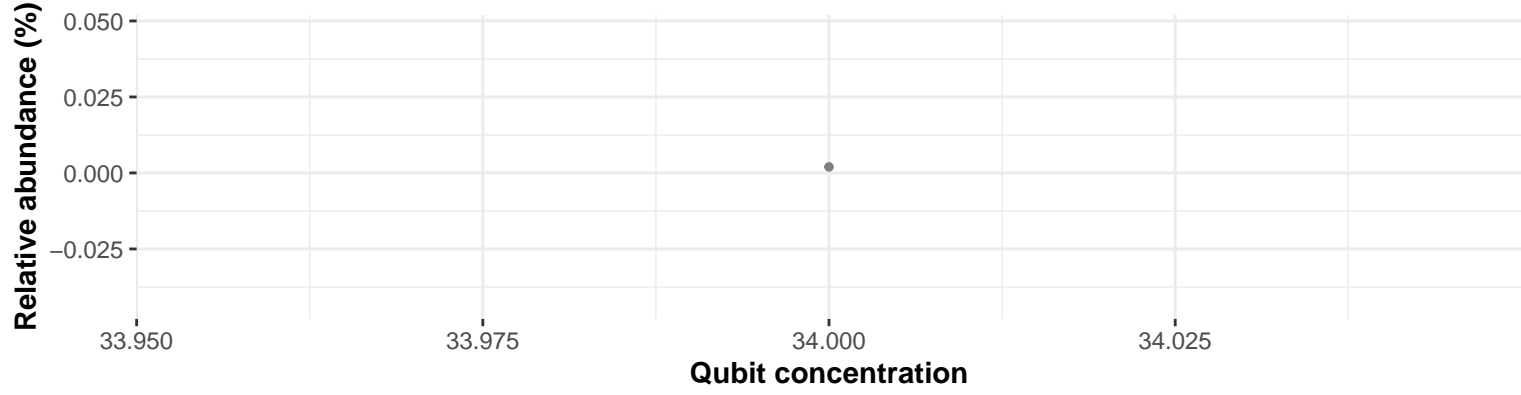
$\log_e(S) = 4.304$, $p = 0.779$, $\hat{\rho}_{\text{Spearman}} = 0.119$, $\text{CI}_{95\%} [-0.654, 0.771]$, $n_{\text{pairs}} = 8$



Correlation within: control



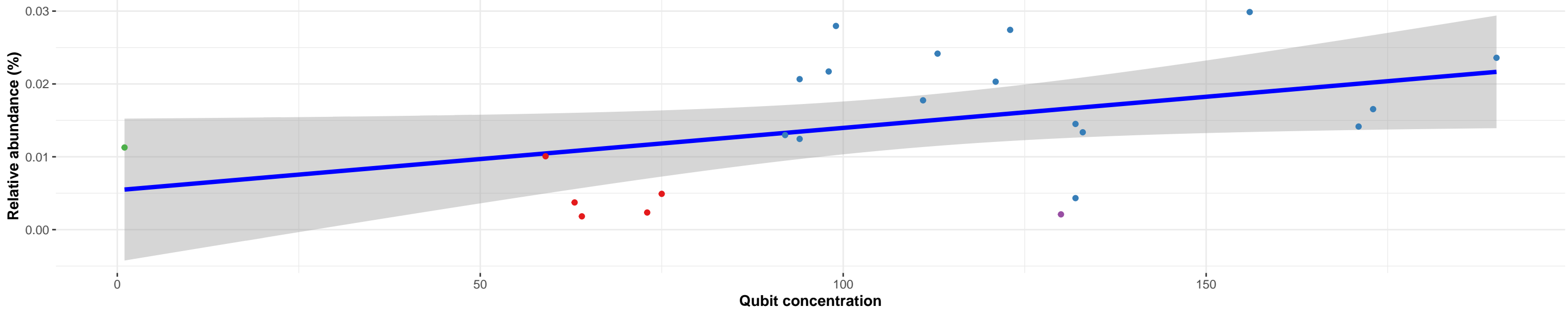
Correlation within: water



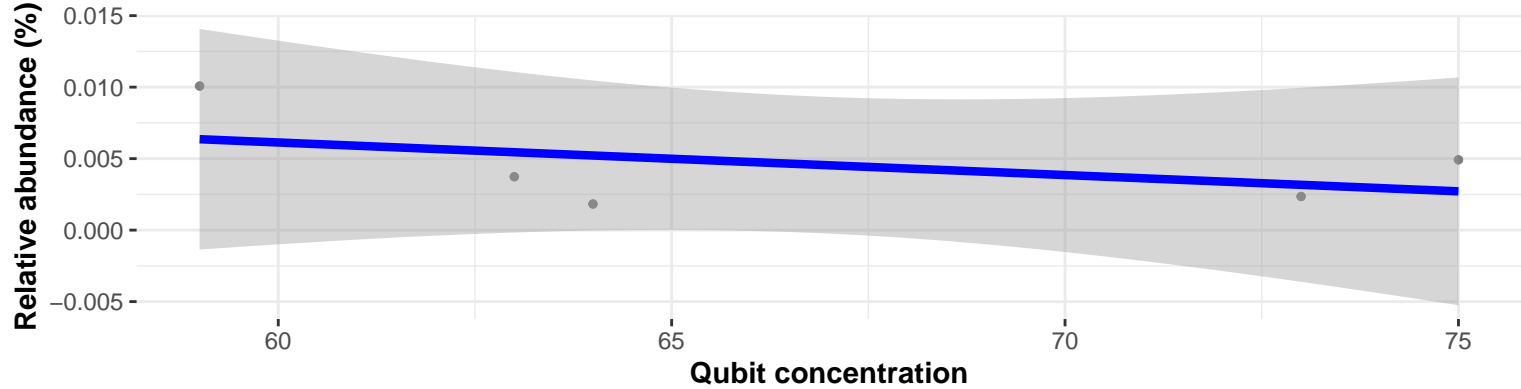
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; NA

Correlation with all samples

$\log_e(S) = 6.966$, $p = 0.022$, $\hat{\rho}_{\text{Spearman}} = 0.477$, $\text{CI}_{95\%} [0.067, 0.749]$, $n_{\text{pairs}} = 23$

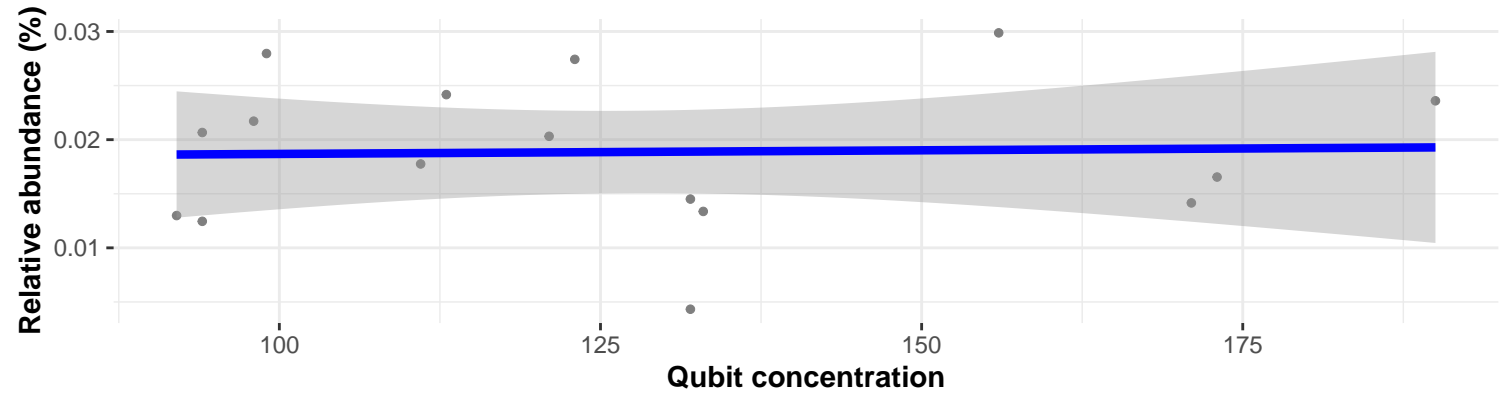


Correlation within: Digesta

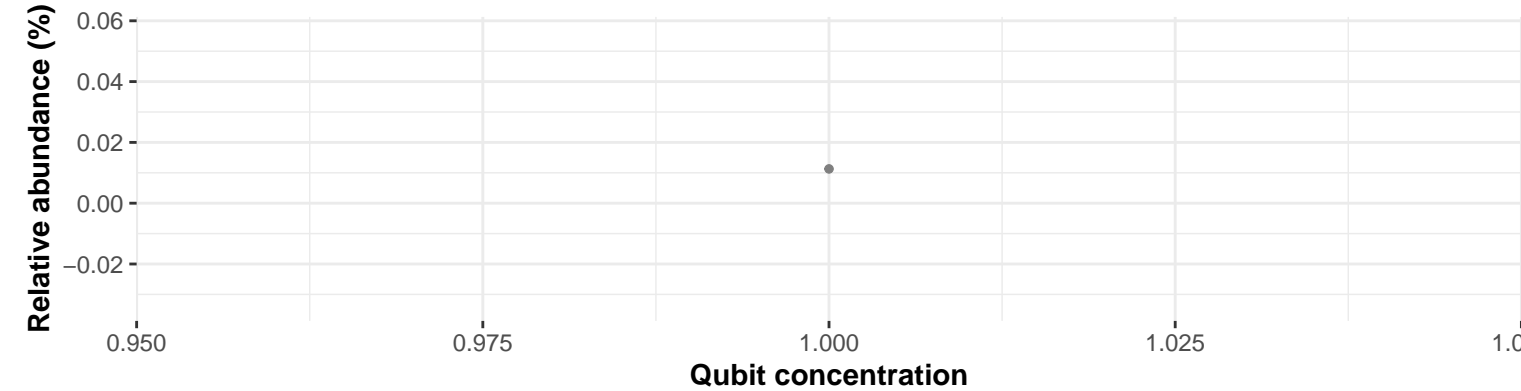


Correlation within: Feed

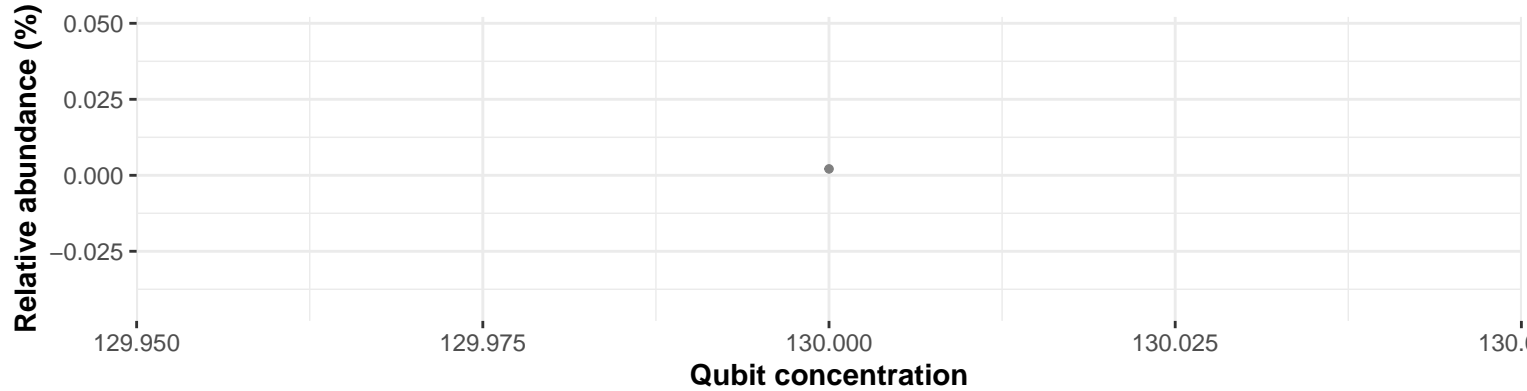
$\log_e(S) = 6.431$, $p = 0.749$, $\hat{\rho}_{\text{Spearman}} = 0.087$, $\text{CI}_{95\%} [-0.440, 0.569]$, $n_{\text{pairs}} = 16$



Correlation within: control



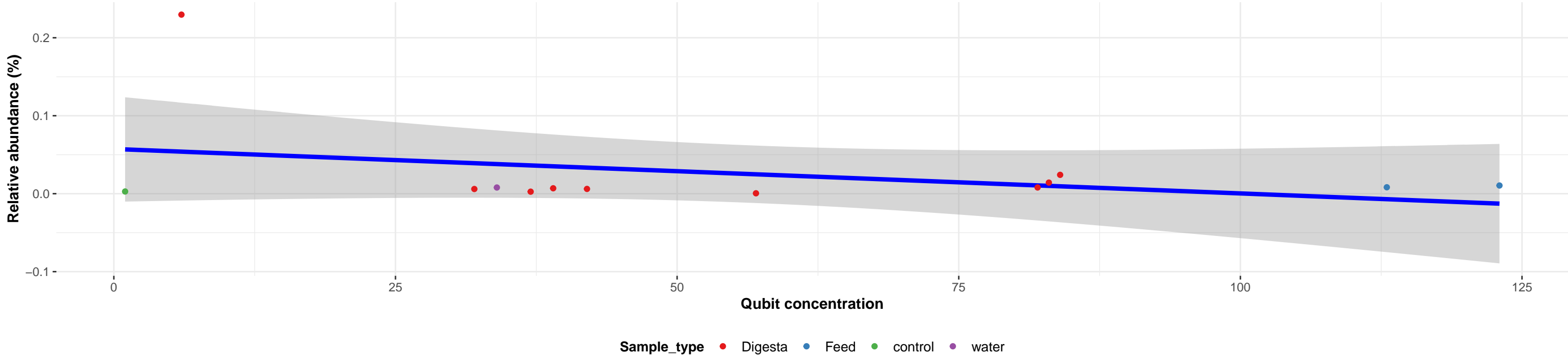
Correlation within: water



Bacteria; Firmicutes; Bacilli; Staphylococcales; Staphylococcaceae; Staphylococcus; NA

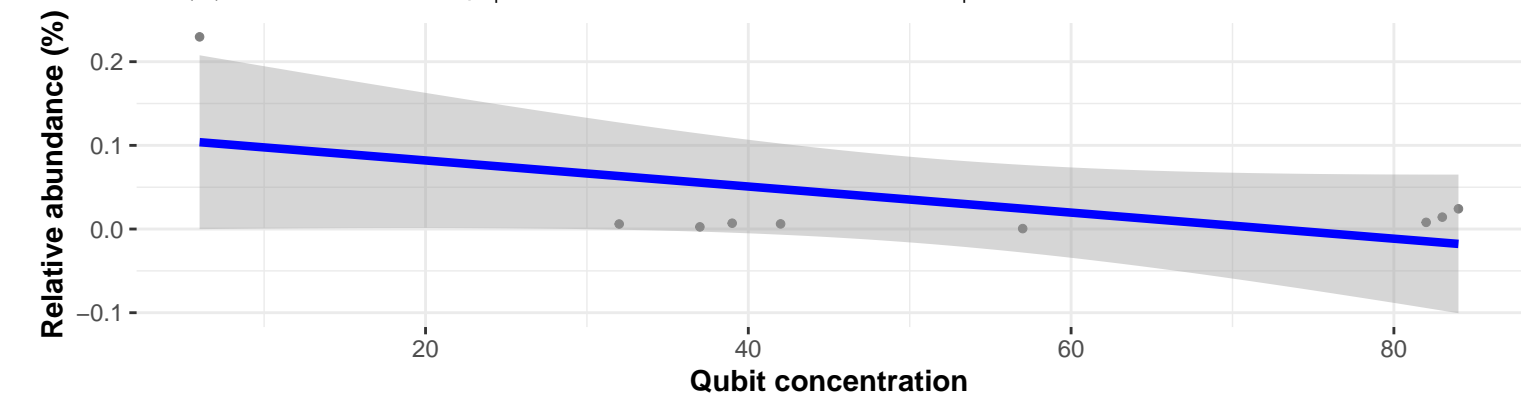
Correlation with all samples

$\log_e(S) = 5.384$, $p = 0.174$, $\hat{\rho}_{\text{Spearman}} = 0.401$, $CI_{95\%} [-0.210, 0.787]$, $n_{\text{pairs}} = 13$

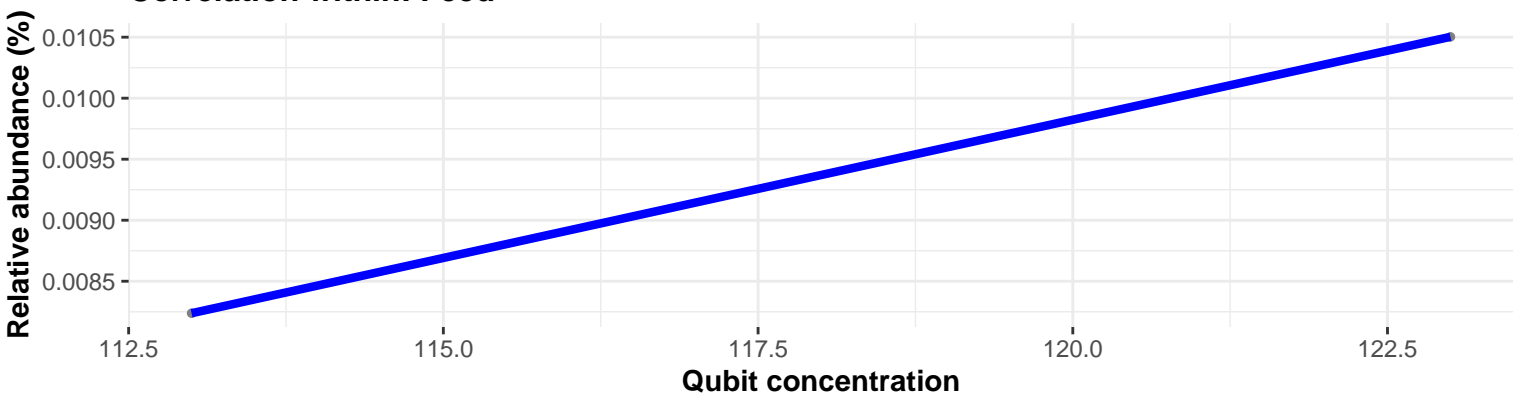


Correlation within: Digesta

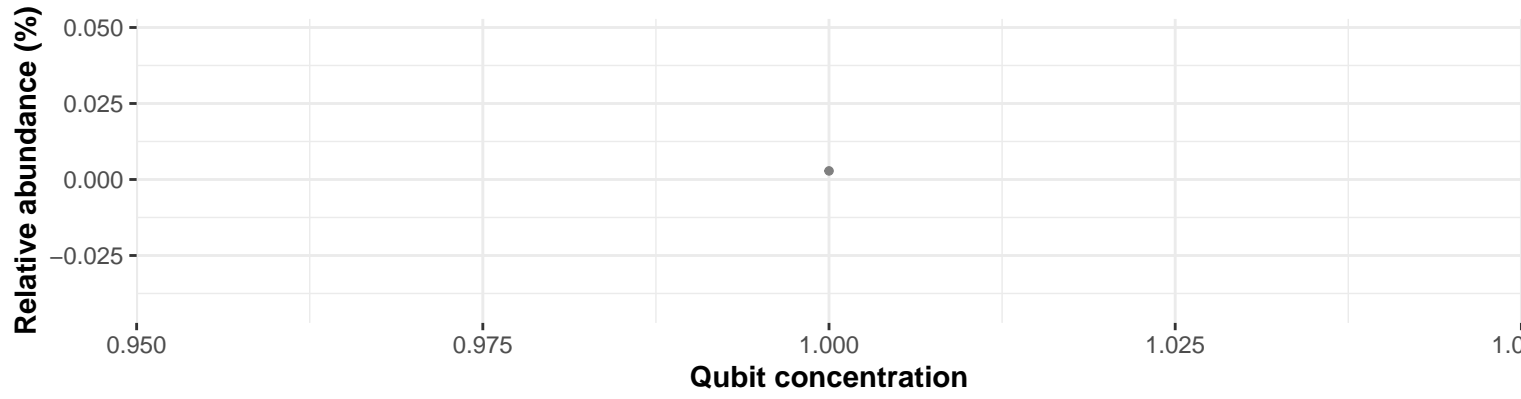
$\log_e(S) = 4.564$, $p = 0.606$, $\hat{\rho}_{\text{Spearman}} = 0.200$, $CI_{95\%} [-0.552, 0.773]$, $n_{\text{pairs}} = 9$



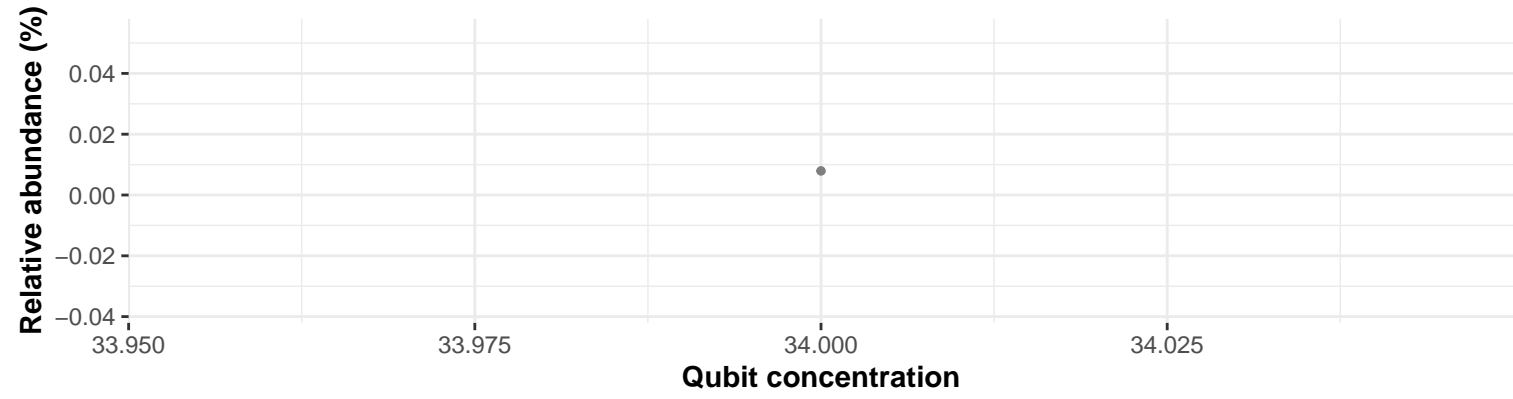
Correlation within: Feed



Correlation within: control



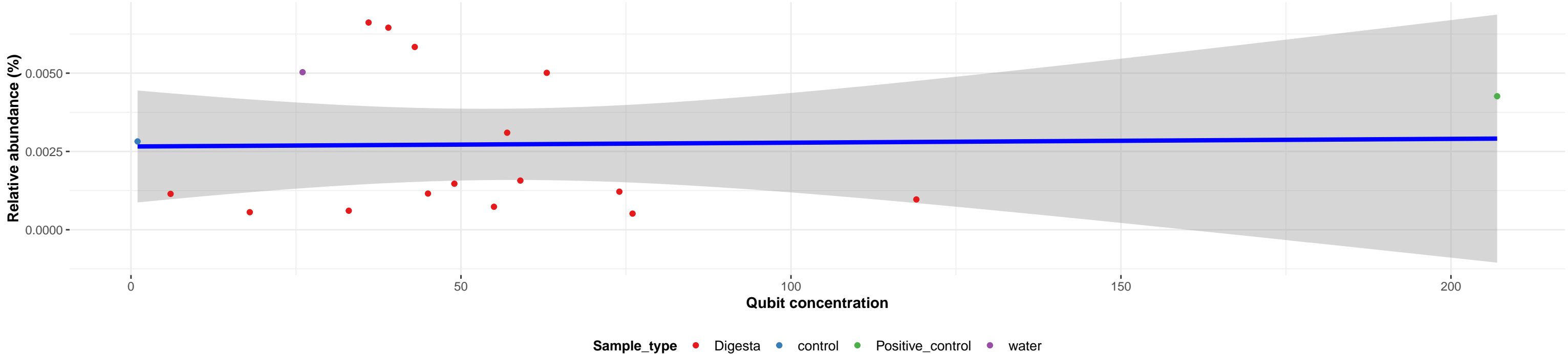
Correlation within: water



Bacteria; Firmicutes; Bacilli; Lactobacillales; NA; NA; NA

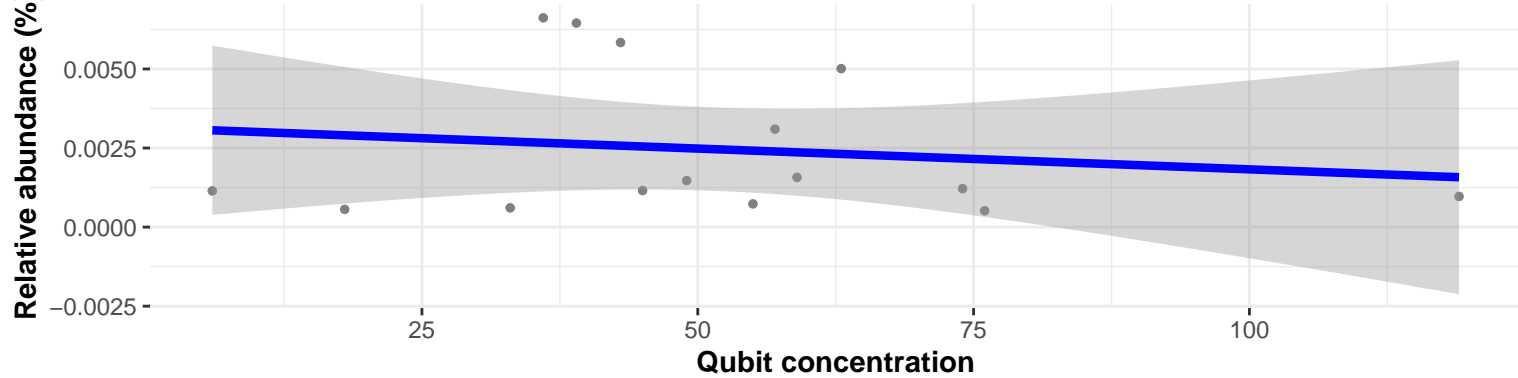
Correlation with all samples

$\log_e(S) = 6.962$, $p = 0.723$, $\hat{\rho}_{\text{Spearman}} = -0.090$, $\text{CI}_{95\%} [-0.545, 0.406]$, $n_{\text{pairs}} = 18$

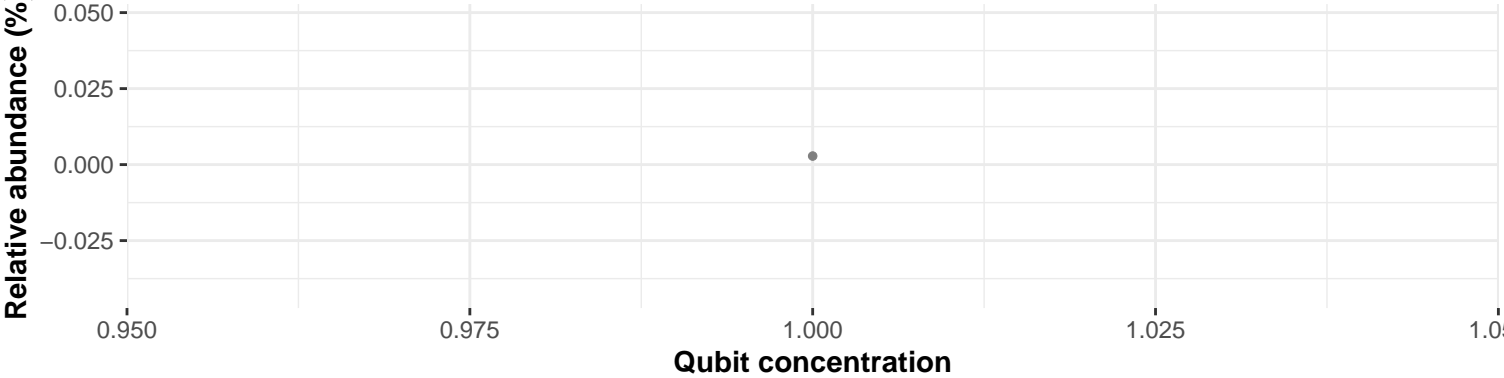


Correlation within: Digesta

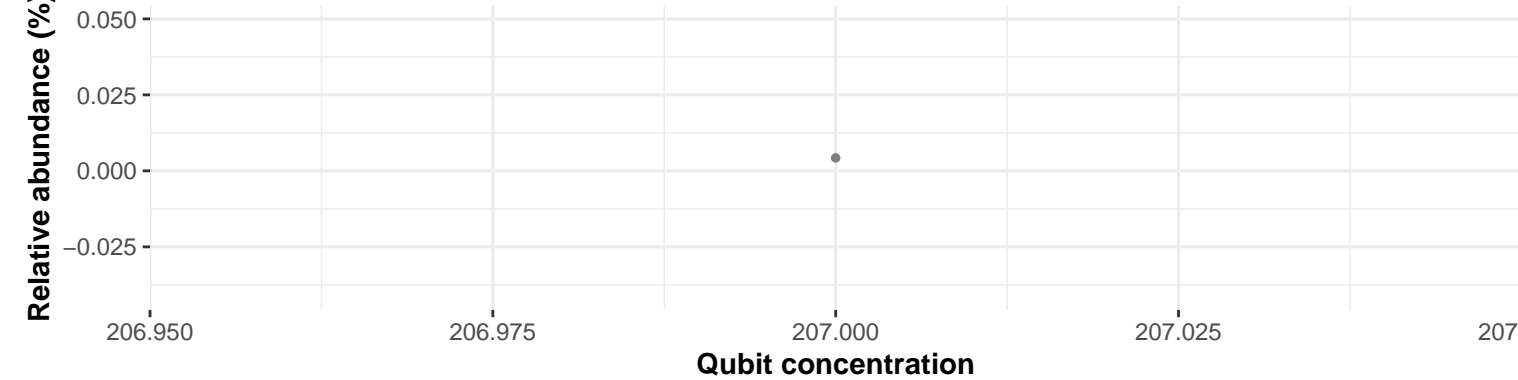
$\log_e(S) = 6.394$, $p = 0.810$, $\hat{\rho}_{\text{Spearman}} = -0.068$, $\text{CI}_{95\%} [-0.572, 0.473]$, $n_{\text{pairs}} = 15$



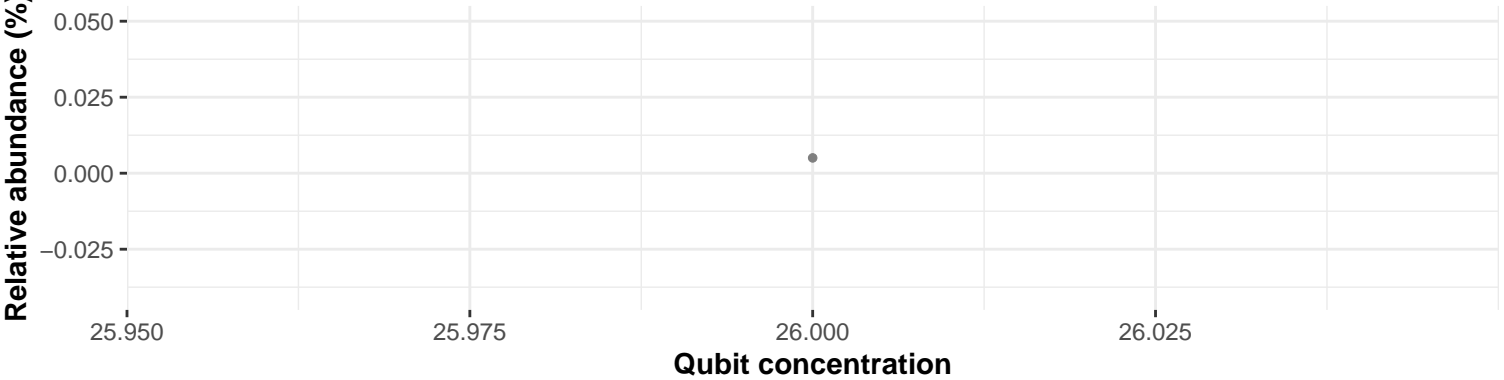
Correlation within: control



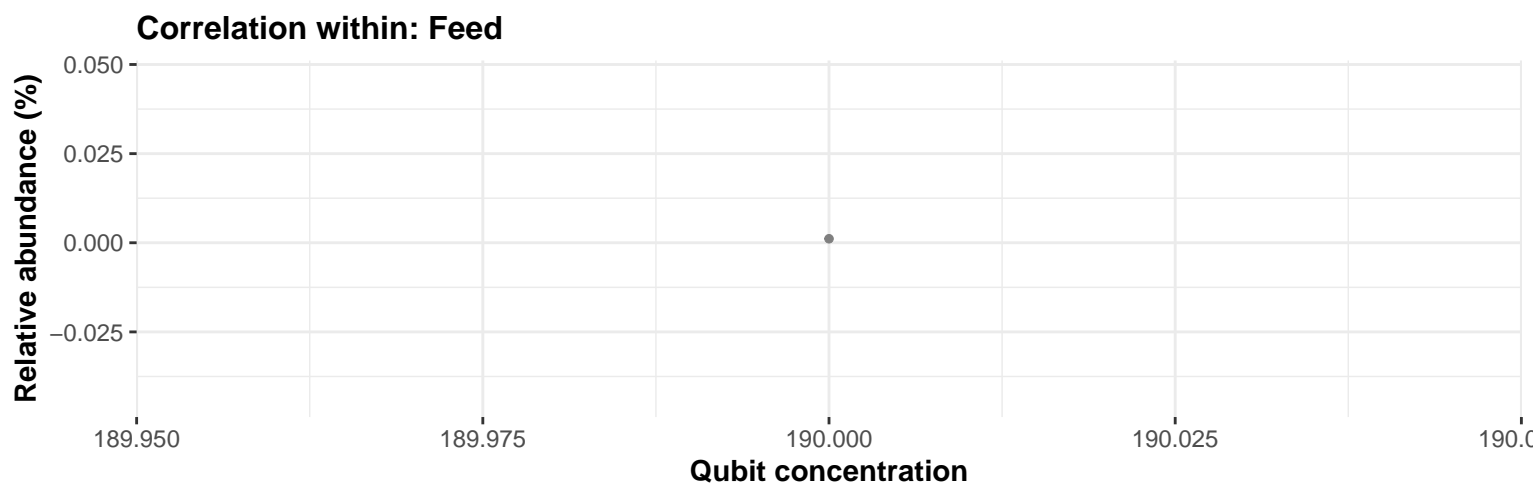
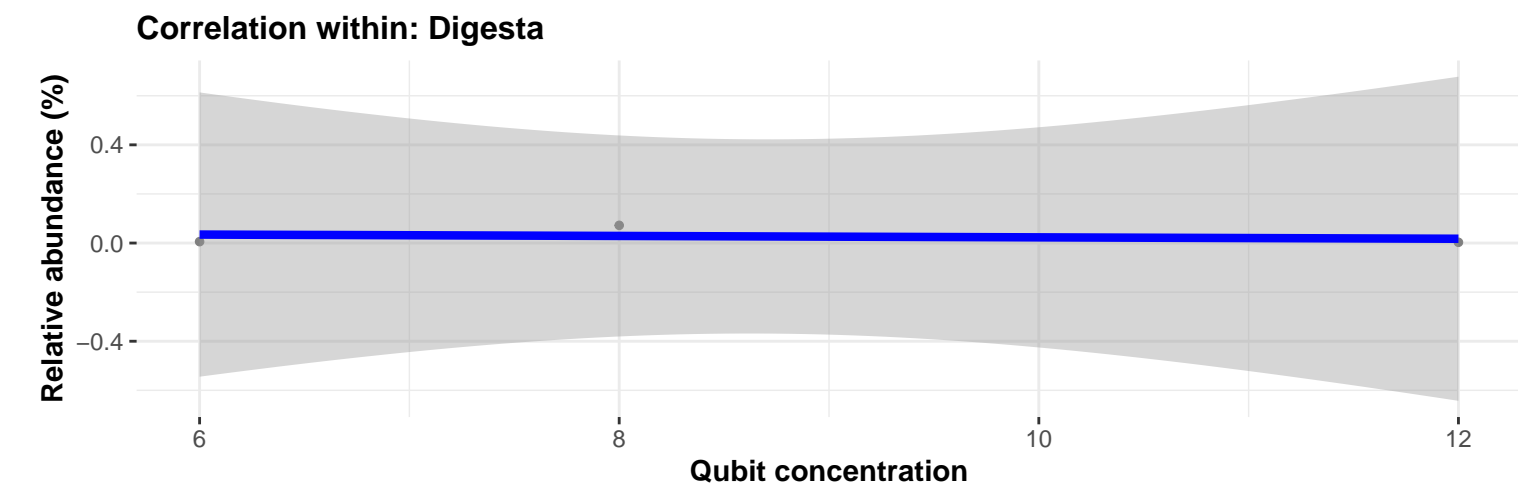
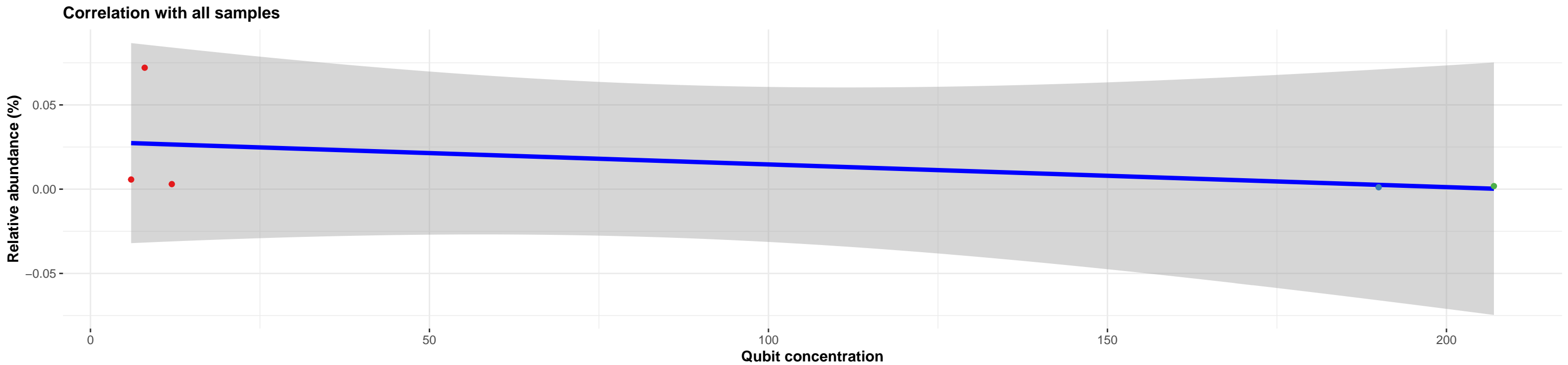
Correlation within: Positive_control



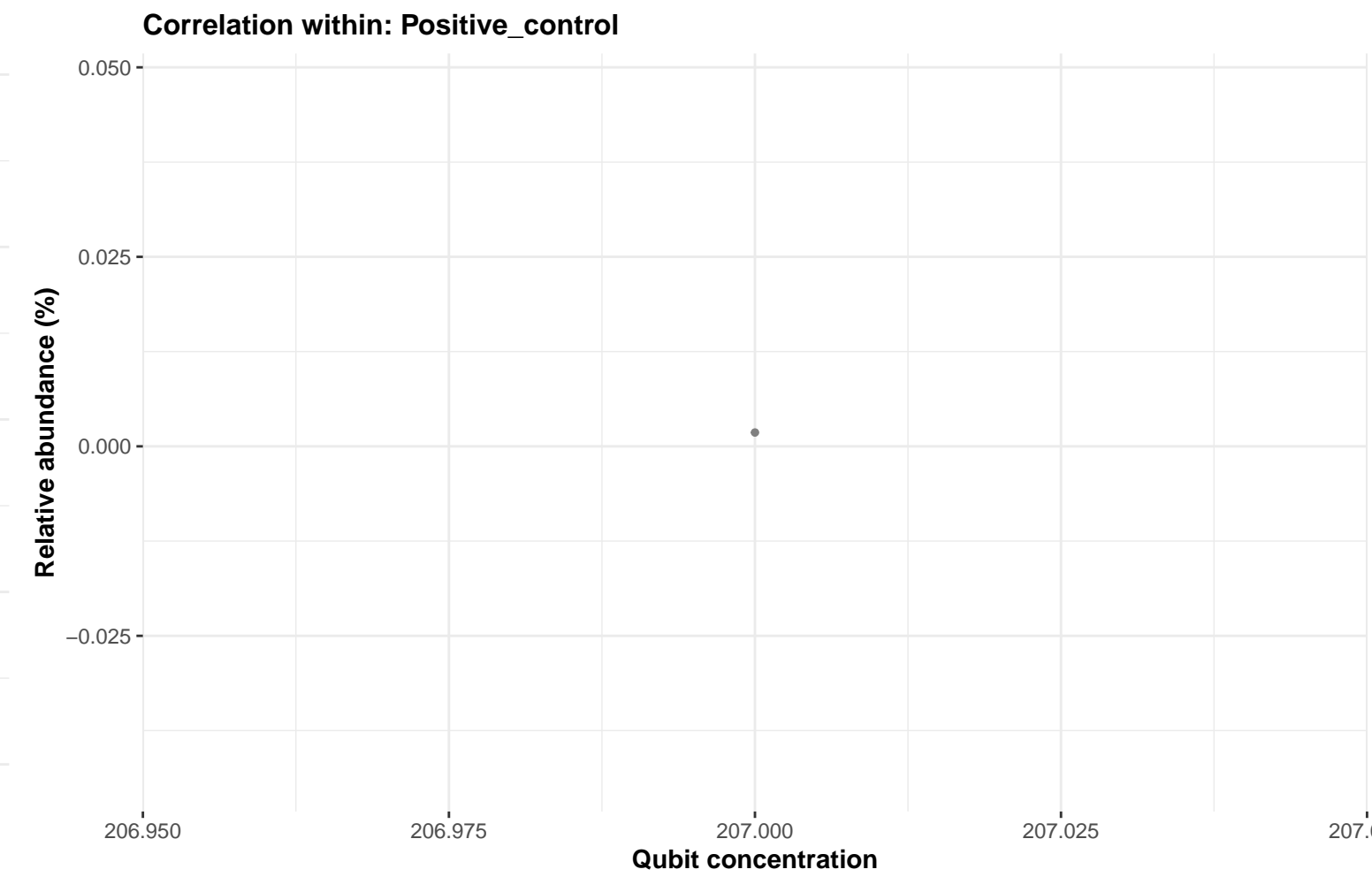
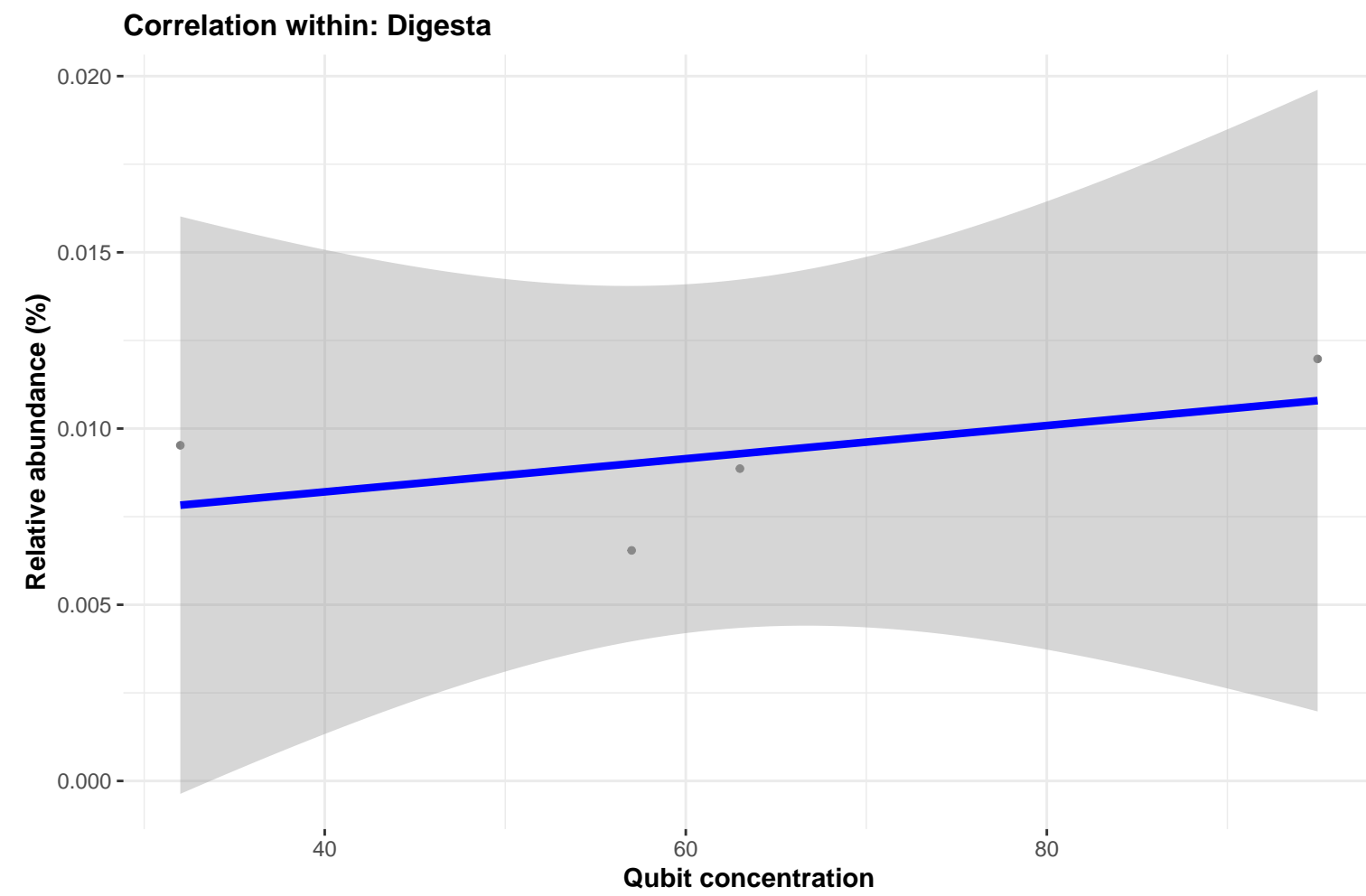
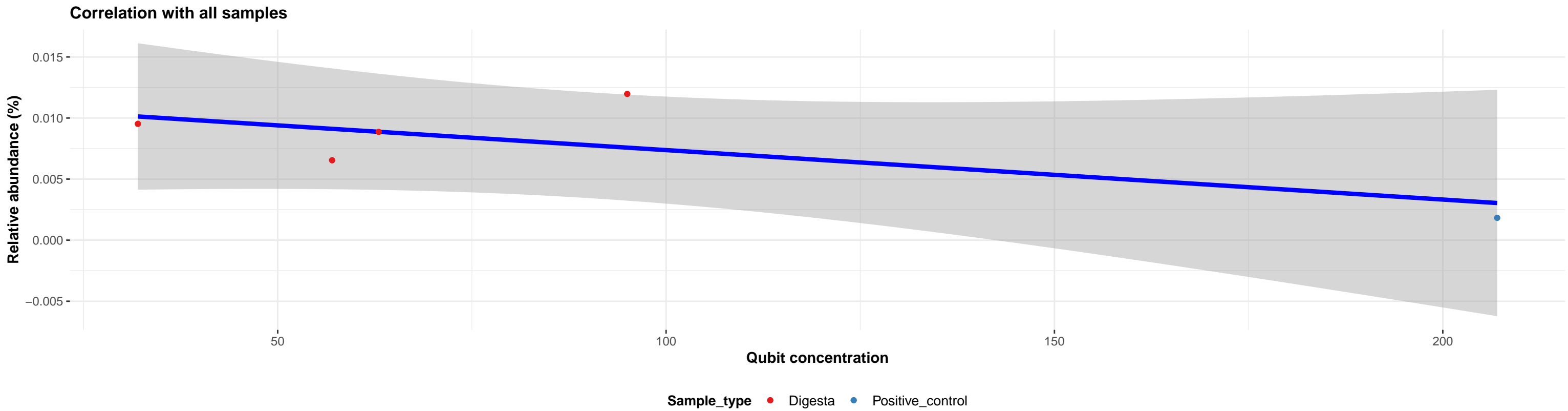
Correlation within: water



Bacteria; Actinobacteriota; Actinobacteria; Corynebacteriales; Corynebacteriaceae; Corynebacterium; urealyticum



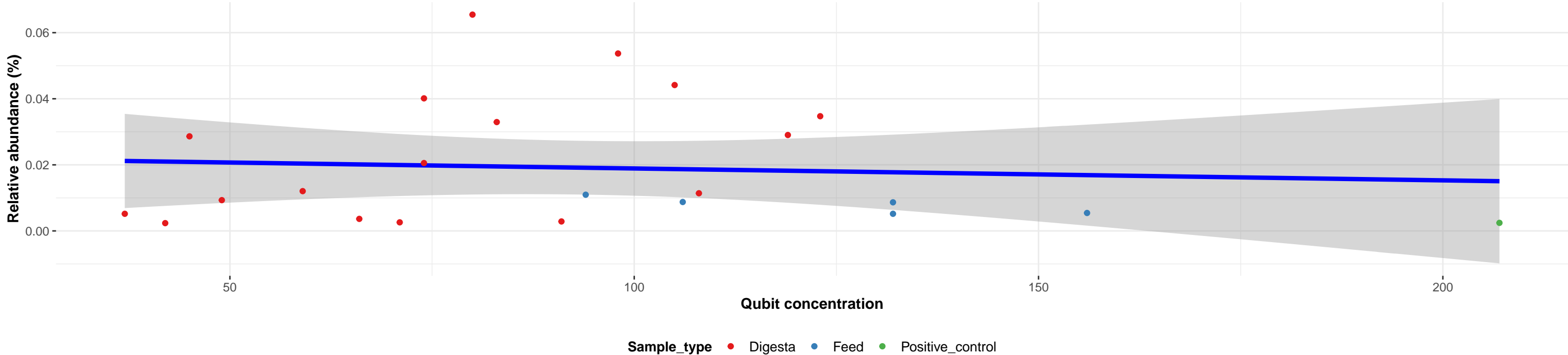
Bacteria; Firmicutes; Bacilli; Lactobacillales; Vagococcaceae; Vagococcus; fluvialis



Bacteria; Firmicutes; Clostridia; Peptostreptococcales–Tissierellales; Anaerovoracaceae; NA; NA

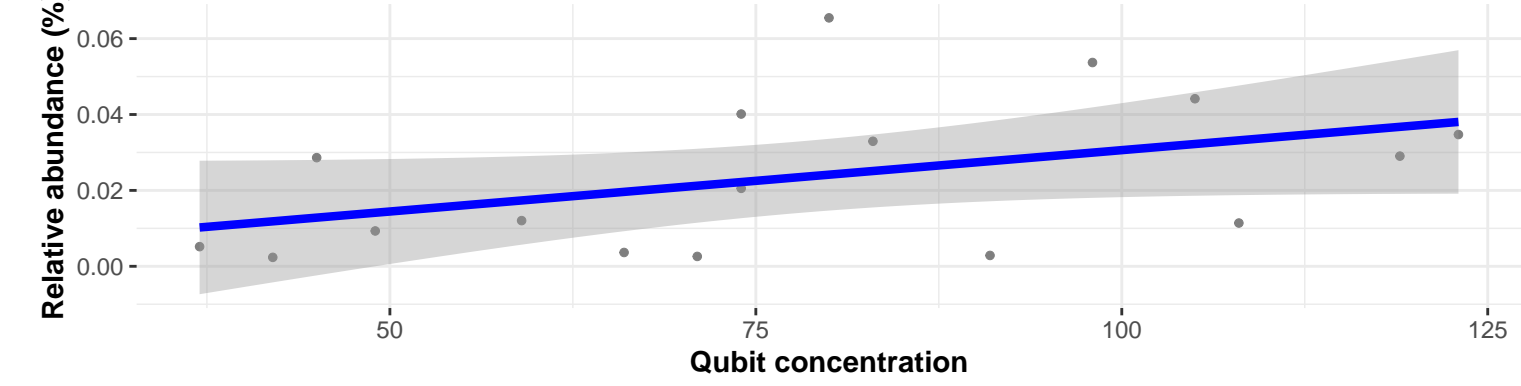
Correlation with all samples

$\log_e(S) = 7.552$, $p = 0.790$, $\hat{\rho}_{\text{Spearman}} = 0.059$, $CI_{95\%} [-0.373, 0.470]$, $n_{\text{pairs}} = 23$

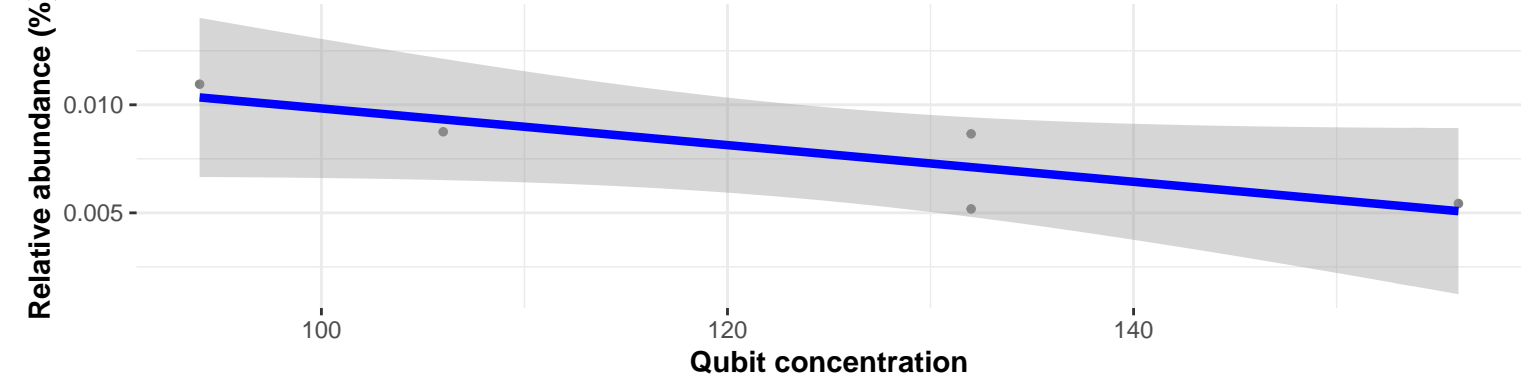


Correlation within: Digesta

$\log_e(S) = 5.953$, $p = 0.029$, $\hat{\rho}_{\text{Spearman}} = 0.529$, $CI_{95\%} [0.049, 0.810]$, $n_{\text{pairs}} = 17$



Correlation within: Feed



Correlation within: Positive_control

