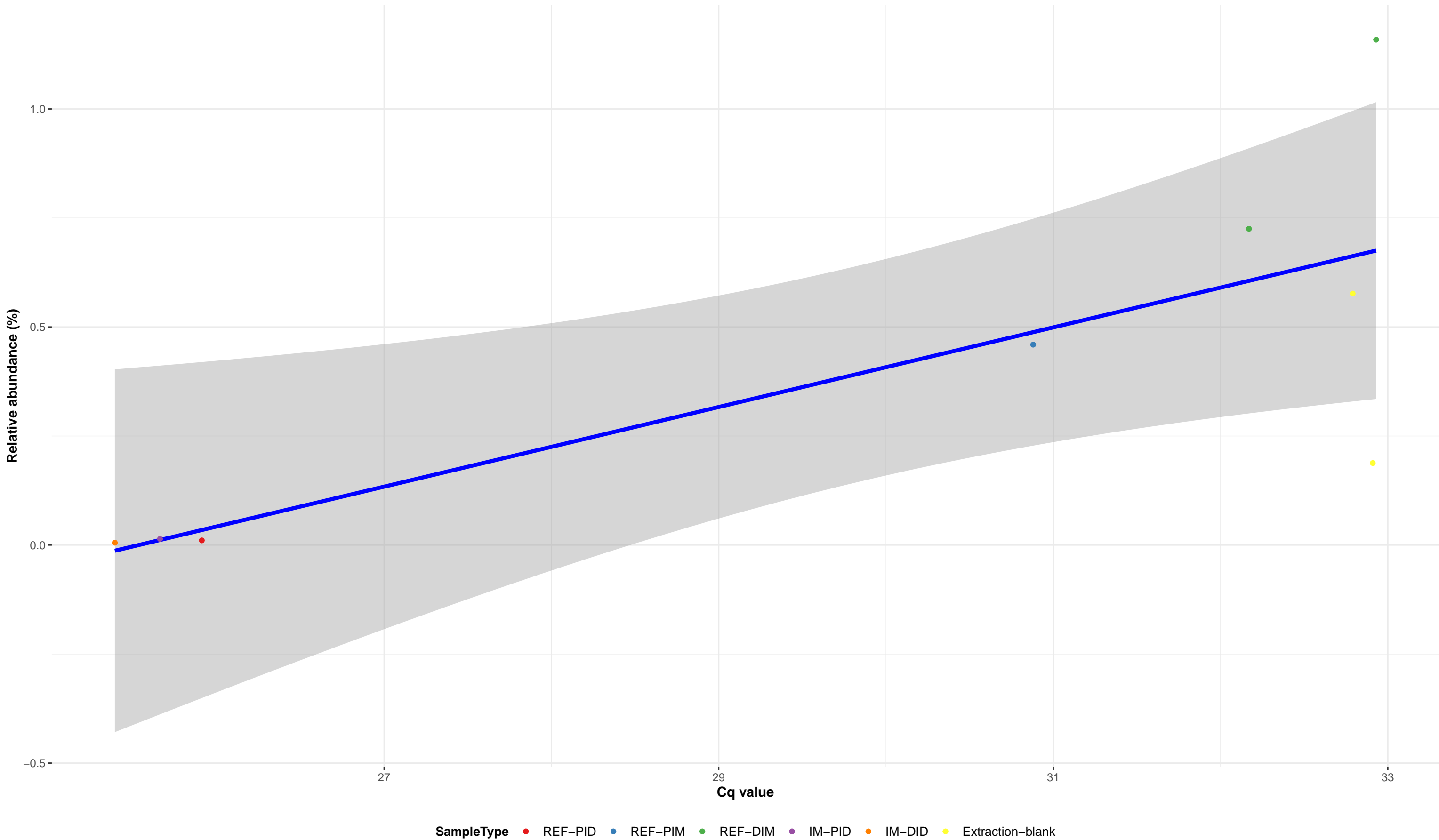
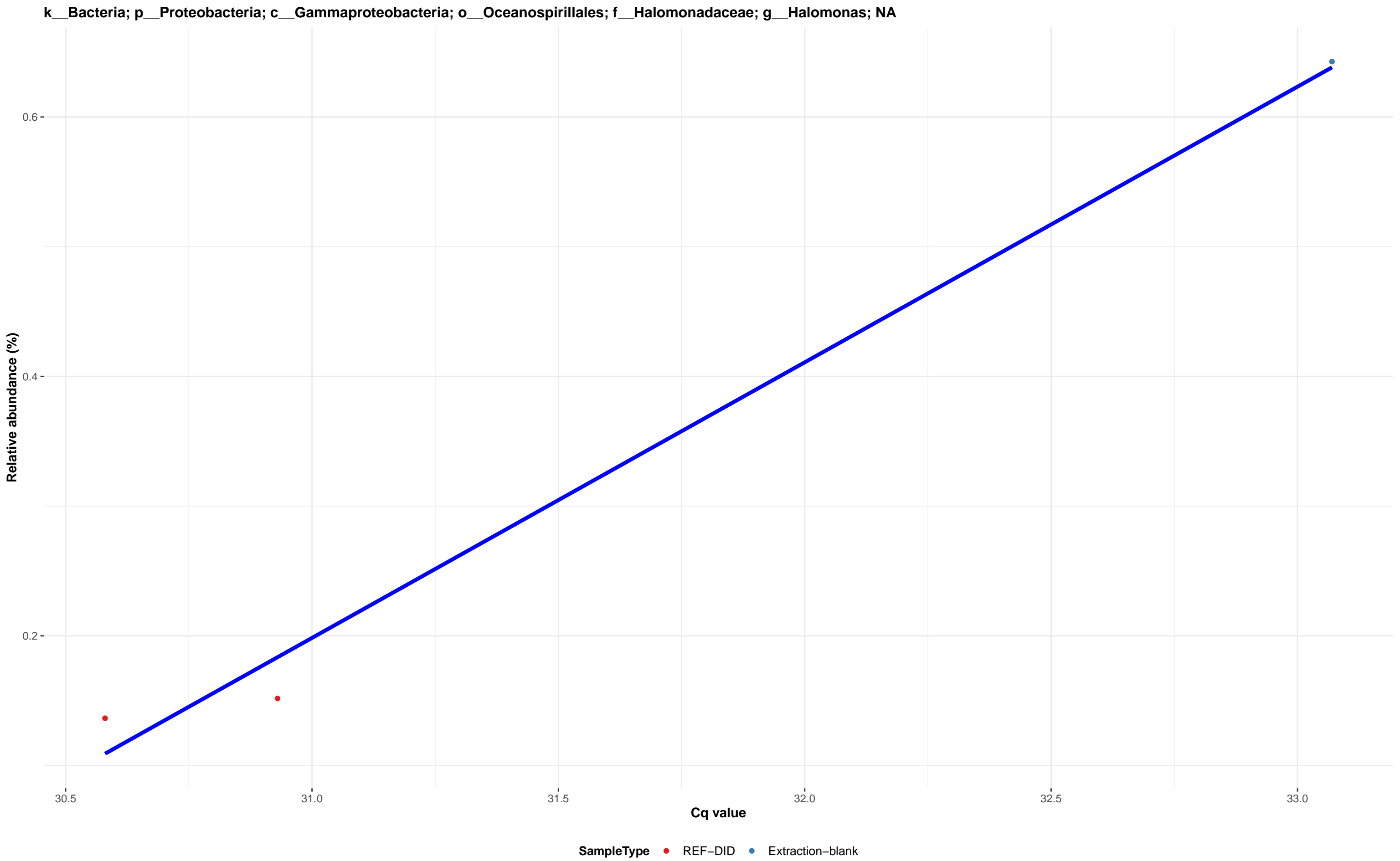


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Betaproteobacteriales; f__Burkholderiaceae; g__Pelomonas; NA

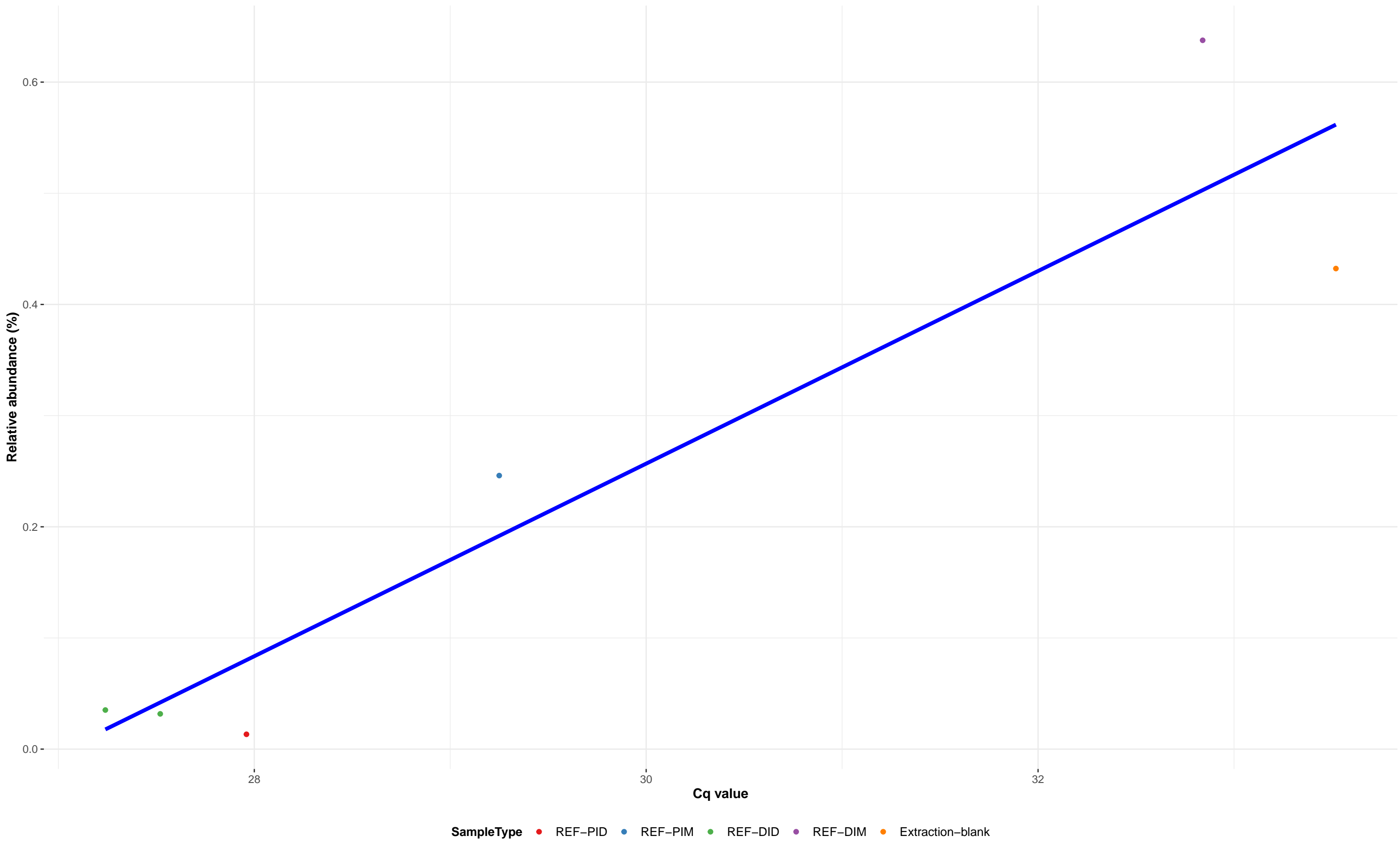
$\log_e(S) = 2.773$, $p = 0.015$, $\hat{\rho}_{\text{Spearman}} = 0.810$, $\text{CI}_{95\%} [0.220, 0.966]$, $n_{\text{pairs}} = 8$



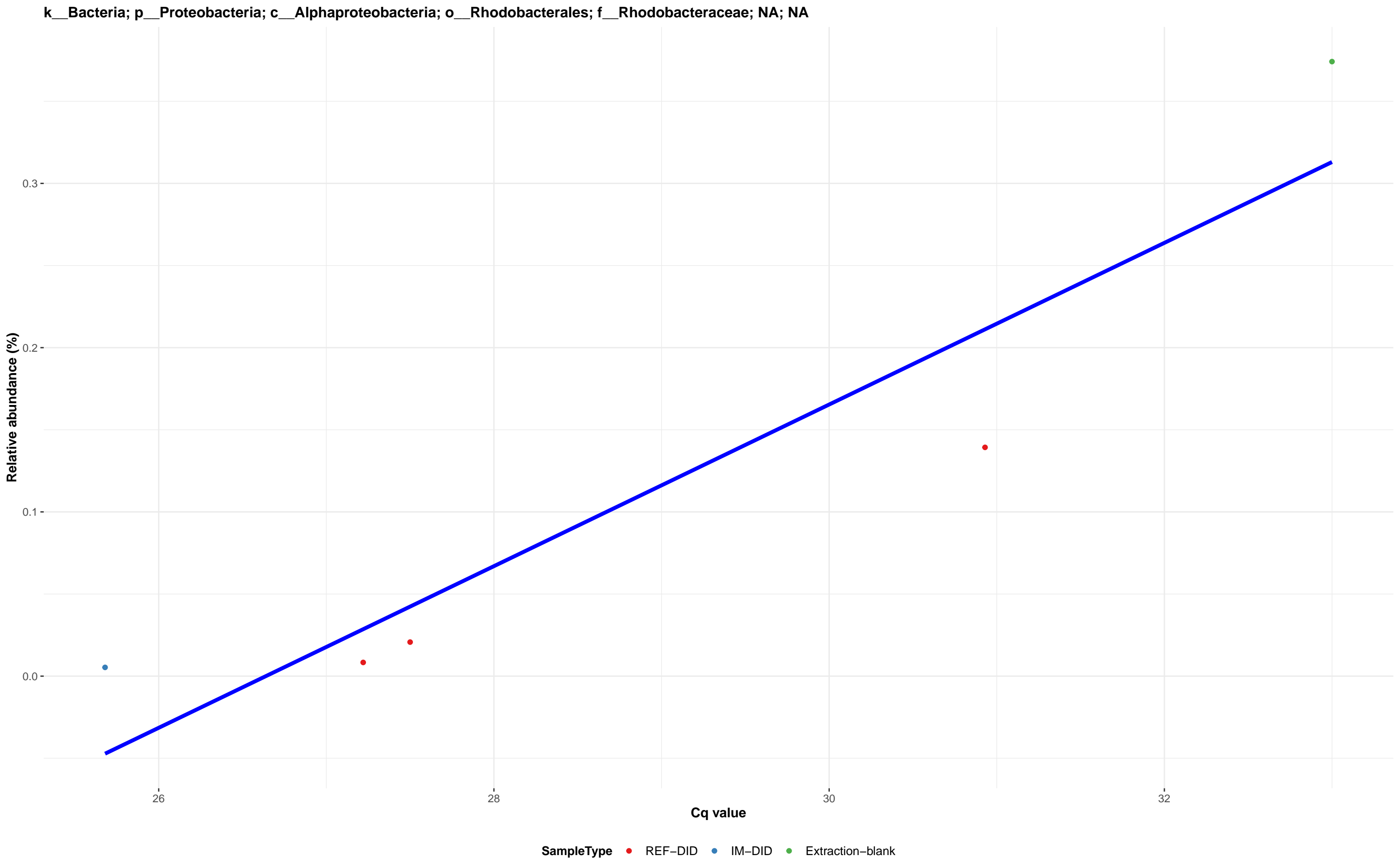
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; NA



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Moraxellaceae; g__Acinetobacter; NA



k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; NA; NA

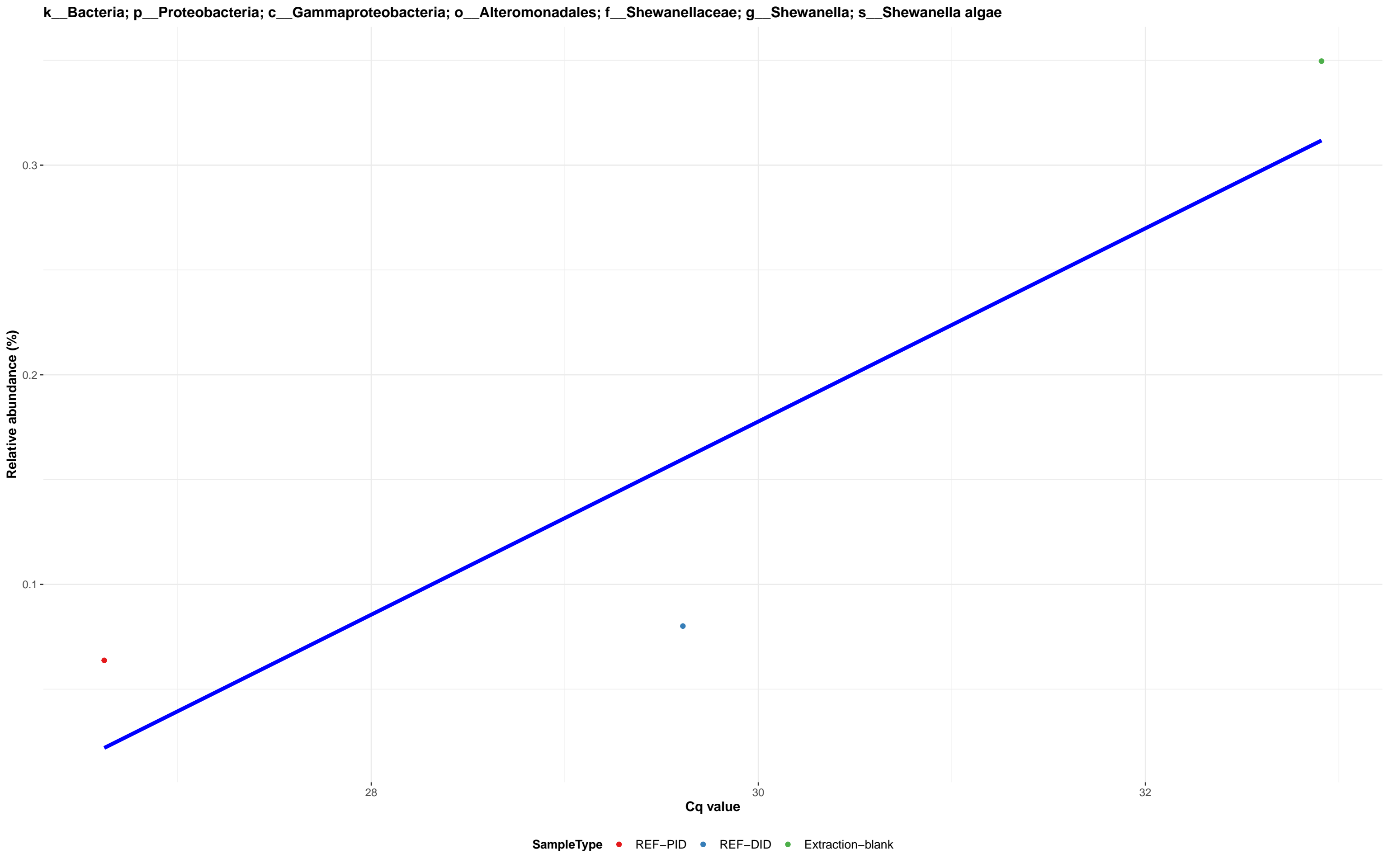


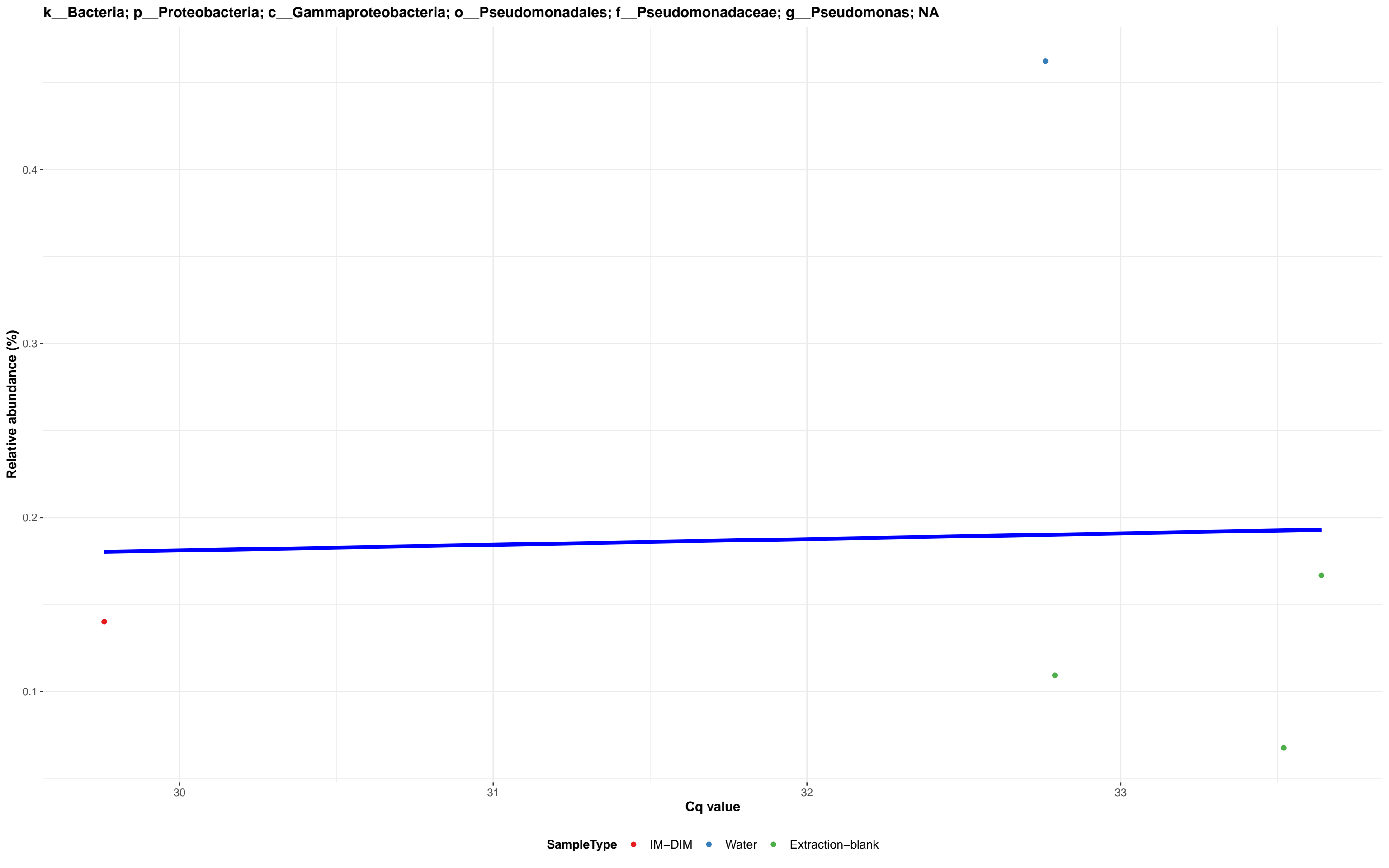
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; s__Shewanella algae

Relative abundance (%)

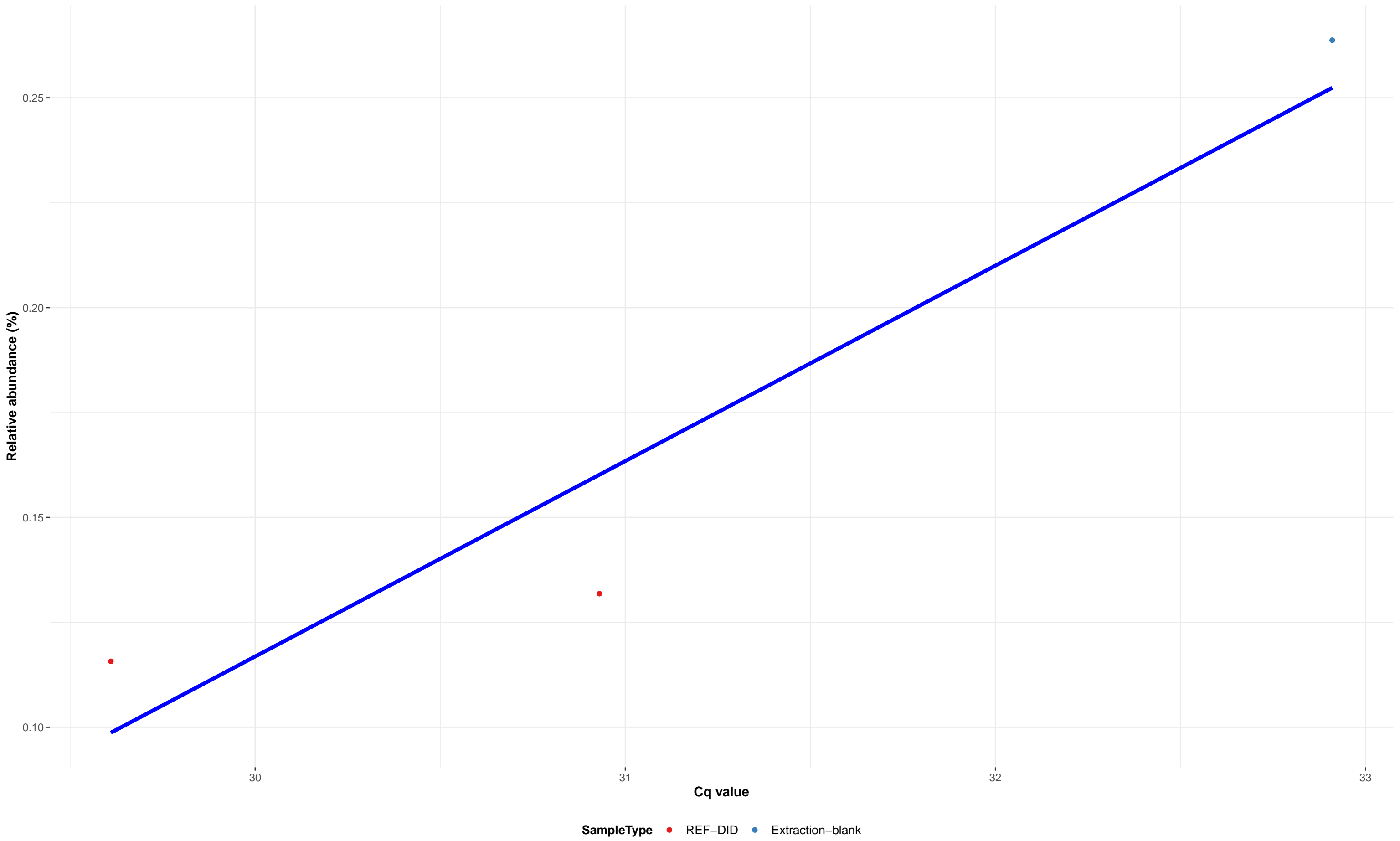
Cq value

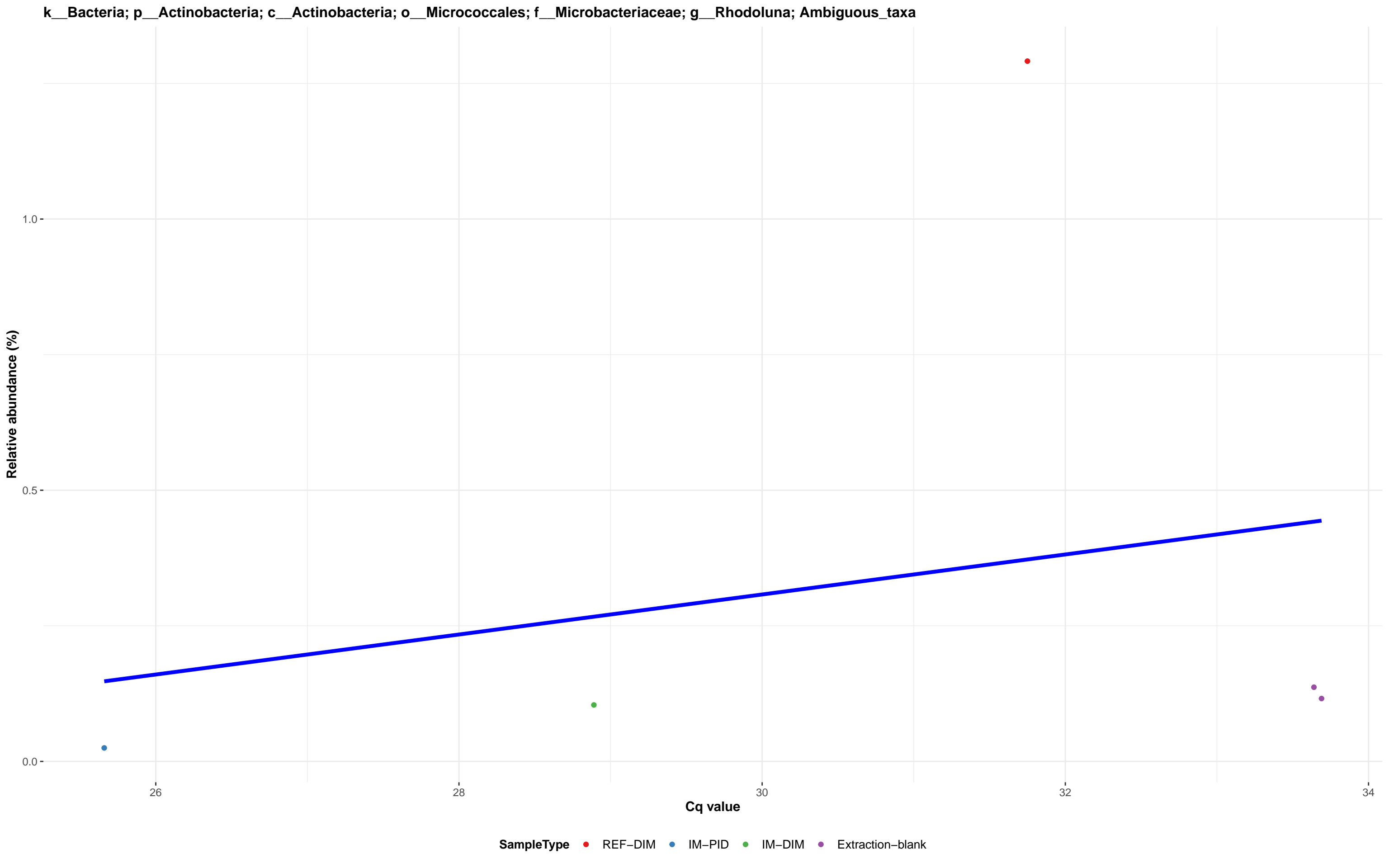
SampleType REF-PID REF-DID Extraction-blank



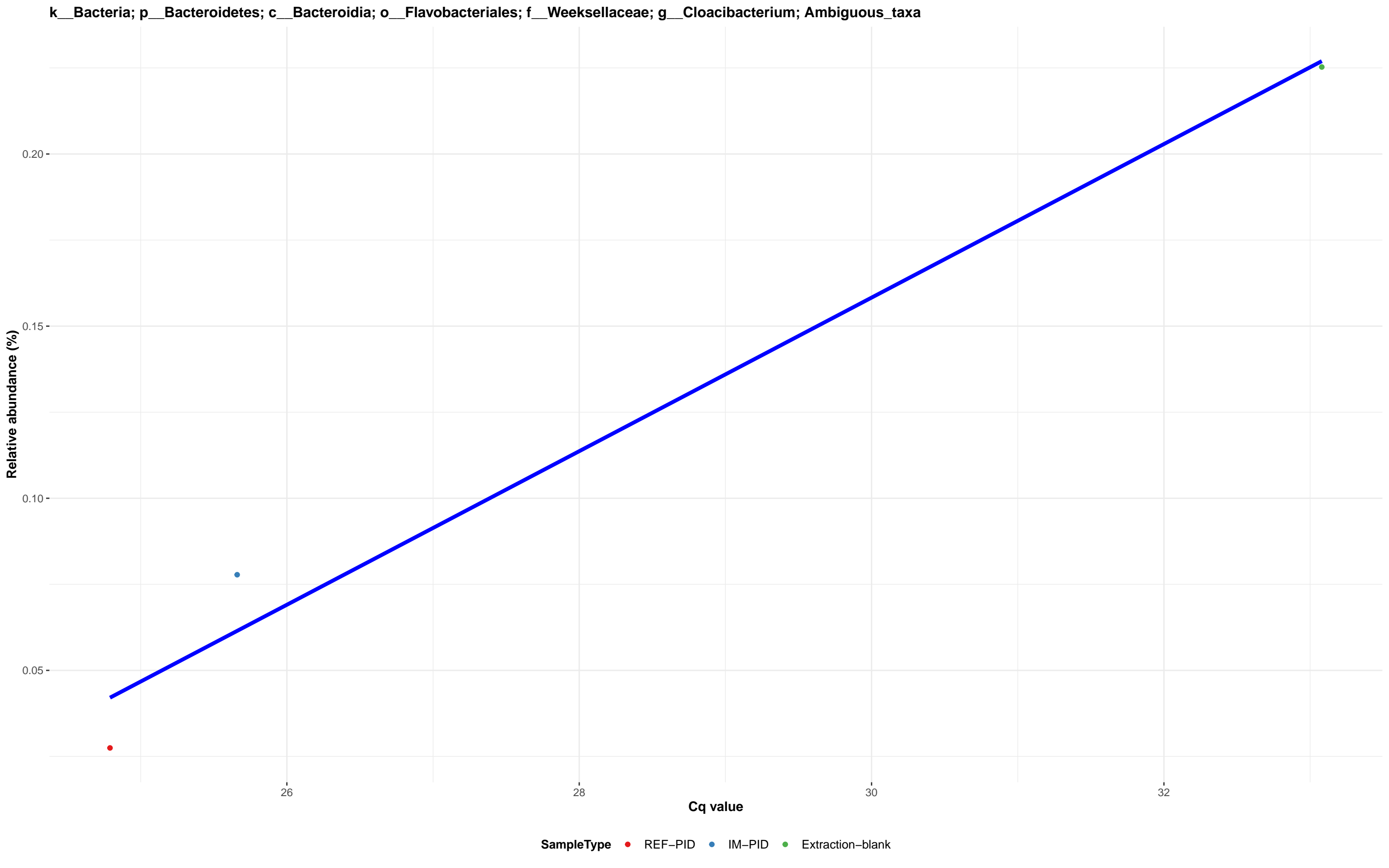


k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas; NA

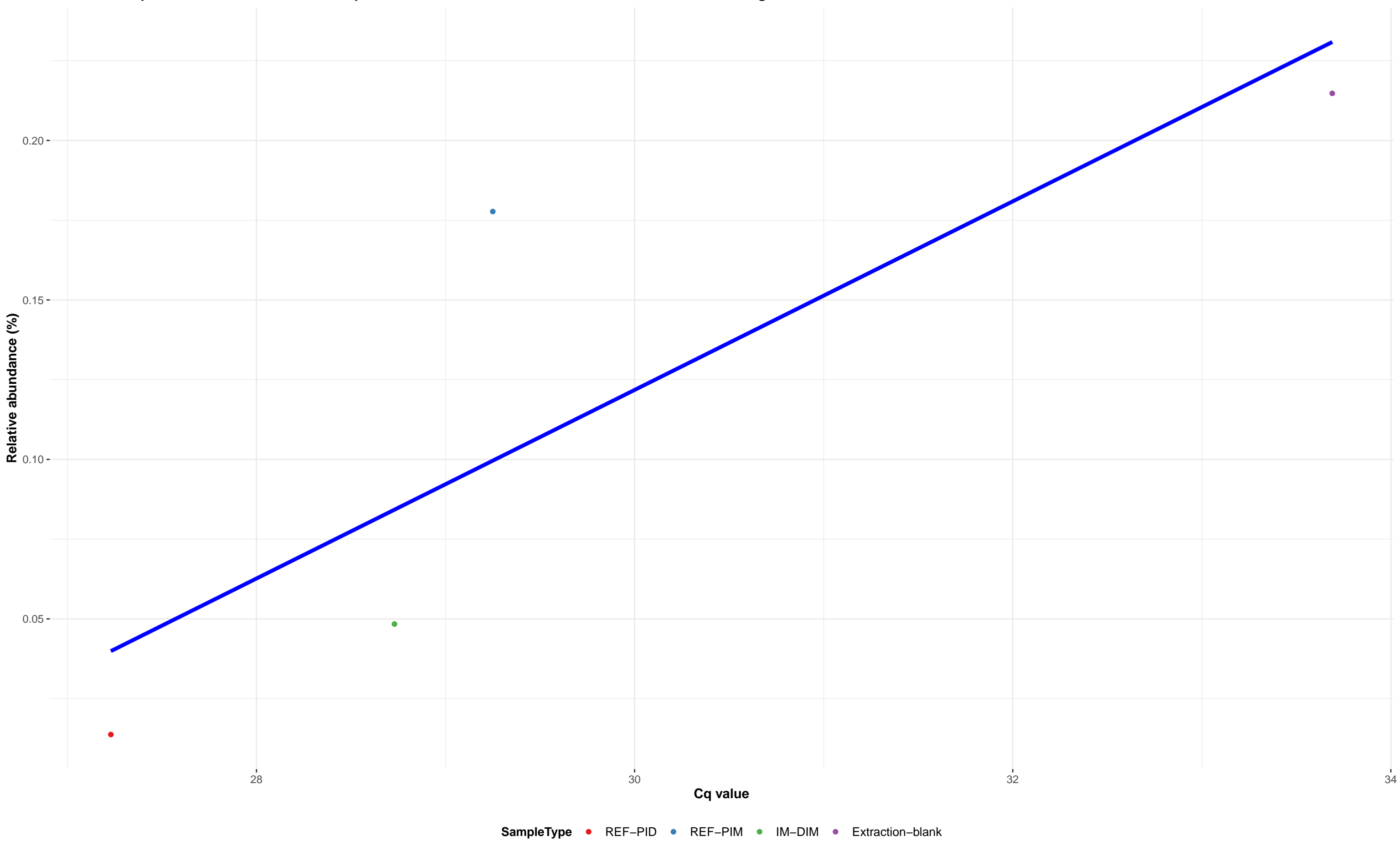


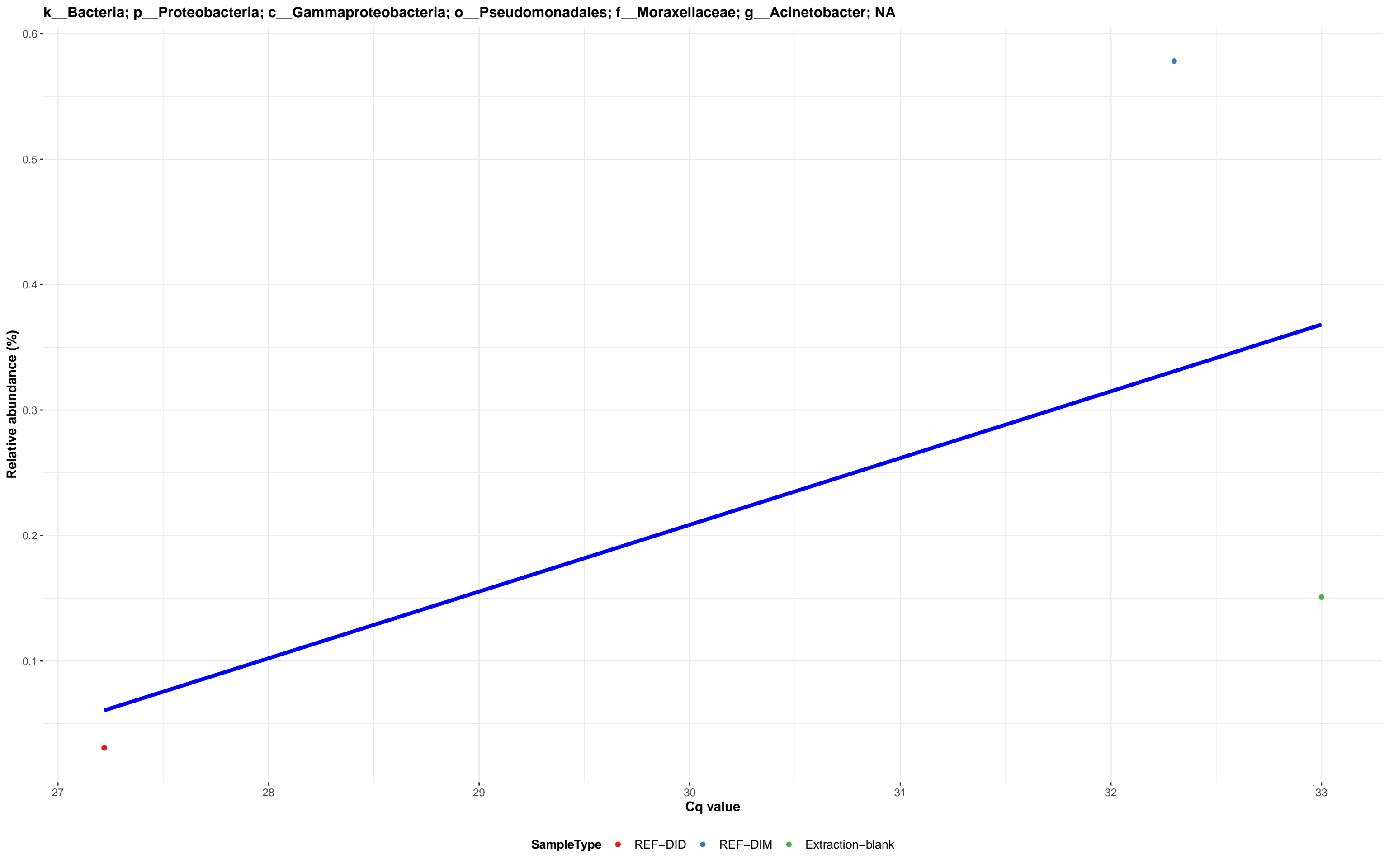


k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Flavobacteriales; f__Weeksellaceae; g__Cloacibacterium; Ambiguous_taxa



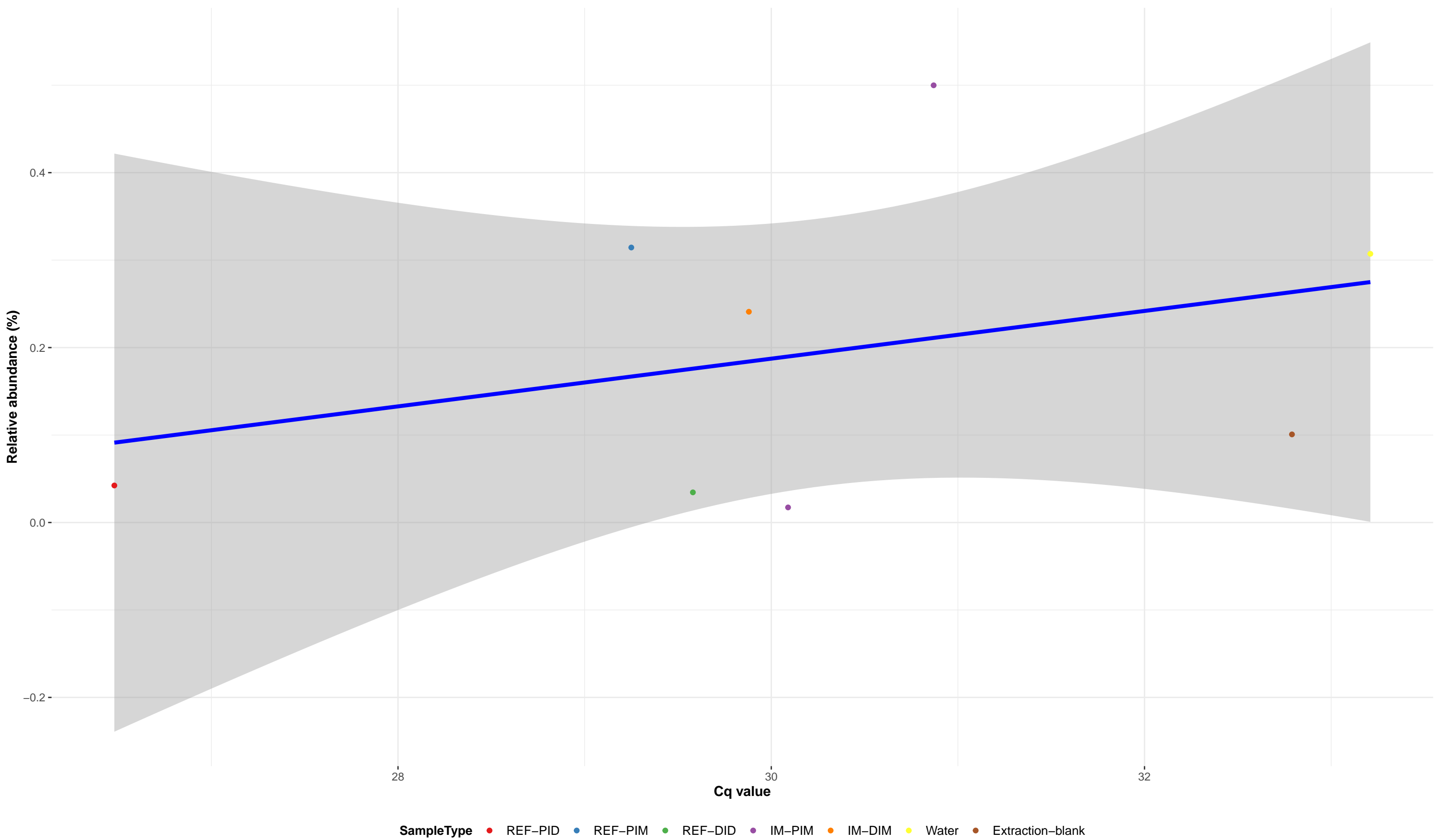
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella; NA





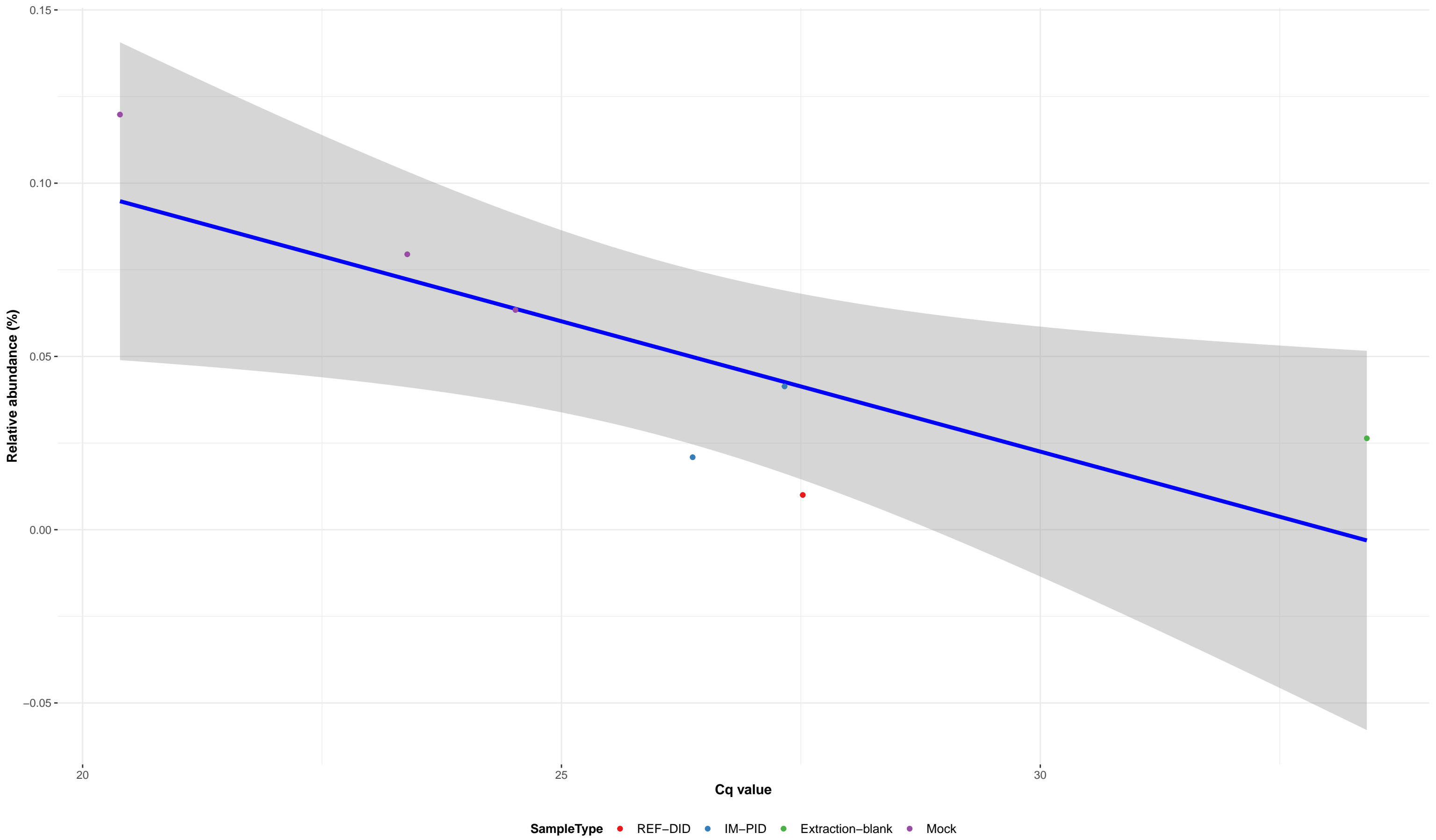
k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; NA

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



k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; NA; NA

$\log_e(S) = 4.625$, $p = 0.023$, $\hat{\rho}_{\text{Spearman}} = -0.821$, $\text{CI}_{95\%} [-0.974, -0.151]$, $n_{\text{pairs}} = 7$



k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; NA

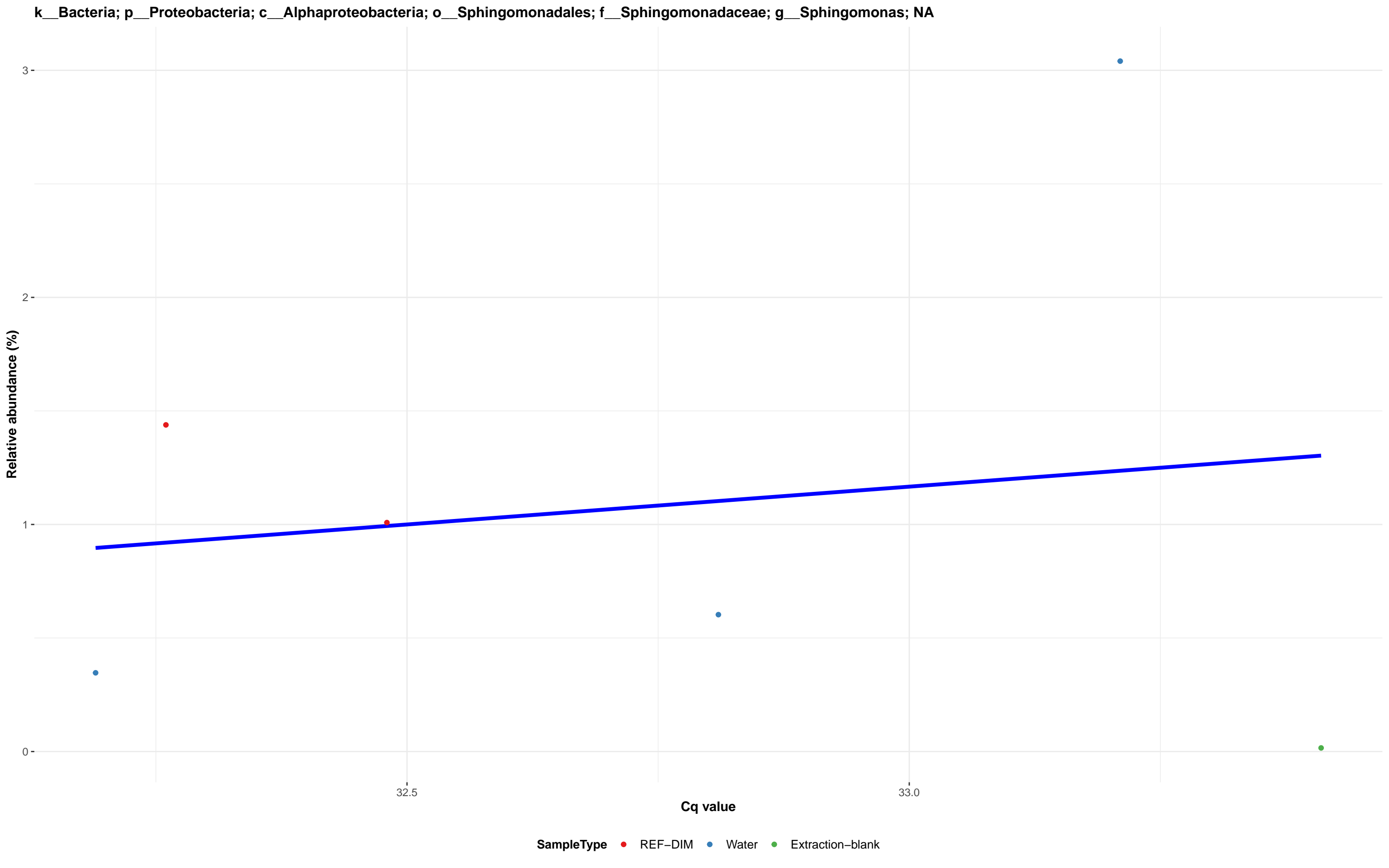
Relative abundance (%)

32.5

Cq value

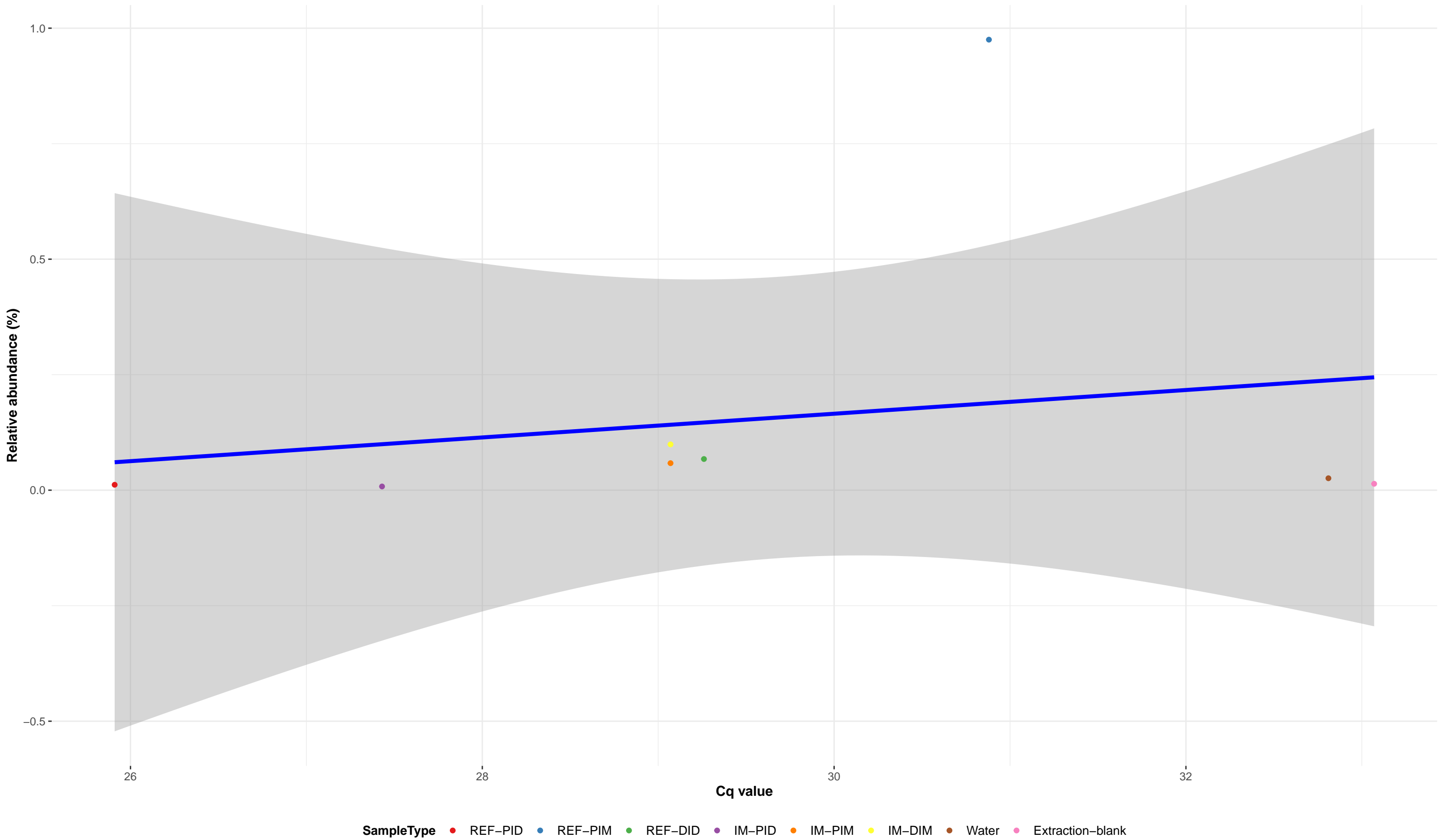
33.0

SampleType REF-DIM Water Extraction-blank



k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Desulfuromonadales; f__Desulfuromonadaceae; NA; NA

$\log_e(S) = 4.022$, $p = 0.417$, $\hat{\rho}_{\text{Spearman}} = 0.335$, $\text{CI}_{95\%} [-0.503, 0.849]$, $n_{\text{pairs}} = 8$



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

