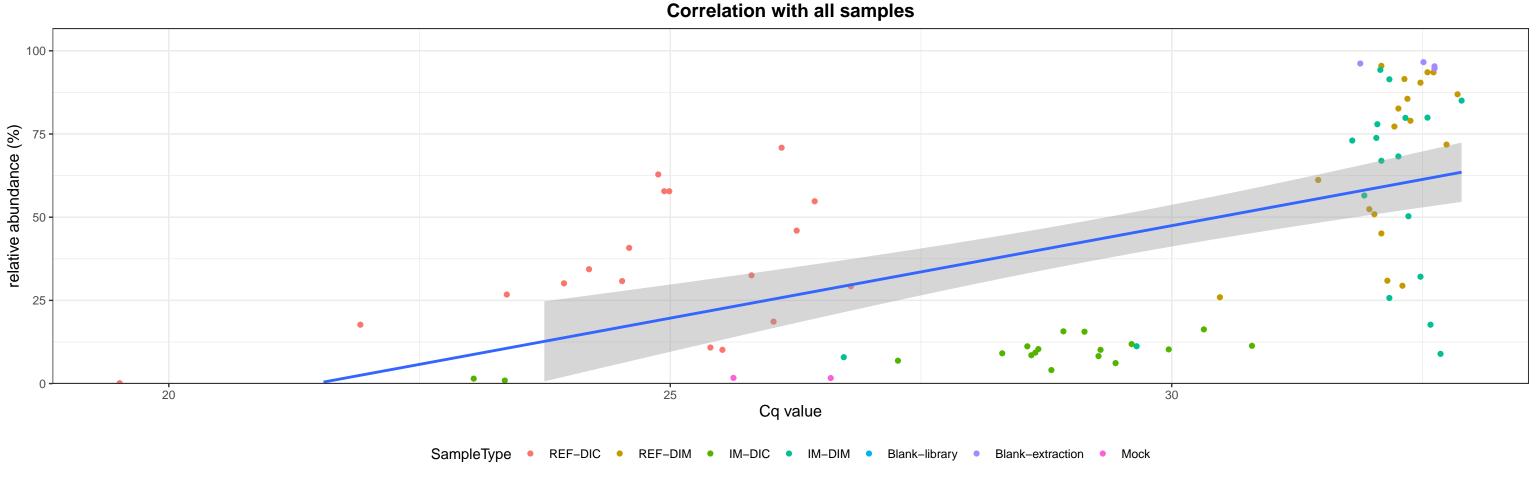
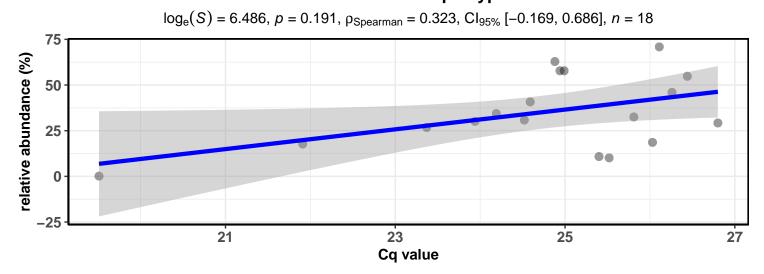
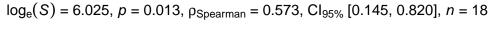
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

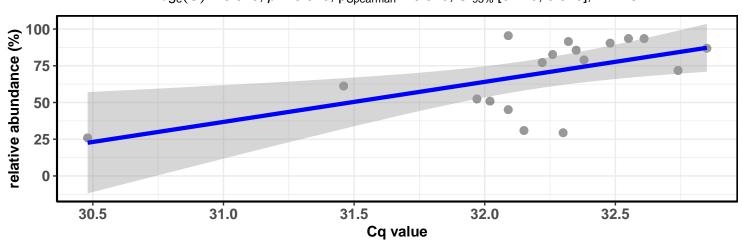




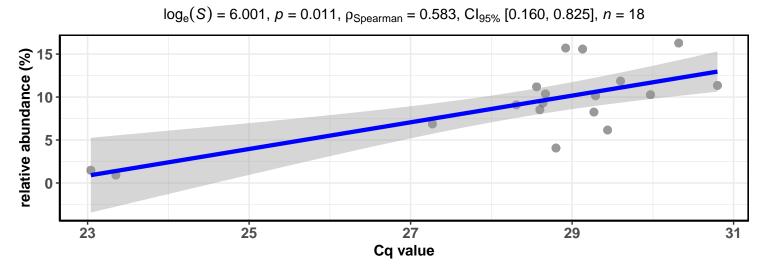


# Correlation within the sample type: REF-DIM

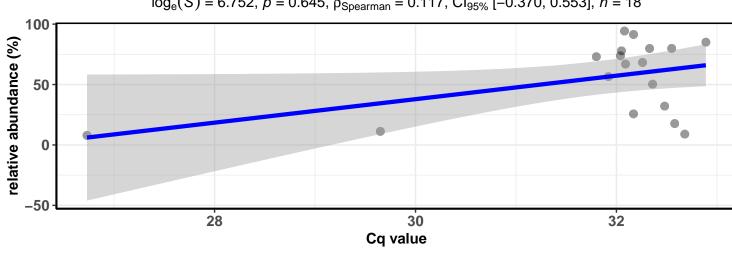




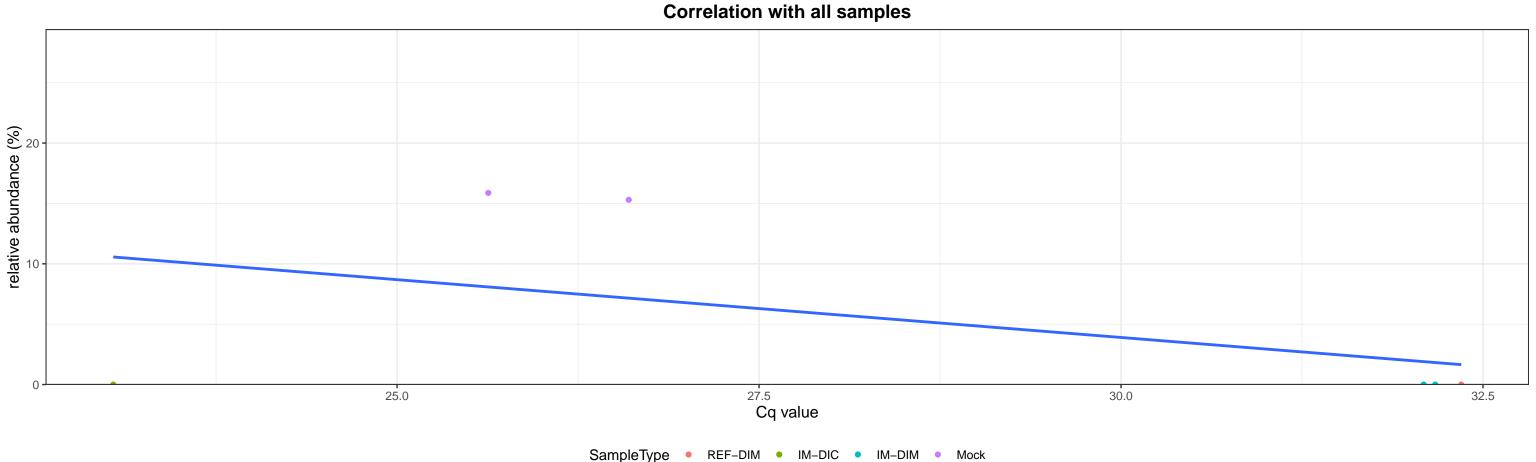
### Correlation within the sample type: IM-DIC

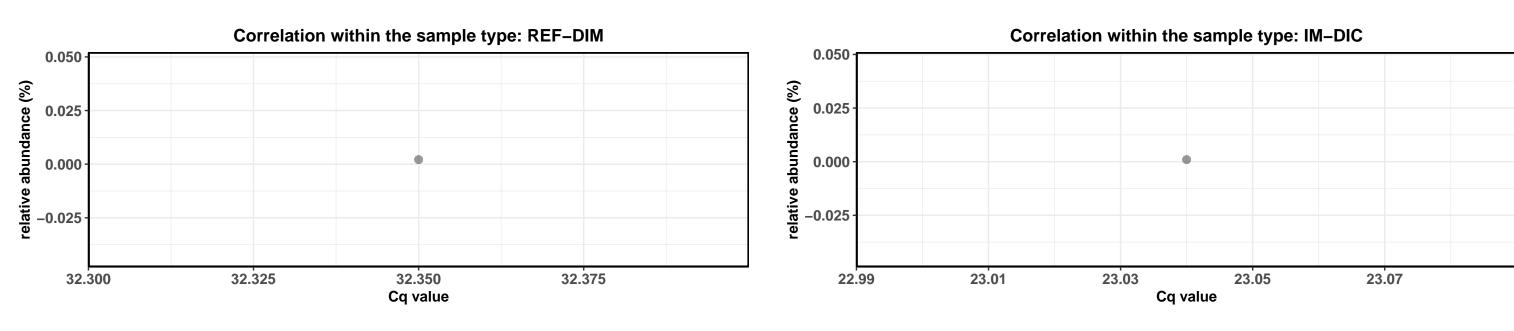


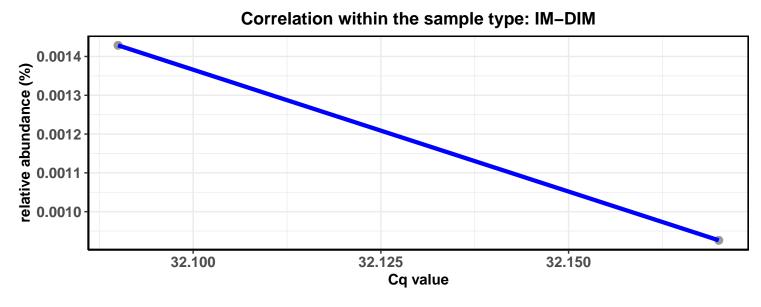
$$log_e(S) = 6.752$$
,  $p = 0.645$ ,  $\rho_{Spearman} = 0.117$ ,  $Cl_{95\%}$  [-0.370, 0.553],  $n = 18$ 



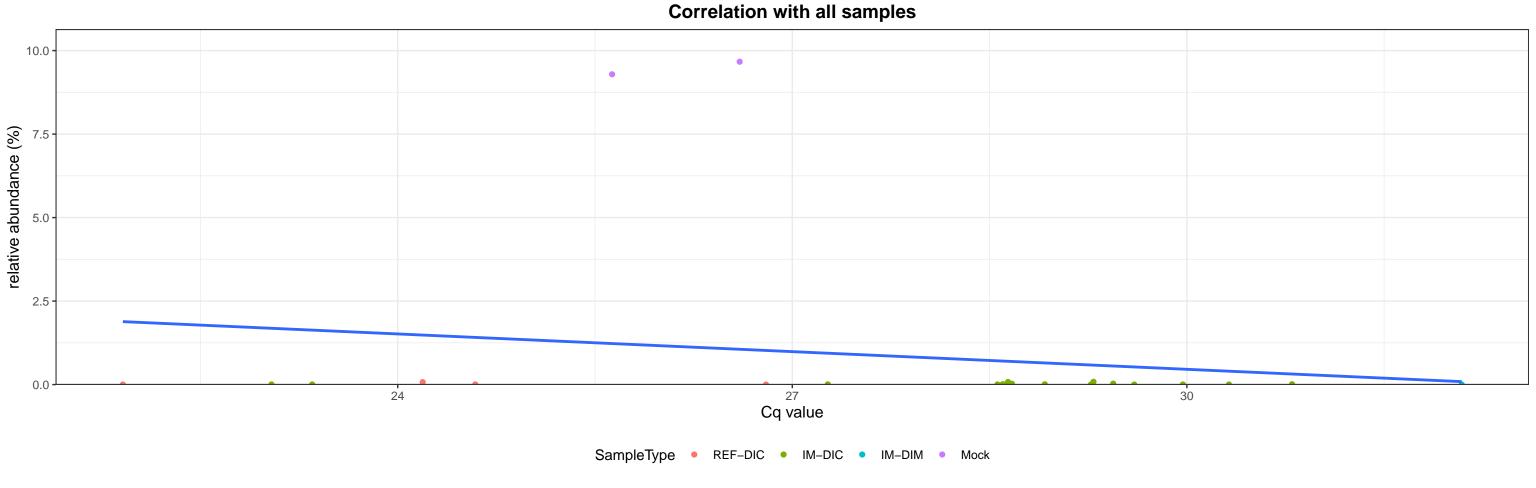
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Enterobacteriales; D\_4\_Enterobacteriaceae; D\_5\_Salmonella

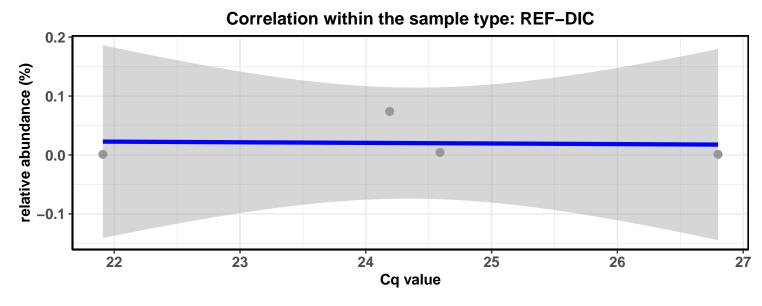


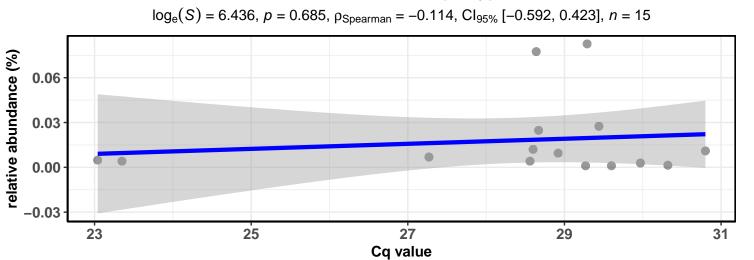


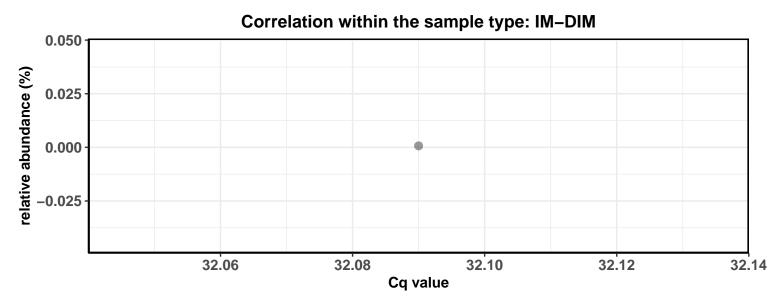


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Enterobacteriales; D\_4\_Enterobacteriaceae; D\_5\_Escherichia-Shigella









D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Bacillus **Correlation with all samples** relative abundance (%) 29 Cq value 27 31 SampleType • REF-DIC • IM-DIM • Mock Correlation within the sample type: REF-DIC Correlation within the sample type: IM-DIM 0.050 0.003 0.025 0.002 relative abundance (%) relative abundance (%) 0.001 0.000 0.000 -0.025-0.00126.23 26.25 32.2 32.3 32.4 32.5 32.6 32.7 26.21 26.31 26.27 26.29

Cq value

Cq value

D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas **Correlation with all samples** 32.5 27.5 30.0 25.0 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC • IM-DIM Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.050 0.0028 celative abundance (%) 0.000 -0.000 -0.025 0.0026 - 0.0026 - 0.0025 - 0.0024 - 0.0 0.0023 25.525 31.0 32.0 25.475 25.500 25.550 30.5 31.5 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM 0.050 0.10 0.10 0.00 0.00 0.00 0.00 0.00 relative aprindance (%) 0.000 - 0.000 - 0.025

32.2

32.4

Cq value

32.6

relative abundance (%)

22.99

23.01

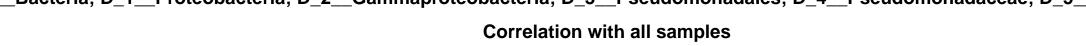
23.03

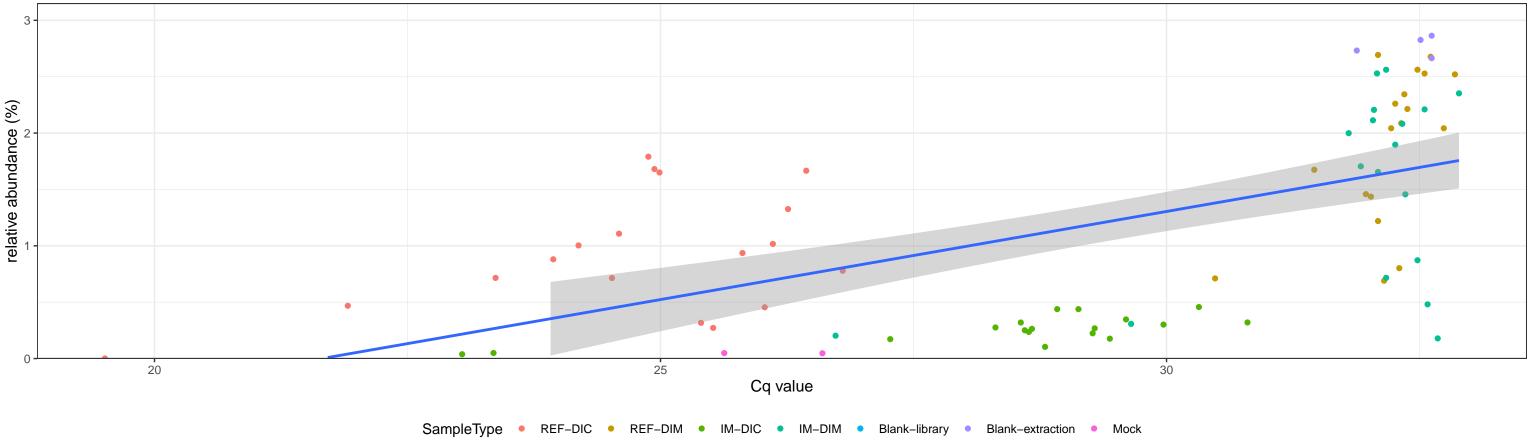
23.05

Cq value

23.07

D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

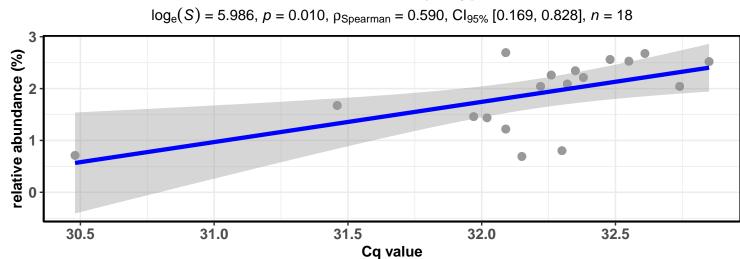




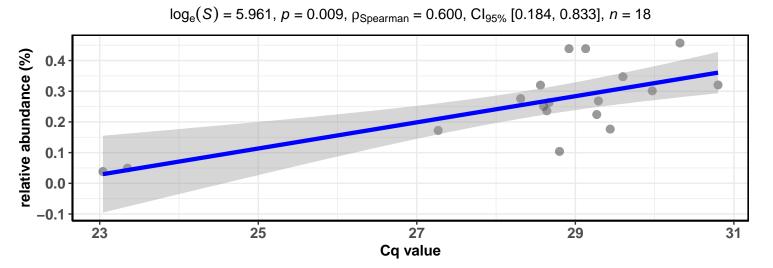
## Correlation within the sample type: REF-DIC

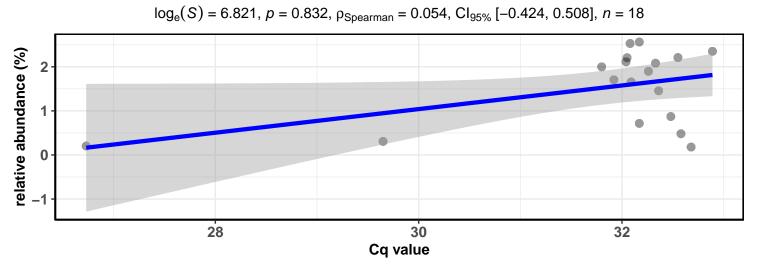
log<sub>e</sub>(S) = 6.548, ρ = 0.261, ρ<sub>Spearman</sub> = 0.280, Cl<sub>95%</sub> [-0.215, 0.660], n = 18

## Correlation within the sample type: REF-DIM



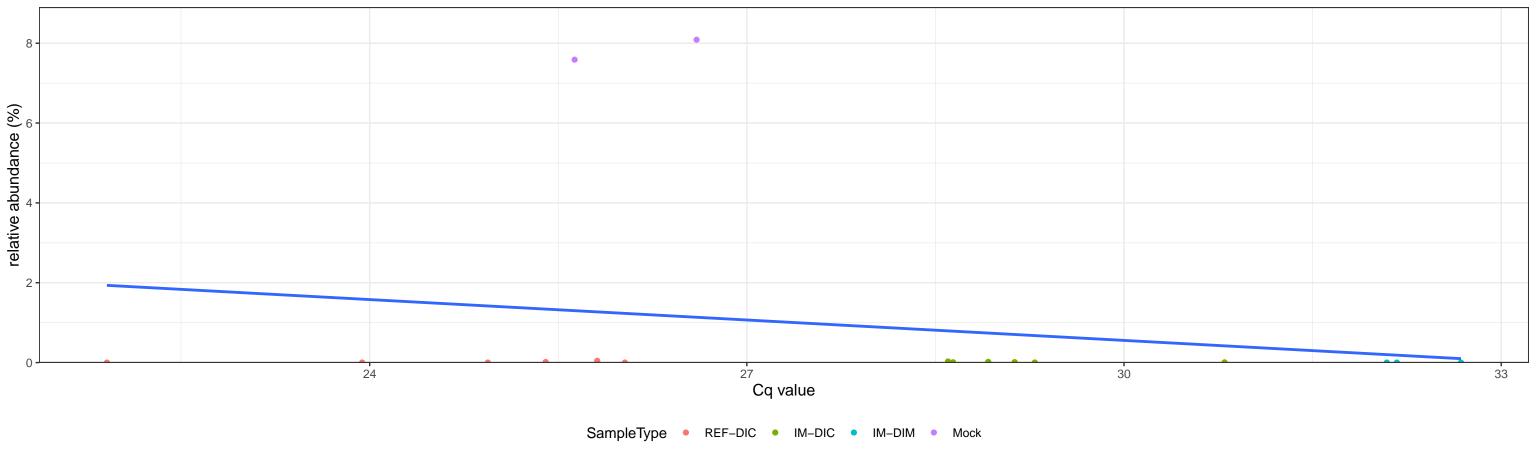
### Correlation within the sample type: IM-DIC



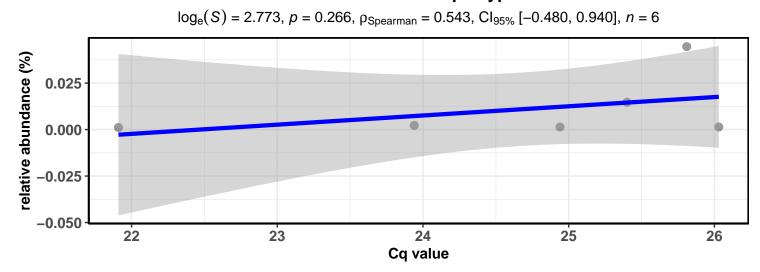


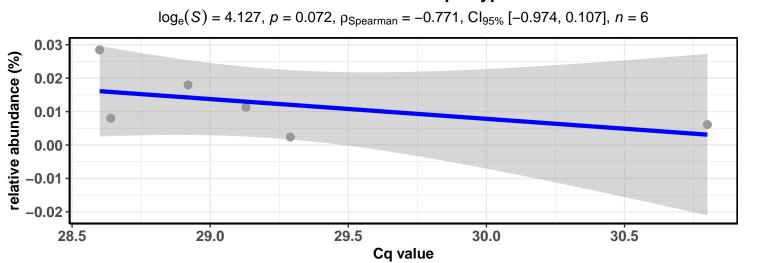
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum



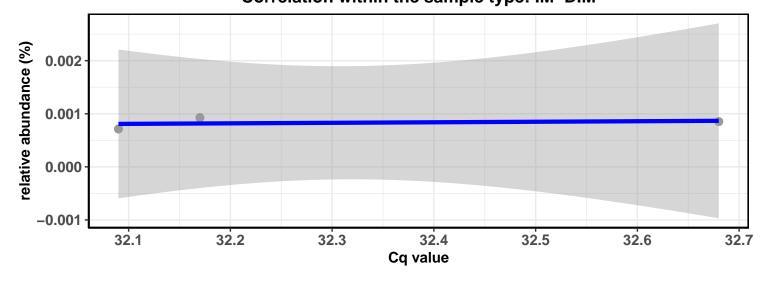




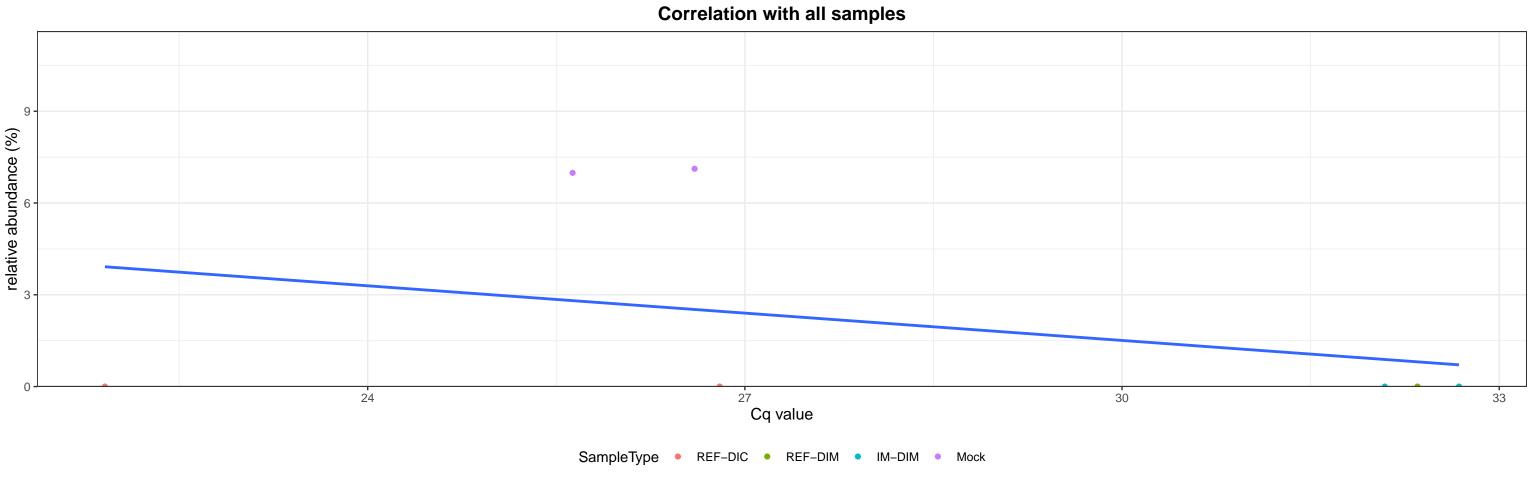


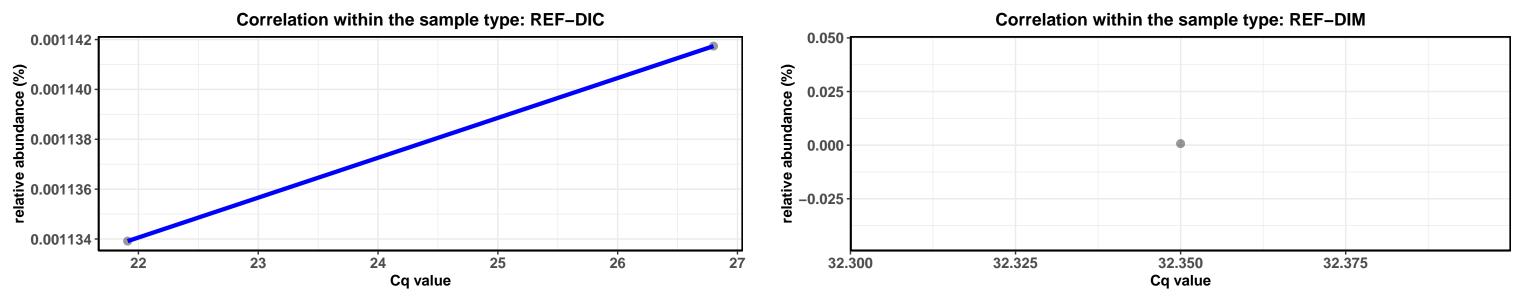


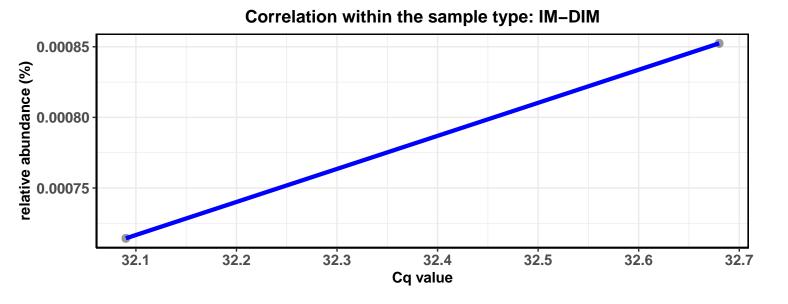




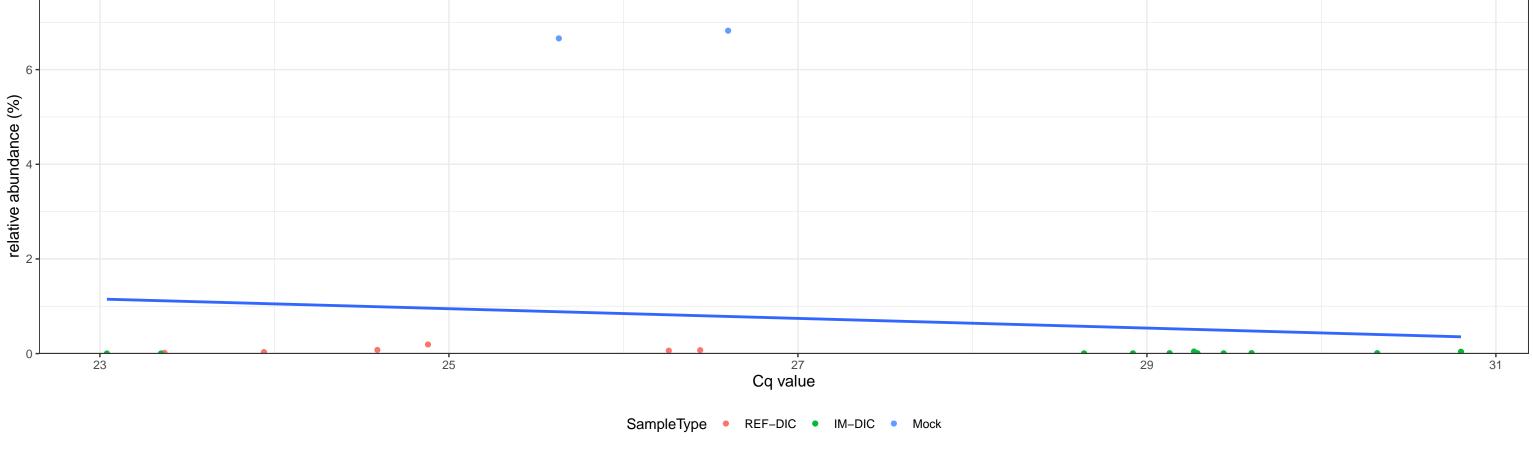
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Enterobacteriales; D\_4\_Enterobacteriaceae; D\_5\_Escherichia-Shigella

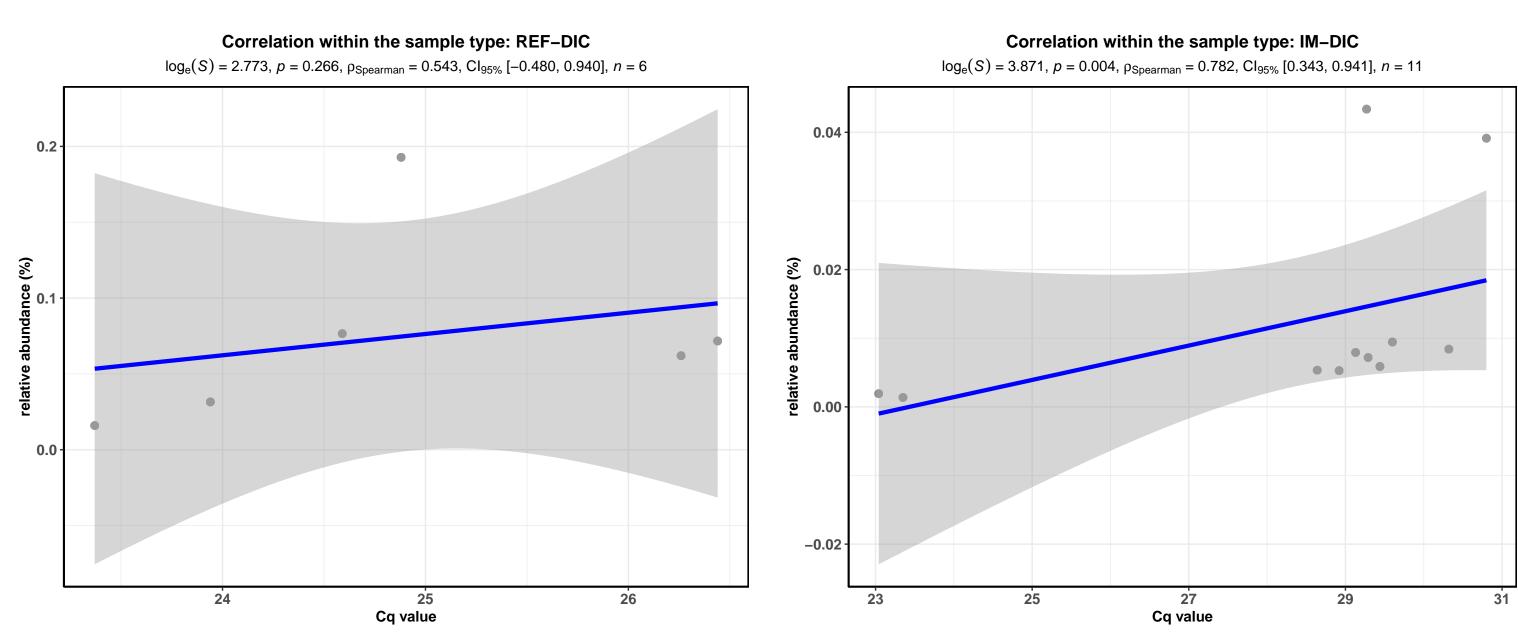




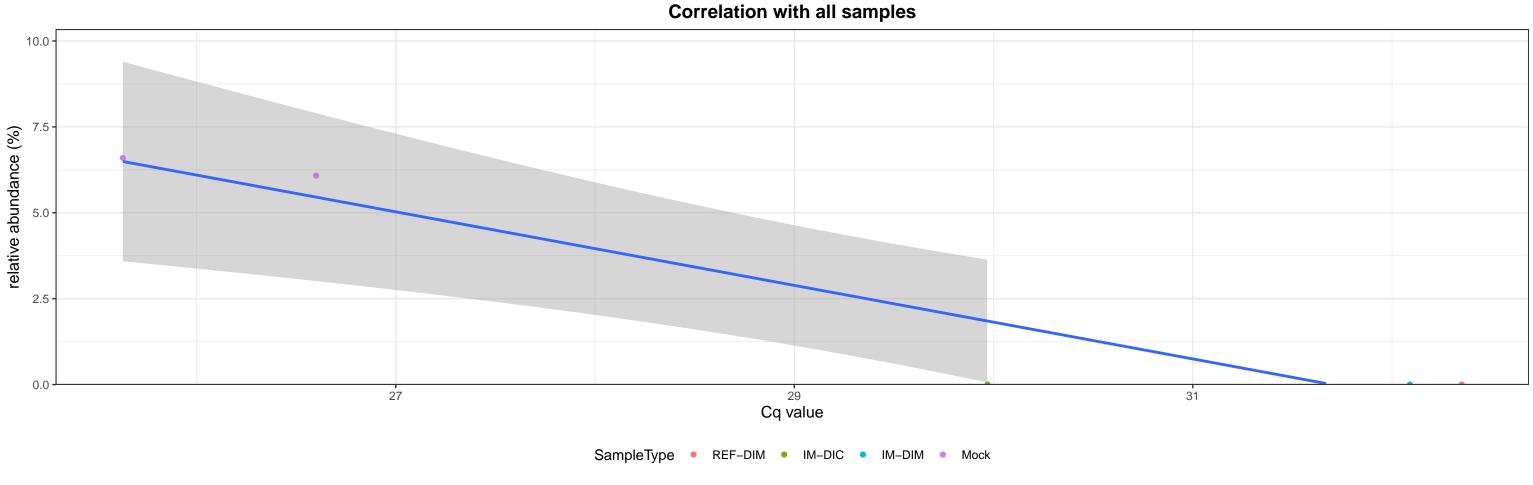


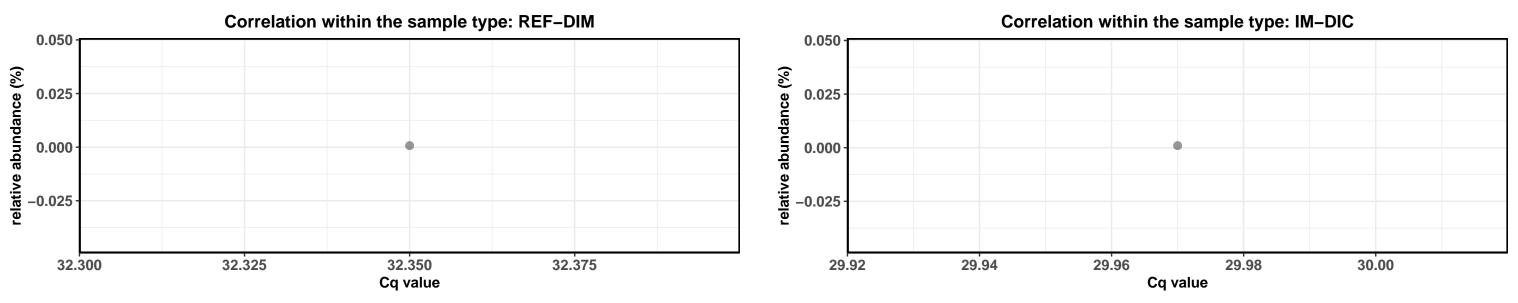
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum **Correlation with all samples** 

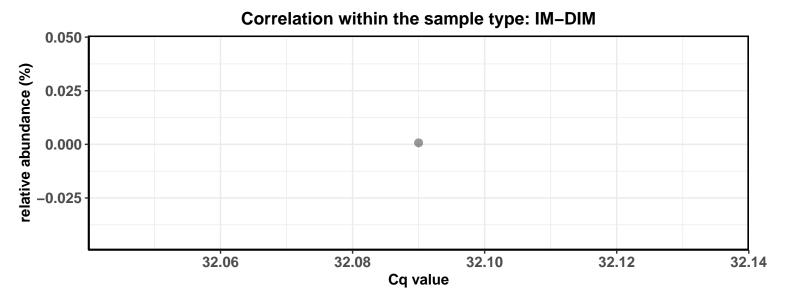




D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

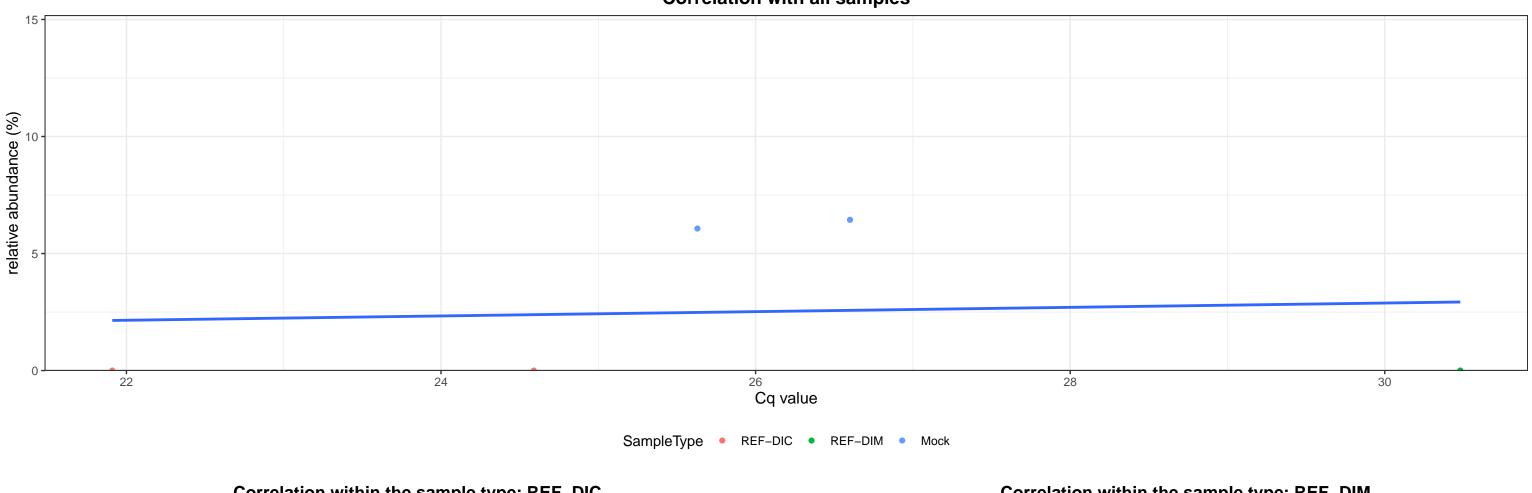


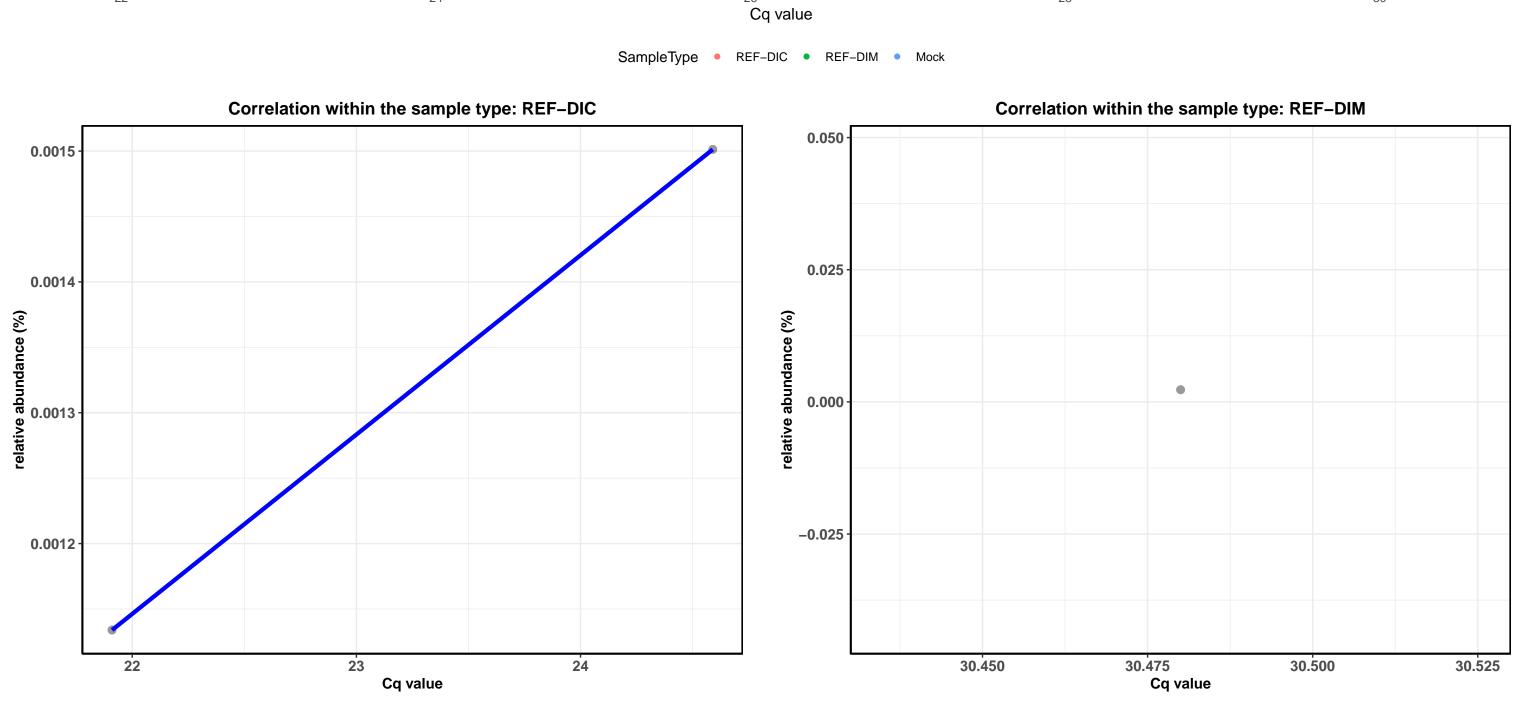




D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Staphylococcaceae; D\_5\_Staphylococcus; D\_6\_Staphylococcus aureus

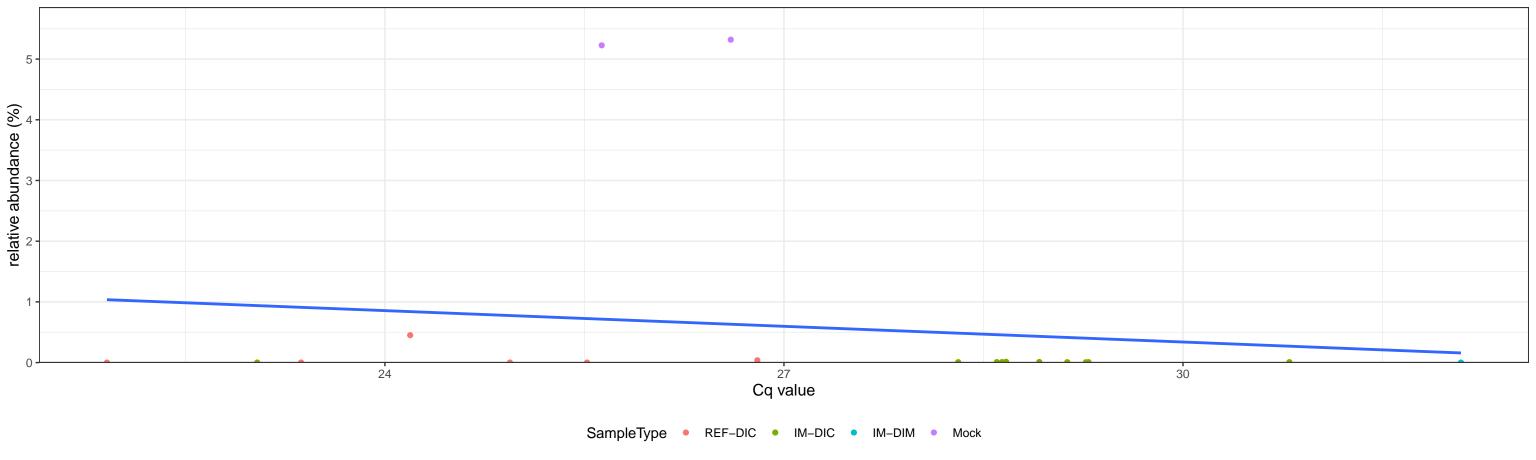
Correlation with all samples





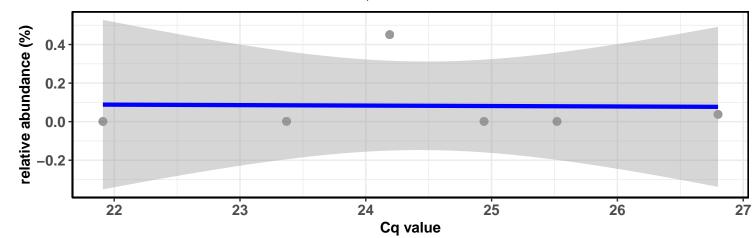
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum





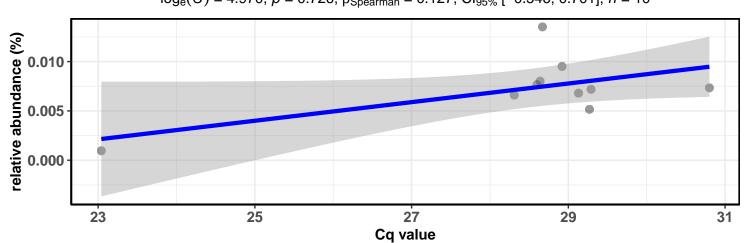
## Correlation within the sample type: REF-DIC

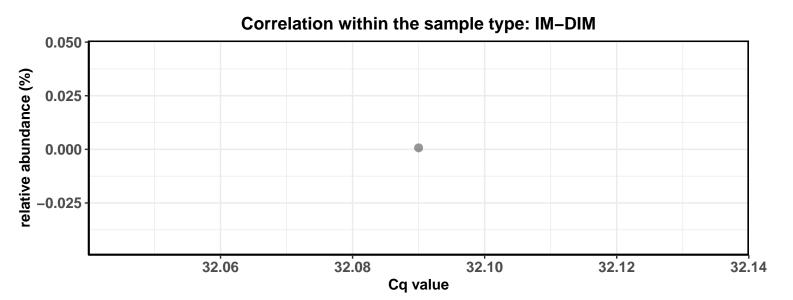
 $log_e(S) = 3.466$ , p = 0.872,  $\rho_{Spearman} = 0.086$ ,  $Cl_{95\%}$  [-0.780, 0.839], n = 6



### Correlation within the sample type: IM-DIC

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





D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum **Correlation with all samples** 22 26 28 Cq value SampleType • REF-DIC • IM-DIC • Mock Correlation within the sample type: REF-DIC Correlation within the sample type: IM-DIC 0.0014 0.050 0.025 relative abundance (%) relative abundance (%) 0.000 0.0012 -0.025

24

Cq value

25

26

29.24

29.26

29.28

29.30

Cq value

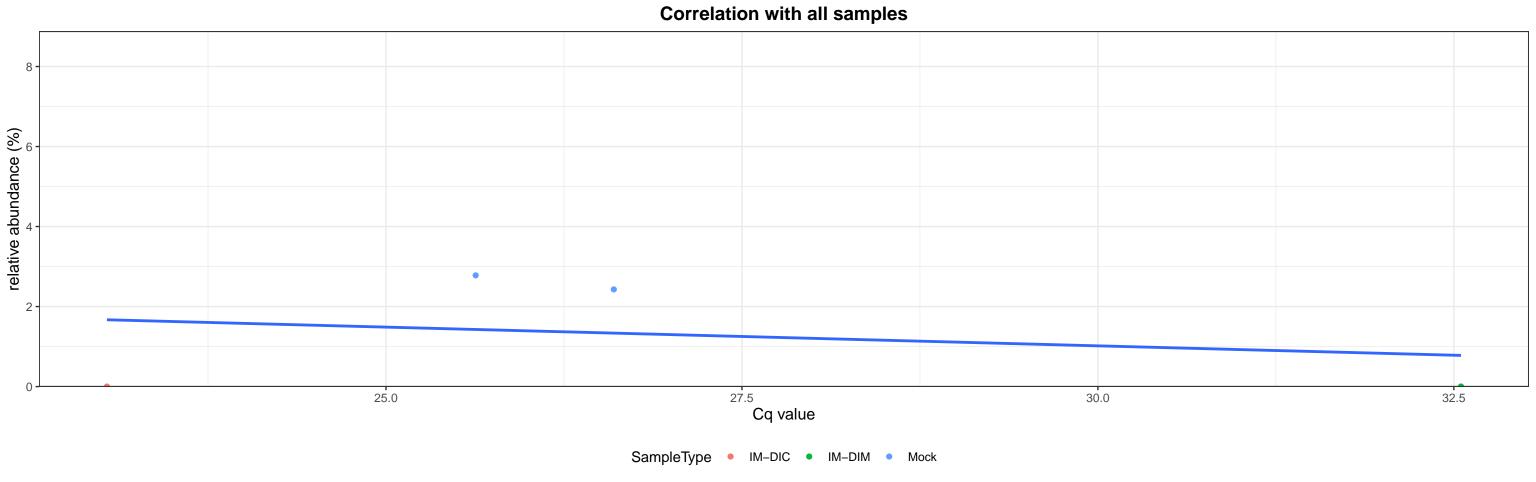
29.32

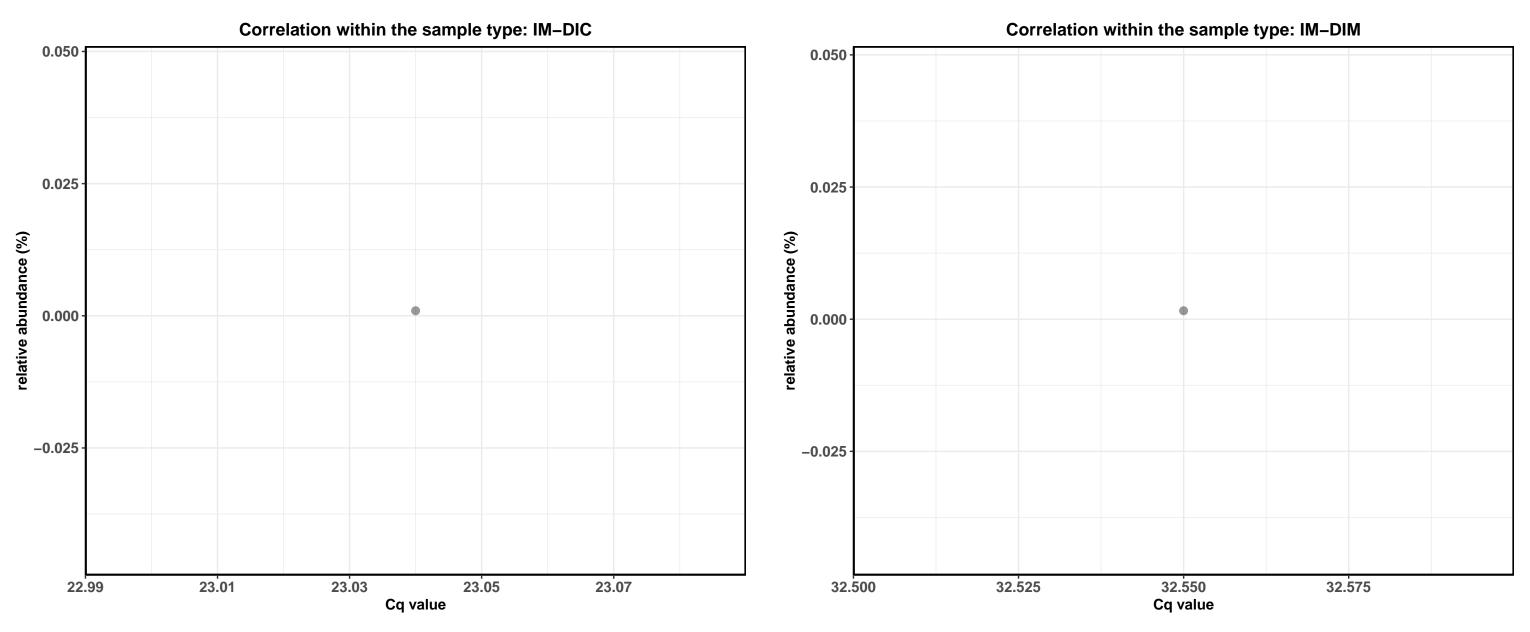
relative abundance (%)

22

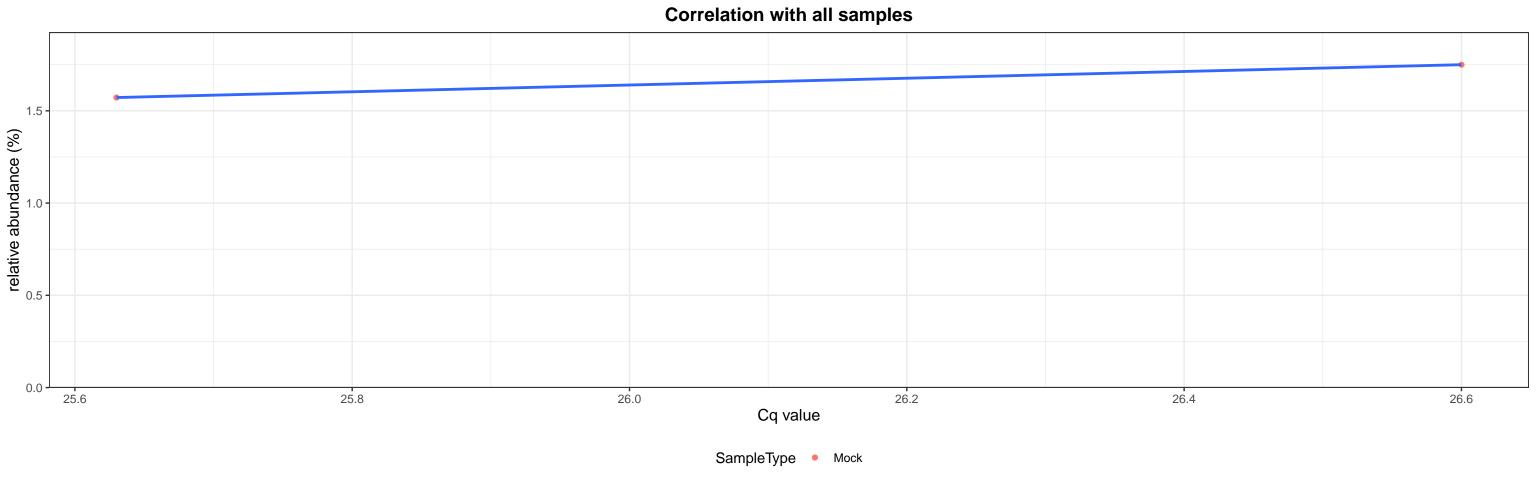
23

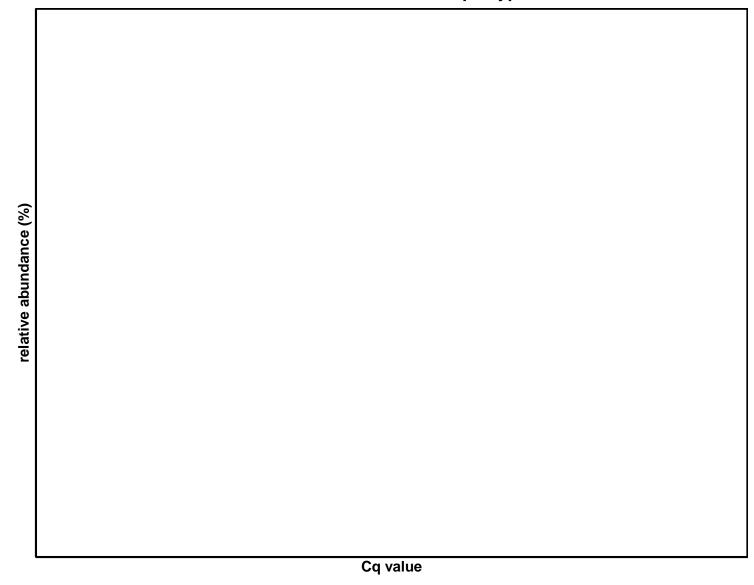
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Enterobacteriales; D\_4\_Enterobacteriaceae; D\_5\_Salmonella



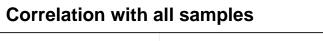


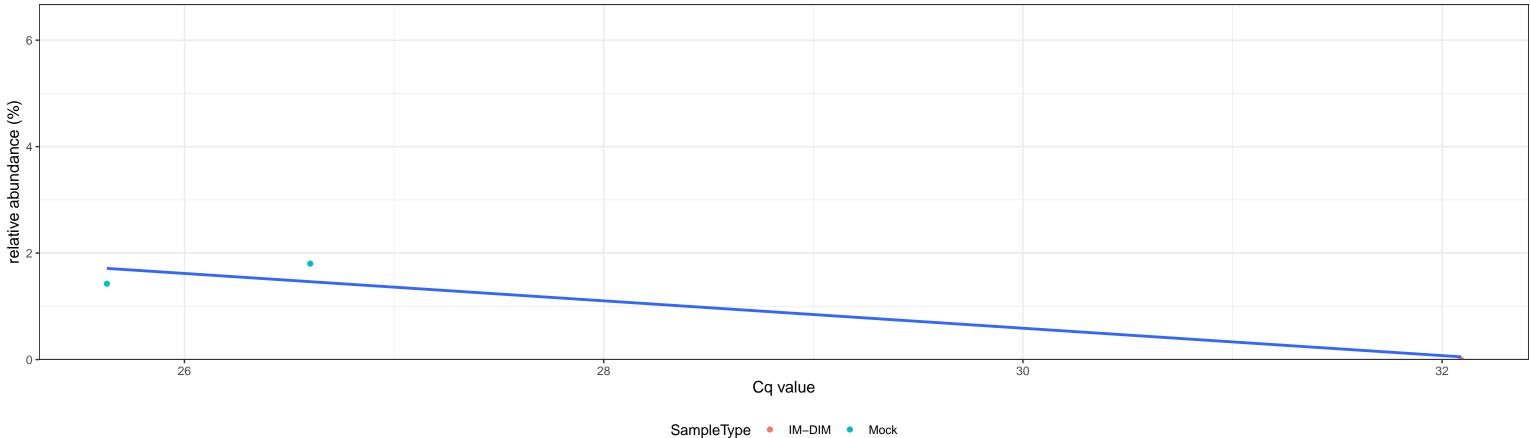
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Staphylococcaceae; D\_5\_Staphylococcus; D\_6\_Staphylococcus aureus

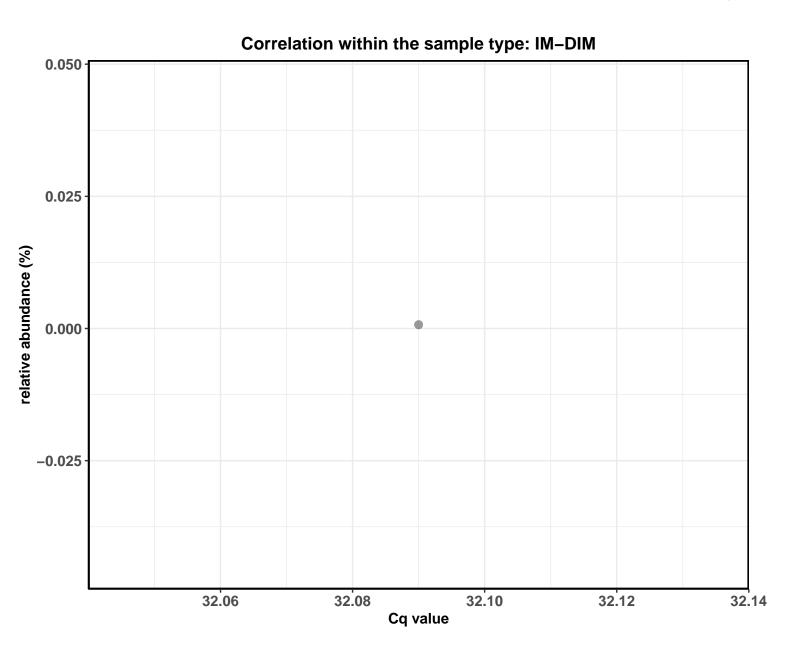




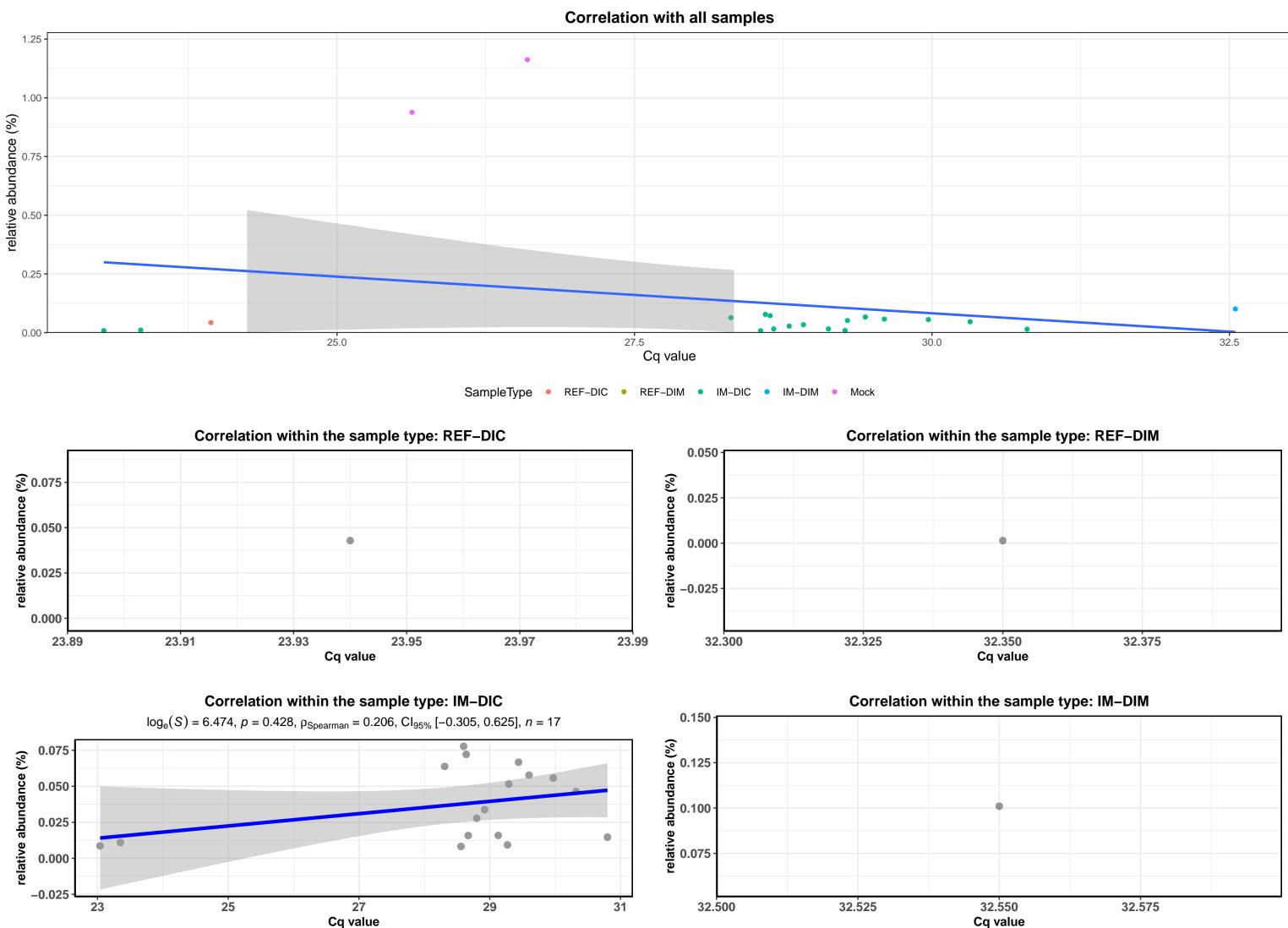
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Staphylococcaceae; D\_5\_Staphylococcus; D\_6\_Staphylococcus aureus





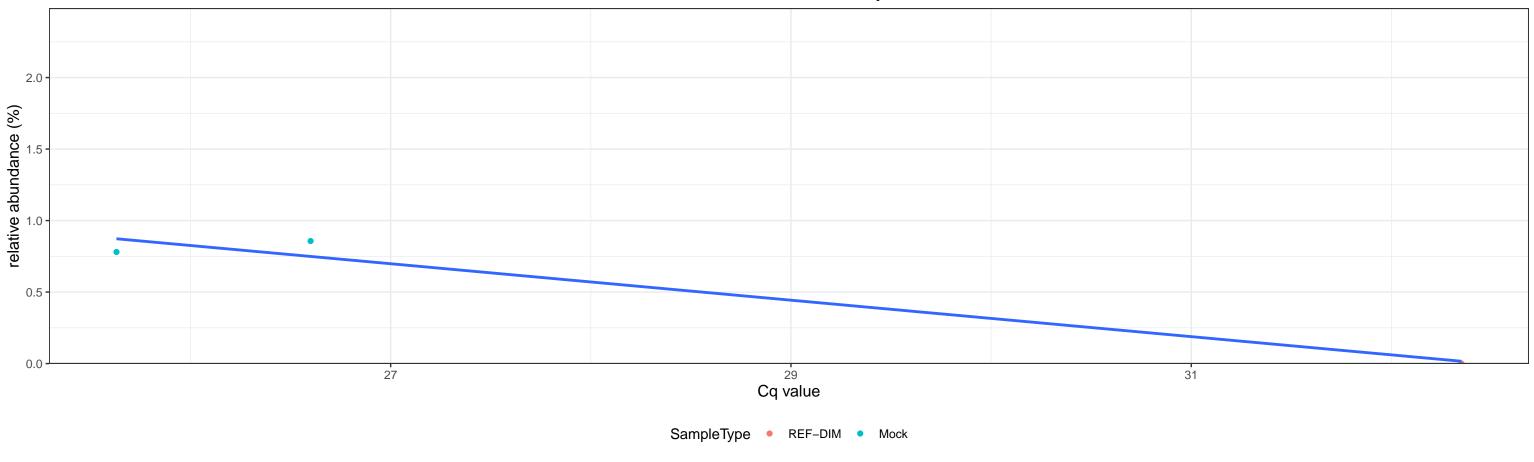


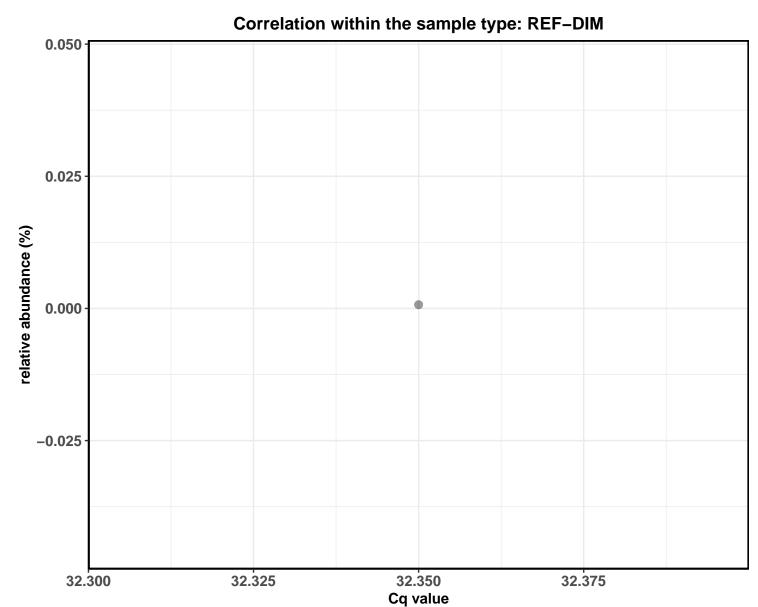
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Enterococcaceae; D\_5\_Enterococcus; D\_6\_Enterococcus faecalis



D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Listeriaceae; D\_5\_Listeria; D\_6\_Listeria monocytogenes

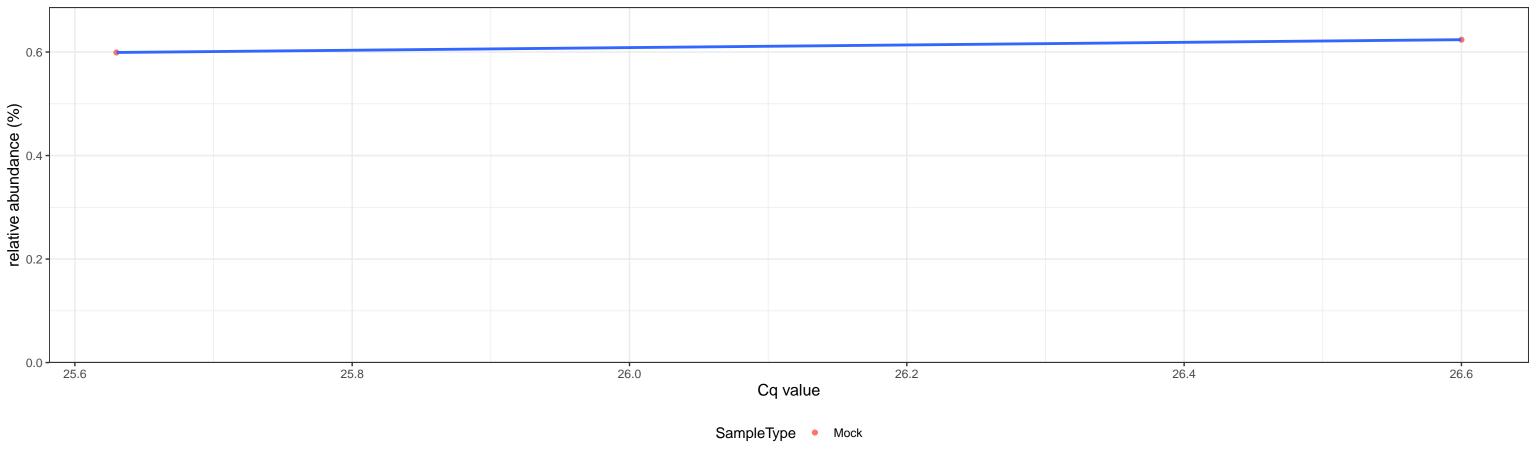


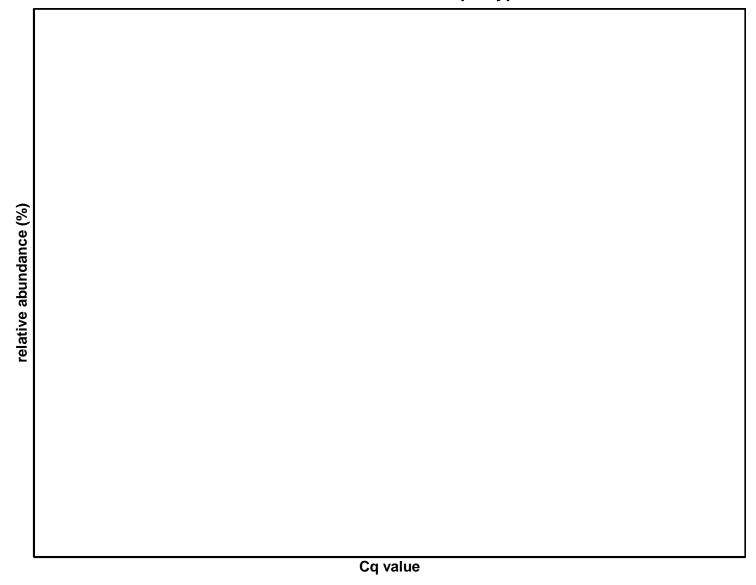




D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Enterococcaceae; D\_5\_Enterococcus; D\_6\_Enterococcus faecalis

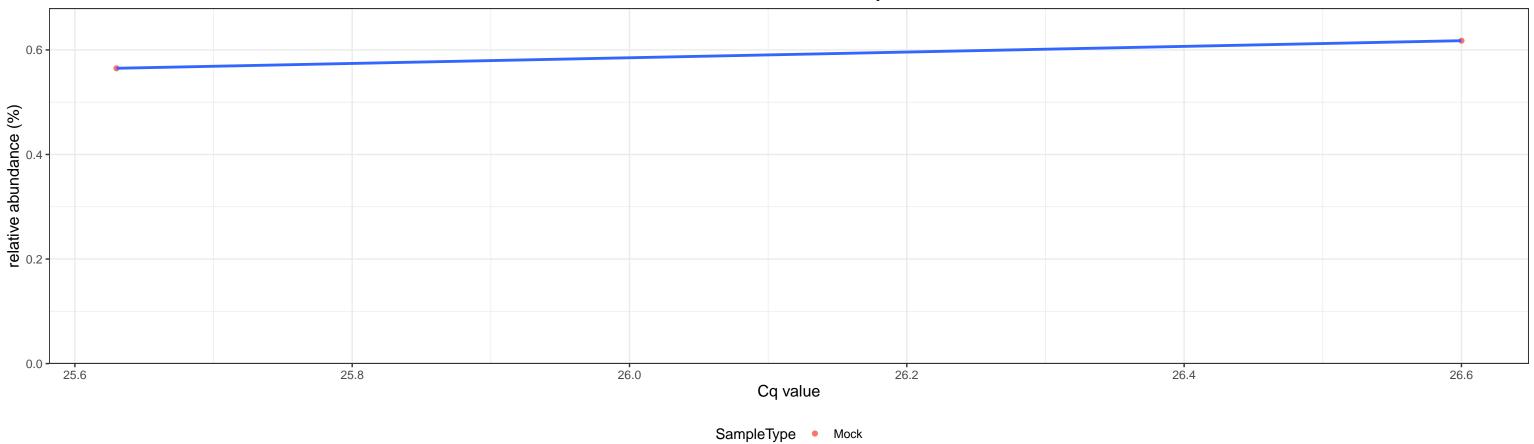


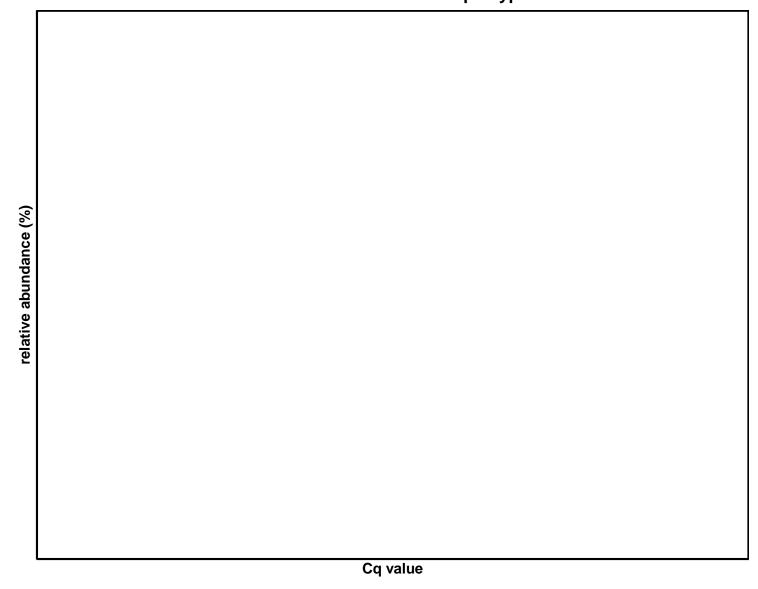




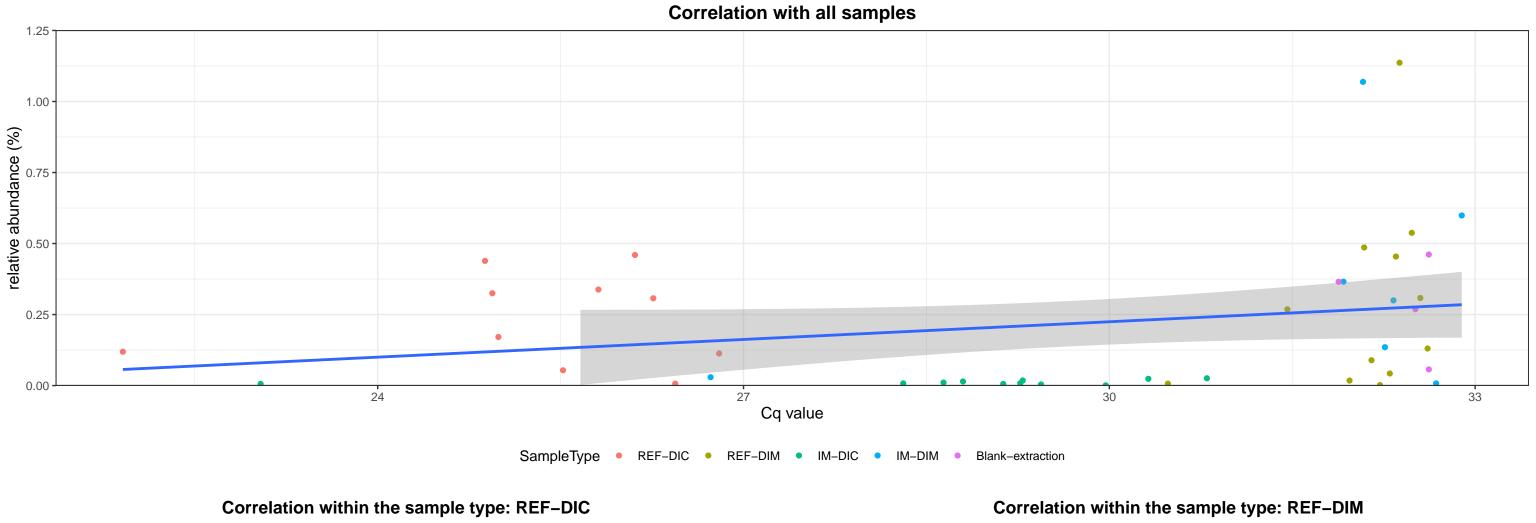
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Listeriaceae; D\_5\_Listeria; D\_6\_Listeria monocytogenes

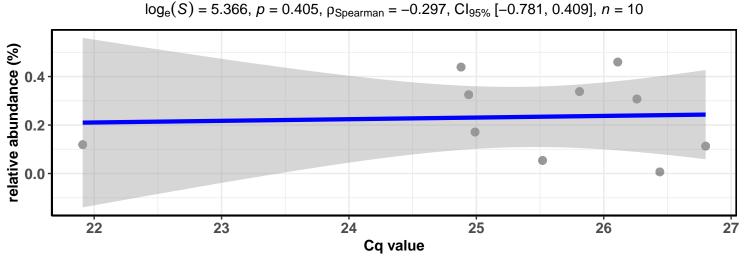


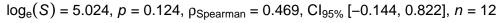


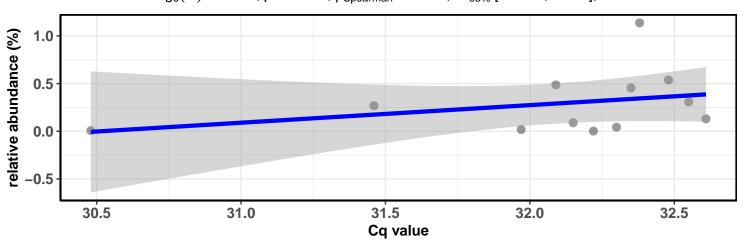


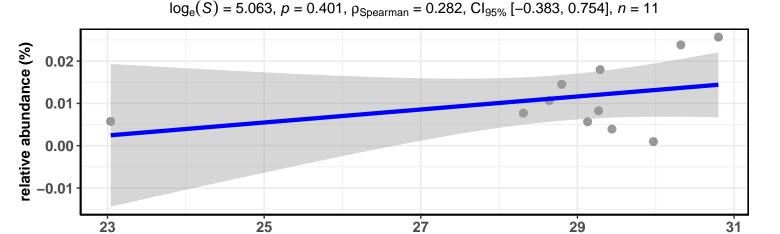
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Propionibacteriales; D\_4\_Propionibacteriaceae; D\_5\_Cutibacterium





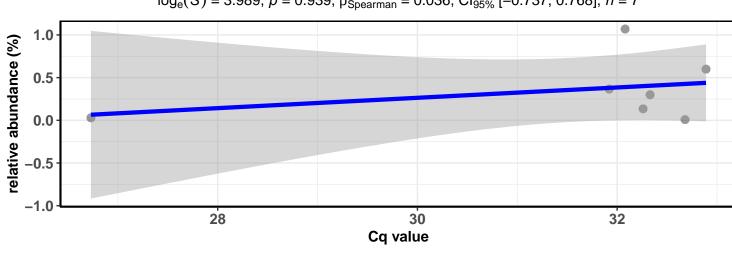




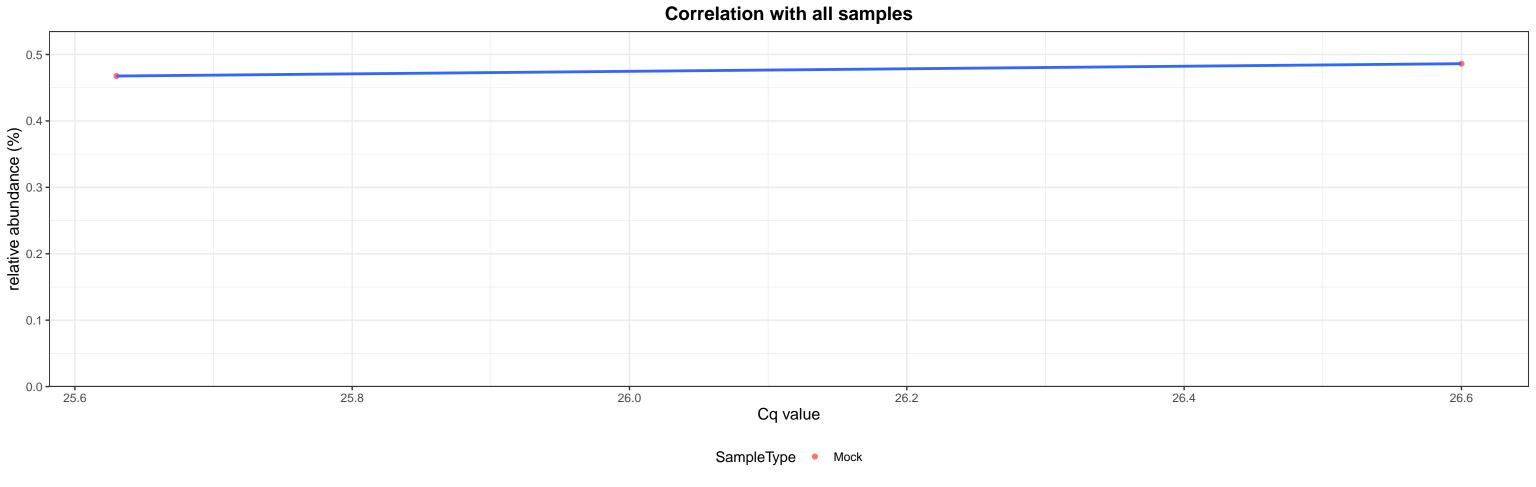


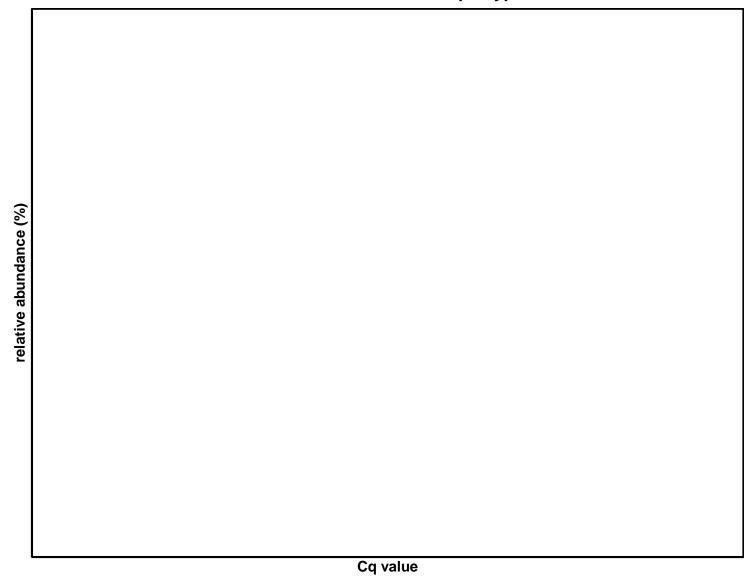
Cq value

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



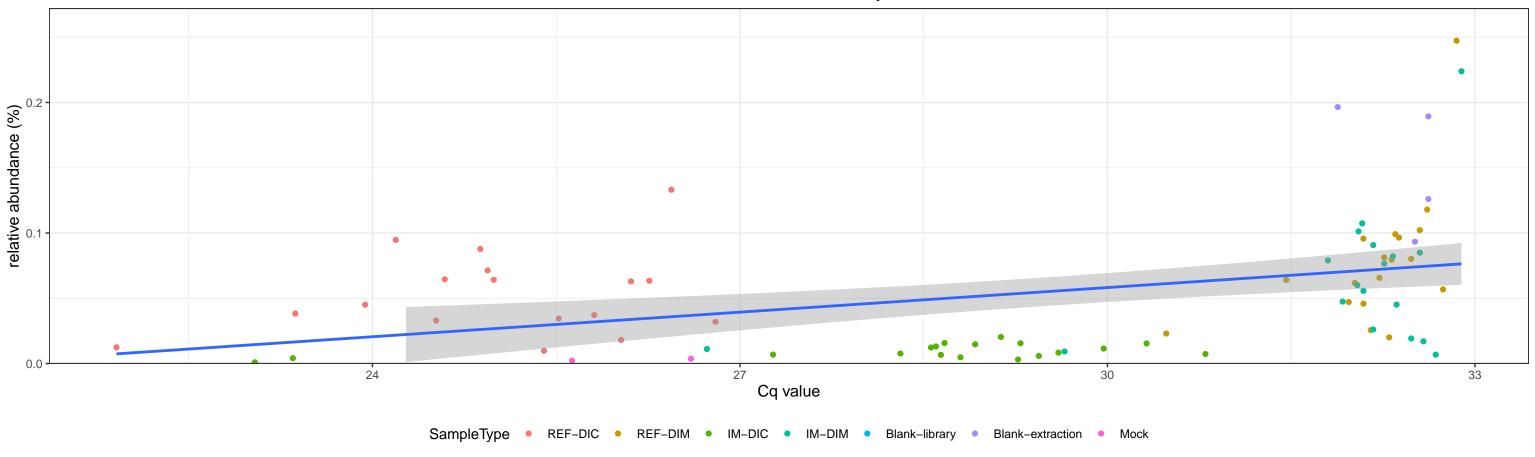
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Enterococcaceae; D\_5\_Enterococcus; D\_6\_Enterococcus faecalis





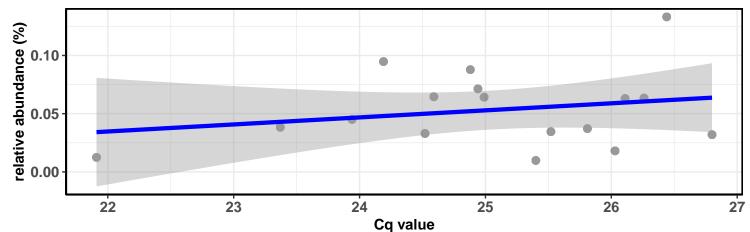
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas





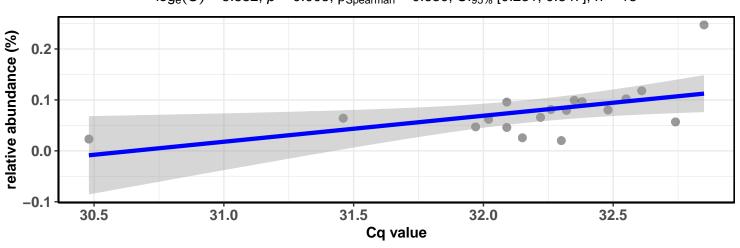
## Correlation within the sample type: REF-DIC

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



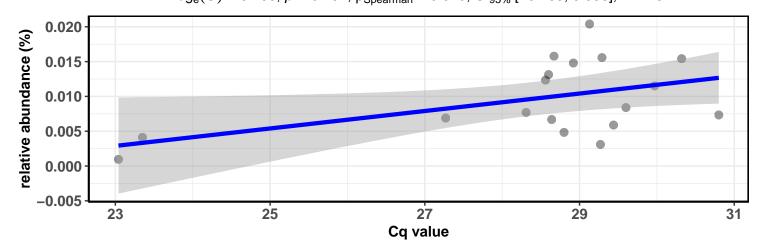
# Correlation within the sample type: REF-DIM

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



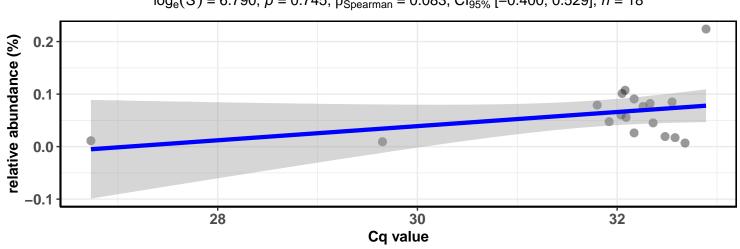
### Correlation within the sample type: IM-DIC

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



# Correlation within the sample type: IM-DIM

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

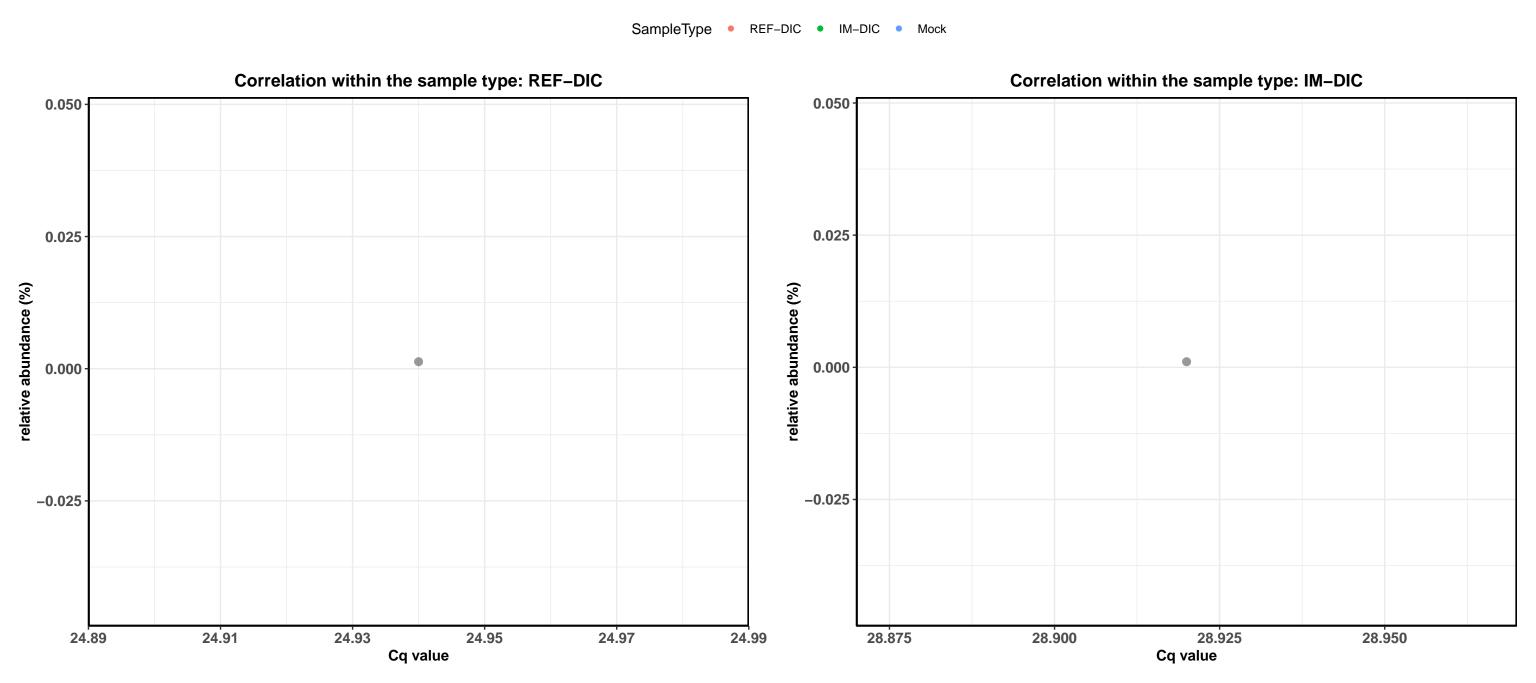


D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

Correlation with all samples

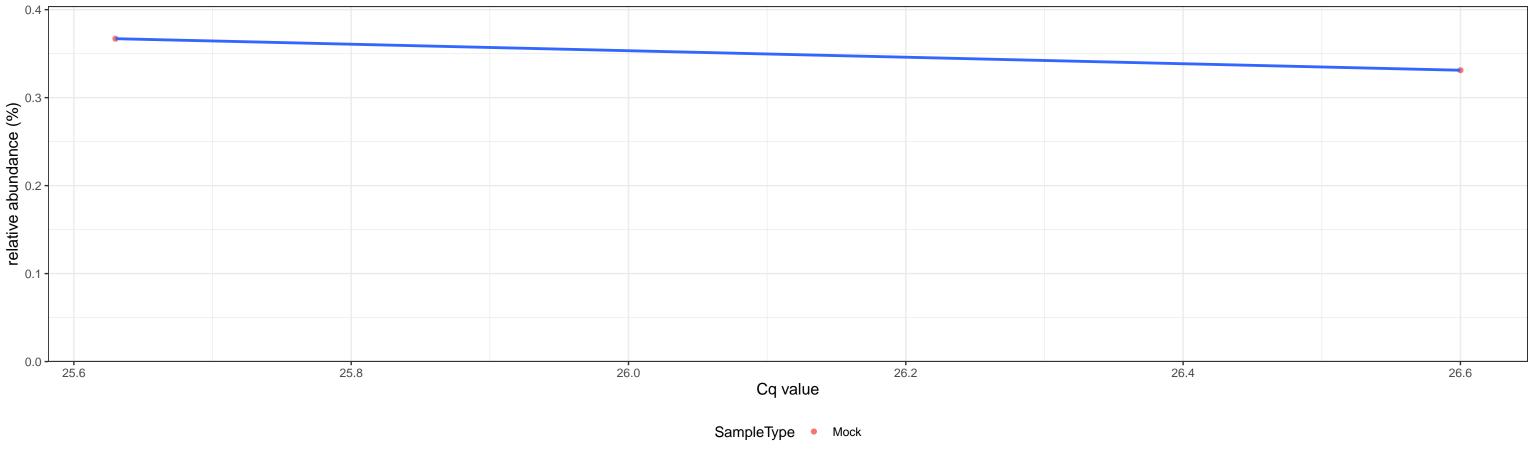
relative abundance (%)

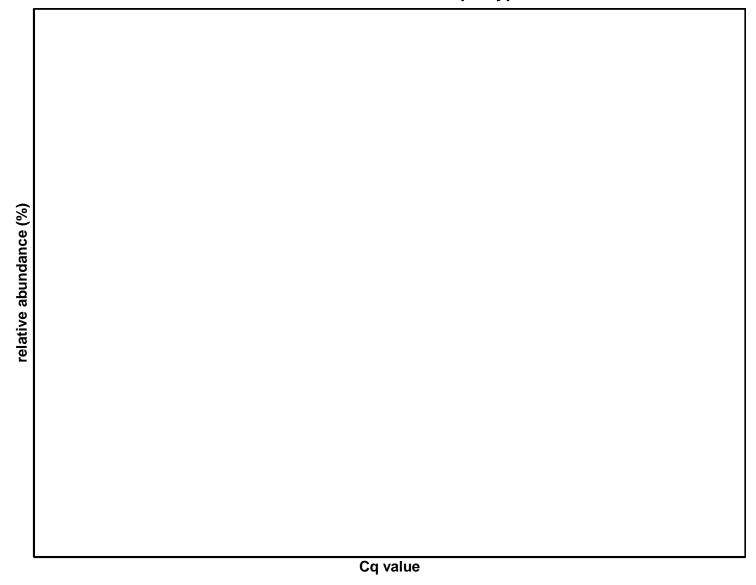
0.0



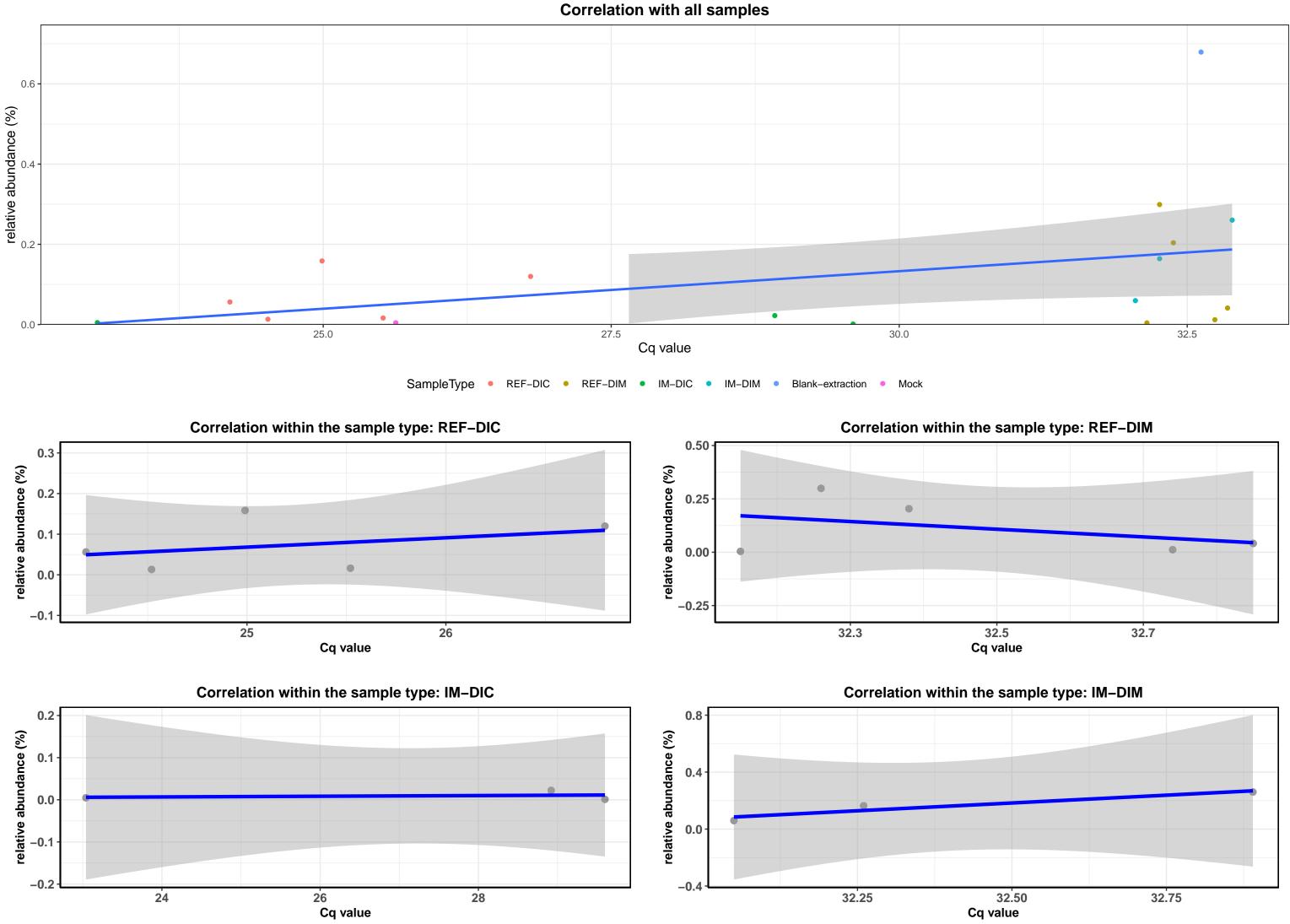
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum





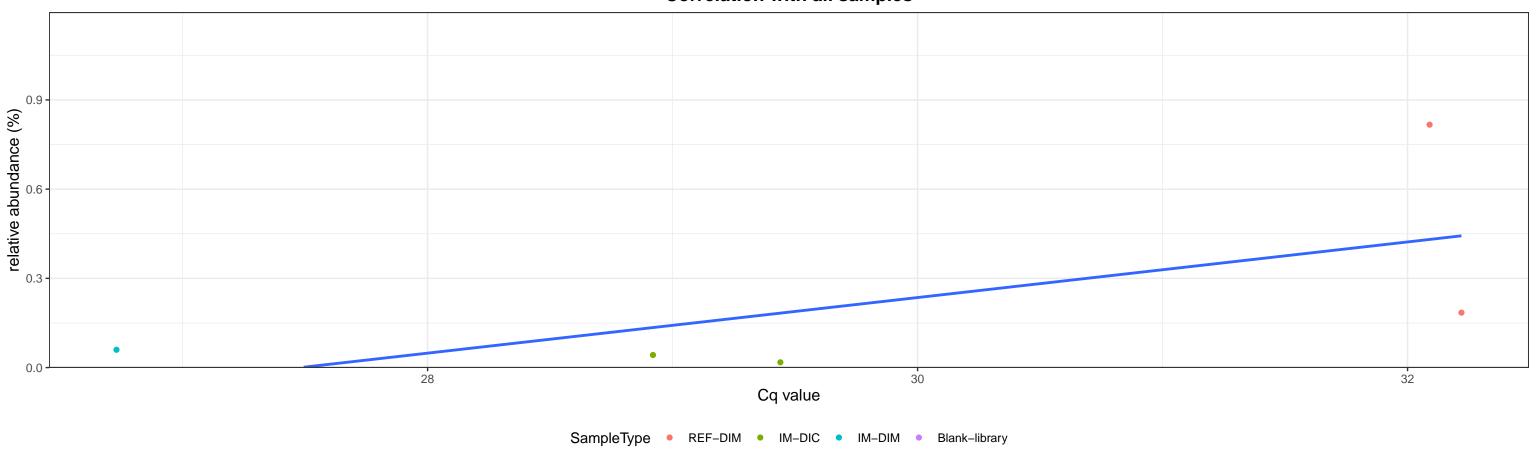


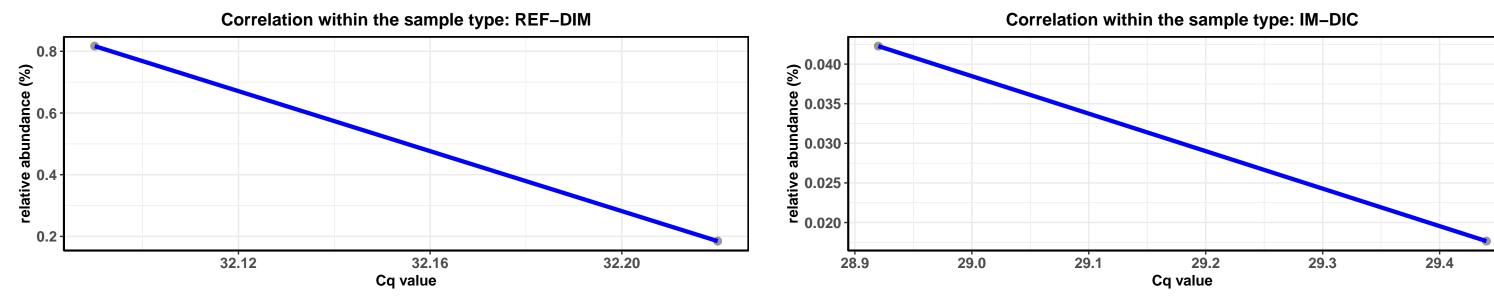
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Micrococcales; D\_4\_Microbacteriaceae; D\_5\_Curtobacterium; Ambiguous\_taxa

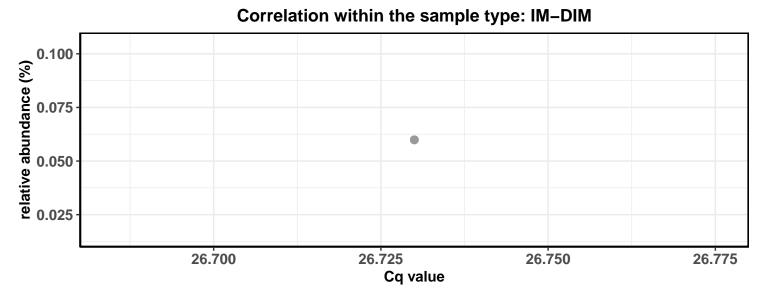


D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Staphylococcaceae; D\_5\_Jeotgalicoccus; Ambiguous\_taxa

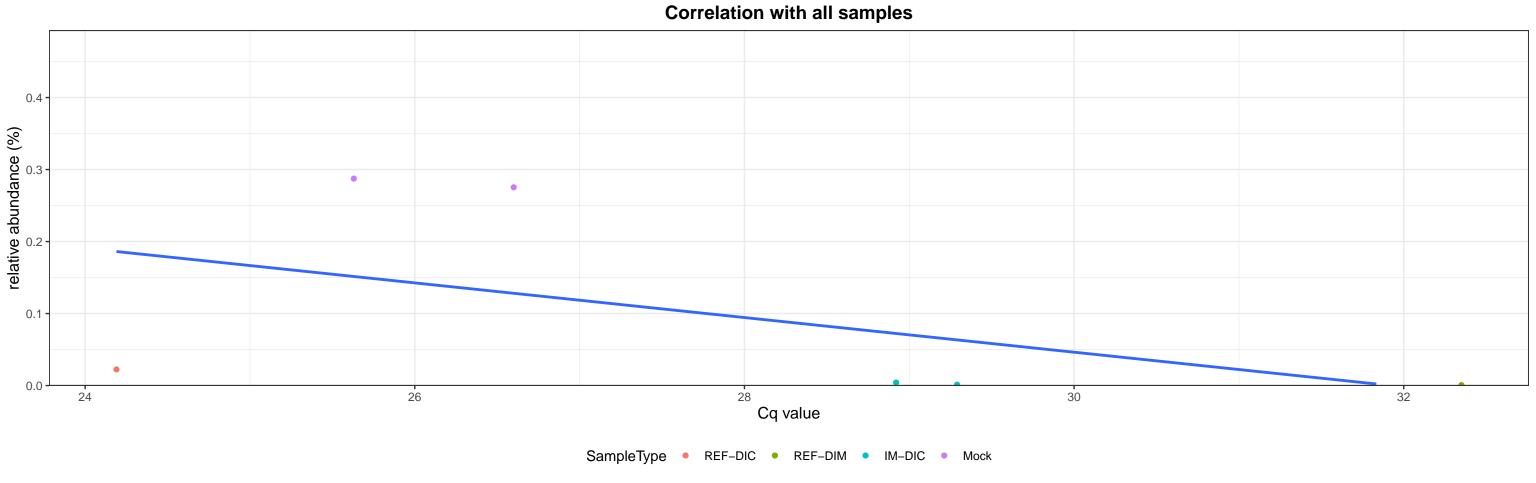
Correlation with all samples

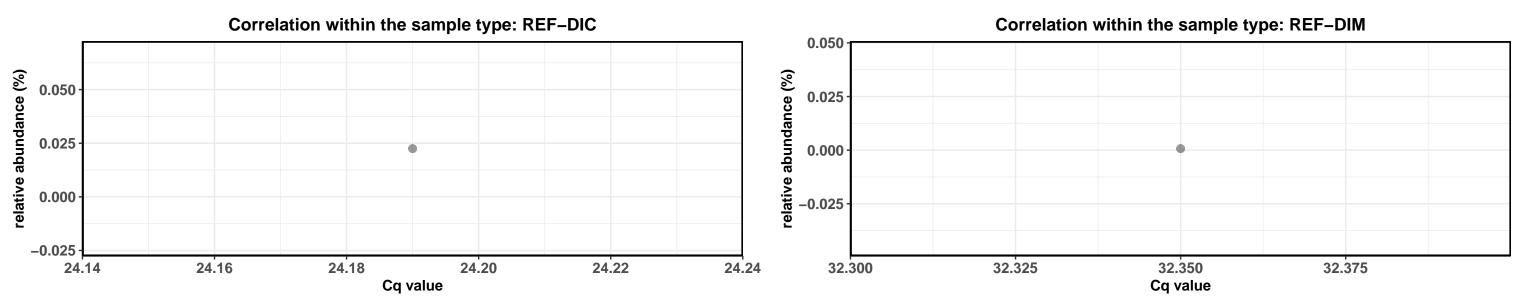


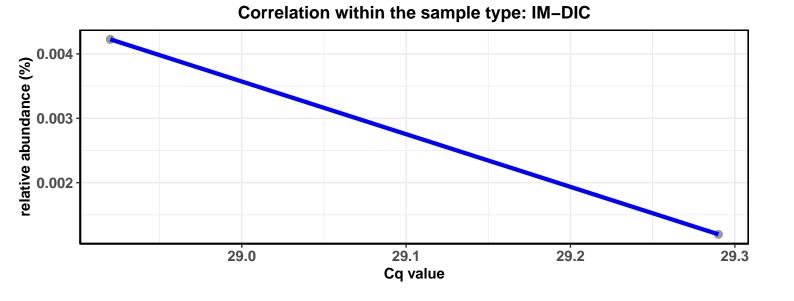




D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

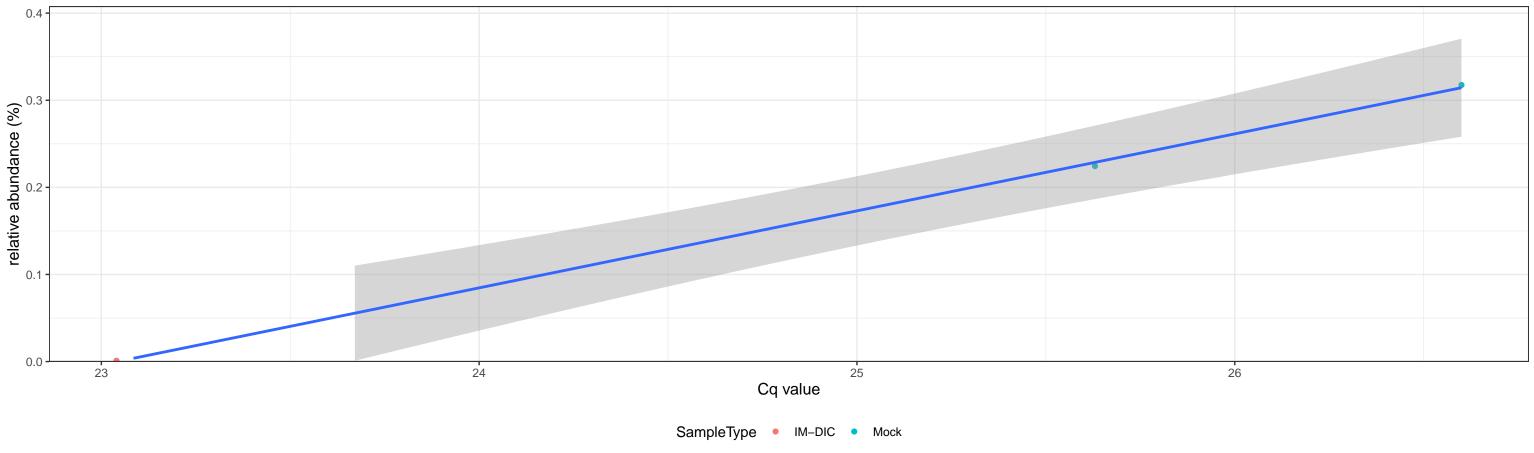




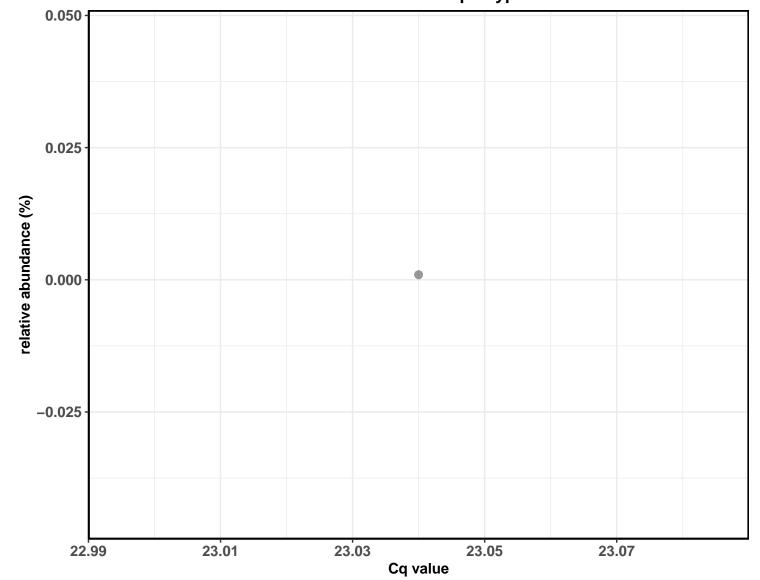


D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Listeriaceae; D\_5\_Listeria; D\_6\_Listeria monocytogenes









D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Frankiales; D\_4\_Geodermatophilaceae; D\_5\_Modestobacter; Ambiguous\_taxa **Correlation with all samples** 26 28 32 30 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC IM-DIM Blank-extraction Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.06 relative abundance (%) relative abundance (%) 0.075 0.050 0.025 26.000 26.025 26.050 32.70 26.075 32.65 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM relative abundance (%) 0.000 0.010 0.010 relative april about 800.0 800.0 800.0 800.0 800.0 0.005

27

28

29

Cq value

30

31

32

0.5

relative abundance (%)

0.1

0.002

28.8

29.2

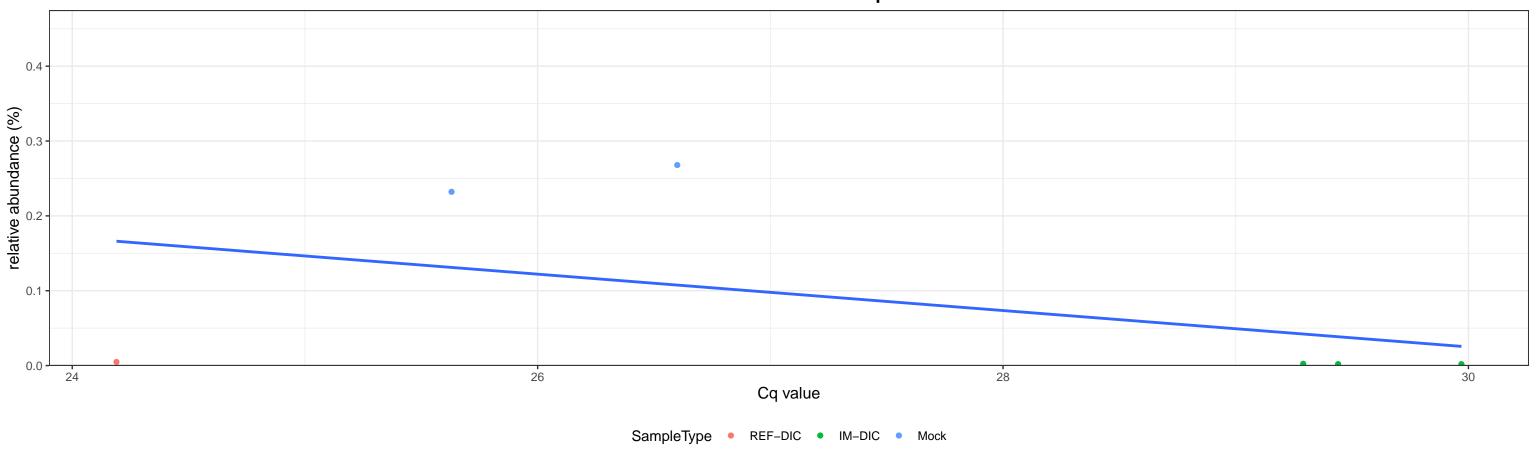
29.6

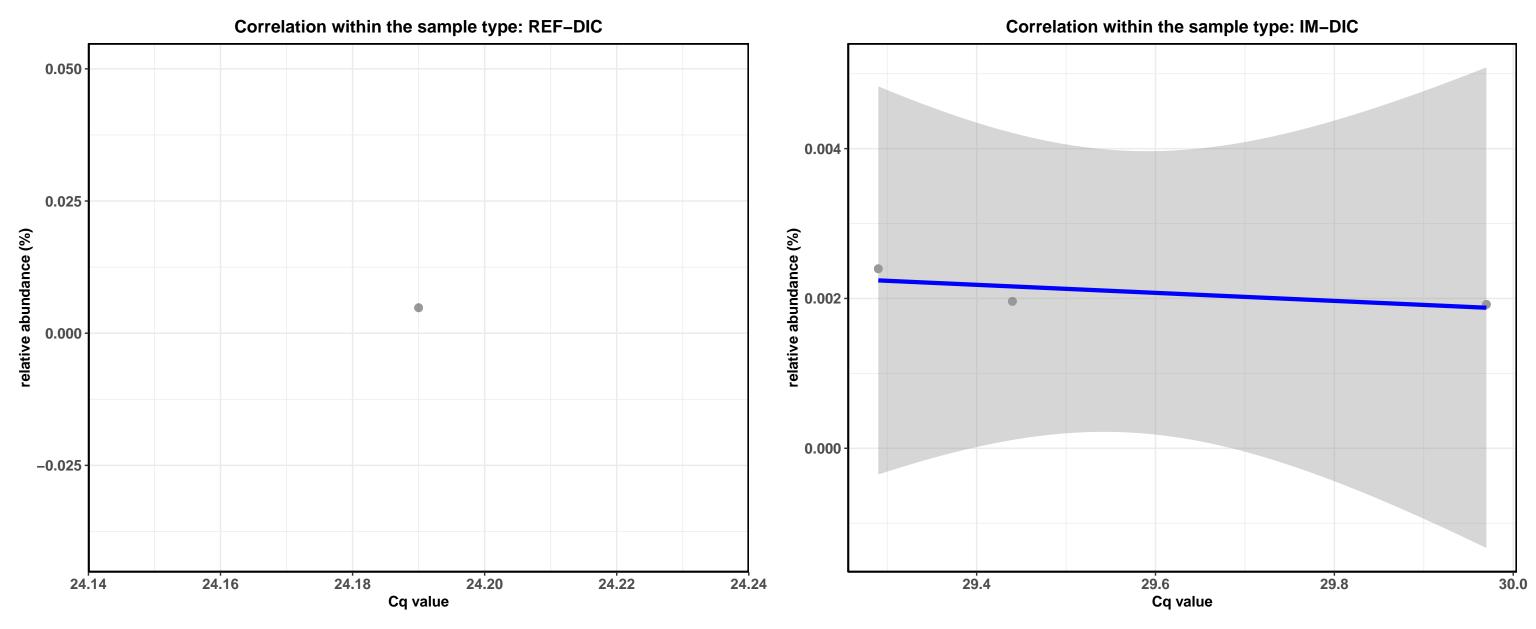
Cq value

30.0

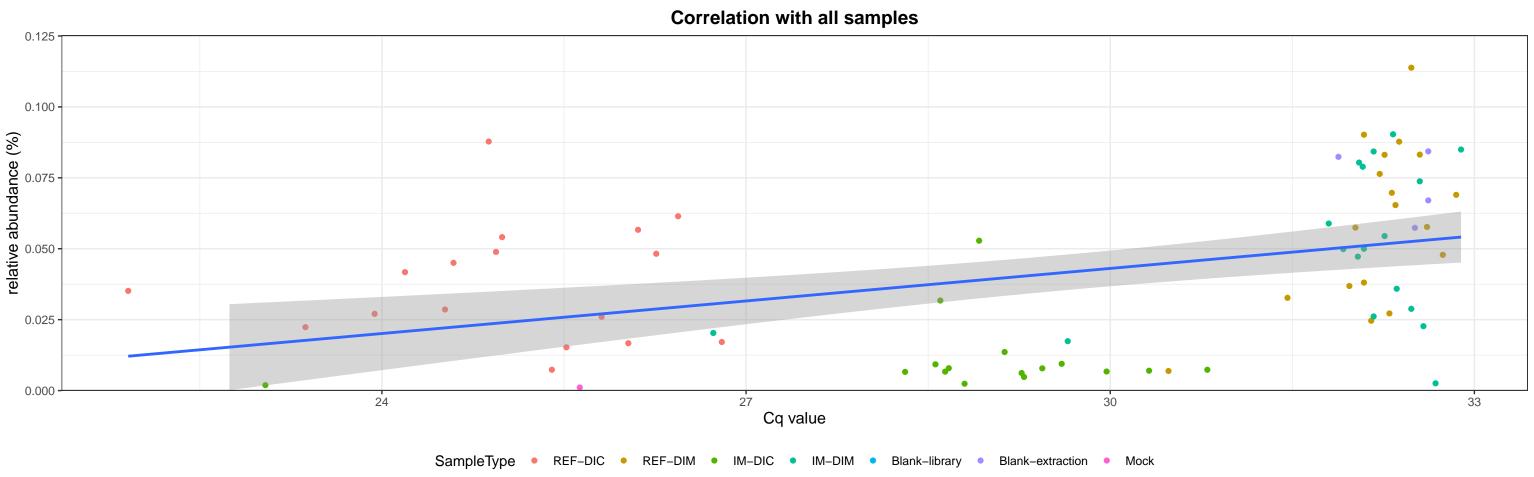
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

Correlation with all samples

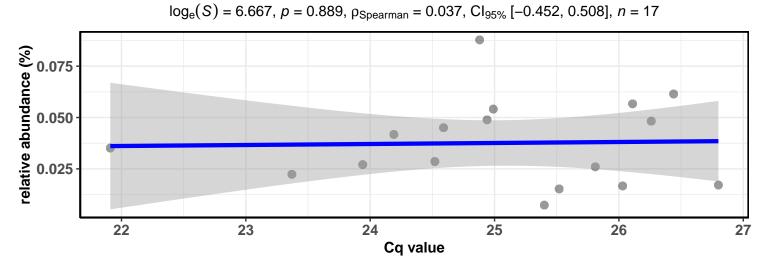




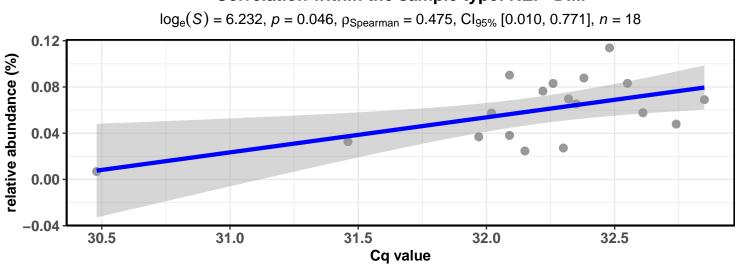
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas



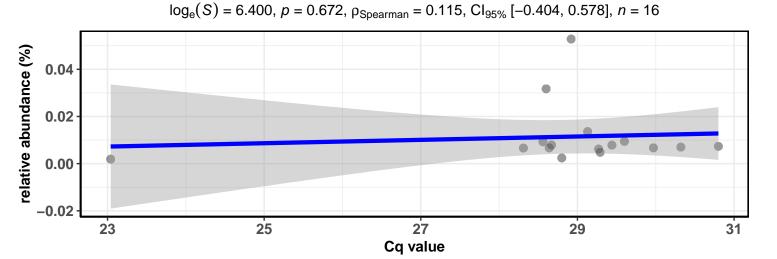


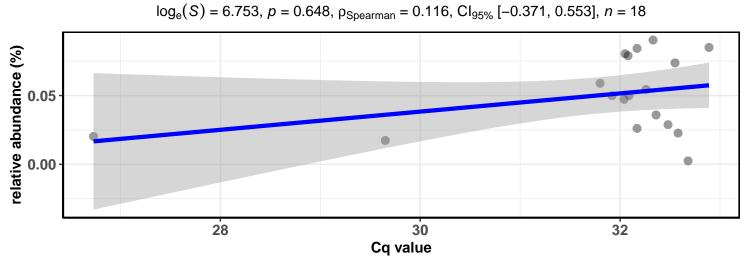


# Correlation within the sample type: REF-DIM

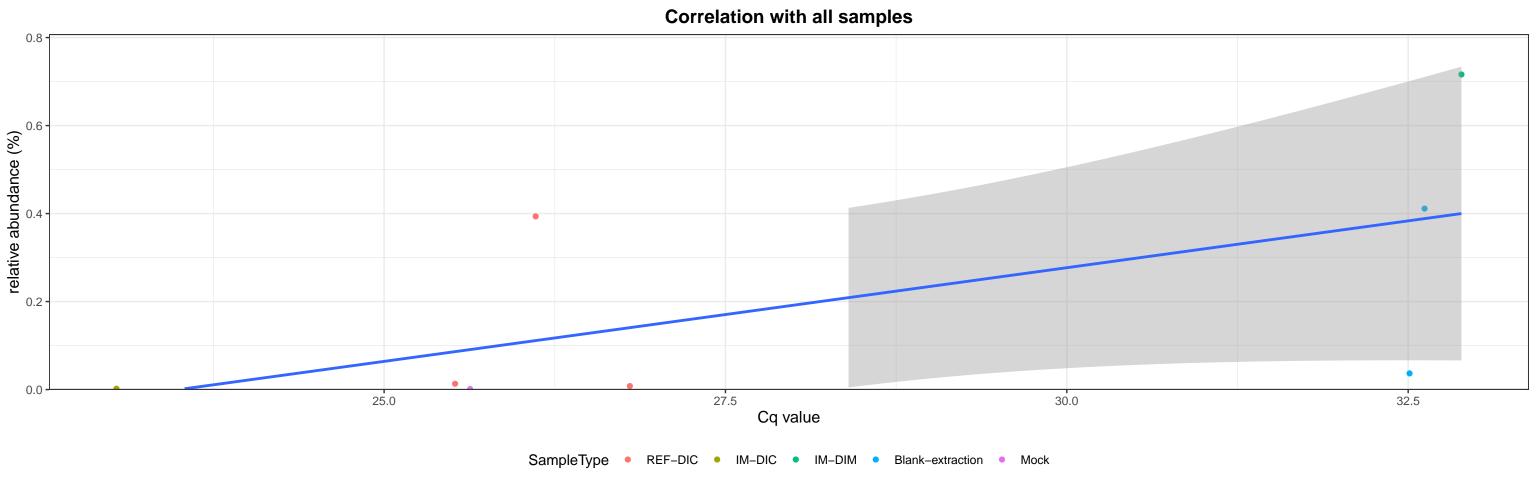


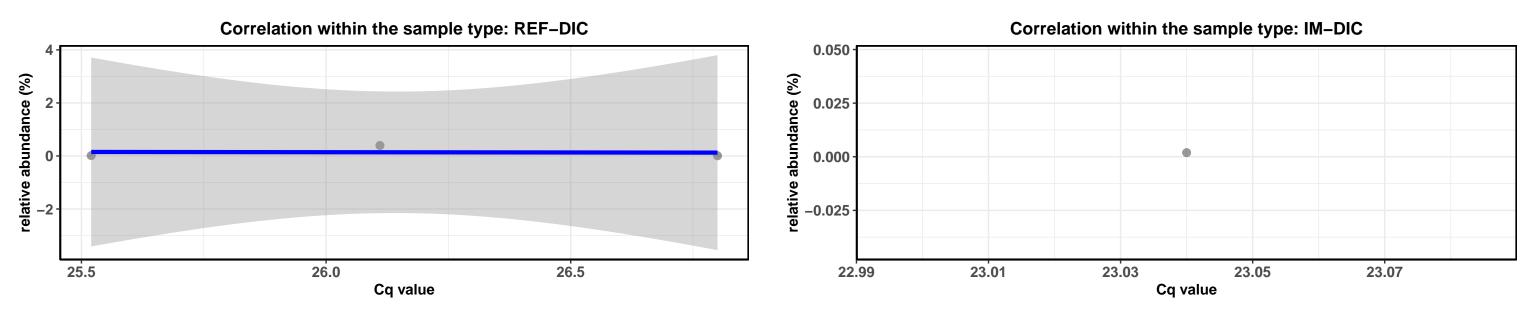
### Correlation within the sample type: IM-DIC

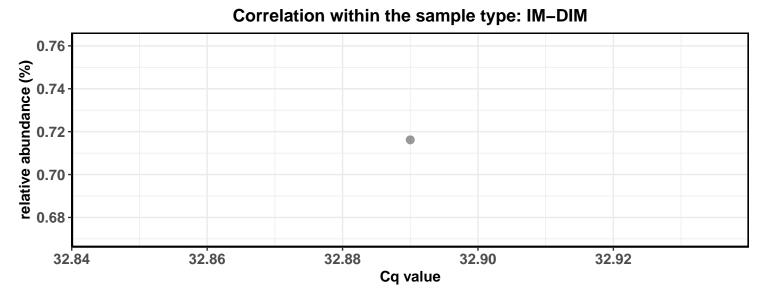




D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium







D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Caulobacterales; D\_4\_Caulobacteraceae; D\_5\_Brevundimonas; Ambiguous\_taxa **Correlation with all samples** 0.6 relative abundance (%) 0.0 30.0 25.0 27.5 32.5 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC • IM-DIM Blank-library Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM  $log_e(S) = 2.079$ , p = 0.072,  $\rho_{Spearman} = 0.771$ ,  $Cl_{95\%}$  [-0.107, 0.974], n = 68.0 relative abundance (%)
0.0
0.0
4.0 0.75 relative abundance (%) 0.50 0.25 0.0 0.00 -0.25 25.0 25.5 26.0 32.0 32.1 32.2 32.3 32.4 32.5 26.5 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM relative abundance (%) relative abundance (%) 0.0

28.8

28.9

29.0

Cq value

29.1

29.2

29.3

32.1

32.0

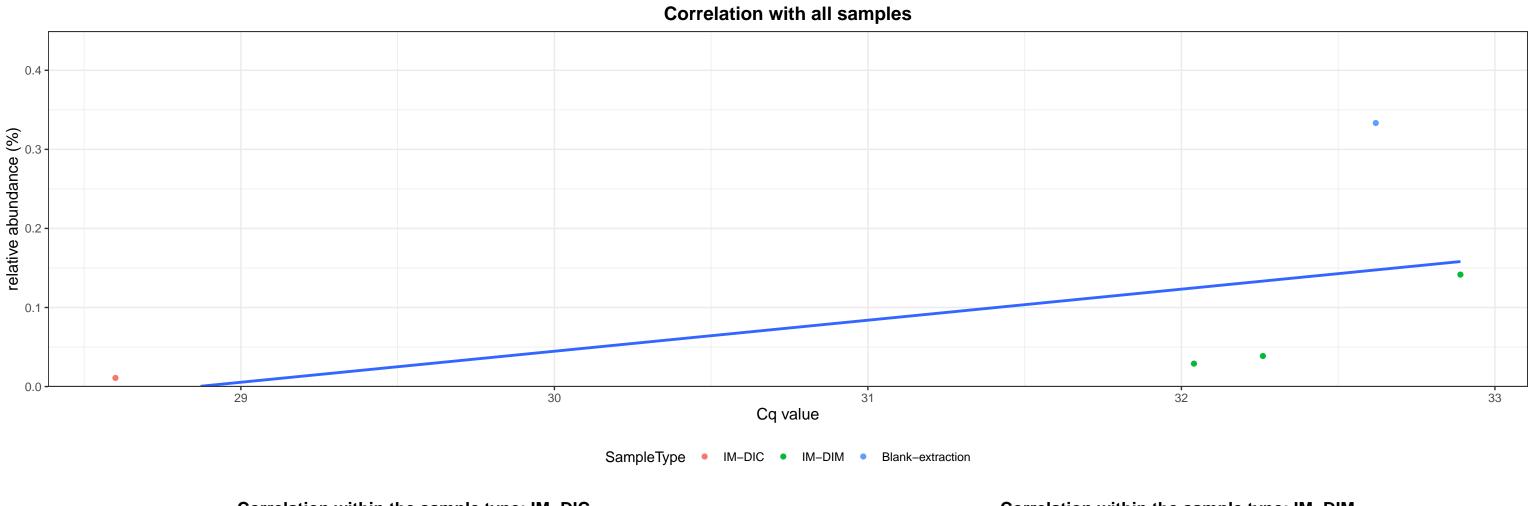
Cq value

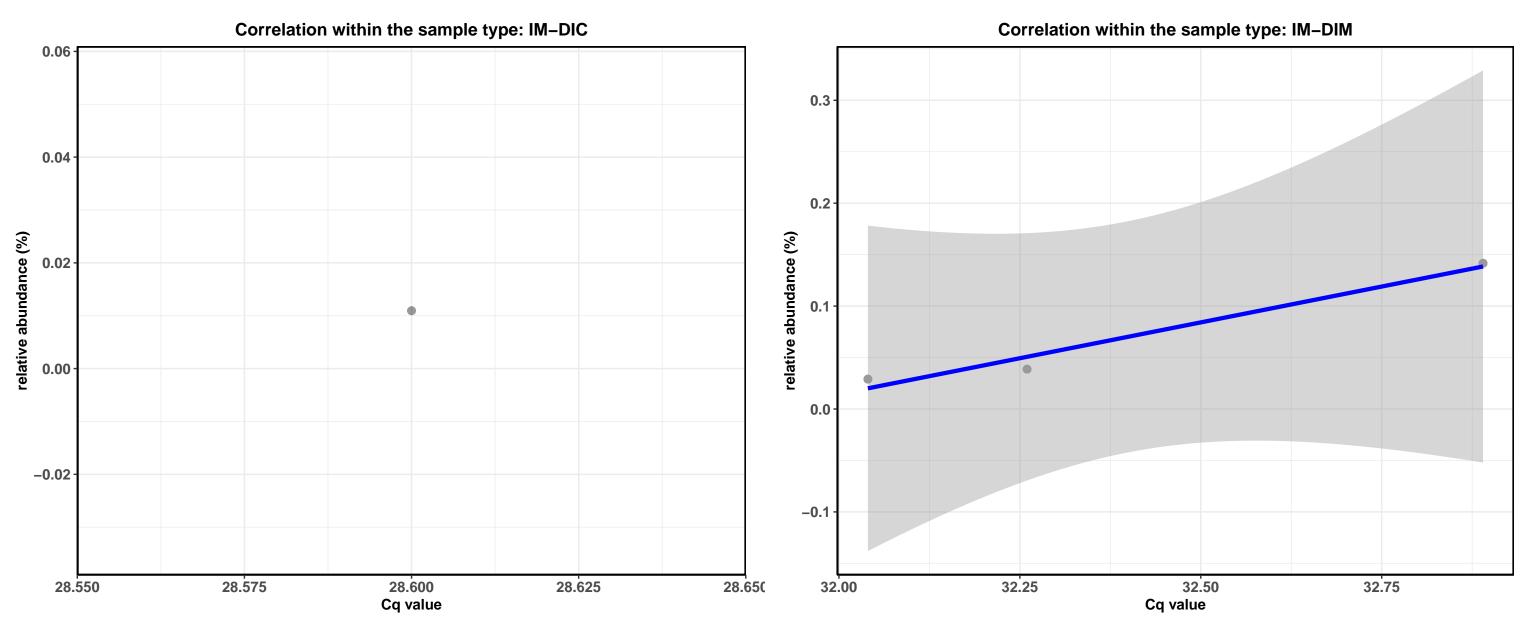
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Caulobacterales; D\_4\_Caulobacteraceae; D\_5\_Brevundimonas; Ambiguous\_taxa **Correlation with all samples** 1.5 relative abundance (%) 24 27 30 33 Cq value SampleType • REF-DIC • REF-DIM IM-DIC
 IM-DIM
 Blank-library Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.50 0.00 0.25 -0.25 relative abundance (%) -0.5022 25 32.0 32.2 32.4 23 24 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM relative abundance (%) 0.03 relative abundance (%) 0.0 23 24 25 27 29 32.0 32.1 26 28

Cq value

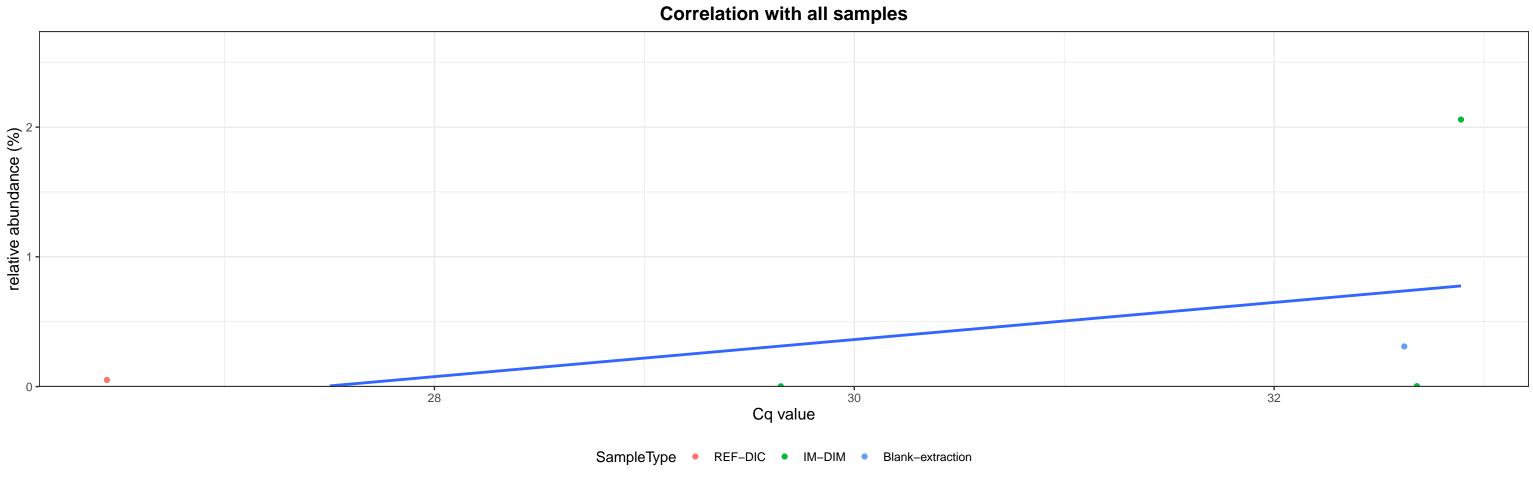
Cq value

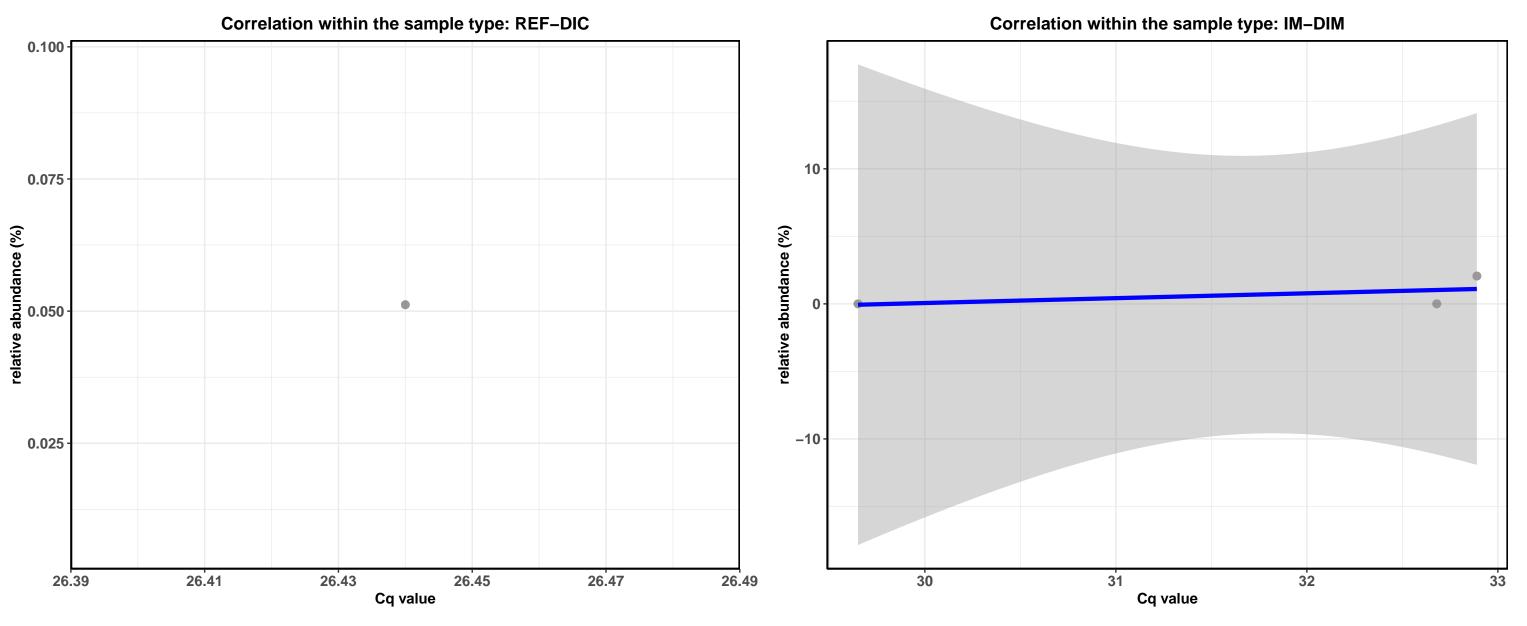
D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium



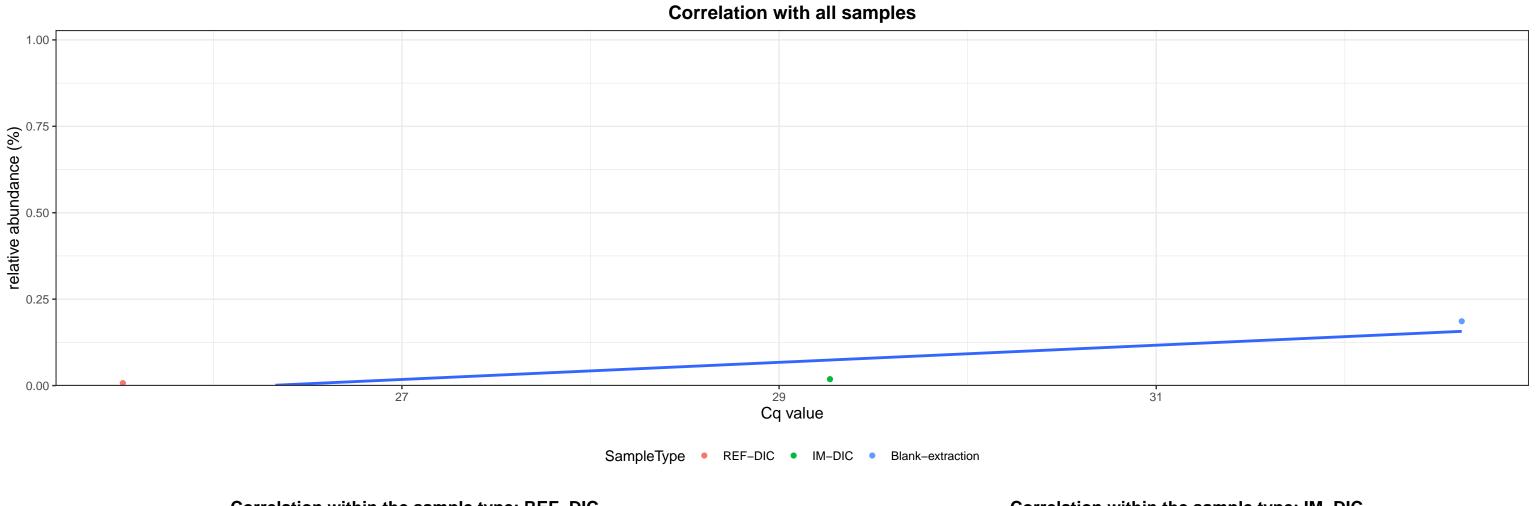


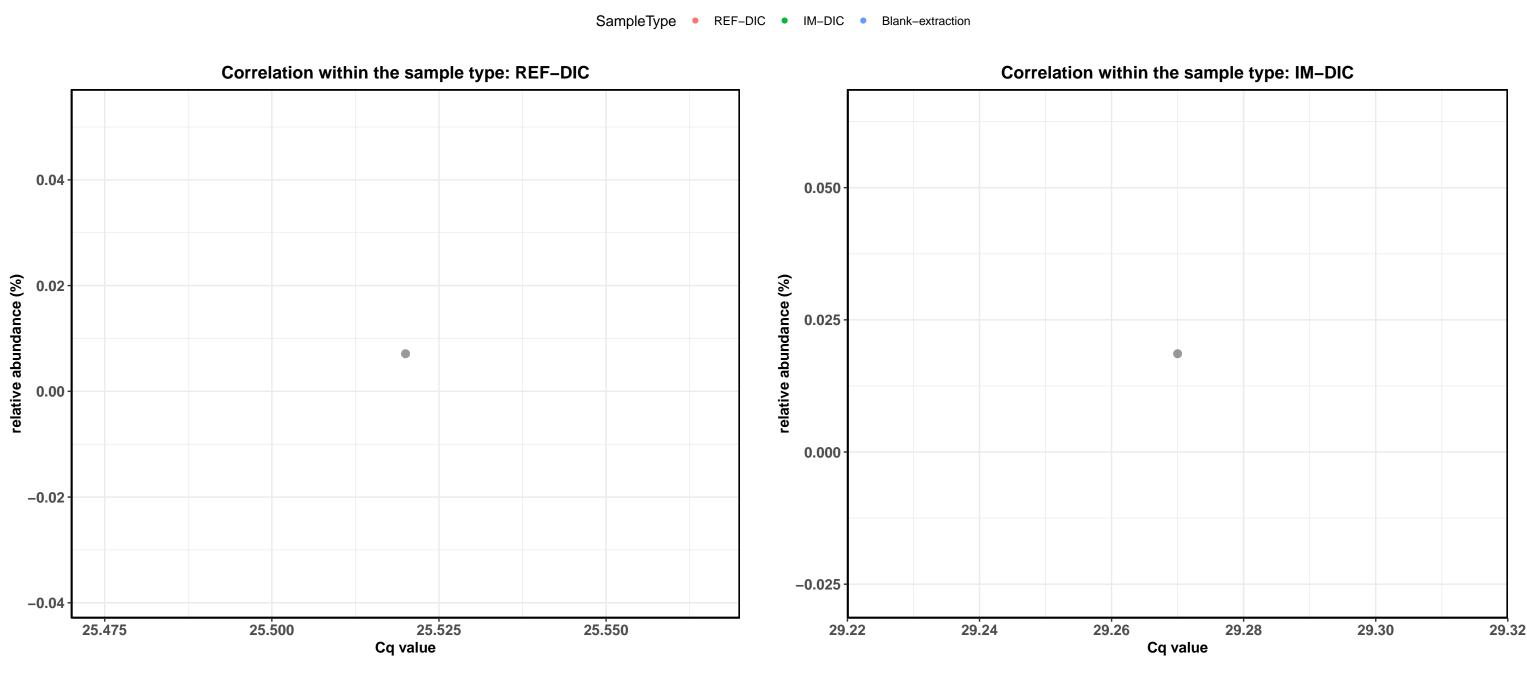
D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium





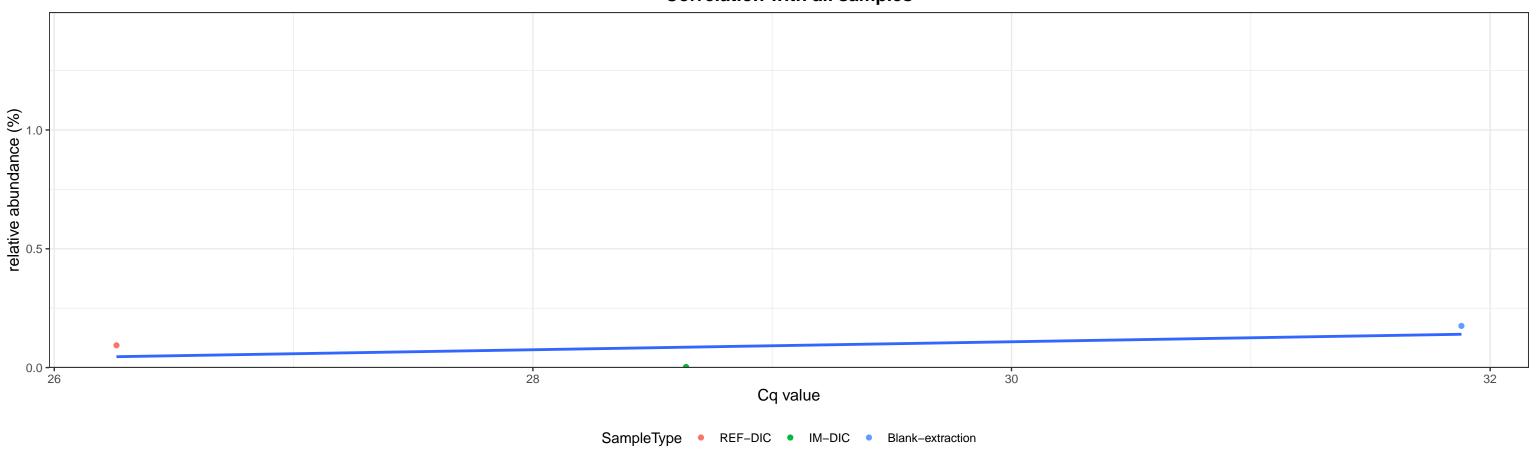
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Micrococcales; D\_4\_Micrococcaceae; D\_5\_Micrococcus; Ambiguous\_taxa

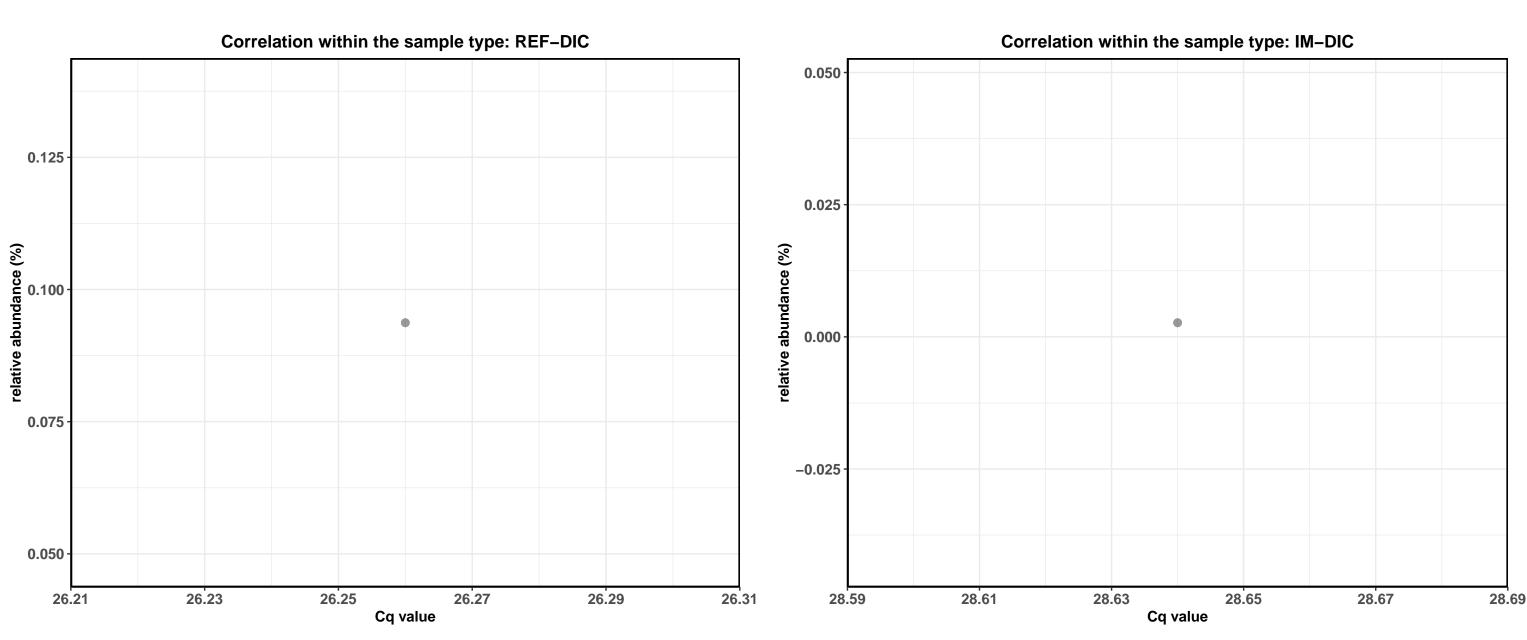




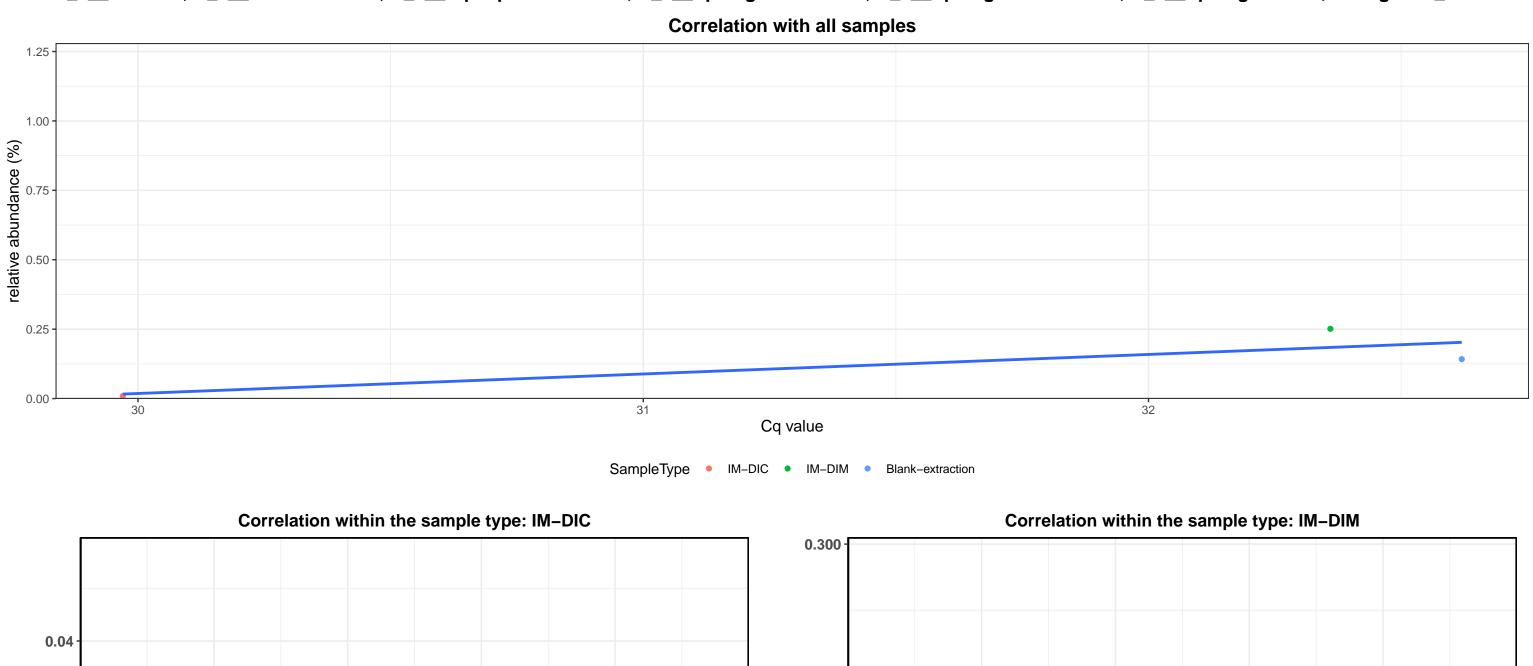
D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium

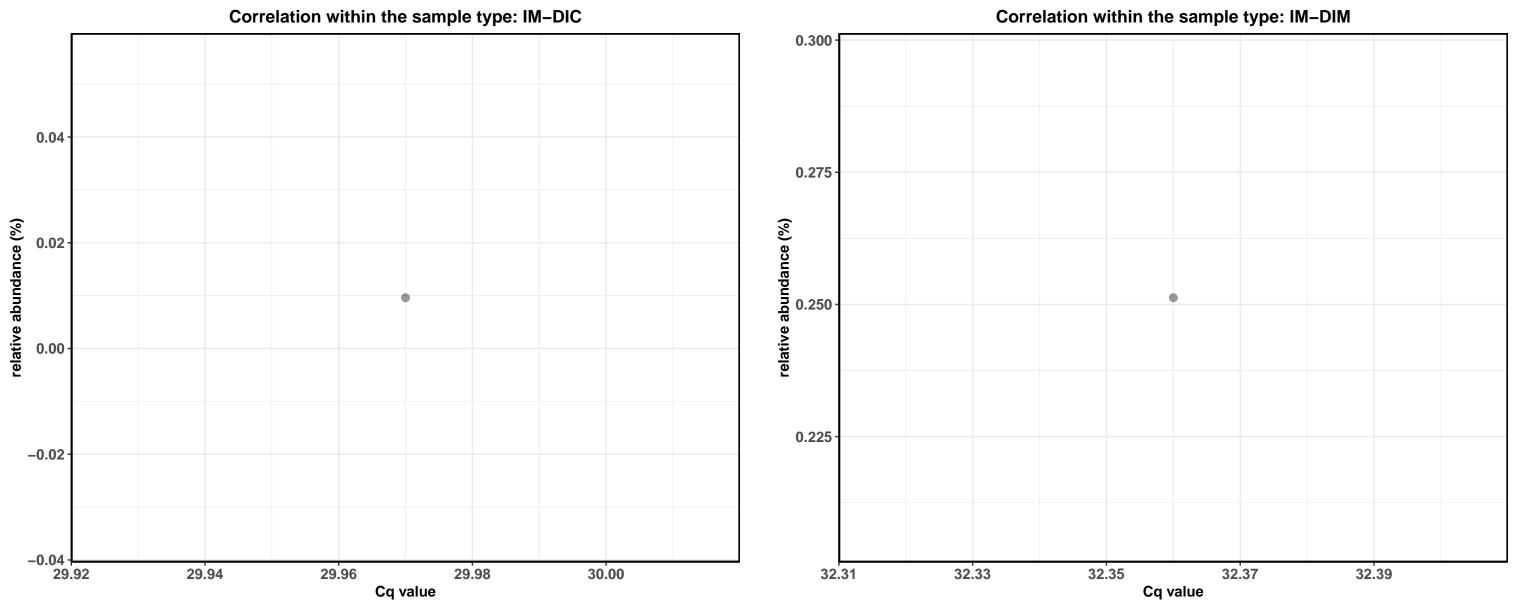
Correlation with all samples



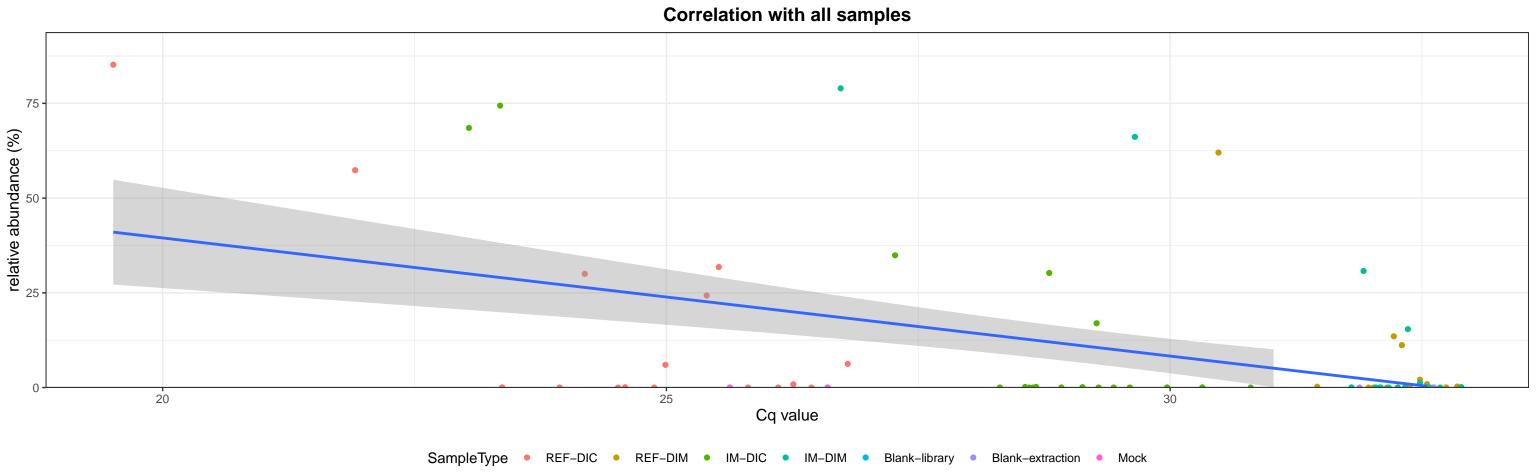


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Sphingomonadales; D\_4\_Sphingomonadaceae; D\_5\_Sphingomonas; Ambiguous\_taxa





D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Aliivibrio; D\_6\_uncultured bacterium



relative abundance (%)

40

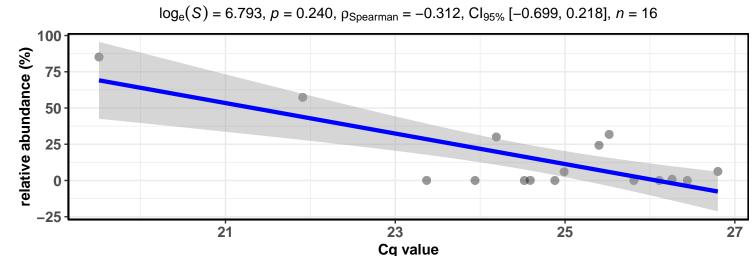
20

0

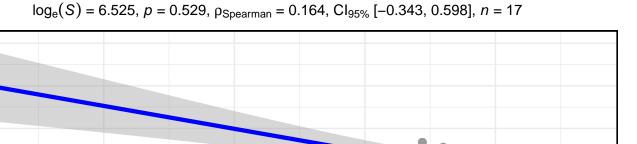
30.5

31.0





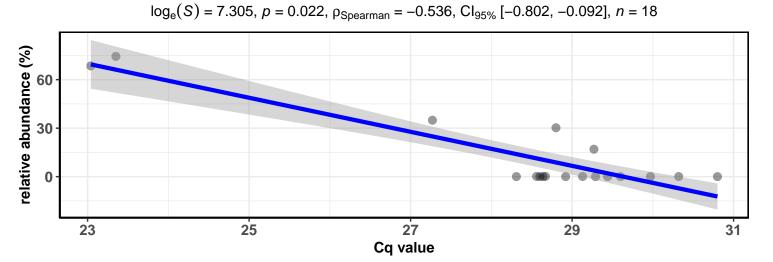
# Correlation within the sample type: REF-DIM



32.0

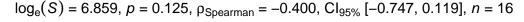
32.5

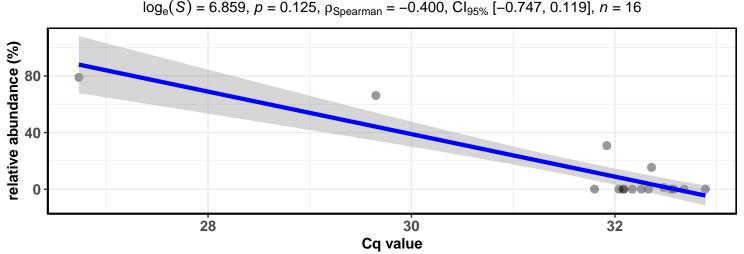
#### Correlation within the sample type: IM-DIC



#### Correlation within the sample type: IM-DIM

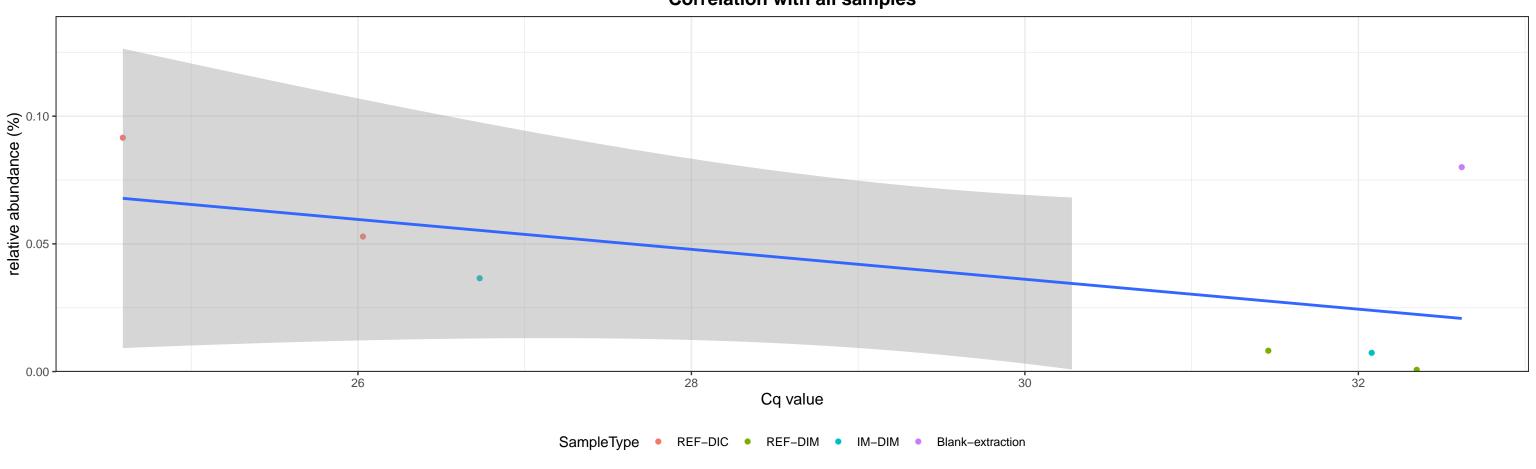
Cq value

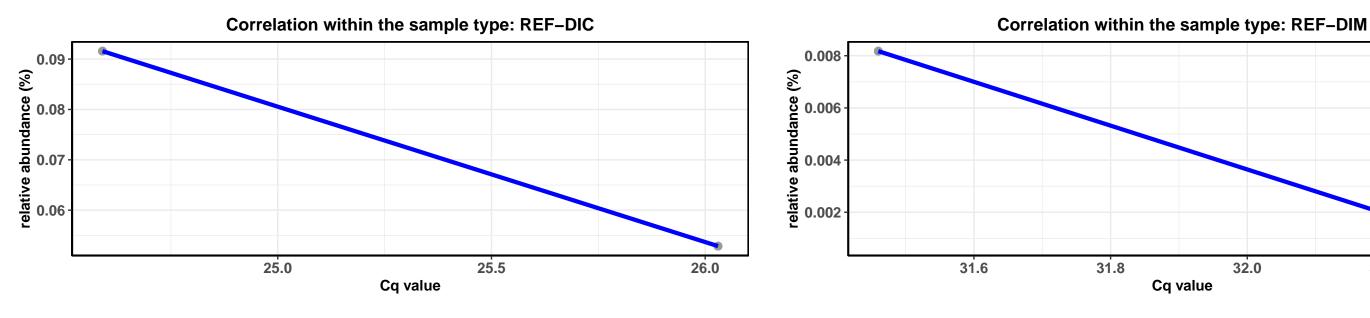


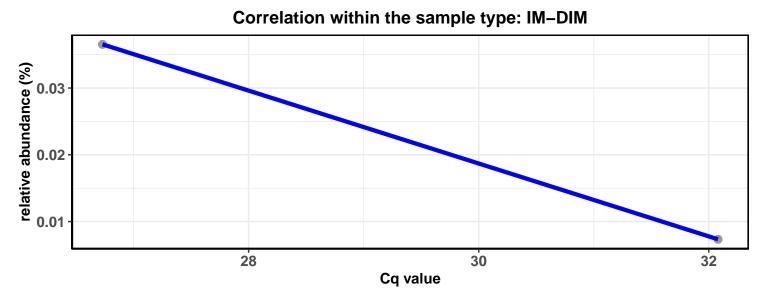


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Sphingomonadales; D\_4\_Sphingomonadaceae; D\_5\_Sphingomonas; Ambiguous\_taxa

Correlation with all samples

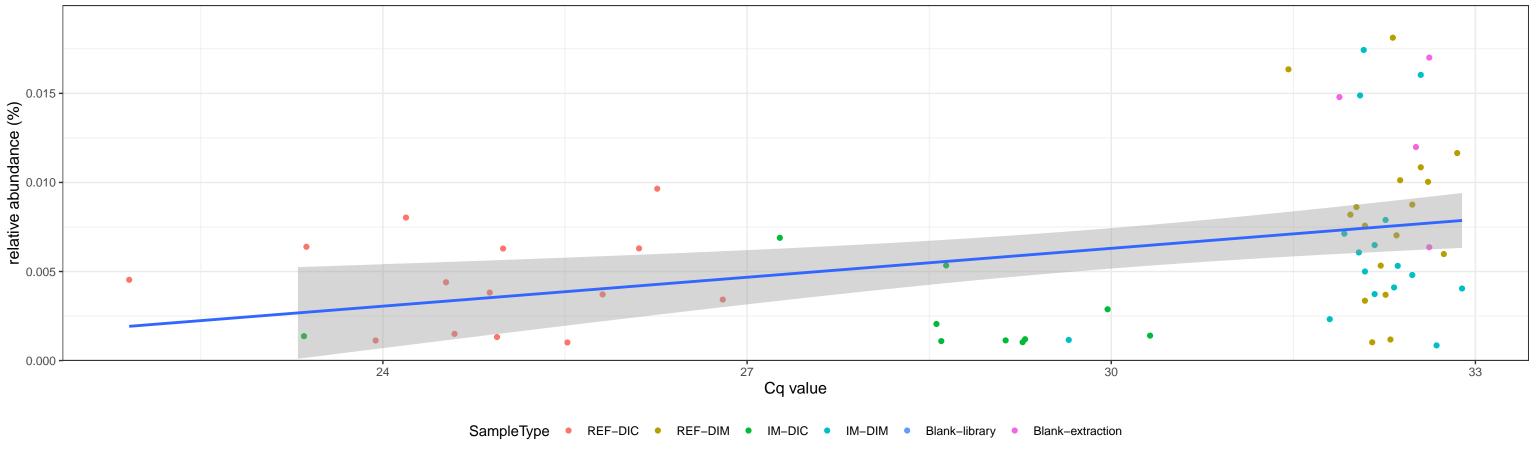




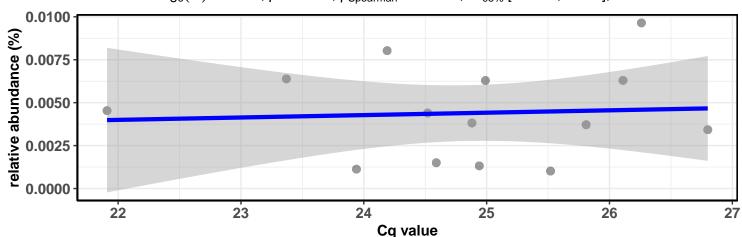


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas



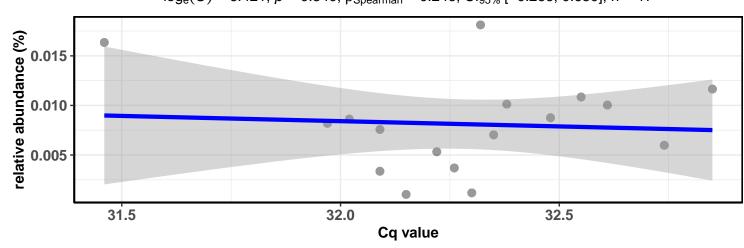


 $log_e(S) = 6.161$ , p = 0.887,  $\rho_{Spearman} = -0.042$ ,  $Cl_{95\%}$  [-0.560, 0.500], n = 14



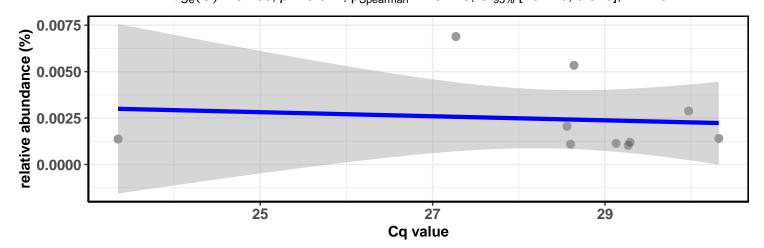
#### Correlation within the sample type: REF-DIM

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

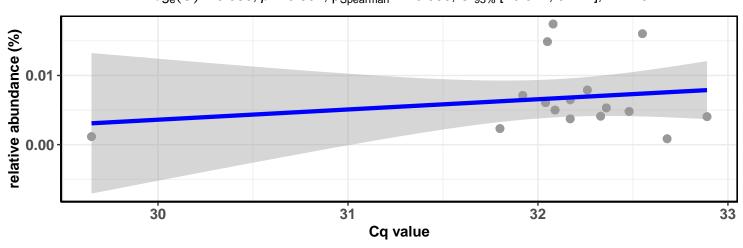


#### Correlation within the sample type: IM-DIC

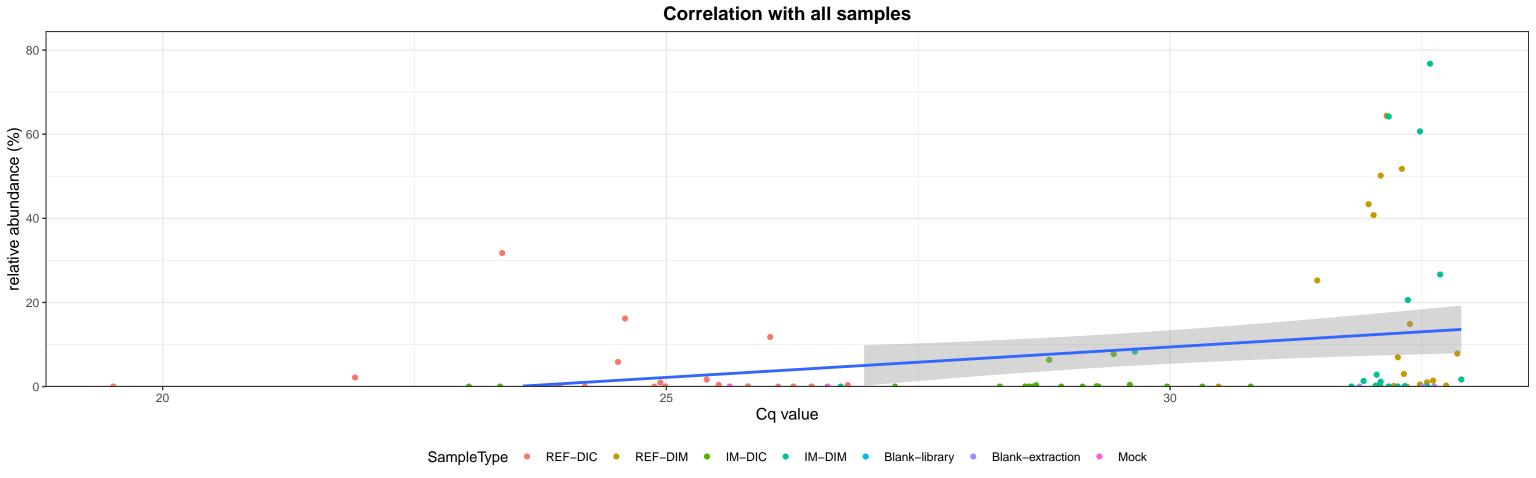
 $log_e(S) = 5.268$ , p = 0.627,  $\rho_{Spearman} = -0.176$ ,  $Cl_{95\%}$  [-0.725, 0.510], n = 10



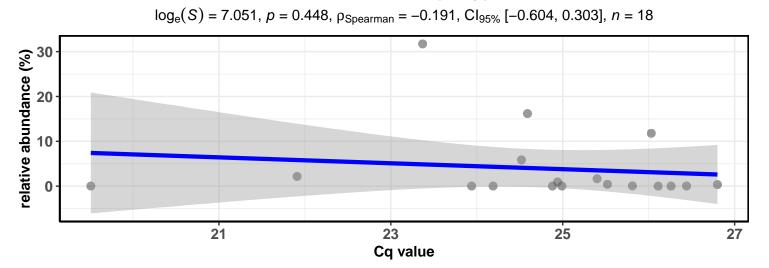
$$log_e(S) = 6.586$$
,  $p = 0.807$ ,  $\rho_{Spearman} = -0.066$ ,  $Cl_{95\%}$  [-0.544, 0.444],  $n = 16$ 

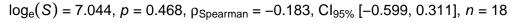


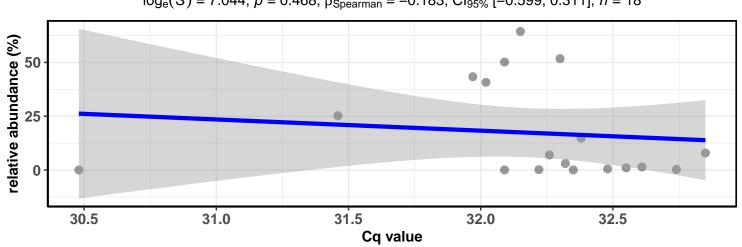
D\_0\_Bacteria; D\_1\_Spirochaetes; D\_2\_Spirochaetia; D\_3\_Brevinematales; D\_4\_Brevinemataceae; D\_5\_Brevinema; D\_6\_Brevinema andersonii



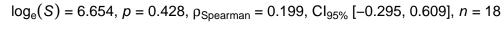


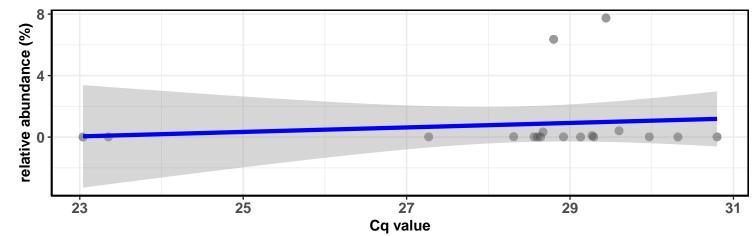




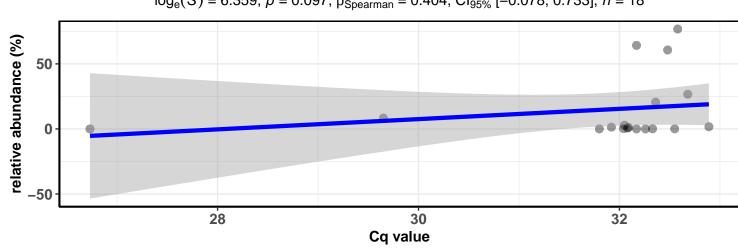


#### Correlation within the sample type: IM-DIC

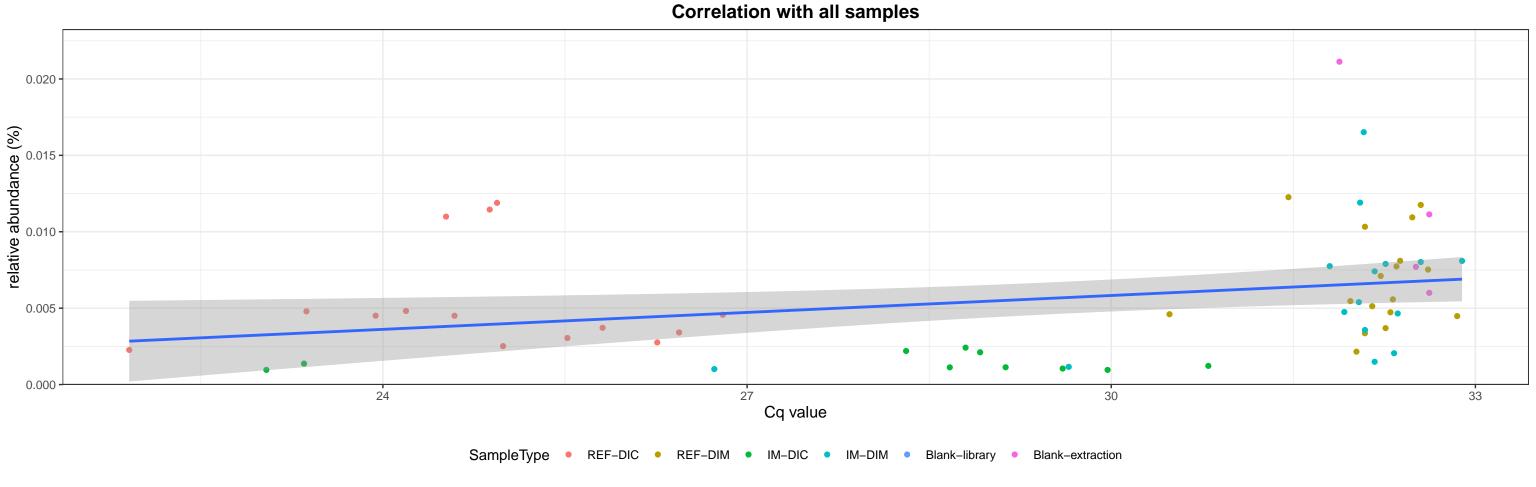




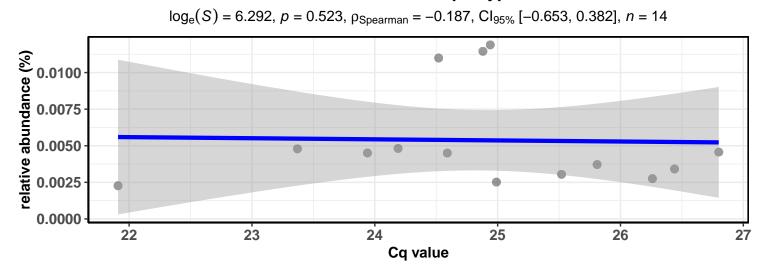
$$log_e(S) = 6.359$$
,  $p = 0.097$ ,  $\rho_{Spearman} = 0.404$ ,  $Cl_{95\%}$  [-0.078, 0.733],  $n = 18$ 

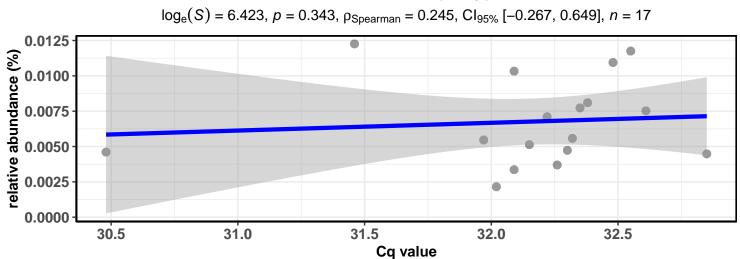


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

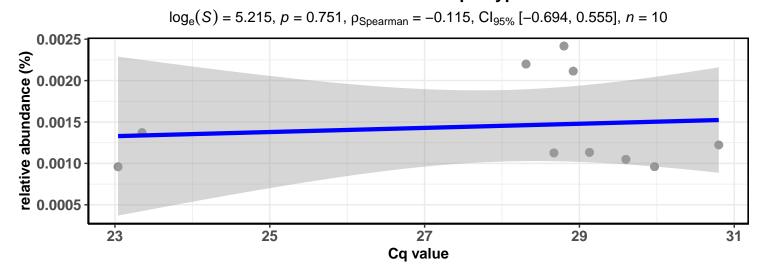


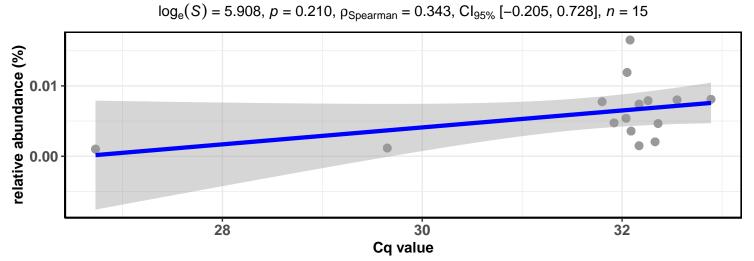




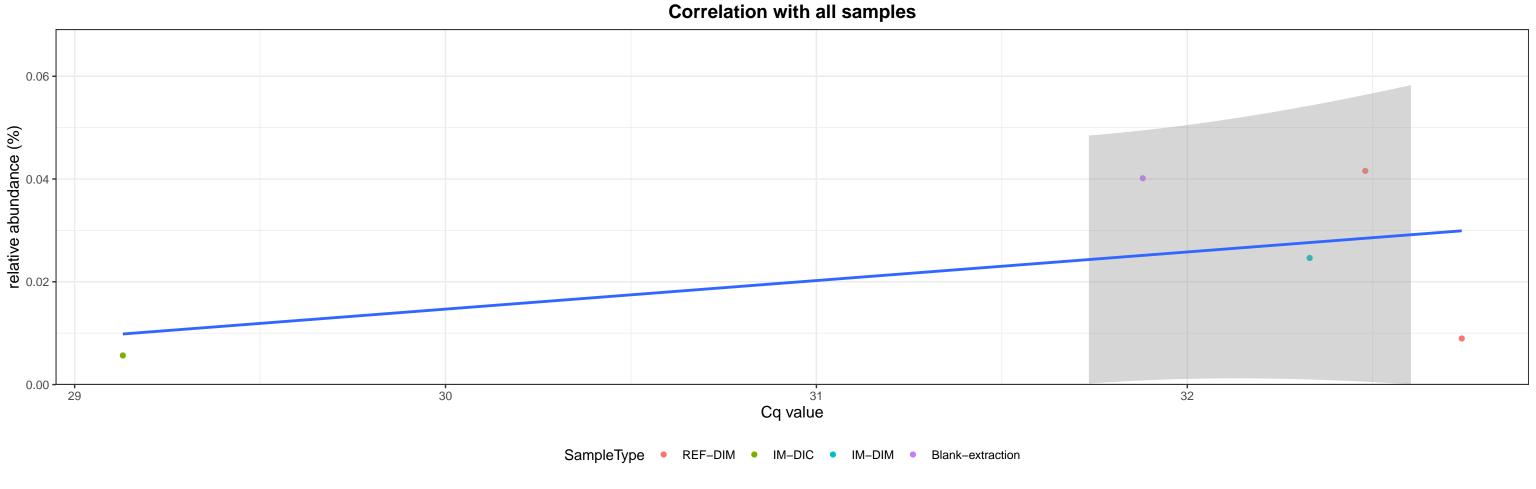


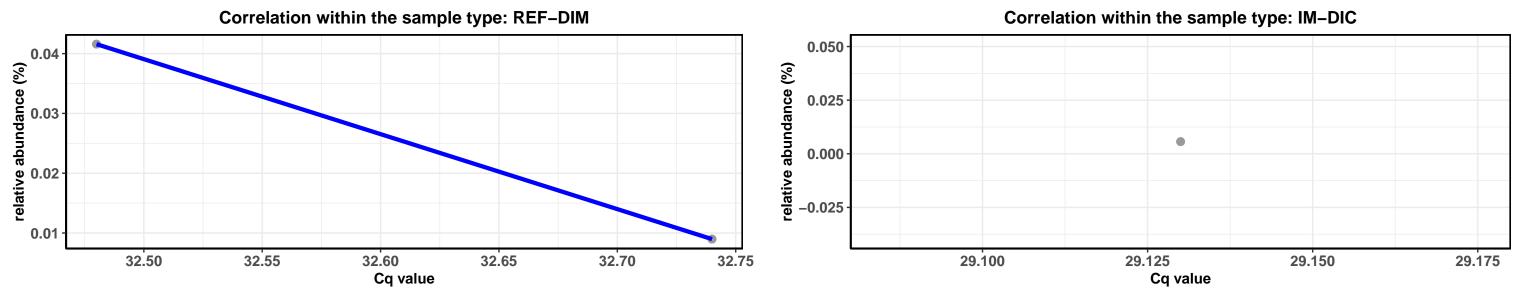
#### Correlation within the sample type: IM-DIC

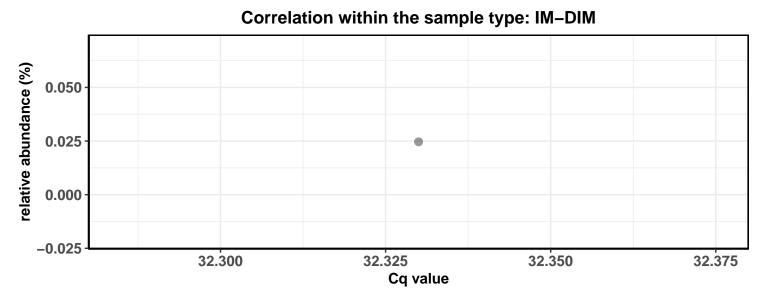




D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Rhizobiales; D\_4\_Devosiaceae; D\_5\_Devosia



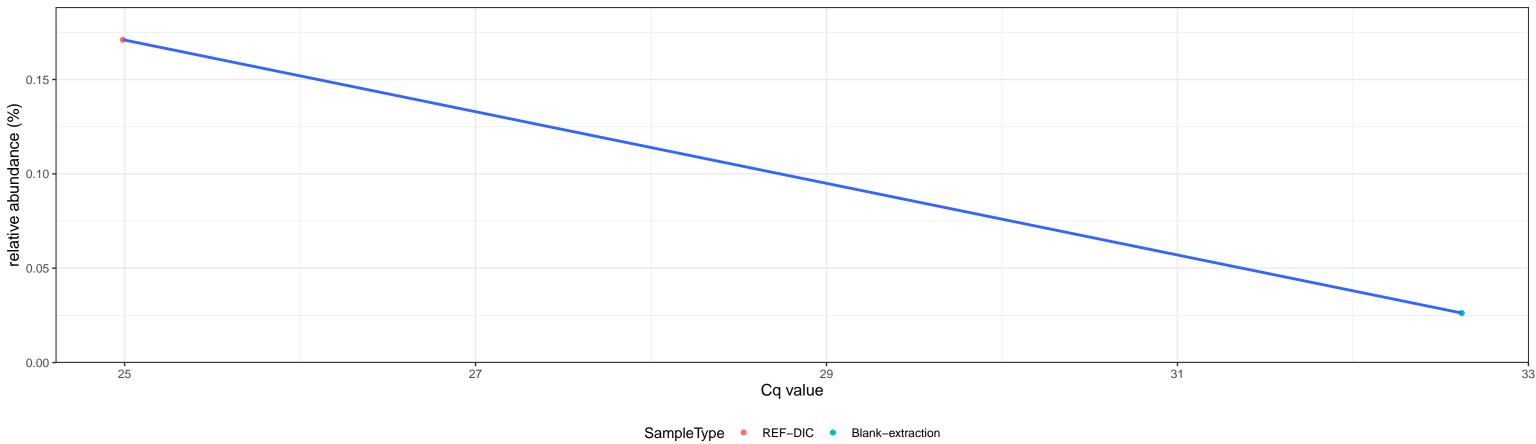


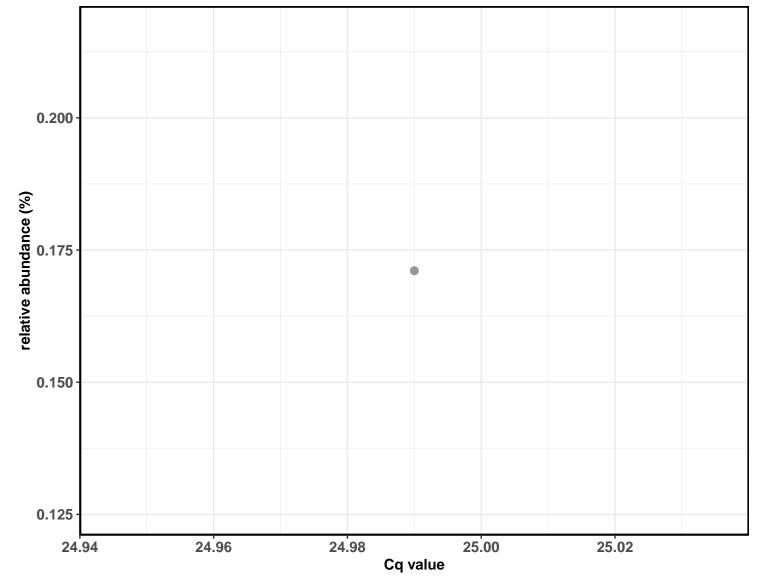


\_0\_\_Bacteria; D\_1\_\_Proteobacteria; D\_2\_\_Alphaproteobacteria; D\_3\_\_Sphingomonadales; D\_4\_\_Sphingomonadaceae; D\_5\_\_Sphingomonas; D\_6\_\_Sphingomonas aurantiad **Correlation with all samples** 0.16 relative abundance (%) 0.04 25.0 27.5 32.5 30.0 Cq value REF-DIC • REF-DIM • IM-DIC IM-DIM Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.125 0.03 (%) 0.002 0.001 0.025 colors of the second of 0.000 24 25 32.40 32.45 32.50 32.55 32.60 Cq value Cq value Correlation within the sample type: IM-DIM Correlation within the sample type: IM-DIC 0.050 0.16 relative abundance (%) relative abundance (%) 0.000 -0.000 -0.025 -0.04 31.75 29.39 29.41 29.43 29.45 29.47 29.49 32.00 32.25 32.50 32.75 Cq value Cq value

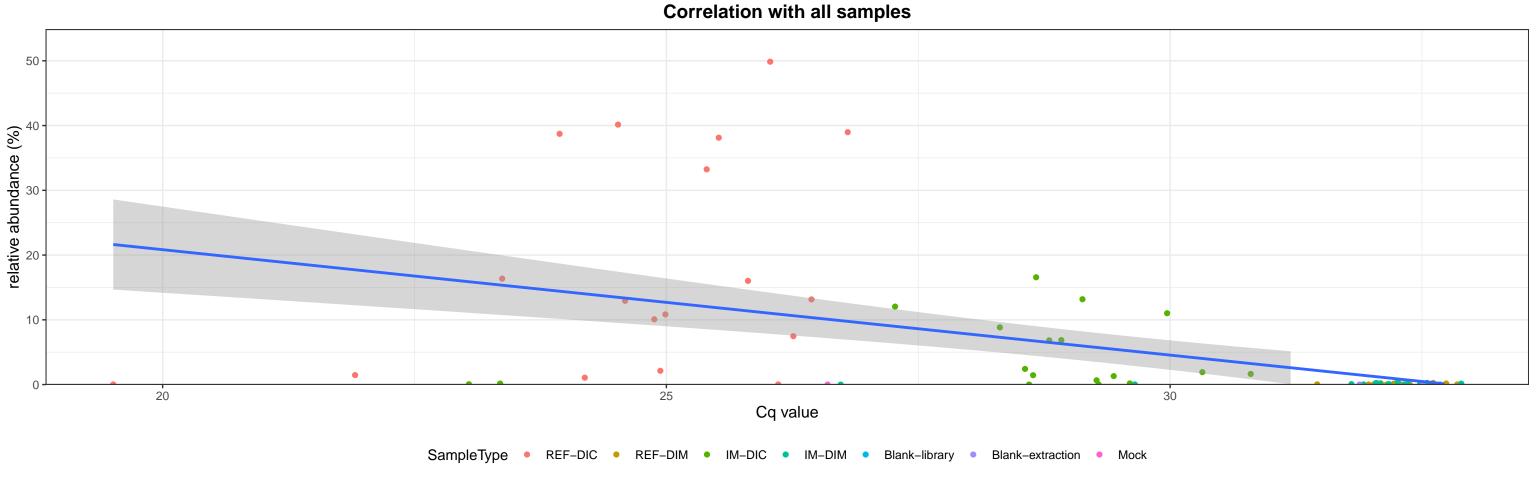
D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured Hymenobacter sp.



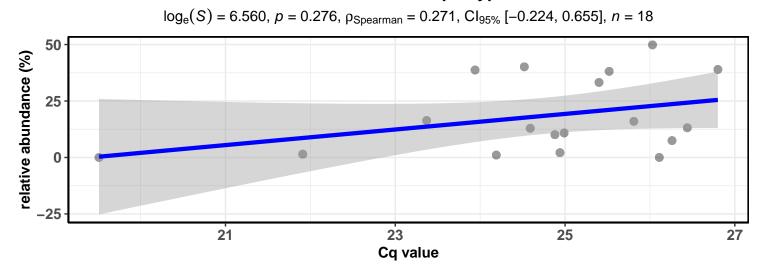


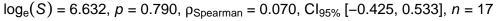


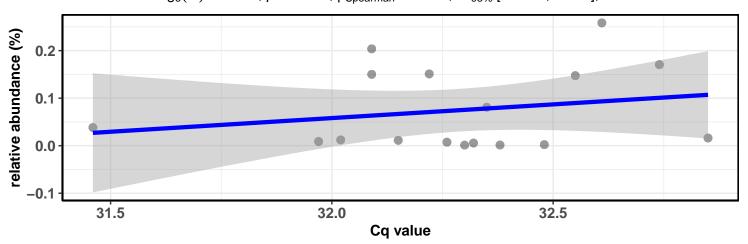
D\_0\_Bacteria; D\_1\_Tenericutes; D\_2\_Mollicutes; D\_3\_Mycoplasmatales; D\_4\_Mycoplasmataceae; D\_5\_Mycoplasma; D\_6\_uncultured bacterium



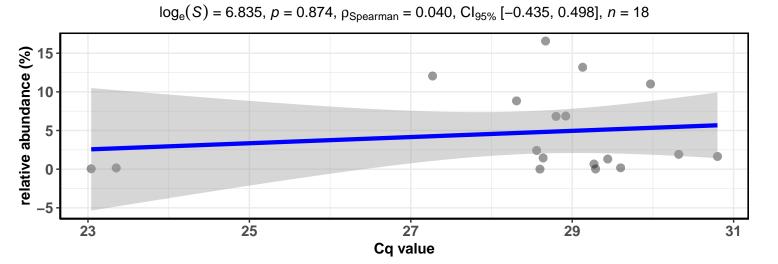




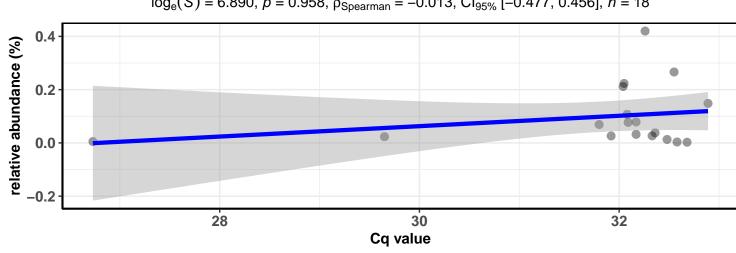




#### Correlation within the sample type: IM-DIC

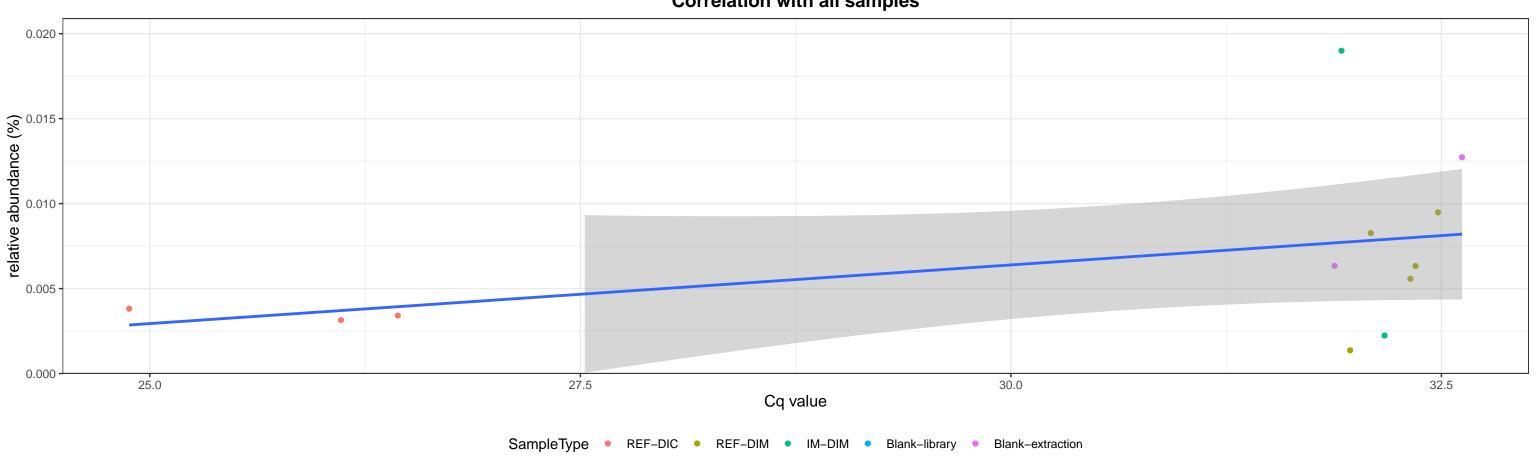


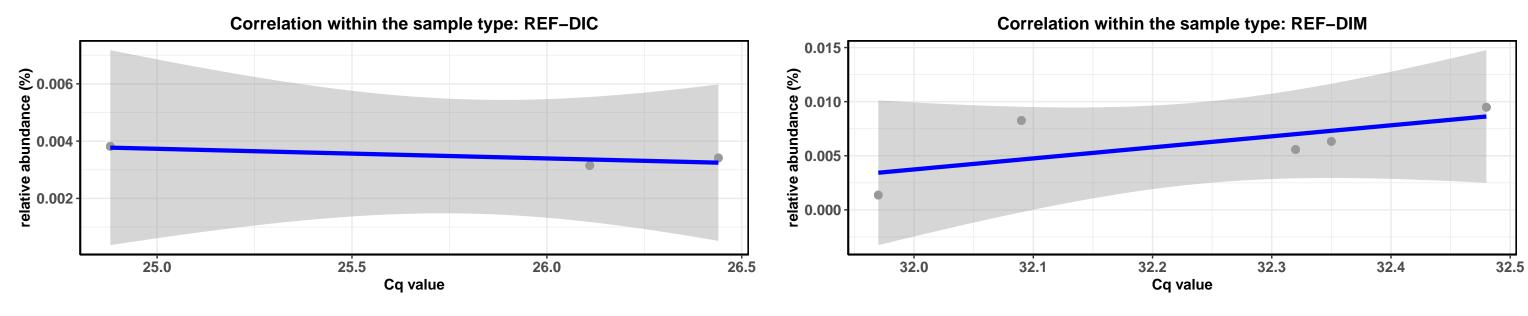
$$log_e(S) = 6.890, p = 0.958, \rho_{Spearman} = -0.013, Cl_{95\%} [-0.477, 0.456], n = 18$$

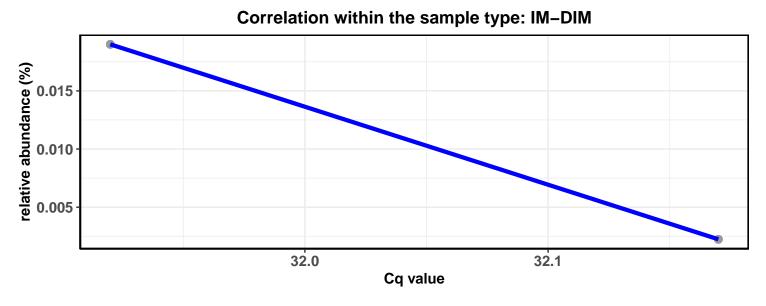


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Caulobacterales; D\_4\_Caulobacteraceae; D\_5\_Brevundimonas; Ambiguous\_taxa

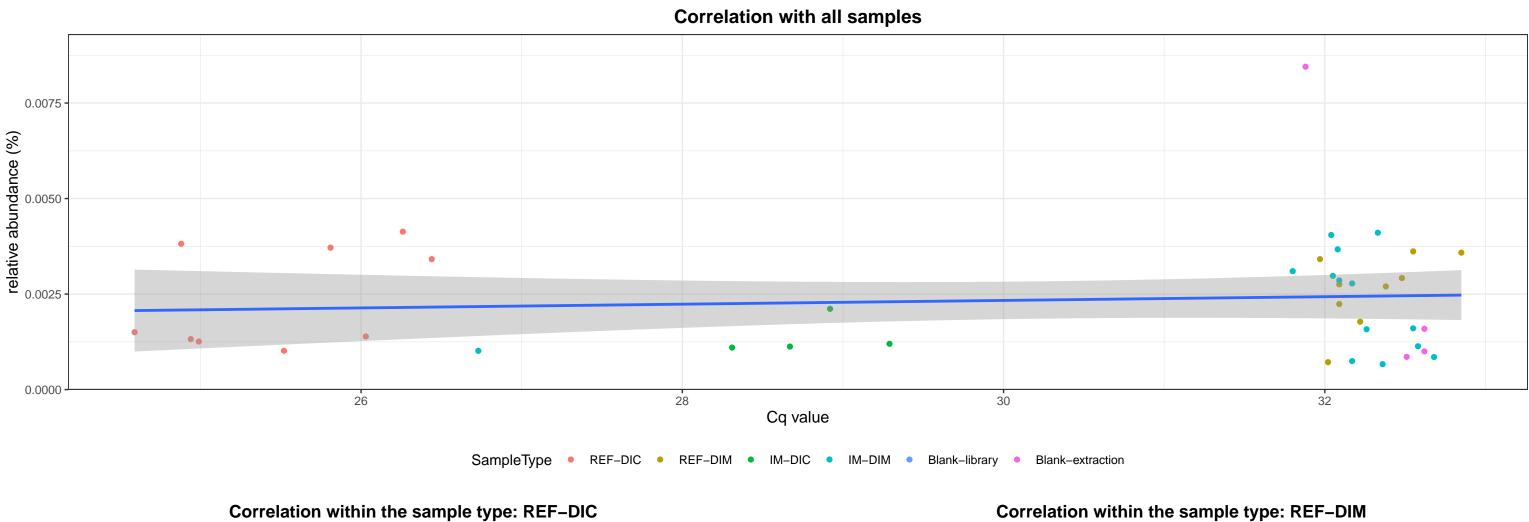
Correlation with all samples

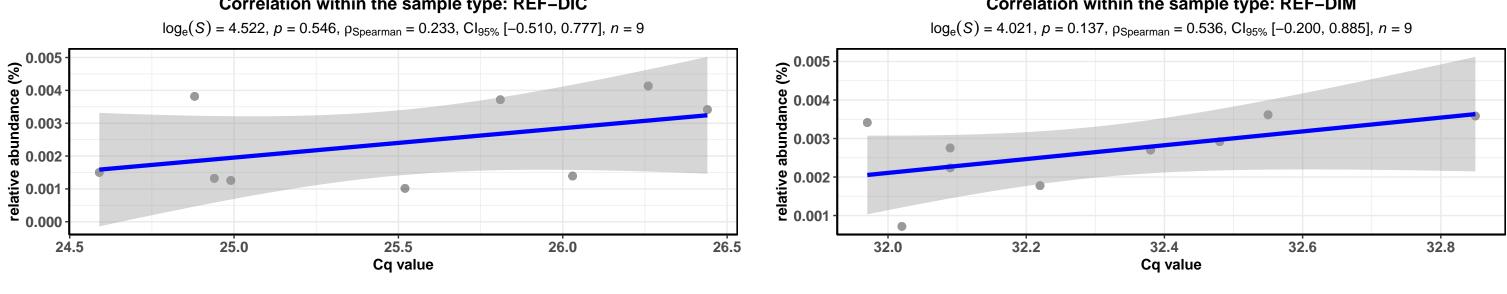


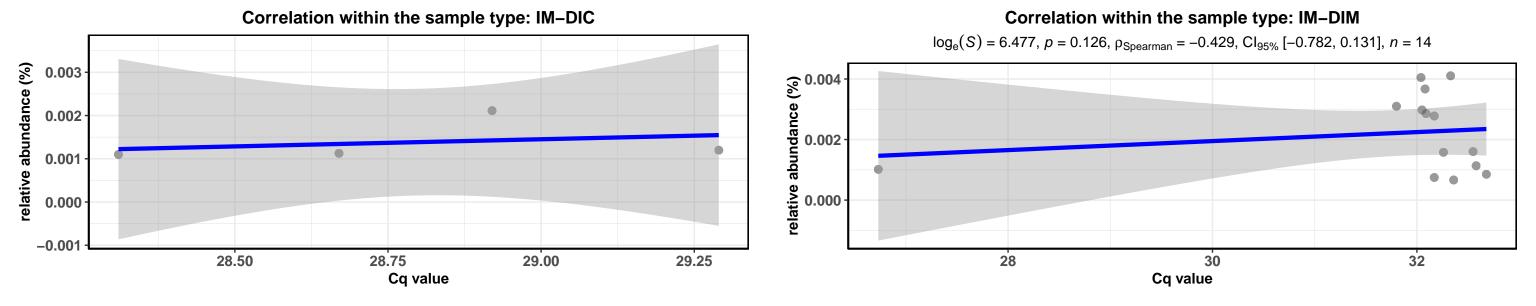




D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

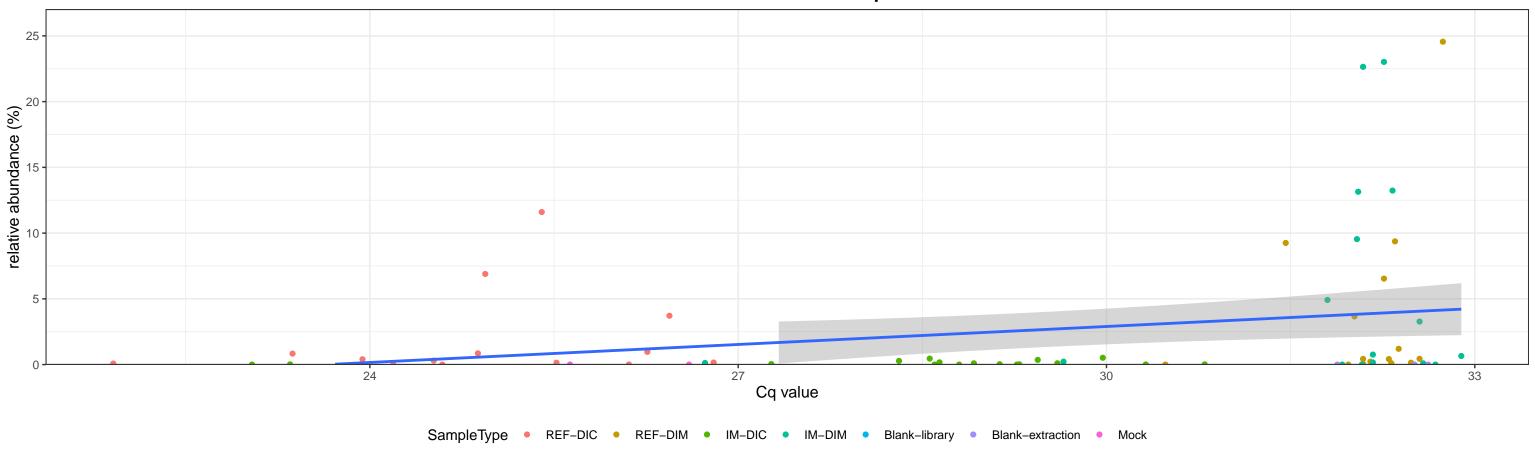




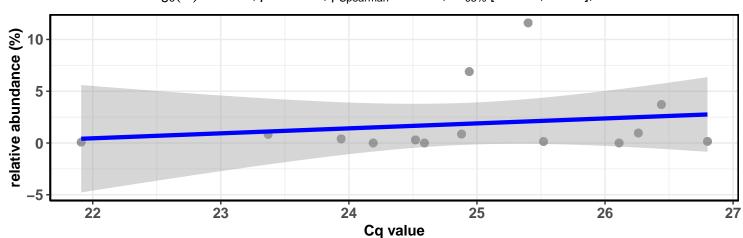


D\_0\_Bacteria; D\_1\_Spirochaetes; D\_2\_Spirochaetia; D\_3\_Spirochaetales; D\_4\_Spirochaetaceae



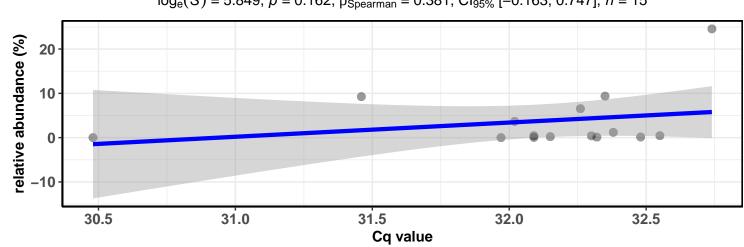


 $log_e(S) = 5.799, p = 0.342, \rho_{Spearman} = 0.275, Cl_{95\%}$  [-0.300, 0.703], n = 14



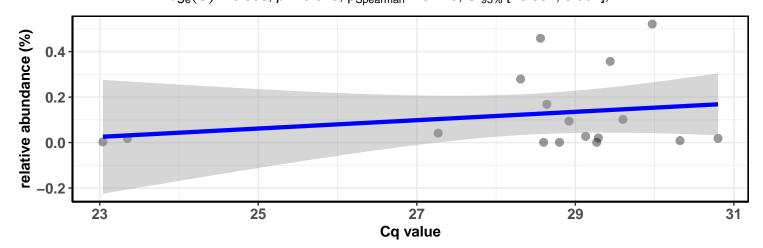
# Correlation within the sample type: REF-DIM

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



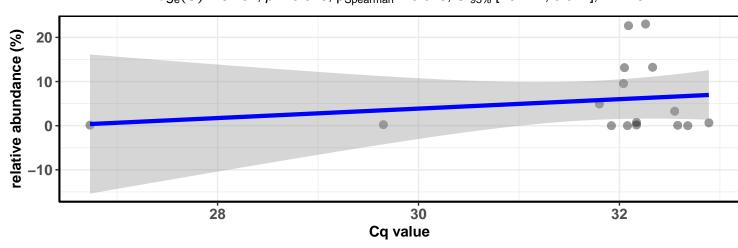
#### Correlation within the sample type: IM-DIC

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

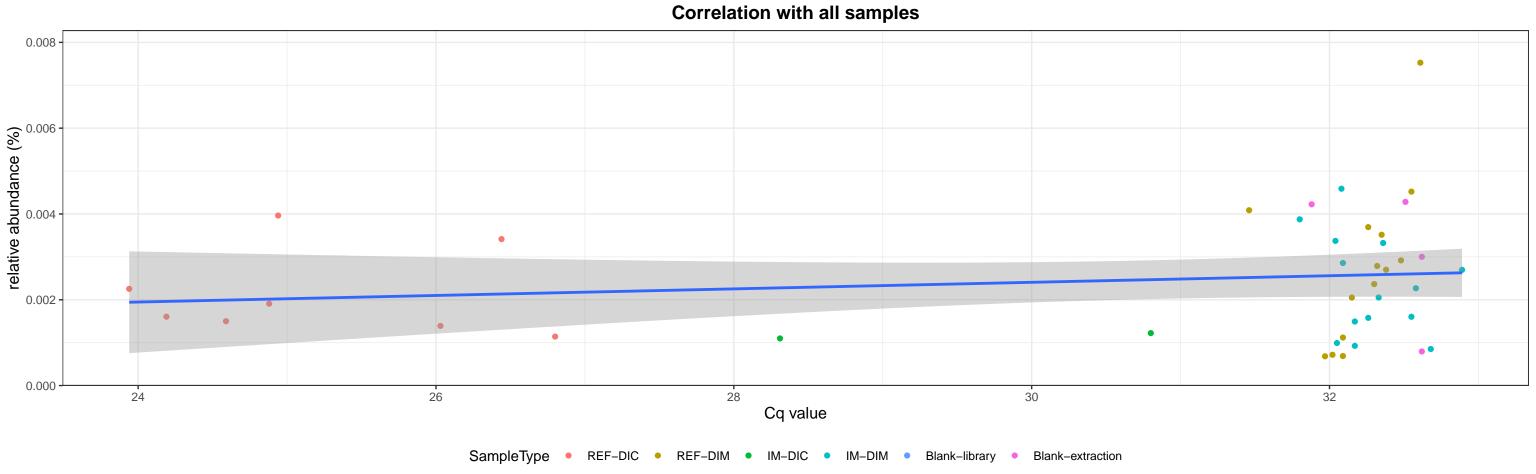


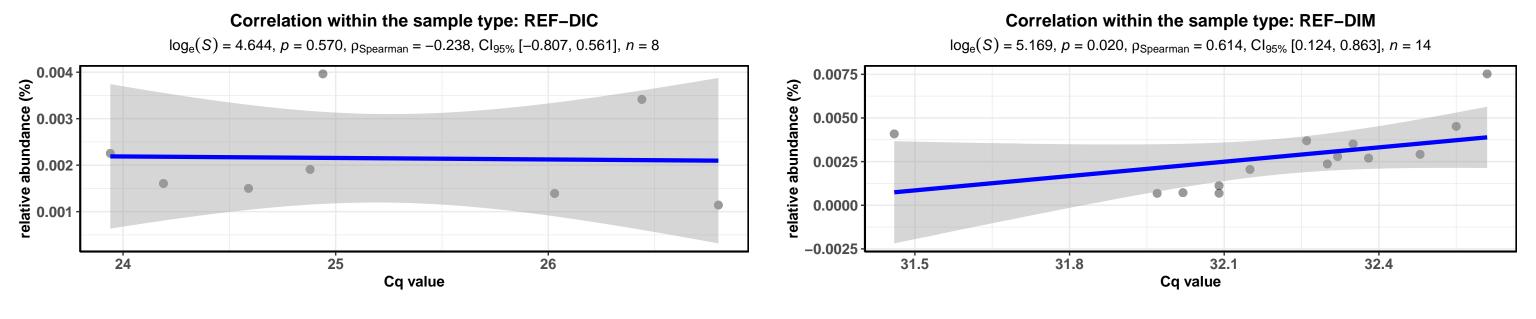
# Correlation within the sample type: IM-DIM

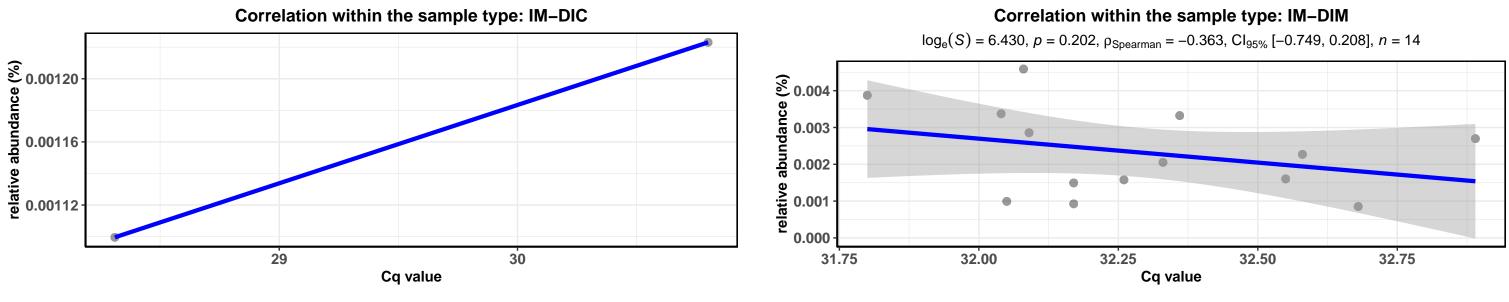
 $log_e(S) = 6.494, p = 0.918, \rho_{Spearman} = 0.028, Cl_{95\%}$  [-0.474, 0.517], n = 16



D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

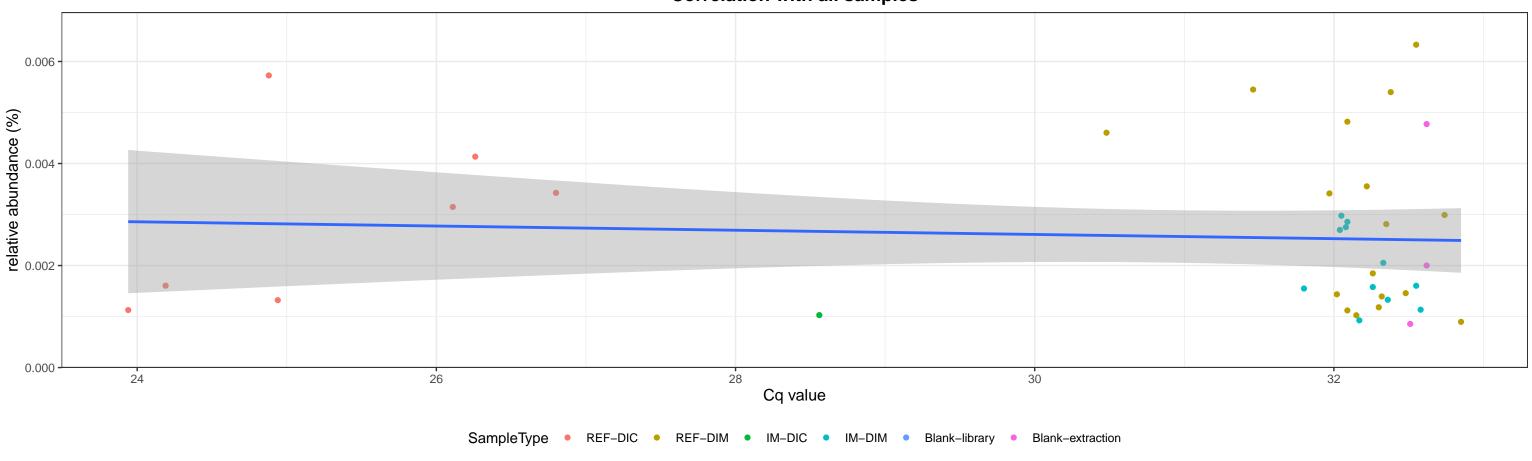


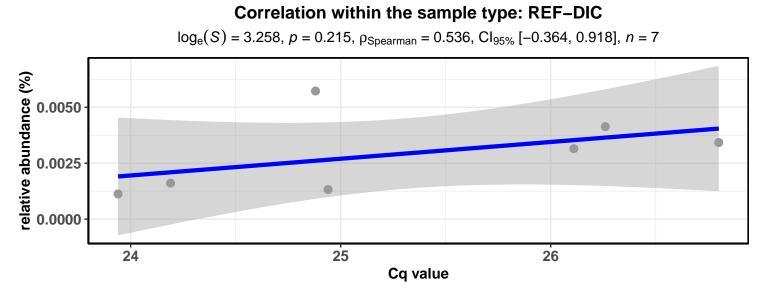


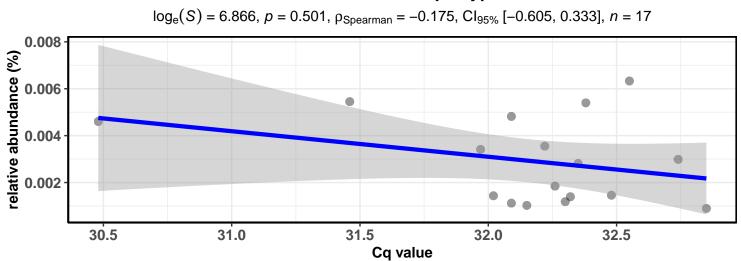


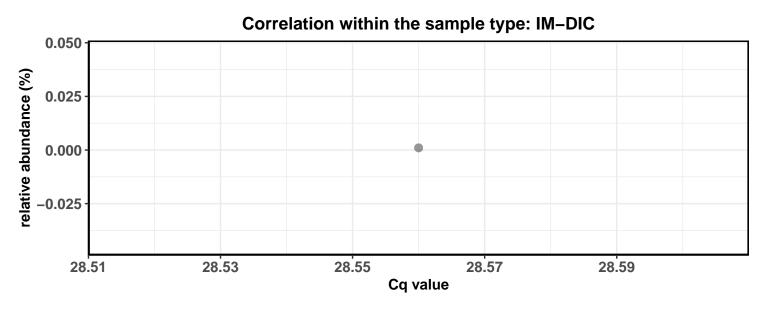
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

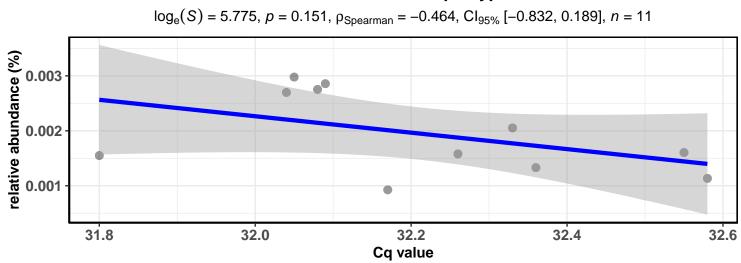
Correlation with all samples





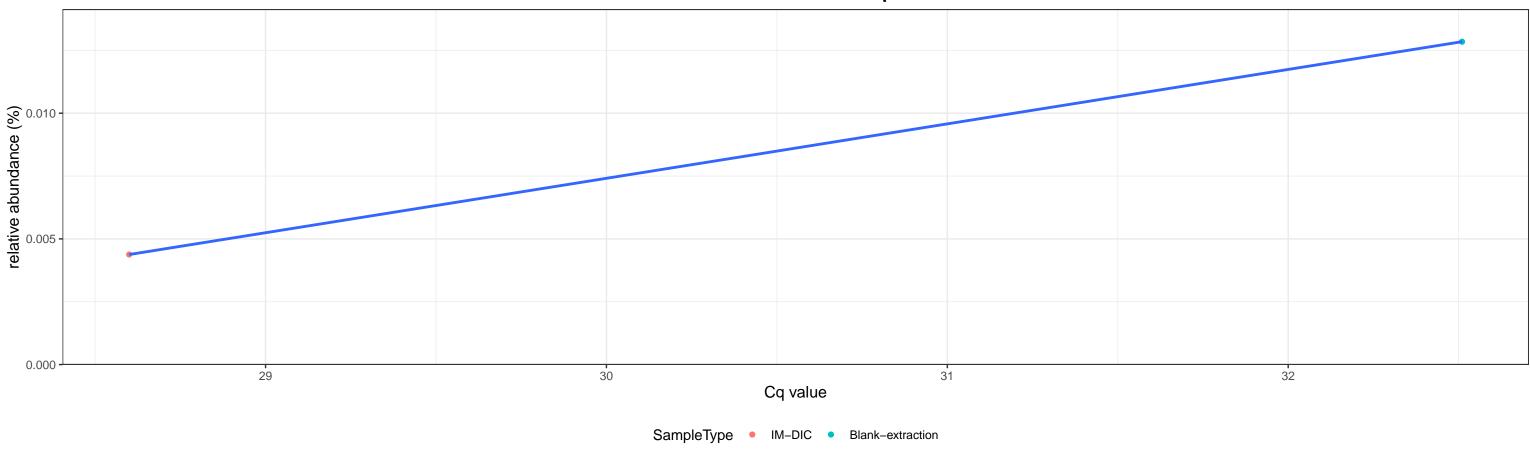




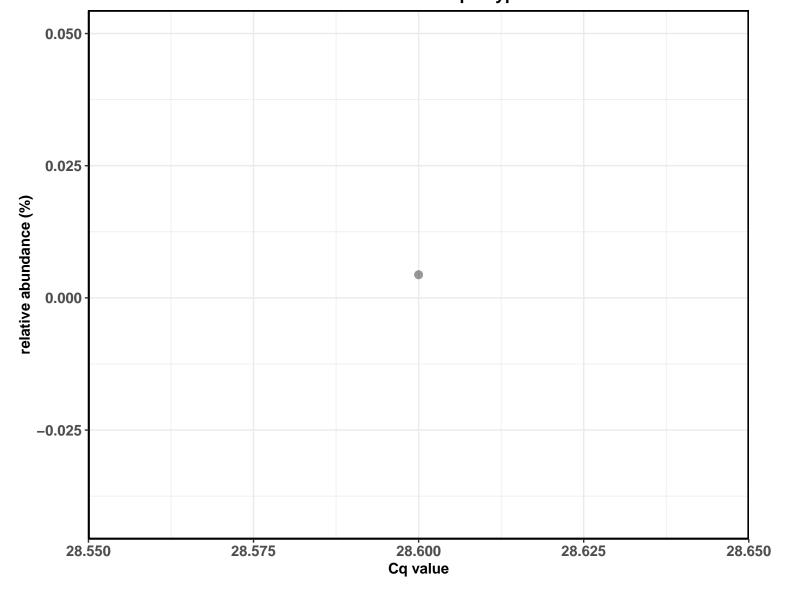


D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Sphingobacteriales; D\_4\_Sphingobacteriaceae; D\_5\_Pedobacter



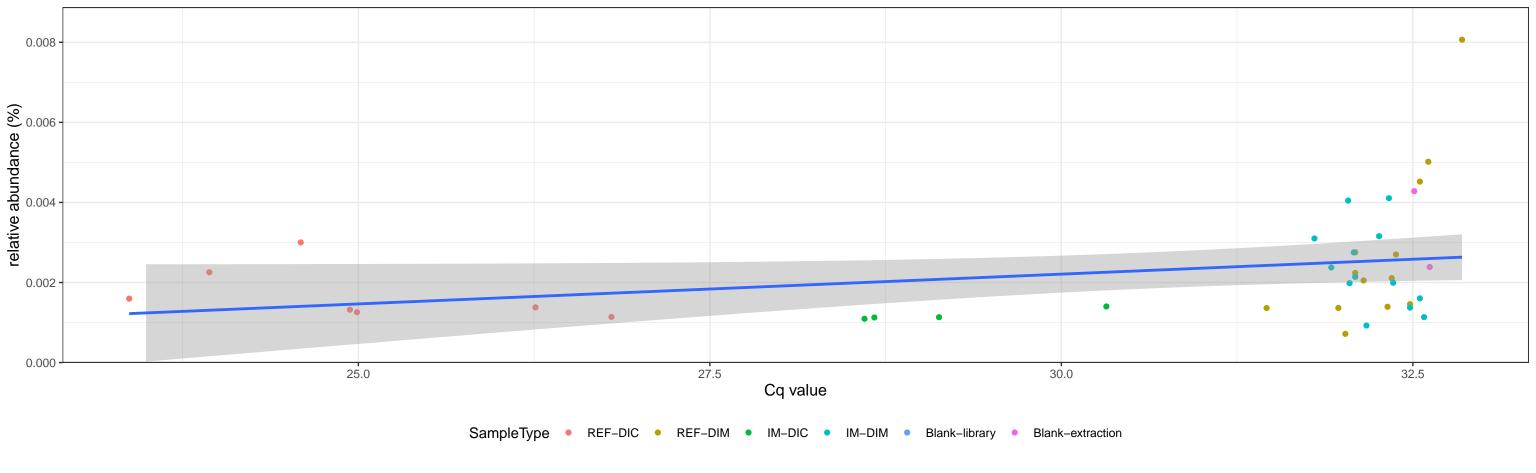






D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

Correlation with all samples



relative abundance (%)

0.006

0.003

0.000

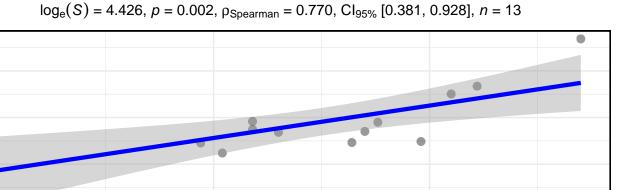
-0.003

31.5



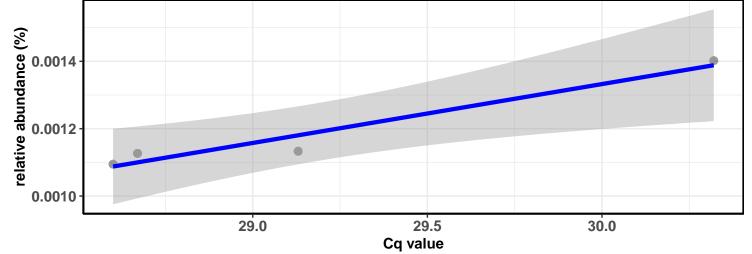
# log<sub>e</sub>(S) = 4.585, ρ = 0.052, ρ<sub>Spearman</sub> = -0.750, Cl<sub>95%</sub> [-0.961, 0.007], n = 7

#### Correlation within the sample type: REF-DIM



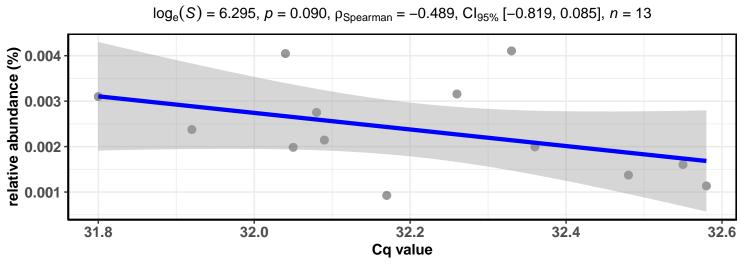
32.5





# Correlation within the sample type: IM-DIM

Cq value



D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum **Correlation with all samples** 28 25 26 27 29 Cq value SampleType • REF-DIC • IM-DIC • Mock Correlation within the sample type: REF-DIC Correlation within the sample type: IM-DIC 0.050 0.14 relative abundance (%) relative abundance (%) 0.025 0.000 0.08 -0.025 0.06

29.26

29.24

29.28

29.32

29.30

Cq value

25.00

24.98

Cq value

25.02

0.8

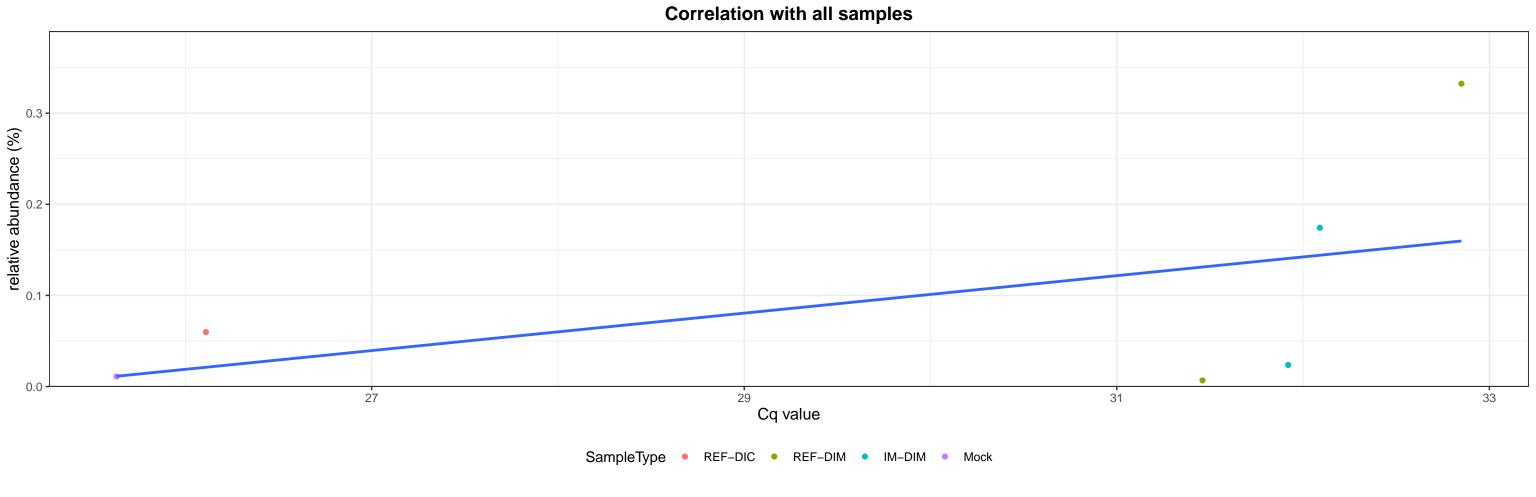
relative abundance (%)

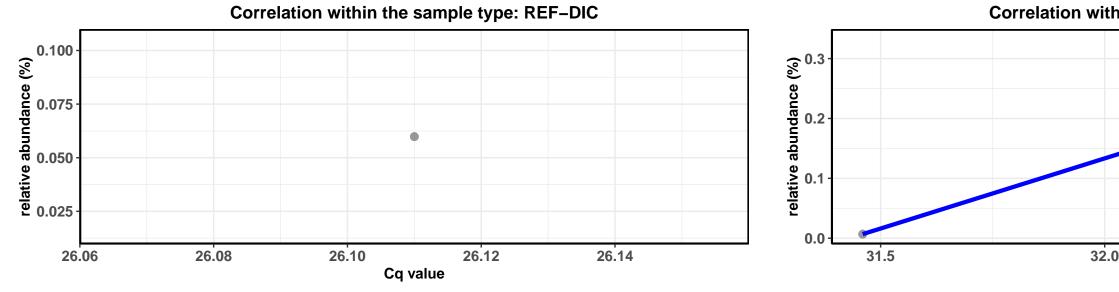
0.2

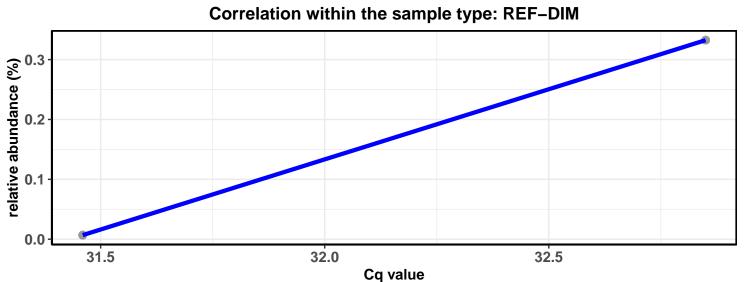
0.0

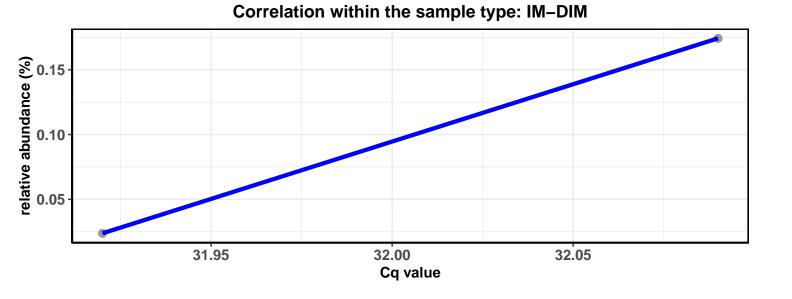
24.94

D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Sphingomonadales; D\_4\_Sphingomonadaceae; D\_5\_Sphingomonas

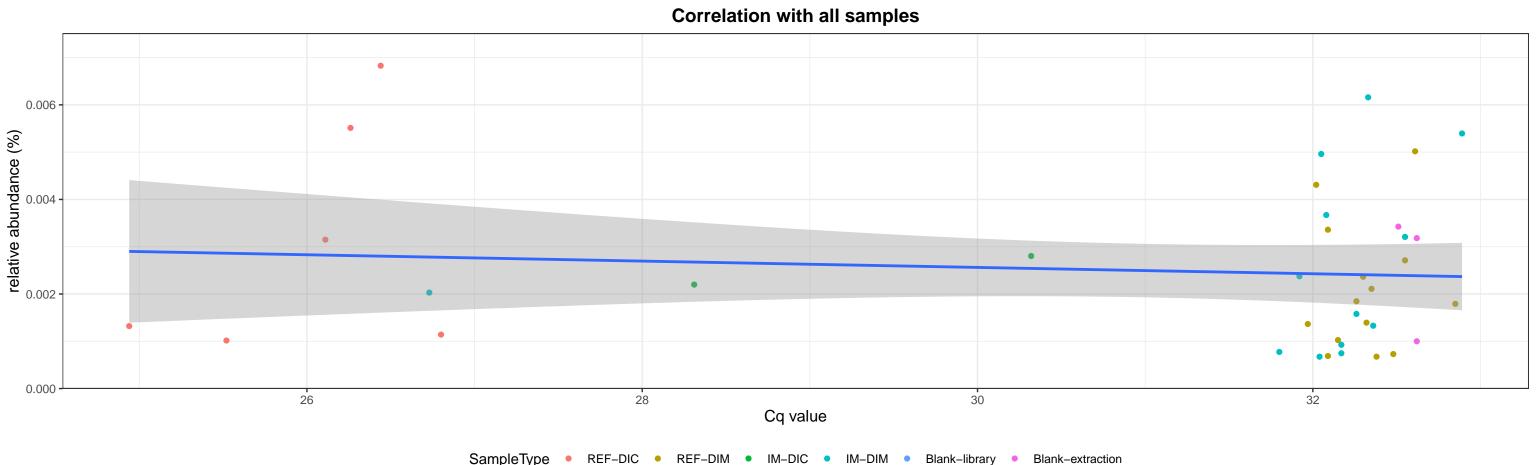




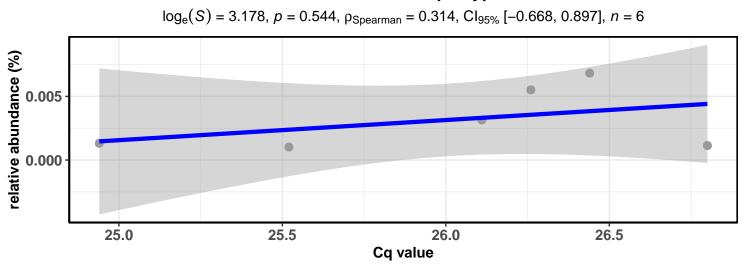


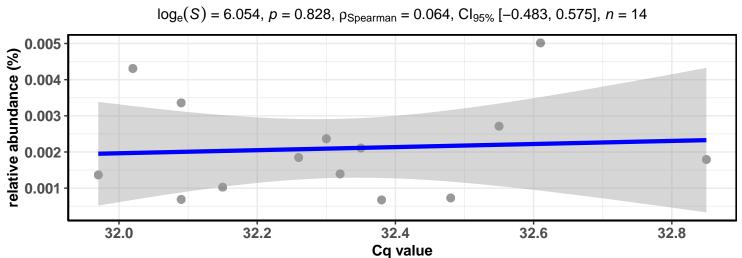


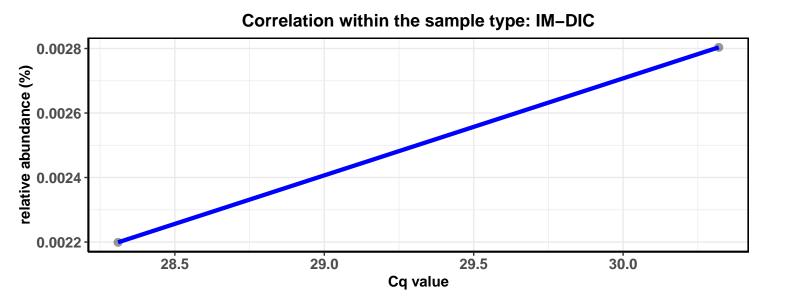
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

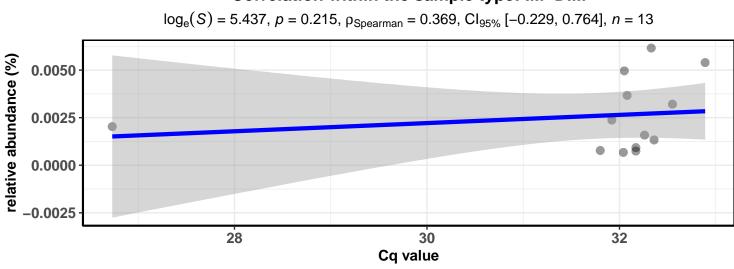




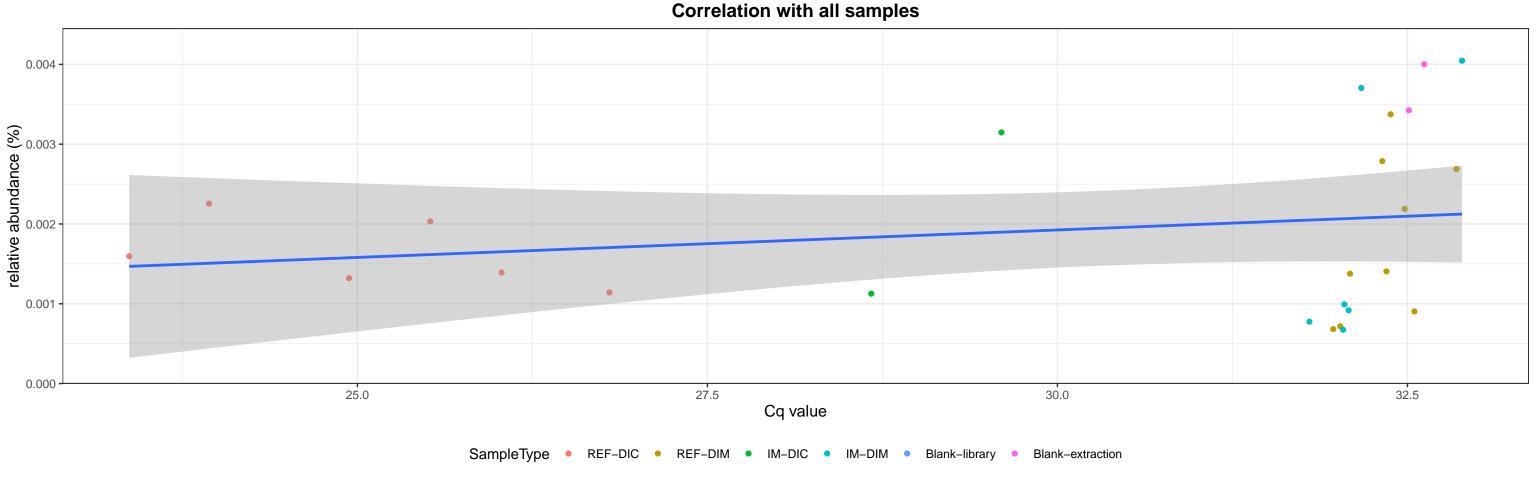






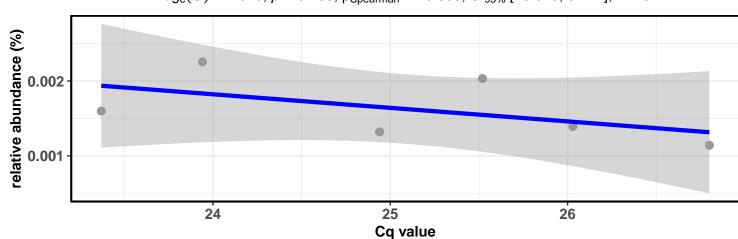


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas



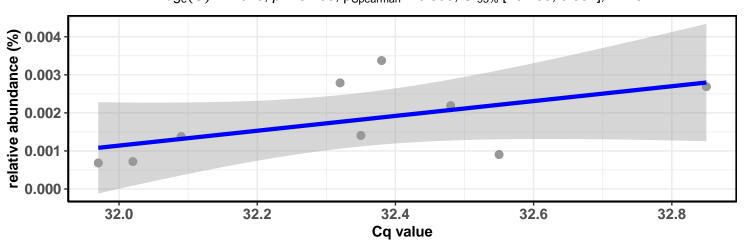


 $log_e(S) = 4.025$ , p = 0.208,  $\rho_{Spearman} = -0.600$ ,  $Cl_{95\%}$  [-0.949, 0.412], n = 6

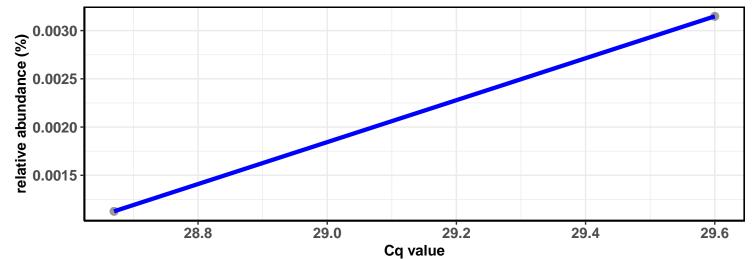


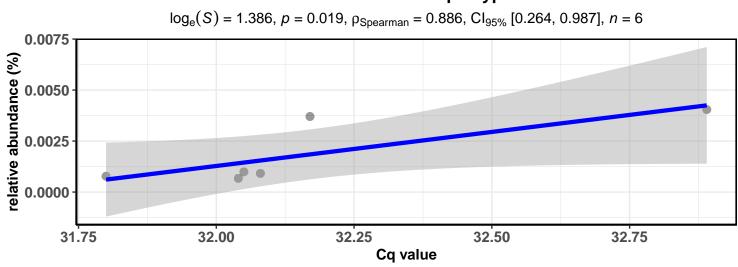
# Correlation within the sample type: REF-DIM

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

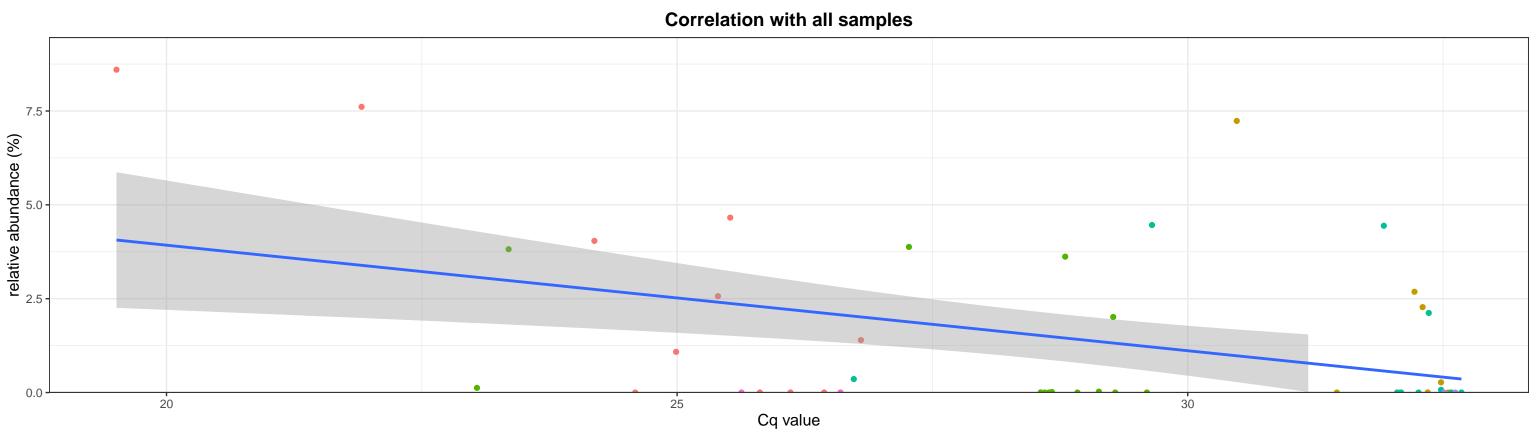


#### Correlation within the sample type: IM-DIC



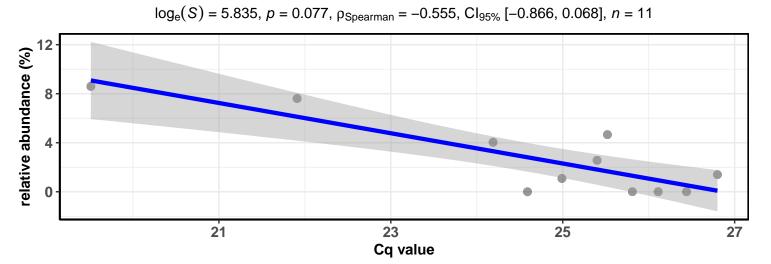


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Aliivibrio; Ambiguous\_taxa

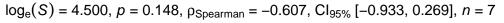


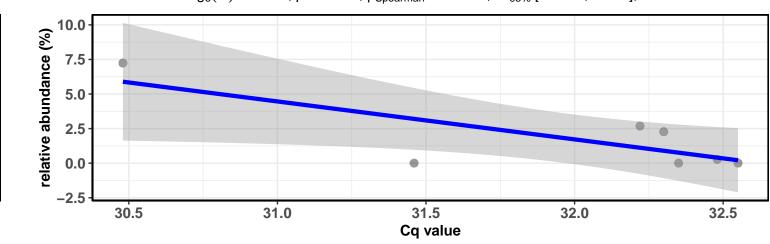
SampleType • REF-DIC • REF-DIM • IM-DIC • IM-DIM • Blank-library •

# Correlation within the sample type: REF-DIC

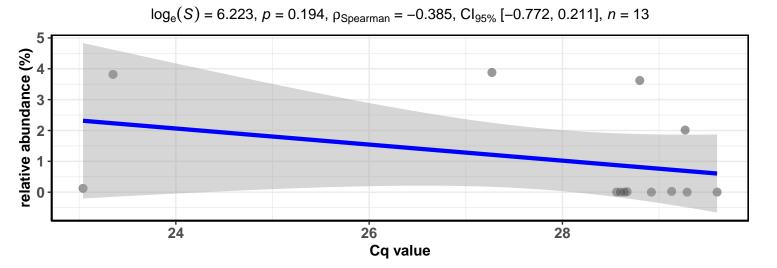


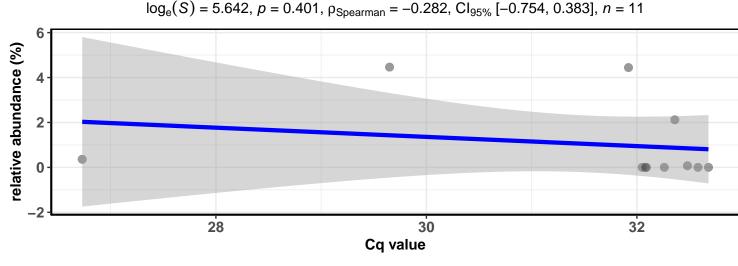
# Correlation within the sample type: REF-DIM





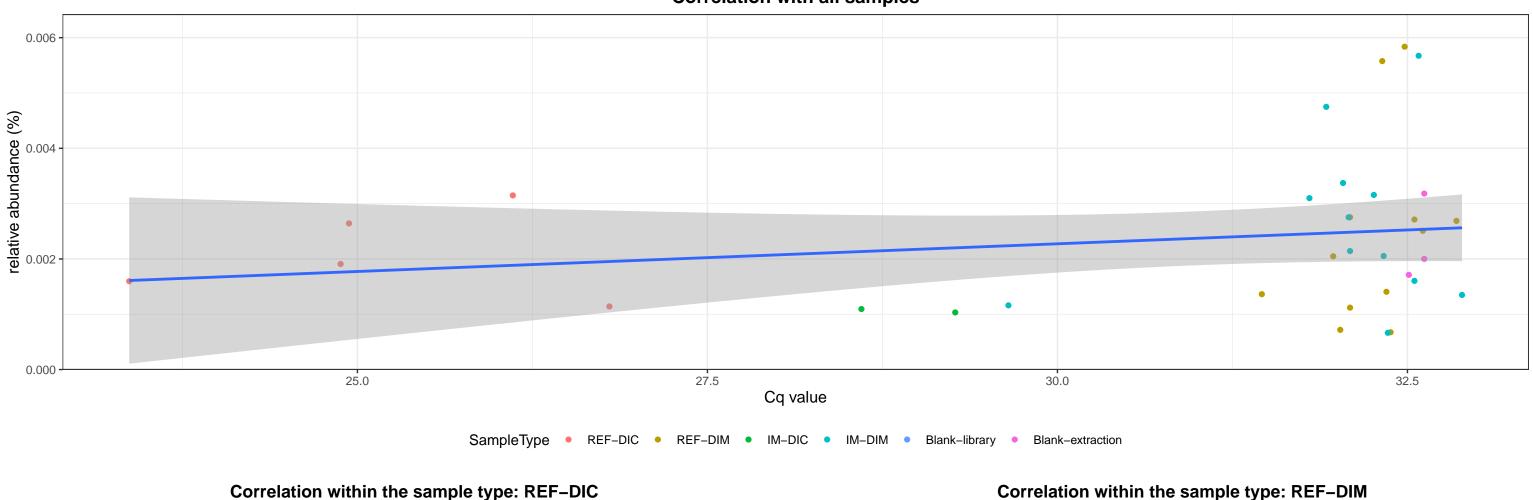
#### Correlation within the sample type: IM-DIC

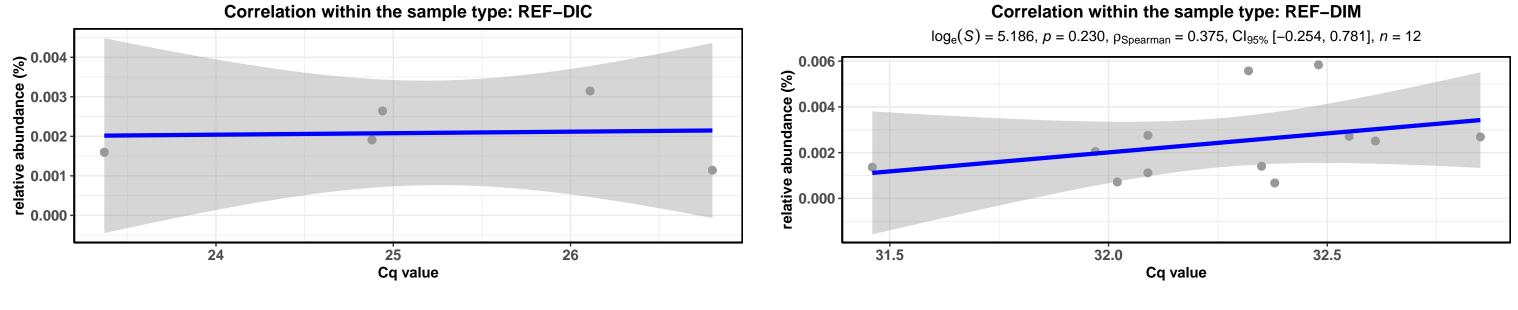


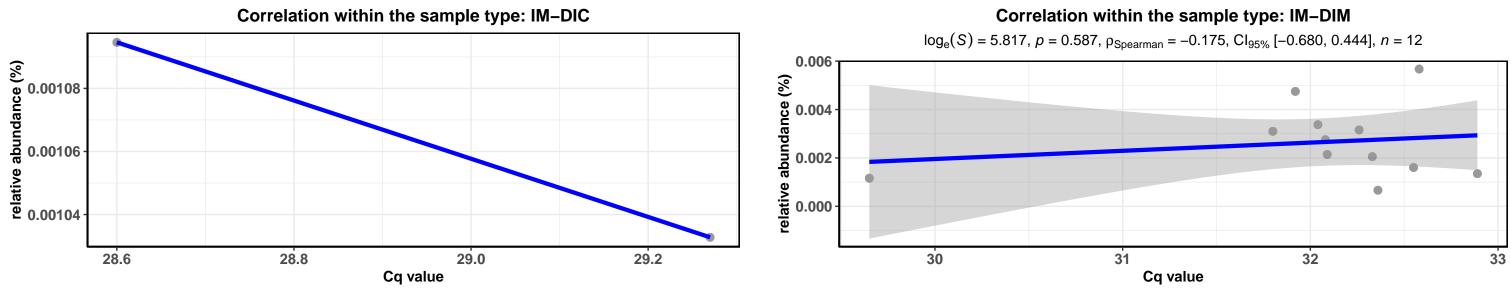


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas

Correlation with all samples



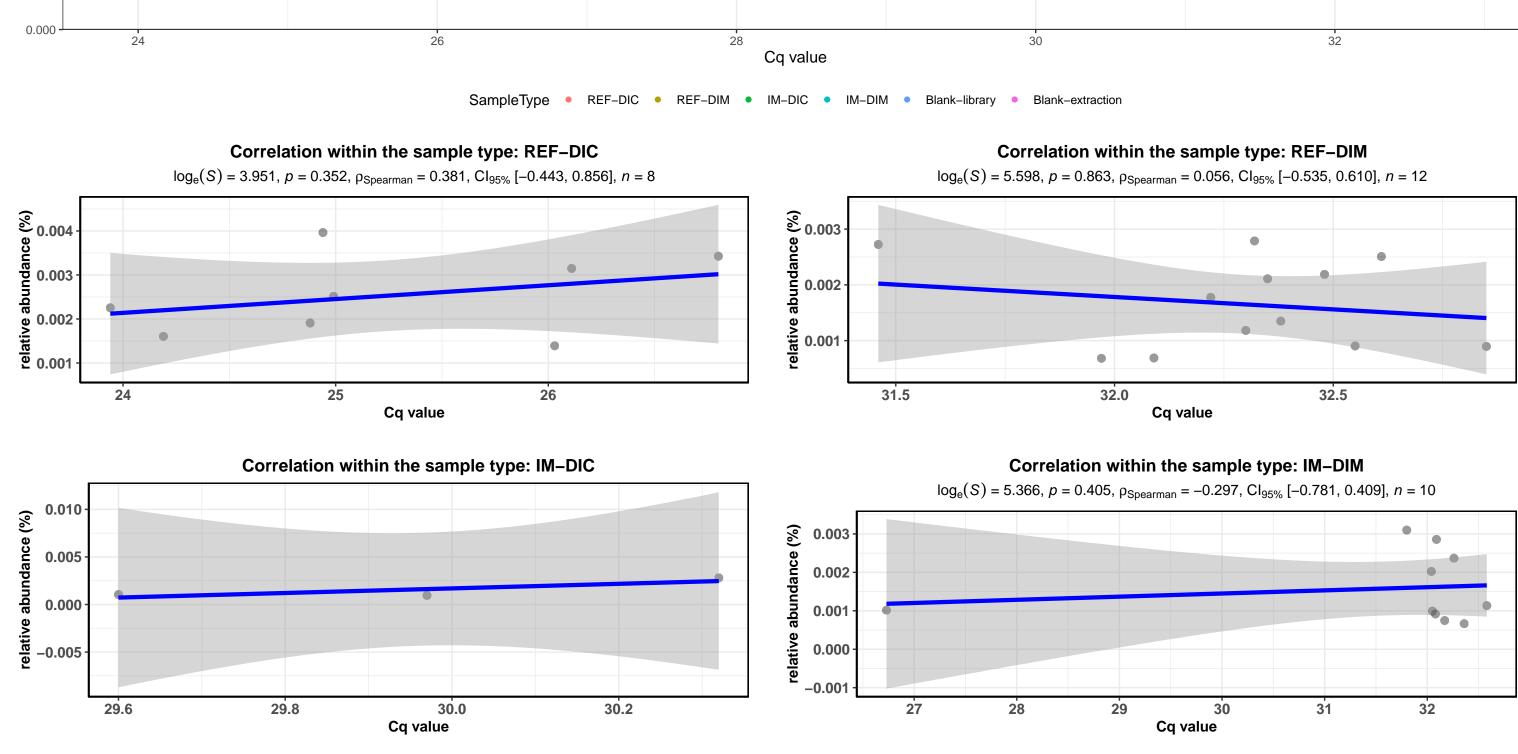




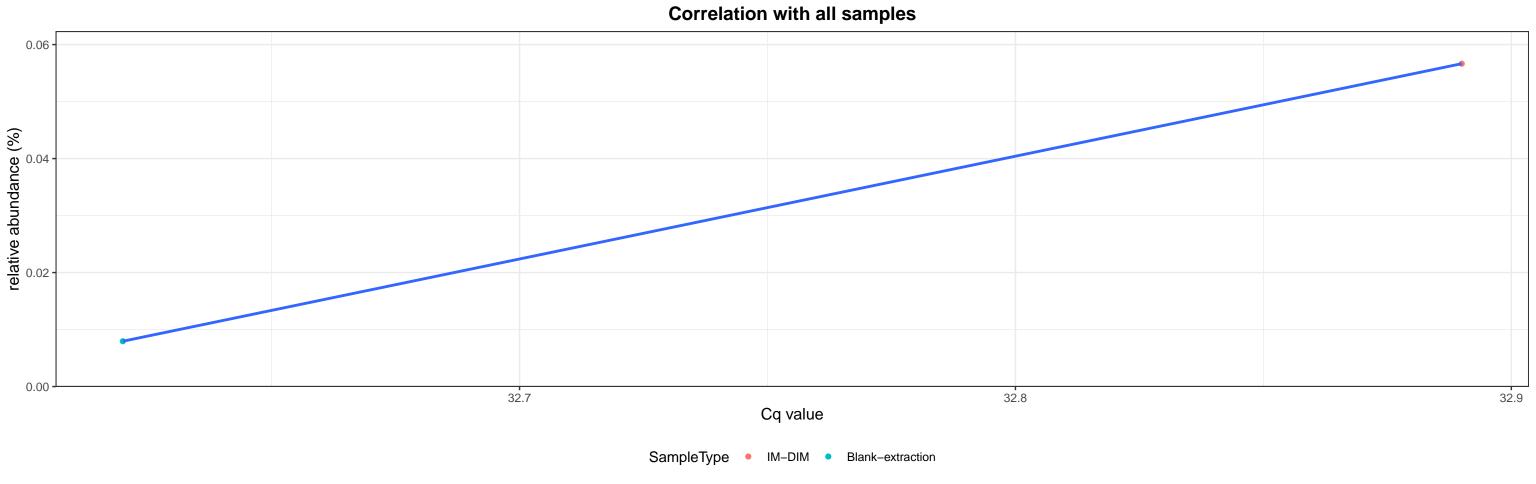
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas **Correlation with all samples** 26 30 24 28 32 Cq value IM-DIC
 IM-DIM
 Blank-library SampleType • REF-DIC • REF-DIM Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM  $log_e(S) = 3.951$ , p = 0.352,  $\rho_{Spearman} = 0.381$ ,  $Cl_{95\%}$  [-0.443, 0.856], n = 8 $log_e(S) = 5.598$ , p = 0.863,  $\rho_{Spearman} = 0.056$ ,  $Cl_{95\%}$  [-0.535, 0.610], n = 12

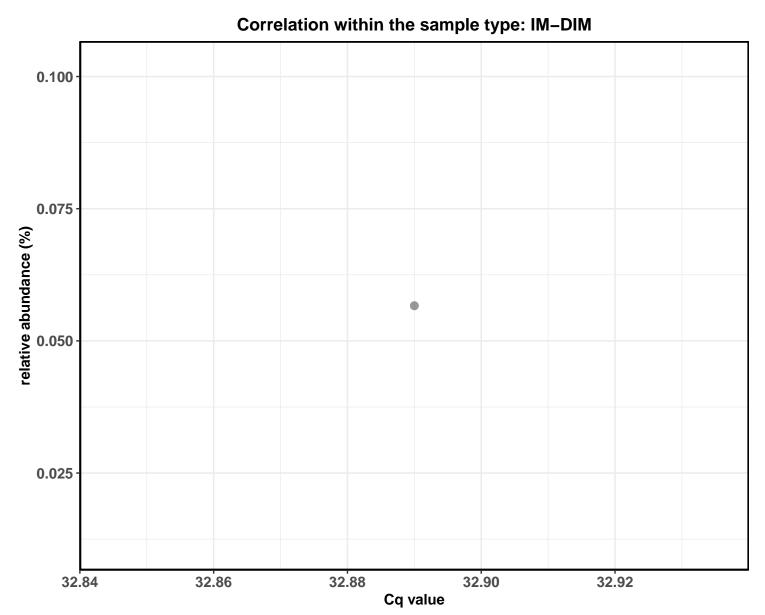
0.004

relative abundance (%)

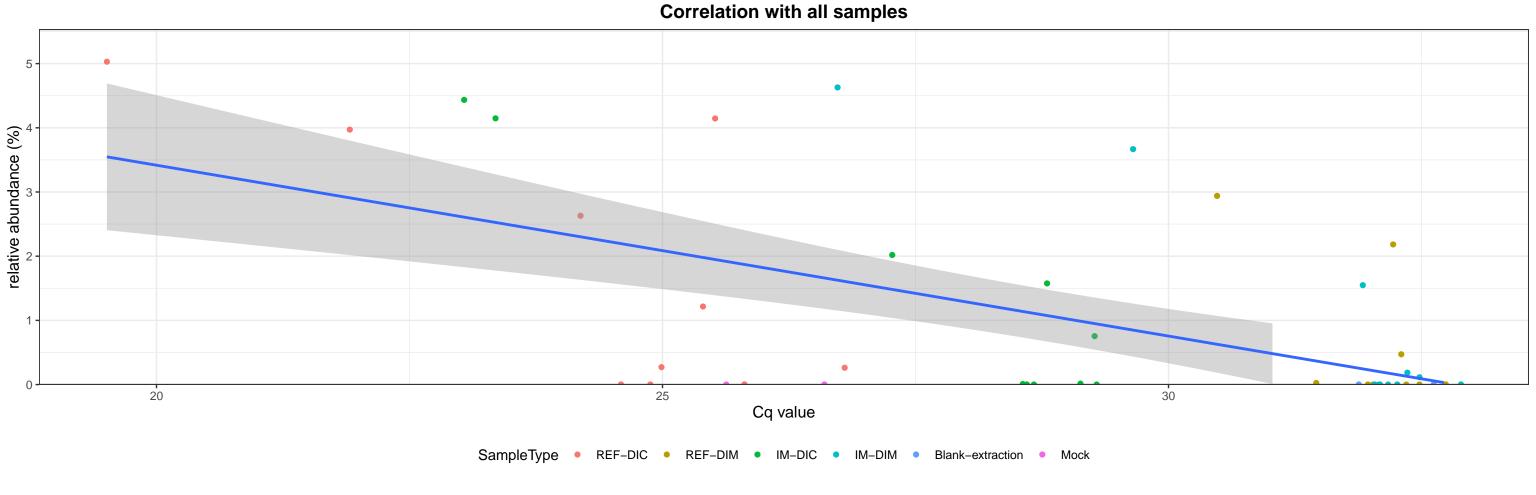


D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium

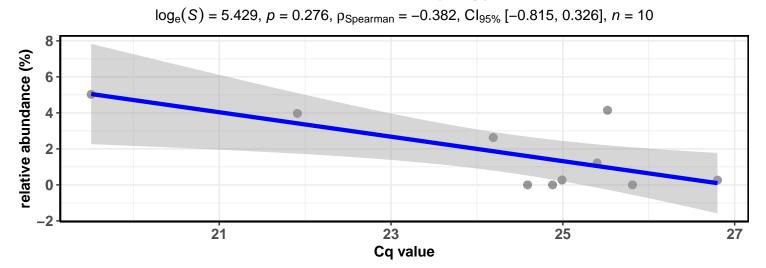


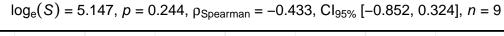


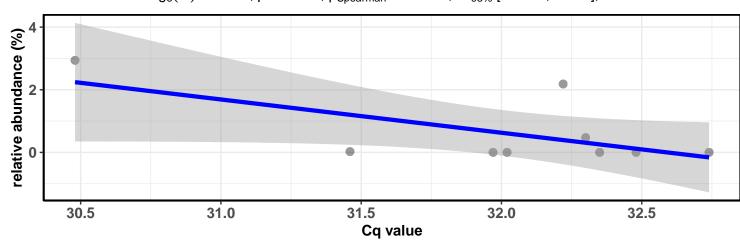
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Aliivibrio; D\_6\_uncultured bacterium



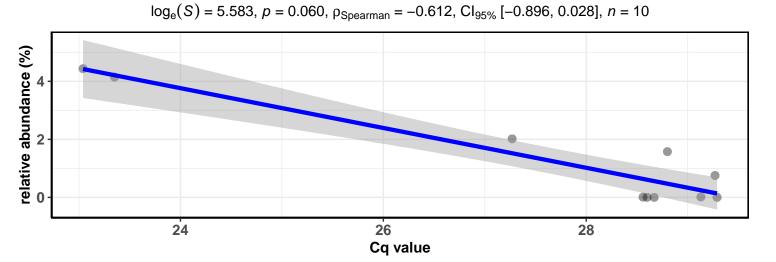




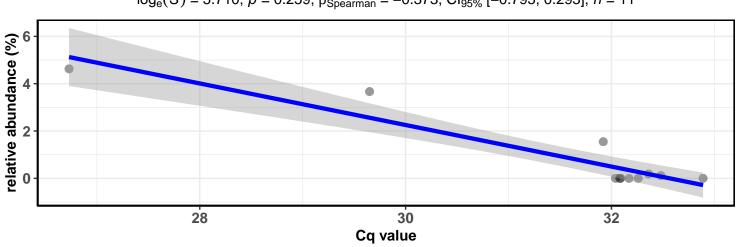




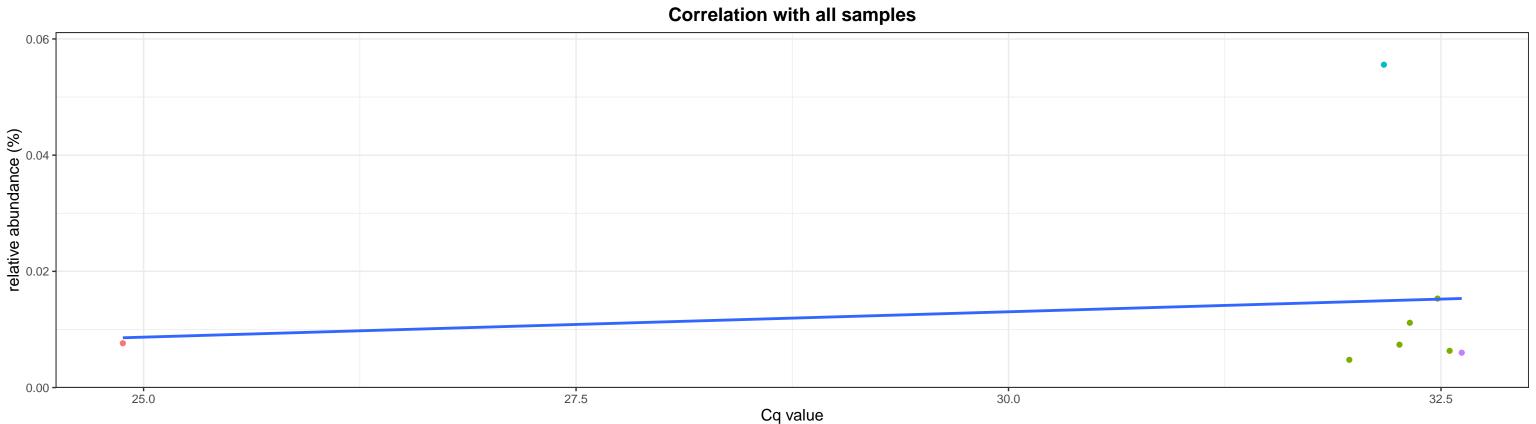
#### Correlation within the sample type: IM-DIC



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

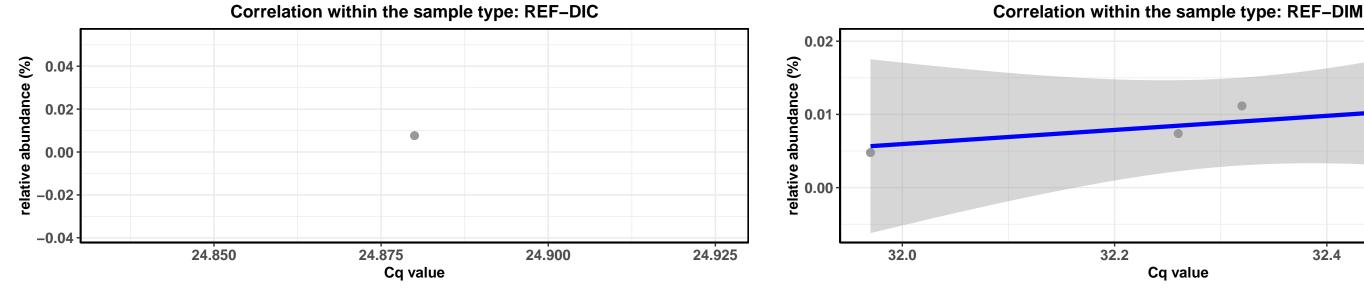


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Alphaproteobacteria; D\_3\_Caulobacterales; D\_4\_Caulobacteraceae; D\_5\_Brevundimonas

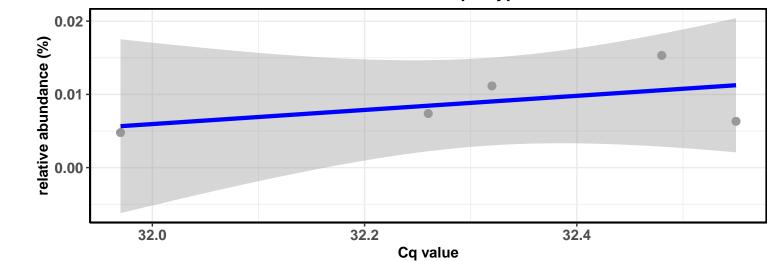


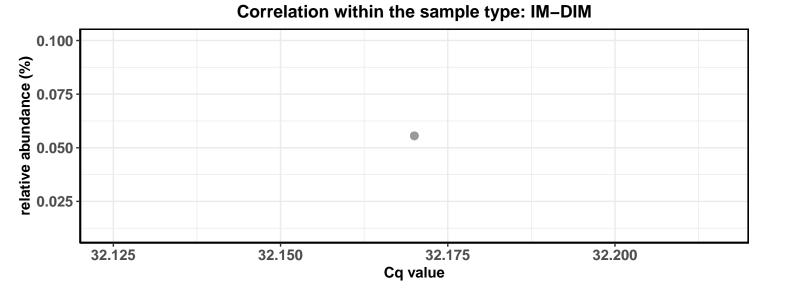
REF-DIMIM-DIM

Blank-extraction

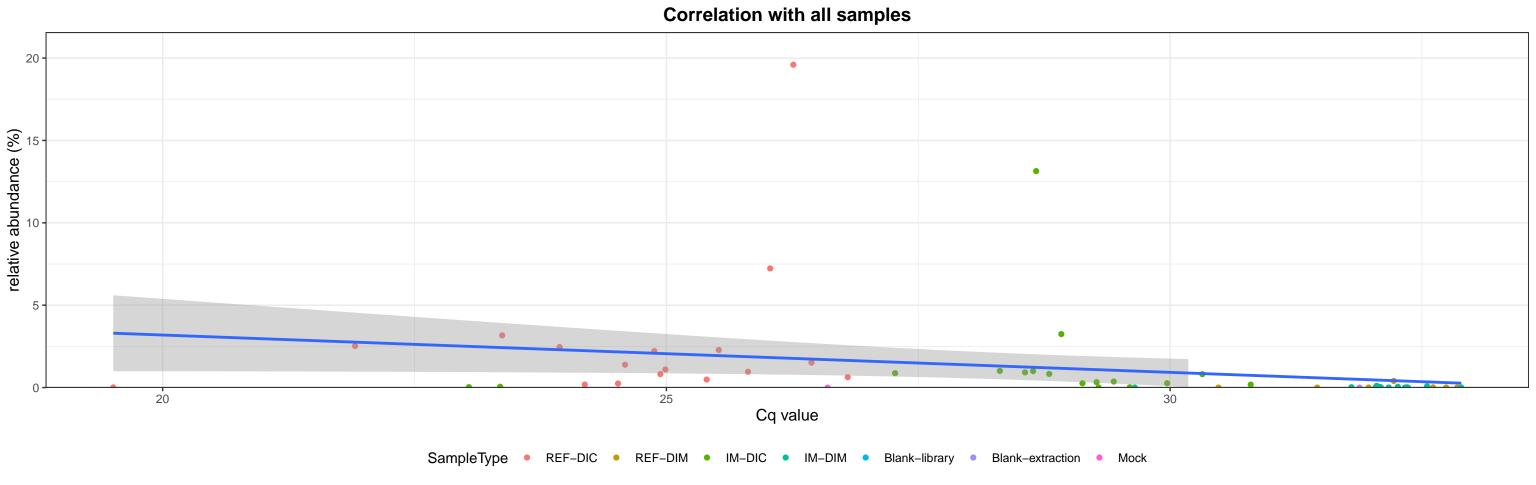


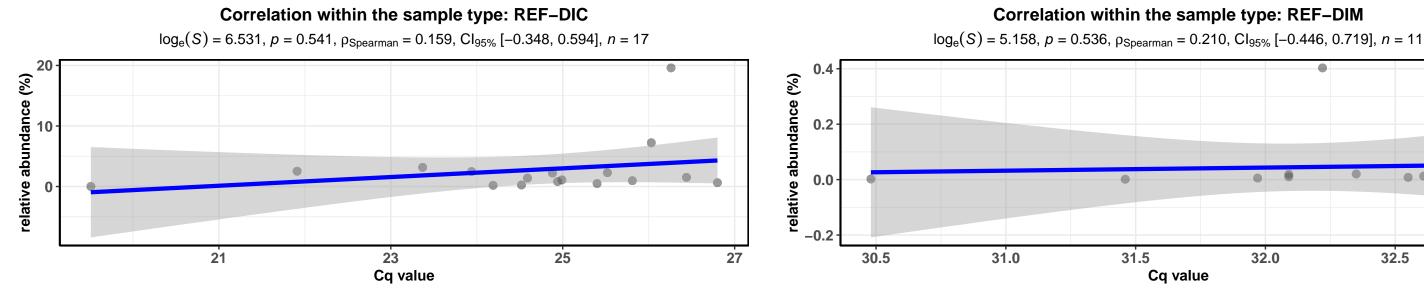
SampleType • REF-DIC

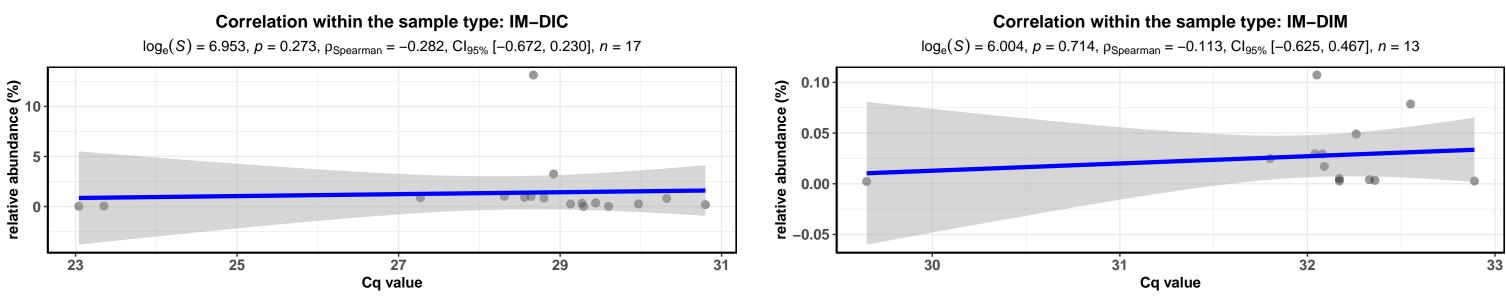




D\_0\_Bacteria; D\_1\_Tenericutes; D\_2\_Mollicutes; D\_3\_Mycoplasmatales; D\_4\_Mycoplasmataceae; D\_5\_Mycoplasma; D\_6\_uncultured bacterium

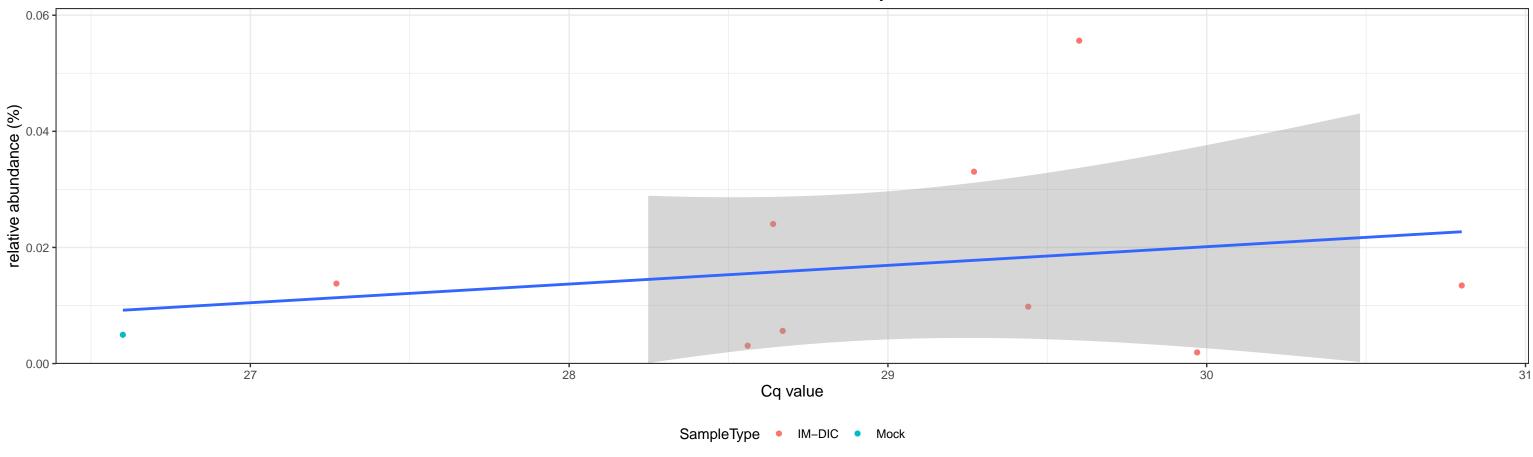




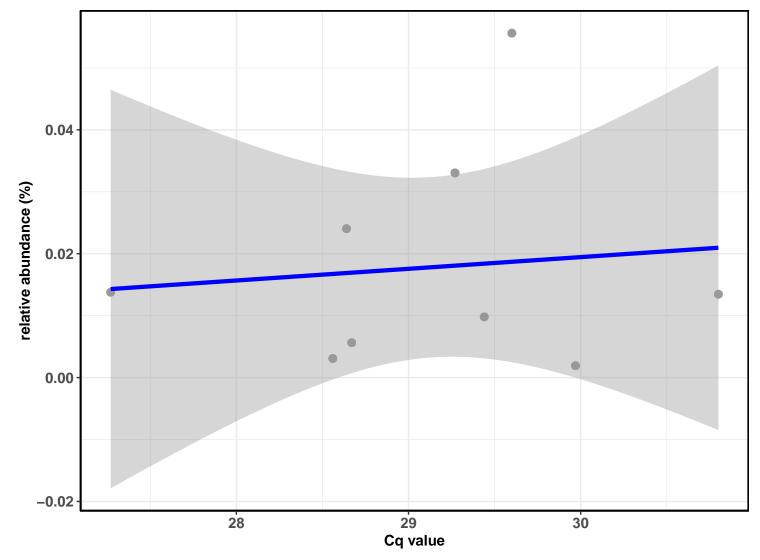


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Enterobacteriales; D\_4\_Enterobacteriaceae; D\_5\_Escherichia-Shigella



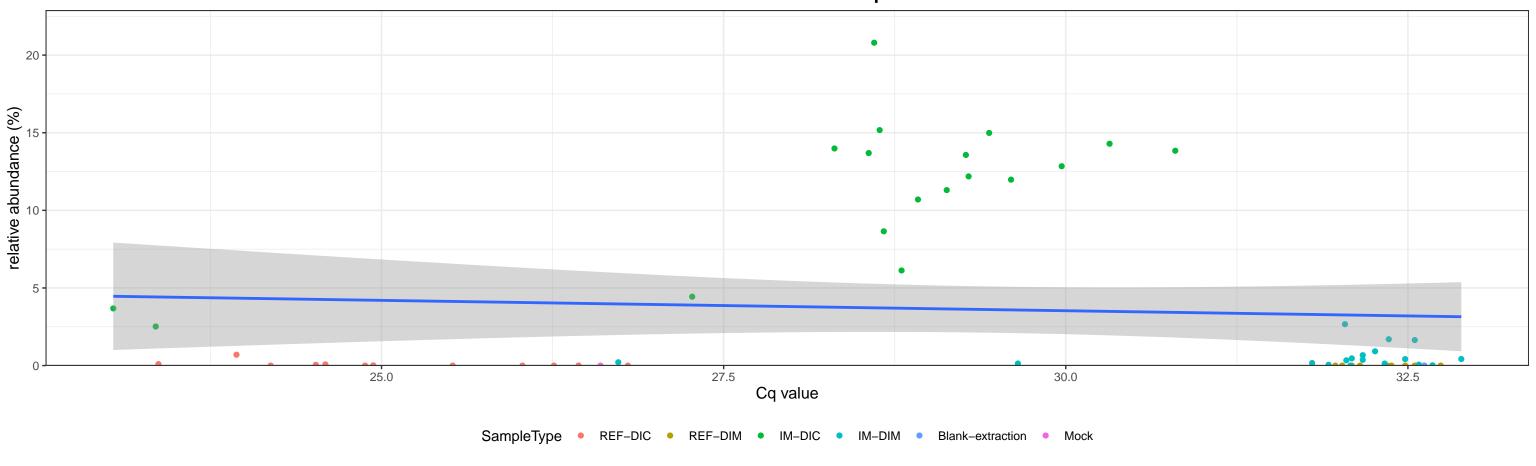


 $log_e(S) = 4.820, p = 0.932, \rho_{Spearman} = -0.033, Cl_{95\%} [-0.682, 0.645], n = 9$ 



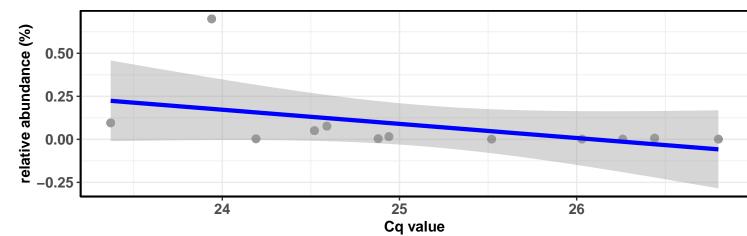
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales

#### **Correlation with all samples**

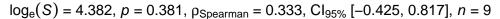


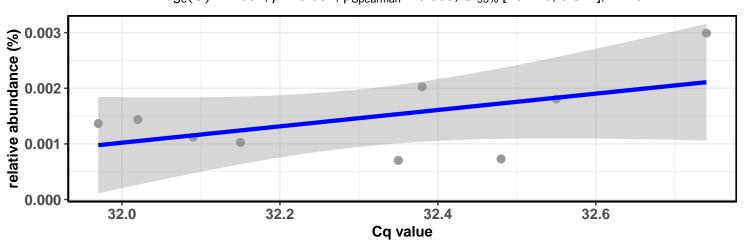
#### Correlation within the sample type: REF-DIC

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



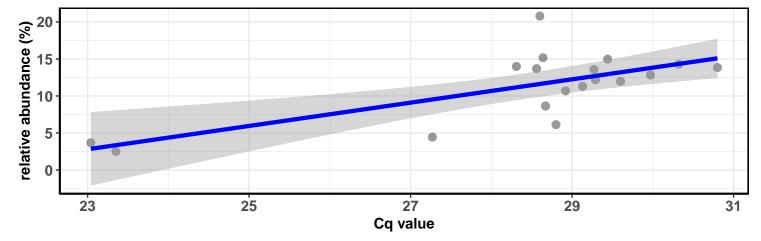
#### Correlation within the sample type: REF-DIM



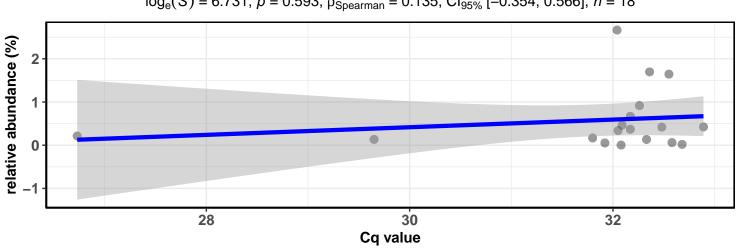


#### Correlation within the sample type: IM-DIC

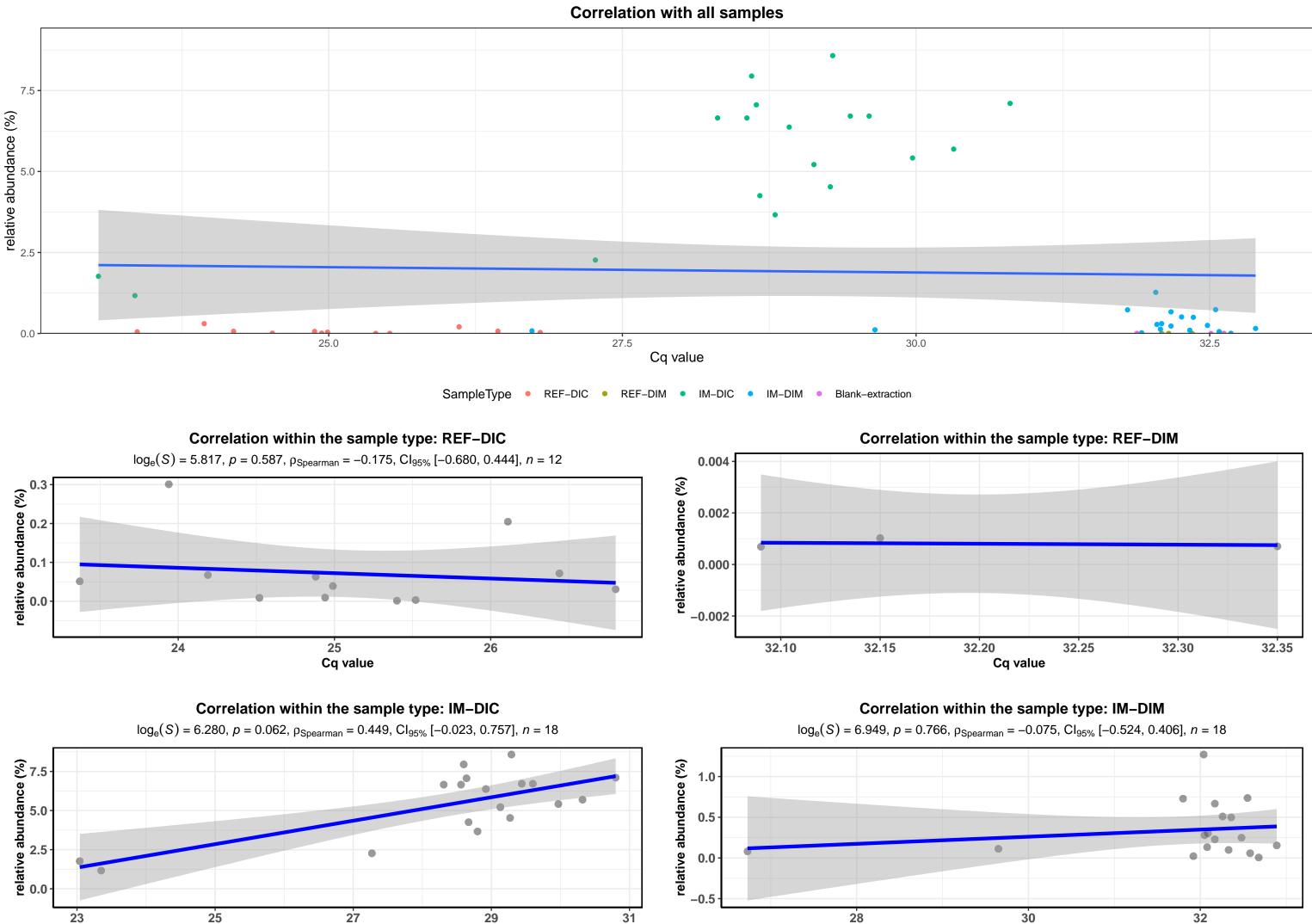
 $log_e(S) = 6.390, p = 0.115, \rho_{Spearman} = 0.385, Cl_{95\%} [-0.100, 0.722], n = 18$ 



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



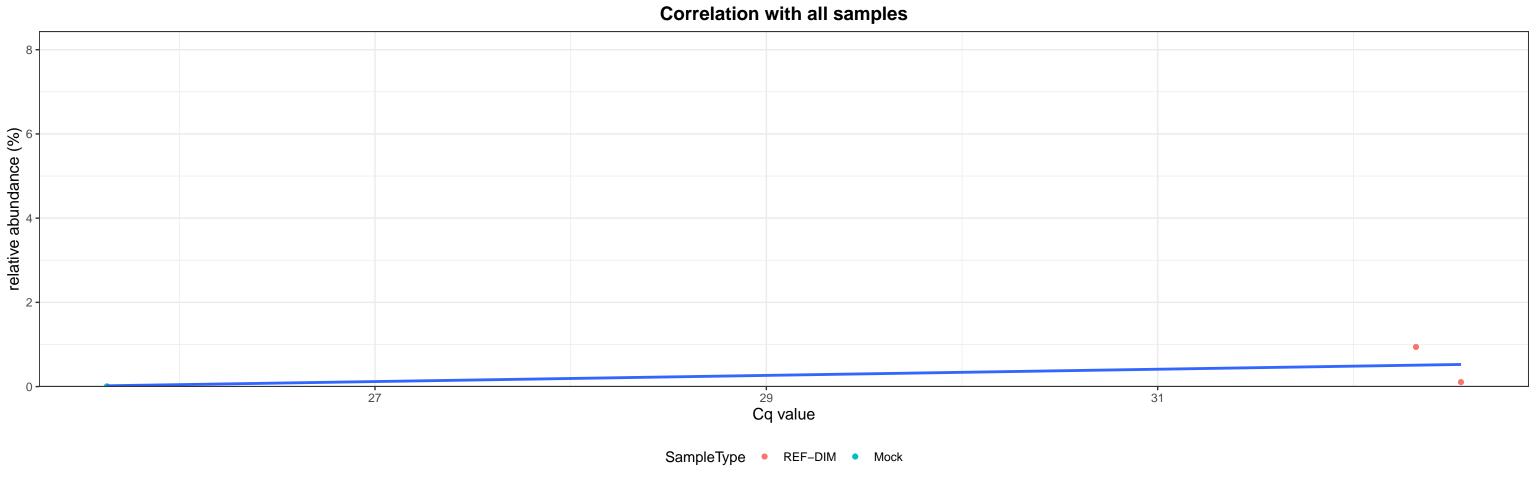
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Corynebacteriales; D\_4\_Corynebacteriaceae; D\_5\_Corynebacterium 1; Ambiguous\_taxa

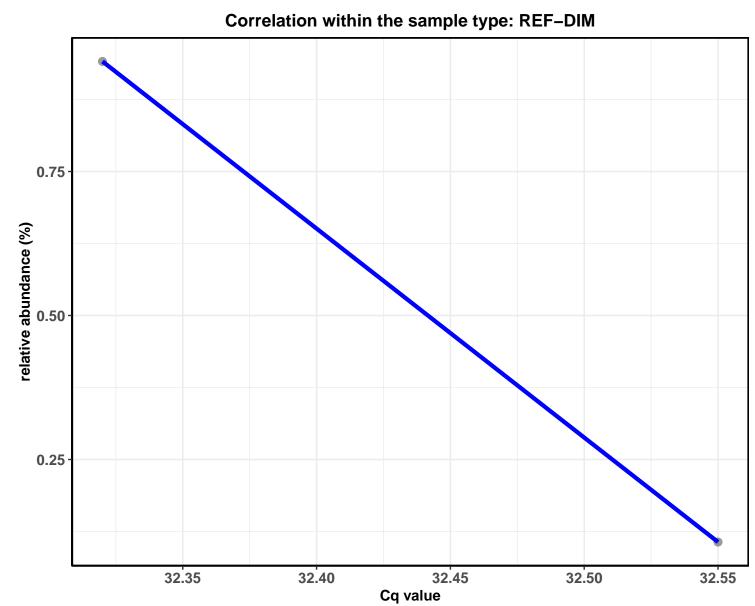


Cq value

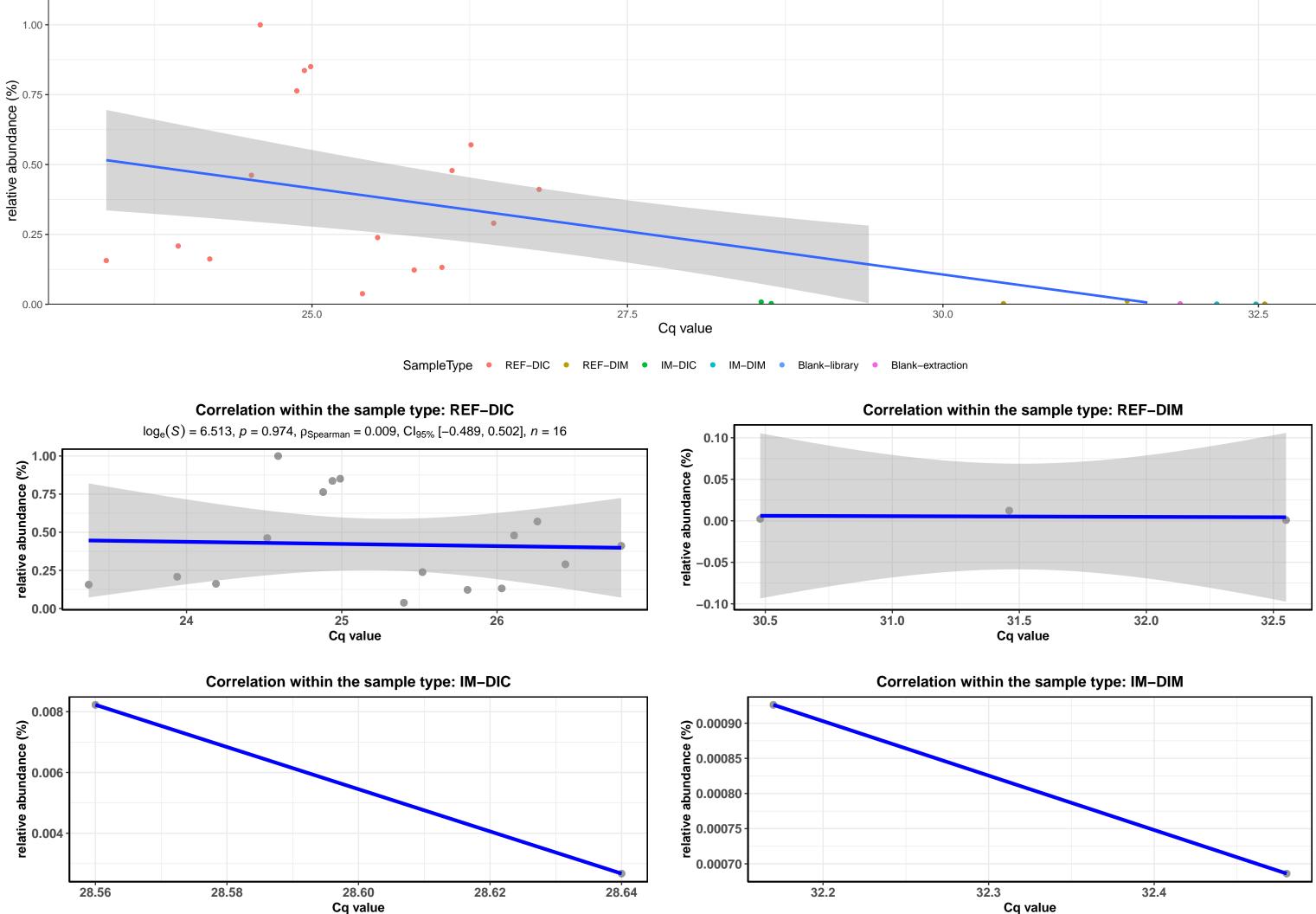
Cq value

D\_0\_Bacteria; D\_1\_Cyanobacteria; D\_2\_Melainabacteria; D\_3\_Obscuribacterales; Ambiguous\_taxa; Ambiguous\_taxa; Ambiguous\_taxa





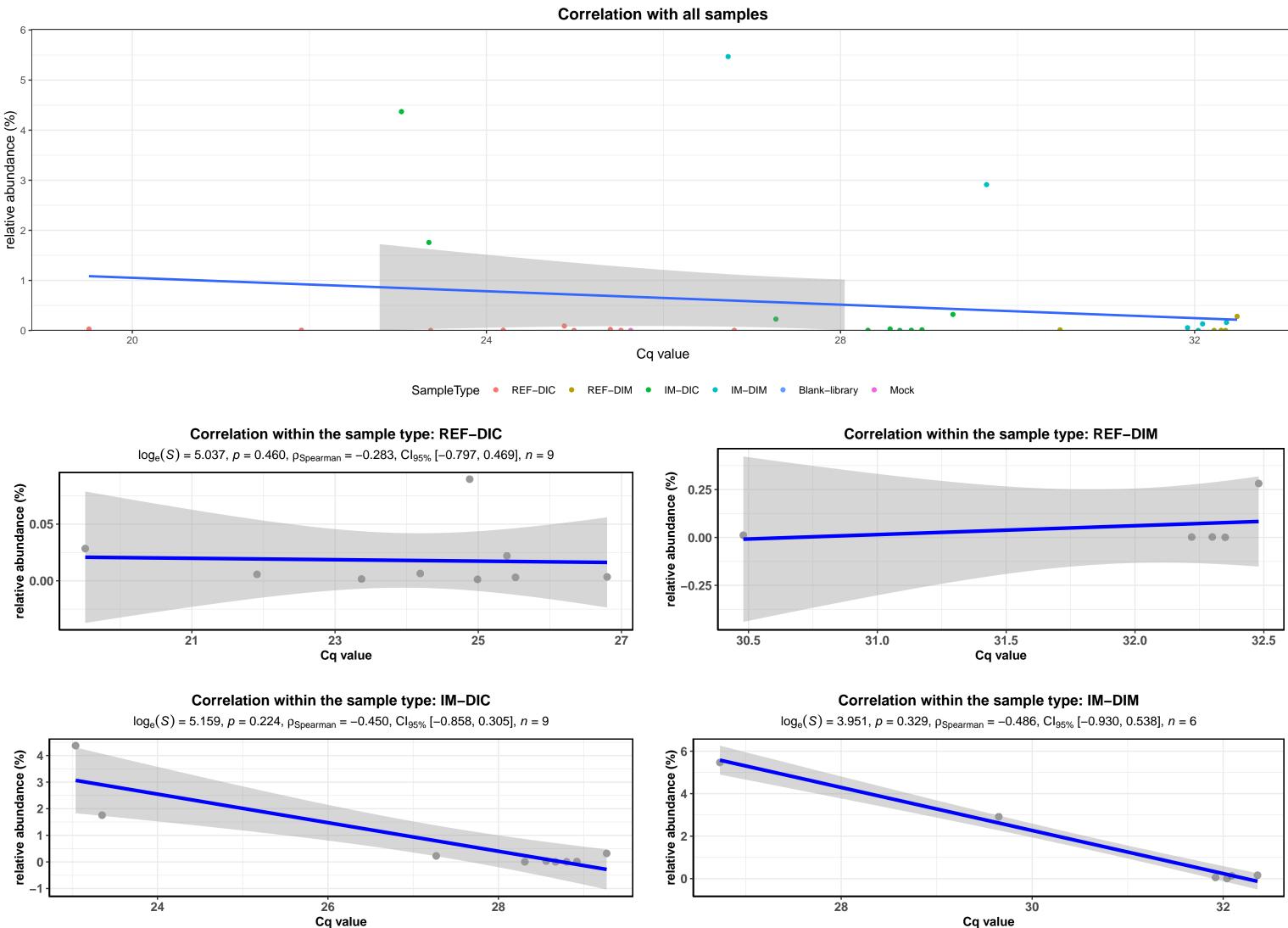
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Clostridia; D\_3\_Clostridiales; D\_4\_Family XI; D\_5\_Tepidimicrobium; D\_6\_Tepidimicrobium sp. GRC1 **Correlation with all samples** 



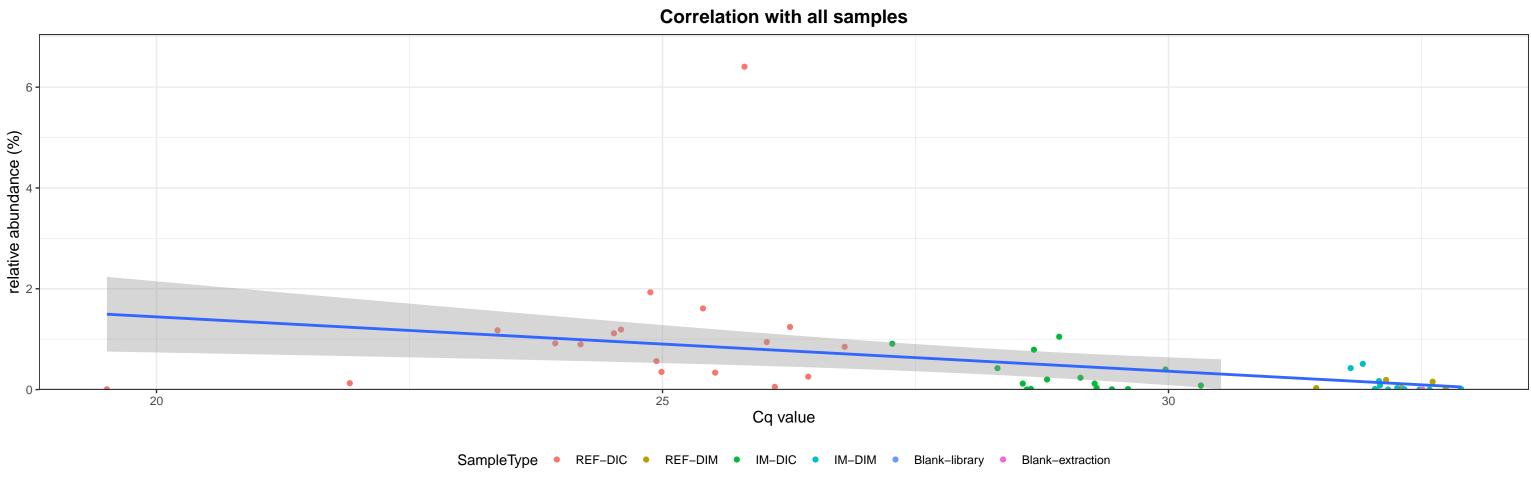
D\_0\_Bacteria; D\_1\_Tenericutes; D\_2\_Mollicutes; D\_3\_Mycoplasmatales; D\_4\_Mycoplasmataceae; D\_5\_Mycoplasma; D\_6\_uncultured Mycoplasma sp. **Correlation with all samples** 60 · relative abundance (%) 24 27 30 33 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC • IM-DIM Blank–extraction Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.02 relative abundance (%)
00.0
10.0relative abundance (%) 0 0 22 23 25 31.0 24 30.5 31.5 32.0 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM 150 relative abundance (%) relative abundance (%) 100 **50** 0 --50 23 24 25 27 28 29 31.75 32.25 32.75 26 32.00 32.50

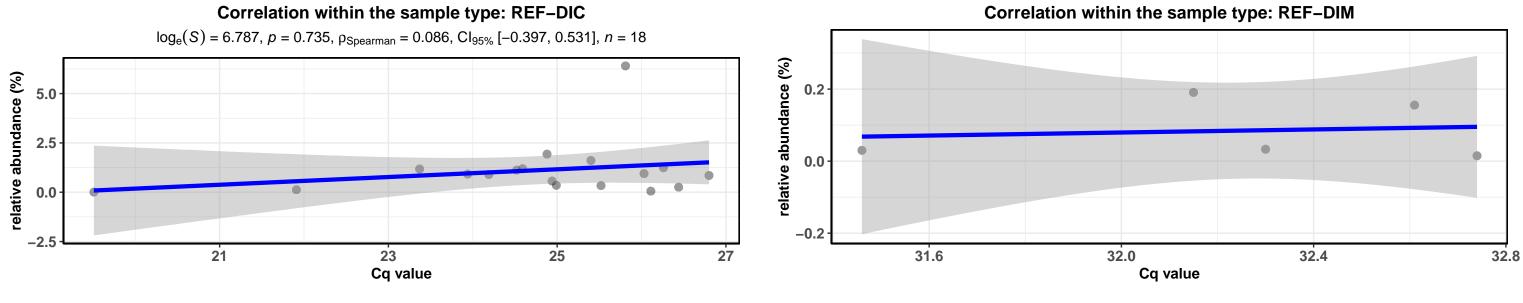
Cq value

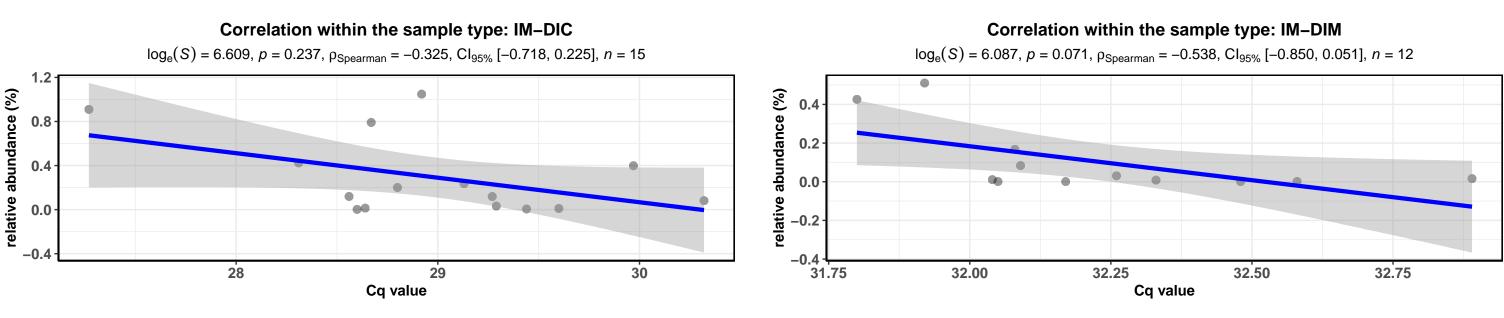
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Aliivibrio; D\_6\_uncultured bacterium



D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Photobacterium

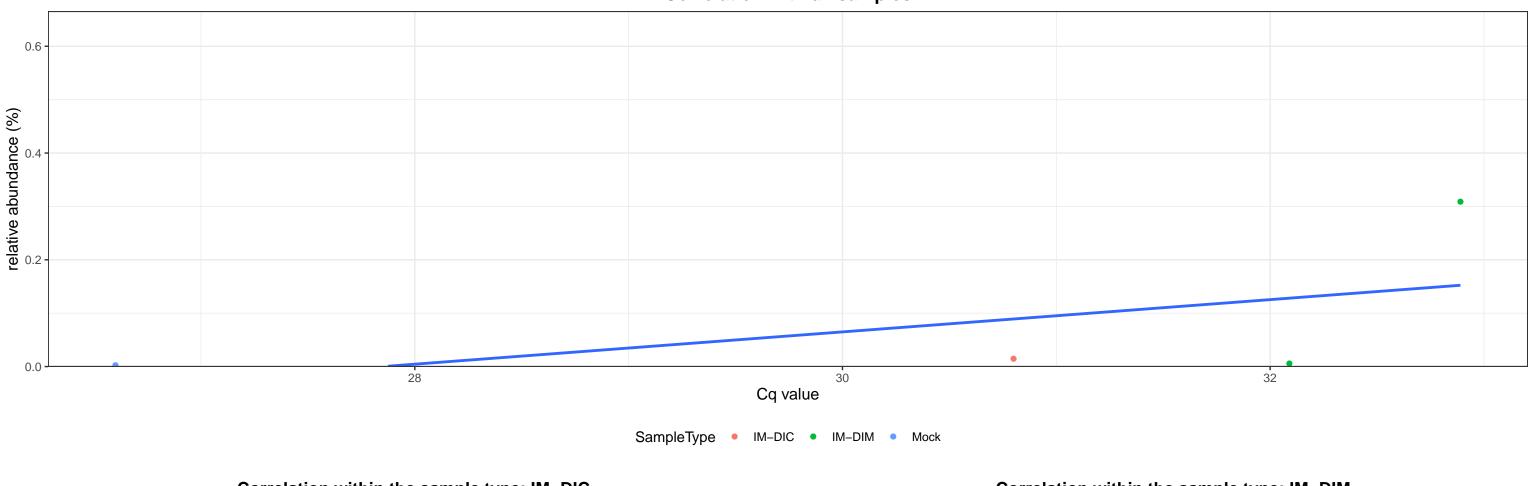


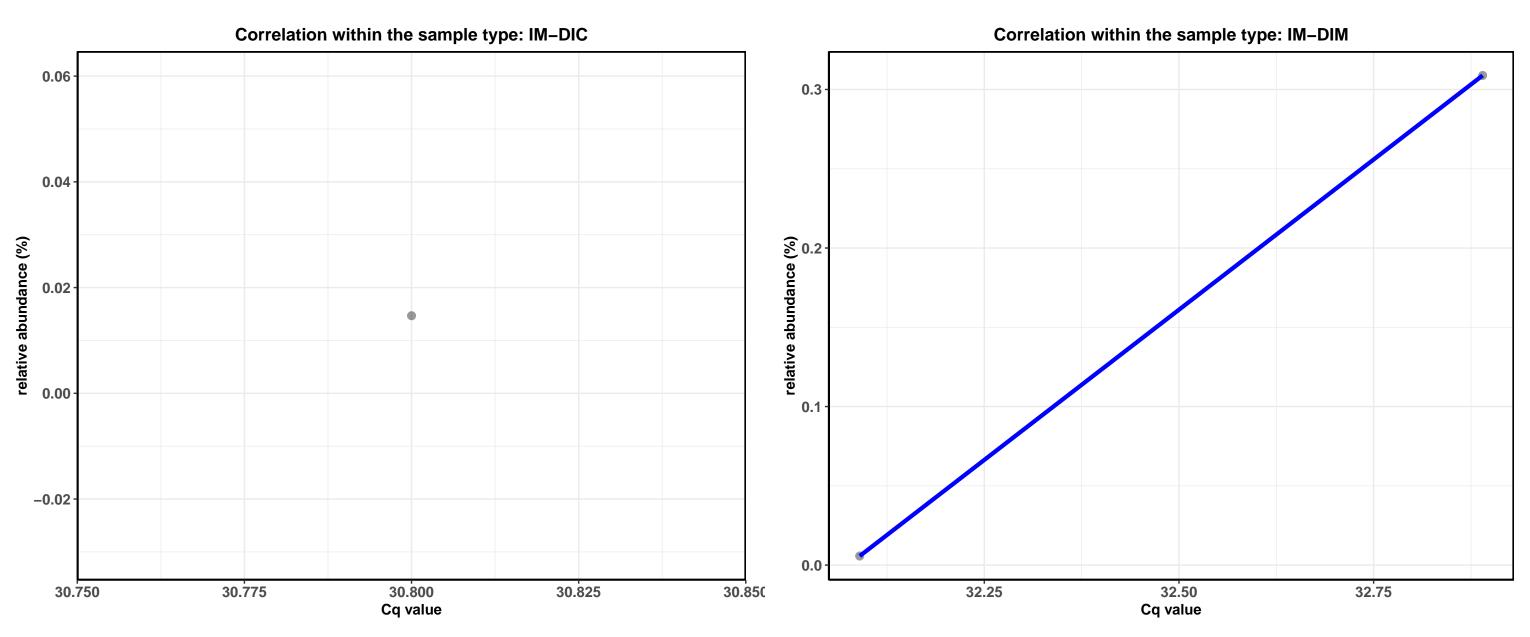




D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Micrococcales; D\_4\_Micrococcaceae; D\_5\_Arthrobacter; Ambiguous\_taxa

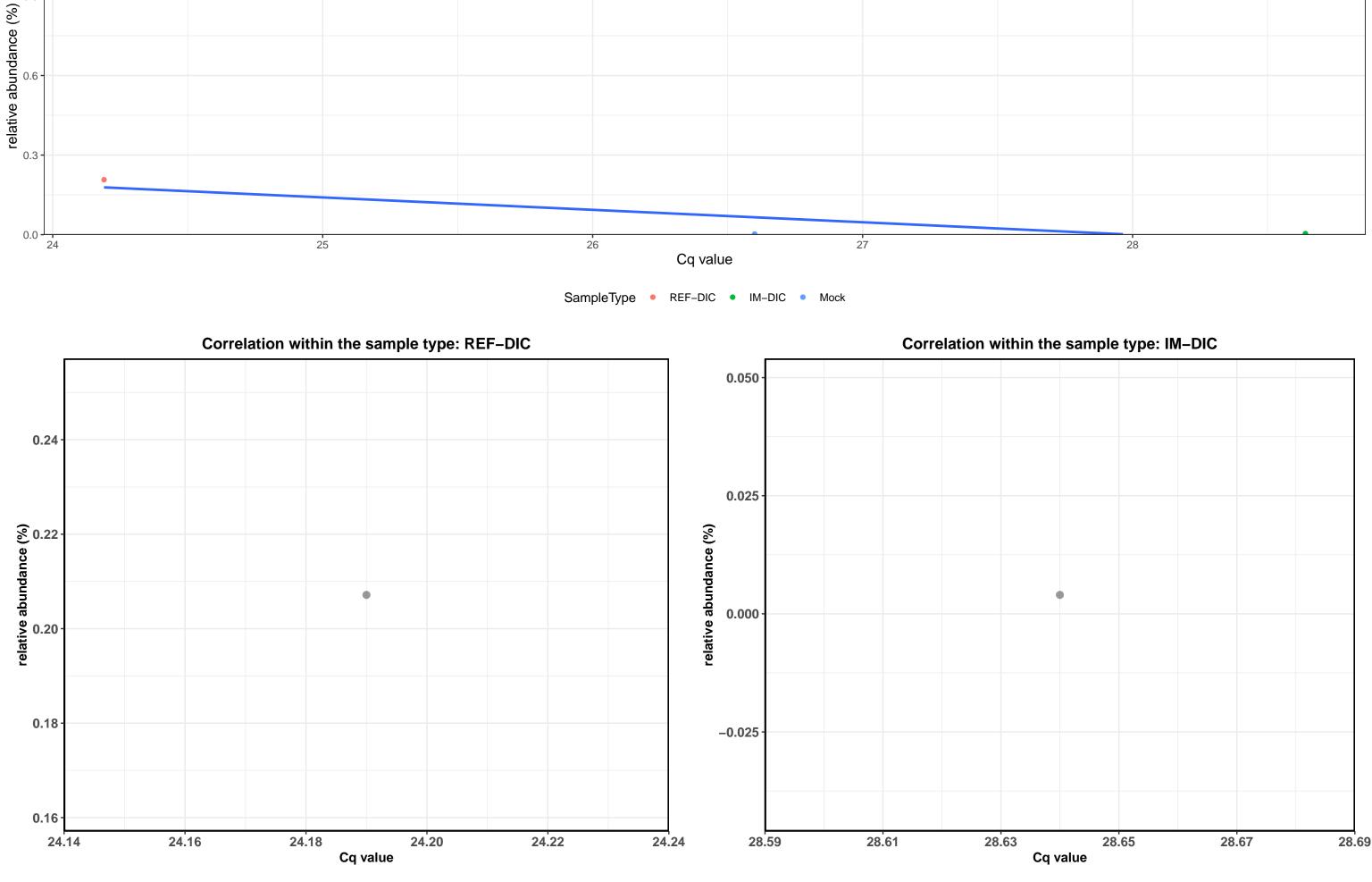
Correlation with all samples



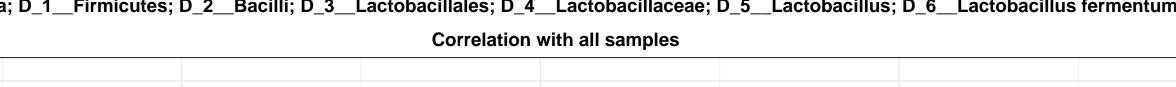


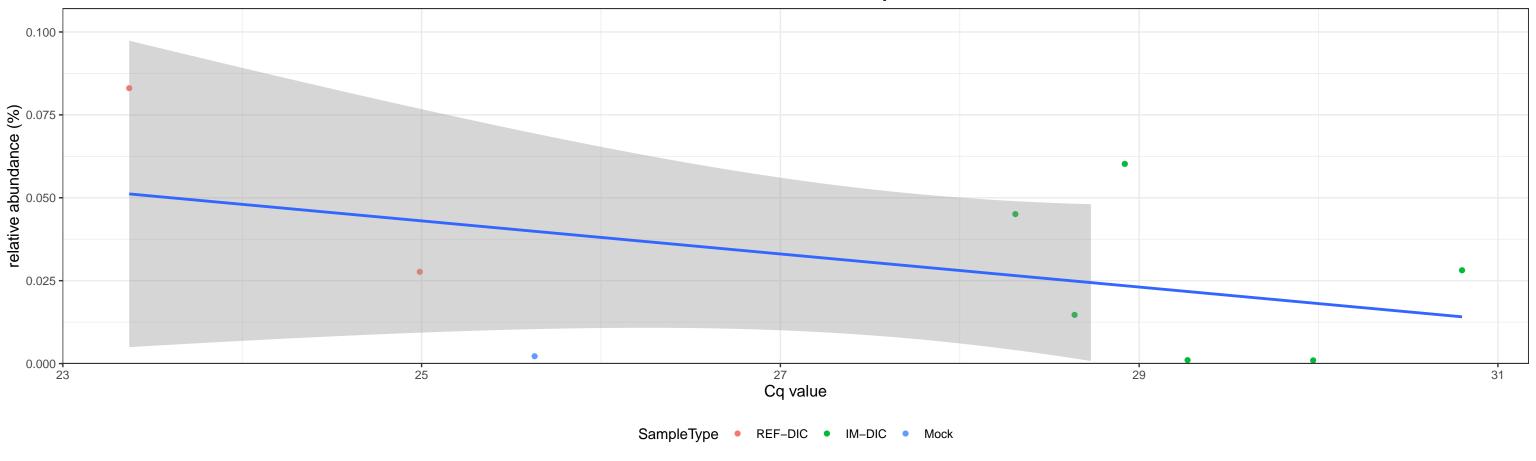
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

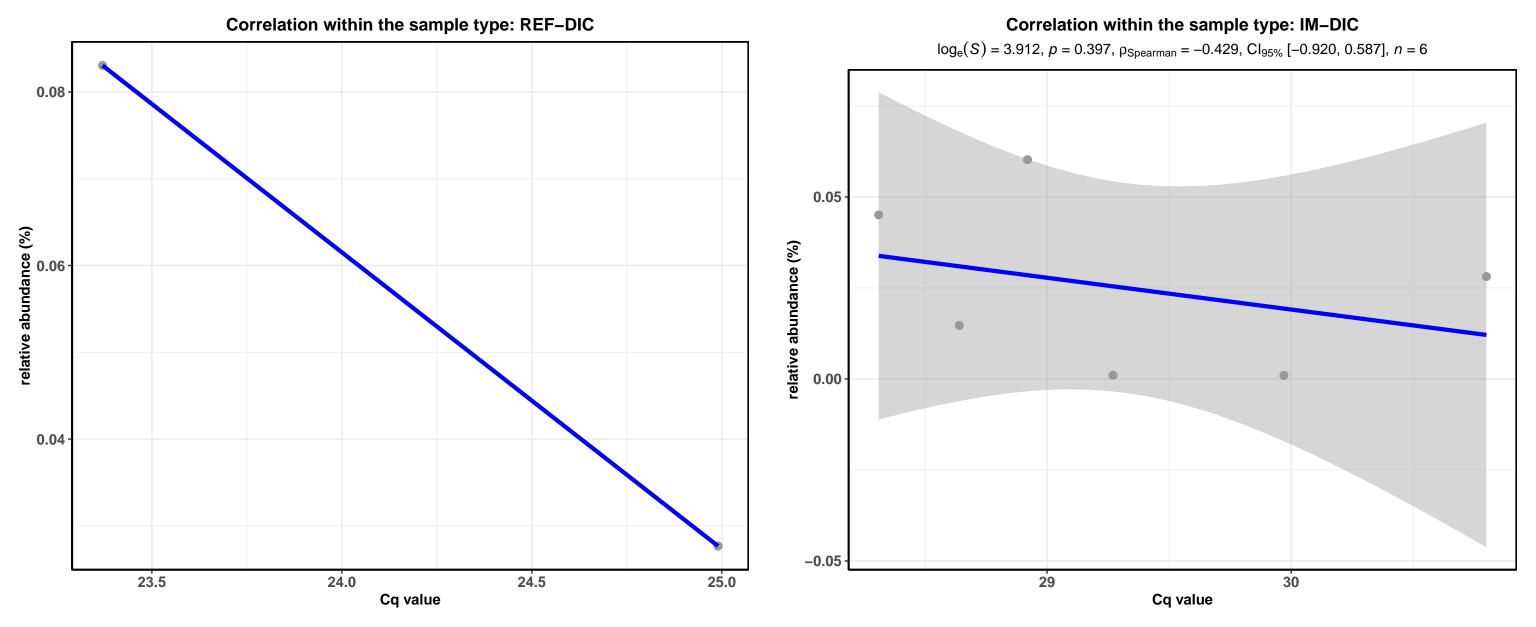
Correlation with all samples



D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum







D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum **Correlation with all samples** 24 26 28 Cq value SampleType • REF-DIC • IM-DIC • Mock Correlation within the sample type: REF-DIC Correlation within the sample type: IM-DIC 0.009 0.008 0.007 relative abundance (%) 900.0 900.0 900.0 0.004 0.003

28.5

28.8

29.1

Cq value

29.4

0.4

relative abundance (%)

0.1

0.0

0.3

relative abundance (%)

0.1

24.00

24.25

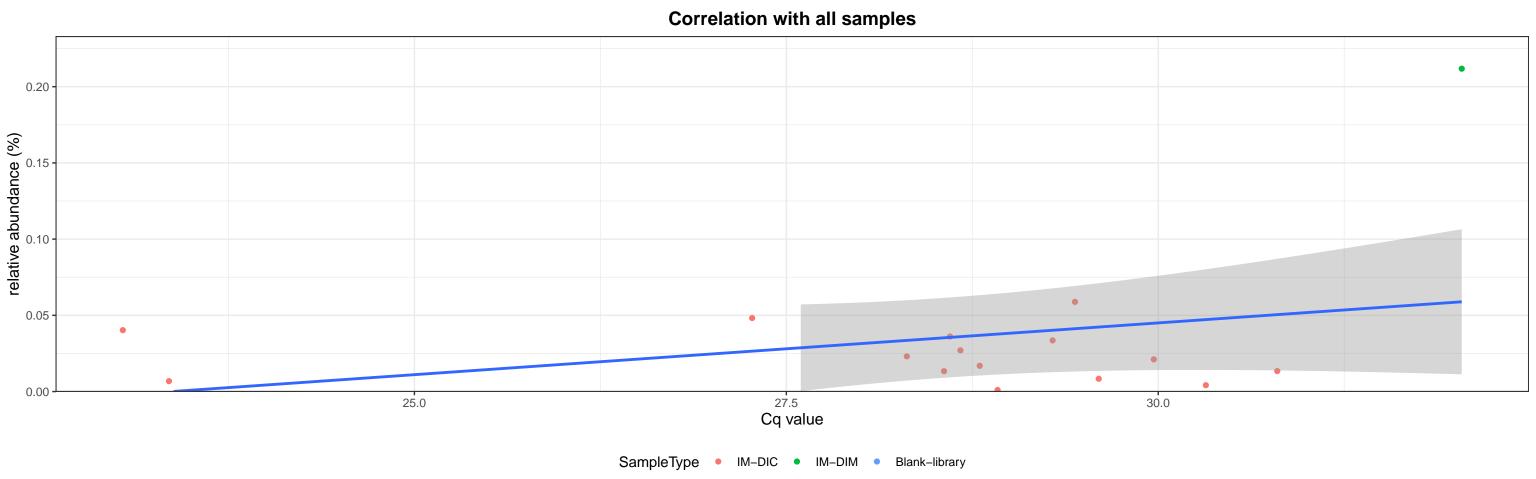
24.50

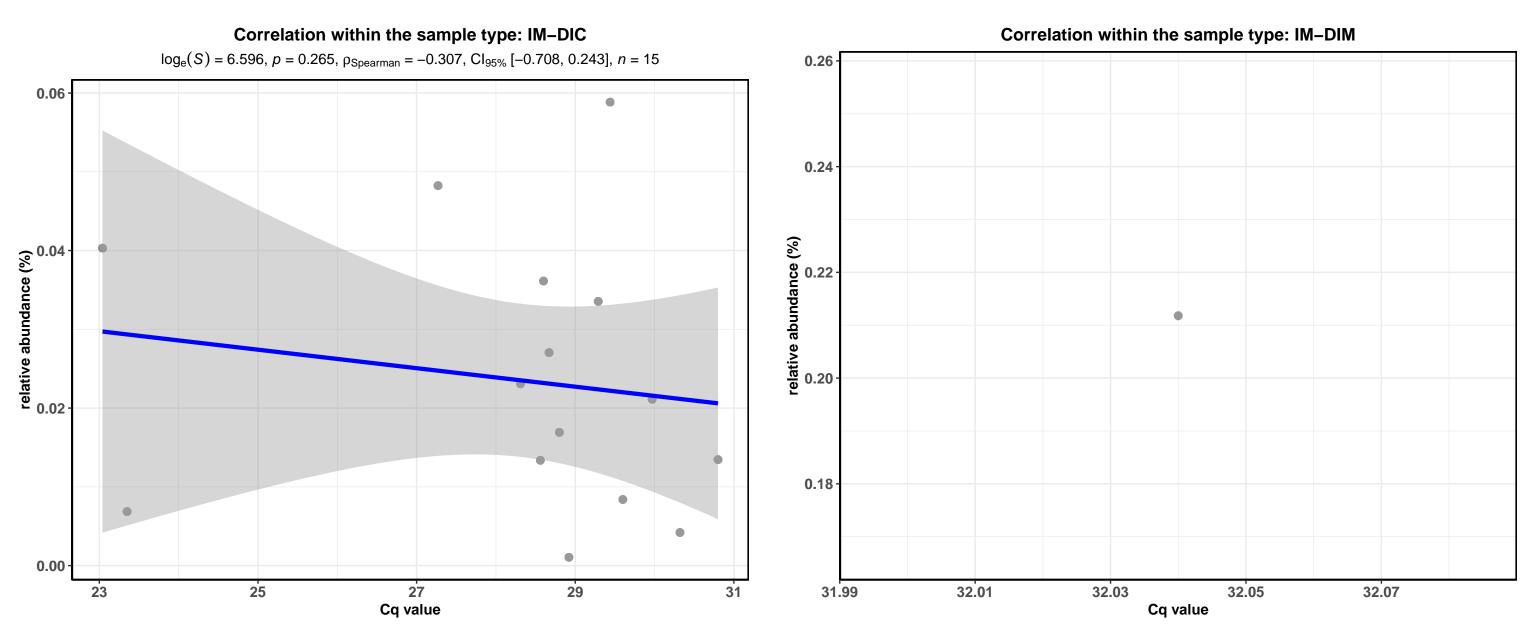
Cq value

24.75

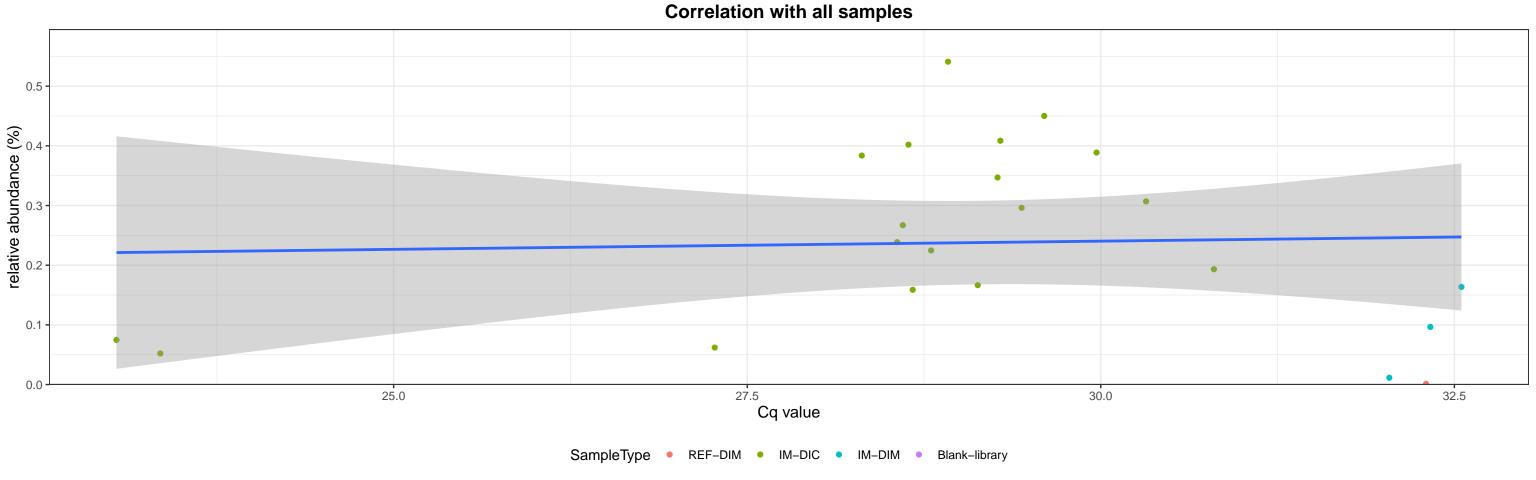
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Alteromonadales; D\_4\_Marinobacteraceae; D\_5\_Marinobacter; D\_6\_Marinobacter adhaerens **Correlation with all samples** relative abundance (%) 0.000 26 28 30 32 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.050 0.050 celative abundance (%) 0.000 - 0.000 - 0.025 relative abundance (%) 0.025 0.000 -0.025 24.850 24.875 24.925 32.08 24.900 32.06 32.10 32.12 32.14 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM 0.050 relative abundance (%) 0.0012 celative abundance (%) 0.000 0.000 0.000 0.000 32.3 28.750 28.775 28.800 28.825 28.850 32.5 32.7 32.9 Cq value Cq value

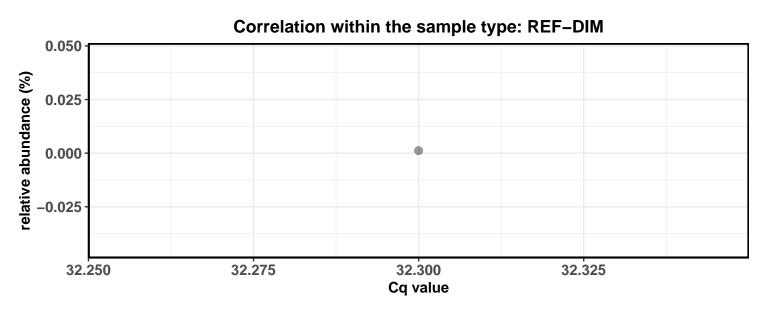
0\_0\_Bacteria; D\_1\_\_Actinobacteria; D\_2\_\_Actinobacteria; D\_3\_\_Actinomycetales; D\_4\_\_Actinomycetaceae; D\_5\_\_Actinomyces; D\_6\_\_uncultured Actinomycetales bacterium





D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Micrococcales; D\_4\_Brevibacteriaceae; D\_5\_Brevibacterium; D\_6\_Brevibacterium album





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

25

23

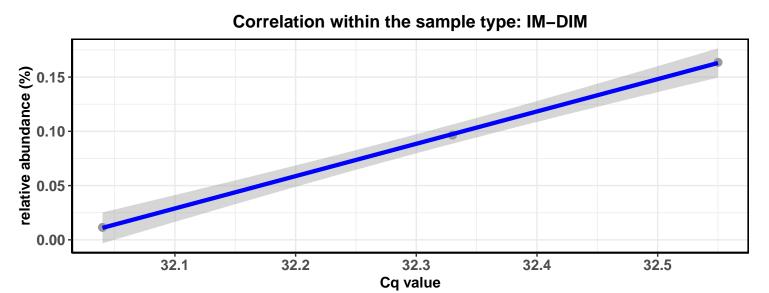
Correlation within the sample type: IM-DIC

27

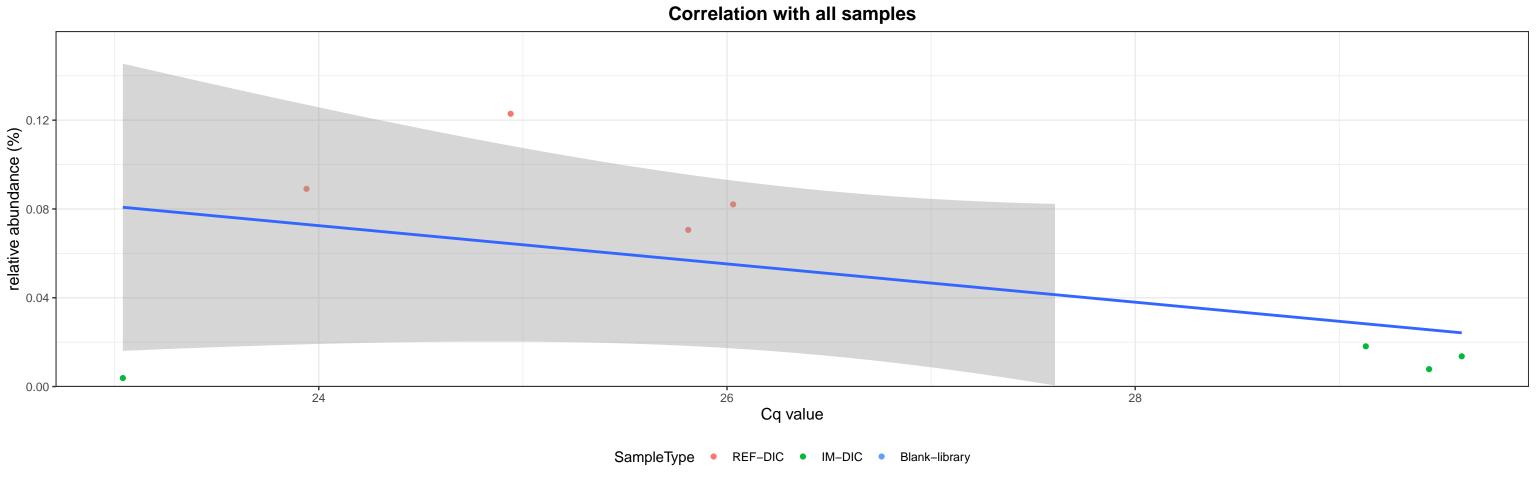
Cq value

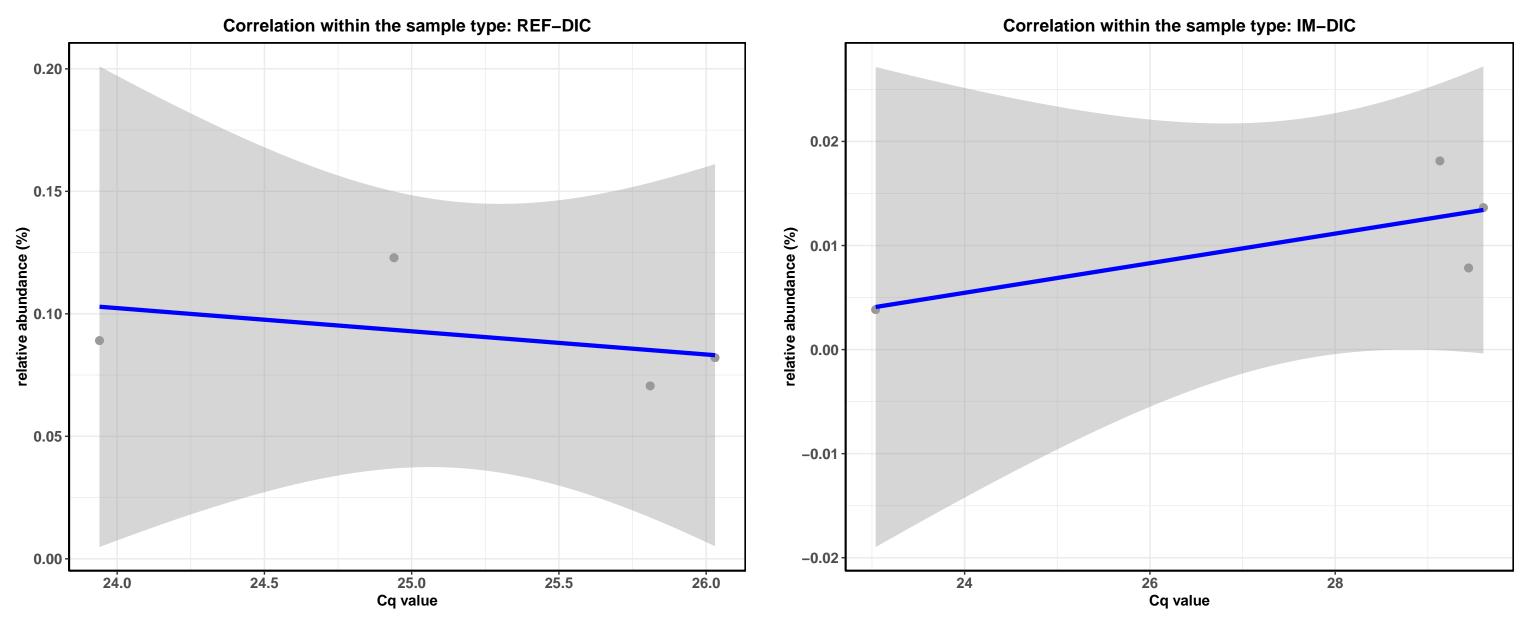
29

31



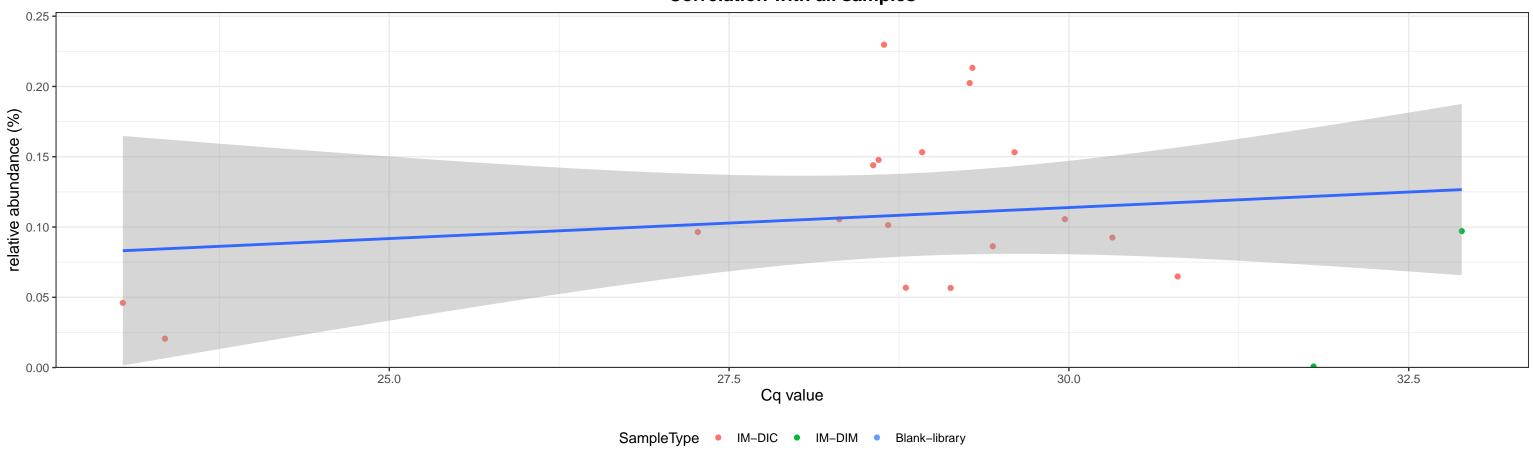
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Bacillus

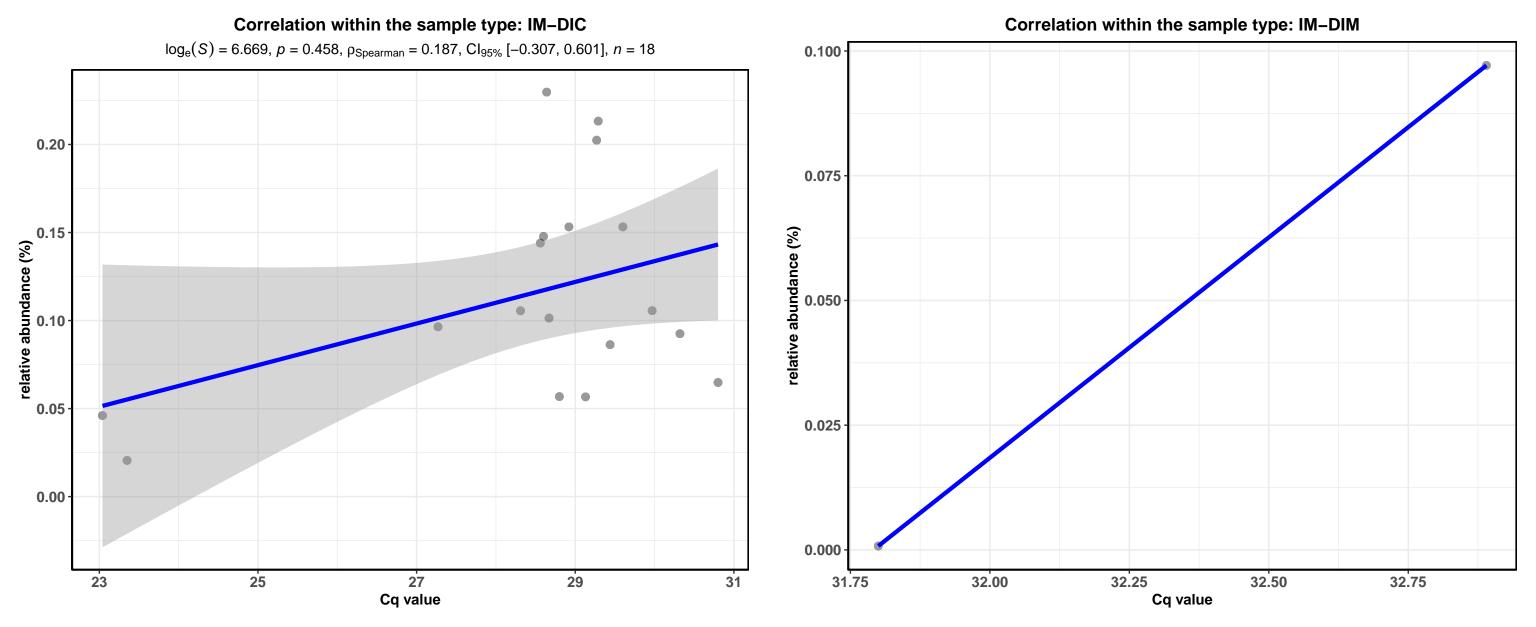




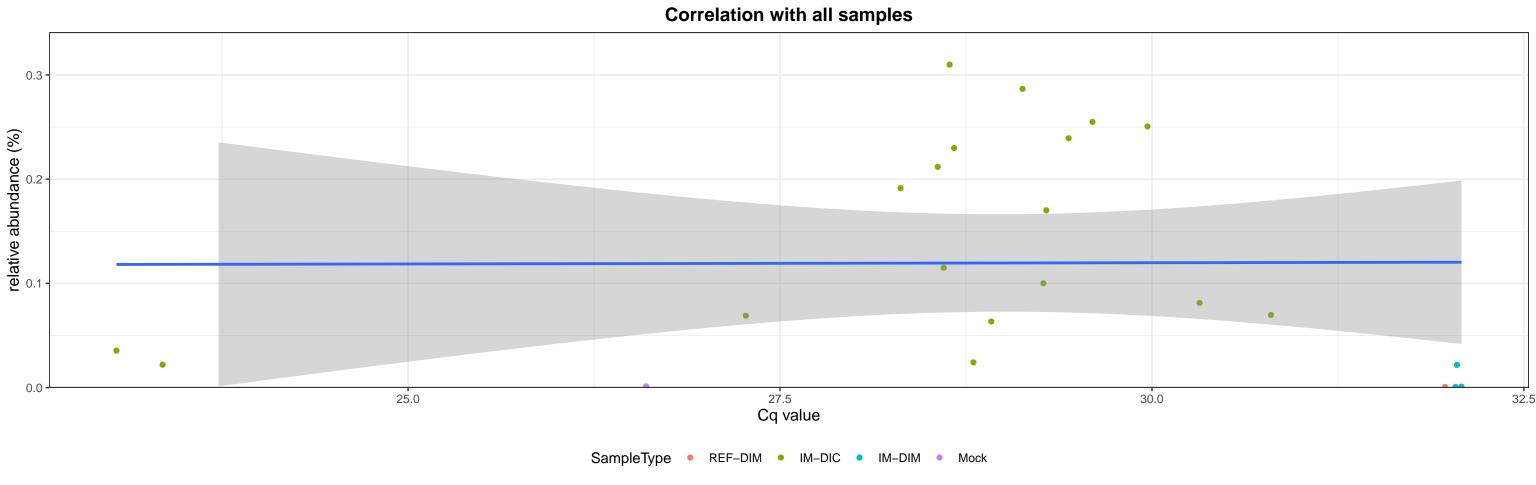
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Micrococcales; D\_4\_Brevibacteriaceae; D\_5\_Brevibacterium

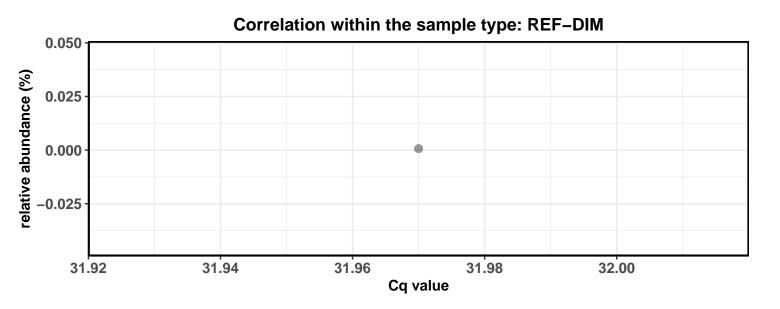


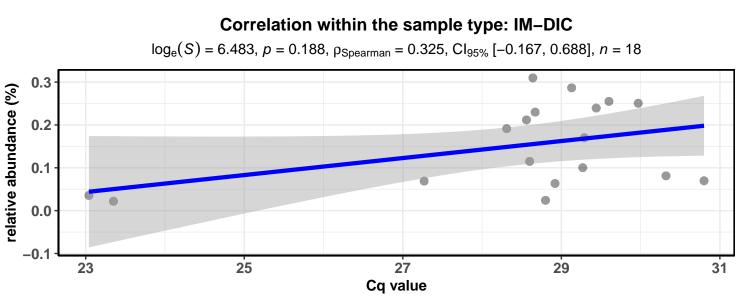


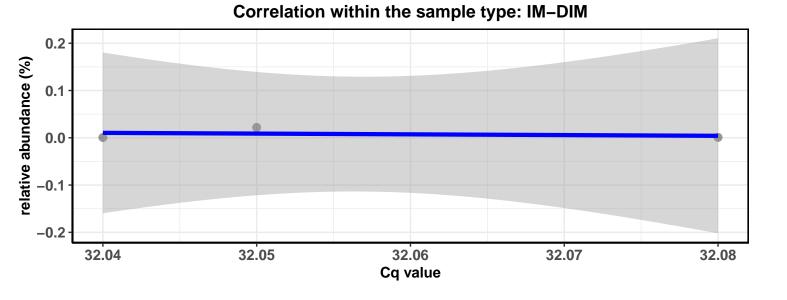


D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Flavobacteriales; D\_4\_Flavobacteriaceae; D\_5\_Flavobacterium

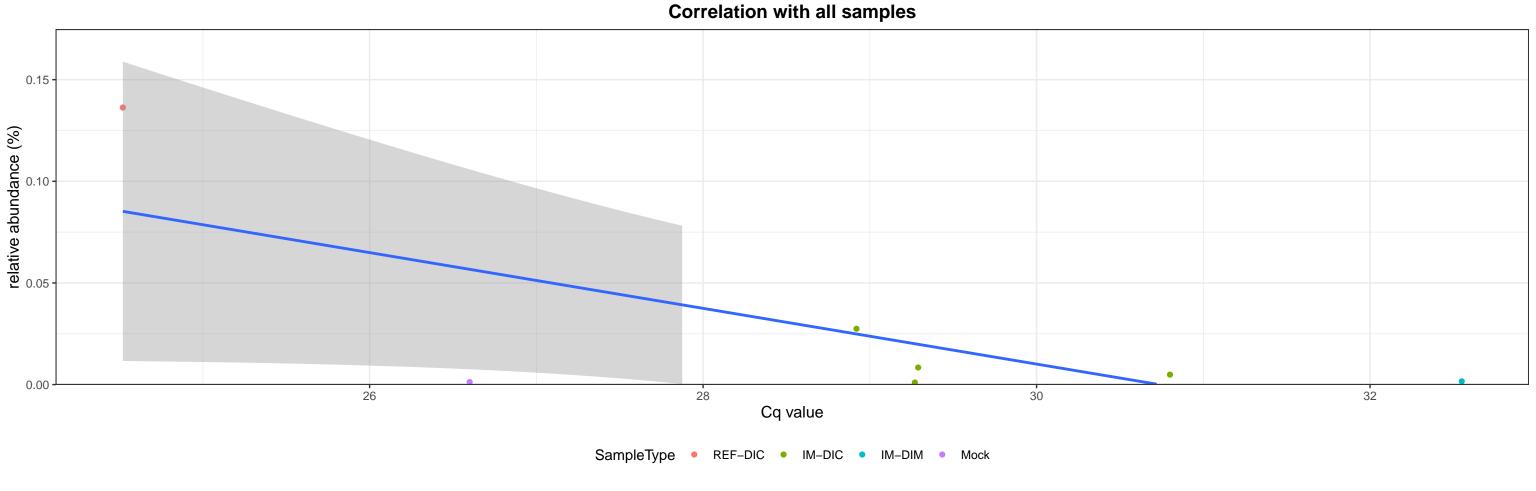


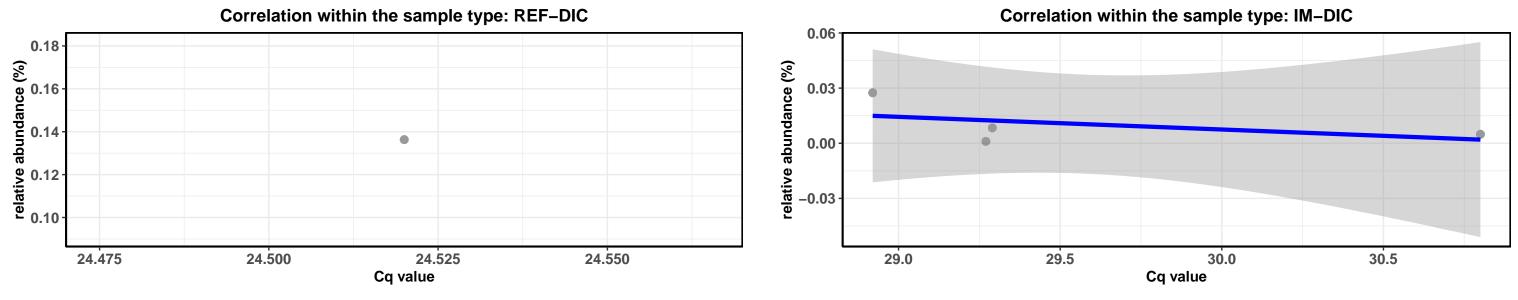


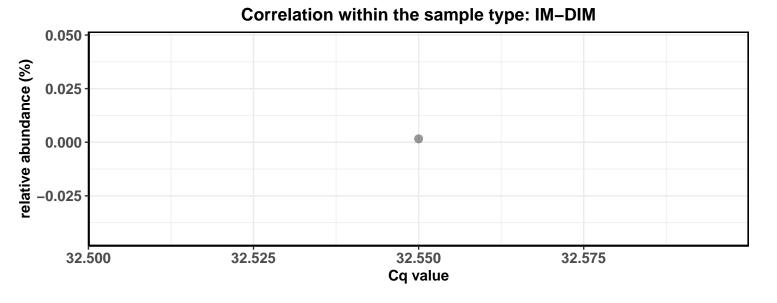




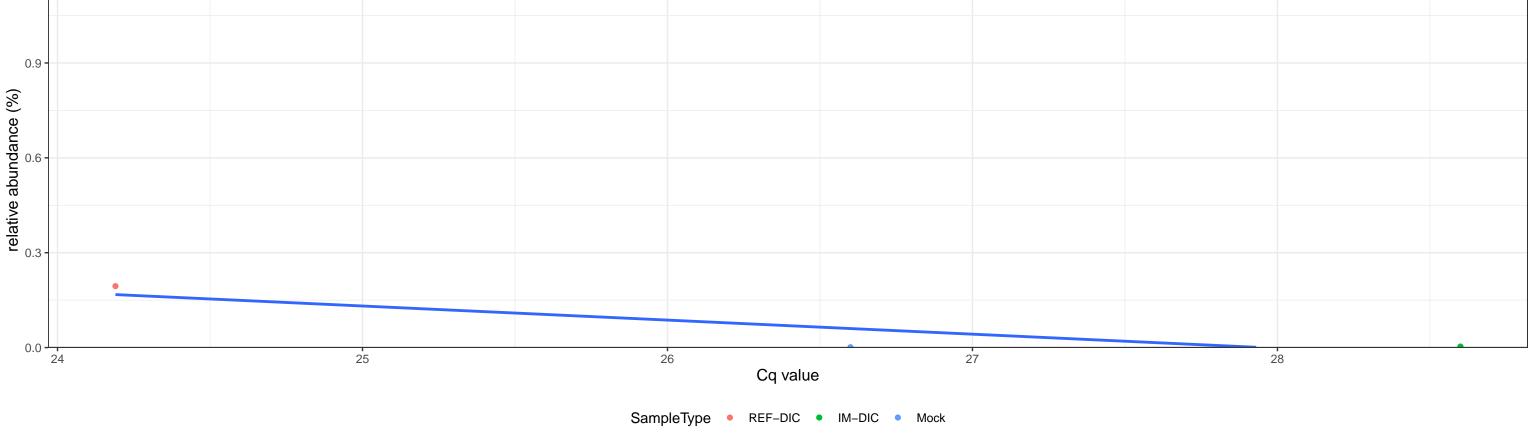
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

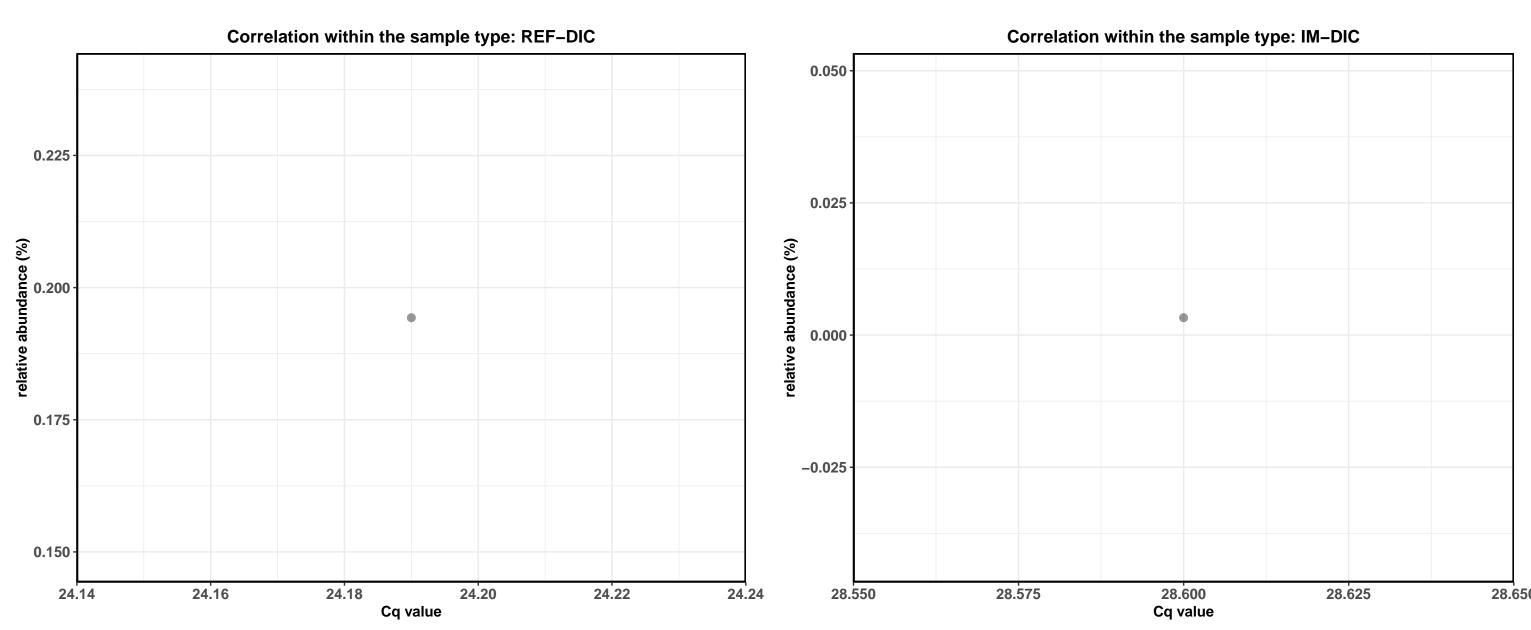






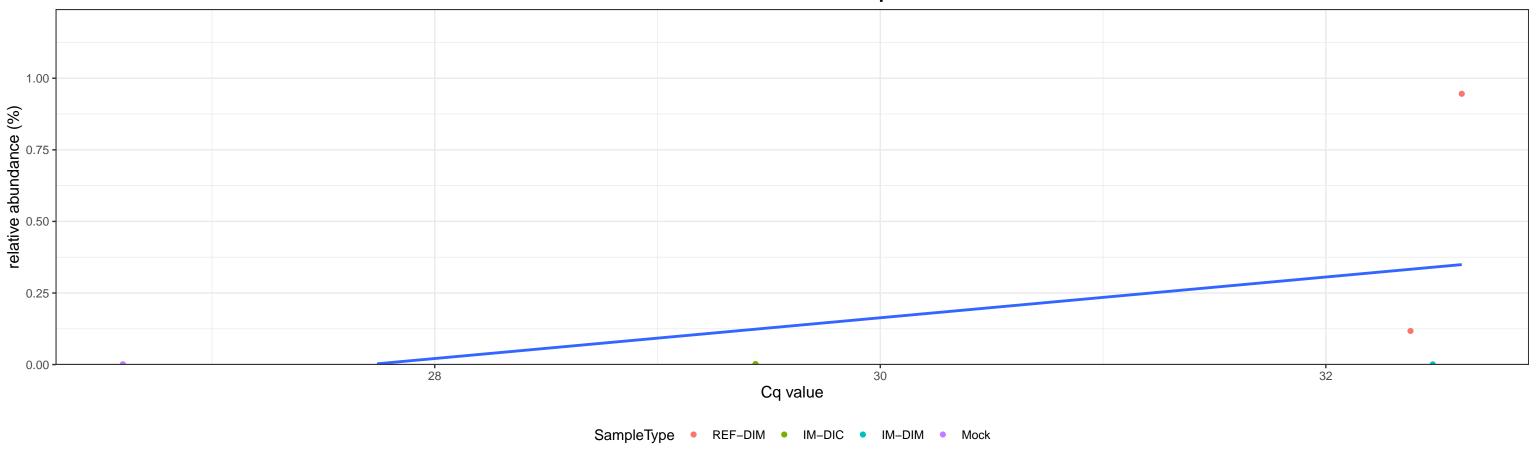
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum **Correlation with all samples** 

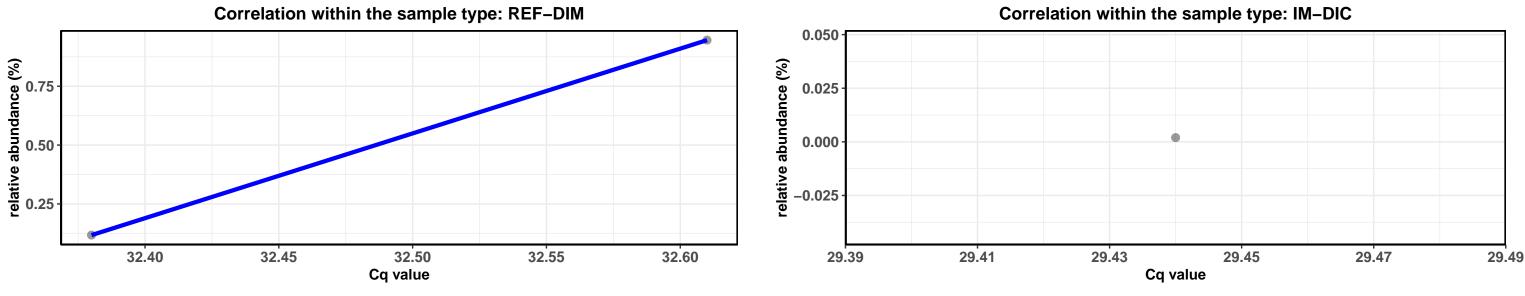


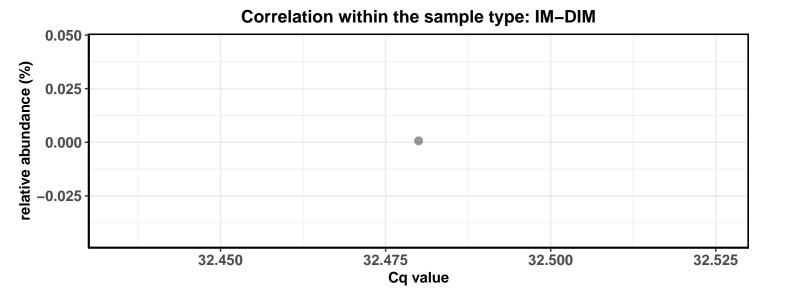


D\_0\_Bacteria; D\_1\_Bacteroidetes; D\_2\_Bacteroidia; D\_3\_Cytophagales; D\_4\_Hymenobacteraceae; D\_5\_Hymenobacter; D\_6\_uncultured bacterium

Correlation with all samples

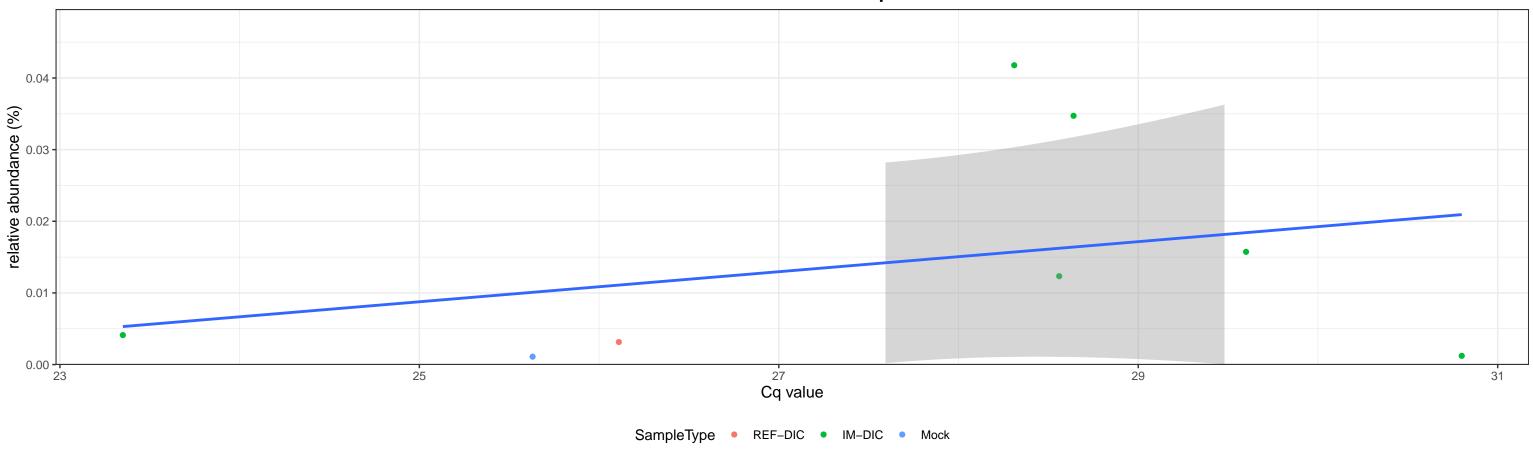


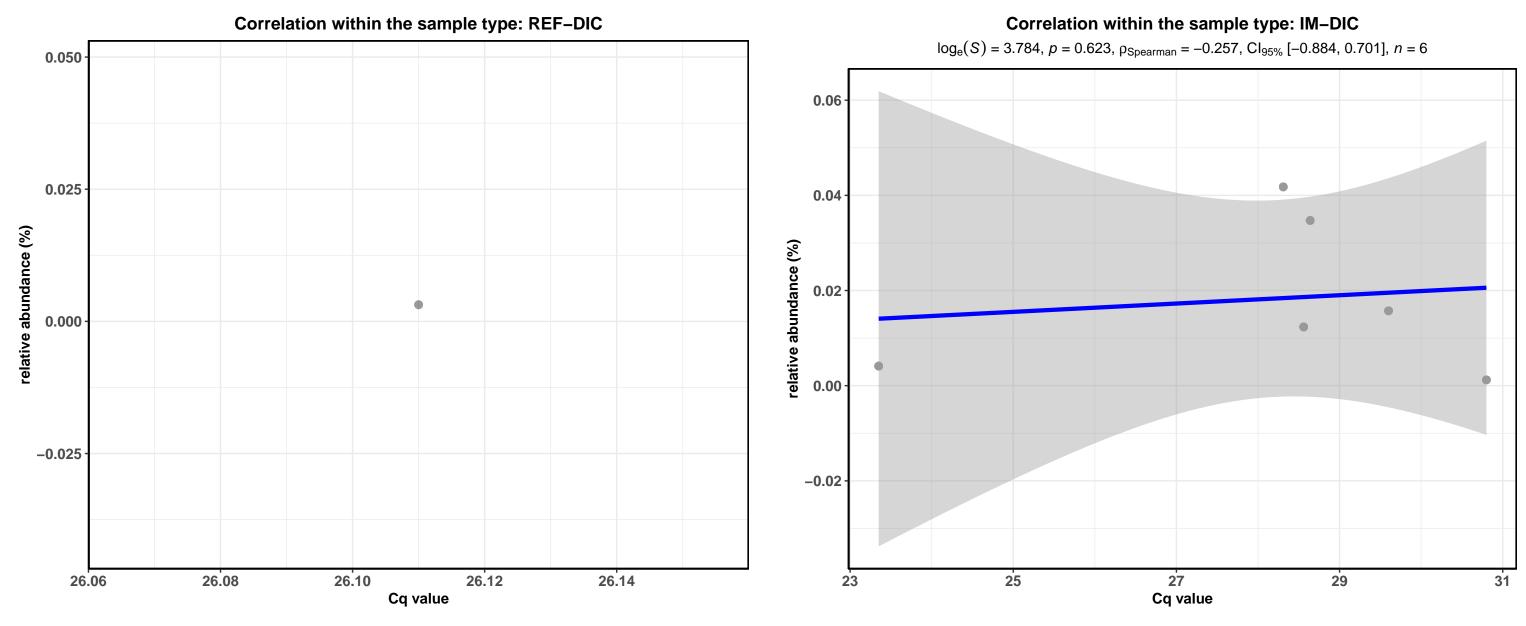




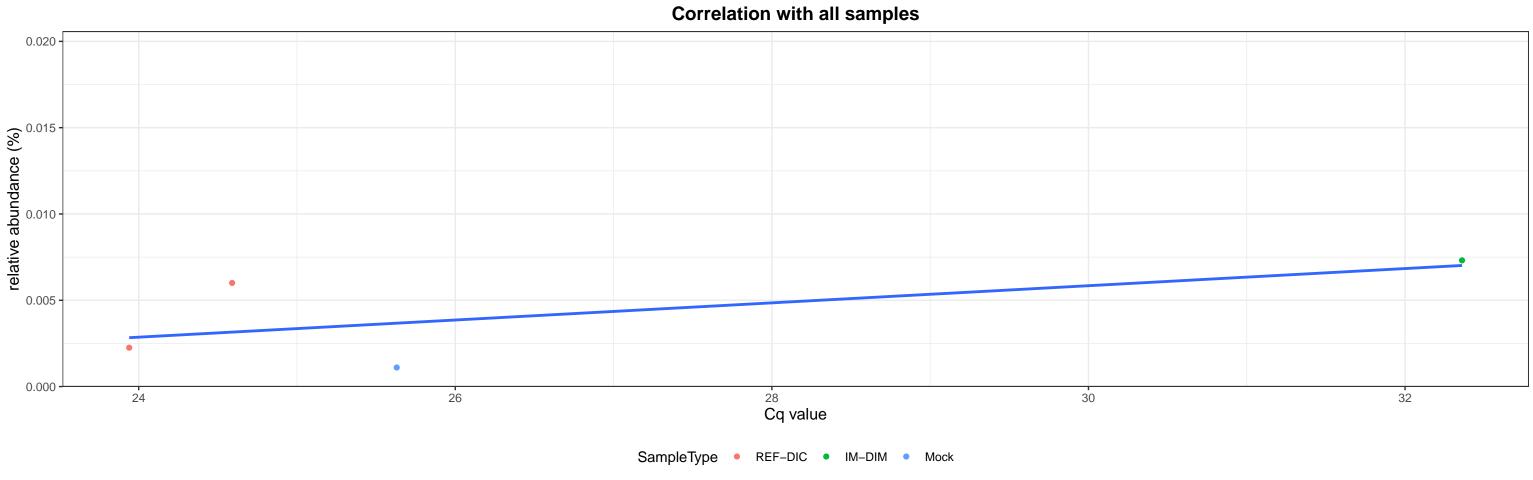
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; D\_6\_Lactobacillus fermentum

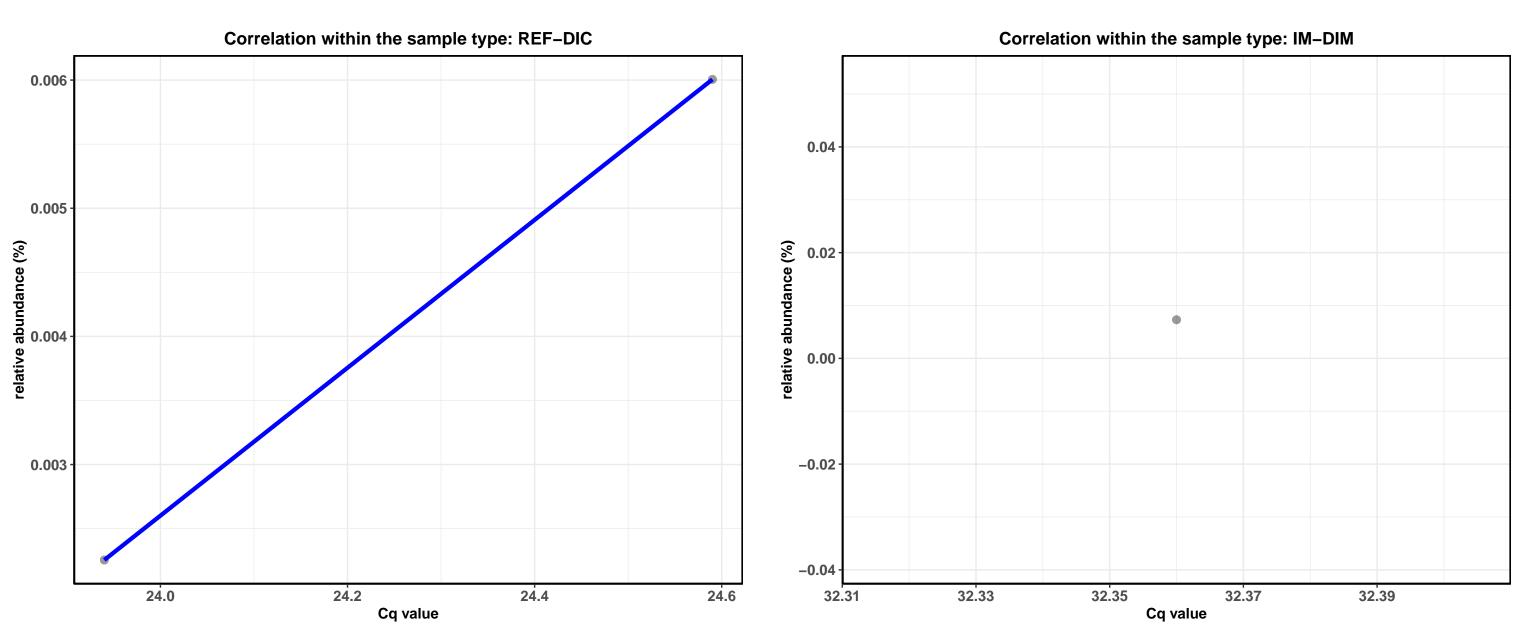




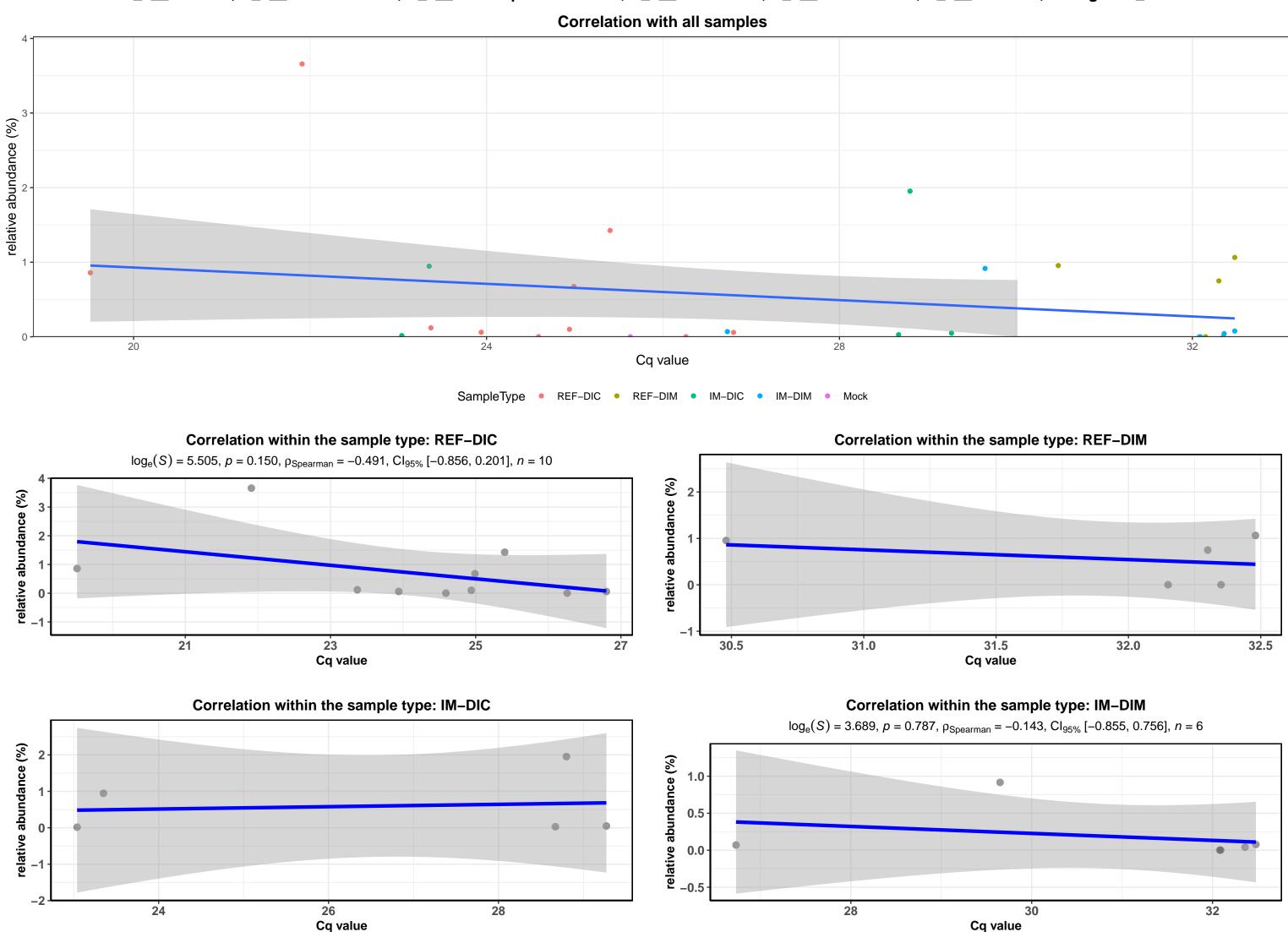


D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Betaproteobacteriales; D\_4\_Burkholderiaceae; D\_5\_Acidovorax

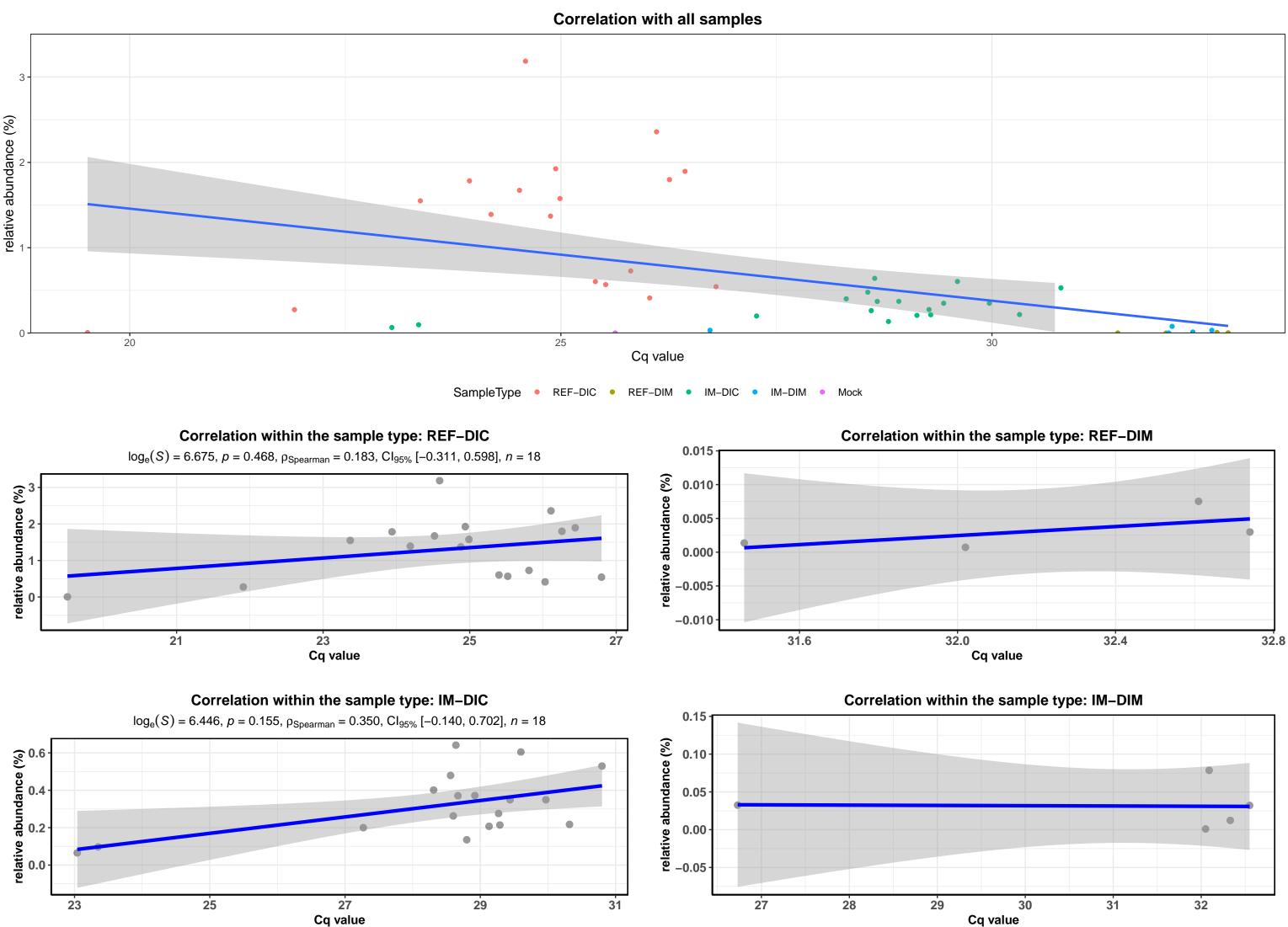




D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Vibrionales; D\_4\_Vibrionaceae; D\_5\_Aliivibrio; Ambiguous\_taxa



D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Leuconostocaceae; D\_5\_Weissella; D\_6\_uncultured bacterium



D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Ornithinibacillus; Ambiguous\_taxa **Correlation with all samples** 25.0 27.5 32.5 30.0 Cq value SampleType • REF-DIC • REF-DIM • IM-DIC • IM-DIM Correlation within the sample type: REF-DIC Correlation within the sample type: REF-DIM 0.050 0.4 relative abundance (%) 0.025 0.2 0.000 0.0 -0.025 -0.2 24 25 32.825 32.850 32.875 26 32.800 Cq value Cq value Correlation within the sample type: IM-DIC Correlation within the sample type: IM-DIM  $log_e(S) = 6.148$ , p = 0.028,  $\rho_{Spearman} = 0.517$ ,  $Cl_{95\%}$  [0.066, 0.793], n = 18relative abundance (%) 0.1 0.0

31

29

28

27

31

30

Cq value

29

32

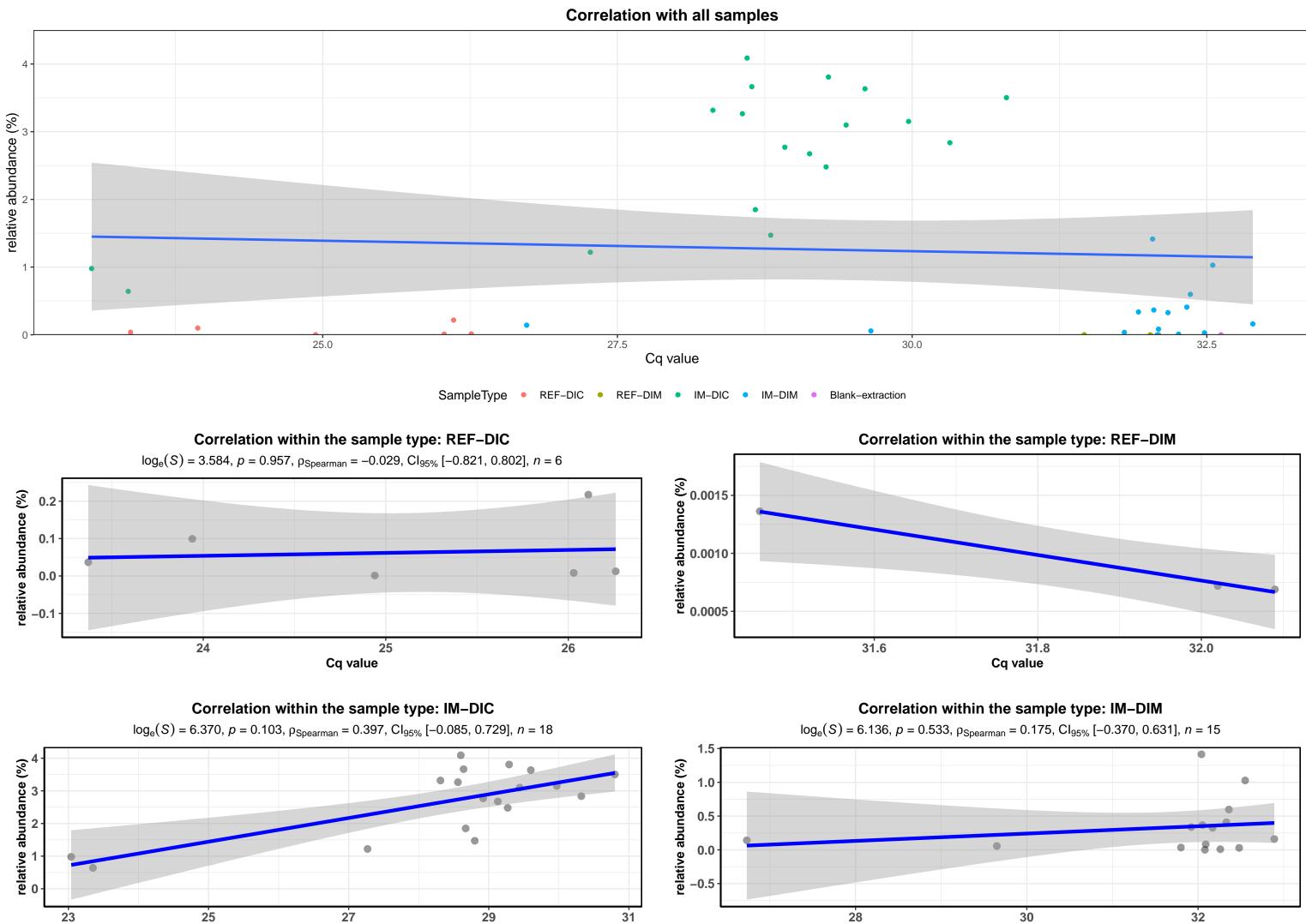
relative abundance (%)

relative abundance (%)

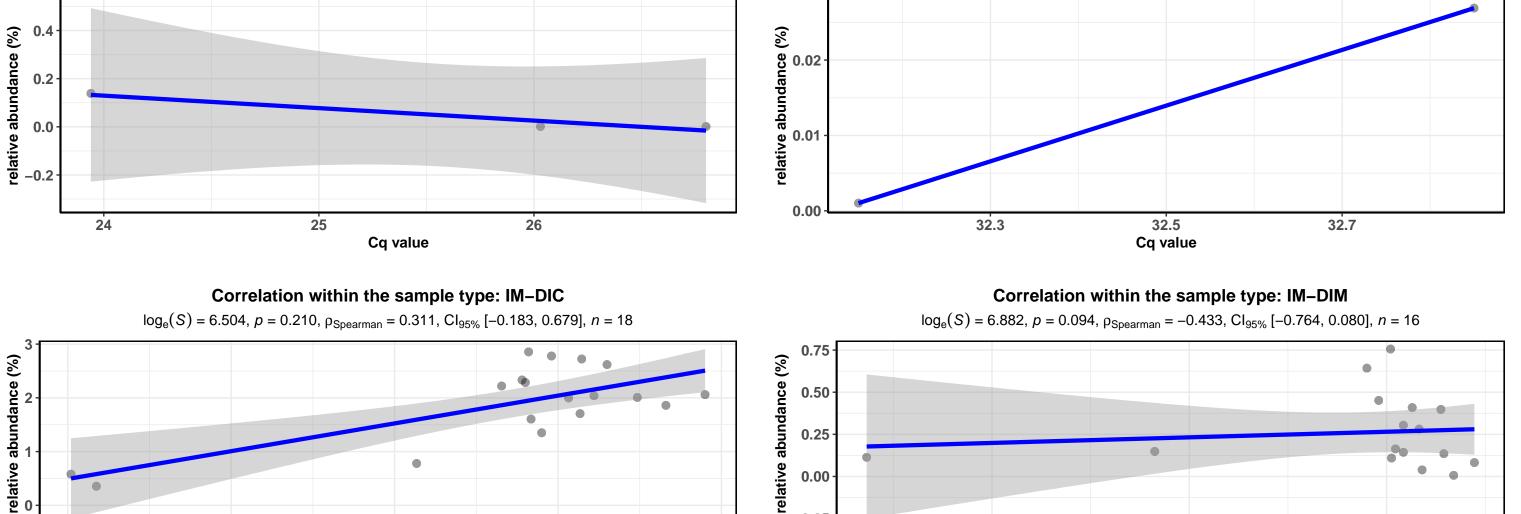
23

25

27



Cq value



0.25

0.00

28

30

Cq value

32

31

29

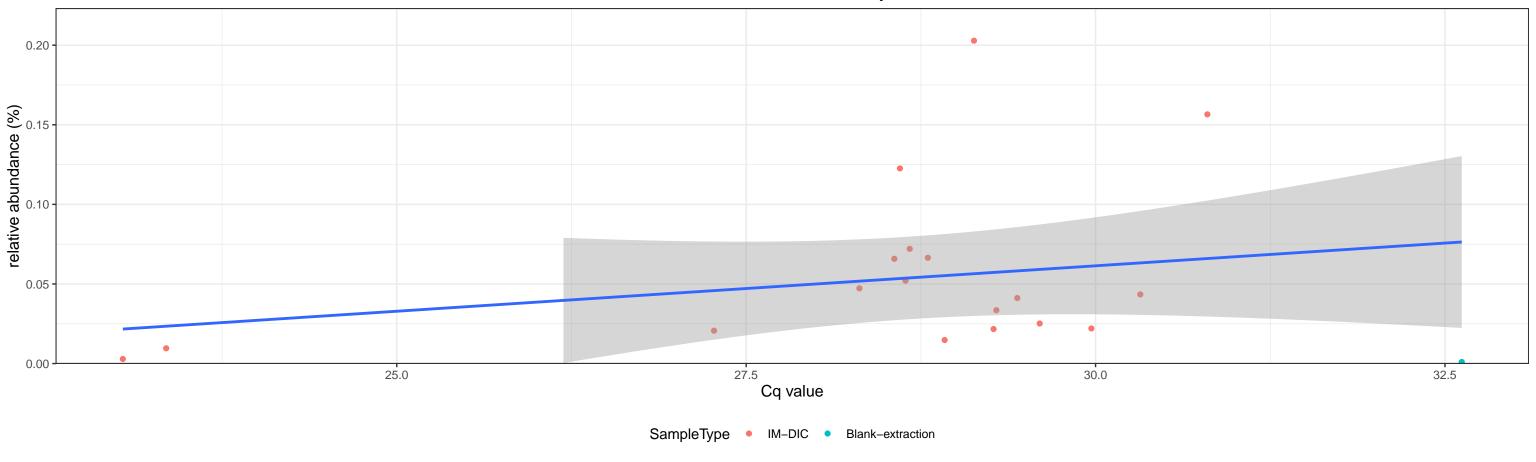
25

23

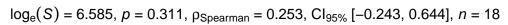
27

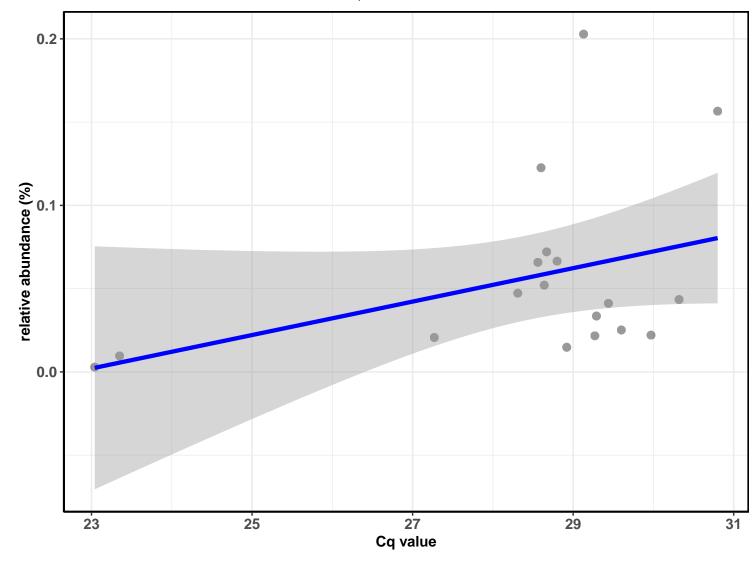
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Lactobacillales; D\_4\_Lactobacillaceae; D\_5\_Lactobacillus; Ambiguous\_taxa



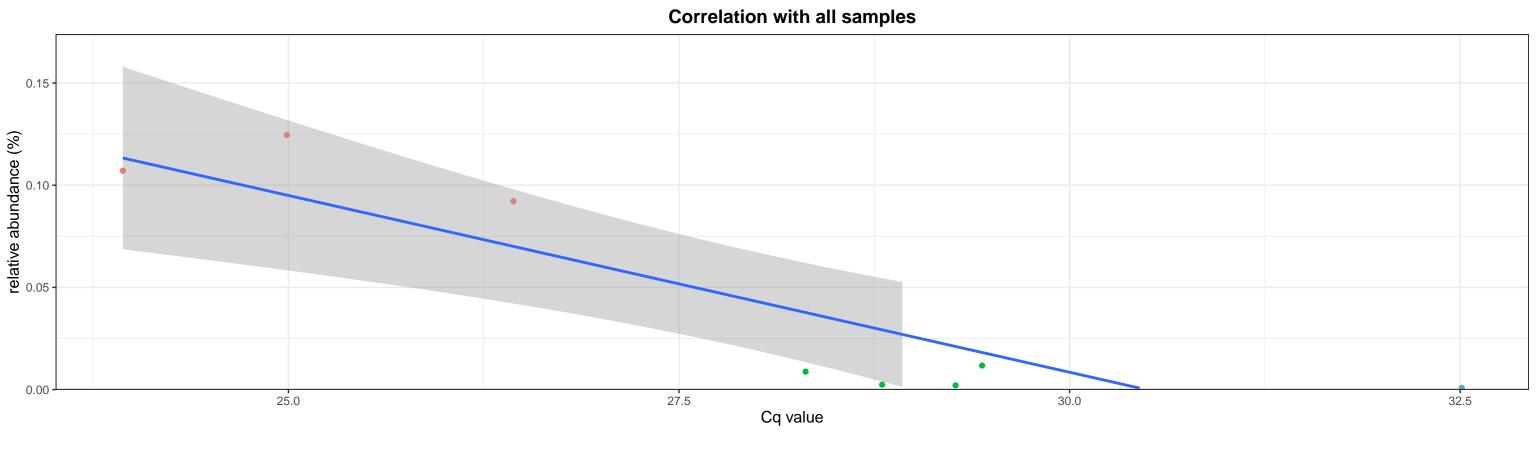


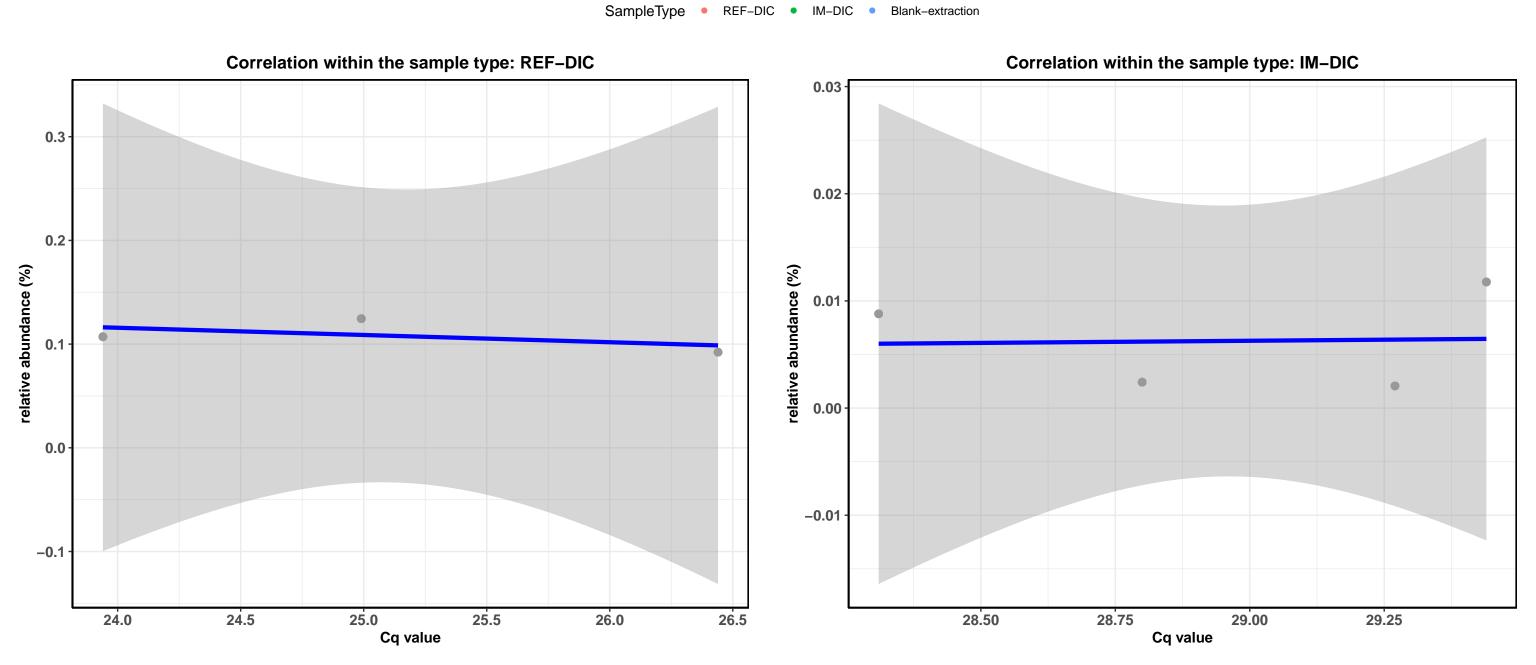
## Correlation within the sample type: IM-DIC



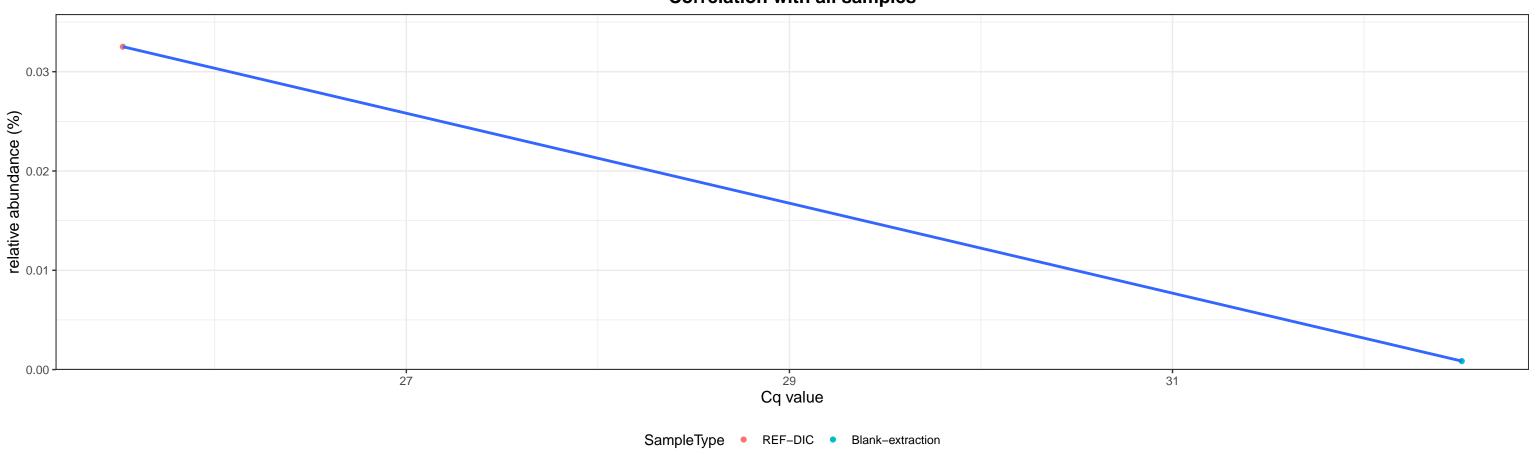


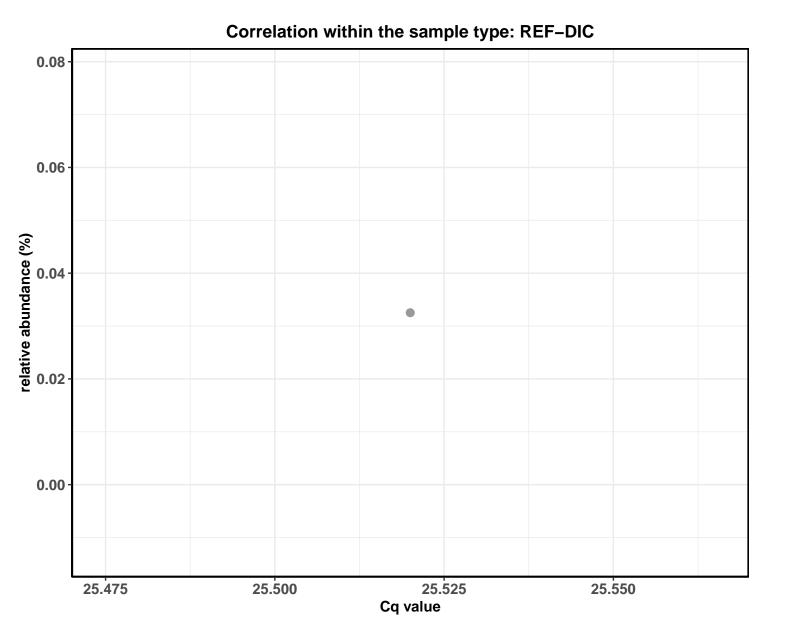
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Erysipelotrichia; D\_3\_Erysipelotrichales; D\_4\_Erysipelotrichaceae



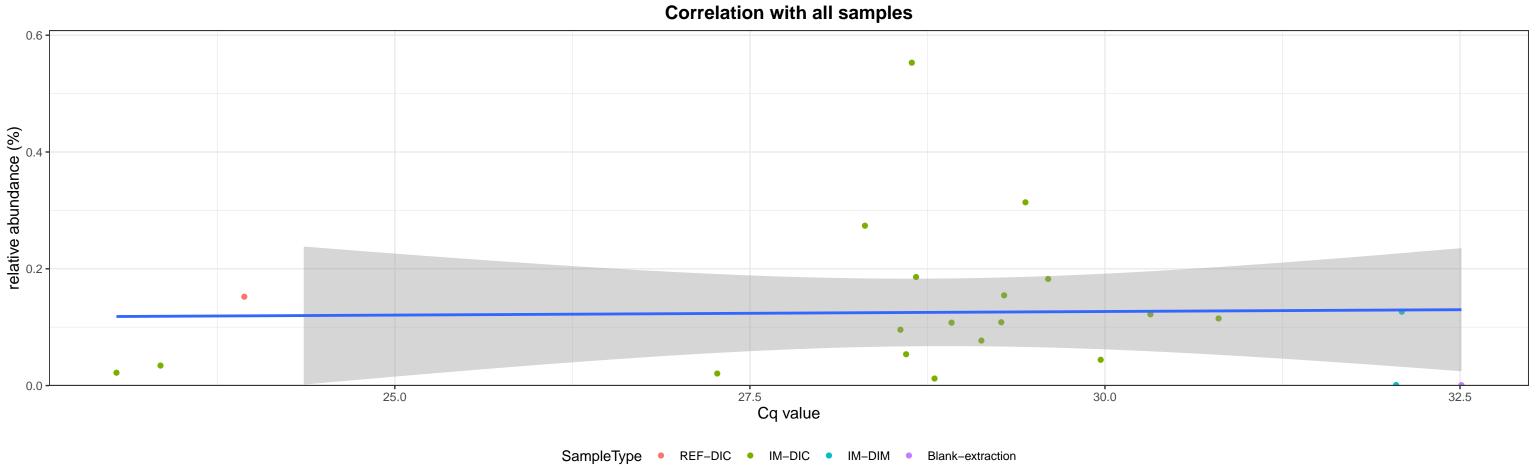


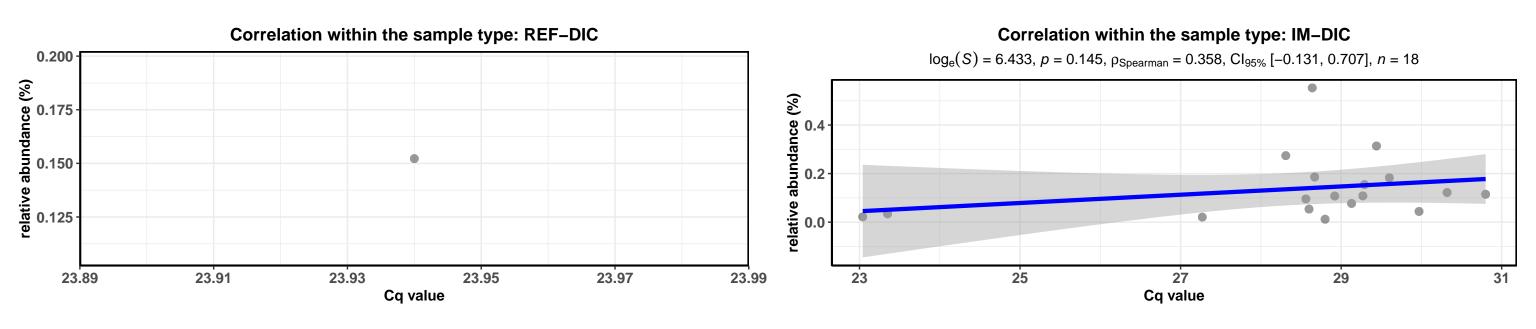
D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Corynebacteriales; D\_4\_Corynebacteriaceae; D\_5\_Corynebacterium 1; D\_6\_uncultured bacterium Correlation with all samples

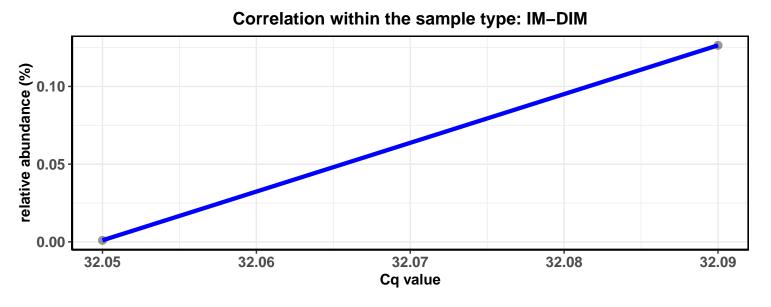




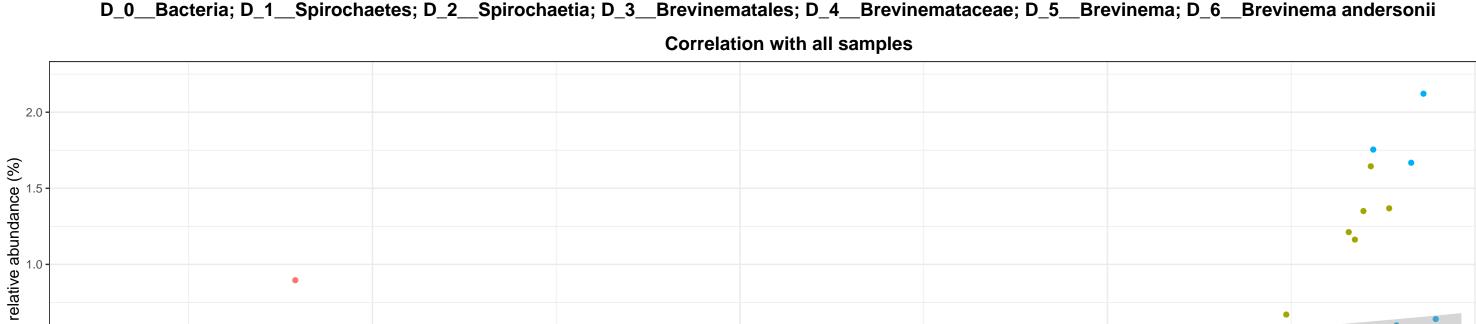
D\_0\_Bacteria; D\_1\_Proteobacteria; D\_2\_Gammaproteobacteria; D\_3\_Pseudomonadales; D\_4\_Pseudomonadaceae; D\_5\_Pseudomonas; D\_6\_uncultured bacterium

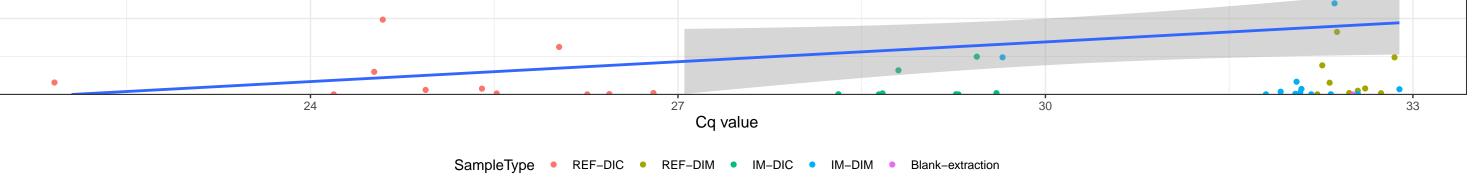


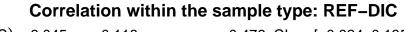




D\_0\_Bacteria; D\_1\_Spirochaetes; D\_2\_Spirochaetia; D\_3\_Brevinematales; D\_4\_Brevinemataceae; D\_5\_Brevinema; D\_6\_Brevinema andersonii





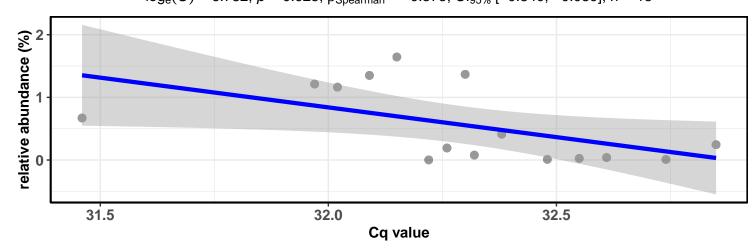


0.5

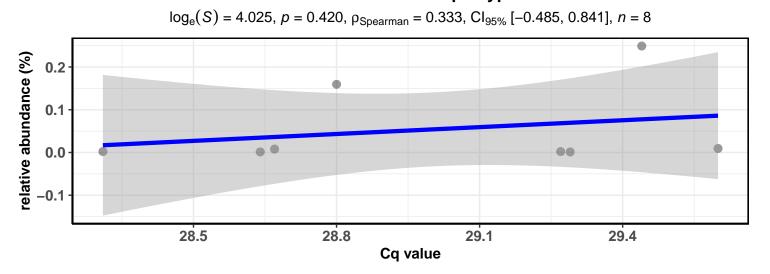
 $log_e(S) = 6.045$ , p = 0.118,  $\rho_{Spearman} = -0.476$ ,  $Cl_{95\%}$  [-0.824, 0.135], n = 12relative abundance (%) 0.6 0.3 0.0 -0.322 23 25 24 26 27 Cq value

## Correlation within the sample type: REF-DIM

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

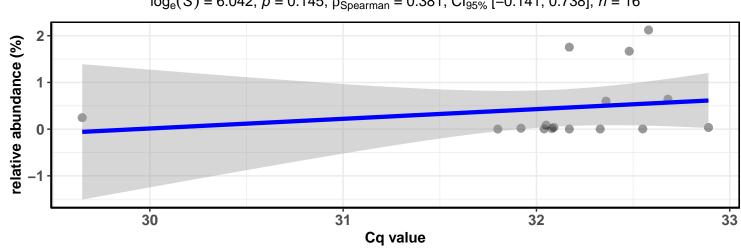


#### Correlation within the sample type: IM-DIC

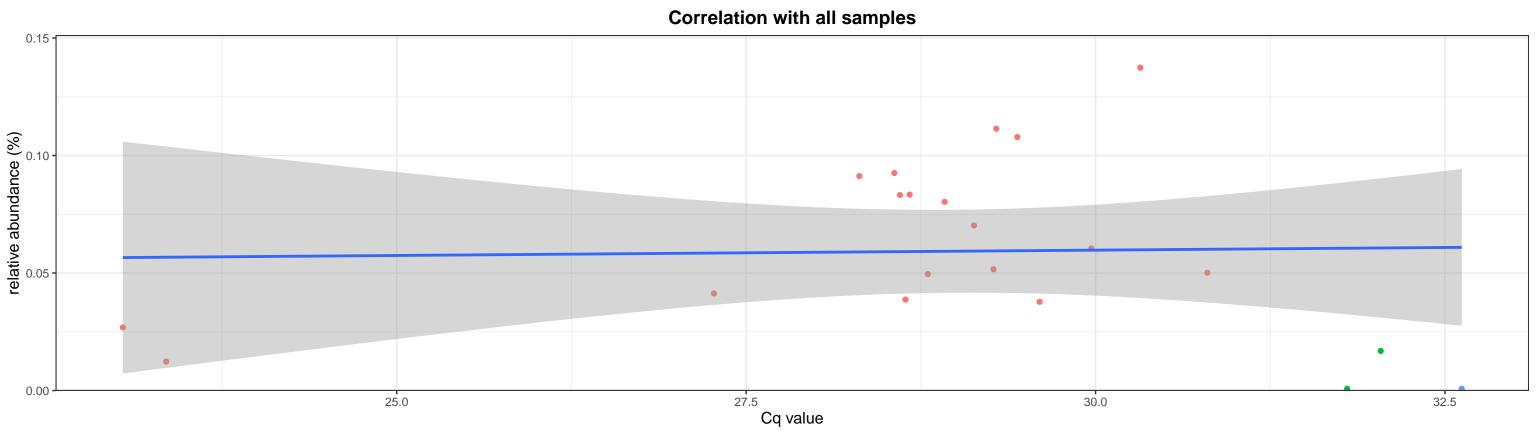


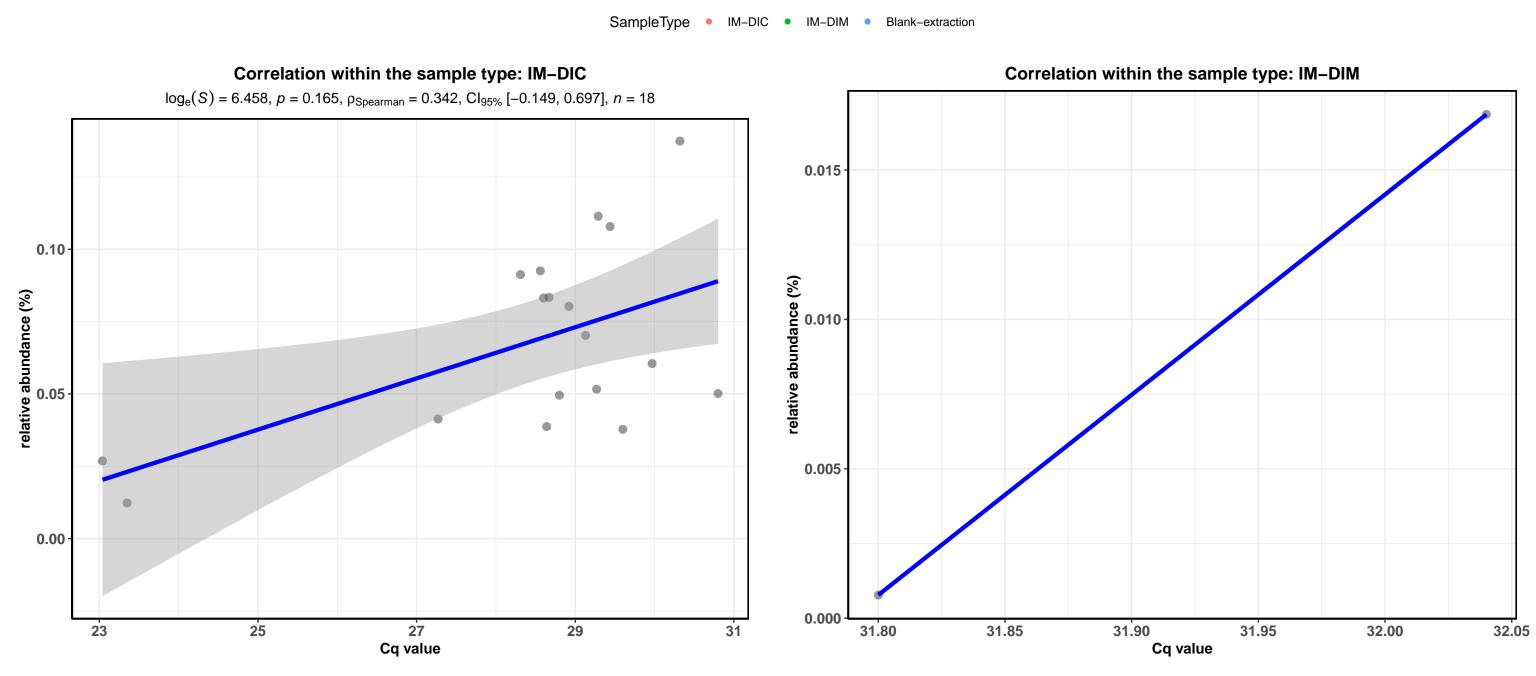
# Correlation within the sample type: IM-DIM

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

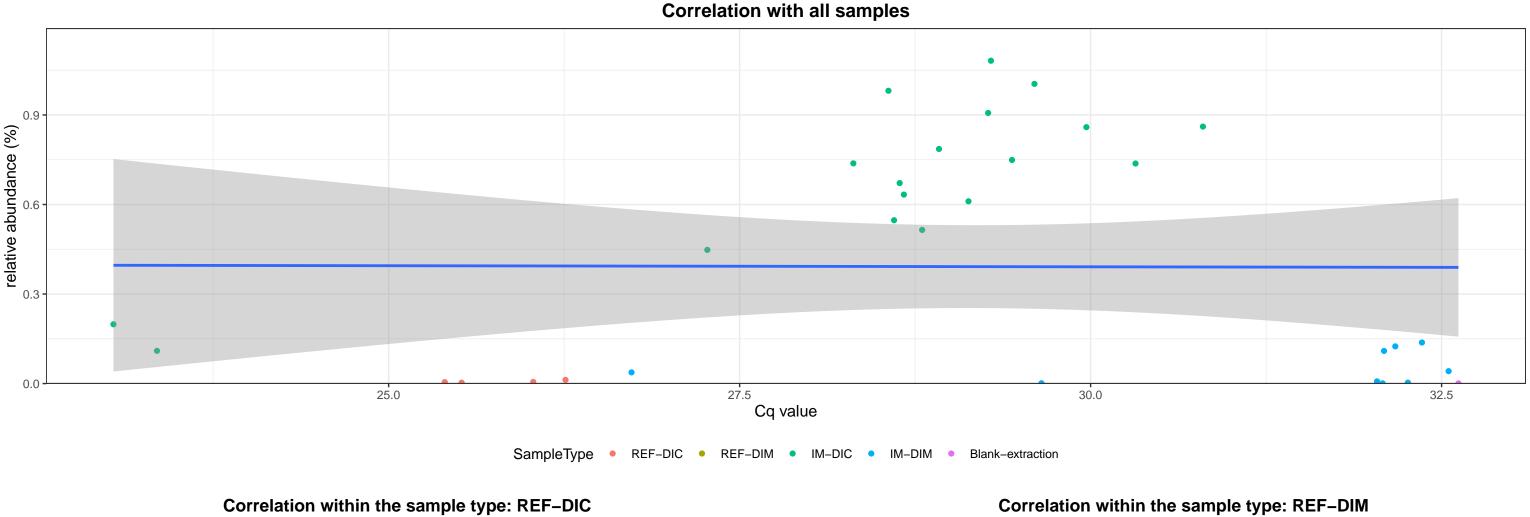


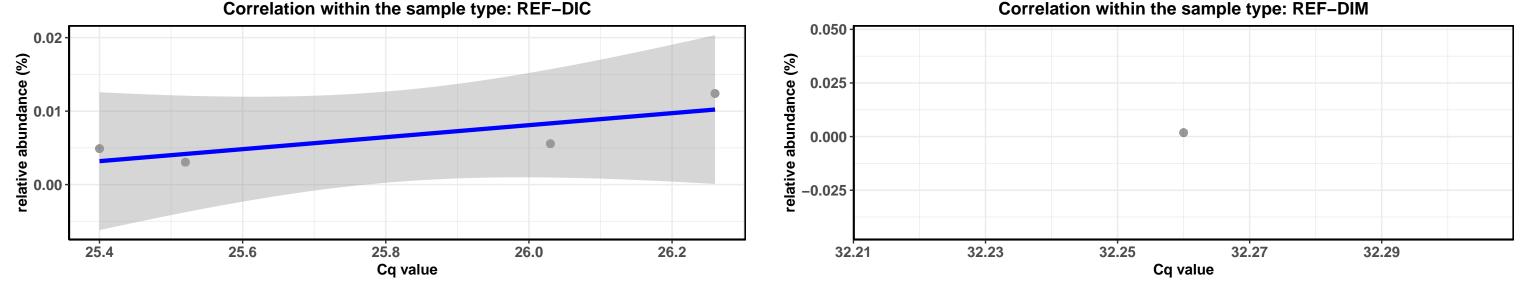
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Gracilibacillus; Ambiguous\_taxa

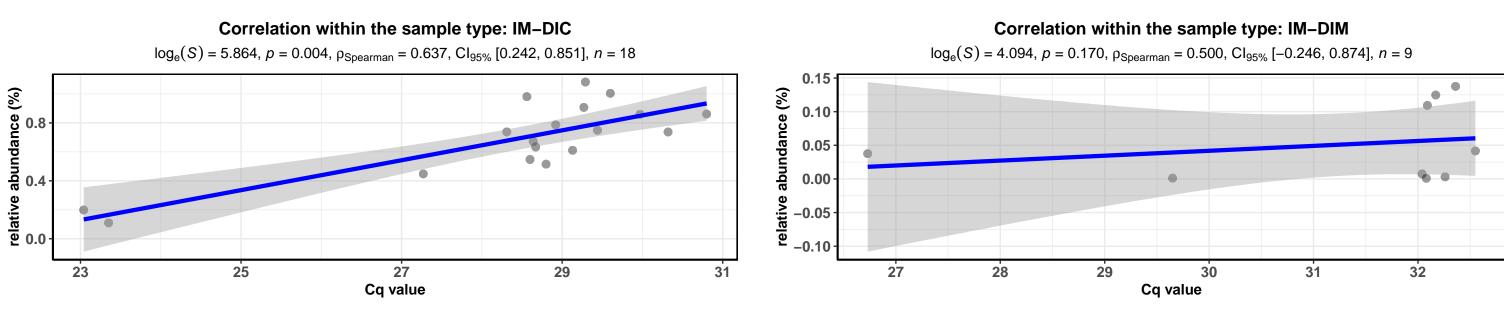




D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Oceanobacillus; D\_6\_Oceanobacillus caeni

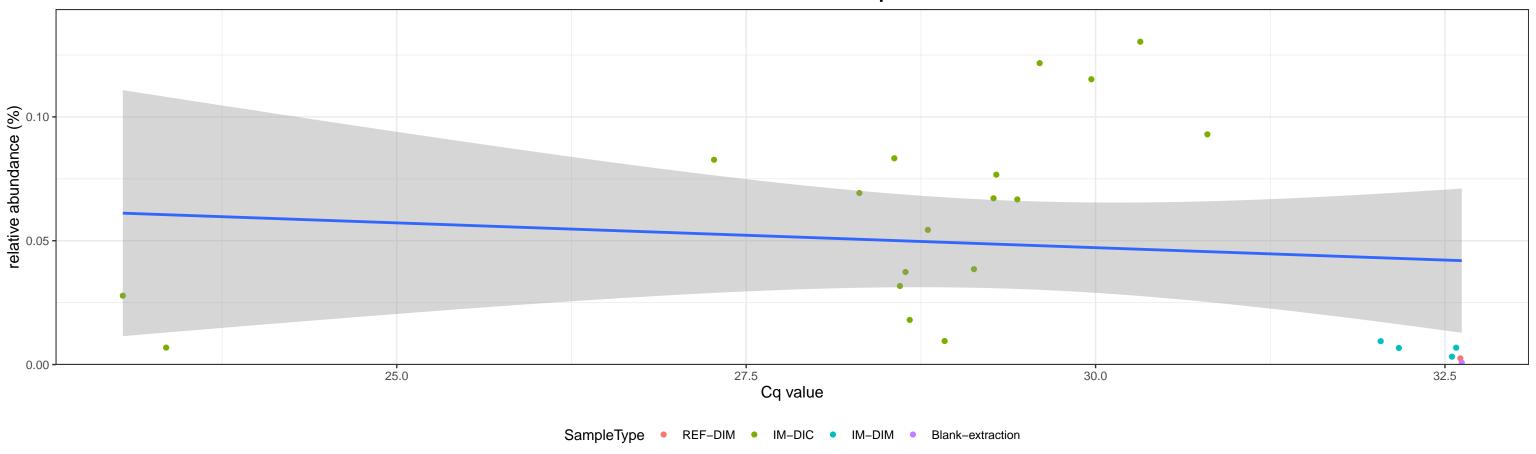


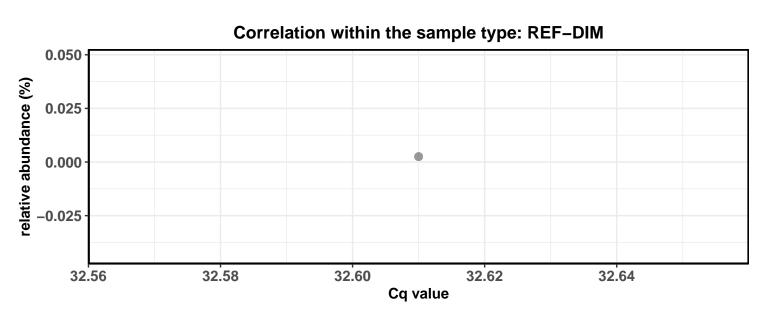




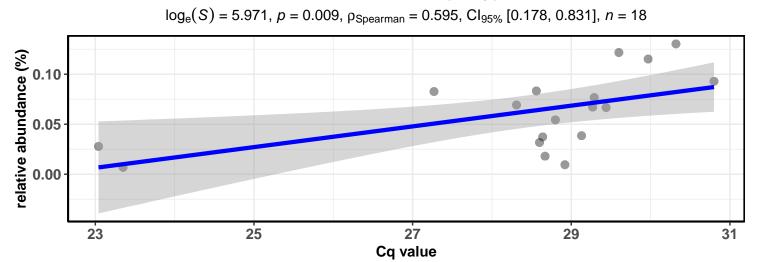
D\_0\_Bacteria; D\_1\_Firmicutes; D\_2\_Bacilli; D\_3\_Bacillales; D\_4\_Bacillaceae; D\_5\_Oceanobacillus; Ambiguous\_taxa

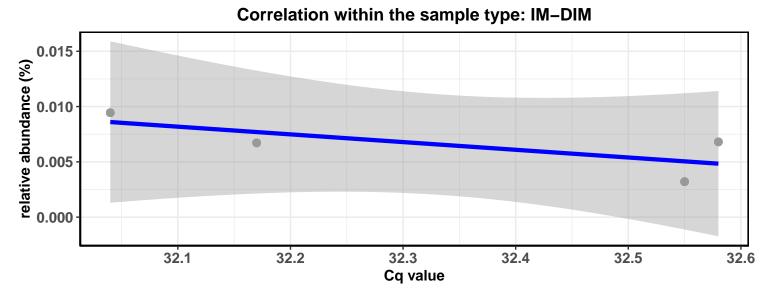






## Correlation within the sample type: IM-DIC





D\_0\_Bacteria; D\_1\_Actinobacteria; D\_2\_Actinobacteria; D\_3\_Propionibacteriales; D\_4\_Propionibacteriaceae; D\_5\_Cutibacterium

