



# Sample QC Report

## 4 Bacteria mRNA Samples

Report Date: 2021-06-15

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### 1. Project General Information

Project Name	4 Bacteria mRNA Sequencing
Client	Dr. Ragıp Silme
Test Date	2021-06-13

### 2. QC Methods

Sample Type		<input type="checkbox"/> DNA; <input checked="" type="checkbox"/> RNA; <input type="checkbox"/> smRNA; <input type="checkbox"/> Tissue; <input type="checkbox"/> Library; <input type="checkbox"/> Others
Assay Type	Sample Concentration	<input type="checkbox"/> Qubit Fluorometer; <input type="checkbox"/> Agarose Gel Electrophoresis; <input checked="" type="checkbox"/> Nanodrop; <input checked="" type="checkbox"/> Agilent 2100 <input type="checkbox"/> Agilent 5400
	Sample Integrity	<input checked="" type="checkbox"/> Agilent 2100; <input type="checkbox"/> Agarose Gel Electrophoresis; <input type="checkbox"/> Agilent 5400
	Sample Purity	<input type="checkbox"/> Nanodrop; <input checked="" type="checkbox"/> Agarose Gel Electrophoresis; <input checked="" type="checkbox"/> Agilent 2100 <input type="checkbox"/> Agilent 5400

### 3. QC Results

#### 3.1. QC Result Summaries

2021-03-24

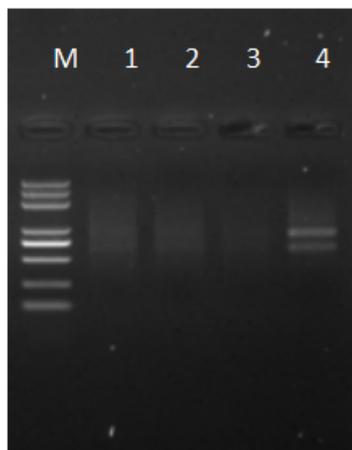
Sample Name	Sample ID	Library	Conc (ng/μl)	Vol (μl)	Amt. ( μg) Min≥3	RIN Min≥6.0	Conclusion	Note
BF-1	FZTR210101587-1B	Prokaryote mRNA	273	32	8.736	9.80	A	-
BF-2	FZTR210101588-1B	Prokaryote mRNA	244	32	7.808	9.50	A	-
B-1	FZTR210101589-1B	Prokaryote mRNA	6	30	0.18	4.00	D	RIN Failed, Insufficient total amount
B-2	FZTR210101590-1B	Prokaryote mRNA	24	30	0.72	7.90	C	Insufficient total amount

#### 3.2. Agarose Gel Electrophoresis Results

##### 3.2.1. Electrophoresis Condition

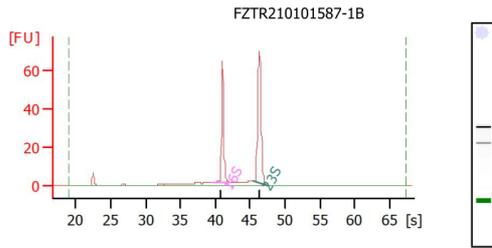
Gel Conc: 1%, Voltage: 180v, Run Time: 16min

##### 3.2.2. Electrophoresis Results



Notes: Marker M: Trans 2k plus DNA ladder; Sample 1-4 loaded 5μl

##### 3.2.3. Agilent 2100 Analysis Results

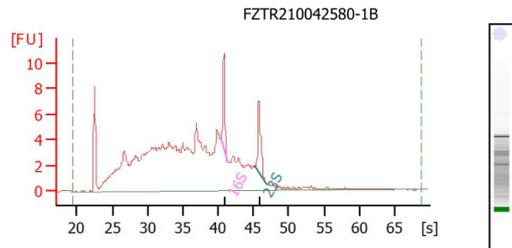


**Overall Results for sample 2 :** FZTR210101587-1B

RNA Area: 200.0  
 RNA Concentration: 273 ng/µl  
 rRNA Ratio [23s / 16s]: 1.6  
 RNA Integrity Number (RIN): 9.8 (B.02.10)  
 Result Flagging Color:    
 Result Flagging Label: RIN: 9.80

**Fragment table for sample 2 :** FZTR210101587-1B

Name	Start Time [s]	End Time [s]	Area	% of total Area
16S	39.48	42.22	56.2	28.1
23S	45.34	47.39	91.4	45.7

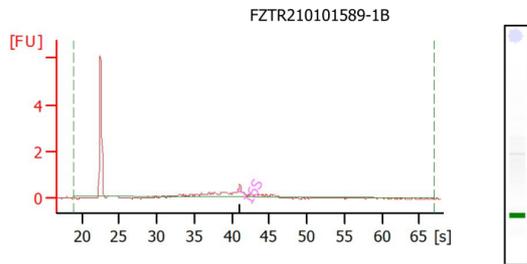


**Overall Results for sample 10 :** FZTR210042580-1B

RNA Area: 196.4  
 RNA Concentration: 220 ng/µl  
 rRNA Ratio [23s / 16s]: 1.1  
 RNA Integrity Number (RIN): 4.4 (B.02.10, Anomaly Threshold(s) manually adapted)  
 Result Flagging Color:    
 Result Flagging Label: RIN: 4.40

**Fragment table for sample 10 :** FZTR210042580-1B

Name	Start Time [s]	End Time [s]	Area	% of total Area
16S	40.46	41.31	5.6	2.9
23S	45.25	46.80	6.0	3.1

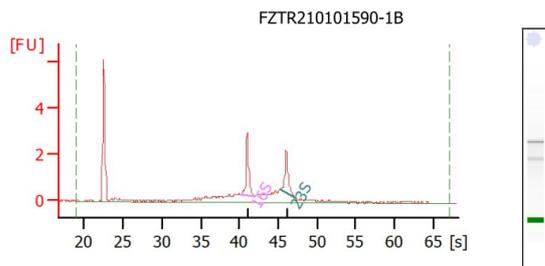


**Overall Results for sample 4 :** FZTR210101589-1B

RNA Area: 4.6  
 RNA Concentration: 6 ng/µl  
 rRNA Ratio [23s / 16s]: 0.0  
 RNA Integrity Number (RIN): 4 (B.02.10)  
 Result Flagging Color:    
 Result Flagging Label: RIN:4

**Fragment table for sample 4 :** FZTR210101589-1B

Name	Start Time [s]	End Time [s]	Area	% of total Area
16S	40.82	41.45	0.3	5.6



**Overall Results for sample 5 :** FZTR210101590-1B

RNA Area: 17.6  
 RNA Concentration: 24 ng/µl  
 rRNA Ratio [23s / 16s]: 0.8  
 RNA Integrity Number (RIN): 7.9 (B.02.10)  
 Result Flagging Color:    
 Result Flagging Label: RIN: 7.90

**Fragment table for sample 5 :** FZTR210101590-1B

Name	Start Time [s]	End Time [s]	Area	% of total Area
16S	40.23	42.03	2.7	15.4
23S	45.24	47.34	2.2	12.5

## Notes

The test result is a comprehensive evaluation based on sample quality requirements for library construction and sequencing. The test result based on the “RNA Samples QC Criteria” explains whether the RNA sample meets the requirement of library construction.

- a) A: The sample is qualified and the library can be prepared regularly;
- b) C: The sample does not totally meet the requirements of library construction and sequencing. We can try to construct library but the sequencing quality is not guaranteed.
- c) D: It is highly recommended that the client resend the sample or the library could be constructed at high risk and the sequencing quality is not guaranteed (not recommended).

### RNA Samples QC Criteria

Sequencing Type	Remarks	Amount (Qubit)	RIN	Volume	Concentration	Purity
Eukaryotic RNA-seq	Strongly Recommended*	≥2 µg	≥6.8 (Animals)	≥20 µL	≥50ng/µL	No degradation or DNA contamination
	Required*	≥1 µg	≥6.3 (Plants/Fungal)			
Prokaryotic RNA-seq	Strongly Recommended	≥6 µg	≥6.0	≥20 µL	≥50ng/µL	
	Required	≥3 µg				
Eukaryotic Long non-coding RNA-Seq	Strongly Recommended	≥4 µg	≥6.8 (Animals)	≥20 µL	≥50ng/µL	
	Required	≥2 µg	≥6.3 (Plants/Fungal)			
Small RNA-Seq	Strongly Recommended	≥6 µg	≥7.5(Animals)	≥20 µL	≥50ng/µL	
	Required	≥3 µg	≥7 (Plants/Fungal)			

**Note:**

1. Strongly Recommended\*: In case of unforeseen circumstances (lib prep failure, low quality, low amount, etc), double sample amount is highly recommended to avoid re-sending of samples.
2. Required\*: Sample amount required for one time library preparation
3. Sample amount required is based on Qubit. If client uses Nanodrop, the figure is expected to be times difference and this is normal due to the different working principle.