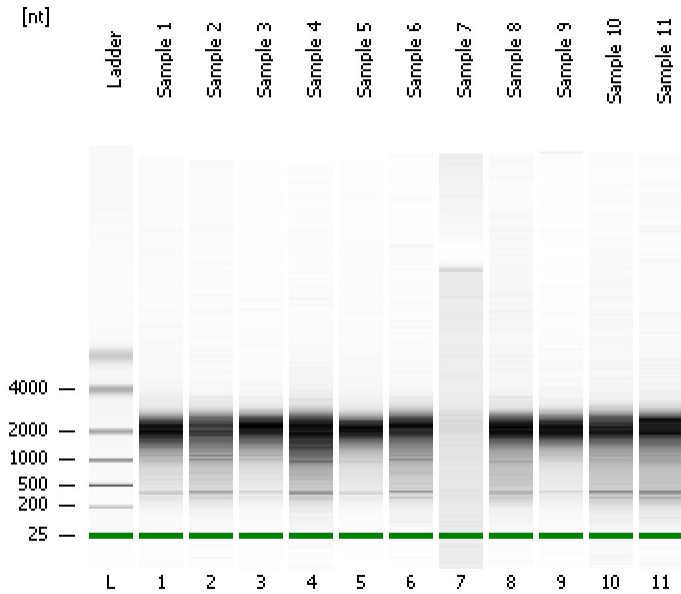


Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electrophoresis File Run Summary



Instrument Information:

Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

Assay Information:

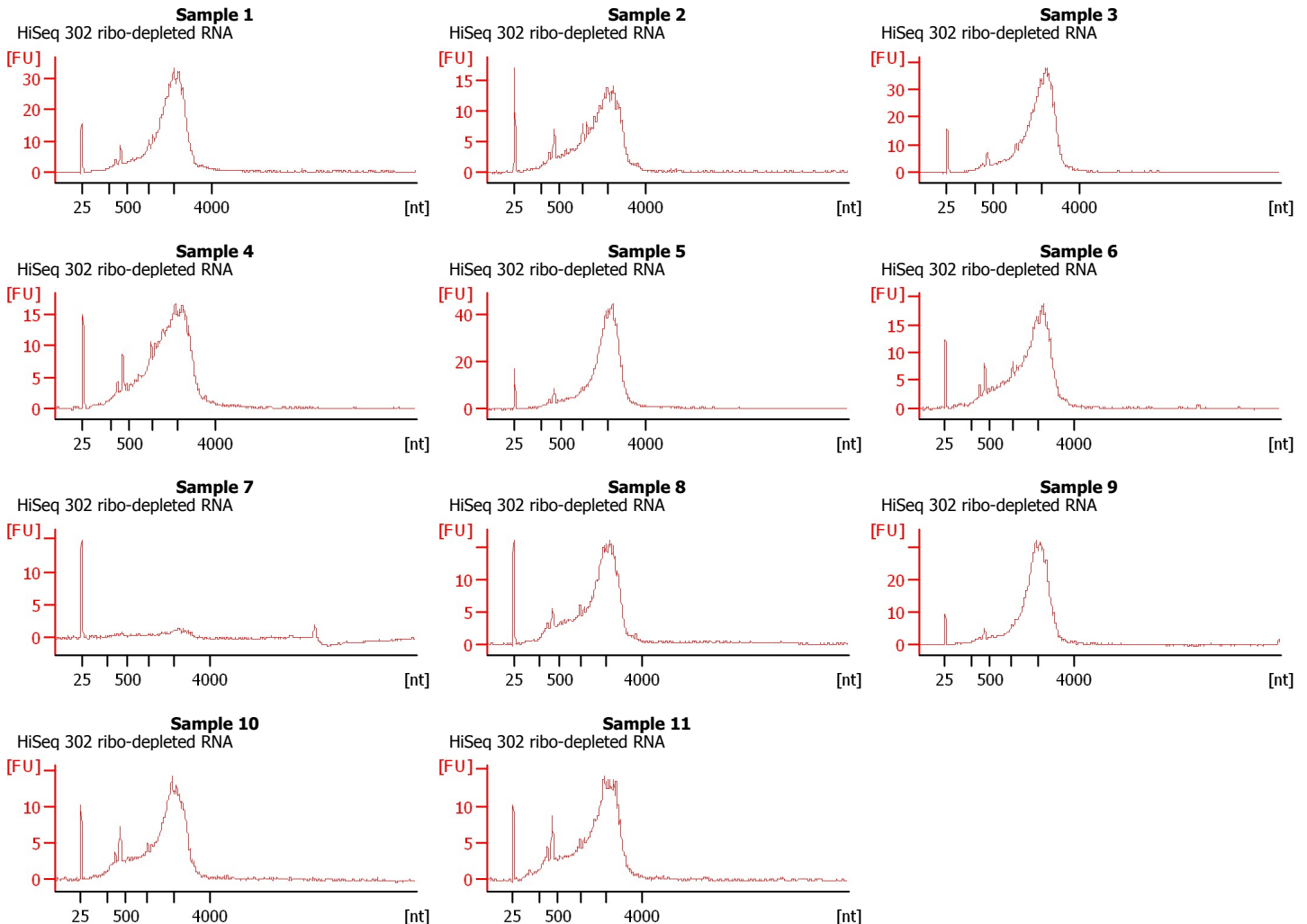
Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\RNA\mRNA Pico Series II.xsy

Assay Class: mRNA Pico
Version: 2.6
Assay Comments: mRNA Analysis pg sensitivity

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Chip Information:

Chip Lot #: Reagent Kit Lot #: Chip Comments:



Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Status	Result Label	Result Color
Sample 1	HiSeq 302 ribo-depleted RNA	✓		
Sample 2	HiSeq 302 ribo-depleted RNA	✓		
Sample 3	HiSeq 302 ribo-depleted RNA	✓		
Sample 4	HiSeq 302 ribo-depleted RNA	✓		
Sample 5	HiSeq 302 ribo-depleted RNA	✓		
Sample 6	HiSeq 302 ribo-depleted RNA	✓		
Sample 7	HiSeq 302 ribo-depleted RNA	✓		
Sample 8	HiSeq 302 ribo-depleted RNA	✓		
Sample 9	HiSeq 302 ribo-depleted RNA	✓		
Sample 10	HiSeq 302 ribo-depleted RNA	✓		
Sample 11	HiSeq 302 ribo-depleted RNA	✓		
Ladder		✓		

Chip Lot #**Reagent Kit Lot #****Chip Comments :**

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electrophoresis Assay Details

General Analysis Settings

Number of Available Sample and Ladder Wells (Max.) : 12
Minimum Visible Range [s] : 14
Maximum Visible Range [s] : 85
Start Analysis Time Range [s] : 15
End Analysis Time Range [s] : 84
Ladder Concentration [pg/μl] : 1000
Lower Marker Concentration [pg/μl] : 0
Upper Marker Concentration [pg/μl] : 0
Used Lower Marker for Quantitation
Standard Curve Fit is Logarithmic
Show Data Aligned to Lower Marker

Integrator Settings

Integration Start Time [s] : 15
Integration End Time [s] : 84
Slope Threshold : 0.2
Height Threshold [FU] : 0.5
Area Threshold : 0.1
Width Threshold [s] : 0.2
Baseline Plateau [s] : 0.5

Filter Settings

Filter Width [s] : 0.5
Polynomial Order : 4

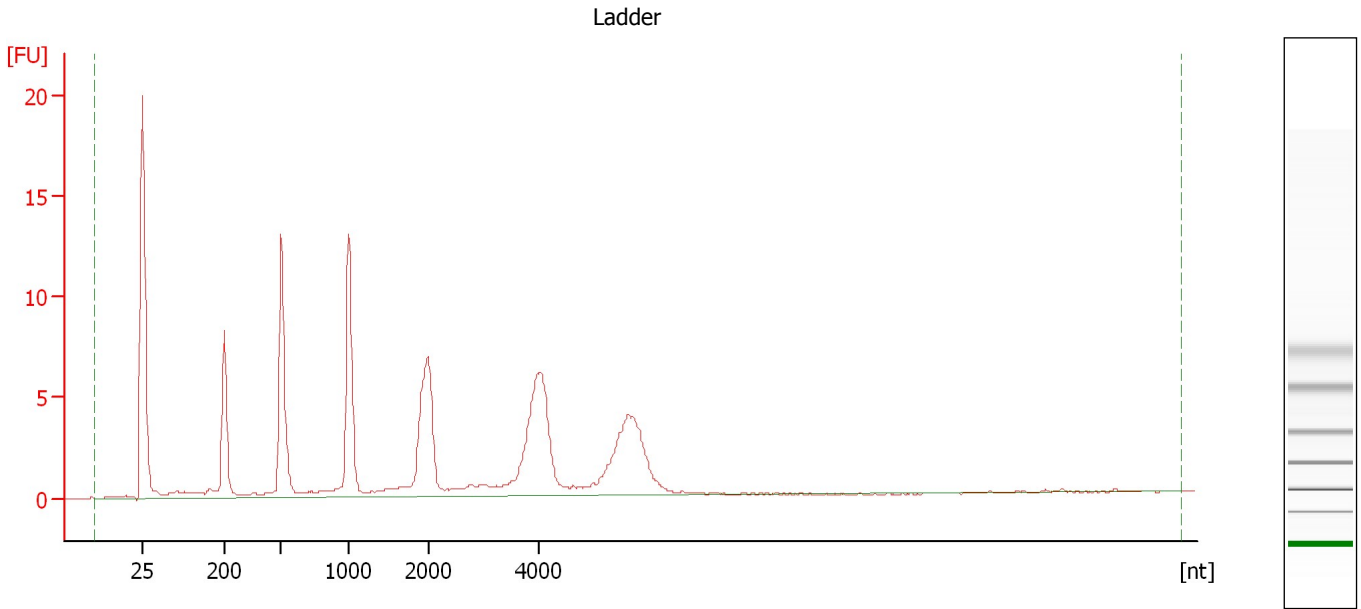
Ladder

Ladder Peak	Size
1	25
2	200
3	500
4	1000
5	2000
6	4000

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary



Overall Results for Ladder

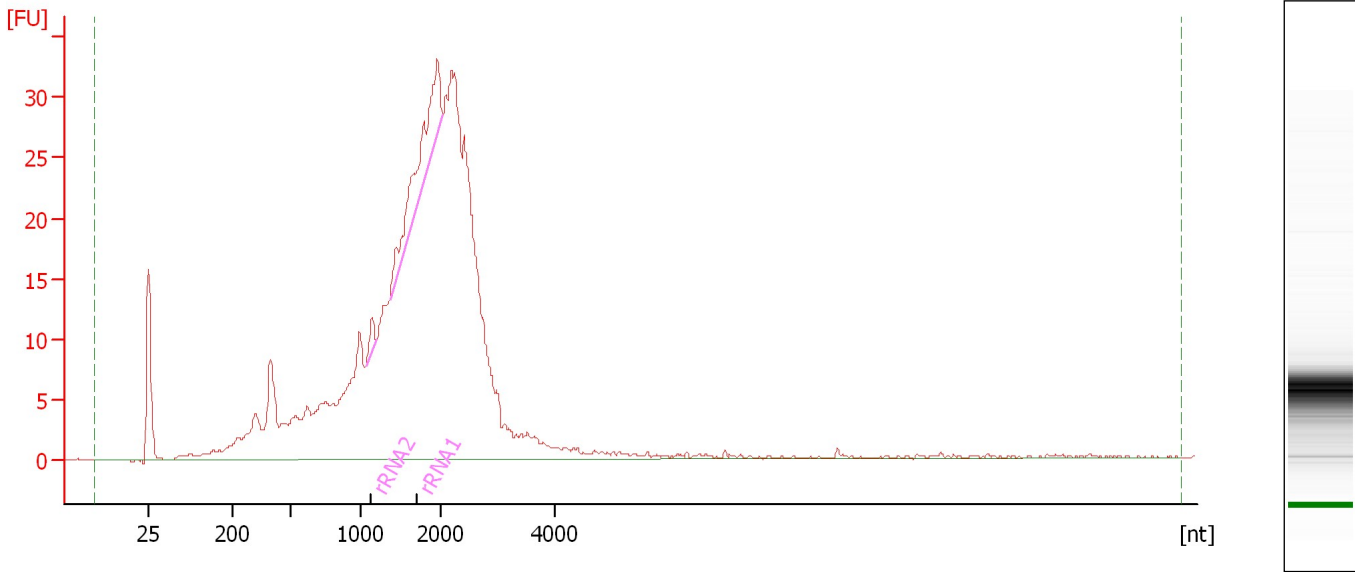
RNA Area: 123.9 RNA Concentration: 1,000 pg/μl

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 1 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 1 : Sample 1

RNA Area: 606.0 rRNA Contamination: 5.2 %
RNA Concentration: 4,892 pg/μl

Fragment table for sample 1 : Sample 1

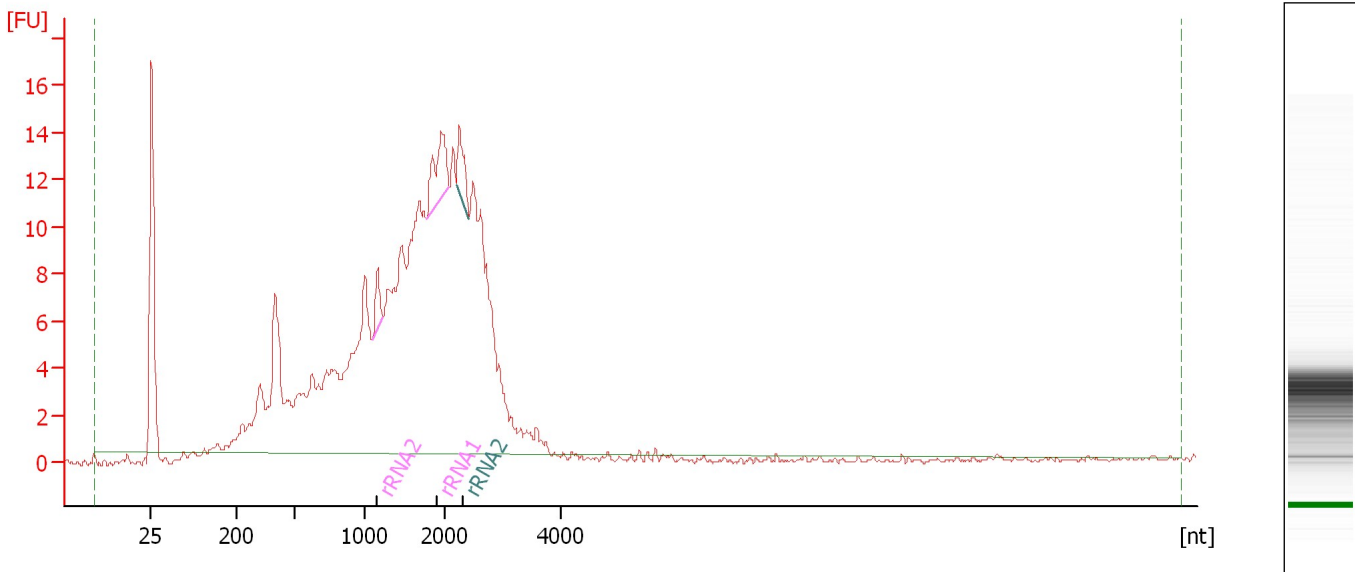
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,074	1,213	2.6	0.4
rRNA1	1,371	2,048	29.0	4.8

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 2 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 2 : Sample 2

RNA Area: 300.0 rRNA Contamination: 4.1 %
RNA Concentration: 2,422 pg/μl

Fragment table for sample 2 : Sample 2

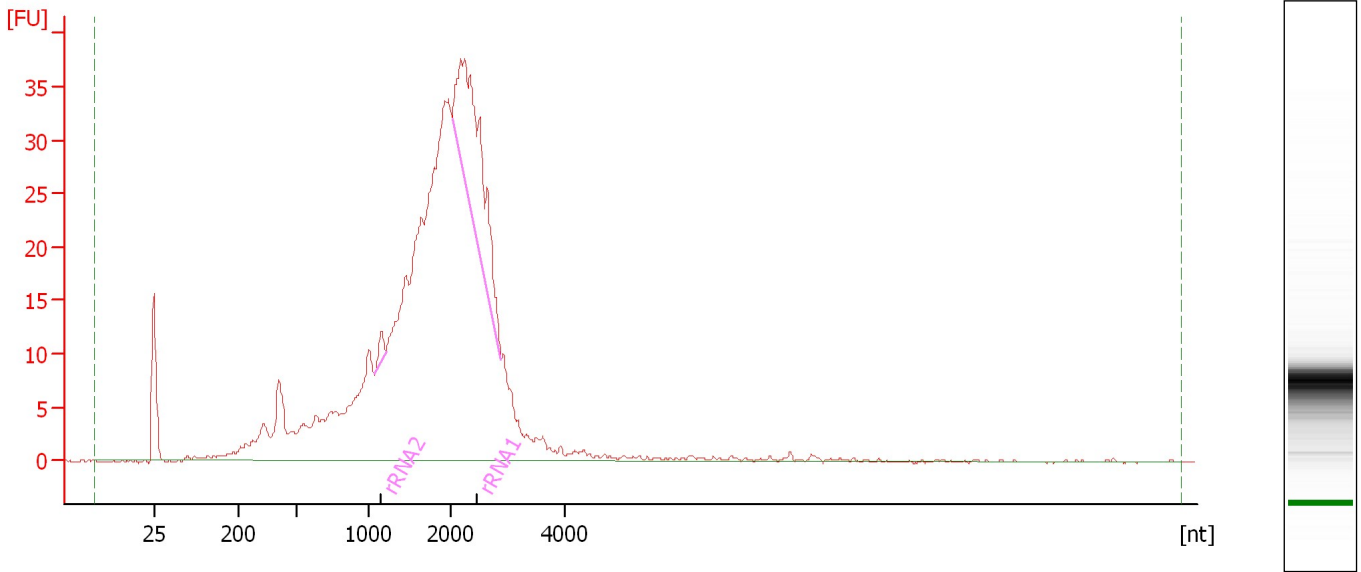
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,102	1,240	2.3	0.8
rRNA1	1,780	2,077	6.5	2.2
rRNA2	2,188	2,411	3.4	1.1

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 3 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 3 : Sample 3

RNA Area: 648.2 rRNA Contamination: 9.8 %
RNA Concentration: 5,232 pg/μl

Fragment table for sample 3 : Sample 3

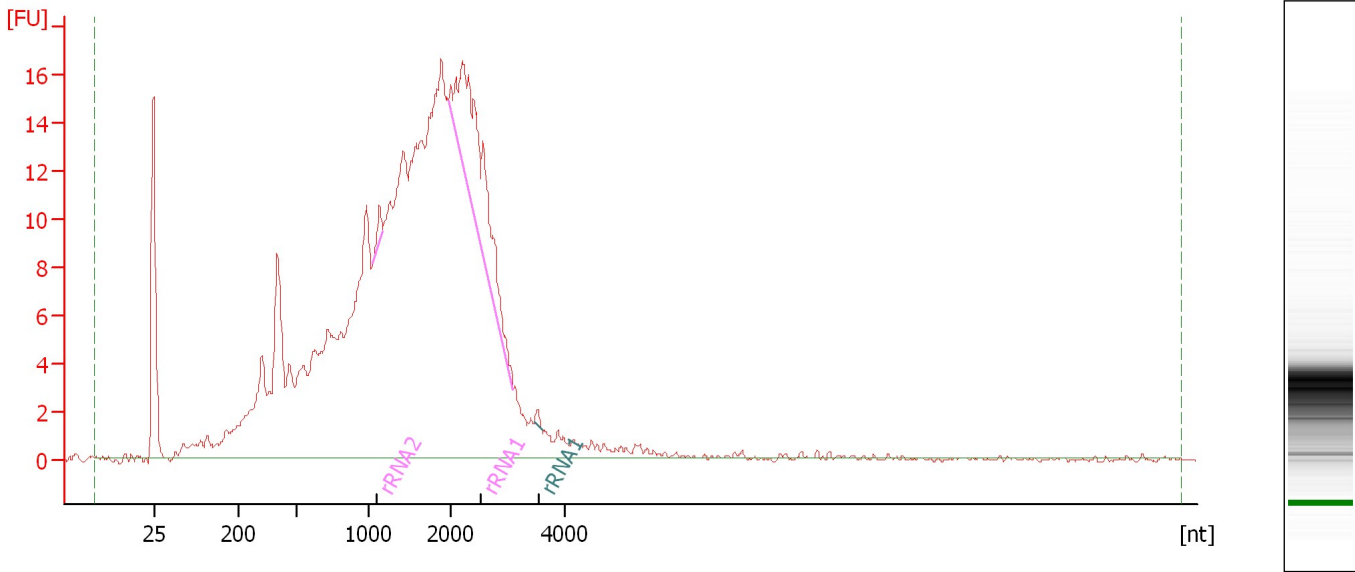
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,091	1,218	2.8	0.4
rRNA1	2,038	2,892	60.5	9.3

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 4 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 4 : Sample 4

RNA Area: 436.8 rRNA Contamination: 6.2 %
RNA Concentration: 3,526 pg/μl

Fragment table for sample 4 : Sample 4

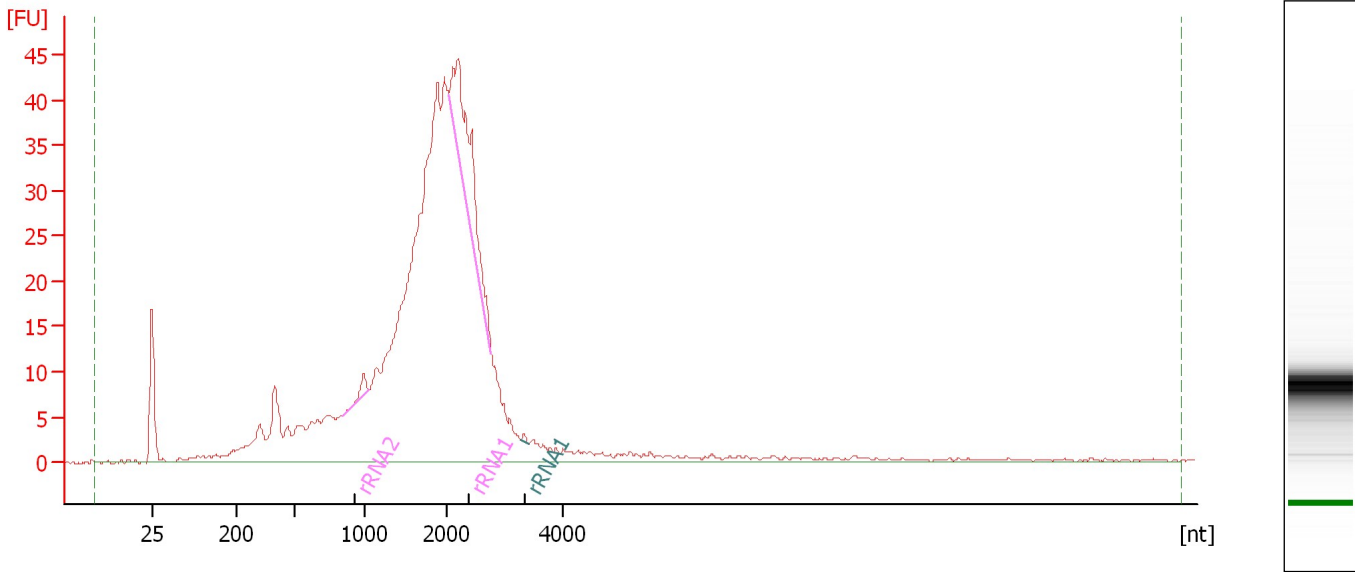
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,062	1,179	1.2	0.3
rRNA1	1,997	3,099	25.6	5.9
rRNA1	3,471	3,595	0.4	0.1

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 5 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 5 : Sample 5

RNA Area: 724.5 rRNA Contamination: 5.8 %
RNA Concentration: 5,848 pg/μl

Fragment table for sample 5 : Sample 5

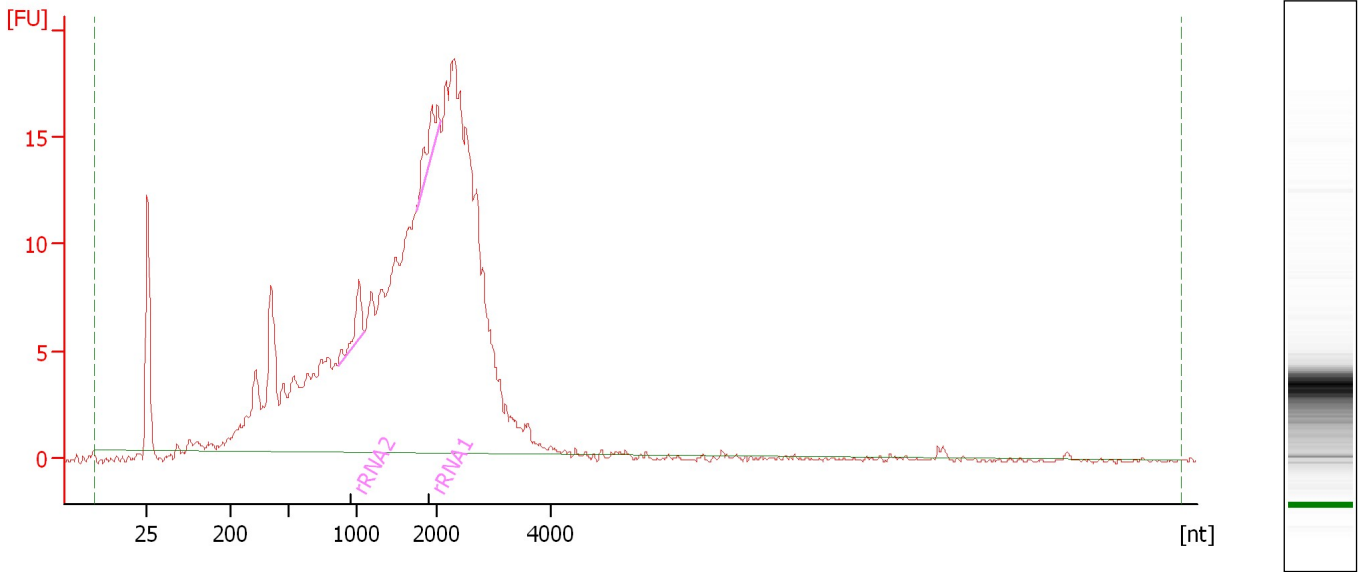
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	844	1,046	3.1	0.4
rRNA1	2,050	2,770	38.1	5.3
rRNA1	3,283	3,435	0.5	0.1

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 6 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 6 : Sample 6

RNA Area: 372.8 rRNA Contamination: 2.2 %
RNA Concentration: 3,009 pg/μl

Fragment table for sample 6 : Sample 6

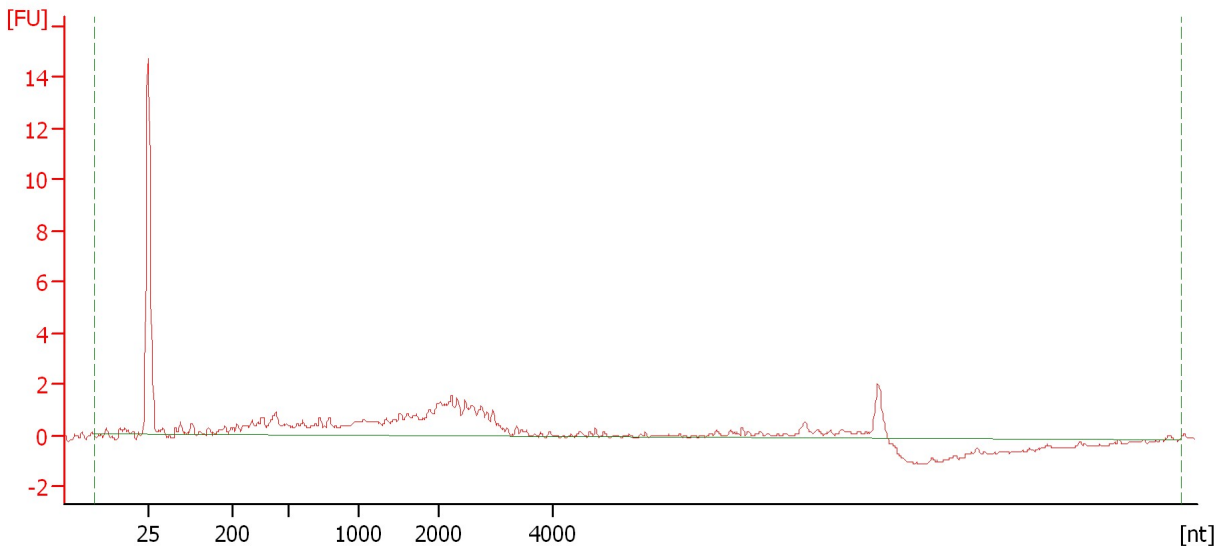
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	860	1,098	3.9	1.0
rRNA1	1,744	2,046	4.3	1.1

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 7 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 7 : Sample 7

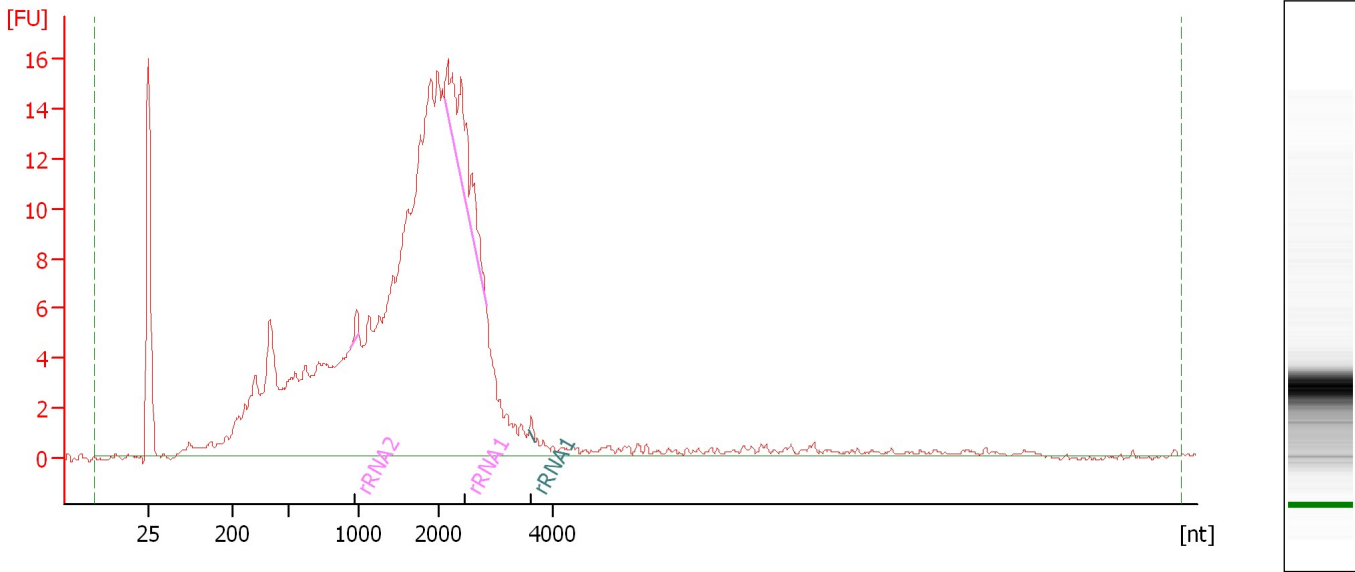
RNA Area: 43.2 rRNA Contamination: 0.0 %
RNA Concentration: 349 pg/μl

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 8 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 8 : Sample 8

RNA Area: 343.9 rRNA Contamination: 4.5 %
RNA Concentration: 2,776 pg/μl

Fragment table for sample 8 : Sample 8

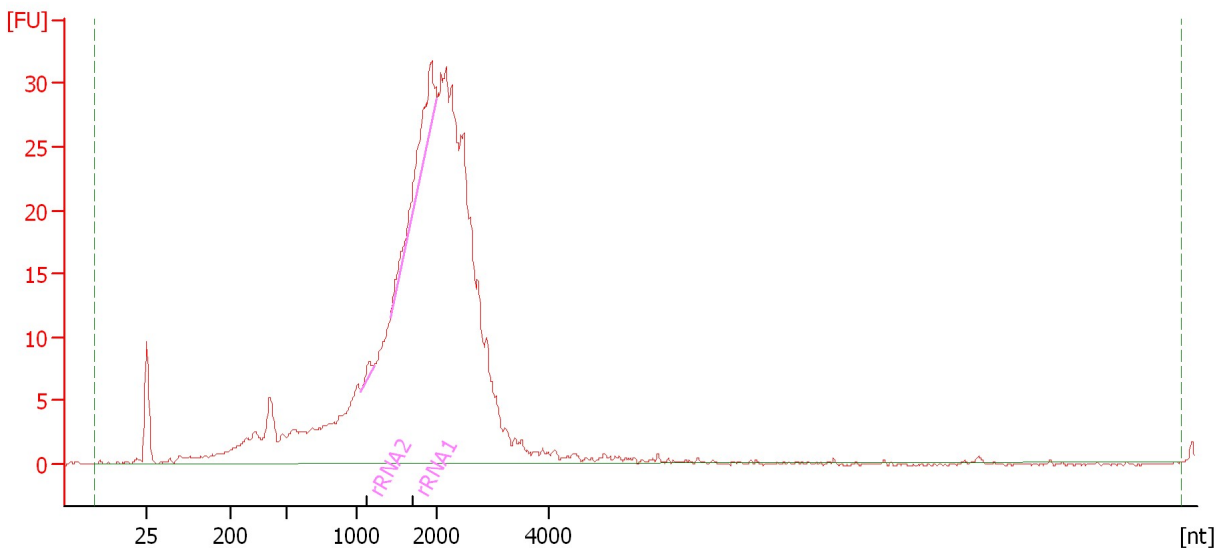
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	949	1,012	0.9	0.3
rRNA1	2,089	2,833	14.3	4.1
rRNA1	3,590	3,688	0.3	0.1

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 9 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 9 : Sample 9

RNA Area: 529.4 rRNA Contamination: 3.6 %
RNA Concentration: 4,273 pg/μl

Fragment table for sample 9 : Sample 9

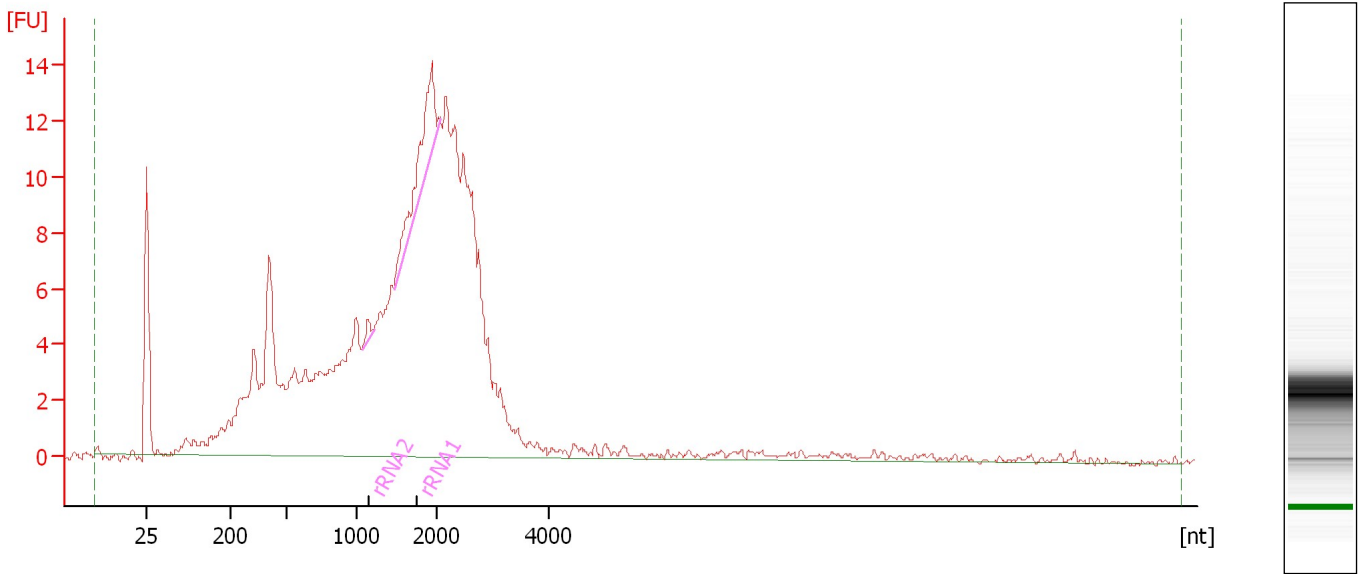
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,065	1,225	1.2	0.2
rRNA1	1,434	2,032	17.6	3.3

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 10 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 10 : Sample 10

RNA Area: 306.8 rRNA Contamination: 3.3 %
RNA Concentration: 2,476 pg/μl

Fragment table for sample 10 : Sample 10

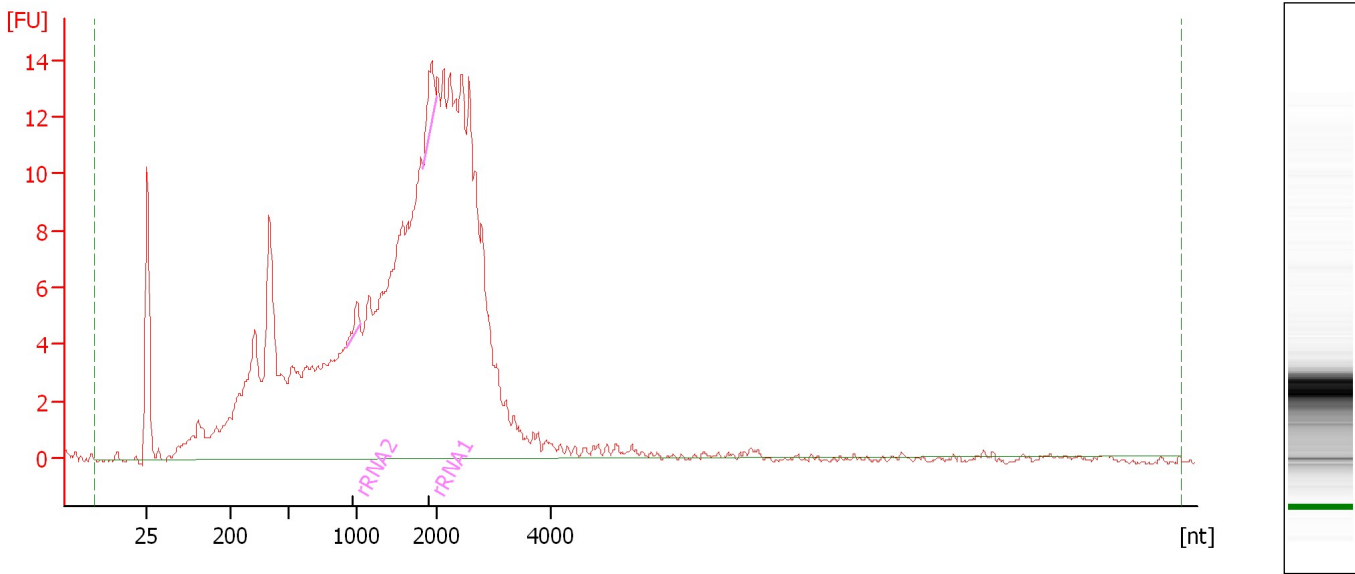
Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	1,085	1,225	0.7	0.2
rRNA1	1,474	2,074	9.3	3.0

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Electropherogram Summary Continued ...

Sample 11 [HiSeq 302 ribo-depleted RNA]



Overall Results for sample 11 : Sample 11

RNA Area: 339.0 rRNA Contamination: 1.1 %
RNA Concentration: 2,736 pg/μl

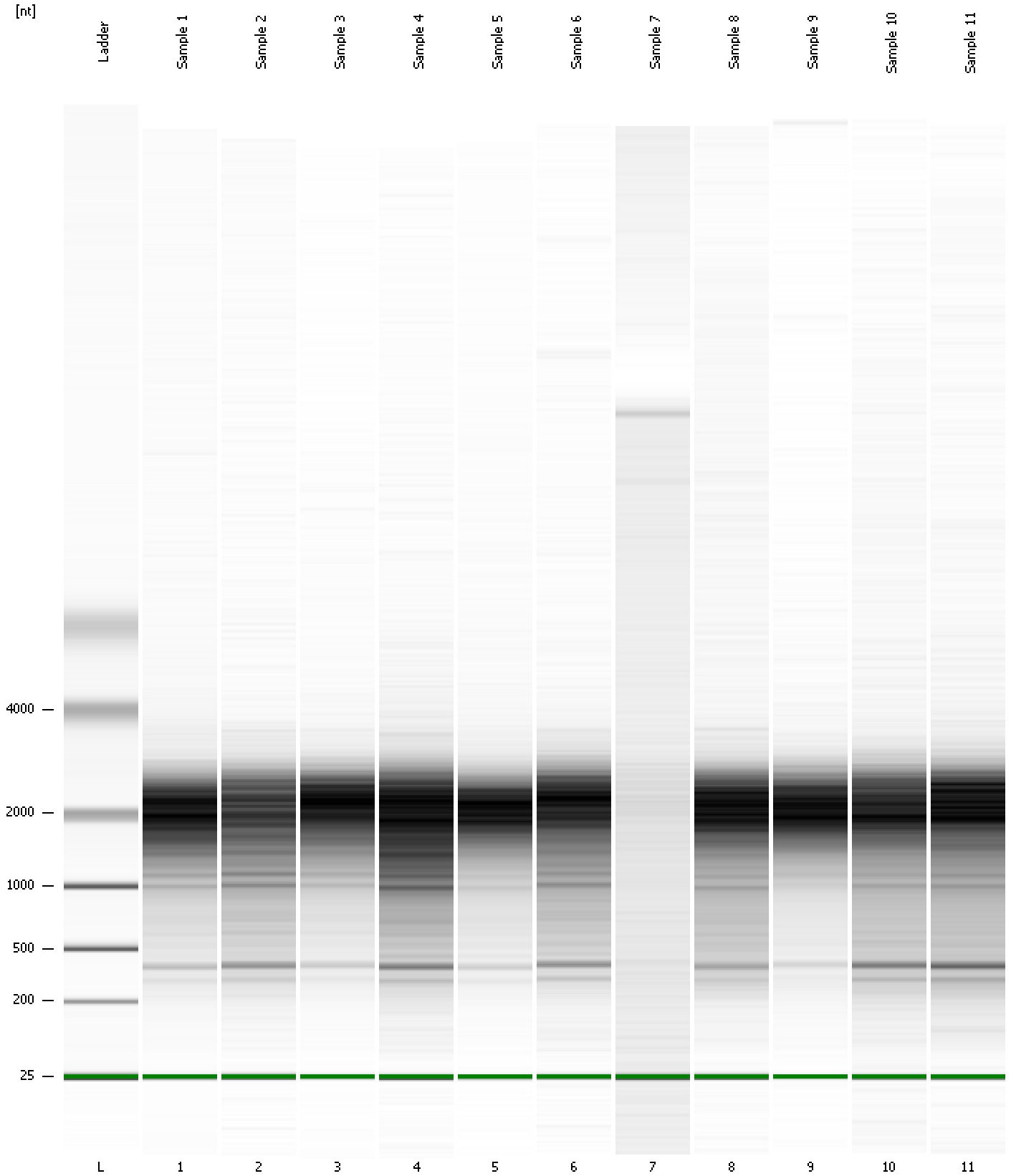
Fragment table for sample 11 : Sample 11

Name	Start Size [nt]	End Size [nt]	Area	% of total Area
rRNA2	918	1,038	1.0	0.3
rRNA1	1,824	1,983	2.7	0.8

Assay Class: mRNA Pico
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
Modified: 1/14/2016 11:24:51 AM

Gel Image



Assay Class: mRNA Pico
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad

Created: 1/14/2016 10:58:58 AM
 Modified: 1/14/2016 11:24:51 AM

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 12)		Instrument	Run		1/14/2016 11:24:51 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-01-14\2016-01-14_001.xad)		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/14/2016 10:59:03 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1