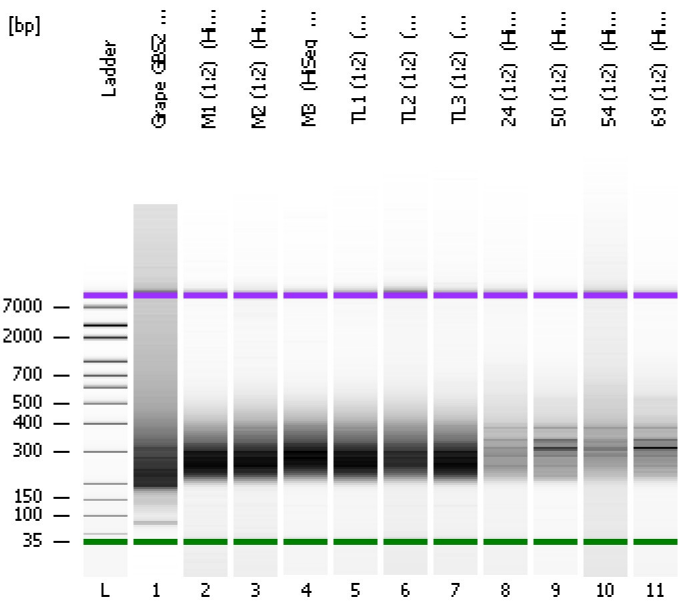
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad

Created: 3/13/2015 4:01:51 PM
Modified: 3/13/2015 4:47:01 PM

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\dsDNA\High Sensitivity DNA.xsy

Assay Class: High Sensitivity DNA Assay

Version: 1.03

Assay Comments: Copyright © 2003-2010 Agilent Technologies

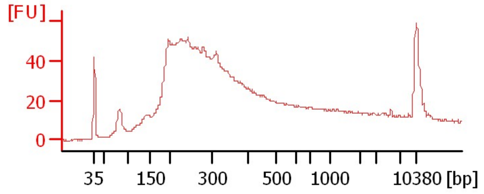
Chip Information:

Chip Lot #:

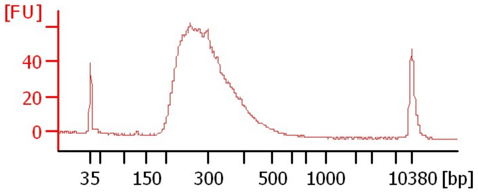
Reagent Kit Lot #:

Chip Comments:

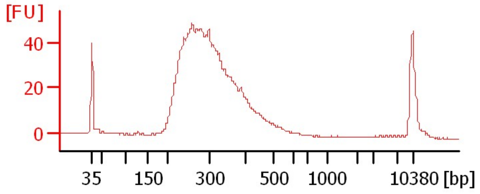
Grape GBS2 1/2x
CBA



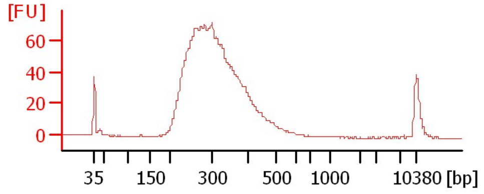
M1 (1:2) (HiSeq_70)
ribo-dep ssRNA libs_TruSeq_Sciclone



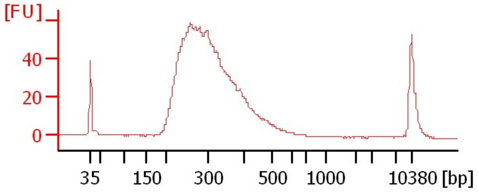
M2 (1:2) (HiSeq_70)
ribo-dep ssRNA libs_TruSeq_Sciclone



M3 (HiSeq_70)
ribo-dep ssRNA libs_TruSeq_Sciclone



TL1 (1:2) (HiSeq_70)
ribo-dep ssRNA libs_TruSeq_Sciclone



TL2 (1:2) (HiSeq_70)
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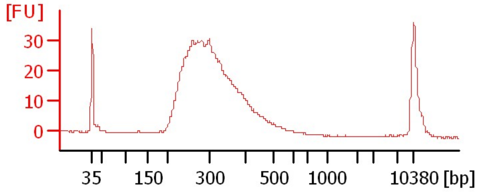
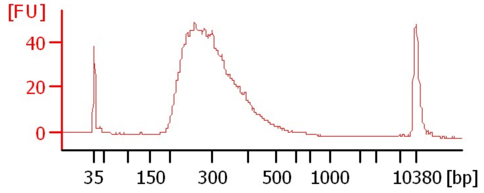
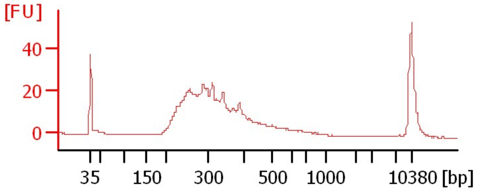


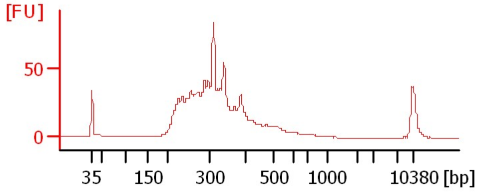
TL3 (1:2) (HiSeq_70)
ribo-dep ssRNA libs_TruSeq_Sciclone



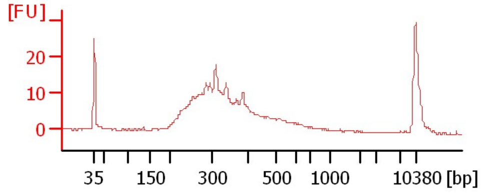
24 (1:2) (HiSeq_67)
ribo-dep ssRNA libs_TruSeq_Sciclone



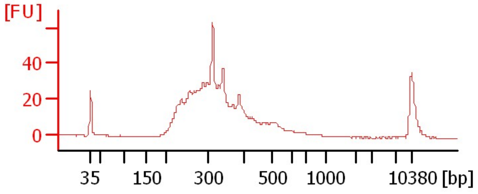
50 (1:2) (HiSeq_67)
ribo-dep ssRNA libs_TruSeq_Sciclone



54 (1:2) (HiSeq_67)
ribo-dep ssRNA libs_TruSeq_Sciclone



69 (1:2) (HiSeq_67)
ribo-dep ssRNA libs_TruSeq_Sciclone



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad
Created: 3/13/2015 4:01:51 PM
Modified: 3/13/2015 4:47:01 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	**Sample Comment**	**Rest. Digest**	**Status**	**Observation**	**Result Label**	**Result Color**
Grape GBS2 1/2x	CBA	☐	✓			
M1 (1:2) (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
M2 (1:2) (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
M3 (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
TL1 (1:2) (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
TL2 (1:2) (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
TL3 (1:2) (HiSeq_70)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
24 (1:2) (HiSeq_67)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
50 (1:2) (HiSeq_67)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
54 (1:2) (HiSeq_67)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
69 (1:2) (HiSeq_67)	ribo-dep ssRNA libs_TruSeq_Sciclone	☐	✓			
Ladder		☐	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Electrophoresis Assay Details

General Analysis Settings

Number of Available Sample and Ladder Wells (Max.) : 12
Minimum Visible Range [s] : 32
Maximum Visible Range [s] : 138
Start Analysis Time Range [s] : 33
End Analysis Time Range [s] : 137.5
Ladder Concentration [pg/µl] : 1950
Uses Standard Area for Ladder Fragments
Lower Marker Concentration [pg/µl] : 125
Upper Marker Concentration [pg/µl] : 75
Used Upper Marker for Quantitation
Standard Curve Fit is Point to Point
Show Data Aligned to Lower and Upper Marker

Integrator Settings

Integration Start Time [s] : 33.05
Integration End Time [s] : 137
Slope Threshold : 0.8
Height Threshold [FU] : 5
Area Threshold : 0.1
Width Threshold [s] : 0.6
Baseline Plateau [s] : 0.5

Filter Settings

Filter Width [s] : 0.5
Polynomial Order : 4

Ladder

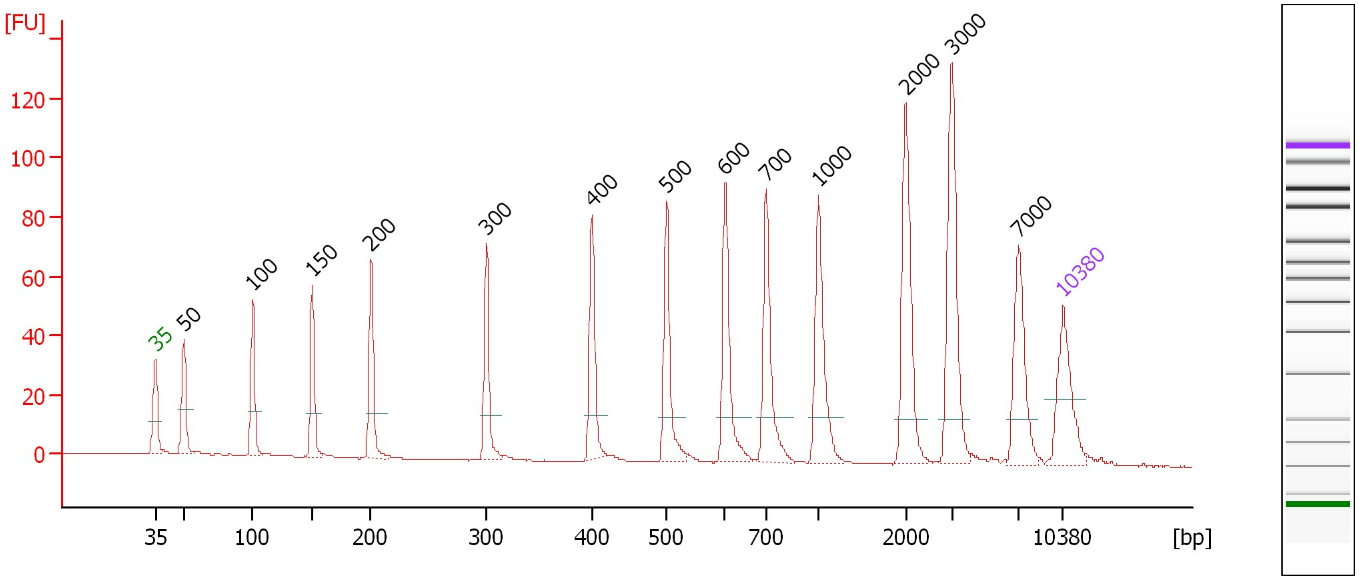
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad

Created: 3/13/2015 4:01:51 PM
Modified: 3/13/2015 4:47:01 PM

Electropherogram Summary

Ladder



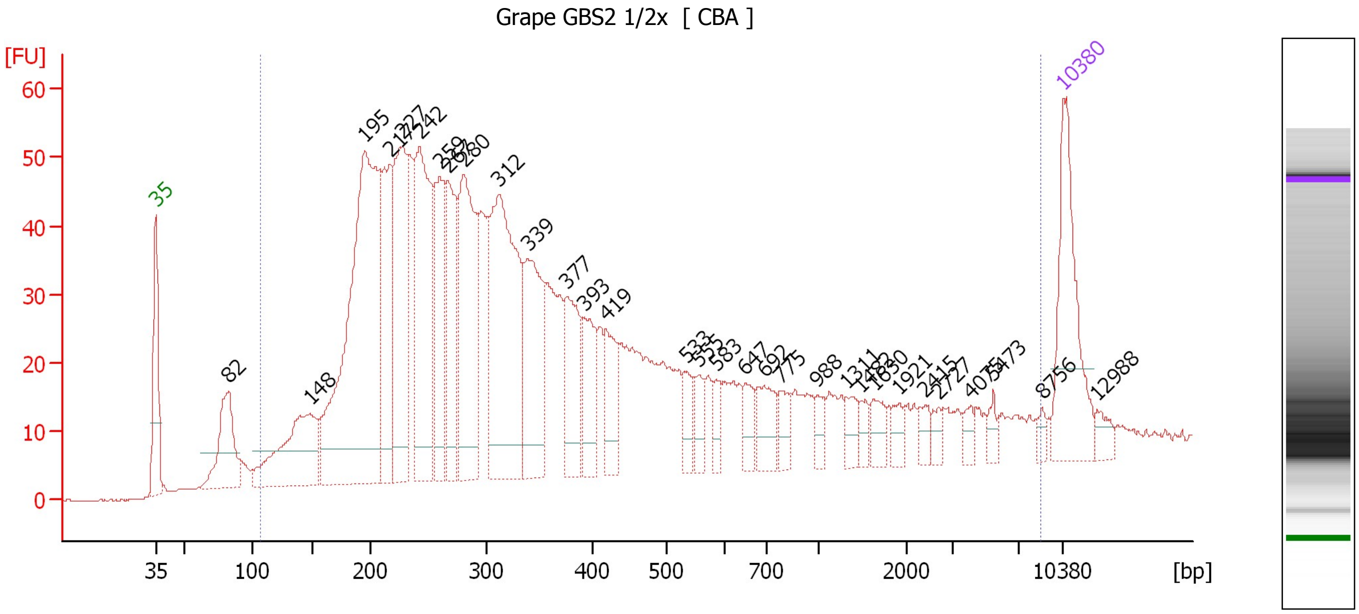
Overall Results for Ladder

Noise: 0.1

Peak table for Ladder

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	∟	50	150.00	4,545.5	Ladder Peak	45.21
3	∟	100	150.00	2,272.7	Ladder Peak	50.51
4	∟	150	150.00	1,515.2	Ladder Peak	55.12
5	∟	200	150.00	1,136.4	Ladder Peak	59.63
6	∟	300	150.00	757.6	Ladder Peak	68.51
7	∟	400	150.00	568.2	Ladder Peak	76.65
8	∟	500	150.00	454.5	Ladder Peak	82.44
9	∟	600	150.00	378.8	Ladder Peak	86.95
10	∟	700	150.00	324.7	Ladder Peak	90.14
11	∟	1,000	150.00	227.3	Ladder Peak	94.16
12	∟	2,000	150.00	113.6	Ladder Peak	100.88
13	∟	3,000	150.00	75.8	Ladder Peak	104.42
14	∟	7,000	150.00	32.5	Ladder Peak	109.57
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...



Overall Results for sample 1 : Grape GBS2 1/2x

Number of peaks found:	31	Corr. Area 1:	1,719.6
Noise:	0.2		

Peak table for sample 1 : Grape GBS2 1/2x

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		82	83.14	1,527.1		48.65
3		148	121.53	1,247.1		54.90
4		195	410.35	3,193.5		59.15
5		217	106.34	744.0		61.10
6		227	155.61	1,040.0		62.00
7		242	181.03	1,131.2		63.40
8		259	96.75	565.2		64.90
9		267	86.73	491.7		65.60
10		280	159.75	863.8		66.75
11		312	219.23	1,066.1		69.45
12		339	105.52	471.4		71.70
13		377	66.58	267.8		74.75
14		393	47.03	181.5		76.05
15		419	39.14	141.5		77.75
16		533	15.59	44.3		83.95
17		555	15.65	42.8		84.90
18		583	13.19	34.3		86.20
19		647	16.78	39.3		88.45
20		692	28.70	62.8		89.90
21		775	15.55	30.4		91.15
22		988	11.39	17.5		94.00
23		1,311	12.12	14.0		96.25
24		1,482	8.30	8.5		97.40
25		1,630	13.24	12.3		98.40

Electropherogram Summary Continued ...

... Peak table for sample 1 : Grape GBS2 1/2x

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		1,921	8.92	7.0		100.35
27		2,415	8.31	5.2		102.35
28		2,727	6.98	3.9		103.45
29		4,075	7.24	2.7		105.80
30		5,473	7.18	2.0		107.60
31		8,756	4.65	0.8		111.35
32	▶	10,380	75.00	10.9	Upper Marker	113.00
33		12,988	0.00	0.0		115.65

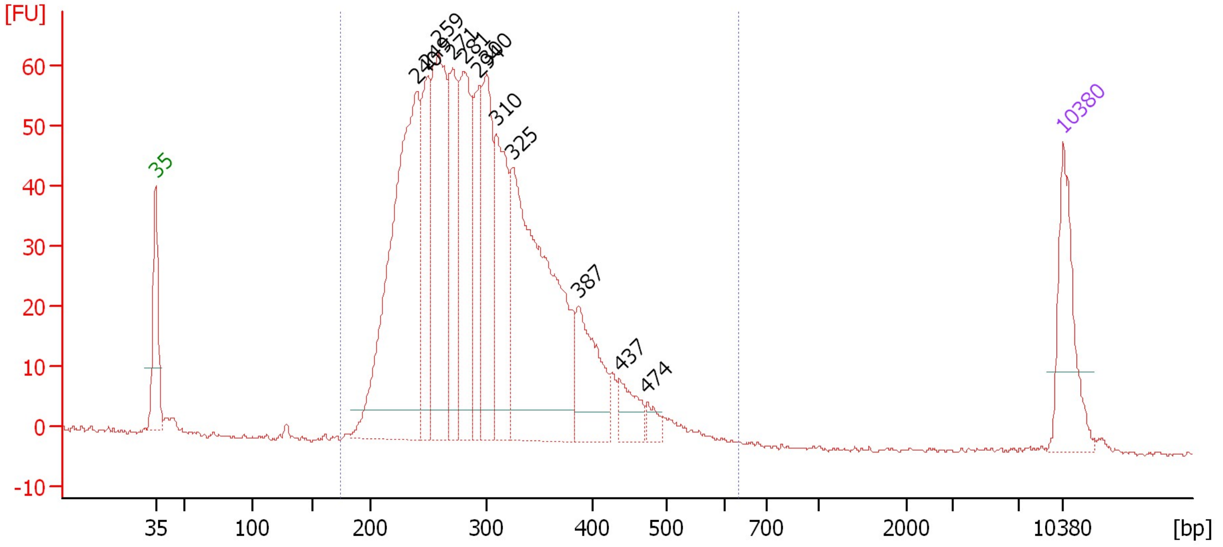
Region table for sample 1 : Grape GBS2 1/2x

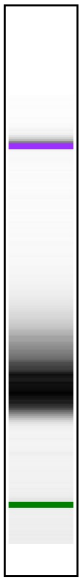
From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
107	688	8,651	1,719.6	14,556.0	94	100.0	2,681.80	🟦

Assay Class:	High Sensitivity DNA Assay	Created:	3/13/2015 4:01:51 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad	Modified:	3/13/2015 4:47:01 PM

Electropherogram Summary Continued ...

M1 (1:2) (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 2 : M1 (1:2) (HiSeq_70)

Number of peaks found:	12	Corr. Area 1:	1,154.0
Noise:	0.3		

Peak table for sample 2 : M1 (1:2) (HiSeq_70)

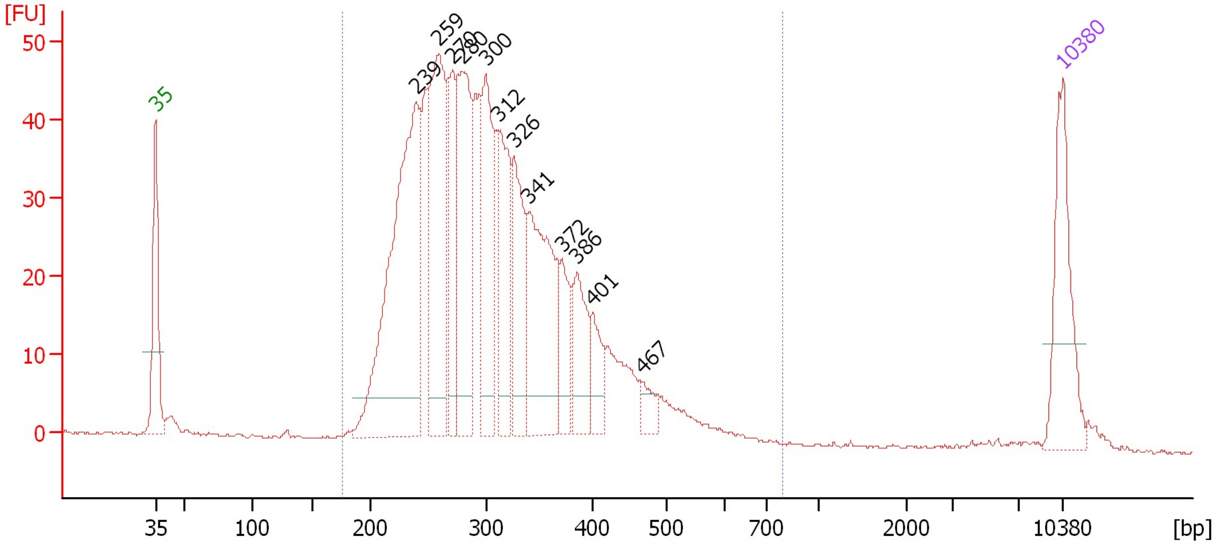
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		240	494.65	3,126.0		63.16
3		249	133.59	813.2		63.97
4		259	254.37	1,490.4		64.83
5		271	139.68	782.2		65.89
6		281	178.25	959.8		66.86
7		294	109.31	563.4		67.97
8		300	162.93	822.2		68.53
9		310	154.01	753.7		69.29
10		325	424.49	1,982.0		70.50
11		387	102.81	402.2		75.62
12		437	37.61	130.3		78.81
13		474	13.74	43.9		80.94
14	▶	10,380	75.00	10.9	Upper Marker	113.00

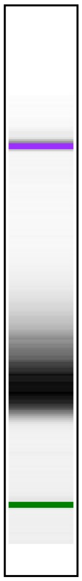
Region table for sample 2 : M1 (1:2) (HiSeq_70)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
174	300	634	1,154.0	11,809.0	99	21.3	2,219.82	🟦

Electropherogram Summary Continued ...

M2 (1:2) (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 3 : M2 (1:2) (HiSeq_70)

Number of peaks found:	12	Corr. Area 1:	950.1
Noise:	0.1		

Peak table for sample 3 : M2 (1:2) (HiSeq_70)

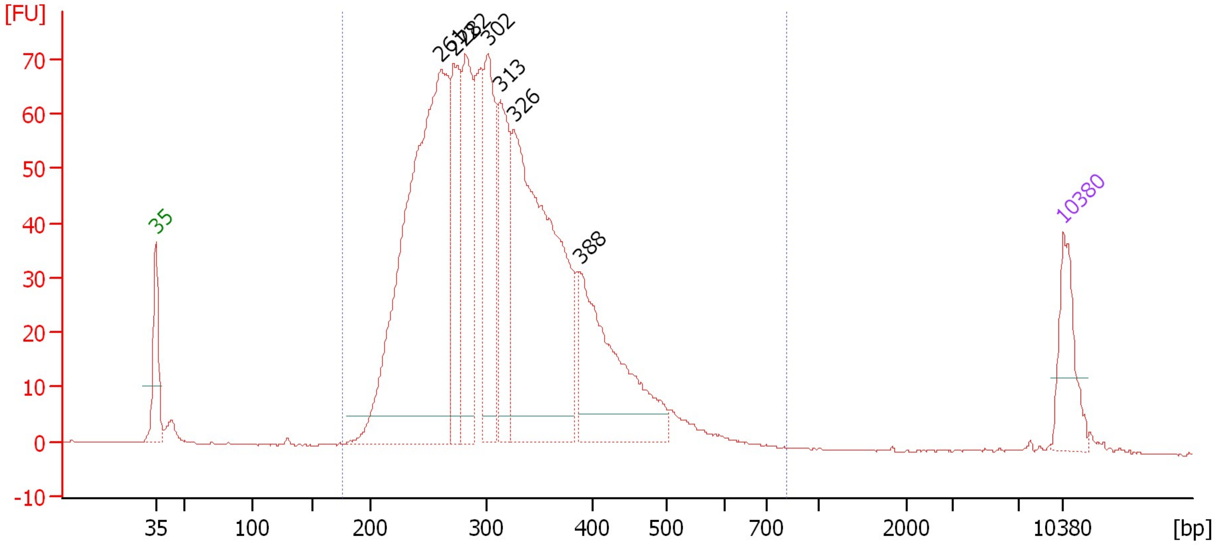
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		239	374.76	2,372.1		63.13
3		259	221.17	1,296.3		64.82
4		270	98.43	552.1		65.85
5		280	168.43	911.6		66.73
6		300	143.98	728.0		68.48
7		312	110.67	538.0		69.46
8		326	100.93	468.9		70.64
9		341	165.43	735.7		71.82
10		372	47.94	195.4		74.35
11		386	61.27	240.4		75.53
12		401	32.43	122.5		76.71
13		467	16.00	51.9		80.52
14	▶	10,380	75.00	10.9	Upper Marker	113.00

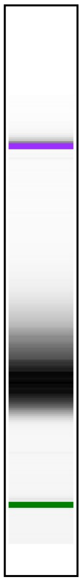
Region table for sample 3 : M2 (1:2) (HiSeq_70)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
175	311	791	950.1	10,028.1	97	24.9	1,923.28	🟦

Electropherogram Summary Continued ...

M3 (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 4 : **M3 (HiSeq 70)**

Number of peaks found:	7	Corr. Area 1:	1,363.0
Noise:	0.1		

Peak table for sample 4 : **M3 (HiSeq 70)**

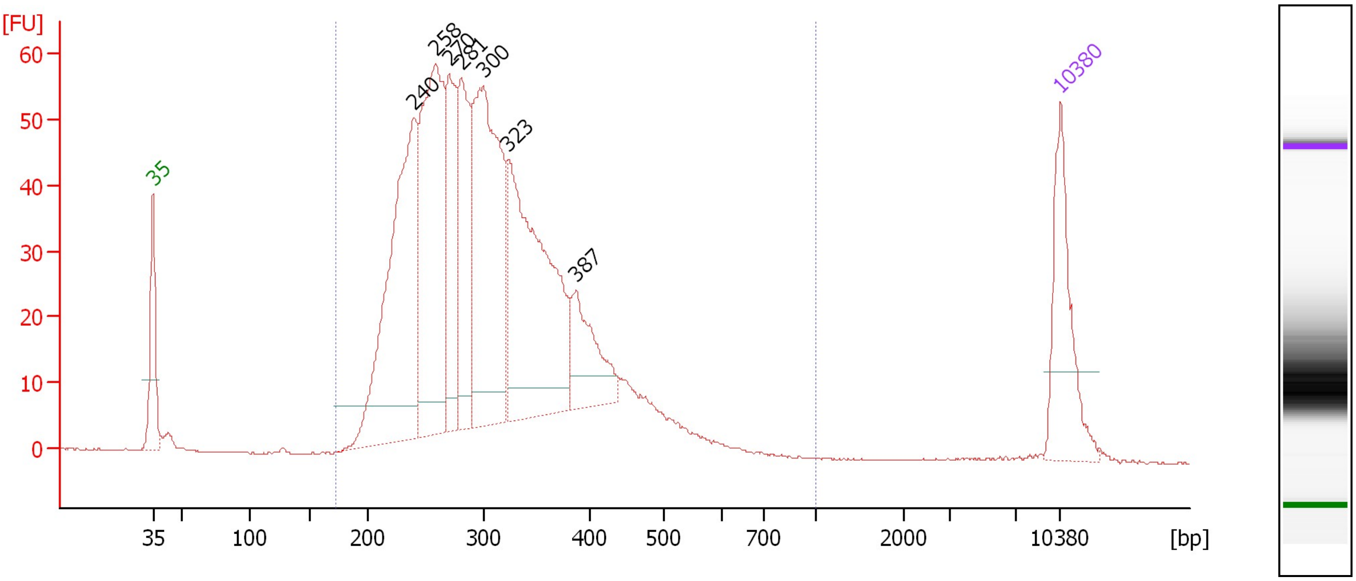
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		261	1,011.40	5,870.2		65.05
3		272	230.90	1,287.4		66.00
4		282	240.84	1,294.7		66.90
5		302	249.47	1,253.4		68.64
6		313	205.20	992.6		69.59
7		326	703.49	3,267.6		70.64
8		388	315.48	1,230.7		75.71
9	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : **M3 (HiSeq 70)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
175	317	809	1,363.0	16,644.0	99	23.4	3,269.09	🟦

Electropherogram Summary Continued ...

TL1 (1:2) (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]



Overall Results for sample 5 : **<u>TL1 (1:2) (HiSeq 70)</u>**

Number of peaks found:	7	Corr. Area 1:	1,122.8
Noise:	0.1		

Peak table for sample 5 : **<u>TL1 (1:2) (HiSeq 70)</u>**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		240	337.64	2,135.9		63.14
3		258	295.35	1,733.0		64.80
4		270	125.66	704.4		65.87
5		281	139.76	754.8		66.78
6		300	307.45	1,553.6		68.49
7		323	299.78	1,404.1		70.42
8		387	76.56	299.5		75.62
9	▶	10,380	75.00	10.9	Upper Marker	113.00

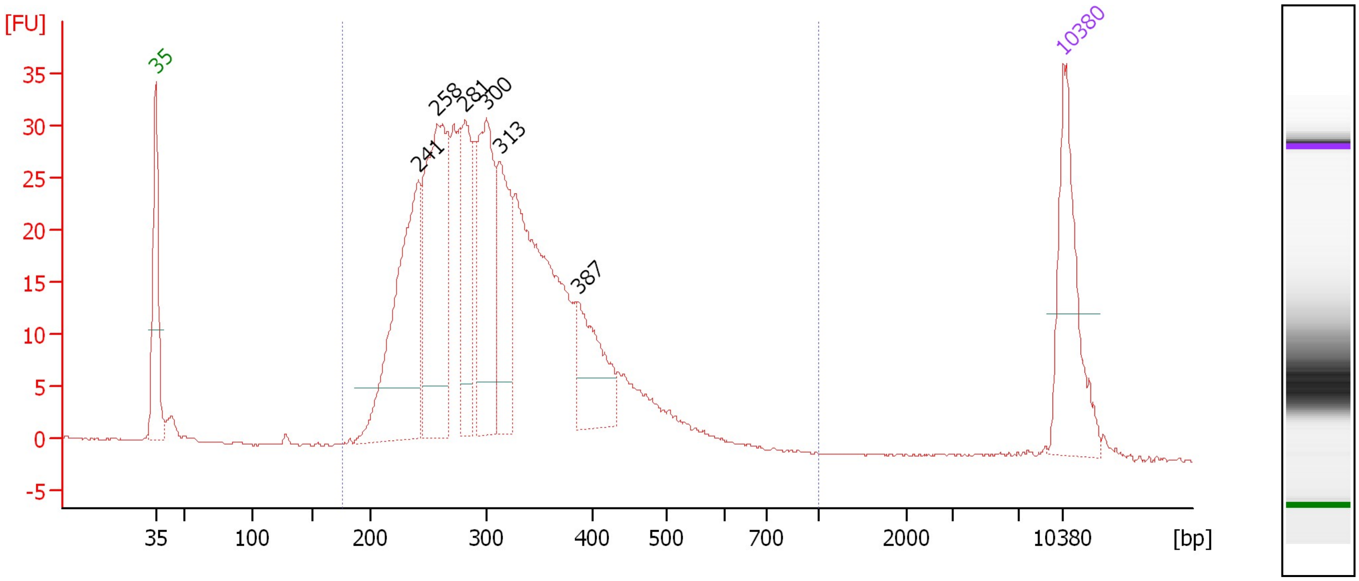
Region table for sample 5 : **<u>TL1 (1:2) (HiSeq 70)</u>**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
172	312	1,000	1,122.8	9,759.5	99	24.7	1,877.14	🟦

Assay Class:	High Sensitivity DNA Assay	Created:	3/13/2015 4:01:51 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad	Modified:	3/13/2015 4:47:01 PM

Electropherogram Summary Continued ...

TL2 (1:2) (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]



Overall Results for sample 6 : <u>TL2 (1:2) (HiSeq_70)</u>

Number of peaks found:	6	Corr. Area 1:	601.4
Noise:	0.1		

Peak table for sample 6 : <u>TL2 (1:2) (HiSeq_70)</u>

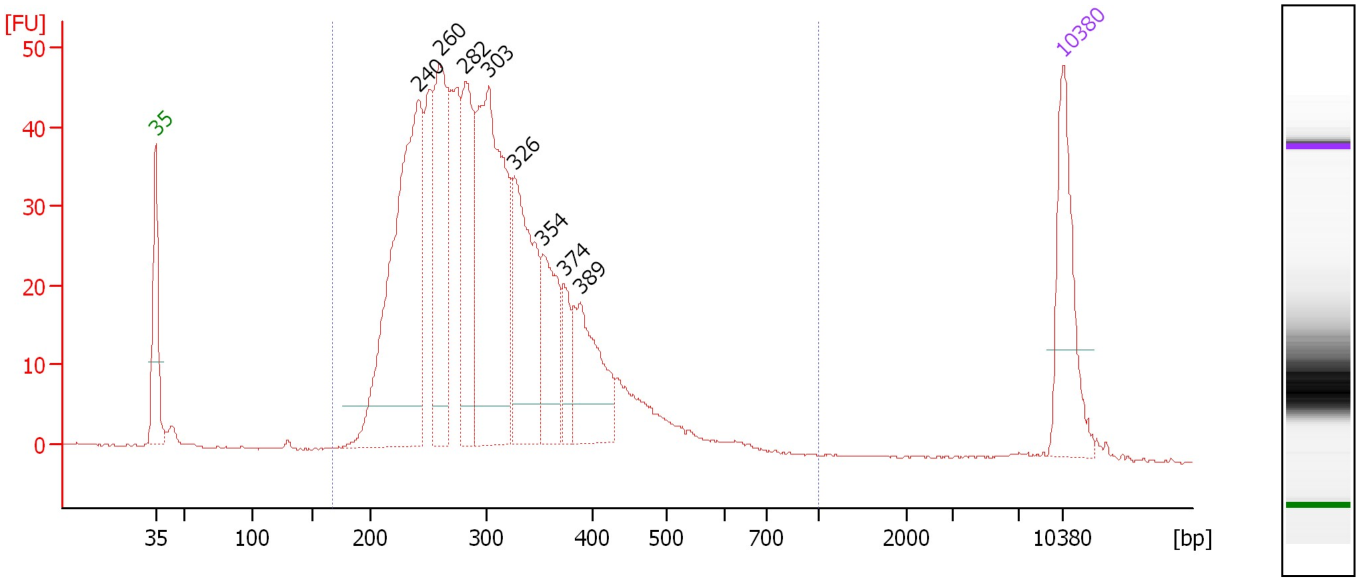
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		241	204.29	1,284.2		63.27
3		258	201.72	1,186.7		64.74
4		281	96.67	520.4		66.86
5		300	138.93	700.6		68.54
6		313	95.83	463.7		69.58
7		387	71.18	279.0		75.55
8	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : <u>TL2 (1:2) (HiSeq_70)</u>

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
175	318	1,000	601.4	6,775.1	98	24.9	1,327.38	🟦

Electropherogram Summary Continued ...

TL3 (1:2) (HiSeq_70) [ribo-dep ssRNA libs_TruSeq_Sciclone]



Overall Results for sample 7 : TL3 (1:2) (HiSeq_70)

Number of peaks found:	8	Corr. Area 1:	897.4
Noise:	0.1		

Peak table for sample 7 : TL3 (1:2) (HiSeq_70)

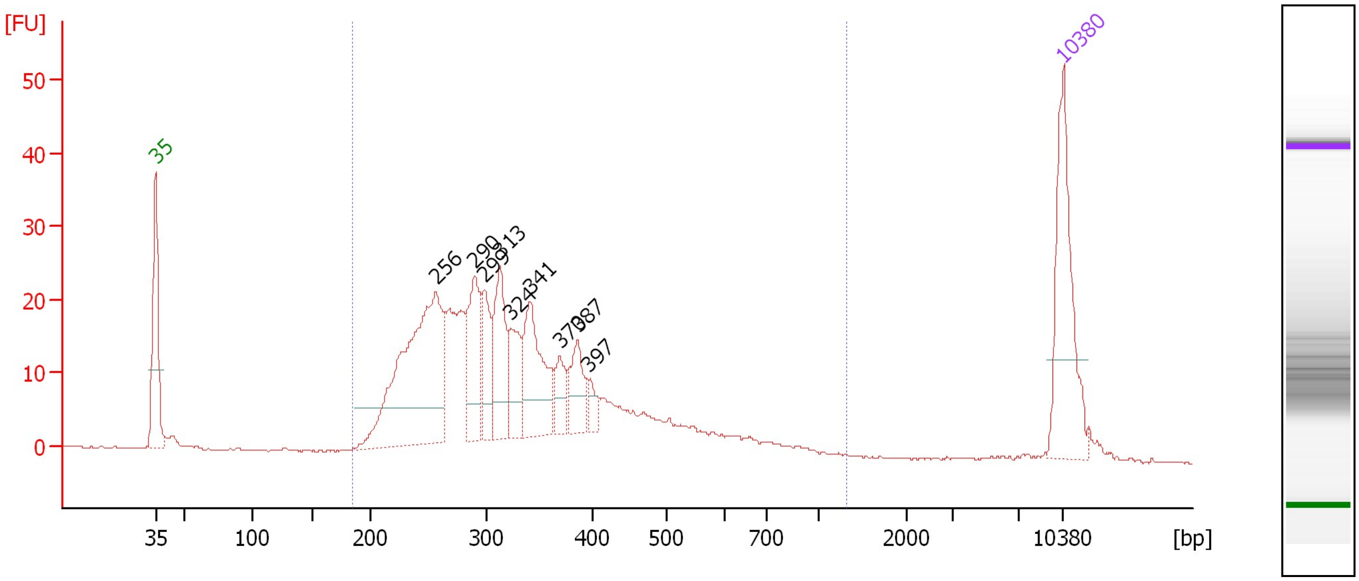
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		240	378.51	2,386.0		63.21
3		260	171.61	1,001.6		64.92
4		282	133.41	717.0		66.90
5		303	304.98	1,527.0		68.72
6		326	162.33	753.8		70.65
7		354	82.31	352.3		72.91
8		374	33.70	136.7		74.50
9		389	95.42	371.5		75.77
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : TL3 (1:2) (HiSeq_70)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
166	309	1,000	897.4	9,100.6	98	25.5	1,734.80	🟦

Electropherogram Summary Continued ...

24 (1:2) (HiSeq_67) [ribo-dep ssRNA libs_TruSeq_Sciclone]



Overall Results for sample 8 : **24 (1:2) (HiSeq_67)**

Number of peaks found:	9	Corr. Area 1:	462.8
Noise:	0.1		

Peak table for sample 8 : **24 (1:2) (HiSeq_67)**

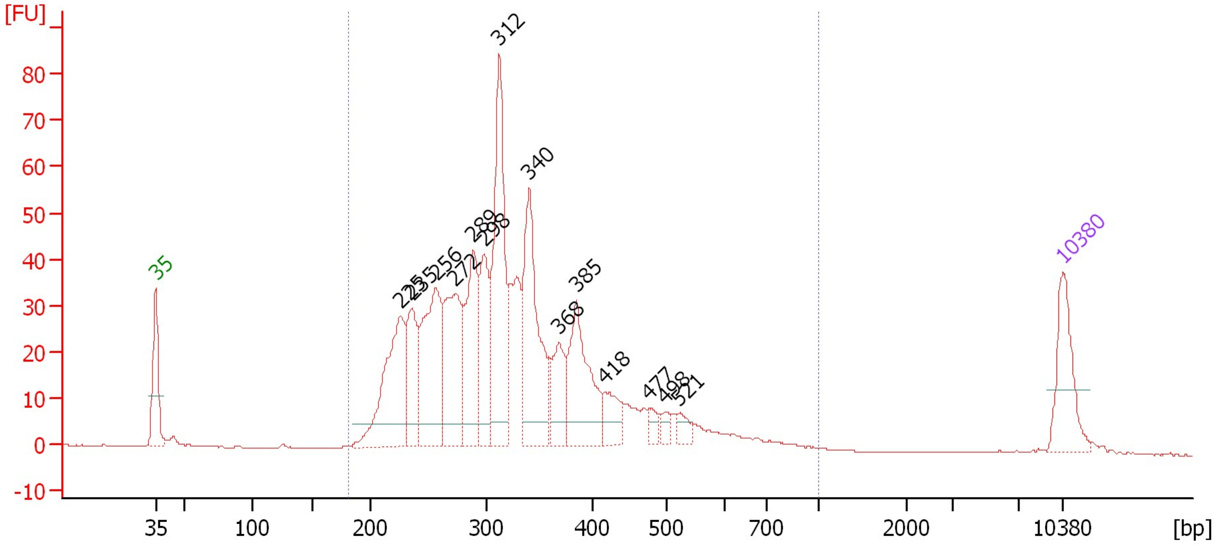
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		256	222.20	1,314.1		64.62
3		290	62.57	327.1		67.61
4		299	39.74	201.7		68.38
5		313	60.90	294.5		69.60
6		324	36.61	171.4		70.42
7		341	72.82	323.4		71.86
8		370	20.68	84.8		74.18
9		387	30.34	118.9		75.57
10		397	10.09	38.5		76.40
11	▶	10,380	75.00	10.9	Upper Marker	113.00

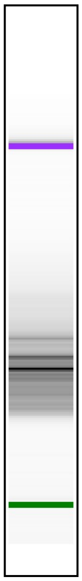
Region table for sample 8 : **24 (1:2) (HiSeq_67)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
183	344	1,318	462.8	4,231.8	98	35.2	857.91	🟦

Electropherogram Summary Continued ...

50 (1:2) (HiSeq_67) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 9 : **50 (1:2) (HiSeq_67)**

Number of peaks found:	14	Corr. Area 1:	873.6
Noise:	0.1		

Peak table for sample 9 : **50 (1:2) (HiSeq_67)**

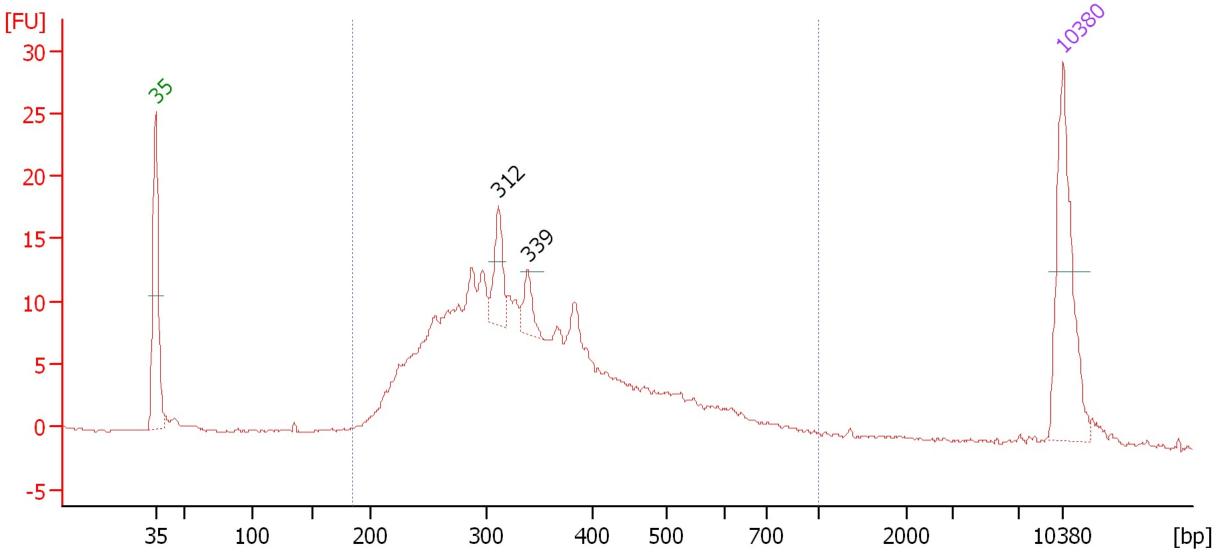
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		225	226.30	1,523.9		61.85
3		235	118.41	763.4		62.74
4		256	223.01	1,318.4		64.63
5		272	185.42	1,033.0		66.02
6		289	166.49	873.3		67.52
7		298	118.65	602.8		68.35
8		312	282.35	1,369.2		69.52
9		340	235.39	1,047.6		71.80
10		368	76.67	315.3		74.08
11		385	157.76	620.0		75.47
12		418	48.07	174.2		77.69
13		477	14.48	46.0		81.09
14		498	14.25	43.4		82.31
15		521	18.60	54.1		83.37
16	▶	10,380	75.00	10.9	Upper Marker	113.00

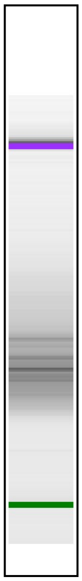
Region table for sample 9 : **50 (1:2) (HiSeq_67)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
181	334	1,000	873.6	10,907.8	99	29.8	2,195.55	🟦

Electropherogram Summary Continued ...

54 (1:2) (HiSeq_67) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 10 : **54 (1:2) (HiSeq_67)**

Number of peaks found: 2
Corr. Area 1: 283.5
Noise: 0.1

Peak table for sample 10 : **54 (1:2) (HiSeq_67)**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		312	34.14	165.9		69.47
3		339	17.28	77.1		71.72
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : **54 (1:2) (HiSeq_67)**

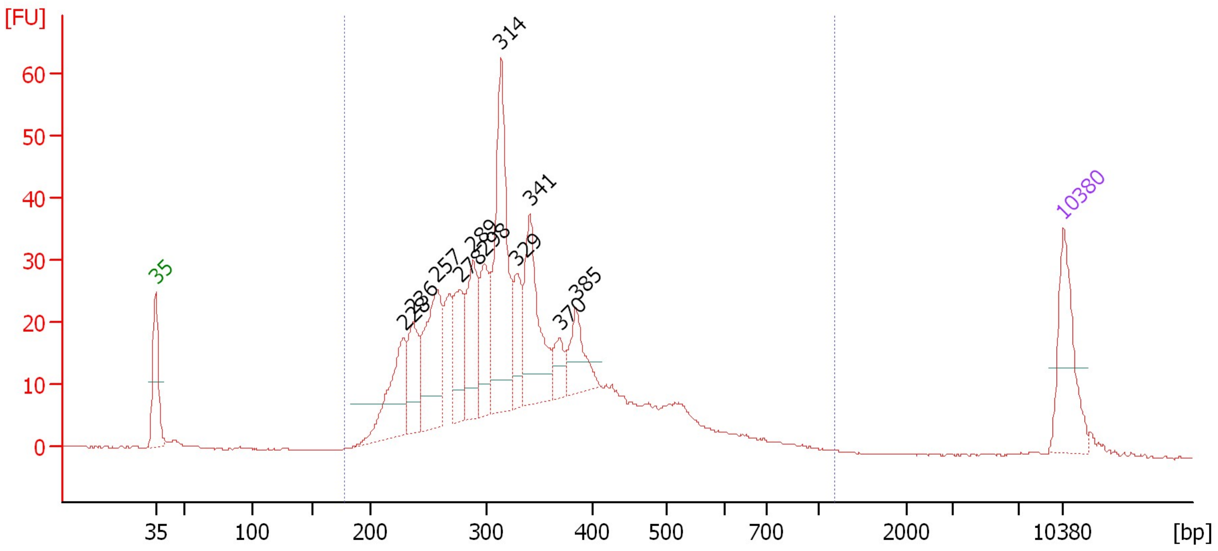
From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
184	368	1,000	283.5	4,311.9	88	35.4	919.95	🟦

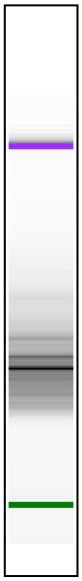
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad

Created: 3/13/2015 4:01:51 PM
Modified: 3/13/2015 4:47:01 PM

Electropherogram Summary Continued ...

69 (1:2) (HiSeq_67) [ribo-dep ssRNA libs_TruSeq_Sciclone]





Overall Results for sample 11 : **69 (1:2) (HiSeq_67)**

Number of peaks found:	11	Corr. Area 1:	654.7
Noise:	0.1		

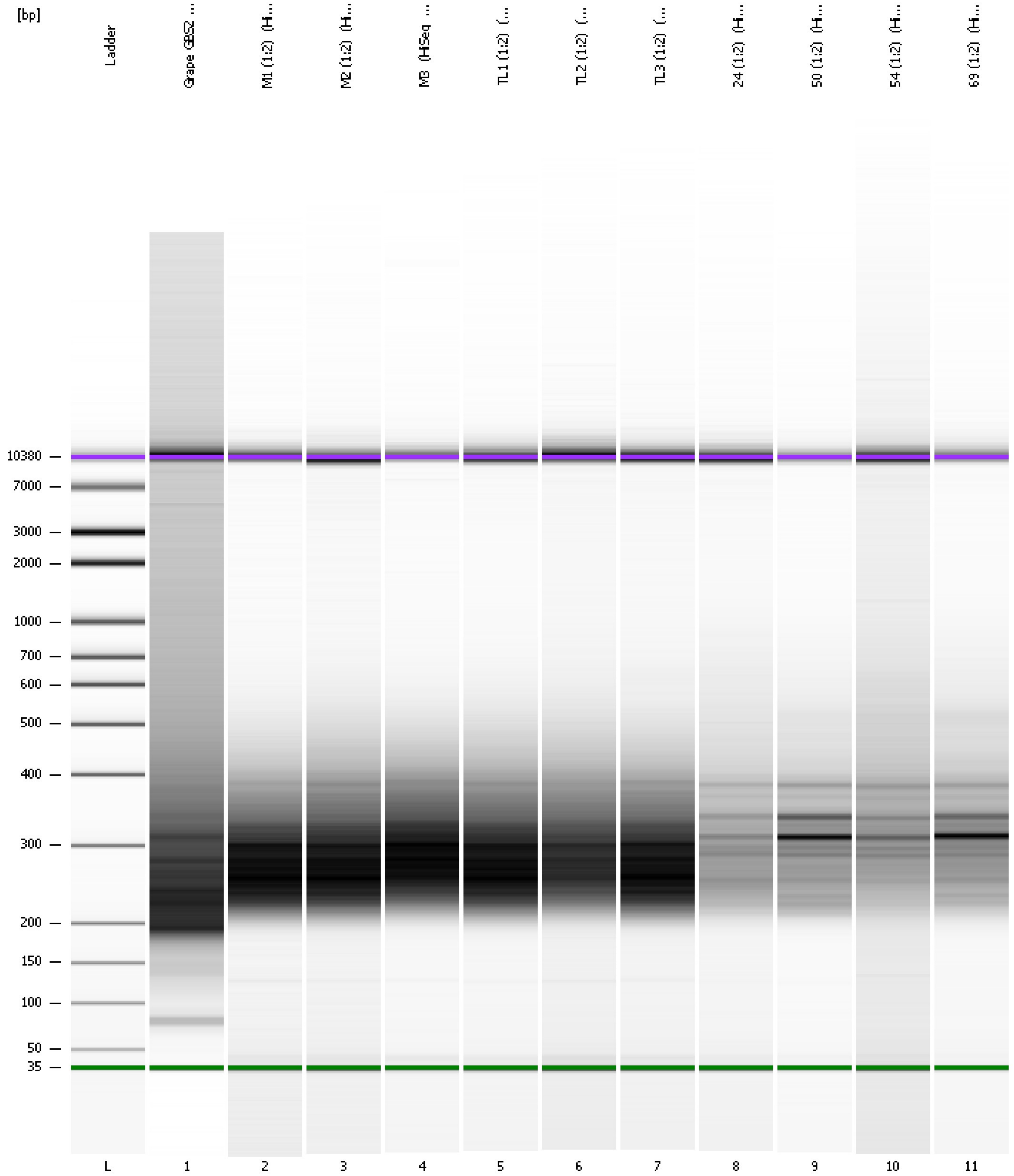
Peak table for sample 11 : **69 (1:2) (HiSeq_67)**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		228	116.25	772.1		62.13
3		236	72.16	462.5		62.86
4		257	143.46	844.3		64.73
5		278	77.81	424.3		66.54
6		289	99.66	523.1		67.50
7		298	78.36	398.1		68.35
8		314	219.08	1,056.9		69.65
9		329	60.52	278.4		70.90
10		341	137.94	612.6		71.86
11		370	30.67	125.7		74.18
12		385	56.11	220.9		75.43
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : **69 (1:2) (HiSeq_67)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Color
177	345	1,184	654.7	8,635.2	98	31.9	1,781.50	🟦

Gel Image


[bp]
Ladder
Grape GBS2 ...
M1 (1:2) (H...
M2 (1:2) (H...
M3 (HiSeq ...
TL1 (1:2) (...
TL2 (1:2) (...
TL3 (1:2) (...
24 (1:2) (H...
50 (1:2) (H...
54 (1:2) (H...
69 (1:2) (H...
10380
7000
3000
2000
1000
700
600
500
400
300
200
150
100
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35
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9
10
11

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad
Created: 3/13/2015 4:01:51 PM
Modified: 3/13/2015 4:47:01 PM

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		3/13/2015 6:42:14 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-03-13\2015-03-13_006.xad)		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		3/13/2015 6:01:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1