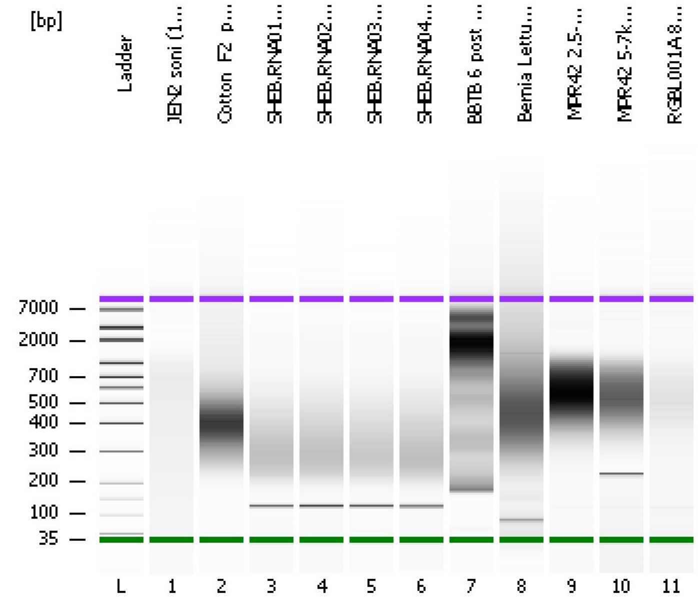
Assay Class:	High Sensitivity DNA Assay	Created:	6/12/2015 4:32:27 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-06-12\2015-06-12_003.xad	Modified:	6/13/2015 9:33:17 AM

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\dsDNA\High Sensitivity DNA.xsy
Assay Class:	High Sensitivity DNA Assay
Version:	1.03
Assay Comments:	Copyright © 2003-2010 Agilent Technologies

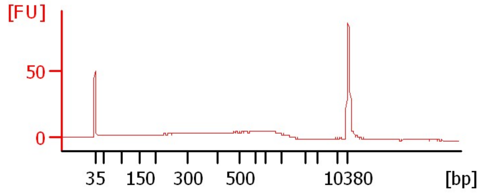
Chip Information:

Chip Lot #:

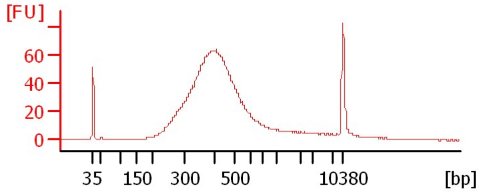
Reagent Kit Lot #:

Chip Comments:

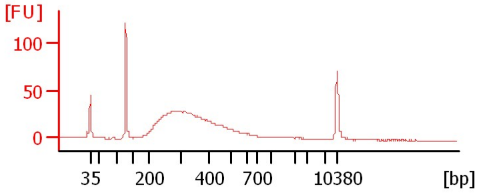
JEN2 soni (1:2)



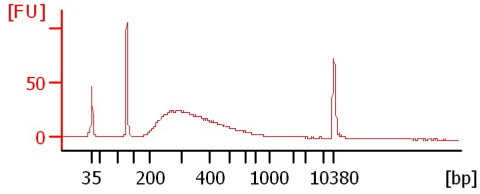
Cotton_F2_pool (1:18)



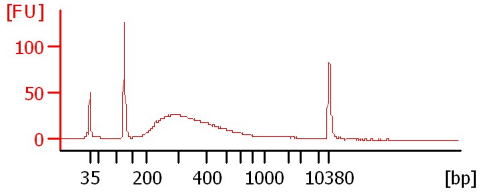
SHEB.RNA01 (1:5)



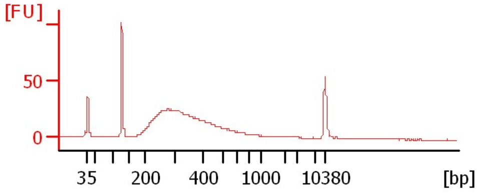
SHEB.RNA02 (1:6)



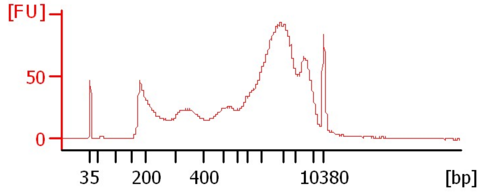
SHEB.RNA03 (1:5)



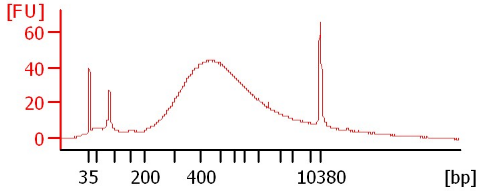
SHEB.RNA04 (1:5)



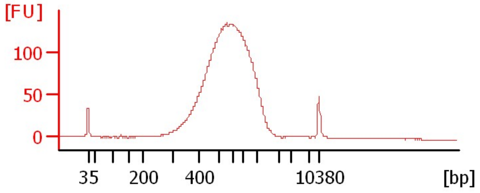
BBTB 6 post beads



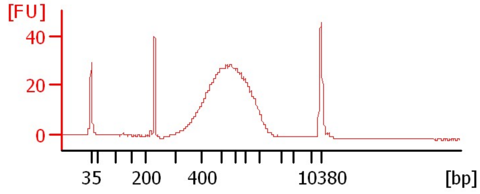
Bernia Lettuce (1:2)



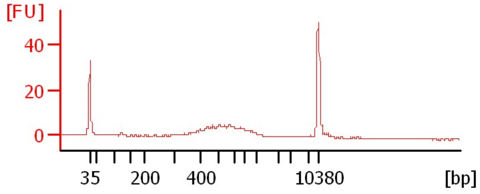
MPR42 2.5-4kb mate pair lib



MPR42 5-7kb mate pair lib



RGBL001A 8kb mate pari lib



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-12\2015-06-12_003.xad
Created: 6/12/2015 4:32:27 PM
Modified: 6/13/2015 9:33:17 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	**Sample Comment**	**Rest. Digest**	**Status**	**Observation**	**Result Label**	**Result Color**
JEN2 soni (1:2)		☐	✓			
Cotton_F2_pool (1:18)		☐	✓			
SHEB.RNA01 (1:5)		☐	✓			
SHEB.RNA02 (1:6)		☐	✓			
SHEB.RNA03 (1:5)		☐	✓			
SHEB.RNA04 (1:5)		☐	✓			
BBTB 6 post beads		☐	✓			
Bernia Lettuce (1:2)		☐	✓			
MPR42 2.5-4kb mate pair lib		☐	✓			
MPR42 5-7kb mate pair lib		☐	✓			
RGBL001A 8kb mate pari lib		☐	✓			
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

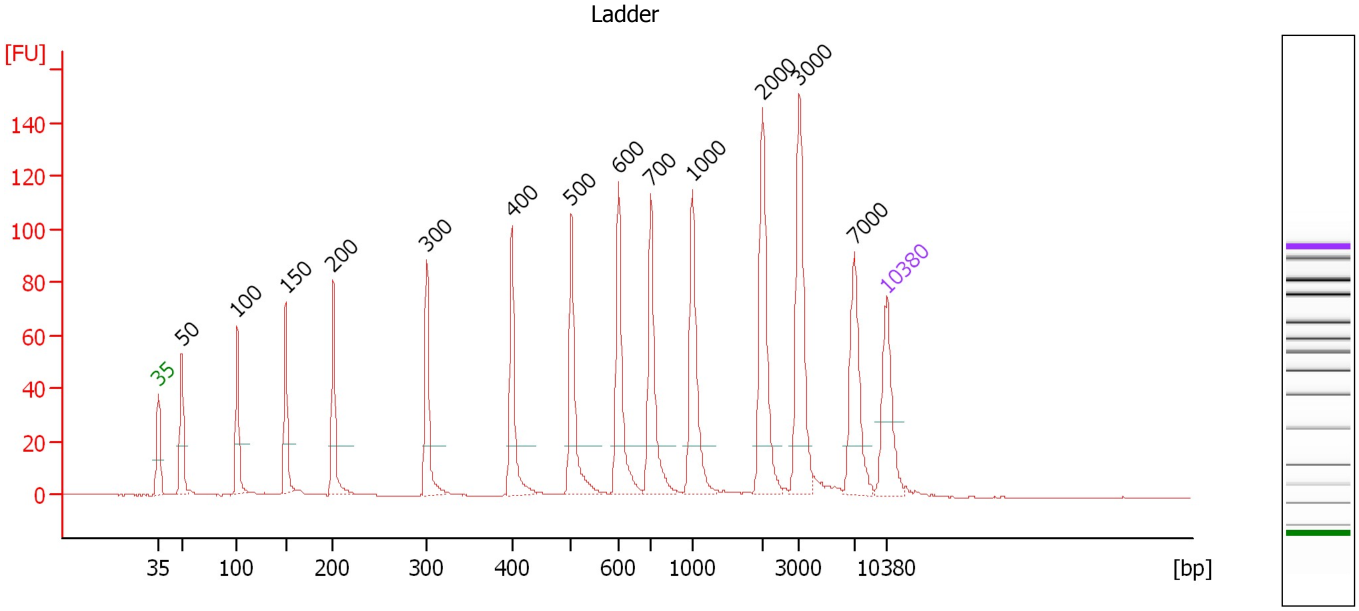
Filter Width [s] : 0.5
Polynomial Order : 4

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	Created:	6/12/2015 4:32:27 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-06-12\2015-06-12_003.xad	Modified:	6/13/2015 9:33:17 AM

Electropherogram Summary



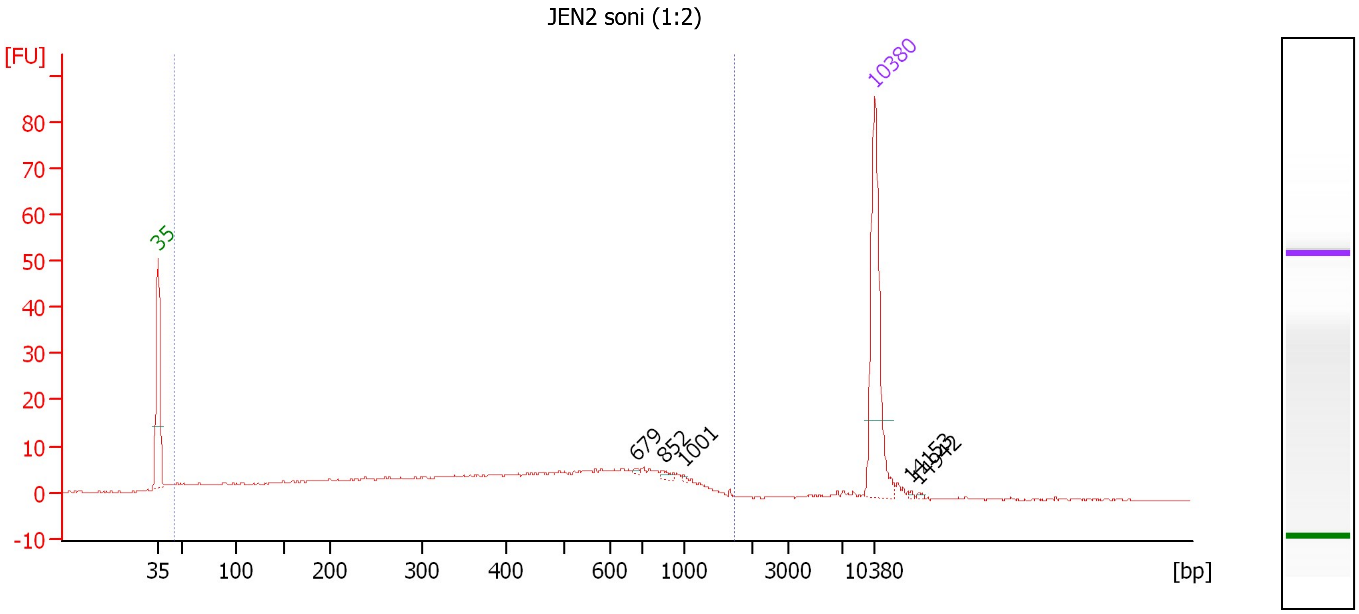
Overall Results for Ladder

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	L	50	150.00	4,545.5	Ladder Peak	45.25
3	L	100	150.00	2,272.7	Ladder Peak	50.58
4	L	150	150.00	1,515.2	Ladder Peak	55.24
5	L	200	150.00	1,136.4	Ladder Peak	59.80
6	L	300	150.00	757.6	Ladder Peak	68.76
7	L	400	150.00	568.2	Ladder Peak	76.95
8	L	500	150.00	454.5	Ladder Peak	82.69
9	L	600	150.00	378.8	Ladder Peak	87.24
10	L	700	150.00	324.7	Ladder Peak	90.32
11	L	1,000	150.00	227.3	Ladder Peak	94.31
12	L	2,000	150.00	113.6	Ladder Peak	101.02
13	L	3,000	150.00	75.8	Ladder Peak	104.60
14	L	7,000	150.00	32.5	Ladder Peak	109.88
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...


JEN2 soni (1:2)

Setpoint Deviations for sample 1 : JEN2 soni (1:2)

Height Threshold [FU] : 1

Overall Results for sample 1 : JEN2 soni (1:2)

Number of peaks found:	5	Corr. Area 1:	278.1
Noise:	0.1		

Peak table for sample 1 : JEN2 soni (1:2)

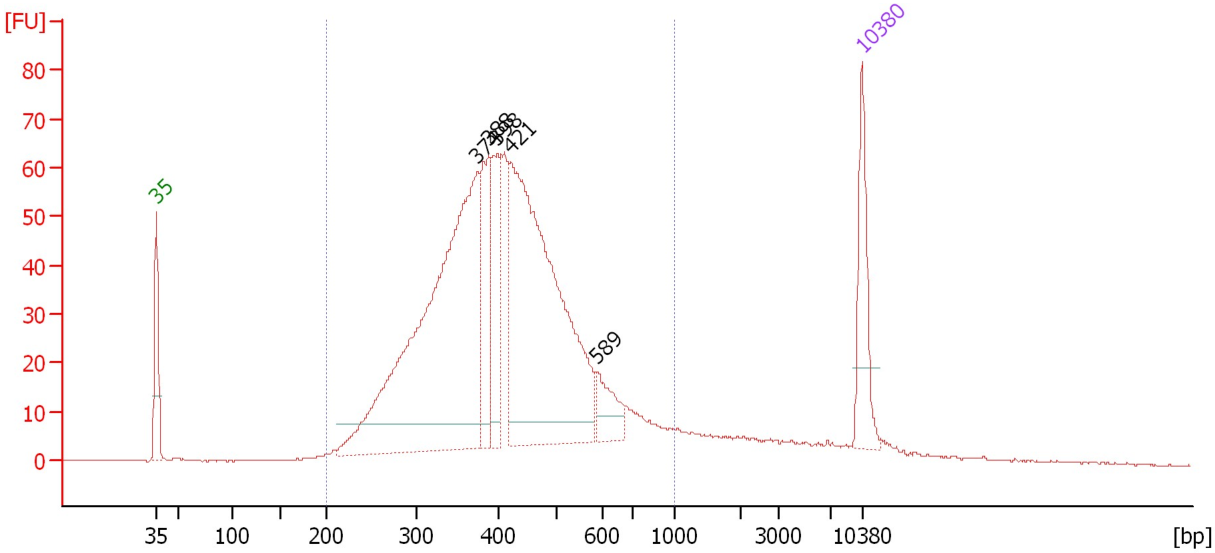
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		679	1.14	2.5		89.68
3		852	2.53	4.5		92.34
4		1,001	0.90	1.4		94.32
5	▶	10,380	75.00	10.9	Upper Marker	113.00
6		14,153	0.00	0.0		116.49
7		14,942	0.00	0.0		117.22

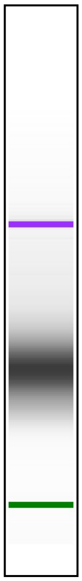
Region table for sample 1 : JEN2 soni (1:2)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
45	462	1,736	278.1	3,087.5	■	94	63.1	428.40

Electropherogram Summary Continued ...

Cotton_F2_pool (1:18)





Overall Results for sample 2 : **Cotton_F2_pool (1:18)**

Number of peaks found:	5	Corr. Area 1:	1,286.7
Noise:	0.1		

Peak table for sample 2 : **Cotton_F2_pool (1:18)**

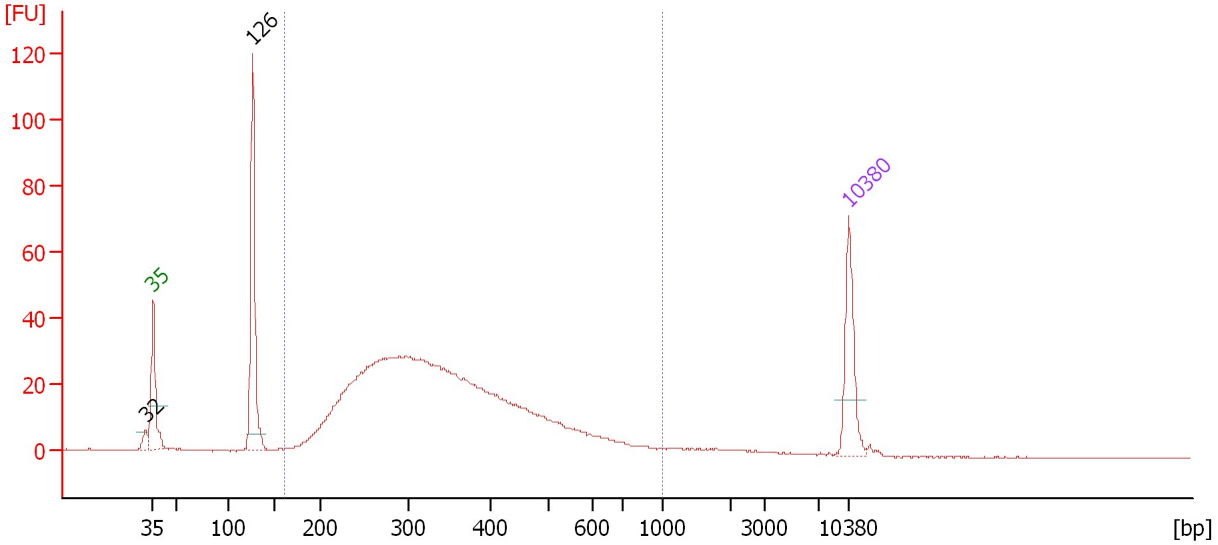
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		374	748.55	3,034.1		74.80
3		388	134.38	524.8		75.97
4		398	114.83	436.8		76.81
5		421	612.98	2,208.2		78.13
6		589	46.16	118.7		86.74
7	▶	10,380	75.00	10.9	Upper Marker	113.00

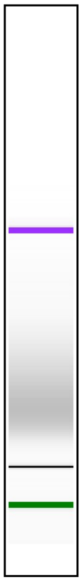
Region table for sample 2 : **Cotton_F2_pool (1:18)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	424	1,000	1,286.7	8,103.3	■	92	28.7	2,057.23

Electropherogram Summary Continued ...

SHEB.RNA01 (1:5)





Overall Results for sample 3 : **SHEB.RNA01 (1:5)**

Number of peaks found:	2	Corr. Area 1:	763.0
Noise:	0.1		

Peak table for sample 3 : **SHEB.RNA01 (1:5)**

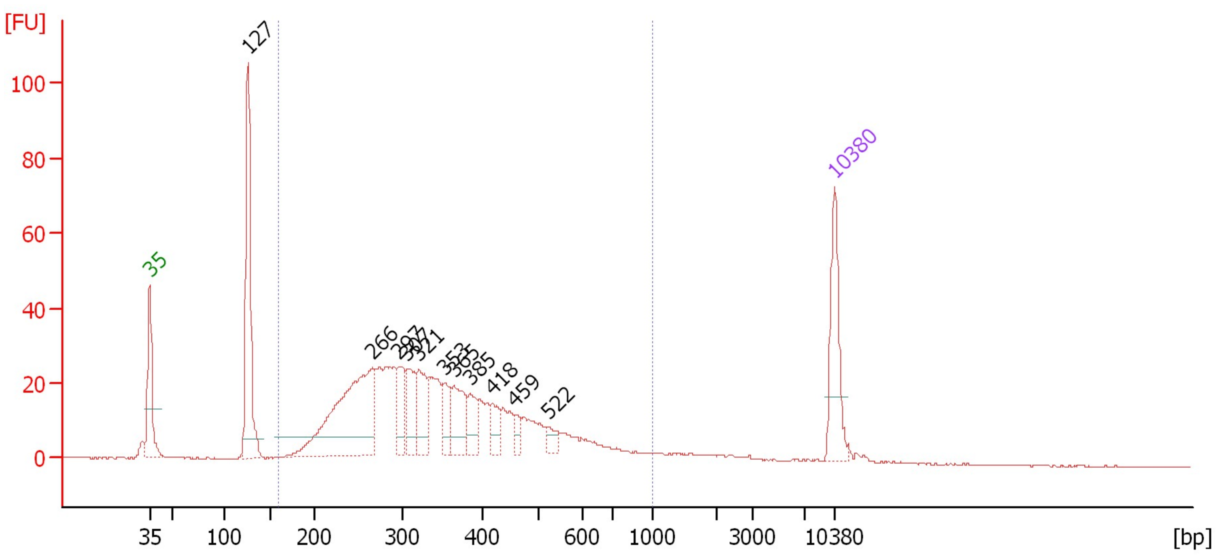
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.25
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		126	278.07	3,337.7		53.02
4	▶	10,380	75.00	10.9	Upper Marker	113.00

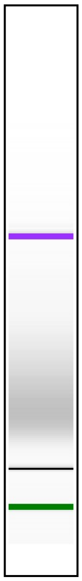
Region table for sample 3 : **SHEB.RNA01 (1:5)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
160	354	1,000	763.0	6,959.1	🟦	83	33.9	1,426.97

Electropherogram Summary Continued ...

SHEB.RNA02 (1:6)





Overall Results for sample 4 : SHEB.RNA02 (1:6)

Number of peaks found:	11	Corr. Area 1:	673.5
Noise:	0.1		

Peak table for sample 4 : SHEB.RNA02 (1:6)

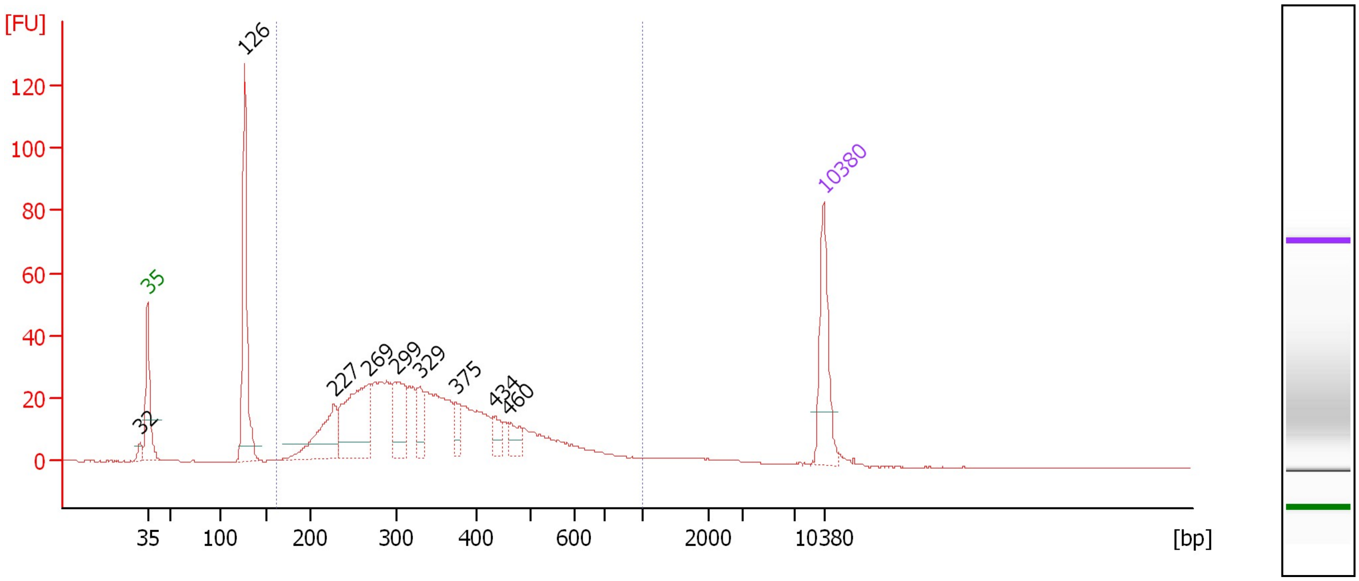
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		127	268.76	3,211.0		53.08
3		266	303.30	1,727.2		65.72
4		297	55.45	282.8		68.49
5		307	55.58	274.5		69.31
6		321	66.51	313.5		70.51
7		353	41.03	176.3		73.07
8		365	67.23	279.4		74.05
9		385	35.55	139.8		75.74
10		418	26.67	96.7		77.97
11		459	14.71	48.6		80.32
12		522	16.12	46.8		83.69
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : SHEB.RNA02 (1:6)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
161	363	1,000	673.5	5,867.1	🟦	80	35.5	1,220.54

Electropherogram Summary Continued ...

SHEB.RNA03 (1:5)



Overall Results for sample 5 : SHEB.RNA03 (1:5)

Number of peaks found:	9	Corr. Area 1:	691.4
Noise:	0.1		

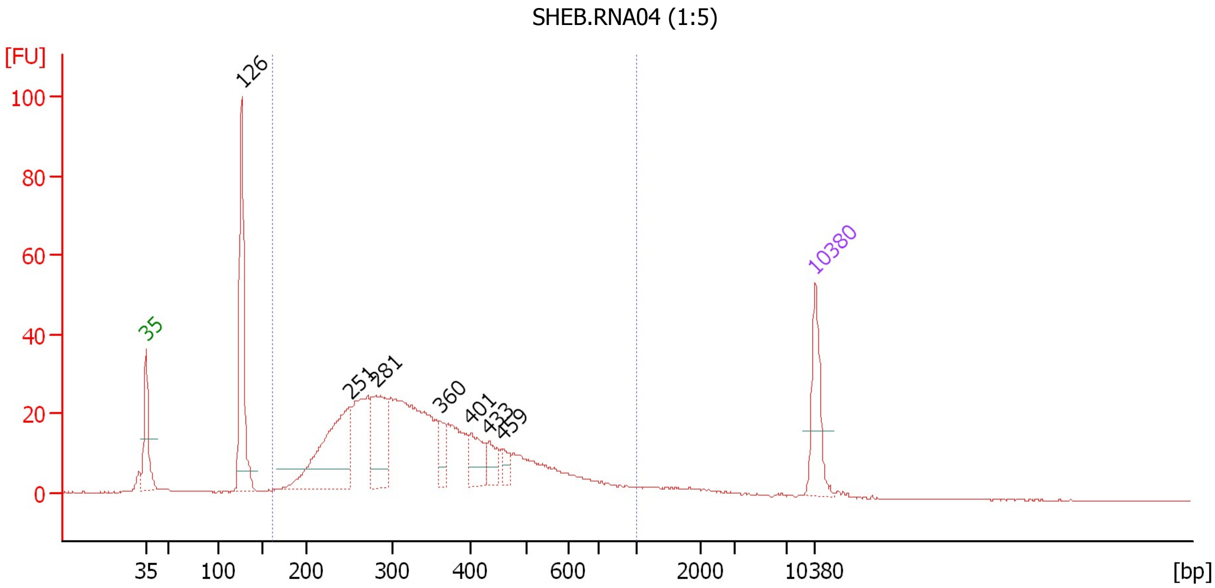
Peak table for sample 5 : SHEB.RNA03 (1:5)

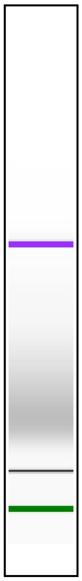
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.23
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		126	249.39	2,989.4		53.04
4		227	105.23	701.1		62.25
5		269	167.72	946.0		65.95
6		299	75.54	383.1		68.65
7		329	39.85	183.5		71.13
8		375	22.63	91.3		74.94
9		434	20.29	70.8		78.91
10		460	22.02	72.5		80.40
11	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : SHEB.RNA03 (1:5)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
162	360	1,000	691.4	5,019.1	🟦	80	35.0	1,039.99

Electropherogram Summary Continued ...





Overall Results for sample 6 : SHEB.RNA04 (1:5)

Number of peaks found:	7	Corr. Area 1:	652.2
Noise:	0.1		

Peak table for sample 6 : SHEB.RNA04 (1:5)

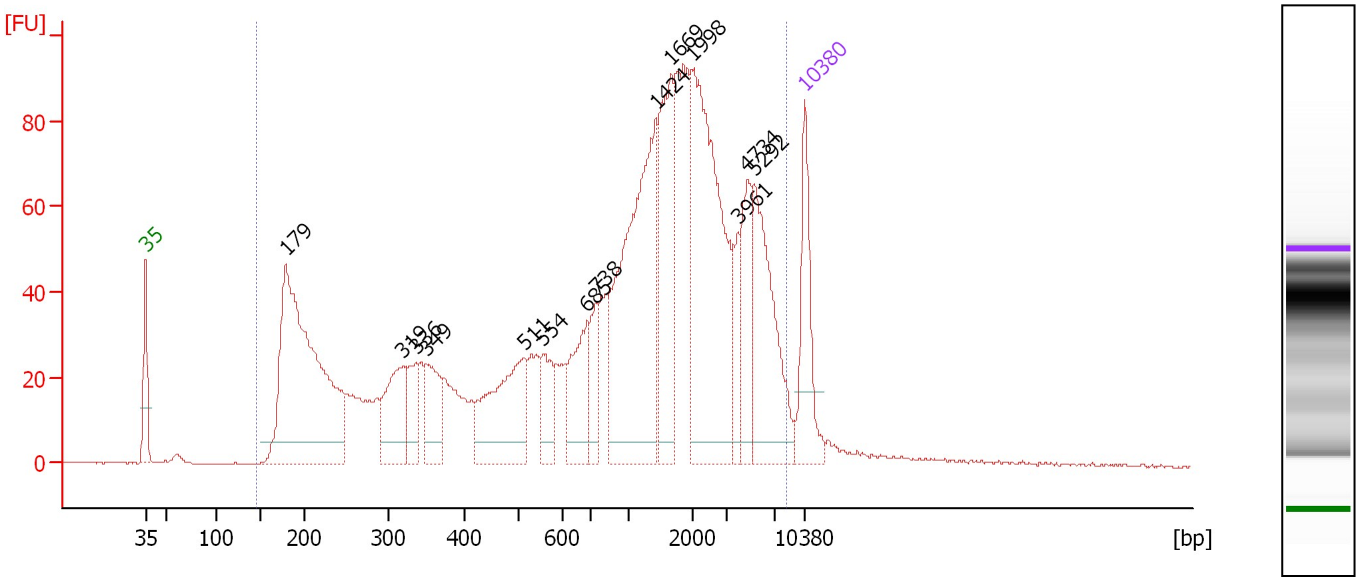
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		126	319.54	3,850.8		52.98
3		251	281.60	1,701.4		64.35
4		281	155.84	839.6		67.08
5		360	38.91	163.6		73.71
6		401	60.16	227.4		77.00
7		433	32.50	113.8		78.84
8		459	21.96	72.5		80.34
9	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : SHEB.RNA04 (1:5)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
160	360	1,000	652.2	7,617.7	🟦 81	36.2	1,566.07

Electropherogram Summary Continued ...

BBTB 6 post beads



Overall Results for sample 7 : BBTB 6 post beads

Number of peaks found:	14	Corr. Area 1:	2,269.5
Noise:	0.1		

Peak table for sample 7 : BBTB 6 post beads

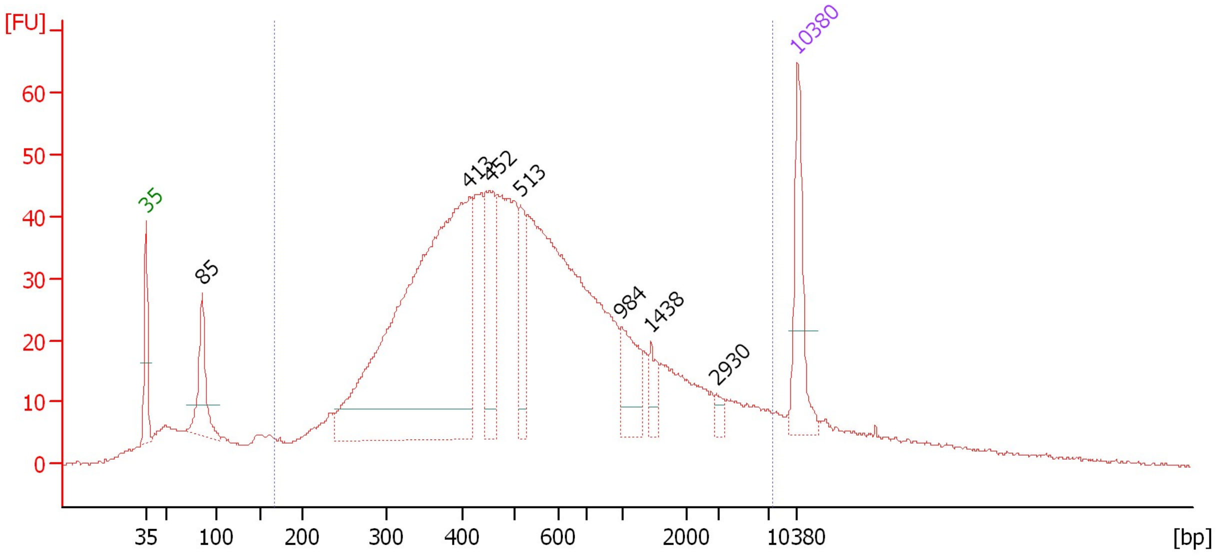
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		179	543.99	4,604.3		57.88
3		319	99.16	470.6		70.33
4		336	50.73	228.9		71.69
5		349	70.60	306.6		72.77
6		511	145.07	430.3		83.18
7		554	47.40	129.6		85.16
8		685	80.08	177.1		89.86
9		738	39.48	81.1		90.82
10		1,424	293.35	312.1		97.16
11		1,669	134.88	122.5		98.80
12		1,998	285.15	216.2		101.00
13		3,961	32.30	12.4		105.87
14		4,734	67.46	21.6		106.89
15		5,292	142.13	40.7		107.62
16	▶	10,380	75.00	10.9	Upper Marker	113.00

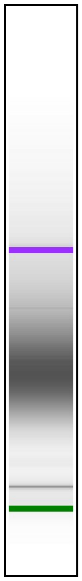
Region table for sample 7 : BBTB 6 post beads

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
145	1,763	8,343	2,269.5	8,078.3	🟦	98	98.6	2,537.69

Electropherogram Summary Continued ...

Bernia Lettuce (1:2)





Overall Results for sample 8 : Bernia Lettuce (1:2)

Number of peaks found:	7	Corr. Area 1:	1,442.4
Noise:	0.3		

Peak table for sample 8 : Bernia Lettuce (1:2)

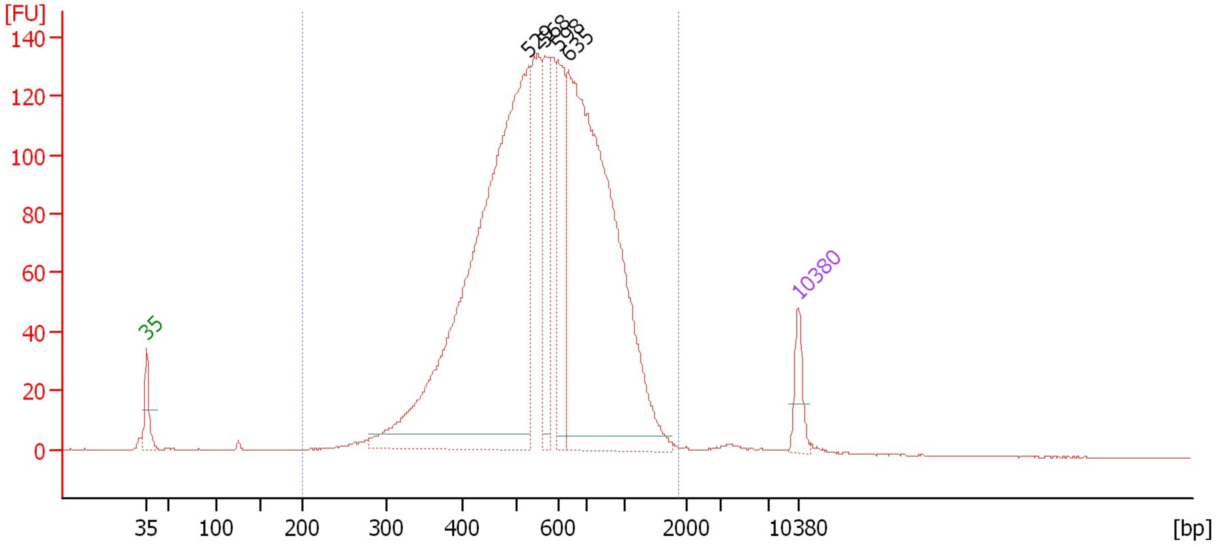
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		85	109.32	1,941.5		49.01
3		413	790.55	2,898.1		77.71
4		452	109.10	365.5		79.95
5		513	68.34	201.9		83.27
6		984	61.26	94.3		94.10
7		1,438	22.43	23.6		97.25
8		2,930	9.04	4.7		104.35
9	▶	10,380	75.00	10.9	Upper Marker	113.00

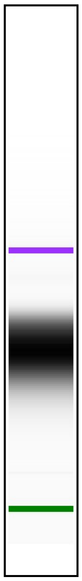
Region table for sample 8 : Bernia Lettuce (1:2)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
167	852	7,395	1,442.4	9,147.7	■ 85	100.0	2,664.22

Electropherogram Summary Continued ...

MPR42 2.5-4kb mate pair lib





Overall Results for sample 9 : **MPR42 2.5-4kb mate pair lib**

Number of peaks found:	4	Corr. Area 1:	2,537.4
Noise:	0.2		

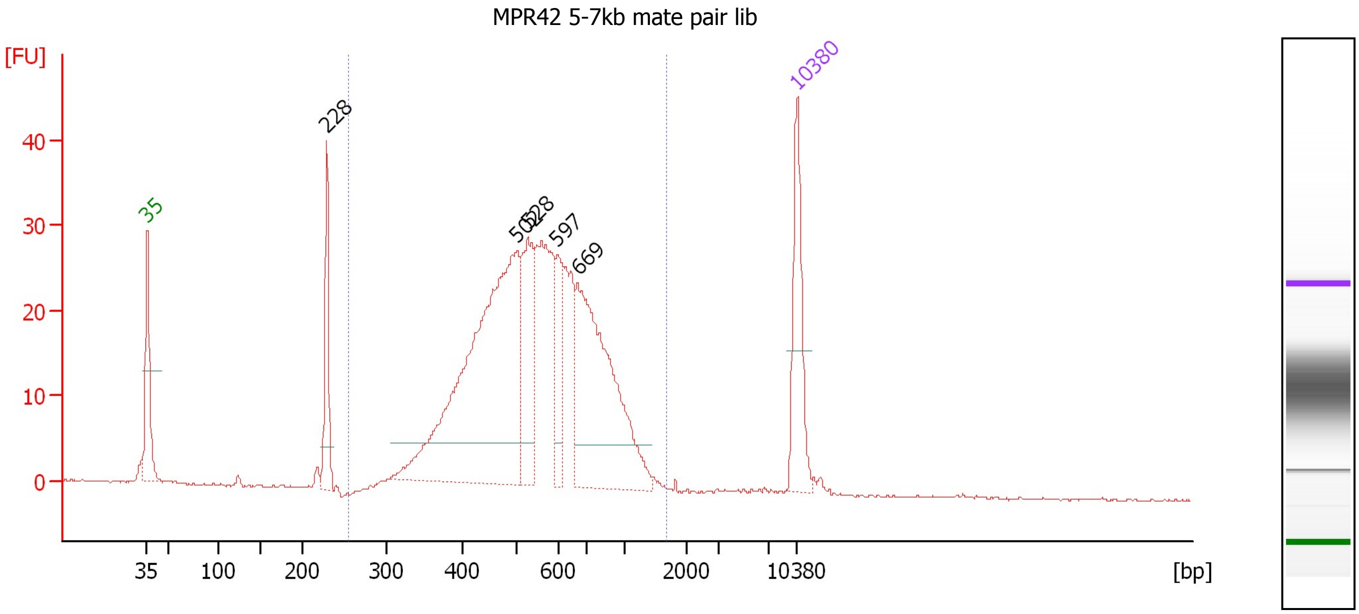
Peak table for sample 9 : **MPR42 2.5-4kb mate pair lib**

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		529	2,477.47	7,093.7		84.01
3		568	319.01	850.8		85.79
4		598	373.86	946.8		87.17
5		635	1,905.51	4,548.4		88.31
6	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : **MPR42 2.5-4kb mate pair lib**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	616	1,887	2,537.4	16,970.8	🟦	98	36.2	6,007.08

Electropherogram Summary Continued ...



Overall Results for sample 10 : **MPR42 5-7kb mate pair lib**

Number of peaks found:	5	Corr. Area 1:	522.2
Noise:	0.1		

Peak table for sample 10 : **MPR42 5-7kb mate pair lib**

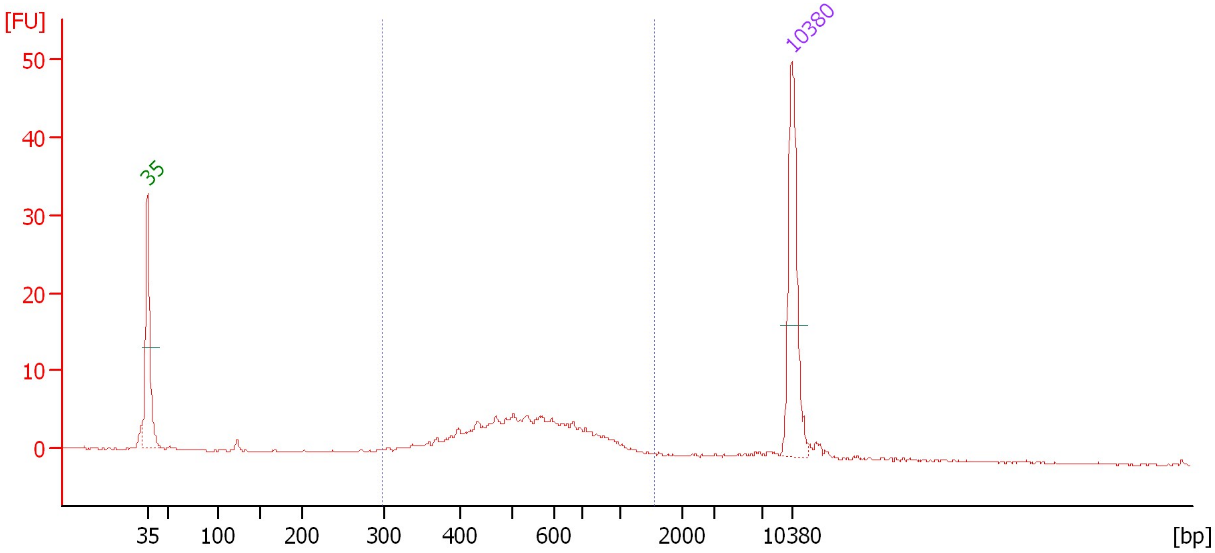
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		228	87.74	582.2		62.34
3		502	484.99	1,464.7		82.76
4		528	103.83	297.9		83.97
5		597	56.20	142.5		87.12
6		669	265.33	601.0		89.36
7	▶	10,380	75.00	10.9	Upper Marker	113.00

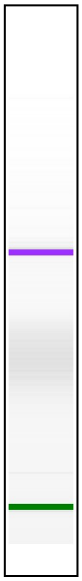
Region table for sample 10 : **MPR42 5-7kb mate pair lib**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
255	587	1,682	522.2	3,478.6	■	93	32.2	1,210.77

Electropherogram Summary Continued ...

RGBL001A 8kb mate pari lib





Overall Results for sample 11 : RGBL001A 8kb mate pari lib

Number of peaks found:	0	Corr. Area 1:	87.1
Noise:	0.1		

Peak table for sample 11 : RGBL001A 8kb mate pari lib

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : RGBL001A 8kb mate pari lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co lor	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
298	573	1,552	87.1	534.5	■	87	32.8	181.02

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-12\2015-06-12_003.xad

Created: 6/12/2015 4:32:27 PM
Modified: 6/13/2015 9:33:17 AM

Gel Image