

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad

Created: 12/23/2014 1:12:32 PM
Modified: 12/23/2014 1:53:53 PM

Electrophoresis File Run Summary

Instrument Information:

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

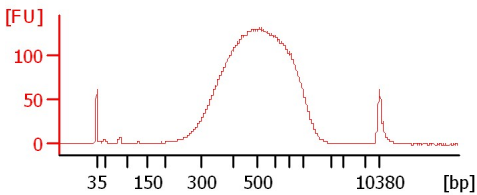
Assay Information:

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

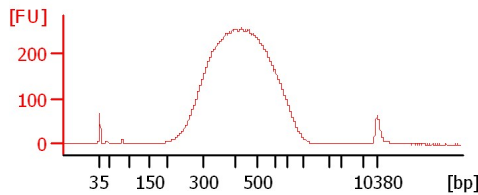
Chip Information:

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

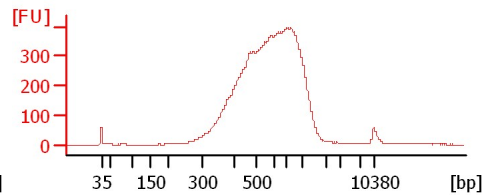
lib drip rnasA I1



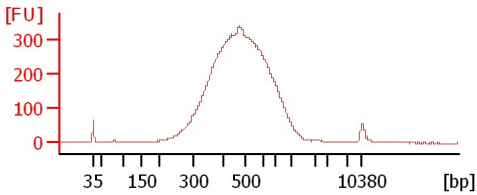
lib drip rnaseH I3



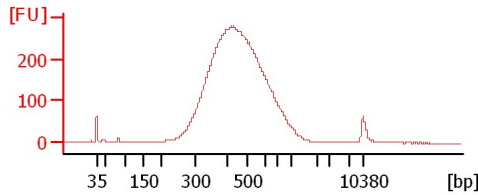
lib input Caro 30c I9



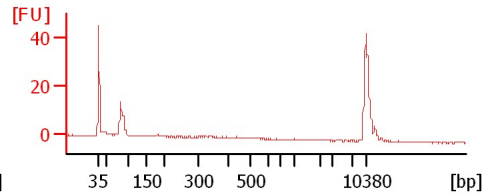
lin input Caro 15c I10



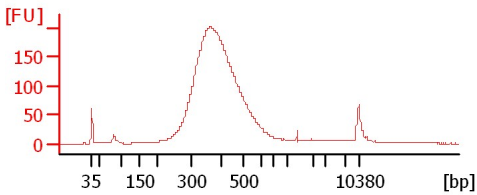
lib drip RnaseA 2 I11



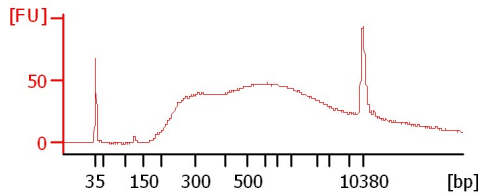
lib drip BS index1



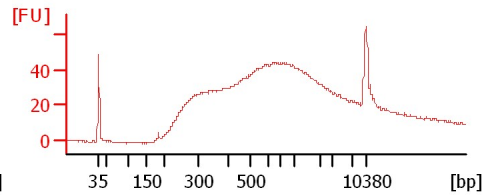
lib Flow T BS index2



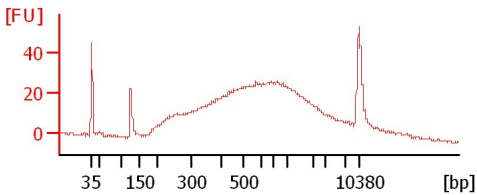
Shally I1



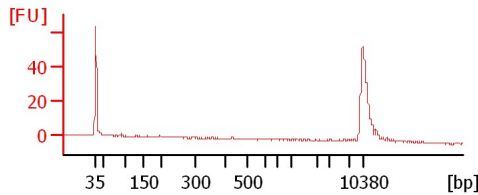
Shally I8



Shally I11



sample 11



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
lib drip rnasA I1		<input type="checkbox"/>	✓			
lib drip rnaseH I3		<input type="checkbox"/>	✓			
lib input Caro 30c I9		<input type="checkbox"/>	✓			
lin input Caro 15c I10		<input type="checkbox"/>	✓			
lib drip RnaseA 2 I11		<input type="checkbox"/>	✓			
lib drip BS index1		<input type="checkbox"/>	✓			
lib Flow T BS index2		<input type="checkbox"/>	✓			
Shally I1		<input type="checkbox"/>	✓			
Shally I8		<input type="checkbox"/>	✓			
Shally I11		<input type="checkbox"/>	✓			
sample 11		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

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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

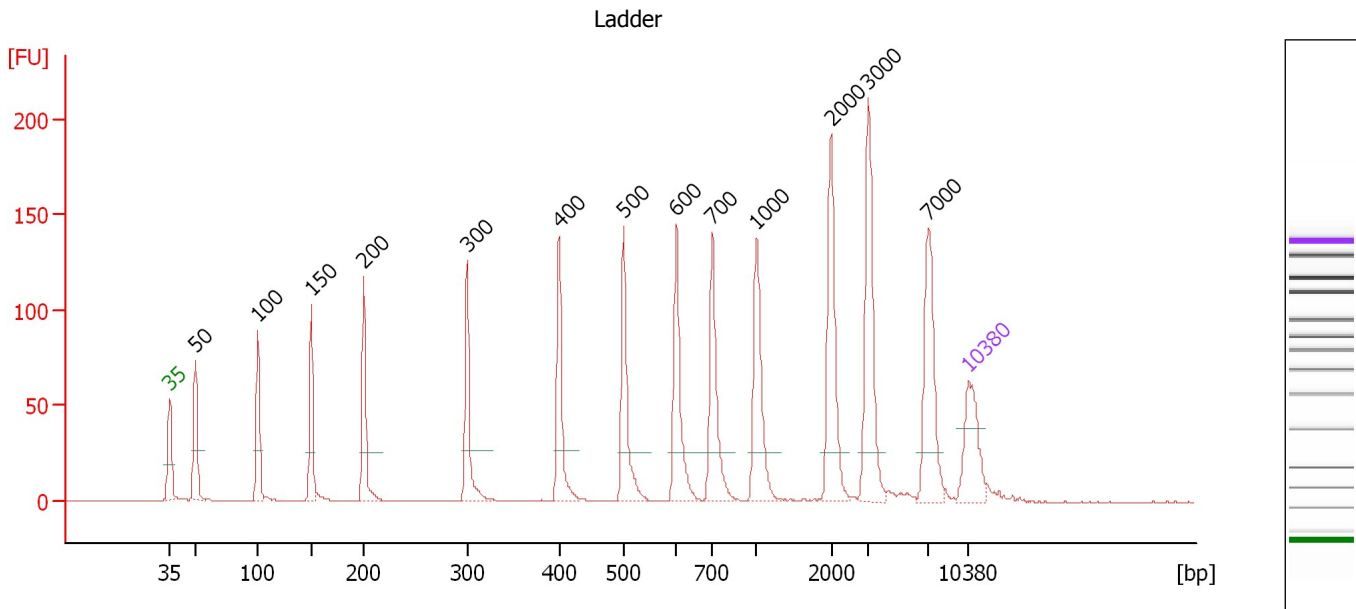
Ladder

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

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Electropherogram Summary



Overall Results for Ladder

Noise: 0.1

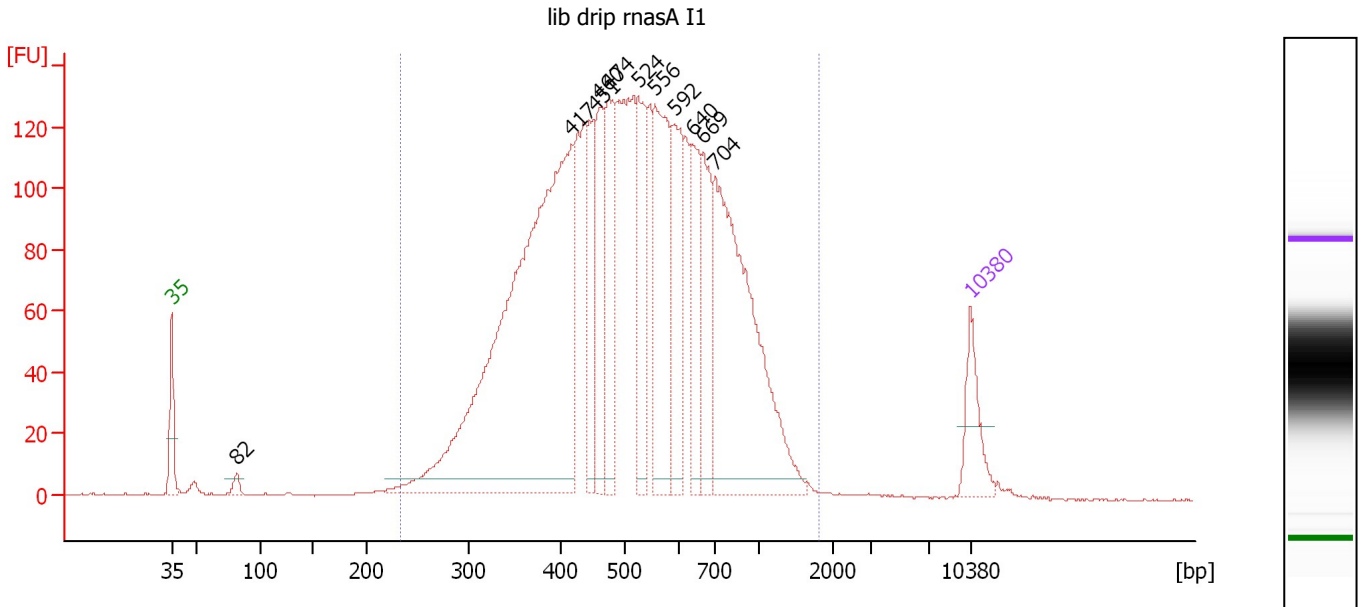
Peak table for Ladder

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	50	150.00	4,545.5	Ladder Peak	45.24
3	100	150.00	2,272.7	Ladder Peak	50.71
4	150	150.00	1,515.2	Ladder Peak	55.38
5	200	150.00	1,136.4	Ladder Peak	60.01
6	300	150.00	757.6	Ladder Peak	69.07
7	400	150.00	568.2	Ladder Peak	77.11
8	500	150.00	454.5	Ladder Peak	82.77
9	600	150.00	378.8	Ladder Peak	87.39
10	700	150.00	324.7	Ladder Peak	90.57
11	1,000	150.00	227.3	Ladder Peak	94.40
12	2,000	150.00	113.6	Ladder Peak	100.94
13	3,000	150.00	75.8	Ladder Peak	104.21
14	7,000	150.00	32.5	Ladder Peak	109.45
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : lib drip rnasA I1

Number of peaks found: 11 Corr. Area 1: 3,428.0
 Noise: 0.3

Peak table for sample 1 : lib drip rnasA I1

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	21.38	396.8		48.70
3	417	1,466.39	5,334.1		78.05
4	451	161.41	542.0		80.01
5	460	198.21	652.4		80.52
6	474	211.38	675.1		81.32
7	524	220.69	637.8		83.89
8	556	329.48	898.6		85.34
9	592	194.92	498.9		87.02
10	640	157.90	374.0		88.65
11	669	174.26	394.6		89.59
12	704	669.29	1,441.1		90.62
13	10,380	75.00	10.9	Upper Marker	113.00

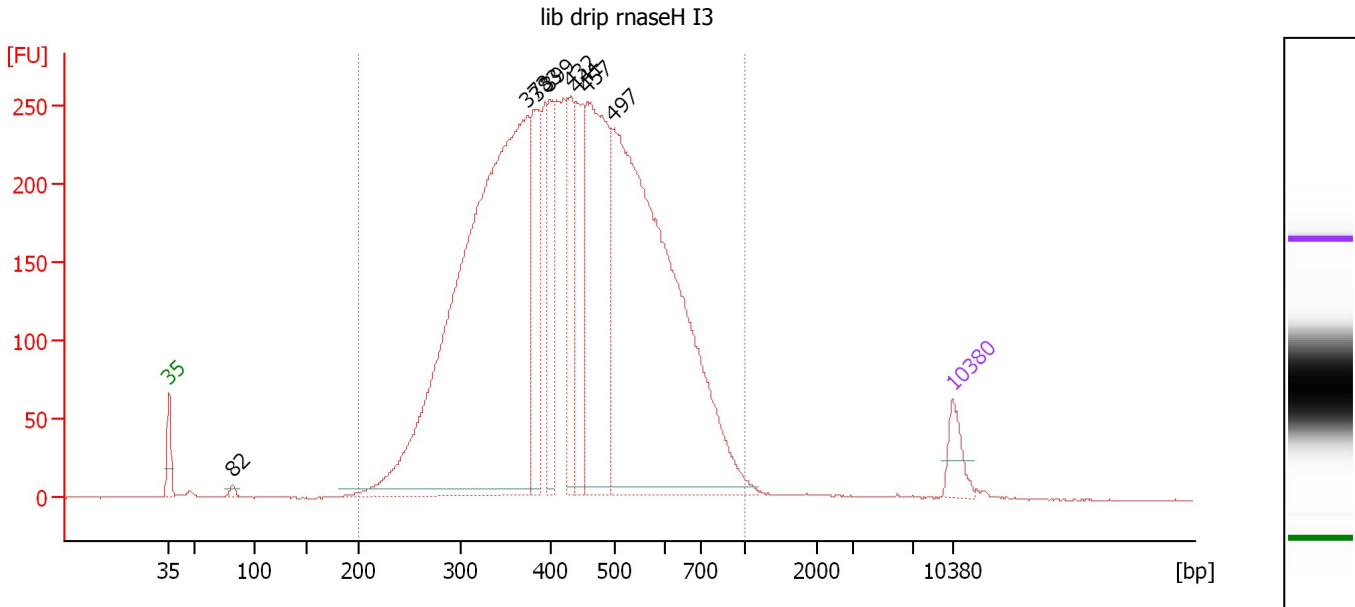
Region table for sample 1 : lib drip rnasA I1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
234	551	1,814	3,428.0	98	38.0	4,870.69	15,617.3	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 2 : lib drip rnaseH I3

Number of peaks found: 8 Corr. Area 1: 6,846.3
 Noise: 0.3

Peak table for sample 2 : lib drip rnaseH I3

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	21.30	394.7		48.72
3	373	3,359.61	13,632.4		74.97
4	383	418.84	1,654.9		75.78
5	399	349.80	1,328.7		77.02
6	432	320.41	1,123.4		78.93
7	441	356.24	1,225.2		79.41
8	457	967.90	3,206.1		80.36
9	497	2,580.83	7,867.4		82.60
10	10,380	75.00	10.9	Upper Marker	113.00

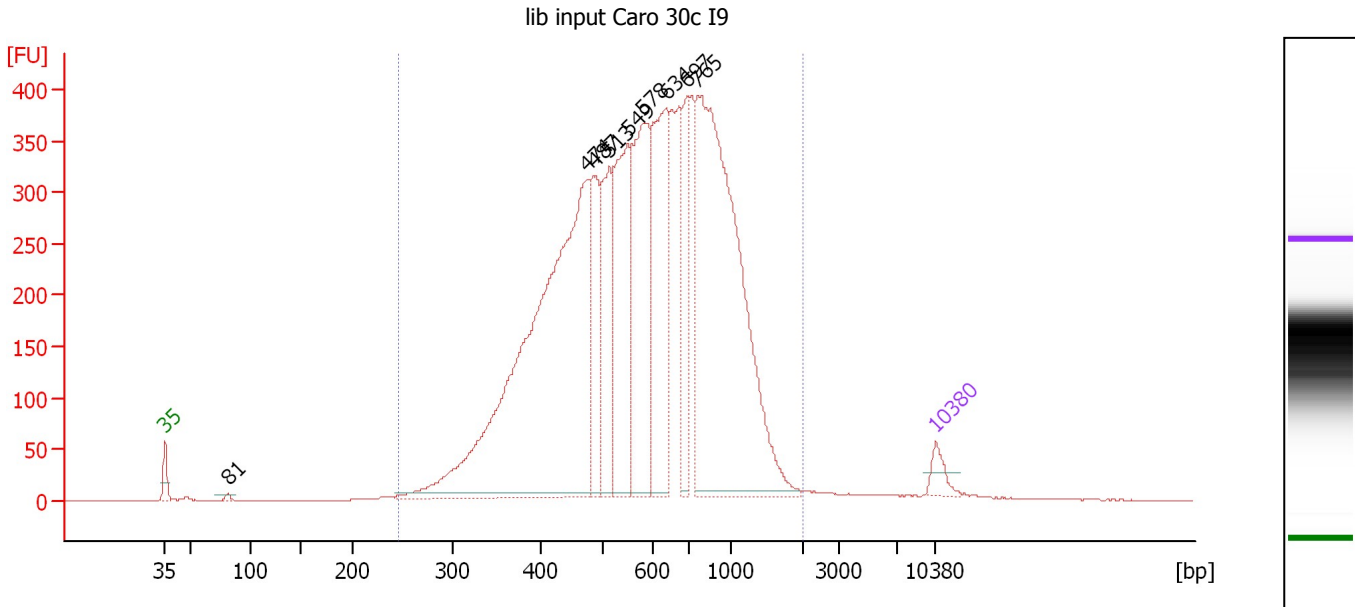
Region table for sample 2 : lib drip rnaseH I3

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	446	1,000	6,846.3	98	28.4	9,429.35	35,657.0	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 3 : lib input Caro 30c I9

Number of peaks found: 9 Corr. Area 1: 8,751.7
 Noise: 0.3

Peak table for sample 3 : lib input Caro 30c I9

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	81	23.43	436.6		48.67
3	474	3,966.66	12,669.1		81.32
4	487	603.59	1,877.0		82.04
5	513	622.32	1,839.2		83.35
6	549	1,071.41	2,955.1		85.05
7	578	1,098.31	2,881.0		86.36
8	634	1,109.55	2,649.7		88.49
9	697	484.36	1,052.9		90.47
10	765	2,967.85	5,881.6		91.39
11	10,380	75.00	10.9	Upper Marker	113.00

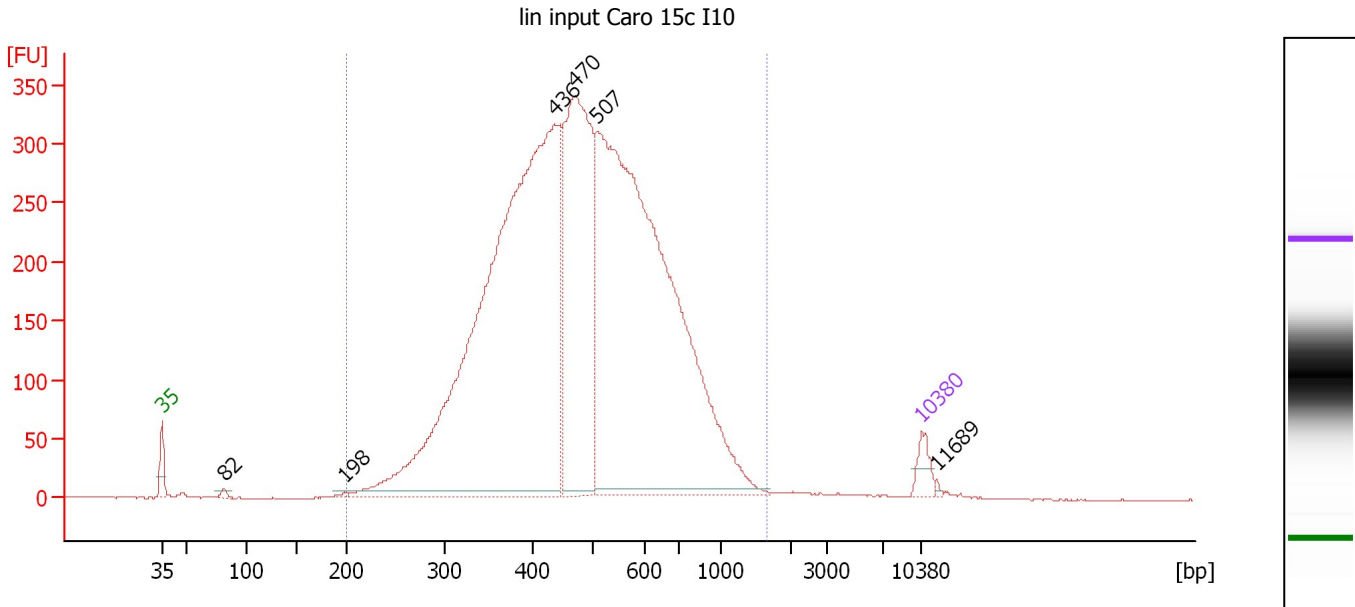
Region table for sample 3 : lib input Caro 30c I9

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
247	648	2,026	8,751.7	98	40.4	13,299.63	37,046.4	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 4 : lin input Caro 15c I10

Number of peaks found: 6 Corr. Area 1: 7,784.3
 Noise: 0.2

Peak table for sample 4 : lin input Caro 15c I10

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	24.84	461.3		48.70
3	198	15.06	115.4		59.80
4	436	5,560.90	19,319.5		79.15
5	470	2,107.78	6,794.9		81.07
6	507	5,031.91	15,041.5		83.08
7	10,380	75.00	10.9	Upper Marker	113.00
8	11,689	0.00	0.0		114.38

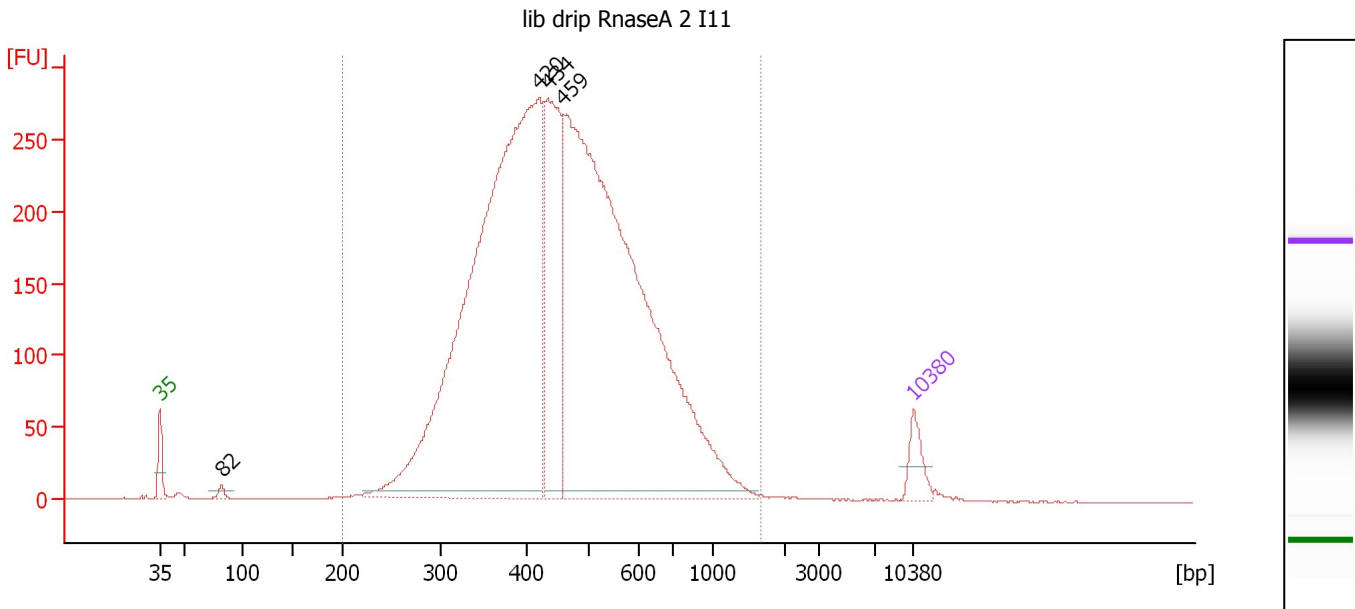
Region table for sample 4 : lin input Caro 15c I10

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	504	1,666	7,784.3	99	33.8	12,996.95	44,294.2	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 5 : lib drip RnaseA 2 I11

Number of peaks found: 4 Corr. Area 1: 6,287.4
 Noise: 0.3

Peak table for sample 5 : lib drip RnaseA 2 I11

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	28.22	521.3		48.74
3	420	3,677.83	13,265.2		78.25
4	434	815.40	2,846.1		79.04
5	459	3,838.10	12,656.3		80.48
6	10,380	75.00	10.9	Upper Marker	113.00

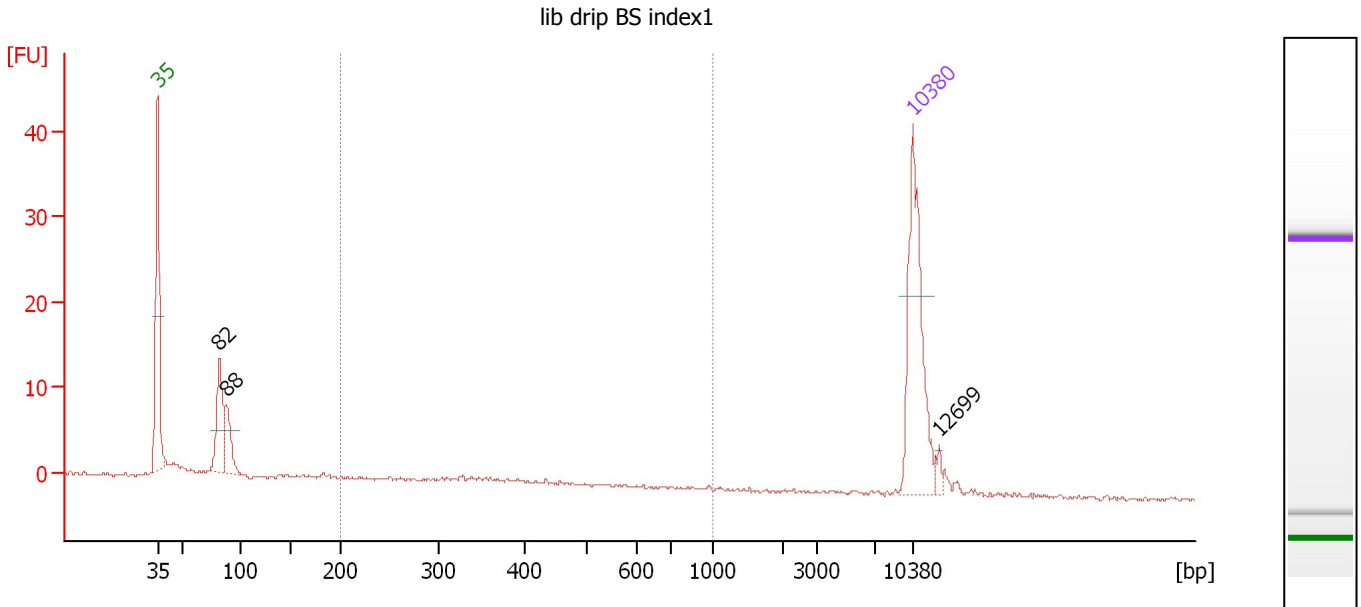
Region table for sample 5 : lib drip RnaseA 2 I11

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	478	1,663	6,287.4	99	32.9	8,567.61	30,324.7	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 6 : lib drip BS index1

Number of peaks found: 3 Corr. Area 1: 9.1
 Noise: 0.2

Peak table for sample 6 : lib drip BS index1

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	56.01	1,037.8		48.72
3	88	32.09	554.5		49.36
4	10,380	75.00	10.9	Upper Marker	113.00
5	12,699	0.00	0.0		115.44

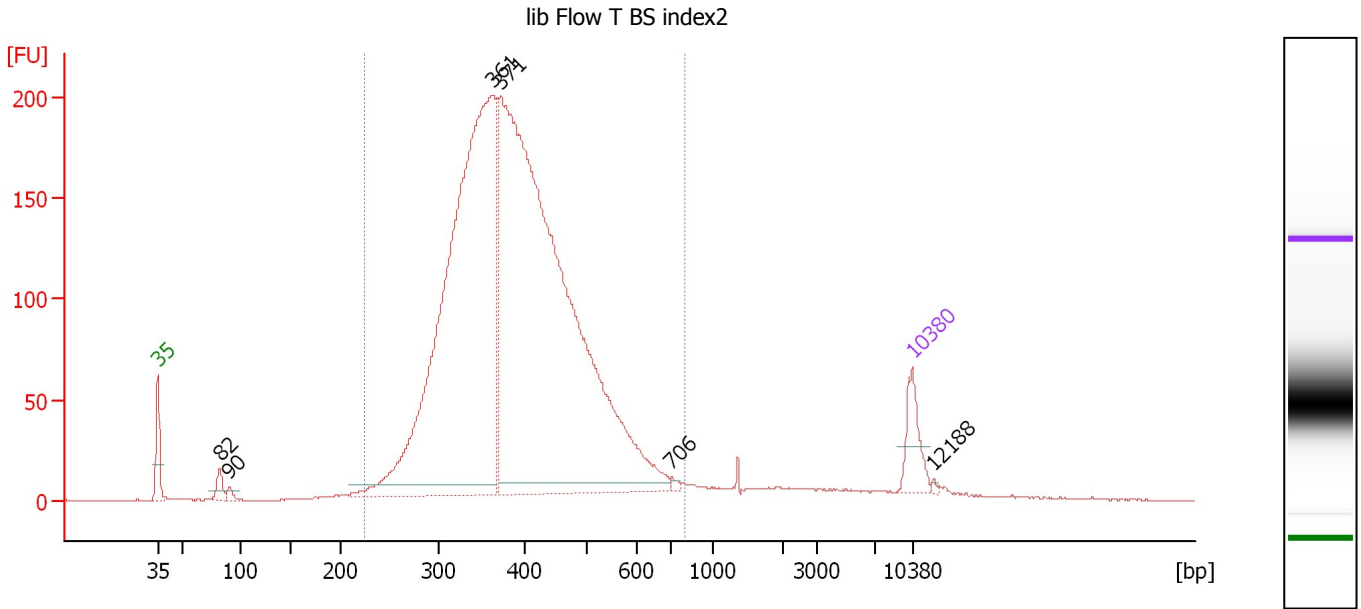
Region table for sample 6 : lib drip BS index1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	350	1,000	9.1	15	29.2	19.23	91.6	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 7 : lib Flow T BS index2

Number of peaks found: 6 Corr. Area 1: 3,507.7
 Noise: 0.2

Peak table for sample 7 : lib Flow T BS index2

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	43.50	803.0		48.75
3	90	19.26	323.1		49.65
4	361	2,157.00	9,046.1		74.00
5	371	2,810.87	11,491.6		74.75
6	706	7.65	16.4		90.65
7	10,380	75.00	10.9	Upper Marker	113.00
8	12,188	0.00	0.0		114.90

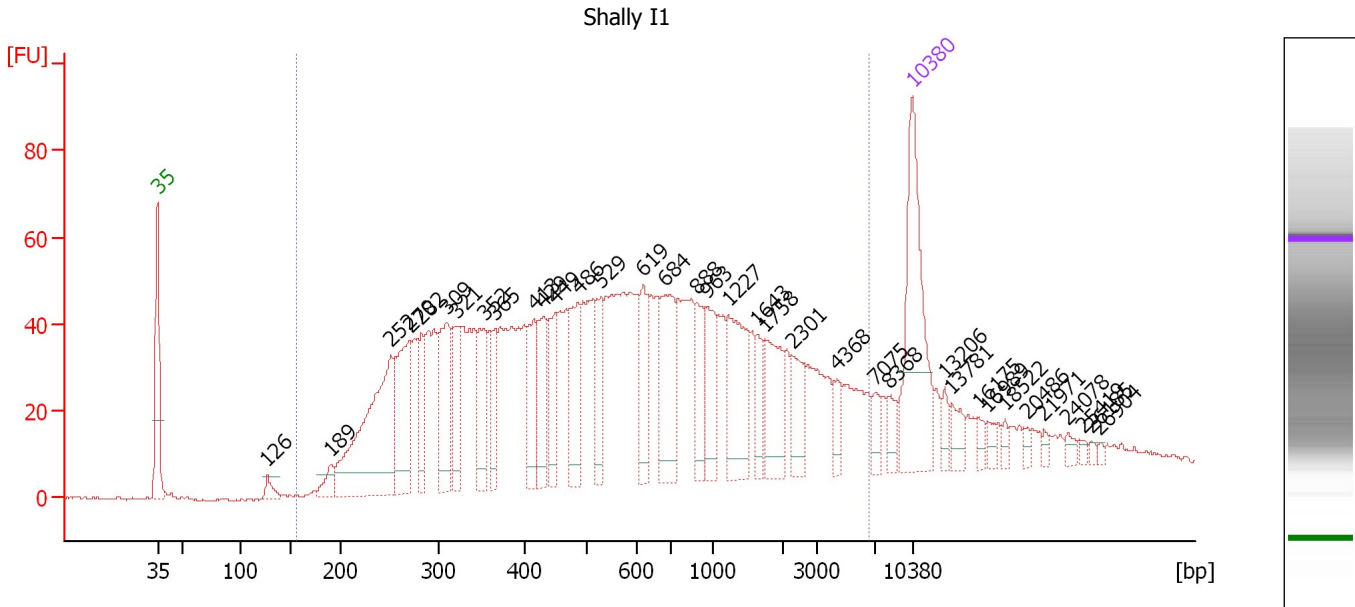
Region table for sample 7 : lib Flow T BS index2

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
224	397	809	3,507.7	94	21.4	5,193.57	20,978.6	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 8 : Shally I1

Number of peaks found: 36 Corr. Area 1: 2,028.5
 Noise: 0.2

Peak table for sample 8 : Shally I1

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	9.14	109.7		53.17
3	189	12.64	101.2		59.00
4	252	148.94	896.8		64.69
5	270	71.63	401.2		66.40
6	282	32.55	174.8		67.46
7	309	61.86	303.7		69.77
8	321	33.72	159.4		70.73
9	352	41.39	178.2		73.24
10	365	29.42	122.1		74.30
11	413	33.76	123.7		77.87
12	429	38.15	134.6		78.78
13	449	31.99	107.9		79.89
14	486	41.06	127.9		82.00
15	529	30.13	86.3		84.11
16	619	35.40	86.7		87.99
17	684	54.59	121.0		90.05
18	888	26.29	44.9		92.97
19	963	30.18	47.5		93.93
20	1,227	54.14	66.8		95.89
21	1,643	15.47	14.3		98.61
22	1,758	33.18	28.6		99.36
23	2,301	20.59	13.6		101.93
24	4,368	9.28	3.2		106.01
25	7,075	8.78	1.9		109.53

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Electropherogram Summary Continued ...

... Peak table for sample 8 : Shally I1

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	8,368	8.35	1.5		110.89
27	10,380	75.00	10.9	Upper Marker	113.00
28	13,206	0.00	0.0		115.97
29	13,781	0.00	0.0		116.57
30	16,175	0.00	0.0		119.09
31	16,989	0.00	0.0		119.94
32	18,522	0.00	0.0		121.55
33	20,486	0.00	0.0		123.62
34	21,971	0.00	0.0		125.18
35	24,078	0.00	0.0		127.39
36	25,419	0.00	0.0		128.80
37	26,185	0.00	0.0		129.61
38	26,904	0.00	0.0		130.36

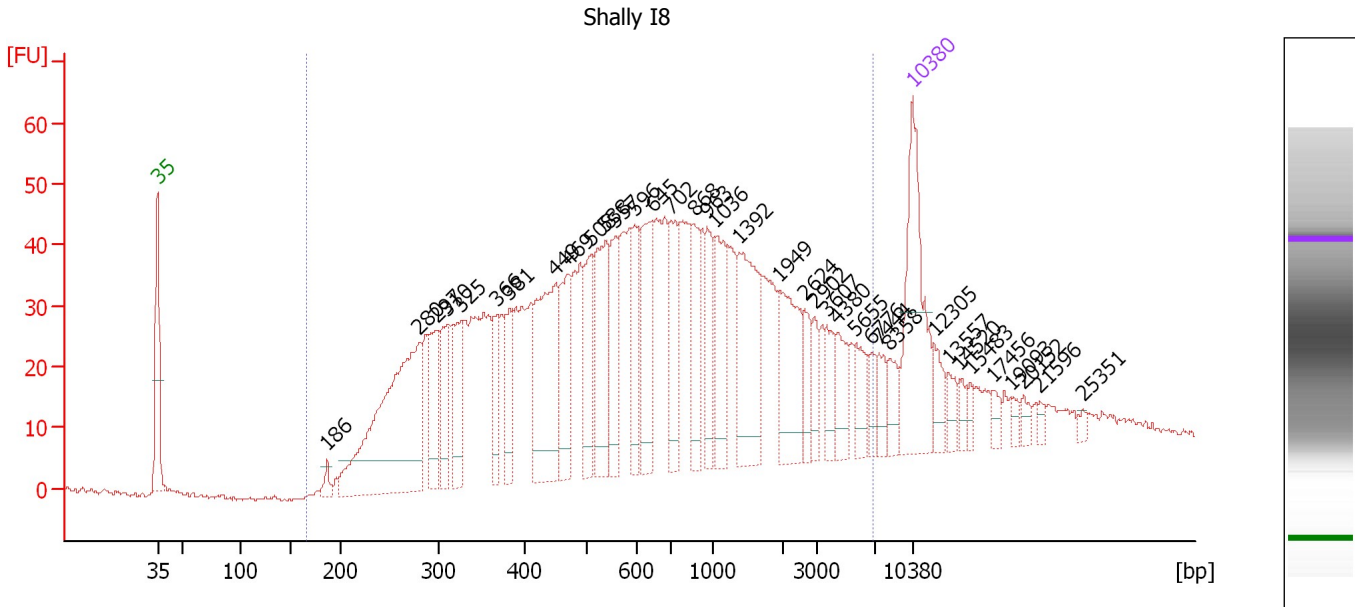
Region table for sample 8 : Shally I1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
156	965	6,550	2,028.5	91	100.0	1,567.80	5,431.7	

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Electropherogram Summary Continued ...



Overall Results for sample 9 : Shally I8

Number of peaks found: 37 Corr. Area 1: 1,556.4
 Noise: 0.4

Peak table for sample 9 : Shally I8

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	186	8.65	70.4		58.73
3	280	216.01	1,168.2		67.28
4	297	47.83	243.6		68.85
5	310	40.27	197.0		69.86
6	325	51.88	241.5		71.12
7	366	29.88	123.6		74.41
8	381	31.70	125.9		75.62
9	449	104.64	353.3		79.87
10	469	52.80	170.4		81.03
11	508	47.89	142.7		83.16
12	538	68.50	192.9		84.52
13	557	40.66	110.7		85.38
14	596	35.19	89.5		87.21
15	645	55.72	130.9		88.82
16	702	43.11	93.1		90.59
17	868	40.53	70.7		92.72
18	963	33.06	52.0		93.93
19	1,036	46.45	67.9		94.64
20	1,392	72.69	79.1		96.97
21	1,949	51.30	39.9		100.61
22	2,624	15.41	8.9		102.99
23	2,902	12.52	6.5		103.90
24	3,607	15.16	6.4		105.01
25	4,380	20.60	7.1		106.02

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad


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Electropherogram Summary Continued ...

... Peak table for sample 9 : Shally I8

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	5,655	17.74	4.8		107.69
27	6,776	9.06	2.0		109.16
28	7,444	12.63	2.6		109.91
29	8,358	13.35	2.4		110.88
30	10,380	75.00	10.9	Upper Marker	113.00
31	12,305	0.00	0.0		115.02
32	13,557	0.00	0.0		116.34
33	14,520	0.00	0.0		117.35
34	15,483	0.00	0.0		118.36
35	17,456	0.00	0.0		120.43
36	19,093	0.00	0.0		122.15
37	20,152	0.00	0.0		123.27
38	21,596	0.00	0.0		124.78
39	25,351	0.00	0.0		128.73

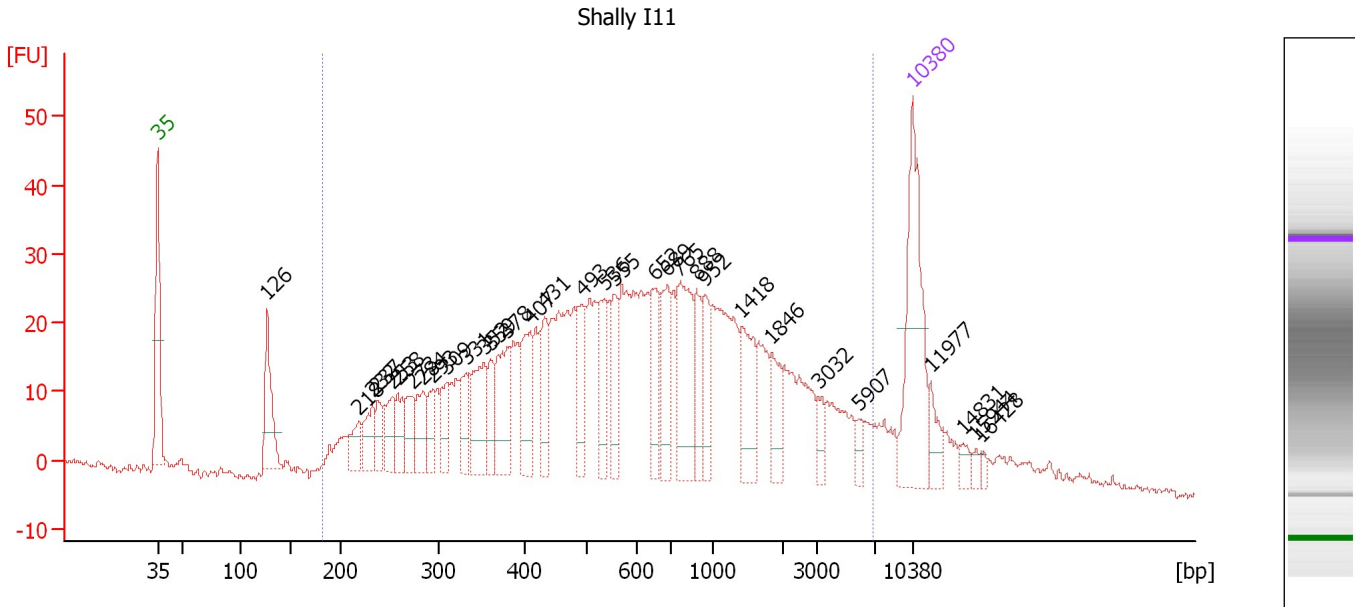
Region table for sample 9 : Shally I8

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
165	1,093	6,859	1,556.4	91	100.0	1,702.61	5,197.2	

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad

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Electropherogram Summary Continued ...



Overall Results for sample 10 : Shally I11

Number of peaks found: 32 Corr. Area 1: 1,065.3
 Noise: 0.6

Peak table for sample 10 : Shally I11

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	58.21	701.4		53.12
3	218	20.88	145.0		61.66
4	232	25.92	169.2		62.93
5	237	18.58	118.7		63.38
6	253	25.64	153.6		64.81
7	258	22.35	131.3		65.27
8	273	23.34	129.7		66.59
9	284	28.81	153.8		67.60
10	293	18.18	93.9		68.47
11	309	21.85	107.2		69.79
12	331	26.29	120.3		71.57
13	352	49.17	211.7		73.25
14	359	23.23	98.1		73.81
15	378	48.14	192.7		75.38
16	407	41.31	153.7		77.52
17	431	32.29	113.4		78.89
18	493	30.23	93.0		82.35
19	536	29.48	83.3		84.43
20	555	27.16	74.2		85.29
21	652	32.87	76.3		89.06
22	689	37.27	81.9		90.23
23	765	64.17	127.2		91.40
24	888	27.10	46.2		92.97
25	952	25.70	40.9		93.78

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad


Created: 12/23/2014 1:12:32 PM
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Electropherogram Summary Continued ...

... Peak table for sample 10 : Shally I11

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,418	37.50	40.1		97.14
27	1,846	21.97	18.0		99.94
28	3,032	8.17	4.1		104.26
29	5,907	6.20	1.6		108.02
30	10,380	75.00	10.9	Upper Marker	113.00
31	11,977	0.00	0.0		114.68
32	14,831	0.00	0.0		117.68
33	15,944	0.00	0.0		118.85
34	16,428	0.00	0.0		119.35

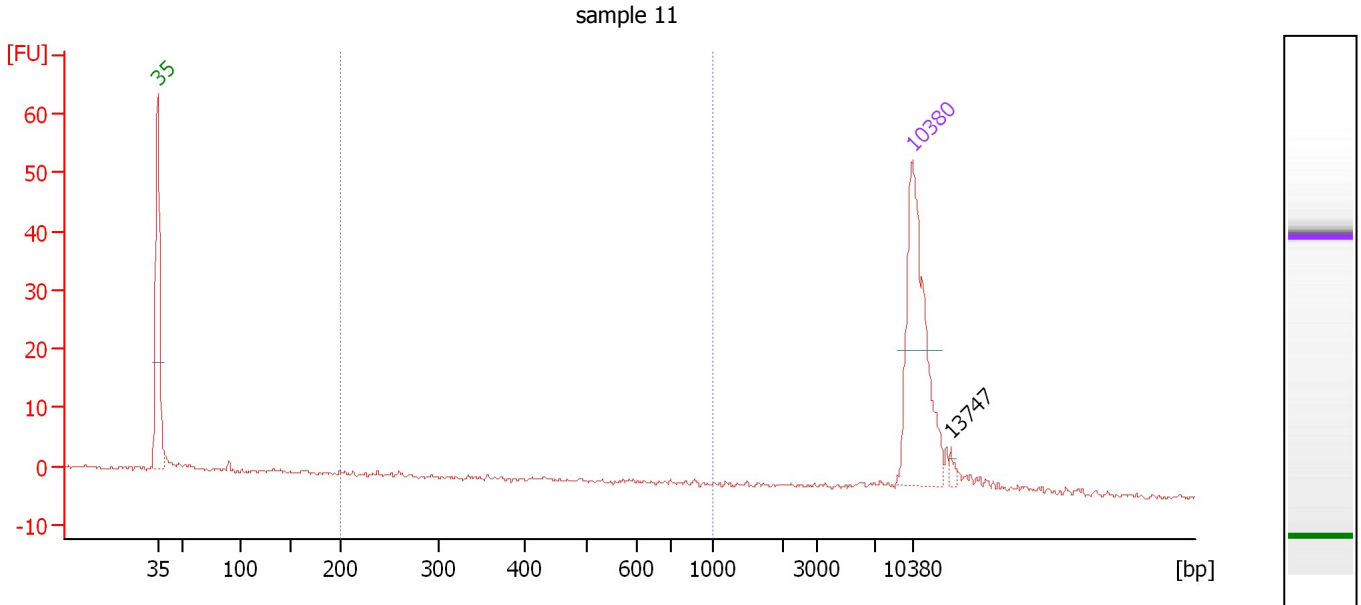
Region table for sample 10 : Shally I11

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
180	1,018	6,829	1,065.3	90	100.0	1,420.57	4,484.5	

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad

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Electropherogram Summary Continued ...



Overall Results for sample 11 : sample 11

Number of peaks found: 1 Corr. Area 1: 5.3
 Noise: 0.3

Peak table for sample 11 : sample 11

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
3	13,747	0.00	0.0		116.54

Region table for sample 11 : sample 11

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	423	1,000	5.3	12	48.6	6.19	29.8	Blue

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad

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Modified: 12/23/2014 1:53:53 PM

Gel Image

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad

Created: 12/23/2014 1:12:32 PM
 Modified: 12/23/2014 1:53:53 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		12/23/2014 1:53:50 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2014-12-23\2014-12-23_002.xad)		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		12/23/2014 1:12:38 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1