

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
Modified: 11/3/2015 12:42:07 PM

**Electrophoresis File Run Summary**

Instrument Information:

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

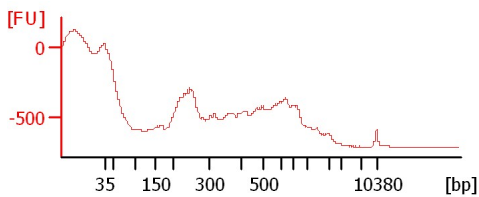
Assay Information:

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

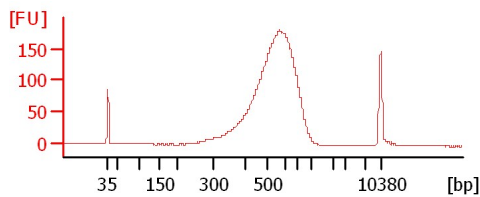
Chip Information:

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

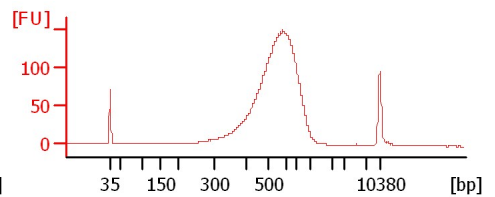
**RS588 SS Library (1:4)**



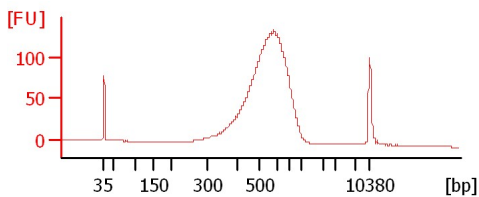
**RS850 SS Library (1:2)**



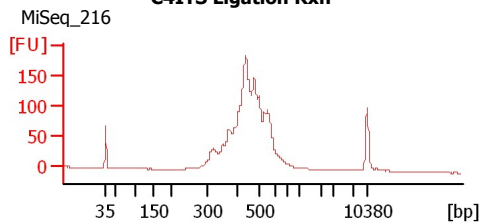
**RS860 SS Library (1:2)**



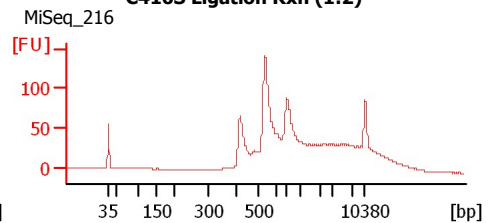
**14-255 SS Library (1:4)**



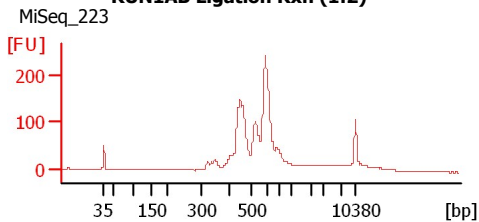
**C4ITS Ligation Rxn**



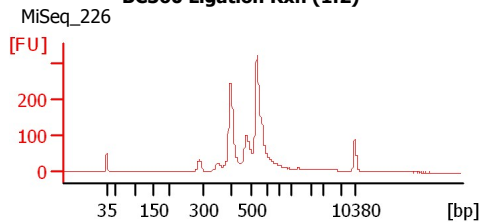
**C416S Ligation Rxn (1:2)**



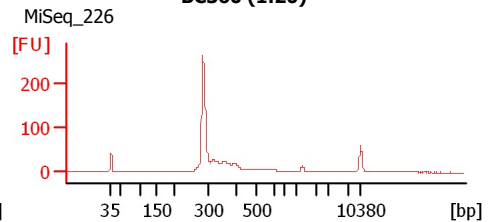
**RUN1AB Ligation Rxn (1:2)**



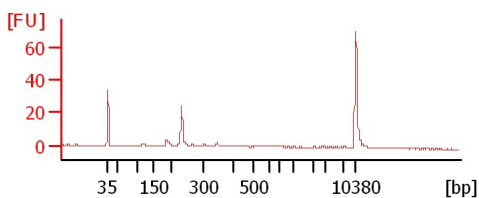
**BC360 Ligation Rxn (1:2)**



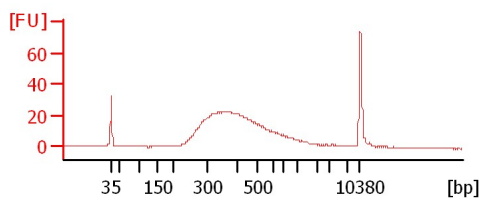
**BC360 (1:20)**



**M219P\_Eva BC 0.9X**



**Bremia Timecourse 11-2-15**



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
RS588 SS Library (1:4)		<input type="checkbox"/>	✓			
RS850 SS Library (1:2)		<input type="checkbox"/>	✓			
RS860 SS Library (1:2)		<input type="checkbox"/>	✓			
14-255 SS Library (1:4)		<input type="checkbox"/>	✓			
C4ITS Ligation Rxn	MiSeq_216	<input type="checkbox"/>	✓			
C416S Ligation Rxn (1:2)	MiSeq_216	<input type="checkbox"/>	✓			
RUN1AB Ligation Rxn (1:2)	MiSeq_223	<input type="checkbox"/>	✓			
BC360 Ligation Rxn (1:2)	MiSeq_226	<input type="checkbox"/>	✓			
BC360 (1:20)	MiSeq_226	<input type="checkbox"/>	✓			
M219P_Eva BC 0.9X		<input type="checkbox"/>	✓			
Bremia Timecourse 11-2-15		<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

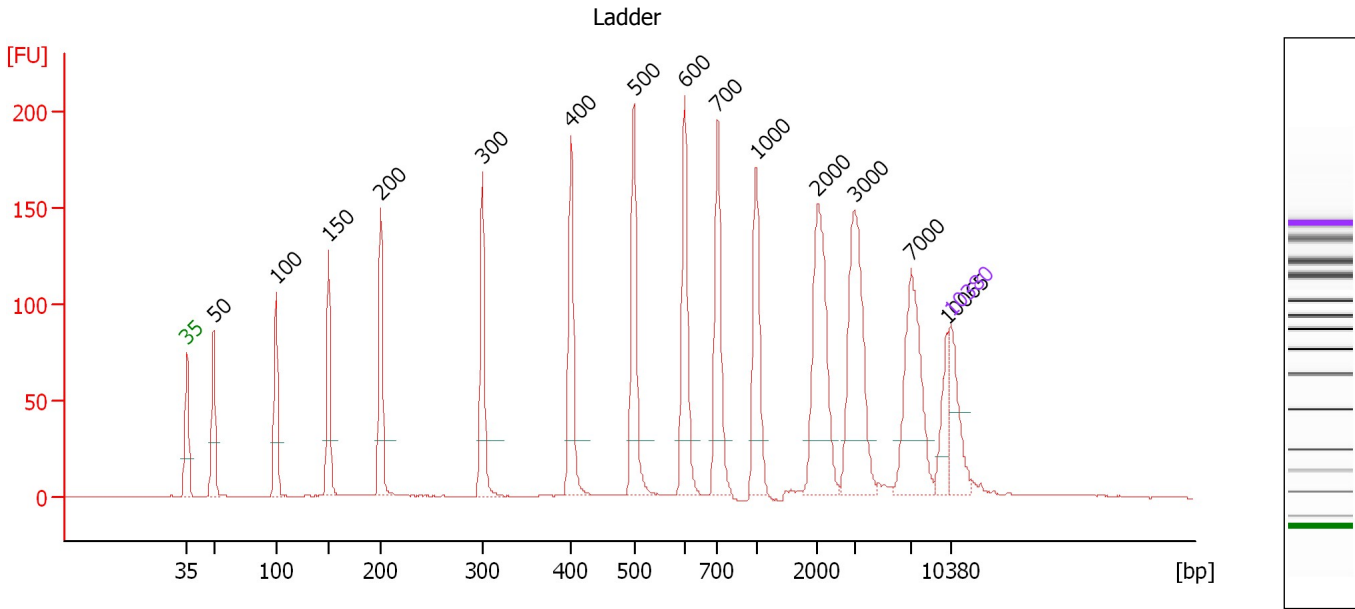
**Ladder**

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

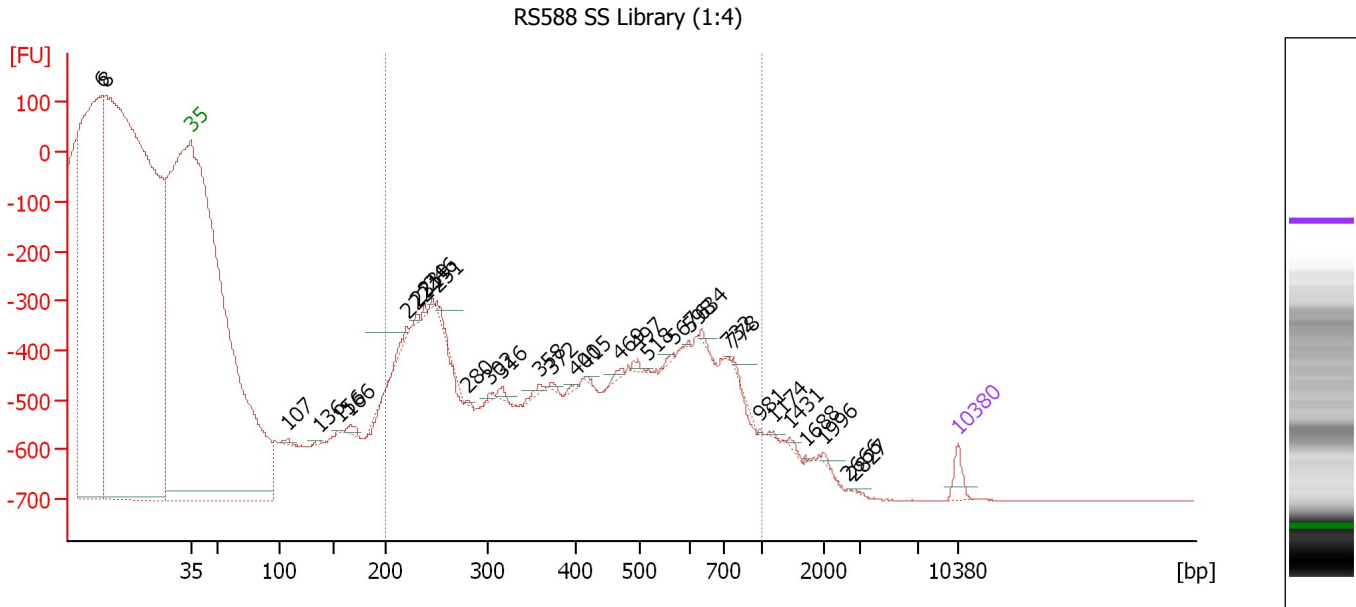
**Peak table for Ladder**

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	45.44
3	100	150.00	2,272.7	Ladder Peak	51.16
4	150	150.00	1,515.2	Ladder Peak	55.99
5	200	150.00	1,136.4	Ladder Peak	60.73
6	300	150.00	757.6	Ladder Peak	70.06
7	400	150.00	568.2	Ladder Peak	78.17
8	500	150.00	454.5	Ladder Peak	83.94
9	600	150.00	378.8	Ladder Peak	88.58
10	700	150.00	324.7	Ladder Peak	91.60
11	1,000	150.00	227.3	Ladder Peak	95.12
12	2,000	150.00	113.6	Ladder Peak	100.79
13	3,000	150.00	75.8	Ladder Peak	104.11
14	7,000	150.00	32.5	Ladder Peak	109.34
15	10,065	0.00	0.0		112.66
16	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : RS588 SS Library (1:4)**

Number of peaks found: 33                      Corr. Area 1: 13.1  
 Noise: 0.5

**Peak table for sample 1 : RS588 SS Library (1:4)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	6	0.00	0.0		34.84
2	8	0.00	0.0		35.18
3	35	125.00	5,411.3	Lower Marker	43.00
4	107	29.36	415.7		51.83
5	136	8.91	99.1		54.65
6	156	11.08	107.4		56.59
7	166	51.28	467.9		57.51
8	222	51.43	351.4		62.76
9	231	19.11	125.3		63.63
10	239	16.35	103.7		64.36
11	246	13.11	80.7		65.04
12	251	43.68	263.8		65.48
13	280	11.37	61.5		68.19
14	302	18.54	93.0		70.23
15	316	31.58	151.2		71.40
16	358	39.21	166.0		74.75
17	372	16.19	66.0		75.86
18	400	13.63	51.7		78.15
19	415	8.11	29.6		79.02
20	469	26.15	84.5		82.13
21	497	22.61	68.9		83.78
22	518	1.61	4.7		84.75
23	567	15.94	42.6		87.03
24	598	5.26	13.3		88.49
25	634	12.72	30.4		89.60

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**Electropherogram Summary Continued ...**

**... Peak table for sample 1 : RS588 SS Library (1:4)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	732	1.78	3.7		91.98
27	778	11.39	22.2		92.51
28	981	3.40	5.3		94.89
29	1,174	6.78	8.7		96.11
30	1,431	15.89	16.8		97.56
31	1,688	3.25	2.9		99.02
32	1,996	11.64	8.8		100.77
33	2,666	1.19	0.7		103.00
34	2,827	4.14	2.2		103.53
35	10,380	75.00	10.9	Upper Marker	113.00

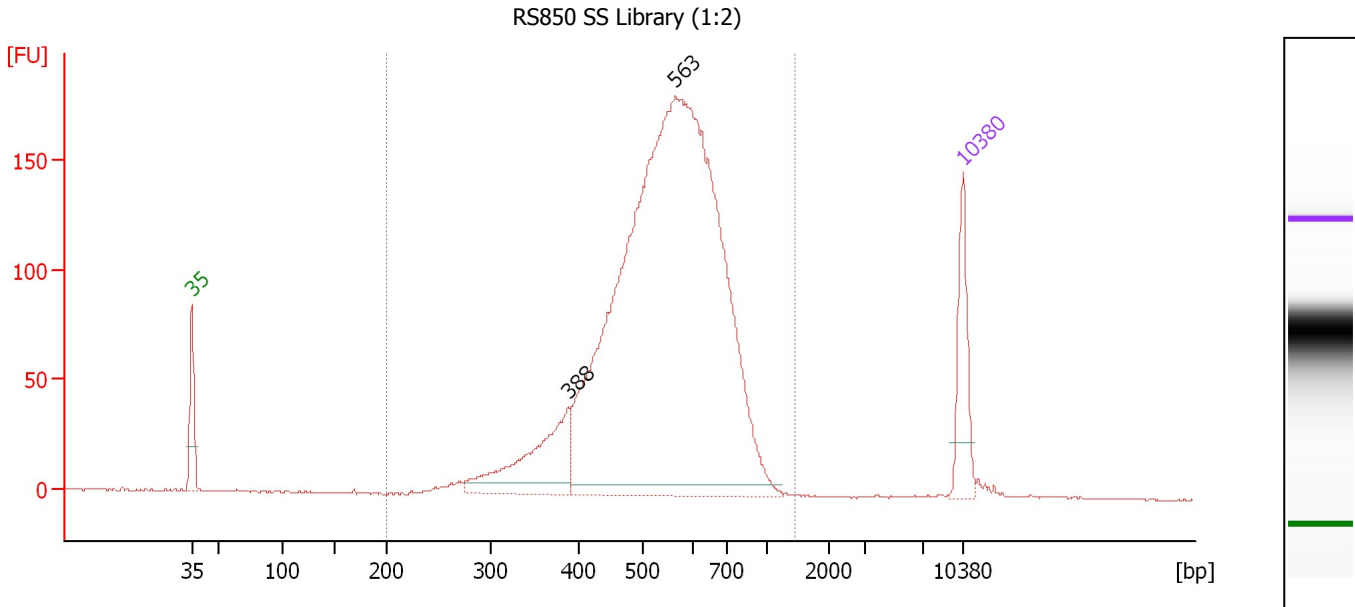
**Region table for sample 1 : RS588 SS Library (1:4)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	631	13.1	33.1	13.77	1	1.2

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : RS850 SS Library (1:2)**

Number of peaks found: 2                      Corr. Area 1: 2,500.8  
 Noise: 0.4

**Peak table for sample 2 : RS850 SS Library (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	388	184.50	721.0		77.18
3	563	1,720.32	4,629.7		86.86
4	10,380	75.00	10.9	Upper Marker	113.00

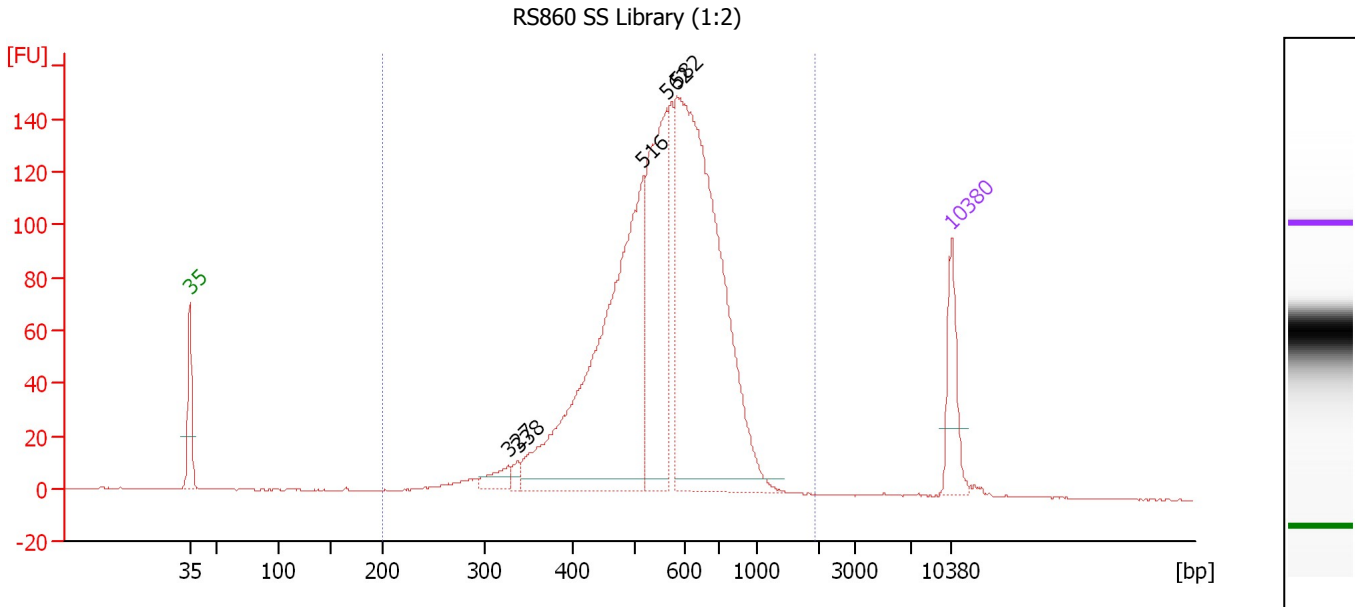
**Region table for sample 2 : RS850 SS Library (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,468	551	2,500.8	5,866.3	1,983.56	99	22.7

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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : RS860 SS Library (1:2)**

Number of peaks found: 5                      Corr. Area 1: 2,055.1  
 Noise: 0.2

**Peak table for sample 3 : RS860 SS Library (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	327	34.63	160.5		72.24
3	338	14.77	66.1		73.17
4	516	797.45	2,340.7		84.69
5	562	370.88	1,000.6		86.79
6	582	922.29	2,402.5		87.72
7	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 3 : RS860 SS Library (1:2)**

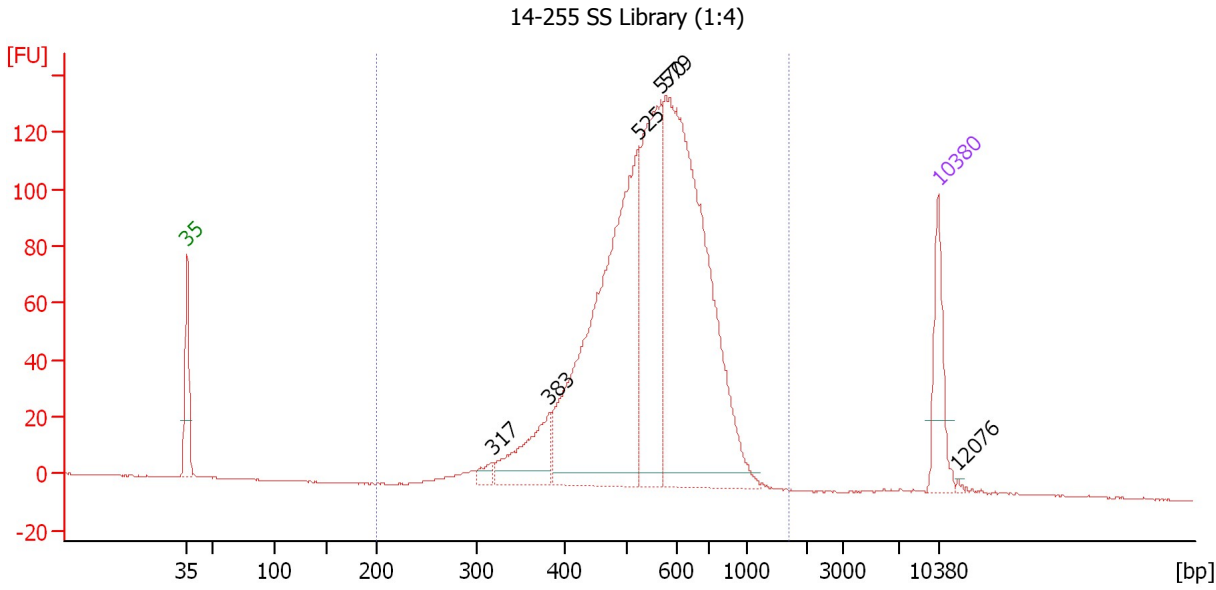
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,933	567	2,055.1	6,935.5	2,388.62	98	25.3



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



**Overall Results for sample 4 : 14-255 SS Library (1:4)**

Number of peaks found: 6                      Corr. Area 1: 1,853.0  
 Noise: 0.1

**Peak table for sample 4 : 14-255 SS Library (1:4)**

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	317	18.34	87.8		71.42
3	383	119.17	471.6		76.78
4	525	720.78	2,081.5		85.08
5	570	340.23	905.0		87.17
6	579	781.51	2,044.2		87.61
7	10,380	75.00	10.9	Upper Marker	113.00
8	12,076	0.00	0.0		114.84

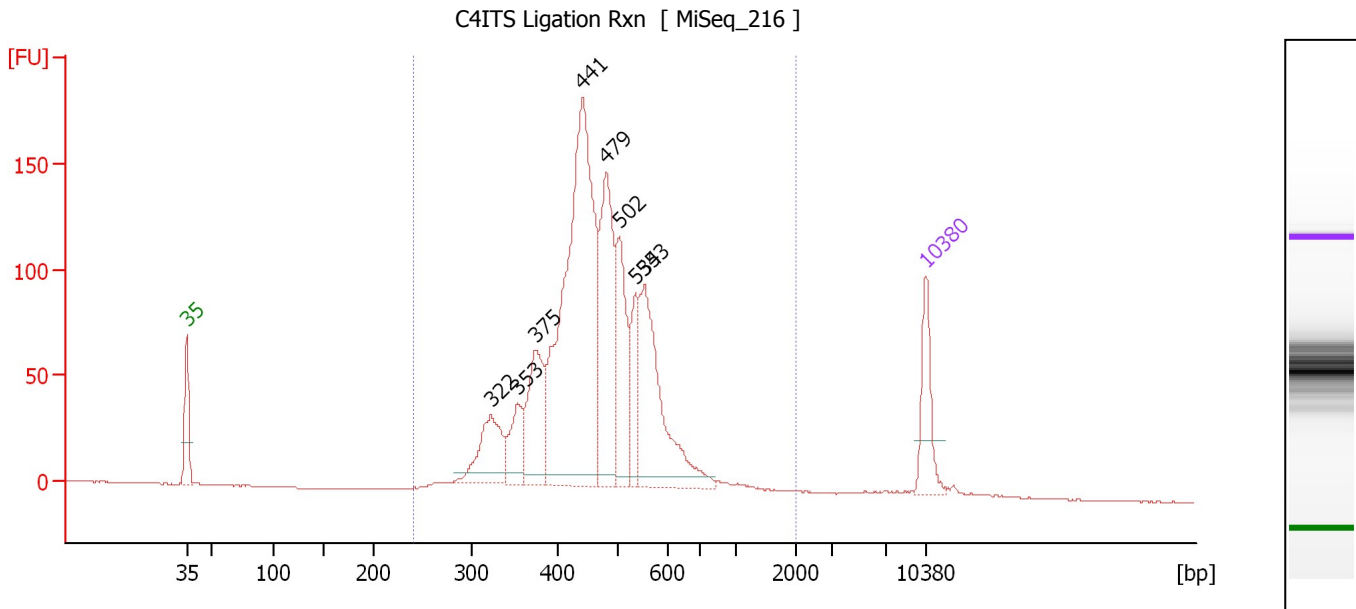
**Region table for sample 4 : 14-255 SS Library (1:4)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,694	559	1,853.0	6,017.8	2,070.80	99	23.1

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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : C4ITS Ligation Rxn**

Number of peaks found: 8                      Corr. Area 1: 1,929.1  
 Noise: 0.1

**Peak table for sample 5 : C4ITS Ligation Rxn**

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	322	135.31	636.9		71.84
3	353	87.12	373.9		74.36
4	375	164.24	663.9		76.13
5	441	804.02	2,763.4		80.53
6	479	294.66	931.3		82.75
7	502	174.32	526.5		84.01
8	534	86.32	244.8		85.53
9	553	298.66	818.6		86.38
10	10,380	75.00	10.9	Upper Marker	113.00

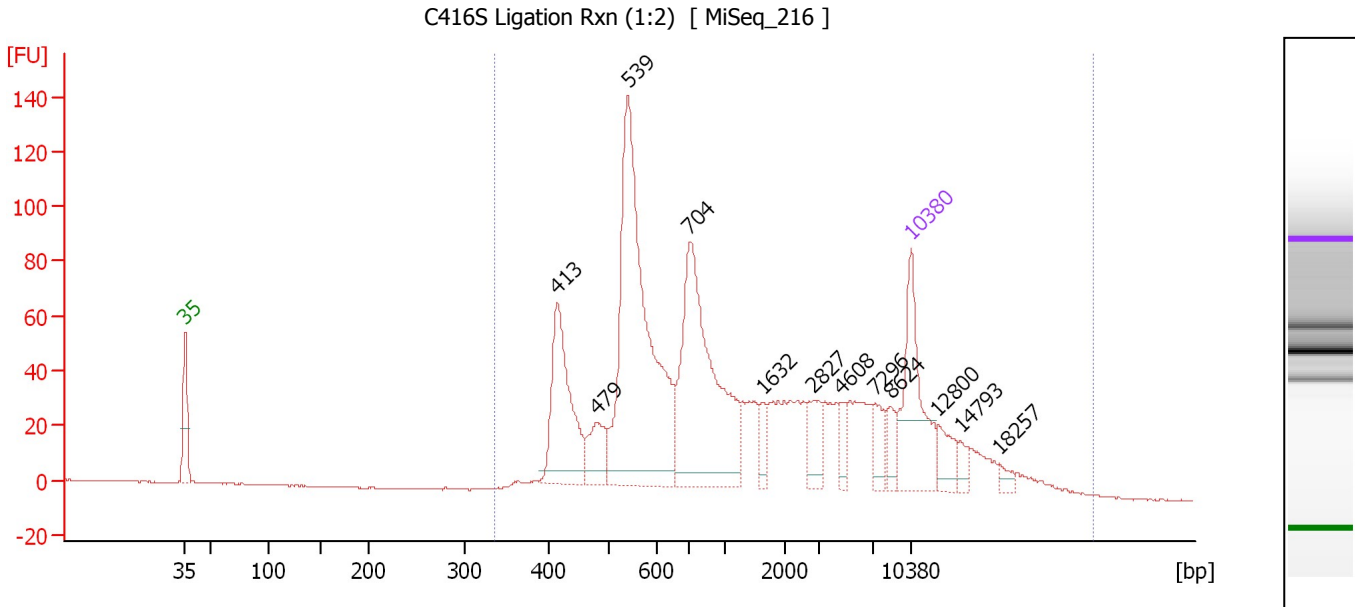
**Region table for sample 5 : C4ITS Ligation Rxn**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
241	1,985	473	1,929.1	7,399.8	2,171.84	98	27.6

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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : C416S Ligation Rxn (1:2)**

Number of peaks found: 12                      Corr. Area 1: 1,691.1  
 Noise: 0.1

**Peak table for sample 6 : C416S Ligation Rxn (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	413	126.27	463.6		78.90
3	479	37.90	120.0		82.71
4	539	339.47	954.4		85.74
5	704	243.17	523.1		91.66
6	1,632	13.62	12.6		98.70
7	2,827	25.78	13.8		103.54
8	4,608	11.85	3.9		106.21
9	7,296	18.34	3.8		109.66
10	8,624	14.16	2.5		111.10
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,800	0.00	0.0		115.62
13	14,793	0.00	0.0		117.78
14	18,257	0.00	0.0		121.54

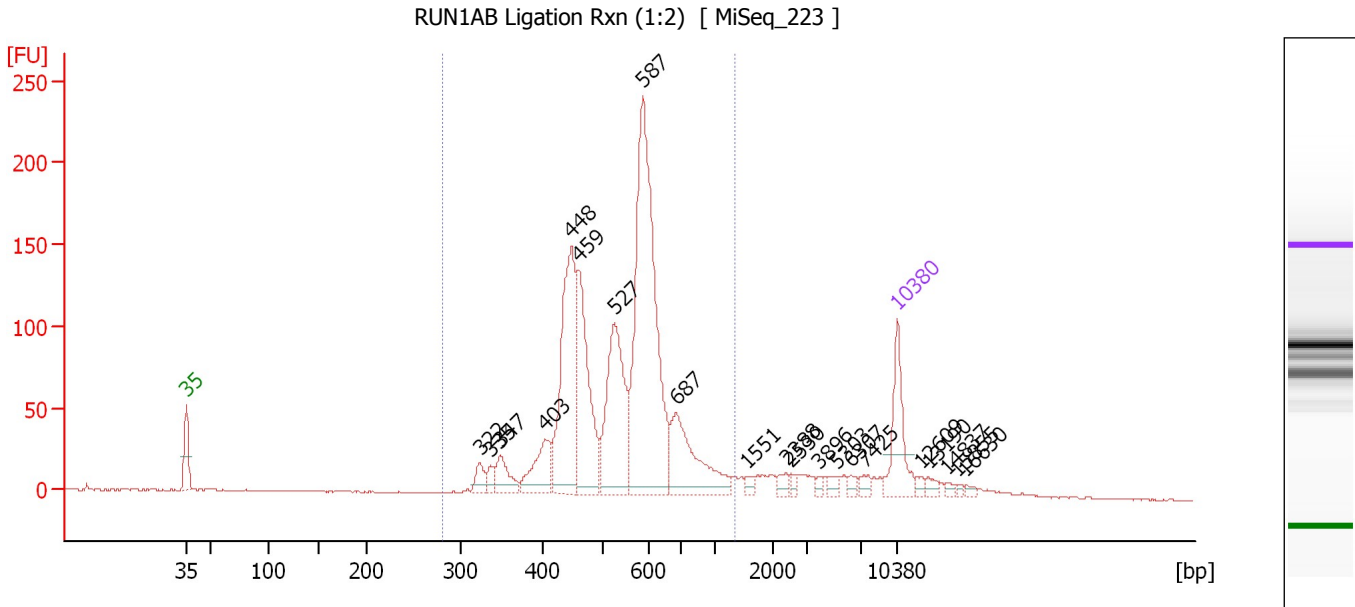
**Region table for sample 6 : C416S Ligation Rxn (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
335	26,555	3,967	1,691.1	2,147.2	1,087.29	100	100.0

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**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : RUN1AB Ligation Rxn (1:2)**

Number of peaks found: 21                      Corr. Area 1: 1,697.6  
 Noise: 0.4

**Peak table for sample 7 : RUN1AB Ligation Rxn (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	322	26.40	124.1		71.88
3	335	19.42	87.7		72.93
4	347	46.48	202.9		73.88
5	403	77.88	292.8		78.34
6	448	296.96	1,005.2		80.91
7	459	215.19	711.1		81.54
8	527	229.01	658.9		85.17
9	587	535.25	1,382.6		87.95
10	687	153.26	338.1		91.21
11	1,551	8.23	8.0		98.24
12	2,388	10.01	6.3		102.08
13	2,530	6.29	3.8		102.55
14	3,896	5.45	2.1		105.28
15	5,303	10.80	3.1		107.12
16	6,307	7.90	1.9		108.43
17	7,425	10.69	2.2		109.80
18	10,380	75.00	10.9	Upper Marker	113.00
19	12,609	0.00	0.0		115.42
20	13,190	0.00	0.0		116.05
21	14,837	0.00	0.0		117.83
22	15,855	0.00	0.0		118.93
23	16,630	0.00	0.0		119.77

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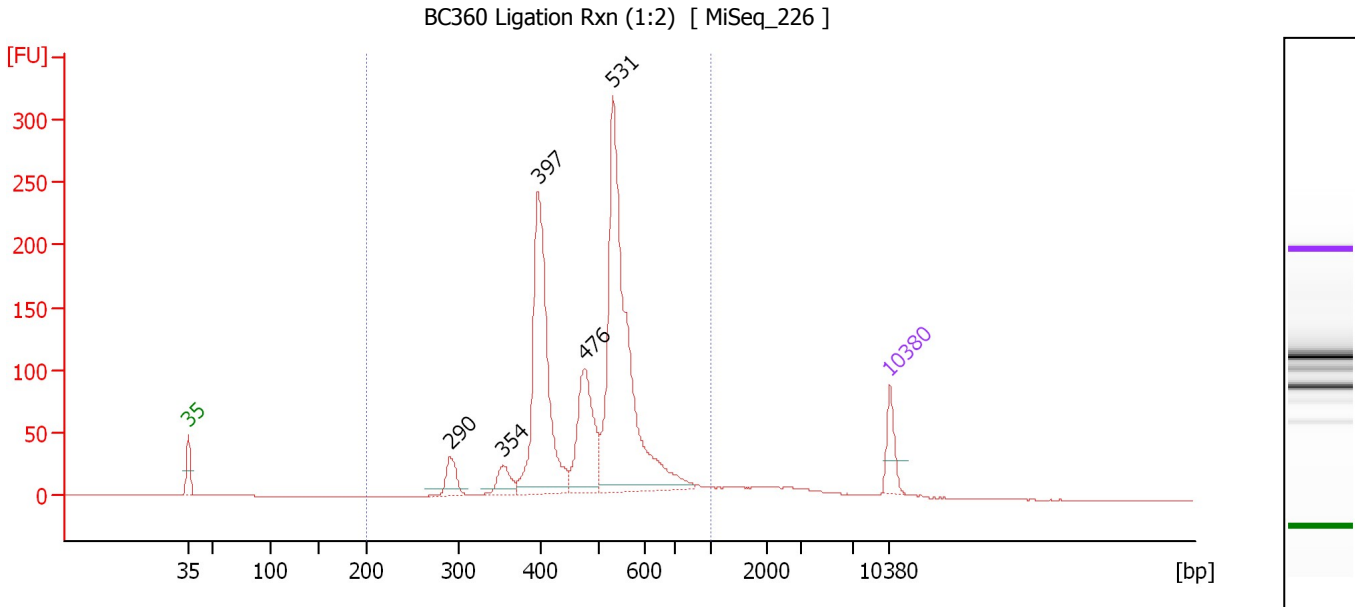
**Electropherogram Summary Continued ...****... Region table for sample 7 : RUN1AB Ligation Rxn (1:2)**

<b>From [bp]</b>	<b>To [bp]</b>	<b>Average Size [bp]</b>	<b>Corr. Area</b>	<b>Molarity [pmol/l]</b>	<b>Co Conc. lor [pg/μl]</b>	<b>% of Total</b>	<b>Size distribution in CV [%]</b>
281	1,330	549	1,697.6	4,767.8	■ 1,611.26	86	24.9

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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : BC360 Ligation Rxn (1:2)**

Number of peaks found: 5                      Corr. Area 1: 1,701.2  
 Noise: 0.2

**Peak table for sample 8 : BC360 Ligation Rxn (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	290	97.26	508.4		69.12
3	354	80.50	344.6		74.44
4	397	814.55	3,112.0		77.89
5	476	352.38	1,120.7		82.57
6	531	1,186.31	3,382.3		85.39
7	10,380	75.00	10.9	Upper Marker	113.00

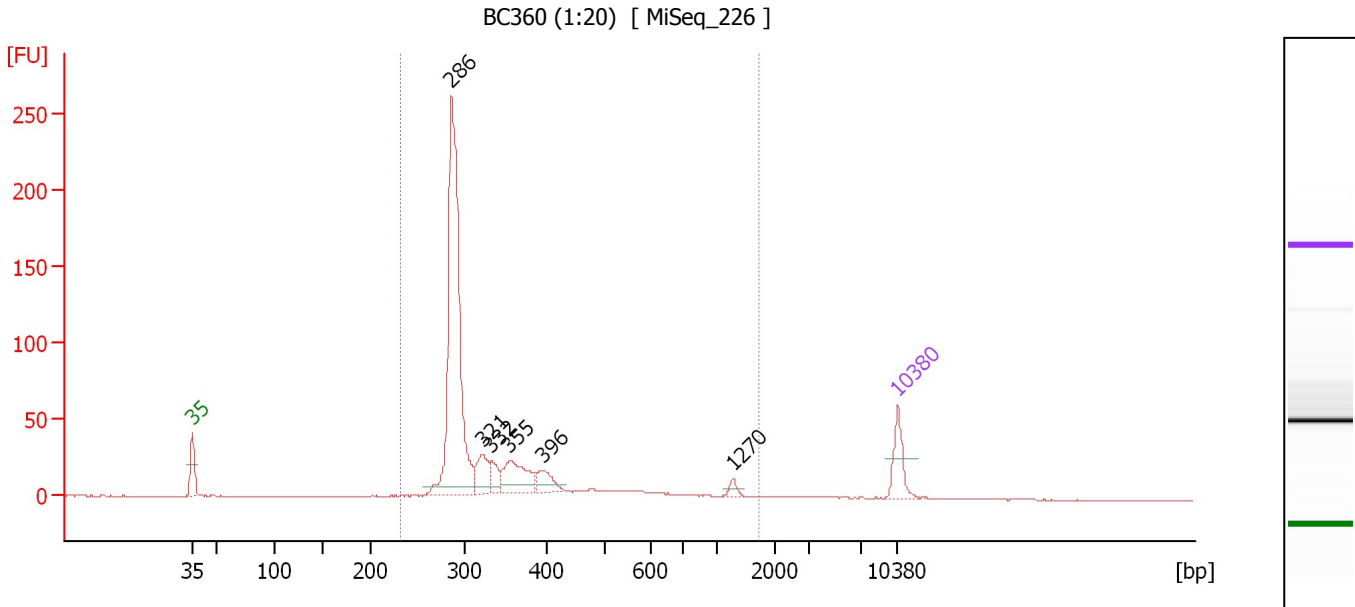
**Region table for sample 8 : BC360 Ligation Rxn (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	495	1,701.2	8,743.4	2,696.24	92	20.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
 Modified: 11/3/2015 12:42:07 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : BC360 (1:20)**

Number of peaks found: 6                      Corr. Area 1: 777.6  
 Noise: 0.1

**Peak table for sample 9 : BC360 (1:20)**

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	286	1,101.09	5,842.4		68.71
3	321	103.59	489.6		71.73
4	332	57.02	260.0		72.68
5	355	156.10	667.2		74.48
6	396	62.48	239.3		77.81
7	1,270	16.16	19.3		96.65
8	10,380	75.00	10.9	Upper Marker	113.00

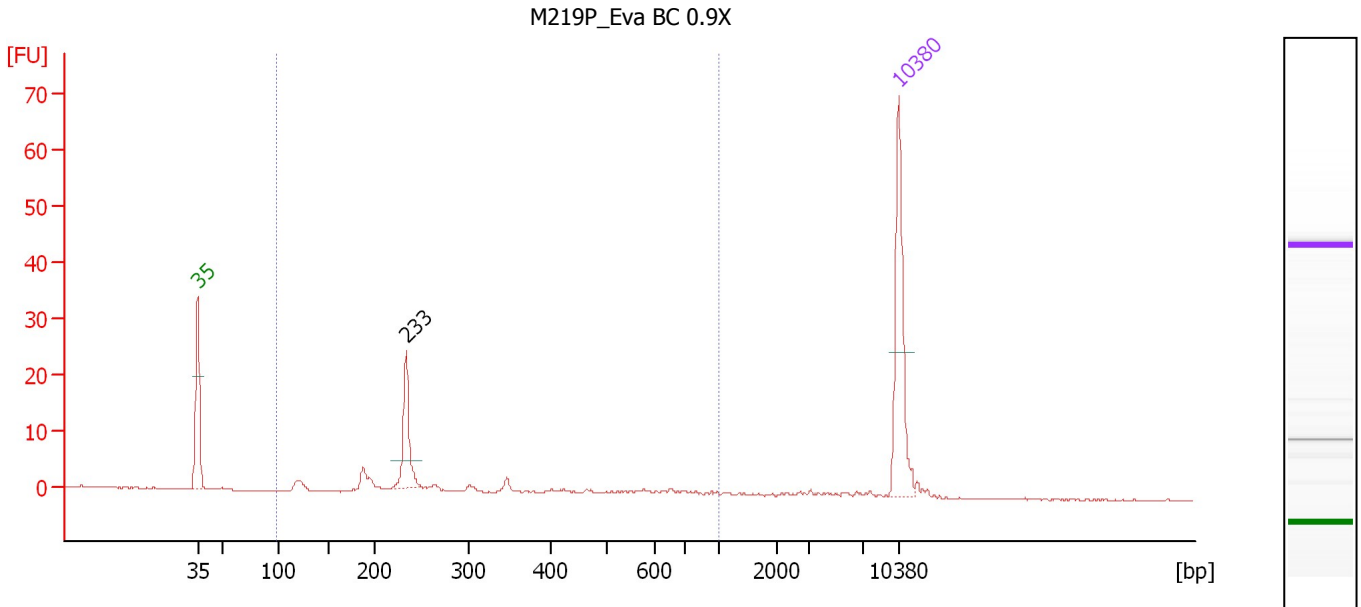
**Region table for sample 9 : BC360 (1:20)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
231	1,721	364	777.6	8,268.4	1,745.93	96	50.3

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
Modified: 11/3/2015 12:42:07 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : M219P Eva BC 0.9X**

Number of peaks found: 1                      Corr. Area 1: 49.8  
Noise: 0.1

**Peak table for sample 10 : M219P Eva BC 0.9X**

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	233	59.15	384.6		63.81
3	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 10 : M219P Eva BC 0.9X**

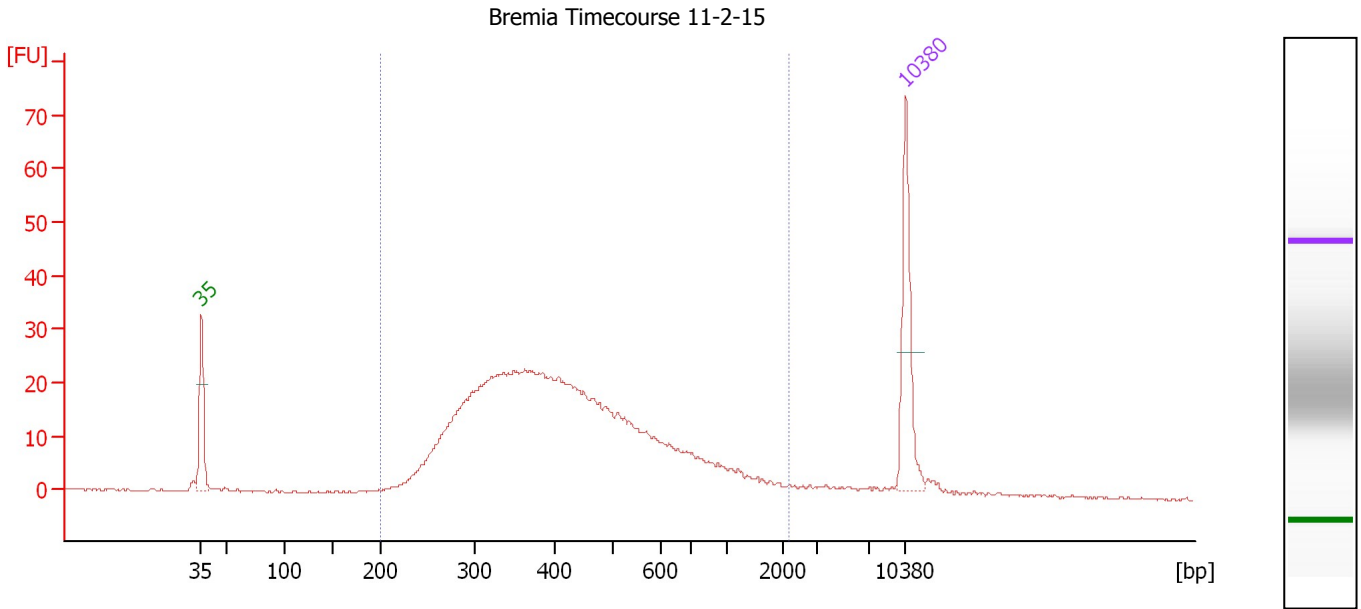
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
98	1,000	299	49.8	768.6	118.06	86	53.4



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
 Modified: 11/3/2015 12:42:07 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : Bremia Timecourse 11-2-15**

Number of peaks found: 0                      Corr. Area 1: 579.9  
 Noise: 0.2

**Peak table for sample 11 : Bremia Timecourse 11-2-15**

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 : Bremia Timecourse 11-2-15**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	2,184	468	579.9	4,336.0	1,096.23	95	54.2

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Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
Modified: 11/3/2015 12:42:07 PM

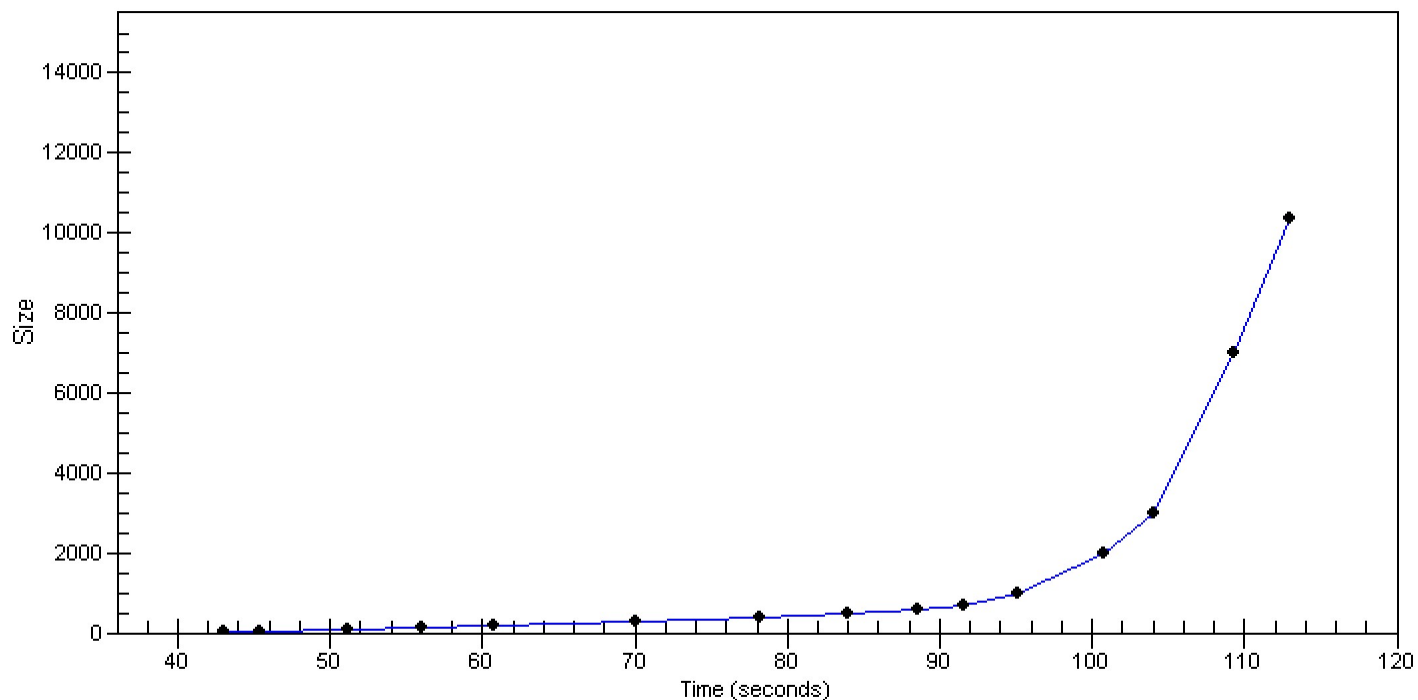
**Gel Image**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
Modified: 11/3/2015 12:42:07 PM

**Curves**

**Standard Curve**



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-03\2015-11-03\_002.xad

Created: 11/3/2015 12:00:07 PM  
 Modified: 11/3/2015 12:42:07 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		11/3/2015 10:41:24 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-11-03\2015-11-03_002.xad)		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		11/3/2015 10:00:12 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1