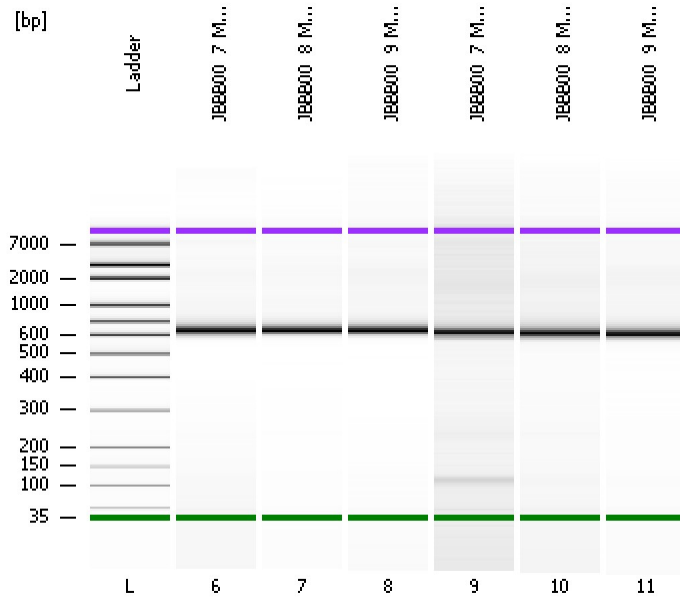


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
Modified: 3/2/2016 4:12:27 PM

**Electrophoresis File Run Summary**



Instrument Information:

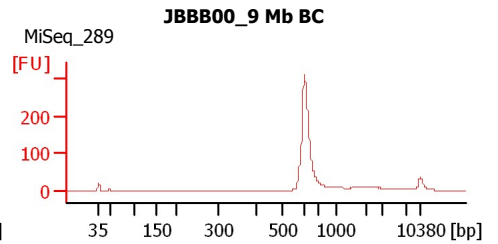
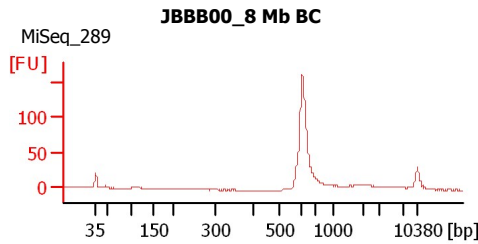
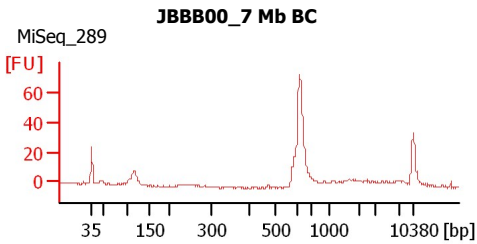
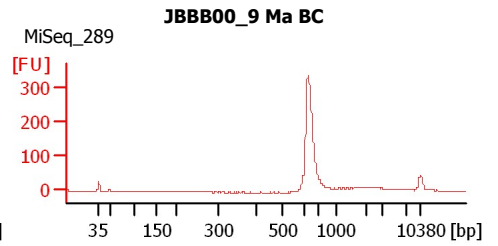
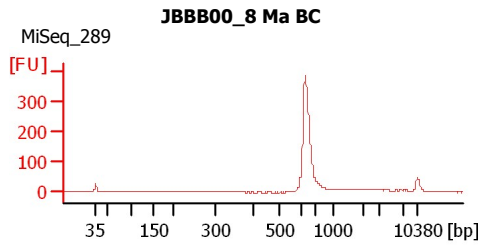
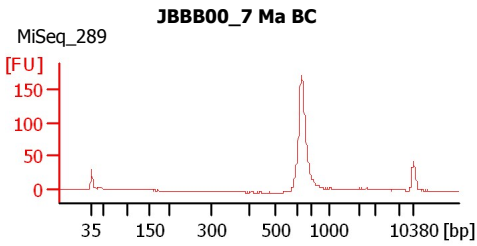
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

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:



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
JBBB00_7 Ma BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
JBBB00_8 Ma BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
JBBB00_9 Ma BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
JBBB00_7 Mb BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
JBBB00_8 Mb BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
JBBB00_9 Mb BC	MiSeq_289	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
Ladder		<input type="checkbox"/>	<input checked="" type="checkbox"/>			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**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

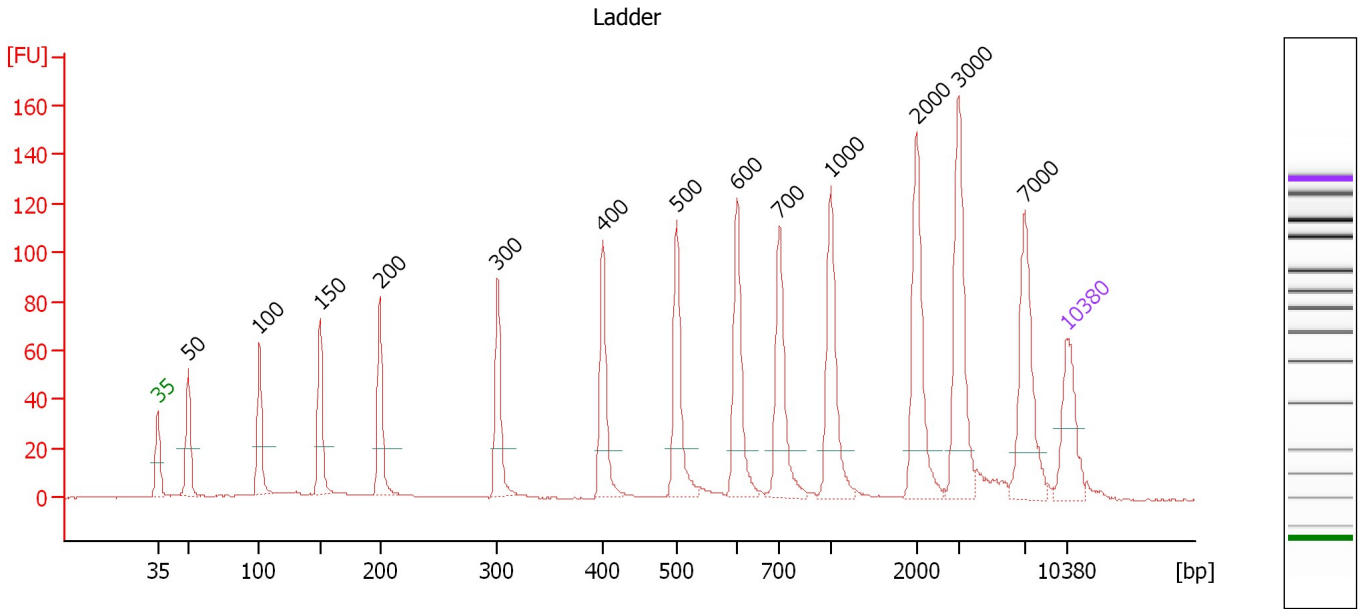
**Ladder**

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:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

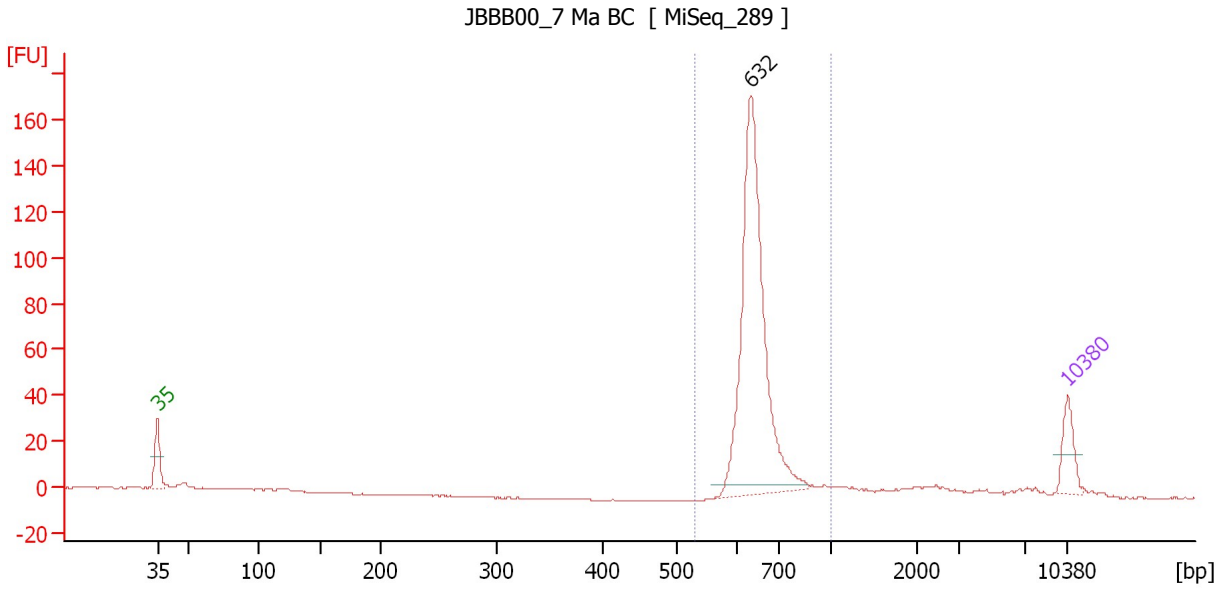
**Peak table for Ladder**

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	45.35
3	100	150.00	2,272.7	Ladder Peak	50.84
4	150	150.00	1,515.2	Ladder Peak	55.49
5	200	150.00	1,136.4	Ladder Peak	60.09
6	300	150.00	757.6	Ladder Peak	69.17
7	400	150.00	568.2	Ladder Peak	77.27
8	500	150.00	454.5	Ladder Peak	82.94
9	600	150.00	378.8	Ladder Peak	87.59
10	700	150.00	324.7	Ladder Peak	90.86
11	1,000	150.00	227.3	Ladder Peak	94.80
12	2,000	150.00	113.6	Ladder Peak	101.40
13	3,000	150.00	75.8	Ladder Peak	104.63
14	7,000	150.00	32.5	Ladder Peak	109.77
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : JBBB00\_7 Ma BC**

Number of peaks found: 1                      Corr. Area 1: 384.3  
 Noise: 0.2

**Peak table for sample 6 : JBBB00\_7 Ma BC**

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	632	1,001.50	2,402.9		88.62
3	10,380	75.00	10.9	Upper Marker	113.00

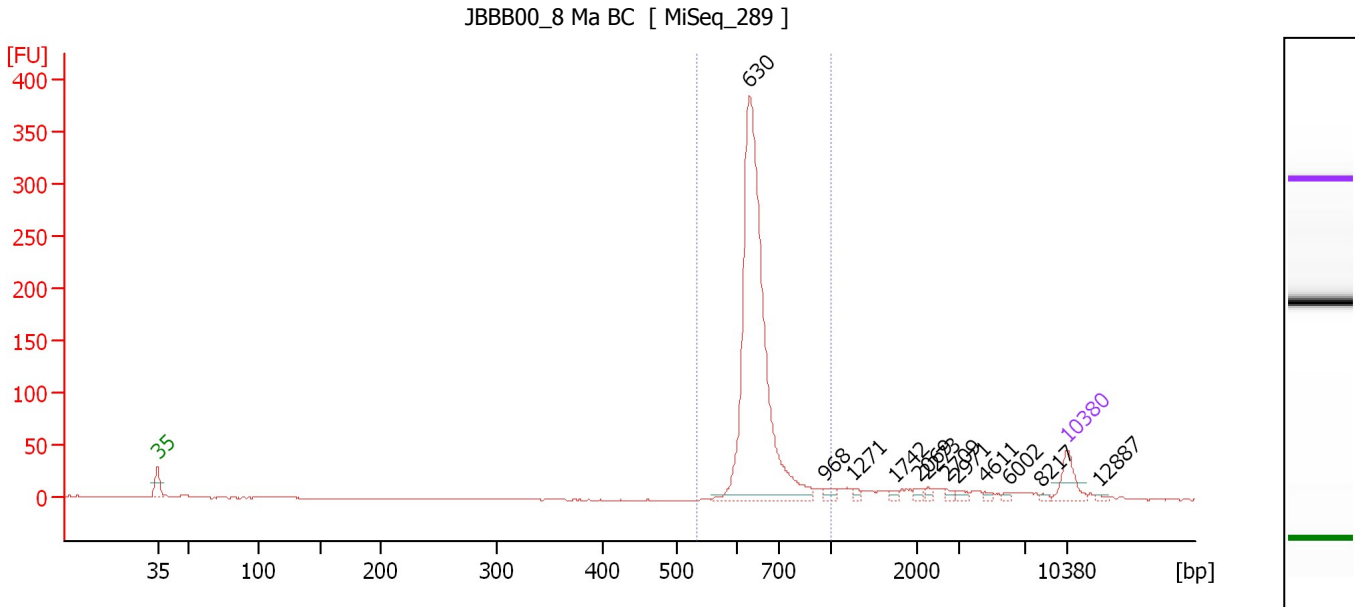
**Region table for sample 6 : JBBB00\_7 Ma BC**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
529	1,000	650	384.3	2,346.7	1,001.84	89	8.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : JBBB00\_8 Ma BC**

Number of peaks found: 12                      Corr. Area 1: 817.0  
 Noise: 0.4

**Peak table for sample 7 : JBBB00\_8 Ma BC**

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	630	1,601.18	3,853.6		88.55
3	968	23.63	37.0		94.38
4	1,271	13.27	15.8		96.59
5	1,742	11.39	9.9		99.70
6	2,069	13.17	9.6		101.62
7	2,273	10.97	7.3		102.28
8	2,709	12.88	7.2		103.69
9	2,971	13.99	7.1		104.54
10	4,611	8.31	2.7		106.70
11	6,002	7.97	2.0		108.49
12	8,217	7.00	1.3		110.93
13	10,380	75.00	10.9	Upper Marker	113.00
14	12,887	0.00	0.0		115.40

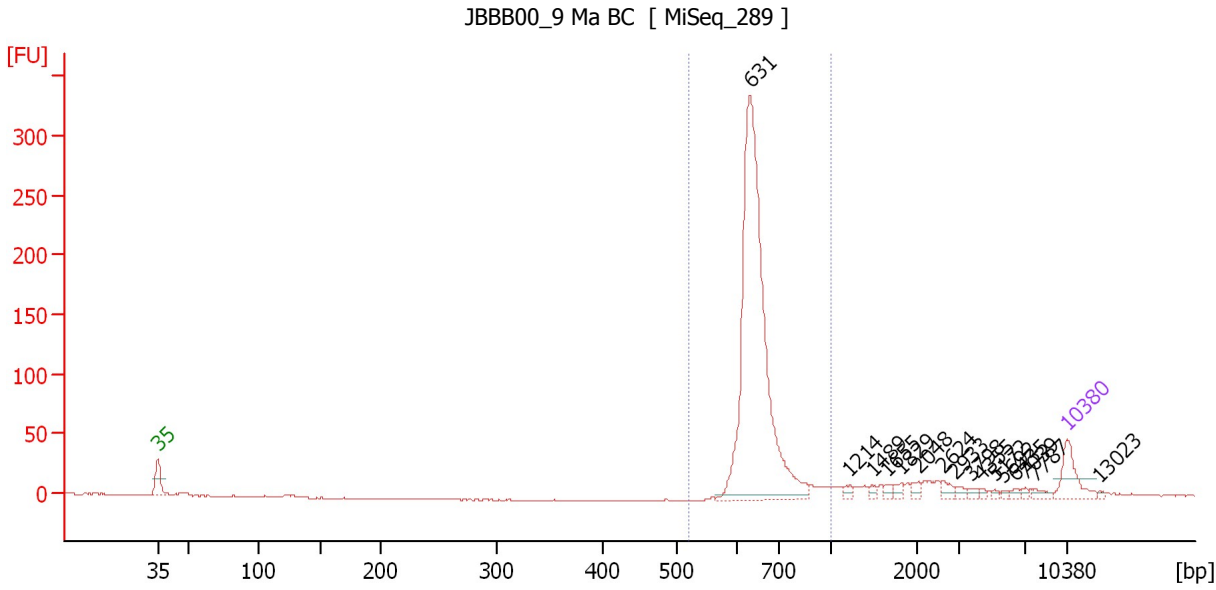
**Region table for sample 7 : JBBB00\_8 Ma BC**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
533	1,000	655	817.0	3,718.5	1,597.62	83	9.0

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : JBBB00\_9 Ma BC**

Number of peaks found: 16                      Corr. Area 1: 722.5  
 Noise: 0.4

**Peak table for sample 8 : JBBB00\_9 Ma BC**

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	631	1,285.67	3,089.5		88.59
3	1,214	14.39	18.0		96.22
4	1,489	10.39	10.6		98.03
5	1,655	11.40	10.4		99.12
6	1,829	14.34	11.9		100.27
7	2,048	14.72	10.9		101.56
8	2,624	18.58	10.7		103.42
9	2,933	11.73	6.1		104.42
10	3,798	10.55	4.2		105.66
11	4,355	6.24	2.2		106.37
12	5,172	5.72	1.7		107.42
13	5,692	5.51	1.5		108.09
14	6,435	9.25	2.2		109.04
15	7,039	6.66	1.4		109.81
16	7,787	13.89	2.7		110.52
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,023	0.00	0.0		115.53

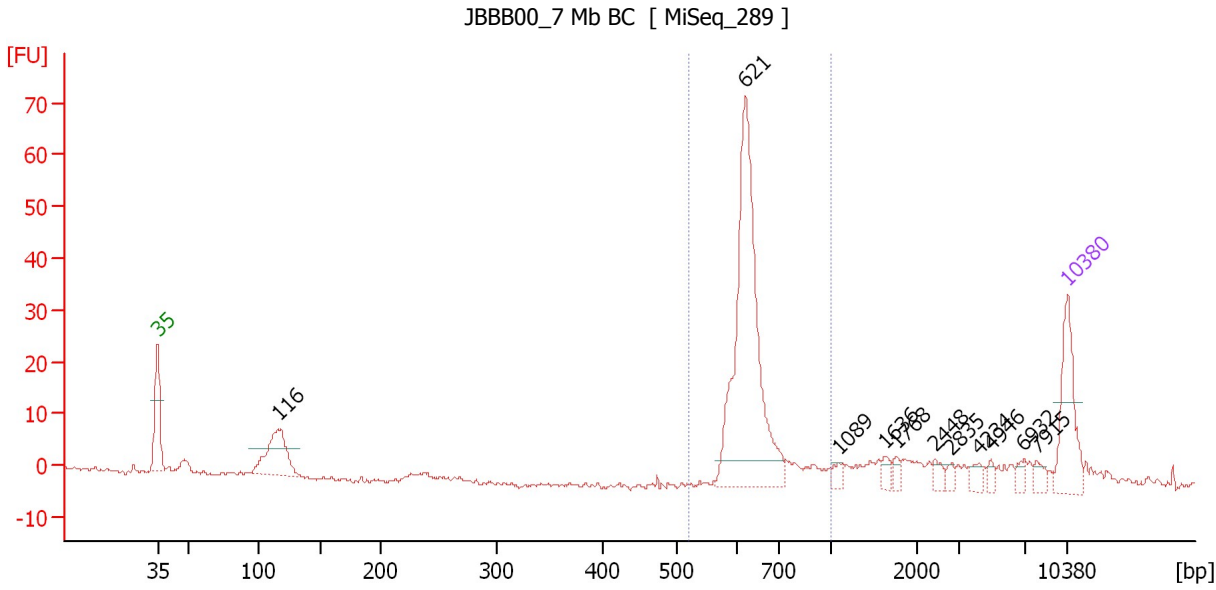
**Region table for sample 8 : JBBB00\_9 Ma BC**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
520	1,000	653	722.5	2,907.4	1,245.98	84	8.4

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : JBBB00 7 Mb BC**

Number of peaks found: 11                      Corr. Area 1: 169.9  
 Noise: 0.5

**Peak table for sample 9 : JBBB00 7 Mb BC**

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	116	115.23	1,510.6		52.29
3	621	394.39	962.4		88.27
4	1,089	8.90	12.4		95.39
5	1,636	10.01	9.3		99.00
6	1,768	8.52	7.3		99.87
7	2,448	10.44	6.5		102.85
8	2,835	6.94	3.7		104.10
9	4,234	10.39	3.7		106.22
10	4,946	7.12	2.2		107.13
11	6,932	8.71	1.9		109.68
12	7,915	10.13	1.9		110.64
13	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 9 : JBBB00 7 Mb BC**

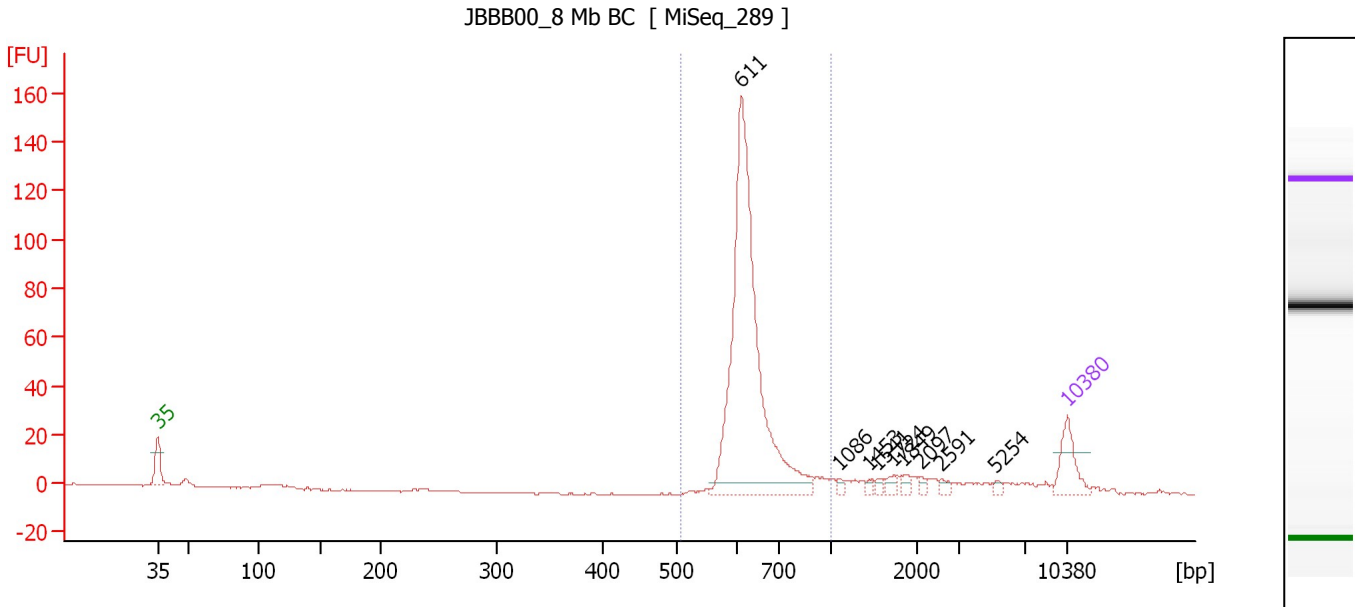
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
521	1,000	648	169.9	1,018.7	430.63	53	11.8



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : JBBB00 8 Mb BC**

Number of peaks found: 9                      Corr. Area 1: 391.0  
 Noise: 0.3

**Peak table for sample 10 : JBBB00 8 Mb BC**

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	611	1,061.08	2,630.1		87.96
3	1,086	9.88	13.8		95.37
4	1,453	8.81	9.2		97.79
5	1,541	9.41	9.3		98.37
6	1,724	14.61	12.8		99.58
7	1,849	14.30	11.7		100.40
8	2,097	9.58	6.9		101.71
9	2,591	11.46	6.7		103.31
10	5,254	8.35	2.4		107.53
11	10,380	75.00	10.9	Upper Marker	113.00

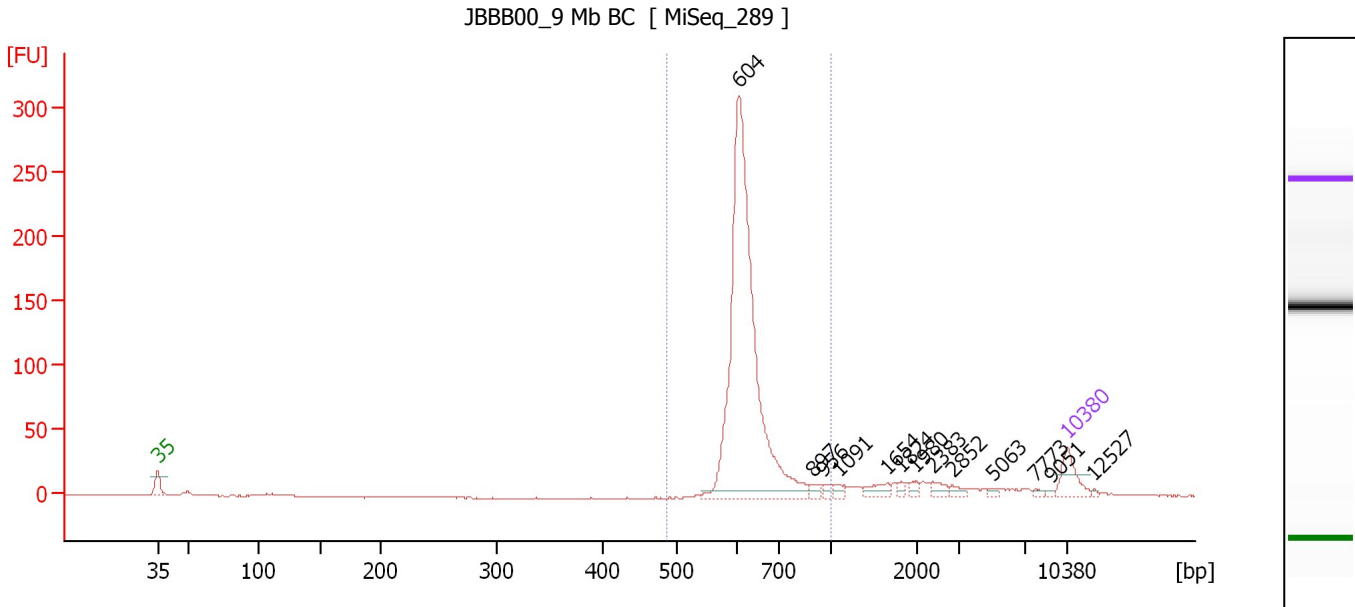
**Region table for sample 10 : JBBB00 8 Mb BC**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
507	1,000	641	391.0	2,557.2	1,071.00	75	11.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
 Modified: 3/2/2016 4:12:27 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : JBBB00\_9 Mb BC**

Number of peaks found: 13                      Corr. Area 1: 716.0  
 Noise: 0.3

**Peak table for sample 11 : JBBB00\_9 Mb BC**

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	604	1,510.19	3,786.3		87.73
3	897	16.98	28.7		93.45
4	956	12.97	20.5		94.23
5	1,091	19.74	27.4		95.40
6	1,654	36.95	33.8		99.12
7	1,824	14.22	11.8		100.24
8	1,980	18.23	13.9		101.27
9	2,383	25.18	16.0		102.64
10	2,852	17.40	9.2		104.15
11	5,063	10.07	3.0		107.28
12	7,773	8.20	1.6		110.51
13	9,051	5.59	0.9		111.73
14	10,380	75.00	10.9	Upper Marker	113.00
15	12,527	0.00	0.0		115.05

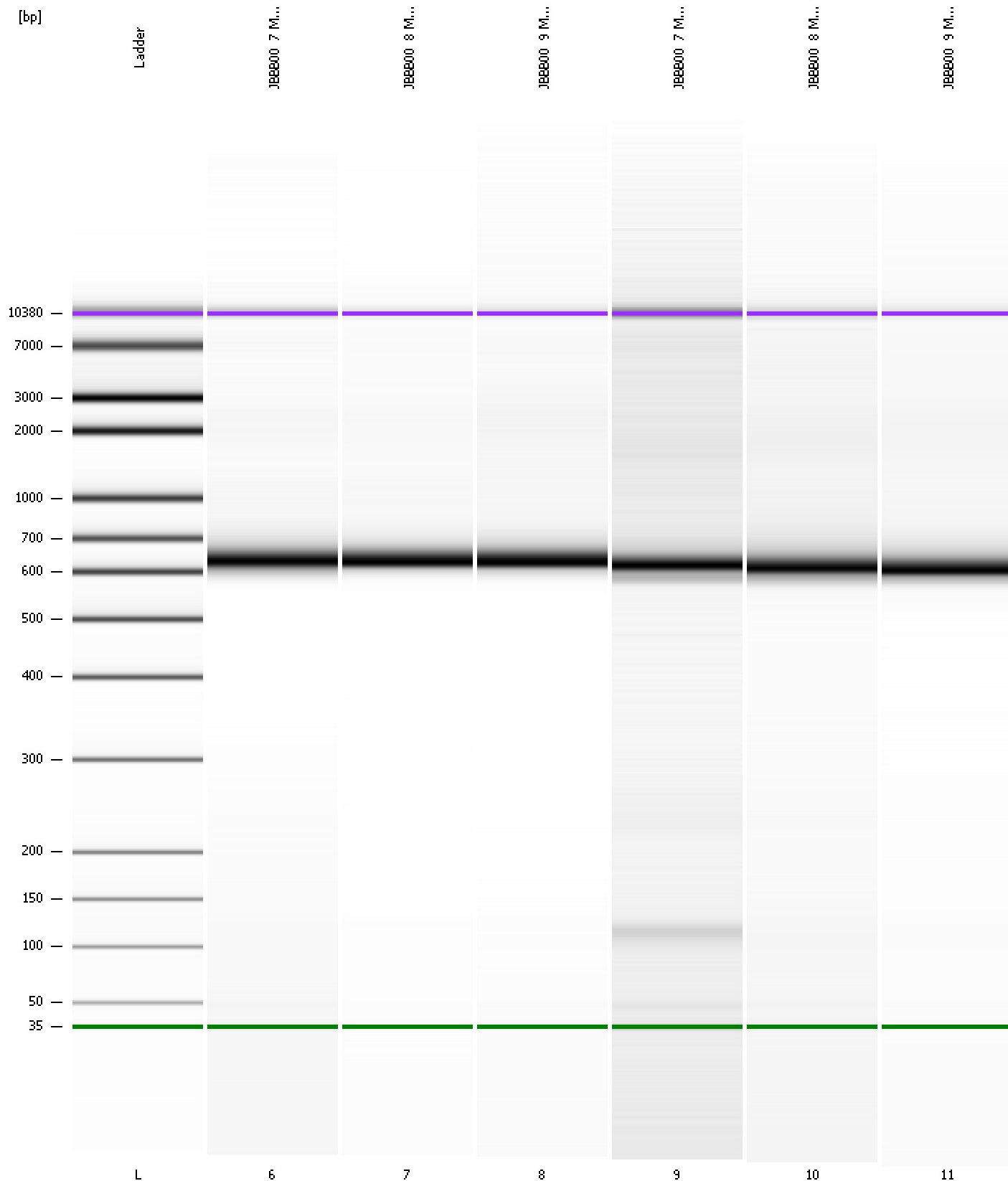
**Region table for sample 11 : JBBB00\_9 Mb BC**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
488	1,000	634	716.0	3,738.8	1,549.74	78	10.6

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad

Created: 3/2/2016 3:28:41 PM  
Modified: 3/2/2016 4:12:27 PM

**Gel Image**



Assay Class: High Sensitivity DNA Assay Created: 3/2/2016 3:28:41 PM  
 Data Path: C:\...analyzer\2016-03-02\2016-03-02\_002\_MiSeq289\_7-9Ma\_7-9Mb.xad Modified: 3/2/2016 4:12:27 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		3/2/2016 4:10:00 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-03-02\2016-03-02_002.xad)		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		3/2/2016 3:28:46 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1