

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

Created: 7/2/2018 4:06:07 PM  
Modified: 7/2/2018 4:51:44 PM

**Electrophoresis File Run Summary**

Instrument Information:

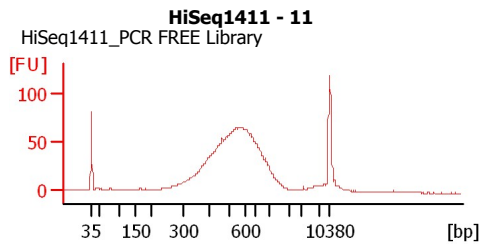
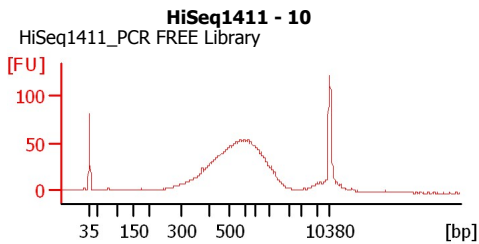
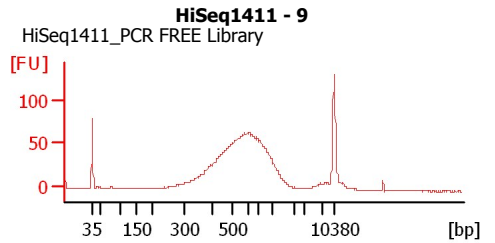
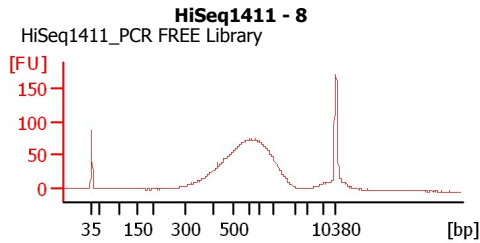
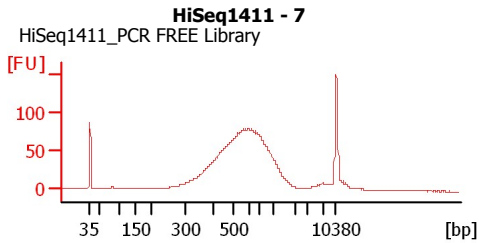
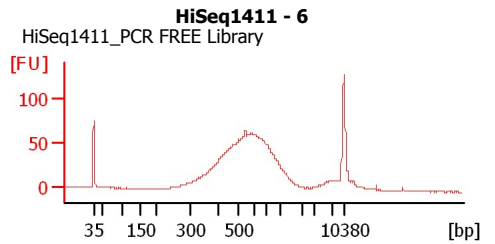
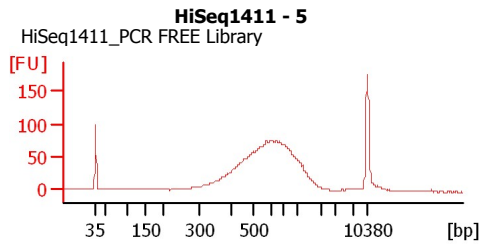
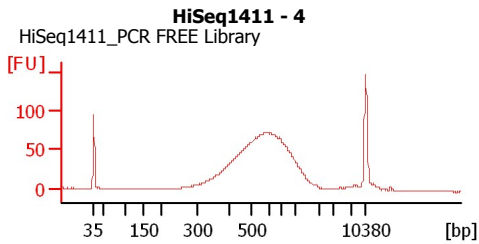
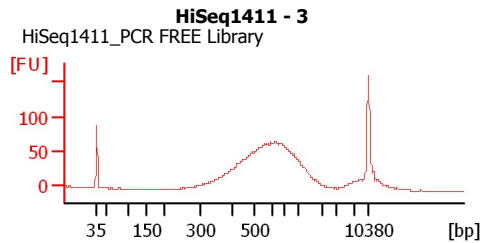
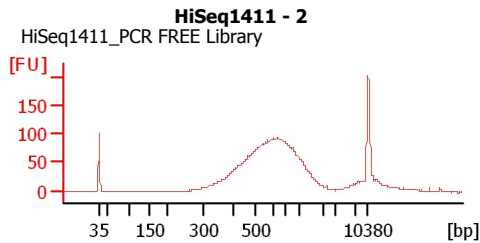
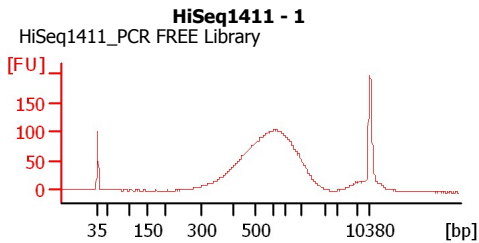
Instrument Name: DE34903152      Firmware: C.01.069  
Serial#: DE34903152      Type: G2938C

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:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq1411 - 1	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 2	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 3	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 4	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 5	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 6	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 7	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 8	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 9	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 10	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
HiSeq1411 - 11	HiSeq1411_PCR FREE Library	<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
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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

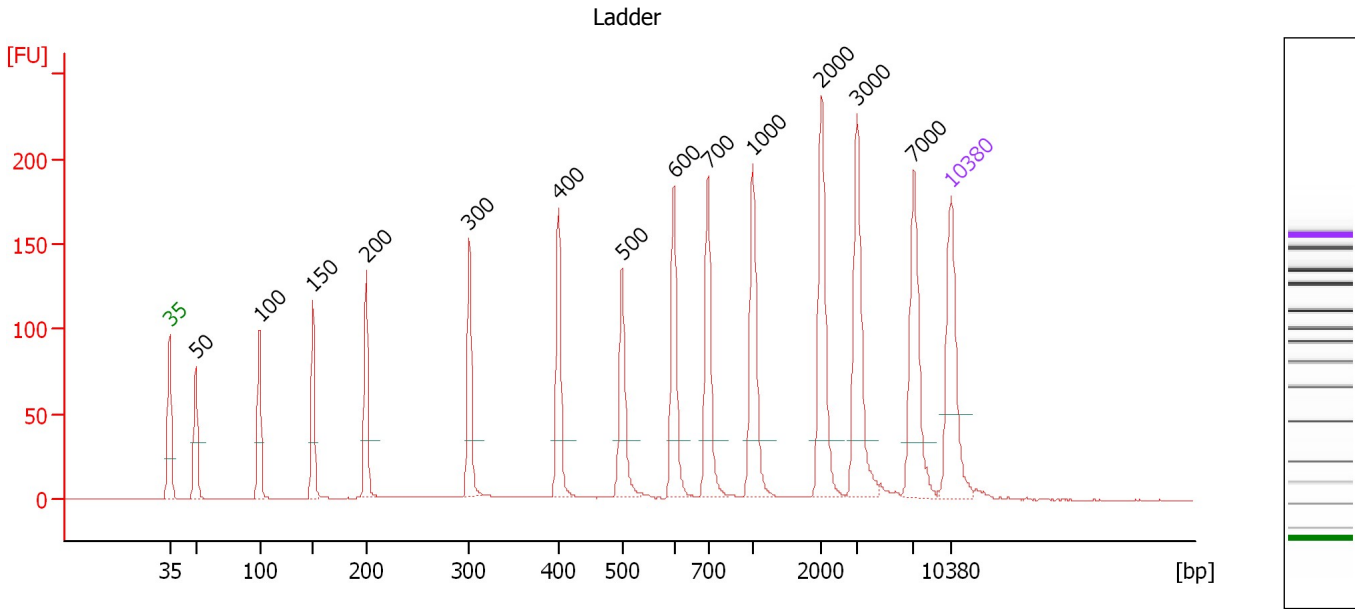
**Ladder**

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: 0.3

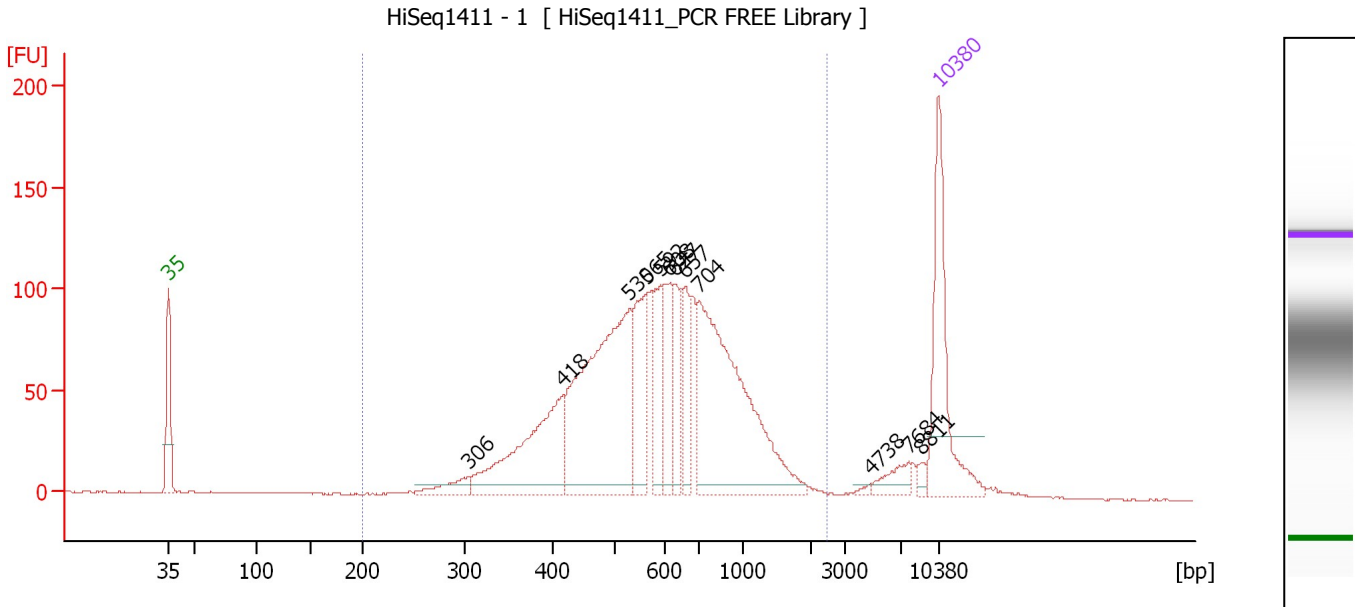
**Peak table for Ladder**

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	45.34
3	100	150.00	2,272.7	Ladder Peak	51.07
4	150	150.00	1,515.2	Ladder Peak	55.84
5	200	150.00	1,136.4	Ladder Peak	60.62
6	300	150.00	757.6	Ladder Peak	69.88
7	400	150.00	568.2	Ladder Peak	77.86
8	500	150.00	454.5	Ladder Peak	83.54
9	600	150.00	378.8	Ladder Peak	88.17
10	700	150.00	324.7	Ladder Peak	91.23
11	1,000	150.00	227.3	Ladder Peak	95.24
12	2,000	150.00	113.6	Ladder Peak	101.40
13	3,000	150.00	75.8	Ladder Peak	104.60
14	7,000	150.00	32.5	Ladder Peak	109.66
15	10,380	75.00	10.9	Upper Marker	113.00

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



**Overall Results for sample 1 : HiSeq1411 - 1**

Number of peaks found: 12                      Corr. Area 1: 2,110.1  
 Noise: 0.3

**Peak table for sample 1 : HiSeq1411 - 1**

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	306	17.14	84.8		70.39
3	418	128.59	466.3		78.87
4	530	235.76	673.9		84.93
5	565	66.08	177.3		86.53
6	592	50.47	129.2		87.79
7	608	43.62	108.7		88.42
8	627	31.35	75.7		89.00
9	657	33.07	76.2		89.93
10	704	225.43	485.0		91.28
11	4,738	1.78	0.6		106.80
12	7,684	12.96	2.6		110.33
13	8,811	4.49	0.8		111.45
14	10,380	75.00	10.9	Upper Marker	113.00

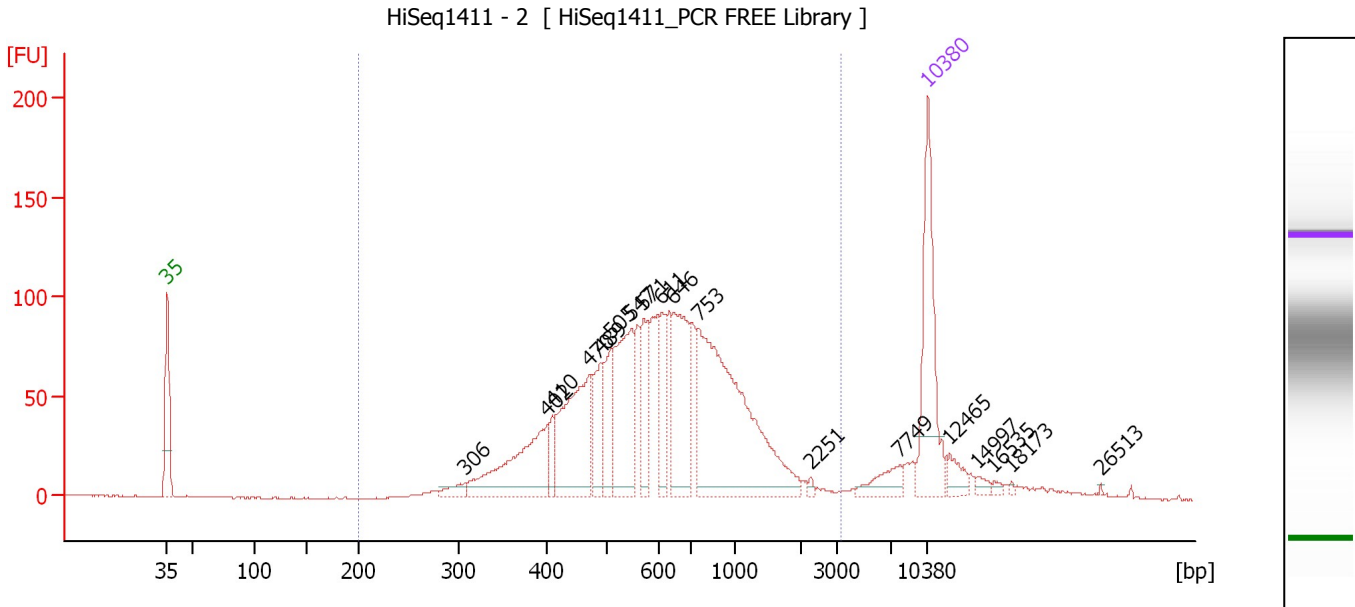
**Region table for sample 1 : HiSeq1411 - 1**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	2,460	649	912.95	2,110.1	2,544.5	95	43.2

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



**Overall Results for sample 2 : HiSeq1411 - 2**

Number of peaks found: 18                      Corr. Area 1: 1,908.9  
 Noise: 0.3

**Peak table for sample 2 : HiSeq1411 - 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	306	11.51	56.9		70.39
3	402	97.70	368.5		77.95
4	410	17.06	63.0		78.44
5	470	110.81	357.3		81.83
6	489	42.58	132.0		82.91
7	505	39.69	119.0		83.79
8	547	92.58	256.5		85.71
9	571	41.97	111.3		86.84
10	611	34.68	86.0		88.50
11	646	83.12	194.9		89.58
12	753	230.39	463.3		91.94
13	2,251	1.88	1.3		102.20
14	7,749	15.12	3.0		110.40
15	10,380	75.00	10.9	Upper Marker	113.00
16	12,465	0.00	0.0		115.06
17	14,997	0.00	0.0		117.57
18	16,535	0.00	0.0		119.09
19	18,173	0.00	0.0		120.71
20	26,513	0.00	0.0		128.95

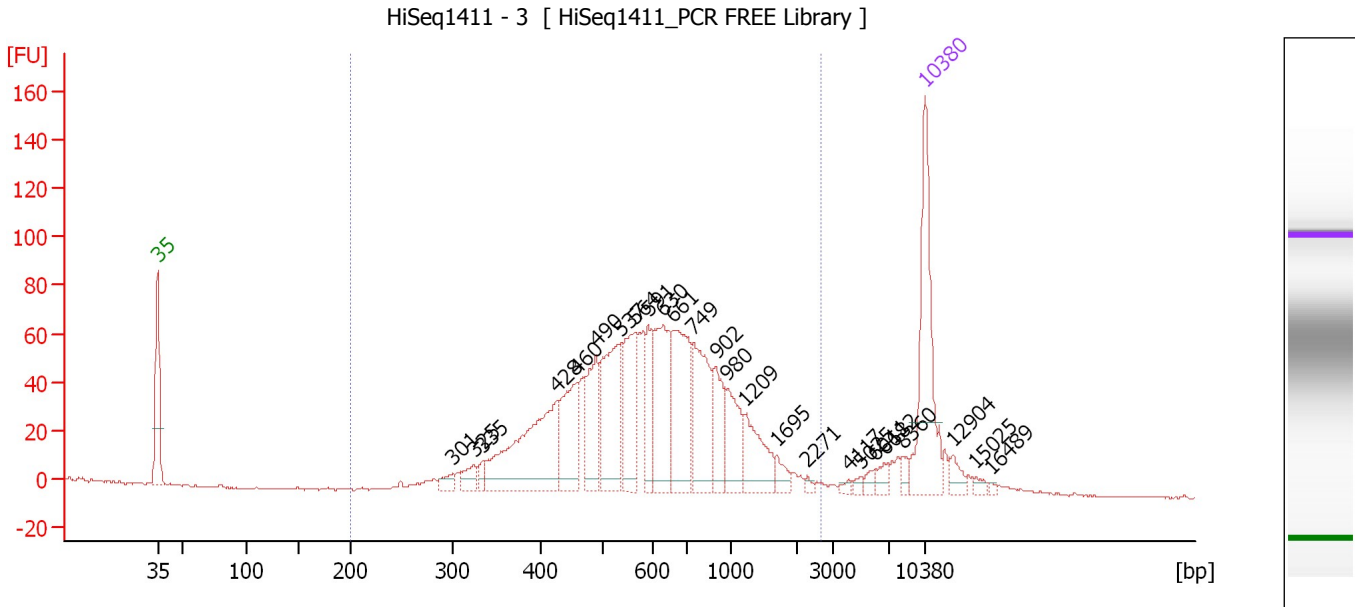
**Region table for sample 2 : HiSeq1411 - 2**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	3,315	699	935.01	1,908.9	2,507.1	92	51.0

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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : HiSeq1411 - 3**

Number of peaks found: 25                      Corr. Area 1: 1,393.6  
 Noise: 0.4

**Peak table for sample 3 : HiSeq1411 - 3**

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	301	8.36	42.1		69.96
3	325	12.59	58.7		71.86
4	335	7.08	32.0		72.66
5	428	125.56	444.5		79.45
6	460	55.53	183.1		81.25
7	490	49.54	153.1		82.99
8	537	81.30	229.5		85.24
9	564	57.79	155.3		86.49
10	591	29.10	74.7		87.74
11	630	77.68	186.9		89.08
12	661	77.85	178.5		90.03
13	749	67.99	137.6		91.88
14	902	31.26	52.5		93.93
15	980	35.66	55.1		94.98
16	1,209	34.87	43.7		96.52
17	1,695	8.19	7.3		99.52
18	2,271	2.21	1.5		102.27
19	4,117	2.45	0.9		106.01
20	5,025	2.81	0.8		107.16
21	6,011	4.19	1.1		108.41
22	6,682	6.01	1.4		109.26
23	8,360	4.87	0.9		111.00
24	10,380	75.00	10.9	Upper Marker	113.00
25	12,904	0.00	0.0		115.50

Assay Class: High Sensitivity DNA Assay  
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**Electropherogram Summary Continued ...****... Peak table for sample 3 : HiSeq1411 - 3**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	15,025	0.00	0.0		117.59
27	16,489	0.00	0.0		119.04

**Region table for sample 3 : HiSeq1411 - 3**

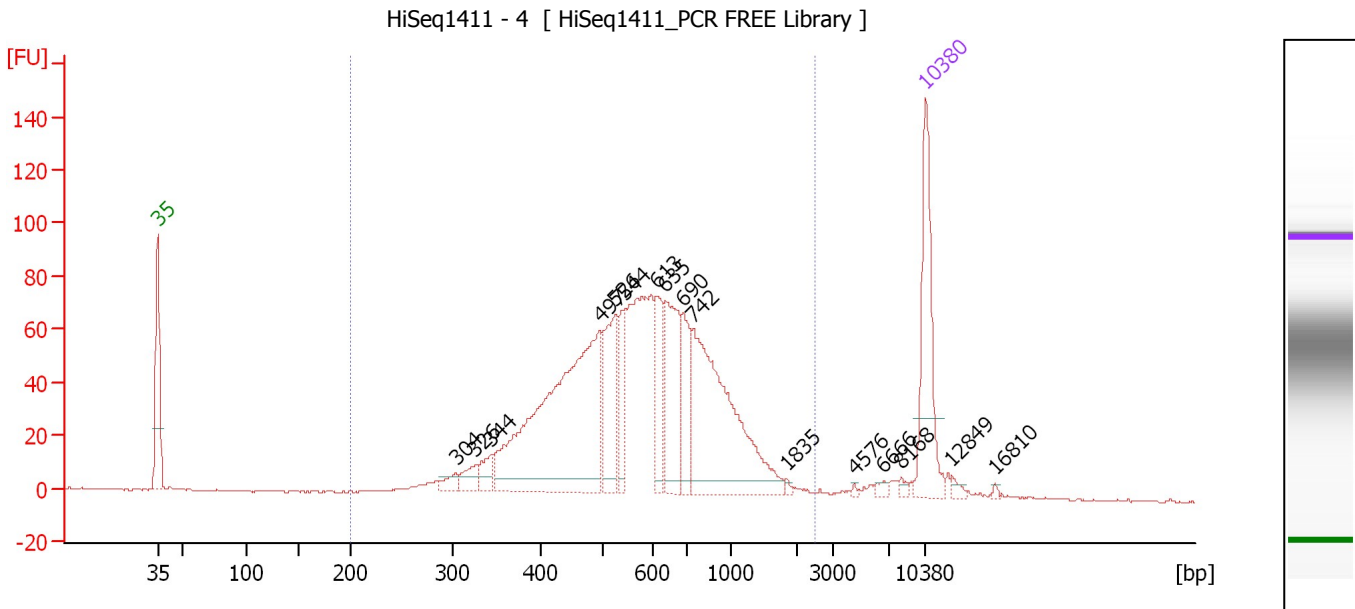
From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ $\mu$ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,658	682	824.88	1,393.6	2,242.6	 93	48.6



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



**Overall Results for sample 4 : HiSeq1411 - 4**

Number of peaks found: 16                      Corr. Area 1: 1,500.4  
 Noise: 0.3

**Peak table for sample 4 : HiSeq1411 - 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	304	10.63	52.9		70.22
3	326	15.90	73.9		71.95
4	344	18.11	79.7		73.42
5	497	326.14	995.2		83.34
6	526	74.56	214.6		84.77
7	544	38.74	107.9		85.58
8	613	47.23	116.7		88.58
9	635	84.93	202.6		89.24
10	690	47.81	105.0		90.92
11	742	205.50	419.7		91.79
12	1,835	2.06	1.7		100.38
13	4,576	1.42	0.5		106.59
14	6,666	3.62	0.8		109.24
15	8,168	2.94	0.5		110.81
16	10,380	75.00	10.9	Upper Marker	113.00
17	12,849	0.00	0.0		115.44
18	16,810	0.00	0.0		119.36

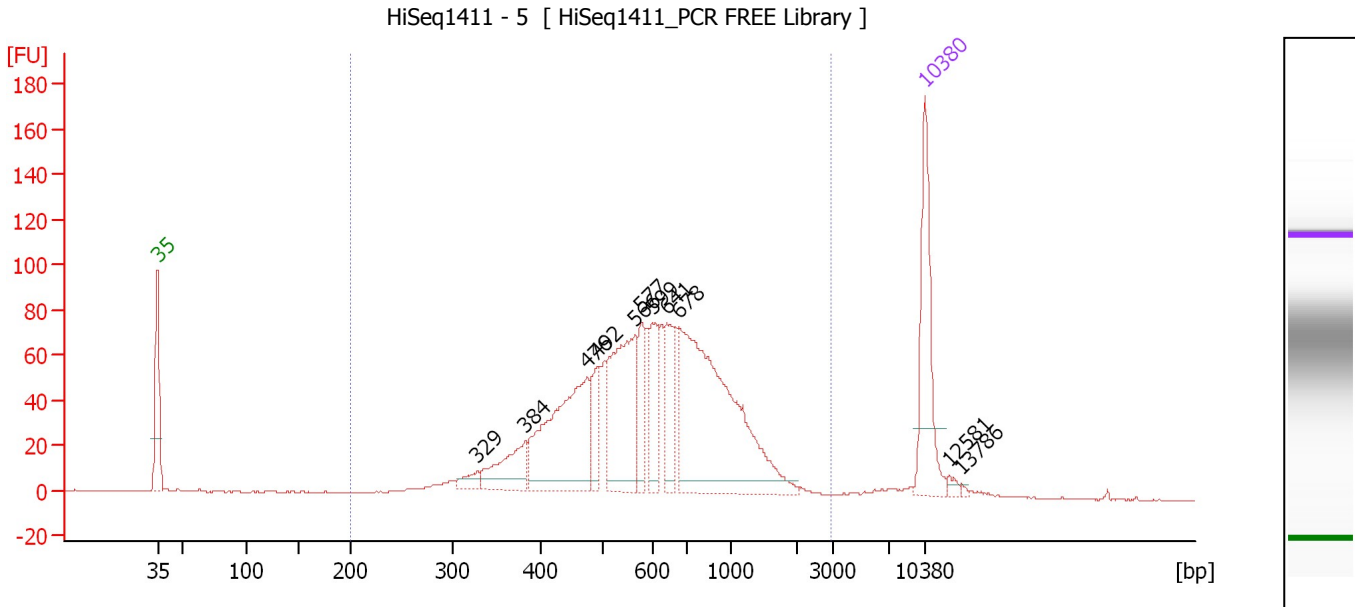
**Region table for sample 4 : HiSeq1411 - 4**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	2,483	634	1,080.24	1,500.4	3,059.4	96	42.9

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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : HiSeq1411 - 5**

Number of peaks found: 11                      Corr. Area 1: 1,525.8  
 Noise: 0.3

**Peak table for sample 5 : HiSeq1411 - 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	329	13.55	62.4		72.17
3	384	53.52	211.2		76.58
4	476	168.35	536.0		82.17
5	492	37.68	116.0		83.10
6	566	130.52	349.7		86.58
7	577	37.94	99.7		87.09
8	599	47.96	121.3		88.13
9	641	50.76	120.0		89.42
10	678	286.03	638.9		90.56
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,581	0.00	0.0		115.18
13	13,786	0.00	0.0		116.37

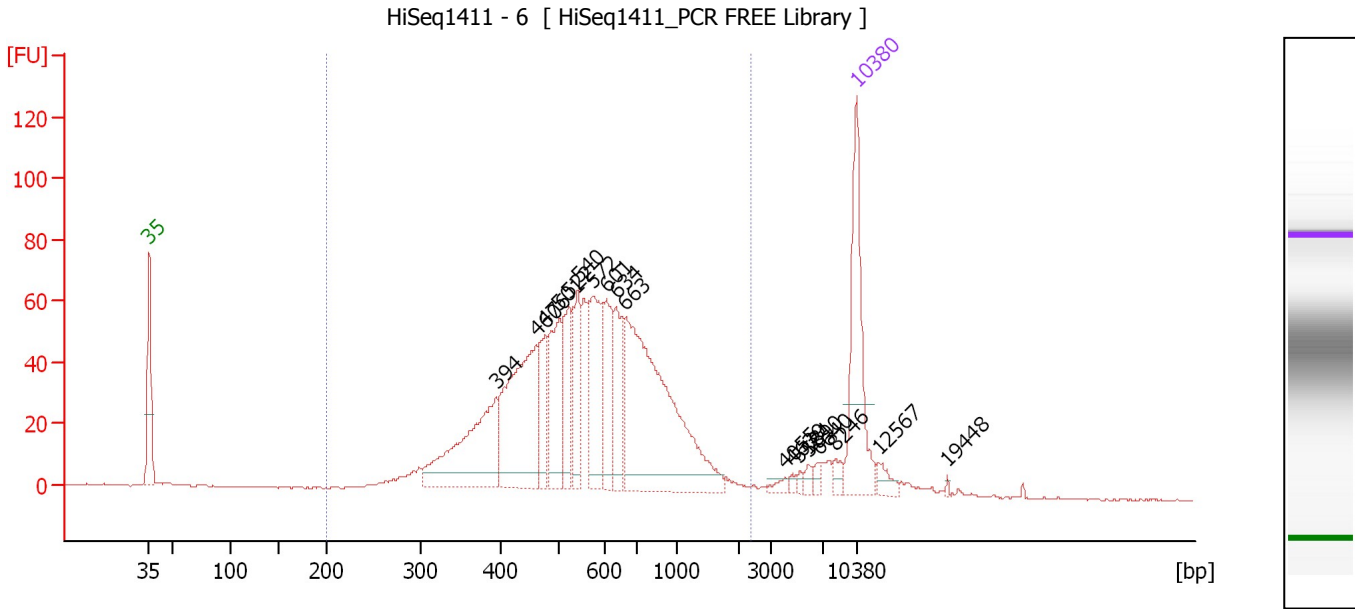
**Region table for sample 5 : HiSeq1411 - 5**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,959	671	962.64	1,525.8	2,640.4	97	46.2

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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : HiSeq1411 - 6**

Number of peaks found: 18                      Corr. Area 1: 1,314.8  
 Noise: 0.2

**Peak table for sample 6 : HiSeq1411 - 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	394	120.71	464.8		77.34
3	460	145.56	479.8		81.24
4	476	43.99	139.9		82.19
5	501	67.56	204.5		83.57
6	522	46.59	135.2		84.57
7	540	48.24	135.2		85.41
8	572	68.40	181.1		86.89
9	601	48.76	122.9		88.21
10	634	44.43	106.2		89.21
11	663	231.57	528.9		90.11
12	4,055	4.17	1.6		105.93
13	4,639	2.23	0.7		106.67
14	5,181	2.77	0.8		107.36
15	5,890	4.22	1.1		108.25
16	6,640	4.30	1.0		109.20
17	8,246	6.00	1.1		110.89
18	10,380	75.00	10.9	Upper Marker	113.00
19	12,567	0.00	0.0		115.16
20	19,448	0.00	0.0		121.97

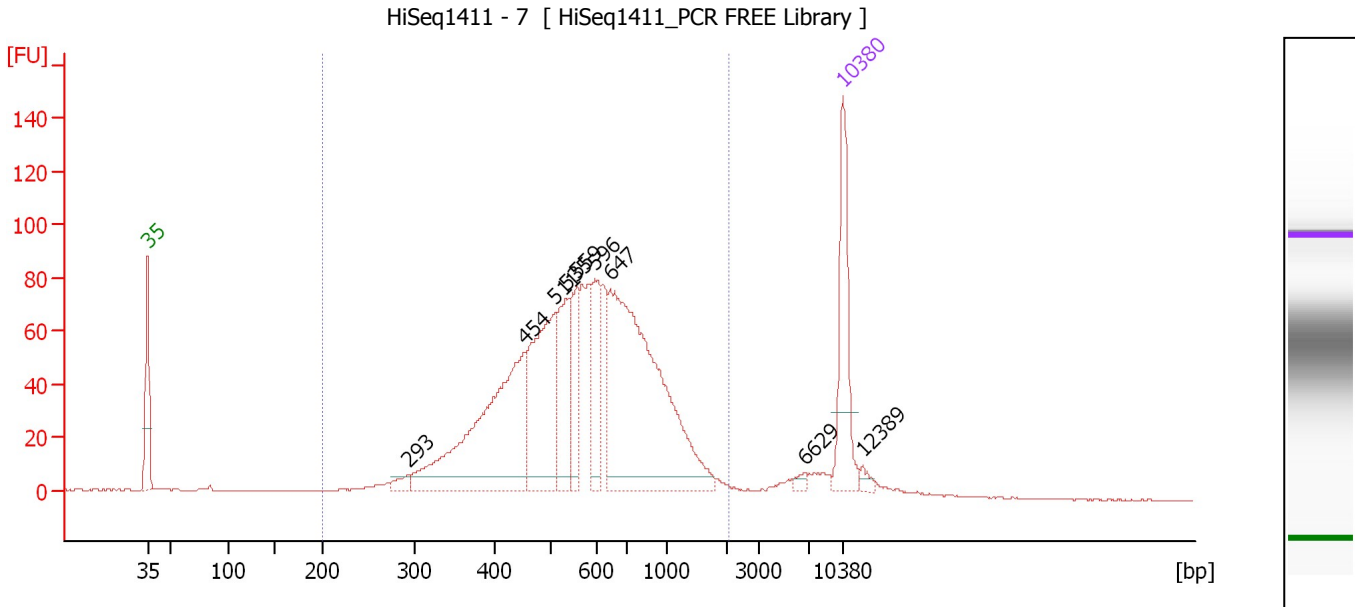
**Region table for sample 6 : HiSeq1411 - 6**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,376	614	982.64	1,314.8	2,887.1	93	43.7

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**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : HiSeq1411 - 7**

Number of peaks found: 9                      Corr. Area 1: 1,621.4  
 Noise: 0.2

**Peak table for sample 7 : HiSeq1411 - 7**

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	293	11.12	57.5		69.25
3	454	271.17	904.0		80.95
4	511	162.85	482.5		84.07
5	535	85.36	241.9		85.14
6	559	60.71	164.6		86.27
7	596	63.94	162.5		87.98
8	647	360.23	844.1		89.60
9	6,629	5.01	1.1		109.19
10	10,380	75.00	10.9	Upper Marker	113.00
11	12,389	0.00	0.0		114.99

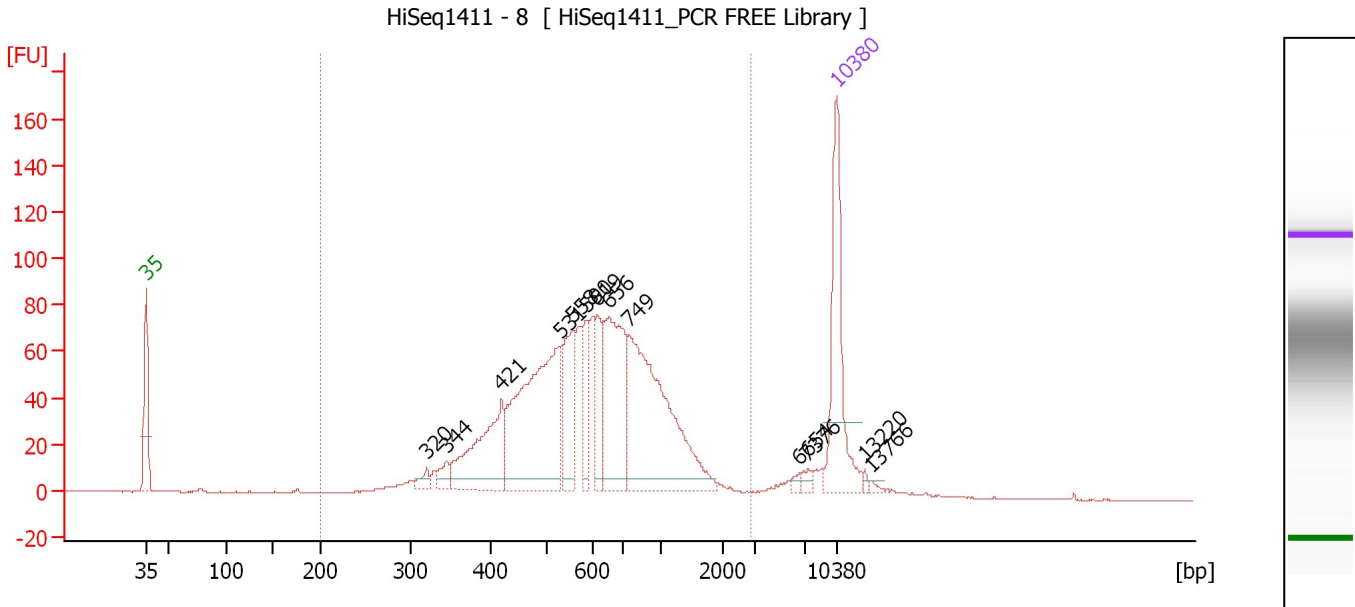
**Region table for sample 7 : HiSeq1411 - 7**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	2,059	629	1,191.49	1,621.4	3,422.3	94	42.2

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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : HiSeq1411 - 8**

Number of peaks found: 13                      Corr. Area 1: 1,514.3  
 Noise: 0.2

**Peak table for sample 8 : HiSeq1411 - 8**

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	320	9.24	43.8		71.46
3	344	11.23	49.4		73.41
4	421	91.92	331.2		79.03
5	531	189.50	540.9		84.97
6	558	61.13	166.1		86.21
7	590	34.25	87.9		87.72
8	619	37.09	90.8		88.75
9	656	105.60	243.9		89.88
10	749	189.11	382.6		91.88
11	6,654	3.23	0.7		109.22
12	7,376	4.41	0.9		110.03
13	10,380	75.00	10.9	Upper Marker	113.00
14	13,220	0.00	0.0		115.81
15	13,766	0.00	0.0		116.35

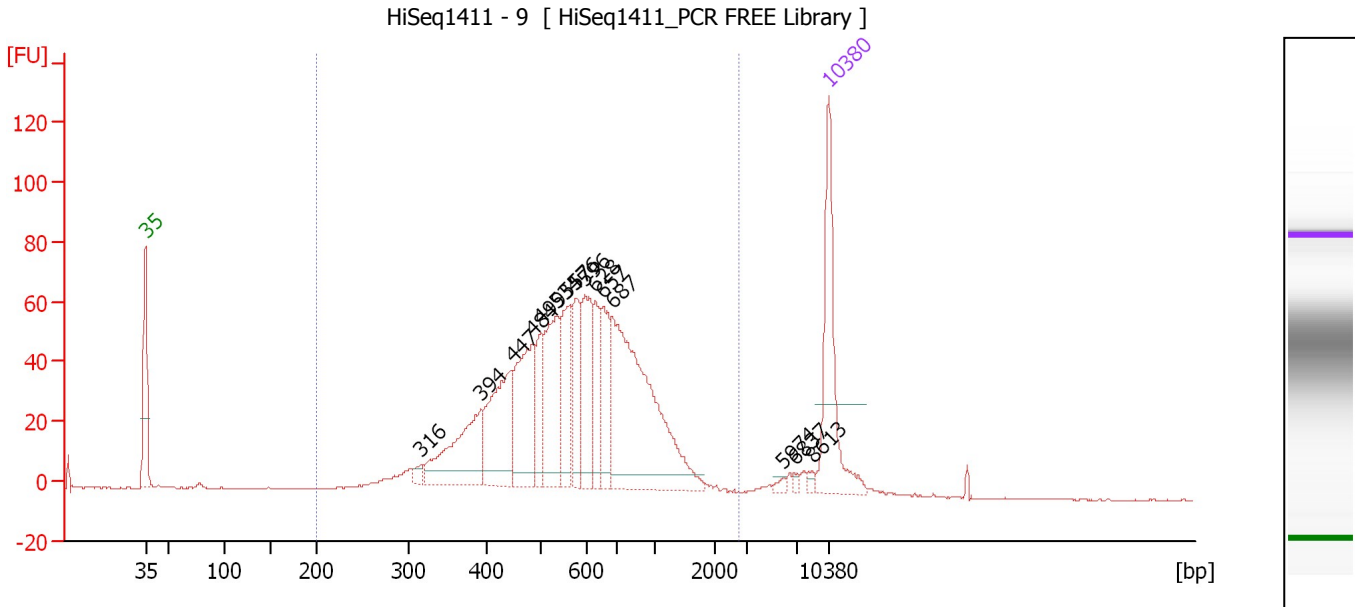
**Region table for sample 8 : HiSeq1411 - 8**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,923	675	856.24	1,514.3	2,339.2	95	47.0

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : HiSeq1411 - 9**

Number of peaks found: 15                      Corr. Area 1: 1,295.2  
 Noise: 0.2

**Peak table for sample 9 : HiSeq1411 - 9**

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	316	6.71	32.2		71.17
3	394	92.25	355.1		77.34
4	447	94.64	321.0		80.51
5	484	92.38	289.1		82.64
6	499	32.88	99.9		83.46
7	534	84.43	239.7		85.10
8	557	52.46	142.6		86.19
9	576	42.38	111.5		87.06
10	596	58.37	148.4		87.99
11	628	43.04	103.8		89.03
12	657	44.37	102.4		89.90
13	687	223.33	492.5		90.83
14	5,974	3.03	0.8		108.36
15	6,837	2.42	0.5		109.45
16	8,613	3.13	0.6		111.25
17	10,380	75.00	10.9	Upper Marker	113.00

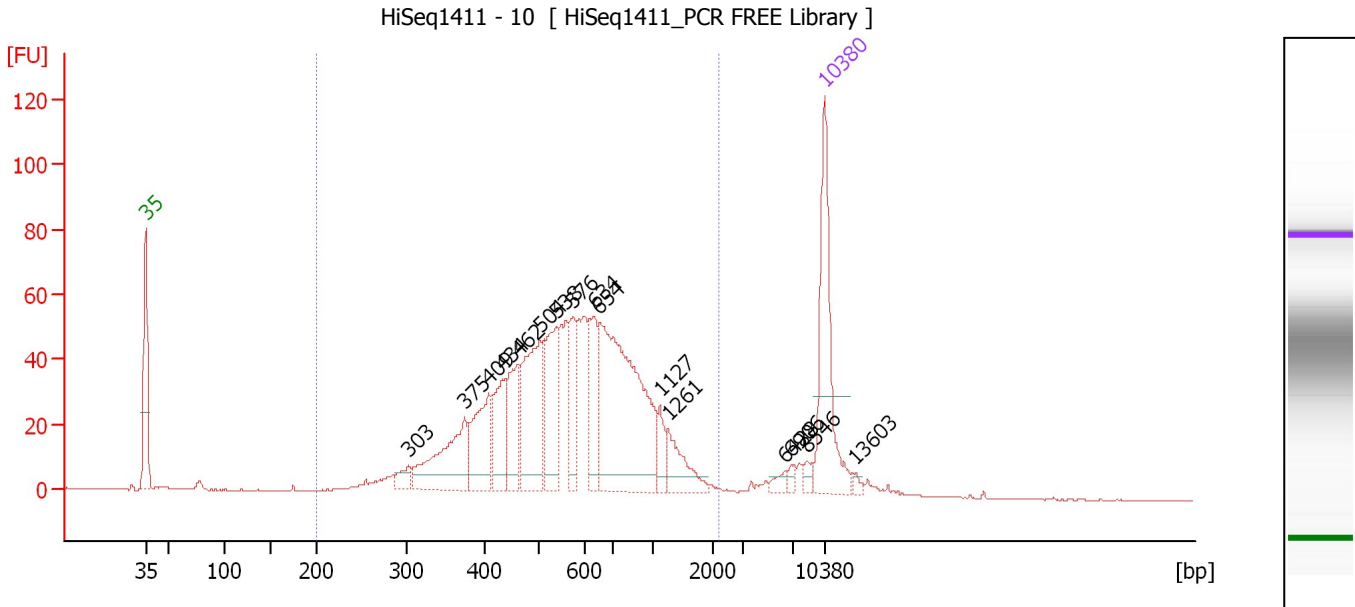
**Region table for sample 9 : HiSeq1411 - 9**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,725	627	966.06	1,295.2	2,783.8	96	43.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : HiSeq1411 - 10**

Number of peaks found: 16                      Corr. Area 1: 1,155.5  
 Noise: 0.2

**Peak table for sample 10 : HiSeq1411 - 10**

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	303	12.38	62.0		70.09
3	375	77.81	314.4		75.86
4	409	60.82	225.1		78.38
5	434	45.54	158.8		79.81
6	462	47.53	155.7		81.41
7	504	93.85	282.2		83.71
8	538	67.12	189.0		85.31
9	576	37.10	97.6		87.07
10	634	40.73	97.3		89.21
11	654	197.38	457.5		89.81
12	1,127	14.45	19.4		96.02
13	1,261	27.66	33.2		96.85
14	6,428	5.29	1.2		108.93
15	6,906	3.77	0.8		109.54
16	8,546	4.90	0.9		111.19
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,603	0.00	0.0		116.19

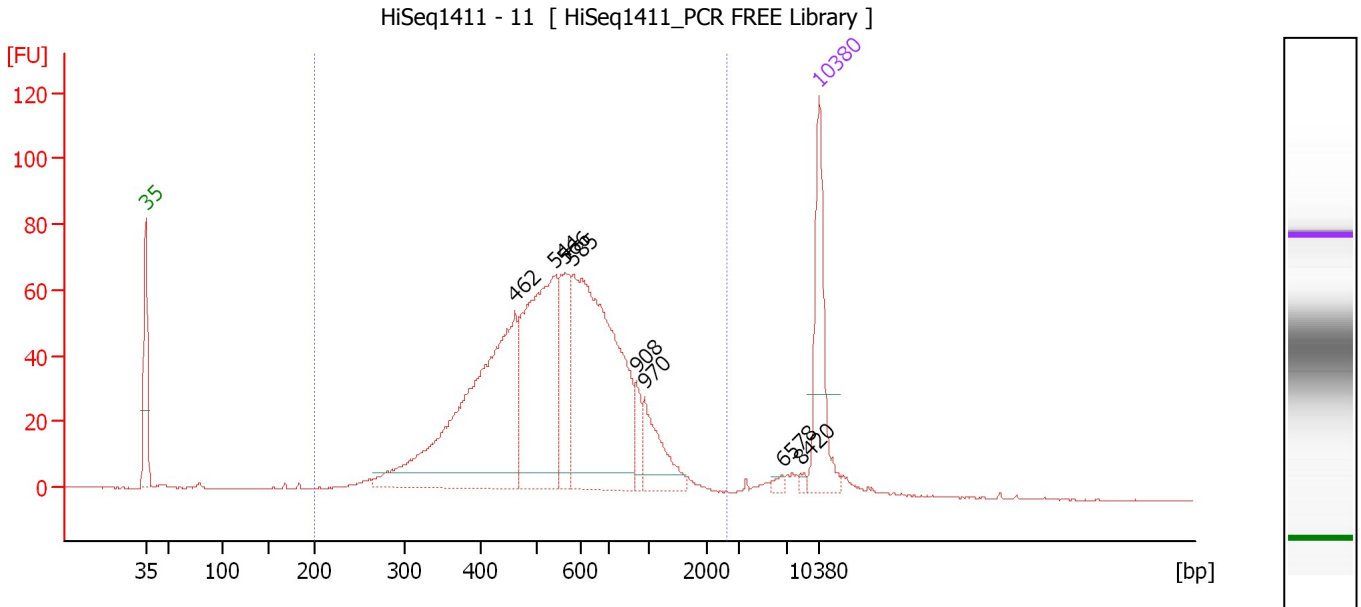
**Region table for sample 10 : HiSeq1411 - 10**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	2,202	629	889.38	1,155.5	2,597.4	94	44.4

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

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 Modified: 7/2/2018 4:51:44 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : HiSeq1411 - 11**

Number of peaks found: 8                      Corr. Area 1: 1,358.2  
 Noise: 0.2

**Peak table for sample 11 : HiSeq1411 - 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	462	356.75	1,170.0		81.38
3	544	241.45	672.2		85.59
4	566	79.13	211.9		86.58
5	585	314.82	815.6		87.47
6	908	22.01	36.7		94.00
7	970	49.05	76.6		94.84
8	6,578	3.74	0.9		109.12
9	8,420	3.26	0.6		111.06
10	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 11 : HiSeq1411 - 11**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,636	590	1,165.66	1,358.2	3,519.9	96	41.6



Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02\_002.xad

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**Gel Image**