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

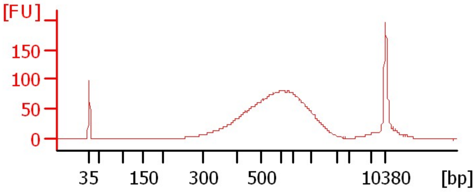
Chip Information:

Chip Lot #:

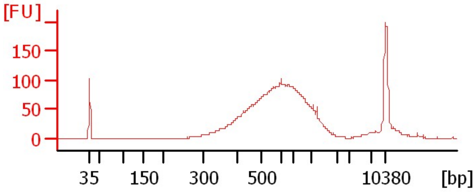
Reagent Kit Lot #:

Chip Comments:

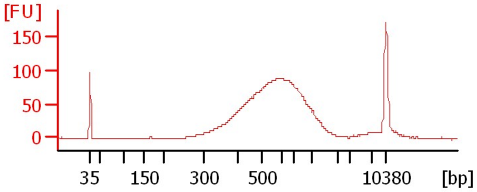
HiSeq1411-15



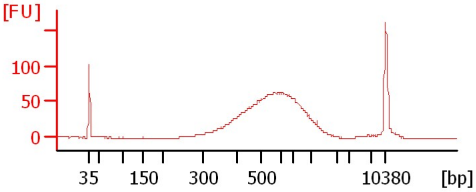
HiSeq1411-23



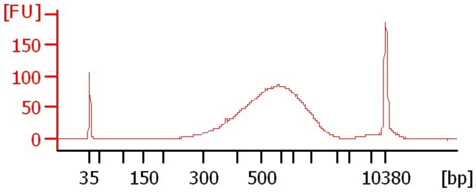
HiSeq1411-24



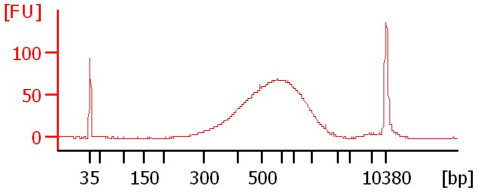
HiSeq1411-25



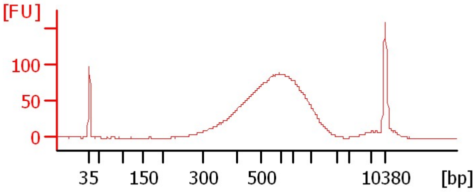
HiSeq1411-26



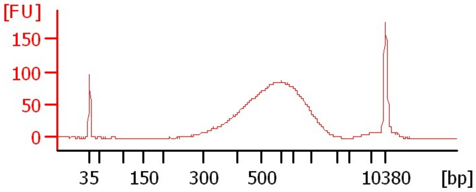
HiSeq1411-27



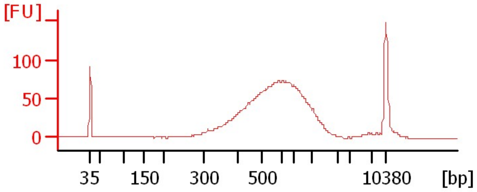
HiSeq1411-28



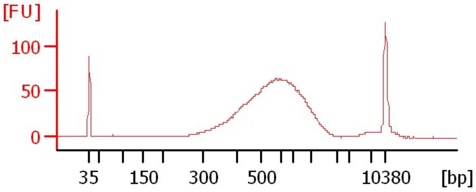
HiSeq1411-29



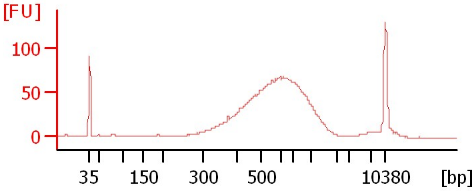
HiSeq1411-30



HiSeq1411-31



HiSeq1411-32



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02_003.xad

Created: 7/2/2018 4:59:12 PM
Modified: 7/3/2018 8:55:33 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq1411-15		☐	✓			
HiSeq1411-23		☐	✓			
HiSeq1411-24		☐	✓			
HiSeq1411-25		☐	✓			
HiSeq1411-26		☐	✓			
HiSeq1411-27		☐	✓			
HiSeq1411-28		☐	✓			
HiSeq1411-29		☐	✓			
HiSeq1411-30		☐	✓			
HiSeq1411-31		☐	✓			
HiSeq1411-32		☐	✓			
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

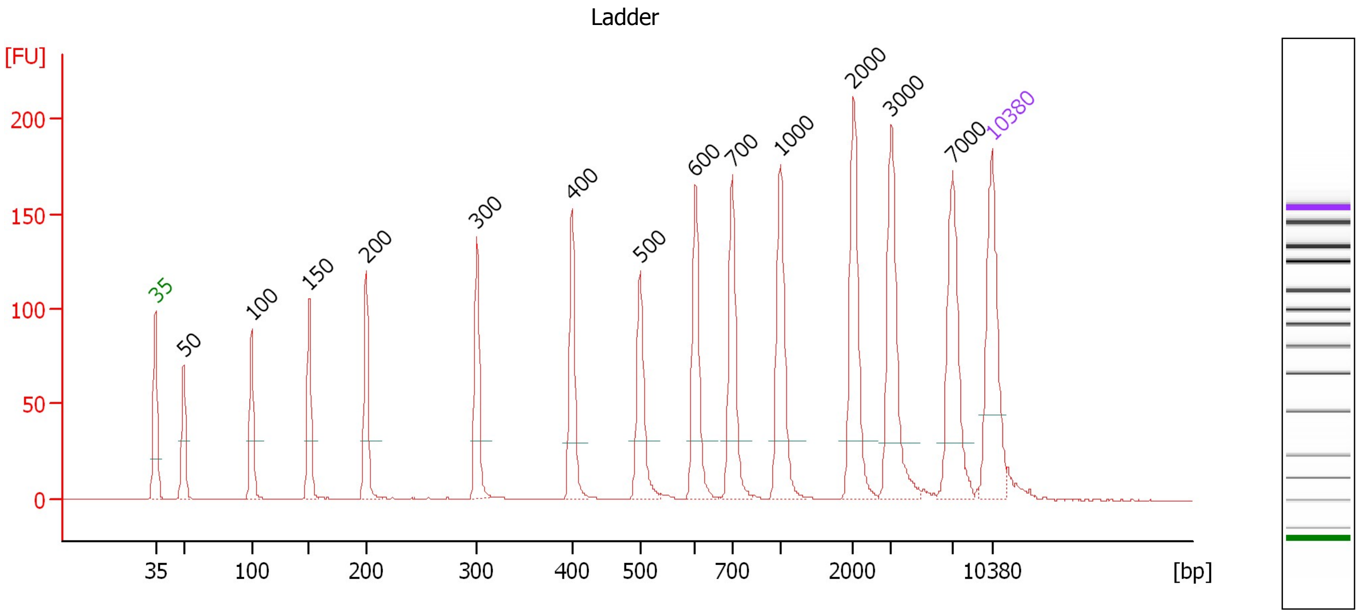
Ladder

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
Data Path: C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02_003.xad

Created: 7/2/2018 4:59:12 PM
Modified: 7/3/2018 8:55:33 AM

Electropherogram Summary



Overall Results for Ladder

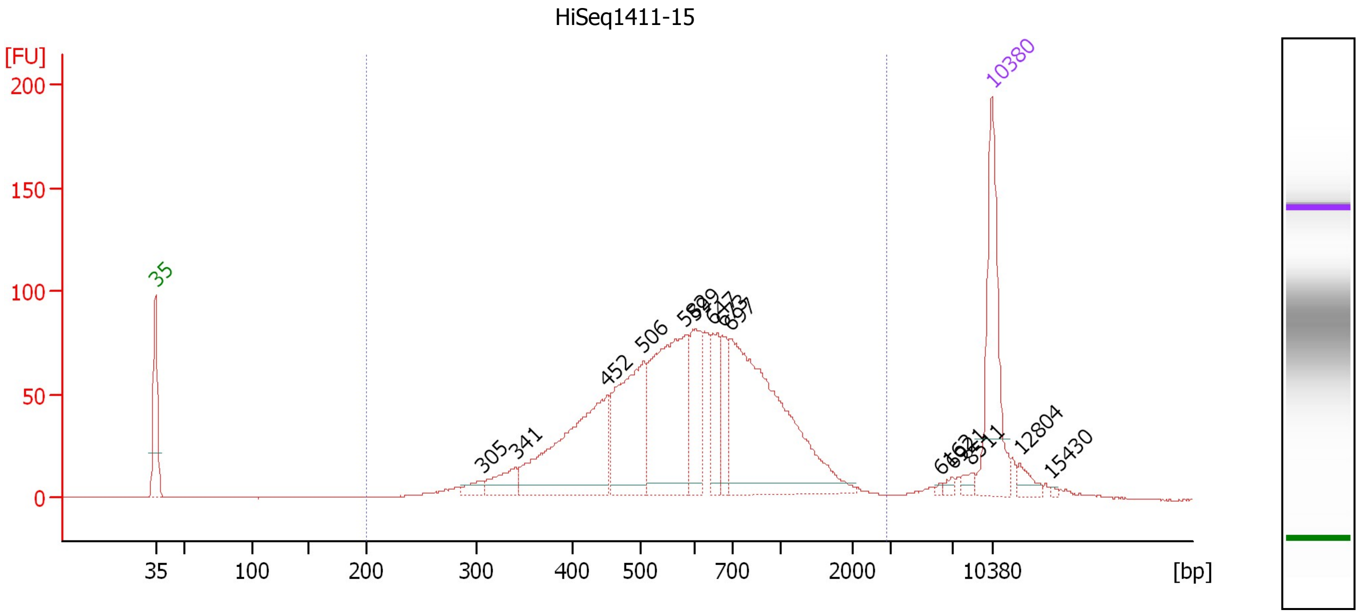
Noise: 0.2

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	45.36
3	∟	100	150.00	2,272.7	Ladder Peak	51.03
4	∟	150	150.00	1,515.2	Ladder Peak	55.84
5	∟	200	150.00	1,136.4	Ladder Peak	60.60
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	83.58
9	∟	600	150.00	378.8	Ladder Peak	88.19
10	∟	700	150.00	324.7	Ladder Peak	91.27
11	∟	1,000	150.00	227.3	Ladder Peak	95.31
12	∟	2,000	150.00	113.6	Ladder Peak	101.41
13	∟	3,000	150.00	75.8	Ladder Peak	104.59
14	∟	7,000	150.00	32.5	Ladder Peak	109.73
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class:	High Sensitivity DNA Assay	Created:	7/2/2018 4:59:12 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02_003.xad	Modified:	7/3/2018 8:55:33 AM

Electropherogram Summary Continued ...



Overall Results for sample 1 : HiSeq1411-15

Number of peaks found:	14	Corr. Area 1:	1,732.1
Noise:	0.3		

Peak table for sample 1 : HiSeq1411-15

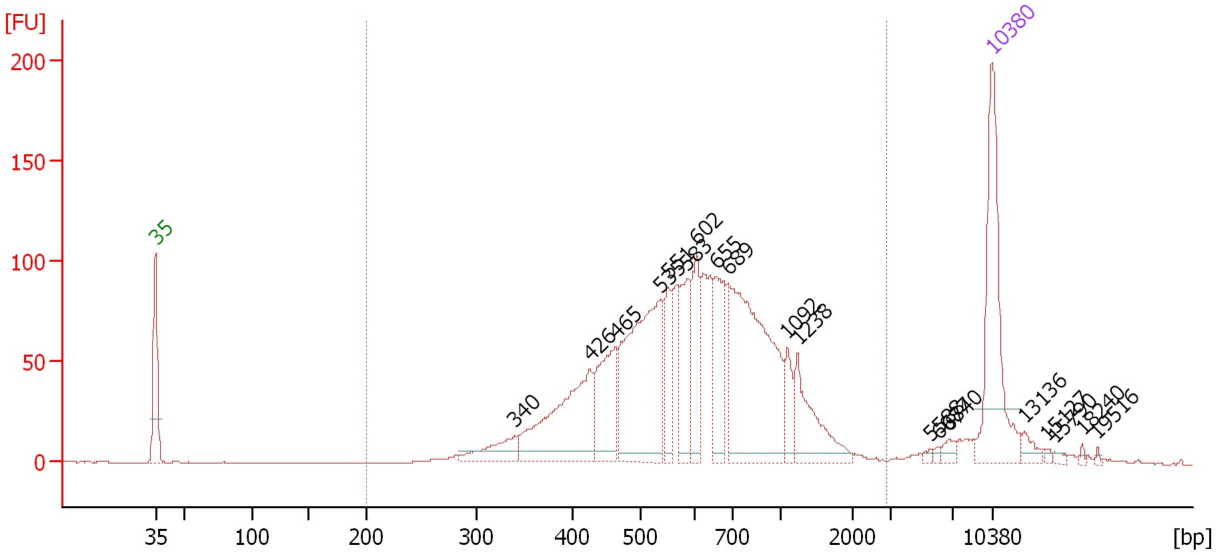
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		305	9.55	47.4		70.31
3		341	23.17	103.0		73.14
4		452	157.00	526.7		80.81
5		506	119.77	358.9		83.84
6		582	151.95	395.7		87.35
7		599	52.17	132.0		88.14
8		647	40.26	94.2		89.65
9		673	30.83	69.4		90.43
10		697	231.49	503.5		91.16
11		6,162	1.32	0.3		108.65
12		6,921	2.70	0.6		109.63
13		8,511	4.67	0.8		111.19
14	▶	10,380	75.00	10.9	Upper Marker	113.00
15		12,804	0.00	0.0		115.34
16		15,430	0.00	0.0		117.88

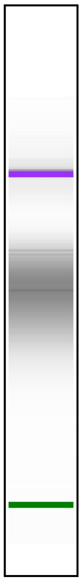
Region table for sample 1 : HiSeq1411-15

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	2,857	668	910.50	1,732.1	2,545.7	🟦 94	48.2

Electropherogram Summary Continued ...

HiSeq1411-23





Overall Results for sample 2 : HiSeq1411-23

Number of peaks found:	19	Corr. Area 1:	1,899.8
Noise:	0.2		

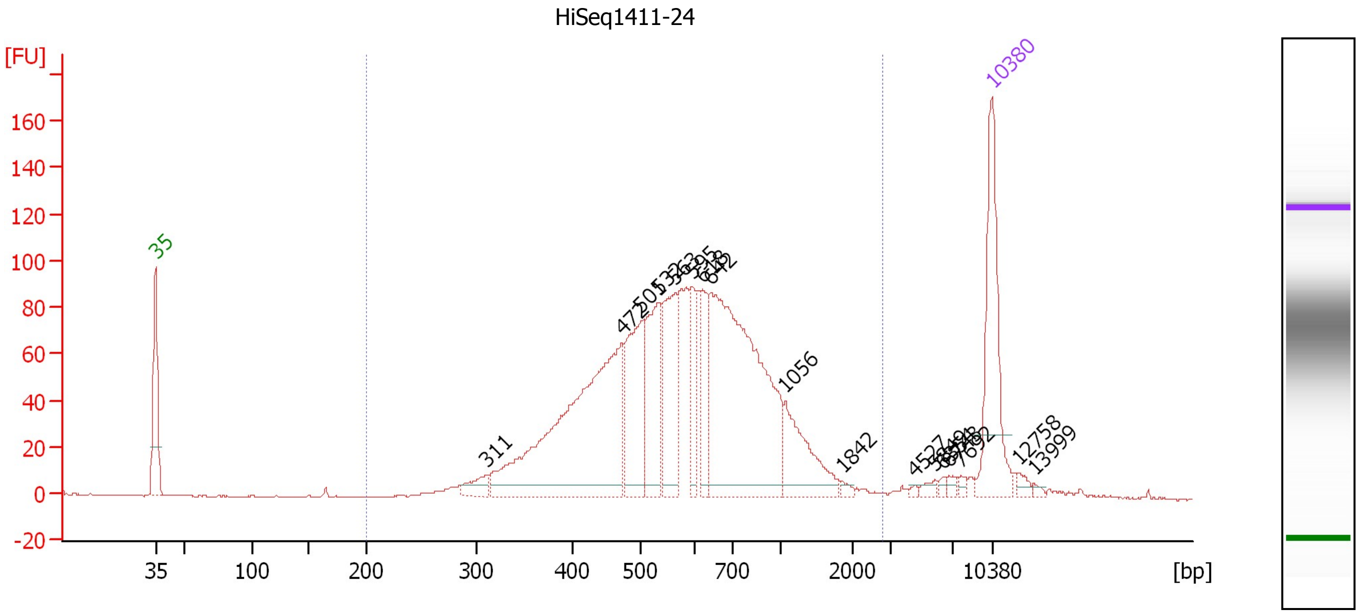
Peak table for sample 2 : HiSeq1411-23

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		340	25.35	113.0		73.06
3		426	105.51	375.4		79.33
4		465	58.24	189.9		81.55
5		535	137.92	390.4		85.21
6		551	28.76	79.0		85.95
7		583	40.22	104.4		87.43
8		602	44.11	110.9		88.27
9		655	44.54	103.0		89.90
10		689	168.99	371.6		90.93
11		1,092	17.13	23.8		95.87
12		1,238	40.15	49.2		96.76
13		5,588	1.95	0.5		107.92
14		6,087	1.70	0.4		108.56
15		6,740	4.40	1.0		109.40
16	▶	10,380	75.00	10.9	Upper Marker	113.00
17		13,136	0.00	0.0		115.67
18		15,127	0.00	0.0		117.59
19		15,790	0.00	0.0		118.23
20		18,240	0.00	0.0		120.60
21		19,516	0.00	0.0		121.84

Region table for sample 2 : HiSeq1411-23

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,884	677	839.10	1,899.8	2,279.3	🟦 94	46.7

Electropherogram Summary Continued ...



Overall Results for sample 3 : HiSeq1411-24

Number of peaks found:	17	Corr. Area 1:	1,818.2
Noise:	0.3		

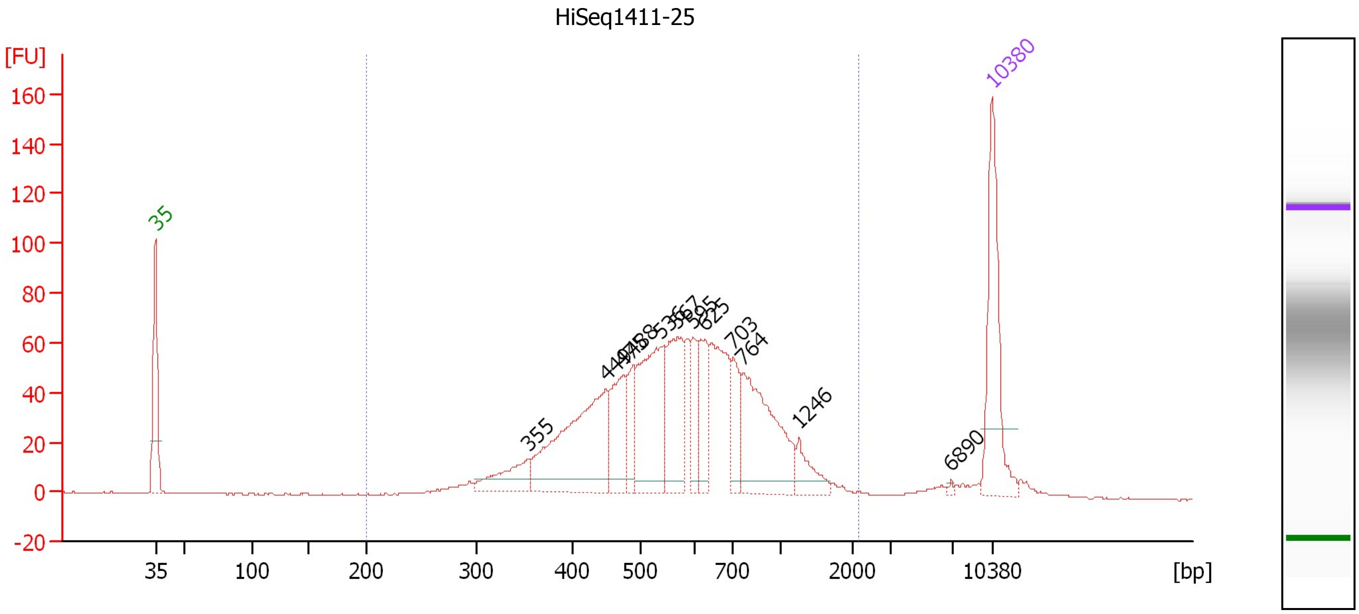
Peak table for sample 3 : HiSeq1411-24

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		311	15.25	74.3		70.75
3		472	280.81	900.6		82.00
4		501	85.86	259.9		83.60
5		532	74.70	212.8		85.05
6		563	76.61	206.1		86.50
7		595	36.80	93.7		87.95
8		618	38.88	95.3		88.75
9		643	268.34	632.8		89.50
10		1,056	52.62	75.5		95.65
11		1,842	2.99	2.5		100.45
12		4,527	1.49	0.5		106.55
13		5,849	4.29	1.1		108.25
14		6,354	2.34	0.6		108.90
15		6,743	3.44	0.8		109.40
16		7,692	2.63	0.5		110.40
17	▶	10,380	75.00	10.9	Upper Marker	113.00
18		12,758	0.00	0.0		115.30
19		13,999	0.00	0.0		116.50

Region table for sample 3 : HiSeq1411-24

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,788	641	1,034.17	1,818.2	2,910.4	🟦 96	44.9

Electropherogram Summary Continued ...



Overall Results for sample 4 : HiSeq1411-25

Number of peaks found:	12	Corr. Area 1:	1,289.6
Noise:	0.3		

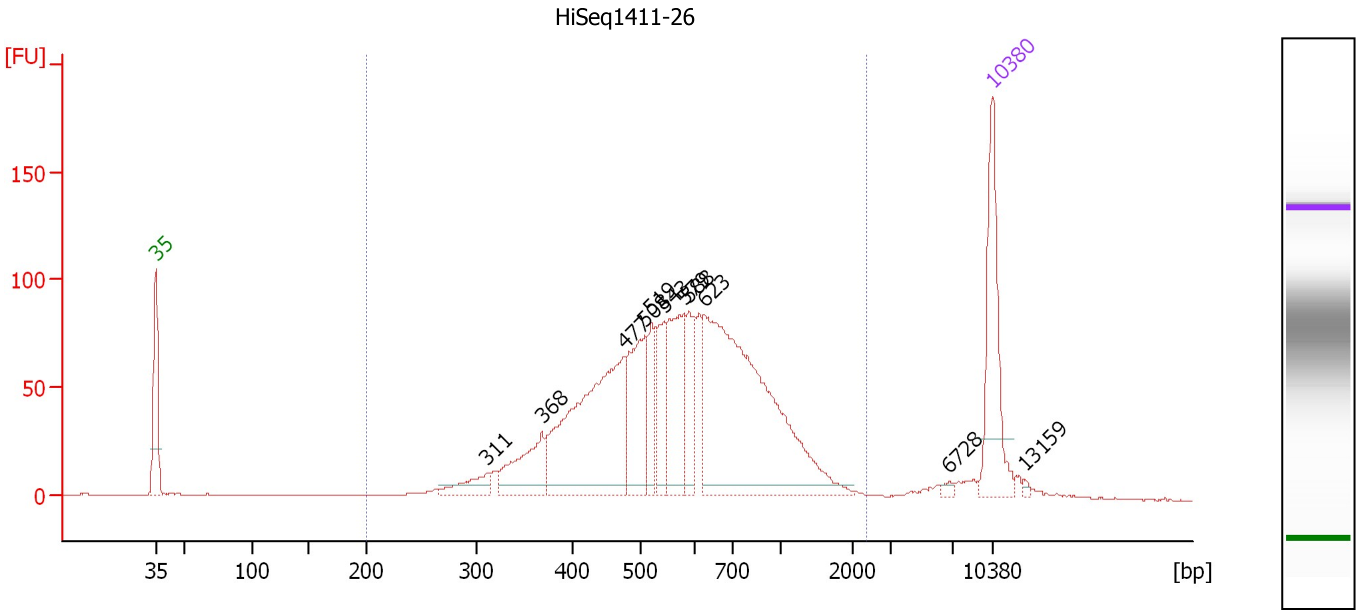
Peak table for sample 4 : HiSeq1411-25

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		355	36.78	157.0		74.26
3		449	157.34	530.7		80.67
4		475	55.33	176.5		82.15
5		488	30.42	94.4		82.91
6		536	109.29	308.7		85.25
7		567	74.90	200.1		86.68
8		595	30.39	77.4		87.95
9		625	41.50	100.6		88.97
10		703	33.38	71.9		91.31
11		764	111.51	221.2		92.13
12		1,246	20.12	24.5		96.81
13		6,890	1.46	0.3		109.59
14	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : HiSeq1411-25

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,126	621	868.91	1,289.6	2,489.5	🟦 97	40.7

Electropherogram Summary Continued ...



Overall Results for sample 5 : **HiSeq1411-26**

Number of peaks found:	11	Corr. Area 1:	1,761.6
Noise:	0.2		

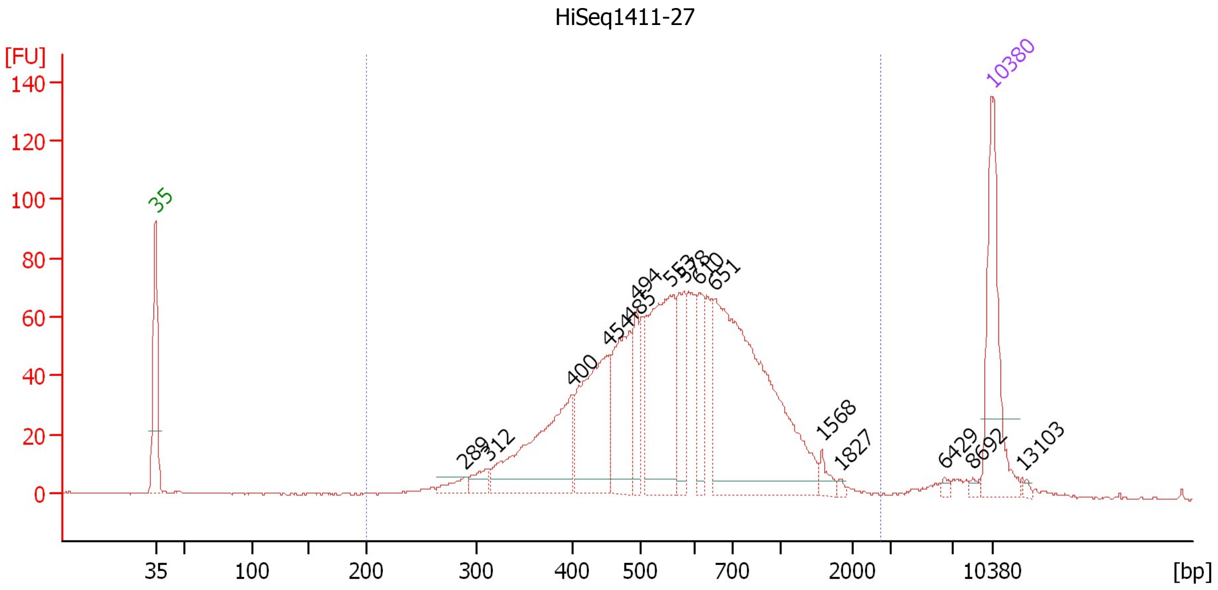
Peak table for sample 5 : **HiSeq1411-26**

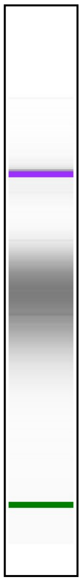
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		311	24.95	121.5		70.76
3		368	62.36	256.7		75.31
4		477	224.10	712.4		82.24
5		508	88.84	265.0		83.95
6		519	36.17	105.6		84.46
7		543	46.86	130.8		85.55
8		579	81.56	213.6		87.20
9		588	35.44	91.4		87.62
10		623	327.03	795.0		88.91
11		6,728	2.60	0.6		109.38
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		13,159	0.00	0.0		115.69

Region table for sample 5 : **HiSeq1411-26**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,342	623	992.56	1,761.6	2,859.7	🟦 97	42.1

Electropherogram Summary Continued ...





Overall Results for sample 6 : **HiSeq1411-27**

Number of peaks found:	15	Corr. Area 1:	1,453.4
Noise:	0.2		

Peak table for sample 6 : **HiSeq1411-27**

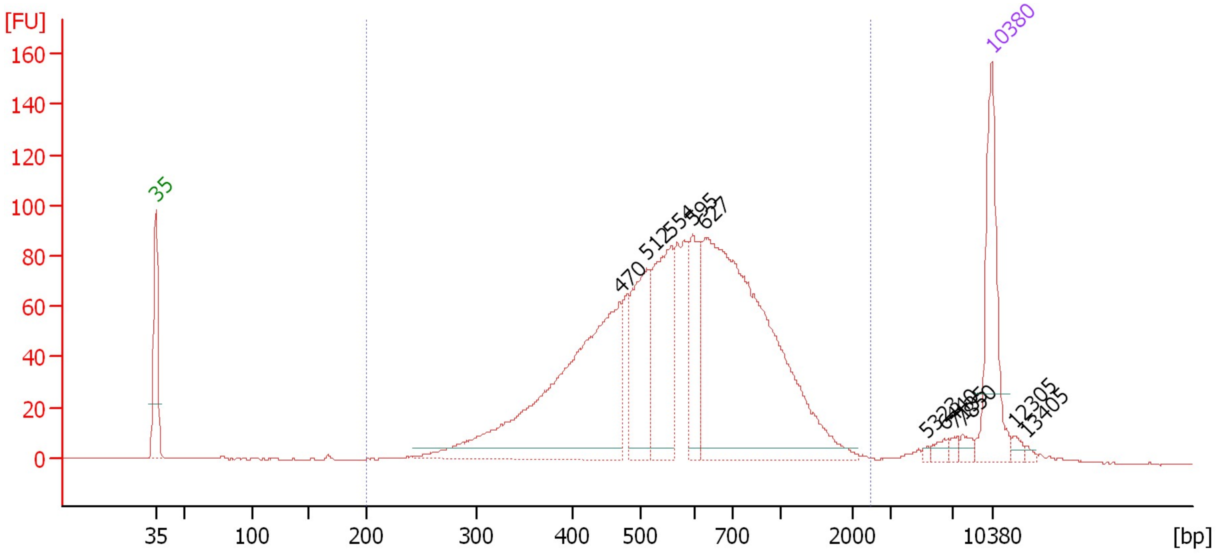
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		289	12.07	63.3		68.86
3		312	14.42	70.1		70.81
4		400	134.58	509.5		77.87
5		454	118.94	397.3		80.92
6		485	88.89	277.7		82.71
7		494	38.32	117.5		83.24
8		553	147.47	403.9		86.03
9		578	54.26	142.2		87.19
10		610	37.89	94.1		88.51
11		651	296.18	689.0		89.77
12		1,568	8.39	8.1		98.78
13		1,827	2.28	1.9		100.36
14		6,429	2.54	0.6		109.00
15		8,692	2.72	0.5		111.37
16	▶	10,380	75.00	10.9	Upper Marker	113.00
17		13,103	0.00	0.0		115.63

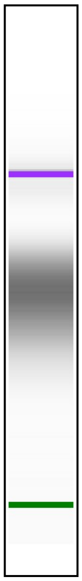
Region table for sample 6 : **HiSeq1411-27**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,691	624	1,085.12	1,453.4	3,143.4	🟦 97	43.9

Electropherogram Summary Continued ...

HiSeq1411-28





Overall Results for sample 7 : HiSeq1411-28

Number of peaks found:	11	Corr. Area 1:	1,816.2
Noise:	0.2		

Peak table for sample 7 : HiSeq1411-28

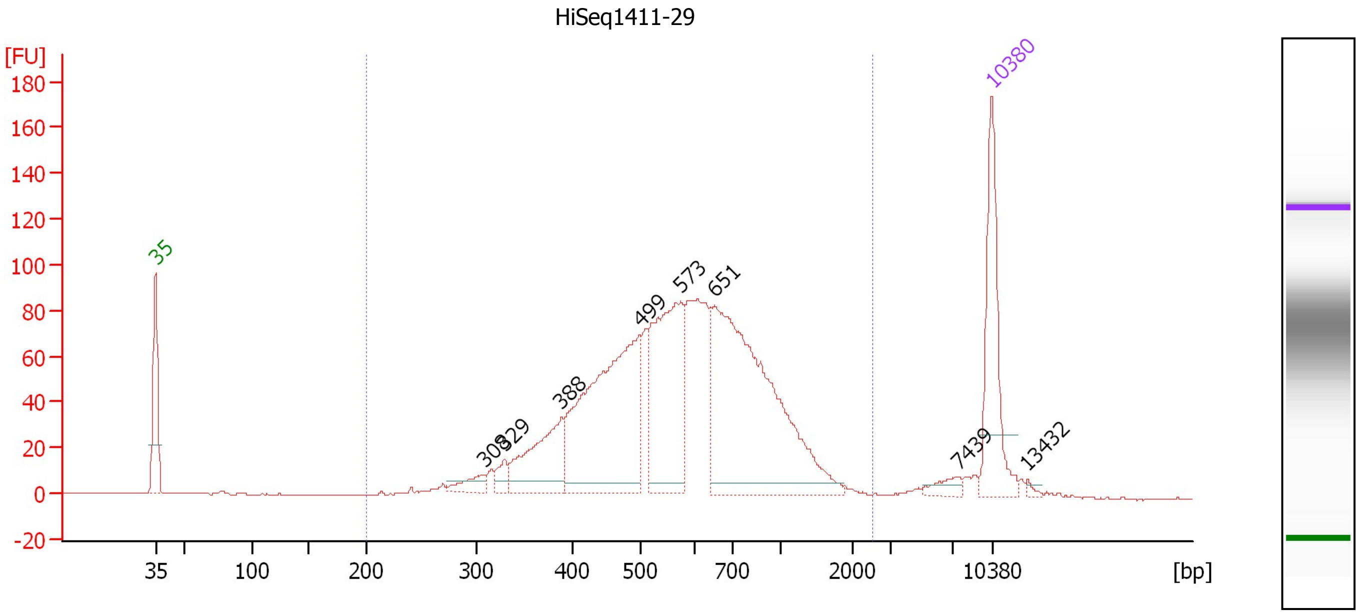
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		470	345.92	1,114.2		81.88
3		512	109.16	323.2		84.12
4		554	119.09	325.5		86.09
5		595	67.69	172.5		87.95
6		627	428.04	1,035.0		89.01
7		5,323	2.04	0.6		107.57
8		6,440	5.31	1.2		109.01
9		7,135	4.08	0.9		109.86
10		7,850	5.75	1.1		110.55
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,305	0.00	0.0		114.86
13		13,405	0.00	0.0		115.93

Region table for sample 7 : HiSeq1411-28

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	2,464	635	1,207.25	1,816.2	3,446.7	🟦 96	43.4

Assay Class:	High Sensitivity DNA Assay	Created:	7/2/2018 4:59:12 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-07-02\2018-07-02_003.xad	Modified:	7/3/2018 8:55:33 AM

Electropherogram Summary Continued ...



Overall Results for sample 8 : **HiSeq1411-29**

Number of peaks found:	8	Corr. Area 1:	1,738.0
Noise:	0.2		

Peak table for sample 8 : **HiSeq1411-29**

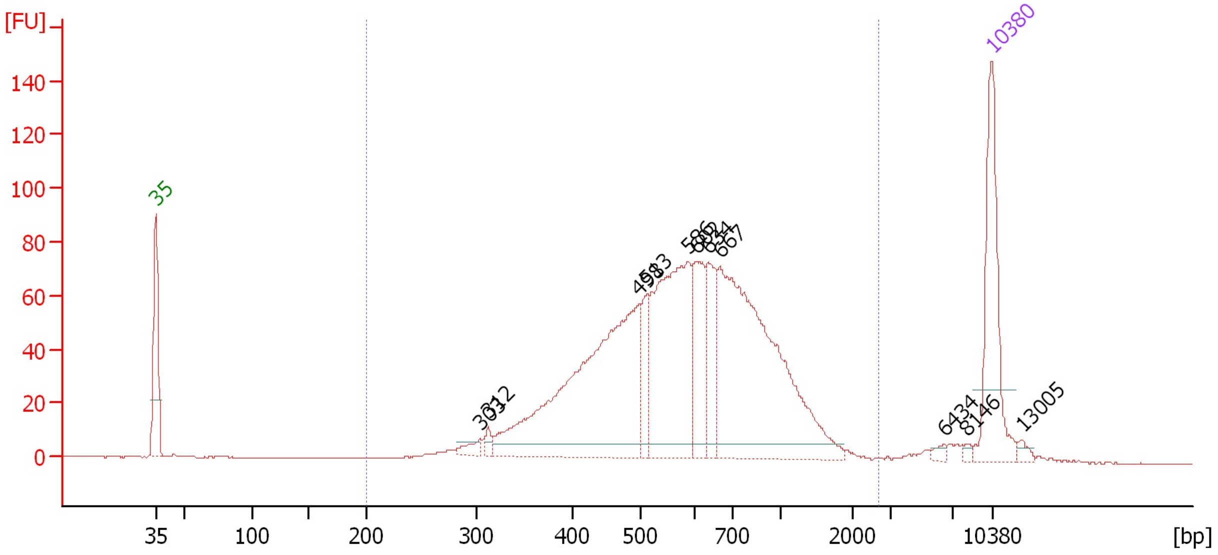
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		308	16.57	81.4		70.54
3		329	13.26	61.0		72.20
4		388	83.25	324.8		76.93
5		499	248.96	755.7		83.53
6		573	159.22	420.7		86.96
7		651	312.07	726.5		89.76
8		7,439	8.99	1.8		110.15
9	▶	10,380	75.00	10.9	Upper Marker	113.00
10		13,432	0.00	0.0		115.95

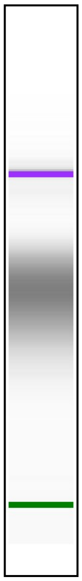
Region table for sample 8 : **HiSeq1411-29**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	2,515	630	1,034.03	1,738.0	2,961.2	■ 96	42.7

Electropherogram Summary Continued ...

HiSeq1411-30





Overall Results for sample 9 : **HiSeq1411-30**

Number of peaks found:	11	Corr. Area 1:	1,479.8
Noise:	0.2		

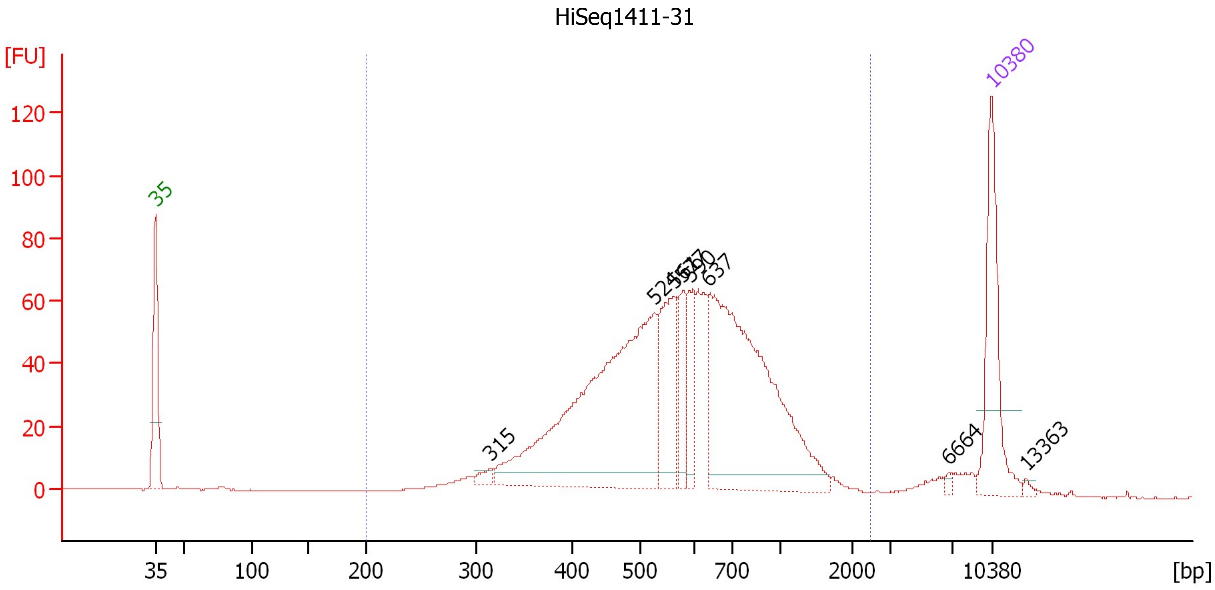
Peak table for sample 9 : **HiSeq1411-30**

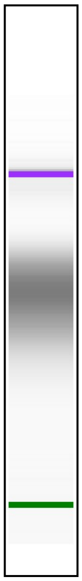
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		303	9.35	46.7		70.11
3		312	6.79	33.0		70.82
4		498	298.95	909.8		83.46
5		513	33.88	100.1		84.16
6		586	179.28	463.3		87.56
7		602	61.81	155.5		88.26
8		634	41.84	100.0		89.23
9		667	291.68	662.4		90.26
10		6,434	3.44	0.8		109.00
11		8,146	2.41	0.4		110.84
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		13,005	0.00	0.0		115.54

Region table for sample 9 : **HiSeq1411-30**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,666	643	979.71	1,479.8	2,758.7	🟦 97	43.4

Electropherogram Summary Continued ...





Overall Results for sample 10 : HiSeq1411-31

Number of peaks found:	8	Corr. Area 1:	1,279.7
Noise:	0.2		

Peak table for sample 10 : HiSeq1411-31

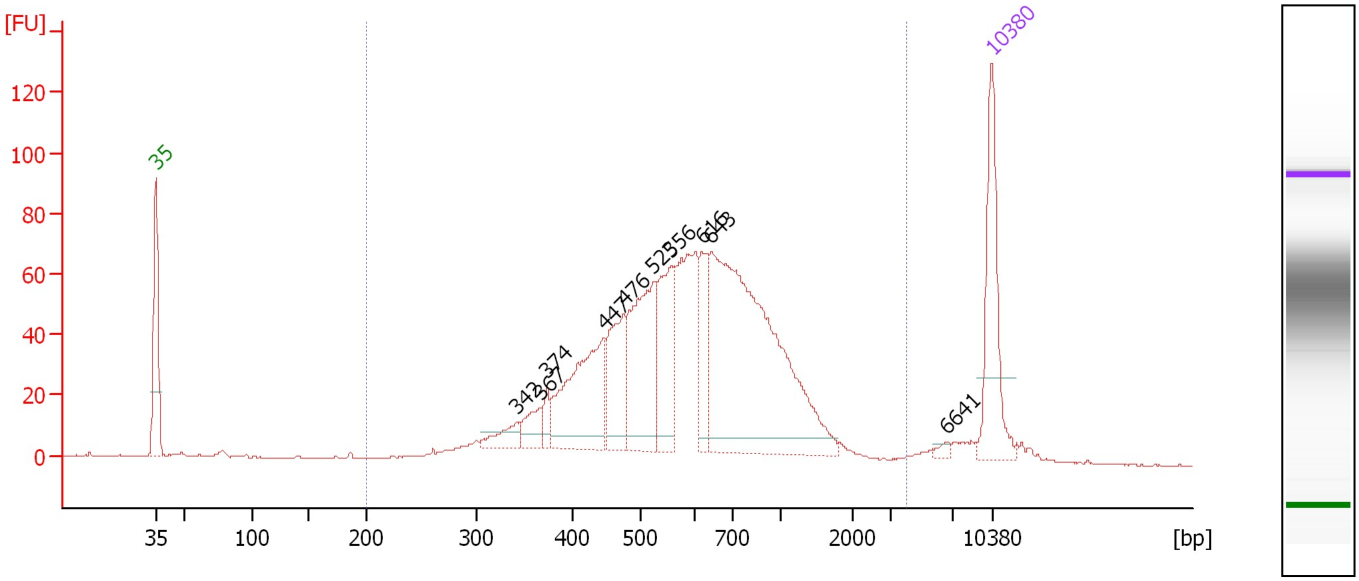
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		315	8.77	42.3		71.03
3		524	381.81	1,103.5		84.70
4		561	86.84	234.6		86.38
5		577	40.01	105.0		87.14
6		590	39.64	101.7		87.74
7		637	321.68	765.5		89.32
8		6,664	2.64	0.6		109.30
9	▶	10,380	75.00	10.9	Upper Marker	113.00
10		13,363	0.00	0.0		115.88

Region table for sample 10 : HiSeq1411-31

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	2,469	628	1,040.62	1,279.7	2,967.3	🟦 96	41.5

Electropherogram Summary Continued ...

HiSeq1411-32



Overall Results for sample 11 : HiSeq1411-32

Number of peaks found:	10	Corr. Area 1:	1,374.6
Noise:	0.2		

Peak table for sample 11 : HiSeq1411-32

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		342	22.06	97.7		73.23
3		367	24.54	101.2		75.26
4		374	14.15	57.4		75.75
5		447	128.48	435.9		80.52
6		476	73.42	233.5		82.22
7		523	122.69	355.4		84.64
8		556	90.76	247.2		86.17
9		616	44.59	109.6		88.70
10		643	370.74	873.4		89.52
11		6,641	3.97	0.9		109.27
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : HiSeq1411-32

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	4,004	662	1,121.07	1,374.6	3,125.6	■ 96	48.7

Gel Image