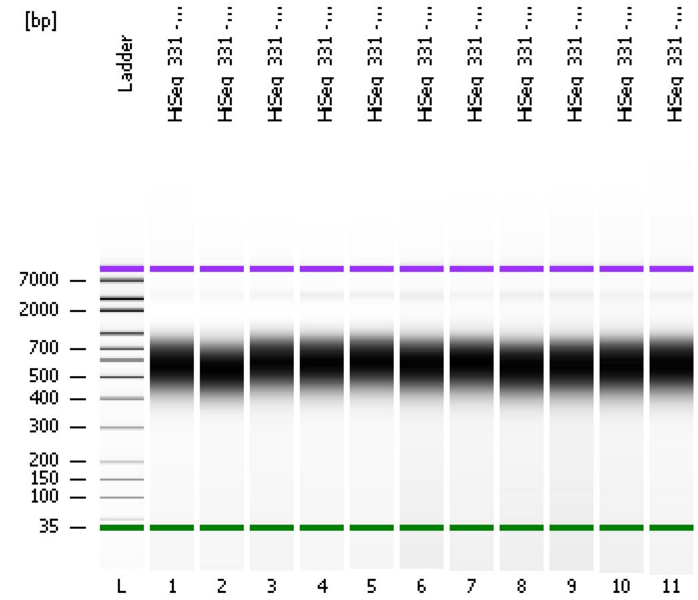
Assay Class:	High Sensitivity DNA Assay	Created:	2/12/2016 4:18:45 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad	Modified:	2/12/2016 5:04:23 PM

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

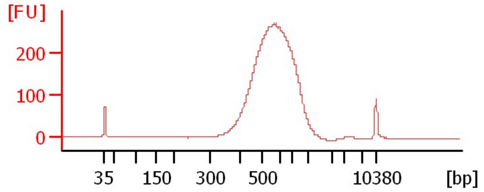
Chip Information:

Chip Lot #:

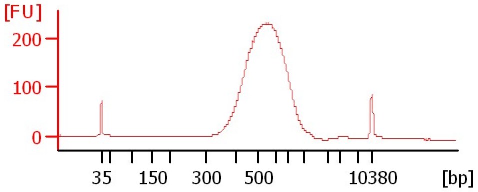
Reagent Kit Lot #:

Chip Comments:

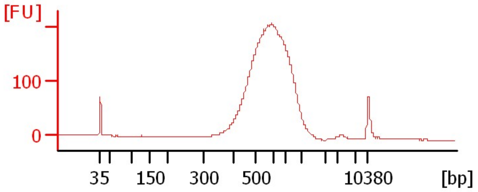
HiSeq_331 - 11 Library



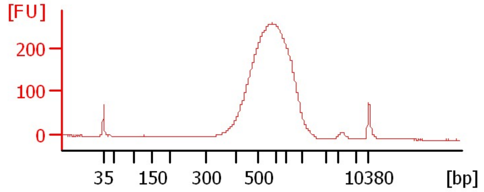
HiSeq_331 - 12 Library



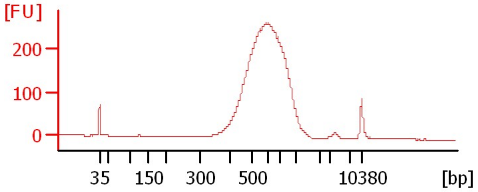
HiSeq_331 - 13 Library



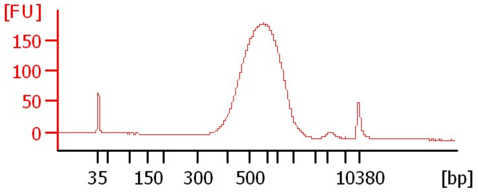
HiSeq_331 - 14 Library



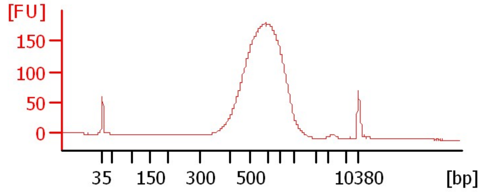
HiSeq_331 - 15 Library



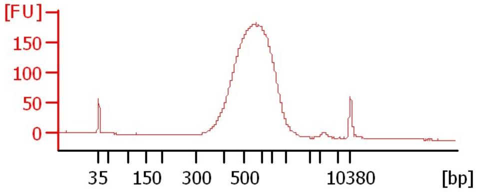
HiSeq_331 - 16 Library



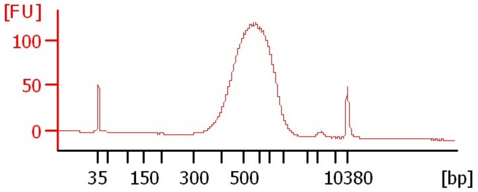
HiSeq_331 - 17 Library



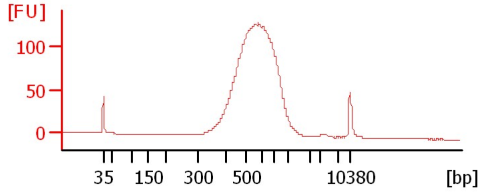
HiSeq_331 - 18 Library



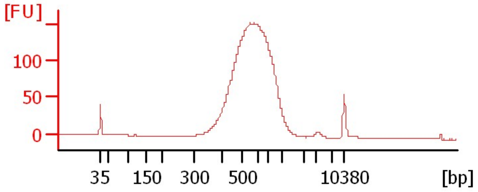
HiSeq_331 - 19 Library



HiSeq_331 - 20 Library



HiSeq_331 - 21 Library



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad

Created: 2/12/2016 4:18:45 PM
Modified: 2/12/2016 5:04:23 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq_331 - 11 Library		☐	✓			
HiSeq_331 - 12 Library		☐	✓			
HiSeq_331 - 13 Library		☐	✓			
HiSeq_331 - 14 Library		☐	✓			
HiSeq_331 - 15 Library		☐	✓			
HiSeq_331 - 16 Library		☐	✓			
HiSeq_331 - 17 Library		☐	✓			
HiSeq_331 - 18 Library		☐	✓			
HiSeq_331 - 19 Library		☐	✓			
HiSeq_331 - 20 Library		☐	✓			
HiSeq_331 - 21 Library		☐	✓			
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

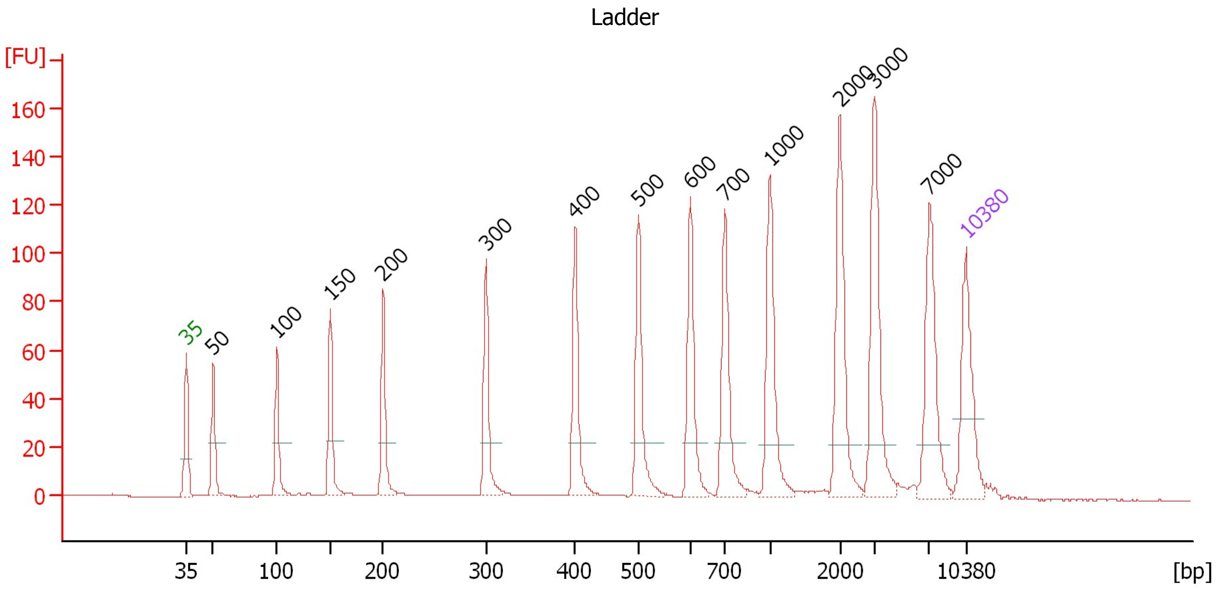
Ladder

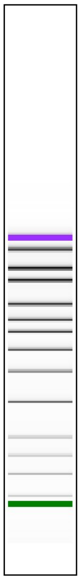
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad

Created: 2/12/2016 4:18:45 PM
Modified: 2/12/2016 5:04:23 PM

Electropherogram Summary





Overall Results for Ladder

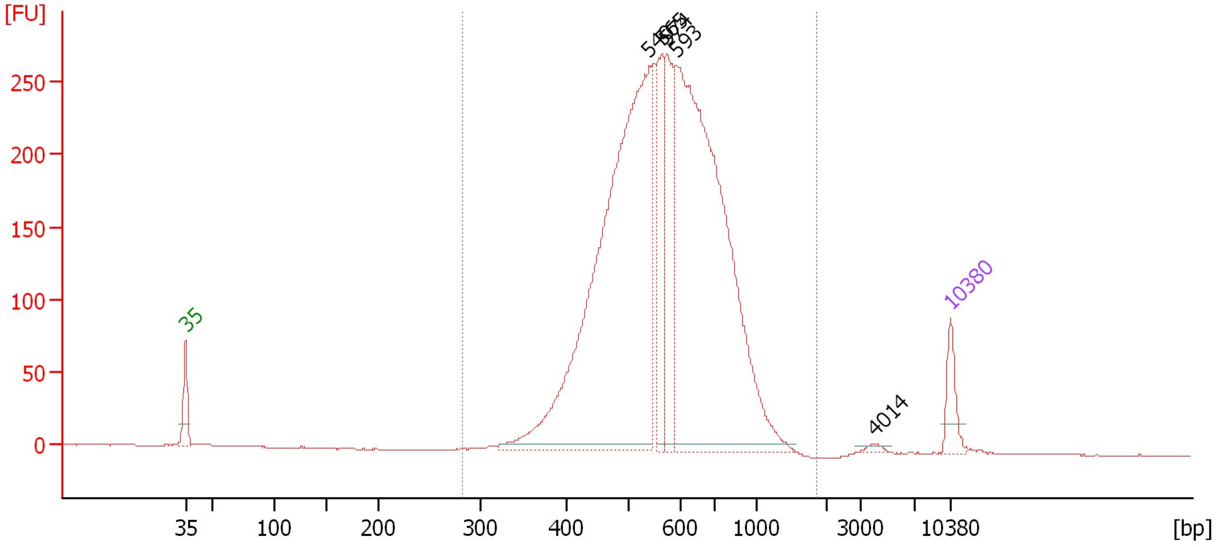
Noise:	0.2

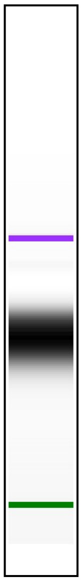
Peak table for Ladder

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	45.44
3	∟	100	150.00	2,272.7	Ladder Peak	51.18
4	∟	150	150.00	1,515.2	Ladder Peak	55.96
5	∟	200	150.00	1,136.4	Ladder Peak	60.69
6	∟	300	150.00	757.6	Ladder Peak	69.92
7	∟	400	150.00	568.2	Ladder Peak	77.90
8	∟	500	150.00	454.5	Ladder Peak	83.59
9	∟	600	150.00	378.8	Ladder Peak	88.23
10	∟	700	150.00	324.7	Ladder Peak	91.34
11	∟	1,000	150.00	227.3	Ladder Peak	95.36
12	∟	2,000	150.00	113.6	Ladder Peak	101.67
13	∟	3,000	150.00	75.8	Ladder Peak	104.78
14	∟	7,000	150.00	32.5	Ladder Peak	109.70
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

HiSeq_331 - 11 Library





Overall Results for sample 1 : <u>HiSeq_331 - 11 Library</u>

Number of peaks found:	5	Corr. Area 1:	3,939.6
Noise:	0.2		

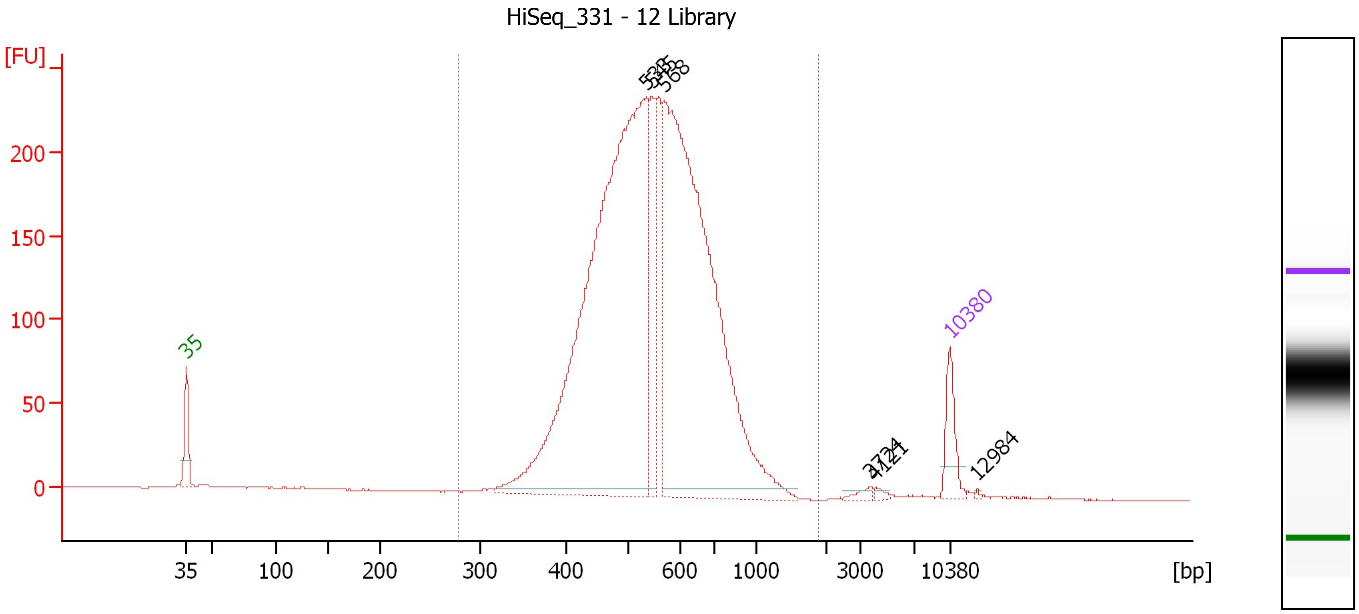
Peak table for sample 1 : <u>HiSeq_331 - 11 Library</u>

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		540	2,274.84	6,385.5		85.44
3		565	344.69	924.3		86.61
4		574	358.40	945.2		87.05
5		593	2,039.66	5,207.8		87.93
6		4,014	10.53	4.0		106.02
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : <u>HiSeq_331 - 11 Library</u>

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
284	1,844	593	3,939.6	14,459.5	🟦	5,302.09	99	24.4

Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq_331 - 12 Library

Number of peaks found:	6	Corr. Area 1:	3,474.3
Noise:	0.2		

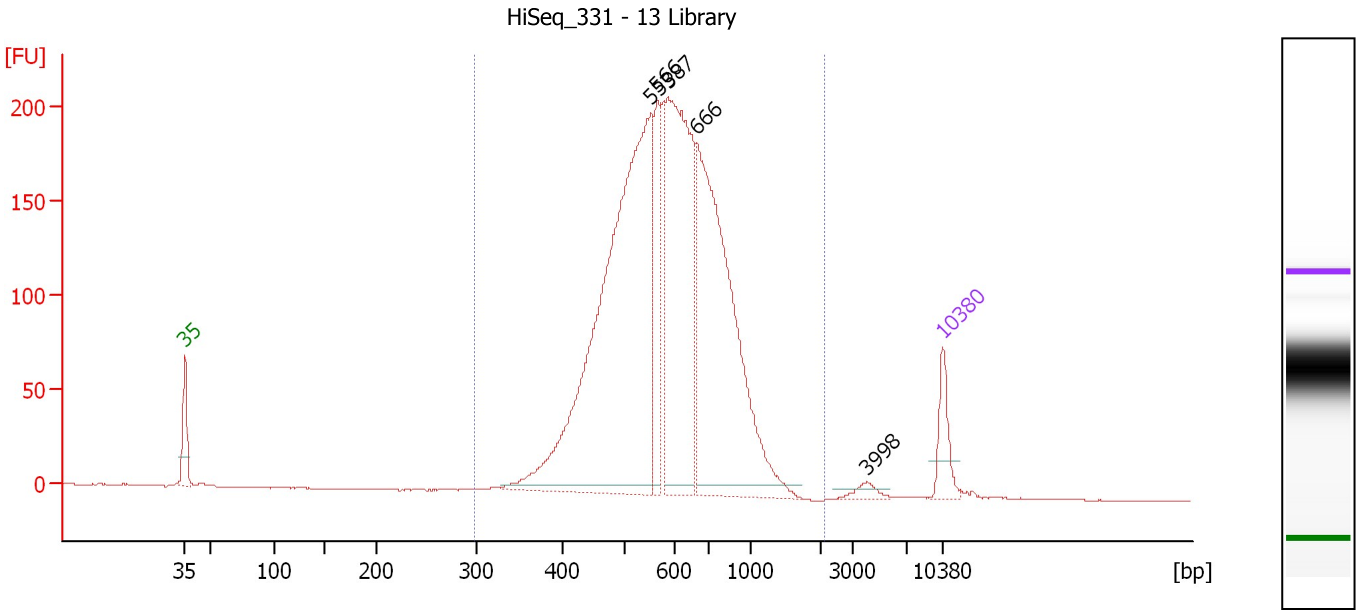
Peak table for sample 2 : HiSeq_331 - 12 Library

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		533	2,281.16	6,481.4		85.14
3		545	233.45	649.2		85.67
4		568	1,816.08	4,844.1		86.75
5		3,724	12.45	5.1		105.67
6		4,121	7.50	2.8		106.16
7	▶	10,380	75.00	10.9	Upper Marker	113.00
8		12,984	0.00	0.0		115.54

Region table for sample 2 : HiSeq_331 - 12 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
279	1,882	561	3,474.3	13,208.2	🟦	4,610.90	99	23.1

Electropherogram Summary Continued ...


HiSeq_331 - 13 Library

Overall Results for sample 3 : **HiSeq_331 - 13 Library**

Number of peaks found:	5	Corr. Area 1:	2,959.2
Noise:	0.2		

Peak table for sample 3 : **HiSeq_331 - 13 Library**

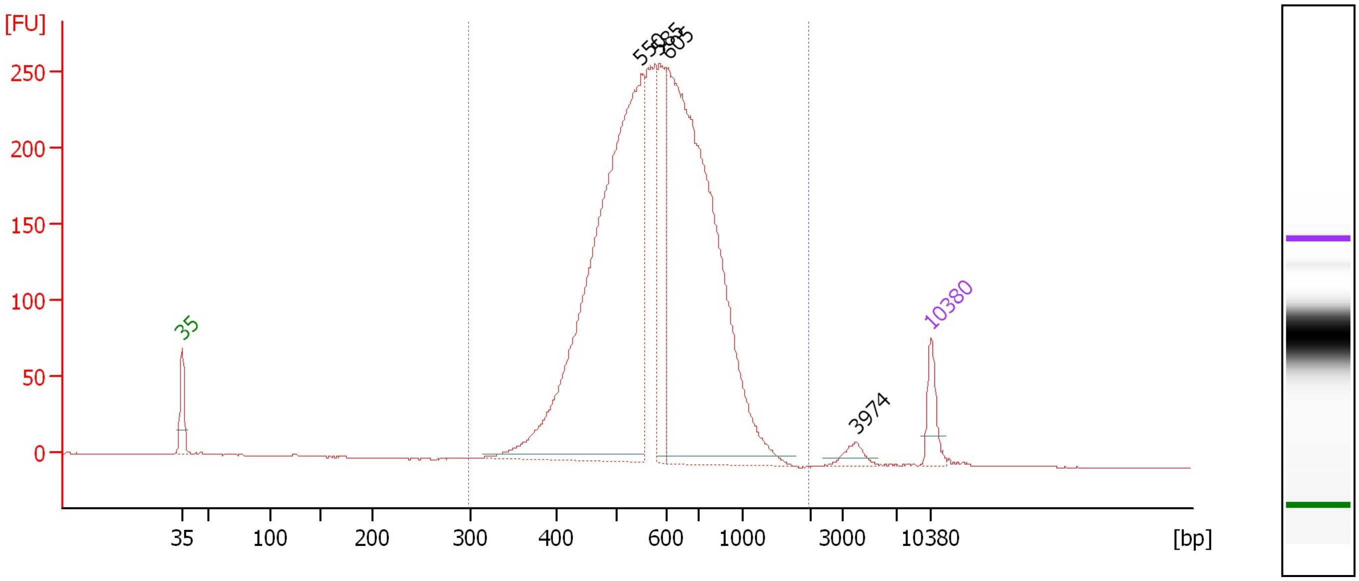
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		553	1,715.49	4,699.9		86.05
3		566	207.63	556.0		86.65
4		587	862.11	2,225.1		87.63
5		666	1,081.97	2,460.6		90.29
6		3,998	22.63	8.6		106.00
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : **HiSeq_331 - 13 Library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
299	2,163	614	2,959.2	10,779.8	■	4,070.05	99	25.9

Electropherogram Summary Continued ...

HiSeq_331 - 14 Library



Overall Results for sample 4 : HiSeq_331 - 14 Library

Number of peaks found:	4	Corr. Area 1:	3,715.3
Noise:	0.2		

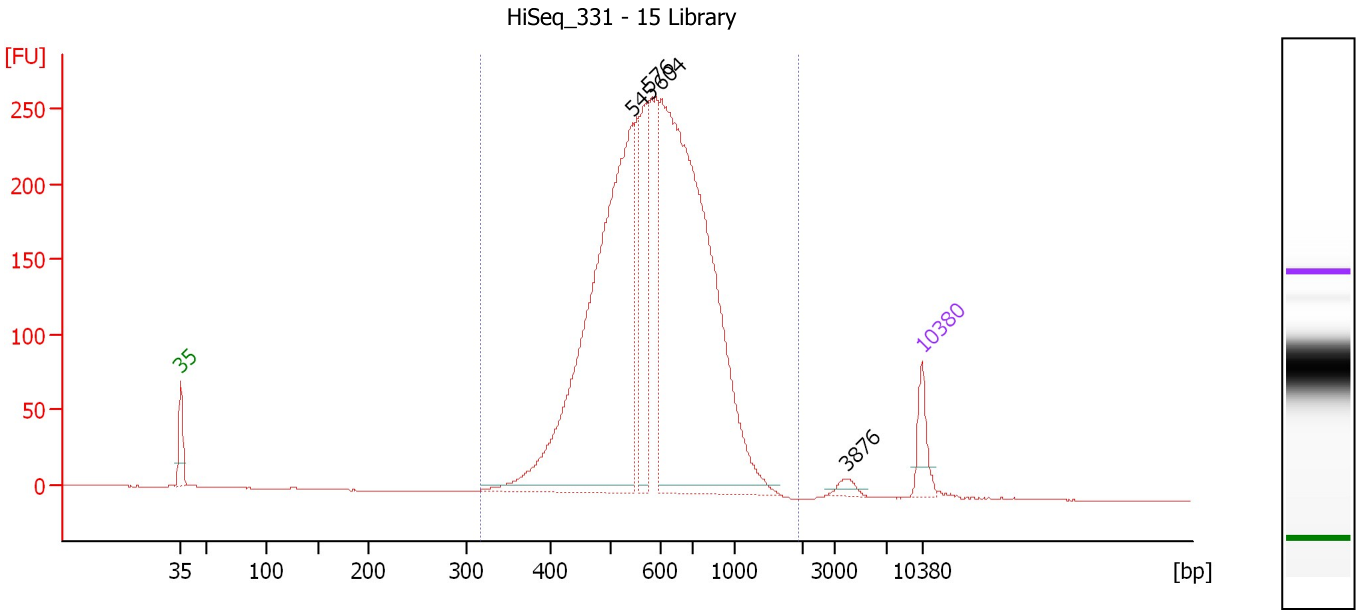
Peak table for sample 4 : HiSeq_331 - 14 Library

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		550	2,320.94	6,397.9		85.90
3		585	348.19	901.7		87.54
4		605	2,118.45	5,305.3		88.39
5		3,974	36.57	13.9		105.98
6	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : HiSeq_331 - 14 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
298	1,981	607	3,715.3	14,188.7	🟦	5,311.02	99	25.4

Electropherogram Summary Continued ...



Overall Results for sample 5 : <u>HiSeq_331 - 15 Library</u>

Number of peaks found: 4 Corr. Area 1: 3,665.5

Noise: 0.1

Peak table for sample 5 : <u>HiSeq_331 - 15 Library</u>

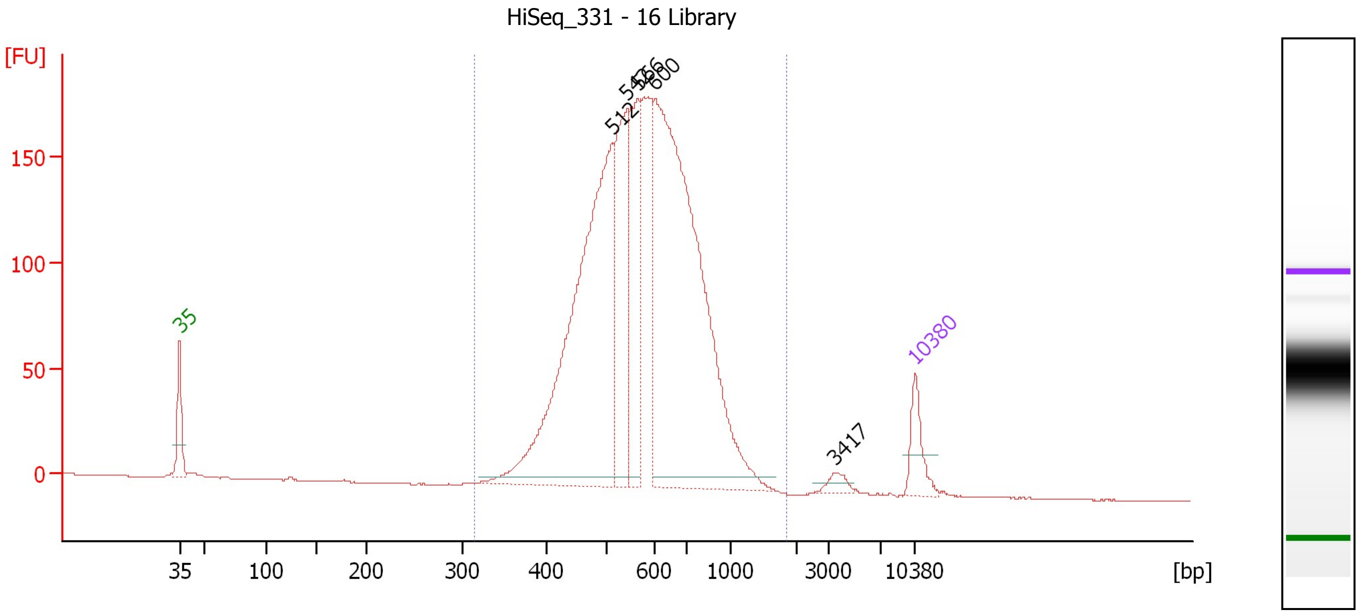
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		545	1,762.06	4,900.1		85.67
3		576	341.38	897.5		87.13
4		604	2,058.68	5,168.4		88.34
5		3,876	22.47	8.8		105.85
6	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : <u>HiSeq_331 - 15 Library</u>

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
317	1,957	621	3,665.5	12,575.2	🟦	4,802.71	99	26.0

Electropherogram Summary Continued ...

HiSeq_331 - 16 Library



Overall Results for sample 6 : HiSeq_331 - 16 Library

Number of peaks found:	5	Corr. Area 1:	2,664.4
Noise:	0.2		

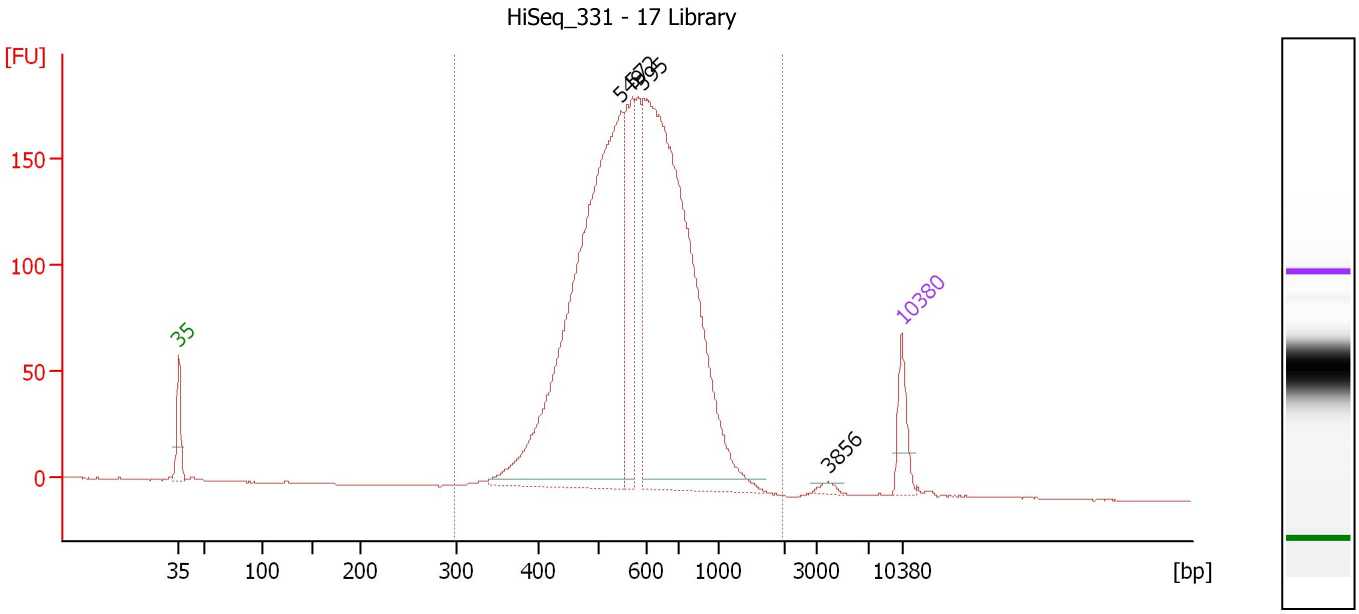
Peak table for sample 6 : HiSeq_331 - 16 Library

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		512	1,429.17	4,231.6		84.14
3		542	451.27	1,260.7		85.56
4		566	407.11	1,089.0		86.67
5		600	1,645.94	4,153.3		88.25
6		3,417	24.80	11.0		105.29
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : HiSeq_331 - 16 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
315	1,868	599	2,664.4	11,790.7	■	4,355.23	99	25.4

Electropherogram Summary Continued ...


HiSeq_331 - 17 Library

Overall Results for sample 7 : HiSeq_331 - 17 Library

Number of peaks found: 4 Corr. Area 1: 2,612.9

Noise: 0.1

Peak table for sample 7 : HiSeq_331 - 17 Library

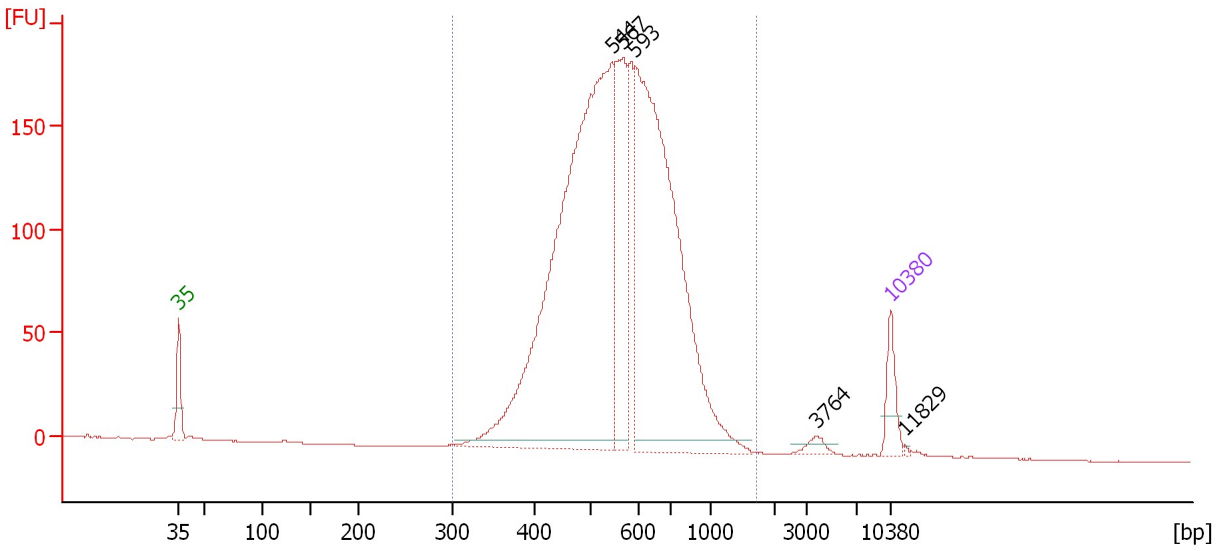
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		549	1,762.34	4,863.8		85.87
3		572	343.36	909.0		86.95
4		595	1,697.92	4,326.6		87.98
5		3,856	12.11	4.8		105.83
6	▶	10,380	75.00	10.9	Upper Marker	113.00

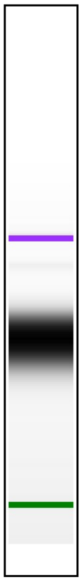
Region table for sample 7 : HiSeq_331 - 17 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
297	1,968	604	2,612.9	11,087.8	■	4,127.09	99	25.6

Electropherogram Summary Continued ...

HiSeq_331 - 18 Library





Overall Results for sample 8 : HiSeq_331 - 18 Library

Number of peaks found:	5	Corr. Area 1:	2,776.6
Noise:	0.2		

Peak table for sample 8 : HiSeq_331 - 18 Library

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		544	2,304.67	6,415.2		85.65
3		567	444.44	1,187.8		86.70
4		593	1,610.58	4,115.9		87.90
5		3,764	24.25	9.8		105.72
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		11,829	0.00	0.0		114.41

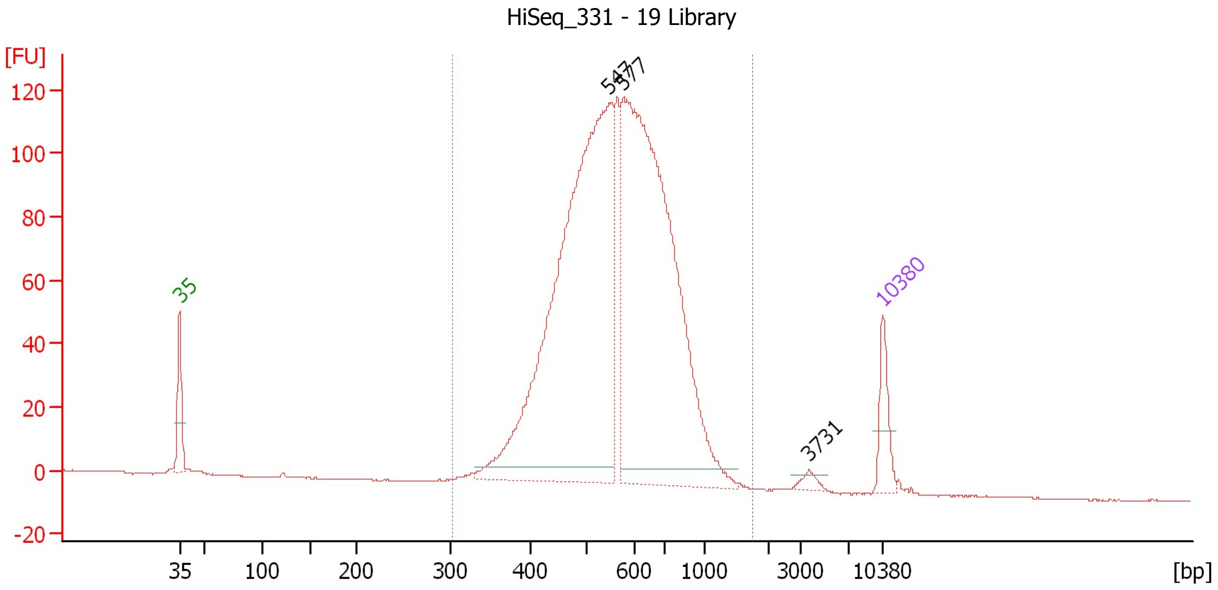
Region table for sample 8 : HiSeq_331 - 18 Library

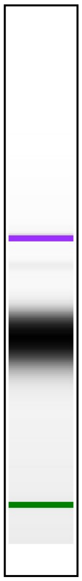
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
299	1,708	576	2,776.6	13,250.6	🟦	4,723.72	99	24.6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad

Created: 2/12/2016 4:18:45 PM
Modified: 2/12/2016 5:04:23 PM

Electropherogram Summary Continued ...


HiSeq_331 - 19 Library



Overall Results for sample 9 : HiSeq_331 - 19 Library

Number of peaks found:	3	Corr. Area 1:	1,776.7
Noise:	0.1		

Peak table for sample 9 : HiSeq_331 - 19 Library

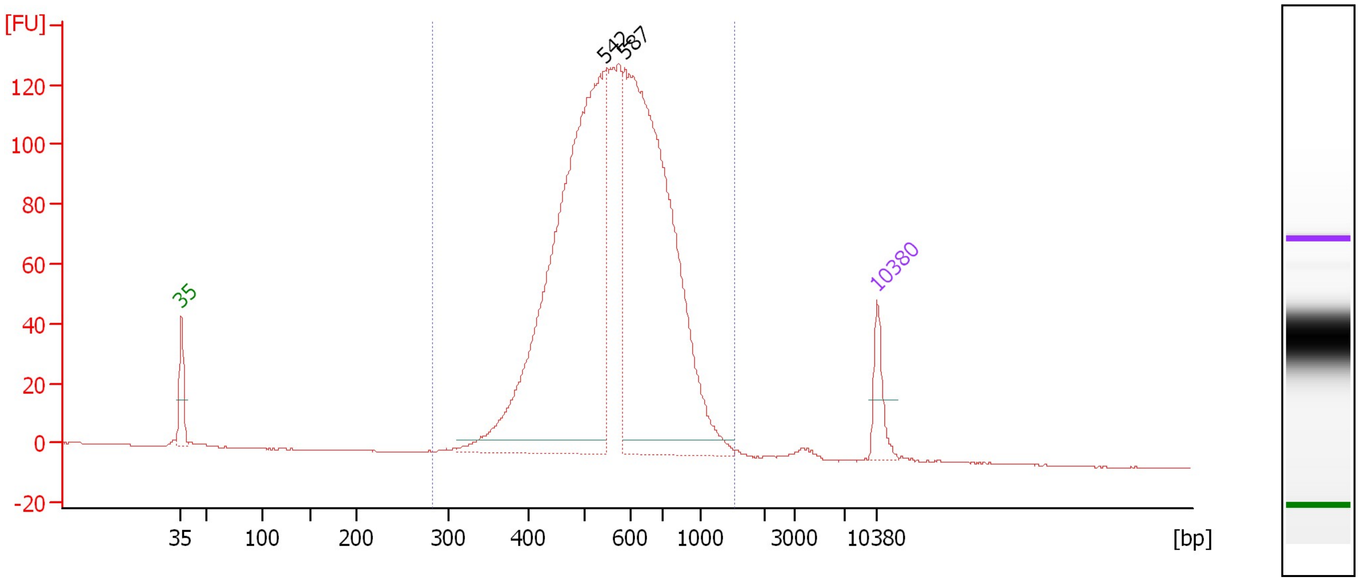
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		547	1,779.87	4,930.0		85.77
3		577	1,636.85	4,300.0		87.15
4		3,731	16.74	6.8		105.68
5	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : HiSeq_331 - 19 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
302	1,733	585	1,776.7	10,271.2	■	3,711.24	99	25.0

Electropherogram Summary Continued ...

HiSeq_331 - 20 Library



Overall Results for sample 10 : HiSeq_331 - 20 Library

Number of peaks found:	2	Corr. Area 1:	1,932.3
Noise:	0.1		

Peak table for sample 10 : HiSeq_331 - 20 Library

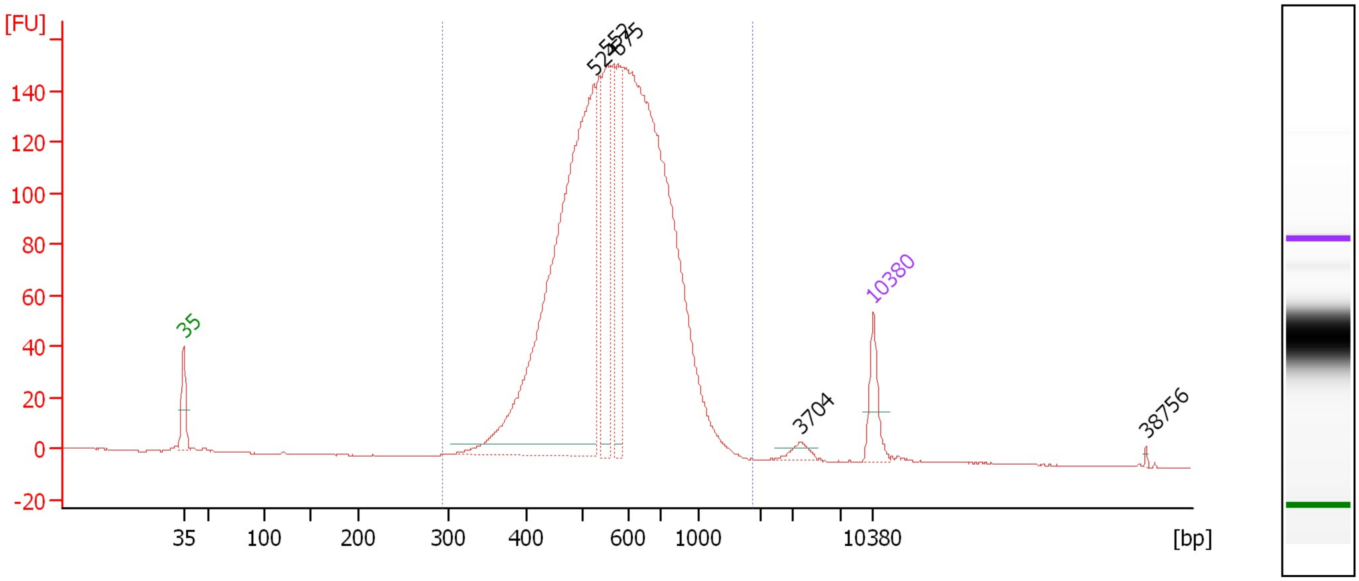
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		542	1,915.92	5,357.2		85.54
3		587	1,686.72	4,353.9		87.63
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : HiSeq_331 - 20 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
282	1,540	589	1,932.3	11,571.8	🟦	4,191.56	99	25.7

Electropherogram Summary Continued ...

HiSeq_331 - 21 Library



Overall Results for sample 11 : **HiSeq_331 - 21 Library**

Number of peaks found:	5	Corr. Area 1:	2,251.0
Noise:	0.1		

Peak table for sample 11 : **HiSeq_331 - 21 Library**

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		524	1,725.36	4,988.8		84.71
3		552	336.14	922.6		86.01
4		575	272.77	718.3		87.09
5		3,704	22.96	9.4		105.64
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		38,756	0.00	0.0		140.70

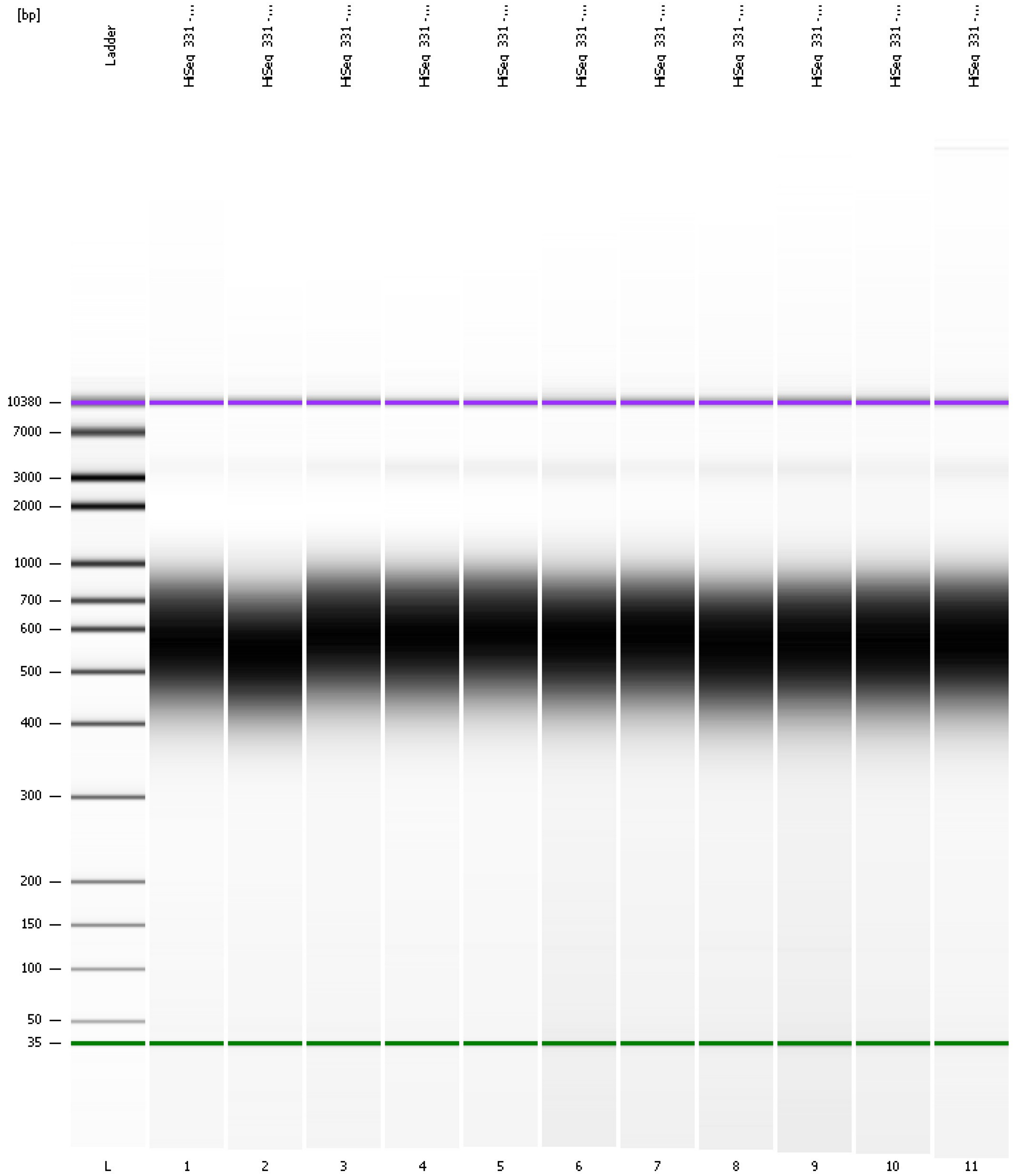
Region table for sample 11 : **HiSeq_331 - 21 Library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
293	1,847	599	2,251.0	12,553.9	■	4,611.18	99	26.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad

Created: 2/12/2016 4:18:45 PM
Modified: 2/12/2016 5:04:23 PM

Gel Image



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		2/12/2016 5:00:03 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-02-12\2016-02-12_002.xad)		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		2/12/2016 4:18:51 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1