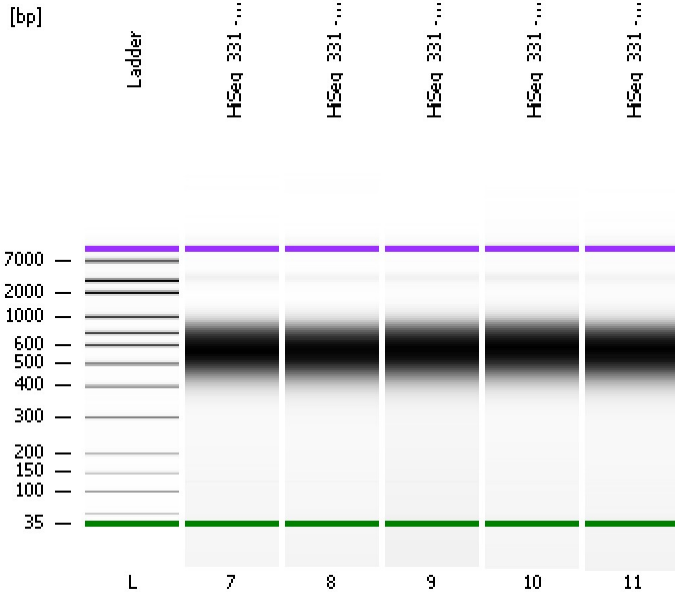


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
Modified: 2/11/2016 5:08:08 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

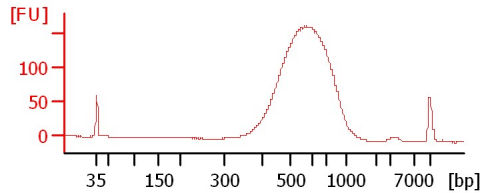
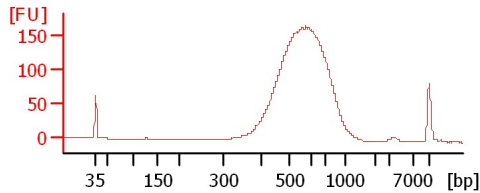
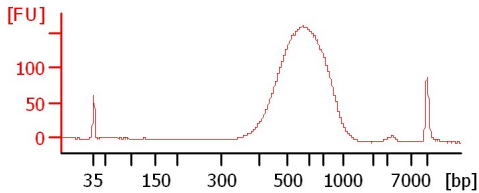
Chip Information:

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

HiSeq_331 - 1 Library (1:15)

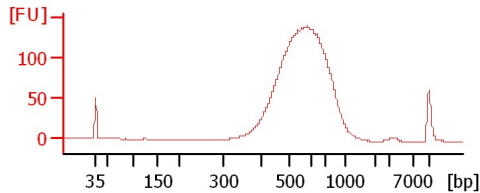
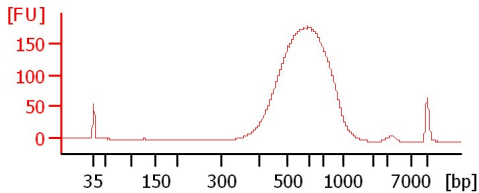
HiSeq_331 - 2 Library (1:15)

HiSeq_331 - 3 Library (1:15)



HiSeq_331 - 4 Library (1:15)

HiSeq_331 - 5 Library (1:15)



Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq_331 - 1 Library (1:15)		<input type="checkbox"/>				
HiSeq_331 - 2 Library (1:15)		<input type="checkbox"/>				
HiSeq_331 - 3 Library (1:15)		<input type="checkbox"/>				
HiSeq_331 - 4 Library (1:15)		<input type="checkbox"/>				
HiSeq_331 - 5 Library (1:15)		<input type="checkbox"/>				
Ladder		<input type="checkbox"/>				

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 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

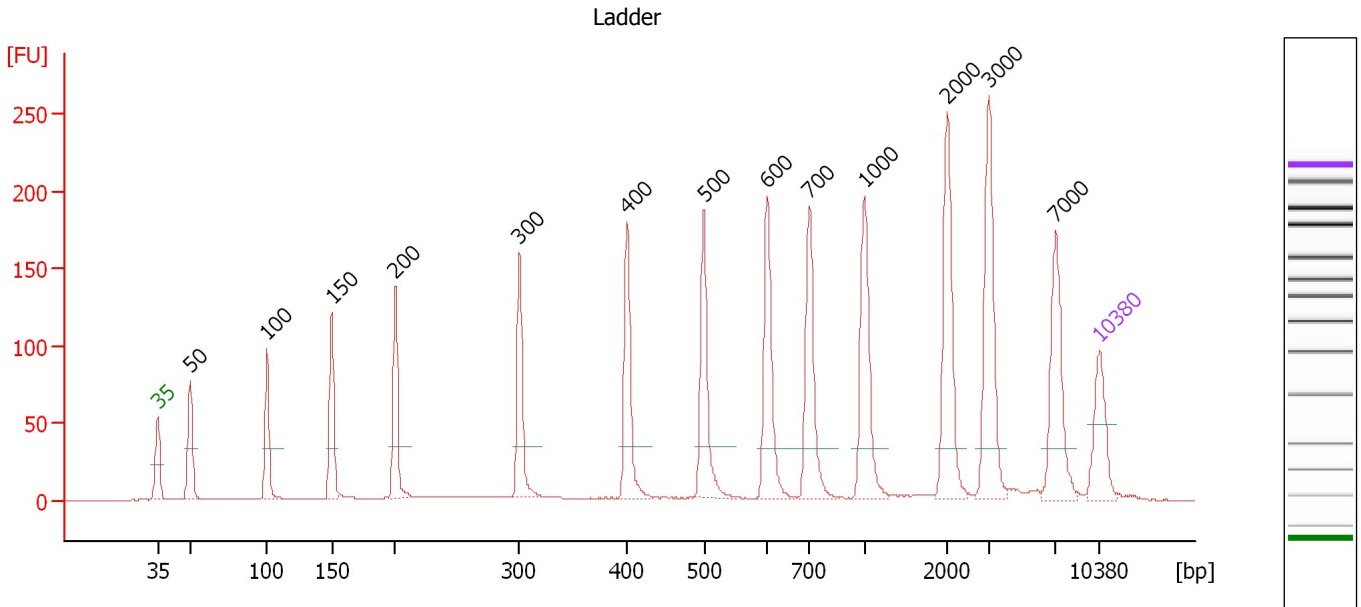
Ladder

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:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

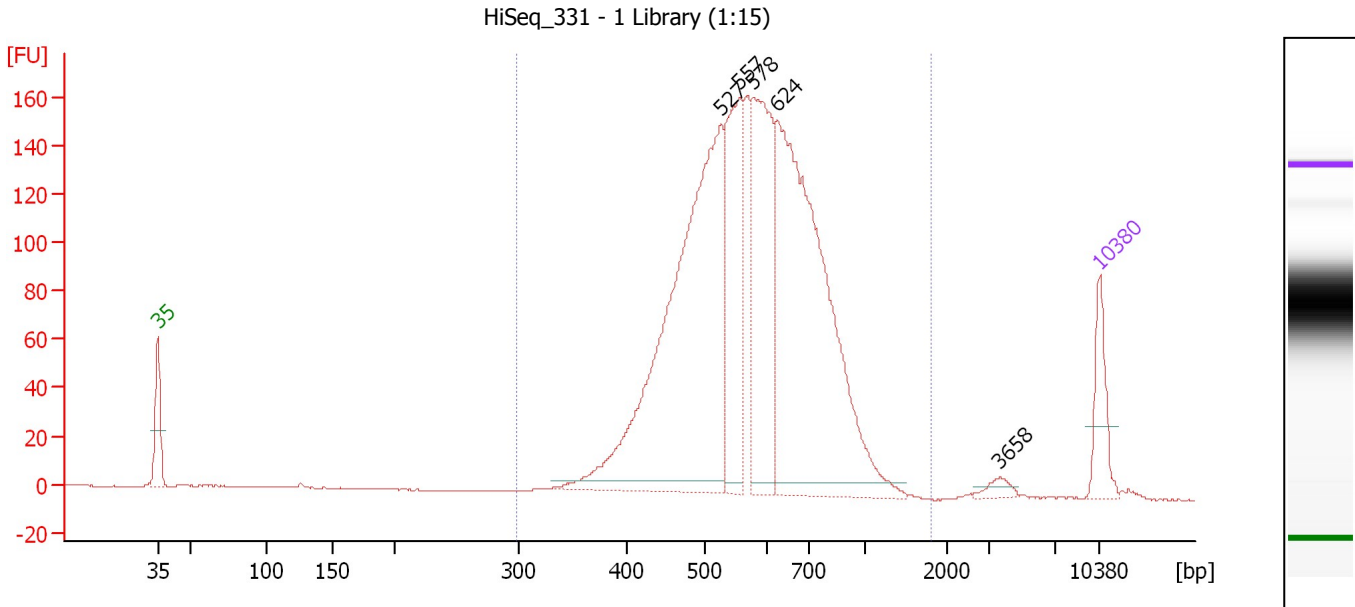
Peak table for Ladder

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	51.12
4	150	150.00	1,515.2	Ladder Peak	55.95
5	200	150.00	1,136.4	Ladder Peak	60.64
6	300	150.00	757.6	Ladder Peak	69.88
7	400	150.00	568.2	Ladder Peak	77.91
8	500	150.00	454.5	Ladder Peak	83.58
9	600	150.00	378.8	Ladder Peak	88.27
10	700	150.00	324.7	Ladder Peak	91.42
11	1,000	150.00	227.3	Ladder Peak	95.50
12	2,000	150.00	113.6	Ladder Peak	101.65
13	3,000	150.00	75.8	Ladder Peak	104.74
14	7,000	150.00	32.5	Ladder Peak	109.72
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : HiSeq 331 - 1 Library (1:15)

Number of peaks found: 5 Corr. Area 1: 2,260.3
 Noise: 0.2

Peak table for sample 7 : HiSeq 331 - 1 Library (1:15)

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	527	1,095.34	3,150.4		84.84
3	557	349.81	952.2		86.24
4	578	389.04	1,020.0		87.24
5	624	963.05	2,337.8		89.03
6	3,658	17.45	7.2		105.56
7	10,380	75.00	10.9	Upper Marker	113.00

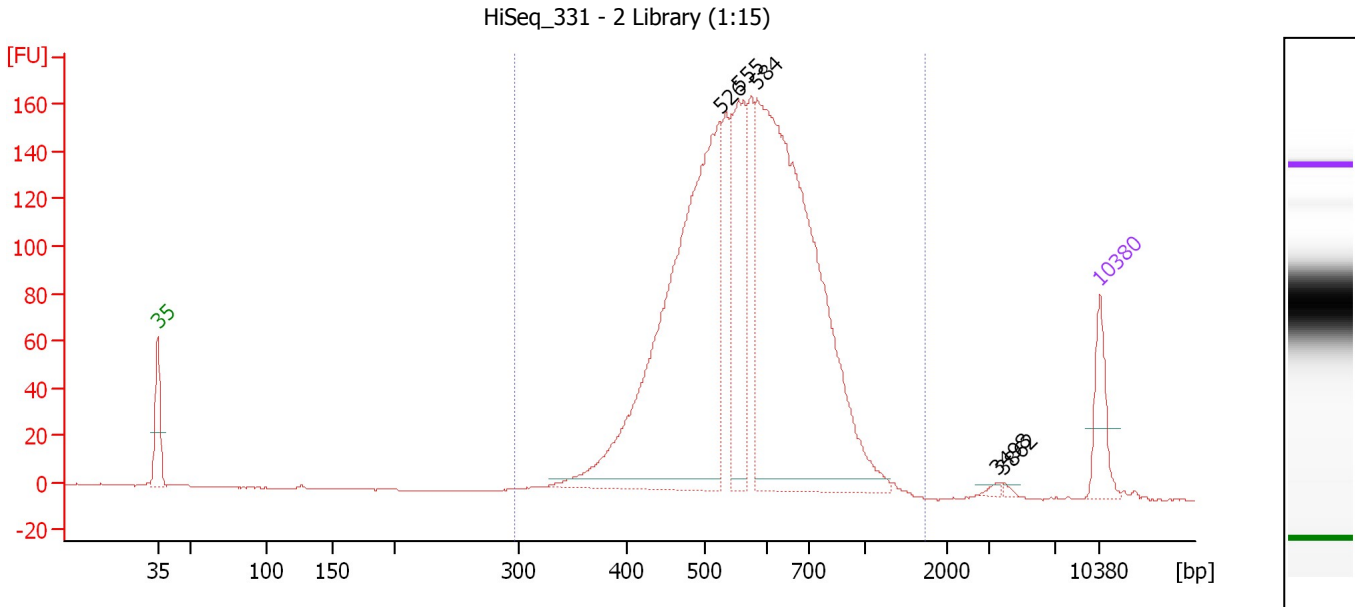
Region table for sample 7 : HiSeq 331 - 1 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
298	1,808	594	2,260.3	8,052.0	2,978.39	99	22.9

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : HiSeq 331 - 2 Library (1:15)

Number of peaks found: 5 Corr. Area 1: 2,323.4
 Noise: 0.2

Peak table for sample 8 : HiSeq 331 - 2 Library (1:15)

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	526	1,218.88	3,510.1		84.81
3	555	331.04	903.7		86.17
4	584	1,341.78	3,481.3		87.52
5	3,498	6.55	2.8		105.36
6	3,862	4.11	1.6		105.81
7	10,380	75.00	10.9	Upper Marker	113.00

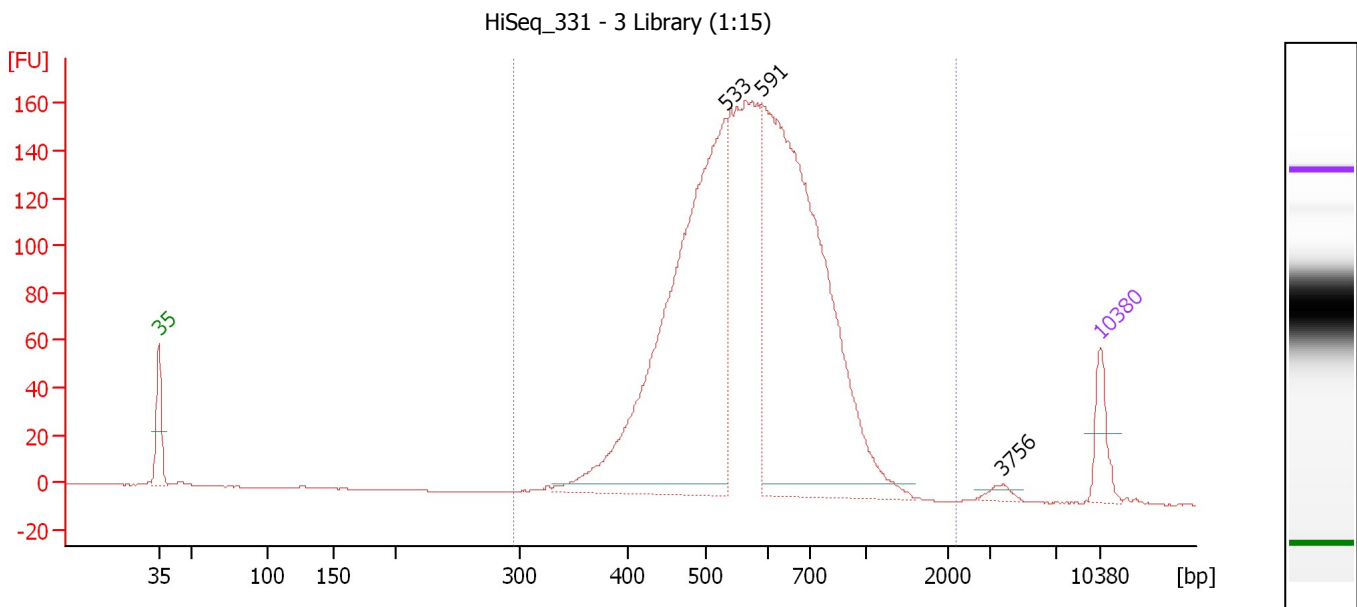
Region table for sample 8 : HiSeq 331 - 2 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
296	1,732	585	2,323.4	9,021.6	3,285.94	99	23.1

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : HiSeq 331 - 3 Library (1:15)

Number of peaks found: 3 Corr. Area 1: 2,361.1
 Noise: 0.2

Peak table for sample 9 : HiSeq 331 - 3 Library (1:15)

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	533	1,608.24	4,569.9		85.14
3	591	1,658.18	4,248.9		87.87
4	3,756	18.17	7.3		105.68
5	10,380	75.00	10.9	Upper Marker	113.00

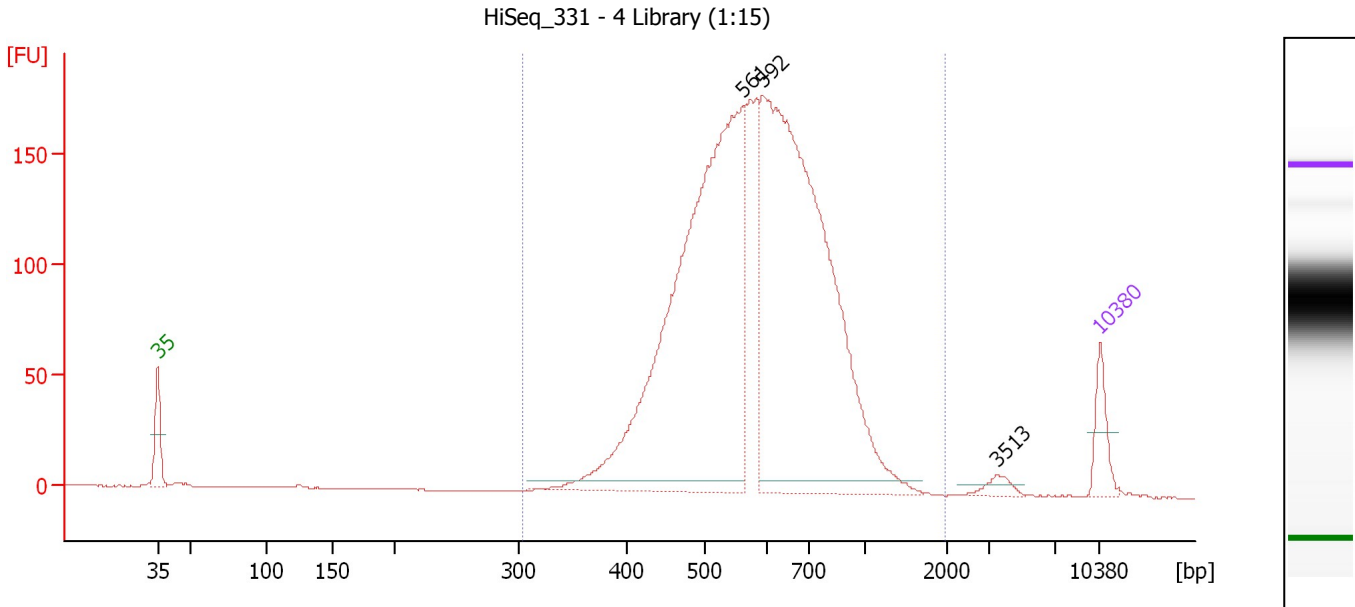
Region table for sample 9 : HiSeq 331 - 3 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
294	2,178	594	2,361.1	11,248.4	4,143.01	99	24.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary Continued ...



Overall Results for sample 10 : HiSeq 331 - 4 Library (1:15)

Number of peaks found: 3 Corr. Area 1: 2,542.9
 Noise: 0.1

Peak table for sample 10 : HiSeq 331 - 4 Library (1:15)

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	561	1,991.65	5,381.6		86.43
3	592	1,947.44	4,983.1		87.91
4	3,513	26.51	11.4		105.38
5	10,380	75.00	10.9	Upper Marker	113.00

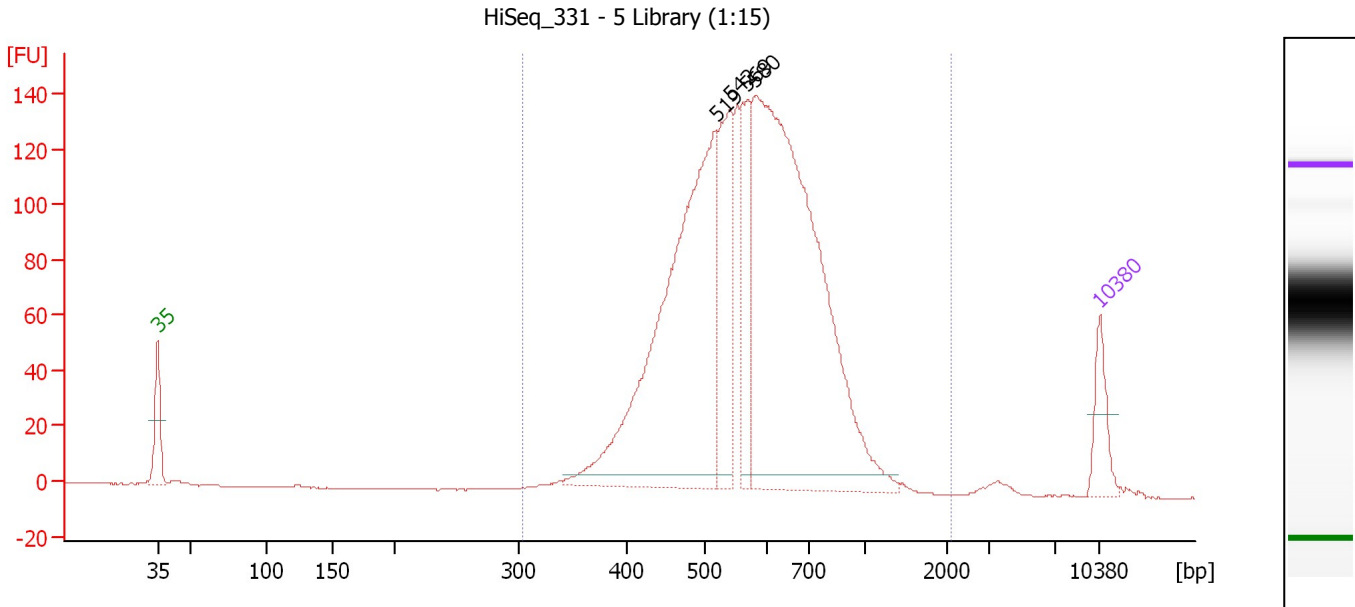
Region table for sample 10 : HiSeq 331 - 4 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
304	1,974	610	2,542.9	11,721.1	4,406.09	99	25.8

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 PM

Electropherogram Summary Continued ...



Overall Results for sample 11 : HiSeq 331 - 5 Library (1:15)

Number of peaks found: 4 Corr. Area 1: 2,007.1
 Noise: 0.2

Peak table for sample 11 : HiSeq 331 - 5 Library (1:15)

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	519	1,226.56	3,581.4		84.47
3	542	333.80	933.6		85.54
4	569	181.84	484.3		86.81
5	580	1,553.41	4,060.0		87.32
6	10,380	75.00	10.9	Upper Marker	113.00

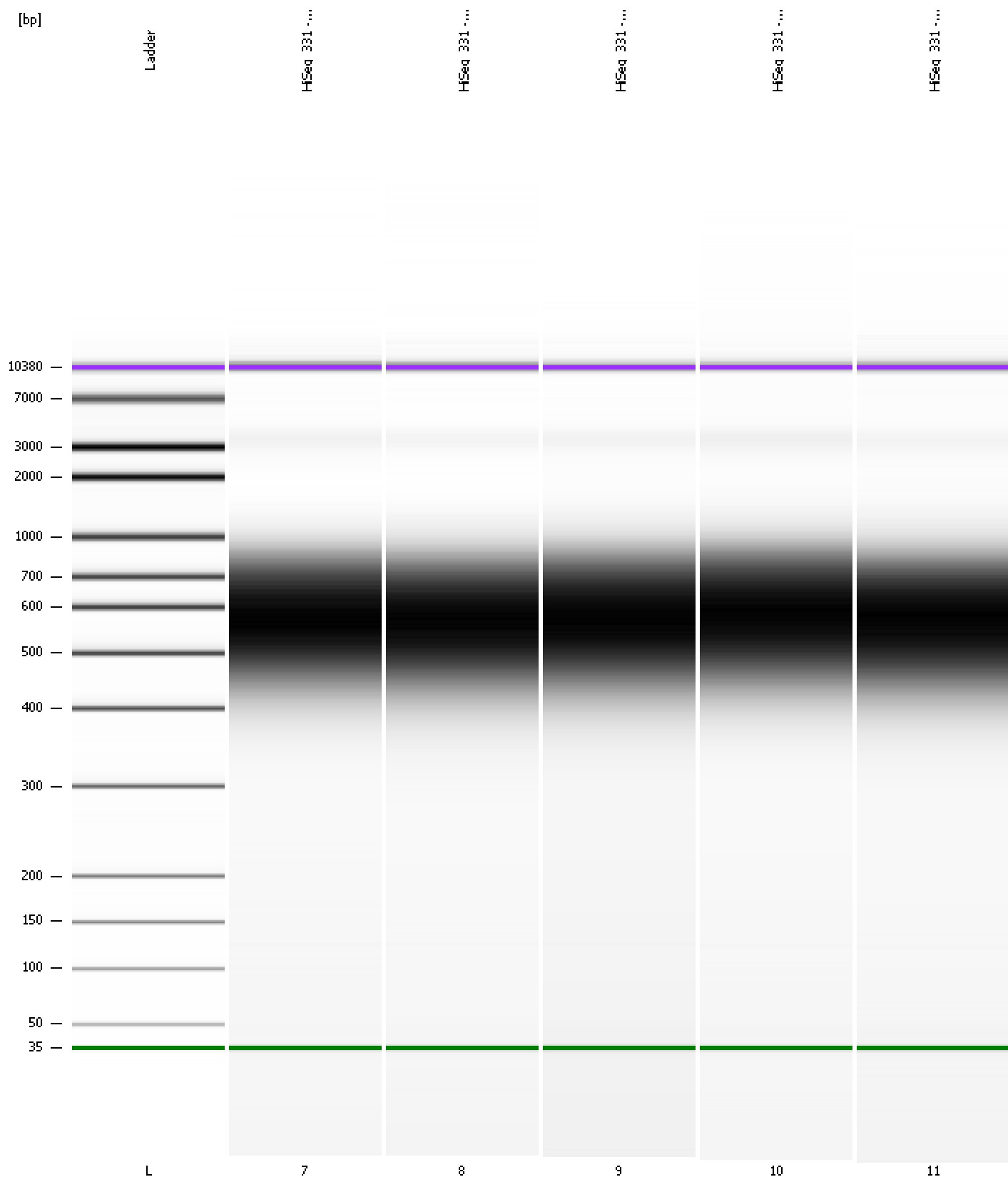
Region table for sample 11 : HiSeq 331 - 5 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
302	2,082	590	2,007.1	9,683.6	3,539.05	99	24.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
Modified: 2/11/2016 5:08:08 PM

Gel Image



Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...alyzer\2016-02-11\2016-02-11_001_HiSeq331_Libraries_1-5.xad

Created: 2/11/2016 10:47:50 AM
 Modified: 2/11/2016 5:08:08 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		2/11/2016 11:29:07 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanal yzer\2016-02-11\2016-02-11_001.xad)		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		2/11/2016 10:47:56 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1