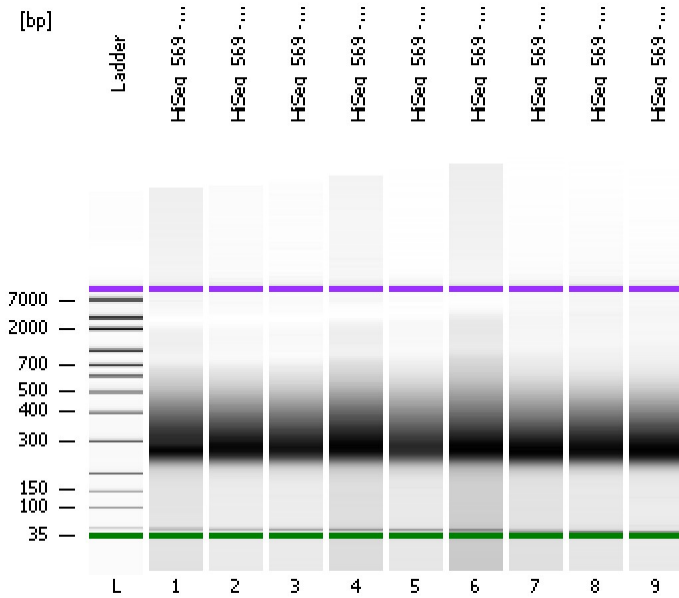


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
Modified: 8/25/2016 4:26:13 PM

Electrophoresis File Run Summary



Instrument Information:

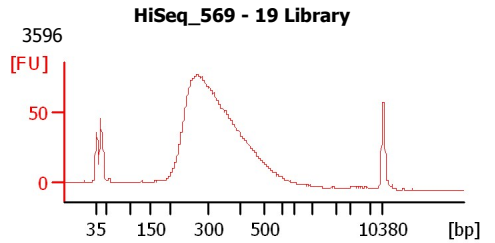
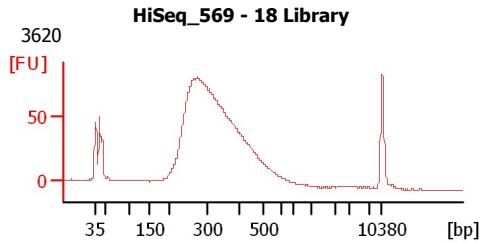
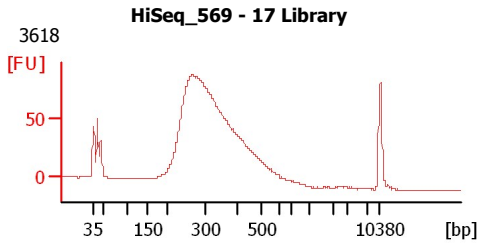
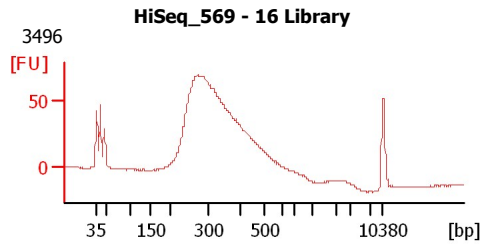
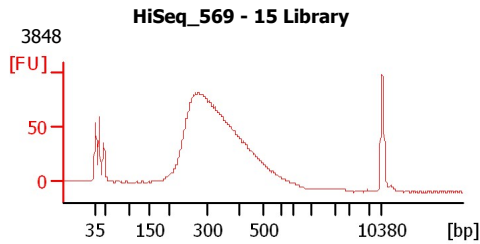
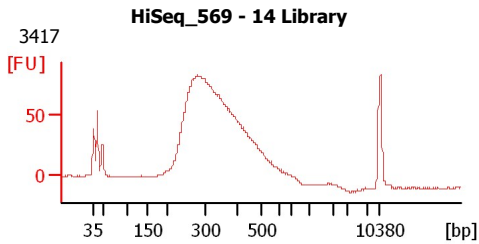
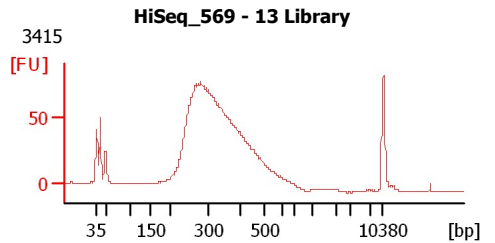
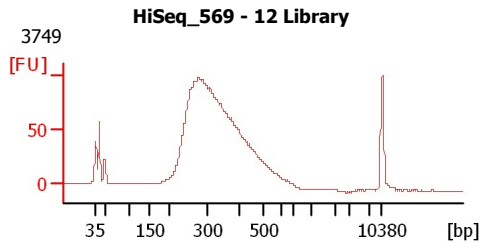
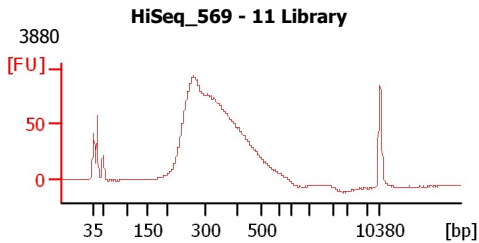
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq_569 - 11 Library	3880	<input type="checkbox"/>	✓			
HiSeq_569 - 12 Library	3749	<input type="checkbox"/>	✓			
HiSeq_569 - 13 Library	3415	<input type="checkbox"/>	✓			
HiSeq_569 - 14 Library	3417	<input type="checkbox"/>	✓			
HiSeq_569 - 15 Library	3848	<input type="checkbox"/>	✓			
HiSeq_569 - 16 Library	3496	<input type="checkbox"/>	✓			
HiSeq_569 - 17 Library	3618	<input type="checkbox"/>	✓			
HiSeq_569 - 18 Library	3620	<input type="checkbox"/>	✓			
HiSeq_569 - 19 Library	3596	<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
Modified: 8/25/2016 4:26:13 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

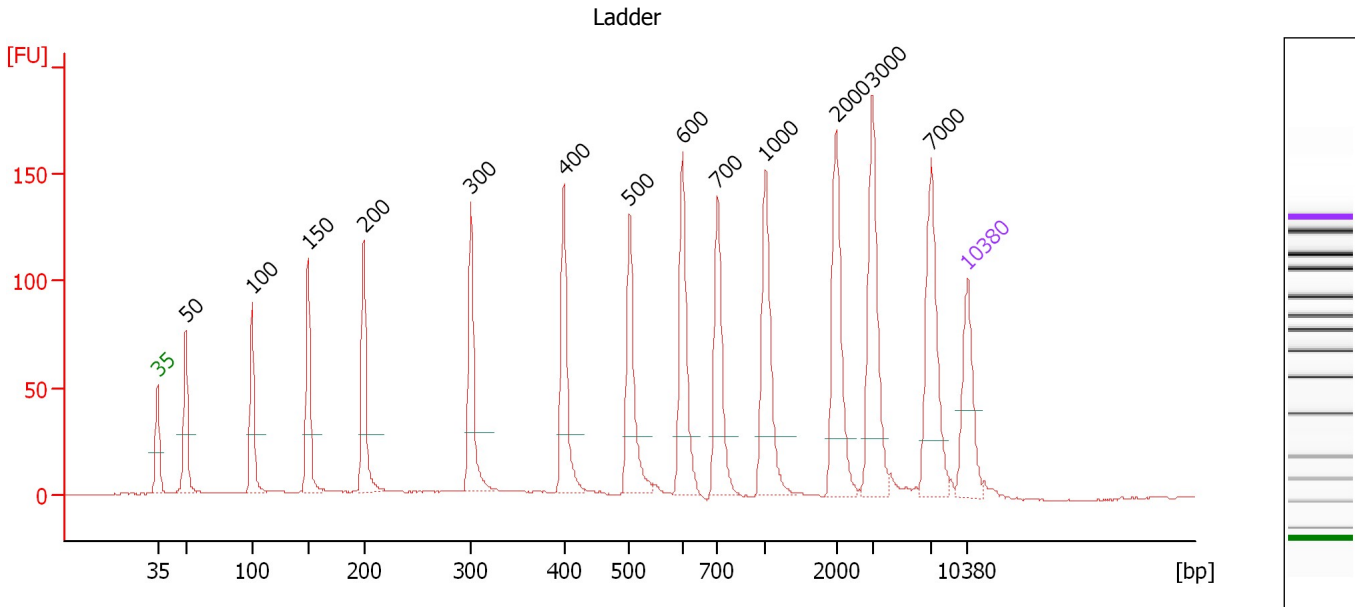
Ladder

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:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

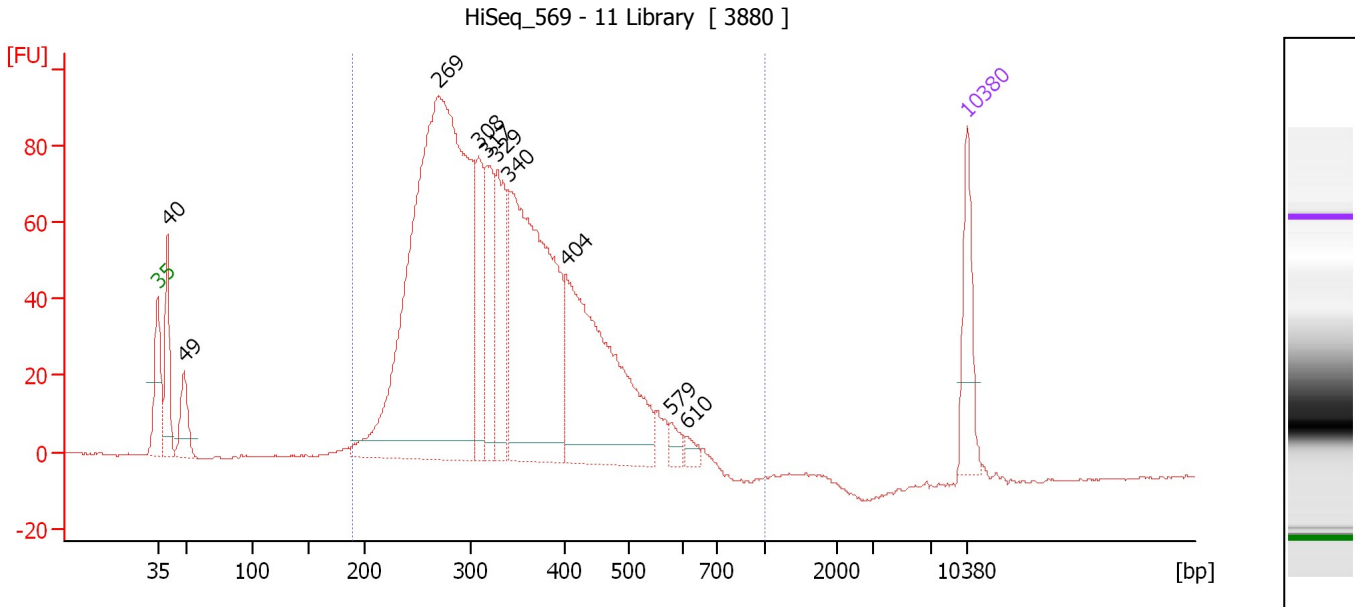
Peak table for Ladder

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	56.00
5	200	150.00	1,136.4	Ladder Peak	60.83
6	300	150.00	757.6	Ladder Peak	70.08
7	400	150.00	568.2	Ladder Peak	78.10
8	500	150.00	454.5	Ladder Peak	83.79
9	600	150.00	378.8	Ladder Peak	88.36
10	700	150.00	324.7	Ladder Peak	91.41
11	1,000	150.00	227.3	Ladder Peak	95.53
12	2,000	150.00	113.6	Ladder Peak	101.62
13	3,000	150.00	75.8	Ladder Peak	104.77
14	7,000	150.00	32.5	Ladder Peak	109.85
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : HiSeq 569 - 11 Library

Number of peaks found: 10 Corr. Area 1: 1,865.0
 Noise: 0.3

Peak table for sample 1 : HiSeq 569 - 11 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	40	135.04	5,072.6		43.87
3	49	78.26	2,413.8		45.30
4	269	1,382.66	7,780.0		67.23
5	308	136.01	668.0		70.76
6	317	138.71	662.2		71.47
7	329	170.17	784.2		72.39
8	340	614.74	2,737.5		73.31
9	404	438.83	1,647.4		78.31
10	579	17.98	47.1		87.39
11	610	13.67	34.0		88.66
12	10,380	75.00	10.9	Upper Marker	113.00

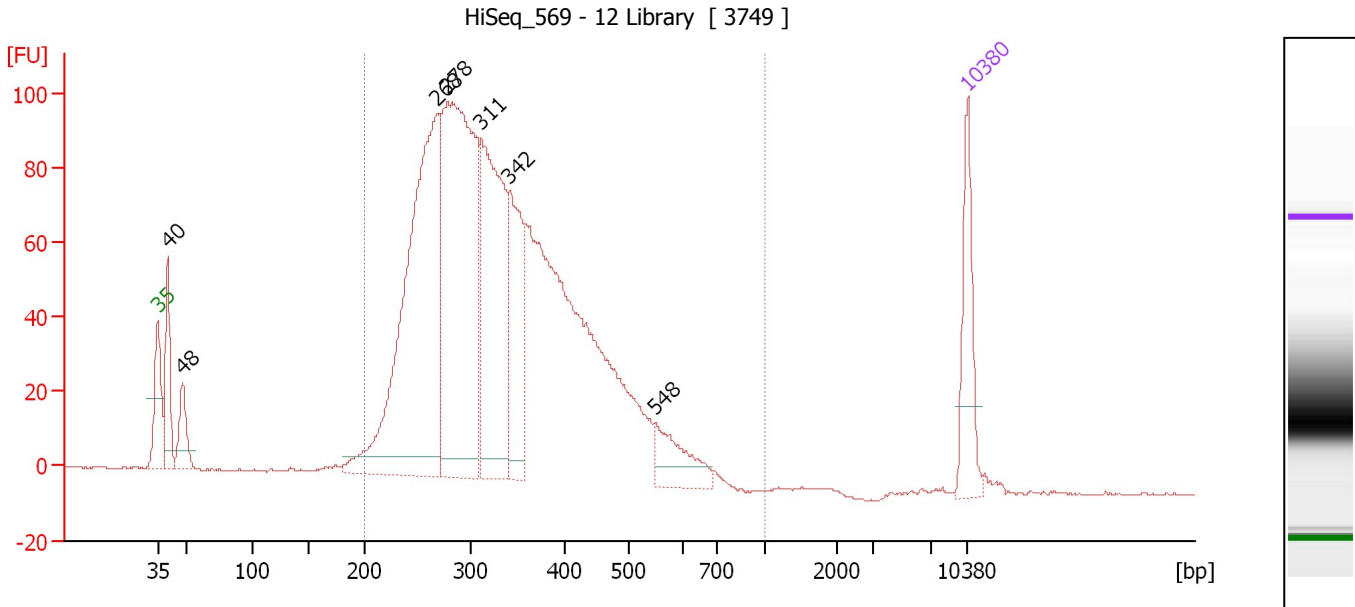
Region table for sample 1 : HiSeq 569 - 11 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
189	1,000	341	1,865.0	14,013.4	2,914.39	95	25.1

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq 569 - 12 Library

Number of peaks found: 7 Corr. Area 1: 2,018.4
 Noise: 0.3

Peak table for sample 2 : HiSeq 569 - 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	40	106.94	4,016.0		43.87
3	48	64.07	2,013.5		45.15
4	268	654.42	3,697.2		67.13
5	278	615.10	3,350.7		68.05
6	311	353.06	1,719.3		70.97
7	342	186.45	826.7		73.42
8	548	66.33	183.3		86.00
9	10,380	75.00	10.9	Upper Marker	113.00

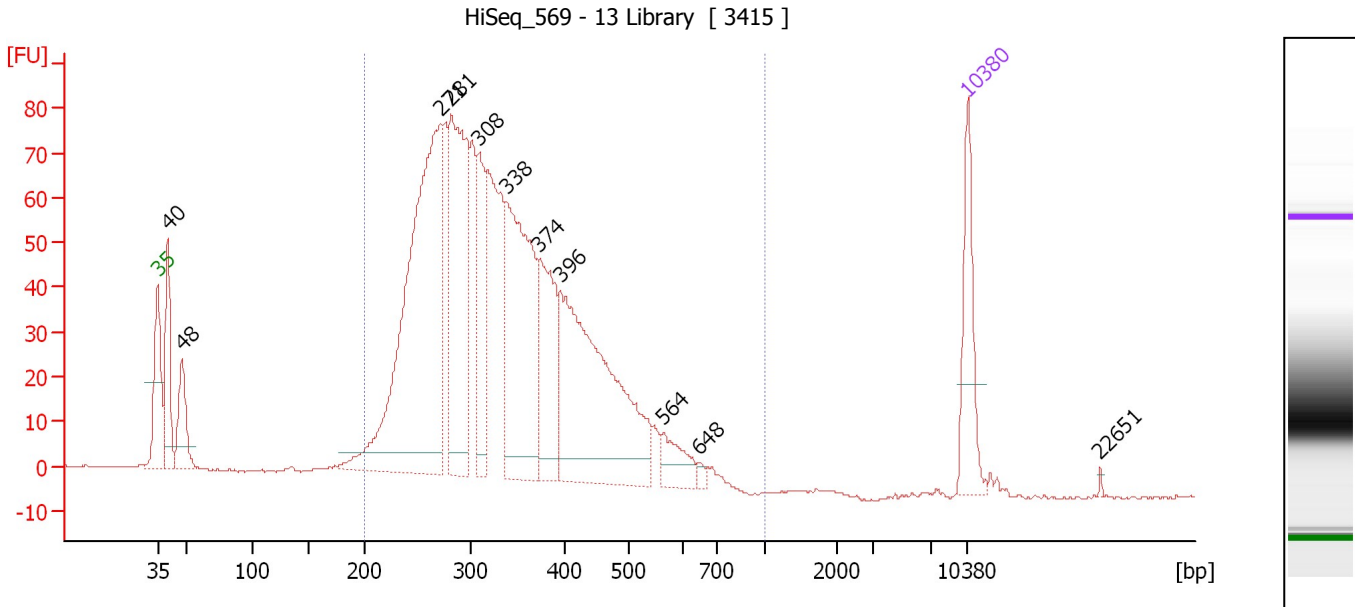
Region table for sample 2 : HiSeq 569 - 12 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	340	2,018.4	12,082.2	2,509.70	94	25.2

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : HiSeq 569 - 13 Library

Number of peaks found: 11 Corr. Area 1: 1,600.9
 Noise: 0.2

Peak table for sample 3 : HiSeq 569 - 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	40	120.16	4,505.1		43.88
3	48	86.33	2,722.3		45.12
4	271	659.33	3,682.5		67.42
5	281	339.31	1,827.3		68.35
6	308	121.48	597.3		70.73
7	338	321.79	1,443.2		73.11
8	374	155.21	628.9		76.01
9	396	397.91	1,523.1		77.77
10	564	41.29	110.9		86.72
11	648	5.74	13.4		89.82
12	10,380	75.00	10.9	Upper Marker	113.00
13	22,651	0.00	0.0		124.43

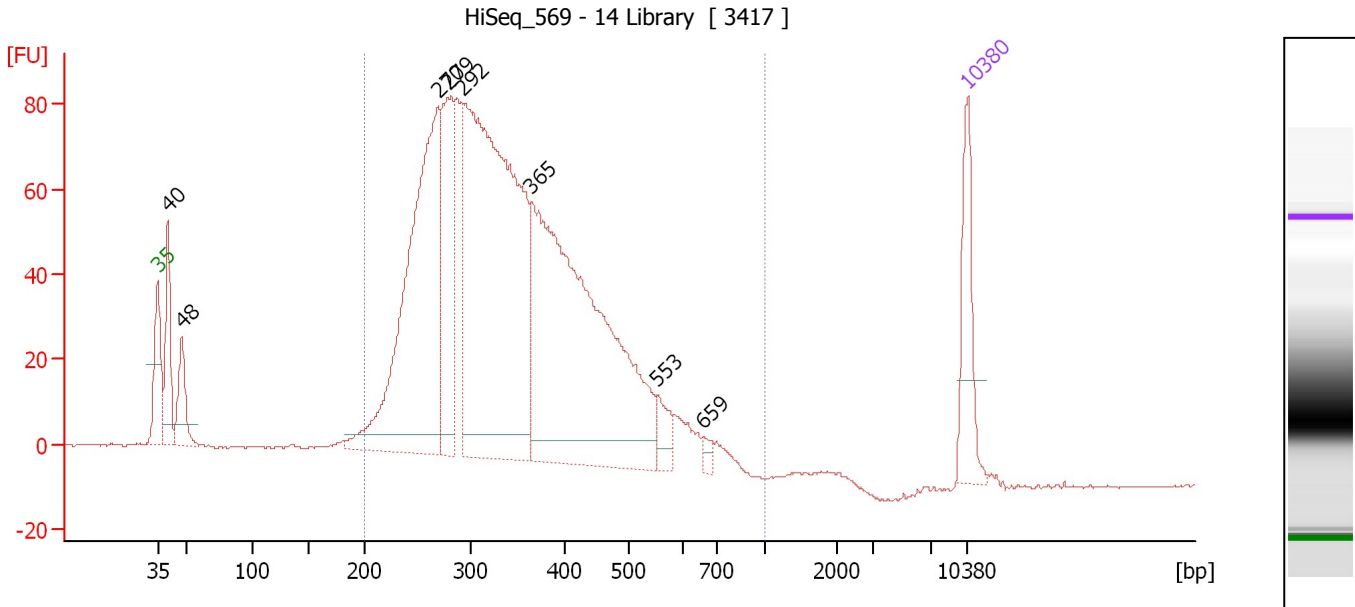
Region table for sample 3 : HiSeq 569 - 13 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	340	1,600.9	11,792.2	2,451.04	93	25.4

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : HiSeq 569 - 14 Library

Number of peaks found: 8 Corr. Area 1: 1,796.8
 Noise: 0.2

Peak table for sample 4 : HiSeq 569 - 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	40	117.10	4,381.6		43.89
3	48	79.34	2,508.6		45.10
4	270	587.36	3,301.5		67.26
5	279	202.62	1,101.8		68.10
6	292	914.53	4,740.9		69.36
7	365	755.45	3,135.6		75.30
8	553	32.03	87.8		86.22
9	659	10.92	25.1		90.16
10	10,380	75.00	10.9	Upper Marker	113.00

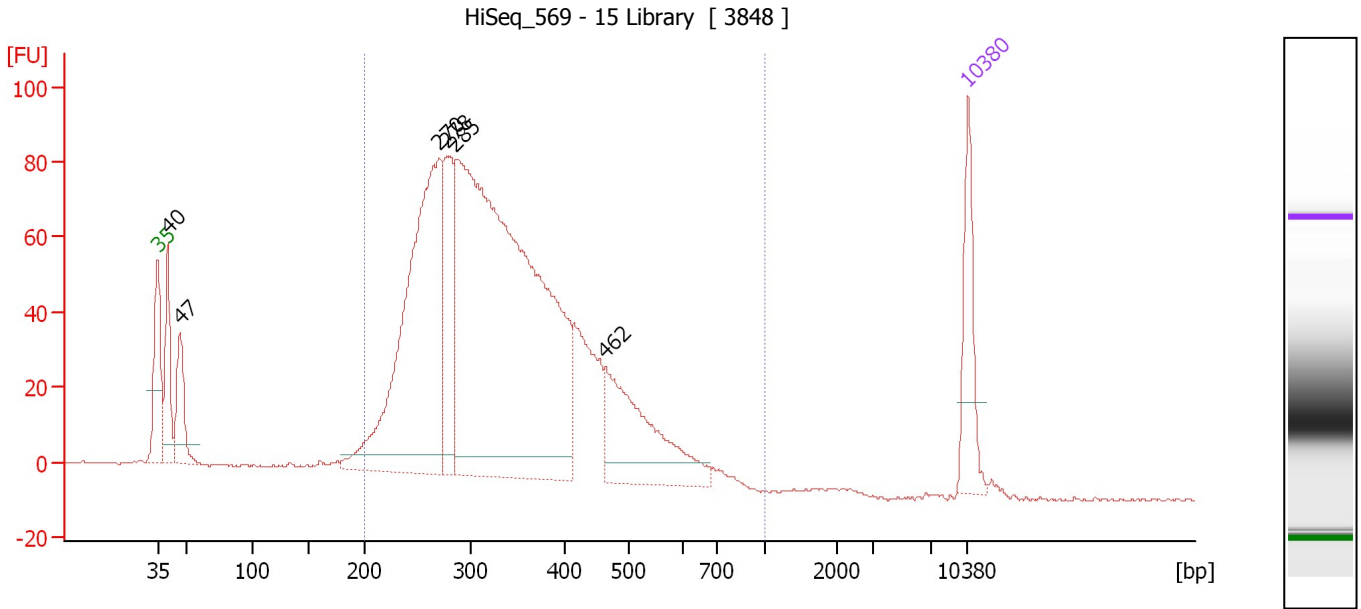
Region table for sample 4 : HiSeq 569 - 14 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	349	1,796.8	12,017.8	2,542.96	93	26.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : HiSeq 569 - 15 Library

Number of peaks found: 6 Corr. Area 1: 1,734.8
 Noise: 0.2

Peak table for sample 5 : HiSeq 569 - 15 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	40	118.30	4,453.8		43.85
3	47	101.38	3,282.5		44.92
4	270	625.13	3,509.4		67.29
5	278	170.89	931.5		68.04
6	285	1,278.59	6,786.6		68.73
7	462	208.69	684.6		81.62
8	10,380	75.00	10.9	Upper Marker	113.00

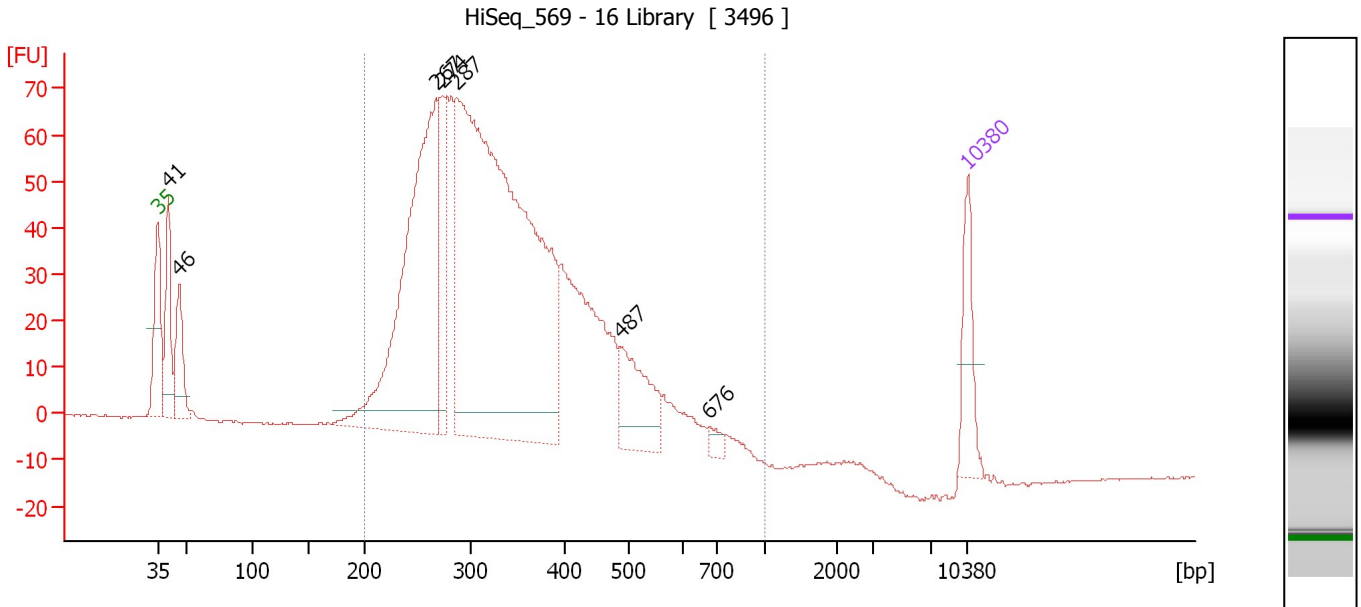
Region table for sample 5 : HiSeq 569 - 15 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	342	1,734.8	10,898.3	2,265.70	91	26.3

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 6 : HiSeq 569 - 16 Library

Number of peaks found: 7 Corr. Area 1: 1,441.2
 Noise: 0.2

Peak table for sample 6 : HiSeq 569 - 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	41	160.33	5,976.0		43.92
3	46	127.54	4,173.9		44.84
4	267	774.23	4,391.6		67.04
5	274	177.38	982.5		67.63
6	287	1,566.93	8,272.8		68.87
7	487	140.98	439.1		83.02
8	676	15.15	33.9		90.69
9	10,380	75.00	10.9	Upper Marker	113.00

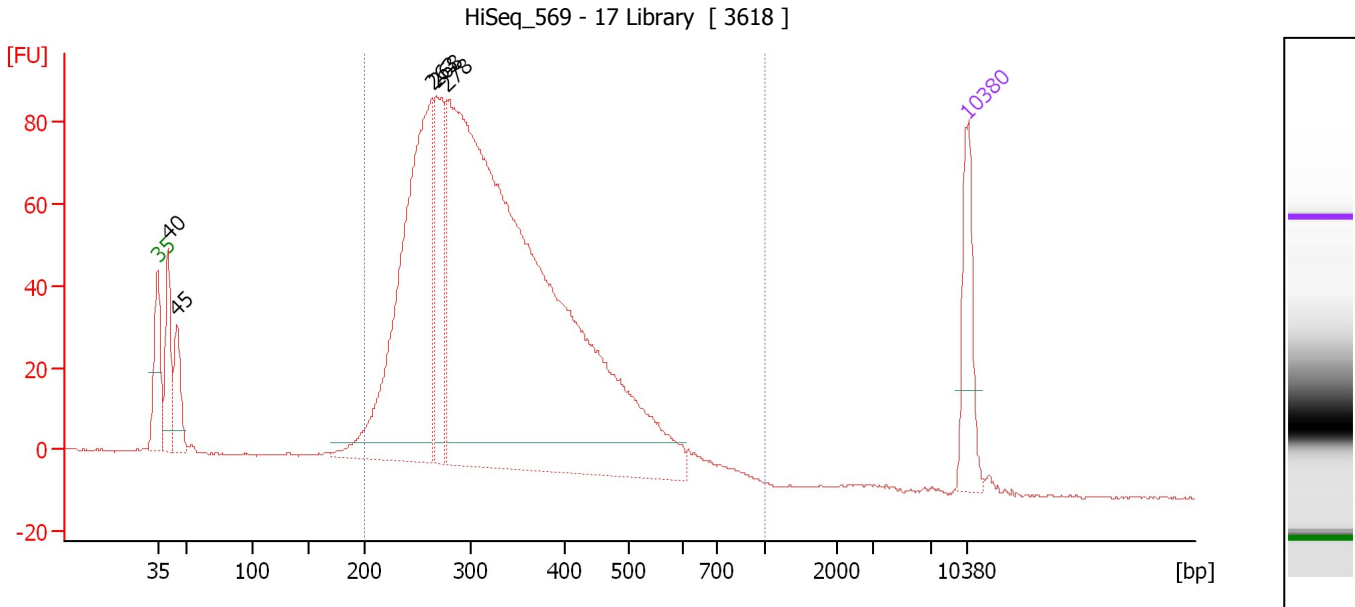
Region table for sample 6 : HiSeq 569 - 16 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	341	1,441.2	14,477.9	3,006.68	92	26.4

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : HiSeq 569 - 17 Library

Number of peaks found: 5 Corr. Area 1: 1,743.2
 Noise: 0.2

Peak table for sample 7 : HiSeq 569 - 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	40	112.05	4,203.7		43.88
3	45	86.79	2,894.2		44.70
4	263	639.35	3,676.8		66.70
5	268	172.06	972.0		67.14
6	278	1,934.97	10,558.2		68.01
7	10,380	75.00	10.9	Upper Marker	113.00

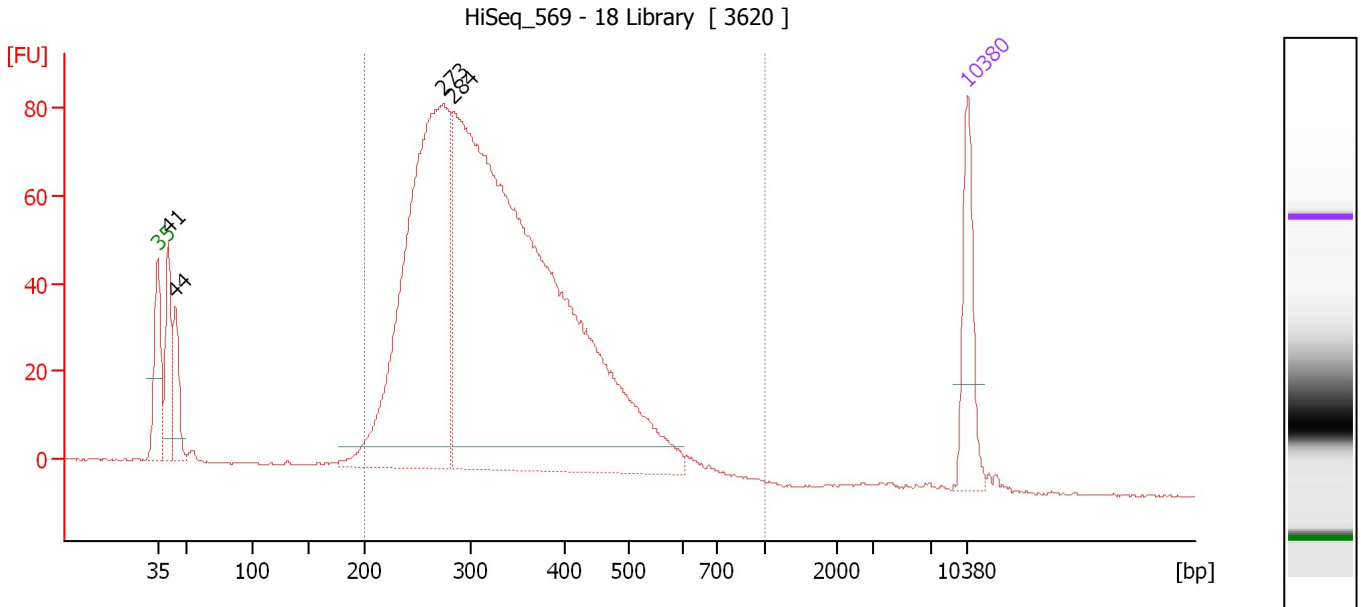
Region table for sample 7 : HiSeq 569 - 17 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	333	1,743.2	12,257.6	2,491.08	93	26.3

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : HiSeq 569 - 18 Library

Number of peaks found: 4 Corr. Area 1: 1,635.7
 Noise: 0.2

Peak table for sample 8 : HiSeq 569 - 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	41	124.16	4,609.6		43.94
3	44	82.86	2,838.8		44.50
4	273	821.23	4,552.1		67.61
5	284	1,695.97	9,062.1		68.56
6	10,380	75.00	10.9	Upper Marker	113.00

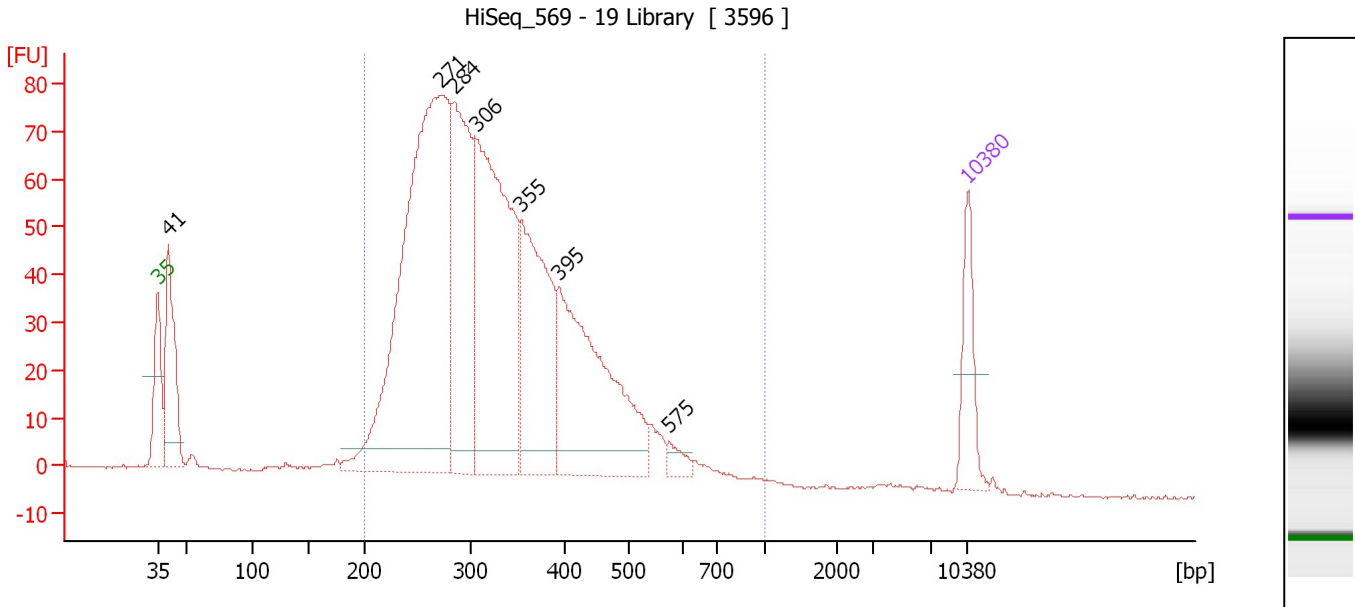
Region table for sample 8 : HiSeq 569 - 18 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	335	1,635.7	11,435.3	2,344.76	93	25.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
 Modified: 8/25/2016 4:26:13 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : HiSeq 569 - 19 Library

Number of peaks found: 7 Corr. Area 1: 1,558.5
 Noise: 0.2

Peak table for sample 9 : HiSeq 569 - 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	41	246.32	9,130.6		43.96
3	271	1,139.80	6,361.4		67.44
4	284	429.84	2,291.3		68.62
5	306	648.90	3,209.4		70.58
6	355	370.11	1,581.3		74.46
7	395	441.70	1,696.3		77.66
8	575	22.40	59.0		87.21
9	10,380	75.00	10.9	Upper Marker	113.00

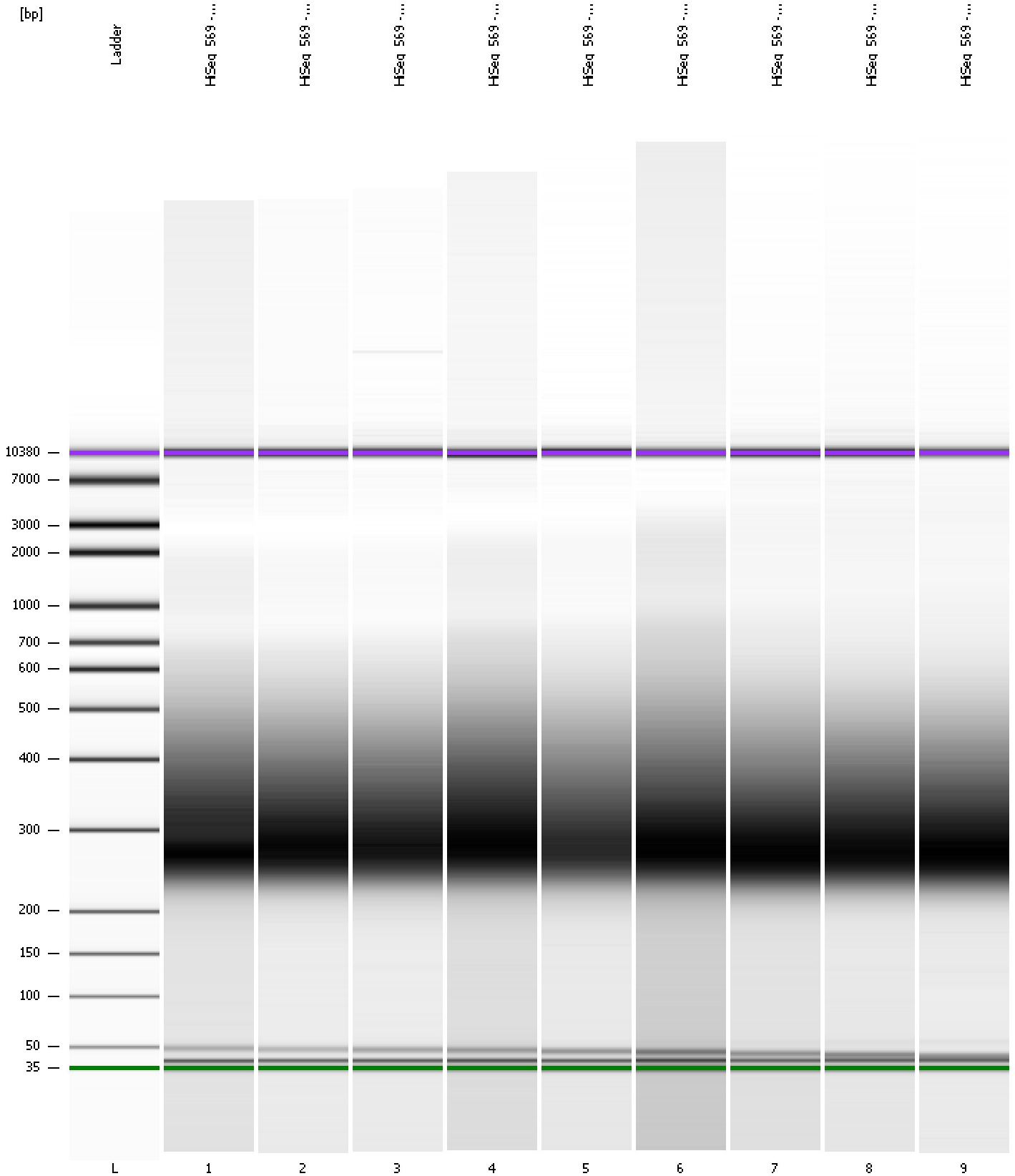
Region table for sample 9 : HiSeq 569 - 19 Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	336	1,558.5	15,385.6	3,144.06	92	27.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad

Created: 8/25/2016 3:37:46 PM
Modified: 8/25/2016 4:26:13 PM

Gel Image



Assay Class: High Sensitivity DNA Assay Created: 8/25/2016 3:37:46 PM
 Data Path: C:\...data\2016-08-25\2016-08-25_003_HiSeq569_Libraries_11-19.xad Modified: 8/25/2016 4:26:13 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		8/25/2016 4:19:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-08-25\2016-08-25_003.xad)		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		8/25/2016 3:37:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1