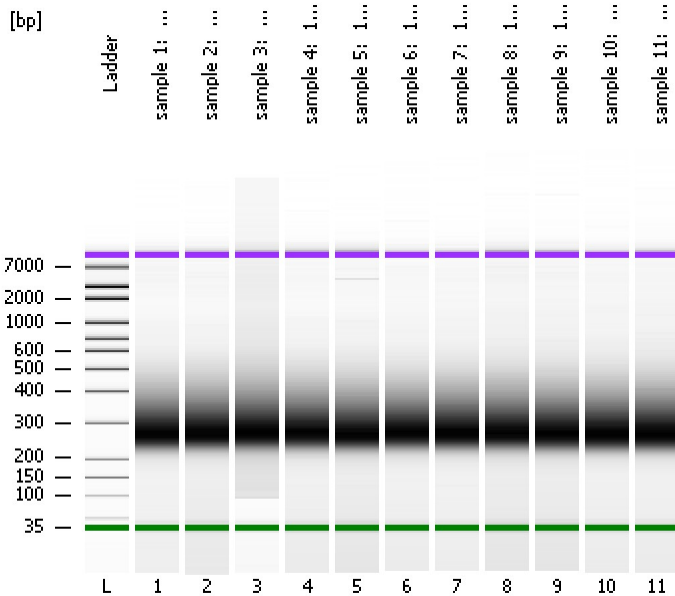


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
Modified: 1/26/2016 4:46:00 PM

**Electrophoresis File Run Summary**



Instrument Information:

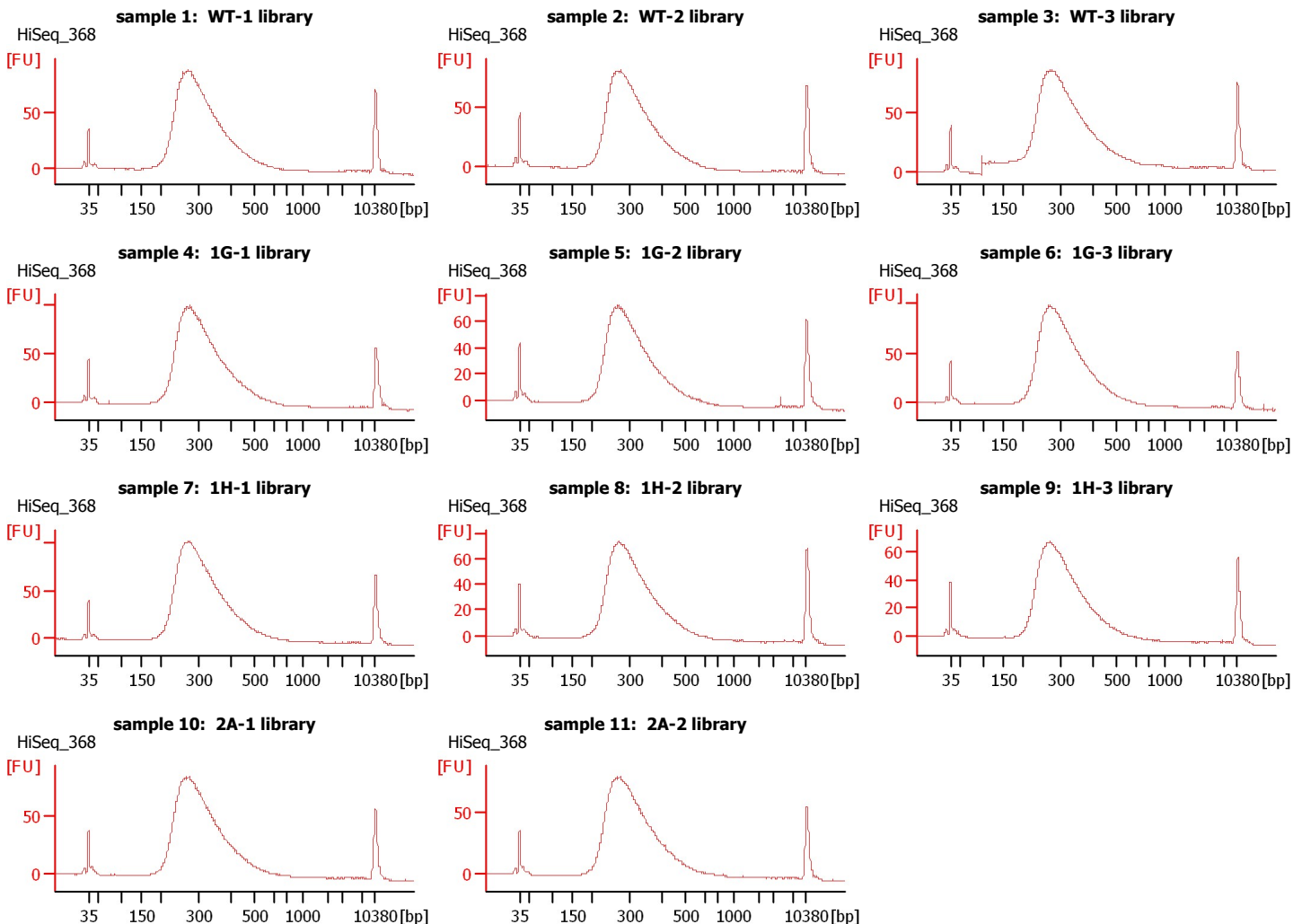
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

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:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
sample 1: WT-1 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 2: WT-2 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 3: WT-3 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 4: 1G-1 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 5: 1G-2 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 6: 1G-3 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 7: 1H-1 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 8: 1H-2 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 9: 1H-3 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 10: 2A-1 library	HiSeq_368	<input type="checkbox"/>	✓			
sample 11: 2A-2 library	HiSeq_368	<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
Modified: 1/26/2016 4:46:00 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

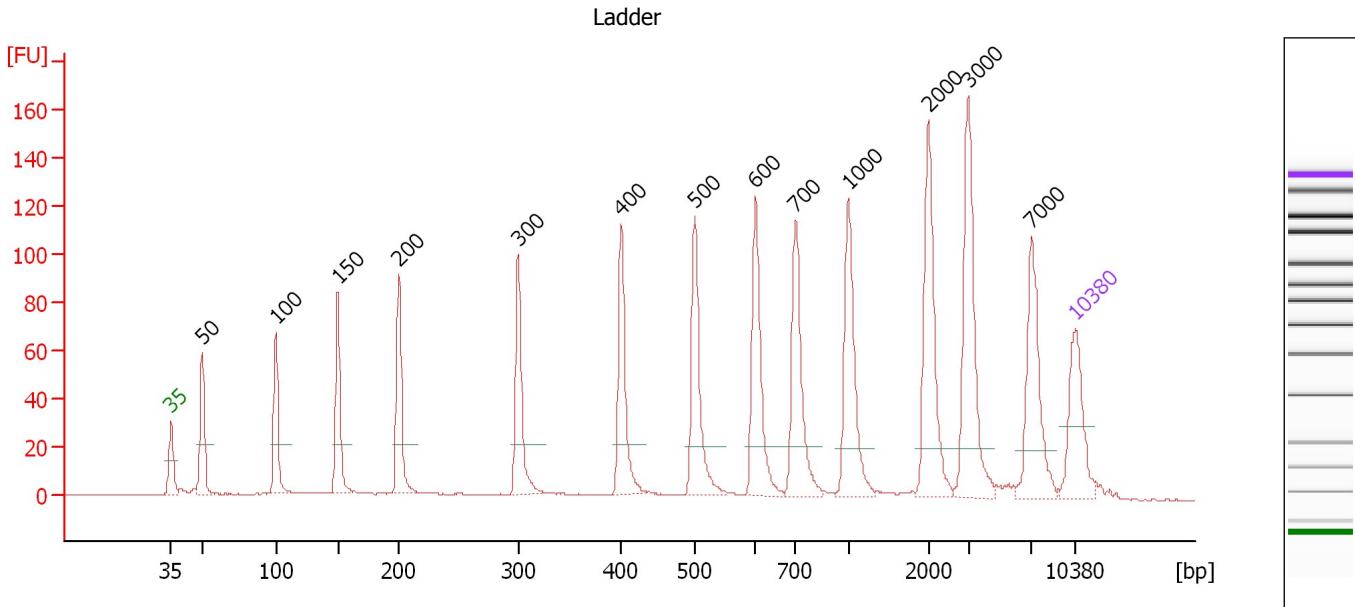
**Ladder**

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:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

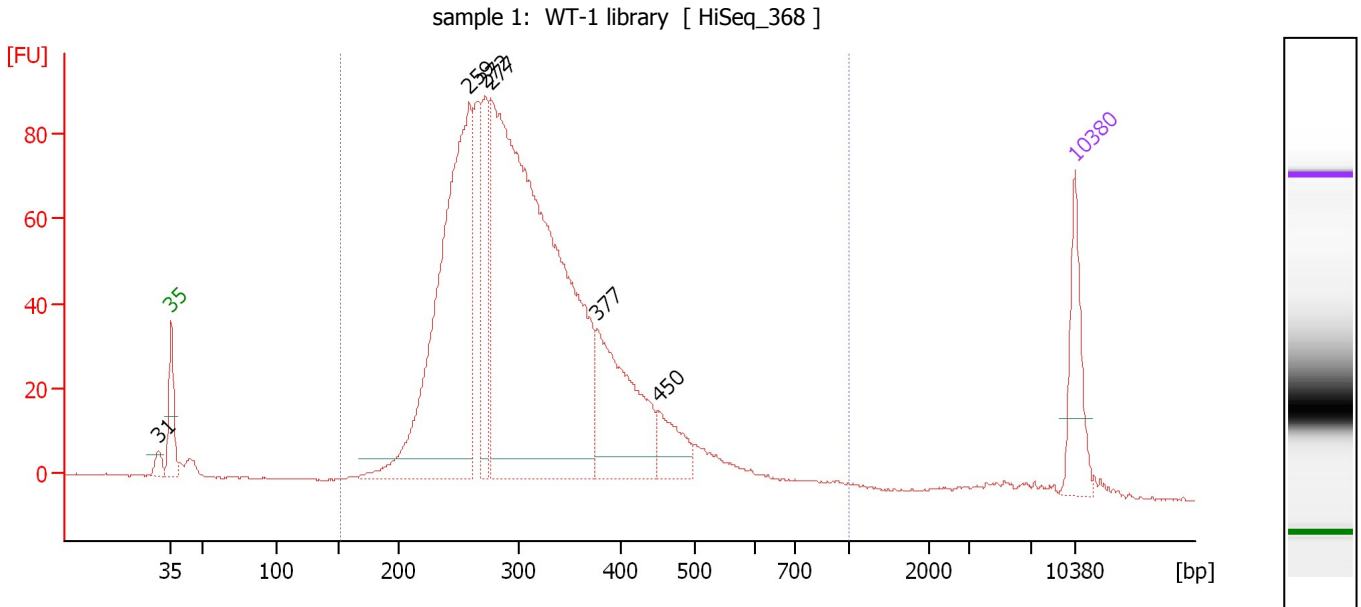
**Peak table for Ladder**

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	45.41
3	100	150.00	2,272.7	Ladder Peak	51.09
4	150	150.00	1,515.2	Ladder Peak	55.91
5	200	150.00	1,136.4	Ladder Peak	60.64
6	300	150.00	757.6	Ladder Peak	69.86
7	400	150.00	568.2	Ladder Peak	77.86
8	500	150.00	454.5	Ladder Peak	83.53
9	600	150.00	378.8	Ladder Peak	88.26
10	700	150.00	324.7	Ladder Peak	91.34
11	1,000	150.00	227.3	Ladder Peak	95.41
12	2,000	150.00	113.6	Ladder Peak	101.60
13	3,000	150.00	75.8	Ladder Peak	104.72
14	7,000	150.00	32.5	Ladder Peak	109.64
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : sample 1: WT-1 library**

Number of peaks found: 6                      Corr. Area 1: 1,609.4  
 Noise: 0.2

**Peak table for sample 1 : sample 1: WT-1 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		42.00
2	35	125.00	5,411.3	Lower Marker	43.00
3	259	759.67	4,444.9		66.08
4	272	152.15	846.3		67.32
5	277	1,375.59	7,537.1		67.70
6	377	249.53	1,003.6		76.00
7	450	65.73	221.5		80.67
8	10,380	75.00	10.9	Upper Marker	113.00

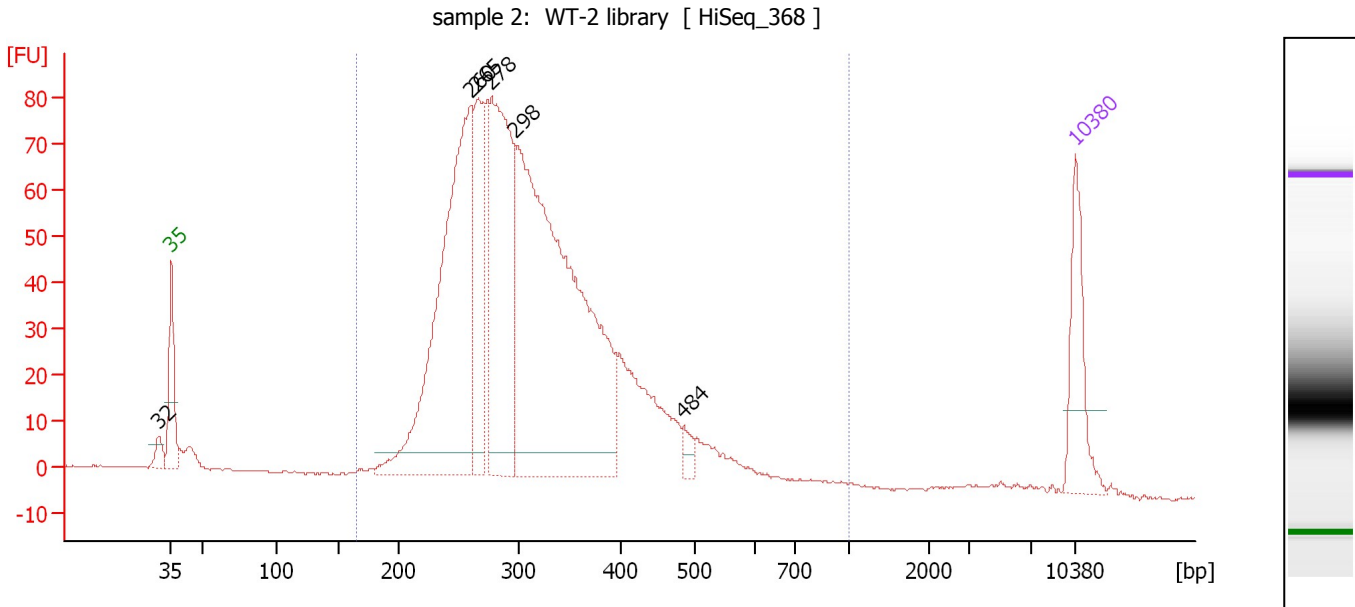
**Region table for sample 1 : sample 1: WT-1 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
151	1,000	320	1,609.4	14,420.1	2,823.79	97	27.9

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : sample 2: WT-2 library**

Number of peaks found: 6                      Corr. Area 1: 1,471.8  
 Noise: 0.2

**Peak table for sample 2 : sample 2: WT-2 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.05
2	35	125.00	5,411.3	Lower Marker	43.00
3	260	613.00	3,577.1		66.14
4	265	178.62	1,020.1		66.67
5	278	397.97	2,171.7		67.80
6	298	899.93	4,580.2		69.65
7	484	16.53	51.7		82.65
8	10,380	75.00	10.9	Upper Marker	113.00

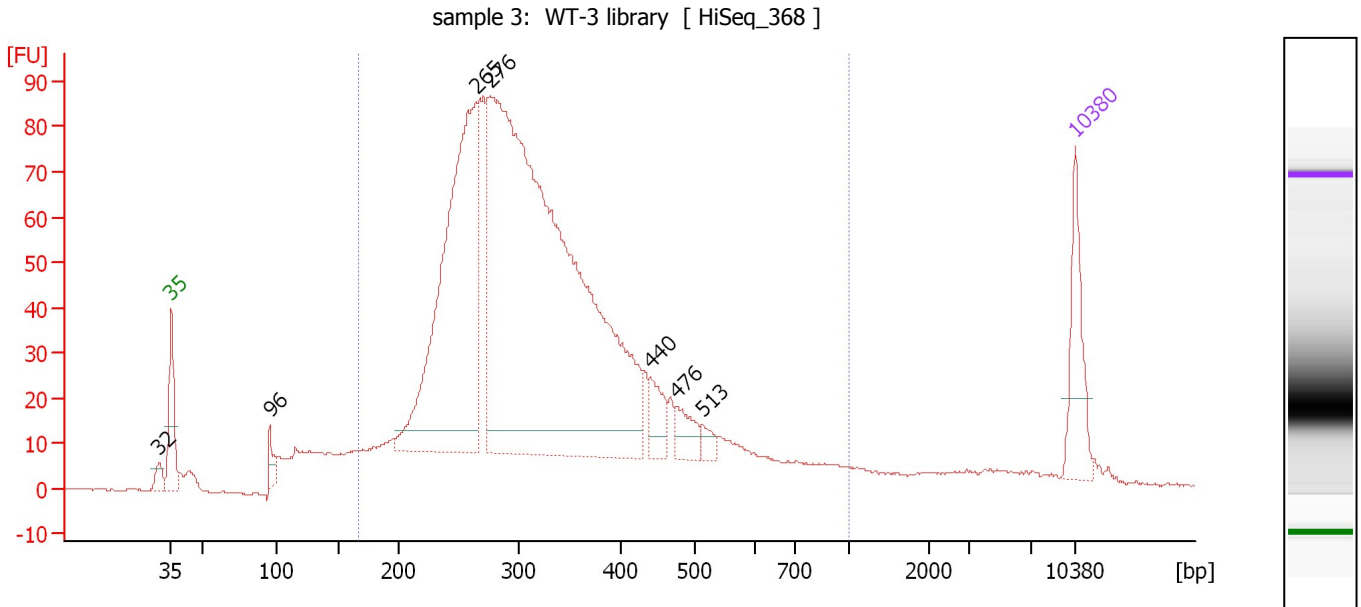
**Region table for sample 2 : sample 2: WT-2 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
165	1,000	321	1,471.8	12,080.4	2,380.80	97	26.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : sample 3: WT-3 library**

Number of peaks found: 7                      Corr. Area 1: 1,719.9  
 Noise: 0.3

**Peak table for sample 3 : sample 3: WT-3 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.04
2	35	125.00	5,411.3	Lower Marker	43.00
3	96	26.48	417.5		50.65
4	265	730.01	4,179.5		66.60
5	276	1,697.21	9,315.7		67.66
6	440	45.28	156.0		80.13
7	476	38.32	121.9		82.18
8	513	16.17	47.8		84.14
9	10,380	75.00	10.9	Upper Marker	113.00

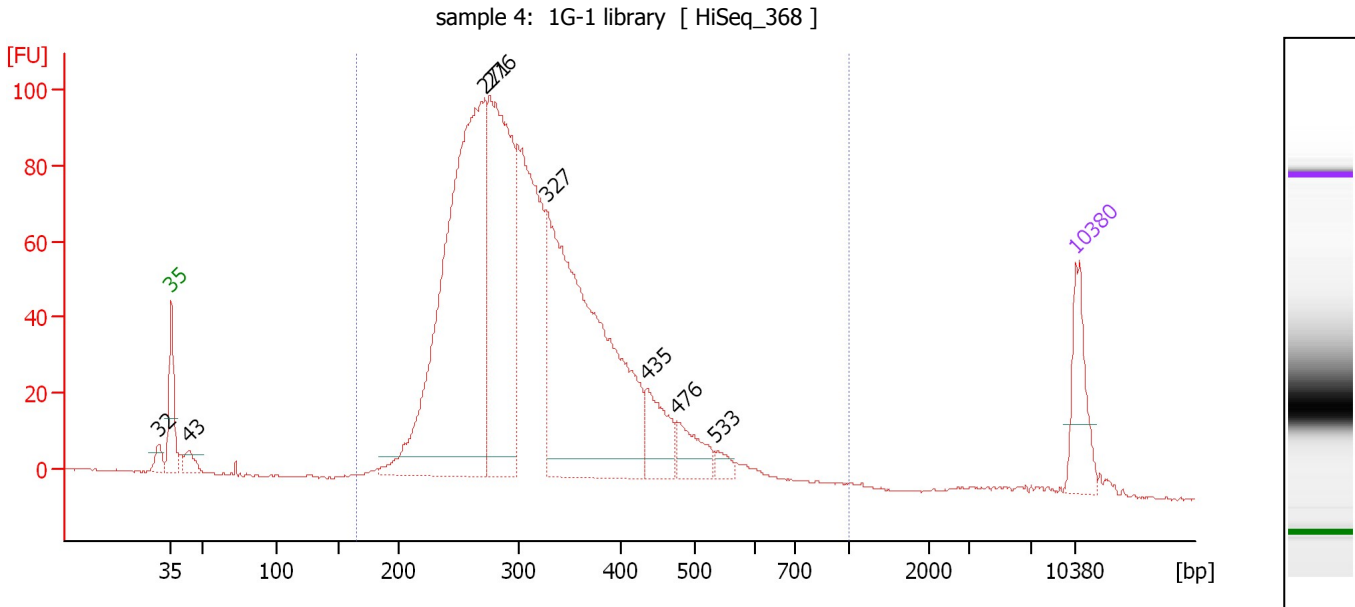
**Region table for sample 3 : sample 3: WT-3 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
166	1,000	335	1,719.9	16,286.4	3,216.85	91	33.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : sample 4: 1G-1 library**

Number of peaks found: 8                      Corr. Area 1: 1,776.3  
 Noise: 0.2

**Peak table for sample 4 : sample 4: 1G-1 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.03
2	35	125.00	5,411.3	Lower Marker	43.00
3	43	29.39	1,024.3		44.36
4	271	1,049.05	5,864.5		67.19
5	276	586.45	3,215.8		67.68
6	327	816.23	3,776.5		72.06
7	435	91.72	319.4		79.85
8	476	61.83	196.7		82.19
9	533	18.27	51.9		85.11
10	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 4 : sample 4: 1G-1 library**

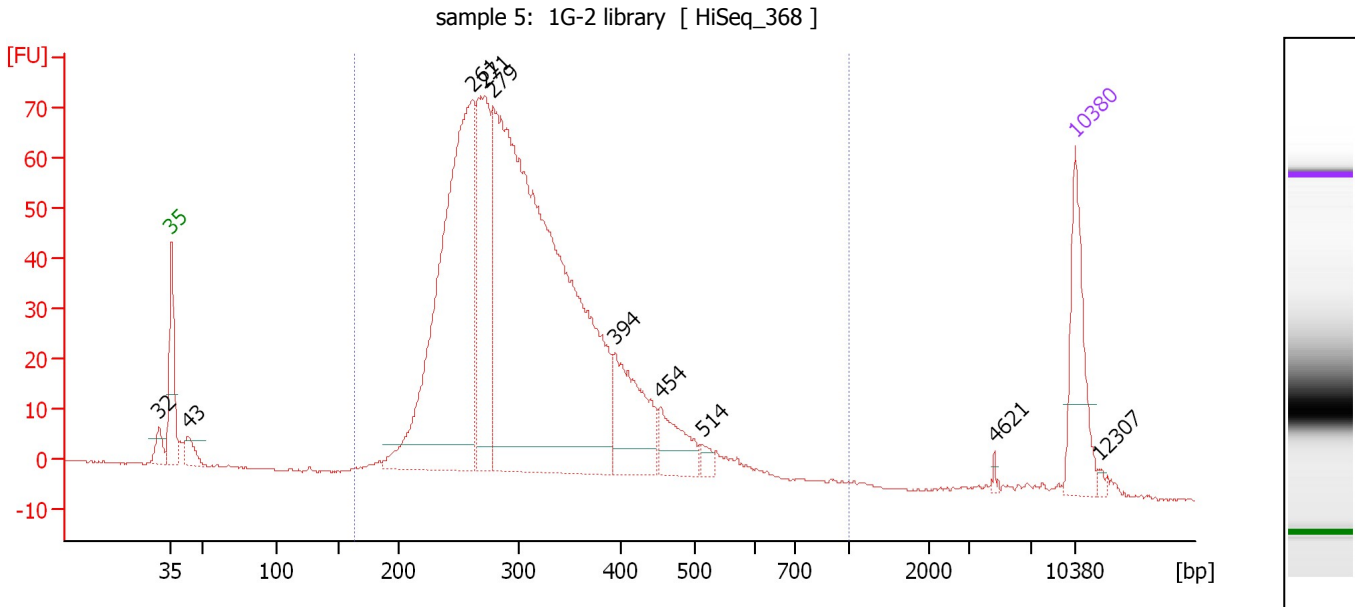
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
166	1,000	323	1,776.3	16,092.1	3,189.10	98	26.3



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : sample 5: 1G-2 library**

Number of peaks found: 10                      Corr. Area 1: 1,289.8  
 Noise: 0.2

**Peak table for sample 5 : sample 5: 1G-2 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.02
2	35	125.00	5,411.3	Lower Marker	43.00
3	43	26.17	916.9		44.33
4	261	624.00	3,622.4		66.27
5	271	235.99	1,318.9		67.20
6	279	1,123.78	6,100.7		67.94
7	394	126.28	485.9		77.36
8	454	56.46	188.6		80.90
9	514	11.06	32.6		84.19
10	4,621	2.70	0.9		106.72
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,307	0.00	0.0		114.91

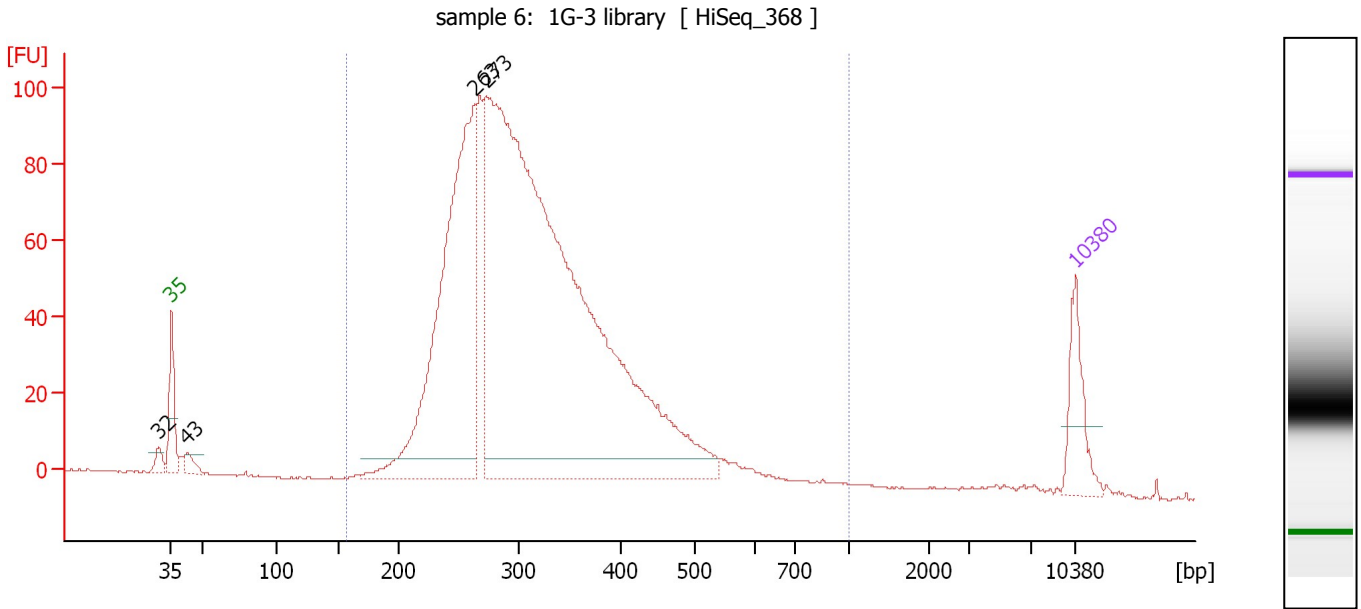
**Region table for sample 5 : sample 5: 1G-2 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
163	1,000	316	1,289.8	11,124.1	2,171.43	97	24.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : sample 6: 1G-3 library**

Number of peaks found: 4                      Corr. Area 1: 1,727.0  
 Noise: 0.3

**Peak table for sample 6 : sample 6: 1G-3 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.01
2	35	125.00	5,411.3	Lower Marker	43.00
3	43	29.15	1,034.5		44.24
4	263	878.34	5,057.5		66.47
5	273	2,394.26	13,297.8		67.36
6	10,380	75.00	10.9	Upper Marker	113.00

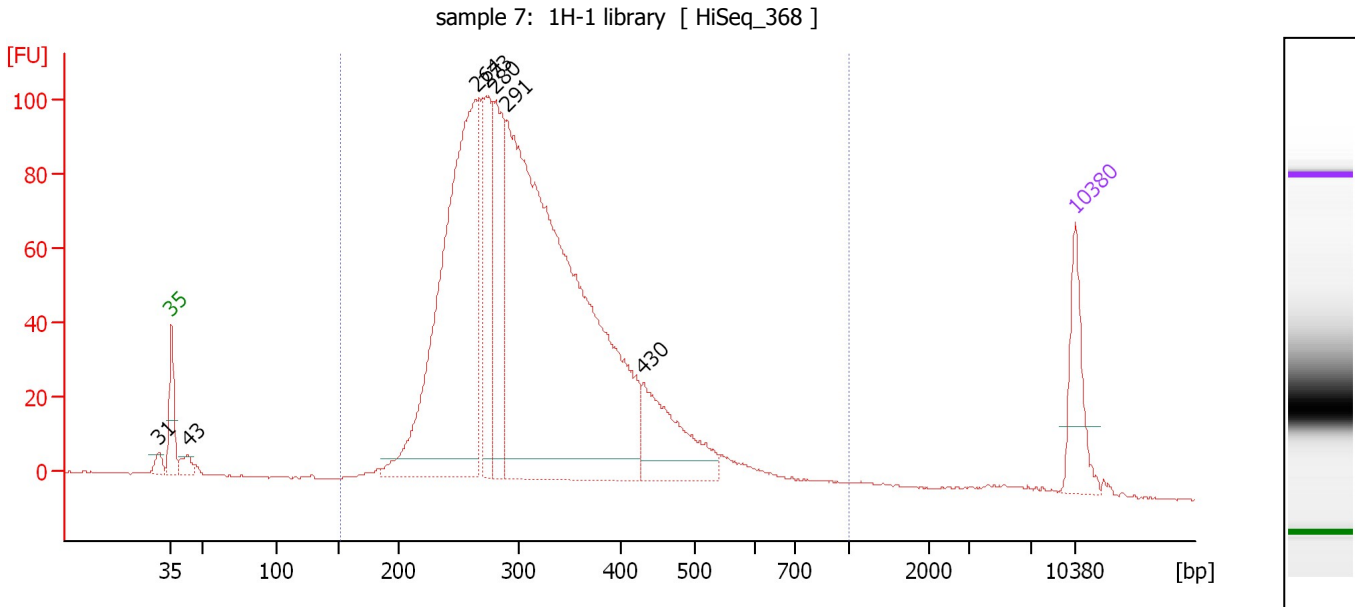
**Region table for sample 6 : sample 6: 1G-3 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
157	1,000	320	1,727.0	16,511.5	3,259.63	98	25.5

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : sample 7: 1H-1 library**

Number of peaks found: 7                      Corr. Area 1: 1,836.3  
 Noise: 0.2

**Peak table for sample 7 : sample 7: 1H-1 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		42.00
2	35	125.00	5,411.3	Lower Marker	43.00
3	43	25.66	908.8		44.25
4	264	881.92	5,053.4		66.58
5	273	210.23	1,166.3		67.38
6	280	225.27	1,218.2		68.04
7	291	1,484.00	7,726.0		69.04
8	430	175.81	619.7		79.55
9	10,380	75.00	10.9	Upper Marker	113.00

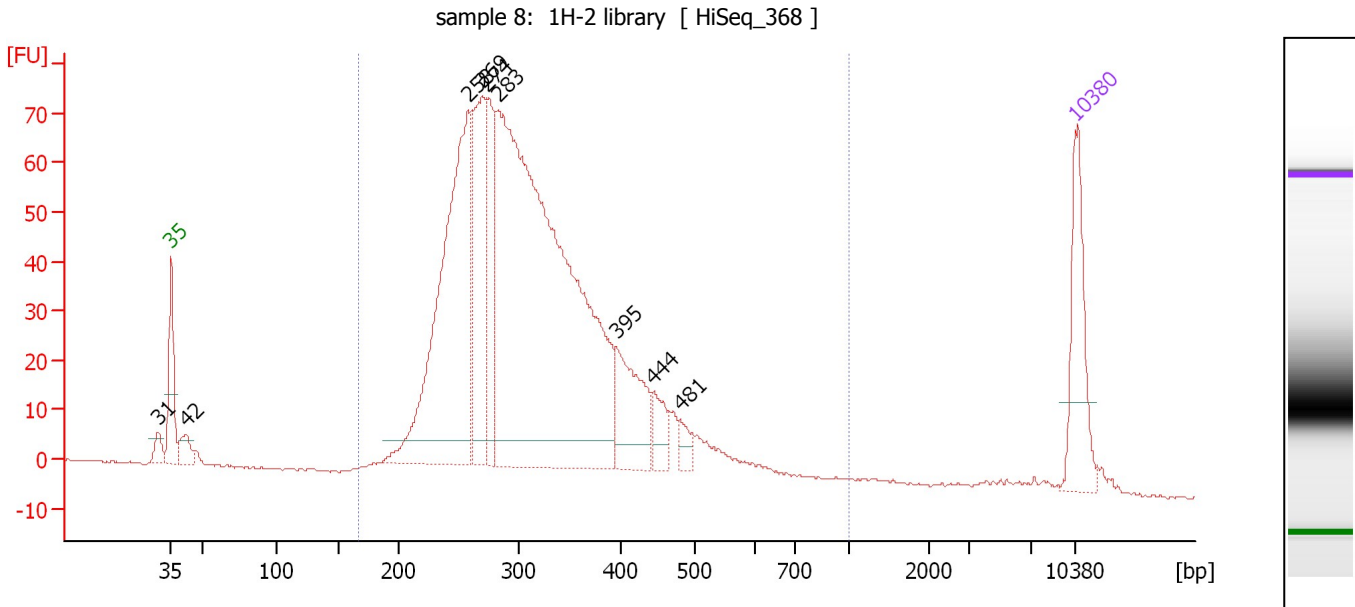
**Region table for sample 7 : sample 7: 1H-1 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
152	1,000	323	1,836.3	15,498.6	3,064.42	98	27.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : sample 8: 1H-2 library**

Number of peaks found: 9                      Corr. Area 1: 1,306.8  
 Noise: 0.3

**Peak table for sample 8 : sample 8: 1H-2 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.99
2	35	125.00	5,411.3	Lower Marker	43.00
3	42	27.98	1,011.2		44.11
4	258	470.07	2,762.0		65.98
5	269	190.41	1,070.9		67.04
6	274	116.42	644.3		67.45
7	283	1,046.94	5,603.0		68.31
8	395	102.44	392.8		77.47
9	444	31.04	105.9		80.35
10	481	16.12	50.8		82.43
11	10,380	75.00	10.9	Upper Marker	113.00

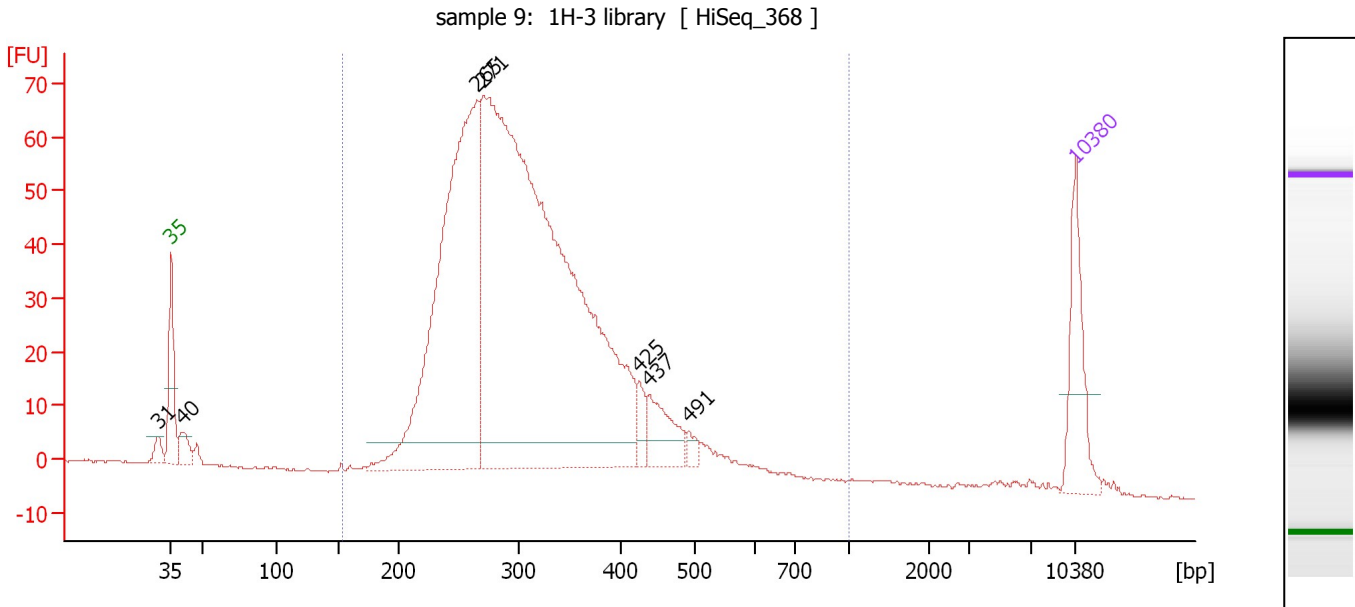
**Region table for sample 8 : sample 8: 1H-2 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
167	1,000	321	1,306.8	10,447.3	2,063.96	97	25.4

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : sample 9: 1H-3 library**

Number of peaks found: 7                      Corr. Area 1: 1,210.6  
 Noise: 0.2

**Peak table for sample 9 : sample 9: 1H-3 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.93
2	35	125.00	5,411.3	Lower Marker	43.00
3	40	33.05	1,250.1		43.81
4	265	755.81	4,324.1		66.62
5	271	1,575.18	8,810.4		67.18
6	425	24.99	89.1		79.27
7	437	63.42	220.1		79.93
8	491	12.08	37.3		83.03
9	10,380	75.00	10.9	Upper Marker	113.00

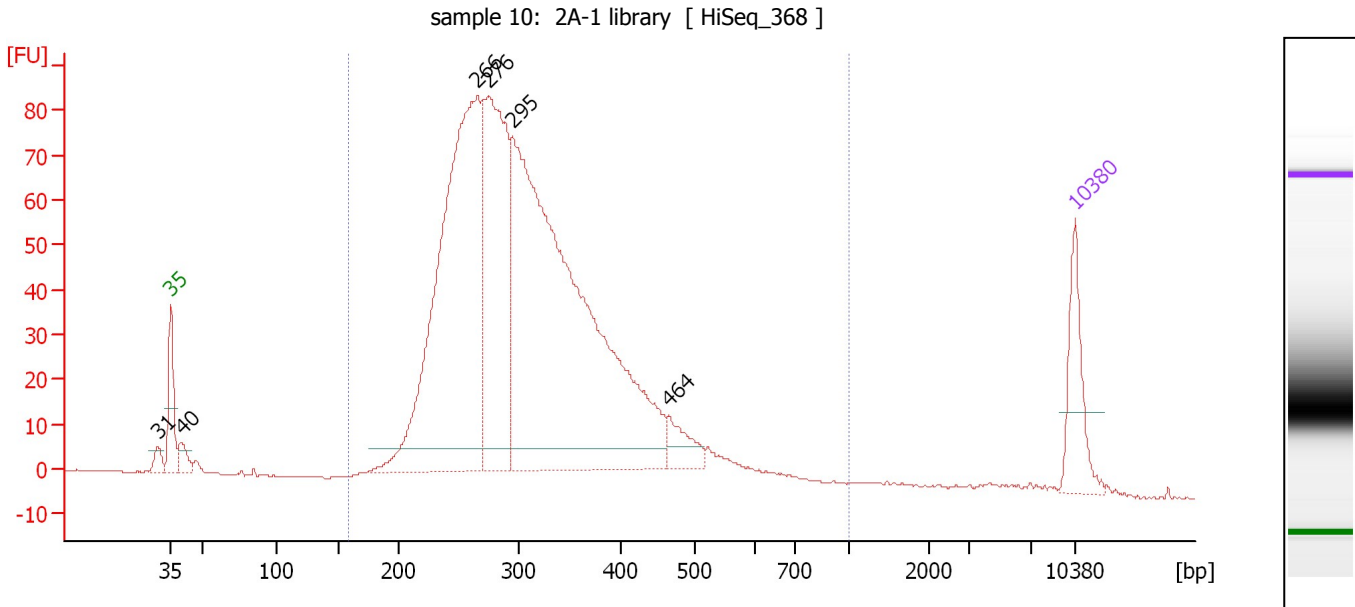
**Region table for sample 9 : sample 9: 1H-3 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
153	1,000	317	1,210.6	12,353.1	2,417.67	97	25.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : sample 10: 2A-1 library**

Number of peaks found: 6                      Corr. Area 1: 1,501.3  
 Noise: 0.2

**Peak table for sample 10 : sample 10: 2A-1 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.93
2	35	125.00	5,411.3	Lower Marker	43.00
3	40	32.56	1,231.1		43.82
4	266	938.43	5,353.9		66.69
5	276	515.15	2,832.9		67.61
6	295	1,293.40	6,633.9		69.44
7	464	47.45	154.8		81.52
8	10,380	75.00	10.9	Upper Marker	113.00

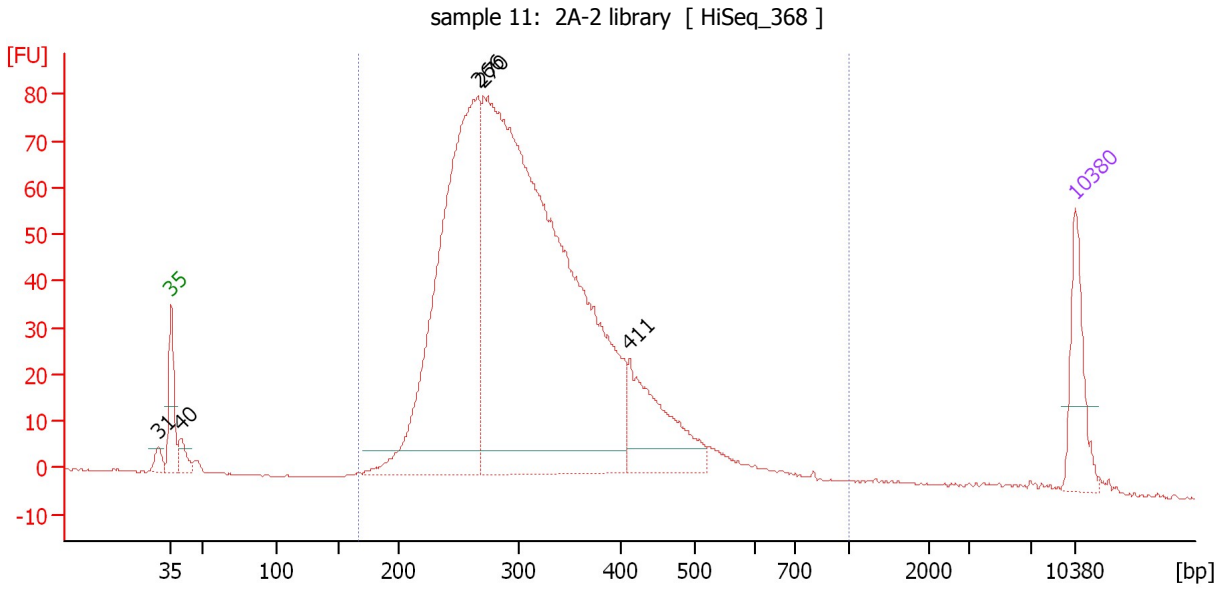
**Region table for sample 10 : sample 10: 2A-1 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
158	1,000	319	1,501.3	14,922.2	2,916.84	97	26.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : sample 11: 2A-2 library**

Number of peaks found: 5                      Corr. Area 1: 1,456.8  
 Noise: 0.2

**Peak table for sample 11 : sample 11: 2A-2 library**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.98
2	35	125.00	5,411.3	Lower Marker	43.00
3	40	30.80	1,173.2		43.77
4	266	912.15	5,196.3		66.73
5	270	1,772.78	9,933.0		67.14
6	411	180.73	666.8		78.46
7	10,380	75.00	10.9	Upper Marker	113.00

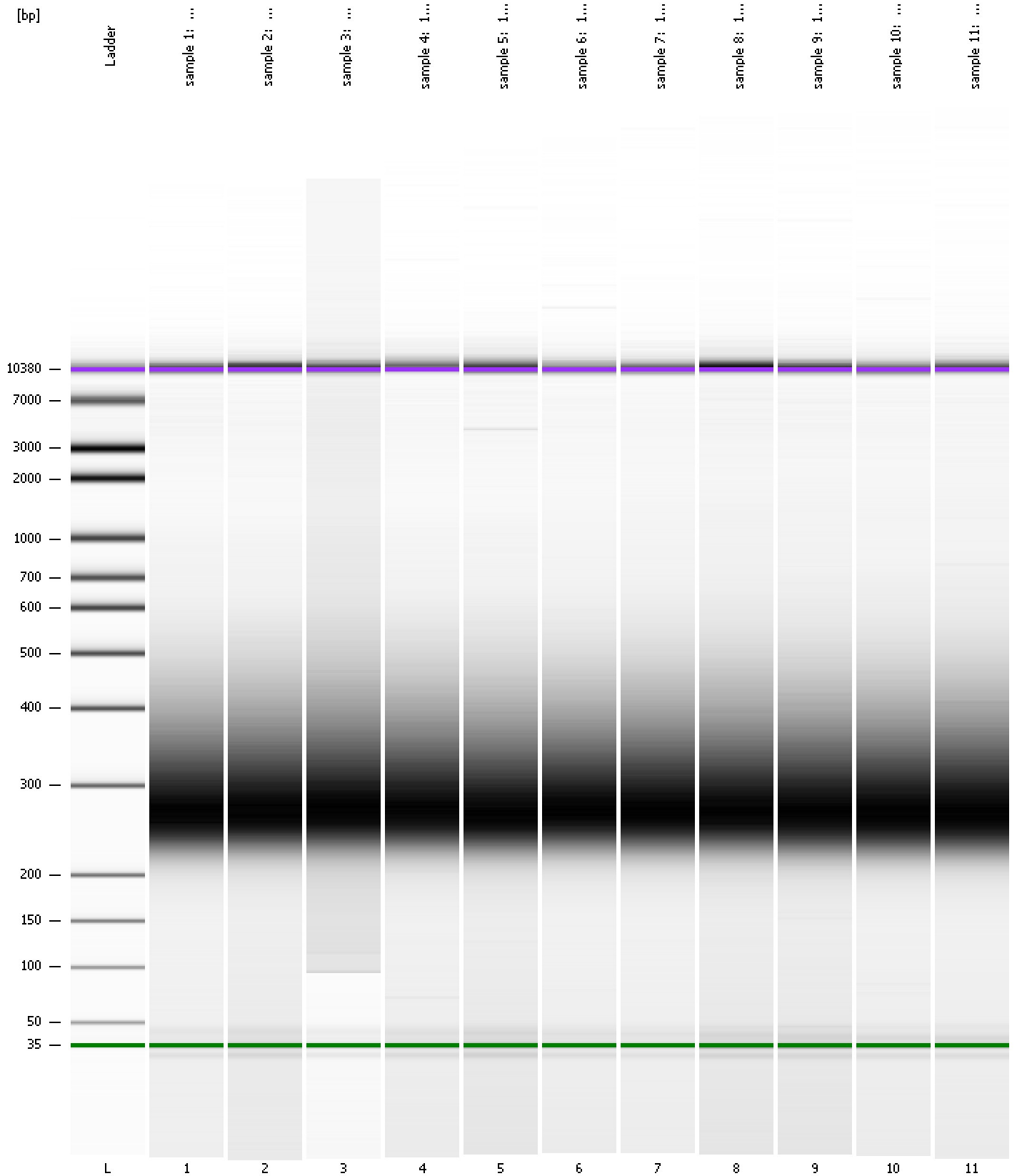
**Region table for sample 11 : sample 11: 2A-2 library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
167	1,000	321	1,456.8	14,555.4	2,860.00	97	27.6

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
Modified: 1/26/2016 4:46:00 PM

**Gel Image**





Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-26\2016-01-26\_002.xad

Created: 1/26/2016 4:02:05 PM  
 Modified: 1/26/2016 4:46:00 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		1/26/2016 4:43:22 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-01-26\2016-01-26_002.xad)		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/26/2016 4:02:11 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1