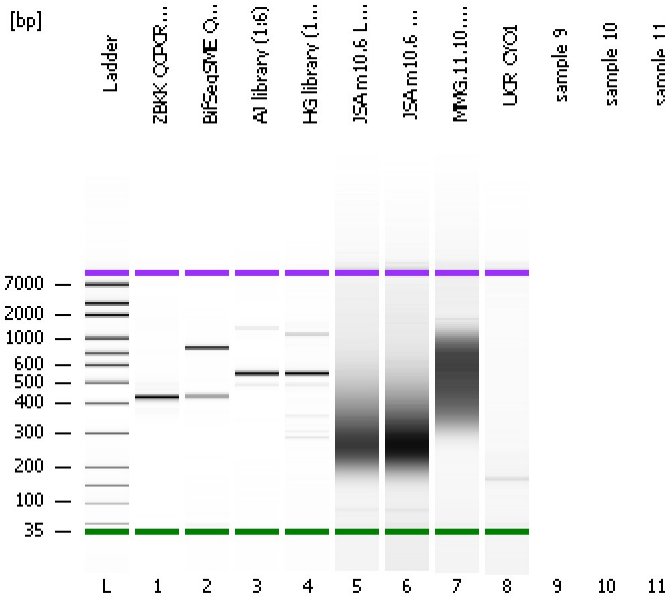


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
Modified: 11/22/2016 3:46:48 PM

**Electrophoresis File Run Summary**



Instrument Information:

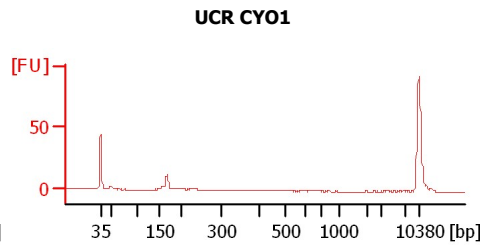
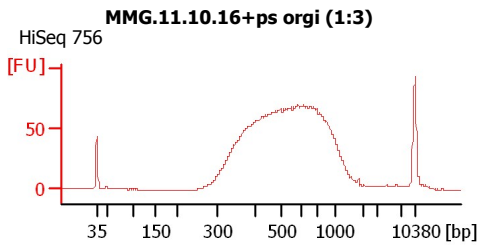
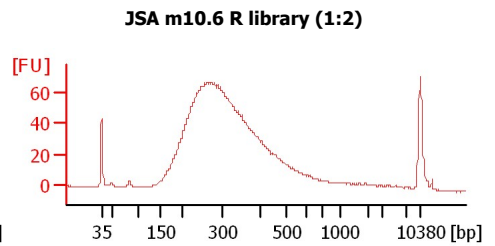
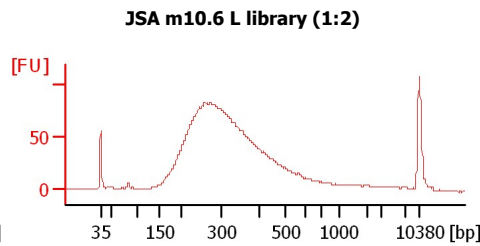
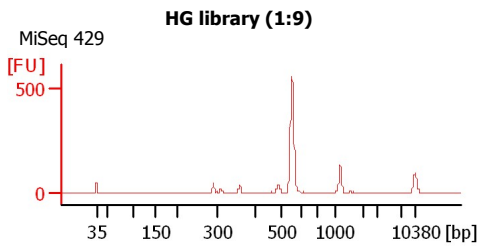
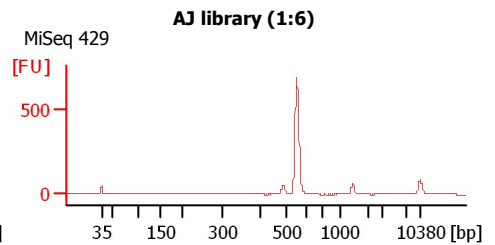
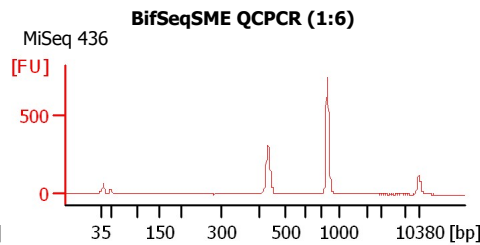
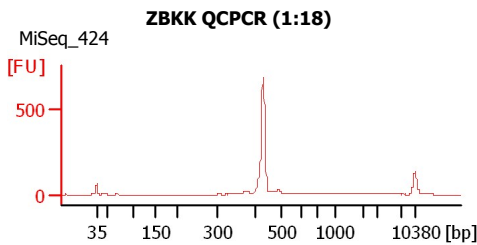
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

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:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
ZBKK QCPCR (1:18)	MiSeq_424	<input type="checkbox"/>	✓			
BifSeqSME QCPCR (1:6)	MiSeq 436	<input type="checkbox"/>	✓			
AJ library (1:6)	MiSeq 429	<input type="checkbox"/>	✓			
HG library (1:9)	MiSeq 429	<input type="checkbox"/>	✓			
JSA m10.6 L library (1:2)		<input type="checkbox"/>	✓			
JSA m10.6 R library (1:2)		<input type="checkbox"/>	✓			
MMG.11.10.16+ps orgi (1:3)	HiSeq 756	<input type="checkbox"/>	✓			
UCR CYO1		<input type="checkbox"/>	✓			
sample 9		<input type="checkbox"/>				
sample 10		<input type="checkbox"/>				
sample 11		<input type="checkbox"/>				
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
Modified: 11/22/2016 3:46:48 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

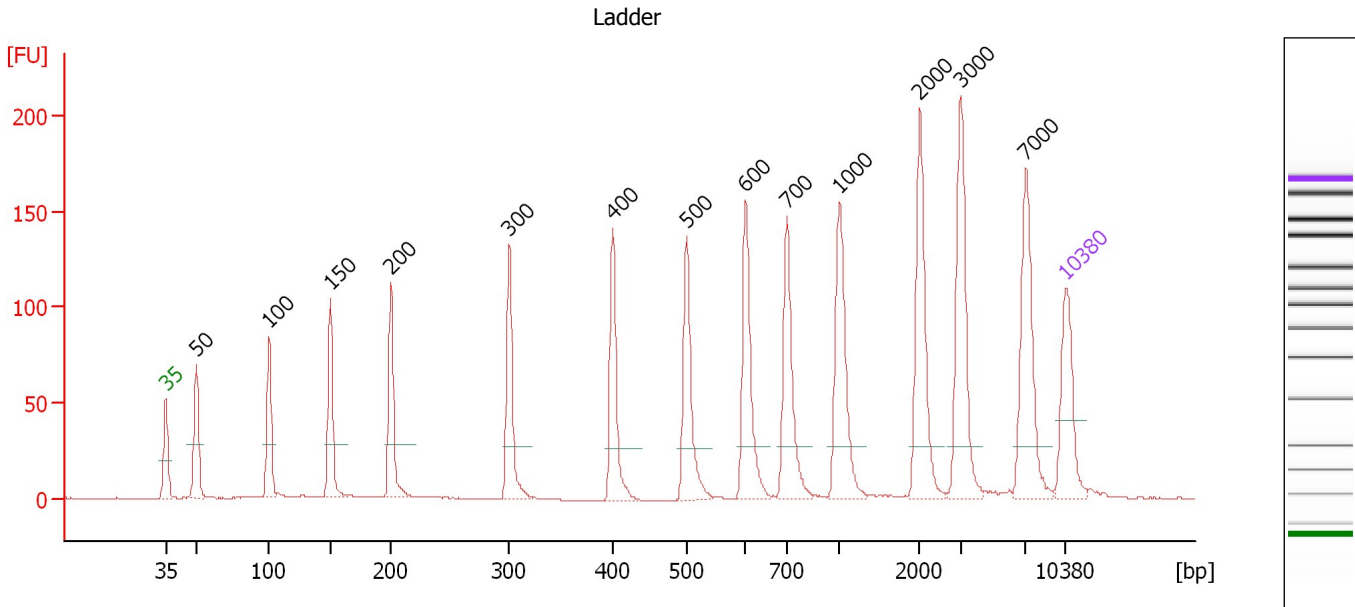
**Ladder**

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:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

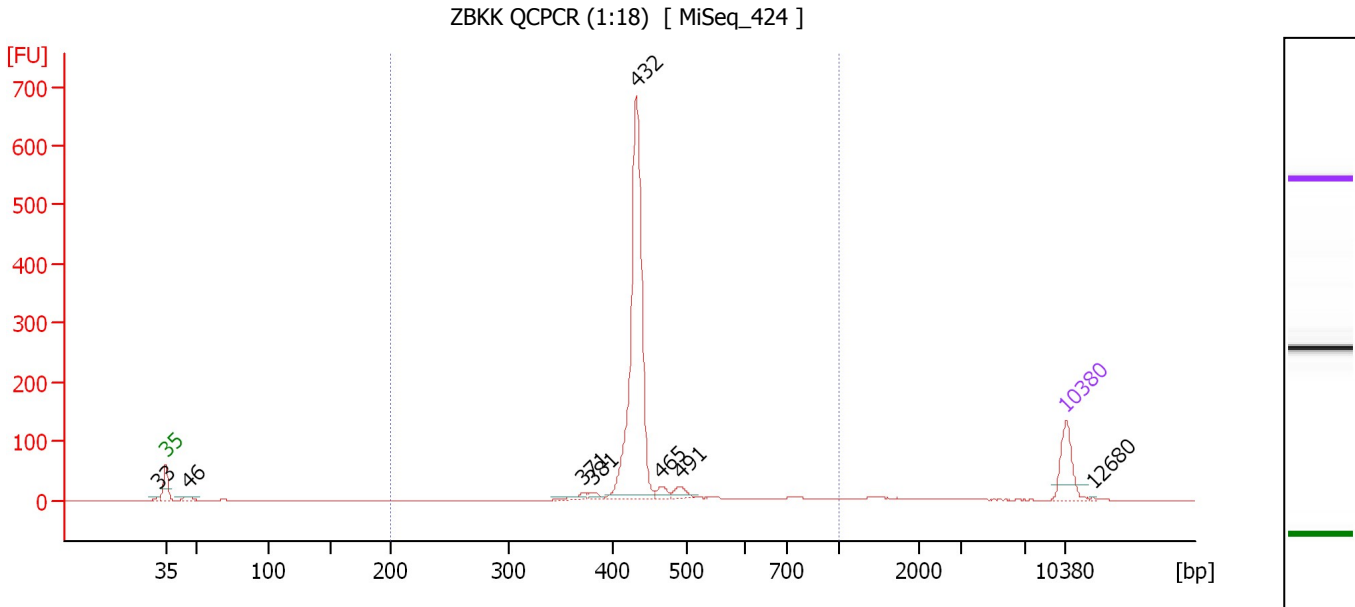
**Peak table for Ladder**

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	45.37
3	100	150.00	2,272.7	Ladder Peak	51.01
4	150	150.00	1,515.2	Ladder Peak	55.80
5	200	150.00	1,136.4	Ladder Peak	60.54
6	300	150.00	757.6	Ladder Peak	69.71
7	400	150.00	568.2	Ladder Peak	77.77
8	500	150.00	454.5	Ladder Peak	83.52
9	600	150.00	378.8	Ladder Peak	88.10
10	700	150.00	324.7	Ladder Peak	91.33
11	1,000	150.00	227.3	Ladder Peak	95.36
12	2,000	150.00	113.6	Ladder Peak	101.66
13	3,000	150.00	75.8	Ladder Peak	104.79
14	7,000	150.00	32.5	Ladder Peak	109.88
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : ZBKK QCPCR (1:18)**

Number of peaks found: 8                      Corr. Area 1: 1,063.3  
 Noise: 0.3

**Peak table for sample 1 : ZBKK QCPCR (1:18)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.34
2	35	125.00	5,411.3	Lower Marker	43.00
3	46	18.32	609.2		44.67
4	371	14.44	58.9		75.44
5	381	12.23	48.7		76.20
6	432	775.41	2,721.5		79.59
7	465	19.05	62.0		81.52
8	491	23.25	71.8		82.99
9	10,380	75.00	10.9	Upper Marker	113.00
10	12,680	0.00	0.0		115.13

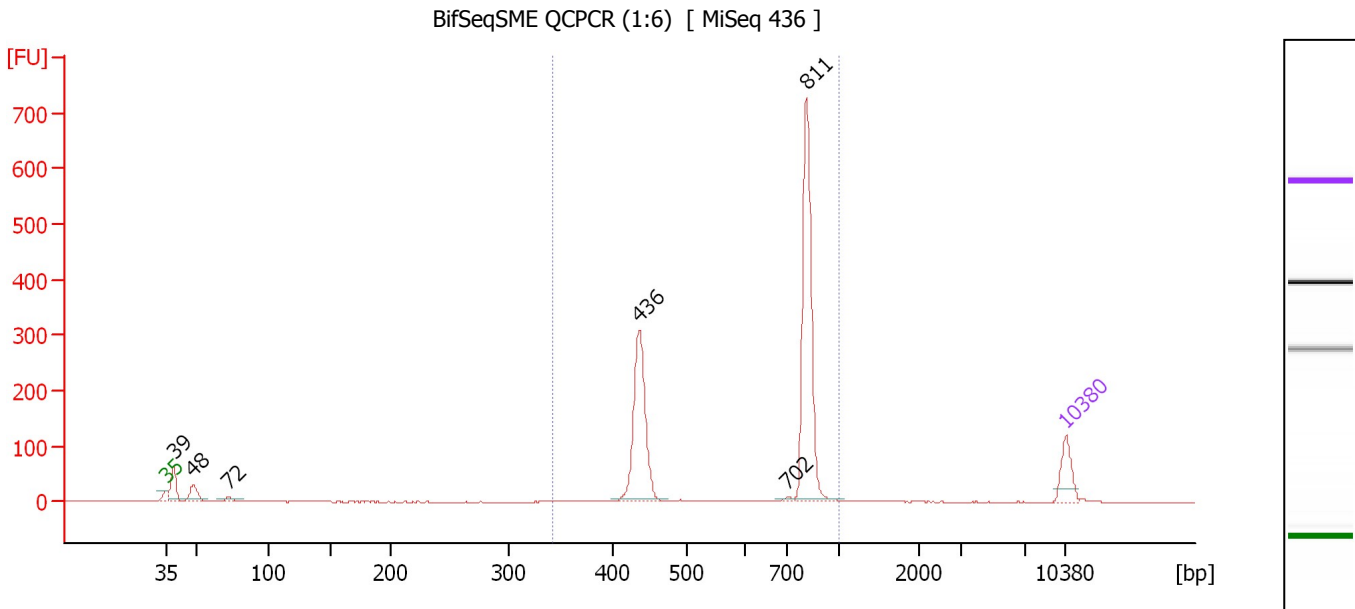
**Region table for sample 1 : ZBKK QCPCR (1:18)**

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	445	1,063.3	3,244.3	935.36	93	15.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : BifSeqSME QCPCR (1:6)**

Number of peaks found: 6                      Corr. Area 1: 1,082.6  
 Noise: 0.2

**Peak table for sample 2 : BifSeqSME QCPCR (1:6)**

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	39	117.61	4,587.6		43.61
3	48	80.77	2,525.7		45.12
4	72	20.35	425.4		47.91
5	436	450.62	1,567.3		79.82
6	702	7.27	15.7		91.35
7	811	599.68	1,120.6		92.82
8	10,380	75.00	10.9	Upper Marker	113.00

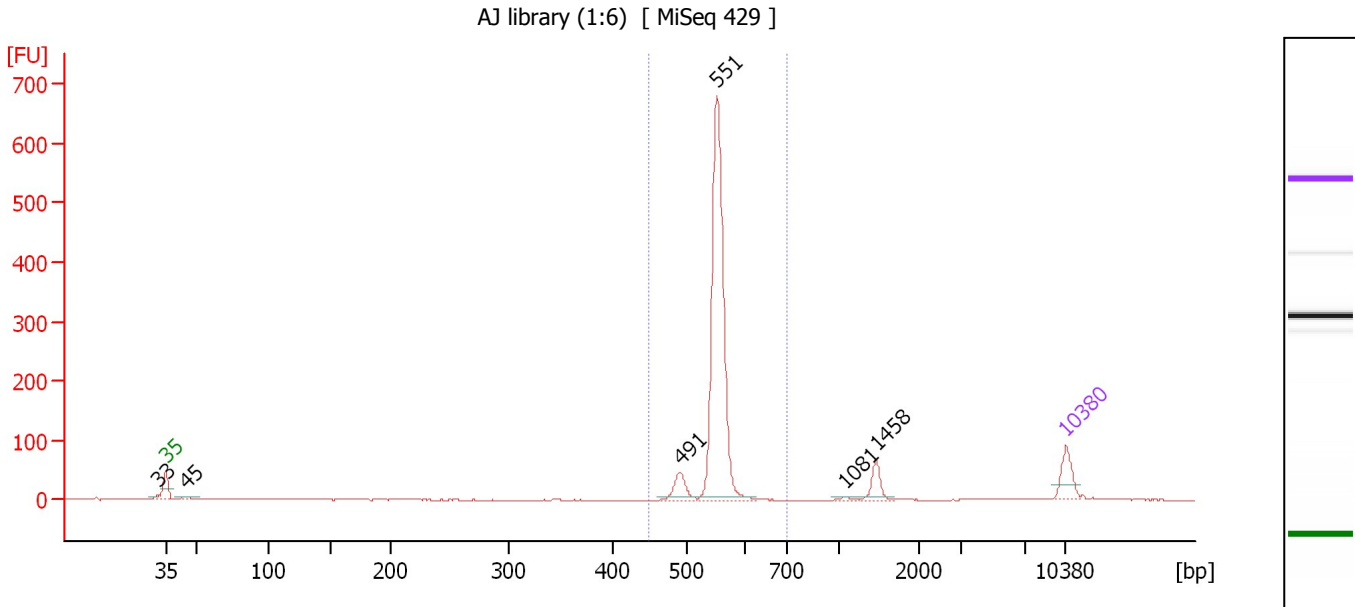
**Region table for sample 2 : BifSeqSME QCPCR (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
341	1,000	673	1,082.6	2,814.0	1,095.68	86	27.7

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : AJ library (1:6)**

Number of peaks found: 6                      Corr. Area 1: 881.1  
 Noise: 0.2

**Peak table for sample 3 : AJ library (1:6)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.38
2	35	125.00	5,411.3	Lower Marker	43.00
3	45	23.49	794.6		44.55
4	491	82.55	255.0		82.98
5	551	1,066.79	2,932.4		85.87
6	1,081	6.22	8.7		95.87
7	1,458	57.88	60.2		98.25
8	10,380	75.00	10.9	Upper Marker	113.00

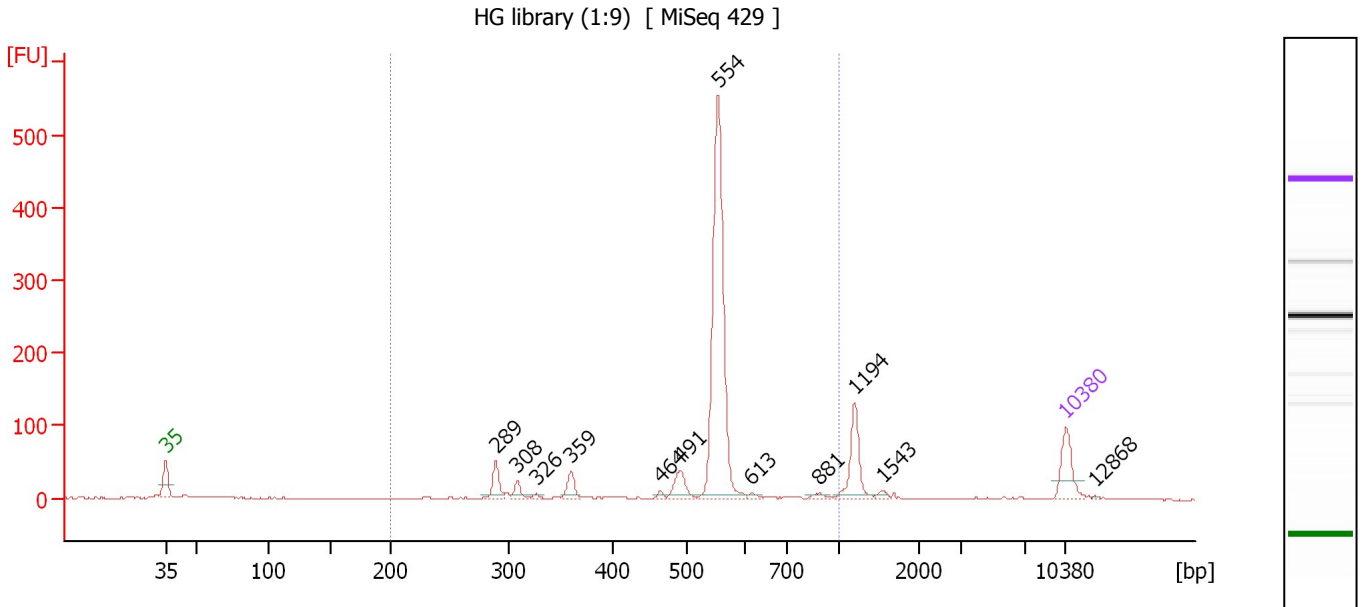
**Region table for sample 3 : AJ library (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
449	701	550	881.1	3,183.9	1,153.75	86	3.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : HG library (1:9)**

Number of peaks found: 12                      Corr. Area 1: 871.7  
 Noise: 0.3

**Peak table for sample 4 : HG library (1:9)**

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	60.66	318.4		68.67
3	308	26.23	129.1		70.34
4	326	5.99	27.8		71.81
5	359	42.97	181.3		74.47
6	464	8.09	26.4		81.48
7	491	58.24	179.8		82.99
8	554	724.34	1,982.8		85.97
9	613	7.40	18.3		88.53
10	881	8.29	14.3		93.76
11	1,194	110.43	140.1		96.58
12	1,543	8.80	8.6		98.78
13	10,380	75.00	10.9	Upper Marker	113.00
14	12,868	0.00	0.0		115.30

**Region table for sample 4 : HG library (1:9)**

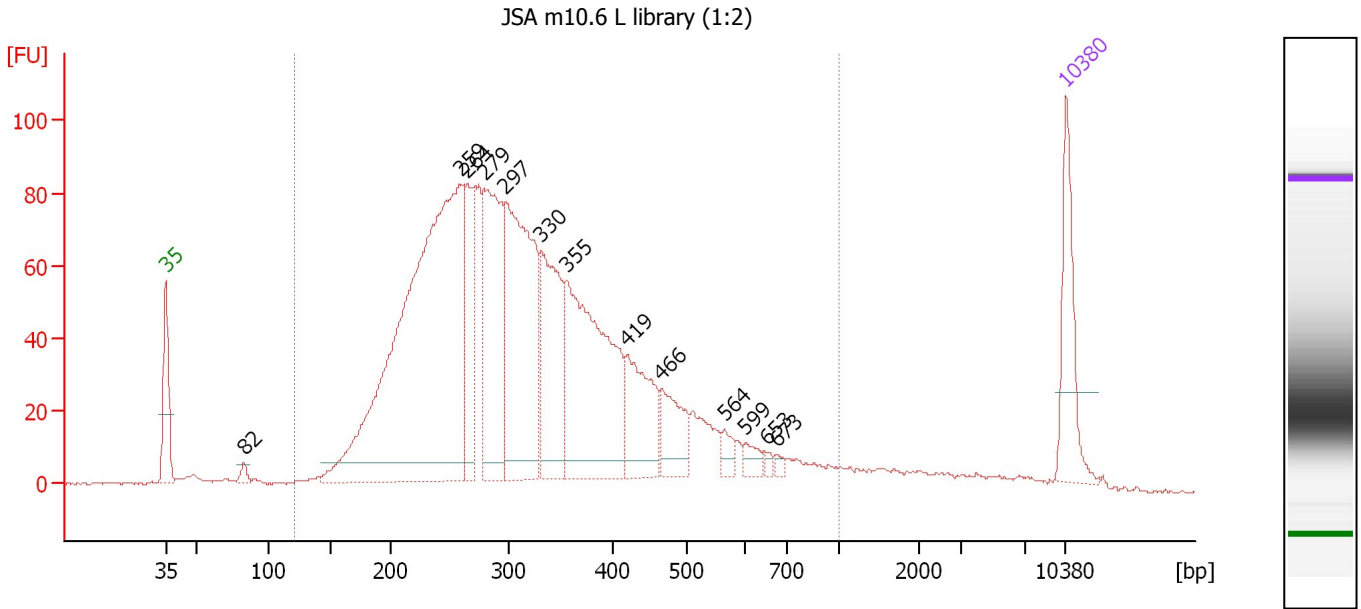
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	525	871.7	3,291.7	1,050.50	79	19.5



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : JSA m10.6 L library (1:2)**

Number of peaks found: 13                      Corr. Area 1: 2,156.1  
 Noise: 0.4

**Peak table for sample 5 : JSA m10.6 L library (1:2)**

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	82	10.81	198.7		49.03
3	259	884.53	5,171.5		65.96
4	264	127.16	730.4		66.39
5	279	236.49	1,285.4		67.76
6	297	351.78	1,796.8		69.40
7	330	183.19	840.3		72.15
8	355	327.17	1,398.0		74.11
9	419	113.19	409.2		78.87
10	466	64.89	210.9		81.57
11	564	14.76	39.7		86.44
12	599	14.27	36.1		88.08
13	653	5.00	11.6		89.83
14	673	5.25	11.8		90.46
15	10,380	75.00	10.9	Upper Marker	113.00

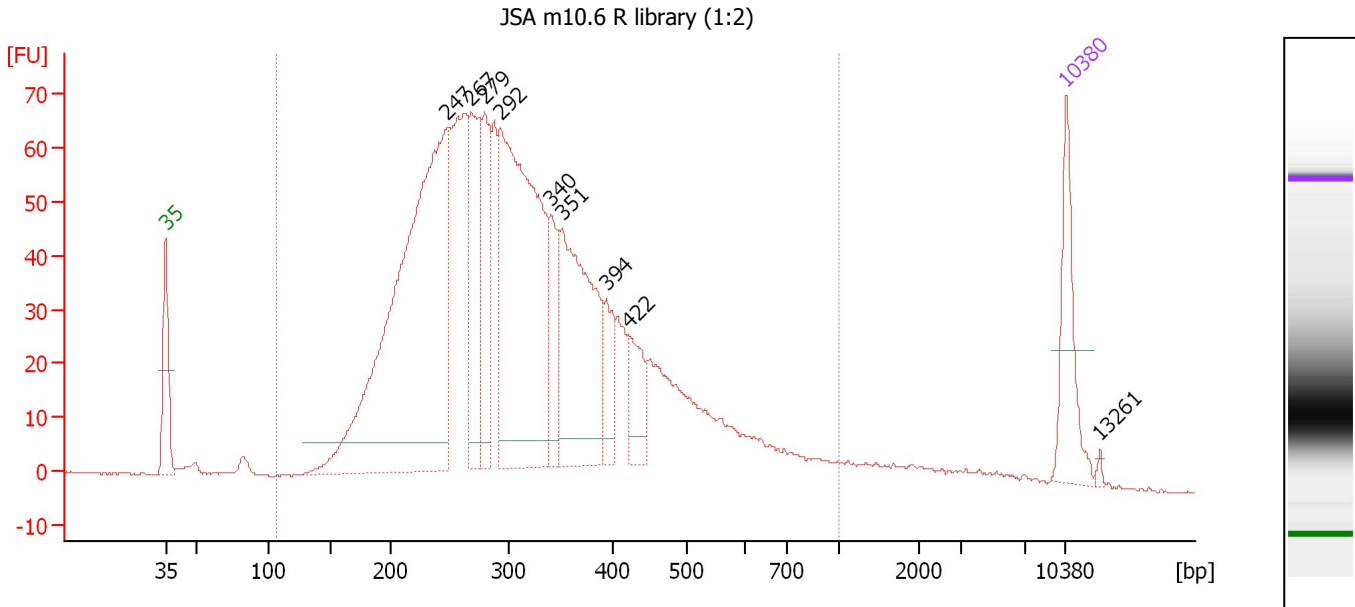
**Region table for sample 5 : JSA m10.6 L library (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
120	1,000	335	2,156.1	14,625.3	2,763.65	94	38.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : JSA m10.6 R library (1:2)**

Number of peaks found: 9                      Corr. Area 1: 1,705.7  
 Noise: 0.2

**Peak table for sample 6 : JSA m10.6 R library (1:2)**

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	247	838.73	5,146.6		64.84
3	267	159.98	907.0		66.71
4	279	126.65	688.1		67.77
5	292	542.86	2,814.6		69.00
6	340	71.42	318.2		72.94
7	351	283.47	1,225.0		73.79
8	394	53.01	204.1		77.25
9	422	56.51	202.7		79.07
10	10,380	75.00	10.9	Upper Marker	113.00
11	13,261	0.00	0.0		115.66

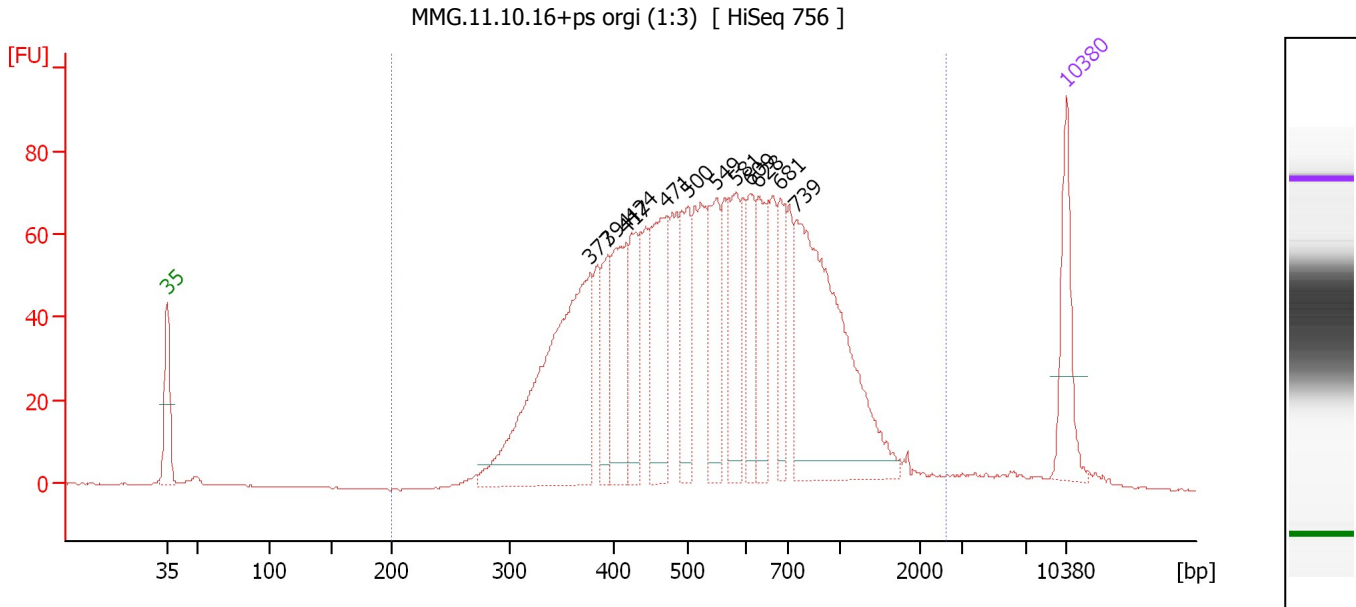
**Region table for sample 6 : JSA m10.6 R library (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
106	1,000	329	1,705.7	16,166.1	3,030.83	96	37.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : MMG.11.10.16+ps orgi (1:3)**

Number of peaks found: 12                      Corr. Area 1: 1,847.6  
 Noise: 0.2

**Peak table for sample 7 : MMG.11.10.16+ps orgi (1:3)**

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	377	440.83	1,769.8		75.95
3	394	80.62	310.0		77.30
4	417	132.25	480.4		78.76
5	424	97.88	350.1		79.13
6	471	158.95	511.8		81.83
7	500	101.50	307.8		83.50
8	549	113.89	314.3		85.77
9	581	100.07	261.1		87.22
10	609	75.97	188.9		88.41
11	628	85.56	206.5		89.00
12	681	69.33	154.2		90.73
13	739	402.17	824.1		91.86
14	10,380	75.00	10.9	Upper Marker	113.00

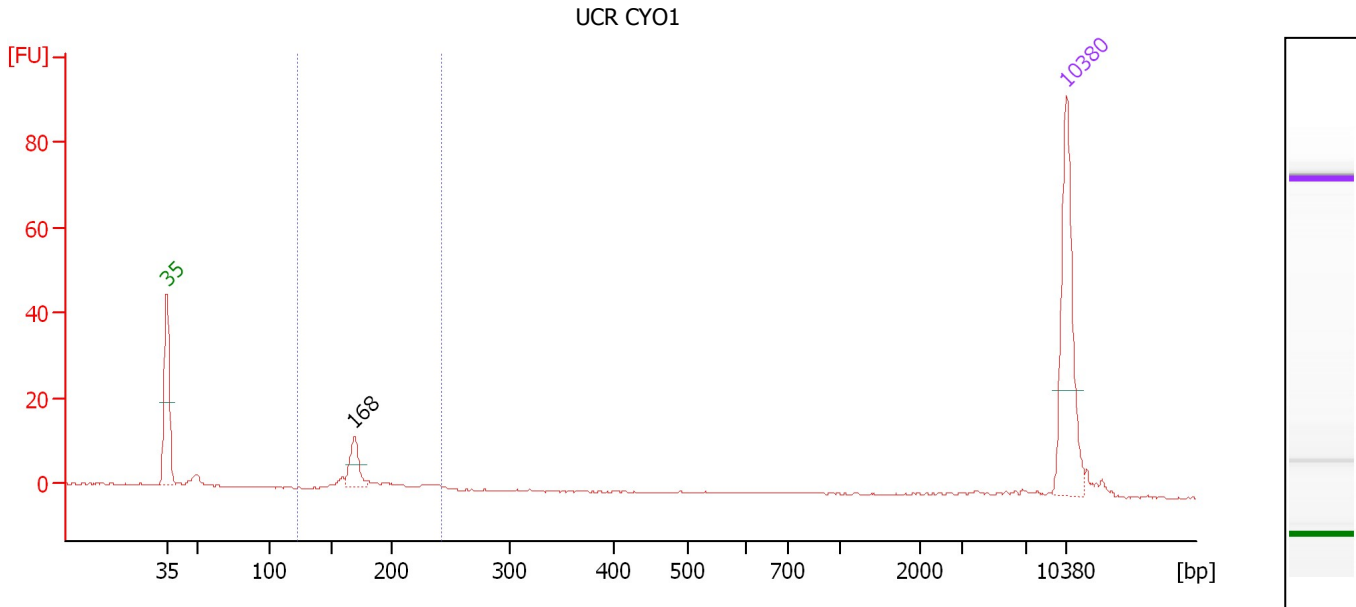
**Region table for sample 7 : MMG.11.10.16+ps orgi (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,599	607	1,847.6	7,904.4	2,598.43	96	47.9

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : UCR CYO1**

Number of peaks found: 1                      Corr. Area 1: 26.1  
 Noise: 0.2

**Peak table for sample 8 : UCR CYO1**

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	168	27.72	249.2		57.55
3	10,380	75.00	10.9	Upper Marker	113.00

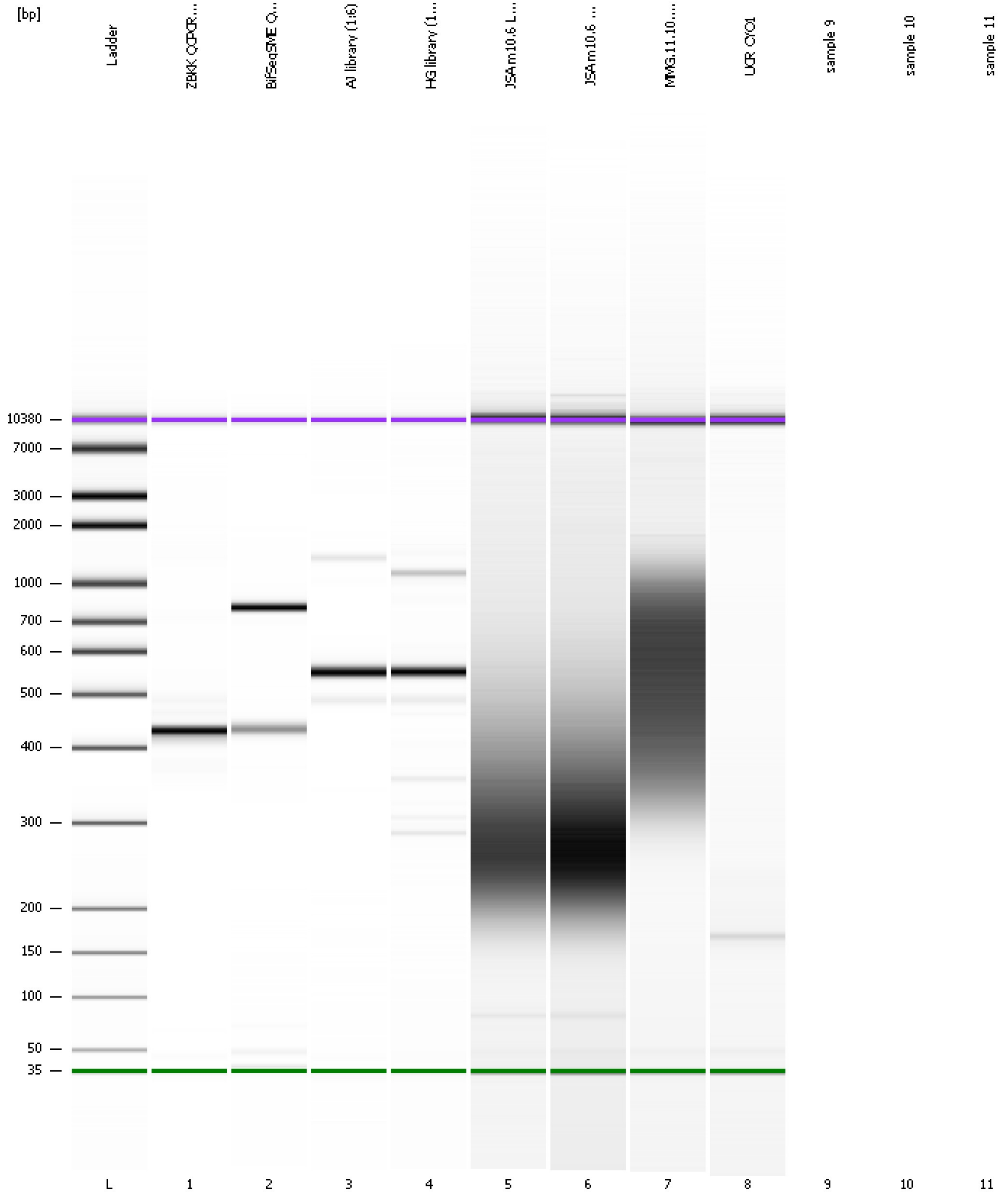
**Region table for sample 8 : UCR CYO1**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
122	242	178	26.1	382.4	44.28	61	11.6

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
Modified: 11/22/2016 3:46:48 PM

**Gel Image**



Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
Modified: 11/22/2016 3:46:48 PM

**Invalid Samples**

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-11-22\2016-11-22\_001.xad

Created: 11/22/2016 3:13:35 PM  
 Modified: 11/22/2016 3:46:48 PM

**Run Logbook**

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 9)		Instrument	Run		11/22/2016 3:46:18 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-11-22\2016-11-22_001.xad)		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		11/22/2016 3:13:41 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1