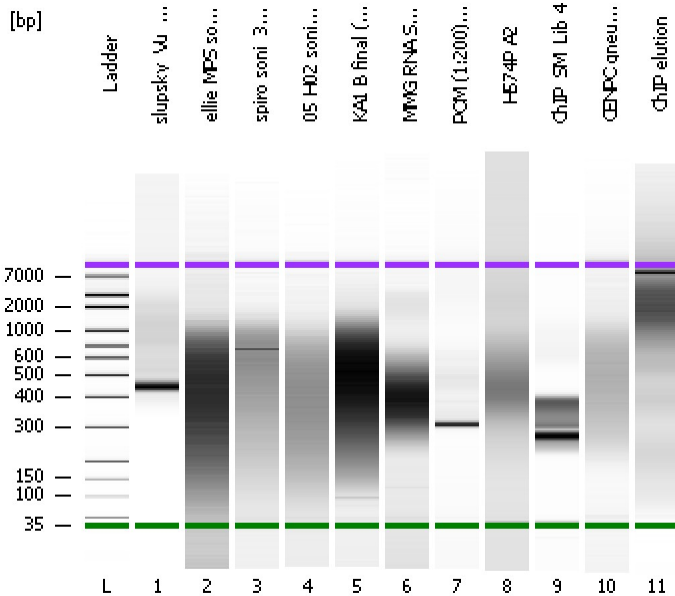


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
Modified: 9/23/2016 4:41:49 PM

Electrophoresis File Run Summary



Instrument Information:

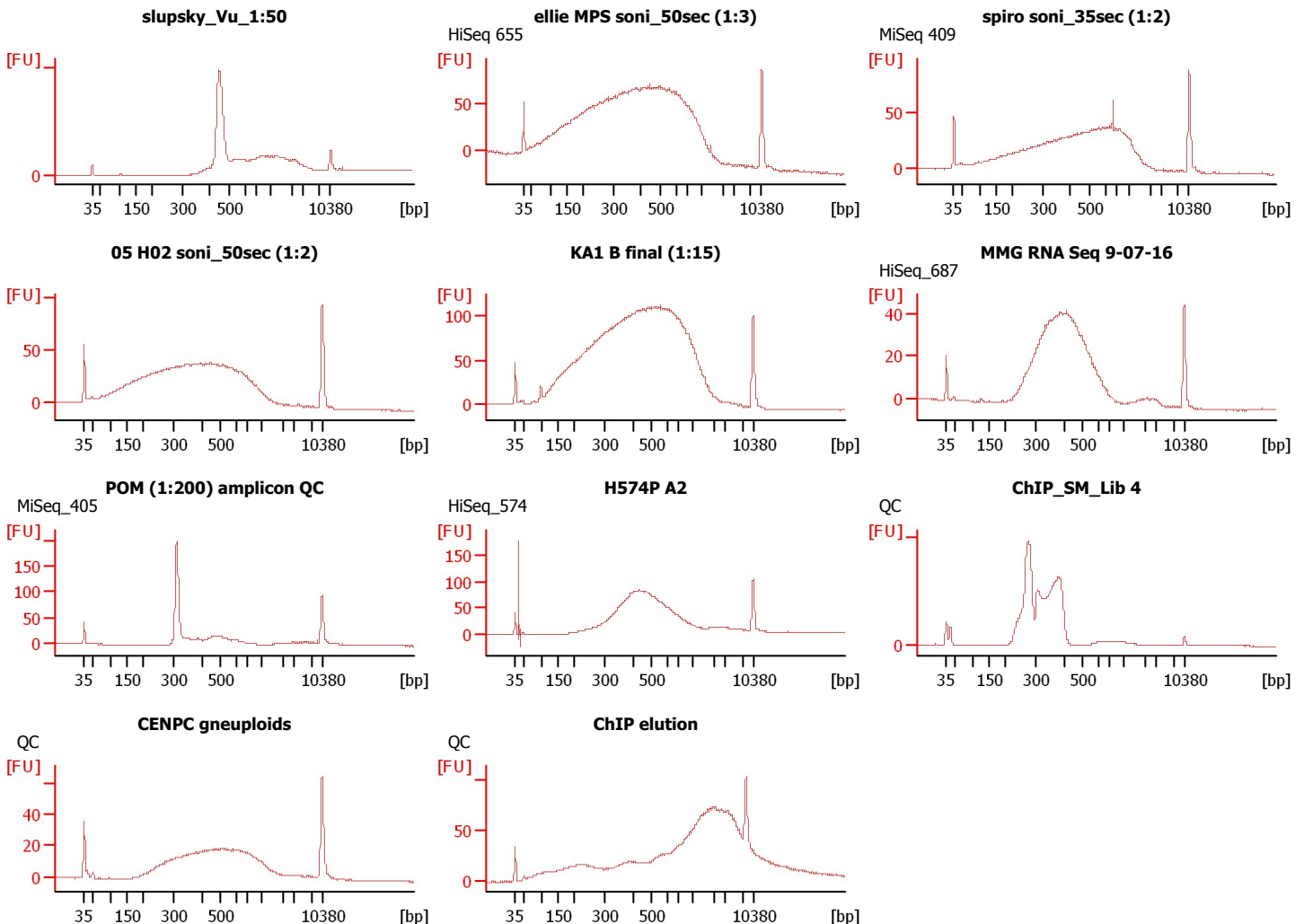
Instrument Name: DE13701086 Firmware: C.01.069  
Serial#: DE13701086 Type: G2938B

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\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
slupsky_Vu_1:50		<input type="checkbox"/>	✓			
ellie MPS soni_50sec (1:3)	HiSeq 655	<input type="checkbox"/>	✓			
spiro soni_35sec (1:2)	MiSeq 409	<input type="checkbox"/>	✓			
05 H02 soni_50sec (1:2)		<input type="checkbox"/>	✓			
KA1 B final (1:15)		<input type="checkbox"/>	✓			
MMG RNA Seq 9-07-16	HiSeq_687	<input type="checkbox"/>	✓			
POM (1:200) amplicon QC	MiSeq_405	<input type="checkbox"/>	✓			
H574P A2	HiSeq_574	<input type="checkbox"/>	✓			
ChIP_SM_Lib 4	QC	<input type="checkbox"/>	✓			
CENPC gneuploids	QC	<input type="checkbox"/>	✓			
ChIP elution	QC	<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\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
Modified: 9/23/2016 4:41:49 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

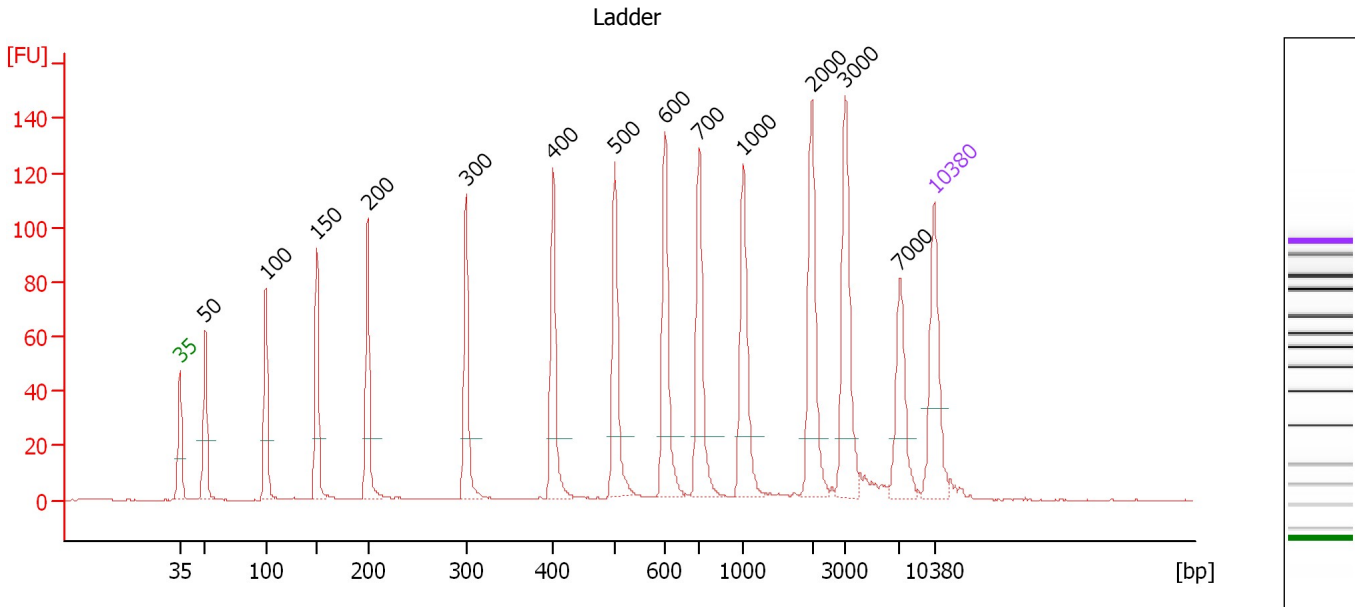
**Ladder**

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\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

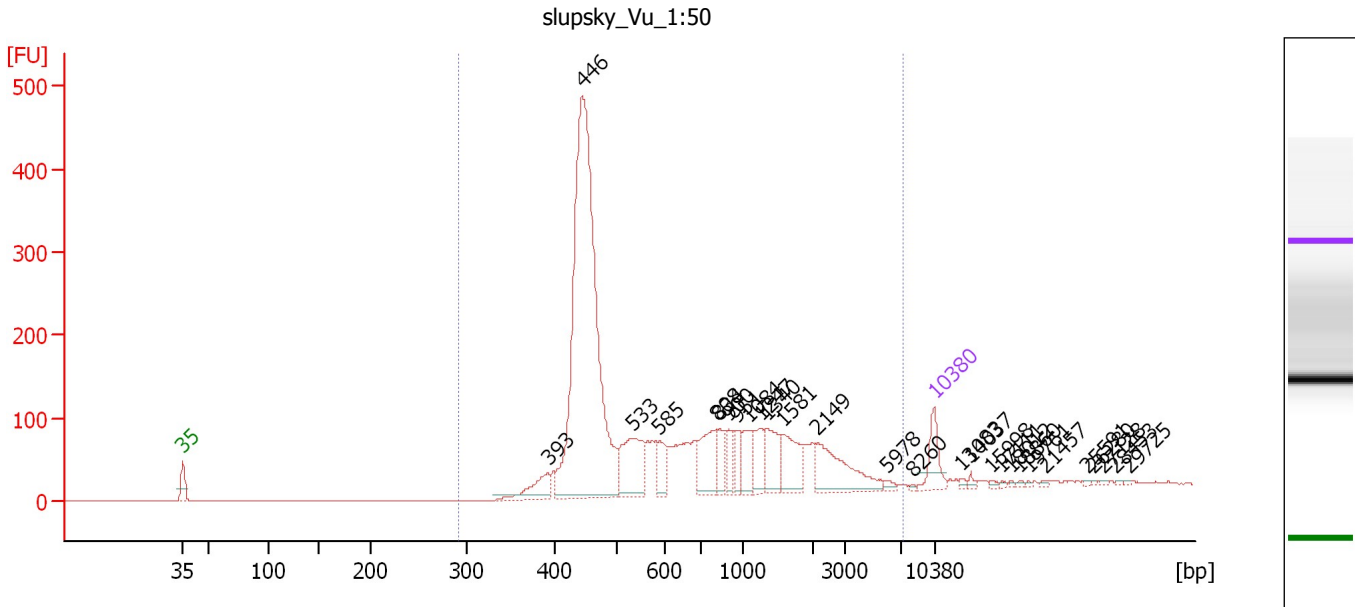
**Peak table for Ladder**

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	45.33
3	100	150.00	2,272.7	Ladder Peak	50.97
4	150	150.00	1,515.2	Ladder Peak	55.72
5	200	150.00	1,136.4	Ladder Peak	60.43
6	300	150.00	757.6	Ladder Peak	69.53
7	400	150.00	568.2	Ladder Peak	77.60
8	500	150.00	454.5	Ladder Peak	83.35
9	600	150.00	378.8	Ladder Peak	88.00
10	700	150.00	324.7	Ladder Peak	91.22
11	1,000	150.00	227.3	Ladder Peak	95.28
12	2,000	150.00	113.6	Ladder Peak	101.66
13	3,000	150.00	75.8	Ladder Peak	104.73
14	7,000	150.00	32.5	Ladder Peak	109.83
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : slupsky Vu 1:50**

Number of peaks found: 28                      Corr. Area 1: 2,958.3  
 Noise: 0.3

**Peak table for sample 1 : slupsky Vu 1:50**

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	393	99.60	384.1		77.03
3	446	1,800.37	6,112.7		80.26
4	533	231.56	658.3		84.88
5	585	80.50	208.4		87.32
6	808	170.52	319.7		92.68
7	834	67.57	122.8		93.03
8	900	60.29	101.5		93.92
9	951	53.47	85.2		94.62
10	1,084	94.63	132.3		95.81
11	1,247	77.47	94.1		96.85
12	1,340	110.20	124.6		97.45
13	1,581	130.31	124.9		98.99
14	2,149	177.43	125.1		102.12
15	5,978	10.45	2.6		108.53
16	8,260	3.30	0.6		111.01
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,083	0.00	0.0		115.53
19	14,037	0.00	0.0		116.43
20	15,998	0.00	0.0		118.27
21	17,111	0.00	0.0		119.31
22	18,012	0.00	0.0		120.15
23	18,860	0.00	0.0		120.95
24	19,761	0.00	0.0		121.79
25	21,457	0.00	0.0		123.38

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
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**Electropherogram Summary Continued ...**

**... Peak table for sample 1 : slupsky\_Vu\_1:50**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	25,591	0.00	0.0		127.26
27	26,280	0.00	0.0		127.90
28	27,128	0.00	0.0		128.70
29	28,453	0.00	0.0		129.94
30	29,725	0.00	0.0		131.13

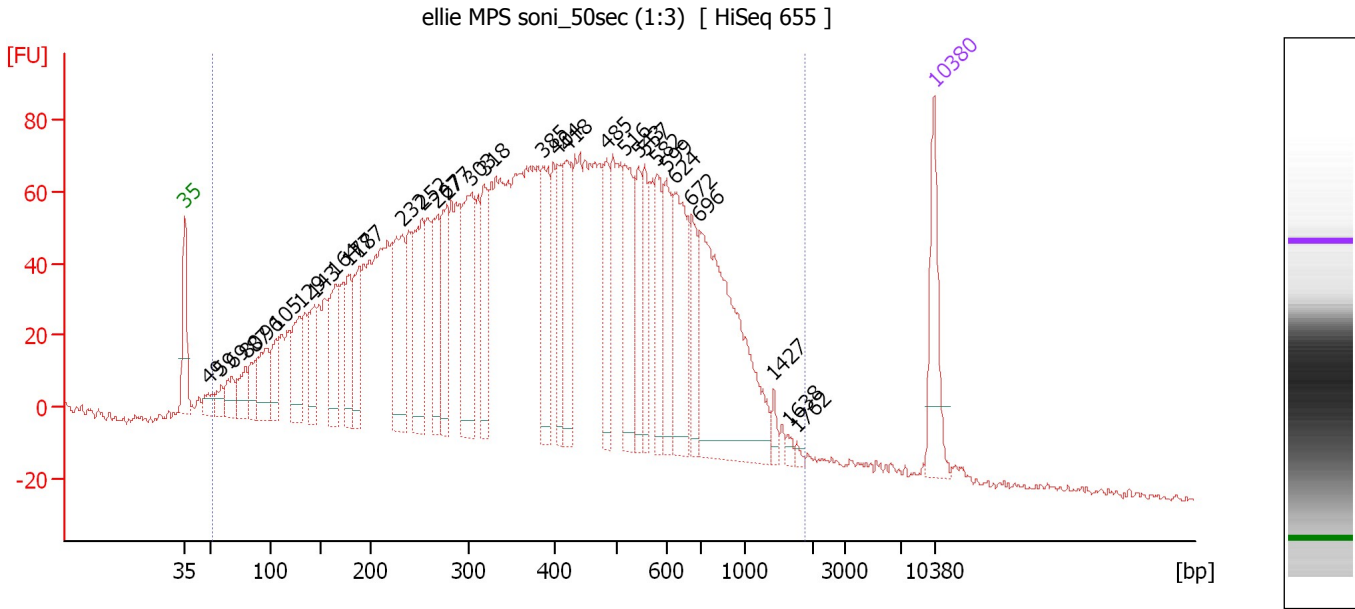
**Region table for sample 1 : slupsky\_Vu\_1:50**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
291	7,335	904	2,958.3	8,740.8	3,316.06	97	92.7

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : ellie MPS soni\_50sec (1:3)**

Number of peaks found: 33                      Corr. Area 1: 3,961.4  
 Noise: 1.1

**Peak table for sample 2 : ellie MPS soni\_50sec (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	49	24.13	739.2		45.24
3	59	24.42	623.0		46.39
4	69	42.07	928.1		47.43
5	80	49.54	941.6		48.68
6	87	47.52	825.5		49.53
7	96	80.37	1,262.1		50.57
8	105	56.19	808.9		51.47
9	129	91.02	1,070.4		53.71
10	143	69.81	739.7		55.06
11	164	103.22	953.0		57.05
12	177	74.91	639.9		58.30
13	187	87.48	707.2		59.24
14	232	146.06	954.5		63.33
15	252	155.10	932.2		65.17
16	267	97.87	554.5		66.57
17	277	105.95	580.2		67.41
18	303	172.09	861.3		69.75
19	318	105.98	505.7		70.95
20	385	113.00	444.2		76.43
21	404	80.33	301.4		77.83
22	418	104.94	380.6		78.62
23	485	77.01	240.8		82.46
24	516	118.16	346.8		84.10
25	543	69.93	195.1		85.35

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**

**... Peak table for sample 2 : ellie MPS soni 50sec (1:3)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	557	73.41	199.7		86.00
27	582	79.21	206.4		87.14
28	599	85.45	216.3		87.94
29	624	129.81	315.0		88.79
30	672	62.06	139.8		90.33
31	696	355.62	774.5		91.08
32	1,427	12.31	13.1		98.00
33	1,638	5.63	5.2		99.35
34	1,762	4.01	3.4		100.15
35	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 2 : ellie MPS soni 50sec (1:3)**

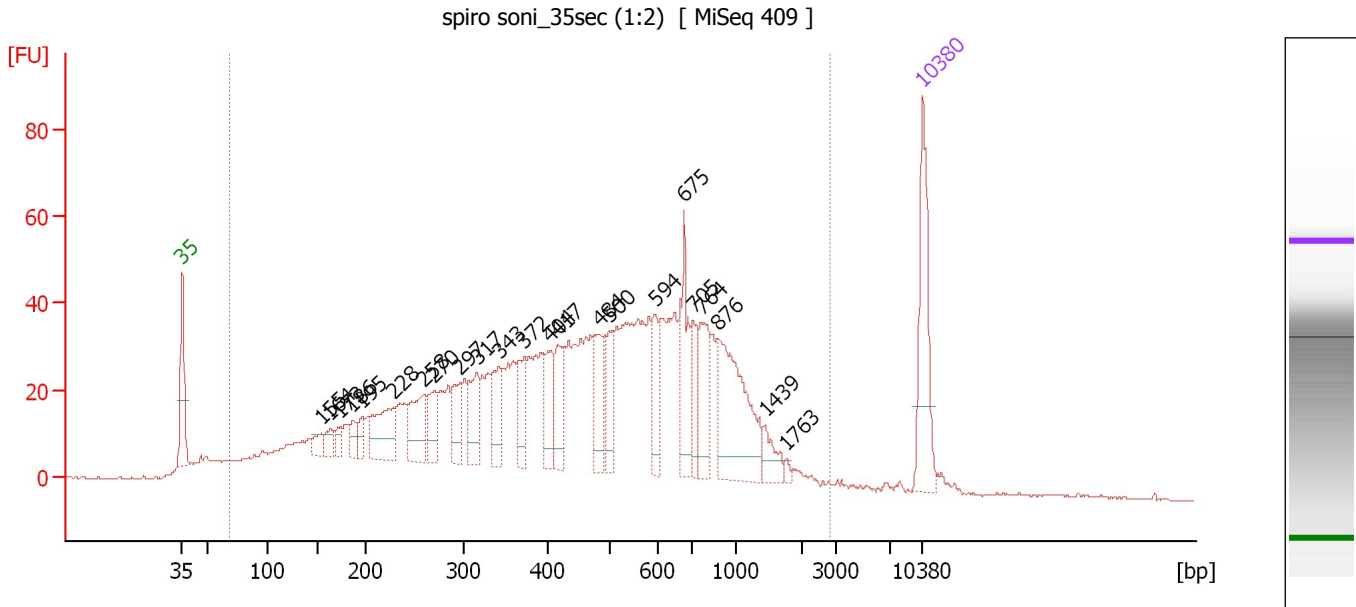
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
53	1,894	430	3,961.4	32,870.3	5,442.77	98	58.4



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : spiro soni 35sec (1:2)**

Number of peaks found: 23                      Corr. Area 1: 1,616.2  
 Noise: 0.2

**Peak table for sample 3 : spiro soni 35sec (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	155	16.71	163.2		56.20
3	164	17.45	161.5		57.01
4	173	15.06	131.6		57.92
5	186	18.90	154.2		59.08
6	195	17.67	137.1		59.98
7	228	69.24	459.4		63.01
8	258	63.46	372.4		65.73
9	270	33.81	189.5		66.84
10	297	37.90	193.0		69.31
11	317	48.99	234.5		70.87
12	343	48.52	214.5		72.99
13	372	43.62	177.6		75.35
14	404	44.37	166.5		77.82
15	417	48.39	175.8		78.58
16	484	48.92	153.2		82.41
17	500	35.62	107.8		83.37
18	594	35.07	89.5		87.70
19	675	61.70	138.4		90.42
20	705	36.58	78.7		91.28
21	764	57.35	113.7		92.09
22	876	132.75	229.6		93.60
23	1,439	19.19	20.2		98.08
24	1,763	3.46	3.0		100.15
25	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**

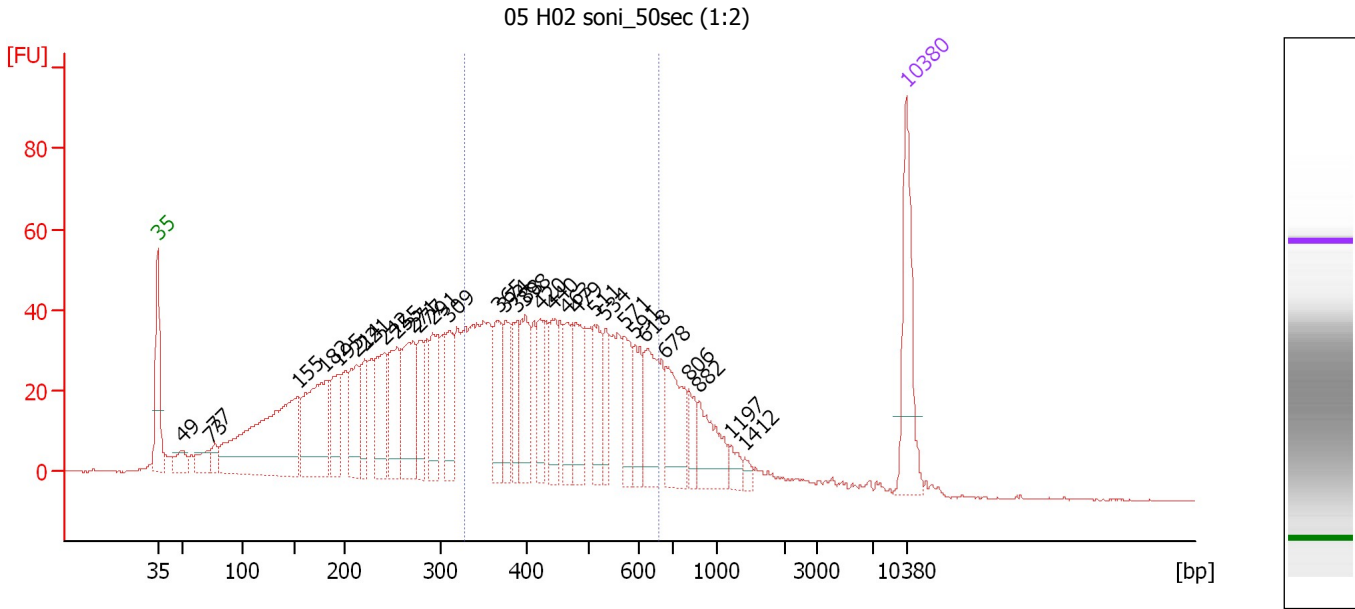
... Region table for sample 3 : spiro soni\_35sec (1:2)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
68	2,807	529	1,616.2	12,260.2	2,426.27	96	64.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : 05 H02 soni 50sec (1:2)**

Number of peaks found: 32                      Corr. Area 1: 866.6  
 Noise: 0.1

**Peak table for sample 4 : 05 H02 soni 50sec (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	49	24.83	760.8		45.24
3	73	27.61	575.0		47.89
4	77	16.67	328.7		48.35
5	155	288.04	2,823.3		56.15
6	182	155.67	1,298.2		58.70
7	195	69.53	541.1		59.93
8	214	71.74	509.0		61.66
9	221	46.12	315.7		62.37
10	242	85.50	535.1		64.26
11	255	86.72	515.4		65.43
12	271	98.28	549.1		66.91
13	277	55.14	301.2		67.47
14	291	66.52	345.9		68.75
15	309	65.72	322.1		70.28
16	365	61.86	256.5		74.81
17	374	50.83	205.8		75.53
18	388	42.88	167.4		76.65
19	398	71.53	272.6		77.41
20	420	48.05	173.4		78.74
21	440	50.61	174.2		79.91
22	463	55.26	180.7		81.24
23	479	57.06	180.4		82.16
24	511	54.34	161.3		83.84
25	534	35.17	99.9		84.91

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

### Electropherogram Summary Continued ...

#### ... Peak table for sample 4 : 05 H02 soni 50sec (1:2)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	571	46.18	122.6		86.64
27	591	40.29	103.4		87.56
28	618	61.75	151.4		88.58
29	678	70.04	156.5		90.52
30	806	23.67	44.5		92.66
31	882	51.99	89.3		93.68
32	1,197	11.75	14.9		96.53
33	1,412	6.80	7.3		97.91
34	10,380	75.00	10.9	Upper Marker	113.00

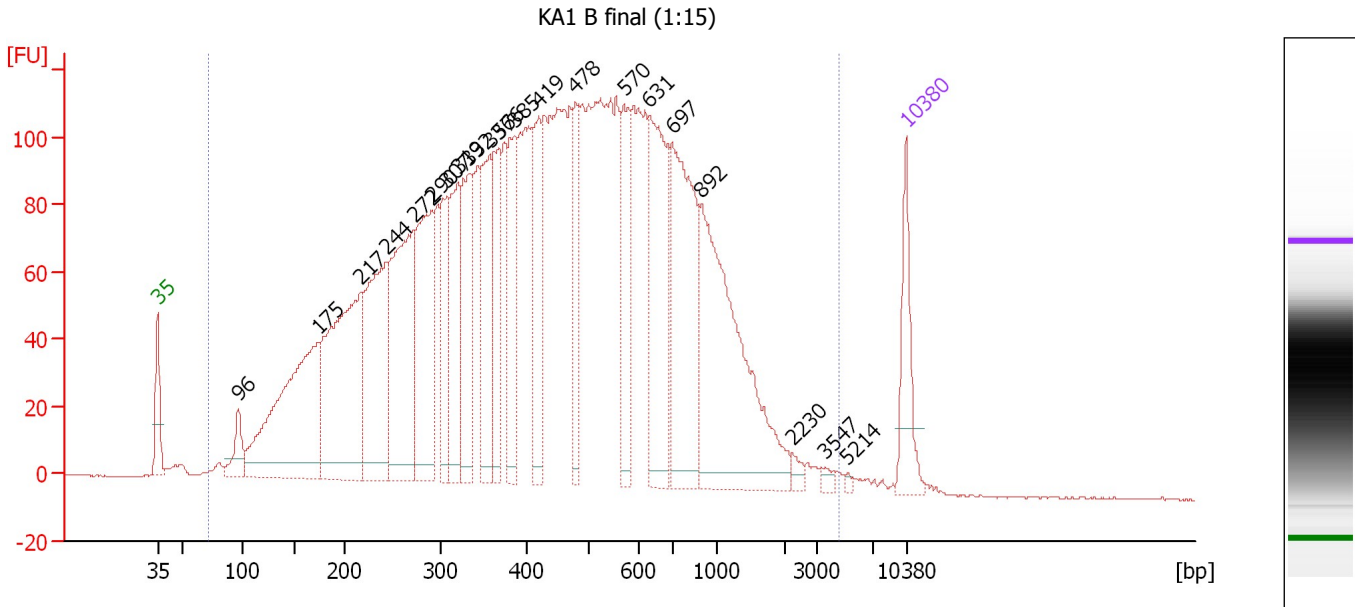
#### Region table for sample 4 : 05 H02 soni 50sec (1:2)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
326	660	461	866.6	3,711.0	1,069.21	42	19.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : KA1 B final (1:15)**

Number of peaks found: 21                      Corr. Area 1: 4,882.6  
 Noise: 0.2

**Peak table for sample 5 : KA1 B final (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	96	59.87	940.5		50.57
3	175	479.80	4,163.5		58.04
4	217	464.72	3,244.2		61.98
5	244	325.49	2,022.9		64.41
6	272	365.37	2,033.4		67.01
7	290	268.91	1,402.7		68.67
8	307	143.23	707.8		70.07
9	319	177.76	843.1		71.10
10	332	179.72	819.5		72.14
11	357	179.60	762.9		74.11
12	366	146.56	606.2		74.89
13	385	146.03	574.7		76.39
14	419	146.21	529.2		78.67
15	478	112.27	355.7		82.10
16	570	137.08	364.3		86.61
17	631	262.44	630.3		88.99
18	697	321.82	699.7		91.12
19	892	415.51	705.8		93.81
20	2,230	11.06	7.5		102.37
21	3,547	6.73	2.9		105.43
22	5,214	3.26	0.9		107.56
23	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**

... Region table for sample 5 :

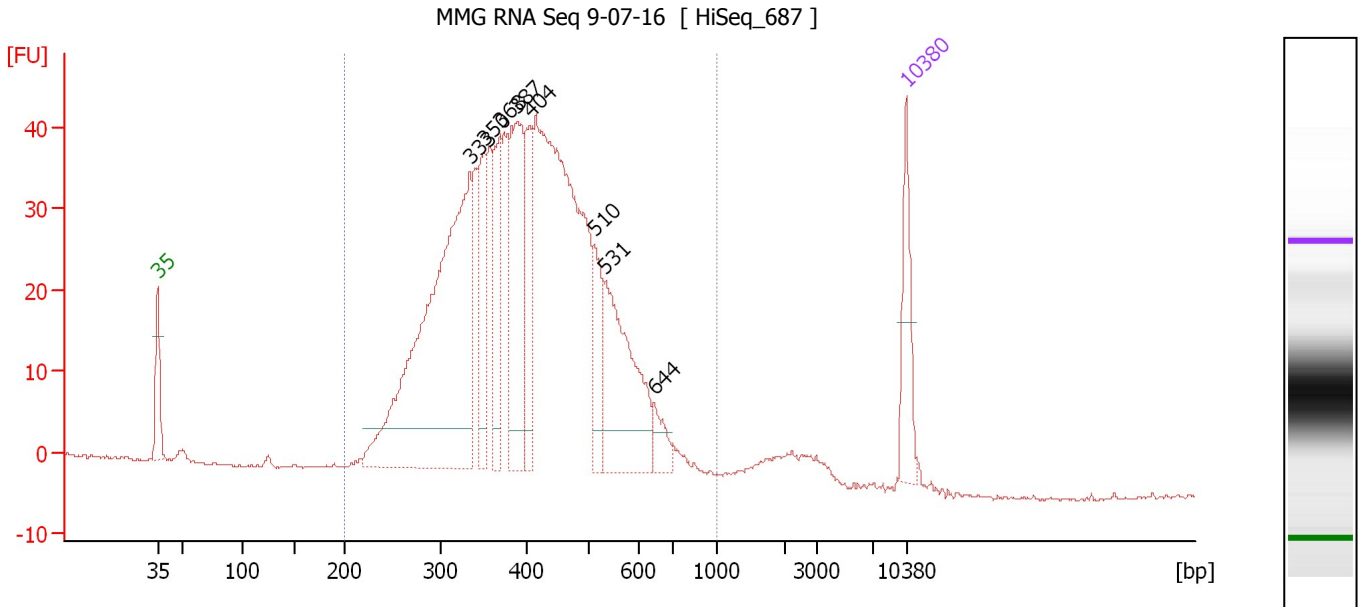
**KA1 B final (1:15)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
72	4,559	526	4,882.6	30,043.3	6,351.65	99	74.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : MMG RNA Seq 9-07-16**

Number of peaks found: 8                      Corr. Area 1: 928.2  
 Noise: 0.2

**Peak table for sample 6 : MMG RNA Seq 9-07-16**

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	333	777.08	3,532.3		72.22
3	350	111.41	482.1		73.58
4	368	120.66	496.4		75.05
5	387	260.37	1,019.1		76.56
6	404	109.25	410.0		77.82
7	510	90.39	268.3		83.83
8	531	247.02	705.4		84.77
9	644	36.11	84.9		89.42
10	10,380	75.00	10.9	Upper Marker	113.00

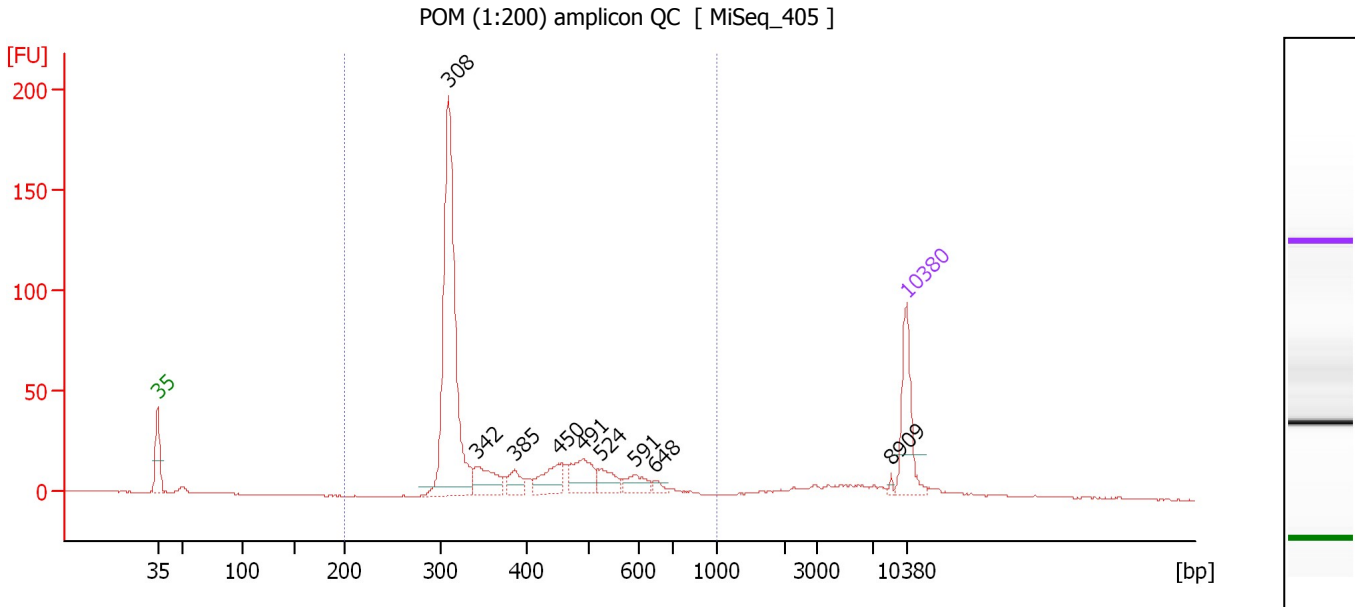
**Region table for sample 6 : MMG RNA Seq 9-07-16**

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	412	928.2	11,625.7	2,918.56	97	24.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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 Modified: 9/23/2016 4:41:49 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : POM (1:200) amplicon QC**

Number of peaks found: 9                      Corr. Area 1: 599.1  
 Noise: 0.2

**Peak table for sample 7 : POM (1:200) amplicon QC**

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	308	491.61	2,416.0		70.20
3	342	61.94	274.5		72.91
4	385	27.93	109.8		76.41
5	450	49.60	166.9		80.49
6	491	57.81	178.4		82.83
7	524	30.21	87.3		84.47
8	591	25.38	65.0		87.60
9	648	6.90	16.1		89.56
10	8,909	3.13	0.5		111.62
11	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 7 : POM (1:200) amplicon QC**

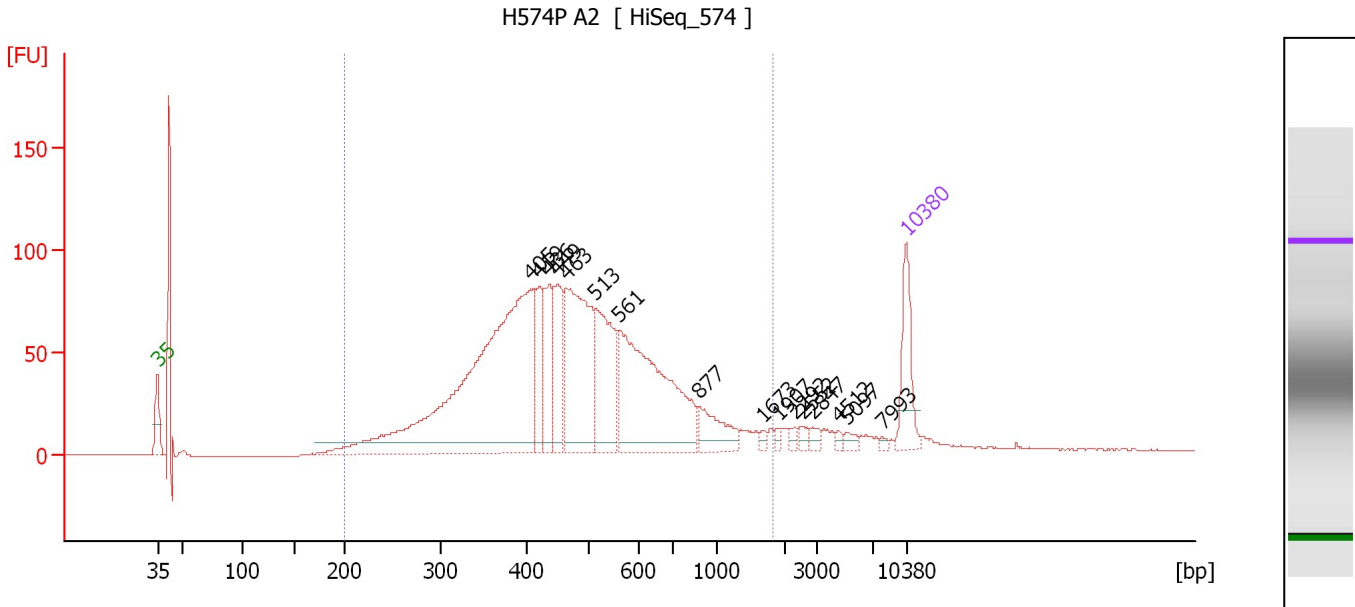
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	391	599.1	3,406.9	803.80	86	29.2



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : H574P A2**

Number of peaks found: 16                      Corr. Area 1: 1,840.9  
 Noise: 0.2

**Peak table for sample 8 : H574P A2**

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	405	870.79	3,257.4		77.89
3	419	89.97	325.4		78.69
4	436	108.66	377.9		79.65
5	449	114.13	385.4		80.40
6	463	316.28	1,036.0		81.20
7	513	186.14	549.4		83.97
8	561	386.13	1,042.1		86.20
9	877	65.76	113.6		93.61
10	1,673	6.60	6.0		99.58
11	1,907	6.62	5.3		101.07
12	2,292	8.07	5.3		102.56
13	2,552	10.24	6.1		103.36
14	2,847	9.63	5.1		104.26
15	4,512	5.11	1.7		106.66
16	5,097	9.28	2.8		107.41
17	7,993	3.80	0.7		110.76
18	10,380	75.00	10.9	Upper Marker	113.00

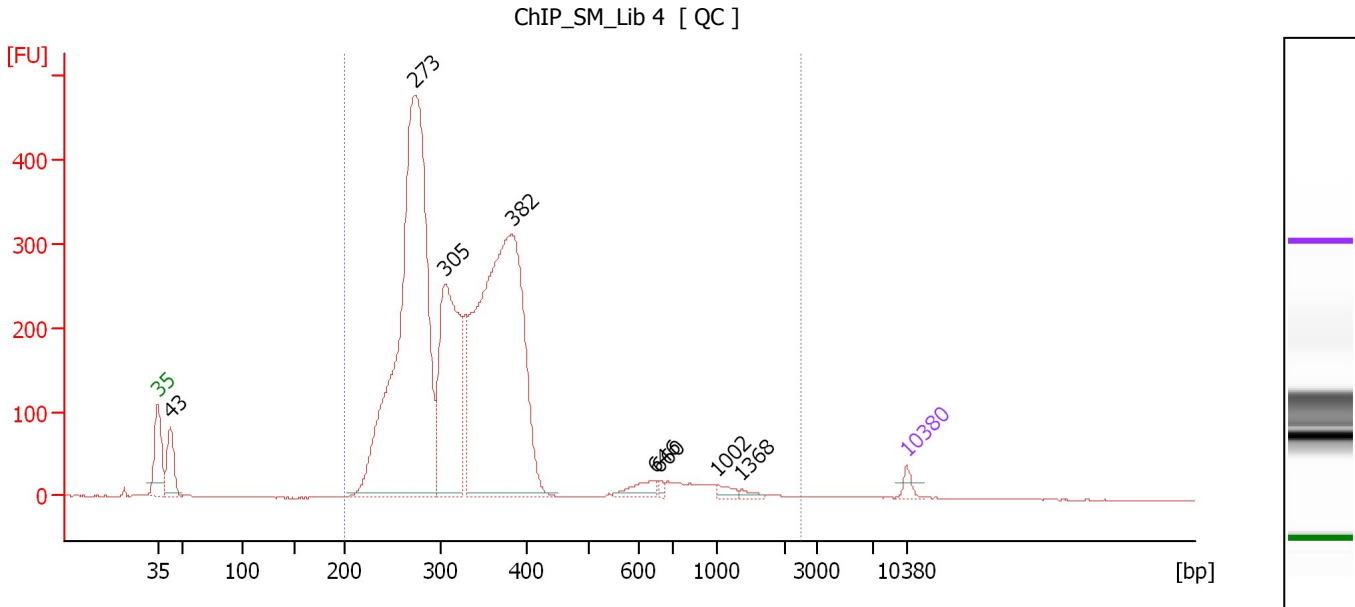
**Region table for sample 8 : H574P A2**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,814	509	1,840.9	7,902.4	2,240.78	89	44.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : ChIP SM Lib 4**

Number of peaks found: 8                      Corr. Area 1: 5,293.3  
 Noise: 0.3

**Peak table for sample 9 : ChIP SM Lib 4**

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	43	668.71	23,815.1		44.17
3	273	8,630.38	47,961.7		67.04
4	305	2,907.11	14,455.3		69.91
5	382	6,921.43	27,464.6		76.14
6	646	194.97	457.1		89.49
7	660	46.88	107.7		89.91
8	1,002	78.48	118.7		95.29
9	1,368	43.39	48.1		97.63
10	10,380	75.00	10.9	Upper Marker	113.00

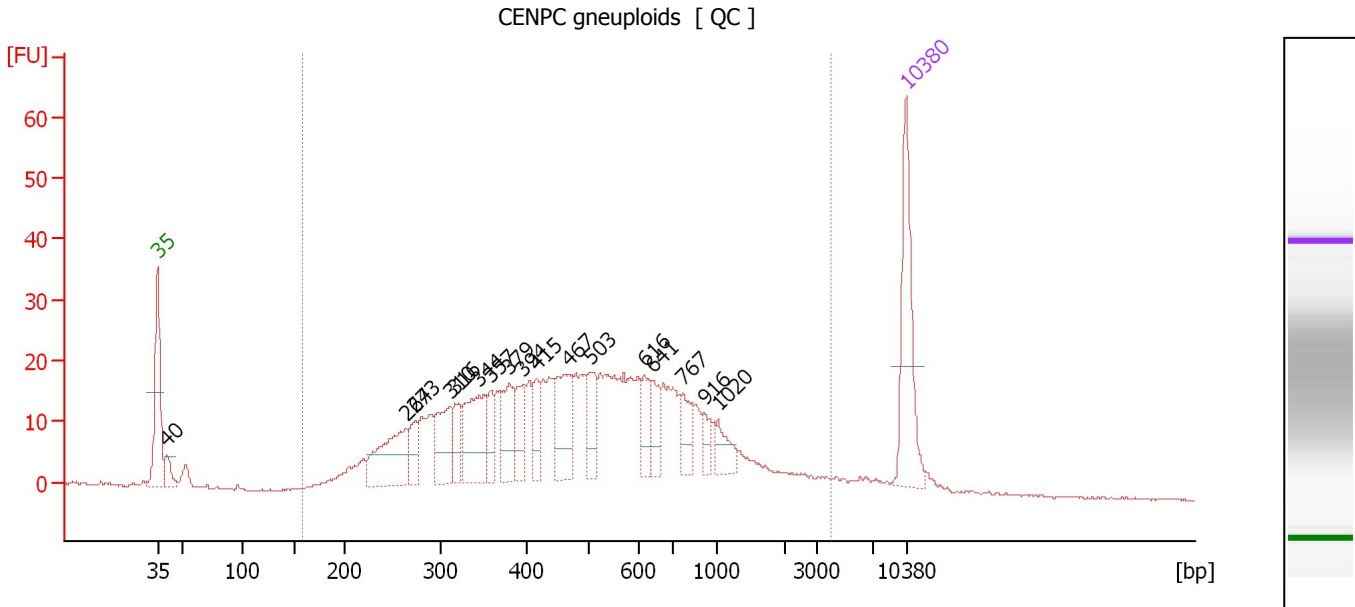
**Region table for sample 9 : ChIP SM Lib 4**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	2,478	351	5,293.3	96,388.7	19,977.64	97	48.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : CENPC gneuploids**

Number of peaks found: 17      Corr. Area 1: 662.6  
 Noise: 0.2

**Peak table for sample 10 : CENPC gneuploids**

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	20.29	759.9		43.85
3	264	84.57	485.2		66.26
4	273	25.42	140.9		67.11
5	310	53.62	262.0		70.34
6	316	27.73	133.0		70.82
7	344	79.28	349.0		73.10
8	357	24.77	105.1		74.16
9	379	45.79	183.1		75.91
10	394	31.95	122.9		77.13
11	415	25.10	91.7		78.45
12	467	57.99	188.0		81.47
13	503	32.31	97.3		83.48
14	616	26.14	64.3		88.52
15	641	22.06	52.2		89.31
16	767	23.34	46.1		92.12
17	916	10.65	17.6		94.14
18	1,020	19.03	28.3		95.41
19	10,380	75.00	10.9	Upper Marker	113.00

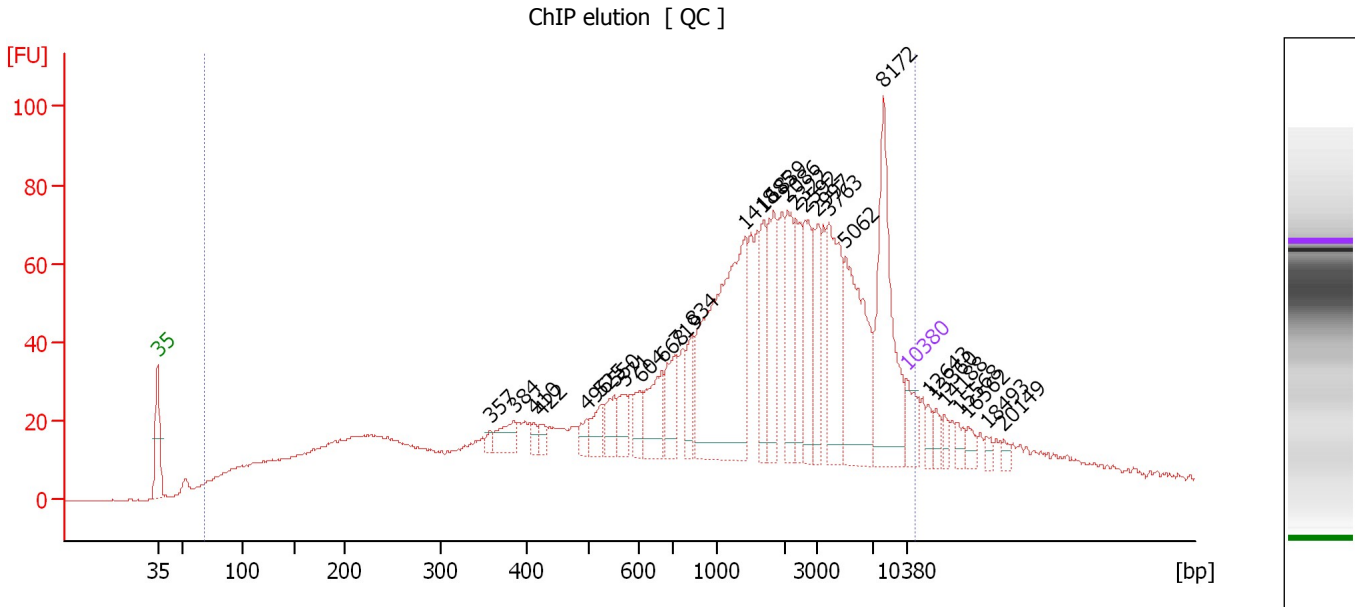
**Region table for sample 10 : CENPC gneuploids**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
158	4,005	598	662.6	4,417.2	1,210.64	95	75.7

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : ChIP elution**

Number of peaks found: 29                      Corr. Area 1: 1,998.9  
 Noise: 0.2

**Peak table for sample 11 : ChIP elution**

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	357	19.54	83.1		74.09
3	384	85.71	338.1		76.32
4	410	30.17	111.5		78.18
5	422	29.19	104.9		78.85
6	496	42.89	131.1		83.10
7	525	73.03	210.9		84.49
8	550	79.53	219.0		85.68
9	571	71.61	189.9		86.67
10	604	65.09	163.4		88.11
11	668	165.13	374.6		90.18
12	719	137.13	288.9		91.48
13	834	97.70	177.5		93.03
14	1,418	769.78	822.7		97.94
15	1,685	145.39	130.7		99.65
16	1,839	208.27	171.6		100.63
17	2,086	174.29	126.6		101.93
18	2,322	129.09	84.2		102.65
19	2,592	186.07	108.8		103.48
20	2,997	134.45	68.0		104.72
21	3,763	281.62	113.4		105.71
22	5,062	366.36	109.7		107.36
23	8,172	411.89	76.4		110.93
24	10,380	75.00	10.9	Upper Marker	113.00
25	12,643	0.00	0.0		115.12

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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 Modified: 9/23/2016 4:41:49 PM

### Electropherogram Summary Continued ...

#### ... Peak table for sample 11 :

#### ChIP elution

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	13,360	0.00	0.0		115.79
27	14,188	0.00	0.0		116.57
28	15,568	0.00	0.0		117.86
29	16,562	0.00	0.0		118.79
30	18,493	0.00	0.0		120.61
31	20,149	0.00	0.0		122.16

#### Region table for sample 11 :

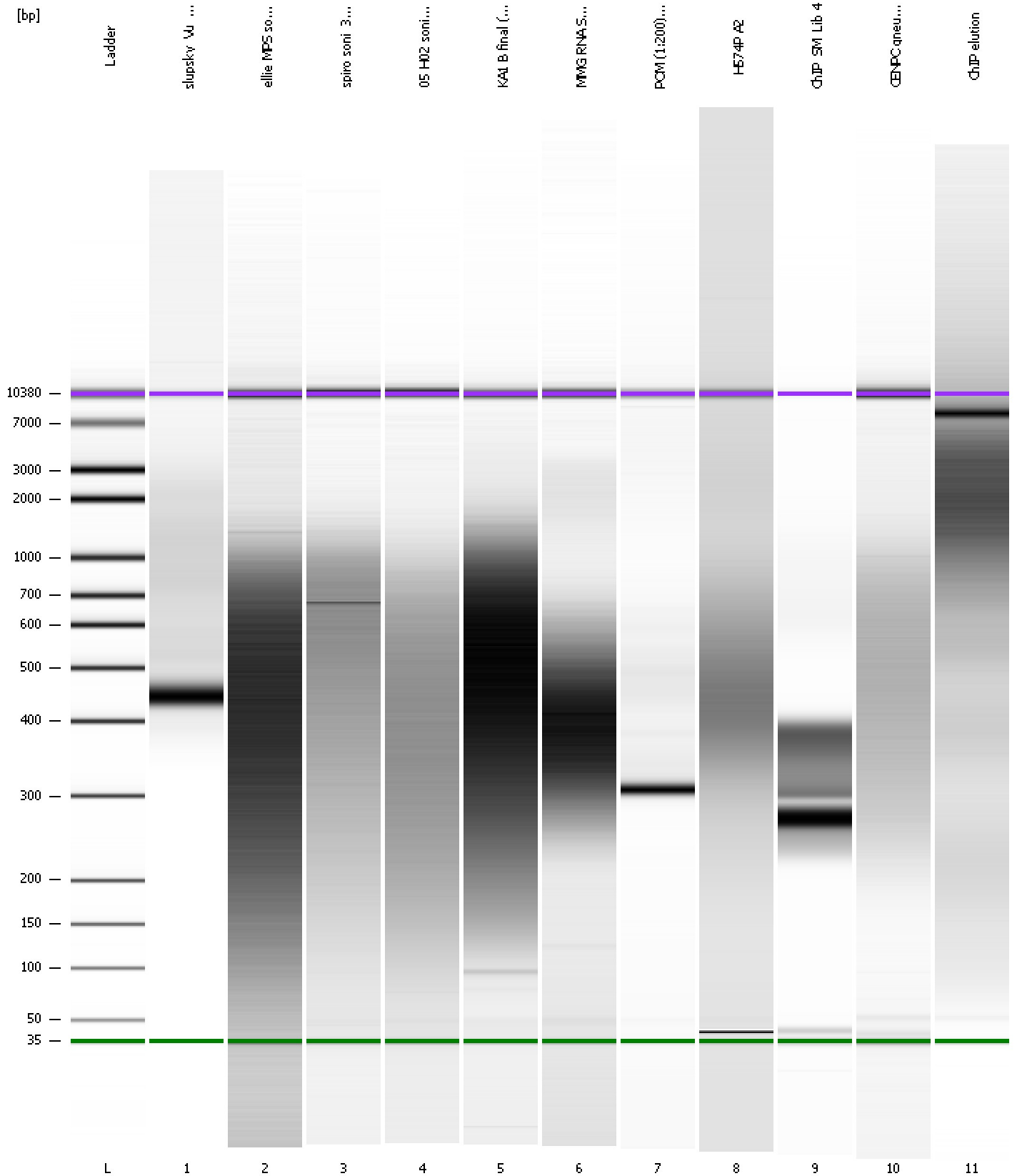
#### ChIP elution

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
67	11,186	2,371	1,998.9	30,942.6	8,279.92	92	100.0

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

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**Gel Image**



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-23\2016-09-23\_001.xad

Created: 9/23/2016 2:14:53 PM  
 Modified: 9/23/2016 4:41:49 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		9/23/2016 2:56:12 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\2016-09-23\2016-09-23_001.xad)		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		9/23/2016 2:14:58 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1