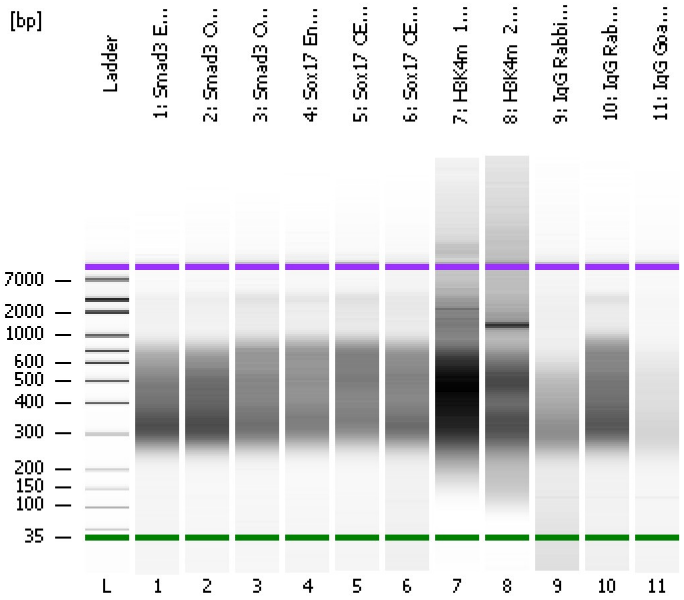
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad

Created: 8/13/2015 9:47:01 AM
Modified: 8/13/2015 10:31:43 AM

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

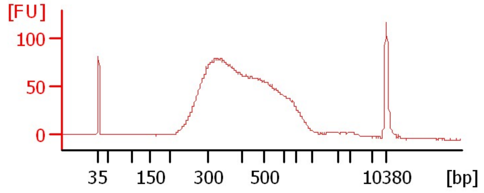
Chip Information:

Chip Lot #:

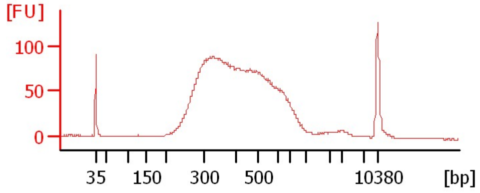
Reagent Kit Lot #:

Chip Comments:

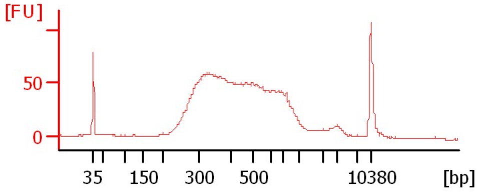
1: Smad3 Endog lib (1:3)
HiSeq_176: Size Selected Lib (0.55X R...



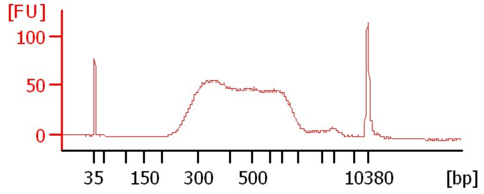
2: Smad3 OE 1 lib (1:3)
HiSeq_176: Size Selected Lib (0.55X R...



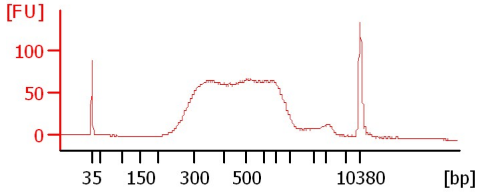
3: Smad3 OE 2 lib (1:5)
HiSeq_176: Size Selected Lib (0.55X R...



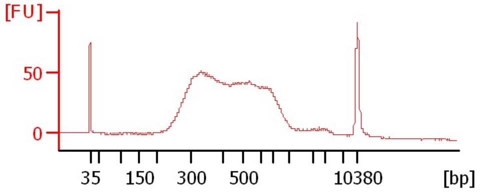
4: Sox17 Endog (1:8)
HiSeq_176: Size Selected Lib (0.55X R...



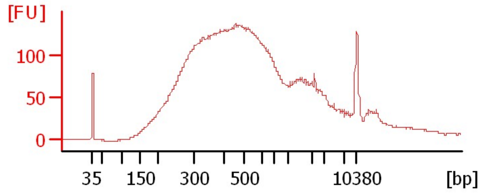
5: Sox17 OE 1 (1:8)
HiSeq_176: Size Selected Lib (0.55X R...



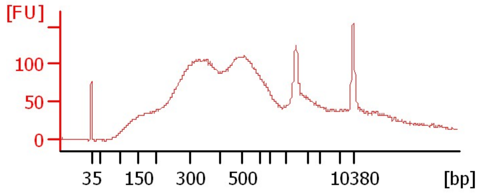
6: Sox17 OE 2 (1:2)
HiSeq_176: Size Selected Lib (0.55X R...



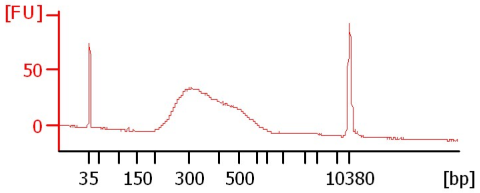
7: H3K4m_1 lib (1:30)
HiSeq_176: Size Selected Lib (0.55X R...



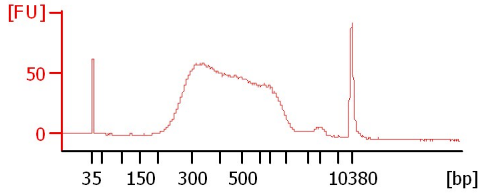
8: H3K4m_2 lib (1:25)
HiSeq_176: Size Selected Lib (0.55X R...



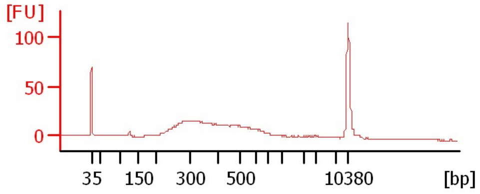
9: IgG Rabbit 1 lib (1:2)
HiSeq_176: Size Selected Lib (0.55X R...



10: IgG Rabbit 2 (1:2)
HiSeq_176: Size Selected Lib (0.55X R...



11: IgG Goat 1 lib
HiSeq_176: Size Selected Lib (0.55X R...



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad

Created: 8/13/2015 9:47:01 AM
Modified: 8/13/2015 10:31:43 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1: Smad3 Endog lib (1:3)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
2: Smad3 OE 1 lib (1:3)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
3: Smad3 OE 2 lib (1:5)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
4: Sox17 Endog (1:8)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
5: Sox17 OE 1 (1:8)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
6: Sox17 OE 2 (1:2)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
7: H3K4m_1 lib (1:30)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
8: H3K4m_2 lib (1:25)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
9: IgG Rabbit 1 lib (1:2)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
10: IgG Rabbit 2 (1:2)	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
11: IgG Goat 1 lib	HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)	☐	✓			
Ladder		☐	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

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

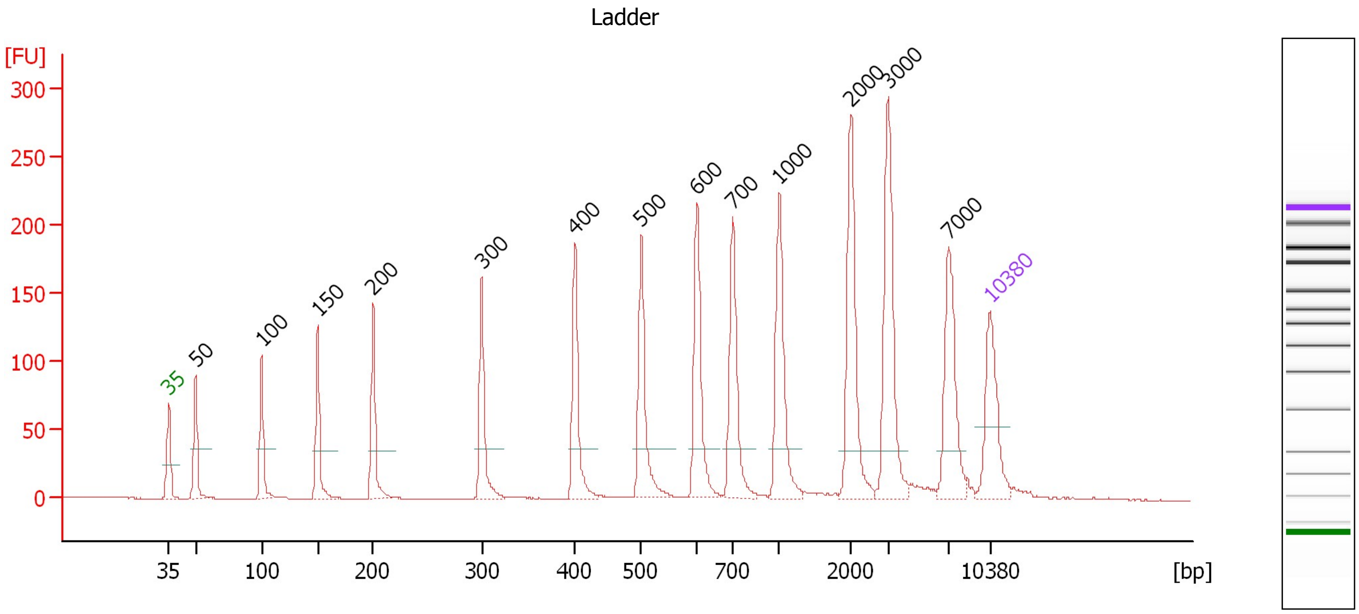
Filter Width [s] : 0.5
Polynomial Order : 4

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	Created:	8/13/2015 9:47:01 AM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad	Modified:	8/13/2015 10:31:43 AM

Electropherogram Summary



Overall Results for Ladder

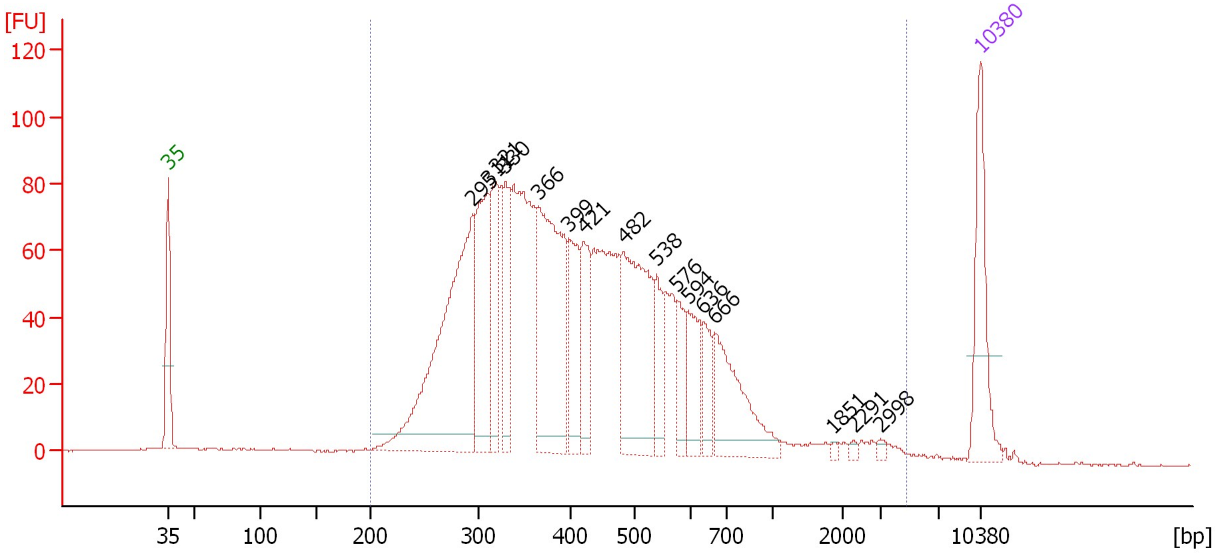
Noise: 0.2

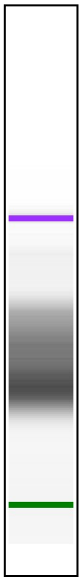
Peak table for Ladder

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	L	50	150.00	4,545.5	Ladder Peak	45.32
3	L	100	150.00	2,272.7	Ladder Peak	50.94
4	L	150	150.00	1,515.2	Ladder Peak	55.71
5	L	200	150.00	1,136.4	Ladder Peak	60.43
6	L	300	150.00	757.6	Ladder Peak	69.69
7	L	400	150.00	568.2	Ladder Peak	77.64
8	L	500	150.00	454.5	Ladder Peak	83.27
9	L	600	150.00	378.8	Ladder Peak	88.03
10	L	700	150.00	324.7	Ladder Peak	91.07
11	L	1,000	150.00	227.3	Ladder Peak	95.02
12	L	2,000	150.00	113.6	Ladder Peak	101.15
13	L	3,000	150.00	75.8	Ladder Peak	104.33
14	L	7,000	150.00	32.5	Ladder Peak	109.46
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

1: Smad3 Endog lib (1:3) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 1 : 1: Smad3 Endog lib (1:3)

Number of peaks found:	16	Corr. Area 1:	2,328.6
Noise:	0.2		

Peak table for sample 1 : 1: Smad3 Endog lib (1:3)

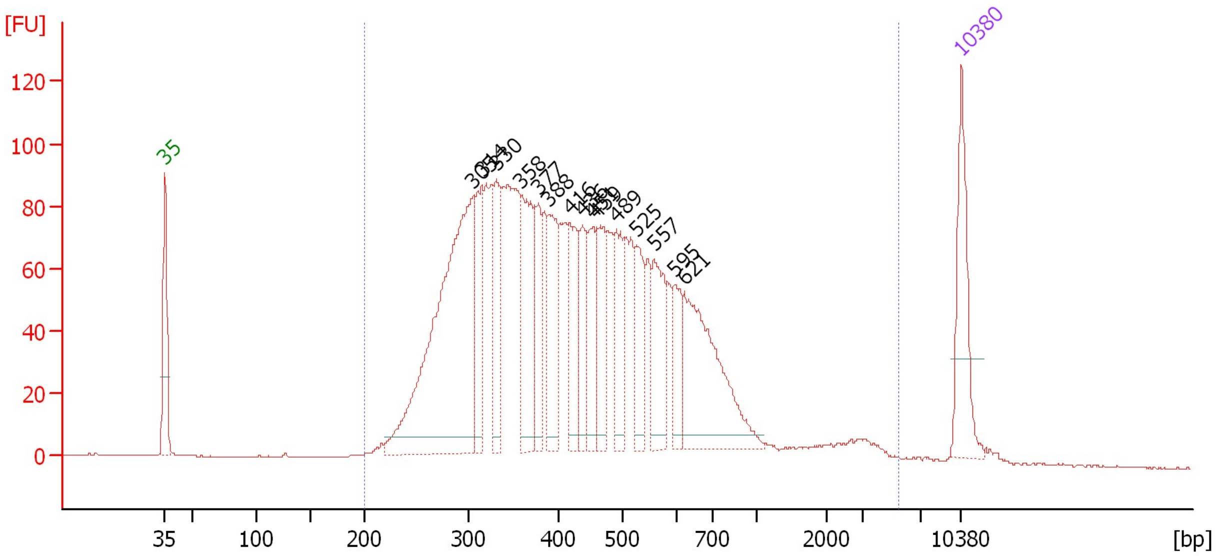
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		295	382.55	1,962.9		69.26
3		311	153.42	748.2		70.54
4		321	101.66	480.6		71.32
5		330	89.01	409.0		72.06
6		366	250.34	1,037.6		74.90
7		399	78.44	297.8		77.56
8		421	72.31	260.4		78.80
9		482	195.20	613.8		82.25
10		538	44.85	126.2		85.09
11		576	39.42	103.7		86.88
12		594	55.43	141.4		87.75
13		636	36.15	86.1		89.13
14		666	110.74	251.8		90.05
15		1,851	3.02	2.5		100.24
16		2,291	2.88	1.9		102.08
17		2,998	4.15	2.1		104.32
18	▶	10,380	75.00	10.9	Upper Marker	113.00

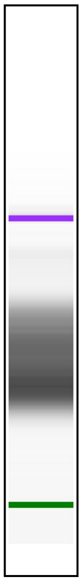
Region table for sample 1 : 1: Smad3 Endog lib (1:3)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	493	4,803	2,328.6	9,002.0	🟦 97	80.9	2,270.29

Electropherogram Summary Continued ...

2: Smad3 OE 1 lib (1:3) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 2 : 2: Smad3 OE 1 lib (1:3)

Number of peaks found:	15	Corr. Area 1:	2,696.9
Noise:	0.2		

Peak table for sample 2 : 2: Smad3 OE 1 lib (1:3)

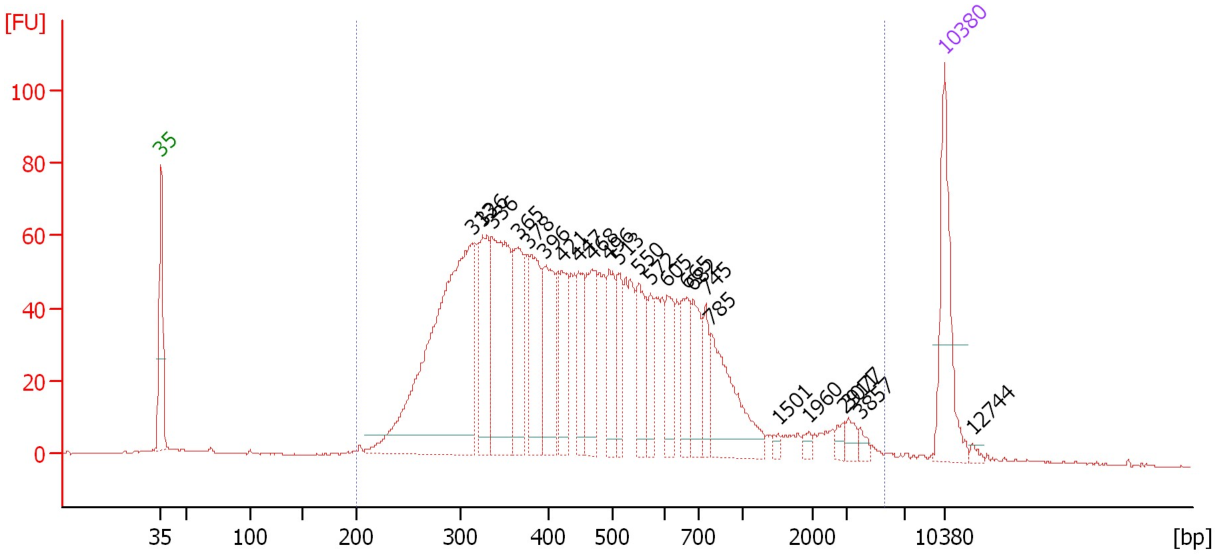
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		305	485.14	2,410.8		70.08
3		314	89.44	431.1		70.83
4		330	88.46	405.8		72.10
5		358	123.68	523.5		74.30
6		377	67.46	271.2		75.80
7		388	94.06	367.2		76.69
8		416	86.92	316.2		78.56
9		436	60.46	209.9		79.69
10		451	67.66	227.1		80.53
11		459	79.35	262.0		80.95
12		489	67.67	209.7		82.64
13		525	68.88	198.7		84.47
14		557	82.42	224.4		85.97
15		595	43.33	110.3		87.79
16		621	179.28	437.2		88.68
17	▶	10,380	75.00	10.9	Upper Marker	113.00

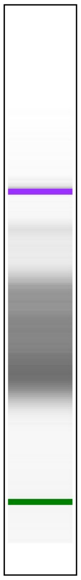
Region table for sample 2 : 2: Smad3 OE 1 lib (1:3)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	506	5,390	2,696.9	9,921.0	🟦	98	86.0	2,537.94

Electropherogram Summary Continued ...

3: Smad3 OE 2 lib (1:5) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 3 : 3: Smad3 OE 2 lib (1:5)

Number of peaks found:	24	Corr. Area 1:	2,007.1
Noise:	0.2		

Peak table for sample 3 : 3: Smad3 OE 2 lib (1:5)

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		313	432.20	2,089.1		70.76
3		326	106.23	493.7		71.76
4		336	176.89	797.1		72.57
5		365	91.86	381.3		74.86
6		378	92.93	372.9		75.86
7		396	88.10	336.9		77.33
8		421	58.43	210.4		78.81
9		447	56.82	192.6		80.29
10		468	72.24	233.8		81.48
11		496	55.02	168.0		83.05
12		513	38.29	113.0		83.90
13		550	53.62	147.6		85.67
14		572	31.11	82.4		86.71
15		605	41.12	102.9		88.19
16		665	45.60	104.0		90.00
17		682	47.90	106.4		90.52
18		745	27.53	56.0		91.67
19		785	95.52	184.4		92.19
20		1,501	4.46	4.5		98.10
21		1,960	5.43	4.2		100.90
22		2,911	6.20	3.2		104.05
23		3,077	8.83	4.3		104.43
24		3,857	5.30	2.1		105.43
25	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Peak table for sample 3 : 3: Smad3 OE 2 lib (1:5)

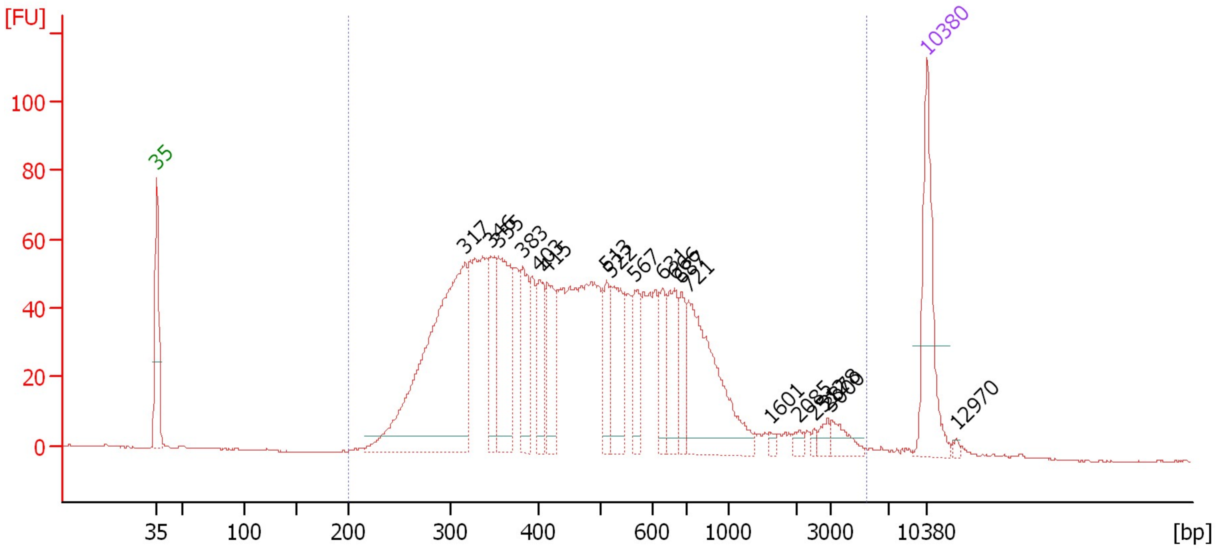
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	12,744	0.00	0.0		115.48

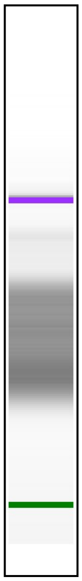
Region table for sample 3 : 3: Smad3 OE 2 lib (1:5)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	585	5,554	2,007.1	7,747.4	🟦	97	97.2	2,070.18

Electropherogram Summary Continued ...

4: Sox17 Endog (1:8) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 4 : **4: Sox17 Endog (1:8)**

Number of peaks found:	19	Corr. Area 1:	1,866.9
Noise:	0.2		

Peak table for sample 4 : **4: Sox17 Endog (1:8)**

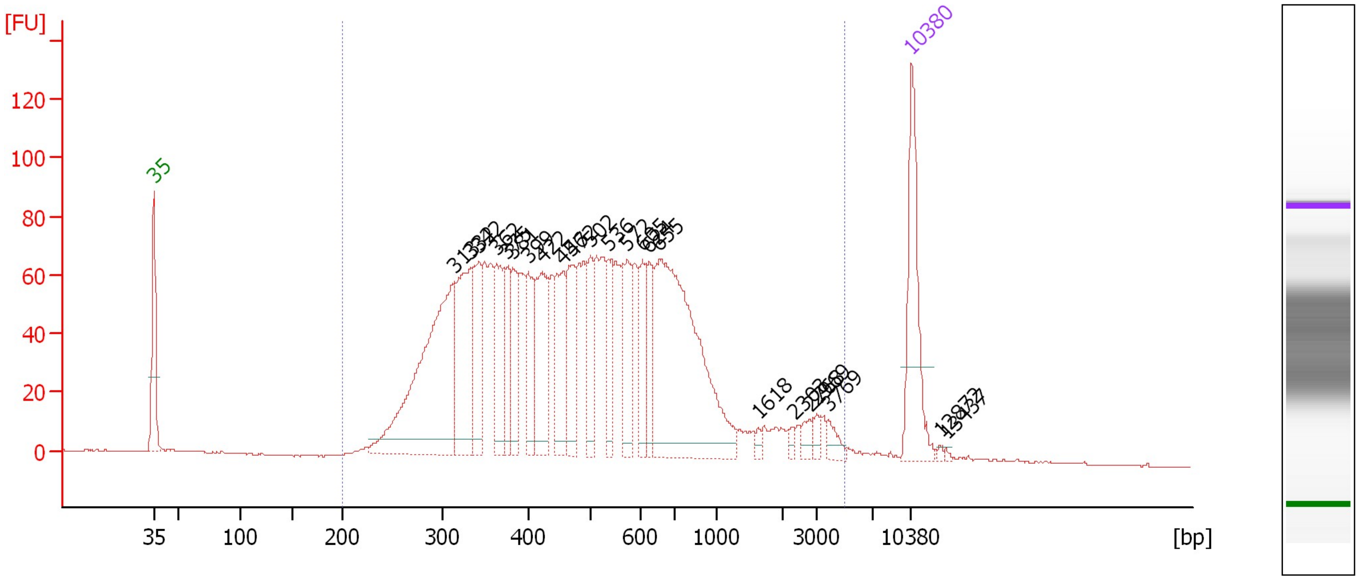
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		317	379.73	1,814.6		71.05
3		346	61.27	268.0		73.37
4		355	124.84	532.1		74.10
5		383	62.16	245.9		76.28
6		403	53.33	200.7		77.78
7		415	57.89	211.1		78.51
8		513	36.52	107.9		83.89
9		522	70.91	205.8		84.32
10		567	42.39	113.3		86.45
11		631	33.50	80.4		88.97
12		666	52.64	119.8		90.04
13		687	32.86	72.5		90.67
14		721	155.34	326.6		91.35
15		1,601	3.72	3.5		98.71
16		2,085	5.42	3.9		101.42
17		2,512	3.33	2.0		102.78
18		2,878	7.60	4.0		103.94
19		3,000	14.06	7.1		104.33
20	▶	10,380	75.00	10.9	Upper Marker	113.00
21		12,970	0.00	0.0		115.71

Region table for sample 4 : **4: Sox17 Endog (1:8)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	585	5,436	1,866.9	6,673.1	🟦	99	91.6	1,834.19

Electropherogram Summary Continued ...

5: Sox17 OE 1 (1:8) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]



Overall Results for sample 5 : **5: Sox17 OE 1 (1:8)**

Number of peaks found: 23

Corr. Area 1: 2,372.2

Noise: 0.2

Peak table for sample 5 : **5: Sox17 OE 1 (1:8)**

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		313	286.10	1,384.4		70.73
3		332	123.21	561.7		72.26
4		342	67.62	299.9		73.00
5		362	67.64	283.0		74.63
6		375	47.00	189.8		75.66
7		381	45.91	182.7		76.10
8		399	55.79	211.7		77.58
9		422	80.89	290.6		78.86
10		456	66.93	222.5		80.78
11		472	62.20	199.8		81.67
12		502	43.31	130.8		83.34
13		536	44.03	124.5		84.97
14		572	50.07	132.6		86.69
15		605	36.64	91.8		88.17
16		624	39.53	96.0		88.76
17		655	280.14	648.2		89.70
18		1,618	4.10	3.8		98.81
19		2,303	4.43	2.9		102.11
20		2,768	9.22	5.0		103.59
21		2,969	6.09	3.1		104.23
22		3,769	9.22	3.7		105.32
23	▶	10,380	75.00	10.9	Upper Marker	113.00
24		12,872	0.00	0.0		115.61
25		13,437	0.00	0.0		116.20

Electropherogram Summary Continued ...

... Region table for sample 5 : 5: Sox17 OE 1 (1:8)

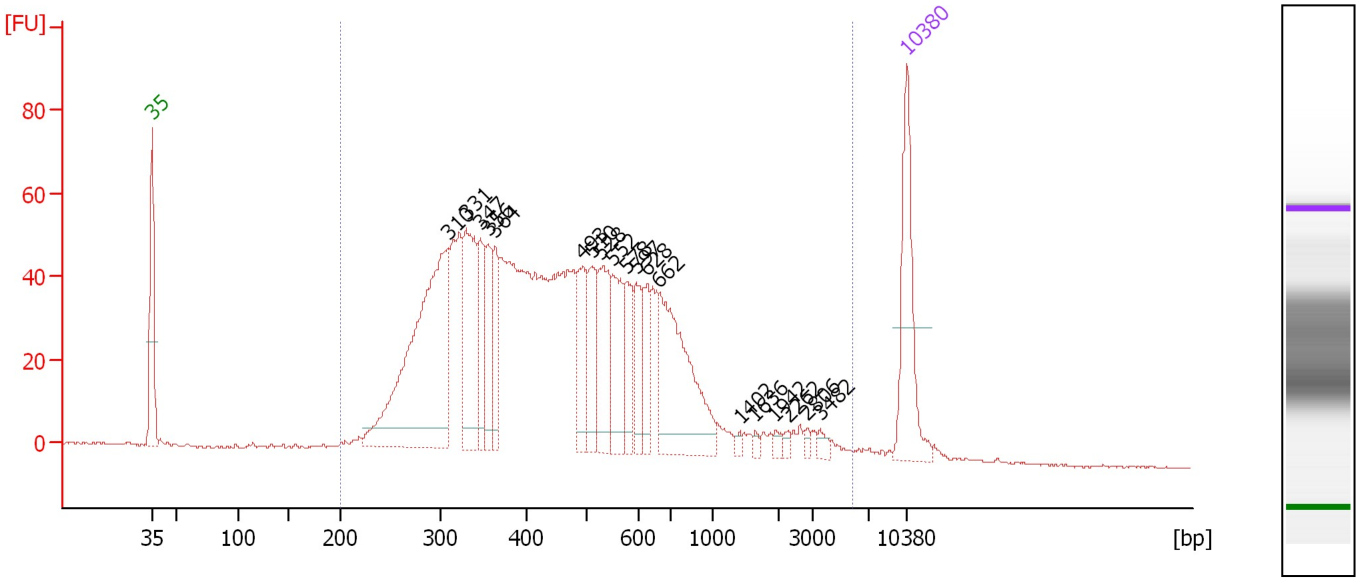
From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	621	4,999	2,372.2	6,730.4	🟦	98	91.4	1,922.31

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad

Created: 8/13/2015 9:47:01 AM
Modified: 8/13/2015 10:31:43 AM

Electropherogram Summary Continued ...

6: Sox17 OE 2 (1:2) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]



Overall Results for sample 6 : **6: Sox17 OE 2 (1:2)**

Number of peaks found:	19	Corr. Area 1:	1,656.8
Noise:	0.2		

Peak table for sample 6 : **6: Sox17 OE 2 (1:2)**

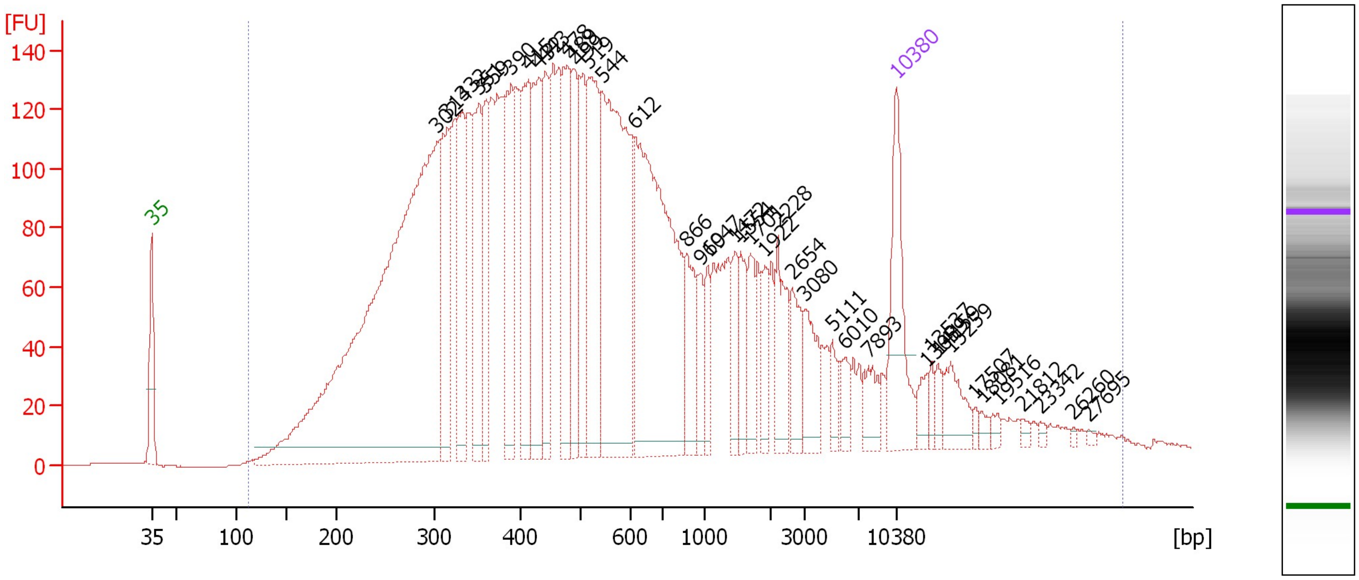
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		310	331.79	1,623.0		70.47
3		331	115.71	529.9		72.15
4		347	56.27	245.7		73.43
5		356	50.24	214.0		74.12
6		364	47.97	199.4		74.81
7		493	55.56	170.8		82.87
8		510	57.44	170.5		83.76
9		528	69.56	199.6		84.59
10		552	58.88	161.7		85.73
11		578	40.71	106.8		86.97
12		597	36.80	93.3		87.90
13		628	29.76	71.8		88.89
14		662	150.24	343.7		89.93
15		1,402	3.41	3.7		97.49
16		1,636	3.33	3.1		98.92
17		1,942	4.19	3.3		100.80
18		2,262	3.73	2.5		101.98
19		2,806	3.51	1.9		103.71
20		3,482	5.19	2.3		104.95
21	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : **6: Sox17 OE 2 (1:2)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	569	5,787	1,656.8	6,774.6	🟦	98	95.0	1,814.49

Electropherogram Summary Continued ...

7: H3K4m_1 lib (1:30) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]



Overall Results for sample 7 : **7: H3K4m_1 lib (1:30)**

Number of peaks found:	39	Corr. Area 1:	5,724.1
Noise:	0.2		

Peak table for sample 7 : **7: H3K4m_1 lib (1:30)**

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		302	954.52	4,787.6		69.86
3		314	125.34	604.7		70.81
4		332	113.54	518.6		72.21
5		351	116.29	501.6		73.77
6		359	83.98	354.6		74.37
7		390	118.42	460.4		76.82
8		415	116.20	424.3		78.48
9		432	121.58	426.6		79.43
10		443	85.70	293.5		80.03
11		478	109.17	346.0		82.03
12		489	77.41	240.0		82.63
13		499	81.41	247.0		83.24
14		519	144.97	422.9		84.19
15		544	299.23	834.1		85.34
16		612	325.55	806.0		88.40
17		866	54.88	96.0		93.26
18		969	26.43	41.3		94.61
19		1,047	26.14	37.8		95.31
20		1,472	26.38	27.1		97.92
21		1,554	31.20	30.4		98.42
22		1,701	30.23	26.9		99.32
23		1,922	24.37	19.2		100.67
24		2,228	45.32	30.8		101.88
25		2,654	33.45	19.1		103.23

Electropherogram Summary Continued ...

... Peak table for sample 7 : 7: H3K4m 1 lib (1:30)

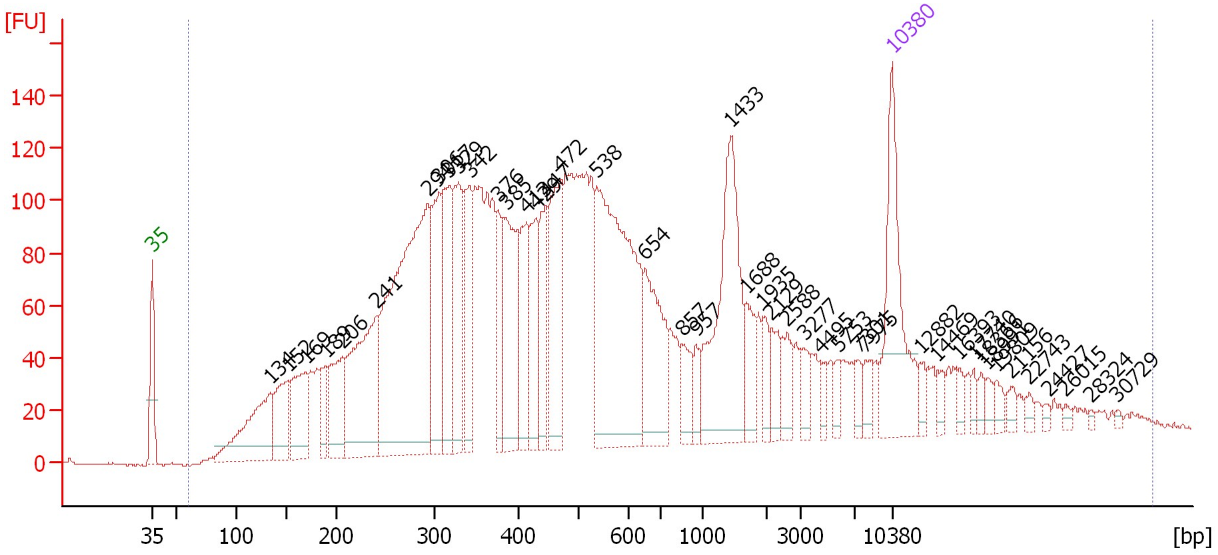
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	3,080	37.61	18.5		104.43
27	5,111	14.25	4.2		107.04
28	6,010	13.80	3.5		108.19
29	7,893	22.08	4.2		110.39
30	▶ 10,380	75.00	10.9	Upper Marker	113.00
31	13,059	0.00	0.0		115.81
32	13,537	0.00	0.0		116.31
33	14,159	0.00	0.0		116.96
34	15,259	0.00	0.0		118.11
35	17,507	0.00	0.0		120.47
36	18,081	0.00	0.0		121.07
37	19,516	0.00	0.0		122.57
38	21,812	0.00	0.0		124.98
39	23,342	0.00	0.0		126.58
40	26,260	0.00	0.0		129.64
41	27,695	0.00	0.0		131.14

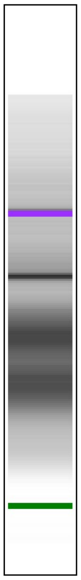
Region table for sample 7 : 7: H3K4m 1 lib (1:30)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
112	2,118	30,790	5,724.1	15,596.1	🟦	100	100.0	4,166.56

Electropherogram Summary Continued ...

8: H3K4m_2 lib (1:25) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 8 : **8: H3K4m_2 lib (1:25)**

Number of peaks found:	44	Corr. Area 1:	5,009.6
Noise:	0.5		

Peak table for sample 8 : **8: H3K4m_2 lib (1:25)**

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		134	104.98	1,186.8		54.19
3		152	57.03	568.4		55.90
4		169	64.41	577.1		57.51
5		189	28.72	229.8		59.43
6		206	61.44	451.8		60.99
7		241	142.56	896.8		64.22
8		294	333.87	1,722.6		69.11
9		306	84.52	418.6		70.16
10		317	85.54	408.4		71.07
11		329	79.47	365.5		72.03
12		342	64.26	284.6		73.04
13		376	43.45	175.2		75.71
14		385	84.05	330.6		76.46
15		413	53.27	195.4		78.38
16		429	53.54	189.0		79.29
17		447	48.85	165.5		80.29
18		472	91.50	293.6		81.70
19		538	233.74	658.2		85.08
20		654	75.34	174.6		89.67
21		857	21.66	38.3		93.14
22		957	12.21	19.3		94.45
23		1,433	120.52	127.4		97.68
24		1,688	22.19	19.9		99.24
25		1,935	14.62	11.4		100.75

Electropherogram Summary Continued ...

... Peak table for sample 8 : 8: H3K4m 2 lib (1:25)

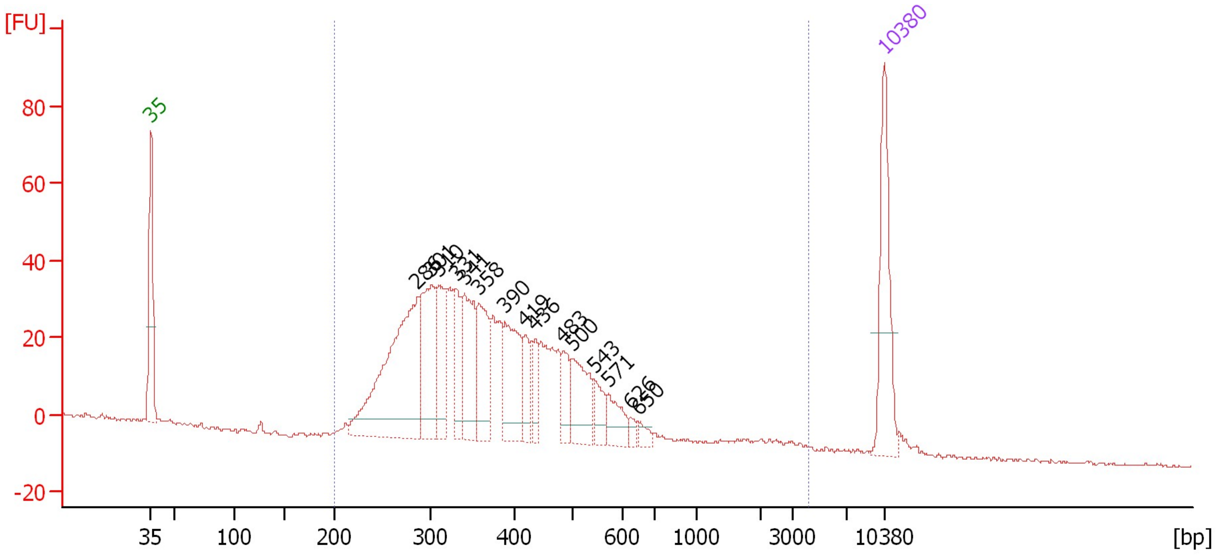
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		2,129	16.28	11.6		101.56
27		2,588	16.57	9.7		103.02
28		3,277	12.45	5.8		104.68
29		4,495	7.24	2.4		106.25
30		5,753	8.47	2.2		107.86
31		7,301	9.21	1.9		109.77
32		7,975	9.58	1.8		110.48
33	▶	10,380	75.00	10.9	Upper Marker	113.00
34		12,882	0.00	0.0		115.62
35		14,469	0.00	0.0		117.28
36		16,393	0.00	0.0		119.30
37		17,740	0.00	0.0		120.71
38		18,366	0.00	0.0		121.37
39		18,991	0.00	0.0		122.02
40		19,809	0.00	0.0		122.88
41		21,156	0.00	0.0		124.29
42		22,743	0.00	0.0		125.95
43		24,427	0.00	0.0		127.72
44		26,015	0.00	0.0		129.38
45		28,324	0.00	0.0		131.80
46		30,729	0.00	0.0		134.32

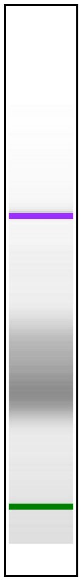
Region table for sample 8 : 8: H3K4m 2 lib (1:25)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
61	2,872	33,919	5,009.6	11,626.6	🟦	100	100.0	2,645.46

Electropherogram Summary Continued ...

9: IgG Rabbit 1 lib (1:2) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 9 : 9: IgG Rabbit 1 lib (1:2)

Number of peaks found:	15	Corr. Area 1:	902.4
Noise:	0.4		

Peak table for sample 9 : 9: IgG Rabbit 1 lib (1:2)

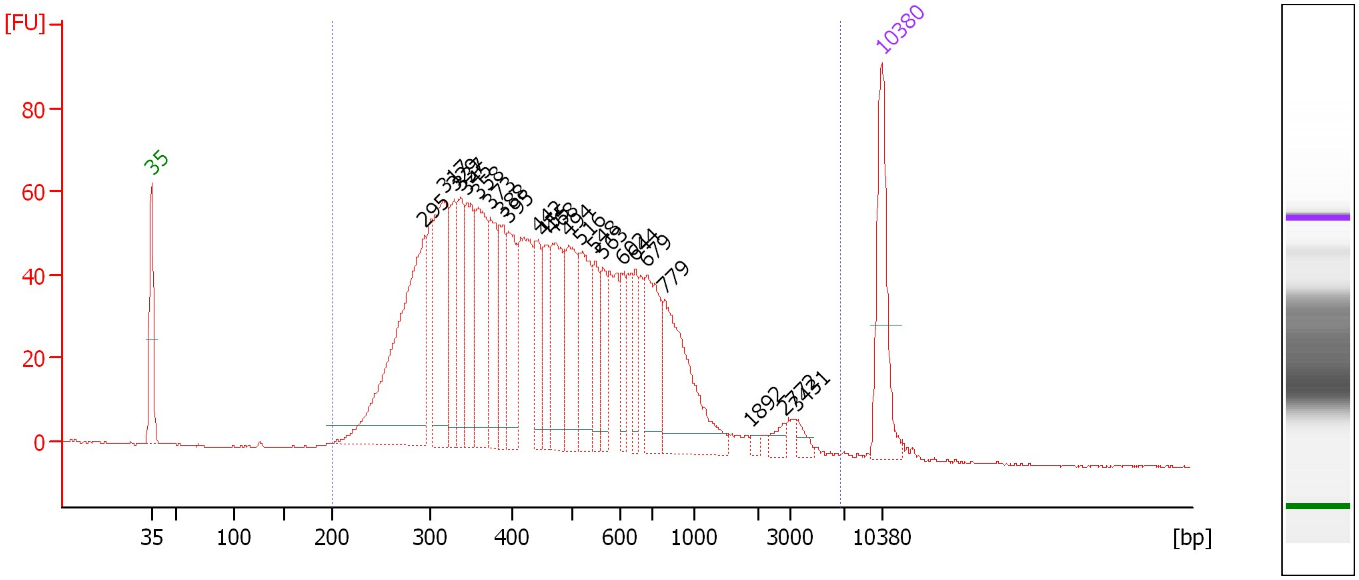
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		286	250.51	1,325.1		68.44
3		301	106.46	536.2		69.76
4		310	66.04	323.0		70.47
5		331	50.82	232.7		72.15
6		341	87.82	390.0		72.96
7		358	70.61	299.0		74.29
8		390	78.82	306.4		76.83
9		419	28.33	102.4		78.71
10		436	25.13	87.3		79.68
11		483	28.11	88.1		82.32
12		500	58.43	177.2		83.24
13		543	23.49	65.5		85.33
14		571	27.45	72.8		86.65
15		626	5.89	14.2		88.84
16		650	8.34	19.5		89.55
17	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : 9: IgG Rabbit 1 lib (1:2)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	418	4,152	902.4	4,667.7	■ 99	69.7	1,079.17

Electropherogram Summary Continued ...

10: IgG Rabbit 2 (1:2) [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]



Overall Results for sample 10 : 10: IgG Rabbit 2 (1:2)

Number of peaks found: 23
Corr. Area 1: 1,902.8
Noise: 0.2

Peak table for sample 10 : 10: IgG Rabbit 2 (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		295	305.19	1,566.7		69.24
3		317	146.26	699.4		71.03
4		329	75.39	347.2		72.00
5		337	74.66	335.9		72.61
6		345	86.27	378.8		73.28
7		358	113.37	479.9		74.30
8		373	71.25	289.1		75.52
9		388	63.67	248.9		76.65
10		395	75.42	289.6		77.21
11		442	56.09	192.2		80.02
12		455	48.02	159.9		80.73
13		468	88.01	285.1		81.45
14		494	85.32	261.7		82.93
15		516	76.52	224.5		84.05
16		548	39.26	108.7		85.53
17		563	37.42	100.8		86.25
18		602	32.17	81.0		88.08
19		644	32.78	77.2		89.36
20		679	80.47	179.6		90.43
21		779	128.10	249.1		92.12
22		1,892	4.15	3.3		100.49
23		2,772	8.53	4.7		103.61
24		3,431	7.93	3.5		104.88
25	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad
Created: 8/13/2015 9:47:01 AM
Modified: 8/13/2015 10:31:43 AM

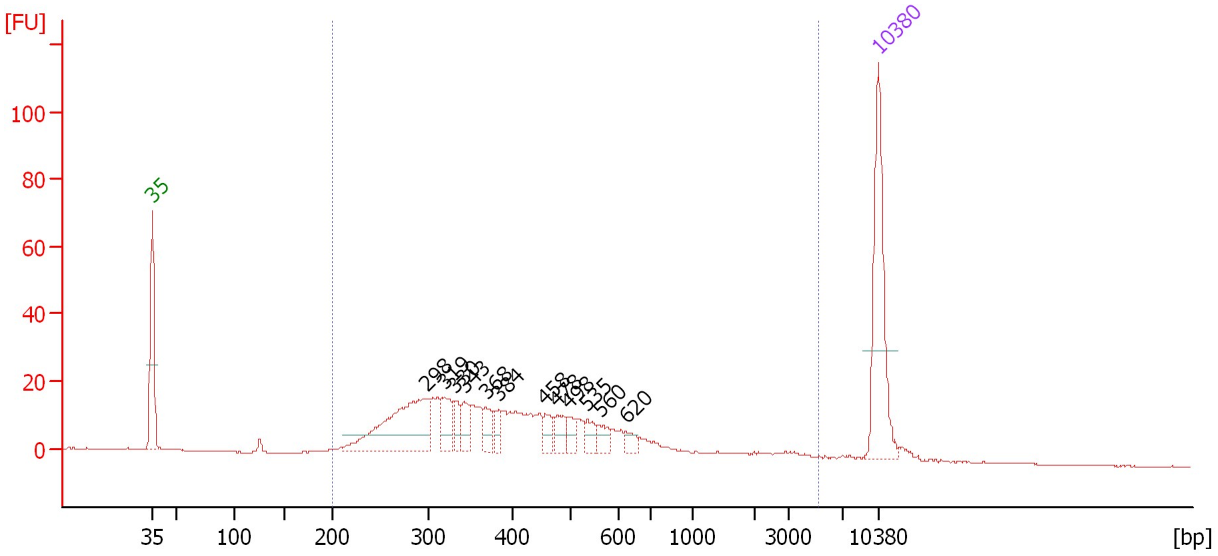
Electropherogram Summary Continued ...

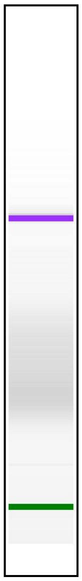
... Region table for sample 10 : **10: IgG Rabbit 2 (1:2)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	560	6,674	1,902.8	7,884.4	🟦 100	92.5	2,096.00

Electropherogram Summary Continued ...

11: IgG Goat 1 lib [HiSeq_176: Size Selected Lib (0.55X Right/0.8X Left)]





Overall Results for sample 11 : **11: IgG Goat 1 lib**

Number of peaks found:	12	Corr. Area 1:	487.2
Noise:	0.2		

Peak table for sample 11 : **11: IgG Goat 1 lib**

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		298	118.59	603.8		69.47
3		319	26.17	124.5		71.16
4		330	15.27	70.1		72.09
5		343	18.56	82.0		73.12
6		368	14.77	60.8		75.12
7		384	10.49	41.4		76.36
8		458	10.59	35.1		80.88
9		478	13.91	44.1		82.01
10		498	9.69	29.5		83.14
11		535	10.48	29.7		84.94
12		560	11.14	30.1		86.12
13		620	7.51	18.4		88.64
14	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : **11: IgG Goat 1 lib**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	529	5,220	487.2	1,961.2	■	96	100.0	474.58

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-13\2015-08-13_001.xad

Created: 8/13/2015 9:47:01 AM
Modified: 8/13/2015 10:31:43 AM

Gel Image