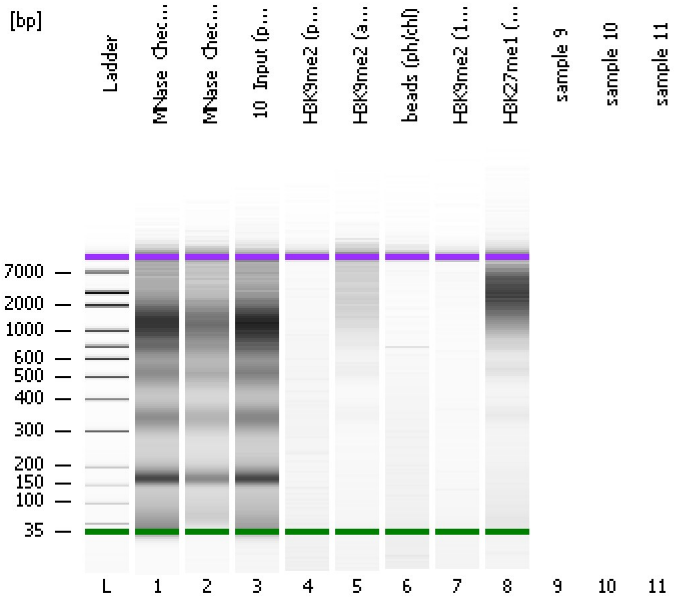
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-02-13\2015-02-13_002.xad
Created: 2/13/2015 3:23:10 PM
Modified: 2/18/2015 9:54:22 AM

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:

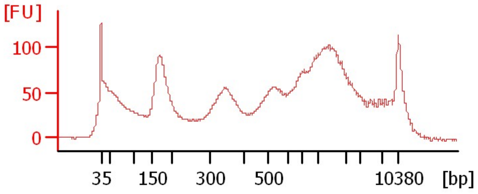
Chip Information:

Chip Lot #:

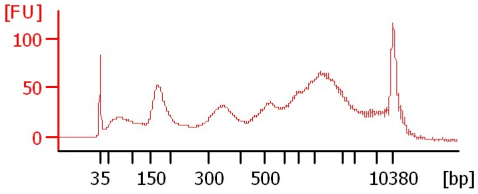
Reagent Kit Lot #:

Chip Comments:

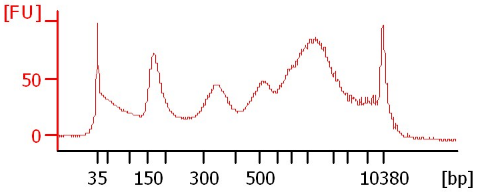
MNase_Check (ph/chl)



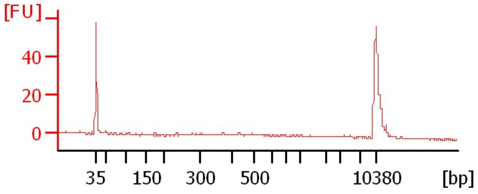
MNase_Check (ampure)



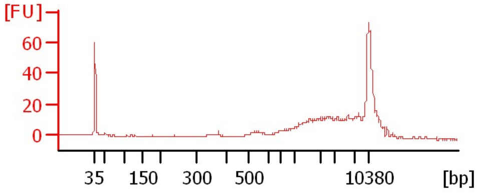
10_Input (ph/chl)



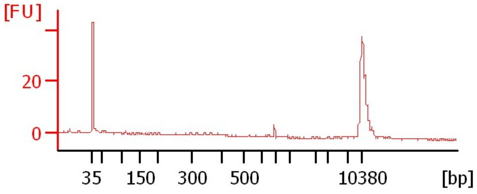
H3K9me2 (ph/chl)



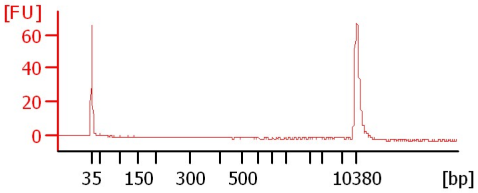
H3K9me2 (ampure)



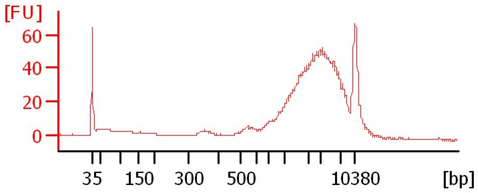
beads (ph/chl)



H3K9me2 (1/31/15)



H3K27me1 (1/31/15)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-02-13\2015-02-13_002.xad

Created: 2/13/2015 3:23:10 PM
Modified: 2/18/2015 9:54:22 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
MNase_Check (ph/chl)		☐	✓			
MNase_Check (ampure)		☐	✓			
10_Input (ph/chl)		☐	✓			
H3K9me2 (ph/chl)		☐	✓			
H3K9me2 (ampure)		☐	✓			
beads (ph/chl)		☐	✓			
H3K9me2 (1/31/15)		☐	✓			
H3K27me1 (1/31/15)		☐	✓			
sample 9		☐				
sample 10		☐				
sample 11		☐				
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

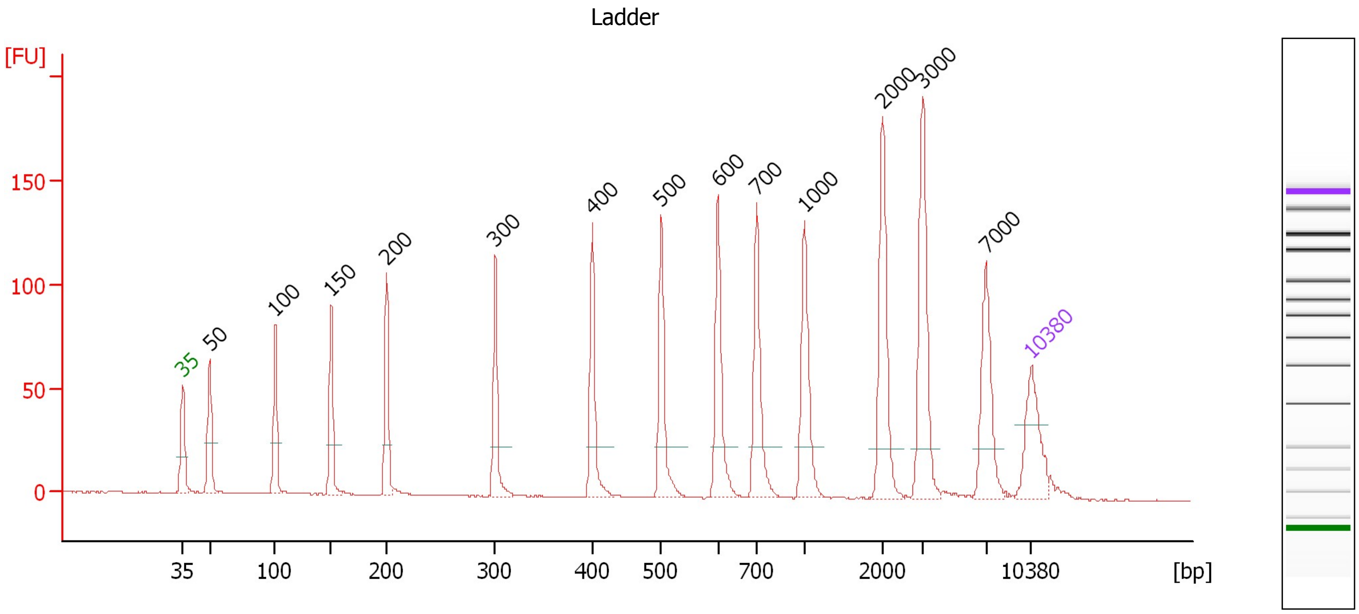
Filter Settings

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

Electropherogram Summary



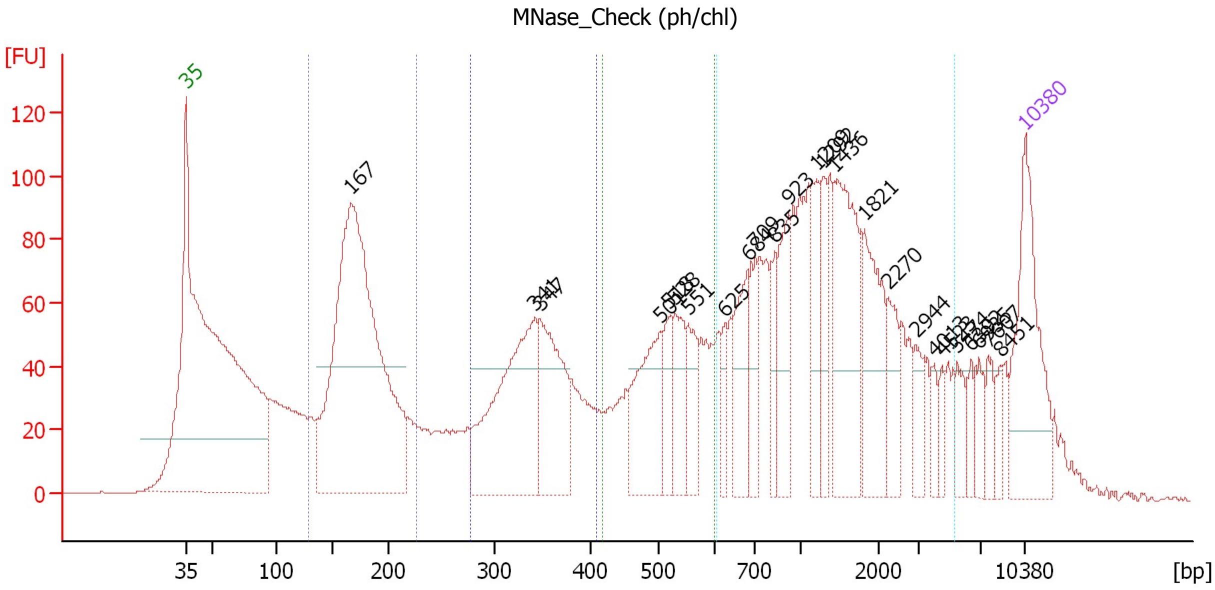
Overall Results for Ladder

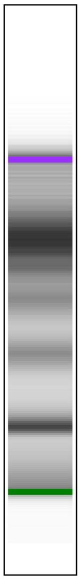
Noise: 0.2

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	45.20
3	∟	100	150.00	2,272.7	Ladder Peak	50.61
4	∟	150	150.00	1,515.2	Ladder Peak	55.22
5	∟	200	150.00	1,136.4	Ladder Peak	59.80
6	∟	300	150.00	757.6	Ladder Peak	68.77
7	∟	400	150.00	568.2	Ladder Peak	76.77
8	∟	500	150.00	454.5	Ladder Peak	82.48
9	∟	600	150.00	378.8	Ladder Peak	87.15
10	∟	700	150.00	324.7	Ladder Peak	90.36
11	∟	1,000	150.00	227.3	Ladder Peak	94.27
12	∟	2,000	150.00	113.6	Ladder Peak	100.73
13	∟	3,000	150.00	75.8	Ladder Peak	104.03
14	∟	7,000	150.00	32.5	Ladder Peak	109.26
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...





Setpoint Deviations for sample 1 : MNase_Check (ph/chl)

Height Threshold [FU] : 40

Overall Results for sample 1 : MNase_Check (ph/chl)

Number of peaks found:	25	Corr. Area 2:	597.4
Noise:	0.3	Corr. Area 3:	519.7
Corr. Area 1:	805.6	Corr. Area 4:	1,527.0

Peak table for sample 1 : MNase_Check (ph/chl)

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		167	498.93	4,526.8		56.78
3		341	164.33	729.7		72.07
4		347	99.89	436.4		72.51
5		501	77.12	233.4		82.51
6		518	27.02	79.1		83.31
7		528	37.59	107.8		83.80
8		551	32.18	88.5		84.87
9		625	16.75	40.6		87.93
10		684	44.92	99.5		89.84
11		709	31.70	67.8		90.47
12		835	21.89	39.7		92.11
13		923	46.19	75.8		93.27
14		1,209	31.22	39.1		95.62
15		1,292	29.01	34.0		96.16
16		1,436	90.05	95.0		97.09
17		1,821	57.66	48.0		99.58
18		2,270	25.04	16.7		101.62
19		2,944	15.86	8.2		103.84
20		4,013	8.47	3.2		105.36
21		4,523	9.01	3.0		106.02

Electropherogram Summary Continued ...

... Peak table for sample 1 : MNase Check (ph/chl)

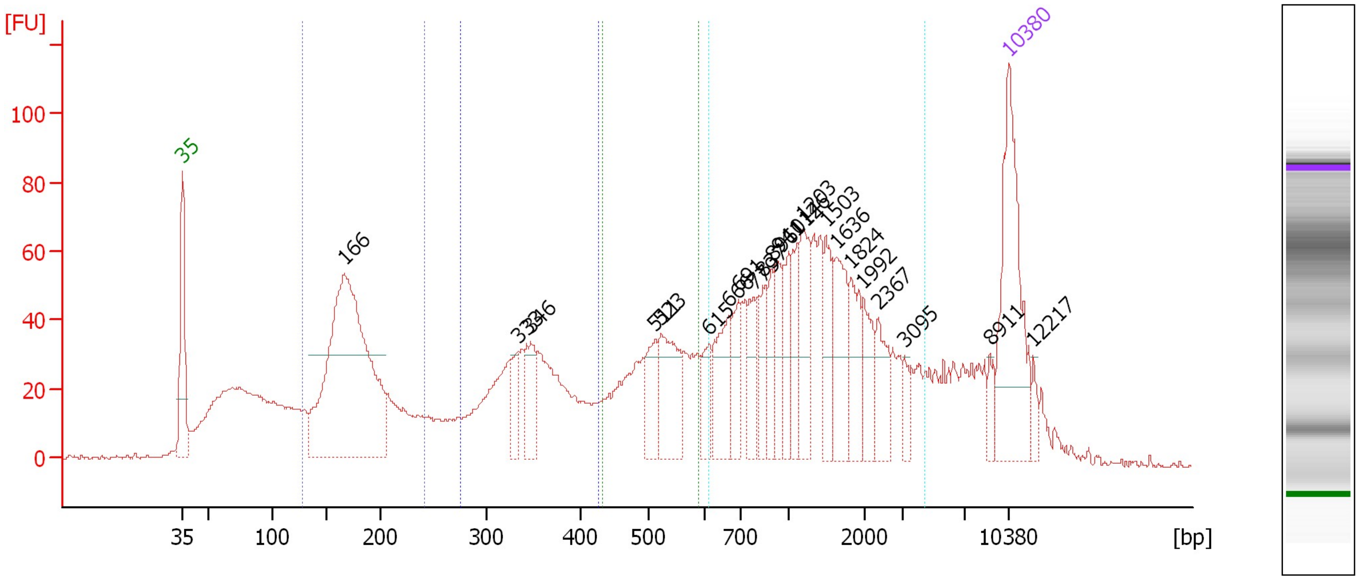
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
22	5,474	13.88	3.8		107.27
23	6,392	9.68	2.3		108.47
24	6,935	12.91	2.8		109.18
25	7,607	11.03	2.2		109.93
26	8,451	8.67	1.6		110.87
27 ▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : MNase Check (ph/chl)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
128	174	227	805.6	20	13.0	528.91	4,685.5	🟦
277	342	408	597.4	15	9.7	318.61	1,423.7	🟦
417	511	597	519.7	13	9.6	251.21	753.0	🟩
603	1,587	5,317	1,527.0	38	62.5	623.59	831.0	🟦

Electropherogram Summary Continued ...

MNase_Check (ampure)



Setpoint Deviations for sample 2 : MNase_Check (ampure)

Height Threshold [FU] : 30

Overall Results for sample 2 : MNase_Check (ampure)

Number of peaks found:	23	Corr. Area 2:	395.3
Noise:	0.7	Corr. Area 3:	302.5
Corr. Area 1:	505.4	Corr. Area 4:	953.6

Peak table for sample 2 : MNase_Check (ampure)

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		166	313.36	2,853.9		56.72
3		333	20.20	92.0		71.39
4		346	31.59	138.2		72.47
5		511	25.59	75.9		82.99
6		523	48.70	141.0		83.57
7		615	17.30	42.6		87.64
8		666	38.46	87.5		89.26
9		691	23.96	52.5		90.07
10		779	20.28	39.5		91.38
11		837	18.28	33.1		92.15
12		896	17.71	29.9		92.92
13		941	22.52	36.3		93.50
14		1,014	19.60	29.3		94.36
15		1,126	18.69	25.1		95.08
16		1,203	34.54	43.5		95.58
17		1,503	24.05	24.2		97.52
18		1,636	36.02	33.4		98.38
19		1,824	24.35	20.2		99.60
20		1,992	21.03	16.0		100.68
21		2,367	20.45	13.1		101.94

Electropherogram Summary Continued ...

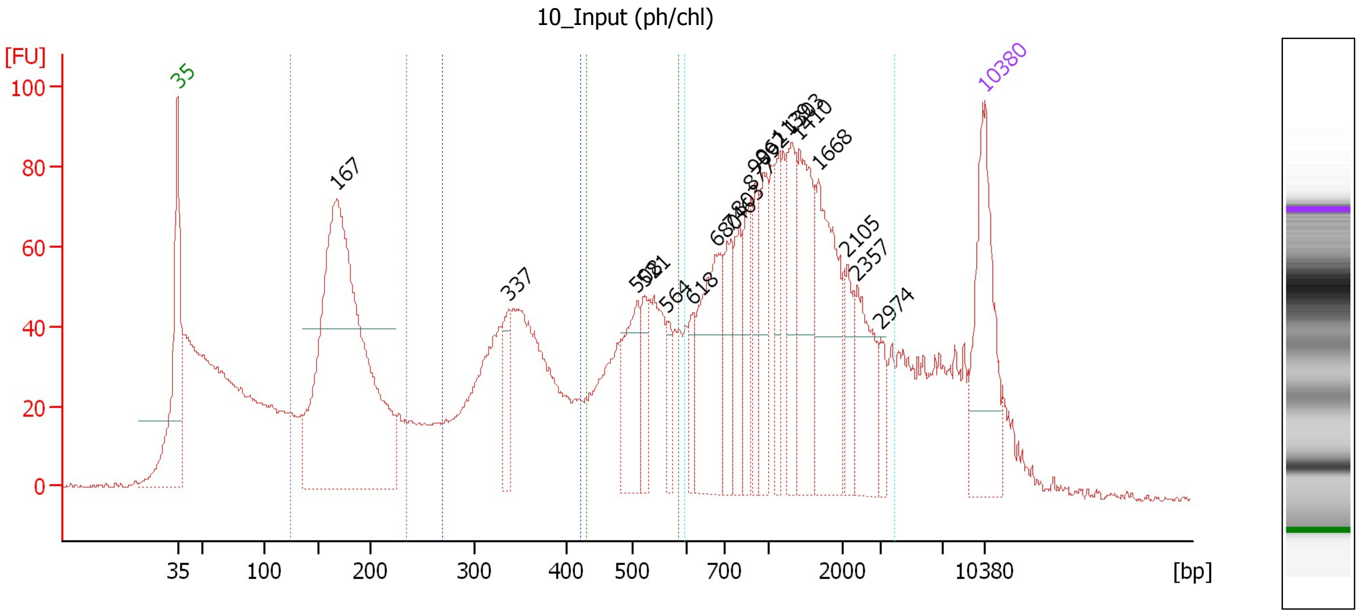
... Peak table for sample 2 : MNase Check (ampure)

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
22		3,095	8.14	4.0		104.15
23		8,911	6.97	1.2		111.38
24	🔒	10,380	75.00	10.9	Upper Marker	113.00
25		12,217	0.00	0.0		115.03

Region table for sample 2 : MNase Check (ampure)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
128	178	242	505.4	18	14.9	383.58	3,346.0	🟪
276	347	427	395.3	14	10.8	243.84	1,077.9	🟦
432	513	591	302.5	11	8.6	169.91	505.8	🟩
611	1,485	4,370	953.6	34	53.9	453.01	610.7	🟦

Electropherogram Summary Continued ...



Setpoint Deviations for sample 3 : 10_Input (ph/chl)

Height Threshold [FU] : 40

Overall Results for sample 3 : 10_Input (ph/chl)

Number of peaks found:	19	Corr. Area 2:	542.7
Noise:	0.3	Corr. Area 3:	384.6
Corr. Area 1:	662.2	Corr. Area 4:	1,242.9

Peak table for sample 3 : 10_Input (ph/chl)

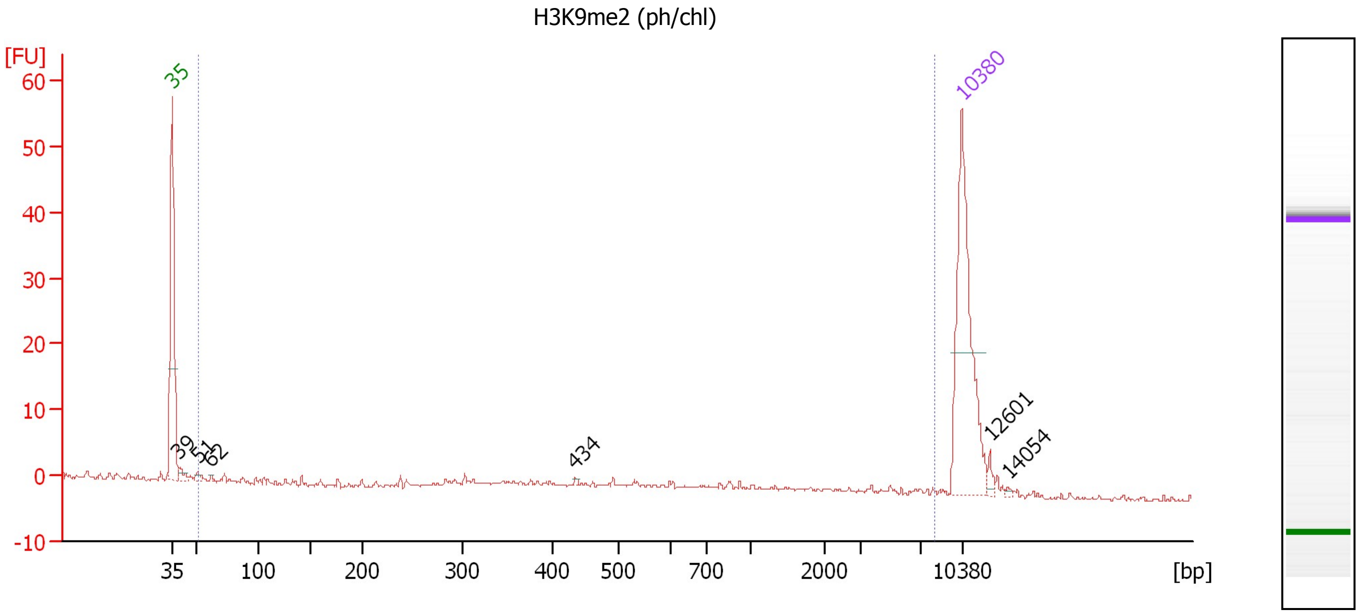
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		167	530.35	4,814.7		56.77
3		337	37.91	170.7		71.69
4		508	63.01	187.8		82.87
5		521	23.39	68.0		83.48
6		564	18.90	50.8		85.46
7		618	21.83	53.5		87.73
8		680	92.82	206.8		89.71
9		746	38.09	77.3		90.96
10		803	34.40	64.9		91.70
11		877	35.77	61.8		92.67
12		909	28.84	48.0		93.09
13		962	35.90	56.5		93.78
14		1,139	31.94	42.5		95.17
15		1,303	45.38	52.8		96.23
16		1,410	71.60	76.9		96.92
17		1,668	85.72	77.9		98.58
18		2,105	24.97	18.0		101.08
19		2,357	44.97	28.9		101.91
20		2,974	14.99	7.6		103.94
21	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Region table for sample 3 : 10 Input (ph/chl)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
124	176	235	662.2	18	14.5	573.97	5,080.7	🟪
269	343	422	542.7	14	11.0	382.48	1,711.6	🟦
431	509	583	384.6	10	8.2	246.61	739.8	🟩
594	1,395	3,836	1,242.9	33	50.6	675.81	951.4	🟦

Electropherogram Summary Continued ...



Setpoint Deviations for sample 4 : H3K9me2 (ph/chl)

Height Threshold [FU] : 1

Overall Results for sample 4 : H3K9me2 (ph/chl)

Number of peaks found:	6	Corr. Area 1:	37.0
Noise:	0.2		

Peak table for sample 4 : H3K9me2 (ph/chl)

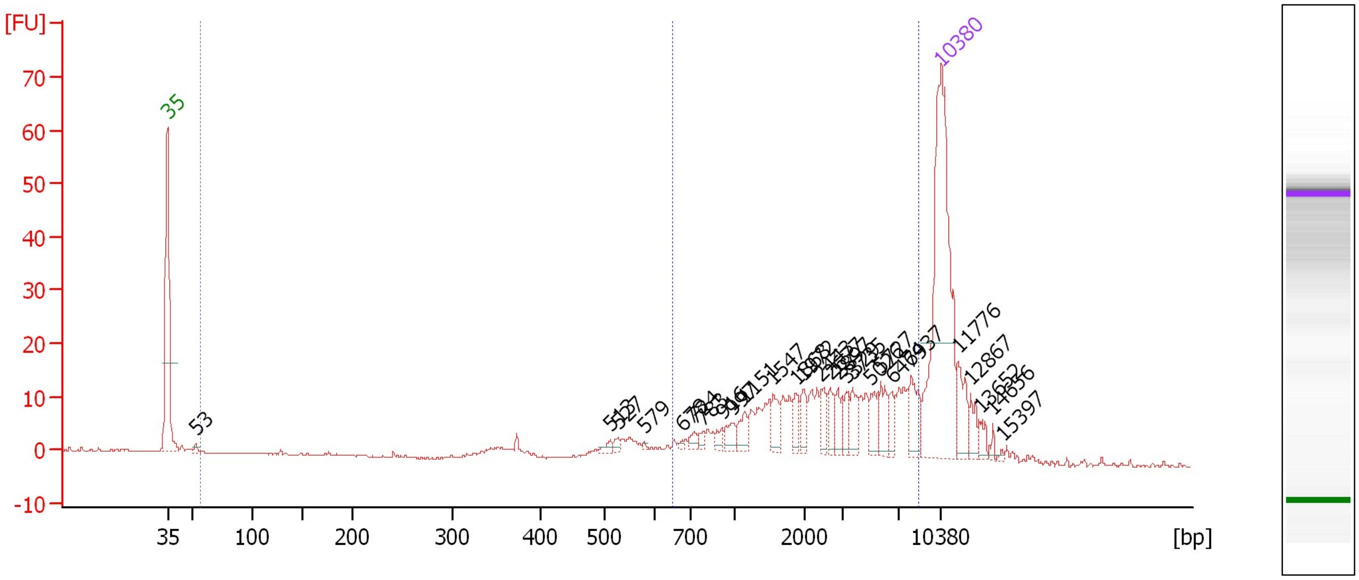
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		39	6.18	240.9		43.57
3		51	3.17	94.9		45.27
4		62	1.46	36.0		46.45
5		434	0.82	2.9		78.71
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		12,601	0.00	0.0		115.46
8		14,054	0.00	0.0		117.06

Region table for sample 4 : H3K9me2 (ph/chl)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
51	1,307	8,170	37.0	67	100.0	53.56	305.2	■

Electropherogram Summary Continued ...

H3K9me2 (ampure)



Setpoint Deviations for sample 5 : H3K9me2 (ampure)

Height Threshold [FU] :	1

Overall Results for sample 5 : H3K9me2 (ampure)

Number of peaks found:	27	Corr. Area 1:	35.6
Noise:	0.2	Corr. Area 2:	224.5

Peak table for sample 5 : H3K9me2 (ampure)

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		53	1.65	47.0		45.56
3		513	2.25	6.6		83.09
4		527	1.66	4.8		83.76
5		579	0.52	1.4		86.18
6		678	0.98	2.2		89.65
7		724	2.38	5.0		90.66
8		783	2.02	3.9		91.44
9		916	2.33	3.9		93.17
10		997	4.45	6.8		94.23
11		1,151	5.04	6.6		95.25
12		1,547	6.14	6.0		97.80
13		1,868	4.73	3.8		99.88
14		1,972	5.24	4.0		100.55
15		2,443	5.11	3.2		102.19
16		2,677	4.97	2.8		102.97
17		2,897	4.72	2.5		103.69
18		3,329	5.10	2.3		104.46
19		3,735	5.90	2.4		104.99
20		5,026	6.20	1.9		106.68
21		5,727	7.80	2.1		107.60
22		6,464	4.82	1.1		108.56

Electropherogram Summary Continued ...

... Peak table for sample 5 : H3K9me2 (ampure)

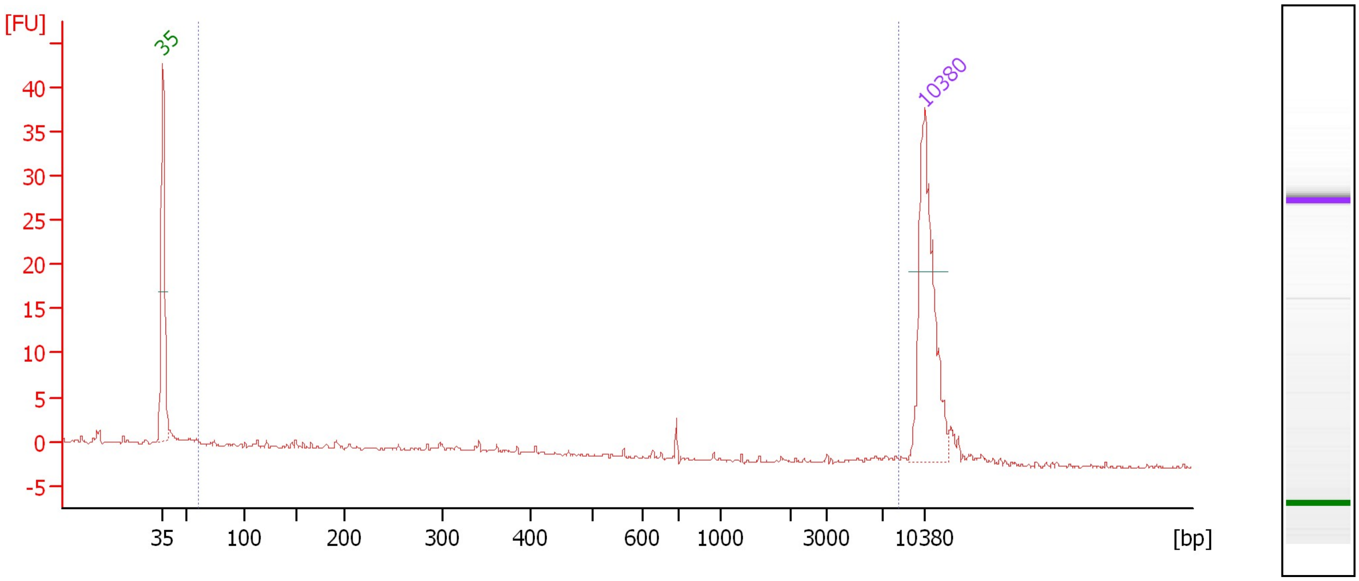
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
23		7,937	10.48	2.0		110.30
24	▶	10,380	75.00	10.9	Upper Marker	113.00
25		11,776	0.00	0.0		114.54
26		12,867	0.00	0.0		115.75
27		13,652	0.00	0.0		116.62
28		14,656	0.00	0.0		117.73
29		15,397	0.00	0.0		118.55

Region table for sample 5 : H3K9me2 (ampure)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
58	483	647	35.6	12	24.2	33.21	139.5	🟦
647	3,311	8,533	224.5	73	68.8	161.66	128.6	🟦

Electropherogram Summary Continued ...

beads (ph/chl)



Overall Results for sample 6 : beads (ph/chl)

Number of peaks found:	0	Corr. Area 1:	5.4
Noise:	0.1		

Peak table for sample 6 : beads (ph/chl)

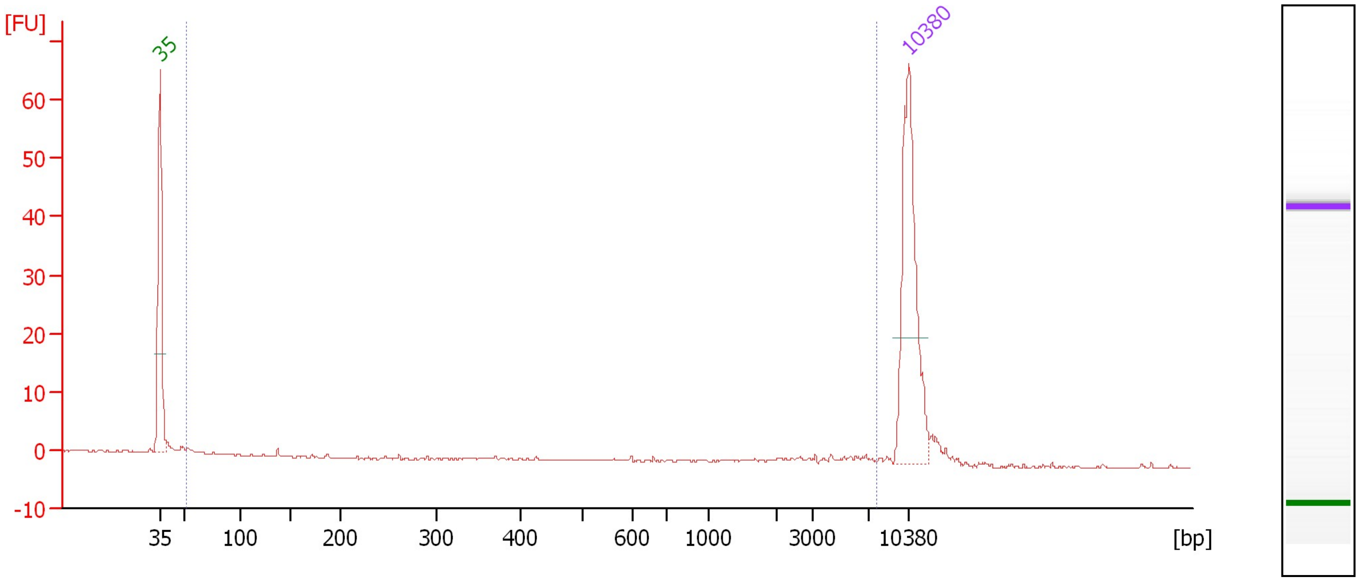
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : beads (ph/chl)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
60	1,050	8,275	5.4	34	100.0	11.67	84.5	🟦

Electropherogram Summary Continued ...

H3K9me2 (1/31/15)



Overall Results for sample 7 : **H3K9me2 (1/31/15)**

Number of peaks found:	0	Corr. Area 1:	5.7
Noise:	0.1		

Peak table for sample 7 : **H3K9me2 (1/31/15)**

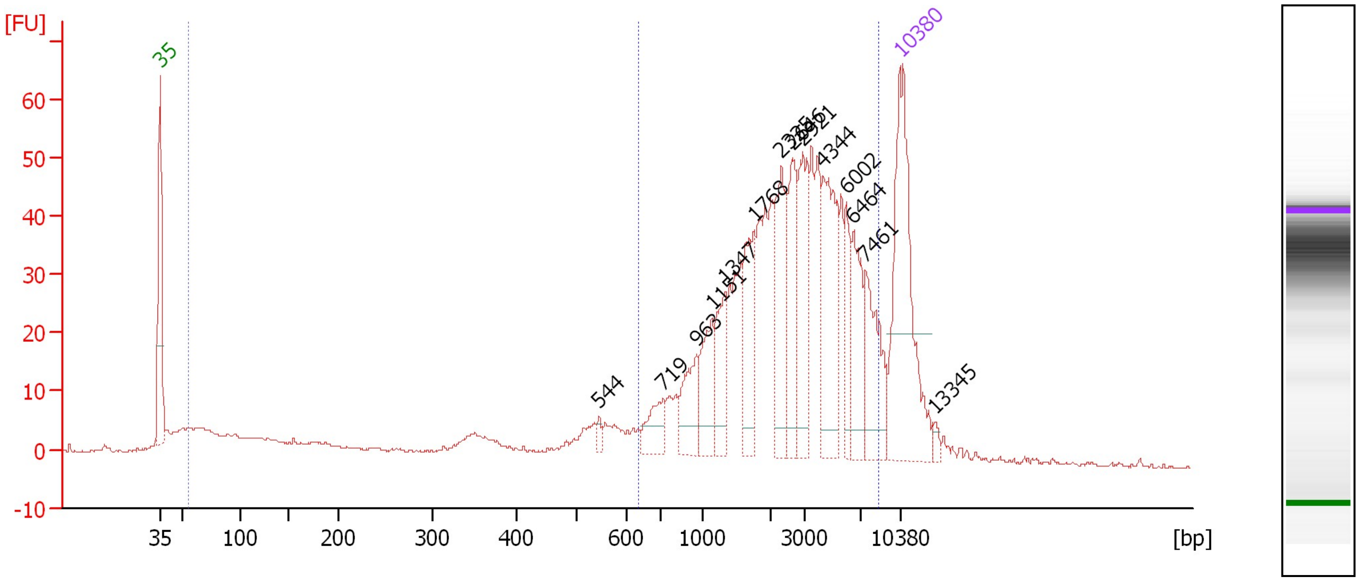
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **H3K9me2 (1/31/15)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
53	4,056	7,695	5.7	35	50.9	5.48	26.3	🟦

Electropherogram Summary Continued ...

H3K27me1 (1/31/15)



Overall Results for sample 8 : H3K27me1 (1/31/15)

Number of peaks found:	14	Corr. Area 1:	176.1
Noise:	0.2	Corr. Area 2:	720.1

Peak table for sample 8 : H3K27me1 (1/31/15)

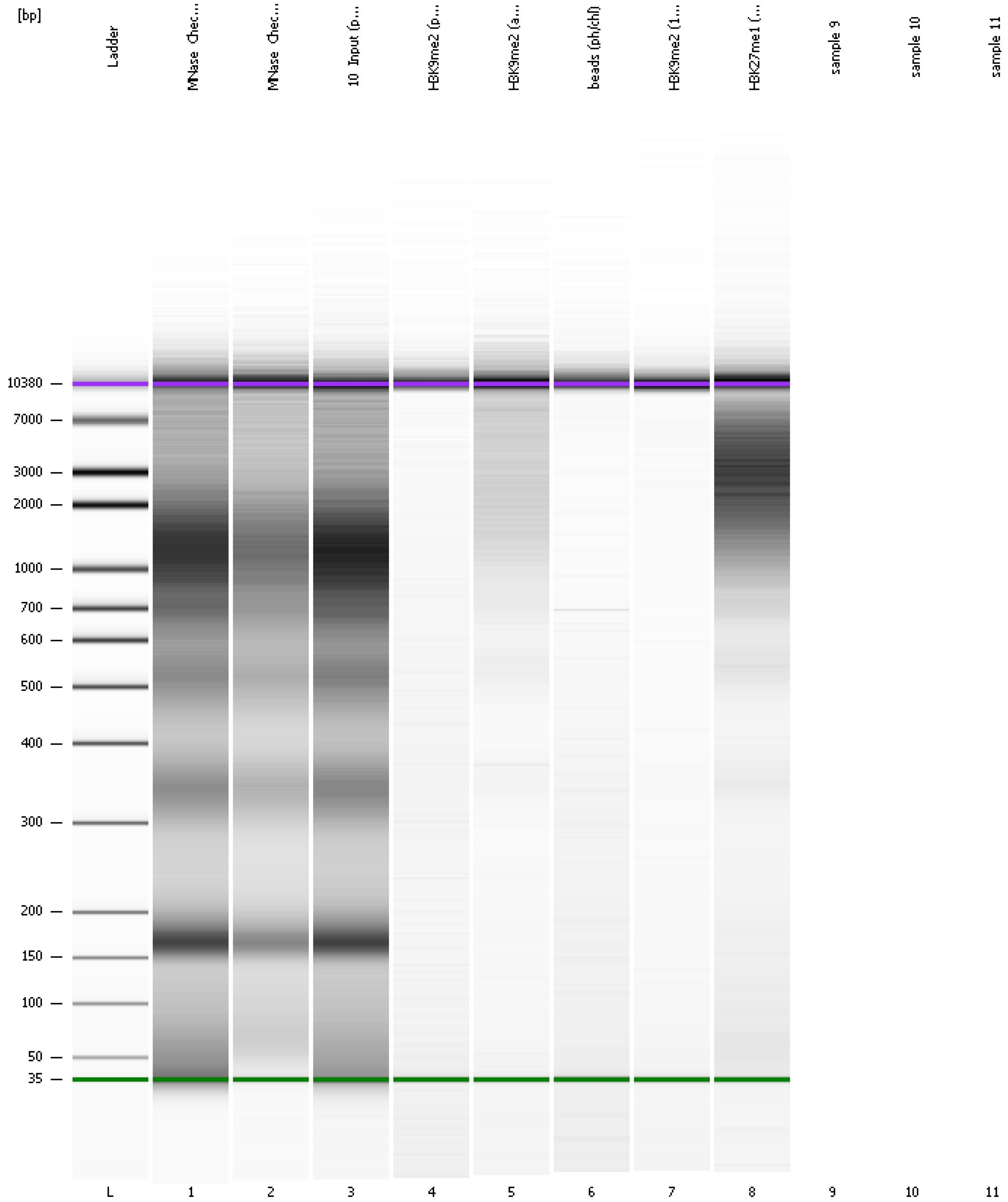
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		544	3.51	9.8		84.56
3		719	15.67	33.0		90.61
4		963	22.40	35.2		93.79
5		1,151	22.98	30.2		95.25
6		1,347	23.61	26.6		96.51
7		1,768	31.19	26.7		99.23
8		2,325	34.34	22.4		101.80
9		2,646	30.99	17.7		102.86
10		2,921	35.04	18.2		103.77
11		4,344	49.87	17.4		105.79
12		6,002	17.28	4.4		107.96
13		6,464	27.52	6.5		108.56
14		7,461	33.79	6.9		109.77
15	▶	10,380	75.00	10.9	Upper Marker	113.00
16		13,345	0.00	0.0		116.28

Region table for sample 8 : H3K27me1 (1/31/15)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
54	324	636	176.1	18	58.1	193.54	1,992.5	🟦
636	3,222	8,617	720.1	75	63.9	505.41	380.1	🟦

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-02-13\2015-02-13_002.xad
Created: 2/13/2015 3:23:10 PM
Modified: 2/18/2015 9:54:22 AM

Gel Image



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.

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		2/13/2015 3:55:55 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-02-13\2015-02-13_002.xad)		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		2/13/2015 3:23:15 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1