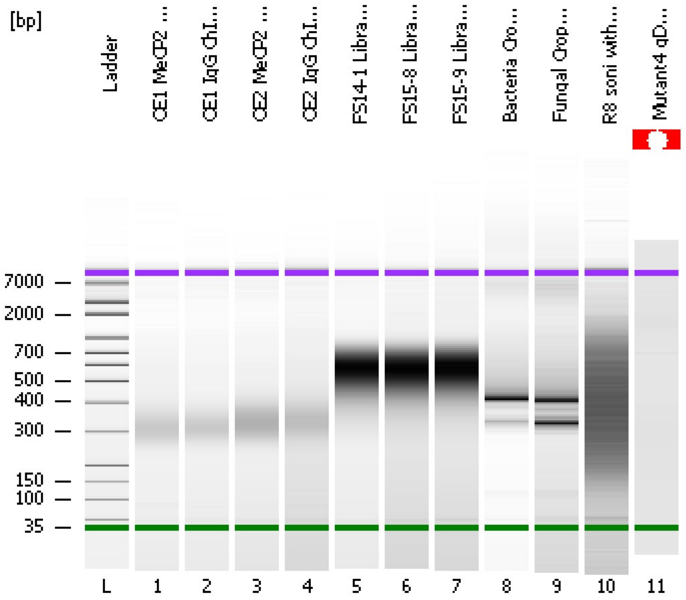
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad

Created: 2/24/2016 2:47:21 PM
Modified: 2/24/2016 3:43:43 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

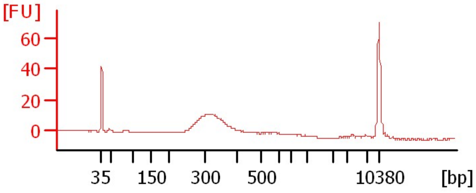
Chip Information:

Chip Lot #:

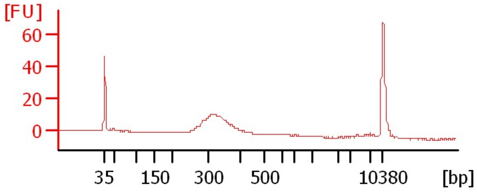
Reagent Kit Lot #:

Chip Comments:

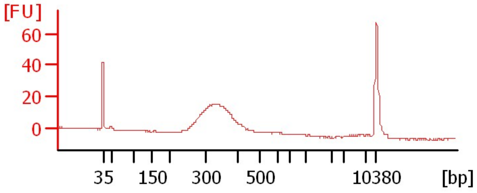
OE1 MeCP2 ChIP-seq



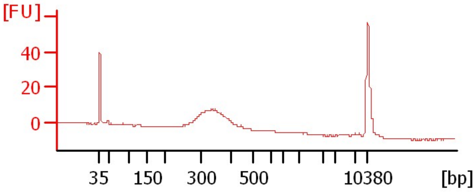
OE1 IgG ChIP-seq



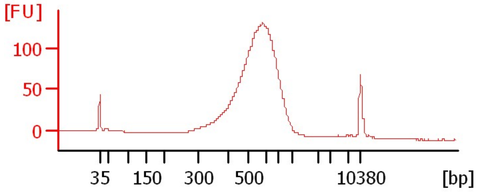
OE2 MeCP2 ChIP-seq



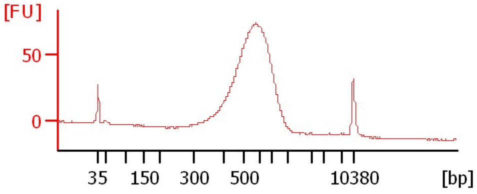
OE2 IgG ChIP-seq



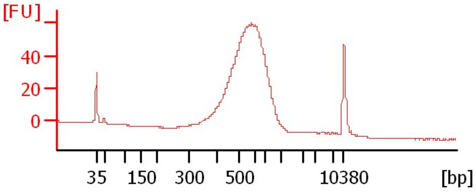
FS14-1 Library (1:10)



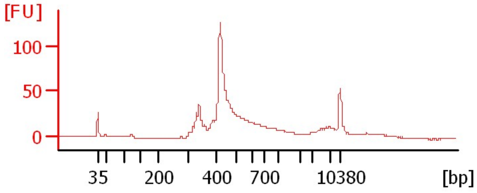
FS15-8 Library (1:10)



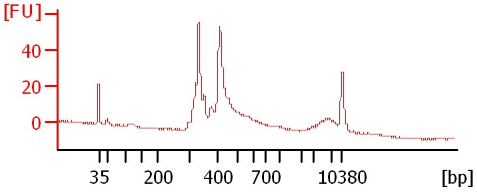
FS15-9 Library (1:10)



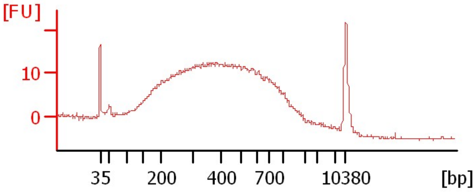
Bacteria CropCover Amplicon with 0.8x...



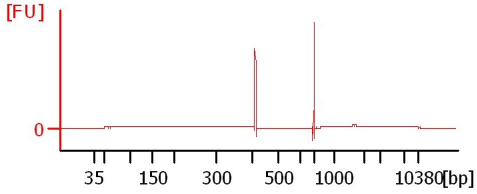
Fungal CropCover Amplicon with 0.8x c...



R8 soni with RNase and Zymo Cleanup



Mutant4 gDNA with RNase and Zymo Cleanup



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad

Created: 2/24/2016 2:47:21 PM
Modified: 2/24/2016 3:43:43 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
OE1 MeCP2 ChIP-seq		☐	✓			
OE1 IgG ChIP-seq		☐	✓			
OE2 MeCP2 ChIP-seq		☐	✓			
OE2 IgG ChIP-seq		☐	✓			
FS14-1 Library (1:10)		☐	✓			
FS15-8 Library (1:10)		☐	✓			
FS15-9 Library (1:10)		☐	✓			
Bacteria CropCover Amplicon with 0.8x cleanup		☐	✓			
Fungal CropCover Amplicon with 0.8x cleanup		☐	✓			
R8 soni with RNase and Zymo Cleanup		☐	✓			
Mutant4 gDNA with RNase and Zymo Cleanup		☐	⚠			
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

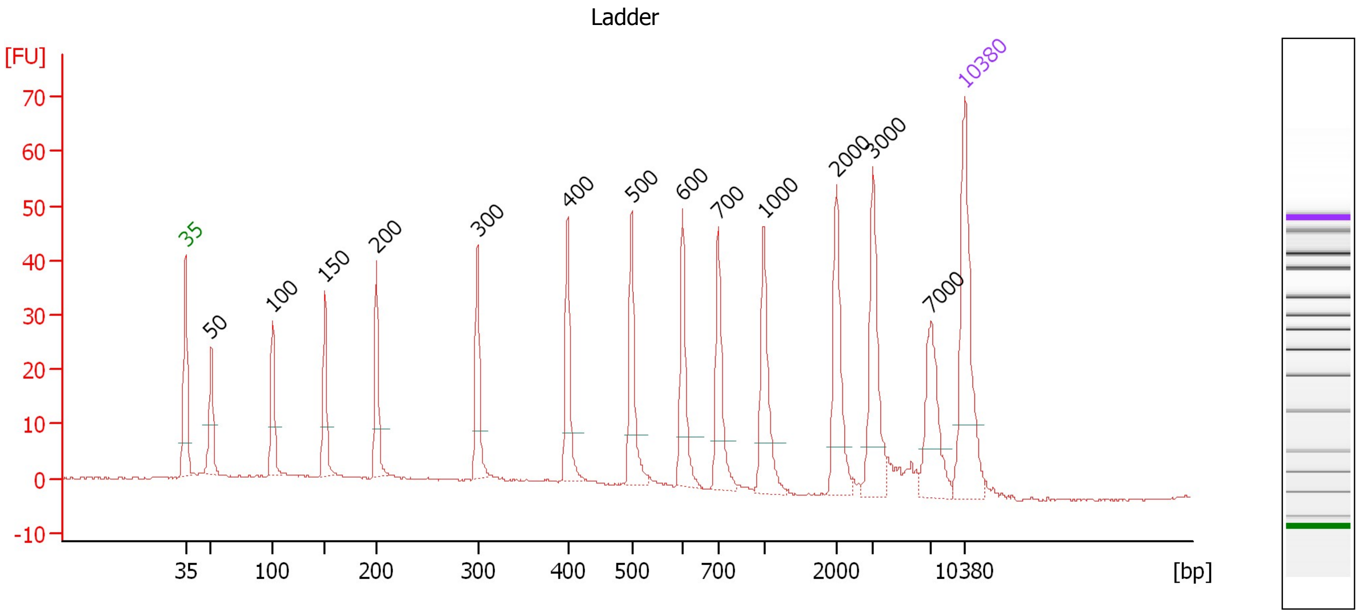
Filter Width [s] : 0.5
Polynomial Order : 4

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
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad
Created: 2/24/2016 2:47:21 PM
Modified: 2/24/2016 3:43:43 PM

Electropherogram Summary



Overall Results for Ladder

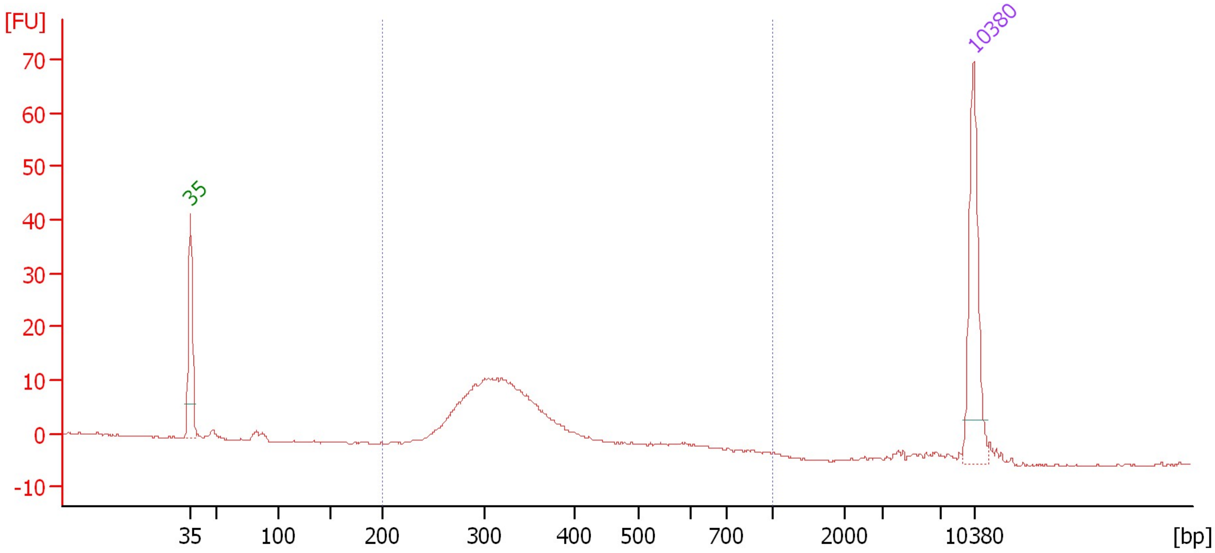
Noise: 0.2

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	45.30
3	∟	100	150.00	2,272.7	Ladder Peak	50.80
4	∟	150	150.00	1,515.2	Ladder Peak	55.50
5	∟	200	150.00	1,136.4	Ladder Peak	60.14
6	∟	300	150.00	757.6	Ladder Peak	69.24
7	∟	400	150.00	568.2	Ladder Peak	77.33
8	∟	500	150.00	454.5	Ladder Peak	83.08
9	∟	600	150.00	378.8	Ladder Peak	87.62
10	∟	700	150.00	324.7	Ladder Peak	90.88
11	∟	1,000	150.00	227.3	Ladder Peak	94.95
12	∟	2,000	150.00	113.6	Ladder Peak	101.51
13	∟	3,000	150.00	75.8	Ladder Peak	104.76
14	∟	7,000	150.00	32.5	Ladder Peak	109.98
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

OE1 MeCP2 ChIP-seq



Overall Results for sample 1 : OE1 MeCP2 ChIP-seq

Number of peaks found:	0	Corr. Area 1:	168.4
Noise:	0.2		

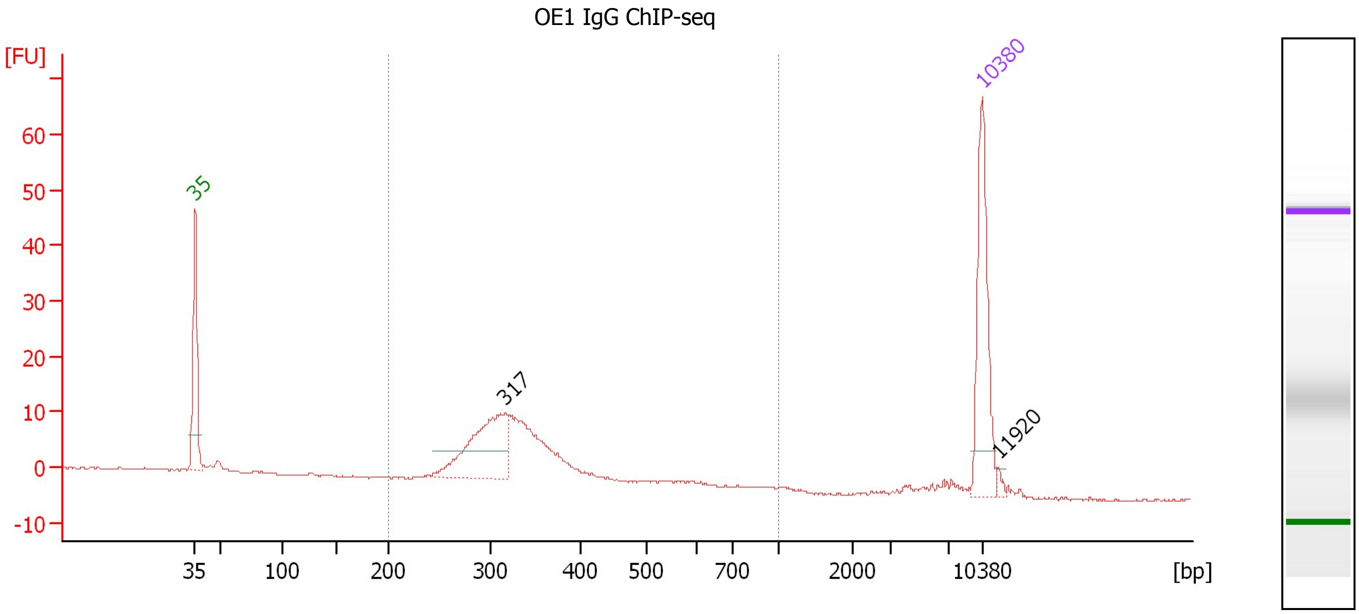
Peak table for sample 1 : OE1 MeCP2 ChIP-seq

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 1 : OE1 MeCP2 ChIP-seq

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	347	168.4	1,408.4	🟦	303.64	95	25.7

Electropherogram Summary Continued ...



Overall Results for sample 2 : OE1 IgG ChIP-seq

Number of peaks found:	2	Corr. Area 1:	140.3
Noise:	0.1		

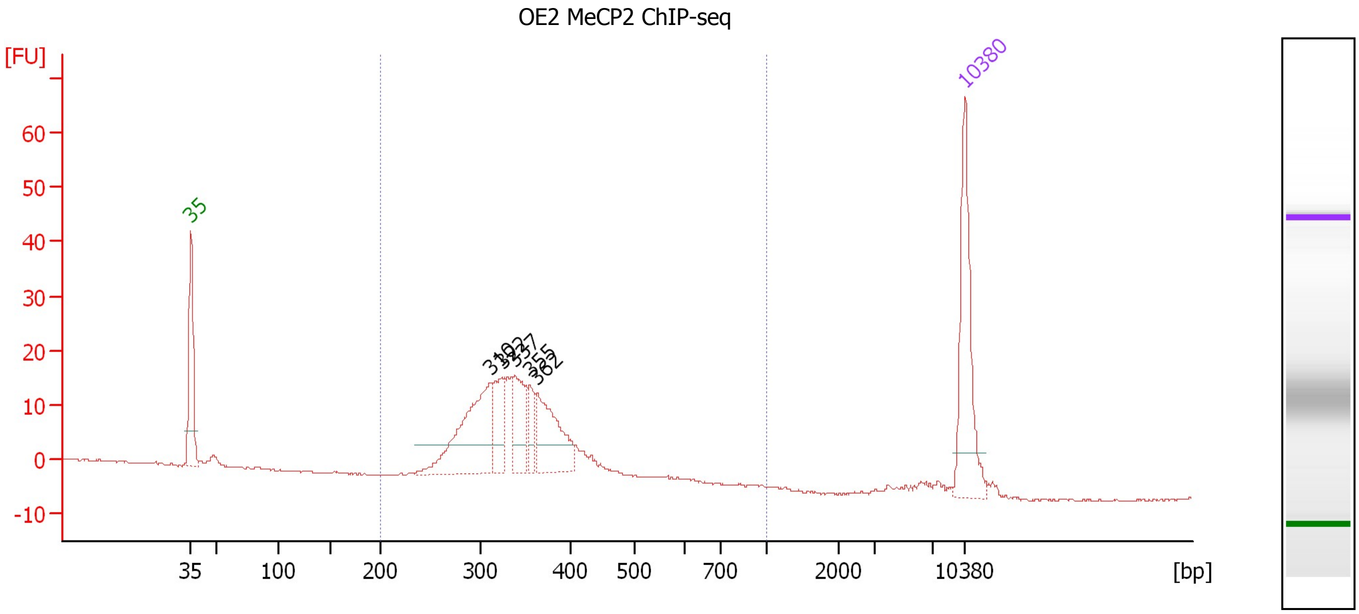
Peak table for sample 2 : OE1 IgG ChIP-seq

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	111.04	531.4		70.58
3	▶	10,380	75.00	10.9	Upper Marker	113.00
4		11,920	0.00	0.0		114.37

Region table for sample 2 : OE1 IgG ChIP-seq

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	338	140.3	1,124.0	🟦 240.88	88	21.1

Electropherogram Summary Continued ...



Overall Results for sample 3 : OE2 MeCP2 ChIP-seq

Number of peaks found:	5	Corr. Area 1:	237.5
Noise:	0.2		

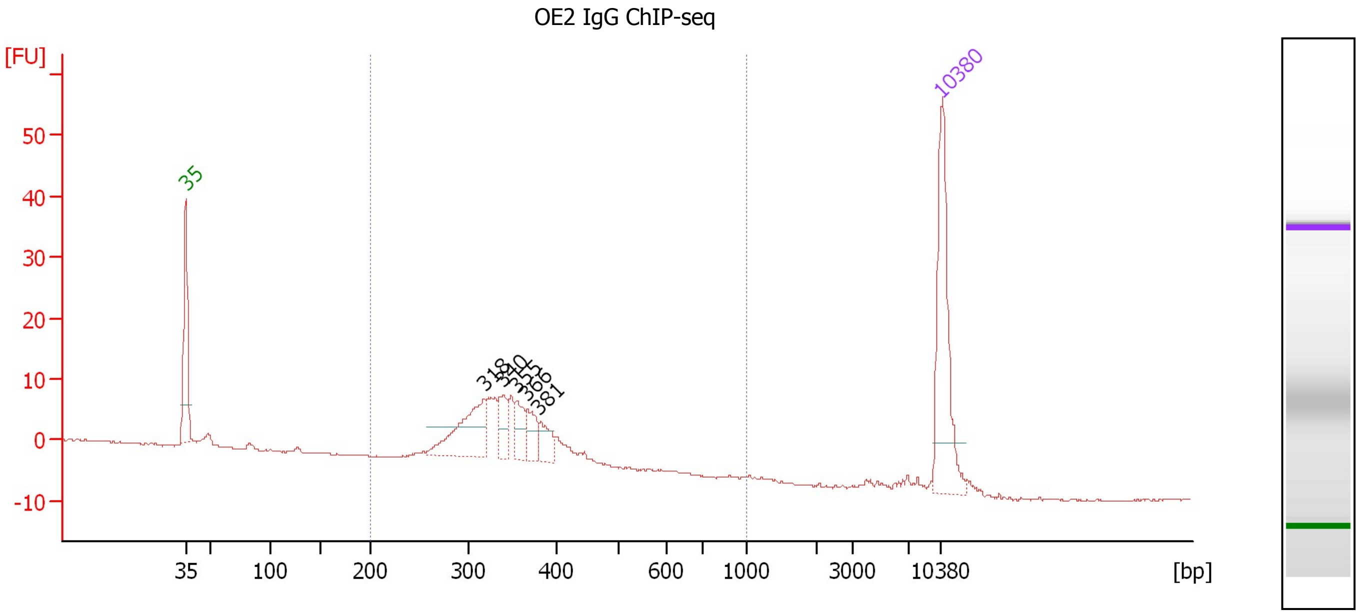
Peak table for sample 3 : OE2 MeCP2 ChIP-seq

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	127.62	623.8		70.05
3		322	41.53	195.1		71.06
4		337	53.04	238.2		72.26
5		355	21.47	91.7		73.66
6		362	74.74	312.5		74.29
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : OE2 MeCP2 ChIP-seq

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	343	237.5	1,804.9	🟦	397.90	97	15.5

Electropherogram Summary Continued ...



Overall Results for sample 4 : **OE2 IgG ChIP-seq**

Number of peaks found:	5	Corr. Area 1:	136.7
Noise:	0.2		

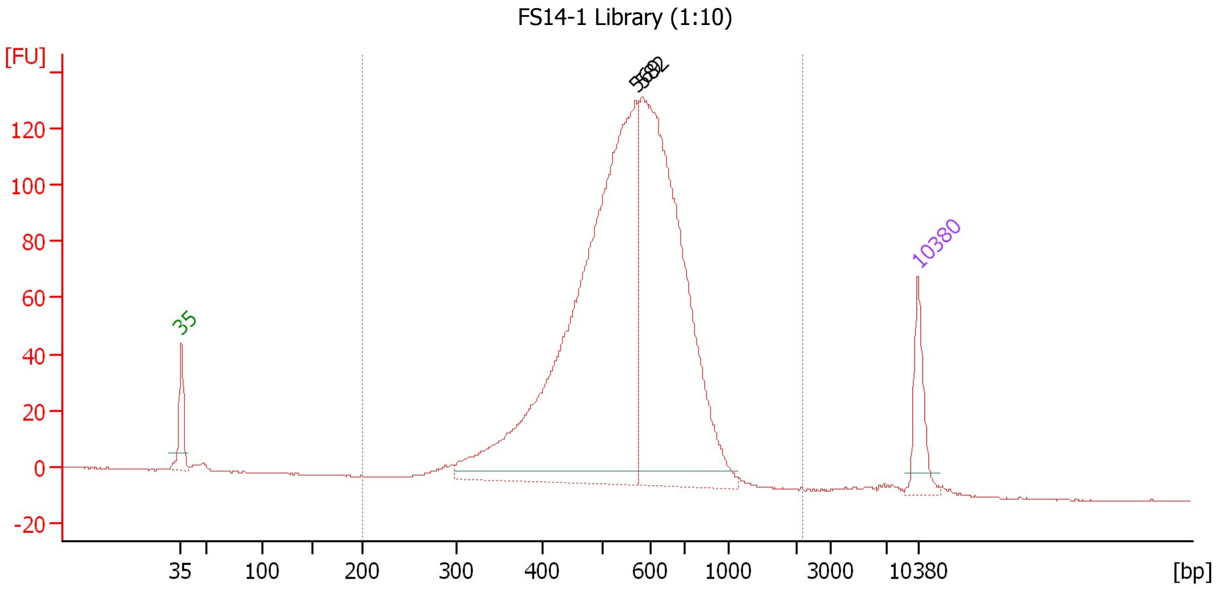
Peak table for sample 4 : **OE2 IgG ChIP-seq**

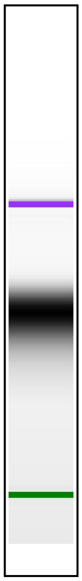
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		318	65.65	313.2		70.66
3		340	22.36	99.8		72.44
4		355	19.16	81.7		73.73
5		366	19.27	79.7		74.62
6		381	17.24	68.5		75.80
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : **OE2 IgG ChIP-seq**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	345	136.7	1,046.1	🟦	232.97	94	13.9

Electropherogram Summary Continued ...


FS14-1 Library (1:10)



Overall Results for sample 5 : **FS14-1 Library (1:10)**

Number of peaks found:	2	Corr. Area 1:	1,856.8
Noise:	0.2		

Peak table for sample 5 : **FS14-1 Library (1:10)**

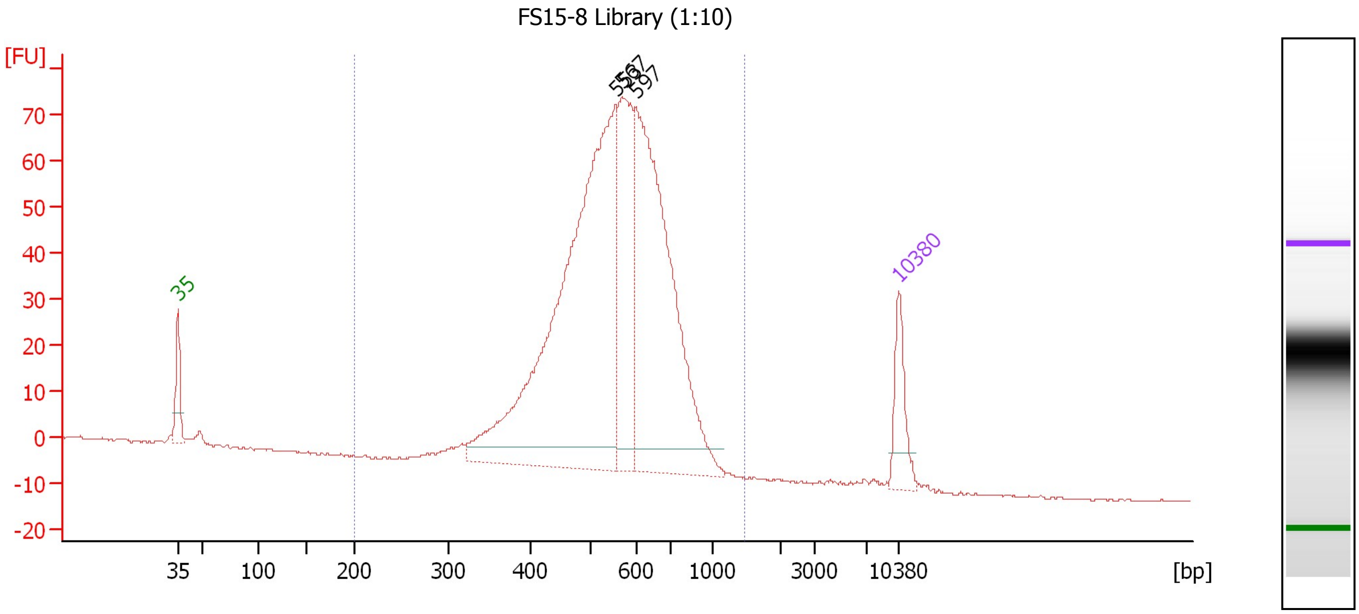
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		569	1,413.78	3,765.9		86.21
3		582	1,033.01	2,688.5		86.81
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : **FS14-1 Library (1:10)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,154	561	1,856.8	7,565.7	🟦	2,612.69	99	22.8

Assay Class:	High Sensitivity DNA Assay	Created:	2/24/2016 2:47:21 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad	Modified:	2/24/2016 3:43:43 PM

Electropherogram Summary Continued ...


FS15-8 Library (1:10)

Overall Results for sample 6 : FS15-8 Library (1:10)

Number of peaks found:	3	Corr. Area 1:	1,080.7
Noise:	0.2		

Peak table for sample 6 : FS15-8 Library (1:10)

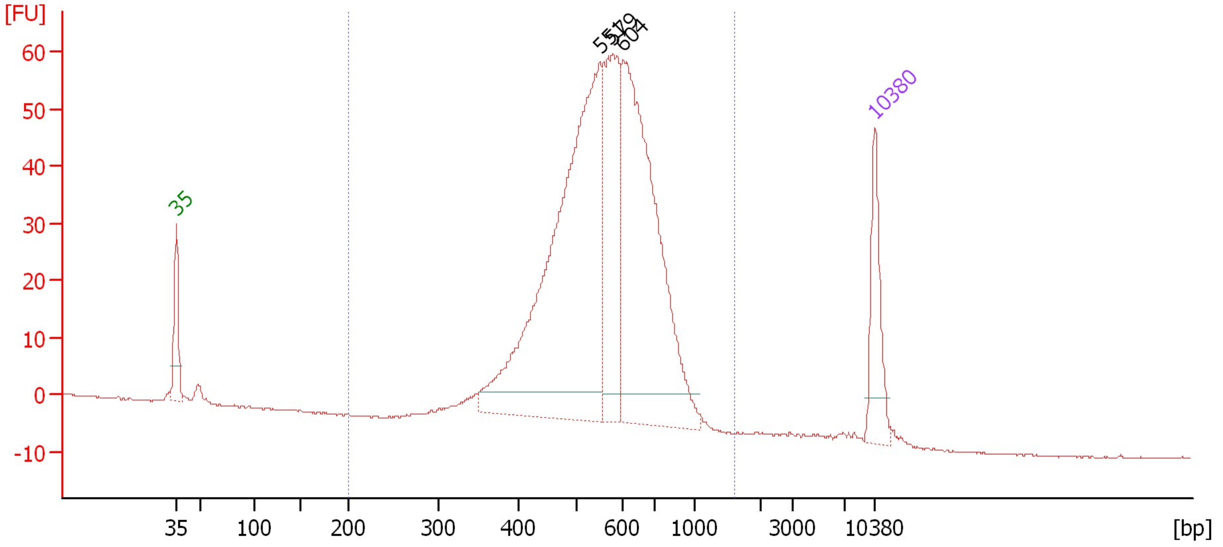
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		553	1,263.98	3,460.2		85.51
3		567	345.23	922.3		86.13
4		597	814.10	2,067.1		87.47
5	▶	10,380	75.00	10.9	Upper Marker	113.00

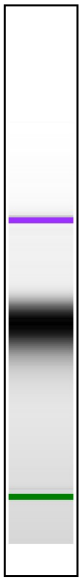
Region table for sample 6 : FS15-8 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,457	560	1,080.7	7,303.3	■	2,540.26	99	21.1

Electropherogram Summary Continued ...

FS15-9 Library (1:10)





Overall Results for sample 7 : **FS15-9 Library (1:10)**

Number of peaks found:	3	Corr. Area 1:	851.8
Noise:	0.1		

Peak table for sample 7 : **FS15-9 Library (1:10)**

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		551	747.13	2,054.5		85.40
3		579	244.84	640.5		86.68
4		604	545.55	1,369.2		87.74
5	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **FS15-9 Library (1:10)**

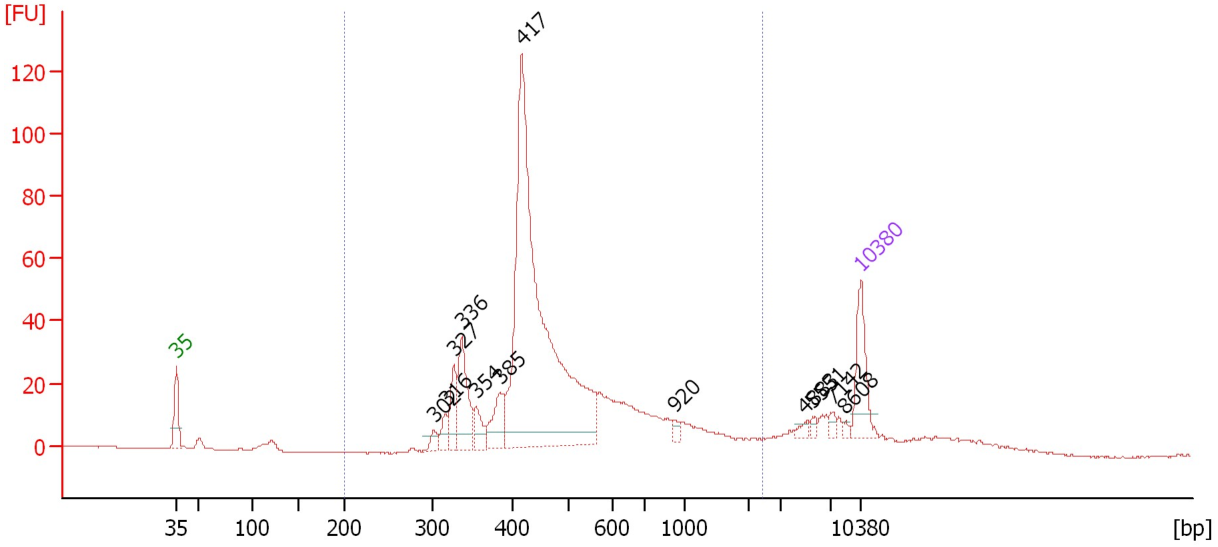
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,619	571	851.8	4,704.7	🟦	1,673.48	99	21.4

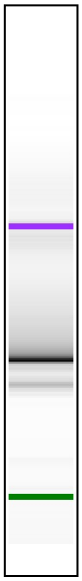
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad

Created: 2/24/2016 2:47:21 PM
Modified: 2/24/2016 3:43:43 PM

Electropherogram Summary Continued ...

Bacteria CropCover Amplicon with 0.8x cleanup





Overall Results for sample 8 : Bacteria CropCover Amplicon with 0.8x cleanup

Number of peaks found:	12	Corr. Area 1:	785.7
Noise:	0.1		

Peak table for sample 8 : Bacteria CropCover Amplicon with 0.8x cleanup

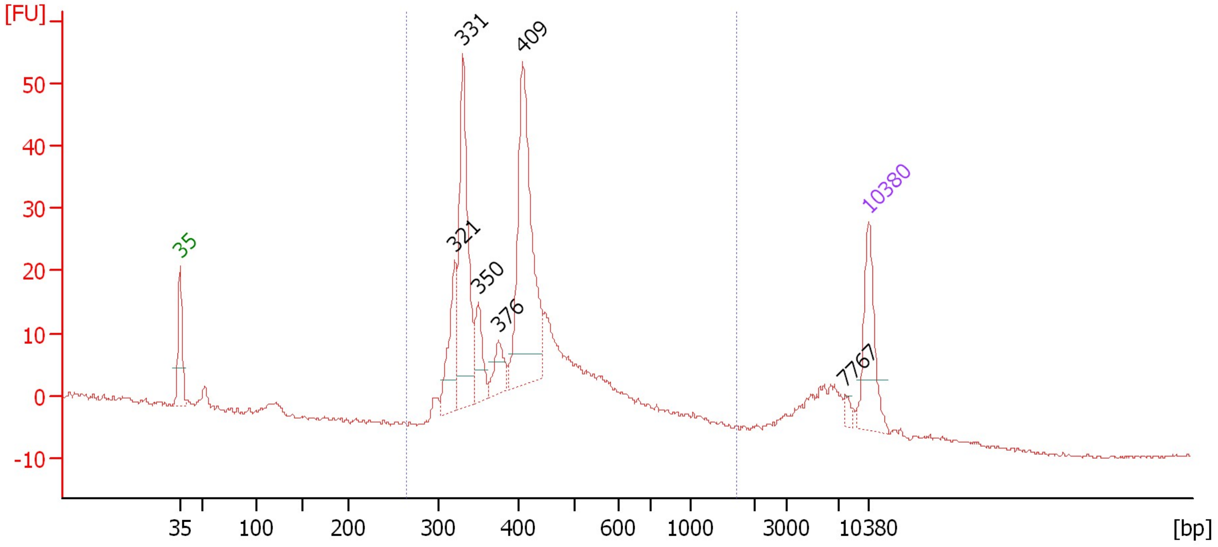
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		302	18.72	93.9		69.39
3		316	26.01	124.7		70.53
4		327	62.19	288.4		71.40
5		336	120.80	544.4		72.17
6		354	37.96	162.3		73.64
7		385	69.71	274.6		76.09
8		417	1,008.25	3,660.3		78.33
9		920	11.17	18.4		93.86
10		4,883	9.97	3.1		107.22
11		5,551	7.42	2.0		108.09
12		7,142	9.13	1.9		110.11
13		8,608	5.03	0.9		111.42
14	▶	10,380	75.00	10.9	Upper Marker	113.00

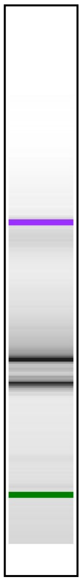
Region table for sample 8 : Bacteria CropCover Amplicon with 0.8x cleanup

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,449	554	785.7	5,547.6	🟦 1,682.24	86	56.7

Electropherogram Summary Continued ...

Fungal CropCover Amplicon with 0.8x cleanup





Overall Results for sample 9 : Fungal CropCover Amplicon with 0.8x cleanup

Number of peaks found:	6	Corr. Area 1:	411.9
Noise:	0.3		

Peak table for sample 9 : Fungal CropCover Amplicon with 0.8x cleanup

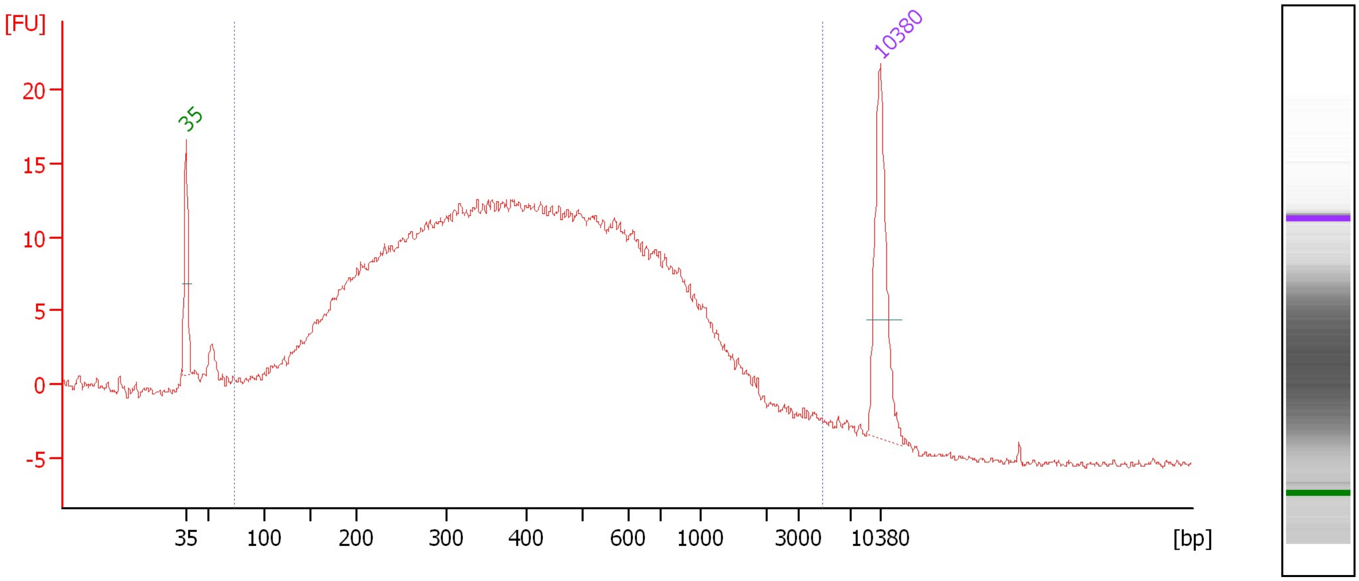
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		321	97.50	460.5		70.92
3		331	236.37	1,082.4		71.74
4		350	55.68	240.8		73.31
5		376	39.01	157.3		75.37
6		409	302.13	1,118.4		77.86
7		7,767	7.88	1.5		110.67
8	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : Fungal CropCover Amplicon with 0.8x cleanup

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
264	1,714	450	411.9	4,526.6	🟦	1,213.51	87	38.0

Electropherogram Summary Continued ...

R8 soni with RNase and Zymo Cleanup



Overall Results for sample 10 : R8 soni with RNase and Zymo Cleanup

Number of peaks found:	0	Corr. Area 1:	673.4
Noise:	0.2		

Peak table for sample 10 : R8 soni with RNase and Zymo Cleanup

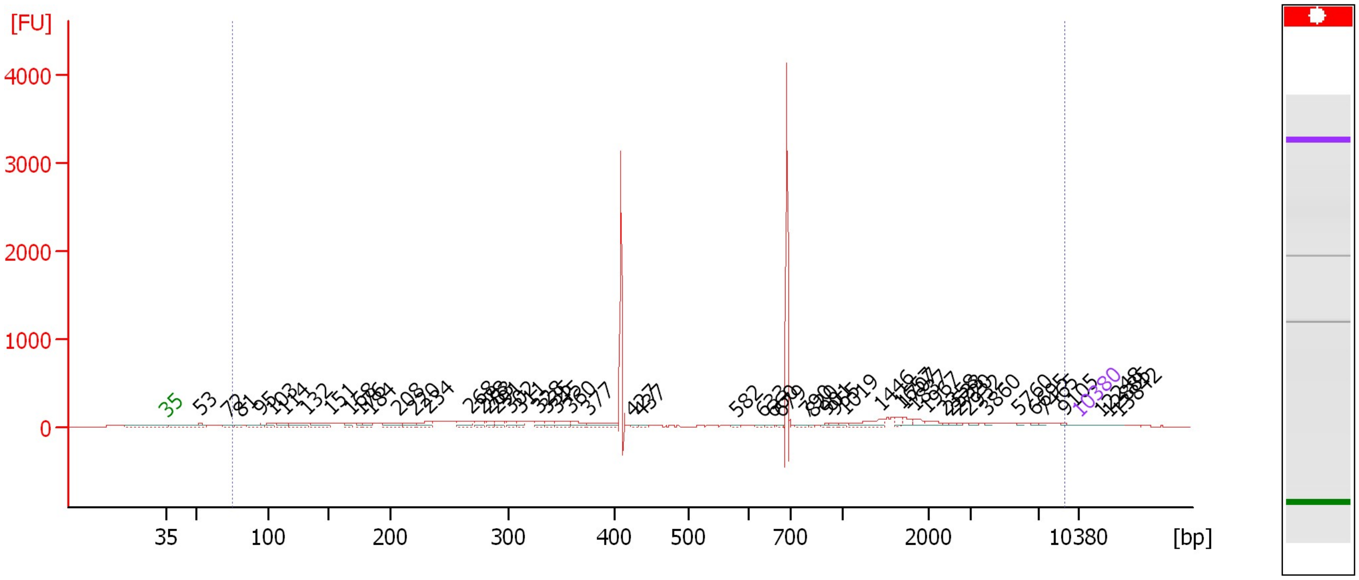
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : R8 soni with RNase and Zymo Cleanup

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
73	4,811	526	673.4	12,940.2	■ 2,575.85	97	89.1

Electropherogram Summary Continued ...

Mutant4 gDNA with RNase and Zymo Cleanup



Overall Results for sample 11 : **Mutant4 gDNA with RNase and Zymo Cleanup**

Number of peaks found:	53	Corr. Area 1:	5,191.2
Noise:	0.5		

Peak table for sample 11 : **Mutant4 gDNA with RNase and Zymo Cleanup**

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	968.39	27,619.3		45.64
3		72	392.87	8,273.3		47.72
4		81	242.54	4,526.9		48.73
5		95	543.27	8,679.5		50.24
6		103	341.50	5,021.7		51.09
7		114	405.64	5,397.6		52.11
8		132	714.30	8,222.3		53.77
9		151	777.00	7,789.8		55.60
10		168	327.39	2,956.8		57.15
11		176	289.98	2,495.3		57.92
12		184	370.69	3,046.0		58.69
13		208	788.99	5,754.3		60.85
14		220	570.69	3,925.8		61.98
15		234	572.95	3,715.2		63.20
16		268	642.73	3,632.8		66.33
17		278	409.04	2,226.6		67.27
18		283	321.36	1,721.7		67.67
19		291	380.28	1,981.0		68.41
20		302	350.85	1,761.5		69.38
21		311	283.78	1,383.3		70.11
22		328	367.53	1,695.7		71.54
23		335	330.55	1,493.1		72.11
24		345	493.42	2,163.9		72.92
25		360	478.07	2,011.8		74.10

Electropherogram Summary Continued ...

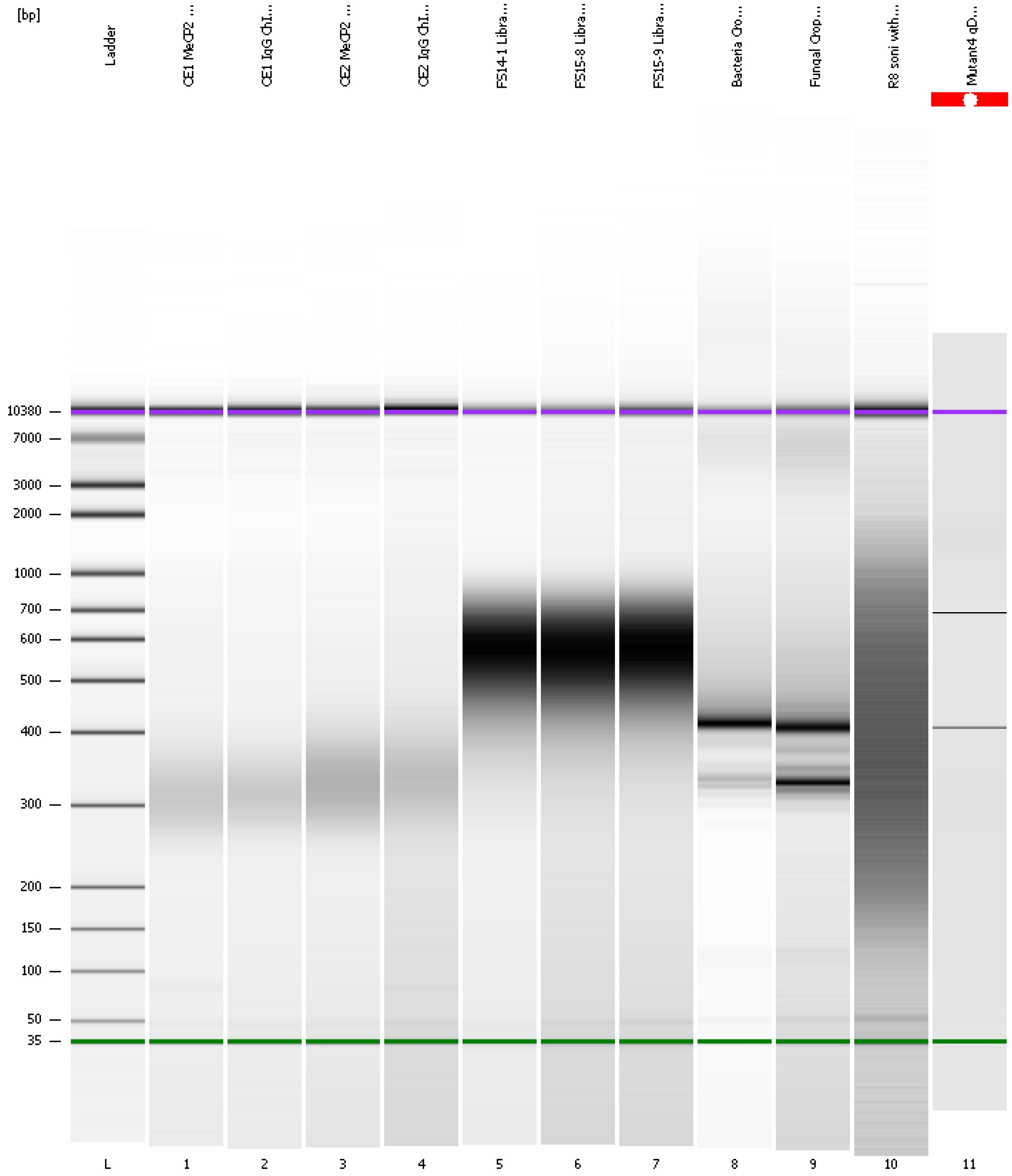
... Peak table for sample 11 : Mutant4 gDNA with RNase and Zymo Cleanup

Peak	**Size [bp]**	**Conc. [pg/µl]**	**Molarity [pmol/l]**	**Observations**	**Aligned Migration Time [s]**
26	377	639.48	2,572.5		75.44
27	427	40.51	143.9		78.85
28	437	35.97	124.7		79.46
29	582	16.47	42.8		86.82
30	633	25.99	62.2		88.69
31	660	41.24	94.6		89.59
32	679	42.75	95.4		90.20
33	790	65.60	125.8		92.11
34	820	51.47	95.1		92.51
35	901	72.17	121.3		93.61
36	955	89.47	141.9		94.34
37	1,019	101.73	151.3		95.07
38	1,446	644.16	674.7		97.88
39	1,657	240.13	219.5		99.26
40	1,707	313.94	278.7		99.59
41	1,837	252.80	208.5		100.44
42	1,967	280.10	215.7		101.29
43	2,358	84.73	54.4		102.67
44	2,533	74.85	44.8		103.24
45	2,720	71.80	40.0		103.85
46	2,932	106.94	55.3		104.54
47	3,860	82.21	32.3		105.89
48	5,760	62.95	16.6		108.37
49	6,695	64.72	14.6		109.59
50	7,465	61.62	12.5		110.40
51	9,105	87.44	14.6		111.86
52 ▶	10,380	75.00	10.9	Upper Marker	113.00
53	12,248	0.00	0.0		114.67
54	12,885	0.00	0.0		115.24
55	13,842	0.00	0.0		116.09

Region table for sample 11 : Mutant4 gDNA with RNase and Zymo Cleanup

From [bp]	**To [bp]**	**Average Size [bp]**	**Corr. Area**	**Molarity [pmol/l]**	**Color**	**Conc. [pg/µl]**	**% of Total**	**Size distribution in CV [%]**
76	9,152	1,046	5,191.2	138,775.7	🟦	26,370.32	94	100.0

Gel Image


[bp]
Ladder
CE1 MeCP2 ...
CE1 IgG ChI...
CE2 MeCP2 ...
CE2 IgG ChI...
FS14-1 Libra...
FS15-8 Libra...
FS15-9 Libra...
Bacteria Cro...
Fungal Crop...
R8 soni with...
Mutant4 qD...
10380
7000
3000
2000
1000
700
600
500
400
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Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad

Created: 2/24/2016 2:47:21 PM
Modified: 2/24/2016 3:43:43 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		2/24/2016 3:27:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Instrument error occurred on port 1, Optical signal too high (1605h)	559	Instrument	Run	Sample 11	2/24/2016 3:26:39 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-02-24\2016-02-24_002.xad)		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		2/24/2016 2:47:26 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1