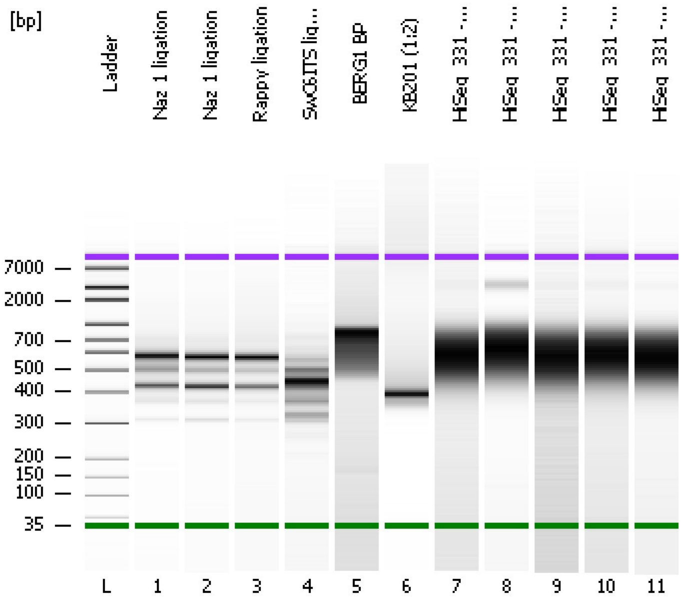
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad
Created: 2/12/2016 12:03:42 PM
Modified: 2/12/2016 3:04:02 PM

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

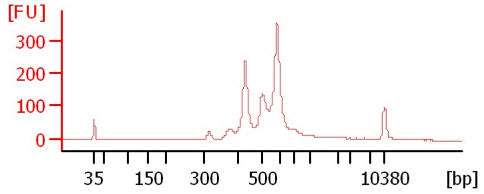
Chip Information:

Chip Lot #:

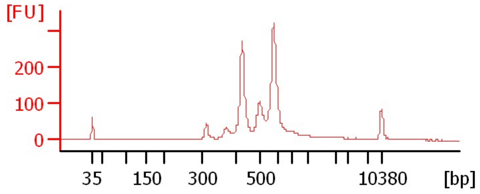
Reagent Kit Lot #:

Chip Comments:

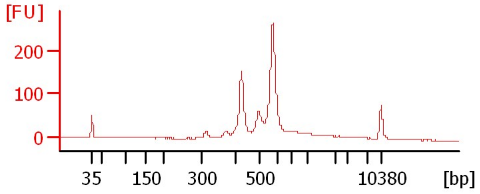
Naz 1 ligation



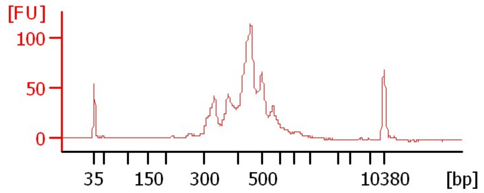
Naz 1 ligation



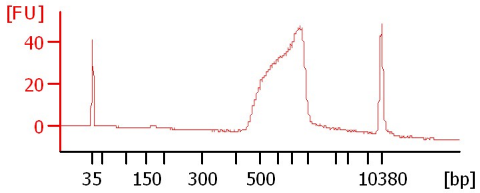
Rappy ligation



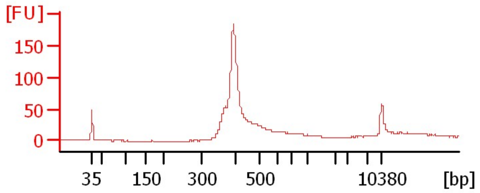
SwC6ITS ligation



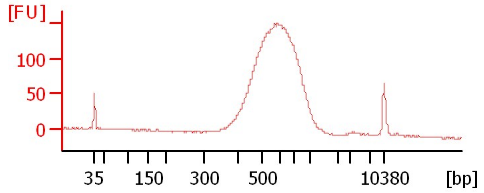
BERG1 BP



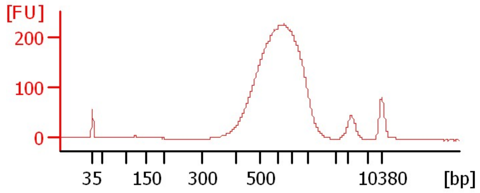
KB201 (1:2)



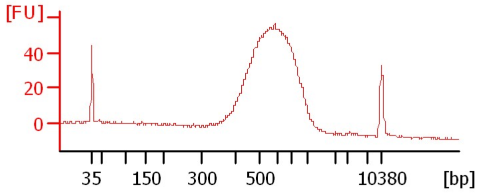
HiSeq_331 - 6 Library (1:15)



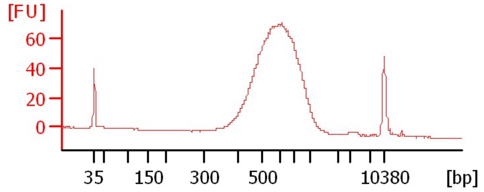
HiSeq_331 - 7 Library (1:15)



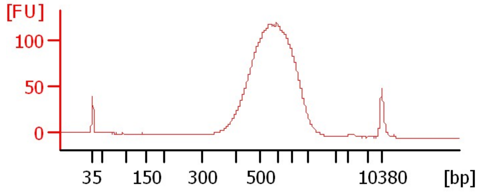
HiSeq_331 - 8 Library (1:15)



HiSeq_331 - 9 Library (1:15)



HiSeq_331 - 10 Library (1:15)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad

Created: 2/12/2016 12:03:42 PM
Modified: 2/12/2016 3:04:02 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
Naz 1 ligation		☐	✓			
Naz 1 ligation		☐	✓			
Rappy ligation		☐	✓			
SwC6ITS ligation		☐	✓			
BERG1 BP		☐	✓			
KB201 (1:2)		☐	✓			
HiSeq_331 - 6 Library (1:15)		☐	✓			
HiSeq_331 - 7 Library (1:15)		☐	✓			
HiSeq_331 - 8 Library (1:15)		☐	✓			
HiSeq_331 - 9 Library (1:15)		☐	✓			
HiSeq_331 - 10 Library (1:15)		☐	✓			
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

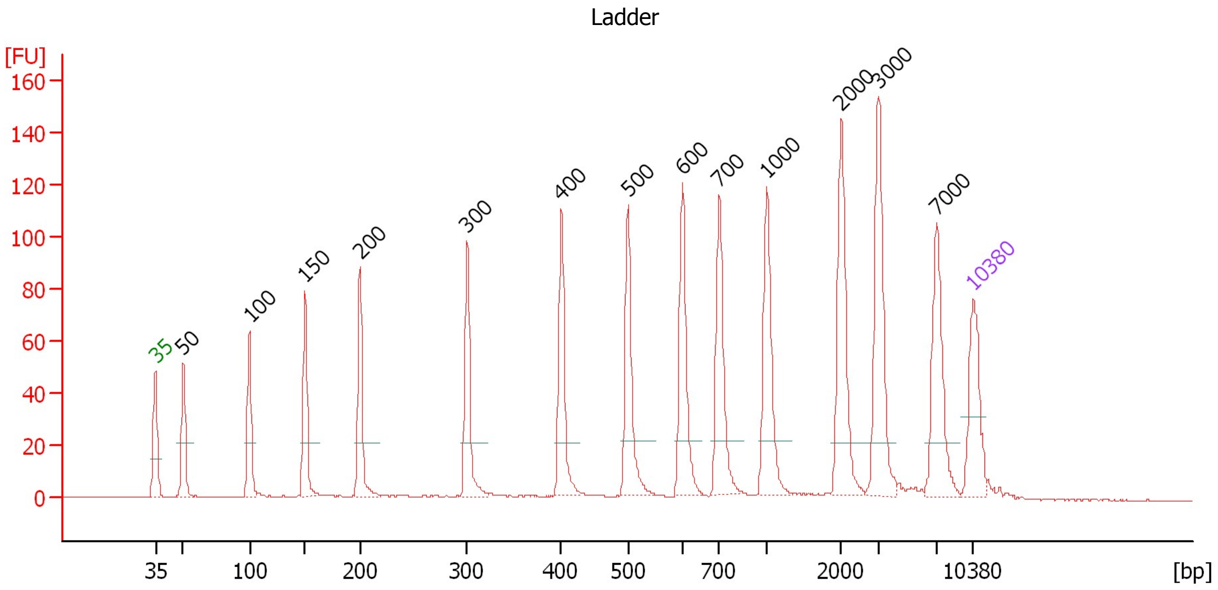
Ladder

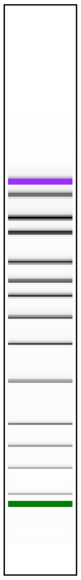
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad

Created: 2/12/2016 12:03:42 PM
Modified: 2/12/2016 3:04:02 PM

Electropherogram Summary





Overall Results for Ladder

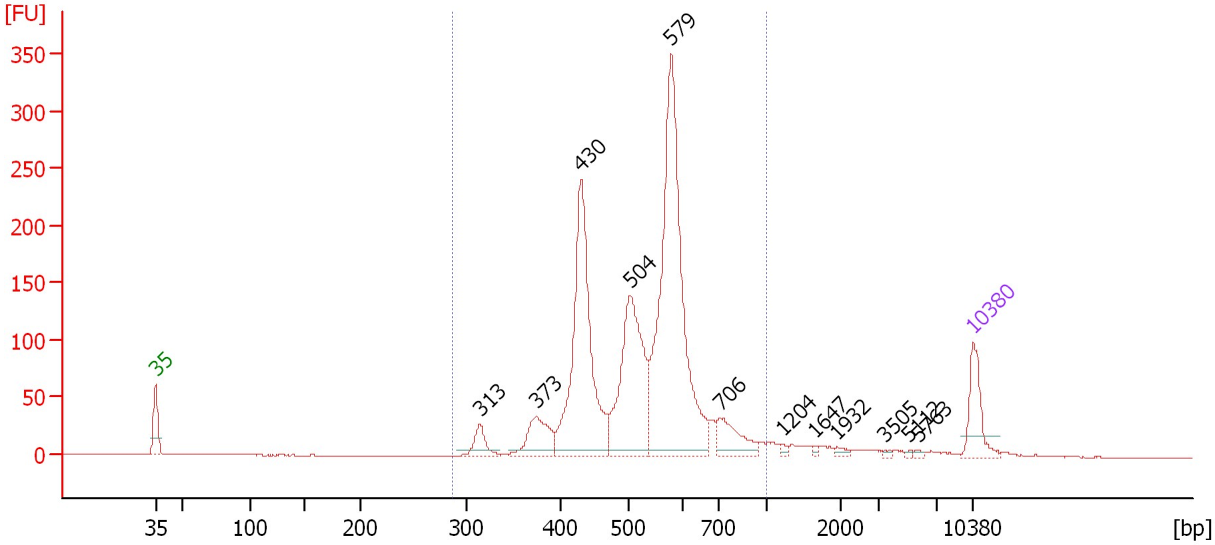
Noise: 0.2

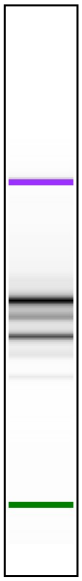
Peak table for Ladder

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	45.38
3	∟	100	150.00	2,272.7	Ladder Peak	51.05
4	∟	150	150.00	1,515.2	Ladder Peak	55.82
5	∟	200	150.00	1,136.4	Ladder Peak	60.49
6	∟	300	150.00	757.6	Ladder Peak	69.68
7	∟	400	150.00	568.2	Ladder Peak	77.74
8	∟	500	150.00	454.5	Ladder Peak	83.46
9	∟	600	150.00	378.8	Ladder Peak	88.13
10	∟	700	150.00	324.7	Ladder Peak	91.27
11	∟	1,000	150.00	227.3	Ladder Peak	95.32
12	∟	2,000	150.00	113.6	Ladder Peak	101.71
13	∟	3,000	150.00	75.8	Ladder Peak	104.85
14	∟	7,000	150.00	32.5	Ladder Peak	109.86
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

Naz 1 ligation





Overall Results for sample 1 : Naz 1 ligation

Number of peaks found:	12	Corr. Area 1:	1,997.7
Noise:	0.2		

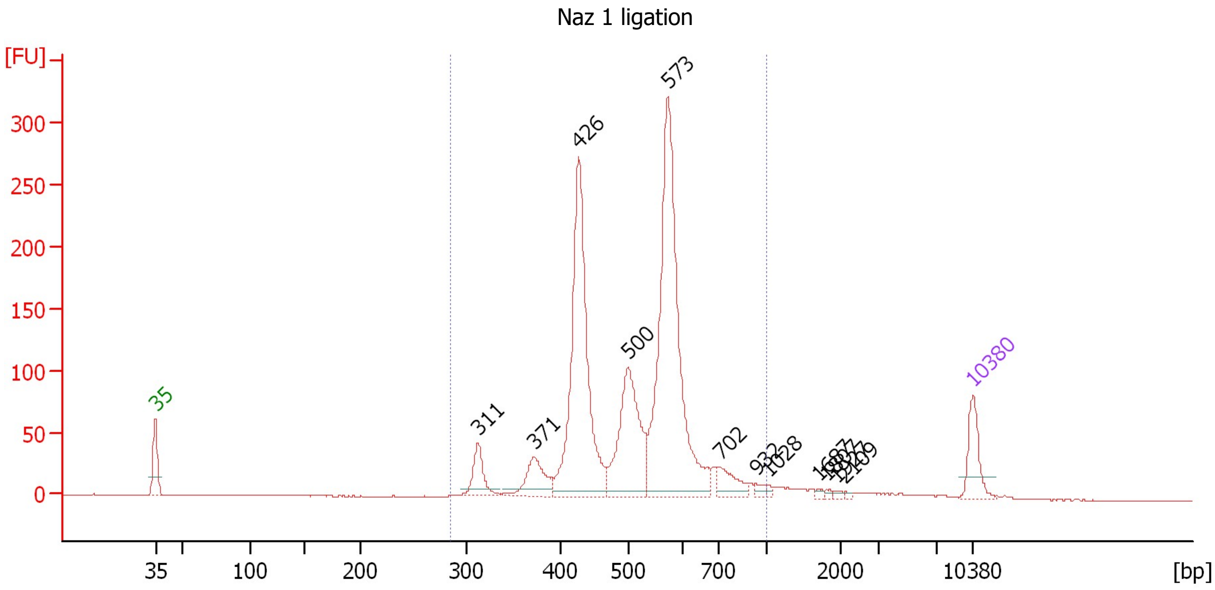
Peak table for sample 1 : Naz 1 ligation

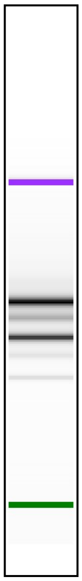
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		313	52.47	253.6		70.77
3		373	109.23	443.8		75.56
4		430	551.22	1,943.6		79.44
5		504	392.60	1,179.9		83.65
6		579	810.60	2,121.2		87.15
7		706	89.04	191.0		91.36
8		1,204	6.76	8.5		96.63
9		1,647	4.73	4.3		99.45
10		1,932	7.41	5.8		101.27
11		3,505	3.29	1.4		105.48
12		5,112	2.41	0.7		107.49
13		5,763	3.83	1.0		108.31
14	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : Naz 1 ligation

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
286	1,000	530	1,997.7	6,066.6	■	2,018.29	94	19.6

Electropherogram Summary Continued ...





Overall Results for sample 2 : **Naz 1 ligation**

Number of peaks found: 12

Corr. Area 1: 1,746.1

Noise: 0.2

Peak table for sample 2 : **Naz 1 ligation**

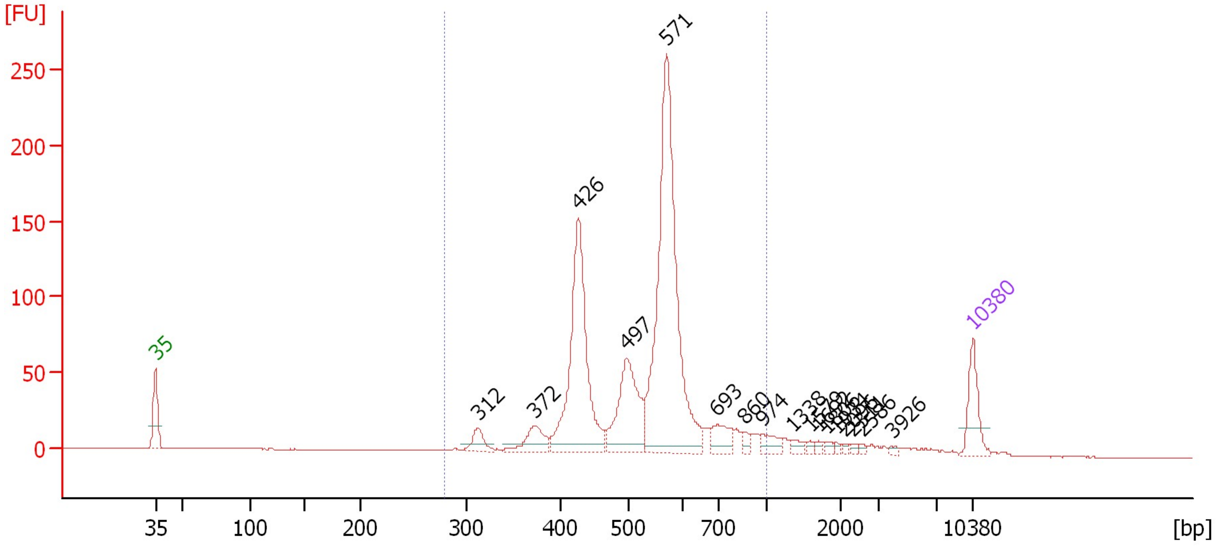
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		311	92.20	448.9		70.59
3		371	109.26	446.0		75.42
4		426	705.43	2,507.1		79.24
5		500	342.14	1,037.0		83.45
6		573	862.88	2,283.3		86.85
7		702	63.29	136.7		91.29
8		932	12.98	21.1		94.40
9		1,028	7.13	10.5		95.50
10		1,687	5.30	4.8		99.71
11		1,807	4.40	3.7		100.47
12		1,927	5.22	4.1		101.24
13		2,109	2.96	2.1		102.05
14	▶	10,380	75.00	10.9	Upper Marker	113.00

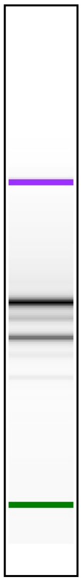
Region table for sample 2 : **Naz 1 ligation**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
285	1,000	517	1,746.1	6,980.0	🟦	2,251.23	94	20.7

Electropherogram Summary Continued ...

Rappy ligation





Overall Results for sample 3 : Rappy ligation

Number of peaks found:	17	Corr. Area 1:	1,204.0
Noise:	0.2		

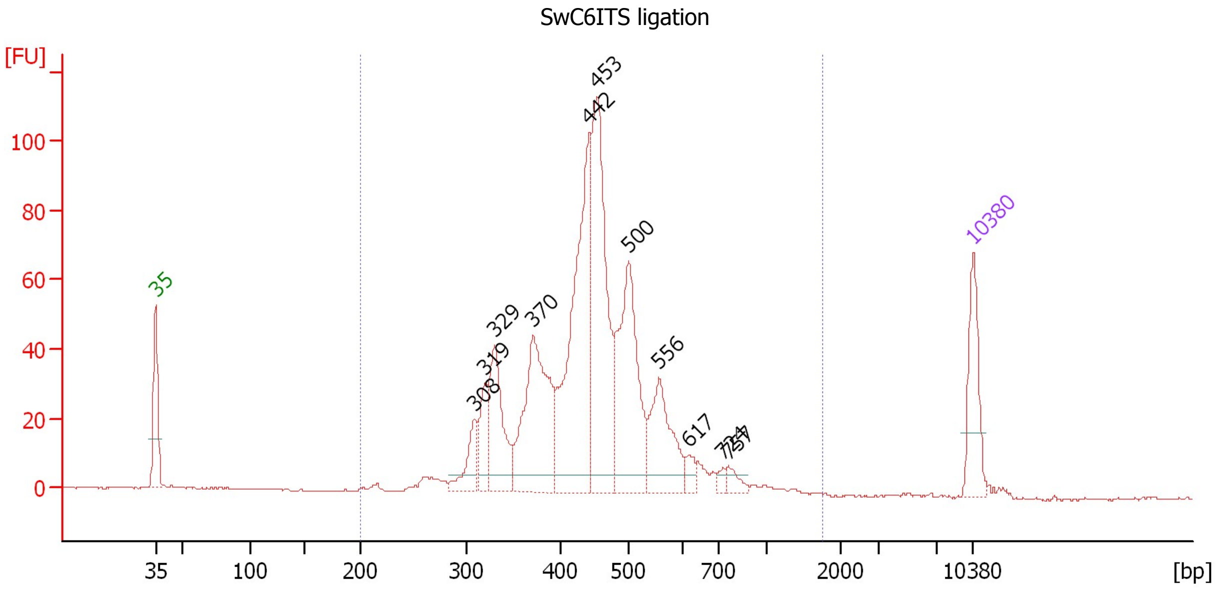
Peak table for sample 3 : Rappy ligation

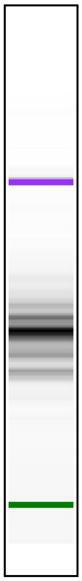
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		312	45.14	219.5		70.62
3		372	70.09	285.4		75.49
4		426	504.74	1,796.6		79.21
5		497	242.55	739.0		83.30
6		571	822.73	2,182.9		86.77
7		693	59.39	129.8		91.06
8		860	15.25	26.9		93.43
9		974	30.06	46.8		94.97
10		1,338	14.17	16.0		97.48
11		1,579	6.65	6.4		99.02
12		1,692	7.55	6.8		99.74
13		1,806	7.48	6.3		100.47
14		1,934	5.45	4.3		101.29
15		2,096	5.22	3.8		102.01
16		2,311	5.36	3.5		102.68
17		2,586	5.05	3.0		103.55
18		3,926	5.57	2.1		106.01
19	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : Rappy ligation

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
279	1,000	533	1,204.0	5,616.5	■	1,862.93	88	21.3

Electropherogram Summary Continued ...





Overall Results for sample 4 : SwC6ITS ligation

Number of peaks found:	11	Corr. Area 1:	1,032.4
Noise:	0.1		

Peak table for sample 4 : SwC6ITS ligation

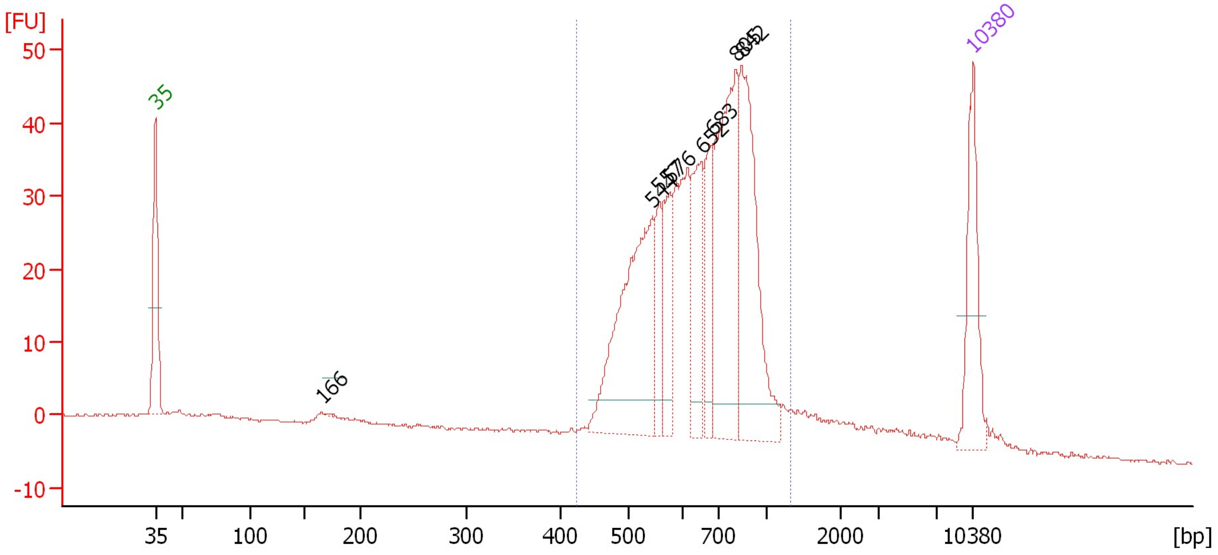
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		308	60.29	297.0		70.30
3		319	60.62	288.3		71.18
4		329	148.16	682.7		72.00
5		370	260.53	1,067.0		75.32
6		442	391.45	1,341.6		80.14
7		453	345.10	1,153.8		80.78
8		500	263.57	798.6		83.46
9		556	130.07	354.2		86.09
10		617	17.66	43.3		88.68
11		724	9.18	19.2		91.60
12		757	17.13	34.3		92.04
13	▶	10,380	75.00	10.9	Upper Marker	113.00

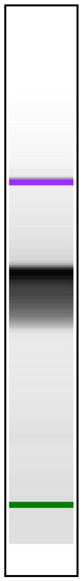
Region table for sample 4 : SwC6ITS ligation

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,743	455	1,032.4	6,415.3	🟦	1,794.07	99	26.9

Electropherogram Summary Continued ...

BERG1 BP





Overall Results for sample 5 : BERG1 BP

Number of peaks found:	8	Corr. Area 1:	542.3
Noise:	0.2		

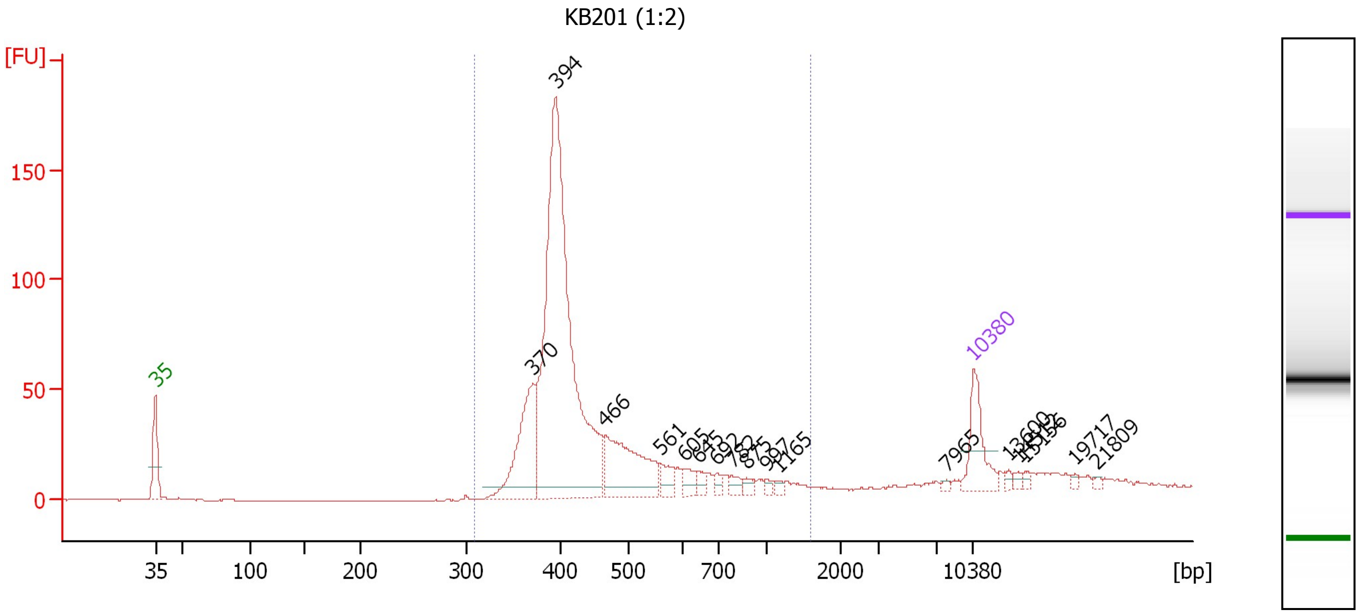
Peak table for sample 5 : BERG1 BP

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	2.62	23.9		57.27
3		544	243.04	676.4		85.53
4		557	48.39	131.6		86.12
5		576	68.67	180.7		87.00
6		652	83.41	194.0		89.75
7		683	71.19	158.0		90.73
8		805	212.17	399.2		92.69
9		842	194.30	349.8		93.18
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : BERG1 BP

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
424	1,327	682	542.3	2,635.9	🟦	1,117.53	83	22.9

Electropherogram Summary Continued ...



Overall Results for sample 6 : **KB201 (1:2)**

Number of peaks found:	17	Corr. Area 1:	895.5
Noise:	0.2		

Peak table for sample 6 : **KB201 (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		370	211.55	866.8		75.30
3		394	1,011.67	3,890.9		77.25
4		466	208.49	678.3		81.50
5		561	30.71	83.0		86.29
6		605	24.91	62.4		88.29
7		645	15.32	36.0		89.53
8		692	13.51	29.6		91.03
9		782	15.93	30.9		92.38
10		875	12.15	21.0		93.63
11		997	7.10	10.8		95.28
12		1,165	7.22	9.4		96.37
13		7,965	4.52	0.9		110.75
14	▶	10,380	75.00	10.9	Upper Marker	113.00
15		13,600	0.00	0.0		116.00
16		14,512	0.00	0.0		116.84
17		15,156	0.00	0.0		117.44
18		19,717	0.00	0.0		121.69
19		21,809	0.00	0.0		123.63

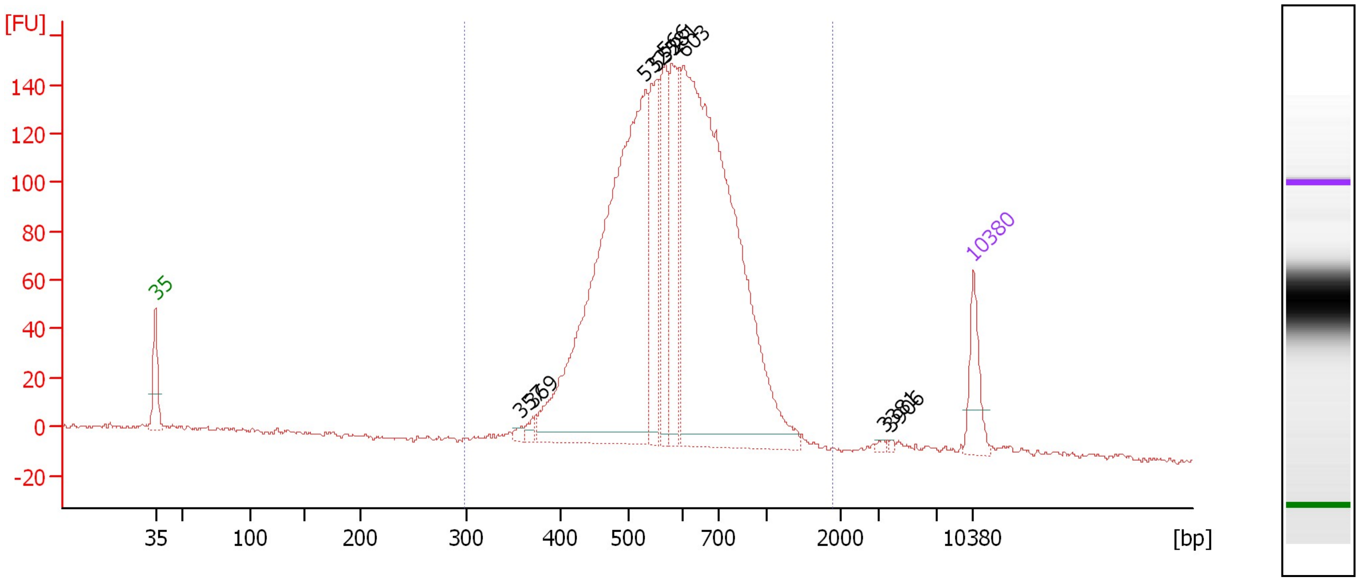
Region table for sample 6 : **KB201 (1:2)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
308	1,579	462	895.5	5,425.6	🟦	1,530.01	90	34.5

Assay Class:	High Sensitivity DNA Assay	Created:	2/12/2016 12:03:42 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad	Modified:	2/12/2016 3:04:02 PM

Electropherogram Summary Continued ...

HiSeq_331 - 6 Library (1:15)



Overall Results for sample 7 : **HiSeq_331 - 6 Library (1:15)**

Number of peaks found:	9	Corr. Area 1:	2,265.5
Noise:	0.8		

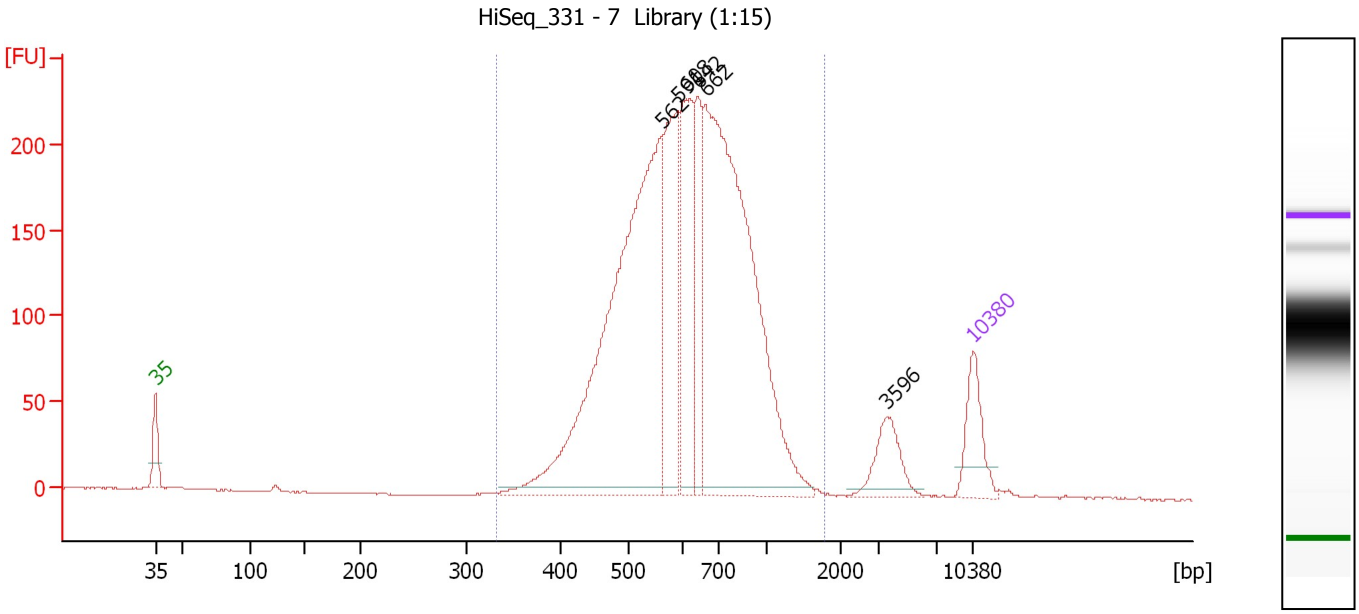
Peak table for sample 7 : **HiSeq_331 - 6 Library (1:15)**

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		357	12.37	52.5		74.29
3		369	17.06	70.0		75.25
4		532	1,318.16	3,755.8		84.94
5		552	247.25	678.3		85.90
6		566	223.47	597.8		86.55
7		581	220.73	575.2		87.26
8		603	1,421.46	3,571.8		88.22
9		3,381	5.04	2.3		105.33
10		3,906	3.65	1.4		105.98
11	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **HiSeq_331 - 6 Library (1:15)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
297	1,879	608	2,265.5	9,698.0	🟦	3,615.51	95	27.3

Electropherogram Summary Continued ...



Overall Results for sample 8 : HiSeq_331 - 7 Library (1:15)

Number of peaks found:	6	Corr. Area 1:	3,280.1
Noise:	0.2		

Peak table for sample 8 : HiSeq_331 - 7 Library (1:15)

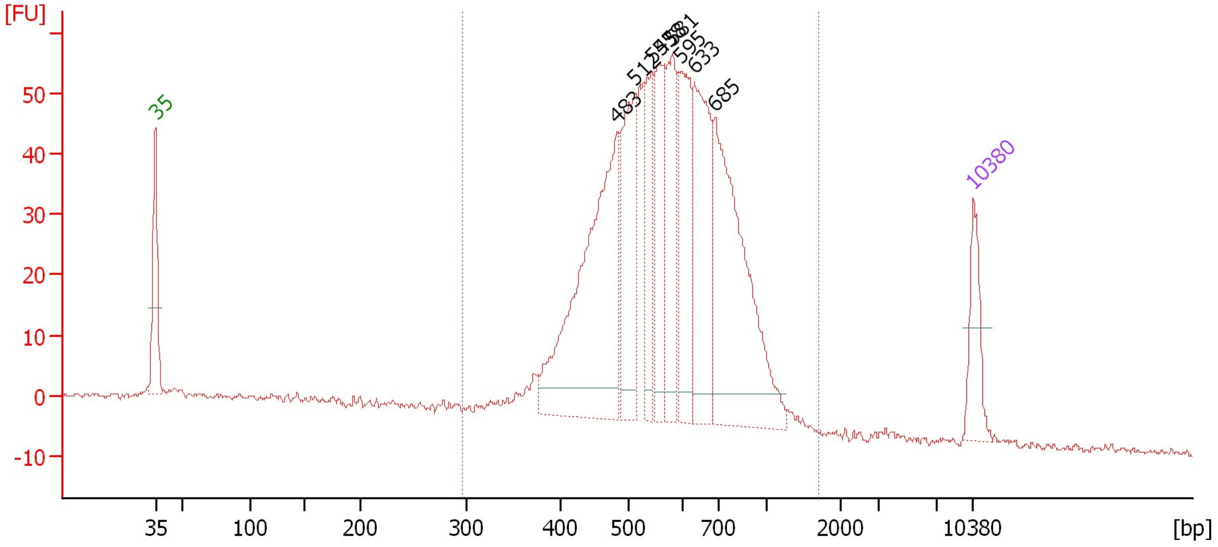
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		562	1,022.62	2,756.1		86.36
3		591	275.85	706.8		87.72
4		608	254.38	634.0		88.37
5		642	160.23	378.4		89.43
6		662	1,004.11	2,297.0		90.09
7		3,596	74.33	31.3		105.60
8	▶	10,380	75.00	10.9	Upper Marker	113.00

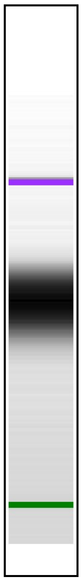
Region table for sample 8 : HiSeq_331 - 7 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
331	1,773	650	3,280.1	6,961.1	🟦	2,756.23	96	27.7

Electropherogram Summary Continued ...

HiSeq_331 - 8 Library (1:15)





Overall Results for sample 9 : **HiSeq_331 - 8 Library (1:15)**

Number of peaks found:	8	Corr. Area 1:	922.1
Noise:	0.4		

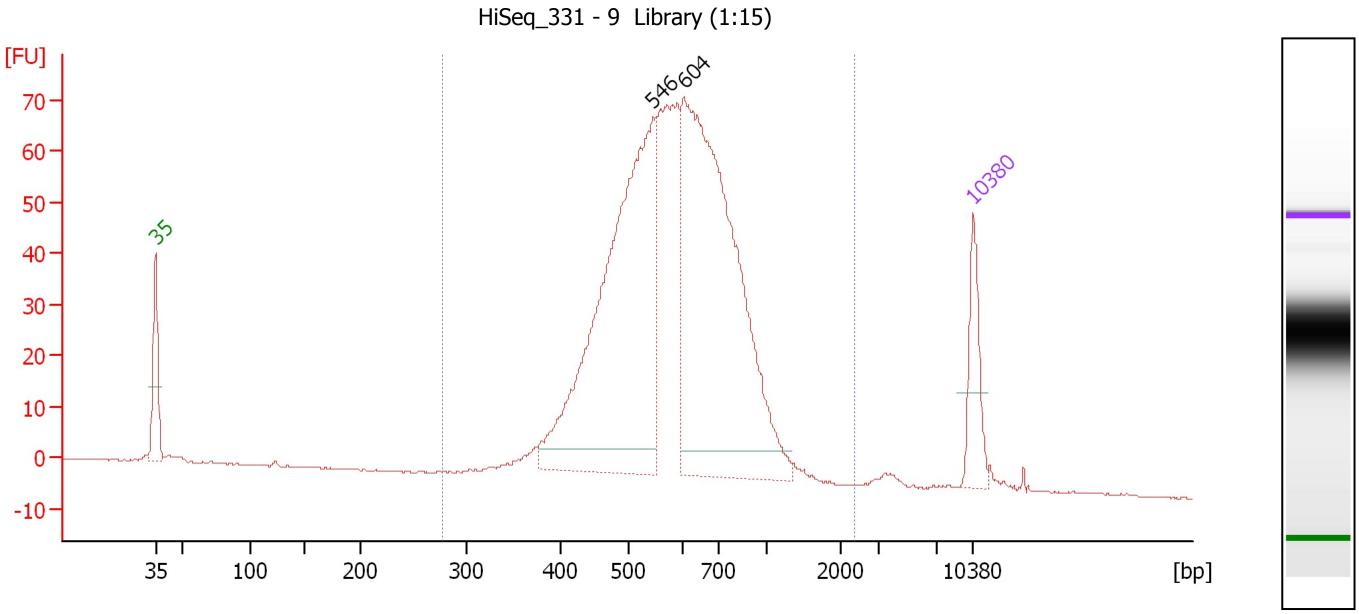
Peak table for sample 9 : **HiSeq_331 - 8 Library (1:15)**

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		483	599.63	1,879.7		82.50
3		512	228.74	676.3		84.04
4		543	154.52	431.1		85.47
5		558	175.87	477.1		86.19
6		581	190.88	497.4		87.26
7		595	226.56	577.3		87.88
8		633	261.99	627.4		89.15
9		685	497.48	1,100.7		90.79
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : **HiSeq_331 - 8 Library (1:15)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
295	1,693	595	922.1	7,334.6	🟦	2,667.60	94	26.7

Electropherogram Summary Continued ...



Overall Results for sample 10 : HiSeq_331 - 9 Library (1:15)

Number of peaks found:	2	Corr. Area 1:	1,054.7
Noise:	0.1		

Peak table for sample 10 : HiSeq_331 - 9 Library (1:15)

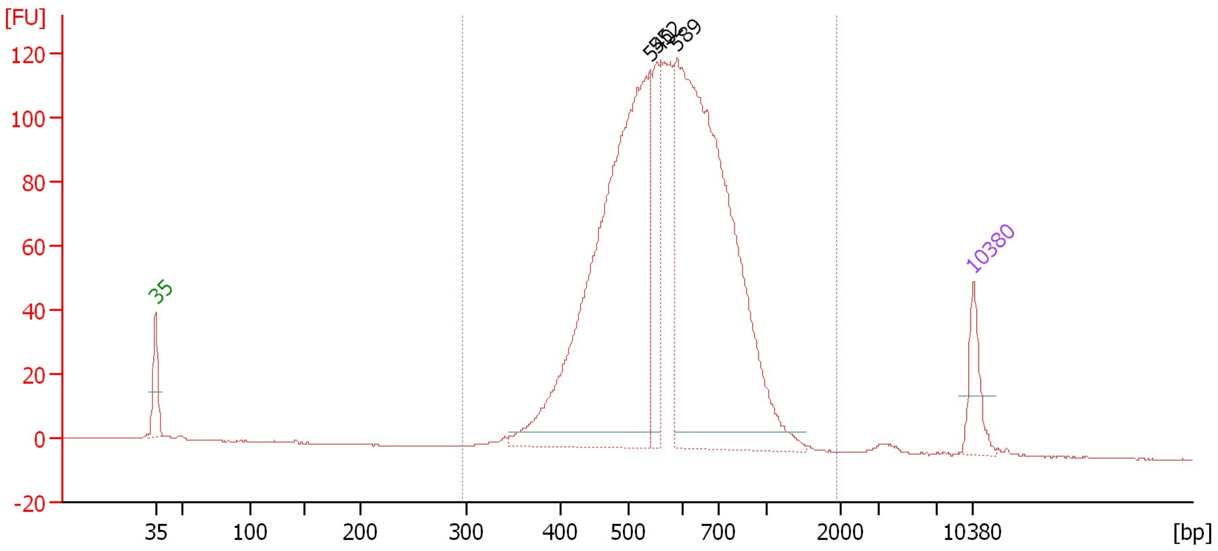
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		546	860.37	2,387.1		85.61
3		604	900.56	2,260.5		88.24
4	▶	10,380	75.00	10.9	Upper Marker	113.00

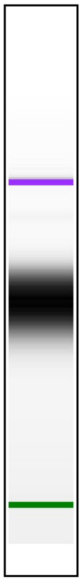
Region table for sample 10 : HiSeq_331 - 9 Library (1:15)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
277	2,381	614	1,054.7	6,015.0	🟦	2,255.53	97	28.0

Electropherogram Summary Continued ...

HiSeq_331 - 10 Library (1:15)





Overall Results for sample 11 : **HiSeq_331 - 10 Library (1:15)**

Number of peaks found:	3	Corr. Area 1:	1,748.1
Noise:	0.1		

Peak table for sample 11 : **HiSeq_331 - 10 Library (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		540	1,444.84	4,055.9		85.31
3		552	228.85	628.2		85.88
4		589	1,484.17	3,819.3		87.60
5	▶	10,380	75.00	10.9	Upper Marker	113.00

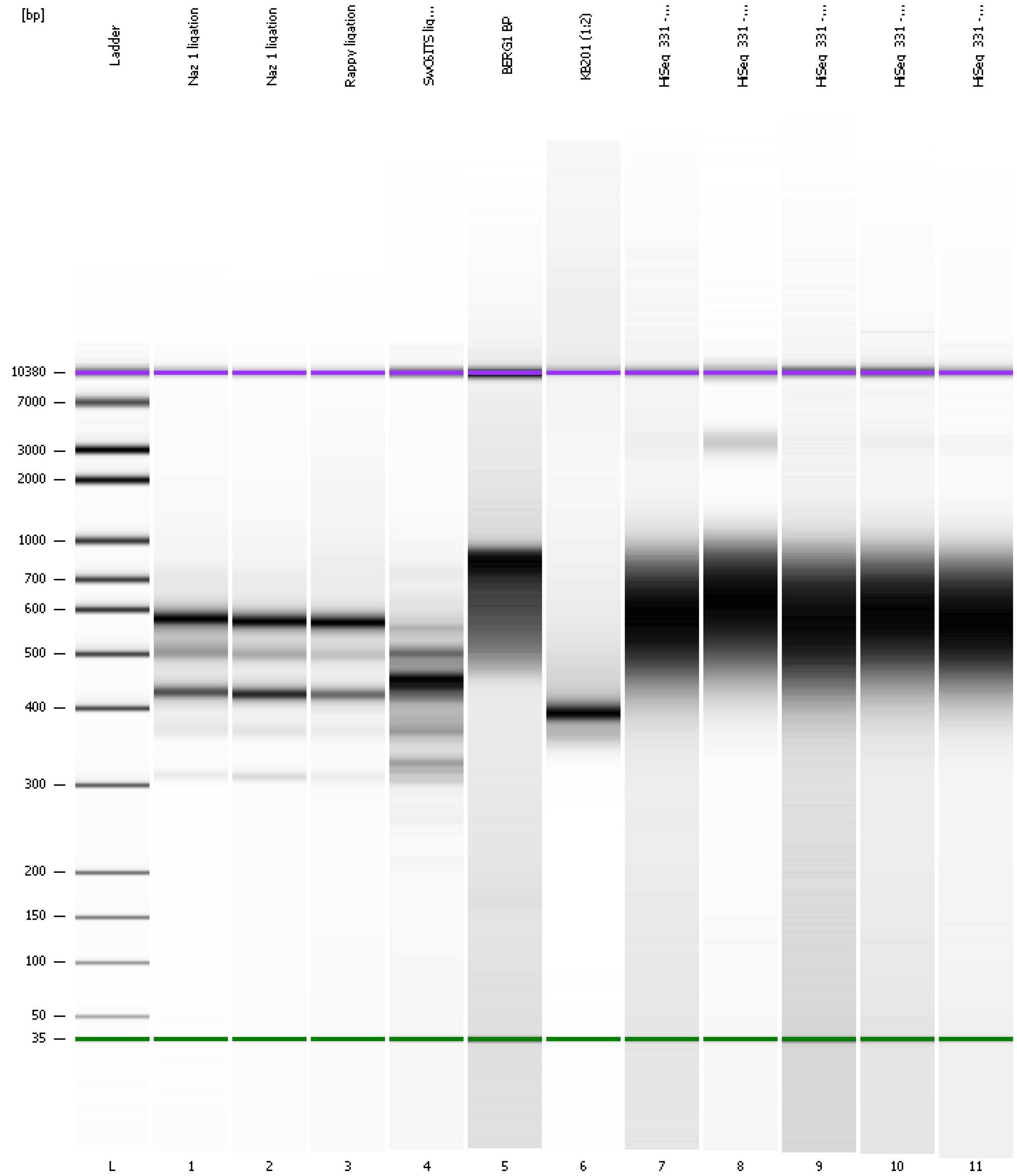
Region table for sample 11 : **HiSeq_331 - 10 Library (1:15)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
295	1,945	597	1,748.1	9,707.6	🟦	3,569.25	98	26.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad

Created: 2/12/2016 12:03:42 PM
Modified: 2/12/2016 3:04:02 PM

Gel Image



Printed: 2/12/2016 3:09:55 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		2/12/2016 12:45:00 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-02-12\2016-02-12_001.xad)		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		2/12/2016 12:03:47 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1