

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-01-27\2015-01-27_001.xad

Created: 1/27/2015 9:08:26 AM
Modified: 1/27/2015 9:42:10 AM

Electrophoresis File Run Summary

Instrument Information:

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

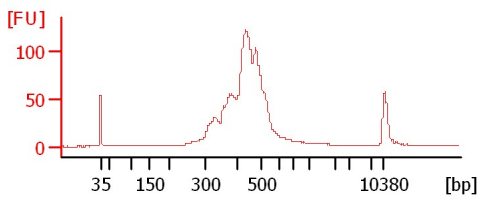
Assay Information:

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

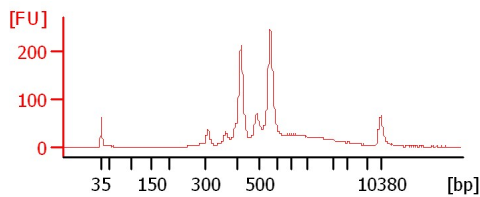
Chip Information:

Chip Lot #:
Reagent Kit Lot #:
Chip Comments:

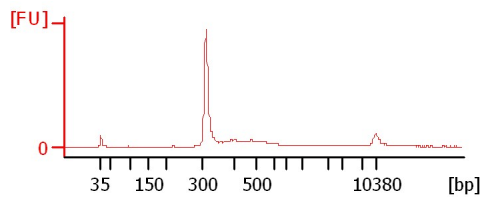
NM14CITS ligation rxn



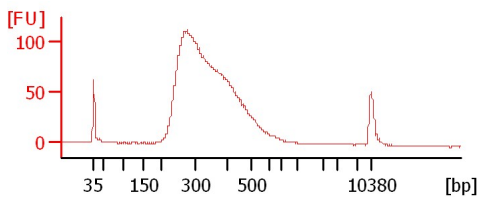
January V4 ligation rxn (1:3)



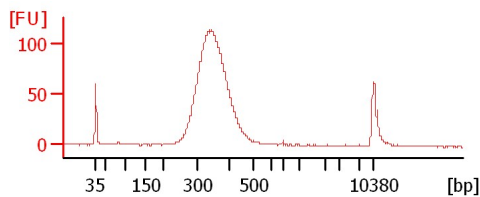
January V4 DNA (1:60)



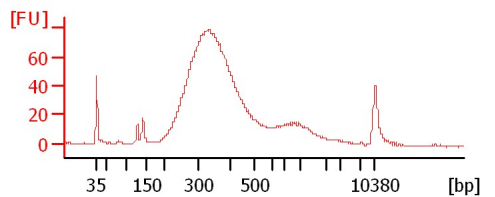
CWZ_23X



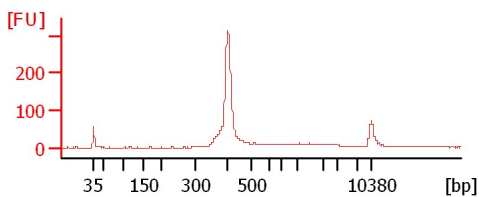
BAC_5X lib



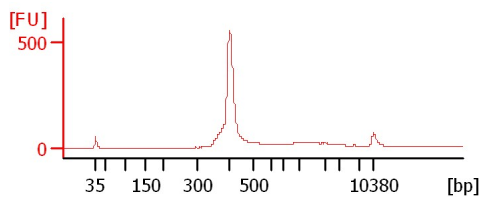
RAD SYM LIB



ARB_5 (1:2)



ARB_5



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
NM14CITS ligation rxn		<input type="checkbox"/>	✓			
January V4 ligation rxn (1:3)		<input type="checkbox"/>	✓			
January V4 DNA (1:60)		<input type="checkbox"/>	✓			
CWZ_23X		<input type="checkbox"/>	✓			
BAC_5X lib		<input type="checkbox"/>	✓			
RAD SYM LIB		<input type="checkbox"/>	✓			
ARB_5 (1:2)		<input type="checkbox"/>	✓			
ARB_5		<input type="checkbox"/>	✓			
sample 9		<input type="checkbox"/>				
sample 10		<input type="checkbox"/>				
sample 11		<input type="checkbox"/>				
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

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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

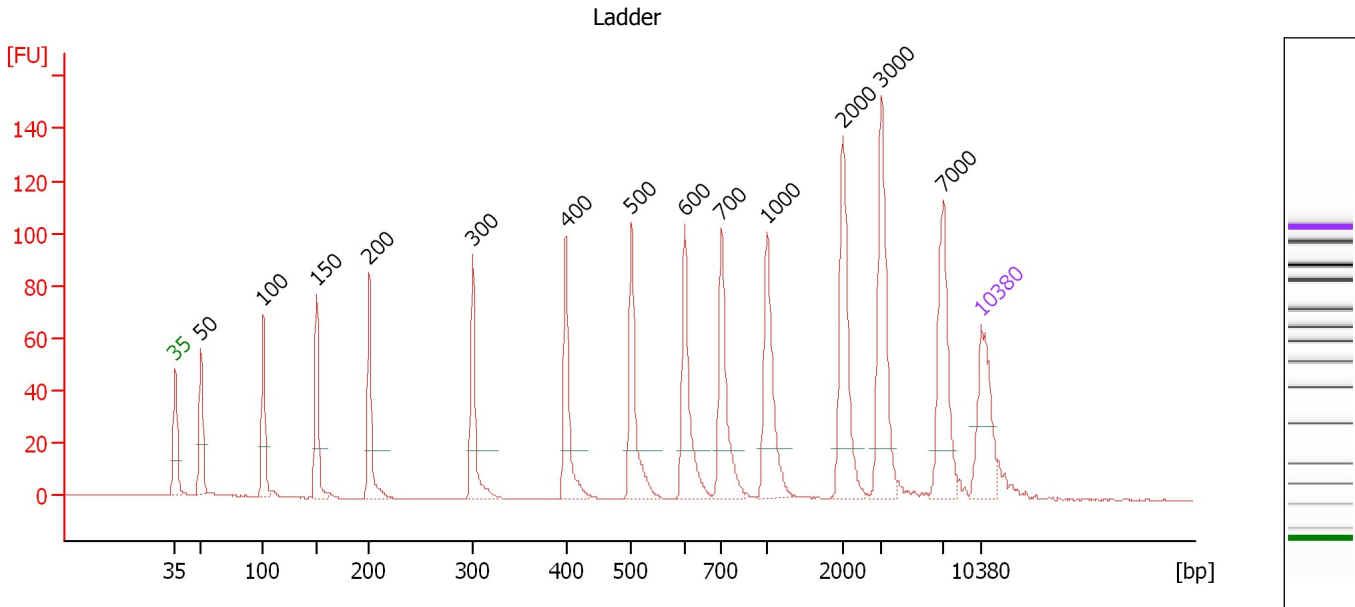
Ladder

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

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Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

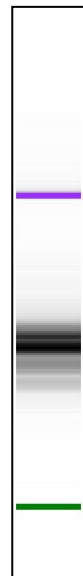
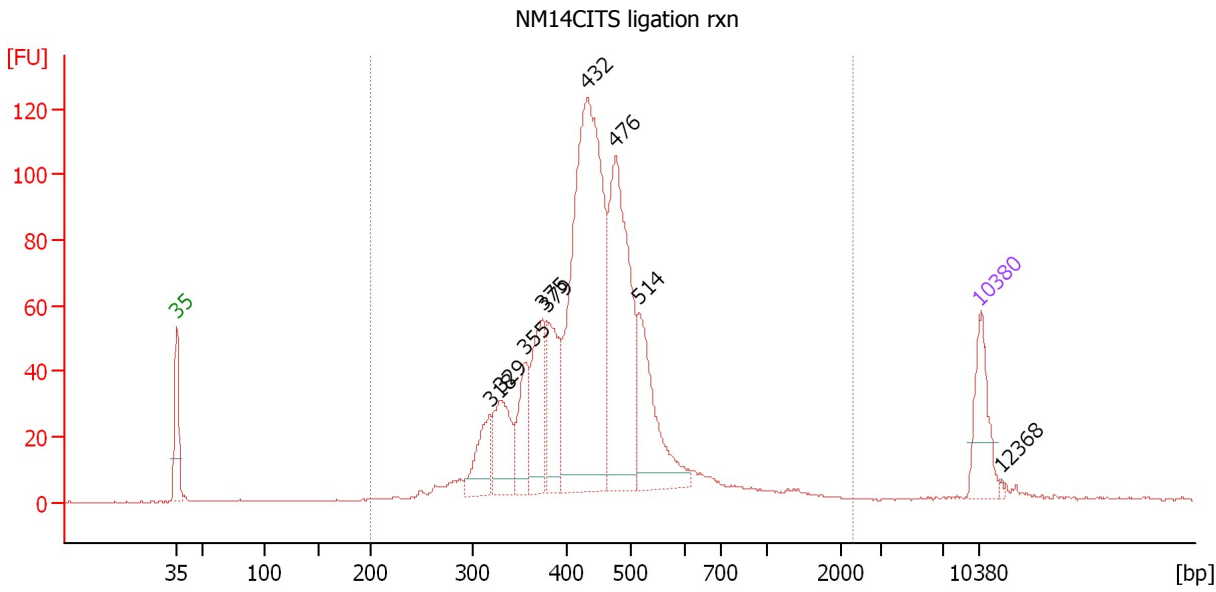
Peak table for Ladder

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	45.22
3	100	150.00	2,272.7	Ladder Peak	50.64
4	150	150.00	1,515.2	Ladder Peak	55.28
5	200	150.00	1,136.4	Ladder Peak	59.86
6	300	150.00	757.6	Ladder Peak	68.85
7	400	150.00	568.2	Ladder Peak	76.96
8	500	150.00	454.5	Ladder Peak	82.66
9	600	150.00	378.8	Ladder Peak	87.24
10	700	150.00	324.7	Ladder Peak	90.49
11	1,000	150.00	227.3	Ladder Peak	94.42
12	2,000	150.00	113.6	Ladder Peak	101.00
13	3,000	150.00	75.8	Ladder Peak	104.38
14	7,000	150.00	32.5	Ladder Peak	109.76
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : NM14CITS ligation rxn

Number of peaks found: 9 Corr. Area 1: 1,432.2
 Noise: 0.2

Peak table for sample 1 : NM14CITS ligation rxn

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	91.30	435.1		70.30
3	329	119.02	547.5		71.23
4	355	101.63	433.5		73.33
5	375	141.74	573.1		74.91
6	379	147.06	588.3		75.23
7	432	762.44	2,675.6		78.77
8	476	407.45	1,297.4		81.28
9	514	189.82	560.0		83.28
10	10,380	75.00	10.9	Upper Marker	113.00
11	12,368	0.00	0.0		114.91

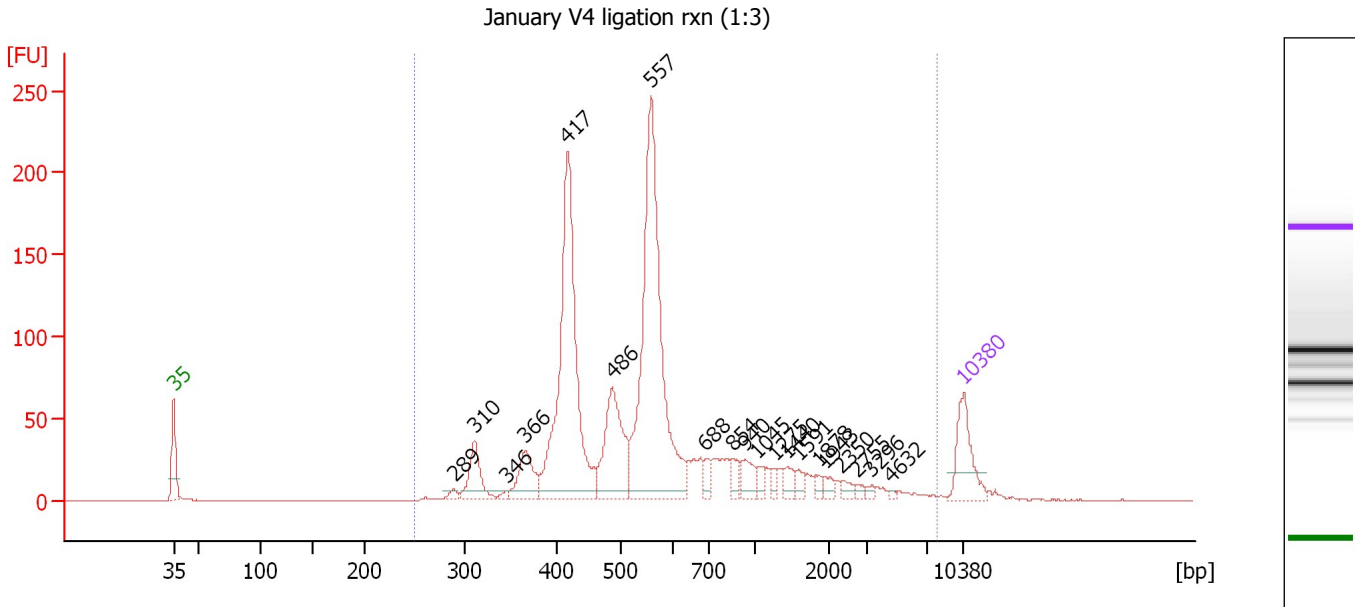
Region table for sample 1 : NM14CITS ligation rxn

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	454	2,279	1,432.2	98	33.0	2,220.92	7,991.2	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 2 : January V4 ligation rxn (1:3)

Number of peaks found: 20 Corr. Area 1: 1,737.9
 Noise: 0.2

Peak table for sample 2 : January V4 ligation rxn (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	289	11.83	62.1		67.84
3	310	84.96	414.8		69.69
4	346	7.25	31.8		72.57
5	366	81.17	336.3		74.17
6	417	578.97	2,105.5		77.91
7	486	197.91	616.7		81.87
8	557	636.63	1,731.5		85.27
9	688	21.52	47.4		90.09
10	854	23.44	41.6		92.50
11	940	35.04	56.5		93.63
12	1,045	14.46	21.0		94.72
13	1,275	13.29	15.8		96.23
14	1,440	19.25	20.3		97.32
15	1,591	14.51	13.8		98.31
16	1,878	10.29	8.3		100.20
17	1,943	13.42	10.5		100.62
18	2,350	11.11	7.2		102.18
19	2,755	6.31	3.5		103.55
20	3,296	6.87	3.2		104.78
21	4,632	2.91	1.0		106.58
22	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...

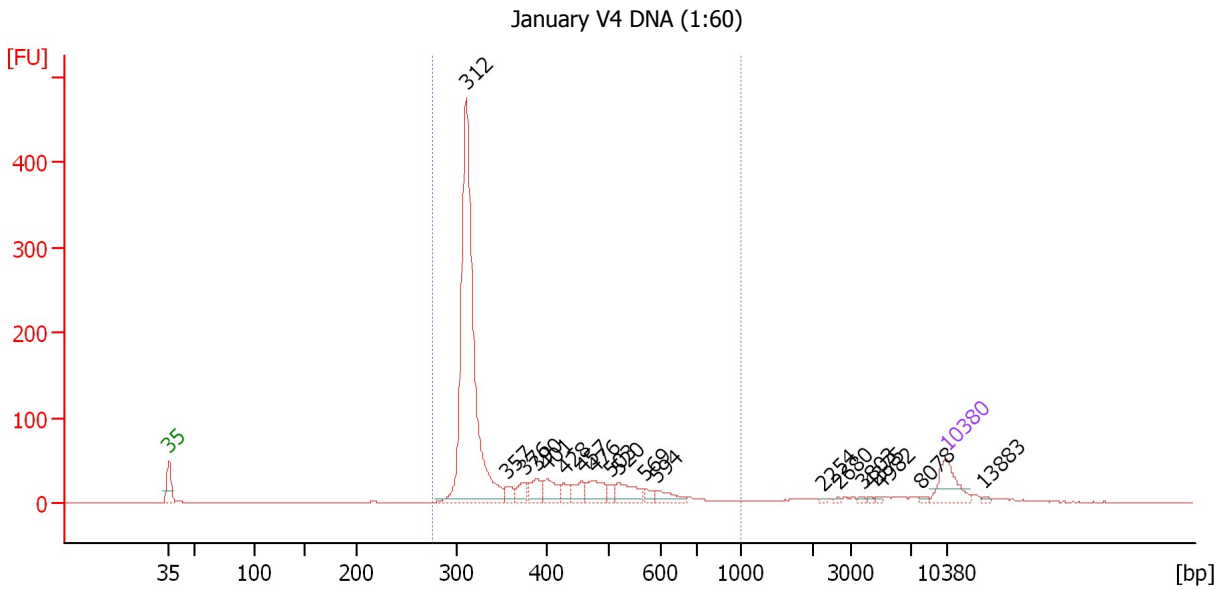
... Region table for sample 2 : January V4 ligation rxn (1:3)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/ μ l]	Molarity [pmol/l]	Color
251	759	7,943	1,737.9	98	100.0	2,013.20	5,949.2	

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Electropherogram Summary Continued ...



Overall Results for sample 3 : January V4 DNA (1:60)

Number of peaks found: 19 Corr. Area 1: 1,344.7
 Noise: 0.2

Peak table for sample 3 : January V4 DNA (1:60)

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	1,237.68	6,018.4		69.79
3	357	32.67	138.8		73.44
4	376	41.29	166.6		74.98
5	390	58.13	226.0		76.13
6	401	61.25	231.2		77.04
7	428	33.52	118.6		78.58
8	457	42.36	140.4		80.21
9	476	72.06	229.2		81.31
10	503	20.52	61.8		82.80
11	520	69.29	201.9		83.57
12	569	20.92	55.7		85.83
13	594	36.44	92.9		86.98
14	2,254	2.94	2.0		101.86
15	2,680	3.87	2.2		103.30
16	3,803	4.65	1.9		105.46
17	4,375	4.08	1.4		106.23
18	4,982	4.50	1.4		107.05
19	8,078	4.74	0.9		110.79
20	10,380	75.00	10.9	Upper Marker	113.00
21	13,883	0.00	0.0		116.36

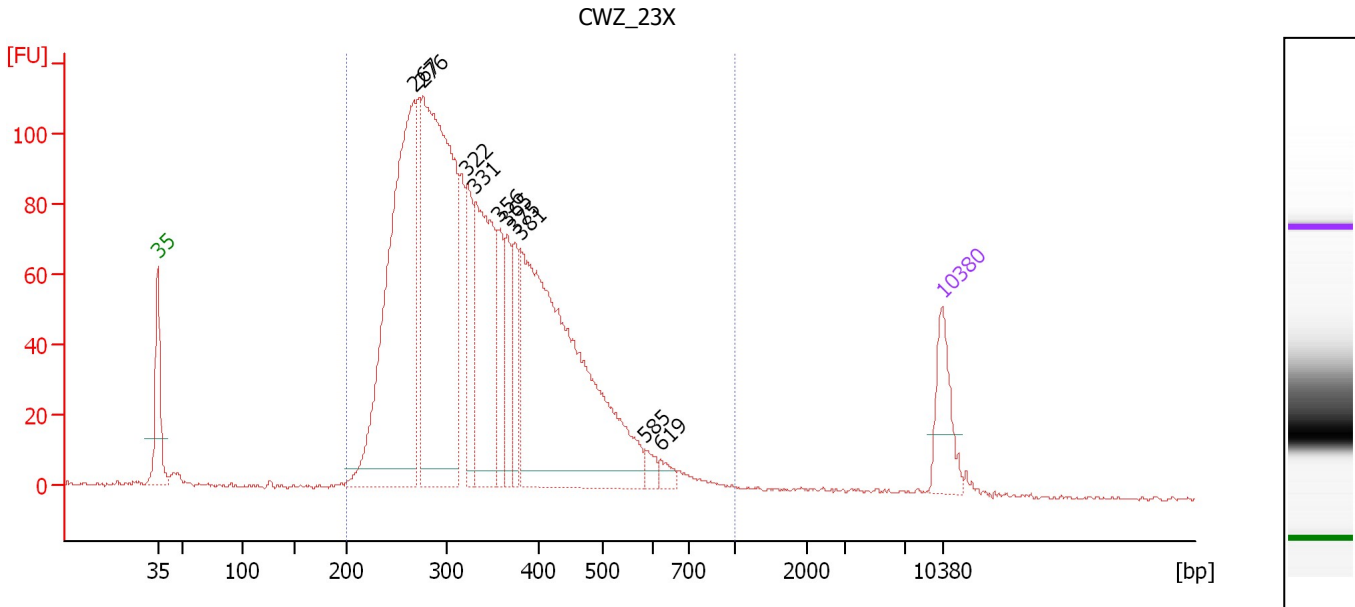
Region table for sample 3 : January V4 DNA (1:60)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
276	375	1,000	1,344.7	91	26.9	1,756.99	7,617.9	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 4 : CWZ_23X

Number of peaks found: 10 Corr. Area 1: 2,319.8
 Noise: 0.5

Peak table for sample 4 : CWZ_23X

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	267	849.65	4,829.6		65.84
3	276	936.31	5,143.7		66.68
4	322	147.85	695.6		70.64
5	331	364.05	1,666.0		71.37
6	356	110.36	469.9		73.38
7	365	112.09	464.7		74.16
8	375	92.65	374.2		74.94
9	381	877.82	3,494.8		75.38
10	585	19.10	49.5		86.54
11	619	17.45	42.7		87.86
12	10,380	75.00	10.9	Upper Marker	113.00

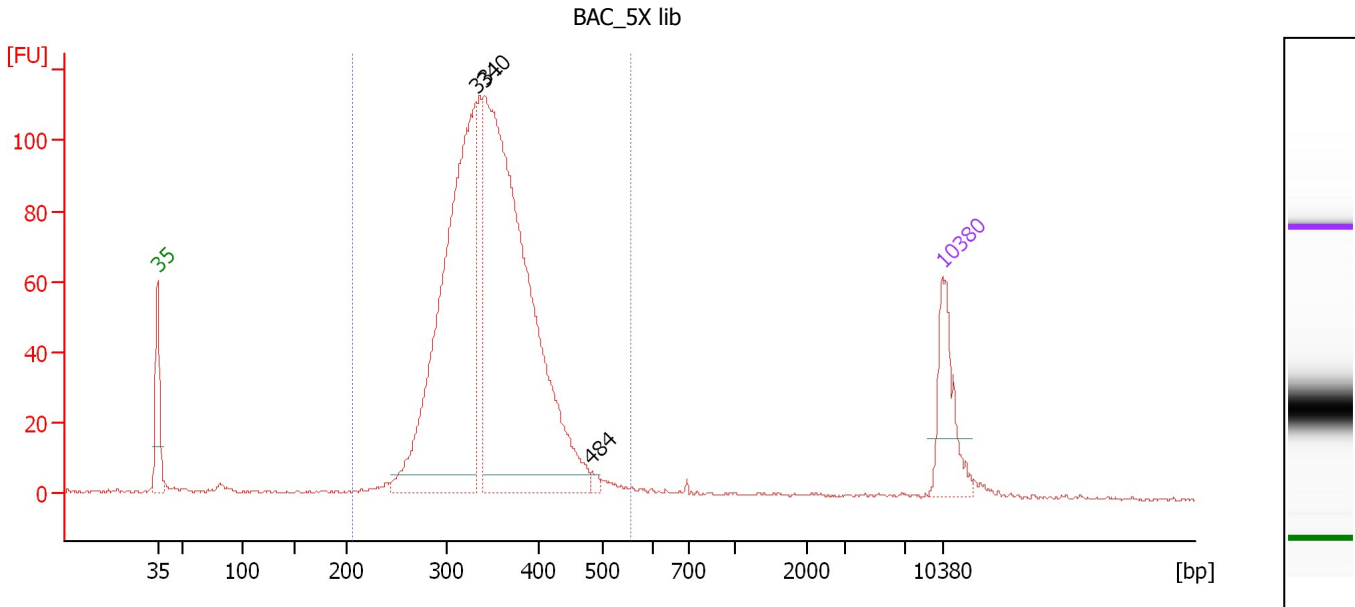
Region table for sample 4 : CWZ_23X

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
200	349	1,000	2,319.8	98	27.9	3,780.18	17,934.3	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 5 : BAC_5X lib

Number of peaks found: 3 Corr. Area 1: 1,407.0
 Noise: 0.5

Peak table for sample 5 : BAC_5X 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	331	706.80	3,232.5		71.39
3	340	935.08	4,161.0		72.13
4	484	7.78	24.4		81.73
5	10,380	75.00	10.9	Upper Marker	113.00

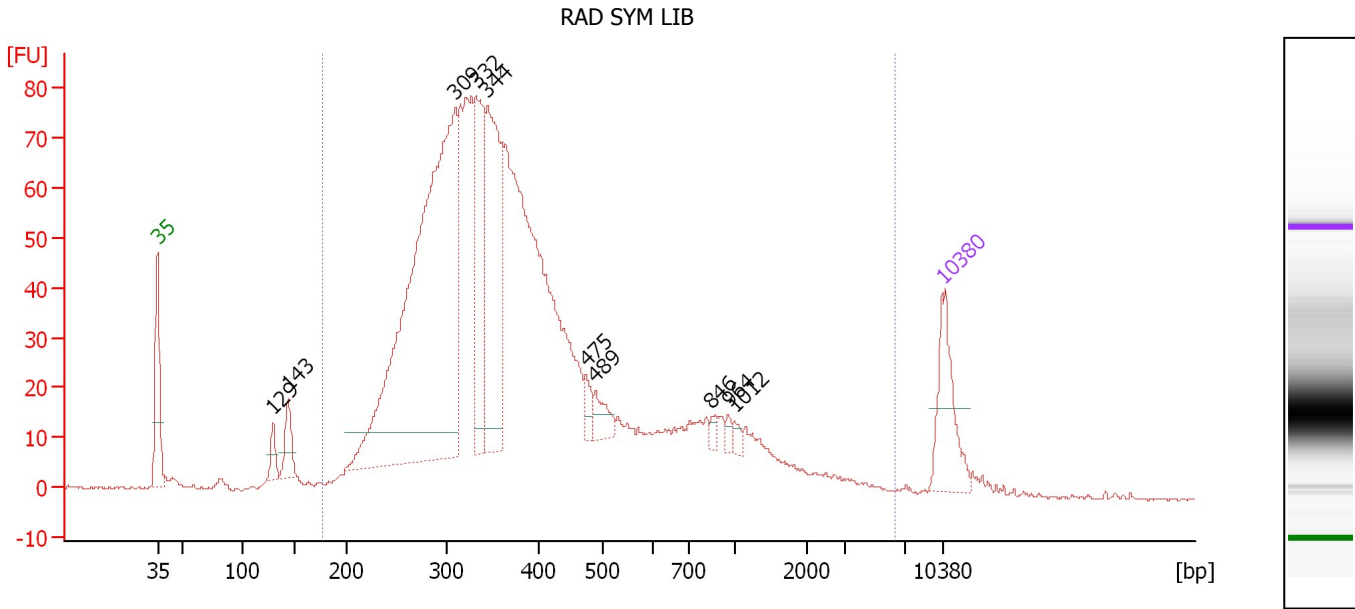
Region table for sample 5 : BAC_5X lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
206	348	557	1,407.0	96	13.6	1,773.90	7,888.6	Blue

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 6 : RAD SYM LIB

Number of peaks found: 10 Corr. Area 1: 1,775.6
 Noise: 0.3

Peak table for sample 6 : RAD SYM 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	129	27.15	319.7		53.30
3	143	50.83	537.6		54.65
4	309	977.24	4,797.6		69.55
5	332	202.33	923.2		71.45
6	344	275.80	1,213.3		72.45
7	475	21.01	67.0		81.25
8	489	29.00	89.8		82.05
9	846	8.04	14.4		92.40
10	964	7.42	11.7		93.95
11	1,012	8.24	12.3		94.50
12	10,380	75.00	10.9	Upper Marker	113.00

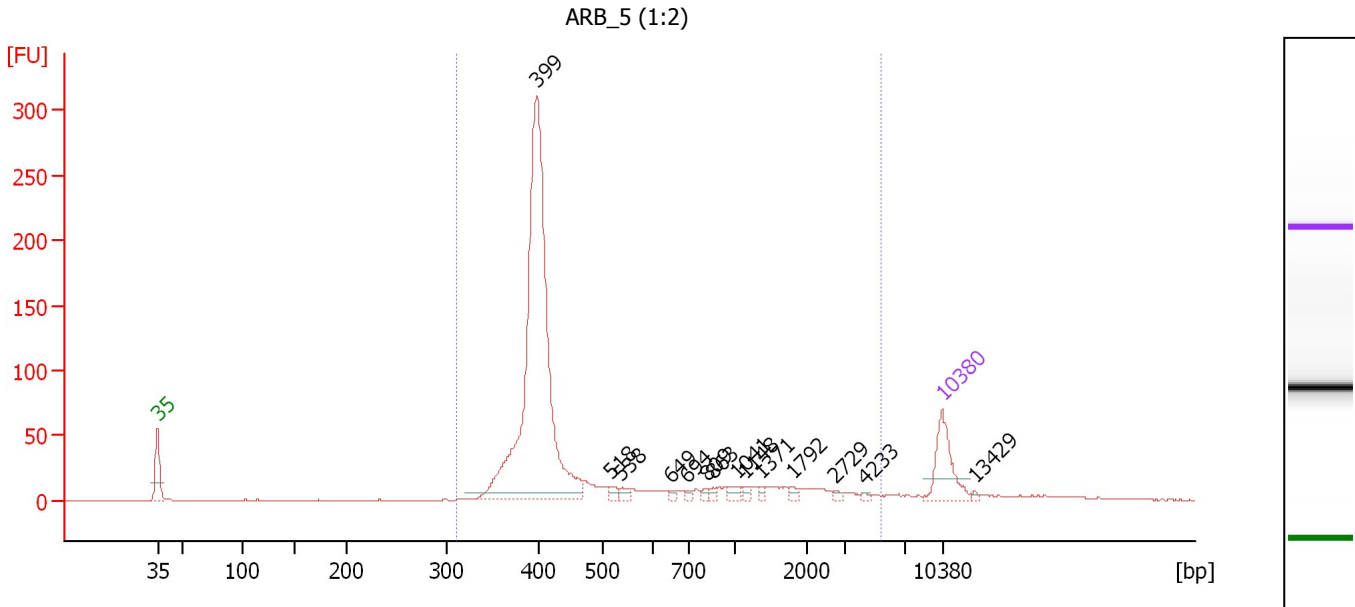
Region table for sample 6 : RAD SYM LIB

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
176	481	6,297	1,775.6	96	98.1	3,449.86	14,990.4	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 7 : ARB 5 (1:2)

Number of peaks found: 14 Corr. Area 1: 1,189.3
 Noise: 0.2

Peak table for sample 7 : ARB 5 (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	399	986.23	3,749.3		76.84
3	518	10.97	32.1		83.50
4	538	10.63	29.9		84.40
5	649	6.06	14.1		88.84
6	694	6.08	13.3		90.31
7	809	7.16	13.4		91.92
8	863	6.29	11.0		92.63
9	1,041	12.85	18.7		94.69
10	1,148	8.33	11.0		95.40
11	1,371	6.10	6.7		96.86
12	1,792	6.09	5.1		99.64
13	2,729	4.47	2.5		103.47
14	4,233	3.61	1.3		106.04
15	10,380	75.00	10.9	Upper Marker	113.00
16	13,429	0.00	0.0		115.93

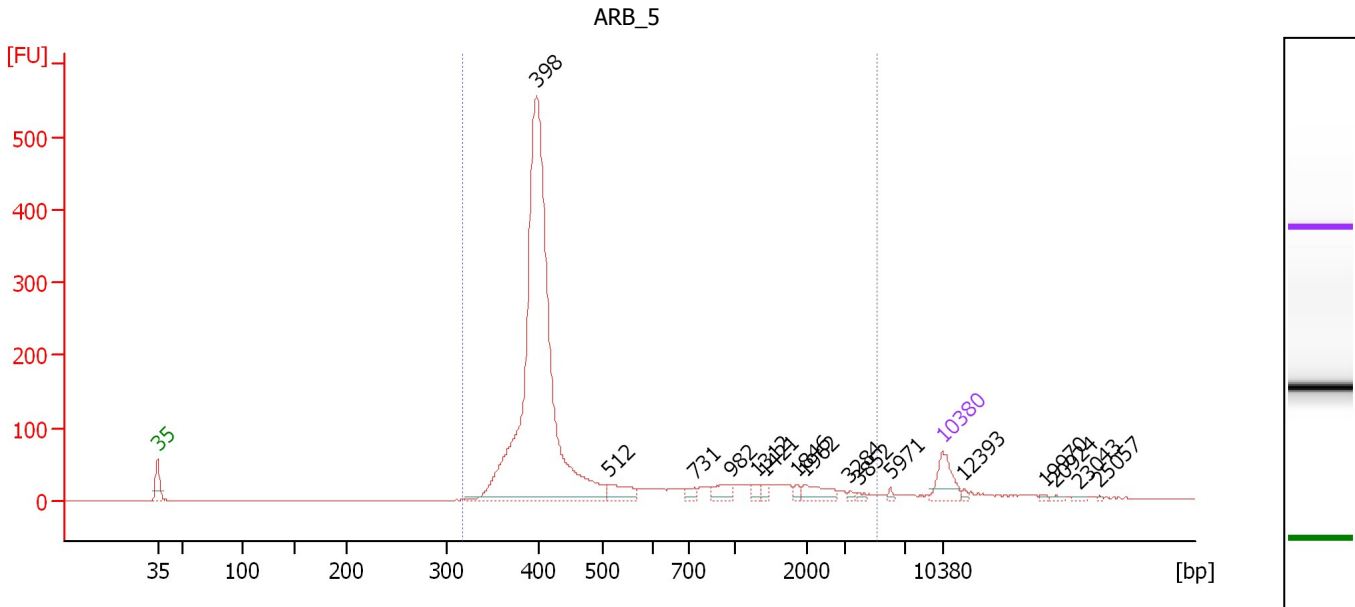
Region table for sample 7 : ARB 5 (1:2)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
310	643	5,339	1,189.3	94	100.0	1,258.32	4,295.9	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 8 : ARB_5

Number of peaks found: 16 Corr. Area 1: 2,312.6
 Noise: 0.4

Peak table for sample 8 : ARB_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	398	2,154.23	8,198.4		76.81
3	512	68.28	202.0		83.21
4	731	22.00	45.6		90.89
5	982	38.84	59.9		94.19
6	1,312	19.42	22.4		96.48
7	1,421	13.70	14.6		97.19
8	1,846	12.68	10.4		99.99
9	1,962	48.47	37.4		100.75
10	3,284	6.74	3.1		104.76
11	3,852	8.17	3.2		105.53
12	5,971	6.78	1.7		108.37
13	10,380	75.00	10.9	Upper Marker	113.00
14	12,393	0.00	0.0		114.93
15	19,970	0.00	0.0		122.20
16	20,924	0.00	0.0		123.12
17	23,043	0.00	0.0		125.15
18	25,057	0.00	0.0		127.08

Region table for sample 8 : ARB_5

From [bp]	Average Size [bp]	To [bp]	Corr. Area	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Molarity [pmol/l]	Color
316	634	5,082	2,312.6	95	97.3	2,623.99	8,931.7	Blue

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Gel Image

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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.

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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		1/27/2015 9:41:09 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-01-27\2015-01-27_001.xad)		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/27/2015 9:08:32 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1