

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
Modified: 1/13/2016 2:51:28 PM

### Electrophoresis File Run Summary

#### Instrument Information:

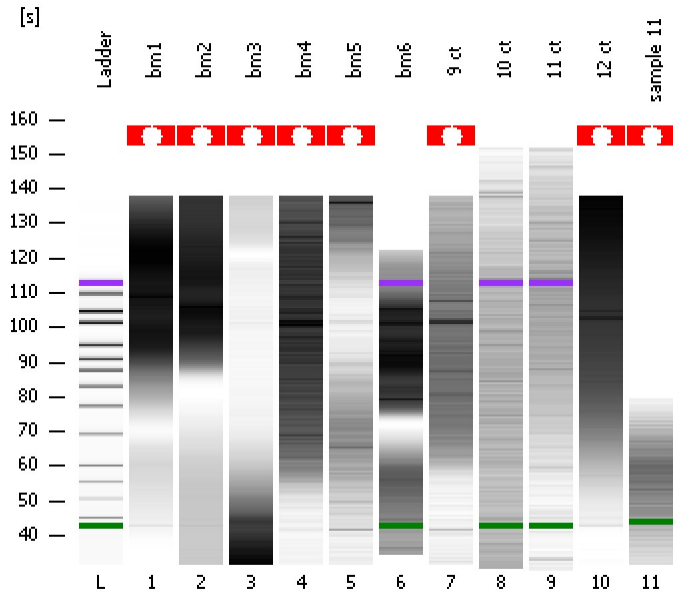
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

#### 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:

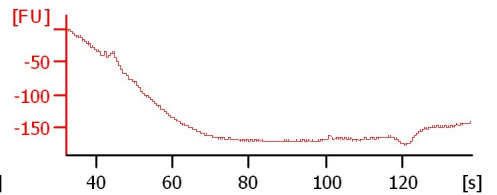
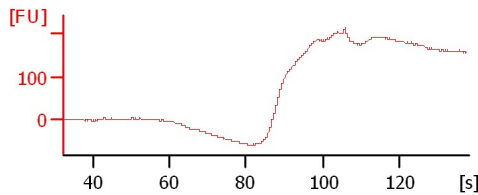
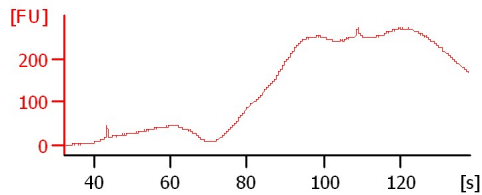
Chip Lot #:      Reagent Kit Lot #:      Chip Comments:



bm1

bm2

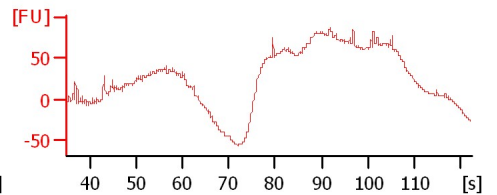
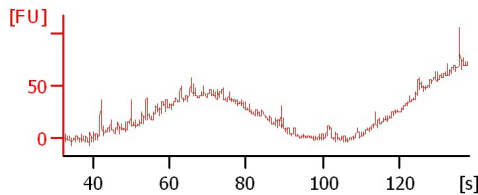
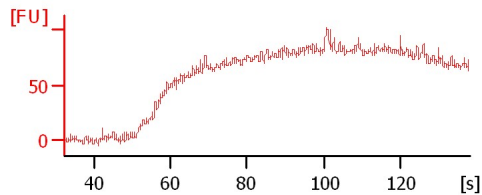
bm3



bm4

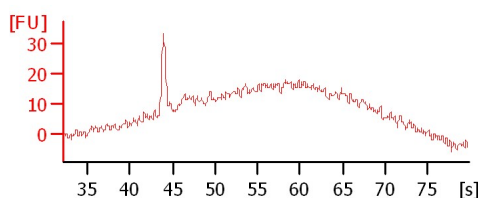
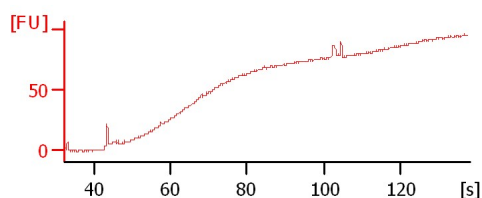
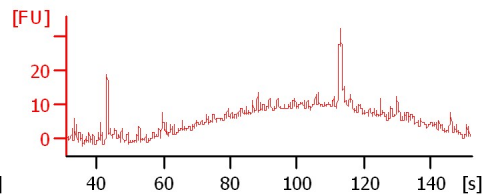
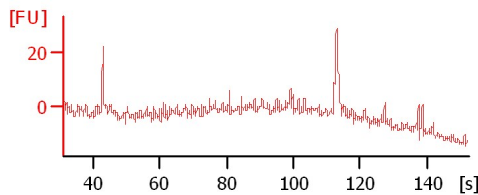
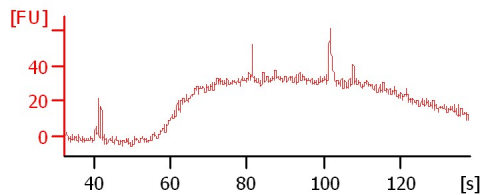
bm5

bm6



12 ct

sample 11



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
bm1		<input type="checkbox"/>	✓			
bm2		<input type="checkbox"/>	✓			
bm3		<input type="checkbox"/>	✓			
bm4		<input type="checkbox"/>	✓			
bm5		<input type="checkbox"/>	✓			
bm6		<input type="checkbox"/>	✓			
9 ct		<input type="checkbox"/>	✓			
10 ct		<input type="checkbox"/>	✓			
11 ct		<input type="checkbox"/>	✓			
12 ct		<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

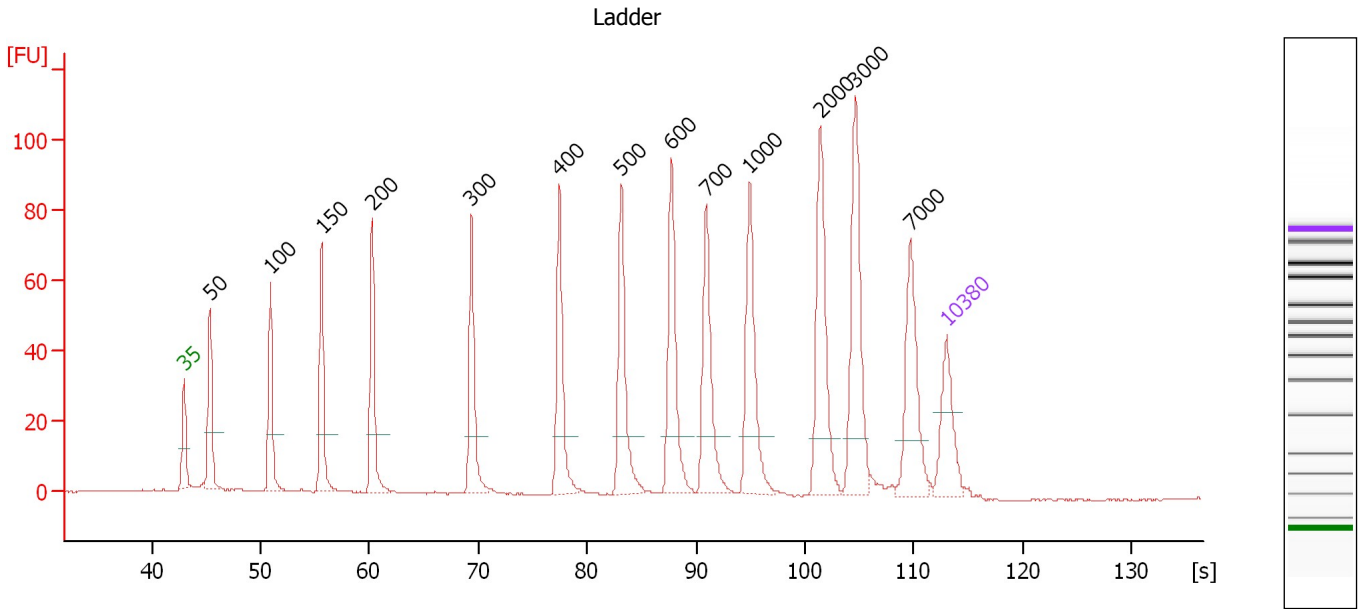
**Ladder**

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

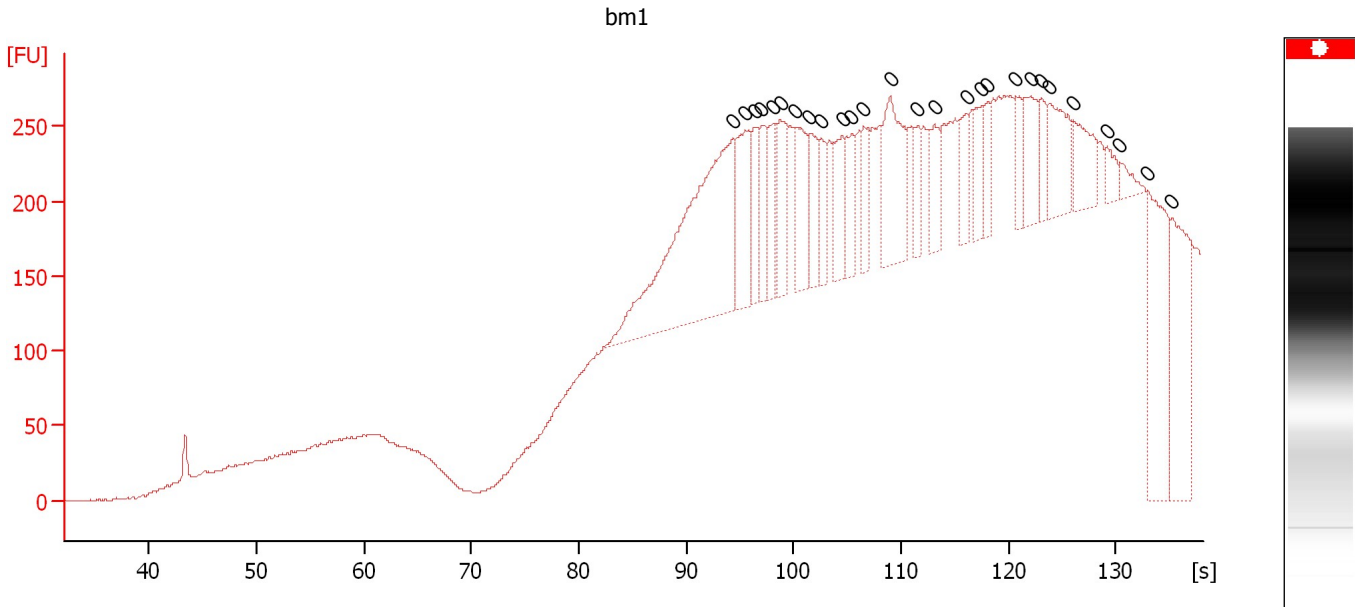
**Peak table for Ladder**

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	45.37
3	100	150.00	2,272.7	Ladder Peak	50.94
4	150	150.00	1,515.2	Ladder Peak	55.62
5	200	150.00	1,136.4	Ladder Peak	60.25
6	300	150.00	757.6	Ladder Peak	69.37
7	400	150.00	568.2	Ladder Peak	77.46
8	500	150.00	454.5	Ladder Peak	83.13
9	600	150.00	378.8	Ladder Peak	87.71
10	700	150.00	324.7	Ladder Peak	90.92
11	1,000	150.00	227.3	Ladder Peak	94.91
12	2,000	150.00	113.6	Ladder Peak	101.42
13	3,000	150.00	75.8	Ladder Peak	104.67
14	7,000	150.00	32.5	Ladder Peak	109.65
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : bm1**

Number of peaks found: 0                      Noise: 0.8

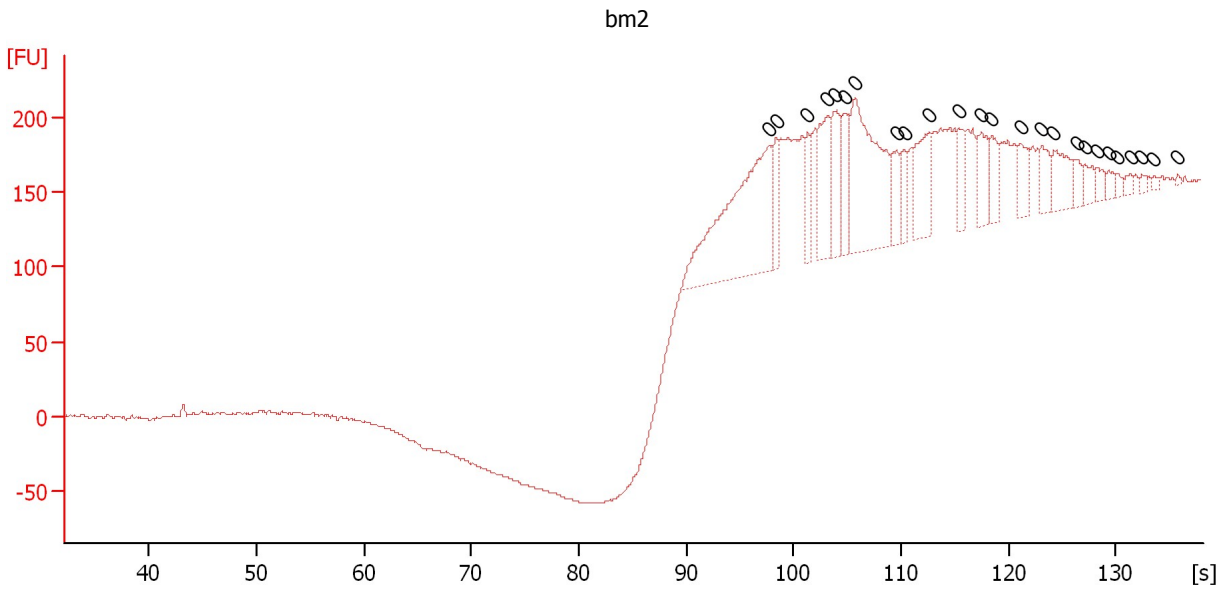
**Peak table for sample 1 : bm1**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		94.40
2	0	0.00	0.0		95.55
3	0	0.00	0.0		96.40
4	0	0.00	0.0		97.00
5	0	0.00	0.0		98.15
6	0	0.00	0.0		98.75
7	0	0.00	0.0		100.20
8	0	0.00	0.0		101.45
9	0	0.00	0.0		102.55
10	0	0.00	0.0		104.55
11	0	0.00	0.0		105.35
12	0	0.00	0.0		106.55
13	0	0.00	0.0		109.00
14	0	0.00	0.0		111.55
15	0	0.00	0.0		113.10
16	0	0.00	0.0		116.10
17	0	0.00	0.0		117.45
18	0	0.00	0.0		118.10
19	0	0.00	0.0		120.70
20	0	0.00	0.0		122.05
21	0	0.00	0.0		123.10
22	0	0.00	0.0		123.70
23	0	0.00	0.0		126.00
24	0	0.00	0.0		129.15
25	0	0.00	0.0		130.40
26	0	0.00	0.0		133.00
27	0	0.00	0.0		135.25

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : bm2**

Number of peaks found: 0                      Noise: 0.8

**Peak table for sample 2 : bm2**

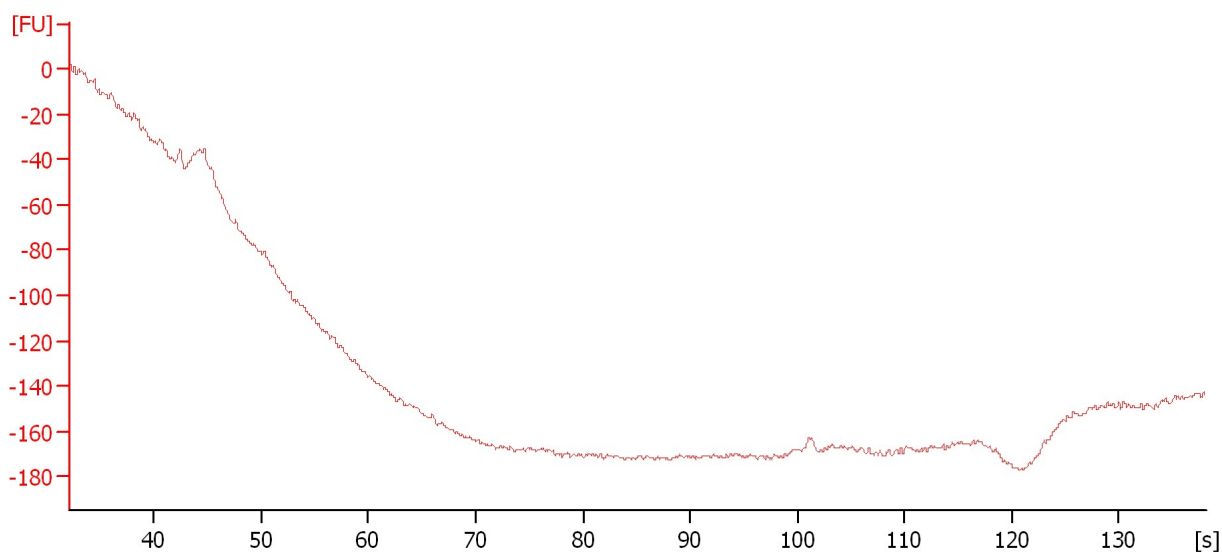
Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		97.75
2	0	0.00	0.0		98.45
3	0	0.00	0.0		101.30
4	0	0.00	0.0		103.15
5	0	0.00	0.0		103.80
6	0	0.00	0.0		104.75
7	0	0.00	0.0		105.70
8	0	0.00	0.0		109.60
9	0	0.00	0.0		110.30
10	0	0.00	0.0		112.65
11	0	0.00	0.0		115.35
12	0	0.00	0.0		117.45
13	0	0.00	0.0		118.45
14	0	0.00	0.0		121.10
15	0	0.00	0.0		123.10
16	0	0.00	0.0		124.25
17	0	0.00	0.0		126.35
18	0	0.00	0.0		127.10
19	0	0.00	0.0		128.25
20	0	0.00	0.0		129.30
21	0	0.00	0.0		130.15
22	0	0.00	0.0		131.35
23	0	0.00	0.0		132.45
24	0	0.00	0.0		133.45
25	0	0.00	0.0		135.75

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**Electropherogram Summary Continued ...**

bm3



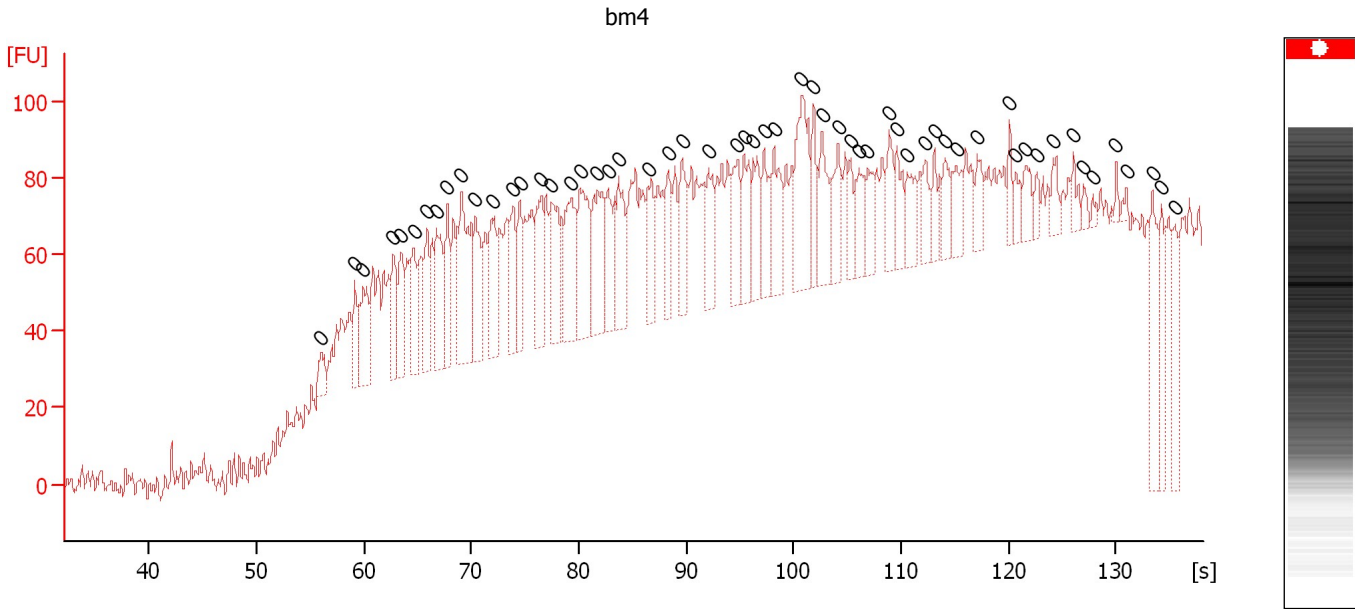
**Overall Results for sample 3 : bm3**

Noise: 1.3

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : bm4**

Number of peaks found: 0                      Noise: 3.9

**Peak table for sample 4 : bm4**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		55.95
2	0	0.00	0.0		59.15
3	0	0.00	0.0		59.95
4	0	0.00	0.0		62.70
5	0	0.00	0.0		63.45
6	0	0.00	0.0		64.65
7	0	0.00	0.0		65.90
8	0	0.00	0.0		66.80
9	0	0.00	0.0		67.75
10	0	0.00	0.0		69.05
11	0	0.00	0.0		70.35
12	0	0.00	0.0		71.90
13	0	0.00	0.0		73.90
14	0	0.00	0.0		74.50
15	0	0.00	0.0		76.50
16	0	0.00	0.0		77.45
17	0	0.00	0.0		79.25
18	0	0.00	0.0		80.10
19	0	0.00	0.0		81.75
20	0	0.00	0.0		82.70
21	0	0.00	0.0		83.70
22	0	0.00	0.0		86.45
23	0	0.00	0.0		88.30
24	0	0.00	0.0		89.60
25	0	0.00	0.0		92.10
26	0	0.00	0.0		94.75
27	0	0.00	0.0		95.40



Assay Class: High Sensitivity DNA Assay  
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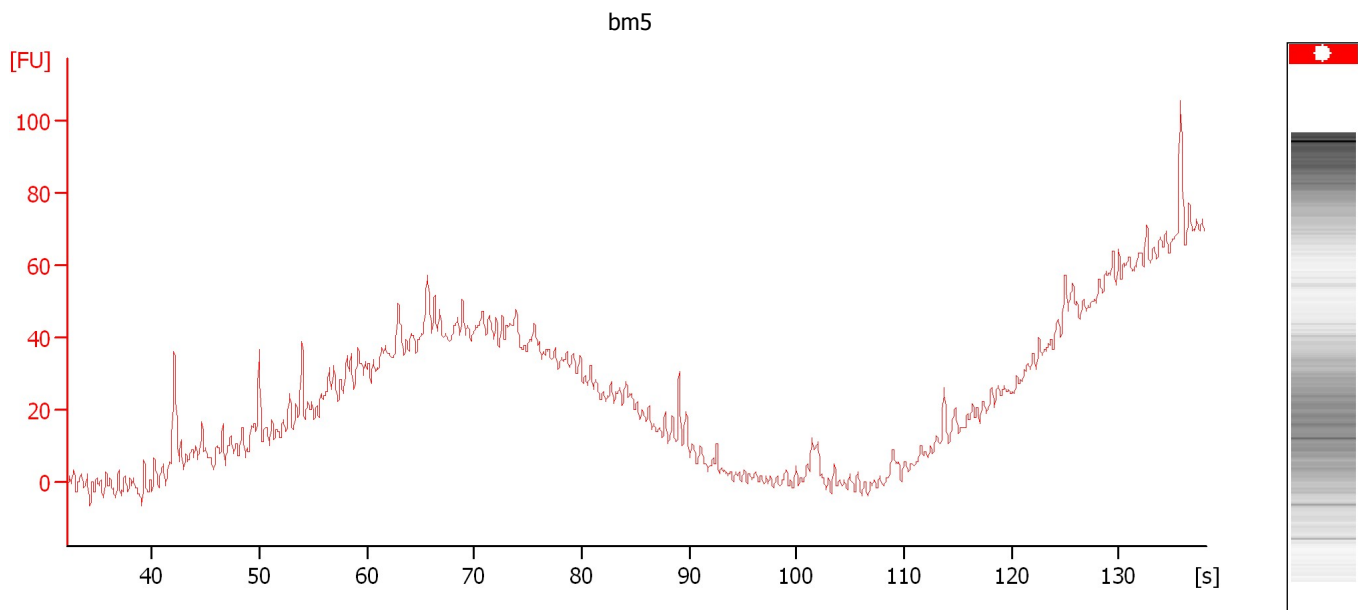
**Electropherogram Summary Continued ...****... Peak table for sample 4 : bm4**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
28	0	0.00	0.0		96.25
29	0	0.00	0.0		97.25
30	0	0.00	0.0		98.20
31	0	0.00	0.0		100.75
32	0	0.00	0.0		101.85
33	0	0.00	0.0		102.65
34	0	0.00	0.0		104.15
35	0	0.00	0.0		105.30
36	0	0.00	0.0		106.05
37	0	0.00	0.0		106.90
38	0	0.00	0.0		108.90
39	0	0.00	0.0		109.65
40	0	0.00	0.0		110.55
41	0	0.00	0.0		112.25
42	0	0.00	0.0		113.10
43	0	0.00	0.0		114.10
44	0	0.00	0.0		115.15
45	0	0.00	0.0		117.10
46	0	0.00	0.0		120.10
47	0	0.00	0.0		120.65
48	0	0.00	0.0		121.60
49	0	0.00	0.0		122.65
50	0	0.00	0.0		124.15
51	0	0.00	0.0		126.05
52	0	0.00	0.0		127.00
53	0	0.00	0.0		127.85
54	0	0.00	0.0		130.00
55	0	0.00	0.0		131.00
56	0	0.00	0.0		133.40
57	0	0.00	0.0		134.25
58	0	0.00	0.0		135.50

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**Electropherogram Summary Continued ...**



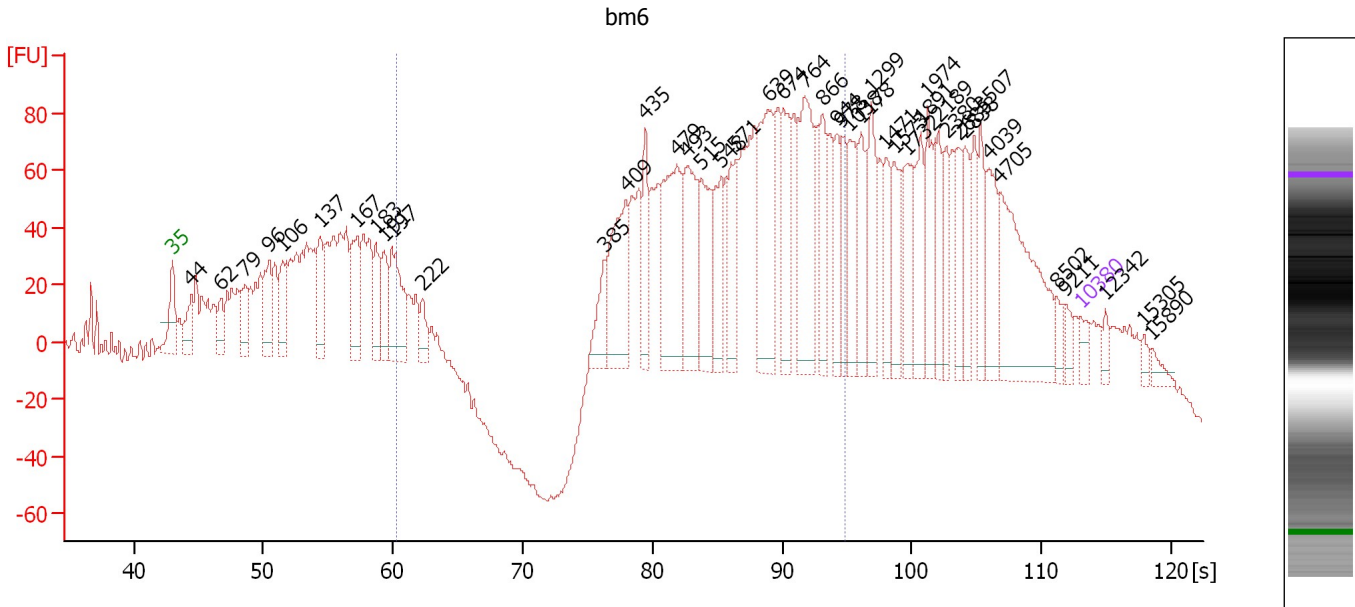
**Overall Results for sample 5 : bm5**

Noise: 3.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : bm6**

Number of peaks found: 45                      Corr. Area 1: 1,992.8  
 Noise: 1.8

**Peak table for sample 6 : bm6**

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	44	297.07	10,187.1		44.45
3	62	203.24	4,950.6		46.73
4	79	298.68	5,707.1		48.63
5	96	441.95	7,001.3		50.45
6	106	351.23	5,026.8		51.49
7	137	368.51	4,081.4		54.38
8	167	498.34	4,508.3		57.24
9	183	317.49	2,626.9		58.69
10	191	317.31	2,520.9		59.39
11	197	625.30	4,821.1		59.93
12	222	167.82	1,143.7		62.29
13	385	250.32	984.0		76.28
14	409	715.50	2,649.3		77.98
15	435	345.40	1,201.7		79.47
16	479	886.58	2,806.9		81.91
17	493	669.37	2,056.5		82.74
18	515	472.32	1,389.5		83.82
19	548	379.92	1,051.3		85.31
20	571	382.28	1,014.4		86.38
21	639	767.77	1,821.5		88.95
22	674	439.65	989.1		90.07
23	764	761.38	1,510.4		91.76
24	866	363.76	636.2		93.13
25	944	251.18	403.1		94.16

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**Electropherogram Summary Continued ...**

**... Peak table for sample 6 : bm6**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	978	244.51	378.7		94.62
27	1,038	328.46	479.3		95.16
28	1,178	301.86	388.1		96.07
29	1,299	356.89	416.2		96.86
30	1,471	231.16	238.1		97.97
31	1,573	266.69	256.9		98.64
32	1,732	304.48	266.4		99.67
33	1,891	296.58	237.6		100.71
34	1,974	283.05	217.3		101.24
35	2,189	229.54	158.9		102.03
36	2,380	190.43	121.2		102.65
37	2,685	205.08	115.7		103.64
38	2,838	202.30	108.0		104.14
39	3,507	203.35	87.8		105.30
40	4,039	331.56	124.4		105.96
41	4,705	873.43	281.3		106.79
42	8,502	77.84	13.9		111.14
43	9,211	67.73	11.1		111.84
44	10,380	75.00	10.9	Upper Marker	113.00
45	12,342	0.00	0.0		114.95
46	15,305	0.00	0.0		117.88
47	15,890	0.00	0.0		118.46

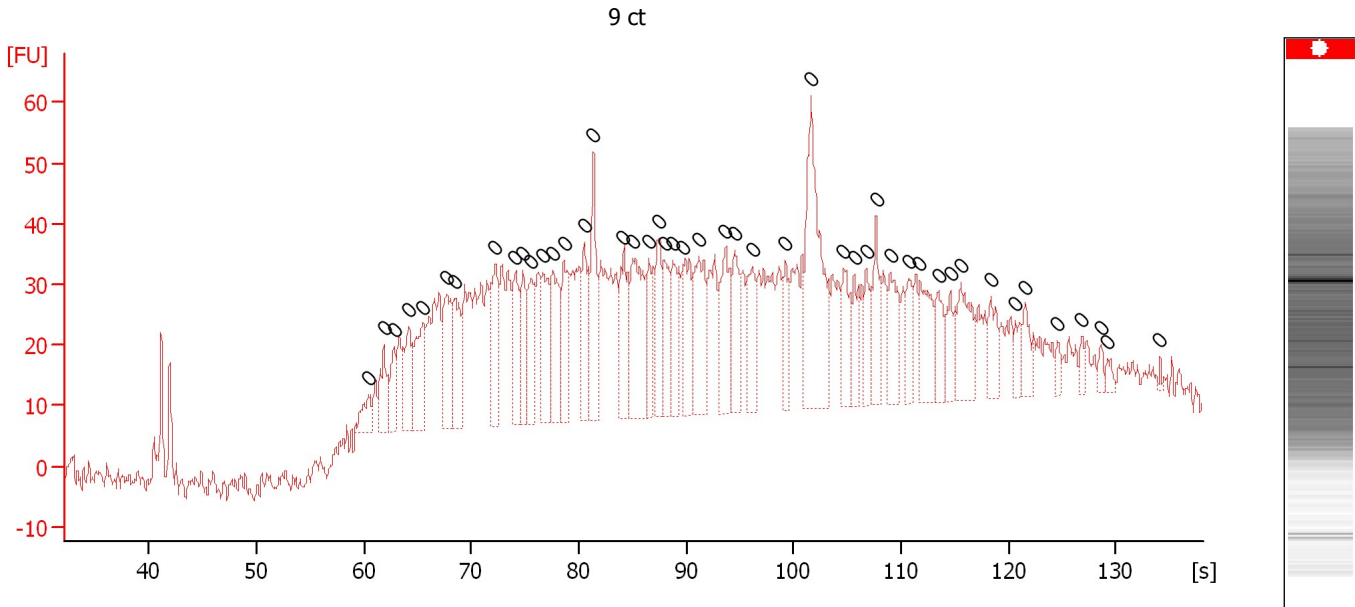
**Region table for sample 6 : bm6**

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	595	1,992.8	33,043.7	10,871.62	44	30.0

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**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : 9 ct**

Number of peaks found: 0                      Noise: 2.3

**Peak table for sample 7 : 9 ct**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		60.45
2	0	0.00	0.0		61.85
3	0	0.00	0.0		62.80
4	0	0.00	0.0		64.15
5	0	0.00	0.0		65.45
6	0	0.00	0.0		67.65
7	0	0.00	0.0		68.35
8	0	0.00	0.0		72.25
9	0	0.00	0.0		74.10
10	0	0.00	0.0		74.80
11	0	0.00	0.0		75.55
12	0	0.00	0.0		76.65
13	0	0.00	0.0		77.60
14	0	0.00	0.0		78.60
15	0	0.00	0.0		80.50
16	0	0.00	0.0		81.35
17	0	0.00	0.0		84.15
18	0	0.00	0.0		85.05
19	0	0.00	0.0		86.55
20	0	0.00	0.0		87.45
21	0	0.00	0.0		87.95
22	0	0.00	0.0		88.75
23	0	0.00	0.0		89.75
24	0	0.00	0.0		91.15
25	0	0.00	0.0		93.65
26	0	0.00	0.0		94.50
27	0	0.00	0.0		96.15

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Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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Modified: 1/13/2016 2:51:28 PM

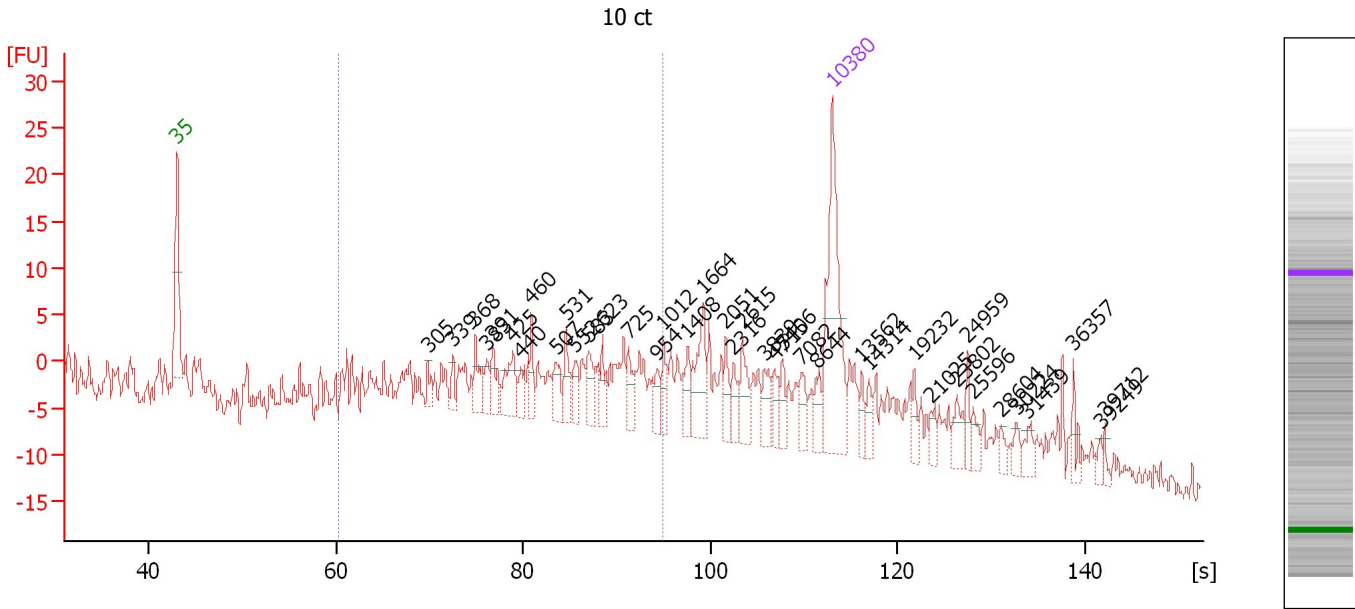
**Electropherogram Summary Continued ...****... Peak table for sample 7 : 9 ct**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
28	0	0.00	0.0		99.25
29	0	0.00	0.0		101.65
30	0	0.00	0.0		104.65
31	0	0.00	0.0		105.65
32	0	0.00	0.0		106.75
33	0	0.00	0.0		107.70
34	0	0.00	0.0		109.05
35	0	0.00	0.0		110.75
36	0	0.00	0.0		111.75
37	0	0.00	0.0		113.45
38	0	0.00	0.0		114.60
39	0	0.00	0.0		115.55
40	0	0.00	0.0		118.35
41	0	0.00	0.0		120.65
42	0	0.00	0.0		121.55
43	0	0.00	0.0		124.55
44	0	0.00	0.0		126.85
45	0	0.00	0.0		128.55
46	0	0.00	0.0		129.25
47	0	0.00	0.0		134.10

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
 Modified: 1/13/2016 2:51:28 PM

**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : 10 ct**

Number of peaks found: 39                      Corr. Area 1: 179.3  
 Noise: 1.8

**Peak table for sample 8 : 10 ct**

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	7.76	38.5		69.80
3	339	7.43	33.3		72.49
4	368	18.55	76.4		74.84
5	383	11.23	44.5		76.05
6	391	13.70	53.1		76.74
7	425	24.15	86.1		78.86
8	440	10.72	36.9		79.72
9	460	15.09	49.7		80.87
10	507	15.61	46.7		83.45
11	531	15.67	44.7		84.54
12	552	11.83	32.5		85.52
13	583	16.21	42.1		86.95
14	623	12.38	30.1		88.44
15	725	14.65	30.6		91.25
16	954	10.16	16.1		94.30
17	1,012	11.72	17.6		94.98
18	1,408	13.69	14.7		97.57
19	1,664	27.78	25.3		99.23
20	2,051	11.03	8.1		101.58
21	2,316	9.27	6.1		102.44
22	2,615	16.79	9.7		103.42
23	3,839	12.64	5.0		105.71
24	4,715	9.22	3.0		106.80
25	5,406	9.03	2.5		107.66

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
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**Electropherogram Summary Continued ...**

**... Peak table for sample 8 : 10 ct**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	7,082	11.30	2.4		109.73
27	8,644	11.06	1.9		111.28
28	10,380	75.00	10.9	Upper Marker	113.00
29	13,562	0.00	0.0		116.16
30	14,314	0.00	0.0		116.90
31	19,232	0.00	0.0		121.78
32	21,025	0.00	0.0		123.56
33	23,802	0.00	0.0		126.31
34	24,959	0.00	0.0		127.46
35	25,596	0.00	0.0		128.09
36	28,604	0.00	0.0		131.07
37	30,224	0.00	0.0		132.68
38	31,439	0.00	0.0		133.89
39	36,357	0.00	0.0		138.76
40	39,249	0.00	0.0		141.63
41	39,712	0.00	0.0		142.09

**Region table for sample 8 : 10 ct**

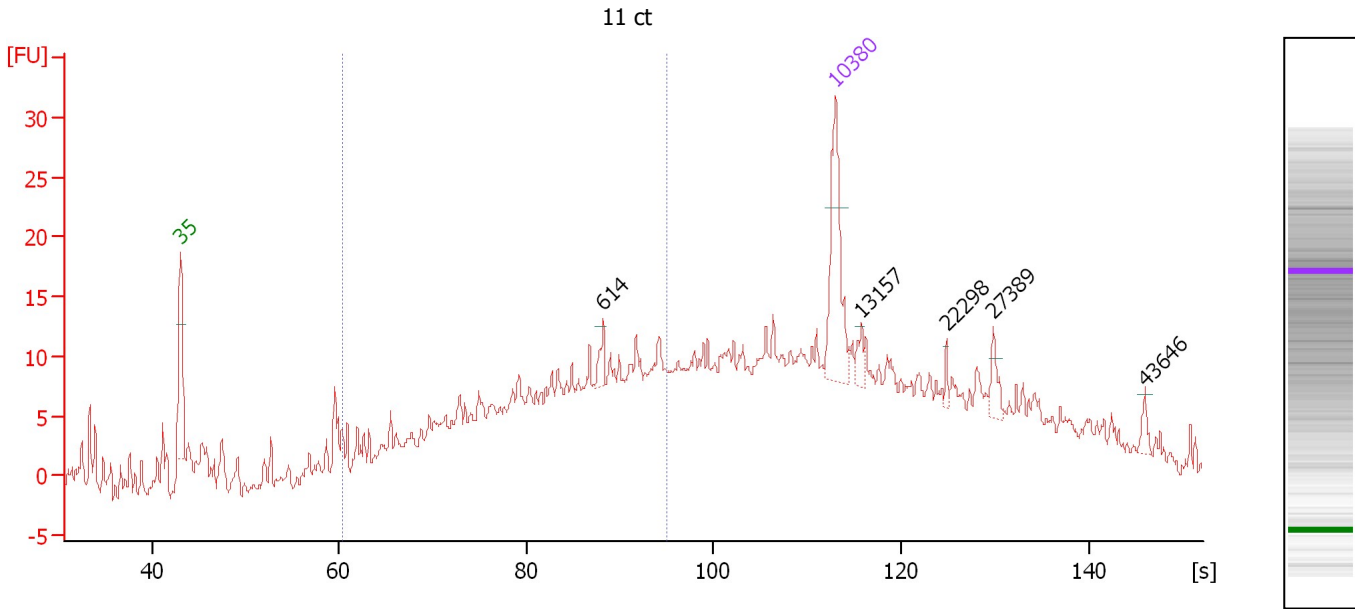
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	523	179.3	1,550.1	433.65	40	36.8



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : 11 ct**

Number of peaks found: 5                      Corr. Area 1: 197.2  
 Noise: 0.8

**Peak table for sample 9 : 11 ct**

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	614	13.81	34.1		88.16
3	10,380	75.00	10.9	Upper Marker	113.00
4	13,157	0.00	0.0		115.75
5	22,298	0.00	0.0		124.82
6	27,389	0.00	0.0		129.87
7	43,646	0.00	0.0		145.99

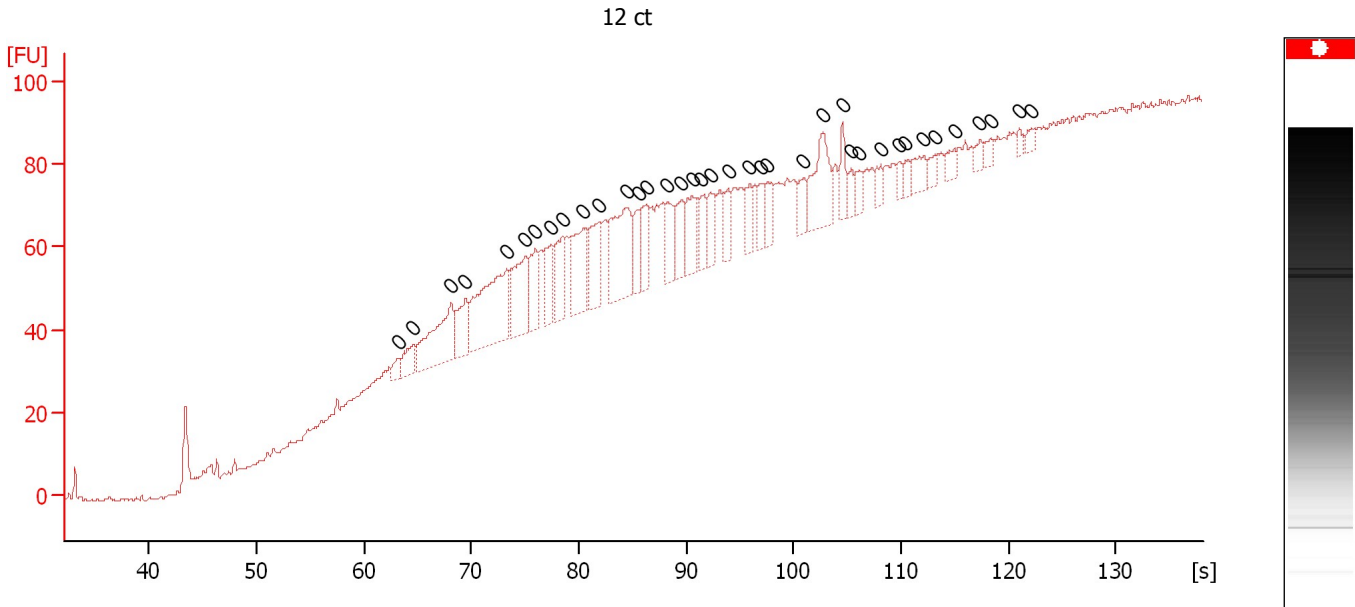
**Region table for sample 9 : 11 ct**

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	530	197.2	3,073.2	868.58	43	37.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : 12 ct**

Number of peaks found: 0                      Noise: 0.6

**Peak table for sample 10 : 12 ct**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		63.15
2	0	0.00	0.0		64.60
3	0	0.00	0.0		68.15
4	0	0.00	0.0		69.45
5	0	0.00	0.0		73.30
6	0	0.00	0.0		74.95
7	0	0.00	0.0		75.95
8	0	0.00	0.0		77.45
9	0	0.00	0.0		78.55
10	0	0.00	0.0		80.40
11	0	0.00	0.0		81.80
12	0	0.00	0.0		84.50
13	0	0.00	0.0		85.50
14	0	0.00	0.0		86.25
15	0	0.00	0.0		88.25
16	0	0.00	0.0		89.50
17	0	0.00	0.0		90.55
18	0	0.00	0.0		91.45
19	0	0.00	0.0		92.25
20	0	0.00	0.0		93.90
21	0	0.00	0.0		95.90
22	0	0.00	0.0		97.00
23	0	0.00	0.0		97.60
24	0	0.00	0.0		100.90
25	0	0.00	0.0		102.70
26	0	0.00	0.0		104.55
27	0	0.00	0.0		105.35

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
Modified: 1/13/2016 2:51:28 PM

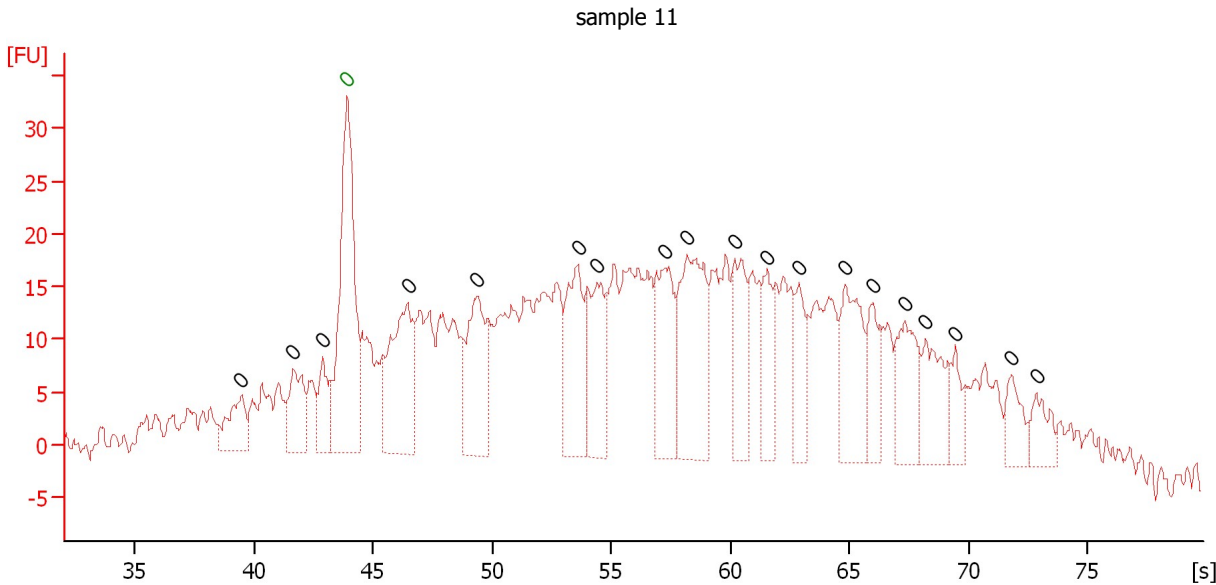
**Electropherogram Summary Continued ...****... Peak table for sample 10 : 12 ct**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
28	0	0.00	0.0		106.15
29	0	0.00	0.0		108.10
30	0	0.00	0.0		109.90
31	0	0.00	0.0		110.40
32	0	0.00	0.0		112.10
33	0	0.00	0.0		113.20
34	0	0.00	0.0		114.95
35	0	0.00	0.0		117.35
36	0	0.00	0.0		118.35
37	0	0.00	0.0		121.00
38	0	0.00	0.0		122.15

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

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**Electropherogram Summary Continued ...**



**Setpoint Deviations for sample 11 : sample 11**

End Analysis Time Range [s] : 79.8

**Overall Results for sample 11 : sample 11**

Number of peaks found: 19                      Noise: 1.6

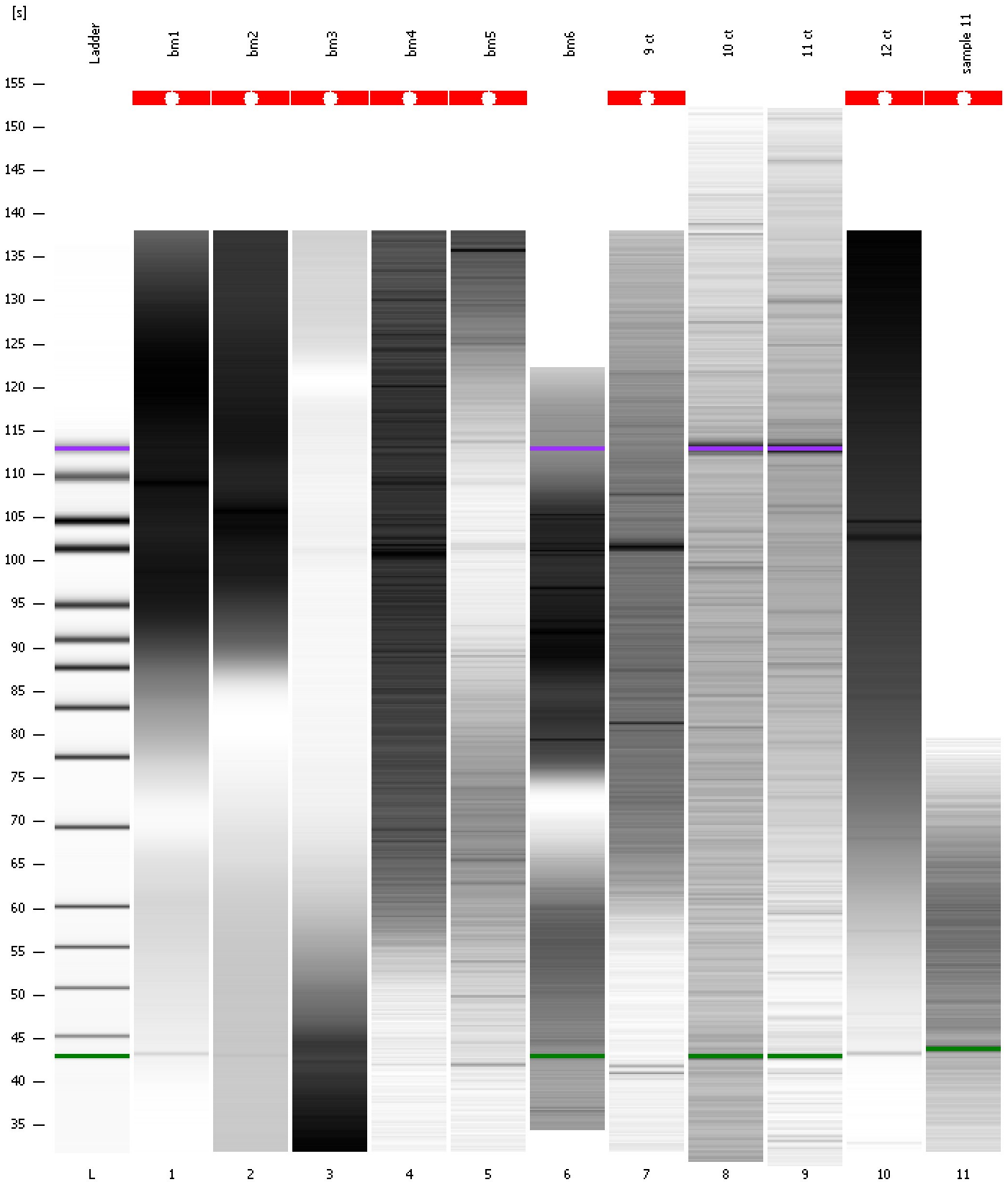
**Peak table for sample 11 : sample 11**

Pea k	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		39.45
2	0	0.00	0.0		41.65
3	0	0.00	0.0		42.90
4	0	0.00	0.0	Lower Marker	43.90
5	0	0.00	0.0		46.45
6	0	0.00	0.0		49.35
7	0	0.00	0.0		53.60
8	0	0.00	0.0		54.40
9	0	0.00	0.0		57.25
10	0	0.00	0.0		58.20
11	0	0.00	0.0		60.15
12	0	0.00	0.0		61.50
13	0	0.00	0.0		62.85
14	0	0.00	0.0		64.80
15	0	0.00	0.0		66.00
16	0	0.00	0.0		67.35
17	0	0.00	0.0		68.20
18	0	0.00	0.0		69.40
19	0	0.00	0.0		71.80
20	0	0.00	0.0		72.85

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
Modified: 1/13/2016 2:51:28 PM

**Gel Image**



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-13\2016-01-13\_001.xad

Created: 1/13/2016 2:11:23 PM  
 Modified: 1/13/2016 2:51:28 PM

**Run Logbook**

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run aborted on port 1		Instrument	Run		1/13/2016 2:51:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-01-13\2016-01-13_001.xad)		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/13/2016 2:11:28 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1