

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

Created: 8/2/2017 3:09:18 PM  
Modified: 8/2/2017 3:51:32 PM

**Electrophoresis File Run Summary**

Instrument Information:

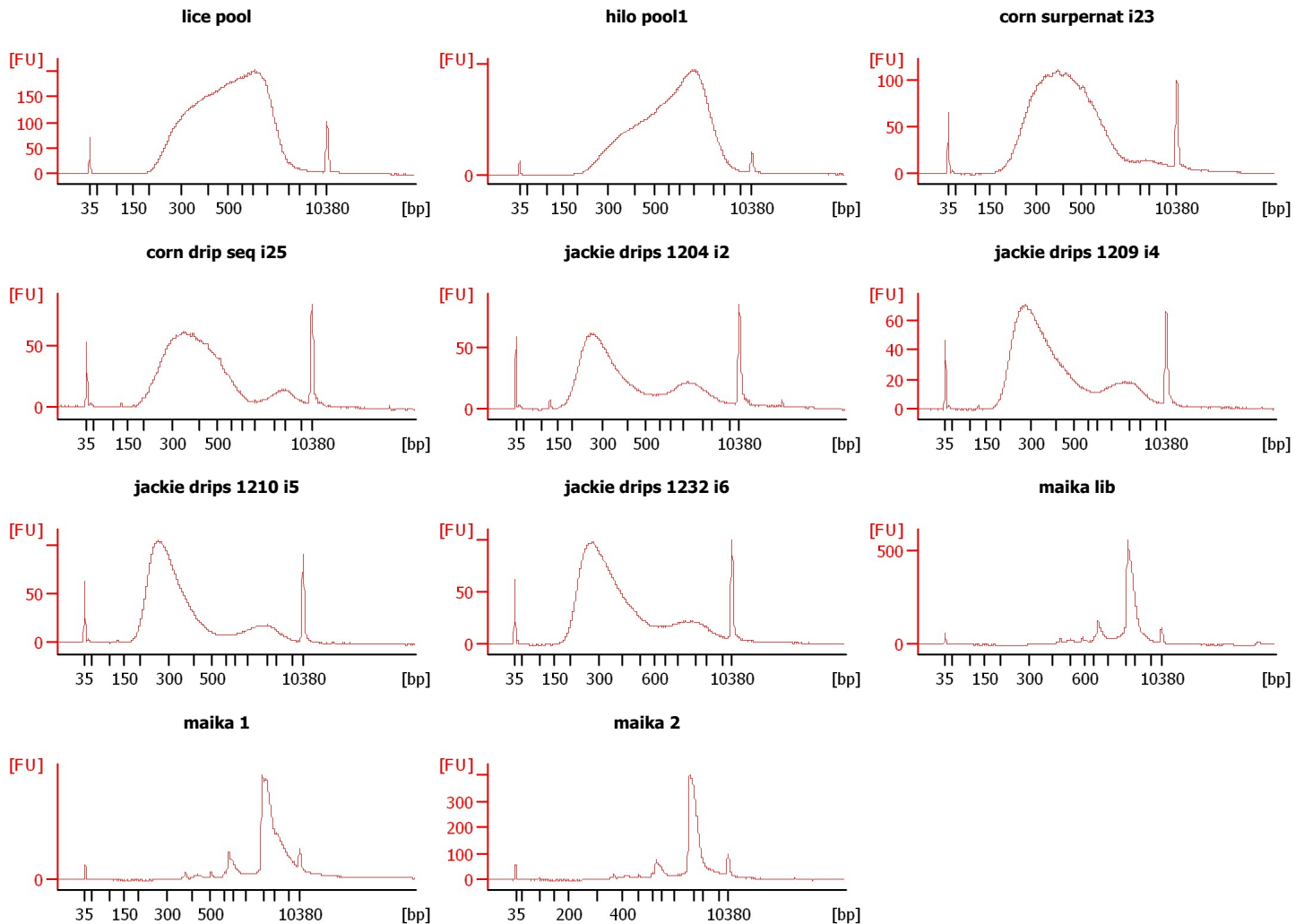
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

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:



Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

Created: 8/2/2017 3:09:18 PM  
Modified: 8/2/2017 3:51:32 PM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
lice pool		<input type="checkbox"/>	✓			
hilo pool1		<input type="checkbox"/>	✓			
corn supernat i23		<input type="checkbox"/>	✓			
corn drip seq i25		<input type="checkbox"/>	✓			
jackie drips 1204 i2		<input type="checkbox"/>	✓			
jackie drips 1209 i4		<input type="checkbox"/>	✓			
jackie drips 1210 i5		<input type="checkbox"/>	✓			
jackie drips 1232 i6		<input type="checkbox"/>	✓			
maika lib		<input type="checkbox"/>	✓			
maika 1		<input type="checkbox"/>	✓			
maika 2		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

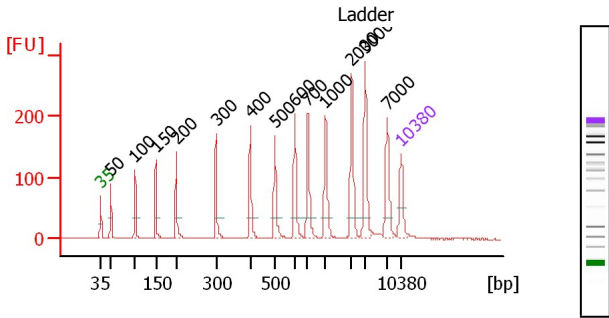
**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

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**Electropherogram Summary**



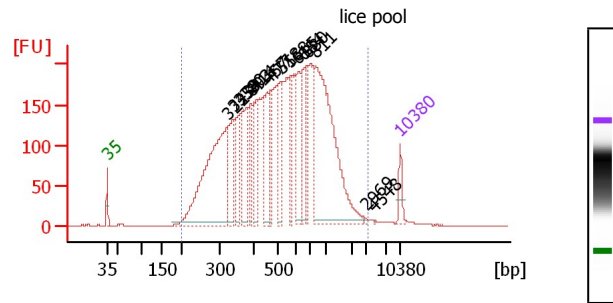
**Peak table for Ladder**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	50	150.00	4,545.5	Ladder Peak	45.34
3	100	150.00	2,272.7	Ladder Peak	51.04
4	150	150.00	1,515.2	Ladder Peak	55.86
5	200	150.00	1,136.4	Ladder Peak	60.63
6	300	150.00	757.6	Ladder Peak	69.89
7	400	150.00	568.2	Ladder Peak	77.93
8	500	150.00	454.5	Ladder Peak	83.63
9	600	150.00	378.8	Ladder Peak	88.25
10	700	150.00	324.7	Ladder Peak	91.32
11	1,000	150.00	227.3	Ladder Peak	95.46
12	2,000	150.00	113.6	Ladder Peak	101.55
13	3,000	150.00	75.8	Ladder Peak	104.67

**Overall Results for Ladder**

Noise: 0.1

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
14	7,000	150.00	32.5	Ladder Peak	109.83
15	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 1 : lice pool**

Number of peaks found: 16  
 Noise: 0.2  
 Corr. Area 1: 6,537.7

**Region table for sample 1 : lice pool**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	3,298	618	6,537.7	28,922.17	8,575.19	99.8	59.6

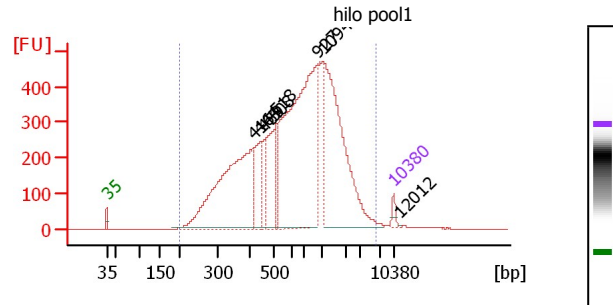
Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

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**Electropherogram Summary Continued ...**

**Peak table for sample 1 : lice pool**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	322	1,502.88	7,082.5		71.62
3	343	402.37	1,779.5		73.31
4	358	309.86	1,311.0		74.56
5	380	312.79	1,247.8		76.30
6	393	224.06	864.2		77.35
7	414	355.34	1,301.9		78.70
8	457	350.00	1,159.7		81.19
9	477	218.49	693.4		82.34
10	518	206.31	602.9		84.48
11	568	174.05	464.3		86.77
12	615	289.02	711.9		88.72
13	654	269.62	624.5		89.92
14	680	178.75	398.2		90.71
15	811	1,421.93	2,655.9		92.86
16	2,969	5.10	2.6		104.57
17	4,548	3.73	1.2		106.67
18	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 2 : hilo pool1**

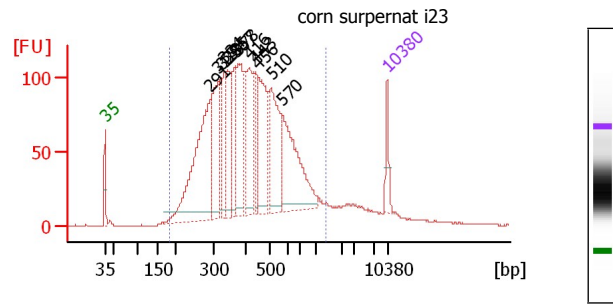
Number of peaks found: 8  
 Noise: 0.1  
 Corr. Area 1: 12,262.2

**Region table for sample 2 : hilo pool1**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution CV [%]
200	5,945	881	12,262.2	40,379.9	14,463.99	76.9	83

**Peak table for sample 2 : hilo pool1**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	416	3,513.07	12,808.0		78.82
3	444	608.87	2,076.9		80.45
4	459	354.35	1,168.7		81.31
5	508	994.50	2,964.3		84.01
6	518	282.47	825.8		84.47
7	927	4,277.25	6,991.2		94.46
8	1,094	2,890.41	4,003.7		96.03
9	10,380	75.00	10.9	Upper Marker	113.00
10	12,012	0.00	0.0		114.53



**Overall Results for sample 3 : corn supernat i23**

Number of peaks found: 12  
 Noise: 0.3  
 Corr. Area 1: 3,316.1

**Region table for sample 3 : corn supernat i23**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution CV [%]
184	1,370	440	3,316.1	21,337.8	5,245.5	93	38.7

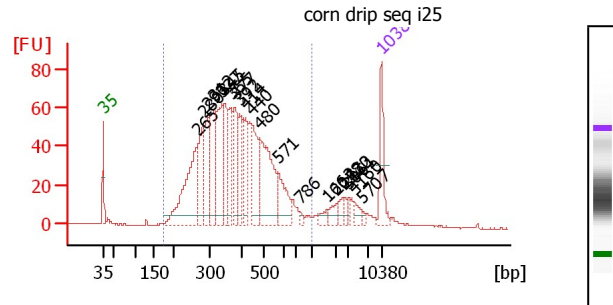
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**Electropherogram Summary Continued ...**

**Peak table for sample 3 : corn supernat i23**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	291	951.88	4,958.6		69.04
3	315	410.93	1,975.1		71.11
4	323	147.68	692.8		71.74
5	334	182.92	830.0		72.62
6	345	282.62	1,241.7		73.50
7	367	293.85	1,213.9		75.26
8	378	397.78	1,595.6		76.14
9	416	324.72	1,183.2		78.83
10	443	121.54	415.6		80.38
11	456	393.21	1,307.1		81.11
12	510	390.65	1,159.6		84.11
13	570	515.10	1,369.9		86.85
14	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 4 : corn drip seq i25**

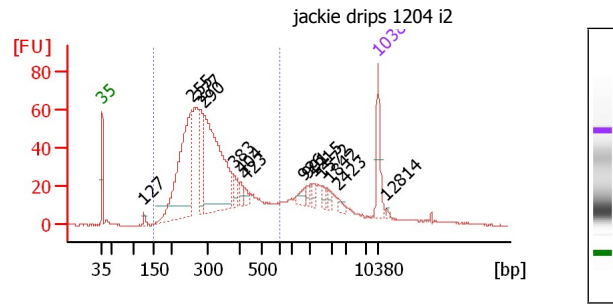
Number of peaks found: 21  
 Noise: 0.3  
 Corr. Area 1: 1,709.5

**Region table for sample 4 : corn drip seq i25**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
173	1,000	393	1,709.5	10,354.9	2,371.7	90	31.4

**Peak table for sample 4 : corn drip seq i25**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	265	350.93	2,006.6		66.65
3	280	130.08	703.1		68.07
4	296	149.39	765.6		69.49
5	312	180.35	875.9		70.85
6	337	219.55	985.7		72.90
7	345	116.12	509.5		73.53
8	365	131.18	544.6		75.11
9	377	97.72	392.3		76.11
10	392	89.97	348.0		77.26
11	414	88.72	324.5		78.74
12	440	164.60	566.8		80.21
13	480	259.84	820.8		82.47
14	571	101.65	269.5		86.93
15	786	8.99	17.3		92.50
16	1,662	15.31	14.0		99.49
17	2,048	20.21	15.0		101.70
18	2,570	17.93	10.6		103.33
19	2,722	11.55	6.4		103.80
20	3,061	10.69	5.3		104.75
21	4,160	18.43	6.7		106.17
22	5,707	5.47	1.5		108.17
23	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 5 : jackie drips 1204 i2**

Number of peaks found: 14  
 Noise: 0.3  
 Corr. Area 1: 1,303.3

**Region table for sample 5 : jackie drips 1204 i2**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
150	591	317	1,303.3	10,947.6	2,088.8	76	27.7

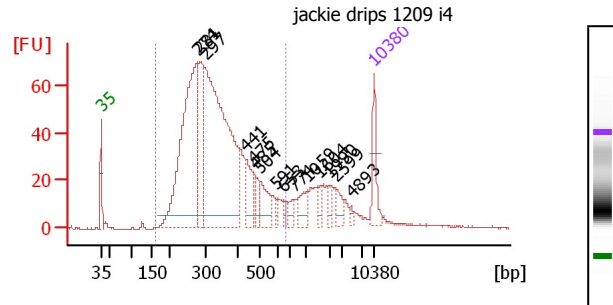
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 Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

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**Electropherogram Summary Continued ...**

**Peak table for sample 5 : jackie drips 1204 i2**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	127	16.24	194.4		53.61
3	255	559.53	3,321.0		65.75
4	277	144.58	790.7		67.77
5	290	555.54	2,900.2		68.98
6	383	20.37	80.6		76.57
7	404	23.39	87.7		78.16
8	423	14.72	52.8		79.22
9	926	21.41	35.0		94.44
10	991	12.43	19.0		95.34
11	1,215	17.85	22.3		96.77
12	1,572	14.64	14.1		98.95
13	1,842	7.14	5.9		100.59
14	2,423	10.66	6.7		102.87
15	10,380	75.00	10.9	Upper Marker	113.00
16	12,814	0.00	0.0		115.28



**Overall Results for sample 6 : jackie drips 1209 i4**

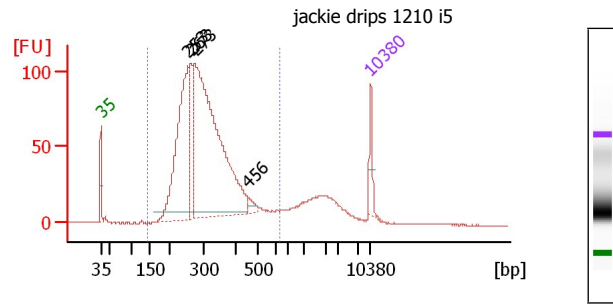
Number of peaks found: 15  
 Noise: 0.2  
 Corr. Area 1: 1,558.6

**Region table for sample 6 : jackie drips 1209 i4**

From To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Size distribution Total in CV [%]
161 - 676	343	1,558.6	13,656.4	2,795.1	83.28

**Peak table for sample 6 : jackie drips 1209 i4**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	274	870.65	4,809.2		67.51
3	281	303.83	1,636.9		68.15
4	297	1,165.63	5,949.5		69.60
5	441	97.32	334.6		80.25
6	475	30.65	97.9		82.17
7	485	33.91	106.0		82.76
8	504	88.70	266.4		83.83
9	591	18.52	47.5		87.85
10	653	13.71	31.8		89.88
11	774	22.74	44.5		92.34
12	1,059	57.11	81.7		95.82
13	1,604	22.03	20.8		99.14
14	1,990	20.29	15.4		101.49
15	2,599	28.84	16.8		103.42
16	4,893	9.48	2.9		107.11
17	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 7 : jackie drips 1210 i5**

Number of peaks found: 4  
 Noise: 0.4  
 Corr. Area 1: 1,991.4

**Region table for sample 7 : jackie drips 1210 i5**

From To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Size distribution Total in CV [%]
144 - 637	311	1,991.4	18,865.6	3,590.5	87.25

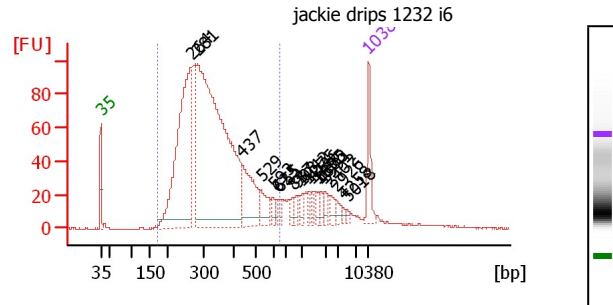
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**Electropherogram Summary Continued ...**

**Peak table for sample 7 : jackie drips 1210 i5**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	253	996.91	5,961.1		65.58
3	263	279.00	1,608.9		66.44
4	273	2,000.18	11,113.5		67.36
5	456	42.67	141.8		81.11
6	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 8 : jackie drips 1232 i6**

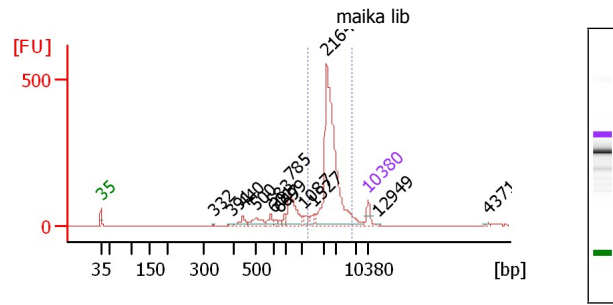
Number of peaks found: 19  
 Noise: 0.1  
 Corr. Area 1: 2,167.3

**Region table for sample 8 : jackie drips 1232 i6**

From To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
168 - 647	335	2,167.3	15,218.9	3,049.5	83	28.5

**Peak table for sample 8 : jackie drips 1232 i6**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	264	861.44	4,945.2		66.55
3	281	1,682.09	9,069.3		68.13
4	437	211.18	732.7		80.02
5	529	66.59	190.6		84.98
6	593	19.55	50.0		87.92
7	625	14.31	34.7		89.01
8	655	14.29	33.1		89.94
9	837	24.35	44.1		93.21
10	908	20.73	34.6		94.19
11	1,042	20.69	30.1		95.72
12	1,275	19.09	22.7		97.14
13	1,436	15.32	16.2		98.12
14	1,695	13.48	12.1		99.70
15	1,803	17.04	14.3		100.35
16	1,991	16.25	12.4		101.50
17	2,402	21.06	13.3		102.81
18	2,926	21.20	11.0		104.44
19	4,258	6.19	2.2		106.29
20	5,018	7.95	2.4		107.28
21	10,380	75.00	10.9	Upper Marker	113.00



**Overall Results for sample 9 : maika lib**

Number of peaks found: 14  
 Noise: 0.3  
 Corr. Area 1: 1,694.8

**Region table for sample 9 : maika lib**

From To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
1,256 - 6,093	2,649	1,694.8	991.7	1,621.9	71	31.9

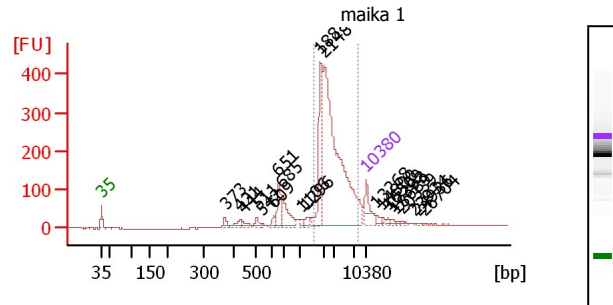
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**Electropherogram Summary Continued ...**

**Peak table for sample 9 : maika lib**

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	332	8.30	37.9		72.48
3	391	13.62	52.7		77.23
4	440	84.24	290.3		80.19
5	500	141.88	429.8		83.63
6	583	68.05	176.9		87.46
7	601	29.88	75.4		88.28
8	647	17.66	41.3		89.70
9	699	57.79	125.3		91.29
10	785	348.00	671.9		92.49
11	1,087	51.95	72.4		95.99
12	1,527	45.20	44.8		98.67
13	2,164	1,625.95	1,138.6		102.06
14	10,380	75.00	10.9	Upper Marker	113.00
15	12,949	0.00	0.0		115.41
16	43,714	0.00	0.0		144.23



**Overall Results for sample 10 : maika 1**

Number of peaks found: 21  
 Noise: 0.7  
 Corr. Area 1: 2,261.8

**Region table for sample 10 : maika 1**

From [bp]	To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Conc. [pg/µl]	% of Total	Size distribution CV [%]
1,627	8,277	3,237	2,261.8	575.4	1,040.2	72	48.9

**Peak table for sample 10 : maika 1**

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	373	19.24	78.2		75.74
3	431	23.63	83.0		79.71
4	444	15.26	52.1		80.43
5	511	18.84	55.9		84.13
6	542	2.85	8.0		85.56
7	609	17.67	43.9		88.54
8	651	74.58	173.6		89.81
9	685	108.20	239.3		90.86
10	1,106	11.63	15.9		96.11
11	1,296	16.10	18.8		97.27
12	1,885	199.54	160.3		100.85
13	2,148	882.42	622.4		102.01
14	10,380	75.00	10.9	Upper Marker	113.00
15	13,268	0.00	0.0		115.71
16	14,800	0.00	0.0		117.14
17	16,509	0.00	0.0		118.74
18	17,393	0.00	0.0		119.57
19	18,689	0.00	0.0		120.78

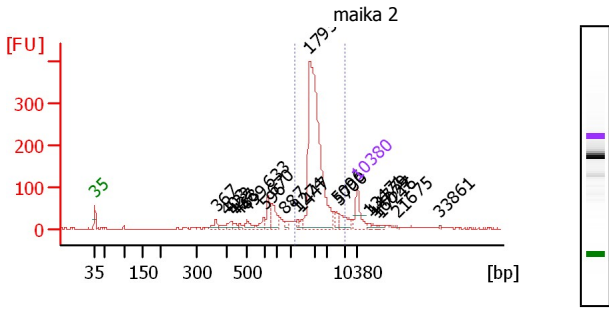
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time
20	20,339	0.00	0.0		122.33
21	23,934	0.00	0.0		125.70
22	24,936	0.00	0.0		126.64
23	26,704	0.00	0.0		128.29



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**Electropherogram Summary Continued ...**



**Peak table for sample 11 : maika 2**

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	367	32.61	134.5		75.30
3	403	21.47	80.8		78.08
4	422	23.92	85.8		79.20
5	437	15.33	53.2		80.03
6	463	12.28	40.2		81.54
7	499	32.25	97.8		83.60
8	596	31.10	79.1		88.05
9	633	75.31	180.2		89.28
10	670	84.79	191.9		90.39
11	887	16.30	27.9		93.90
12	1,274	10.04	12.0		97.13
13	1,447	10.90	11.4		98.19
14	1,795	900.89	760.5		100.30
15	5,096	16.20	4.8		107.38
16	5,700	56.30	15.0		108.16
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,471	0.00	0.0		115.90
19	14,779	0.00	0.0		117.12
20	16,027	0.00	0.0		118.29
21	17,216	0.00	0.0		119.40

**Overall Results for sample 11 : maika 2**

Number of peaks found: 21  
 Noise: 1.0  
 Corr. Area 1: 1,501.0

**Region table for sample 11 : maika 2**

From [bp]	To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/µl]	% of Total	CV [%]
1,177	6,852	2,409	1,501.0	667.3	961.45	70	42.2

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time
22	21,675	0.00	0.0		123.58
23	33,861	0.00	0.0		135.00

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Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

Created: 8/2/2017 3:09:18 PM  
Modified: 8/2/2017 3:51:32 PM

**Gel Image**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-08-02\2017-08-02\_001.xad

Created: 8/2/2017 3:09:18 PM  
Modified: 8/2/2017 3:51:32 PM

**Curves**

**Standard Curve**

