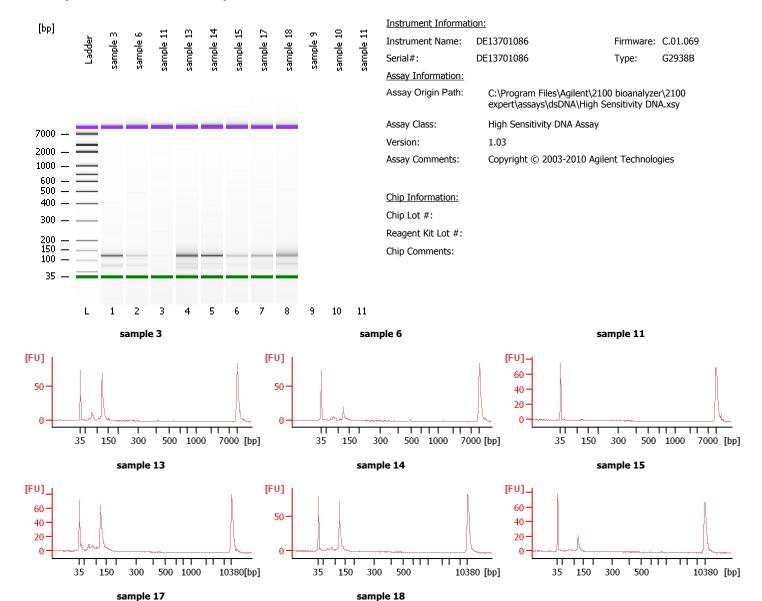
**2014-02-18\_001.xad** Page 1 of 14

Assay Class: High Sensitivity DNA Assay Created: 2/18/2014 11:29:08 AM Data Path: C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\_001.xad Created: 2/18/2014 12:01:55 PM

# **Electrophoresis File Run Summary**



[FU]

50

0

35 150

500

10380

[bp]

Printed:

2/18/2014 12:03:34 PM

[FU]

50

35

150

300

10380 [bp]

500

300

**2014-02-18\_001.xad** Page 2 of 14

 $\label{light} \begin{tabular}{ll} High Sensitivity DNA Assay \\ C:\...ttings\Bioanalyzer\2014-02-18\2014-02-1$ 2/18/2014 11:29:08 AM 2/18/2014 12:01:55 PM Assay Class: Created: Data Path: Modified: **Electrophoresis File Run Summary (Chip Summary) Sample Name** Sample Comment Rest. Digest Status Observation **Result Label Result Color** sample 3 sample 6 sample 11 sample 13 sample 14 sample 15 sample 17

Chip Lot # Reagent Kit Lot #

**Chip Comments:** 

sample 18 sample 9 sample 10 sample 11 Ladder

**2014-02-18\_001.xad** Page 3 of 14

Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad Created: 2/18/2014 11:29:08 AM Modified: 2/18/2014 12:01:55 PM

#### **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

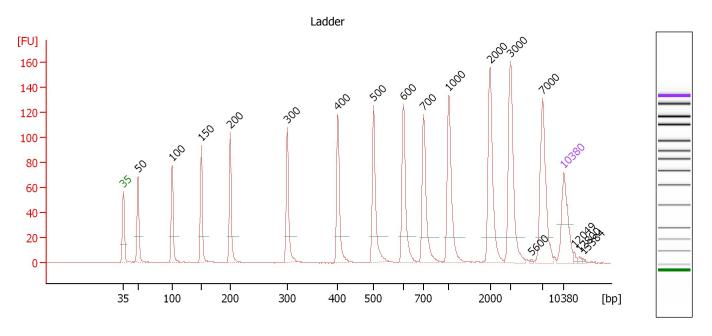
# Ladder

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

**2014-02-18\_001.xad** Page 4 of 14

Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary**



### **Overall Results for Ladder**

Noise: 0.2

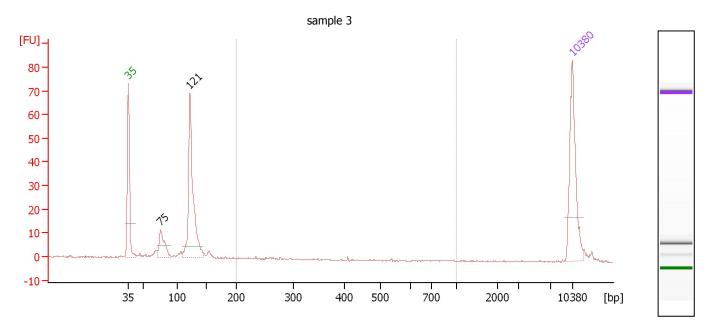
# **Peak table for Ladder**

· can	car table for Educi										
Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations					
1	4	43.00	35	125.00	5,411.3	Lower Marker					
2	L	45.33	50	150.00	4,545.5	Ladder Peak					
3	L	50.75	100	150.00	2,272.7	Ladder Peak					
4	L	55.37	150	150.00	1,515.2	Ladder Peak					
5	L	59.98	200	150.00	1,136.4	Ladder Peak					
6	L	69.04	300	150.00	757.6	Ladder Peak					
7	L	77.09	400	150.00	568.2	Ladder Peak					
8	L	82.76	500	150.00	454.5	Ladder Peak					
9	L	87.51	600	150.00	378.8	Ladder Peak					
10	L	90.73	700	150.00	324.7	Ladder Peak					
11	L	94.71	1,000	150.00	227.3	Ladder Peak					
12	L	101.27	2,000	150.00	113.6	Ladder Peak					
13	L	104.49	3,000	150.00	75.8	Ladder Peak					
14		107.79	5,600	0.00	0.0						
15	L	109.57	7,000	150.00	32.5	Ladder Peak					
16		113.00	10,380	75.00	10.9	Upper Marker					
17		114.69	12,049	0.00	0.0						
18		115.46	12,800	0.00	0.0						
19		116.05	13,384	0.00	0.0						

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



# Overall Results for sample 1: sample 3

Number of peaks found: 2 Corr. Area 1: 2.3

Noise: 0.2

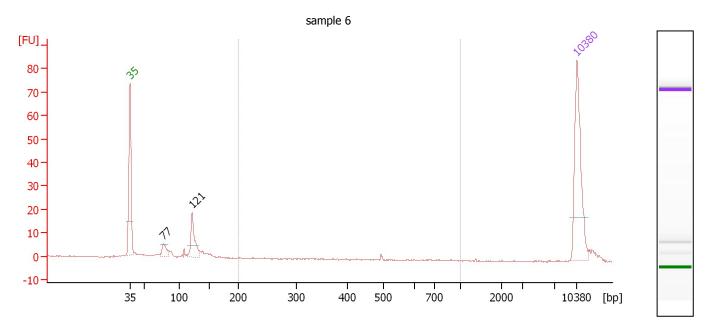
Peak	Peak table for sample 1: <u>sample 3</u>									
Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations				
1	18	43.00	35	125.00	5,411.3	Lower Marker				
2		48.08	75	48.49	974.3					
3		52.71	121	211.45	2,643.6					
4	8	113.00	10,380	75.00	10.9	Upper Marker				
Reai	Region table for sample 1: sample 3									

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/µl]	Co Corr. Ior Area	% of Total	Size distribution in CV [%]
200	1,000	308	18.5	3.33	2.3	1	39.0

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



# Overall Results for sample 2: sample 6

Number of peaks found: 2 Corr. Area 1: 0.8

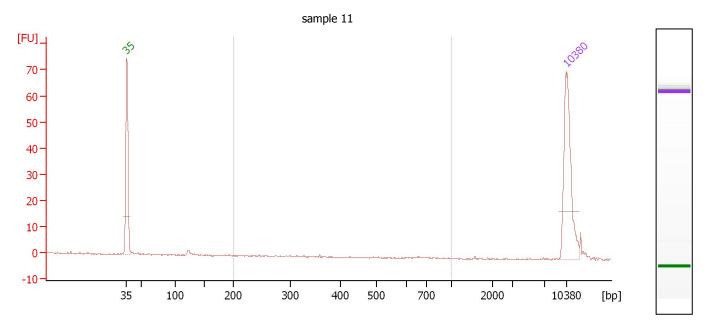
Noise: 0.2

Peak	Peak table for sample 2 : <u>sample 6</u>									
Pea	Aligned Migration Tin	ne [s] Size [l	bp] Cond	c. [pg/µl]	Molarity [	pmol/I] Observations				
k	•									
1	<b>1</b> 6 43.00	35	125.0	00	5,411.3	Lower Marker				
2	48.30	77	16.70	0	326.8					
3	52.73	121	45.3	4	565.8					
4	113.00	10,380	75.00	0	10.9	Upper Marker				
Regio	on table for sample 2:	sample 6								
From	To [bp] Average Size	Molarity	Conc.	Co Corr.	% of	Size distribution in				
[bp]	[bp]	[pmol/l]	[pg/µl]	<u>lor</u> Area	Total	CV [%]				
200	1,000 483	3.4	0.99	0.8	1	22.9				

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 3: sample 11

Number of peaks found: 0 Corr. Area 1: 0.4

Noise: 0.2

Peak table for sample 3: <u>sample 11</u>

Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1	18	43.00	35	125.00	5,411.3	Lower Marker
2	Pa	113.00	10,380	75.00	10.9	Upper Marker

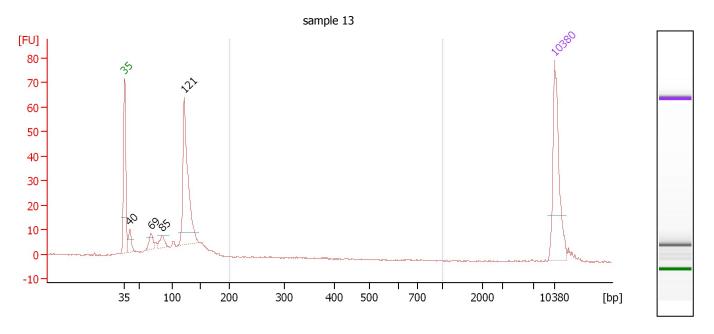
Region table for sample 3: <u>sample 11</u>

Size distribution in **From** To [bp] Average Size Molarity Co Corr. % of Conc. [bp] [bp] [pmol/l] [pg/µl] lor Area Total **CV** [%] 200 487 1.9 0.4 1,000 0.49 37.1

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 4: <u>sample 13</u>

Number of peaks found: 4 Corr. Area 1: 0.7

Noise: 0.1

Peak	Peak table for sample 4: sample 13										
Pea k		Aligned Migration Tim	e [s] Size [b	p] Cor	nc. [pg/µl]	Molarity [p	mol/I] Observations				
1	4	43.00	35	125	.00	5,411.3	Lower Marker				
2		43.82	40	23.9	90	898.4					
3		47.34	69	20.4	10	451.1					
4		49.07	85	19.2	25	345.1					
5		52.71	121	205	.03	2,561.2					
6		113.00	10,380	75.0	00	10.9	Upper Marker				
Region table for sample 4:			sample 13								
From	l	To [bp] Average Size	Molarity [pmol/l]	Conc. [pg/ul]	Co Corr. Ior Area	% of Total	Size distribution in CV [%]				

0.98

200

1,000

296

5.3

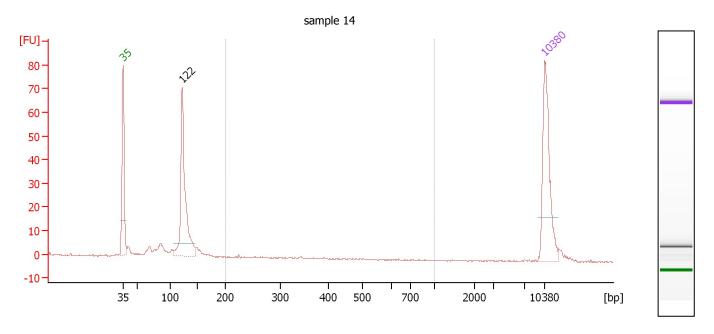
0.7

19.6

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 5 : <u>sample 14</u>

Number of peaks found: 1 Corr. Area 1: 0.7

Noise: 0.2

Peak table for sample 5 : sample 14

Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1	4	43.00	35	125.00	5,411.3	Lower Marker
2		52.78	122	178.39	2,215.8	
3		113.00	10,380	75.00	10.9	Upper Marker

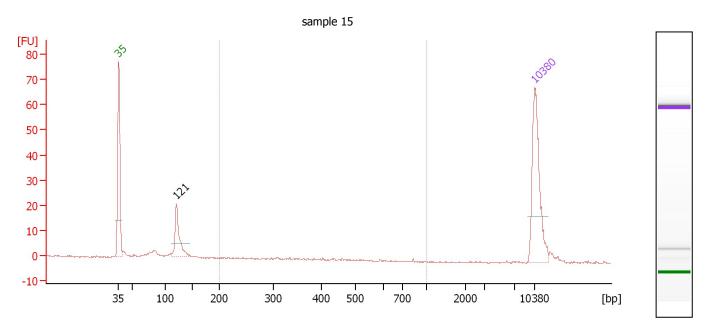
Region table for sample 5: <u>sample 14</u>

Size distribution in To [bp] Average Size **Molarity** Co Corr. % of From Conc. [pmol/l] lor Area Total **CV** [%] [bp] [bp] [pg/µl] 200 277 5.3 0.91 0.7 1,000 21.7

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 6: <u>sample 15</u>

Number of peaks found: 1 Corr. Area 1: 4.8

Noise: 0.2

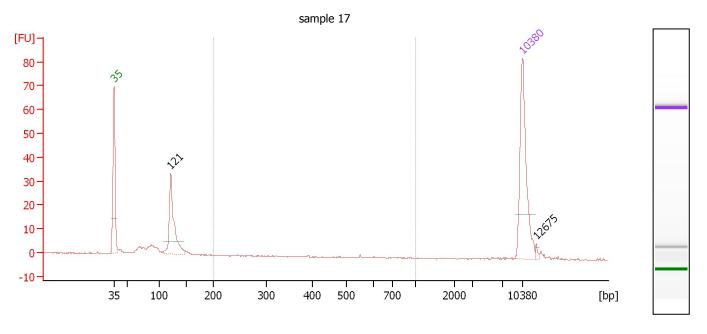
Peak	Peak table for sample 6: <u>sample 15</u>									
Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations				
1	4	43.00	35	125.00	5,411.3	Lower Marker				
2		52.69	121	57.25	717.0					
3		113.00	10,380	75.00	10.9	Upper Marker				
Regi	Region table for sample 6 : sample 15									

Size distribution in **Molarity** Co Corr. % of From To [bp] Average Size Conc. lor Area Total **CV** [%] [bp] [bp] [pmol/l] [pg/µl] 200 30.2 4.8 37.3 1,000 360 6.20

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 7: <u>sample 17</u>

Number of peaks found: 2 Corr. Area 1: 0.4

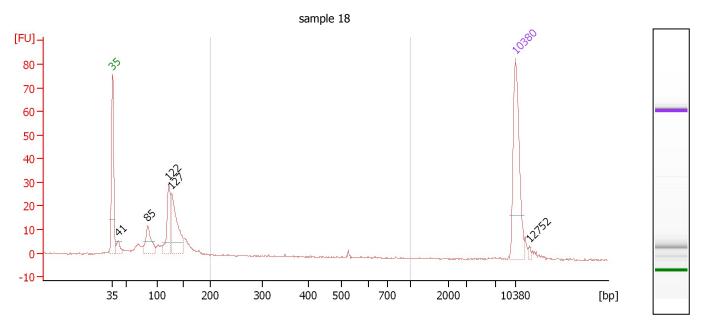
Noise: 0.1

Peak	Peak table for sample 7: sample 17									
Pea		Aligned Migration Tim	ne [s] Size	[bp]	Conc.	[pg/µl]	Molarity [	pmol/l]	Observations	
k										
1	•	43.00	35		125.00	)	5,411.3		Lower Marker	
2		52.73	121		97.06		1,211.3			
3		113.00	10,3	80	75.00		10.9		Upper Marker	
4		115.33	12,6	75	0.00		0.0			
Regi	on t	table for sample 7:	sample 1	<u>.7</u>						
From [bp]		To [bp] Average Size [bp]	Molarity [pmol/l]	Con [pg		Co Corr. Ior Area	% of Total	Size d CV [%	istribution in	
200		1.000 518	1.6	0.48		0.4	0	28.8	<b>,</b> 1	

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Assay Class: High Sensitivity DNA Assay C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\_001.xad C:\...ttings\Bioanalyzer\2014-02-18\2

# **Electropherogram Summary Continued ...**



Overall Results for sample 8 : <u>sample 18</u>

Number of peaks found: 5 Corr. Area 1: 2.2

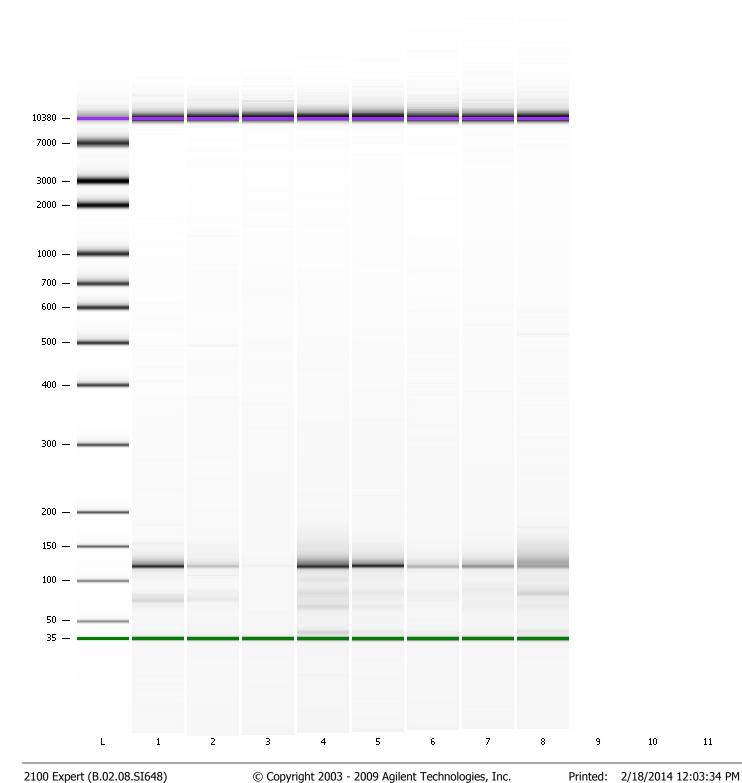
Noise: 0.1

Peak	Peak table for sample 8 : sample 18									
Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations				
1	4	43.00	35	125.00	5,411.3	Lower Marker				
2		43.97	41	16.45	604.1					
3		49.11	85	47.55	848.7					
4		52.77	122	65.29	811.7					
5		53.28	127	98.21	1,168.1					
6		113.00	10,380	75.00	10.9	Upper Marker				
7		115.41	12,752	0.00	0.0					

Region table for sample 8:			sample 1	<u>8</u>			
From [bp]	To [bp	] Average Size [bp]	Molarity [pmol/l]	Conc. [pg/µl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
200	1,000	424	11.7	2.60	2.2	1	33.6

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 $\label{light} \begin{tabular}{ll} High Sensitivity DNA Assay \\ C:\...ttings\Bioanalyzer\2014-02-18\2014-02-18\2014-02-18\2014-02-18\Data \\ \end{tabular}$ Created: Modified: 2/18/2014 11:29:08 AM 2/18/2014 12:01:55 PM Assay Class: Data Path: **Gel Image** [bp] sample 17 sample 10 sample 11 sample 3 sample 6



10

11

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Assay Class:

 $\label{light} \begin{tabular}{ll} High Sensitivity DNA Assay \\ C:\...ttings\Bioanalyzer\2014-02-18\2014-02-1$ 2/18/2014 11:29:08 AM 2/18/2014 12:01:55 PM Created: Data Path: Modified:

### **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.