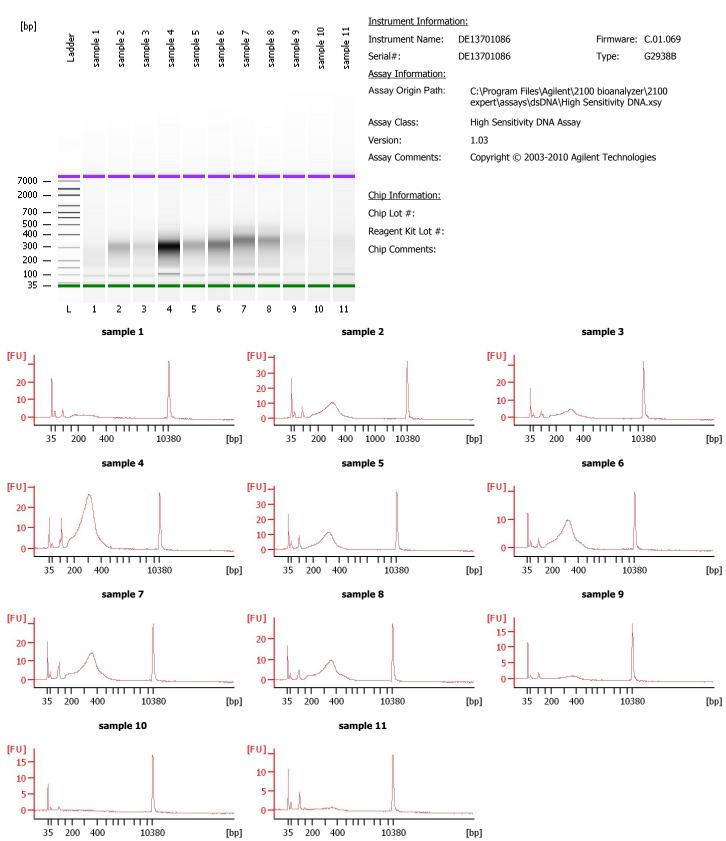
2015-06-26_001.xad Page 1 of 16

Assay Class: High Sensitivity DNA Assay Created: 6/26/2015 10:57:46 AM Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 11:39:22 AM

Electrophoresis File Run Summary



Printed:

6/26/2015 11:43:24 AM

2015-06-26_001.xad Page 2 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
sample 1			~			
sample 2			~			
sample 3			~			
sample 4			~			
sample 5			~			
sample 6			~			
sample 7			~			
sample 8			~			
sample 9			~			
sample 10			~			
sample 11			~			
Ladder			~			
Chip Lot #			Reago	ent Kit Lot #		

Chip Comments:

2015-06-26_001.xad Page 3 of 16

Assay Class: High Sensitivity DNA Assay Created: 6/26/2015 10:57:46 AM Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 11:39:22 AM

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

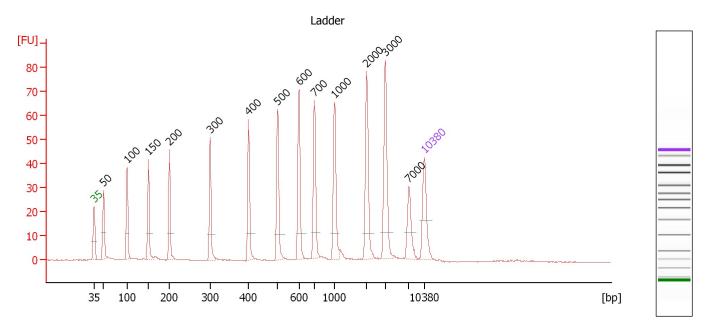
Ladder

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

2015-06-26_001.xad Page 4 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.1

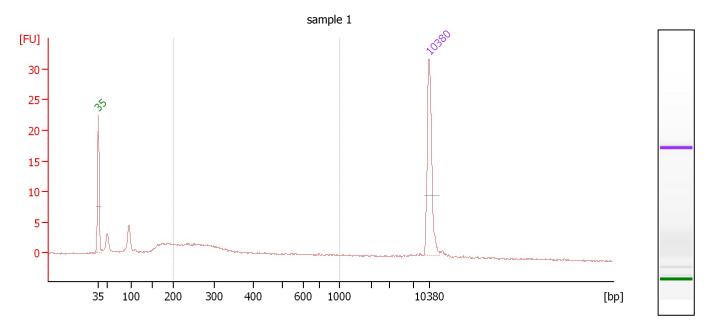
Peak table for Ladder

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2	L	50	150.00	4,545.5	Ladder Peak	44.98
3	L	100	150.00	2,272.7	Ladder Peak	50.00
4	L	150	150.00	1,515.2	Ladder Peak	54.52
5		200	150.00	1,136.4	Ladder Peak	58.98
6	L	300	150.00	757.6	Ladder Peak	67.61
7	L	400	150.00	568.2	Ladder Peak	75.74
8		500	150.00	454.5	Ladder Peak	81.90
9		600	150.00	378.8	Ladder Peak	86.41
10	L	700	150.00	324.7	Ladder Peak	89.69
11		1,000	150.00	227.3	Ladder Peak	93.92
12	L	2,000	150.00	113.6	Ladder Peak	100.75
13	L	3,000	150.00	75.8	Ladder Peak	104.70
14		7,000	150.00	32.5	Ladder Peak	109.67
15		10,380	75.00	10.9	Upper Marker	113.00

2015-06-26_001.xad Page 5 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 1 : sample 1

Number of peaks found: 0 Corr. Area 1: 36.8

Noise: 0.1

Peak table for sample 1 : <u>sample 1</u>

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

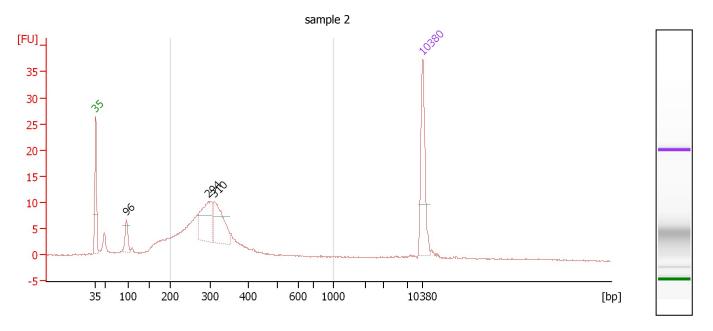
Region table for sample 1: sample 1

From	Average Size	To [bp]	Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	lor Total	CV [%]	[pg/µl]
200	251	1 000	26.0	72/1 5	10	/E 0	1/11 70

2015-06-26_001.xad Page 6 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 2 : <u>sample 2</u>

Number of peaks found: 3 Corr. Area 1: 155.7

Noise: 0.1

Peak table for sample 2 : <u>sample 2</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2		96	37.30	587.6		49.62
3		294	101.71	523.4		67.13
4		310	91.38	447.3		68.39
5		10,380	75.00	10.9	Upper Marker	113.00

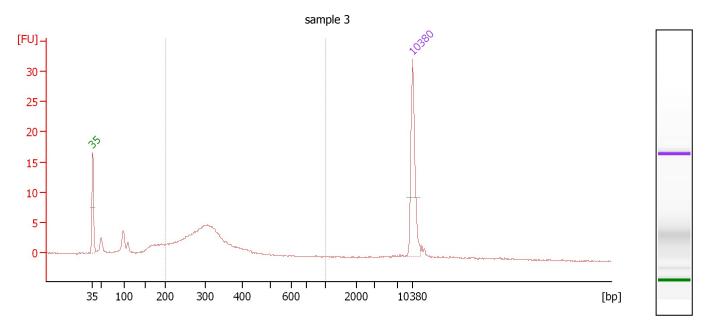
Region table for sample 2: <u>sample 2</u>

From	Average Size	To [bp] Corr.	Molarity	Co % of	Size distribution in	
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	311	1 000	155 7	2 830 4	72	27 7	545 02

2015-06-26_001.xad Page 7 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 3: sample 3

Number of peaks found: 0 Corr. Area 1: 78.1

Noise: 0.1

Peak table for sample 3: sample 3

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

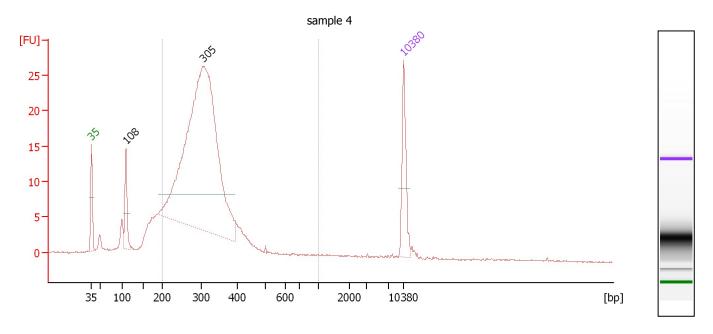
Region table for sample 3: sample 3

From	Average Size	To [bp]] Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	318	1,000	78.1	1,657.7	66	28.0	324.48

2015-06-26_001.xad Page 8 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 4: sample 4

Number of peaks found: 2 Corr. Area 1: 363.0

Noise: 0.1

Peak table for sample 4: <u>sample 4</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2		108	89.78	1,261.0		50.71
3		305	1,256.80	6,251.5		67.99
4		10,380	75.00	10.9	Upper Marker	113.00

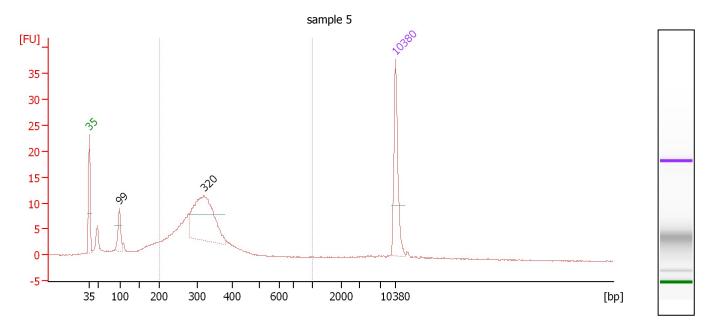
Region table for sample 4: <u>sample 4</u>

From	Average Size	To [bp]] Corr.	Molarity	Co % of	Size distribution in	
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	307	1,000	363.0	9,225.6	83	21.8	1,790.82

2015-06-26_001.xad Page 9 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 5 : sample 5

Number of peaks found: 2 Corr. Area 1: 163.0

Noise: 0.1

Peak table for sample 5 : <u>sample 5</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2		99	51.82	793.8		49.89
3		320	222.17	1,052.7		69.22
4	PA	10,380	75.00	10.9	Upper Marker	113.00

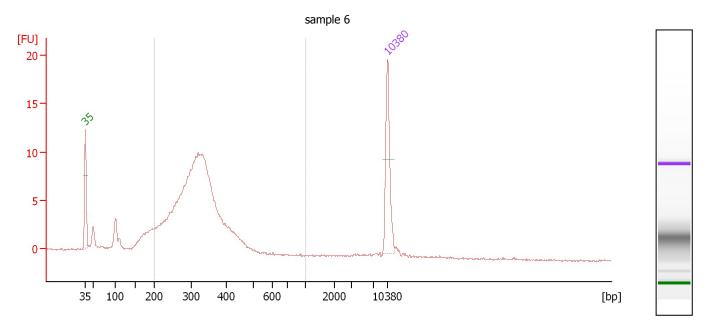
Region table for sample 5: <u>sample 5</u>

From	Average Size	To [bp]	Corr.	Molarity	Co % of	Size distribution in	
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	315	1,000	163.0	2.922.6	73	22.4	578.48

2015-06-26_001.xad Page 10 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 6: sample 6

Number of peaks found: 0 Corr. Area 1: 143.9

Noise: 0.1

Peak table for sample 6: sample 6

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

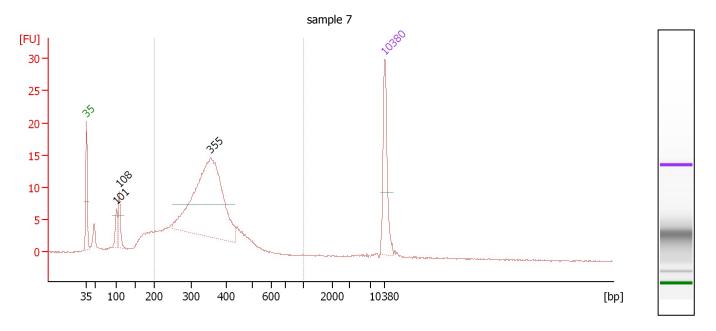
Region table for sample 6: <u>sample 6</u>

From [bp]	Average Size [bp]	To [bp]] Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	210	1 000	1/13 0	4 E34 O	9/1	10 5	010 88

2015-06-26_001.xad Page 11 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 7: sample 7

Number of peaks found: 3 Corr. Area 1: 224.6

Noise: 0.1

Peak table for sample 7: <u>sample 7</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/I]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2		101	34.74	522.8		50.06
3		108	48.07	676.8		50.69
4		355	459.79	1,963.8		72.06
5	PA	10,380	75.00	10.9	Upper Marker	113.00

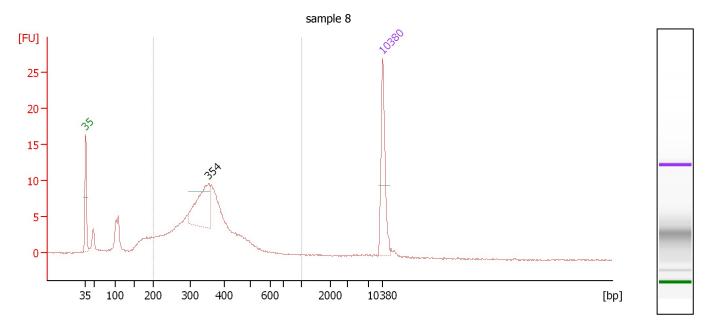
Region table for sample 7: <u>sample 7</u>

From	Average Size	To [bp] Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	348	1 000	224.6	4 134 4	79	22 B	889 23

2015-06-26_001.xad Page 12 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 8: sample 8

Number of peaks found: 1 Corr. Area 1: 153.7

Noise: 0.1

Peak table for sample 8 : <u>sample 8</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2		354	117.39	502.4		72.00
3	0	10,380	75.00	10.9	Upper Marker	113.00

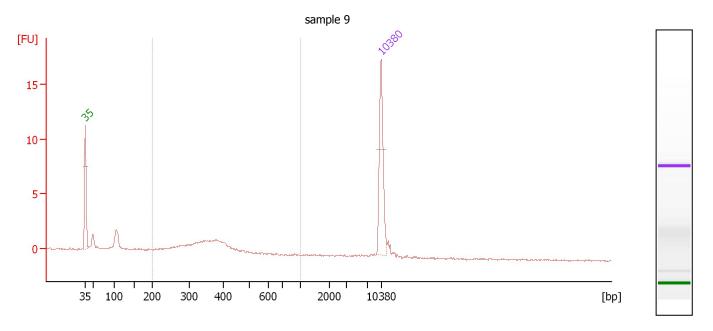
Region table for sample 8: sample 8

From	Average Size	To [bp]	Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	lor Total	CV [%]	[pg/µl]
200	352	1 000	153.7	3 238 6	79	25 4	698 30

2015-06-26_001.xad Page 13 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 9: sample 9

Number of peaks found: 0 Corr. Area 1: 17.3

Noise: 0.1

Peak table for sample 9 : <u>sample 9</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	4	35	125.00	5,411.3	Lower Marker	43.00
2	8	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9: <u>sample 9</u>

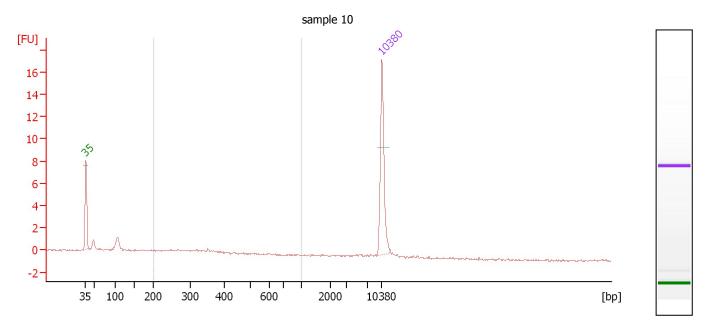
From	Average Size	To [bp]	Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	lor Total	CV [%]	[pg/µl]
200	2/17	1 000	172	E02 6	6 1	10.2	126.02

2015-06-26_001.xad Page 14 of 16

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad

Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 10 : sample 10

Number of peaks found: 0 Corr. Area 1: 5.8

Noise: 0.1

Peak table for sample 10 : <u>sample 10</u>

Pea k		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	PB	10,380	75.00	10.9	Upper Marker	113.00

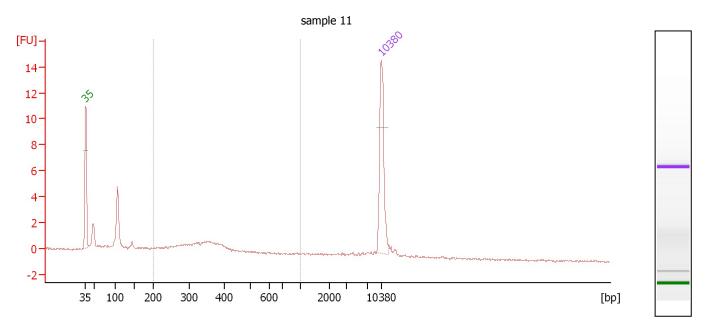
Region table for sample 10 : sample 10

From	Average Size	To [bp]	Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	337	1,000	5.8	237.1	36	33.3	47.39

2015-06-26_001.xad Page 15 of 16

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: 6/26/2015 10:57:46 AM Modified: 6/26/2015 11:39:22 AM

Electropherogram Summary Continued ...



Overall Results for sample 11: sample 11

Number of peaks found: 0 Corr. Area 1: 11.9

Noise: 0.1

Peak table for sample 11 : sample 11

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

Region table for sample 11: sample 11

From	Average Size	To [bp] Corr.	Molarity	Co % of	Size distribution in	Conc.
[bp]	[bp]		Area	[pmol/l]	<u>lor</u> Total	CV [%]	[pg/µl]
200	339	1,000	11.9	443.0	44	23.2	93.20

2015-06-26_001.xad Page 16 of 16

High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-06-26\2015-06-26_001.xad Created: Modified: 6/26/2015 10:57:46 AM 6/26/2015 11:39:22 AM Assay Class: Data Path: **Gel Image** [bp] sample 10 sample 11 sample 2 sample 5 sample 7 10380 -7000 — — 3000 **—** 2000 --1000 — 700 — 600 — 500 — 400 — 300 — 200 — 150 — 100 — L 1 3 5 6 7 8 9 10 11