

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-11\2015-06-11_001.xad

Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Electrophoresis File Run Summary

Instrument Information:

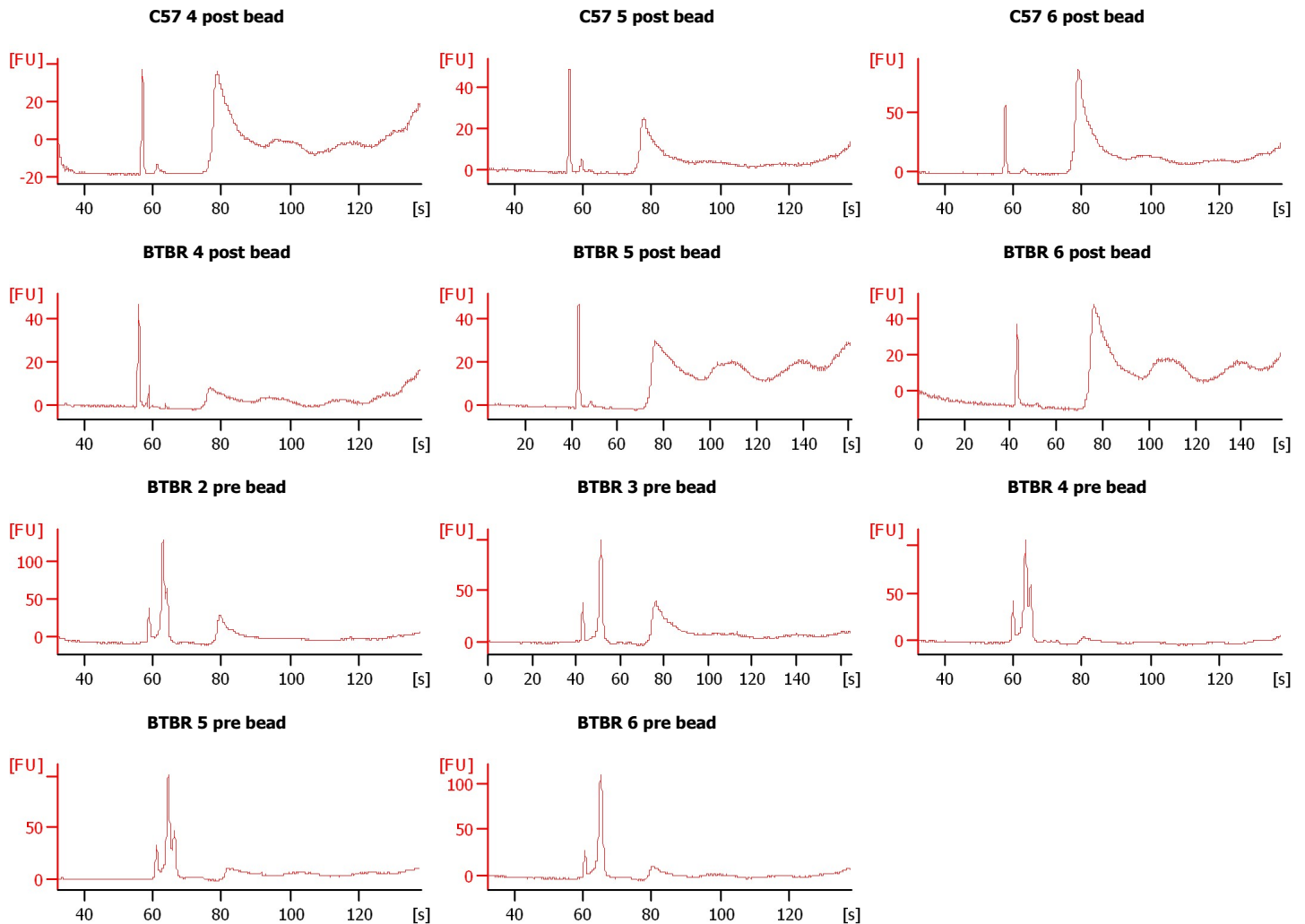
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
C57 4 post bead		<input type="checkbox"/>	✓			
C57 5 post bead		<input type="checkbox"/>	✓			
C57 6 post bead		<input type="checkbox"/>	✓			
BTBR 4 post bead		<input type="checkbox"/>	✓			
BTBR 5 post bead		<input type="checkbox"/>	✓			
BTBR 6 post bead		<input type="checkbox"/>	✓			
BTBR 2 pre bead		<input type="checkbox"/>	✓			
BTBR 3 pre bead		<input type="checkbox"/>	✓			
BTBR 4 pre bead		<input type="checkbox"/>	✓			
BTBR 5 pre bead		<input type="checkbox"/>	✓			
BTBR 6 pre bead		<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

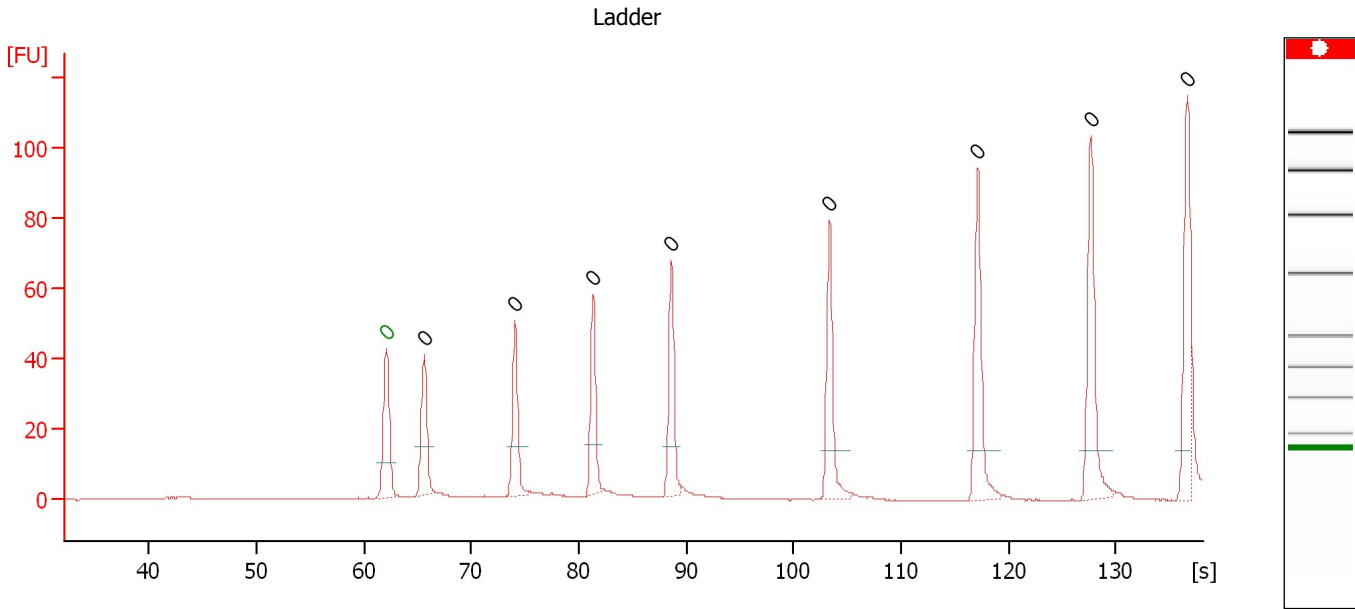
Ladder

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

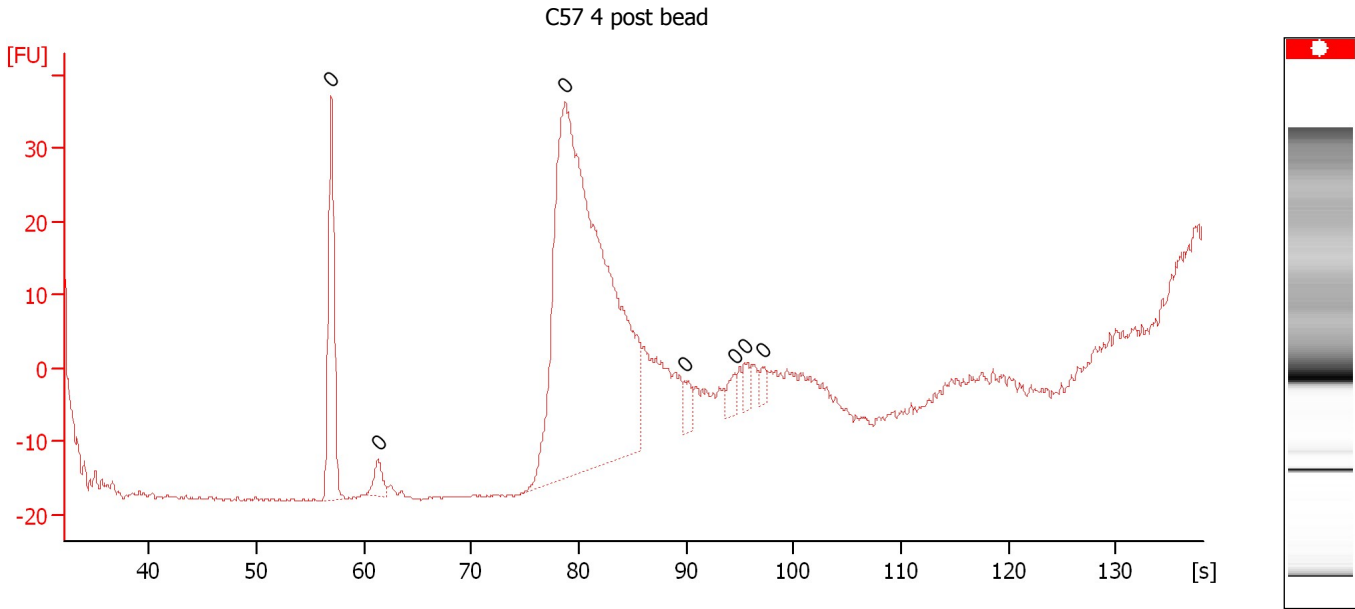
Peak table for Ladder

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	62.10
2	0	0.00	0.0	Ladder Peak	65.60
3	0	0.00	0.0	Ladder Peak	74.05
4	0	0.00	0.0	Ladder Peak	81.35
5	0	0.00	0.0	Ladder Peak	88.60
6	0	0.00	0.0	Ladder Peak	103.35
7	0	0.00	0.0	Ladder Peak	117.15
8	0	0.00	0.0	Ladder Peak	127.70
9	0	0.00	0.0	Ladder Peak	136.65

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Electropherogram Summary Continued ...



Overall Results for sample 1 : C57 4 post bead

Number of peaks found: 0 Noise: 0.2

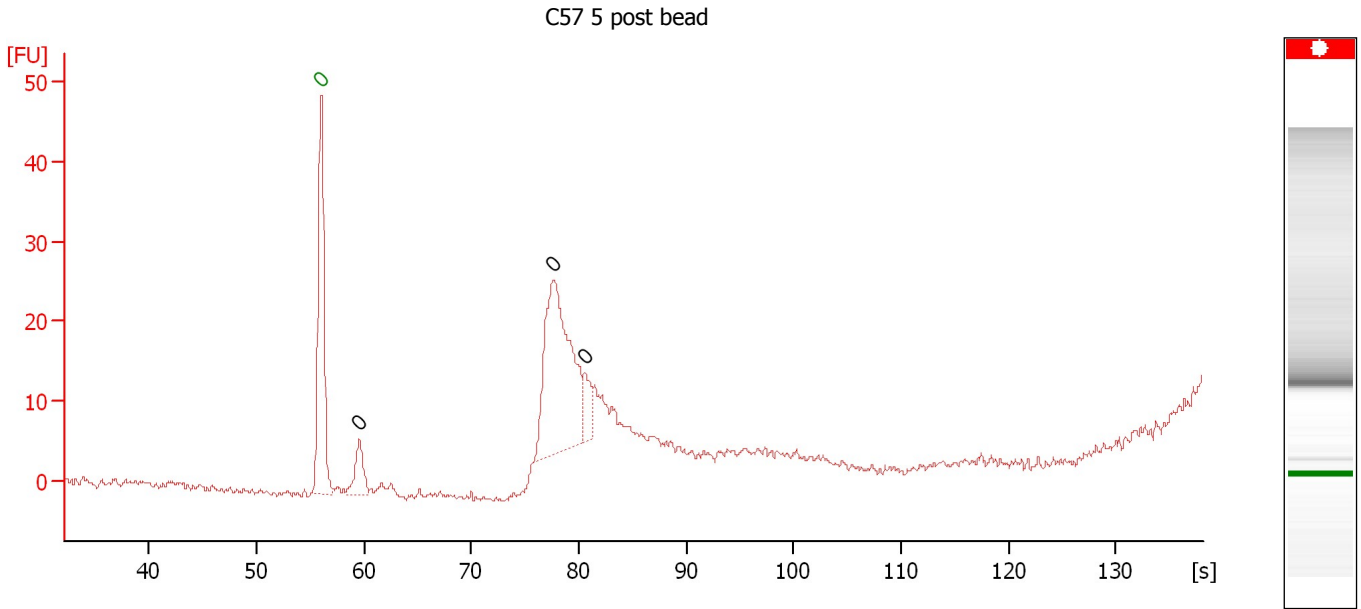
Peak table for sample 1 : C57 4 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		56.95
2	0	0.00	0.0		61.30
3	0	0.00	0.0		78.75
4	0	0.00	0.0		89.85
5	0	0.00	0.0		94.50
6	0	0.00	0.0		95.40
7	0	0.00	0.0		97.10

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Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : C57 5 post bead

Number of peaks found: 3 Noise: 0.4

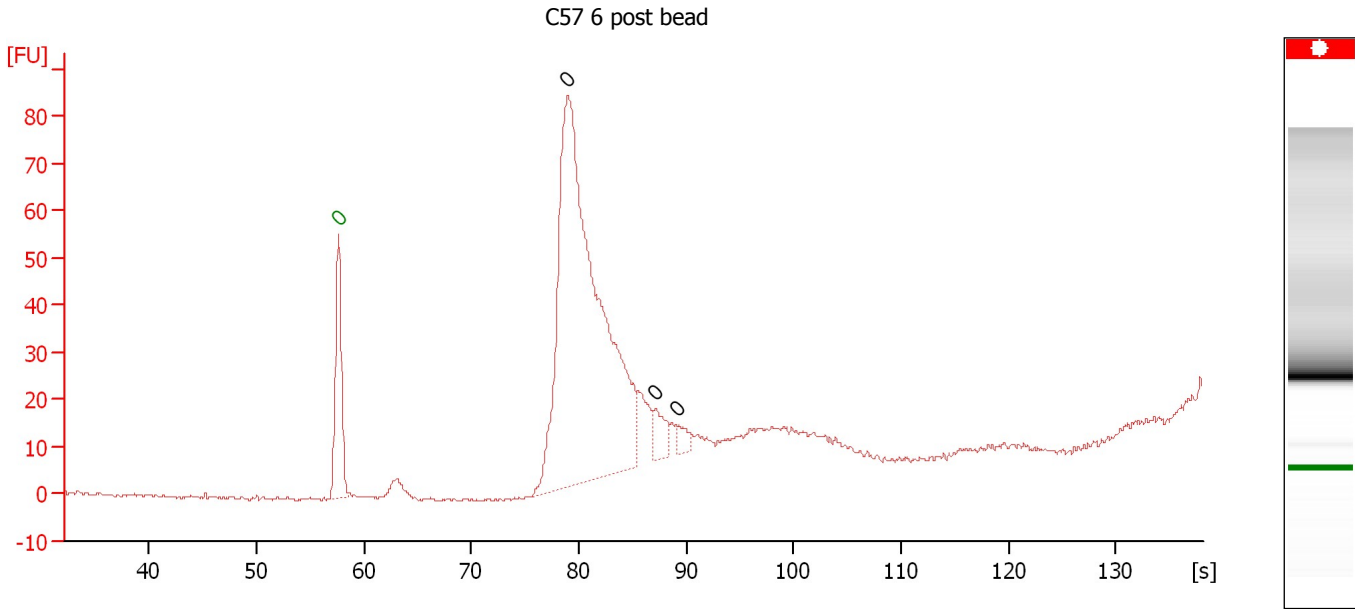
Peak table for sample 2 : C57 5 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	56.00
2	0	0.00	0.0		59.55
3	0	0.00	0.0		77.60
4	0	0.00	0.0		80.60

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : C57 6 post bead

Number of peaks found: 3 Noise: 0.3

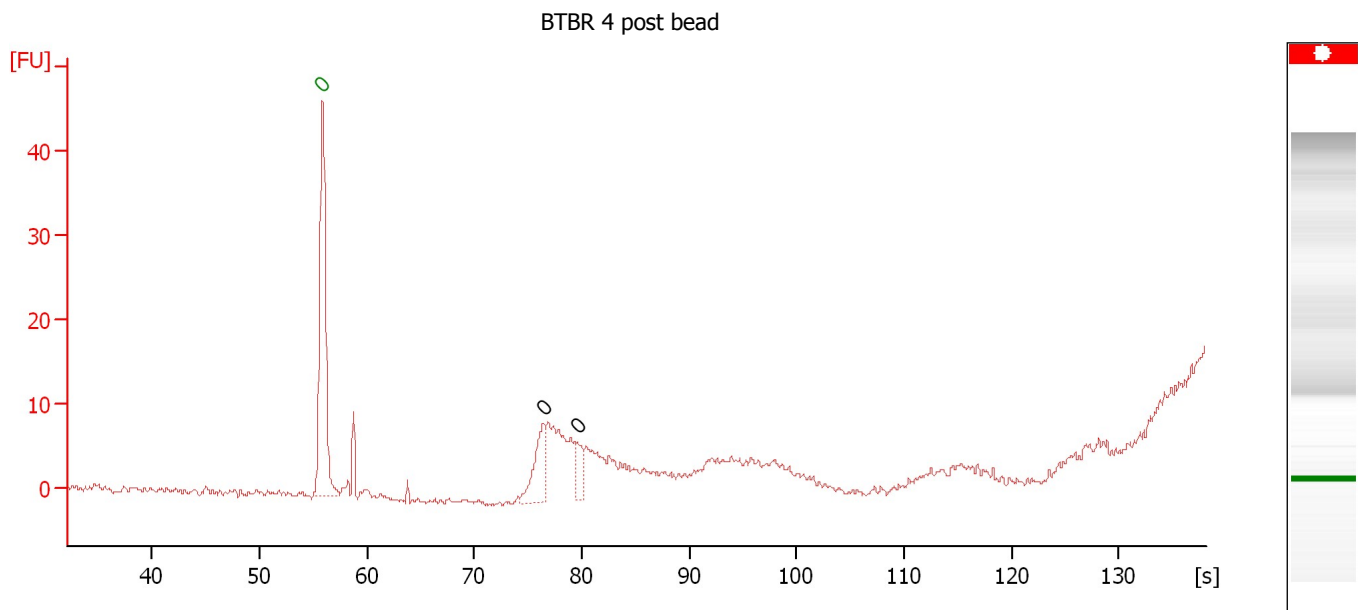
Peak table for sample 3 : C57 6 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	57.65
2	0	0.00	0.0		78.95
3	0	0.00	0.0		87.10
4	0	0.00	0.0		89.15

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : BTBR 4 post bead

Number of peaks found: 2 Noise: 0.4

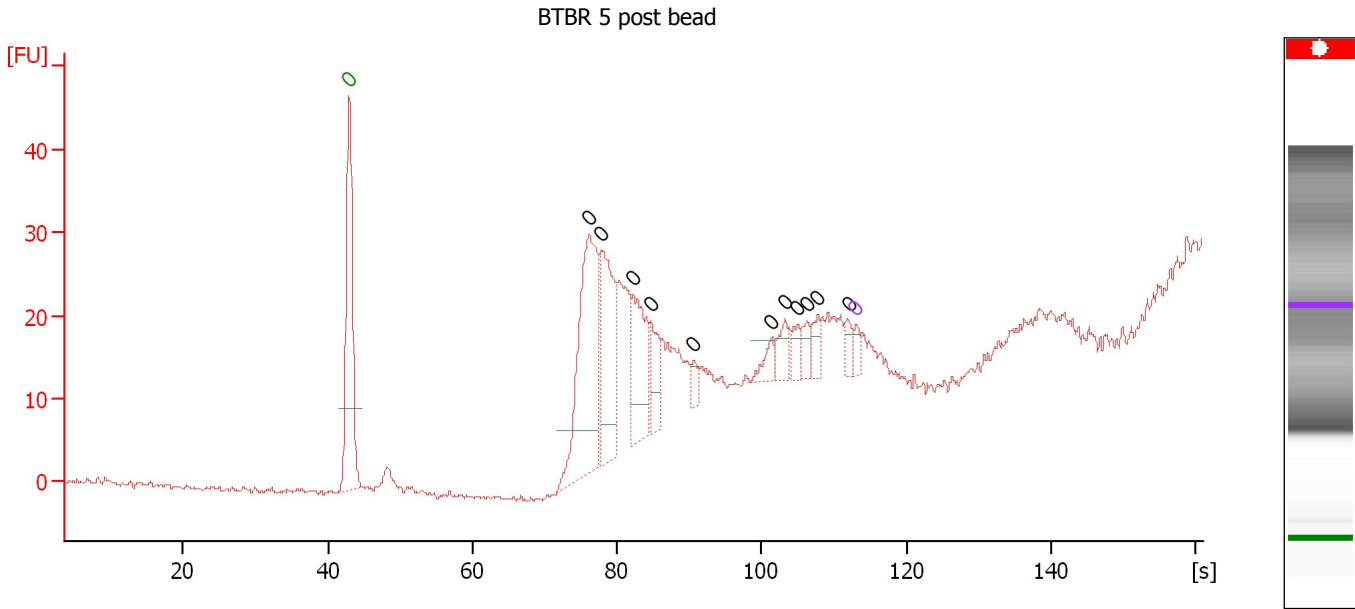
Peak table for sample 4 : BTBR 4 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	55.85
2	0	0.00	0.0		76.45
3	0	0.00	0.0		79.65

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : BTBR 5 post bead

Number of peaks found: 11 Noise: 0.3

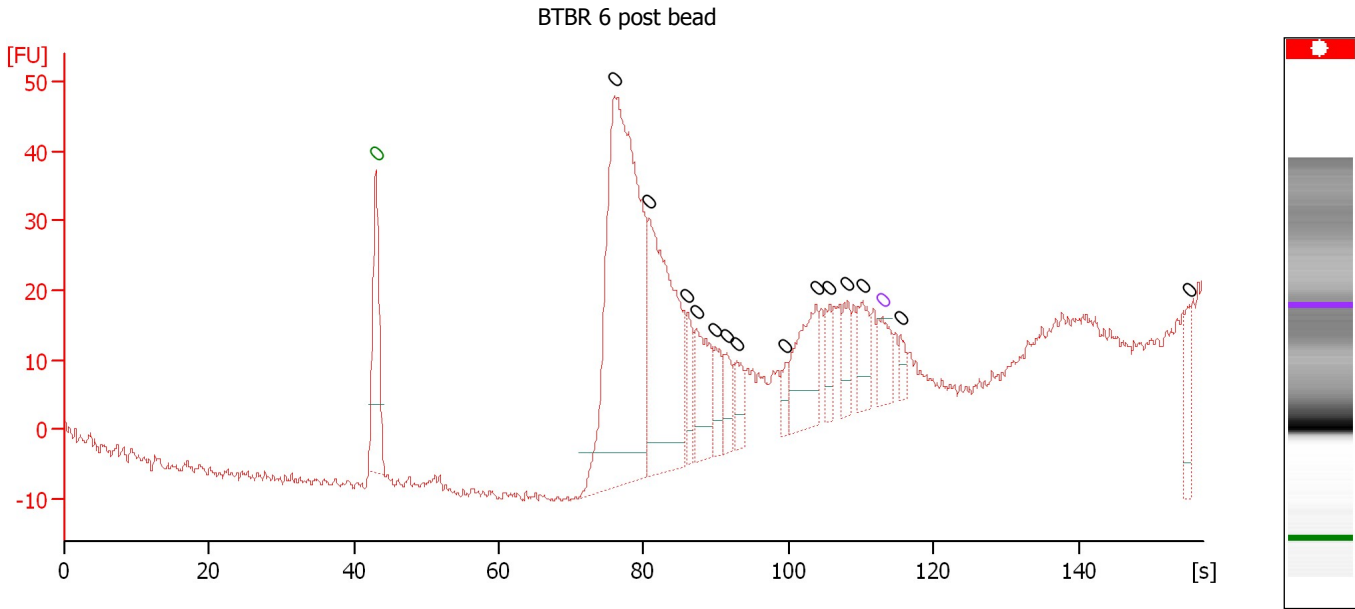
Peak table for sample 5 : BTBR 5 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	43.00
2	0	0.00	0.0		76.11
3	0	0.00	0.0		77.81
4	0	0.00	0.0		82.19
5	0	0.00	0.0		84.64
6	0	0.00	0.0		90.58
7	0	0.00	0.0		101.35
8	0	0.00	0.0		103.13
9	0	0.00	0.0		104.83
10	0	0.00	0.0		106.17
11	0	0.00	0.0		107.73
12	0	0.00	0.0		111.96
13	0	0.00	0.0	Upper Marker	113.00

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 6 : BTBR 6 post bead

Number of peaks found: 14 Noise: 0.7

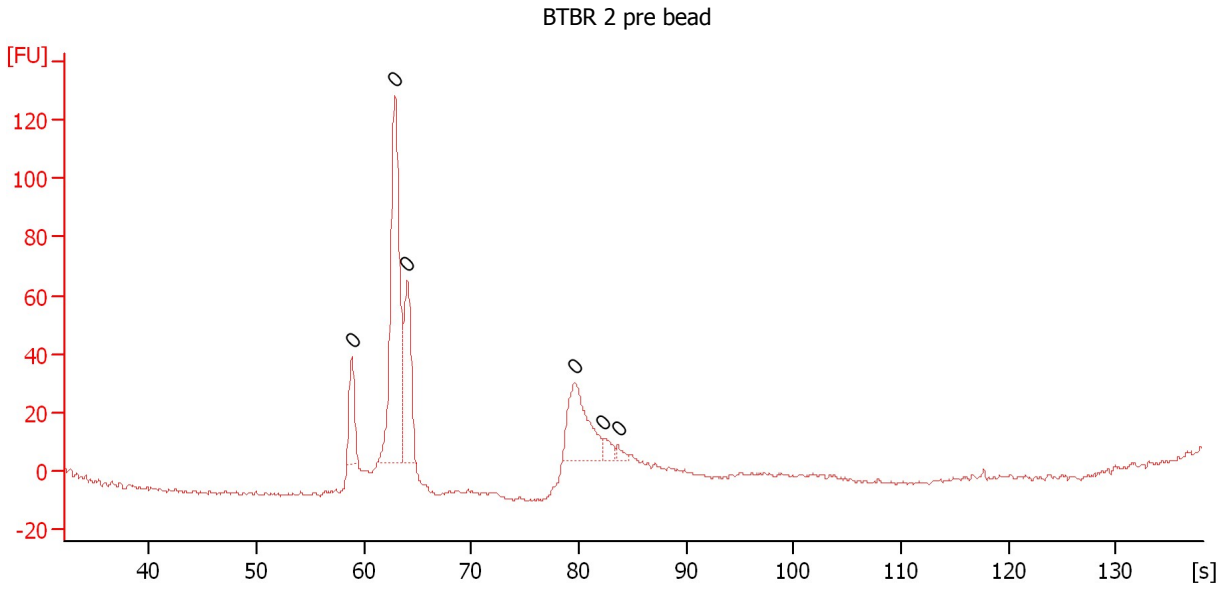
Peak table for sample 6 : BTBR 6 post bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	43.00
2	0	0.00	0.0		76.00
3	0	0.00	0.0		80.74
4	0	0.00	0.0		86.08
5	0	0.00	0.0		87.34
6	0	0.00	0.0		89.94
7	0	0.00	0.0		91.42
8	0	0.00	0.0		92.83
9	0	0.00	0.0		99.50
10	0	0.00	0.0		103.81
11	0	0.00	0.0		105.58
12	0	0.00	0.0		108.18
13	0	0.00	0.0		110.18
14	0	0.00	0.0	Upper Marker	113.00
15	0	0.00	0.0		115.52
16	0	0.00	0.0		155.27

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Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : BTBR 2 pre bead

Number of peaks found: 0 Noise: 0.7

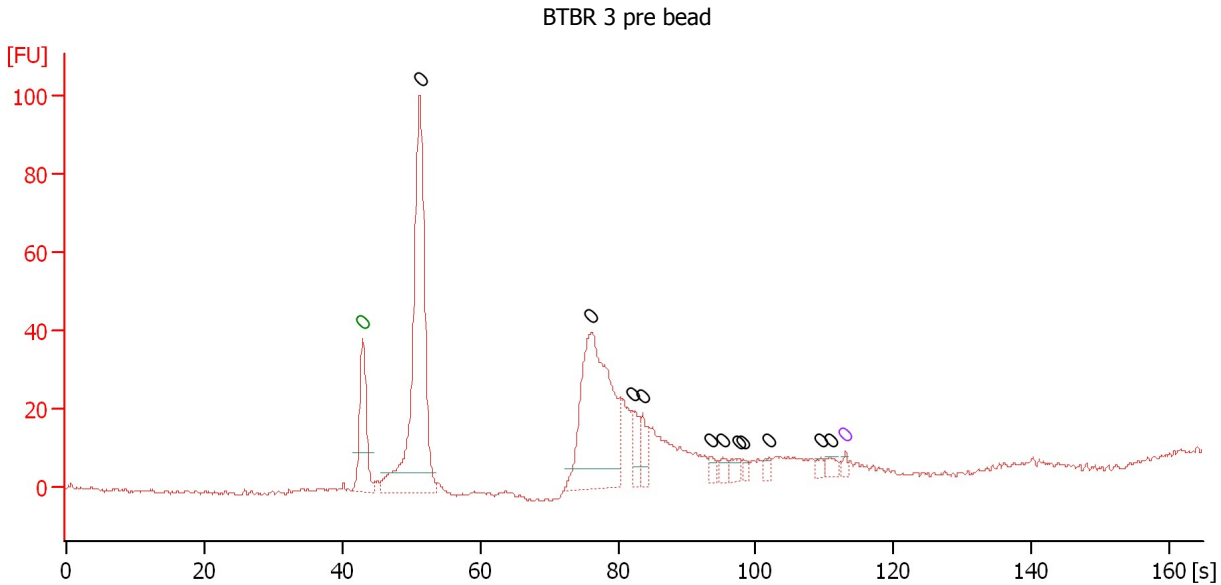
Peak table for sample 7 : BTBR 2 pre bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		58.90
2	0	0.00	0.0		62.90
3	0	0.00	0.0		64.05
4	0	0.00	0.0		79.65
5	0	0.00	0.0		82.30
6	0	0.00	0.0		83.65

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : BTBR 3 pre bead

Number of peaks found: 11 Noise: 0.6

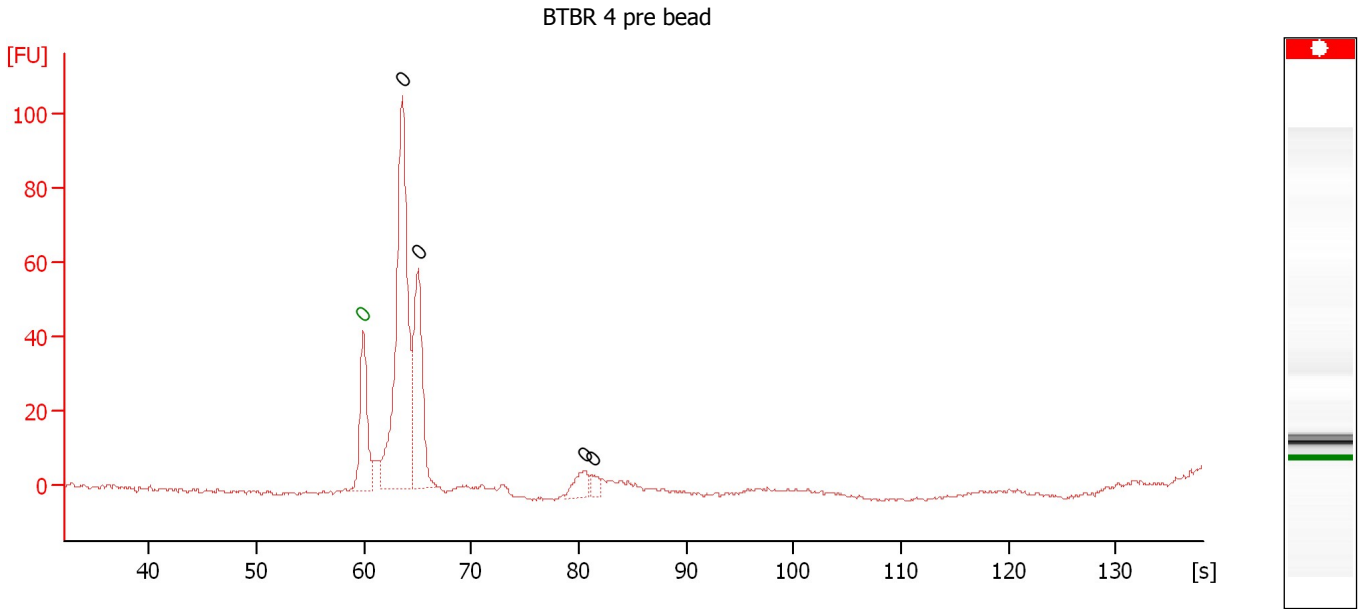
Peak table for sample 8 : BTBR 3 pre bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	43.00
2	0	0.00	0.0		51.26
3	0	0.00	0.0		76.21
4	0	0.00	0.0		82.21
5	0	0.00	0.0		83.61
6	0	0.00	0.0		93.59
7	0	0.00	0.0		95.23
8	0	0.00	0.0		97.57
9	0	0.00	0.0		98.19
10	0	0.00	0.0		101.93
11	0	0.00	0.0		109.49
12	0	0.00	0.0		110.82
13	0	0.00	0.0	Upper Marker	113.00

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Created: 6/11/2015 11:17:54 AM
 Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : BTBR 4 pre bead

Number of peaks found: 4 Noise: 0.5

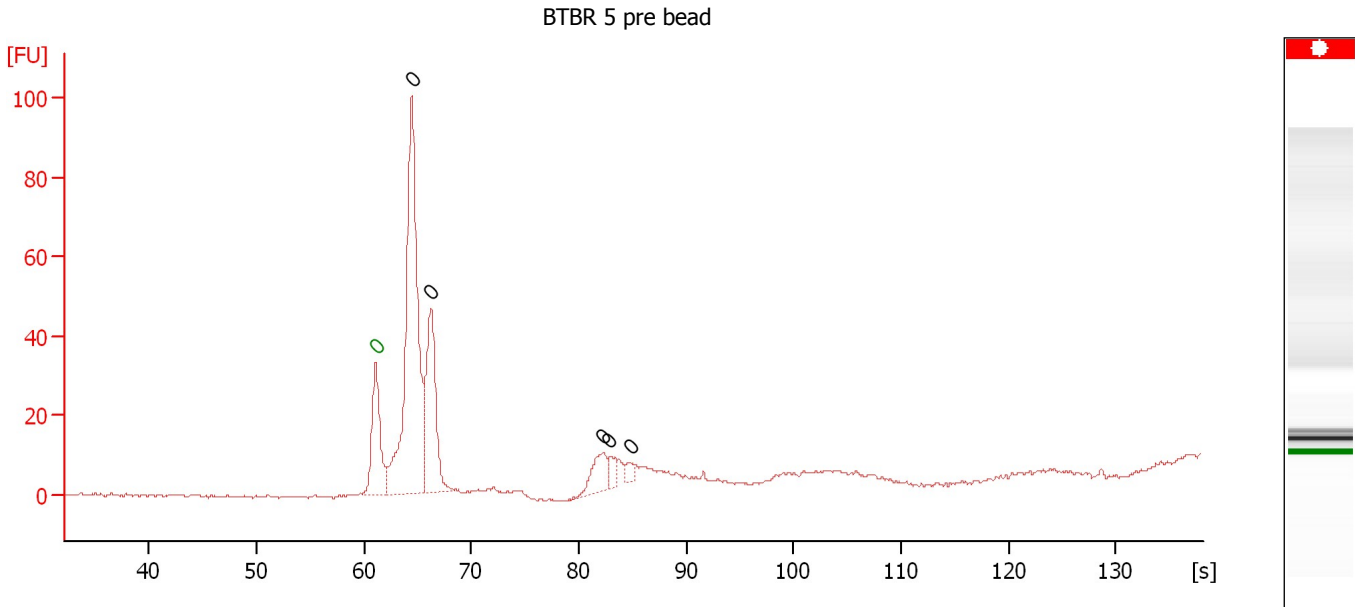
Peak table for sample 9 : BTBR 4 pre bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	59.95
2	0	0.00	0.0		63.55
3	0	0.00	0.0		65.05
4	0	0.00	0.0		80.50
5	0	0.00	0.0		81.25

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Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...



Overall Results for sample 10 : BTBR 5 pre bead

Number of peaks found: 5 Noise: 0.4

Peak table for sample 10 : BTBR 5 pre bead

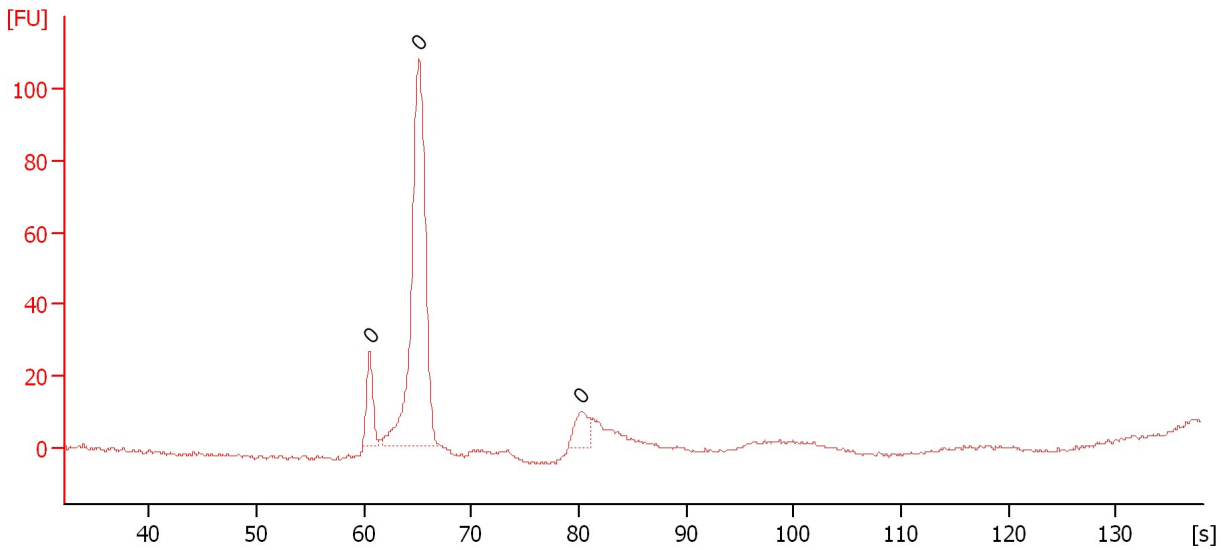
Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0	Lower Marker	61.10
2	0	0.00	0.0		64.45
3	0	0.00	0.0		66.25
4	0	0.00	0.0		82.30
5	0	0.00	0.0		82.85
6	0	0.00	0.0		84.75

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Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Electropherogram Summary Continued ...

BTBR 6 pre bead



Overall Results for sample 11 : BTBR 6 pre bead

Number of peaks found: 0 Noise: 0.5

Peak table for sample 11 : BTBR 6 pre bead

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	0	0.00	0.0		60.55
2	0	0.00	0.0		65.10
3	0	0.00	0.0		80.25

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-06-11\2015-06-11_001.xad

Created: 6/11/2015 11:17:54 AM
Modified: 6/11/2015 12:01:39 PM

Gel Image