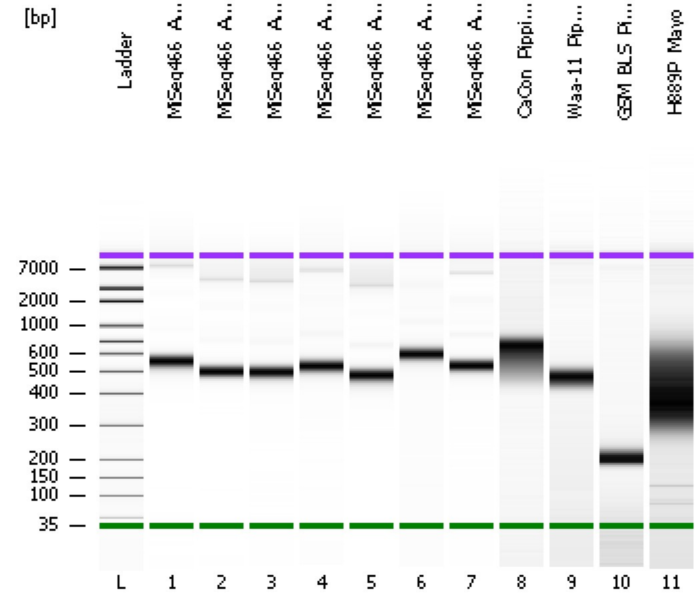
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad

Created: 3/14/2017 4:43:42 PM
Modified: 3/14/2017 5:25:01 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

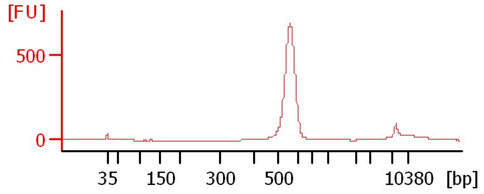
Chip Information:

Chip Lot #:

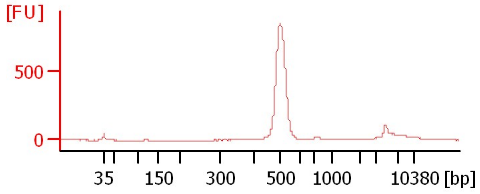
Reagent Kit Lot #:

Chip Comments:

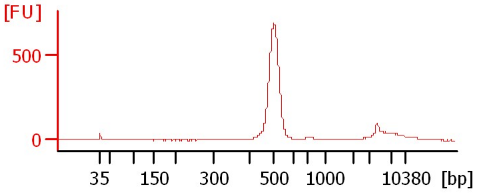
MiSeq466_AP6 (1:50)



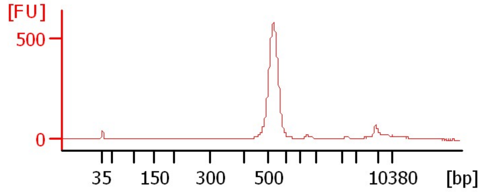
MiSeq466_AP7 (1:50)



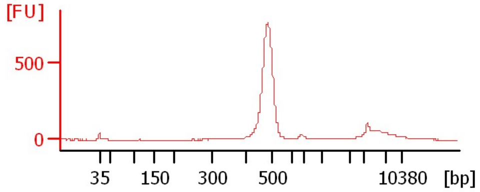
MiSeq466_AP8 (1:50)



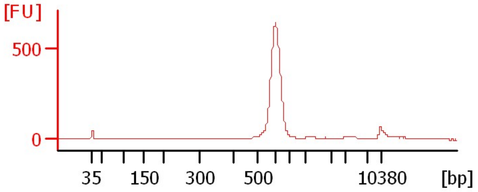
MiSeq466_AP9 (1:50)



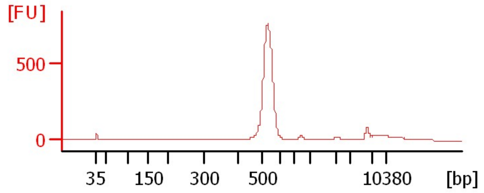
MiSeq466_AP10 (1:50)



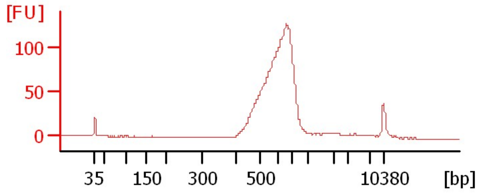
MiSeq466_AP11 (1:50)



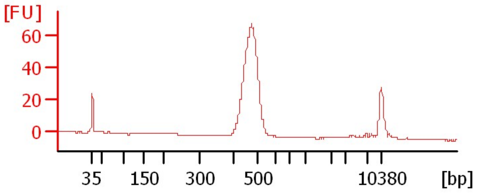
MiSeq466_AP12 (1:50)



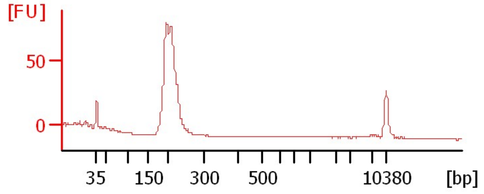
CaCon_PippinHT



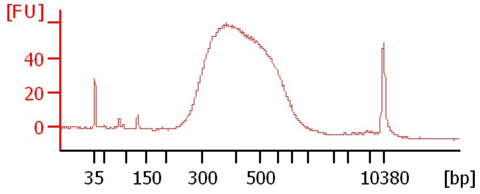
Waa-11_PippinHT



GSM_BLS_PippinHT



H889P_Mayo



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad

Created: 3/14/2017 4:43:42 PM
Modified: 3/14/2017 5:25:01 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
MiSeq466_AP6 (1:50)		☐	✓			
MiSeq466_AP7 (1:50)		☐	✓			
MiSeq466_AP8 (1:50)		☐	✓			
MiSeq466_AP9 (1:50)		☐	✓			
MiSeq466_AP10 (1:50)		☐	✓			
MiSeq466_AP11 (1:50)		☐	✓			
MiSeq466_AP12 (1:50)		☐	✓			
CaCon_PippinHT		☐	✓			
Waa-11_PippinHT		☐	✓			
GSM_BLS_PippinHT		☐	✓			
H889P_Mayo		☐	✓			
Ladder		☐	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

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

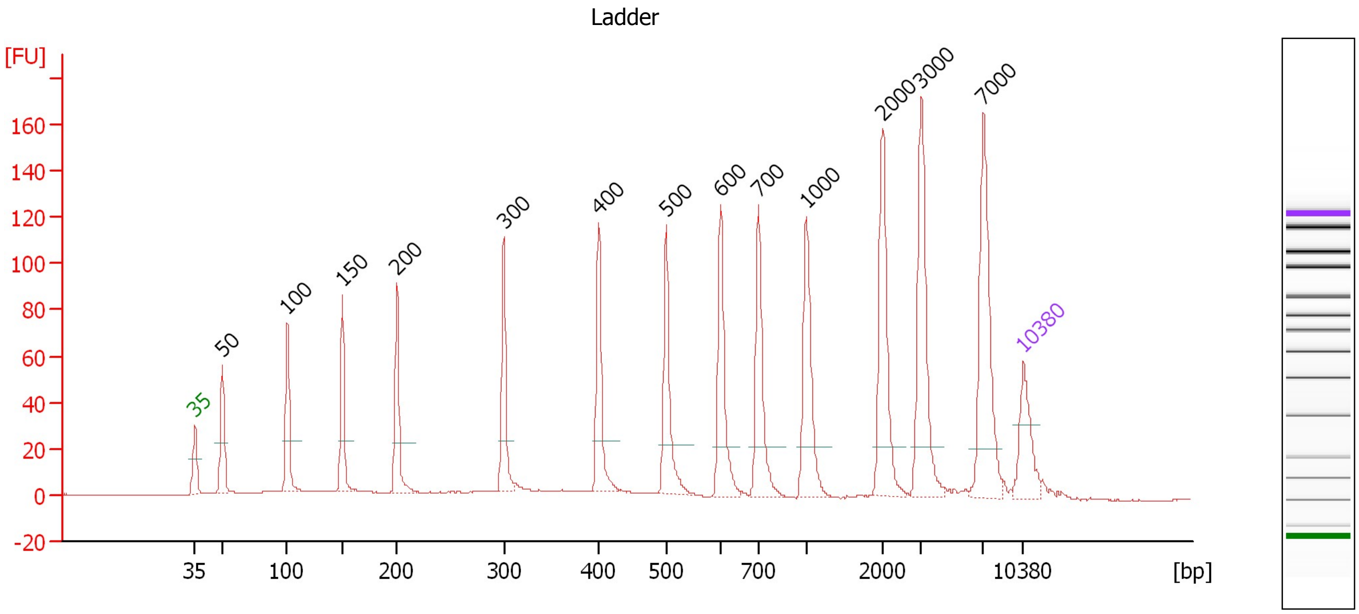
Filter Width [s] : 0.5
Polynomial Order : 4

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

Assay Class:	High Sensitivity DNA Assay	Created:	3/14/2017 4:43:42 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad	Modified:	3/14/2017 5:25:01 PM

Electropherogram Summary



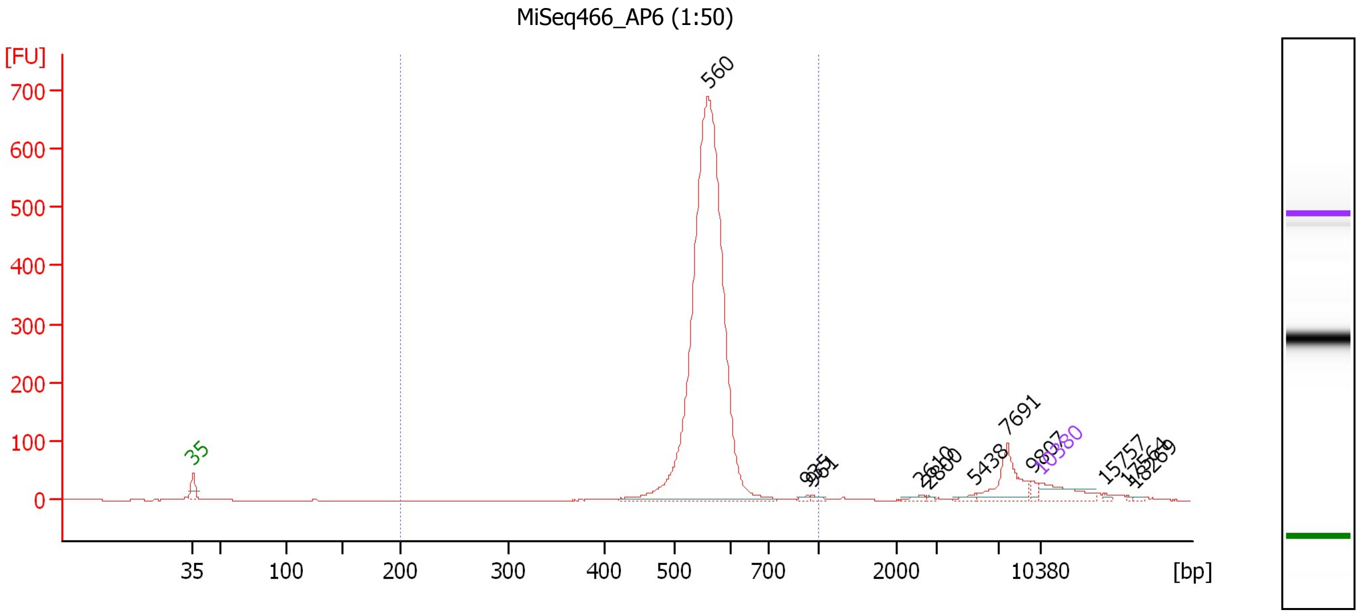
Overall Results for Ladder

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	45.30
3	∟	100	150.00	2,272.7	Ladder Peak	50.79
4	∟	150	150.00	1,515.2	Ladder Peak	55.43
5	∟	200	150.00	1,136.4	Ladder Peak	60.07
6	∟	300	150.00	757.6	Ladder Peak	69.08
7	∟	400	150.00	568.2	Ladder Peak	77.10
8	∟	500	150.00	454.5	Ladder Peak	82.82
9	∟	600	150.00	378.8	Ladder Peak	87.41
10	∟	700	150.00	324.7	Ladder Peak	90.61
11	∟	1,000	150.00	227.3	Ladder Peak	94.67
12	∟	2,000	150.00	113.6	Ladder Peak	101.15
13	∟	3,000	150.00	75.8	Ladder Peak	104.40
14	∟	7,000	150.00	32.5	Ladder Peak	109.62
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...



Overall Results for sample 1 : MiSeq466_AP6 (1:50)

Number of peaks found:	11	Corr. Area 1:	2,499.7
Noise:	0.2		

Peak table for sample 1 : MiSeq466_AP6 (1:50)

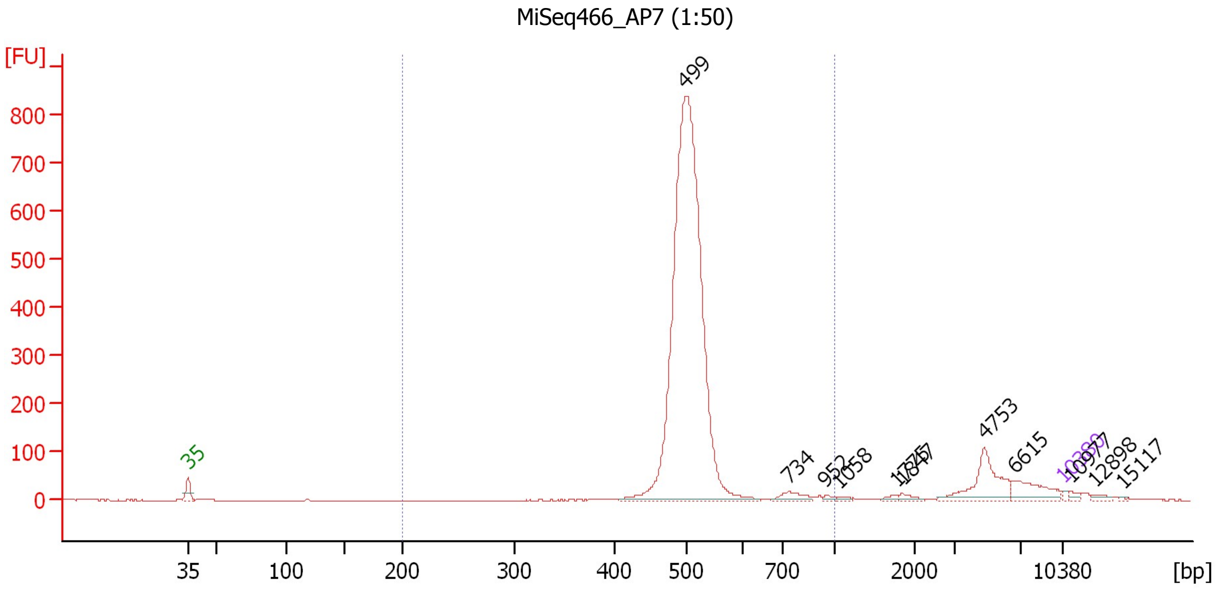
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		560	2,785.11	7,541.8		85.56
3		935	9.07	14.7		93.79
4		961	8.93	14.1		94.15
5		2,610	11.36	6.6		103.13
6		2,800	4.25	2.3		103.75
7		5,438	12.52	3.5		107.58
8		7,691	139.60	27.5		110.31
9		9,807	19.66	3.0		112.43
10	▶	10,380	75.00	10.9	Upper Marker	113.00
11		15,757	0.00	0.0		118.37
12		17,564	0.00	0.0		120.18
13		18,269	0.00	0.0		120.89

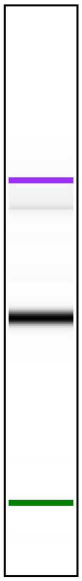
Region table for sample 1 : MiSeq466_AP6 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	560	2,499.7	7,632.4	🟦	2,807.18	90	8.0

Electropherogram Summary Continued ...

MiSeq466_AP7 (1:50)





Overall Results for sample 2 : MiSeq466_AP7 (1:50)

Number of peaks found:	11	Corr. Area 1:	2,903.4
Noise:	0.6		

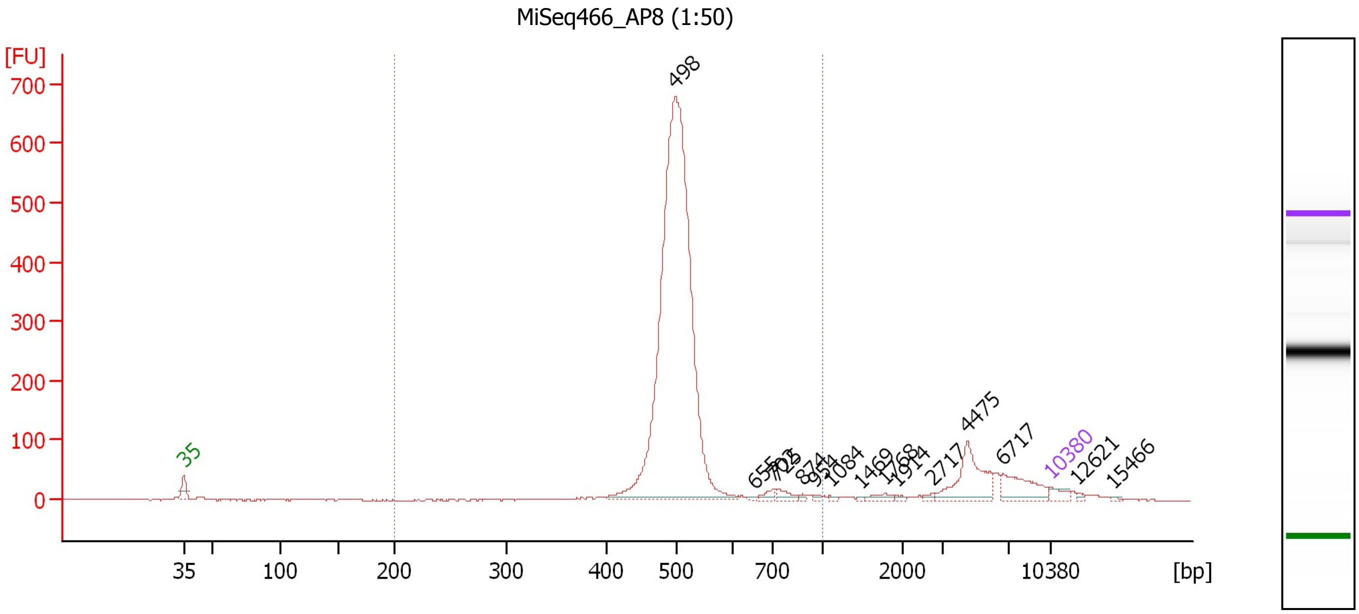
Peak table for sample 2 : MiSeq466_AP7 (1:50)

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		499	30,662.88	93,124.7		82.76
3		734	470.08	970.1		91.07
4		952	104.56	166.4		94.02
5		1,058	74.47	106.7		95.04
6		1,775	106.50	90.9		99.69
7		1,847	155.88	127.9		100.16
8		4,753	1,805.19	575.4		106.69
9		6,615	972.36	222.7		109.12
10	▶	10,380	75.00	10.9	Upper Marker	113.00
11		10,977	0.00	0.0		113.60
12		12,898	0.00	0.0		115.52
13		15,117	0.00	0.0		117.73

Region table for sample 2 : MiSeq466_AP7 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	512	2,903.4	91,659.1	🟦	30,679.63	87	10.2

Electropherogram Summary Continued ...



Overall Results for sample 3 : MiSeq466_AP8 (1:50)

Number of peaks found:	15	Corr. Area 1:	2,603.3
Noise:	0.7		

Peak table for sample 3 : MiSeq466_AP8 (1:50)

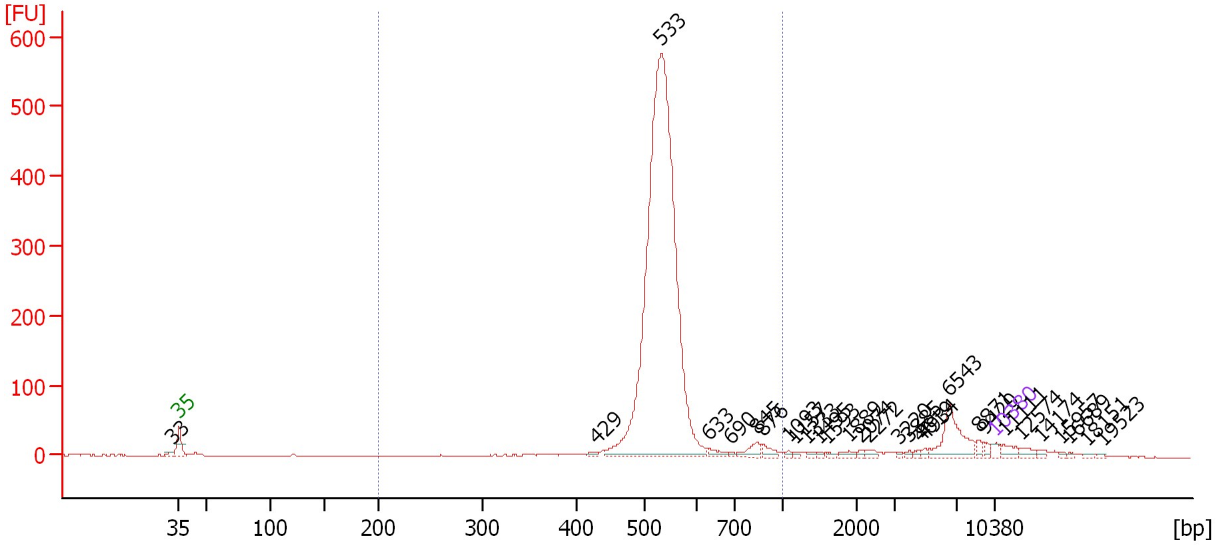
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		498	8,120.01	24,694.9		82.72
3		655	21.25	49.1		89.18
4		702	66.31	143.1		90.64
5		725	85.17	178.1		90.94
6		874	20.13	34.9		92.97
7		954	19.18	30.5		94.05
8		1,084	15.54	21.7		95.21
9		1,469	9.29	9.6		97.71
10		1,768	56.94	48.8		99.65
11		1,914	15.37	12.2		100.59
12		2,717	22.62	12.6		103.48
13		4,475	511.91	173.3		106.32
14		6,717	302.48	68.2		109.25
15	▶	10,380	75.00	10.9	Upper Marker	113.00
16		12,621	0.00	0.0		115.24
17		15,466	0.00	0.0		118.08

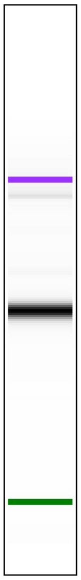
Region table for sample 3 : MiSeq466_AP8 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	509	2,603.3	25,368.2	🟦	8,412.38	84	12.0

Electropherogram Summary Continued ...

MiSeq466_AP9 (1:50)





Overall Results for sample 4 : MiSeq466_AP9 (1:50)

Number of peaks found:	29	Corr. Area 1:	2,128.0
Noise:	0.7		

Peak table for sample 4 : MiSeq466_AP9 (1:50)

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.41
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		429	64.64	228.5		78.73
4		533	14,463.55	41,089.9		84.35
5		633	125.49	300.5		88.46
6		690	35.64	78.3		90.29
7		845	203.19	364.2		92.58
8		876	133.63	231.2		92.99
9		1,093	32.99	45.7		95.27
10		1,157	36.02	47.2		95.68
11		1,333	40.05	45.5		96.83
12		1,495	26.70	27.1		97.88
13		1,593	35.06	33.3		98.52
14		1,889	68.43	54.9		100.43
15		2,074	39.38	28.8		101.39
16		2,272	70.21	46.8		102.03
17		3,220	26.71	12.6		104.68
18		3,885	32.61	12.7		105.55
19		4,619	43.81	14.4		106.51
20		4,934	42.52	13.1		106.92
21		6,543	733.62	169.9		109.02
22		8,871	75.51	12.9		111.49
23		9,420	62.63	10.1		112.04
24	▶	10,380	75.00	10.9	Upper Marker	113.00
25		11,111	0.00	0.0		113.73

Electropherogram Summary Continued ...

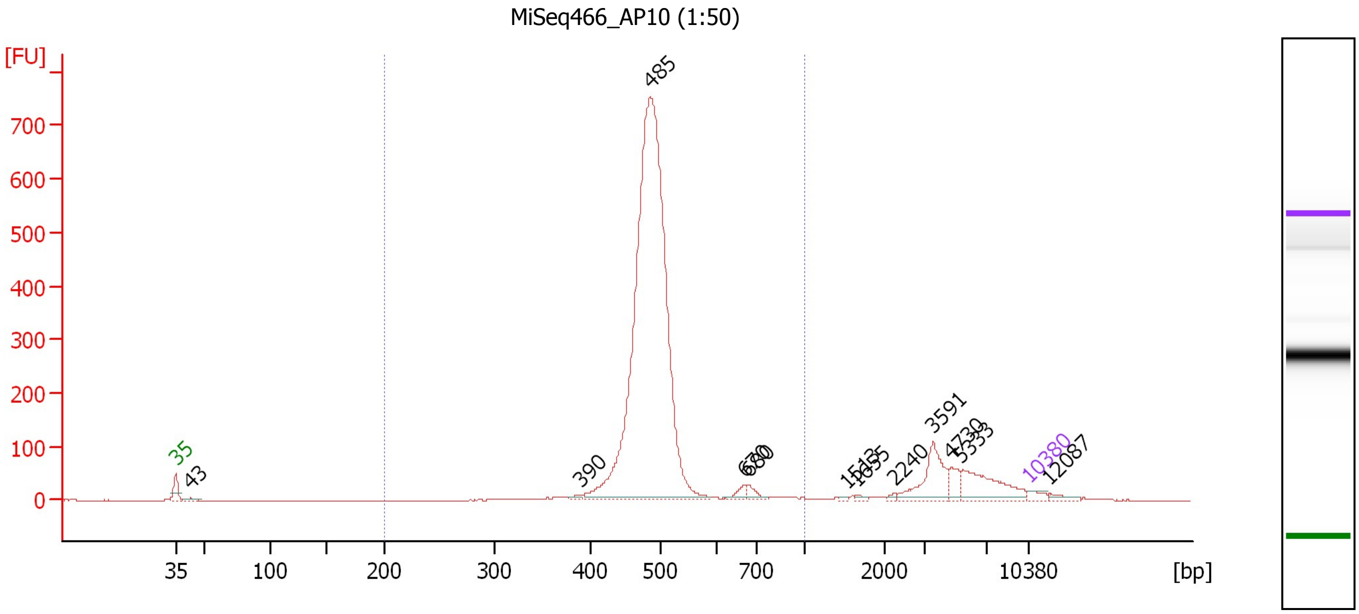
... Peak table for sample 4 : MiSeq466_AP9 (1:50)

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	12,574	0.00	0.0		115.19
27	14,174	0.00	0.0		116.79
28	15,957	0.00	0.0		118.57
29	16,689	0.00	0.0		119.31
30	18,151	0.00	0.0		120.77
31	19,523	0.00	0.0		122.14

Region table for sample 4 : MiSeq466_AP9 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	540	2,128.0	43,477.4	🟦	15,277.80	86	12.1

Electropherogram Summary Continued ...



Overall Results for sample 5 : MiSeq466_AP10 (1:50)

Number of peaks found:	12	Corr. Area 1:	3,079.9
Noise:	0.5		

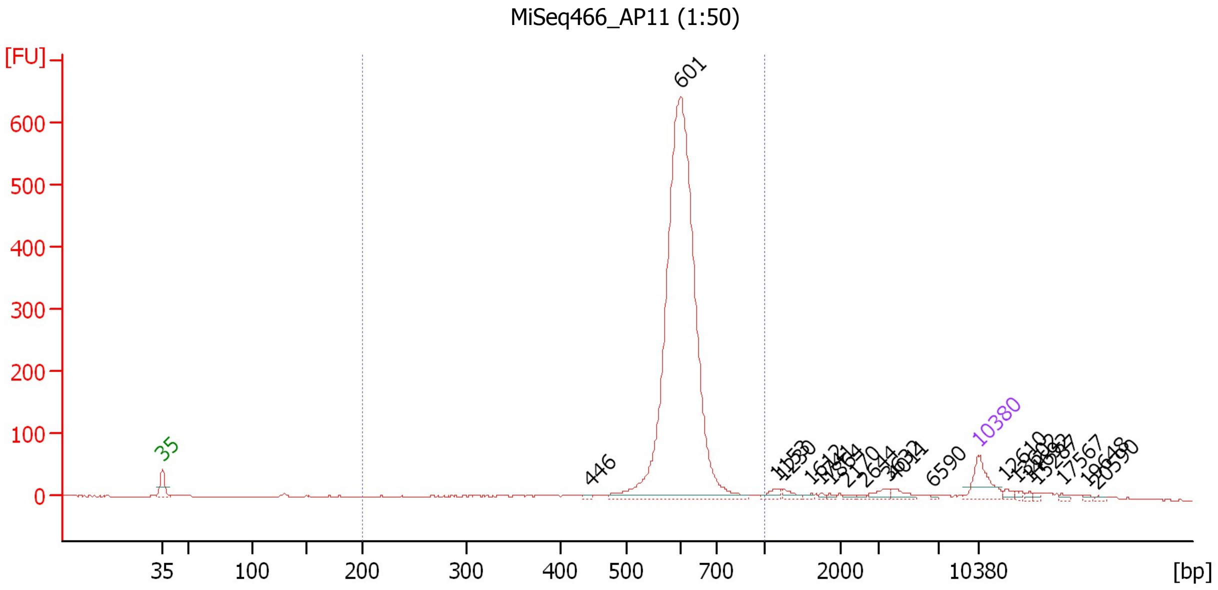
Peak table for sample 5 : MiSeq466_AP10 (1:50)

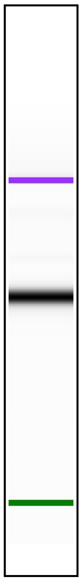
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		43	69.06	2,417.3		44.27
3		390	49.88	193.8		76.29
4		485	11,658.71	36,396.4		81.98
5		670	124.42	281.6		89.64
6		680	107.68	239.8		89.99
7		1,513	15.62	15.6		97.99
8		1,655	29.35	26.9		98.91
9		2,240	23.57	15.9		101.93
10		3,591	596.75	251.8		105.17
11		4,730	166.95	53.5		106.66
12		5,333	616.22	175.1		107.44
13	▶	10,380	75.00	10.9	Upper Marker	113.00
14		12,087	0.00	0.0		114.71

Region table for sample 5 : MiSeq466_AP10 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	490	3,079.9	38,366.3	🟦	12,271.47	85	11.0

Electropherogram Summary Continued ...





Overall Results for sample 6 : MiSeq466_AP11 (1:50)

Number of peaks found: 19
Corr. Area 1: 2,232.1
Noise: 0.7

Peak table for sample 6 : MiSeq466_AP11 (1:50)

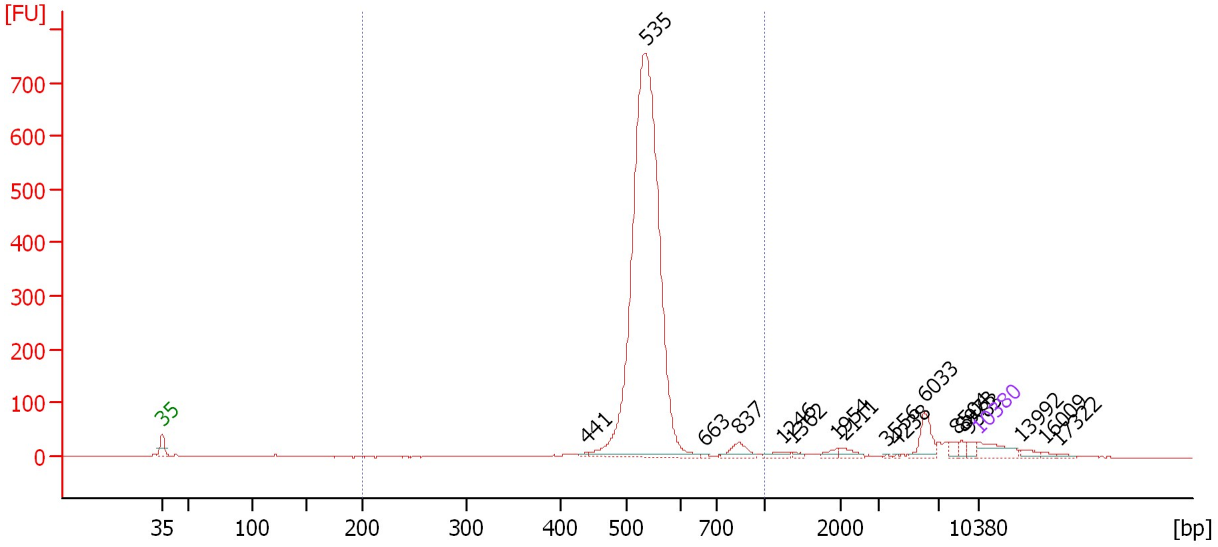
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		446	5.01	17.0		79.71
3		601	2,050.83	5,172.7		87.44
4		1,153	17.77	23.4		95.66
5		1,230	16.30	20.1		96.16
6		1,612	5.92	5.6		98.63
7		1,741	4.68	4.1		99.48
8		1,864	5.42	4.4		100.27
9		2,170	6.68	4.7		101.70
10		2,644	4.28	2.5		103.24
11		3,632	19.50	8.1		105.22
12		4,011	19.17	7.2		105.72
13		6,590	3.42	0.8		109.09
14	▶	10,380	75.00	10.9	Upper Marker	113.00
15		12,610	0.00	0.0		115.23
16		13,602	0.00	0.0		116.22
17		14,692	0.00	0.0		117.31
18		15,287	0.00	0.0		117.90
19		17,567	0.00	0.0		120.18
20		19,648	0.00	0.0		122.26
21		20,590	0.00	0.0		123.21

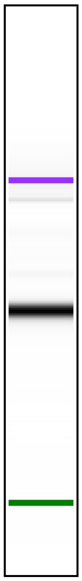
Region table for sample 6 : MiSeq466_AP11 (1:50)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	600	2,232.1	5,645.7	🟦	2,181.21	89	10.5

Electropherogram Summary Continued ...

MiSeq466_AP12 (1:50)





Overall Results for sample 7 : **MiSeq466_AP12 (1:50)**

Number of peaks found:	17	Corr. Area 1:	2,627.3
Noise:	0.5		

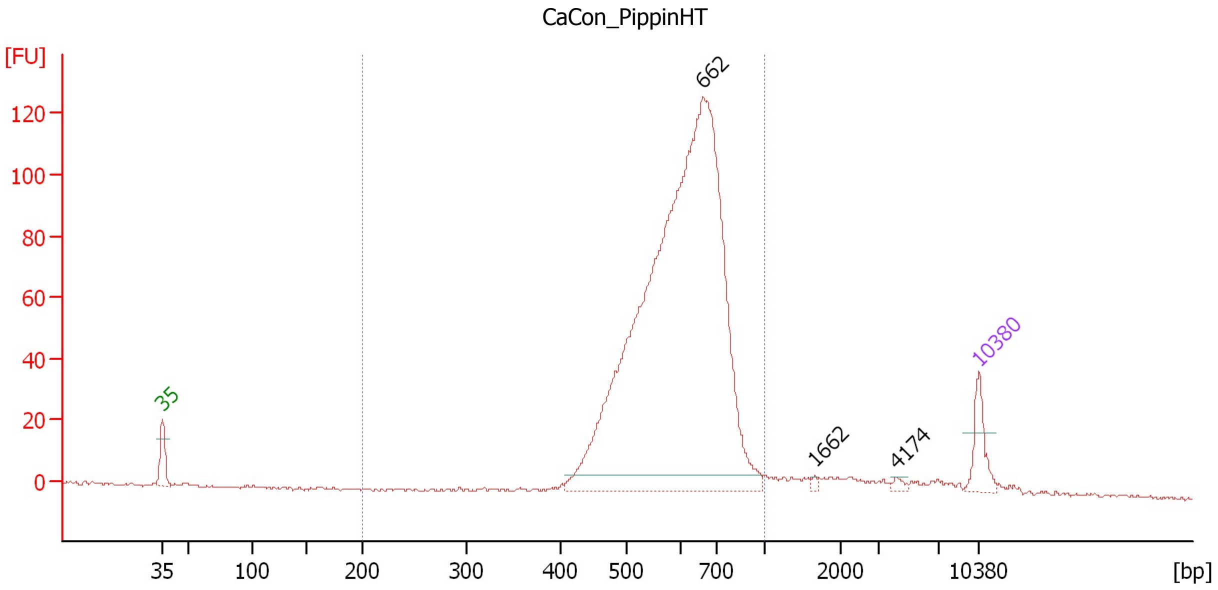
Peak table for sample 7 : **MiSeq466_AP12 (1:50)**

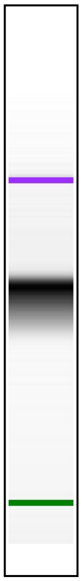
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		441	10.24	35.2		79.43
3		535	3,417.28	9,670.5		84.45
4		663	5.49	12.6		89.42
5		837	67.91	122.9		92.46
6		1,246	23.42	28.5		96.26
7		1,362	10.36	11.5		97.01
8		1,954	19.29	15.0		100.86
9		2,111	28.05	20.1		101.51
10		3,556	3.36	1.4		105.12
11		4,238	2.98	1.1		106.01
12		6,033	97.52	24.5		108.36
13		8,504	26.90	4.8		111.12
14		8,973	18.98	3.2		111.59
15		9,583	20.79	3.3		112.20
16	▶	10,380	75.00	10.9	Upper Marker	113.00
17		13,992	0.00	0.0		116.61
18		16,009	0.00	0.0		118.63
19		17,322	0.00	0.0		119.94

Region table for sample 7 : **MiSeq466_AP12 (1:50)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	542	2,627.3	10,003.4	■	3,544.20	88	10.5

Electropherogram Summary Continued ...





Overall Results for sample 8 : CaCon_PippinHT

Number of peaks found:	3	Corr. Area 1:	1,112.0
Noise:	0.5		

Peak table for sample 8 : CaCon_PippinHT

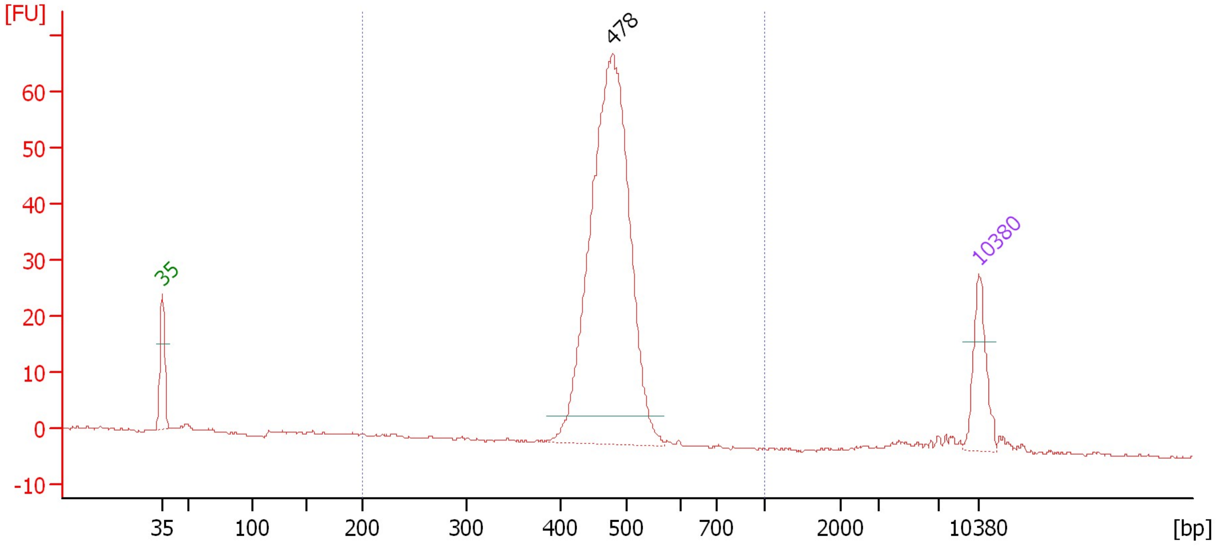
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		662	2,996.06	6,862.0		89.38
3		1,662	6.88	6.3		98.96
4		4,174	10.53	3.8		105.93
5	▶	10,380	75.00	10.9	Upper Marker	113.00

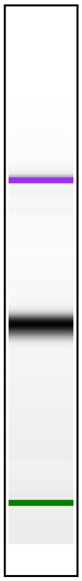
Region table for sample 8 : CaCon_PippinHT

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	613	1,112.0	7,964.4	🟦	3,128.33	92	15.7

Electropherogram Summary Continued ...

Waa-11_PippinHT





Overall Results for sample 9 : **Waa-11 PippinHT**

Number of peaks found:	1	Corr. Area 1:	334.0
Noise:	0.2		

Peak table for sample 9 : **Waa-11 PippinHT**

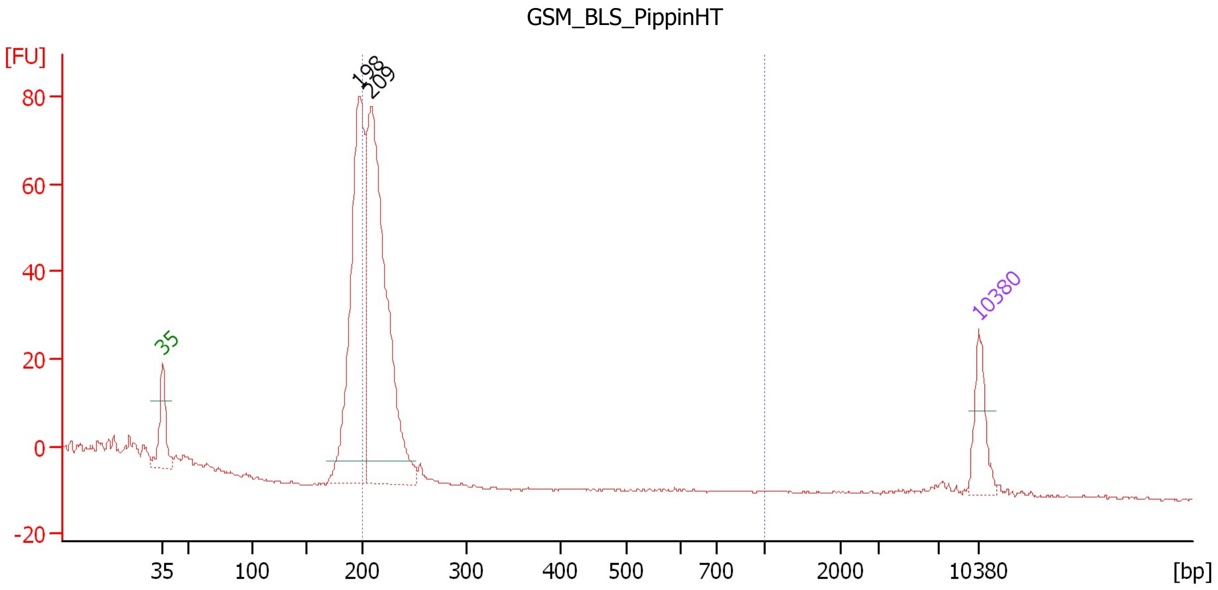
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		478	985.03	3,123.0		81.56
3	▶	10,380	75.00	10.9	Upper Marker	113.00

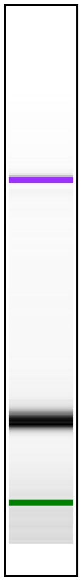
Region table for sample 9 : **Waa-11 PippinHT**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	474	334.0	3,136.5	🟦	977.49	95	6.2

Assay Class:	High Sensitivity DNA Assay	Created:	3/14/2017 4:43:42 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad	Modified:	3/14/2017 5:25:01 PM

Electropherogram Summary Continued ...





Overall Results for sample 10 : **GSM_BLS_PippinHT**

Number of peaks found:	2	Corr. Area 1:	281.2
Noise:	0.3		

Peak table for sample 10 : **GSM_BLS_PippinHT**

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		198	776.30	5,944.0		59.88
3		209	1,018.52	7,379.0		60.90
4	▶	10,380	75.00	10.9	Upper Marker	113.00

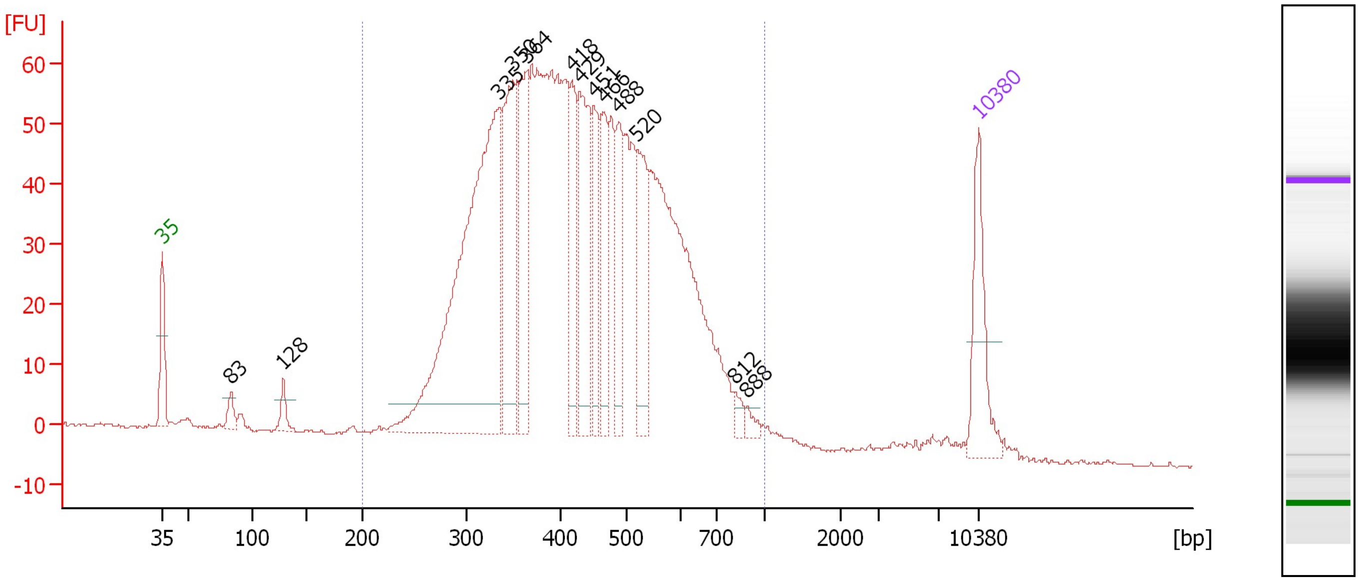
Region table for sample 10 : **GSM_BLS_PippinHT**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	213	281.2	7,303.4	■	1,028.36	69	4.4

Assay Class:	High Sensitivity DNA Assay	Created:	3/14/2017 4:43:42 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad	Modified:	3/14/2017 5:25:01 PM

Electropherogram Summary Continued ...

H889P_Mayo



Overall Results for sample 11 : **H889P_Mayo**

Number of peaks found:	13	Corr. Area 1:	1,478.5
Noise:	0.3		

Peak table for sample 11 : **H889P_Mayo**

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		83	20.49	376.0		48.88
3		128	23.19	275.2		53.36
4		335	614.30	2,780.6		71.87
5		350	199.57	863.6		73.10
6		364	152.18	632.9		74.24
7		418	97.28	353.0		78.10
8		429	156.87	553.7		78.77
9		451	88.29	296.7		80.01
10		466	86.10	279.8		80.89
11		488	87.84	272.8		82.12
12		520	104.02	303.3		83.72
13		812	12.13	22.6		92.12
14		888	8.65	14.8		93.15
15	▶	10,380	75.00	10.9	Upper Marker	113.00

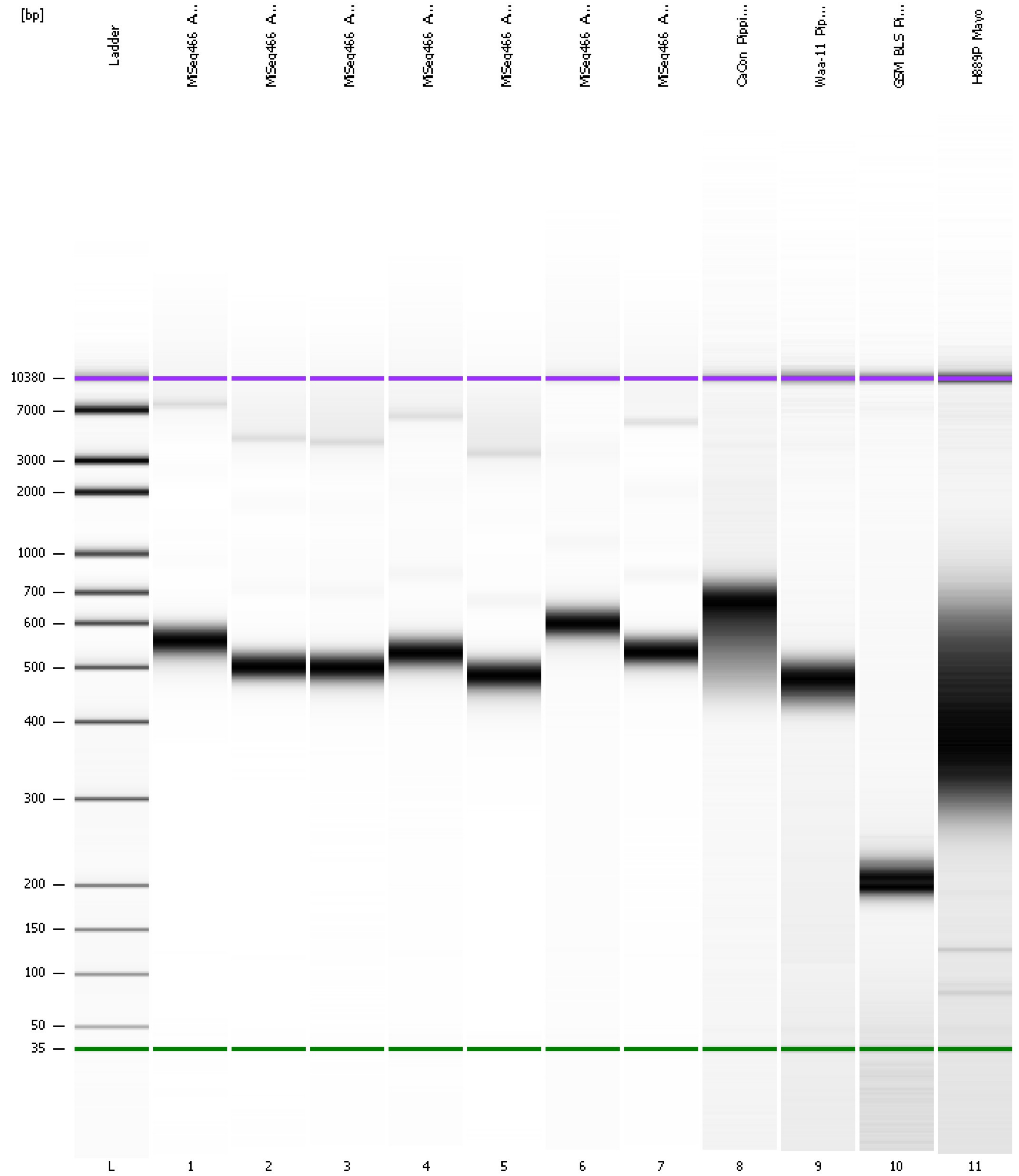
Region table for sample 11 : **H889P_Mayo**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	441	1,478.5	11,298.2	■	2,993.75	96	27.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad

Created: 3/14/2017 4:43:42 PM
Modified: 3/14/2017 5:25:01 PM

Gel Image



Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 12)		Instrument	Run		3/14/2017 5:25:00 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2017-03-14\2017-03-14_003.xad)		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		3/14/2017 4:43:47 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1