

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-05-23\2016-05-23_003.xad

Created: 5/23/2016 2:36:52 PM
Modified: 5/23/2016 5:12:46 PM

Electrophoresis File Run Summary

Instrument Information:

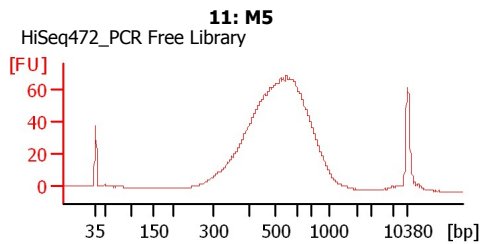
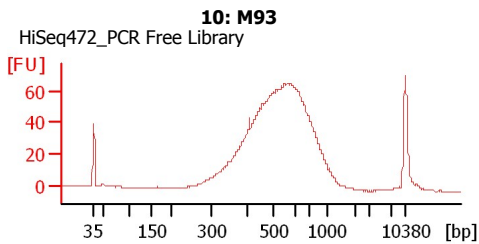
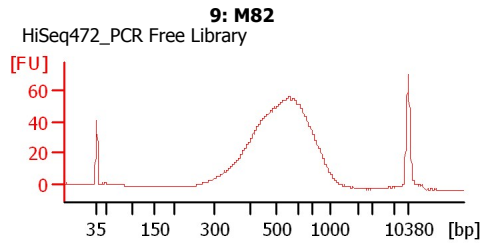
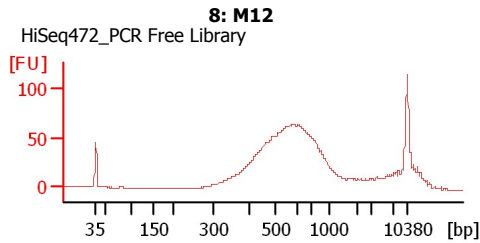
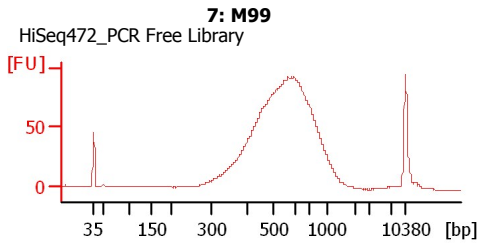
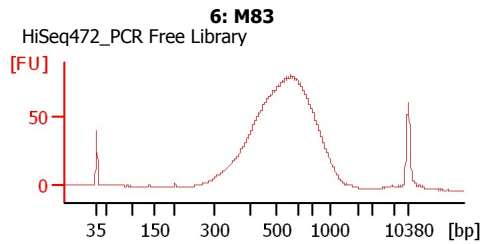
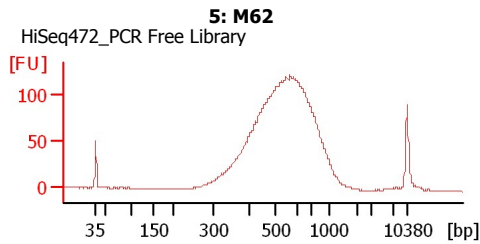
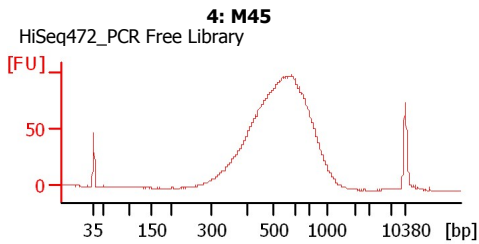
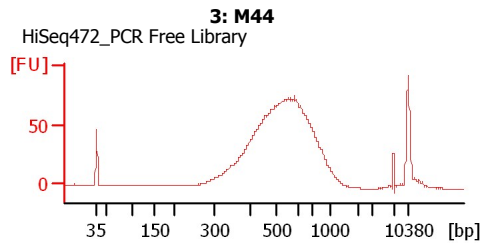
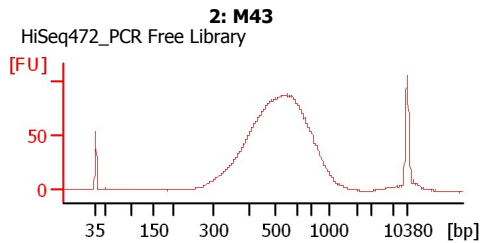
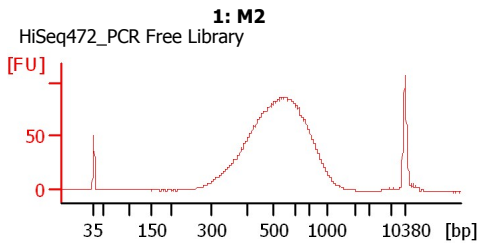
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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
1: M2	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
2: M43	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
3: M44	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
4: M45	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
5: M62	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
6: M83	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
7: M99	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
8: M12	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
9: M82	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
10: M93	HiSeq472_PCR Free Library	<input type="checkbox"/>	✓			
11: M5	HiSeq472_PCR Free Library	<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

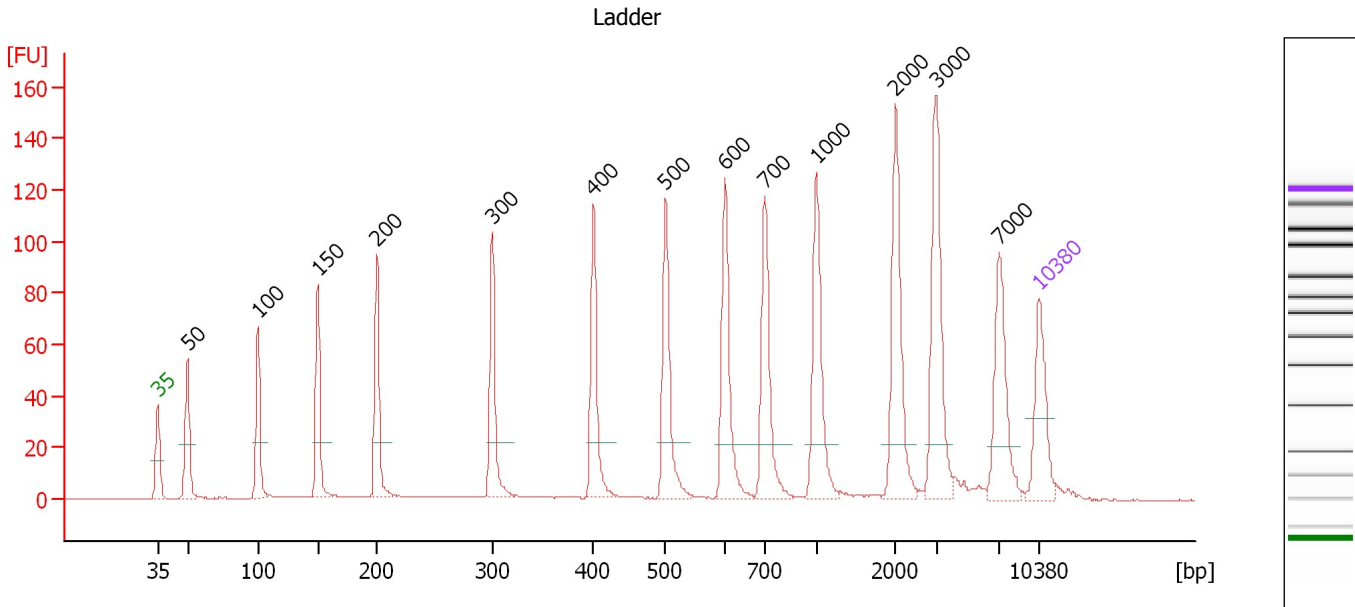
Ladder

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

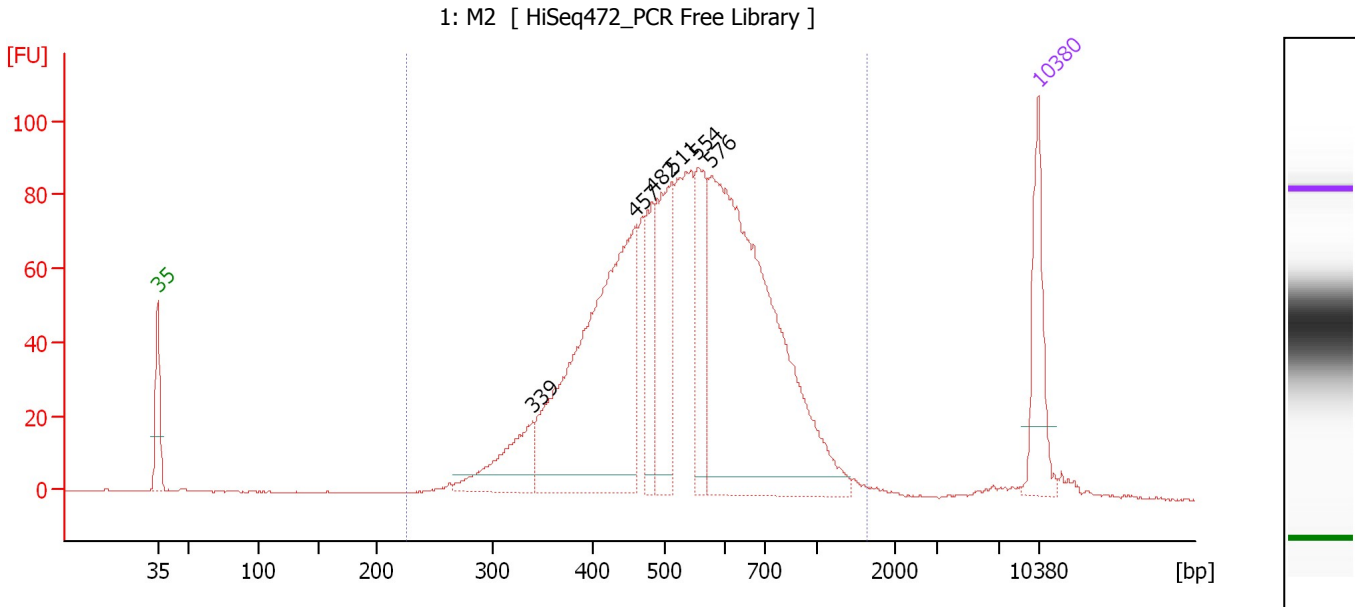
Peak table for Ladder

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	50	150.00	4,545.5	Ladder Peak	45.38
3	100	150.00	2,272.7	Ladder Peak	50.97
4	150	150.00	1,515.2	Ladder Peak	55.73
5	200	150.00	1,136.4	Ladder Peak	60.44
6	300	150.00	757.6	Ladder Peak	69.63
7	400	150.00	568.2	Ladder Peak	77.65
8	500	150.00	454.5	Ladder Peak	83.39
9	600	150.00	378.8	Ladder Peak	88.10
10	700	150.00	324.7	Ladder Peak	91.27
11	1,000	150.00	227.3	Ladder Peak	95.33
12	2,000	150.00	113.6	Ladder Peak	101.62
13	3,000	150.00	75.8	Ladder Peak	104.89
14	7,000	150.00	32.5	Ladder Peak	109.88
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : 1: M2

Number of peaks found: 6 Corr. Area 1: 1,753.4
 Noise: 0.2

Peak table for sample 1 : 1: M2

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	339	100.79	449.9		72.79
3	457	518.56	1,719.3		80.92
4	482	89.89	282.4		82.37
5	511	163.74	485.4		83.91
6	554	113.13	309.6		85.92
7	576	642.18	1,690.7		86.94
8	10,380	75.00	10.9	Upper Marker	113.00

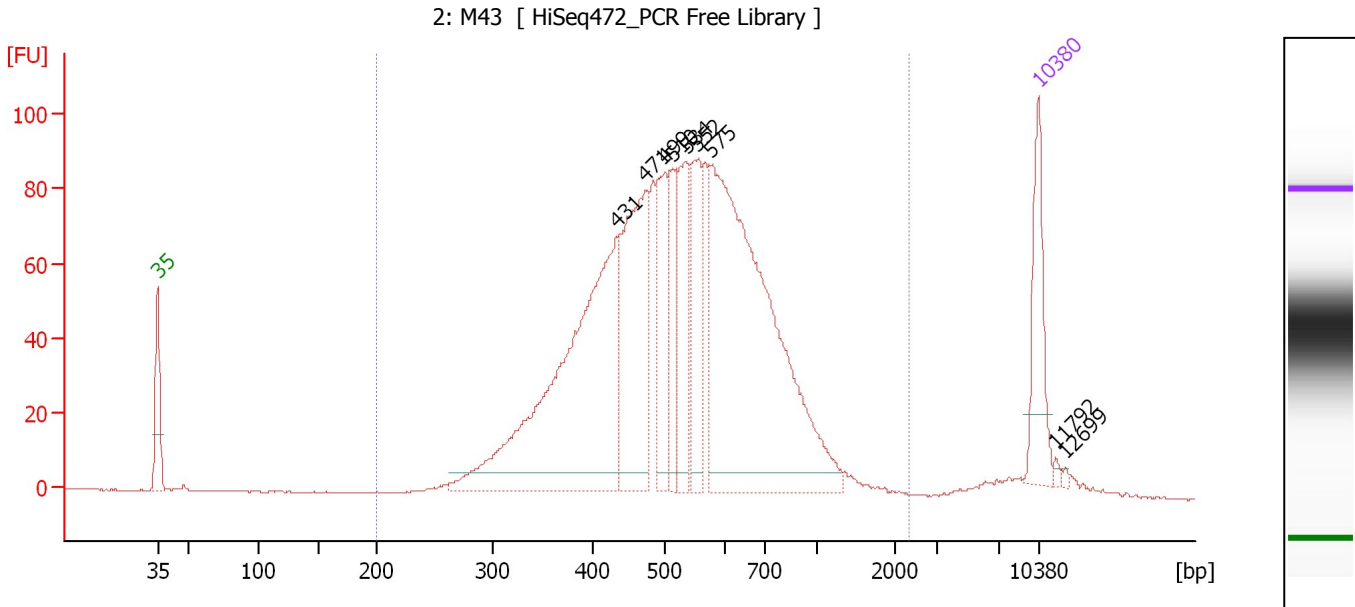
Region table for sample 1 : 1: M2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
226	1,651	554	1,753.4	5,814.7	1,902.20	98	31.7

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Electropherogram Summary Continued ...



Overall Results for sample 2 : 2: M43

Number of peaks found: 9 Corr. Area 1: 1,812.3
 Noise: 0.2

Peak table for sample 2 : 2: M43

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	431	545.25	1,915.5		79.44
3	471	261.56	841.2		81.73
4	499	107.23	325.8		83.31
5	510	84.85	251.9		83.87
6	534	110.88	314.6		84.99
7	552	109.09	299.5		85.83
8	575	622.49	1,641.3		86.90
9	10,380	75.00	10.9	Upper Marker	113.00
10	11,792	0.00	0.0		114.30
11	12,699	0.00	0.0		115.14

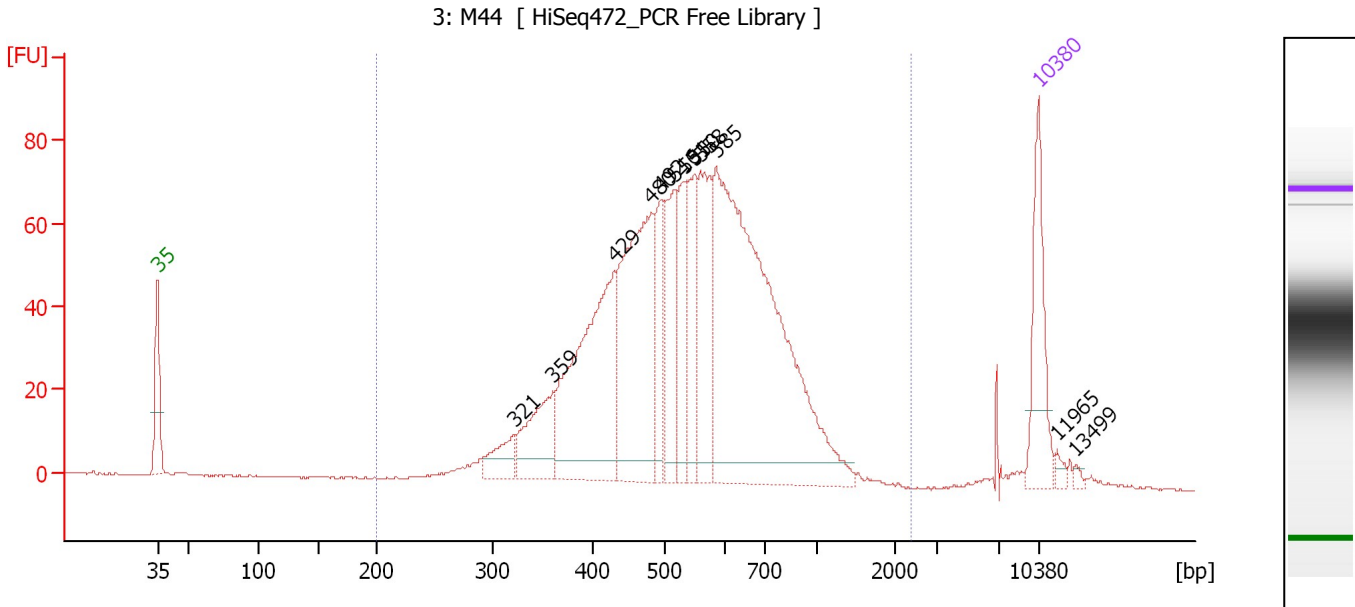
Region table for sample 2 : 2: M43

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,345	552	1,812.3	6,411.6	2,074.21	98	34.9

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 3 : 3: M44

Number of peaks found: 12 Corr. Area 1: 1,449.7
 Noise: 0.2

Peak table for sample 3 : 3: M44

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	321	39.16	184.8		71.31
3	359	91.66	386.6		74.38
4	429	281.31	994.1		79.30
5	480	274.43	866.5		82.23
6	492	73.48	226.2		82.94
7	516	93.74	275.5		84.12
8	531	80.15	228.8		84.83
9	550	84.52	232.9		85.73
10	558	123.65	335.9		86.11
11	585	583.24	1,511.0		87.38
12	10,380	75.00	10.9	Upper Marker	113.00
13	11,965	0.00	0.0		114.47
14	13,499	0.00	0.0		115.88

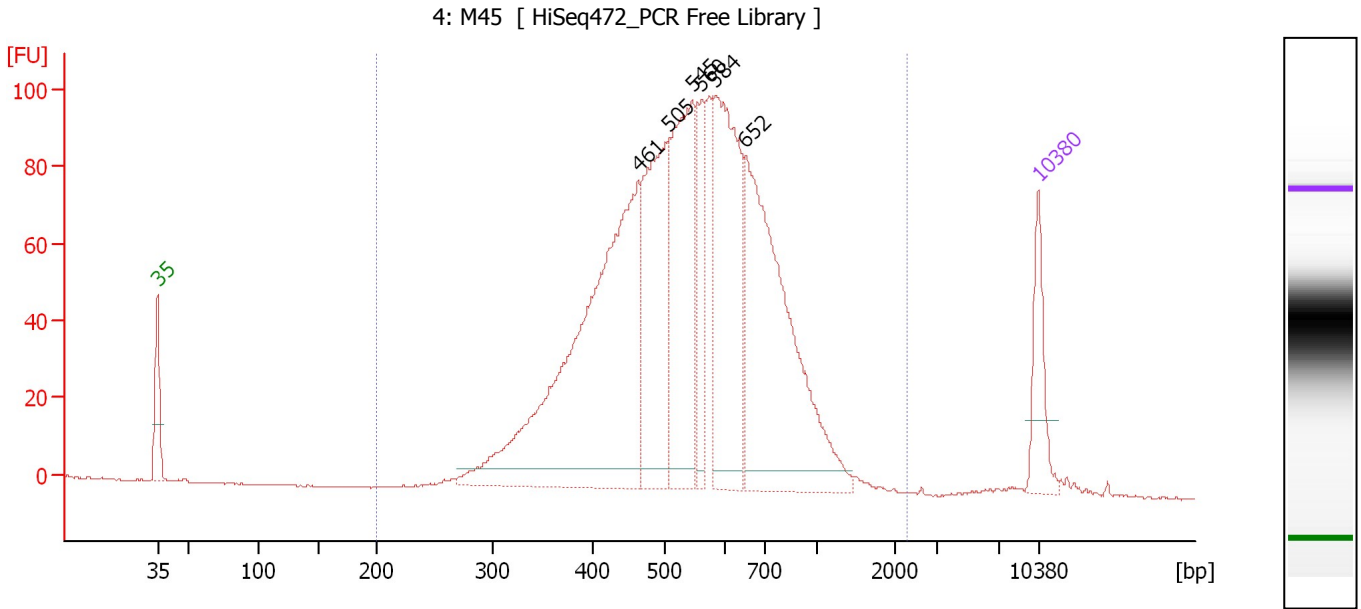
Region table for sample 3 : 3: M44

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,404	559	1,449.7	5,393.6	1,780.26	98	32.0

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Electropherogram Summary Continued ...



Overall Results for sample 4 : 4: M45

Number of peaks found: 6 Corr. Area 1: 1,890.8
 Noise: 0.2

Peak table for sample 4 : 4: M45

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	461	889.95	2,921.8		81.18
3	505	366.65	1,099.6		83.63
4	545	355.52	988.2		85.51
5	560	109.58	296.3		86.23
6	584	397.62	1,031.7		87.34
7	652	571.73	1,328.5		89.75
8	10,380	75.00	10.9	Upper Marker	113.00

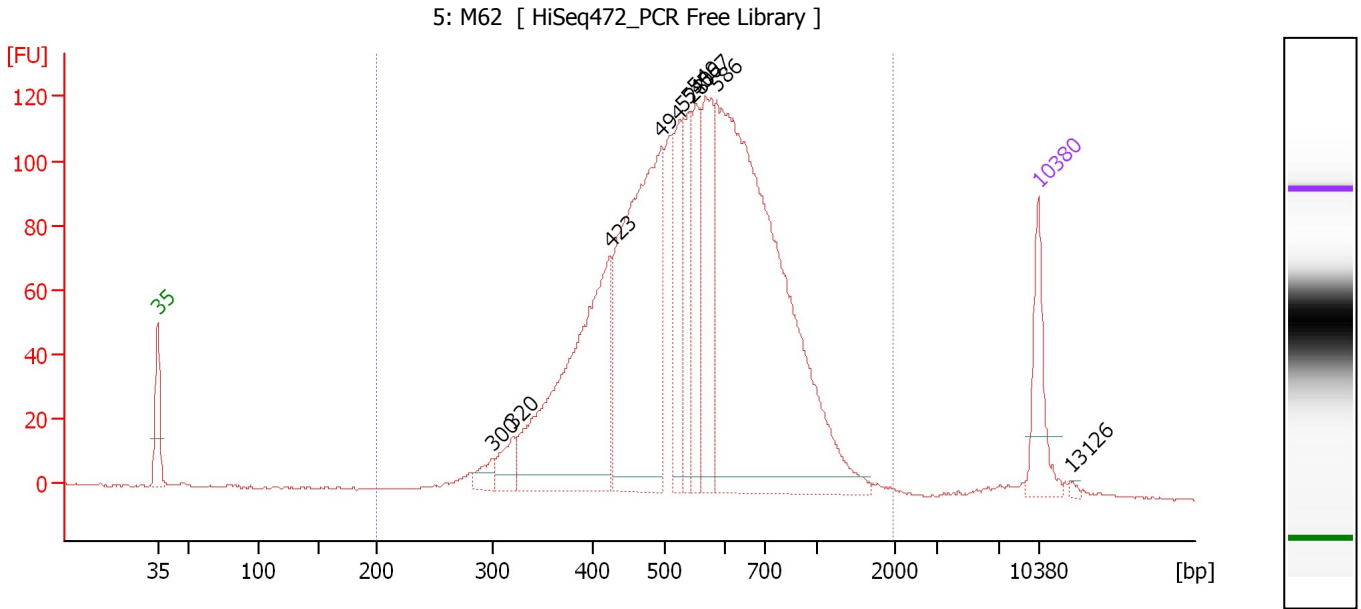
Region table for sample 4 : 4: M45

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,281	565	1,890.8	8,596.2	2,886.01	99	31.5

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 5 : 5: M62

Number of peaks found: 10 Corr. Area 1: 2,313.1
 Noise: 0.2

Peak table for sample 5 : 5: M62

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	300	28.26	142.9		69.60
3	320	46.28	219.3		71.21
4	423	518.93	1,858.3		78.98
5	494	611.64	1,876.9		83.03
6	528	154.65	444.1		84.69
7	540	112.64	316.0		85.27
8	549	139.59	385.0		85.71
9	567	172.82	461.8		86.54
10	586	1,038.38	2,686.4		87.42
11	10,380	75.00	10.9	Upper Marker	113.00
12	13,126	0.00	0.0		115.54

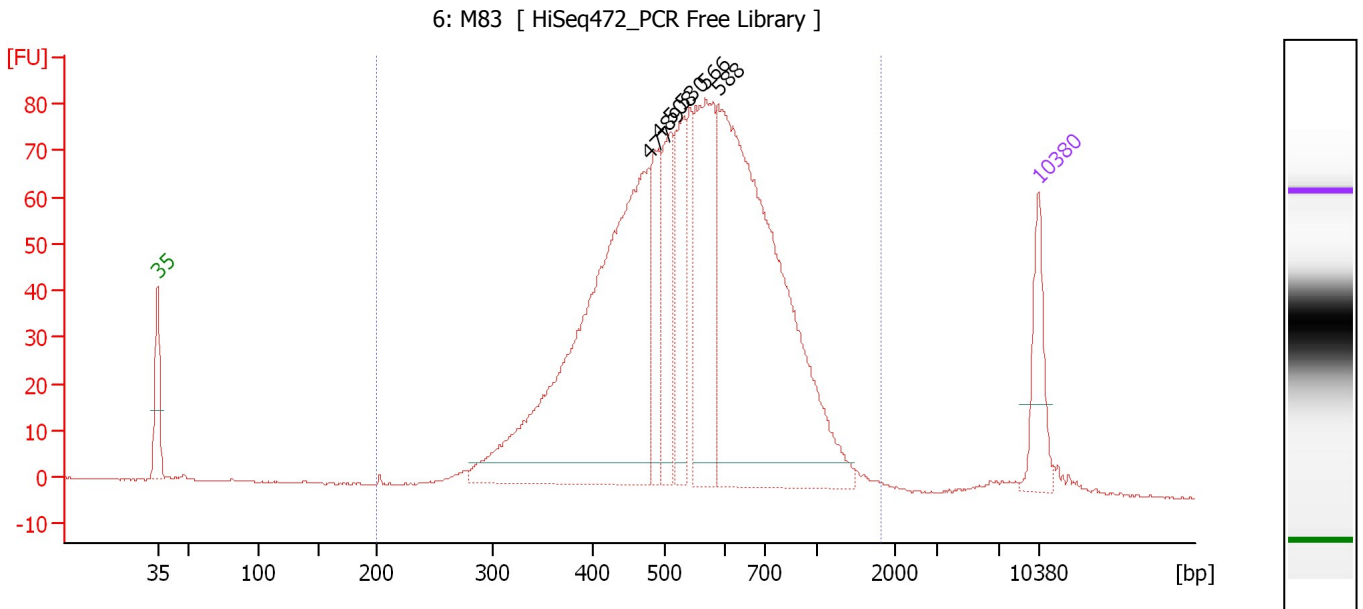
Region table for sample 5 : 5: M62

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,982	577	2,313.1	8,811.6	2,982.30	99	33.8

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 6 : 6: M83

Number of peaks found: 6 Corr. Area 1: 1,596.2
 Noise: 0.1

Peak table for sample 6 : 6: M83

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	477	918.58	2,917.5		82.07
3	489	134.43	416.4		82.76
4	508	138.40	413.1		83.75
5	530	147.55	422.1		84.78
6	566	293.82	786.1		86.51
7	588	866.92	2,232.7		87.55
8	10,380	75.00	10.9	Upper Marker	113.00

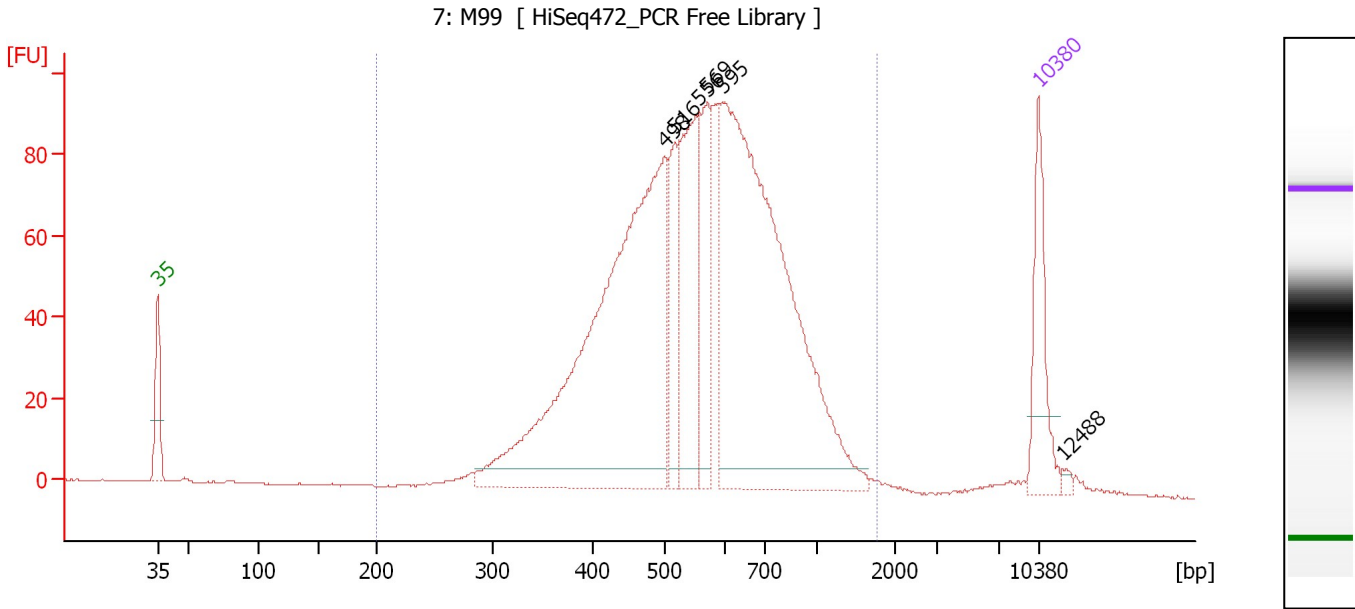
Region table for sample 6 : 6: M83

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,831	572	1,596.2	8,108.9	2,720.56	99	33.5

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Electropherogram Summary Continued ...



Overall Results for sample 7 : 7: M99

Number of peaks found: 6 Corr. Area 1: 1,760.3
 Noise: 0.2

Peak table for sample 7 : 7: M99

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	783.25	2,383.1		83.27
3	516	95.24	279.9		84.12
4	556	202.59	552.2		86.02
5	569	111.01	295.8		86.62
6	595	726.07	1,848.5		87.87
7	10,380	75.00	10.9	Upper Marker	113.00
8	12,488	0.00	0.0		114.95

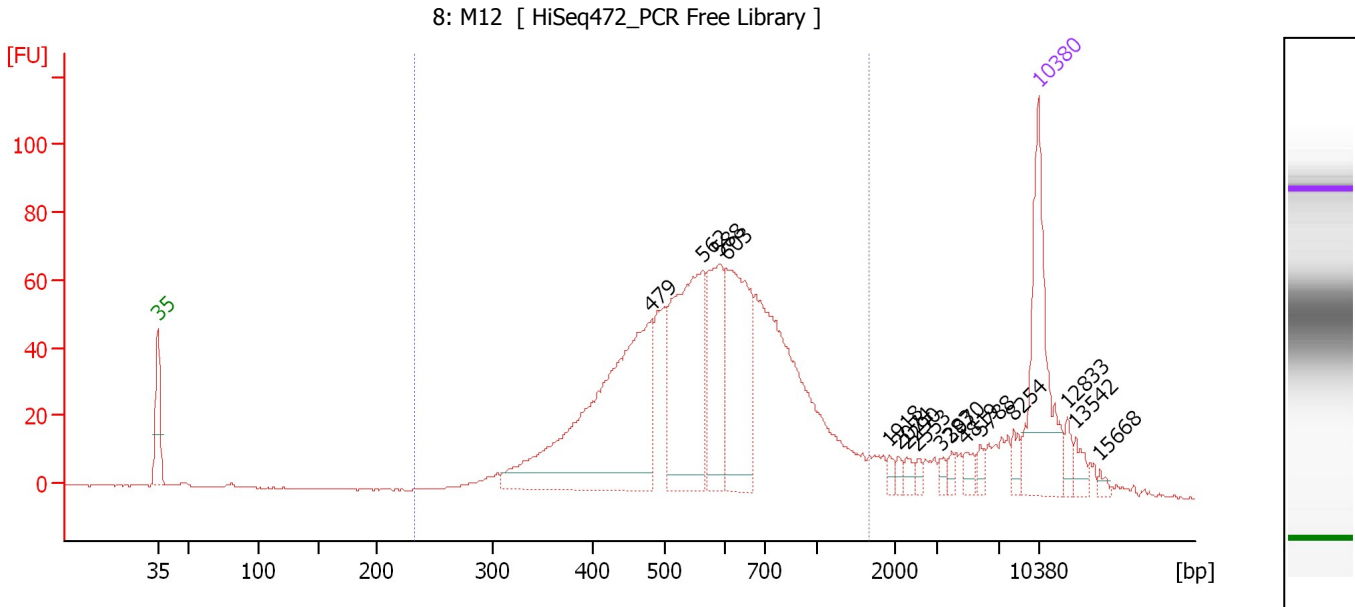
Region table for sample 7 : 7: M99

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,769	588	1,760.3	5,960.2	2,055.09	98	33.4

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Electropherogram Summary Continued ...



Overall Results for sample 8 : 8: M12

Number of peaks found: 16 Corr. Area 1: 1,249.9
 Noise: 0.2

Peak table for sample 8 : 8: M12

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	479	261.47	826.3		82.21
3	562	146.05	394.0		86.29
4	588	76.81	197.8		87.55
5	603	109.27	274.4		88.21
6	1,918	3.87	3.1		101.11
7	2,074	3.69	2.7		101.86
8	2,290	4.70	3.1		102.57
9	2,553	3.55	2.1		103.42
10	3,283	4.03	1.9		105.24
11	3,970	4.14	1.6		106.10
12	4,819	6.83	2.1		107.15
13	5,788	4.75	1.2		108.36
14	8,254	7.62	1.4		111.03
15	10,380	75.00	10.9	Upper Marker	113.00
16	12,833	0.00	0.0		115.27
17	13,542	0.00	0.0		115.92
18	15,668	0.00	0.0		117.89

Region table for sample 8 : 8: M12

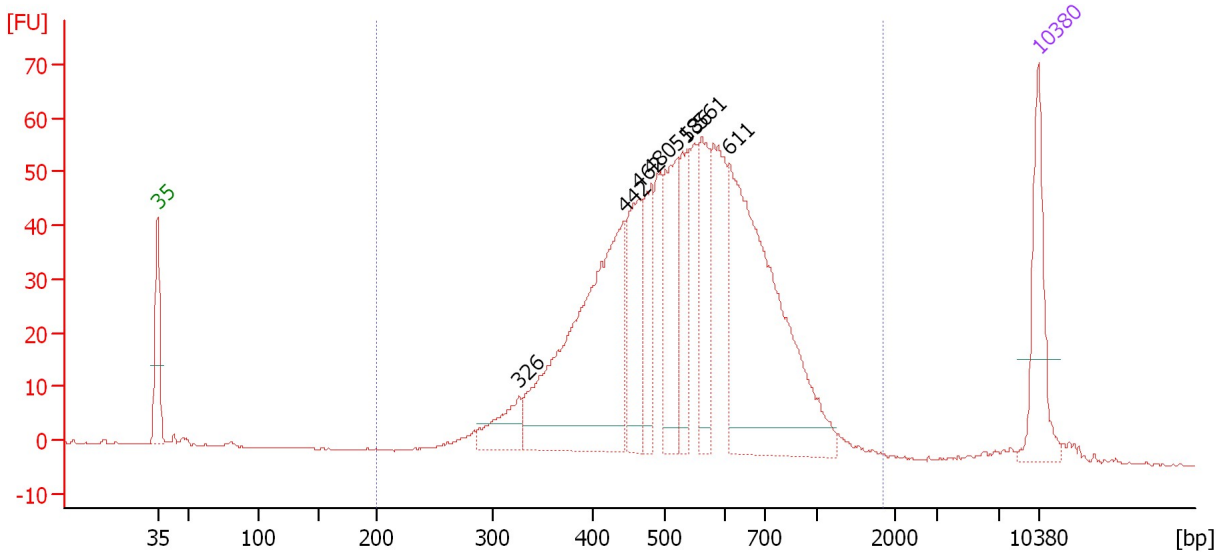
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
232	1,661	615	1,249.9	2,562.9	907.85	87	37.0

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Electropherogram Summary Continued ...

9: M82 [HiSeq472_PCR Free Library]



Overall Results for sample 9 : 9: M82

Number of peaks found: 8 Corr. Area 1: 1,087.1
 Noise: 0.1

Peak table for sample 9 : 9: M82

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	326	54.36	252.5		71.73
3	442	393.91	1,350.5		80.06
4	462	115.95	380.0		81.22
5	480	65.12	205.5		82.24
6	518	122.83	359.5		84.22
7	536	85.06	240.4		85.08
8	561	94.93	256.5		86.25
9	611	387.15	960.7		88.43
10	10,380	75.00	10.9	Upper Marker	113.00

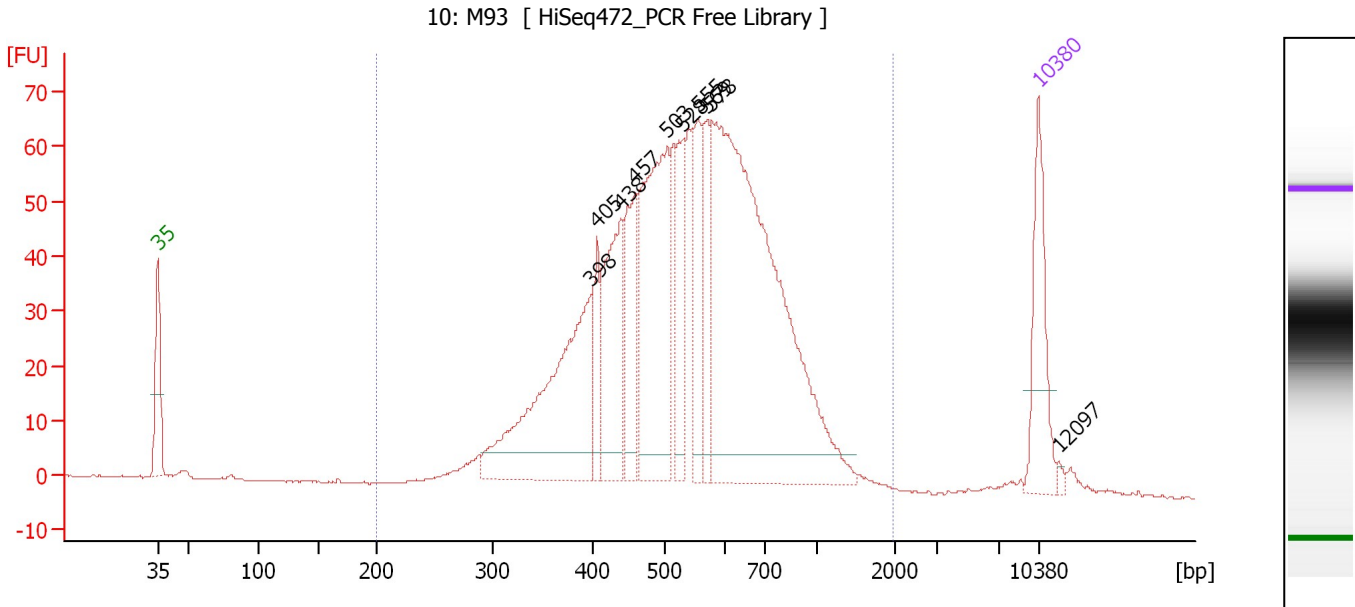
Region table for sample 9 : 9: M82

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,833	554	1,087.1	5,029.4	1,653.23	99	31.1

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Overall Results for sample 10 : 10: M93

Number of peaks found: 10 Corr. Area 1: 1,297.7
 Noise: 0.2

Peak table for sample 10 : 10: M93

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	398	289.59	1,103.4		77.46
3	405	55.10	206.3		77.92
4	438	146.20	506.0		79.82
5	457	104.11	344.8		80.94
6	503	269.27	811.9		83.50
7	528	73.20	210.2		84.68
8	555	85.56	233.7		85.96
9	569	72.98	194.4		86.63
10	578	647.90	1,699.8		87.04
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,097	0.00	0.0		114.59

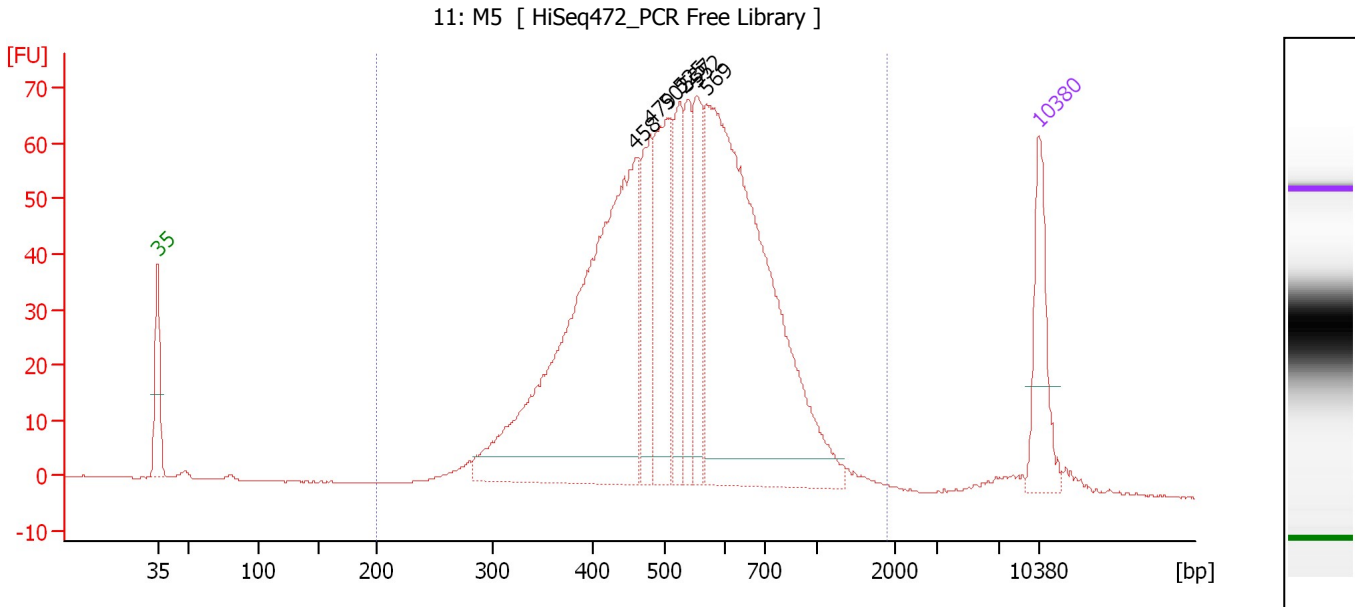
Region table for sample 10 : 10: M93

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,964	563	1,297.7	5,970.6	1,967.74	98	33.6

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-05-23\2016-05-23_003.xad

Created: 5/23/2016 2:36:52 PM
 Modified: 5/23/2016 5:12:46 PM

Electropherogram Summary Continued ...



Overall Results for sample 11 : 11: M5

Number of peaks found: 7 Corr. Area 1: 1,329.9
 Noise: 0.2

Peak table for sample 11 : 11: M5

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	458	710.64	2,351.2		80.97
3	479	122.73	388.5		82.16
4	502	172.95	522.5		83.46
5	525	109.79	317.1		84.54
6	537	83.86	236.8		85.11
7	552	108.03	296.5		85.84
8	569	694.43	1,850.7		86.61
9	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : 11: M5

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,893	546	1,329.9	6,537.7	2,113.55	98	32.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-05-23\2016-05-23_003.xad

Created: 5/23/2016 2:36:52 PM
Modified: 5/23/2016 5:12:46 PM

Gel Image

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-05-23\2016-05-23_003.xad

Created: 5/23/2016 2:36:52 PM
 Modified: 5/23/2016 5:12:46 PM

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		5/23/2016 3:18:08 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\2016-05-23\2016-05-23_003.xad)		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		5/23/2016 2:36:57 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1