

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-29\2018-06-29_001.xad

Created: 6/29/2018 2:01:01 PM
Modified: 6/29/2018 2:43:24 PM

Electrophoresis File Run Summary

Instrument Information:

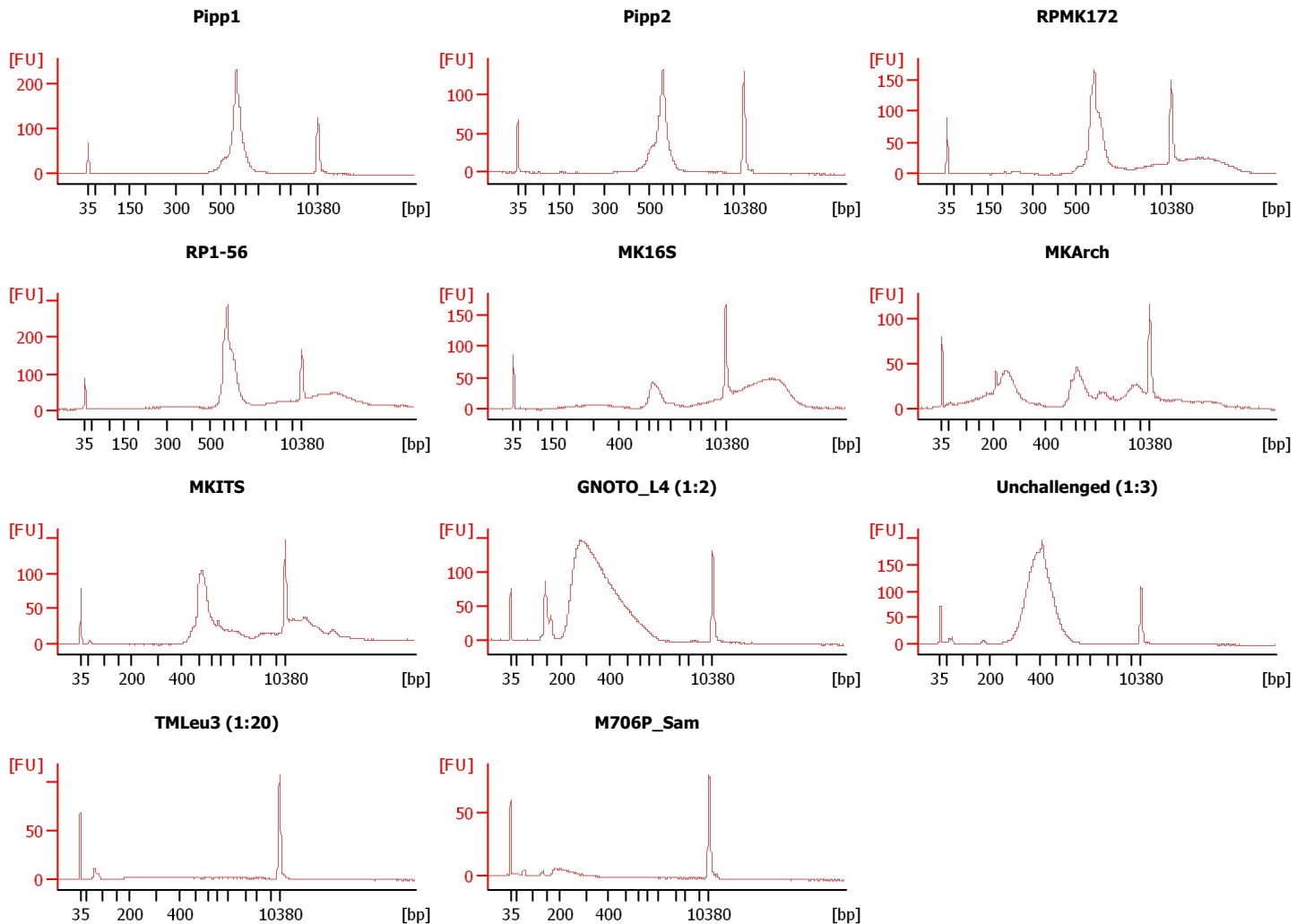
Instrument Name: DE34903152 Firmware: C.01.069
Serial#: DE34903152 Type: G2938C

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
Pipp1		<input type="checkbox"/>	✓			
Pipp2		<input type="checkbox"/>	✓			
RPMK172		<input type="checkbox"/>	✓			
RP1-56		<input type="checkbox"/>	✓			
MK16S		<input type="checkbox"/>	✓			
MKArch		<input type="checkbox"/>	✓			
MKITS		<input type="checkbox"/>	✓			
GNOTO_L4 (1:2)		<input type="checkbox"/>	✓			
Unchallenged (1:3)		<input type="checkbox"/>	✓			
TMLeu3 (1:20)		<input type="checkbox"/>	✓			
M706P_Sam		<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

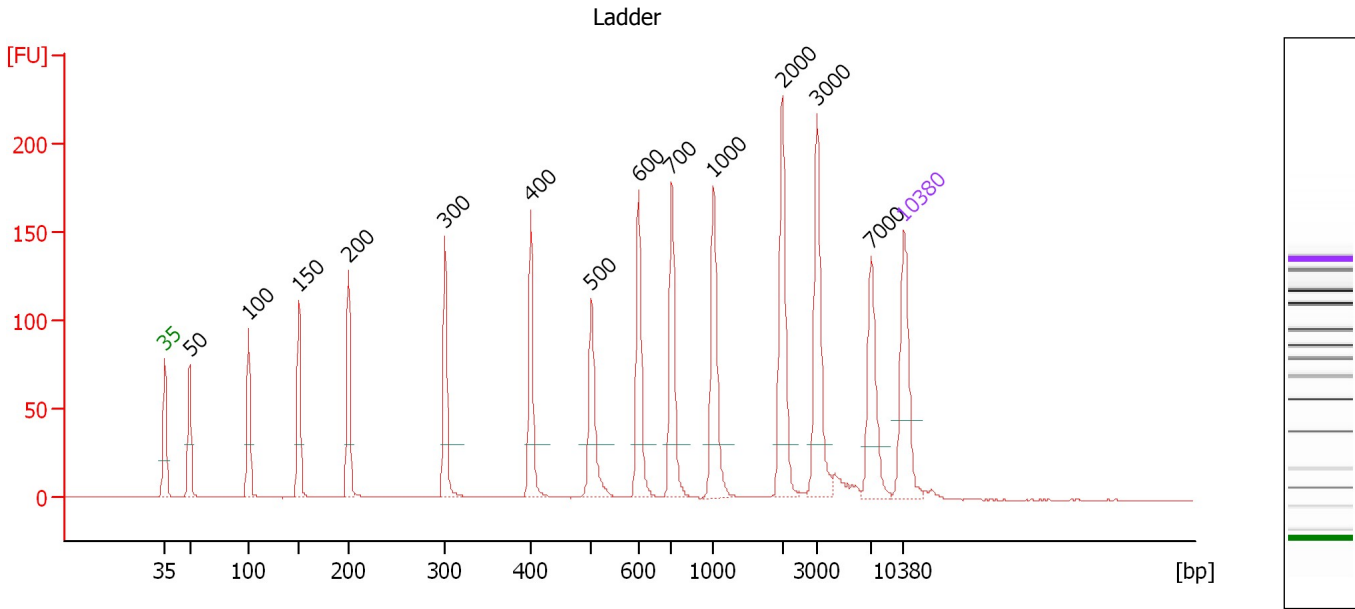
Ladder

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

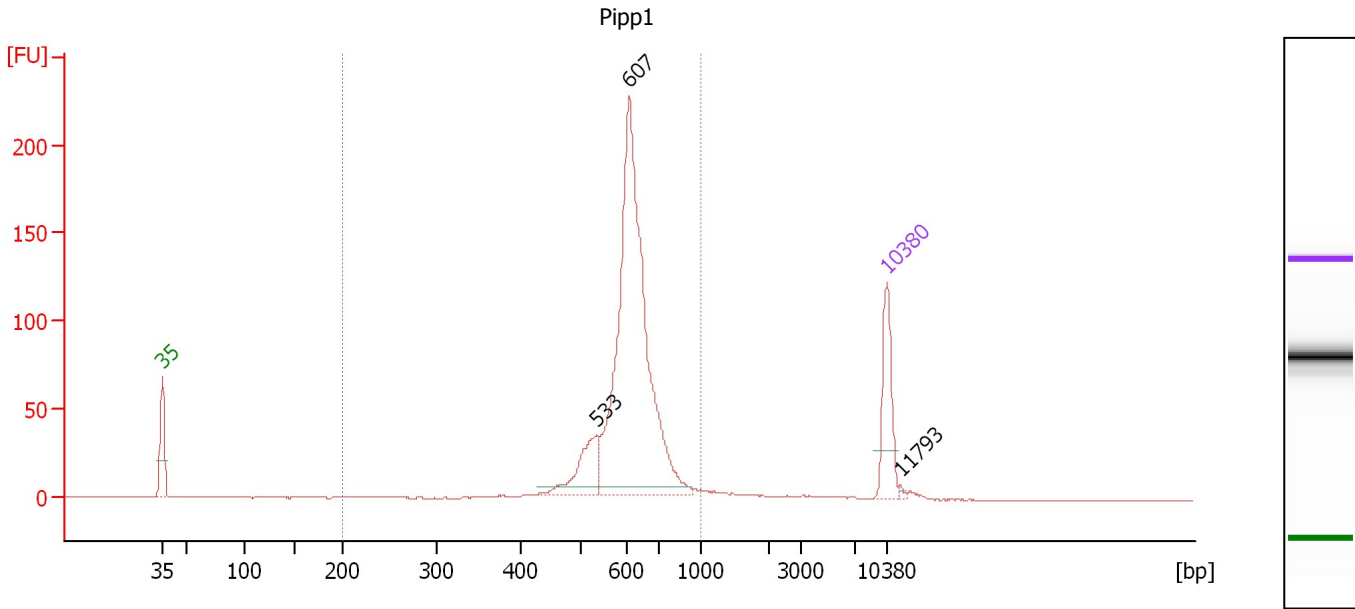
Peak table for Ladder

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	45.37
3	100	150.00	2,272.7	Ladder Peak	50.98
4	150	150.00	1,515.2	Ladder Peak	55.73
5	200	150.00	1,136.4	Ladder Peak	60.42
6	300	150.00	757.6	Ladder Peak	69.57
7	400	150.00	568.2	Ladder Peak	77.70
8	500	150.00	454.5	Ladder Peak	83.45
9	600	150.00	378.8	Ladder Peak	87.90
10	700	150.00	324.7	Ladder Peak	91.03
11	1,000	150.00	227.3	Ladder Peak	95.02
12	2,000	150.00	113.6	Ladder Peak	101.48
13	3,000	150.00	75.8	Ladder Peak	104.77
14	7,000	150.00	32.5	Ladder Peak	109.92
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : Pipp1

Number of peaks found: 3 Corr. Area 1: 895.8
 Noise: 0.2

Peak table for sample 1 : Pipp1

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	533	88.63	251.9		84.93
3	607	652.22	1,627.8		88.12
4	10,380	75.00	10.9	Upper Marker	113.00
5	11,793	0.00	0.0		114.29

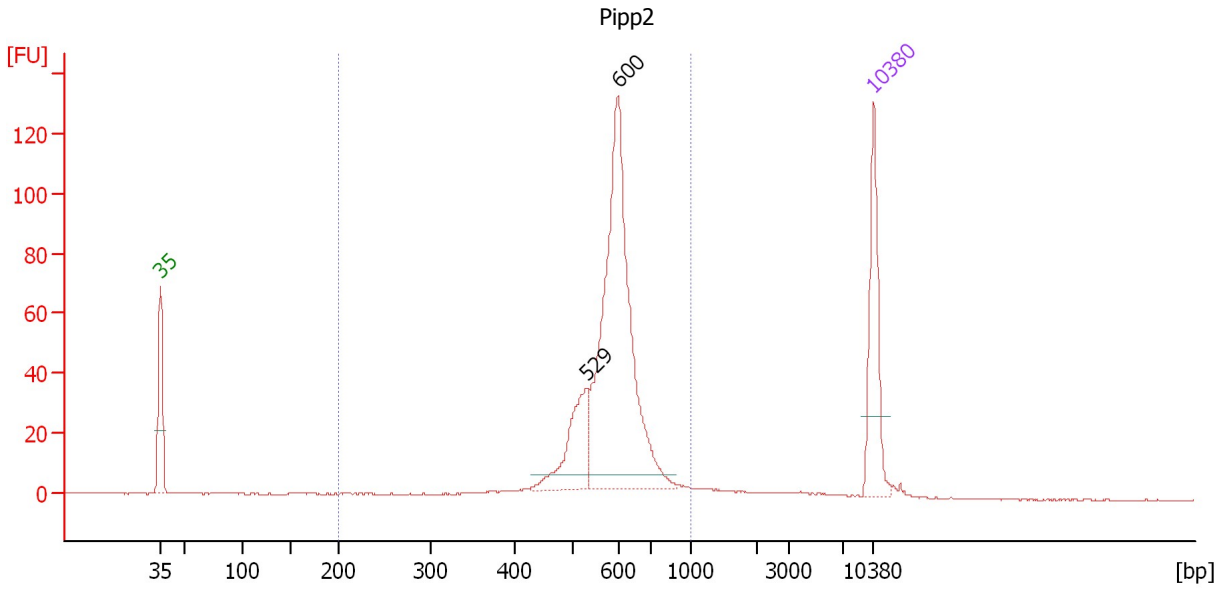
Region table for sample 1 : Pipp1

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	613	795.54	895.8	2,006.2	95	12.7

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Electropherogram Summary Continued ...



Overall Results for sample 2 : Pipp2

Number of peaks found: 2 Corr. Area 1: 595.9
 Noise: 0.2

Peak table for sample 2 : Pipp2

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	529	85.97	246.2		84.75
3	600	373.31	943.1		87.89
4	10,380	75.00	10.9	Upper Marker	113.00

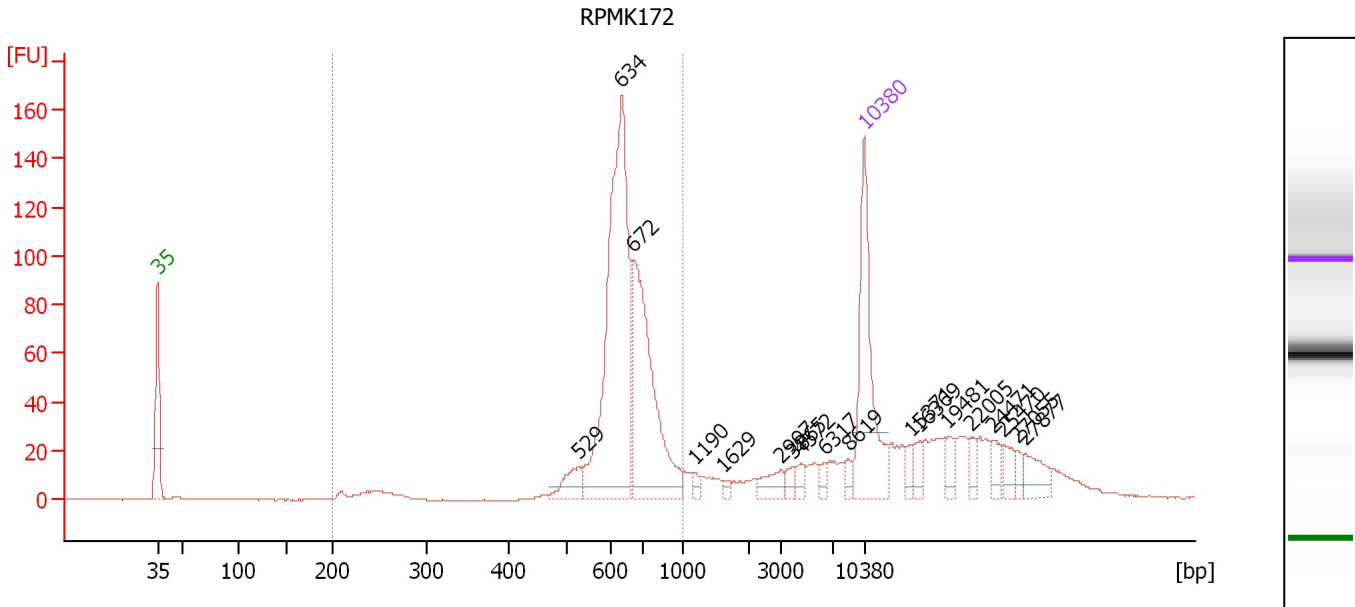
Region table for sample 2 : Pipp2

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	588	527.60	595.9	1,404.6	93	14.3

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Electropherogram Summary Continued ...



Overall Results for sample 3 : RPMK172

Number of peaks found: 18 Corr. Area 1: 747.5
 Noise: 0.2

Peak table for sample 3 : RPMK172

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	529	18.72	53.6		84.74
3	634	239.67	572.6		88.97
4	672	146.69	330.8		90.15
5	1,190	4.31	5.5		96.25
6	1,629	2.57	2.4		99.09
7	2,997	11.14	5.6		104.76
8	3,865	5.36	2.1		105.88
9	4,572	5.85	1.9		106.79
10	6,317	5.17	1.2		109.04
11	8,619	4.94	0.9		111.39
12	10,380	75.00	10.9	Upper Marker	113.00
13	15,371	0.00	0.0		117.55
14	16,369	0.00	0.0		118.46
15	19,481	0.00	0.0		121.30
16	22,005	0.00	0.0		123.60
17	24,471	0.00	0.0		125.84
18	25,470	0.00	0.0		126.75
19	27,055	0.00	0.0		128.20
20	27,877	0.00	0.0		128.95

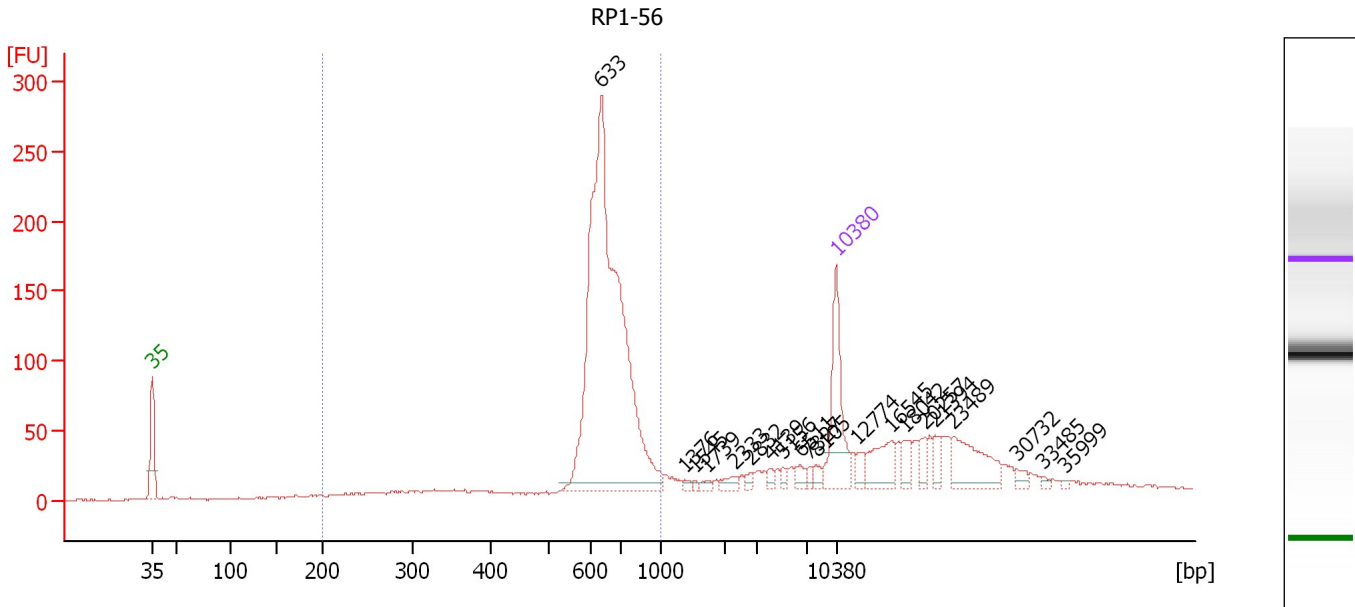
Region table for sample 3 : RPMK172

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	650	422.39	747.5	1,052.6	60	16.5

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Electropherogram Summary Continued ...



Overall Results for sample 4 : RP1-56

Number of peaks found: 20 Corr. Area 1: 1,214.1
 Noise: 0.8

Peak table for sample 4 : RP1-56

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	633	659.64	1,578.4		88.94
3	1,376	3.13	3.4		97.45
4	1,545	2.18	2.1		98.54
5	1,739	4.05	3.5		99.80
6	2,333	7.85	5.1		102.58
7	2,832	4.90	2.6		104.22
8	4,139	5.30	1.9		106.23
9	5,156	4.99	1.5		107.54
10	6,511	8.33	1.9		109.29
11	7,327	5.04	1.0		110.22
12	8,105	6.74	1.3		110.93
13	10,380	75.00	10.9	Upper Marker	113.00
14	12,774	0.00	0.0		115.18
15	16,545	0.00	0.0		118.62
16	18,042	0.00	0.0		119.98
17	20,257	0.00	0.0		122.00
18	21,394	0.00	0.0		123.04
19	23,489	0.00	0.0		124.95
20	30,732	0.00	0.0		131.55
21	33,485	0.00	0.0		134.06
22	35,999	0.00	0.0		136.35

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Electropherogram Summary Continued ...

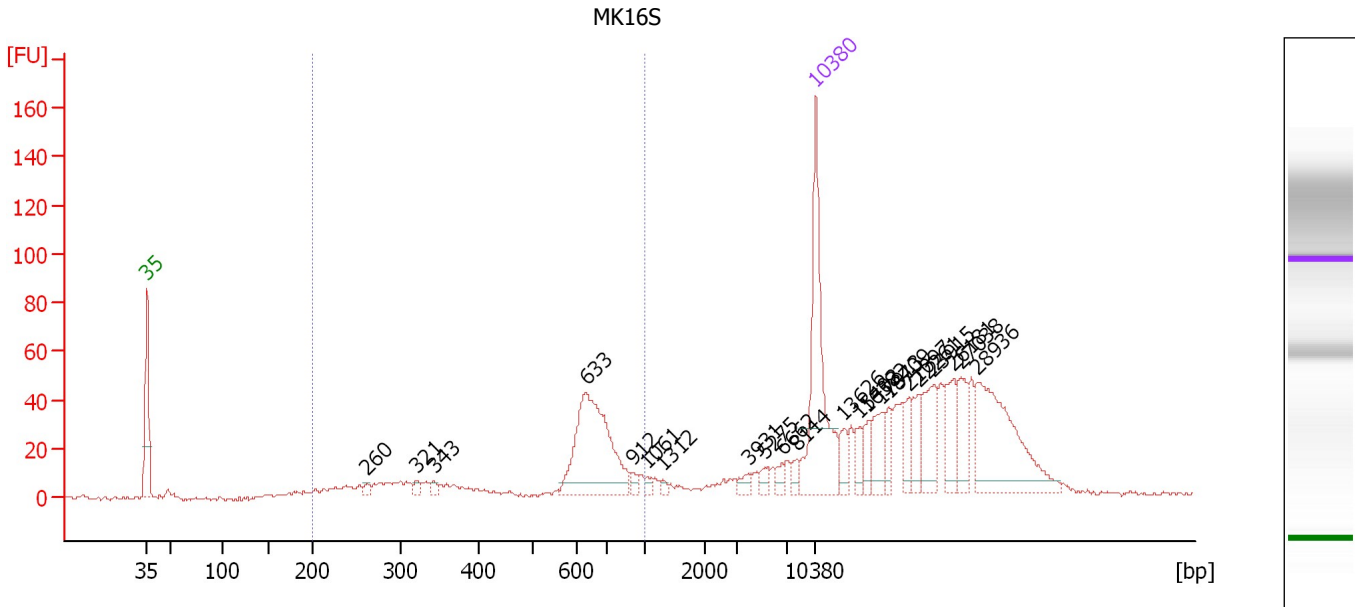
... Region table for sample 4 : RP1-56

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ μ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	646	746.86	1,214.1	1,901.8	 62	18.1

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Electropherogram Summary Continued ...



Overall Results for sample 5 : MK16S

Number of peaks found: 22 Corr. Area 1: 334.6
 Noise: 0.8

Peak table for sample 5 : MK16S


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	260	3.62	21.0		65.94
3	321	3.62	17.1		71.25
4	343	3.17	14.0		73.09
5	633	103.42	247.4		88.94
6	912	3.84	6.4		93.85
7	1,061	2.57	3.7		95.42
8	1,312	2.10	2.4		97.04
9	3,931	4.36	1.7		105.97
10	5,275	4.71	1.4		107.70
11	6,662	4.48	1.0		109.48
12	8,114	4.73	0.9		110.93
13	10,380	75.00	10.9	Upper Marker	113.00
14	13,626	0.00	0.0		115.96
15	15,402	0.00	0.0		117.58
16	16,382	0.00	0.0		118.47
17	17,913	0.00	0.0		119.87
18	18,709	0.00	0.0		120.59
19	21,097	0.00	0.0		122.77
20	22,261	0.00	0.0		123.83
21	23,915	0.00	0.0		125.34
22	26,181	0.00	0.0		127.40
23	27,038	0.00	0.0		128.18
24	28,936	0.00	0.0		129.91

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Electropherogram Summary Continued ...

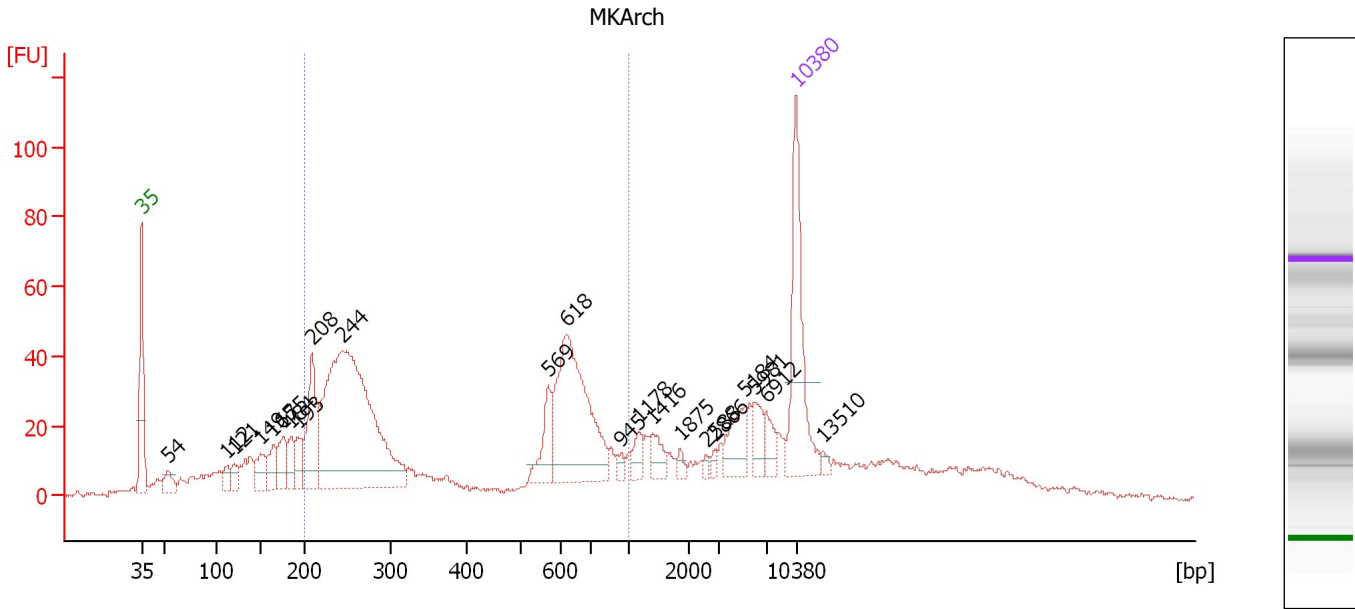
... Region table for sample 5 : MK16S

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ μ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	572	193.21	334.6	662.5	 31	34.2

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



Overall Results for sample 6 : MKArch

Number of peaks found: 22 Corr. Area 1: 785.1
 Noise: 0.7

Peak table for sample 6 : MKArch

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	54	19.45	548.1		45.80
3	112	13.56	183.3		52.13
4	121	12.57	158.1		52.93
5	149	26.09	264.7		55.67
6	165	23.71	218.3		57.09
7	175	31.06	268.3		58.12
8	184	20.43	168.2		58.92
9	193	24.72	194.0		59.77
10	208	74.95	544.7		61.20
11	244	376.01	2,334.4		64.45
12	569	31.17	83.0		86.53
13	618	146.56	359.2		88.47
14	945	5.49	8.8		94.29
15	1,178	11.23	14.4		96.17
16	1,416	13.87	14.8		97.71
17	1,875	4.49	3.6		100.68
18	2,588	2.75	1.6		103.42
19	2,866	3.45	1.8		104.33
20	5,184	26.49	7.7		107.58
21	5,981	15.65	4.0		108.61
22	6,912	12.65	2.8		109.81
23	10,380	75.00	10.9	Upper Marker	113.00
24	13,510	0.00	0.0		115.85

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Electropherogram Summary Continued ...

... Region table for sample 6 :

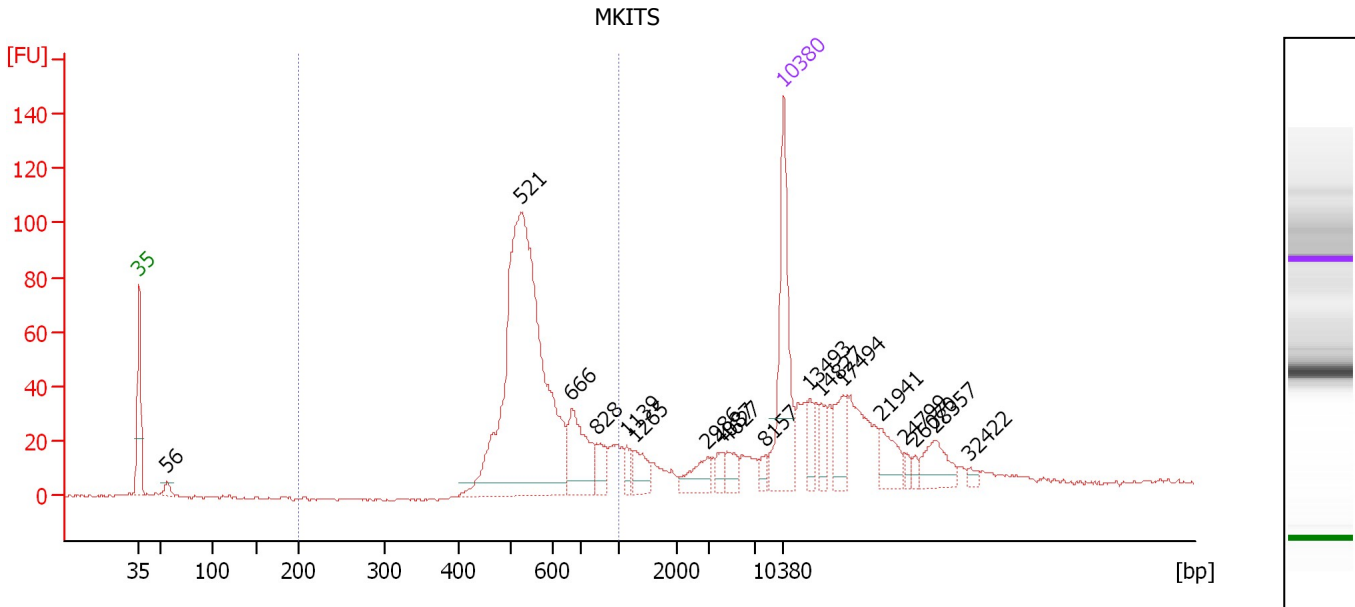
MKArch

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ μ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	438	767.80	785.1	3,680.7	 52	48.8

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Electropherogram Summary Continued ...



Overall Results for sample 7 : MKITS

Number of peaks found: 18 Corr. Area 1: 659.8
 Noise: 0.4

Peak table for sample 7 : MKITS

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	56	8.38	227.9		46.01
3	521	405.49	1,178.7		84.40
4	666	52.37	119.2		89.96
5	828	16.43	30.1		92.74
6	1,139	7.61	10.1		95.92
7	1,265	15.32	18.4		96.73
8	2,986	16.05	8.1		104.72
9	4,087	7.70	2.9		106.17
10	4,627	10.48	3.4		106.86
11	8,157	5.55	1.0		110.97
12	10,380	75.00	10.9	Upper Marker	113.00
13	13,493	0.00	0.0		115.84
14	14,827	0.00	0.0		117.05
15	17,494	0.00	0.0		119.48
16	21,941	0.00	0.0		123.54
17	24,799	0.00	0.0		126.14
18	26,070	0.00	0.0		127.30
19	28,357	0.00	0.0		129.39
20	32,422	0.00	0.0		133.09

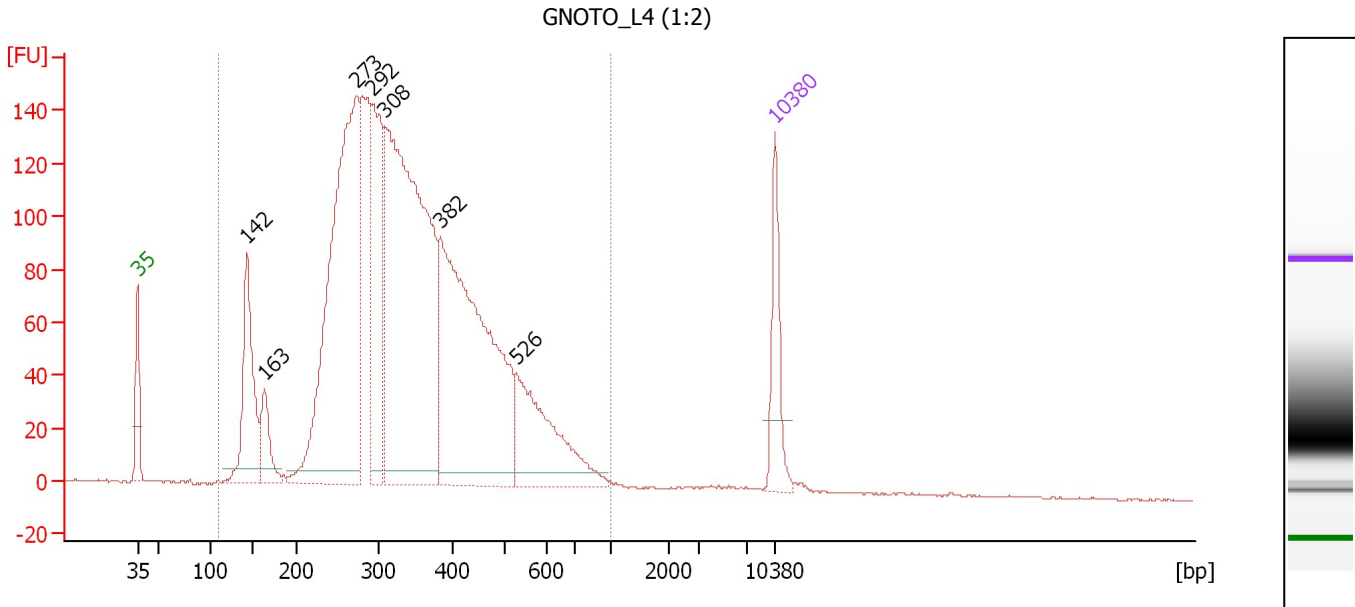
Region table for sample 7 : MKITS

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	580	454.58	659.8	1,232.1	56	19.4

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Electropherogram Summary Continued ...



Overall Results for sample 8 : GNOTO_L4 (1:2)

Number of peaks found: 7 Corr. Area 1: 3,433.5
 Noise: 0.4

Peak table for sample 8 : GNOTO_L4 (1:2)

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	142	243.81	2,593.6		55.01
3	163	83.01	771.9		56.94
4	273	818.38	4,546.0		67.08
5	292	264.55	1,372.8		68.83
6	308	966.96	4,763.7		70.18
7	382	666.72	2,641.2		76.27
8	526	213.15	614.5		84.59
9	10,380	75.00	10.9	Upper Marker	113.00

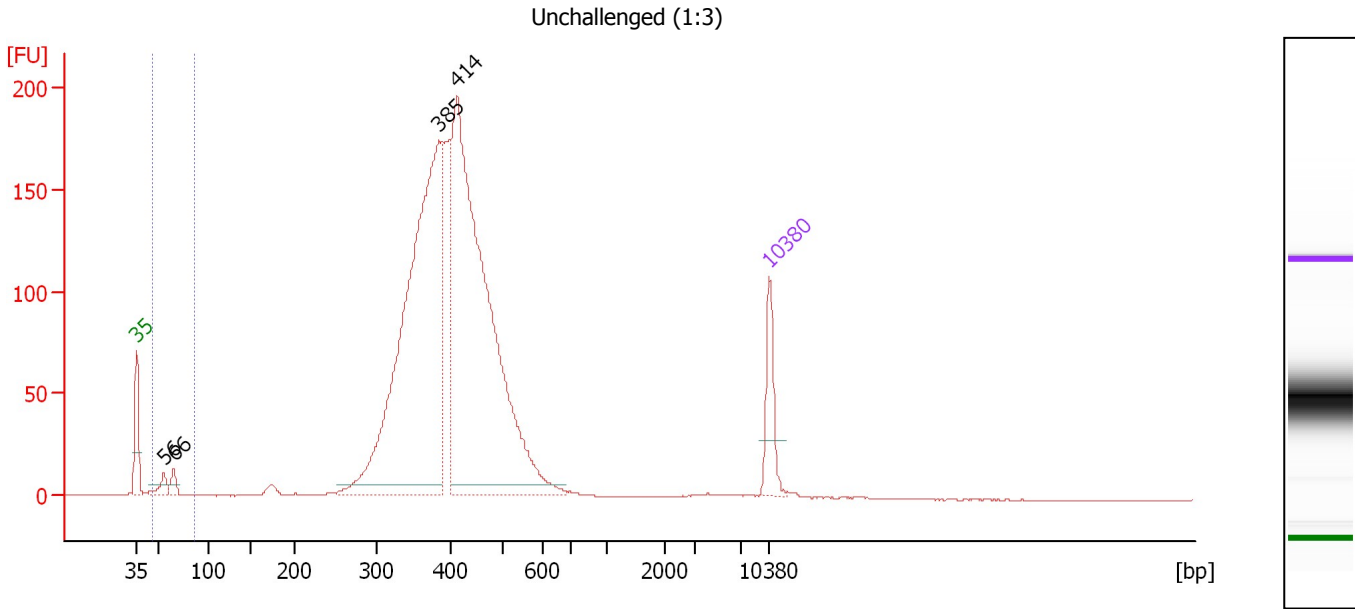
Region table for sample 8 : GNOTO_L4 (1:2)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
109	1,000	348	3,504.62	3,433.5	18,173.9	99	34.3

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Electropherogram Summary Continued ...



Overall Results for sample 9 : Unchallenged (1:3)

Number of peaks found: 4 Corr. Area 1: 38.0
 Noise: 0.2

Peak table for sample 9 : Unchallenged (1:3)

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	56	34.38	935.7		46.01
3	66	28.30	652.8		47.13
4	385	1,221.65	4,809.6		76.47
5	414	1,261.69	4,612.0		78.53
6	10,380	75.00	10.9	Upper Marker	113.00

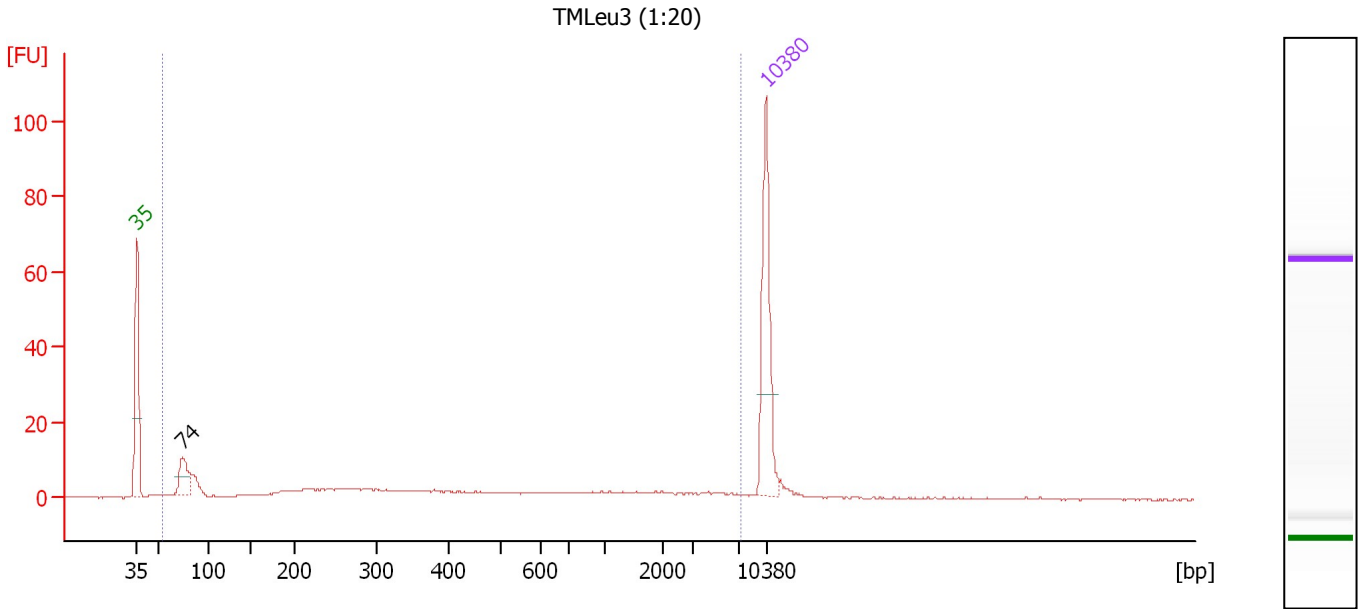
Region table for sample 9 : Unchallenged (1:3)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
46	86	60	64.49	38.0	1,640.9	2	10.9

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Electropherogram Summary Continued ...



Overall Results for sample 10 : TMLeu3 (1:20)

Number of peaks found: 1 Corr. Area 1: 150.1
 Noise: 0.2

Peak table for sample 10 : TMLeu3 (1:20)

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	74	37.45	768.8		48.04
3	10,380	75.00	10.9	Upper Marker	113.00

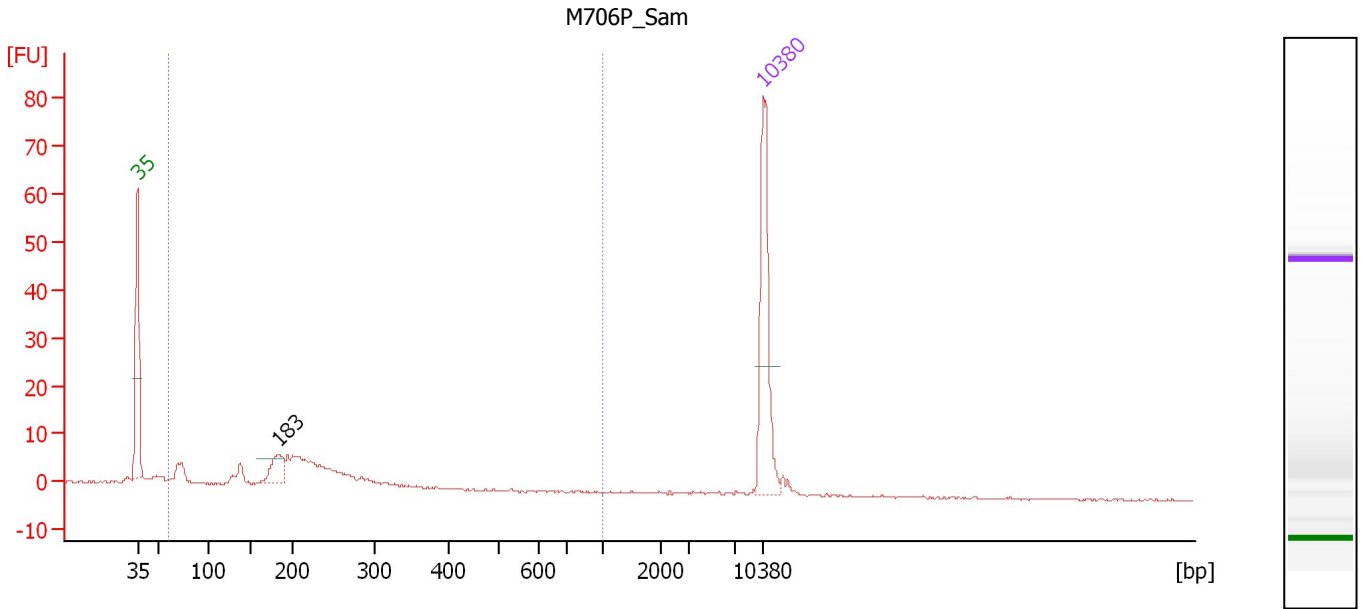
Region table for sample 10 : TMLeu3 (1:20)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
54	7,189	853	205.61	150.1	1,912.9	89	100.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-29\2018-06-29_001.xad

Created: 6/29/2018 2:01:01 PM
 Modified: 6/29/2018 2:43:24 PM

Electropherogram Summary Continued ...



Overall Results for sample 11 : M706P_Sam

Number of peaks found: 1 Corr. Area 1: 99.5
 Noise: 0.2

Peak table for sample 11 : M706P_Sam

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	183	29.01	240.6		58.80
3	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : M706P_Sam

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
59	1,000	201	174.81	99.5	1,640.4	87	30.9

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-29\2018-06-29_001.xad

Created: 6/29/2018 2:01:01 PM
Modified: 6/29/2018 2:43:24 PM

Gel Image