

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-18\2018-09-18_001.xad

Created: 9/18/2018 2:48:07 PM
Modified: 9/18/2018 3:23:41 PM

Electrophoresis File Run Summary

Instrument Information:

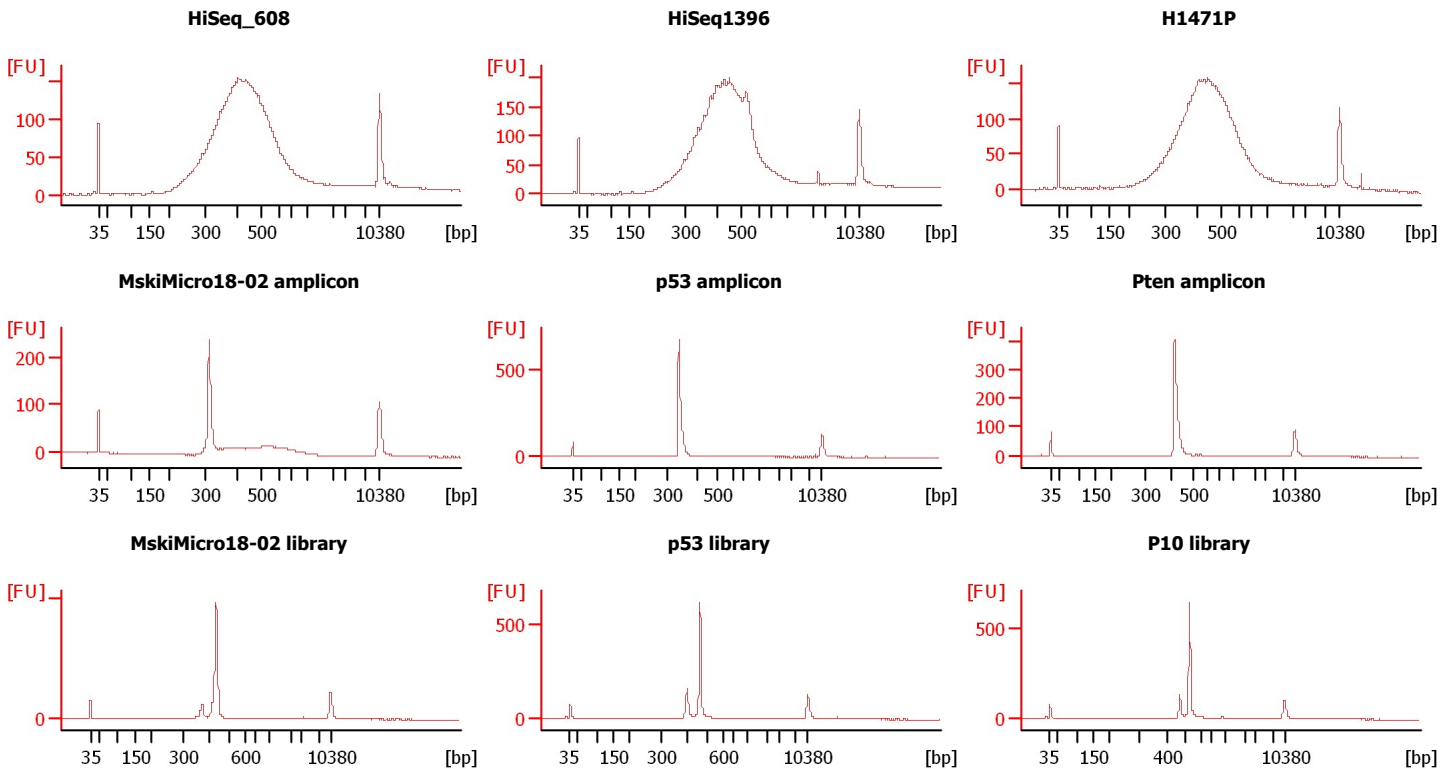
Instrument Name: DE34903152 Firmware: C.01.069
Serial#: DE34903152 Type: G2938C

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
HiSeq_608		<input type="checkbox"/>	✓			
HiSeq1396		<input type="checkbox"/>	✓			
H1471P		<input type="checkbox"/>	✓			
MskiMicro18-02 amplicon		<input type="checkbox"/>	✓			
p53 amplicon		<input type="checkbox"/>	✓			
Pten amplicon		<input type="checkbox"/>	✓			
MskiMicro18-02 library		<input type="checkbox"/>	✓			
p53 library		<input type="checkbox"/>	✓			
P10 library		<input type="checkbox"/>	✓			
sample 10		<input type="checkbox"/>				
sample 11		<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

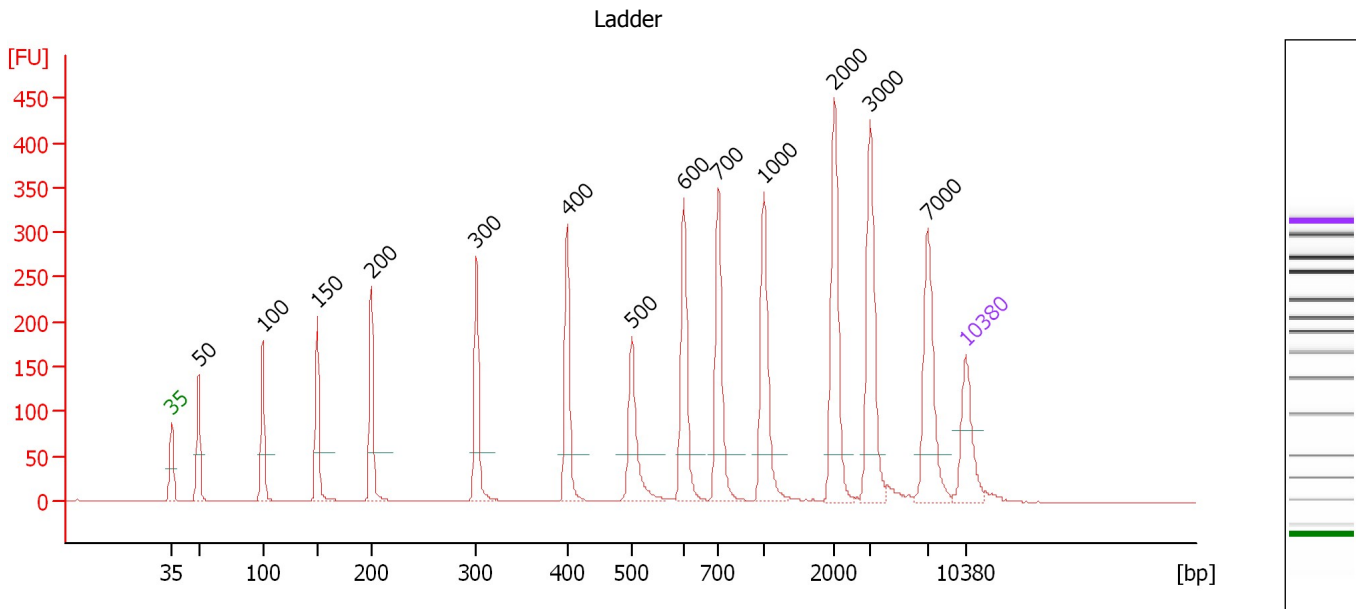
Ladder

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

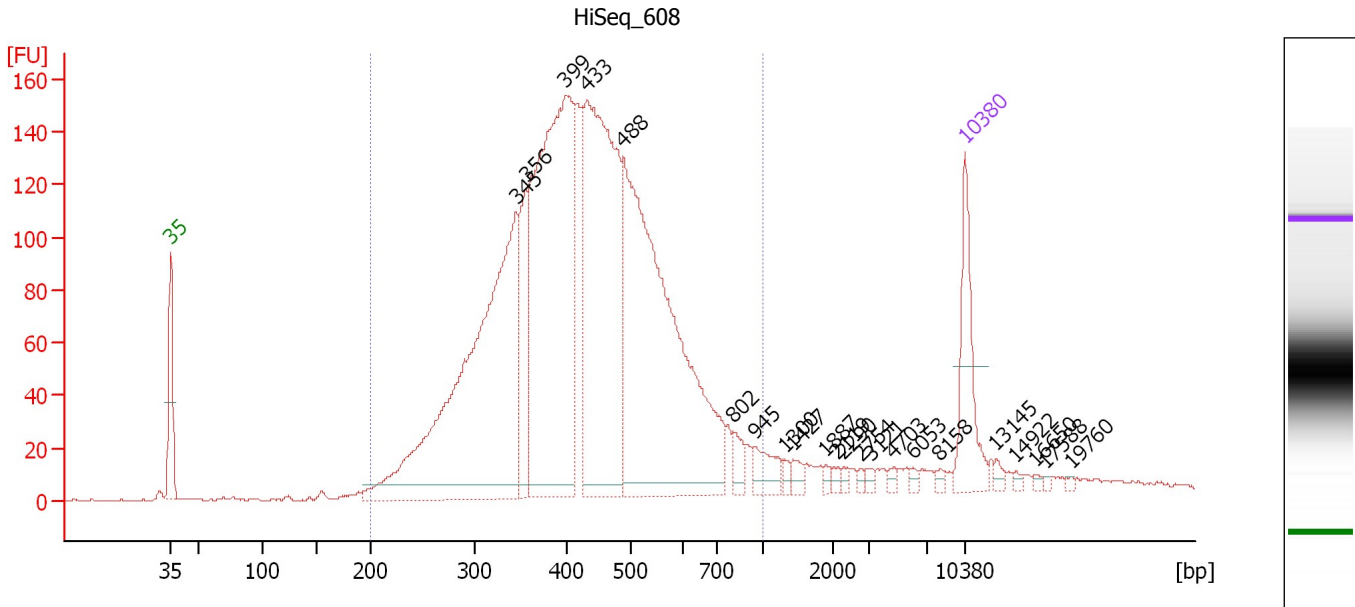
Peak table for Ladder

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	45.35
3	100	150.00	2,272.7	Ladder Peak	51.01
4	150	150.00	1,515.2	Ladder Peak	55.80
5	200	150.00	1,136.4	Ladder Peak	60.55
6	300	150.00	757.6	Ladder Peak	69.85
7	400	150.00	568.2	Ladder Peak	77.81
8	500	150.00	454.5	Ladder Peak	83.56
9	600	150.00	378.8	Ladder Peak	88.12
10	700	150.00	324.7	Ladder Peak	91.18
11	1,000	150.00	227.3	Ladder Peak	95.21
12	2,000	150.00	113.6	Ladder Peak	101.40
13	3,000	150.00	75.8	Ladder Peak	104.56
14	7,000	150.00	32.5	Ladder Peak	109.64
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : HiSeq_608

Number of peaks found: 22 Corr. Area 1: 3,262.8
 Noise: 0.4

Peak table for sample 1 : HiSeq_608


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	345	667.73	2,931.4		73.44
3	356	111.38	473.7		74.32
4	399	613.25	2,326.8		77.75
5	433	497.48	1,740.2		79.72
6	488	653.91	2,031.6		82.85
7	802	20.02	37.8		92.56
8	945	29.77	47.7		94.47
9	1,300	5.63	6.6		97.07
10	1,427	9.67	10.3		97.85
11	1,887	4.11	3.3		100.70
12	2,119	4.94	3.5		101.77
13	2,290	4.05	2.7		102.31
14	2,754	3.45	1.9		103.78
15	3,121	4.75	2.3		104.72
16	4,703	4.41	1.4		106.73
17	6,053	4.09	1.0		108.44
18	8,158	3.93	0.7		110.79
19	10,380	75.00	10.9	Upper Marker	113.00
20	13,145	0.00	0.0		115.75
21	14,922	0.00	0.0		117.51
22	16,650	0.00	0.0		119.23
23	17,588	0.00	0.0		120.16
24	19,760	0.00	0.0		122.31

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Electropherogram Summary Continued ...

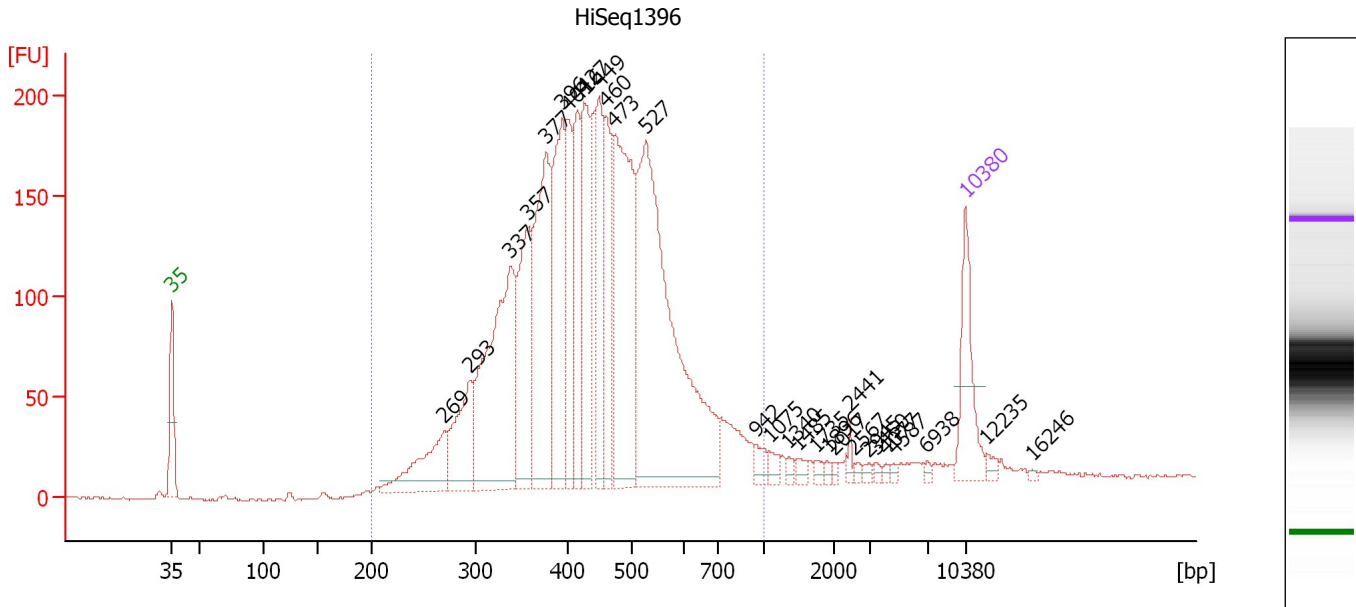
... Region table for sample 1 : HiSeq 608

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	439	2,727.37	3,262.8	10,404.3	 93	28.0

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Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq1396

Number of peaks found: 29 Corr. Area 1: 3,818.1
 Noise: 0.6

Peak table for sample 2 : HiSeq1396

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	269	116.94	657.8		67.00
3	293	118.60	612.4		69.24
4	337	367.12	1,648.9		72.82
5	357	174.36	739.2		74.42
6	377	280.12	1,126.5		75.96
7	396	212.43	813.8		77.45
8	401	119.89	453.3		77.85
9	416	129.19	470.2		78.75
10	427	168.40	598.0		79.34
11	449	148.07	499.4		80.64
12	460	131.13	431.5		81.29
13	473	310.81	994.7		82.03
14	527	583.18	1,678.1		84.77
15	942	16.46	26.5		94.43
16	1,075	10.58	14.9		95.67
17	1,340	5.52	6.2		97.32
18	1,485	7.30	7.5		98.21
19	1,735	6.16	5.4		99.76
20	1,896	4.18	3.3		100.75
21	2,017	3.90	2.9		101.45
22	2,441	6.79	4.2		102.79
23	2,567	3.80	2.2		103.19
24	2,945	4.73	2.4		104.39
25	3,450	3.82	1.7		105.13

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Electropherogram Summary Continued ...

... Peak table for sample 2 : HiSeq1396

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	4,077	3.26	1.2		105.93
27	4,587	3.35	1.1		106.58
28	6,938	3.34	0.7		109.56
29	10,380	75.00	10.9	Upper Marker	113.00
30	12,235	0.00	0.0		114.84
31	16,246	0.00	0.0		118.83

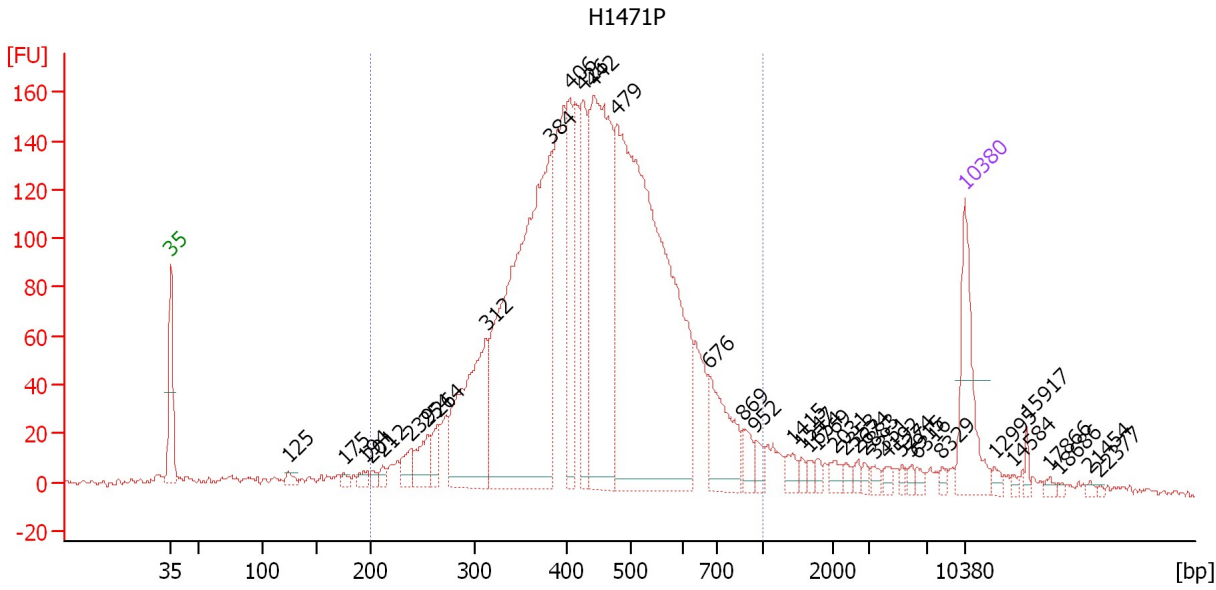
Region table for sample 2 : HiSeq1396

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	448	3,030.09	3,818.1	11,186.5	94	26.4

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Electropherogram Summary Continued ...



Overall Results for sample 3 : H1471P

Number of peaks found: 38 Corr. Area 1: 3,359.8
 Noise: 1.4

Peak table for sample 3 : H1471P

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	125	10.26	124.5		53.39
3	175	7.12	61.5		58.22
4	194	8.94	69.7		60.00
5	201	6.94	52.3		60.67
6	212	8.63	61.8		61.63
7	239	25.67	162.7		64.18
8	254	39.10	232.9		65.60
9	264	28.14	161.3		66.52
10	312	210.22	1,021.2		70.80
11	384	610.97	2,409.6		76.55
12	406	111.59	416.0		78.18
13	426	117.26	417.1		79.30
14	442	368.25	1,262.8		80.21
15	479	772.95	2,445.0		82.35
16	676	86.23	193.3		90.45
17	869	20.13	35.1		93.45
18	952	13.00	20.7		94.57
19	1,415	12.13	13.0		97.78
20	1,547	5.80	5.7		98.59
21	1,654	5.60	5.1		99.25
22	1,769	6.28	5.4		99.97
23	2,031	9.84	7.3		101.49
24	2,353	5.98	3.8		102.51
25	2,674	5.19	2.9		103.53

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Electropherogram Summary Continued ...

... Peak table for sample 3 : H1471P

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	2,883	4.88	2.6		104.19
27	3,351	5.43	2.5		105.01
28	4,192	6.47	2.3		106.08
29	5,274	4.26	1.2		107.45
30	5,915	4.58	1.2		108.27
31	6,316	4.75	1.1		108.77
32	8,329	4.13	0.8		110.96
33	10,380	75.00	10.9	Upper Marker	113.00
34	12,995	0.00	0.0		115.60
35	14,584	0.00	0.0		117.17
36	15,917	0.00	0.0		118.50
37	17,866	0.00	0.0		120.43
38	18,686	0.00	0.0		121.25
39	21,454	0.00	0.0		124.00
40	22,377	0.00	0.0		124.91

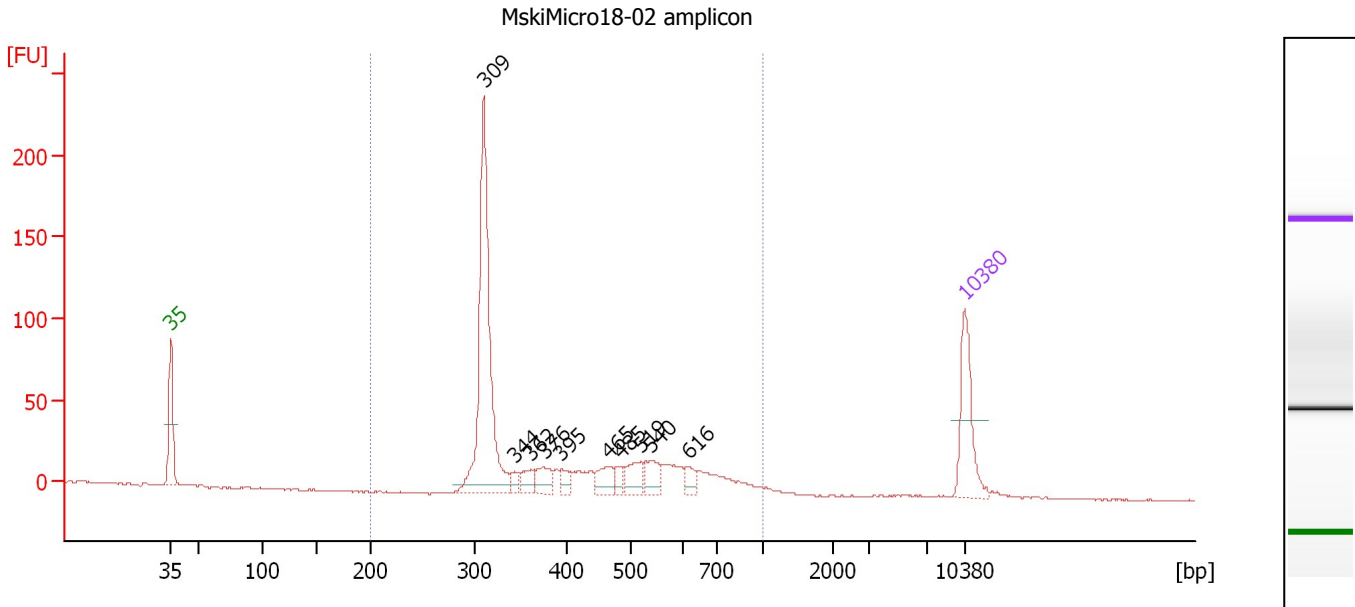
Region table for sample 3 : H1471P

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	454	2,807.02	3,359.8	10,363.8	91	27.9

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Electropherogram Summary Continued ...



Overall Results for sample 4 : MskiMicro18-02 amplicon

Number of peaks found: 10 Corr. Area 1: 663.3
 Noise: 0.4

Peak table for sample 4 : MskiMicro18-02 amplicon

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	309	373.19	1,829.2		70.57
3	344	12.69	56.0		73.33
4	362	22.17	92.8		74.78
5	376	31.03	125.1		75.87
6	395	16.02	61.4		77.43
7	465	30.50	99.4		81.53
8	485	14.62	45.7		82.67
9	519	31.30	91.3		84.44
10	540	32.19	90.3		85.37
11	616	15.22	37.5		88.59
12	10,380	75.00	10.9	Upper Marker	113.00

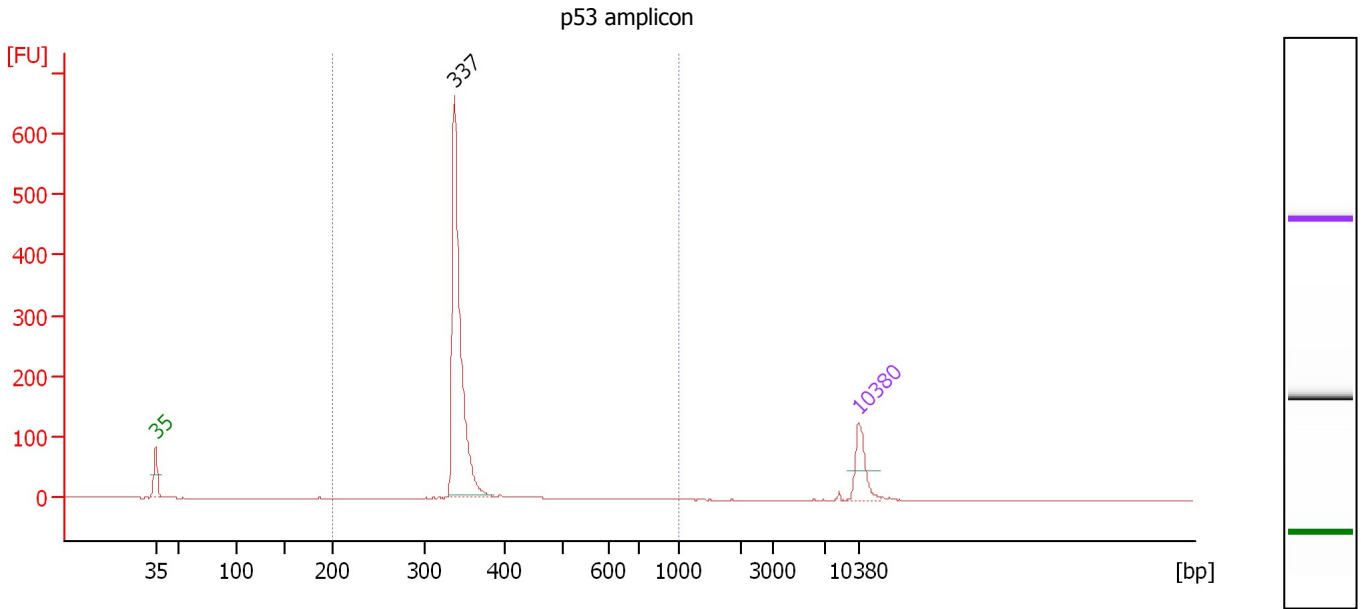
Region table for sample 4 : MskiMicro18-02 amplicon

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	423	638.70	663.3	2,593.5	99	34.0

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Electropherogram Summary Continued ...



Overall Results for sample 5 : p53 amplicon

Number of peaks found: 1 Corr. Area 1: 898.2
 Noise: 0.3

Peak table for sample 5 : p53 amplicon

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	337	752.93	3,385.0		72.80
3	10,380	75.00	10.9	Upper Marker	113.00

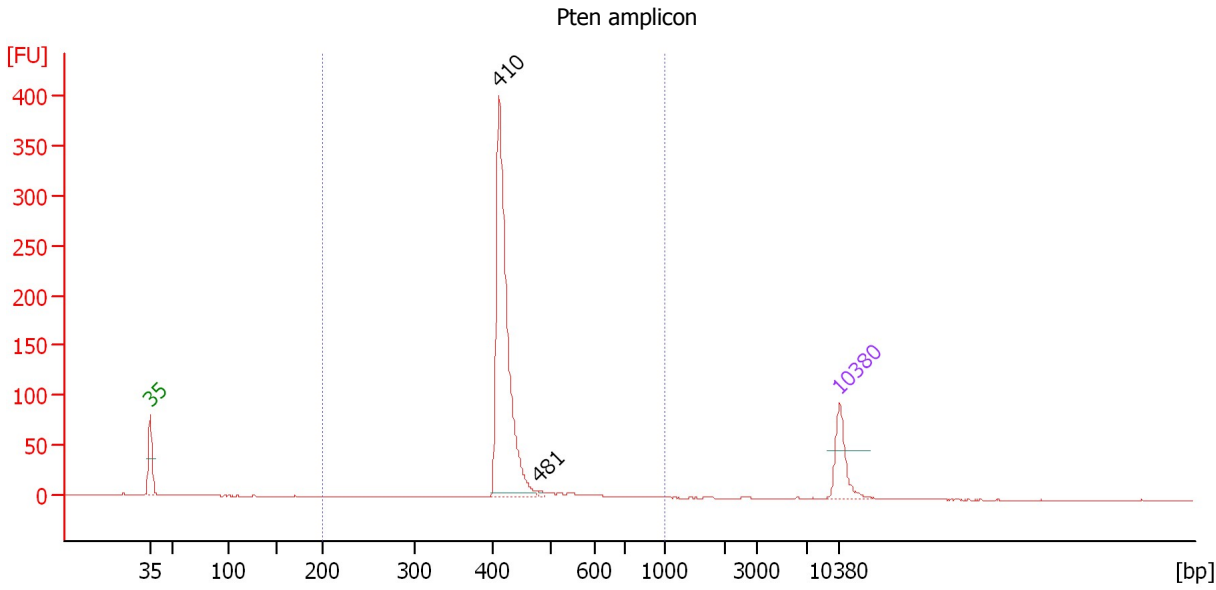
Region table for sample 5 : p53 amplicon

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	347	786.21	898.2	3,454.1	99	8.4

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Electropherogram Summary Continued ...



Overall Results for sample 6 : Pten amplicon

Number of peaks found: 2 Corr. Area 1: 691.0
 Noise: 0.3

Peak table for sample 6 : Pten amplicon

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	410	690.28	2,548.5		78.41
3	481	4.51	14.2		82.47
4	10,380	75.00	10.9	Upper Marker	113.00

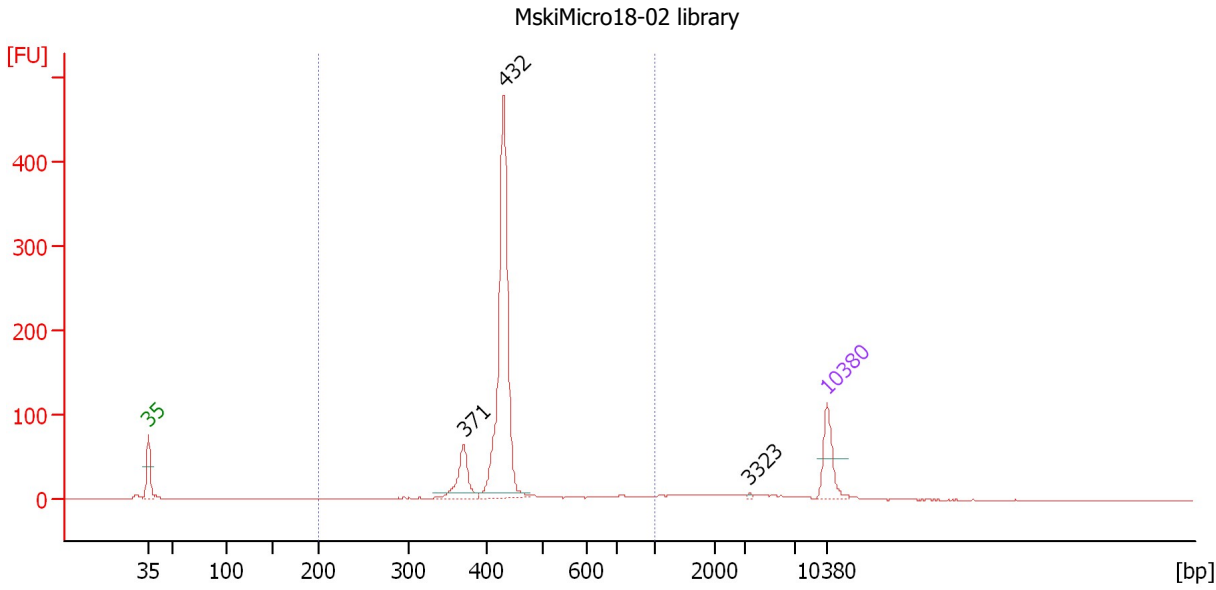
Region table for sample 6 : Pten amplicon

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	430	725.43	691.0	2,579.8	97	11.9

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Electropherogram Summary Continued ...



Overall Results for sample 7 : MskiMicro18-02 library

Number of peaks found: 3 Corr. Area 1: 841.6
 Noise: 0.2

Peak table for sample 7 : MskiMicro18-02 library

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	371	102.02	416.7		75.50
3	432	632.84	2,222.0		79.62
4	3,323	2.45	1.1		104.97
5	10,380	75.00	10.9	Upper Marker	113.00

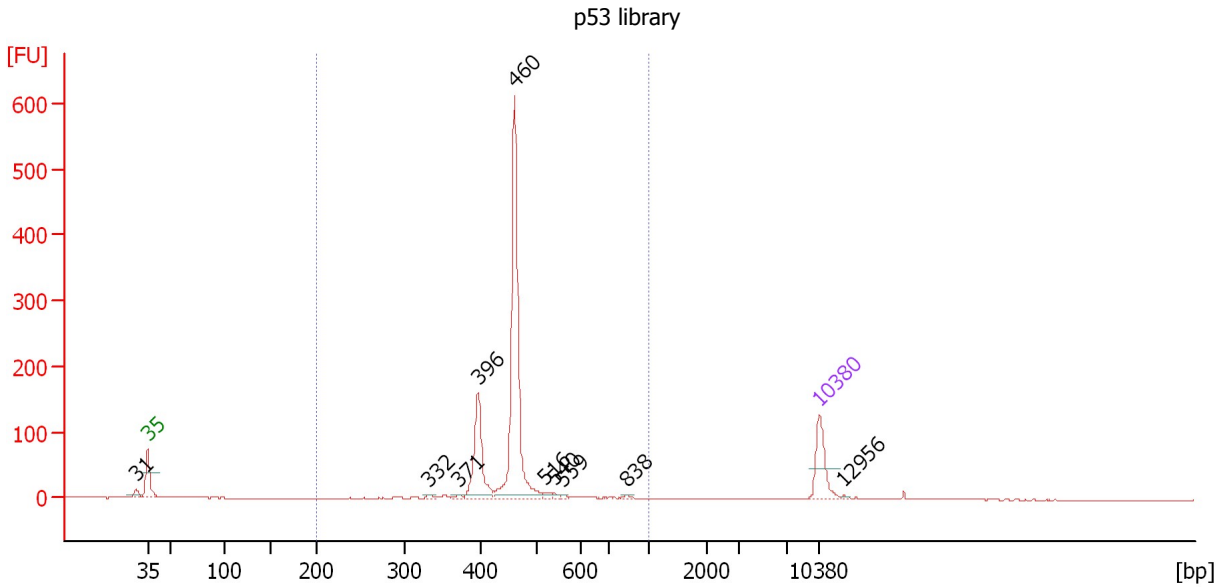
Region table for sample 7 : MskiMicro18-02 library

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	435	820.32	841.6	2,942.3	87	18.4

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Electropherogram Summary Continued ...



Overall Results for sample 8 : p53 library

Number of peaks found: 10 Corr. Area 1: 889.3
 Noise: 0.3

Peak table for sample 8 : p53 library

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.83
2	35	125.00	5,411.3	Lower Marker	43.00
3	332	5.98	27.3		72.36
4	371	6.17	25.2		75.53
5	396	171.66	657.2		77.47
6	460	527.95	1,739.5		81.25
7	516	7.91	23.2		84.31
8	540	5.05	14.2		85.37
9	559	4.77	12.9		86.26
10	838	4.26	7.7		93.04
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,956	0.00	0.0		115.56

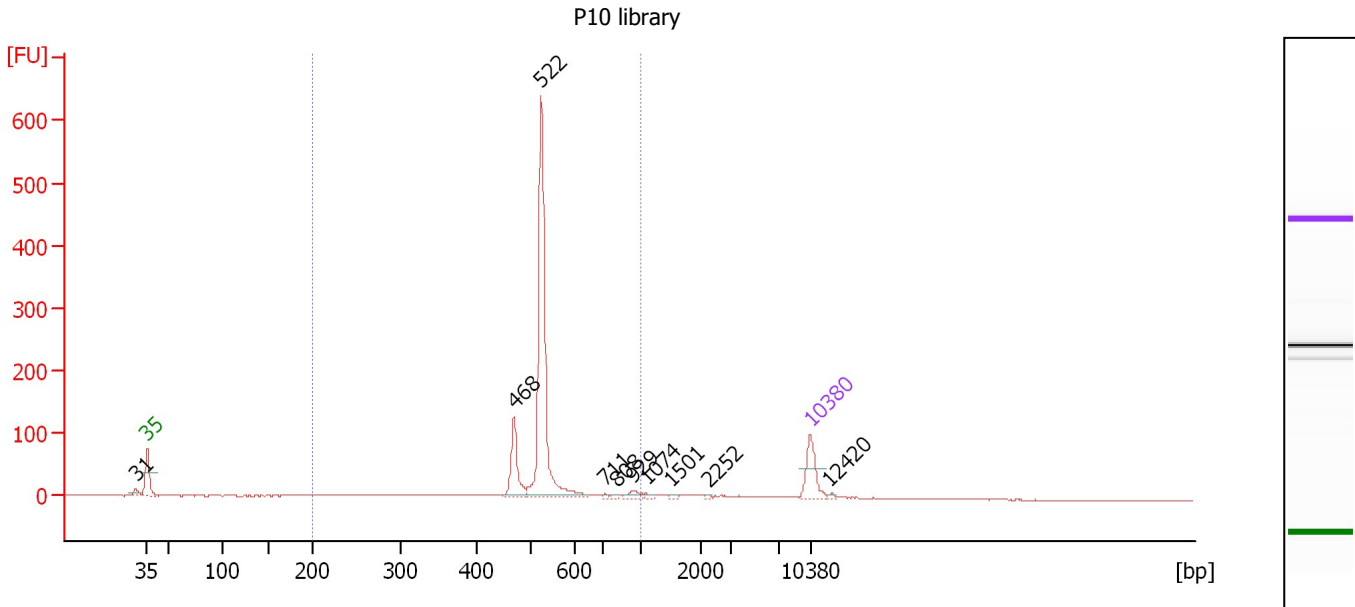
Region table for sample 8 : p53 library

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	454	757.23	889.3	2,573.3	94	13.6

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Electropherogram Summary Continued ...



Overall Results for sample 9 : P10 library

Number of peaks found: 10 Corr. Area 1: 886.0
 Noise: 0.3

Peak table for sample 9 : P10 library

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	31	0.00	0.0		41.82
2	35	125.00	5,411.3	Lower Marker	43.00
3	468	130.06	421.2		81.71
4	522	629.00	1,824.2		84.58
5	711	4.89	10.4		91.34
6	808	5.08	9.5		92.63
7	929	16.24	26.5		94.26
8	1,074	5.39	7.6		95.67
9	1,501	4.01	4.0		98.31
10	2,252	2.86	1.9		102.20
11	10,380	75.00	10.9	Upper Marker	113.00
12	12,420	0.00	0.0		115.03

Region table for sample 9 : P10 library

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	517	908.06	886.0	2,842.8	84	19.3

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Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-18\2018-09-18_001.xad

Created: 9/18/2018 2:48:07 PM
Modified: 9/18/2018 3:23:41 PM

Invalid Samples

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.