

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-26\2018-09-26_001.xad

Created: 9/26/2018 3:48:42 PM
Modified: 9/26/2018 4:29:58 PM

Electrophoresis File Run Summary

Instrument Information:

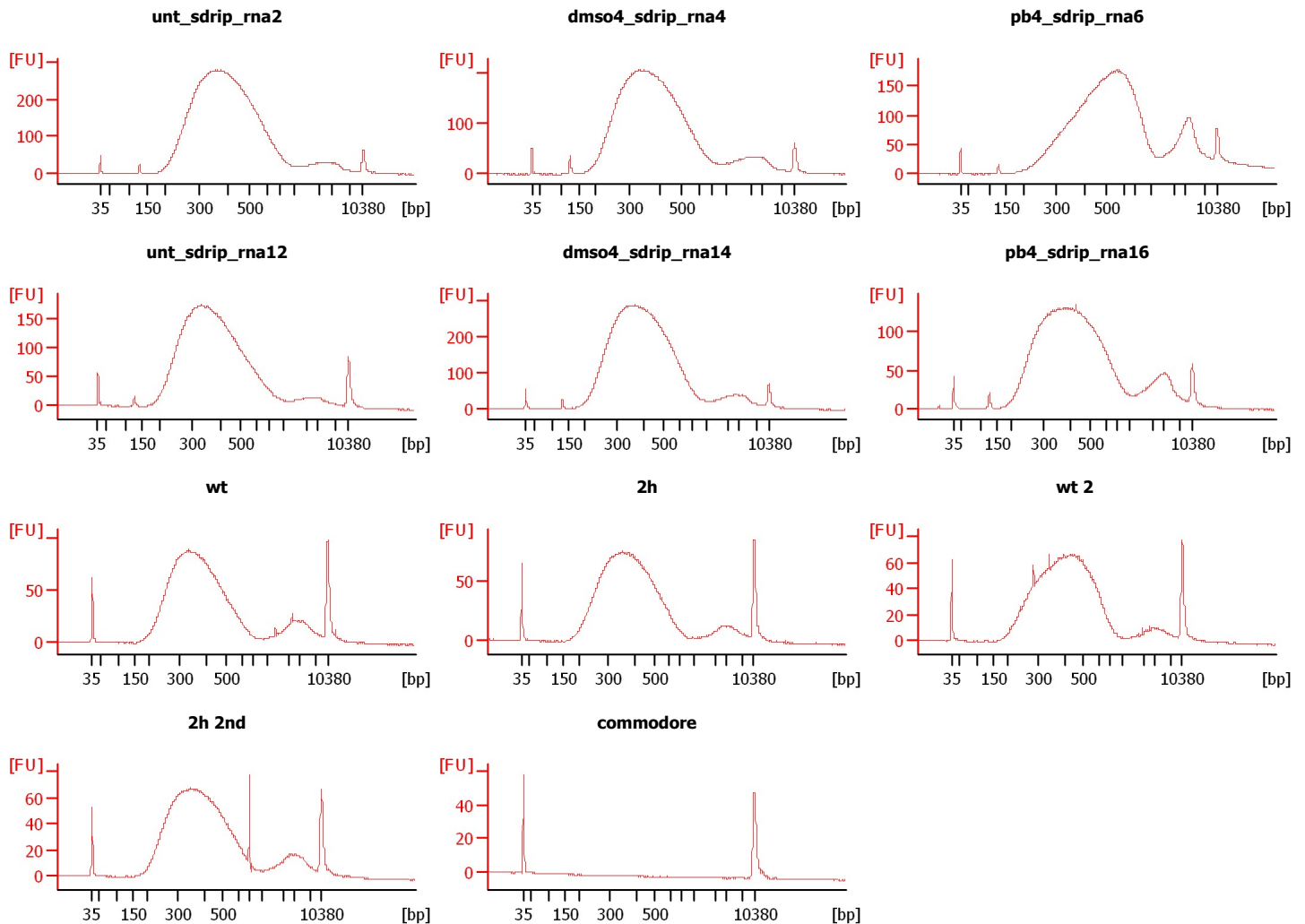
Instrument Name: DE34903152 Firmware: C.01.069
Serial#: DE34903152 Type: G2938C

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
unt_sdrip_rna2		<input type="checkbox"/>	✓			
dms04_sdrip_rna4		<input type="checkbox"/>	✓			
pb4_sdrip_rna6		<input type="checkbox"/>	✓			
unt_sdrip_rna12		<input type="checkbox"/>	✓			
dms04_sdrip_rna14		<input type="checkbox"/>	✓			
pb4_sdrip_rna16		<input type="checkbox"/>	✓			
wt		<input type="checkbox"/>	✓			
2h		<input type="checkbox"/>	✓			
wt 2		<input type="checkbox"/>	✓			
2h 2nd		<input type="checkbox"/>	✓			
commodore		<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

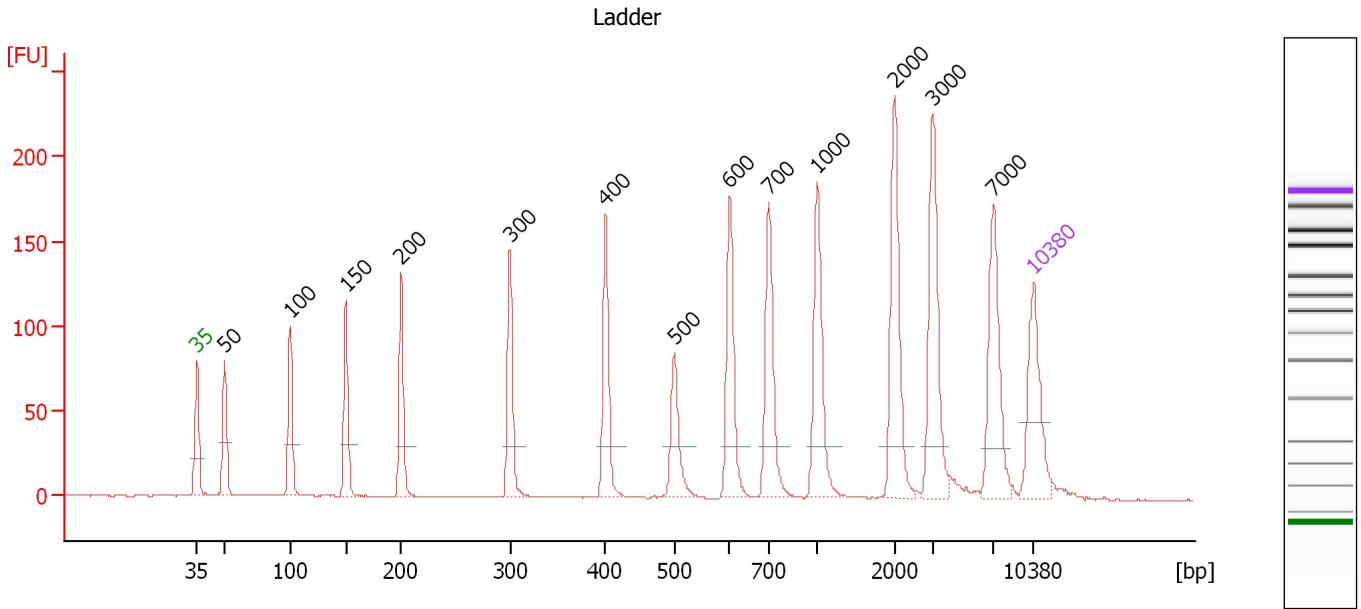
Ladder

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

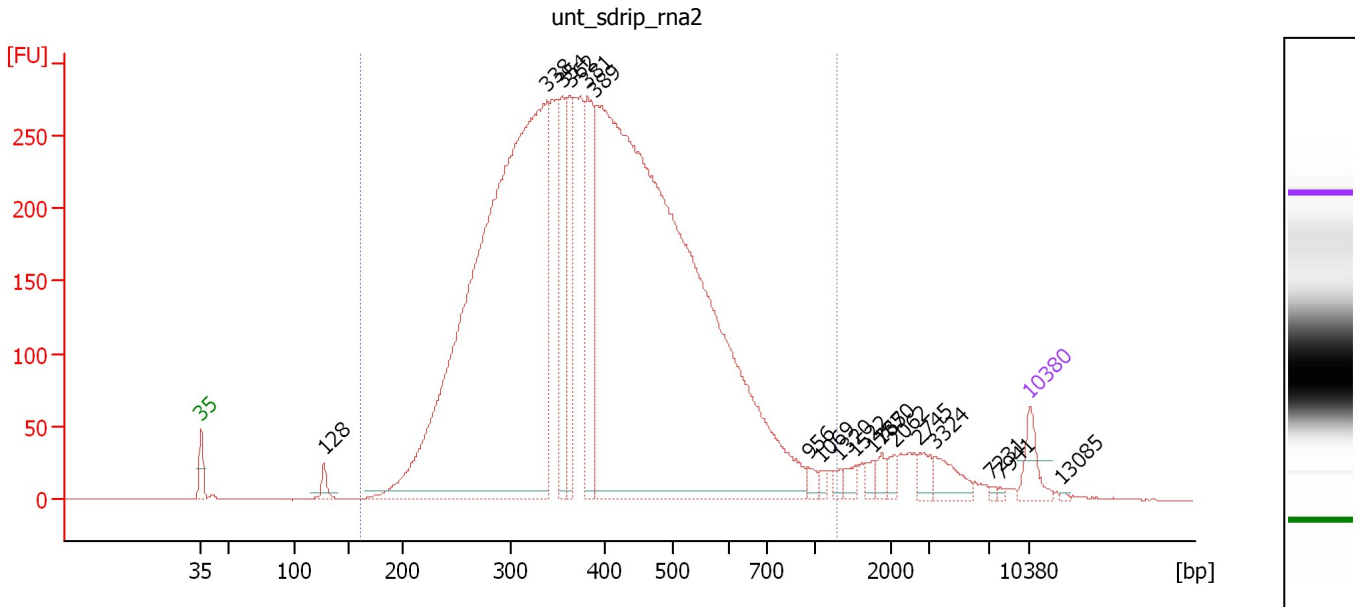
Peak table for Ladder

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	45.32
3	100	150.00	2,272.7	Ladder Peak	50.81
4	150	150.00	1,515.2	Ladder Peak	55.45
5	200	150.00	1,136.4	Ladder Peak	60.09
6	300	150.00	757.6	Ladder Peak	69.19
7	400	150.00	568.2	Ladder Peak	77.17
8	500	150.00	454.5	Ladder Peak	82.93
9	600	150.00	378.8	Ladder Peak	87.57
10	700	150.00	324.7	Ladder Peak	90.83
11	1,000	150.00	227.3	Ladder Peak	94.89
12	2,000	150.00	113.6	Ladder Peak	101.36
13	3,000	150.00	75.8	Ladder Peak	104.52
14	7,000	150.00	32.5	Ladder Peak	109.56
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : unt_sdrrip_rna2

Number of peaks found: 18 Corr. Area 1: 7,849.6
 Noise: 0.3

Peak table for sample 1 : unt_sdrrip_rna2

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	128	56.15	666.8		53.37
3	338	4,528.36	20,310.8		72.21
4	354	391.28	1,676.6		73.47
5	362	384.30	1,608.1		74.15
6	381	468.75	1,865.6		75.63
7	389	5,482.93	21,346.7		76.31
8	956	28.79	45.6		94.29
9	1,069	15.39	21.8		95.33
10	1,320	19.95	22.9		96.95
11	1,522	32.89	32.7		98.26
12	1,765	26.17	22.5		99.84
13	1,870	28.95	23.5		100.51
14	2,062	31.85	23.4		101.55
15	2,745	45.00	24.8		103.71
16	3,324	80.16	36.5		104.93
17	7,231	5.60	1.2		109.80
18	7,941	5.05	1.0		110.52
19	10,380	75.00	10.9	Upper Marker	113.00
20	13,085	0.00	0.0		115.75

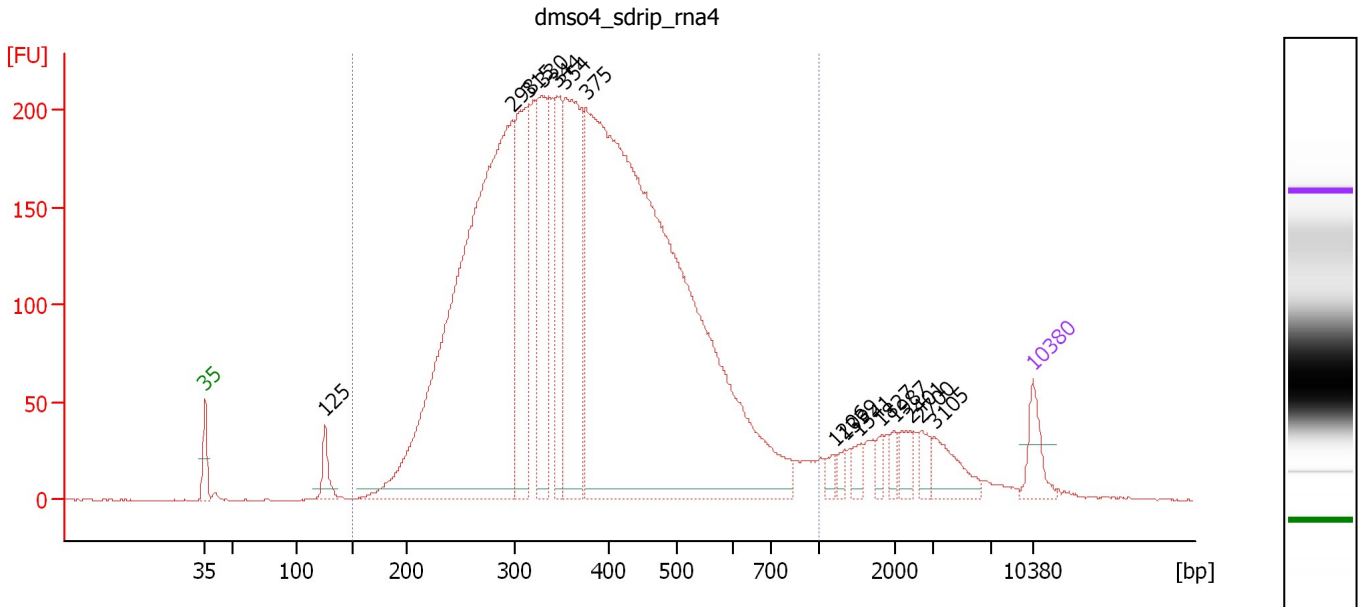
Region table for sample 1 : unt_sdrrip_rna2

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
162	1,277	409	12,439.62	7,849.6	52,349.6	95	33.3

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Electropherogram Summary Continued ...



Overall Results for sample 2 : dms04_sdrip_rna4

Number of peaks found: 15 Corr. Area 1: 5,912.2
 Noise: 0.3

Peak table for sample 2 : dms04_sdrip_rna4

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	96.56	1,168.4		53.15
3	298	2,984.63	15,190.3		68.98
4	315	660.60	3,178.6		70.38
5	330	566.07	2,602.4		71.55
6	344	386.45	1,700.8		72.72
7	354	834.65	3,573.8		73.49
8	375	4,320.69	17,442.5		75.20
9	1,206	24.31	30.5		96.22
10	1,339	24.77	28.0		97.08
11	1,541	34.92	34.3		98.39
12	1,827	24.85	20.6		100.24
13	1,987	29.36	22.4		101.27
14	2,401	51.33	32.4		102.63
15	2,700	42.40	23.8		103.57
16	3,105	99.35	48.5		104.66
17	10,380	75.00	10.9	Upper Marker	113.00

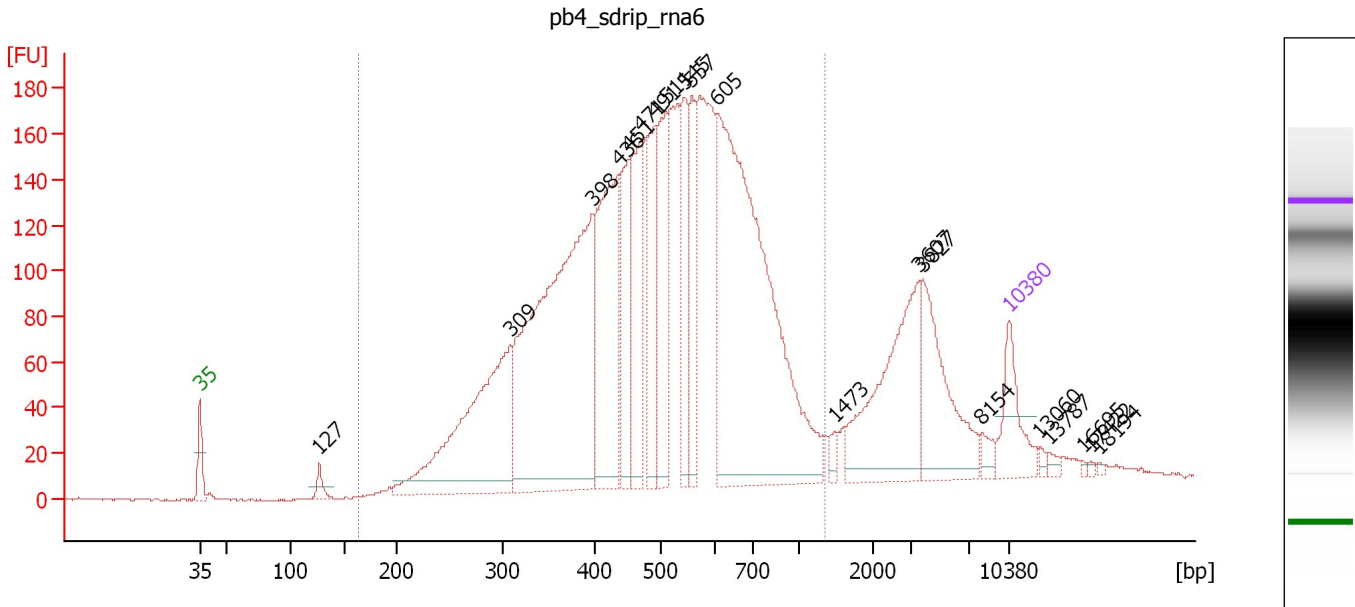
Region table for sample 2 : dms04_sdrip_rna4

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
150	1,000	385	10,220.35	5,912.2	45,523.4	93	31.7

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Electropherogram Summary Continued ...



Overall Results for sample 3 : pb4_sdrrip_rna6

Number of peaks found: 20 Corr. Area 1: 4,266.6
 Noise: 0.3

Peak table for sample 3 : pb4_sdrrip_rna6

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	127	25.28	300.9		53.34
3	309	521.46	2,560.5		69.87
4	398	912.47	3,477.1		76.98
5	436	384.59	1,336.5		79.25
6	451	167.14	561.2		80.12
7	471	199.65	642.9		81.23
8	491	170.15	524.7		82.43
9	511	200.33	593.8		83.45
10	545	151.63	421.5		85.02
11	557	130.47	354.9		85.57
12	605	923.63	2,311.9		87.74
13	1,473	13.83	14.2		97.95
14	3,607	252.13	105.9		105.29
15	3,827	178.24	70.6		105.57
16	8,154	16.82	3.1		110.74
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,060	0.00	0.0		115.72
19	13,787	0.00	0.0		116.46
20	16,695	0.00	0.0		119.42
21	17,422	0.00	0.0		120.16
22	18,194	0.00	0.0		120.94

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Electropherogram Summary Continued ...

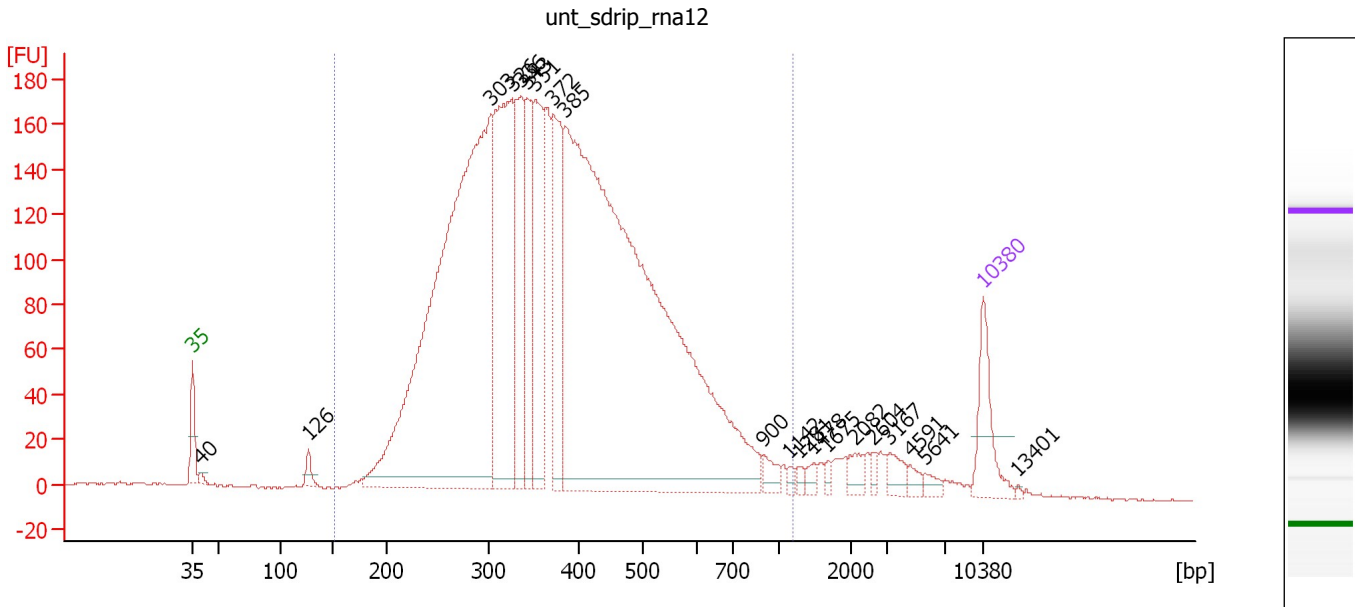
... Region table for sample 3 : pb4_sdrrip_rna6

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ μ l]	Corr. Area	Molarity [pmol/l]	Co lor % of Total	Size distribution in CV [%]
165	1,353	516	4,499.91	4,266.6	15,416.1	 86	33.9

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Electropherogram Summary Continued ...



Overall Results for sample 4 : unt_sdrip_rna12

Number of peaks found: 20 Corr. Area 1: 4,848.2
 Noise: 0.6

Peak table for sample 4 : unt_sdrip_rna12


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	40	9.31	356.4		43.71
3	126	22.84	275.1		53.20
4	303	1,581.55	7,916.6		69.40
5	326	526.33	2,448.1		71.25
6	336	275.19	1,241.6		72.05
7	343	179.92	795.0		72.62
8	351	274.35	1,183.6		73.28
9	372	239.28	974.9		74.93
10	385	2,139.15	8,407.7		76.02
11	900	22.08	37.2		93.54
12	1,142	8.05	10.7		95.81
13	1,281	8.39	9.9		96.70
14	1,478	11.38	11.7		97.98
15	1,675	7.30	6.6		99.26
16	2,082	20.09	14.6		101.62
17	2,604	8.76	5.1		103.27
18	3,167	22.65	10.8		104.73
19	4,591	11.99	4.0		106.53
20	5,641	10.65	2.9		107.85
21	10,380	75.00	10.9	Upper Marker	113.00
22	13,401	0.00	0.0		116.07

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

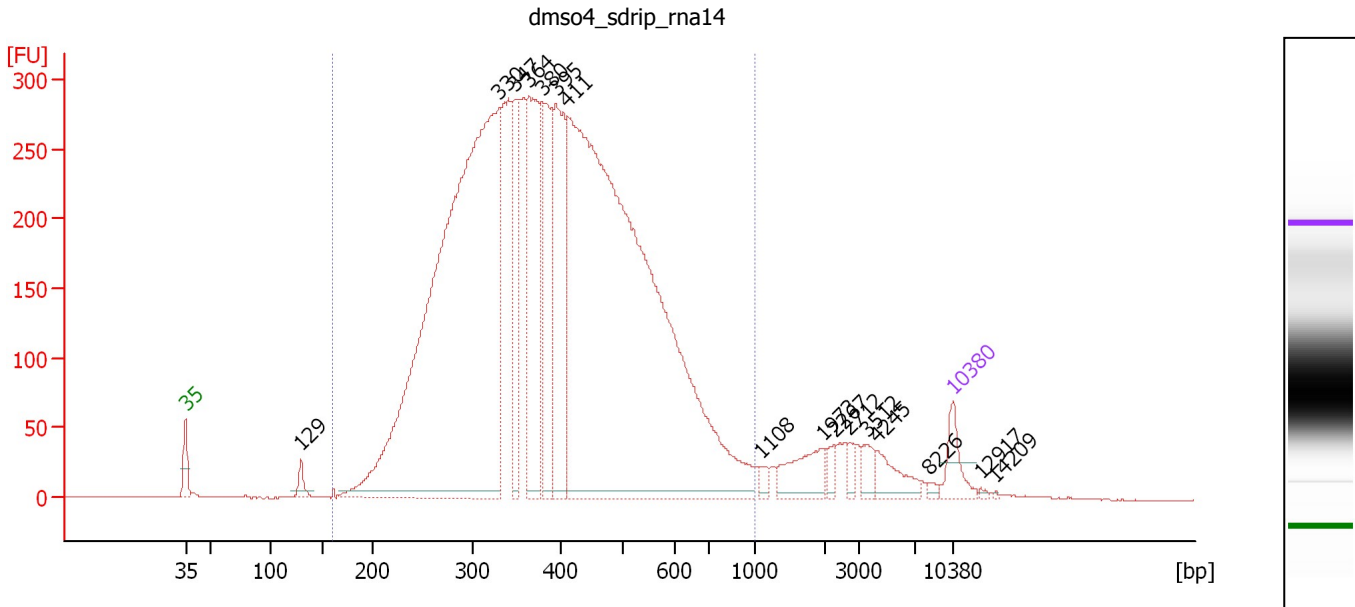
... Region table for sample 4 : unt_sdrp_rna12

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ μ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
152	1,186	393	5,406.74	4,848.2	23,767.8	 95	33.8

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



Overall Results for sample 5 : dms04_sdrip_rna14

Number of peaks found: 16 Corr. Area 1: 8,121.4
 Noise: 0.4

Peak table for sample 5 : dms04_sdrip_rna14

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	129	51.29	601.9		53.51
3	330	3,691.64	16,937.6		71.60
4	347	364.30	1,589.4		72.97
5	364	677.44	2,821.9		74.28
6	380	453.19	1,806.1		75.59
7	395	567.75	2,175.5		76.81
8	411	4,047.05	14,905.5		77.83
9	1,108	22.01	30.1		95.59
10	1,973	124.56	95.7		101.18
11	2,267	30.64	20.5		102.20
12	2,712	25.00	14.0		103.61
13	3,512	45.11	19.5		105.17
14	4,245	79.65	28.4		106.09
15	8,226	11.76	2.2		110.81
16	10,380	75.00	10.9	Upper Marker	113.00
17	12,917	0.00	0.0		115.58
18	14,209	0.00	0.0		116.89

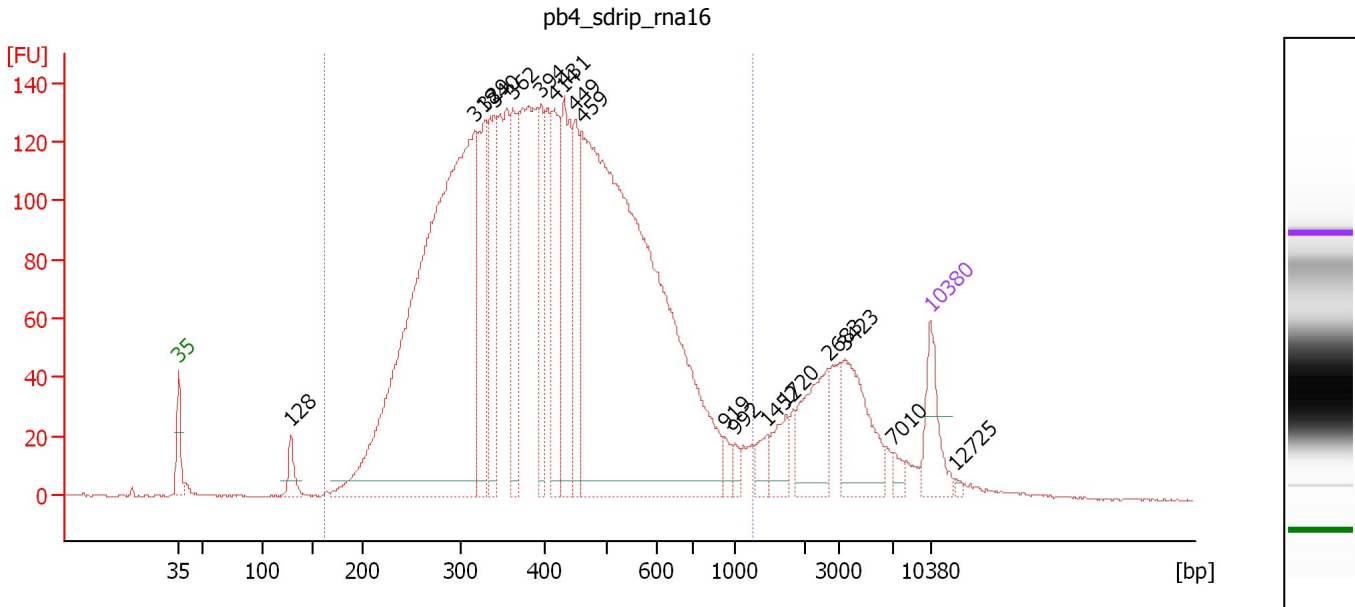
Region table for sample 5 : dms04_sdrip_rna14

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
161	1,000	405	10,810.08	8,121.4	45,650.6	94	30.7

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Electropherogram Summary Continued ...



Overall Results for sample 6 : pb4_sdrip_rna16

Number of peaks found: 18 Corr. Area 1: 4,121.0
 Noise: 0.2

Peak table for sample 6 : pb4_sdrip_rna16

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	128	48.92	578.1		53.43
3	318	1,852.67	8,835.4		70.60
4	329	252.05	1,161.2		71.50
5	340	251.08	1,118.6		72.39
6	362	215.96	904.3		74.13
7	394	164.94	634.0		76.71
8	414	219.88	804.1		78.00
9	431	275.07	967.6		78.94
10	449	149.35	504.2		79.99
11	459	1,856.47	6,125.5		80.58
12	919	20.33	33.5		93.79
13	992	16.57	25.3		94.78
14	1,452	31.95	33.3		97.81
15	1,720	50.11	44.1		99.55
16	2,683	121.35	68.5		103.52
17	3,423	138.80	61.4		105.06
18	7,010	15.59	3.4		109.57
19	10,380	75.00	10.9	Upper Marker	113.00
20	12,725	0.00	0.0		115.38

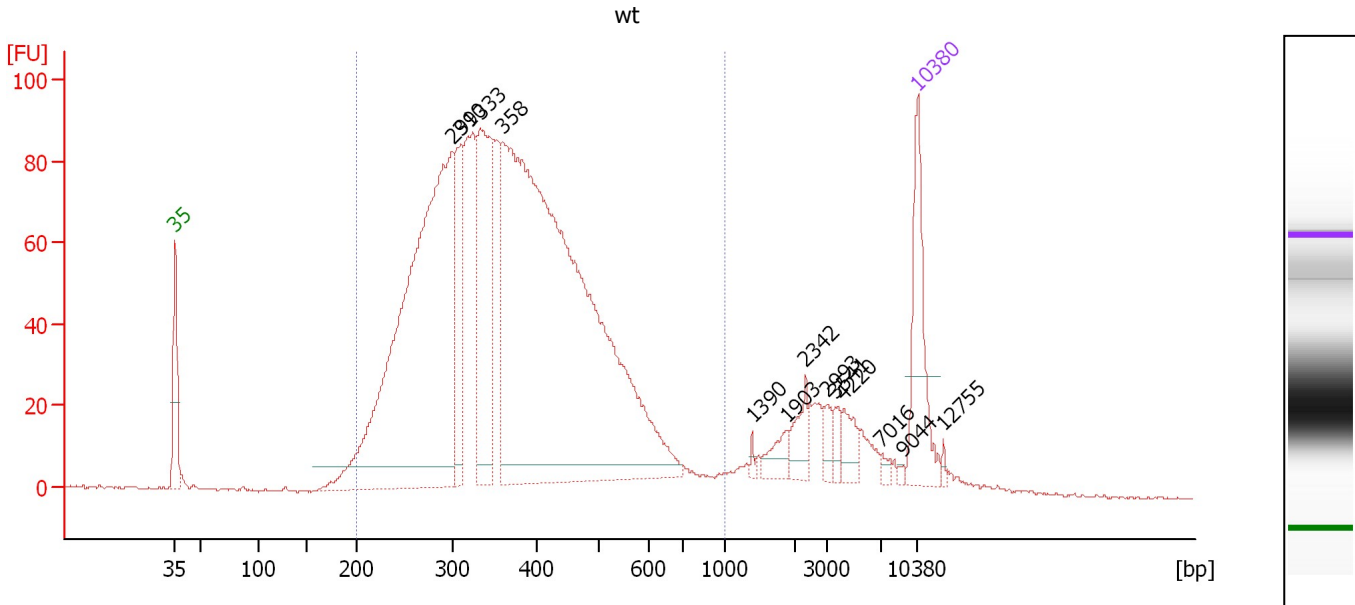
Region table for sample 6 : pb4_sdrip_rna16

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
162	1,241	425	6,316.02	4,121.0	26,200.9	89	35.6

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Electropherogram Summary Continued ...



Overall Results for sample 7 : wt

Number of peaks found: 13 Corr. Area 1: 2,248.8
 Noise: 0.3

Peak table for sample 7 : wt

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	299	752.90	3,815.0		69.10
3	310	109.77	537.2		69.95
4	333	208.48	948.9		71.81
5	358	1,104.82	4,675.0		73.83
6	1,390	3.34	3.6		97.41
7	1,903	16.79	13.4		100.73
8	2,342	23.14	15.0		102.44
9	2,993	11.46	5.8		104.50
10	3,541	10.55	4.5		105.21
11	4,220	18.55	6.7		106.06
12	7,016	4.93	1.1		109.58
13	9,044	2.18	0.4		111.64
14	10,380	75.00	10.9	Upper Marker	113.00
15	12,755	0.00	0.0		115.41

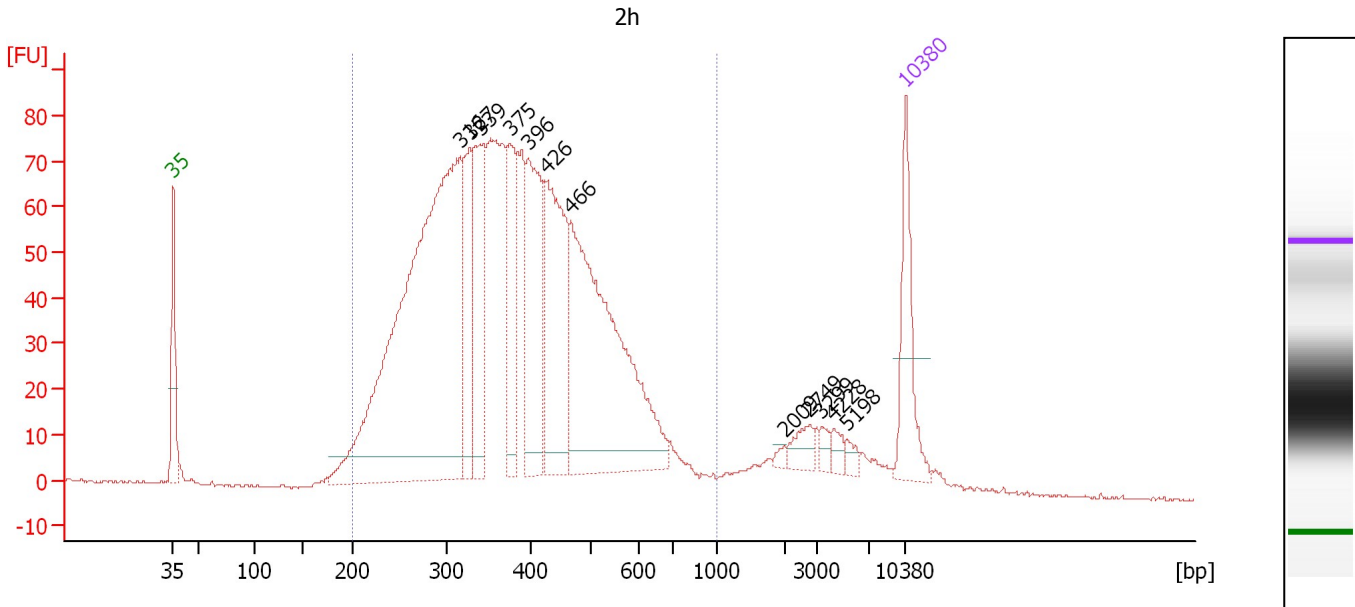
Region table for sample 7 : wt

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	377	2,461.98	2,248.8	10,975.7	89	29.3

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Electropherogram Summary Continued ...



Overall Results for sample 8 : 2h

Number of peaks found: 12 Corr. Area 1: 2,064.7
 Noise: 0.3

Peak table for sample 8 : 2h

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	316	924.71	4,434.9		70.46
3	327	120.37	557.0		71.38
4	339	161.86	723.7		72.29
5	375	128.04	517.0		75.20
6	396	187.87	718.3		76.88
7	426	217.38	773.4		78.66
8	466	450.73	1,466.5		80.95
9	2,009	4.55	3.4		101.38
10	2,749	18.91	10.4		103.73
11	3,299	8.26	3.8		104.90
12	4,228	10.33	3.7		106.07
13	5,198	7.84	2.3		107.29
14	10,380	75.00	10.9	Upper Marker	113.00

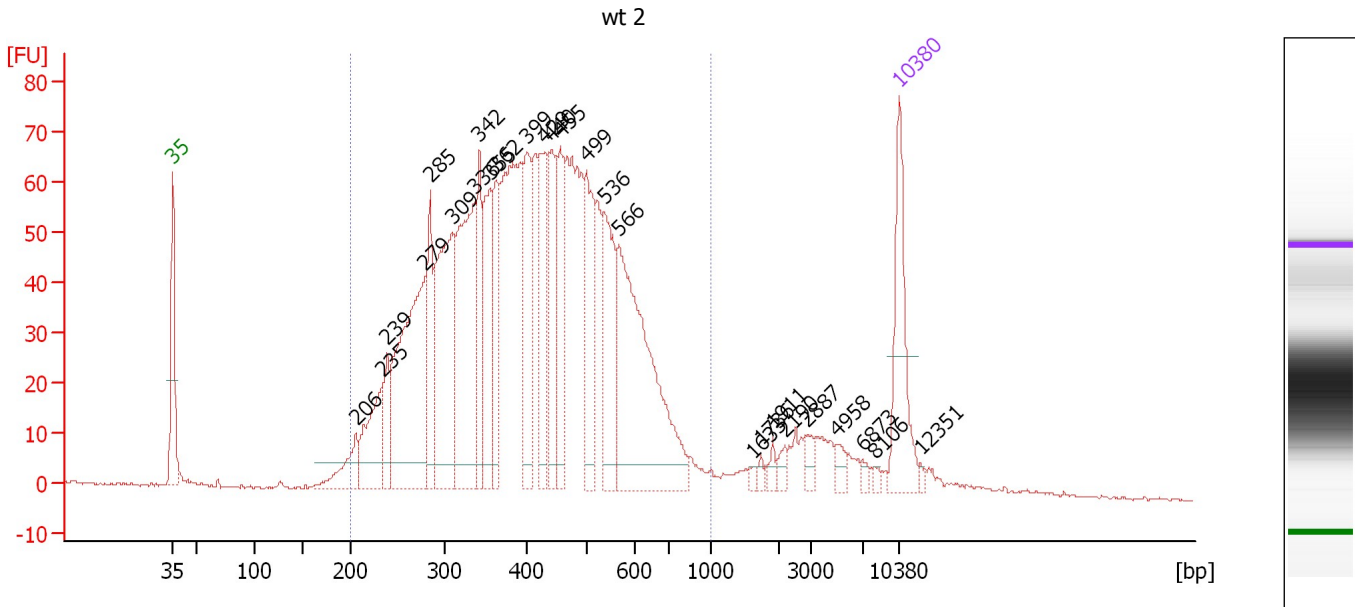
Region table for sample 8 : 2h

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	389	2,786.53	2,064.7	12,114.0	91	29.4

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Electropherogram Summary Continued ...



Overall Results for sample 9 : wt 2

Number of peaks found: 26 Corr. Area 1: 1,900.0
 Noise: 0.3

Peak table for sample 9 : wt 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	206	45.71	335.6		60.67
3	235	87.80	567.1		63.23
4	239	39.82	252.4		63.65
5	279	263.57	1,430.5		67.29
6	285	78.21	416.1		67.81
7	309	208.25	1,021.0		69.91
8	336	212.87	959.8		72.07
9	342	84.29	373.6		72.53
10	355	97.19	415.1		73.56
11	362	75.42	315.3		74.17
12	399	93.31	354.3		77.10
13	429	86.40	305.1		78.85
14	440	91.46	315.1		79.46
15	455	78.86	262.6		80.34
16	499	103.09	313.2		82.85
17	536	104.74	296.1		84.60
18	566	265.33	710.4		85.99
19	1,633	4.33	4.0		98.98
20	1,736	4.16	3.6		99.65
21	1,911	6.40	5.1		100.78
22	2,190	7.86	5.4		101.96
23	2,887	10.18	5.3		104.17
24	4,958	9.80	3.0		106.99
25	6,873	4.07	0.9		109.40

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-26\2018-09-26_001.xad

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Electropherogram Summary Continued ...**... Peak table for sample 9 : wt 2**

Peak	Size [bp]	Conc. [pg/ μ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	8,106	3.48	0.6		110.69
27	10,380	75.00	10.9	Upper Marker	113.00
28	12,351	0.00	0.0		115.00

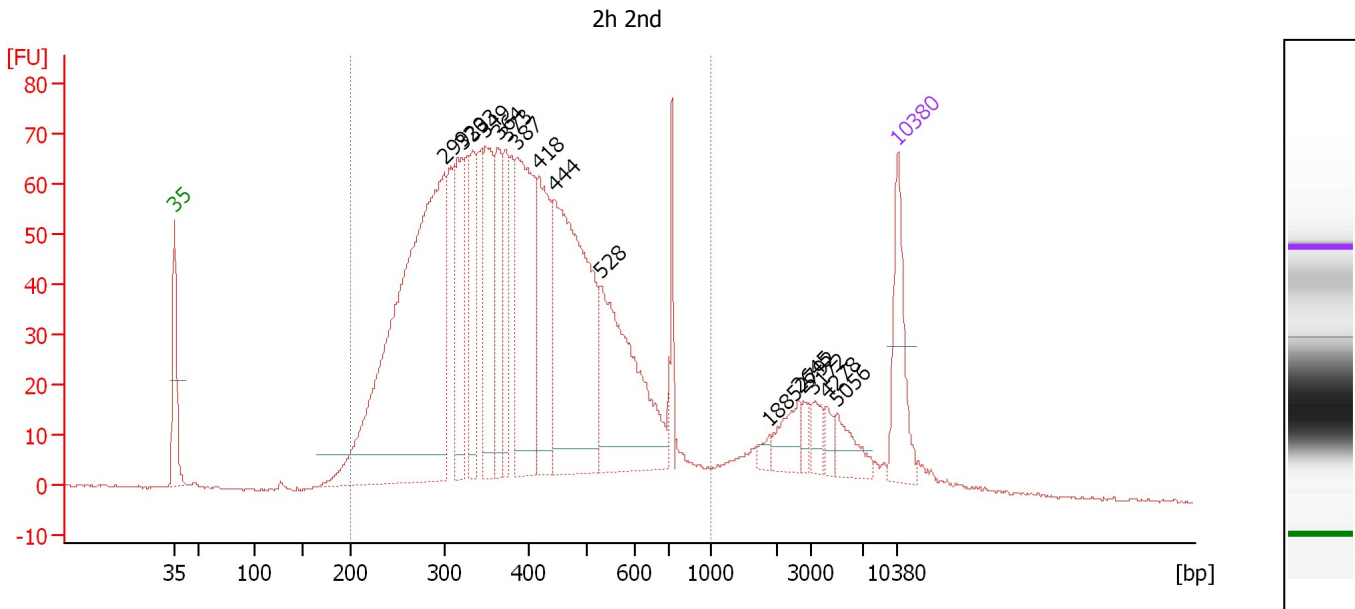
Region table for sample 9 : wt 2

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	420	2,620.12	1,900.0	10,698.4	92	29.8

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-26\2018-09-26_001.xad

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Electropherogram Summary Continued ...



Overall Results for sample 10 : 2h 2nd

Number of peaks found: 16 Corr. Area 1: 1,956.0
 Noise: 0.2

Peak table for sample 10 : 2h 2nd

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	299	844.44	4,275.4		69.12
3	320	147.01	695.0		70.82
4	333	107.22	487.2		71.86
5	349	149.00	647.0		73.10
6	364	107.55	447.9		74.28
7	373	90.39	366.7		75.06
8	387	263.42	1,031.2		76.14
9	418	153.88	557.9		78.21
10	444	405.68	1,384.6		79.70
11	528	265.35	760.9		84.25
12	1,885	8.84	7.1		100.61
13	2,645	34.28	19.6		103.40
14	2,792	11.77	6.4		103.86
15	3,172	19.33	9.2		104.74
16	4,278	13.47	4.8		106.13
17	5,056	31.56	9.5		107.12
18	10,380	75.00	10.9	Upper Marker	113.00

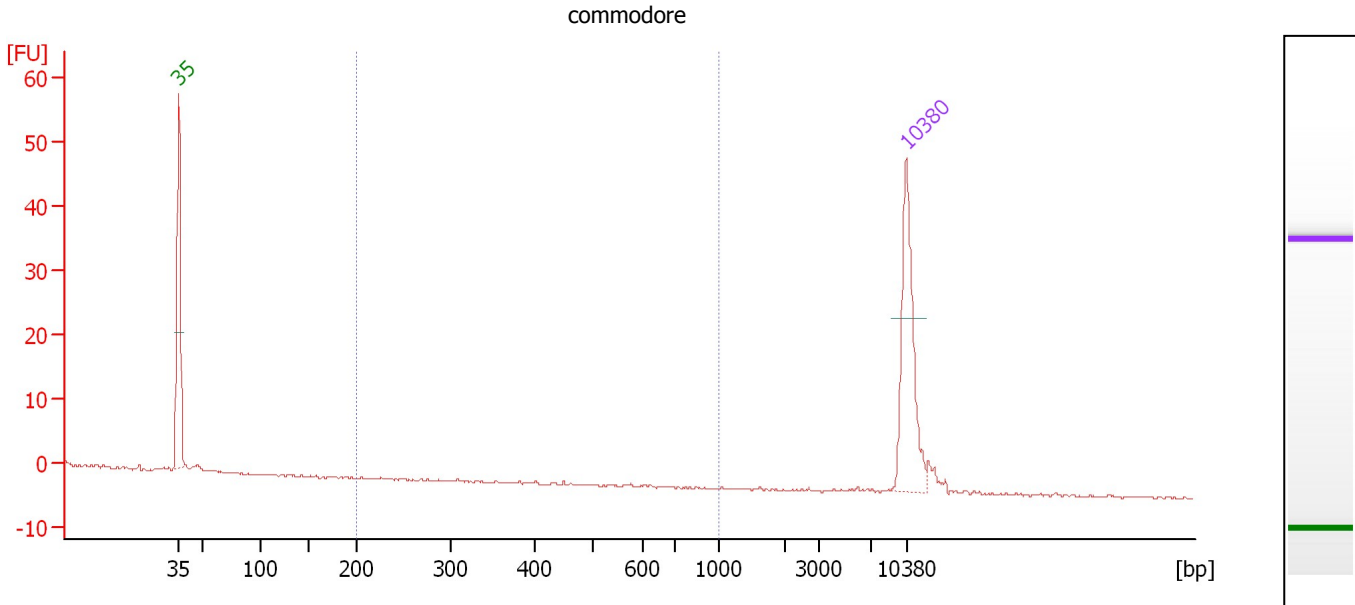
Region table for sample 10 : 2h 2nd

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	401	3,174.99	1,956.0	13,650.2	89	32.1

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-26\2018-09-26_001.xad

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Electropherogram Summary Continued ...



Overall Results for sample 11 : commodore

Number of peaks found: 0 Corr. Area 1: 0.0
 Noise: 0.2

Peak table for sample 11 : commodore

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	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : commodore

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	0	0.00	0.0	0.0	0	0.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-09-26\2018-09-26_001.xad

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