

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-05-22\2015-05-22_001.xad

Created: 5/22/2015 10:02:41 AM
Modified: 5/22/2015 10:35:25 AM

Electrophoresis File Run Summary

Instrument Information:

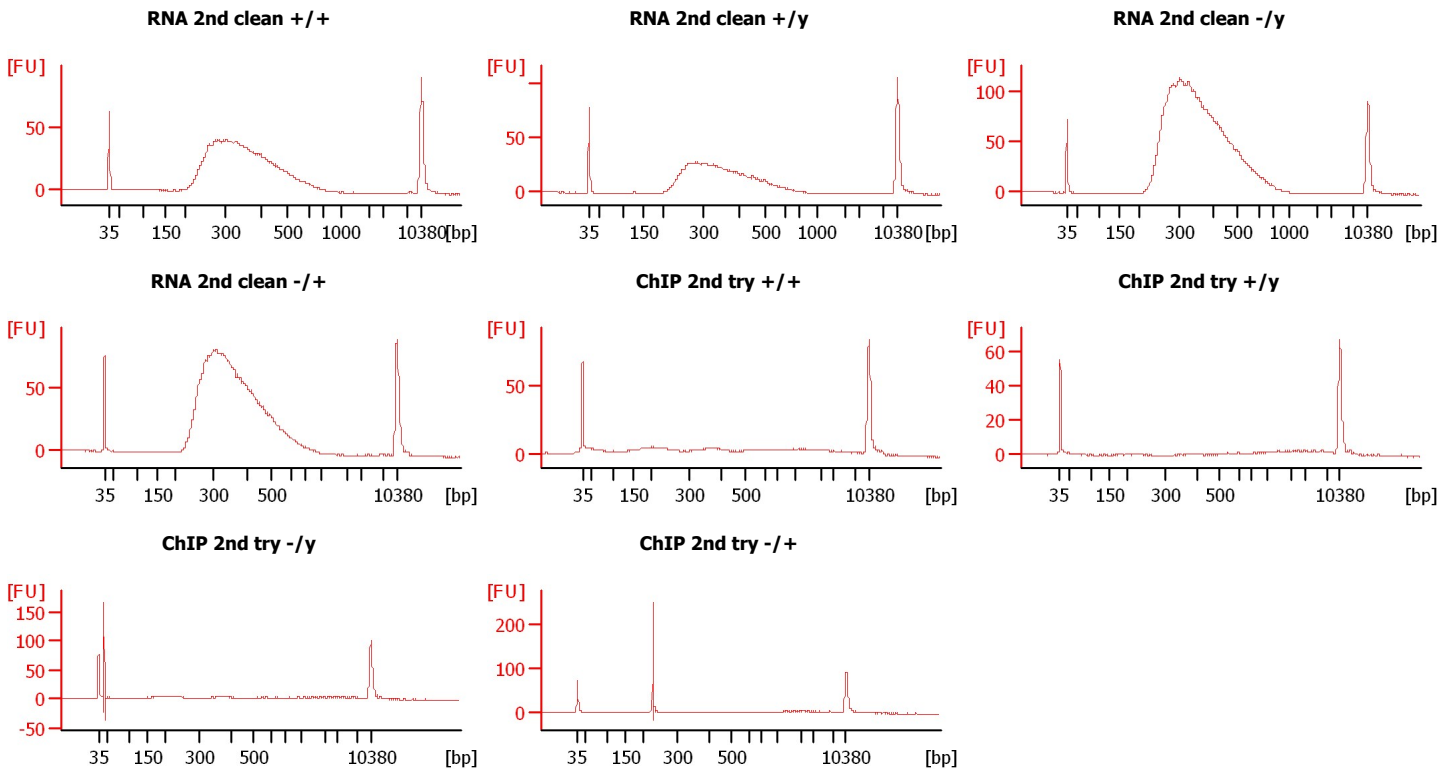
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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
RNA 2nd clean +/+		<input type="checkbox"/>	✓			
RNA 2nd clean +/y		<input type="checkbox"/>	✓			
RNA 2nd clean -/y		<input type="checkbox"/>	✓			
RNA 2nd clean -/+		<input type="checkbox"/>	✓			
ChIP 2nd try +/+		<input type="checkbox"/>	✓			
ChIP 2nd try +/y		<input type="checkbox"/>	✓			
ChIP 2nd try -/y		<input type="checkbox"/>	✓			
ChIP 2nd try -/+		<input type="checkbox"/>	✓			
sample 9		<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

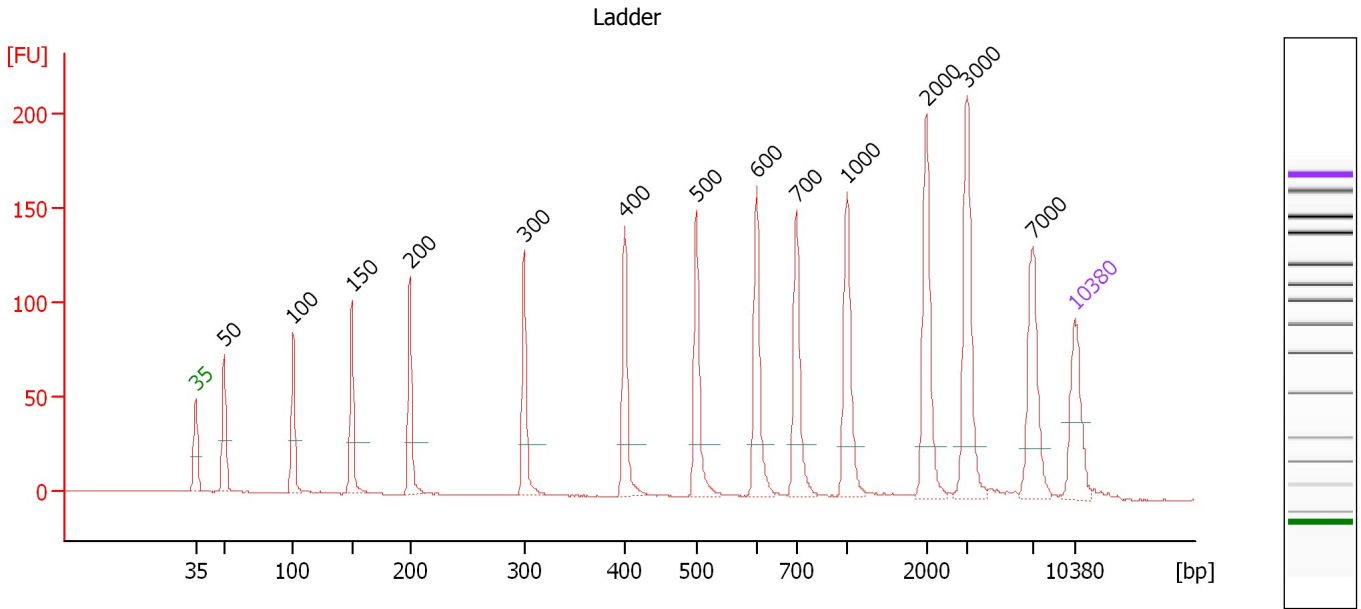
Ladder

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

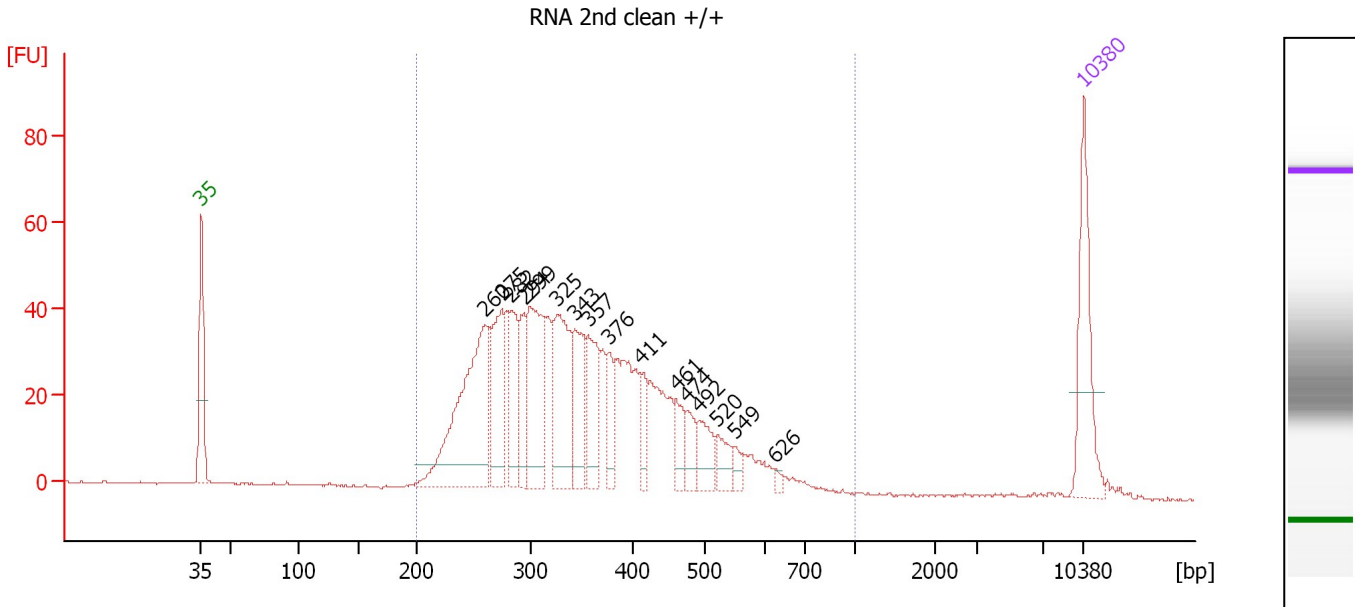
Peak table for Ladder

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	45.29
3	100	150.00	2,272.7	Ladder Peak	50.77
4	150	150.00	1,515.2	Ladder Peak	55.45
5	200	150.00	1,136.4	Ladder Peak	60.08
6	300	150.00	757.6	Ladder Peak	69.17
7	400	150.00	568.2	Ladder Peak	77.19
8	500	150.00	454.5	Ladder Peak	82.93
9	600	150.00	378.8	Ladder Peak	87.68
10	700	150.00	324.7	Ladder Peak	90.87
11	1,000	150.00	227.3	Ladder Peak	94.91
12	2,000	150.00	113.6	Ladder Peak	101.19
13	3,000	150.00	75.8	Ladder Peak	104.46
14	7,000	150.00	32.5	Ladder Peak	109.73
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : RNA 2nd clean +/+

Number of peaks found: 16 Corr. Area 1: 1,065.0
 Noise: 0.2

Peak table for sample 1 : RNA 2nd clean +/+

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	251.30	1,466.2		65.50
3	275	104.52	576.7		66.85
4	282	72.98	392.0		67.53
5	294	58.47	301.2		68.63
6	299	130.01	659.3		69.05
7	325	122.29	570.2		71.17
8	343	72.15	318.8		72.61
9	357	74.59	316.9		73.71
10	376	34.51	139.0		75.27
11	411	27.92	102.8		77.85
12	461	30.07	98.9		80.69
13	474	26.10	83.4		81.45
14	492	35.46	109.2		82.46
15	520	24.46	71.3		83.86
16	549	11.17	30.8		85.25
17	626	4.24	10.3		88.51
18	10,380	75.00	10.9	Upper Marker	113.00

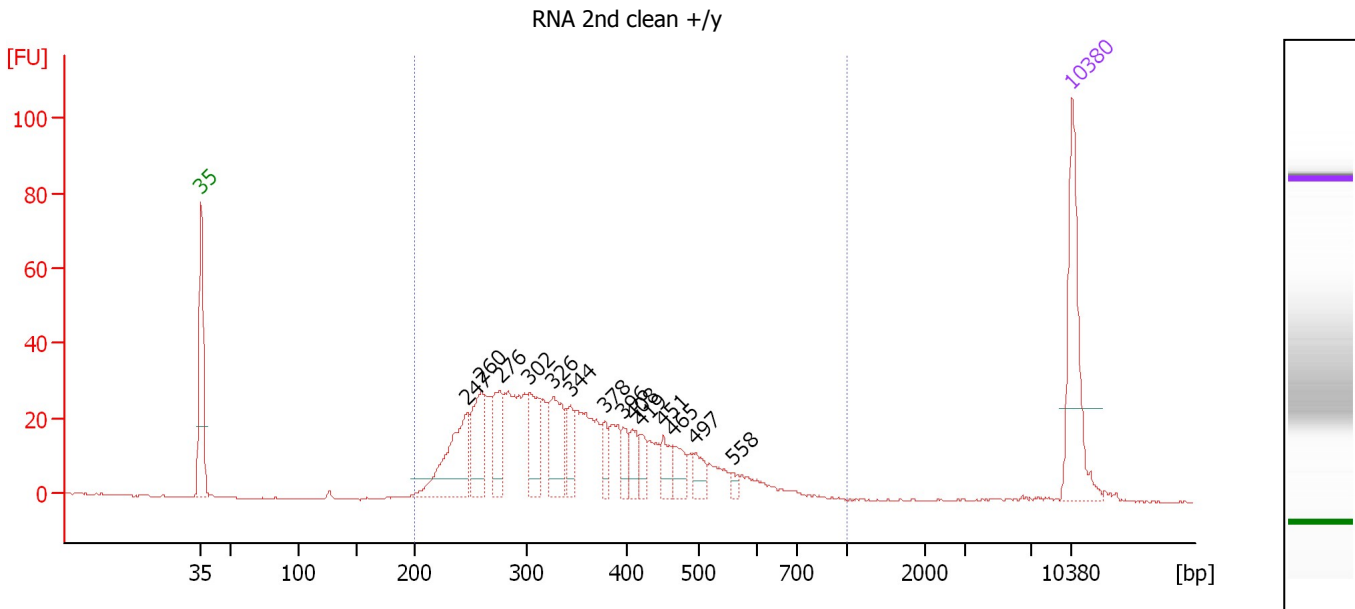
Region table for sample 1 : RNA 2nd clean +/+

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	360	1,000	1,065.0	6,917.2	97	28.0	1,493.25	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 2 : RNA 2nd clean +/y

Number of peaks found: 14 Corr. Area 1: 718.7
 Noise: 0.2

Peak table for sample 2 : RNA 2nd clean +/y

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	247	99.97	612.1		64.39
3	260	67.69	394.8		65.50
4	276	50.49	276.9		67.00
5	302	50.59	253.4		69.36
6	326	58.37	271.3		71.25
7	344	26.18	115.4		72.66
8	378	17.36	69.6		75.41
9	396	17.72	67.8		76.86
10	408	20.26	75.3		77.64
11	419	14.60	52.8		78.28
12	451	20.79	69.8		80.12
13	465	20.95	68.3		80.89
14	497	16.84	51.4		82.74
15	558	5.74	15.6		85.69
16	10,380	75.00	10.9	Upper Marker	113.00

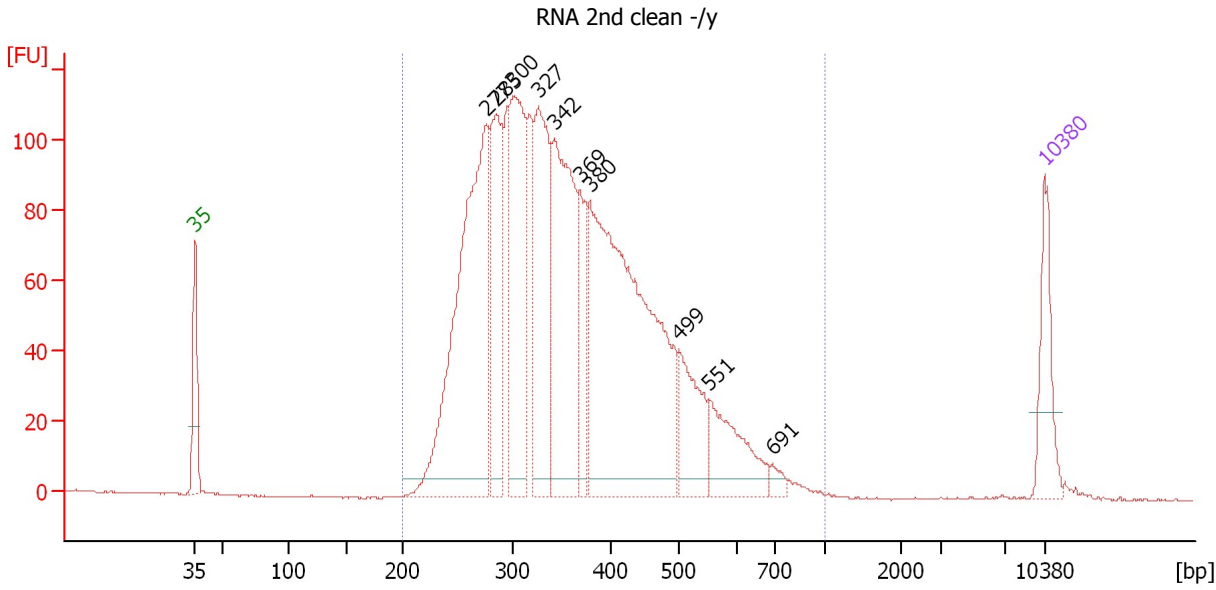
Region table for sample 2 : RNA 2nd clean +/y

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	359	1,000	718.7	3,984.2	98	29.0	852.63	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 3 : RNA 2nd clean -/y

Number of peaks found: 10 Corr. Area 1: 2,569.1
 Noise: 0.2

Peak table for sample 3 : RNA 2nd clean -/y

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	277	696.75	3,816.9		67.04
3	285	249.13	1,325.4		67.78
4	300	344.86	1,739.9		69.19
5	327	308.68	1,432.1		71.30
6	342	399.77	1,768.7		72.57
7	369	121.21	497.3		74.73
8	380	802.44	3,202.2		75.56
9	499	128.74	391.1		82.86
10	551	127.72	351.1		85.36
11	691	14.46	31.7		90.59
12	10,380	75.00	10.9	Upper Marker	113.00

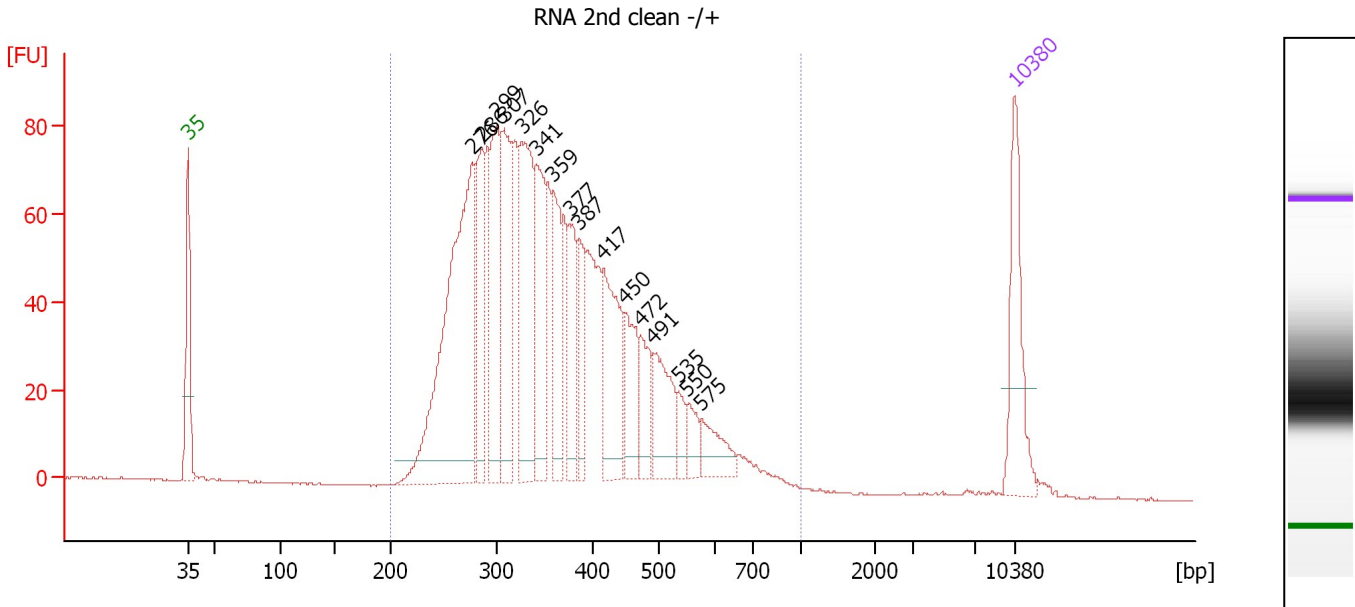
Region table for sample 3 : RNA 2nd clean -/y

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	368	1,000	2,569.1	15,300.1	100	27.4	3,395.94	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 4 : RNA 2nd clean -/+

Number of peaks found: 16 Corr. Area 1: 1,808.2
 Noise: 0.1

Peak table for sample 4 : RNA 2nd clean -/+

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	276	418.31	2,292.5		67.03
3	286	111.01	588.3		67.88
4	299	156.65	792.9		69.10
5	307	139.18	686.7		69.74
6	326	191.07	887.4		71.27
7	341	114.33	508.2		72.45
8	359	88.31	372.3		73.94
9	377	76.77	308.7		75.34
10	387	55.04	215.5		76.15
11	417	122.30	444.1		78.18
12	450	67.47	227.4		80.03
13	472	47.28	151.9		81.30
14	491	75.42	232.6		82.43
15	535	19.46	55.1		84.59
16	550	23.16	63.8		85.32
17	575	36.49	96.2		86.49
18	10,380	75.00	10.9	Upper Marker	113.00

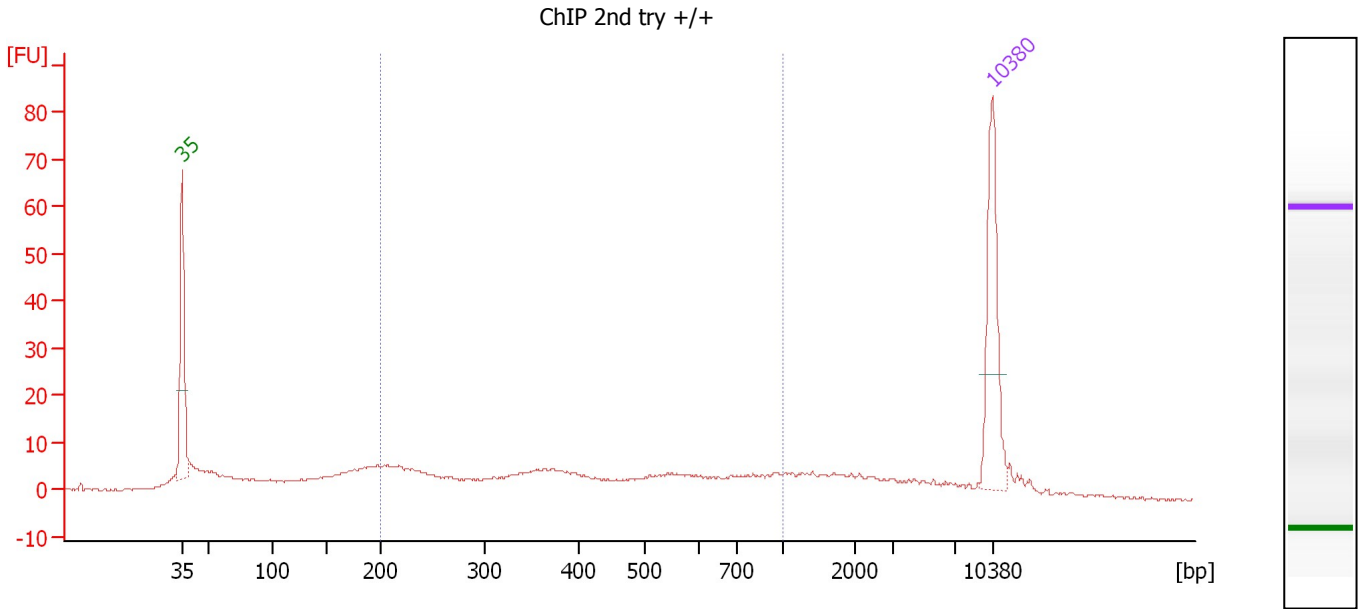
Region table for sample 4 : RNA 2nd clean -/+

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	371	1,000	1,808.2	10,031.3	99	27.8	2,244.80	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 5 : ChIP 2nd try +/-

Number of peaks found: 0 Corr. Area 1: 200.6
 Noise: 0.2

Peak table for sample 5 : ChIP 2nd try +/-

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

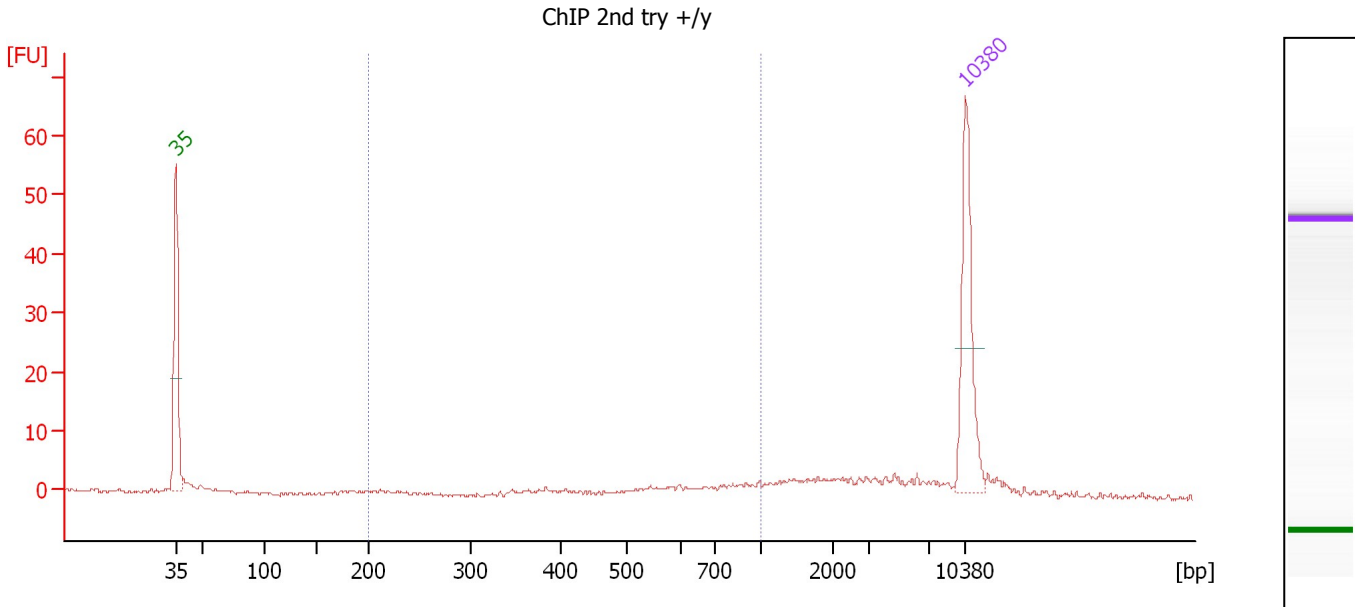
Region table for sample 5 : ChIP 2nd try +/-

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	454	1,000	200.6	1,256.1	48	44.2	288.22	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 6 : ChIP 2nd try +/-

Number of peaks found: 0 Corr. Area 1: 24.4
 Noise: 0.4

Peak table for sample 6 : ChIP 2nd try +/-

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

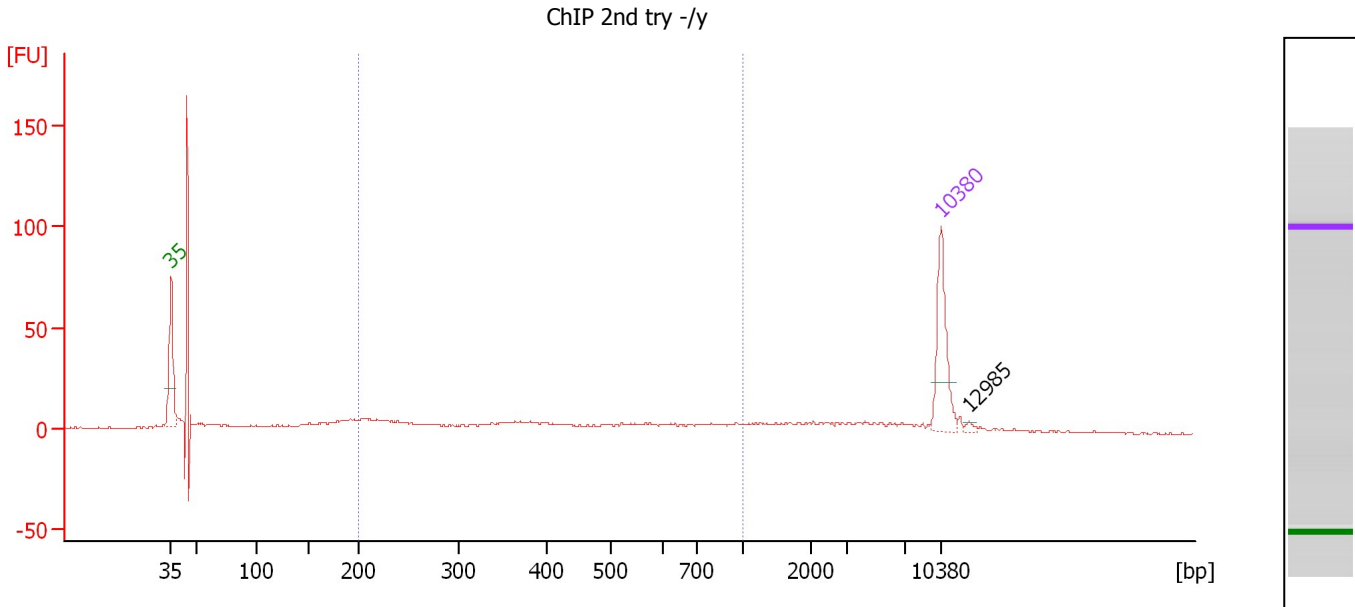
Region table for sample 6 : ChIP 2nd try +/-

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	630	1,000	24.4	114.9	28	30.8	39.68	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 7 : ChIP 2nd try -/y

Number of peaks found: 1 Corr. Area 1: 168.7
 Noise: 0.5

Peak table for sample 7 : ChIP 2nd try -/y

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
3	12,985	0.00	0.0		115.52

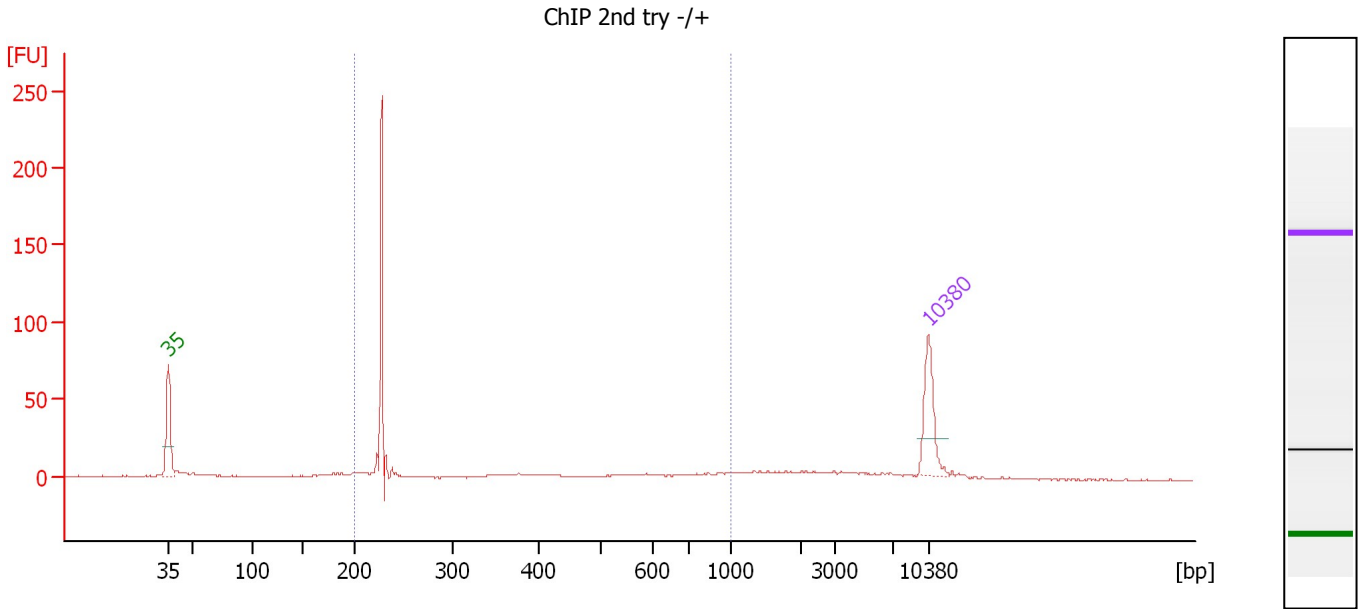
Region table for sample 7 : ChIP 2nd try -/y

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	452	1,000	168.7	925.8	39	44.6	210.65	Blue

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Electropherogram Summary Continued ...



Overall Results for sample 8 : ChIP 2nd try -/+

Number of peaks found: 0 Corr. Area 1: 189.6
 Noise: 0.5

Peak table for sample 8 : ChIP 2nd try -/+

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 8 : ChIP 2nd try -/+

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	382	1,000	189.6	1,487.2	57	56.0	271.59	Blue

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Gel Image

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Invalid Samples

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.