

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-06\2015-08-06_001.xad

Created: 8/6/2015 12:06:11 PM
Modified: 8/6/2015 1:01:41 PM

Electrophoresis File Run Summary

Instrument Information:

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

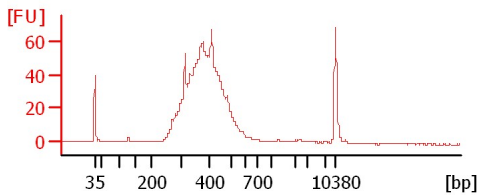
Assay Information:

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

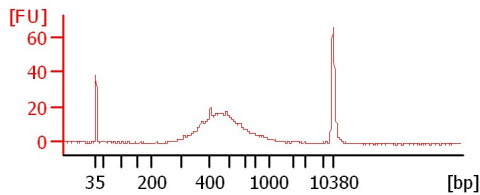
Chip Information:

Chip Lot #:
Reagent Kit Lot #:
Chip Comments:

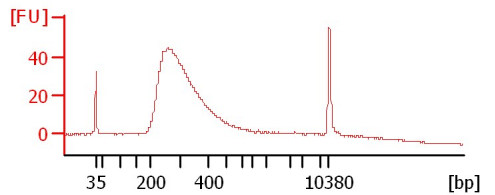
MiSeq 155 library pool (1:4)



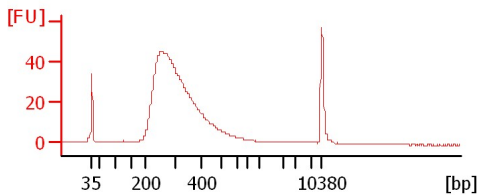
M155P 0.55x



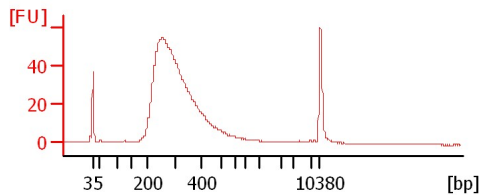
PC1 lib



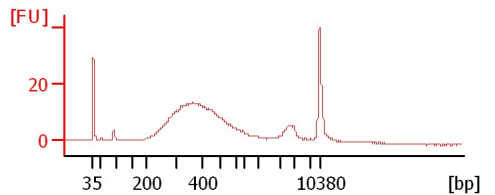
PC2 lib



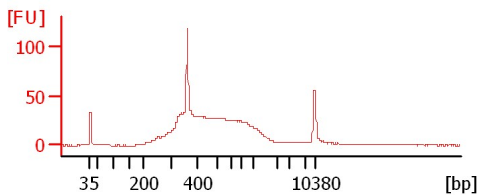
PC3 lib



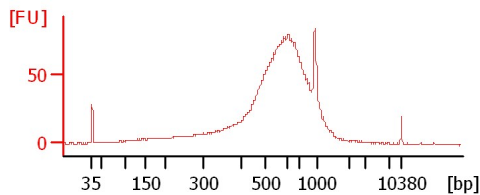
RAD ANTHO 8-5-15 Final



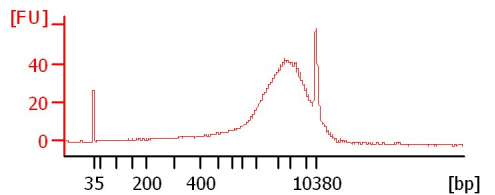
Greg and Fu



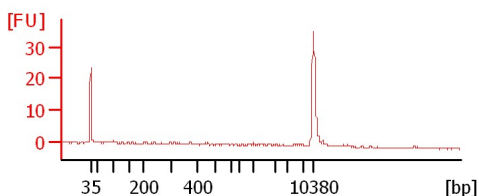
H3K4m 1



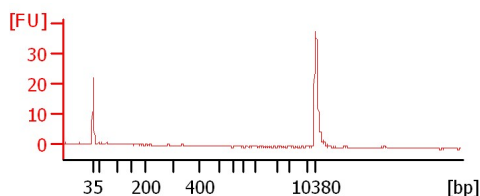
H3K4m 2



igG Rabbit 1



igG Rabbit 2



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
MiSeq 155 library pool (1:4)		<input type="checkbox"/>	✓			
M155P 0.55x		<input type="checkbox"/>	✓			
PC1 lib		<input type="checkbox"/>	✓			
PC2 lib		<input type="checkbox"/>	✓			
PC3 lib		<input type="checkbox"/>	✓			
RAD ANTHO 8-5-15 Final		<input type="checkbox"/>	✓			
Greg and Fu		<input type="checkbox"/>	✓			
H3K4m 1		<input type="checkbox"/>	✓			
H3K4m 2		<input type="checkbox"/>	✓			
igG Rabbit 1		<input type="checkbox"/>	✓			
igG Rabbit 2		<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

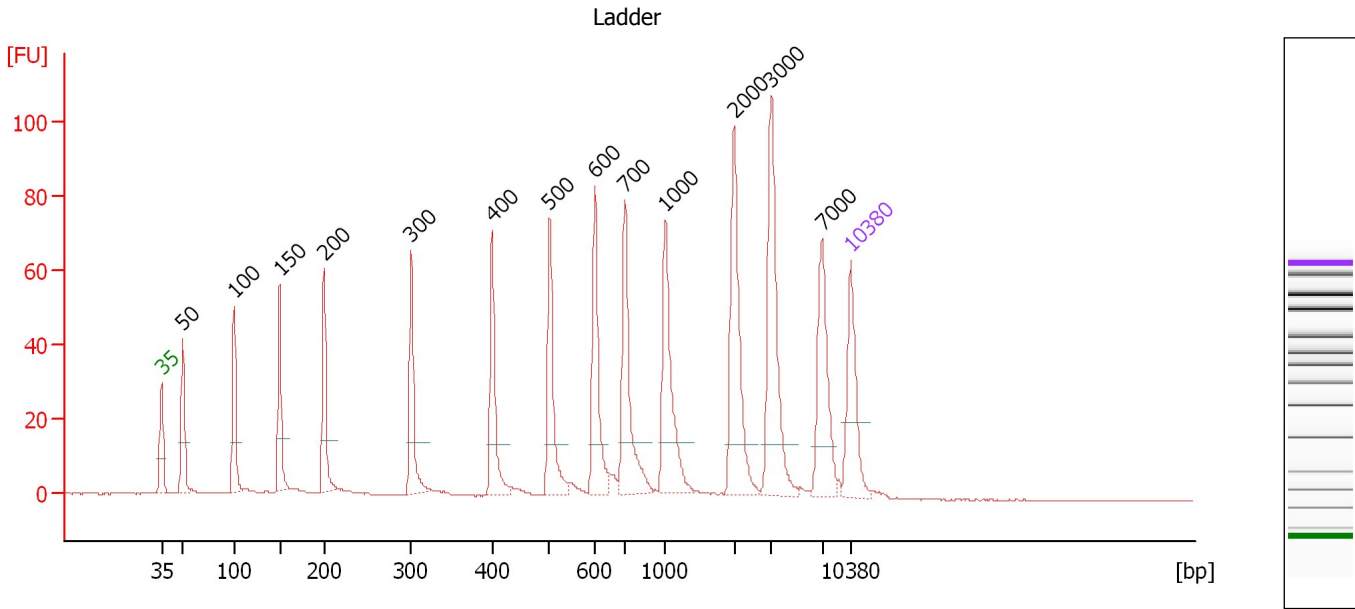
Ladder

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: 0.1

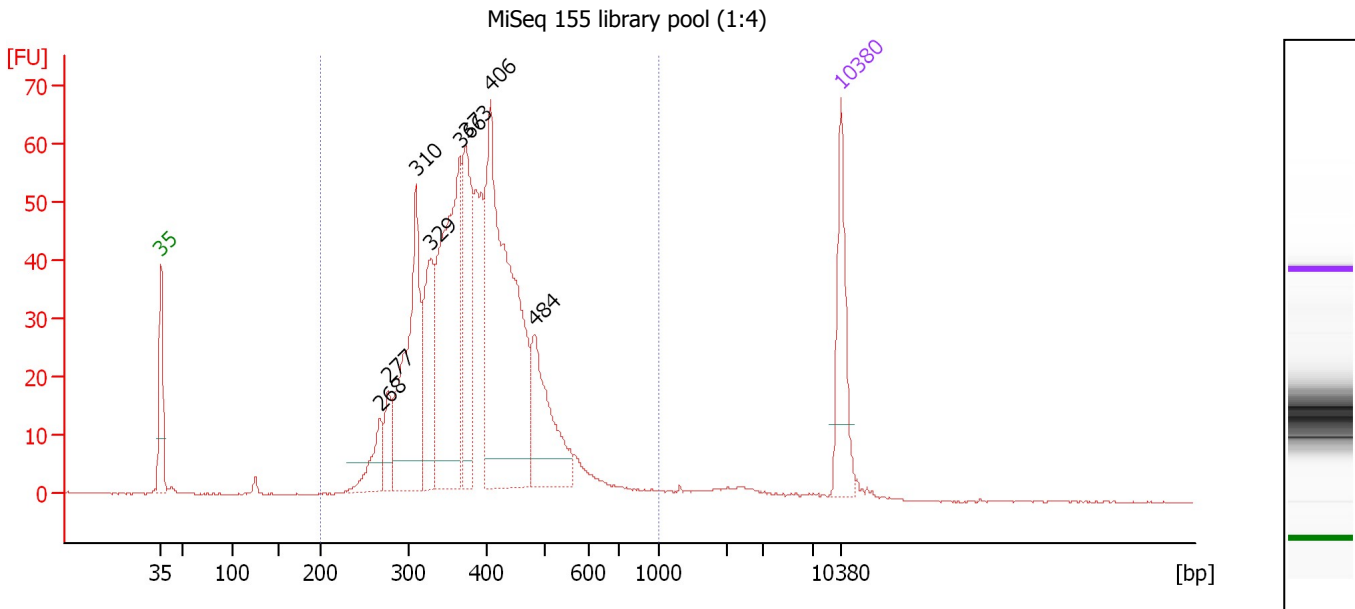
Peak table for Ladder

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	45.17
3	100	150.00	2,272.7	Ladder Peak	50.36
4	150	150.00	1,515.2	Ladder Peak	55.02
5	200	150.00	1,136.4	Ladder Peak	59.51
6	300	150.00	757.6	Ladder Peak	68.39
7	400	150.00	568.2	Ladder Peak	76.57
8	500	150.00	454.5	Ladder Peak	82.41
9	600	150.00	378.8	Ladder Peak	87.01
10	700	150.00	324.7	Ladder Peak	90.05
11	1,000	150.00	227.3	Ladder Peak	94.16
12	2,000	150.00	113.6	Ladder Peak	101.14
13	3,000	150.00	75.8	Ladder Peak	104.93
14	7,000	150.00	32.5	Ladder Peak	110.08
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : MiSeq 155 library pool (1:4)

Number of peaks found: 8 Corr. Area 1: 950.4
 Noise: 0.1

Peak table for sample 1 : MiSeq 155 library pool (1:4)

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	268	53.05	299.9		65.55
3	277	39.87	217.9		66.37
4	310	237.52	1,160.2		69.22
5	329	125.29	577.0		70.76
6	366	315.32	1,305.8		73.78
7	373	154.55	627.4		74.38
8	406	444.19	1,658.6		76.90
9	484	128.71	403.2		81.46
10	10,380	75.00	10.9	Upper Marker	113.00

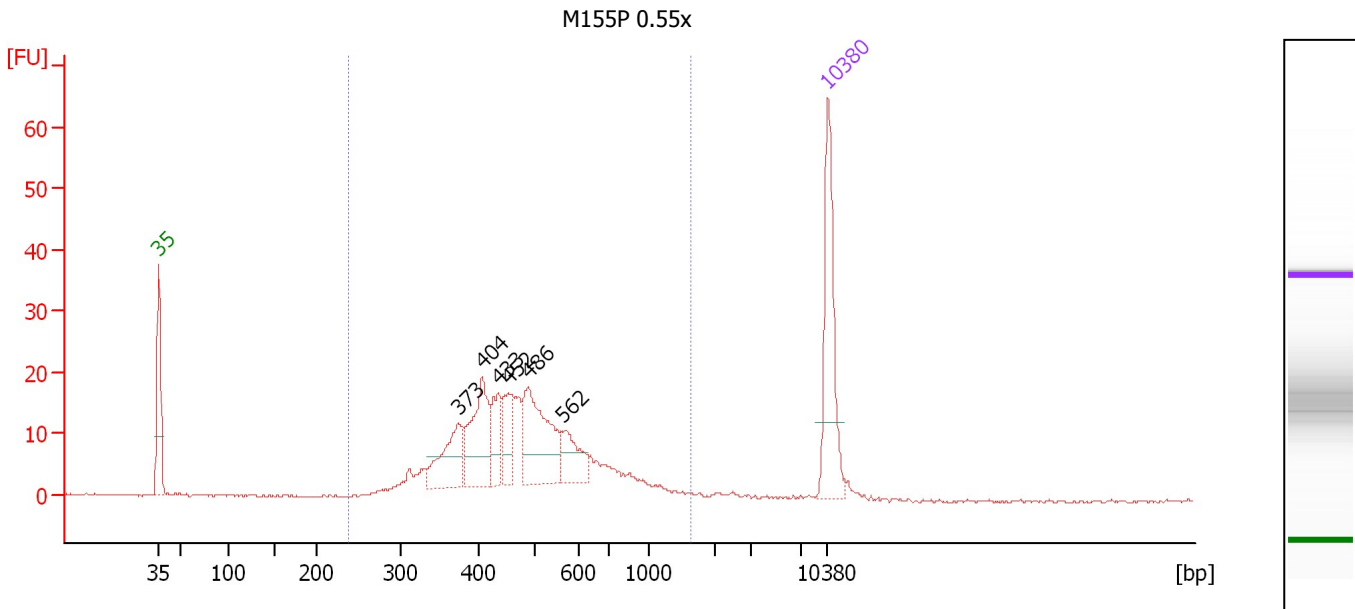
Region table for sample 1 : MiSeq 155 library pool (1:4)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
200	392	1,000	950.4	7,223.4	96	21.7	1,770.83

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Electropherogram Summary Continued ...



Overall Results for sample 2 : M155P 0.55x

Number of peaks found: 6 Corr. Area 1: 307.2
 Noise: 0.2

Peak table for sample 2 : M155P 0.55x

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	373	56.86	231.1		74.35
3	404	74.12	278.0		76.80
4	433	33.17	116.1		78.47
5	452	35.38	118.7		79.59
6	486	92.71	289.0		81.60
7	562	32.81	88.4		85.28
8	10,380	75.00	10.9	Upper Marker	113.00

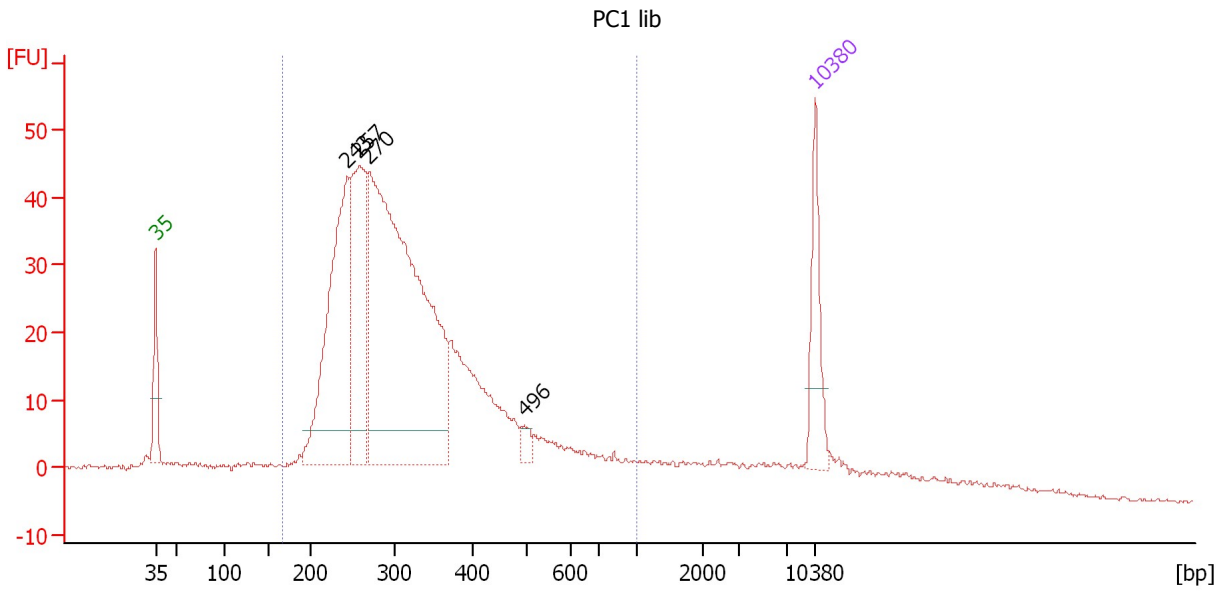
Region table for sample 2 : M155P 0.55x

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
239	501	1,637	307.2	1,717.9	97	34.2	511.79

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Electropherogram Summary Continued ...



Overall Results for sample 3 : PC1 lib

Number of peaks found: 4 Corr. Area 1: 899.6
 Noise: 0.2

Peak table for sample 3 : PC1 lib

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	243	426.81	2,656.1		63.37
3	257	292.62	1,726.1		64.56
4	270	973.23	5,469.4		65.69
5	496	15.87	48.5		82.16
6	10,380	75.00	10.9	Upper Marker	113.00

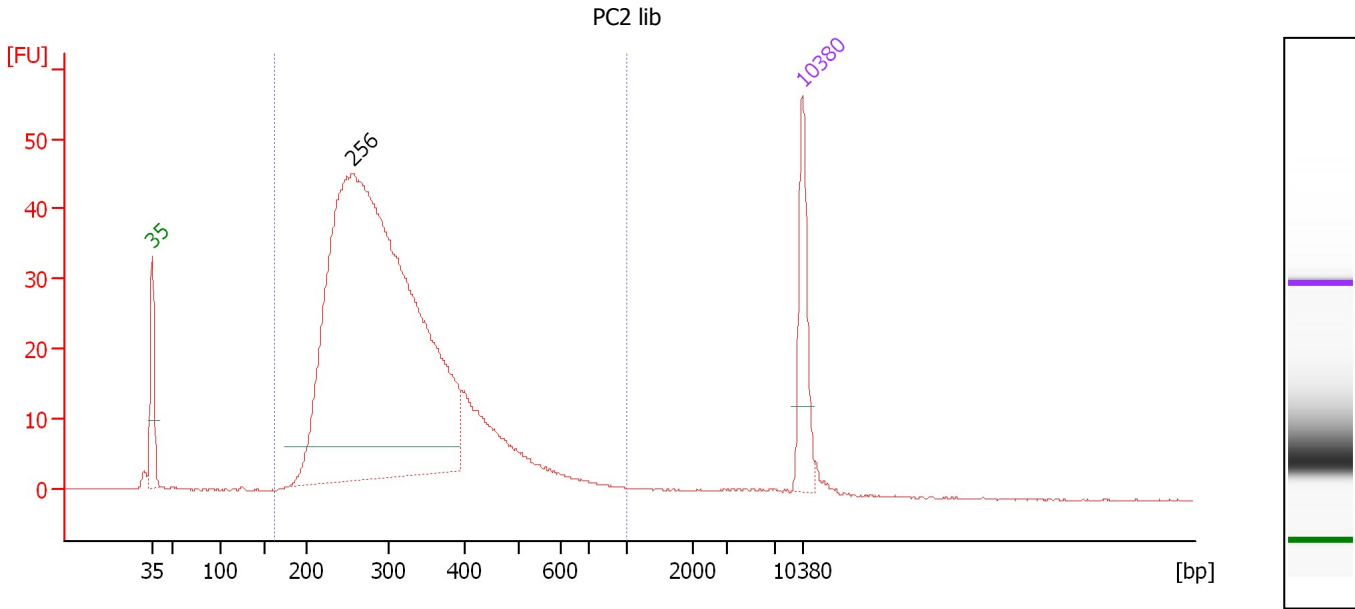
Region table for sample 3 : PC1 lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
167	336	1,000	899.6	11,180.2	87	36.6	2,193.76

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Electropherogram Summary Continued ...



Overall Results for sample 4 : PC2 lib

Number of peaks found: 1 Corr. Area 1: 834.8
 Noise: 0.1

Peak table for sample 4 : PC2 lib

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	256	1,674.55	9,914.1		64.48
3	10,380	75.00	10.9	Upper Marker	113.00

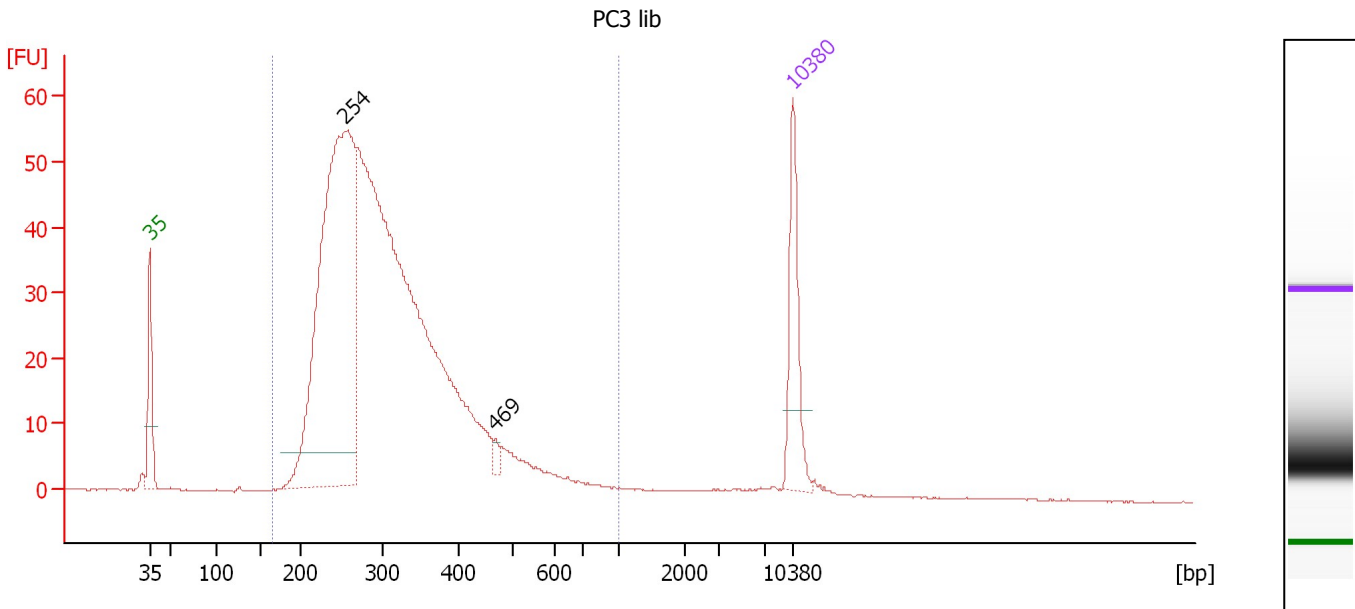
Region table for sample 4 : PC2 lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
163	321	1,000	834.8	9,795.0	97	30.6	1,892.58

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-06\2015-08-06_001.xad

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Electropherogram Summary Continued ...



Overall Results for sample 5 : PC3 lib

Number of peaks found: 2 Corr. Area 1: 972.6
 Noise: 0.1

Peak table for sample 5 : PC3 lib

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	254	768.52	4,585.3		64.30
3	469	9.40	30.4		80.61
4	10,380	75.00	10.9	Upper Marker	113.00

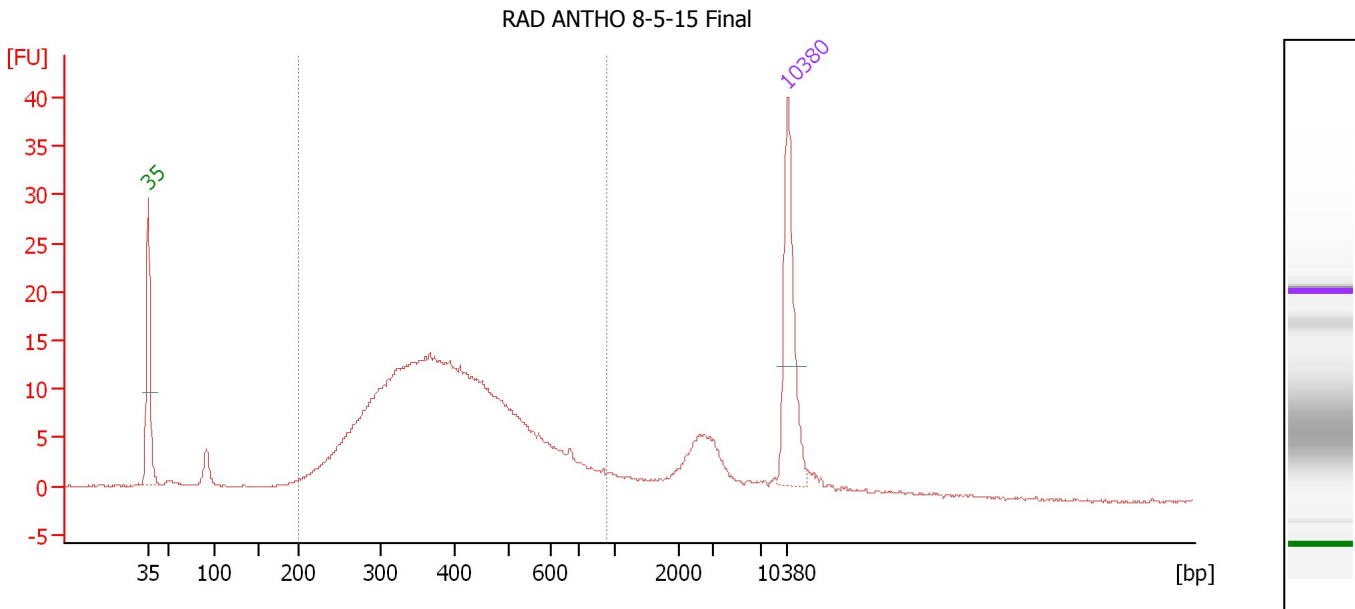
Region table for sample 5 : PC3 lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
165	316	1,000	972.6	10,622.8	97	30.4	2,029.05

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-06\2015-08-06_001.xad

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Electropherogram Summary Continued ...



Overall Results for sample 6 : RAD ANTHO 8-5-15 Final

Number of peaks found: 0 Corr. Area 1: 336.7
 Noise: 0.1

Peak table for sample 6 : RAD ANTHO 8-5-15 Final

Pea k	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

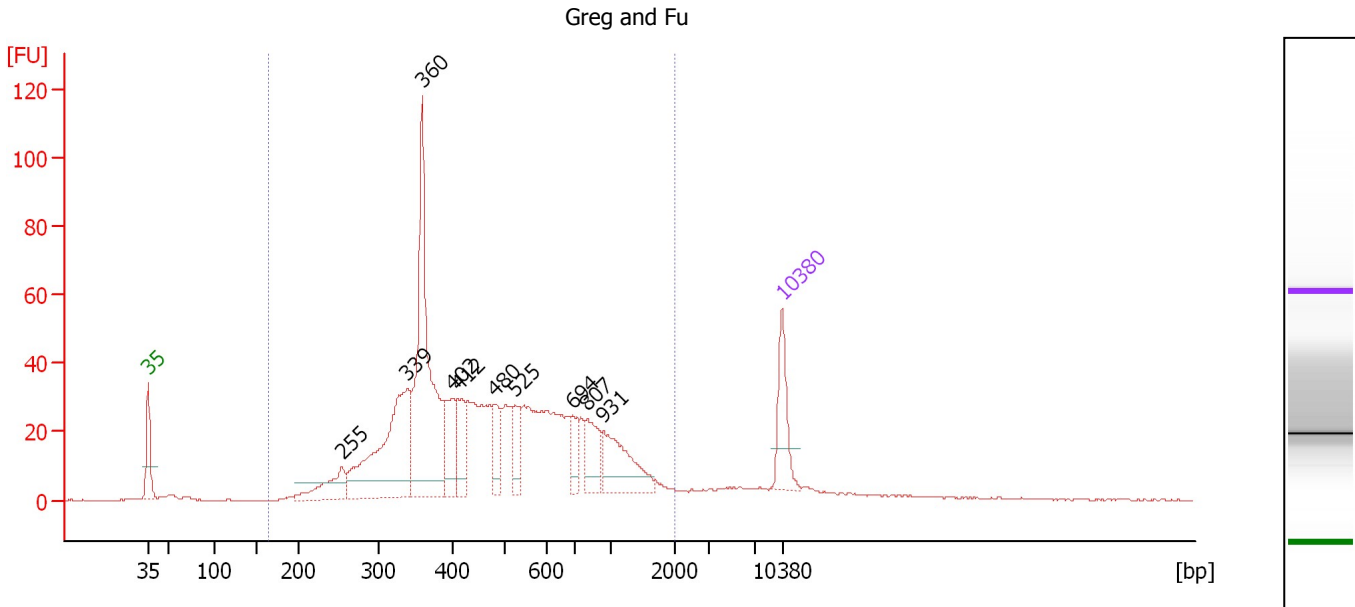
Region table for sample 6 : RAD ANTHO 8-5-15 Final

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
200	411	932	336.7	3,594.2	82	30.5	869.24

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



Overall Results for sample 7 : Greg and Fu

Number of peaks found: 10 Corr. Area 1: 1,051.3
 Noise: 0.2

Peak table for sample 7 : Greg and Fu

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	255	89.57	532.7		64.37
3	339	378.50	1,689.7		71.61
4	360	484.62	2,042.0		73.26
5	402	88.11	332.2		76.68
6	412	73.99	272.1		77.26
7	480	61.39	193.6		81.27
8	525	54.09	156.1		83.56
9	694	42.65	93.1		89.86
10	807	73.80	138.6		91.51
11	931	120.79	196.5		93.22
12	10,380	75.00	10.9	Upper Marker	113.00

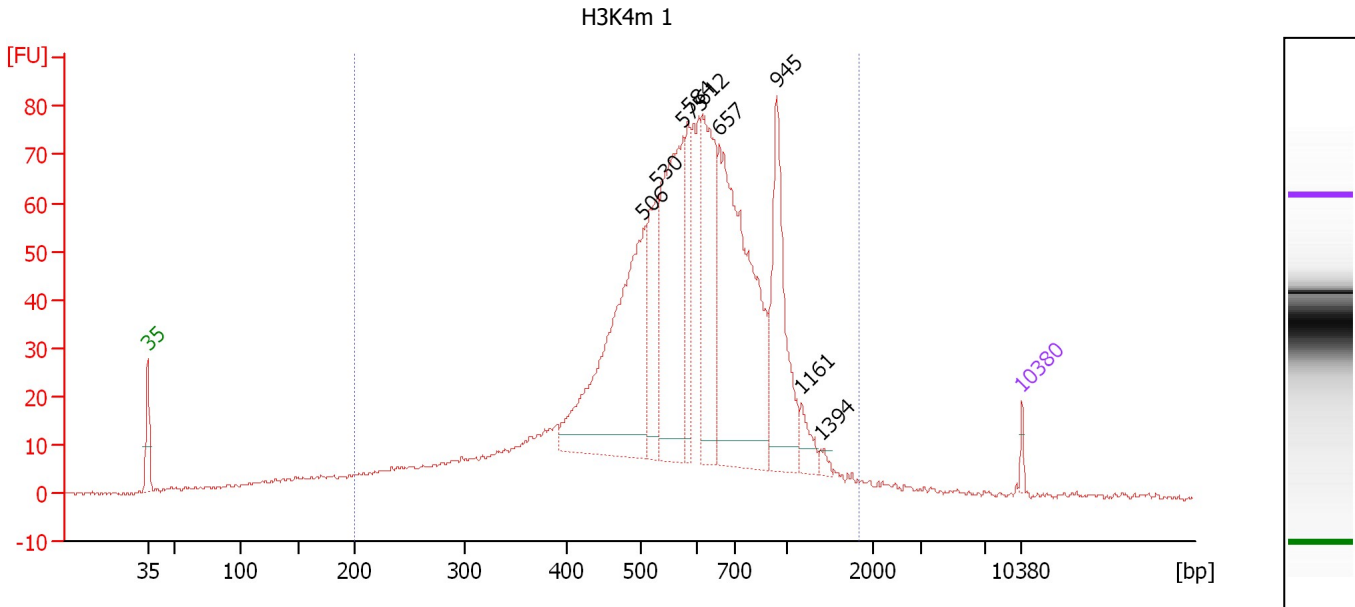
Region table for sample 7 : Greg and Fu

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
164	545	2,008	1,051.3	8,045.1	93	54.0	2,246.23

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Electropherogram Summary Continued ...



Overall Results for sample 8 : H3K4m 1

Number of peaks found: 9 Corr. Area 1: 1,499.2
 Noise: 0.4

Peak table for sample 8 : H3K4m 1

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	506	4,964.67	14,861.7		82.70
3	530	1,556.36	4,447.1		83.80
4	575	3,455.90	9,109.8		85.85
5	584	1,029.32	2,670.2		86.28
6	612	2,245.58	5,555.7		87.39
7	657	5,221.64	12,033.4		88.76
8	945	2,116.55	3,392.8		93.41
9	1,161	304.21	396.9		95.29
10	1,394	88.22	95.9		96.91
11	10,380	75.00	10.9	Upper Marker	113.00

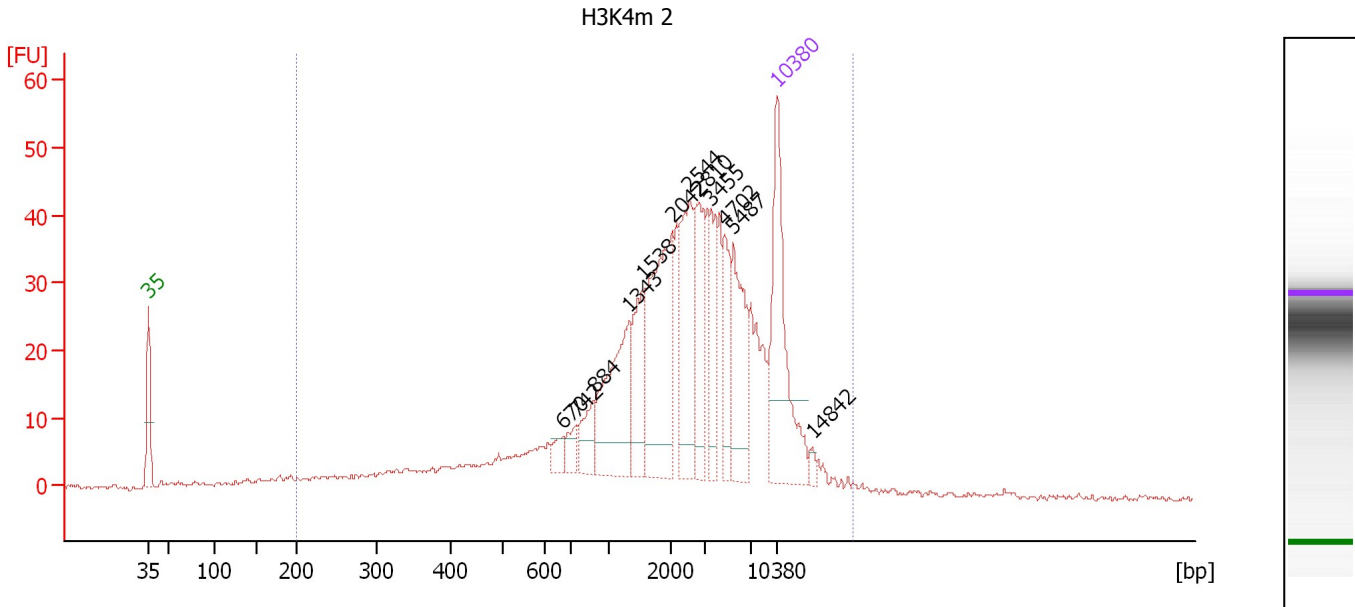
Region table for sample 8 : H3K4m 1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
200	624	1,838	1,499.2	95,823.4	93	37.8	32,468.38

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Electropherogram Summary Continued ...



Overall Results for sample 9 : H3K4m 2

Number of peaks found: 12 Corr. Area 1: 722.1
 Noise: 0.3

Peak table for sample 9 : H3K4m 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	670	8.68	19.6		89.13
3	742	10.57	21.6		90.62
4	884	18.58	31.8		92.58
5	1,343	65.48	73.9		96.55
6	1,538	36.57	36.0		97.92
7	2,042	84.91	63.0		101.30
8	2,544	56.93	33.9		103.20
9	2,810	43.07	23.2		104.21
10	3,455	27.72	12.2		105.52
11	4,702	24.71	8.0		107.12
12	5,487	47.80	13.2		108.13
13	10,380	75.00	10.9	Upper Marker	113.00
14	14,842	0.00	0.0		116.86

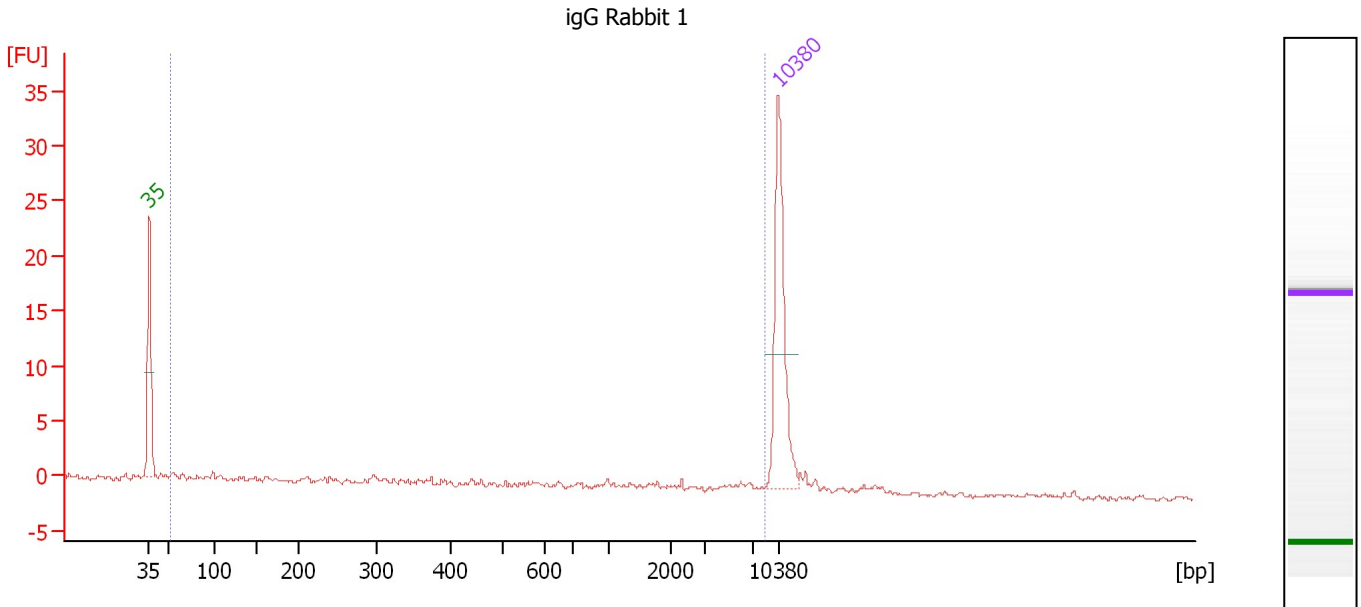
Region table for sample 9 : H3K4m 2

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
200	3,990	20,155	722.1	1,027.8	97	93.6	737.37

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Electropherogram Summary Continued ...



Overall Results for sample 10 : igG Rabbit 1

Number of peaks found: 0 Corr. Area 1: 9.9
 Noise: 0.2

Peak table for sample 10 : igG Rabbit 1

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

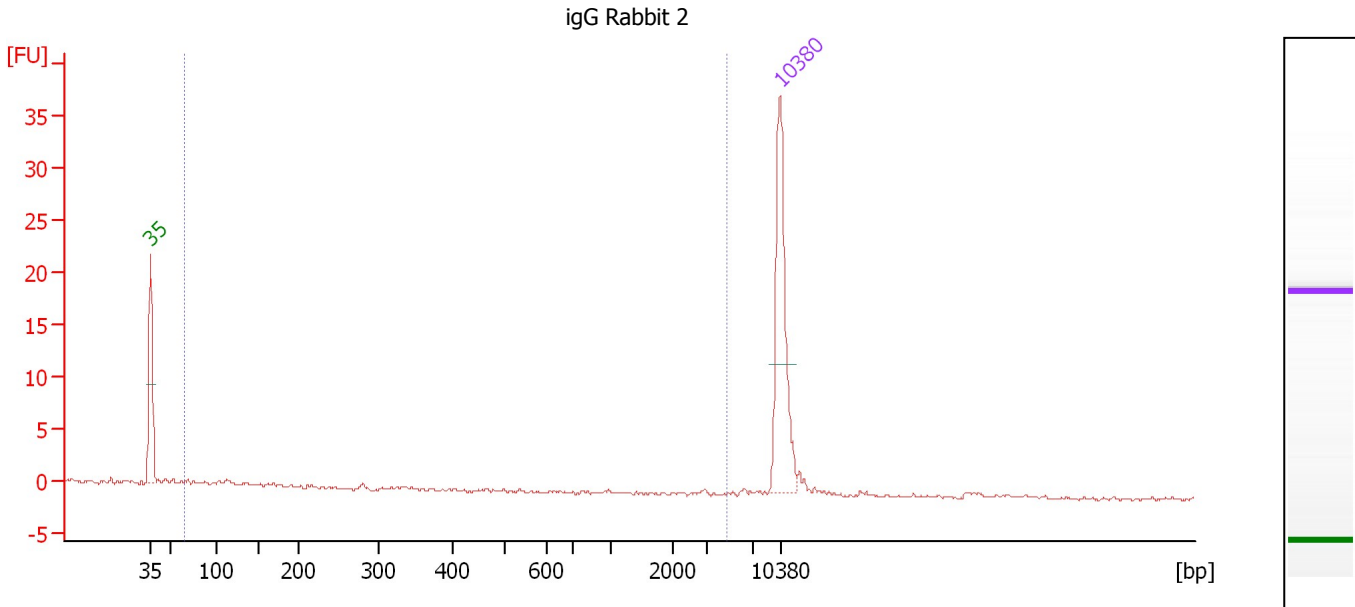
Region table for sample 10 : igG Rabbit 1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
53	1,533	8,689	9.9	256.5	70	100.0	30.90

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Electropherogram Summary Continued ...



Overall Results for sample 11 : igG Rabbit 2

Number of peaks found: 0 Corr. Area 1: 1.9
 Noise: 0.2

Peak table for sample 11 : igG Rabbit 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	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : igG Rabbit 2

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
65	299	4,761	1.9	104.2	27	100.0	7.17

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Gel Image