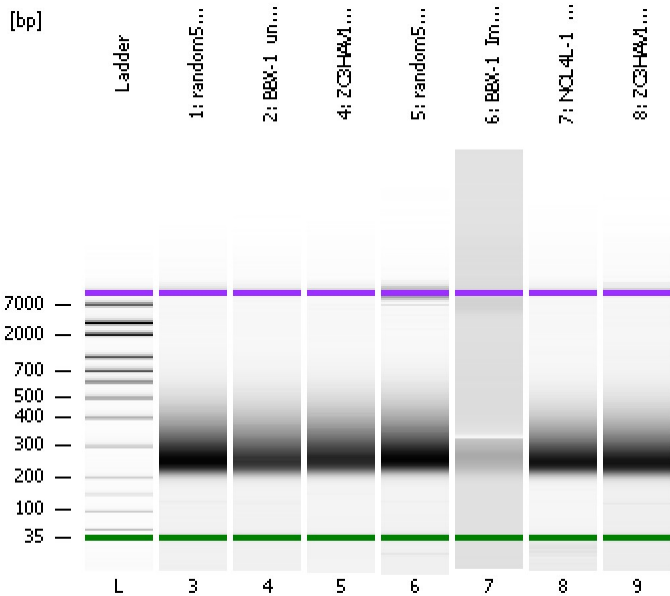


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
Modified: 8/10/2015 10:30:21 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

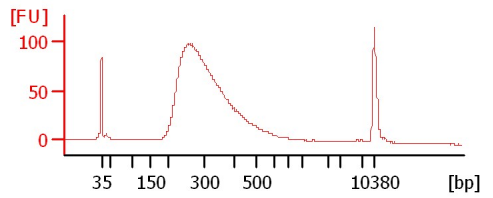
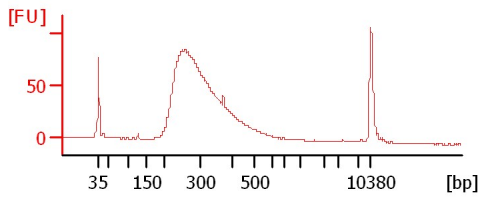
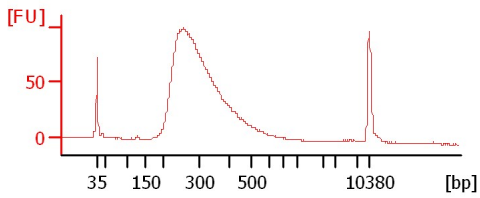
Chip Information:

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

1: random5305\_untreated

2: BBX-1\_untreated

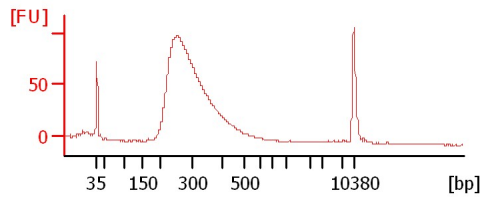
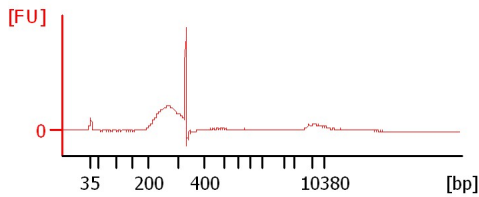
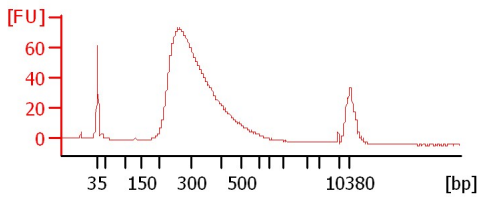
4: ZC3HAV1\_2\_untreated



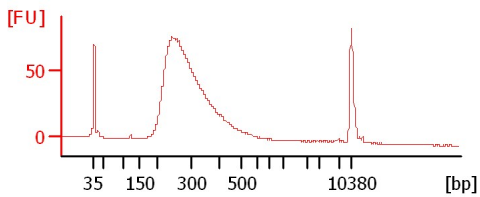
5: random5305\_Imatinib

6: BBX-1\_Imatinib

7: NOL4L-1\_Imatinib



8: ZC3HAV1\_2\_Imatinib



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1: random5305_untreated		<input type="checkbox"/>	✓			
2: BBX-1_untreated		<input type="checkbox"/>	✓			
4: ZC3HAV1_2_untreated		<input type="checkbox"/>	✓			
5: random5305_Imatinib		<input type="checkbox"/>	✓			
6: BBX-1_Imatinib		<input type="checkbox"/>	✓			
7: NOL4L-1_Imatinib		<input type="checkbox"/>	✓			
8: ZC3HAV1_2_Imatinib		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
Modified: 8/10/2015 10:30:21 AM

**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

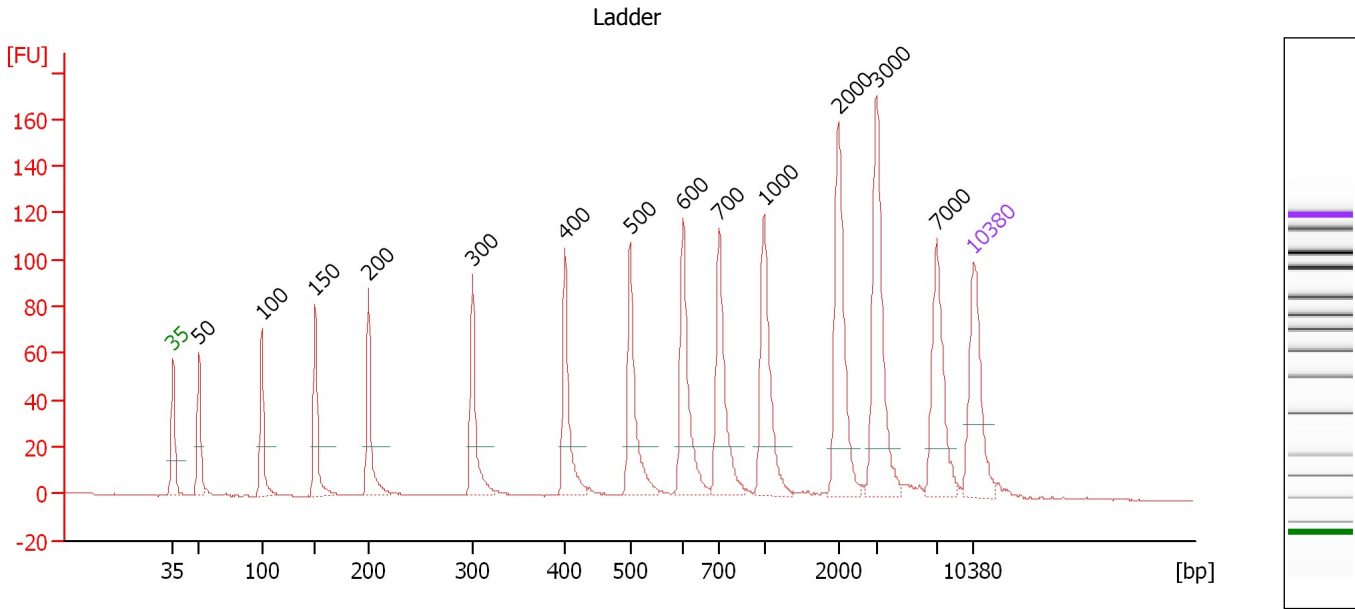
**Ladder**

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

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...\Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

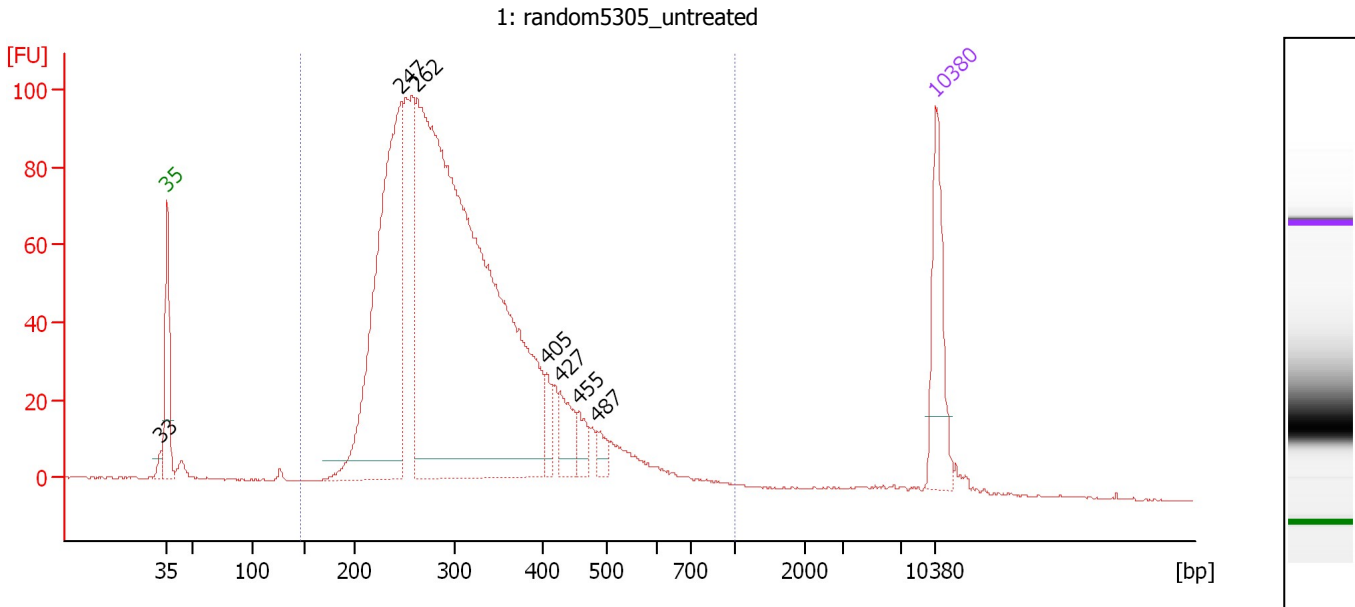
**Peak table for Ladder**

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	50.74
4	150	150.00	1,515.2	Ladder Peak	55.45
5	200	150.00	1,136.4	Ladder Peak	60.07
6	300	150.00	757.6	Ladder Peak	69.16
7	400	150.00	568.2	Ladder Peak	77.28
8	500	150.00	454.5	Ladder Peak	82.97
9	600	150.00	378.8	Ladder Peak	87.58
10	700	150.00	324.7	Ladder Peak	90.75
11	1,000	150.00	227.3	Ladder Peak	94.67
12	2,000	150.00	113.6	Ladder Peak	101.15
13	3,000	150.00	75.8	Ladder Peak	104.51
14	7,000	150.00	32.5	Ladder Peak	109.78
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : 1: random5305\_untreated**

Number of peaks found: 7                      Corr. Area 1: 1,936.1  
 Noise: 0.3

**Peak table for sample 3 : 1: random5305\_untreated**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.37
2	35	125.00	5,411.3	Lower Marker	43.00
3	247	519.18	3,187.2		64.33
4	262	1,383.02	7,988.9		65.73
5	405	24.15	90.4		77.54
6	427	40.65	144.3		78.80
7	455	22.43	74.7		80.40
8	487	14.76	46.0		82.20
9	10,380	75.00	10.9	Upper Marker	113.00

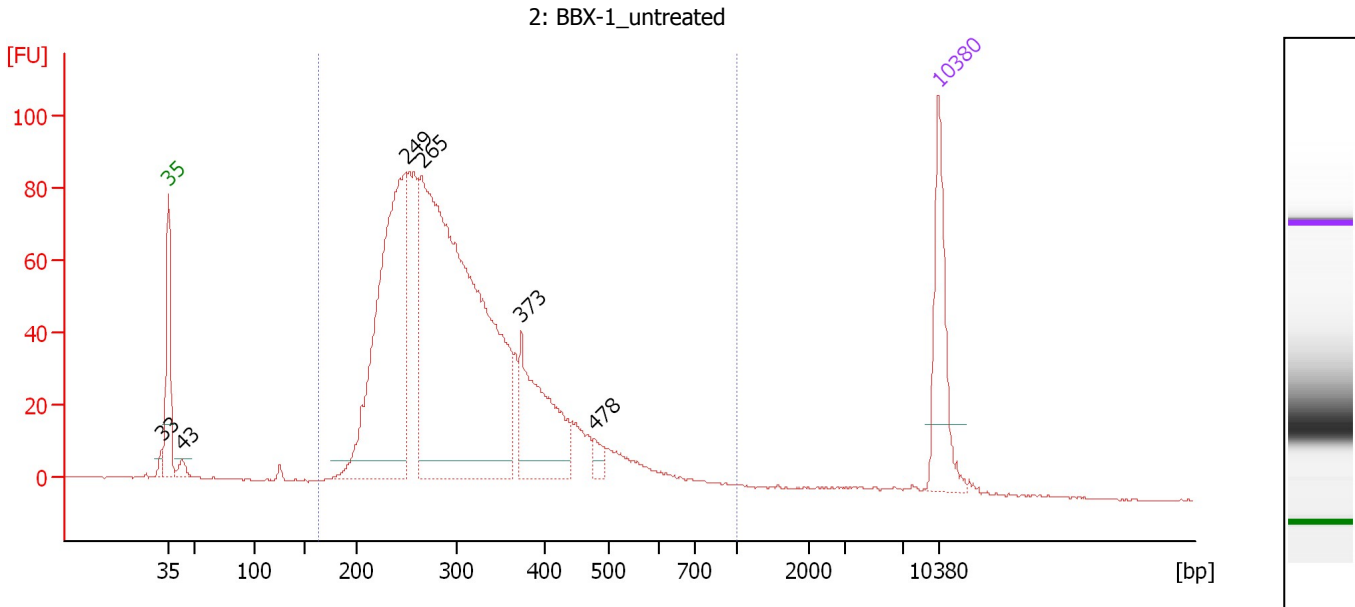
**Region table for sample 3 : 1: random5305\_untreated**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
147	317	1,000	1,936.1	11,870.2	97	29.8	2,274.49

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : 2: BBX-1 untreated**

Number of peaks found: 6                      Corr. Area 1: 1,670.2  
 Noise: 0.2

**Peak table for sample 4 : 2: BBX-1 untreated**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.42
2	35	125.00	5,411.3	Lower Marker	43.00
3	43	13.14	463.6		44.21
4	249	447.27	2,717.7		64.56
5	265	861.89	4,921.6		66.01
6	373	150.54	611.8		75.07
7	478	12.93	41.0		81.71
8	10,380	75.00	10.9	Upper Marker	113.00

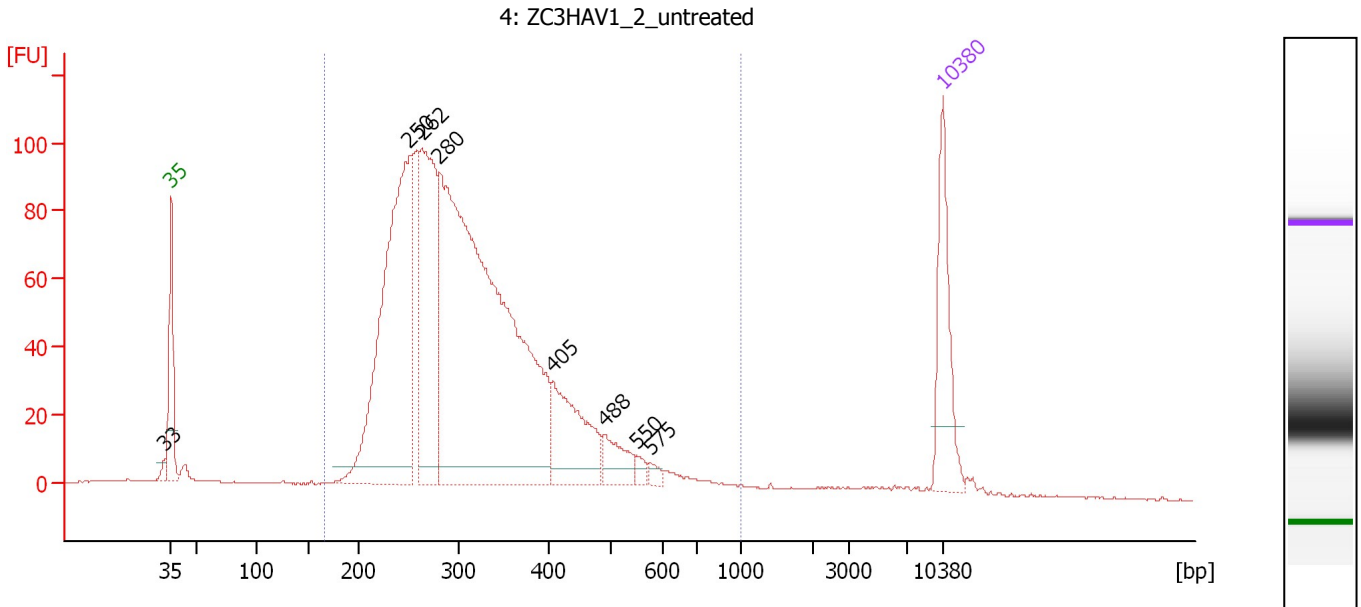
**Region table for sample 4 : 2: BBX-1 untreated**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
163	316	1,000	1,670.2	9,035.6	97	29.9	1,724.02

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : 4: ZC3HAV1\_2\_untreated**

Number of peaks found: 8                      Corr. Area 1: 2,000.1  
 Noise: 0.2

**Peak table for sample 5 : 4: ZC3HAV1\_2\_untreated**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.37
2	35	125.00	5,411.3	Lower Marker	43.00
3	250	481.55	2,917.4		64.62
4	262	269.63	1,557.3		65.74
5	280	929.81	5,033.5		67.33
6	405	117.90	440.6		77.59
7	488	38.12	118.4		82.28
8	550	8.40	23.1		85.28
9	575	7.51	19.8		86.44
10	10,380	75.00	10.9	Upper Marker	113.00

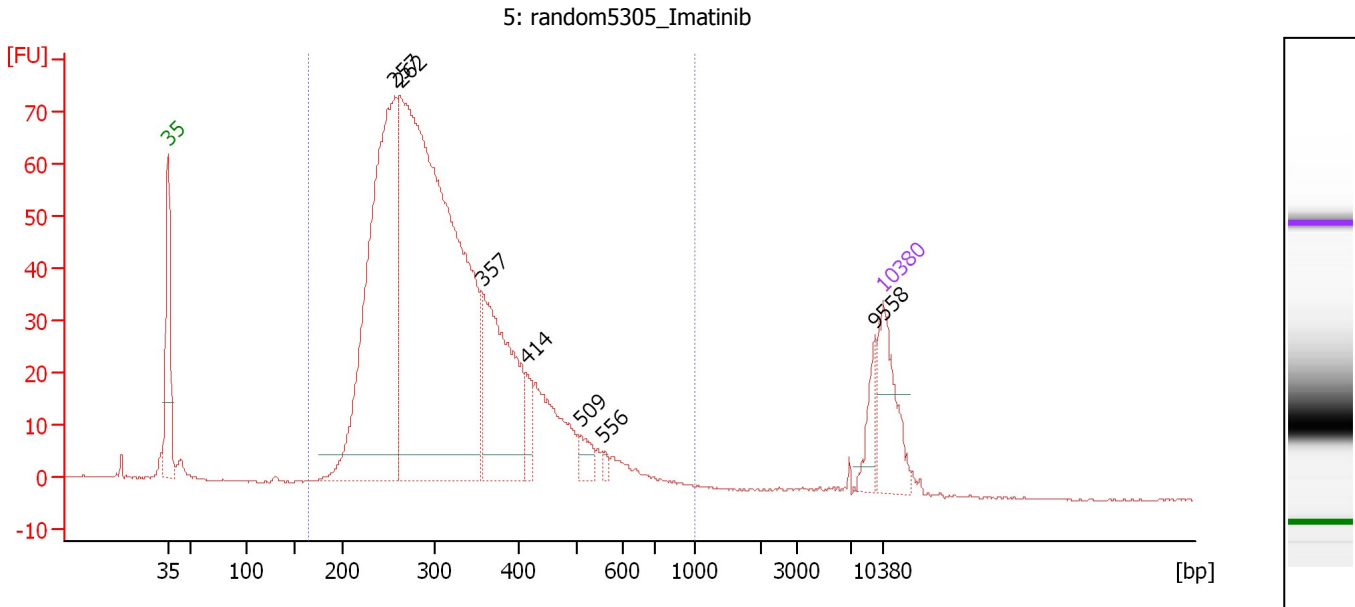
**Region table for sample 5 : 4: ZC3HAV1\_2\_untreated**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
167	323	1,000	2,000.1	10,065.9	95	30.5	1,955.60

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : 5: random5305 Imatinib**

Number of peaks found: 7                      Corr. Area 1: 1,356.7  
 Noise: 0.2

**Peak table for sample 6 : 5: random5305 Imatinib**

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	257	711.70	4,198.5		65.24
3	262	1,326.99	7,674.0		65.71
4	357	277.41	1,177.0		73.80
5	414	30.36	111.1		78.08
6	509	23.86	71.0		83.40
7	556	7.00	19.1		85.54
8	9,558	27.28	4.3		112.22
9	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 6 : 5: random5305 Imatinib**

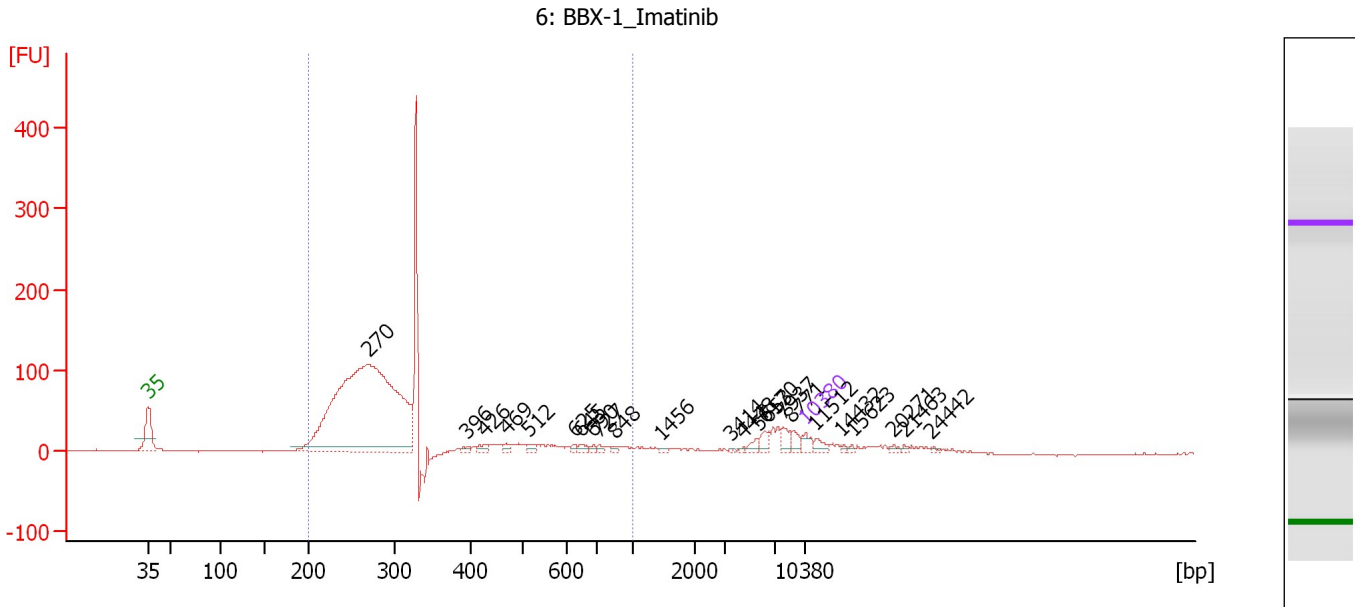
From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
164	322	1,000	1,356.7	12,861.1	96	28.3	2,515.72



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : 6: BBX-1\_Imatinib**

Number of peaks found: 23                      Corr. Area 1: 1,569.5  
 Noise: 0.8

**Peak table for sample 7 : 6: BBX-1\_Imatinib**


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	270	6,542.45	36,723.8		66.43
3	396	35.87	137.1		76.98
4	426	67.11	238.9		78.74
5	469	43.11	139.4		81.18
6	512	47.11	139.5		83.50
7	625	29.20	70.8		88.38
8	645	52.02	122.2		89.00
9	690	27.68	60.8		90.42
10	727	29.34	61.2		91.10
11	848	23.33	41.7		92.69
12	1,456	20.53	21.4		97.63
13	3,414	10.22	4.5		105.06
14	4,448	14.29	4.9		106.42
15	5,653	57.85	15.5		108.01
16	6,170	88.03	21.6		108.69
17	7,937	92.59	17.7		110.67
18	8,771	86.98	15.0		111.47
19	10,380	75.00	10.9	Upper Marker	113.00
20	11,512	0.00	0.0		114.08
21	14,432	0.00	0.0		116.86
22	15,623	0.00	0.0		117.99
23	20,271	0.00	0.0		122.42
24	21,463	0.00	0.0		123.55
25	24,442	0.00	0.0		126.39

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary Continued ...**

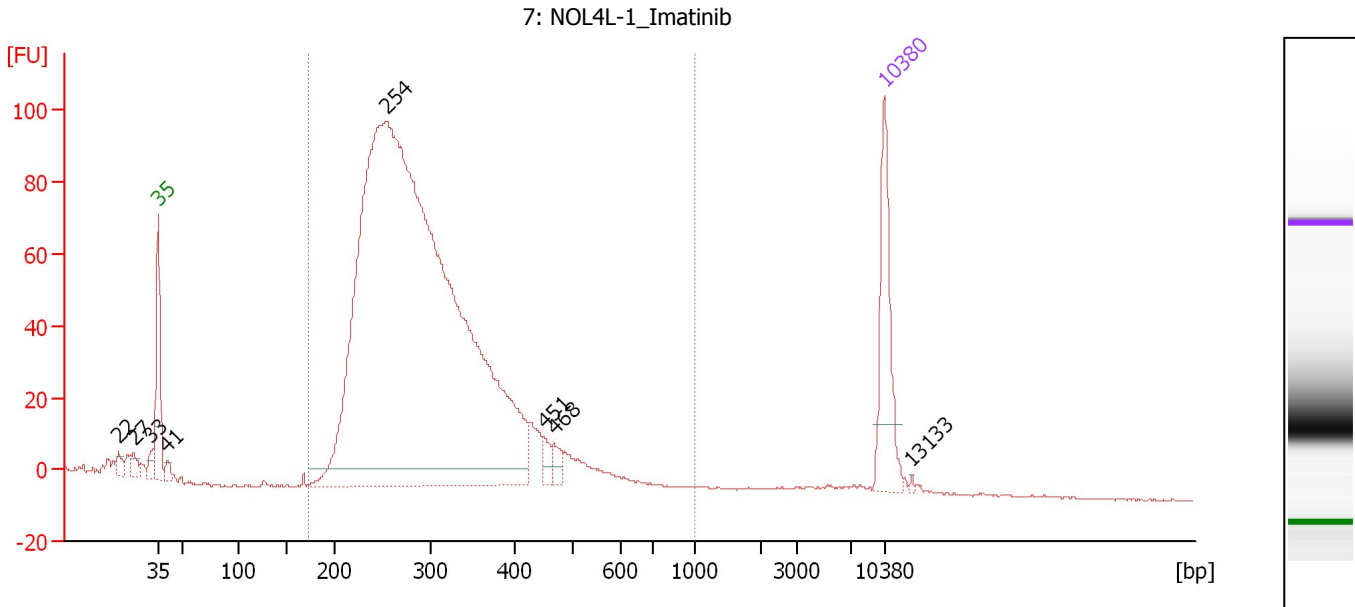
... Region table for sample 7 : **6: BBX-1 Imatinib**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
200	317	1,000	1,569.5	43,666.7	 83	38.9	8,215.88

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : 7: NOL4L-1 Imatinib**

Number of peaks found: 8                      Corr. Area 1: 1,658.1  
 Noise: 0.2

**Peak table for sample 8 : 7: NOL4L-1 Imatinib**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	22	0.00	0.0		39.20
2	27	0.00	0.0		40.64
3	33	0.00	0.0		42.33
4	35	125.00	5,411.3	Lower Marker	43.00
5	41	11.56	429.9		43.87
6	254	1,959.35	11,678.8		65.00
7	451	12.44	41.8		80.16
8	468	13.02	42.2		81.14
9	10,380	75.00	10.9	Upper Marker	113.00
10	13,133	0.00	0.0		115.62

**Region table for sample 8 : 7: NOL4L-1 Imatinib**

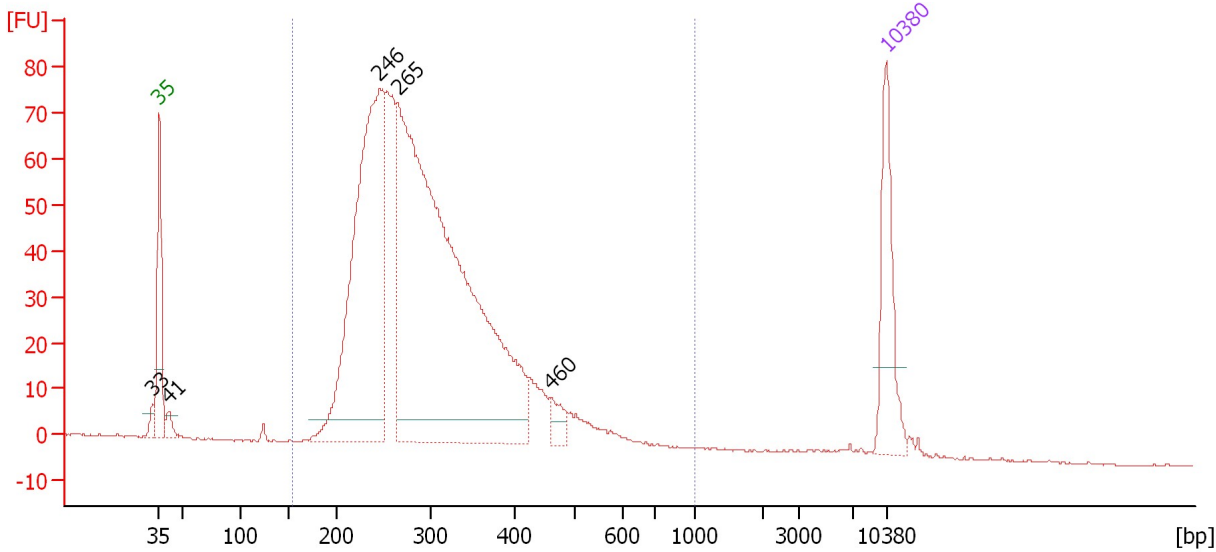
From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
171	301	1,000	1,658.1	9,865.1	97	23.9	1,844.88

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
 Modified: 8/10/2015 10:30:21 AM

**Electropherogram Summary Continued ...**

8: ZC3HAV1\_2\_Imatinib



**Overall Results for sample 9 : 8: ZC3HAV1\_2\_Imatinib**

Number of peaks found: 5                      Corr. Area 1: 1,378.7  
 Noise: 0.2

**Peak table for sample 9 : 8: ZC3HAV1\_2\_Imatinib**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	33	0.00	0.0		42.33
2	35	125.00	5,411.3	Lower Marker	43.00
3	41	16.18	601.7		43.87
4	246	529.09	3,264.7		64.21
5	265	1,019.89	5,836.8		65.96
6	460	20.52	67.6		80.70
7	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 9 : 8: ZC3HAV1\_2\_Imatinib**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
154	305	1,000	1,378.7	9,440.6	97	27.9	1,761.25

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...Bioanalyzer\2015-08-06\2015-08-06\_002\_HiSeq158\_Libraries.xad

Created: 8/6/2015 3:53:09 PM  
Modified: 8/10/2015 10:30:21 AM

**Gel Image**

