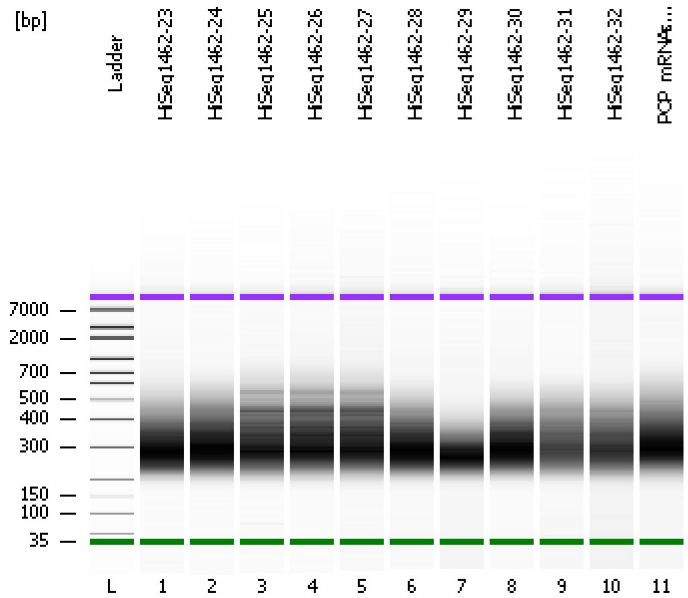
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad
Created: 8/16/2018 3:24:04 PM
Modified: 8/16/2018 4:05:23 PM

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

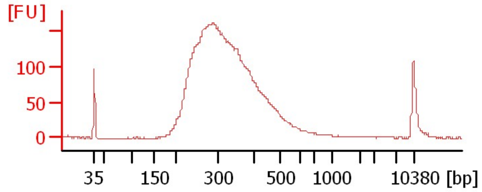
Chip Information:

Chip Lot #:

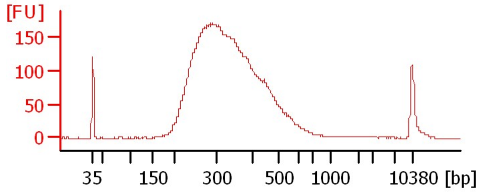
Reagent Kit Lot #:

Chip Comments:

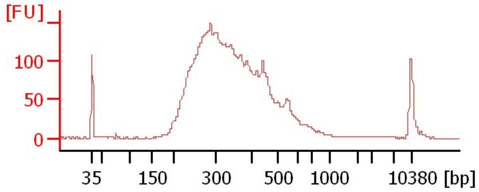
HiSeq1462-23



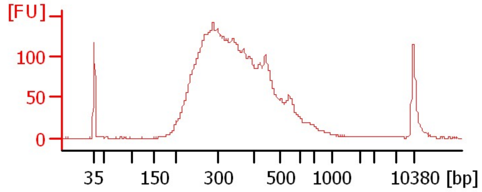
HiSeq1462-24



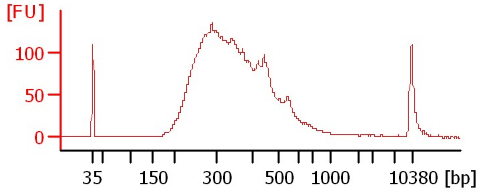
HiSeq1462-25



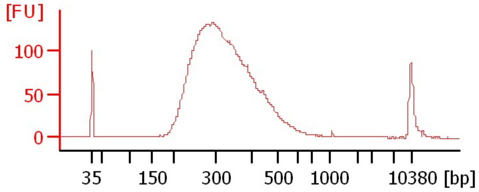
HiSeq1462-26



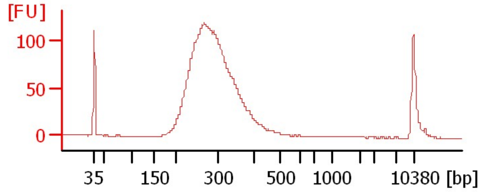
HiSeq1462-27



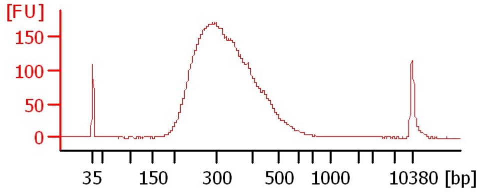
HiSeq1462-28



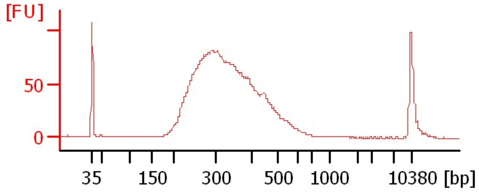
HiSeq1462-29



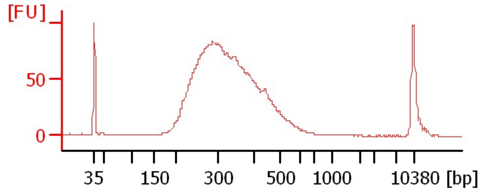
HiSeq1462-30



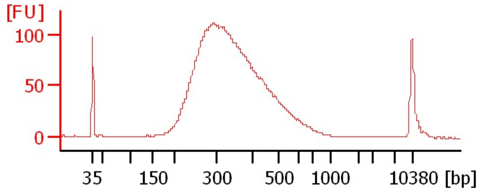
HiSeq1462-31



HiSeq1462-32



POP_mRNAseq_BC



Assay Class:	High Sensitivity DNA Assay	Created:	8/16/2018 3:24:04 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad	Modified:	8/16/2018 4:05:23 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq1462-23		☐	✓			
HiSeq1462-24		☐	✓			
HiSeq1462-25		☐	✓			
HiSeq1462-26		☐	✓			
HiSeq1462-27		☐	✓			
HiSeq1462-28		☐	✓			
HiSeq1462-29		☐	✓			
HiSeq1462-30		☐	✓			
HiSeq1462-31		☐	✓			
HiSeq1462-32		☐	✓			
POP_mRNAseq_BC		☐	✓			
Ladder		☐	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

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

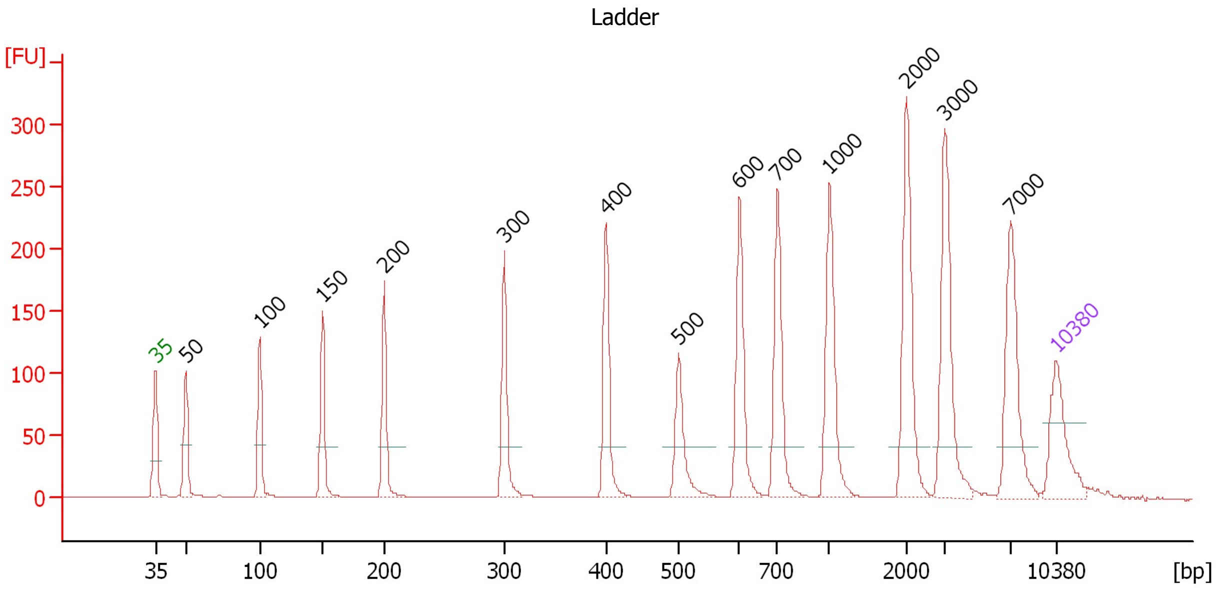
Ladder

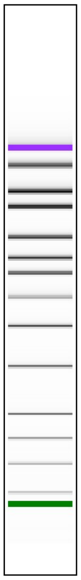
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

Assay Class:	High Sensitivity DNA Assay	Created:	8/16/2018 3:24:04 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad	Modified:	8/16/2018 4:05:23 PM

Electropherogram Summary

Ladder





Overall Results for Ladder

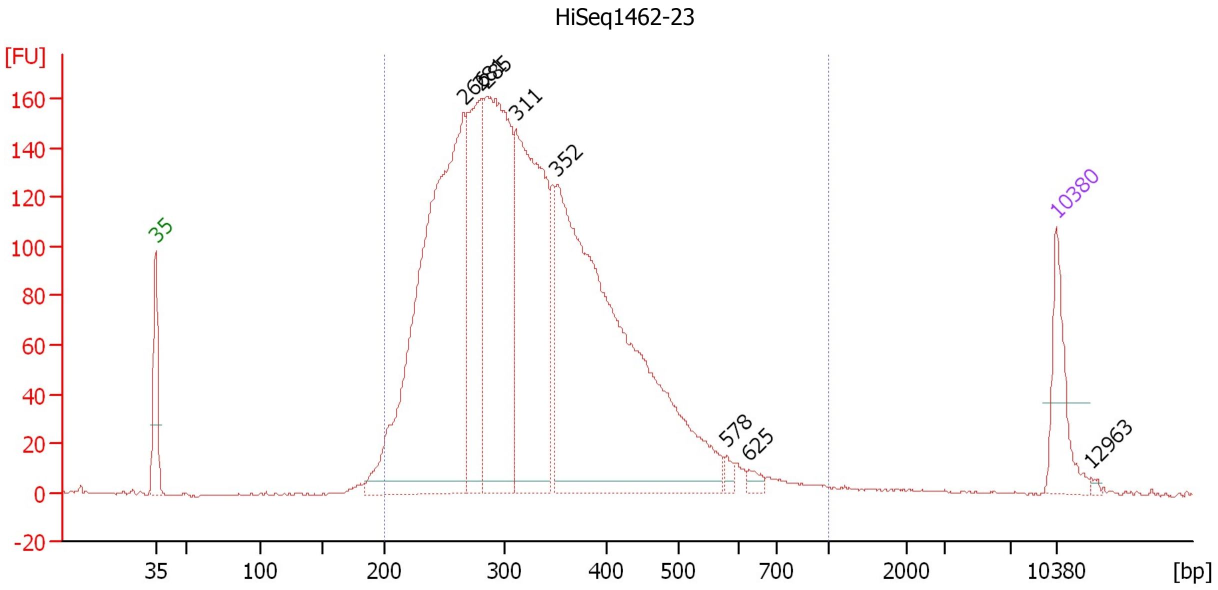
Noise: 0.3

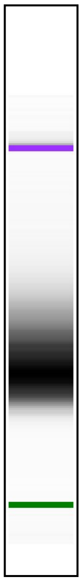
Peak table for Ladder

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	L	50	150.00	4,545.5	Ladder Peak	45.33
3	L	100	150.00	2,272.7	Ladder Peak	51.10
4	L	150	150.00	1,515.2	Ladder Peak	55.95
5	L	200	150.00	1,136.4	Ladder Peak	60.76
6	L	300	150.00	757.6	Ladder Peak	70.10
7	L	400	150.00	568.2	Ladder Peak	78.00
8	L	500	150.00	454.5	Ladder Peak	83.67
9	L	600	150.00	378.8	Ladder Peak	88.38
10	L	700	150.00	324.7	Ladder Peak	91.33
11	L	1,000	150.00	227.3	Ladder Peak	95.38
12	L	2,000	150.00	113.6	Ladder Peak	101.38
13	L	3,000	150.00	75.8	Ladder Peak	104.33
14	L	7,000	150.00	32.5	Ladder Peak	109.43
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class:	High Sensitivity DNA Assay	Created:	8/16/2018 3:24:04 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad	Modified:	8/16/2018 4:05:23 PM

Electropherogram Summary Continued ...





Overall Results for sample 1 : HiSeq1462-23

Number of peaks found:	8	Corr. Area 1:	3,613.6
Noise:	0.4		

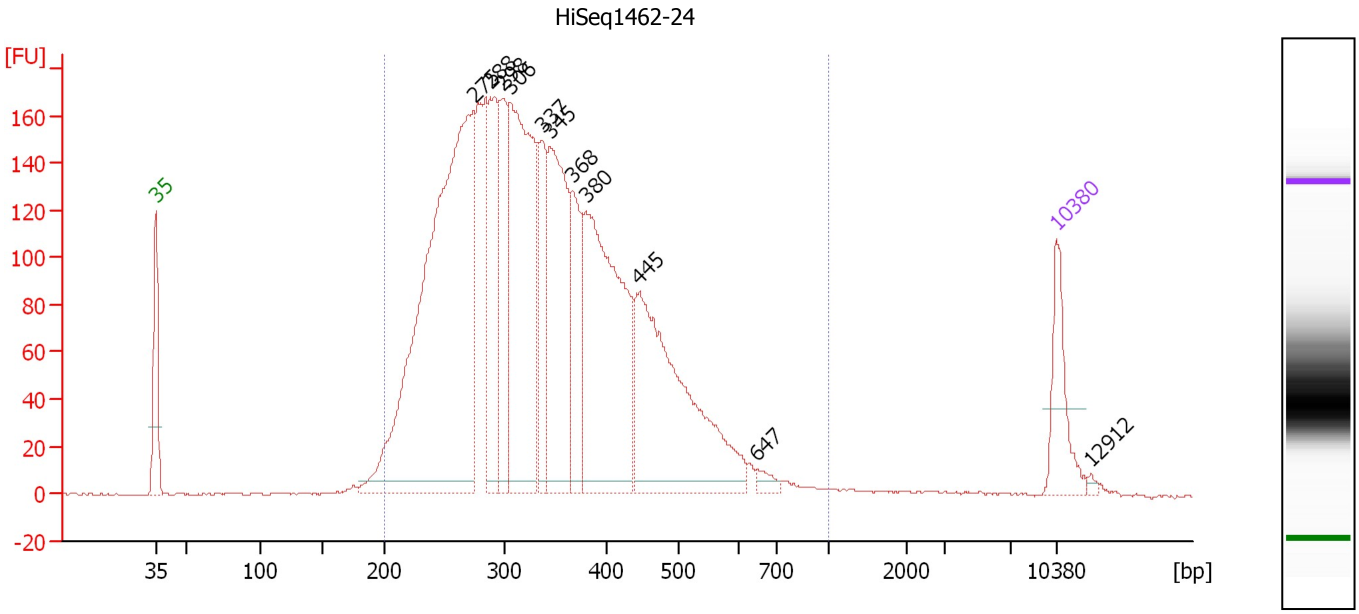
Peak table for sample 1 : HiSeq1462-23

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		266	1,060.17	6,035.7		66.93
3		281	316.59	1,708.5		68.30
4		285	611.02	3,249.1		68.69
5		311	599.38	2,918.2		70.98
6		352	1,099.93	4,735.9		74.20
7		578	10.83	28.4		87.36
8		625	11.12	27.0		89.11
9	▶	10,380	75.00	10.9	Upper Marker	113.00
10		12,963	0.00	0.0		115.73

Region table for sample 1 : HiSeq1462-23

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	337	3,749.97	3,613.6	18,432.9	🟦 97	29.1

Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq1462-24

Number of peaks found:	11	Corr. Area 1:	4,020.7
Noise:	0.4		

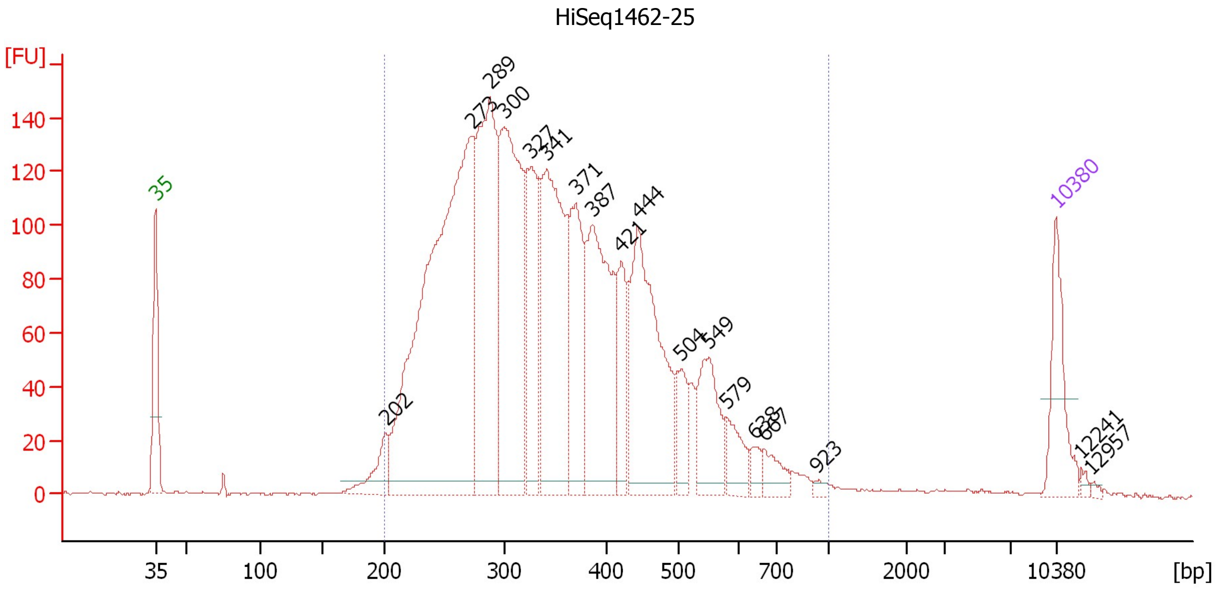
Peak table for sample 2 : HiSeq1462-24

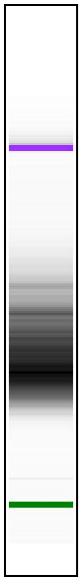
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		275	1,154.66	6,372.1		67.72
3		288	234.54	1,232.4		69.01
4		298	190.14	965.3		69.95
5		306	514.93	2,547.1		70.59
6		337	133.27	599.2		73.02
7		345	341.19	1,497.7		73.67
8		368	152.43	628.1		75.45
9		380	500.65	1,994.9		76.44
10		445	456.93	1,555.7		80.55
11		647	12.98	30.4		89.77
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		12,912	0.00	0.0		115.68

Region table for sample 2 : HiSeq1462-24

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co lor	% of Total	Size distribution in CV [%]
200	1,000	347	4,060.57	4,020.7	19,444.3	🟦	98	28.4

Electropherogram Summary Continued ...





Overall Results for sample 3 : HiSeq1462-25

Number of peaks found:	18	Corr. Area 1:	3,450.8
Noise:	0.4		

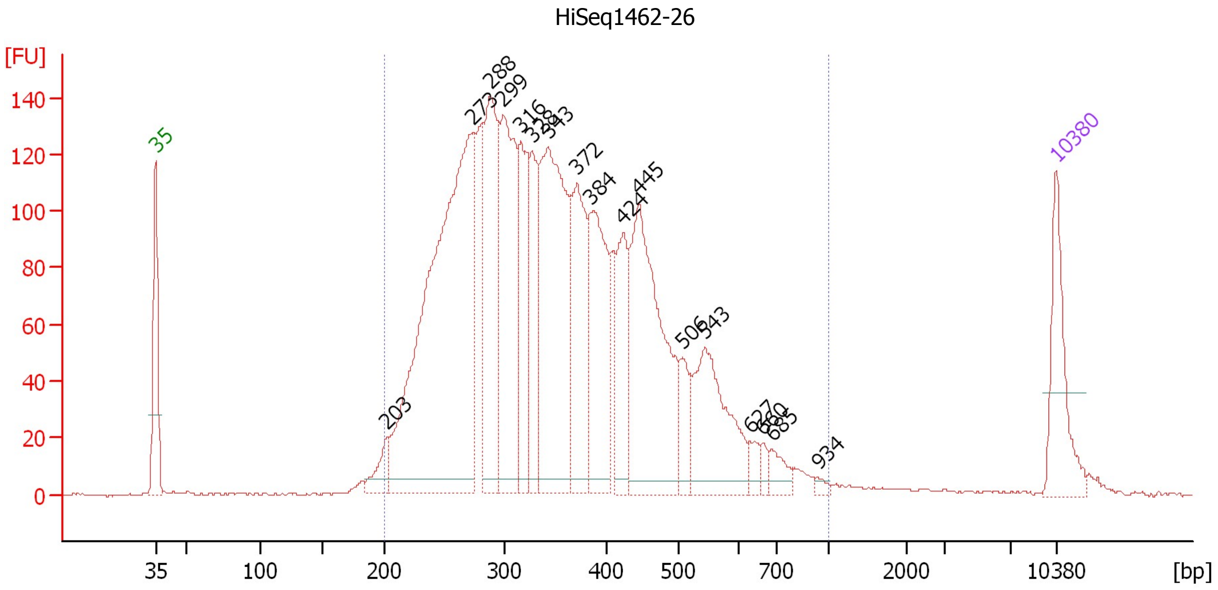
Peak table for sample 3 : HiSeq1462-25

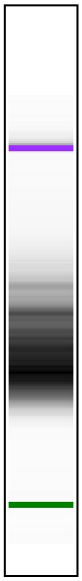
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		202	61.18	460.0		60.90
3		273	969.18	5,371.4		67.61
4		289	411.37	2,160.3		69.02
5		300	415.87	2,101.3		70.08
6		327	166.85	774.0		72.20
7		341	363.23	1,612.5		73.36
8		371	179.51	733.8		75.68
9		387	287.48	1,126.7		76.94
10		421	96.66	347.6		79.21
11		444	320.26	1,093.9		80.47
12		504	54.29	163.2		83.85
13		549	102.96	284.2		85.97
14		579	44.01	115.2		87.38
15		638	16.90	40.1		89.50
16		667	30.04	68.2		90.36
17		923	6.00	9.9		94.34
18	▶	10,380	75.00	10.9	Upper Marker	113.00
19		12,241	0.00	0.0		114.97
20		12,957	0.00	0.0		115.72

Region table for sample 3 : HiSeq1462-25

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	1,000	360	3,702.76	3,450.8	17,416.8	🟦 96	31.4

Electropherogram Summary Continued ...





Overall Results for sample 4 : HiSeq1462-26

Number of peaks found:	17	Corr. Area 1:	3,414.6
Noise:	0.3		

Peak table for sample 4 : HiSeq1462-26

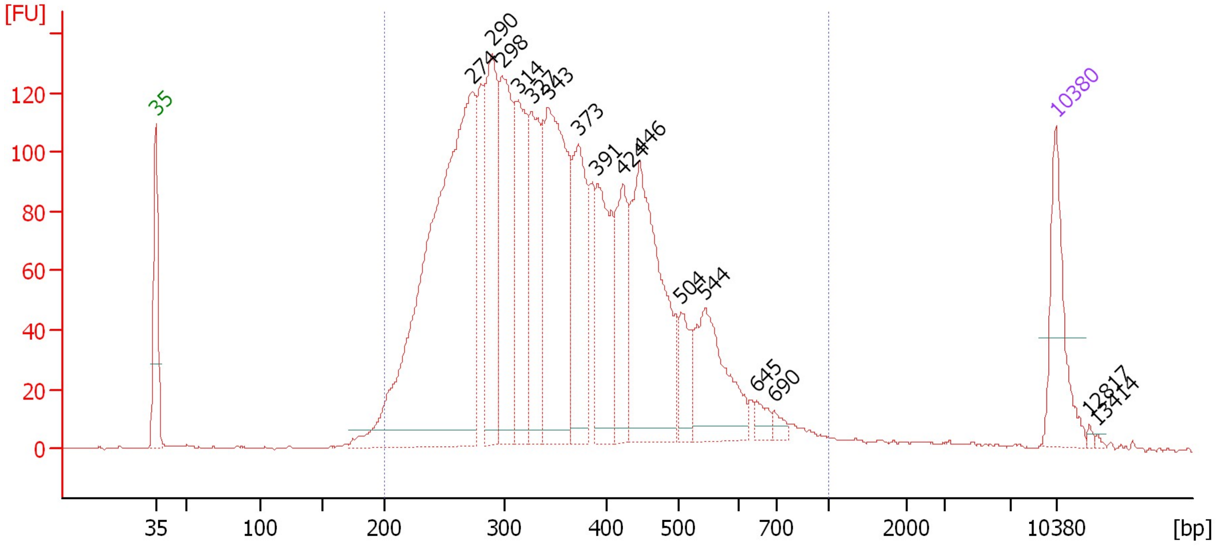
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		203	34.39	257.3		61.00
3		273	782.29	4,340.1		67.58
4		288	245.55	1,291.9		68.97
5		299	264.12	1,338.4		70.00
6		316	154.59	741.8		71.34
7		328	122.16	564.1		72.32
8		343	357.27	1,577.9		73.50
9		372	168.39	686.4		75.76
10		384	192.89	761.0		76.74
11		424	106.44	380.3		79.36
12		445	307.25	1,046.3		80.55
13		506	44.18	132.3		83.94
14		543	156.73	437.4		85.69
15		627	15.63	37.8		89.19
16		660	10.54	24.2		90.16
17		685	21.10	46.7		90.88
18		934	5.32	8.6		94.48
19	▶	10,380	75.00	10.9	Upper Marker	113.00

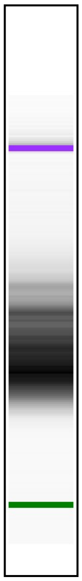
Region table for sample 4 : HiSeq1462-26

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	366	3,209.03	3,414.6	14,875.7	🟦 96	31.4

Electropherogram Summary Continued ...

HiSeq1462-27





Overall Results for sample 5 : HiSeq1462-27

Number of peaks found:	16	Corr. Area 1:	3,168.4
Noise:	0.4		

Peak table for sample 5 : HiSeq1462-27

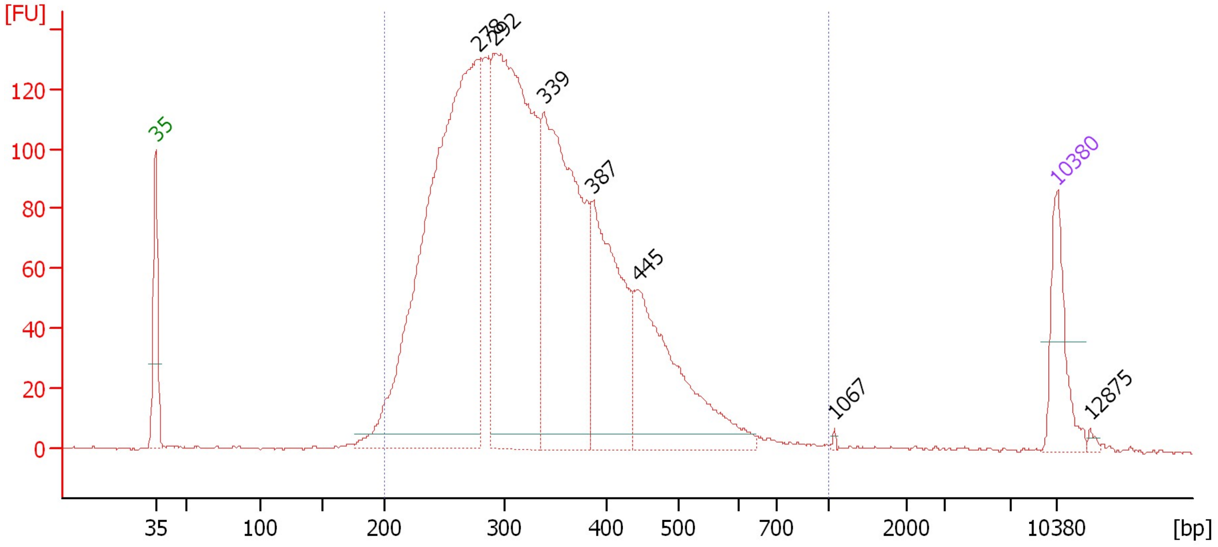
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		274	825.83	4,570.5		67.65
3		290	216.72	1,134.1		69.12
4		298	221.47	1,126.1		69.91
5		314	175.33	847.2		71.17
6		327	172.41	799.2		72.22
7		343	327.88	1,446.3		73.53
8		373	159.85	649.8		75.85
9		391	147.18	569.8		77.32
10		424	107.40	383.7		79.37
11		446	296.72	1,007.2		80.63
12		504	47.19	142.0		83.83
13		544	130.91	364.8		85.73
14		645	15.21	35.7		89.72
15		690	9.29	20.4		91.03
16	▶	10,380	75.00	10.9	Upper Marker	113.00
17		12,817	0.00	0.0		115.58
18		13,414	0.00	0.0		116.21

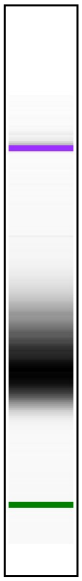
Region table for sample 5 : HiSeq1462-27

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	365	3,173.04	3,168.4	14,723.0	🟦 96	30.9

Electropherogram Summary Continued ...

HiSeq1462-28





Overall Results for sample 6 : HiSeq1462-28

Number of peaks found:	7	Corr. Area 1:	2,875.5
Noise:	0.4		

Peak table for sample 6 : HiSeq1462-28

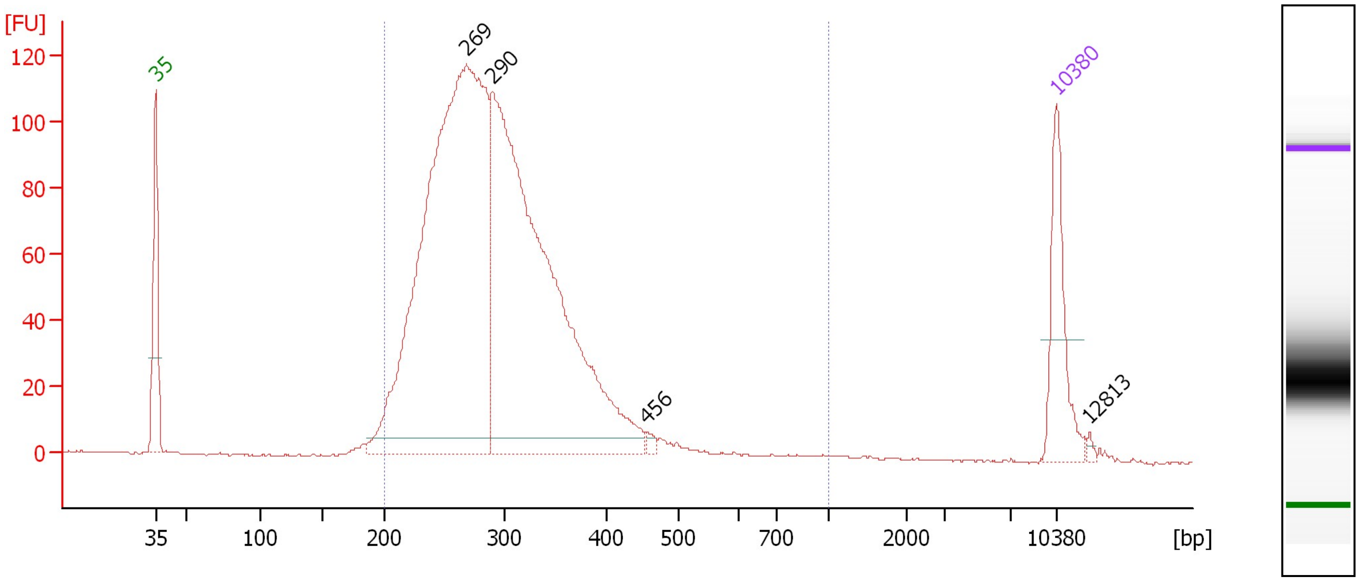
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		278	1,133.40	6,169.8		68.07
3		292	844.14	4,386.3		69.31
4		339	592.08	2,645.6		73.18
5		387	312.17	1,220.9		77.00
6		445	303.06	1,031.6		80.56
7		1,067	2.27	3.2		95.78
8	▶	10,380	75.00	10.9	Upper Marker	113.00
9		12,875	0.00	0.0		115.64

Region table for sample 6 : HiSeq1462-28

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	336	3,380.79	2,875.5	16,542.9	🟦	97	27.2

Electropherogram Summary Continued ...

HiSeq1462-29



Overall Results for sample 7 : HiSeq1462-29

Number of peaks found:	4	Corr. Area 1:	1,859.4
Noise:	0.3		

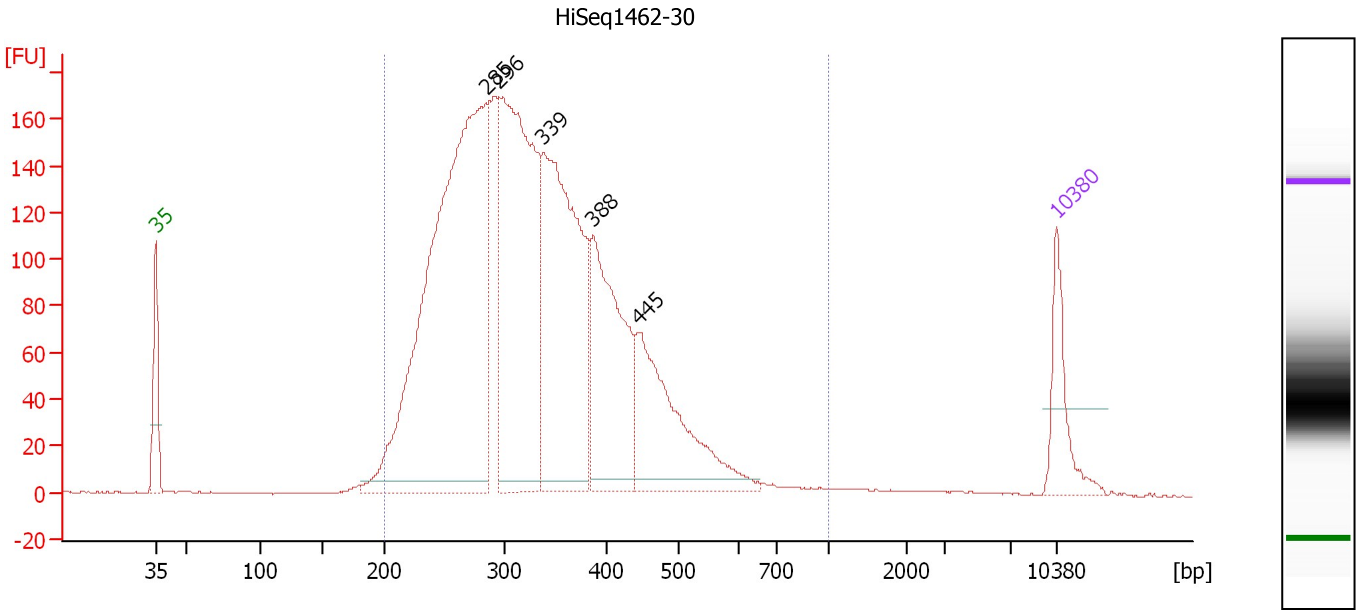
Peak table for sample 7 : HiSeq1462-29

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	1,071.31	6,041.4		67.17
3		290	888.63	4,637.1		69.20
4		456	5.68	18.9		81.17
5	▶	10,380	75.00	10.9	Upper Marker	113.00
6		12,813	0.00	0.0		115.57

Region table for sample 7 : HiSeq1462-29

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	300	1,959.53	1,859.4	10,391.6	🟦 98	23.3

Electropherogram Summary Continued ...



Overall Results for sample 8 : **HiSeq1462-30**

Number of peaks found:	5	Corr. Area 1:	3,627.6
Noise:	0.3		

Peak table for sample 8 : **HiSeq1462-30**

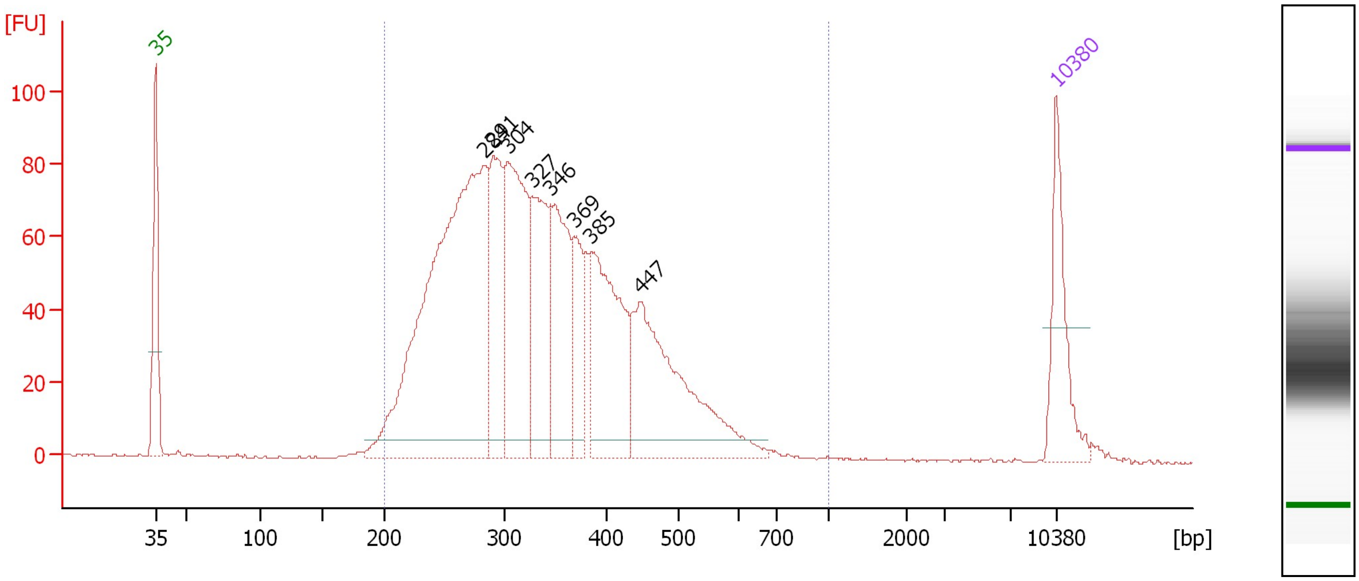
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		285	1,272.68	6,764.3		68.70
3		296	732.62	3,752.9		69.70
4		339	628.63	2,813.3		73.14
5		388	345.82	1,351.4		77.03
6		445	294.48	1,003.6		80.53
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 8 : **HiSeq1462-30**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	337	3,535.00	3,627.6	17,176.9	🟦	98	26.8

Electropherogram Summary Continued ...

HiSeq1462-31



Overall Results for sample 9 : HiSeq1462-31

Number of peaks found:	8	Corr. Area 1:	1,842.3
Noise:	0.4		

Peak table for sample 9 : HiSeq1462-31

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		284	727.11	3,877.6		68.61
3		291	164.15	855.5		69.23
4		304	265.81	1,325.1		70.41
5		327	161.80	749.0		72.26
6		346	171.96	753.6		73.71
7		369	85.05	349.1		75.56
8		385	203.86	801.3		76.85
9		447	257.49	872.8		80.66
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : HiSeq1462-31

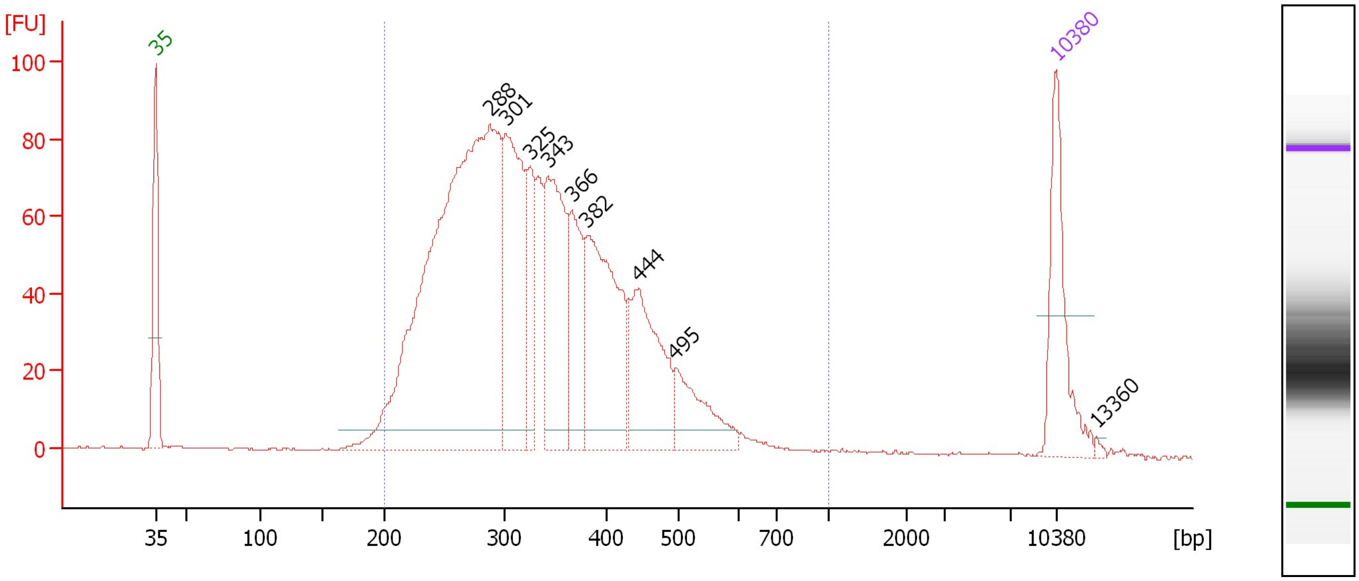
From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	344	2,106.57	1,842.3	10,115.4	🟦 98	26.7

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad

Created: 8/16/2018 3:24:04 PM
Modified: 8/16/2018 4:05:23 PM

Electropherogram Summary Continued ...

HiSeq1462-32



Overall Results for sample 10 : **HiSeq1462-32**

Number of peaks found:	9	Corr. Area 1:	1,852.3
Noise:	0.3		

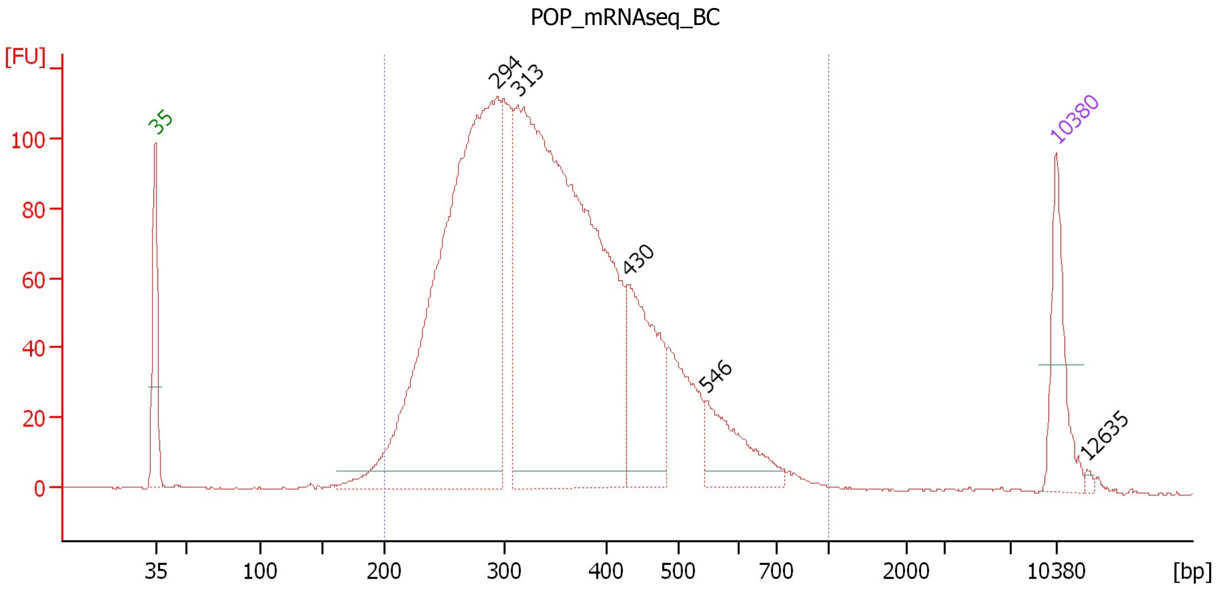
Peak table for sample 10 : **HiSeq1462-32**

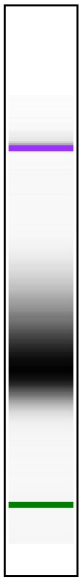
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		288	794.78	4,181.2		68.98
3		301	205.41	1,032.3		70.21
4		325	73.40	342.3		72.07
5		343	165.77	731.3		73.53
6		366	91.70	379.4		75.33
7		382	194.58	772.0		76.57
8		444	130.62	445.6		80.50
9		495	65.61	200.9		83.37
10	▶	10,380	75.00	10.9	Upper Marker	113.00
11		13,360	0.00	0.0		116.15

Region table for sample 10 : **HiSeq1462-32**

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	341	1,875.74	1,852.3	9,073.2	🟦 96	27.5

Electropherogram Summary Continued ...


POP_mRNAseq_BC



Overall Results for sample 11 : POP_mRNAseq_BC

Number of peaks found:	5	Corr. Area 1:	2,498.4
Noise:	0.3		

Peak table for sample 11 : POP_mRNAseq_BC

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		294	1,088.57	5,607.5		69.55
3		313	1,247.35	6,034.9		71.14
4		430	204.35	720.0		79.70
5		546	101.41	281.5		85.83
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		12,635	0.00	0.0		115.38

Region table for sample 11 : POP_mRNAseq_BC

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	356	2,905.78	2,498.4	13,612.6	■	98	29.1

Assay Class:	High Sensitivity DNA Assay	Created:	8/16/2018 3:24:04 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-08-16\2018-08-16_003.xad	Modified:	8/16/2018 4:05:23 PM

Gel Image