Assay Class:	High Sensitivity DNA Assay	Created:	8/13/2015 1:19:48 PM
Data Path:	C:\...r\2015-08-13\2015-08-13_003_HiSeq176_SizeSelLib_Repeats.xad	Modified:	8/13/2015 3:14:13 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

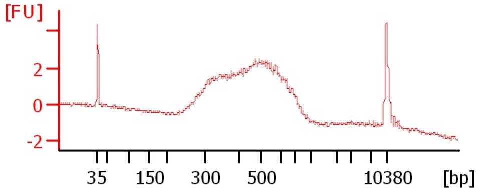
Chip Information:

Chip Lot #:

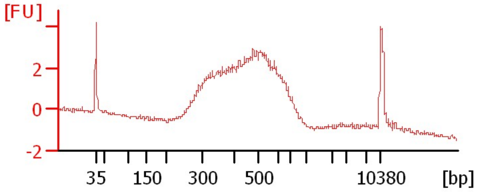
Reagent Kit Lot #:

Chip Comments:

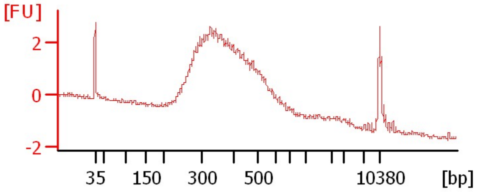
7: H3K4m_1 lib (1:8)
HiSeq_176: Size Selected Lib (0.55X R...



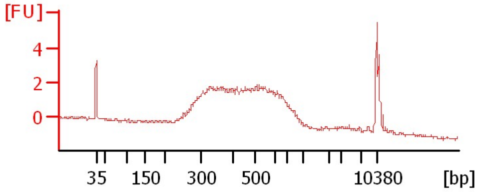
8: H3K4m_2 lib (1:8)
HiSeq_176: Size Selected Lib (0.55X R...



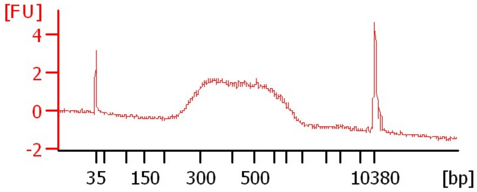
14: IgG Mouse 2 lib
HiSeq_176: Size Selected Lib (0.55X R...



15: CoupTF::1 lib (1:5)
HiSeq_176: Size Selected Lib (0.55X R...



16: CopuTF::2 lib (1:6)
HiSeq_176: Size Selected Lib (0.55X R...



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...r\2015-08-13\2015-08-13_003_HiSeq176_SizeSelLib_Repeats.xad

Created: 8/13/2015 1:19:48 PM
Modified: 8/13/2015 3:14:13 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
7: H3K4m_1 lib (1:8)	HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat	☐	✓			
8: H3K4m_2 lib (1:8)	HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat	☐	✓			
14: IgG Mouse 2 lib	HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat	☐	✓			
15: CoupTF::1 lib (1:5)	HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat	☐	✓			
16: CopuTF::2 lib (1:6)	HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat	☐	✓			
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

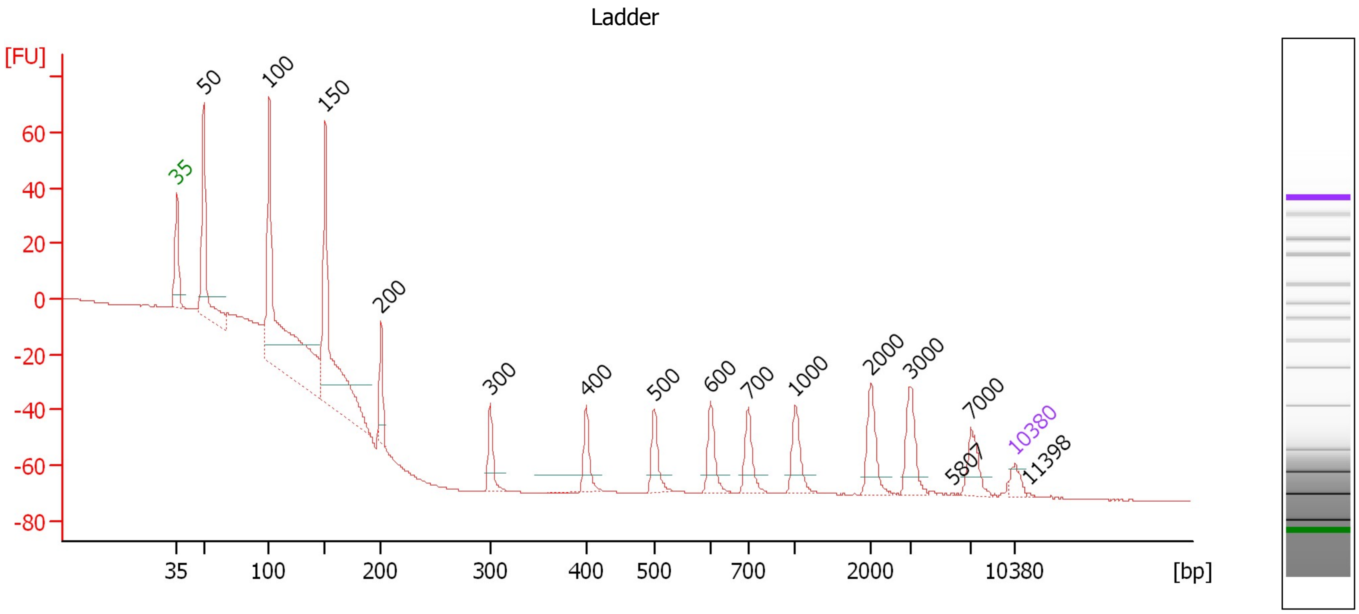
Filter Width [s] : 0.5
Polynomial Order : 4

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:	8/13/2015 1:19:48 PM
Data Path:	C:\...r\2015-08-13\2015-08-13_003_HiSeq176_SizeSelLib_Repeats.xad	Modified:	8/13/2015 3:14:13 PM

Electropherogram Summary



Overall Results for Ladder

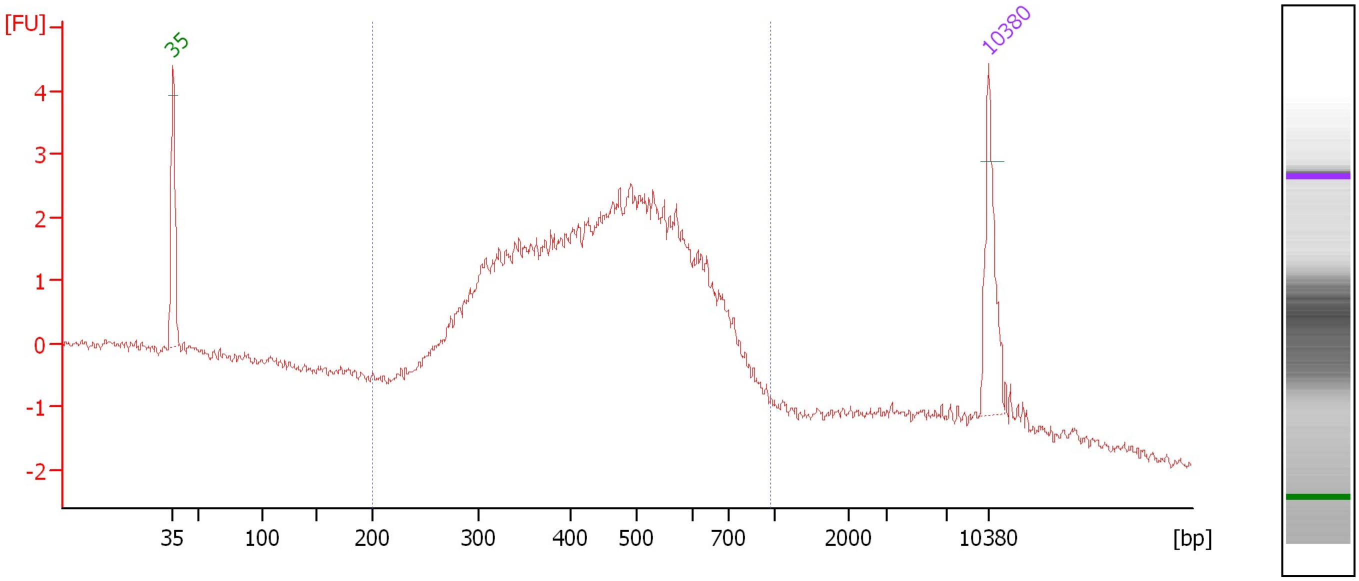
Noise: 0.1

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	L	50	150.00	4,545.5	Ladder Peak	45.23
3	L	100	150.00	2,272.7	Ladder Peak	50.70
4	L	150	150.00	1,515.2	Ladder Peak	55.37
5	L	200	150.00	1,136.4	Ladder Peak	60.04
6	L	300	150.00	757.6	Ladder Peak	69.17
7	L	400	150.00	568.2	Ladder Peak	77.18
8	L	500	150.00	454.5	Ladder Peak	82.83
9	L	600	150.00	378.8	Ladder Peak	87.55
10	L	700	150.00	324.7	Ladder Peak	90.71
11	L	1,000	150.00	227.3	Ladder Peak	94.62
12	L	2,000	150.00	113.6	Ladder Peak	100.98
13	L	3,000	150.00	75.8	Ladder Peak	104.23
14		5,807	0.00	0.0		107.79
15	L	7,000	150.00	32.5	Ladder Peak	109.31
16	▶	10,380	75.00	10.9	Upper Marker	113.00
17		11,398	0.00	0.0		114.11

Electropherogram Summary Continued ...

7: H3K4m_1 lib (1:8) [HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat]



Setpoint Deviations for sample 4 : 7: H3K4m_1 lib (1:8)

Height Threshold [FU] : 4

Overall Results for sample 4 : 7: H3K4m_1 lib (1:8)

Number of peaks found:	0	Corr. Area 1:	84.2
Noise:	0.1		

Peak table for sample 4 : 7: H3K4m_1 lib (1:8)

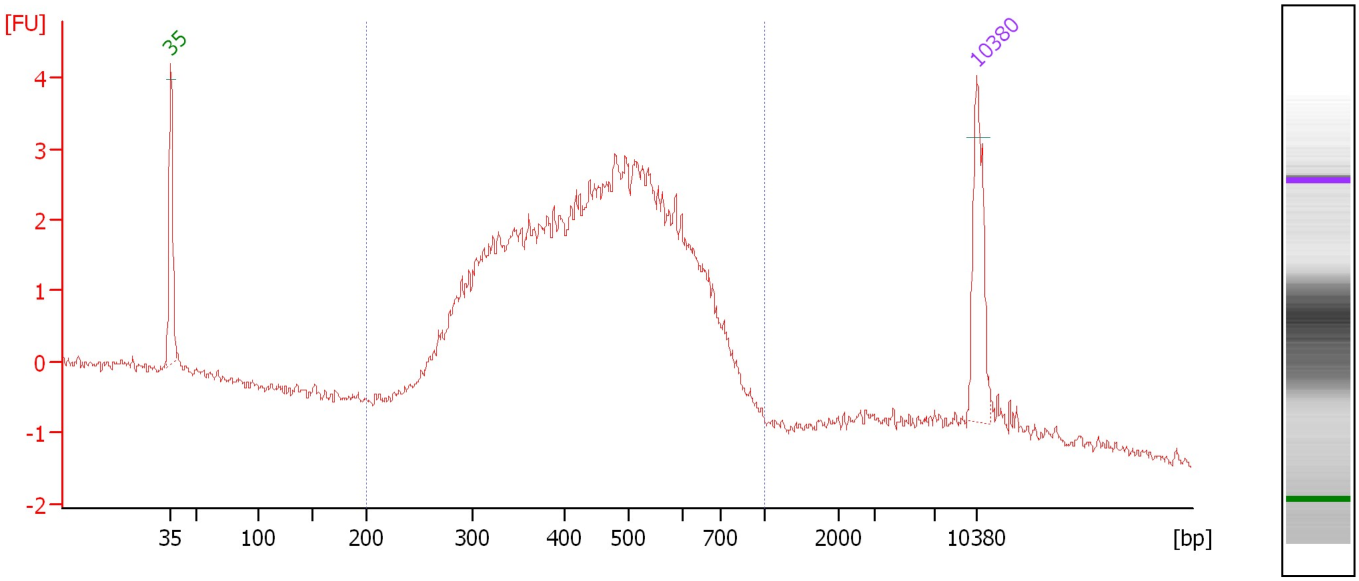
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : 7: H3K4m_1 lib (1:8)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	468	971	84.2	7,038.8	🟦 88	28.4	1,939.09

Electropherogram Summary Continued ...

8: H3K4m_2 lib (1:8) [HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat]



Setpoint Deviations for sample 5 : 8: H3K4m_2 lib (1:8)

Height Threshold [FU] : 4

Overall Results for sample 5 : 8: H3K4m_2 lib (1:8)

Number of peaks found:	0	Corr. Area 1:	83.9
Noise:	0.1		

Peak table for sample 5 : 8: H3K4m_2 lib (1:8)

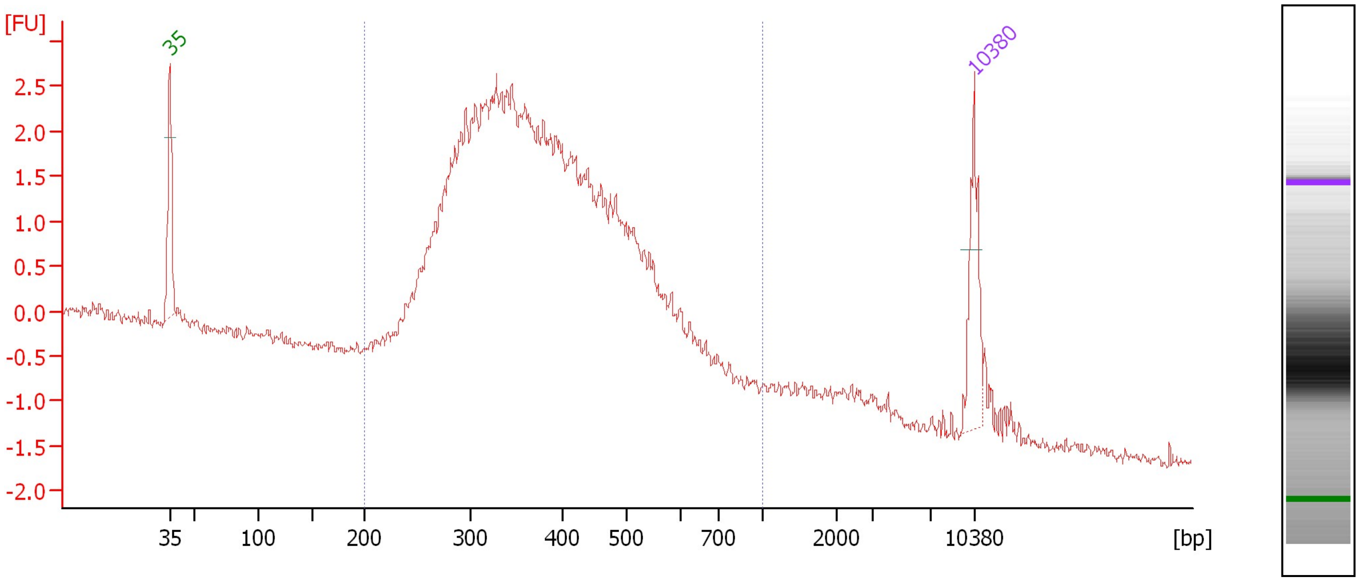
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : 8: H3K4m_2 lib (1:8)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	466	1,000	83.9	7,042.9	■	94	27.2	1,948.88

Electropherogram Summary Continued ...

14: IgG Mouse 2 lib [HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat]



Setpoint Deviations for sample 6 : 14: IgG Mouse 2 lib

Height Threshold [FU] : 2

Overall Results for sample 6 : 14: IgG Mouse 2 lib

Number of peaks found:	0	Corr. Area 1:	73.8
Noise:	0.1		

Peak table for sample 6 : 14: IgG Mouse 2 lib

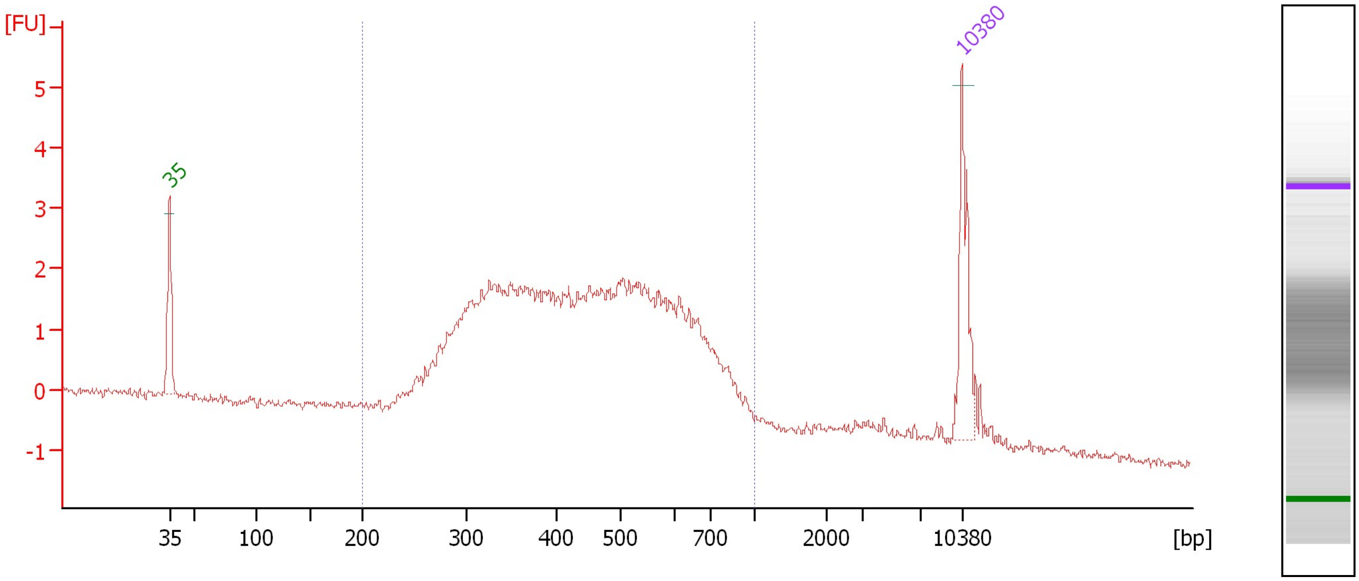
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : 14: IgG Mouse 2 lib

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co lor	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	398	1,000	73.8	11,656.9	■	95	28.7	2,775.35

Electropherogram Summary Continued ...

15: CoupTF::1 lib (1:5) [HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat]



Setpoint Deviations for sample 7 : **15: CoupTF::1 lib (1:5)**

Height Threshold [FU] : 3

Overall Results for sample 7 : **15: CoupTF::1 lib (1:5)**

Number of peaks found:	0	Corr. Area 1:	73.4
Noise:	0.1		

Peak table for sample 7 : **15: CoupTF::1 lib (1:5)**

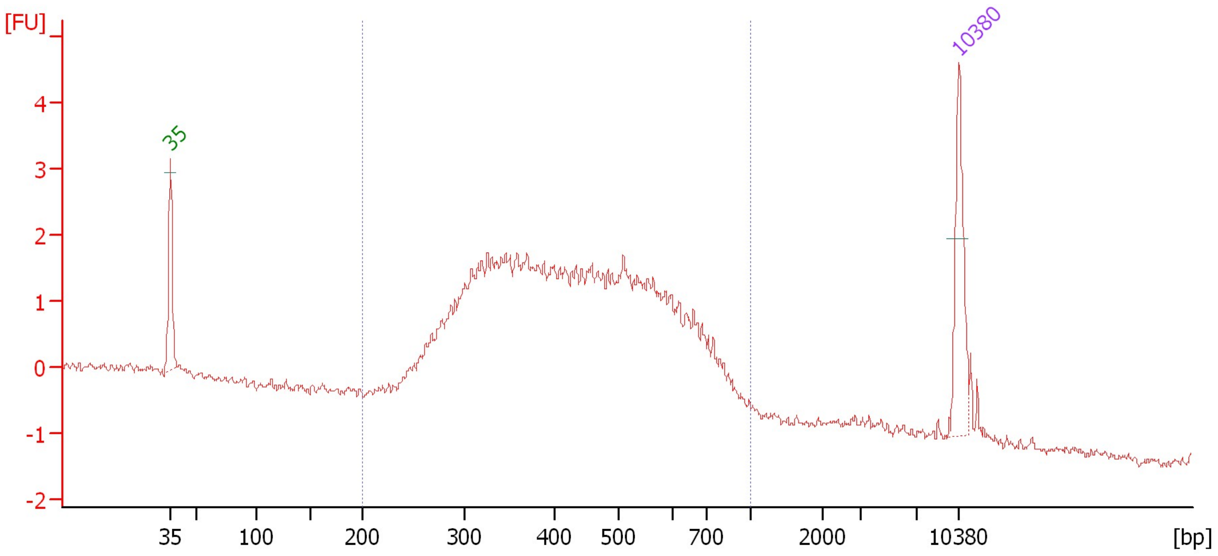
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

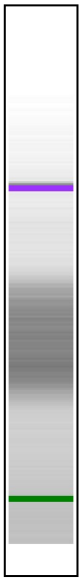
Region table for sample 7 : **15: CoupTF::1 lib (1:5)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	466	1,000	73.4	6,266.7	■	89	32.0	1,675.67

Electropherogram Summary Continued ...

16: CopuTF::2 lib (1:6) [HiSeq_176: Size Selected Lib (0.55X Right/1X Left) Repeat]





Setpoint Deviations for sample 8 : 16: CopuTF::2 lib (1:6)

Height Threshold [FU] : 3

Overall Results for sample 8 : 16: CopuTF::2 lib (1:6)

Number of peaks found:	0	Corr. Area 1:	66.4
Noise:	0.1		

Peak table for sample 8 : 16: CopuTF::2 lib (1:6)

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 : 16: CopuTF::2 lib (1:6)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	455	1,000	66.4	6,472.4	■	94	31.0	1,711.77

Gel Image