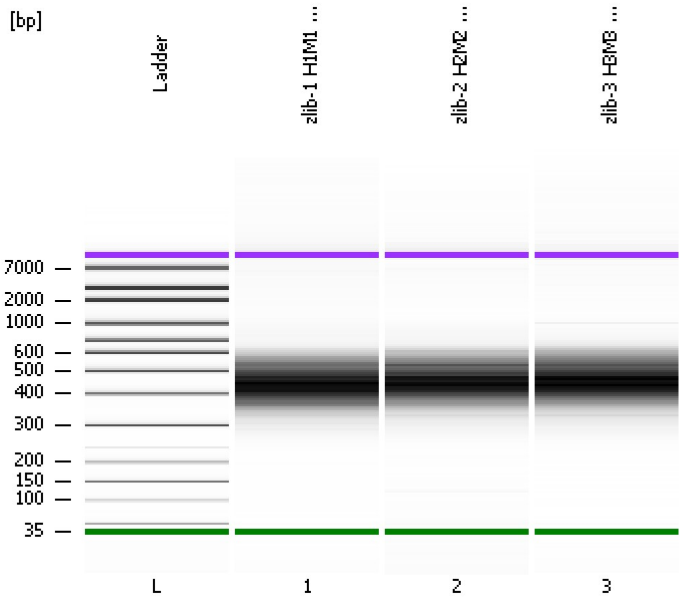
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-03\2016-10-03_001_HiSeq660_SizeSelected_Libraries.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:35:25 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

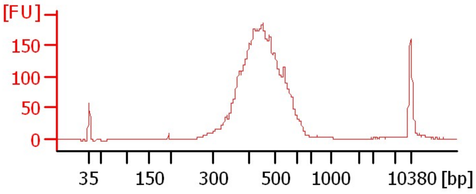
Chip Information:

Chip Lot #:

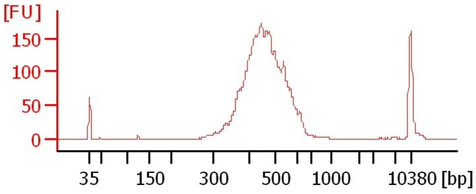
Reagent Kit Lot #:

Chip Comments:

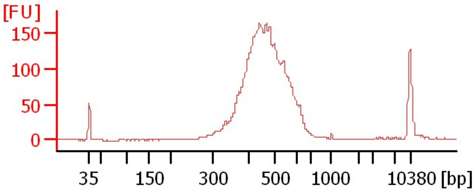
zlib-1 H1M1 0.72X Size Sel Library (1:3)
HiSeq_660



zlib-2 H2M2 0.72X Size Sel Library (1:3)
HiSeq_660



zlib-3 H3M3 0.72X Size Sel Library (1:3)
HiSeq_660



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-03\2016-10-03_001_HiSeq660_SizeSelected_Libraries.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:35:25 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
zlib-1 H1M1 0.72X Size Sel Library (1:3)	HiSeq_660	☐	✓			
zlib-2 H2M2 0.72X Size Sel Library (1:3)	HiSeq_660	☐	✓			
zlib-3 H3M3 0.72X Size Sel Library (1:3)	HiSeq_660	☐	✓			
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

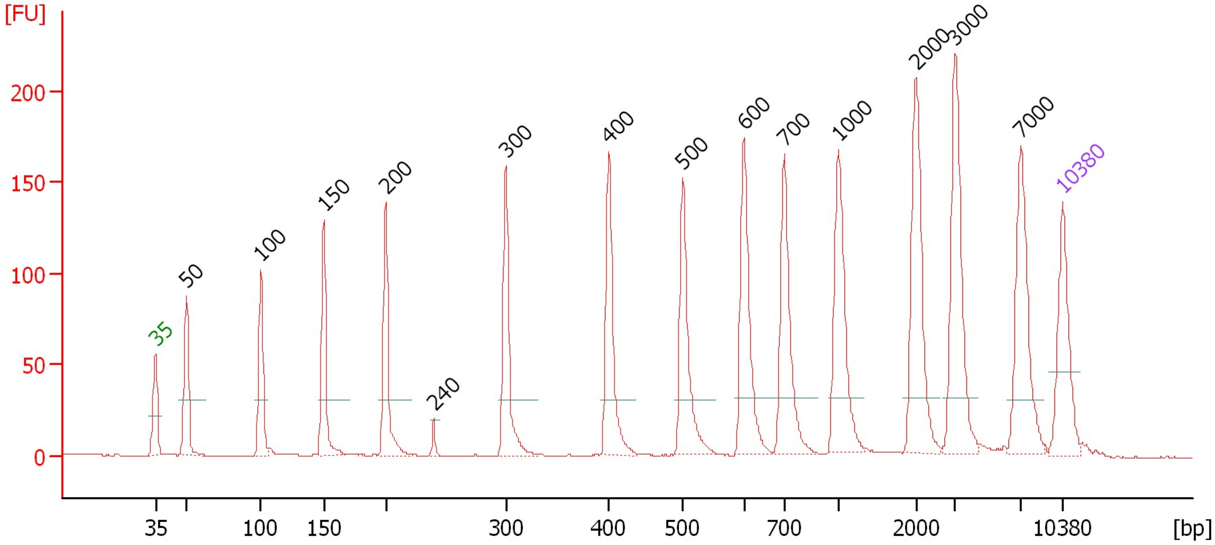
Filter Width [s] : 0.5
Polynomial Order : 4

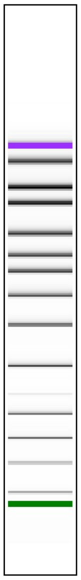
Ladder

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

Electropherogram Summary

Ladder





Overall Results for Ladder

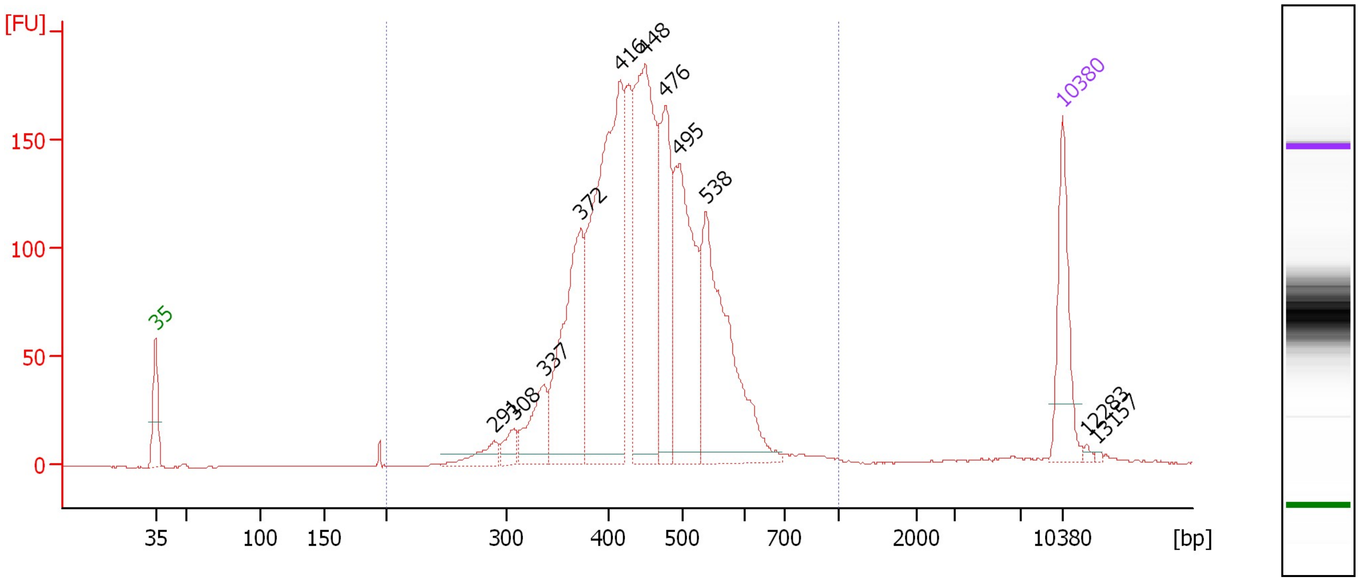
Noise: 0.2

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	45.37
3	∟	100	150.00	2,272.7	Ladder Peak	51.13
4	∟	150	150.00	1,515.2	Ladder Peak	55.96
5	∟	200	150.00	1,136.4	Ladder Peak	60.75
6		240	0.00	0.0		64.44
7	∟	300	150.00	757.6	Ladder Peak	70.01
8	∟	400	150.00	568.2	Ladder Peak	78.00
9	∟	500	150.00	454.5	Ladder Peak	83.67
10	∟	600	150.00	378.8	Ladder Peak	88.40
11	∟	700	150.00	324.7	Ladder Peak	91.51
12	∟	1,000	150.00	227.3	Ladder Peak	95.70
13	∟	2,000	150.00	113.6	Ladder Peak	101.66
14	∟	3,000	150.00	75.8	Ladder Peak	104.72
15	∟	7,000	150.00	32.5	Ladder Peak	109.75
16	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

zlib-1 H1M1 0.72X Size Sel Library (1:3) [HiSeq_660]



Overall Results for sample 1 : zlib-1 H1M1 0.72X Size Sel Library (1:3)

Number of peaks found:	11	Corr. Area 1:	2,445.9
Noise:	0.2		

Peak table for sample 1 : zlib-1 H1M1 0.72X Size Sel Library (1:3)

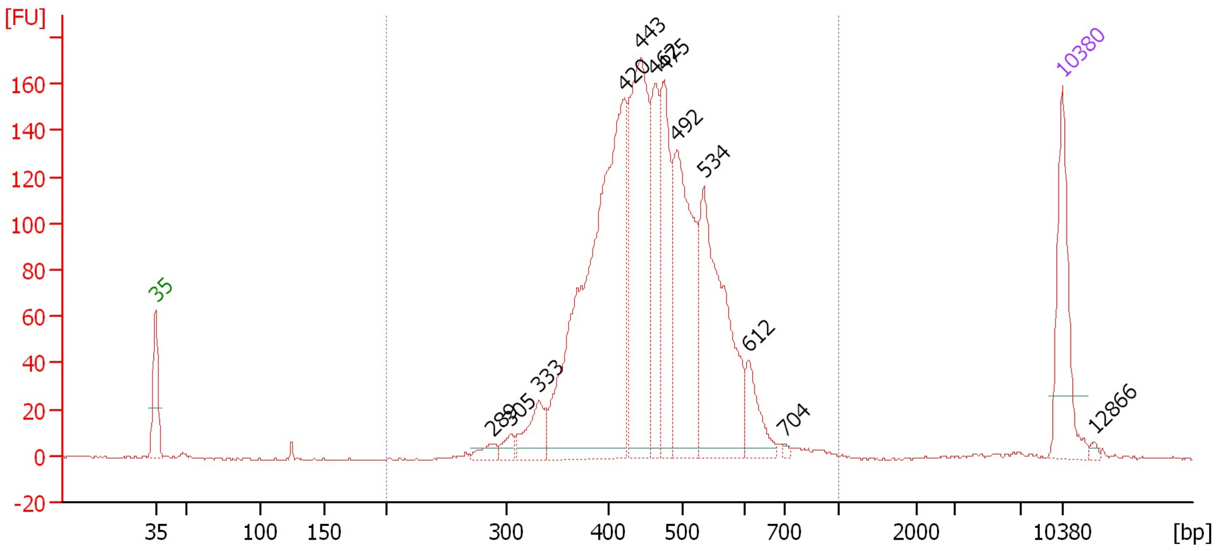
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		291	29.19	152.2		69.14
3		308	22.14	109.0		70.62
4		337	70.15	315.6		72.95
5		372	222.59	906.4		75.77
6		416	447.40	1,630.6		78.89
7		448	351.72	1,189.4		80.72
8		476	161.64	514.6		82.31
9		495	228.51	699.2		83.40
10		538	262.81	739.9		85.48
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,283	0.00	0.0		114.83
13		13,157	0.00	0.0		115.67

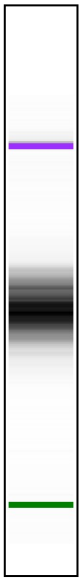
Region table for sample 1 : zlib-1 H1M1 0.72X Size Sel Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	451	2,445.9	6,706.4	🟦	1,919.90	98	18.0

Electropherogram Summary Continued ...

zlib-2 H2M2 0.72X Size Sel Library (1:3) [HiSeq_660]





Overall Results for sample 2 : zlib-2 H2M2 0.72X Size Sel Library (1:3)

Number of peaks found:	12	Corr. Area 1:	2,140.6
Noise:	0.4		

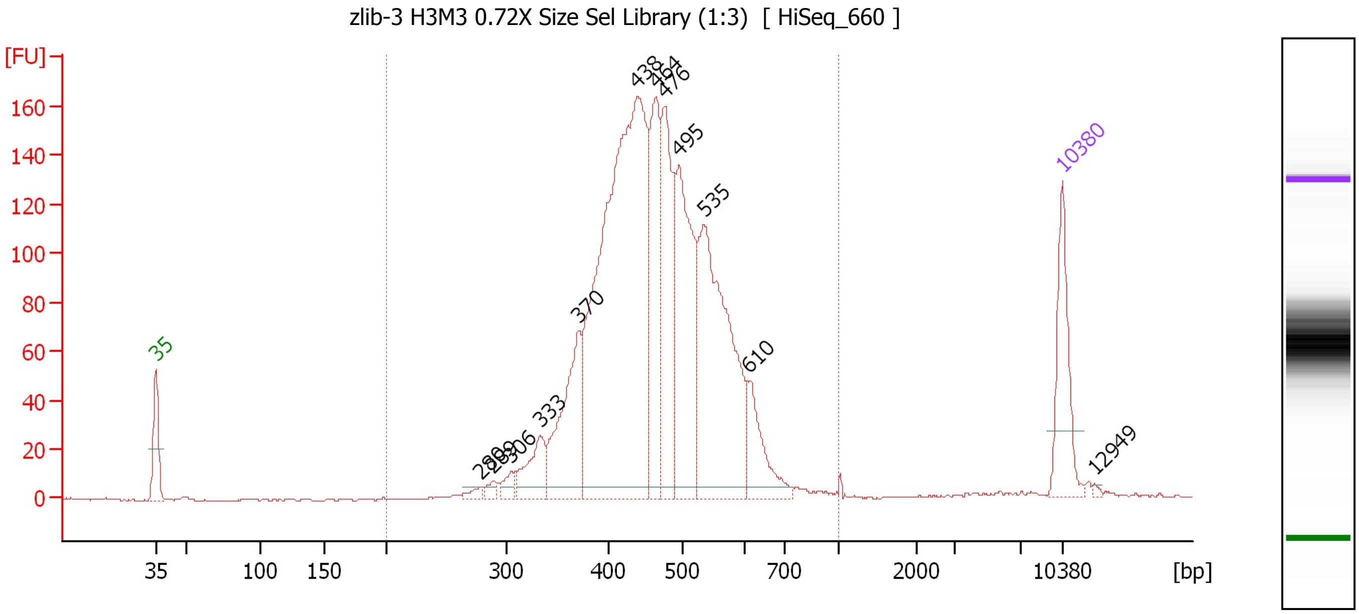
Peak table for sample 2 : zlib-2 H2M2 0.72X Size Sel Library (1:3)

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		289	12.77	66.9		69.03
3		305	12.96	64.3		70.42
4		333	46.51	211.9		72.62
5		420	503.53	1,815.5		79.15
6		443	255.98	875.3		80.44
7		462	107.92	353.6		81.54
8		475	128.39	409.7		82.24
9		492	201.56	620.3		83.24
10		534	229.69	651.7		85.28
11		612	40.86	101.2		88.77
12		704	3.21	6.9		91.56
13	▶	10,380	75.00	10.9	Upper Marker	113.00
14		12,866	0.00	0.0		115.39

Region table for sample 2 : zlib-2 H2M2 0.72X Size Sel Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	462	2,140.6	5,361.1	🟦 1,573.78	98	17.6

Electropherogram Summary Continued ...


zlib-3 H3M3 0.72X Size Sel Library (1:3) [HiSeq_660]

Overall Results for sample 3 : **zlib-3 H3M3 0.72X Size Sel Library (1:3)**

Number of peaks found:	12	Corr. Area 1:	2,168.0
Noise:	0.3		

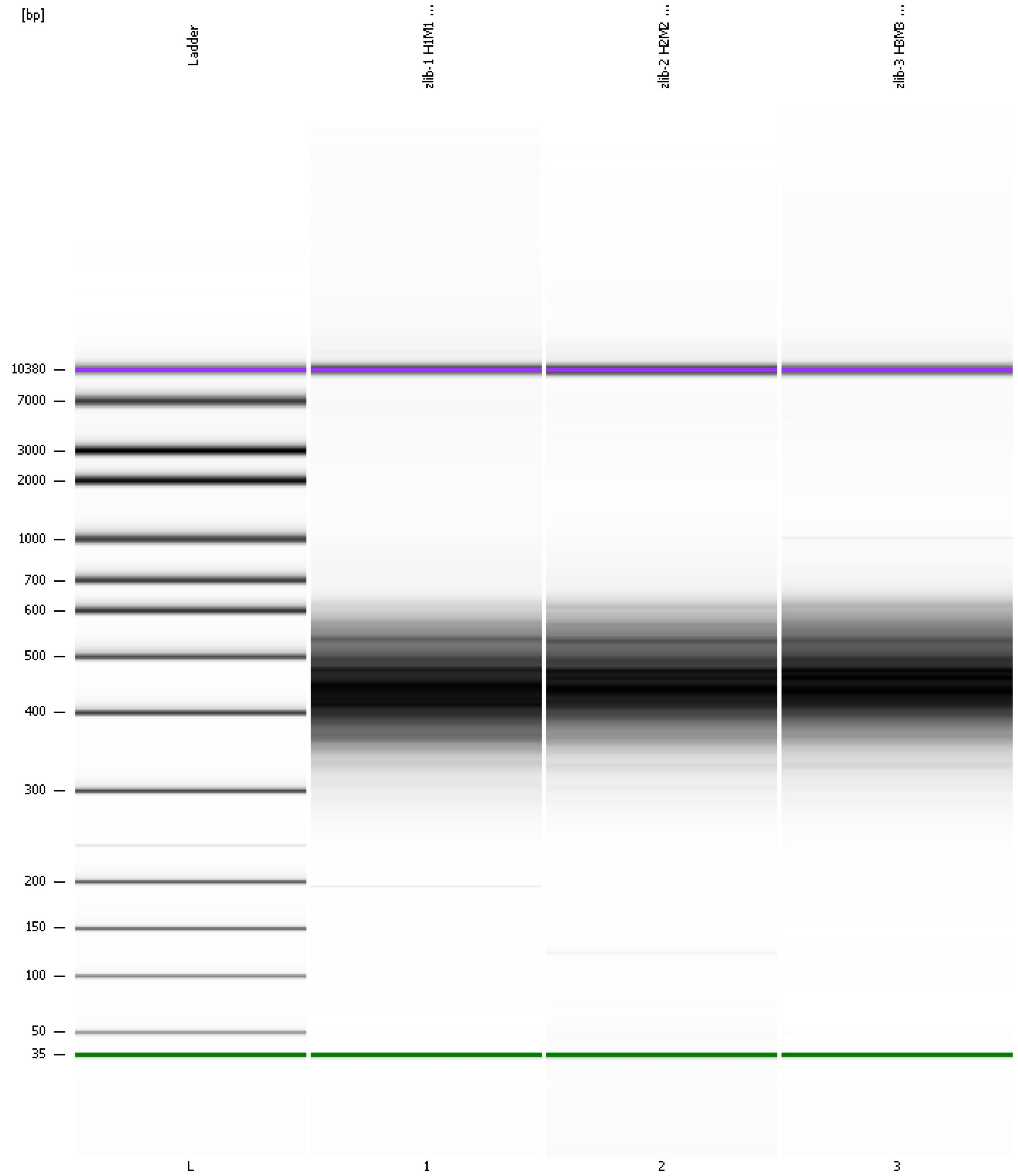
Peak table for sample 3 : **zlib-3 H3M3 0.72X Size Sel Library (1:3)**

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		280	9.25	50.1		68.13
3		289	9.36	49.1		68.99
4		306	16.12	79.9		70.45
5		333	59.45	270.7		72.63
6		370	152.42	624.2		75.60
7		438	764.09	2,644.2		80.14
8		464	174.44	570.0		81.61
9		476	170.10	541.3		82.32
10		495	239.21	732.5		83.37
11		535	329.64	932.9		85.34
12		610	65.35	162.2		88.72
13	▶	10,380	75.00	10.9	Upper Marker	113.00
14		12,949	0.00	0.0		115.47

Region table for sample 3 : **zlib-3 H3M3 0.72X Size Sel Library (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	466	2,168.0	6,836.3	■	2,016.82	98	17.9

Gel Image


[bp]
Ladder
zlib-1 H1M1 ...
zlib-2 H2M2 ...
zlib-3 H3M3 ...
10380
7000
3000
2000
1000
700
600
500
400
300
200
150
100
50
35
L
1
2
3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-03\2016-10-03_001_HiSeq660_SizeSelected_Libraries.xad
Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:35:25 AM

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 12)		Instrument	Run		10/3/2016 11:33:29 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad)		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/3/2016 10:52:18 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1