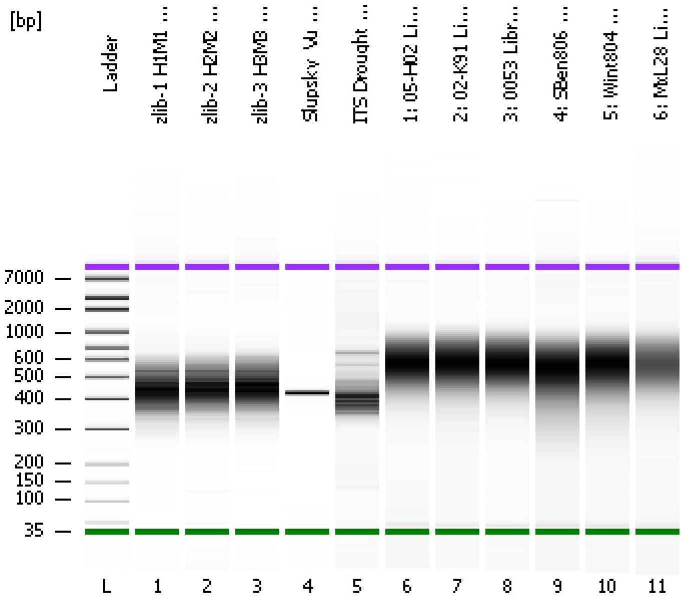
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 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

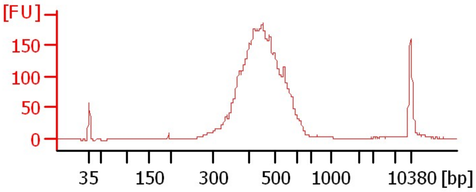
Assay Comments: Copyright © 2003-2010 Agilent Technologies

Chip Information:

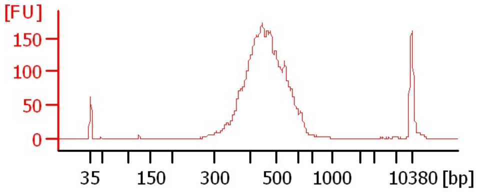
Chip Lot #:

Reagent Kit Lot #:

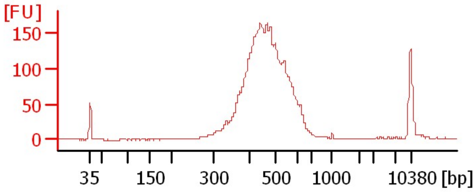
Chip Comments:



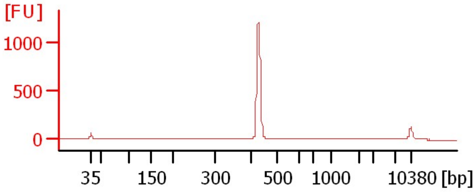
zlib-1 H1M1 0.72X Size Sel Library (1:3)
HiSeq_660



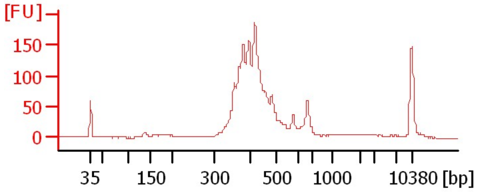
zlib-2 H2M2 0.72X Size Sel Library (1:3)
HiSeq_660



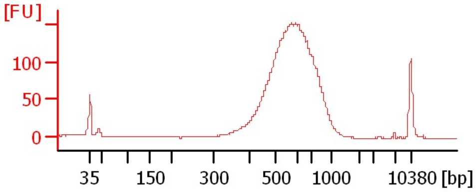
zlib-3 H3M3 0.72X Size Sel Library (1:3)
HiSeq_660



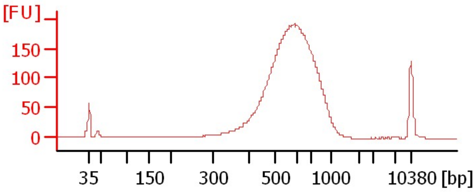
Slupsky_Vu QC-PCR (1:3)



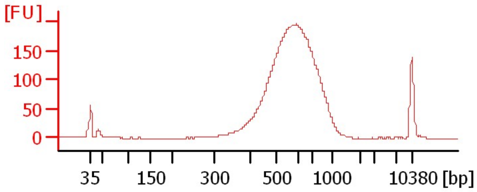
ITS Drought (1:9)



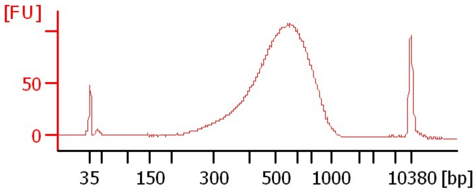
1: 05-H02 Library (1:2)
HiSeq_667



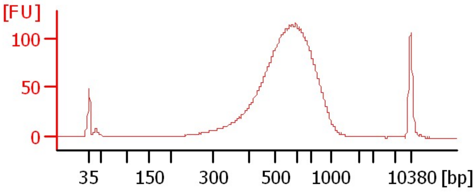
2: 02-K91 Library (1:3)
HiSeq_667



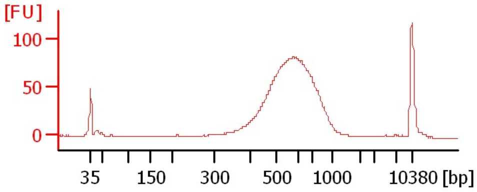
3: 0053 Library (1:2)
HiSeq_667



4: SBen806 Library (1:4)
HiSeq_667



5: Wint804 Library (1:3)
HiSeq_667



6: MxL28 Library (1:3)
HiSeq_667

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 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	☐	✓			
Slupsky_Vu QC-PCR (1:3)		☐	✓			
ITS Drought (1:9)		☐	✓			
1: 05-H02 Library (1:2)	HiSeq_667	☐	✓			
2: 02-K91 Library (1:3)	HiSeq_667	☐	✓			
3: 0053 Library (1:2)	HiSeq_667	☐	✓			
4: SBen806 Library (1:4)	HiSeq_667	☐	✓			
5: Wint804 Library (1:3)	HiSeq_667	☐	✓			
6: MxL28 Library (1:3)	HiSeq_667	☐	✓			
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

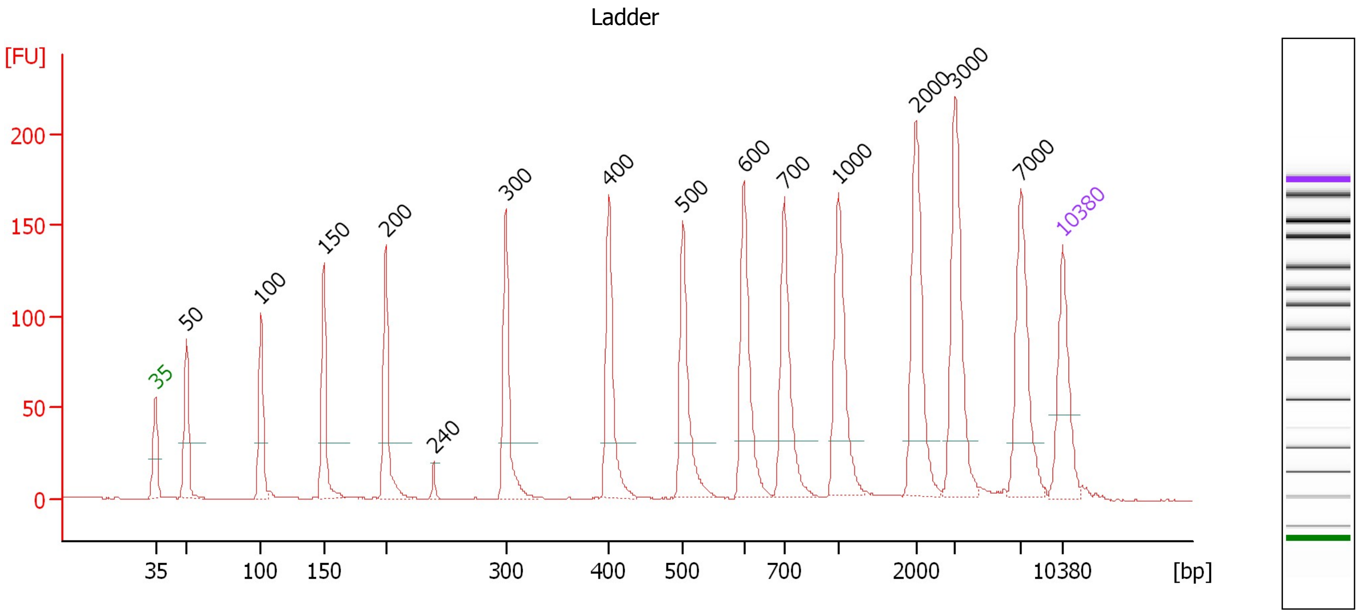
Filter Settings

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



Overall Results for Ladder

Noise: 0.2

Peak table for Ladder

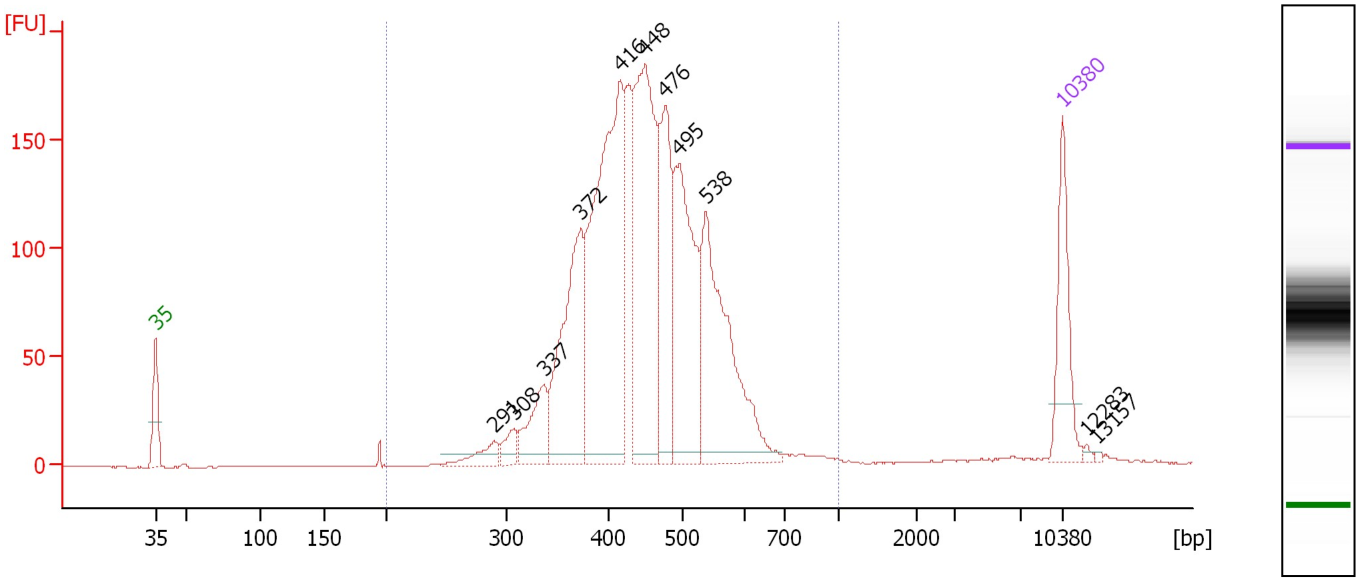
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	L	50	150.00	4,545.5	Ladder Peak	45.37
3	L	100	150.00	2,272.7	Ladder Peak	51.13
4	L	150	150.00	1,515.2	Ladder Peak	55.96
5	L	200	150.00	1,136.4	Ladder Peak	60.75
6		240	0.00	0.0		64.44
7	L	300	150.00	757.6	Ladder Peak	70.01
8	L	400	150.00	568.2	Ladder Peak	78.00
9	L	500	150.00	454.5	Ladder Peak	83.67
10	L	600	150.00	378.8	Ladder Peak	88.40
11	L	700	150.00	324.7	Ladder Peak	91.51
12	L	1,000	150.00	227.3	Ladder Peak	95.70
13	L	2,000	150.00	113.6	Ladder Peak	101.66
14	L	3,000	150.00	75.8	Ladder Peak	104.72
15	L	7,000	150.00	32.5	Ladder Peak	109.75
16	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 AM

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

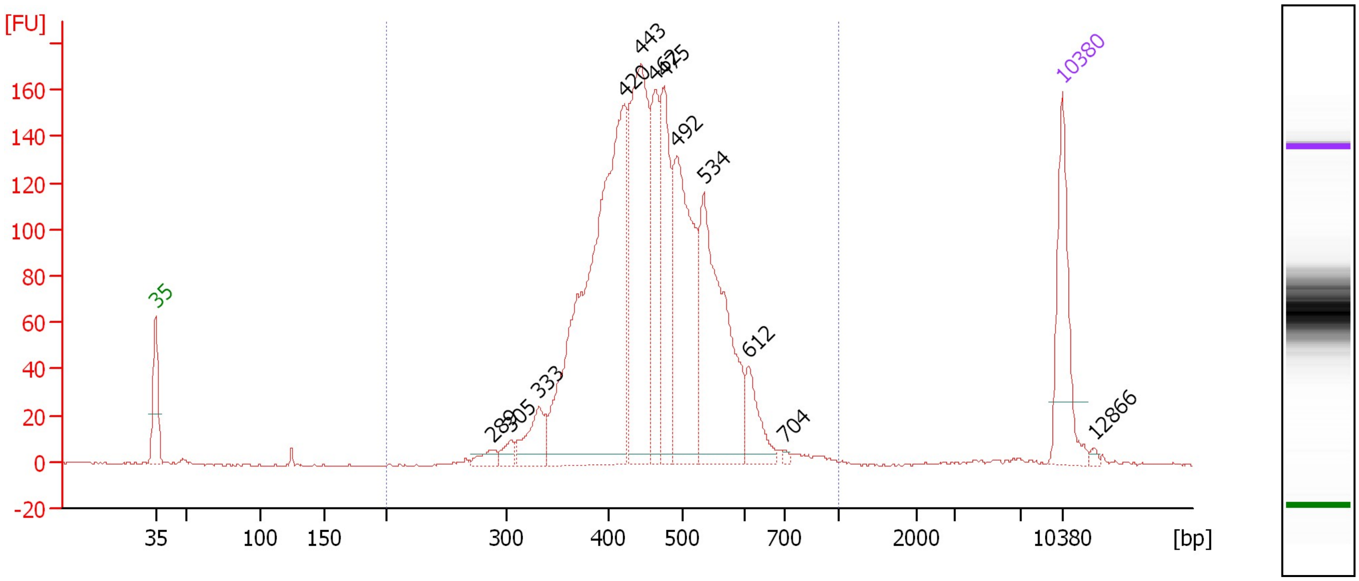
Region table for sample 1 : zlib-1 H1M1 0.72X Size Sel Library (1:3)

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

Assay Class:	High Sensitivity DNA Assay	Created:	10/3/2016 10:52:12 AM
Data Path:	C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad	Modified:	10/3/2016 11:33:30 AM

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)

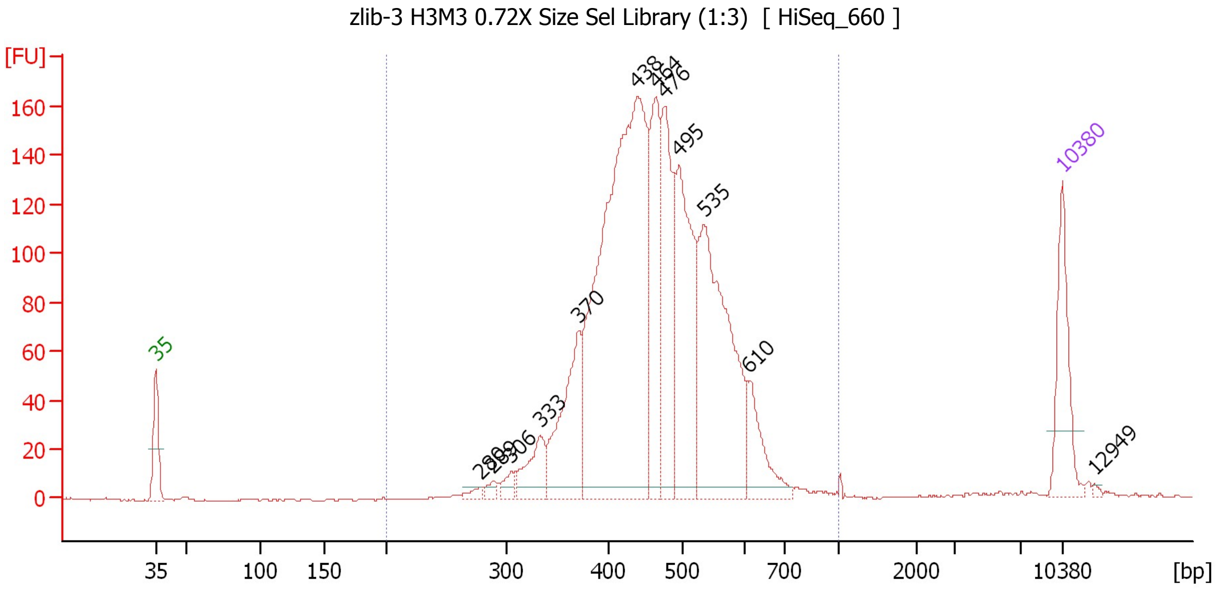
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		289	12.77	66.9		69.03
3		305	12.96	64.3		70.42
4		333	46.51	211.9		72.62
5		420	503.53	1,815.5		79.15
6		443	255.98	875.3		80.44
7		462	107.92	353.6		81.54
8		475	128.39	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

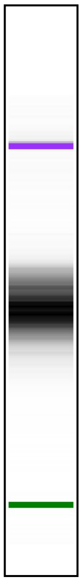
Region table for sample 2 : zlib-2 H2M2 0.72X Size Sel Library (1:3)

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

Assay Class:	High Sensitivity DNA Assay	Created:	10/3/2016 10:52:12 AM
Data Path:	C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad	Modified:	10/3/2016 11:33:30 AM

Electropherogram Summary Continued ...





Overall Results for sample 3 : <u>zlib-3 H3M3 0.72X Size Sel Library (1:3)</u>

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

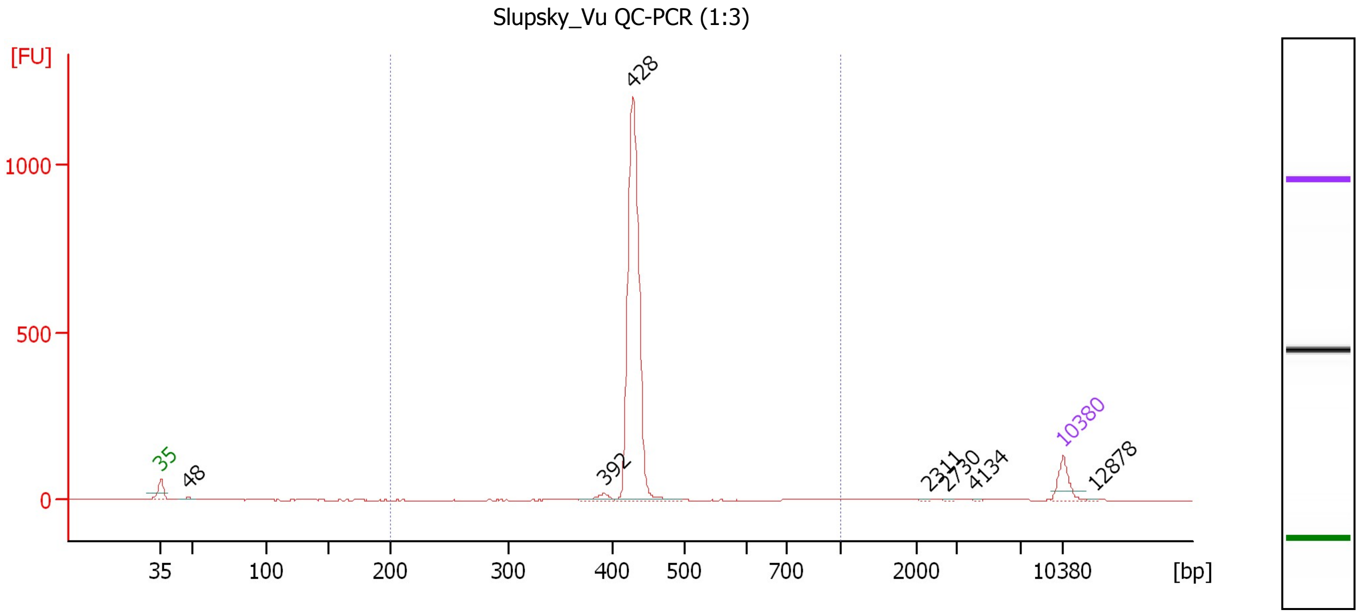
Peak table for sample 3 : <u>zlib-3 H3M3 0.72X Size Sel Library (1:3)</u>

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 : <u>zlib-3 H3M3 0.72X Size Sel Library (1:3)</u>

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

Electropherogram Summary Continued ...



Overall Results for sample 4 : **Slupsky_Vu QC-PCR (1:3)**

Number of peaks found:	7	Corr. Area 1:	1,628.6
Noise:	0.3		

Peak table for sample 4 : **Slupsky_Vu QC-PCR (1:3)**

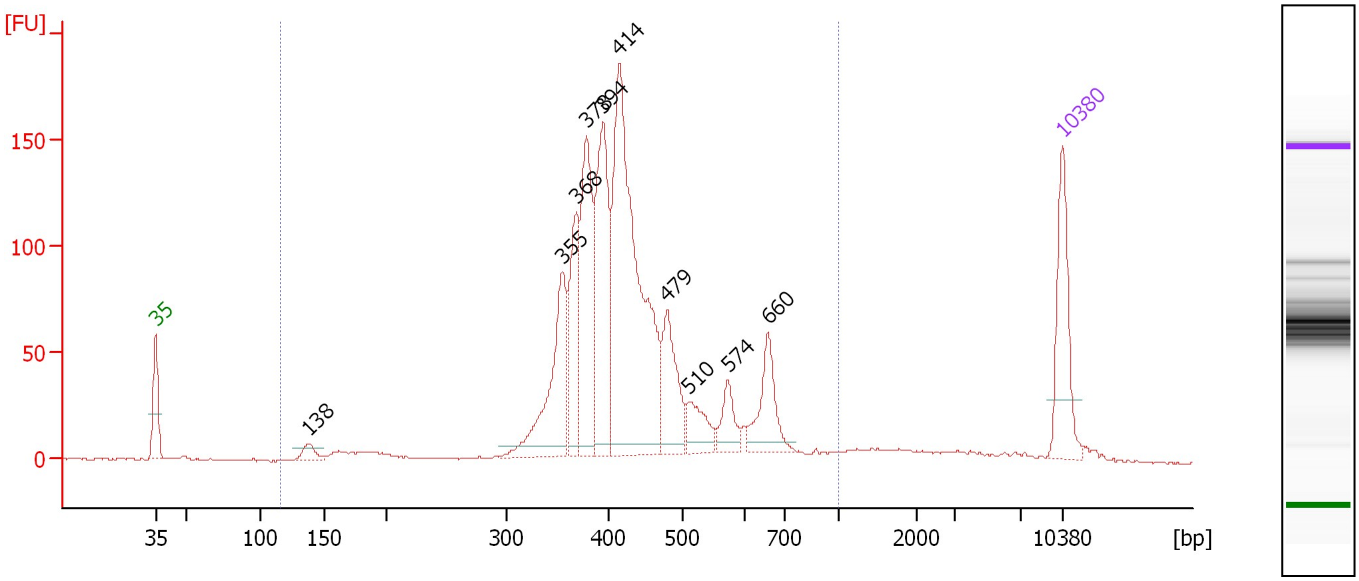
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		48	14.47	453.9		45.10
3		392	29.66	114.7		77.33
4		428	1,462.45	5,177.4		79.59
5		2,311	3.53	2.3		102.61
6		2,730	3.96	2.2		103.89
7		4,134	2.05	0.8		106.14
8	▶	10,380	75.00	10.9	Upper Marker	113.00
9		12,878	0.00	0.0		115.40

Region table for sample 4 : **Slupsky_Vu QC-PCR (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	434	1,628.6	5,568.3	🟦	1,571.61	91	12.4

Electropherogram Summary Continued ...

ITS Drought (1:9)



Overall Results for sample 5 : **ITS Drought (1:9)**

Number of peaks found:	10	Corr. Area 1:	1,715.5
Noise:	0.3		

Peak table for sample 5 : **ITS Drought (1:9)**

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		138	16.83	185.0		54.79
3		355	146.95	627.7		74.38
4		368	99.12	407.8		75.47
5		378	162.85	652.8		76.24
6		394	185.26	712.1		77.53
7		414	420.12	1,538.7		78.78
8		479	82.58	261.0		82.50
9		510	39.28	116.6		84.15
10		574	32.41	85.6		87.15
11		660	61.58	141.5		90.25
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : **ITS Drought (1:9)**

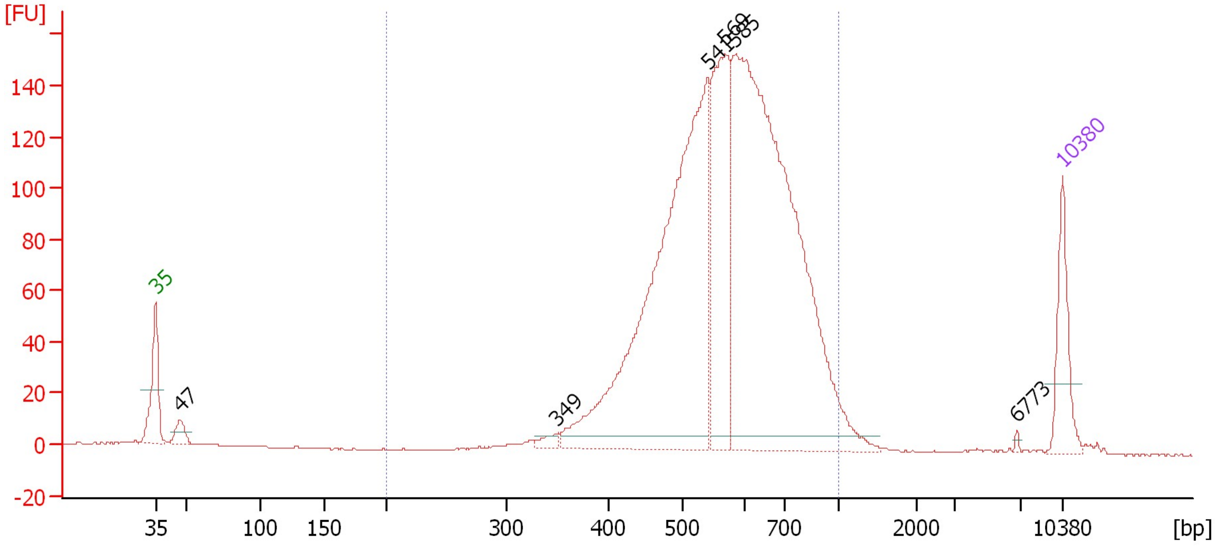
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
116	1,000	434	1,715.5	5,408.5	■	1,406.47	93	24.6

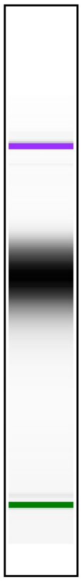
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 AM

Electropherogram Summary Continued ...

1: 05-H02 Library (1:2) [HiSeq_667]





Overall Results for sample 6 : 1: 05-H02 Library (1:2)

Number of peaks found:	6	Corr. Area 1:	2,044.5
Noise:	0.2		

Peak table for sample 6 : 1: 05-H02 Library (1:2)

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		47	31.32	1,005.4		44.93
3		349	13.78	59.9		73.91
4		541	896.87	2,510.3		85.62
5		569	304.08	810.0		86.93
6		585	1,091.51	2,825.5		87.71
7		6,773	2.11	0.5		109.46
8	▶	10,380	75.00	10.9	Upper Marker	113.00

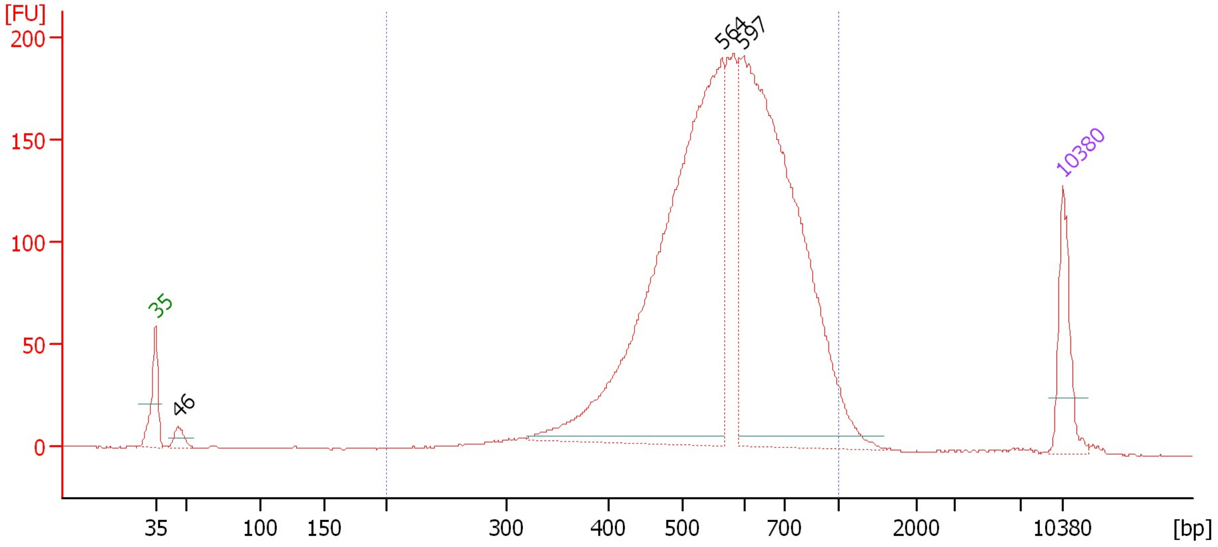
Region table for sample 6 : 1: 05-H02 Library (1:2)

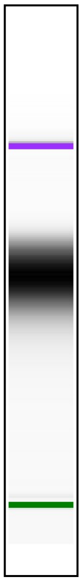
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	589	2,044.5	6,389.2	🟦	2,348.72	96	21.1

Printed: 10/3/2016 11:42:34 AM

Electropherogram Summary Continued ...

2: 02-K91 Library (1:3) [HiSeq_667]





Overall Results for sample 7 : 2: 02-K91 Library (1:3)

Number of peaks found:	3	Corr. Area 1:	2,655.4
Noise:	0.1		

Peak table for sample 7 : 2: 02-K91 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		46	25.86	846.1		44.79
3		564	1,030.94	2,770.3		86.69
4		597	928.80	2,356.7		88.27
5	▶	10,380	75.00	10.9	Upper Marker	113.00

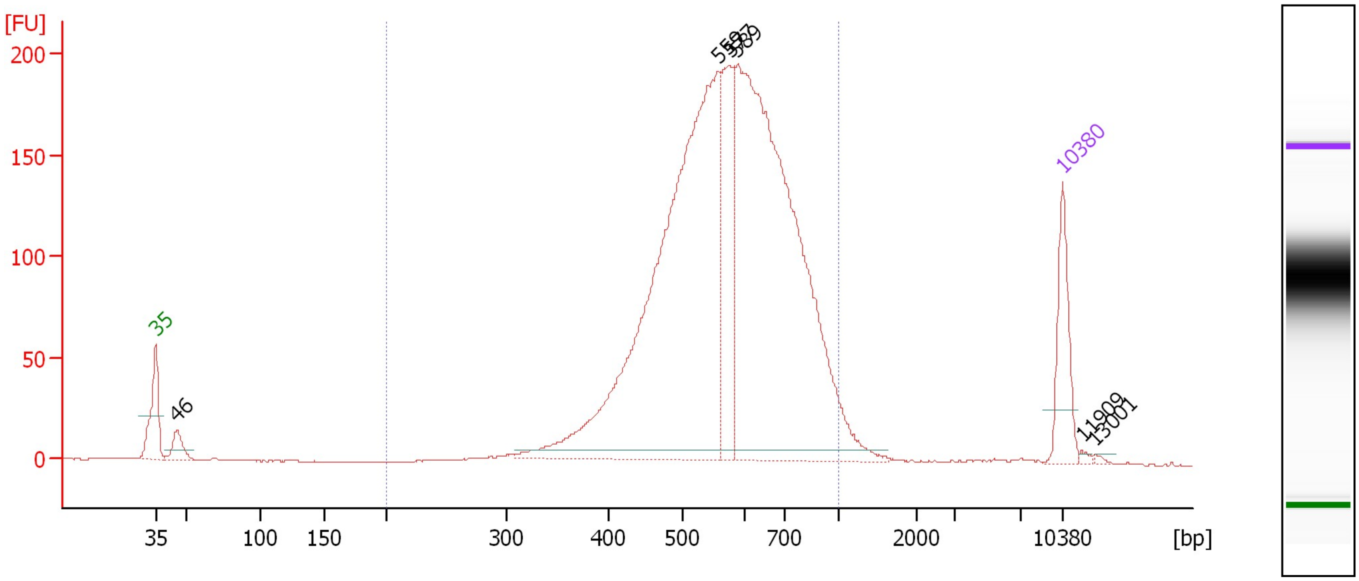
Region table for sample 7 : 2: 02-K91 Library (1:3)

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	588	2,655.4	6,403.9	■	2,318.69	97	22.5

Assay Class:	High Sensitivity DNA Assay	Created:	10/3/2016 10:52:12 AM
Data Path:	C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad	Modified:	10/3/2016 11:33:30 AM

Electropherogram Summary Continued ...

3: 0053 Library (1:2) [HiSeq_667]



Overall Results for sample 8 : **3: 0053 Library (1:2)**

Number of peaks found:	6	Corr. Area 1:	2,679.2
Noise:	0.2		

Peak table for sample 8 : **3: 0053 Library (1:2)**

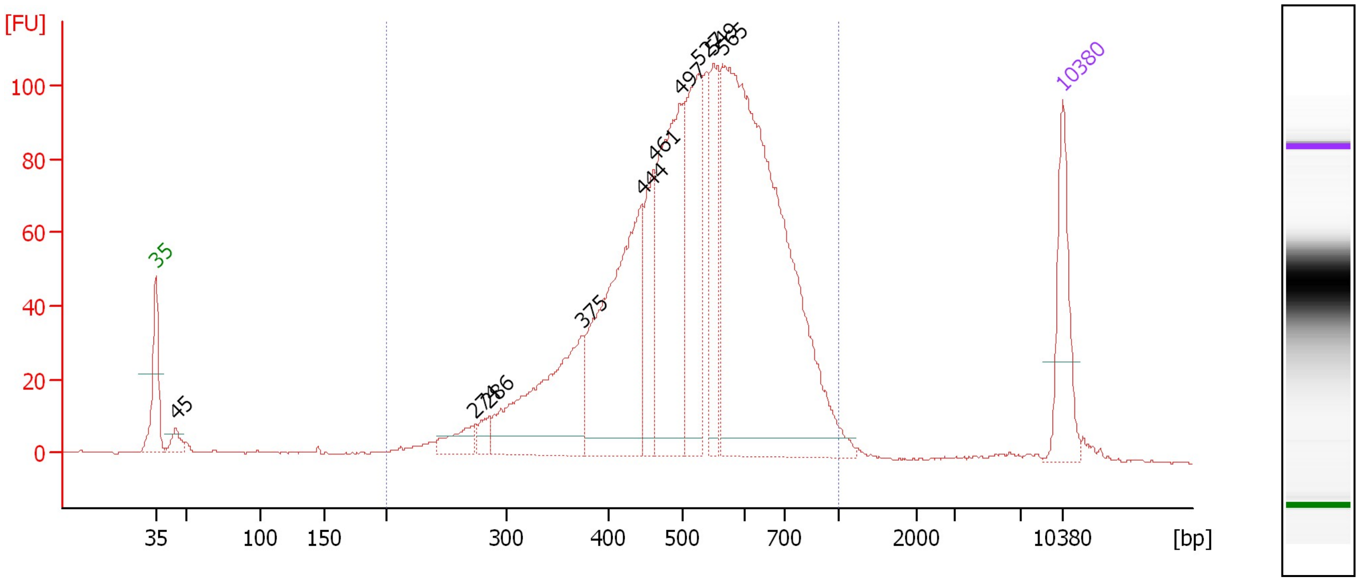
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		46	36.42	1,208.6		44.68
3		559	1,020.84	2,767.0		86.46
4		577	191.72	503.6		87.30
5		589	987.85	2,541.2		87.88
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		11,909	0.00	0.0		114.47
8		13,001	0.00	0.0		115.52

Region table for sample 8 : **3: 0053 Library (1:2)**

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	588	2,679.2	6,253.1	🟦	2,280.06	96	22.0

Electropherogram Summary Continued ...

4: SBen806 Library (1:4) [HiSeq_667]



Overall Results for sample 9 : 4: SBen806 Library (1:4)

Number of peaks found:	10	Corr. Area 1:	1,861.9
Noise:	0.2		

Peak table for sample 9 : 4: SBen806 Library (1:4)

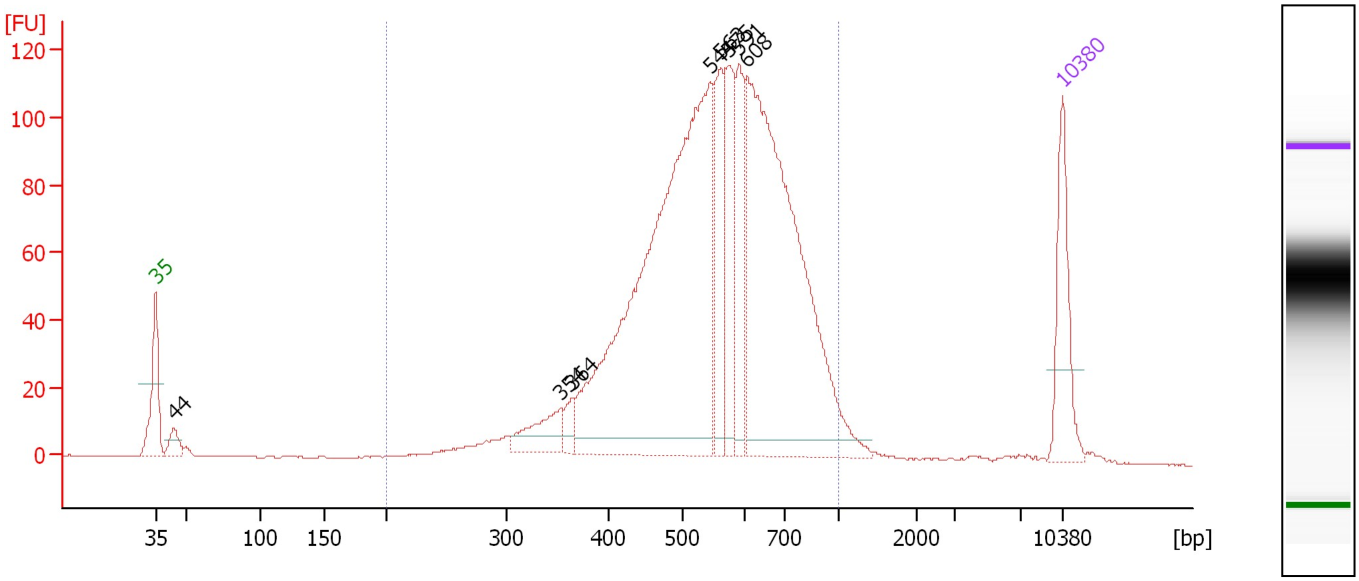
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		45	20.57	692.9		44.58
3		274	34.21	189.0		67.63
4		286	18.83	99.7		68.73
5		375	226.15	914.5		75.98
6		444	323.36	1,103.5		80.49
7		461	94.13	309.6		81.44
8		497	279.70	853.0		83.49
9		527	192.12	552.1		84.96
10		549	101.31	279.4		86.01
11		565	747.53	2,004.8		86.74
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : 4: SBen806 Library (1:4)

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	530	1,861.9	6,881.9	■	2,173.11	95	25.6

Electropherogram Summary Continued ...

5: Wint804 Library (1:3) [HiSeq_667]



Overall Results for sample 10 : 5: Wint804 Library (1:3)

Number of peaks found:	8	Corr. Area 1:	1,781.4
Noise:	0.1		

Peak table for sample 10 : 5: Wint804 Library (1:3)

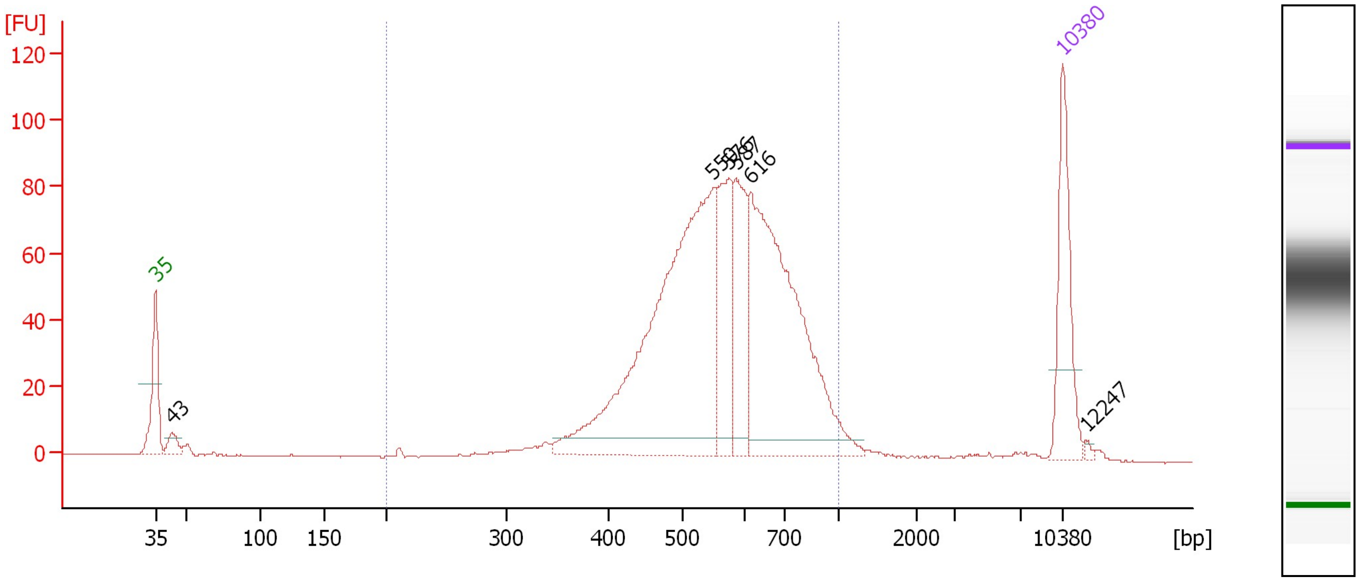
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		44	25.35	872.8		44.42
3		354	52.89	226.6		74.29
4		364	20.22	84.1		75.13
5		544	772.11	2,150.0		85.76
6		563	112.04	301.5		86.65
7		575	97.78	257.6		87.23
8		591	94.91	243.4		87.97
9		608	573.62	1,429.5		88.65
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : 5: Wint804 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	565	1,781.4	5,558.3	■	1,901.03	96	24.2

Electropherogram Summary Continued ...

6: MxL28 Library (1:3) [HiSeq_667]



Overall Results for sample 11 : **6: MxL28 Library (1:3)**

Number of peaks found:	6	Corr. Area 1:	1,143.4
Noise:	0.1		

Peak table for sample 11 : **6: MxL28 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		43	18.08	631.5		44.32
3		550	478.75	1,318.8		86.04
4		576	103.27	271.8		87.25
5		587	91.70	236.8		87.78
6		616	346.52	852.6		88.89
7	▶	10,380	75.00	10.9	Upper Marker	113.00
8		12,247	0.00	0.0		114.80

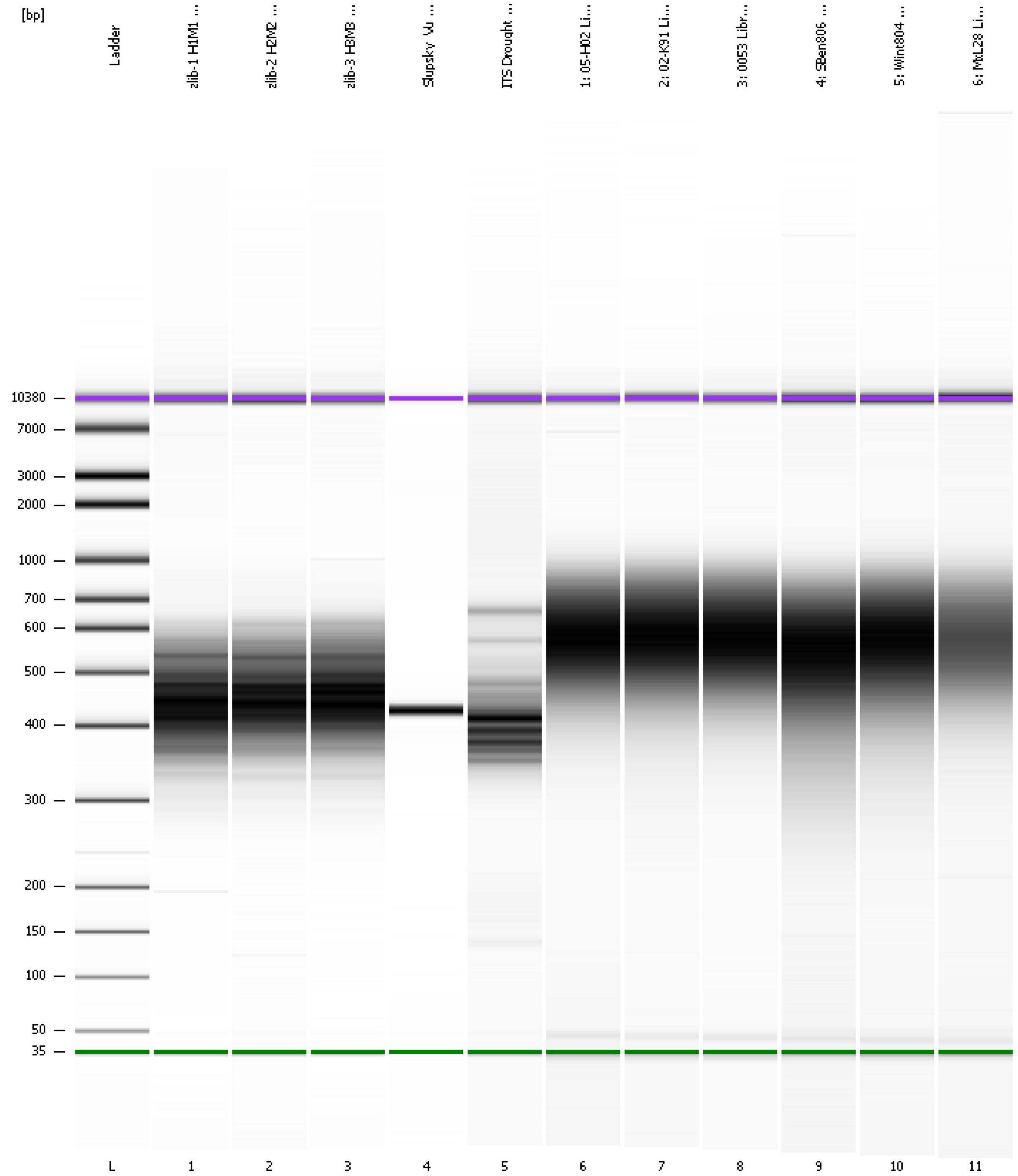
Region table for sample 11 : **6: MxL28 Library (1:3)**

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	580	1,143.4	3,030.6	🟦	1,088.39	95	22.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad

Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 AM

Gel Image



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-10-03\2016-10-03_001.xad
Created: 10/3/2016 10:52:12 AM
Modified: 10/3/2016 11:33:30 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