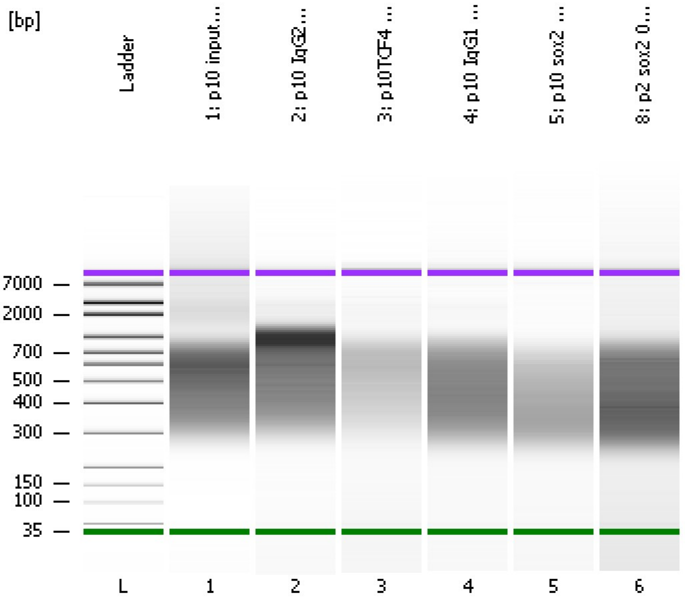
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-04\2016-10-04_001_HiSeq642_SizeSelected_Libraries.xad

Created: 10/4/2016 12:45:40 PM
Modified: 10/4/2016 1:33:43 PM

Electrophoresis File Run Summary



Instrument Information:

Instrument Name: DE13701086
Firmware: C.01.069
Serial#: DE13701086
Type: G2938B

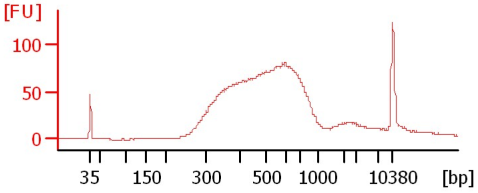
Assay Information:

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

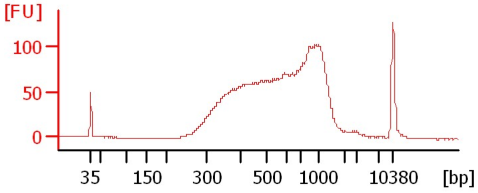
Chip Information:

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

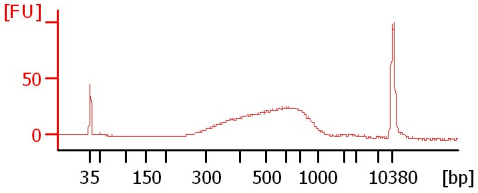
1: p10 input 0.55XR / 0.8X L SS lib
14 cyc PCR



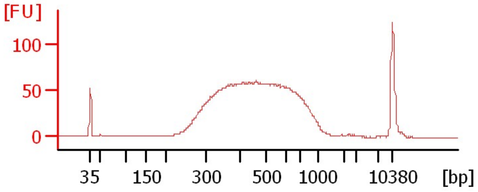
2: p10 IgG2a 0.55XR / 0.8X L SS lib
14 cyc PCR



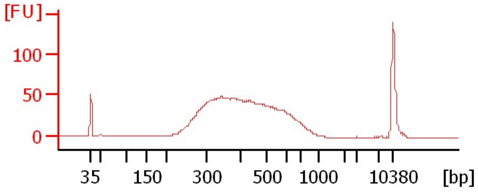
3: p10TCF4 0.55XR / 0.8X L SS lib
14 cyc PCR



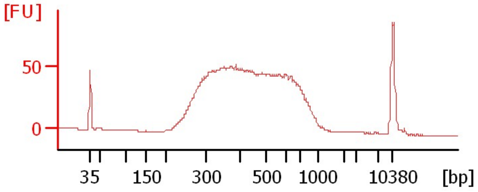
4: p10 IgG1 0.55XR / 0.8X L SS lib
19 cyc PCR



5: p10 sox2 0.55XR / 0.8X L SS lib
19 cyc PCR



8: p2 sox2 0.55XR / 0.8X L SS lib
19 cyc PCR



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-04\2016-10-04_001_HiSeq642_SizeSelected_Libraries.xad
Created: 10/4/2016 12:45:40 PM
Modified: 10/4/2016 1:33:43 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1: p10 input 0.55XR / 0.8X L SS	14 cyc PCR	☐	✓			
2: p10 IgG2a 0.55XR / 0.8X L SS lib	14 cyc PCR	☐	✓			
3: p10TCF4 0.55XR / 0.8X L SS lib	14 cyc PCR	☐	✓			
4: p10 IgG1 0.55XR / 0.8X L SS	19 cyc PCR	☐	✓			
5: p10 sox2 0.55XR / 0.8X L SS	19 cyc PCR	☐	✓			
8: p2 sox2 0.55XR / 0.8X L SS lib	19 cyc PCR	☐	✓			
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

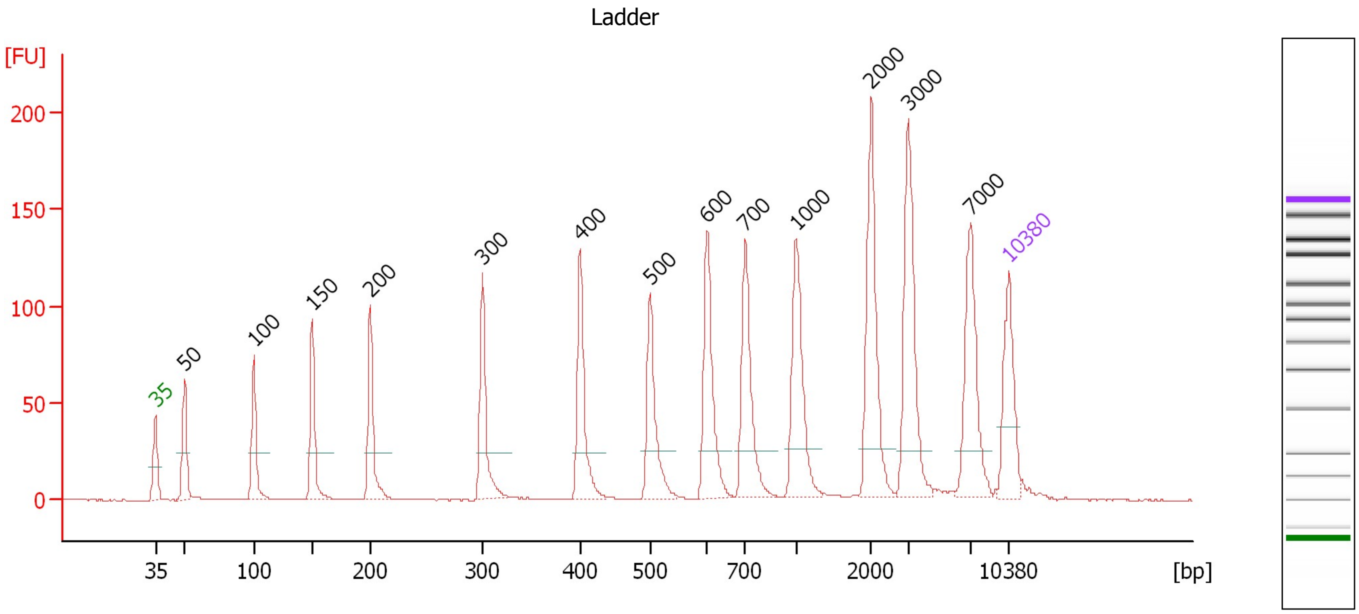
Filter Width [s] : 0.5
Polynomial Order : 4

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:	10/4/2016 12:45:40 PM
Data Path:	C:\...16-10-04\2016-10-04_001_HiSeq642_SizeSelected_Libraries.xad	Modified:	10/4/2016 1:33:43 PM

Electropherogram Summary



Overall Results for Ladder

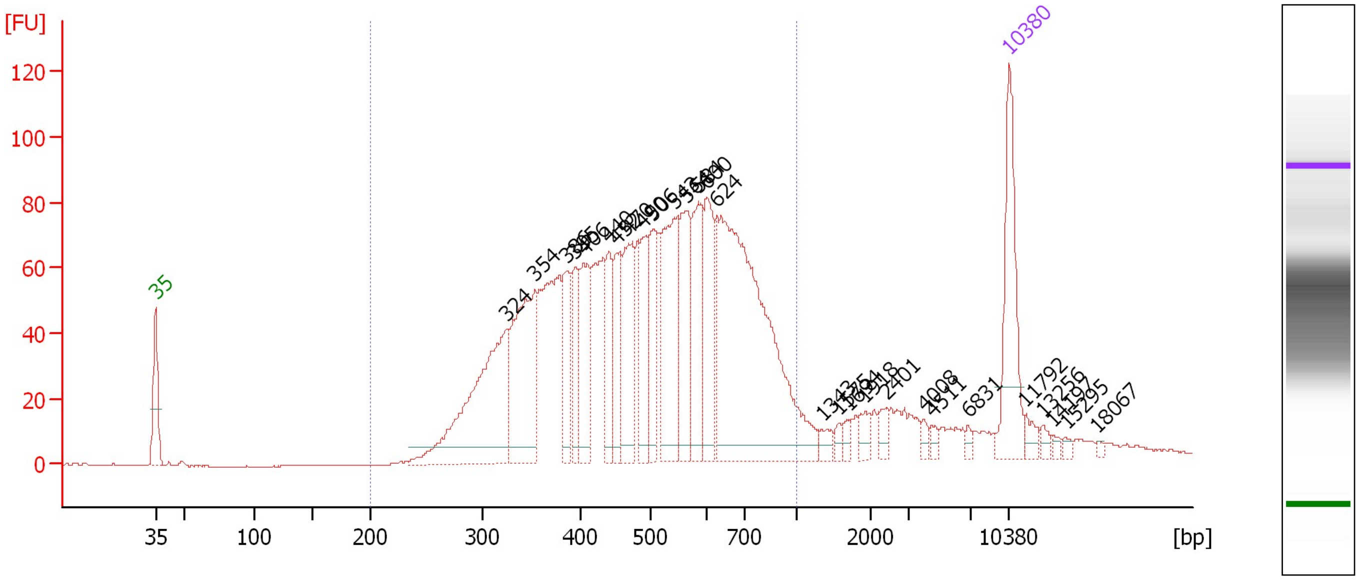
Noise: 0.2

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	45.40
3	∟	100	150.00	2,272.7	Ladder Peak	51.08
4	∟	150	150.00	1,515.2	Ladder Peak	55.87
5	∟	200	150.00	1,136.4	Ladder Peak	60.62
6	∟	300	150.00	757.6	Ladder Peak	69.83
7	∟	400	150.00	568.2	Ladder Peak	77.80
8	∟	500	150.00	454.5	Ladder Peak	83.53
9	∟	600	150.00	378.8	Ladder Peak	88.23
10	∟	700	150.00	324.7	Ladder Peak	91.36
11	∟	1,000	150.00	227.3	Ladder Peak	95.52
12	∟	2,000	150.00	113.6	Ladder Peak	101.69
13	∟	3,000	150.00	75.8	Ladder Peak	104.73
14	∟	7,000	150.00	32.5	Ladder Peak	109.82
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

1: p10 input 0.55XR / 0.8X L SS lib [14 cyc PCR]



Overall Results for sample 1 : **1: p10 input 0.55XR / 0.8X L SS lib**

Number of peaks found:	28	Corr. Area 1:	1,923.1
Noise:	0.2		

Peak table for sample 1 : **1: p10 input 0.55XR / 0.8X L SS 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		324	214.99	1,005.0		71.75
3		354	153.40	657.1		74.11
4		386	55.47	217.8		76.67
5		395	47.89	183.7		77.41
6		406	70.12	261.7		78.15
7		440	52.71	181.3		80.12
8		452	52.64	176.3		80.81
9		470	80.54	259.9		81.79
10		490	55.24	170.7		82.97
11		506	63.74	190.9		83.81
12		543	112.41	313.9		85.53
13		564	82.48	221.8		86.52
14		584	74.10	192.1		87.50
15		600	73.11	184.5		88.24
16		624	363.47	882.8		88.98
17		1,343	8.70	9.8		97.64
18		1,575	5.65	5.4		99.07
19		1,694	6.17	5.5		99.81
20		1,918	10.56	8.3		101.19
21		2,401	9.00	5.7		102.91
22		4,008	4.92	1.9		106.01
23		4,511	5.06	1.7		106.65
24		6,831	4.03	0.9		109.60
25	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Peak table for sample 1 : 1: p10 input 0.55XR / 0.8X L SS lib

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	11,792	0.00	0.0		114.33
27	13,256	0.00	0.0		115.71
28	14,197	0.00	0.0		116.59
29	15,295	0.00	0.0		117.63
30	18,067	0.00	0.0		120.24

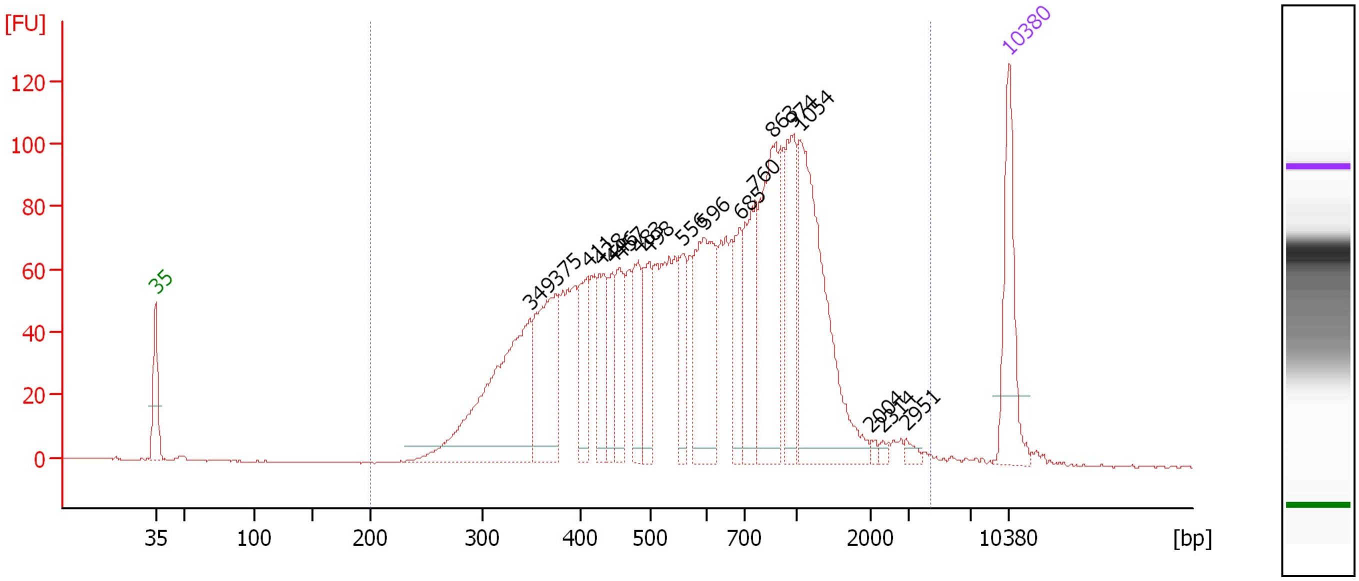
Region table for sample 1 : 1: p10 input 0.55XR / 0.8X L SS lib

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	511	1,923.1	6,192.1	🟦	1,844.12	88	30.2

Assay Class:	High Sensitivity DNA Assay	Created:	10/4/2016 12:45:40 PM
Data Path:	C:\...16-10-04\2016-10-04_001_HiSeq642_SizeSelected_Libraries.xad	Modified:	10/4/2016 1:33:43 PM

Electropherogram Summary Continued ...

2: p10 IgG2a 0.55XR / 0.8X L SS lib [14 cyc PCR]



Overall Results for sample 2 : **2: p10 IgG2a 0.55XR / 0.8X L SS lib**

Number of peaks found:	18	Corr. Area 1:	2,309.1
Noise:	0.2		

Peak table for sample 2 : **2: p10 IgG2a 0.55XR / 0.8X L SS lib**

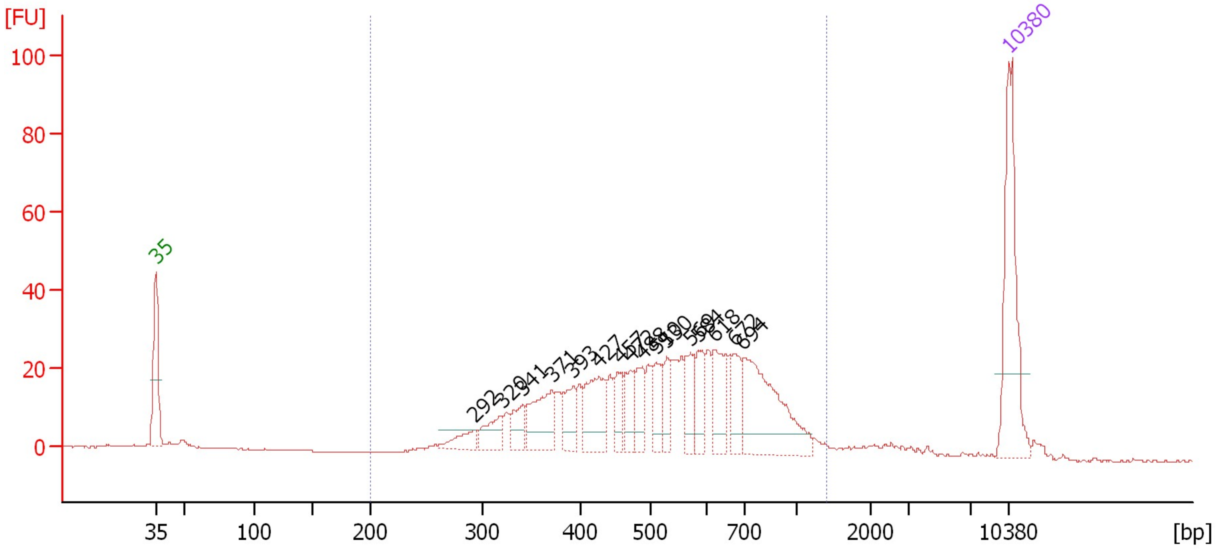
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		349	265.06	1,151.6		73.71
3		375	145.13	586.7		75.80
4		411	67.22	248.0		78.42
5		428	61.31	217.0		79.41
6		446	46.36	157.4		80.45
7		457	57.75	191.6		81.05
8		483	65.61	206.0		82.53
9		498	54.21	164.9		83.42
10		556	52.21	142.4		86.15
11		596	145.59	370.3		88.03
12		685	51.15	113.1		90.91
13		760	86.99	173.5		92.19
14		863	164.50	288.7		93.63
15		974	96.38	149.9		95.17
16		1,054	228.28	328.1		95.86
17		2,004	3.27	2.5		101.70
18		2,314	3.58	2.3		102.65
19		2,951	5.78	3.0		104.58
20	▶	10,380	75.00	10.9	Upper Marker	113.00

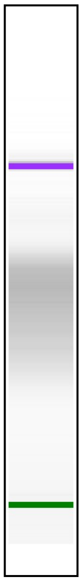
Region table for sample 2 : **2: p10 IgG2a 0.55XR / 0.8X L SS lib**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	4,376	706	2,309.1	6,147.7	■	2,123.68	99	59.2

Electropherogram Summary Continued ...

3: p10TCF4 0.55XR / 0.8X L SS lib [14 cyc PCR]





Overall Results for sample 3 : **3: p10TCF4 0.55XR / 0.8X L SS lib**

Number of peaks found:	16	Corr. Area 1:	612.8
Noise:	0.2		

Peak table for sample 3 : **3: p10TCF4 0.55XR / 0.8X L SS lib**

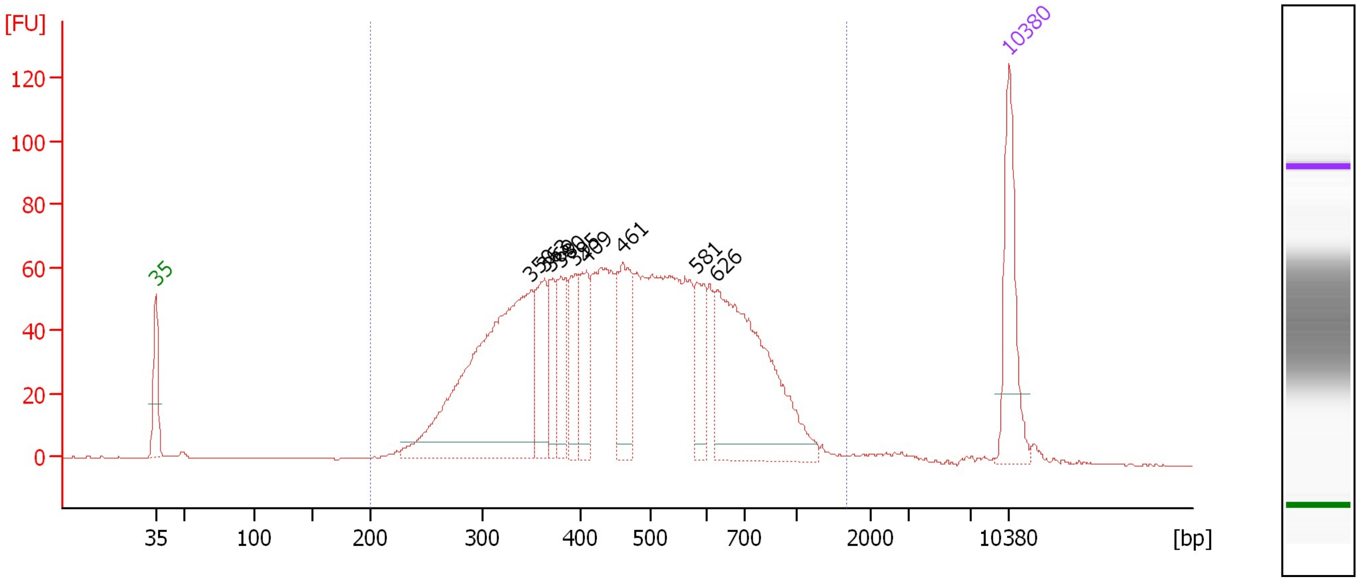
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		292	16.91	87.7		69.11
3		320	22.57	107.0		71.38
4		341	20.92	92.9		73.10
5		371	46.78	191.2		75.47
6		393	23.40	90.2		77.24
7		427	46.94	166.5		79.36
8		457	18.57	61.5		81.08
9		472	22.98	73.7		81.94
10		488	23.77	73.8		82.85
11		510	25.90	76.9		84.01
12		530	19.02	54.4		84.92
13		569	24.85	66.1		86.79
14		584	23.58	61.1		87.49
15		618	33.15	81.2		88.81
16		672	28.29	63.8		90.47
17		694	96.28	210.2		91.18
18	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : **3: p10TCF4 0.55XR / 0.8X L SS lib**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,400	552	612.8	2,052.7	🟦	645.81	93	34.0

Electropherogram Summary Continued ...

4: p10 IgG1 0.55XR / 0.8X L SS lib [19 cyc PCR]



Overall Results for sample 4 : 4: p10 IgG1 0.55XR / 0.8X L SS lib

Number of peaks found:	9	Corr. Area 1:	1,819.5
Noise:	0.1		

Peak table for sample 4 : 4: p10 IgG1 0.55XR / 0.8X L SS lib

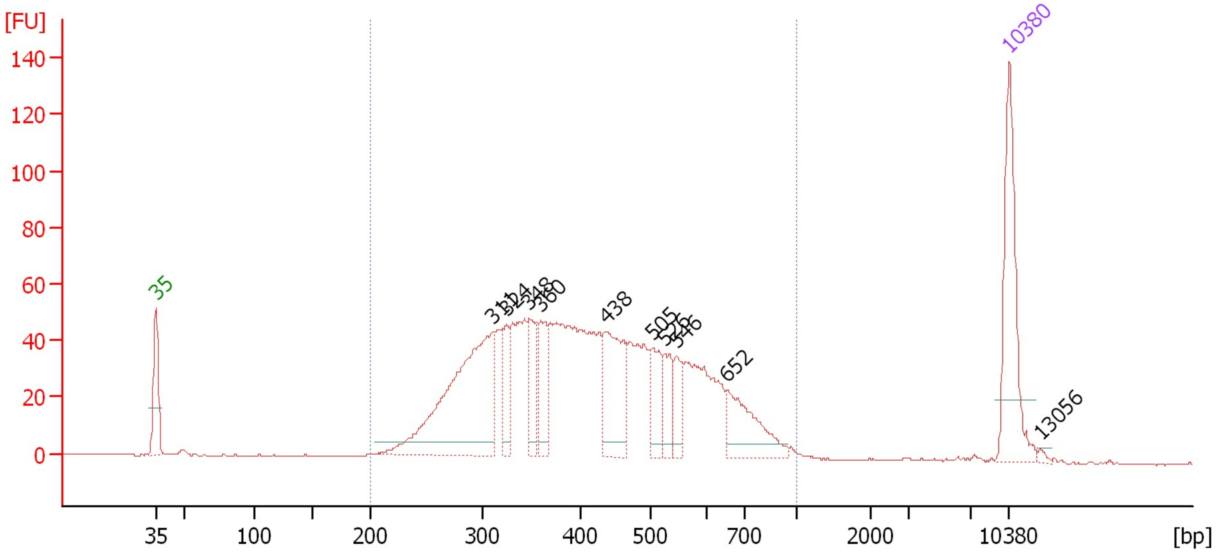
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		350	399.62	1,729.3		73.82
3		363	75.10	313.4		74.86
4		369	50.61	207.9		75.32
5		380	56.82	226.3		76.25
6		395	59.40	228.0		77.38
7		409	62.43	231.4		78.31
8		461	95.69	314.5		81.30
9		581	57.26	149.4		87.33
10		626	254.79	617.1		89.03
11	▶	10,380	75.00	10.9	Upper Marker	113.00

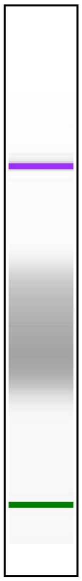
Region table for sample 4 : 4: p10 IgG1 0.55XR / 0.8X L SS lib

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,667	496	1,819.5	5,946.7	🟦	1,659.13	97	37.5

Electropherogram Summary Continued ...

5: p10 sox2 0.55XR / 0.8X L SS lib [19 cyc PCR]





Overall Results for sample 5 : **5: p10 sox2 0.55XR / 0.8X L SS lib**

Number of peaks found:	10	Corr. Area 1:	1,334.0
Noise:	0.2		

Peak table for sample 5 : **5: p10 sox2 0.55XR / 0.8X L SS lib**

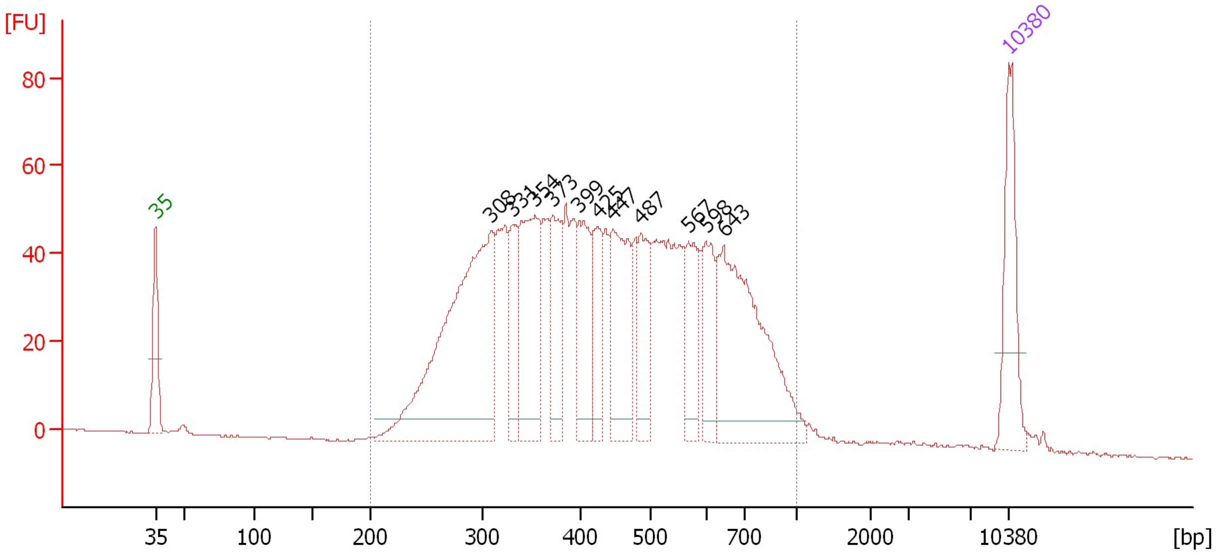
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		311	230.75	1,124.1		70.71
3		324	37.56	175.5		71.76
4		348	40.09	174.6		73.64
5		360	46.76	197.0		74.59
6		438	85.41	295.3		79.99
7		505	36.93	110.8		83.77
8		526	27.34	78.7		84.77
9		546	25.56	70.9		85.71
10		652	56.23	130.7		89.86
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		13,056	0.00	0.0		115.52

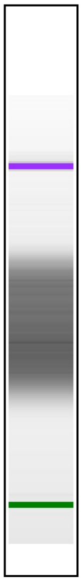
Region table for sample 5 : **5: p10 sox2 0.55XR / 0.8X L SS lib**

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	433	1,334.0	4,363.6	■	1,102.38	98	31.0

Electropherogram Summary Continued ...

8: p2 sox2 0.55XR / 0.8X L SS lib [19 cyc PCR]





Overall Results for sample 6 : **8: p2 sox2 0.55XR / 0.8X L SS lib**

Number of peaks found:	11	Corr. Area 1:	1,601.9
Noise:	0.1		

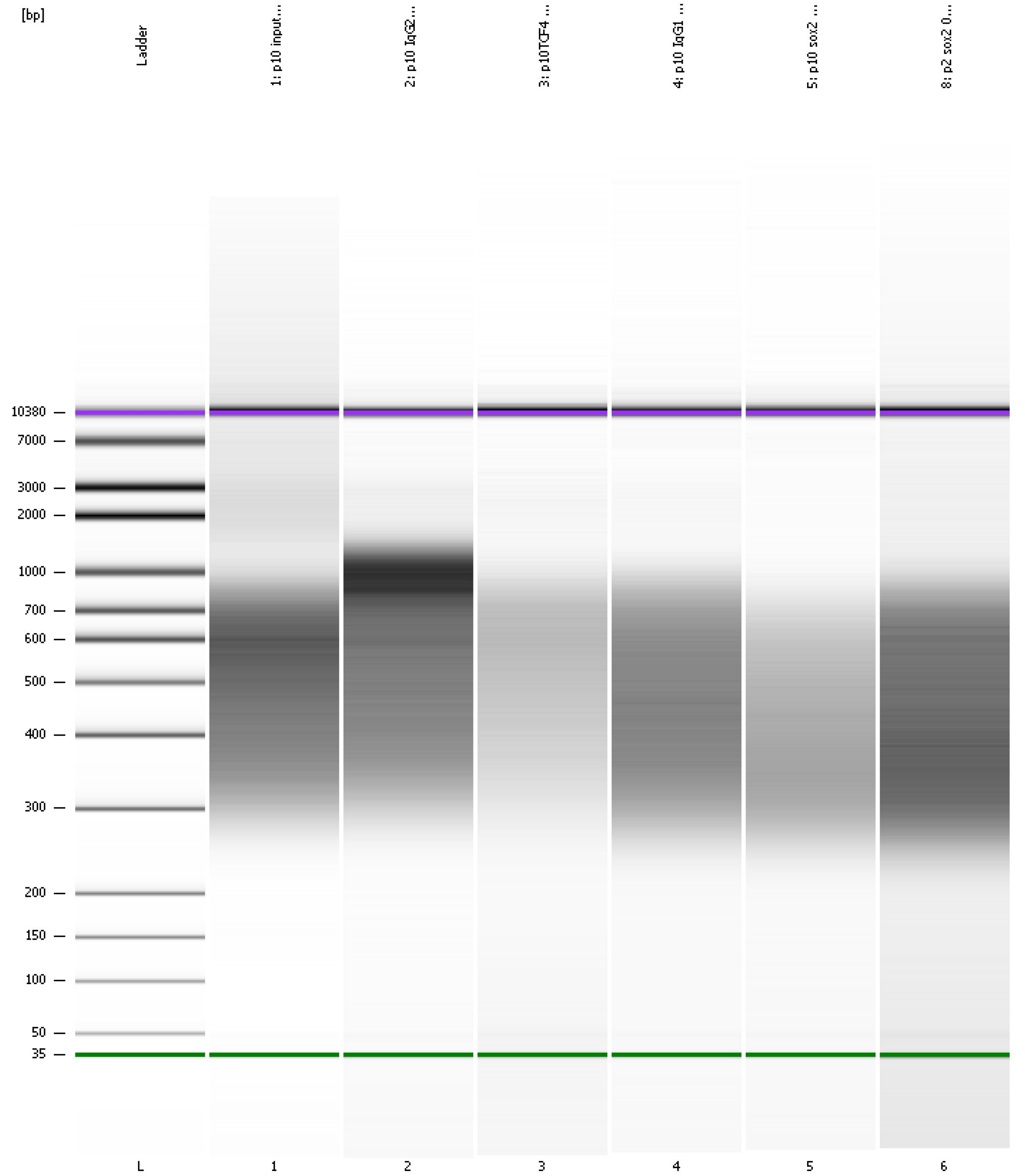
Peak table for sample 6 : **8: p2 sox2 0.55XR / 0.8X L SS lib**

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		308	428.55	2,106.2		70.49
3		331	64.26	294.1		72.30
4		354	163.93	701.9		74.12
5		373	83.75	340.5		75.62
6		399	98.11	372.8		77.71
7		425	65.71	234.1		79.26
8		447	128.29	435.0		80.49
9		487	74.86	232.9		82.79
10		567	74.78	199.8		86.69
11		598	64.65	163.8		88.13
12		643	252.52	595.1		89.58
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : **8: p2 sox2 0.55XR / 0.8X L SS lib**

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	461	1,601.9	8,028.5	🟦	2,103.54	97	33.8

Gel Image


[bp]
Ladder
1: p10 input...
2: p10 IgG2...
3: p10TCF4 ...
4: p10 IgG1 ...
5: p10 sox2 ...
8: p2 sox2 0...
10380
7000
3000
2000
1000
700
600
500
400
300
200
150
100
50
35
L
1
2
3
4
5
6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...16-10-04\2016-10-04_001_HiSeq642_SizeSelected_Libraries.xad
Created: 10/4/2016 12:45:40 PM
Modified: 10/4/2016 1:33:43 PM

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		10/4/2016 1:26:59 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-10-04\2016-10-04_001.xad)		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/4/2016 12:45:46 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1