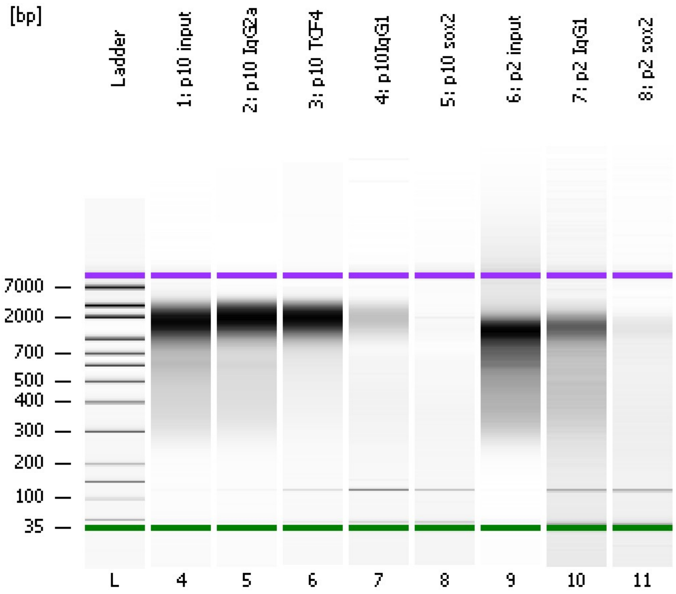
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-09-07\2016-09-07_002_HiSeq642_libraries.xad

Created: 9/7/2016 12:18:19 PM
Modified: 9/7/2016 12:59:44 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:

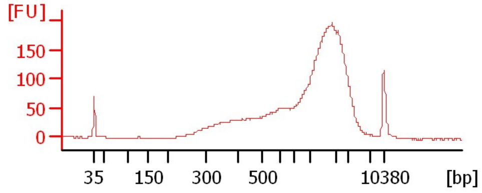
Chip Lot #:

Reagent Kit Lot #:

Chip Comments:

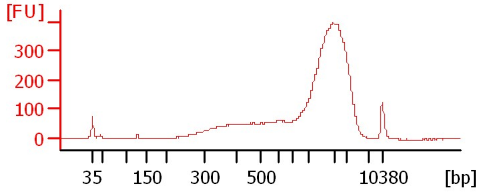
1: p10 input

Hi Seq_642 Library



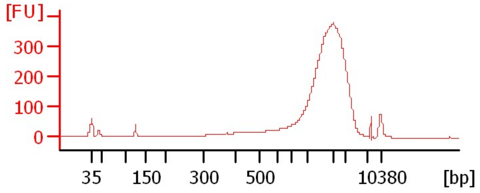
2: p10 IgG2a

Hi Seq_642 Library



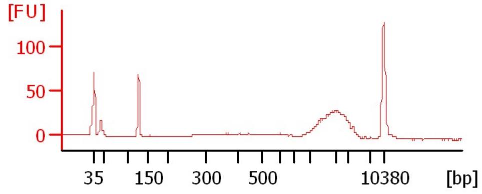
3: p10 TCF4

Hi Seq_642 Library



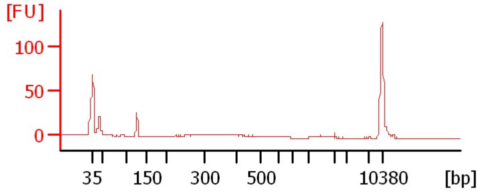
4: p10IgG1

Hi Seq_642 Library



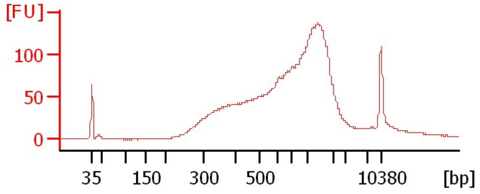
5: p10 sox2

Hi Seq_642 Library



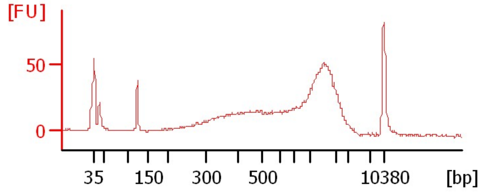
6: p2 input

Hi Seq_642 Library



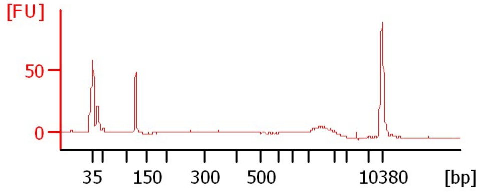
7: p2 IgG1

Hi Seq_642 Library



8: p2 sox2

Hi Seq_642 Library



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-09-07\2016-09-07_002_HiSeq642_libraries.xad

Created: 9/7/2016 12:18:19 PM
Modified: 9/7/2016 12:59:44 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1: p10 input	Hi Seq_642 Library	☐	✓			
2: p10 IgG2a	Hi Seq_642 Library	☐	✓			
3: p10 TCF4	Hi Seq_642 Library	☐	✓			
4: p10IgG1	Hi Seq_642 Library	☐	✓			
5: p10 sox2	Hi Seq_642 Library	☐	✓			
6: p2 input	Hi Seq_642 Library	☐	✓			
7: p2 IgG1	Hi Seq_642 Library	☐	✓			
8: p2 sox2	Hi Seq_642 Library	☐	✓			
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

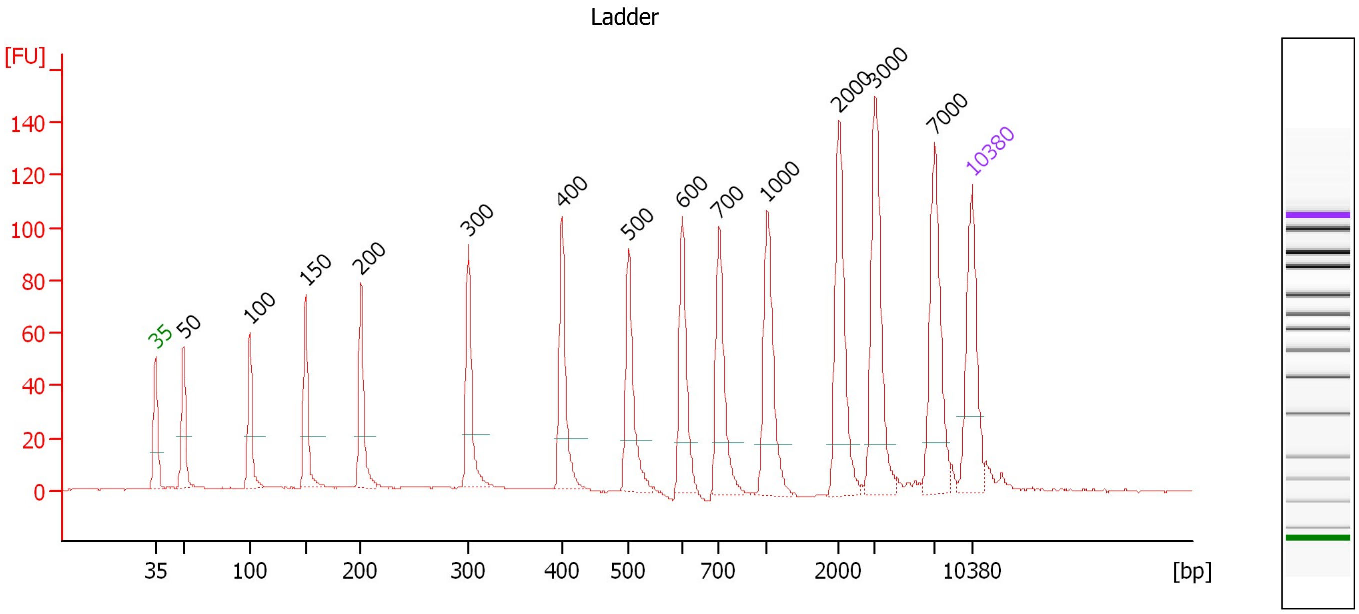
Ladder

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
Data Path: C:\...xpert\data\2016-09-07\2016-09-07_002_HiSeq642_libraries.xad

Created: 9/7/2016 12:18:19 PM
Modified: 9/7/2016 12:59:44 PM

Electropherogram Summary



Overall Results for Ladder

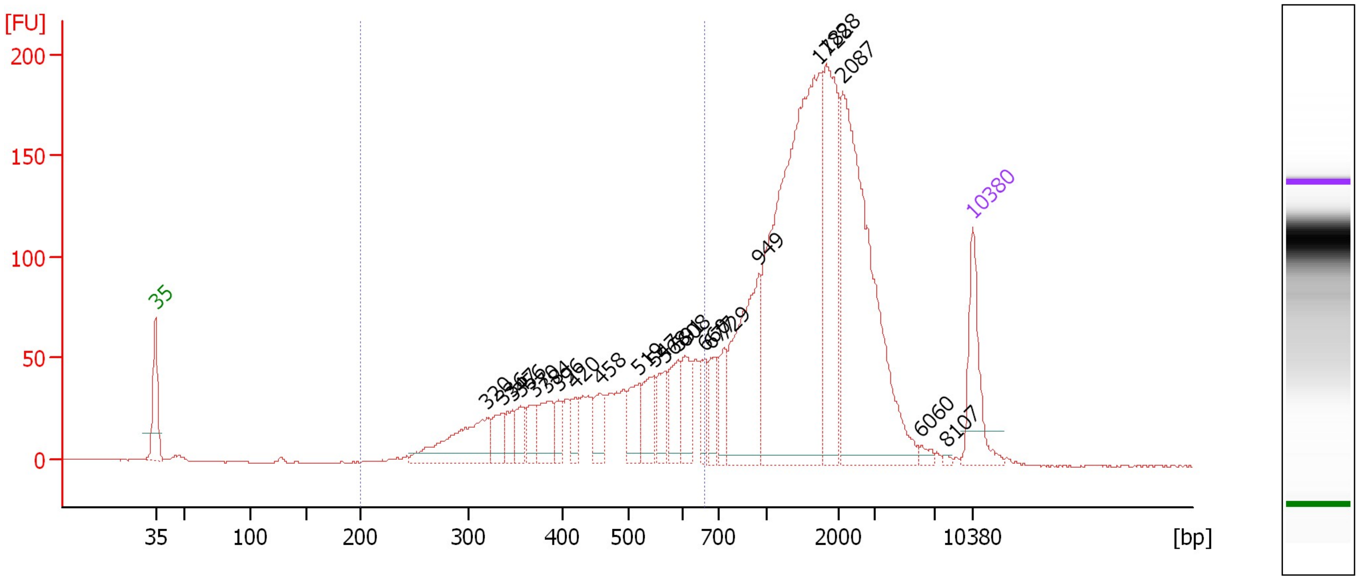
Noise: 0.3

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	45.42
3	L	100	150.00	2,272.7	Ladder Peak	51.08
4	L	150	150.00	1,515.2	Ladder Peak	55.87
5	L	200	150.00	1,136.4	Ladder Peak	60.61
6	L	300	150.00	757.6	Ladder Peak	69.85
7	L	400	150.00	568.2	Ladder Peak	77.83
8	L	500	150.00	454.5	Ladder Peak	83.54
9	L	600	150.00	378.8	Ladder Peak	88.13
10	L	700	150.00	324.7	Ladder Peak	91.33
11	L	1,000	150.00	227.3	Ladder Peak	95.44
12	L	2,000	150.00	113.6	Ladder Peak	101.58
13	L	3,000	150.00	75.8	Ladder Peak	104.68
14	L	7,000	150.00	32.5	Ladder Peak	109.81
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

1: p10 input [Hi Seq_642 Library]



Overall Results for sample 4 : 1: p10 input

Number of peaks found:	23	Corr. Area 1:	910.9
Noise:	0.3		

Peak table for sample 4 : 1: p10 input

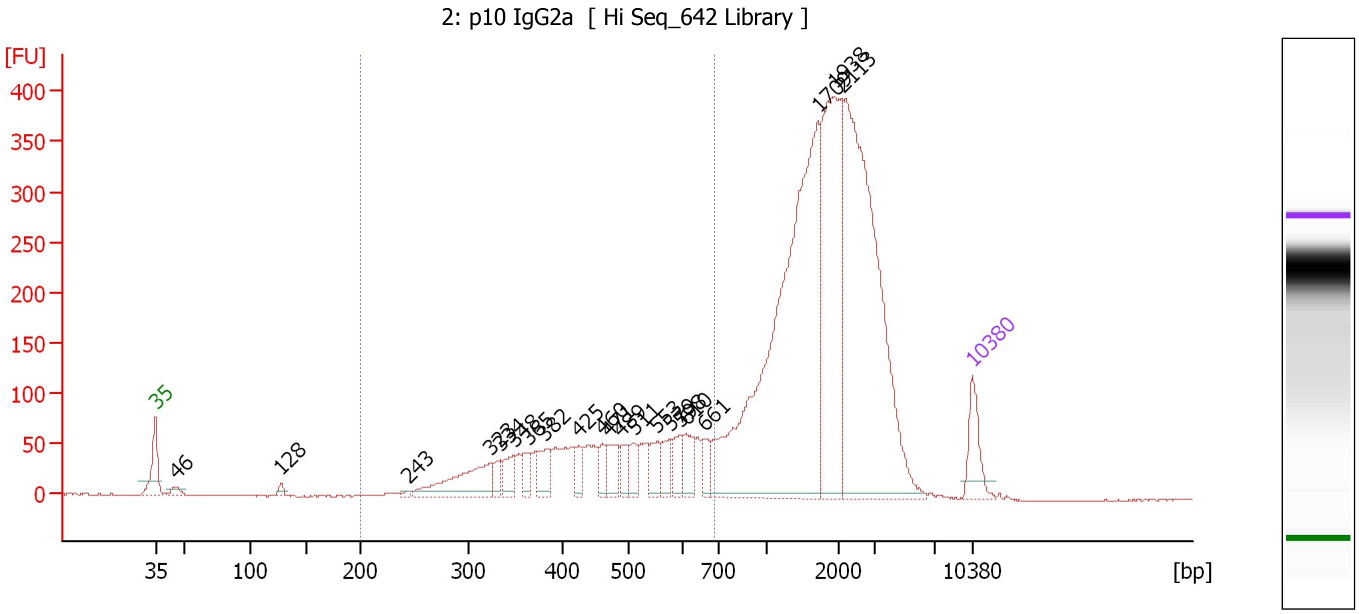
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		320	129.67	614.3		71.43
3		336	36.98	166.5		72.76
4		347	31.98	139.8		73.58
5		356	31.74	135.2		74.29
6		370	33.80	138.5		75.42
7		384	53.71	212.0		76.54
8		396	26.97	103.2		77.51
9		420	25.56	92.3		78.95
10		458	33.98	112.4		81.14
11		519	46.79	136.6		84.42
12		547	51.11	141.6		85.70
13		568	41.98	112.0		86.67
14		591	51.76	132.6		87.74
15		608	46.70	116.3		88.41
16		660	33.32	76.5		90.04
17		677	36.65	82.0		90.60
18		729	40.94	85.1		91.73
19		949	181.39	289.5		94.75
20		1,728	584.11	512.3		99.91
21		1,828	194.56	161.3		100.52
22		2,087	388.65	282.1		101.85
23		6,060	7.40	1.9		108.60
24		8,107	2.52	0.5		110.85
25	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Region table for sample 4 : 1: p10 input

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	662	464	910.9	3,119.8	🟦	869.69	31	23.8

Electropherogram Summary Continued ...



Overall Results for sample 5 : 2: p10 IgG2a

Number of peaks found: 21
Corr. Area 1: 1,315.7
Noise: 0.3

Peak table for sample 5 : 2: p10 IgG2a

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	22.56	748.3		44.72
3		128	13.81	163.6		53.75
4		243	7.28	45.3		64.61
5		323	190.53	894.7		71.66
6		334	33.62	152.6		72.55
7		348	58.53	254.7		73.69
8		365	44.70	185.5		75.05
9		382	67.93	269.3		76.41
10		425	40.74	145.1		79.28
11		460	40.69	134.0		81.26
12		471	68.82	221.4		81.89
13		489	43.11	133.5		82.93
14		511	46.02	136.5		84.03
15		553	53.63	147.0		85.96
16		579	50.49	132.2		87.16
17		598	55.87	141.5		88.05
18		610	62.85	156.0		88.47
19		661	38.54	88.3		90.08
20		1,709	1,183.10	1,049.1		99.79
21		1,938	516.35	403.7		101.20
22		2,113	937.92	672.5		101.93
23	▶	10,380	75.00	10.9	Upper Marker	113.00

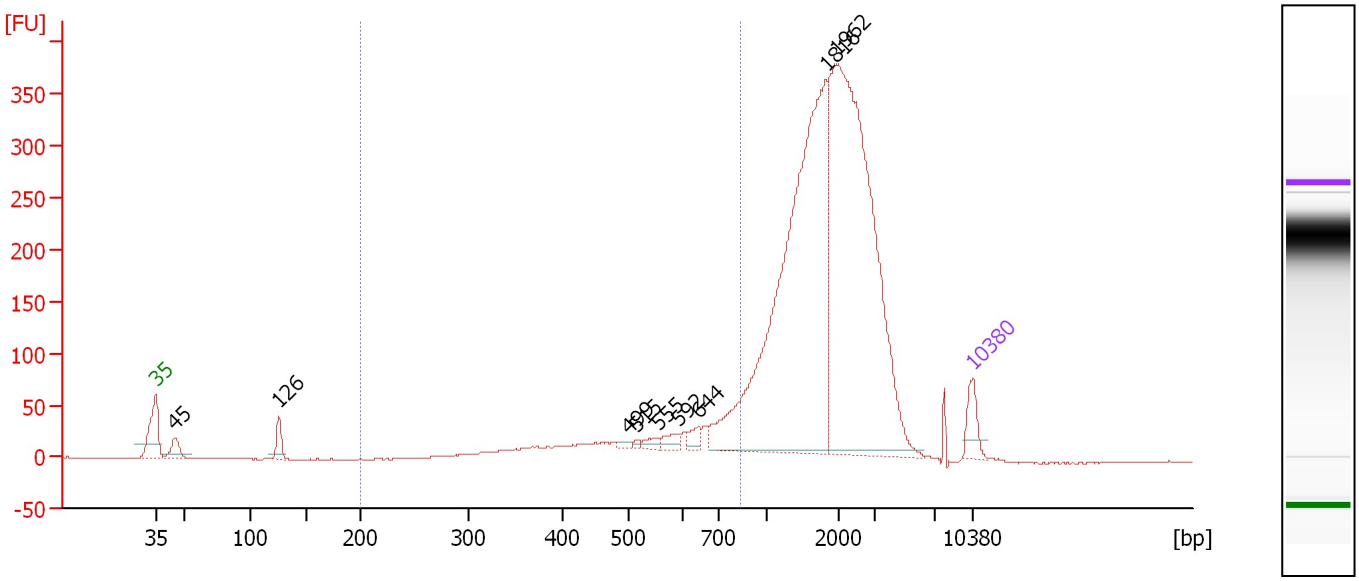
Electropherogram Summary Continued ...

... Region table for sample 5 : 2: p10 IgG2a

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	688	465	1,315.7	4,596.4	🟦	1,279.63	27	24.7

Electropherogram Summary Continued ...

3: p10 TCF4 [Hi Seq_642 Library]



Overall Results for sample 6 : **3: p10 TCF4**

Number of peaks found:	9	Corr. Area 1:	524.3
Noise:	0.3		

Peak table for sample 6 : **3: p10 TCF4**

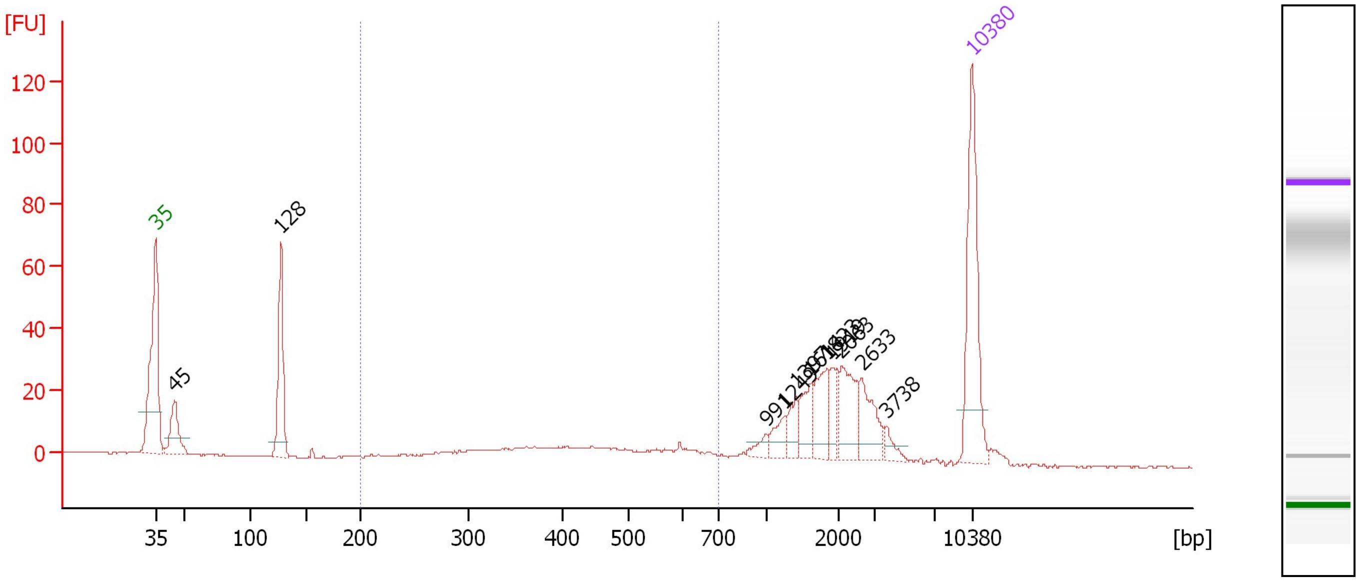
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		45	88.30	2,964.4		44.63
3		126	79.49	953.9		53.59
4		499	14.07	42.7		83.48
5		515	10.01	29.5		84.22
6		555	25.62	70.0		86.06
7		592	38.75	99.2		87.75
8		644	36.98	87.0		89.54
9		1,816	1,863.82	1,554.8		100.45
10		1,962	1,842.82	1,423.0		101.35
11	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : **3: p10 TCF4**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	832	557	524.3	2,449.6	🟦	803.58	14	26.3

Electropherogram Summary Continued ...

4: p10IgG1 [Hi Seq_642 Library]



Overall Results for sample 7 : **4: p10IgG1**

Number of peaks found:	11	Corr. Area 1:	49.6
Noise:	0.2		

Peak table for sample 7 : **4: p10IgG1**

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	43.79	1,476.4		44.60
3		128	82.36	976.5		53.74
4		991	6.74	10.3		95.31
5		1,249	13.21	16.0		96.97
6		1,397	14.10	15.3		97.88
7		1,614	17.98	16.9		99.21
8		1,823	26.58	22.1		100.50
9		1,919	14.15	11.2		101.08
10		2,063	31.16	22.9		101.78
11		2,633	26.35	15.2		103.54
12		3,738	7.11	2.9		105.63
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **4: p10IgG1**

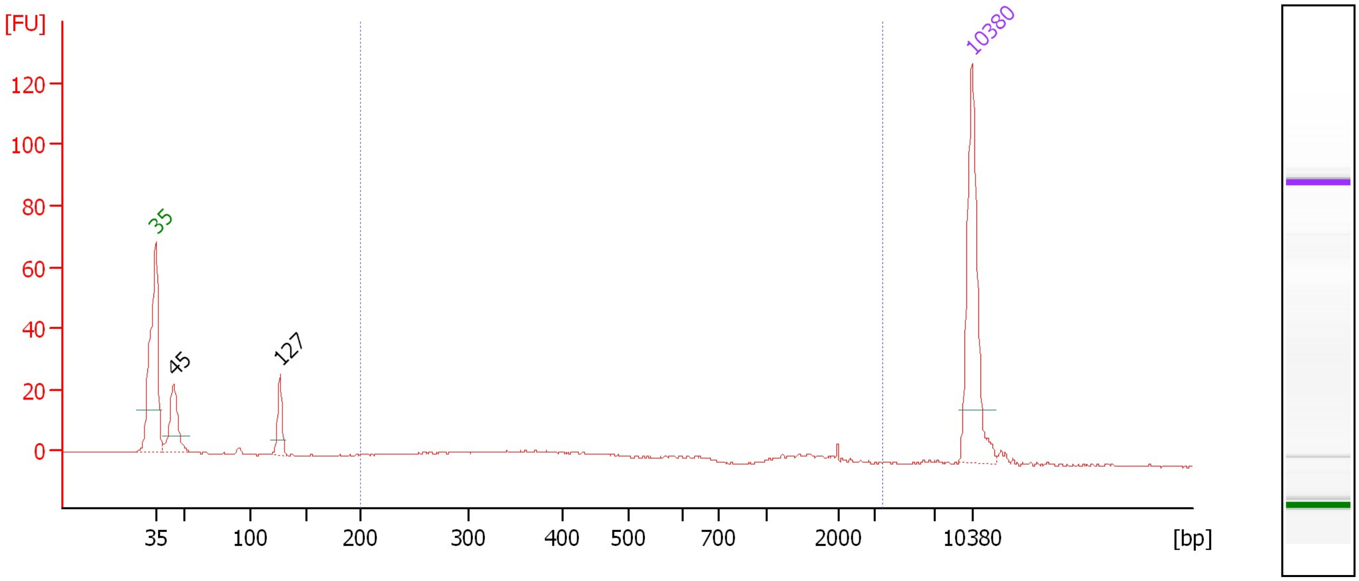
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	699	446	49.6	175.3	🟦	47.86	14	23.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-09-07\2016-09-07_002_HiSeq642_libraries.xad

Created: 9/7/2016 12:18:19 PM
Modified: 9/7/2016 12:59:44 PM

Electropherogram Summary Continued ...

5: p10 sox2 [Hi Seq_642 Library]



Overall Results for sample 8 : 5: p10 sox2

Number of peaks found:	2	Corr. Area 1:	43.9
Noise:	0.2		

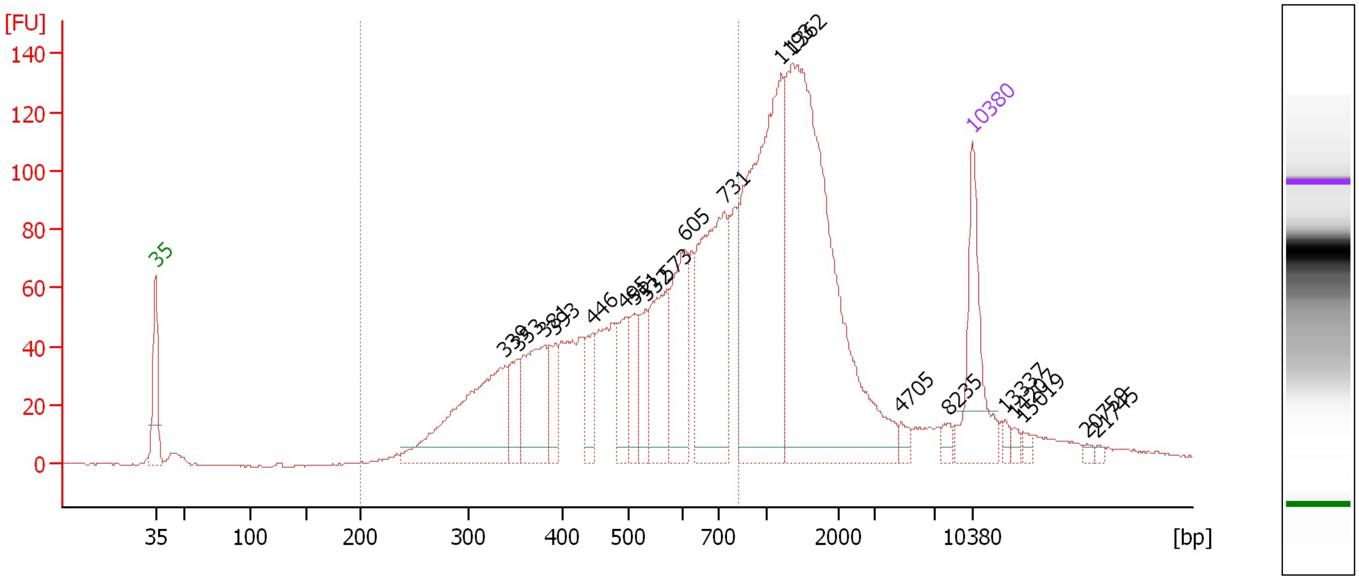
Peak table for sample 8 : 5: p10 sox2

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	53.09	1,799.6		44.56
3		127	28.60	340.8		53.68
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 8 : 5: p10 sox2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	3,550	665	43.9	155.3	🟦	40.34	40	82.4

Electropherogram Summary Continued ...


6: p2 input [Hi Seq_642 Library]

Overall Results for sample 9 : 6: p2 input

Number of peaks found:	20	Corr. Area 1:	1,499.1
Noise:	0.2		

Peak table for sample 9 : 6: p2 input

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		339	194.59	869.7		72.96
3		353	41.42	177.9		74.06
4		381	99.77	396.9		76.30
5		393	37.16	143.5		77.23
6		446	38.38	130.3		80.46
7		495	54.55	167.0		83.26
8		511	36.91	109.5		84.03
9		532	36.48	103.9		85.01
10		573	85.92	227.4		86.87
11		605	98.98	247.9		88.30
12		731	189.14	392.2		91.75
13		1,193	301.90	383.5		96.62
14		1,362	436.15	485.2		97.66
15		4,705	8.23	2.7		106.87
16		8,235	7.30	1.3		110.97
17	▶	10,380	75.00	10.9	Upper Marker	113.00
18		13,337	0.00	0.0		115.79
19		14,207	0.00	0.0		116.62
20		15,019	0.00	0.0		117.38
21		20,759	0.00	0.0		122.80
22		21,745	0.00	0.0		123.74

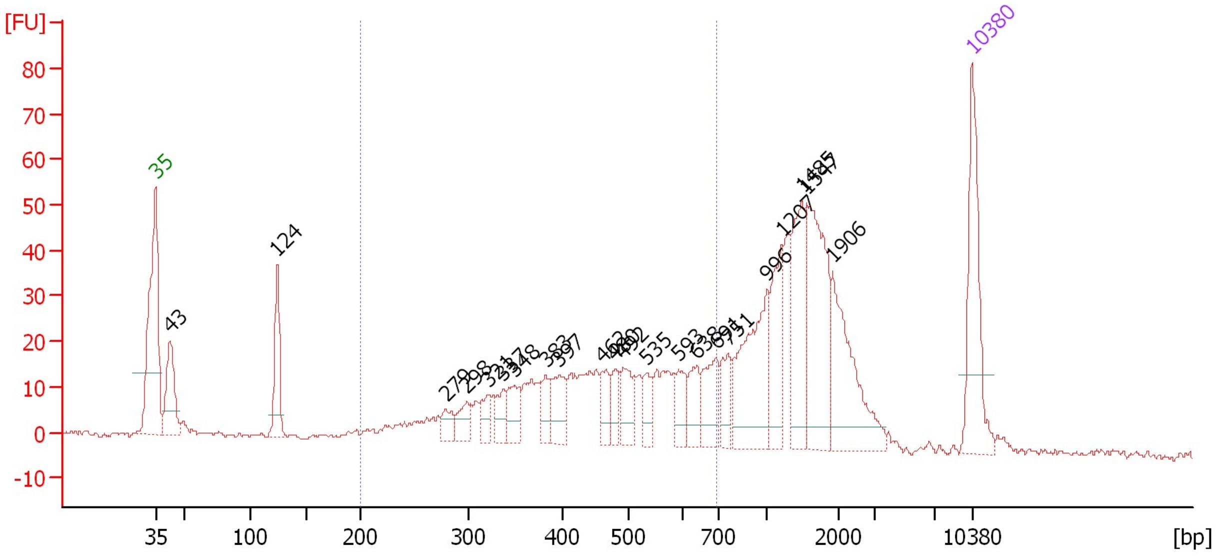
Electropherogram Summary Continued ...

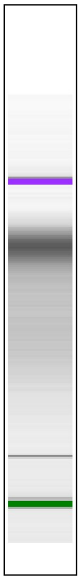
... Region table for sample 9 : 6: p2 input

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	826	515	1,499.1	4,215.1	🟦	1,252.75	54	28.7

Electropherogram Summary Continued ...

7: p2 IgG1 [Hi Seq_642 Library]





Overall Results for sample 10 : **7: p2 IgG1**

Number of peaks found: 22 Corr. Area 1: 434.0

Noise: 0.7

Peak table for sample 10 : **7: p2 IgG1**

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	72.21	2,553.2		44.27
3		124	63.86	778.7		53.40
4		279	17.11	93.1		67.87
5		298	20.82	106.0		69.64
6		321	17.17	81.1		71.51
7		337	20.74	93.4		72.77
8		348	27.77	120.8		73.71
9		383	17.90	70.8		76.46
10		397	32.66	124.6		77.61
11		462	21.30	69.9		81.36
12		480	18.44	58.2		82.40
13		492	31.09	95.8		83.06
14		535	17.90	50.7		85.15
15		593	23.43	59.9		87.80
16		638	27.93	66.4		89.34
17		691	38.33	84.0		91.04
18		751	26.04	52.5		92.03
19		996	93.02	141.5		95.39
20		1,207	54.05	67.9		96.71
21		1,485	71.73	73.2		98.42
22		1,547	107.82	105.6		98.80
23		1,906	82.48	65.6		101.00
24	▶	10,380	75.00	10.9	Upper Marker	113.00

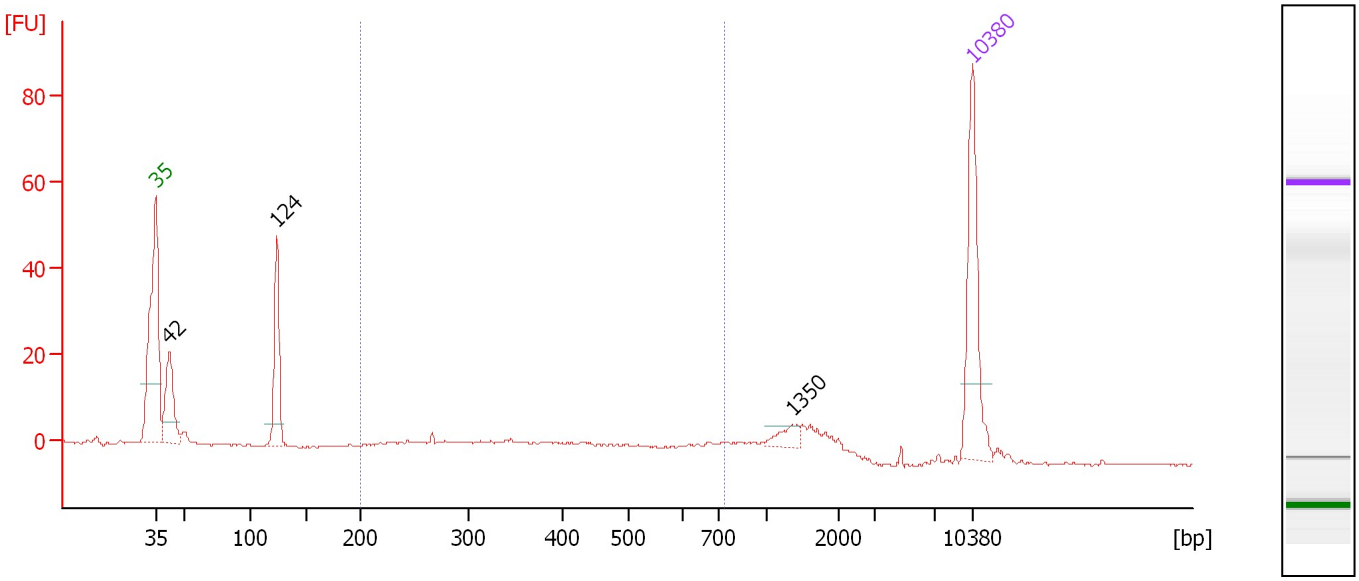
Electropherogram Summary Continued ...

... Region table for sample 10 : 7: p2 IgG1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	690	451	434.0	2,280.1	🟦 600.93	43	27.1

Electropherogram Summary Continued ...

8: p2 sox2 [Hi Seq_642 Library]



Overall Results for sample 11 : **8: p2 sox2**

Number of peaks found:	3	Corr. Area 1:	65.6
Noise:	0.2		

Peak table for sample 11 : **8: p2 sox2**

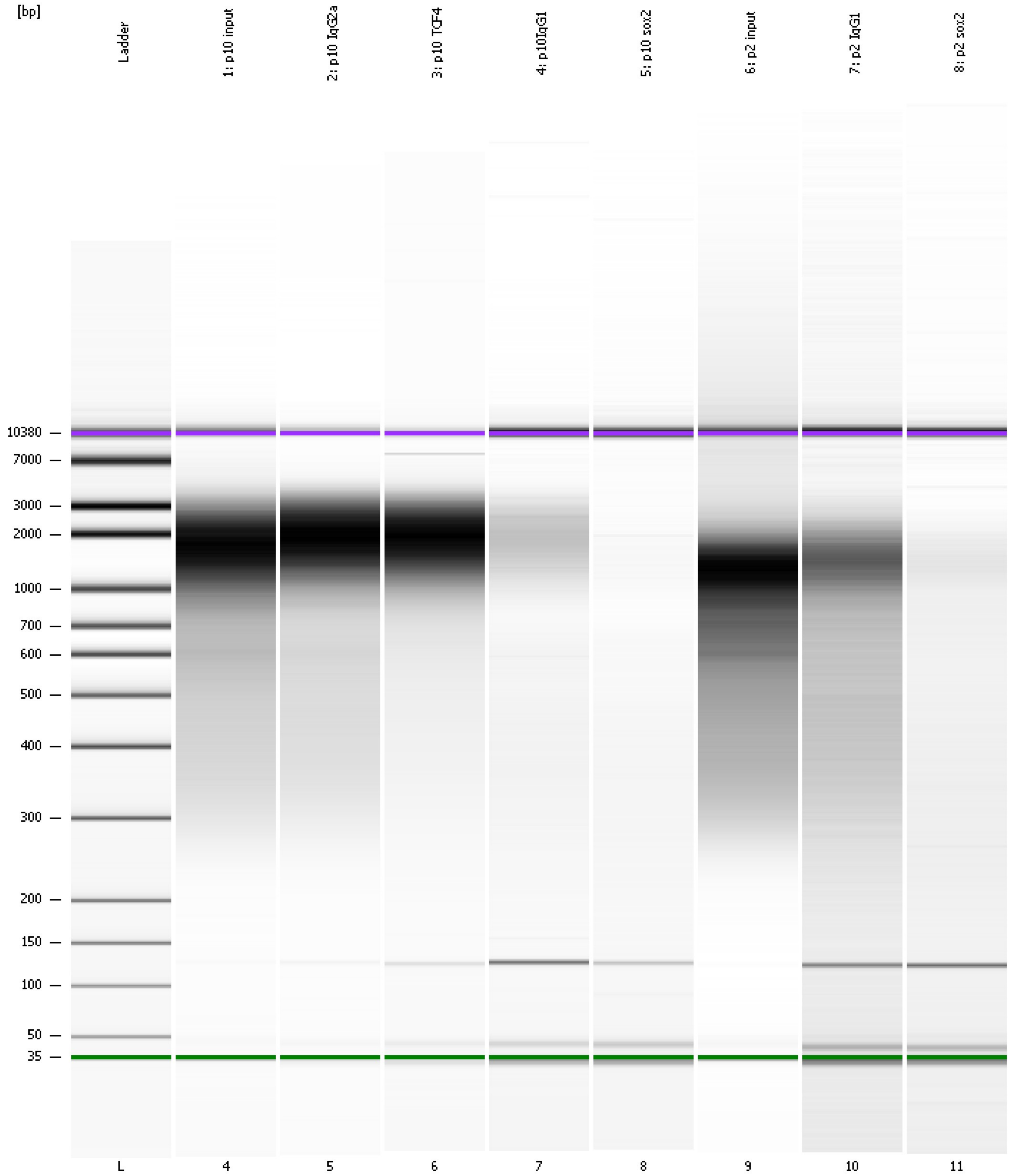
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		42	70.69	2,537.0		44.16
3		124	77.49	943.5		53.42
4		1,350	10.71	12.0		97.59
5	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : **8: p2 sox2**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	731	416	65.6	400.4	🟦	93.24	32	33.8

Assay Class:	High Sensitivity DNA Assay	Created:	9/7/2016 12:18:19 PM
Data Path:	C:\...xpert\data\2016-09-07\2016-09-07_002_HiSeq642_libraries.xad	Modified:	9/7/2016 12:59:44 PM

Gel Image



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		9/7/2016 12:58:48 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\2016-09-07\2016-09-07_002.xad)		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		9/7/2016 12:18:24 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1