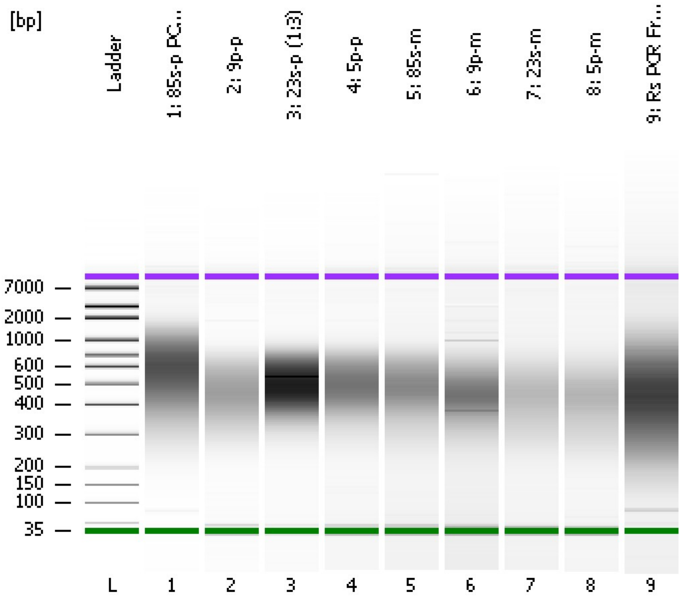
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-10-31\2016-10-31_001_HiSeq663_Libraries.xad

Created: 10/31/2016 9:47:45 AM
Modified: 10/31/2016 11:08:54 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:

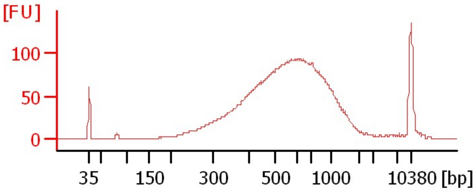
Chip Lot #:

Reagent Kit Lot #:

Chip Comments:

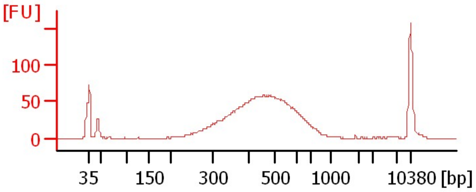
1: 85s-p PCR Free (1:3)

HiSeq_663 Library



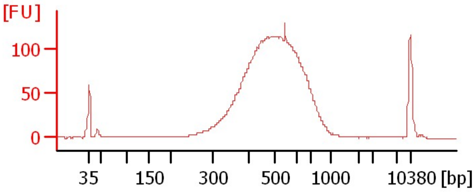
2: 9p-p

HiSeq_663 Library



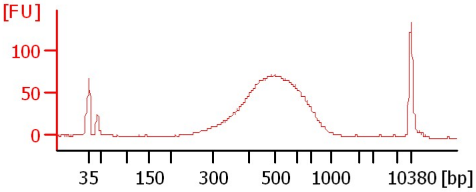
3: 23s-p (1:3)

HiSeq_663 Library



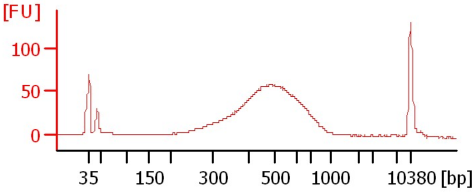
4: 5p-p

HiSeq_663 Library



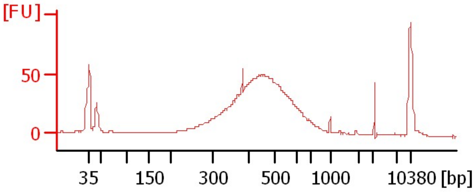
5: 85s-m

HiSeq_663 Library



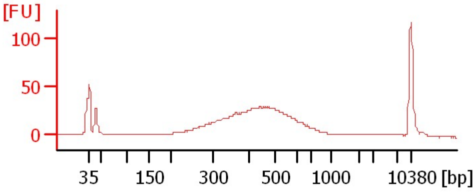
6: 9p-m

HiSeq_663 Library



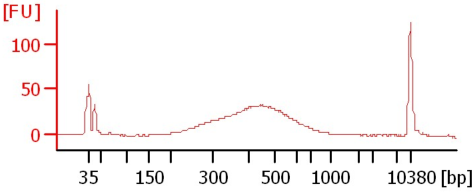
7: 23s-m

HiSeq_663 Library



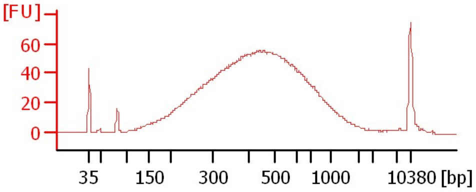
8: 5p-m

HiSeq_663 Library



9: Rs PCR Free (1:2)

HiSeq_663 Library



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-10-31\2016-10-31_001_HiSeq663_Libraries.xad

Created: 10/31/2016 9:47:45 AM
Modified: 10/31/2016 11:08:54 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1: 85s-p PCR Free (1:3)	HiSeq_663 Library	☐	✓			
2: 9p-p	HiSeq_663 Library	☐	✓			
3: 23s-p (1:3)	HiSeq_663 Library	☐	✓			
4: 5p-p	HiSeq_663 Library	☐	✓			
5: 85s-m	HiSeq_663 Library	☐	✓			
6: 9p-m	HiSeq_663 Library	☐	✓			
7: 23s-m	HiSeq_663 Library	☐	✓			
8: 5p-m	HiSeq_663 Library	☐	✓			
9: Rs PCR Free (1:2)	HiSeq_663 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

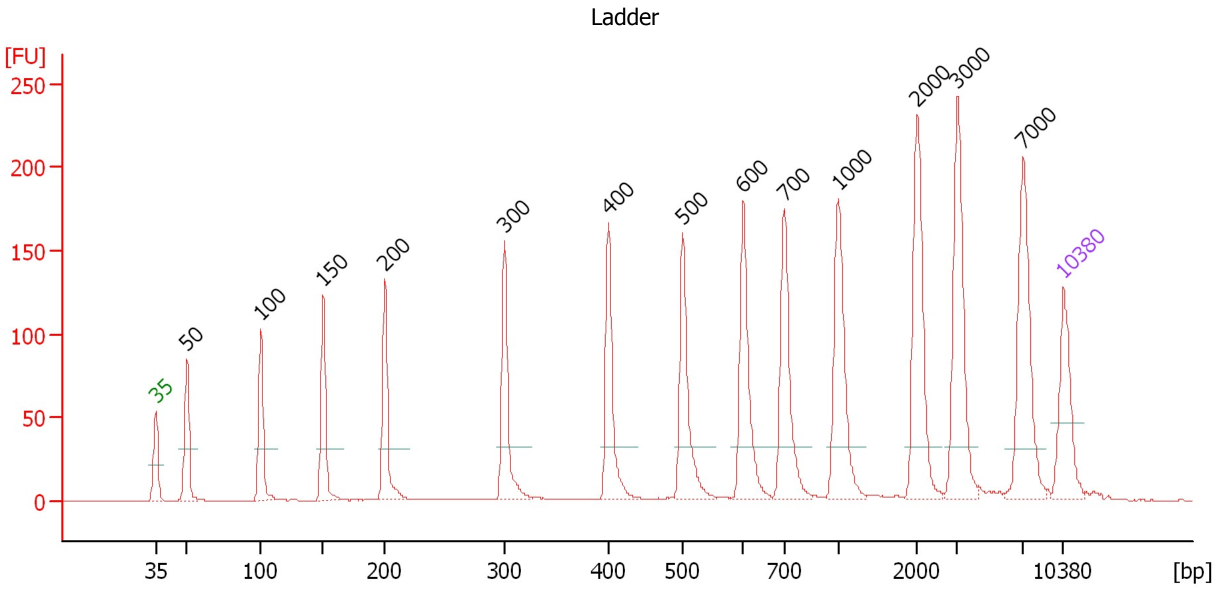
Filter Width [s] : 0.5
Polynomial Order : 4

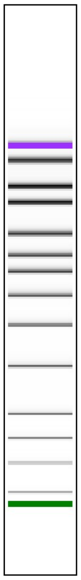
Ladder

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	Created:	10/31/2016 9:47:45 AM
Data Path:	C:\...xpert\data\2016-10-31\2016-10-31_001_HiSeq663_Libraries.xad	Modified:	10/31/2016 11:08:54 AM

Electropherogram Summary





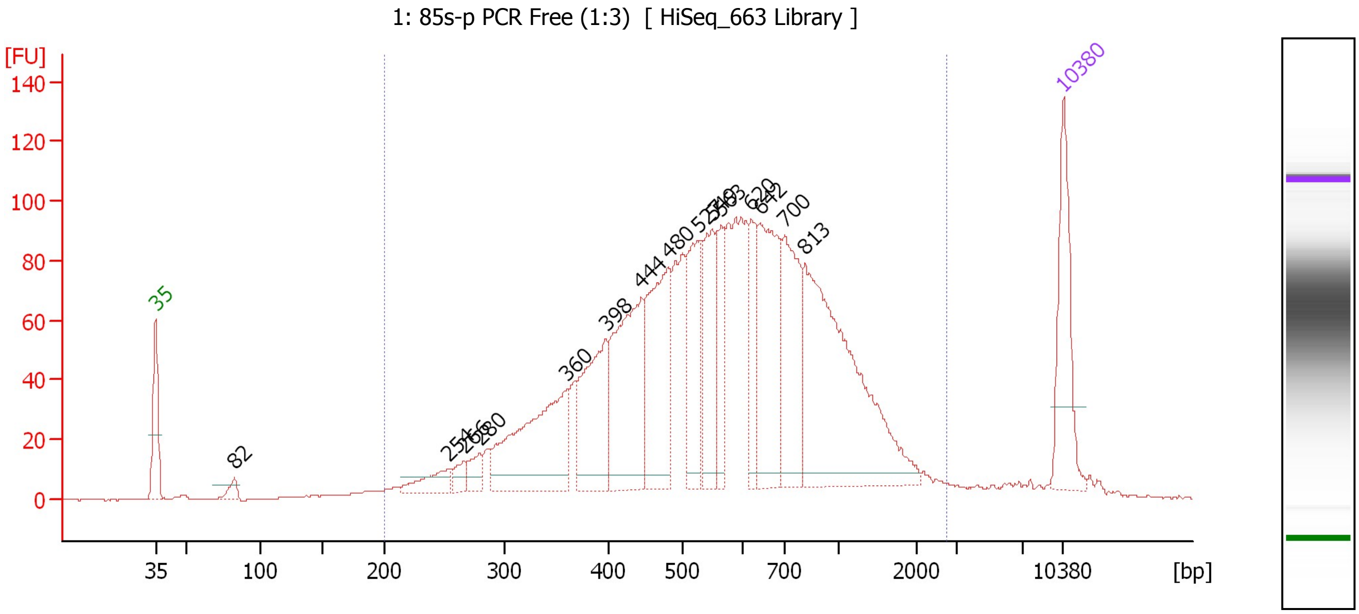
Overall Results for Ladder

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	45.41
3	L	100	150.00	2,272.7	Ladder Peak	51.13
4	L	150	150.00	1,515.2	Ladder Peak	55.91
5	L	200	150.00	1,136.4	Ladder Peak	60.68
6	L	300	150.00	757.6	Ladder Peak	69.90
7	L	400	150.00	568.2	Ladder Peak	77.93
8	L	500	150.00	454.5	Ladder Peak	83.64
9	L	600	150.00	378.8	Ladder Peak	88.32
10	L	700	150.00	324.7	Ladder Peak	91.47
11	L	1,000	150.00	227.3	Ladder Peak	95.66
12	L	2,000	150.00	113.6	Ladder Peak	101.72
13	L	3,000	150.00	75.8	Ladder Peak	104.82
14	L	7,000	150.00	32.5	Ladder Peak	109.90
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...


1: 85s-p PCR Free (1:3) [HiSeq_663 Library]

Overall Results for sample 1 : **1: 85s-p PCR Free (1:3)**

Number of peaks found:	15	Corr. Area 1:	2,334.5
Noise:	0.2		

Peak table for sample 1 : **1: 85s-p PCR Free (1:3)**

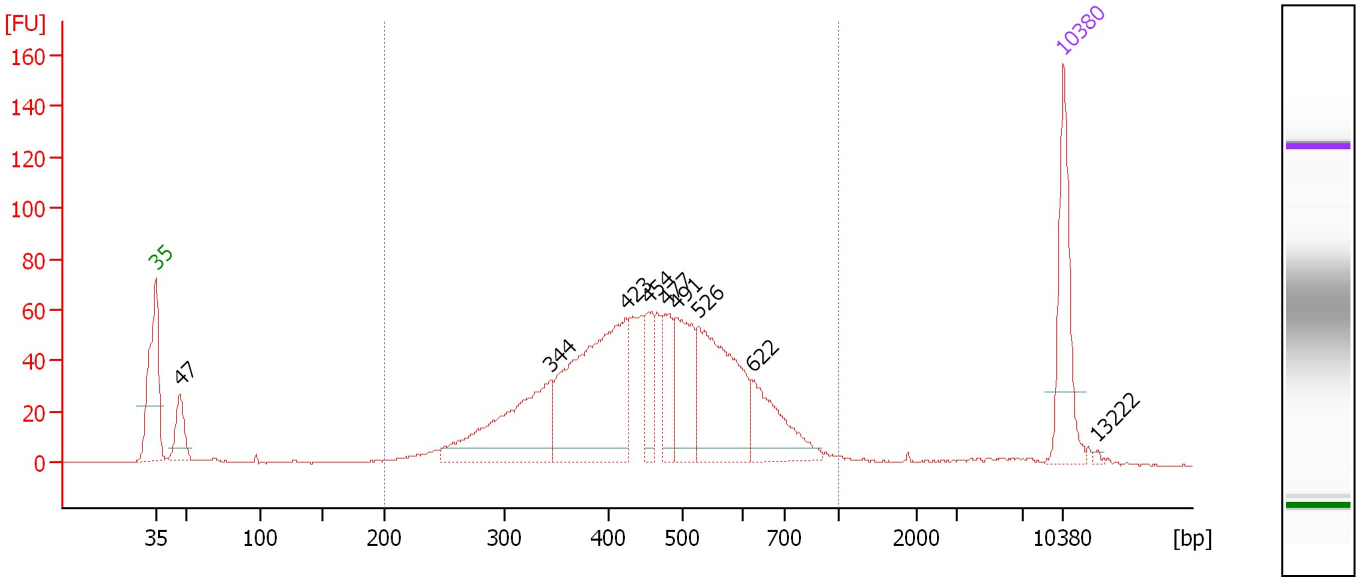
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		82	14.21	263.1		49.05
3		254	29.45	175.9		65.62
4		266	15.14	86.2		66.76
5		280	19.39	105.0		68.05
6		360	169.80	713.7		74.75
7		398	123.08	469.1		77.73
8		444	168.89	576.0		80.46
9		480	144.18	455.2		82.49
10		527	88.09	253.1		84.92
11		549	85.26	235.5		85.91
12		563	52.71	141.7		86.61
13		620	51.28	125.4		88.94
14		642	141.02	333.0		89.63
15		700	113.65	246.0		91.47
16		813	293.62	546.9		93.06
17	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : **1: 85s-p PCR Free (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	2,745	644	2,334.5	5,908.3	🟦	1,939.97	97	52.9

Electropherogram Summary Continued ...

2: 9p-p [HiSeq_663 Library]



Overall Results for sample 2 : **2: 9p-p**

Number of peaks found:	9	Corr. Area 1:	1,300.1
Noise:	0.3		

Peak table for sample 2 : **2: 9p-p**

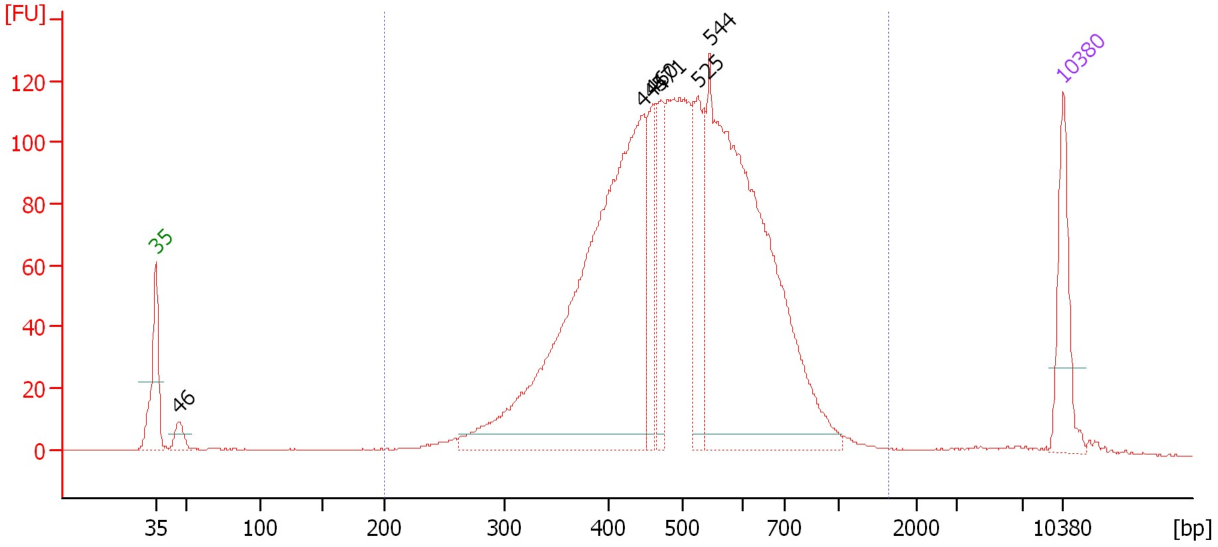
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		47	50.32	1,638.2		44.86
3		344	166.27	731.6		73.46
4		423	256.96	920.8		79.23
5		454	44.37	148.2		80.99
6		477	48.27	153.3		82.34
7		491	86.11	265.6		83.14
8		526	162.15	467.2		84.85
9		622	71.27	173.6		89.01
10	▶	10,380	75.00	10.9	Upper Marker	113.00
11		13,222	0.00	0.0		115.61

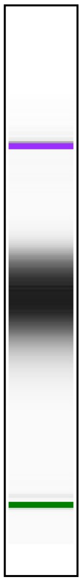
Region table for sample 2 : **2: 9p-p**

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	463	1,300.1	3,679.0	🟦	1,014.17	91	26.8

Electropherogram Summary Continued ...

3: 23s-p (1:3) [HiSeq_663 Library]





Overall Results for sample 3 : **3: 23s-p (1:3)**

Number of peaks found:	6	Corr. Area 1:	2,230.2
Noise:	0.2		

Peak table for sample 3 : **3: 23s-p (1:3)**

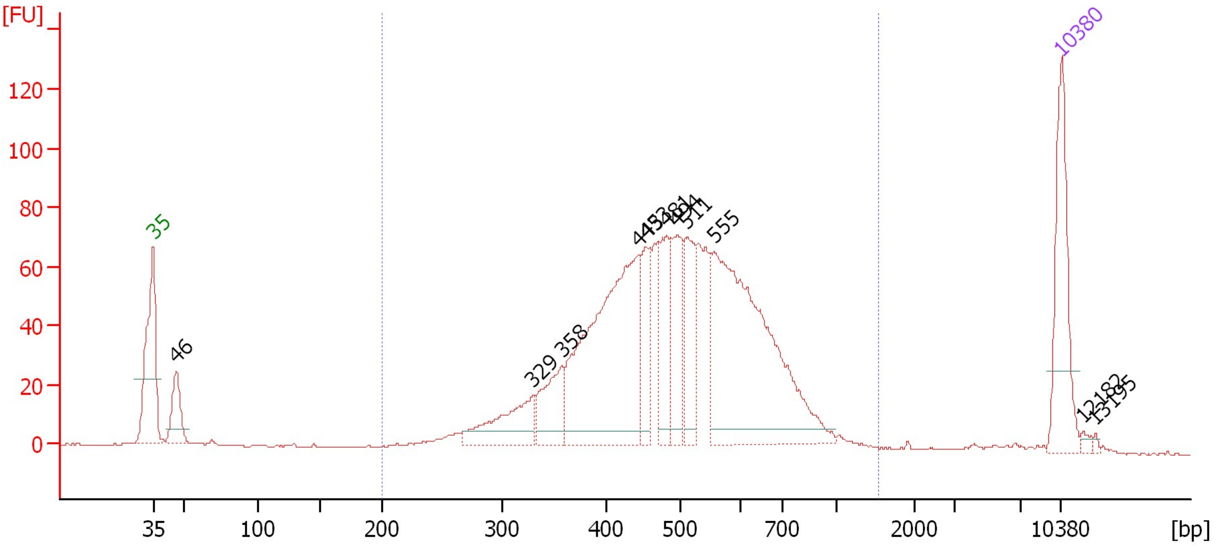
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		46	24.73	807.7		44.83
3		445	781.25	2,657.7		80.52
4		460	96.80	319.1		81.33
5		471	91.13	293.0		82.00
6		525	131.48	379.7		84.80
7		544	704.66	1,961.6		85.71
8	▶	10,380	75.00	10.9	Upper Marker	113.00

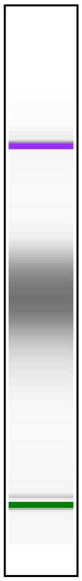
Region table for sample 3 : **3: 23s-p (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,646	508	2,230.2	7,200.8	■	2,209.15	97	27.3

Electropherogram Summary Continued ...

4: 5p-p [HiSeq_663 Library]





Overall Results for sample 4 : **4: 5p-p**

Number of peaks found:	11	Corr. Area 1:	1,405.8
Noise:	0.2		

Peak table for sample 4 : **4: 5p-p**

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	54.40	1,794.9		44.76
3		329	73.63	338.6		72.26
4		358	58.79	249.0		74.54
5		443	299.74	1,025.4		80.38
6		453	48.46	162.1		80.95
7		481	69.11	217.7		82.55
8		494	69.03	211.5		83.32
9		511	70.23	208.2		84.15
10		555	322.44	880.1		86.22
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,182	0.00	0.0		114.65
13		13,195	0.00	0.0		115.58

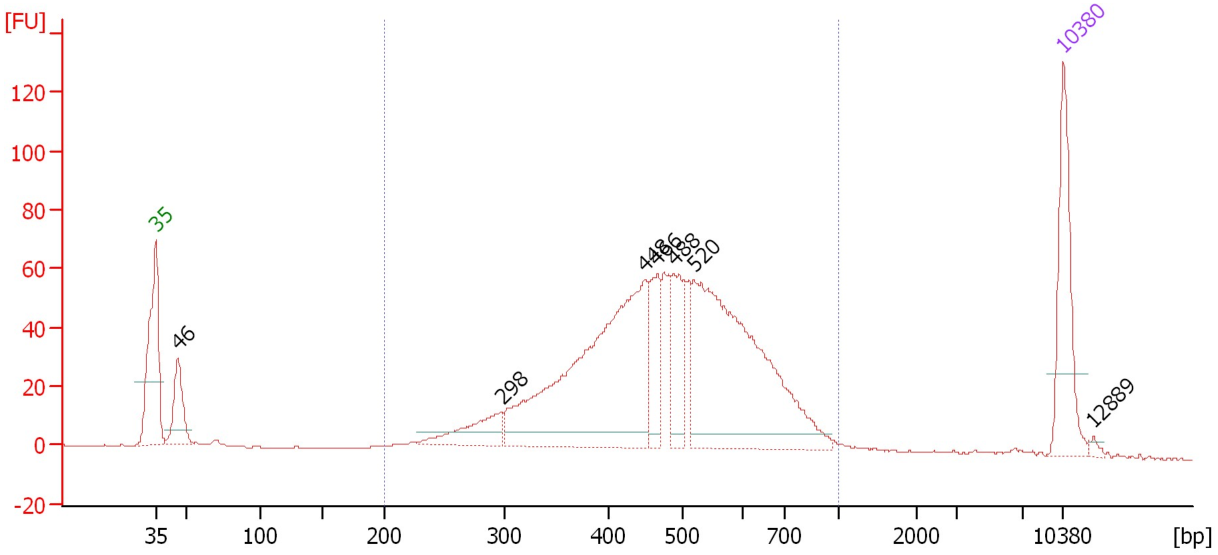
Region table for sample 4 : **4: 5p-p**

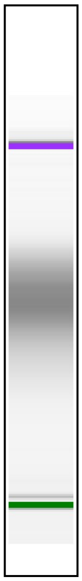
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,536	507	1,405.8	4,088.6	🟦	1,236.94	93	28.5

Assay Class:	High Sensitivity DNA Assay	Created:	10/31/2016 9:47:45 AM
Data Path:	C:\...xpert\data\2016-10-31\2016-10-31_001_HiSeq663_Libraries.xad	Modified:	10/31/2016 11:08:54 AM

Electropherogram Summary Continued ...

5: 85s-m [HiSeq_663 Library]





Overall Results for sample 5 : **5: 85s-m**

Number of peaks found:	7	Corr. Area 1:	1,219.9
Noise:	0.1		

Peak table for sample 5 : **5: 85s-m**

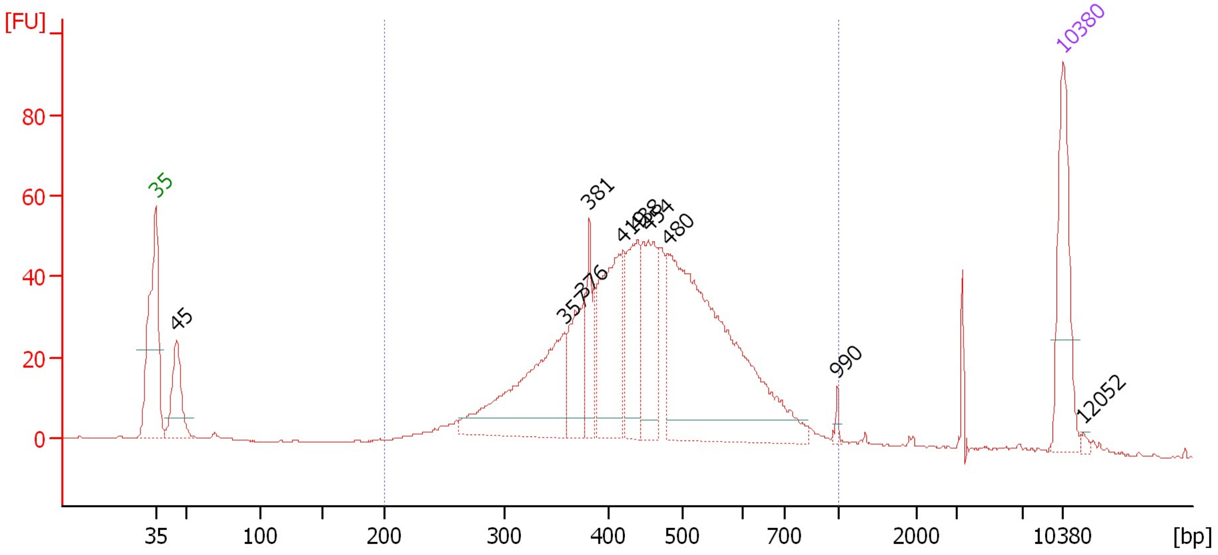
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		46	67.16	2,224.9		44.73
3		298	53.89	273.6		69.75
4		448	372.44	1,258.2		80.70
5		466	57.49	187.0		81.69
6		488	66.77	207.3		82.95
7		520	345.06	1,005.6		84.57
8	▶	10,380	75.00	10.9	Upper Marker	113.00
9		12,889	0.00	0.0		115.30

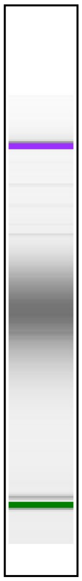
Region table for sample 5 : **5: 85s-m**

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	486	1,219.9	3,691.2	🟦	1,065.90	90	26.8

Electropherogram Summary Continued ...

6: 9p-m [HiSeq_663 Library]





Overall Results for sample 6 : 6: 9p-m

Number of peaks found:	10	Corr. Area 1:	989.0
Noise:	0.2		

Peak table for sample 6 : 6: 9p-m

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	80.85	2,729.9		44.59
3		357	183.89	779.6		74.51
4		376	70.53	284.3		75.99
5		381	49.54	196.9		76.41
6		419	132.06	477.6		79.01
7		438	91.94	317.8		80.12
8		454	100.09	333.9		81.02
9		480	385.81	1,217.7		82.50
10		990	4.48	6.9		95.53
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,052	0.00	0.0		114.54

Region table for sample 6 : 6: 9p-m

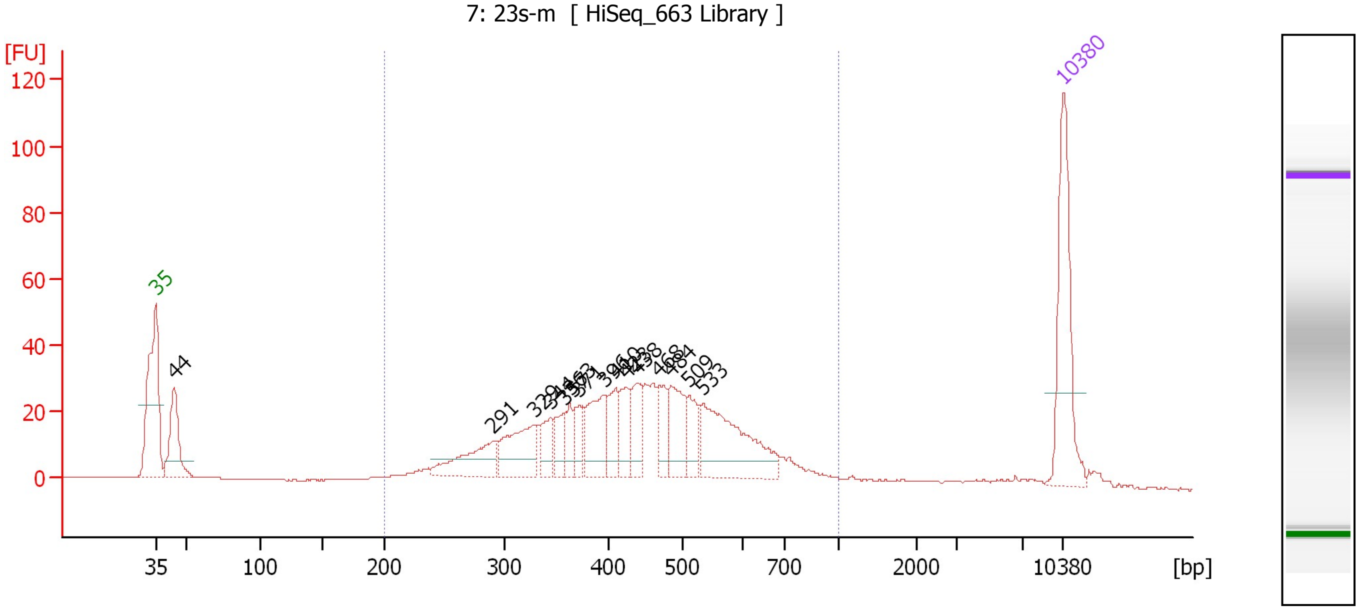
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	460	989.0	4,493.9	🟦	1,238.18	88	26.9

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...xpert\data\2016-10-31\2016-10-31_001_HiSeq663_Libraries.xad

Created: 10/31/2016 9:47:45 AM
Modified: 10/31/2016 11:08:54 AM

Electropherogram Summary Continued ...

7: 23s-m [HiSeq_663 Library]



Overall Results for sample 7 : 7: 23s-m

Number of peaks found:	15	Corr. Area 1:	687.4
Noise:	0.2		

Peak table for sample 7 : 7: 23s-m

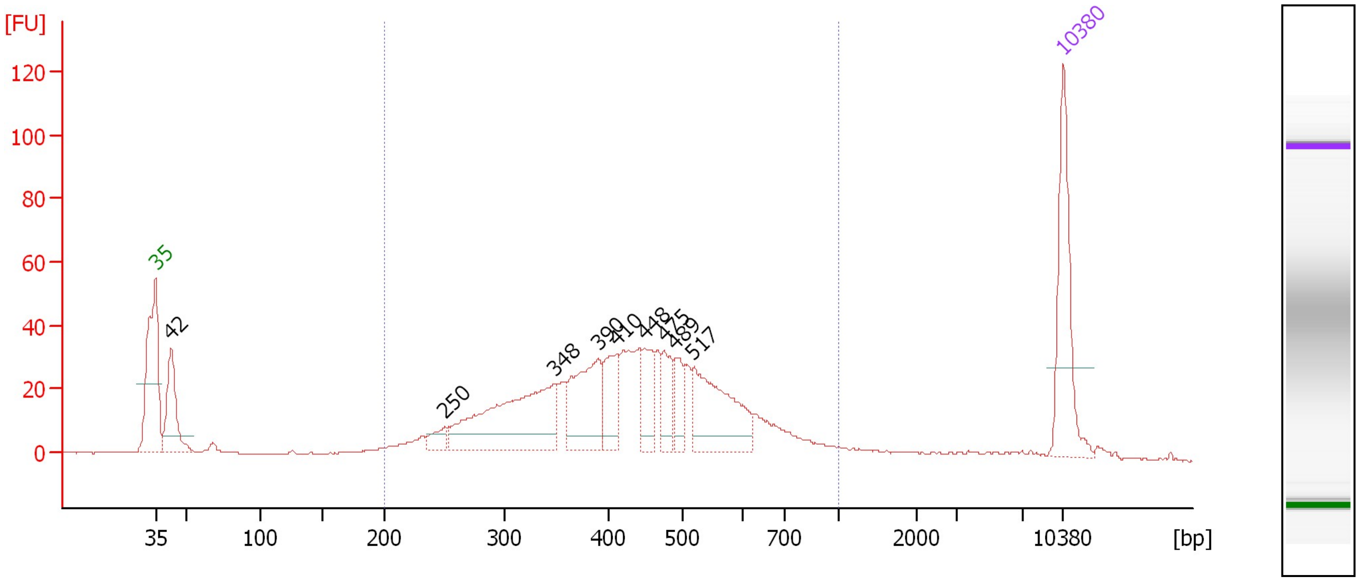
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		44	70.49	2,426.1		44.45
3		291	50.48	263.3		69.02
4		329	56.14	258.9		72.19
5		344	23.80	104.8		73.43
6		357	19.99	84.8		74.51
7		363	19.13	79.9		74.94
8		371	19.36	79.0		75.63
9		396	46.17	176.9		77.57
10		410	28.55	105.6		78.48
11		423	27.68	99.2		79.24
12		438	30.21	104.5		80.10
13		468	25.80	83.5		81.82
14		484	40.56	126.9		82.73
15		509	25.54	76.0		84.08
16		533	96.72	274.7		85.20
17	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : 7: 23s-m

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	449	687.4	2,587.3	🟦	683.75	85	29.0

Electropherogram Summary Continued ...

8: 5p-m [HiSeq_663 Library]



Overall Results for sample 8 : **8: 5p-m**

Number of peaks found:	9	Corr. Area 1:	788.8
Noise:	0.2		

Peak table for sample 8 : **8: 5p-m**

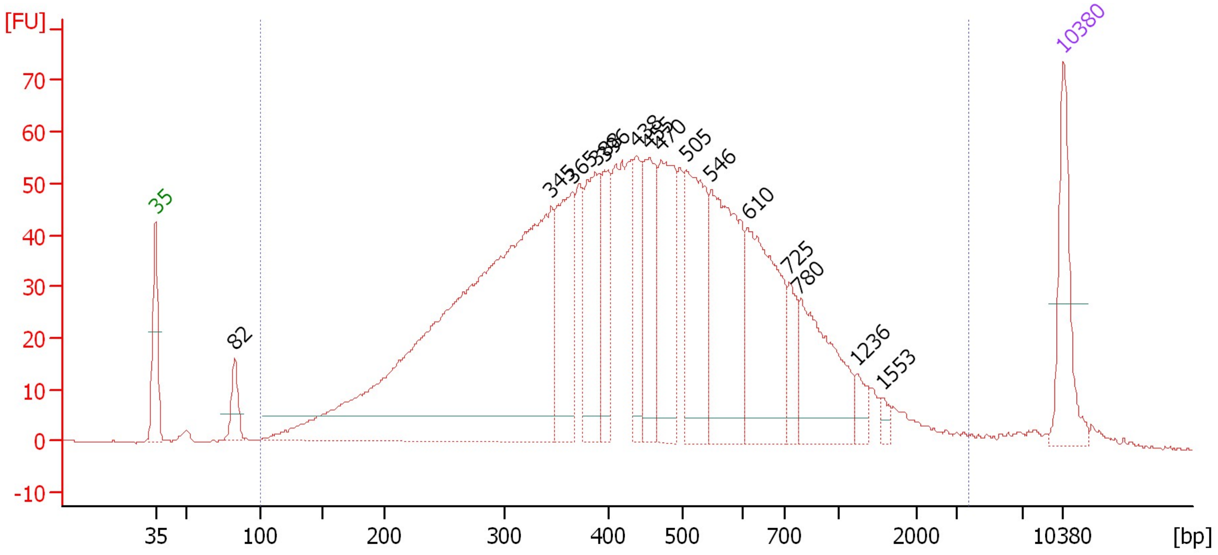
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		42	89.92	3,211.3		44.19
3		250	16.16	97.8		65.32
4		348	162.83	709.3		73.74
5		390	88.49	344.0		77.10
6		410	43.43	160.4		78.52
7		448	37.20	125.7		80.69
8		475	32.49	103.6		82.21
9		489	25.27	78.3		83.02
10		517	100.19	293.6		84.44
11	▶	10,380	75.00	10.9	Upper Marker	113.00

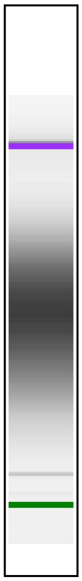
Region table for sample 8 : **8: 5p-m**

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	441	788.8	3,121.6	🟦	802.61	84	30.3

Electropherogram Summary Continued ...

9: Rs PCR Free (1:2) [HiSeq_663 Library]





Overall Results for sample 9 : 9: Rs PCR Free (1:2)

Number of peaks found:	15	Corr. Area 1:	1,905.5
Noise:	0.2		

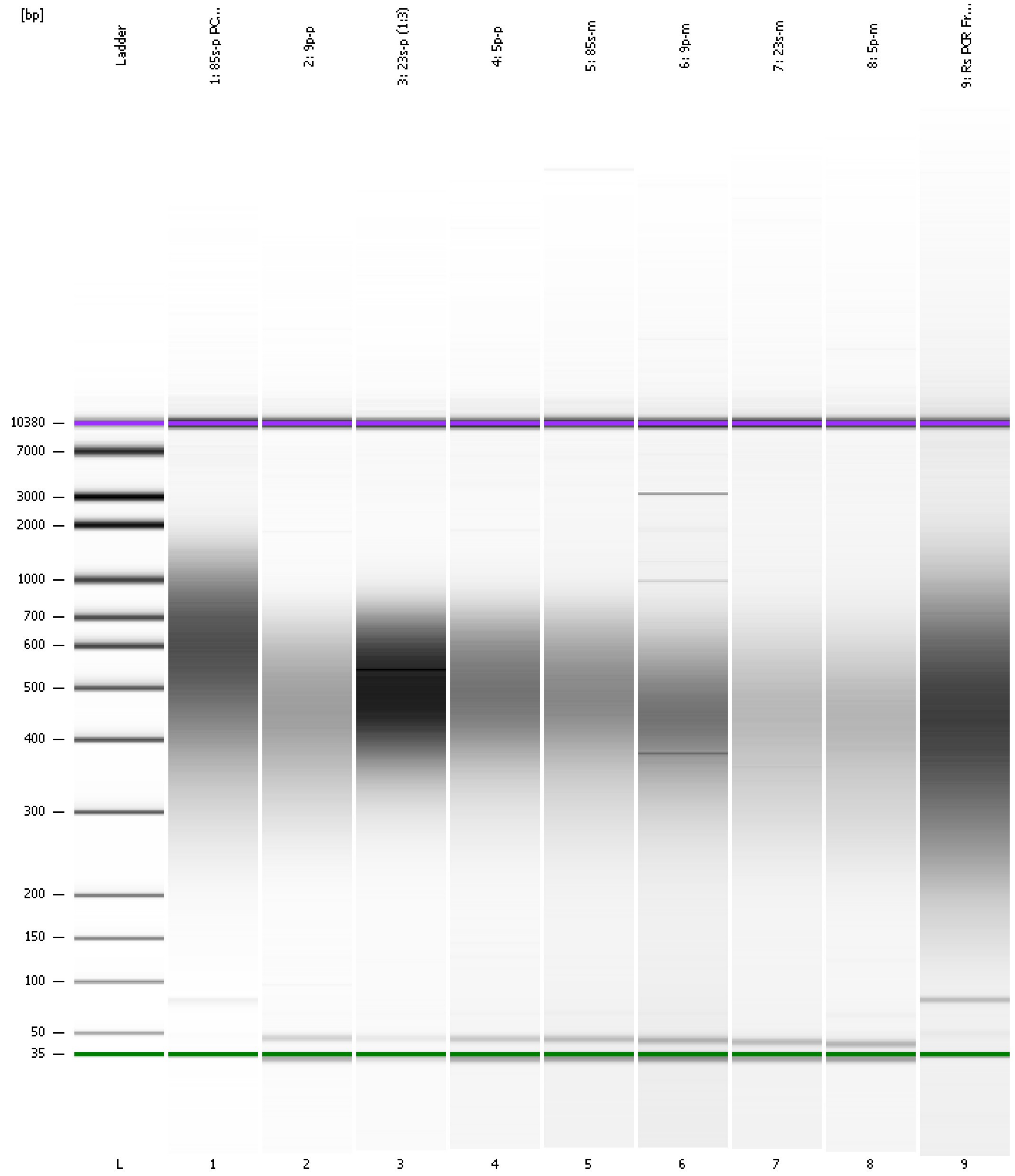
Peak table for sample 9 : 9: Rs PCR Free (1:2)

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		82	43.21	796.9		49.09
3		345	972.47	4,272.1		73.50
4		365	148.91	617.5		75.15
5		388	131.53	513.7		76.96
6		396	86.41	330.5		77.62
7		438	81.76	283.0		80.08
8		455	120.02	399.6		81.07
9		470	155.99	502.4		81.95
10		505	169.35	508.2		83.87
11		546	219.61	609.5		85.79
12		610	187.49	465.5		88.64
13		725	38.88	81.2		91.82
14		780	136.54	265.2		92.59
15		1,236	16.06	19.7		97.09
16		1,553	7.22	7.0		99.01
17	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : 9: Rs PCR Free (1:2)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
99	3,673	514	1,905.5	13,469.6	🟦	3,182.07	96	69.7

Gel Image


[bp]
Ladder
1: 85s-p PC...
2: 9p-p
3: 23s-p (1:3)
4: 5p-p
5: 85s-m
6: 9p-m
7: 23s-m
8: 5p-m
9: Rs PCR Fr...
10380
7000
3000
2000
1000
700
600
500
400
300
200
150
100
50
35
L
1
2
3
4
5
6
7
8
9

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		10/31/2016 10:29:04 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\2016-10-31\2016-10-31_001.xad)		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/31/2016 9:47:50 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1