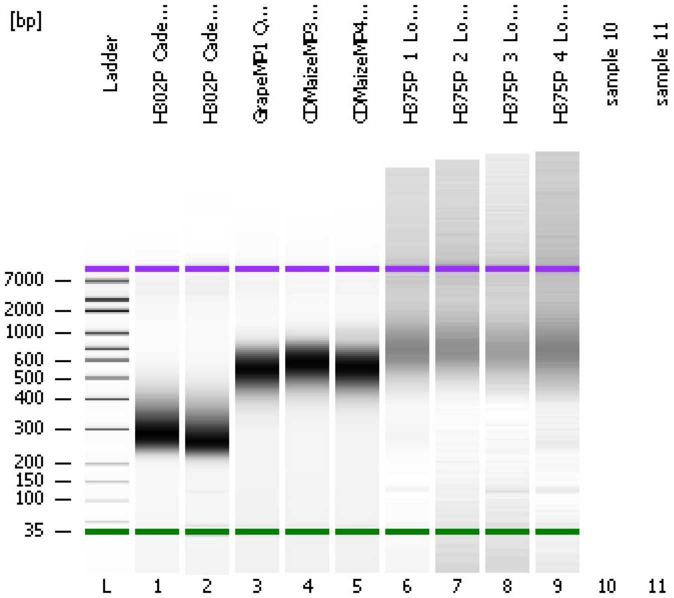
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-18\2016-01-18_002.xad
Created: 1/18/2016 10:15:29 AM
Modified: 1/18/2016 10:51:53 AM

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

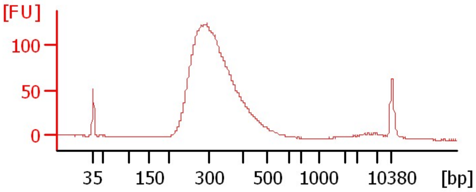
Chip Information:

Chip Lot #:

Reagent Kit Lot #:

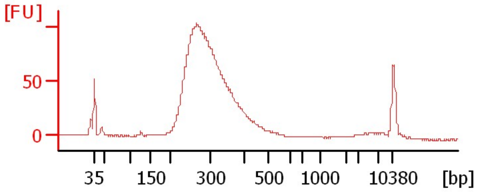
Chip Comments:

H302P_Cadena with 0.9X cleanup (1:2)



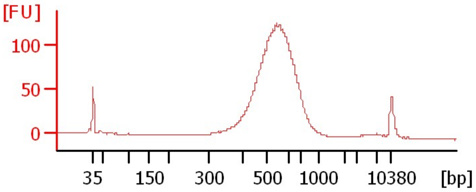
H302P_Cadena (1:3)

before cleanup



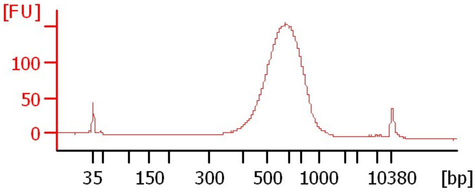
GrapeMP1 QC PCR

HiSeq_382



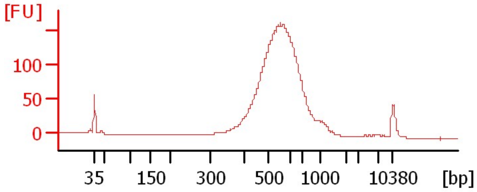
CDMaizeMP3 QC PCR

HiSeq_382



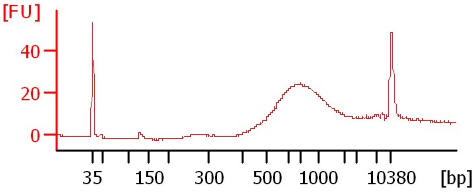
CDMaizeMP4 QC PCR

HiSeq_382



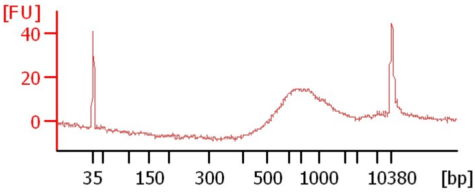
H375P_1_Lott (1:6)

HiSeq_375



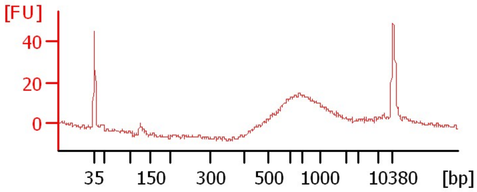
H375P_2_Lott (1:6)

HiSeq_375



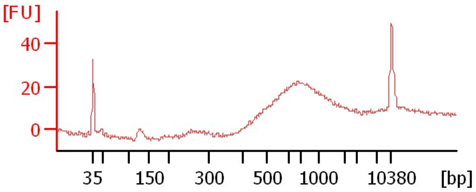
H375P_3_Lott (1:6)

HiSeq_375



H375P_4_Lott (1:6)

HiSeq_375



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-18\2016-01-18_002.xad

Created: 1/18/2016 10:15:29 AM
Modified: 1/18/2016 10:51:53 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
H302P_Cadena with 0.9X cleanup (1:2)		☐	✓			
H302P_Cadena (1:3)	before cleanup	☐	✓			
GrapeMP1 QC PCR	HiSeq_382	☐	✓			
CDMaizeMP3 QC PCR	HiSeq_382	☐	✓			
CDMaizeMP4 QC PCR	HiSeq_382	☐	✓			
H375P_1_Lott (1:6)	HiSeq_375	☐	✓			
H375P_2_Lott (1:6)	HiSeq_375	☐	✓			
H375P_3_Lott (1:6)	HiSeq_375	☐	✓			
H375P_4_Lott (1:6)	HiSeq_375	☐	✓			
sample 10		☐				
sample 11		☐				
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

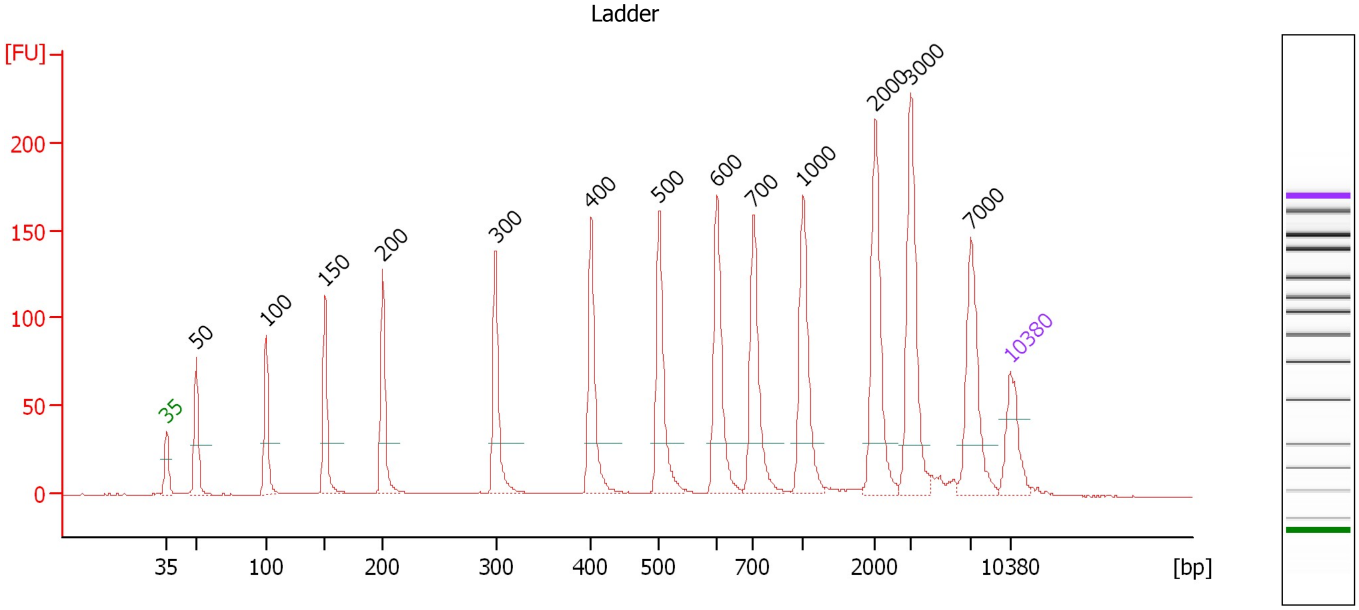
Ladder

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:\...ents and Settings\Bioanalyzer\2016-01-18\2016-01-18_002.xad

Created: 1/18/2016 10:15:29 AM
Modified: 1/18/2016 10:51:53 AM

Electropherogram Summary



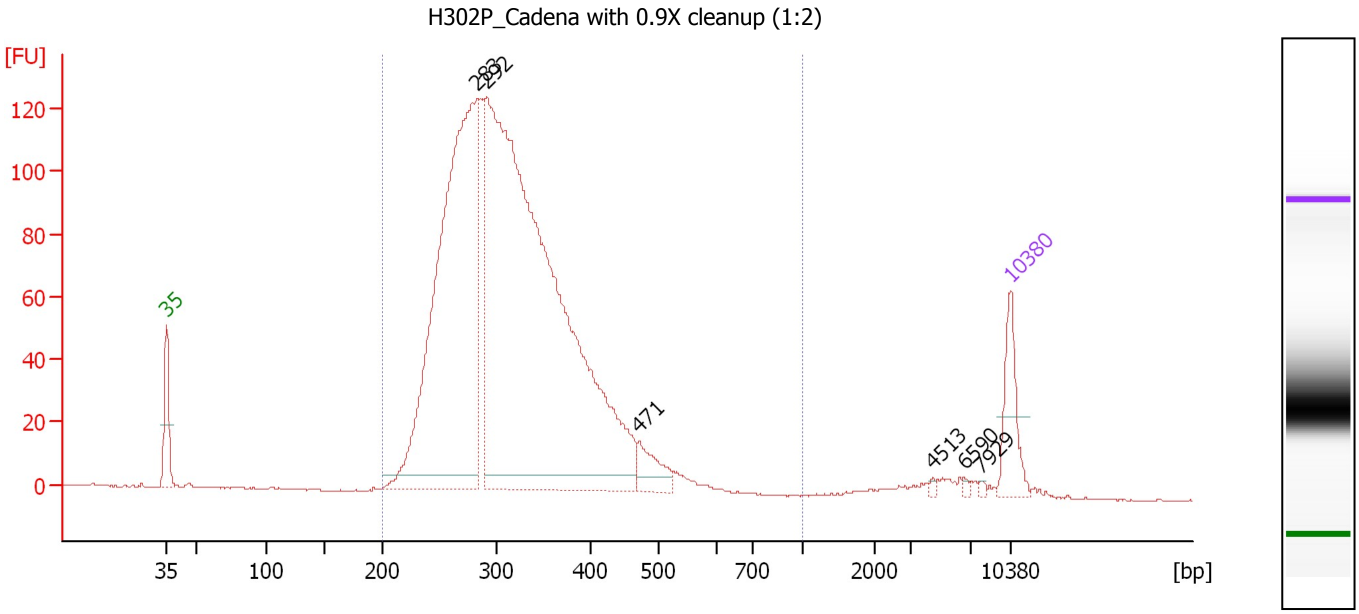
Overall Results for Ladder

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	45.45
3	∟	100	150.00	2,272.7	Ladder Peak	51.24
4	∟	150	150.00	1,515.2	Ladder Peak	56.13
5	∟	200	150.00	1,136.4	Ladder Peak	60.94
6	∟	300	150.00	757.6	Ladder Peak	70.30
7	∟	400	150.00	568.2	Ladder Peak	78.21
8	∟	500	150.00	454.5	Ladder Peak	83.86
9	∟	600	150.00	378.8	Ladder Peak	88.66
10	∟	700	150.00	324.7	Ladder Peak	91.68
11	∟	1,000	150.00	227.3	Ladder Peak	95.82
12	∟	2,000	150.00	113.6	Ladder Peak	101.80
13	∟	3,000	150.00	75.8	Ladder Peak	104.71
14	∟	7,000	150.00	32.5	Ladder Peak	109.66
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...



Overall Results for sample 1 : **H302P_Cadena with 0.9X cleanup (1:2)**

Number of peaks found:	6	Corr. Area 1:	2,031.4
Noise:	0.2		

Peak table for sample 1 : **H302P_Cadena with 0.9X cleanup (1:2)**

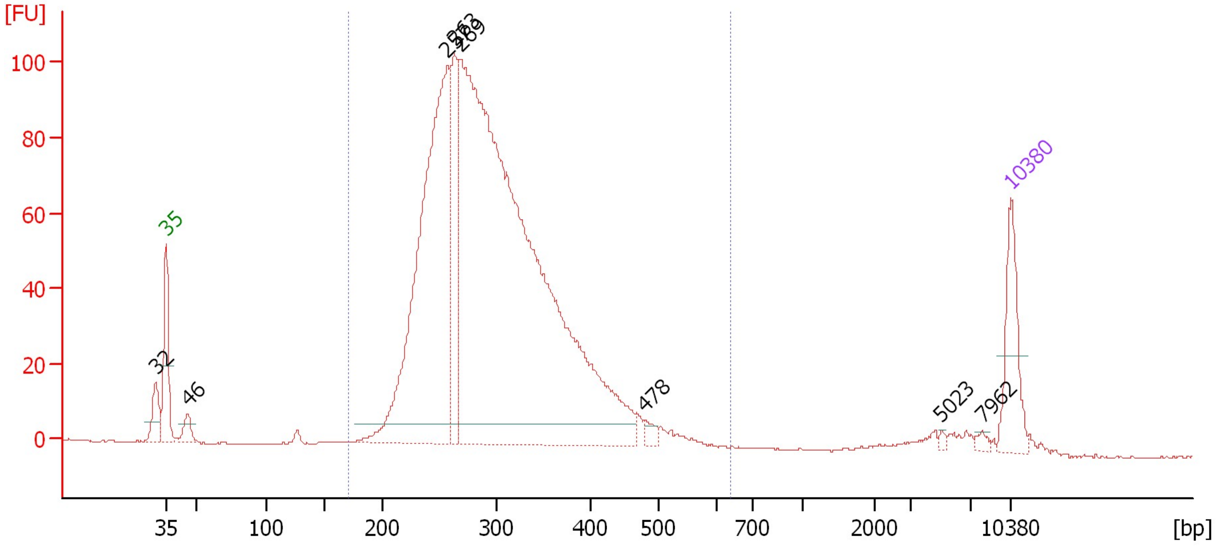
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		283	1,286.51	6,888.2		68.71
3		292	2,203.09	11,427.0		69.56
4		471	61.66	198.5		82.21
5		4,513	3.60	1.2		106.58
6		6,590	3.87	0.9		109.15
7		7,929	3.79	0.7		110.58
8	▶	10,380	75.00	10.9	Upper Marker	113.00

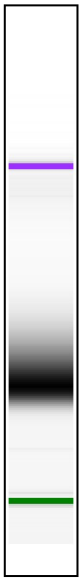
Region table for sample 1 : **H302P_Cadena with 0.9X cleanup (1:2)**

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	320	2,031.4	17,578.8	■	3,550.07	98	20.0

Electropherogram Summary Continued ...

H302P_Cadena (1:3) [before cleanup]





Overall Results for sample 2 : **H302P_Cadena (1:3)**

Number of peaks found:	8	Corr. Area 1:	1,603.6
Noise:	0.2		

Peak table for sample 2 : **H302P_Cadena (1:3)**

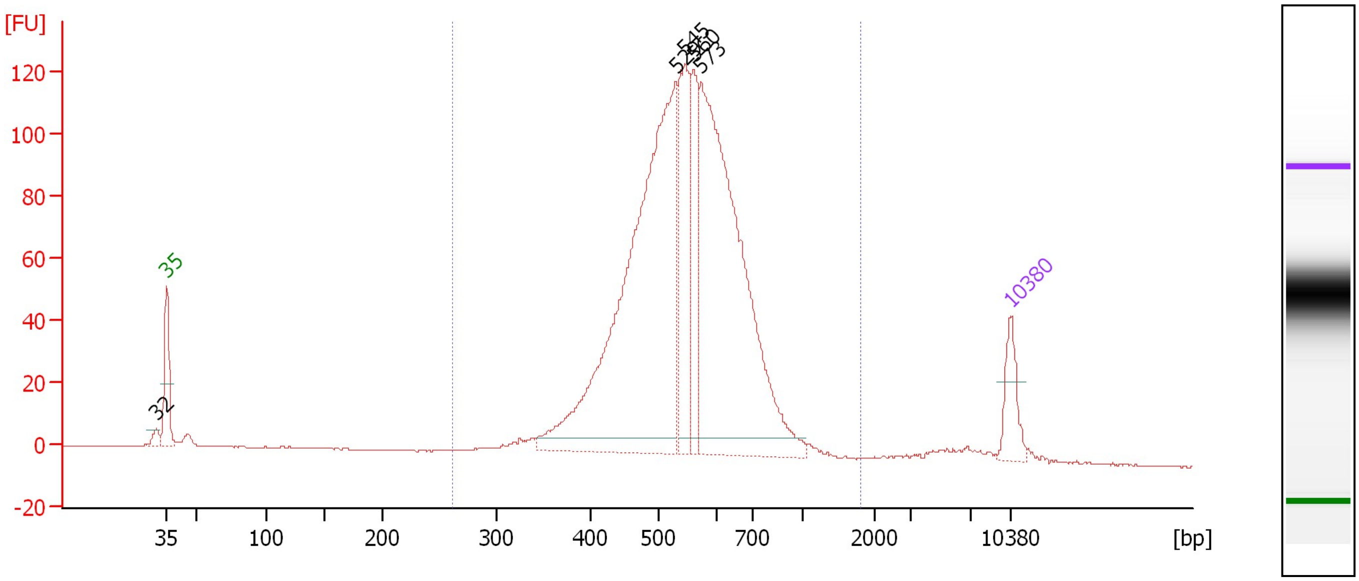
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.09
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		46	29.88	987.7		44.77
4		257	790.46	4,658.2		66.29
5		263	172.73	994.2		66.86
6		269	1,899.95	10,707.5		67.39
7		478	13.06	41.4		82.64
8		5,023	3.08	0.9		107.21
9		7,962	5.73	1.1		110.61
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 2 : **H302P_Cadena (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
170	639	302	1,603.5	14,554.9	■	2,769.76	95	20.8

Electropherogram Summary Continued ...

GrapeMP1 QC PCR [HiSeq_382]



Overall Results for sample 3 : GrapeMP1 QC PCR

Number of peaks found:	5	Corr. Area 1:	1,540.6
Noise:	0.2		

Peak table for sample 3 : GrapeMP1 QC PCR

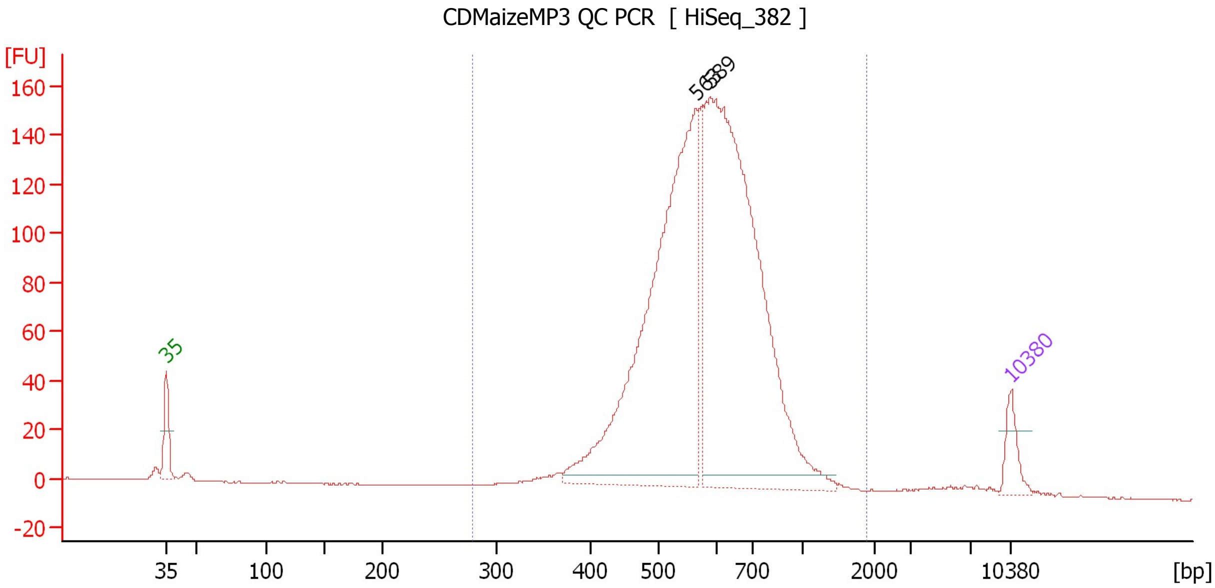
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.13
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		529	1,424.71	4,082.5		85.24
4		545	331.79	922.7		86.01
5		560	219.25	593.3		86.74
6		573	1,166.02	3,083.3		87.37
7	▶	10,380	75.00	10.9	Upper Marker	113.00

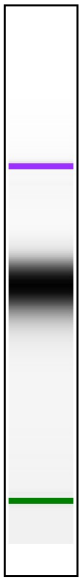
Region table for sample 3 : GrapeMP1 QC PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
262	1,803	554	1,540.6	9,696.1	🟦	3,362.06	95	21.8

Electropherogram Summary Continued ...

CDMaizeMP3 QC PCR [HiSeq_382]





Overall Results for sample 4 : **CDMaizeMP3 QC PCR**

Number of peaks found:	2	Corr. Area 1:	1,902.0
Noise:	0.1		

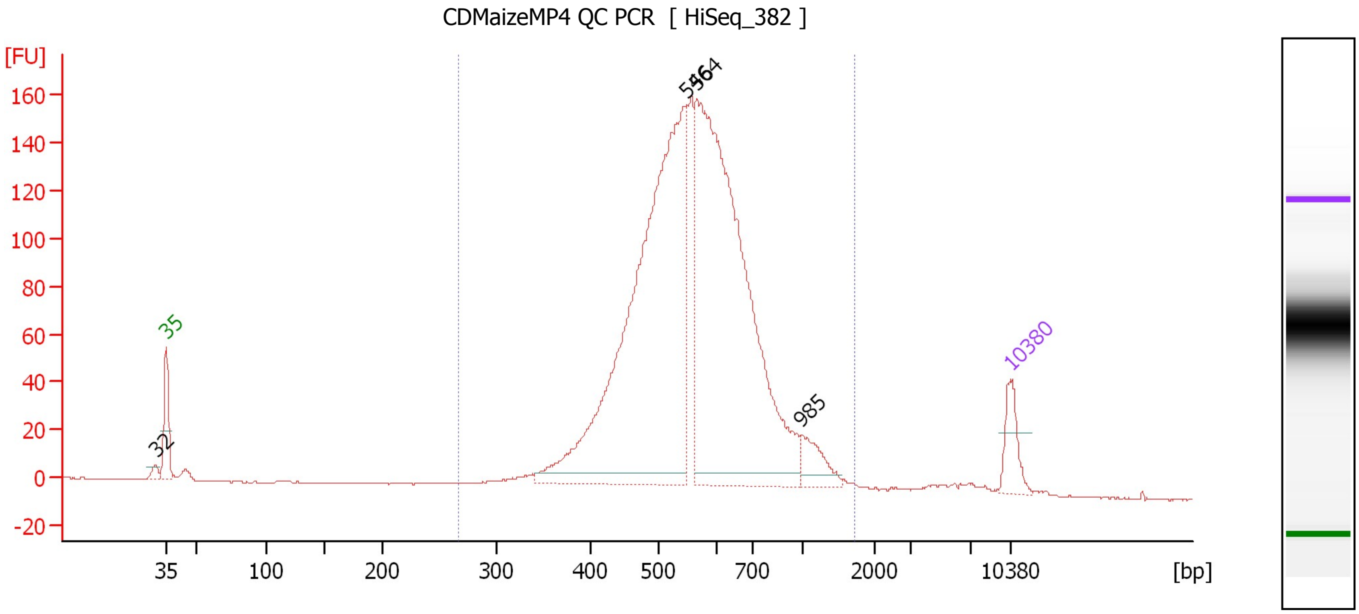
Peak table for sample 4 : **CDMaizeMP3 QC PCR**

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		563	1,893.32	5,093.1		86.90
3		589	2,192.68	5,642.0		88.13
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : **CDMaizeMP3 QC PCR**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
280	1,890	604	1,902.0	12,076.1	■	4,532.50	96	24.4

Electropherogram Summary Continued ...



Overall Results for sample 5 : CDMaizeMP4 QC PCR

Number of peaks found:	4	Corr. Area 1:	2,064.8
Noise:	0.2		

Peak table for sample 5 : CDMaizeMP4 QC PCR

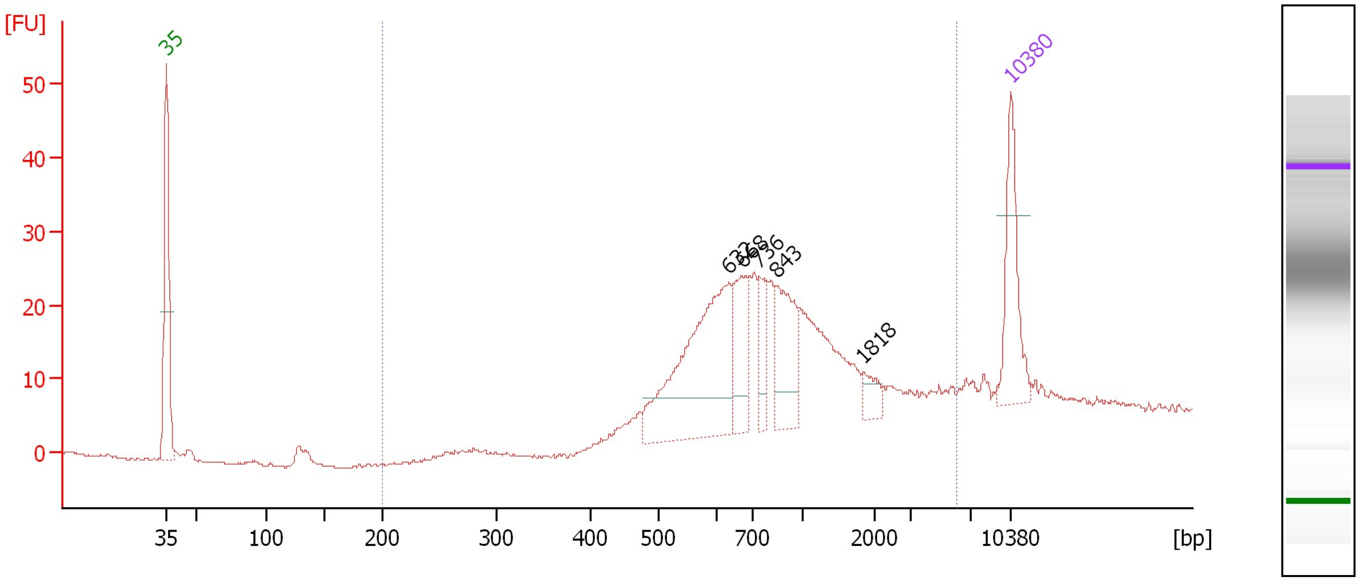
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.10
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		546	1,797.09	4,991.4		86.05
4		564	1,692.98	4,546.5		86.94
5		985	83.18	127.9		95.61
6	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : CDMaizeMP4 QC PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
268	1,699	585	2,064.8	11,154.5	🟦	4,003.91	97	27.8

Electropherogram Summary Continued ...

H375P_1_Lott (1:6) [HiSeq_375]



Overall Results for sample 6 : **H375P_1_Lott (1:6)**

Number of peaks found:	5	Corr. Area 1:	319.1
Noise:	0.2		

Peak table for sample 6 : **H375P_1_Lott (1:6)**

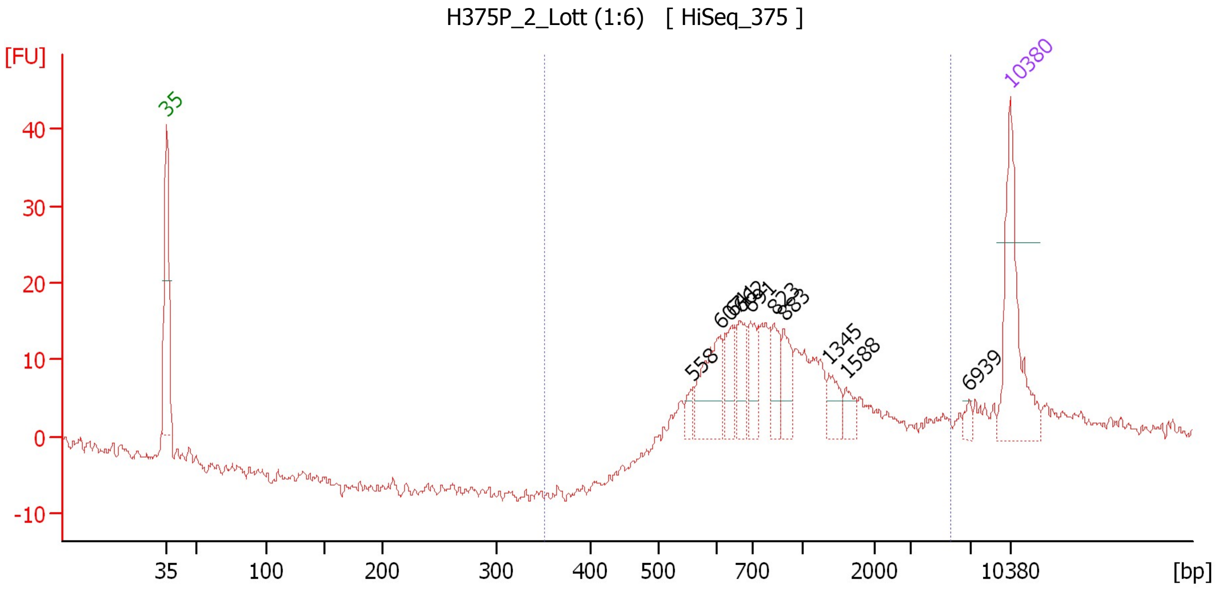
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		632	248.18	594.8		89.63
3		668	73.41	166.6		90.70
4		736	40.85	84.1		92.17
5		843	82.68	148.7		93.65
6		1,818	18.91	15.8		100.71
7	▶	10,380	75.00	10.9	Upper Marker	113.00

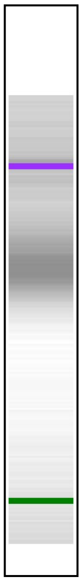
Region table for sample 6 : **H375P_1_Lott (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	6,067	1,139	319.1	1,399.7	🟦	721.02	88	86.0

Electropherogram Summary Continued ...

H375P_2_Lott (1:6) [HiSeq_375]





Overall Results for sample 7 : **H375P_2_Lott (1:6)**

Number of peaks found: 10 Corr. Area 1: 207.4

Noise: 0.7

Peak table for sample 7 : **H375P_2_Lott (1:6)**

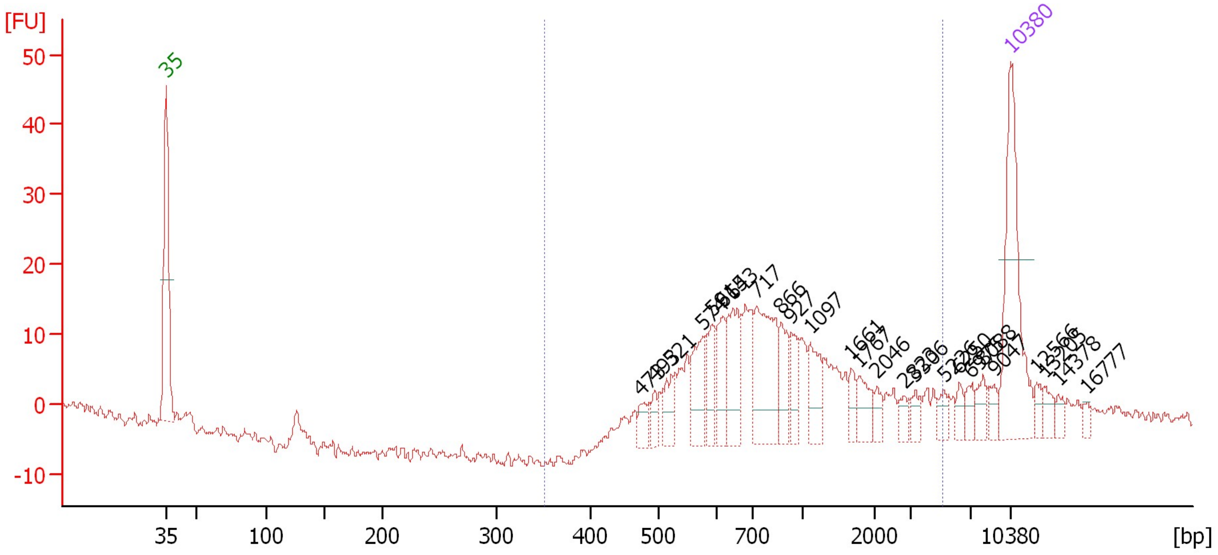
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		558	9.74	26.5		86.65
3		607	52.83	131.9		88.87
4		641	25.48	60.2		89.91
5		662	30.51	69.8		90.53
6		691	26.94	59.1		91.41
7		823	24.24	44.6		93.38
8		883	25.00	42.9		94.21
9		1,345	17.89	20.1		97.88
10		1,588	11.07	10.6		99.33
11		6,939	4.97	1.1		109.58
12	▶	10,380	75.00	10.9	Upper Marker	113.00

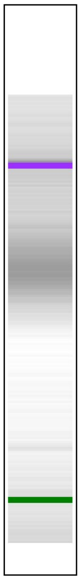
Region table for sample 7 : **H375P_2_Lott (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
350	5,707	1,119	207.4	725.7	■	390.06	82	78.4

Electropherogram Summary Continued ...

H375P_3_Lott (1:6) [HiSeq_375]





Overall Results for sample 8 : **H375P_3_Lott (1:6)**

Number of peaks found:	25	Corr. Area 1:	224.6
Noise:	0.8		

Peak table for sample 8 : **H375P_3_Lott (1:6)**

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		473	11.77	37.7		82.32
3		493	10.69	32.8		83.48
4		521	18.32	53.3		84.85
5		574	33.00	87.0		87.44
6		591	21.73	55.7		88.23
7		615	26.25	64.6		89.12
8		643	39.97	94.2		89.97
9		717	67.95	143.5		91.92
10		866	19.54	34.2		93.97
11		927	17.70	28.9		94.81
12		1,097	24.18	33.4		96.40
13		1,661	8.88	8.1		99.77
14		1,767	14.29	12.3		100.40
15		2,046	7.43	5.5		101.93
16		2,823	5.88	3.2		104.20
17		3,306	6.66	3.1		105.09
18		5,226	7.46	2.2		107.47
19		6,250	6.61	1.6		108.73
20		6,975	7.43	1.6		109.63
21		8,088	8.70	1.6		110.73
22		9,047	6.59	1.1		111.68
23	▶	10,380	75.00	10.9	Upper Marker	113.00
24		12,566	0.00	0.0		115.16
25		13,205	0.00	0.0		115.79

Electropherogram Summary Continued ...

... Peak table for sample 8 : H375P_3_Lott (1:6)

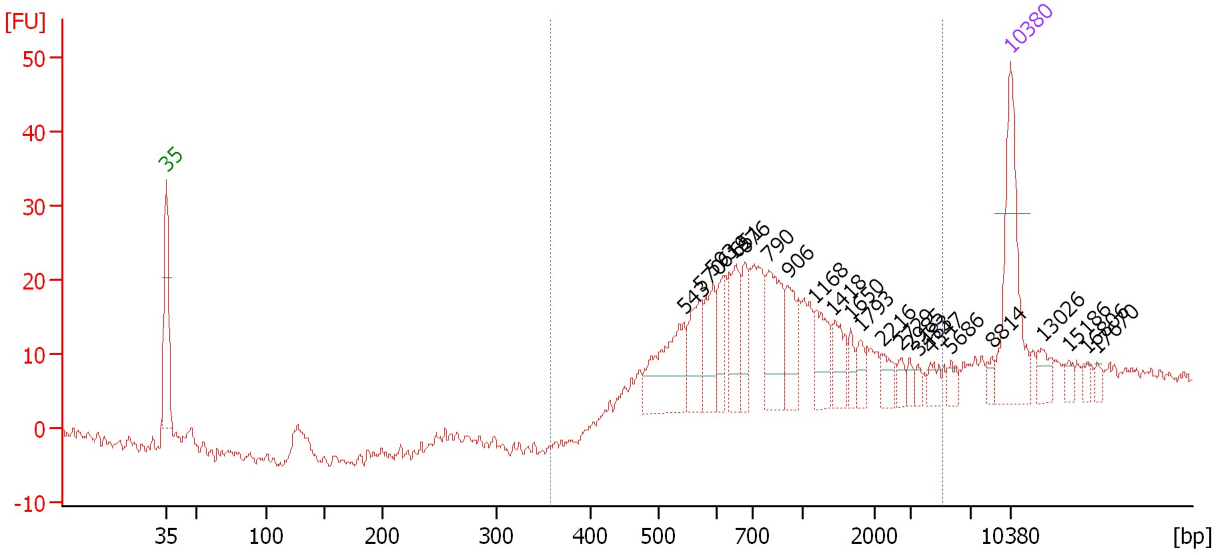
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	14,378	0.00	0.0		116.95
27	16,777	0.00	0.0		119.33

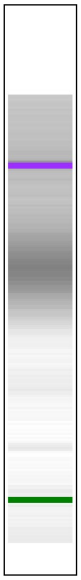
Region table for sample 8 : H375P_3_Lott (1:6)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
351	5,206	1,120	224.6	656.8	🟦	343.09	78	77.7

Electropherogram Summary Continued ...

H375P_4_Lott (1:6) [HiSeq_375]





Overall Results for sample 9 : **H375P_4_Lott (1:6)**

Number of peaks found:	23	Corr. Area 1:	319.3
Noise:	0.8		

Peak table for sample 9 : **H375P_4_Lott (1:6)**

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		543	77.37	215.9		85.93
3		570	38.37	102.0		87.21
4		593	36.78	94.0		88.33
5		619	26.44	64.7		89.24
6		651	41.35	96.2		90.20
7		676	28.97	65.0		90.95
8		790	58.77	112.7		92.92
9		906	34.33	57.4		94.53
10		1,168	28.34	36.8		96.82
11		1,418	22.27	23.8		98.32
12		1,650	10.44	9.6		99.70
13		1,793	11.38	9.6		100.56
14		2,216	11.63	8.0		102.43
15		2,729	6.60	3.7		103.92
16		2,985	5.77	2.9		104.67
17		3,483	5.15	2.2		105.31
18		4,347	9.11	3.2		106.38
19		5,686	7.25	1.9		108.03
20		8,814	5.67	1.0		111.45
21	▶	10,380	75.00	10.9	Upper Marker	113.00
22		13,026	0.00	0.0		115.62
23		15,186	0.00	0.0		117.75
24		16,806	0.00	0.0		119.35
25		17,670	0.00	0.0		120.21

Electropherogram Summary Continued ...

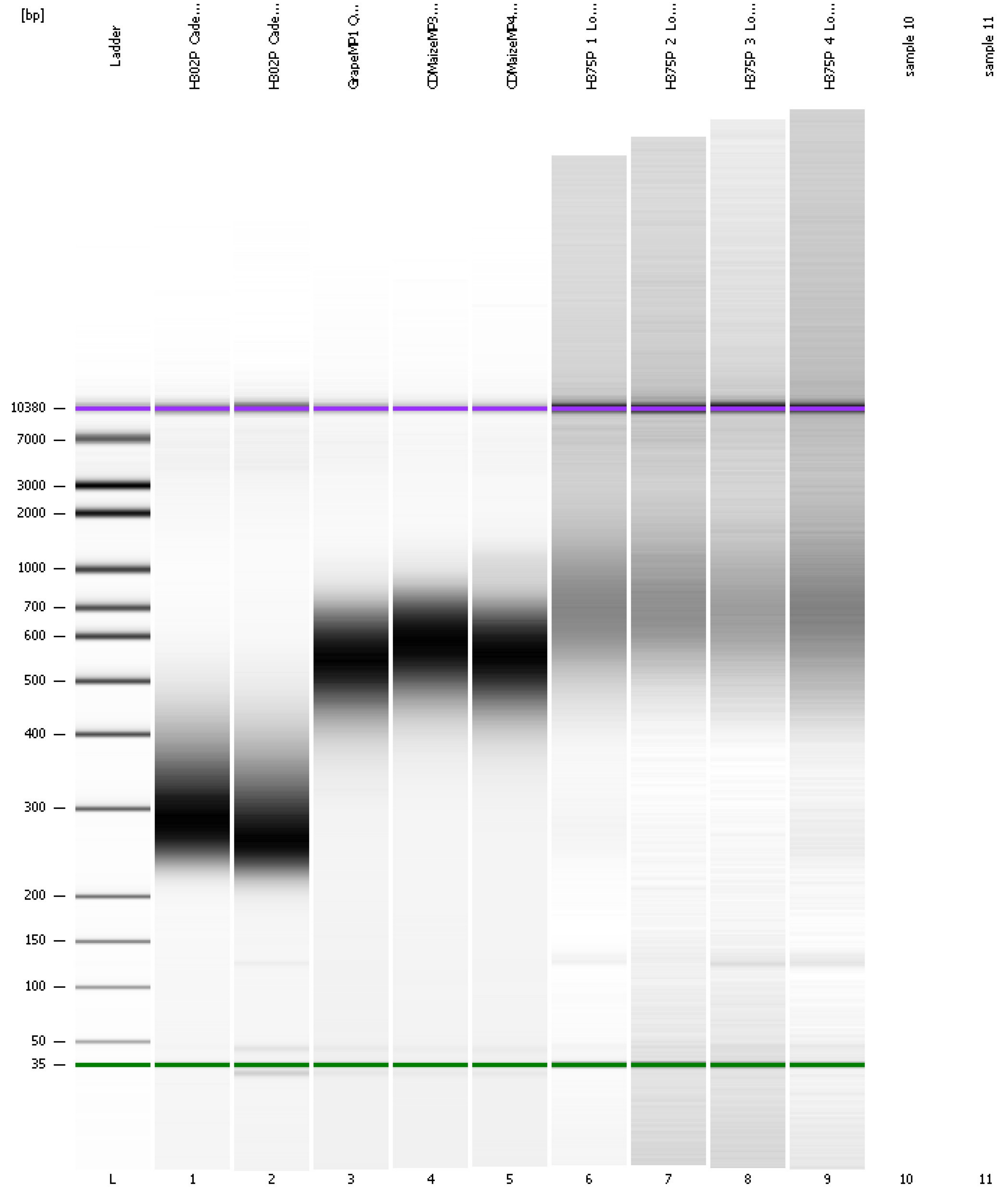
... Region table for sample 9 : **H375P 4 Lott (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
358	5,125	1,091	319.3	1,209.2	🟦 606.52	78	76.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-18\2016-01-18_002.xad

Created: 1/18/2016 10:15:29 AM
Modified: 1/18/2016 10:51:53 AM

Gel Image



Invalid Samples

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 10)		Instrument	Run		1/18/2016 10:51:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-01-18\2016-01-18_002.xad)		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/18/2016 10:15:35 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1