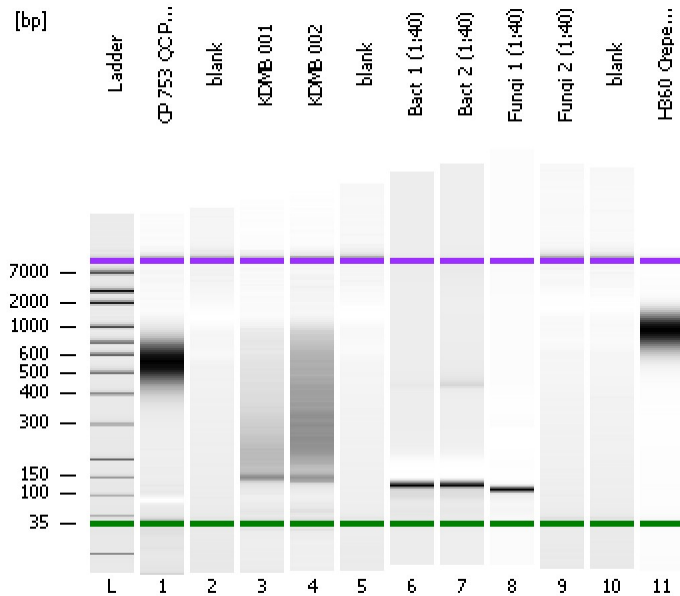


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
Modified: 1/8/2016 12:28:12 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

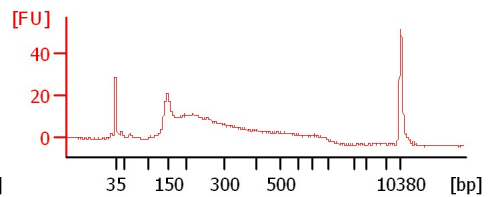
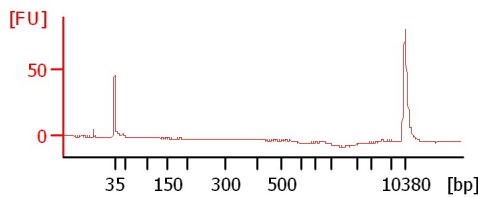
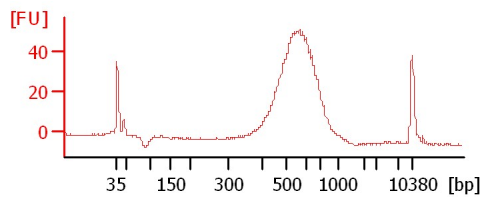
Chip Information:

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

CP 753 QC PCR

blank

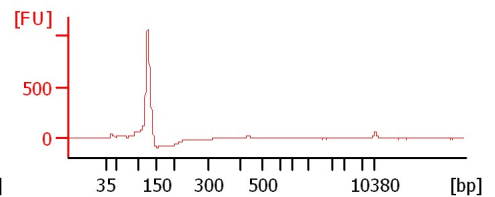
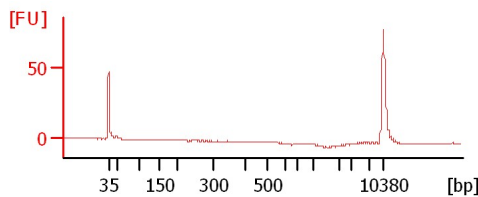
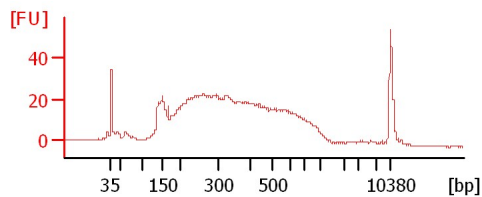
KDMB 001



KDMB 002

blank

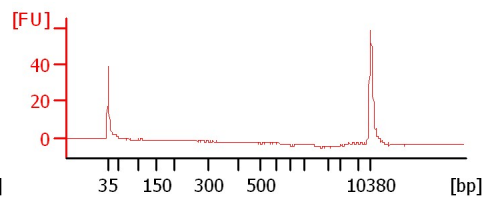
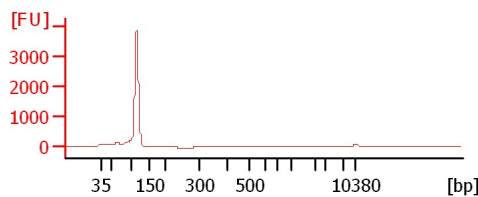
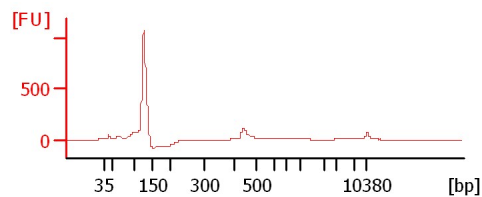
Bact 1 (1:40)



Bact 2 (1:40)

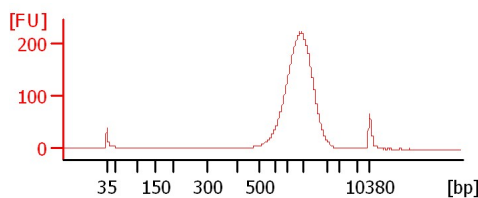
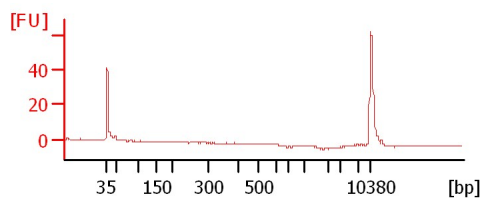
Fungi 1 (1:40)

Fungi 2 (1:40)



blank

H360 Crepeau QC PCR (1:2)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
Modified: 1/8/2016 12:28:12 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
CP 753 QC PCR		<input type="checkbox"/>	✓			
blank		<input type="checkbox"/>	✓			
KDMB 001		<input type="checkbox"/>	✓			
KDMB 002		<input type="checkbox"/>	✓			
blank		<input type="checkbox"/>	✓			
Bact 1 (1:40)		<input type="checkbox"/>	✓			
Bact 2 (1:40)		<input type="checkbox"/>	✓			
Fungi 1 (1:40)		<input type="checkbox"/>	✓			
Fungi 2 (1:40)		<input type="checkbox"/>	✓			
blank		<input type="checkbox"/>	✓			
H360 Crepeau QC PCR (1:2)		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
Modified: 1/8/2016 12:28:12 PM

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

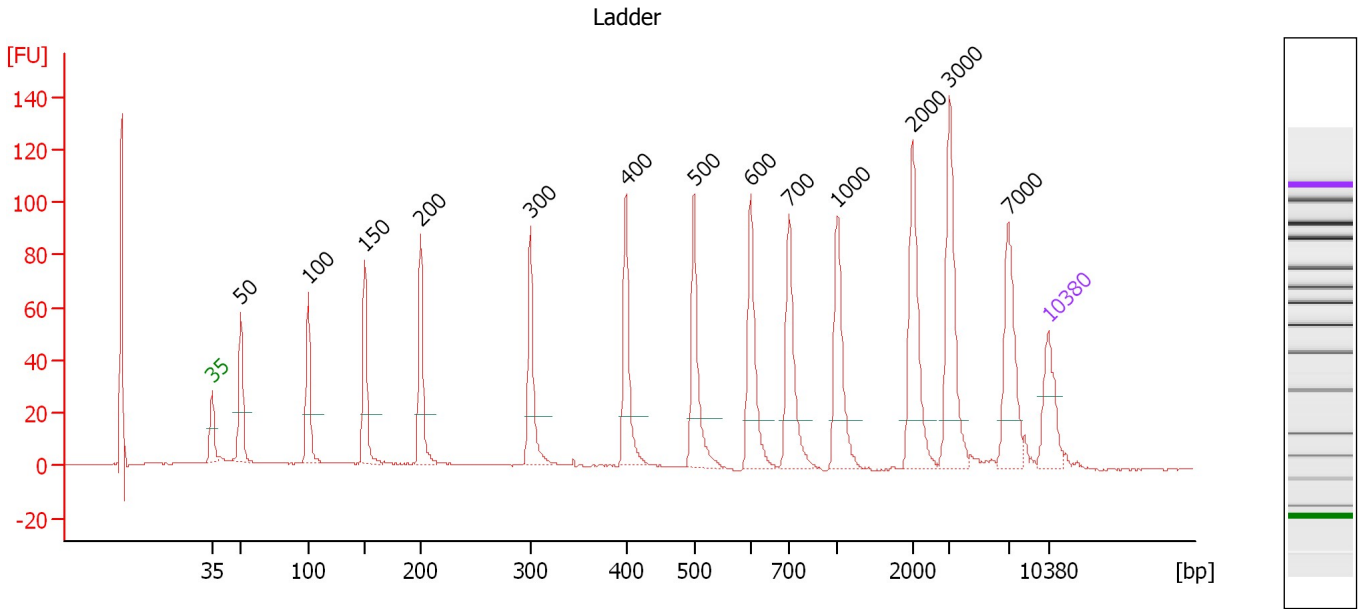
Ladder

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\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

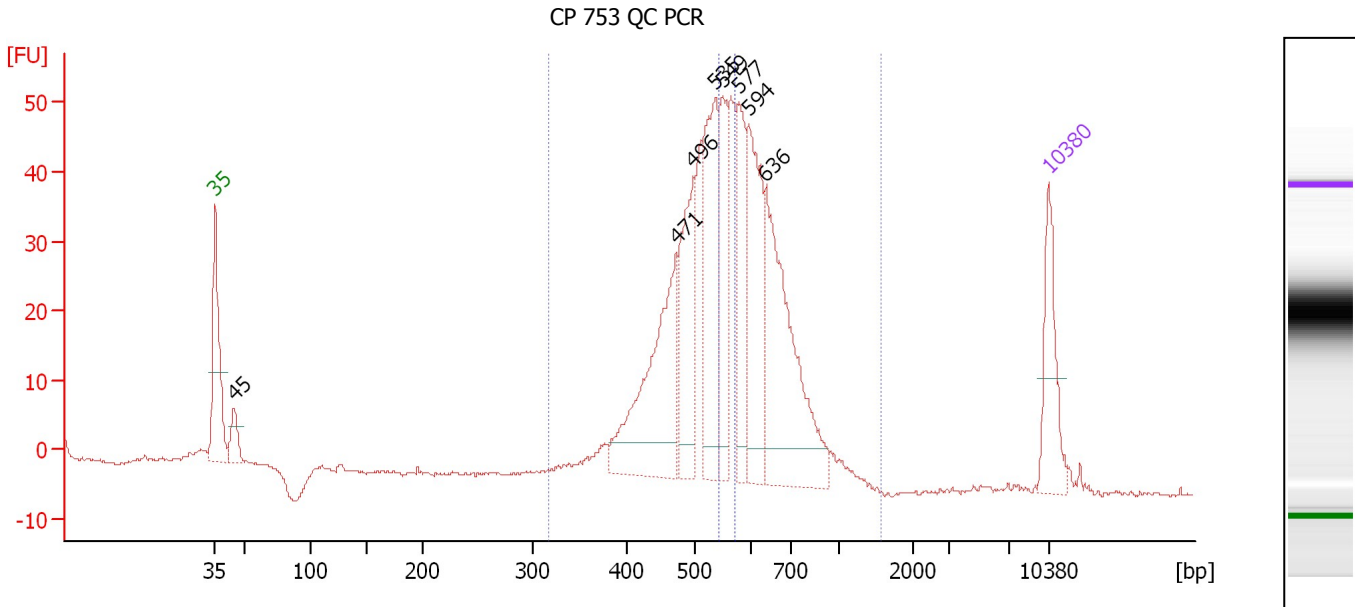
Peak table for Ladder

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	45.41
3	100	150.00	2,272.7	Ladder Peak	51.04
4	150	150.00	1,515.2	Ladder Peak	55.77
5	200	150.00	1,136.4	Ladder Peak	60.46
6	300	150.00	757.6	Ladder Peak	69.65
7	400	150.00	568.2	Ladder Peak	77.64
8	500	150.00	454.5	Ladder Peak	83.36
9	600	150.00	378.8	Ladder Peak	88.09
10	700	150.00	324.7	Ladder Peak	91.30
11	1,000	150.00	227.3	Ladder Peak	95.37
12	2,000	150.00	113.6	Ladder Peak	101.62
13	3,000	150.00	75.8	Ladder Peak	104.74
14	7,000	150.00	32.5	Ladder Peak	109.65
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : CP 753 QC PCR

Number of peaks found: 8 Corr. Area 1: 676.5
 Noise: 0.3 Corr. Area 2: 80.9

Peak table for sample 1 : CP 753 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	45	45.17	1,529.0		44.57
3	471	267.38	859.5		81.72
4	496	169.72	518.0		83.15
5	535	210.66	596.1		85.04
6	549	114.57	316.3		85.66
7	577	112.93	296.5		87.01
8	594	180.78	461.0		87.81
9	636	292.46	696.7		89.25
10	10,380	75.00	10.9	Upper Marker	113.00

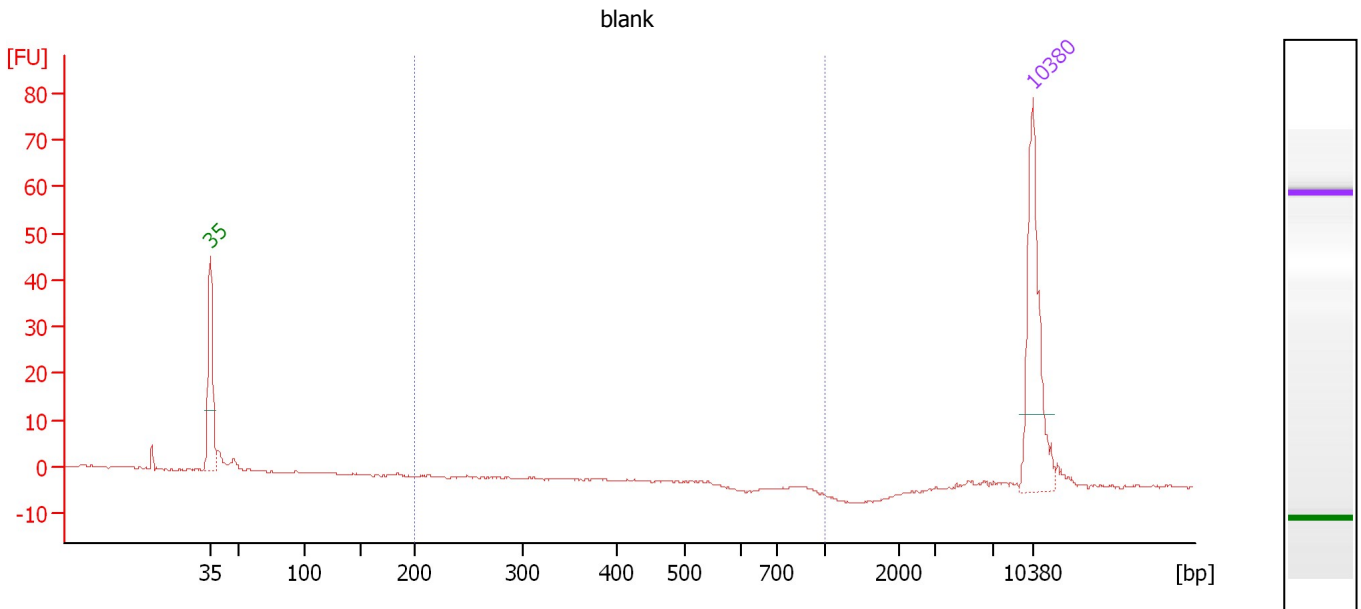
Region table for sample 1 : CP 753 QC PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
317	1,580	565	676.5	4,424.4	1,573.90	96	20.0
543	570	555	80.9	507.0	185.82	11	1.4

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : blank

Number of peaks found: 0 Corr. Area 1: 0.0
 Noise: 0.2

Peak table for sample 2 : blank

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	10,380	75.00	10.9	Upper Marker	113.00

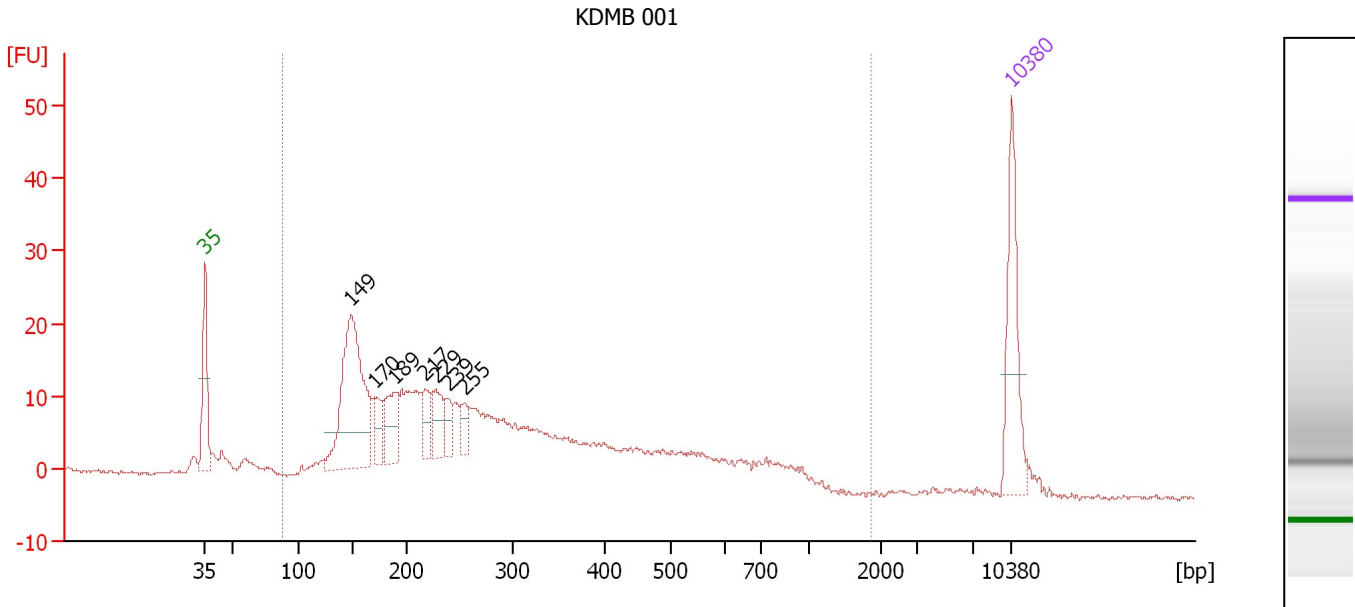
Region table for sample 2 : blank

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	0	0.0	0.0	0.00	0	0.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : KDMB 001

Number of peaks found: 7 Corr. Area 1: 469.1
 Noise: 0.3

Peak table for sample 3 : KDMB 001

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	149	261.71	2,660.6		55.68
3	170	33.38	297.1		57.67
4	189	59.92	481.6		59.38
5	217	29.30	204.2		62.06
6	229	39.27	260.4		63.08
7	239	22.85	144.8		64.05
8	255	18.26	108.6		65.49
9	10,380	75.00	10.9	Upper Marker	113.00

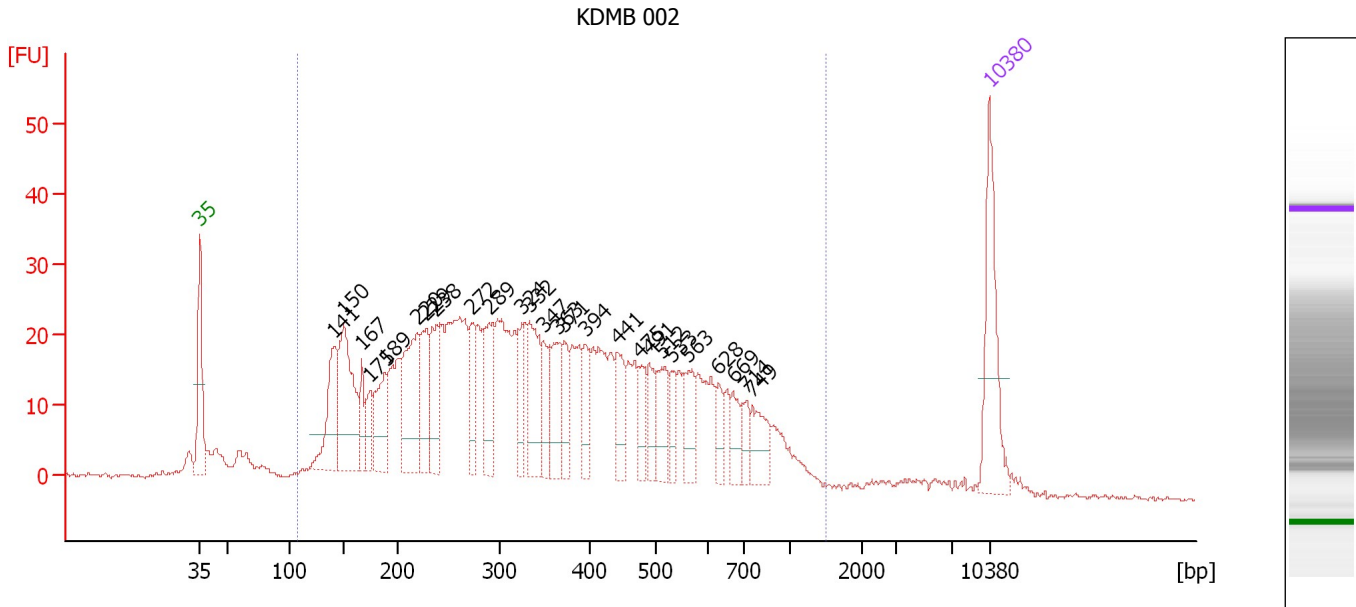
Region table for sample 3 : KDMB 001

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
88	1,863	318	469.1	8,398.2	1,244.44	93	56.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : KDMB 002

Number of peaks found: 26 Corr. Area 1: 1,048.0
 Noise: 0.2

Peak table for sample 4 : KDMB 002

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	141	89.00	956.8		54.91
3	150	151.23	1,528.2		55.76
4	167	34.48	312.7		57.37
5	175	31.07	268.7		58.12
6	189	62.49	500.3		59.45
7	220	121.24	835.4		62.28
8	229	63.38	420.1		63.09
9	238	67.44	428.7		63.99
10	272	46.01	256.0		67.11
11	289	61.06	320.4		68.62
12	324	40.68	190.4		71.55
13	332	80.22	366.1		72.21
14	347	39.48	172.2		73.44
15	363	48.38	201.8		74.72
16	371	32.48	132.6		75.33
17	394	32.73	125.8		77.17
18	441	39.91	137.0		80.01
19	475	26.22	83.6		81.95
20	491	27.58	85.1		82.84
21	512	42.65	126.2		83.93
22	533	22.05	62.7		84.92
23	563	37.37	100.6		86.34
24	628	18.87	45.5		88.99
25	669	23.00	52.1		90.31

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...

... Peak table for sample 4 : KDMB 002

Peak	Size [bp]	Conc. [pg/ μ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	714	19.18	40.7		91.49
27	749	37.23	75.3		91.97
28	10,380	75.00	10.9	Upper Marker	113.00

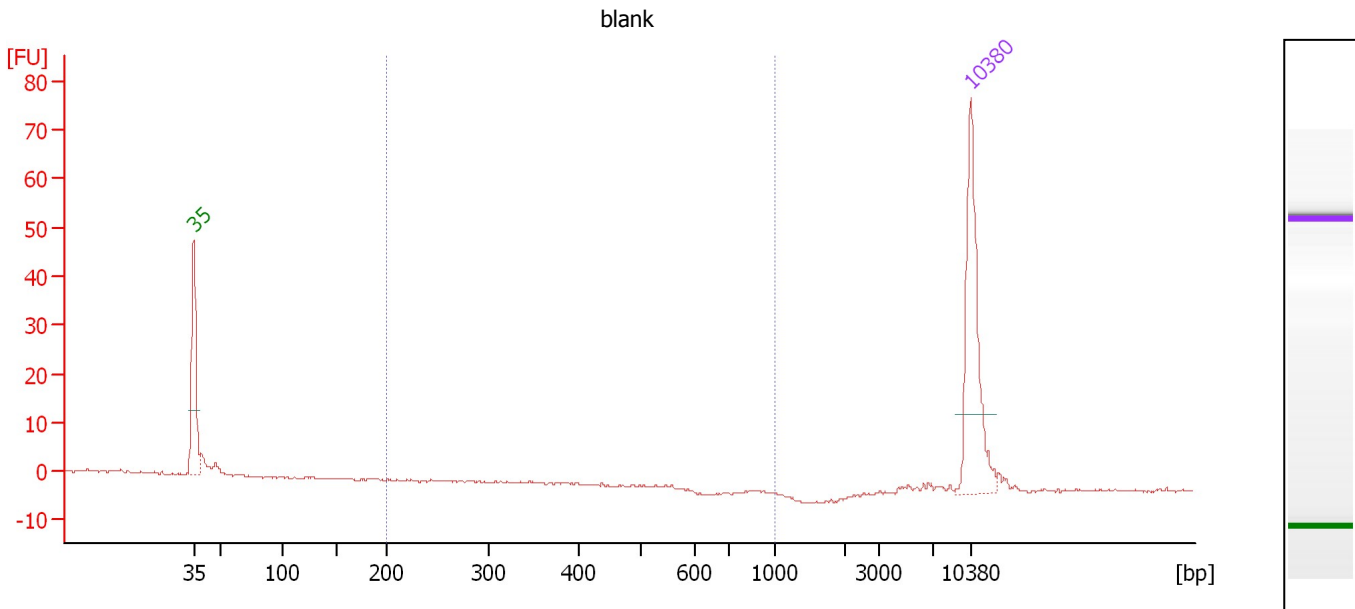
Region table for sample 4 : KDMB 002

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/ μ l]	% of Total	Size distribution in CV [%]
106	1,507	385	1,048.0	13,030.5	2,342.32	94	51.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : blank

Number of peaks found: 0 Corr. Area 1: 0.0
 Noise: 0.2

Peak table for sample 5 : blank

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	10,380	75.00	10.9	Upper Marker	113.00

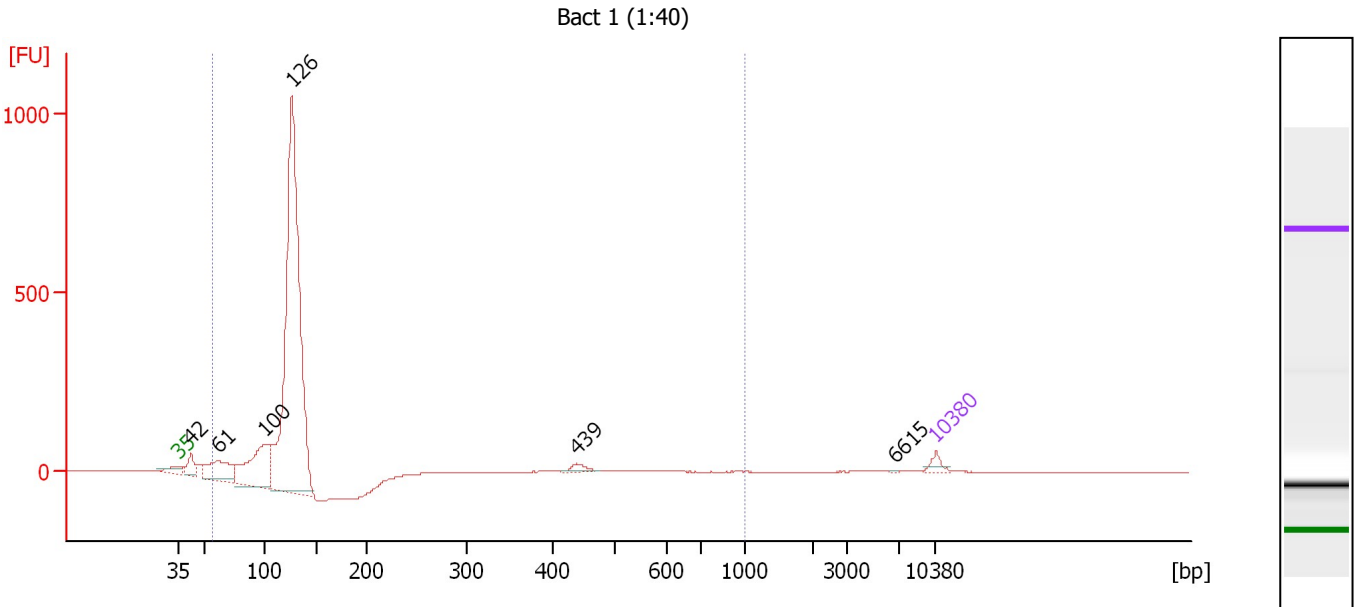
Region table for sample 5 : blank

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	0	0.0	0.0	0.00	0	0.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
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Electropherogram Summary Continued ...



Overall Results for sample 6 : Bact 1 (1:40)

Number of peaks found: 6 Corr. Area 1: 3,154.3
 Noise: 0.2

Peak table for sample 6 : Bact 1 (1:40)

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	316.29	11,325.0		44.18
3	61	897.29	22,204.1		46.67
4	100	1,618.13	24,521.8		51.03
5	126	8,665.30	103,891.7		53.53
6	439	88.73	306.1		79.89
7	6,615	6.86	1.6		109.18
8	10,380	75.00	10.9	Upper Marker	113.00

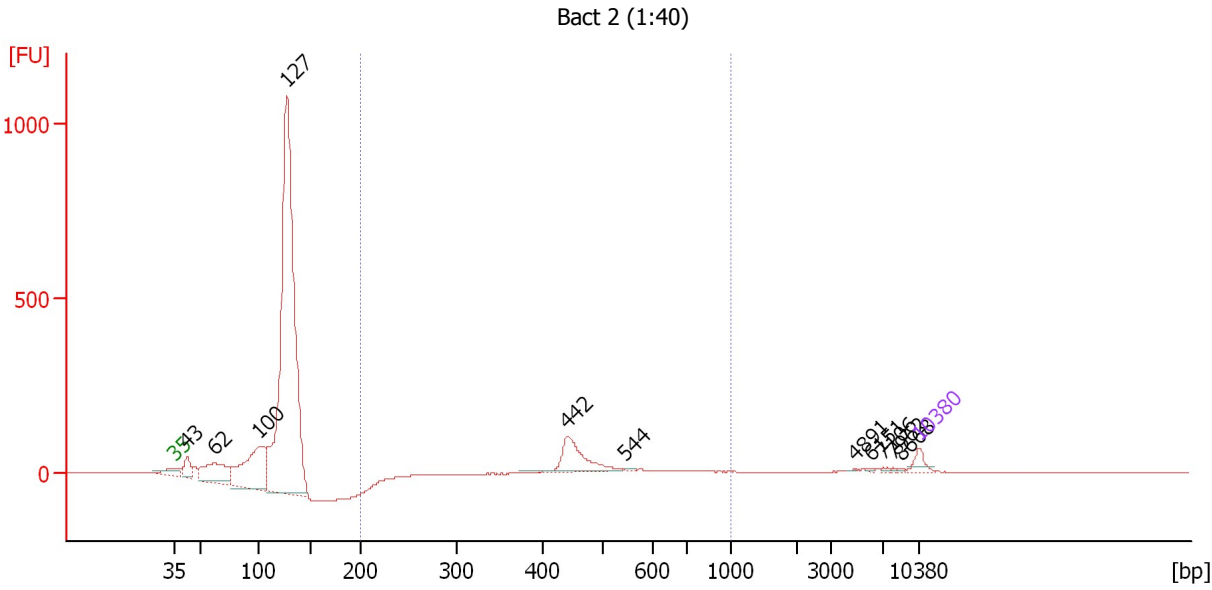
Region table for sample 6 : Bact 1 (1:40)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
57	1,000	130	3,154.3	108,968.5	8,696.37	95	41.1

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
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Electropherogram Summary Continued ...



Overall Results for sample 7 : Bact 2 (1:40)

Number of peaks found: 11 Corr. Area 1: 428.6
 Noise: 0.3

Peak table for sample 7 : Bact 2 (1:40)

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	242.36	8,587.5		44.25
3	62	717.29	17,451.0		46.79
4	100	1,319.66	20,000.0		51.03
5	127	6,977.65	82,995.9		53.63
6	442	516.58	1,772.4		80.02
7	544	12.82	35.7		85.46
8	4,891	5.25	1.6		107.06
9	6,151	9.04	2.2		108.61
10	7,106	10.78	2.3		109.76
11	7,962	6.94	1.3		110.61
12	8,668	6.39	1.1		111.30
13	10,380	75.00	10.9	Upper Marker	113.00

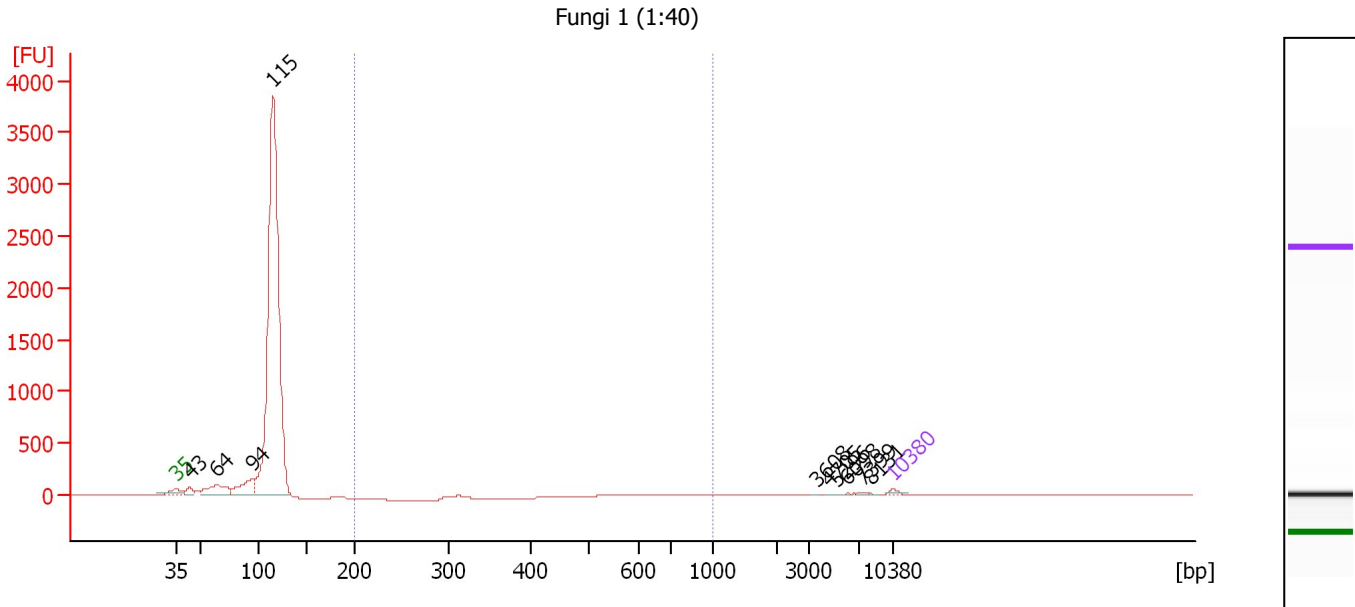
Region table for sample 7 : Bact 2 (1:40)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	502	428.6	2,074.5	662.04	11	20.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

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Electropherogram Summary Continued ...



Overall Results for sample 8 : Fungi 1 (1:40)

Number of peaks found: 10 Corr. Area 1: 0.0
 Noise: 0.3

Peak table for sample 8 : Fungi 1 (1:40)

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	317.38	11,167.8		44.30
3	64	1,135.85	27,070.3		46.94
4	94	1,152.23	18,578.1		50.36
5	115	20,717.30	273,591.0		52.43
6	3,608	5.90	2.5		105.49
7	4,705	10.15	3.3		106.83
8	5,296	11.87	3.4		107.56
9	6,098	13.60	3.4		108.54
10	7,399	25.65	5.3		110.05
11	8,131	15.25	2.8		110.77
12	10,380	75.00	10.9	Upper Marker	113.00

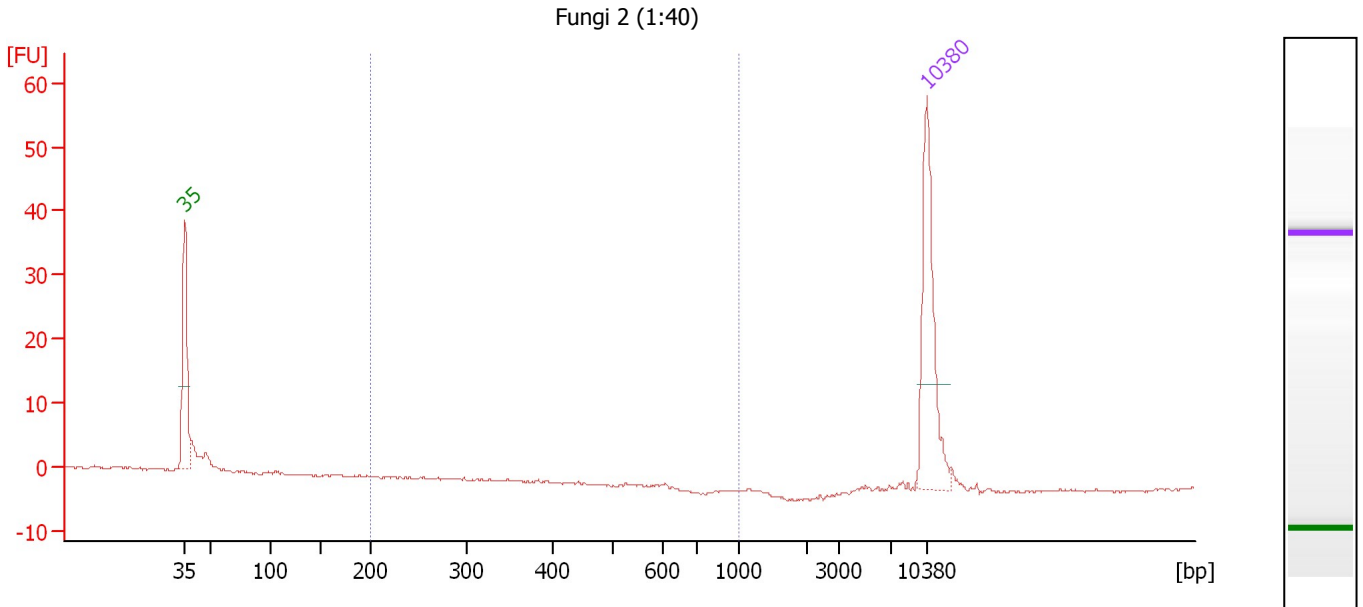
Region table for sample 8 : Fungi 1 (1:40)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	0	0.0	0.0	0.00	0	0.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : Fungi 2 (1:40)

Number of peaks found: 0 Corr. Area 1: 0.0
 Noise: 0.1

Peak table for sample 9 : Fungi 2 (1:40)

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	10,380	75.00	10.9	Upper Marker	113.00

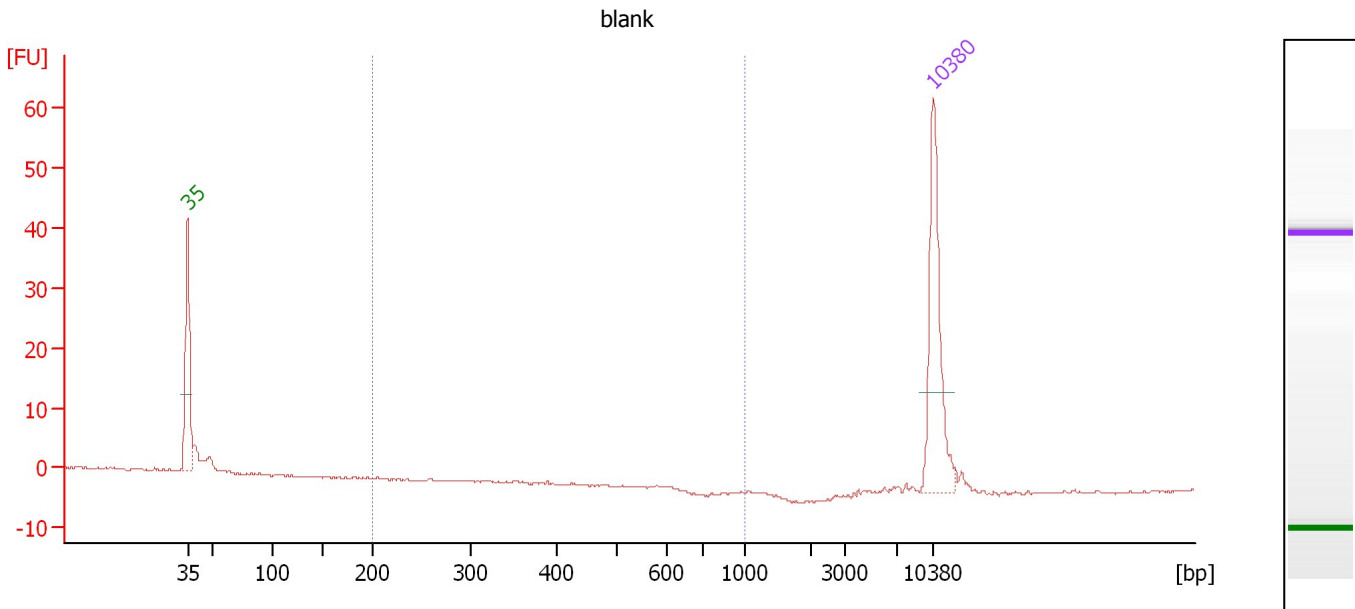
Region table for sample 9 : Fungi 2 (1:40)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	0	0.0	0.0	0.00	0	0.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 10 : blank

Number of peaks found: 0 Corr. Area 1: 0.0
 Noise: 0.2

Peak table for sample 10 : blank

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	10,380	75.00	10.9	Upper Marker	113.00

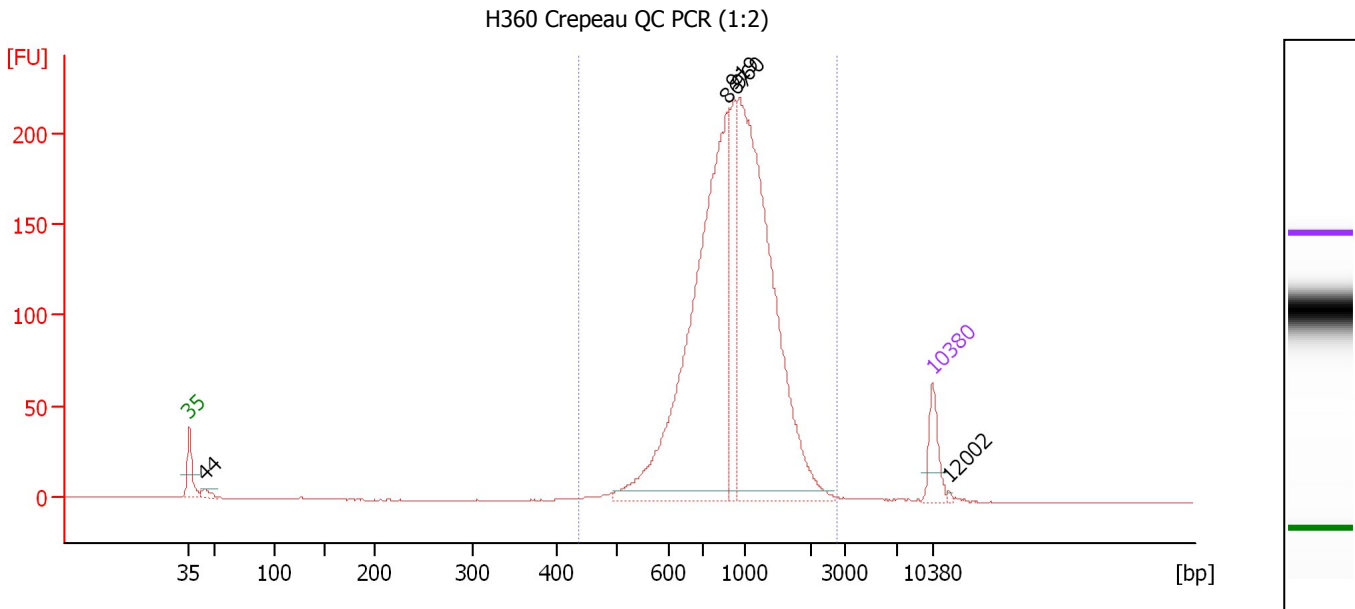
Region table for sample 10 : blank

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	0	0.0	0.0	0.00	0	0.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 PM

Electropherogram Summary Continued ...



Overall Results for sample 11 : H360 Crepeau QC PCR (1:2)

Number of peaks found: 5 Corr. Area 1: 1,945.6
 Noise: 0.2

Peak table for sample 11 : H360 Crepeau QC PCR (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	44	29.36	1,002.4		44.51
3	867	1,399.57	2,445.5		93.57
4	919	271.34	447.3		94.27
5	960	1,379.12	2,177.0		94.82
6	10,380	75.00	10.9	Upper Marker	113.00
7	12,002	0.00	0.0		114.61

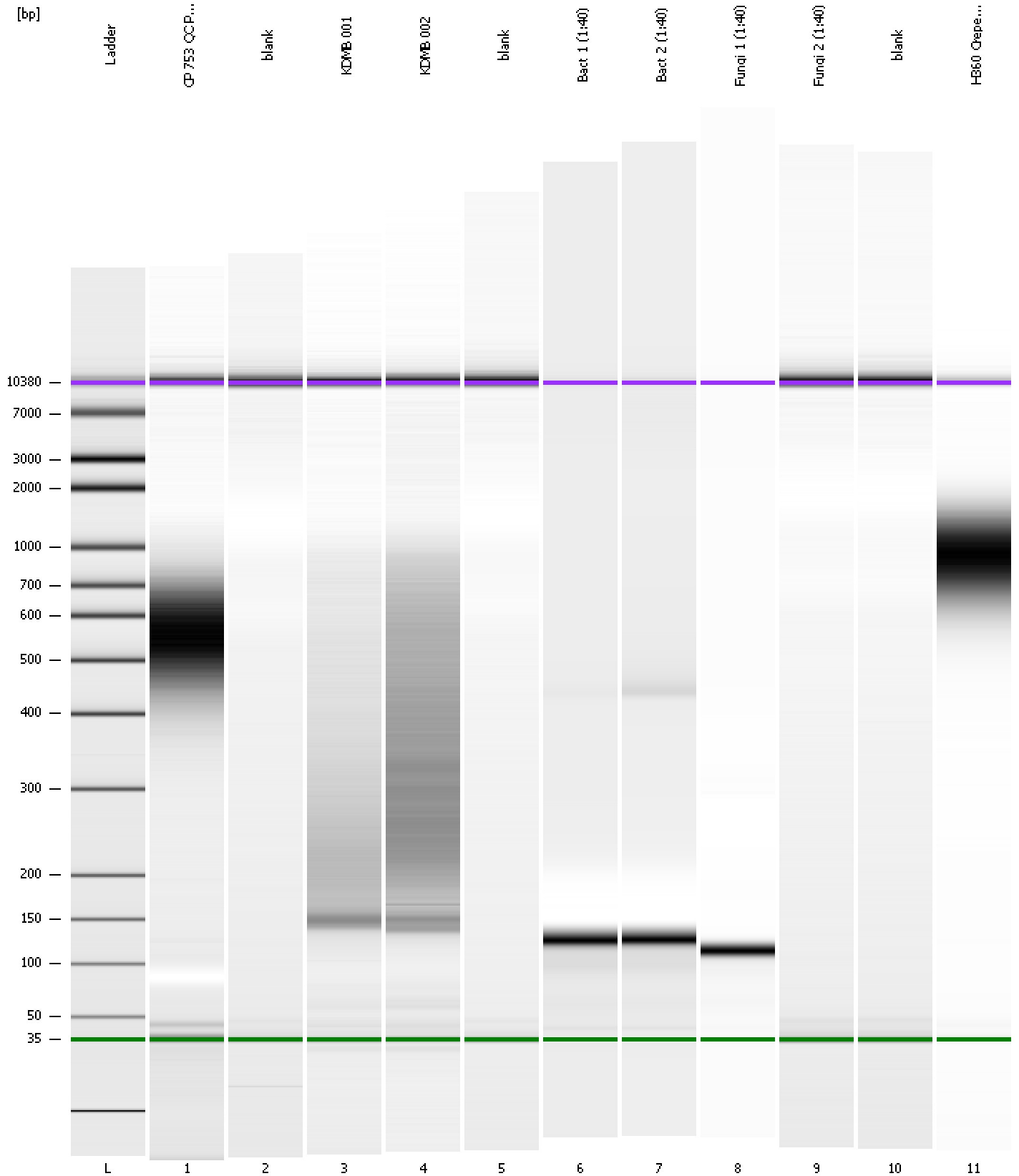
Region table for sample 11 : H360 Crepeau QC PCR (1:2)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
437	2,787	994	1,945.6	5,220.1	3,065.00	99	33.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
Modified: 1/8/2016 12:28:12 PM

Gel Image



Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad

Created: 1/8/2016 11:33:57 AM
 Modified: 1/8/2016 12:28:12 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		1/8/2016 12:14:20 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-01-08\2016-01-08_002.xad)		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/8/2016 11:33:57 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1