

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...2016-11-04\2016-11-04_002_HiSeq693_LibrariesForPippinHT.xad

Created: 11/4/2016 2:20:51 PM
Modified: 11/4/2016 4:46:51 PM

Electrophoresis File Run Summary

Instrument Information:

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

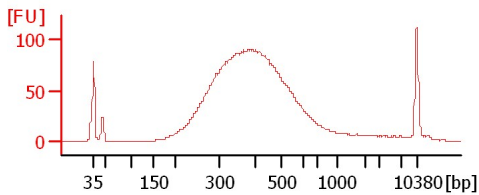
Assay Information:

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

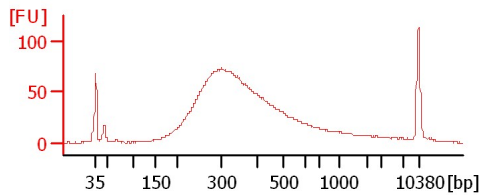
Chip Information:

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

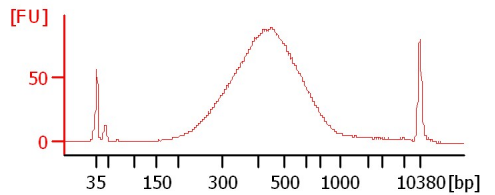
9: Rs library with 4 cyc PCR



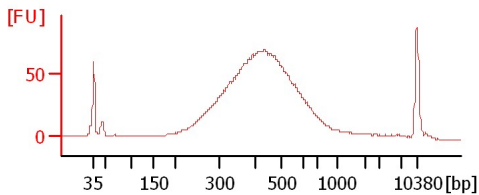
10: Rp library with 4 cyc PCR



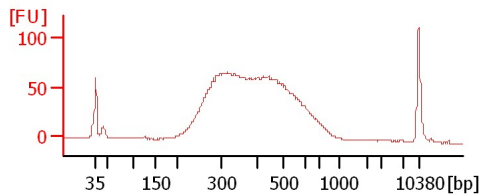
13: W library with 4 cyc PCR



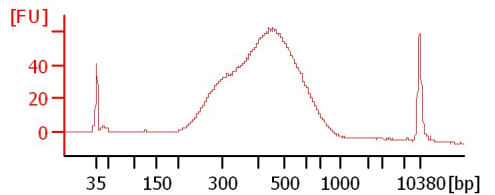
14: H library with 4 cyc PCR



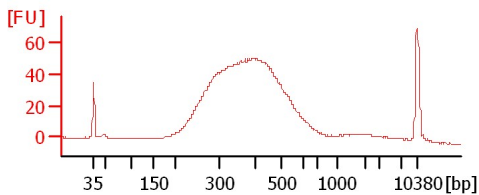
15: C library with 9 cyc PCR



16: O library with 9 cyc PCR



11: 1s library with 9 cyc PCR



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
9: Rs library with 4 cyc PCR		<input type="checkbox"/>	✓			
10: Rp library with 4 cyc PCR		<input type="checkbox"/>	✓			
13: W library with 4 cyc PCR		<input type="checkbox"/>	✓			
14: H library with 4 cyc PCR		<input type="checkbox"/>	✓			
15: C library with 9 cyc PCR		<input type="checkbox"/>	✓			
16: O library with 9 cyc PCR		<input type="checkbox"/>	✓			
11: 1s library with 9 cyc PCR		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

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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

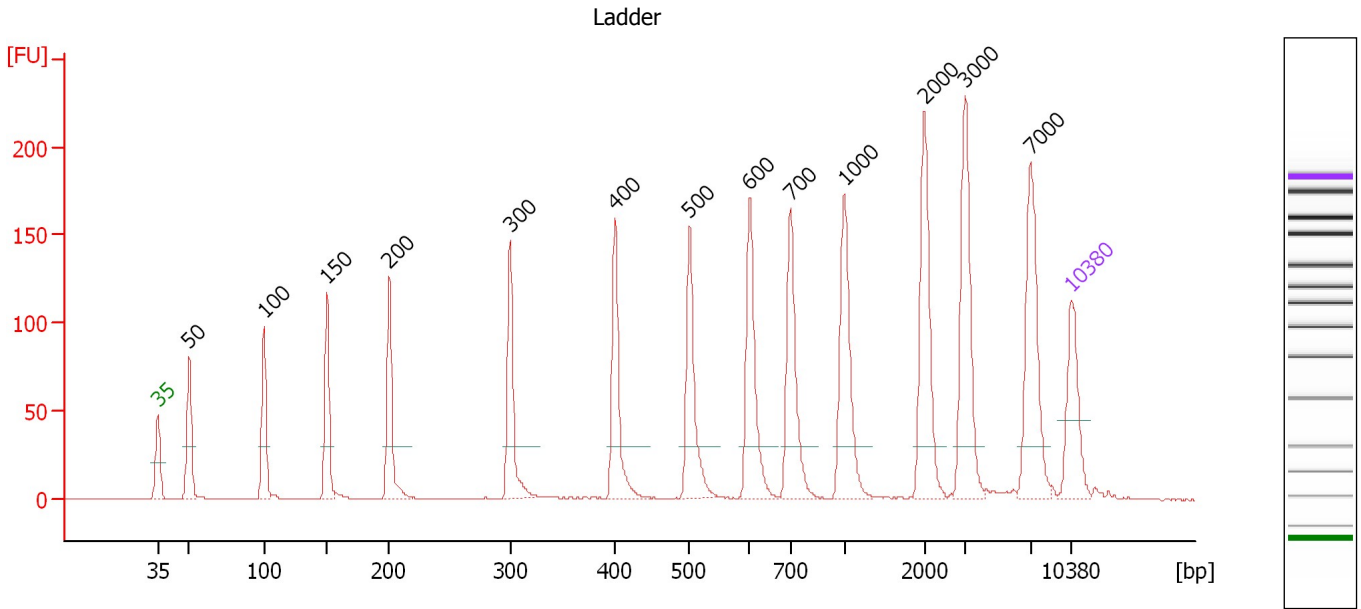
Ladder

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

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 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

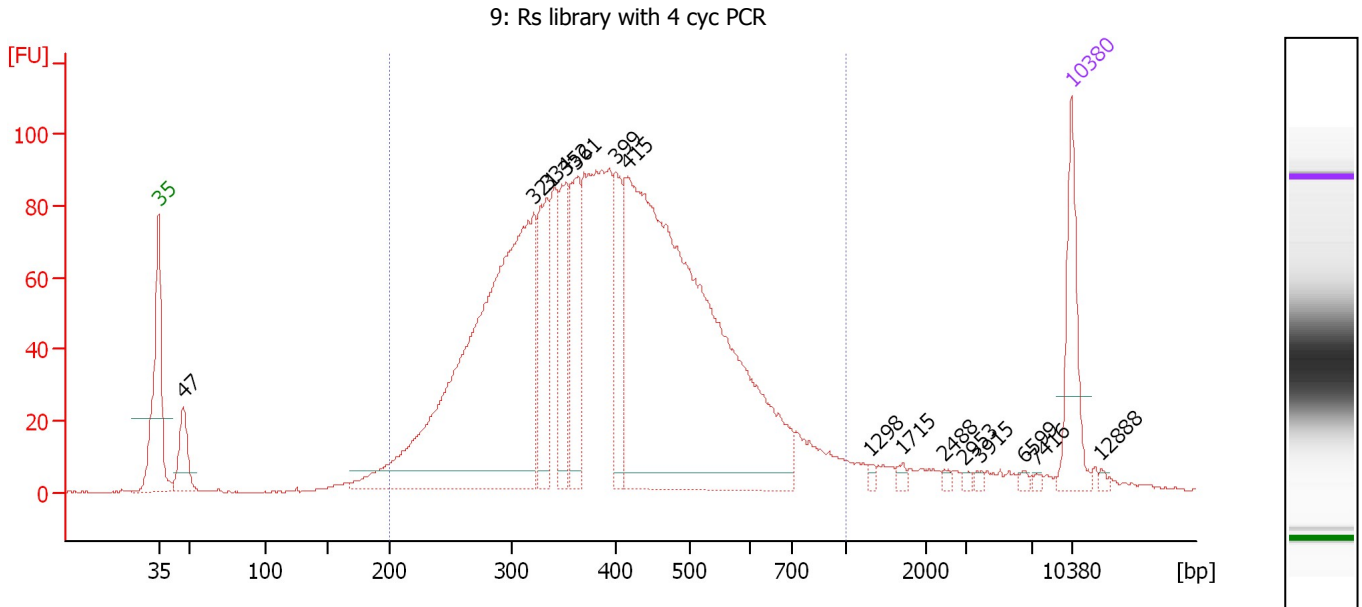
Peak table for Ladder

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	51.14
4	150	150.00	1,515.2	Ladder Peak	56.01
5	200	150.00	1,136.4	Ladder Peak	60.77
6	300	150.00	757.6	Ladder Peak	70.04
7	400	150.00	568.2	Ladder Peak	78.13
8	500	150.00	454.5	Ladder Peak	83.81
9	600	150.00	378.8	Ladder Peak	88.42
10	700	150.00	324.7	Ladder Peak	91.54
11	1,000	150.00	227.3	Ladder Peak	95.69
12	2,000	150.00	113.6	Ladder Peak	101.79
13	3,000	150.00	75.8	Ladder Peak	104.91
14	7,000	150.00	32.5	Ladder Peak	109.93
15	10,380	75.00	10.9	Upper Marker	113.00

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 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : 9: Rs library with 4 cyc PCR

Number of peaks found: 15 Corr. Area 1: 2,344.7
 Noise: 0.2

Peak table for sample 1 : 9: Rs library with 4 cyc 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	47	69.40	2,239.8		44.92
3	321	821.94	3,876.6		71.76
4	334	135.77	615.8		72.79
5	352	94.95	408.7		74.24
6	361	109.55	459.9		74.97
7	399	101.79	386.8		78.03
8	415	996.56	3,641.8		78.96
9	1,298	4.97	5.8		97.51
10	1,715	4.92	4.3		100.05
11	2,488	3.65	2.2		103.31
12	2,953	3.69	1.9		104.76
13	3,915	3.14	1.2		106.06
14	6,599	3.68	0.8		109.42
15	7,416	2.96	0.6		110.31
16	10,380	75.00	10.9	Upper Marker	113.00
17	12,888	0.00	0.0		115.28

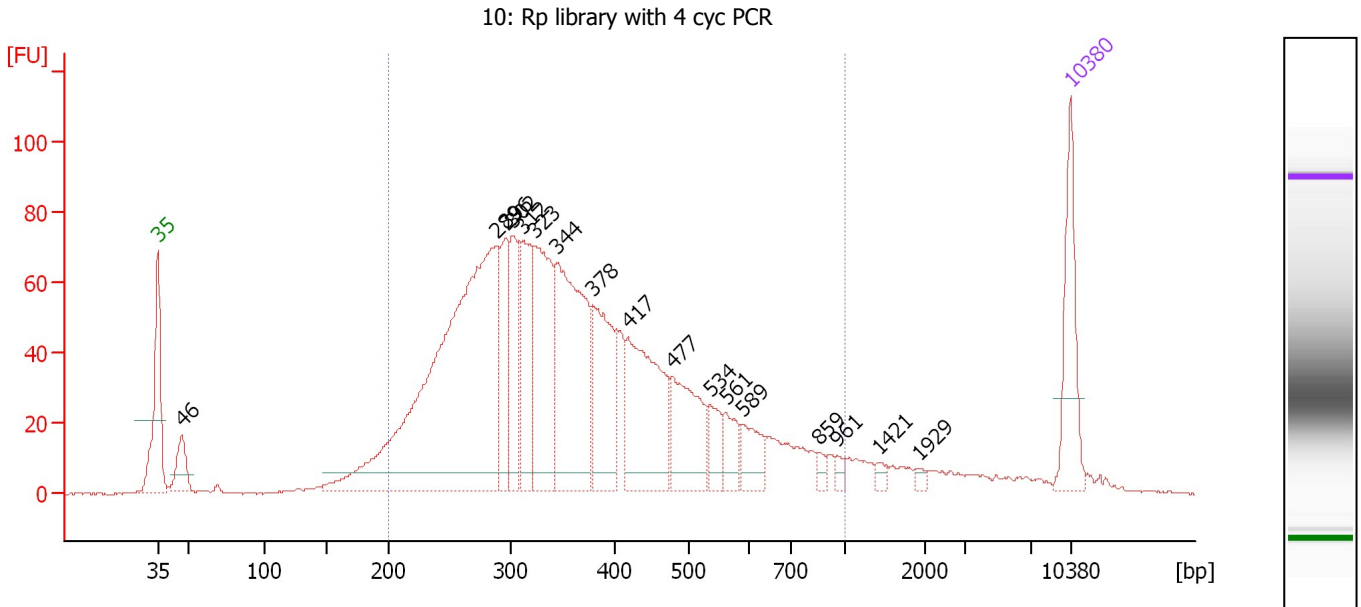
Region table for sample 1 : 9: Rs library with 4 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	412	2,344.7	11,975.7	2,884.66	90	31.4

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Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : 10: Rp library with 4 cyc PCR

Number of peaks found: 17 Corr. Area 1: 1,840.1
 Noise: 0.2

Peak table for sample 2 : 10: Rp library with 4 cyc 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	46	49.20	1,605.0		44.84
3	289	767.75	4,023.7		69.03
4	296	99.28	507.4		69.71
5	302	99.27	498.4		70.18
6	312	115.47	561.6		70.97
7	323	196.32	922.2		71.86
8	344	278.73	1,227.9		73.59
9	378	146.63	587.3		76.37
10	417	187.02	679.3		79.10
11	477	112.99	358.8		82.51
12	534	34.17	96.9		85.40
13	561	34.72	93.8		86.61
14	589	38.85	99.9		87.92
15	859	8.74	15.4		93.74
16	961	7.48	11.8		95.16
17	1,421	6.50	6.9		98.25
18	1,929	5.14	4.0		101.35
19	10,380	75.00	10.9	Upper Marker	113.00

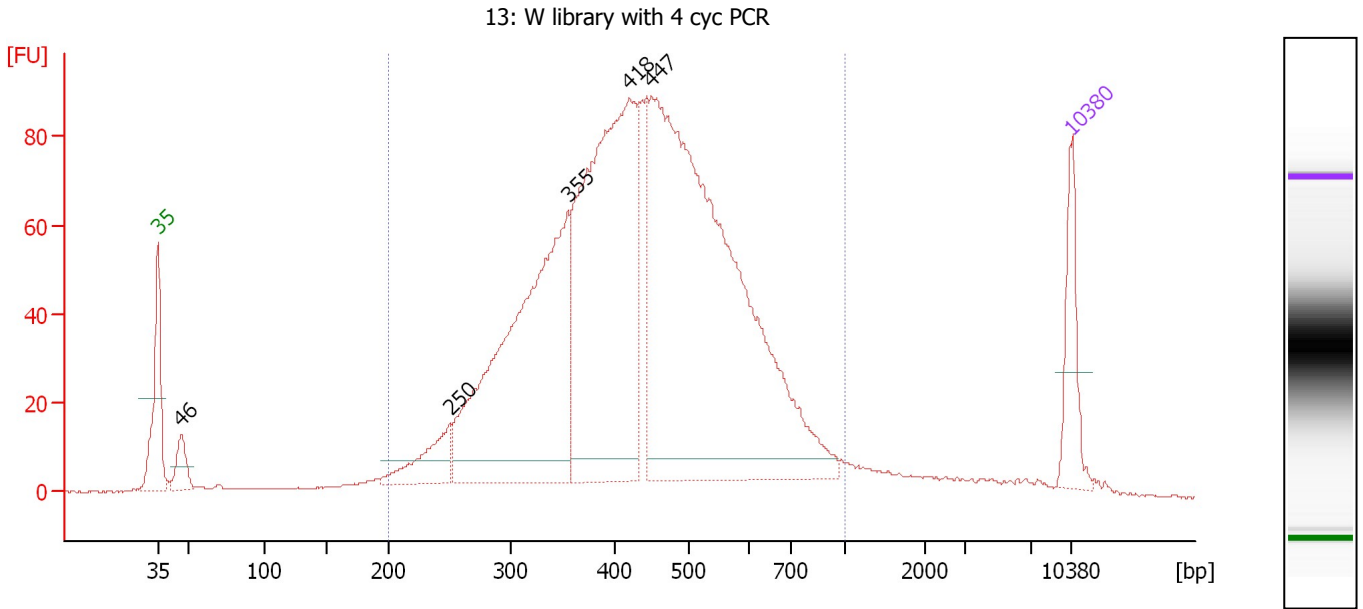
Region table for sample 2 : 10: Rp library with 4 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	382	1,840.1	10,724.5	2,347.19	87	36.8

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Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : 13: W library with 4 cyc PCR

Number of peaks found: 5 Corr. Area 1: 1,969.4
 Noise: 0.2

Peak table for sample 3 : 13: W library with 4 cyc 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	46	55.14	1,804.9		44.81
3	250	94.49	572.1		65.43
4	355	711.55	3,037.3		74.48
5	418	775.07	2,807.0		79.17
6	447	1,262.05	4,273.8		80.82
7	10,380	75.00	10.9	Upper Marker	113.00

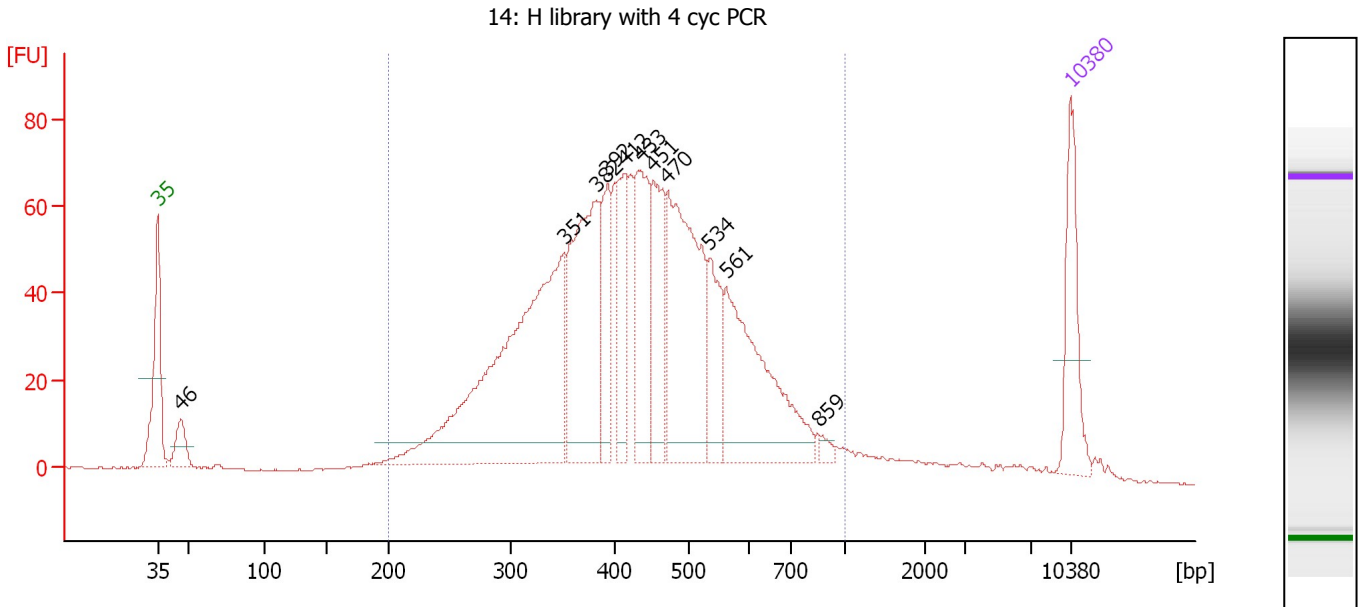
Region table for sample 3 : 13: W library with 4 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	445	1,969.4	12,045.9	3,171.17	94	28.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...2016-11-04\2016-11-04_002_HiSeq693_LibrariesForPippinHT.xad

Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : 14: H library with 4 cyc PCR

Number of peaks found: 11 Corr. Area 1: 1,592.1
 Noise: 0.2

Peak table for sample 4 : 14: H library with 4 cyc 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	46	44.87	1,473.9		44.79
3	351	531.99	2,296.8		74.16
4	382	259.52	1,028.3		76.70
5	392	89.47	345.5		77.51
6	412	85.97	316.1		78.81
7	433	145.57	509.4		80.00
8	451	109.50	367.8		81.03
9	470	283.61	914.1		82.11
10	534	82.77	235.1		85.36
11	561	227.36	614.6		86.60
12	859	8.55	15.1		93.74
13	10,380	75.00	10.9	Upper Marker	113.00

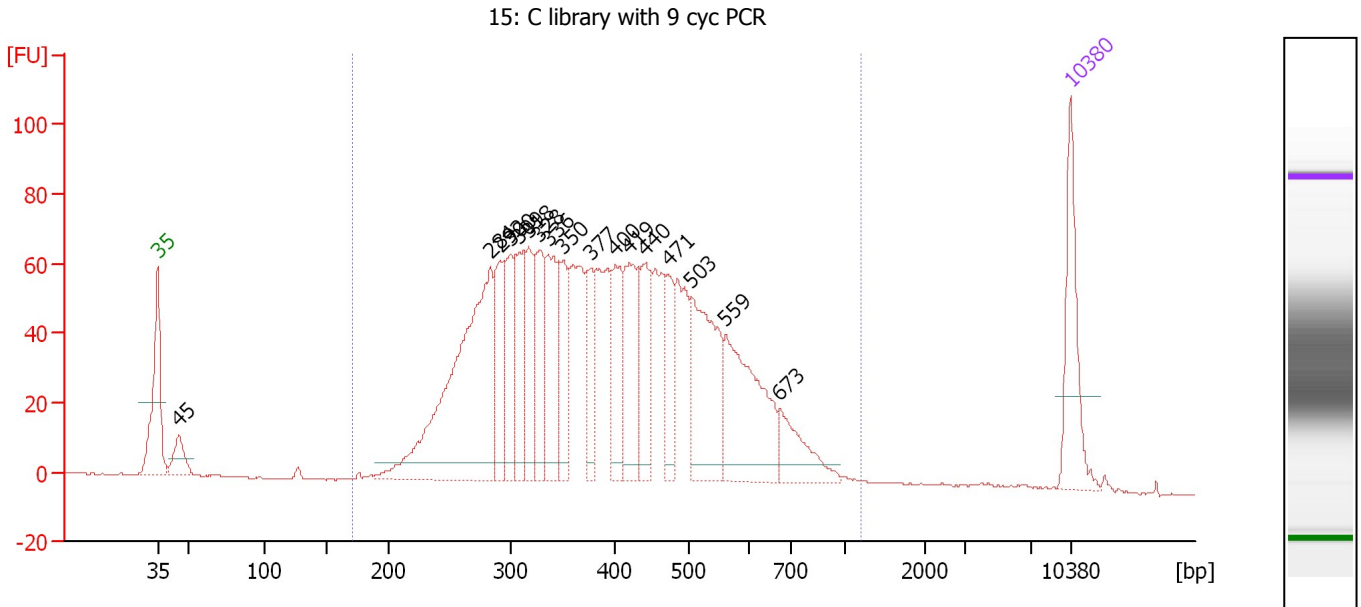
Region table for sample 4 : 14: H library with 4 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	442	1,592.1	8,654.0	2,253.84	90	29.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...2016-11-04\2016-11-04_002_HiSeq693_LibrariesForPippinHT.xad

Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : 15: C library with 9 cyc PCR

Number of peaks found: 17 Corr. Area 1: 1,883.4
 Noise: 0.2

Peak table for sample 5 : 15: C library with 9 cyc 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	41.61	1,393.6		44.64
3	284	416.85	2,226.4		68.52
4	292	83.02	430.9		69.29
5	300	90.33	455.8		70.06
6	309	83.73	410.5		70.77
7	318	82.74	394.4		71.48
8	328	92.43	427.0		72.30
9	336	112.49	507.1		72.96
10	350	72.88	315.8		74.06
11	377	66.54	267.6		76.25
12	400	83.66	317.1		78.11
13	419	107.66	389.3		79.21
14	440	81.55	280.7		80.41
15	471	58.18	187.2		82.16
16	503	161.34	485.6		83.97
17	559	165.95	449.6		86.54
18	673	58.67	132.1		90.71
19	10,380	75.00	10.9	Upper Marker	113.00

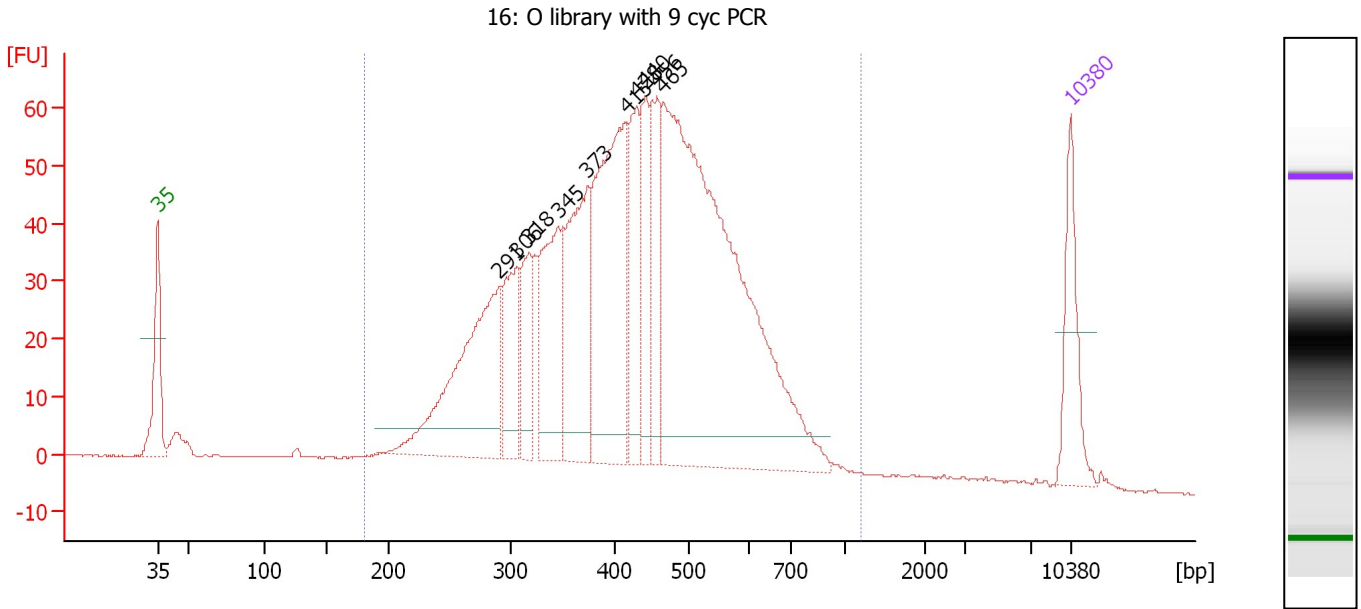
Region table for sample 5 : 15: C library with 9 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
170	1,206	412	1,883.4	9,655.7	2,314.80	97	31.7

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Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 6 : 16: O library with 9 cyc PCR

Number of peaks found: 10 Corr. Area 1: 1,434.2
 Noise: 0.2

Peak table for sample 6 : 16: O library with 9 cyc 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	291	333.14	1,733.8		69.22
3	306	120.76	597.4		70.55
4	318	90.55	431.5		71.49
5	345	180.70	792.8		73.70
6	373	230.80	936.5		75.98
7	415	340.25	1,242.8		78.97
8	428	121.34	429.1		79.75
9	440	108.63	373.9		80.41
10	456	115.47	383.9		81.30
11	465	907.22	2,959.0		81.80
12	10,380	75.00	10.9	Upper Marker	113.00

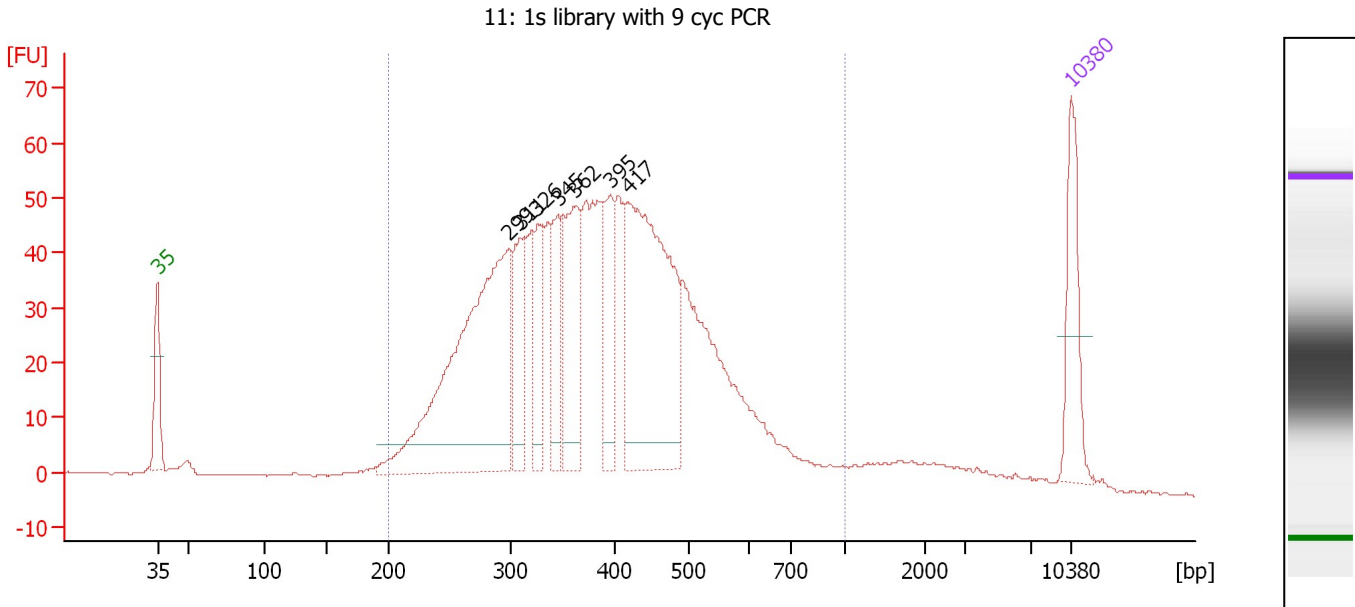
Region table for sample 6 : 16: O library with 9 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
180	1,211	433	1,434.2	10,664.2	2,724.60	97	28.1

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Created: 11/4/2016 2:20:51 PM
 Modified: 11/4/2016 4:46:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : 11: 1s library with 9 cyc PCR

Number of peaks found: 7 Corr. Area 1: 1,261.3
 Noise: 0.2

Peak table for sample 7 : 11: 1s library with 9 cyc 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	299	532.48	2,700.0		69.93
3	311	98.44	480.4		70.89
4	326	82.16	382.0		72.13
5	345	81.13	355.9		73.71
6	362	148.47	621.2		75.06
7	395	90.43	346.9		77.72
8	417	394.44	1,434.5		79.07
9	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : 11: 1s library with 9 cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	396	1,261.3	9,838.0	2,316.78	94	28.9

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Created: 11/4/2016 2:20:51 PM
Modified: 11/4/2016 4:46:51 PM

Gel Image

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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		11/4/2016 3:01:13 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\2016-11-04\2016-11-04_002.xad)		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		11/4/2016 2:20:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1