

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...analyzer\2015-10-26\2015-10-26_001_HiSeq177_cDNAQC_Test.xad

Created: 10/26/2015 2:52:59 PM
Modified: 10/26/2015 3:42:05 PM

Electrophoresis File Run Summary

Instrument Information:

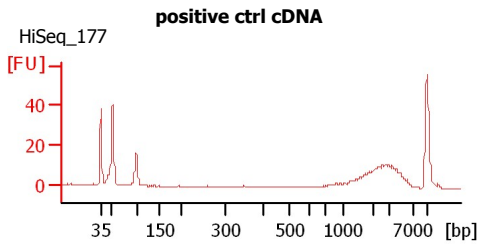
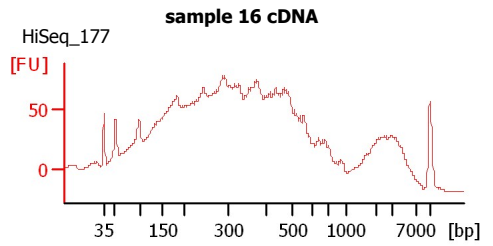
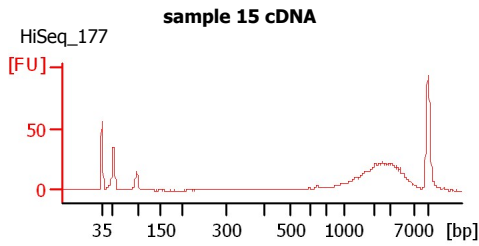
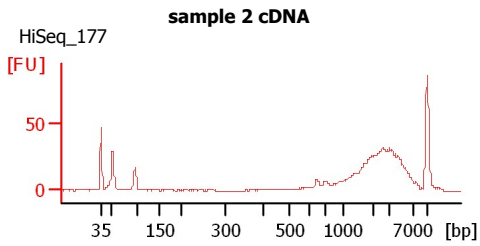
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
sample 2 cDNA	HiSeq_177	<input type="checkbox"/>				
sample 15 cDNA	HiSeq_177	<input type="checkbox"/>				
sample 16 cDNA	HiSeq_177	<input type="checkbox"/>				
positive ctrl cDNA	HiSeq_177	<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

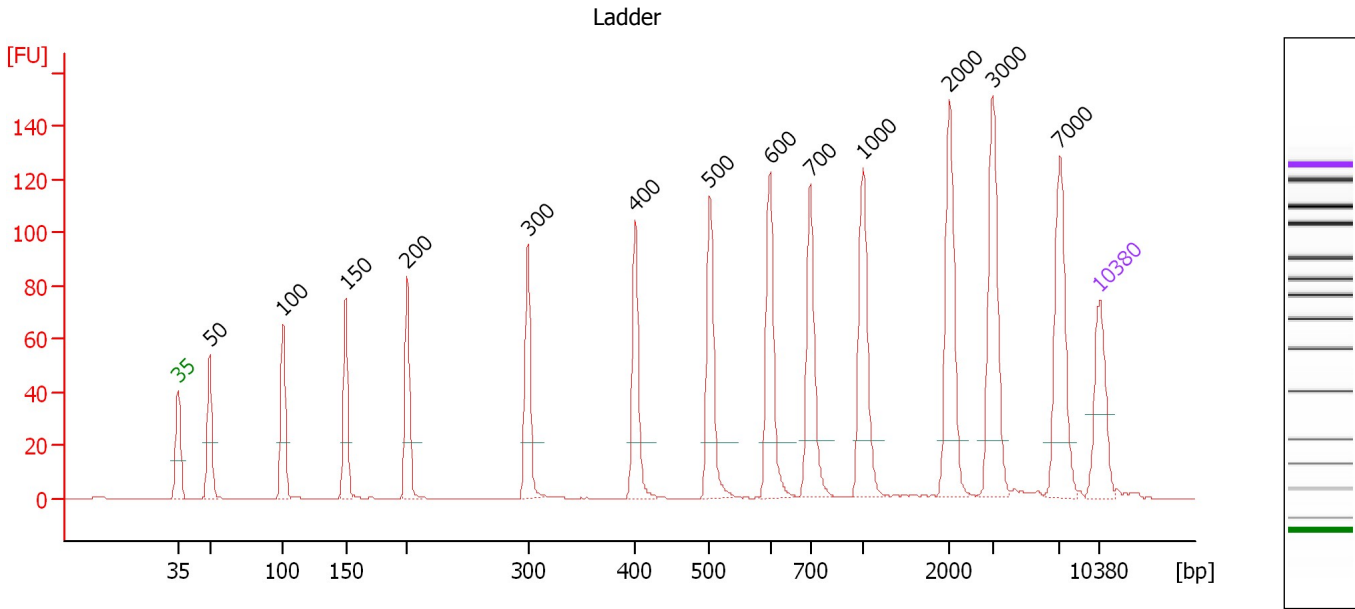
Ladder

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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Electropherogram Summary



Overall Results for Ladder

Noise: 0.1

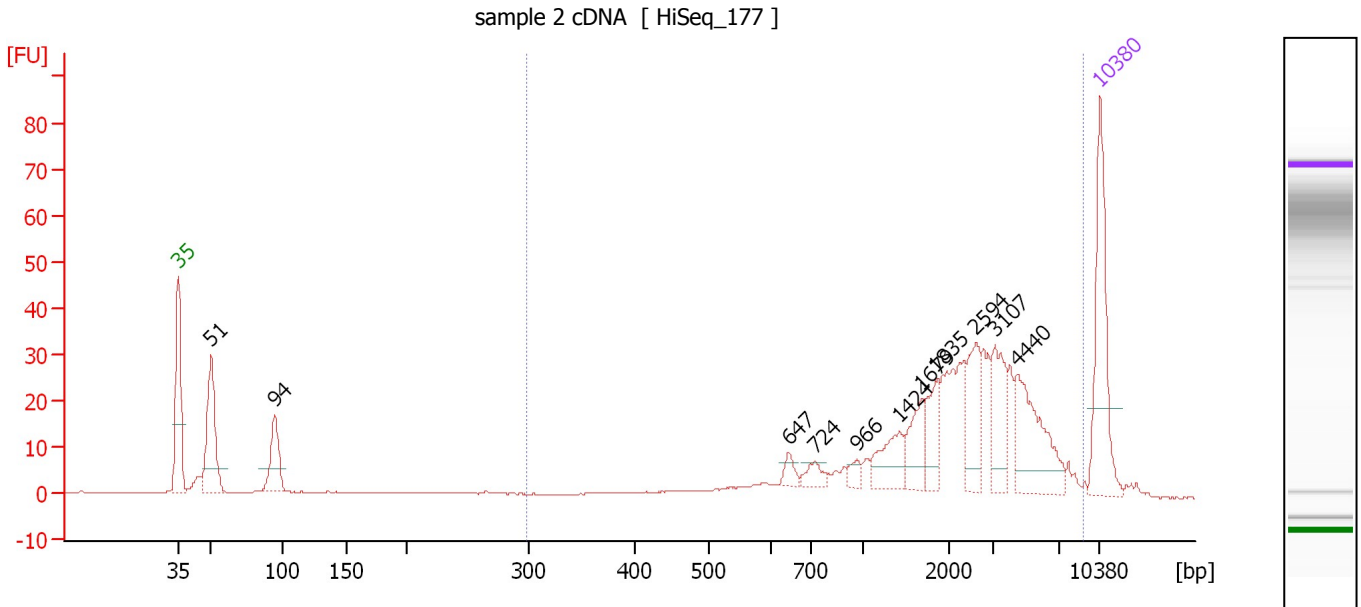
Peak table for Ladder

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	50	150.00	4,545.5	Ladder Peak	45.42
3	100	150.00	2,272.7	Ladder Peak	50.96
4	150	150.00	1,515.2	Ladder Peak	55.74
5	200	150.00	1,136.4	Ladder Peak	60.42
6	300	150.00	757.6	Ladder Peak	69.56
7	400	150.00	568.2	Ladder Peak	77.73
8	500	150.00	454.5	Ladder Peak	83.38
9	600	150.00	378.8	Ladder Peak	87.95
10	700	150.00	324.7	Ladder Peak	91.01
11	1,000	150.00	227.3	Ladder Peak	94.99
12	2,000	150.00	113.6	Ladder Peak	101.60
13	3,000	150.00	75.8	Ladder Peak	104.88
14	7,000	150.00	32.5	Ladder Peak	109.94
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : sample 2 cDNA

Number of peaks found: 11 Corr. Area 1: 372.6
 Noise: 0.1

Peak table for sample 1 : sample 2 cDNA

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	51	99.98	2,987.2		45.50
3	94	52.62	845.0		50.33
4	647	9.51	22.3		89.38
5	724	11.97	25.0		91.33
6	966	8.25	12.9		94.54
7	1,424	30.64	32.6		97.79
8	1,679	28.89	26.1		99.48
9	1,835	24.27	20.0		100.51
10	2,594	41.34	24.1		103.55
11	3,107	38.10	18.6		105.02
12	4,440	65.28	22.3		106.70
13	10,380	75.00	10.9	Upper Marker	113.00

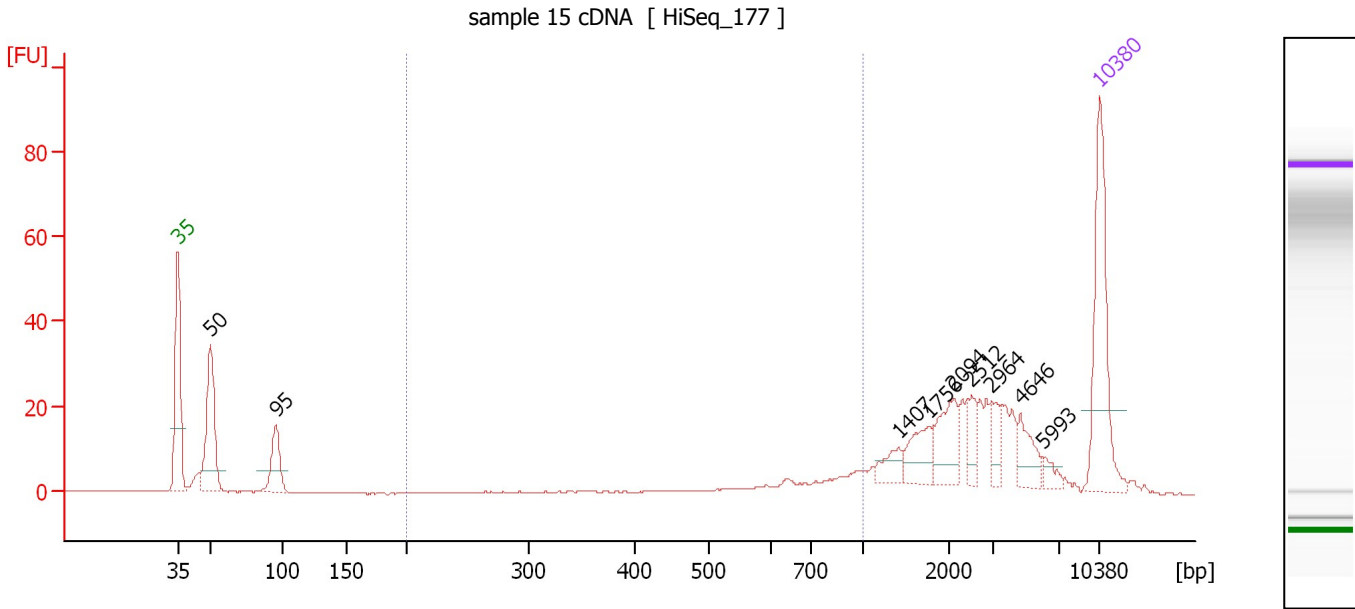
Region table for sample 1 : sample 2 cDNA

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
299	9,010	2,711	372.6	456.6	459.88	80	64.3

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Electropherogram Summary Continued ...



Overall Results for sample 2 : sample 15 cDNA

Number of peaks found: 9 Corr. Area 1: 49.1
 Noise: 0.1

Peak table for sample 2 : sample 15 cDNA

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	93.55	2,808.7		45.47
3	95	40.94	652.4		50.41
4	1,407	13.32	14.3		97.68
5	1,756	24.18	20.9		99.99
6	2,094	30.21	21.9		101.91
7	2,512	14.03	8.5		103.28
8	2,964	14.16	7.2		104.76
9	4,646	19.89	6.5		106.96
10	5,993	7.23	1.8		108.66
11	10,380	75.00	10.9	Upper Marker	113.00

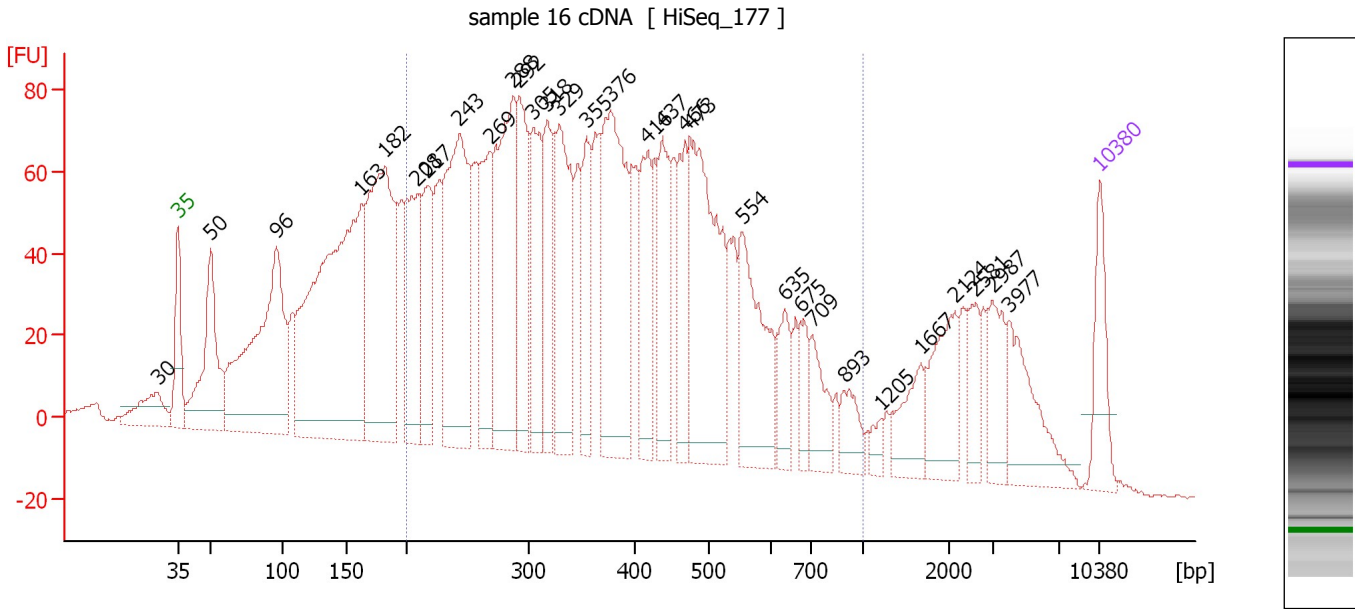
Region table for sample 2 : sample 15 cDNA

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	651	49.1	167.1	59.65	13	31.6

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Electropherogram Summary Continued ...



Overall Results for sample 3 : sample 16 cDNA

Number of peaks found: 31 Corr. Area 1: 2,614.2
 Noise: 0.2

Peak table for sample 3 : sample 16 cDNA

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	30	0.00	0.0		41.45
2	35	125.00	5,411.3	Lower Marker	43.00
3	50	269.42	8,130.2		45.44
4	96	564.01	8,918.3		50.49
5	163	881.16	8,204.0		56.93
6	182	536.53	4,473.3		58.71
7	208	249.54	1,817.6		61.15
8	217	176.41	1,234.4		61.93
9	243	444.16	2,766.6		64.37
10	269	198.43	1,116.2		66.76
11	288	386.48	2,031.9		68.48
12	292	195.06	1,010.6		68.87
13	305	189.28	939.9		69.98
14	318	153.88	733.1		71.03
15	329	262.16	1,207.7		71.92
16	355	133.17	568.8		74.03
17	376	397.92	1,601.5		75.81
18	416	158.13	575.9		78.64
19	437	152.79	530.1		79.80
20	466	141.24	459.0		81.47
21	473	383.51	1,228.2		81.86
22	554	212.69	581.4		85.85
23	635	69.47	165.8		89.02
24	675	45.79	102.8		90.24
25	709	71.39	152.6		91.13

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Electropherogram Summary Continued ...

... Peak table for sample 3 : sample 16 cDNA

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	893	48.62	82.5		93.57
27	1,205	16.87	21.2		96.35
28	1,667	67.79	61.6		99.40
29	2,124	103.77	74.0		102.01
30	2,581	49.56	29.1		103.51
31	2,987	70.17	35.6		104.84
32	3,977	117.70	44.8		106.12
33	10,380	75.00	10.9	Upper Marker	113.00

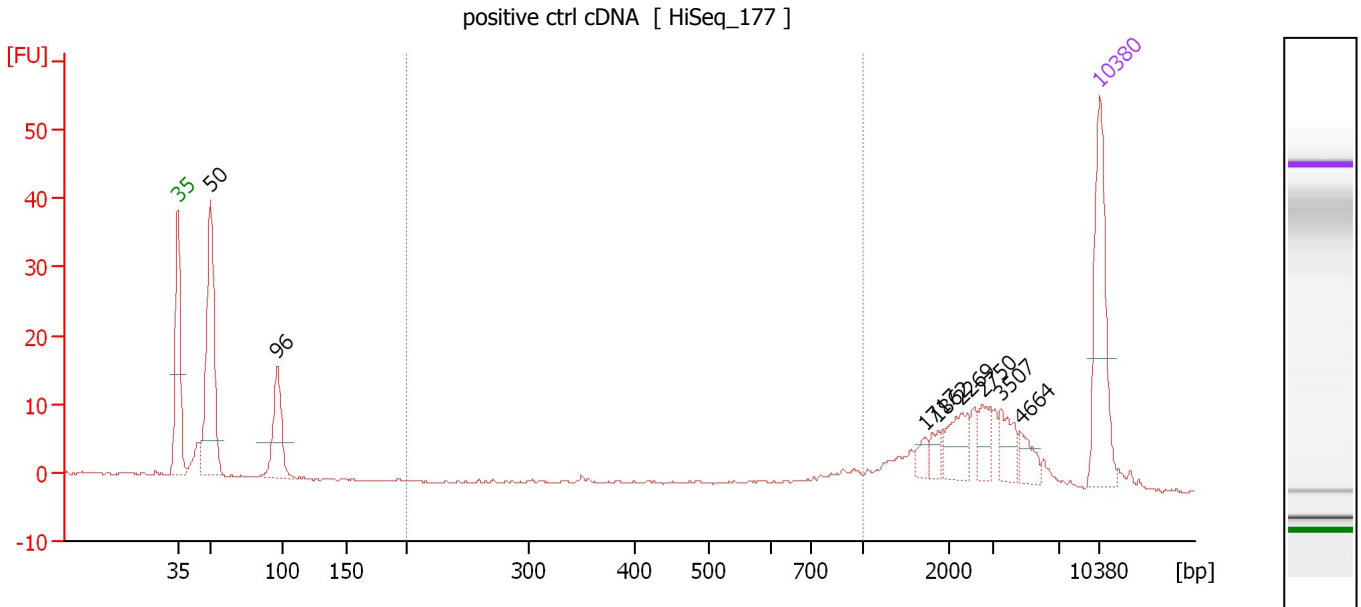
Region table for sample 3 : sample 16 cDNA

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	391	2,614.2	21,514.2	4,712.53	64	36.6

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Electropherogram Summary Continued ...



Overall Results for sample 4 : positive ctrl cDNA

Number of peaks found: 8 Corr. Area 1: 17.3
 Noise: 0.2

Peak table for sample 4 : positive ctrl cDNA

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	175.77	5,274.4		45.47
3	96	72.08	1,135.5		50.53
4	1,717	8.37	7.4		99.73
5	1,862	9.75	7.9		100.69
6	2,269	25.84	17.2		102.49
7	2,750	15.39	8.5		104.06
8	3,507	19.55	8.4		105.52
9	4,664	13.07	4.2		106.98
10	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : positive ctrl cDNA

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	688	17.3	90.6	35.38	8	29.2

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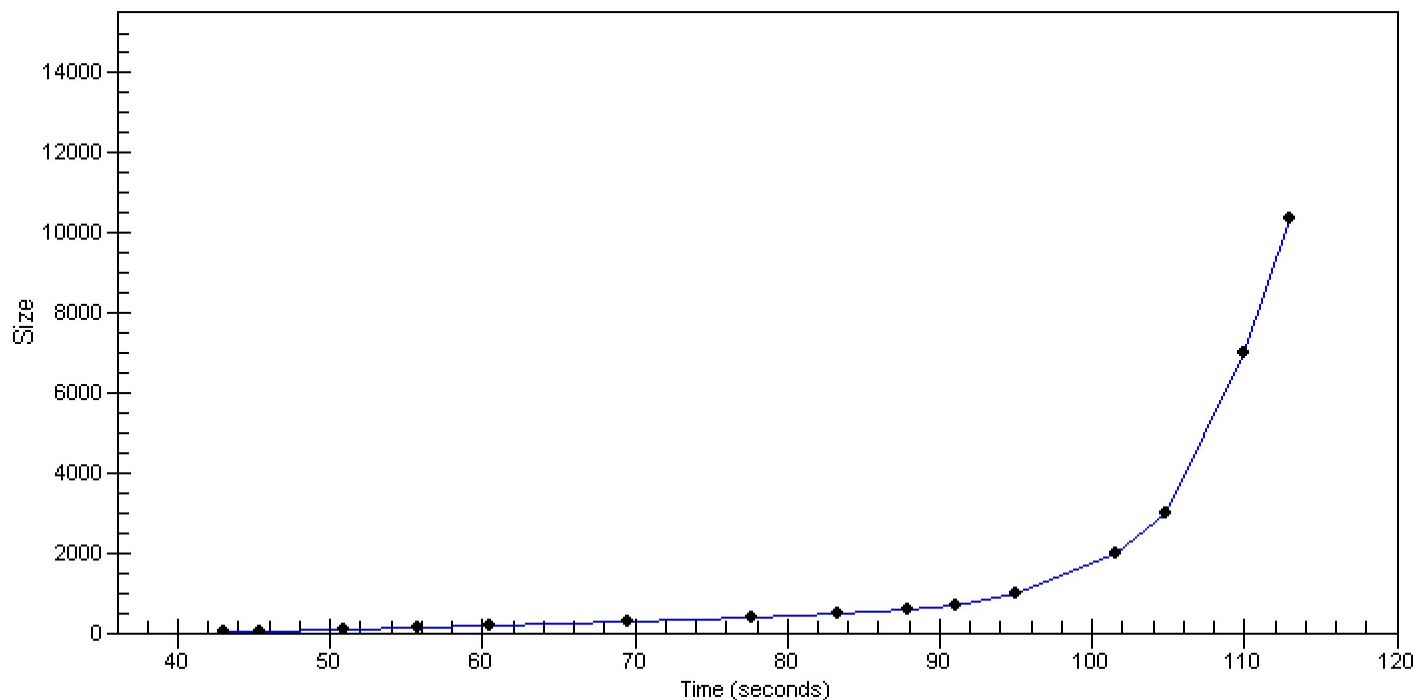
Gel Image

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Curves

Standard Curve



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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		10/26/2015 3:34:15 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-10-26\2015-10-26_001.xad)		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/26/2015 2:53:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1