

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...10-28\2015-10-28_001_HiSeq177_cDNA_3of3_ctrlRNASoni5min.xad

Created: 10/28/2015 11:09:36 AM
Modified: 10/28/2015 11:54:07 AM

Electrophoresis File Run Summary

Instrument Information:

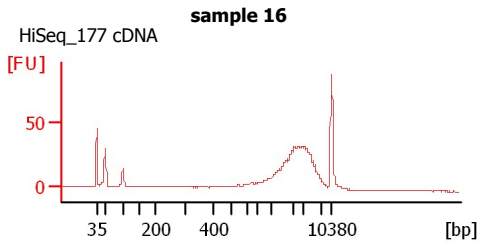
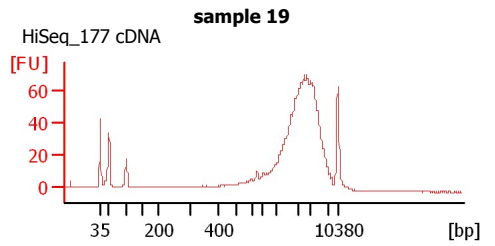
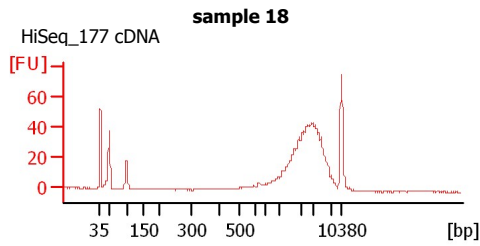
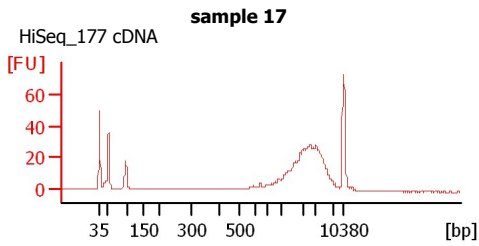
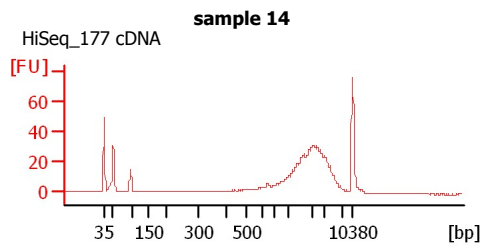
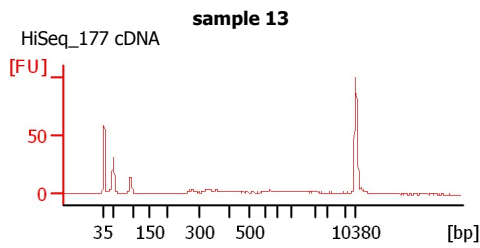
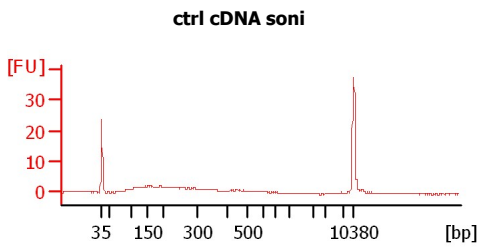
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
ctrl cDNA soni		<input type="checkbox"/>				
sample 13	HiSeq_177 cDNA	<input type="checkbox"/>		✓		
sample 14	HiSeq_177 cDNA	<input type="checkbox"/>		✓		
sample 17	HiSeq_177 cDNA	<input type="checkbox"/>		✓		
sample 18	HiSeq_177 cDNA	<input type="checkbox"/>		✓		
sample 19	HiSeq_177 cDNA	<input type="checkbox"/>		✓		
sample 16	HiSeq_177 cDNA	<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

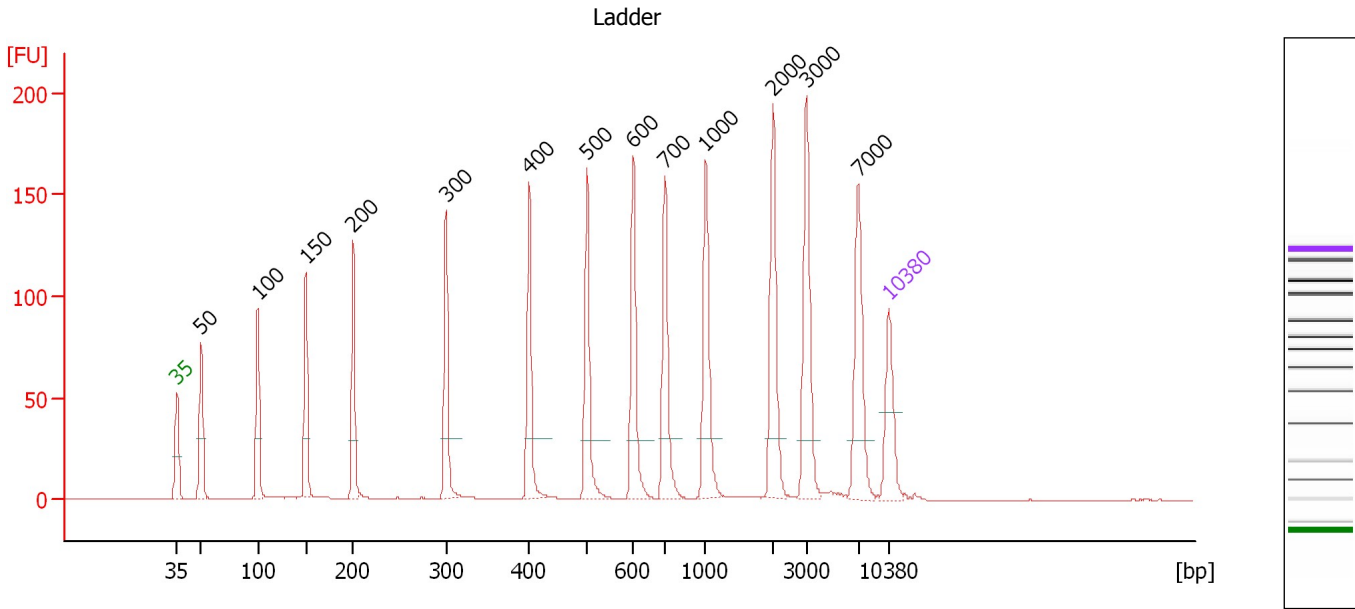
Ladder

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

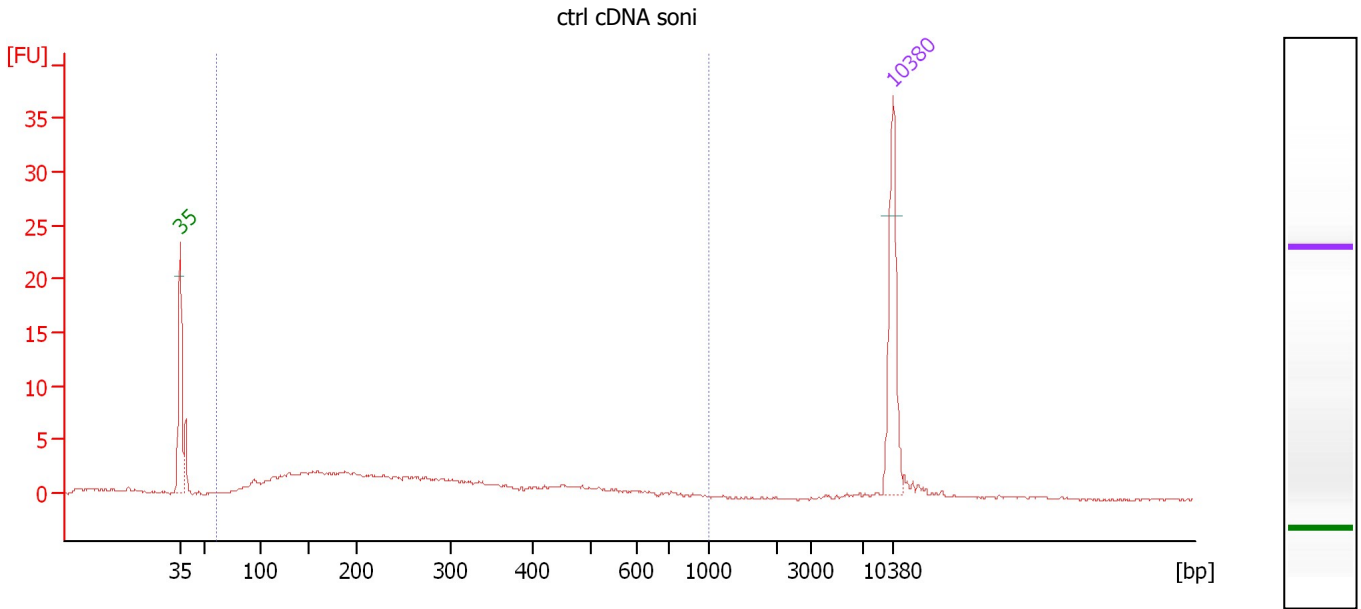
Peak table for Ladder

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	45.41
3	100	150.00	2,272.7	Ladder Peak	50.97
4	150	150.00	1,515.2	Ladder Peak	55.69
5	200	150.00	1,136.4	Ladder Peak	60.36
6	300	150.00	757.6	Ladder Peak	69.48
7	400	150.00	568.2	Ladder Peak	77.66
8	500	150.00	454.5	Ladder Peak	83.32
9	600	150.00	378.8	Ladder Peak	87.88
10	700	150.00	324.7	Ladder Peak	90.98
11	1,000	150.00	227.3	Ladder Peak	95.01
12	2,000	150.00	113.6	Ladder Peak	101.62
13	3,000	150.00	75.8	Ladder Peak	104.87
14	7,000	150.00	32.5	Ladder Peak	110.01
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 1 : ctrl cDNA soni

Number of peaks found: 0 Corr. Area 1: 68.1
 Noise: 0.1

Peak table for sample 1 : ctrl cDNA soni

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

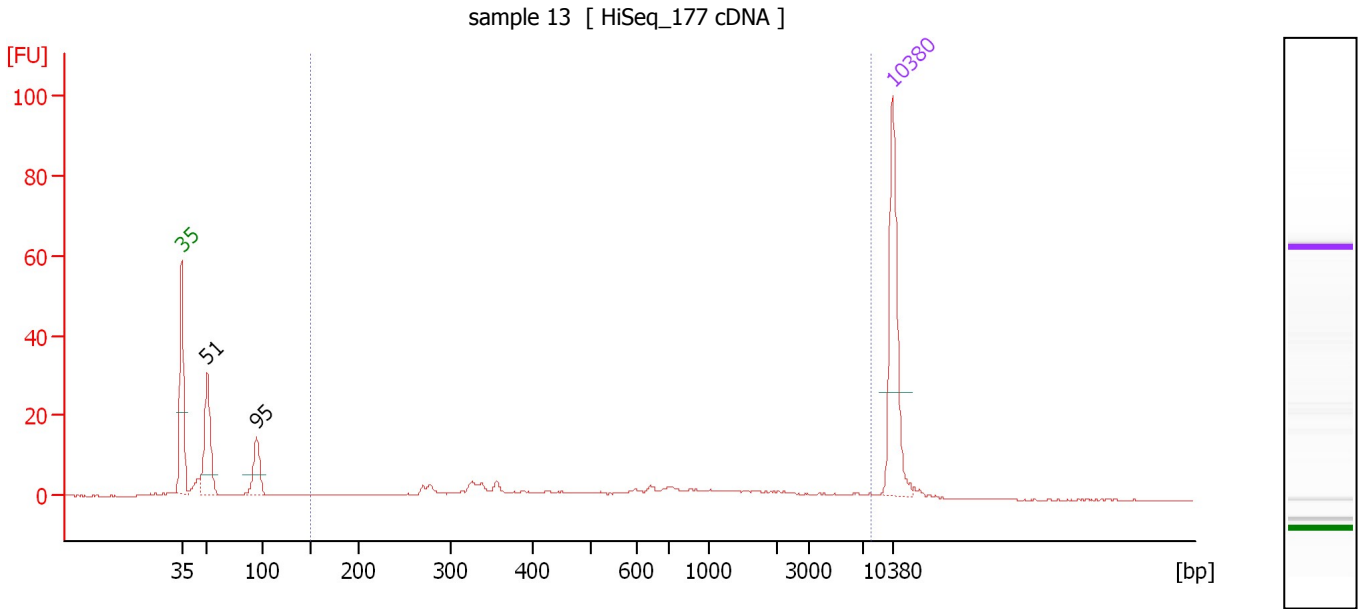
Region table for sample 1 : ctrl cDNA soni

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
61	1,000	266	68.1	2,617.2	327.22	87	50.8

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Electropherogram Summary Continued ...



Overall Results for sample 2 : sample 13

Number of peaks found: 2 Corr. Area 1: 100.0
 Noise: 0.1

Peak table for sample 2 : sample 13

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	85.37	2,537.4		45.52
3	95	39.42	629.4		50.40
4	10,380	75.00	10.9	Upper Marker	113.00

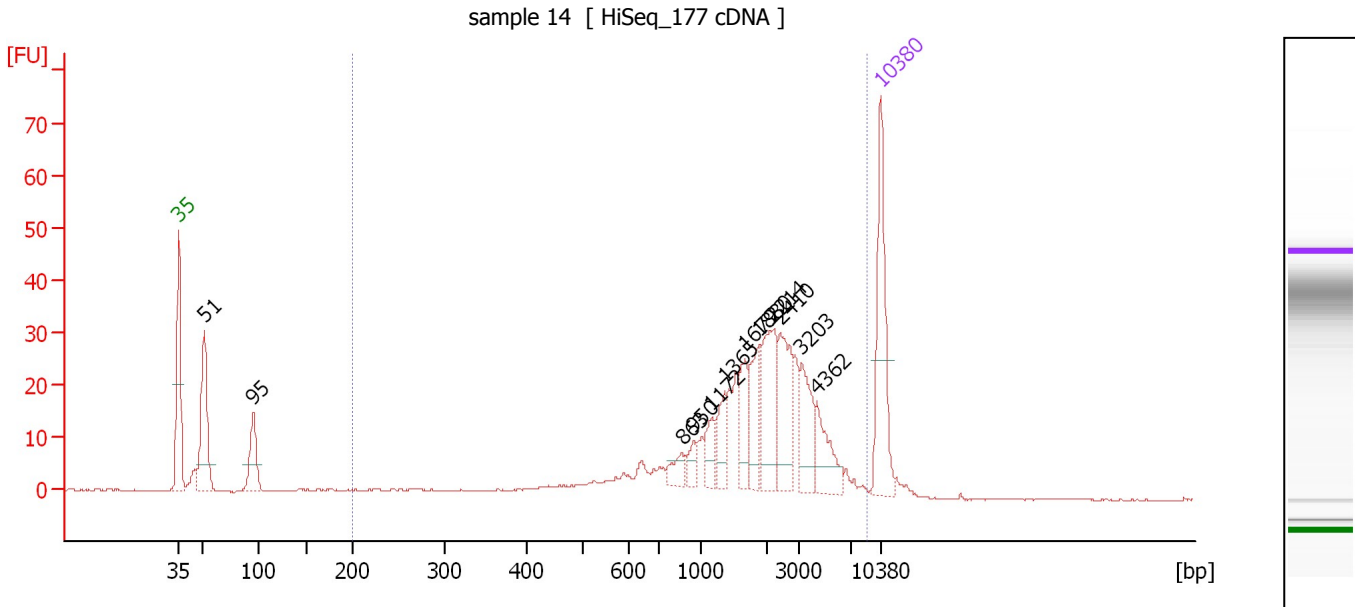
Region table for sample 2 : sample 13

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
150	8,038	1,193	100.0	460.3	130.05	51	100.0

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 Data Path: C:\...10-28\2015-10-28_001_HiSeq177_cDNA_3of3_ctrlRNASoni5min.xad

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Electropherogram Summary Continued ...



Overall Results for sample 3 : sample 14

Number of peaks found: 12 Corr. Area 1: 374.0
 Noise: 0.1

Peak table for sample 3 : sample 14

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	111.26	3,289.0		45.55
3	95	52.09	828.7		50.44
4	863	15.15	26.6		93.17
5	950	10.44	16.6		94.34
6	1,172	19.12	24.7		96.15
7	1,365	23.31	25.9		97.43
8	1,679	30.53	27.6		99.50
9	1,880	33.44	26.9		100.83
10	2,214	57.01	39.0		102.32
11	2,410	50.61	31.8		102.95
12	3,203	36.75	17.4		105.13
13	4,362	32.98	11.5		106.62
14	10,380	75.00	10.9	Upper Marker	113.00

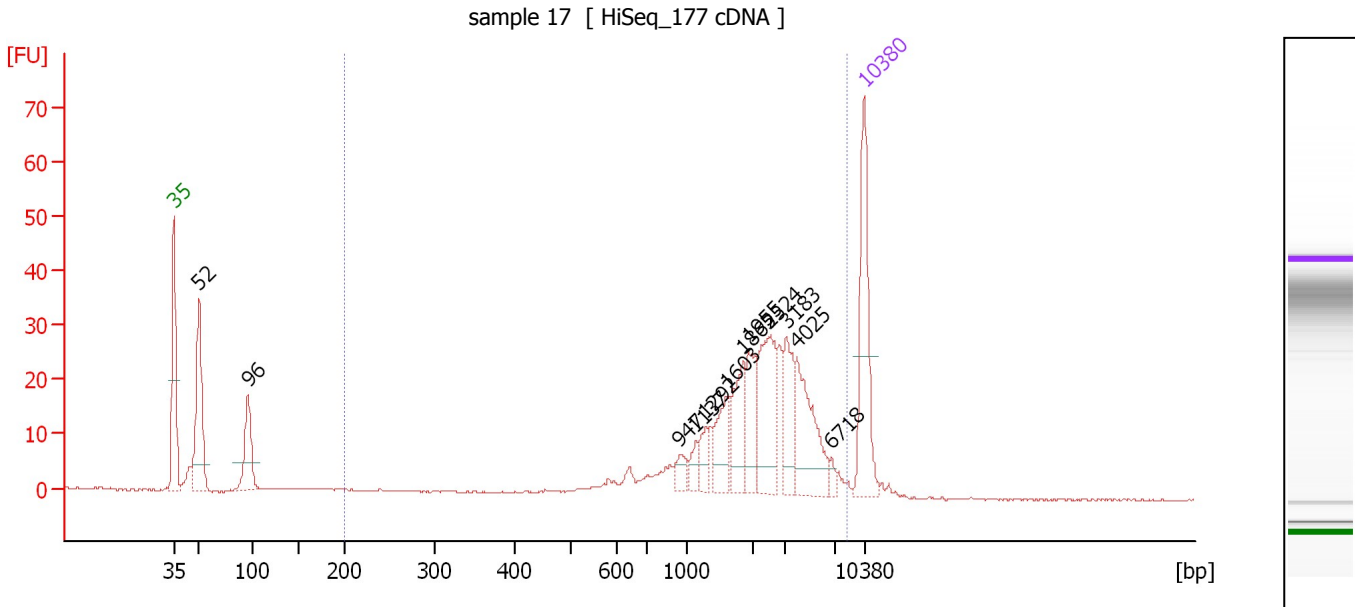
Region table for sample 3 : sample 14

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	8,893	2,188	374.0	656.4	512.94	82	65.0

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Electropherogram Summary Continued ...



Overall Results for sample 4 : sample 17

Number of peaks found: 12 Corr. Area 1: 318.6
 Noise: 0.1

Peak table for sample 4 : sample 17

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	52	126.76	3,719.2		45.59
3	96	63.41	1,002.0		50.51
4	947	12.54	20.1		94.30
5	1,137	11.35	15.1		95.92
6	1,292	14.58	17.1		96.95
7	1,603	31.73	30.0		99.00
8	1,865	40.54	32.9		100.73
9	1,955	31.65	24.5		101.32
10	2,524	70.55	42.4		103.32
11	3,183	37.29	17.7		105.11
12	4,025	61.09	23.0		106.19
13	6,718	5.18	1.2		109.65
14	10,380	75.00	10.9	Upper Marker	113.00

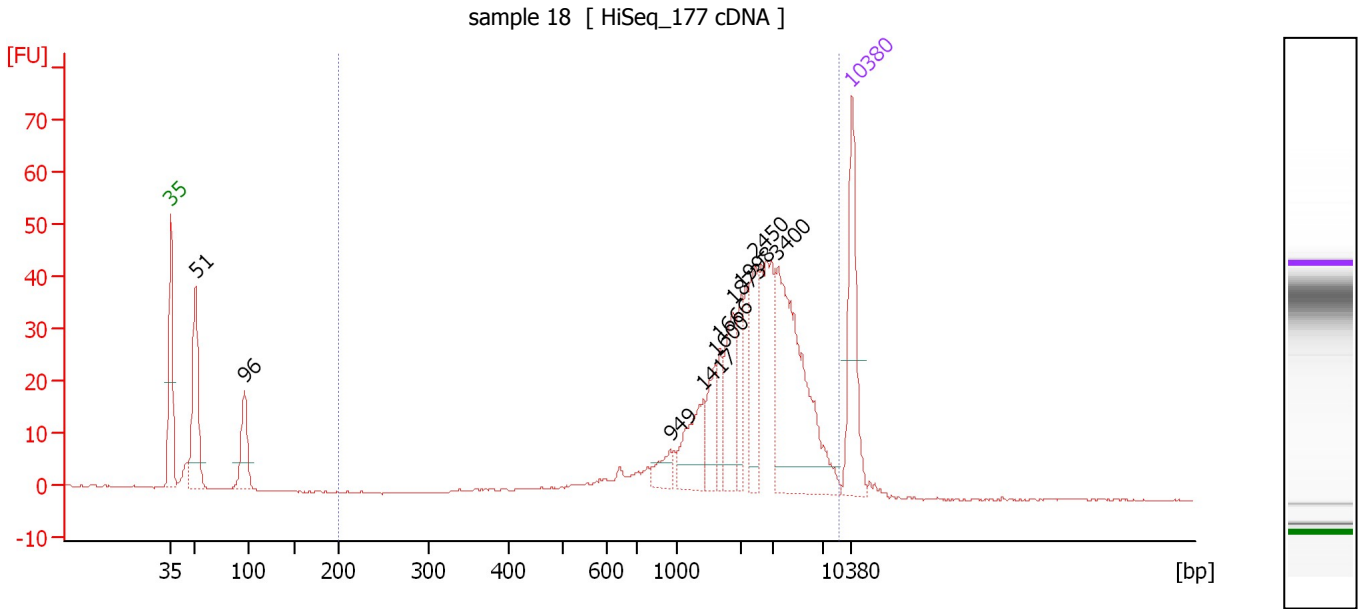
Region table for sample 4 : sample 17

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	8,362	2,584	318.6	424.9	424.64	77	60.1

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Electropherogram Summary Continued ...



Overall Results for sample 5 : sample 18

Number of peaks found: 10 Corr. Area 1: 465.5
 Noise: 0.1

Peak table for sample 5 : sample 18

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	132.09	3,889.2		45.57
3	96	63.74	1,002.9		50.56
4	949	18.36	29.3		94.32
5	1,417	48.85	52.2		97.77
6	1,600	29.19	27.6		98.98
7	1,666	22.84	20.8		99.42
8	1,873	49.04	39.7		100.79
9	1,998	29.79	22.6		101.61
10	2,450	49.99	30.9		103.09
11	3,400	167.19	74.5		105.39
12	10,380	75.00	10.9	Upper Marker	113.00

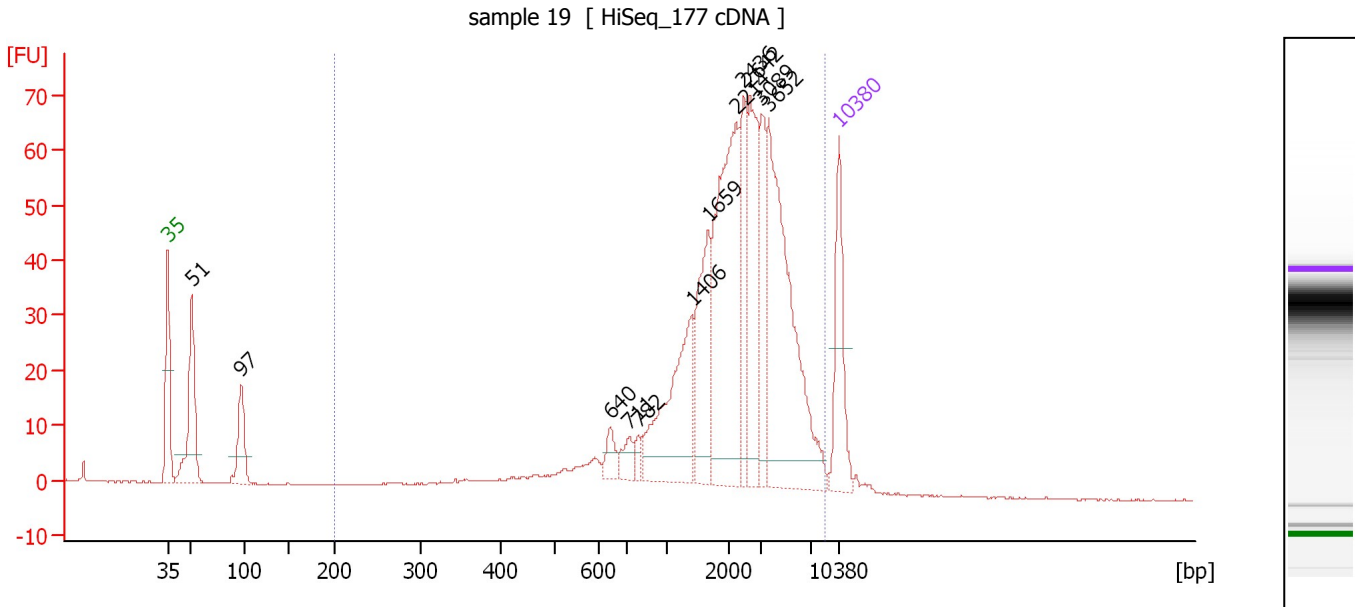
Region table for sample 5 : sample 18

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	8,787	2,803	465.5	508.7	599.36	83	58.9

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...10-28\2015-10-28_001_HiSeq177_cDNA_3of3_ctrlRNASoni5min.xad

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Electropherogram Summary Continued ...



Overall Results for sample 6 : sample 19

Number of peaks found: 12 Corr. Area 1: 792.0
 Noise: 0.1

Peak table for sample 6 : sample 19

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	158.28	4,718.1		45.50
3	97	75.29	1,171.4		50.68
4	640	20.43	48.3		89.13
5	711	21.00	44.7		91.13
6	782	10.69	20.7		92.08
7	1,406	147.20	158.6		97.70
8	1,659	105.36	96.2		99.37
9	2,214	243.70	166.8		102.32
10	2,436	74.80	46.5		103.04
11	2,642	115.49	66.2		103.71
12	3,089	66.03	32.4		104.99
13	3,652	263.25	109.2		105.71
14	10,380	75.00	10.9	Upper Marker	113.00

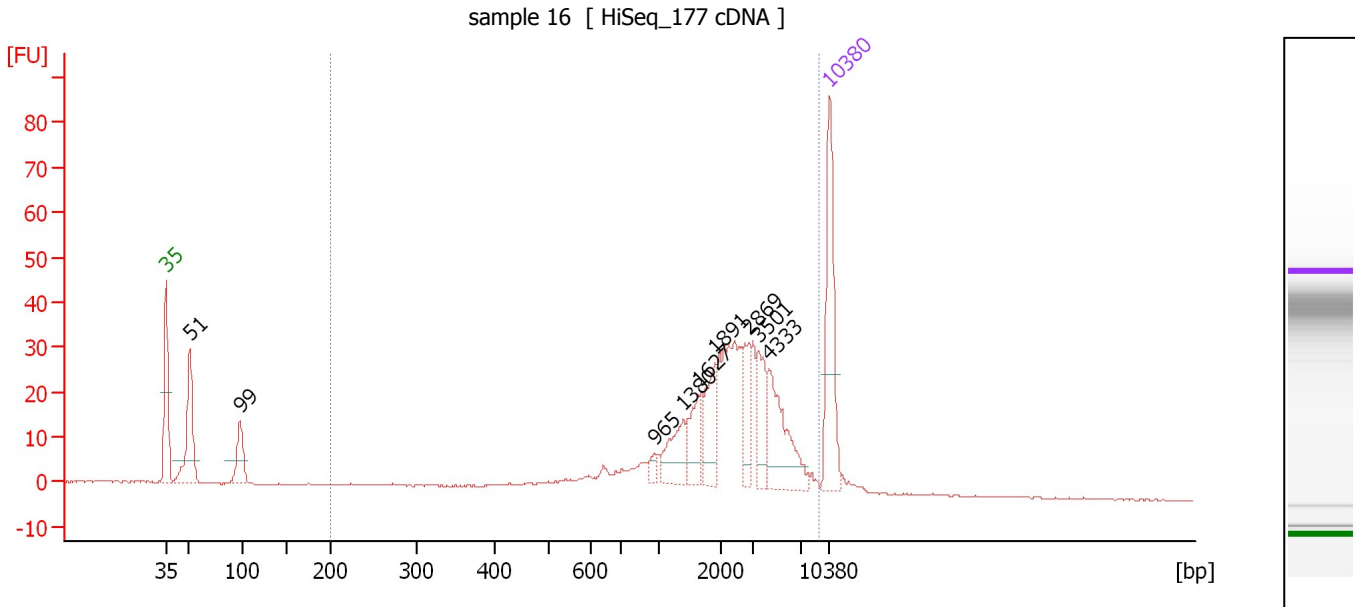
Region table for sample 6 : sample 19

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	8,852	2,625	792.0	1,273.5	1,248.67	90	62.1

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Electropherogram Summary Continued ...



Overall Results for sample 7 : sample 16

Number of peaks found: 9 Corr. Area 1: 389.2
 Noise: 0.2

Peak table for sample 7 : sample 16

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	101.51	3,041.0		45.48
3	99	43.54	668.6		50.82
4	965	6.50	10.2		94.54
5	1,380	33.43	36.7		97.53
6	1,627	31.87	29.7		99.16
7	1,891	35.60	28.5		100.90
8	2,869	31.25	16.5		104.45
9	3,501	31.48	13.6		105.52
10	4,333	61.48	21.5		106.59
11	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : sample 16

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	9,084	2,600	389.2	519.2	463.67	82	64.4

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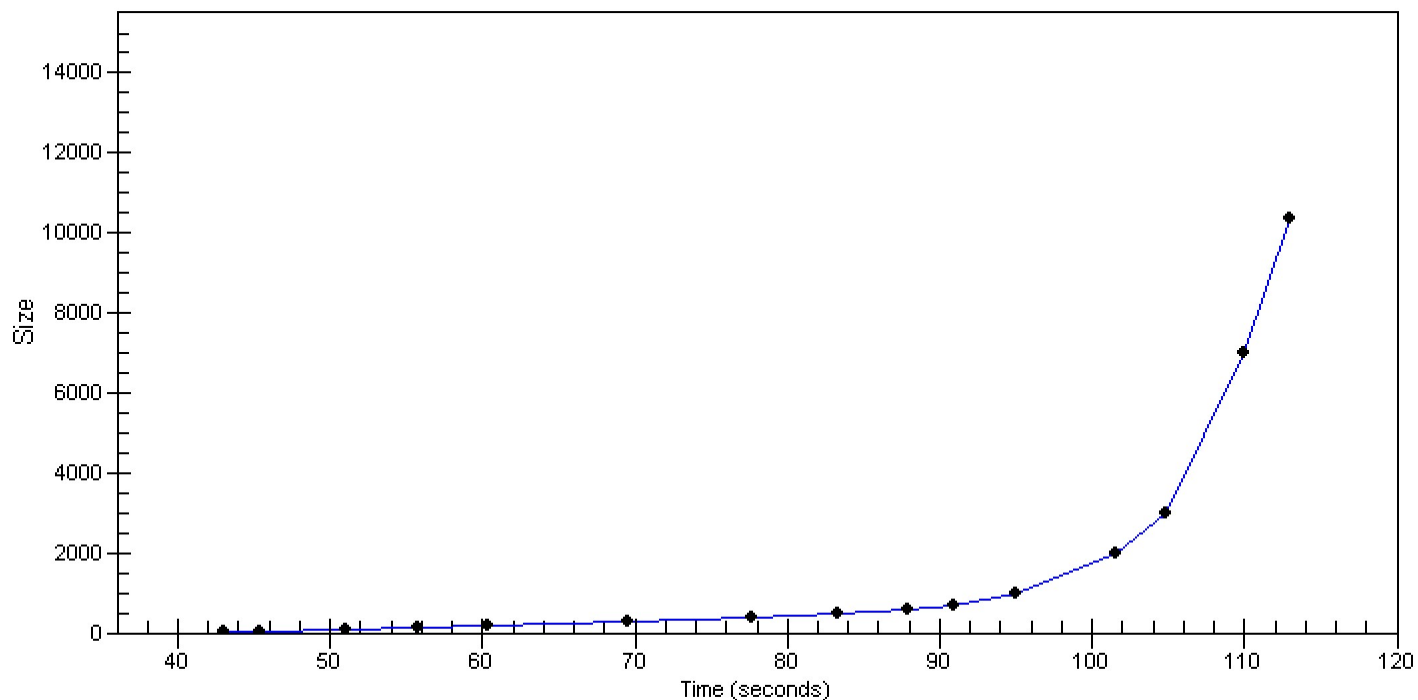
Gel Image

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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		10/28/2015 11:50:52 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyser\2015-10-28\2015-10-28_001.xad)		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/28/2015 11:09:41 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1