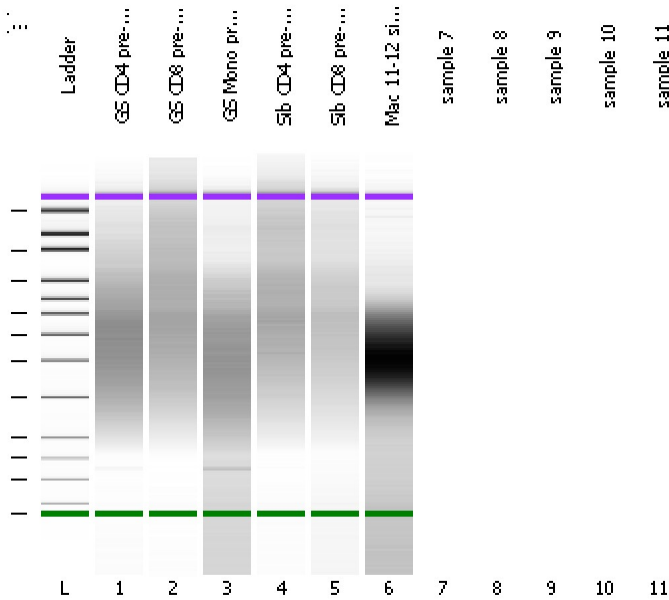


Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electrophoresis File Run Summary



Instrument Information:

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

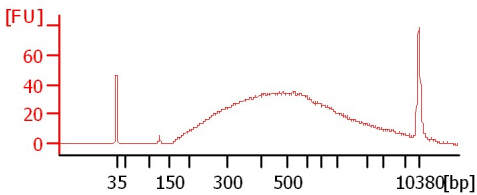
Assay Information:

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

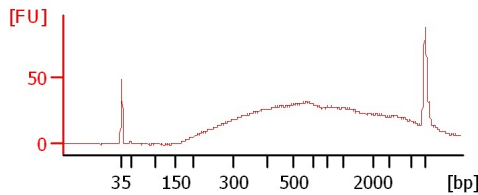
Chip Information:

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

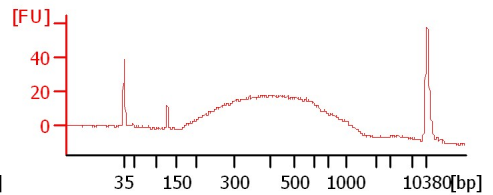
GS CD4 pre-cap library (1:20)



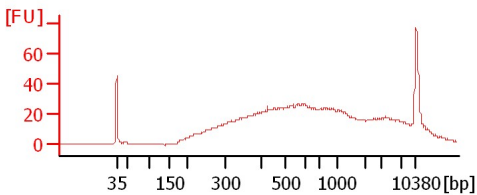
GS CD8 pre-cap library (1:20)



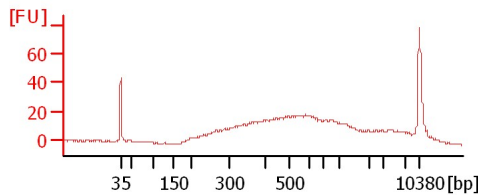
GS Mono pre-cap library (1:20)



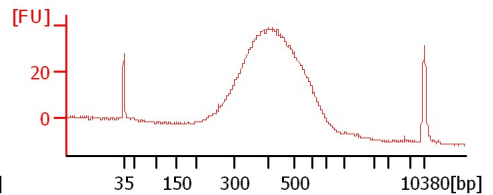
Sib CD4 pre-cap library (1:20)



Sib CD8 pre-cap library (1:20)



Mac 11-12 size sel. soni gDNA
 0.6X R / 0.72X L SS



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
Modified: 4/14/2016 9:45:12 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
GS CD4 pre-cap library (1:20)		<input type="checkbox"/>	✓			
GS CD8 pre-cap library (1:20)		<input type="checkbox"/>	✓			
GS Mono pre-cap library (1:20)		<input type="checkbox"/>	✓			
Sib CD4 pre-cap library (1:20)		<input type="checkbox"/>	✓			
Sib CD8 pre-cap library (1:20)		<input type="checkbox"/>	✓			
Mac 11-12 size sel. soni gDNA sample 7	0.6X R / 0.72X L SS	<input type="checkbox"/>	✓			
sample 8		<input type="checkbox"/>				
sample 9		<input type="checkbox"/>				
sample 10		<input type="checkbox"/>				
sample 11		<input type="checkbox"/>				
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
Modified: 4/14/2016 9:45:12 AM

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

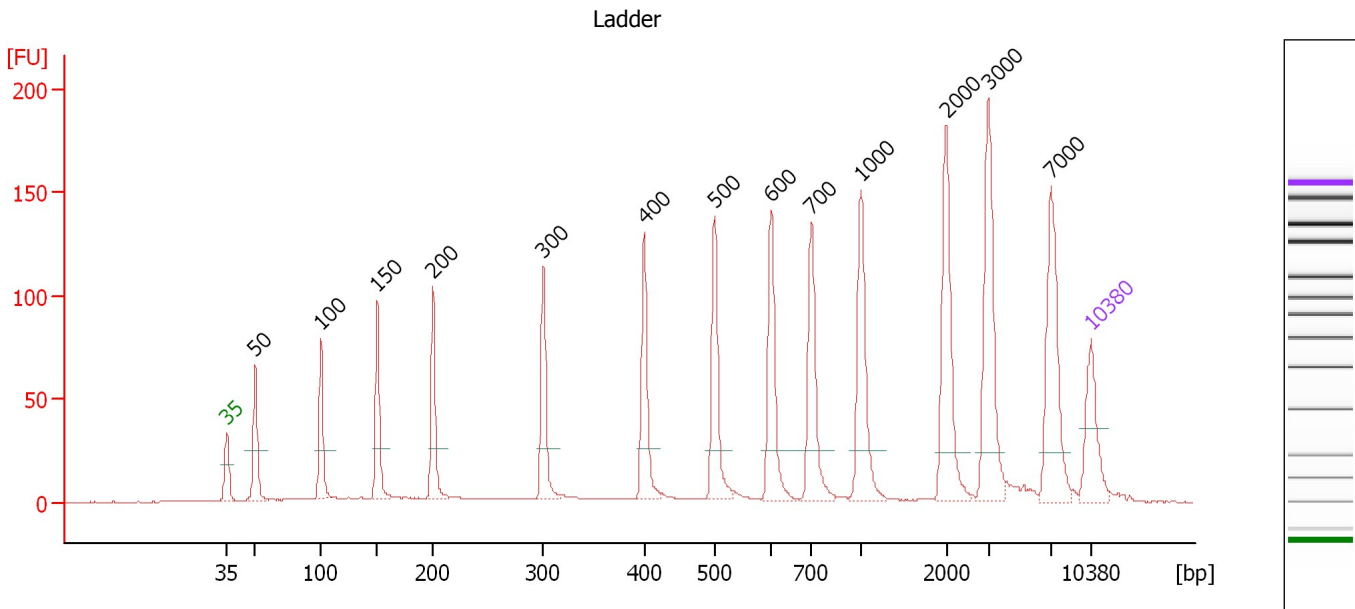
Ladder

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:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
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Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

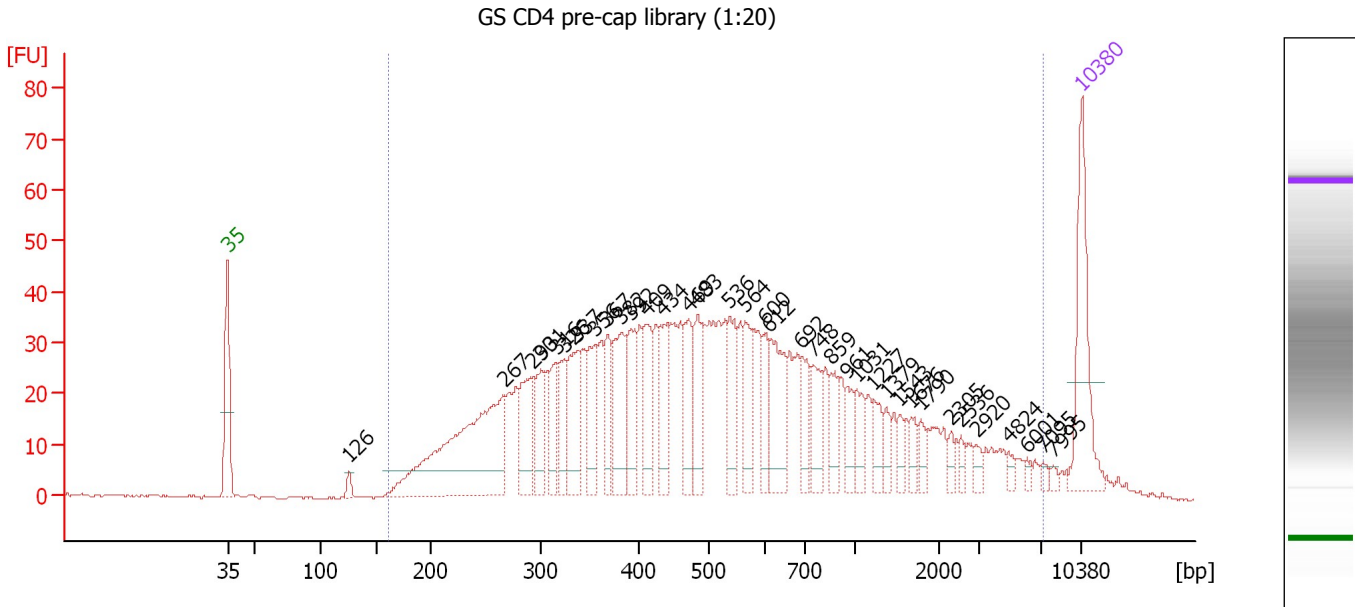
Peak table for Ladder

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	45.29
3	100	150.00	2,272.7	Ladder Peak	50.60
4	150	150.00	1,515.2	Ladder Peak	55.18
5	200	150.00	1,136.4	Ladder Peak	59.67
6	300	150.00	757.6	Ladder Peak	68.61
7	400	150.00	568.2	Ladder Peak	76.77
8	500	150.00	454.5	Ladder Peak	82.51
9	600	150.00	378.8	Ladder Peak	87.05
10	700	150.00	324.7	Ladder Peak	90.33
11	1,000	150.00	227.3	Ladder Peak	94.34
12	2,000	150.00	113.6	Ladder Peak	101.25
13	3,000	150.00	75.8	Ladder Peak	104.67
14	7,000	150.00	32.5	Ladder Peak	109.72
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 1 : GS CD4 pre-cap library (1:20)

Number of peaks found: 36 Corr. Area 1: 1,449.1
 Noise: 0.3

Peak table for sample 1 : GS CD4 pre-cap library (1:20)

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	126	8.93	107.6		52.96
3	267	278.12	1,576.9		65.68
4	293	69.37	358.6		67.99
5	301	45.71	230.0		68.69
6	316	38.46	184.4		69.92
7	326	41.74	194.2		70.70
8	337	68.18	306.1		71.66
9	356	57.06	243.1		73.15
10	367	40.90	168.6		74.11
11	382	77.48	307.4		75.29
12	392	52.07	201.5		76.08
13	409	49.36	182.7		77.30
14	434	54.50	190.1		78.74
15	469	48.02	155.0		80.75
16	483	45.21	141.8		81.54
17	536	47.05	132.9		84.16
18	564	48.99	131.5		85.43
19	600	28.49	71.9		87.04
20	612	66.64	165.0		87.44
21	692	29.68	65.0		90.06
22	748	39.12	79.2		90.98
23	859	27.07	47.7		92.46
24	961	22.39	35.3		93.82
25	1,031	23.17	34.0		94.56

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...

... Peak table for sample 1 : GS CD4 pre-cap library (1:20)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,227	19.89	24.6		95.92
27	1,379	12.30	13.5		96.96
28	1,543	10.30	10.1		98.10
29	1,676	12.64	11.4		99.02
30	1,790	10.29	8.7		99.80
31	2,305	6.94	4.6		102.29
32	2,536	6.30	3.8		103.08
33	2,920	7.14	3.7		104.39
34	4,824	4.75	1.5		106.97
35	6,001	3.93	1.0		108.46
36	7,095	4.08	0.9		109.81
37	7,995	3.37	0.6		110.68
38	10,380	75.00	10.9	Upper Marker	113.00

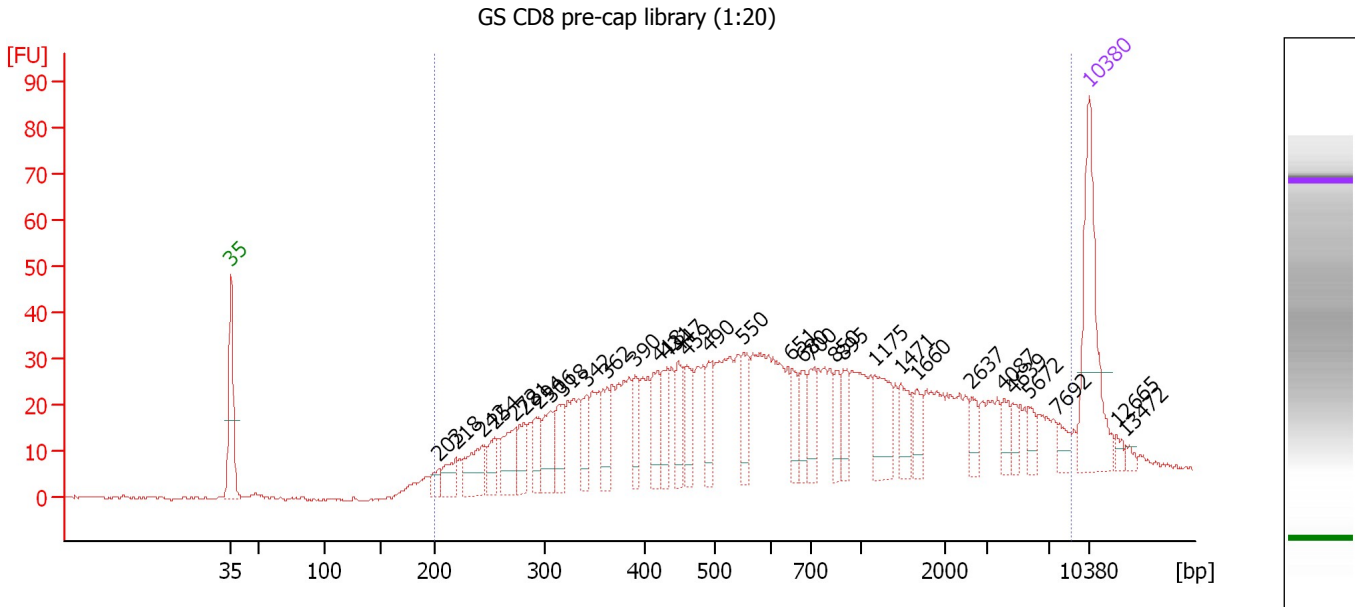
Region table for sample 1 : GS CD4 pre-cap library (1:20)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
161	7,123	804	1,449.1	8,050.3	2,193.30	98	100.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
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Electropherogram Summary Continued ...



Overall Results for sample 2 : GS CD8 pre-cap library (1:20)

Number of peaks found: 33 Corr. Area 1: 1,150.3
 Noise: 0.3

Peak table for sample 2 : GS CD8 pre-cap library (1:20)

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	203	12.04	89.9		59.92
3	218	22.78	158.0		61.32
4	242	38.29	239.5		63.45
5	254	20.49	122.3		64.49
6	272	38.45	213.8		66.14
7	281	25.75	138.7		66.93
8	294	25.51	131.3		68.10
9	306	35.28	174.9		69.06
10	318	29.67	141.5		70.06
11	342	24.20	107.3		72.02
12	362	27.97	117.0		73.67
13	390	22.15	86.1		75.93
14	418	30.40	110.2		77.80
15	431	27.59	97.0		78.54
16	447	28.06	95.1		79.46
17	459	30.69	101.3		80.15
18	490	22.40	69.3		81.94
19	550	26.81	73.9		84.77
20	651	17.31	40.3		88.72
21	680	18.50	41.2		89.68
22	700	24.27	52.5		90.33
23	850	15.60	27.8		92.33
24	895	18.82	31.9		92.94
25	1,175	36.24	46.7		95.55

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...

... Peak table for sample 2 : GS CD8 pre-cap library (1:20)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,471	19.06	19.6		97.60
27	1,660	12.95	11.8		98.90
28	2,637	11.08	6.4		103.43
29	4,087	11.21	4.2		106.04
30	4,639	7.31	2.4		106.74
31	5,672	9.73	2.6		108.04
32	7,692	9.07	1.8		110.39
33	10,380	75.00	10.9	Upper Marker	113.00
34	12,665	0.00	0.0		115.22
35	13,472	0.00	0.0		116.00

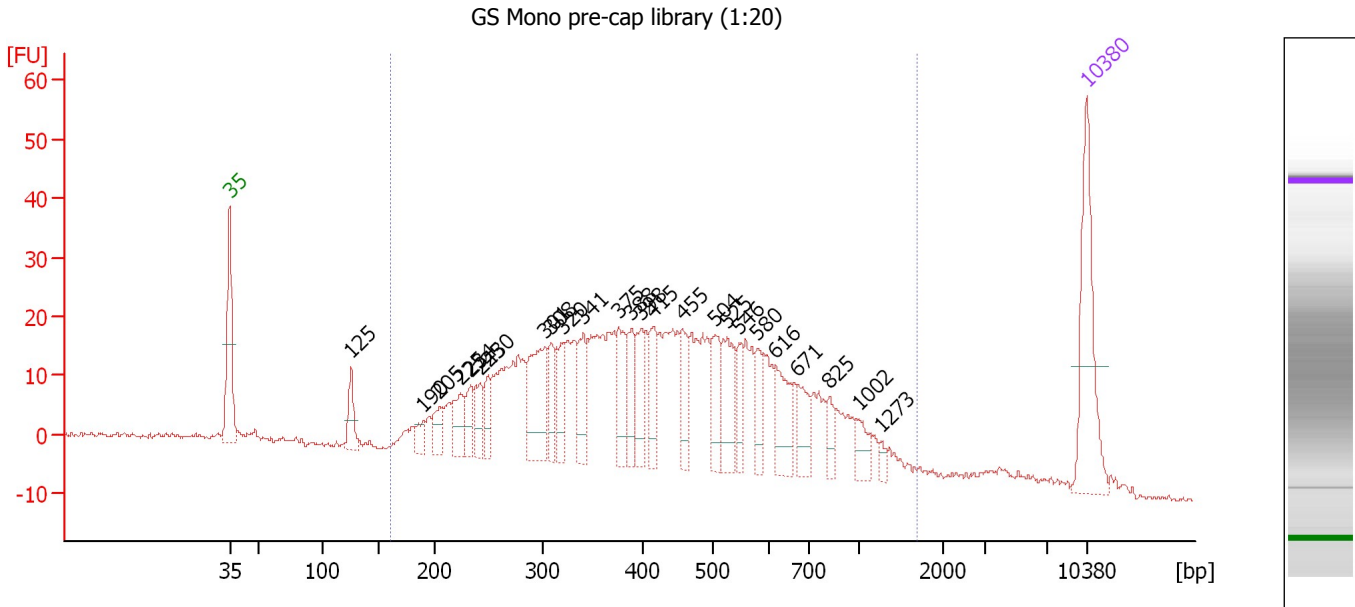
Region table for sample 2 : GS CD8 pre-cap library (1:20)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	8,819	1,219	1,150.3	4,068.8	1,306.49	98	100.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 3 : GS Mono pre-cap library (1:20)

Number of peaks found: 25 Corr. Area 1: 898.5
 Noise: 0.5

Peak table for sample 3 : GS Mono pre-cap library (1:20)

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	125	30.82	372.1		52.93
3	190	15.37	122.6		58.77
4	205	22.46	165.9		60.12
5	225	32.12	216.3		61.90
6	234	24.98	161.9		62.69
7	243	29.52	184.4		63.47
8	250	22.95	139.2		64.13
9	301	83.31	419.2		68.70
10	308	29.39	144.8		69.22
11	320	30.91	146.2		70.27
12	341	40.31	179.3		71.92
13	375	40.16	162.3		74.71
14	388	36.90	144.1		75.80
15	398	34.11	129.9		76.58
16	415	34.32	125.3		77.63
17	455	32.87	109.4		79.94
18	504	36.70	110.4		82.68
19	525	49.02	141.5		83.64
20	546	22.61	62.7		84.60
21	580	25.41	66.4		86.12
22	616	43.32	106.6		87.56
23	671	28.54	64.4		89.39
24	825	14.20	26.1		92.00
25	1,002	17.24	26.1		94.36

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...

... Peak table for sample 3 : GS Mono pre-cap library (1:20)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,273	4.84	5.8		96.23
27	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : GS Mono pre-cap library (1:20)

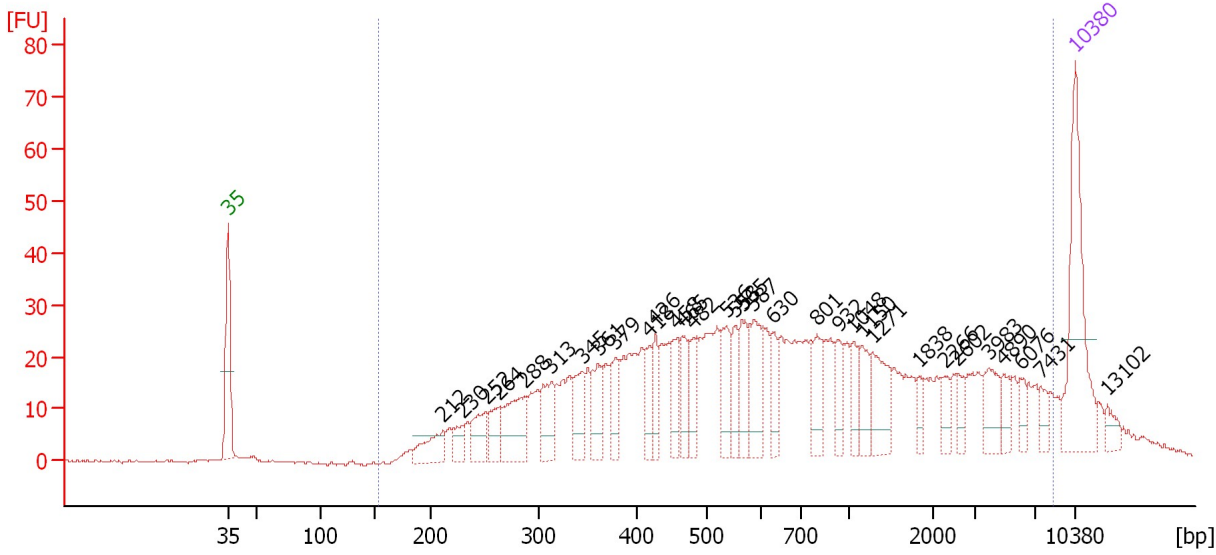
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
161	1,698	475	898.5	6,228.4	1,497.10	89	49.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
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Electropherogram Summary Continued ...

Sib CD4 pre-cap library (1:20)



Overall Results for sample 4 : Sib CD4 pre-cap library (1:20)

Number of peaks found: 32 Corr. Area 1: 1,065.2
 Noise: 0.2

Peak table for sample 4 : Sib CD4 pre-cap library (1:20)

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	212	31.20	222.8		60.75
3	230	14.62	96.4		62.34
4	252	29.10	174.9		64.32
5	264	25.00	143.5		65.38
6	288	54.07	284.9		67.49
7	313	34.47	166.7		69.70
8	345	27.99	122.9		72.30
9	361	31.92	134.0		73.57
10	379	23.95	95.8		75.03
11	418	22.03	79.9		77.80
12	426	21.49	76.3		78.29
13	458	22.85	75.6		80.09
14	465	24.60	80.2		80.49
15	482	27.38	86.1		81.46
16	536	32.29	91.3		84.15
17	553	20.61	56.5		84.89
18	565	29.00	77.8		85.47
19	587	40.34	104.2		86.44
20	630	18.18	43.7		88.02
21	801	28.09	53.1		91.68
22	932	19.49	31.7		93.44
23	1,048	15.99	23.1		94.67
24	1,150	18.96	25.0		95.38
25	1,271	33.79	40.3		96.22

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
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Electropherogram Summary Continued ...

... Peak table for sample 4 : Sib CD4 pre-cap library (1:20)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,838	8.23	6.8		100.14
27	2,266	11.59	7.7		102.16
28	2,602	7.93	4.6		103.31
29	3,983	20.59	7.8		105.91
30	4,890	10.57	3.3		107.05
31	6,076	8.83	2.2		108.55
32	7,431	8.42	1.7		110.14
33	10,380	75.00	10.9	Upper Marker	113.00
34	13,102	0.00	0.0		115.64

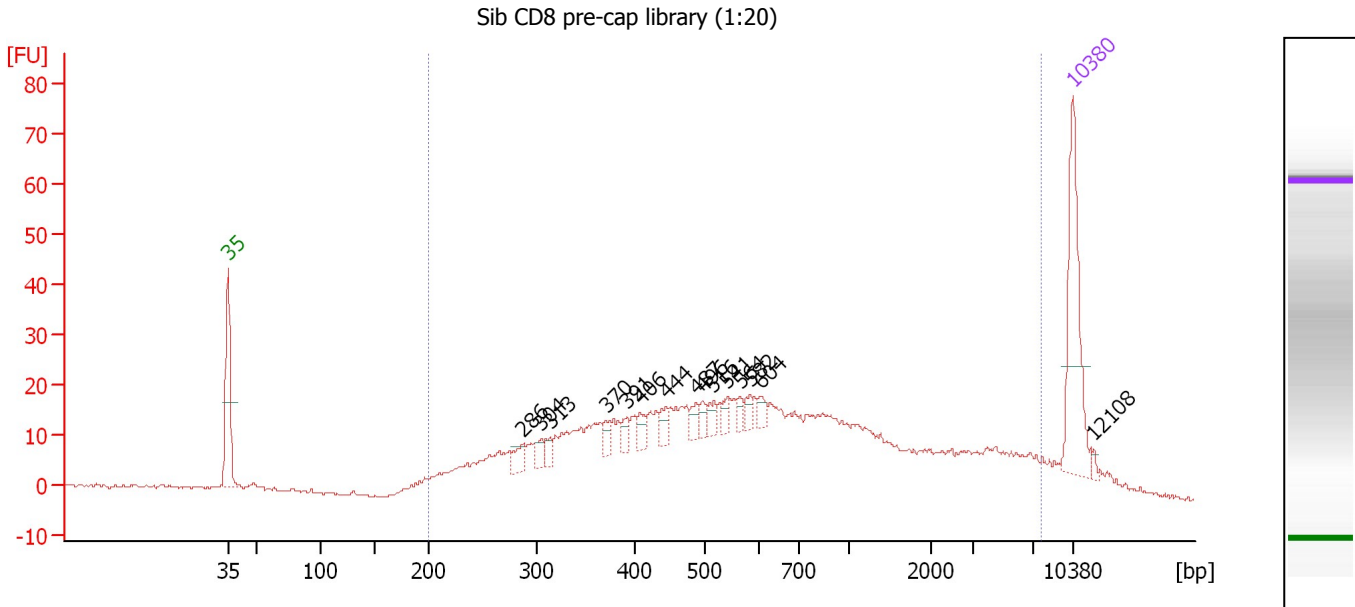
Region table for sample 4 : Sib CD4 pre-cap library (1:20)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
153	8,420	1,270	1,065.2	4,051.5	1,298.48	97	100.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 5 : Sib CD8 pre-cap library (1:20)

Number of peaks found: 15 Corr. Area 1: 726.9
 Noise: 0.4

Peak table for sample 5 : Sib CD8 pre-cap library (1:20)

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	286	15.31	81.2		67.33
3	304	11.01	54.9		68.92
4	313	9.71	47.0		69.68
5	370	9.15	37.4		74.36
6	391	9.15	35.4		76.03
7	406	11.12	41.4		77.14
8	444	10.70	36.5		79.30
9	487	10.28	32.0		81.78
10	496	7.65	23.4		82.31
11	516	10.14	29.8		83.23
12	541	6.94	19.4		84.38
13	564	6.44	17.3		85.40
14	582	8.59	22.4		86.24
15	604	8.09	20.3		87.16
16	10,380	75.00	10.9	Upper Marker	113.00
17	12,108	0.00	0.0		114.68

Region table for sample 5 : Sib CD8 pre-cap library (1:20)

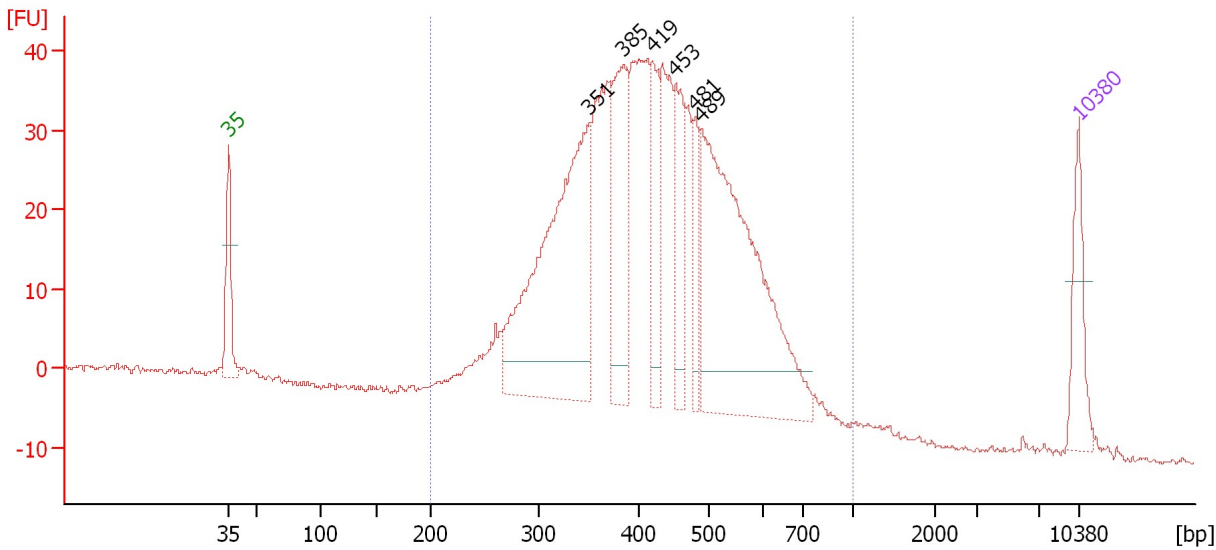
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	7,621	1,086	726.9	3,412.9	1,075.22	96	100.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Electropherogram Summary Continued ...

Mac 11-12 size sel. soni gDNA [0.6X R / 0.72X L SS]



Overall Results for sample 6 : Mac 11-12 size sel. soni gDNA

Number of peaks found: 6 Corr. Area 1: 1,011.3
 Noise: 0.4

Peak table for sample 6 : Mac 11-12 size sel. soni gDNA

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	351	652.23	2,819.4		72.73
3	385	257.54	1,013.7		75.54
4	419	122.12	441.5		77.87
5	453	142.97	478.4		79.80
6	481	75.84	238.9		81.43
7	489	665.18	2,059.0		81.91
8	10,380	75.00	10.9	Upper Marker	113.00

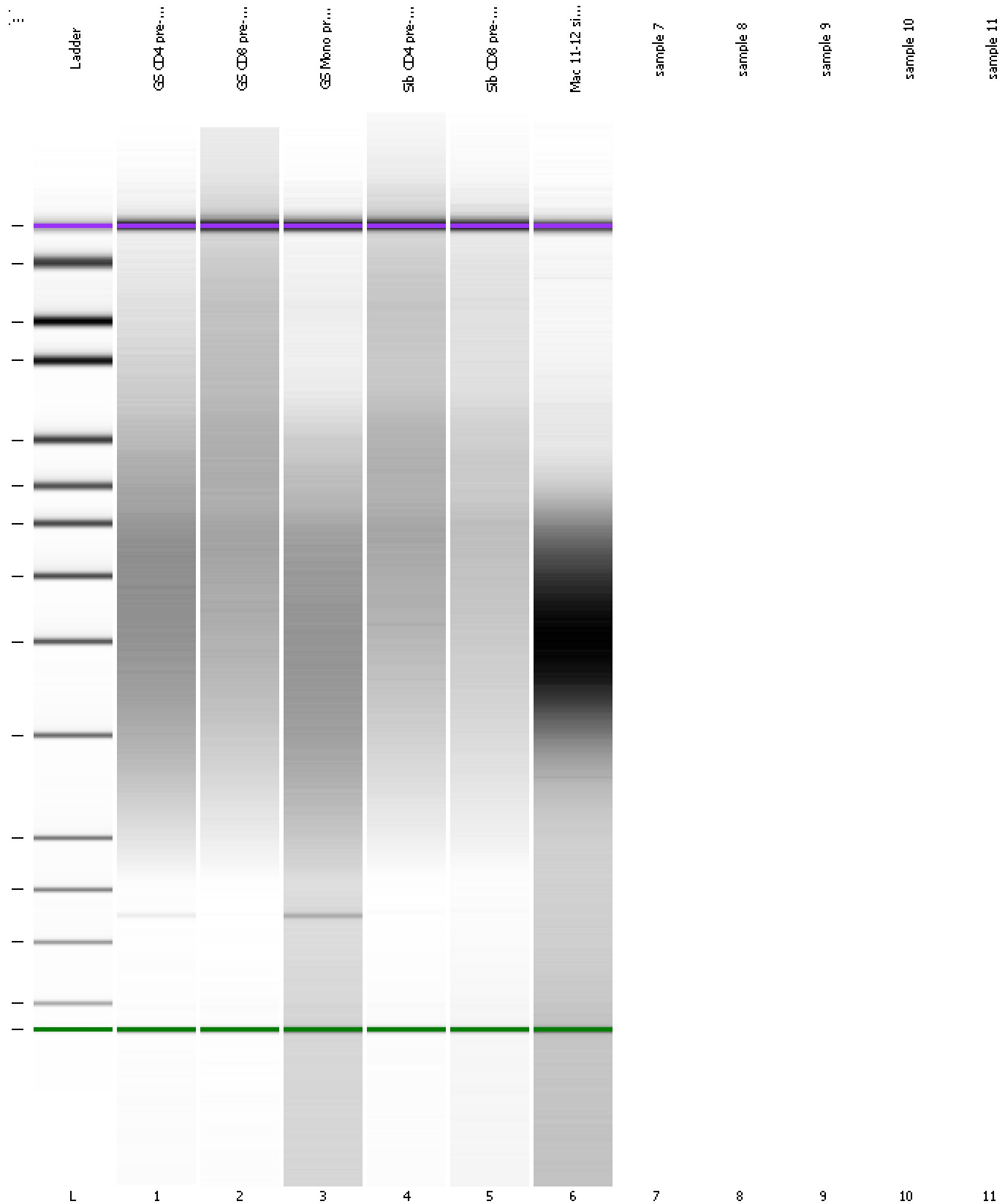
Region table for sample 6 : Mac 11-12 size sel. soni gDNA

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	429	1,011.3	11,690.1	3,029.93	96	25.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
Modified: 4/14/2016 9:45:12 AM

Gel Image

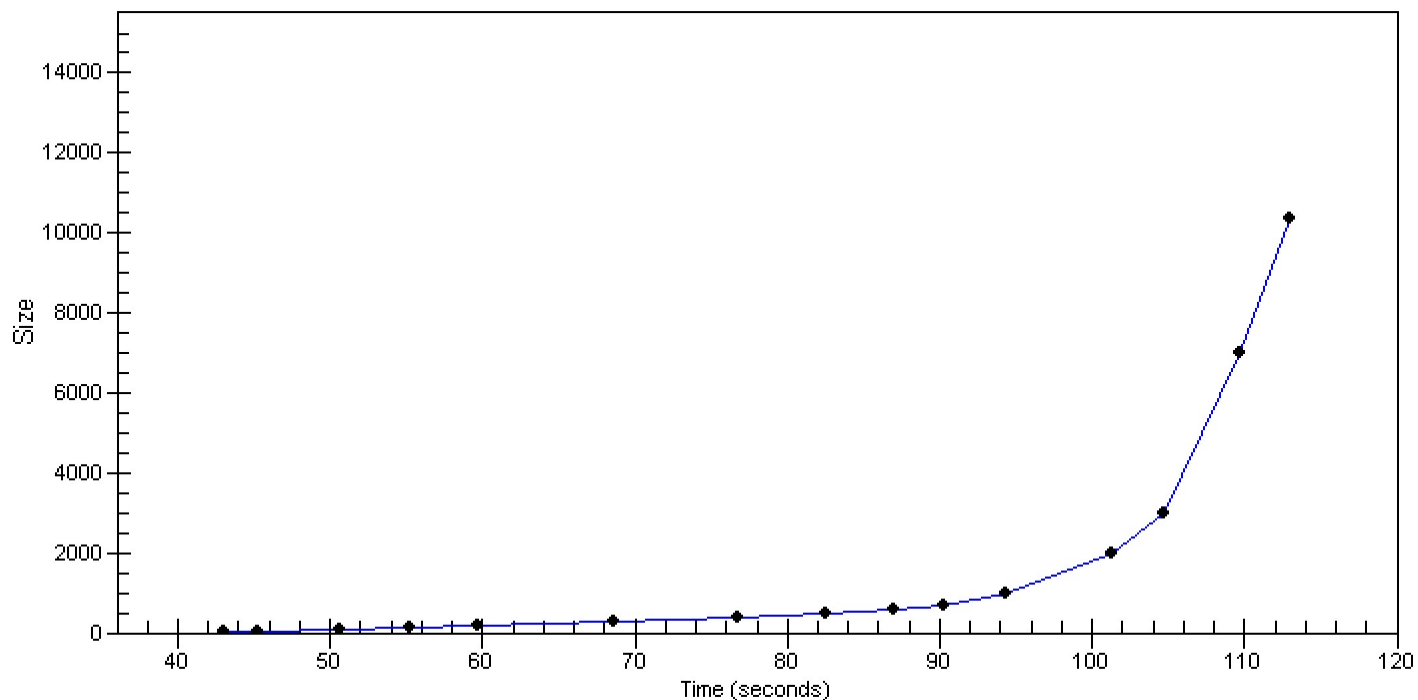


Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
Modified: 4/14/2016 9:45:12 AM

Curves

Standard Curve



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
Modified: 4/14/2016 9:45:12 AM

Invalid Samples

Sample 7 has not been run, no results available.

Sample 8 has not been run, no results available.

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad

Created: 4/14/2016 9:15:28 AM
 Modified: 4/14/2016 9:45:12 AM

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 7)		Instrument	Run		4/14/2016 9:42:27 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-04-14\2016-04-14_001.xad)		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		4/14/2016 9:15:33 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1