

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...04-12\2016-04-12_006_HiSeq426_SizeSelectedLibraries_1-6.xad

Created: 4/12/2016 4:42:09 PM
Modified: 4/12/2016 6:33:14 PM

Electrophoresis File Run Summary

Instrument Information:

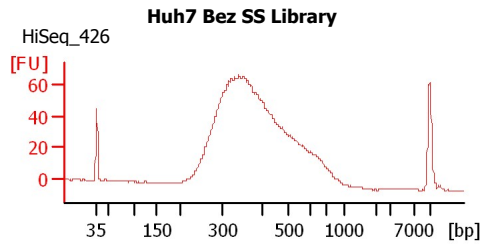
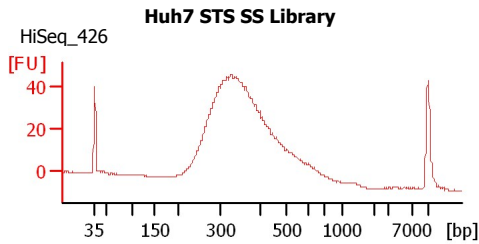
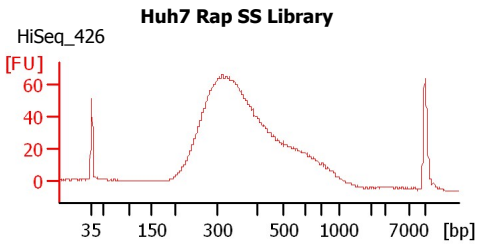
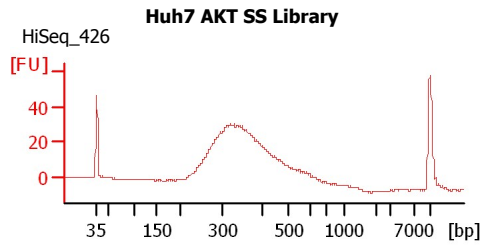
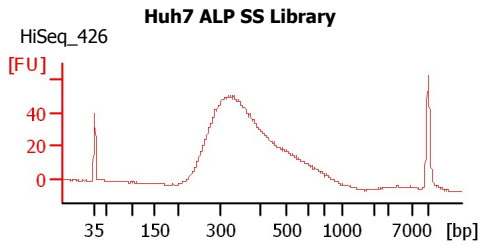
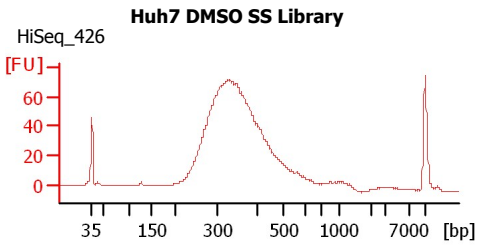
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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
Huh7 DMSO SS Library	HiSeq_426	<input type="checkbox"/>	✓			
Huh7 ALP SS Library	HiSeq_426	<input type="checkbox"/>	✓			
Huh7 AKT SS Library	HiSeq_426	<input type="checkbox"/>	✓			
Huh7 Rap SS Library	HiSeq_426	<input type="checkbox"/>	✓			
Huh7 STS SS Library	HiSeq_426	<input type="checkbox"/>	✓			
Huh7 Bez SS Library	HiSeq_426	<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/ μ l] : 1950
Uses Standard Area for Ladder Fragments
Lower Marker Concentration [pg/ μ l] : 125
Upper Marker Concentration [pg/ μ l] : 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

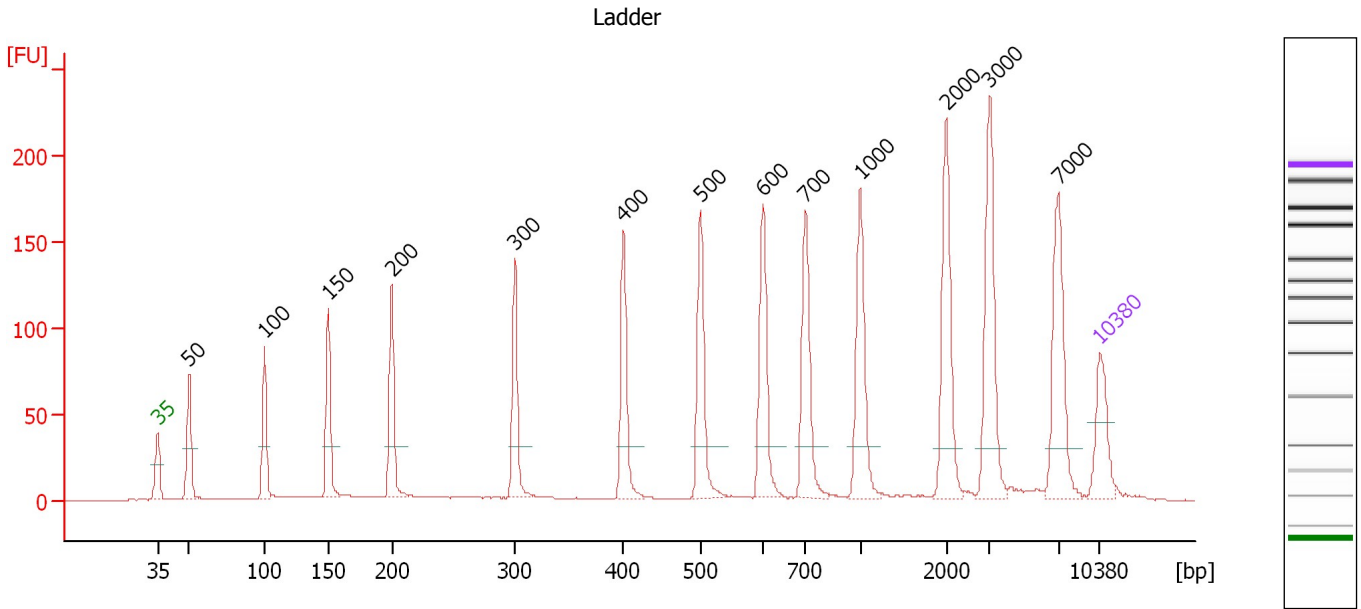
Ladder

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: 0.2

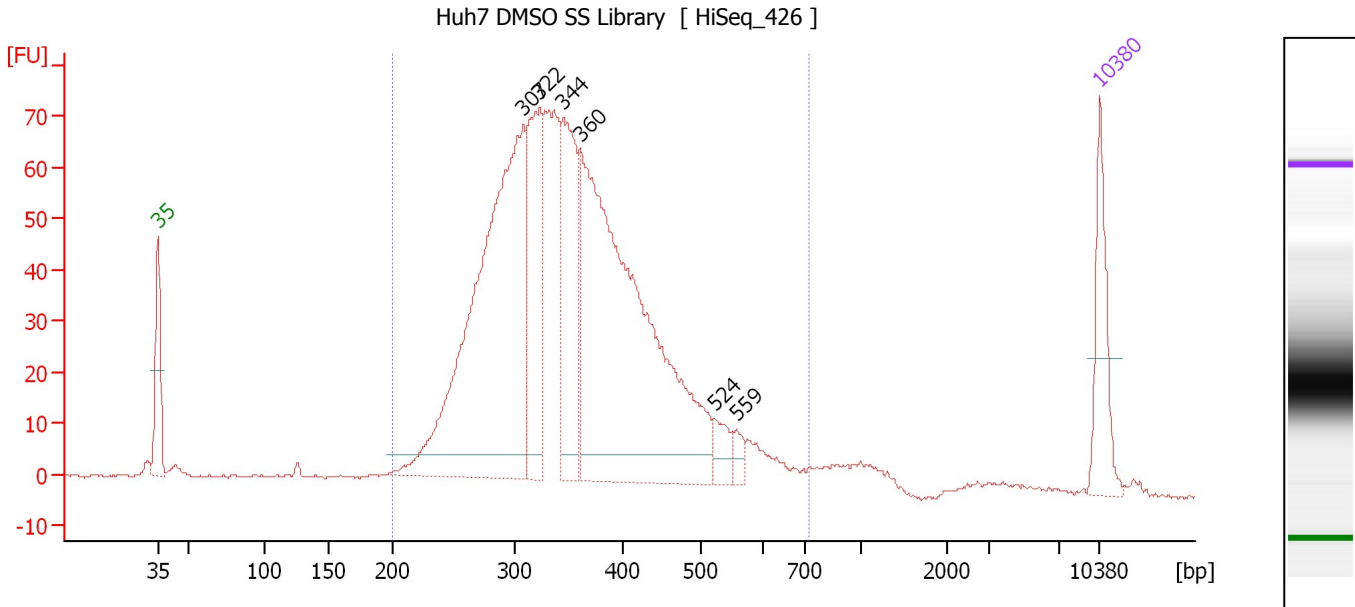
Peak table for Ladder

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	45.32
3	100	150.00	2,272.7	Ladder Peak	50.97
4	150	150.00	1,515.2	Ladder Peak	55.71
5	200	150.00	1,136.4	Ladder Peak	60.41
6	300	150.00	757.6	Ladder Peak	69.56
7	400	150.00	568.2	Ladder Peak	77.62
8	500	150.00	454.5	Ladder Peak	83.31
9	600	150.00	378.8	Ladder Peak	87.96
10	700	150.00	324.7	Ladder Peak	91.14
11	1,000	150.00	227.3	Ladder Peak	95.22
12	2,000	150.00	113.6	Ladder Peak	101.57
13	3,000	150.00	75.8	Ladder Peak	104.80
14	7,000	150.00	32.5	Ladder Peak	109.92
15	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Overall Results for sample 2 : Huh7 DMSO SS Library

Number of peaks found: 6 Corr. Area 1: 1,360.8
 Noise: 0.3

Peak table for sample 2 : Huh7 DMSO SS Library

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	307	779.79	3,850.4		70.11
3	322	232.25	1,091.9		71.35
4	344	220.48	970.5		73.12
5	360	824.89	3,469.6		74.41
6	524	31.82	92.1		84.41
7	559	15.93	43.2		86.03
8	10,380	75.00	10.9	Upper Marker	113.00

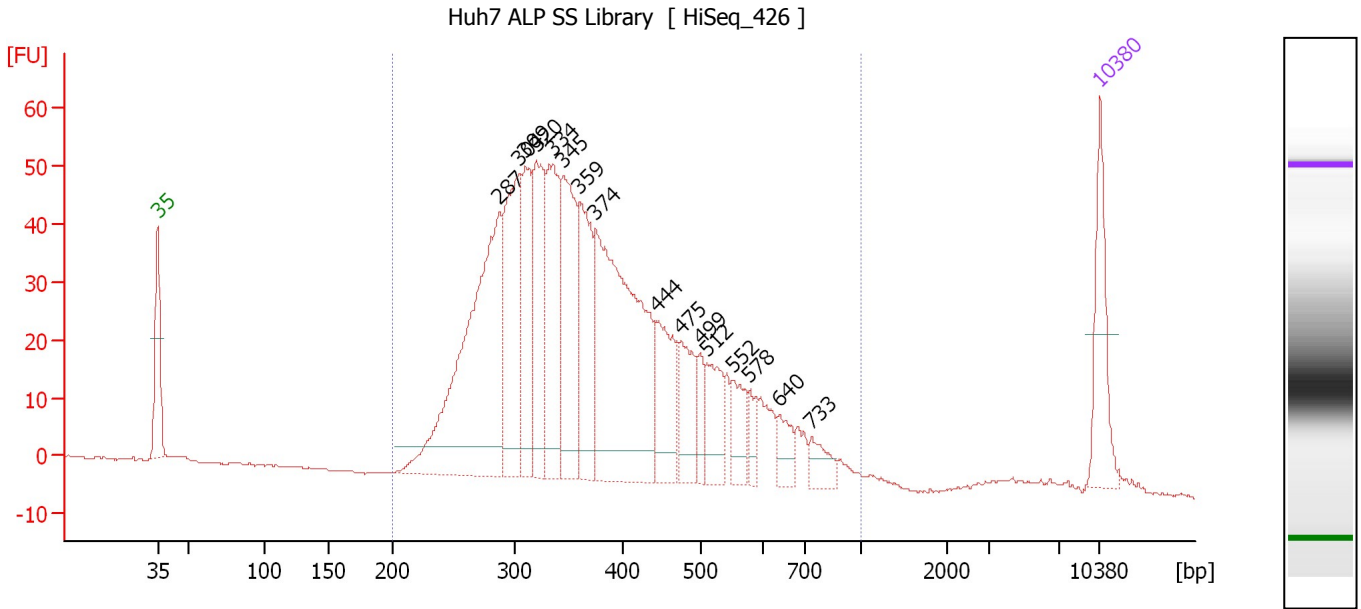
Region table for sample 2 : Huh7 DMSO SS Library

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	715	359	1,360.8	11,095.1	2,465.33	95	23.1

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Electropherogram Summary Continued ...



Overall Results for sample 3 : Huh7 ALP SS Library

Number of peaks found: 16 Corr. Area 1: 1,120.7
 Noise: 0.3

Peak table for sample 3 : Huh7 ALP SS Library

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	287	489.07	2,581.2		68.38
3	304	220.01	1,097.0		69.87
4	309	141.57	693.6		70.31
5	320	164.49	778.8		71.17
6	334	181.04	821.7		72.28
7	345	195.29	858.8		73.15
8	359	152.45	643.6		74.31
9	374	441.35	1,788.5		75.52
10	444	106.25	363.0		80.10
11	475	72.47	231.2		81.88
12	499	35.75	108.4		83.28
13	512	65.33	193.4		83.86
14	552	46.76	128.3		85.74
15	578	21.33	55.9		86.95
16	640	31.17	73.8		89.22
17	733	29.39	60.8		91.58
18	10,380	75.00	10.9	Upper Marker	113.00

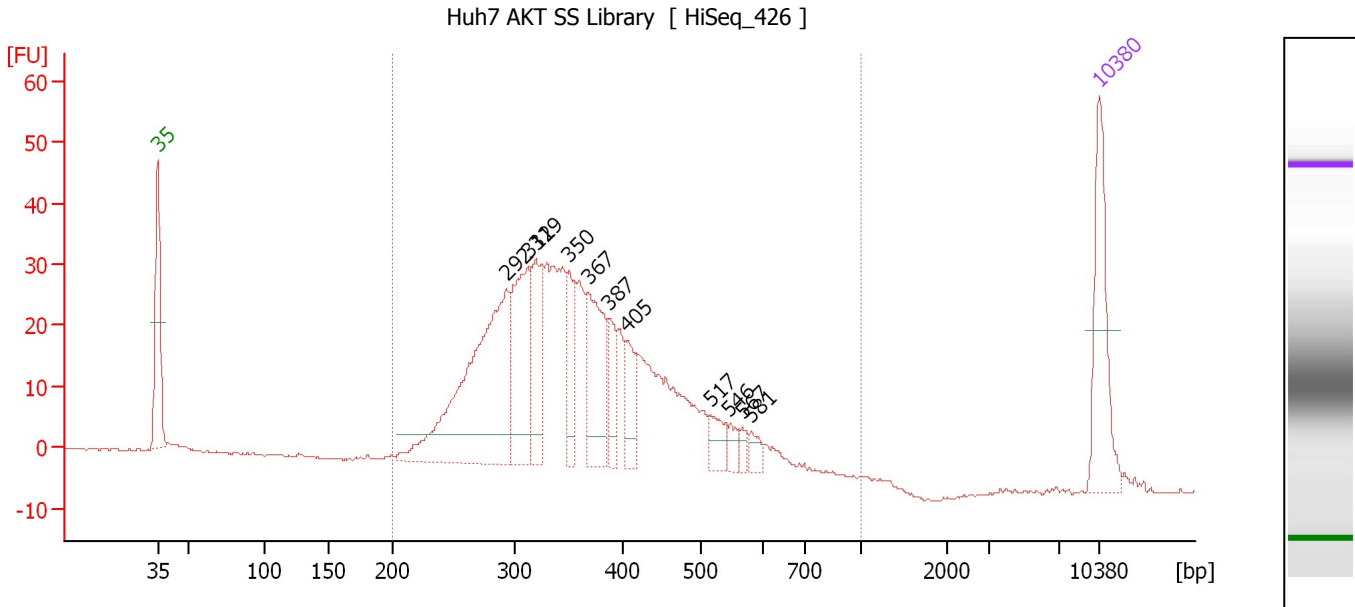
Region table for sample 3 : Huh7 ALP SS Library

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	389	1,120.7	10,396.2	2,410.38	99	30.0

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Electropherogram Summary Continued ...



Overall Results for sample 4 : Huh7 AKT SS Library

Number of peaks found: 11 Corr. Area 1: 650.3
 Noise: 0.2

Peak table for sample 4 : Huh7 AKT SS Library

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	292	306.31	1,586.7		68.87
3	312	131.29	637.4		70.53
4	319	76.19	361.5		71.12
5	350	51.14	221.6		73.56
6	367	103.15	425.6		74.97
7	387	35.82	140.2		76.58
8	405	35.94	134.5		77.90
9	517	22.30	65.3		84.10
10	546	12.72	35.3		85.47
11	567	8.36	22.3		86.44
12	581	11.24	29.3		87.08
13	10,380	75.00	10.9	Upper Marker	113.00

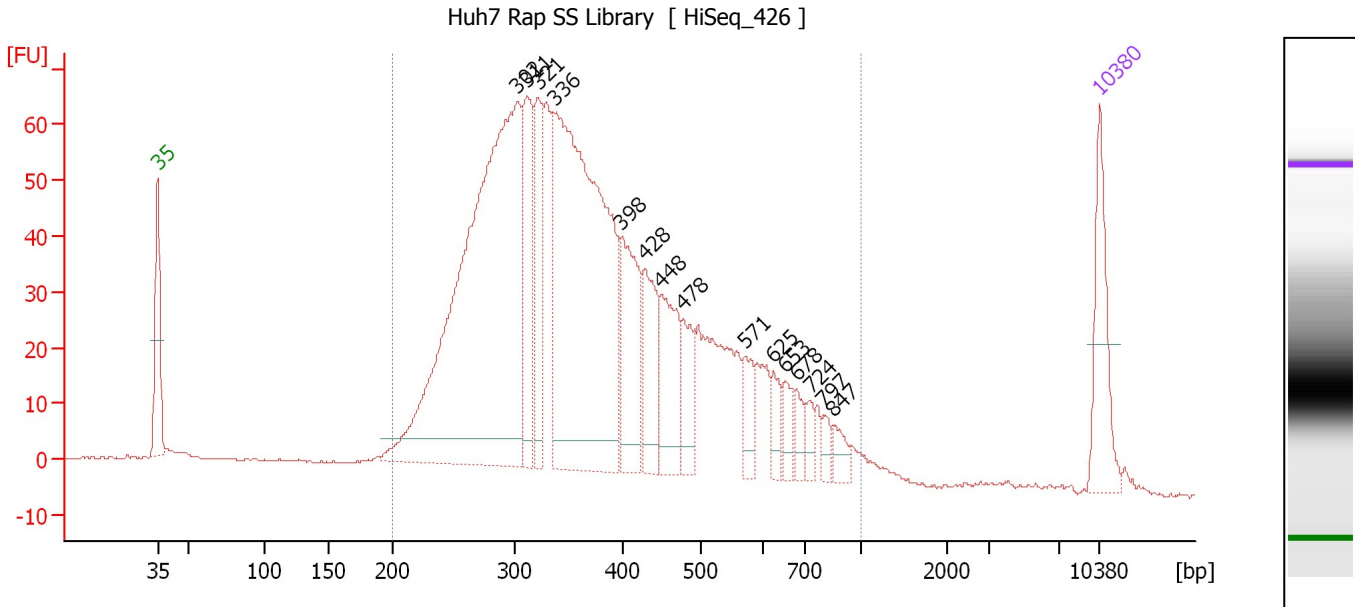
Region table for sample 4 : Huh7 AKT SS Library

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	366	650.3	5,505.7	1,237.59	99	24.2

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 5 : Huh7 Rap SS Library

Number of peaks found: 15 Corr. Area 1: 1,568.7
 Noise: 0.2

Peak table for sample 5 : Huh7 Rap SS Library

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	302	909.76	4,563.2		69.73
3	311	151.62	738.1		70.47
4	321	113.23	534.3		71.26
5	336	673.19	3,032.2		72.49
6	398	144.47	550.4		77.43
7	428	93.64	331.5		79.21
8	448	106.88	361.5		80.35
9	478	53.30	168.9		82.08
10	571	35.18	93.3		86.62
11	625	25.67	62.3		88.74
12	653	22.79	52.9		89.63
13	678	21.52	48.1		90.42
14	724	16.08	33.7		91.46
15	797	14.26	27.1		92.45
16	847	20.01	35.8		93.14
17	10,380	75.00	10.9	Upper Marker	113.00

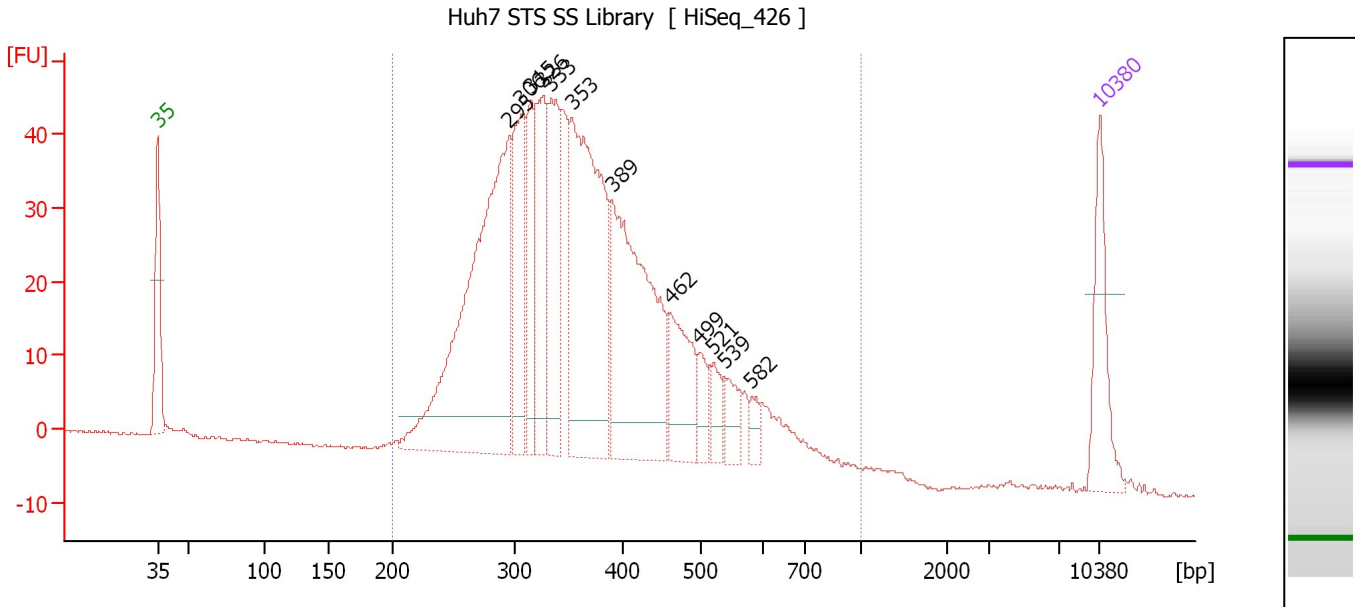
Region table for sample 5 : Huh7 Rap SS Library

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	1,568.7	12,734.3	2,892.72	95	34.4

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Electropherogram Summary Continued ...



Overall Results for sample 6 : Huh7 STS SS Library

Number of peaks found: 12 Corr. Area 1: 963.5
 Noise: 0.2

Peak table for sample 6 : Huh7 STS SS Library

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	295	579.76	2,973.6		69.14
3	306	163.71	810.9		70.03
4	315	108.92	524.7		70.73
5	326	158.32	736.6		71.63
6	333	154.59	703.2		72.22
7	353	399.40	1,715.1		73.82
8	389	343.34	1,336.4		76.76
9	462	103.18	338.5		81.14
10	499	28.92	87.7		83.28
11	521	31.59	91.9		84.27
12	539	34.92	98.2		85.12
13	582	17.06	44.4		87.11
14	10,380	75.00	10.9	Upper Marker	113.00

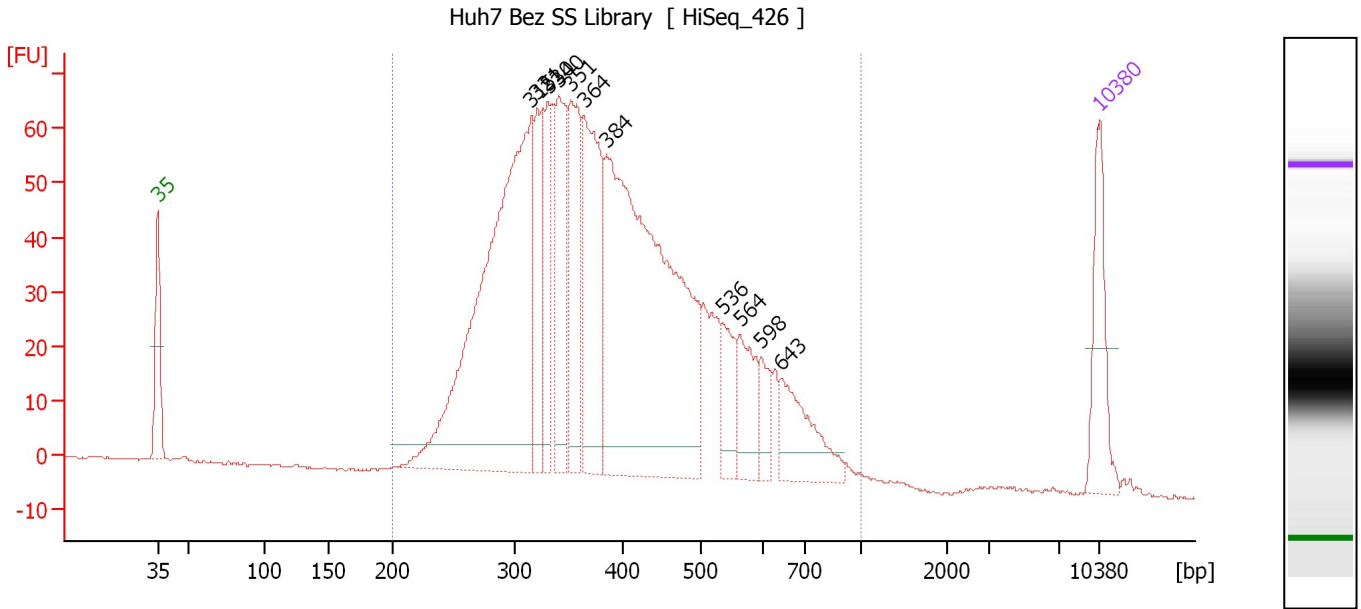
Region table for sample 6 : Huh7 STS SS Library

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	372	963.5	10,337.6	2,339.10	99	26.4

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Electropherogram Summary Continued ...



Overall Results for sample 7 : Huh7 Bez SS Library

Number of peaks found: 11 Corr. Area 1: 1,491.5
 Noise: 0.2

Peak table for sample 7 : Huh7 Bez SS Library

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	315	733.76	3,527.8		70.78
3	321	114.17	539.3		71.23
4	330	113.87	522.7		71.98
5	340	164.70	733.9		72.79
6	351	166.97	720.3		73.69
7	364	233.00	970.8		74.69
8	384	738.39	2,916.8		76.30
9	536	58.38	165.1		84.97
10	564	74.36	199.9		86.27
11	598	34.15	86.5		87.88
12	643	93.91	221.2		89.33
13	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : Huh7 Bez SS Library

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	402	1,491.5	11,245.5	2,700.49	99	29.0

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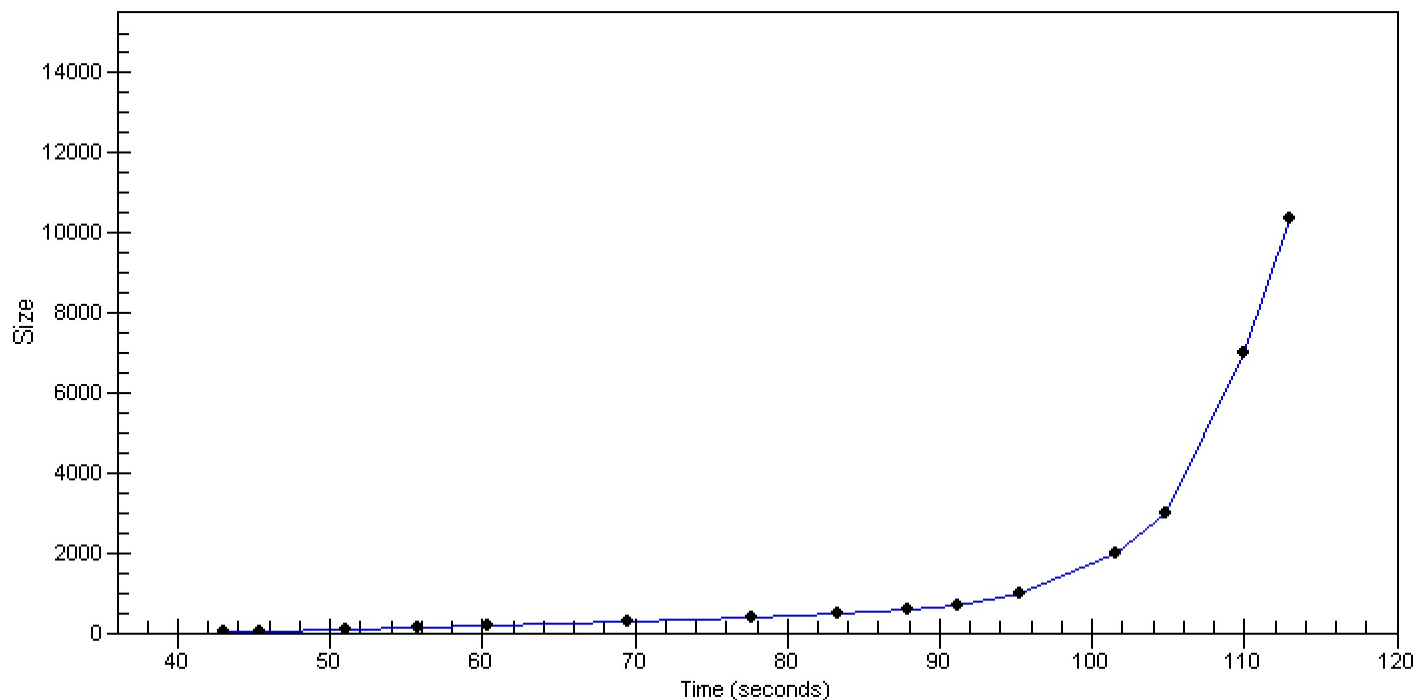
Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...04-12\2016-04-12_006_HiSeq426_SizeSelectedLibraries_1-6.xad

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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		4/12/2016 5:22:30 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\2016-04-12\2016-04-12_006.xad)		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		4/12/2016 4:42:09 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1