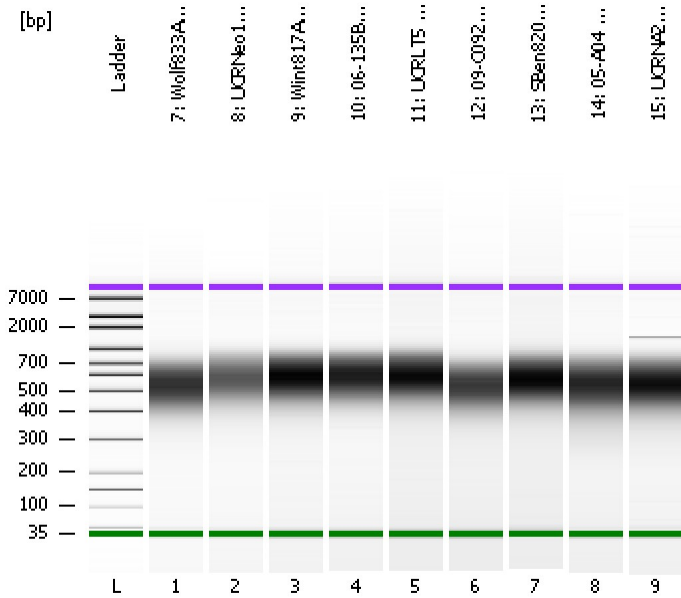


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
Modified: 10/3/2016 3:50:51 PM

Electrophoresis File Run Summary



Instrument Information:

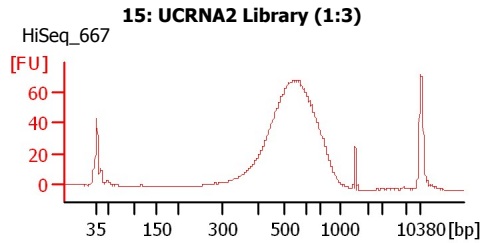
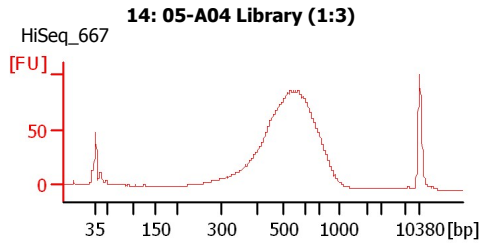
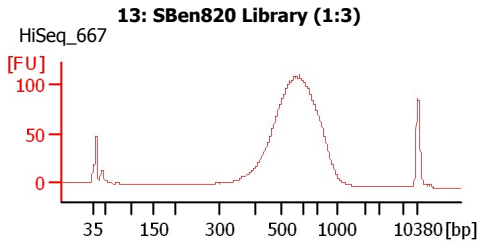
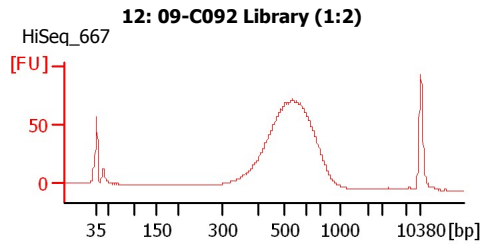
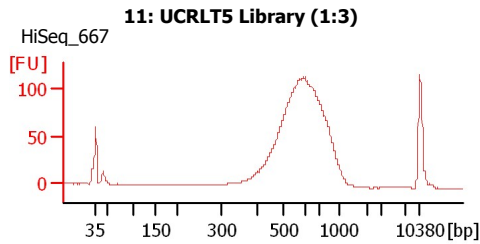
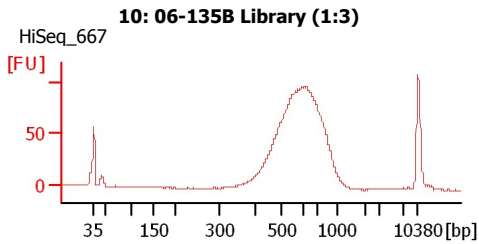
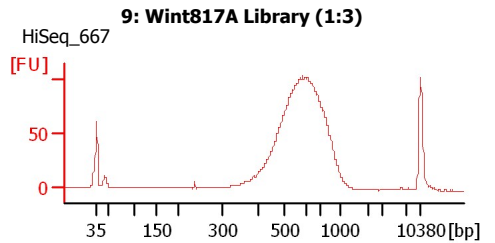
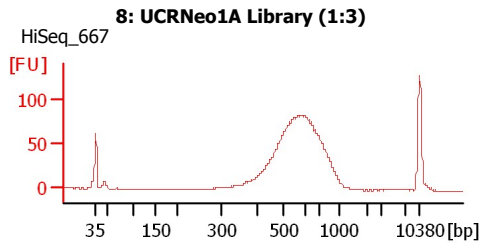
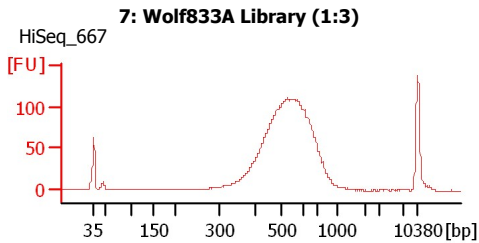
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:



Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
7: Wolf833A Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
8: UCRNeo1A Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
9: Wint817A Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
10: 06-135B Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
11: UCRLT5 Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
12: 09-C092 Library (1:2)	HiSeq_667	<input type="checkbox"/>		✓		
13: SBen820 Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
14: 05-A04 Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
15: UCRNA2 Library (1:3)	HiSeq_667	<input type="checkbox"/>		✓		
Ladder		<input type="checkbox"/>		✓		

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

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

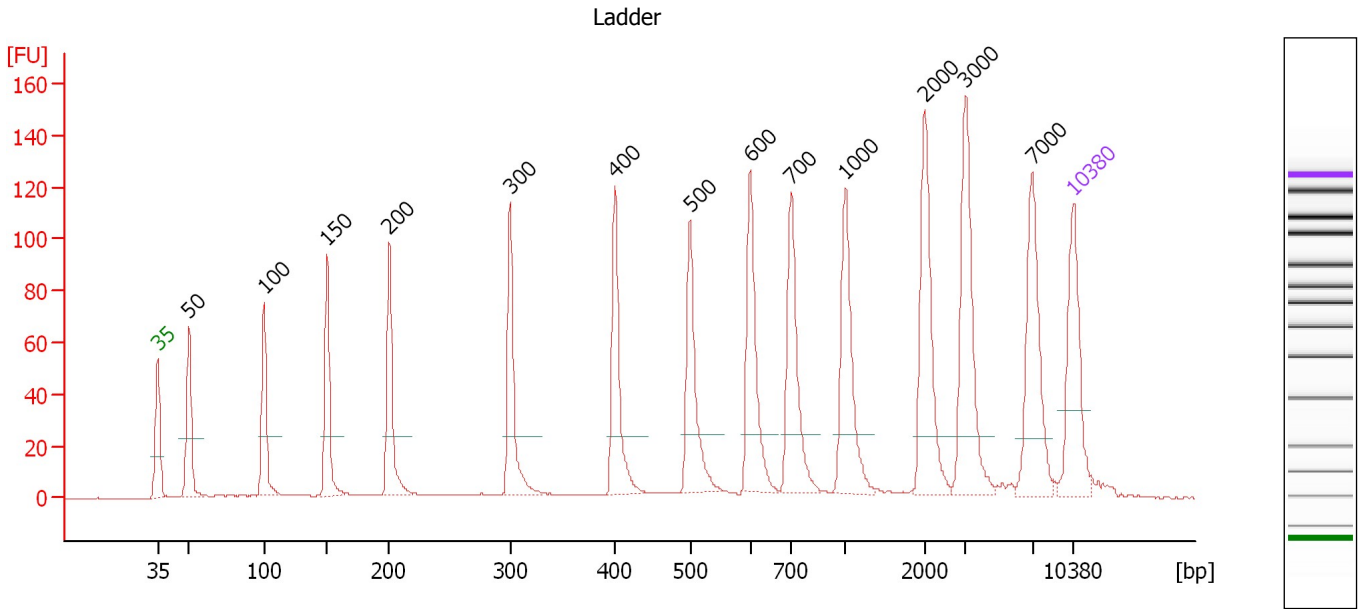
Ladder

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:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

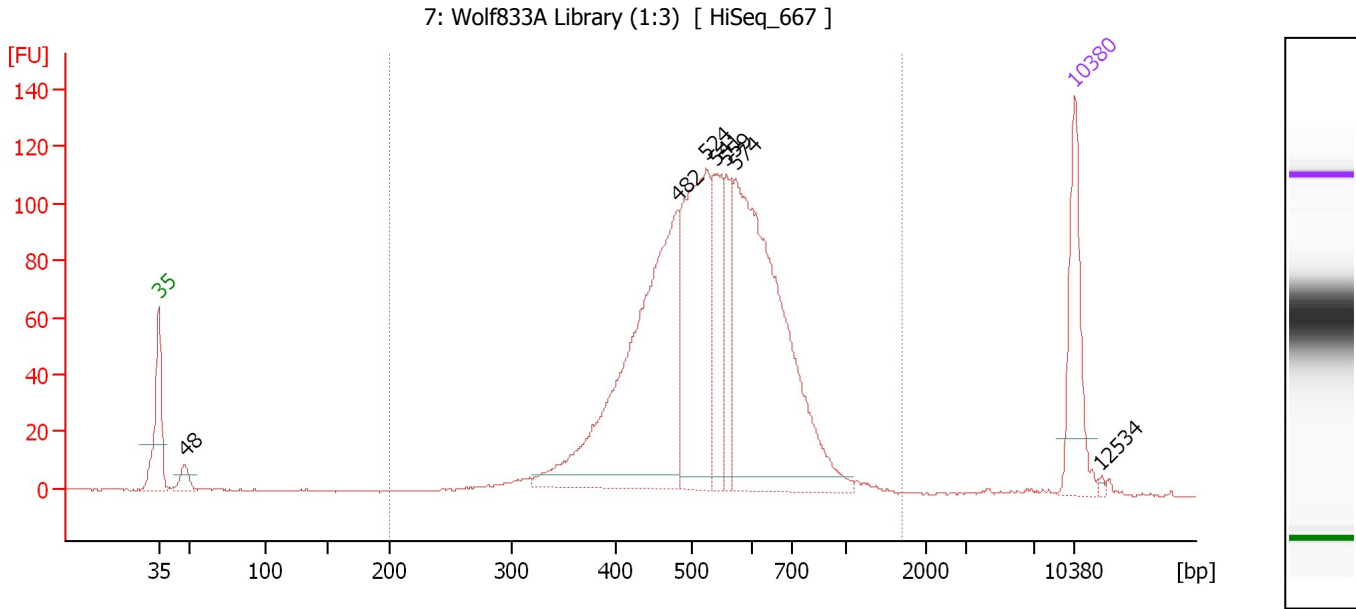
Peak table for Ladder

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	45.40
3	100	150.00	2,272.7	Ladder Peak	51.10
4	150	150.00	1,515.2	Ladder Peak	55.95
5	200	150.00	1,136.4	Ladder Peak	60.70
6	300	150.00	757.6	Ladder Peak	69.95
7	400	150.00	568.2	Ladder Peak	77.95
8	500	150.00	454.5	Ladder Peak	83.70
9	600	150.00	378.8	Ladder Peak	88.30
10	700	150.00	324.7	Ladder Peak	91.45
11	1,000	150.00	227.3	Ladder Peak	95.55
12	2,000	150.00	113.6	Ladder Peak	101.60
13	3,000	150.00	75.8	Ladder Peak	104.75
14	7,000	150.00	32.5	Ladder Peak	109.85
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : 7: Wolf833A Library (1:3)

Number of peaks found: 7 Corr. Area 1: 1,681.6
 Noise: 0.2

Peak table for sample 1 : 7: Wolf833A Library (1:3)

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	48	19.49	621.1		45.01
3	482	440.20	1,382.4		82.69
4	524	250.58	724.7		84.80
5	541	100.27	280.6		85.60
6	559	66.33	179.8		86.41
7	574	437.57	1,154.9		87.11
8	10,380	75.00	10.9	Upper Marker	113.00
9	12,534	0.00	0.0		115.01

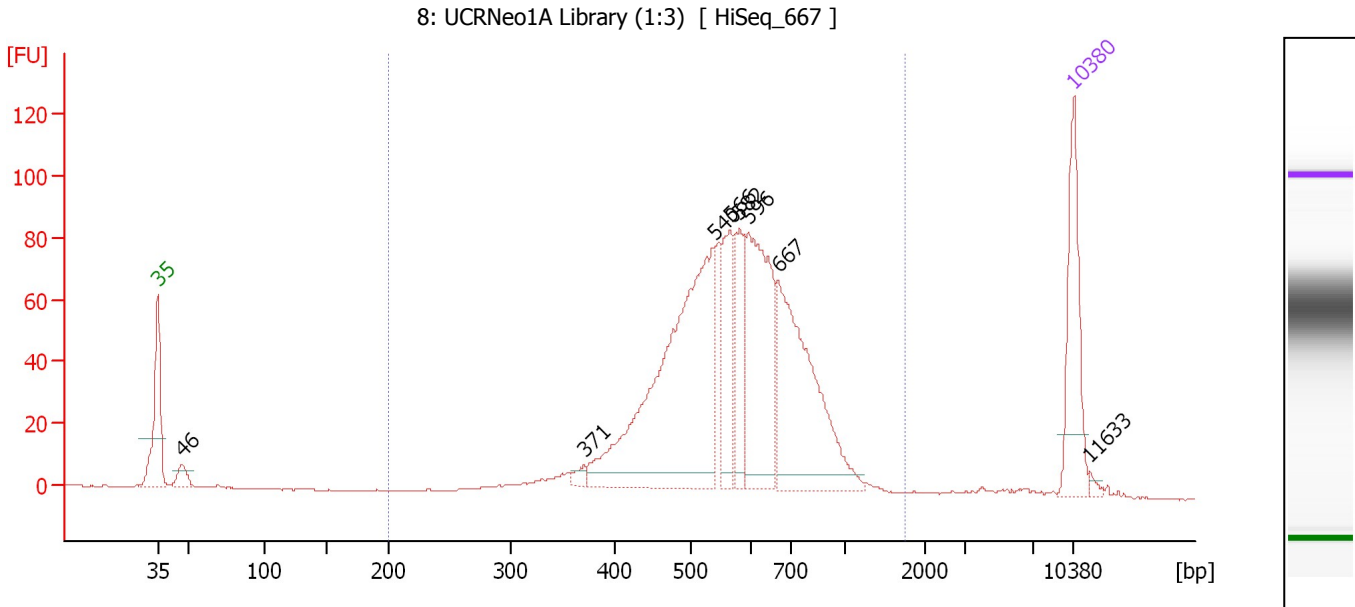
Region table for sample 1 : 7: Wolf833A Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,699	544	1,681.6	4,117.7	1,380.93	97	24.4

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : 8: UCRNeo1A Library (1:3)

Number of peaks found: 8 Corr. Area 1: 1,164.0
 Noise: 0.2

Peak table for sample 2 : 8: UCRNeo1A Library (1:3)

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	19.75	644.7		44.83
3	371	8.18	33.4		75.64
4	540	380.67	1,068.2		85.54
5	566	76.33	204.2		86.76
6	582	62.88	163.7		87.47
7	596	175.58	446.2		88.13
8	667	215.64	489.8		90.41
9	10,380	75.00	10.9	Upper Marker	113.00
10	11,633	0.00	0.0		114.17

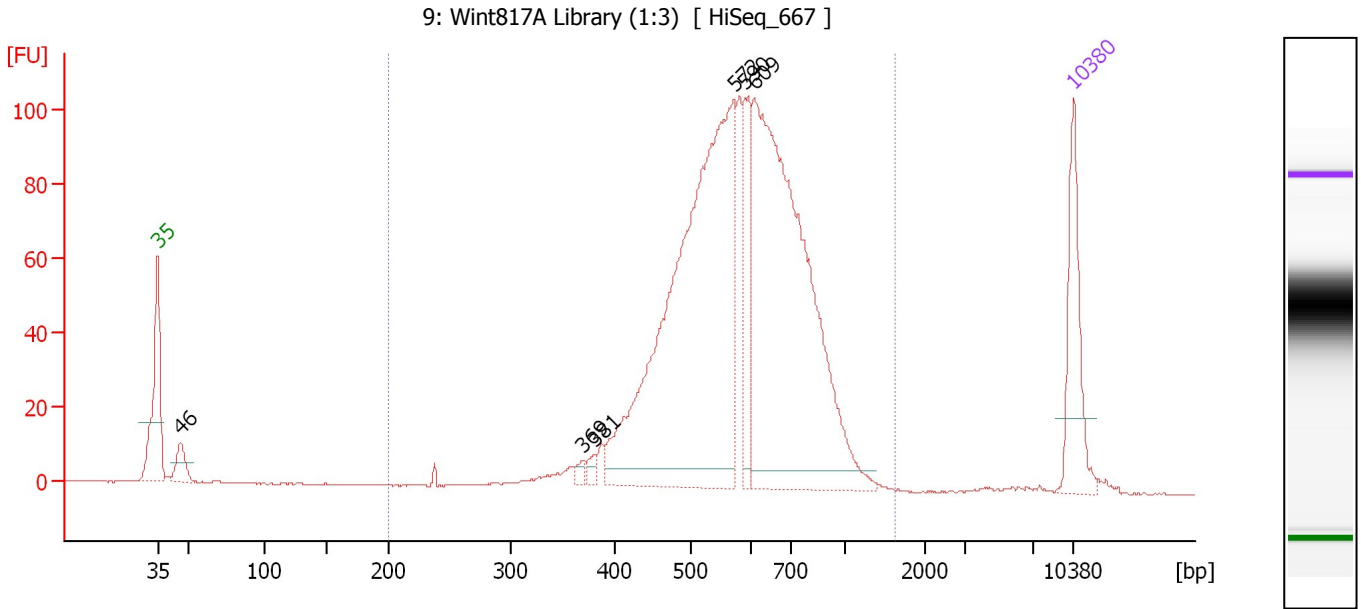
Region table for sample 2 : 8: UCRNeo1A Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,758	591	1,164.0	2,888.6	1,049.14	97	25.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : 9: Wint817A Library (1:3)

Number of peaks found: 6 Corr. Area 1: 1,411.4
 Noise: 0.2

Peak table for sample 3 : 9: Wint817A Library (1:3)

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	31.37	1,034.0		44.76
3	369	7.17	29.4		75.47
4	381	8.44	33.6		76.40
5	572	642.96	1,701.7		87.03
6	590	81.38	208.8		87.86
7	609	569.78	1,417.6		88.58
8	10,380	75.00	10.9	Upper Marker	113.00

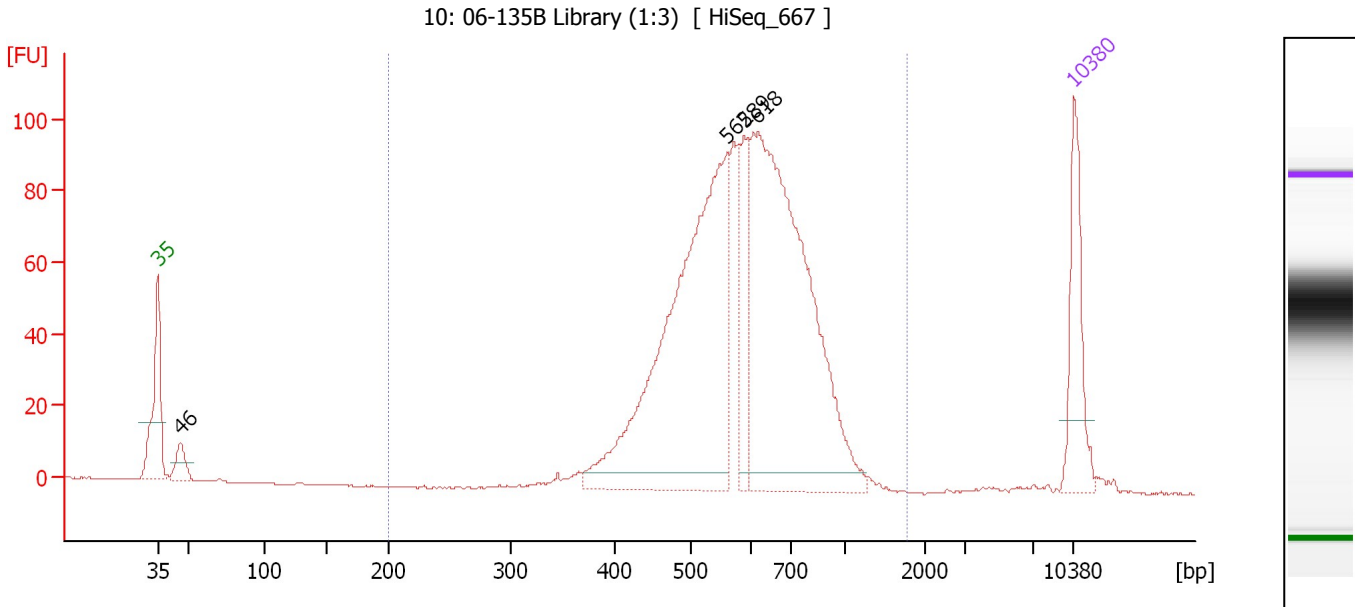
Region table for sample 3 : 9: Wint817A Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,639	602	1,411.4	4,061.5	1,501.29	96	24.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : 10: 06-135B Library (1:3)

Number of peaks found: 4 Corr. Area 1: 1,276.4
 Noise: 0.2

Peak table for sample 4 : 10: 06-135B Library (1:3)

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	30.43	1,005.6		44.74
3	562	540.01	1,456.2		86.55
4	589	78.81	202.6		87.81
5	618	543.15	1,332.1		88.86
6	10,380	75.00	10.9	Upper Marker	113.00

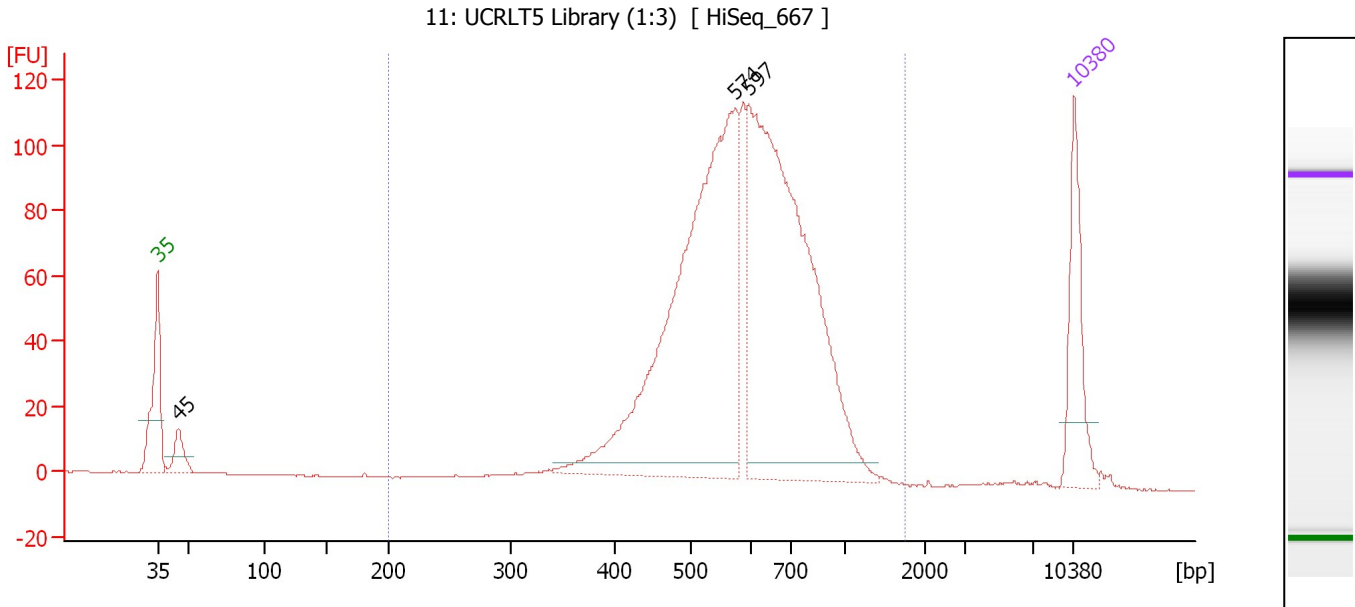
Region table for sample 4 : 10: 06-135B Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,780	611	1,276.4	3,350.1	1,272.79	97	23.1

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : 11: UCRLT5 Library (1:3)

Number of peaks found: 3 Corr. Area 1: 1,526.2
 Noise: 0.2

Peak table for sample 5 : 11: UCRLT5 Library (1:3)

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	36.75	1,237.0		44.60
3	574	616.60	1,627.6		87.10
4	597	603.01	1,529.9		88.17
5	10,380	75.00	10.9	Upper Marker	113.00

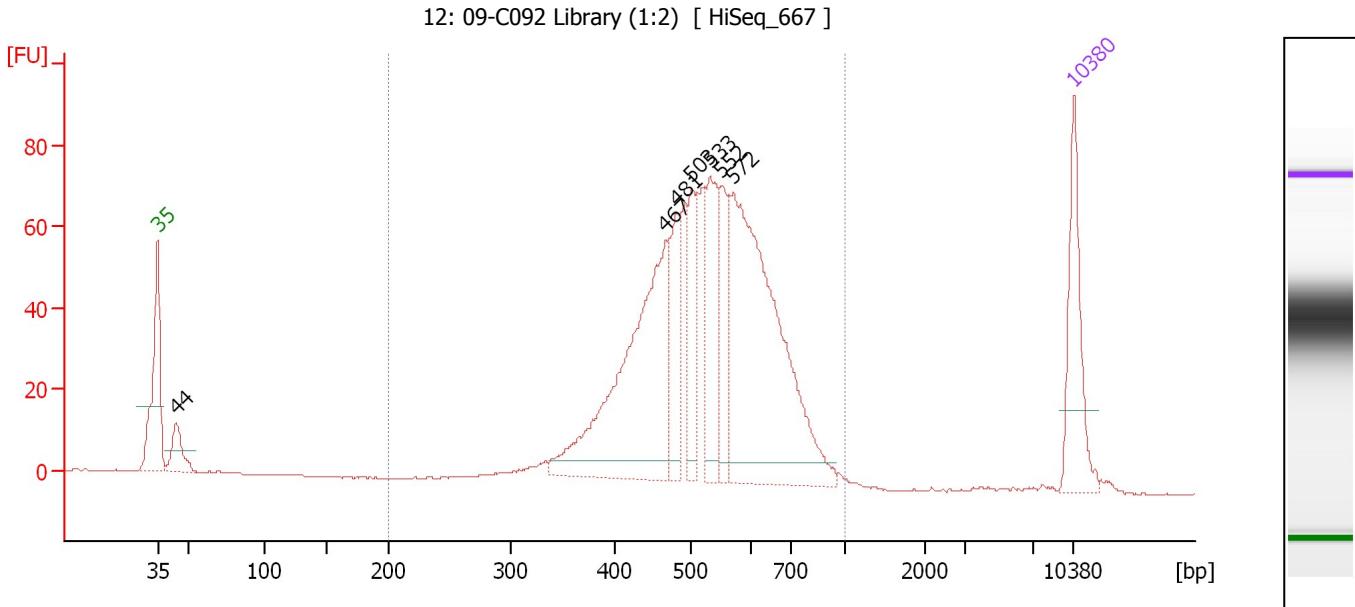
Region table for sample 5 : 11: UCRLT5 Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,749	615	1,526.2	3,730.6	1,400.62	96	26.0

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 6 : 12: 09-C092 Library (1:2)

Number of peaks found: 7 Corr. Area 1: 1,021.8
 Noise: 0.2

Peak table for sample 6 : 12: 09-C092 Library (1:2)

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	44	43.34	1,487.7		44.46
3	467	326.74	1,059.5		81.82
4	481	78.21	246.2		82.63
5	503	69.34	209.0		83.82
6	533	106.24	301.9		85.23
7	552	70.91	194.6		86.09
8	572	382.93	1,014.3		87.01
9	10,380	75.00	10.9	Upper Marker	113.00

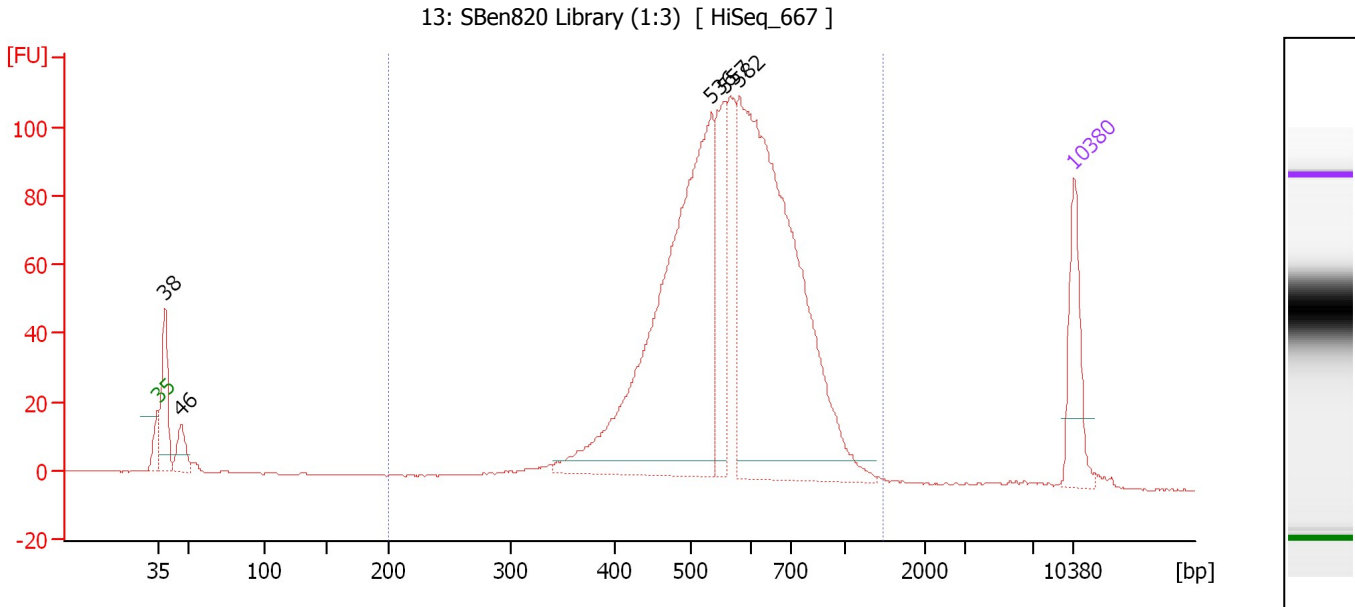
Region table for sample 6 : 12: 09-C092 Library (1:2)

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	533	1,021.8	3,570.1	1,193.20	97	19.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : 13: SBen820 Library (1:3)

Number of peaks found: 5 Corr. Area 1: 1,510.6
 Noise: 0.2

Peak table for sample 7 : 13: SBen820 Library (1:3)

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	38	116.53	4,595.3		43.55
3	46	45.97	1,504.4		44.81
4	536	716.75	2,027.5		85.34
5	557	132.86	361.4		86.33
6	582	784.36	2,041.7		87.48
7	10,380	75.00	10.9	Upper Marker	113.00

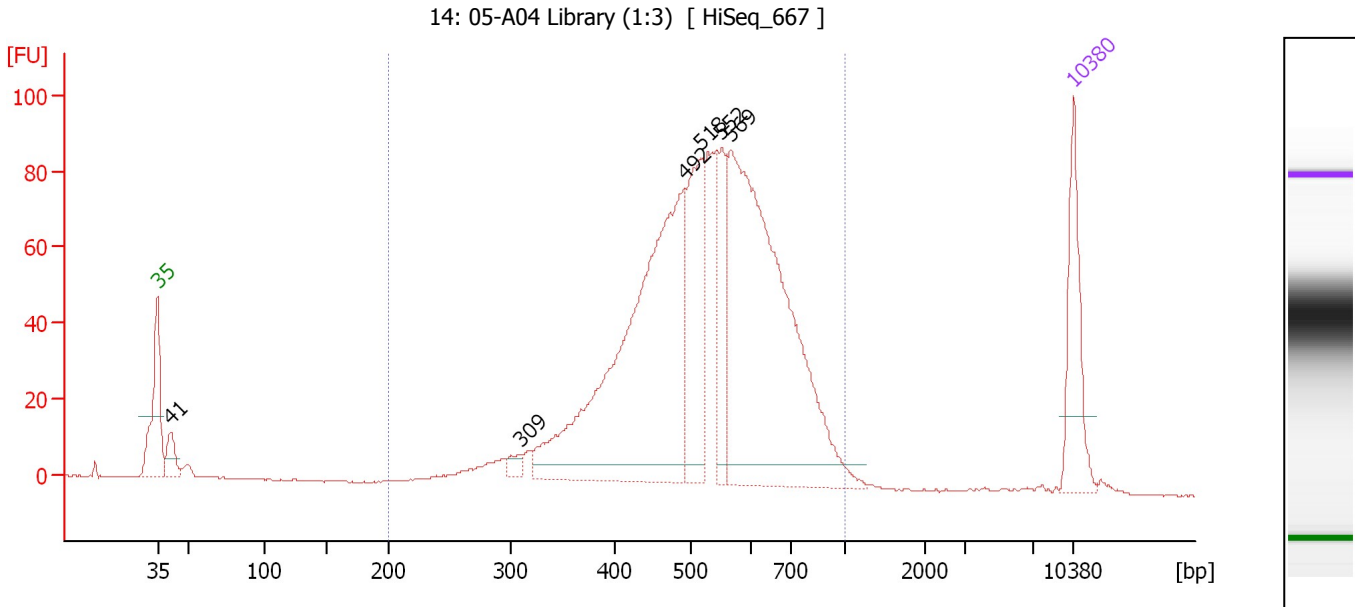
Region table for sample 7 : 13: SBen820 Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,482	583	1,510.6	5,338.0	1,902.83	91	24.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : 14: 05-A04 Library (1:3)

Number of peaks found: 6 Corr. Area 1: 1,353.4
 Noise: 0.2

Peak table for sample 8 : 14: 05-A04 Library (1:3)

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	41	33.44	1,226.8		44.01
3	309	11.80	57.8		70.70
4	492	560.55	1,726.8		83.23
5	518	151.93	444.6		84.52
6	552	79.77	219.0		86.09
7	569	548.76	1,461.5		86.87
8	10,380	75.00	10.9	Upper Marker	113.00

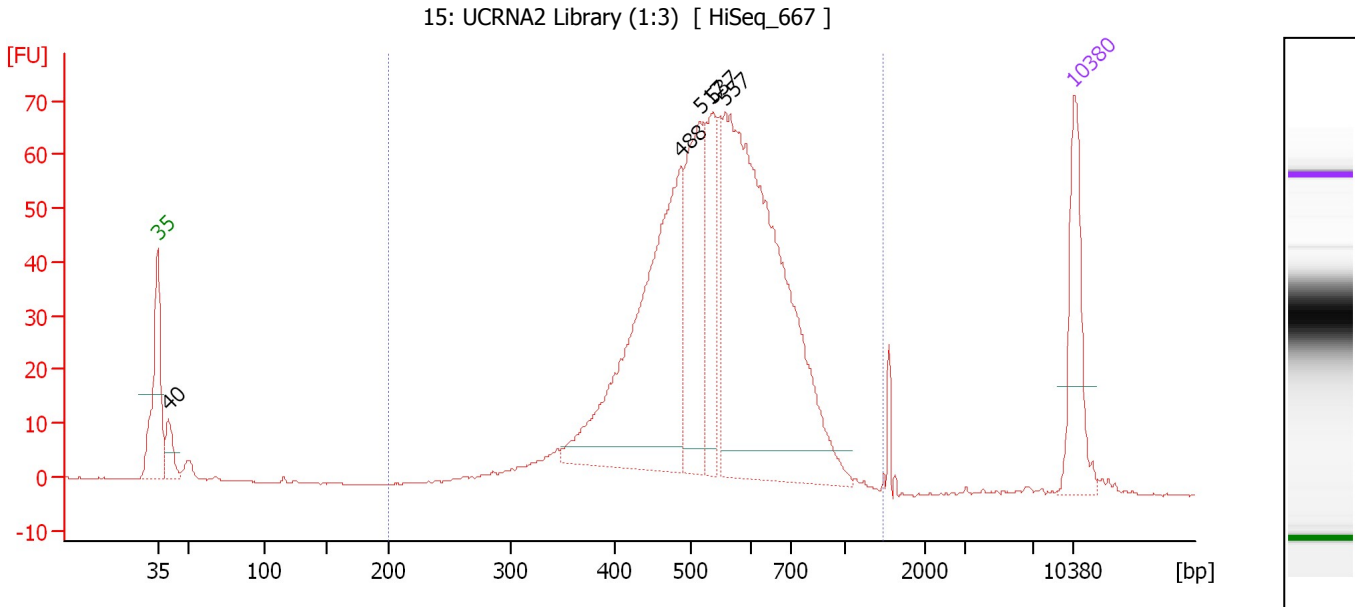
Region table for sample 8 : 14: 05-A04 Library (1:3)

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	535	1,353.4	4,781.9	1,560.07	97	23.3

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
 Modified: 10/3/2016 3:50:51 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : 15: UCRNA2 Library (1:3)

Number of peaks found: 5 Corr. Area 1: 961.5
 Noise: 0.1

Peak table for sample 9 : 15: UCRNA2 Library (1:3)

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	40	35.33	1,328.4		43.85
3	488	404.81	1,255.9		83.03
4	517	167.59	490.7		84.50
5	537	105.40	297.3		85.41
6	557	575.39	1,565.8		86.31
7	10,380	75.00	10.9	Upper Marker	113.00

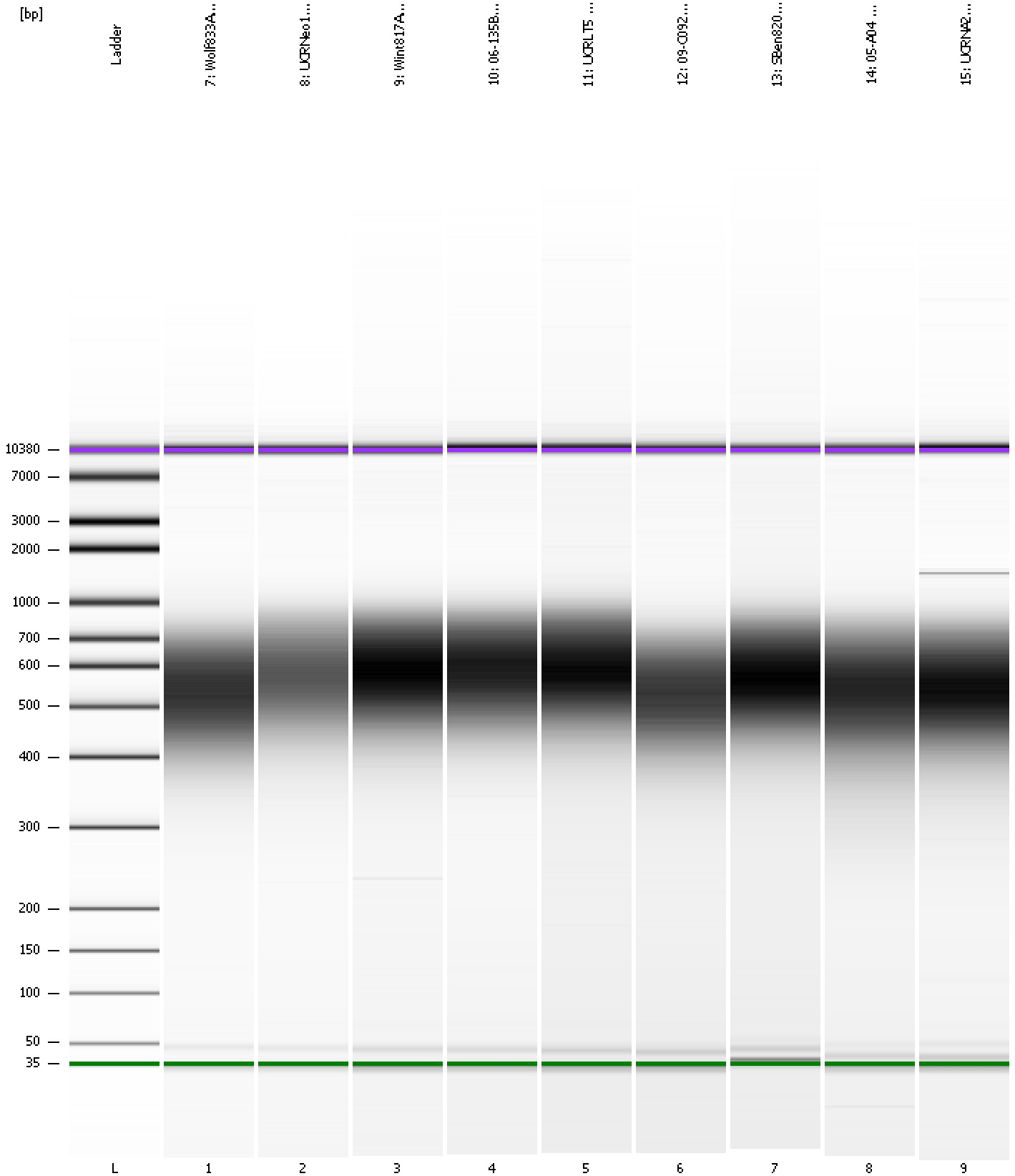
Region table for sample 9 : 15: UCRNA2 Library (1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,480	548	961.5	4,217.5	1,425.72	96	22.6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad

Created: 10/3/2016 2:57:23 PM
Modified: 10/3/2016 3:50:51 PM

Gel Image



Assay Class: High Sensitivity DNA Assay Created: 10/3/2016 2:57:23 PM
 Data Path: C:\...\data\2016-10-03\2016-10-03_004_HiSeq667_Libraries_7-15.xad Modified: 10/3/2016 3:50:51 PM

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		10/3/2016 3:38:40 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\2016-10-03\2016-10-03_004.xad)		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/3/2016 2:57:28 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1