Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electrophoresis File Run Summary

Instrument Information:

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

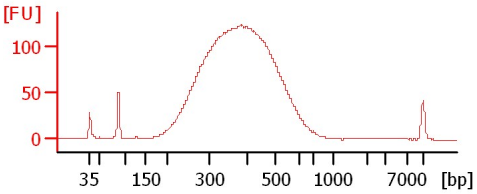
Assay Information:

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

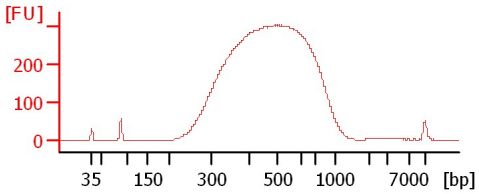
Chip Information:

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

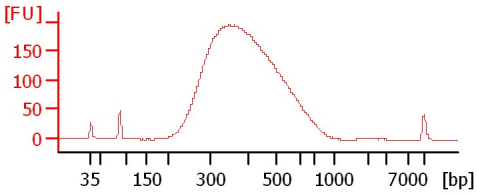
dripseq hela1 i3



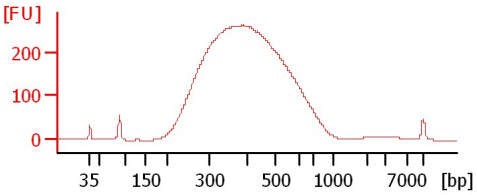
dripseq hela2 i8



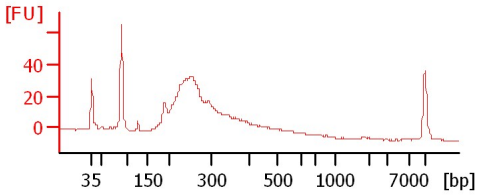
dripseq hela1RH i9



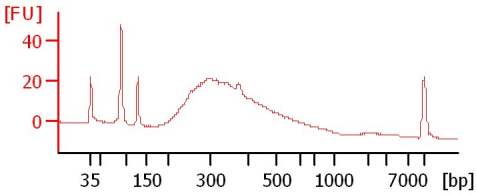
dripCseq hela1 i20



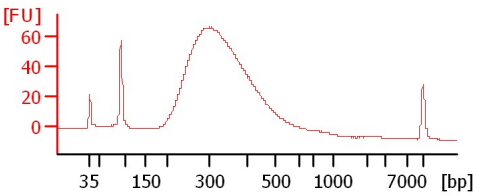
dripCseq hela2 i21



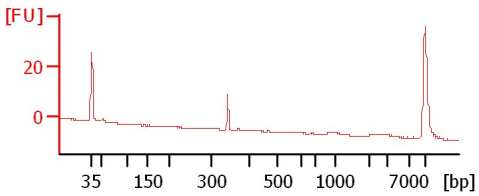
dripCseq nt2 RA i22



dripseq nt2 sonic i23



sample 8



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
dripseq hela1 i3		☐	✔			
dripseq hela2 i8		☐	✔			
dripseq hela1RH i9		☐	✔			
dripCseq hela1 i20		☐	✔			
dripCseq hela2 i21		☐	✔			
dripCseq nt2 RA i22		☐	✔			
dripseq nt2 sonic i23		☐	✔			
sample 8		☐	✔			
sample 9		☐				
sample 10		☐				
sample 11		☐				
Ladder		☐	✔			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 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

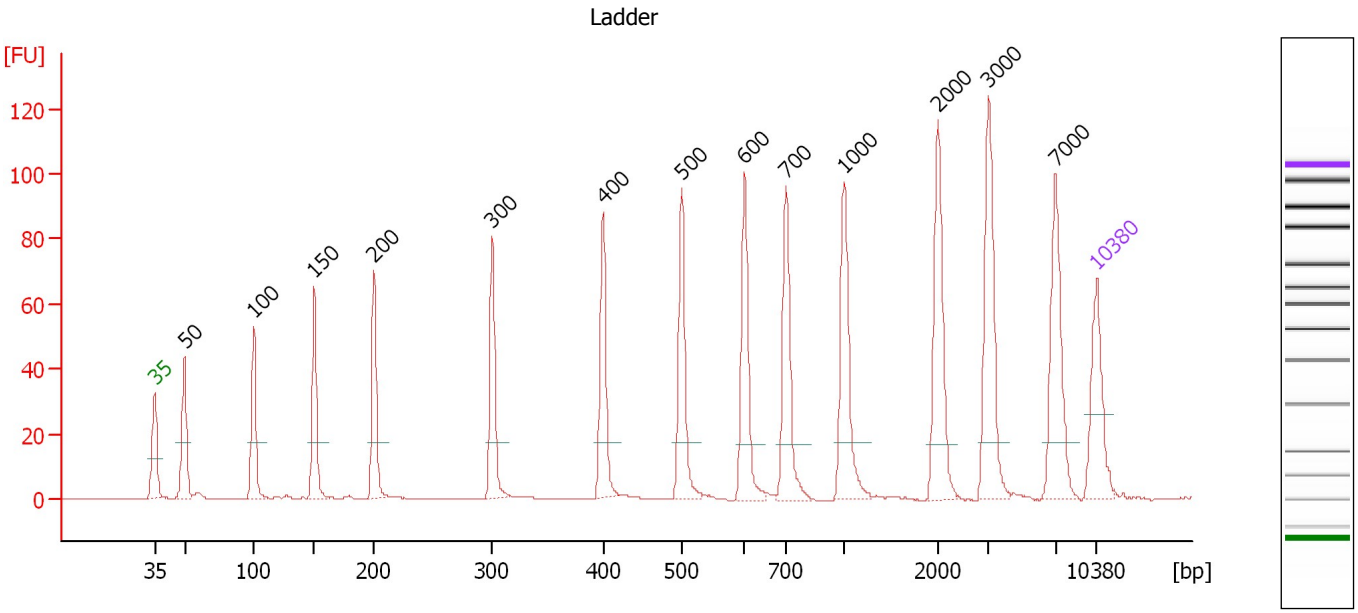
Ladder

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:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

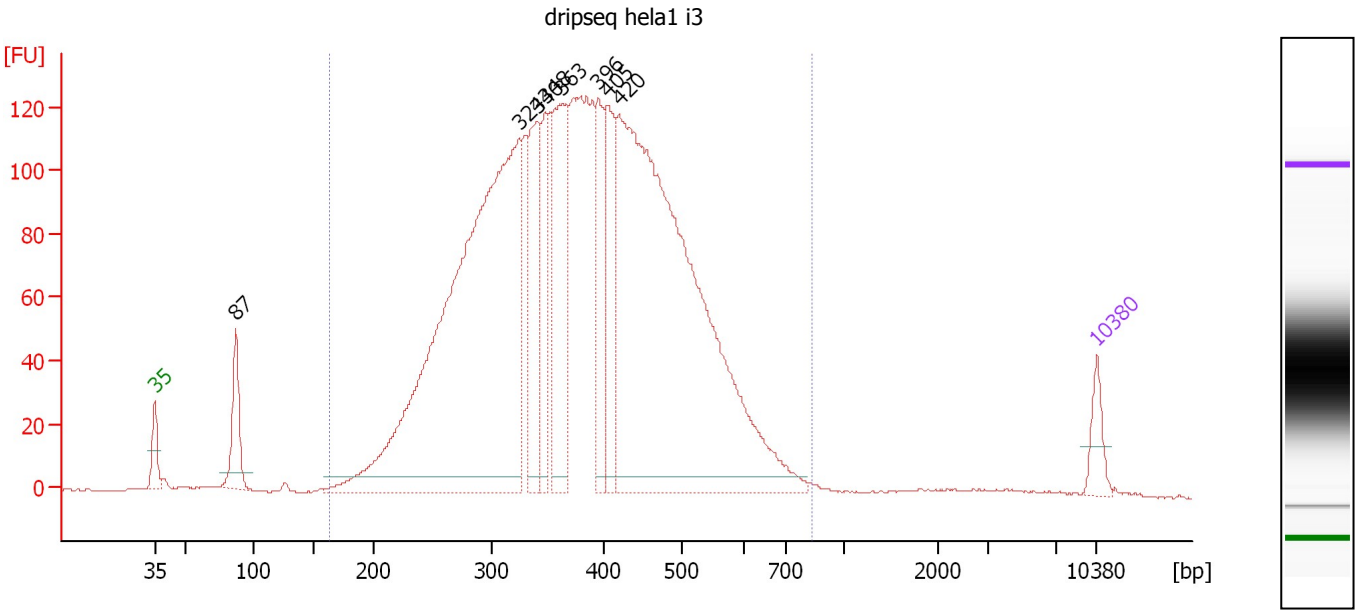
Peak table for Ladder

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	45.23
3		100	150.00	2,272.7	Ladder Peak	50.38
4		150	150.00	1,515.2	Ladder Peak	54.88
5		200	150.00	1,136.4	Ladder Peak	59.28
6		300	150.00	757.6	Ladder Peak	68.10
7		400	150.00	568.2	Ladder Peak	76.31
8		500	150.00	454.5	Ladder Peak	82.15
9		600	150.00	378.8	Ladder Peak	86.84
10		700	150.00	324.7	Ladder Peak	89.90
11		1,000	150.00	227.3	Ladder Peak	94.26
12		2,000	150.00	113.6	Ladder Peak	101.17
13		3,000	150.00	75.8	Ladder Peak	104.93
14		7,000	150.00	32.5	Ladder Peak	109.89
15		10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : dripseq hela1 i3

Number of peaks found:	8	Corr. Area 1:	3,123.9
Noise:	0.1		

Peak table for sample 1 : dripseq hela1 i3

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	87	266.45	4,645.0		49.03
3	324	3,194.33	14,943.9		70.06
4	340	483.70	2,153.1		71.41
5	348	317.65	1,383.9		72.02
6	363	653.52	2,731.0		73.23
7	396	339.14	1,297.1		75.99
8	405	394.90	1,477.4		76.60
9	420	3,088.98	11,138.9		77.49
10	10,380	75.00	10.9	Upper Marker	113.00

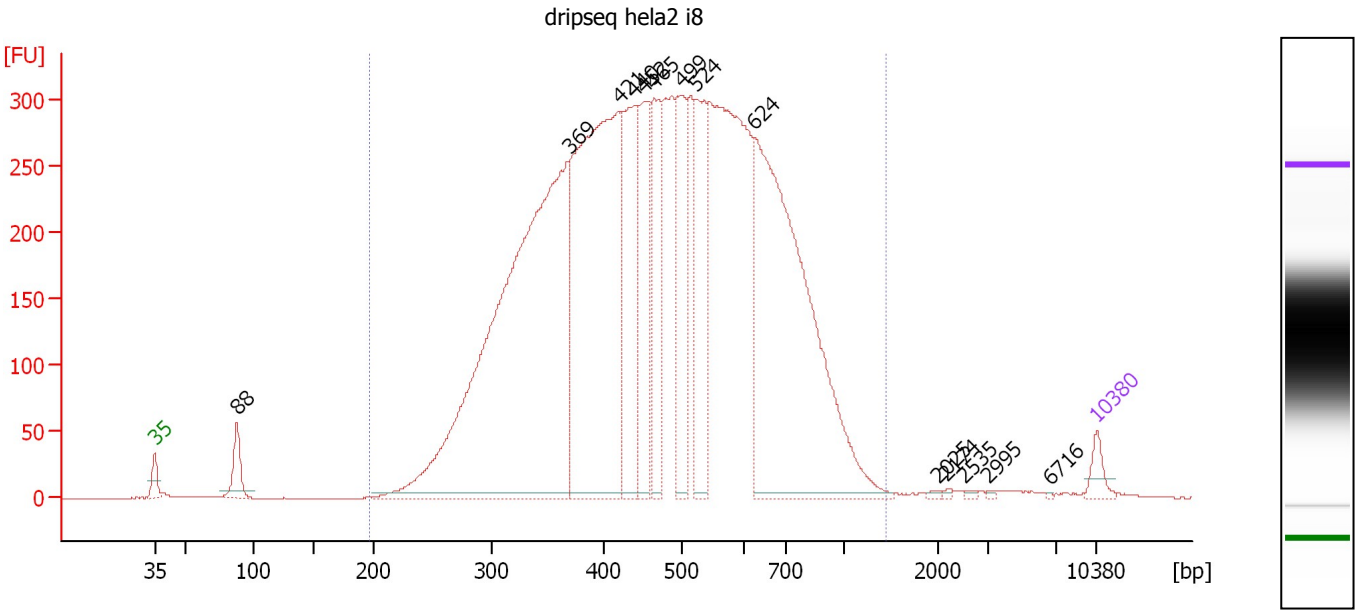
Region table for sample 1 : dripseq hela1 i3

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
162	829	388	3,123.9	42,972.1	10,023.29	96	25.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : dripseq hela2 i8

Number of peaks found:	14	Corr. Area 1:	8,378.4
Noise:	0.2		

Peak table for sample 2 : dripseq hela2 i8

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	88	230.56	3,976.0		49.13
3	369	4,832.19	19,837.1		73.77
4	421	3,097.08	11,157.6		77.51
5	440	1,016.22	3,501.2		78.63
6	452	746.82	2,504.7		79.33
7	465	625.86	2,037.7		80.13
8	499	692.29	2,102.2		82.09
9	524	733.67	2,122.8		83.26
10	624	2,932.21	7,123.2		87.56
11	2,025	12.42	9.3		101.26
12	2,174	8.96	6.2		101.82
13	2,535	10.62	6.3		103.18
14	2,995	7.95	4.0		104.91
15	6,716	5.06	1.1		109.54
16	10,380	75.00	10.9	Upper Marker	113.00

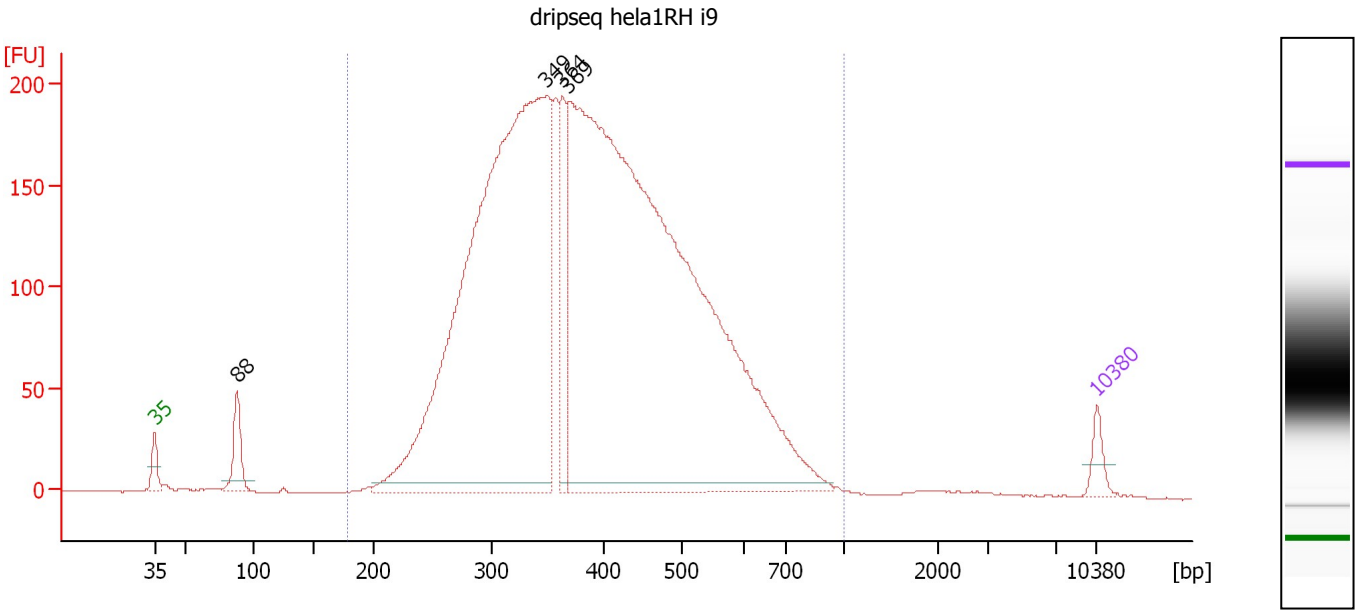
Region table for sample 2 : dripseq hela2 i8

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
196	1,452	497	8,378.4	66,421.6	19,063.27	98	32.8

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 3 : dripseq hela1RH i9

Number of peaks found:	4	Corr. Area 1:	4,724.3
Noise:	0.3		

Peak table for sample 3 : dripseq hela1RH i9

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	88	265.18	4,575.9		49.12
3	349	5,764.43	25,049.5		72.09
4	364	483.45	2,014.7		73.32
5	369	7,914.44	32,520.8		73.74
6	10,380	75.00	10.9	Upper Marker	113.00

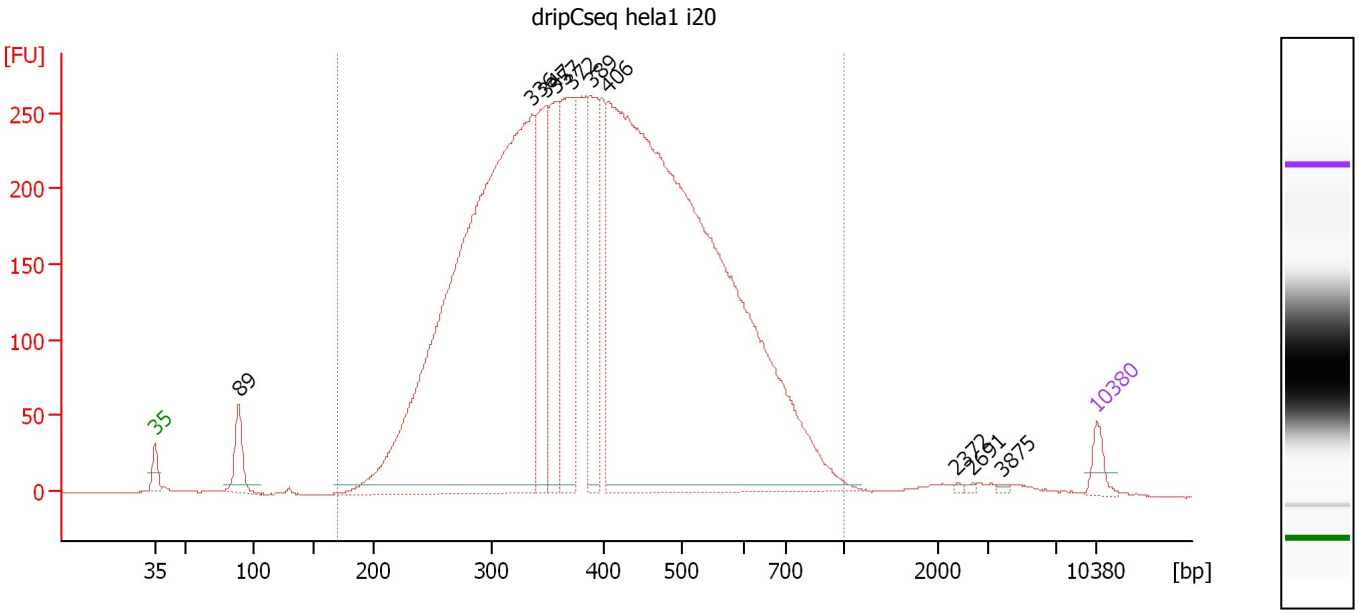
Region table for sample 3 : dripseq hela1RH i9

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
178	1,000	404	4,724.3	59,596.3	14,440.88	98	27.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 4 : dripCseq hela1 i20

Number of peaks found:	10	Corr. Area 1:	7,309.6
Noise:	0.3		

Peak table for sample 4 : dripCseq hela1 i20

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	89	269.59	4,577.0		49.27
3	336	6,307.21	28,406.4		71.09
4	347	833.76	3,635.4		72.00
5	357	785.15	3,328.6		72.81
6	372	1,066.81	4,345.5		74.00
7	389	741.10	2,883.3		75.44
8	406	7,994.44	29,861.1		76.64
9	2,372	7.74	4.9		102.57
10	2,691	8.92	5.0		103.77
11	3,875	10.72	4.2		106.01
12	10,380	75.00	10.9	Upper Marker	113.00

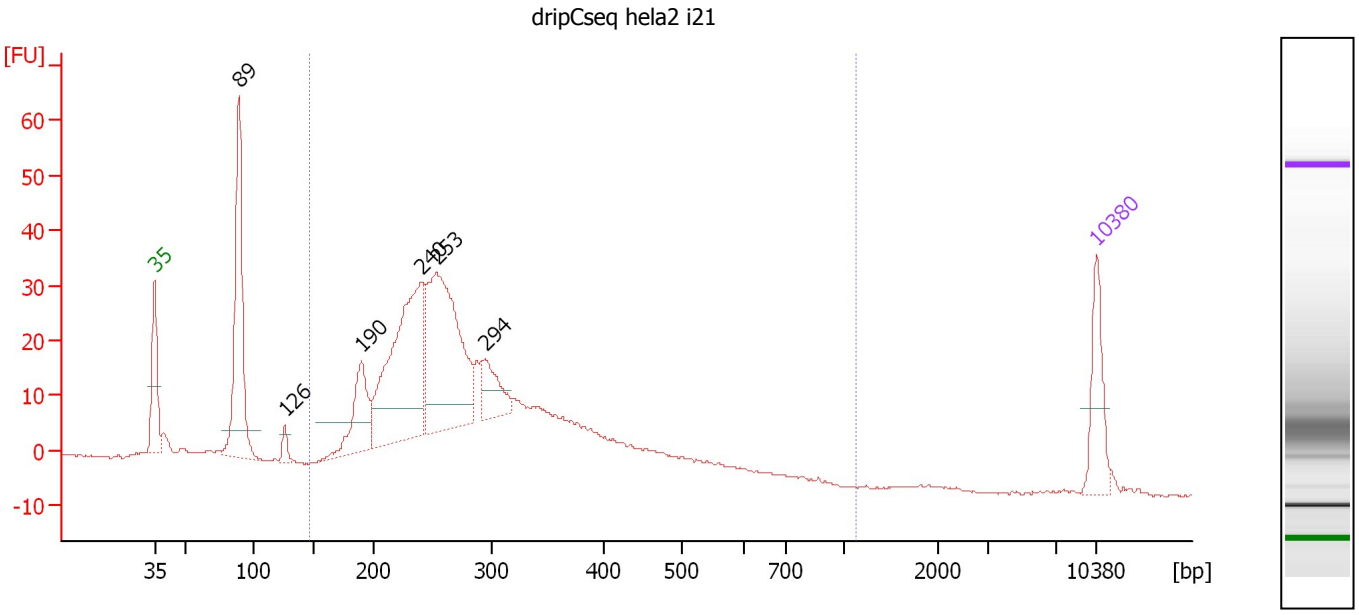
Region table for sample 4 : dripCseq hela1 i20

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
169	1,000	415	7,309.6	79,009.2	19,204.92	97	30.2

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : dripCseq hela2 i21

Number of peaks found:	6	Corr. Area 1:	577.5
Noise:	0.2		

Peak table for sample 5 : dripCseq hela2 i21

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	89	369.33	6,291.5		49.24
3	126	22.20	267.6		52.69
4	190	135.45	1,080.1		58.40
5	240	428.60	2,711.0		62.77
6	253	411.02	2,460.1		63.97
7	294	76.91	396.4		67.56
8	10,380	75.00	10.9	Upper Marker	113.00

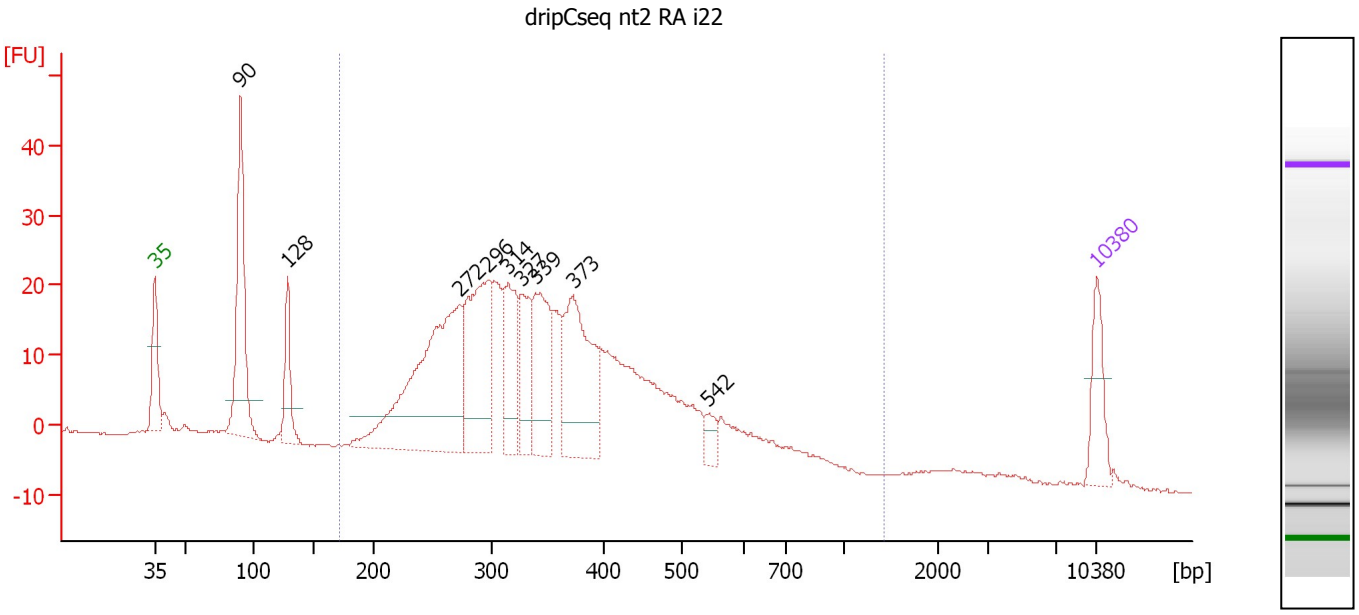
Region table for sample 5 : dripCseq hela2 i21

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
146	1,123	297	577.5	11,274.7	1,981.97	83	32.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 6 : dripCseq nt2 RA i22

Number of peaks found:	9	Corr. Area 1:	586.0
Noise:	0.1		

Peak table for sample 6 : dripCseq nt2 RA i22

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	90	388.87	6,524.9		49.38
3	128	126.94	1,507.9		52.86
4	272	596.79	3,327.1		65.61
5	296	330.05	1,686.9		67.78
6	314	164.42	792.3		69.28
7	327	132.84	615.9		70.29
8	339	214.08	956.5		71.31
9	373	298.87	1,215.1		74.06
10	542	31.63	88.4		84.11
11	10,380	75.00	10.9	Upper Marker	113.00

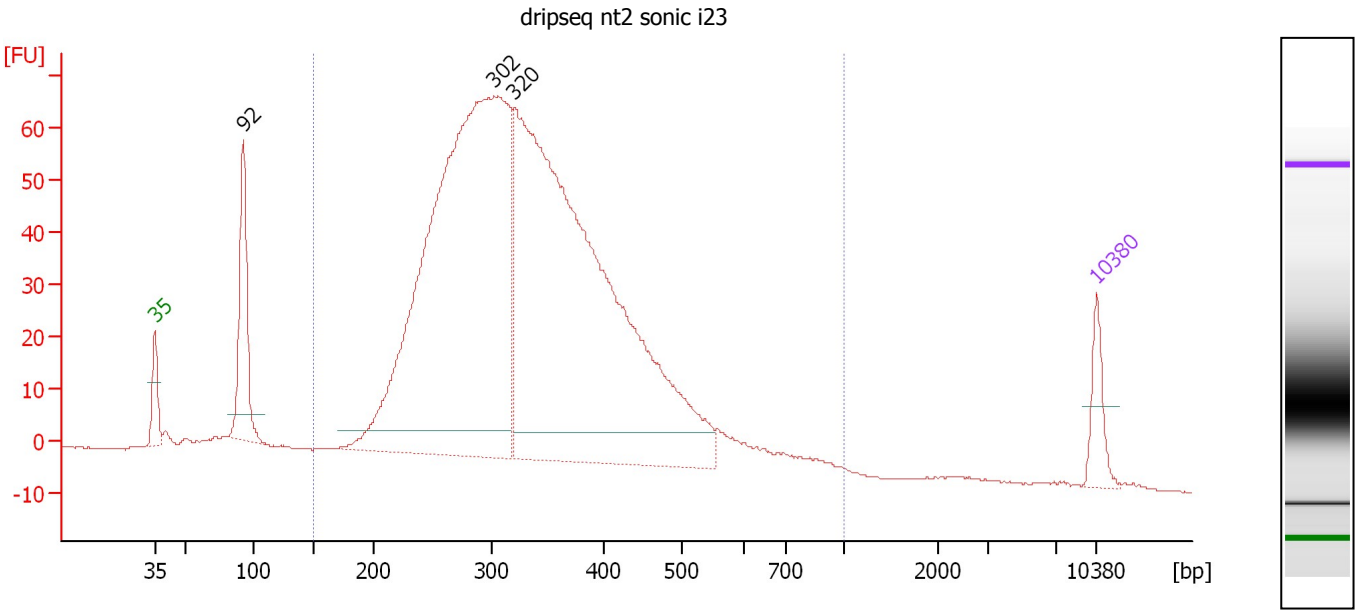
Region table for sample 6 : dripCseq nt2 RA i22

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
172	1,432	371	586.0	12,232.6	2,661.39	84	32.7

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 7 : dripseq nt2 sonic i23

Number of peaks found:	3	Corr. Area 1:	1,479.7
Noise:	0.1		

Peak table for sample 7 : dripseq nt2 sonic i23

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		92	389.32	6,389.2		49.59
3		302	2,756.12	13,850.4		68.22
4		320	2,847.64	13,486.5		69.73
5	▶	10,380	75.00	10.9	Upper Marker	113.00

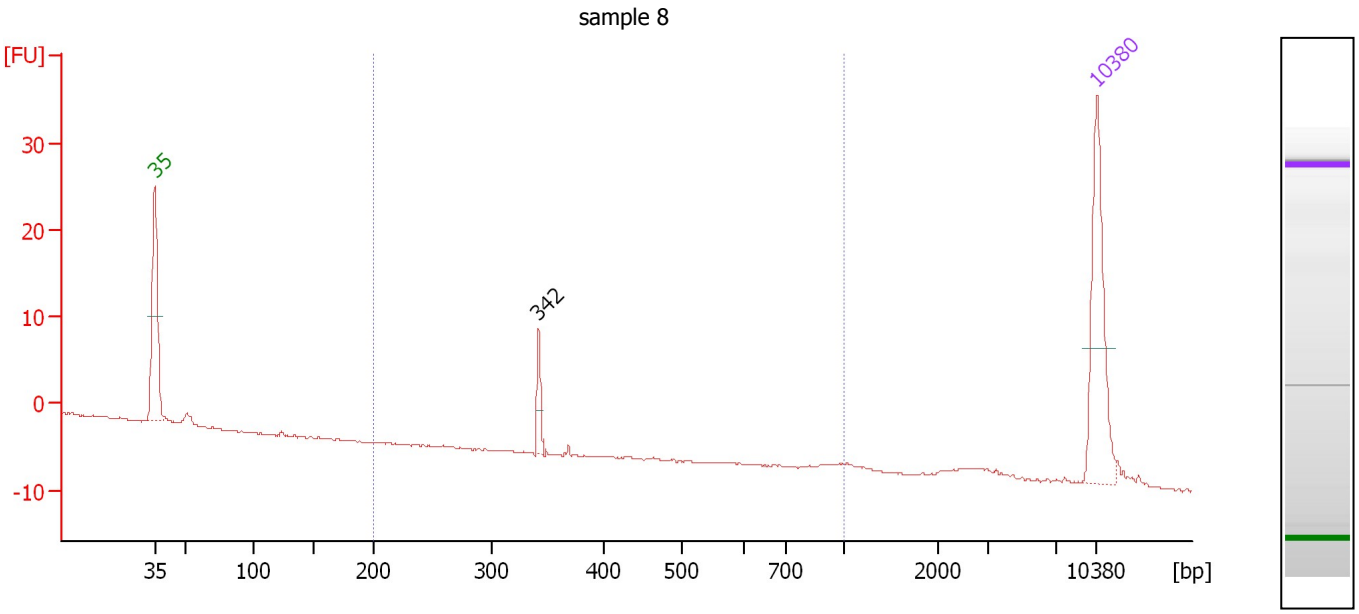
Region table for sample 7 : dripseq nt2 sonic i23

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
149	1,000	345	1,479.7	28,069.1	5,824.32	92	29.6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : sample 8

Number of peaks found:	1	Corr. Area 1:	5.1
Noise:	0.1		

Peak table for sample 8 : sample 8

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	342	17.60	78.1		71.51
3	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 8 : sample 8

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	354	5.1	66.5	15.11	51	24.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

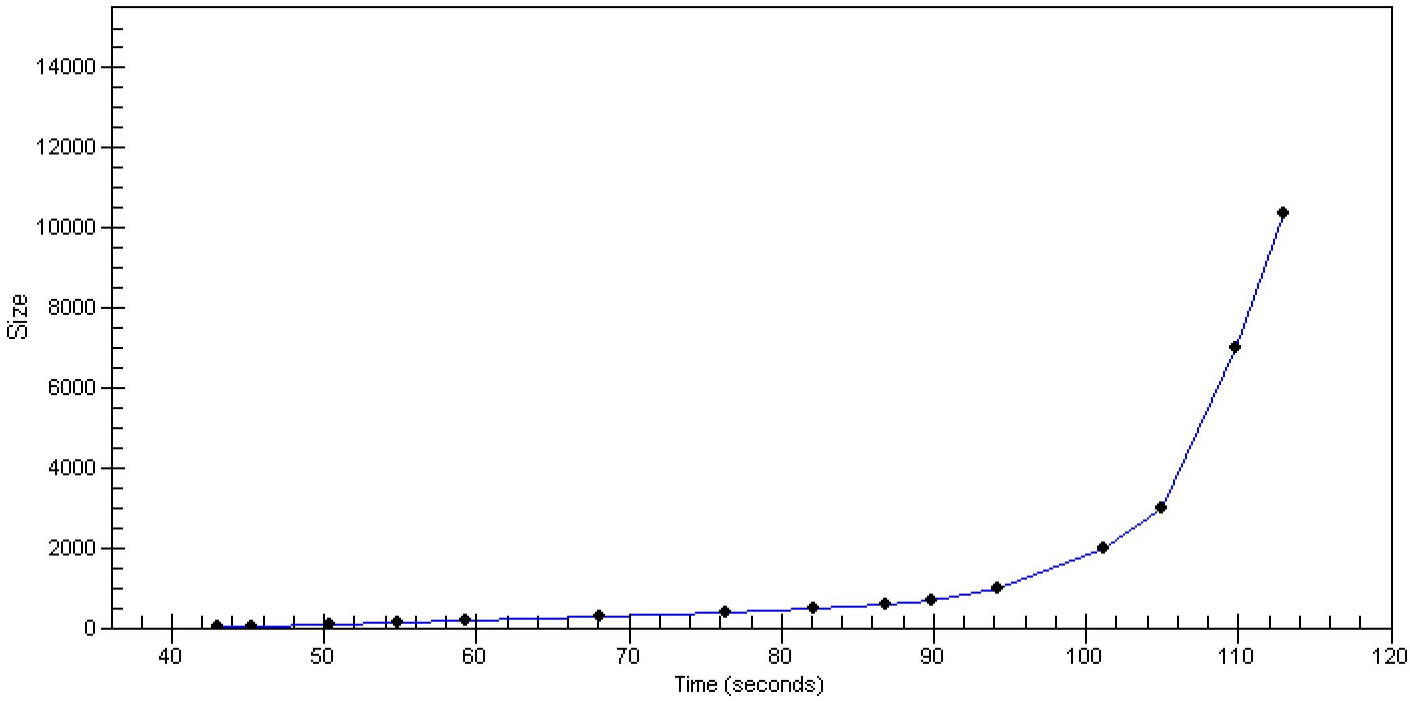
Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Curves

Standard Curve



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Invalid Samples

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\2016-04-18\2016-04-18_002.xad

Created: 4/18/2016 2:55:49 PM
Modified: 4/18/2016 3:28:34 PM

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 9)		Instrument	Run		4/18/2016 3:28:32 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\2016-04-18\2016-04-18_002.xad)		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		4/18/2016 2:55:54 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1