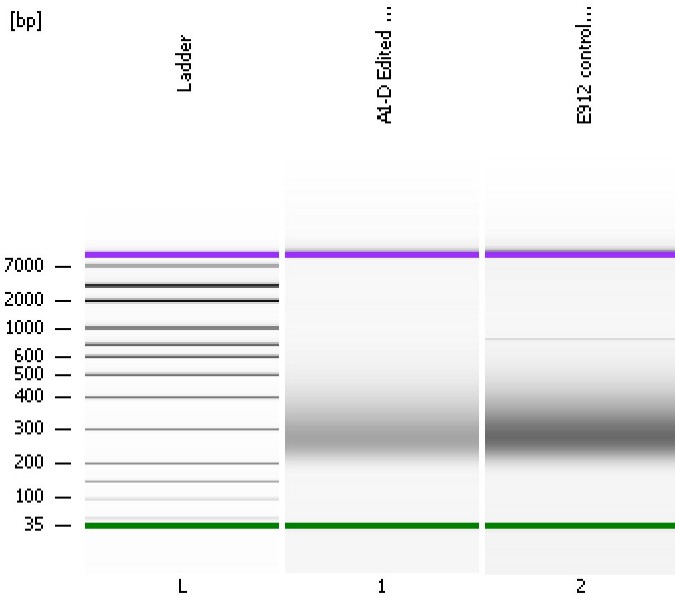


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

Created: 6/29/2015 2:08:07 PM
Modified: 7/1/2015 3:47:22 PM

Electrophoresis File Run Summary



Instrument Information:

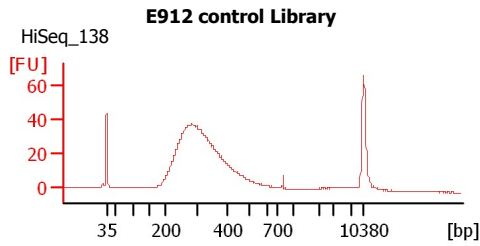
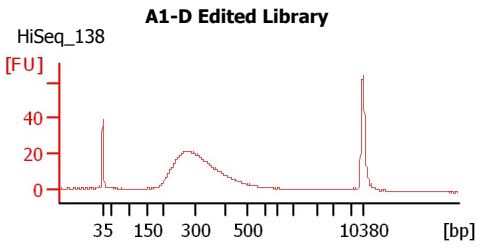
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
A1-D Edited Library	HiSeq_138	<input type="checkbox"/>	✓			
E912 control Library	HiSeq_138	<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

Created: 6/29/2015 2:08:07 PM
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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

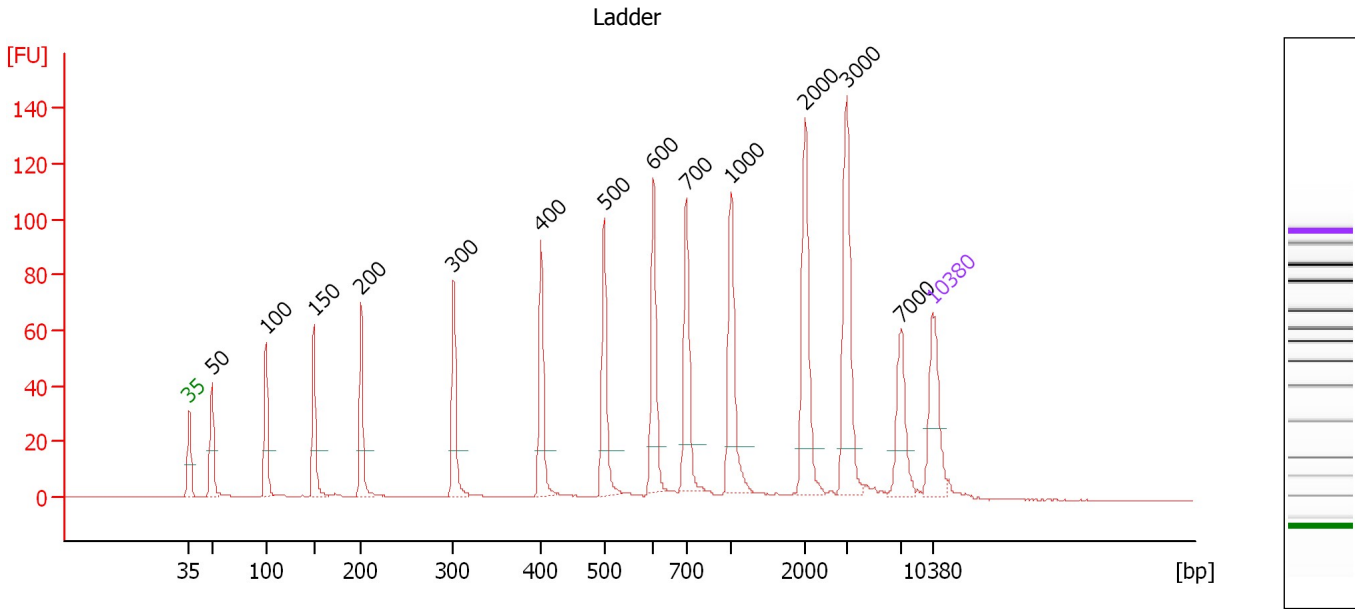
Ladder

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

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

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Electropherogram Summary



Overall Results for Ladder

Noise: 0.1

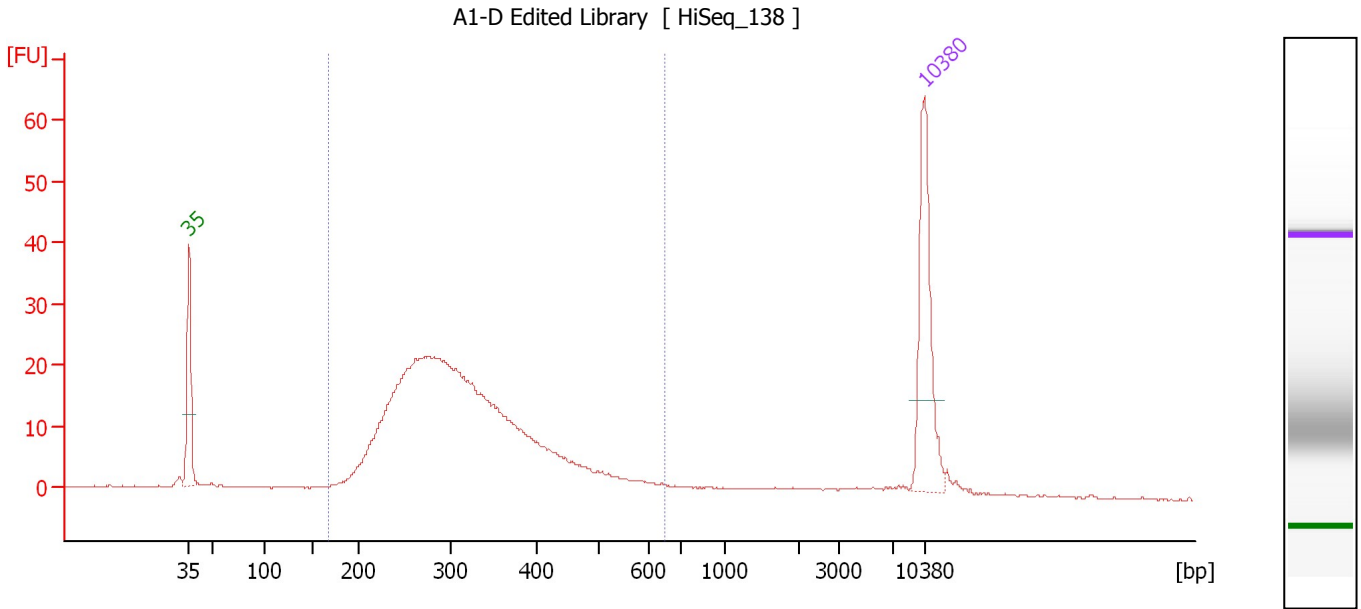
Peak table for Ladder

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	45.16
3	100	150.00	2,272.7	Ladder Peak	50.23
4	150	150.00	1,515.2	Ladder Peak	54.75
5	200	150.00	1,136.4	Ladder Peak	59.22
6	300	150.00	757.6	Ladder Peak	67.91
7	400	150.00	568.2	Ladder Peak	76.14
8	500	150.00	454.5	Ladder Peak	82.07
9	600	150.00	378.8	Ladder Peak	86.74
10	700	150.00	324.7	Ladder Peak	89.80
11	1,000	150.00	227.3	Ladder Peak	94.02
12	2,000	150.00	113.6	Ladder Peak	101.00
13	3,000	150.00	75.8	Ladder Peak	104.92
14	7,000	150.00	32.5	Ladder Peak	110.04
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

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Electropherogram Summary Continued ...



Overall Results for sample 1 : A1-D Edited Library

Number of peaks found: 0 Corr. Area 1: 441.7
 Noise: 0.1

Peak table for sample 1 : A1-D Edited Library

Pea k	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

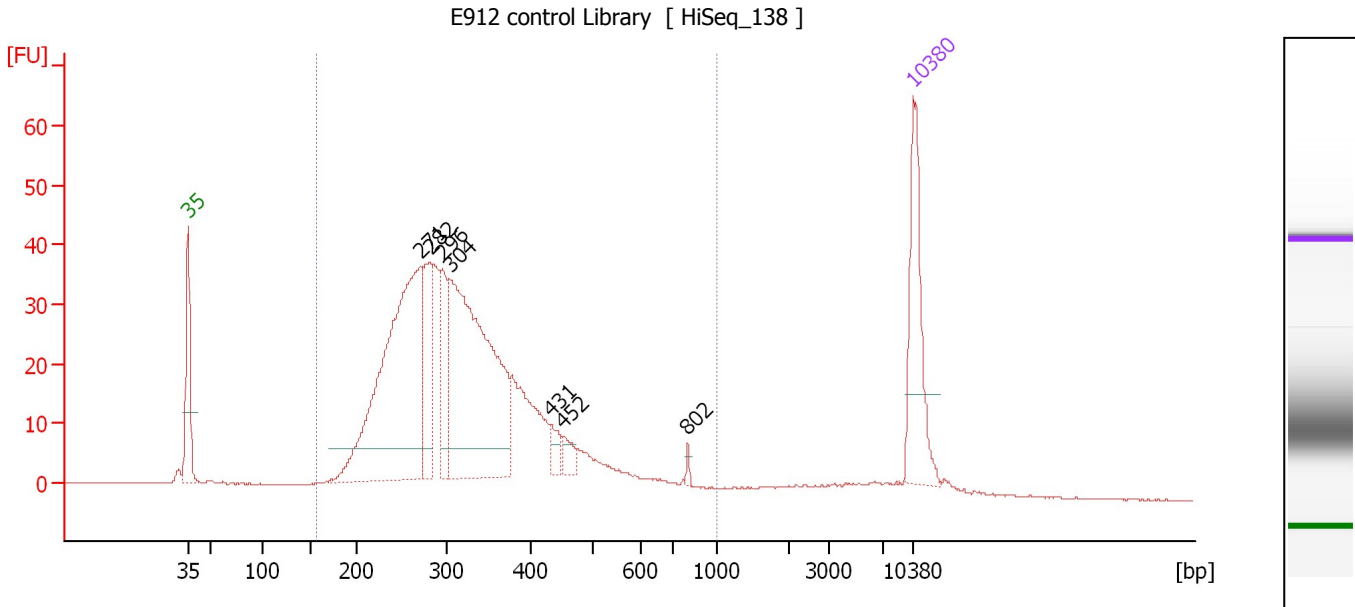
Region table for sample 1 : A1-D Edited Library

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/μl]
168	321	649	441.7	3,776.9	90	26.0	738.96

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

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Electropherogram Summary Continued ...



Overall Results for sample 2 : E912 control Library

Number of peaks found: 7 Corr. Area 1: 759.6
 Noise: 0.1

Peak table for sample 2 : E912 control 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	271	387.76	2,167.7		65.39
3	282	82.39	442.2		66.37
4	296	63.37	324.4		67.55
5	304	347.34	1,728.7		68.27
6	431	14.77	51.9		78.00
7	452	12.85	43.0		79.24
8	802	2.87	5.4		91.23
9	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 2 : E912 control Library

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]	Conc. [pg/μl]
156	329	1,000	759.6	6,283.2	94	30.7	1,241.80

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ings\Bioanalyzer\2015-06-29\2015-06-29_002_HiSeq138Libs.xad

Created: 6/29/2015 2:08:07 PM
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Gel Image

