

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...ert\data\2018-05-09\2018-05-09\_001\_NuGen\_Test\_mRNA\_Libs.xad

Created: 5/9/2018 9:50:48 AM  
Modified: 5/9/2018 11:09:23 AM

**Electrophoresis File Run Summary**

Instrument Information:

Instrument Name: DE34903152                      Firmware: C.01.069  
Serial#: DE34903152                                Type: G2938C

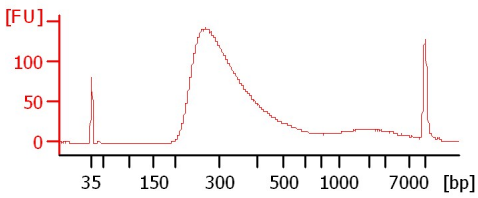
Assay Information:

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

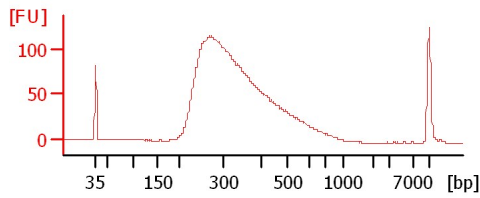
Chip Information:

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

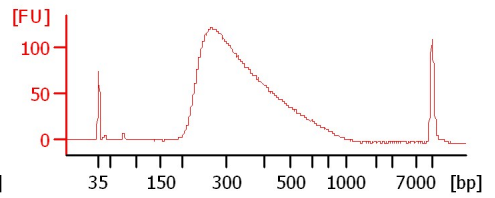
**1 NuGen mRNA Lib (1:23)**



**2 NuGen mRNA Lib (1:23)**



**3 NuGen mRNA Lib (1:4)**



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
1 NuGen mRNA Lib (1:23)		<input type="checkbox"/>	✓			
2 NuGen mRNA Lib (1:23)		<input type="checkbox"/>	✓			
3 NuGen mRNA Lib (1:4)		<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/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

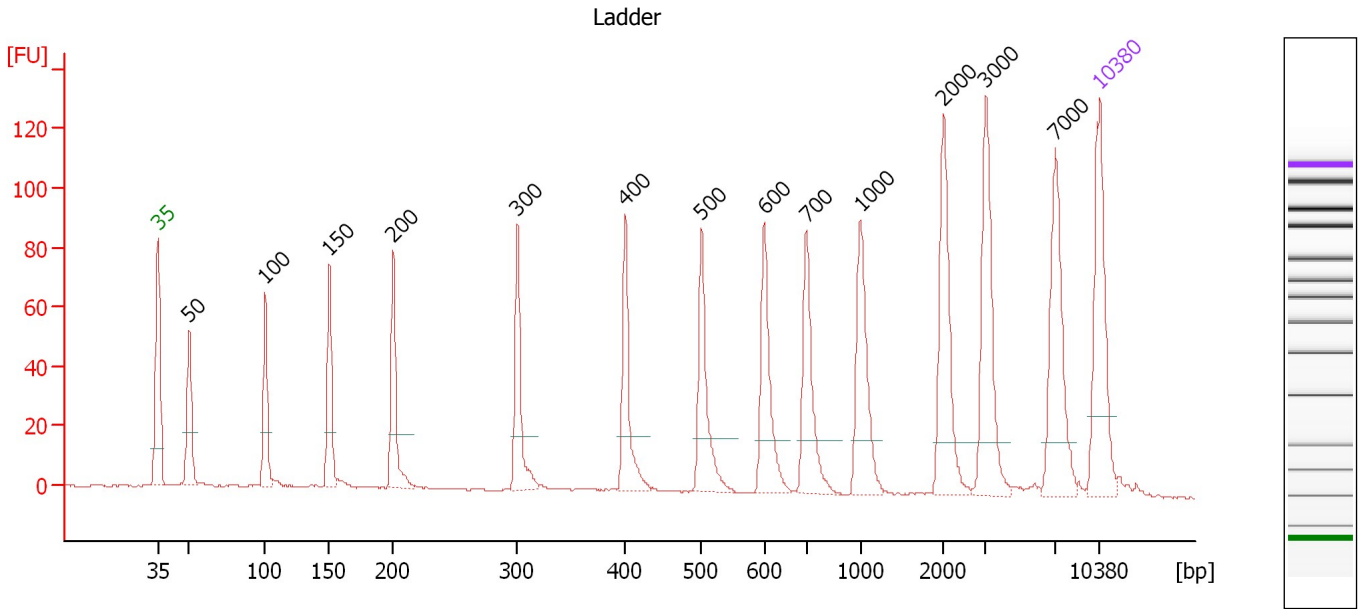
**Ladder**

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

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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.3

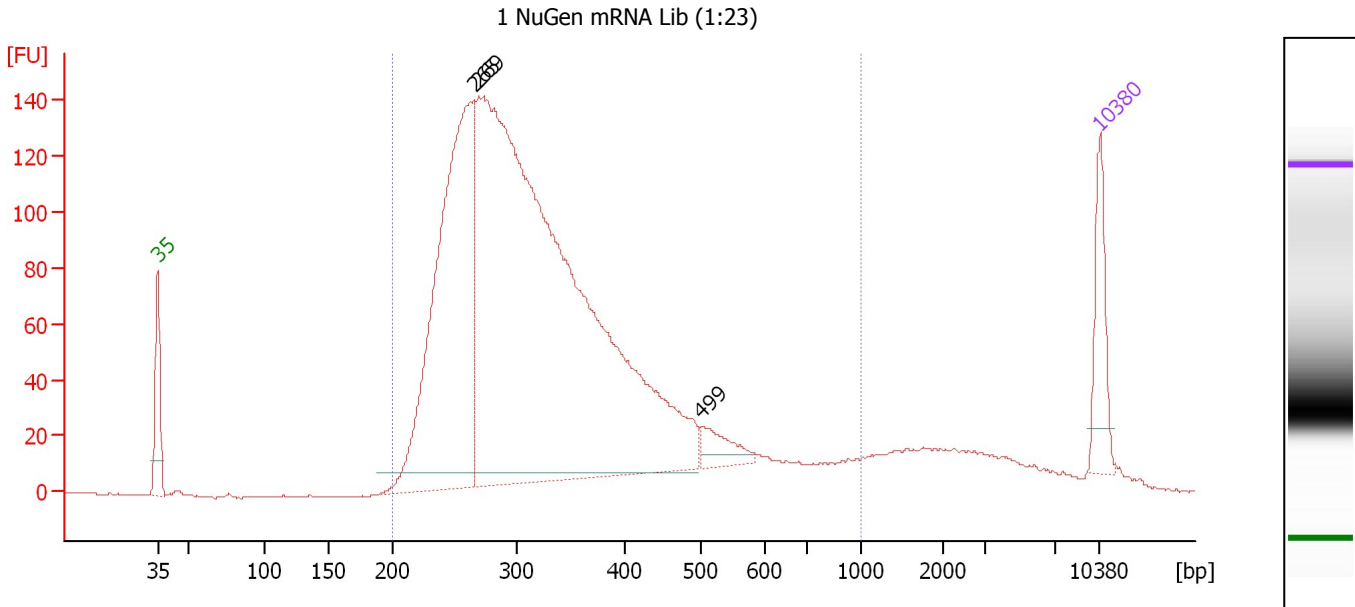
**Peak table for Ladder**

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	45.35
3	100	150.00	2,272.7	Ladder Peak	51.01
4	150	150.00	1,515.2	Ladder Peak	55.76
5	200	150.00	1,136.4	Ladder Peak	60.51
6	300	150.00	757.6	Ladder Peak	69.72
7	400	150.00	568.2	Ladder Peak	77.74
8	500	150.00	454.5	Ladder Peak	83.40
9	600	150.00	378.8	Ladder Peak	88.05
10	700	150.00	324.7	Ladder Peak	91.17
11	1,000	150.00	227.3	Ladder Peak	95.20
12	2,000	150.00	113.6	Ladder Peak	101.39
13	3,000	150.00	75.8	Ladder Peak	104.51
14	7,000	150.00	32.5	Ladder Peak	109.69
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : 1 NuGen mRNA Lib (1:23)**

Number of peaks found: 3                      Corr. Area 1: 2,705.2  
 Noise: 0.3

**Peak table for sample 1 : 1 NuGen mRNA Lib (1:23)**

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	265	879.62	5,026.5		66.51
3	269	2,304.72	12,962.2		66.90
4	499	50.87	154.3		83.36
5	10,380	75.00	10.9	Upper Marker	113.00

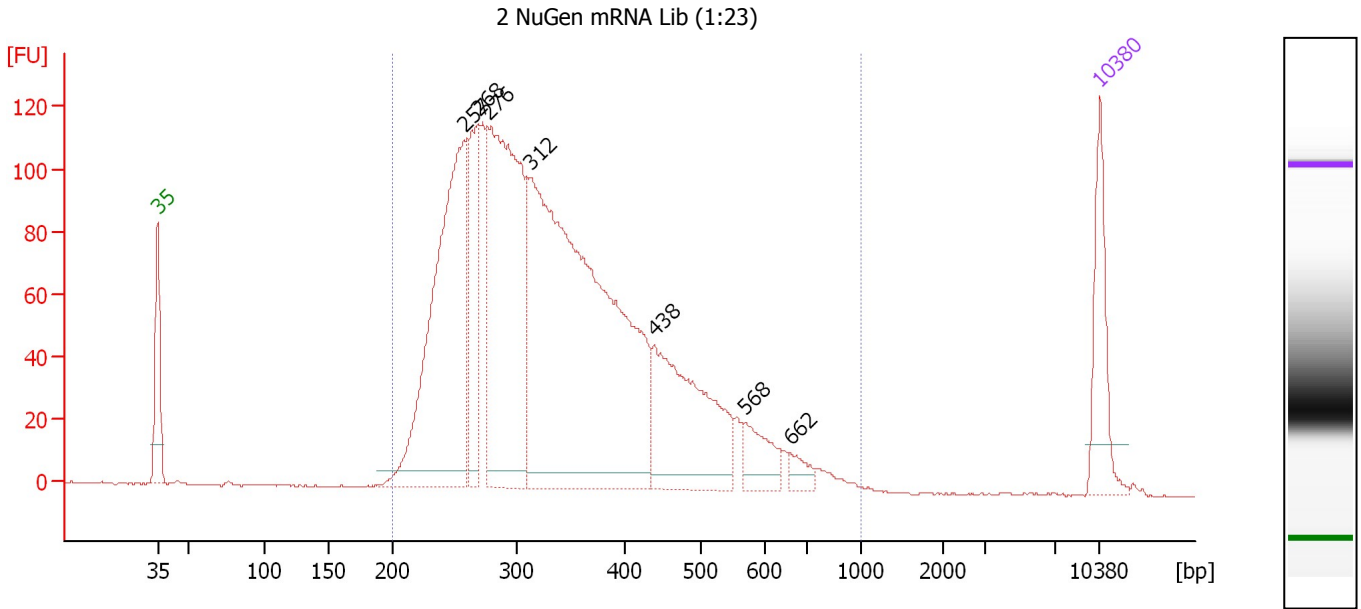
**Region table for sample 1 : 1 NuGen mRNA Lib (1:23)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	345	3,303.03	2,705.2	16,231.4	91	35.8

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : 2 NuGen mRNA Lib (1:23)**

Number of peaks found: 7                      Corr. Area 1: 2,506.1  
 Noise: 0.2

**Peak table for sample 2 : 2 NuGen mRNA Lib (1:23)**

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	257	554.41	3,262.8		65.80
3	268	166.12	938.4		66.80
4	276	537.20	2,946.0		67.54
5	312	1,022.26	4,959.0		70.71
6	438	257.26	890.1		79.88
7	568	52.86	140.9		86.58
8	662	19.01	43.5		90.00
9	10,380	75.00	10.9	Upper Marker	113.00

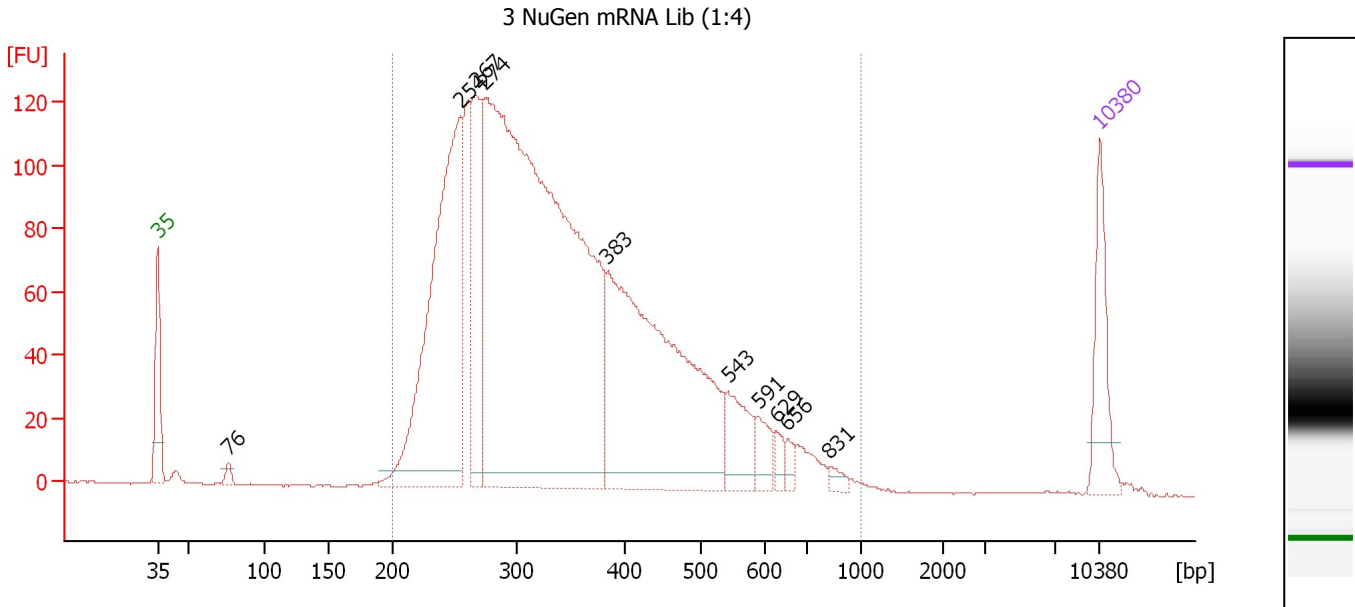
**Region table for sample 2 : 2 NuGen mRNA Lib (1:23)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	350	2,670.77	2,506.1	12,847.0	99	31.4

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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : 3 NuGen mRNA Lib (1:4)**

Number of peaks found: 10                      Corr. Area 1: 2,735.3  
 Noise: 0.3

**Peak table for sample 3 : 3 NuGen mRNA Lib (1:4)**

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	76	11.57	231.7		48.26
3	254	606.43	3,616.7		65.49
4	267	195.36	1,110.0		66.65
5	274	1,698.73	9,381.6		67.36
6	383	644.34	2,546.2		76.41
7	543	73.74	205.7		85.40
8	591	32.55	83.5		87.63
9	629	16.43	39.6		88.94
10	656	11.82	27.3		89.80
11	831	9.80	17.9		92.94
12	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 3 : 3 NuGen mRNA Lib (1:4)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	355	3,299.93	2,735.3	15,786.5	99	32.7

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**Gel Image**



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**Curves**

**Standard Curve**

