

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...lyzer\2015-05-21\2015-05-21\_001\_MatePair\_BluePippinLibs.xad

Created: 5/21/2015 8:42:25 AM  
Modified: 5/21/2015 9:28:07 AM

**Electrophoresis File Run Summary**

Instrument Information:

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

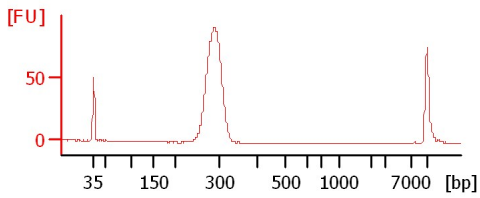
Assay Information:

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

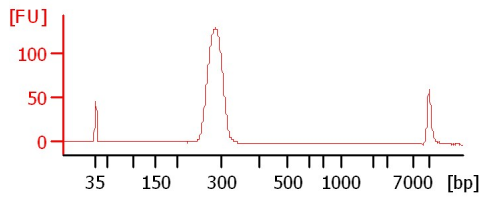
Chip Information:

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

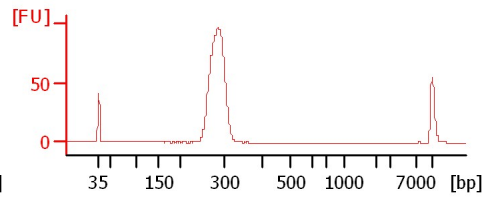
**950 Blue Pippin Library**



**107MI Blue Pippin Library**



**81S Blue Pippin Library**



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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
950 Blue Pippin Library		<input type="checkbox"/>	✓			
107MI Blue Pippin Library		<input type="checkbox"/>	✓			
81S Blue Pippin Library		<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

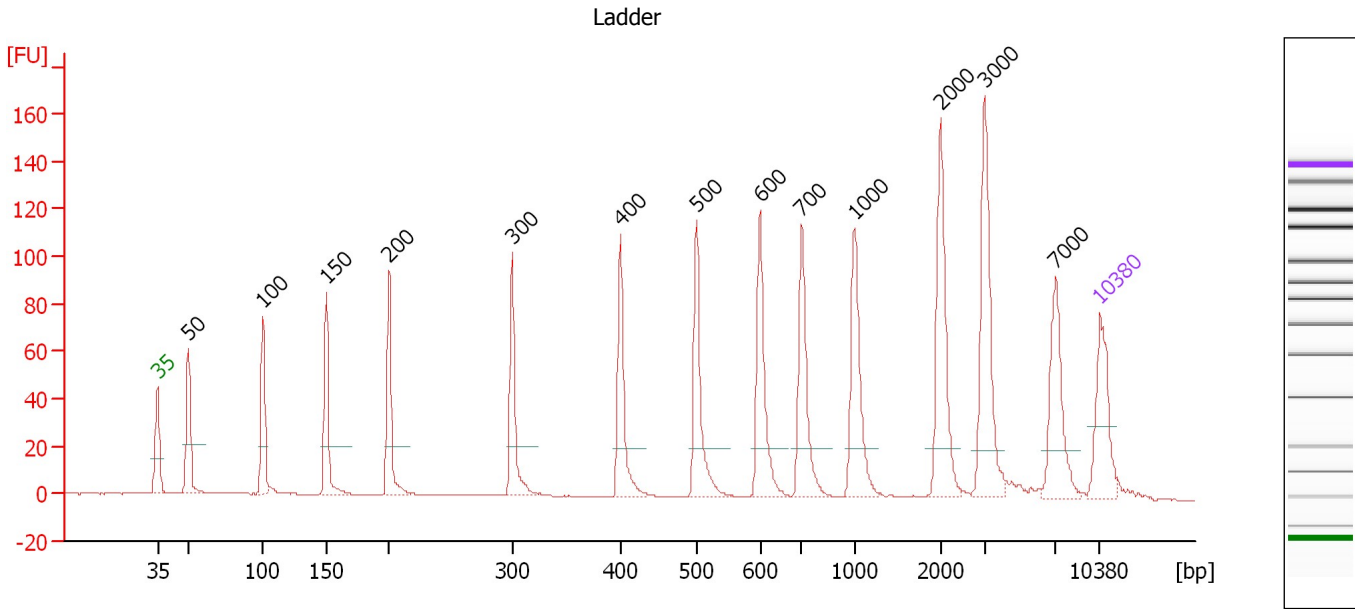
**Ladder**

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: 0.2

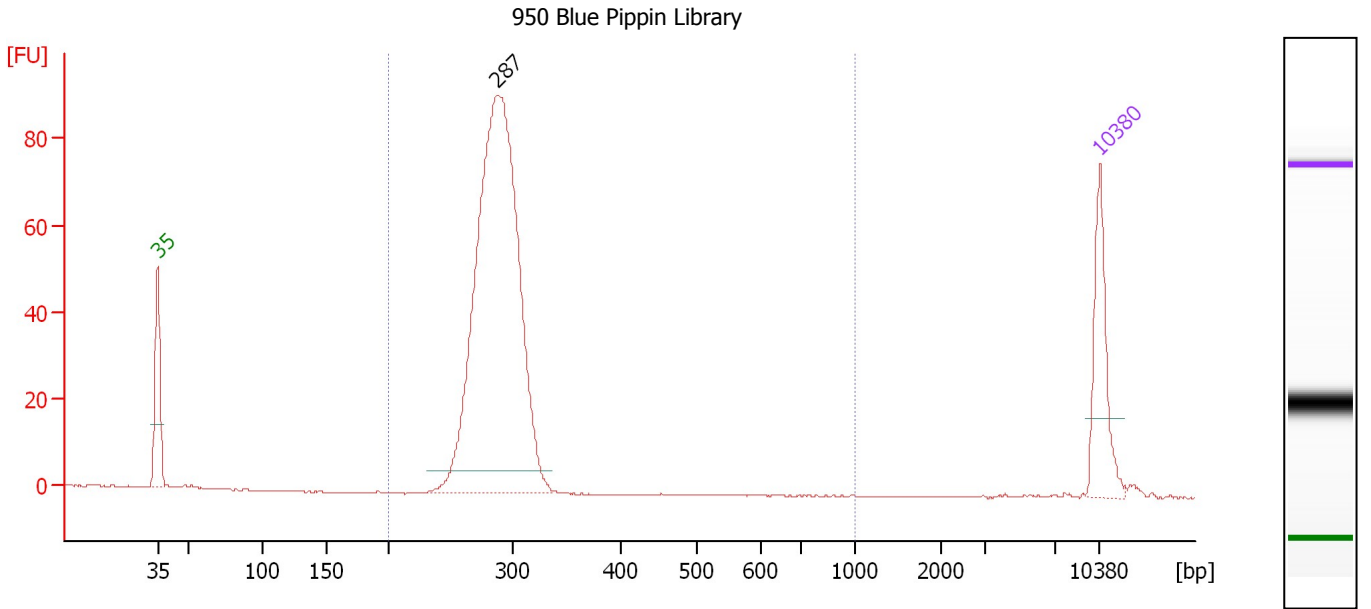
**Peak table for Ladder**

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	45.30
3	100	150.00	2,272.7	Ladder Peak	50.84
4	150	150.00	1,515.2	Ladder Peak	55.54
5	200	150.00	1,136.4	Ladder Peak	60.19
6	300	150.00	757.6	Ladder Peak	69.36
7	400	150.00	568.2	Ladder Peak	77.38
8	500	150.00	454.5	Ladder Peak	83.05
9	600	150.00	378.8	Ladder Peak	87.75
10	700	150.00	324.7	Ladder Peak	90.85
11	1,000	150.00	227.3	Ladder Peak	94.75
12	2,000	150.00	113.6	Ladder Peak	101.17
13	3,000	150.00	75.8	Ladder Peak	104.41
14	7,000	150.00	32.5	Ladder Peak	109.72
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : 950 Blue Pippin Library**

Number of peaks found: 1                      Corr. Area 1: 508.3  
 Noise: 0.2

**Peak table for sample 8 : 950 Blue Pippin 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	885.67	4,677.7		68.16
3	10,380	75.00	10.9	Upper Marker	113.00

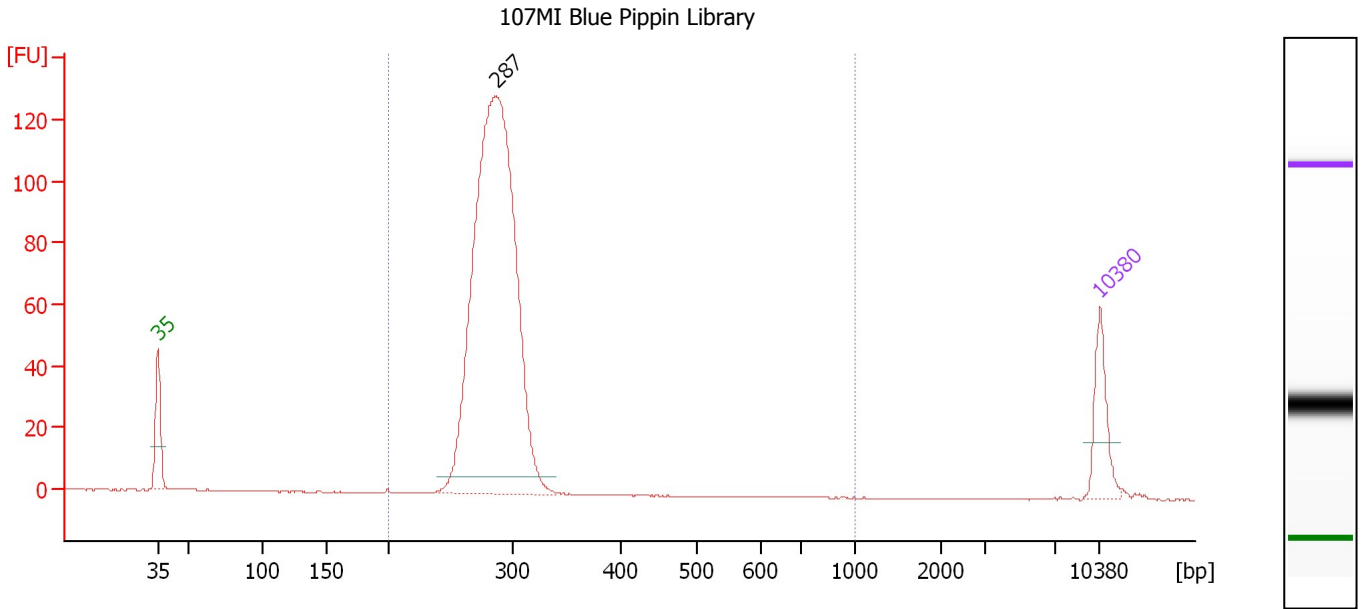
**Region table for sample 8 : 950 Blue Pippin Library**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	288	1,000	508.3	4,581.3	99	5.4	868.10	Blue

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : 107MI Blue Pippin Library**

Number of peaks found: 1                      Corr. Area 1: 715.7  
 Noise: 0.1

**Peak table for sample 9 : 107MI Blue Pippin 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	1,517.93	8,024.3		68.13
3	10,380	75.00	10.9	Upper Marker	113.00

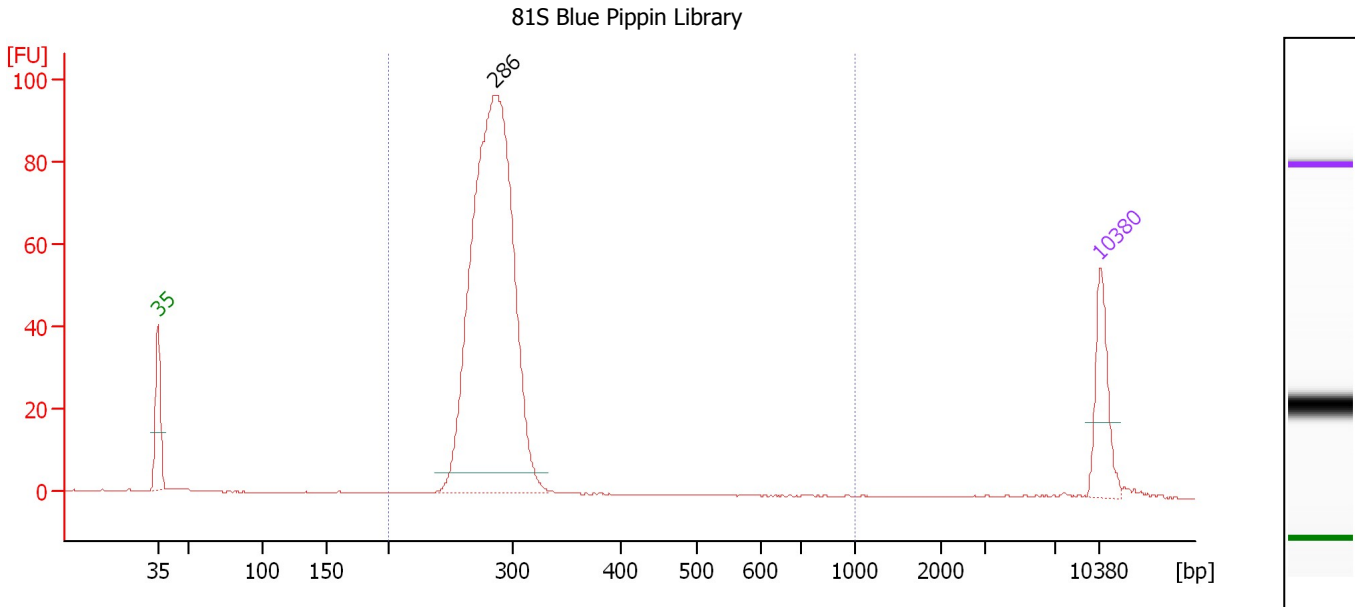
**Region table for sample 9 : 107MI Blue Pippin Library**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	286	1,000	715.7	8,090.8	99	5.3	1,522.87	Blue

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**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : 81S Blue Pippin Library**

Number of peaks found: 1      Corr. Area 1: 543.1  
 Noise: 0.1

**Peak table for sample 10 : 81S Blue Pippin 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	286	1,209.57	6,419.0		68.03
3	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 10 : 81S Blue Pippin Library**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/μl]	Color
200	285	1,000	543.1	6,581.5	97	10.1	1,232.90	Blue

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**Gel Image**