

Instrument Information:

Instrument Name:

Serial#:

DE13701086

DE13701086

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**Electrophoresis File Run Summary** 

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2013-05-31\_001.xad

C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xad Data Path:

> LC. യ

Ladder

[s]

Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

Firmware: C.01.069

Type:

G2938B

High Sensitivity DNA Assay Assay Class:

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\	Sensitivity DNA Assay .ents and Settings\Bioanalyzer\2013-05-31\2013-05-31_001.xad					13 12:20:40 PM 013 1:02:00 PM
Electrophore	sis File Run Summary (Chip Su	mmary)					
Sample Name	Sample Comment	Rest. Digest	Status Obse	ervation	Result	Label	Result Color
sample 1			×				
sample 2			×				
sample 3			× .				
sample 4			× .				
sample 5			×				
sample 6			×				
sample 7			×				
sample 8			×				
sample 9			×				
sample 10			~				
sample 11			×				
Ladder			×				

Chip Lot #

Reagent Kit Lot #

Chip Comments :

2013-05-31\_001.xad

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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] : 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

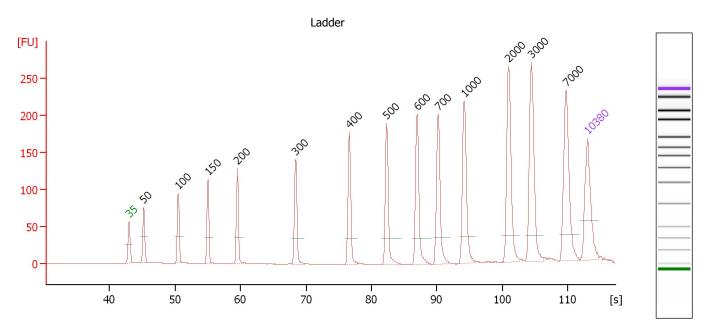
Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

#### High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xad Assay Class: Data Path:

Created: Modified:

### 5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM

#### **Electropherogram Summary**



### **Overall Results for Ladder**

Noise:

0.2

### Peak table for Ladder

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1		35	125.00	5,411.3	Lower Marker
2		50	150.00	4,545.5	Ladder Peak
3	L	100	150.00	2,272.7	Ladder Peak
4	L	150	150.00	1,515.2	Ladder Peak
5	L	200	150.00	1,136.4	Ladder Peak
6	L	300	150.00	757.6	Ladder Peak
7	L	400	150.00	568.2	Ladder Peak
8		500	150.00	454.5	Ladder Peak
9	L	600	150.00	378.8	Ladder Peak
10	L	700	150.00	324.7	Ladder Peak
11		1,000	150.00	227.3	Ladder Peak
12		2,000	150.00	113.6	Ladder Peak
13		3,000	150.00	75.8	Ladder Peak
14	L	7,000	150.00	32.5	Ladder Peak
15	Þ	10,380	75.00	10.9	Upper Marker

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013-05-31\2013-05-31_001.xad	Created: Modified:	5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM
Electropher	ogram Summary Continued		
	sample 1		
[FU]_		0	
100 -			
80 -	0		
60 -			
40 -			
20 -			
0		www.	<i>∧</i> .
4	50 60 70 80 90 100 110 120	130	[s]

#### Overall Results for sample 1 : <u>sample 1</u>

Number of peaks found:			1	Noise:	0.2
Peak ta Peak	able	for sample 1 : Size [bp]	<u>sample 1</u> Conc. [pg/µl]	Molarity [pmol/l]	Observations
1 2	•	0 0	0.00 0.00	0.0 0.0	Lower Marker

2013-05-31\_001.xad

Assay Class: Data Path:	High Sensitivit C:\ents and	Created: Modified:	5/31/2013 12: 5/31/2013 1:	20:40 PM 02:00 PM						
Electrophe	rogram Summa	ary Continued								
			samp	ole 2						
[FU]								0	•	
120-								0		
100 -										
80 -	0									
60 -										
40 -										
20 -								0		
0	, <u> </u>				~			- Junger	-n-	
	1 1 10 50	60 70	80	90	100	110	120	130	_ [s]	

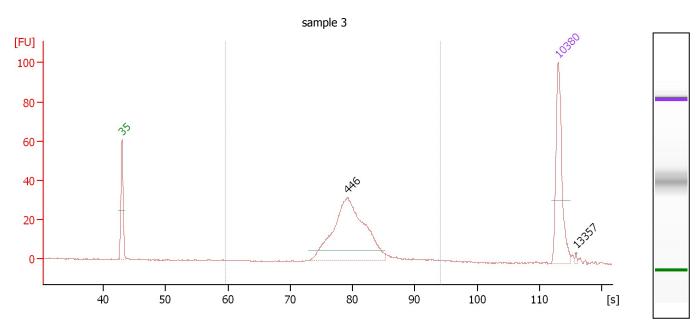
#### Overall Results for sample 2 : sample 2

Peak table for sample 2 : sample 2 : sample 2 :   Peak Size [bp] Conc. [pg]   1 ● 0 0.00   2 0 0.00   3 0 0.00	<b>Observations</b> Lower Marker

2013-05-31\_001.xad

Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

### Electropherogram Summary Continued ...



Overa	Overall Results for sample 3 : <u>sample 3</u>										
Number of peaks found:		2	Corr.	Corr. Area 1:		268.7					
Noise:			0.1								
Peak table for sample 3 : <u>sample 3</u>											
Peak		Size [bp]	Conc. [pg/µl]	Mola	ity [pmol/	<b>'</b> ]]	Observations				
1	-	35	125.00	5,411.	3		Lower Marker				
2		446	247.23	840.5							
3		10,380	75.00	10.9			Upper Marker				
4		13,357	0.00	0.0							
Regior	n tab	le for sample 3	: <u>sample 3</u>								
From [bp]	T	o [bp] Average S [bp]	ize Molarity [pmol/l]	Conc. [pg/µl]	Corr. Area	% of Total	Size distribution in CV [%]				

271.41

268.7

94

17.5

200

1,000

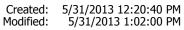
471

898.1

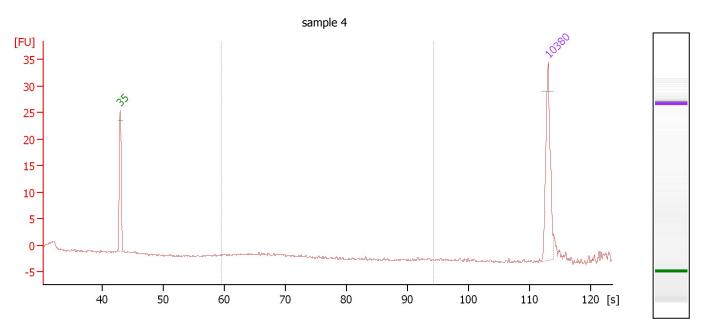
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#### High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xad Assay Class: Data Path:



### **Electropherogram Summary Continued ...**



From [bp]	Т	o [bp] Average [bp]	Size Molarity [pmol/l]	Conc. [pg/µl]	Corr. Area	% of Total	Size distribution in CV [%]
Regior	ı tab	le for sample	4 : <u>sample</u>	<u>e 4</u>			
2		10,380	75.00	10.9			Upper Marker
1		35	125.00	5,411.3			Lower Marker
Peak		Size [bp]	Conc. [pg/µl	] Molarit	y [pmol	/I]	Observations
Peak t	able	for sample 4	: <u>sample 4</u>	:			
Noise:			0.1				
Number	Number of peaks found:		0	0 Corr. Area 1:			0.0
Overal	l Re	sults for samp	le 4 : <u>samp</u>	<u>le 4</u>			

0.00

200

0

0.0

1,000

0

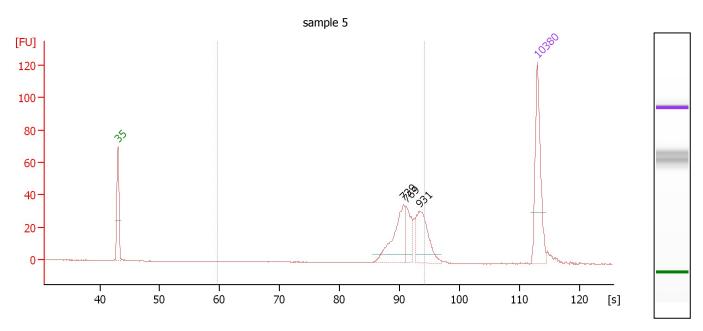
0.0

0.0

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Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

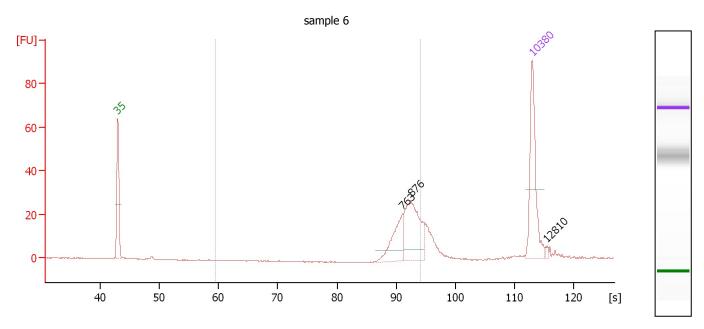


Overall Results for sample 5 : <u>sample 5</u>										
Number of peaks found:		eaks found:	3	Corr. Area 1:	194.0					
Noise:			0.1							
Peak table for sample 5 : <u>sample 5</u>										
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations					
1	- ◀-	35	125.00	5,411.3	Lower Marker					
1 2		35 739	125.00 76.29	5,411.3 156.5	Lower Marker					
-	•			,	Lower Marker					
2	•	739	76.29	156.5	Lower Marker					

Region table for sample 5 :			sample 5					
<b>From</b> [bp] 200	<b>To [bp</b> 1,000	J Average Size [bp] 789	Molarity [pmol/l] 312.0	<b>Conc.</b> [pg/µl] 159.42	<b>Corr.</b> Area 194.0	<b>% of</b> Total 81	Size distribution in CV [%] 14.4	Co lor

Created: 5/31/20 Modified: 5/31/2

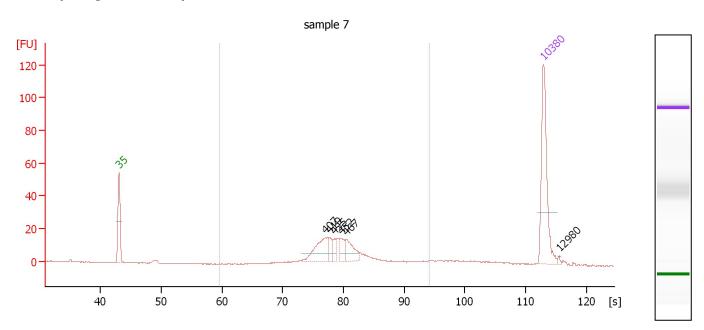
5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM



	Overall Results for sample 6 : <u>sample 6</u>											
Number of peaks found:			eaks found:	3	Corr. Area 1:	114.4						
Noise:			0.1									
Peak table for sample 6 : <u>sample 6</u>												
	Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations						
	1	-	35	125.00	5,411.3	Lower Marker						
	2		763	51.98	103.2							
	3		876	91.10	157.5							
	4		10,380	75.00	10.9	Upper Marker						
	5		12.810	0.00	0.0							

5	12,810	0.0	0	0.0					
Region	Region table for sample 6 : <u>sample 6</u>								
From [bp]	To [bp] Aver [bp]		Molarity [pmol/l]	Conc. [pg/µl]	Corr. Area	% of Total	Size distribution in CV [%]	Co lor	
200	1,000 820		222.7	119.12	114.4	68	12.3		

Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

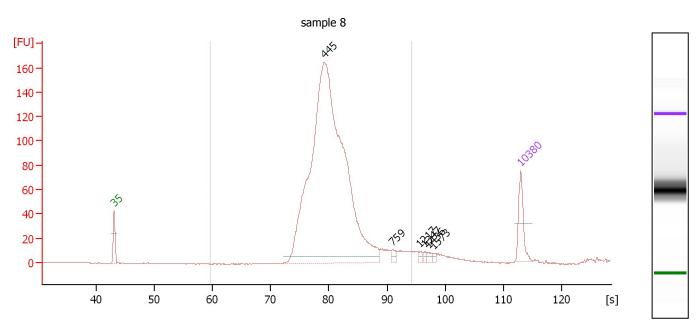


Overall Results for sample 7 :	sample 7
Overall Results for sample 7:	sample 7

Number of peaks found:	6	Corr. Area 1:	181.1
Noise:	0.1		

Peak t	able	for sample 7 :	sample 7					
Peak		Size [bp]	Conc. [pg/µl]	Molar	ity [pmol/	/I]	Observations	
1		35	125.00	5,411.	3		Lower Marker	
2		407	43.31	161.4				
3		419	9.89	35.7				
4		435	9.34	32.6				
5		452	14.96	50.1				
6		467	23.75	77.0				
7		10,380	75.00	10.9			Upper Marker	
8		12,980	0.00	0.0				
Region table for sample 7 : <u>sample 7</u>								
<b>From</b> [bp] 200		o [bp] Average S [bp] .000 473	ize Molarity [pmol/l] 554.1	<b>Conc. [pg/μl]</b> 164.64	<b>Corr.</b> Area 181.1	<b>% of</b> Total 83	Size distribution in CV [%] 23.5	Co lor

### Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

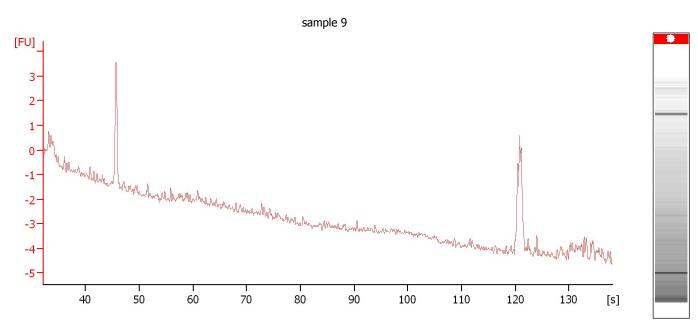


Overall Results for sam	ole 8: <u>sample 8</u>		
Number of peaks found:	6	Corr. Area 1:	1,409.6
Noise:	0.1		
Peak table for sample 8	: <u>sample 8</u>		

Peak		Size [bp]	Conc. [pg/µl]	Molar	ity [pmol/	1]	Observations	
1		35	125.00	5,411.	3		Lower Marker	
2		445	2,305.28	7,852.	7			
3		759	15.15	30.3				
4		1,217	8.53	10.6				
5		1,347	7.51	8.4				
6		1,436	9.80	10.3				
7		1,573	6.64	6.4				
8		10,380	75.00	10.9			Upper Marker	
Region table for sample 8 : <u>sample 8</u>								
From [bp]	Т	o [bp] Average S [bp]	Size Molarity [pmol/l]	Conc. [pg/µl]	Corr. Area	% of Total	Size distribution in CV [%]	Co lor
200	1,	,000 476	7,573.3	2,308.17	1,409.6	96	18.6	

Created: Modified: 5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM

### **Electropherogram Summary Continued ...**

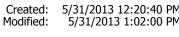


<b>Overall Res</b>	sults for sample 9 :	sample 9
Noise:	0.1	

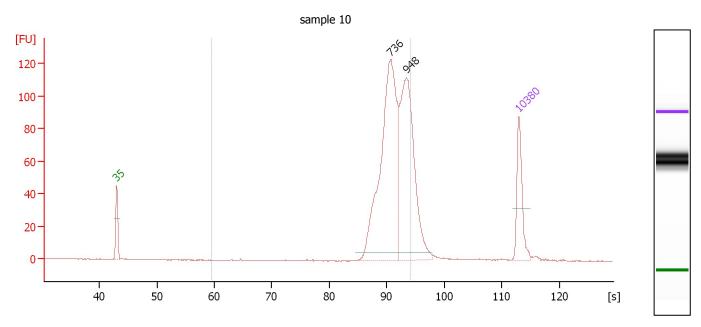
Noise:

#### High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xad Assay Class: Data Path:

### 5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM



### **Electropherogram Summary Continued ...**



Overall Results for sample 10 : <u>sample 10</u>									
Number of	peaks found:	2	Corr. Area 1:	688.7					
Noise:		0.1							
	Peak table for sample 10 : <u>sample 10</u>								
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations					
1 🔺	35	125.00	5,411.3	Lower Marker					
2	736	541.62	1,114.9						
3	948	375.94	601.0						
4 🕨	10,380	75.00	10.9	Upper Marker					
Region ta	Region table for sample 10 : <u>sample 10</u>								
From	To [bp] Average S	Size Molarity Co	onc. Corr. % of	Size distribution in					

[pg/µl]

785.38

Area

688.7

Total

83

CV [%]

14.7

[pmol/l]

1,543.1

[bp]

786

1,000

[bp]

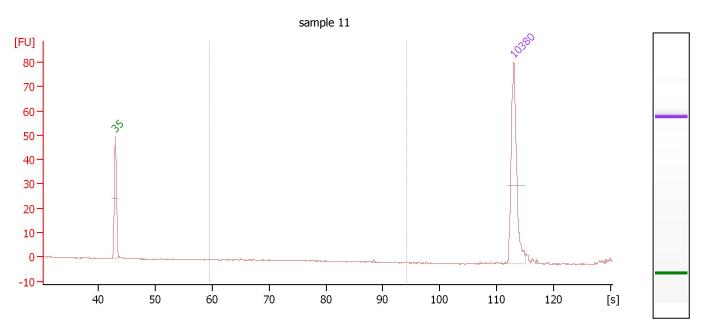
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Created: 5/31/2013 12:20:40 PM Modified: 5/31/2013 1:02:00 PM

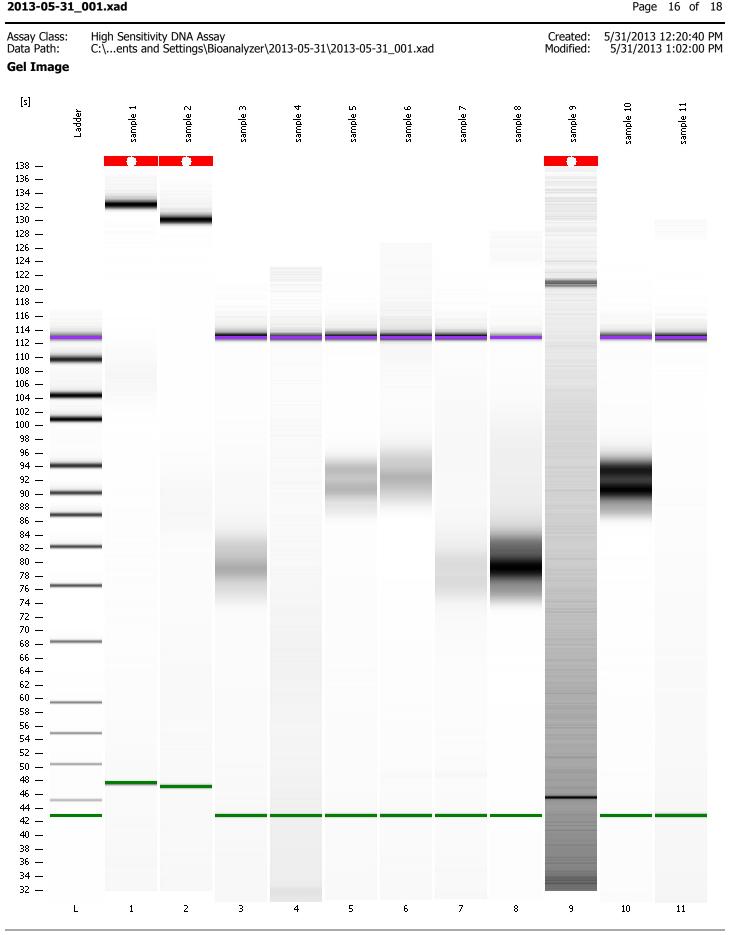
### Electropherogram Summary Continued ...



### Overall Results for sample 11 : <u>sample 11</u>

Number of peaks found: Noise:	0 0.1	Corr. Area 1:	0.0				
Peak table for sample 11 : <u>sample 11</u>							

Peak	Size [bp] Conc. [pg/µl]		Mola	rity [pmol	/I]	Observations		
1 2		35 10,380	125.00 5,411.3 75.00 10.9		.3	Lower Marker Upper Marker		
Region table for sample 11 : <u>sample 11</u>								
<b>From</b> [bp] 200		<b>b [bp] Average S</b> [bp] 000 0	ize Molarity [pmol/l] 0.0	<b>Conc. [pg/µl]</b> 0.00	<b>Corr.</b> Area 0.0	<b>% of Total</b> 0	Size distribution in CV [%] 0.0	Co lor

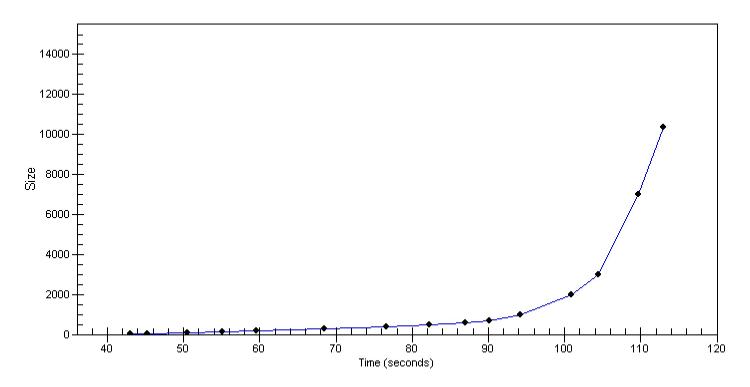


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# Assay Class:High Sensitivity DNA AssayCreated:5/31/2013 12:20:40 PMData Path:C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xadModified:5/31/2013 1:02:00 PM

### Curves

### Standard Curve



### 2013-05-31\_001.xad

### Assay Class: Data Path: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2013-05-31\2013-05-31\_001.xad

Created: Modified: 5/31/2013 12:20:40 PM 5/31/2013 1:02:00 PM

### **Run Logbook**

<b>Description</b> Run ended on port 1 (Number of wells	Number	<b>Source</b> Instrument	<b>Category</b> Run	Sub Category	<b>Time</b> 5/31/2013 1:01:58 PM	<b>Time Zone</b> (GMT07:00) Pacific Standard Time	<b>User</b> UC Davis	<b>Host</b> D8XSMGH1
acquired: 12) Run started on port 1 (File: C:\Documents and Settings\Bioana yzer\2013-05-3: \2013-05-31_00 1.xad)	1	Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time		D8XSMGH1
Product Number : G2938B	r	Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time		D8XSMGH1
Vendor : Agilent Technologies	t	Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time		D8XSMGH1
Serial# : DE13701086		Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time		D8XSMGH1
Firmware : C.01.069		Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time		D8XSMGH1
Cartridge : Electrode		Instrument	Run		5/31/2013 12:20:45 PM	(GMT07:00) Pacific Standard Time	UC Davis	D8XSMGH1