

2013-12-06_	005.xad					Page	2 of 17
Assay Class: Data Path: Electrophore	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013 esis File Run Summary (Chip Summ	-	2-06_005.	xad	Created: Modified:	12/6/2013 2 12/6/2013 3	
Sample Name	Sample Comment	Rest. Digest	Status	Observation	Re	esult Label	Res ult Col or
sample 1			~				
sample 2			$\sim$				
sample 3			$\sim$				
sample 4			$\sim$				
sample 5			$\sim$				
sample 6			$\sim$				
sample 7			$\sim$				
sample 8			$\checkmark$				
sample 9			$\checkmark$				
sample 10			~				
sample 11			$\checkmark$				
Ladder		Ō	~				

# Chip Lot #

Reagent Kit Lot #

# **Chip Comments :**

Assay Class: High Sensitivity DNA Assay Data Path: C:\...ents and Settings\Bioanalyzer\2013-12-06\2013-12-06\_005.xad

## 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

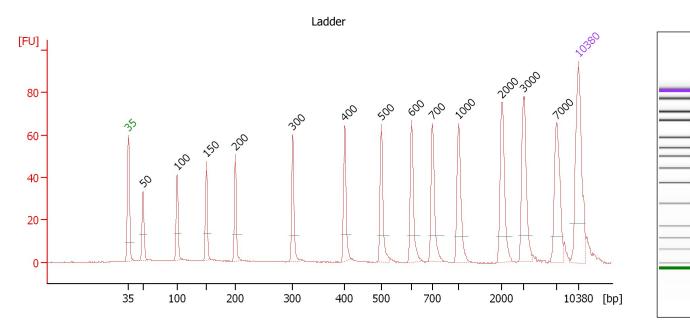
Created: 12/6/2013 2:28:33 PM Modified: 12/6/2013 3:11:09 PM

#### High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2013-12-06\2013-12-06\_005.xad Assay Class: Data Path:

Created: Modified:

# 12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM

#### **Electropherogram Summary**



## **Overall Results for Ladder**

Noise:

0.1

## Peak table for Ladder

Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1		43.00	35	125.00	5,411.3	Lower Marker
2	L	45.28	50	150.00	4,545.5	Ladder Peak
3		50.58	100	150.00	2,272.7	Ladder Peak
4	L	55.14	150	150.00	1,515.2	Ladder Peak
5	L	59.62	200	150.00	1,136.4	Ladder Peak
6	L	68.57	300	150.00	757.6	Ladder Peak
7	L	76.65	400	150.00	568.2	Ladder Peak
8		82.33	500	150.00	454.5	Ladder Peak
9	L	87.06	600	150.00	378.8	Ladder Peak
10	L	90.29	700	150.00	324.7	Ladder Peak
11		94.35	1,000	150.00	227.3	Ladder Peak
12	L	101.06	2,000	150.00	113.6	Ladder Peak
13		104.46	3,000	150.00	75.8	Ladder Peak
14	L	109.60	7,000	150.00	32.5	Ladder Peak
15		113.00	10,380	75.00	10.9	Upper Marker

2013-12-06_	005.xad						Page 5 of 17
Assay Class: Data Path: <b>Electropher</b> e	High Sensitivity DNA Assa C:\ents and Settings\Bic Ogram Summary Contin		2013-12-06_0	05.xad		Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
		sample	1				
<sup>[FU]</sup> -]						10380	
80 -						h	
70 -	ŝ						
60 -							
50 -							
40 -							
30 -							
20-							
10-						f t	
0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛			~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	- Mille	
L	35 100 2	00 300 4	1 1	700	2000	10380 [bp	

Overall Results for sample 1 : <u>sample</u>	s for sample 1 : sample 1	
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Number of peaks found:	0	Corr. Area 1:	0.8
Noise:	0.2		

Peak table for sample 1	:	<u>sample 1</u>
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Pea k	Aligned Migration Tir	ne [s] Size	[bp] Coi	nc. [pg/µl]	Molarity	/ [pmol/l]	Observat	ions
1	👌 43.00	35	125	.00	5,411.3		Lower Mar	'ker
2 🎙	🔒 113.00	10,3	80 75.0	00	10.9		Upper Mar	ker
Regior	table for sample 1 :	sample 1						
<b>From</b> [bp] 200	To [bp] Average Size [bp] 1,000 346	Molarity [pmol/l] 4.9	<b>Conc.</b> [pg/μl] 1.04	<b>Corr.</b> Area 0.8	<b>% of</b> Total 4	Size distr CV [%] 29.7	ibution in	Co lor

2013-12-06_	005.xad					Page 6 of 17
Assay Class: Data Path: Electrophere	High Sensitivity DNA Assay C:\ents and Settings\Bioanaly ogram Summary Continued		2-06_005.xad	C M	Created: odified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
		sample 2				
<sup>[FU]</sup>					10380	
80 -	25					
60 -						
40 -						
20 -						
0				and and and a second	wal	
	35 100 200	300 400	500 700	2000	10380 [bp	)

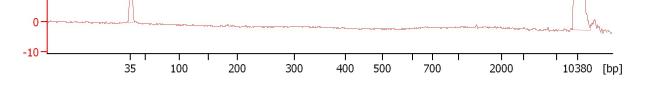
Overall Results for sample 2 :	sample 2
Overall Results for sample 2:	<u>sample 2</u>

Number of peaks found:	0	Corr. Area 1:	67.5
Noise:	0.2		

Peak table for sample	2	:	sample 2
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Pea k	Align	ed Migration Tim	ie [s] Size	e [bp]	Conc. [pg/	/µl] Molar	ity [pmol/l]	Observat	ions
1 1	6 43.00		35		125.00	5,411.	3	Lower Mar	ker
2	113.00	)	10,3	80	75.00	10.9		Upper Mar	ker
Regio	n table fo	or sample 2 :	sample 2	2					
<b>From</b> [bp] 242	<b>To [b</b> ] 463	p] Average Size [bp] 345	<b>Molarity [pmol/l]</b> 370.8	<b>Conc</b> [pg/ 82.78	µl] Area	a Total	Size distr CV [%] 12.8	ibution in	Co lor

2013-12-06 <u>-</u>	_005.xad		Page 7 of 17
Assay Class: Data Path: <b>Electropher</b>	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad ogram Summary Continued	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
	sample 3		
[FU]		10380	
60 -		l l	
50 -	5		
40 -			
30 -			
20 -			
10-			



# Overall Results for sample 3 : <u>sample 3</u>

Number of peaks found: 0 Noise: 0.2

Peak	Peak table for sample 3 : <u>sample 3</u>								
Pea k		Aligned Migration Time [s]	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations			
1	18	43.00	35	125.00	5,411.3	Lower Marker			
2	8	113.00	10,380	75.00	10.9	Upper Marker			

2013-12-06_	005.xad		Page 8 of 17	
Assay Class: Data Path:	Data Path: C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad Mod			
Electrophen	ogram Summary Continued			
	sample 4			
[FU]		10380		
80 -		Ň		
70 -		-		
60 -	<b>参</b>			
50 -				
40 -				
30 -				
20 -				
10-				
0		mand have an		
-10-				
	35 100 200 300 400 500 700 2000	10380 [b	p]	

Overall Results for sample 4	:	sample 4
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Number of peaks found:	0	Corr. Area 1:	11.5
Noise:	0.1		

Peak table for sample 4	:	sample 4
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Pea k	Aligned Migration Tim	ne [s] Size	[bp] C	onc. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1 🍾	43.00	35	12	25.00	5,411.3		Lower Mar	'ker
2 隆	113.00	10,38	30 75	5.00	10.9		Upper Mar	ker
Region	table for sample 4 :	sample 4						
<b>From</b> [bp] 200	To [bp] Average Size   [bp]   1,000 632	<b>Molarity [pmol/l]</b> 44.6	<b>Conc.</b> [pg/μl] 13.77	<b>Corr.</b> <b>Area</b> 11.5	<b>% of</b> Total 29	<b>Size distr CV [%]</b> 37.5	ibution in	Co lor

2013-12-06_	_005.xad				Page 9 of 17
Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioa	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM		
Electropher	ogram Summary Continu	ed			
		sample 5			
[FU] 100 -				10380	
80 -	సా				
60 -					
40 -					
20-					
0		h		man Manan	
	35 100 200	300 400 500	700 2000	10380 [bp	)]

# Overall Results for sample 5 : <u>sample 5</u>

Number of peaks found:	0	Corr. Area 1:	13.0
Noise:	0.2		

Peak table for sample 5	:	sample 5
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Pea k		Aligned Migra	tion Time [s]	Size [b	op] (	Conc. [pg	g/μl]	Molarity	[pmol/l]	Observat	ions
1	-	43.00		35	1	125.00		5,411.3		Lower Mar	ker
2		113.00		10,380	7	75.00		10.9		Upper Mar	ker
Regi	on 1	able for samp	le 5 : <u>sa</u>	mple 5							
<b>From</b> [bp] 200	l	<b>To [bp] Avera</b> [bp] 1,000 769	-	arity ol/l]	<b>Conc.</b> [pg/µl 13.00	Co [] Ard 13.	ea	<b>% of</b> Total 20	<b>Size distri</b> <b>CV [%]</b> 23.9	bution in	Co lor

2013-12-06_	005.xad		Page 10 of 17
Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
Electropher	ogram Summary Continued		
	sample 6		
[FU] 40 - 30 - 20 -	*	10 <sup>380</sup>	
10-			
0	have a final for the second of	norman management	
	35 100 200 300 400 500 700 2000	10380 [b	p]

# Overall Results for sample 6 : <u>sample 6</u>

Number of peaks found:	0	Corr. Area 1:	5.2
Noise:	0.1		

Peak table for sample 6	:	sample 6
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Pea k		Aligned Migration Ti	ne [s] S	ize [bp]	Conc. [pg/µ	I] Molarity	[pmol/l]	Observat	ions
1	•	43.00	3	5	125.00	5,411.3		Lower Mar	ker
2		113.00	1	0,380	75.00	10.9		Upper Mar	ker
Regi	ont	table for sample 6 :	sample	<u>e 6</u>					
<b>From</b> [bp] 200	1	To [bp] Average Size [bp] 1,000 809	Molarity [pmol/l] 18.1			<b>% of</b> Total 10	<b>Size distri</b> <b>CV [%]</b> 15.7	ibution in	Co lor

Assay Class: Data Path:	High Sensitivity DNA C:\ents and Setting	Assay s∖Bioanalyzer∖	2013-12-06\2	2013-12-0	6_005.xad		Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
Electropher	ogram Summary Co	ntinued						
			sample	7				
[FU] 60 -							10380	
50 - 40 -	35 I							
30 -								
20- 10-								
0	man di la come de	v	du, <u>v n</u>		····	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	monton management	
-10-	35 100	200 30	00 400	500	700	2000	1 1	- - pp]

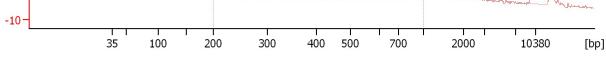
#### Overall Results for sample 7 : sample 7

Number of peaks found:	0	Corr. Area 1:	3.2
Noise:	0.1		

#### Peak table for sample 7 : sample 7

Pea k	Aligned Migration Tir	ne [s] Size [	[bp] Con	c. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1 •	43.00	35	125.	00	5,411.3		Lower Mar	ker
2	113.00	10,380	0 75.0	0	10.9		Upper Mar	ker
Region table for sample 7 : <u>sample 7</u>								
<b>From</b> [ <b>bp]</b> 200	To [bp] Average Size [bp] 1,000 821	Molarity [pmol/l] 8.8	<b>Conc.</b> [pg/μl] 4.65	<b>Corr.</b> Area 3.2	<b>% of</b> Total 9	Size distr CV [%] 15.2	ibution in	Co lor

Assay Class: Data Path:	High Sensitivity DNA Assa C:\ents and Settings\Big	y banalyzer\2013-12-06\2013-12-06_005.xad	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
	ogram Summary Contin			
		sample 8		
[FU]			10380	
50 -	n's		¥	
40 -				
30 -				
20-				
10-	4			
0				



Number of peaks found:	0	Corr. Area 1:	13.0
Noise:	0.1		

Peak table for sample 8	:	sample 8
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Pea k		Aligned Migration Tin	ne [s]	Size [bp]	Conc. [p	g/µl]	Molarity	[pmol/l]	Observati	ions
1		43.00		35	125.00		5,411.3		Lower Mar	ker
2		113.00		10,380	75.00		10.9		Upper Mar	ker
Regi	on 1	table for sample 8 :	<u>samp</u>	ole 8						
<b>From</b> [bp] 200	l	To [bp] Average Size   [bp]   1,000 726	Molarit [pmol/ 51.6		μl] Aι	rea	<b>% of</b> Total 33	<b>Size distri</b> <b>CV [%]</b> 20.5	bution in	Co lor

2013-12-06_	005.xad		Page 13 of 17
Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad Ogram Summary Continued	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
Electrophen	Sgram Summary Continued		
	sample 9		
[FU] 50 -		10380	
40 -	32	Å	
30 -		ß	
20 -			
10-		H	
0		Magnetin	
	35 100 200 300 400 500 700 2000	10380 [bj	p]

<b>Overall Results for sample 9</b>	:	sample 9
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Number of peaks found:	0	Corr. Area 1:	75.6
Noise:	0.1		

Peak ta	able for	sample	e 9 :	:	<u>samp</u>	le 9	
_						~ .	

Pea k	Aligne	ed Migration Tim	ne [s] Size	e [bp]	Conc. [pg/µ	l] Molarit	/ [pmol/l]	Observat	ions
1 2	<ul><li>43.00</li><li>113.00</li></ul>	)	35 10,3		125.00 75.00	5,411.3 10.9		Lower Mar Upper Mar	
Regio	n table fo	or sample 9 :	sample 9	<u>9</u>					
<b>From</b> [bp] 578	<b>To [b;</b> 9,023	D] Average Size [bp] 2,270	Molarity [pmol/l] 142.2	<b>Conc.</b> [pg/µ 135.14	Corr. Area 75.6	<b>% of</b> Total 92	<b>Size distr CV [%]</b> 73.7	ibution in	Co lor

Assay Class: High Sensitivity DNA Assay Data Path: C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad Electropherogram Summary Continued sample 10 [FU] 40- 35- 30- 25- 5- 10- 5-			
[FU] - 40 - 55 - 57 - 57 - 57 - 57 - 57 - 57 - 5	Data Path:		12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
40- 35- 30- 25- 20- 15- 10-		sample 10	
0 -5 -5 -5 - 35 100 200 300 400 500 700 2000 10380 [bp]	40 - 35 - 30 - 25 - 20 - 15 - 10 - 5 - 0 -		

Overall Results for sample 10 : <u>sample 1</u>	Overall	Results for	sample 10	:	sample 10
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2013-12-06\_005.xad

Number of peaks found:	0	Corr. Area 1:	153.1
Noise:	0.1		

Peak ta	ble for sample 10 :	sample 10	<u>)</u>				
Pea	Aligned Migration Tin	ne [s] Size	[bp] Cor	ic. [pg/µl]	Molarity	/ [pmol/l] Observa	tions
k							
1 指	43.00	35	125	.00	5,411.3	Lower M	arker
2 🍾	113.00	10,3	80 75.0	00	10.9	Upper Ma	arker
Region	table for sample 10 :	sample	<u>10</u>				
From	To [bp] Average Size	Molarity	Conc.	Corr.	% of	Size distribution in	Со
[bp]	[bp]	[pmol/l]	[pg/µl]	Area	Total	CV [%]	lor
386	7,756 1,644	567.4	329.73	153.1	92	86.7	

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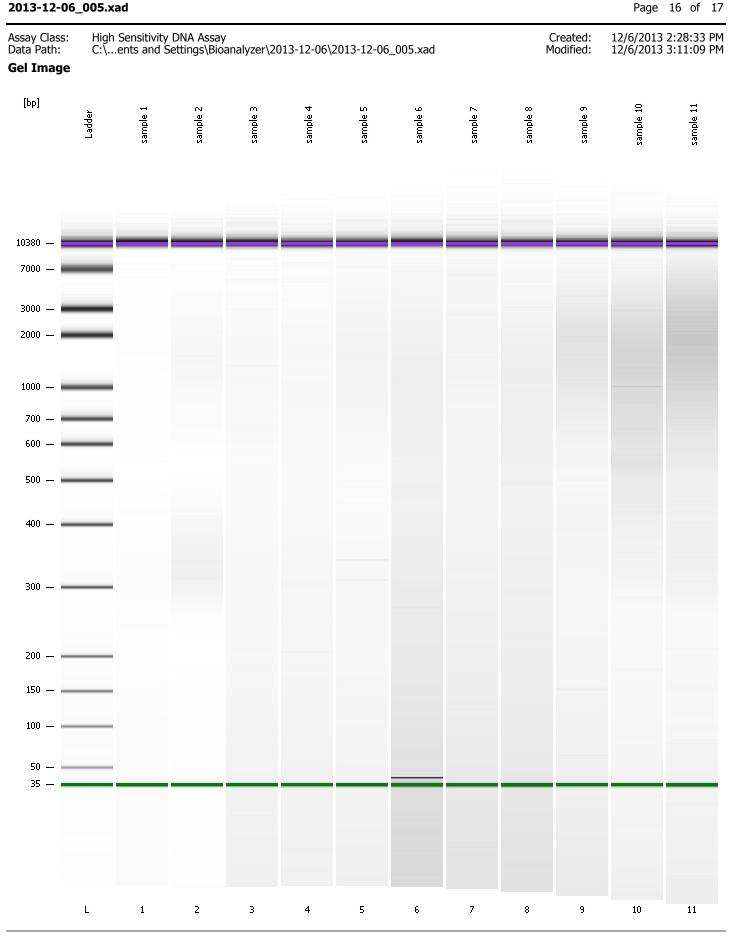
2013-12-06_	005.xad		Page 15 of 17
Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad	Created: Modified:	12/6/2013 2:28:33 PM 12/6/2013 3:11:09 PM
Electrophere	ogram Summary Continued		
	sample 11		
[FU]-		10380	
30 -	35		
25-			
20 -			
15-			
10-		+	
5-	and the second se	man	
0 - wirmonderman	when when a source and a source and the source and	where a show a s	
-5-			
	35 100 200 300 400 500 700 2000	) 10380 [b	p]

#### Overall Results for sample 11 : sample 11

Number of peaks found:	0	Corr. Area 1:	46.9
Noise:	0.2		

Peak table for sample 11	:	sample 11
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Pea k	Aligned Migration Tin	ne [s] Size	[bp] Con	c. [pg/µl]	Molarity	[pmol/l]	Observat	ions		
1	👌 43.00	35	125.	00	5,411.3		Lower Mar	'ker		
2	👌 113.00	10,38	0 75.0	0	10.9		Upper Mar	ker		
Region table for sample 11 : <u>sample 11</u>										
<b>From</b> [bp] 200	To [bp] Average Size [bp] 1,000 658	Molarity [pmol/l] 436.2	<b>Conc.</b> [pg/µl] 164.99	<b>Corr.</b> Area 46.9	<b>% of</b> Total 35	<b>Size distr CV [%]</b> 29.0	ibution in	Co lor		



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Assay Class:	High Sensitivity DNA Assay	Created:	12/6/2013 2:28:33 PM
Data Path:	C:\ents and Settings\Bioanalyzer\2013-12-06\2013-12-06_005.xad	Modified:	12/6/2013 3:11:09 PM

# Curves

# **Standard Curve**

