

2014-01-08_	001.xad					Page	2 of 16
Assay Class: High Sensitivity DNA Assay Data Path: C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad Electrophoresis File Run Summary (Chip Summary)					Created: Modified:		10:37:46 AM 11:20:02 AM
Sample Name	Sample Comment	Rest. Digest	Status	Observation	Resu	lt Label	Result Color
sample 2 sample 3		Ä	÷.				
sample 4		ğ	× .				
sample 5 sample 6		ğ	×.				
sample 7 sample 8		<u> </u>	×.				
sample 9 sample 10			×				
sample 11 Ladder			¥.				

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad Data Path:

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

Created: Modified:

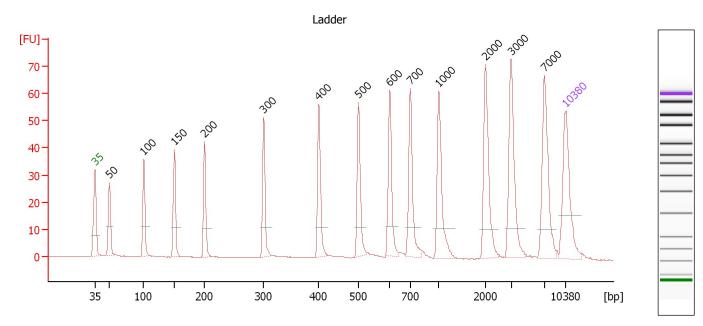
1/8/2014 10:37:46 AM 1/8/2014 11:20:02 AM

High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad Assay Class: Data Path:

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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		45.14	50	150.00	4,545.5	Ladder Peak
3		50.25	100	150.00	2,272.7	Ladder Peak
4		54.79	150	150.00	1,515.2	Ladder Peak
5	L	59.27	200	150.00	1,136.4	Ladder Peak
6		68.09	300	150.00	757.6	Ladder Peak
7	L	76.28	400	150.00	568.2	Ladder Peak
8	L	82.17	500	150.00	454.5	Ladder Peak
9		86.82	600	150.00	378.8	Ladder Peak
10	L	89.89	700	150.00	324.7	Ladder Peak
11	L	94.12	1,000	150.00	227.3	Ladder Peak
12	L	101.06	2,000	150.00	113.6	Ladder Peak
13	L	104.86	3,000	150.00	75.8	Ladder Peak
14	L	109.77	7,000	150.00	32.5	Ladder Peak
15		113.00	10,380	75.00	10.9	Upper Marker

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad	Created: Modified:	1/8/2014 10:37:46 AN 1/8/2014 11:20:02 AN
Electrophe	ogram Summary Continued		
	sample 1		
[FU]-]			
70 -	Ń		
60 -		10380	
50 -			
40-	*		
30 -			
20 -			
10-		+	
0		N	
L	1 1 1 1 1 1 1 35 100 200 300 400 500 700 2000 1	l.0380 [bj	o]

Overall Results for sample 1 : <u>sample 1</u>	Overall	Results	for	sample 1	:	sample 1
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2014-01-08_001.xad

Number of peaks found:	1	Corr. Area 1:	687.6
Noise:	0.1		

Peak	tal	ble for s	ample 1 :	sample	<u>1</u>						
Pea k		Aligne	d Migration Tim	ie [s]	Size [bp	o] Cor	ic. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1		43.00			35	125	.00	5,411.3		Lower Mar	ker
2		56.68			171	1,62	23.23	14,380.1			
3		113.00			10,380	75.0	00	10.9		Upper Mar	ker
Region table for sample 1: <u>sample 1</u> From To [bp] Average Size Molarity Conc. Corr. % of Size distribution in Co											
[bp]	-		[bp]	[pmol/	-	pg/µl]	Area	Total	CV [%]		lor
83		384	201	14,724.	3 1	,835.23	687.6	89	24.1		

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Assay Class: Data Path: Electropher	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad ogram Summary Continued	Created: Modified:	1/8/2014 10:37:46 AM 1/8/2014 11:20:02 AM
	sample 2		
[FU] 60 - 50 - 40 -	5°	10,000	
30 - 20 -			
10-			
	35 100 200 300 400 500 700 2000	10380 [b	p]

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

2014-01-08_001.xad

Number of peaks found:	1	Corr. Area 1:	447.2
Noise:	0.1		

Peak ta	able for	sample 2 :	sample 2						
Pea	Align	ed Migration Tin	ne [s] Siz	e [bp] C	Conc. [pg/µl] Molarity	[pmol/l]	Observat	ions
k	43.00		35	1	25.00	5,411.3		Lower Mar	kor
1	56.42		168		22.90	7,411.7		LOWEI Mai	Kei
3	113.00		10.		5.00	10.9		Upper Mar	ker
Decien			- ,						
Region		or sample 2 :	<u>sample</u>	<u> </u>					
From	To [b	p] Average Size	Molarity	Conc.	Corr.	% of	Size distri	bution in	Со
[bp]	253	[bp] 190	[pmol/l]	[pg/µ]	-	Total 92	CV [%] 20.6		lor
83	352	190	8,134.8	973.85	447.2	92	20.0		

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad rogram Summary Continued	Created: Modified:	1/8/2014 10:37:46 AM 1/8/2014 11:20:02 AM
Liecciopiie	ogram Summary Continueu		
	sample 3		
[FU]	49	10380	
40-	1 ¹⁹	~~··	
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30 -	*		
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20-			
15-			
10-		++	
5-			
		1 John	
0			
L	I I	10380 [b	nl
	55 100 200 500 1 00 500 700 2000	10200 [D	

Overall Results for sample 3 : sample 3

Number of peaks found:	1	Corr. Area 1:	434.1
Noise:	0.1		

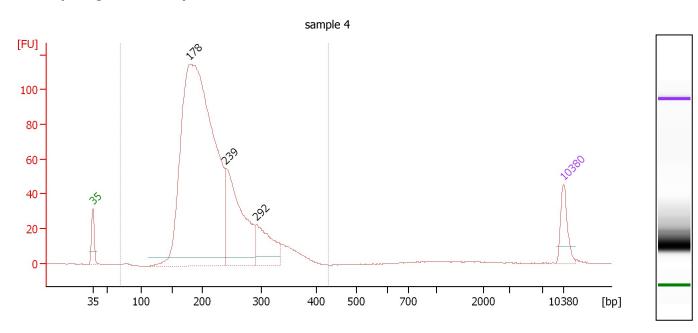
Peak	tał	ble for s	ample 3 :	sampl	<u>e 3</u>							
Pea k		Aligne	d Migration Tim	ne [s]	Size [l	bp]	Conc.	[pg/µl]	Molarit	ty [pmol/l]	Observat	ions
1 2 3	•	43.00 57.41 113.00			35 179 10,380)	125.00 494.73 75.00		5,411.3 4,181.2 10.9		Lower Mar Upper Mar	
Regi From [bp] 89			r sample 3 :] Average Size [bp] 209	<u>sam</u> Molar [pmol 10,972	/í]	Conc. [pg/µ 1,451.	ul]	Corr. Area 434.1	% of Total 99	Size distr CV [%] 20.1	ibution in	Co lor

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Electropherogram Summary Continued ...



Overall	Results	for	sample 4	:	sample 4
orcian	1.Courto		Sumple 1		Sumple 1

Number of peaks found:	3	Corr. Area 1:	1,379.2
Noise:	0.1		

Peak	Peak table for sample 4 : <u>sample 4</u>										
Pea		Aligne	d Migration Tim	e [s] Size [bp]	Conc. [pg/	/µl] №	Iolarity	[pmol/l]	Observat	ions
k 1	•	43.00		35		125.00	5	,411.3		Lower Mar	ker
2		57.34		178		3,239.88	2	7,517.9			
3		62.74		239		653.99	4	,139.6			
4		67.34		292		241.99	1	,257.7			
5		113.00		10,380)	75.00	1	0.9		Upper Mar	ker
Regi	on t	table fo	r sample 4 :	sample 4							
From [bp]] Average Size [bp]	Molarity [pmol/l]	Conc. [pg/]	I] Area	a To	o of otal	Size distri CV [%]	bution in	Co lor
70		430	219	28,842.1	3,951	.49 1,37	9.2 99)	22.2		

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Assay Class: Data Path:	ta Path: C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad Modified: 1							
Electropher	ogram Summary Continued							
		sample 5						
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80-								
60 -			10380					

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	35	100	200	300	400	500	700	2000			
				_							
Overa	all Results fo	r sample	5: <u>san</u>	nple 5							

Number of peaks found:	1	Corr. Area 1:	1,156.8
Noise:	0.1		

Peak table for sample 5	:	sample 5
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3

40

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0.

Pea k		Aligne	d Migration Tim	e [s] S	ize [bp]	Conc.	[pg/µl]	Molarity	[pmol/l]	Observat	ions
1	•	43.00		3	5	125.00	1	5,411.3		Lower Mar	ker
2		56.52		10	69	3,287.0	65	29,429.5			
3		113.00		10	0,380	75.00		10.9		Upper Mar	ker
Regi	ont	table fo	r sample 5 :	sample	<u>e 5</u>						
From [bp] 72	1	To [bp 402	•] Average Size [bp] 199	Molarity [pmol/l] 25,227.0		μl]	Corr. Area 1,156.8	% of Total 99	Size distri CV [%] 20.8	bution in	Co lor

10380

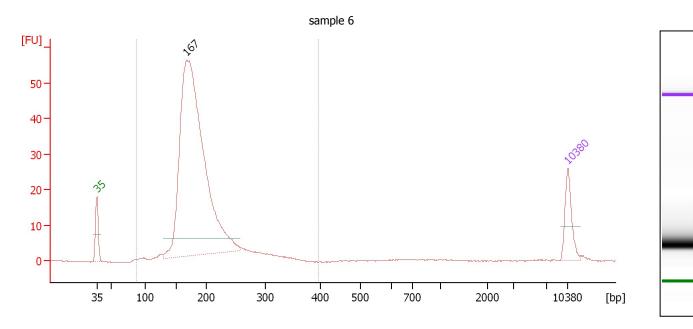
[bp]

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Electropherogram Summary Continued ...



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

Number of peaks found:	1	Corr. Area 1:	421.8
Noise:	0.1		

Peak table for samp	ele 6 :	sample 6
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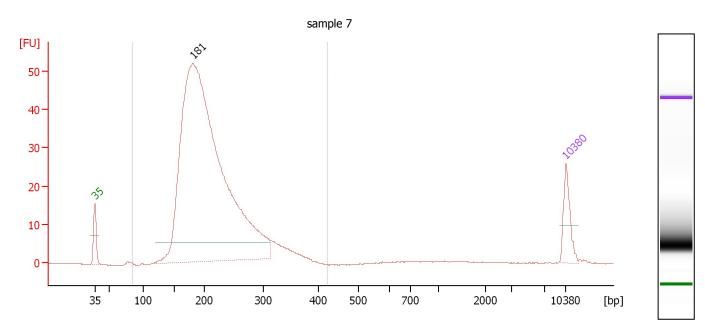
Pea k		Aligned	Migration Tim	e [s]	Size [bp]	Conc	. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1	€.	43.00			35	125.0	0	5,411.3		Lower Mar	ker
2		56.35			167	2,104	.87	19,051.8			
3		113.00			10,380	75.00		10.9		Upper Mar	ker
Regio	n t	able for	sample 6 :	sam	<u>ple 6</u>						
From [bp] 86		To [bp] 396	Average Size [bp] 188	Molarit [pmol/ 19,189.	/i] [p	onc. g/μl] 298.67	Corr. Area 421.8	% of Total 100	Size distri CV [%] 18.5	ibution in	Co lor

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Assay Class:High Sensitivity DNA AssayData Path:C:\...ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad

Electropherogram Summary Continued ...



Overall Results for sample 7 : <u>sample 7</u>

Number of peaks found:	1	Corr. Area 1:	589.9
Noise:	0.1		

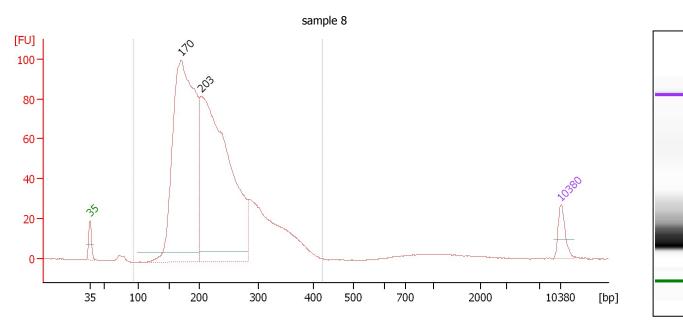
Peak table for sample 7 : <u>sample 7</u>

Pea k		Aligne	d Migration Tim	e [s] S	Size [bp]	Conc.	[pg/µl]	Molarity	[pmol/l]	Observat	ions
1		43.00		3	35	125.00)	5,411.3		Lower Mar	ker
2		57.57		1	.81	3,272.	95	27,402.0			
3		113.00		1	.0,380	75.00		10.9		Upper Mar	ker
Regi	on 1	able fo	r sample 7 :	<u>sampl</u>	<u>le 7</u>						
From [bp] 84	Ì	To [bp 423] Average Size [bp] 213	Molarity [pmol/l] 24,436.2] [pg/	µI]	Corr. Area 589.9	% of Total 99	Size distr CV [%] 22.4	ibution in	Co lor

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Electropherogram Summary Continued ...



Overall Results for sample 8 : sample 8

Number of peaks found:	2	Corr. Area 1:	1,410.2
Noise:	0.1		

Peak table for sample 8	:	sample 8
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Pea k	Aligned Migration Tin	ne [s] Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1 📢	43.00	35	125.00	5,411.3	Lower Marker
2	56.57	170	3,168.66	28,271.6	
3	59.51	203	3,009.86	22,497.2	
4 🕨	113.00	10,380	75.00	10.9	Upper Marker
Region	table for sample 8 :	sample 8			
From [bp] 93	To [bp] Average Size [bp] 421 225		hc. Corr. μ/μ] Area 92.99 1,410.2	% of Size dist Total CV [%] 98 24.8	ribution in Co lor

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad	Created: Modified:	1/8/2014 10:37:46 A 1/8/2014 11:20:02 A
Electrophe	rogram Summary Continued		
	sample 9		
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	1 1 <th1< th=""> <th1< th=""> <th1< th=""> <th1< th=""></th1<></th1<></th1<></th1<>	10380 [b	p]

sample 9 Overall Results for sample 9 :

2014-01-08_001.xad

Number of peaks found:	1	Corr. Area 1:	190.4
Noise:	0.1		

Peak table for sample 9	:	sample 9
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Pea k		Aligne	d Migration Tim	ie [s] Sizo	e [bp]	Conc.	[pg/µl]	Molarity	[pmol/l]	Observat	ions
1		43.00		35		125.00)	5,411.3		Lower Mar	ker
2		54.18		143		35.53		375.7			
3		113.00		10,3	380	75.00		10.9		Upper Mar	ker
Regi	on t	table fo	r sample 9 :	sample	<u>9</u>						
From [bp] 32	1	To [bp 291] Average Size [bp] 121	Molarity [pmol/l] 22,559.8	Con [pg/ 1,33	/μl]	Corr. Area 190.4	% of Total 82	Size distr CV [%] 54.2	ibution in	Co lor

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Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-01-08\2014-01-08_001.xad	Created: Modified:	1/8/2014 10:37:46 A 1/8/2014 11:20:02 A
Electrophere	ogram Summary Continued		
	sample 10		
16- 14- 12- 10- 8- 6- 4- 2- 0- -2-	5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7	10380 [b	p]

Overall Results for sample 10 : sample 10

Number of peaks found:	4	Corr. Area 1:	254.3
Noise:	0.1		

Peak ta	ble for	sample 10 :	sample 10						
Pea k	Aligno	ed Migration Tim	ie [s] Size	[bp] Con	c. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1	43.00		35	125.	.00	5,411.3		Lower Mar	rker
2	44.80		48	352	.81	11,216.5			
3	46.23		61	426	.52	10,656.8			
4	47.81		76	258	.34	5,139.8			
5	49.45		92	230	.58	3,789.1			
6 🕨	113.00)	10,38	0 75.0	0	10.9		Upper Mar	rker
Region	table fo	or sample 10 :	sample 1	<u>LO</u>					
From [bp] 4	To [bj 290	b] Average Size [bp] 99	Molarity [pmol/l] 49,222.4	Conc. [pg/μl] 2,551.45	Corr. Area 254.3	% of Total 96	Size distr CV [%] 57.1	ibution in	Co lor

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Electropher	ogram Summary Continued		
	sample 11		
16- 14- 12- 10- 8- 6- 4- 2- 0- -2-	5	10380 [b	

Overall Results for sample 11 : sample 11

Number of peaks found:	3	Corr. Area 1:	252.6	
Noise:	0.1			

Peak table for sample 11 : <u>sample 11</u>										
Pea		Aligne	d Migration Tim	e [s] Size	[bp]	Conc. [pg	/µl] Mol	arity [pmol/l]] Observat	ions
k		40.00								
1	٩.	43.00		35		125.00	5,41	1.3	Lower Mar	rker
2		44.79		48		378.71	12,0)57.6		
3		46.15		60		267.92	6,77	2.7		
4		47.90		77		141.78	2,79	91.1		
5		113.00		10,3	80	75.00	10.9	9	Upper Mar	rker
Region table for sample 11 :				sample	<u>11</u>					
From [bp]	I] Average Size [bp]	Molarity [pmol/l]	Conc. [pg/µ	-	a Tota	I CV [%]	tribution in	Co lor
0		315	115	41,756.6	2,260.6	51 252	.6 90	65.3		

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