

Assay Class: Data Path: Electrophore	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad sis File Run Summary (Chip Summary)	Created: Modified:		5 11:16:21 AM 5 11:49:07 AM
Sample Name sample 1 sample 2 sample 3 sample 4 sample 5 sample 6 sample 7 sample 8 sample 9 sample 10 sample 11 Ladder	Sample Comment Rest. Digest Status Observation	Result I	.abel	Result Color
Chip Lot #	Reagent Kit Lot #			

Chip Comments :

2015-07-09_001.xad

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Assay Class: High Sensitivity DNA Assay Data Path: C:\...ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.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

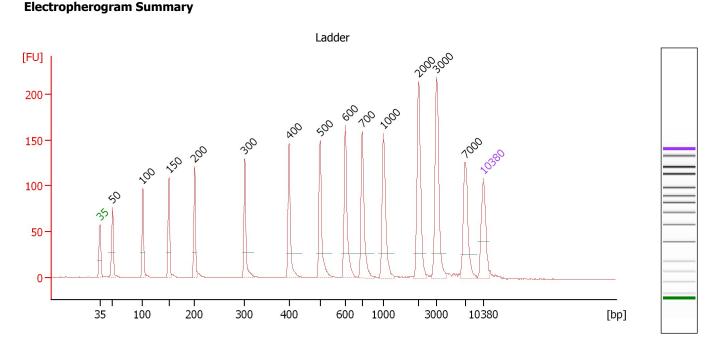
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

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Created: Modified:

High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad Assay Class: Data Path:



Overall Results for Ladder

Noise:

0.2

Peak table for Ladder

Pea k		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	45.29
3		100	150.00	2,272.7	Ladder Peak	50.83
4		150	150.00	1,515.2	Ladder Peak	55.60
5		200	150.00	1,136.4	Ladder Peak	60.32
6		300	150.00	757.6	Ladder Peak	69.46
7		400	150.00	568.2	Ladder Peak	77.54
8		500	150.00	454.5	Ladder Peak	83.18
9		600	150.00	378.8	Ladder Peak	87.80
10		700	150.00	324.7	Ladder Peak	90.87
11		1,000	150.00	227.3	Ladder Peak	94.76
12		2,000	150.00	113.6	Ladder Peak	101.18
13		3,000	150.00	75.8	Ladder Peak	104.49
14	L	7,000	150.00	32.5	Ladder Peak	109.69
15		10,380	75.00	10.9	Upper Marker	113.00

Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad	Created: Modified:	7/9/2015 11:16:21 AM 7/9/2015 11:49:07 AM
Electropher	ogram Summary Continued		
	sample 1		
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140-			
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Overall	Results	for	sample	1	:	sample 1
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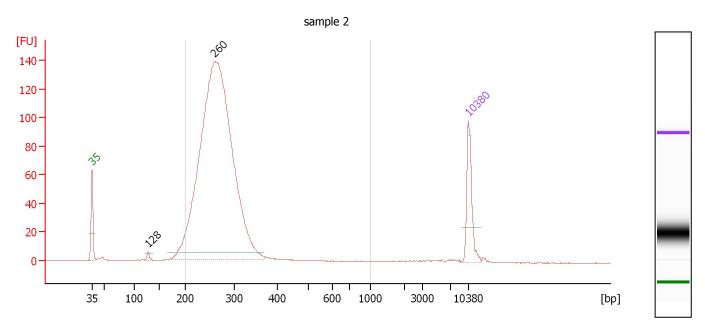
Number of peaks found:	4	Corr. Area 1:	2,778.4
Noise:	0.2		

Peak	tal	ble for sampl	e1: <u>samp</u>	<u>le 1</u>				
Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observati	ions	Aligned Migra	ation Time [s]
1		35	125.00	5,411.3	Lower Mar	ker	43.00	
2		130	49.75	581.3			53.66	
3		189	19.27	154.6			59.26	
4		289	1,586.70	8,306.7			68.49	
5		296	2,215.26	11,324.1			69.13	
6		10,380	75.00	10.9	Upper Marl	ker	113.00	
Regi From	Region table for sample 1 : <u>sample 1</u> From Average Size To [bp] Corr. Molarity Co % of Size distribution in Conc.							
[bp] 200	•	[bp] 316	Area 1,000 2,778	[pmol/l]	or Total 96	CV [% 21.0		[pg/µl] 3,753.44

Assay Class:High Sensitivity DNA AssayData Path:C:\...ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad

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Electropherogram Summary Continued ...



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

Number of peaks found:	2	Corr. Area 1:	1,551.0
Noise:	0.1		

Peak table for sample 2 : <u>sample 2</u>

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observati	ons A	Aligned Migra	ation Time [s]
1 🔹	€.	35	125.00	5,411.3	Lower Mark	ker 4	13.00	
2		128	10.95	130.0		5	53.46	
3		260	1,956.17	11,410.2		6	55.78	
4		10,380	75.00	10.9	Upper Mark	ker 1	13.00	
Regior	n t	able for sam	ple 2 : <u>sar</u>	nple 2				
From [bp] 200		Average Size [bp] 271	e To [bp] Corr. Area 1,000 1,551	[pmol/l] le	co % of or Total 95	Size dis CV [%] 18.9	tribution in	Conc. [pg/μl] 1,957.85

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	ults for sampl		ample 3			L- F	
Overall Resu	ults for sampl	e3: <u>s</u>	-	rea 1:	3.515.1	L- F	
Overall Resu Number of pea	ults for sampl	e3: <u>s</u> 2	ample 3 Corr. A	rea 1:	3,515.1	L- P	
Overall Resu Number of pea	ults for sampl	e3: <u>s</u>	-	rea 1:	3,515.1	L" P	
Overall Resu Number of pea Noise:	ults for samp aks found:	e 3 : <u>s</u> 2 0.2	Corr. A	rea 1:	3,515.1	L - P	
Overall Resu Number of pea Noise: Peak table f o	ults for sampl aks found: or sample 3	e 3 : <u>s</u> 2 0.2 : <u>sam</u>	Corr. A				
Overall Resu Number of pea Noise: Peak table fi Pea Siz	ults for sampl aks found: or sample 3	e 3 : <u>s</u> 2 0.2	Corr. A	rea 1: Observations	3,515.1 Aligned Migration Time		
Overall Resu Number of pea Noise: Peak table fo Pea Siz k 1 4 35	ults for sampl aks found: or sample 3 e [bp] Con 125.	e 3 : <u>sam</u> 0.2 : <u>sam</u> c. [pg/µl]	Corr. A ple <u>3</u> Molarity [pmol/l] 5,411.3		Aligned Migration Time		
Overall Resu Number of pea Noise: Peak table fe Pea Siz k 1 4 35 2 130	ults for sampl aks found: or sample 3 e [bp] Con 125.) 21.0	e 3 : <u>sam</u> 0.2 : <u>sam</u> c. [pg/µl] 00 2	Corr. A ple <u>3</u> Molarity [pmol/l] 5,411.3 244.9	Observations	Aligned Migration Tim 43.00 53.70		
Overall Resu	ults for sampl aks found: or sample 3 e [bp] Con 125.) 21.0	e 3 : <u>sam</u> 0.2 : <u>sam</u> c. [pg/µl] 00 2 7.56	Corr. A ple <u>3</u> Molarity [pmol/l] 5,411.3	Observations	Aligned Migration Time		

Molarity

[pmol/l]

28,681.5

Co % of

lor Total

98

Size distribution in Conc.

[pg/µl]

5,308.97

CV [%]

18.2

From

[bp]

288

[bp]

200

Average Size To [bp] Corr.

Area

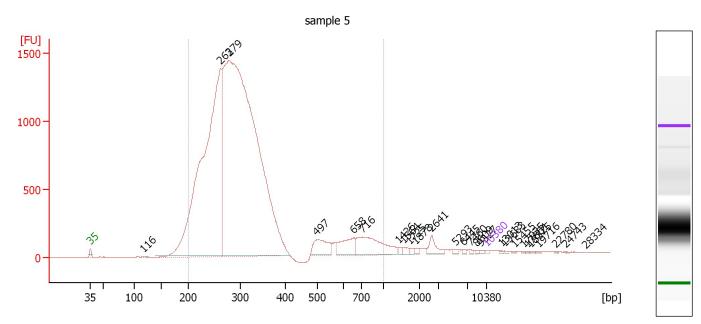
1,000 3,515.1

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Data Path	ss: High S i: C:\e	Sensitivity DNA As ents and Settings\l	say Bioanalyzer\2015-07-09	9\2015-07-09_001	.xad	Created: Modified:	7/9/2015 11:16:21 AN 7/9/2015 11:49:07 AN
Electrop		Summary Cont					
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L	35 10	0 200 3	300 400 600	1000 3000	10380	[b	- p]
		0 200 3	1 I I I 300 400 600	1000 3000	10380	[b	[p]
Overall F			ample 4	1000 3000	10380	[b	[p]
	35 10	ample 4 : <u>s</u>			4,274.2	[b	- p]
	35 10 Results for s	ample 4 : <u>s</u>	ample 4			[b	p]
Number o Noise:	35 10 Results for s	sample 4 : <u>s</u> : 2 0.1	ample 4			[b	- [p]
lumber o loise: Peak tab	35 10 Results for s f peaks found: ole for samp	sample 4 : <u>s</u> 2 0.1 le 4 : <u>sam</u> p	ample 4 Corr. Ar <u>ble 4</u>	ea 1:	4,274.2		p]
Number o Noise: Peak tab Pea	35 10 Results for s	sample 4 : <u>s</u> : 2 0.1	ample 4 Corr. Ar		4,274.2	[b ation Time [s]	pp]
Number o Noise: Peak tab Pea	35 10 Results for s f peaks found: ole for samp	sample 4 : <u>s</u> 2 0.1 le 4 : <u>sam</u> p	ample 4 Corr. Ar Die 4 Molarity [pmol/l]	ea 1:	4,274.2		p]
Number of Noise: Peak tab Pea K L 4 2	35 10 Results for s f peaks found: ble for samp Size [bp] 35 128	sample 4 : <u>s</u> 2 0.1 le 4 : <u>sam</u> Conc. [pg/μl] 125.00 32.63	ample 4 Corr. Ar Die 4 Molarity [pmol/l] 5,411.3 385.3	ea 1: Observations	4,274.2 Aligned Migr 43.00 53.53		pp]
Number of Noise: Peak tab Pea	35 10 Results for s f peaks found: ble for samp Size [bp] 35 128 255	sample 4 : <u>s</u> 2 0.1 le 4 : <u>samp</u> Conc. [pg/μl] 125.00 32.63 6,489.65	ample 4 Corr. Ar Die 4 Molarity [pmol/I] 5,411.3 385.3 38,617.3	ea 1: Observations Lower Marker	4,274.2 Aligned Migr 43.00 53.53 65.31		pp]
Number of Noise: Peak tab Pea C L 4	35 10 Results for s f peaks found: ble for samp Size [bp] 35 128 255 10,380	sample 4 : _s 2 0.1 le 4 : <u>samp</u> Conc. [pg/μ] 125.00 32.63 6,489.65 75.00	ample 4 Corr. Ar Die 4 Molarity [pmol/l] 5,411.3 385.3	ea 1: Observations	4,274.2 Aligned Migr 43.00 53.53		- [9]
Number of Noise: Peak tab Pea C L L 2 3 4 Pea C C C Region t	35 10 Results for s f peaks found: ble for samp Size [bp] 35 128 255 10,380 able for sam	sample 4 : <u>s</u> 2 0.1 le 4 : <u>samp</u> Conc. [pg/μl] 125.00 32.63 6,489.65 75.00 mple 4 : <u>sa</u>	ample 4 Corr. Ar Die 4 Molarity [pmol/l] 5,411.3 385.3 38,617.3 10.9 mple 4	ea 1: Observations Lower Marker Upper Marker	4,274.2 Aligned Migr 43.00 53.53 65.31 113.00	ation Time [s]	pp]
Number of Noise: Peak tab Pea C L 4	35 10 Results for s f peaks found: ble for samp Size [bp] 35 128 255 10,380	sample 4 : <u>s</u> 2 0.1 le 4 : <u>samp</u> Conc. [pg/μl] 125.00 32.63 6,489.65 75.00 mple 4 : <u>sa</u>	ample 4 Corr. Ar Die 4 Molarity [pmol/I] 5,411.3 385.3 38,617.3 10.9 mple 4 . Molarity C	ea 1: Observations Lower Marker Upper Marker	4,274.2 Aligned Migr 43.00 53.53 65.31 113.00 distribution in		p]

Assay Class: High Sensitivity DNA Assay Data Path: C:\...ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad Created: 7/9/2015 11:16:21 AM Modified: 7/9/2015 11:49:07 AM

Electropherogram Summary Continued ...



Overall Results for sam	ple 5 :	sample 5		
Number of peaks found:	26		Corr. Area 1:	25,557.8
Noise:	0.2			

Peak table for sample 5 : <u>sample 5</u>

Pea k	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	116	77.92	1,016.6		52.37
3	263	59,997.80	346,035.5		66.05
4	279	105,563.40	574,124.3		67.50
5	497	2,634.63	8,031.3		83.01
6	658	2,384.04	5,491.4		89.57
7	716	4,665.46	9,874.7		91.07
8	1,426	171.98	182.8		97.49
9	1,564	281.85	273.0		98.38
10	1,725	183.80	161.5		99.41
11	1,878	179.54	144.8		100.40
12	2,641	896.43	514.2		103.30
13	5,293	135.61	38.8		107.47
14	6,445	105.43	24.8		108.97
15	7,460	75.78	15.4		110.14
16	8,609	69.18	12.2		111.27
17	9,327	97.22	15.8		111.97
18	10,380	75.00	10.9	Upper Marker	113.00
19	13,013	0.00	0.0		115.58
20	13,683	0.00	0.0		116.23
21	15,455	0.00	0.0		117.97
22	17,035	0.00	0.0		119.51
23	17,801	0.00	0.0		120.26
24	18,375	0.00	0.0		120.82
25	19,716	0.00	0.0		122.14

Assay Class:	High Sensitivity DNA Assay
Data Path:	C:\ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad

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Electropherogram Summary Continued ...

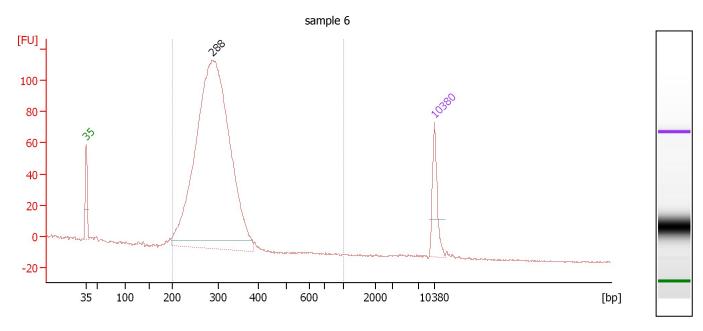
Pea	k table for sa	mple 5 : _	<u>sample 5</u>			
Pea k	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]	
26	22,780	0.00	0.0		125.14	
27	24,743	0.00	0.0		127.06	
28	28,334	0.00	0.0		130.57	
Region table for sample 5 : <u>sample 5</u>						

From [bp]	Average Size [bp]	To [bp] Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
200	318	1,000	25,557.8	867,769.8	94	37.5	164,953.83

Assay Class:High Sensitivity DNA AssayData Path:C:\...ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad

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Electropherogram Summary Continued ...



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

Number of peaks found:	1	Corr. Area 1:	1,338.6
Noise:	0.5		

Peak	tal	ble for sampl	e6: <u>sam</u> p	<u>ole 6</u>				
Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observat	tions	Aligned Migr	ation Time [s]
1	•	35	125.00	5,411.3	Lower Ma	rker	43.00	
2		288	2,001.12	10,540.8			68.33	
3		10,380	75.00	10.9	Upper Ma	rker	113.00	
Regi	Region table for sample 6 : <u>sample 6</u>							
From [bp] 200	1	Average Size [bp] 290	e To [bp] Corr Area 1,000 1,338	[pmol/l]	Co % of lor Total 100	Size c CV [% 11.9	listribution in 6]	Conc. [pg/μl] 1,880.21

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Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad	Created: Modified:	7/9/2015 11:16:21 AM 7/9/2015 11:49:07 AM	
Electropher	ogram Summary Continued			
	sample 7			
[FU] 350 -	A C C C C C C C C C C C C C C C C C C C			
300 -				
250 -				
200 -				

100-

50-

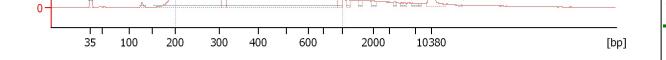
Number of peaks found:	4	Corr. Area 1:	5,618.1
Noise:	0.3		

Peak table for sample 7 : <u>sample 7</u>										
Pea k		Size [bp]	Conc. [pg/	μ] M	olarity [pmol/	I] O I	bservati	ons	Aligned Migra	ation Time [s]
1		35	125.00	5,	411.3	Lo	wer Mar	ker	43.00	
2		129	24.08	28	32.3				53.62	
3		299	3,465.71	17	7,565.7				69.37	
4		309	4,863.63	23	3,854.7				70.18	
5		10,380	75.00	10).9	Up	oper Marl	ker	113.00	
6		11,772	0.00	0.	0				114.36	
Region table for sample 7 : <u>sample 7</u>										
From [bp] 200	l	Average Size [bp] 332	/	Corr. Area 5,618.1	Molarity [pmol/l] 39,666.9	Co % lor To	otal	Size d CV [% 22.4	istribution in []]	Conc. [pg/µl] 8,242.78

[bp]

2015-07-09 <u>-</u>	_001.xad		Page 13 of 15
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Electropher	ogram Summary Continued		
	sample 8		
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Overall Results for samp	le 8:	sample 8		
Number of peaks found:	13		Corr. Area 1:	12,985.6
Noise:	0.2			

Peak table for sample 8 : <u>sample 8</u>									
Pea k	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migr	ation Time [s]			
1 📢	35	125.00	5,411.3	Lower Marker	43.00				
2	128	17.73	209.4		53.52				
3	298	5,116.43	26,036.0		69.26				
4	309	826.41	4,052.4		70.19				
5	321	8,290.81	39,190.8		71.12				
6	948	17.78	28.4		94.09				
7	1,160	13.96	18.2		95.79				
8	1,596	11.22	10.7		98.58				
9	1,963	12.76	9.8		100.94				
10	3,813	7.15	2.8		105.55				
11	5,372	9.74	2.7		107.57				
12	6,635	8.62	2.0		109.22				
13	7,915	4.37	0.8		110.59				
14 🕨	10,380	75.00	10.9	Upper Marker	113.00				
15	16,765	0.00	0.0		119.25				
Region table for sample 8 : <u>sample 8</u>									
From [bp]	Average Siz [bp]	ze To [bp] Cori Area		Co % of Size	distribution in [%]	Conc. [pg/µl]			
200	359	1,000 12,9	85.6 62,036.1	96 28.7		13,417.41			

400-

300-

200-

100-

s'

28

Assay Class: Data Path: Gel Image	High S C:\e	Sensitivity ents and S	DNA Assay ettings\Bioa	analyzer\20)15-07-09\2	2015-07-09	_001.xad		Cr Mc	eated: dified:	7/9/2015 1 7/9/2015 1	1:16:21 AN 1:49:07 AN
[bp]		Ŧ	N	m	र ा	ю	ى	5	œ	σ	9	Ξ
	Ladder	sample 1	sample 2	sample 3	sample 4	sample 5	sample 6	sample 7	sample 8	sample 9	sample 10	sample 11
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7000 — 💼	_											
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Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2015-07-09\2015-07-09_001.xad	Created: Modified:	7/9/2015 11:16:21 AM 7/9/2015 11:49:07 AM				
Invalid Samples							

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.