

Assay Class: Data Path:	High Sensitivity C:\ents and S	v DNA Assay Settings\Bioanalyzer\20	015-05-22\2015	5-05-22_	001.xad	Created: Modified:	5/22/20 5/22/20	15 10:02:41 AM 15 10:35:25 AM
Electrophore	esis File Run Sı	ummary (Chip Sum	nmary)					
Sample Name	2	Sample Comment	Rest. Digest	Status	Observation	Result	Label	Result Color
RNA 2nd clean	+/+			~				
RNA 2nd clean	+/y			\checkmark				
RNA 2nd clean	-/y			\checkmark				
RNA 2nd clean	-/+			×				
ChIP 2nd try +/	/+			×				
ChIP 2nd try +/	′y		Π	×				
ChIP 2nd try -/y	4		Ē	~				
ChIP 2nd try -/-	+		Ē	~				
sample 9			Π					
sample 10			Ē					
sample 11			Ē					
Ladder			$\overline{\Box}$	×				
Chip Lot #				Reag	ent Kit Lot #			

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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] : 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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High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2015-05-22\2015-05-22_001.xad Assay Class: Data Path:

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Electropherogram Summary



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	50.77
4		150	150.00	1,515.2	Ladder Peak	55.45
5		200	150.00	1,136.4	Ladder Peak	60.08
6		300	150.00	757.6	Ladder Peak	69.17
7		400	150.00	568.2	Ladder Peak	77.19
8		500	150.00	454.5	Ladder Peak	82.93
9		600	150.00	378.8	Ladder Peak	87.68
10		700	150.00	324.7	Ladder Peak	90.87
11		1,000	150.00	227.3	Ladder Peak	94.91
12		2,000	150.00	113.6	Ladder Peak	101.19
13		3,000	150.00	75.8	Ladder Peak	104.46
14		7,000	150.00	32.5	Ladder Peak	109.73
15		10,380	75.00	10.9	Upper Marker	113.00



Electropherogram Summary Continued ...



Overall Results for sam	ple1:	<u>RNA 2nd clean +/+</u>	
Number of peaks found:	16	Corr. Area 1:	1,065.0
Noise:	0.2		

Peak table for sample 1 : RNA 2nd clean +/+

Pea k		Size [bp]	Conc. [pg	յ/μ]]	Molarity [pmol/	I] Obser	vations	Aligned M	ligration Tir	ne [s]
1	•	35	125.00		5,411.3	Lower	Marker	43.00		
2		260	251.30		1,466.2			65.50		
3		275	104.52		576.7			66.85		
4		282	72.98		392.0			67.53		
5		294	58.47		301.2			68.63		
6		299	130.01		659.3			69.05		
7		325	122.29		570.2			71.17		
8		343	72.15		318.8			72.61		
9		357	74.59		316.9			73.71		
10		376	34.51		139.0			75.27		
11		411	27.92		102.8			77.85		
12		461	30.07		98.9			80.69		
13		474	26.10		83.4			81.45		
14		492	35.46		109.2			82.46		
15		520	24.46		71.3			83.86		
16		549	11.17		30.8			85.25		
17		626	4.24		10.3			88.51		
18		10,380	75.00		10.9	Upper	Marker	113.00		
Regio	on t	able for sam	ple 1:	RNA	2nd clean +/+					
From		Average Size	e To [bp] Corr.	Molarity	% of Total	Size dist	ribution in	Conc.	Co
200		360	1,000	1,065.0) 6,917.2	97	28.0		ניי <i>יין ופיז</i> ו 1,493.25	

Assay Cl Data Pat Electro	ass: High Sensitivity DNA Assay h: C:\ents and Settings\Bioanalyzer\2015-05-22\2015-05-22_001.xad pherogram Summary Continued	Created: Modified:	5/22/2015 10:02:41 AM 5/22/2015 10:35:25 AM
	RNA 2nd clean +/y		
[FU]		N0380	
100-			
80 -	35		
60 -			
40 -	24 ⁶²¹⁶ 20 ⁶ 25 ⁶ 26 ⁴		
20-	A A A A A A A A A A A A A A A A A A A		
0		1 Mar	-
	35 100 200 300 400 500 700 2000 10)380 [t	_ [qc

Overall Results for sam	ple 2 :	<u>RNA 2nd clean +/y</u>	
Number of peaks found:	14	Corr. Area 1:	718.7
Noise:	0.2		

Peak tab	le for sar	nple 2	:	RNA	2nd	clean	+/y

Pea k	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l] Observation	s Aligned M	ligration Ti	ne [s]
1 📢	35	125.00	5,411.3	Lower Marker	43.00		
2	247	99.97	612.1		64.39		
3	260	67.69	394.8		65.50		
4	276	50.49	276.9		67.00		
5	302	50.59	253.4		69.36		
6	326	58.37	271.3		71.25		
7	344	26.18	115.4		72.66		
8	378	17.36	69.6		75.41		
9	396	17.72	67.8		76.86		
10	408	20.26	75.3		77.64		
11	419	14.60	52.8		78.28		
12	451	20.79	69.8		80.12		
13	465	20.95	68.3		80.89		
14	497	16.84	51.4		82.74		
15	558	5.74	15.6		85.69		
16 🕨	10,380	75.00	10.9	Upper Marker	113.00		
Region	table for sa	mple 2 : <u>RN</u>	IA 2nd clean +/y				
From [bp] 200	Average Si [bp] 359	ze To [bp] Corr Area 1.000 718.7	Molarity [pmol/l] 3.984.2	% of Size Total CV [98	distribution in %]	Conc. [pg/µl] 852.63	Co lor

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Electropherogram Summary Continued ...



Overall Results for sam	ple 3 :	<u>RNA 2nd clean -/y</u>	
Number of peaks found:	10	Corr. Area 1:	2,569.1
Noise:	0.2		

Peak table for sample 3 : <u>RNA 2nd clean -/y</u>

1,000

2,569.1

Pea k		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Obser	vations	Aligned M	igration Tin	ne [s]
1	•	35	125.00	5,411.3	Lower	Marker	43.00		
2		277	696.75	3,816.9			67.04		
3		285	249.13	1,325.4			67.78		
4		300	344.86	1,739.9			69.19		
5		327	308.68	1,432.1			71.30		
6		342	399.77	1,768.7			72.57		
7		369	121.21	497.3			74.73		
8		380	802.44	3,202.2			75.56		
9		499	128.74	391.1			82.86		
10		551	127.72	351.1			85.36		
11		691	14.46	31.7			90.59		
12		10,380	75.00	10.9	Upper	Marker	113.00		
Regio	on t	able for sam	nple 3 : <u>RN</u>	<u>A 2nd clean -/y</u>					
From [bp]		Average Siz [bp]	e To [bp] Corr. Area	Molarity [pmol/l]	% of Total	Size dist CV [%]	ribution in	Conc. [pg/µl]	Co lor

100

15,300.1

368

200

27.4

3,395.94

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Electropherogram Summary Continued ...



Overall Results for sam	ple 4 :	<u>RNA 2nd clean -/+</u>	
Number of peaks found:	16	Corr. Area 1:	1,808.2
Noise:	0.1		

Peak table for sample 4 :	RNA 2nd clean -/+
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Pea k		Size [bp]	Conc. [pg	/µI]	Molarity [p	mol/l]	Observ	vations	Aligned M	ligration Tin	ne [s]
1	٠	35	125.00		5,411.3		Lower	Marker	43.00		
2		276	418.31		2,292.5				67.03		
3		286	111.01		588.3				67.88		
4		299	156.65		792.9				69.10		
5		307	139.18		686.7				69.74		
6		326	191.07		887.4				71.27		
7		341	114.33		508.2				72.45		
8		359	88.31		372.3				73.94		
9		377	76.77		308.7				75.34		
10		387	55.04		215.5				76.15		
11		417	122.30		444.1				78.18		
12		450	67.47		227.4				80.03		
13		472	47.28		151.9				81.30		
14		491	75.42		232.6				82.43		
15		535	19.46		55.1				84.59		
16		550	23.16		63.8				85.32		
17		575	36.49		96.2				86.49		
18		10,380	75.00		10.9		Upper l	Marker	113.00		
Regio	n t	able for sam	ple 4 :	RNA	2nd clean	<u>-/+</u>					
From [bp]		Average Size [bp]	e To [bp]] Corr. Area	Molarit [pmol/	у %] Т	% of otal	Size disti CV [%]	ibution in	Conc. [pg/µl]	Co lor
200		371	1,000	1,808.2	2 10,031.3	3 9 [°]	9	27.8		2,244.80	

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Assay Class Data Path:	s: High : C:\e	Sensitivity ents and S	DNA Ase ettings\l		Created: Modified:	5/22/2015 10:02:41 AM 5/22/2015 10:35:25 AM				
Electroph	erogram	Summar	y Conti	nuea						
					ChIP 2nd	try +/+				
[FU]_								0380		
80-								Ĩ		
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	Í									
60-										
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40-										
30 -										
20-	4									
10-										
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-10-										
10	35	100	200	300	400 5	500 700	2000	10380	[t	[qq
Overall Re	esults for s	sample 5	: <u>c</u>	<u>hIP 2nd t</u>	ry +/+					
Number of p	beaks found	: C)		Corr. A	rea 1:	200.6			
Noise:		C).2							
Peak table	e for samp	le 5 :	<u>ChIP</u>	2nd try +	<u>-/+</u>					
Pea S k	Size [bp]	Conc. [p	og/µl]	Molarity	y [pmol/l]	Observations	Aligned	Migration Tin	ne [s]	
1 4 3	35	125.00		5,411.3		Lower Marker	43.00			
2 🕨 1	10,380	75.00		10.9		Upper Marker	113.00			
Pegion tal	hla for sar	nnlo 5 ·	Ch	ID 2nd try	/ 1/1					

Region t	able for sample	e5:	ChIP 2	<u>2nd try +/+</u>				
From	Average Size	To [bp]] Corr.	Corr. Molarity		Size distribution in	Conc.	Со
[bp]	[bp]		Area	[pmol/l]	Total	CV [%]	[pg/µl]	lor
200	454	1,000	200.6	1,256.1	48	44.2	288.22	

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Electropherogram Summary Continued ...



Overall Results for sample 6 : <u>ChIP 2nd try +/y</u>

Number of peaks found:	0	Corr. Area 1:	24.4
Noise:	0.4		

Peak table for sa	mple 6 :	ChIP	2nd	try	+/	/y
	-					_

Pea k		Size [bp]	Conc. [pg	/µI]	Molarity [pmol/l]] Obs	ervations	Aligned M	igration Tin	ne [s]
1	٠	35	125.00		5,411.3	Lowe	er Marker	43.00		
2		10,380	75.00		10.9	Uppe	er Marker	113.00		
Regio	n t	able for sam	ple 6 :	ChIF	<u>2nd try +/y</u>					
From [bp]		Average Size [bp]	• To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distr CV [%]	ibution in	Conc. [pg/µl]	Co lor
200		020	1,000	24.4	114.9	20	20.8		22.00	

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Electropherogram Summary Continued ...



Overall Results for sample 7 : <u>ChIP 2nd try -/y</u>

Number of peaks found:	1	Corr. Area 1:	168.7
Noise:	0.5		

Peak table for sample 7	:	ChIP 2nd try -/y
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Pea k		Size [bp]	Conc. [pg	/µI]	Molarity [pmol/l]] Obse	rvations	Aligned M	igration Tir	ne [s]
1 2	<.	35 10,380	125.00 75.00		5,411.3 10.9	Lower Upper	⁻ Marker Marker	43.00 113.00		
3 Regio	n t	12,985 able for sam	0.00 ple 7 :	ChIF	0.0 • 2nd try -/y			115.52		
From [bp] 200		Average Size [bp] 452	• To [bp]	Corr. Area 168.7	Molarity [pmol/l] 925.8	% of Total 39	Size distr CV [%] 44.6	ibution in	Conc. [pg/µl] 210.65	Co lor

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Electropherogram Summary Continued ...



Overall Results for sample 8 : <u>ChIP 2nd try -/+</u>

Number of peaks found:	0	Corr. Area 1:	189.6
Noise:	0.5		

Peak table for sample 8 : ChI	<u>2nd 2</u>	try -/+	
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Pea k		Size [bp]	Conc. [pg	/µI]	Molarity [pmol/	I] Ob	servations	Aligned M	ligration Ti	me [s]
1	€.	35	125.00		5,411.3	Lov	ver Marker	43.00		
2		10,380	75.00		10.9	Up	per Marker	113.00		
Region table for sample 8 : ChIP 2nd try -/+										
From [bp]		Average Size [bp]	e To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size dist CV [%]	ribution in	Conc. [pg/µl]	Co Ior
200		382	1,000	189.6	1,487.2	57	56.0		271.59	



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.

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