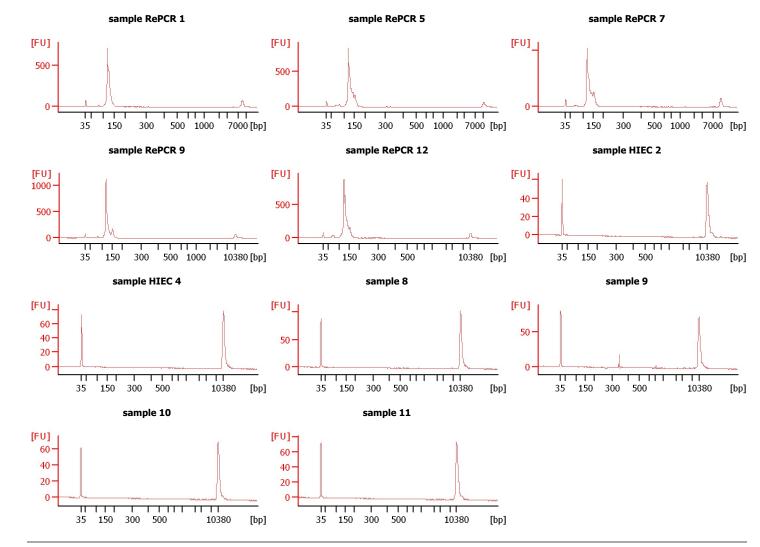
2014-02-14 <u></u>	_004.xad				Pag	ge 1	of	16
Assay Class: High Sensitivity DNA Assay Data Path: C:\ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad Electrophoresis File Run Summary)14 1:24)14 2:0!		
		Instrument Informa	tion:					
		Instrument Name:	DE13701086	Firr	nware:	C.01.069		
		Serial#:	DE13701086	Тур	be:	G2938B		
		Assay Information:						
		Assay Origin Path:		gram Files\Agilent\2100 bioanalyzer\2100 \assays\dsDNA\High Sensitivity DNA.xsy				
		Assay Class:	High Sensitivity DNA	Assay				
		Version:	1.03					
		Assay Comments:	Copyright © 2003-20	10 Agilent Te	echnolog	ies		
		Chip Information:						
		Chip Lot #:						
		Reagent Kit Lot #						

Reagent Kit Lot #: Chip Comments:



2014-02-14_	004.xad					Page	2 of	f 16
Assay Class: Data Path:	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\	2014-02-14\20	14-02-14	_004.xad	Created: Modified:	2/14/2014 2/14/2014		
Electrophore	sis File Run Summary (Chip Su	mmary)						
Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Labe	el Re	esult Co	olor
sample RePCR 1			~					
sample RePCR 5	1		×					
sample RePCR 7	1		\checkmark					
sample RePCR 9	1		\sim					
sample RePCR 1	2		× .					
sample HIEC 2			\checkmark					
sample HIEC 4			× .					
sample 8			× .					
sample 9			\checkmark					
sample 10			× .					
sample 11			\sim					
Ladder			×					

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay Data Path: C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.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: 2/14/2014 1:24:33 PM Modified: 2/14/2014 2:05:57 PM

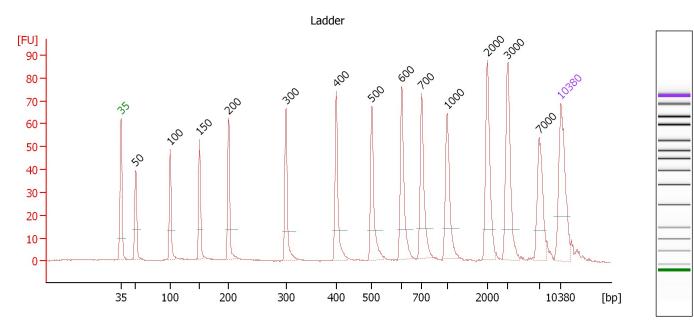
High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad Assay Class: Data Path:

Created:

Modified:

2/14/2014 1:24:33 PM 2/14/2014 2:05:57 PM

Electropherogram Summary



Overall Results for Ladder

Noise:

0.2

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	45.33	50	150.00	4,545.5	Ladder Peak
3		50.84	100	150.00	2,272.7	Ladder Peak
4	L	55.51	150	150.00	1,515.2	Ladder Peak
5	L	60.13	200	150.00	1,136.4	Ladder Peak
6	L	69.24	300	150.00	757.6	Ladder Peak
7	L	77.26	400	150.00	568.2	Ladder Peak
8		82.90	500	150.00	454.5	Ladder Peak
9	L	87.69	600	150.00	378.8	Ladder Peak
10	L	90.83	700	150.00	324.7	Ladder Peak
11		94.90	1,000	150.00	227.3	Ladder Peak
12	L	101.30	2,000	150.00	113.6	Ladder Peak
13		104.56	3,000	150.00	75.8	Ladder Peak
14	L	109.52	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\2014-02-14\2014-02-14_0	04.xad Created: Modified:	2/14/2014 1:24:33 Pr 2/14/2014 2:05:57 Pr
Electropher	ogram Summary Continued		
	sample RePCR 1		
[FU]	1 ⁸		
700 -			
600 -			
500 -	-13		
400 -			
300 -			
200 -		ŝ	
100-	min and a start and a start a	86 ²	
0		<u>\</u>	
L	35 100 200 300 400 500	700 2000 10380 [b	p]

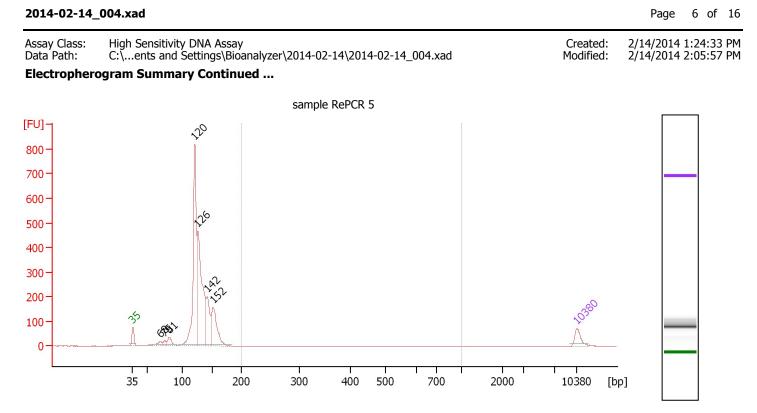
Overall Results for sample 1 : sar	<u>nple RePCR 1</u>
------------------------------------	---------------------

2014-02-14_004.xad

Number of peaks found:	4	Corr. Area 1:	19.2
Noise:	0.2		

Peak table for sample 1 : <u>sample RePCR 1</u>								
Pea k	Aligned Migration Tim	ie [s] Size [bp]] Conc	. [pg/µl]	Molarity	[pmol/l]	Observat	ions
	43.00	35	125.0	0	5,411.3		Lower Mar	ker
2	48.71	81	2,054	.34	38,596.7			
3	52.49	118	53,84	4.74	693,476.	7		
4	52.98	123	58,76	0.48	724,251.9	9		
5	111.19	8,623	2,698	.59	474.2			
6	113.00	10,380	75.00	1	10.9		Upper Mar	ker
Regio	on table for sample 1 :	sample RePC	<u>R 1</u>					
From [bp] 200	To [bp] Average Size [bp] 1,000 486	[pmol/l] [l	conc. pg/μl] 21.65	Corr. Area 19.2	% of Total 1	Size distr CV [%] 45.1	ibution in	Co lor

PM PM



Overall Results for sample 2 :	sample RePCR 5
--------------------------------	----------------

Number of peaks found:	7	Corr. Area 1:	2.3
Noise:	0.1		

Peak t	table for sample 2 :	sample RePCR 5			
Pea k	Aligned Migration Tim	ne [s] Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations
1	43.00	35	125.00	5,411.3	Lower Marker
2	47.33	68	62.59	1,392.5	
3	48.04	75	46.08	936.1	
4	48.76	81	112.18	2,096.8	
5	52.75	120	1,868.34	23,509.0	
6	53.25	126	1,654.55	19,924.5	
7	54.72	142	501.48	5,366.5	
8	55.69	152	601.35	5,995.8	
9	113.00	10,380	75.00	10.9	Upper Marker
Regio	on table for sample 2 :	sample RePCR	5		
From [bp] 200	To [bp] Average Size [bp] 1,000 474	Molarity Con [pmol/l] [pg 13.3 3.27	/µl] Area	% of Size dist Total CV [%] 0 42.4	ribution in Co lor

2014-02-14_004.xad				
Assay Class: Data Path: Electropher	Assay Class: High Sensitivity DNA Assay Created: Created: Data Path: C:\ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad Modified: Description Electropherogram Summary Continued Continued Created: Crea			
	sample RePCR 7			
[FU] 500 - 400 - 300 - 200 -	128 	-		
0-	35 100 200 300 400 500 700 2000	10380 [b	p]	

Overall Results for sample 3 :	sample RePCR 7
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Number of peaks found:	5	Corr. Area 1:	0.3
Noise:	0.2		

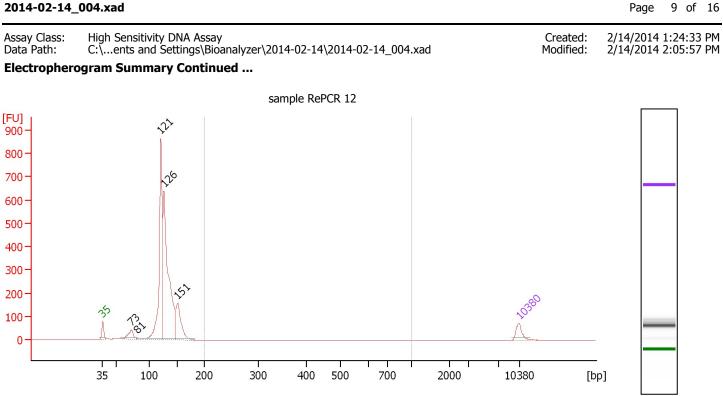
Peak	tał	ble for sample 3 :	sample ReF	<u>PCR 7</u>						
Pea k		Aligned Migration Tin	ne [s] Size	[bp]	Conc	. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1		43.00	35		125.0	0	5,411.3		Lower Mar	ker
2		47.17	67		23.81		540.8			
3		48.02	74		43.23		880.1			
4		52.71	120		2,025	.99	25,583.5			
5		54.67	141		295.9	0	3,180.0			
6		55.65	151		523.6	1	5,236.7			
7		113.00	10,38	30	75.00		10.9		Upper Mar	ker
Regio	on t	table for sample 3 :	sample R	ePCR 7	2					
From [bp] 200		To [bp] Average Size [bp] 1,000 668	Molarity [pmol/l] 1.1	Cond [pg/ 0.38		Corr. Area 0.3	% of Total 0	Size distr CV [%] 25.8	ibution in	Co lor

2014-02-14	_004.xad		Page 8 of 16
Assay Class: Data Path: Electropher	High Sensitivity DNA Assay C:\ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad ogram Summary Continued	Created: Modified:	2/14/2014 1:24:33 PM 2/14/2014 2:05:57 PM
	sample RePCR 9		
[FU]	-2 ⁰		
1000 -			
500 -			
	53	-80 -	
0	35 682 /	10380 A	
	35 100 200 300 400 500 700 2000	10380 [b	p]

Overall Results for sample 4 :	sample RePCR 9
--------------------------------	----------------

Number of peaks found:	4	Corr. Area 1:	2.3
Noise:	0.2		

Peak ta	ble for sample 4 :	sample RePC	<u>R 9</u>					
Pea k	Aligned Migration Tin	ne [s] Size [ł	op] Con	c. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1 📢	43.00	35	125.	00	5,411.3		Lower Ma	rker
2	47.34	68	35.5	7	790.3			
3	48.87	82	64.3	7	1,188.1			
4	52.68	120	4,08	2.02	51,671.7			
5	55.75	153	622.	15	6,177.6			
6 🕨	113.00	10,380	75.0	0	10.9		Upper Ma	rker
Region	table for sample 4 :	sample Rel	PCR 9					
From [bp] 200	To [bp] Average Size [bp] 1,000 391	Molarity [pmol/l] 16.0	Conc. [pg/μl] 3.46	Corr. Area 2.3	% of Total 0	Size distr CV [%] 42.2	ibution in	Co lor

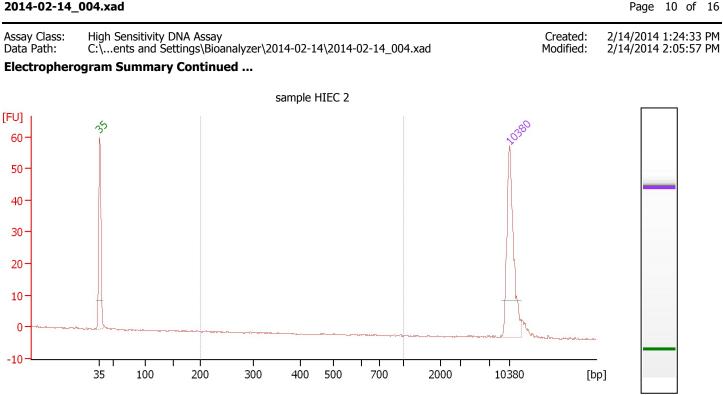


Overall Results for sample 5 : <u>sa</u>	ample RePCR 12
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Number of peaks found:	5	Corr. Area 1:	0.9
Noise:	0.2		

Peak table for sample 5	:	sample RePCR 12
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Pea k		Aligned Migration Tim	e [s] Size	[bp] Co	nc. [pg/µl]	Molarity	[pmol/l]	Observat	tions
1		43.00	35	125	5.00	5,411.3		Lower Ma	rker
2		47.84	73	165	5.77	3,452.5			
3		48.78	81	12.	15	226.5			
4		52.77	121	1,8	95.00	23,798.6			
5		53.31	126	2,4	63.12	29,522.6			
6		55.59	151	553	8.92	5,561.0			
7		113.00	10,38	io 75.	00	10.9		Upper Ma	rker
Regi	on t	able for sample 5 :	sample R	ePCR 12					
From [bp] 200	1	To [bp] Average Size [bp] 1,000 351	Molarity [pmol/l] 6.5	Conc. [pg/μl] 1.39	Corr. Area 0.9	% of Total 0	Size distr CV [%] 31.1	ibution in	Co lor

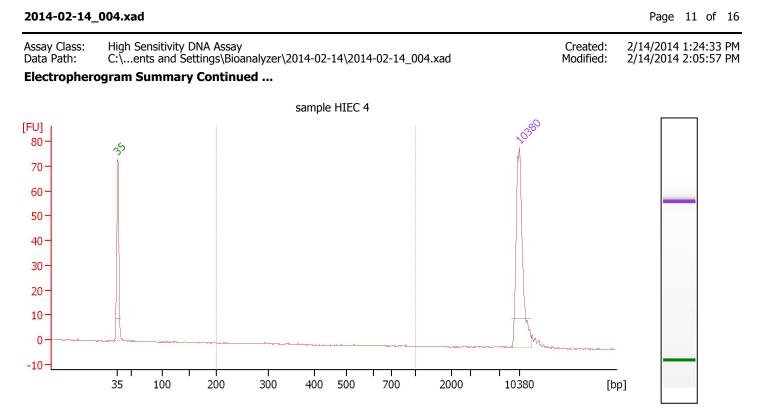


Overall Results for sample 6 : sample HIEC 2

Number of peaks found:	0	Corr. Area 1:	0.0
Noise:	0.2		

Peak table for sample 6 : sample HIEC 2

Pea k		Aligned Migration Tin	1e [s]	Size [bp]	Conc. [pg/	µl] Molari	ty [pmol/l]	Observat	ions
1		43.00		35	125.00	5,411.3		Lower Mar	ker
2	Þ	113.00		10,380	75.00	10.9		Upper Mar	ker
Regio	on t	table for sample 6 :	samp	ple HIEC 2					
From [bp]		To [bp] Average Size [bp]	Molarit [pmol/	/l] [pg/	µl] Area	a Total	Size distr CV [%]	ibution in	Co lor
200		1,000 928	0.0	0.00	0.0	0	4.1		



Overall Results for sample 7 : <u>sample HIEC 4</u>

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

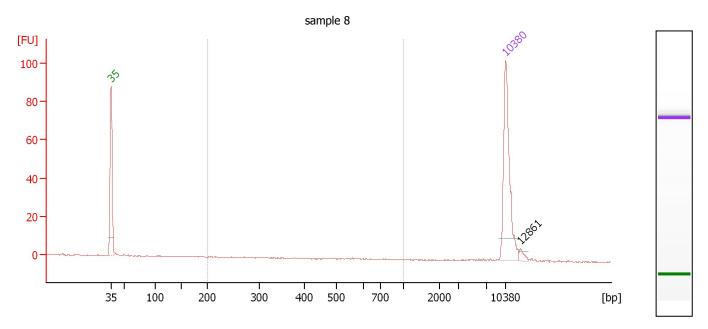
Peak table for sample 7 : <u>sample HIEC 4</u>

Pea k	Aligned Migration Tim	e [s] Size [l	bp] Con	c. [pg/µl]	Molarity	[pmol/l]	Observat	ions
1	43.00	35	125.0	00	5,411.3		Lower Mar	ker
2 🕨	113.00	10,380	75.0)	10.9		Upper Mar	ker
Region	table for sample 7 :	sample HI	<u>EC 4</u>					
From [bp]	To [bp] Average Size [bp]	Molarity [pmol/l]	Conc. [pg/µl]	Corr. Area	% of Total	Size distr CV [%]	ibution in	Co lor
200	1,000 641	0.5	0.14	0.1	1	41.9		

Assay Class:High Sensitivity DNA AssayData Path:C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad

Created: 2/14/2014 1:24:33 PM Modified: 2/14/2014 2:05:57 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : <u>sample 8</u>

Number of peaks found:	1	Corr. Area 1:	0.1
Noise:	0.2		

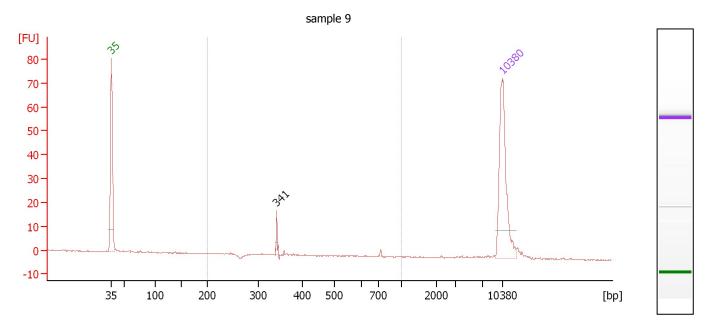
Peak table for sample 8 : <u>sample 8</u>

Pea k		Aligned Migration Tin	ne [s] Size	[bp]	Conc. [pg/	/µl] Molari	ty [pmol/l]	Observat	tions
1		43.00	35		125.00	5,411.3	3	Lower Ma	rker
2		113.00	10,3	80	75.00	10.9		Upper Ma	rker
3		115.55	12,8	61	0.00	0.0			
Regi	on 1	table for sample 8 :	sample 8	<u>l</u>					
From [bp] 200	1	To [bp] Average Size [bp] 1,000 512	Molarity [pmol/l] 0.4	Con [pg/ 0.10			Size distr CV [%] 37.5	ibution in	Co lor

High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad Assay Class: Data Path:

2/14/2014 1:24:33 PM 2/14/2014 2:05:57 PM Created: Modified:

Electropherogram Summary Continued ...



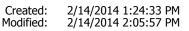
Overall Results for sample 9 : sample 9

Number of peaks found:	1	Corr. Area 1:	7.3
Noise:	0.2		

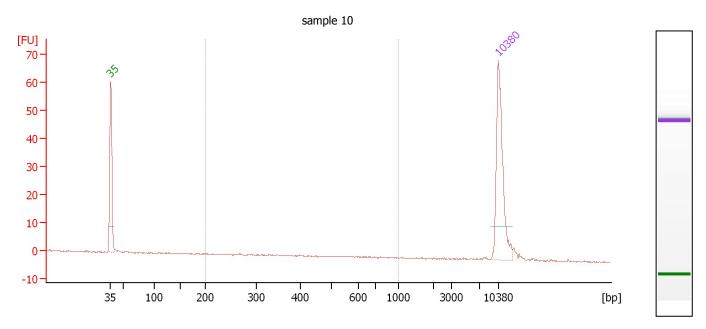
Peak table for sample 9 : sample 9

Pea k	Aligned Migration T	ime [s] Size [b	p] Conc. [pg/µ	ul] Molarity [pmol/l] Observations
1	43.00	35	125.00	5,411.3	Lower Marker
2	72.56	341	7.75	34.4	
3	113.00	10,380	75.00	10.9	Upper Marker
Regio	n table for sample 9 :	sample 9			
From [bp] 200	To [bp] Average Siz [bp] 1,000 385	e Molarity [pmol/l] 36.6	Conc. Corr. [pg/µ] Area 8.63 7.3	% of Size dis Total CV [%] 45 31.3	stribution in Co lor

High Sensitivity DNA Assay C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad Assay Class: Data Path:



Electropherogram Summary Continued ...



Overall Results for sample 10 : sample 10

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

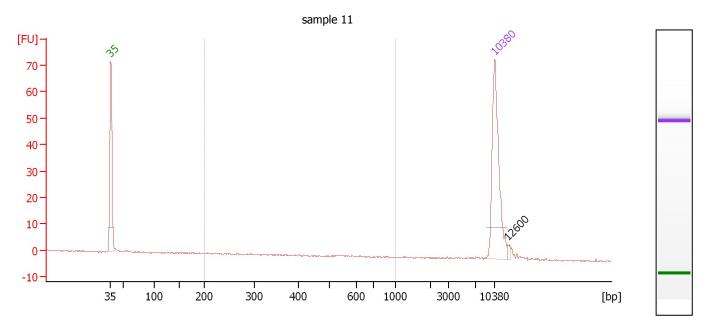
Peak table for sample 10 : sample 10

Pea k		Aligned Migration Tim	ne [s]	Size [bp]	Conc. [pg/µl]	Molarity	[pmol/l]	Observat	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 t	table for sample 10 :	sam	ple 10						
From [bp] 200		To [bp] Average Size [bp] 1,000 487	Molarit [pmol/ 16.1		μl] A	Corr. Area 3.2	% of Total 21	Size distri CV [%] 38.6	bution in	Co lor

Assay Class:High Sensitivity DNA AssayData Path:C:\...ents and Settings\Bioanalyzer\2014-02-14\2014-02-14_004.xad

Created: 2/14/2014 1:24:33 PM Modified: 2/14/2014 2:05:57 PM

Electropherogram Summary Continued ...



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

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

Peak table for sample 11	:	sample 11
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Pea k	ł	Aligned	I Migration Tim	e [s] Si	ize [bp]	Conc.	[pg/µl]	Molarity	[pmol/l]	Observat	ions
1	4	43.00		35	5	125.00		5,411.3		Lower Mar	ker
2	> 1	113.00		10	0,380	75.00		10.9		Upper Mar	ker
3	1	115.28		12	2,600	0.00		0.0			
Regior	ı tal	ble for	sample 11 :	samp	<u>le 11</u>						
From [bp] 200		Fo [bp] 1,000	Average Size [bp] 329	Molarity [pmol/l] 1.5	Conc [pg/ 0.27		Corr. Area 0.2	% of Total 2	Size distr CV [%] 40.2	ibution in	Co lor