Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electrophoresis File Run Summary

Instrument Information:

Instrument Name:	DE13701086	Firmware:	C.01.069
Serial#:	DE13701086	Type:	G2938B

Assay Information:

Assay Origin Path:	C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy
Assay Class:	High Sensitivity DNA Assay
Version:	1.03
Assay Comments:	Copyright © 2003-2010 Agilent Technologies

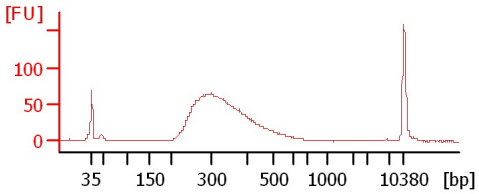
Chip Information:

Chip Lot #:

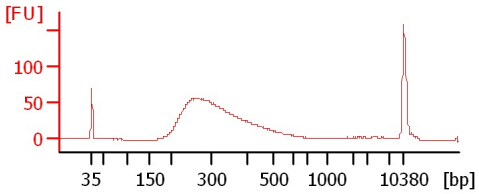
Reagent Kit Lot #:

Chip Comments:

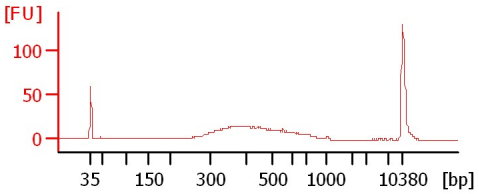
NP Native 08-23-16



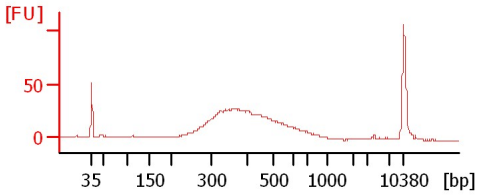
TL2 500ng RTS



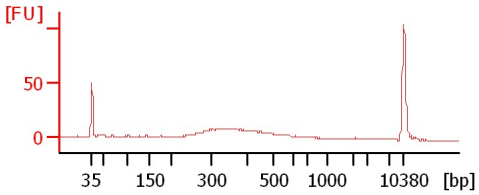
TL2 500ng RTL



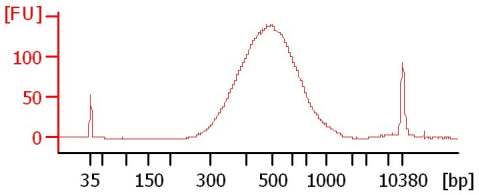
TL2 100ng RTL



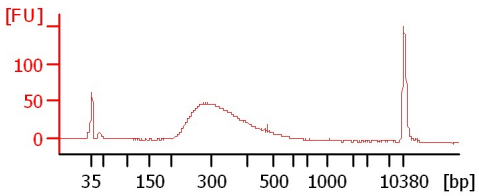
TL2 10ng RTL



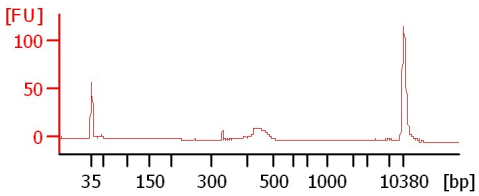
SC4 Pool (1:2)



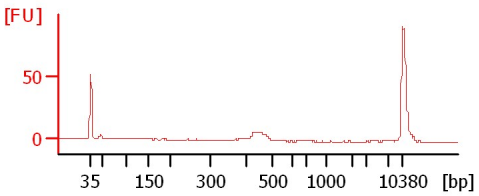
NP Native 08-23-16



Slupsky (1:600)



Slupsky (1:1200)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
NP Native 08-23-16		☐	✔			
TL2 500ng RTS		☐	✔			
TL2 500ng RTL		☐	✔			
TL2 100ng RTL		☐	✔			
TL2 10ng RTL		☐	✔			
SC4 Pool (1:2)		☐	✔			
NP Native 08-23-16		☐	✔			
Slupsky (1:600)		☐	✔			
Slupsky (1:1200)		☐	✔			
sample 10		☐				
sample 11		☐				
Ladder		☐	✔			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

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

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
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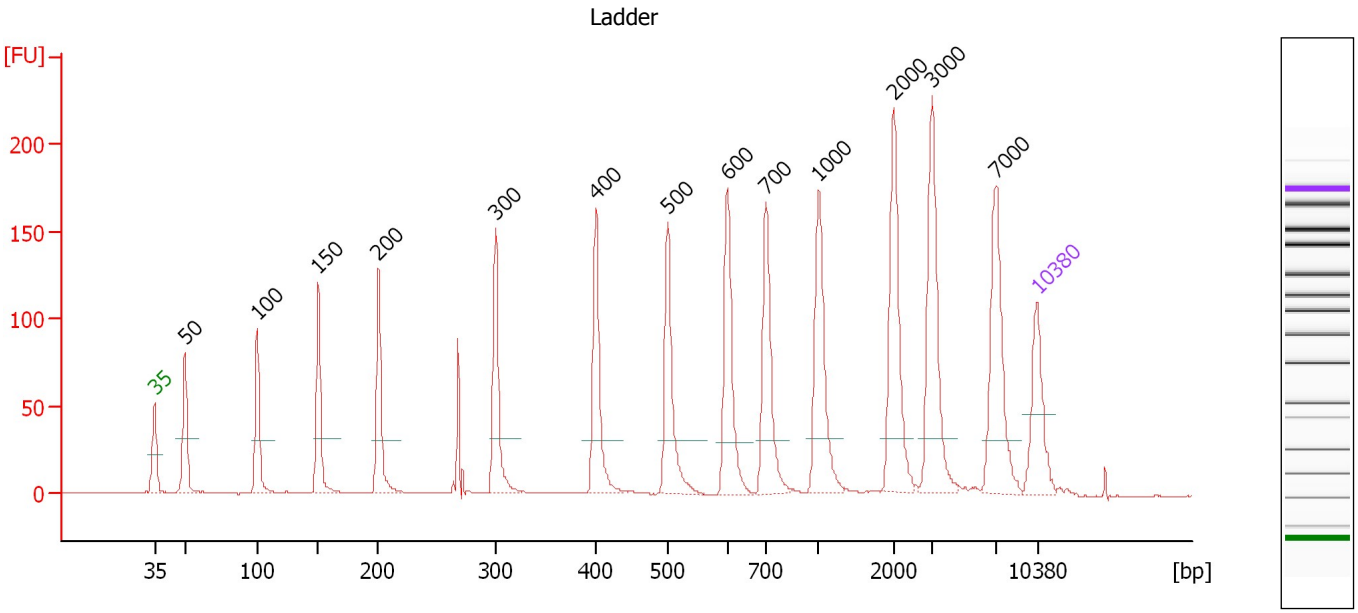
Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

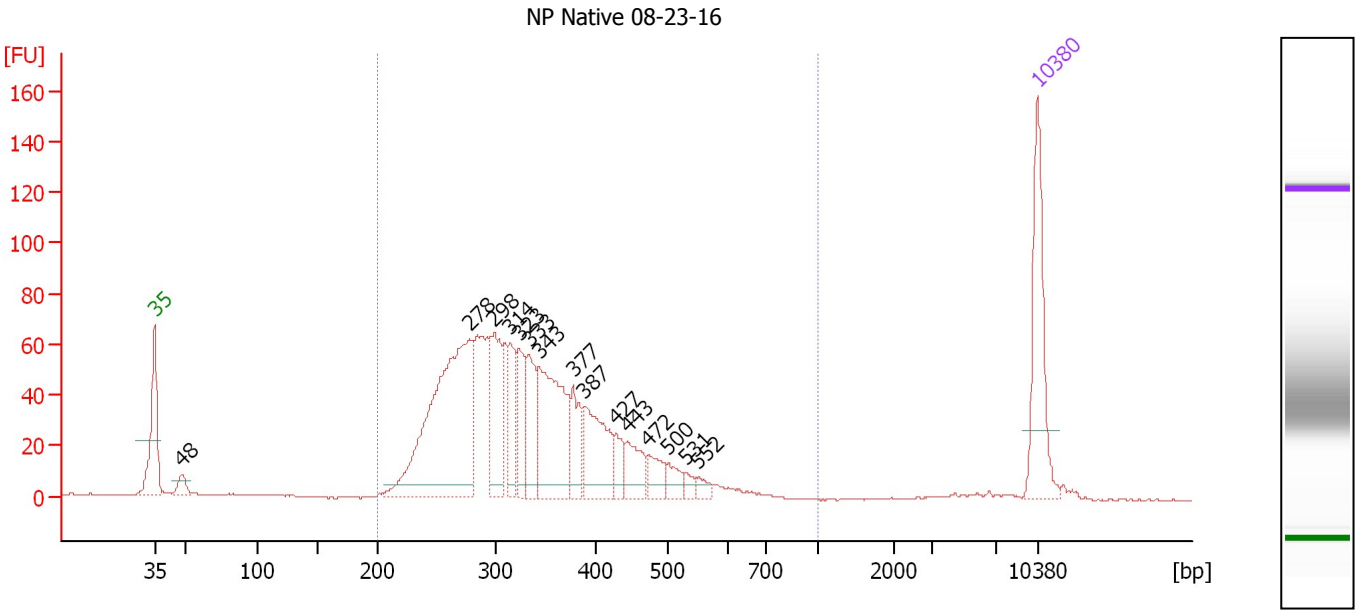
Peak table for Ladder

Peak		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	45.41
3		100	150.00	2,272.7	Ladder Peak	51.13
4		150	150.00	1,515.2	Ladder Peak	55.99
5		200	150.00	1,136.4	Ladder Peak	60.75
6		300	150.00	757.6	Ladder Peak	70.04
7		400	150.00	568.2	Ladder Peak	78.02
8		500	150.00	454.5	Ladder Peak	83.70
9		600	150.00	378.8	Ladder Peak	88.42
10		700	150.00	324.7	Ladder Peak	91.49
11		1,000	150.00	227.3	Ladder Peak	95.68
12		2,000	150.00	113.6	Ladder Peak	101.60
13		3,000	150.00	75.8	Ladder Peak	104.68
14		7,000	150.00	32.5	Ladder Peak	109.73
15		10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 1 : NP Native 08-23-16

Number of peaks found:	15	Corr. Area 1:	1,272.0
Noise:	0.2		

Peak table for sample 1 : NP Native 08-23-16

Peak	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	48	14.58	455.5		45.16
3	278	311.81	1,701.1		67.97
4	298	76.83	390.1		69.89
5	314	49.37	237.9		71.19
6	323	52.96	248.1		71.91
7	333	51.89	236.0		72.68
8	343	139.70	616.4		73.50
9	377	39.21	157.5		76.20
10	387	76.70	300.0		77.01
11	427	21.28	75.5		79.56
12	443	32.22	110.2		80.48
13	472	21.10	67.7		82.11
14	500	14.92	45.2		83.70
15	531	7.69	22.0		85.14
16	552	7.65	21.0		86.15
17	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : NP Native 08-23-16

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	340	1,272.0	5,140.2	1,075.02	95	24.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
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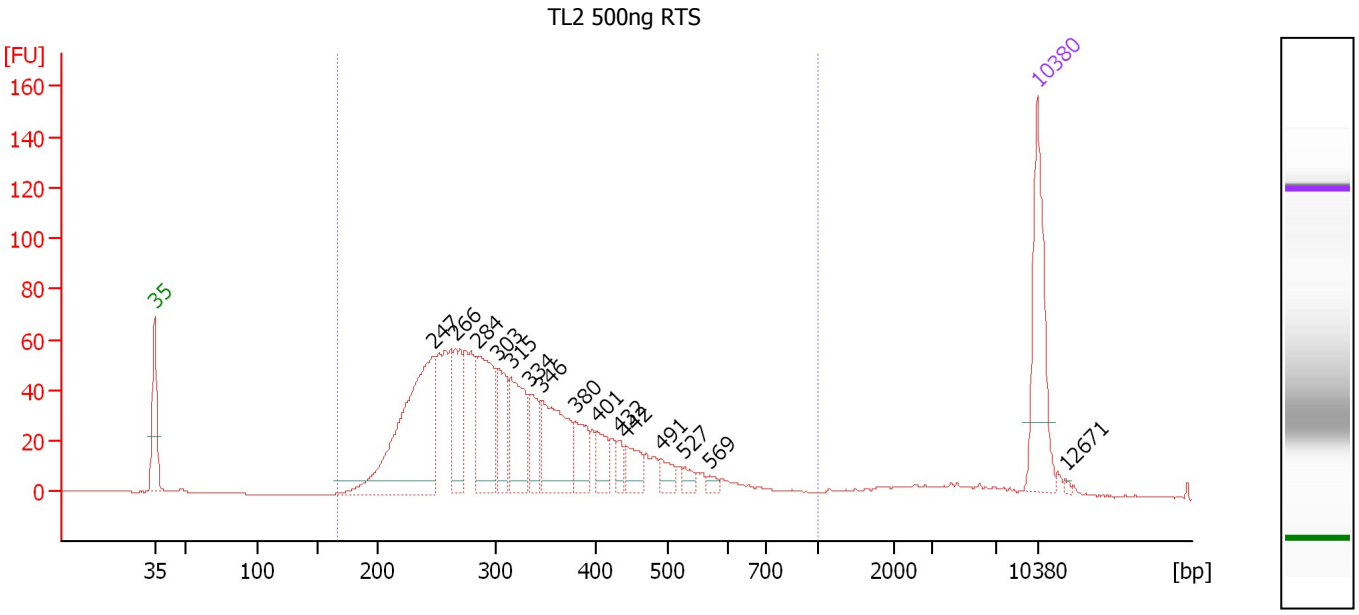
Electropherogram Summary Continued ...



Overall Results for sample 2 : TL2 500ng RTS

Number of peaks found:	15	Corr. Area 1:	1,248.3
Noise:	0.2		

Peak table for sample 2 : TL2 500ng RTS

Peak	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	247	239.95	1,474.3		65.08
3	266	61.48	350.4		66.86
4	284	106.12	566.2		68.55
5	303	53.28	266.3		70.29
6	315	77.82	374.1		71.25
7	334	35.42	160.7		72.75
8	346	89.04	390.0		73.71
9	380	35.61	142.1		76.41
10	401	23.67	89.4		78.10
11	432	12.74	44.7		79.83
12	442	23.10	79.2		80.41
13	491	15.01	46.3		83.21
14	527	8.70	25.0		84.99
15	569	5.24	13.9		86.97
16	10,380	75.00	10.9	Upper Marker	113.00
17	12,671	0.00	0.0		115.22

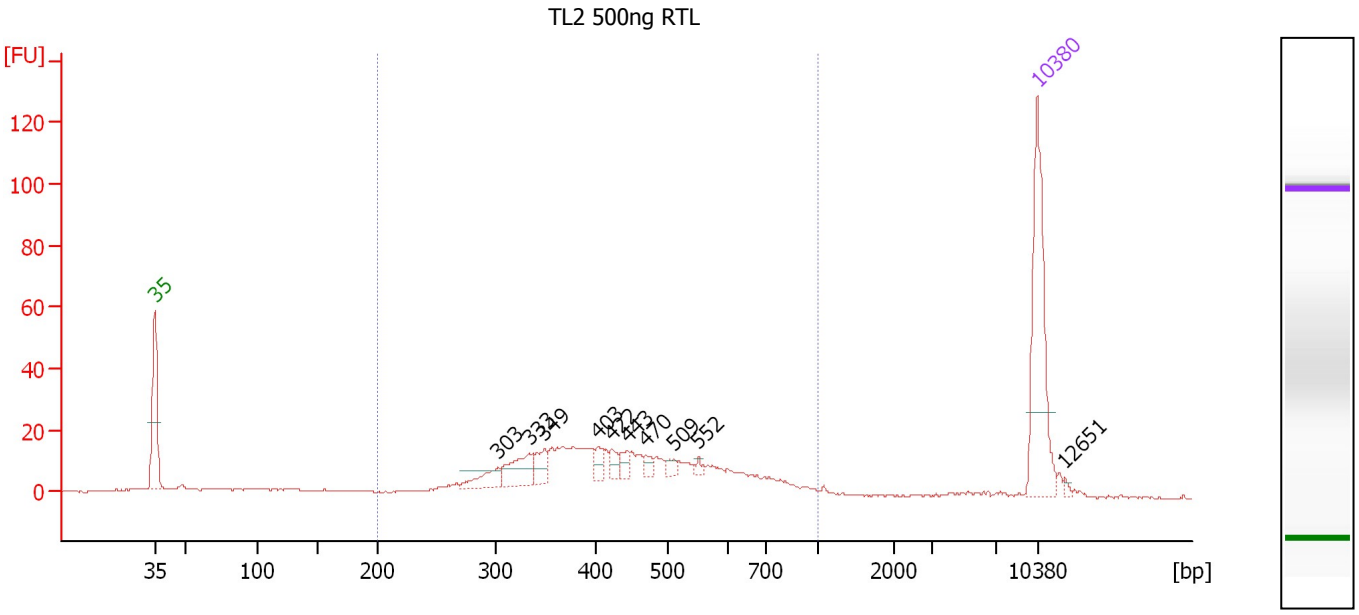
Region table for sample 2 : TL2 500ng RTS

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
166	1,000	330	1,248.3	5,299.7	1,042.84	95	31.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 3 : TL2 500ng RTL

Number of peaks found:	10	Corr. Area 1:	386.3
Noise:	0.2		

Peak table for sample 3 : TL2 500ng RTL

Peak		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		303	16.80	84.1		70.26
3		333	27.06	123.0		72.70
4		349	14.85	64.6		73.92
5		403	8.29	31.2		78.17
6		422	8.15	29.3		79.25
7		443	7.59	26.0		80.47
8		470	5.42	17.5		81.98
9		509	4.45	13.3		84.13
10		552	2.52	6.9		86.13
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,651	0.00	0.0		115.20

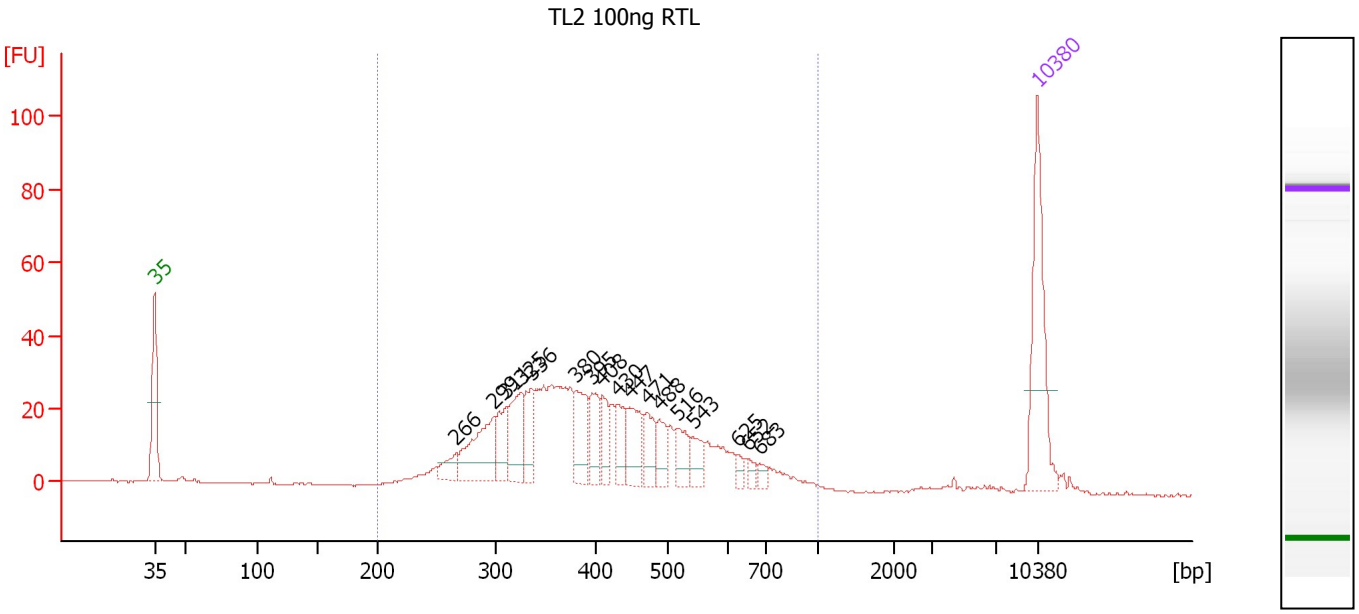
Region table for sample 3 : TL2 500ng RTL

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	452	386.3	1,330.2	351.82	82	31.2

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 4 : TL2 100ng RTL

Number of peaks found:	17	Corr. Area 1:	665.8
Noise:	0.2		

Peak table for sample 4 : TL2 100ng RTL

Peak	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	266	16.59	94.4		66.91
3	299	66.71	338.2		69.93
4	311	31.83	155.0		70.92
5	325	48.49	225.8		72.06
6	336	35.22	158.9		72.90
7	380	40.92	163.2		76.42
8	395	31.86	122.1		77.65
9	408	23.18	86.0		78.50
10	430	25.62	90.3		79.73
11	447	37.11	125.9		80.67
12	471	24.37	78.4		82.06
13	488	21.02	65.3		83.00
14	516	22.62	66.5		84.44
15	543	17.29	48.2		85.72
16	625	6.64	16.1		89.19
17	652	6.67	15.5		90.03
18	683	5.32	11.8		90.97
19	10,380	75.00	10.9	Upper Marker	113.00

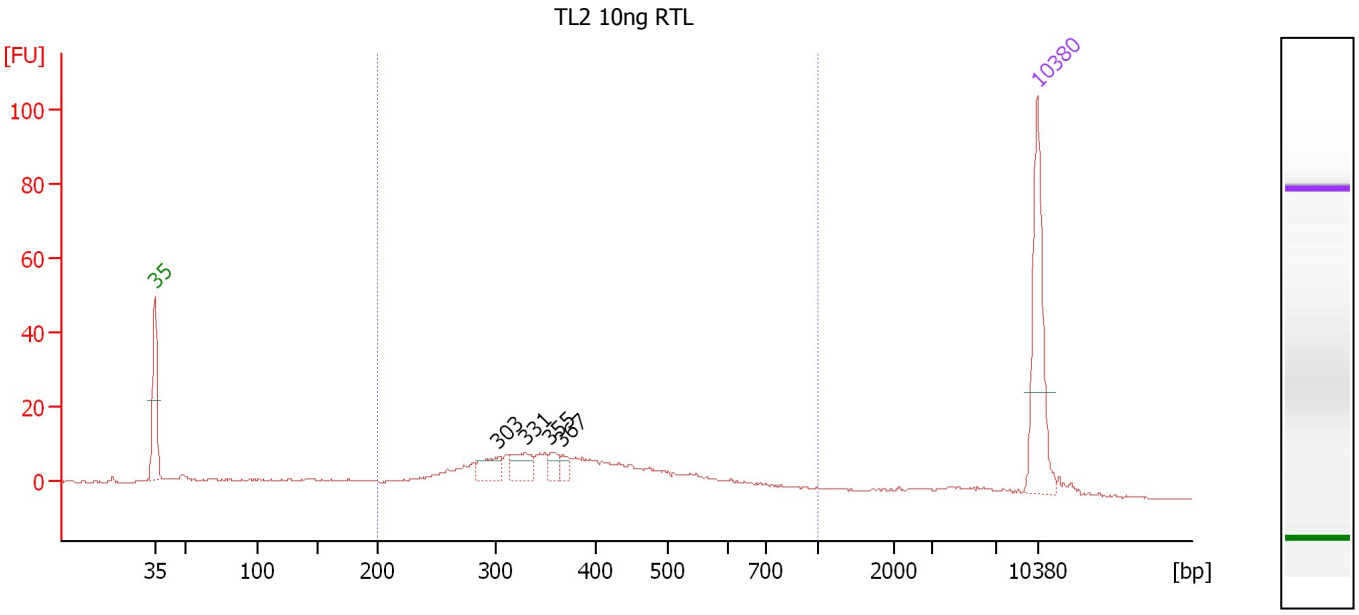
Region table for sample 4 : TL2 100ng RTL

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	422	665.8	3,097.3	774.07	92	30.2

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 5 : TL2 10ng RTL

Number of peaks found:	4	Corr. Area 1:	226.3
Noise:	0.2		

Peak table for sample 5 : TL2 10ng RTL

Peak		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		303	22.78	114.0		70.25
3		331	23.96	109.7		72.50
4		355	10.53	45.0		74.40
5		367	8.52	35.2		75.35
6	▶	10,380	75.00	10.9	Upper Marker	113.00

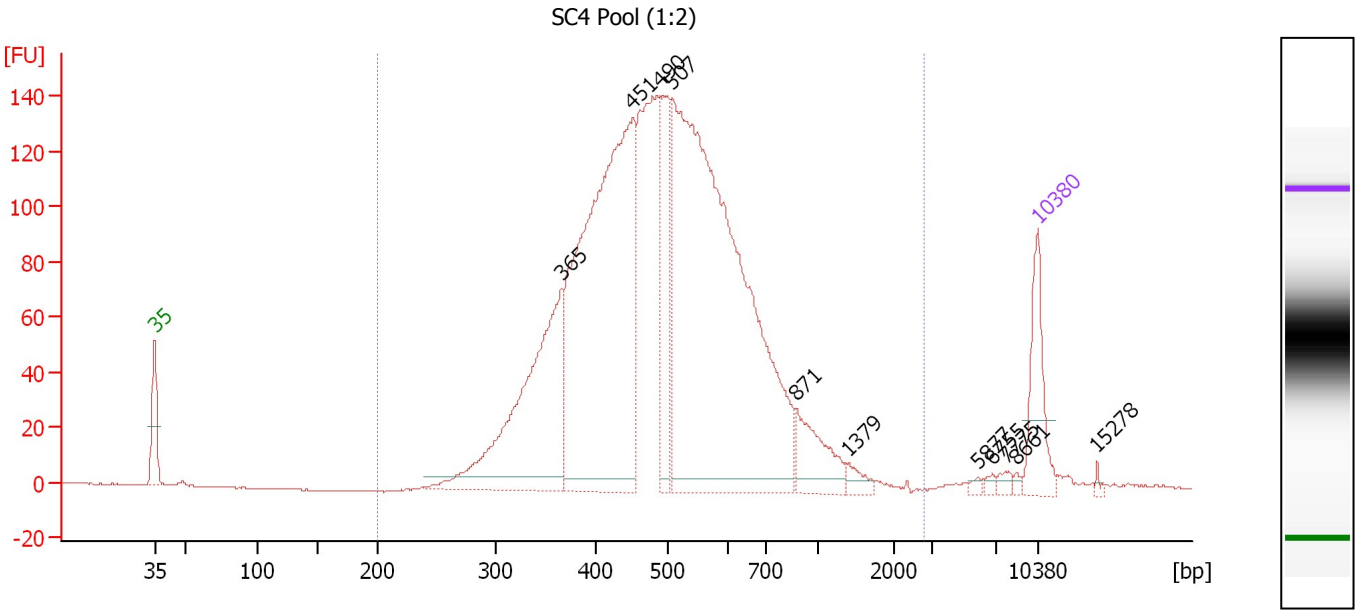
Region table for sample 5 : TL2 10ng RTL

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	404	226.3	1,229.8	289.12	78	33.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 6 : SC4 Pool (1:2)

Number of peaks found:	11	Corr. Area 1:	2,744.5
Noise:	0.2		

Peak table for sample 6 : SC4 Pool (1:2)

Peak	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	365	420.39	1,745.2		75.23
3	451	858.21	2,882.5		80.93
4	490	134.18	414.7		83.14
5	507	1,147.05	3,424.9		84.05
6	871	82.32	143.1		93.89
7	1,379	15.20	16.7		97.92
8	5,877	4.52	1.2		108.31
9	6,755	5.24	1.2		109.42
10	7,775	7.73	1.5		110.48
11	8,661	3.58	0.6		111.34
12	10,380	75.00	10.9	Upper Marker	113.00
13	15,278	0.00	0.0		117.74

Region table for sample 6 : SC4 Pool (1:2)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	2,772	525	2,744.5	9,689.8	2,985.92	97	38.8

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
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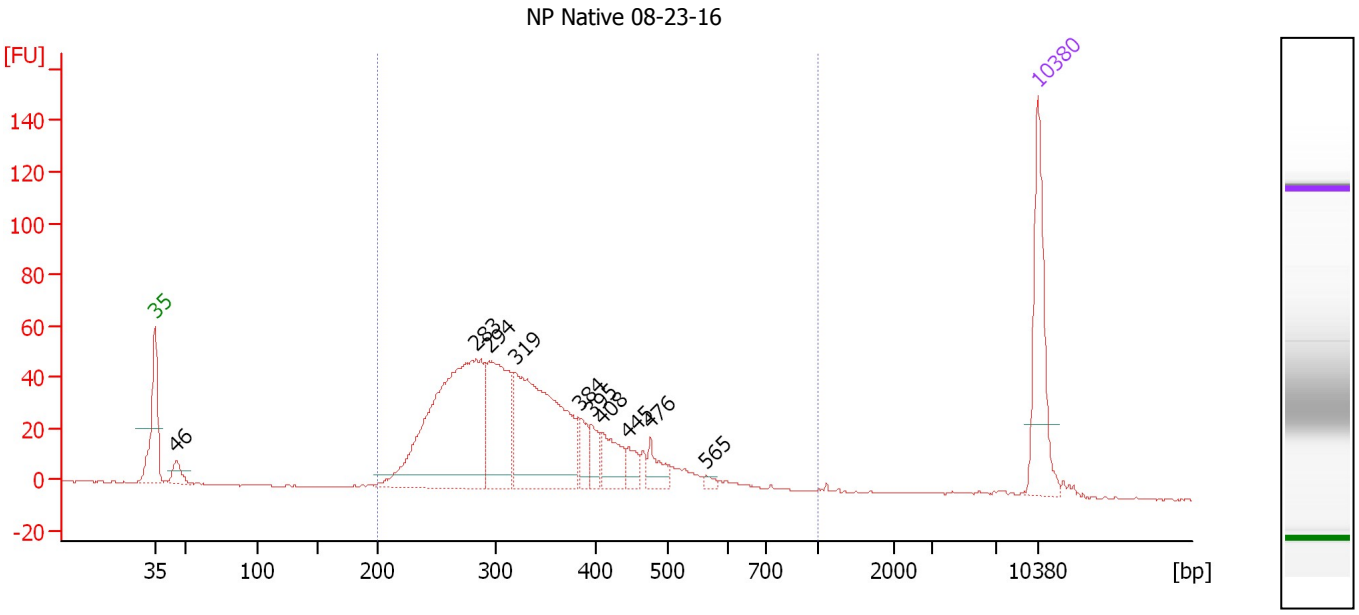
Electropherogram Summary Continued ...



Overall Results for sample 7 : NP Native 08-23-16

Number of peaks found:	10	Corr. Area 1:	947.2
Noise:	0.3		

Peak table for sample 7 : NP Native 08-23-16

Peak	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	46	20.28	674.6		44.69
3	283	325.85	1,742.7		68.49
4	294	134.20	690.8		69.51
5	319	233.36	1,108.0		71.56
6	384	22.82	90.1		76.74
7	395	19.79	75.9		77.62
8	408	36.62	135.9		78.49
9	445	15.96	54.3		80.59
10	476	20.71	65.9		82.33
11	565	4.56	12.3		86.74
12	10,380	75.00	10.9	Upper Marker	113.00

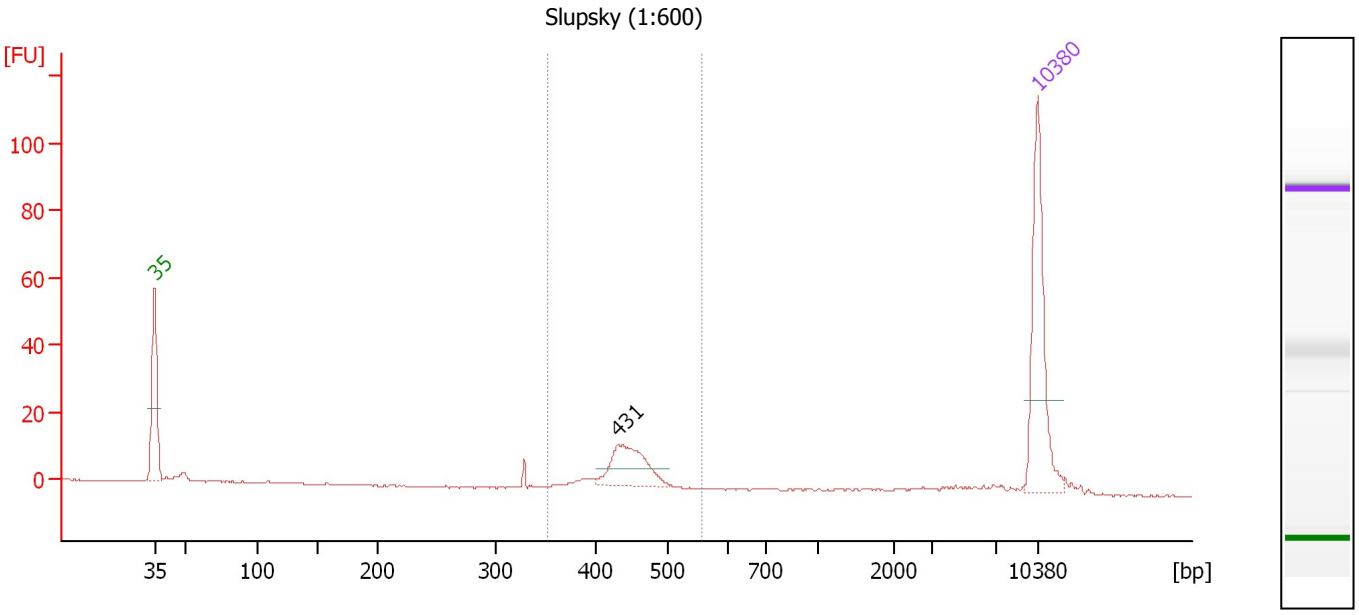
Region table for sample 7 : NP Native 08-23-16

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	339	947.2	4,055.1	841.50	98	25.9

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 8 : Slupsky (1:600)

Number of peaks found:	1	Corr. Area 1:	59.7
Noise:	0.2		

Peak table for sample 8 : Slupsky (1:600)

Peak		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		431	49.85	175.1		79.81
3	▶	10,380	75.00	10.9	Upper Marker	113.00

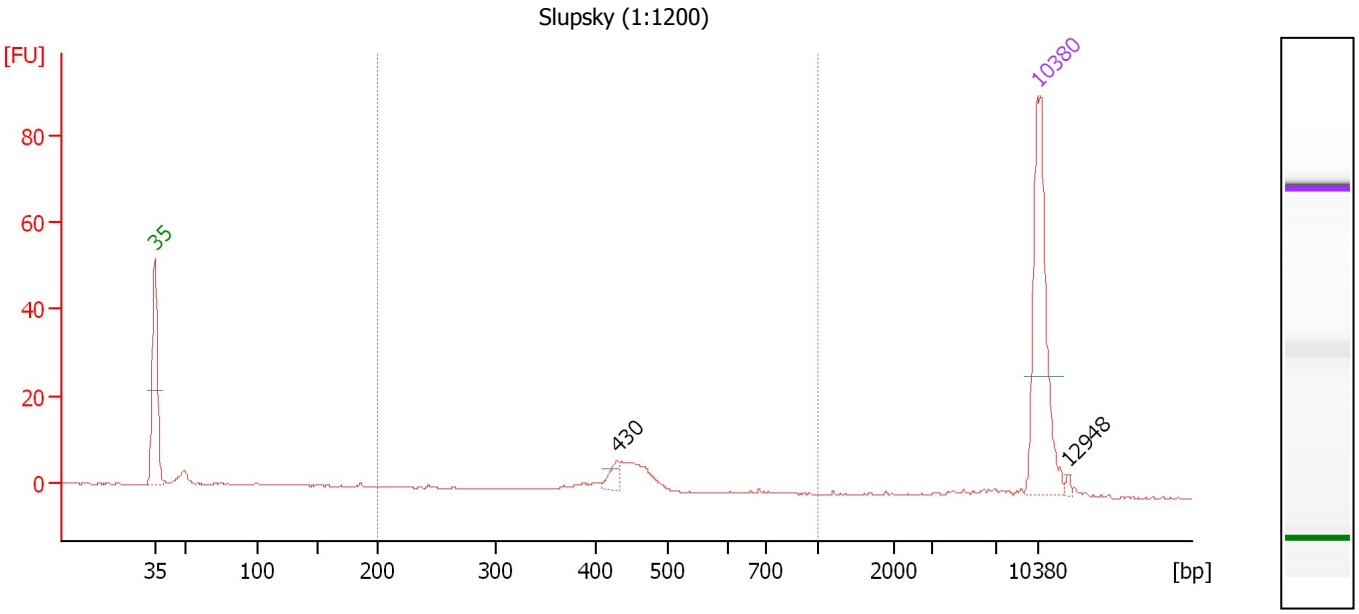
Region table for sample 8 : Slupsky (1:600)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color Conc. [pg/µl]	% of Total	Size distribution in CV [%]
352	558	441	59.7	203.7	59.14	67	6.7

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Electropherogram Summary Continued ...



Overall Results for sample 9 : Slupsky (1:1200)

Number of peaks found:	2	Corr. Area 1:	33.8
Noise:	0.1		

Peak table for sample 9 : Slupsky (1:1200)

Peak		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		430	8.96	31.6		79.71
3	▶	10,380	75.00	10.9	Upper Marker	113.00
4		12,948	0.00	0.0		115.49

Region table for sample 9 : Slupsky (1:1200)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	438	33.8	129.0		36.81	63	9.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Invalid Samples

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad

Created: 9/21/2016 10:34:19 AM
Modified: 9/21/2016 11:24:07 AM

Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 10)		Instrument	Run		9/21/2016 11:09:52 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-09-21\2016-09-21_001.xad)		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		9/21/2016 10:34:24 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1