Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad

Created: 9/20/2016 12:50:06 PM
Modified: 9/20/2016 1:35:10 PM

Electrophoresis File Run Summary

Instrument Information:

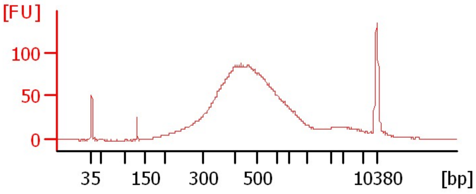
Instrument Name: DE13701086
Firmware: C.01.069
Serial#: DE13701086
Type: G2938B

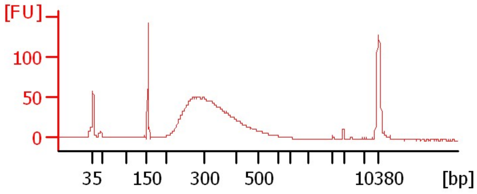
Assay Information:

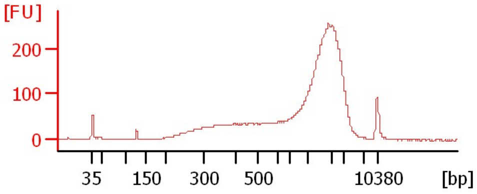
Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy
Assay Class: High Sensitivity DNA Assay
Version: 1.03
Assay Comments: Copyright © 2003-2010 Agilent Technologies

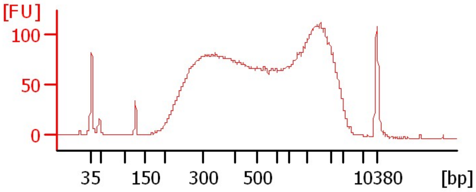
Chip Information:

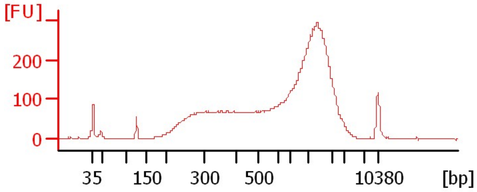
Chip Lot #:
Reagent Kit Lot #:
Chip Comments:

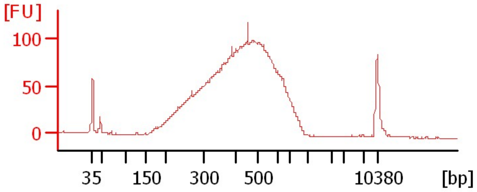

H574P-G-3

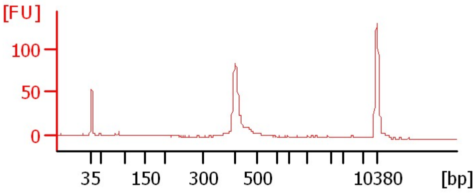

NP Native 08-23-16
QC 117

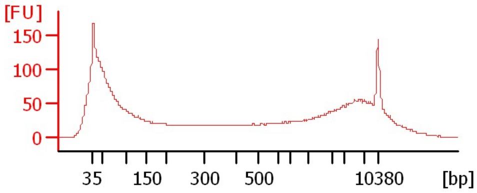

4: p10IgG1 (1:3) with 5 extra cyc PCR
HiSeq_642

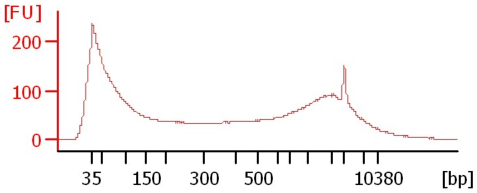

5: p10sox2 with 5 extra cyc PCR
HiSeq_642


8: p2sox2 with 5 extra cyc PCR
HiSeq_642


M398P QC PCR
MiSeq_398


isolates (1:20)
MiSeq_407


DNase (1:4)
QC_118


DNase

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad

Created: 9/20/2016 12:50:06 PM
Modified: 9/20/2016 1:35:10 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
H574P-G-3		☐	✓			
NP Native 08-23-16	QC 117	☐	✓			
4: p10IgG1 (1:3) with 5 extra cyc PCR	HiSeq_642	☐	✓			
5: p10sox2 with 5 extra cyc PCR	HiSeq_642	☐	✓			
8: p2sox2 with 5 extra cyc PCR	HiSeq_642	☐	✓			
M398P QC PCR	MiSeq_398	☐	✓			
isolates (1:20)	MiSeq_407	☐	✓			
DNase (1:4)	QC_118	☐	✓			
DNase		☐	✓			
sample 10		☐				
sample 11		☐				
Ladder		☐	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

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

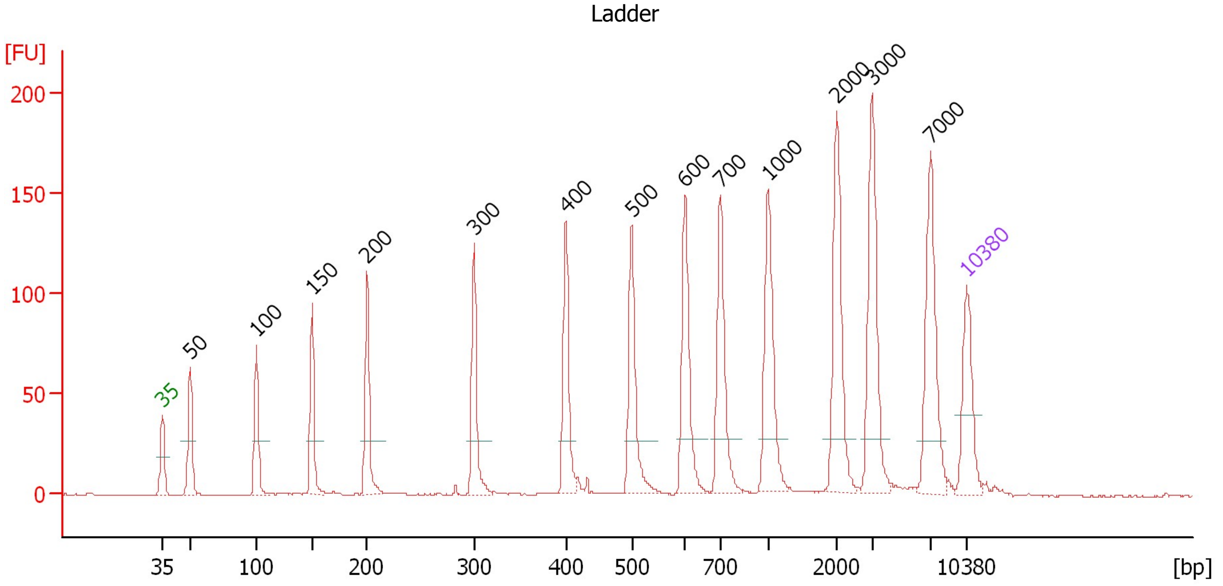
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

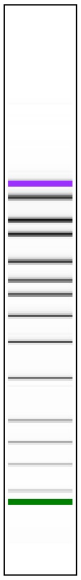
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad

Created: 9/20/2016 12:50:06 PM
Modified: 9/20/2016 1:35:10 PM

Electropherogram Summary

Ladder





Overall Results for Ladder

Noise: 0.2

Peak table for Ladder

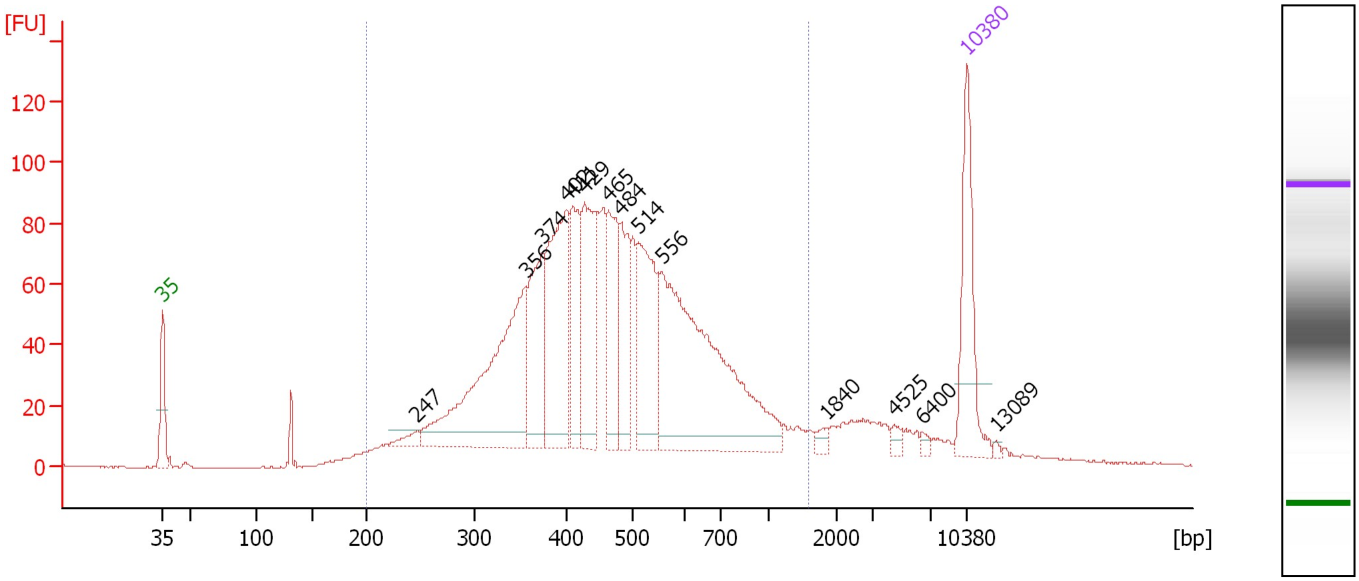
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	L	50	150.00	4,545.5	Ladder Peak	45.43
3	L	100	150.00	2,272.7	Ladder Peak	51.14
4	L	150	150.00	1,515.2	Ladder Peak	56.01
5	L	200	150.00	1,136.4	Ladder Peak	60.82
6	L	300	150.00	757.6	Ladder Peak	70.11
7	L	400	150.00	568.2	Ladder Peak	78.10
8	L	500	150.00	454.5	Ladder Peak	83.81
9	L	600	150.00	378.8	Ladder Peak	88.48
10	L	700	150.00	324.7	Ladder Peak	91.55
11	L	1,000	150.00	227.3	Ladder Peak	95.67
12	L	2,000	150.00	113.6	Ladder Peak	101.68
13	L	3,000	150.00	75.8	Ladder Peak	104.71
14	L	7,000	150.00	32.5	Ladder Peak	109.82
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad

Created: 9/20/2016 12:50:06 PM
Modified: 9/20/2016 1:35:10 PM

Electropherogram Summary Continued ...

H574P-G-3



Overall Results for sample 1 : **H574P-G-3**

Number of peaks found:	14	Corr. Area 1:	2,021.9
Noise:	0.2		

Peak table for sample 1 : **H574P-G-3**

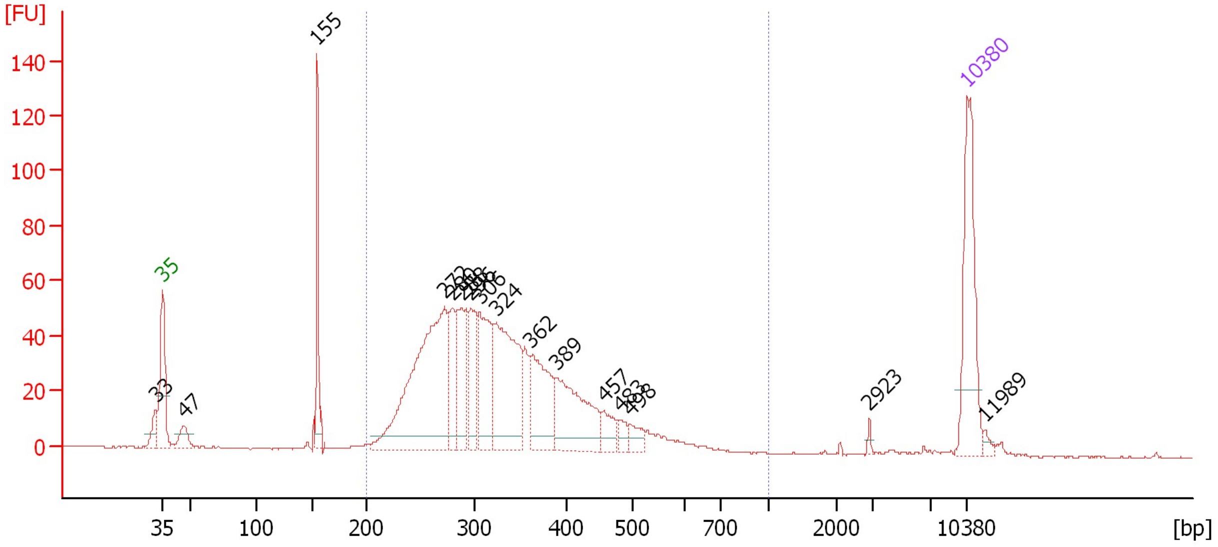
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		247	11.66	71.6		65.17
3		356	267.45	1,137.4		74.60
4		374	105.78	428.1		76.05
5		402	174.32	657.4		78.20
6		411	83.23	307.2		78.70
7		429	125.78	444.4		79.75
8		465	85.99	280.3		81.79
9		484	75.75	237.1		82.89
10		514	124.35	366.9		84.44
11		556	333.92	909.4		86.44
12		1,840	6.28	5.2		100.72
13		4,525	5.59	1.9		106.66
14		6,400	3.99	0.9		109.06
15	▶	10,380	75.00	10.9	Upper Marker	113.00
16		13,089	0.00	0.0		115.55

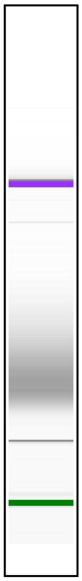
Region table for sample 1 : **H574P-G-3**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,575	495	2,021.9	6,371.3	🟦	1,774.05	91	39.8

Electropherogram Summary Continued ...

NP Native 08-23-16 [QC 117]





Overall Results for sample 2 : NP Native 08-23-16

Number of peaks found:	16	Corr. Area 1:	983.6
Noise:	0.3		

Peak table for sample 2 : NP Native 08-23-16

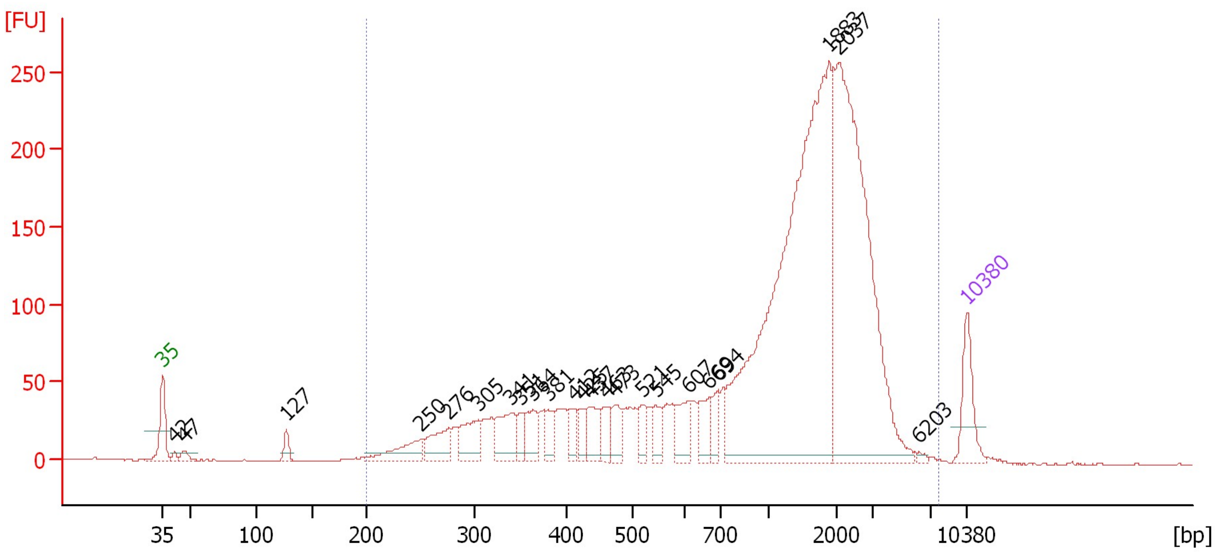
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.39
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		47	19.05	620.5		44.87
4		155	68.92	674.8		56.47
5		272	253.42	1,411.5		67.51
6		280	47.26	256.1		68.22
7		288	68.01	357.4		69.02
8		296	52.14	266.5		69.78
9		306	83.36	412.8		70.59
10		324	134.88	631.4		72.00
11		362	75.69	316.7		75.07
12		389	87.79	341.7		77.24
13		457	18.32	60.7		81.38
14		483	9.52	29.9		82.84
15		498	12.04	36.6		83.70
16		2,923	2.63	1.4		104.48
17	▶	10,380	75.00	10.9	Upper Marker	113.00
18		11,989	0.00	0.0		114.51

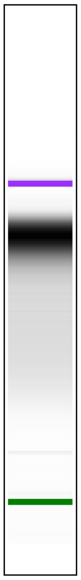
Region table for sample 2 : NP Native 08-23-16

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	335	983.6	4,382.4	🟦	905.61	90	24.1

Electropherogram Summary Continued ...

4: p10IgG1 (1:3) with 5 extra cyc PCR [HiSeq_642]





Overall Results for sample 3 : 4: p10IgG1 (1:3) with 5 extra cyc PCR

Number of peaks found: 23

Corr. Area 1: 3,309.8

Noise: 0.3

Peak table for sample 3 : 4: p10IgG1 (1:3) with 5 extra cyc PCR

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		42	9.42	342.8		44.07
3		47	20.41	658.1		44.94
4		127	29.89	355.7		53.80
5		250	82.28	498.7		65.46
6		276	87.12	478.4		67.87
7		305	94.84	471.7		70.48
8		341	99.72	443.7		73.34
9		351	34.84	150.2		74.21
10		364	59.06	245.7		75.24
11		381	37.24	148.2		76.57
12		412	41.90	154.2		78.77
13		425	36.41	129.8		79.54
14		437	59.95	207.9		80.20
15		463	46.43	152.0		81.68
16		473	49.56	158.9		82.25
17		521	37.90	110.2		84.81
18		545	38.43	106.7		85.93
19		607	63.76	159.1		88.69
20		669	55.35	125.4		90.59
21		694	41.72	91.1		91.36
22		1,883	1,125.91	906.2		100.98
23		2,037	774.18	575.8		101.79
24		6,203	5.63	1.4		108.80
25	▶	10,380	75.00	10.9	Upper Marker	113.00

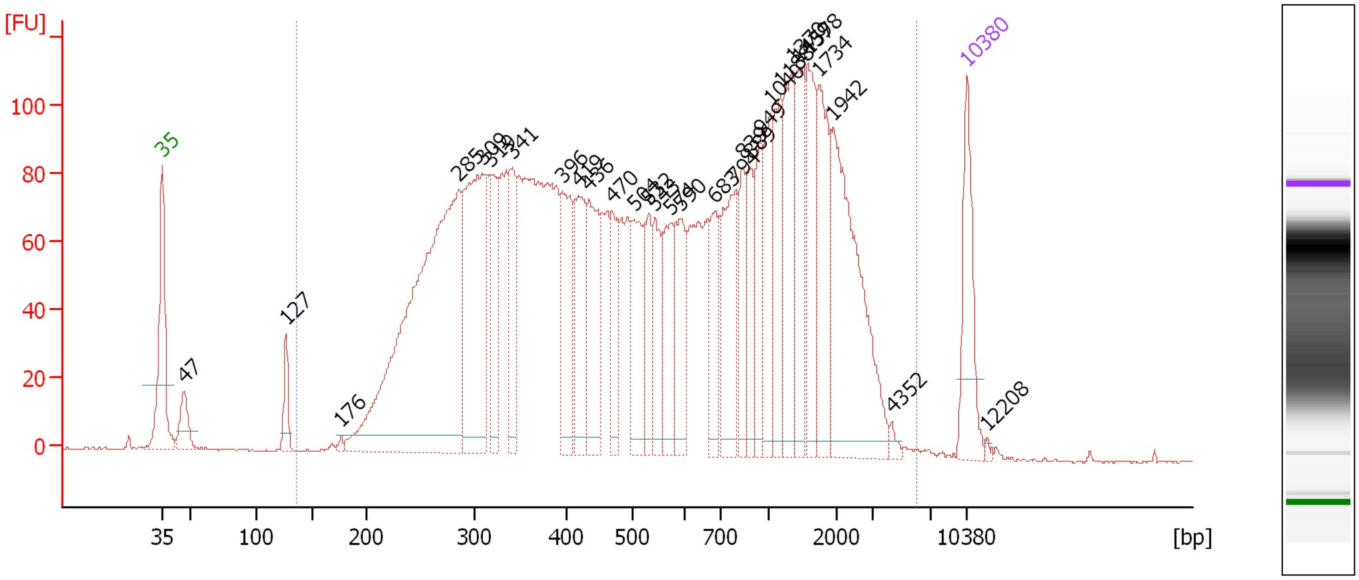
Electropherogram Summary Continued ...

... Region table for sample 3 : 4: p10IgG1 (1:3) with 5 extra cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	7,770	1,515	3,309.8	7,081.4	🟦 3,358.79	99	65.2

Electropherogram Summary Continued ...

5: p10sox2 with 5 extra cyc PCR [HiSeq_642]



Overall Results for sample 4 : 5: p10sox2 with 5 extra cyc PCR

Number of peaks found:	30	Corr. Area 1:	3,924.6
Noise:	0.2		

Peak table for sample 4 : 5: p10sox2 with 5 extra cyc PCR

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		47	47.62	1,549.7		44.88
3		127	43.09	515.7		53.73
4		176	5.34	46.0		58.52
5		285	705.19	3,746.8		68.73
6		309	282.11	1,381.1		70.86
7		319	91.36	434.4		71.59
8		341	88.01	390.6		73.42
9		396	104.41	399.3		77.79
10		419	106.36	384.4		79.20
11		436	126.66	440.5		80.14
12		470	71.60	230.6		82.11
13		504	99.64	299.6		83.99
14		532	61.39	174.9		85.29
15		543	66.91	186.7		85.81
16		574	76.11	200.8		87.27
17		590	79.55	204.4		88.00
18		683	69.85	155.0		91.02
19		794	118.91	226.9		92.84
20		839	66.06	119.2		93.47
21		889	56.70	96.7		94.15
22		949	58.13	92.8		94.98
23		1,040	75.31	109.7		95.92
24		1,188	77.47	98.8		96.80
25		1,370	105.33	116.5		97.90

Electropherogram Summary Continued ...

... Peak table for sample 4 : 5: p10sox2 with 5 extra cyc PCR

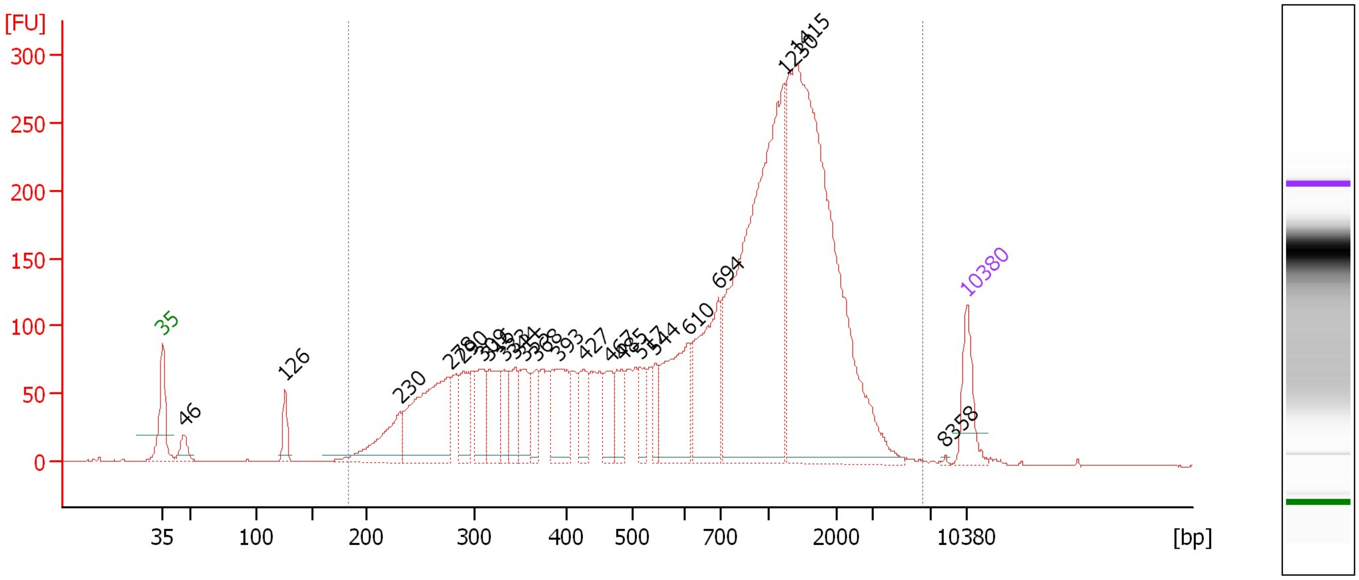
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		1,439	86.87	91.4		98.31
27		1,578	88.60	85.1		99.15
28		1,734	101.62	88.8		100.08
29		1,942	215.02	167.7		101.33
30		4,352	5.77	2.0		106.44
31	▶	10,380	75.00	10.9	Upper Marker	113.00
32		12,208	0.00	0.0		114.72

Region table for sample 4 : 5: p10sox2 with 5 extra cyc PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
137	6,067	831	3,924.6	14,453.3	🟦	4,155.75	98	85.3

Electropherogram Summary Continued ...

8: p2sox2 with 5 extra cyc PCR [HiSeq_642]



Overall Results for sample 5 : 8: p2sox2 with 5 extra cyc PCR

Number of peaks found:	22	Corr. Area 1:	5,168.9
Noise:	0.3		

Peak table for sample 5 : 8: p2sox2 with 5 extra cyc PCR

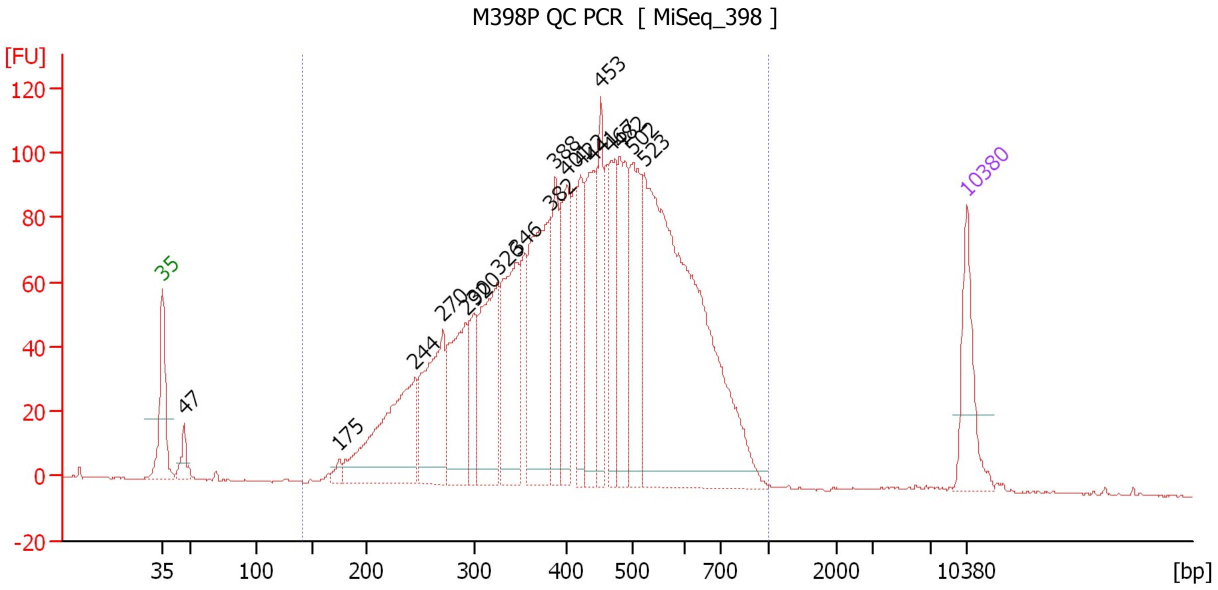
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		46	46.84	1,529.7		44.85
3		126	58.12	699.4		53.66
4		230	151.92	999.2		63.64
5		278	356.09	1,943.9		68.02
6		290	94.17	491.9		69.18
7		309	108.81	533.7		70.82
8		316	111.39	533.7		71.40
9		333	66.29	301.3		72.77
10		344	80.48	354.5		73.62
11		355	87.68	374.7		74.46
12		368	70.29	289.1		75.57
13		393	144.29	556.6		77.52
14		427	77.37	274.6		79.64
15		467	74.74	242.7		81.91
16		485	74.60	233.0		82.96
17		517	53.43	156.6		84.60
18		544	53.16	148.0		85.87
19		610	215.08	534.6		88.77
20		694	261.52	571.3		91.36
21		1,230	847.56	1,043.8		97.06
22		1,415	1,094.20	1,171.8		98.17
23		8,358	1.71	0.3		111.10
24	▶	10,380	75.00	10.9	Upper Marker	113.00

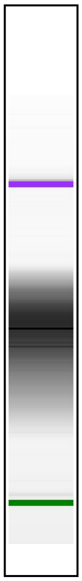
Electropherogram Summary Continued ...

... Region table for sample 5 : **8: p2sox2 with 5 extra cyc PCR**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
184	6,440	998	5,168.9	13,207.0	🟦	4,602.51	98	69.7

Electropherogram Summary Continued ...





Overall Results for sample 6 : M398P QC PCR

Number of peaks found:	18	Corr. Area 1:	2,664.7
Noise:	0.2		

Peak table for sample 6 : M398P QC PCR

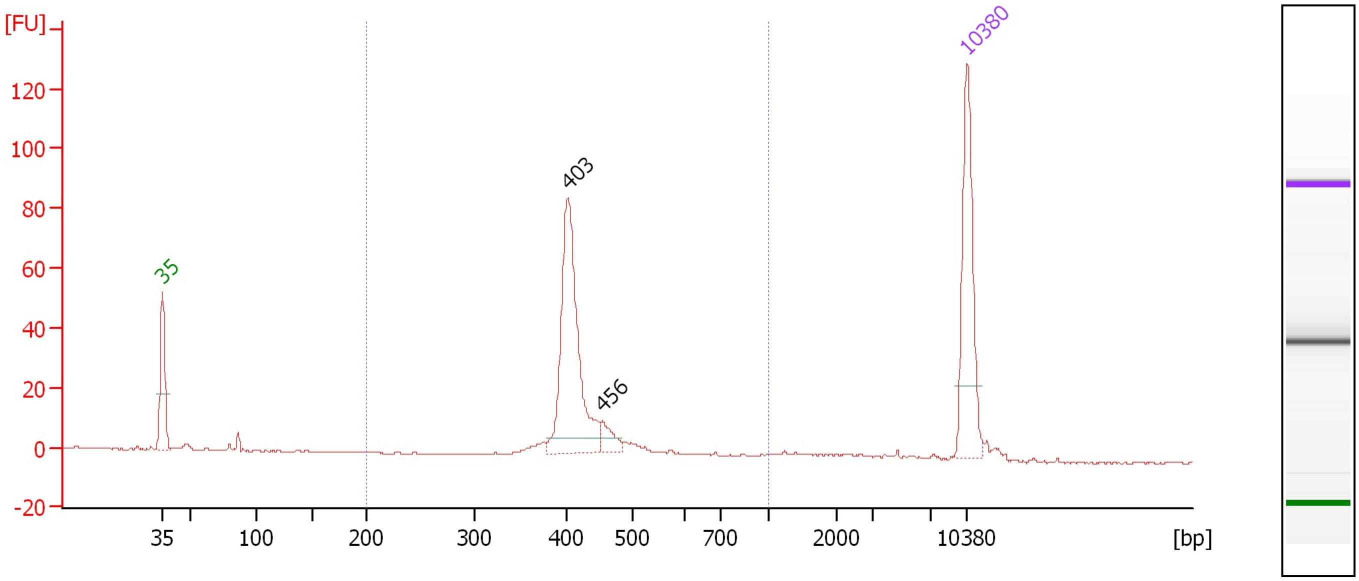
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		47	33.15	1,071.9		44.92
3		175	13.02	113.0		58.38
4		244	266.51	1,652.2		64.95
5		270	199.75	1,119.8		67.35
6		292	168.97	876.3		69.38
7		300	74.45	376.5		70.07
8		326	193.03	898.2		72.15
9		346	193.49	848.2		73.76
10		382	258.88	1,025.8		76.69
11		388	103.56	404.0		77.17
12		401	124.97	472.6		78.13
13		422	105.88	380.0		79.36
14		441	152.91	525.6		80.43
15		453	108.15	361.8		81.12
16		467	101.53	329.4		81.92
17		482	153.96	484.0		82.78
18		502	148.81	449.2		83.90
19		523	760.20	2,204.2		84.86
20	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : M398P QC PCR

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
141	1,000	439	2,664.7	13,362.0	■	3,330.34	98	30.8

Electropherogram Summary Continued ...

isolates (1:20) [MiSeq_407]



Overall Results for sample 7 : **isolates (1:20)**

Number of peaks found:	2	Corr. Area 1:	233.9
Noise:	0.2		

Peak table for sample 7 : **isolates (1:20)**

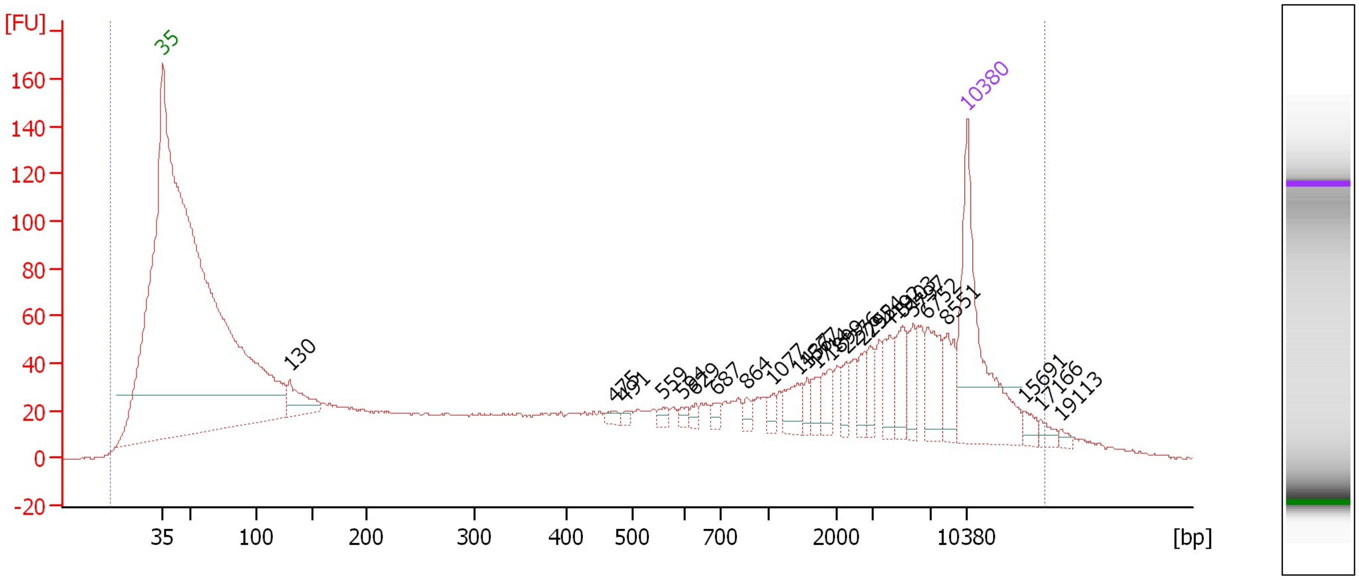
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		403	161.35	606.6		78.27
3		456	14.15	47.0		81.31
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **isolates (1:20)**

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	428	233.9	736.6	🟦	204.55	87	15.6

Electropherogram Summary Continued ...

DNase (1:4) [QC_118]



Overall Results for sample 8 : DNase (1:4)

Number of peaks found:	24	Corr. Area 1:	1,910.6
Noise:	0.5		

Peak table for sample 8 : DNase (1:4)

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		130	30.00	348.7		54.09
3		475	3.83	12.2		82.38
4		491	2.48	7.7		83.27
5		559	4.03	10.9		86.54
6		594	3.69	9.4		88.21
7		629	3.90	9.4		89.37
8		687	4.59	10.1		91.15
9		864	4.43	7.8		93.81
10		1,077	5.46	7.7		96.14
11		1,437	12.91	13.6		98.30
12		1,567	5.79	5.6		99.08
13		1,714	6.55	5.8		99.97
14		1,899	10.52	8.4		101.07
15		2,276	7.32	4.9		102.52
16		2,752	8.27	4.6		103.96
17		2,954	9.53	4.9		104.57
18		4,192	13.74	5.0		106.23
19		5,103	17.13	5.1		107.40
20		5,797	13.51	3.5		108.29
21		6,752	23.55	5.3		109.51
22		8,551	14.77	2.6		111.28
23	▶	10,380	75.00	10.9	Upper Marker	113.00
24		15,691	0.00	0.0		117.99
25		17,166	0.00	0.0		119.38

Electropherogram Summary Continued ...

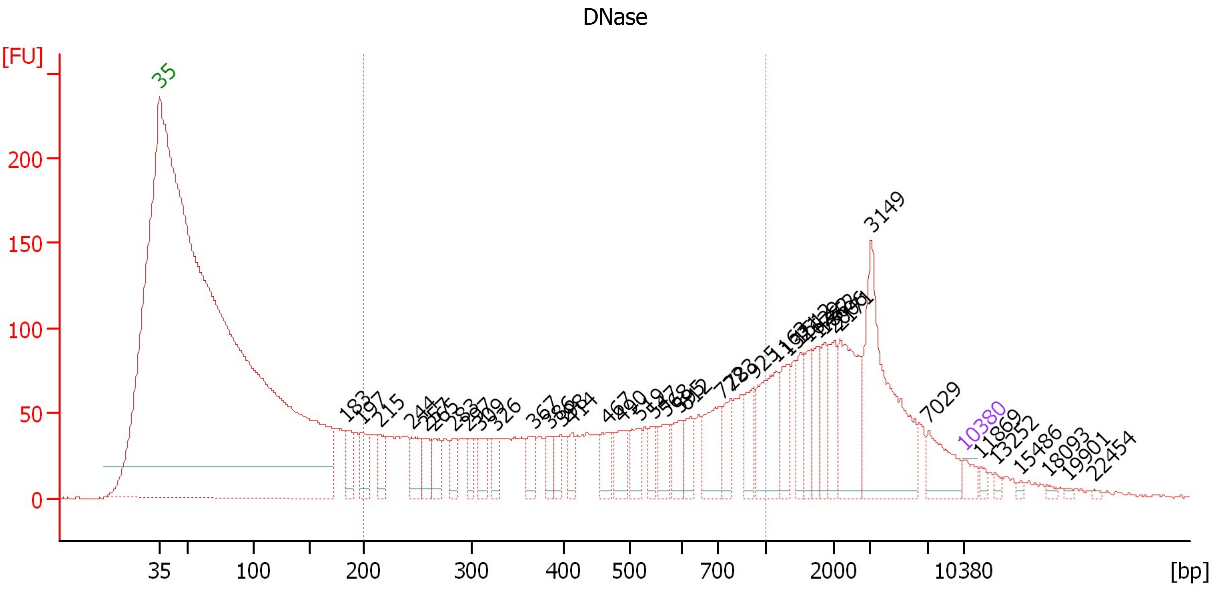
... Peak table for sample 8 : DNase (1:4)

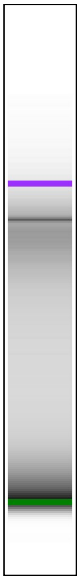
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	19,113	0.00	0.0		121.21

Region table for sample 8 : DNase (1:4)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
7	17,653	2,602	1,910.6	4,041.8	🟦	889.24	95	100.0

Electropherogram Summary Continued ...





Overall Results for sample 9 : **DNase**

Number of peaks found:	40	Corr. Area 1:	1,888.6
Noise:	0.6		

Peak table for sample 9 : **DNase**

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		183	267.09	2,215.9		59.15
3		197	294.63	2,270.1		60.50
4		215	210.48	1,484.5		62.20
5		244	268.25	1,662.6		64.95
6		257	191.72	1,131.0		66.10
7		265	211.01	1,204.4		66.90
8		283	190.89	1,023.1		68.50
9		297	151.21	772.2		69.80
10		309	191.12	936.2		70.85
11		326	142.46	663.0		72.15
12		367	192.84	795.1		75.50
13		386	127.00	499.0		76.95
14		398	134.90	514.2		77.90
15		414	125.36	458.8		78.90
16		467	209.91	681.7		81.90
17		490	260.79	806.0		83.25
18		519	219.96	642.0		84.70
19		547	142.67	395.2		86.00
20		568	198.23	528.4		87.00
21		595	190.08	483.9		88.25
22		612	196.33	485.9		88.85
23		722	376.67	790.9		91.85
24		783	205.02	396.5		92.70
25		925	198.79	325.5		94.65

Electropherogram Summary Continued ...

... Peak table for sample 9 : **DNase**

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	1,163	507.56	661.5		96.65
27	1,321	244.96	281.0		97.60
28	1,512	176.66	177.0		98.75
29	1,629	191.59	178.2		99.45
30	1,762	205.13	176.4		100.25
31	1,862	178.04	144.9		100.85
32	2,006	215.70	162.9		101.70
33	2,171	529.46	369.4		102.20
34	3,149	1,086.81	522.9		104.90
35	7,029	266.10	57.4		109.85
36	▶ 10,380	75.00	10.9	Upper Marker	113.00
37	11,869	0.00	0.0		114.40
38	13,252	0.00	0.0		115.70
39	15,486	0.00	0.0		117.80
40	18,093	0.00	0.0		120.25
41	19,901	0.00	0.0		121.95
42	22,454	0.00	0.0		124.35

Region table for sample 9 : **DNase**

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	489	1,888.6	31,985.8	🟦	7,802.07	56	43.8

Assay Class:	High Sensitivity DNA Assay	Created:	9/20/2016 12:50:06 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad	Modified:	9/20/2016 1:35:10 PM

Gel Image

Invalid Samples

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

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		9/20/2016 1:25:42 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-09-20\2016-09-20_001.xad)		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		9/20/2016 12:50:12 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1