

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-21\2018-06-21\_002.xad

Created: 6/21/2018 11:39:51 AM  
Modified: 6/21/2018 12:15:25 PM

**Electrophoresis File Run Summary**

Instrument Information:

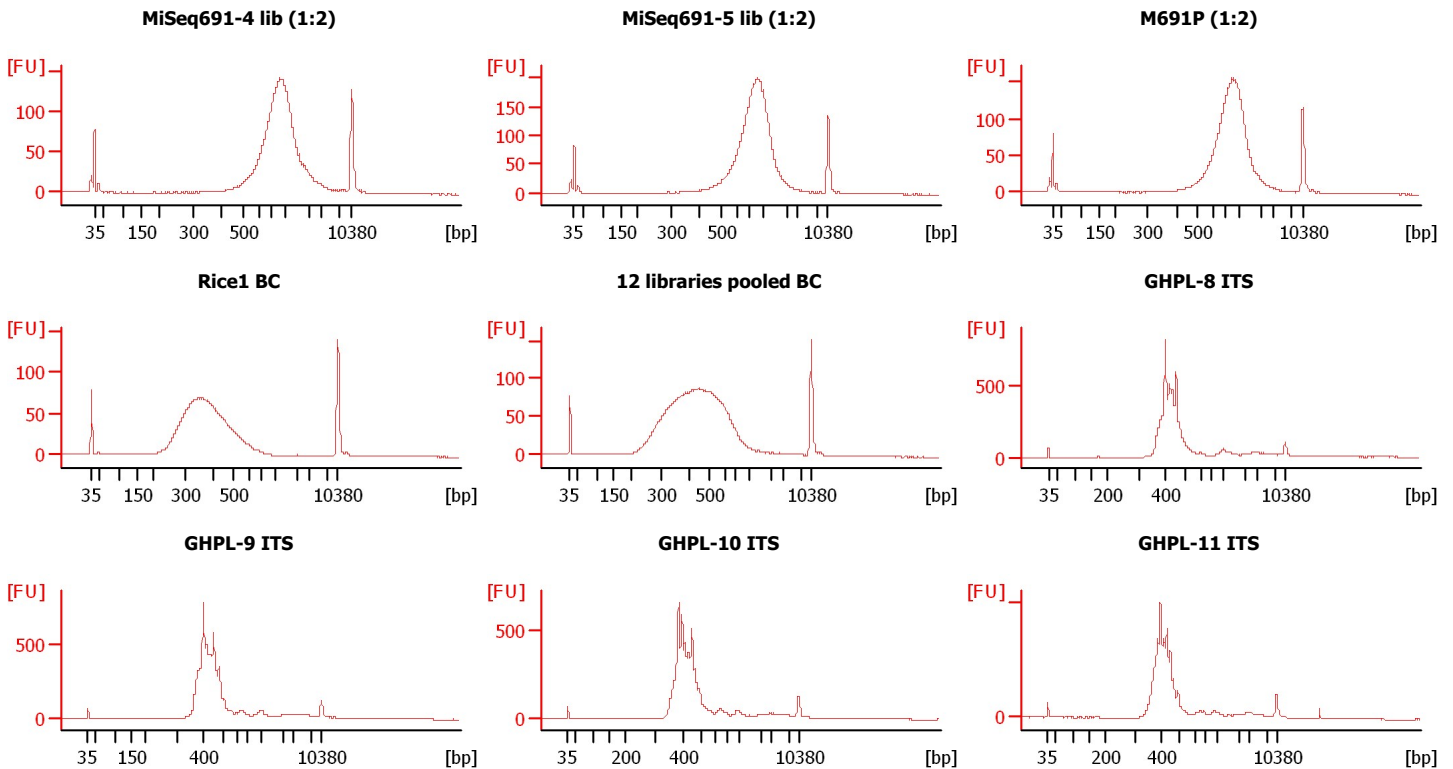
Instrument Name: DE34903152      Firmware: C.01.069  
Serial#: DE34903152      Type: G2938C

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:



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
MiSeq691-4 lib (1:2)		<input type="checkbox"/>	✓			
MiSeq691-5 lib (1:2)		<input type="checkbox"/>	✓			
M691P (1:2)		<input type="checkbox"/>	✓			
Rice1 BC		<input type="checkbox"/>	✓			
12 libraries pooled BC		<input type="checkbox"/>	✓			
GHPL-8 ITS		<input type="checkbox"/>	✓			
GHPL-9 ITS		<input type="checkbox"/>	✓			
GHPL-10 ITS		<input type="checkbox"/>	✓			
GHPL-11 ITS		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #** **Reagent Kit Lot #**

**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] : 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

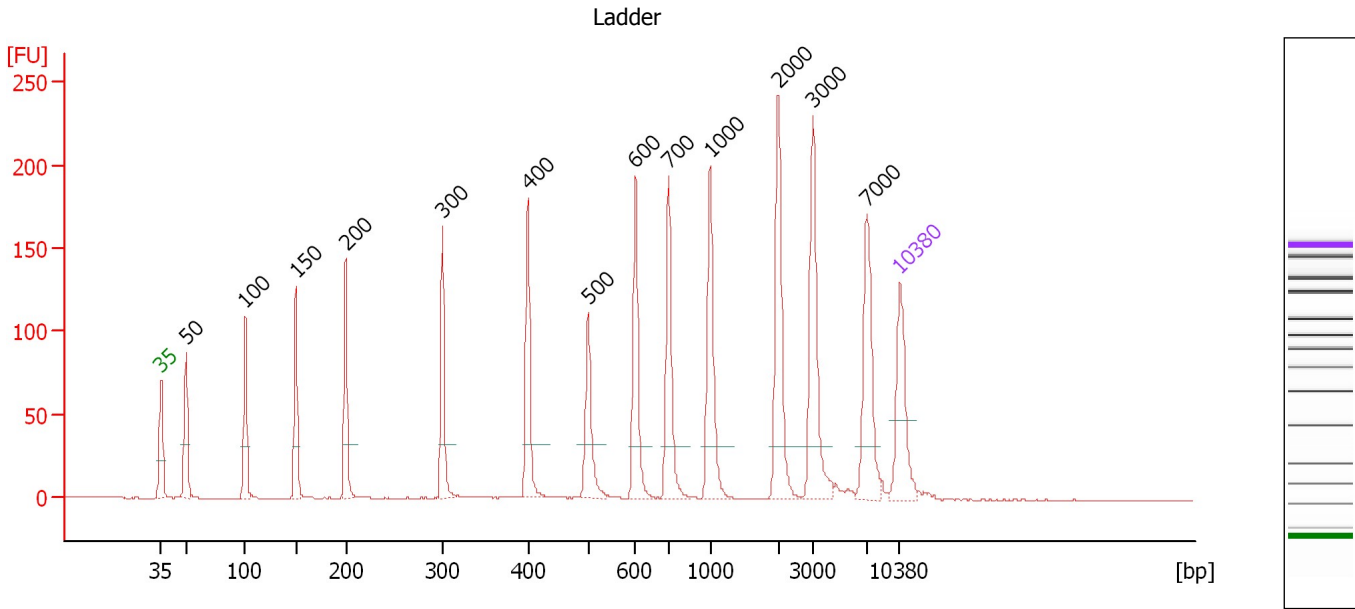
**Ladder**

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

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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

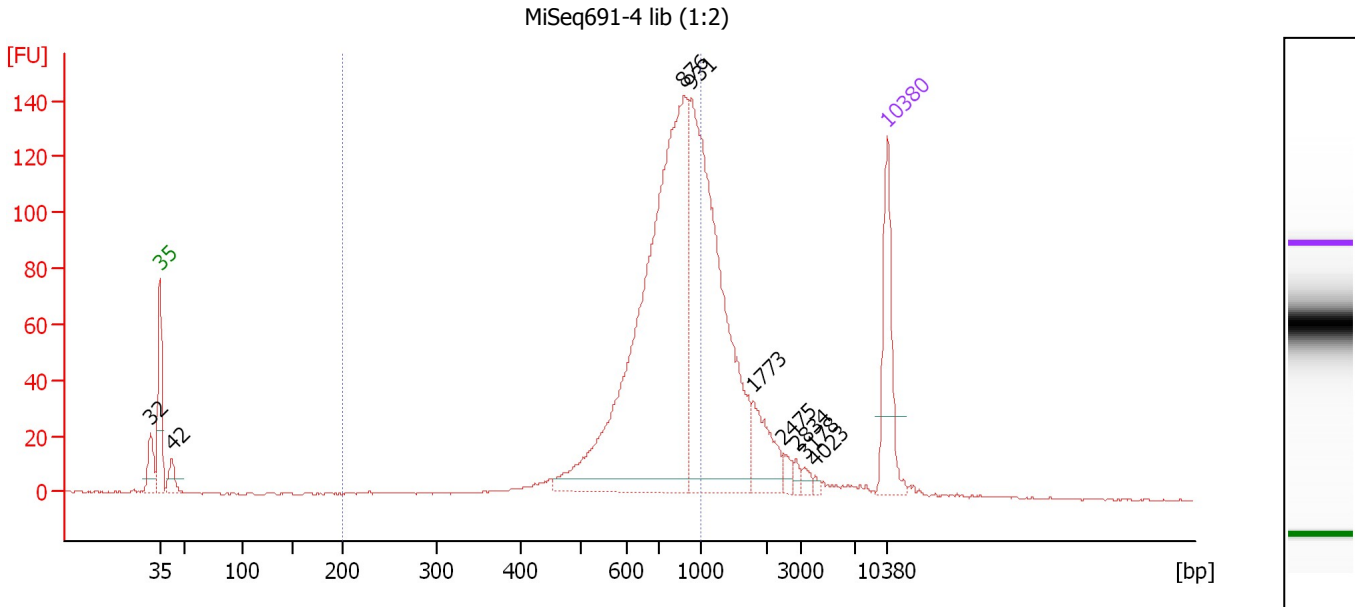
**Peak table for Ladder**

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	45.37
3	100	150.00	2,272.7	Ladder Peak	50.98
4	150	150.00	1,515.2	Ladder Peak	55.78
5	200	150.00	1,136.4	Ladder Peak	60.53
6	300	150.00	757.6	Ladder Peak	69.67
7	400	150.00	568.2	Ladder Peak	77.75
8	500	150.00	454.5	Ladder Peak	83.45
9	600	150.00	378.8	Ladder Peak	87.95
10	700	150.00	324.7	Ladder Peak	91.08
11	1,000	150.00	227.3	Ladder Peak	95.02
12	2,000	150.00	113.6	Ladder Peak	101.48
13	3,000	150.00	75.8	Ladder Peak	104.77
14	7,000	150.00	32.5	Ladder Peak	109.87
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : MiSeq691-4 lib (1:2)**

Number of peaks found: 9                      Corr. Area 1: 1,017.6  
 Noise: 0.3

**Peak table for sample 1 : MiSeq691-4 lib (1:2)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.13
2	35	125.00	5,411.3	Lower Marker	43.00
3	42	28.49	1,024.4		44.13
4	876	639.05	1,104.9		93.40
5	931	443.37	721.5		94.11
6	1,773	50.27	43.0		100.02
7	2,475	8.26	5.1		103.04
8	2,834	5.89	3.1		104.22
9	3,178	5.68	2.7		104.99
10	4,023	2.66	1.0		106.07
11	10,380	75.00	10.9	Upper Marker	113.00

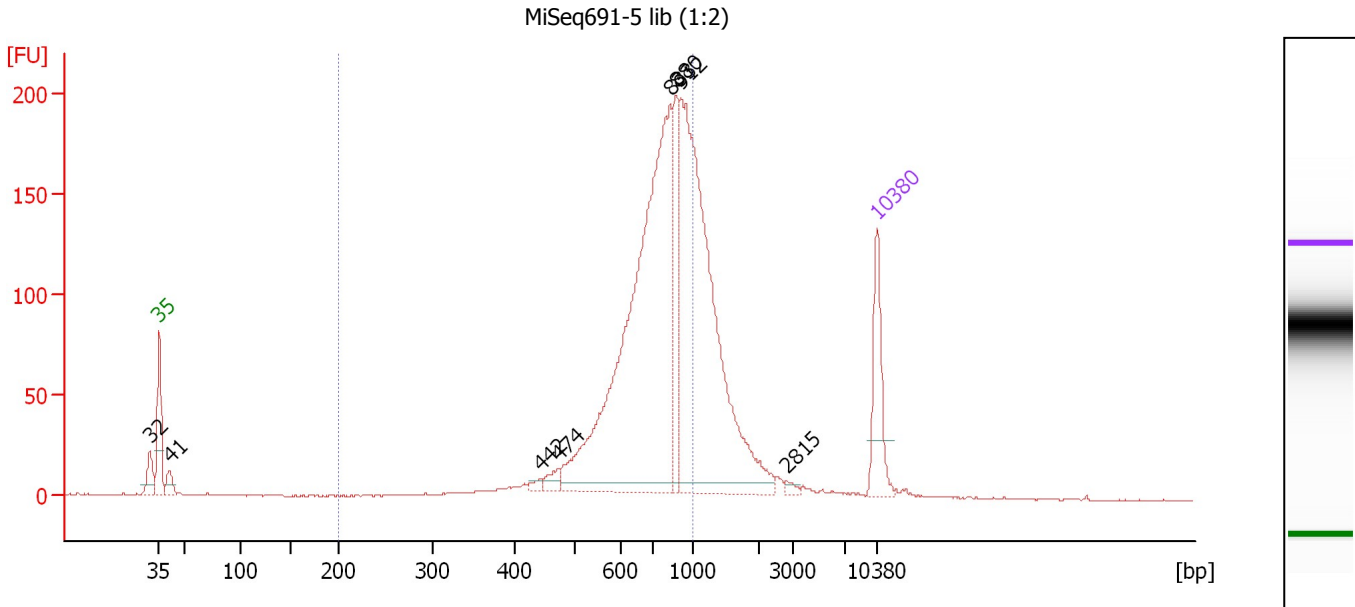
**Region table for sample 1 : MiSeq691-4 lib (1:2)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	746	878.46	1,017.6	1,901.0	64	20.2

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : MiSeq691-5 lib (1:2)**

Number of peaks found: 8                      Corr. Area 1: 1,491.1  
 Noise: 0.2

**Peak table for sample 2 : MiSeq691-5 lib (1:2)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.12
2	35	125.00	5,411.3	Lower Marker	43.00
3	41	27.31	1,003.4		43.99
4	442	8.29	28.4		80.13
5	474	16.61	53.1		81.95
6	833	801.01	1,457.7		92.82
7	880	118.15	203.4		93.45
8	912	645.53	1,072.7		93.86
9	2,815	5.77	3.1		104.16
10	10,380	75.00	10.9	Upper Marker	113.00

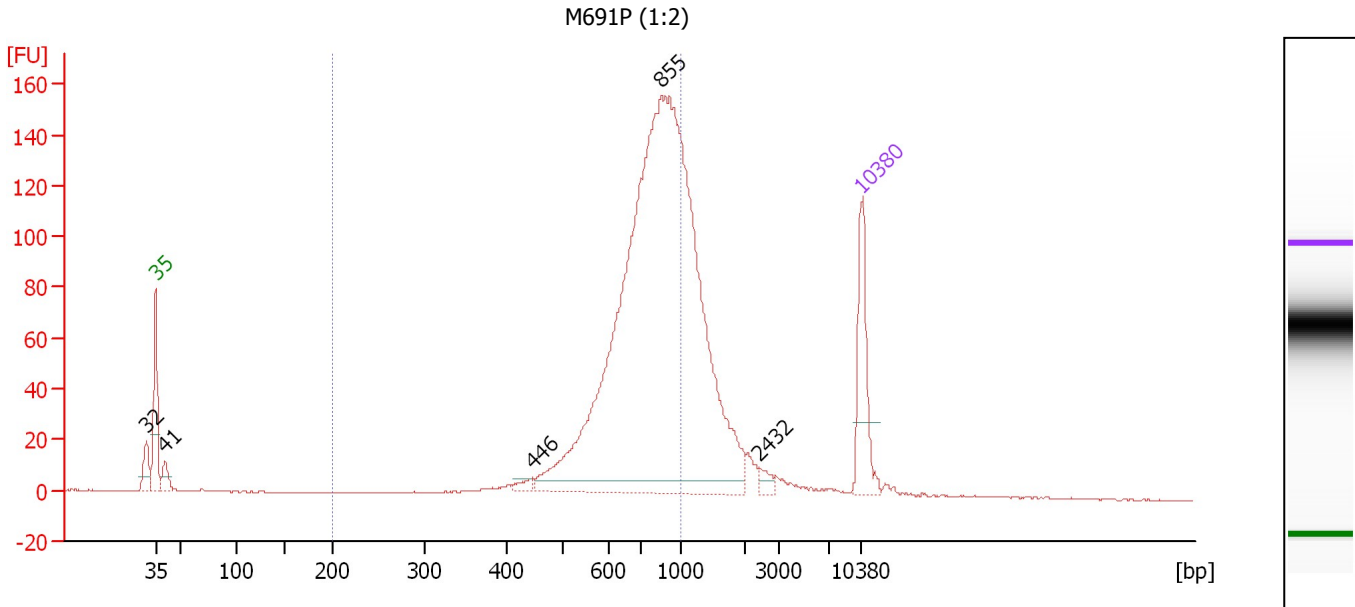
**Region table for sample 2 : MiSeq691-5 lib (1:2)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	735	1,285.93	1,491.1	2,830.8	70	20.7

Assay Class: High Sensitivity DNA Assay  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : M691P (1:2)**

Number of peaks found: 5                      Corr. Area 1: 1,143.7  
 Noise: 0.2

**Peak table for sample 3 : M691P (1:2)**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	32	0.00	0.0		42.10
2	35	125.00	5,411.3	Lower Marker	43.00
3	41	26.60	982.7		43.95
4	446	9.78	33.2		80.38
5	855	1,317.24	2,333.3		93.12
6	2,432	8.92	5.6		102.90
7	10,380	75.00	10.9	Upper Marker	113.00

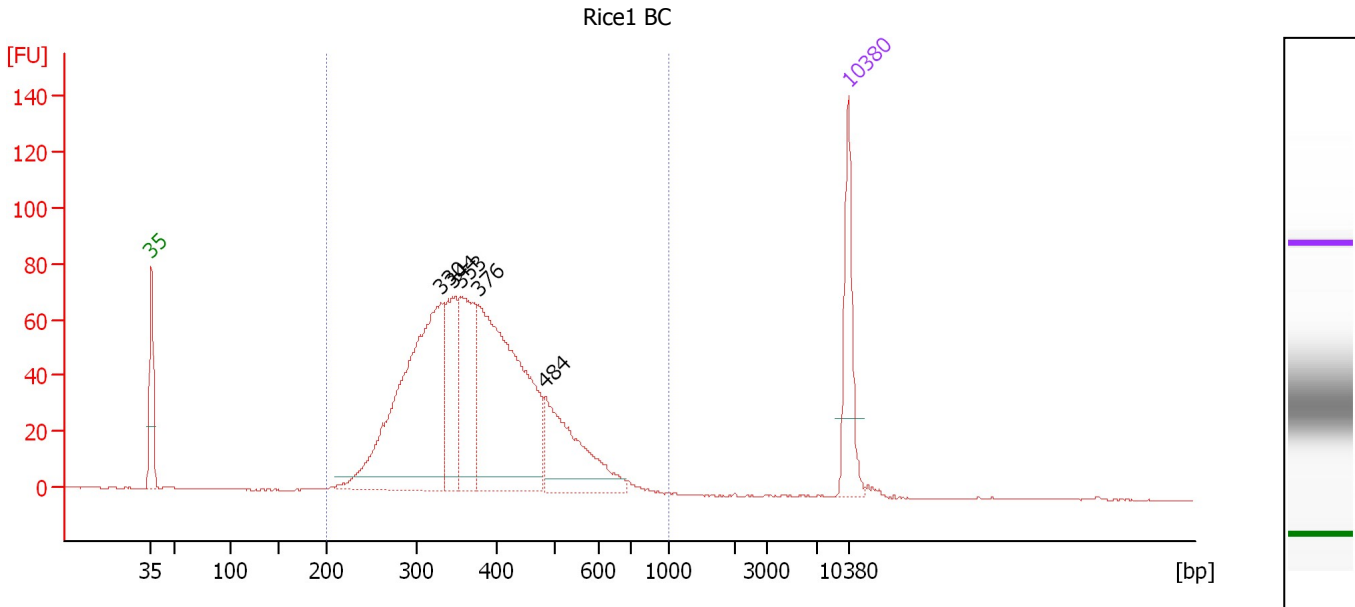
**Region table for sample 3 : M691P (1:2)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	742	1,032.03	1,143.7	2,228.1	68	19.9

Assay Class: High Sensitivity DNA Assay  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : Rice1 BC**

Number of peaks found: 5                      Corr. Area 1: 1,409.2  
 Noise: 0.2

**Peak table for sample 4 : Rice1 BC**

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	330	454.43	2,084.7		72.11
3	344	126.25	555.8		73.24
4	353	160.71	688.9		73.99
5	376	411.69	1,659.1		75.81
6	484	152.54	477.4		82.55
7	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 4 : Rice1 BC**

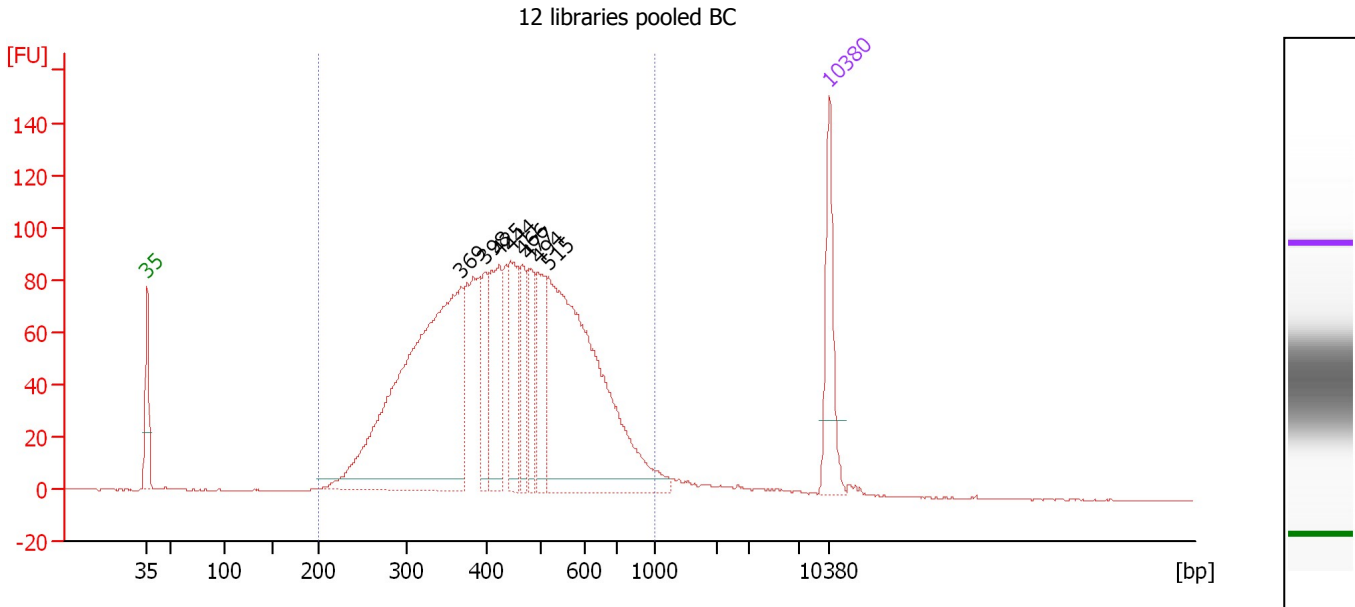
From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	385	1,354.29	1,409.2	5,724.0	99	24.3



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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : 12 libraries pooled BC**

Number of peaks found: 8                      Corr. Area 1: 2,276.4  
 Noise: 0.2

**Peak table for sample 5 : 12 libraries pooled BC**

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	369	664.95	2,728.2		75.27
3	398	65.50	249.1		77.62
4	425	131.04	467.7		79.15
5	444	96.50	329.5		80.24
6	466	64.12	208.6		81.50
7	477	67.72	215.0		82.16
8	494	93.64	286.9		83.14
9	515	525.32	1,545.8		84.13
10	10,380	75.00	10.9	Upper Marker	113.00

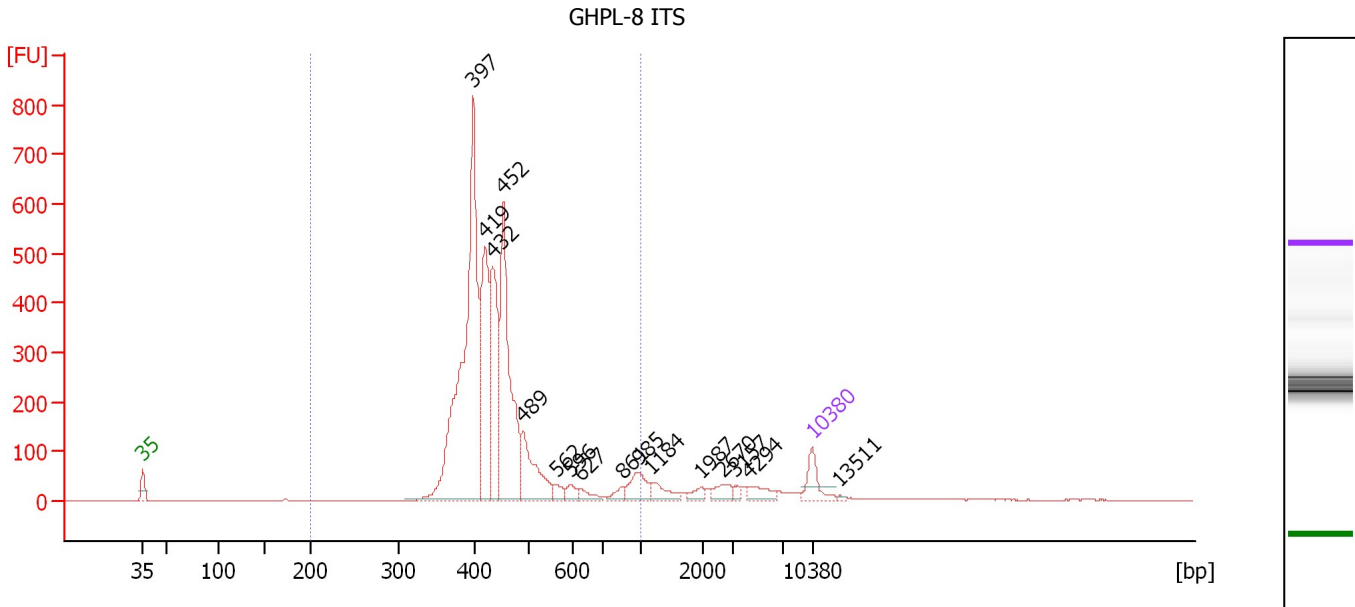
**Region table for sample 5 : 12 libraries pooled BC**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	451	2,009.71	2,276.4	7,580.3	97	29.4

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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : GHPL-8 ITS**

Number of peaks found: 16                      Corr. Area 1: 4,221.8  
 Noise: 0.2

**Peak table for sample 6 : GHPL-8 ITS**

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	397	1,537.04	5,862.3		77.53
3	419	563.05	2,038.0		78.81
4	432	489.82	1,716.8		79.59
5	452	761.99	2,555.3		80.71
6	489	263.72	817.2		82.82
7	562	35.27	95.1		86.23
8	596	35.27	89.6		87.79
9	627	37.85	91.5		88.79
10	861	29.67	52.2		93.20
11	985	89.97	138.5		94.82
12	1,184	60.02	76.8		96.21
13	1,987	26.46	20.2		101.40
14	2,670	43.05	24.4		103.69
15	3,157	14.32	6.9		104.97
16	4,294	48.02	16.9		106.42
17	10,380	75.00	10.9	Upper Marker	113.00
18	13,511	0.00	0.0		115.90

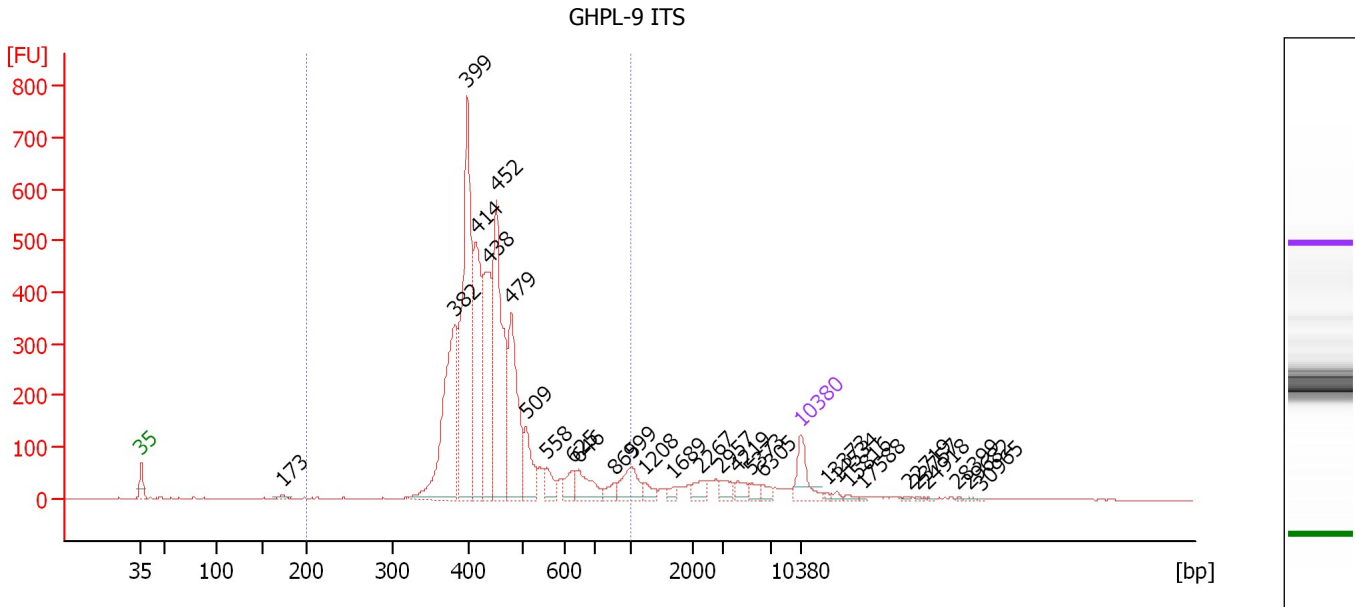
**Region table for sample 6 : GHPL-8 ITS**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	445	3,820.23	4,221.8	13,479.1	90	21.9

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**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : GHPL-9 ITS**

Number of peaks found: 30                      Corr. Area 1: 4,987.9  
 Noise: 1.0

**Peak table for sample 7 : GHPL-9 ITS**

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	173	16.28	142.8		57.94
3	382	568.57	2,252.4		76.33
4	399	804.76	3,059.2		77.63
5	414	422.94	1,548.4		78.54
6	438	407.17	1,409.6		79.90
7	452	615.77	2,066.3		80.69
8	479	376.62	1,190.6		82.27
9	509	123.92	368.9		83.86
10	558	55.33	150.2		86.06
11	625	49.92	121.1		88.72
12	646	84.82	198.8		89.40
13	865	27.52	48.2		93.25
14	999	85.27	129.4		95.00
15	1,208	24.70	31.0		96.36
16	1,689	14.56	13.1		99.48
17	2,267	30.39	20.3		102.36
18	2,957	29.52	15.1		104.62
19	4,219	29.24	10.5		106.32
20	5,373	18.02	5.1		107.79
21	6,305	18.42	4.4		108.98
22	10,380	75.00	10.9	Upper Marker	113.00
23	13,373	0.00	0.0		115.77
24	14,534	0.00	0.0		116.85
25	15,816	0.00	0.0		118.04

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### Electropherogram Summary Continued ...

#### ... Peak table for sample 7 : GHPL-9 ITS

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	17,588	0.00	0.0		119.68
27	22,719	0.00	0.0		124.43
28	23,757	0.00	0.0		125.39
29	24,918	0.00	0.0		126.47
30	28,399	0.00	0.0		129.69
31	29,682	0.00	0.0		130.88
32	30,965	0.00	0.0		132.07

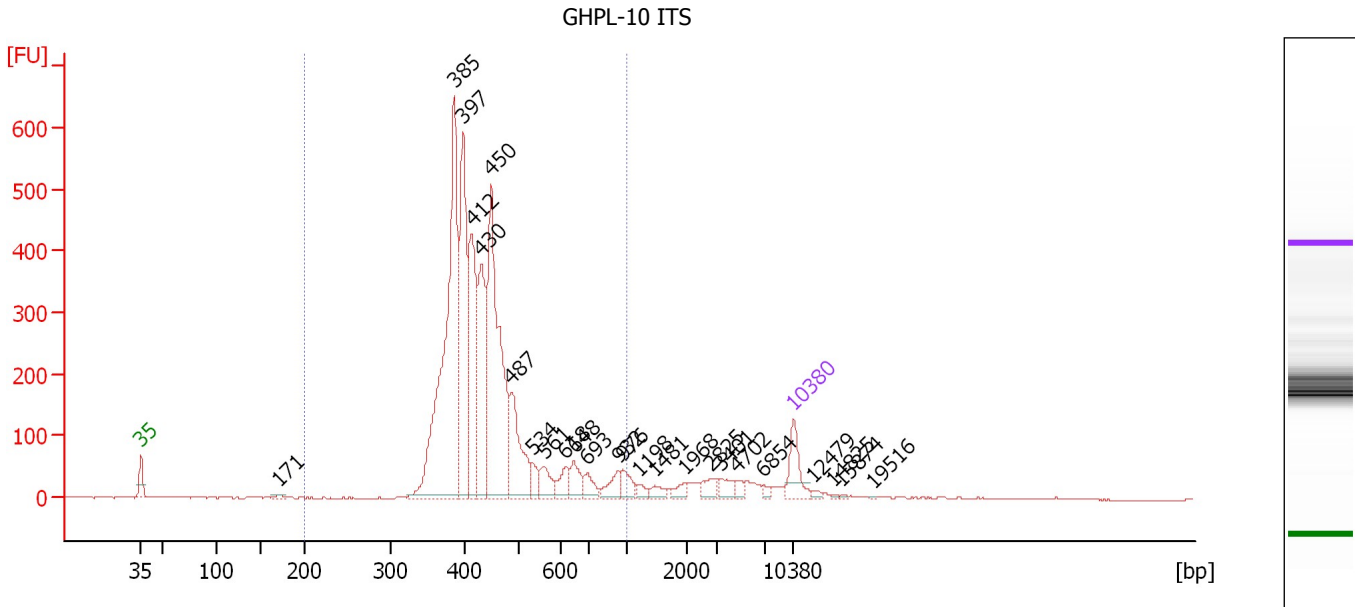
#### Region table for sample 7 : GHPL-9 ITS

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ $\mu$ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	453	3,695.12	4,987.9	12,906.4	 87	22.5

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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : GHPL-10 ITS**

Number of peaks found: 25                      Corr. Area 1: 4,452.6  
 Noise: 0.9

**Peak table for sample 8 : GHPL-10 ITS**

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	171	9.61	85.2		57.75
3	385	1,025.34	4,030.6		76.57
4	397	496.00	1,890.8		77.54
5	412	375.19	1,378.3		78.46
6	430	337.44	1,187.7		79.49
7	450	705.67	2,378.5		80.57
8	487	221.88	690.9		82.69
9	534	36.63	104.0		84.98
10	561	55.41	149.8		86.18
11	618	51.13	125.3		88.52
12	648	59.75	139.8		89.44
13	693	41.01	89.6		90.87
14	932	44.82	72.9		94.13
15	976	41.06	63.8		94.70
16	1,198	18.32	23.2		96.30
17	1,481	22.71	23.2		98.13
18	1,968	21.70	16.7		101.28
19	2,825	30.58	16.4		104.19
20	3,401	25.79	11.5		105.28
21	4,702	17.67	5.7		106.94
22	6,854	10.26	2.3		109.68
23	10,380	75.00	10.9	Upper Marker	113.00
24	12,479	0.00	0.0		114.94
25	14,825	0.00	0.0		117.12

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### Electropherogram Summary Continued ...

#### ... Peak table for sample 8 : GHPL-10 ITS

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	15,874	0.00	0.0		118.09
27	19,516	0.00	0.0		121.46

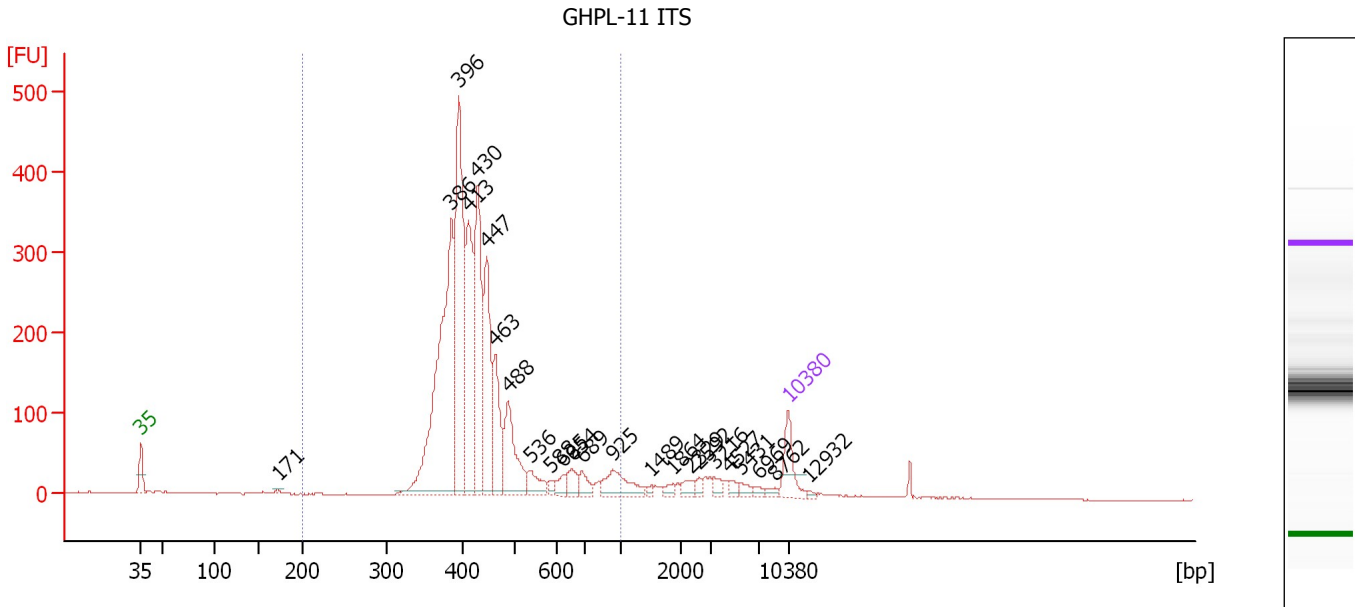
#### Region table for sample 8 : GHPL-10 ITS

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ $\mu$ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	447	3,477.97	4,452.6	12,310.1	 90	22.8

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : GHPL-11 ITS**

Number of peaks found: 24                      Corr. Area 1: 3,145.5  
 Noise: 0.7

**Peak table for sample 9 : GHPL-11 ITS**

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	171	9.40	83.0		57.82
3	386	853.03	3,348.4		76.62
4	396	622.39	2,381.4		77.42
5	413	374.05	1,373.9		78.46
6	430	412.91	1,456.0		79.44
7	447	289.82	982.7		80.42
8	463	186.63	610.7		81.34
9	488	199.01	617.5		82.79
10	536	57.07	161.2		85.09
11	588	14.02	36.1		87.40
12	625	27.15	65.8		88.72
13	654	42.32	98.0		89.65
14	689	36.03	79.2		90.74
15	925	91.67	150.2		94.03
16	1,489	7.72	7.9		98.18
17	1,864	12.79	10.4		100.60
18	2,329	22.01	14.3		102.56
19	2,592	12.25	7.2		103.43
20	3,216	16.76	7.9		105.04
21	4,527	13.81	4.6		106.71
22	5,431	15.50	4.3		107.87
23	6,969	10.79	2.3		109.83
24	8,762	10.45	1.8		111.50
25	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-21\2018-06-21\_002.xad

Created: 6/21/2018 11:39:51 AM  
Modified: 6/21/2018 12:15:25 PM

**Electropherogram Summary Continued ...****... Peak table for sample 9 : GHPL-11 ITS**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	12,932	0.00	0.0		115.36

**Region table for sample 9 : GHPL-11 ITS**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/ $\mu$ l]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	441	3,192.99	3,145.5	11,432.1	 91	22.8



Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-21\2018-06-21\_002.xad

Created: 6/21/2018 11:39:51 AM  
Modified: 6/21/2018 12:15:25 PM

**Gel Image**

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2018-06-21\2018-06-21\_002.xad

Created: 6/21/2018 11:39:51 AM  
Modified: 6/21/2018 12:15:25 PM

**Invalid Samples**

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.