

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-07-24\2017-07-24_002.xad

Created: 7/24/2017 11:49:19 AM
Modified: 7/24/2017 12:30:41 PM

Electrophoresis File Run Summary

Instrument Information:

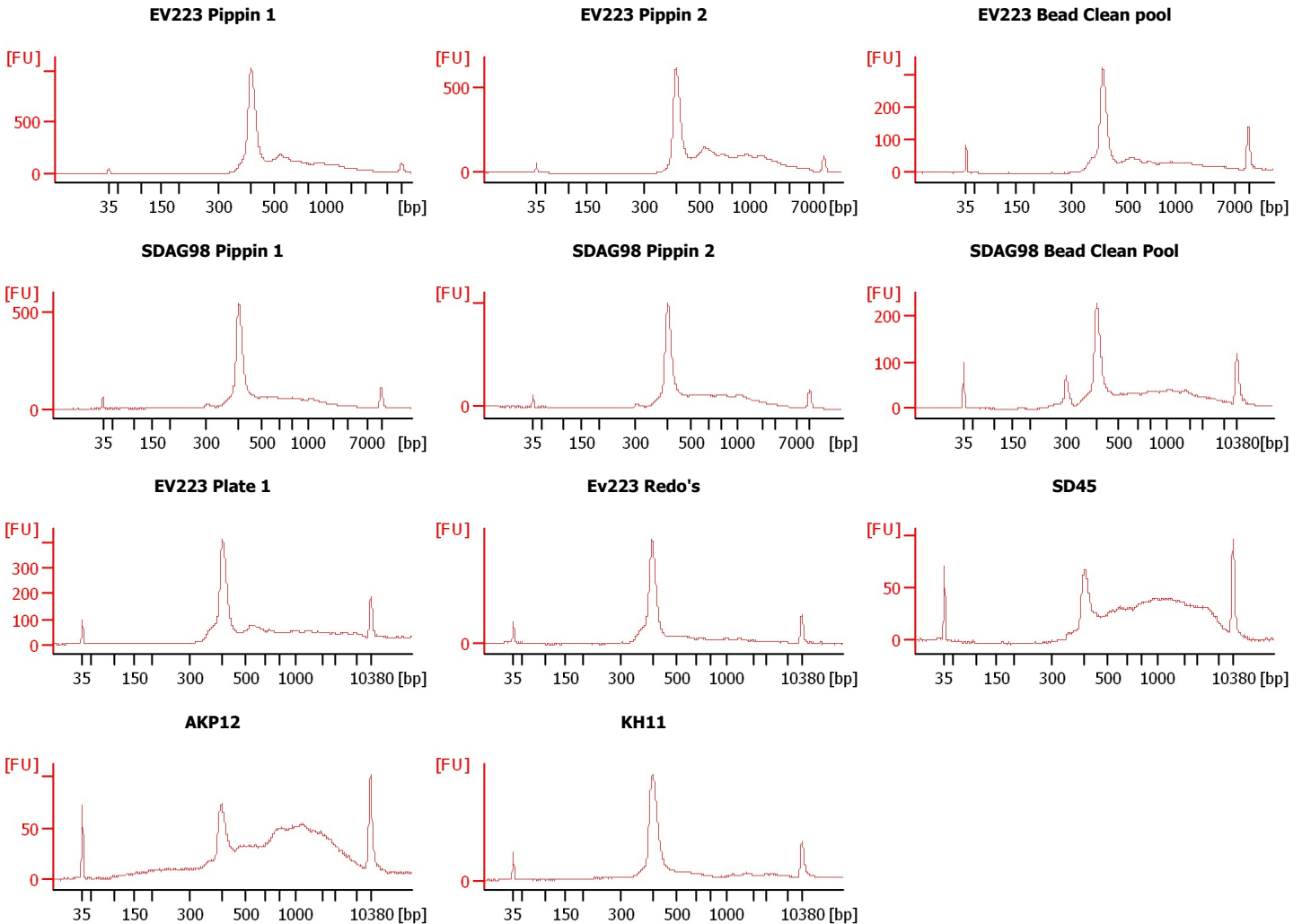
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:



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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
EV223 Pippin 1		<input type="checkbox"/>	✓			
EV223 Pippin 2		<input type="checkbox"/>	✓			
EV223 Bead Clean pool		<input type="checkbox"/>	✓			
SDAG98 Pippin 1		<input type="checkbox"/>	✓			
SDAG98 Pippin 2		<input type="checkbox"/>	✓			
SDAG98 Bead Clean Pool		<input type="checkbox"/>	✓			
EV223 Plate 1		<input type="checkbox"/>	✓			
Ev223 Redo's		<input type="checkbox"/>	✓			
SD45		<input type="checkbox"/>	✓			
AKP12		<input type="checkbox"/>	✓			
KH11		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

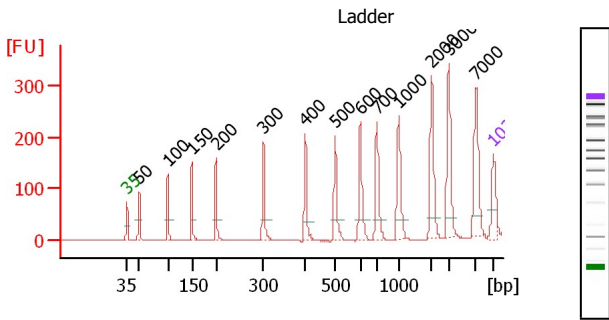
Reagent Kit Lot #

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Electropherogram Summary



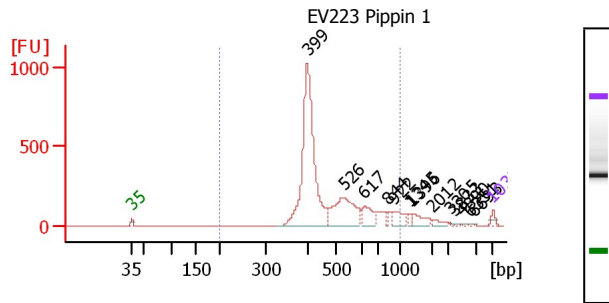
Peak table for Ladder

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	50	150.00	4,545.5	Ladder Peak	45.31
3	100	150.00	2,272.7	Ladder Peak	50.78
4	150	150.00	1,515.2	Ladder Peak	55.40
5	200	150.00	1,136.4	Ladder Peak	59.99
6	300	150.00	757.6	Ladder Peak	69.05
7	400	150.00	568.2	Ladder Peak	77.06
8	500	150.00	454.5	Ladder Peak	82.77
9	600	150.00	378.8	Ladder Peak	87.55
10	700	150.00	324.7	Ladder Peak	90.70
11	1,000	150.00	227.3	Ladder Peak	94.85
12	2,000	150.00	113.6	Ladder Peak	101.19
13	3,000	150.00	75.8	Ladder Peak	104.46

Overall Results for Ladder

Noise: 0.3

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
14	7,000	150.00	32.5	Ladder Peak	109.65
15	10,380	75.00	10.9	Upper Marker	113.00



Overall Results for sample 1 : EV223 Pippin 1

Number of peaks found: 13
 Noise: 0.2
 Corr. Area 1: 5,545.4

Region table for sample 1 : EV223 Pippin 1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total in CV	Size distribution [%]
200	1,000	490	5,545.4	24,643.8	7,386.6	90	28.2

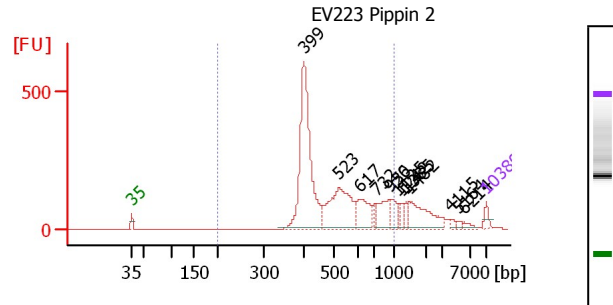
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Electropherogram Summary Continued ...

Peak table for sample 1 : EV223 Pippin 1

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	399	4,966.34	18,841.3		77.01
3	526	1,428.87	4,113.6		84.02
4	617	451.78	1,109.1		88.09
5	844	68.24	122.6		92.69
6	922	267.36	439.2		93.78
7	1,345	46.69	52.6		97.04
8	1,396	248.13	269.3		97.36
9	2,012	87.29	65.7		101.23
10	3,305	10.89	5.0		104.86
11	3,833	21.06	8.3		105.54
12	4,890	9.64	3.0		106.91
13	6,351	7.16	1.7		108.81
14	6,693	4.36	1.0		109.25
15	10,380	75.00	10.9	Upper Marker	113.00



Overall Results for sample 2 : EV223 Pippin 2

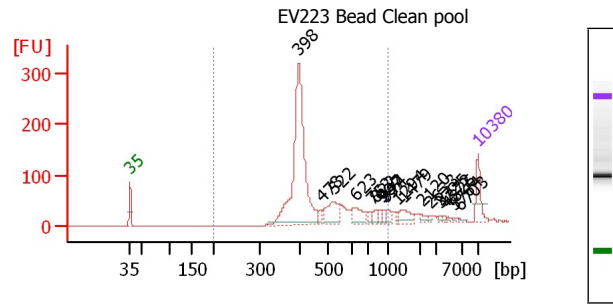
Number of peaks found: 13
 Noise: 0.2
 Corr. Area 1: 3,778.6

Region table for sample 2 : EV223 Pippin 2

From [bp]	To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Total	Size distribution CV [%]
200	1,000	526	3,778.6	14,849.6	4,699.6	80	29.9

Peak table for sample 2 : EV223 Pippin 2

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	399	2,577.16	9,777.8		77.01
3	523	1,185.42	3,436.0		83.85
4	617	453.15	1,112.1		88.10
5	732	65.90	136.3		91.15
6	926	302.51	494.9		93.83
7	950	171.60	273.7		94.16
8	1,125	55.39	74.6		95.64
9	1,242	54.52	66.5		96.39
10	1,385	79.85	87.4		97.29
11	1,482	498.10	509.1		97.91
12	4,115	34.83	12.8		105.91
13	5,164	26.30	7.7		107.27
14	6,214	36.94	9.0		108.63
15	10,380	75.00	10.9	Upper Marker	113.00



Overall Results for sample 3 : EV223 Bead Clean pool

Number of peaks found: 18
 Noise: 0.2
 Corr. Area 1: 1,539.7

Region table for sample 3 : EV223 Bead Clean pool

From [bp]	To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Total	Size distribution CV [%]
200	1,000	479	1,539.7	4,472.4	1,308.9	87	29.2

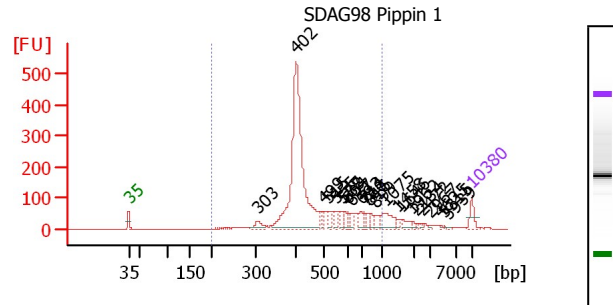
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Electropherogram Summary Continued ...

Peak table for sample 3 : EV223 Bead Clean pool

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	398	966.16	3,682.2		76.87
3	478	27.42	87.0		81.48
4	522	137.15	397.9		83.83
5	623	77.96	189.6		88.28
6	752	15.43	31.1		91.43
7	822	19.66	36.2		92.39
8	907	18.81	31.4		93.57
9	947	12.37	19.8		94.12
10	974	21.83	34.0		94.49
11	1,294	9.65	11.3		96.72
12	1,479	47.87	49.0		97.89
13	2,120	13.57	9.7		101.59
14	2,633	6.60	3.8		103.26
15	3,725	6.77	2.8		105.40
16	4,372	6.15	2.1		106.24
17	4,826	4.21	1.3		106.83
18	5,764	3.53	0.9		108.05
19	6,703	4.94	1.1		109.26
20	10,380	75.00	10.9	Upper Marker	113.00



Overall Results for sample 4 : SDAG98 Pippin 1

Number of peaks found: 24
 Noise: 0.6
 Corr. Area 1: 2,806.5

Region table for sample 4 : SDAG98 Pippin 1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	% of Size distribution in CV [%]
200	1,000	484	2,806.5	11,476.6	3,346.2	88	29.9

Peak table for sample 4 : SDAG98 Pippin 1

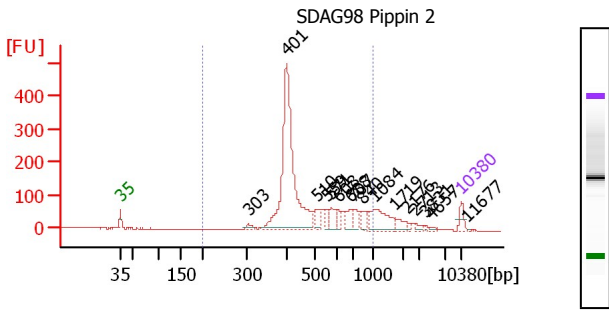
Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	303	95.15	476.1		69.27
3	402	2,290.49	8,643.6		77.15
4	499	62.03	188.2		82.73
5	515	68.58	201.7		83.49
6	555	63.78	174.0		85.41
7	577	59.65	156.5		86.47
8	588	46.11	118.8		86.98
9	604	37.48	94.1		87.67
10	627	47.95	116.0		88.39
11	693	62.51	136.7		90.48
12	714	37.86	80.3		90.90
13	760	45.49	90.6		91.54
14	816	61.32	113.9		92.31
15	899	47.06	79.3		93.46
16	1,075	165.88	233.7		95.33
17	1,458	18.99	19.7		97.76
18	1,646	50.38	46.4		98.95
19	1,962	11.95	9.2		100.95
20	2,134	10.77	7.6		101.63
21	2,472	11.72	7.2		102.74
22	2,967	8.95	4.6		104.36
23	4,625	4.98	1.6		106.57
24	5,315	3.29	0.9		107.46

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
25	5,939	5.19	1.3		108.27
26	10,380	75.00	10.9	Upper Marker	113.00

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Electropherogram Summary Continued ...



Peak table for sample 5 : SDAG98 Pippin 2

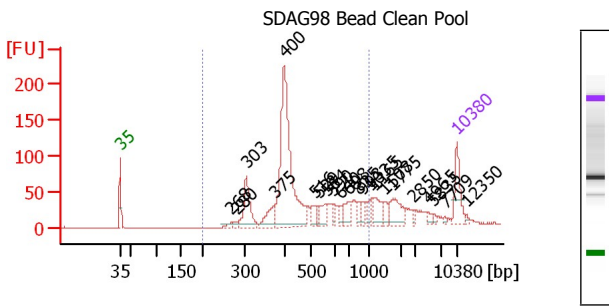
Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	303	48.27	241.1		69.32
3	401	2,287.01	8,640.7		77.12
4	510	127.68	379.2		83.25
5	559	75.03	203.2		85.61
6	571	159.94	424.4		86.17
7	608	55.71	138.9		87.79
8	688	116.06	255.6		90.32
9	707	119.86	257.0		90.80
10	840	80.42	145.1		92.64
11	1,084	305.59	427.3		95.38
12	1,719	75.68	66.7		99.41
13	2,176	19.32	13.5		101.77
14	2,713	33.39	18.6		103.53
15	3,831	7.99	3.2		105.54
16	4,657	12.82	4.2		106.61
17	10,380	75.00	10.9	Upper Marker	113.00
18	11,677	0.00	0.0		114.29

Overall Results for sample 5 : SDAG98 Pippin 2

Number of peaks found: 16
 Noise: 0.6
 Corr. Area 1: 2,710.1

Region table for sample 5 : SDAG98 Pippin 2

From To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Total in CV [%]	Size distribution
200 - 1,000	503	2,710.1	11,100.2	3,364.7	86	30.3



Peak table for sample 6 : SDAG98 Bead Clean Pool

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	268	18.14	102.4		66.17
3	280	13.34	72.2		67.22
4	303	151.13	756.7		69.26
5	375	71.28	287.9		75.07
6	400	628.15	2,378.9		77.07
7	516	40.65	119.4		83.53
8	529	16.24	46.5		84.14
9	564	46.67	125.4		85.83
10	590	21.47	55.1		87.09
11	640	15.98	37.8		88.83
12	698	46.89	101.7		90.65
13	825	16.82	30.9		92.43
14	903	18.23	30.6		93.51
15	1,035	22.18	32.5		95.08
16	1,165	46.52	60.5		95.90
17	1,508	25.97	26.1		98.07
18	1,775	73.02	62.3		99.76
19	2,850	8.01	4.3		103.97
20	4,965	9.68	3.0		107.01
21	5,835	8.72	2.3		108.14
22	7,709	4.67	0.9		110.35
23	10,380	75.00	10.9	Upper Marker	113.00

Overall Results for sample 6 : SDAG98 Bead Clean Pool

Number of peaks found: 22
 Noise: 0.3
 Corr. Area 1: 1,392.7

Region table for sample 6 : SDAG98 Bead Clean Pool

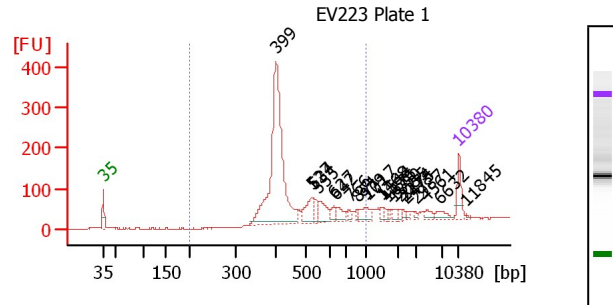
From To [bp]	Average Size [bp]	Corrected Area	Molarity [pmol/l]	Concentration [pg/μl]	% of Total in CV [%]	Size distribution
200 - 1,000	491	1,392.7	3,999.3	1,153.1	78	33.4

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Electropherogram Summary Continued ...

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
24	12,350	0.00	0.0		114.95



Overall Results for sample 7 : EV223 Plate 1

Number of peaks found: 21
 Noise: 0.6
 Corr. Area 1: 1,940.9

Region table for sample 7 : EV223 Plate 1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	480	1,940.9	5,355.9	1,575.8	83	28.3

Peak table for sample 7 : EV223 Plate 1

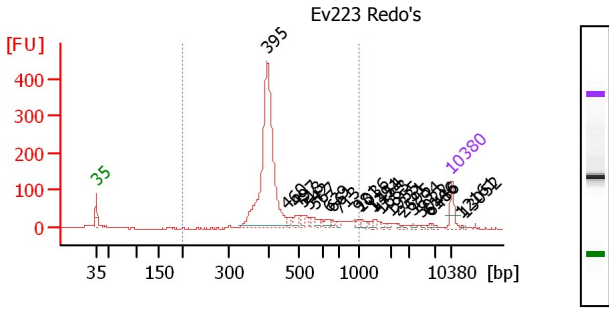
Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	399	1,131.52	4,293.1		77.01
3	527	109.13	313.9		84.05
4	534	51.89	147.2		84.40
5	555	99.03	270.2		85.41
6	627	32.89	79.5		88.41
7	642	51.64	121.8		88.89
8	766	19.55	38.7		91.62
9	871	13.68	23.8		93.07
10	979	37.38	57.8		94.57
11	1,017	29.89	44.5		94.96
12	1,468	18.38	19.0		97.82
13	1,544	15.36	15.1		98.30
14	1,676	10.59	9.6		99.14
15	1,850	16.23	13.3		100.24
16	2,085	14.17	10.3		101.47
17	2,274	9.23	6.2		102.09
18	2,475	11.04	6.8		102.75
19	2,987	7.42	3.8		104.42
20	4,561	22.00	7.3		106.49
21	6,632	32.52	7.4		109.17
22	10,380	75.00	10.9	Upper Marker	113.00

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
23	11,845	0.00	0.0		114.45

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Electropherogram Summary Continued ...



Peak table for sample 8 : Ev223 Redo's

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	395	1,462.62	5,615.7		76.63
3	460	27.45	90.5		80.47
4	497	41.90	127.7		82.59
5	518	23.32	68.3		83.61
6	542	18.93	52.9		84.80
7	567	32.75	87.5		85.99
8	639	35.30	83.7		88.77
9	661	15.44	35.4		89.48
10	713	11.81	25.1		90.89
11	981	19.46	30.0		94.60
12	1,036	21.26	31.1		95.08
13	1,391	12.69	13.8		97.33
14	1,454	14.60	15.2		97.73
15	1,683	9.82	8.8		99.19
16	1,955	8.34	6.5		100.91
17	2,331	7.46	4.9		102.27
18	2,695	6.29	3.5		103.47
19	3,694	8.50	3.5		105.36
20	5,022	4.39	1.3		107.09
21	6,146	5.29	1.3		108.54
22	6,486	9.69	2.3		108.98
23	10,380	75.00	10.9	Upper Marker	113.00

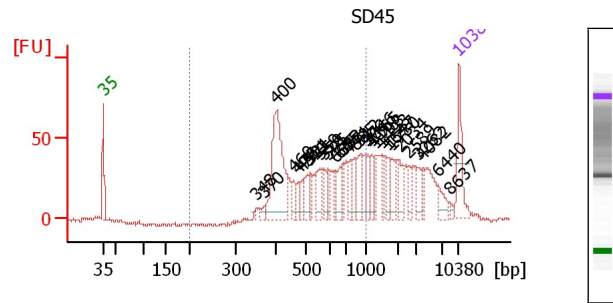
Overall Results for sample 8 : Ev223 Redo's

Number of peaks found: 23
 Noise: 1.3
 Corr. Area 1: 1,950.1

Region table for sample 8 : Ev223 Redo's

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	449	1,950.1	6,685.0	1,866.6	88	27.0

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
24	12,161	0.00	0.0		114.77
25	13,052	0.00	0.0		115.65



Overall Results for sample 9 : SD45

Number of peaks found: 30
 Noise: 0.8
 Corr. Area 1: 773.0

Region table for sample 9 : SD45

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	586	773.0	2,558.6	886.67	60	30.0

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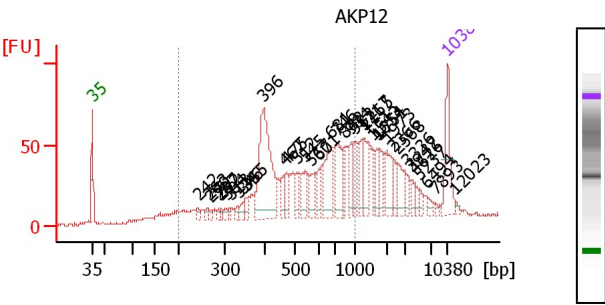
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Electropherogram Summary Continued ...

Peak table for sample 9 : SD45

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	348	4.17	18.1		72.91
3	370	12.66	51.8		74.68
4	400	277.46	1,050.7		77.07
5	460	23.29	76.7		80.48
6	475	20.97	66.8		81.37
7	490	26.27	81.2		82.21
8	511	40.73	120.9		83.27
9	521	24.54	71.4		83.76
10	559	44.95	121.9		85.58
11	579	29.79	77.9		86.55
12	595	27.28	69.5		87.30
13	636	25.16	60.0		88.68
14	665	33.34	75.9		89.61
15	682	30.63	68.0		90.14
16	771	29.65	58.2		91.69
17	835	32.84	59.6		92.58
18	912	52.35	86.9		93.64
19	976	37.86	58.7		94.53
20	1,046	25.65	37.2		95.15
21	1,165	28.75	37.4		95.90
22	1,298	22.86	26.7		96.74
23	1,493	23.83	24.2		97.98
24	1,647	22.18	20.4		98.96
25	1,780	37.83	32.2		99.80
26	2,034	38.16	28.4		101.30

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
27	2,589	26.52	15.5		103.12
28	3,262	25.30	11.8		104.80
29	4,082	16.82	6.2		105.87
30	6,440	27.61	6.5		108.92
31	8,637	6.95	1.2		111.27
32	10,380	75.00	10.9	Upper Marker	113.00



Peak table for sample 10 : AKP12

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	242	14.71	92.1		63.78
3	263	10.85	62.4		65.72
4	270	7.58	42.5		66.33
5	287	7.57	40.0		67.87
6	292	7.27	37.7		68.36
7	304	11.42	56.9		69.37
8	313	7.29	35.3		70.08
9	334	9.89	44.9		71.75
10	346	15.57	68.2		72.72
11	355	16.07	68.6		73.47
12	396	290.54	1,112.3		76.72
13	467	37.75	122.6		80.86
14	475	22.63	72.2		81.35
15	512	33.59	99.5		83.33
16	545	43.66	121.4		84.91
17	567	32.01	85.5		85.97
18	601	22.07	55.6		87.60
19	681	95.12	211.6		90.11
20	746	83.23	169.0		91.34
21	842	29.85	53.8		92.66
22	934	31.79	51.6		93.94
23	982	43.93	67.8		94.60
24	1,217	44.78	55.8		96.23
25	1,265	51.90	62.1		96.53

Overall Results for sample 10 : AKP12

Number of peaks found: 37
 Noise: 0.7
 Corr. Area 1: 1,067.5

Region table for sample 10 : AKP12

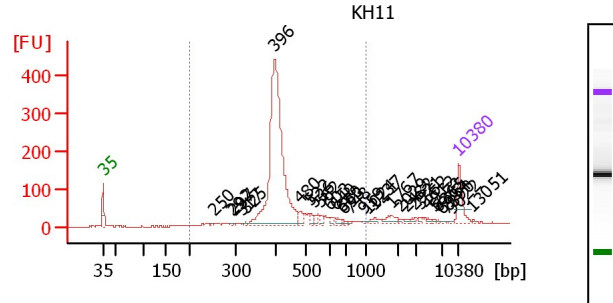
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Conc. [pg/μl]	% of Total in CV [%]	Size distribution
200	1,000	551	1,067.5	4.0626	1,210.6	64	35.8

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-07-24\2017-07-24_002.xad

Created: 7/24/2017 11:49:19 AM
 Modified: 7/24/2017 12:30:41 PM

Electropherogram Summary Continued ...

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
26	1,543	21.95	21.6		98.30
27	1,654	26.48	24.3		99.00
28	1,751	33.05	28.6		99.62
29	1,973	47.89	36.8		101.03
30	2,366	16.21	10.4		102.39
31	2,568	46.10	27.2		103.05
32	3,336	14.94	6.8		104.90
33	3,947	13.86	5.3		105.69
34	4,626	13.31	4.4		106.57
35	5,237	11.61	3.4		107.36
36	6,494	10.59	2.5		108.99
37	7,893	4.40	0.8		110.53
38	10,380	75.00	10.9	Upper Marker	113.00
39	12,023	0.00	0.0		114.63



Overall Results for sample 11 : KH11

Number of peaks found: 30
 Noise: 1.4
 Corr. Area 1: 2,010.1

Region table for sample 11 : KH11

From To [bp]	Average Size [bp]	Area	Corrected Molarity [pmol/l]	Concentration [pg/μl]	% of Total	% of CV
200 - 1,000	431	2,010.1	4,909.5	1,334.7	88	21.3

Peak table for sample 11 : KH11

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
1	35	125.00	5,411.3	Lower Marker	43.00
2	250	3.47	21.0		64.54
3	292	3.09	16.0		68.35
4	297	3.04	15.5		68.80
5	317	3.89	18.6		70.37
6	325	4.02	18.7		71.04
7	396	1,097.93	4,200.6		76.74
8	480	29.77	93.9		81.63
9	522	16.88	49.0		83.83
10	536	11.77	33.3		84.51
11	562	11.81	31.9		85.72
12	603	10.48	26.3		87.65
13	640	10.64	25.2		88.81
14	680	4.40	9.8		90.07
15	693	4.79	10.5		90.47
16	748	3.42	6.9		91.37
17	959	2.55	4.0		94.29
18	1,024	3.02	4.5		95.01
19	1,237	12.67	15.5		96.35
20	1,767	27.22	23.3		99.72
21	2,029	4.25	3.2		101.29
22	2,482	5.51	3.4		102.77
23	2,921	7.16	3.7		104.21
24	3,562	5.67	2.4		105.19

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time
25	4,912	6.04	1.9		106.94
26	5,673	4.43	1.2		107.93
27	6,365	2.68	0.6		108.83
28	6,954	3.09	0.7		109.59
29	7,890	1.59	0.3		110.53
30	9,022	1.90	0.3		111.65
31	10,380	75.00	10.9	Upper Marker	113.00
32	13,051	0.00	0.0		115.65

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-07-24\2017-07-24_002.xad

Created: 7/24/2017 11:49:19 AM
Modified: 7/24/2017 12:30:41 PM

Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-07-24\2017-07-24_002.xad

Created: 7/24/2017 11:49:19 AM
Modified: 7/24/2017 12:30:41 PM

Curves

Standard Curve

