

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2014-04-24\2014-04-24_002.xad

Created: 4/24/2014 12:52:46 PM
Modified: 4/24/2014 1:34:08 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:

600lib 1:2

600lib1:4

600lib 1:8

600lib 1:16

600lib1:32

pcr 1:2

pcr1:4

pcr 1:8

pcr1:16

hic peanut

sample 11

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Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
600lib 1:2		<input type="checkbox"/>				
600lib1:4		<input type="checkbox"/>				
600lib 1:8		<input type="checkbox"/>				
600lib 1:16		<input type="checkbox"/>				
600lib1:32		<input type="checkbox"/>				
pcr 1:2		<input type="checkbox"/>				
pcr1:4		<input type="checkbox"/>				
pcr 1:8		<input type="checkbox"/>				
pcr1:16		<input type="checkbox"/>				
hic peanut		<input type="checkbox"/>				
sample 11		<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

Ladder



Overall Results for Ladder

Noise: 0.1

Peak table for Ladder

Peak	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	45.30	50	150.00	4,545.5	Ladder Peak
3	50.68	100	150.00	2,272.7	Ladder Peak
4	55.27	150	150.00	1,515.2	Ladder Peak
5	59.86	200	150.00	1,136.4	Ladder Peak
6	68.84	300	150.00	757.6	Ladder Peak
7	76.89	400	150.00	568.2	Ladder Peak
8	82.57	500	150.00	454.5	Ladder Peak
9	87.33	600	150.00	378.8	Ladder Peak
10	90.54	700	150.00	324.7	Ladder Peak
11	94.59	1,000	150.00	227.3	Ladder Peak
12	101.15	2,000	150.00	113.6	Ladder Peak
13	104.40	3,000	150.00	75.8	Ladder Peak
14	109.45	7,000	150.00	32.5	Ladder Peak
15	113.00	10,380	75.00	10.9	Upper Marker

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Electropherogram Summary Continued ...

600lib 1:2



Overall Results for sample 1 : 600lib 1:2

Number of peaks found: 5 Corr. Area 1: 5,140.9
 Noise: 0.2

Peak table for sample 1 : 600lib 1:2

Peak	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	48.69	81	44.31	823.9	
3	87.35	601	2,622.46	6,615.2	
4	87.90	618	3,337.76	8,187.3	
5	103.35	2,679	3.84	2.2	
6	105.38	3,772	21.21	8.5	
7	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 1 : 600lib 1:2

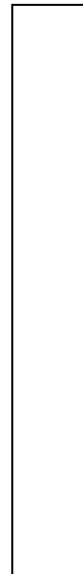
From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
369	1,924	693	14,510.3	6,041.03	5,140.9	96	32.6

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Electropherogram Summary Continued ...

600lib1:4



Overall Results for sample 2 : 600lib1:4

Number of peaks found: 6 Corr. Area 1: 3,162.2
 Noise: 0.2

Peak table for sample 2 : 600lib1:4

Peak	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	48.66	81	25.34	472.4	
3	74.41	369	25.93	106.5	
4	77.66	414	72.54	265.8	
5	87.60	608	1,411.93	3,516.9	
6	88.10	624	1,770.83	4,299.3	
7	113.00	10,380	75.00	10.9	Upper Marker
8	115.24	12,514	0.00	0.0	

Region table for sample 2 : 600lib1:4

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
298	2,465	691	8,230.6	3,382.98	3,162.2	98	34.2

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Electropherogram Summary Continued ...

600lib 1:8



Overall Results for sample 3 : 600lib 1:8

Number of peaks found: 4 Corr. Area 1: 1,518.3
 Noise: 0.2

Peak table for sample 3 : 600lib 1:8

Peak	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	87.16	597	628.54	1,596.5	
3	88.02	622	188.68	459.9	
4	89.31	662	82.58	189.1	
5	91.03	736	433.56	892.8	
6	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 3 : 600lib 1:8

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
356	1,954	694	4,078.0	1,700.41	1,518.3	97	32.3

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Electropherogram Summary Continued ...

600lib 1:16



Overall Results for sample 4 : 600lib 1:16

Number of peaks found: 6 Corr. Area 1: 646.7
 Noise: 0.2

Peak table for sample 4 : 600lib 1:16

Peak	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	78.98	437	7.36	25.6	
3	86.08	574	214.82	567.2	
4	86.86	590	68.40	175.6	
5	87.77	614	60.27	148.8	
6	88.42	634	168.32	402.2	
7	91.07	739	192.63	395.0	
8	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 4 : 600lib 1:16

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
395	2,004	687	1,871.6	783.56	646.7	96	30.2

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Electropherogram Summary Continued ...

600lib1:32



Overall Results for sample 5 : 600lib1:32

Number of peaks found: 7 Corr. Area 1: 837.6
 Noise: 0.1

Peak table for sample 5 : 600lib1:32

Peak	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	81.21	476	31.48	100.2	
3	86.45	582	215.56	561.6	
4	86.98	593	45.67	116.7	
5	87.60	608	62.66	156.1	
6	88.48	636	42.48	101.2	
7	88.92	649	174.40	406.9	
8	91.74	788	165.53	318.1	
9	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 5 : 600lib1:32

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
392	2,403	701	1,894.5	798.49	837.6	94	33.5

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Electropherogram Summary Continued ...

pcr 1:2



Overall Results for sample 6 : pcr 1:2

Number of peaks found: 6 Corr. Area 1: 383.0
 Noise: 0.2

Peak table for sample 6 : pcr 1:2

Peak	Aligned Migration Time [s]	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations
1	42.00	31	0.00	0.0	
2	43.00	35	125.00	5,411.3	Lower Marker
3	44.05	42	664.87	24,075.0	
4	45.31	50	287.36	8,680.3	
5	46.40	60	54.67	1,374.0	
6	90.18	689	275.48	606.2	
7	90.61	705	272.65	585.9	
8	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 6 : pcr 1:2

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
502	1,490	715	1,287.5	594.89	383.0	44	15.2

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Electropherogram Summary Continued ...

pcr1:4



Overall Results for sample 7 : pcr1:4

Number of peaks found: 5 Corr. Area 1: 276.2
 Noise: 0.2

Peak table for sample 7 : pcr1:4

Peak	Aligned Migration Time [s]	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations
1	42.03	32	0.00	0.0	
2	43.00	35	125.00	5,411.3	Lower Marker
3	44.02	42	383.91	13,964.7	
4	45.26	50	151.47	4,612.8	
5	46.45	61	21.34	532.2	
6	90.51	699	311.49	675.3	
7	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 7 : pcr1:4

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
519	1,309	715	710.1	329.10	276.2	42	14.1

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Electropherogram Summary Continued ...

pcr 1:8



Overall Results for sample 8 : pcr 1:8

Number of peaks found: 4 Corr. Area 1: 131.4
 Noise: 0.1

Peak table for sample 8 : pcr 1:8

Peak	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	44.03	42	266.21	9,668.8	
3	45.15	49	85.38	2,638.9	
4	90.34	694	85.81	187.5	
5	91.01	734	55.47	114.4	
6	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 8 : pcr 1:8

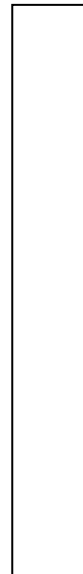
From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
556	1,097	716	337.4	157.28	131.4	37	12.4

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 Data Path: C:\...ents and Settings\Bioanalyzer\2014-04-24\2014-04-24_002.xad

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Electropherogram Summary Continued ...

pcr1:16



Overall Results for sample 9 : pcr1:16

Number of peaks found: 5 Corr. Area 1: 69.6
 Noise: 0.1

Peak table for sample 9 : pcr1:16

Peak	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	43.98	41	777.96	28,462.7	
3	44.87	47	221.60	7,107.1	
4	89.89	680	136.55	304.4	
5	112.69	10,082	94.07	14.1	
6	113.00	10,380	75.00	10.9	Upper Marker
7	113.62	10,975	0.00	0.0	

Region table for sample 9 : pcr1:16

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
530	1,105	706	756.2	346.81	69.6	27	13.1

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Electropherogram Summary Continued ...

Peak table for sample 10 : hic peanut

Peak	Aligned Migration Time [s]	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations
1	42.03	32	0.00	0.0	
2	43.00	35	125.00	5,411.3	Lower Marker
3	113.00	10,380	75.00	10.9	Upper Marker

Region table for sample 10 : hic peanut

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
233	529	352	1,004.0	227.41	88.8	79	14.8

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Electropherogram Summary Continued ...

Peak table for sample 11 : sample 11

Peak	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	113.00	10,380	75.00	10.9	Upper Marker
3	114.94	12,229	0.00	0.0	

Region table for sample 11 : sample 11

From [bp]	To [bp]	Average Size [bp]	Molarity [pmol/l]	Conc. [pg/μl]	Co Corr. lor Area	% of Total	Size distribution in CV [%]
200	1,000	542	1.0	0.33	0.2	2	19.5

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Gel Image

Assay Class: High Sensitivity DNA Assay
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Curves

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Run Logbook

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 12)		Instrument	Run		4/24/2014 1:34:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2014-04-24\2014-04-24_002.xad)		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		4/24/2014 12:52:52 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1