Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2019-10-30\2019-10-30_001.xad

Created: 10/30/2019 10:44:27 AM
Modified: 10/30/2019 11:47:30 AM

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

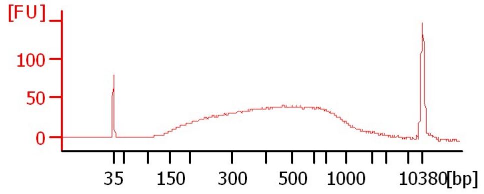
Chip Information:

Chip Lot #:

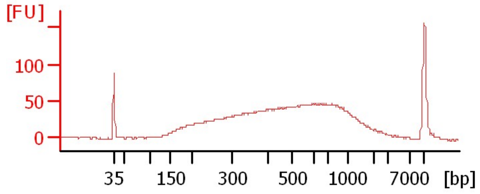
Reagent Kit Lot #:

Chip Comments:

101981 soni DNA

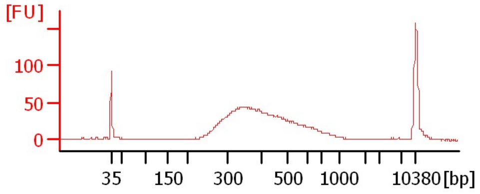


109072 soni DNA

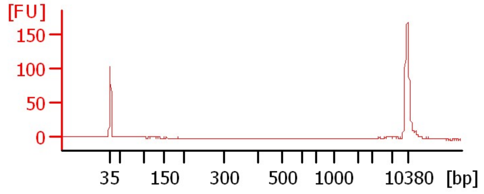


lamend2 0.8 BC

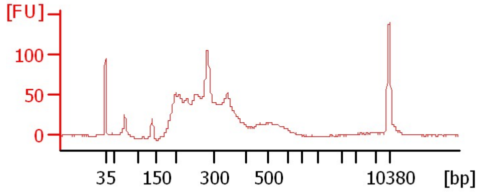
2nd 0.8x BC



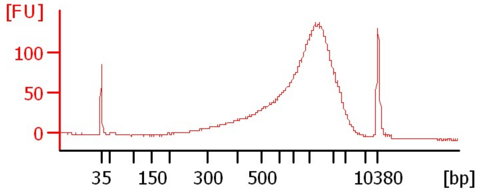
HiSeq-Coy4(1:10)



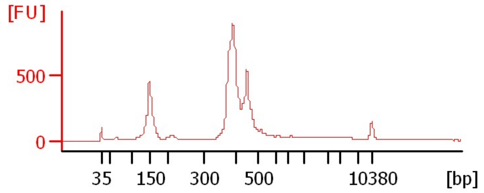
HiSeq1983-FGGBS002 #2 (1:2)



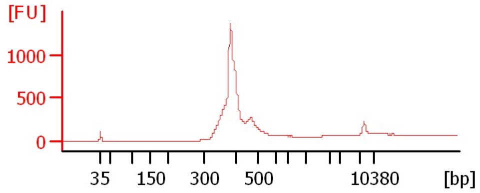
MiSeq930-NARMS092019



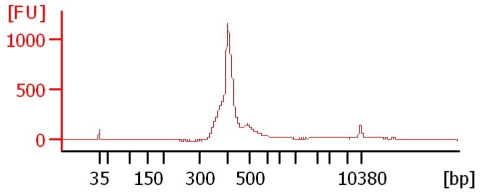
MiSeq927-Fungi(1:4)



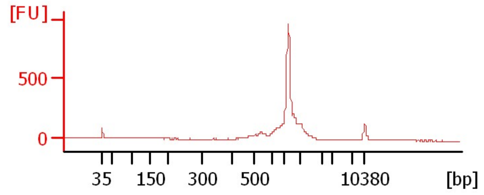
MiSeq931-SYNERGIE Run 1 (1:3)



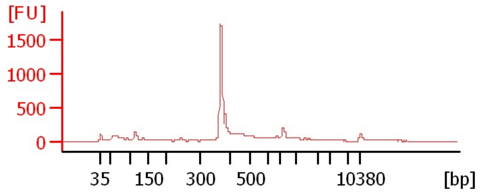
MiSeq931-SYNERGIE Run 2 (1:3)



MiSeq929-EqTRG2



MiSeq962-AmNif (1:4)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2019-10-30\2019-10-30_001.xad

Created: 10/30/2019 10:44:27 AM
Modified: 10/30/2019 11:47:30 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
101981 soni DNA		☐	✓			
109072 soni DNA		☐	✓			
lamend2 0.8 BC	2nd 0.8x BC	☐	✓			
HiSeq-Coy4(1:10)		☐	✓			
HiSeq1983-FGGBS002 #2 (1:2)		☐	✓			
MiSeq930-NARMS092019		☐	✓			
MiSeq927-Fungi(1:4)		☐	✓			
MiSeq931-SYNERGIE Run 1 (1:3)		☐	✓			
MiSeq931-SYNERGIE Run 2 (1:3)		☐	✓			
MiSeq929-EqTRG2		☐	✓			
MiSeq962-AmNif (1:4)		☐	✓			
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

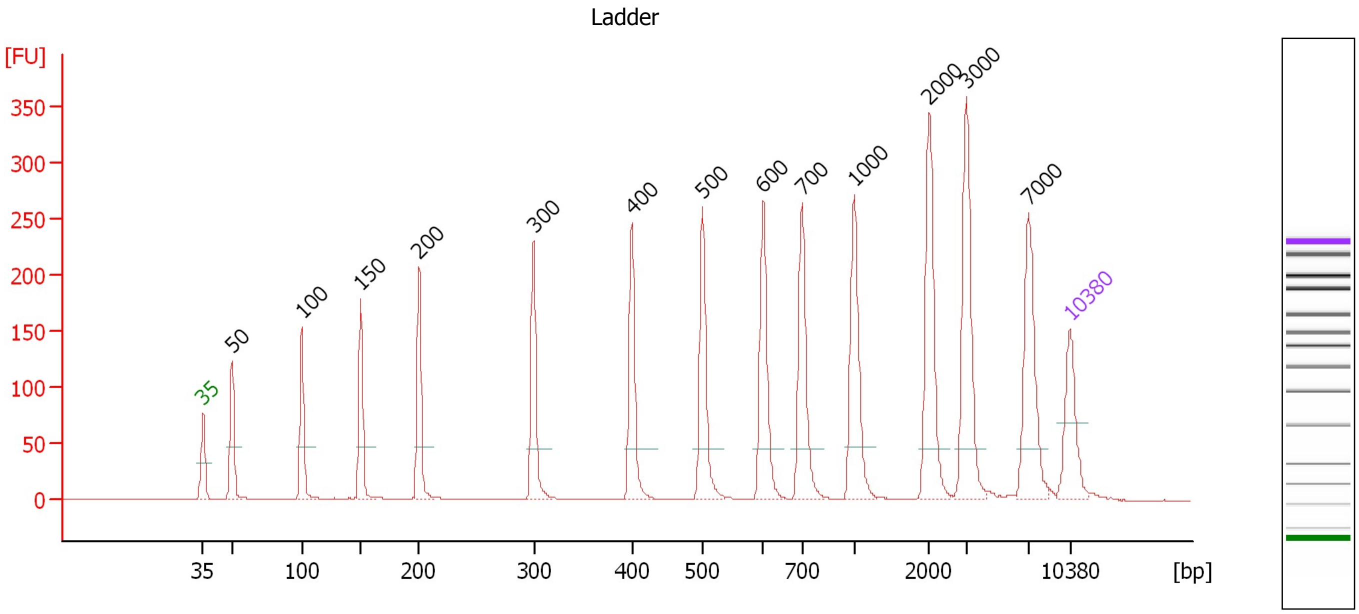
Ladder

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\2019-10-30\2019-10-30_001.xad

Created:	10/30/2019 10:44:27 AM
Modified:	10/30/2019 11:47:30 AM

Electropherogram Summary


Ladder

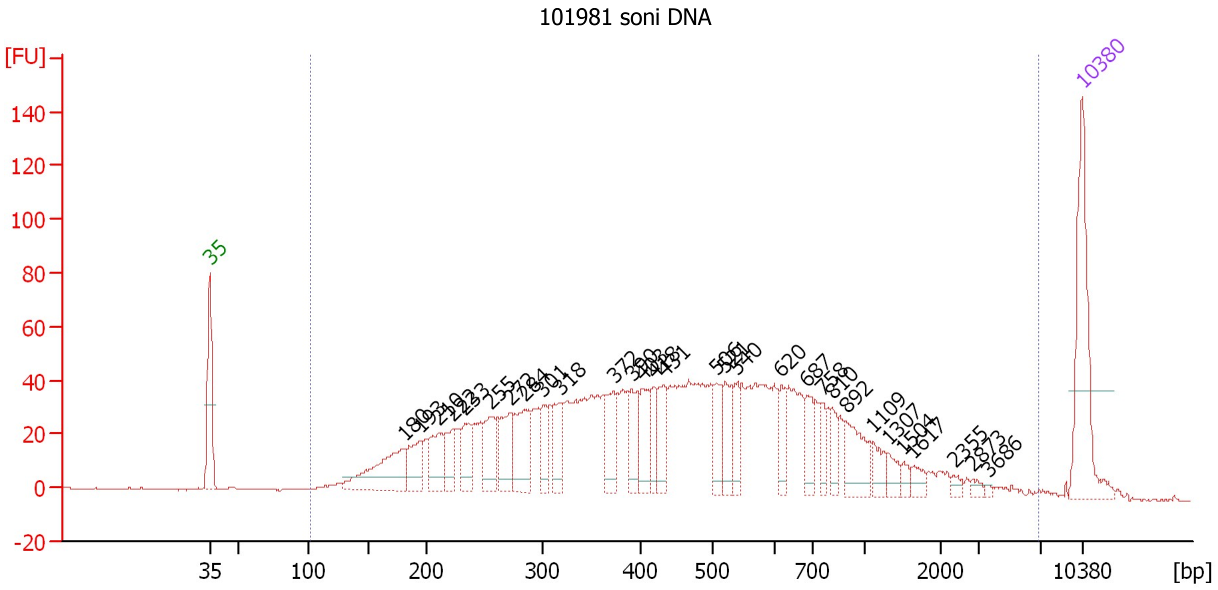
Overall Results for Ladder

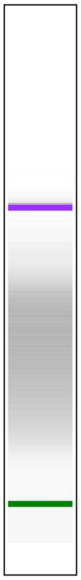
Noise: 0.3

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	45.32
3	L	100	150.00	2,272.7	Ladder Peak	50.96
4	L	150	150.00	1,515.2	Ladder Peak	55.74
5	L	200	150.00	1,136.4	Ladder Peak	60.42
6	L	300	150.00	757.6	Ladder Peak	69.67
7	L	400	150.00	568.2	Ladder Peak	77.59
8	L	500	150.00	454.5	Ladder Peak	83.31
9	L	600	150.00	378.8	Ladder Peak	88.22
10	L	700	150.00	324.7	Ladder Peak	91.36
11	L	1,000	150.00	227.3	Ladder Peak	95.58
12	L	2,000	150.00	113.6	Ladder Peak	101.64
13	L	3,000	150.00	75.8	Ladder Peak	104.61
14	L	7,000	150.00	32.5	Ladder Peak	109.64
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...





Overall Results for sample 1 : 101981 soni DNA

Number of peaks found:	30	Corr. Area 1:	1,933.4
Noise:	0.3		

Peak table for sample 1 : 101981 soni DNA

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	180	81.55	685.8		58.57
3	193	36.16	283.3		59.81
4	210	41.87	302.2		61.34
5	222	25.34	172.6		62.50
6	233	32.35	210.7		63.44
7	255	40.11	238.5		65.49
8	272	44.95	250.5		67.07
9	284	52.93	282.0		68.23
10	301	24.67	124.3		69.73
11	318	34.94	166.5		71.09
12	372	32.65	132.8		75.41
13	390	28.70	111.4		76.82
14	403	33.57	126.2		77.76
15	418	23.63	85.7		78.62
16	431	32.16	113.0		79.39
17	506	27.76	83.1		83.62
18	521	27.09	78.8		84.35
19	540	21.70	60.8		85.29
20	620	18.01	44.0		88.84
21	687	20.33	44.9		90.94
22	758	16.00	32.0		92.18
23	810	15.46	28.9		92.90
24	892	35.54	60.4		94.06
25	1,109	13.10	17.9		96.24

Electropherogram Summary Continued ...

... Peak table for sample 1 : 101981 soni DNA

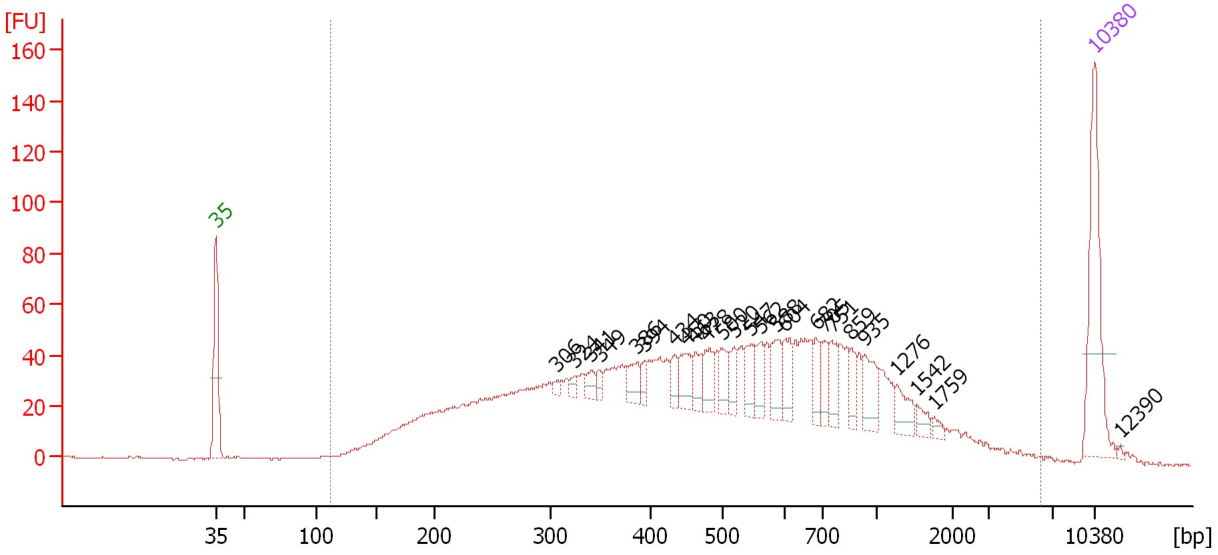
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		1,307	10.51	12.2		97.43
27		1,504	5.66	5.7		98.63
28		1,617	7.67	7.2		99.32
29		2,355	4.27	2.8		102.69
30		2,873	3.52	1.9		104.23
31		3,686	1.81	0.7		105.47
32	▶	10,380	75.00	10.9	Upper Marker	113.00

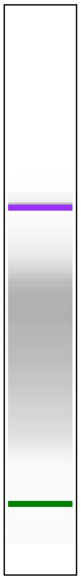
Region table for sample 1 : 101981 soni DNA

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
100	6,810	588	1,520.28	1,933.4	6,749.0	🟦	98	100.0

Electropherogram Summary Continued ...

109072 soni DNA





Overall Results for sample 2 : 109072 soni DNA

Number of peaks found:	25	Corr. Area 1:	2,052.0
Noise:	0.3		

Peak table for sample 2 : 109072 soni DNA

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		306	3.63	18.0		70.17
3		324	6.07	28.4		71.57
4		341	10.33	46.0		72.88
5		349	7.10	30.8		73.56
6		386	16.76	65.8		76.49
7		394	9.78	37.6		77.13
8		434	13.09	45.7		79.55
9		450	23.78	80.1		80.44
10		463	16.92	55.4		81.20
11		478	20.04	63.5		82.05
12		500	17.47	53.0		83.29
13		520	16.35	47.6		84.30
14		547	18.11	50.2		85.62
15		562	18.47	49.8		86.34
16		588	26.48	68.3		87.61
17		604	21.16	53.1		88.34
18		682	16.33	36.3		90.80
19		705	15.11	32.4		91.44
20		751	22.64	45.7		92.07
21		859	12.80	22.6		93.60
22		935	24.70	40.0		94.66
23		1,276	16.13	19.2		97.25
24		1,542	7.85	7.7		98.86
25		1,759	4.30	3.7		100.18

Electropherogram Summary Continued ...

... Peak table for sample 2 : 109072 soni DNA

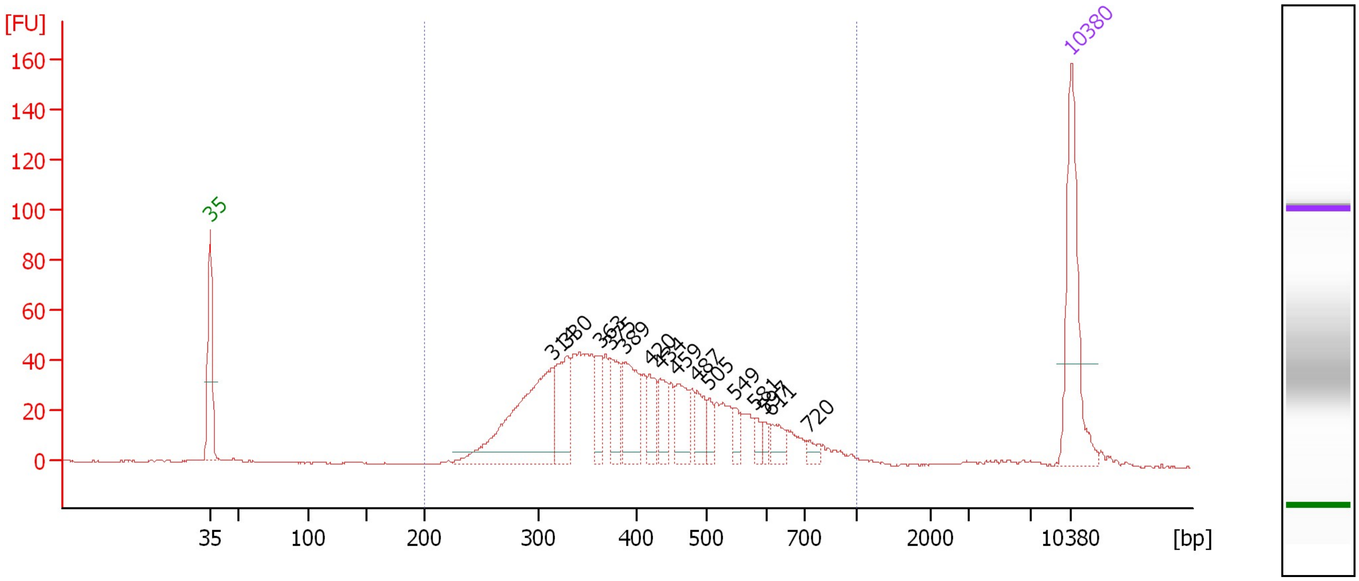
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	▶	10,380	75.00	10.9	Upper Marker	113.00
27		12,390	0.00	0.0		115.00

Region table for sample 2 : 109072 soni DNA

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
111	6,182	637	1,624.05	2,052.0	6,686.0	🟦	99	91.0

Electropherogram Summary Continued ...

lamend2 0.8 BC [2nd 0.8x BC]



Overall Results for sample 3 : lamend2 0.8 BC

Number of peaks found:	15	Corr. Area 1:	1,059.6
Noise:	0.2		

Peak table for sample 3 : lamend2 0.8 BC

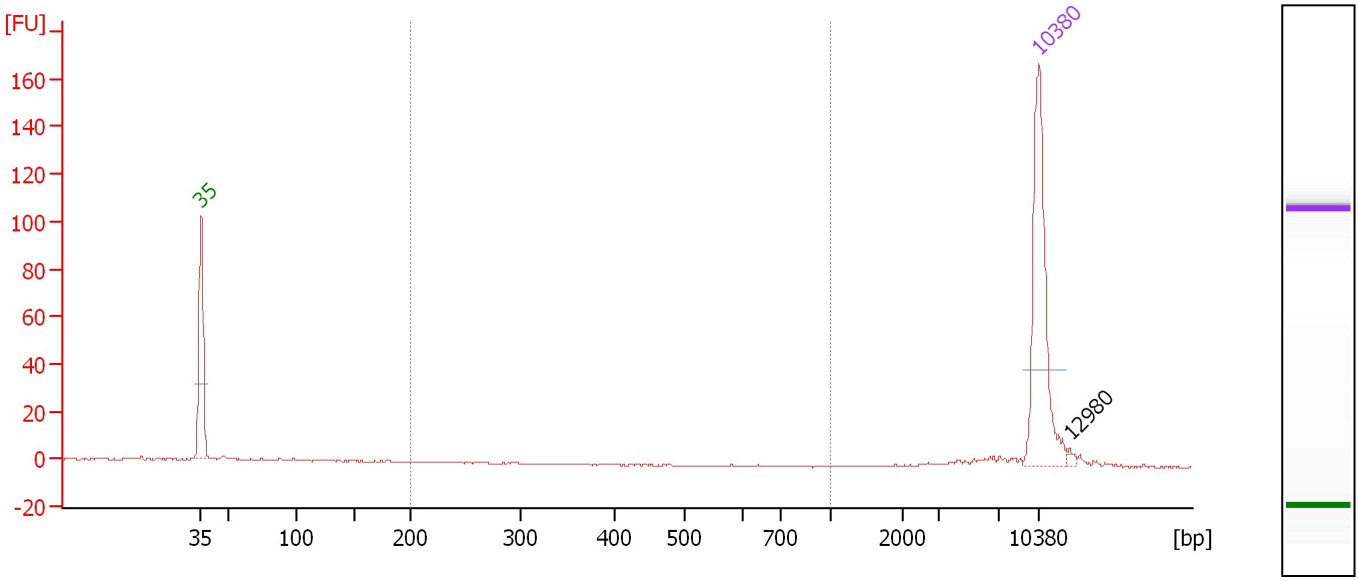
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		314	161.35	777.7		70.81
3		330	57.25	263.1		72.02
4		363	27.89	116.4		74.66
5		375	36.31	146.9		75.57
6		389	51.48	200.4		76.74
7		420	25.69	92.7		78.74
8		434	25.70	89.6		79.56
9		459	34.09	112.4		80.99
10		487	21.41	66.6		82.59
11		505	12.05	36.2		83.54
12		549	10.40	28.7		85.71
13		581	8.06	21.0		87.27
14		597	6.82	17.3		88.05
15		611	14.38	35.7		88.57
16		720	7.04	14.8		91.64
17	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : lamend2 0.8 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	424	744.92	1,059.6	2,963.8	🟦 96	30.2

Electropherogram Summary Continued ...

HiSeq-Coy4(1:10)



Overall Results for sample 4 : HiSeq-Coy4(1:10)

Number of peaks found:	1	Corr. Area 1:	0.0
Noise:	0.3		

Peak table for sample 4 : HiSeq-Coy4(1:10)

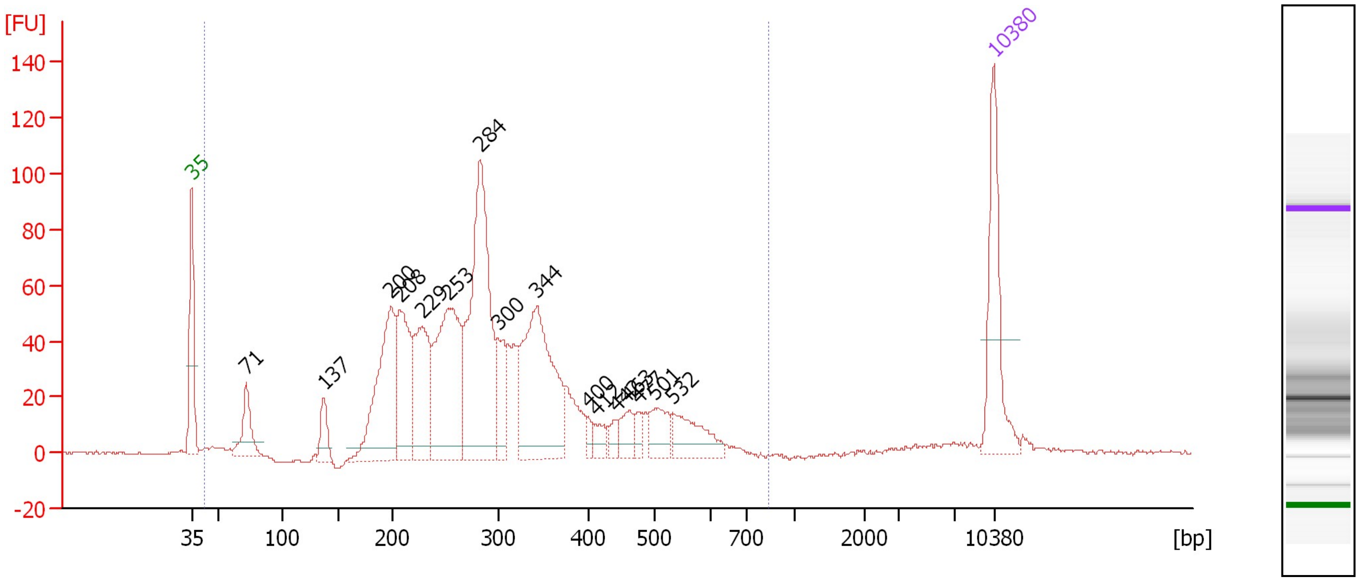
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00
3		12,980	0.00	0.0		115.58

Region table for sample 4 : HiSeq-Coy4(1:10)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	0	0.00	0.0	0.0	■	0	0.0

Electropherogram Summary Continued ...

HiSeq1983-FGGBS002 #2 (1:2)



Overall Results for sample 5 : HiSeq1983-FGGBS002 #2 (1:2)

Number of peaks found:	16	Corr. Area 1:	1,485.9
Noise:	0.4		

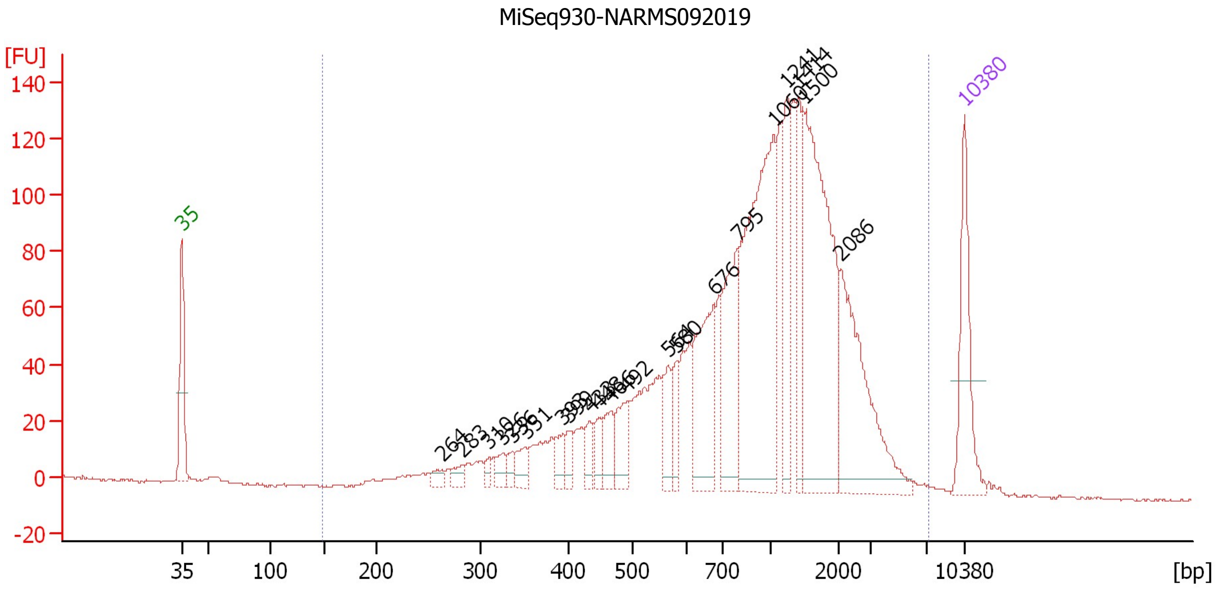
Peak table for sample 5 : HiSeq1983-FGGBS002 #2 (1:2)

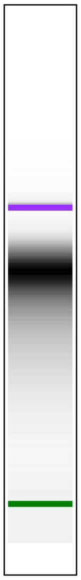
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		71	55.71	1,180.9		47.74
3		137	33.73	373.1		54.49
4		200	175.55	1,332.0		60.40
5		208	113.78	827.9		61.19
6		229	121.35	803.5		63.09
7		253	198.20	1,187.0		65.33
8		284	281.00	1,498.3		68.21
9		300	50.12	252.9		69.70
10		344	198.88	876.6		73.14
11		400	8.88	33.7		77.56
12		412	14.58	53.6		78.30
13		442	11.56	39.7		79.98
14		463	20.49	67.1		81.19
15		477	9.67	30.7		82.02
16		501	30.51	92.2		83.37
17		532	47.39	134.8		84.91
18	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : HiSeq1983-FGGBS002 #2 (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 [%]
42	839	302	1,370.95	1,485.9	8,621.1	■ 99	34.1

Electropherogram Summary Continued ...





Overall Results for sample 6 : **MiSeq930-NARMS092019**

Number of peaks found:	21	Corr. Area 1:	2,291.1
Noise:	0.5		

Peak table for sample 6 : **MiSeq930-NARMS092019**

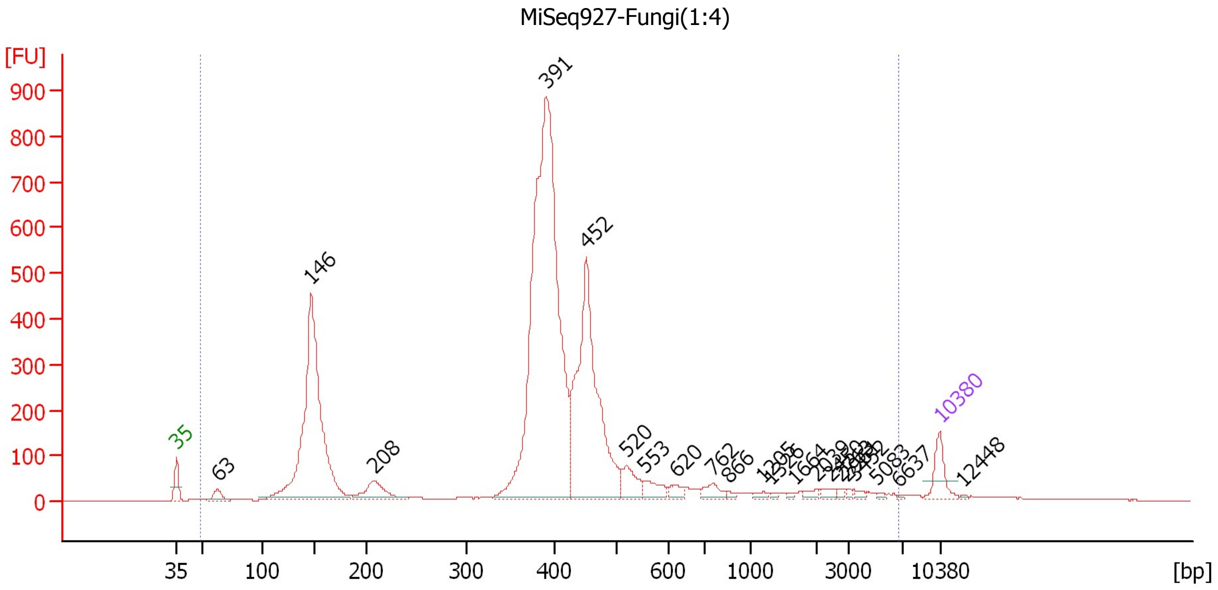
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		264	11.79	67.8		66.30
3		283	13.61	72.9		68.11
4		310	10.01	48.9		70.49
5		326	19.15	89.0		71.73
6		336	10.94	49.3		72.54
7		351	22.29	96.2		73.74
8		393	24.29	93.5		77.07
9		399	17.74	67.3		77.55
10		433	21.15	73.9		79.50
11		448	23.66	80.1		80.31
12		466	29.80	96.9		81.36
13		492	45.56	140.4		82.84
14		564	37.49	100.7		86.46
15		580	27.98	73.1		87.22
16		676	122.17	273.8		90.60
17		795	110.53	210.5		92.70
18		1,060	294.82	421.3		95.94
19		1,241	82.23	100.4		97.04
20		1,414	70.41	75.5		98.09
21		1,500	265.20	267.9		98.61
22		2,086	149.56	108.6		101.90
23	▶	10,380	75.00	10.9	Upper Marker	113.00

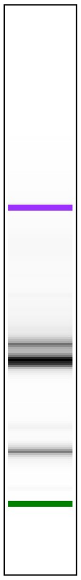
Electropherogram Summary Continued ...

... Region table for sample 6 : MiSeq930-NARMS092019

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
149	7,110	1,198	1,865.17	2,291.1	3,919.1	🟦	99	68.8

Electropherogram Summary Continued ...





Overall Results for sample 7 : MiSeq927-Fungi(1:4)

Number of peaks found:	21	Corr. Area 1:	7,228.2
Noise:	0.3		

Peak table for sample 7 : MiSeq927-Fungi(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		63	48.97	1,181.7		46.76
3		146	1,504.98	15,657.1		55.32
4		208	129.49	944.7		61.14
5		391	2,345.70	9,090.7		76.88
6		452	1,033.45	3,461.0		80.59
7		520	95.56	278.3		84.31
8		553	59.91	164.1		85.92
9		620	34.67	84.7		88.85
10		762	45.47	90.5		92.22
11		866	8.27	14.5		93.69
12		1,205	14.33	18.0		96.82
13		1,326	7.67	8.8		97.55
14		1,664	6.16	5.6		99.61
15		2,039	13.92	10.3		101.76
16		2,450	18.40	11.4		102.98
17		2,763	9.26	5.1		103.91
18		2,961	7.26	3.7		104.49
19		3,452	11.99	5.3		105.18
20		5,083	6.57	2.0		107.23
21		6,637	3.39	0.8		109.19
22	▶	10,380	75.00	10.9	Upper Marker	113.00
23		12,448	0.00	0.0		115.05

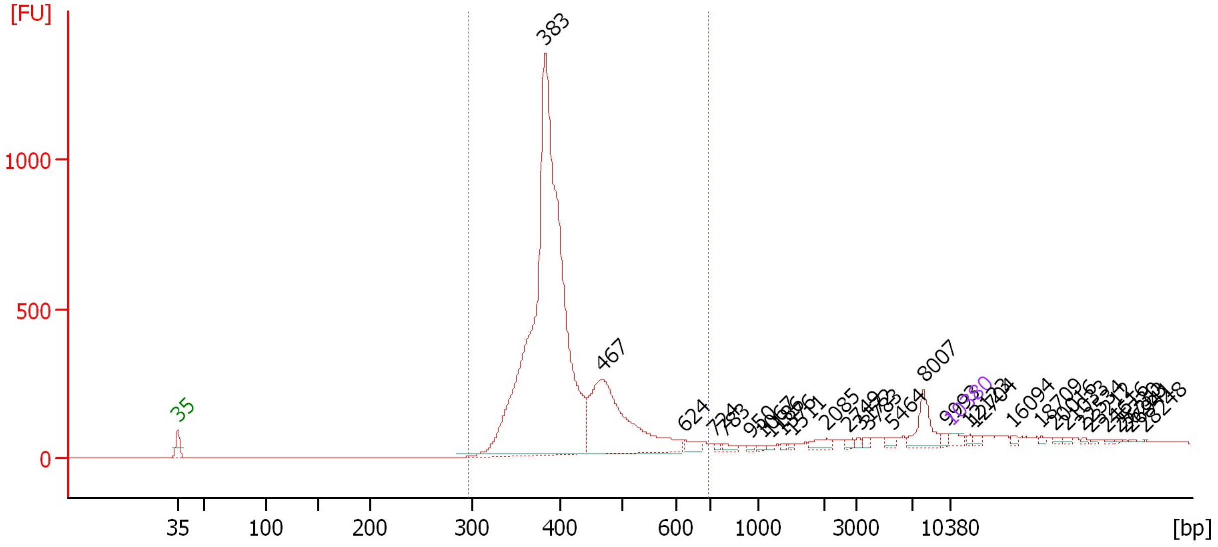
Electropherogram Summary Continued ...

... Region table for sample 7 : MiSeq927-Fungi(1:4)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
50	6,631	497	5,770.43	7,228.2	33,084.3	🟦	99	100.0

Electropherogram Summary Continued ...

MiSeq931-SYNERGIE Run 1 (1:3)



Overall Results for sample 8 : **MiSeq931-SYNERGIE Run 1 (1:3)**

Number of peaks found:	30	Corr. Area 1:	6,357.4
Noise:	0.3		

Peak table for sample 8 : **MiSeq931-SYNERGIE Run 1 (1:3)**

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		383	11,019.97	43,560.9		76.27
3		467	2,651.22	8,605.5		81.41
4		624	138.63	336.8		88.96
5		724	37.48	78.4		91.70
6		783	70.53	136.6		92.52
7		950	24.63	39.3		94.88
8		1,067	28.44	40.4		95.98
9		1,186	20.42	26.1		96.70
10		1,376	20.27	22.3		97.86
11		1,511	20.23	20.3		98.67
12		2,085	105.34	76.5		101.89
13		2,749	41.81	23.0		103.87
14		3,172	30.48	14.6		104.83
15		3,783	38.91	15.6		105.60
16		5,464	50.27	13.9		107.71
17		8,007	349.33	66.1		110.64
18		9,993	47.12	7.1		112.62
19	▶	10,380	75.00	10.9	Upper Marker	113.00
20		12,123	0.00	0.0		114.73
21		12,704	0.00	0.0		115.31
22		16,094	0.00	0.0		118.67
23		18,709	0.00	0.0		121.27
24		20,016	0.00	0.0		122.57
25		21,033	0.00	0.0		123.58

Electropherogram Summary Continued ...

... Peak table for sample 8 : **MiSeq931-SYNERGIE Run 1 (1:3)**

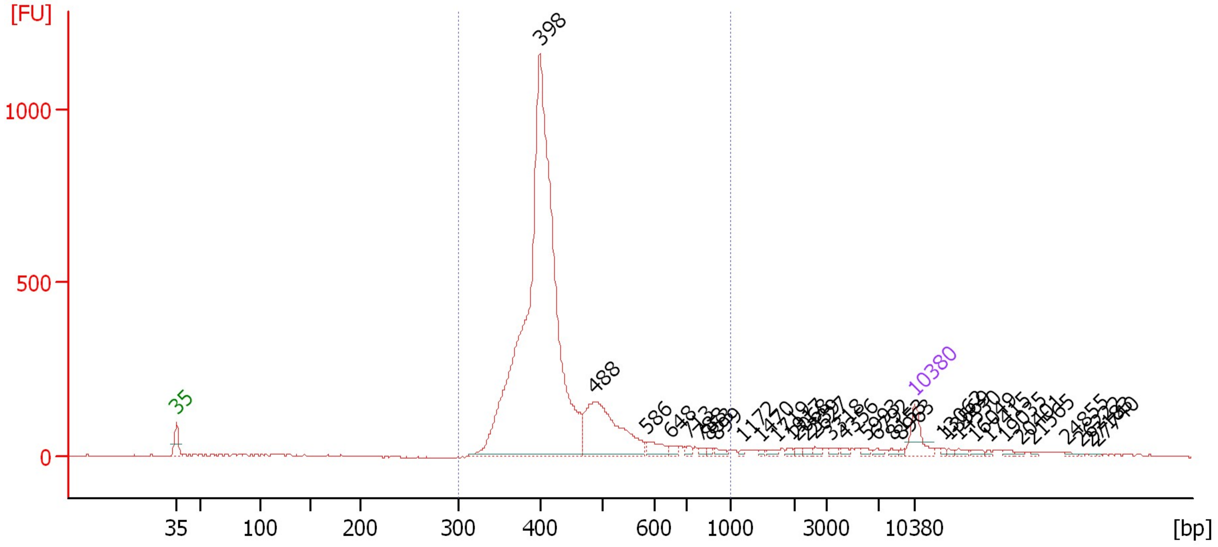
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	22,534	0.00	0.0		125.07
27	23,212	0.00	0.0		125.74
28	24,616	0.00	0.0		127.13
29	25,730	0.00	0.0		128.24
30	26,263	0.00	0.0		128.77
31	26,941	0.00	0.0		129.44
32	28,248	0.00	0.0		130.74

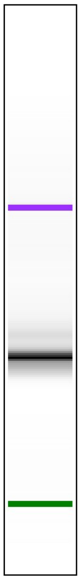
Region table for sample 8 : **MiSeq931-SYNERGIE Run 1 (1:3)**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
297	692	410	13,020.65	6,357.4	49,045.1	🟦	88	14.0

Electropherogram Summary Continued ...

MiSeq931-SYNERGIE Run 2 (1:3)





Overall Results for sample 9 : **MiSeq931-SYNERGIE Run 2 (1:3)**

Number of peaks found:	33	Corr. Area 1:	5,553.4
Noise:	1.8		

Peak table for sample 9 : **MiSeq931-SYNERGIE Run 2 (1:3)**

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		398	3,062.01	11,660.8		77.42
3		488	478.47	1,484.4		82.65
4		586	52.50	135.8		87.52
5		648	16.87	39.4		89.73
6		713	14.48	30.8		91.54
7		788	11.16	21.5		92.60
8		853	9.16	16.3		93.50
9		899	13.74	23.2		94.16
10		1,172	5.95	7.7		96.62
11		1,470	5.70	5.9		98.43
12		1,719	10.89	9.6		99.93
13		1,917	8.27	6.5		101.14
14		2,068	8.36	6.1		101.84
15		2,339	9.67	6.3		102.65
16		2,627	12.43	7.2		103.50
17		3,318	10.94	5.0		105.01
18		4,356	8.94	3.1		106.32
19		5,993	8.73	2.2		108.38
20		6,792	9.82	2.2		109.38
21		8,153	7.59	1.4		110.79
22		8,963	5.50	0.9		111.59
23	▶	10,380	75.00	10.9	Upper Marker	113.00
24		13,062	0.00	0.0		115.66
25		13,569	0.00	0.0		116.17

Electropherogram Summary Continued ...

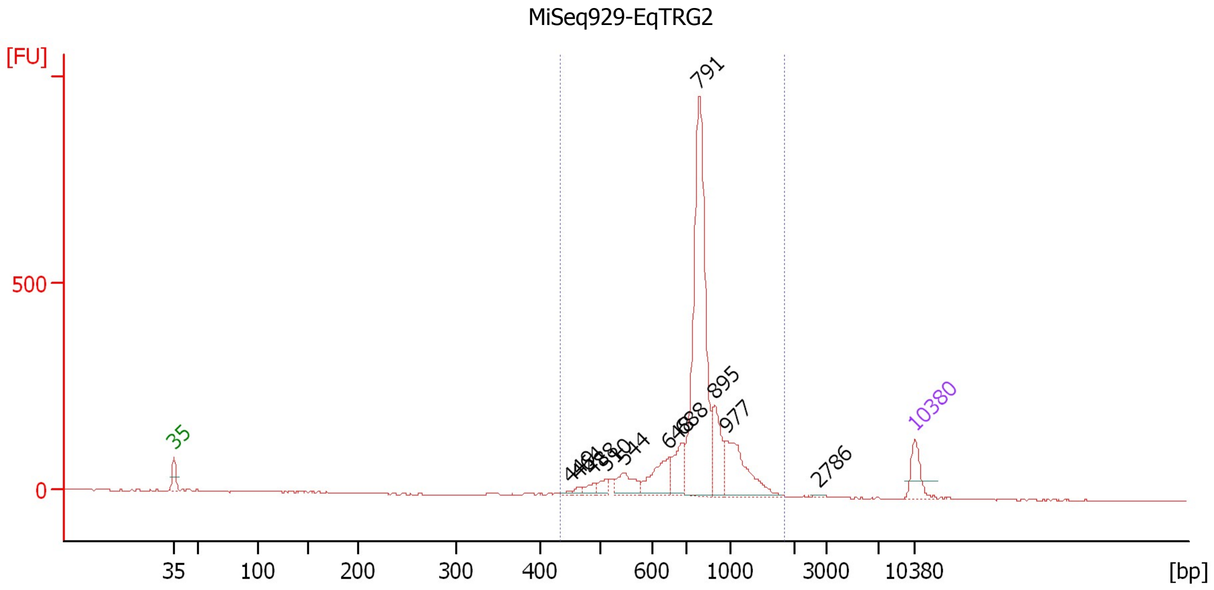
... Peak table for sample 9 : MiSeq931-SYNERGIE Run 2 (1:3)

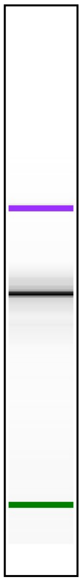
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	14,530	0.00	0.0		117.12
27	16,049	0.00	0.0		118.63
28	17,415	0.00	0.0		119.98
29	19,035	0.00	0.0		121.59
30	20,401	0.00	0.0		122.95
31	21,565	0.00	0.0		124.11
32	24,855	0.00	0.0		127.37
33	26,222	0.00	0.0		128.73
34	27,183	0.00	0.0		129.68
35	27,740	0.00	0.0		130.24

Region table for sample 9 : MiSeq931-SYNERGIE Run 2 (1:3)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
301	999	430	3,726.16	5,553.4	13,569.7	🟦	90	19.7

Electropherogram Summary Continued ...





Overall Results for sample 10 : **MiSeq929-EqTRG2**

Number of peaks found:	11	Corr. Area 1:	2,557.5
Noise:	1.3		

Peak table for sample 10 : **MiSeq929-EqTRG2**

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		449	7.07	23.9		80.41
3		464	13.32	43.5		81.26
4		488	31.27	97.1		82.61
5		510	37.76	112.1		83.82
6		544	100.41	279.7		85.47
7		648	153.48	358.7		89.73
8		688	123.79	272.5		90.99
9		791	998.21	1,911.4		92.64
10		895	158.03	267.6		94.10
11		977	242.49	376.1		95.25
12		2,786	4.08	2.2		103.97
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : **MiSeq929-EqTRG2**

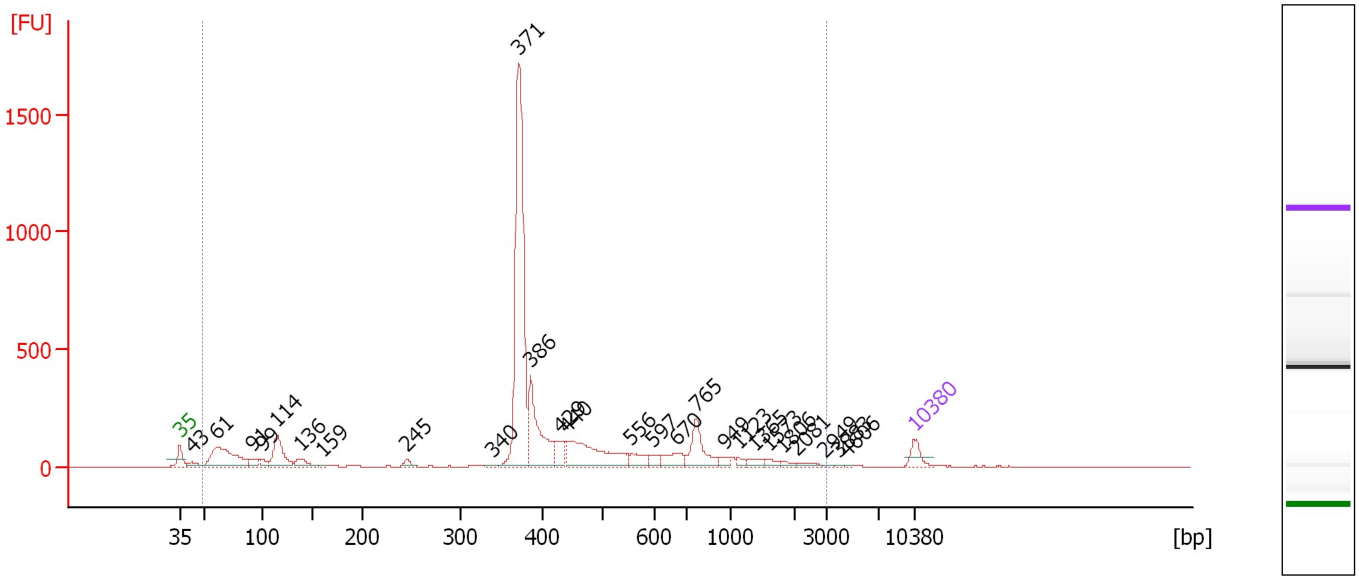
From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
433	1,832	811	1,858.92	2,557.4	3,684.5	🟦 99	23.6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2019-10-30\2019-10-30_001.xad

Created: 10/30/2019 10:44:27 AM
Modified: 10/30/2019 11:47:30 AM

Electropherogram Summary Continued ...

MiSeq962-AmNif (1:4)



Overall Results for sample 11 : **MiSeq962-AmNif (1:4)**

Number of peaks found:	26	Corr. Area 1:	5,560.0
Noise:	0.6		

Peak table for sample 11 : **MiSeq962-AmNif (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		43	79.53	2,835.1		44.16
3		61	643.47	16,042.0		46.54
4		91	83.04	1,378.6		49.97
5		99	59.92	914.0		50.88
6		114	372.87	4,954.4		52.30
7		136	105.21	1,169.9		54.42
8		159	8.18	78.1		56.55
9		245	37.06	228.8		64.63
10		340	8.05	35.9		72.82
11		371	1,989.99	8,126.9		75.30
12		386	555.50	2,182.2		76.46
13		429	123.16	435.2		79.24
14		440	521.29	1,794.0		79.90
15		556	101.58	276.8		86.06
16		597	46.87	118.9		88.08
17		670	120.34	272.3		90.41
18		765	252.30	499.5		92.28
19		949	33.71	53.8		94.86
20		1,123	28.77	38.8		96.32
21		1,365	35.64	39.6		97.79
22		1,573	29.48	28.4		99.05
23		1,806	20.15	16.9		100.47
24		2,081	22.03	16.0		101.88
25		2,949	6.32	3.2		104.46

Electropherogram Summary Continued ...

... Peak table for sample 11 : MiSeq962-AmNif (1:4)

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		3,883	3.78	1.5		105.72
27		4,606	2.51	0.8		106.63
28	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : MiSeq962-AmNif (1:4)

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
50	3,035	478	5,612.21	5,560.0	39,478.4	🟦	97	75.4

Gel Image

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		10/30/2019 11:25:45 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\2019-10-30\2019-10-30_001.xad)		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938C		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE34903152		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/30/2019 10:44:32 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1