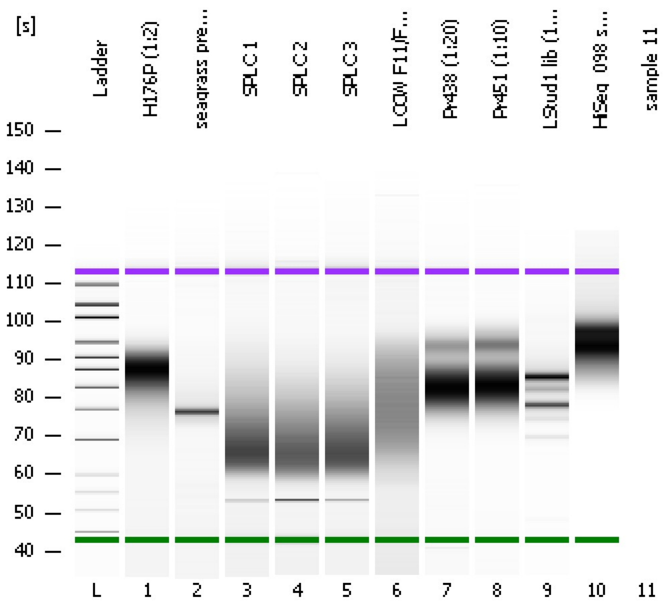
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad

Created: 8/24/2015 4:02:11 PM
Modified: 8/24/2015 4:40:37 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

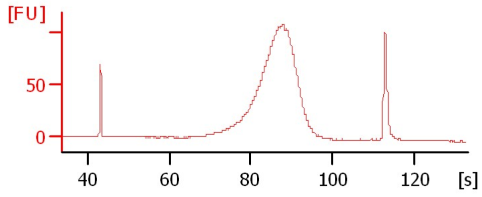
Chip Information:

Chip Lot #:

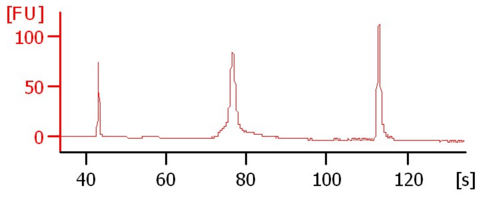
Reagent Kit Lot #:

Chip Comments:

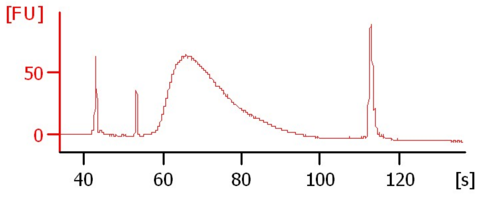
H176P (1:2)



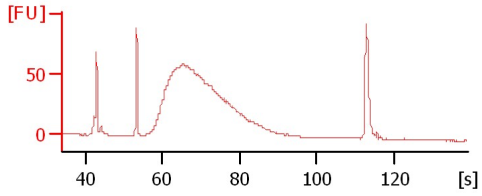
seagrass preservation pool



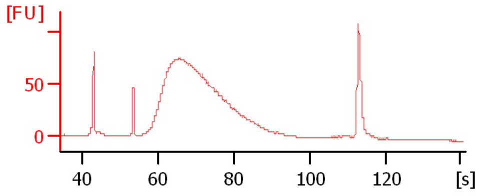
SPLC 1



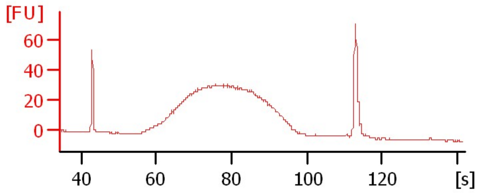
SPLC 2



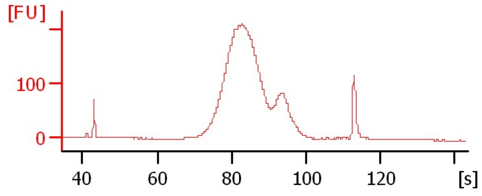
SPLC 3



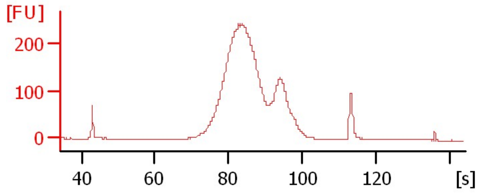
LCCW F11/F13 (1:6)



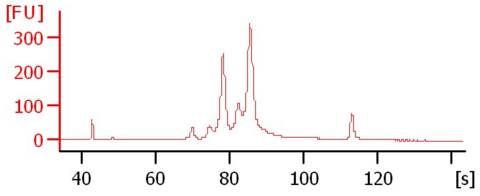
Pr438 (1:20)



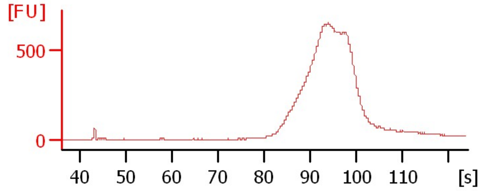
Pr451 (1:10)



LStud1 lib (1:2)



HiSeq_098 strand displaced DNA



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad
Created: 8/24/2015 4:02:11 PM
Modified: 8/24/2015 4:40:37 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
H176P (1:2)		☐	✓			
seagrass preservation pool		☐	✓			
SPLC 1		☐	✓			
SPLC 2		☐	✓			
SPLC 3		☐	✓			
LCCW F11/F13 (1:6)		☐	✓			
Pr438 (1:20)		☐	✓			
Pr451 (1:10)		☐	✓			
LStud1 lib (1:2)		☐	✓			
HiSeq_098 strand displaced DNA		☐	✓			
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

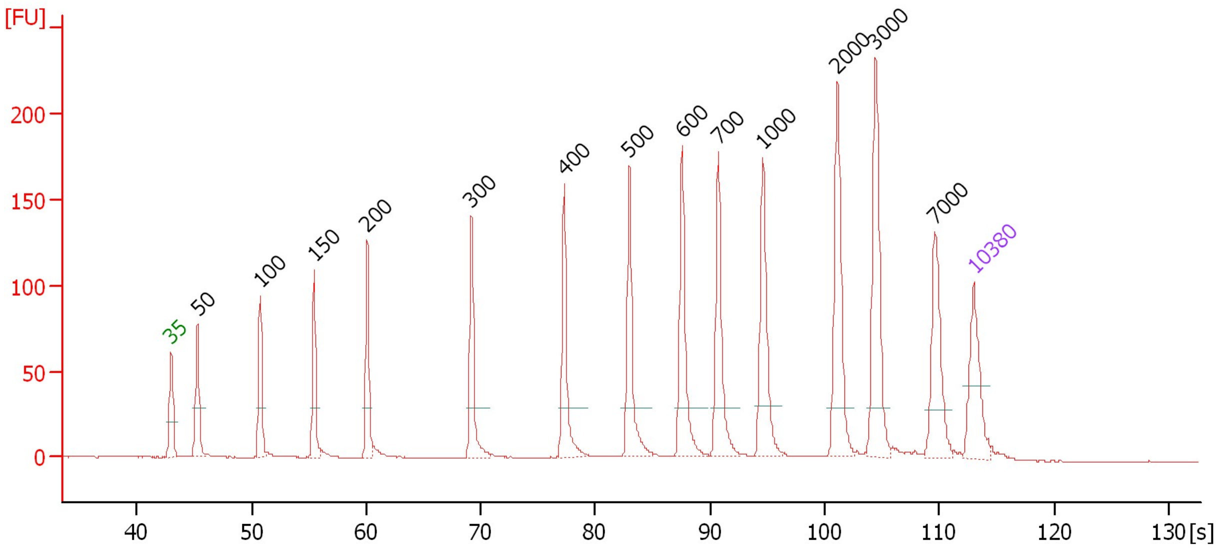
Ladder

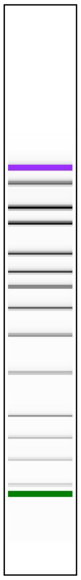
Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

Assay Class:	High Sensitivity DNA Assay	Created:	8/24/2015 4:02:11 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad	Modified:	8/24/2015 4:40:37 PM

Electropherogram Summary

Ladder





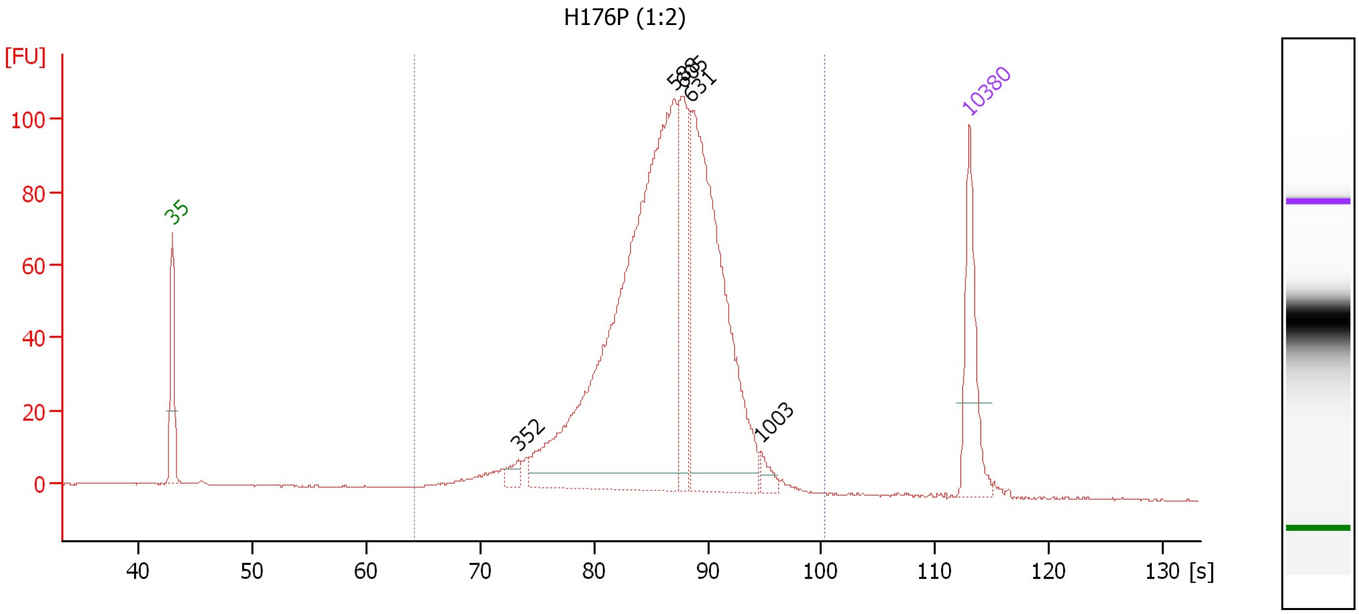
Overall Results for Ladder

Noise: 0.1

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	45.29
3	L	100	150.00	2,272.7	Ladder Peak	50.77
4	L	150	150.00	1,515.2	Ladder Peak	55.45
5	L	200	150.00	1,136.4	Ladder Peak	60.09
6	L	300	150.00	757.6	Ladder Peak	69.17
7	L	400	150.00	568.2	Ladder Peak	77.27
8	L	500	150.00	454.5	Ladder Peak	82.94
9	L	600	150.00	378.8	Ladder Peak	87.58
10	L	700	150.00	324.7	Ladder Peak	90.71
11	L	1,000	150.00	227.3	Ladder Peak	94.60
12	L	2,000	150.00	113.6	Ladder Peak	101.11
13	L	3,000	150.00	75.8	Ladder Peak	104.43
14	L	7,000	150.00	32.5	Ladder Peak	109.58
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...



Overall Results for sample 1 : H176P (1:2)

Number of peaks found:	5	Corr. Area 1:	1,406.3
Noise:	0.1		

Peak table for sample 1 : H176P (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		352	15.19	65.4		73.36
3		588	754.78	1,944.3		87.03
4		605	120.09	300.7		87.73
5		631	411.51	988.7		88.54
6		1,003	12.39	18.7		94.62
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 1 : H176P (1:2)

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
64.25	592	100.20	1,406.3	4,125.7	■ 97	25.4	1,488.68

Assay Class:	High Sensitivity DNA Assay	Created:	8/24/2015 4:02:11 PM
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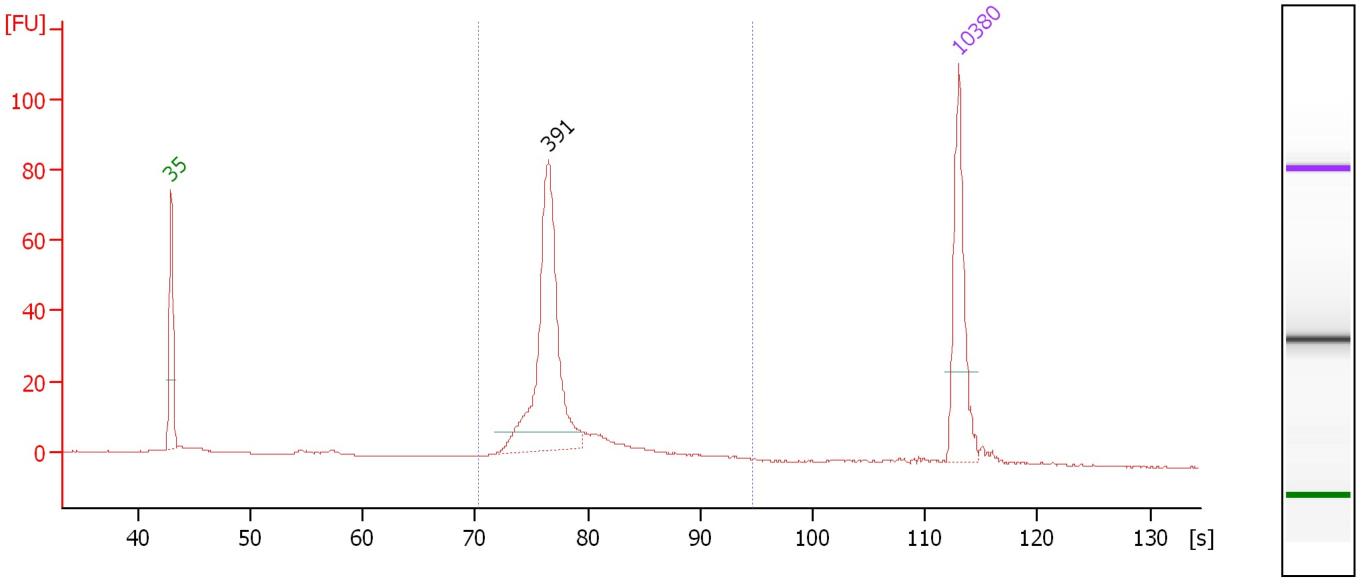
Electropherogram Summary Continued ...

seagrass preservation pool



Overall Results for sample 2 : seagrass preservation pool

Number of peaks found:	1	Corr. Area 1:	294.6
Noise:	0.2		

Peak table for sample 2 : seagrass preservation pool

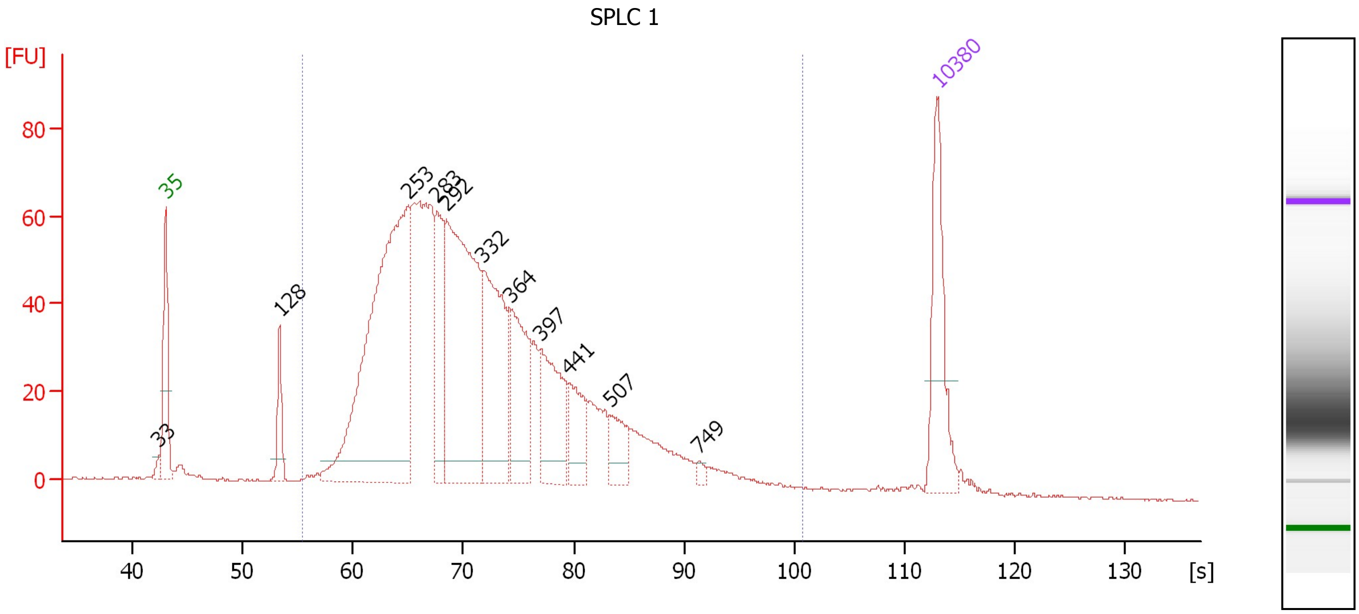
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		391	219.67	851.2		76.54
3	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 2 : seagrass preservation pool

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
70.36	419	94.60	294.6	1,085.6	🟦 89	19.1	291.25

Electropherogram Summary Continued ...

SPLC 1



Overall Results for sample 3 : **SPLC 1**

Number of peaks found:	11	Corr. Area 1:	1,630.5
Noise:	0.3		

Peak table for sample 3 : **SPLC 1**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.42
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		128	45.30	537.7		53.36
4		253	513.28	3,069.3		64.94
5		283	94.37	505.5		67.61
6		292	339.29	1,757.7		68.49
7		332	179.22	816.9		71.80
8		364	106.51	443.8		74.33
9		397	95.41	364.5		77.00
10		441	49.70	170.9		79.58
11		507	33.99	101.5		83.28
12		749	4.70	9.5		91.35
13	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : **SPLC 1**

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
55.49	352	100.77	1,630.5	9,748.6	🟦 96	46.3	1,928.59

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad
Created: 8/24/2015 4:02:11 PM
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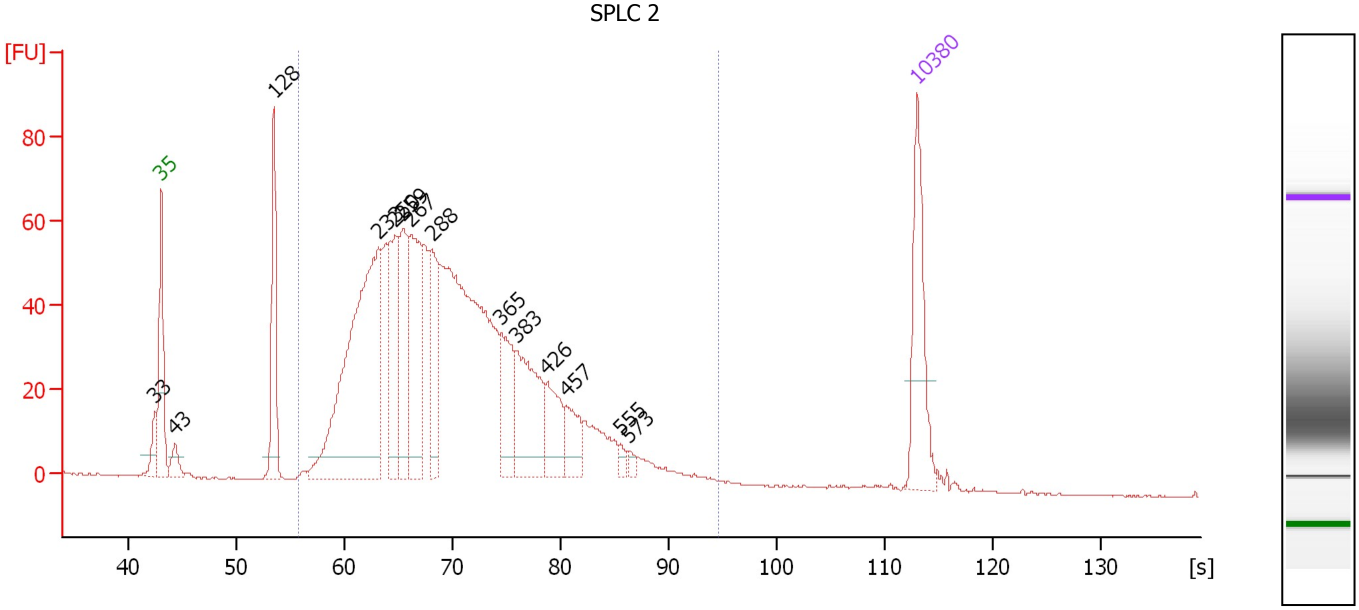
Electropherogram Summary Continued ...

SPLC 2



Overall Results for sample 4 : SPLC 2

Number of peaks found:	14	Corr. Area 1:	1,506.8
Noise:	0.2		

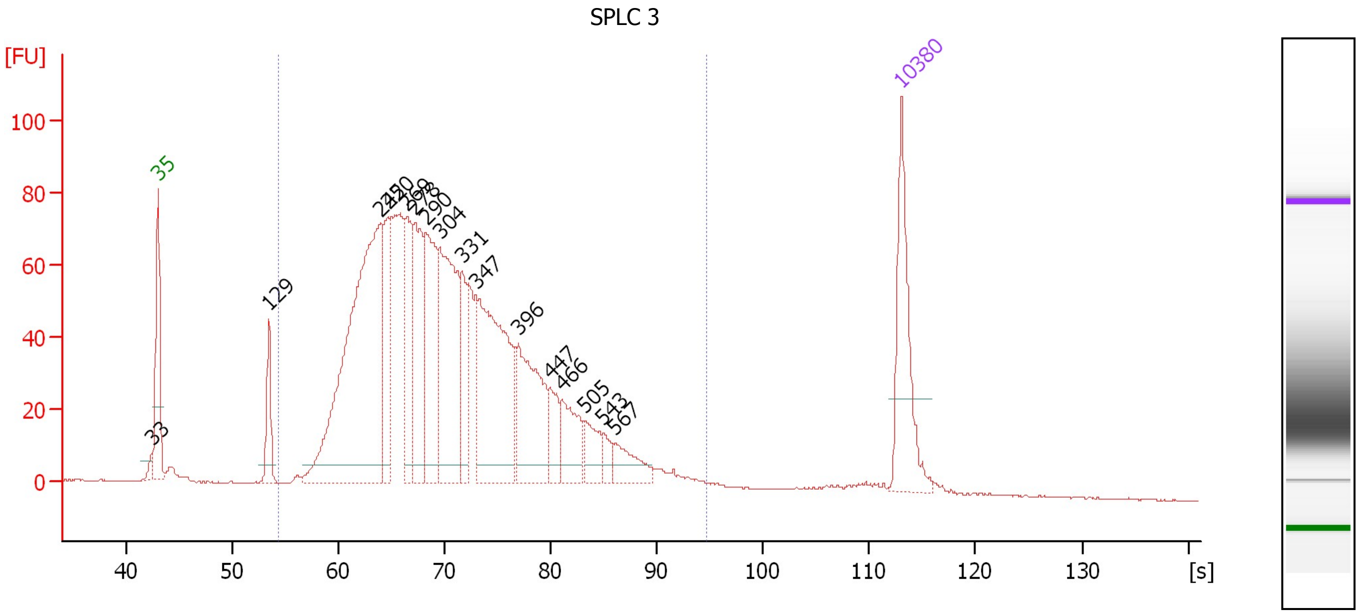
Peak table for sample 4 : SPLC 2

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.40
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		43	25.31	882.6		44.29
4		128	120.55	1,422.4		53.43
5		233	412.64	2,685.4		63.07
6		250	112.69	683.6		64.61
7		259	112.89	661.6		65.41
8		267	141.50	803.8		66.15
9		288	85.48	449.6		68.09
10		365	71.55	296.9		74.45
11		383	107.38	424.9		75.89
12		426	50.17	178.6		78.72
13		457	36.70	121.7		80.51
14		555	6.46	17.6		85.48
15		573	4.44	11.7		86.32
16	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : SPLC 2

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
55.77	324	94.60	1,506.8	9,919.0	■	92	33.6	1,876.04

Electropherogram Summary Continued ...



Overall Results for sample 5 : SPLC 3

Number of peaks found:	16	Corr. Area 1:	1,939.1
Noise:	0.2		

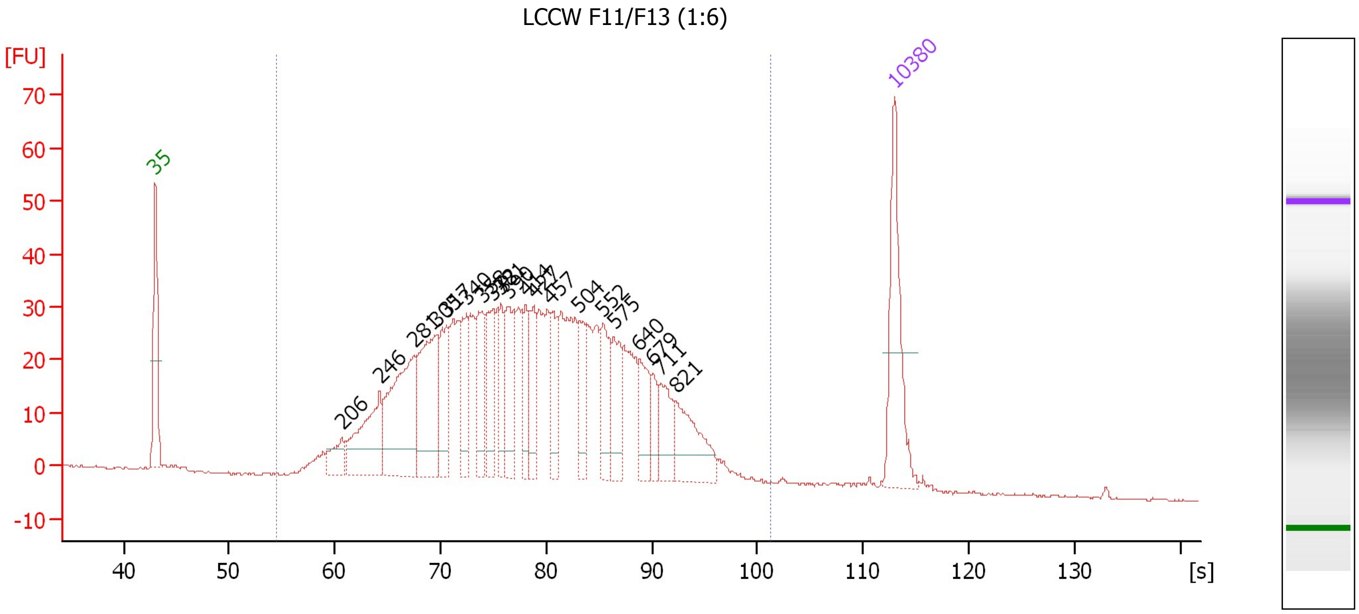
Peak table for sample 5 : SPLC 3

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		129	49.79	586.1		53.46
4		242	453.67	2,844.5		63.87
5		250	104.79	635.1		64.63
6		269	87.94	495.5		66.35
7		278	110.92	603.7		67.21
8		290	129.12	675.8		68.22
9		304	186.24	926.8		69.53
10		331	55.21	253.0		71.66
11		347	220.07	961.2		72.97
12		396	115.15	441.1		76.91
13		447	31.25	105.9		79.95
14		466	47.58	154.8		81.01
15		505	28.28	84.8		83.18
16		543	12.03	33.5		84.95
17		567	28.38	75.8		86.06
18	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : SPLC 3

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
54.31	332	94.60	1,939.1	9,938.1	🟦	95	34.1	1,915.02

Electropherogram Summary Continued ...



Overall Results for sample 6 : LCCW F11/F13 (1:6)

Number of peaks found:	20	Corr. Area 1:	1,124.0
Noise:	0.2		

Peak table for sample 6 : LCCW F11/F13 (1:6)

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		206	27.92	205.5		60.63
3		246	95.82	591.1		64.23
4		281	150.21	808.8		67.48
5		305	123.27	611.4		69.62
6		317	57.89	276.9		70.53
7		340	49.57	220.9		72.41
8		358	58.64	248.1		73.89
9		372	51.25	208.8		75.00
10		381	41.46	165.0		75.71
11		390	56.20	218.6		76.43
12		414	39.28	143.9		78.05
13		427	41.78	148.2		78.81
14		457	36.89	122.4		80.49
15		504	41.82	125.7		83.13
16		552	47.90	131.4		85.37
17		575	41.28	108.7		86.43
18		640	36.17	85.7		88.82
19		679	19.49	43.5		90.04
20		711	37.70	80.4		90.85
21		821	57.46	106.1		92.27
22	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Region table for sample 6 : **LCCW F11/F13 (1:6)**

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
54.42	470	101.33	1,124.0	6,642.1	🟦	98	46.3	1,654.69

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad

Created: 8/24/2015 4:02:11 PM
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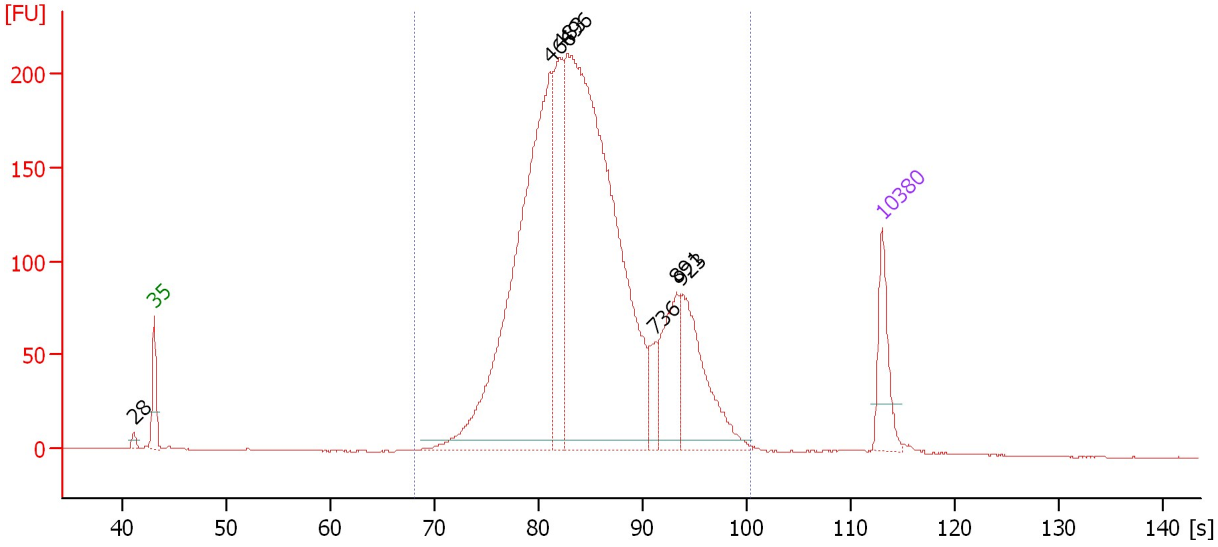
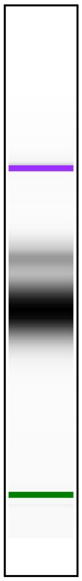
Electropherogram Summary Continued ...

Pr438 (1:20)





Overall Results for sample 7 : Pr438 (1:20)

Number of peaks found:	7	Corr. Area 1:	3,248.7
Noise:	0.1		

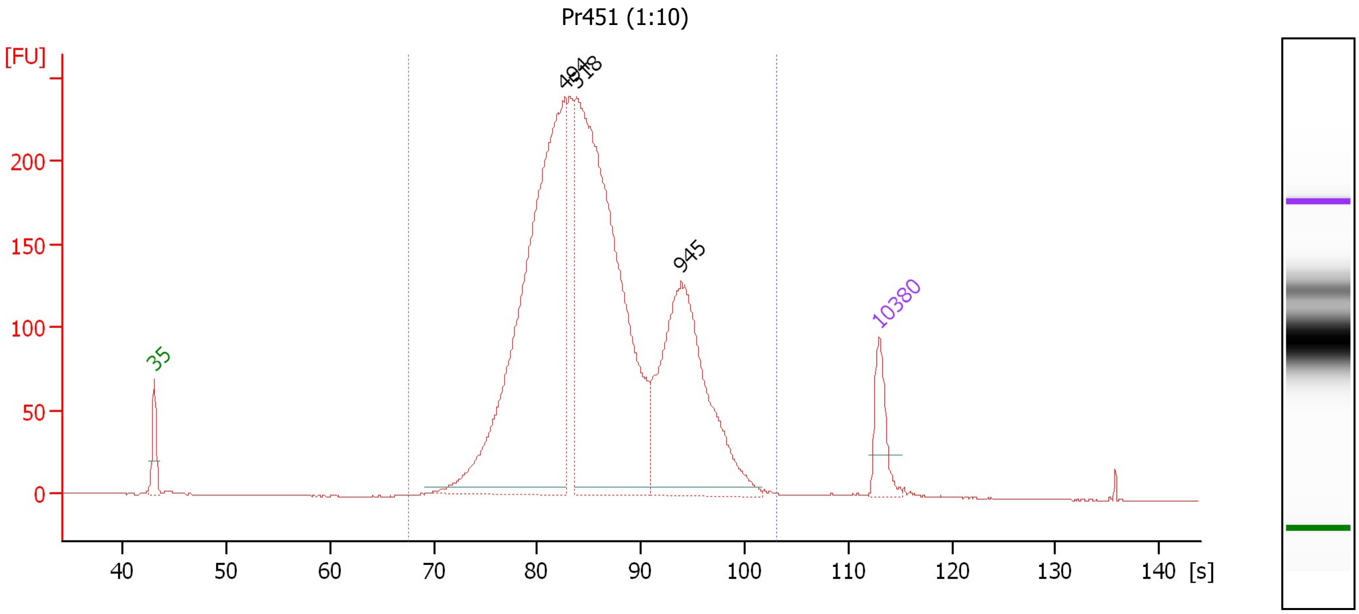
Peak table for sample 7 : Pr438 (1:20)

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		28	0.00	0.0		41.04
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		466	940.49	3,057.4		81.02
4		483	240.88	755.0		82.00
5		496	1,290.78	3,942.0		82.72
6		736	47.22	97.2		91.18
7		891	132.01	224.4		93.19
8		923	199.88	328.0		93.60
9	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : Pr438 (1:20)

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
68.00	587	100.32	3,248.7	8,307.8	■	98	38.4	2,853.16

Electropherogram Summary Continued ...



Overall Results for sample 8 : **Pr451 (1:10)**

Number of peaks found:	3	Corr. Area 1:	3,762.9
Noise:	0.2		

Peak table for sample 8 : **Pr451 (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		494	1,374.46	4,217.8		82.59
3		518	1,338.72	3,915.3		83.78
4		945	616.91	989.5		93.88
5	▶	10,380	75.00	10.9	Upper Marker	113.00

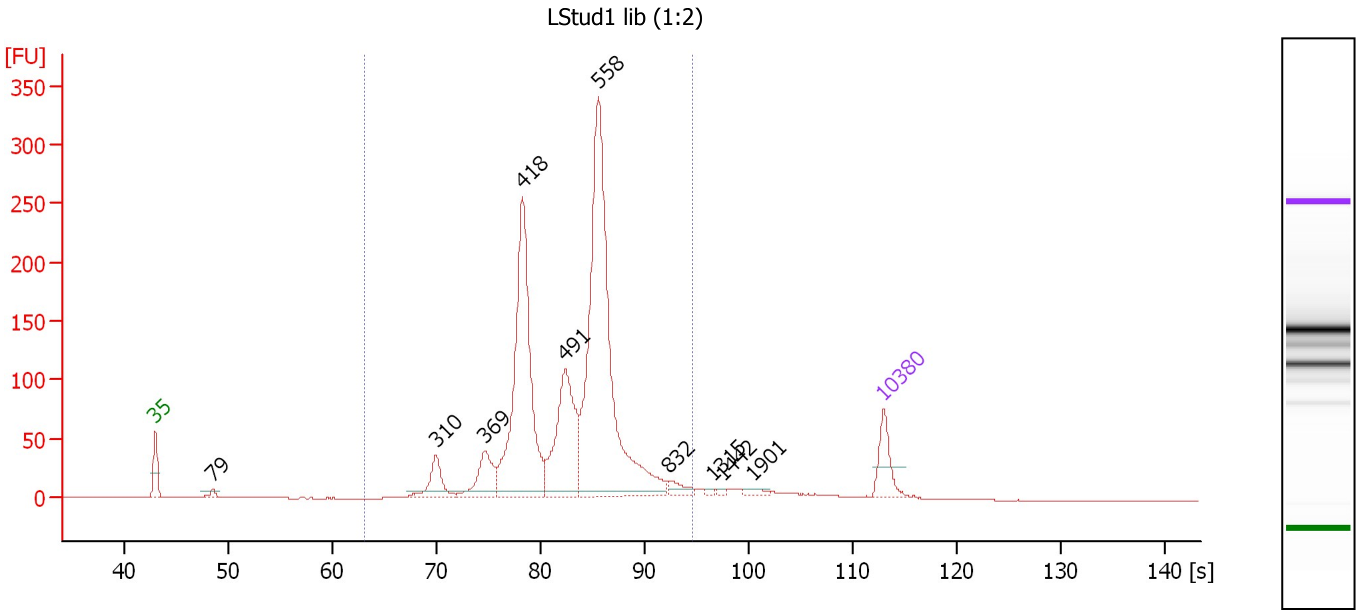
Region table for sample 8 : **Pr451 (1:10)**

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]	Conc. [pg/µl]
67.51	635	103.00	3,762.9	9,822.3	🟦 99	44.6	3,524.53

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-08-24\2015-08-24_001.xad

Created: 8/24/2015 4:02:11 PM
Modified: 8/24/2015 4:40:37 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : **LStud1 lib (1:2)**

Number of peaks found:	10	Corr. Area 1:	2,030.7
Noise:	0.2		

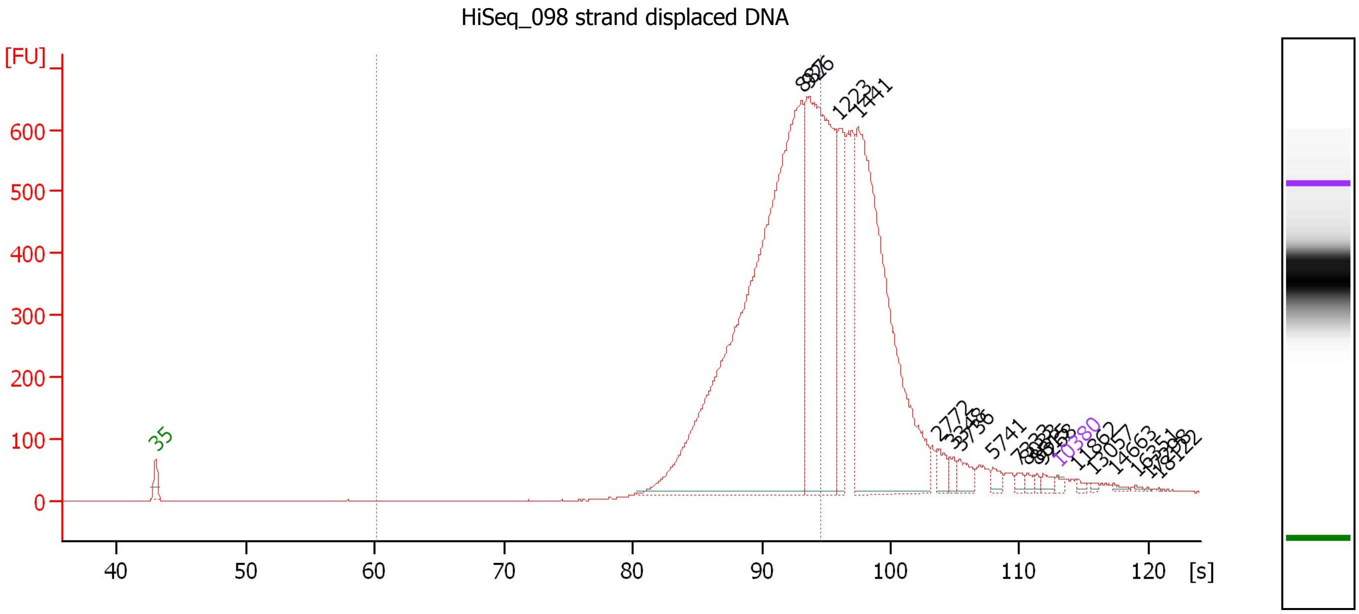
Peak table for sample 9 : **LStud1 lib (1:2)**

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		79	21.11	402.6		48.52
3		310	103.12	504.1		69.98
4		369	129.55	532.6		74.72
5		418	774.64	2,809.1		78.28
6		491	377.87	1,166.9		82.41
7		558	1,155.26	3,139.3		85.61
8		832	32.07	58.4		92.42
9		1,315	5.71	6.6		96.65
10		1,442	5.66	6.0		97.47
11		1,901	14.00	11.2		100.47
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : **LStud1 lib (1:2)**

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
63.08	507	94.60	2,030.7	8,457.3	🟦	94	20.6	2,674.02

Electropherogram Summary Continued ...



Overall Results for sample 10 : HiSeq_098 strand displaced DNA

Number of peaks found: 18 Corr. Area 1: 4,949.6

Noise: 0.8

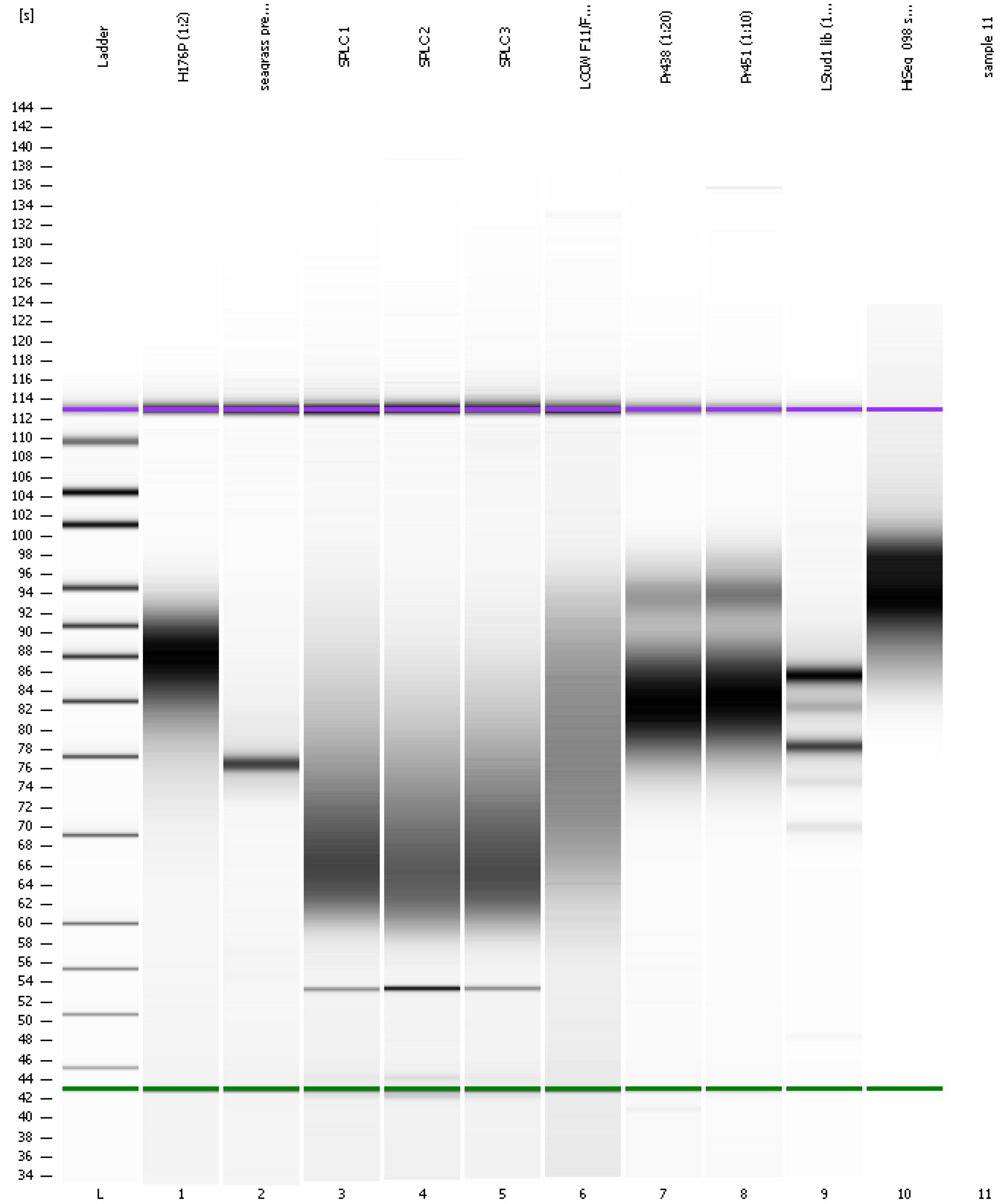
Peak table for sample 10 : HiSeq_098 strand displaced DNA

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		887	19,860.89	33,920.0		93.14
3		926	9,552.75	15,635.1		93.64
4		1,223	1,887.47	2,337.8		96.05
5		1,441	9,307.98	9,788.3		97.47
6		2,772	289.23	158.1		103.67
7		3,348	183.15	82.9		104.88
8		3,736	300.88	122.0		105.38
9		5,741	161.71	42.7		107.96
10		7,333	107.19	22.1		109.92
11		8,033	87.23	16.5		110.63
12		8,815	64.77	11.1		111.42
13		9,268	119.31	19.5		111.88
14	▶	10,380	75.00	10.9	Upper Marker	113.00
15		11,862	0.00	0.0		114.50
16		13,057	0.00	0.0		115.71
17		14,663	0.00	0.0		117.33
18		16,351	0.00	0.0		119.04
19		17,298	0.00	0.0		120.00
20		18,122	0.00	0.0		120.83

Region table for sample 10 : HiSeq_098 strand displaced DNA

From [s]	Average Size [bp]	To [s]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
60.09	751	94.60	4,949.6	55,928.4	■	53	18.6	26,586.83

Gel Image


[s]
Ladder
H176P (1:2)
seagrass pre...
SPLC1
SPLC2
SPLC3
LCCW F11/F...
Px438 (1:20)
Px451 (1:10)
LSud1 lib (1...
HiSeq 098 s...
sample 11
144
142
140
138
136
134
132
130
128
126
124
122
120
118
116
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112
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108
106
104
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