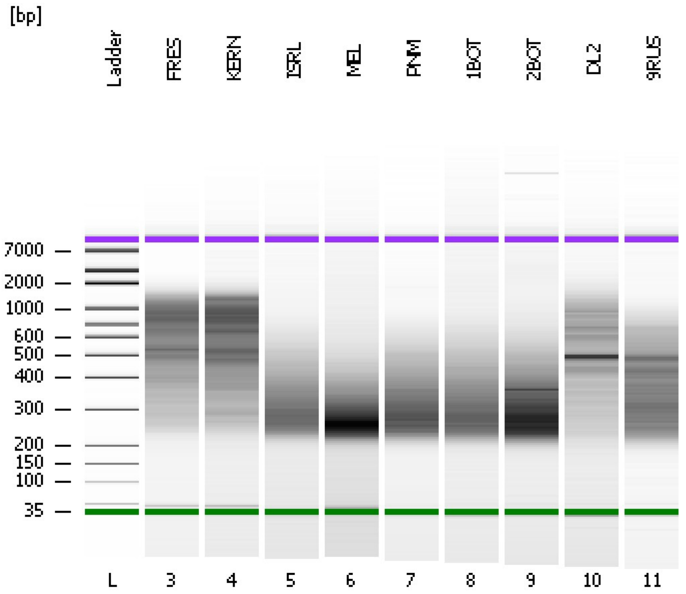
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...016-06-21\2016-06-21_004_HiSeq_517_Libraries_17-24_9rpt.xad
Created: 6/21/2016 2:29:33 PM
Modified: 6/21/2016 3:36:44 PM

Electrophoresis File Run Summary



Instrument Information:

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

Assay Information:

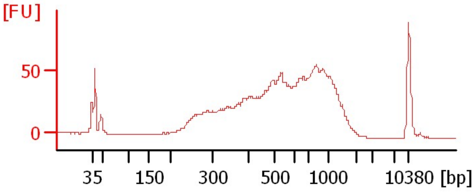
Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy
Assay Class: High Sensitivity DNA Assay
Version: 1.03
Assay Comments: Copyright © 2003-2010 Agilent Technologies

Chip Information:

Chip Lot #:
Reagent Kit Lot #:
Chip Comments:

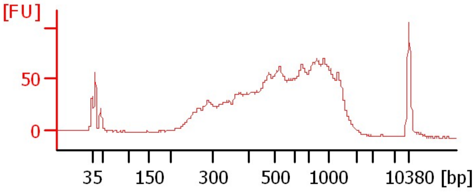
FRES

HiSeq_517 Library



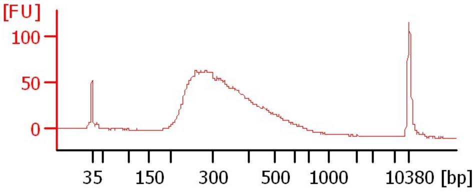
KERN

HiSeq_517 Library



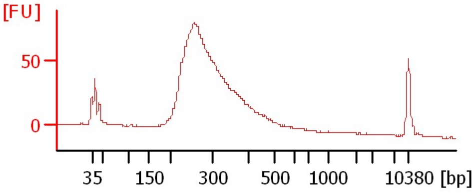
ISRL

HiSeq_517 Library



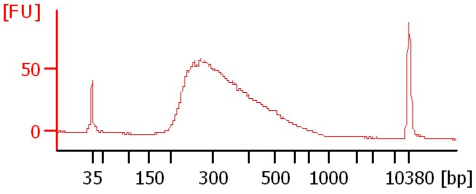
MEL

HiSeq_517 Library



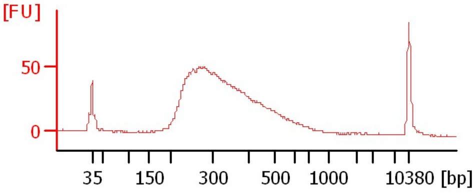
PNM

HiSeq_517 Library



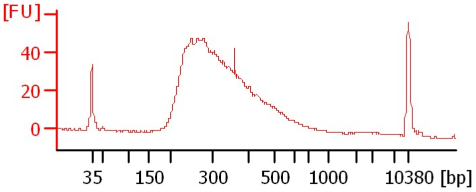
1BOT

HiSeq_517 Library



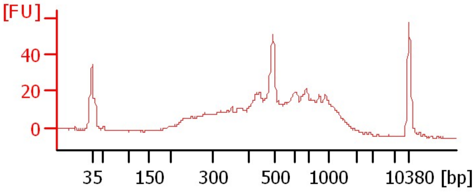
2BOT

HiSeq_517 Library



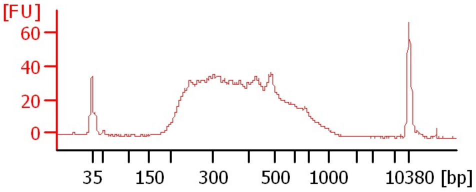
DL2

HiSeq_517 Library



9RUS

HiSeq_517 Library



Assay Class:	High Sensitivity DNA Assay	Created:	6/21/2016 2:29:33 PM
Data Path:	C:\...016-06-21\2016-06-21_004_HiSeq_517_Libraries_17-24_9rpt.xad	Modified:	6/21/2016 3:36:44 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
FRES	HiSeq_517 Library	☐	✓			
KERN	HiSeq_517 Library	☐	✓			
ISRL	HiSeq_517 Library	☐	✓			
MEL	HiSeq_517 Library	☐	✓			
PNM	HiSeq_517 Library	☐	✓			
1BOT	HiSeq_517 Library	☐	✓			
2BOT	HiSeq_517 Library	☐	✓			
DL2	HiSeq_517 Library	☐	✓			
9RUS	HiSeq_517 Library	☐	✓			
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

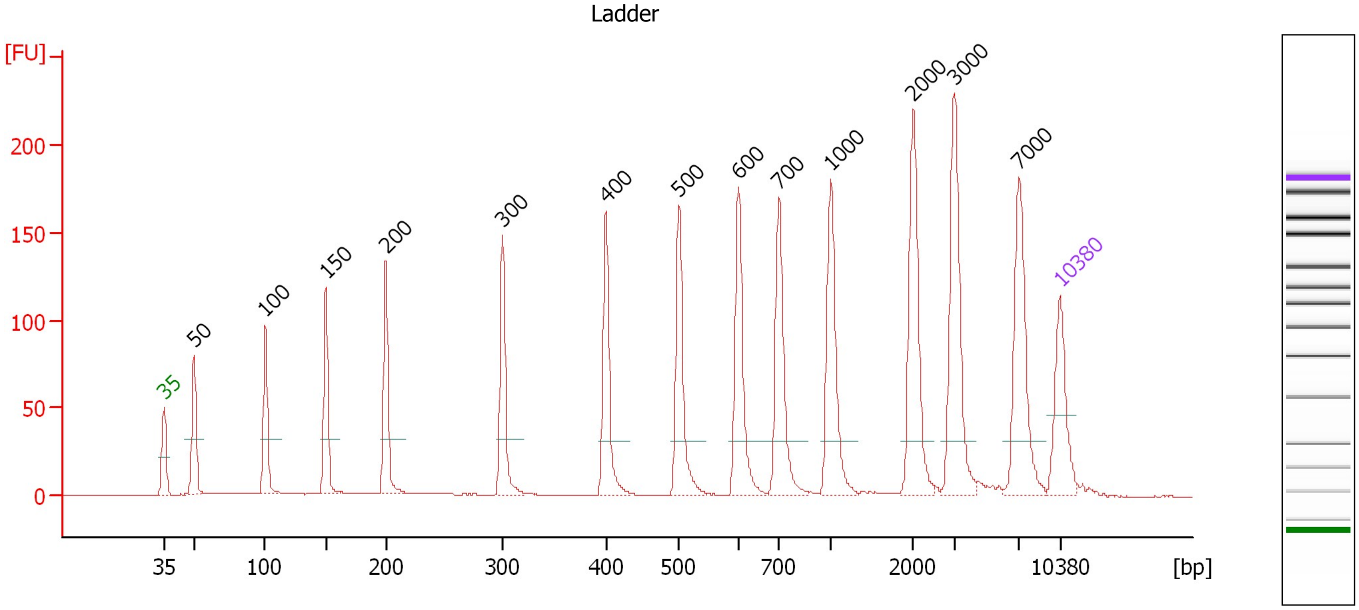
Filter Width [s] : 0.5
Polynomial Order : 4

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:\...016-06-21\2016-06-21_004_HiSeq_517_Libraries_17-24_9rpt.xad
Created: 6/21/2016 2:29:33 PM
Modified: 6/21/2016 3:36:44 PM

Electropherogram Summary



Overall Results for Ladder

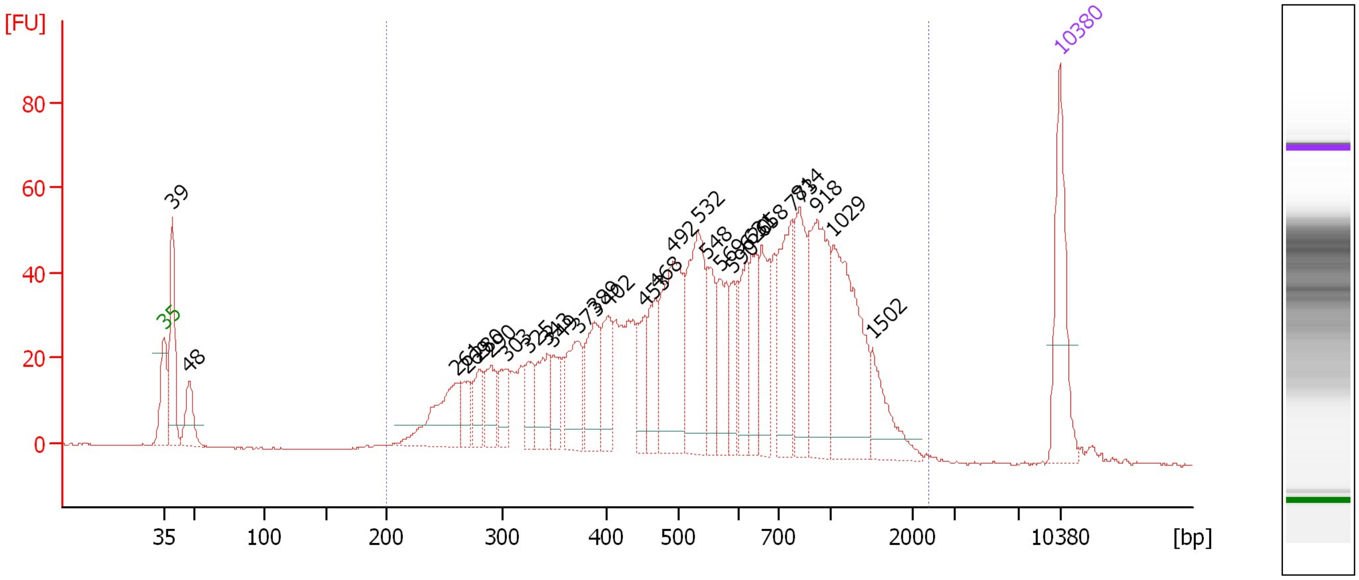
Noise: 0.2

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	L	50	150.00	4,545.5	Ladder Peak	45.32
3	L	100	150.00	2,272.7	Ladder Peak	50.90
4	L	150	150.00	1,515.2	Ladder Peak	55.64
5	L	200	150.00	1,136.4	Ladder Peak	60.34
6	L	300	150.00	757.6	Ladder Peak	69.45
7	L	400	150.00	568.2	Ladder Peak	77.54
8	L	500	150.00	454.5	Ladder Peak	83.25
9	L	600	150.00	378.8	Ladder Peak	87.90
10	L	700	150.00	324.7	Ladder Peak	91.06
11	L	1,000	150.00	227.3	Ladder Peak	95.10
12	L	2,000	150.00	113.6	Ladder Peak	101.57
13	L	3,000	150.00	75.8	Ladder Peak	104.77
14	L	7,000	150.00	32.5	Ladder Peak	109.84
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

FRES [HiSeq_517 Library]



Overall Results for sample 3 : **FRES**

Number of peaks found:	28	Corr. Area 1:	1,513.1
Noise:	0.2		

Peak table for sample 3 : **FRES**

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		39	120.57	4,661.5		43.65
3		48	52.40	1,669.2		44.95
4		261	88.14	511.5		65.90
5		269	28.76	161.9		66.64
6		280	34.83	188.5		67.62
7		290	42.41	221.9		68.50
8		303	35.41	177.0		69.70
9		325	33.10	154.4		71.46
10		343	48.80	215.4		72.95
11		349	33.88	147.1		73.41
12		373	66.64	270.6		75.36
13		389	65.51	255.5		76.61
14		402	52.37	197.1		77.68
15		453	36.45	122.0		80.55
16		468	53.31	172.5		81.43
17		492	132.94	409.7		82.77
18		532	122.32	348.6		84.72
19		548	53.74	148.7		85.46
20		569	57.53	153.3		86.44
21		590	34.63	88.9		87.46
22		620	39.67	97.0		88.52
23		631	51.65	123.9		88.89
24		658	61.48	141.6		89.73
25		773	90.55	177.5		92.05

Electropherogram Summary Continued ...

... Peak table for sample 3 : FRES

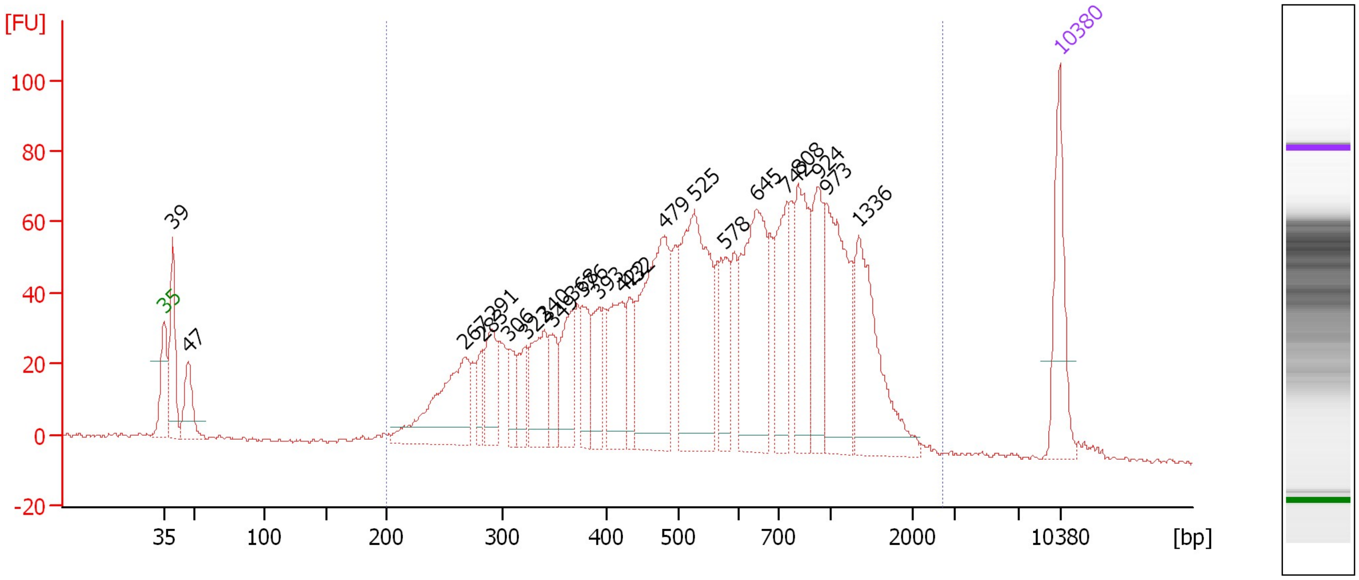
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		814	78.20	145.5		92.60
27		918	119.45	197.2		93.99
28		1,029	142.39	209.7		95.29
29		1,502	45.01	45.4		98.35
30	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : FRES

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,353	650	1,513.1	6,165.6	🟦	1,935.17	94	51.8

Electropherogram Summary Continued ...

KERN [HiSeq_517 Library]



Overall Results for sample 4 : **KERN**

Number of peaks found:	23	Corr. Area 1:	2,067.9
Noise:	0.5		

Peak table for sample 4 : **KERN**

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		39	113.94	4,398.0		43.66
3		47	67.21	2,159.5		44.88
4		267	169.07	959.4		66.44
5		283	31.94	171.3		67.86
6		291	69.48	362.0		68.61
7		306	34.35	170.1		69.93
8		322	42.70	200.8		71.24
9		340	87.12	387.9		72.70
10		349	40.94	177.7		73.41
11		368	69.42	286.1		74.92
12		376	51.57	207.6		75.62
13		393	52.10	200.7		76.99
14		422	87.85	315.6		78.78
15		432	42.04	147.6		79.34
16		479	217.90	688.7		82.07
17		525	228.02	657.8		84.43
18		578	71.78	188.2		86.87
19		645	183.01	429.9		89.32
20		742	95.33	194.7		91.63
21		808	111.49	209.0		92.52
22		924	78.90	129.4		94.08
23		973	150.49	234.5		94.74
24		1,336	132.16	149.9		97.28
25	▶	10,380	75.00	10.9	Upper Marker	113.00

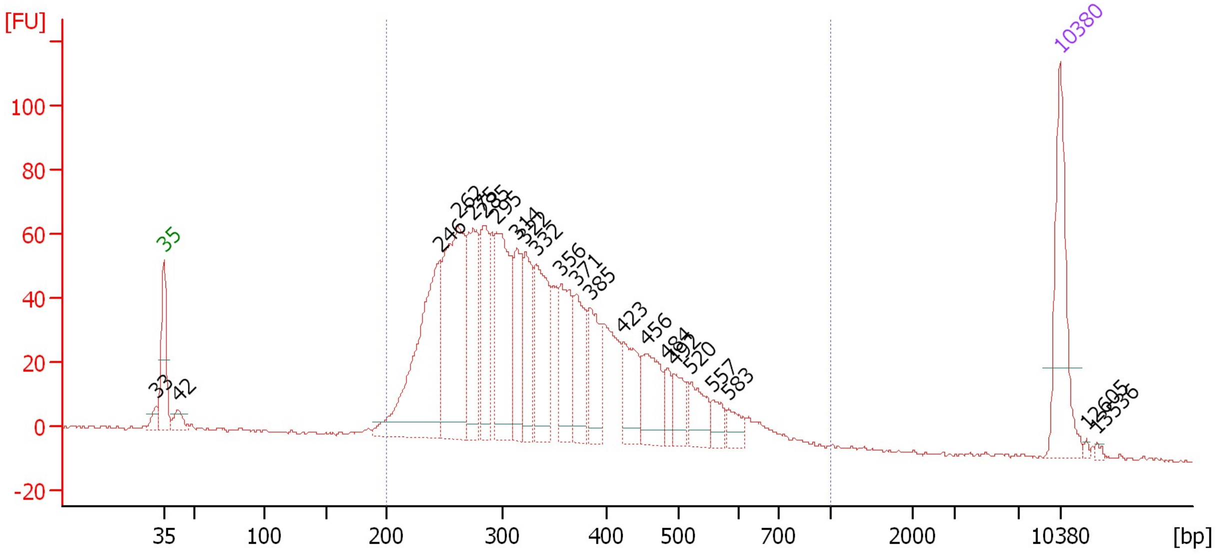
Electropherogram Summary Continued ...

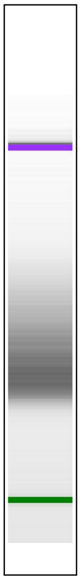
... Region table for sample 4 : KERN

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,714	660	2,067.9	7,540.1	🟦	2,361.18	94	54.1

Electropherogram Summary Continued ...

ISRL [HiSeq_517 Library]





Overall Results for sample 5 : ISRL

Number of peaks found:	22	Corr. Area 1:	1,521.9
Noise:	0.6		

Peak table for sample 5 : ISRL

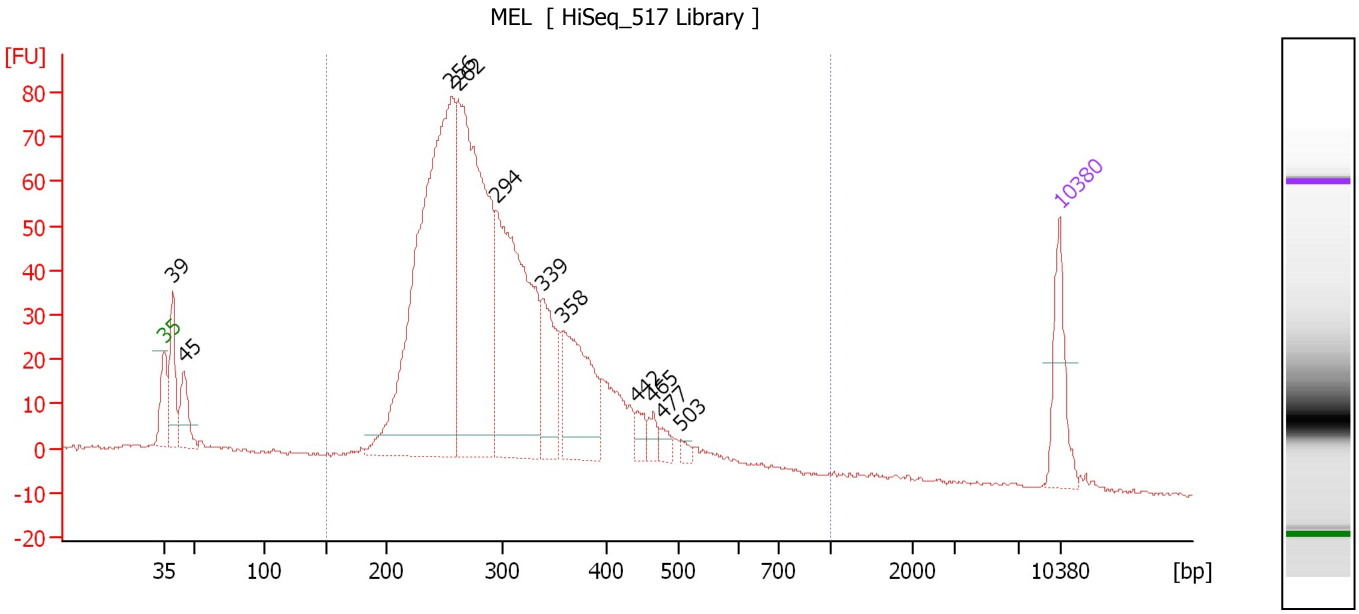
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.32
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		42	17.87	646.5		44.06
4		246	221.92	1,366.9		64.53
5		262	206.14	1,192.5		65.98
6		275	115.03	634.6		67.14
7		285	83.18	442.6		68.06
8		295	128.46	660.2		68.98
9		314	69.29	334.4		70.57
10		322	69.82	328.9		71.20
11		332	103.19	470.3		72.07
12		356	79.36	337.4		74.01
13		371	62.32	254.7		75.17
14		385	62.03	244.4		76.28
15		423	51.68	185.1		78.85
16		456	55.72	185.2		80.73
17		484	17.21	53.9		82.33
18		492	27.55	84.8		82.81
19		520	34.78	101.4		84.17
20		557	16.84	45.8		85.91
21		583	16.43	42.7		87.12
22	▶	10,380	75.00	10.9	Upper Marker	113.00
23		12,605	0.00	0.0		115.08
24		13,536	0.00	0.0		115.95

Electropherogram Summary Continued ...

... Region table for sample 5 : ISRL

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	352	1,521.9	7,700.2	🟦	1,610.25	96	30.4

Electropherogram Summary Continued ...



Overall Results for sample 6 : MEL

Number of peaks found:	11	Corr. Area 1:	1,361.5
Noise:	0.4		

Peak table for sample 6 : MEL

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		39	125.59	4,832.2		43.68
3		45	84.17	2,853.2		44.50
4		256	947.83	5,608.5		65.44
5		262	696.80	4,030.9		65.98
6		294	517.03	2,661.2		68.93
7		339	136.06	608.8		72.57
8		358	199.50	844.8		74.12
9		442	23.86	81.8		79.94
10		465	20.86	68.0		81.25
11		477	16.54	52.5		81.93
12		503	10.67	32.1		83.38
13	▶	10,380	75.00	10.9	Upper Marker	113.00

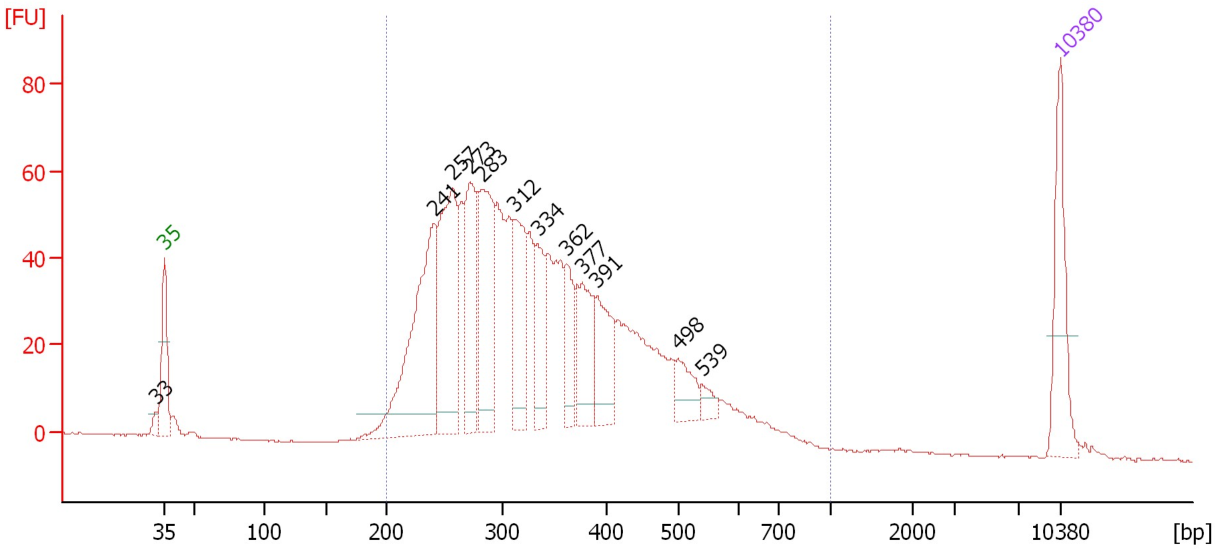
Region table for sample 6 : MEL

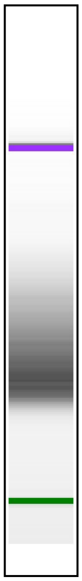
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
150	1,000	312	1,361.5	15,697.2	🟦 2,966.89	90	29.6

Assay Class:	High Sensitivity DNA Assay	Created:	6/21/2016 2:29:33 PM
Data Path:	C:\...016-06-21\2016-06-21_004_HiSeq_517_Libraries_17-24_9rpt.xad	Modified:	6/21/2016 3:36:44 PM

Electropherogram Summary Continued ...

PNM [HiSeq_517 Library]





Overall Results for sample 7 : PNM

Number of peaks found:	12	Corr. Area 1:	1,316.9
Noise:	0.2		

Peak table for sample 7 : PNM

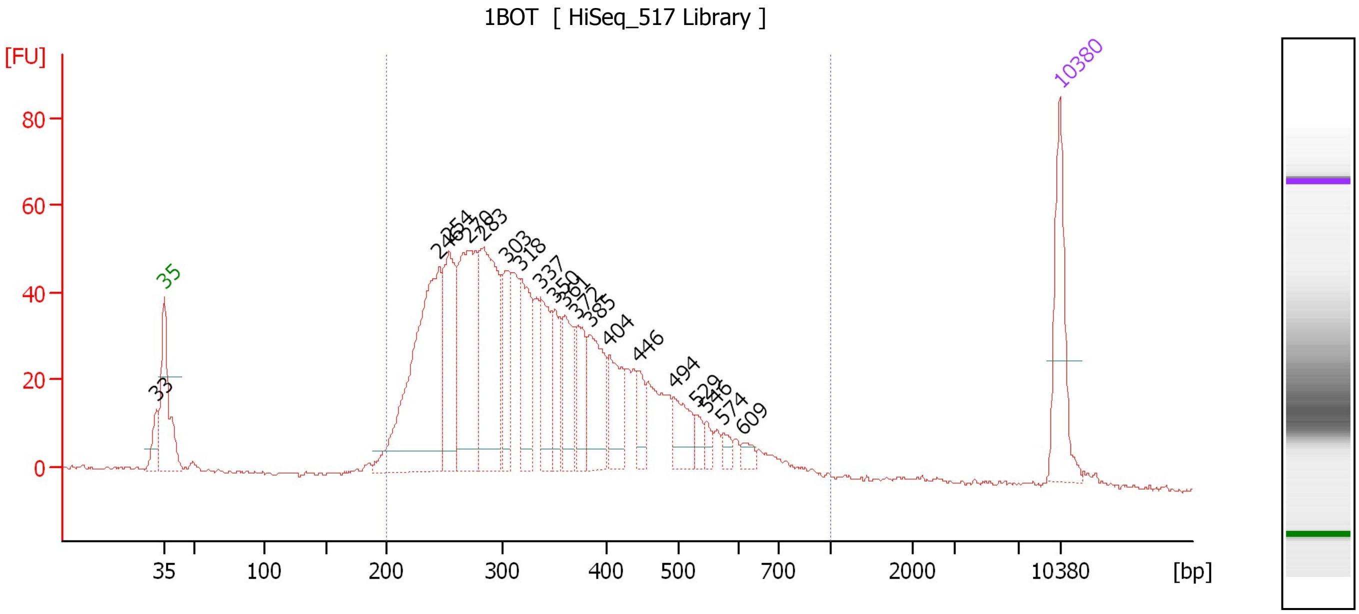
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.35
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		241	285.40	1,795.7		64.05
4		257	210.87	1,242.0		65.55
5		273	134.46	747.4		66.95
6		283	160.57	859.8		67.90
7		312	108.66	527.2		70.44
8		334	73.32	332.7		72.19
9		362	51.96	217.7		74.43
10		377	80.14	322.0		75.68
11		391	78.17	302.7		76.83
12		498	36.52	111.0		83.16
13		539	14.44	40.6		85.06
14	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : PNM

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	347	1,316.9	9,923.9	🟦	2,049.71	98	30.1

Electropherogram Summary Continued ...

1BOT [HiSeq_517 Library]



Overall Results for sample 8 : 1BOT

Number of peaks found:	19	Corr. Area 1:	1,224.5
Noise:	0.5		

Peak table for sample 8 : 1BOT

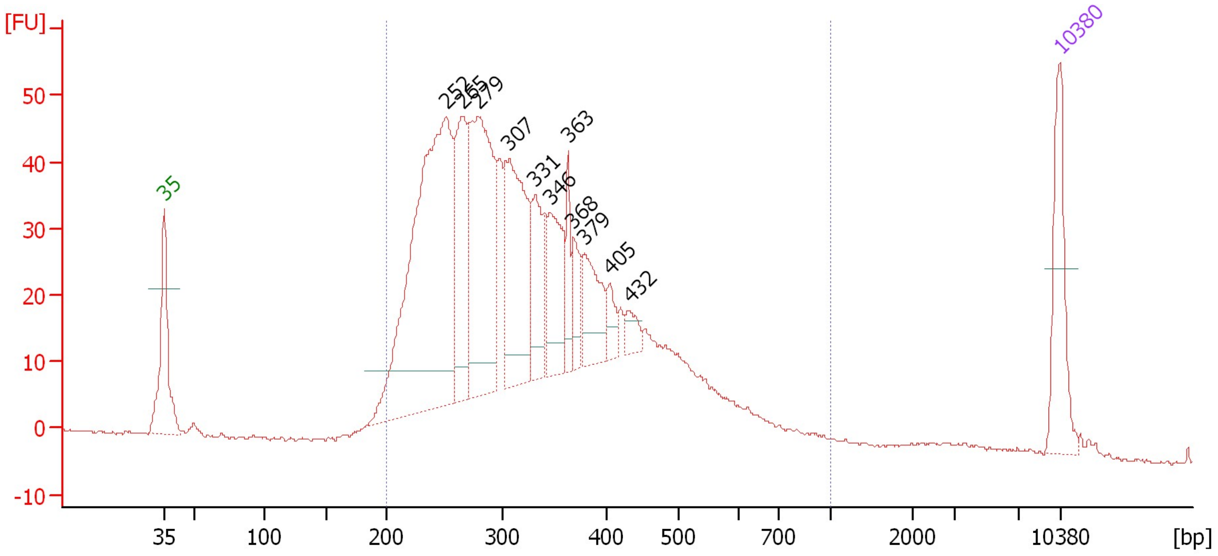
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.40
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		246	329.63	2,033.9		64.49
4		254	139.64	833.5		65.24
5		270	200.87	1,125.4		66.75
6		283	208.83	1,119.8		67.86
7		303	74.56	372.3		69.72
8		318	99.20	473.1		70.88
9		337	77.59	348.8		72.44
10		350	48.81	211.3		73.50
11		361	62.67	263.3		74.35
12		372	57.69	235.1		75.26
13		385	83.81	329.9		76.31
14		404	58.85	220.6		77.77
15		446	26.98	91.7		80.14
16		494	41.46	127.2		82.91
17		529	12.67	36.3		84.62
18		546	11.06	30.7		85.37
19		574	9.23	24.4		86.68
20		609	9.61	23.9		88.19
21	▶	10,380	75.00	10.9	Upper Marker	113.00

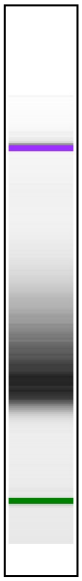
Region table for sample 8 : 1BOT

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	355	1,224.5	9,467.2	■	1,968.89	95	33.2

Electropherogram Summary Continued ...

2BOT [HiSeq_517 Library]





Overall Results for sample 9 : 2BOT

Number of peaks found:	11	Corr. Area 1:	1,081.9
Noise:	0.2		

Peak table for sample 9 : 2BOT

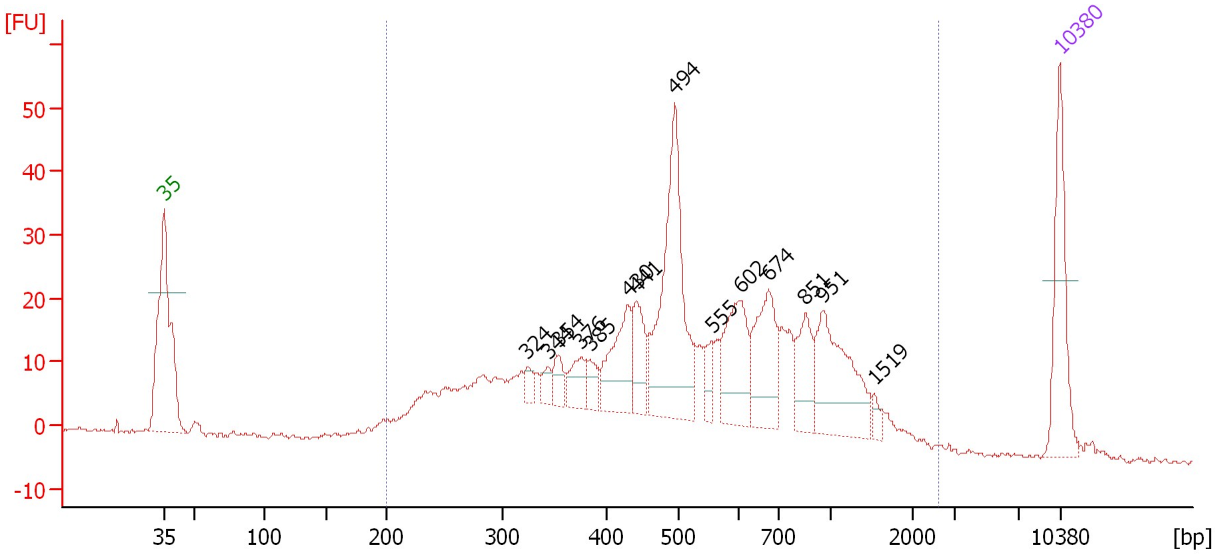
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		252	562.80	3,388.7		65.04
3		265	151.39	864.1		66.30
4		279	292.32	1,589.1		67.51
5		307	200.48	991.1		69.97
6		331	85.36	390.3		71.99
7		346	86.34	377.7		73.19
8		363	41.96	175.1		74.55
9		368	35.01	144.1		74.96
10		379	66.58	265.9		75.86
11		405	21.55	80.6		77.82
12		432	17.67	61.9		79.38
13	▶	10,380	75.00	10.9	Upper Marker	113.00

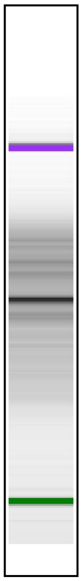
Region table for sample 9 : 2BOT

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	342	1,081.9	11,916.5	🟦	2,406.79	97	32.6

Electropherogram Summary Continued ...

DL2 [HiSeq_517 Library]





Overall Results for sample 10 : DL2

Number of peaks found:	14	Corr. Area 1:	702.3
Noise:	0.3		

Peak table for sample 10 : DL2

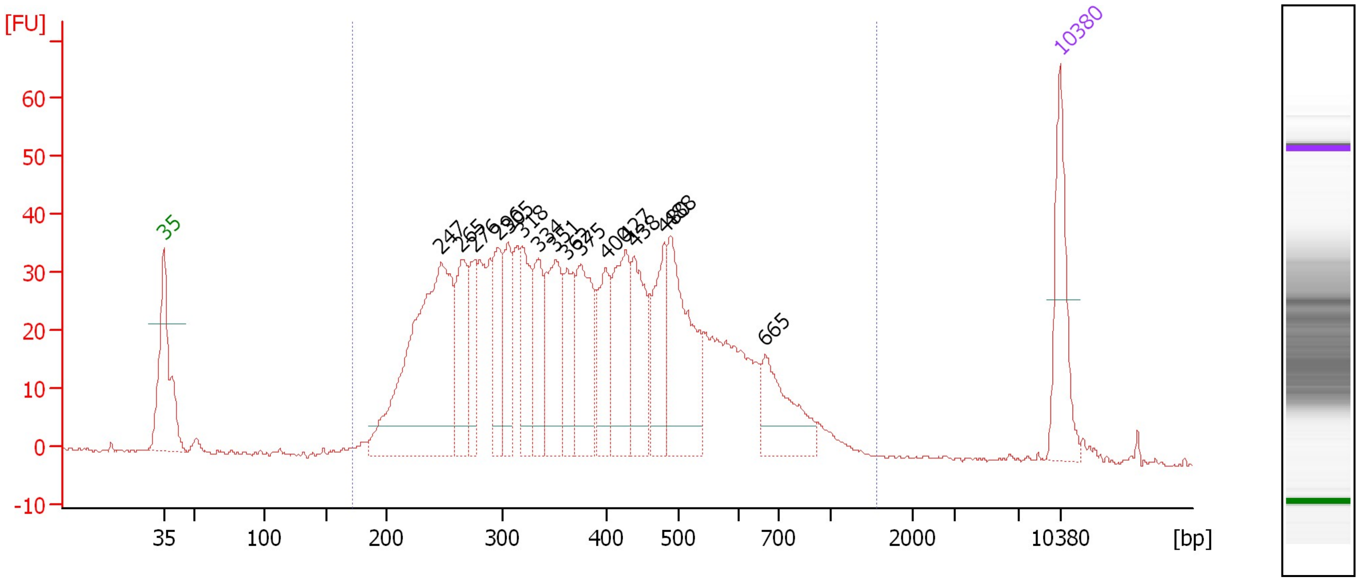
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		324	11.87	55.5		71.38
3		344	12.60	55.5		73.04
4		354	20.38	87.3		73.79
5		376	28.53	115.0		75.59
6		385	18.40	72.5		76.30
7		430	73.68	259.6		79.25
8		441	45.49	156.1		79.91
9		494	209.74	643.2		82.91
10		555	20.27	55.3		85.82
11		602	82.47	207.4		87.98
12		674	84.92	190.9		90.23
13		851	46.90	83.5		93.09
14		951	106.30	169.3		94.45
15		1,519	6.65	6.6		98.46
16	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : DL2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,615	610	702.3	4,848.1	■	1,424.61	98	56.5

Electropherogram Summary Continued ...

9RUS [HiSeq_517 Library]



Overall Results for sample 11 : 9RUS

Number of peaks found:	16	Corr. Area 1:	1,147.9
Noise:	0.2		

Peak table for sample 11 : 9RUS

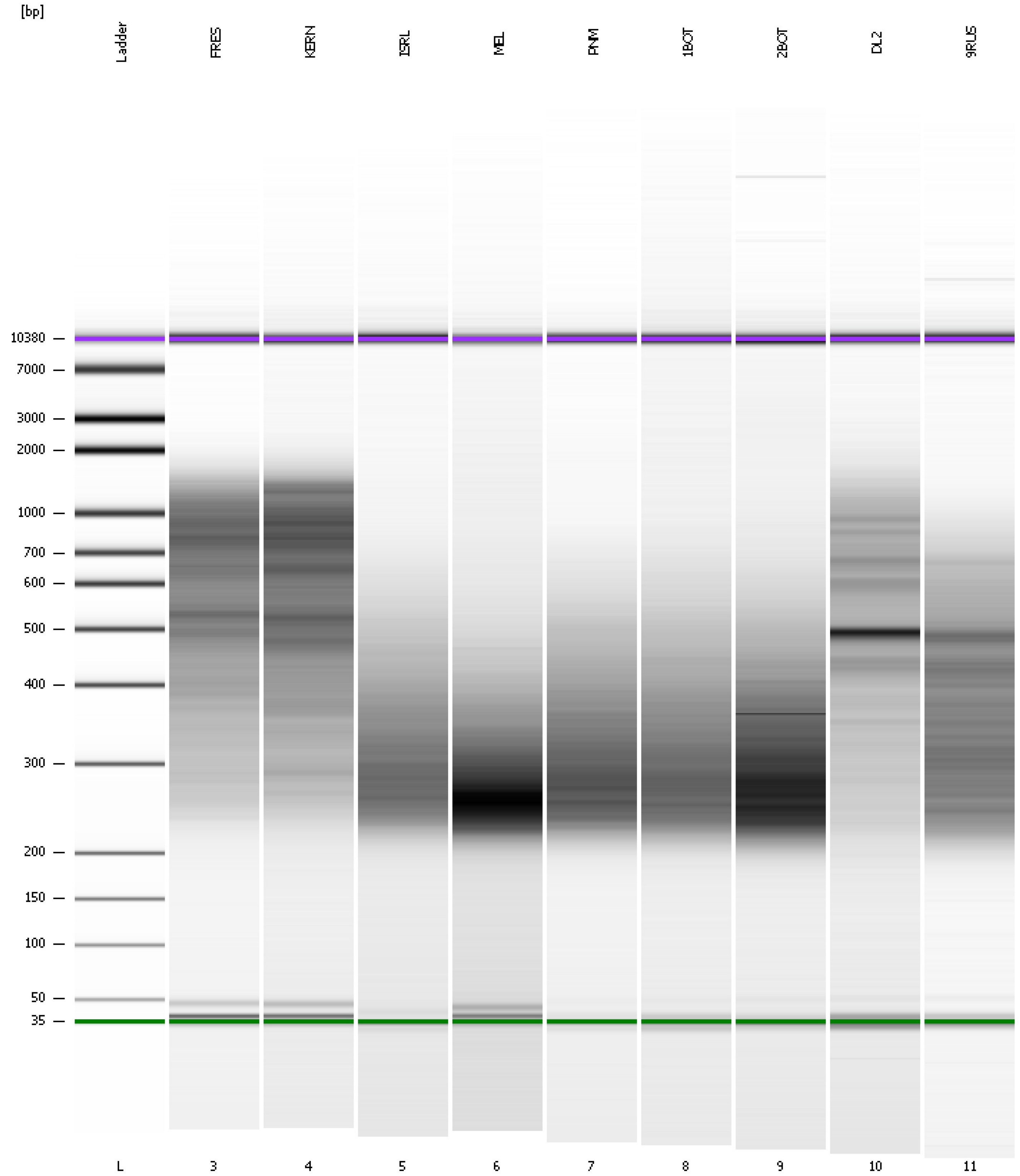
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		247	403.78	2,475.6		64.63
3		265	107.43	614.9		66.23
4		276	63.47	348.8		67.23
5		296	73.66	377.0		69.09
6		305	73.40	364.1		69.89
7		318	85.80	408.2		70.94
8		334	75.55	342.8		72.19
9		351	115.48	499.0		73.54
10		362	68.08	284.6		74.49
11		375	112.09	452.4		75.55
12		400	74.47	282.4		77.50
13		427	107.99	382.8		79.10
14		438	96.75	334.8		79.70
15		480	85.48	269.9		82.11
16		488	156.74	486.8		82.56
17		665	81.33	185.2		89.97
18	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : 9RUS

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
173	1,563	407	1,147.9	9,629.3	■	2,168.96	99	39.6

Assay Class:	High Sensitivity DNA Assay	Created:	6/21/2016 2:29:33 PM
Data Path:	C:\...016-06-21\2016-06-21_004_HiSeq_517_Libraries_17-24_9rpt.xad	Modified:	6/21/2016 3:36:44 PM

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		6/21/2016 3:10:51 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-06-21\2016-06-21_004.xad)		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		6/21/2016 2:29:39 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1