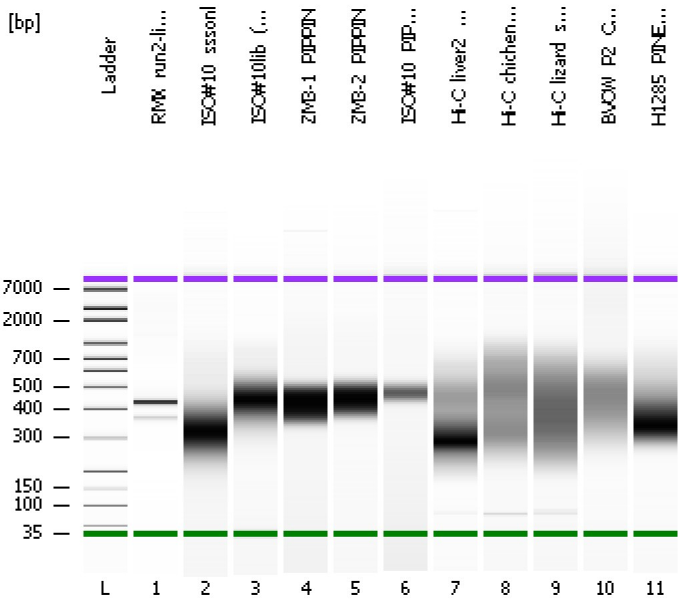
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-02-13\2018-02-13_002.xad

Created: 2/13/2018 12:54:40 PM
Modified: 2/13/2018 1:39:21 PM

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

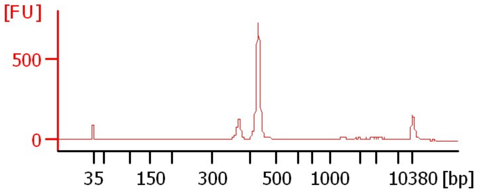
Chip Information:

Chip Lot #:

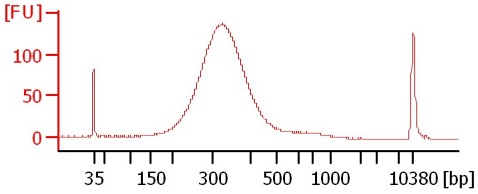
Reagent Kit Lot #:

Chip Comments:

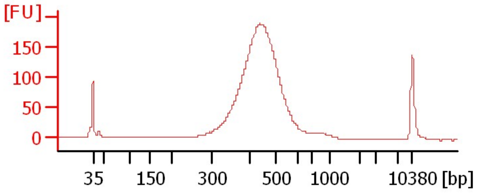
RMX_run2-lib_(1:20)



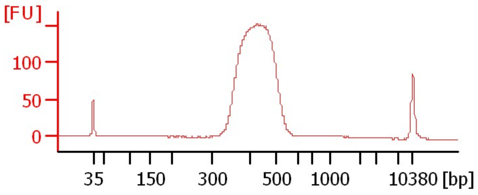
ISO#10_sssonl



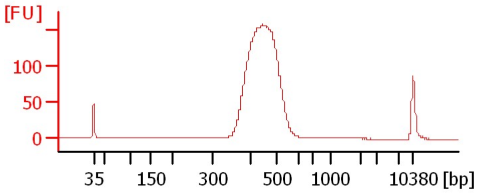
ISO#10lib_(1:3)



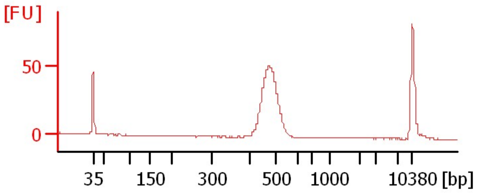
ZM3-1_PIPPIN



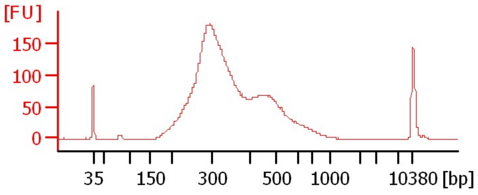
ZM3-2_PIPPIN



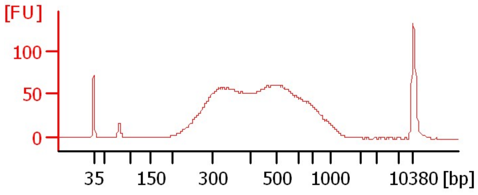
ISO#10_PIPPIN



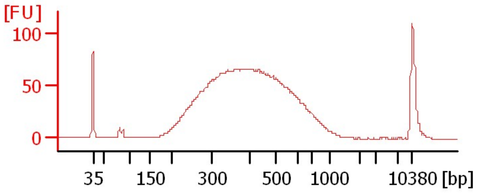
Hi-C_liver2_Seq_lib



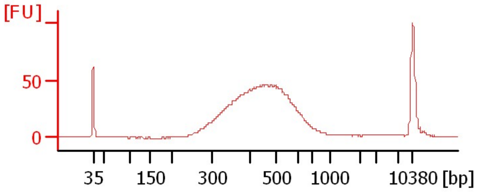
Hi-C_chichenA_liver_seq_lib



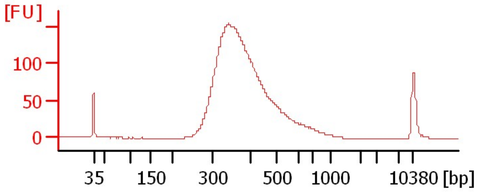
Hi-C_lizard_seq_lib



BVOW_P2_CCWB_BS



H1285_PINE_pool_BC



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-02-13\2018-02-13_002.xad

Created: 2/13/2018 12:54:40 PM
Modified: 2/13/2018 1:39:21 PM

Electrophoresis File Run Summary (Chip Summary)

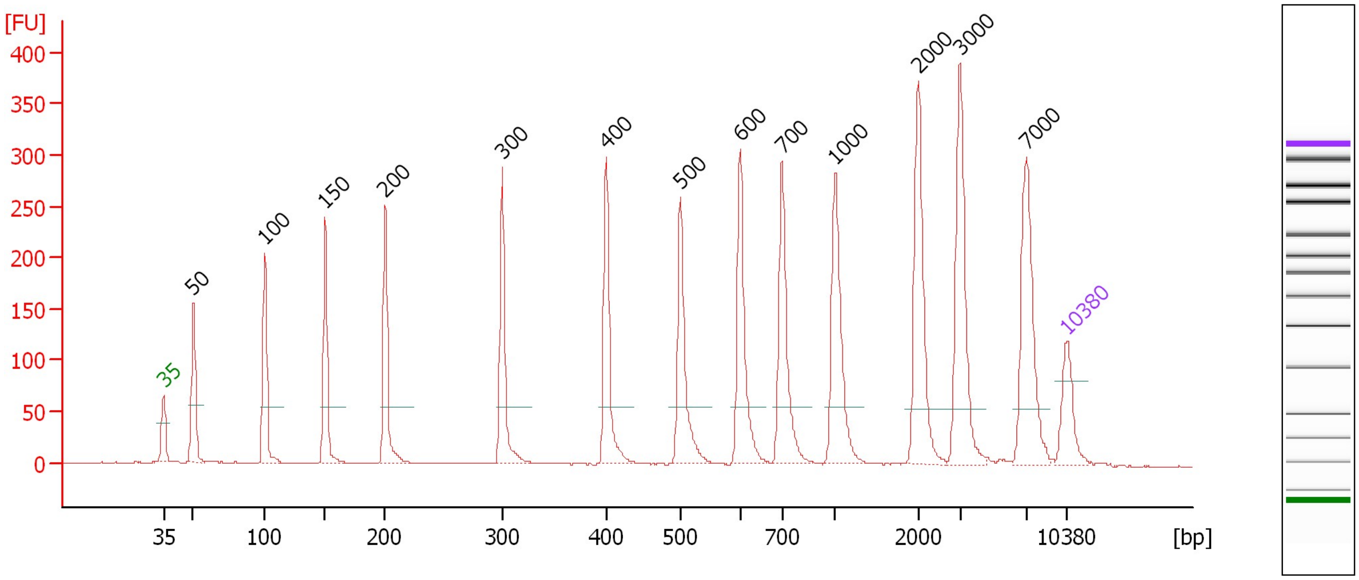
Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
RMX_run2-lib_(1:20)		☐	✓			
ISO#10_sssonl		☐	✓			
ISO#10lib_(1:3)		☐	✓			
ZM3-1_PIPPIN		☐	✓			
ZM3-2_PIPPIN		☐	✓			
ISO#10_PIPPIN		☐	✓			
Hi-C_liver2_Seq_lib		☐	✓			
Hi-C_chichenA_liver_seq_lib		☐	✓			
Hi-C_lizard_seq_lib		☐	✓			
BVOW_P2_CCWB_BS		☐	✓			
H1285_PINE_pool_BC		☐	✓			
Ladder		☐	✓			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Electropherogram Summary

Ladder



Overall Results for Ladder

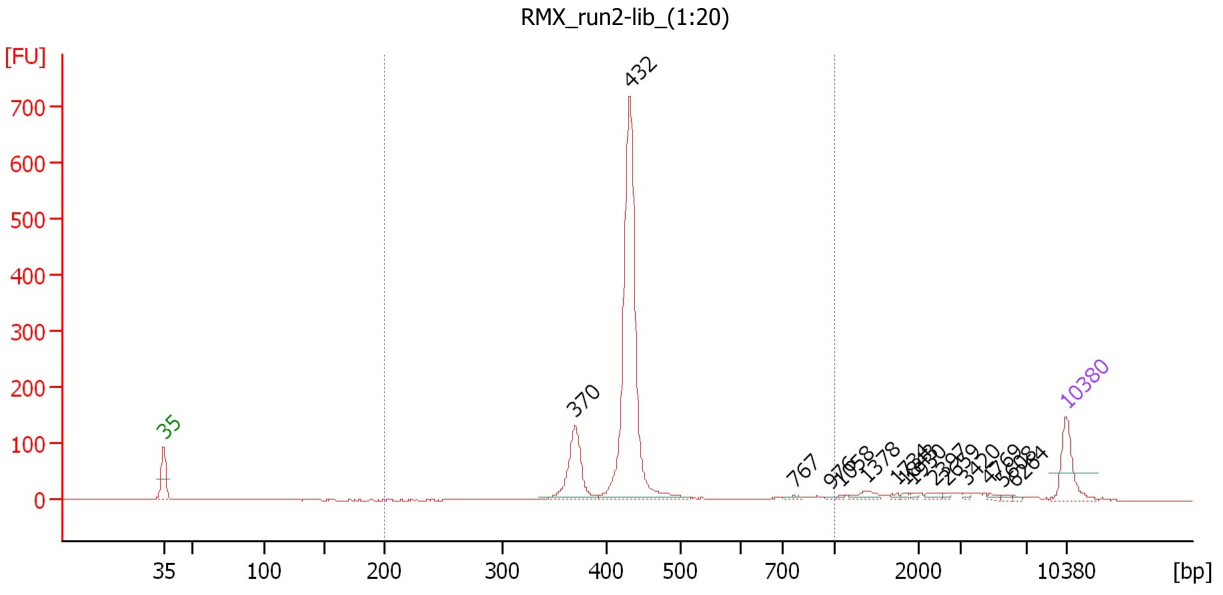
Noise: 0.4

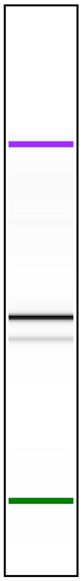
Peak table for Ladder

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	50.86
4	L	150	150.00	1,515.2	Ladder Peak	55.54
5	L	200	150.00	1,136.4	Ladder Peak	60.17
6	L	300	150.00	757.6	Ladder Peak	69.25
7	L	400	150.00	568.2	Ladder Peak	77.34
8	L	500	150.00	454.5	Ladder Peak	83.10
9	L	600	150.00	378.8	Ladder Peak	87.73
10	L	700	150.00	324.7	Ladder Peak	90.96
11	L	1,000	150.00	227.3	Ladder Peak	95.08
12	L	2,000	150.00	113.6	Ladder Peak	101.54
13	L	3,000	150.00	75.8	Ladder Peak	104.76
14	L	7,000	150.00	32.5	Ladder Peak	109.91
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

RMX_run2-lib_(1:20)





Overall Results for sample 1 : RMX_run2-lib_(1:20)

Number of peaks found:	15	Corr. Area 1:	1,322.7
Noise:	0.3		

Peak table for sample 1 : RMX_run2-lib_(1:20)

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		370	171.40	702.2		74.90
3		432	779.52	2,735.5		79.17
4		767	5.61	11.1		91.89
5		976	2.90	4.5		94.75
6		1,058	2.82	4.0		95.45
7		1,378	17.50	19.2		97.52
8		1,734	4.73	4.1		99.82
9		1,843	4.53	3.7		100.52
10		1,930	3.97	3.1		101.08
11		2,397	8.42	5.3		102.82
12		2,659	4.42	2.5		103.66
13		3,420	4.20	1.9		105.31
14		4,769	5.27	1.7		107.04
15		5,608	4.04	1.1		108.12
16		6,264	2.75	0.7		108.97
17	▶	10,380	75.00	10.9	Upper Marker	113.00

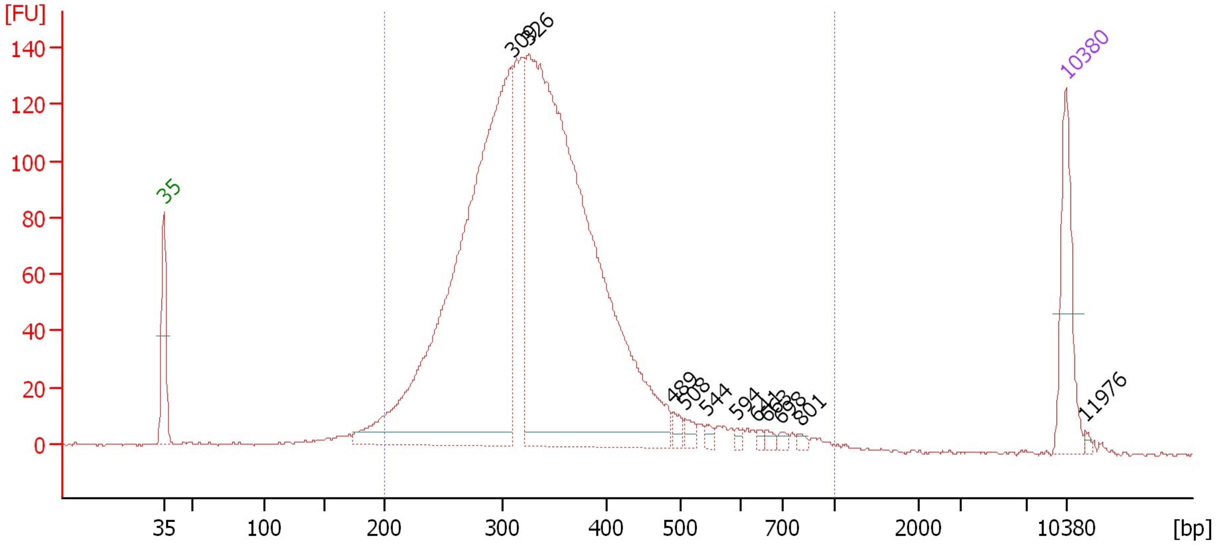
Region table for sample 1 : RMX_run2-lib_(1:20)

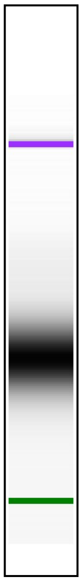
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	438	1,322.7	1,020.18	3,632.6	🟦 87	19.0

Assay Class:	High Sensitivity DNA Assay	Created:	2/13/2018 12:54:40 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2018-02-13\2018-02-13_002.xad	Modified:	2/13/2018 1:39:21 PM

Electropherogram Summary Continued ...

ISO#10_sssonl





Overall Results for sample 2 : **ISO#10_sssonl**

Number of peaks found:	11	Corr. Area 1:	2,395.3
Noise:	0.4		

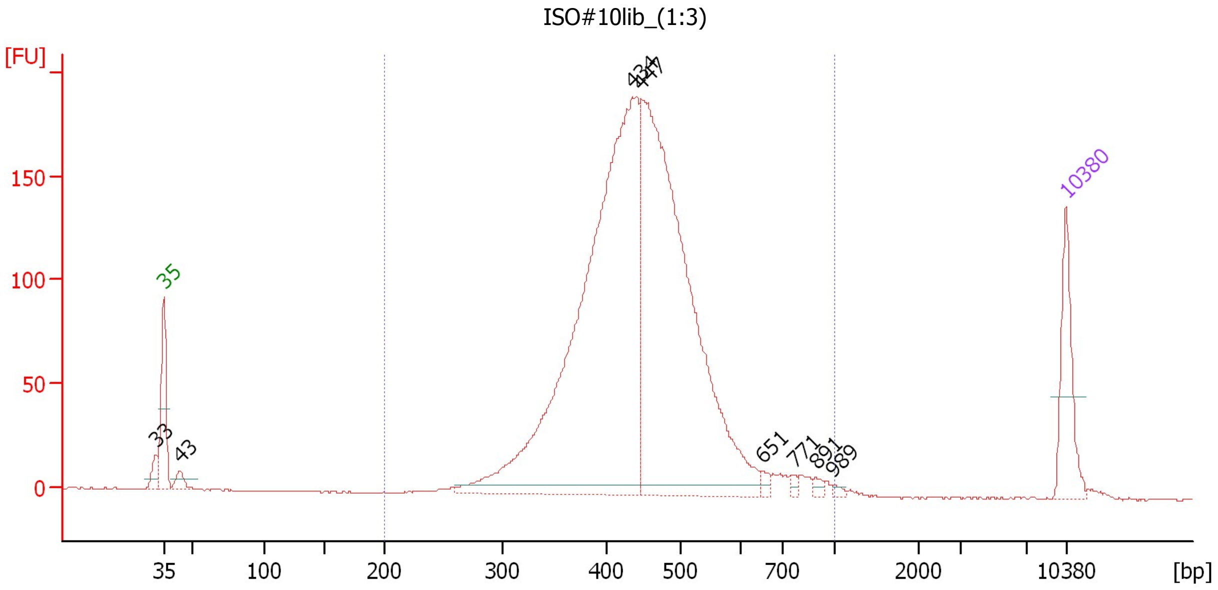
Peak table for sample 2 : **ISO#10_sssonl**

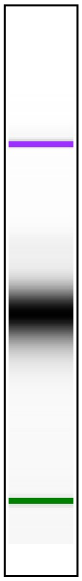
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		309	971.83	4,760.7		70.00
3		326	1,184.48	5,512.4		71.32
4		489	11.92	36.9		82.47
5		508	10.22	30.5		83.46
6		544	5.71	15.9		85.15
7		594	5.03	12.8		87.46
8		641	4.10	9.7		89.06
9		663	6.05	13.8		89.76
10		698	4.98	10.8		90.89
11		801	4.62	8.7		92.35
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		11,976	0.00	0.0		114.46

Region table for sample 2 : **ISO#10_sssonl**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	343	2,395.3	2,428.22	11,469.2	🟦 96	26.6

Electropherogram Summary Continued ...





Overall Results for sample 3 : ISO#10lib_(1:3)

Number of peaks found:	8	Corr. Area 1:	2,348.4
Noise:	0.3		

Peak table for sample 3 : ISO#10lib_(1:3)

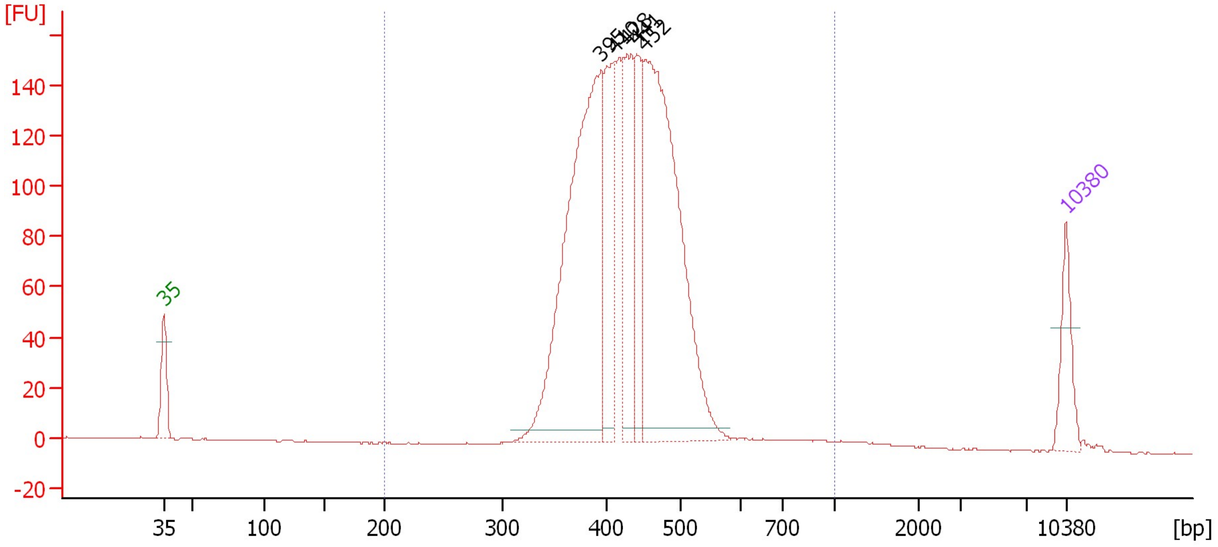
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.37
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		43	22.32	782.5		44.26
4		434	1,094.66	3,817.5		79.33
5		447	923.58	3,130.2		80.05
6		651	7.16	16.7		89.38
7		771	6.09	12.0		91.94
8		891	6.14	10.4		93.58
9		989	4.02	6.2		94.93
10	▶	10,380	75.00	10.9	Upper Marker	113.00

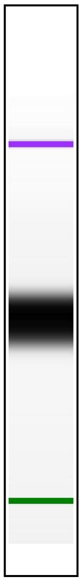
Region table for sample 3 : ISO#10lib_(1:3)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	450	2,348.4	2,081.58	7,299.4	🟦	98	19.4

Electropherogram Summary Continued ...

ZM3-1_PIPPIN





Overall Results for sample 4 : ZM3-1_PIPPIN

Number of peaks found: 5

Corr. Area 1: 1,916.2

Noise: 0.2

Peak table for sample 4 : ZM3-1_PIPPIN

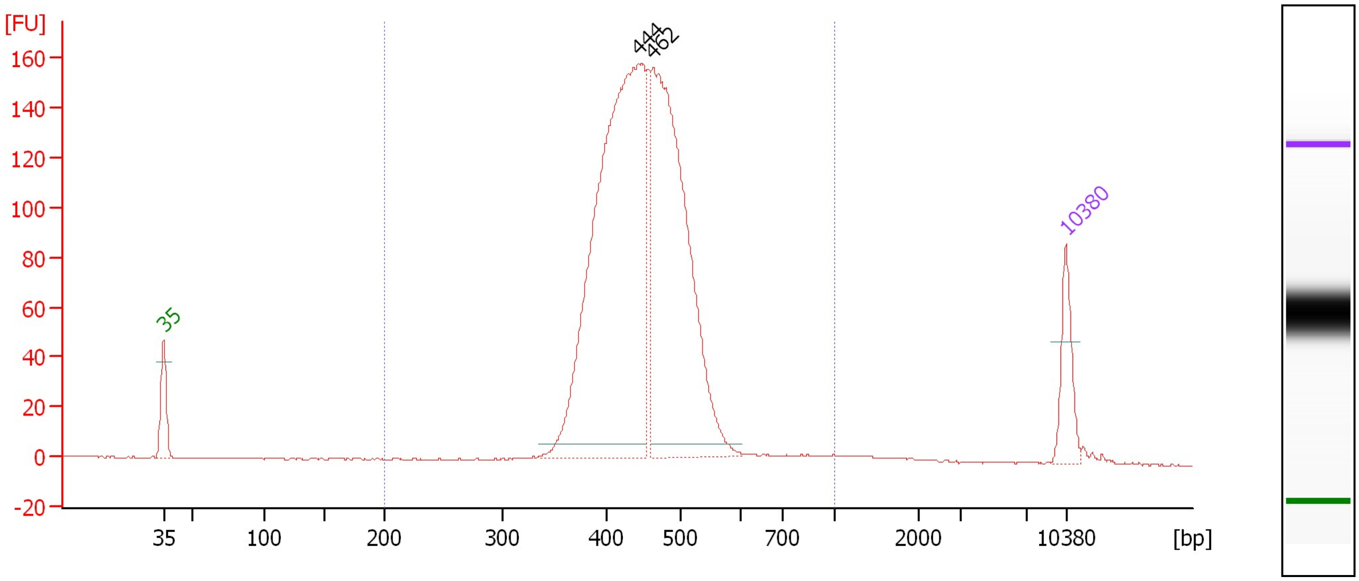
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		395	890.78	3,419.5		76.92
3		410	245.88	909.4		77.90
4		428	262.01	928.3		78.94
5		441	177.17	609.4		79.68
6		452	882.17	2,959.5		80.32
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : ZM3-1_PIPPIN

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	434	1,916.2	2,753.95	9,848.0	■ 97	15.7

Electropherogram Summary Continued ...

ZM3-2_PIPPIN



Overall Results for sample 5 : ZM3-2_PIPPIN

Number of peaks found:	2	Corr. Area 1:	1,649.2
Noise:	0.2		

Peak table for sample 5 : ZM3-2_PIPPIN

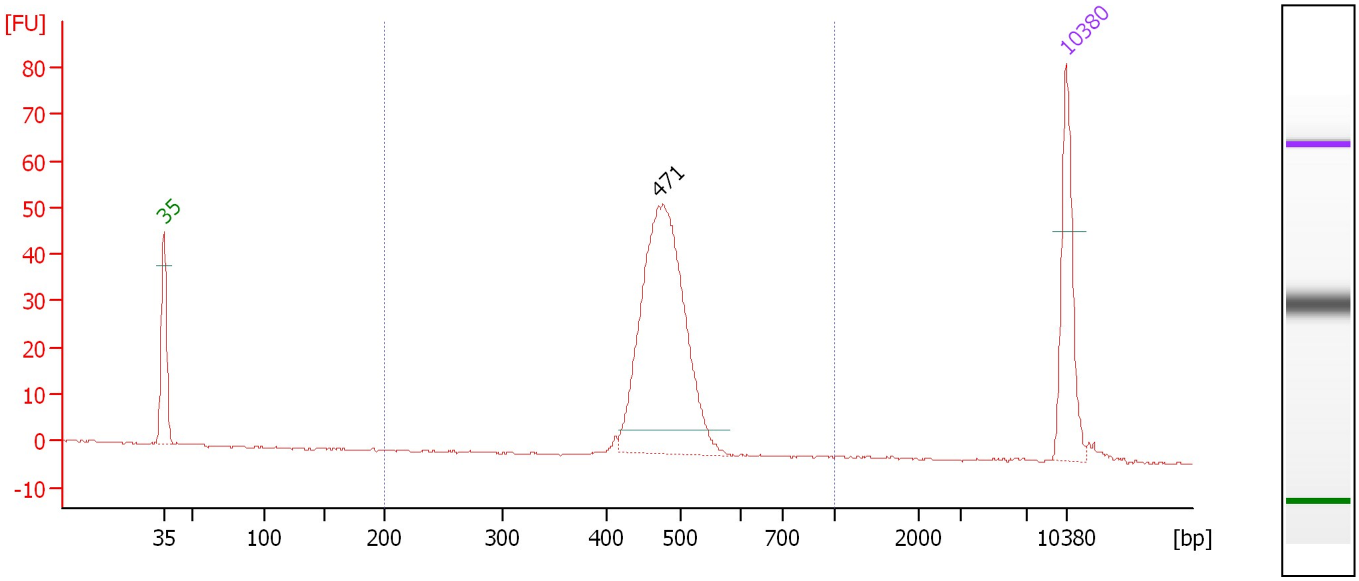
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		444	1,276.65	4,361.2		79.85
3		462	910.36	2,985.4		80.91
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : ZM3-2_PIPPIN

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	453	1,649.2	2,350.07	8,020.8	🟦 97	14.3

Electropherogram Summary Continued ...

ISO#10_PIPPIN



Overall Results for sample 6 : ISO#10 PIPPIN

Number of peaks found:	1	Corr. Area 1:	255.5
Noise:	0.2		

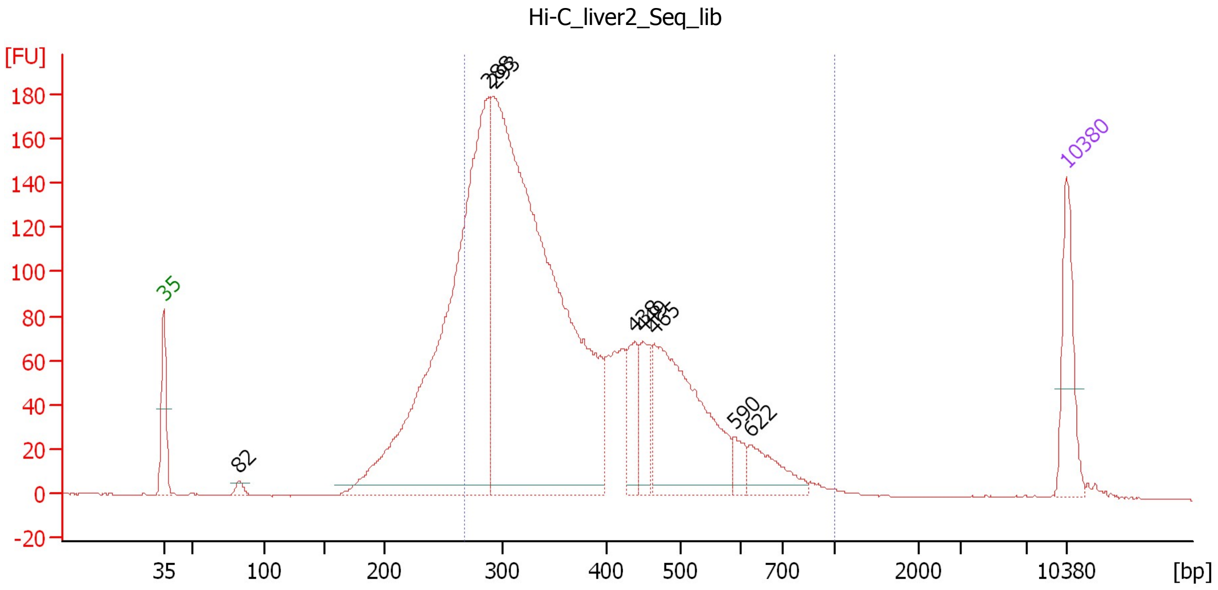
Peak table for sample 6 : ISO#10 PIPPIN

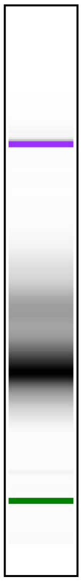
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		471	364.23	1,172.9		81.40
3	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : ISO#10 PIPPIN

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
200	1,000	477	255.5	359.86	1,145.2	🟦	98	5.8

Electropherogram Summary Continued ...


Hi-C_liver2_Seq_lib



Overall Results for sample 7 : Hi-C_liver2_Seq_lib

Number of peaks found:	8	Corr. Area 1:	2,642.8
Noise:	0.2		

Peak table for sample 7 : Hi-C_liver2_Seq_lib

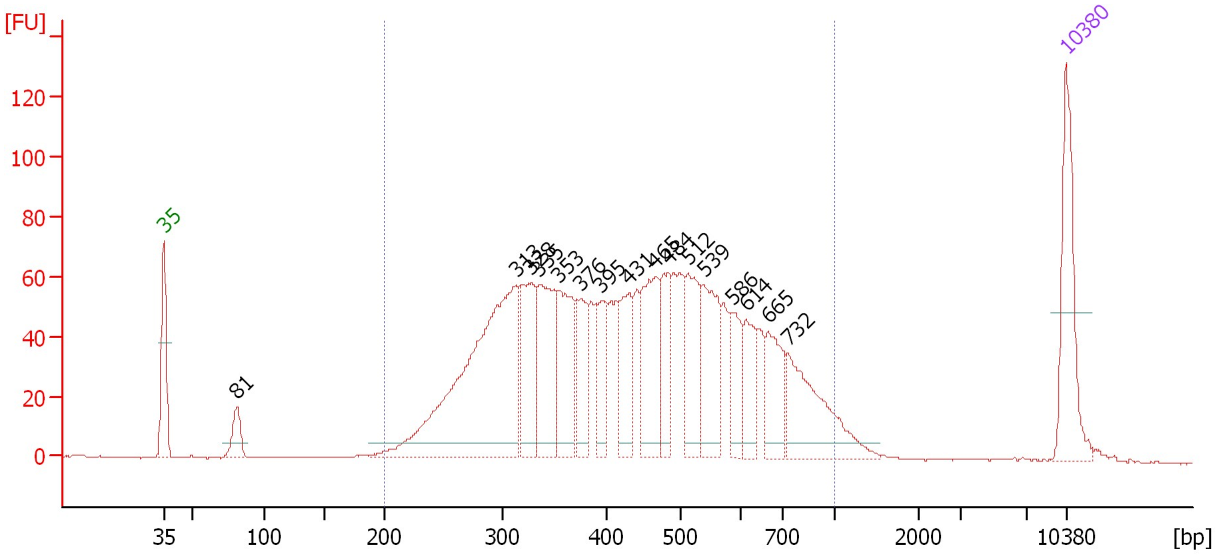
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		82	11.21	207.0		48.86
3		288	1,005.26	5,281.1		68.20
4		293	1,378.63	7,126.6		68.62
5		438	72.76	251.6		79.54
6		449	69.06	232.9		80.18
7		465	308.62	1,005.5		81.09
8		590	25.35	65.1		87.27
9		622	59.84	145.8		88.44
10	▶	10,380	75.00	10.9	Upper Marker	113.00

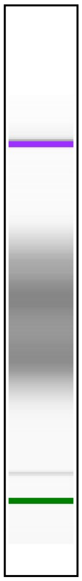
Region table for sample 7 : Hi-C_liver2_Seq_lib

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
267	1,000	383	2,642.8	2,407.55	10,435.0	🟦 81	28.9

Electropherogram Summary Continued ...

Hi-C_chichenA_liver_seq_lib





Overall Results for sample 8 : **Hi-C_chichenA_liver_seq_lib**

Number of peaks found:	16	Corr. Area 1:	1,884.2
Noise:	0.2		

Peak table for sample 8 : **Hi-C_chichenA_liver_seq_lib**

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		81	33.12	622.9		48.69
3		313	363.15	1,758.7		70.29
4		328	93.43	431.4		71.53
5		335	109.88	496.4		72.12
6		353	90.12	386.4		73.57
7		376	49.58	199.8		75.39
8		395	46.95	180.0		76.95
9		431	59.70	210.1		79.10
10		465	96.54	314.5		81.09
11		484	51.52	161.4		82.16
12		512	75.10	222.1		83.67
13		539	83.65	235.2		84.90
14		586	43.94	113.5		87.11
15		614	40.77	100.6		88.18
16		665	54.83	124.9		89.85
17		732	102.93	213.0		91.40
18	▶	10,380	75.00	10.9	Upper Marker	113.00

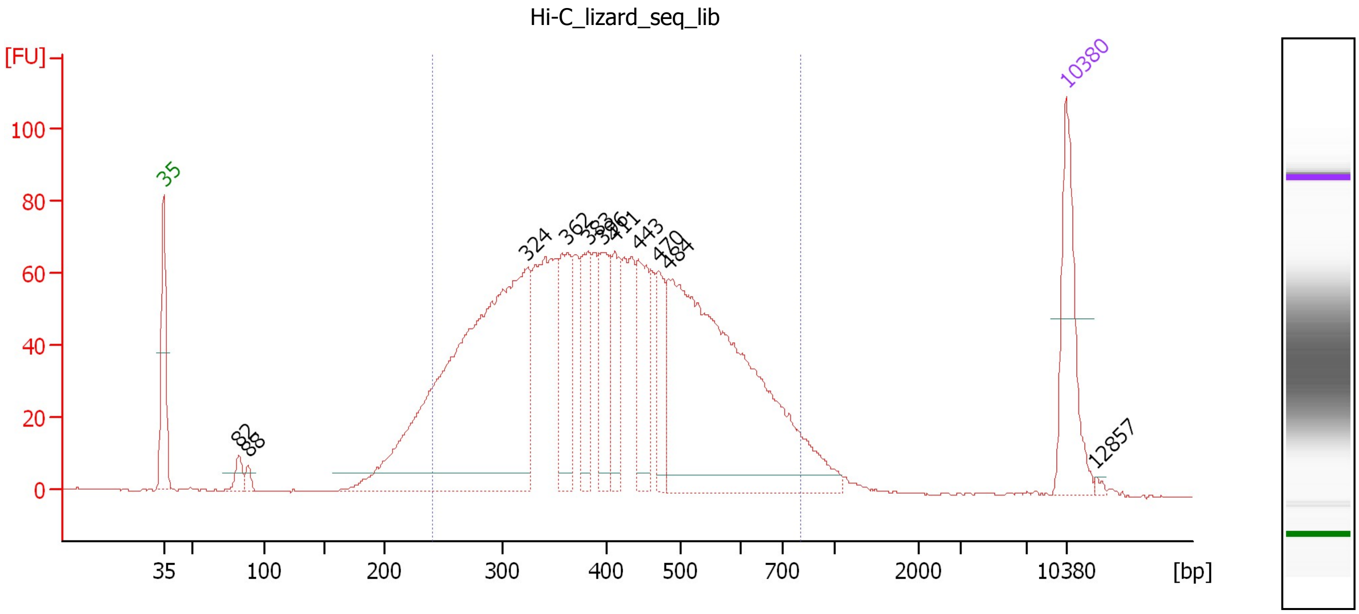
Region table for sample 8 : **Hi-C_chichenA_liver_seq_lib**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	458	1,884.2	1,692.98	6,525.2	■ 95	34.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2018-02-13\2018-02-13_002.xad

Created: 2/13/2018 12:54:40 PM
Modified: 2/13/2018 1:39:21 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : **Hi-C_lizard_seq_lib**

Number of peaks found:	11	Corr. Area 1:	1,881.1
Noise:	0.1		

Peak table for sample 9 : **Hi-C_lizard_seq_lib**

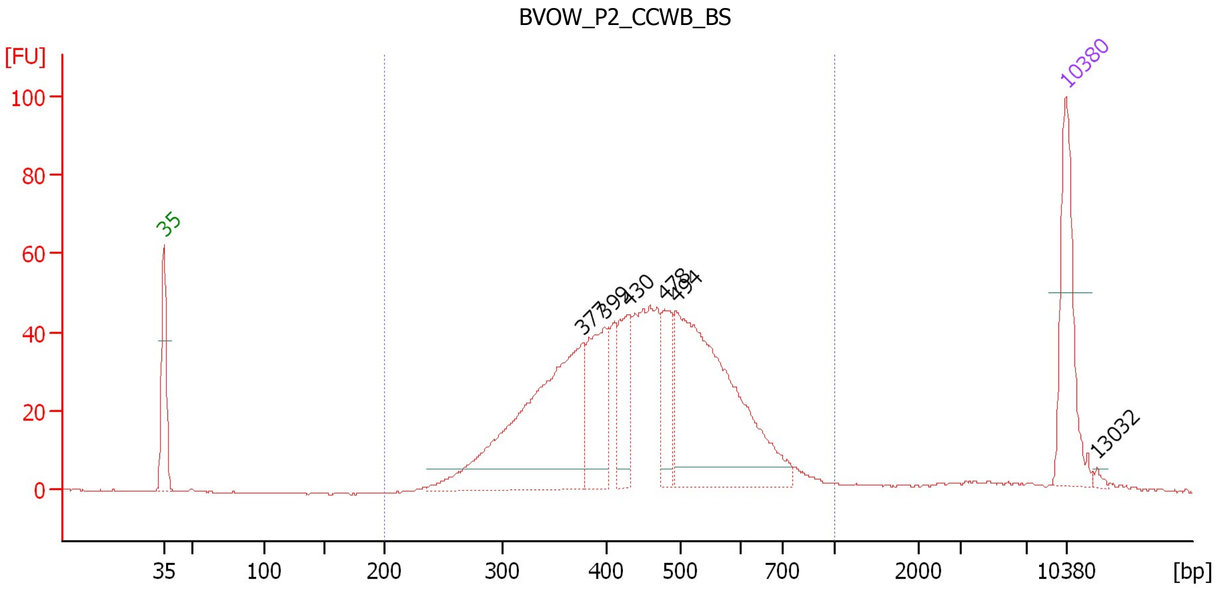
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		82	16.54	306.9		48.82
3		88	9.69	165.9		49.57
4		324	619.97	2,900.3		71.18
5		362	95.39	398.7		74.31
6		383	56.69	224.2		75.98
7		396	76.38	291.9		77.06
8		411	53.94	198.9		77.97
9		443	73.89	252.9		79.81
10		470	54.60	176.1		81.37
11		484	493.03	1,543.6		82.18
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		12,857	0.00	0.0		115.26

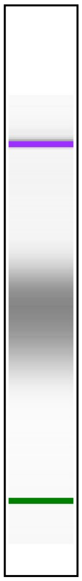
Region table for sample 9 : **Hi-C_lizard_seq_lib**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]
241	799	421	1,881.1	1,814.39	7,296.6	🟦	90	28.2

Electropherogram Summary Continued ...

BVOW_P2_CCWB_BS





Overall Results for sample 10 : BVOW_P2_CCWB_BS

Number of peaks found:	6	Corr. Area 1:	986.9
Noise:	0.2		

Peak table for sample 10 : BVOW_P2_CCWB_BS

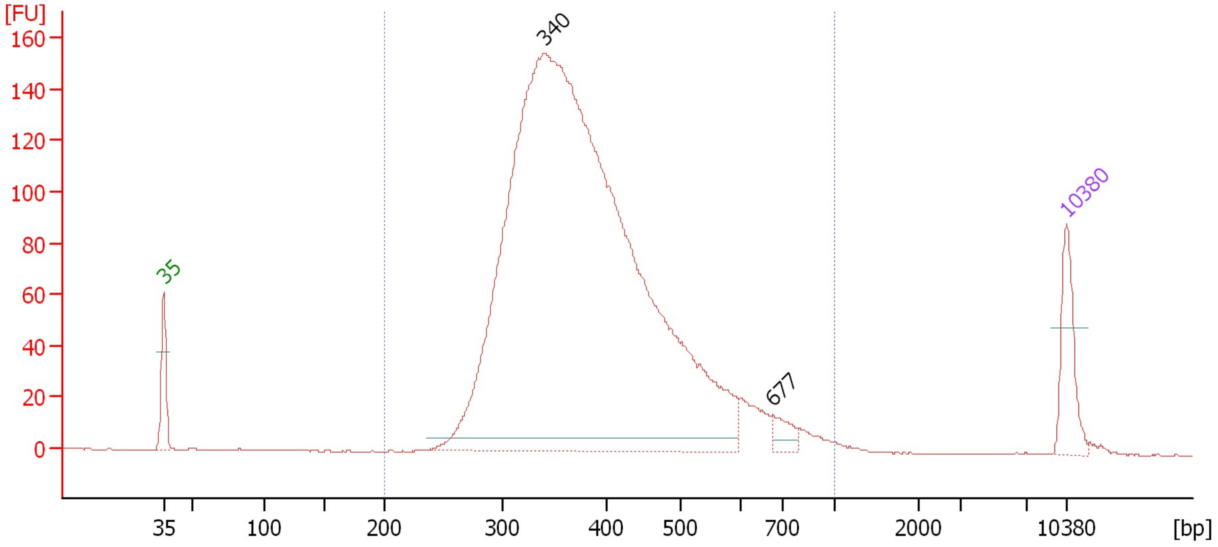
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		377	288.17	1,156.6		75.52
3		399	93.83	356.5		77.25
4		430	61.09	215.2		79.08
5		478	49.07	155.6		81.82
6		494	296.03	908.5		82.74
7	▶	10,380	75.00	10.9	Upper Marker	113.00
8		13,032	0.00	0.0		115.42

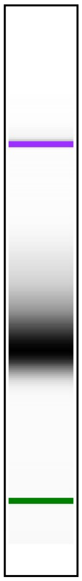
Region table for sample 10 : BVOW_P2_CCWB_BS

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	456	986.9	1,058.59	3,828.0	🟦 92	25.4

Electropherogram Summary Continued ...

H1285_PINE_pool_BC





Overall Results for sample 11 : H1285_PINE_pool_BC

Number of peaks found:	2	Corr. Area 1:	2,368.6
Noise:	0.2		

Peak table for sample 11 : H1285_PINE_pool_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		340	3,032.23	13,523.8		72.47
3		677	30.62	68.5		90.21
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : H1285_PINE_pool_BC

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Conc. [pg/µl]	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]
200	1,000	397	2,368.6	2,964.74	12,063.9	🟦 99	25.4

Assay Class: High Sensitivity DNA Assay
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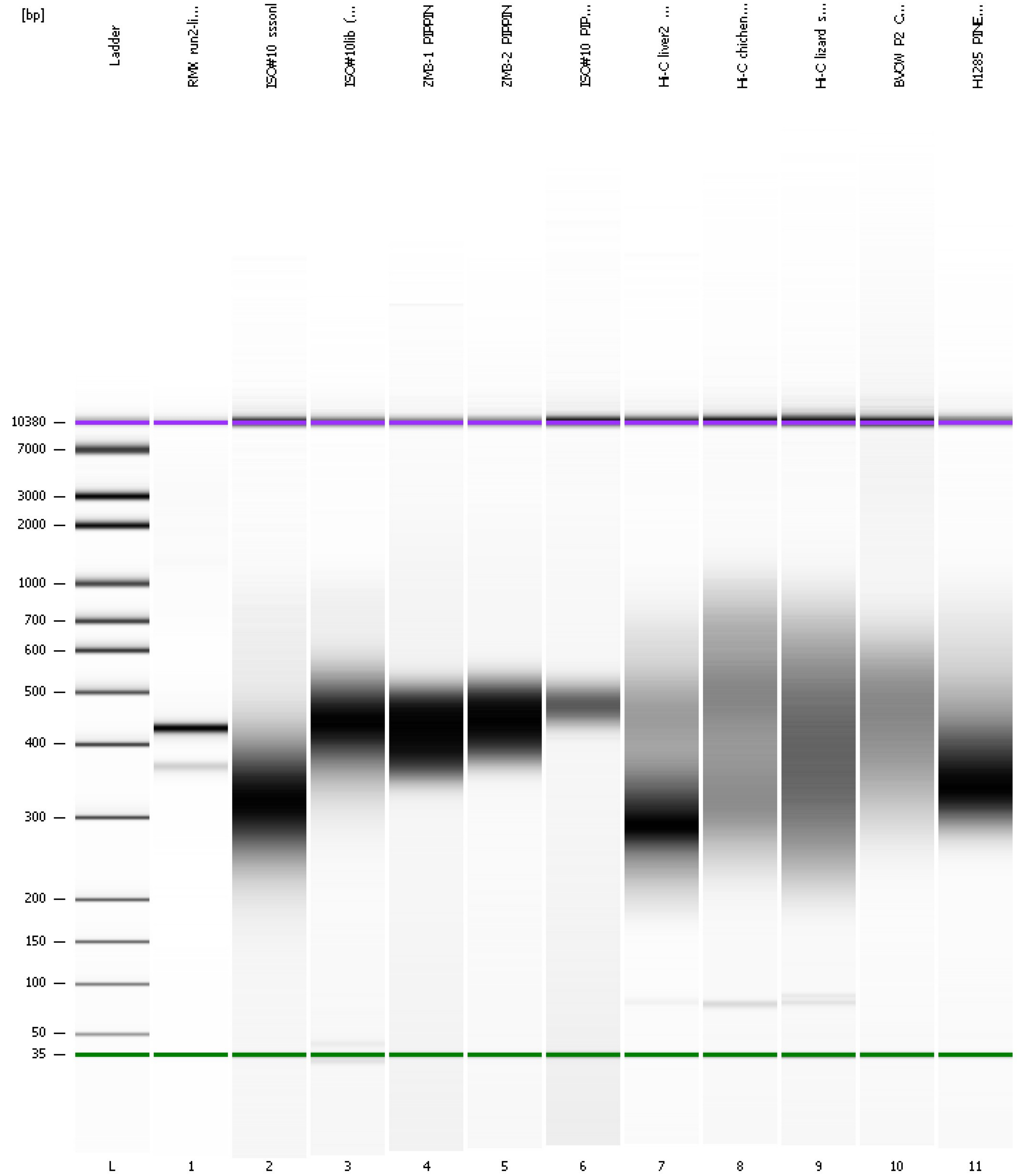
Modified: 2/13/2018 1:39:21 PM

Gel Image



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