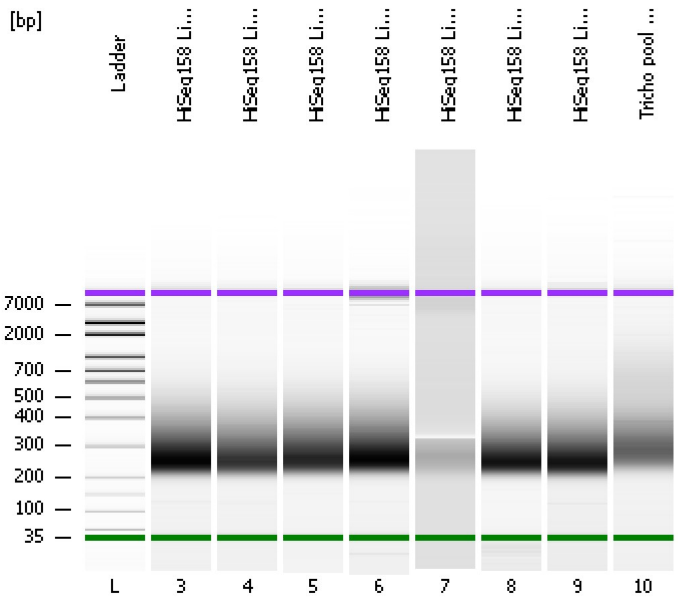
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ings\Bioanalyzer\2015-08-06\2015-08-06_002_HiSeq158Libs.xad
Created: 8/6/2015 3:53:09 PM
Modified: 8/6/2015 5:10:43 PM

Electrophoresis File Run Summary



Instrument Information:

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

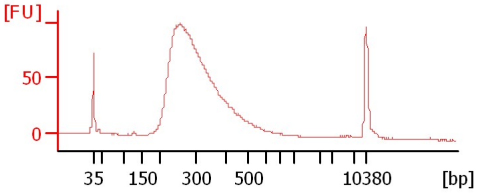
Assay Information:

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

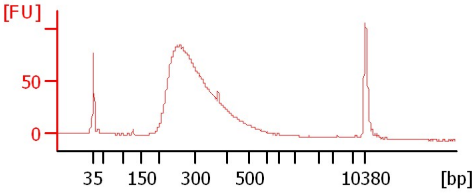
Chip Information:

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

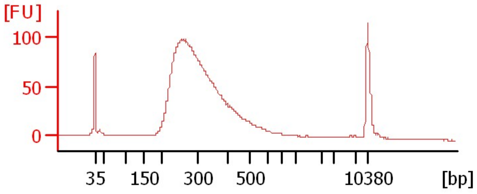
HiSeq158 Library - sample 1



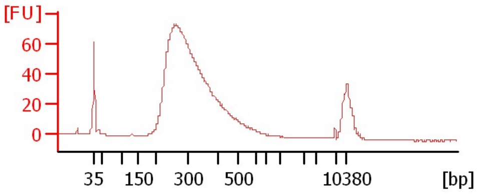
HiSeq158 Library - sample 2



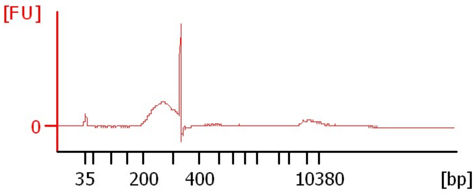
HiSeq158 Library - sample 4



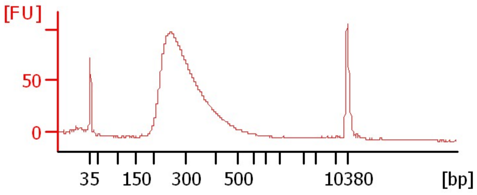
HiSeq158 Library - sample 5



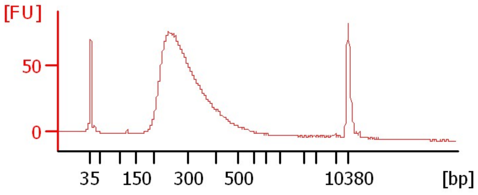
HiSeq158 Library - sample 6



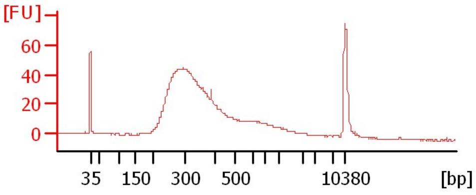
HiSeq158 Library - sample 7



HiSeq158 Library - sample 8



Tricho pool 26 (1:5)



Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq158 Library - sample 1		☐	✓			
HiSeq158 Library - sample 2		☐	✓			
HiSeq158 Library - sample 4		☐	✓			
HiSeq158 Library - sample 5		☐	✓			
HiSeq158 Library - sample 6		☐	✓			
HiSeq158 Library - sample 7		☐	✓			
HiSeq158 Library - sample 8		☐	✓			
Tricho pool 26 (1:5)		☐	✓			
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

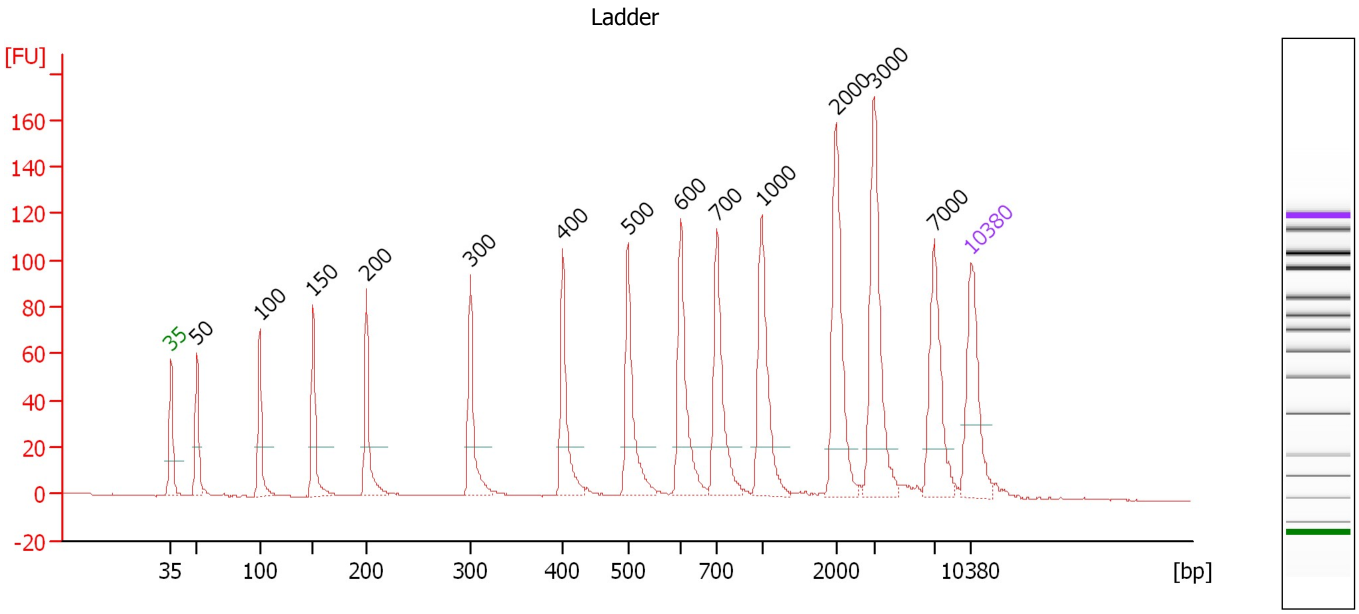
Filter Width [s] : 0.5
Polynomial Order : 4

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:	8/6/2015 3:53:09 PM
Data Path:	C:\...ings\Bioanalyzer\2015-08-06\2015-08-06_002_HiSeq158Libs.xad	Modified:	8/6/2015 5:10:43 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

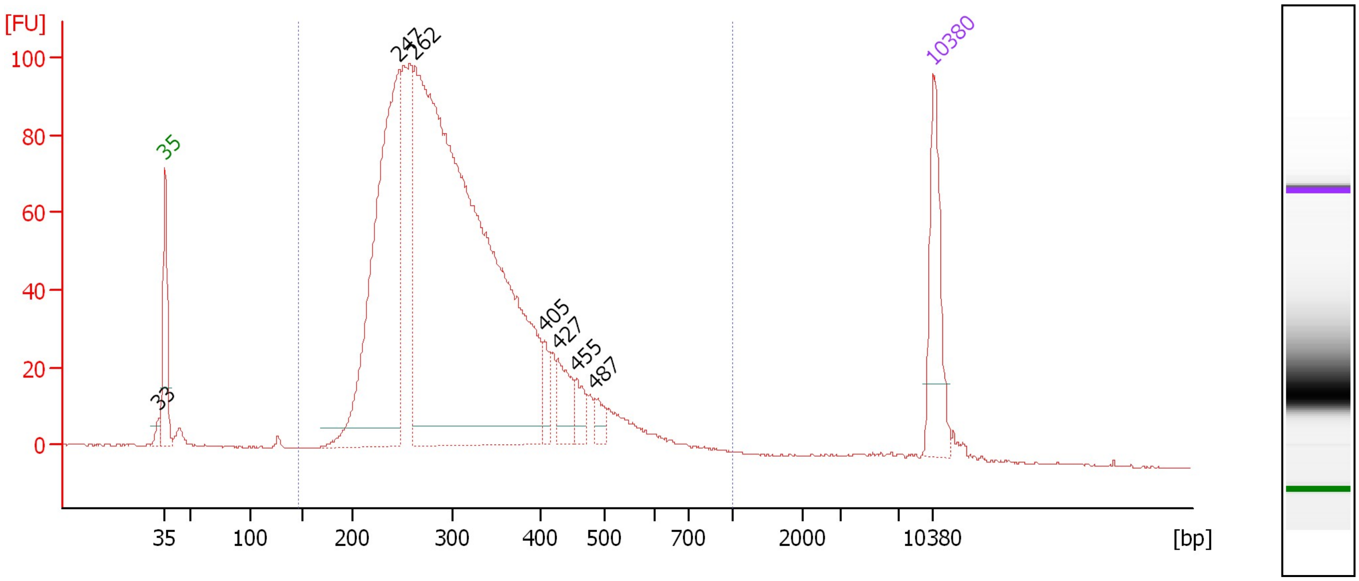
Peak table for Ladder

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	∟	50	150.00	4,545.5	Ladder Peak	45.29
3	∟	100	150.00	2,272.7	Ladder Peak	50.74
4	∟	150	150.00	1,515.2	Ladder Peak	55.45
5	∟	200	150.00	1,136.4	Ladder Peak	60.07
6	∟	300	150.00	757.6	Ladder Peak	69.16
7	∟	400	150.00	568.2	Ladder Peak	77.28
8	∟	500	150.00	454.5	Ladder Peak	82.97
9	∟	600	150.00	378.8	Ladder Peak	87.58
10	∟	700	150.00	324.7	Ladder Peak	90.75
11	∟	1,000	150.00	227.3	Ladder Peak	94.67
12	∟	2,000	150.00	113.6	Ladder Peak	101.15
13	∟	3,000	150.00	75.8	Ladder Peak	104.51
14	∟	7,000	150.00	32.5	Ladder Peak	109.78
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ings\Bioanalyzer\2015-08-06\2015-08-06_002_HiSeq158Libs.xad
Created: 8/6/2015 3:53:09 PM
Modified: 8/6/2015 5:10:43 PM

Electropherogram Summary Continued ...

HiSeq158 Library - sample 1



Overall Results for sample 3 : **HiSeq158 Library - sample 1**

Number of peaks found: 7

Corr. Area 1: 1,936.1

Noise: 0.3

Peak table for sample 3 : **HiSeq158 Library - sample 1**

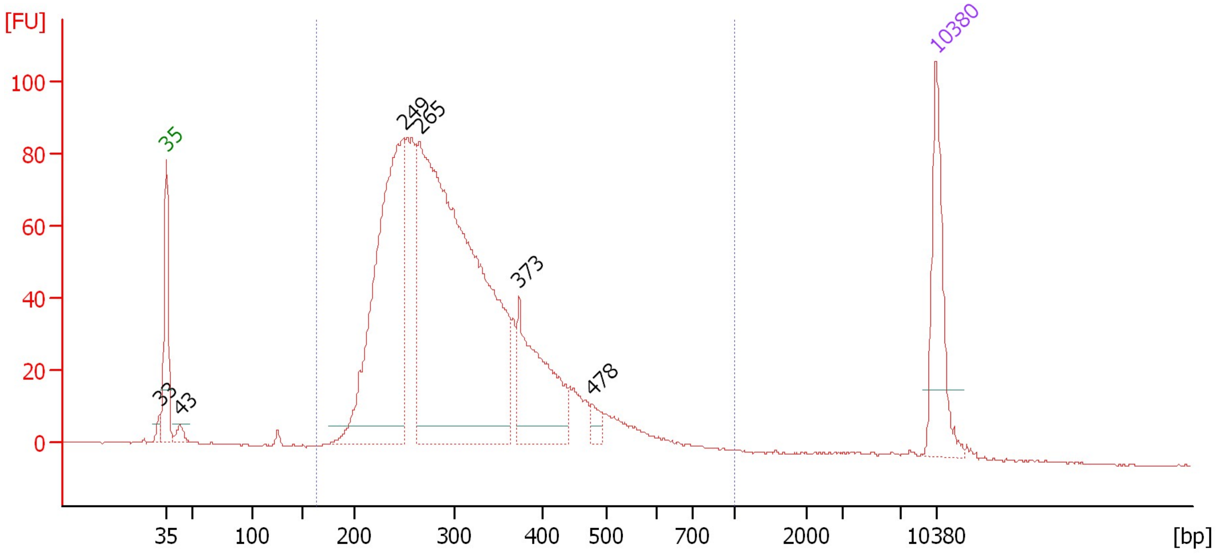
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.37
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		247	519.18	3,187.2		64.33
4		262	1,383.02	7,988.9		65.73
5		405	24.15	90.4		77.54
6		427	40.65	144.3		78.80
7		455	22.43	74.7		80.40
8		487	14.76	46.0		82.20
9	▶	10,380	75.00	10.9	Upper Marker	113.00

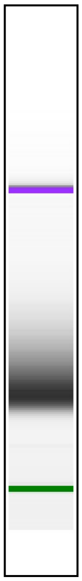
Region table for sample 3 : **HiSeq158 Library - sample 1**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
147	317	1,000	1,936.1	11,870.2	🟦	97	29.8	2,274.49

Electropherogram Summary Continued ...

HiSeq158 Library - sample 2





Overall Results for sample 4 : HiSeq158 Library - sample 2

Number of peaks found:	6	Corr. Area 1:	1,670.2
Noise:	0.2		

Peak table for sample 4 : HiSeq158 Library - sample 2

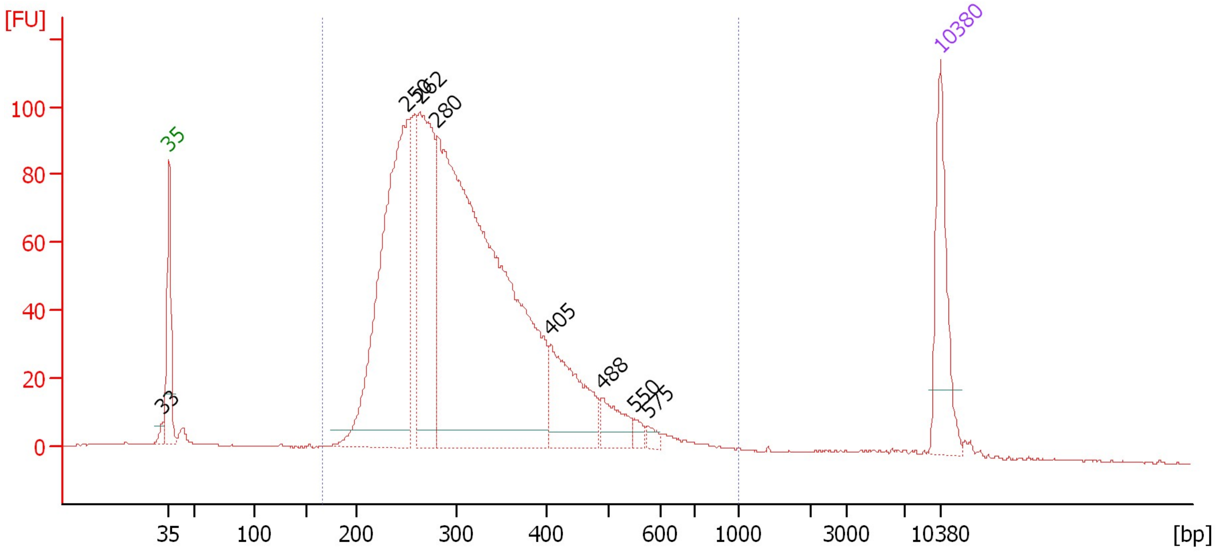
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.42
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		43	13.14	463.6		44.21
4		249	447.27	2,717.7		64.56
5		265	861.89	4,921.6		66.01
6		373	150.54	611.8		75.07
7		478	12.93	41.0		81.71
8	▶	10,380	75.00	10.9	Upper Marker	113.00

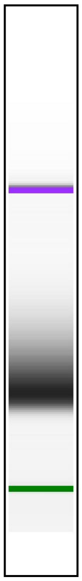
Region table for sample 4 : HiSeq158 Library - sample 2

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]	Conc. [pg/µl]
163	316	1,000	1,670.2	9,035.6	🟦 97	29.9	1,724.02

Electropherogram Summary Continued ...

HiSeq158 Library - sample 4





Overall Results for sample 5 : **HiSeq158 Library - sample 4**

Number of peaks found:	8	Corr. Area 1:	2,000.1
Noise:	0.2		

Peak table for sample 5 : **HiSeq158 Library - sample 4**

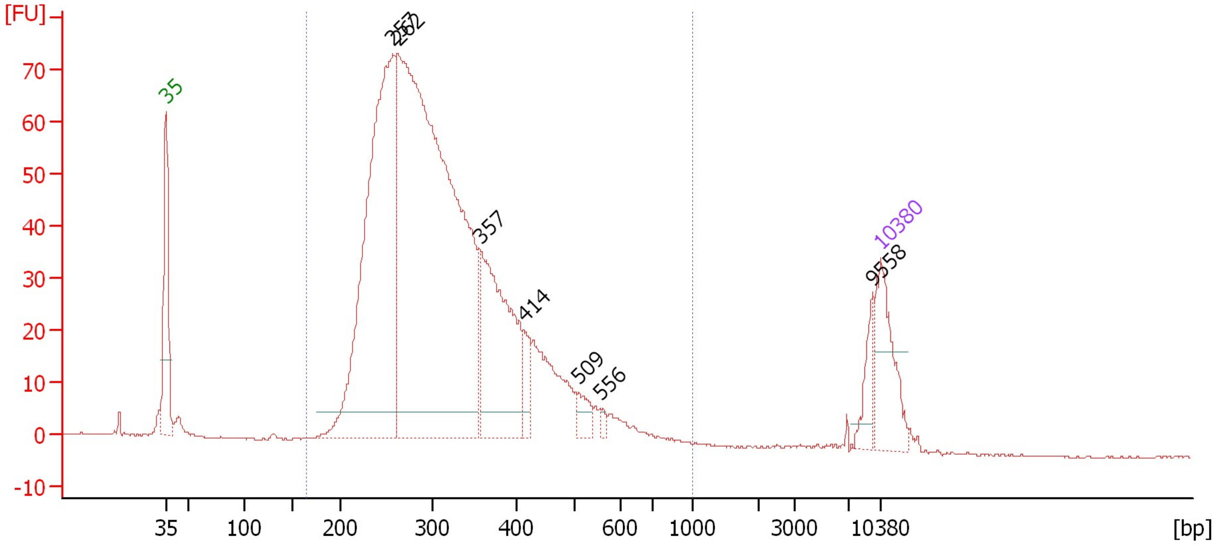
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.37
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		250	481.55	2,917.4		64.62
4		262	269.63	1,557.3		65.74
5		280	929.81	5,033.5		67.33
6		405	117.90	440.6		77.59
7		488	38.12	118.4		82.28
8		550	8.40	23.1		85.28
9		575	7.51	19.8		86.44
10	▶	10,380	75.00	10.9	Upper Marker	113.00

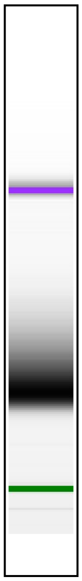
Region table for sample 5 : **HiSeq158 Library - sample 4**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
167	323	1,000	2,000.1	10,065.9	🟦	95	30.5	1,955.60

Electropherogram Summary Continued ...

HiSeq158 Library - sample 5





Overall Results for sample 6 : **HiSeq158 Library - sample 5**

Number of peaks found:	7	Corr. Area 1:	1,356.7
Noise:	0.2		

Peak table for sample 6 : **HiSeq158 Library - sample 5**

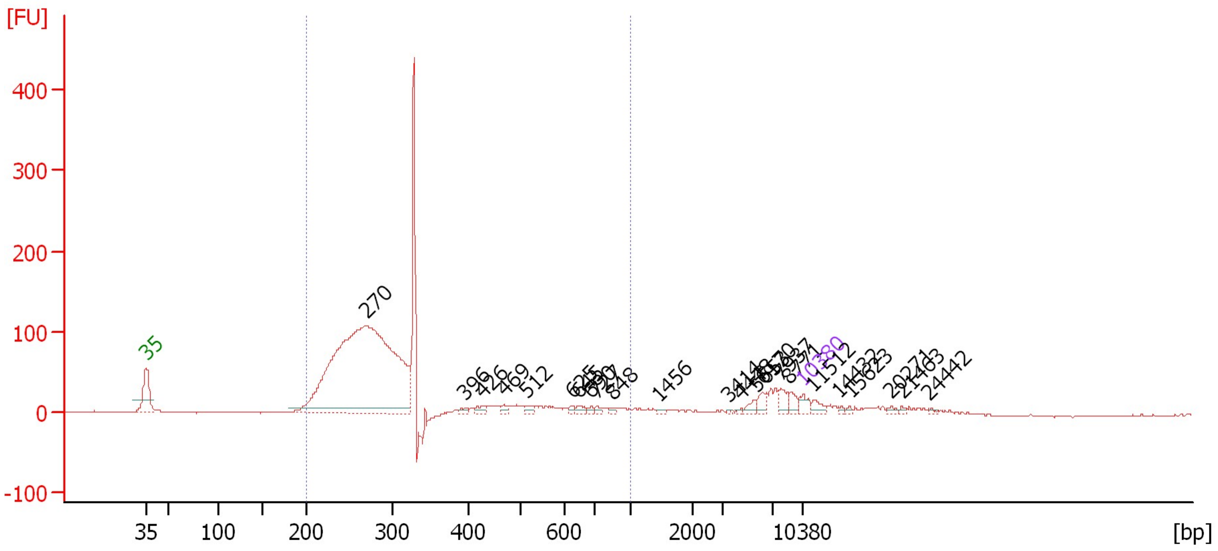
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		257	711.70	4,198.5		65.24
3		262	1,326.99	7,674.0		65.71
4		357	277.41	1,177.0		73.80
5		414	30.36	111.1		78.08
6		509	23.86	71.0		83.40
7		556	7.00	19.1		85.54
8		9,558	27.28	4.3		112.22
9	▶	10,380	75.00	10.9	Upper Marker	113.00

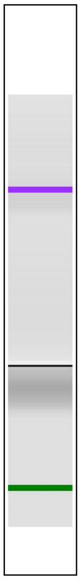
Region table for sample 6 : **HiSeq158 Library - sample 5**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
164	322	1,000	1,356.7	12,861.1	🟦	96	28.3	2,515.72

Electropherogram Summary Continued ...

HiSeq158 Library - sample 6





Overall Results for sample 7 : HiSeq158 Library - sample 6

Number of peaks found:	23	Corr. Area 1:	1,569.5
Noise:	0.8		

Peak table for sample 7 : HiSeq158 Library - sample 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		270	6,542.45	36,723.8		66.43
3		396	35.87	137.1		76.98
4		426	67.11	238.9		78.74
5		469	43.11	139.4		81.18
6		512	47.11	139.5		83.50
7		625	29.20	70.8		88.38
8		645	52.02	122.2		89.00
9		690	27.68	60.8		90.42
10		727	29.34	61.2		91.10
11		848	23.33	41.7		92.69
12		1,456	20.53	21.4		97.63
13		3,414	10.22	4.5		105.06
14		4,448	14.29	4.9		106.42
15		5,653	57.85	15.5		108.01
16		6,170	88.03	21.6		108.69
17		7,937	92.59	17.7		110.67
18		8,771	86.98	15.0		111.47
19	▶	10,380	75.00	10.9	Upper Marker	113.00
20		11,512	0.00	0.0		114.08
21		14,432	0.00	0.0		116.86
22		15,623	0.00	0.0		117.99
23		20,271	0.00	0.0		122.42
24		21,463	0.00	0.0		123.55
25		24,442	0.00	0.0		126.39

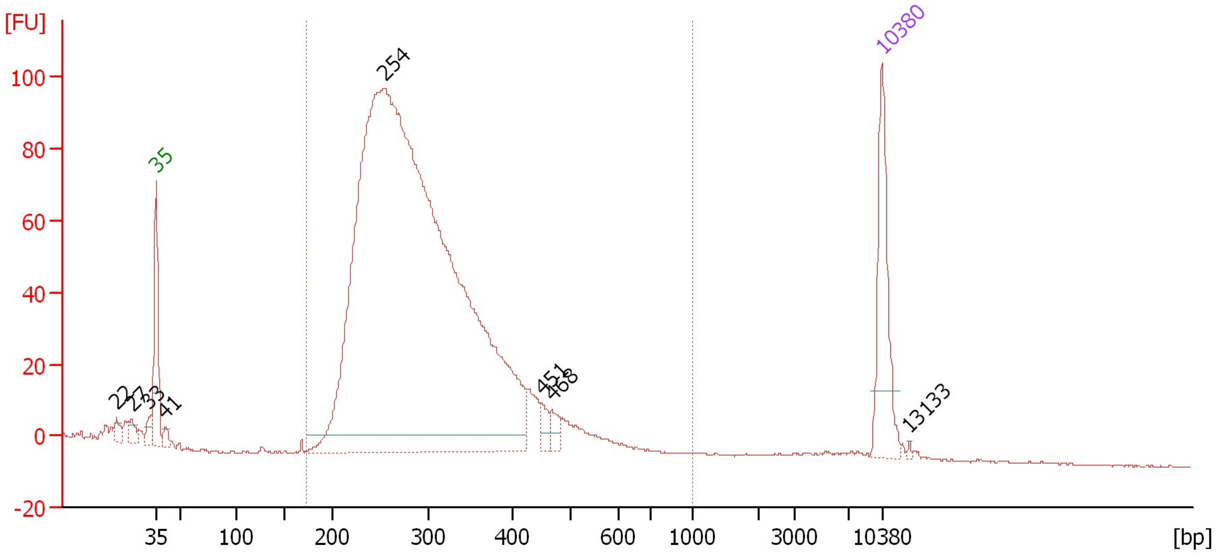
Electropherogram Summary Continued ...

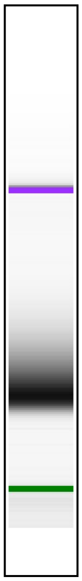
... Region table for sample 7 : HiSeq158 Library - sample 6

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co lor	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	317	1,000	1,569.5	43,666.7	🟦	83	38.9	8,215.88

Electropherogram Summary Continued ...

HiSeq158 Library - sample 7





Overall Results for sample 8 : **HiSeq158 Library - sample 7**

Number of peaks found:	8	Corr. Area 1:	1,658.1
Noise:	0.2		

Peak table for sample 8 : **HiSeq158 Library - sample 7**

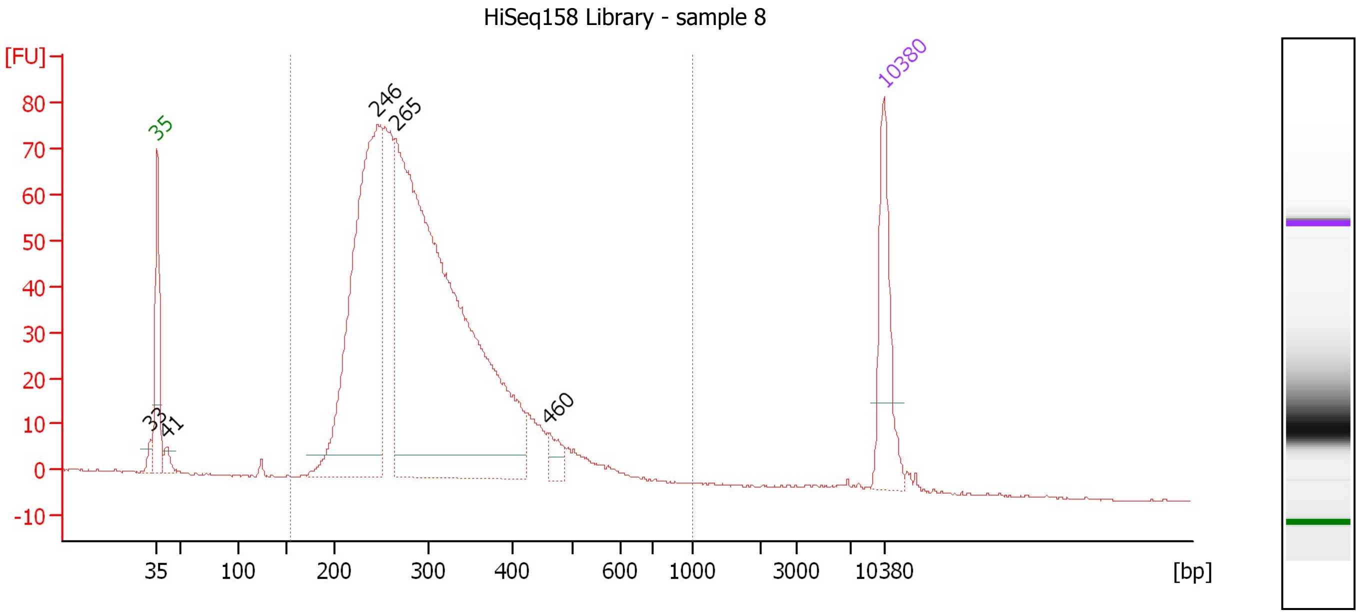
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		22	0.00	0.0		39.20
2		27	0.00	0.0		40.64
3		33	0.00	0.0		42.33
4	◀	35	125.00	5,411.3	Lower Marker	43.00
5		41	11.56	429.9		43.87
6		254	1,959.35	11,678.8		65.00
7		451	12.44	41.8		80.16
8		468	13.02	42.2		81.14
9	▶	10,380	75.00	10.9	Upper Marker	113.00
10		13,133	0.00	0.0		115.62

Region table for sample 8 : **HiSeq158 Library - sample 7**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
171	301	1,000	1,658.1	9,865.1	🟦	97	23.9	1,844.88

Assay Class:	High Sensitivity DNA Assay	Created:	8/6/2015 3:53:09 PM
Data Path:	C:\...ings\Bioanalyzer\2015-08-06\2015-08-06_002_HiSeq158Libs.xad	Modified:	8/6/2015 5:10:43 PM

Electropherogram Summary Continued ...



Overall Results for sample 9 : HiSeq158 Library - sample 8

Number of peaks found:	5	Corr. Area 1:	1,378.7
Noise:	0.2		

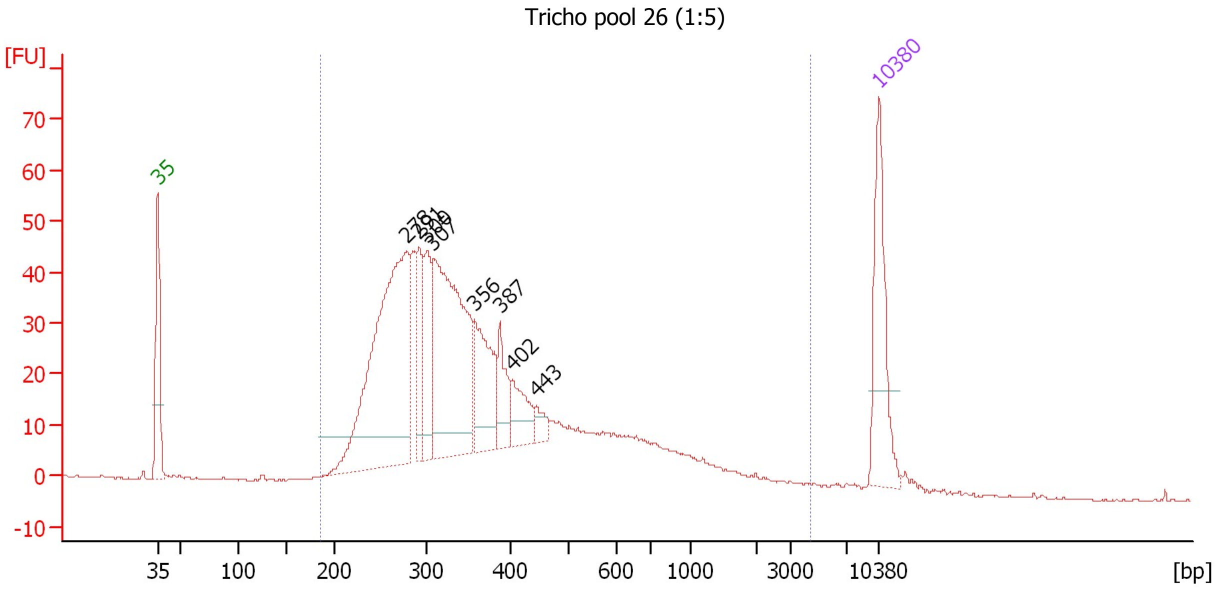
Peak table for sample 9 : HiSeq158 Library - sample 8

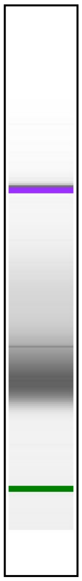
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.33
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		41	16.18	601.7		43.87
4		246	529.09	3,264.7		64.21
5		265	1,019.89	5,836.8		65.96
6		460	20.52	67.6		80.70
7	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : HiSeq158 Library - sample 8

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
154	305	1,000	1,378.7	9,440.6	🟦	97	27.9	1,761.25

Electropherogram Summary Continued ...


Tricho pool 26 (1:5)



Overall Results for sample 10 : **Tricho pool 26 (1:5)**

Number of peaks found:	8	Corr. Area 1:	1,061.1
Noise:	0.1		

Peak table for sample 10 : **Tricho pool 26 (1:5)**

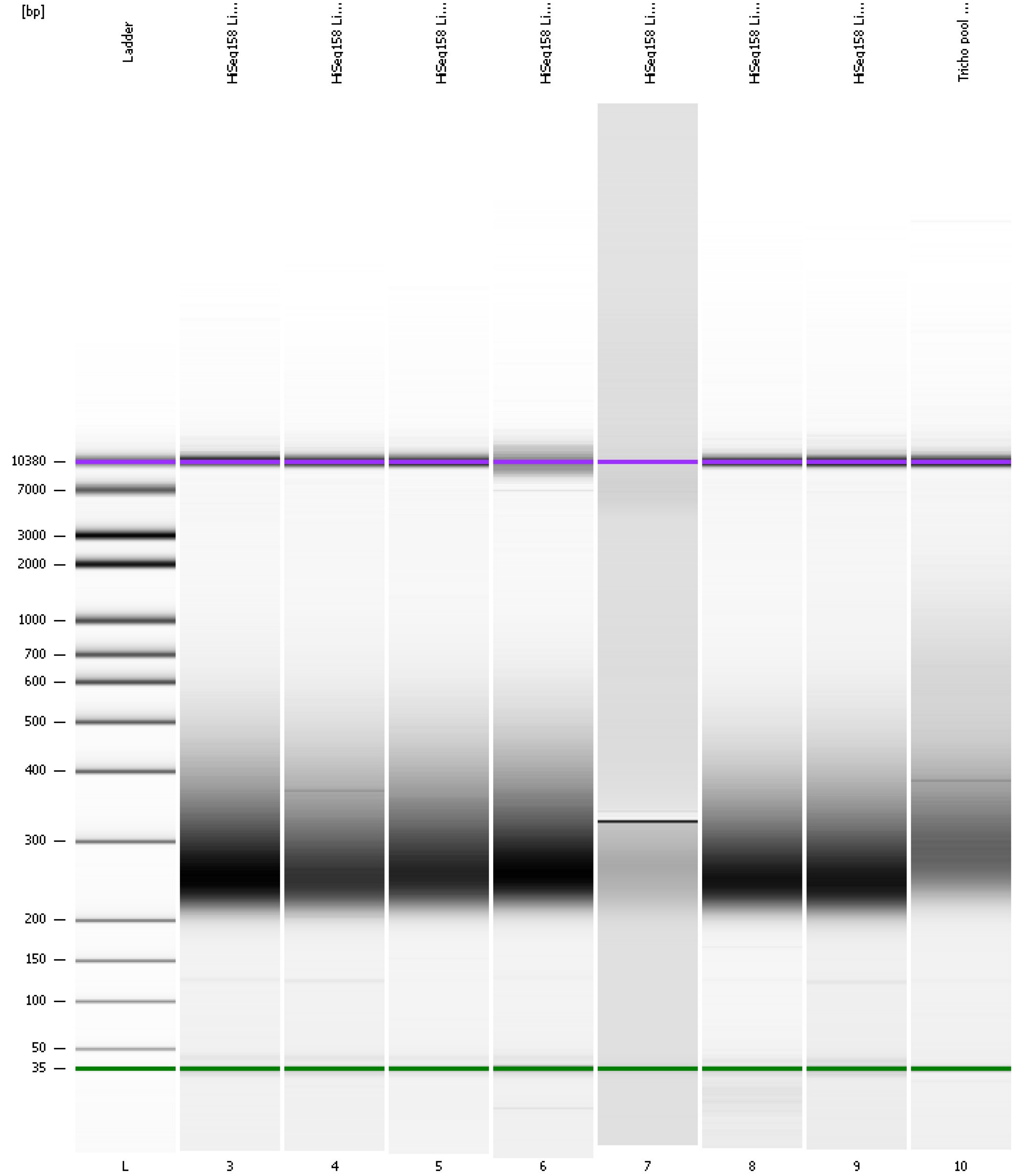
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		278	366.46	1,997.3		67.16
3		291	58.99	307.1		68.35
4		300	69.45	351.2		69.13
5		307	266.04	1,312.1		69.75
6		356	87.98	374.1		73.73
7		387	38.78	151.9		76.22
8		402	36.94	139.2		77.41
9		443	11.89	40.6		79.73
10	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : **Tricho pool 26 (1:5)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]	Conc. [pg/µl]
187	449	4,460	1,061.1	6,597.3	🟦 98	86.6	1,447.74

Assay Class:	High Sensitivity DNA Assay	Created:	8/6/2015 3:53:09 PM
Data Path:	C:\...ings\Bioanalyzer\2015-08-06\2015-08-06_002_HiSeq158Libs.xad	Modified:	8/6/2015 5:10:43 PM

Gel Image



Printed: 8/6/2015 5:13:15 PM