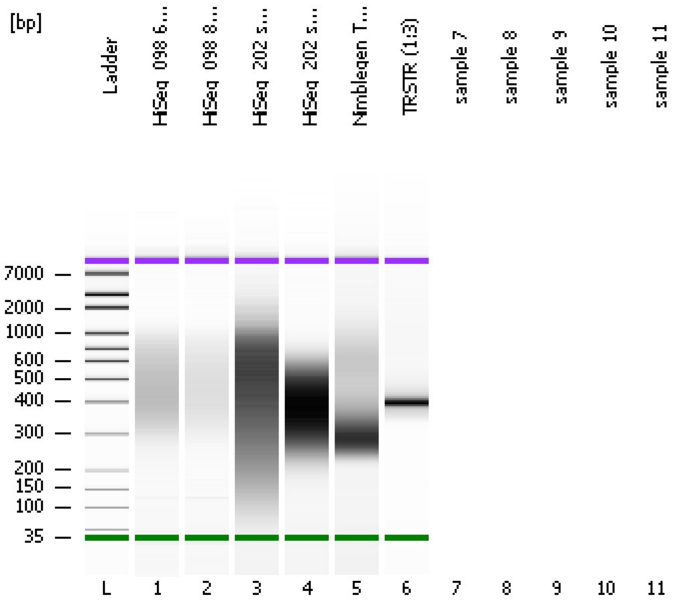
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-04\2015-09-04_002.xad

Created: 9/4/2015 4:25:22 PM
Modified: 9/4/2015 4:56:56 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

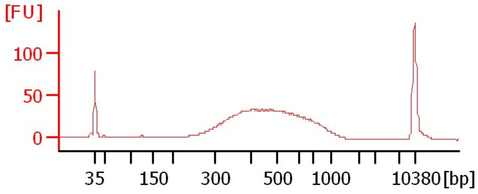
Chip Information:

Chip Lot #:

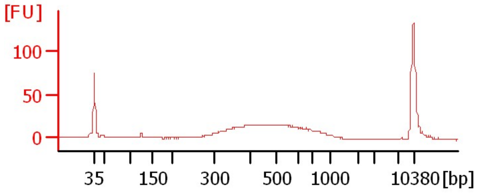
Reagent Kit Lot #:

Chip Comments:

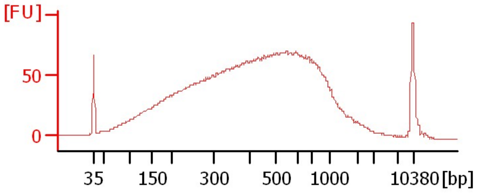
HiSeq_098 6kb lib (0.75X)



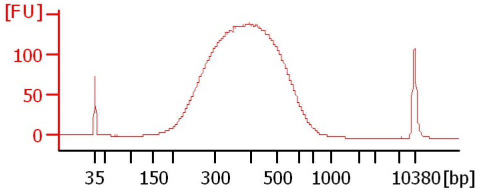
HiSeq_098 8kb lib (0.75X)



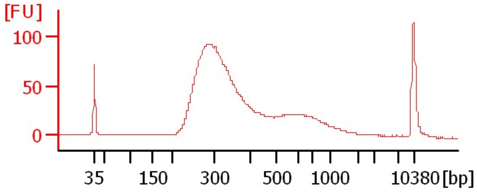
HiSeq_202 soni 1 (1:5)



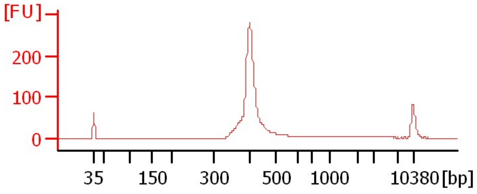
HiSeq_202 size sel soni 1 (1:3)



Nimblegen Test Exome Capture Library ...



TRSTR (1:3)



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-04\2015-09-04_002.xad

Created: 9/4/2015 4:25:22 PM
Modified: 9/4/2015 4:56:56 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq_098 6kb lib (0.75X)		☐	✓			
HiSeq_098 8kb lib (0.75X)		☐	✓			
HiSeq_202 soni 1 (1:5)		☐	✓			
HiSeq_202 size sel soni 1 (1:3)		☐	✓			
Nimblegen Test Exome Capture Library (1:20)		☐	✓			
TRSTR (1:3)		☐	✓			
sample 7		☐				
sample 8		☐				
sample 9		☐				
sample 10		☐				
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

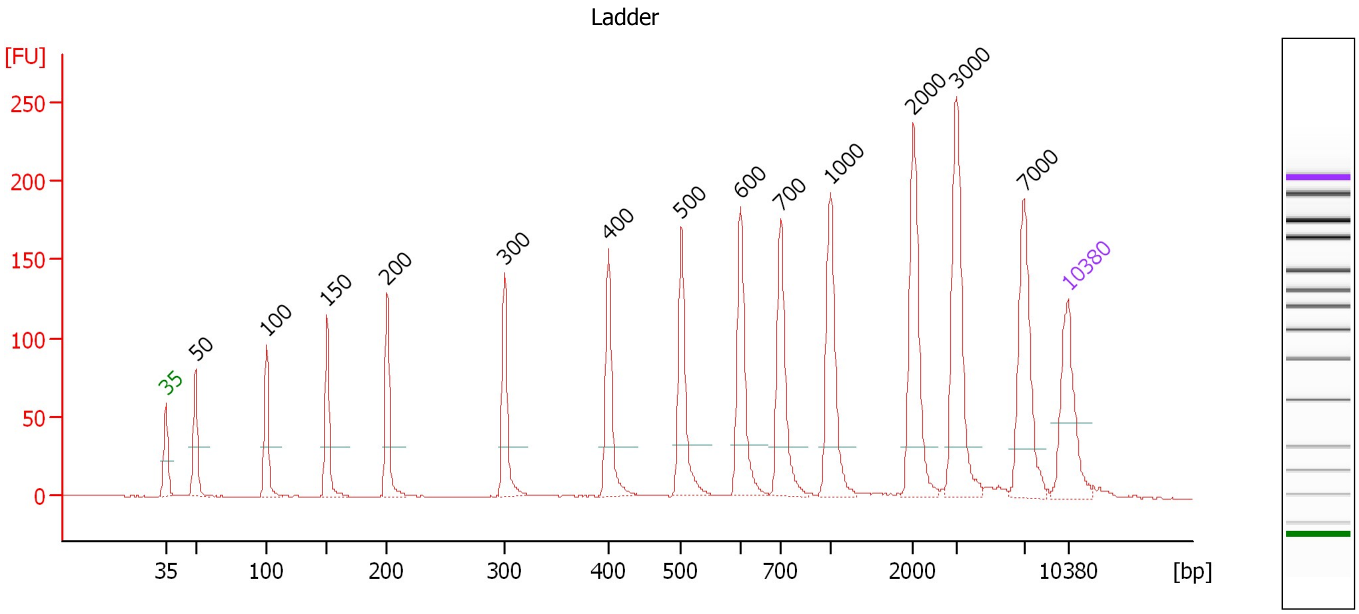
Filter Settings

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

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

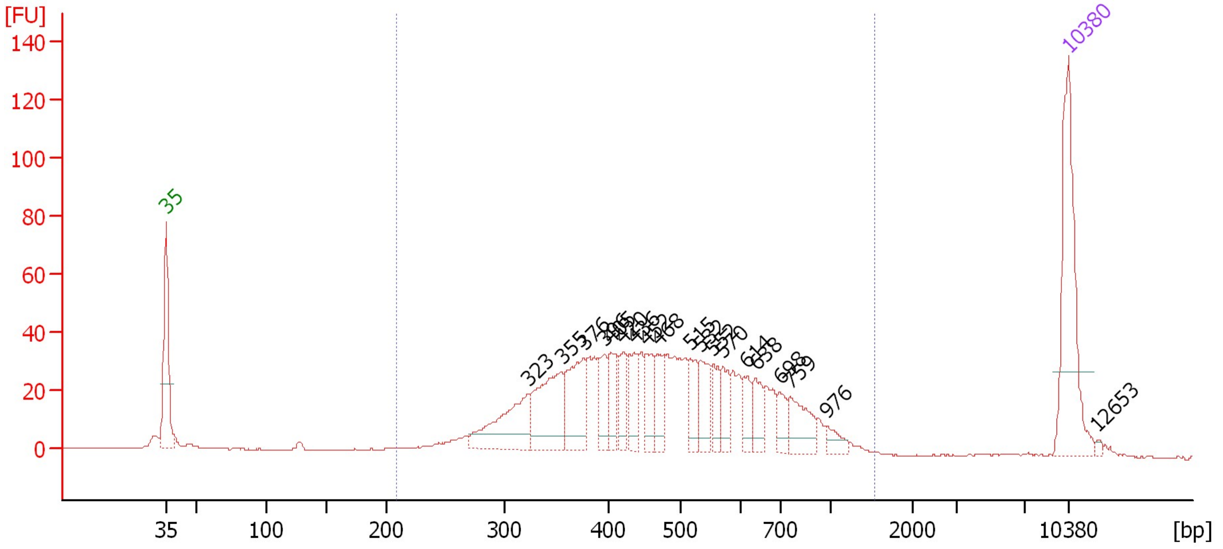
Peak table for Ladder

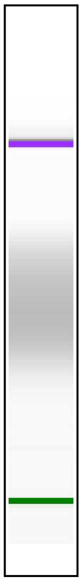
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	L	50	150.00	4,545.5	Ladder Peak	45.27
3	L	100	150.00	2,272.7	Ladder Peak	50.77
4	L	150	150.00	1,515.2	Ladder Peak	55.51
5	L	200	150.00	1,136.4	Ladder Peak	60.16
6	L	300	150.00	757.6	Ladder Peak	69.26
7	L	400	150.00	568.2	Ladder Peak	77.31
8	L	500	150.00	454.5	Ladder Peak	83.00
9	L	600	150.00	378.8	Ladder Peak	87.60
10	L	700	150.00	324.7	Ladder Peak	90.68
11	L	1,000	150.00	227.3	Ladder Peak	94.56
12	L	2,000	150.00	113.6	Ladder Peak	101.01
13	L	3,000	150.00	75.8	Ladder Peak	104.37
14	L	7,000	150.00	32.5	Ladder Peak	109.59
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-04\2015-09-04_002.xad
Created: 9/4/2015 4:25:22 PM
Modified: 9/4/2015 4:56:56 PM

Electropherogram Summary Continued ...

HiSeq_098 6kb lib (0.75X)





Overall Results for sample 1 : HiSeq_098 6kb lib (0.75X)

Number of peaks found: 19
Corr. Area 1: 942.3
Noise: 0.2

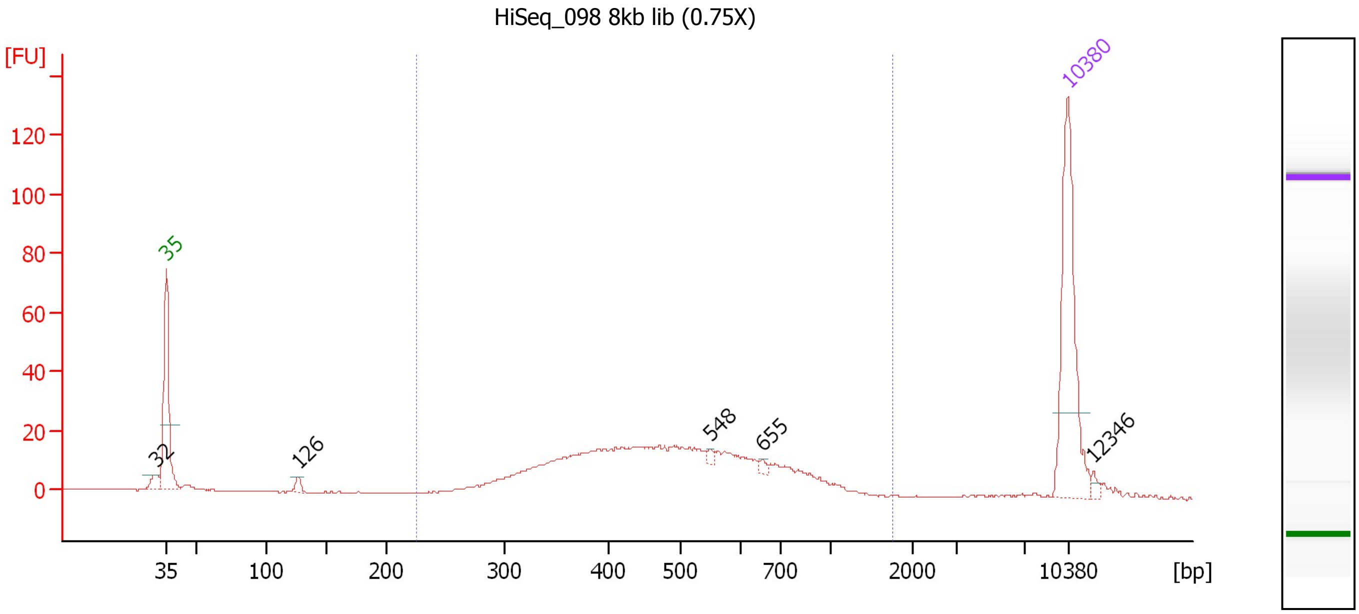
Peak table for sample 1 : HiSeq_098 6kb lib (0.75X)

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		323	65.46	307.0		71.11
3		355	68.55	292.5		73.70
4		376	51.06	205.5		75.42
5		396	22.35	85.5		77.00
6		405	24.18	90.6		77.57
7		420	22.33	80.5		78.48
8		436	25.26	87.9		79.34
9		452	23.30	78.0		80.30
10		468	23.03	74.6		81.16
11		515	20.78	61.1		83.69
12		532	26.44	75.4		84.45
13		552	17.06	46.8		85.41
14		570	17.23	45.8		86.22
15		614	13.88	34.2		88.04
16		638	18.87	44.8		88.76
17		698	13.28	28.8		90.62
18		759	27.86	55.6		91.44
19		976	8.41	13.0		94.26
20	▶	10,380	75.00	10.9	Upper Marker	113.00
21		12,653	0.00	0.0		115.30

Region table for sample 1 : HiSeq_098 6kb lib (0.75X)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
208	499	1,534	942.3	2,497.0	🟦	95	35.8	713.15

Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq_098 8kb lib (0.75X)

Number of peaks found:	5	Corr. Area 1:	425.0
Noise:	0.2		

Peak table for sample 2 : HiSeq_098 8kb lib (0.75X)

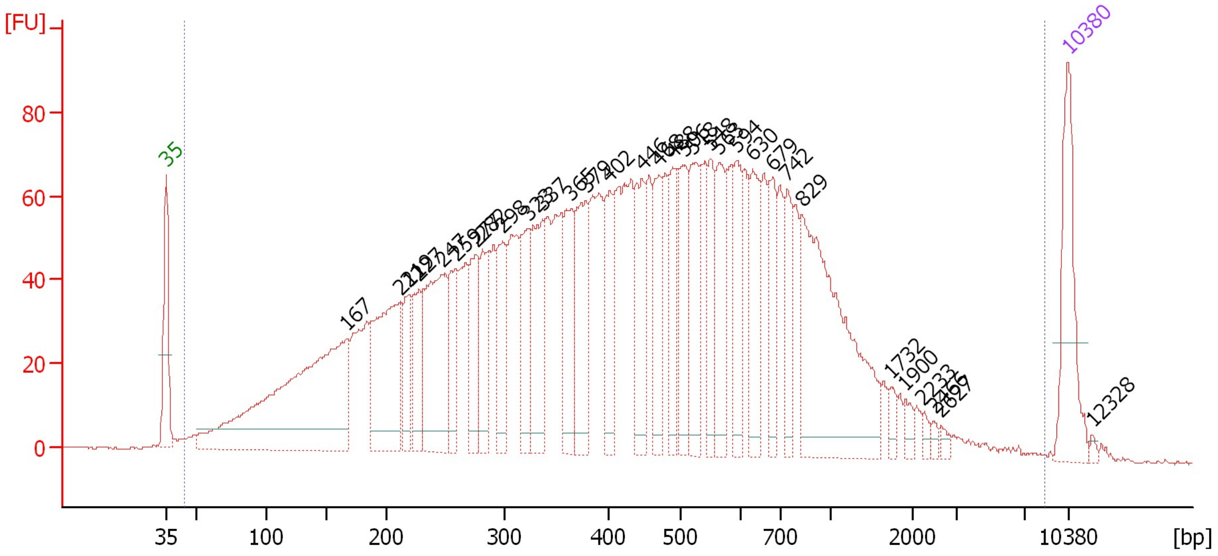
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.18
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		126	5.38	64.6		53.26
4		548	2.46	6.8		85.21
5		655	2.30	5.3		89.28
6	▶	10,380	75.00	10.9	Upper Marker	113.00
7		12,346	0.00	0.0		114.98

Region table for sample 2 : HiSeq_098 8kb lib (0.75X)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
225	512	1,739	425.0	1,066.7	🟦	91	35.7	314.61

Electropherogram Summary Continued ...

HiSeq_202 soni 1 (1:5)



Overall Results for sample 3 : **HiSeq_202 soni 1 (1:5)**

Number of peaks found:	32	Corr. Area 1:	3,309.8
Noise:	0.2		

Peak table for sample 3 : **HiSeq_202 soni 1 (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		167	449.55	4,087.1		57.06
3		211	189.29	1,360.6		61.14
4		219	54.40	376.6		61.88
5		227	67.83	452.7		62.61
6		247	172.62	1,058.9		64.43
7		259	66.34	388.3		65.51
8		277	77.20	422.7		67.14
9		282	74.03	398.4		67.58
10		298	69.59	353.4		69.10
11		323	74.25	348.9		71.07
12		337	106.21	478.2		72.20
13		365	78.43	325.9		74.46
14		379	96.18	384.9		75.59
15		402	72.69	274.2		77.41
16		446	78.00	265.1		79.92
17		468	64.45	208.5		81.20
18		488	60.67	188.3		82.33
19		506	78.76	236.0		83.26
20		518	87.06	254.4		83.85
21		548	57.22	158.1		85.23
22		563	72.44	194.8		85.91
23		594	61.66	157.2		87.34
24		630	70.76	170.2		88.52
25		679	53.90	120.2		90.04

Electropherogram Summary Continued ...

... Peak table for sample 3 : HiSeq 202 soni 1 (1:5)

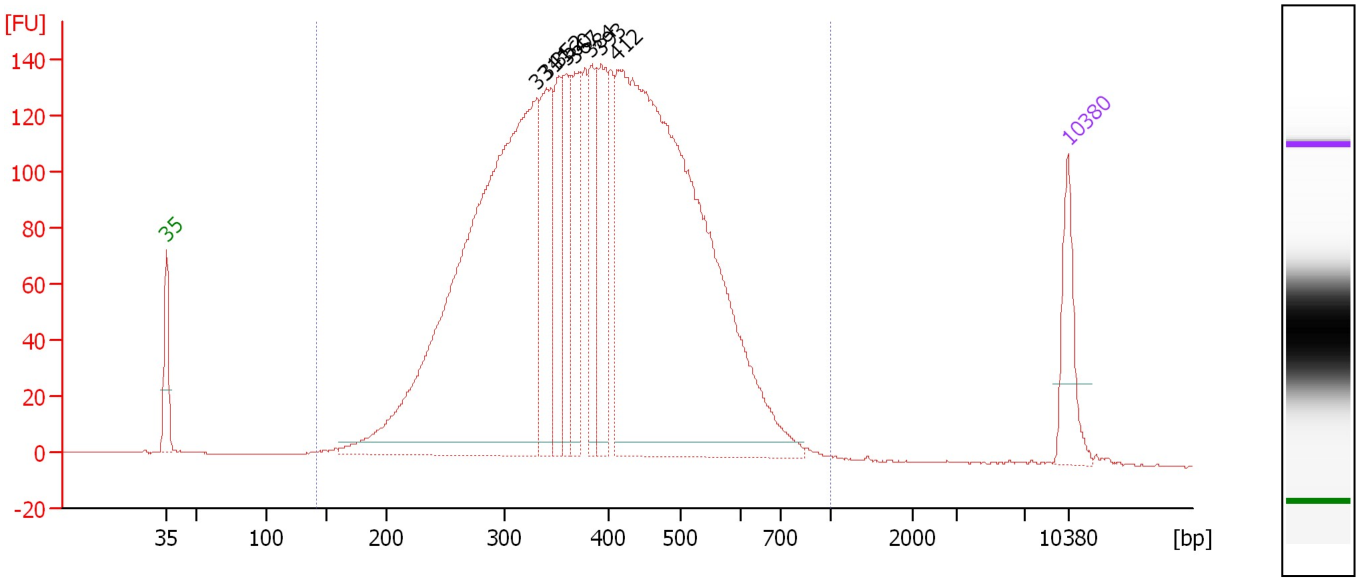
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	742	50.07	102.2		91.22
27	829	252.24	460.8		92.35
28	1,732	9.99	8.7		99.29
29	1,900	8.27	6.6		100.37
30	2,233	5.36	3.6		101.79
31	2,466	4.55	2.8		102.58
32	2,627	4.56	2.6		103.12
33 ▶	10,380	75.00	10.9	Upper Marker	113.00
34	12,328	0.00	0.0		114.97

Region table for sample 3 : HiSeq 202 soni 1 (1:5)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
45	557	8,636	3,309.8	21,328.3	🟦	99	100.0	3,948.32

Electropherogram Summary Continued ...

HiSeq_202 size sel soni 1 (1:3)



Overall Results for sample 4 : **HiSeq_202 size sel soni 1 (1:3)**

Number of peaks found:	8	Corr. Area 1:	3,826.3
Noise:	0.1		

Peak table for sample 4 : **HiSeq_202 size sel soni 1 (1:3)**

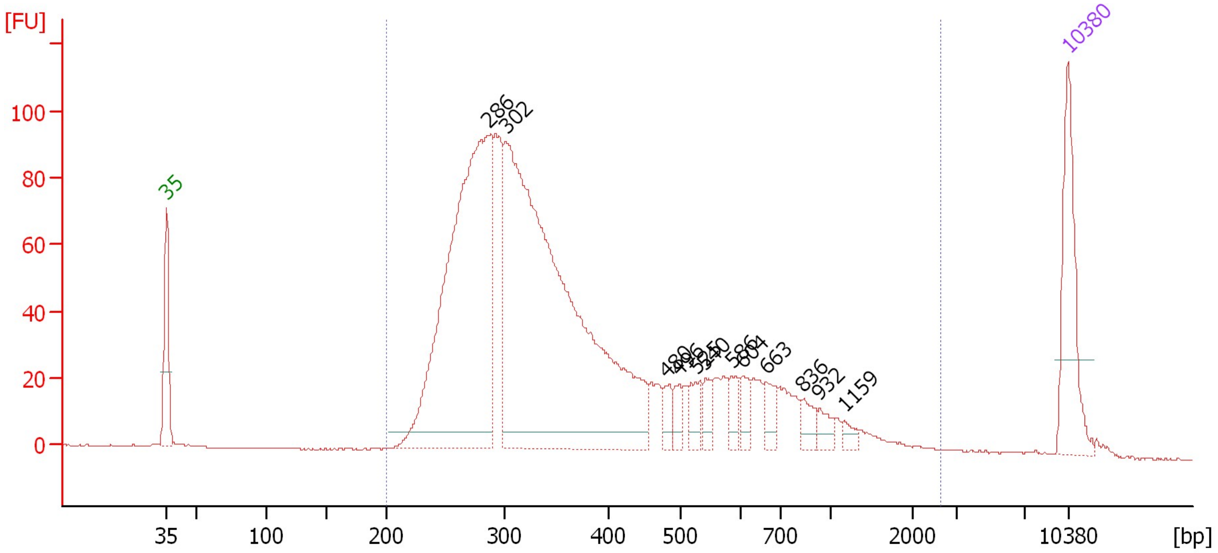
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		331	1,368.28	6,265.4		71.74
3		341	222.44	989.1		72.54
4		352	142.01	610.5		73.48
5		360	131.43	553.4		74.08
6		367	149.83	618.1		74.67
7		384	136.97	540.6		76.01
8		393	172.19	663.6		76.76
9		412	1,483.05	5,452.9		78.00
10	▶	10,380	75.00	10.9	Upper Marker	113.00

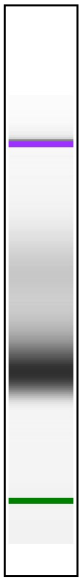
Region table for sample 4 : **HiSeq_202 size sel soni 1 (1:3)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
142	395	1,000	3,826.3	17,754.3	■	100	27.2	4,150.55

Electropherogram Summary Continued ...

Nimblegen Test Exome Capture Library (1:20)





Overall Results for sample 5 : **Nimblegen Test Exome Capture Library (1:20)**

Number of peaks found:	12	Corr. Area 1:	1,857.3
Noise:	0.1		

Peak table for sample 5 : **Nimblegen Test Exome Capture Library (1:20)**

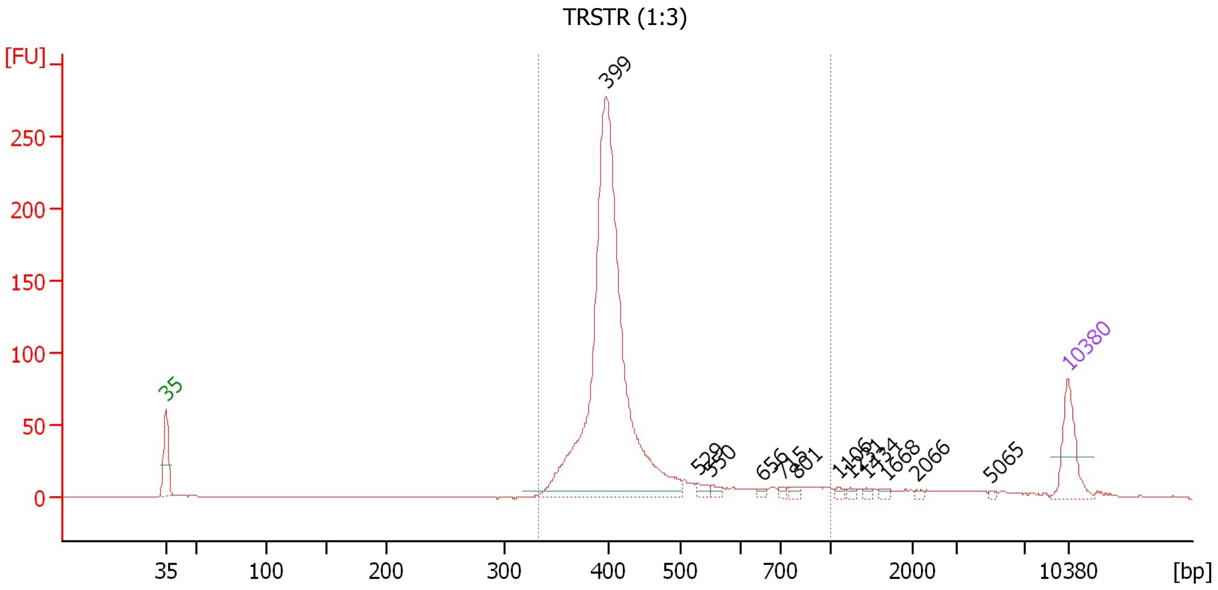
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		286	575.49	3,050.4		67.97
3		302	826.83	4,147.9		69.42
4		480	16.33	51.5		81.88
5		496	15.12	46.2		82.78
6		525	21.61	62.4		84.13
7		540	16.71	46.9		84.83
8		586	16.19	41.9		86.93
9		604	15.77	39.5		87.73
10		663	18.28	41.8		89.53
11		836	15.60	28.3		92.44
12		932	12.60	20.5		93.69
13		1,159	6.97	9.1		95.59
14	▶	10,380	75.00	10.9	Upper Marker	113.00

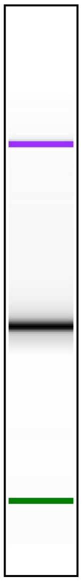
Region table for sample 5 : **Nimblegen Test Exome Capture Library (1:20)**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	427	2,619	1,857.3	8,285.0	🟦	98	63.8	1,837.80

Electropherogram Summary Continued ...

TRSTR (1:3)





Overall Results for sample 6 : TRSTR (1:3)

Number of peaks found:	12	Corr. Area 1:	1,094.6
Noise:	0.2		

Peak table for sample 6 : TRSTR (1:3)

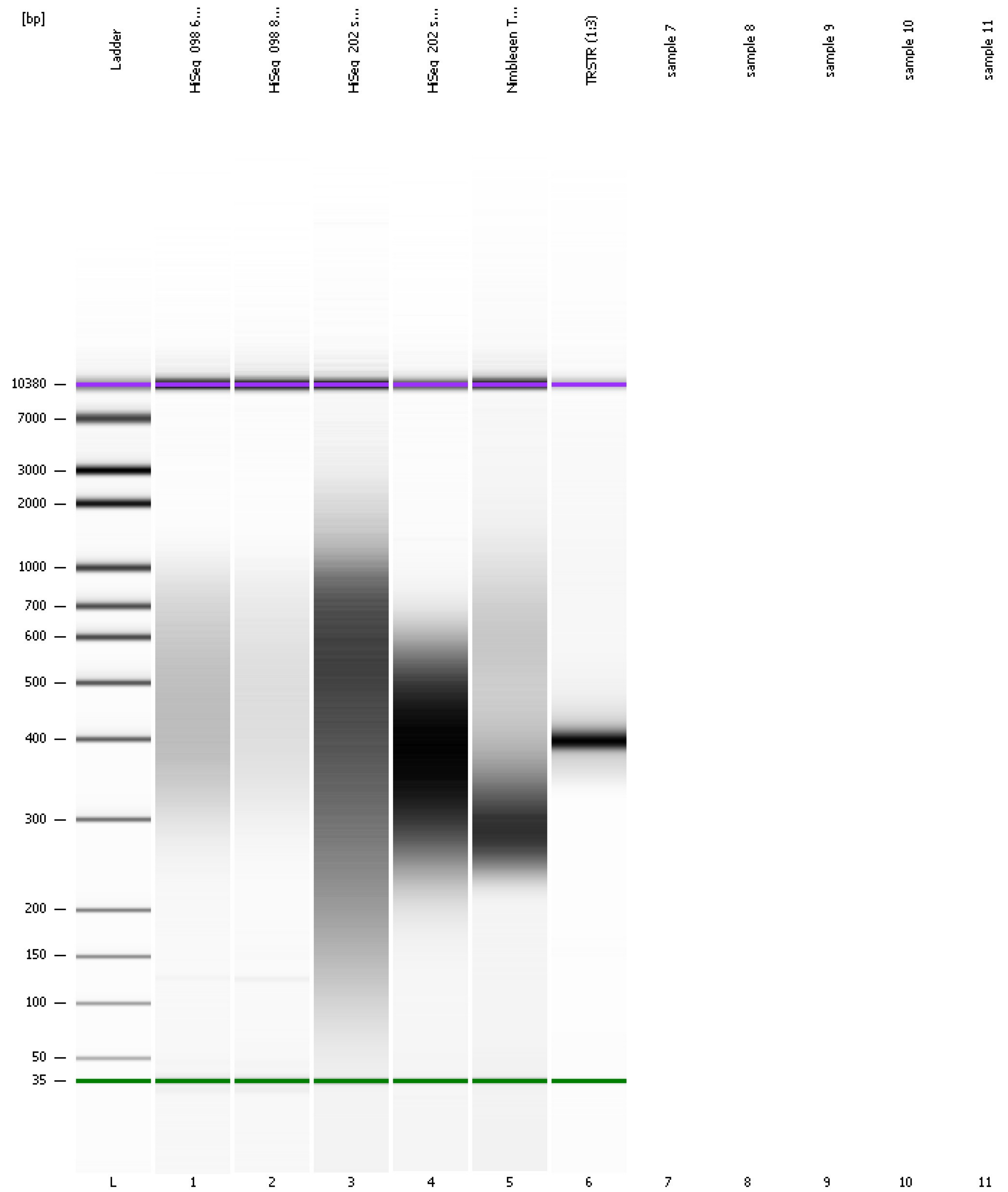
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		399	1,239.25	4,711.3		77.20
3		529	13.48	38.6		84.34
4		550	10.62	29.3		85.29
5		656	6.72	15.5		89.31
6		715	6.26	13.3		90.87
7		801	8.84	16.7		91.98
8		1,106	5.04	6.9		95.25
9		1,231	5.53	6.8		96.05
10		1,434	4.42	4.7		97.36
11		1,668	5.33	4.8		98.87
12		2,066	3.59	2.6		101.23
13		5,065	2.87	0.9		107.07
14	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : TRSTR (1:3)

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]	Conc. [pg/µl]
332	434	1,000	1,094.6	4,994.4	🟦 88	22.9	1,373.96

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-04\2015-09-04_002.xad
Created: 9/4/2015 4:25:22 PM
Modified: 9/4/2015 4:56:56 PM

Gel Image



Invalid Samples

Sample 7 has not been run, no results available.

Sample 8 has not been run, no results available.

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.