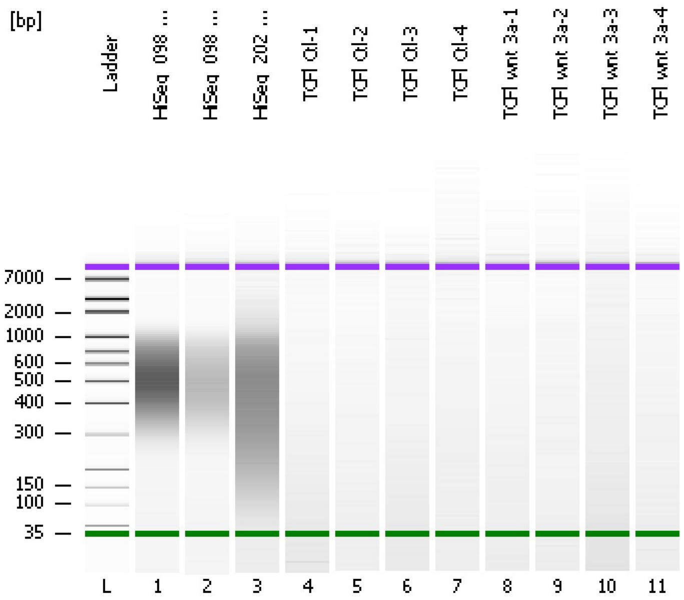
Assay Class:	High Sensitivity DNA Assay	Created:	9/8/2015 11:15:54 AM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-09-08\2015-09-08_001.xad	Modified:	9/8/2015 11:57:14 AM

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

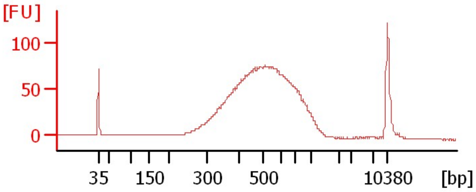
Chip Information:

Chip Lot #:

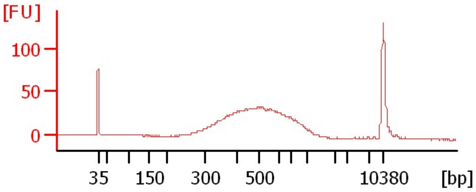
Reagent Kit Lot #:

Chip Comments:

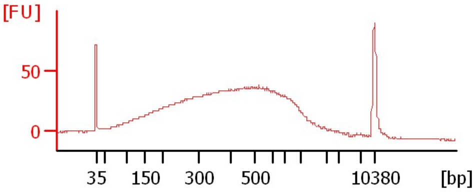
HiSeq_098 Mate Pair Library 6kb



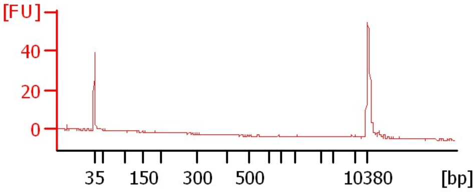
HiSeq_098 Mate Pair Library 8kb



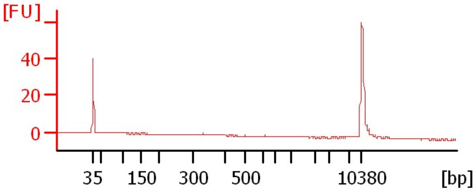
HiSeq_202 #2 soni



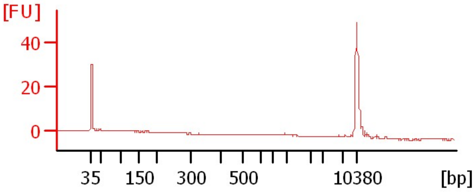
TCFl Ctl-1



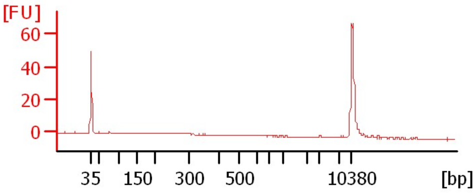
TCFl Ctl-2



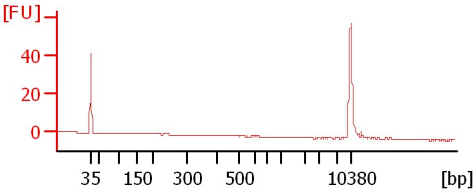
TCFl Ctl-3



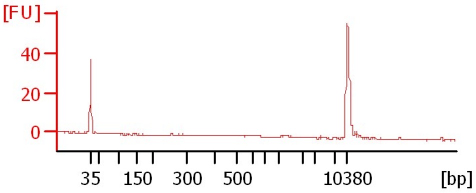
TCFl Ctl-4



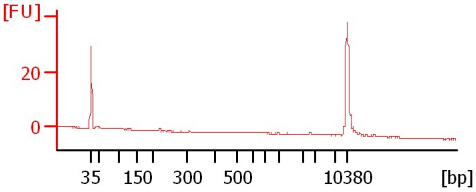
TCFl wnt 3a-1



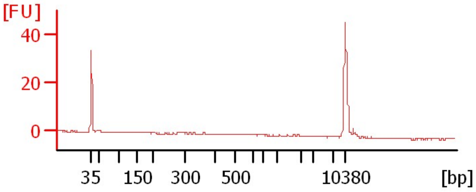
TCFl wnt 3a-2



TCFl wnt 3a-3



TCFl wnt 3a-4



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-08\2015-09-08_001.xad
Created: 9/8/2015 11:15:54 AM
Modified: 9/8/2015 11:57:14 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
HiSeq_098 Mate Pair Library 6kb		☐	✓			
HiSeq_098 Mate Pair Library 8kb		☐	✓			
HiSeq_202 #2 soni		☐	✓			
TCFl Ctl-1		☐	✓			
TCFl Ctl-2		☐	✓			
TCFl Ctl-3		☐	✓			
TCFl Ctl-4		☐	✓			
TCFl wnt 3a-1		☐	✓			
TCFl wnt 3a-2		☐	✓			
TCFl wnt 3a-3		☐	✓			
TCFl wnt 3a-4		☐	✓			
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

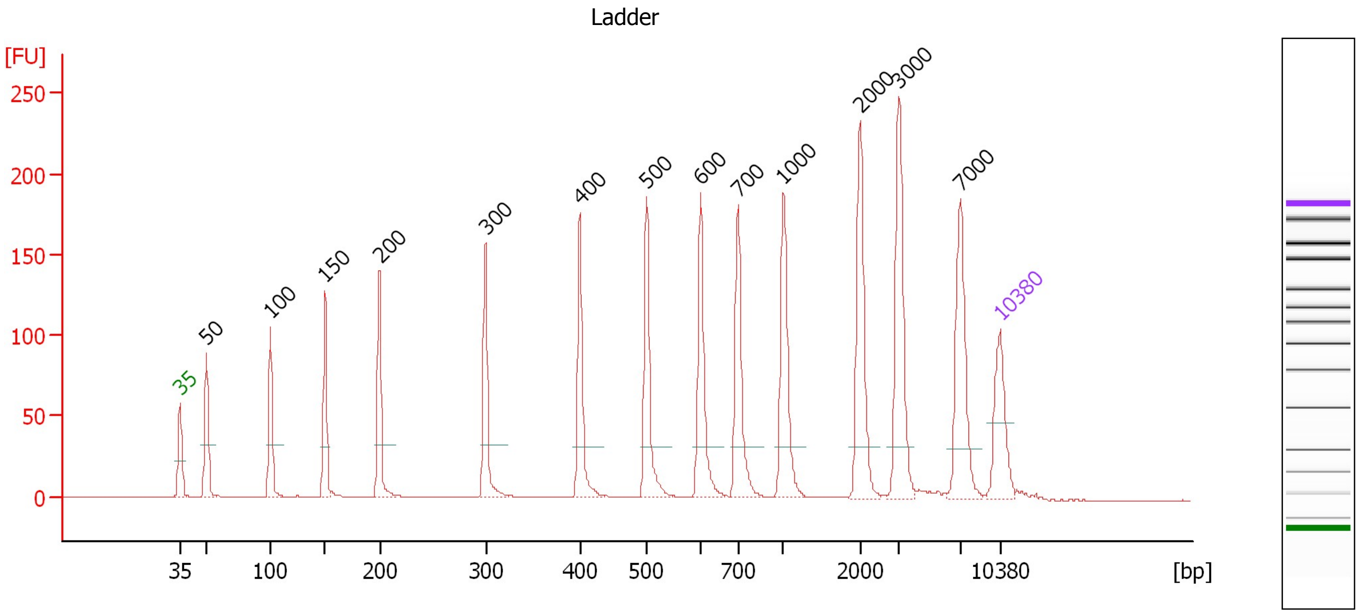
Filter Width [s] : 0.5
Polynomial Order : 4

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:\...ents and Settings\Bioanalyzer\2015-09-08\2015-09-08_001.xad
Created: 9/8/2015 11:15:54 AM
Modified: 9/8/2015 11:57:14 AM

Electropherogram Summary



Overall Results for Ladder

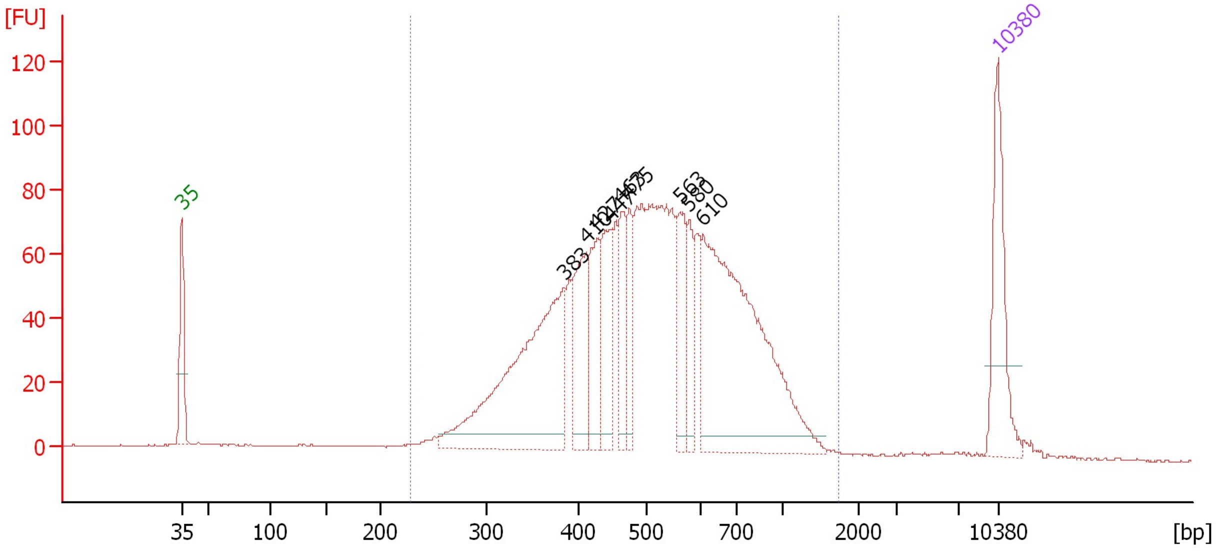
Noise: 0.1

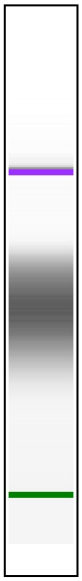
Peak table for Ladder

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	∟	50	150.00	4,545.5	Ladder Peak	45.27
3	∟	100	150.00	2,272.7	Ladder Peak	50.69
4	∟	150	150.00	1,515.2	Ladder Peak	55.37
5	∟	200	150.00	1,136.4	Ladder Peak	60.01
6	∟	300	150.00	757.6	Ladder Peak	69.06
7	∟	400	150.00	568.2	Ladder Peak	77.11
8	∟	500	150.00	454.5	Ladder Peak	82.80
9	∟	600	150.00	378.8	Ladder Peak	87.44
10	∟	700	150.00	324.7	Ladder Peak	90.62
11	∟	1,000	150.00	227.3	Ladder Peak	94.49
12	∟	2,000	150.00	113.6	Ladder Peak	101.04
13	∟	3,000	150.00	75.8	Ladder Peak	104.31
14	∟	7,000	150.00	32.5	Ladder Peak	109.59
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

HiSeq_098 Mate Pair Library 6kb





Overall Results for sample 1 : **HiSeq_098 Mate Pair Library 6kb**

Number of peaks found:	9	Corr. Area 1:	1,894.5
Noise:	0.2		

Peak table for sample 1 : **HiSeq_098 Mate Pair Library 6kb**

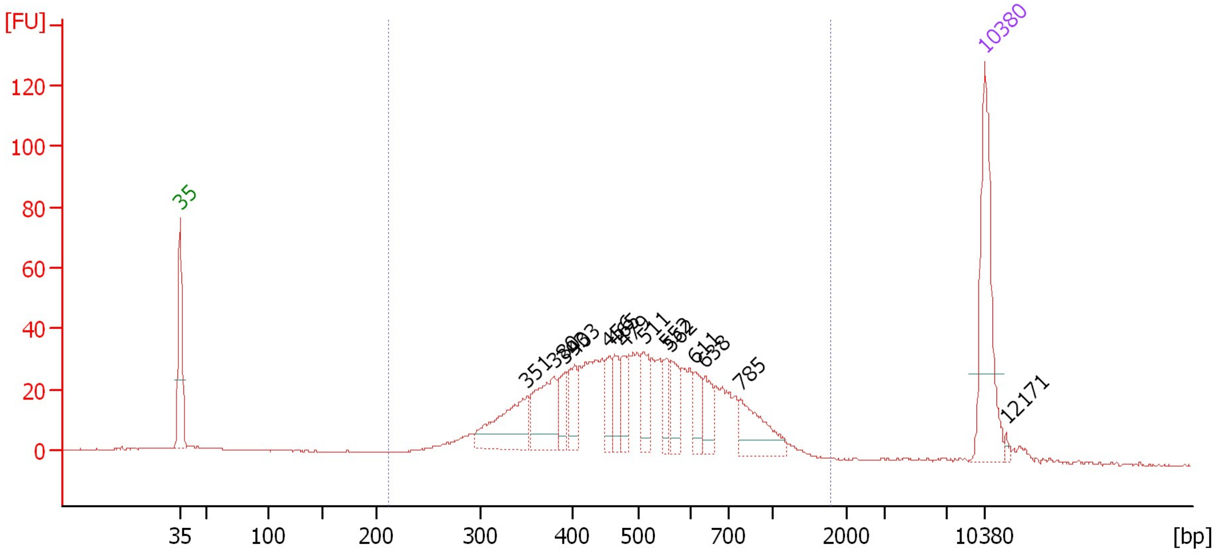
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		383	305.72	1,207.9		75.78
3		410	93.69	345.9		77.70
4		427	72.27	256.3		78.66
5		447	79.11	267.9		79.81
6		463	55.03	179.9		80.72
7		475	47.64	152.0		81.36
8		563	61.64	166.0		85.70
9		580	45.09	117.7		86.53
10		610	346.34	860.0		87.76
11	▶	10,380	75.00	10.9	Upper Marker	113.00

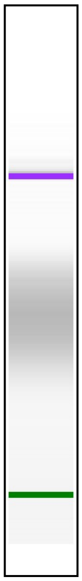
Region table for sample 1 : **HiSeq_098 Mate Pair Library 6kb**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
229	541	1,740	1,894.5	5,076.9	🟦	96	35.9	1,572.04

Electropherogram Summary Continued ...

HiSeq_098 Mate Pair Library 8kb





Overall Results for sample 2 : **HiSeq_098 Mate Pair Library 8kb**

Number of peaks found:	14	Corr. Area 1:	854.5
Noise:	0.2		

Peak table for sample 2 : **HiSeq_098 Mate Pair Library 8kb**

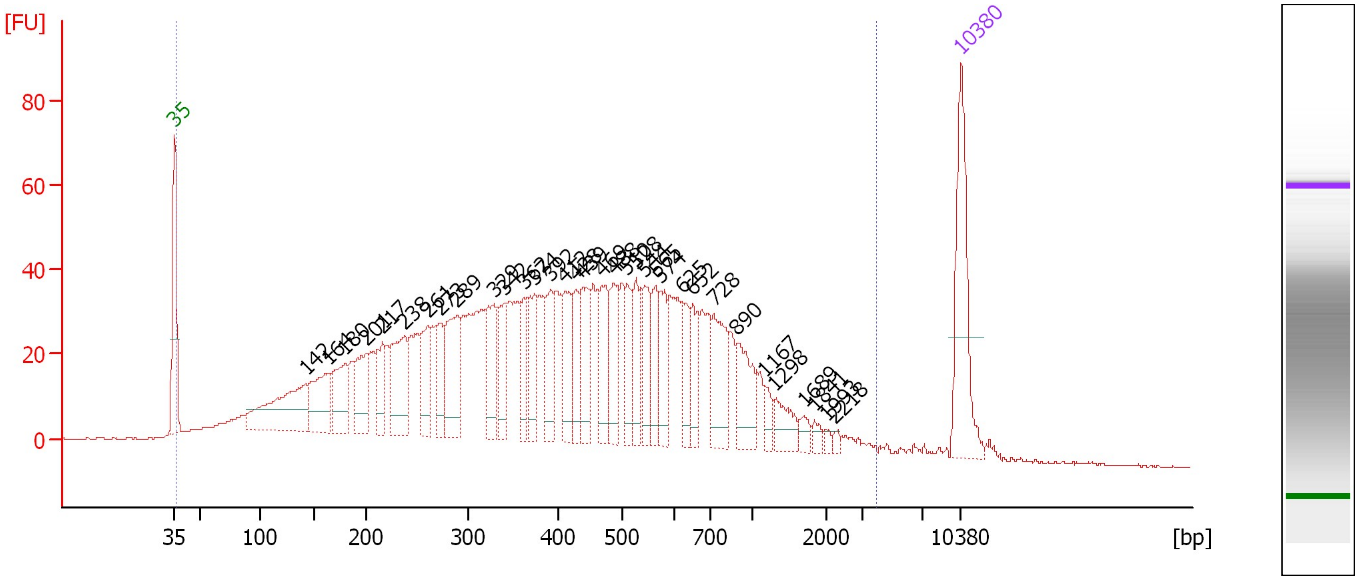
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		351	65.76	284.2		73.13
3		380	59.14	235.9		75.50
4		393	19.43	75.0		76.52
5		403	25.07	94.2		77.30
6		456	21.37	71.0		80.32
7		465	21.49	70.1		80.78
8		479	22.89	72.4		81.62
9		511	27.14	80.4		83.33
10		552	17.61	48.3		85.23
11		562	22.98	61.9		85.70
12		611	19.32	47.9		87.78
13		638	18.86	44.7		88.66
14		785	41.87	80.8		91.72
15	▶	10,380	75.00	10.9	Upper Marker	113.00
16		12,171	0.00	0.0		114.81

Region table for sample 2 : **HiSeq_098 Mate Pair Library 8kb**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color % of Total	Size distribution in CV [%]	Conc. [pg/µl]
212	525	1,764	854.5	2,322.0	🟦 93	36.2	696.89

Electropherogram Summary Continued ...

HiSeq_202 #2 soni



Overall Results for sample 3 : HiSeq_202 #2 soni

Number of peaks found: 34
Corr. Area 1: 1,984.8
Noise: 0.2

Peak table for sample 3 : HiSeq_202 #2 soni

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		142	118.52	1,264.2		54.63
3		164	71.59	659.4		56.72
4		180	58.85	495.8		58.14
5		201	50.04	376.5		60.13
6		217	40.76	285.2		61.51
7		238	78.72	502.2		63.41
8		261	44.65	259.6		65.49
9		273	40.61	225.3		66.63
10		289	74.36	389.3		68.11
11		329	57.25	263.8		71.38
12		342	38.47	170.6		72.42
13		362	33.35	139.5		74.08
14		374	45.89	185.8		75.03
15		392	47.61	183.8		76.51
16		412	44.41	163.4		77.79
17		428	34.44	122.0		78.69
18		439	47.30	163.1		79.35
19		469	51.53	166.3		81.06
20		488	44.26	137.5		82.11
21		510	33.52	99.7		83.24
22		528	30.70	88.1		84.10
23		544	31.76	88.4		84.86
24		565	30.57	82.0		85.81
25		574	33.67	88.9		86.23

Electropherogram Summary Continued ...

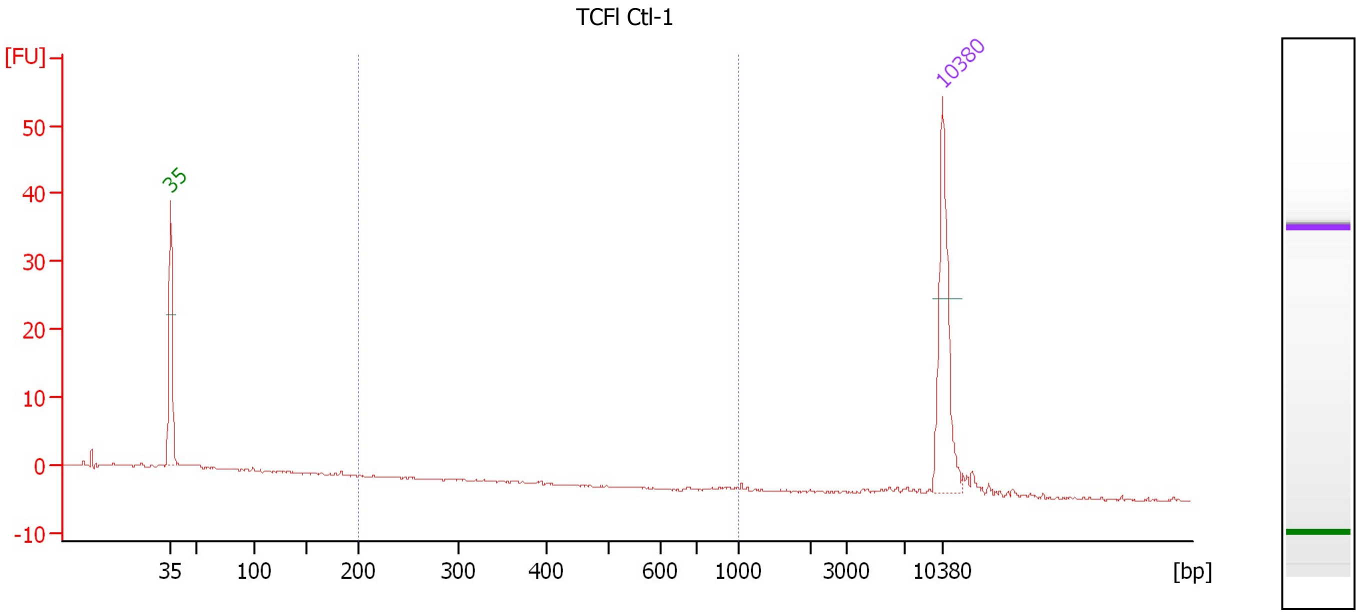
... Peak table for sample 3 : <u>HiSeq_202 #2 soni</u>

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26		625	28.50	69.1		88.23
27		652	25.95	60.3		89.08
28		728	54.49	113.4		90.98
29		890	42.30	72.0		93.07
30		1,167	10.27	13.3		95.58
31		1,298	20.45	23.9		96.44
32		1,689	7.75	7.0		99.00
33		1,841	5.81	4.8		100.00
34		1,993	3.04	2.3		100.99
35		2,218	3.19	2.2		101.75
36	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : <u>HiSeq_202 #2 soni</u>

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
36	499	3,852	1,984.8	14,215.3	🟦	98	81.3	2,394.52

Electropherogram Summary Continued ...



Overall Results for sample 4 : TCFl Ctl-1

Number of peaks found: 0

Corr. Area 1: 0.0

Noise: 0.1

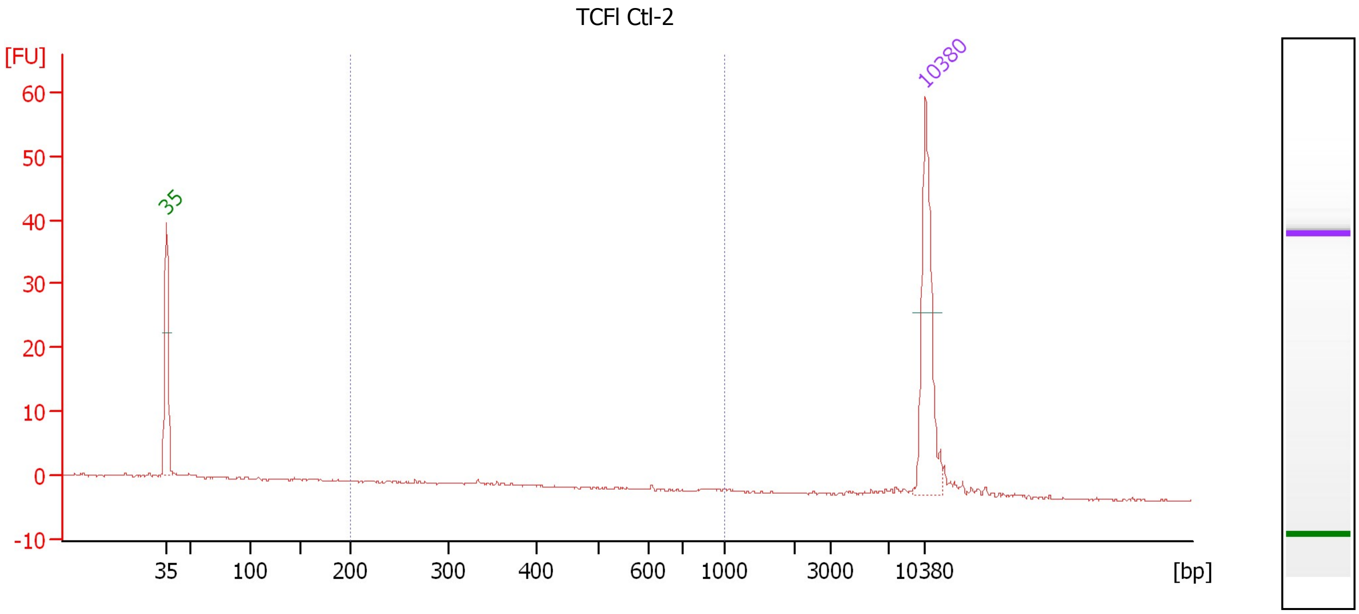
Peak table for sample 4 : TCFl Ctl-1

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : TCFl Ctl-1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	0	1,000	0.0	0.0	■	0	0.0	0.00

Electropherogram Summary Continued ...



Overall Results for sample 5 : TCFl Ctl-2

Number of peaks found:	0	Corr. Area 1:	2.1
Noise:	0.1		

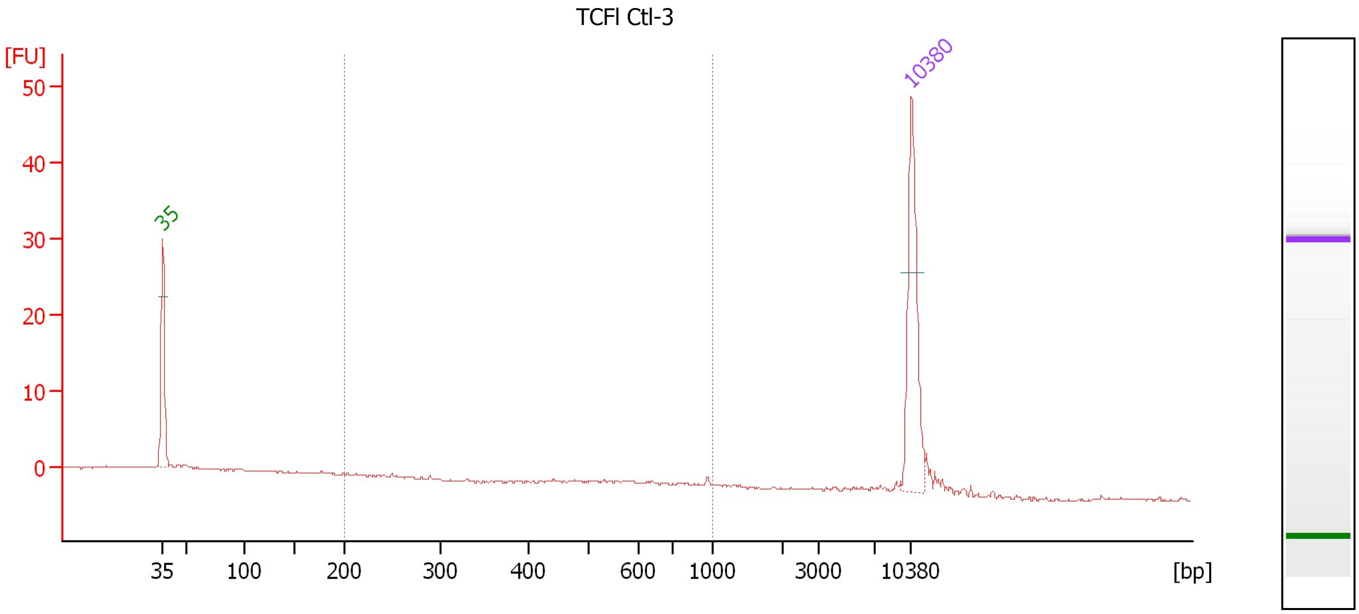
Peak table for sample 5 : TCFl Ctl-2

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : TCFl Ctl-2

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	345	1,000	2.1	20.9	🟦	13	38.3	4.21

Electropherogram Summary Continued ...



Overall Results for sample 6 : TCFl Ctl-3

Number of peaks found:	0	Corr. Area 1:	2.4
Noise:	0.1		

Peak table for sample 6 : TCFl Ctl-3

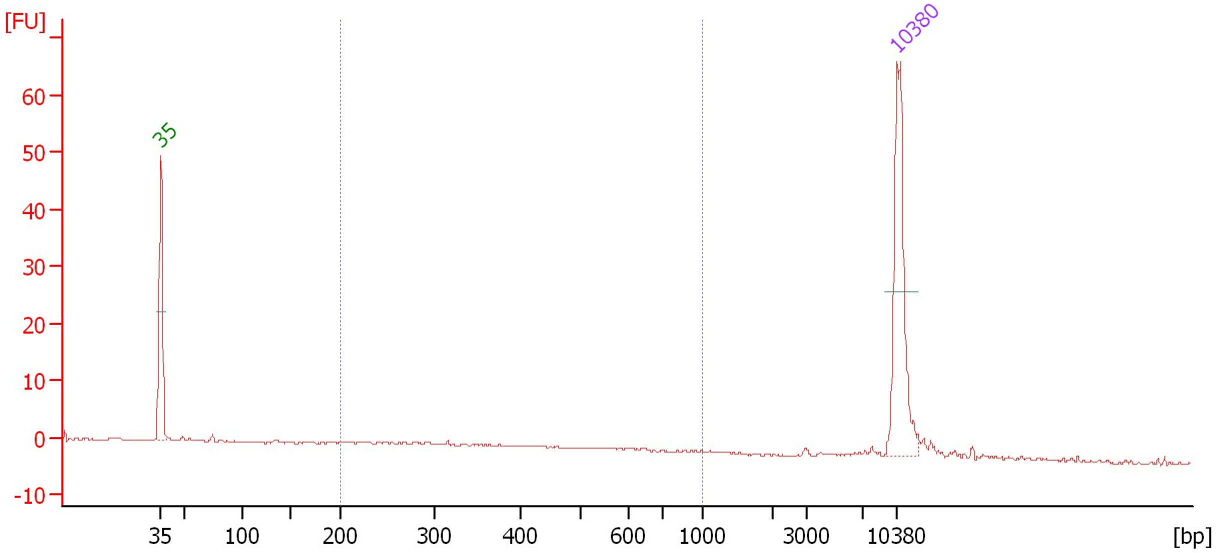
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

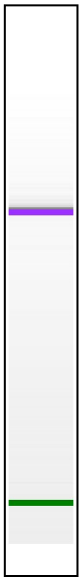
Region table for sample 6 : TCFl Ctl-3

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	609	1,000	2.4	20.3	■	11	39.8	5.56

Electropherogram Summary Continued ...

TCFl Ctl-4





Overall Results for sample 7 : TCFl Ctl-4

Number of peaks found:	0	Corr. Area 1:	25.7
Noise:	0.1		

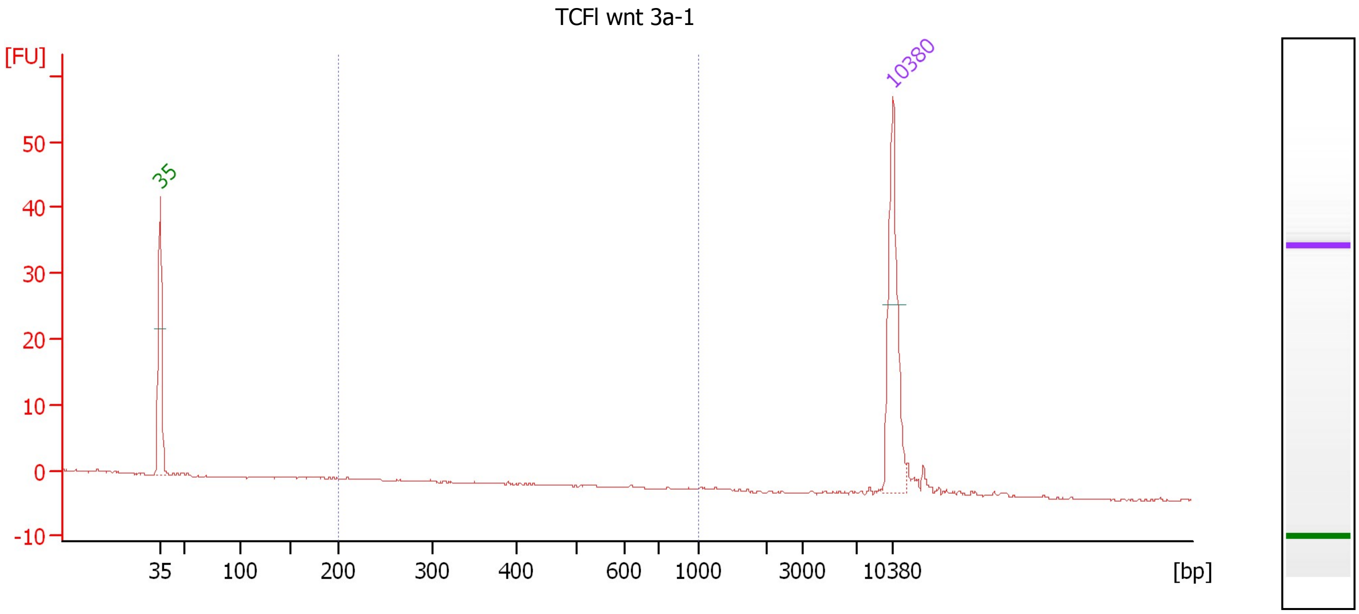
Peak table for sample 7 : TCFl Ctl-4

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : TCFl Ctl-4

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	415	1,000	25.7	192.4	■	44	41.8	42.76

Electropherogram Summary Continued ...



Overall Results for sample 8 : TCFl wnt 3a-1

Number of peaks found:	0	Corr. Area 1:	0.1
Noise:	0.1		

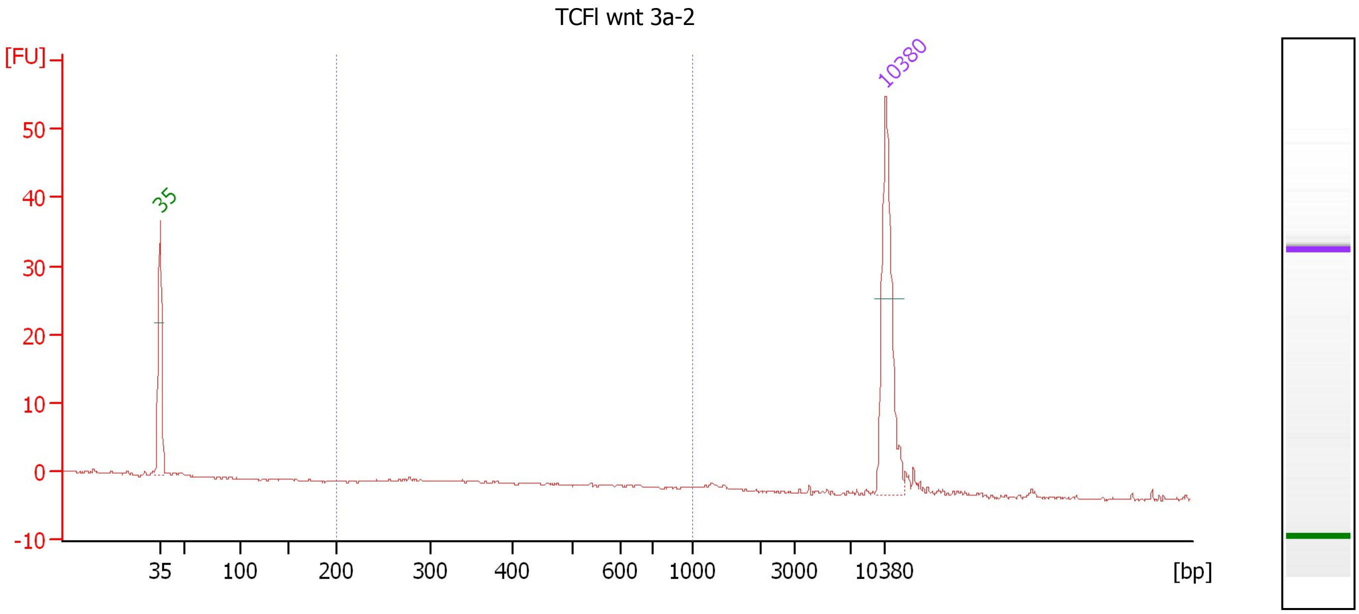
Peak table for sample 8 : TCFl wnt 3a-1

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 8 : TCFl wnt 3a-1

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Co lor	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	401	1,000	0.1	0.6	■	1	45.9	0.12

Electropherogram Summary Continued ...



Overall Results for sample 9 : **TCFl wnt 3a-2**

Number of peaks found:	0	Corr. Area 1:	0.2
Noise:	0.1		

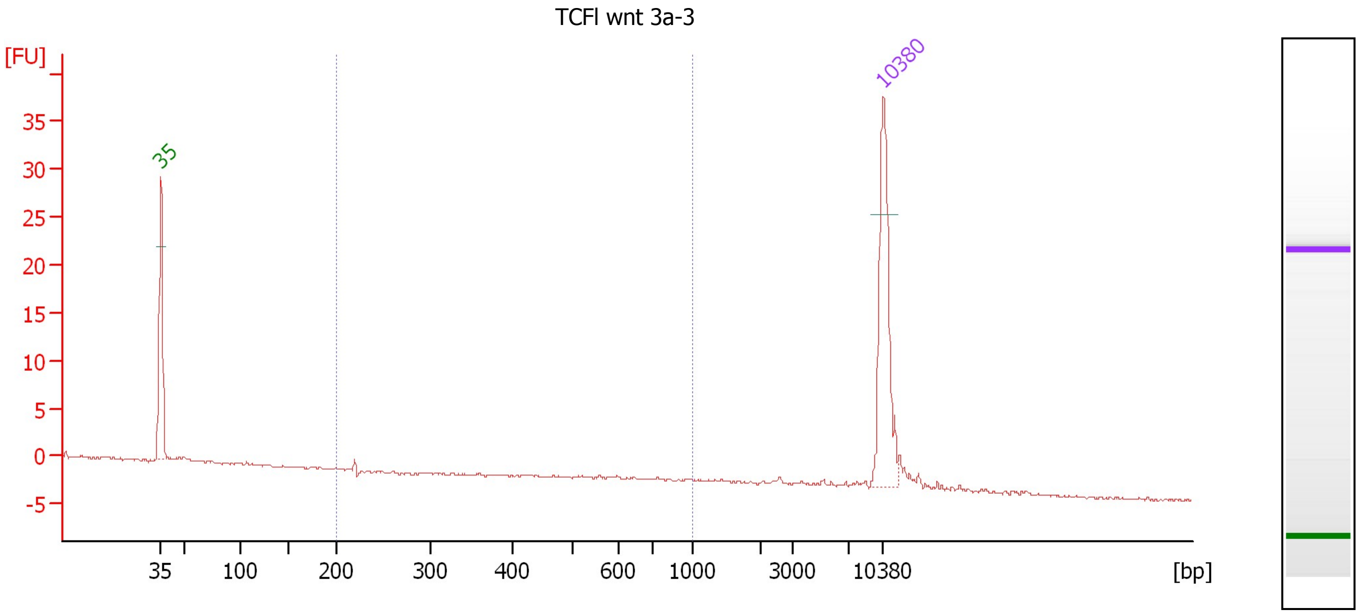
Peak table for sample 9 : **TCFl wnt 3a-2**

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : **TCFl wnt 3a-2**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	319	1,000	0.2	1.7	🟦	4	25.3	0.33

Electropherogram Summary Continued ...



Overall Results for sample 10 : TCFl wnt 3a-3

Number of peaks found:	0	Corr. Area 1:	1.0
Noise:	0.1		

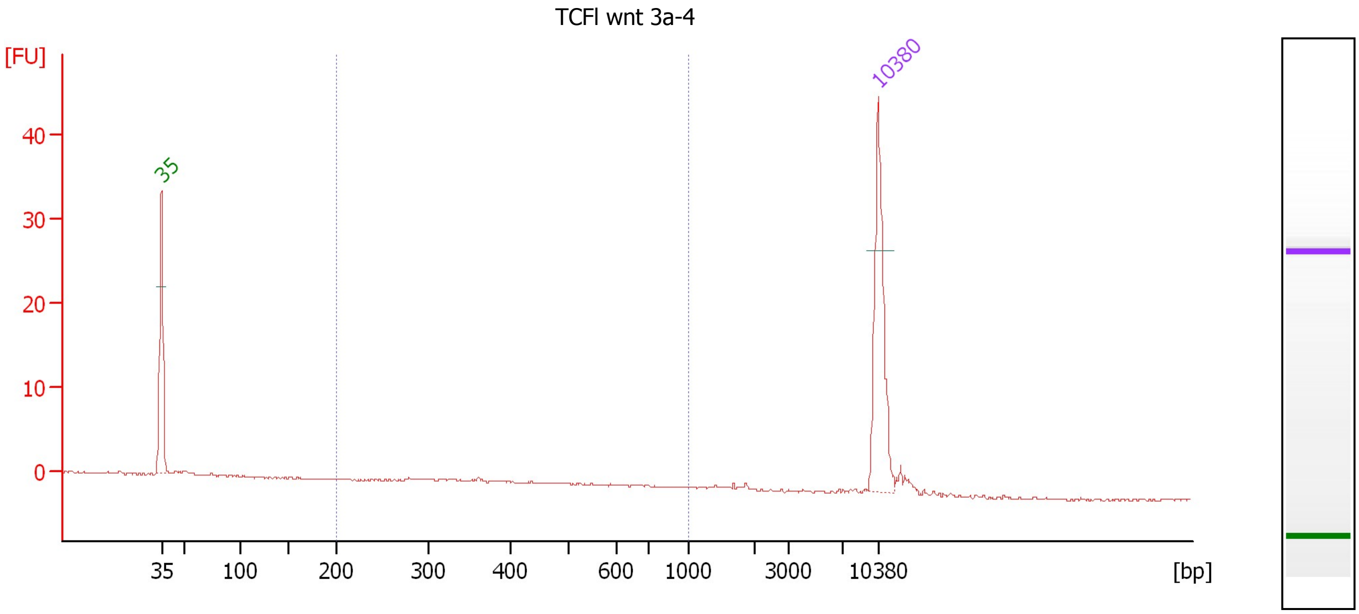
Peak table for sample 10 : TCFl wnt 3a-3

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : TCFl wnt 3a-3

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	631	1,000	1.0	9.2	■	8	36.2	2.63

Electropherogram Summary Continued ...



Overall Results for sample 11 : **TCFl wnt 3a-4**

Number of peaks found:	0	Corr. Area 1:	3.0
Noise:	0.1		

Peak table for sample 11 : **TCFl wnt 3a-4**

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	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 11 : **TCFl wnt 3a-4**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	Color	% of Total	Size distribution in CV [%]	Conc. [pg/µl]
200	400	1,000	3.0	34.0	🟦	36	28.5	8.21

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-09-08\2015-09-08_001.xad
Created: 9/8/2015 11:15:54 AM
Modified: 9/8/2015 11:57:14 AM

Gel Image