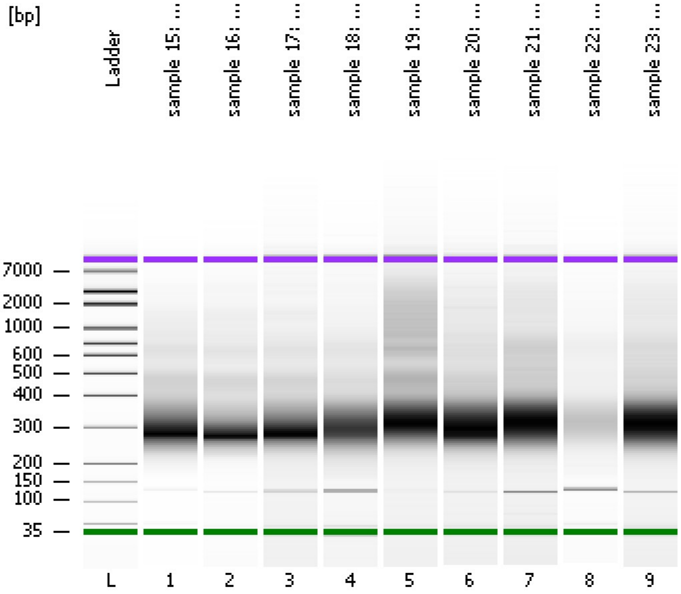
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...yzer\2015-10-05\2015-10-05_003_HiSeq224_Libraries_15-23.xad

Created: 10/5/2015 3:43:37 PM
Modified: 10/5/2015 4:29:59 PM

Electrophoresis File Run Summary



Instrument Information:

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

Assay Information:

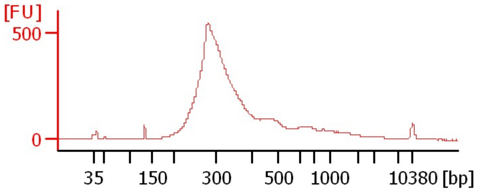
Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy

Assay Class: High Sensitivity DNA Assay
Version: 1.03
Assay Comments: Copyright © 2003-2010 Agilent Technologies

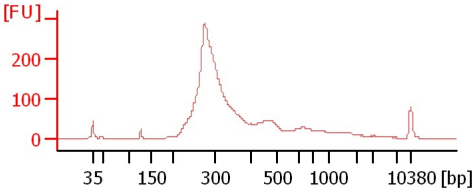
Chip Information:

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

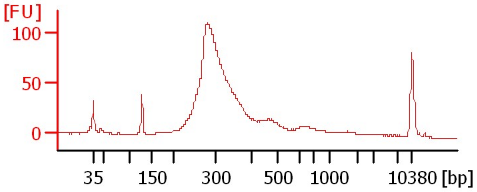
sample 15: B-Cat_Wnt3a-3
HiSeq224 library



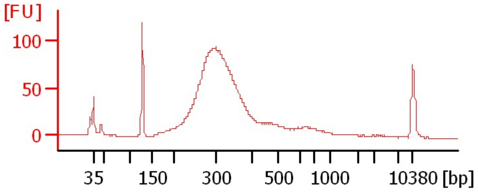
sample 16: B-Cat_Wnt3a-4
HiSeq224 library



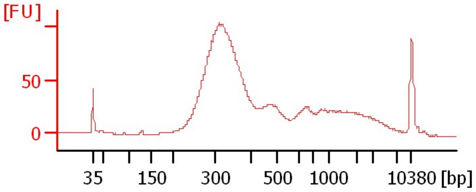
sample 17: Tcf4_Ctl-1
HiSeq224 library



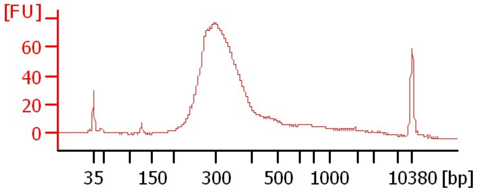
sample 18: Tcf4_Ctl-2
HiSeq224 library



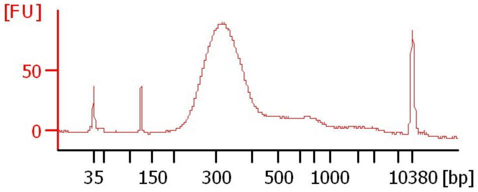
sample 19: Tcf4_Ctl-3
HiSeq224 library



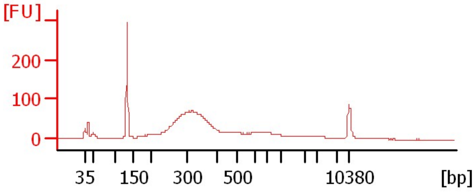
sample 20: Tcf4_Ctl-4
HiSeq224 library



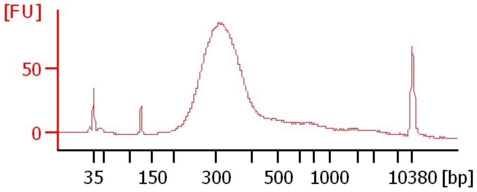
sample 21: Tcf4_Wnt3a-1
HiSeq224 library



sample 22: Tcf4_Wnt3a-2
HiSeq224 library



sample 23: Tcf4_Wnt3a-3
HiSeq224 library



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...yzer\2015-10-05\2015-10-05_003_HiSeq224_Libraries_15-23.xad
Created: 10/5/2015 3:43:37 PM
Modified: 10/5/2015 4:29:59 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
sample 15: B-Cat_Wnt3a-3	HiSeq224 library	☐	✓			
sample 16: B-Cat_Wnt3a-4	HiSeq224 library	☐	✓			
sample 17: Tcf4_Ctl-1	HiSeq224 library	☐	✓			
sample 18: Tcf4_Ctl-2	HiSeq224 library	☐	✓			
sample 19: Tcf4_Ctl-3	HiSeq224 library	☐	✓			
sample 20: Tcf4_Ctl-4	HiSeq224 library	☐	✓			
sample 21: Tcf4_Wnt3a-1	HiSeq224 library	☐	✓			
sample 22: Tcf4_Wnt3a-2	HiSeq224 library	☐	✓			
sample 23: Tcf4_Wnt3a-3	HiSeq224 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

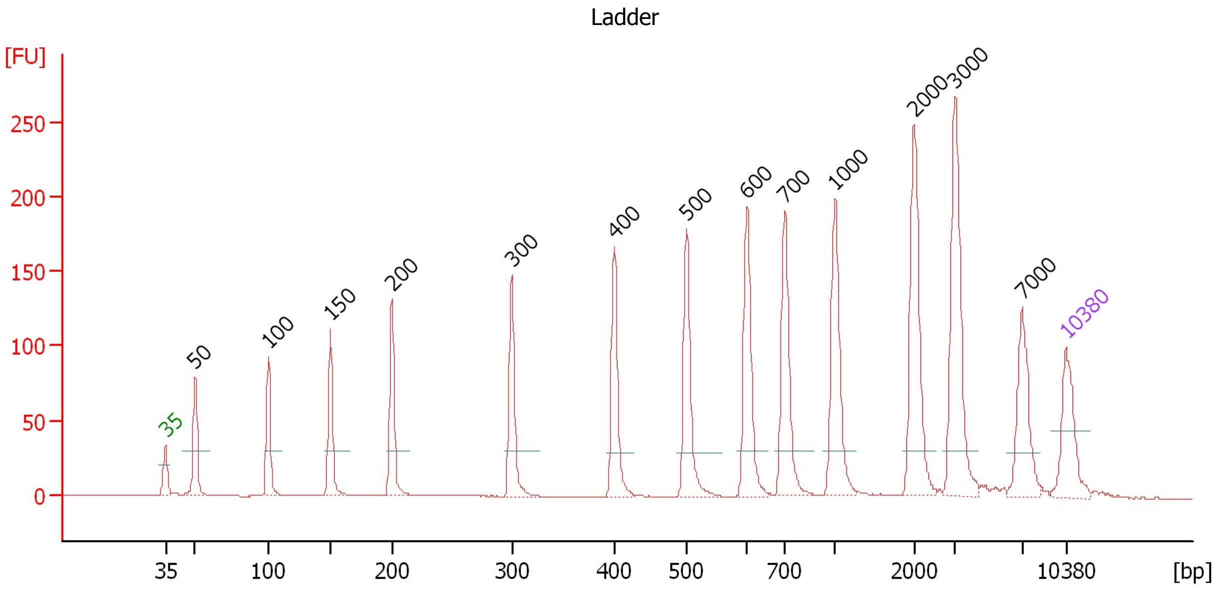
Filter Width [s] : 0.5
Polynomial Order : 4

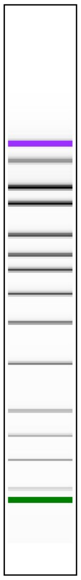
Ladder

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	Created:	10/5/2015 3:43:37 PM
Data Path:	C:\...yzer\2015-10-05\2015-10-05_003_HiSeq224_Libraries_15-23.xad	Modified:	10/5/2015 4:29:59 PM

Electropherogram Summary





Overall Results for Ladder

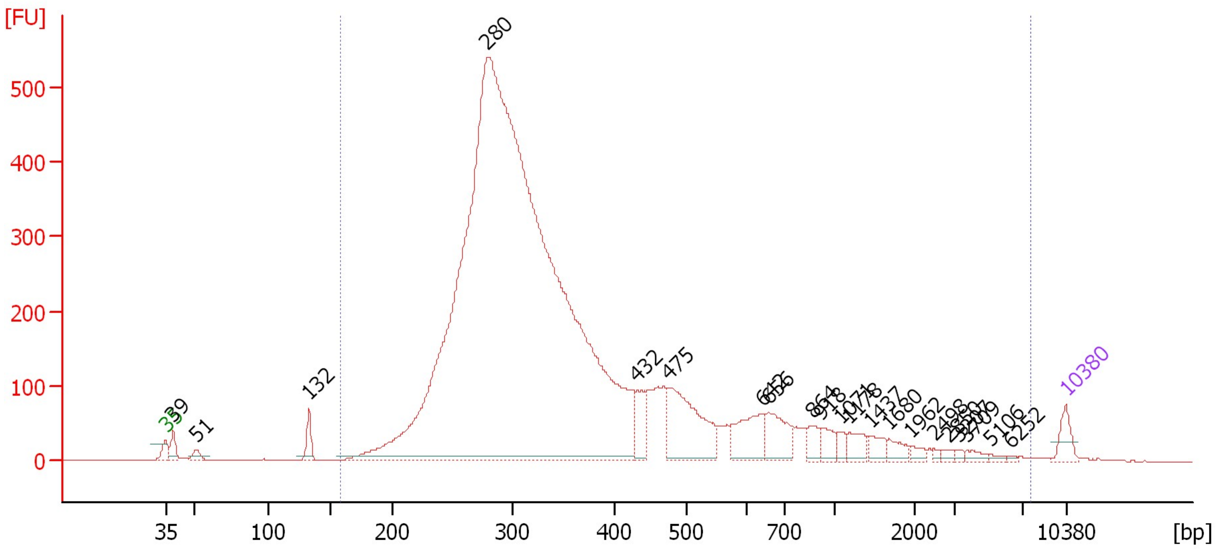
Noise: 0.1

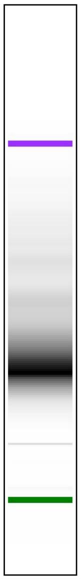
Peak table for Ladder

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	L	50	150.00	4,545.5	Ladder Peak	45.31
3	L	100	150.00	2,272.7	Ladder Peak	51.00
4	L	150	150.00	1,515.2	Ladder Peak	55.85
5	L	200	150.00	1,136.4	Ladder Peak	60.62
6	L	300	150.00	757.6	Ladder Peak	69.91
7	L	400	150.00	568.2	Ladder Peak	77.91
8	L	500	150.00	454.5	Ladder Peak	83.50
9	L	600	150.00	378.8	Ladder Peak	88.22
10	L	700	150.00	324.7	Ladder Peak	91.18
11	L	1,000	150.00	227.3	Ladder Peak	95.06
12	L	2,000	150.00	113.6	Ladder Peak	101.21
13	L	3,000	150.00	75.8	Ladder Peak	104.40
14	L	7,000	150.00	32.5	Ladder Peak	109.62
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

sample 15: B-Cat_Wnt3a-3 [HiSeq224 library]





Overall Results for sample 1 : **sample 15: B-Cat_Wnt3a-3**

Number of peaks found:	21	Corr. Area 1:	8,470.0
Noise:	0.2		

Peak table for sample 1 : **sample 15: B-Cat_Wnt3a-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		39	109.89	4,275.0		43.61
3		51	55.33	1,655.1		45.39
4		132	125.67	1,439.1		54.14
5		280	13,068.19	70,760.8		68.03
6		432	178.45	626.2		79.68
7		475	599.93	1,912.6		82.12
8		642	272.92	644.0		89.46
9		656	213.13	492.0		89.89
10		864	75.03	131.6		93.30
11		918	88.09	145.3		94.00
12		1,071	41.96	59.3		95.50
13		1,178	79.48	102.2		96.16
14		1,437	58.99	62.2		97.75
15		1,680	56.25	50.7		99.24
16		1,962	28.37	21.9		100.97
17		2,498	11.25	6.8		102.80
18		2,850	19.09	10.1		103.92
19		3,207	13.16	6.2		104.67
20		3,709	26.51	10.8		105.33
21		5,106	12.53	3.7		107.15
22		6,252	6.30	1.5		108.65
23	▶	10,380	75.00	10.9	Upper Marker	113.00

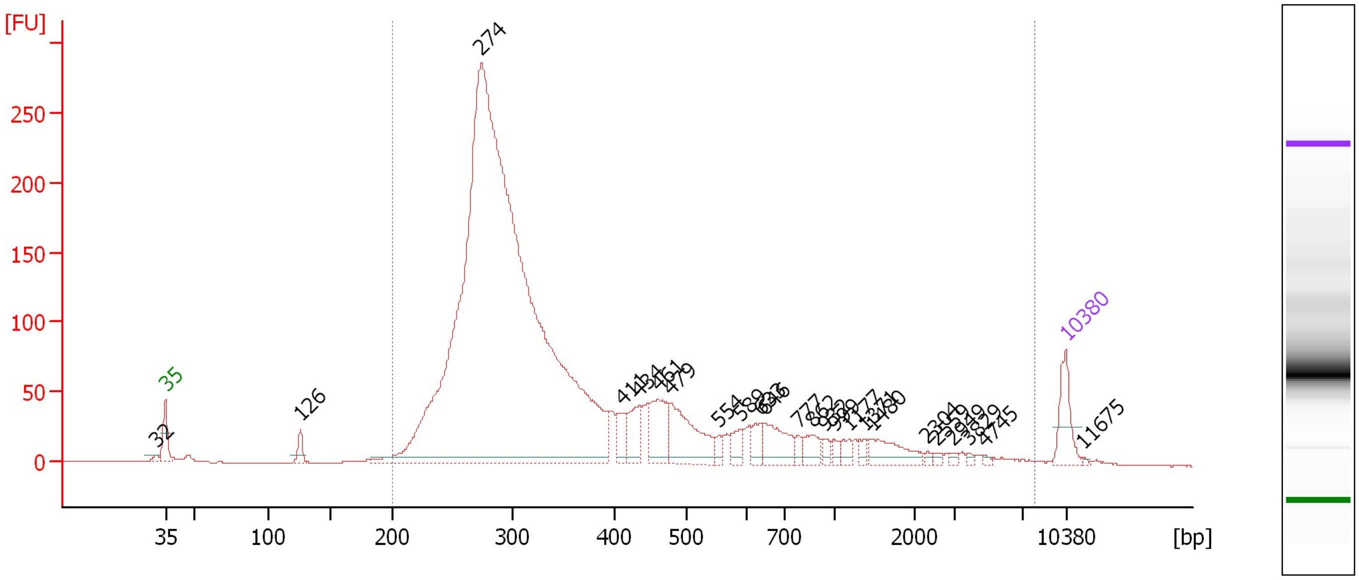
Electropherogram Summary Continued ...

... Region table for sample 1 : sample 15: B-Cat_Wnt3a-3

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
158	7,698	457	8,470.0	69,340.0	🟦 14,701.44	98	100.0

Electropherogram Summary Continued ...

sample 16: B-Cat_Wnt3a-4 [HiSeq224 library]



Overall Results for sample 2 : **sample 16: B-Cat_Wnt3a-4**

Number of peaks found:	24	Corr. Area 1:	3,426.3
Noise:	0.2		

Peak table for sample 2 : **sample 16: B-Cat_Wnt3a-4**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.23
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		126	41.62	502.0		53.49
4		274	4,593.74	25,380.5		67.51
5		411	54.59	201.2		78.53
6		434	86.81	303.0		79.82
7		461	121.55	399.7		81.30
8		479	198.30	627.7		82.31
9		554	20.86	57.1		86.04
10		589	39.60	101.8		87.72
11		633	38.87	93.0		89.20
12		646	95.42	223.7		89.59
13		777	19.11	37.3		92.17
14		862	39.01	68.6		93.27
15		932	16.71	27.2		94.18
16		999	15.49	23.5		95.05
17		1,177	19.26	24.8		96.15
18		1,371	14.78	16.3		97.34
19		1,480	72.63	74.3		98.01
20		2,304	6.34	4.2		102.18
21		2,559	6.84	4.0		102.99
22		2,949	6.22	3.2		104.24
23		3,829	5.31	2.1		105.48
24		4,745	4.88	1.6		106.68
25	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

... Peak table for sample 2 : **sample 16: B-Cat Wnt3a-4**

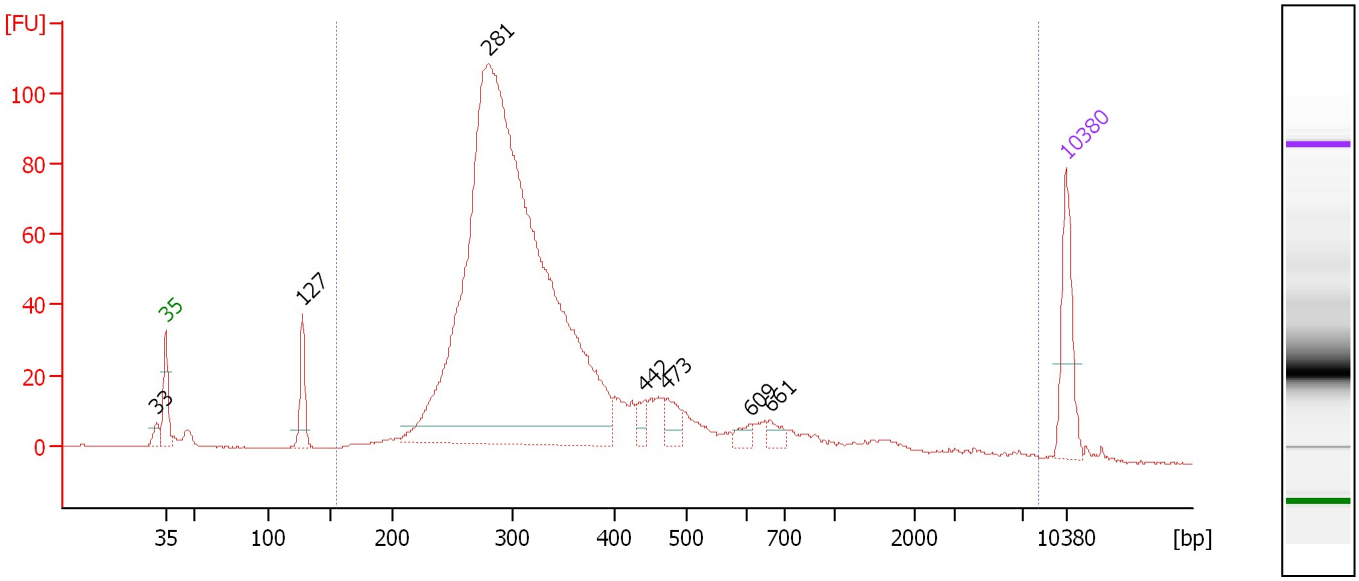
Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	11,675	0.00	0.0		114.29

Region table for sample 2 : **sample 16: B-Cat Wnt3a-4**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	7,997	496	3,426.3	25,604.8	🟦	5,444.26	98	100.0

Electropherogram Summary Continued ...

sample 17: Tcf4_Ctl-1 [HiSeq224 library]



Overall Results for sample 3 : **sample 17: Tcf4_Ctl-1**

Number of peaks found:	7	Corr. Area 1:	1,482.1
Noise:	0.2		

Peak table for sample 3 : **sample 17: Tcf4_Ctl-1**

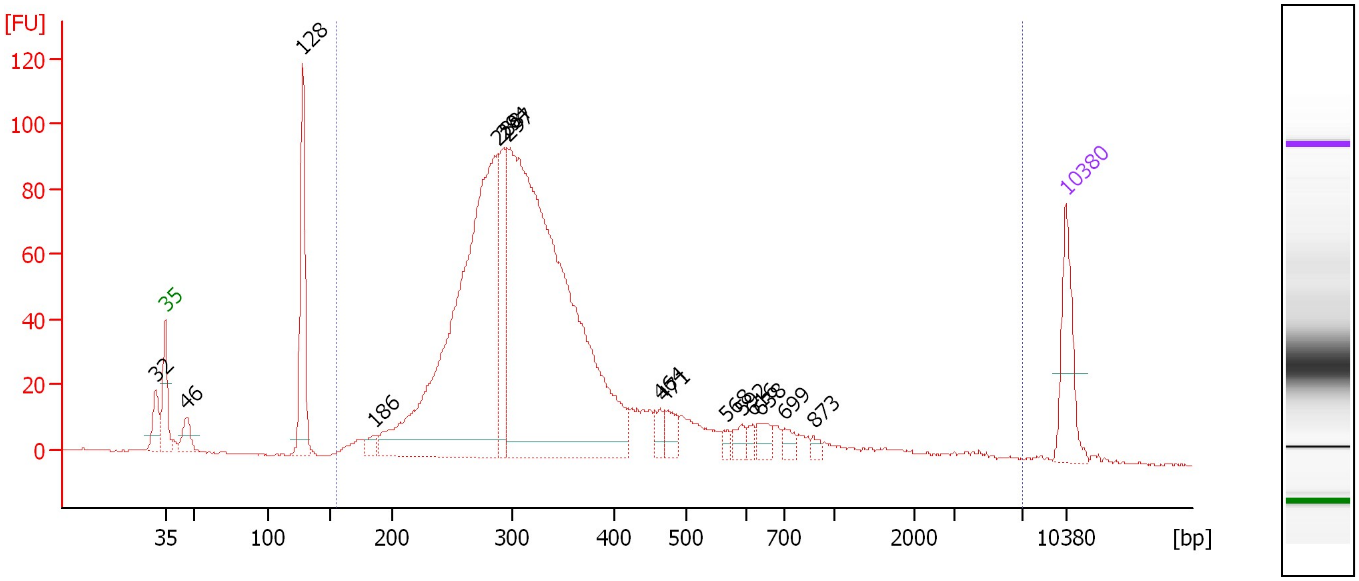
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		33	0.00	0.0		42.32
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		127	71.76	853.0		53.66
4		281	2,005.60	10,827.6		68.11
5		442	21.64	74.1		80.28
6		473	30.70	98.4		81.98
7		609	14.34	35.7		88.47
8		661	15.55	35.6		90.02
9	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : **sample 17: Tcf4_Ctl-1**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
155	8,285	475	1,482.1	11,699.6	■	2,454.25	94	100.0

Electropherogram Summary Continued ...

sample 18: Tcf4_Ctl-2 [HiSeq224 library]



Overall Results for sample 4 : sample 18: Tcf4_Ctl-2

Number of peaks found:	15	Corr. Area 1:	1,630.3
Noise:	0.2		

Peak table for sample 4 : sample 18: Tcf4_Ctl-2

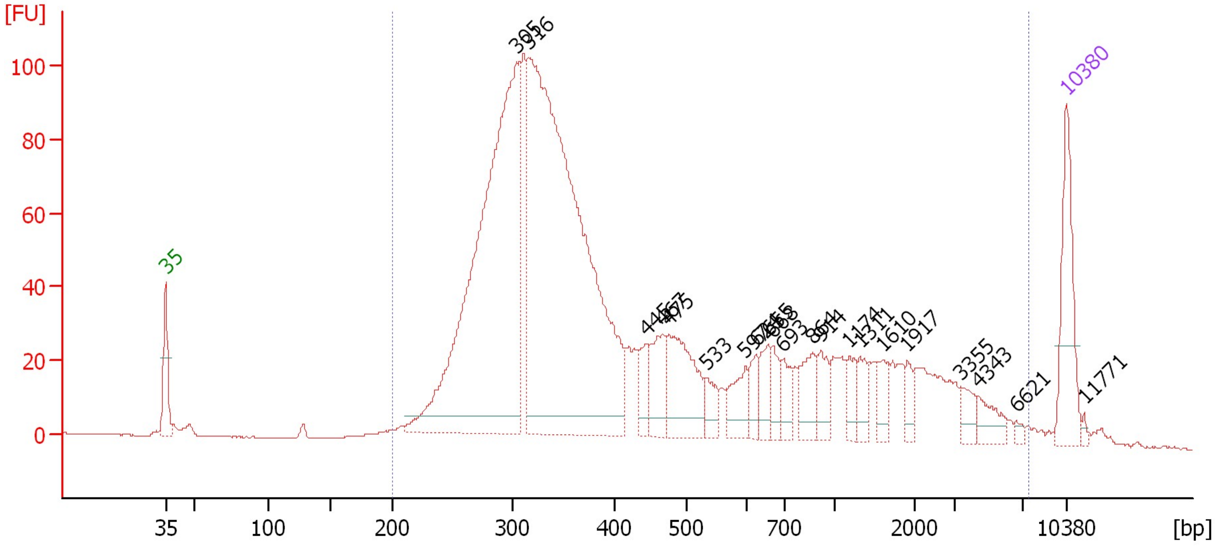
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		32	0.00	0.0		42.26
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		46	43.44	1,436.1		44.67
4		128	210.97	2,500.5		53.70
5		186	16.98	138.2		59.30
6		288	925.78	4,865.6		68.82
7		294	154.18	795.8		69.31
8		297	1,286.21	6,555.7		69.65
9		464	19.10	62.4		81.49
10		471	31.26	100.6		81.88
11		568	10.65	28.4		86.69
12		592	16.68	42.7		87.82
13		616	10.53	25.9		88.70
14		638	21.48	51.0		89.34
15		699	15.91	34.5		91.16
16		873	7.96	13.8		93.41
17	▶	10,380	75.00	10.9	Upper Marker	113.00

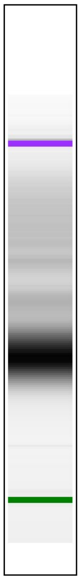
Region table for sample 4 : sample 18: Tcf4_Ctl-2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
154	6,985	424	1,630.3	12,971.9	🟦	2,682.20	91	100.0

Electropherogram Summary Continued ...

sample 19: Tcf4_Ctl-3 [HiSeq224 library]





Overall Results for sample 5 : sample 19: Tcf4_Ctl-3

Number of peaks found: 21 Corr. Area 1: 2,130.4

Noise: 0.2

Peak table for sample 5 : sample 19: Tcf4_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		305	782.55	3,891.2		70.29
3		316	995.82	4,776.6		71.18
4		445	33.84	115.3		80.41
5		467	55.58	180.4		81.65
6		475	107.61	343.4		82.09
7		533	26.63	75.7		85.07
8		597	38.03	96.4		88.10
9		624	23.31	56.6		88.94
10		655	26.38	61.1		89.83
11		668	25.64	58.2		90.23
12		693	23.77	52.0		90.97
13		864	37.88	66.4		93.30
14		914	27.47	45.5		93.95
15		1,174	21.02	27.1		96.13
16		1,311	22.71	26.2		96.98
17		1,610	20.07	18.9		98.81
18		1,917	15.12	12.0		100.70
19		3,355	15.87	7.2		104.86
20		4,343	21.68	7.6		106.15
21		6,621	3.75	0.9		109.13
22	▶	10,380	75.00	10.9	Upper Marker	113.00
23		11,771	0.00	0.0		114.39

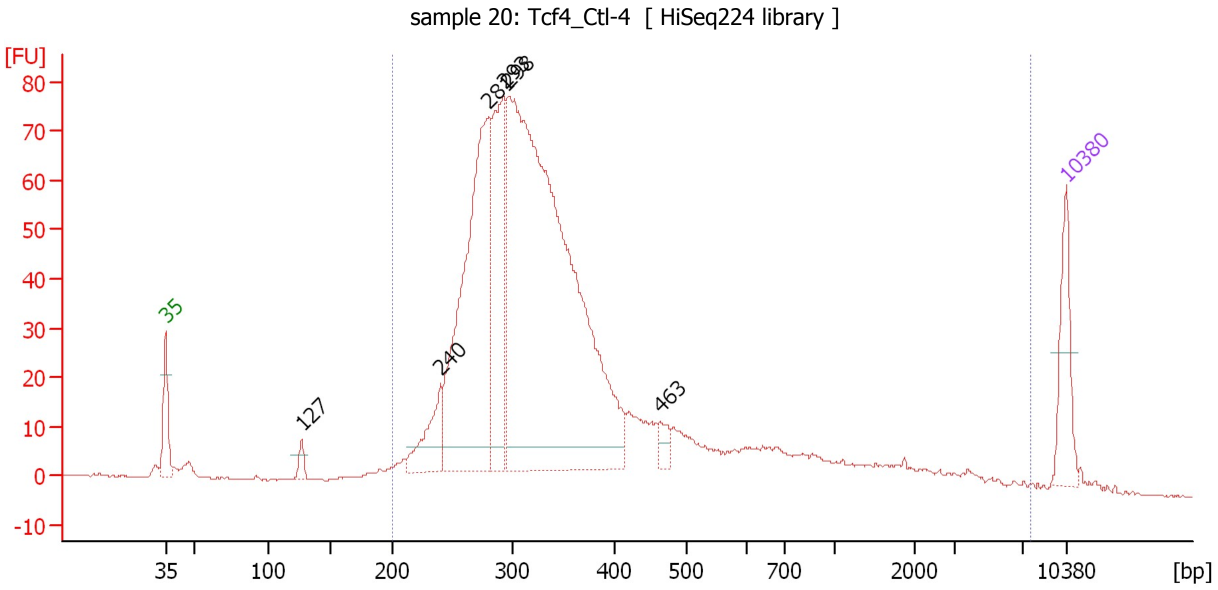
Assay Class:	High Sensitivity DNA Assay	Created:	10/5/2015 3:43:37 PM
Data Path:	C:\...yzer\2015-10-05\2015-10-05_003_HiSeq224_Libraries_15-23.xad	Modified:	10/5/2015 4:29:59 PM

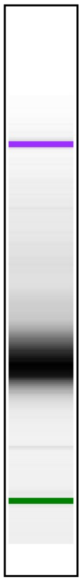
Electropherogram Summary Continued ...

... Region table for sample 5 : sample 19: Tcf4 Ctl-3

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
200	7,454	766	2,130.4	11,197.6	🟦 2,789.76	97	100.0

Electropherogram Summary Continued ...





Overall Results for sample 6 : **sample 20: Tcf4_Ctl-4**

Number of peaks found:	6	Corr. Area 1:	1,353.4
Noise:	0.2		

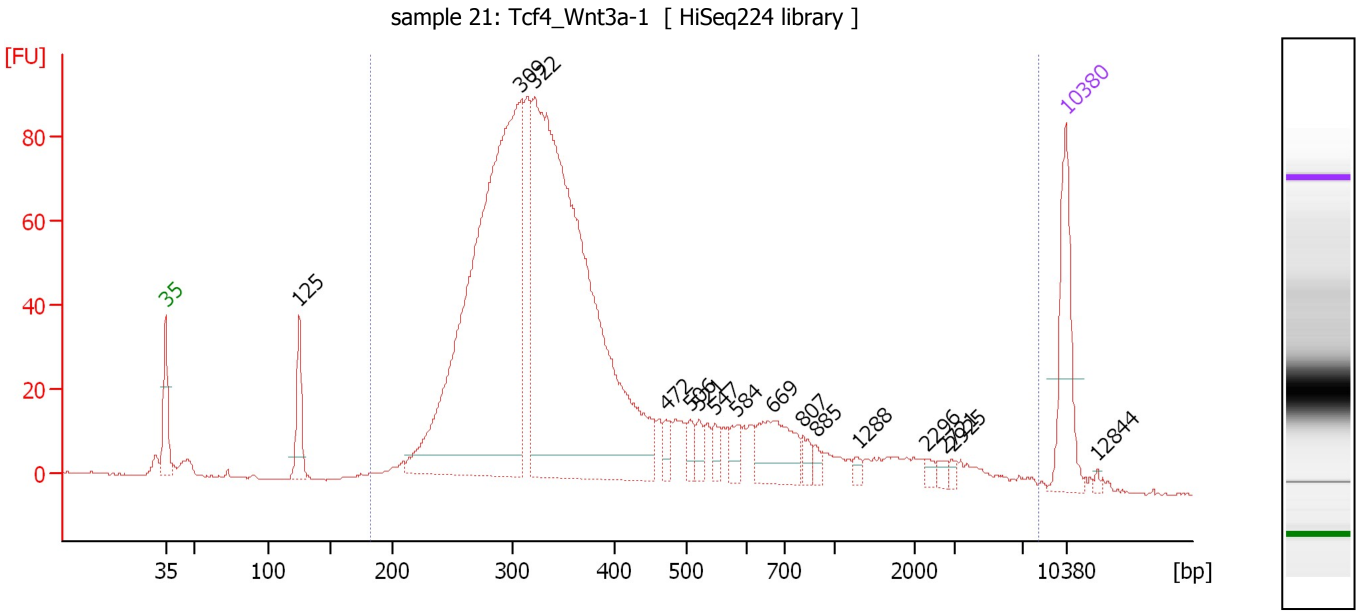
Peak table for sample 6 : **sample 20: Tcf4_Ctl-4**

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		127	21.51	256.9		53.60
3		240	104.35	658.0		64.36
4		281	673.41	3,631.1		68.14
5		293	287.30	1,484.1		69.29
6		298	1,524.31	7,746.7		69.74
7		463	21.79	71.3		81.44
8	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : **sample 20: Tcf4_Ctl-4**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	7,625	494	1,353.4	14,646.6	■	3,179.54	97	100.0

Electropherogram Summary Continued ...



Overall Results for sample 7 : **sample 21: Tcf4 Wnt3a-1**

Number of peaks found:	16	Corr. Area 1:	1,704.8
Noise:	0.1		

Peak table for sample 7 : **sample 21: Tcf4 Wnt3a-1**

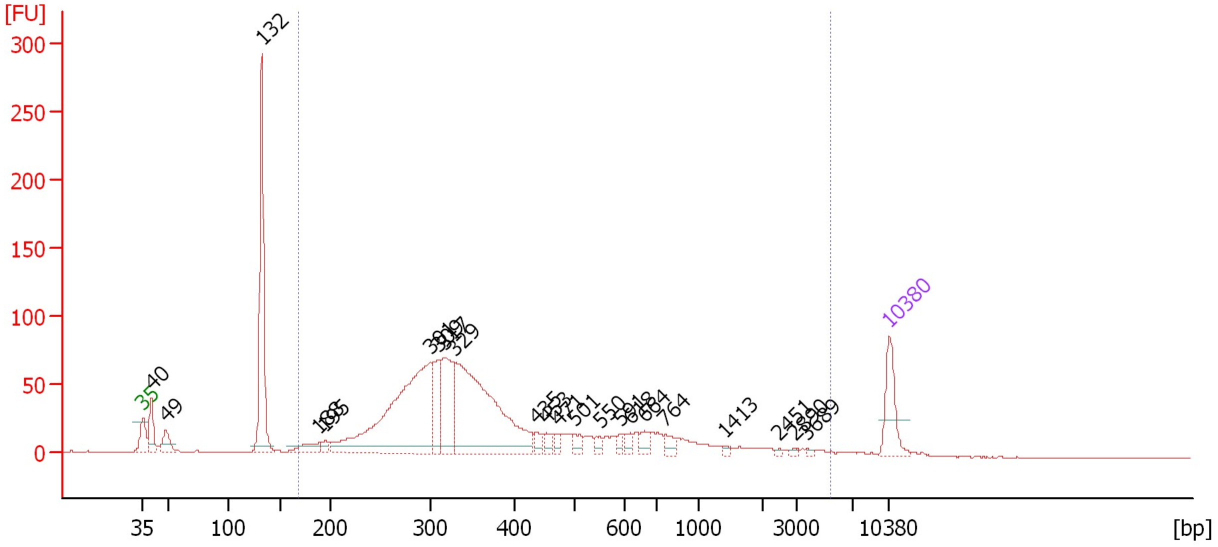
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		125	63.71	774.2		53.39
3		309	881.62	4,316.0		70.67
4		322	990.16	4,658.3		71.67
5		472	15.76	50.6		81.92
6		506	15.12	45.3		83.77
7		521	15.87	46.2		84.48
8		547	13.42	37.2		85.73
9		584	18.69	48.5		87.44
10		669	69.67	157.8		90.25
11		807	12.87	24.2		92.56
12		885	7.45	12.8		93.57
13		1,288	5.66	6.7		96.83
14		2,296	5.71	3.8		102.15
15		2,721	5.45	3.0		103.51
16		2,925	4.27	2.2		104.16
17	▶	10,380	75.00	10.9	Upper Marker	113.00
18		12,844	0.00	0.0		115.46

Region table for sample 7 : **sample 21: Tcf4 Wnt3a-1**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
182	8,205	562	1,704.8	10,838.8	■	2,455.60	96	100.0

Electropherogram Summary Continued ...

sample 22: Tcf4_Wnt3a-2 [HiSeq224 library]



Overall Results for sample 8 : **sample 22: Tcf4 Wnt3a-2**

Number of peaks found:	22	Corr. Area 1:	1,451.3
Noise:	0.2		

Peak table for sample 8 : **sample 22: Tcf4 Wnt3a-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		40	83.29	3,140.1		43.80
3		49	52.64	1,629.4		45.15
4		132	455.79	5,213.7		54.15
5		188	44.32	356.6		59.50
6		195	18.25	142.1		60.10
7		301	641.86	3,236.2		69.95
8		309	106.77	523.1		70.65
9		317	169.43	808.8		71.30
10		329	585.67	2,695.0		72.25
11		435	19.23	67.0		79.85
12		453	20.74	69.4		80.85
13		471	16.67	53.6		81.90
14		501	20.19	61.1		83.55
15		550	15.98	44.0		85.85
16		591	12.98	33.3		87.80
17		618	17.80	43.6		88.75
18		664	23.14	52.8		90.10
19		764	19.01	37.7		92.00
20		1,413	5.22	5.6		97.60
21		2,451	2.91	1.8		102.65
22		2,890	4.45	2.3		104.05
23		3,689	3.49	1.4		105.30
24	▶	10,380	75.00	10.9	Upper Marker	113.00

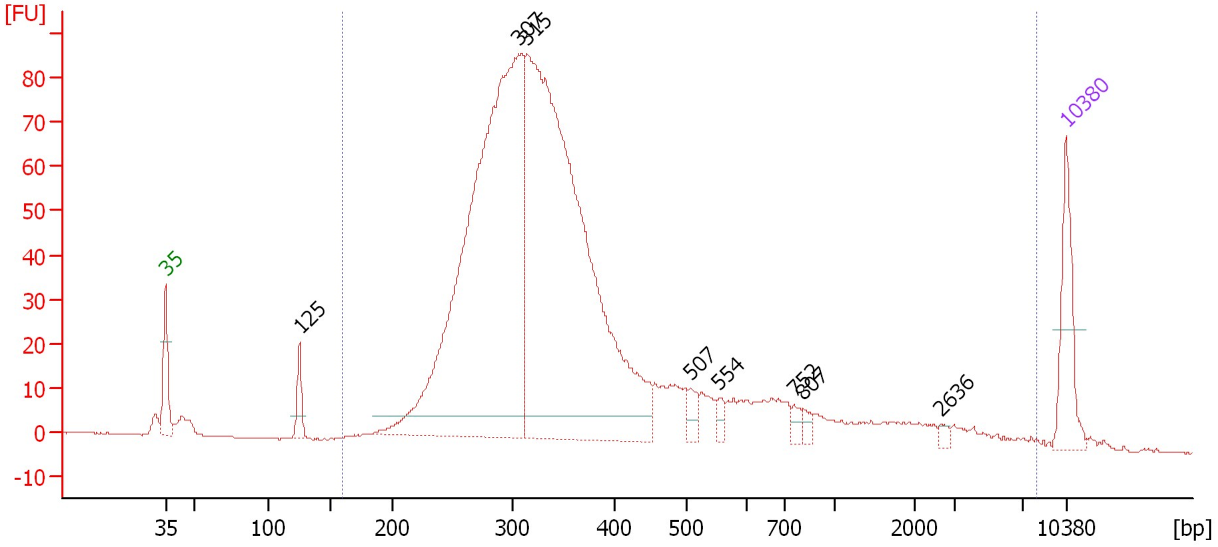
Electropherogram Summary Continued ...

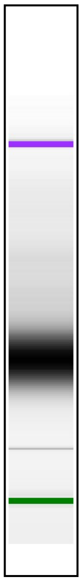
... Region table for sample 8 : sample 22: Tcf4 Wnt3a-2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
168	5,433	501	1,451.3	8,799.4	🟦 1,947.13	80	100.0

Electropherogram Summary Continued ...

sample 23: Tcf4_Wnt3a-3 [HiSeq224 library]





Overall Results for sample 9 : sample 23: Tcf4 Wnt3a-3

Number of peaks found:	8	Corr. Area 1:	1,552.7
Noise:	0.1		

Peak table for sample 9 : sample 23: Tcf4 Wnt3a-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		125	45.35	549.9		53.42
3		307	1,199.87	5,926.1		70.45
4		315	1,269.54	6,105.7		71.11
5		507	20.91	62.5		83.82
6		554	13.46	36.8		86.06
7		752	12.09	24.4		91.85
8		807	11.02	20.7		92.56
9		2,636	6.06	3.5		103.24
10	▶	10,380	75.00	10.9	Upper Marker	113.00

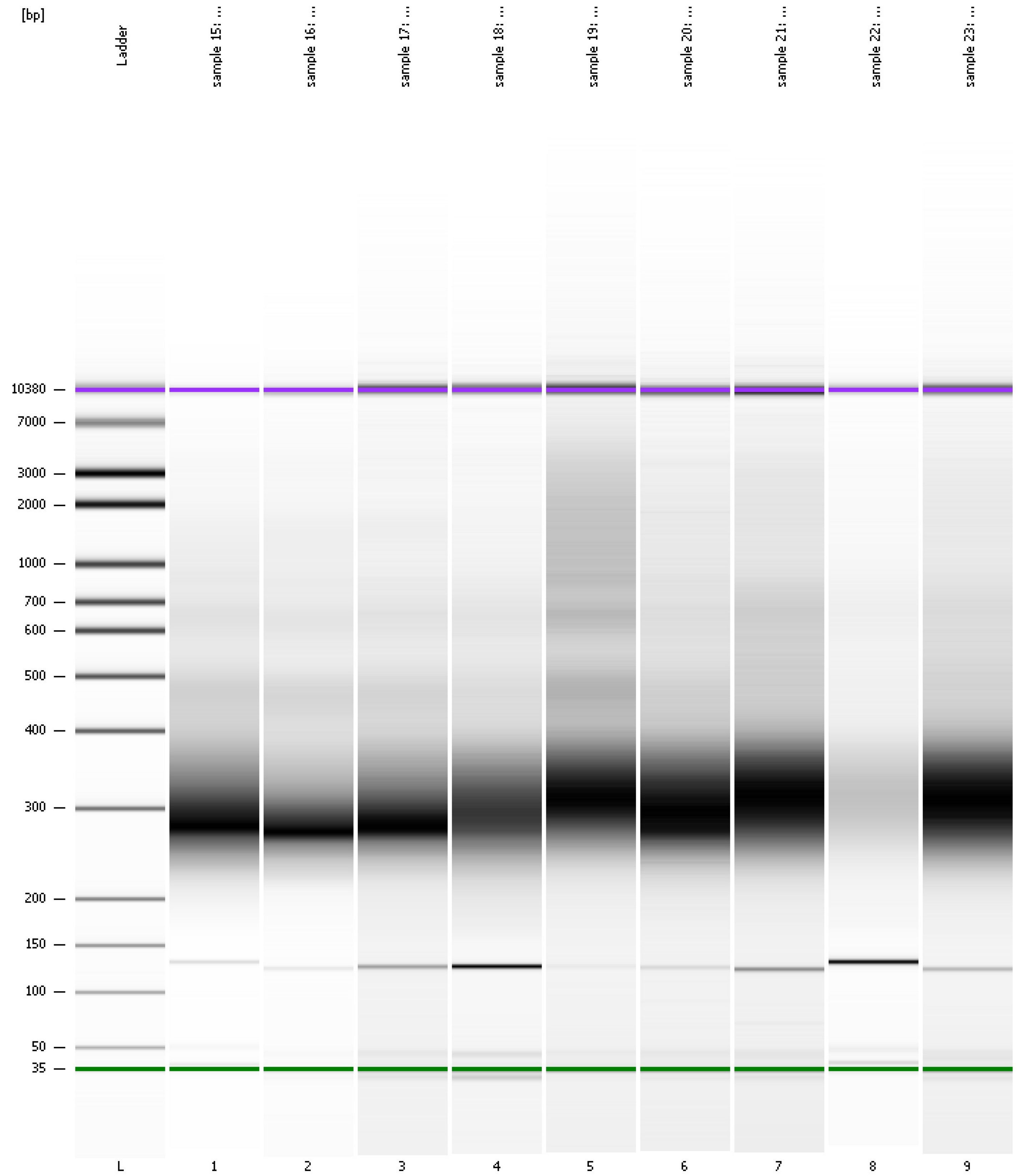
Region table for sample 9 : sample 23: Tcf4 Wnt3a-3

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
160	8,104	515	1,552.7	13,217.2	🟦	2,900.72	97	100.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...yzer\2015-10-05\2015-10-05_003_HiSeq224_Libraries_15-23.xad

Created: 10/5/2015 3:43:37 PM
Modified: 10/5/2015 4:29:59 PM

Gel Image



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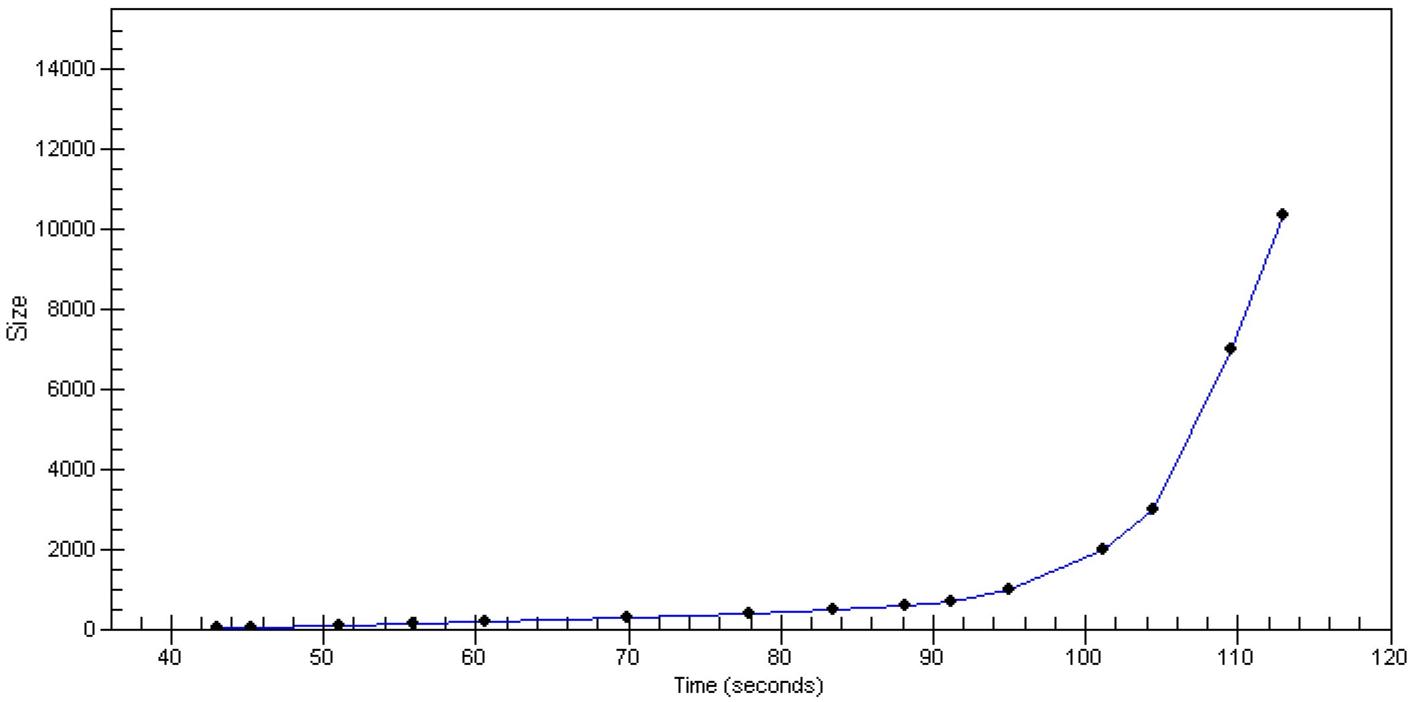
Curves

Standard Curve



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Created: 10/5/2015 3:43:37 PM
Modified: 10/5/2015 4:29:59 PM

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		10/5/2015 4:24:04 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-10-05\2015-10-05_003.xad)		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/5/2015 3:43:43 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1