

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

Created: 10/19/2016 1:55:00 PM  
Modified: 10/19/2016 3:05:41 PM

**Electrophoresis File Run Summary**

Instrument Information:

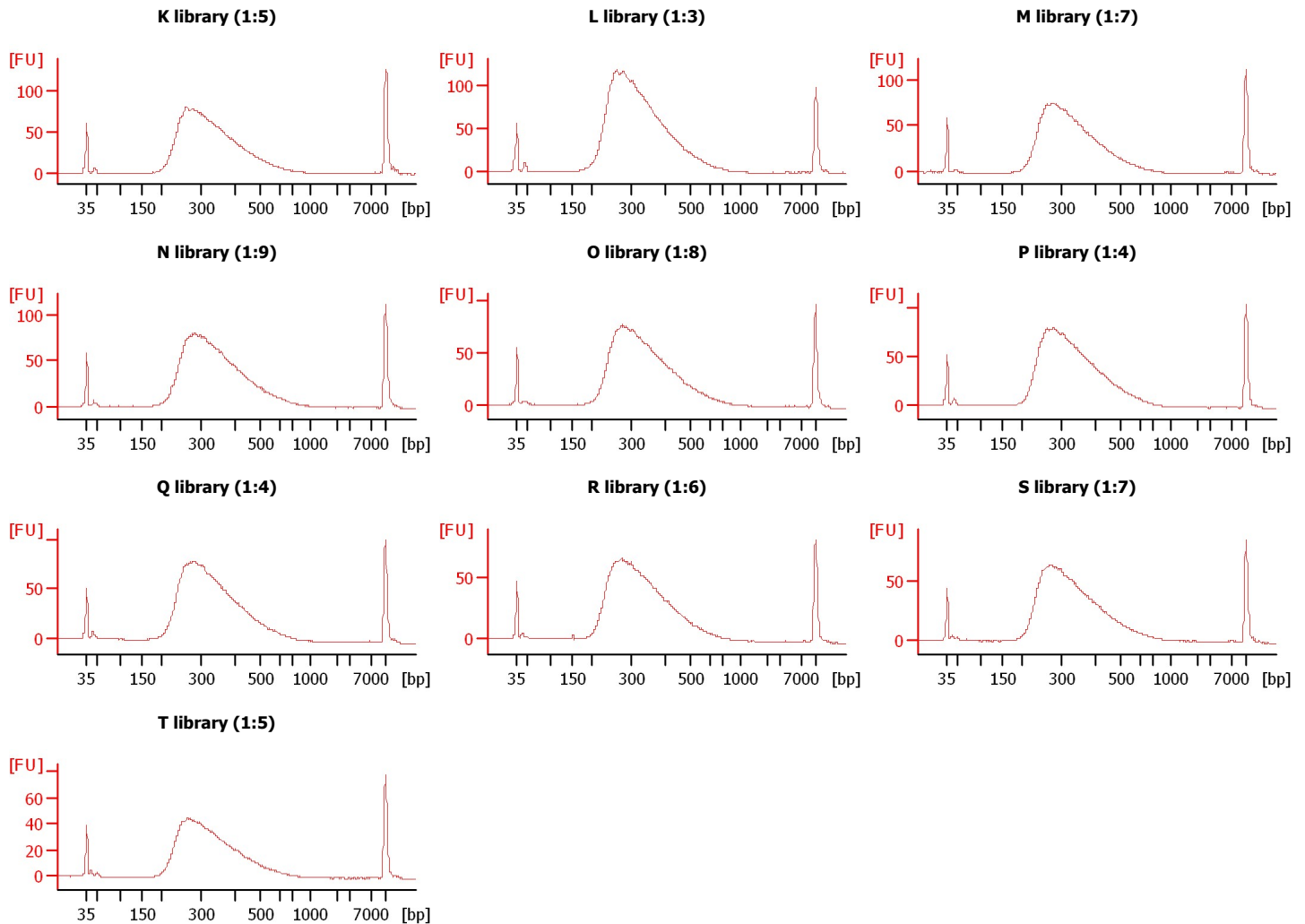
Instrument Name: DE13701086                      Firmware: C.01.069  
Serial#: DE13701086                              Type: G2938B

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:



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
K library (1:5)		<input type="checkbox"/>	✓			
L library (1:3)		<input type="checkbox"/>	✓			
M library (1:7)		<input type="checkbox"/>	✓			
N library (1:9)		<input type="checkbox"/>	✓			
O library (1:8)		<input type="checkbox"/>	✓			
P library (1:4)		<input type="checkbox"/>	✓			
Q library (1:4)		<input type="checkbox"/>	✓			
R library (1:6)		<input type="checkbox"/>	✓			
S library (1:7)		<input type="checkbox"/>	✓			
T library (1:5)		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

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**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

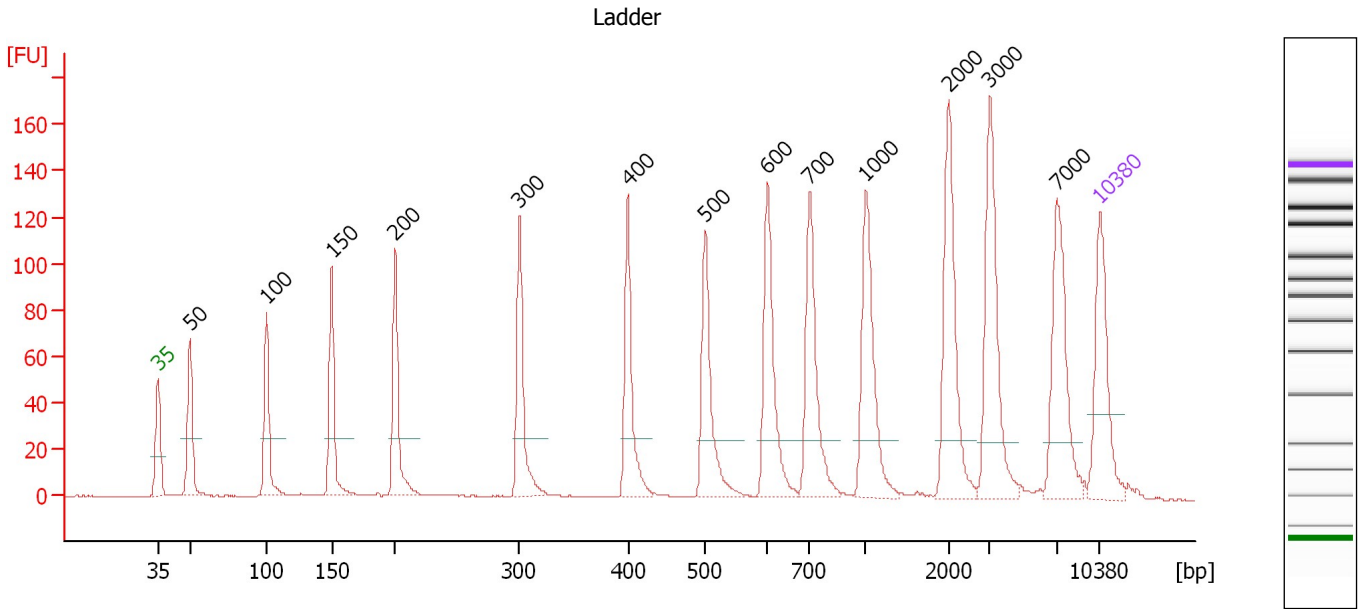
**Ladder**

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

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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

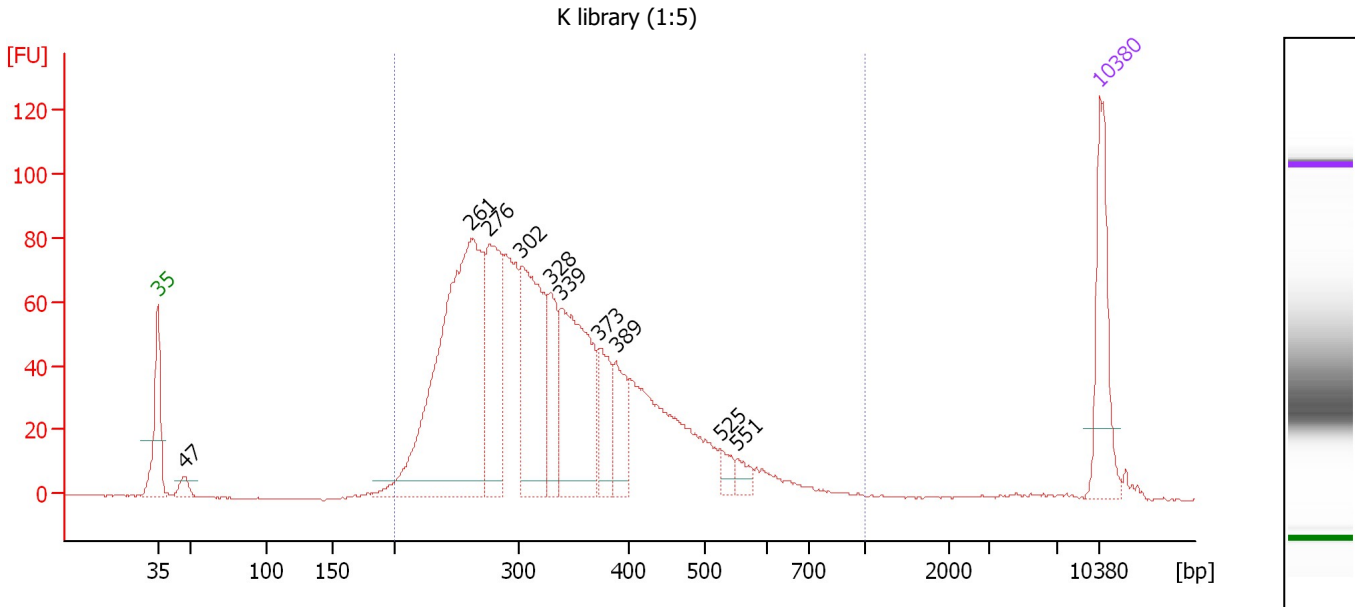
**Peak table for Ladder**

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	45.39
3	100	150.00	2,272.7	Ladder Peak	51.10
4	150	150.00	1,515.2	Ladder Peak	55.93
5	200	150.00	1,136.4	Ladder Peak	60.66
6	300	150.00	757.6	Ladder Peak	69.88
7	400	150.00	568.2	Ladder Peak	77.93
8	500	150.00	454.5	Ladder Peak	83.68
9	600	150.00	378.8	Ladder Peak	88.32
10	700	150.00	324.7	Ladder Peak	91.44
11	1,000	150.00	227.3	Ladder Peak	95.59
12	2,000	150.00	113.6	Ladder Peak	101.78
13	3,000	150.00	75.8	Ladder Peak	104.80
14	7,000	150.00	32.5	Ladder Peak	109.83
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : K library (1:5)**

Number of peaks found: 10                      Corr. Area 1: 1,636.9  
 Noise: 0.2

**Peak table for sample 2 : K library (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	47	16.78	540.1		44.93
3	261	527.96	3,060.5		66.32
4	276	174.53	958.7		67.65
5	302	209.26	1,050.6		70.02
6	328	78.44	362.1		72.15
7	339	209.77	938.6		72.99
8	373	61.98	251.8		75.75
9	389	60.35	235.1		77.04
10	525	15.07	43.5		84.84
11	551	13.79	37.9		86.03
12	10,380	75.00	10.9	Upper Marker	113.00

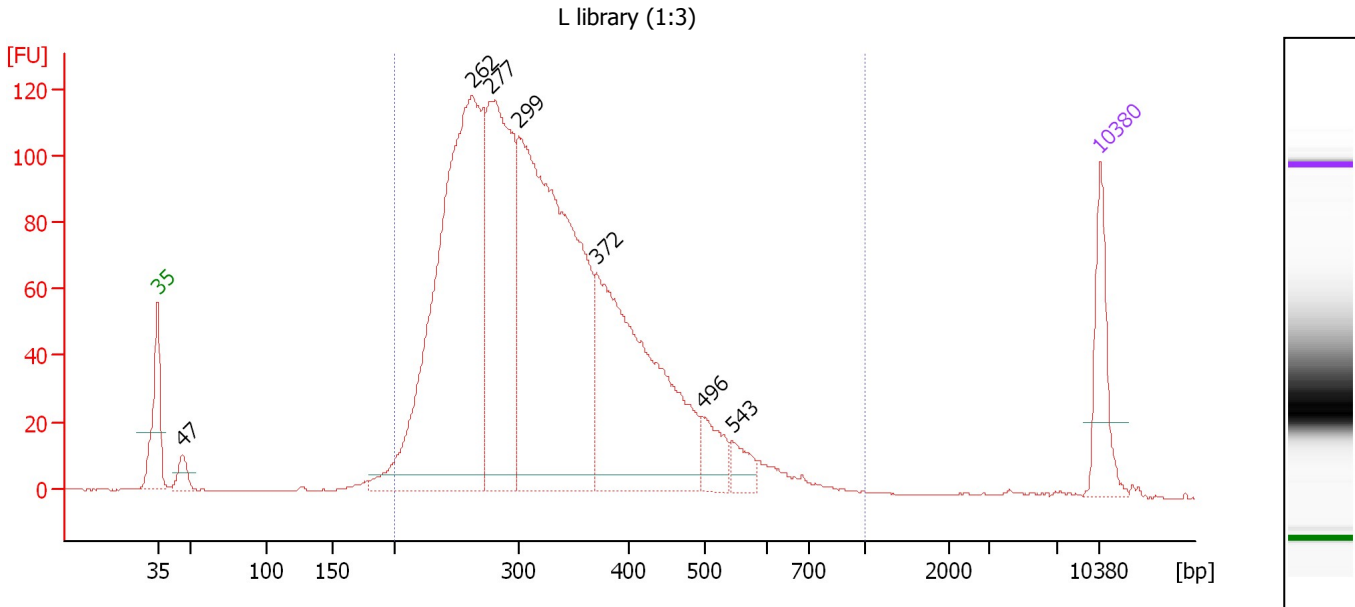
**Region table for sample 2 : K library (1:5)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	339	1,636.9	8,351.3	1,709.92	98	28.3

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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : L library (1:3)**

Number of peaks found: 7                      Corr. Area 1: 2,377.2  
 Noise: 0.2

**Peak table for sample 3 : L library (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	47	33.46	1,087.0		44.86
3	262	988.81	5,720.2		66.37
4	277	518.15	2,832.7		67.77
5	299	947.74	4,795.5		69.83
6	372	533.95	2,177.0		75.64
7	496	53.17	162.4		83.47
8	543	32.14	89.7		85.67
9	10,380	75.00	10.9	Upper Marker	113.00

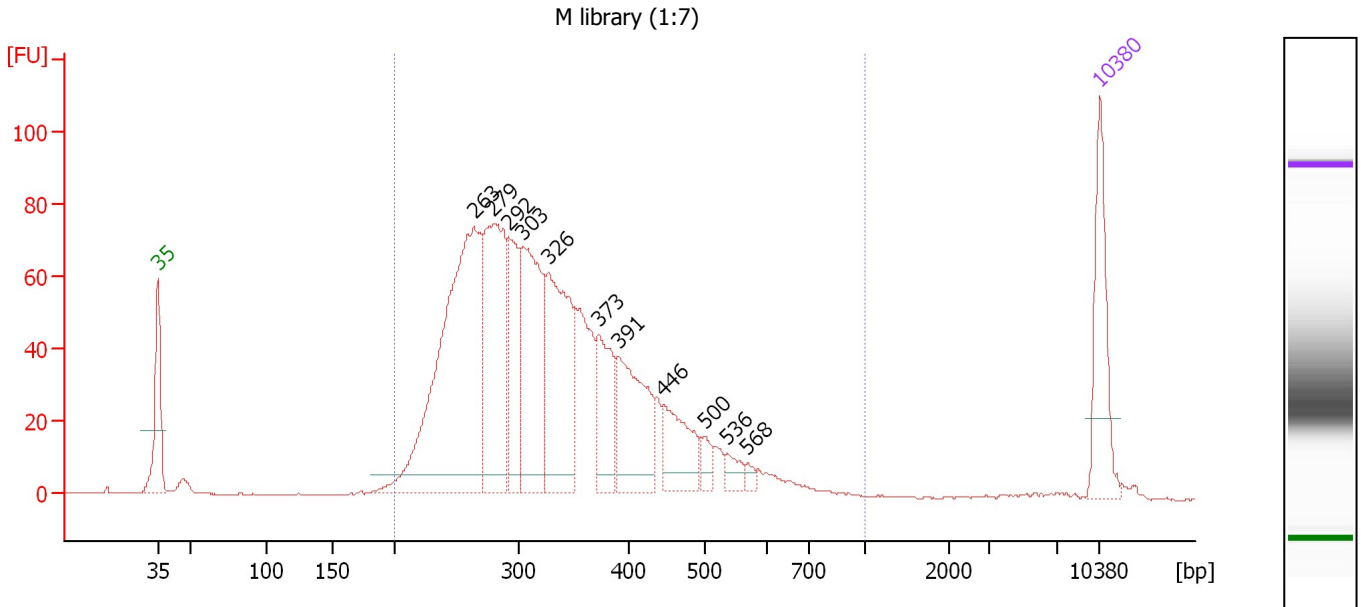
**Region table for sample 3 : L library (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	333	2,377.2	15,244.7	3,082.05	97	28.0

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : M library (1:7)**

Number of peaks found: 11                      Corr. Area 1: 1,509.7  
 Noise: 0.2

**Peak table for sample 4 : M library (1:7)**

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	263	509.10	2,930.6		66.49
3	279	251.58	1,365.1		67.96
4	292	102.69	532.9		69.14
5	303	205.42	1,027.9		70.10
6	326	211.34	981.6		71.99
7	373	90.48	367.5		75.76
8	391	129.92	502.9		77.24
9	446	72.16	244.9		80.60
10	500	17.17	52.0		83.71
11	536	16.15	45.7		85.34
12	568	7.17	19.1		86.81
13	10,380	75.00	10.9	Upper Marker	113.00

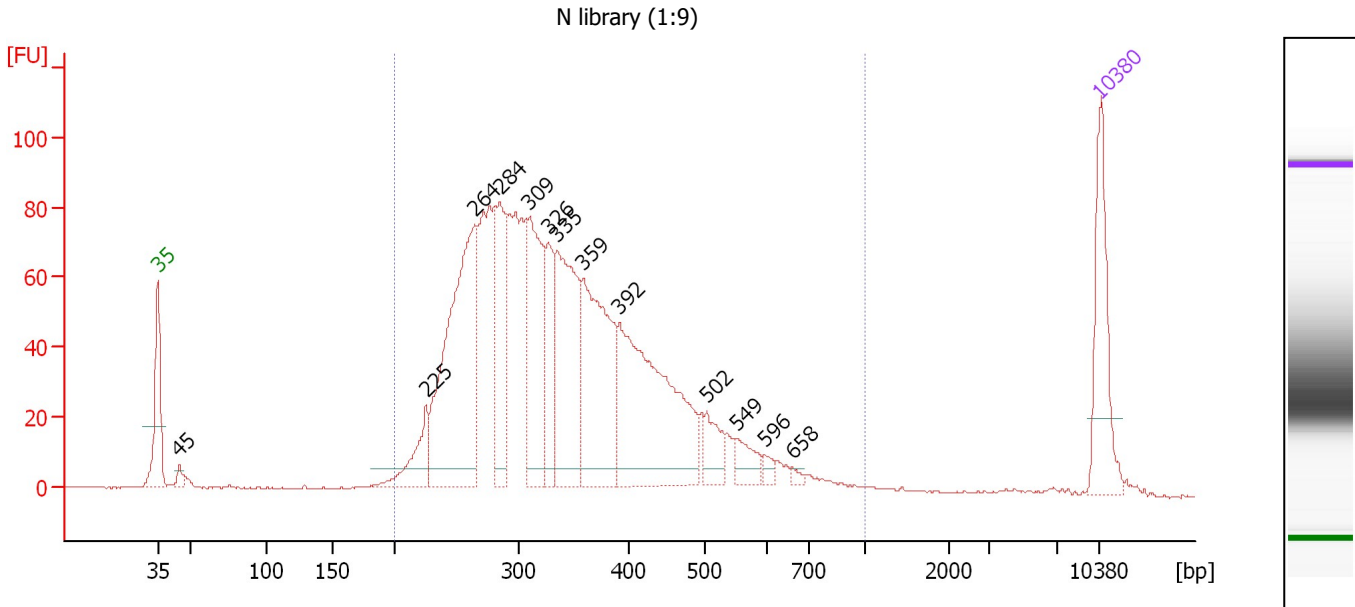
**Region table for sample 4 : M library (1:7)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	338	1,509.7	8,991.3	1,845.84	98	27.1

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**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : N library (1:9)**

Number of peaks found: 13                      Corr. Area 1: 1,723.1  
 Noise: 0.2

**Peak table for sample 5 : N library (1:9)**

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	45	10.32	347.4		44.60
3	225	54.56	368.0		62.93
4	264	312.77	1,796.5		66.54
5	284	133.35	710.3		68.45
6	309	163.56	801.8		70.61
7	326	81.58	378.7		72.00
8	335	182.93	828.2		72.67
9	359	197.32	832.8		74.63
10	392	267.89	1,034.7		77.30
11	502	35.08	105.8		83.79
12	549	24.52	67.6		85.96
13	596	7.89	20.1		88.12
14	658	4.75	10.9		90.13
15	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 5 : N library (1:9)**

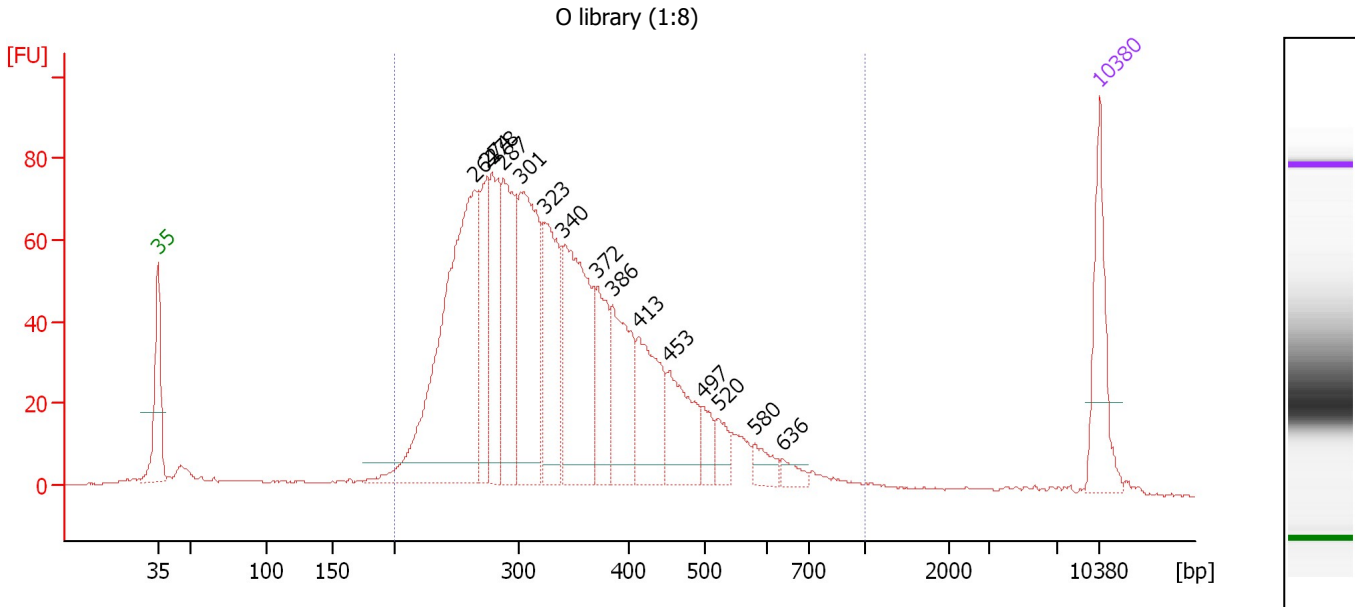
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	353	1,723.1	9,140.6	1,936.75	97	29.8



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**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : O library (1:8)**

Number of peaks found: 15                      Corr. Area 1: 1,628.4  
 Noise: 0.2

**Peak table for sample 6 : O library (1:8)**

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	264	515.97	2,961.4		66.56
3	274	109.17	604.7		67.44
4	278	143.83	783.8		67.85
5	287	184.49	973.9		68.68
6	301	250.56	1,260.4		69.97
7	323	168.86	791.9		71.74
8	340	242.55	1,079.5		73.13
9	372	96.21	391.9		75.67
10	386	125.91	494.1		76.81
11	413	117.10	429.7		78.67
12	453	93.86	314.3		80.95
13	497	30.02	91.6		83.49
14	520	25.38	73.9		84.63
15	580	21.56	56.4		87.37
16	636	13.50	32.1		89.44
17	10,380	75.00	10.9	Upper Marker	113.00

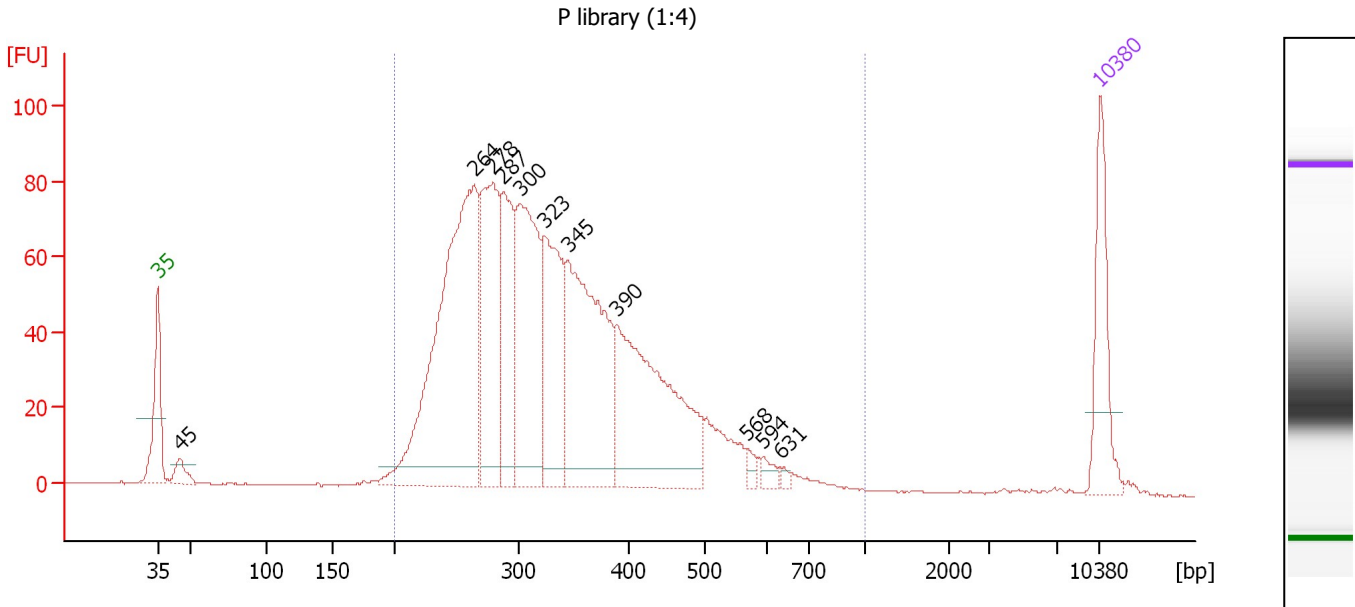
**Region table for sample 6 : O library (1:8)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	351	1,628.4	10,972.4	2,302.81	94	30.5

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**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : P library (1:4)**

Number of peaks found: 11                      Corr. Area 1: 1,668.9  
 Noise: 0.1

**Peak table for sample 7 : P library (1:4)**

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	45	23.78	797.3		44.62
3	264	541.95	3,110.2		66.56
4	278	239.43	1,303.9		67.87
5	287	142.70	752.6		68.71
6	300	253.94	1,280.8		69.91
7	323	178.45	836.6		71.74
8	345	310.92	1,366.9		73.47
9	390	294.58	1,145.8		77.08
10	568	9.78	26.1		86.82
11	594	11.53	29.4		88.03
12	631	5.10	12.3		89.28
13	10,380	75.00	10.9	Upper Marker	113.00

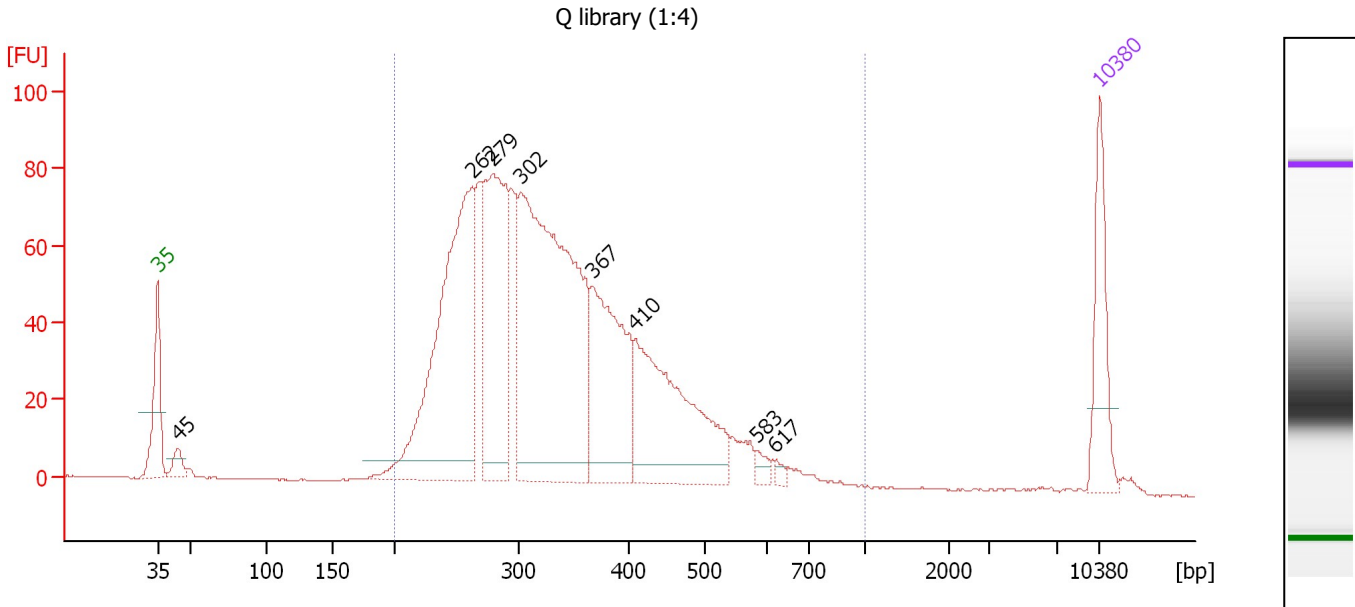
**Region table for sample 7 : P library (1:4)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	341	1,668.9	10,264.2	2,114.29	97	28.4

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : Q library (1:4)**

Number of peaks found: 8                      Corr. Area 1: 1,640.8  
 Noise: 0.2

**Peak table for sample 8 : Q library (1:4)**

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	45	25.36	862.0		44.53
3	262	499.31	2,884.1		66.40
4	279	321.87	1,748.8		67.93
5	302	664.84	3,336.4		70.03
6	367	241.03	994.4		75.29
7	410	267.69	989.4		78.50
8	583	11.11	28.9		87.55
9	617	6.40	15.7		88.86
10	10,380	75.00	10.9	Upper Marker	113.00

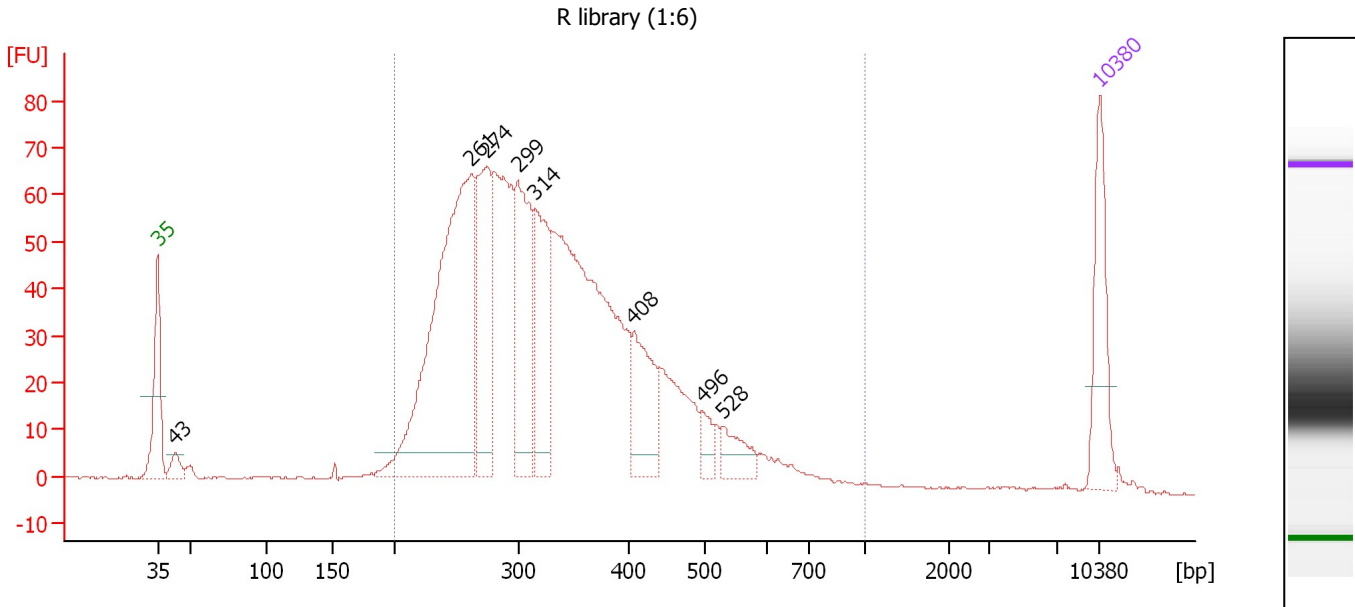
**Region table for sample 8 : Q library (1:4)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	343	1,640.8	10,795.7	2,233.93	97	28.4

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

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**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : R library (1:6)**

Number of peaks found: 8      Corr. Area 1: 1,415.9  
 Noise: 0.2

**Peak table for sample 9 : R library (1:6)**

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	43	20.99	735.1		44.32
3	261	548.37	3,181.3		66.30
4	274	180.87	1,001.1		67.46
5	299	200.30	1,015.3		69.78
6	314	150.92	727.1		71.04
7	408	98.82	367.3		78.37
8	496	21.82	66.7		83.43
9	528	34.92	100.3		84.96
10	10,380	75.00	10.9	Upper Marker	113.00

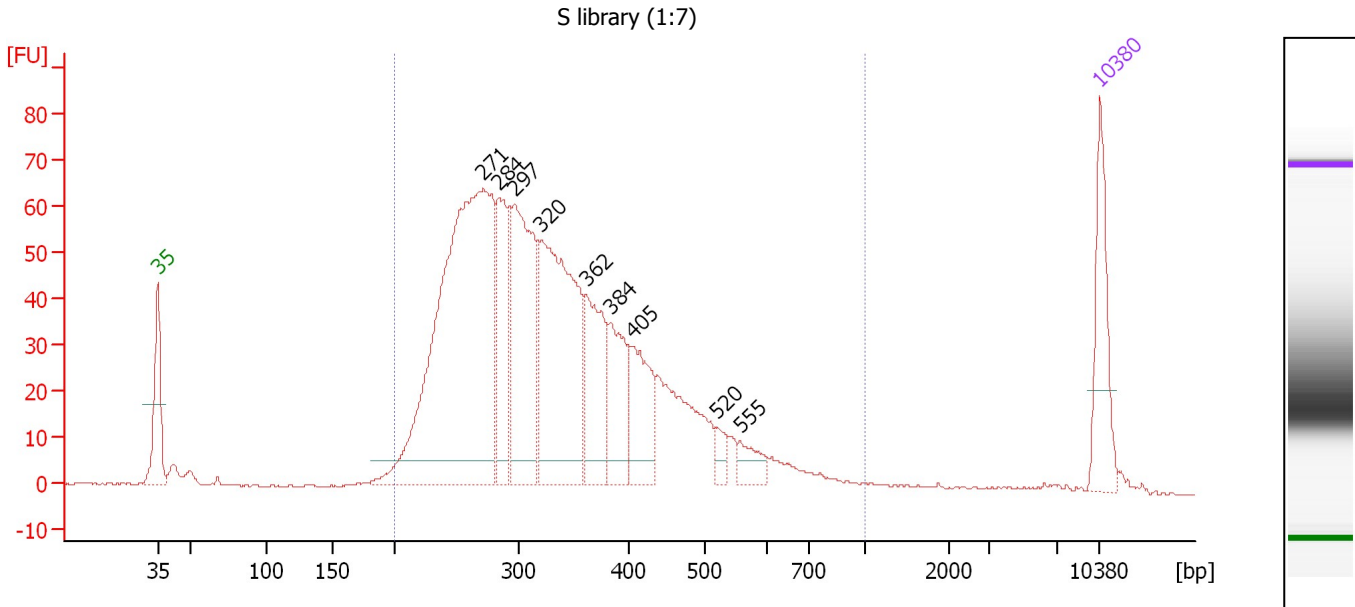
**Region table for sample 9 : R library (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	341	1,415.9	10,931.2	2,239.86	95	29.4

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**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : S library (1:7)**

Number of peaks found: 9                      Corr. Area 1: 1,338.7  
 Noise: 0.2

**Peak table for sample 10 : S library (1:7)**

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	271	764.53	4,275.2		67.20
3	284	134.28	717.3		68.37
4	297	262.73	1,340.9		69.59
5	320	355.70	1,683.5		71.50
6	362	131.77	552.0		74.84
7	384	100.10	394.9		76.65
8	405	96.98	362.4		78.24
9	520	17.54	51.1		84.61
10	555	27.04	73.8		86.25
11	10,380	75.00	10.9	Upper Marker	113.00

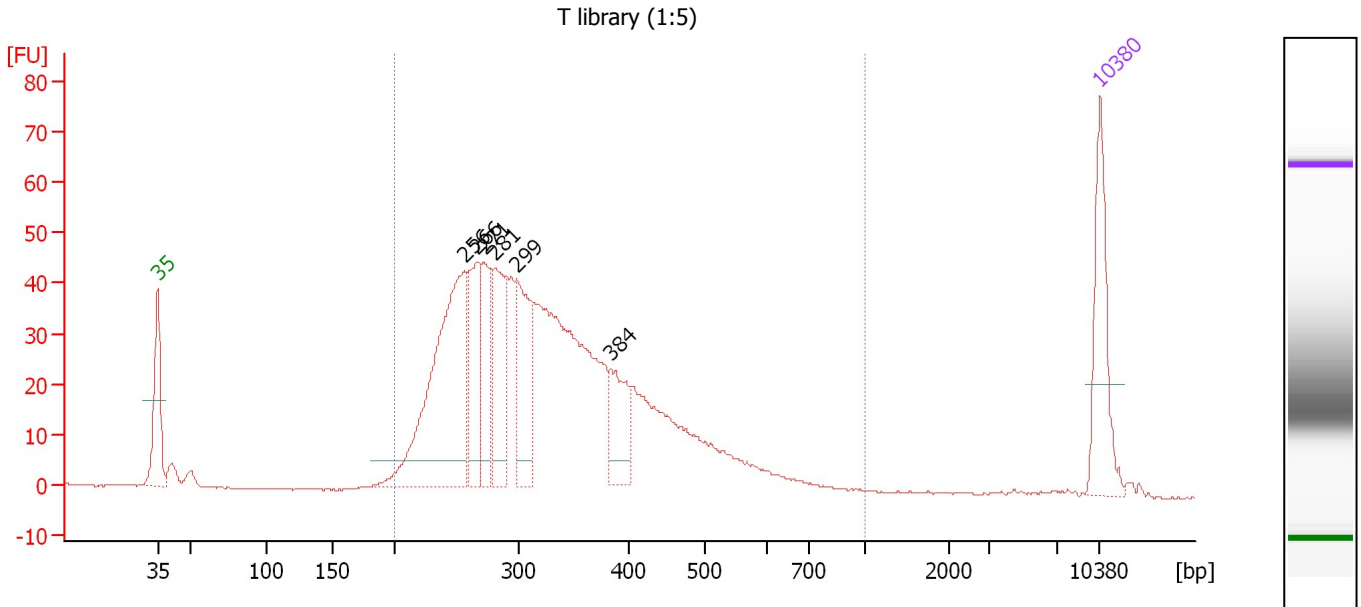
**Region table for sample 10 : S library (1:7)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	345	1,338.7	10,698.8	2,206.05	95	31.2

Assay Class: High Sensitivity DNA Assay  
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**Electropherogram Summary Continued ...**



**Overall Results for sample 11 : T library (1:5)**

Number of peaks found: 6                      Corr. Area 1: 895.8  
 Noise: 0.1

**Peak table for sample 11 : T library (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	256	326.98	1,936.9		65.80
3	266	100.77	574.9		66.71
4	271	82.29	459.4		67.24
5	281	111.12	600.0		68.09
6	299	105.69	536.4		69.74
7	384	66.14	261.2		76.61
8	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 11 : T library (1:5)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	337	895.8	7,357.3	1,498.09	97	28.8

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

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**Gel Image**

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...t\data\2016-10-19\2016-10-19\_004\_HiSeq670\_Libraries\_K-T.xad

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**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		10/19/2016 2:35:26 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2016-10-19\2016-10-19_004.xad)		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		10/19/2016 1:55:05 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1