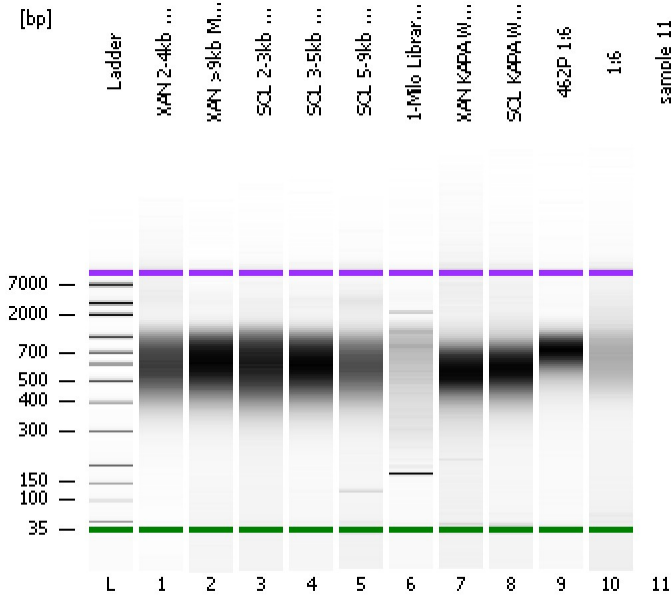


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
Modified: 1/26/2017 11:33:26 AM

Electrophoresis File Run Summary



Instrument Information:

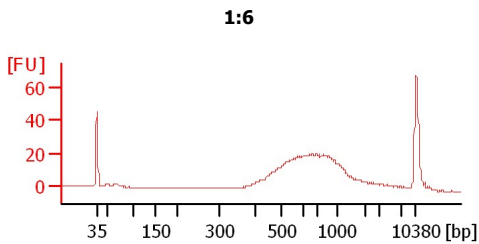
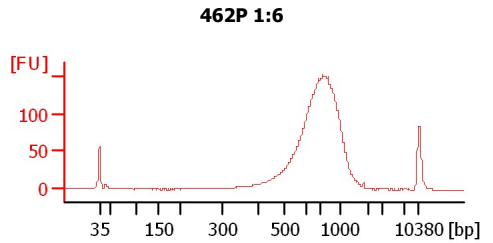
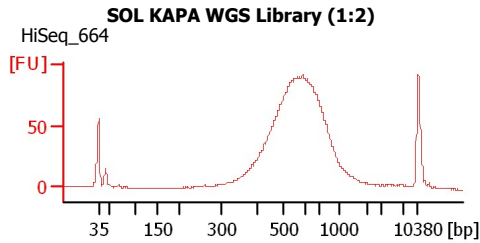
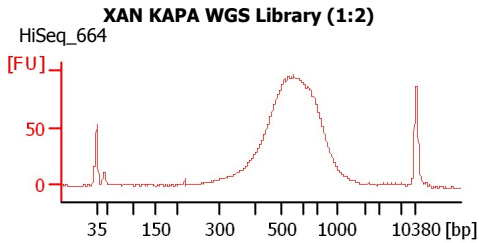
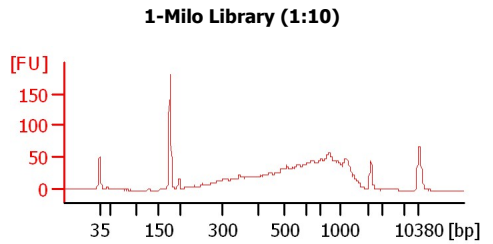
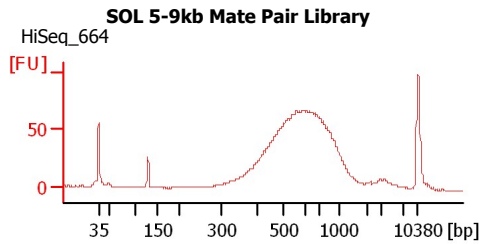
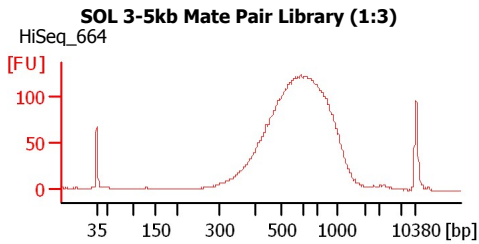
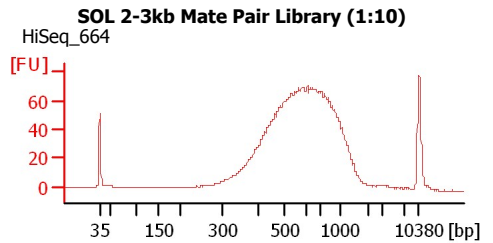
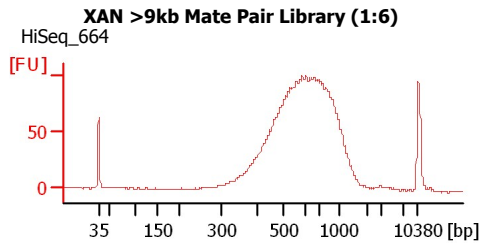
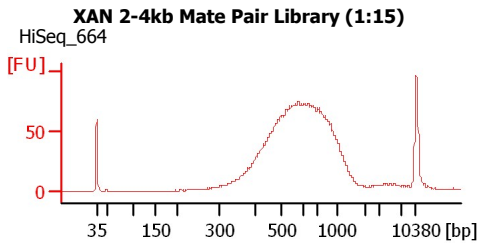
Instrument Name: DE13701086      Firmware: C.01.069  
Serial#: DE13701086      Type: G2938B

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:



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
XAN 2-4kb Mate Pair Library (1:15)	HiSeq_664	<input type="checkbox"/>	✓			
XAN >9kb Mate Pair Library (1:6)	HiSeq_664	<input type="checkbox"/>	✓			
SOL 2-3kb Mate Pair Library (1:10)	HiSeq_664	<input type="checkbox"/>	✓			
SOL 3-5kb Mate Pair Library (1:3)	HiSeq_664	<input type="checkbox"/>	✓			
SOL 5-9kb Mate Pair Library	HiSeq_664	<input type="checkbox"/>	✓			
1-Milo Library (1:10)		<input type="checkbox"/>	✓			
XAN KAPA WGS Library (1:2)	HiSeq_664	<input type="checkbox"/>	✓			
SOL KAPA WGS Library (1:2)	HiSeq_664	<input type="checkbox"/>	✓			
462P 1:6		<input type="checkbox"/>	✓			
1:6		<input type="checkbox"/>	✓			
sample 11		<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
Modified: 1/26/2017 11:33:26 AM

**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

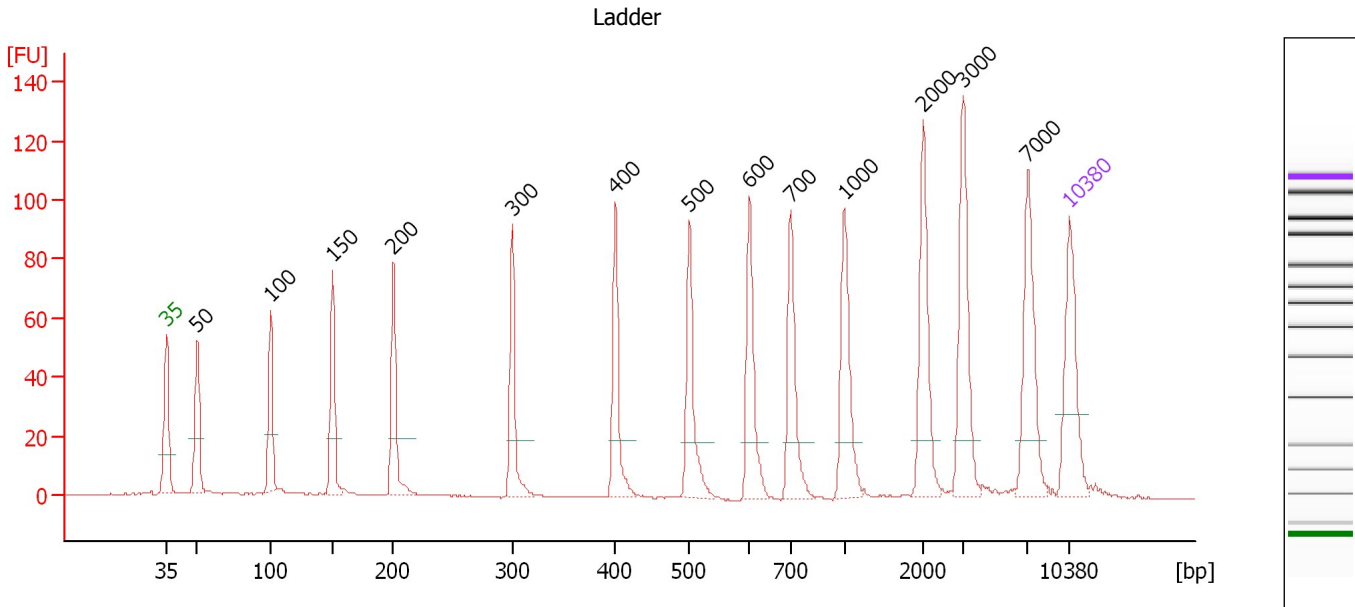
**Ladder**

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:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

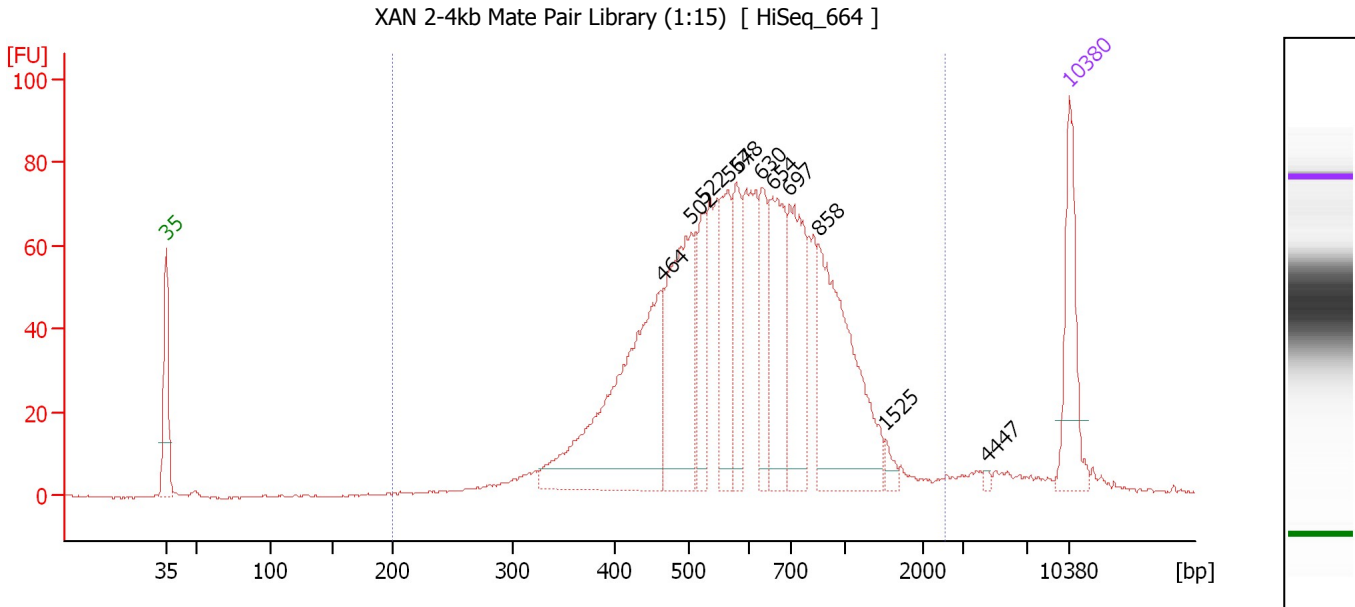
**Peak table for Ladder**

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	45.38
3	100	150.00	2,272.7	Ladder Peak	51.07
4	150	150.00	1,515.2	Ladder Peak	55.88
5	200	150.00	1,136.4	Ladder Peak	60.60
6	300	150.00	757.6	Ladder Peak	69.83
7	400	150.00	568.2	Ladder Peak	77.81
8	500	150.00	454.5	Ladder Peak	83.54
9	600	150.00	378.8	Ladder Peak	88.21
10	700	150.00	324.7	Ladder Peak	91.42
11	1,000	150.00	227.3	Ladder Peak	95.55
12	2,000	150.00	113.6	Ladder Peak	101.67
13	3,000	150.00	75.8	Ladder Peak	104.74
14	7,000	150.00	32.5	Ladder Peak	109.79
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : XAN 2-4kb Mate Pair Library (1:15)**

Number of peaks found: 11                      Corr. Area 1: 1,507.3  
 Noise: 0.2

**Peak table for sample 1 : XAN 2-4kb Mate Pair Library (1:15)**

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	464	343.39	1,122.0		81.46
3	502	214.93	648.2		83.65
4	522	65.70	190.6		84.58
5	564	100.71	270.5		86.53
6	578	76.53	200.7		87.16
7	630	73.60	177.1		89.16
8	654	125.22	290.1		89.94
9	697	140.10	304.7		91.31
10	858	221.26	390.5		93.60
11	1,525	9.28	9.2		98.77
12	4,447	2.61	0.9		106.57
13	10,380	75.00	10.9	Upper Marker	113.00

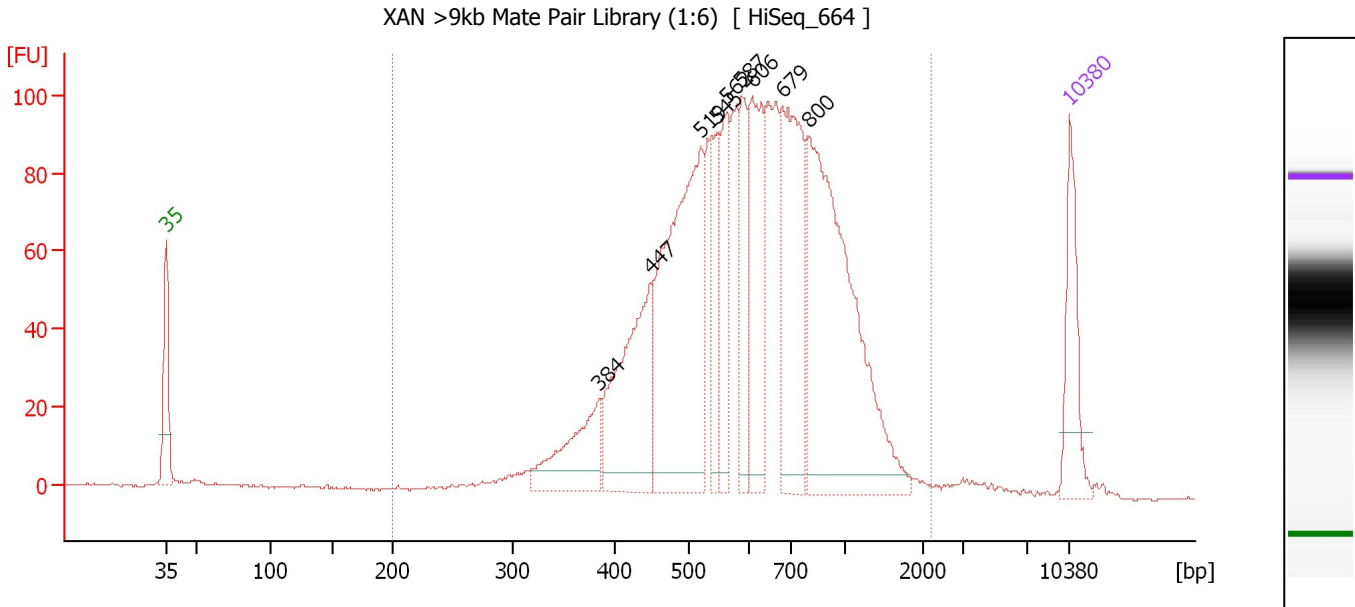
**Region table for sample 1 : XAN 2-4kb Mate Pair Library (1:15)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,564	659	1,507.3	4,971.2	1,813.79	95	43.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : XAN >9kb Mate Pair Library (1:6)**

Number of peaks found: 9                      Corr. Area 1: 1,936.5  
 Noise: 0.2

**Peak table for sample 2 : XAN >9kb Mate Pair 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	384	119.72	472.7		76.51
3	447	230.95	782.3		80.52
4	519	420.17	1,226.4		84.43
5	545	88.85	246.9		85.66
6	562	102.87	277.3		86.44
7	587	104.20	268.9		87.61
8	606	159.11	397.9		88.39
9	679	247.04	551.3		90.74
10	800	465.10	880.6		92.80
11	10,380	75.00	10.9	Upper Marker	113.00

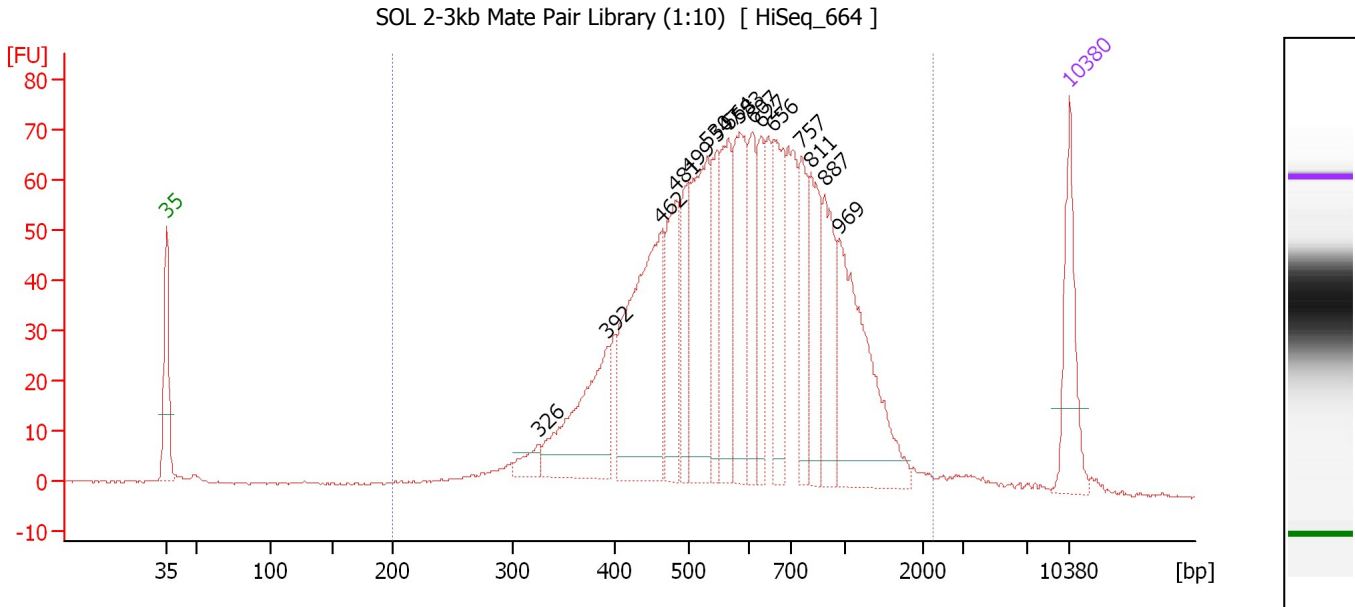
**Region table for sample 2 : XAN >9kb Mate Pair Library (1:6)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	2,212	663	1,936.5	6,086.9	2,293.50	98	38.6

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : SOL 2-3kb Mate Pair Library (1:10)**

Number of peaks found: 16                      Corr. Area 1: 1,520.7  
 Noise: 0.2

**Peak table for sample 3 : SOL 2-3kb Mate Pair Library (1:10)**

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	326	24.62	114.5		71.89
3	392	169.02	652.5		77.21
4	462	286.96	940.6		81.38
5	481	118.75	373.9		82.47
6	499	77.31	234.9		83.46
7	530	185.31	529.6		84.95
8	547	75.19	208.2		85.74
9	564	115.90	311.2		86.54
10	583	132.62	344.4		87.43
11	607	78.81	196.8		88.43
12	627	73.24	177.0		89.07
13	656	116.94	270.0		90.01
14	757	76.36	152.9		92.20
15	811	97.56	182.3		92.94
16	887	95.82	163.8		93.99
17	969	197.71	309.0		95.13
18	10,380	75.00	10.9	Upper Marker	113.00

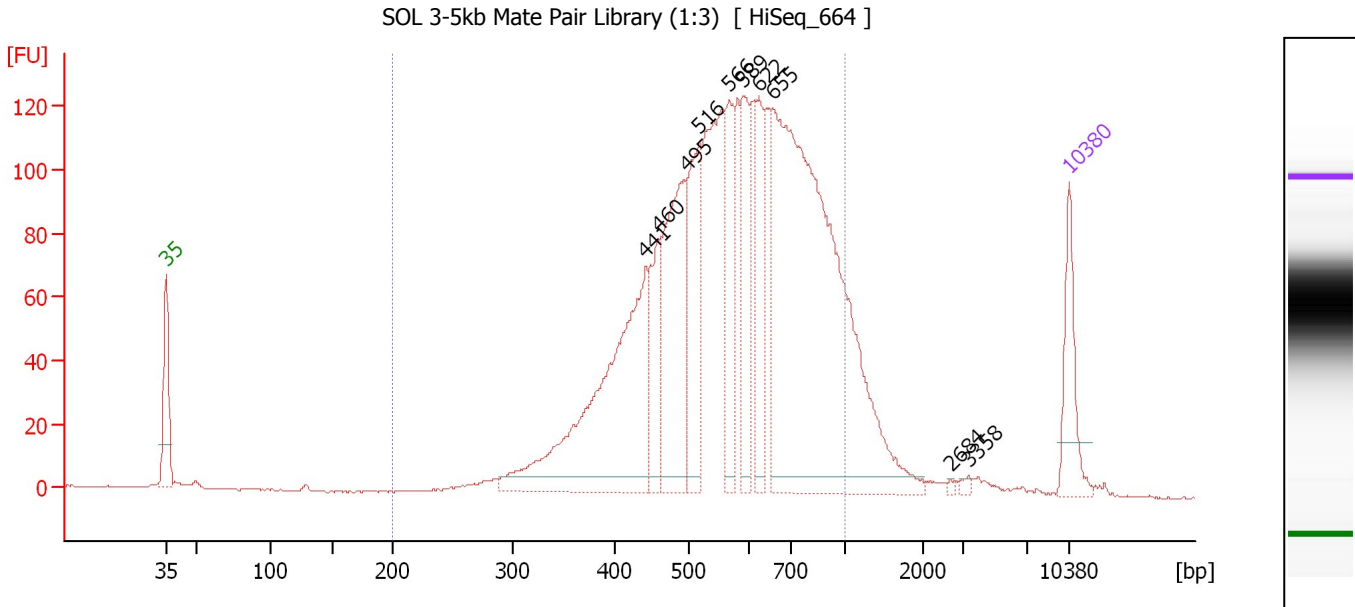
**Region table for sample 3 : SOL 2-3kb Mate Pair Library (1:10)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	2,268	656	1,520.7	6,397.7	2,308.23	97	42.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : SOL 3-5kb Mate Pair Library (1:3)**

Number of peaks found: 10                      Corr. Area 1: 2,219.9  
 Noise: 0.3

**Peak table for sample 4 : SOL 3-5kb Mate Pair 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	441	495.36	1,703.7		80.13
3	460	104.20	343.2		81.25
4	495	288.73	883.1		83.28
5	516	178.49	524.1		84.29
6	566	123.03	329.3		86.62
7	589	120.71	310.6		87.69
8	622	126.28	307.7		88.91
9	655	965.46	2,233.5		89.97
10	2,684	2.74	1.5		103.77
11	3,358	5.19	2.3		105.19
12	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 4 : SOL 3-5kb Mate Pair Library (1:3)**

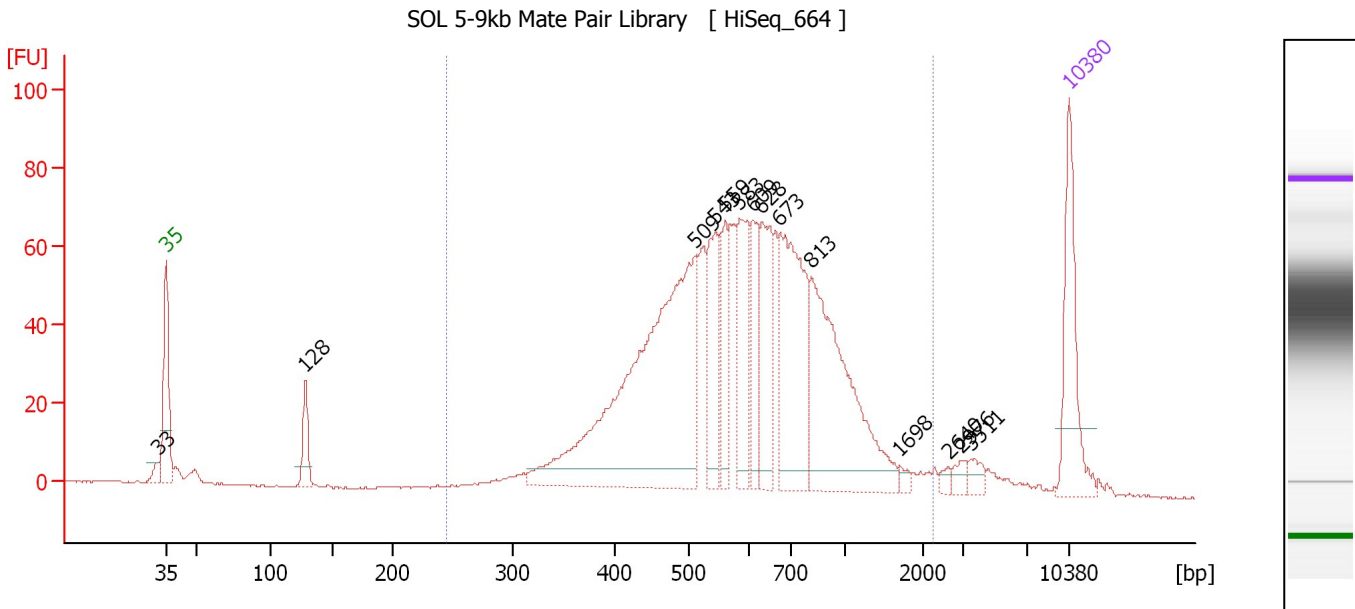
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	591	2,219.9	7,871.4	2,792.47	91	26.4



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 5 : SOL 5-9kb Mate Pair Library**

Number of peaks found: 14                      Corr. Area 1: 1,307.2  
 Noise: 0.2

**Peak table for sample 5 : SOL 5-9kb Mate Pair Library**

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	128	37.97	449.7		53.76
4	509	463.30	1,378.6		83.97
5	543	81.23	226.5		85.57
6	559	56.63	153.6		86.29
7	583	77.63	201.7		87.42
8	609	54.57	135.8		88.50
9	628	86.83	209.4		89.12
10	673	169.04	380.4		90.56
11	813	212.76	396.3		92.98
12	1,698	4.95	4.4		99.82
13	2,640	4.65	2.7		103.63
14	2,976	7.68	3.9		104.66
15	3,511	9.72	4.2		105.38
16	10,380	75.00	10.9	Upper Marker	113.00

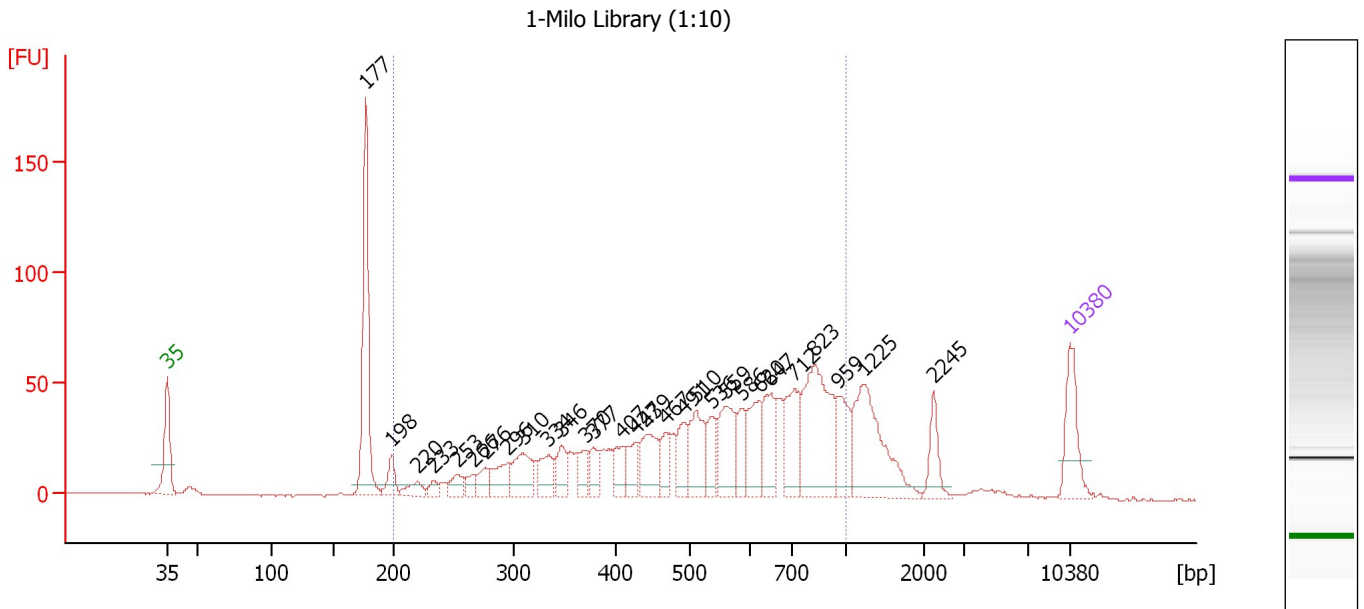
**Region table for sample 5 : SOL 5-9kb Mate Pair Library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
245	2,251	650	1,307.2	3,927.8	1,444.98	93	41.5

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 6 : 1-Milo Library (1:10)**

Number of peaks found: 29                      Corr. Area 1: 1,087.0  
 Noise: 0.2

**Peak table for sample 6 : 1-Milo Library (1:10)**

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	177	345.69	2,965.5		58.39
3	198	44.14	338.3		60.38
4	220	30.18	208.0		62.42
5	233	17.06	110.8		63.68
6	253	33.34	199.9		65.46
7	266	21.24	120.8		66.72
8	276	33.74	185.3		67.61
9	296	59.59	305.3		69.44
10	310	85.84	420.2		70.59
11	334	60.76	275.8		72.53
12	346	50.82	222.3		73.52
13	370	40.08	164.2		75.41
14	377	41.03	164.8		75.98
15	407	48.34	180.1		78.18
16	427	50.45	179.1		79.34
17	439	90.01	310.3		80.07
18	467	45.76	148.5		81.64
19	491	58.12	179.5		83.00
20	510	96.67	287.3		83.99
21	536	53.94	152.6		85.20
22	559	107.05	290.1		86.30
23	586	55.43	143.3		87.55
24	620	85.06	207.7		88.86
25	647	88.23	206.8		89.70

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

### Electropherogram Summary Continued ...

#### ... Peak table for sample 6 : 1-Milo Library (1:10)

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	712	104.23	221.7		91.59
27	823	237.59	437.6		93.10
28	959	76.60	121.0		94.99
29	1,225	193.02	238.7		96.93
30	2,245	44.84	30.3		102.42
31	10,380	75.00	10.9	Upper Marker	113.00

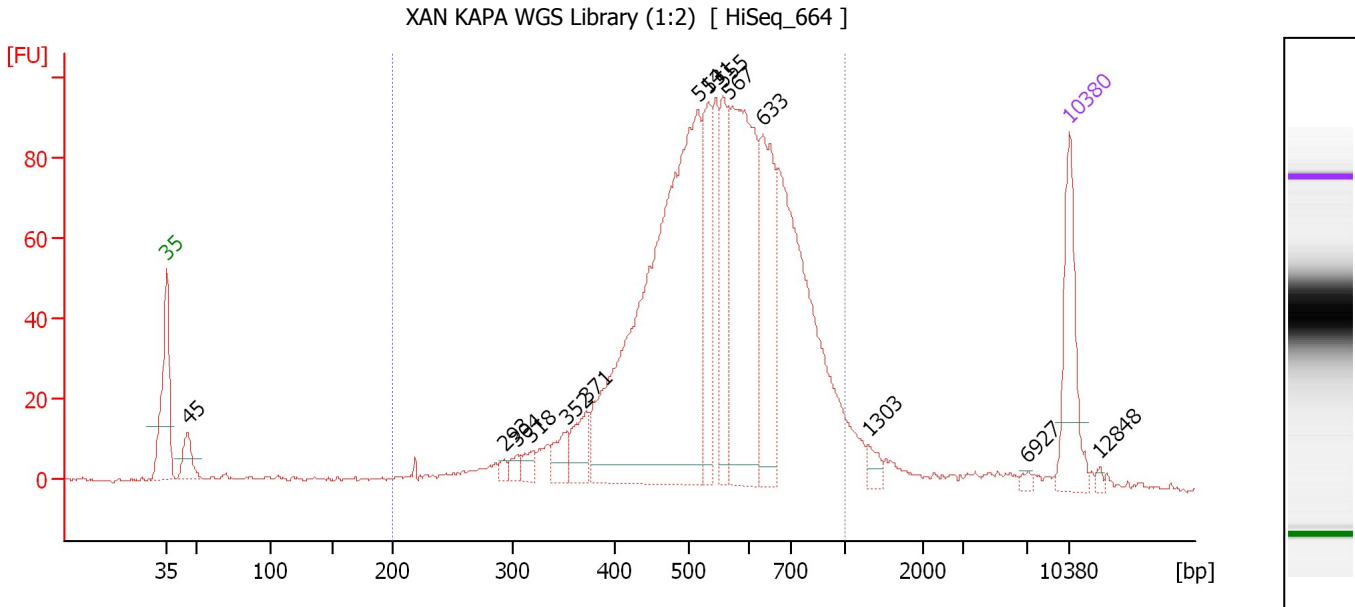
#### Region table for sample 6 : 1-Milo Library (1:10)

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	560	1,087.0	6,127.7	1,851.38	73	35.2

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 7 : XAN KAPA WGS Library (1:2)**

Number of peaks found: 14                      Corr. Area 1: 1,579.6  
 Noise: 0.6

**Peak table for sample 7 : XAN KAPA WGS Library (1:2)**

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	45	40.15	1,340.2		44.65
3	293	7.76	40.1		69.19
4	304	11.62	57.9		70.15
5	318	14.19	67.6		71.27
6	352	27.73	119.3		73.98
7	371	42.74	174.4		75.52
8	514	692.35	2,040.3		84.20
9	531	110.03	313.8		85.00
10	555	93.35	254.8		86.12
11	567	298.75	798.9		86.65
12	633	143.29	343.1		89.26
13	1,303	11.77	13.7		97.40
14	6,927	3.82	0.8		109.70
15	10,380	75.00	10.9	Upper Marker	113.00
16	12,848	0.00	0.0		115.34

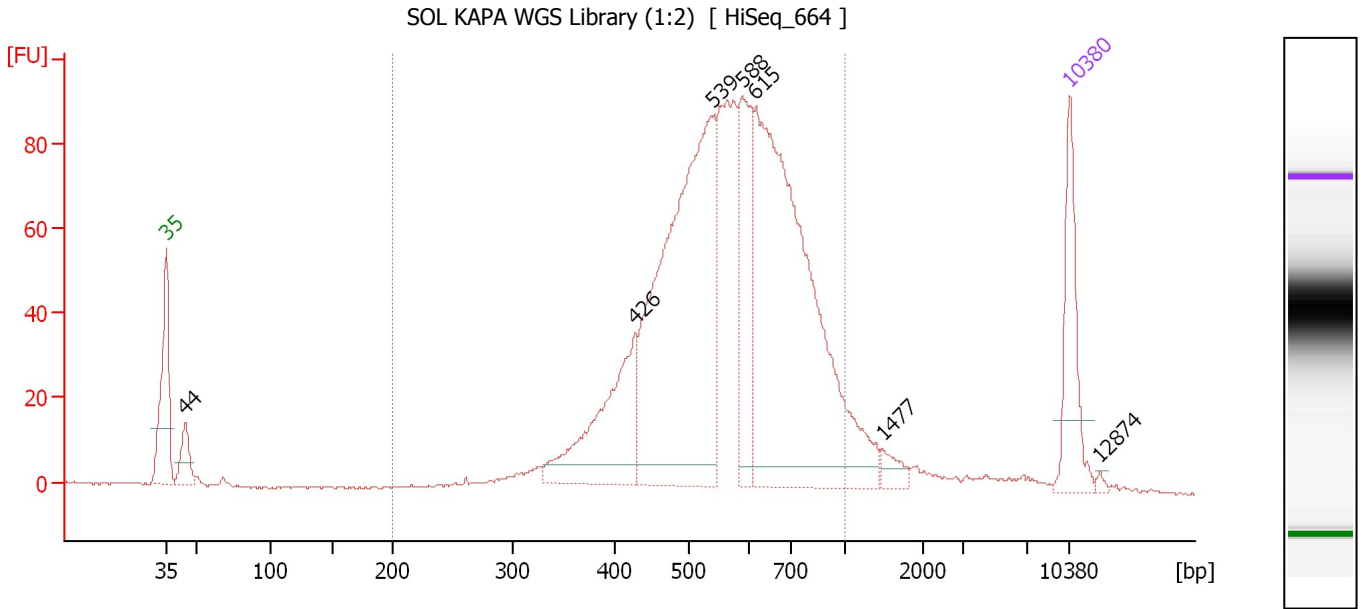
**Region table for sample 7 : XAN KAPA WGS Library (1:2)**

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	557	1,579.6	5,997.6	2,005.27	89	25.0

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

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 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 8 : SOL KAPA WGS Library (1:2)**

Number of peaks found: 7                      Corr. Area 1: 1,396.1  
 Noise: 0.3

**Peak table for sample 8 : SOL KAPA WGS Library (1:2)**

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	44	46.72	1,603.4		44.45
3	426	183.20	651.0		79.32
4	539	555.31	1,562.1		85.34
5	588	135.17	348.2		87.66
6	615	591.31	1,457.5		88.68
7	1,477	16.36	16.8		98.47
8	10,380	75.00	10.9	Upper Marker	113.00
9	12,874	0.00	0.0		115.37

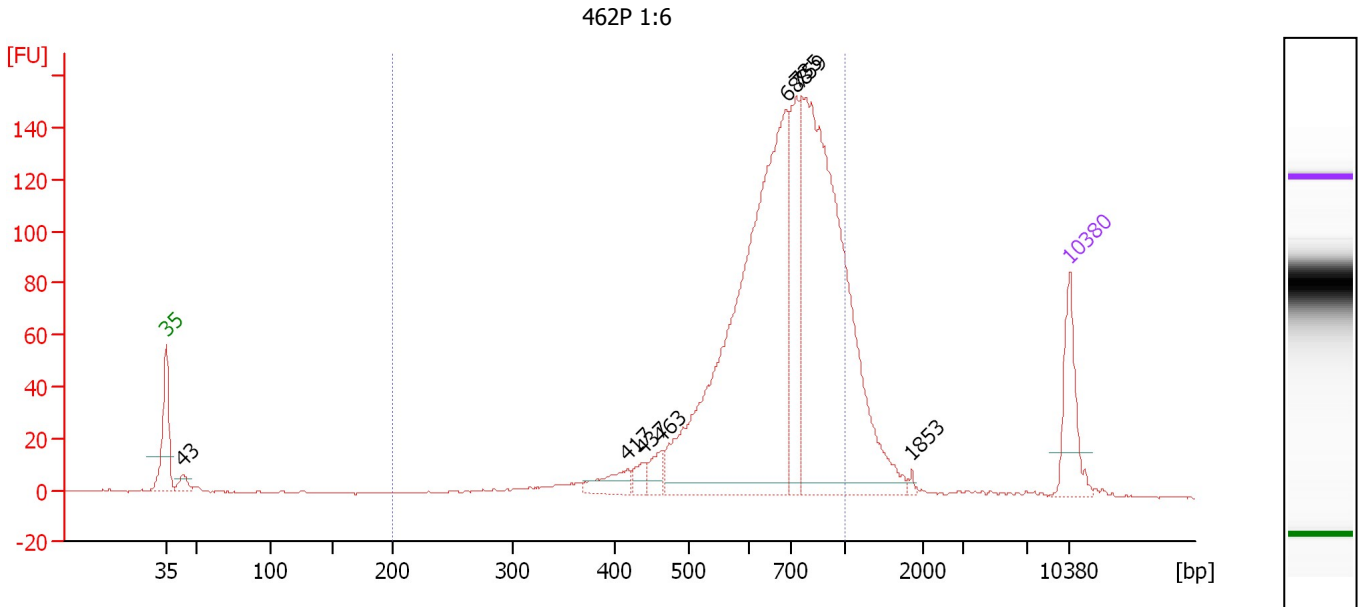
**Region table for sample 8 : SOL KAPA WGS Library (1:2)**

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	578	1,396.1	4,857.4	1,721.89	91	23.5

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 9 : 462P 1:6**

Number of peaks found: 8                      Corr. Area 1: 1,475.0  
 Noise: 0.3

**Peak table for sample 9 : 462P 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	23.92	846.2		44.24
3	417	40.38	146.9		78.76
4	437	20.66	71.6		79.95
5	463	28.16	92.2		81.41
6	688	949.76	2,091.1		91.04
7	735	187.97	387.3		91.90
8	759	808.63	1,614.5		92.23
9	1,853	4.57	3.7		100.77
10	10,380	75.00	10.9	Upper Marker	113.00

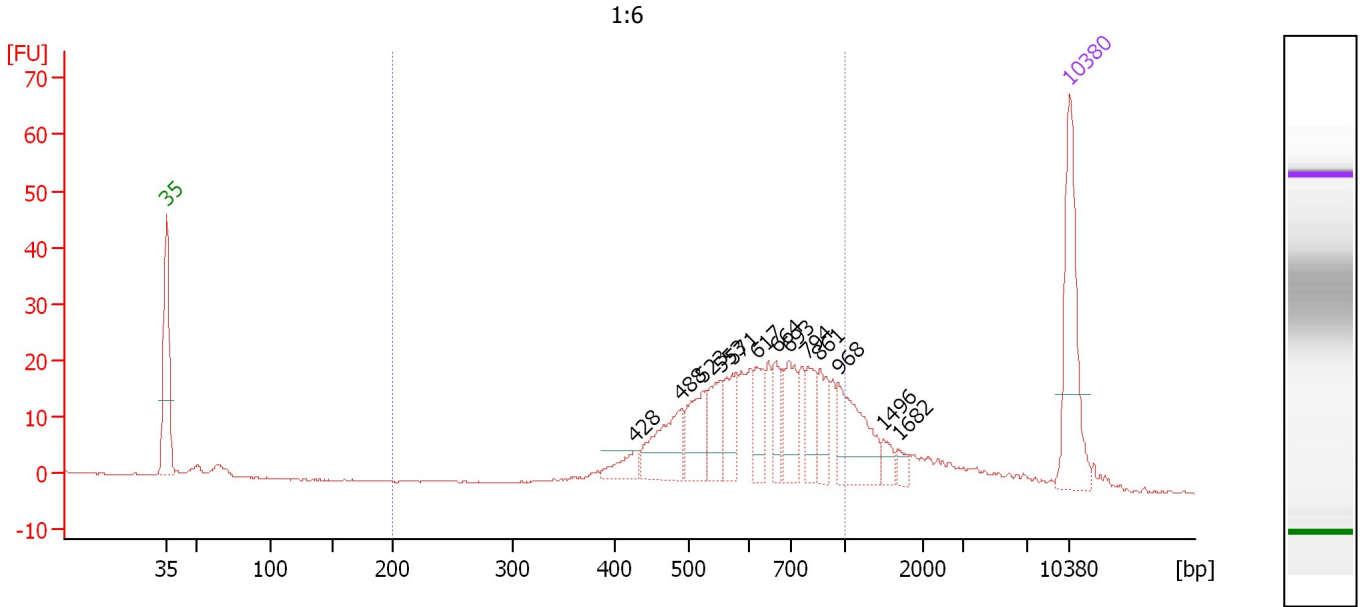
**Region table for sample 9 : 462P 1:6**

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	690	1,475.0	4,390.1	1,860.44	87	21.8

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 10 : 1:6**

Number of peaks found: 13                      Corr. Area 1: 312.7  
 Noise: 0.1

**Peak table for sample 10 : 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	428	18.10	64.2		79.39
3	488	58.07	180.2		82.87
4	523	42.61	123.5		84.61
5	553	37.13	101.7		86.02
6	571	30.62	81.3		86.84
7	617	26.78	65.8		88.74
8	664	23.92	54.6		90.26
9	693	38.67	84.6		91.19
10	794	27.39	52.3		92.71
11	861	26.48	46.6		93.64
12	968	60.69	95.0		95.11
13	1,496	9.95	10.1		98.59
14	1,682	7.05	6.3		99.73
15	10,380	75.00	10.9	Upper Marker	113.00

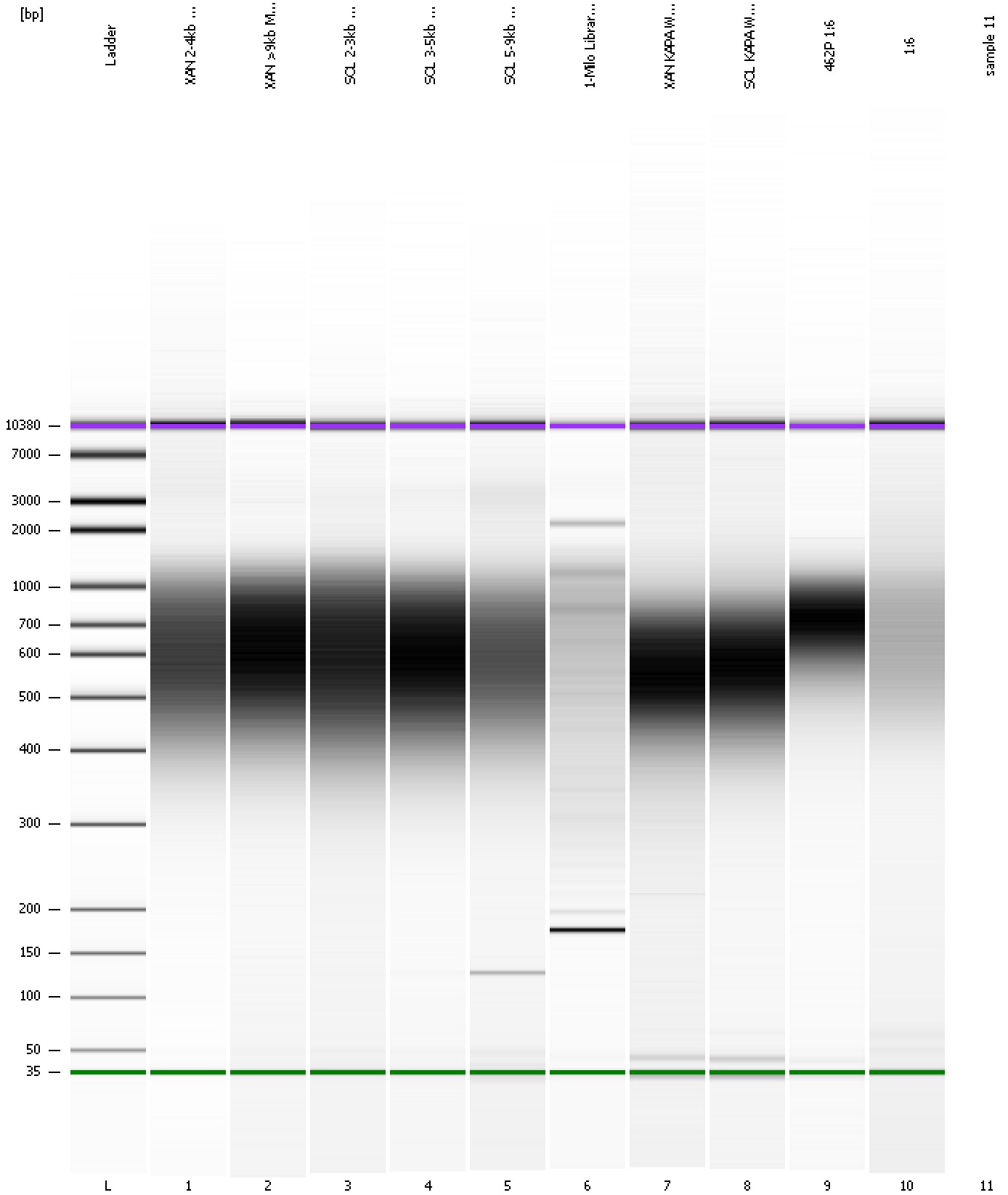
**Region table for sample 10 : 1:6**

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	640	312.7	1,213.7	477.23	76	23.9

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
Modified: 1/26/2017 11:33:26 AM

**Gel Image**





Assay Class: High Sensitivity DNA Assay  
Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
Modified: 1/26/2017 11:33:26 AM

**Invalid Samples**

Sample 11 has not been run, no results available.

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-01-26\2017-01-26\_001.xad

Created: 1/26/2017 10:54:59 AM  
 Modified: 1/26/2017 11:33:26 AM

**Run Logbook**

Description	Number	Source	Category	Sub Category	Time	Time Zone	User	Host
Run ended on port 1 (Number of wells acquired: 11)		Instrument	Run		1/26/2017 11:33:24 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2017-01-26\2017-01-26_001.xad)		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		1/26/2017 10:55:04 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1