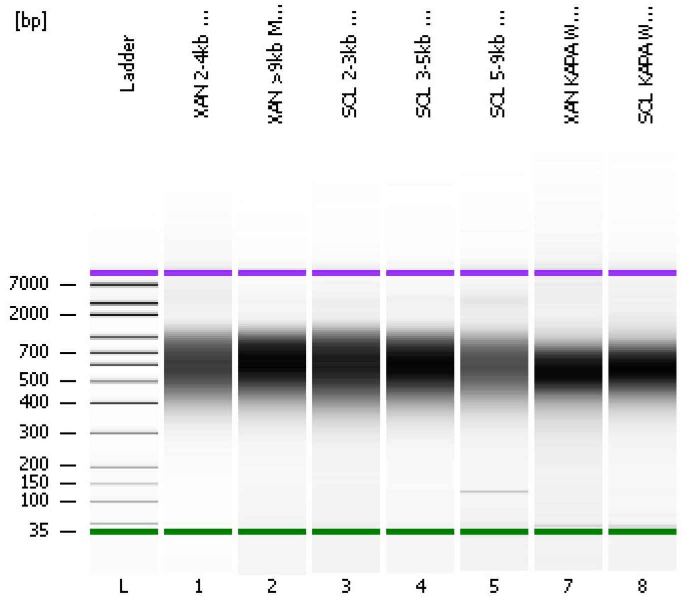
Assay Class:	High Sensitivity DNA Assay	Created:	1/26/2017 10:54:59 AM
Data Path:	C:\...1-26\2017-01-26_001_HiSeq664_MatePair_and_WGS_Libraries.xad	Modified:	1/26/2017 11:43:55 AM

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:

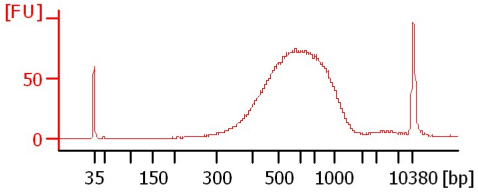
Chip Lot #:

Reagent Kit Lot #:

Chip Comments:

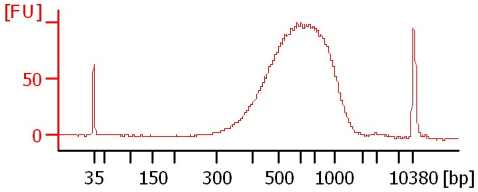
XAN 2-4kb Mate Pair Library (1:15)

HiSeq_664



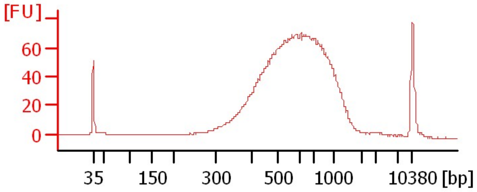
XAN >9kb Mate Pair Library (1:6)

HiSeq_664



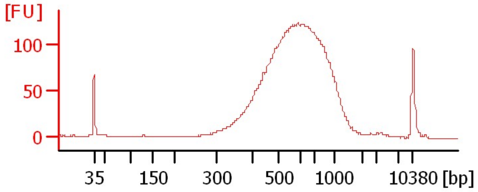
SOL 2-3kb Mate Pair Library (1:10)

HiSeq_664



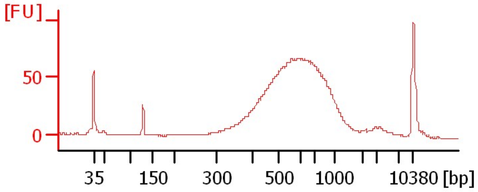
SOL 3-5kb Mate Pair Library (1:3)

HiSeq_664



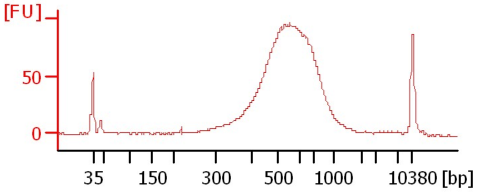
SOL 5-9kb Mate Pair Library

HiSeq_664



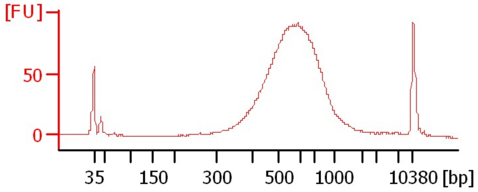
XAN KAPA WGS Library (1:2)

HiSeq_664



SOL KAPA WGS Library (1:2)

HiSeq_664



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	☐	✓			
XAN >9kb Mate Pair Library (1:6)	HiSeq_664	☐	✓			
SOL 2-3kb Mate Pair Library (1:10)	HiSeq_664	☐	✓			
SOL 3-5kb Mate Pair Library (1:3)	HiSeq_664	☐	✓			
SOL 5-9kb Mate Pair Library	HiSeq_664	☐	✓			
XAN KAPA WGS Library (1:2)	HiSeq_664	☐	✓			
SOL KAPA WGS Library (1:2)	HiSeq_664	☐	✓			
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

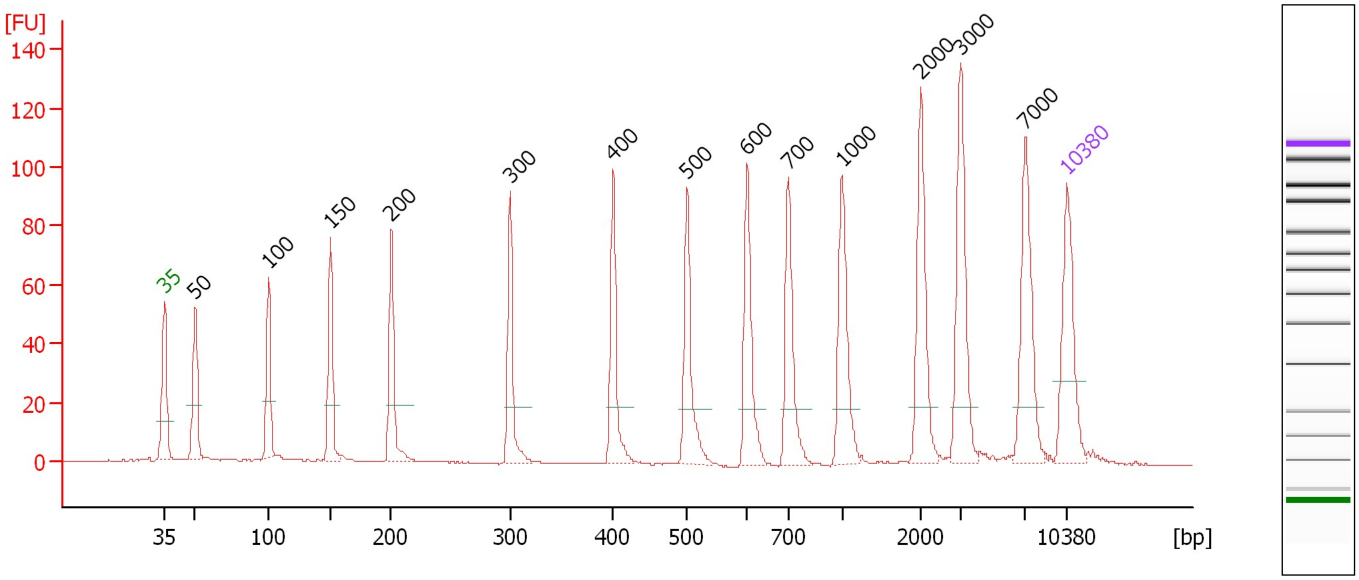
Filter Width [s] : 0.5
Polynomial Order : 4

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

Ladder



Overall Results for Ladder

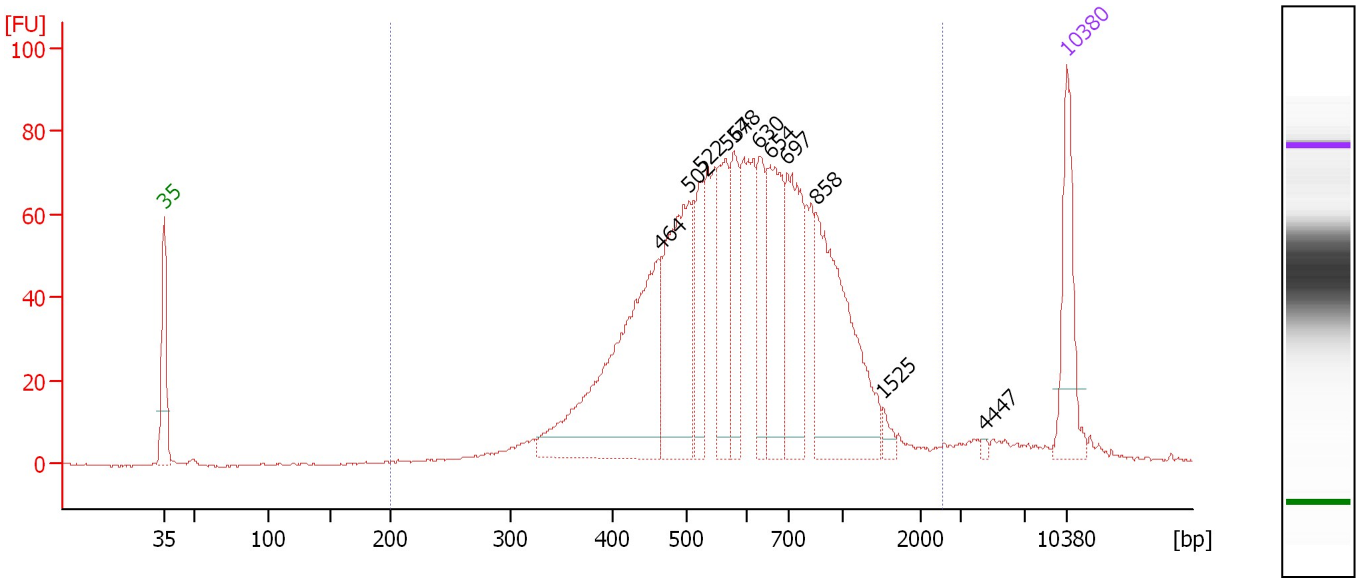
Noise: 0.2

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

Electropherogram Summary Continued ...

XAN 2-4kb Mate Pair Library (1:15) [HiSeq_664]



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)

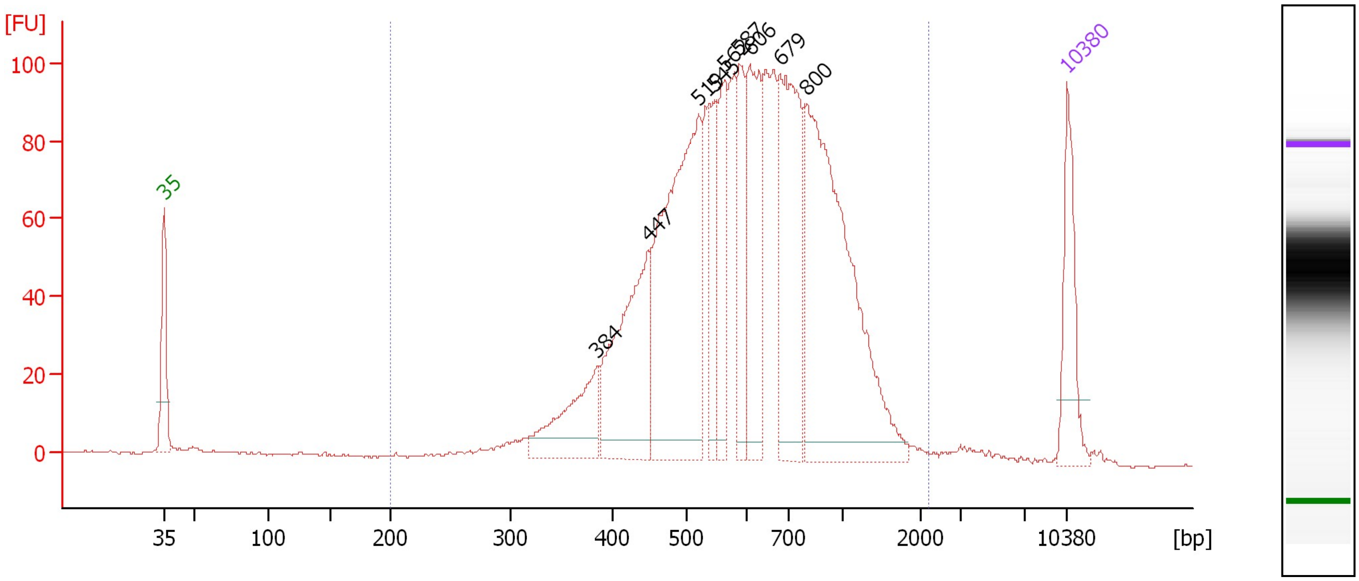
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		464	343.39	1,122.0		81.46
3		502	214.93	648.2		83.65
4		522	65.70	190.6		84.58
5		564	100.71	270.5		86.53
6		578	76.53	200.7		87.16
7		630	73.60	177.1		89.16
8		654	125.22	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]	Color	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

Electropherogram Summary Continued ...

XAN >9kb Mate Pair Library (1:6) [HiSeq_664]



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)**

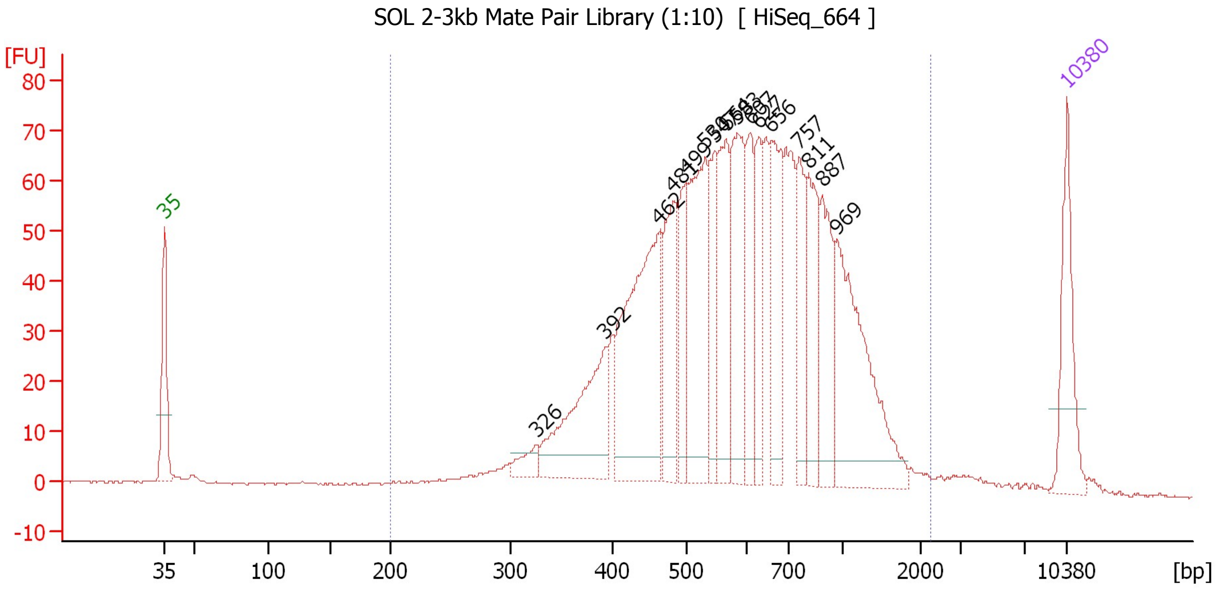
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		384	119.72	472.7		76.51
3		447	230.95	782.3		80.52
4		519	420.17	1,226.4		84.43
5		545	88.85	246.9		85.66
6		562	102.87	277.3		86.44
7		587	104.20	268.9		87.61
8		606	159.11	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

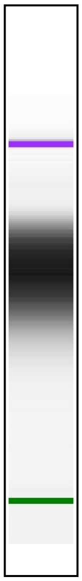
Region table for sample 2 : **XAN >9kb Mate Pair Library (1:6)**

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

Electropherogram Summary Continued ...

SOL 2-3kb Mate Pair Library (1:10) [HiSeq_664]





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)

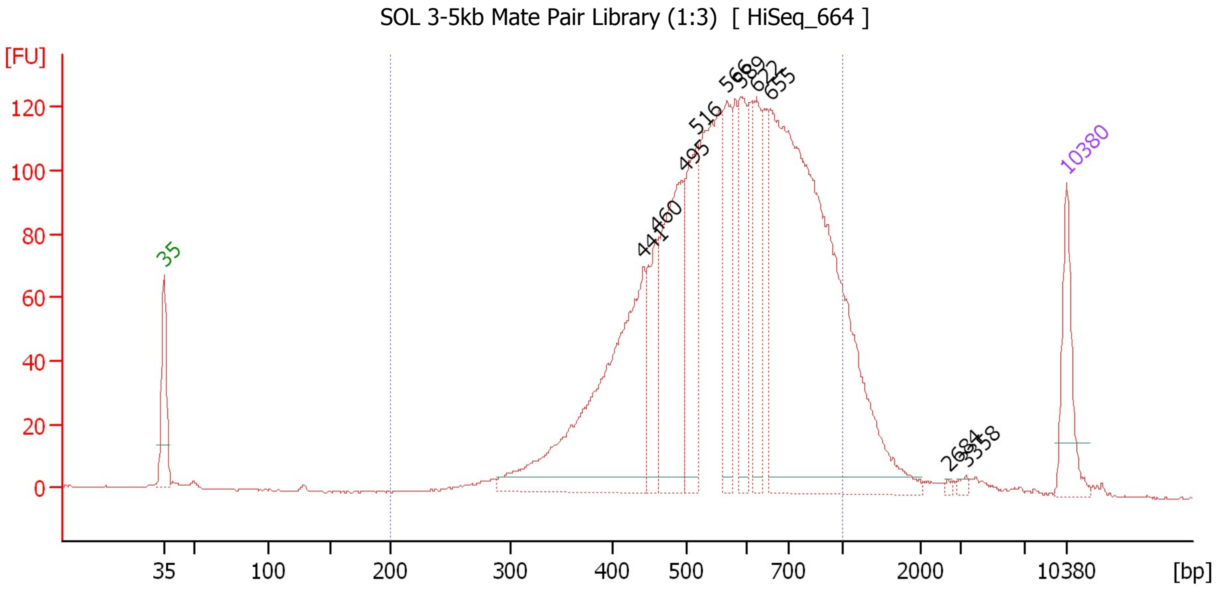
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		326	24.62	114.5		71.89
3		392	169.02	652.5		77.21
4		462	286.96	940.6		81.38
5		481	118.75	373.9		82.47
6		499	77.31	234.9		83.46
7		530	185.31	529.6		84.95
8		547	75.19	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

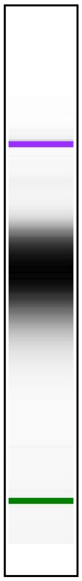
Region table for sample 3 : SOL 2-3kb Mate Pair Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	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	Created:	1/26/2017 10:54:59 AM
Data Path:	C:\...1-26\2017-01-26_001_HiSeq664_MatePair_and_WGS_Libraries.xad	Modified:	1/26/2017 11:43:55 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

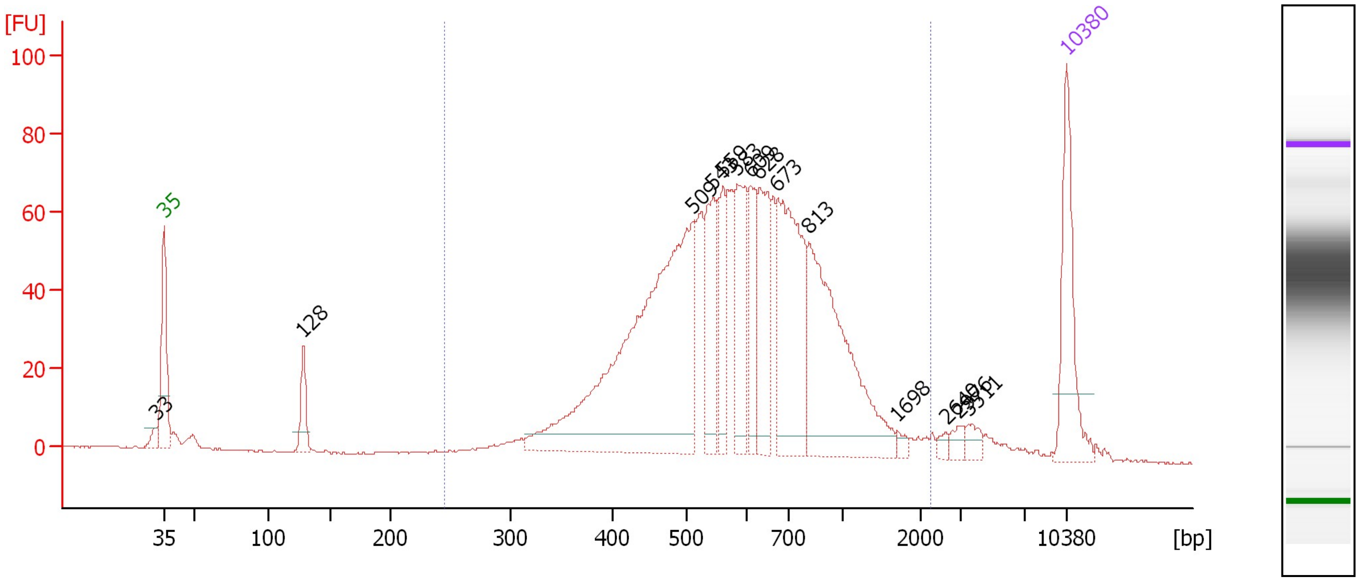
Region table for sample 4 : **SOL 3-5kb Mate Pair Library (1:3)**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [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:\...1-26\2017-01-26_001_HiSeq664_MatePair_and_WGS_Libraries.xad
Created: 1/26/2017 10:54:59 AM
Modified: 1/26/2017 11:43:55 AM

Electropherogram Summary Continued ...

SOL 5-9kb Mate Pair Library [HiSeq_664]



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**

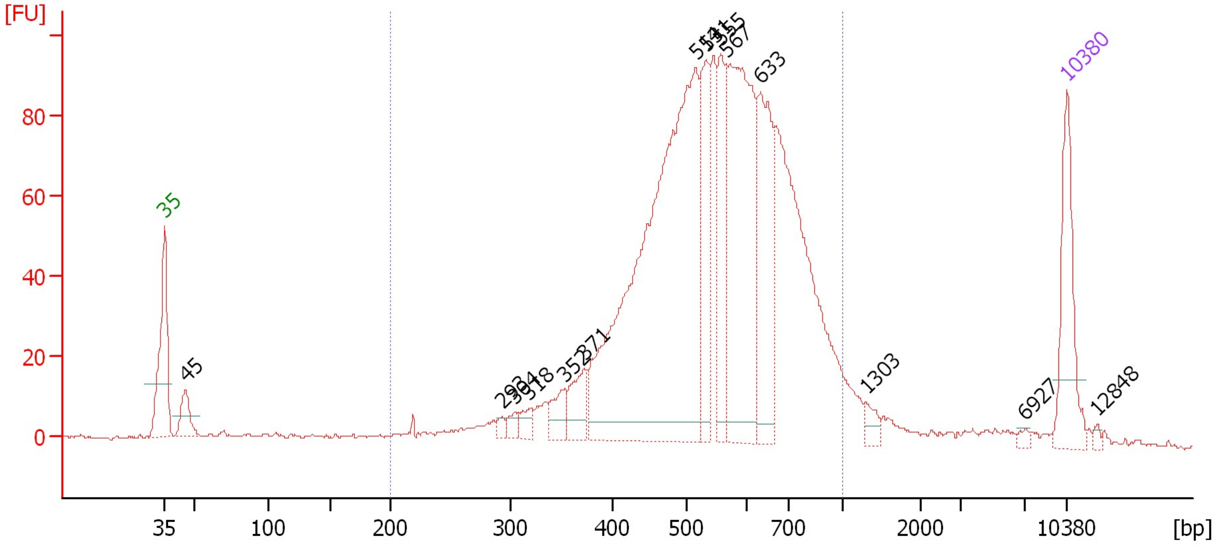
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. lor [pg/µl]	% of Total	Size distribution in CV [%]
245	2,251	650	1,307.2	3,927.8	■ 1,444.98	93	41.5

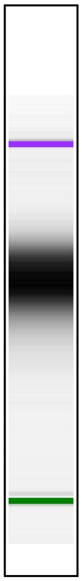
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...1-26\2017-01-26_001_HiSeq664_MatePair_and_WGS_Libraries.xad

Created: 1/26/2017 10:54:59 AM
Modified: 1/26/2017 11:43:55 AM

Electropherogram Summary Continued ...

XAN KAPA WGS Library (1:2) [HiSeq_664]





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)**

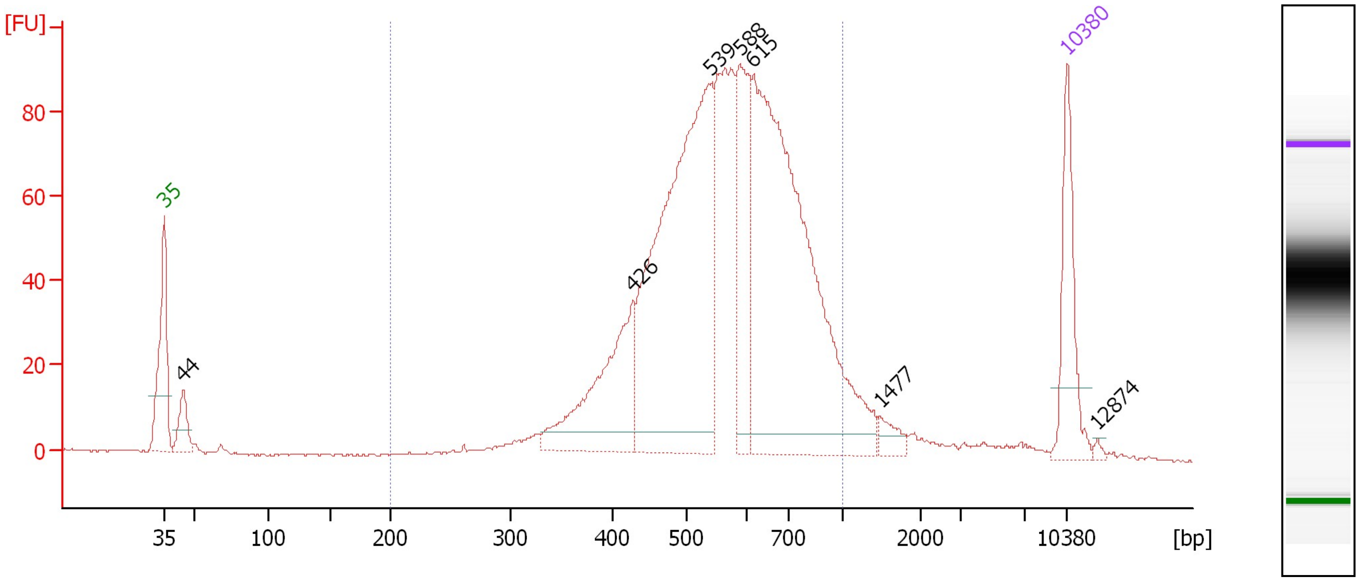
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		45	40.15	1,340.2		44.65
3		293	7.76	40.1		69.19
4		304	11.62	57.9		70.15
5		318	14.19	67.6		71.27
6		352	27.73	119.3		73.98
7		371	42.74	174.4		75.52
8		514	692.35	2,040.3		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]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	557	1,579.6	5,997.6	🟦	2,005.27	89	25.0

Electropherogram Summary Continued ...

SOL KAPA WGS Library (1:2) [HiSeq_664]



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)**

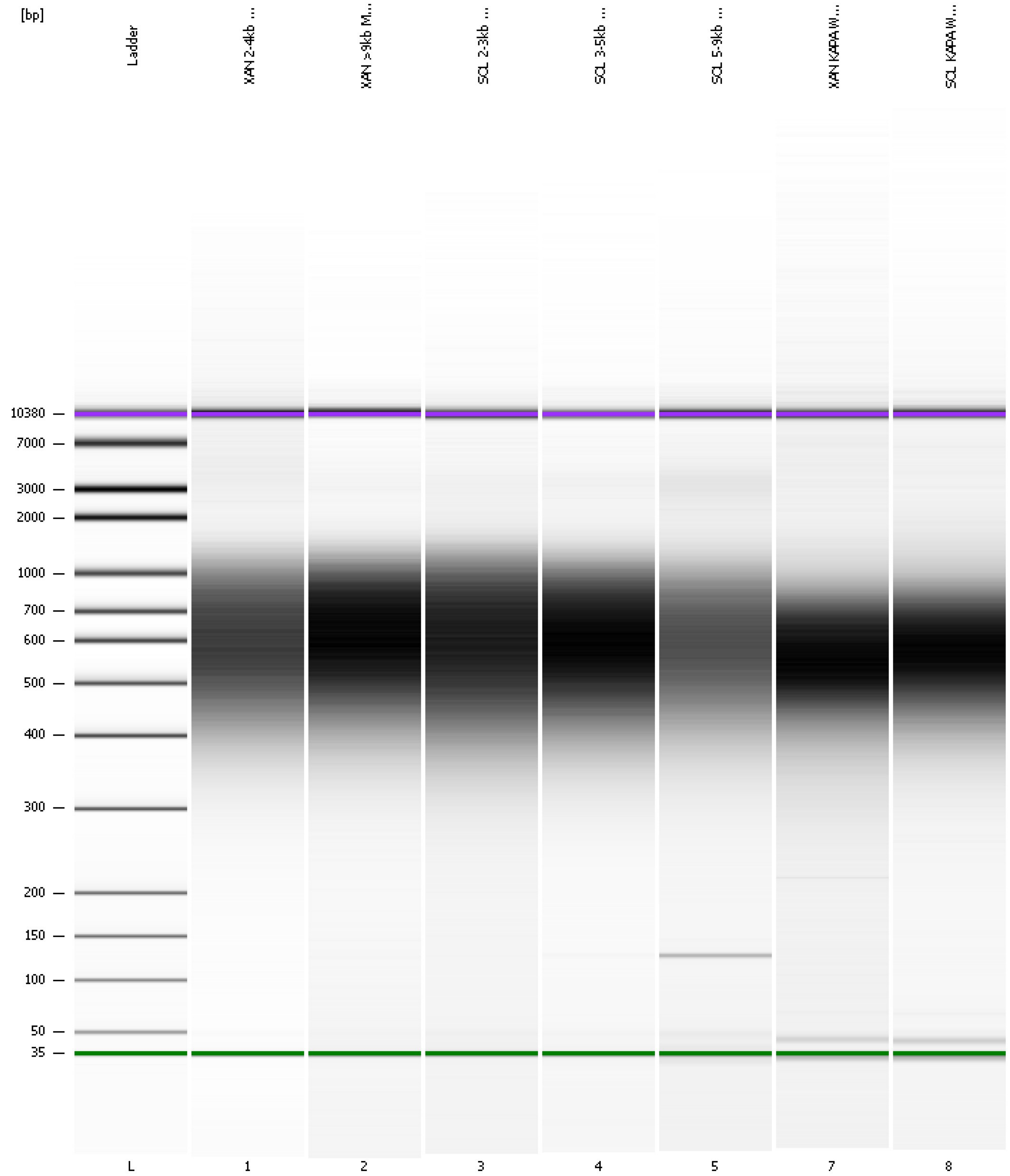
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		44	46.72	1,603.4		44.45
3		426	183.20	651.0		79.32
4		539	555.31	1,562.1		85.34
5		588	135.17	348.2		87.66
6		615	591.31	1,457.5		88.68
7		1,477	16.36	16.8		98.47
8	▶	10,380	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]	Color	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	Created:	1/26/2017 10:54:59 AM
Data Path:	C:\...1-26\2017-01-26_001_HiSeq664_MatePair_and_WGS_Libraries.xad	Modified:	1/26/2017 11:43:55 AM

Gel Image



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