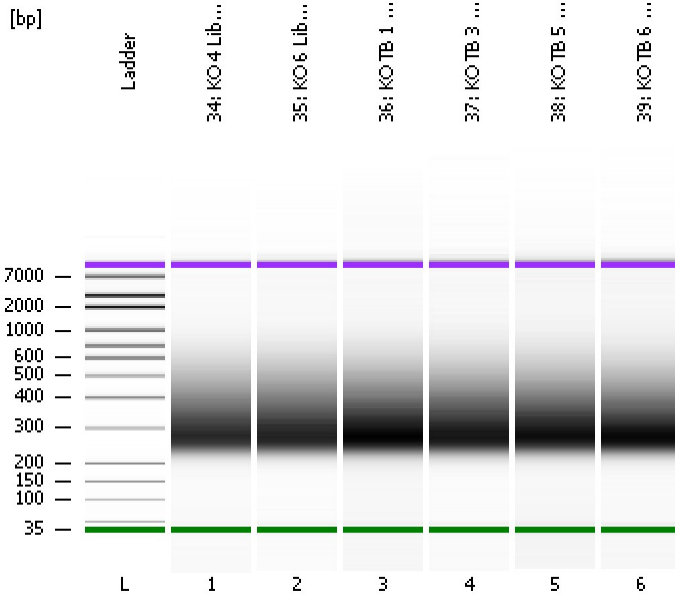


Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
Modified: 12/9/2016 11:48:23 AM

Electrophoresis File Run Summary



Instrument Information:

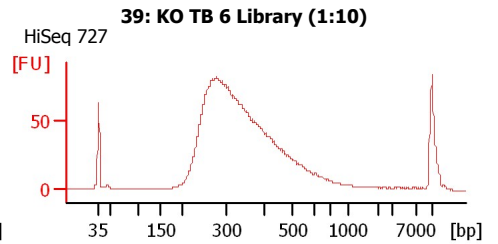
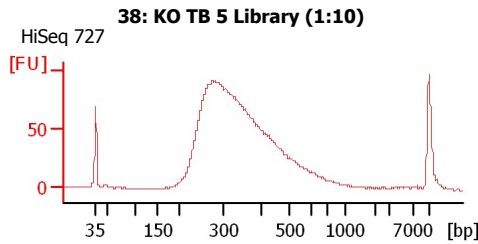
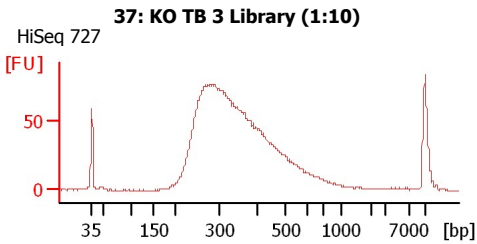
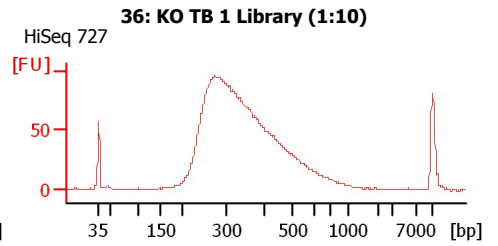
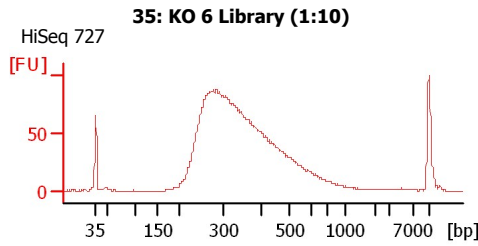
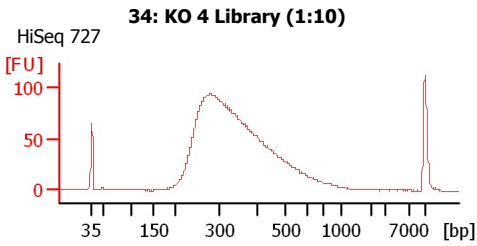
Instrument Name: DE13701086 Firmware: C.01.069
Serial#: DE13701086 Type: G2938B

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:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
34: KO 4 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
35: KO 6 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
36: KO TB 1 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
37: KO TB 3 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
38: KO TB 5 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
39: KO TB 6 Library (1:10)	HiSeq 727	<input type="checkbox"/>	<input checked="" type="checkbox"/>			
Ladder		<input type="checkbox"/>	<input checked="" type="checkbox"/>			

Chip Lot #

Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
Modified: 12/9/2016 11:48:23 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/ μ l] : 1950
Uses Standard Area for Ladder Fragments
Lower Marker Concentration [pg/ μ l] : 125
Upper Marker Concentration [pg/ μ l] : 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

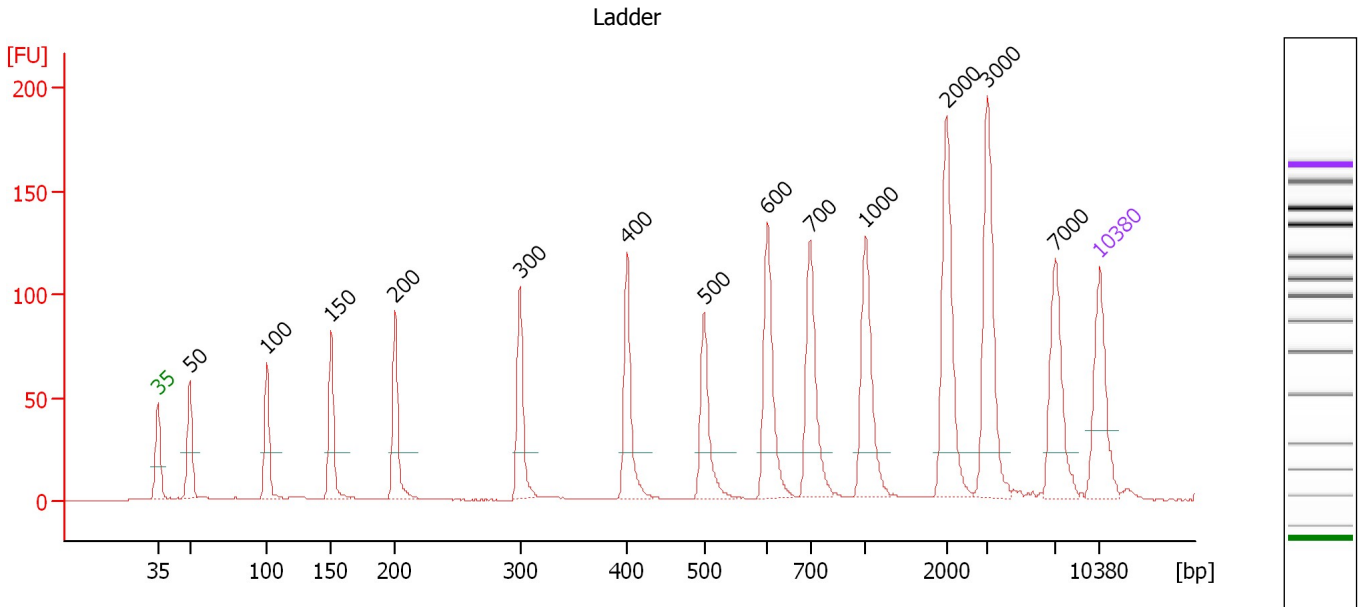
Ladder

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:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.2

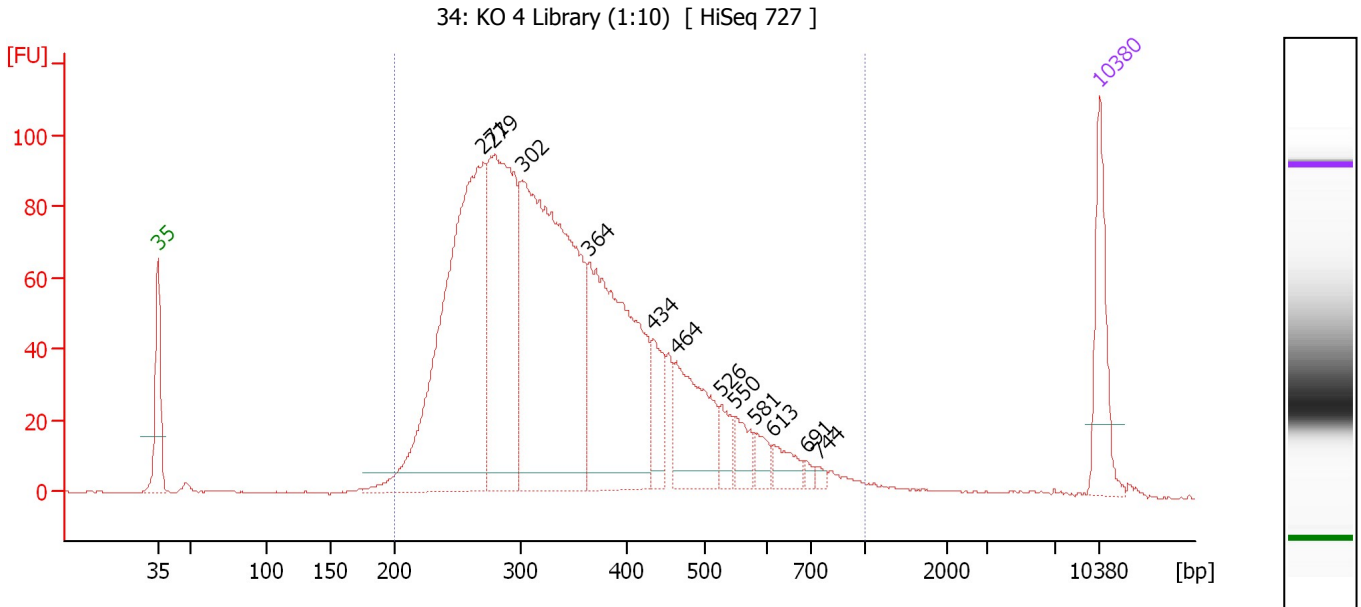
Peak table for Ladder

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	45.40
3	100	150.00	2,272.7	Ladder Peak	51.12
4	150	150.00	1,515.2	Ladder Peak	55.91
5	200	150.00	1,136.4	Ladder Peak	60.66
6	300	150.00	757.6	Ladder Peak	69.90
7	400	150.00	568.2	Ladder Peak	77.88
8	500	150.00	454.5	Ladder Peak	83.60
9	600	150.00	378.8	Ladder Peak	88.30
10	700	150.00	324.7	Ladder Peak	91.48
11	1,000	150.00	227.3	Ladder Peak	95.59
12	2,000	150.00	113.6	Ladder Peak	101.60
13	3,000	150.00	75.8	Ladder Peak	104.64
14	7,000	150.00	32.5	Ladder Peak	109.67
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 1 : 34: KO 4 Library (1:10)

Number of peaks found: 12 Corr. Area 1: 2,105.8
 Noise: 0.2

Peak table for sample 1 : 34: KO 4 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	271	687.06	3,846.0		67.19
3	279	429.92	2,337.1		67.94
4	302	714.20	3,582.5		70.07
5	364	407.18	1,693.8		75.03
6	434	60.42	210.9		79.83
7	464	139.25	455.1		81.52
8	526	31.40	90.4		84.84
9	550	31.67	87.3		85.93
10	581	22.33	58.2		87.42
11	613	27.21	67.3		88.71
12	691	6.18	13.5		91.19
13	744	5.48	11.1		92.08
14	10,380	75.00	10.9	Upper Marker	113.00

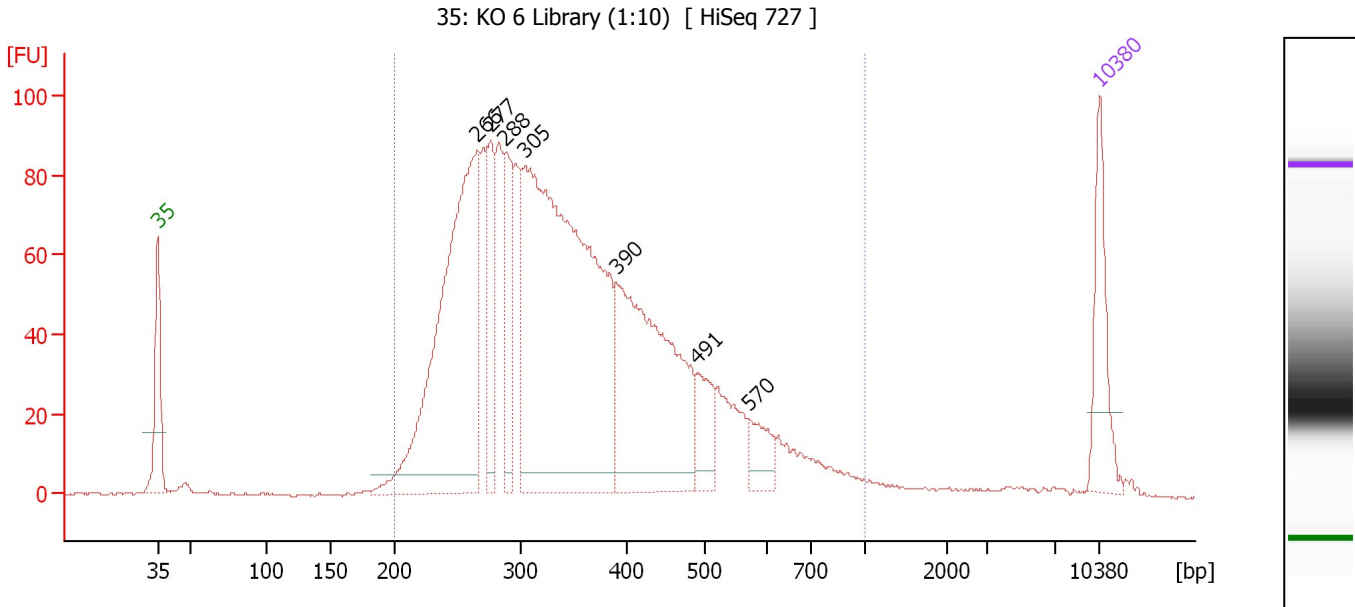
Region table for sample 1 : 34: KO 4 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	360	2,105.8	12,473.3	2,648.30	97	32.3

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 2 : 35: KO 6 Library (1:10)

Number of peaks found: 7 Corr. Area 1: 2,028.4
 Noise: 0.3

Peak table for sample 2 : 35: KO 6 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	266	601.17	3,426.0		66.75
3	277	119.30	653.3		67.75
4	288	121.13	637.2		68.79
5	305	923.44	4,589.6		70.29
6	390	399.05	1,550.5		77.08
7	491	59.91	184.7		83.11
8	570	42.53	113.0		86.91
9	10,380	75.00	10.9	Upper Marker	113.00

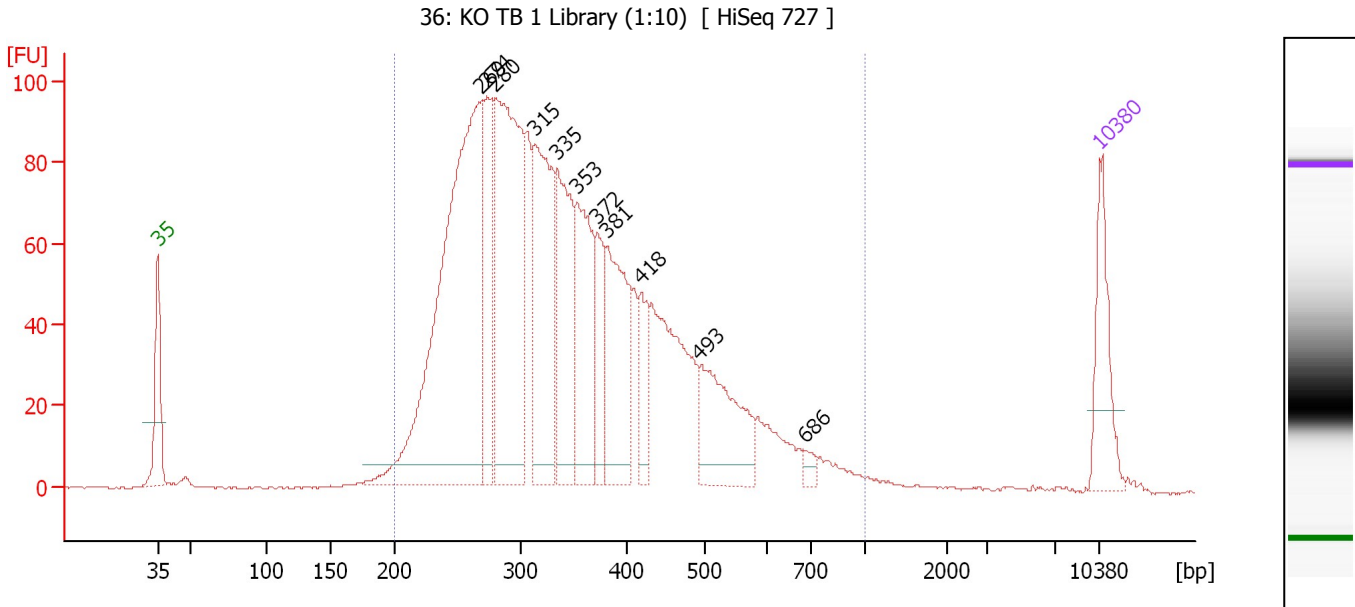
Region table for sample 2 : 35: KO 6 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	363	2,028.4	12,698.4	2,708.91	97	32.9

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 3 : 36: KO TB 1 Library (1:10)

Number of peaks found: 11 Corr. Area 1: 2,171.8
 Noise: 0.3

Peak table for sample 3 : 36: KO TB 1 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	269	779.00	4,384.0		67.06
3	274	157.48	872.0		67.46
4	280	479.69	2,599.1		68.02
5	315	276.93	1,334.1		71.06
6	335	201.37	911.2		72.68
7	353	187.92	806.0		74.15
8	372	85.60	348.9		75.62
9	381	187.87	748.0		76.33
10	418	59.98	217.4		78.91
11	493	156.93	482.0		83.22
12	686	11.60	25.6		91.02
13	10,380	75.00	10.9	Upper Marker	113.00

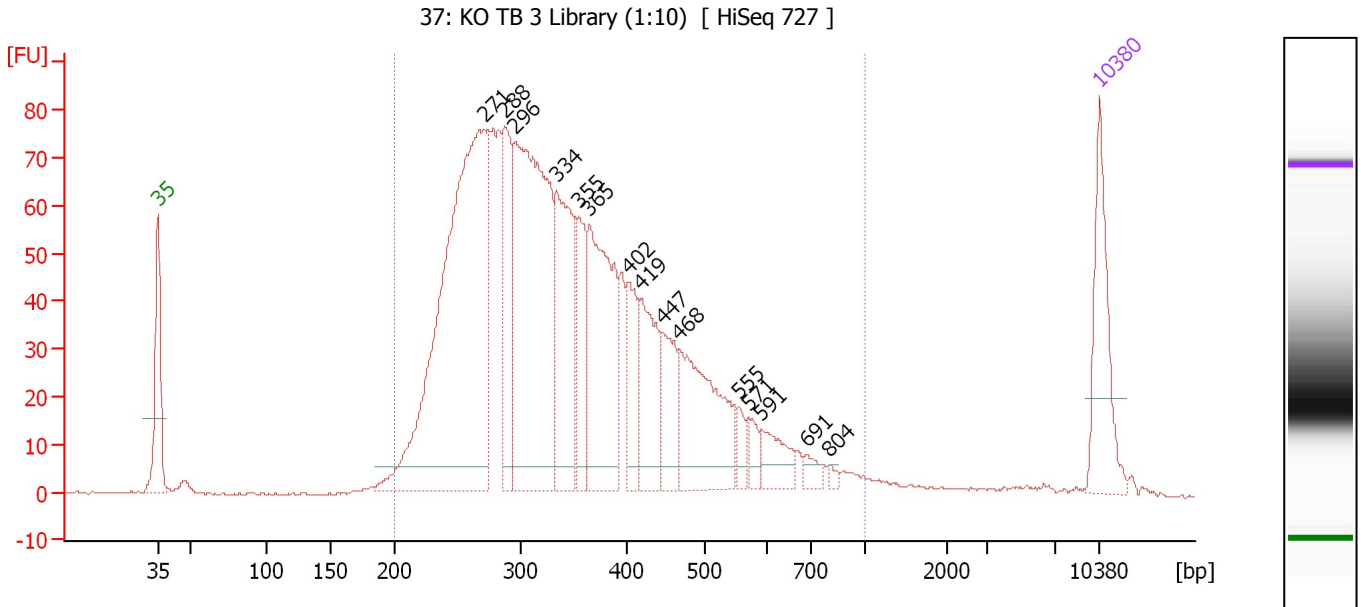
Region table for sample 3 : 36: KO TB 1 Library (1:10)

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	360	2,171.8	15,074.5	3,195.75	96	32.7

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 4 : 37: KO TB 3 Library (1:10)

Number of peaks found: 15 Corr. Area 1: 1,744.4
 Noise: 0.2

Peak table for sample 4 : 37: KO TB 3 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	271	660.20	3,686.3		67.26
3	288	130.17	684.8		68.79
4	296	432.30	2,214.6		69.51
5	334	181.13	822.5		72.59
6	355	78.24	334.0		74.28
7	365	208.50	866.5		75.05
8	402	63.34	238.9		77.97
9	419	97.13	351.5		78.95
10	447	61.23	207.4		80.59
11	468	149.22	483.1		81.77
12	555	16.18	44.2		86.18
13	571	16.43	43.6		86.95
14	591	35.39	90.7		87.87
15	691	12.07	26.4		91.21
16	804	4.65	8.8		92.90
17	10,380	75.00	10.9	Upper Marker	113.00

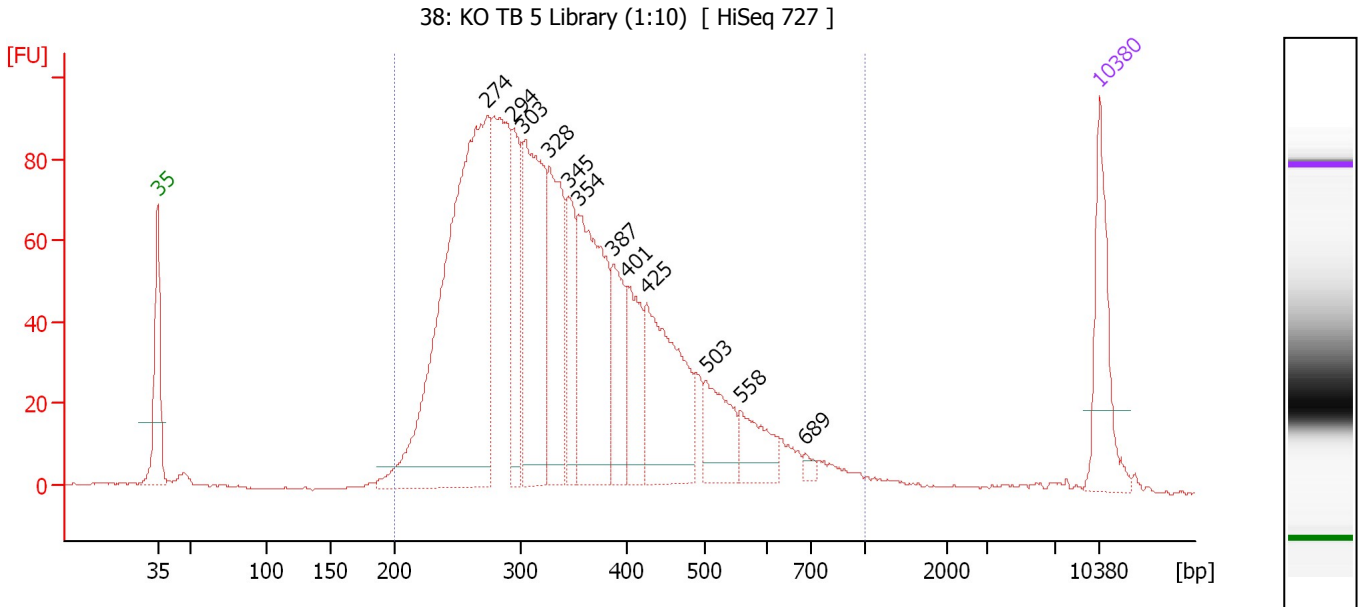
Region table for sample 4 : 37: KO TB 3 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	360	1,744.4	11,431.7	2,428.53	97	32.5

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 5 : 38: KO TB 5 Library (1:10)

Number of peaks found: 12 Corr. Area 1: 2,020.5
 Noise: 0.3

Peak table for sample 5 : 38: KO TB 5 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	274	683.83	3,785.0		67.48
3	294	114.52	590.2		69.35
4	303	264.17	1,319.0		70.18
5	328	170.58	789.0		72.10
6	345	92.70	406.9		73.50
7	354	233.77	999.8		74.23
8	387	87.09	341.1		76.83
9	401	82.01	310.0		77.92
10	425	187.18	666.9		79.33
11	503	73.29	220.8		83.74
12	558	50.79	137.8		86.34
13	689	6.80	15.0		91.12
14	10,380	75.00	10.9	Upper Marker	113.00

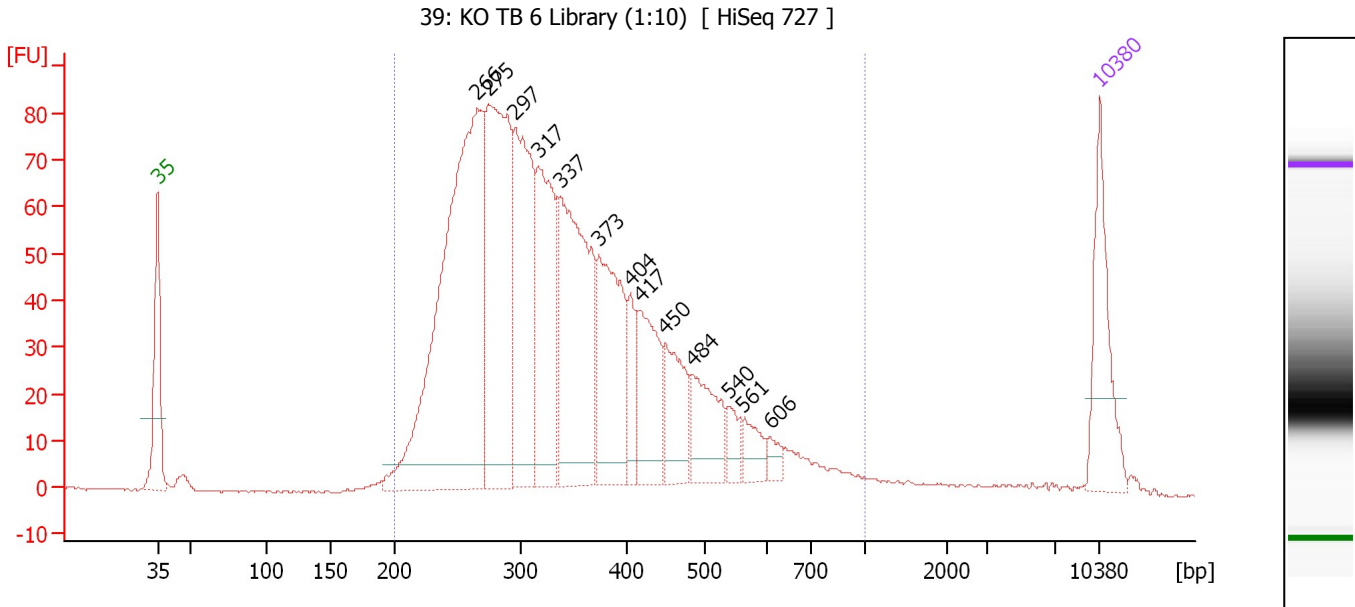
Region table for sample 5 : 38: KO TB 5 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	359	2,020.5	11,618.3	2,466.89	96	32.3

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

Electropherogram Summary Continued ...



Overall Results for sample 6 : 39: KO TB 6 Library (1:10)

Number of peaks found: 13 Corr. Area 1: 1,755.2
 Noise: 0.2

Peak table for sample 6 : 39: KO TB 6 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	266	602.66	3,431.7		66.77
3	275	349.28	1,927.5		67.55
4	297	227.89	1,164.2		69.59
5	317	195.22	933.0		71.26
6	337	274.15	1,231.4		72.88
7	373	163.79	664.7		75.75
8	404	43.40	162.8		78.10
9	417	99.32	361.1		78.84
10	450	71.32	240.4		80.72
11	484	75.88	237.4		82.70
12	540	19.94	56.0		85.47
13	561	25.95	70.1		86.46
14	606	12.24	30.6		88.50
15	10,380	75.00	10.9	Upper Marker	113.00

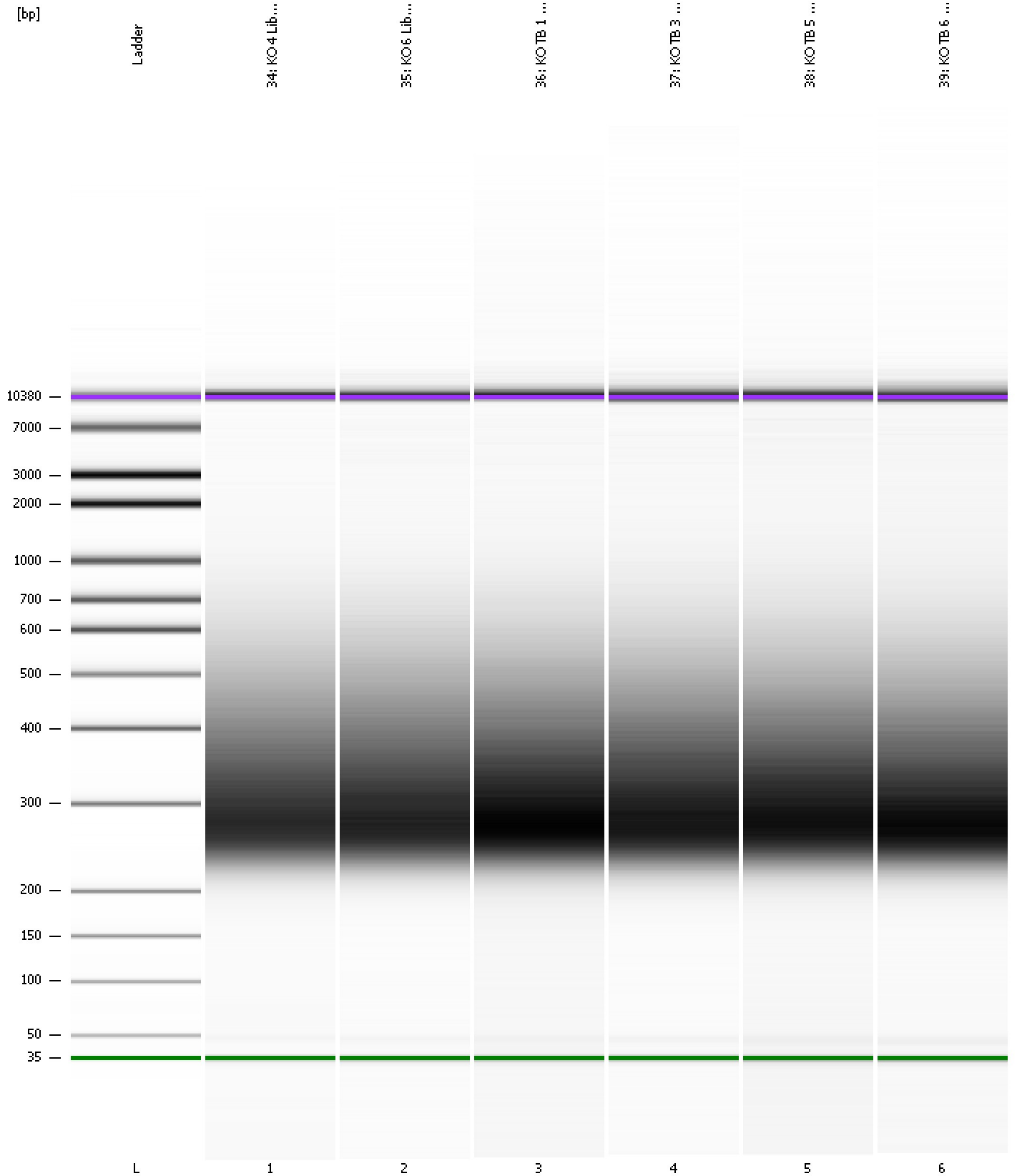
Region table for sample 6 : 39: KO TB 6 Library (1:10)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co Conc. [pg/μl]	% of Total	Size distribution in CV [%]
200	1,000	355	1,755.2	10,893.0	2,289.07	97	32.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
Modified: 12/9/2016 11:48:23 AM

Gel Image



Assay Class: High Sensitivity DNA Assay
 Data Path: C:\...data\2016-12-09\2016-12-09_002_HiSeq727_Libraries_34-39.xad

Created: 12/9/2016 11:02:32 AM
 Modified: 12/9/2016 11:48:23 AM

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		12/9/2016 11:43:49 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\2016-12-09\2016-12-09_002.xad)		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		12/9/2016 11:02:38 AM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1