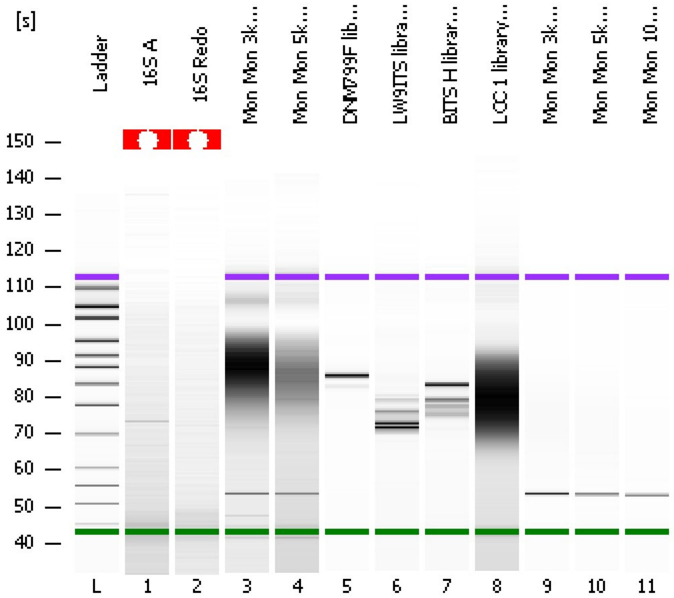
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 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

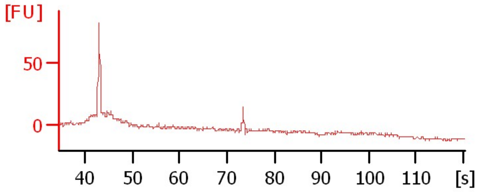
Chip Information:

Chip Lot #:

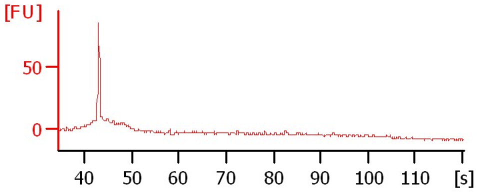
Reagent Kit Lot #:

Chip Comments:

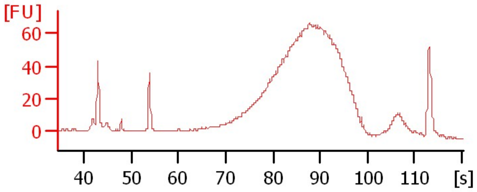
16S A



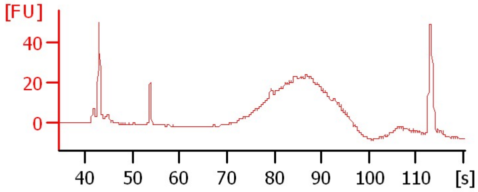
16S Redo



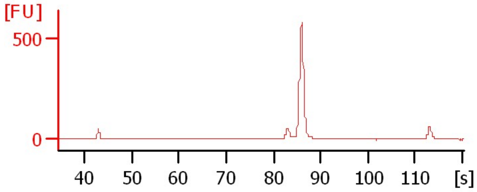
Mon Mon 3k Mate Pair Library



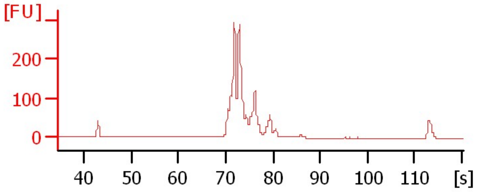
Mon Mon 5k Mate Pair Library



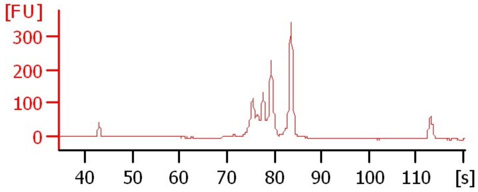
DNM799F library (5cyc PCR)



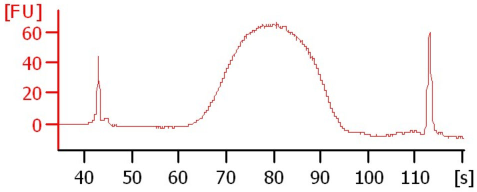
LW9ITS library (5cyc PCR)



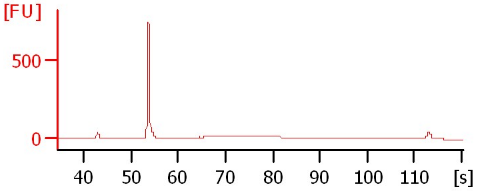
BITS H library (5cyc PCR)



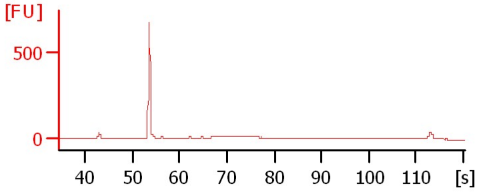
LCC 1 library (5cyc PCR)



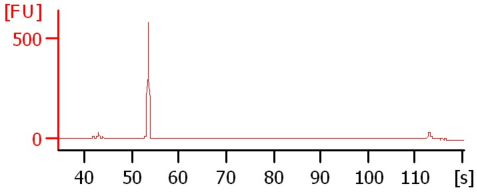
Mon Mon 3k supernatant from library b...



Mon Mon 5k supernatant from library b...



Mon Mon 10k supernatant from library ...



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad
Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
16S A		☐	✓			
16S Redo		☐	✓			
Mon Mon 3k Mate Pair Library		☐	✓			
Mon Mon 5k Mate Pair Library		☐	✓			
DNM799F library (5cyc PCR)		☐	✓			
LW9ITS library (5cyc PCR)		☐	✓			
BITS H library (5cyc PCR)		☐	✓			
LCC 1 library (5cyc PCR)		☐	✓			
Mon Mon 3k supernatant from library bead cleanup		☐	✓			
Mon Mon 5k supernatant from library bead cleanup		☐	✓			
Mon Mon 10k supernatant from library bead cleanup		☐	✓			
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

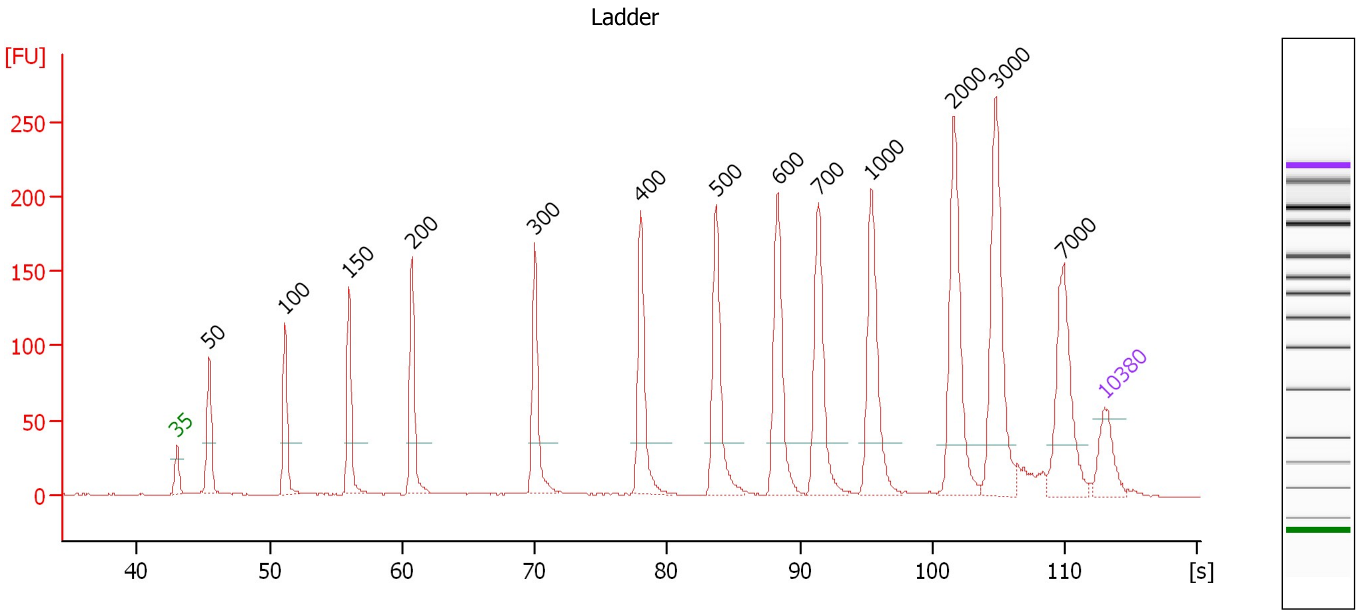
Ladder

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
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.3

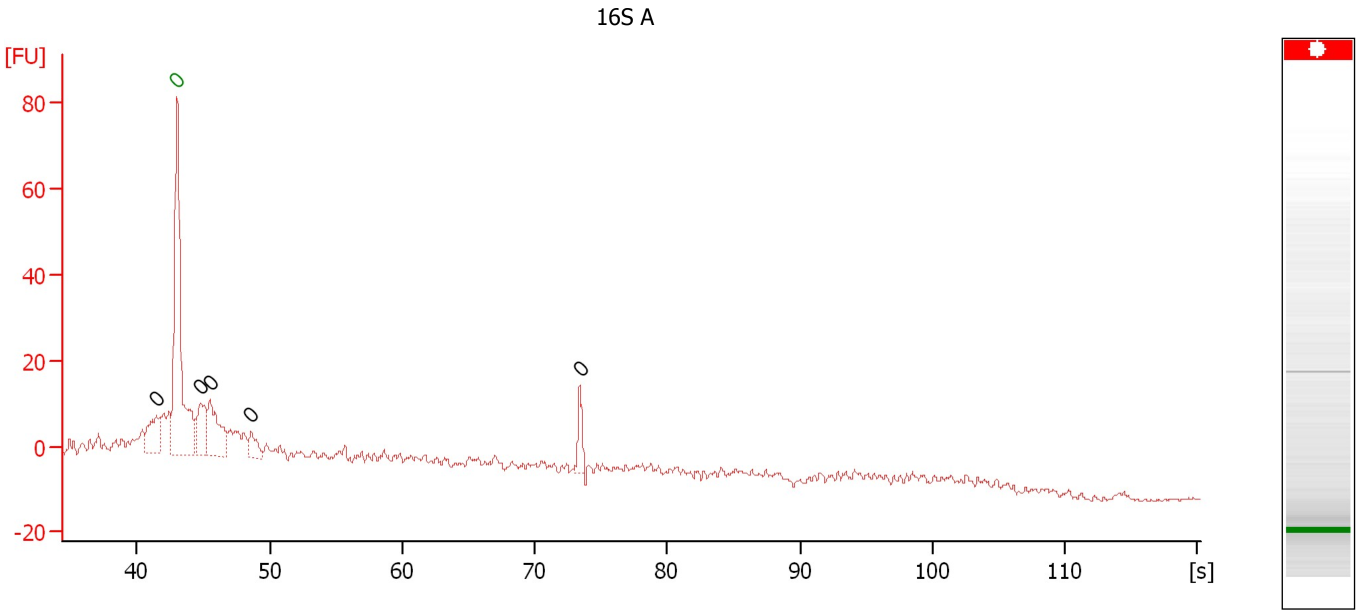
Peak table for Ladder

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	45.44
3	▙	100	150.00	2,272.7	Ladder Peak	51.19
4	▙	150	150.00	1,515.2	Ladder Peak	56.02
5	▙	200	150.00	1,136.4	Ladder Peak	60.74
6	▙	300	150.00	757.6	Ladder Peak	70.01
7	▙	400	150.00	568.2	Ladder Peak	78.00
8	▙	500	150.00	454.5	Ladder Peak	83.65
9	▙	600	150.00	378.8	Ladder Peak	88.33
10	▙	700	150.00	324.7	Ladder Peak	91.41
11	▙	1,000	150.00	227.3	Ladder Peak	95.40
12	▙	2,000	150.00	113.6	Ladder Peak	101.59
13	▙	3,000	150.00	75.8	Ladder Peak	104.81
14	▙	7,000	150.00	32.5	Ladder Peak	109.88
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Electropherogram Summary Continued ...



Overall Results for sample 1 : 16S A

Number of peaks found: 5 Noise: 0.4

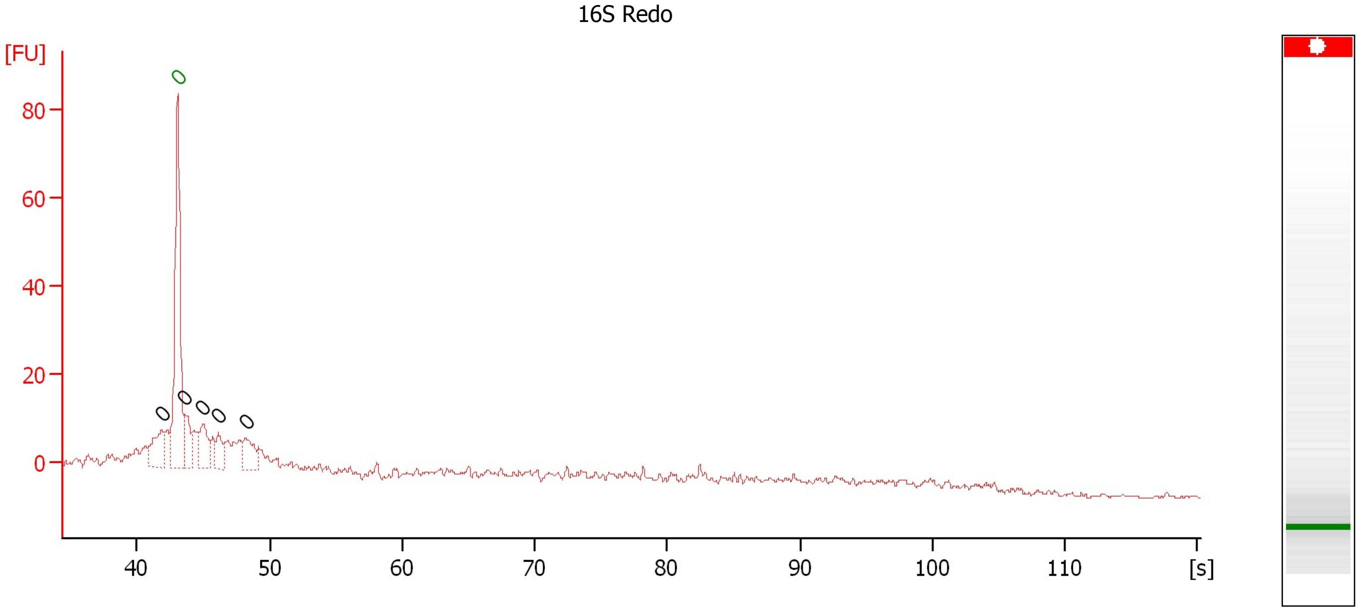
Peak table for sample 1 : 16S A

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		0	0.00	0.0		41.45
2	◀	0	0.00	0.0	Lower Marker	43.00
3		0	0.00	0.0		44.80
4		0	0.00	0.0		45.50
5		0	0.00	0.0		48.60
6		0	0.00	0.0		73.40

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Electropherogram Summary Continued ...



Overall Results for sample 2 : **16S Redo**

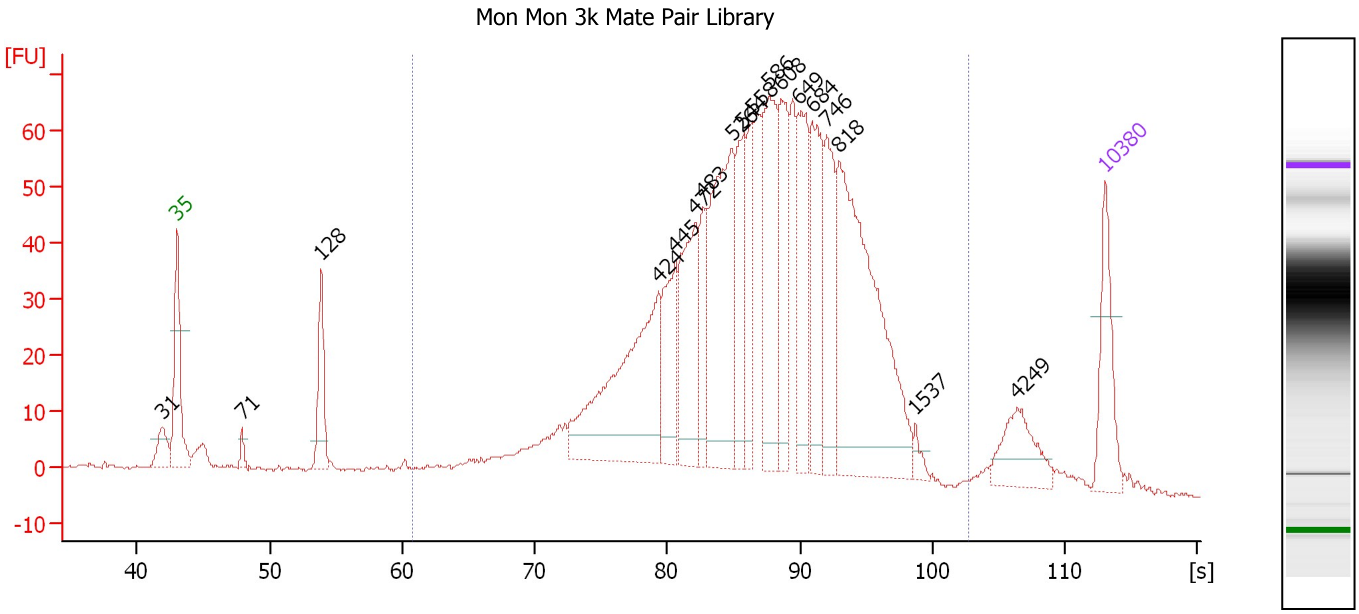
Number of peaks found: 5

Noise: 0.3

Peak table for sample 2 : **16S Redo**

Peak		**Size [bp]**	**Conc. [pg/µl]**	**Molarity [pmol/l]**	**Observations**	**Aligned Migration Time [s]**
1		0	0.00	0.0		41.90
2	◀	0	0.00	0.0	Lower Marker	43.05
3		0	0.00	0.0		43.60
4		0	0.00	0.0		45.00
5		0	0.00	0.0		46.15
6		0	0.00	0.0		48.20

Electropherogram Summary Continued ...



Overall Results for sample 3 : **Mon Mon 3k Mate Pair Library**

Number of peaks found:	18	Corr. Area 1:	1,336.1
Noise:	0.3		

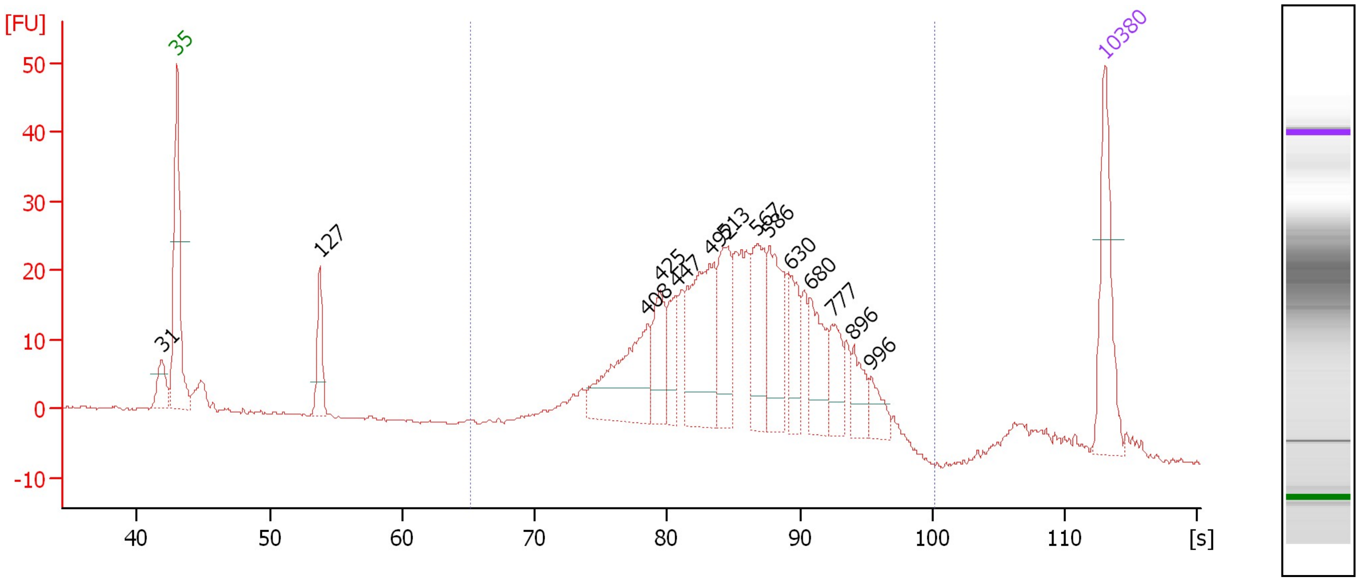
Peak table for sample 3 : **Mon Mon 3k Mate Pair Library**

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		31	0.00	0.0		41.84
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		71	13.06	277.4		47.89
4		128	100.37	1,187.9		53.89
5		424	315.08	1,125.7		79.36
6		445	104.52	355.5		80.57
7		472	162.95	522.8		82.09
8		483	79.19	248.4		82.69
9		526	280.95	809.7		84.86
10		544	94.16	262.2		85.72
11		558	96.15	261.0		86.37
12		586	183.98	475.6		87.68
13		608	127.74	318.1		88.59
14		649	132.10	308.2		89.85
15		684	141.70	313.9		90.91
16		746	124.46	252.7		92.02
17		818	416.25	770.9		92.98
18		1,537	10.49	10.3		98.73
19		4,249	63.86	22.8		106.39
20	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 3 : **Mon Mon 3k Mate Pair Library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	2,342	628	1,336.1	8,077.1	■	2,826.80	90	38.4

Electropherogram Summary Continued ...



Overall Results for sample 4 : **Mon Mon 5k Mate Pair Library**

Number of peaks found:	14	Corr. Area 1:	489.9
Noise:	0.2		

Peak table for sample 4 : **Mon Mon 5k Mate Pair Library**

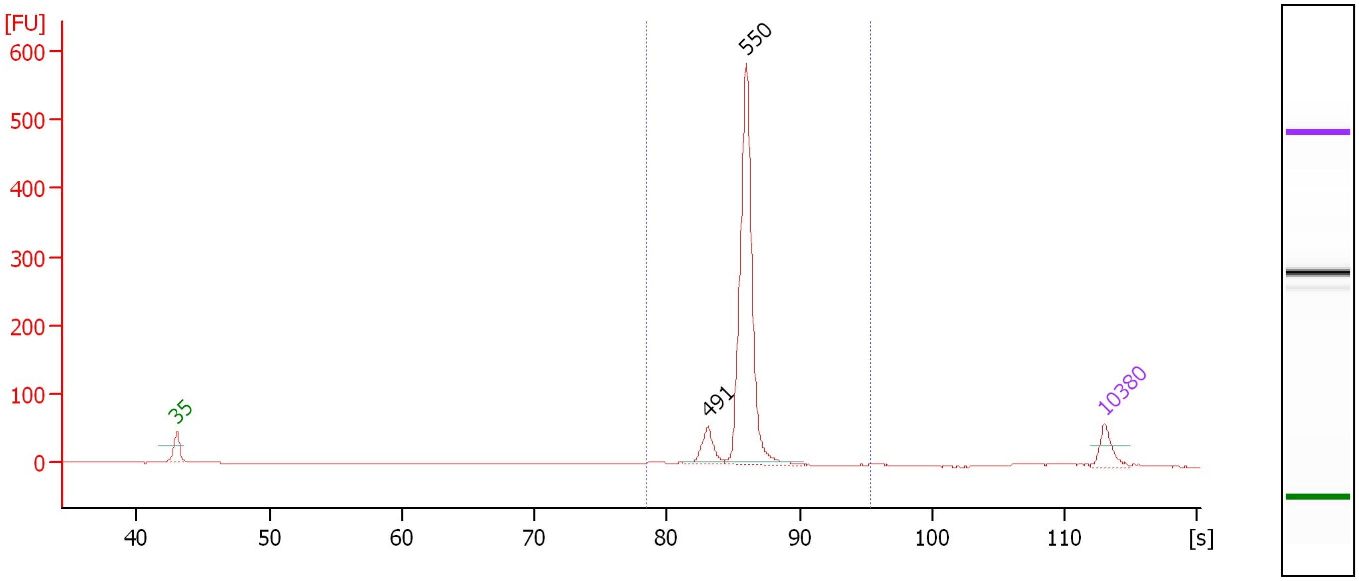
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		31	0.00	0.0		41.87
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		127	56.24	670.8		53.80
4		408	119.63	444.1		78.46
5		425	53.51	190.6		79.43
6		447	37.32	126.5		80.66
7		492	136.97	421.5		83.22
8		513	69.83	206.4		84.24
9		567	69.88	186.7		86.80
10		586	78.43	202.8		87.67
11		630	42.44	102.1		89.26
12		680	57.50	128.1		90.79
13		777	38.94	75.9		92.43
14		896	28.74	48.6		94.02
15		996	19.28	29.3		95.35
16	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 4 : **Mon Mon 5k Mate Pair Library**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
248	1,763	566	489.9	3,067.3	■	1,033.71	89	30.1

Electropherogram Summary Continued ...

DNM799F library (5cyc PCR)



Overall Results for sample 5 : DNM799F library (5cyc PCR)

Number of peaks found:	2	Corr. Area 1:	810.1
Noise:	0.2		

Peak table for sample 5 : DNM799F library (5cyc PCR)

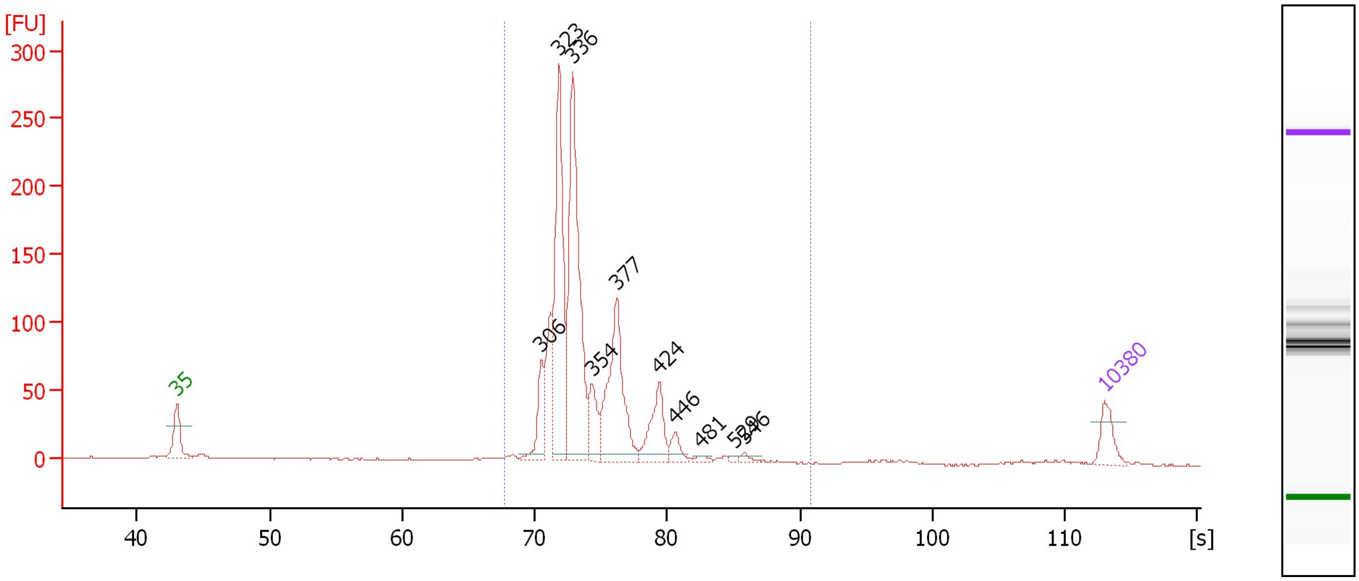
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		491	125.17	386.5		83.13
3		550	1,202.45	3,315.3		85.97
4	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 5 : DNM799F library (5cyc PCR)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
407	1,000	545	810.1	3,809.3	🟦	1,364.84	91	6.4

Electropherogram Summary Continued ...

LW9ITS library (5cyc PCR)



Overall Results for sample 6 : LW9ITS library (5cyc PCR)

Number of peaks found:	10	Corr. Area 1:	1,152.8
Noise:	0.4		

Peak table for sample 6 : LW9ITS library (5cyc PCR)

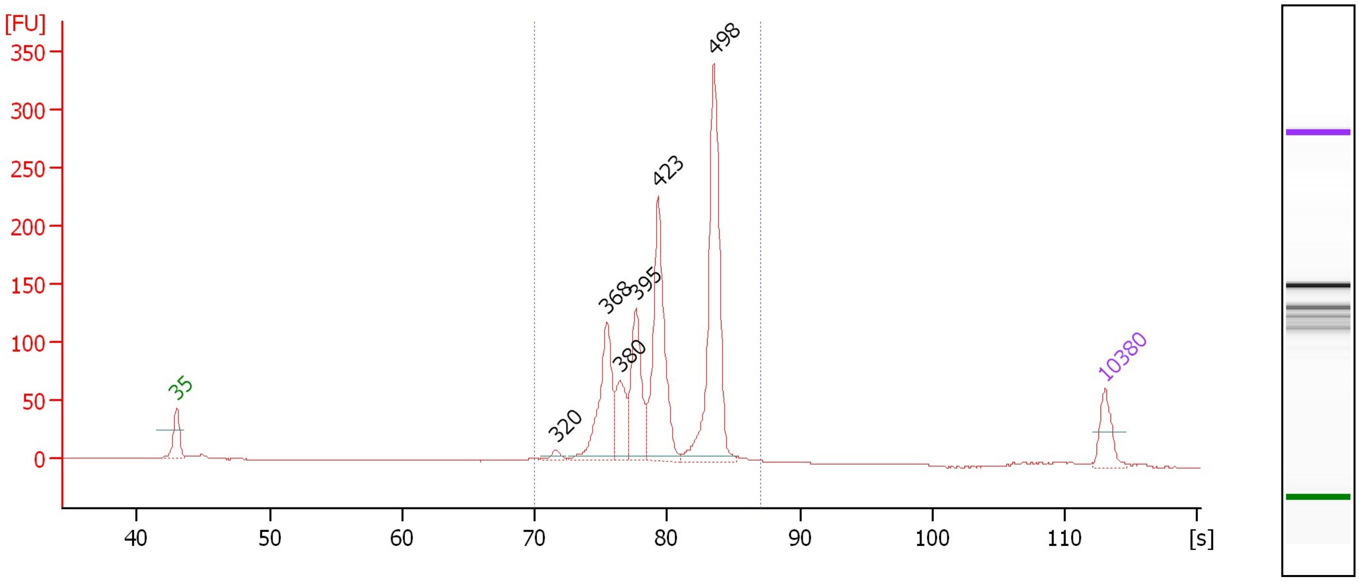
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		306	153.10	757.7		70.50
3		323	691.31	3,241.2		71.86
4		336	872.18	3,937.8		72.85
5		354	137.41	588.3		74.31
6		377	474.80	1,906.0		76.20
7		424	186.68	666.3		79.39
8		446	54.04	183.7		80.59
9		481	14.68	46.3		82.57
10		529	8.82	25.2		85.03
11		546	15.92	44.2		85.82
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 6 : LW9ITS library (5cyc PCR)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
276	683	352	1,152.8	12,436.0	🟦	2,848.20	96	12.5

Electropherogram Summary Continued ...

BITS H library (5cyc PCR)



Overall Results for sample 7 : BITS H library (5cyc PCR)

Number of peaks found:	6	Corr. Area 1:	1,117.3
Noise:	0.2		

Peak table for sample 7 : BITS H library (5cyc PCR)

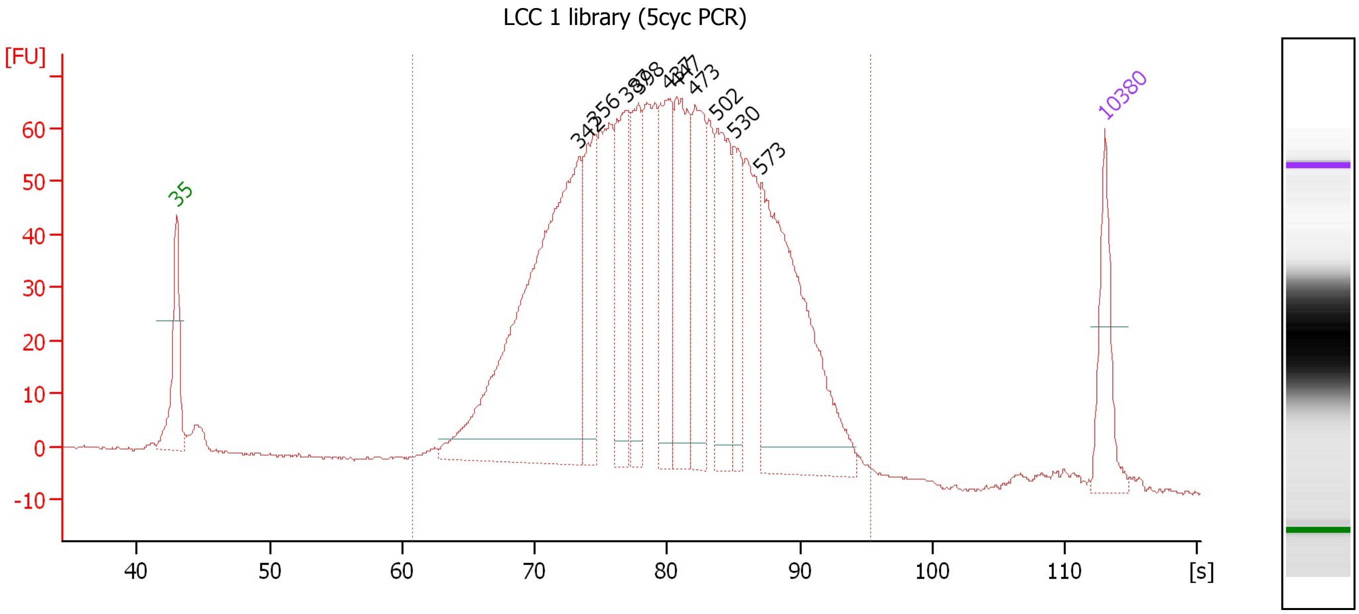
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		320	23.38	110.6		71.62
3		368	320.99	1,321.9		75.43
4		380	135.40	539.2		76.44
5		395	258.49	991.4		77.60
6		423	481.01	1,723.2		79.30
7		498	671.16	2,042.9		83.53
8	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : BITS H library (5cyc PCR)

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
300	573	435	1,117.3	6,802.6	🟦	1,920.61	98	12.4

Assay Class:	High Sensitivity DNA Assay	Created:	3/17/2016 12:29:29 PM
Data Path:	C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad	Modified:	3/17/2016 1:12:17 PM

Electropherogram Summary Continued ...



Overall Results for sample 8 : LCC 1 library (5cyc PCR)

Number of peaks found:	10	Corr. Area 1:	1,720.9
Noise:	0.3		

Peak table for sample 8 : LCC 1 library (5cyc PCR)

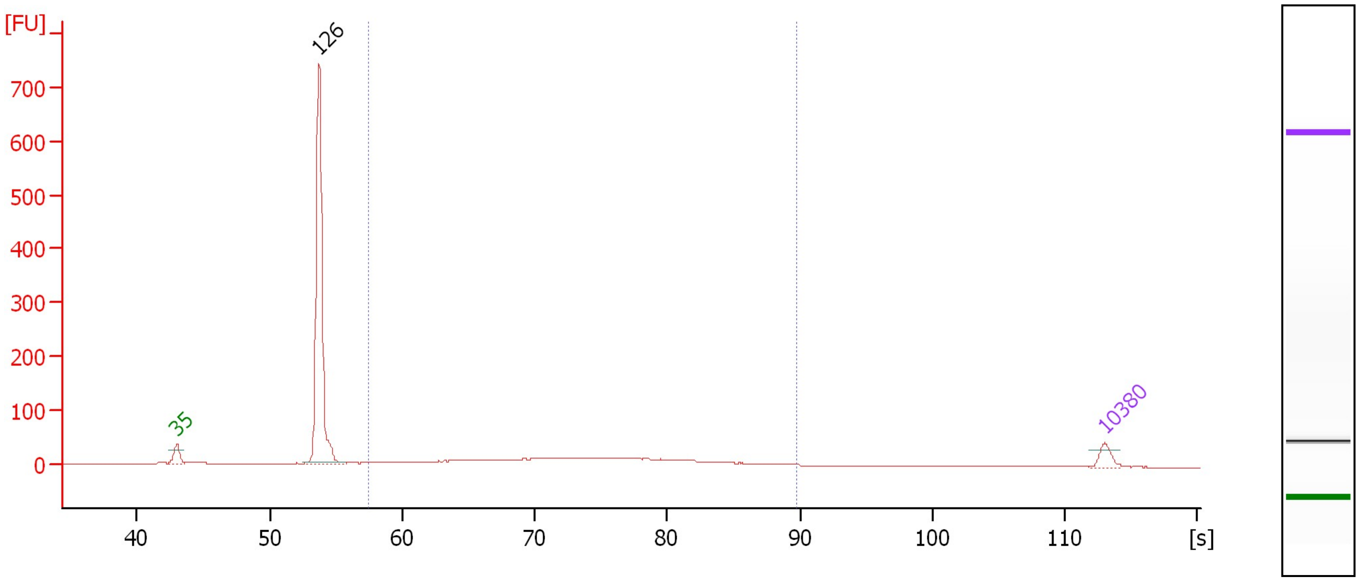
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		342	743.70	3,295.4		73.36
3		356	151.53	645.0		74.48
4		387	170.51	667.0		76.99
5		398	129.96	494.7		77.84
6		437	160.62	557.2		80.08
7		447	197.34	668.6		80.67
8		473	175.42	562.3		82.11
9		502	180.73	545.1		83.76
10		530	96.05	274.8		85.04
11		573	401.17	1,060.8		87.07
12	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 8 : LCC 1 library (5cyc PCR)

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	447	1,720.9	11,680.6	🟦	3,111.00	98	27.2

Electropherogram Summary Continued ...

Mon Mon 3k supernatant from library bead cleanup



Overall Results for sample 9 : **Mon Mon 3k supernatant from library bead cleanup**

Number of peaks found:	1	Corr. Area 1:	375.6
Noise:	0.2		

Peak table for sample 9 : **Mon Mon 3k supernatant from library bead cleanup**

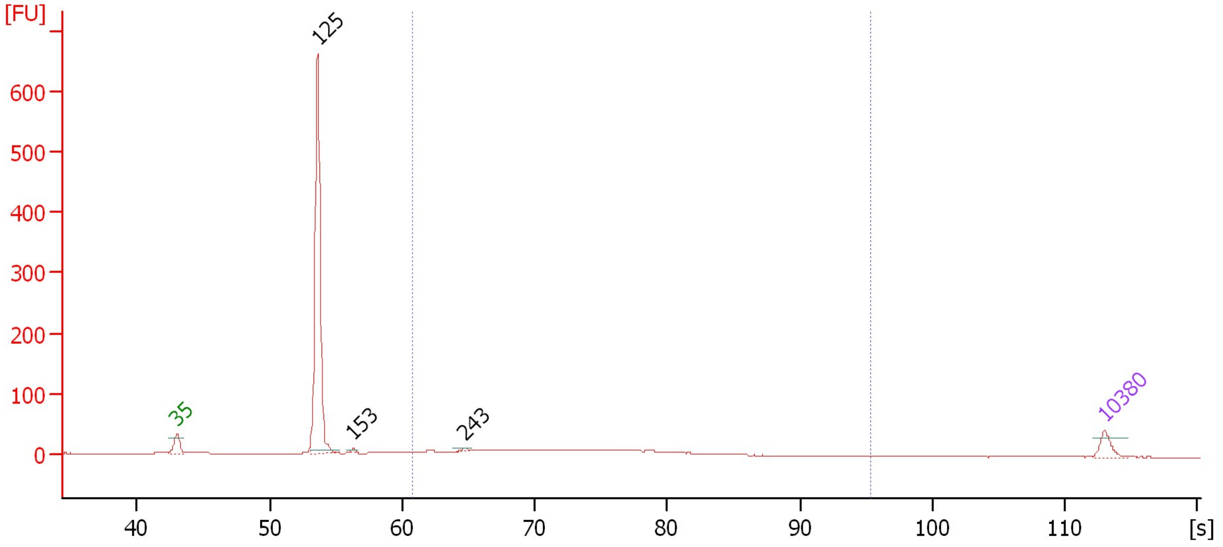
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		126	2,547.65	30,603.6		53.71
3	▶	10,380	75.00	10.9	Upper Marker	113.00

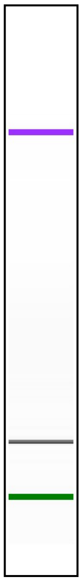
Region table for sample 9 : **Mon Mon 3k supernatant from library bead cleanup**

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
166	645	351	375.6	5,208.0	🟦	1,058.06	33	28.8

Electropherogram Summary Continued ...

Mon Mon 5k supernatant from library bead cleanup





Overall Results for sample 10 : **Mon Mon 5k supernatant from library bead cleanup**

Number of peaks found:	3	Corr. Area 1:	221.1
Noise:	0.2		

Peak table for sample 10 : **Mon Mon 5k supernatant from library bead cleanup**

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	2,294.13	27,739.0		53.63
3		153	17.87	177.2		56.28
4		243	13.15	81.9		64.75
5	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : **Mon Mon 5k supernatant from library bead cleanup**

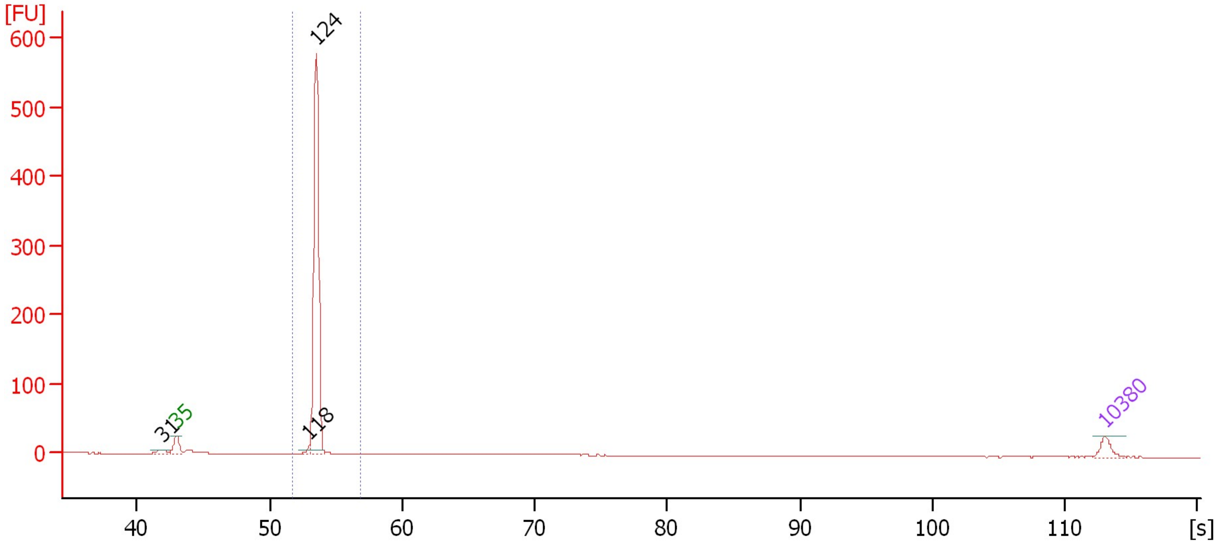
From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	336	221.1	3,363.5	🟦	687.88	26	24.7

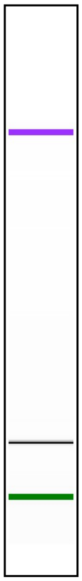
Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Electropherogram Summary Continued ...

Mon Mon 10k supernatant from library bead cleanup





Overall Results for sample 11 : Mon Mon 10k supernatant from library bead cleanup

Number of peaks found:	3	Corr. Area 1:	451.9
Noise:	0.1		

Peak table for sample 11 : Mon Mon 10k supernatant from library bead cleanup

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1		31	0.00	0.0		41.86
2	◀	35	125.00	5,411.3	Lower Marker	43.00
3		118	30.31	389.9		52.91
4		124	2,704.15	33,043.0		53.51
5	▶	10,380	75.00	10.9	Upper Marker	113.00

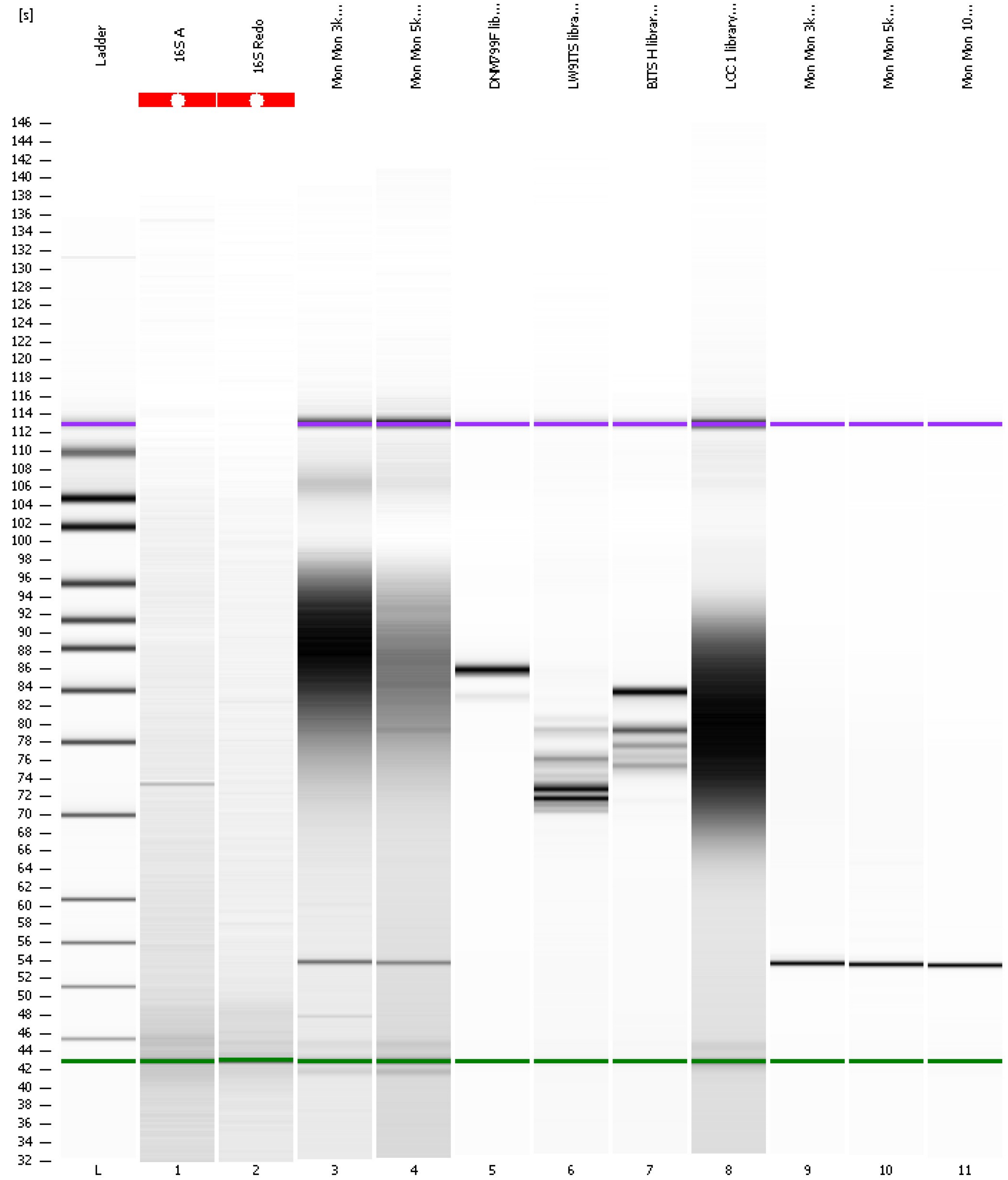
Region table for sample 11 : Mon Mon 10k supernatant from library bead cleanup

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
106	159	124	451.9	33,492.1	🟦	2,745.55	95	1.6

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2016-03-17\2016-03-17_002.xad

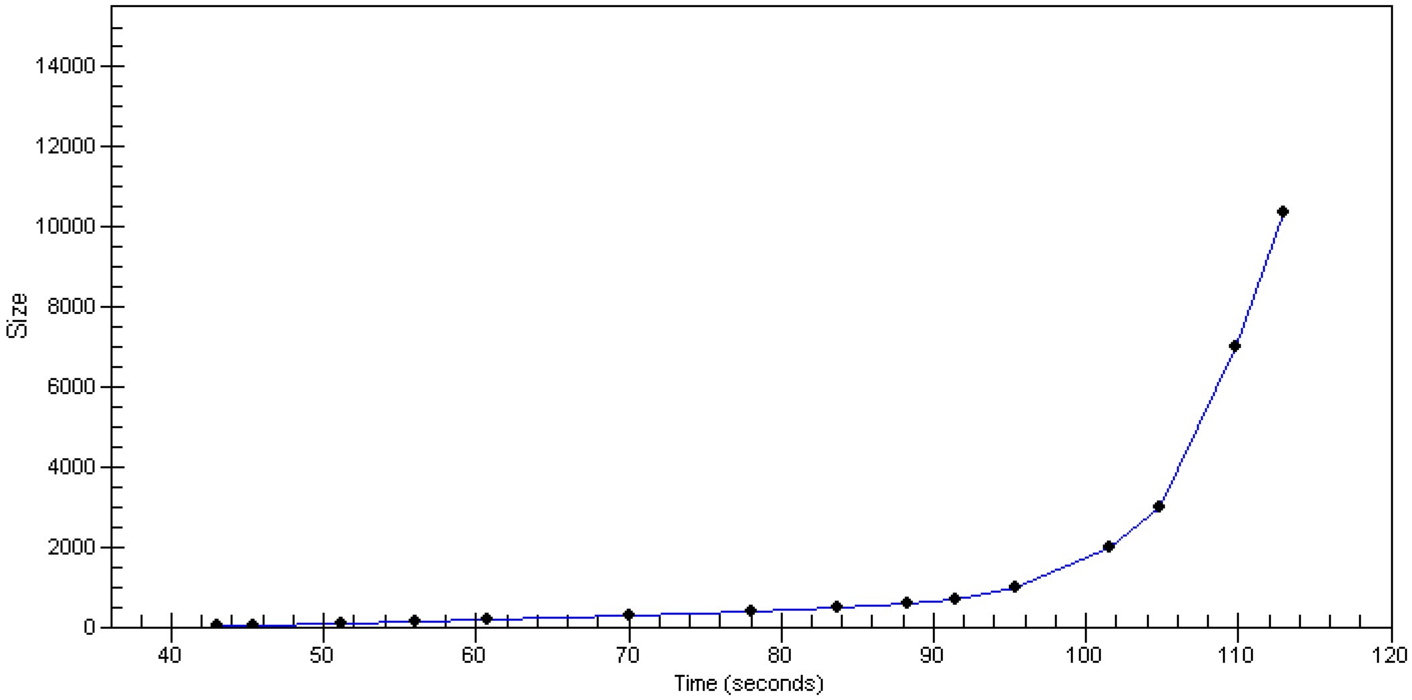
Created: 3/17/2016 12:29:29 PM
Modified: 3/17/2016 1:12:17 PM

Gel Image



Curves

Standard Curve



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		3/17/2016 1:10:46 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\2016-03-17\2016-03-17_002.xad)		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		3/17/2016 12:29:34 PM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1