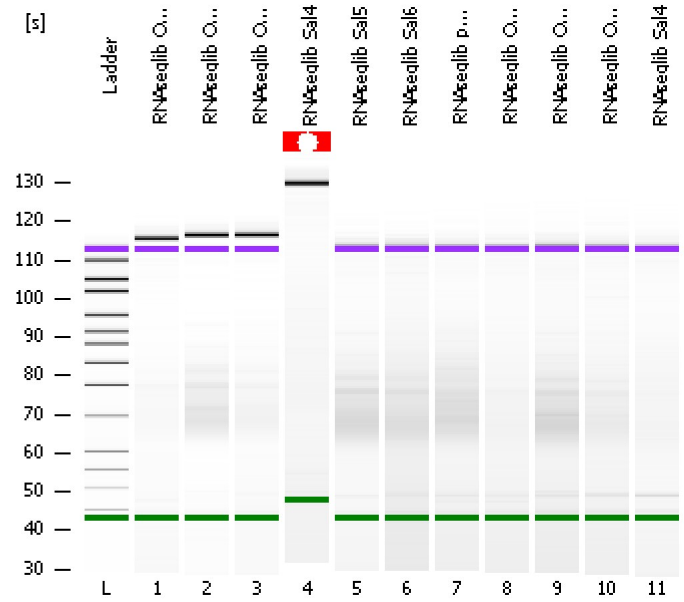
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad

Created: 11/25/2015 1:17:43 PM
Modified: 11/25/2015 2:00:56 PM

Electrophoresis File Run Summary



Instrument Information:

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

Assay Information:

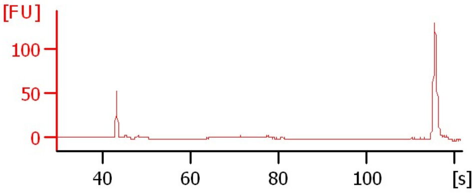
Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy

Assay Class: High Sensitivity DNA Assay
Version: 1.03
Assay Comments: Copyright © 2003-2010 Agilent Technologies

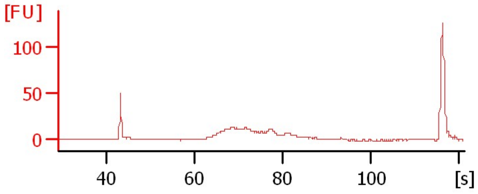
Chip Information:

Chip Lot #:
Reagent Kit Lot #:
Chip Comments:

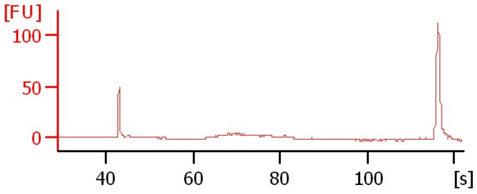
RNAseqlib OVA1



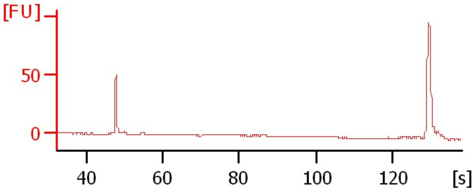
RNAseqlib OVA2



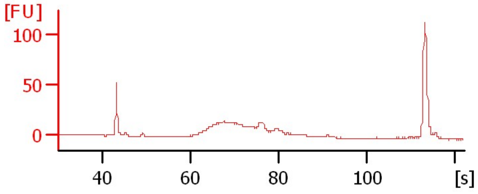
RNAseqlib OVA3



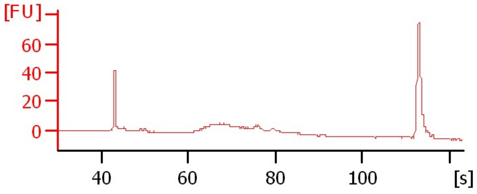
RNAseqlib Sal4



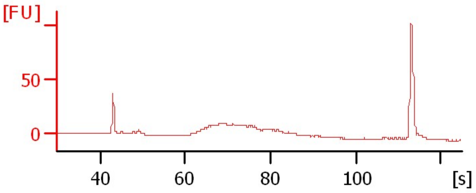
RNAseqlib Sal5



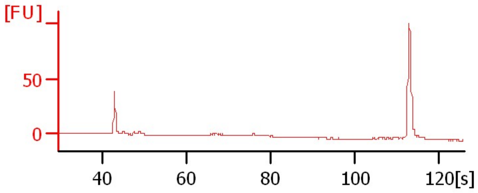
RNAseqlib Sal6



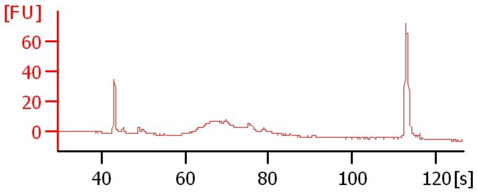
RNAseqlib pos ctrl



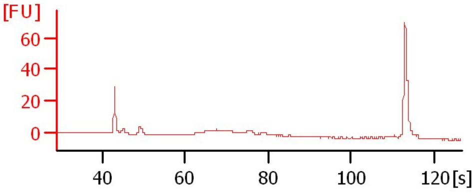
RNAseqlib OVA1



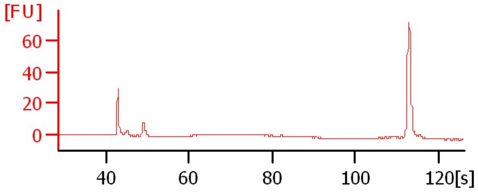
RNAseqlib OVA2



RNAseqlib OVA3



RNAseqlib Sal4



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad

Created: 11/25/2015 1:17:43 PM
Modified: 11/25/2015 2:00:56 PM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
RNAseqlib OVA1		☐	✓			
RNAseqlib OVA2		☐	✓			
RNAseqlib OVA3		☐	✓			
RNAseqlib Sal4		☐	✓			
RNAseqlib Sal5		☐	✓			
RNAseqlib Sal6		☐	✓			
RNAseqlib pos ctrl		☐	✓			
RNAseqlib OVA1		☐	✓			
RNAseqlib OVA2		☐	✓			
RNAseqlib OVA3		☐	✓			
RNAseqlib Sal4		☐	✓			
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

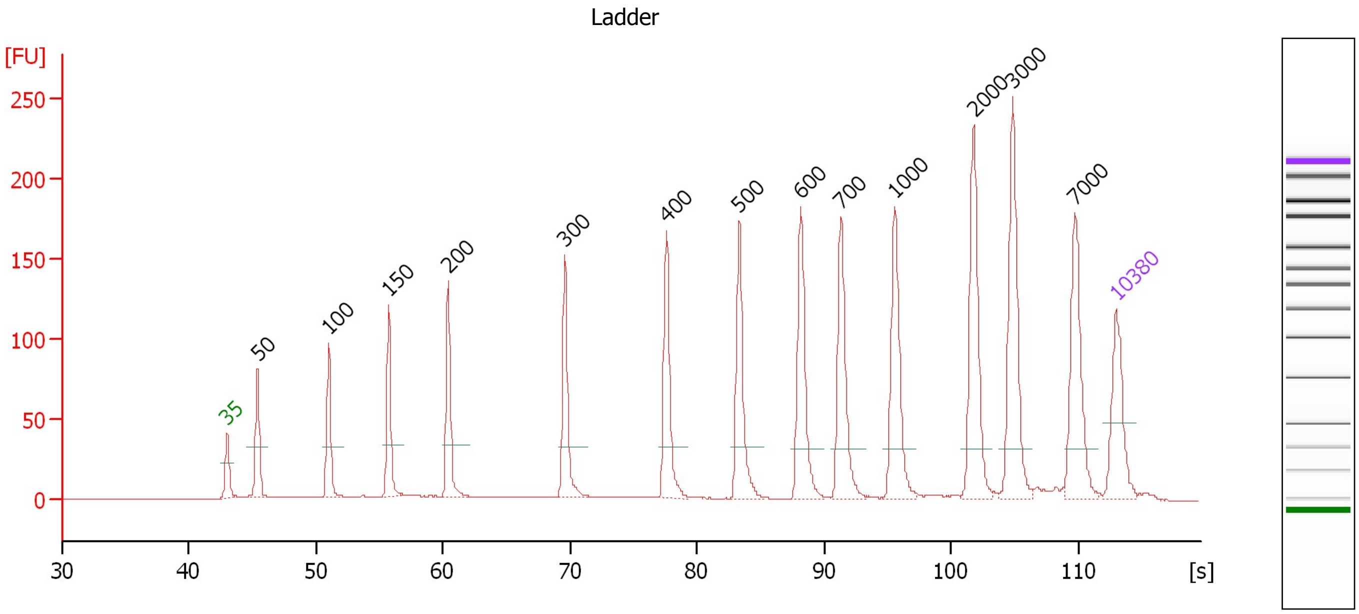
Filter Width [s] : 0.5
Polynomial Order : 4

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	Created:	11/25/2015 1:17:43 PM
Data Path:	C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad	Modified:	11/25/2015 2:00:56 PM

Electropherogram Summary



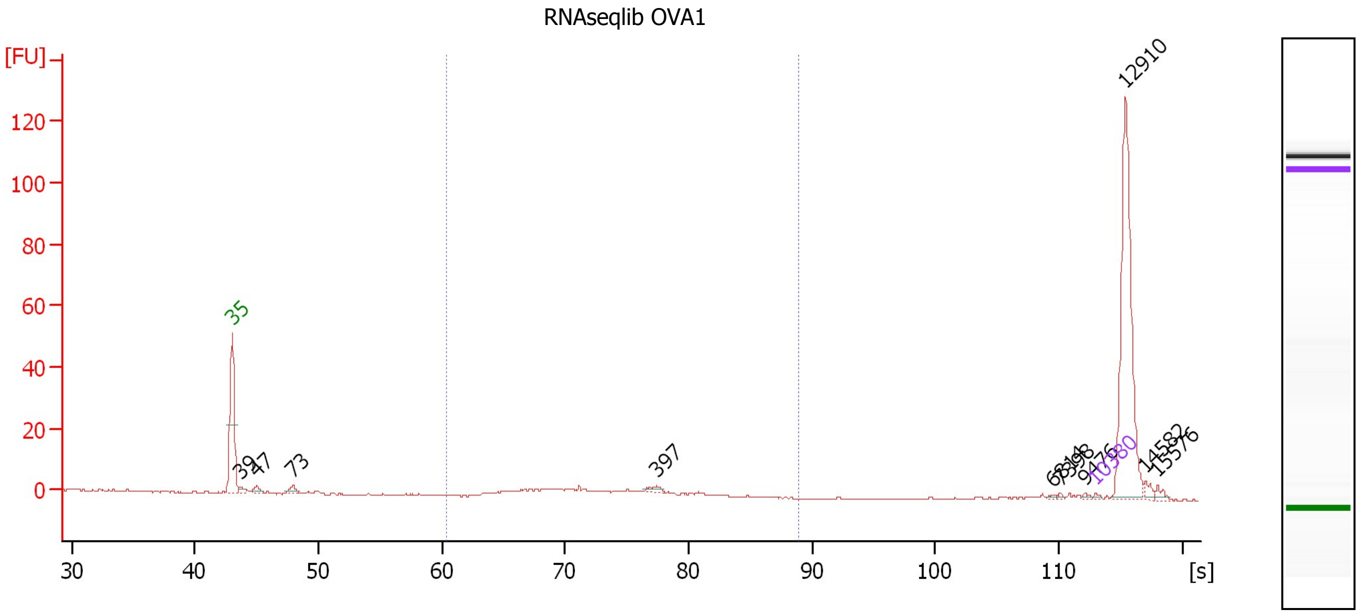
Overall Results for Ladder

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	45.41
3	∟	100	150.00	2,272.7	Ladder Peak	50.99
4	∟	150	150.00	1,515.2	Ladder Peak	55.72
5	∟	200	150.00	1,136.4	Ladder Peak	60.42
6	∟	300	150.00	757.6	Ladder Peak	69.59
7	∟	400	150.00	568.2	Ladder Peak	77.62
8	∟	500	150.00	454.5	Ladder Peak	83.33
9	∟	600	150.00	378.8	Ladder Peak	88.19
10	∟	700	150.00	324.7	Ladder Peak	91.36
11	∟	1,000	150.00	227.3	Ladder Peak	95.58
12	∟	2,000	150.00	113.6	Ladder Peak	101.80
13	∟	3,000	150.00	75.8	Ladder Peak	104.88
14	∟	7,000	150.00	32.5	Ladder Peak	109.75
15	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...



Setpoint Deviations for sample 1 : RNAseqlib OVA1

Height Threshold [FU] : 1

Overall Results for sample 1 : RNAseqlib OVA1

Number of peaks found:	10	Corr. Area 1:	31.5
Noise:	0.2		

Peak table for sample 1 : RNAseqlib OVA1

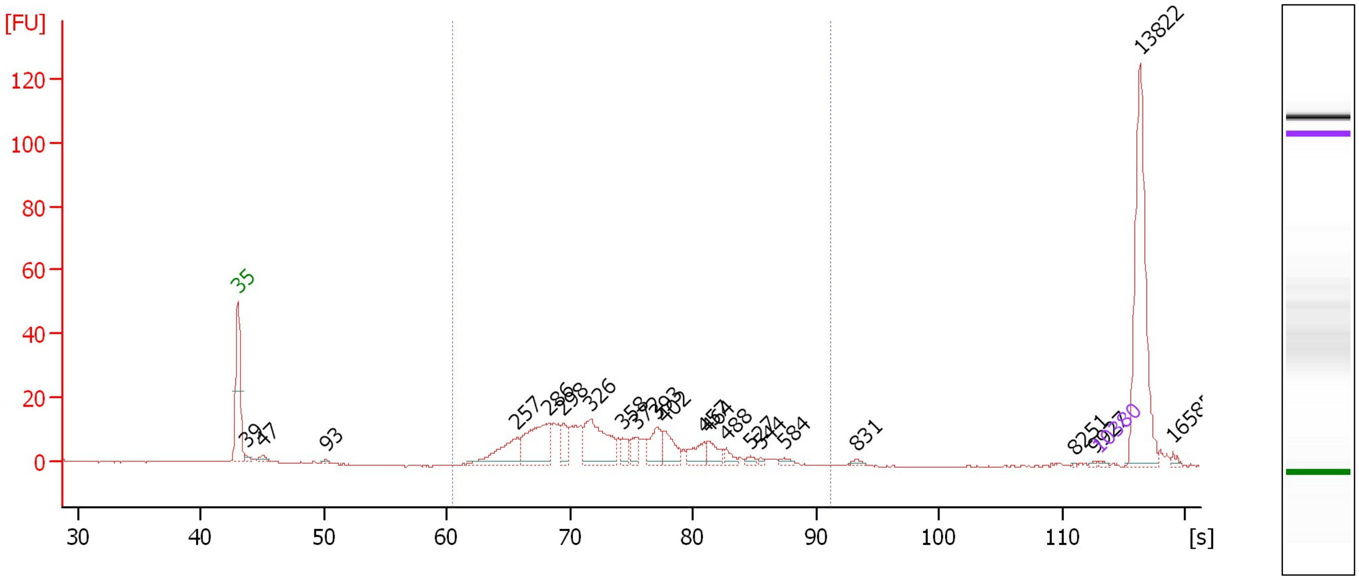
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		39	333.97	12,864.6		43.70
3		47	510.42	16,295.3		45.00
4		73	521.16	10,838.9		47.96
5		397	243.36	927.8		77.41
6		6,814	71.76	16.0		109.52
7		7,398	57.65	11.8		110.13
8		9,476	83.29	13.3		112.13
9	▶	10,380	75.00	10.9	Upper Marker	113.00
10		12,910	0.00	0.0		115.44
11		14,582	0.00	0.0		117.05
12		15,576	0.00	0.0		118.00

Region table for sample 1 : RNAseqlib OVA1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	621	342	31.5	16,339.2	🟦	3,545.04	20	17.2

Electropherogram Summary Continued ...

RNAseqlib OVA2



Setpoint Deviations for sample 2 : RNAseqlib OVA2

Height Threshold [FU] : 1

Overall Results for sample 2 : RNAseqlib OVA2

Number of peaks found:	22	Corr. Area 1:	243.8
Noise:	0.1		

Peak table for sample 2 : RNAseqlib OVA2

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		39	277.17	10,823.4		43.61
3		47	381.05	12,157.3		45.01
4		93	162.72	2,665.2		50.15
5		257	3,002.94	17,677.5		65.68
6		286	4,362.14	23,116.5		68.30
7		298	1,233.85	6,267.6		69.43
8		326	4,208.05	19,541.7		71.70
9		358	653.74	2,764.4		74.27
10		372	835.84	3,405.4		75.36
11		393	1,537.88	5,936.3		77.02
12		402	1,353.79	5,106.3		77.72
13		457	1,089.57	3,614.6		80.86
14		464	853.48	2,789.3		81.25
15		488	464.18	1,441.0		82.64
16		527	242.69	697.4		84.65
17		544	122.97	342.3		85.48
18		584	210.85	547.2		87.40
19		831	156.85	286.1		93.20
20		8,251	26.98	5.0		110.95
21		9,927	58.71	9.0		112.56
22	▶	10,380	75.00	10.9	Upper Marker	113.00

Electropherogram Summary Continued ...

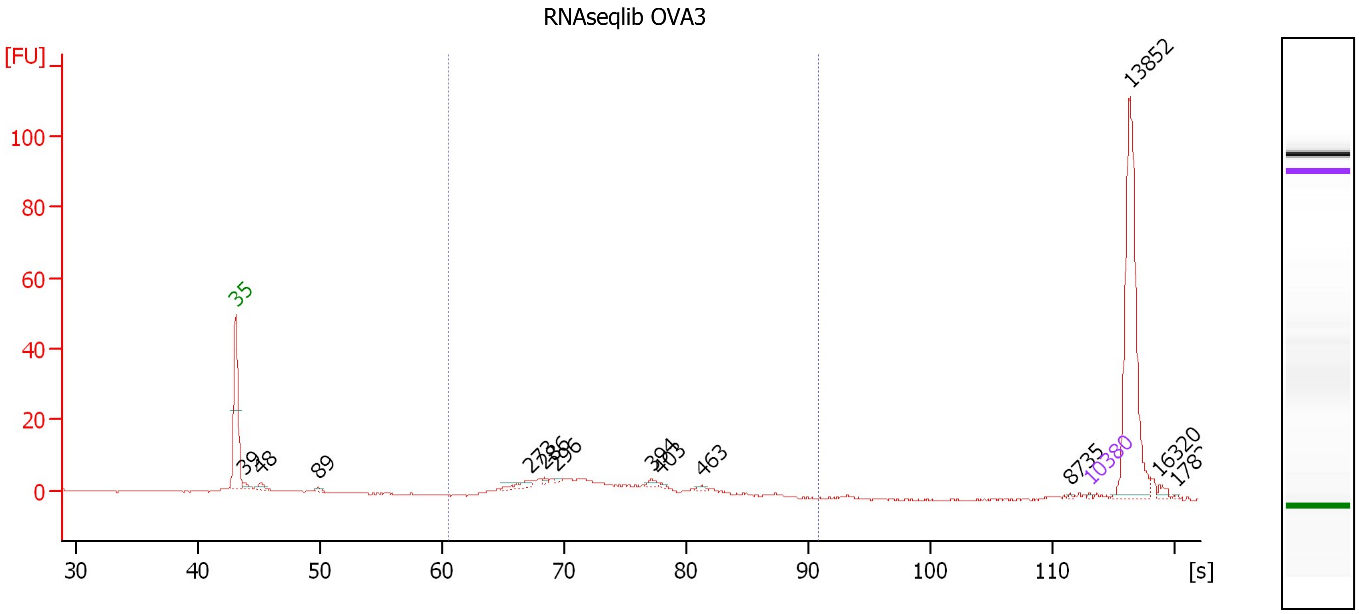
... Peak table for sample 2 : RNAseqlib OVA2

Peak	Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
23	13,822	0.00	0.0		116.31
24	16,585	0.00	0.0		118.98

Region table for sample 2 : RNAseqlib OVA2

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	695	350	243.8	112,333.0	🟦	24,303.79	66	22.5

Electropherogram Summary Continued ...



Setpoint Deviations for sample 3 : RNAseqlib OVA3

Height Threshold [FU] : 1

Overall Results for sample 3 : RNAseqlib OVA3

Number of peaks found:	13	Corr. Area 1:	92.1
Noise:	0.2		

Peak table for sample 3 : RNAseqlib OVA3

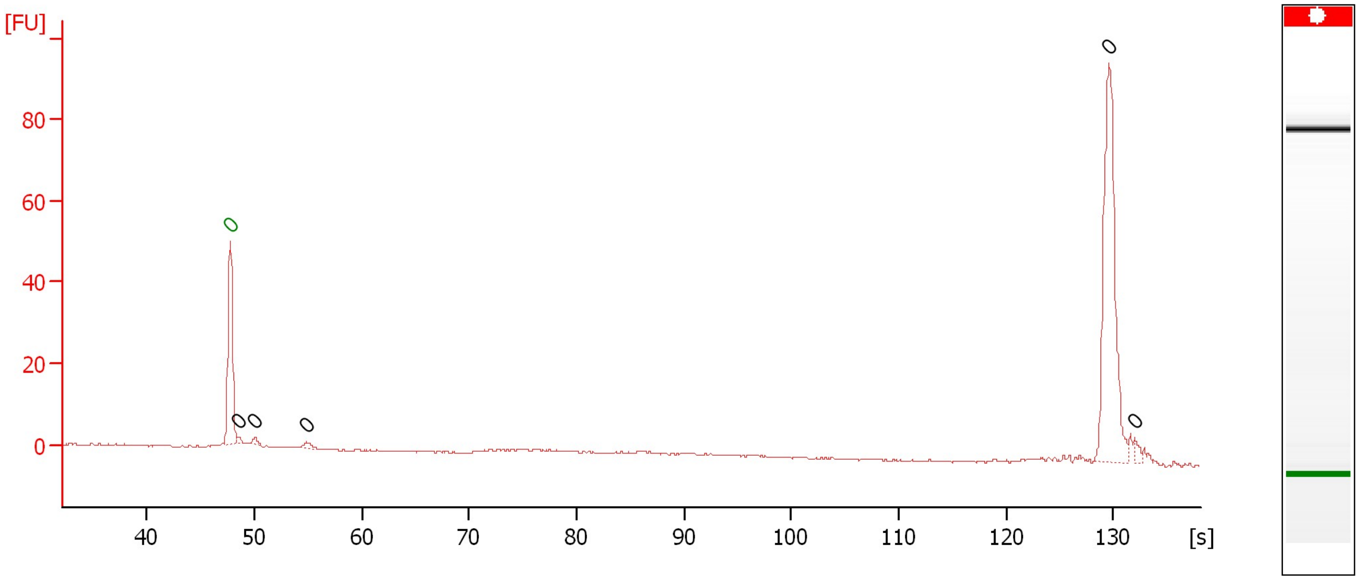
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2		39	673.96	25,929.0		43.70
3		48	749.13	23,709.3		45.07
4		89	448.67	7,627.5		49.78
5		273	1,051.46	5,825.6		67.15
6		286	285.85	1,514.7		68.30
7		296	193.23	989.0		69.22
8		394	443.25	1,706.7		77.10
9		403	137.42	516.4		77.80
10		463	213.90	700.7		81.19
11		8,735	81.70	14.2		111.42
12	▶	10,380	75.00	10.9	Upper Marker	113.00
13		13,852	0.00	0.0		116.34
14		16,320	0.00	0.0		118.72
15		17,827	0.00	0.0		120.17

Region table for sample 3 : RNAseqlib OVA3

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Color	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	683	355	92.1	85,708.0	■	18,777.13	39	22.8

Electropherogram Summary Continued ...

RNAseqlib Sal4



Setpoint Deviations for sample 4 : RNAseqlib Sal4

Height Threshold [FU] : 1

Overall Results for sample 4 : RNAseqlib Sal4

Number of peaks found:	5	Noise:	0.1

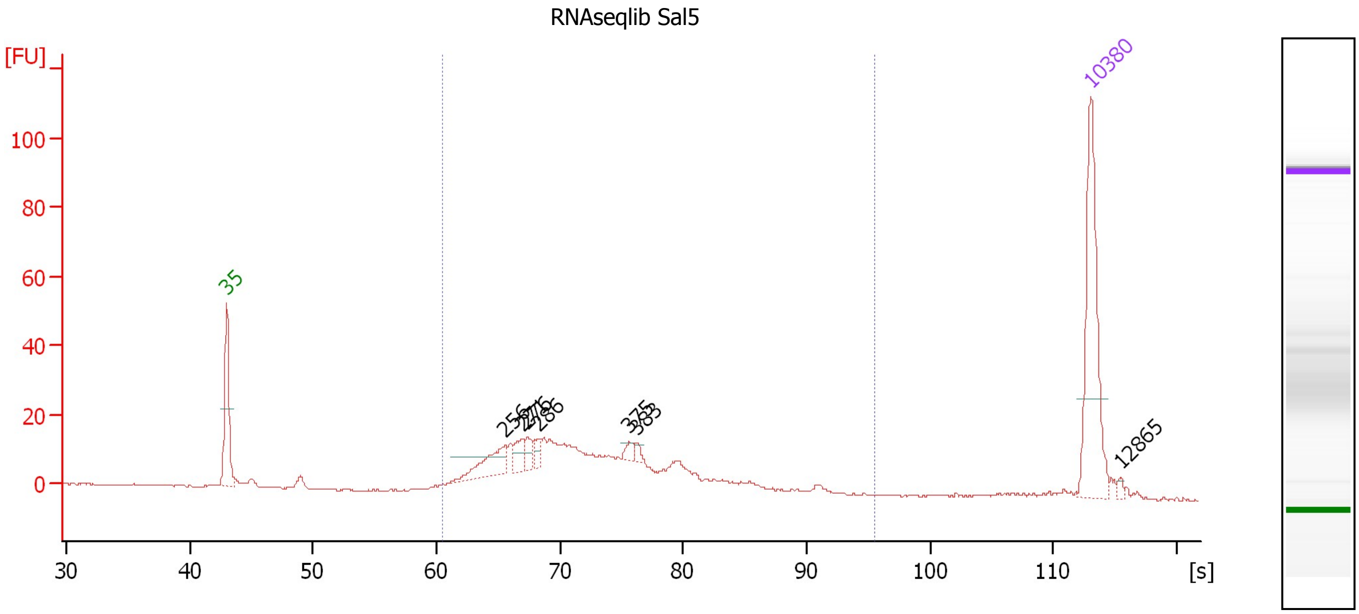
Peak table for sample 4 : RNAseqlib Sal4

Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	0	0.00	0.0	Lower Marker	47.75
2		0	0.00	0.0		48.50
3		0	0.00	0.0		50.05
4		0	0.00	0.0		54.85
5		0	0.00	0.0		129.60
6		0	0.00	0.0		131.95

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad

Created: 11/25/2015 1:17:43 PM
Modified: 11/25/2015 2:00:56 PM

Electropherogram Summary Continued ...



Overall Results for sample 5 : RNAseqlib Sal5

Number of peaks found:	7	Corr. Area 1:	332.6
Noise:	0.2		

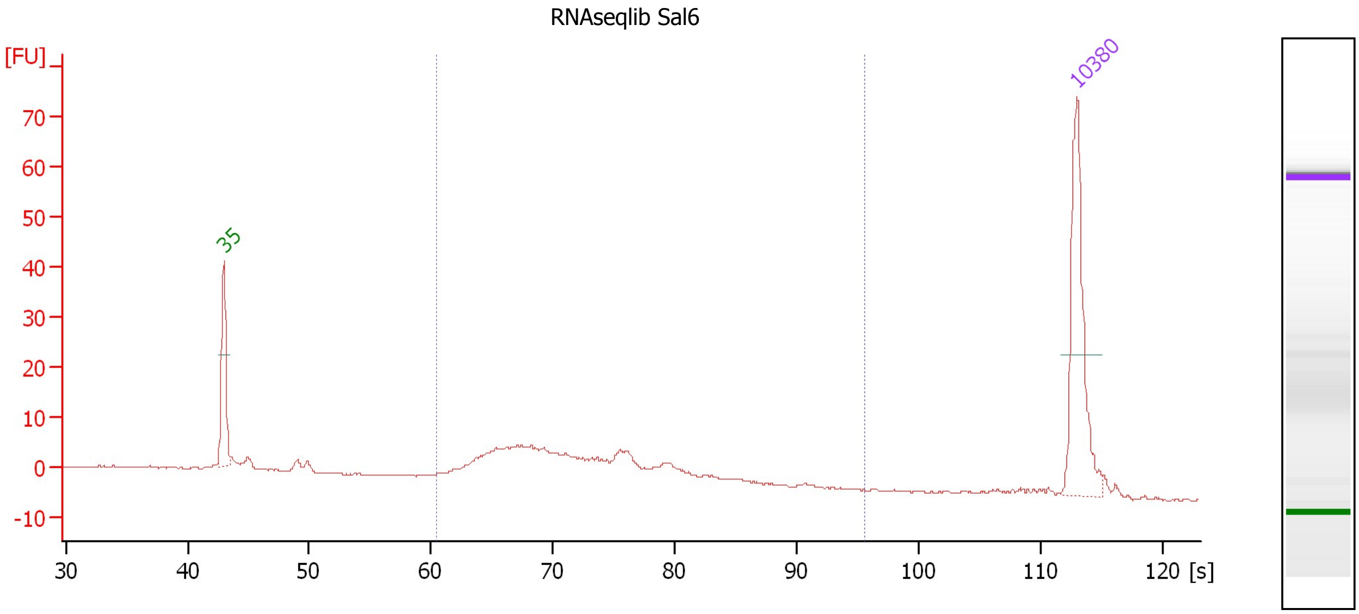
Peak table for sample 5 : RNAseqlib Sal5

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	33.01	195.1		65.58
3		271	13.84	77.4		66.93
4		276	9.22	50.7		67.36
5		286	7.77	41.2		68.28
6		375	5.44	22.0		75.63
7		383	3.73	14.7		76.28
8	▶	10,380	75.00	10.9	Upper Marker	113.00
9		12,865	0.00	0.0		115.39

Region table for sample 5 : RNAseqlib Sal5

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	349	332.6	1,707.8	■	357.29	91	29.6

Electropherogram Summary Continued ...



Overall Results for sample 6 : RNAseqlib Sal6

Number of peaks found:	0	Corr. Area 1:	150.6
Noise:	0.1		

Peak table for sample 6 : RNAseqlib Sal6

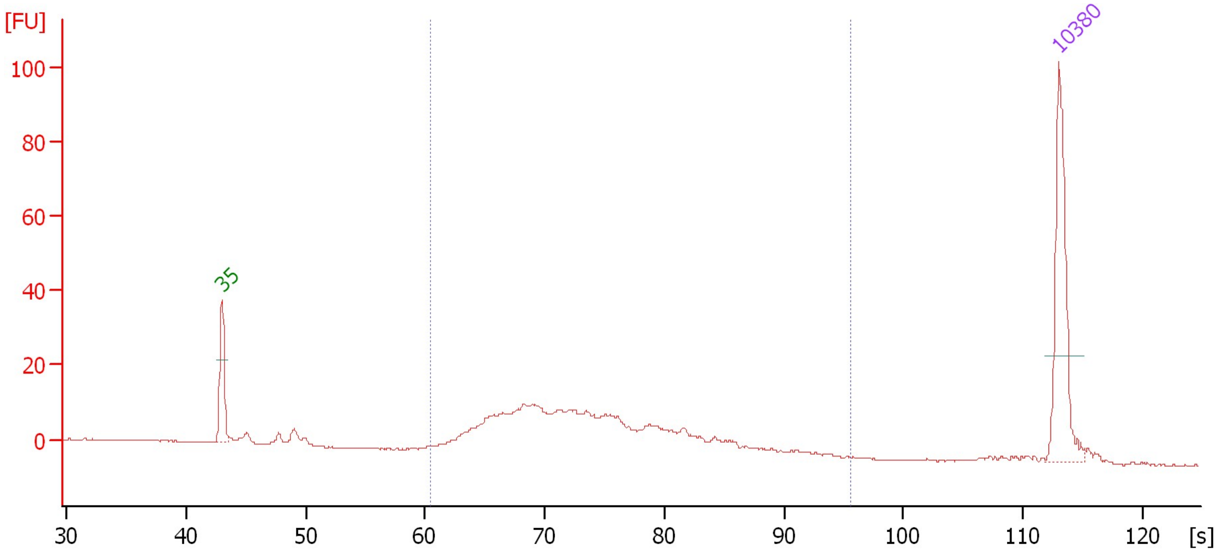
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

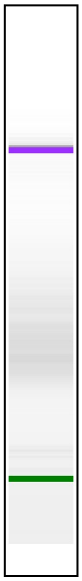
Region table for sample 6 : RNAseqlib Sal6

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	350	150.6	999.7	🟦	209.15	79	30.1

Electropherogram Summary Continued ...

RNAseqlib pos ctrl





Overall Results for sample 7 : **RNAseqlib pos ctrl**

Number of peaks found:	0	Corr. Area 1:	276.4
Noise:	0.1		

Peak table for sample 7 : **RNAseqlib pos ctrl**

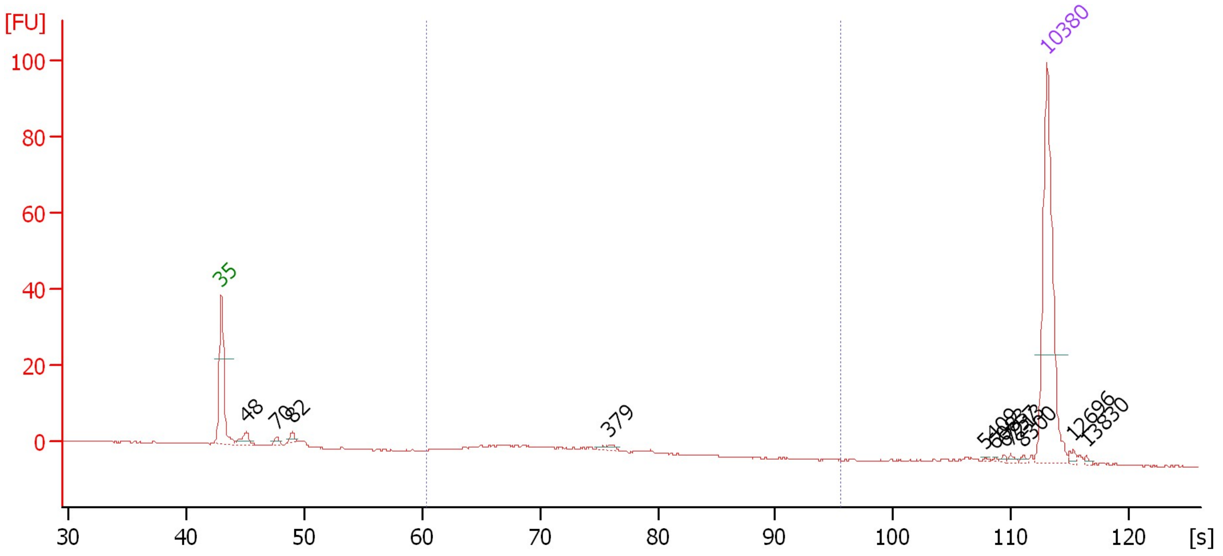
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 7 : **RNAseqlib pos ctrl**

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	369	276.4	1,521.2	🟦	332.69	88	30.8

Electropherogram Summary Continued ...

RNAseqlib OVA1



Setpoint Deviations for sample 8 : RNAseqlib OVA1

Height Threshold [FU] : 1

Overall Results for sample 8 : RNAseqlib OVA1

Number of peaks found:	11	Corr. Area 1:	26.3
Noise:	0.2		

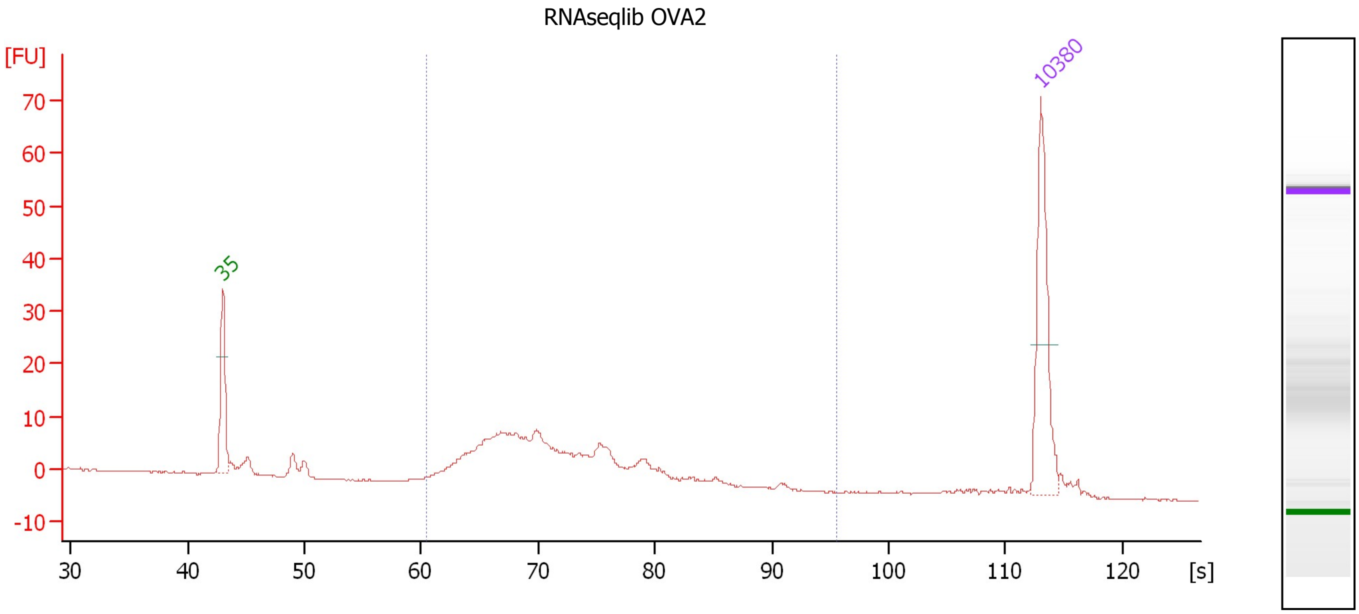
Peak table for sample 8 : RNAseqlib OVA1

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		48	9.79	308.9		45.09
3		70	3.77	81.1		47.69
4		82	4.91	90.4		49.01
5		379	3.14	12.6		75.91
6		5,409	0.43	0.1		107.81
7		6,083	0.41	0.1		108.63
8		6,757	0.75	0.2		109.45
9		7,213	0.98	0.2		109.95
10		8,300	0.72	0.1		111.00
11	▶	10,380	75.00	10.9	Upper Marker	113.00
12		12,696	0.00	0.0		115.23
13		13,830	0.00	0.0		116.32

Region table for sample 8 : RNAseqlib OVA1

From [bp]	To [bp]	Average Size [bp]	Corr. Area	Molarity [pmol/l]	Co lor	Conc. [pg/µl]	% of Total	Size distribution in CV [%]
200	1,000	328	26.3	165.4	🟦	34.33	51	17.5

Electropherogram Summary Continued ...


RNAseqlib OVA2

Overall Results for sample 9 : **RNAseqlib OVA2**

Number of peaks found:	0	Corr. Area 1:	175.1
Noise:	0.1		

Peak table for sample 9 : **RNAseqlib OVA2**

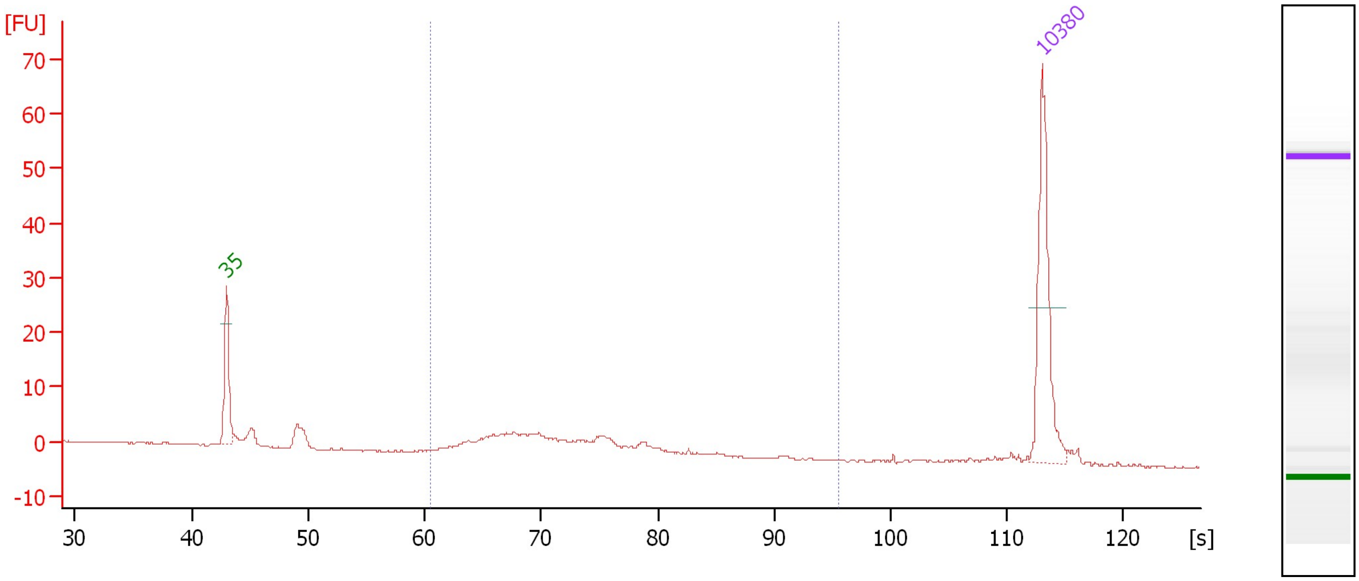
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 9 : **RNAseqlib OVA2**

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	332	175.1	1,479.7	■	301.53	86	25.3

Electropherogram Summary Continued ...

RNAseqlib OVA3



Overall Results for sample 10 : RNAseqlib OVA3

Number of peaks found:	0	Corr. Area 1:	61.8
Noise:	0.1		

Peak table for sample 10 : RNAseqlib OVA3

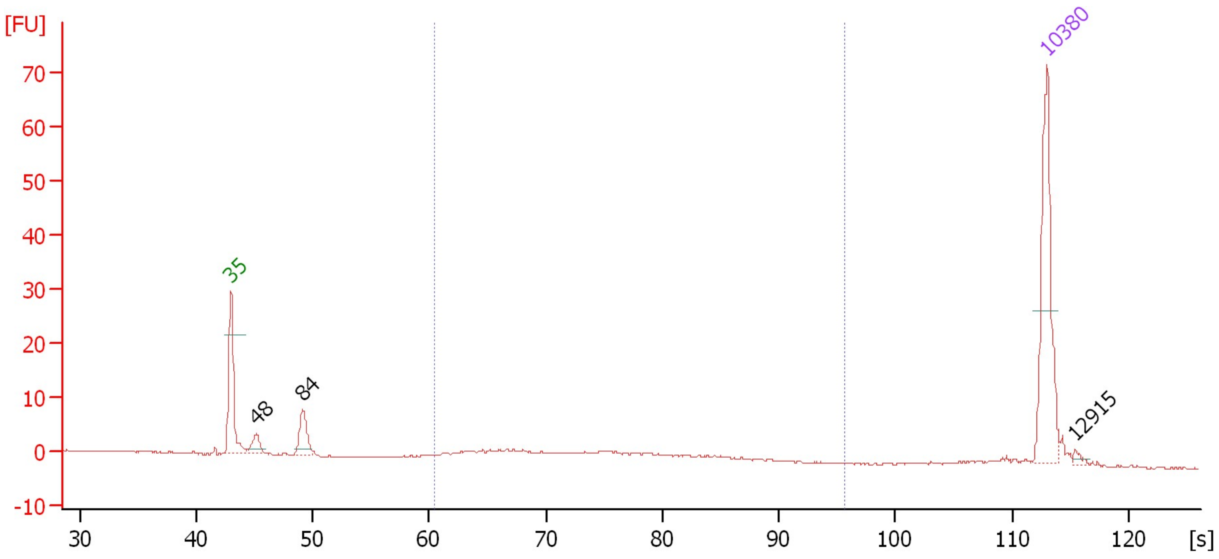
Peak		Size [bp]	Conc. [pg/µl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	◀	35	125.00	5,411.3	Lower Marker	43.00
2	▶	10,380	75.00	10.9	Upper Marker	113.00

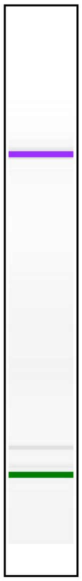
Region table for sample 10 : RNAseqlib OVA3

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	332	61.8	546.0	🟦	112.37	72	22.5

Electropherogram Summary Continued ...

RNAseqlib Sal4





Setpoint Deviations for sample 11 : RNAseqlib Sal4

Height Threshold [FU] : 1

Overall Results for sample 11 : RNAseqlib Sal4

Number of peaks found:	3	Corr. Area 1:	43.4
Noise:	0.2		

Peak table for sample 11 : RNAseqlib Sal4

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		48	16.28	508.9		45.16
3		84	31.22	565.1		49.17
4	▶	10,380	75.00	10.9	Upper Marker	113.00
5		12,915	0.00	0.0		115.44

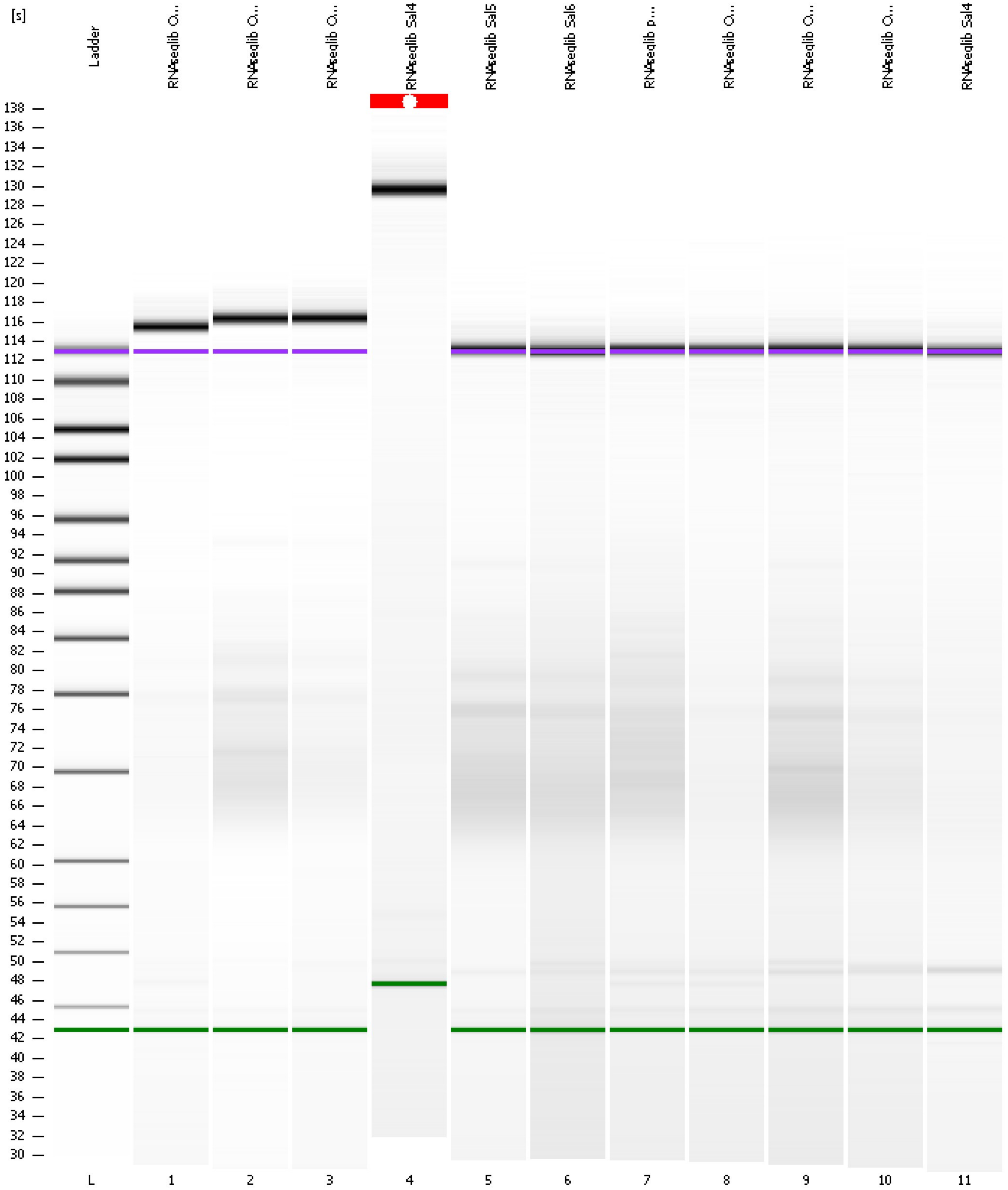
Region table for sample 11 : RNAseqlib Sal4

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	384	43.4	366.5	🟦	80.30	53	34.1

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad

Created: 11/25/2015 1:17:43 PM
Modified: 11/25/2015 2:00:56 PM

Gel Image



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad
Created: 11/25/2015 1:17:43 PM
Modified: 11/25/2015 2:00:56 PM

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		11/25/2015 1:59:02 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2015-11-25\2015-11-25_002.xad)		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938B		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE13701086		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		11/25/2015 1:17:48 PM	(GMT --08:00) Pacific Standard Time	UC Davis	D8XSMGH1