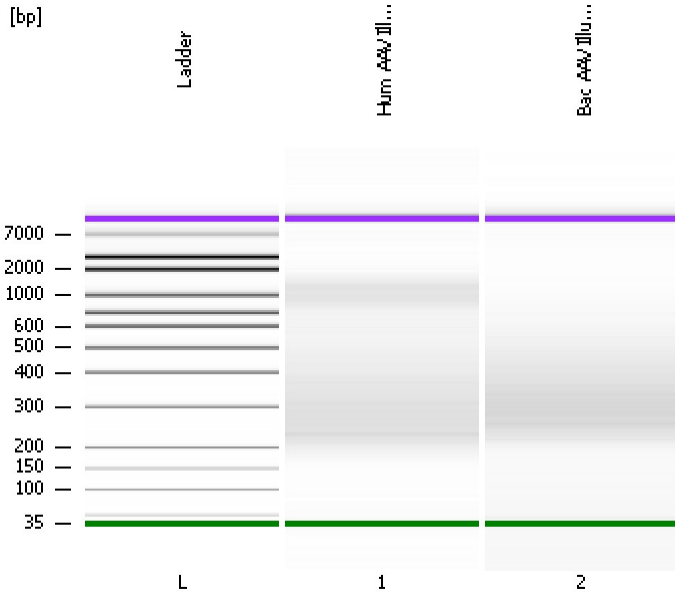


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
Modified: 9/26/2019 9:42:49 AM

**Electrophoresis File Run Summary**



Instrument Information:

Instrument Name: DE34903152      Firmware: C.01.069  
Serial#: DE34903152      Type: G2938C

Assay Information:

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

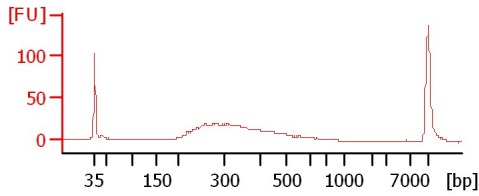
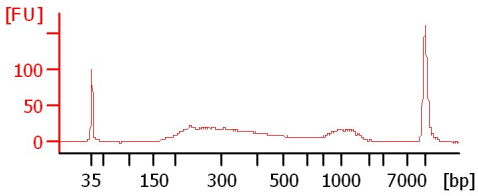
Assay Class: High Sensitivity DNA Assay  
Version: 1.03  
Assay Comments: Copyright © 2003-2010 Agilent Technologies

Chip Information:

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

**Hum AAV Illumina MethylSeq Lib**

**Bac AAV Illumina MethylSeq Lib**



Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
 Modified: 9/26/2019 9:42:49 AM

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

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
Hum AAV Illumina MethylSeq Lib		<input type="checkbox"/>	<input checked="" type="checkbox"/>			
Bac AAV Illumina MethylSeq Lib		<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:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
Modified: 9/26/2019 9:42:49 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

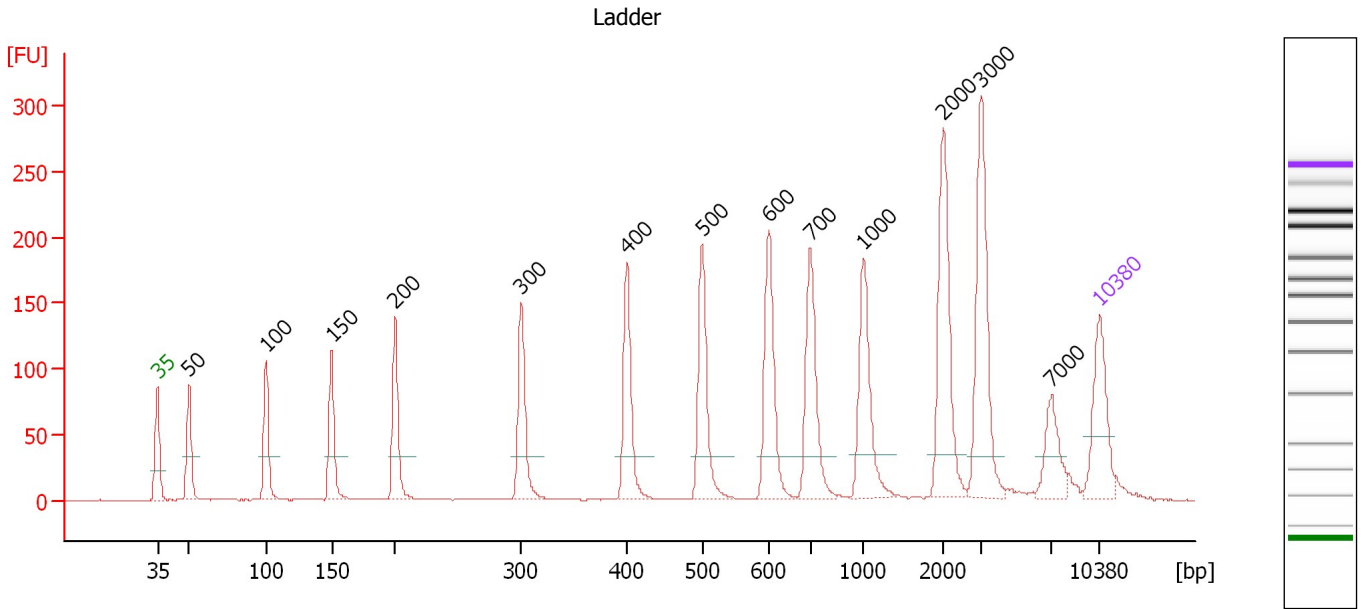
**Ladder**

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:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
 Modified: 9/26/2019 9:42:49 AM

**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

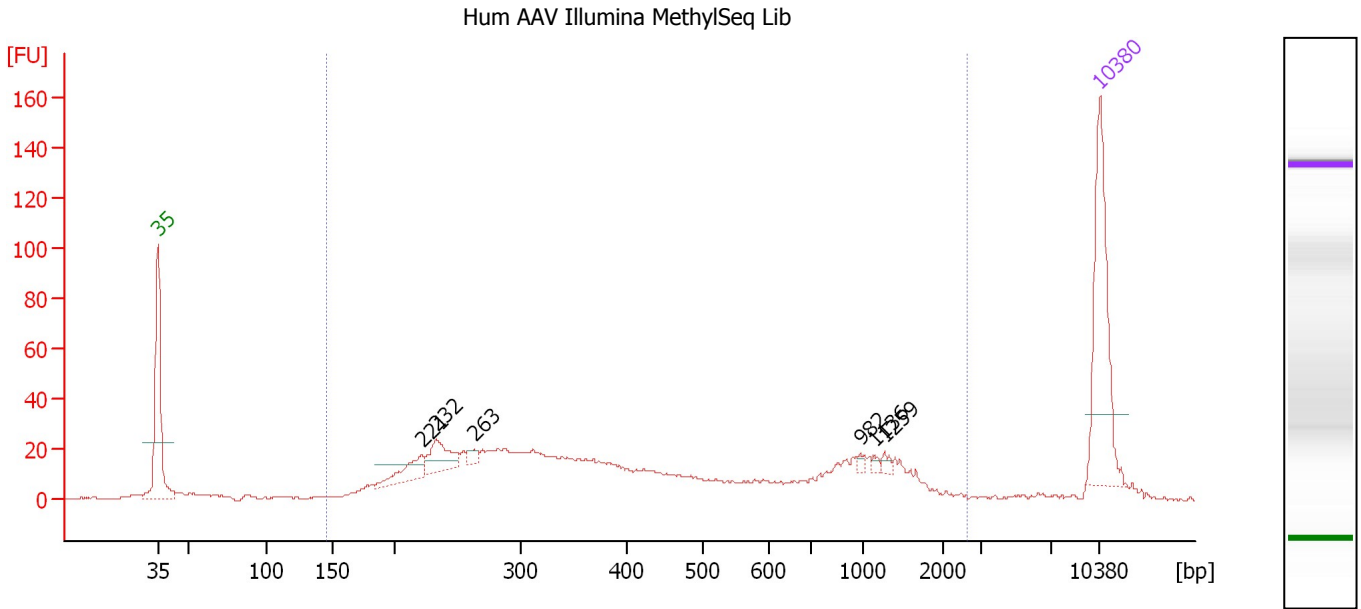
**Peak table for Ladder**

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	45.33
3	100	150.00	2,272.7	Ladder Peak	51.04
4	150	150.00	1,515.2	Ladder Peak	55.93
5	200	150.00	1,136.4	Ladder Peak	60.65
6	300	150.00	757.6	Ladder Peak	70.03
7	400	150.00	568.2	Ladder Peak	77.84
8	500	150.00	454.5	Ladder Peak	83.46
9	600	150.00	378.8	Ladder Peak	88.39
10	700	150.00	324.7	Ladder Peak	91.49
11	1,000	150.00	227.3	Ladder Peak	95.44
12	2,000	150.00	113.6	Ladder Peak	101.37
13	3,000	150.00	75.8	Ladder Peak	104.15
14	7,000	150.00	32.5	Ladder Peak	109.41
15	10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
 Modified: 9/26/2019 9:42:49 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : Hum AAV Illumina MethylSeq Lib**

Number of peaks found: 6                      Corr. Area 1: 748.2  
 Noise: 0.4

**Peak table for sample 1 : Hum AAV Illumina MethylSeq Lib**

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	221	23.97	164.4		62.62
3	232	30.33	198.0		63.66
4	263	6.12	35.3		66.53
5	982	2.41	3.7		95.20
6	1,136	2.57	3.4		96.25
7	1,259	3.19	3.8		96.98
8	10,380	75.00	10.9	Upper Marker	113.00

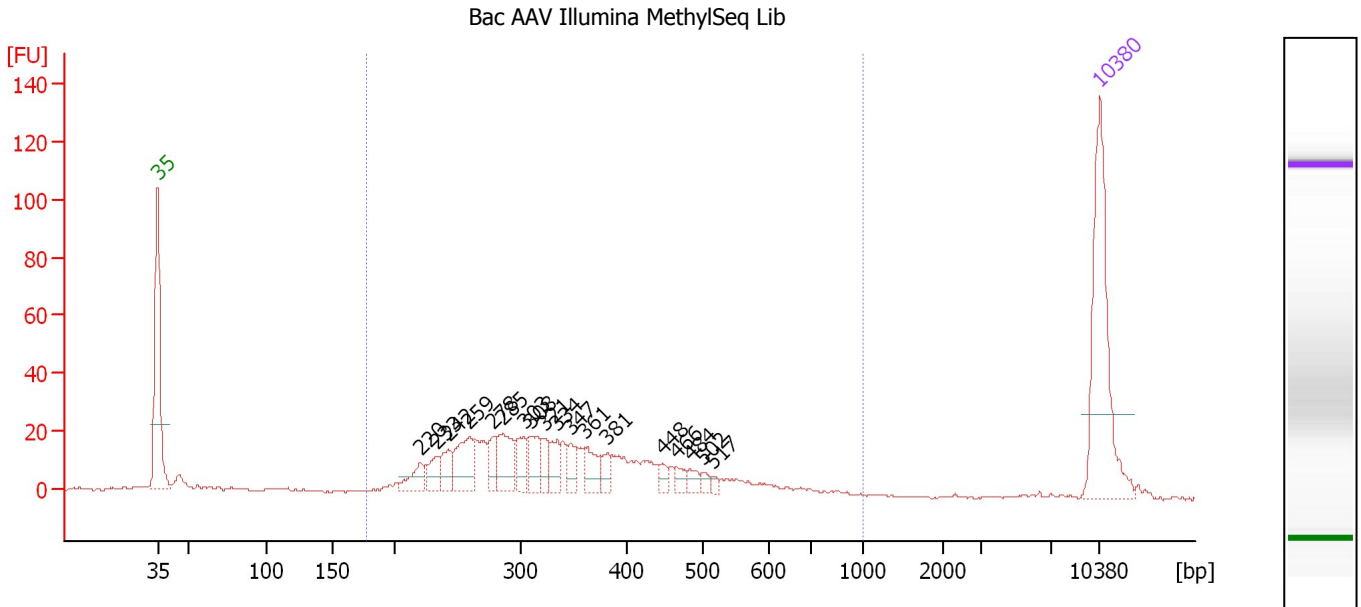
**Region table for sample 1 : Hum AAV Illumina MethylSeq Lib**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
147	2,650	531	538.93	748.2	2,491.4	95	75.1

Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
 Modified: 9/26/2019 9:42:49 AM

**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : Bac AAV Illumina MethylSeq Lib**

Number of peaks found: 18                      Corr. Area 1: 520.2  
 Noise: 0.4

**Peak table for sample 2 : Bac AAV Illumina MethylSeq Lib**

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	220	15.67	108.0		62.50
3	233	14.11	91.7		63.74
4	242	17.11	107.0		64.61
5	259	32.49	190.2		66.17
6	278	13.28	72.4		67.95
7	285	32.07	170.4		68.64
8	303	15.59	78.0		70.24
9	308	19.61	96.5		70.65
10	321	11.79	55.6		71.71
11	334	14.41	65.4		72.67
12	347	12.17	53.2		73.67
13	361	16.56	69.6		74.77
14	381	9.68	38.5		76.37
15	448	5.83	19.7		80.54
16	466	6.43	20.9		81.55
17	484	6.72	21.0		82.56
18	502	4.16	12.5		83.56
19	517	2.77	8.1		84.29
20	10,380	75.00	10.9	Upper Marker	113.00

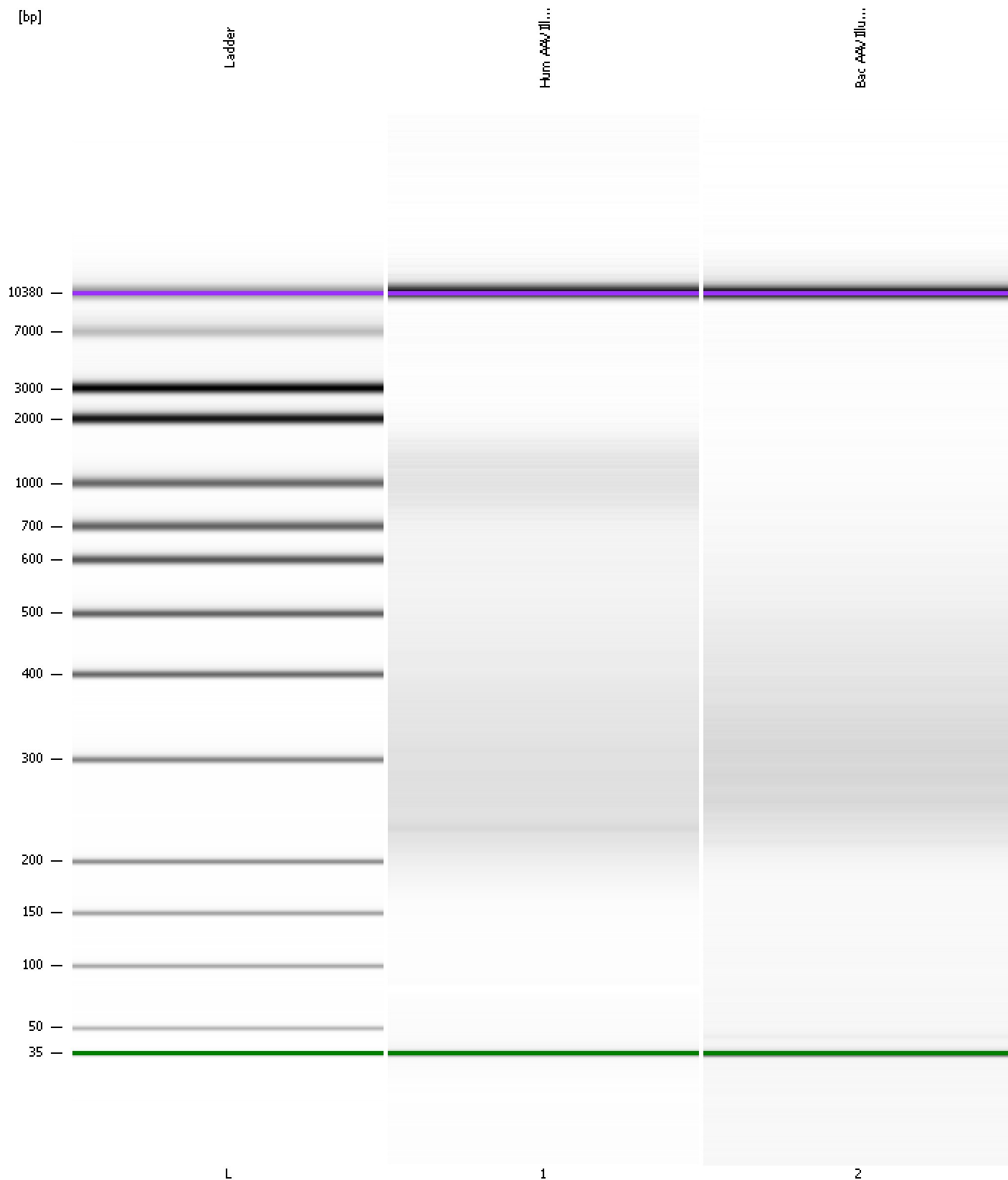
**Region table for sample 2 : Bac AAV Illumina MethylSeq Lib**

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/μl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
178	1,000	357	386.74	520.2	1,854.1	91	32.6

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
Modified: 9/26/2019 9:42:49 AM

**Gel Image**

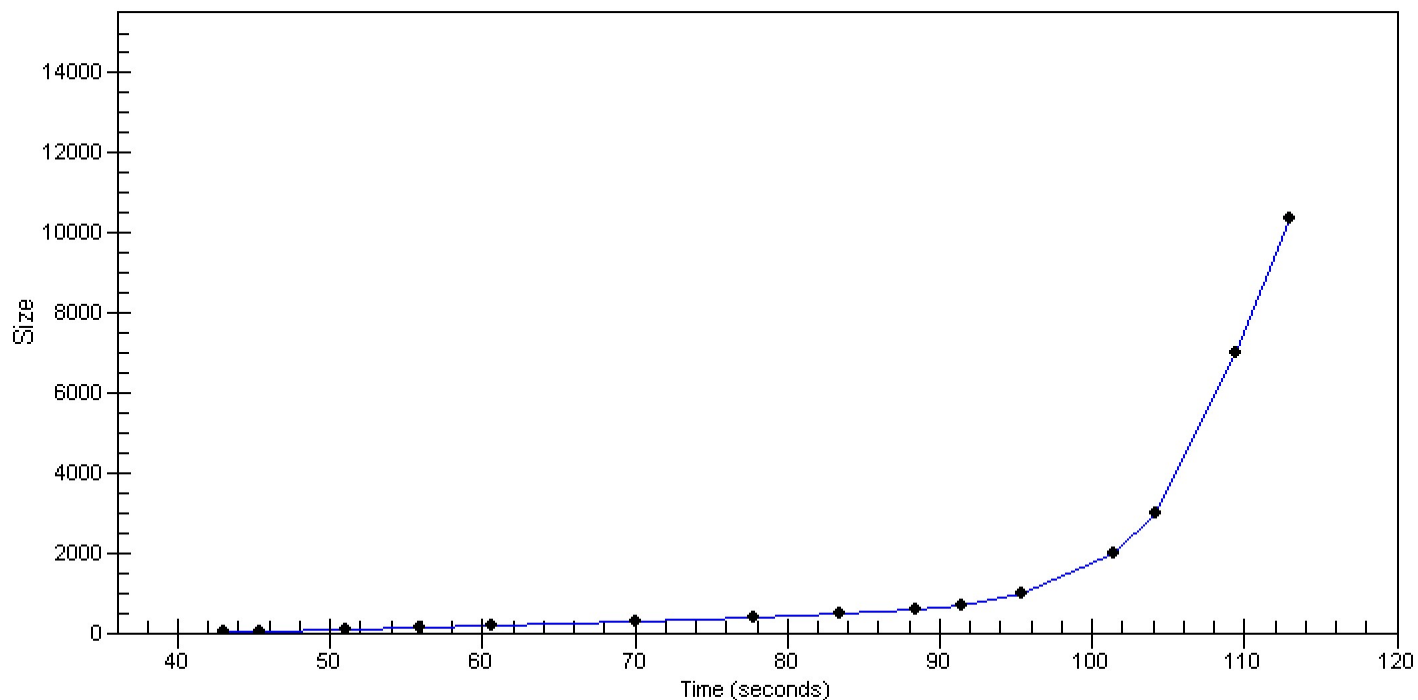


Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
Modified: 9/26/2019 9:42:49 AM

### Curves

#### Standard Curve





Assay Class: High Sensitivity DNA Assay  
 Data Path: C:\...19-09-24\2019-09-24\_001\_HiSeq1885\_IlluminaMethylSeqLibs.xad

Created: 9/24/2019 9:53:07 AM  
 Modified: 9/26/2019 9:42:49 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		9/24/2019 10:34:23 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Run started on port 1 (File: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\data\2019-09-24\2019-09-24_001.xad)		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Product Number : G2938C		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Name :		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Vendor : Agilent Technologies		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Serial# : DE34903152		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Firmware : C.01.069		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1
Cartridge : Electrode		Instrument	Run		9/24/2019 9:53:12 AM	(GMT --07:00) Pacific Standard Time	UC Davis	D8XSMGH1