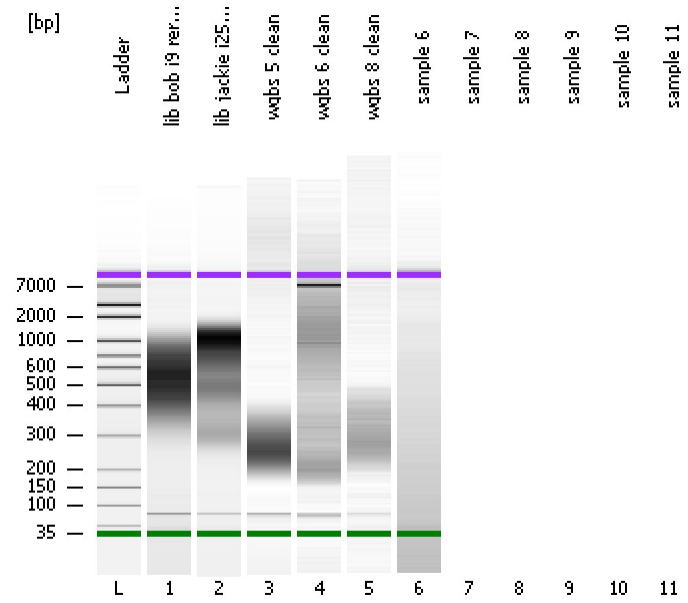
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

## Electrophoresis File Run Summary




Instrument Information:

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

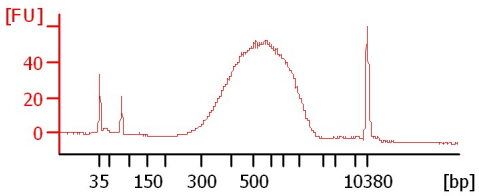
Assay Information:

| | |
|---|---|
| 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 |

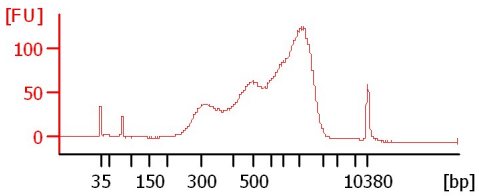
Chip Information:

| | |
|---|---|
| Chip Lot #: | |
| Reagent Kit Lot #: | |
| Chip Comments: | |

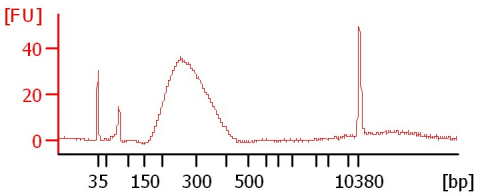
**lib bob i9 rerun**



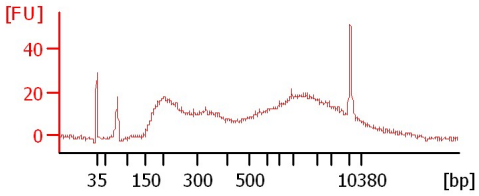

**lib jackie i25 rerun**



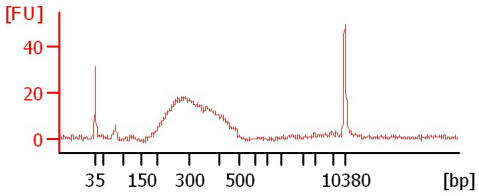

**wgbs 5 clean**



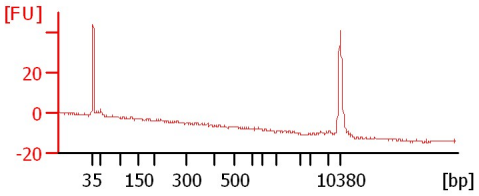

**wgbs 6 clean**




**wgbs 8 clean**




**sample 6**



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

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

| Sample Name | Sample Comment | Rest. Digest | Status | Observation | Result Label | Result Color |
|---|---|---|---|---|---|---|
| lib bob i9 rerun | | ☐ | ✔ | | | |
| lib jackie i25 rerun | | ☐ | ✔ | | | |
| wgbs 5 clean | | ☐ | ✔ | | | |
| wgbs 6 clean | | ☐ | ✔ | | | |
| wgbs 8 clean | | ☐ | ✔ | | | |
| sample 6 | | ☐ | ✔ | | | |
| sample 7 | | ☐ | | | | |
| sample 8 | | ☐ | | | | |
| sample 9 | | ☐ | | | | |
| sample 10 | | ☐ | | | | |
| sample 11 | | ☐ | | | | |
| Ladder | | ☐ | ✔ | | | |

**Chip Lot #** **Reagent Kit Lot #**

**Chip Comments :**

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

## 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

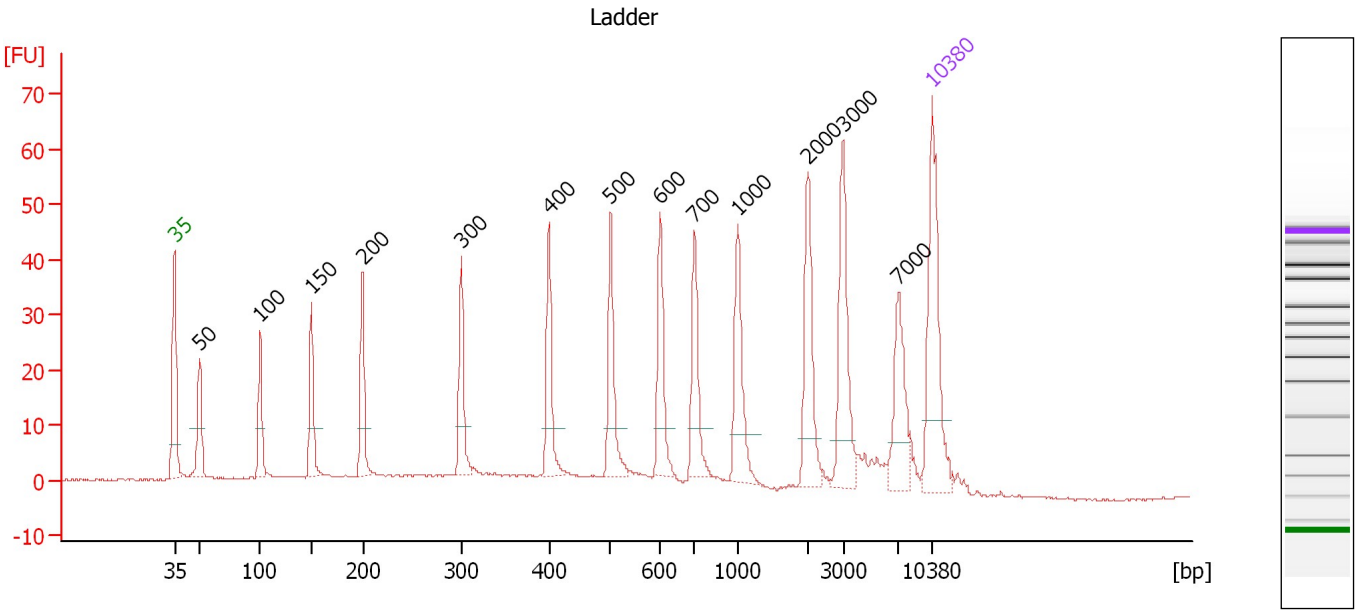
### Ladder

| 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:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

## Electropherogram Summary




### Overall Results for Ladder

Noise: 0.1

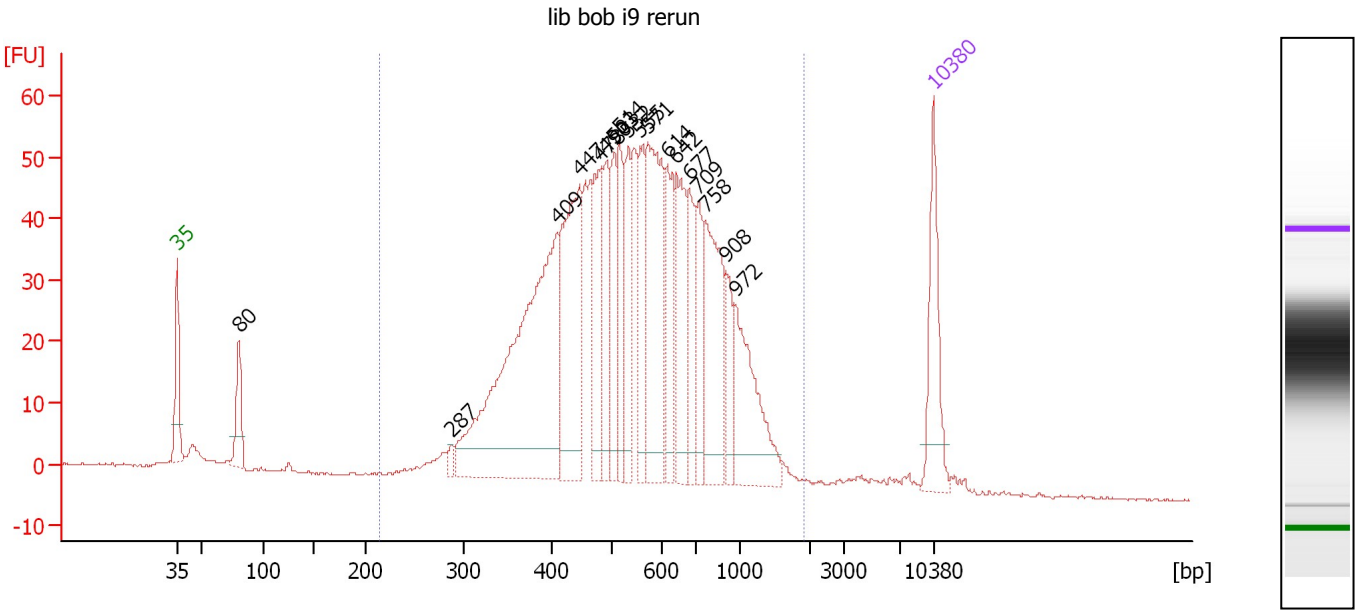
### Peak table for Ladder

| 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 | 45.32 |
| 3 | | 100 | 150.00 | 2,272.7 | Ladder Peak | 50.94 |
| 4 | | 150 | 150.00 | 1,515.2 | Ladder Peak | 55.67 |
| 5 | | 200 | 150.00 | 1,136.4 | Ladder Peak | 60.40 |
| 6 | | 300 | 150.00 | 757.6 | Ladder Peak | 69.52 |
| 7 | | 400 | 150.00 | 568.2 | Ladder Peak | 77.61 |
| 8 | | 500 | 150.00 | 454.5 | Ladder Peak | 83.32 |
| 9 | | 600 | 150.00 | 378.8 | Ladder Peak | 87.91 |
| 10 | | 700 | 150.00 | 324.7 | Ladder Peak | 91.11 |
| 11 | | 1,000 | 150.00 | 227.3 | Ladder Peak | 95.06 |
| 12 | | 2,000 | 150.00 | 113.6 | Ladder Peak | 101.56 |
| 13 | | 3,000 | 150.00 | 75.8 | Ladder Peak | 104.82 |
| 14 | | 7,000 | 150.00 | 32.5 | Ladder Peak | 109.89 |
| 15 | | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 1 : lib bob i9 rerun**

| | | | |
|---|---|---|---|
| Number of peaks found: | 18 | Corr. Area 1: | 1,267.1 |
| Noise: | 0.2 | | |

**Peak table for sample 1 : lib bob i9 rerun**

| 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 | 80 | 66.98 | 1,263.3 | | 48.73 |
| 3 | 287 | 9.90 | 52.2 | | 68.37 |
| 4 | 409 | 505.60 | 1,870.8 | | 78.15 |
| 5 | 447 | 233.38 | 791.7 | | 80.27 |
| 6 | 478 | 101.66 | 322.5 | | 82.05 |
| 7 | 490 | 97.53 | 301.7 | | 82.74 |
| 8 | 503 | 79.80 | 240.2 | | 83.48 |
| 9 | 514 | 79.88 | 235.4 | | 83.97 |
| 10 | 532 | 77.66 | 221.0 | | 84.81 |
| 11 | 555 | 82.34 | 224.8 | | 85.85 |
| 12 | 571 | 198.18 | 525.7 | | 86.59 |
| 13 | 614 | 92.68 | 228.6 | | 88.37 |
| 14 | 642 | 109.48 | 258.4 | | 89.26 |
| 15 | 677 | 76.60 | 171.3 | | 90.39 |
| 16 | 709 | 68.26 | 145.9 | | 91.23 |
| 17 | 758 | 148.85 | 297.6 | | 91.87 |
| 18 | 908 | 41.68 | 69.6 | | 93.85 |
| 19 | 972 | 122.25 | 190.6 | | 94.69 |
| 20 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

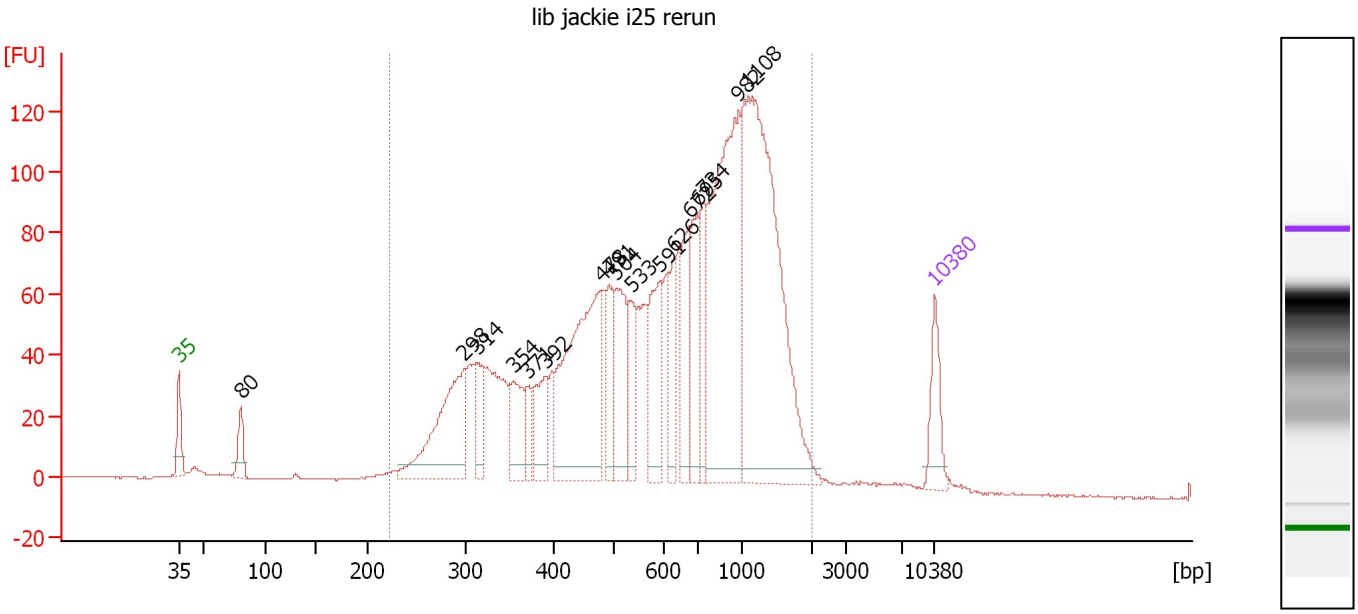
**Region table for sample 1 : lib bob i9 rerun**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 214 | 1,924 | 587 | 1,267.1 | 7,337.5 | 2,429.22 | 95 | 39.2 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 2 : lib jackie i25 rerun**

| | | | |
|---|---|---|---|
| Number of peaks found: | 17 | Corr. Area 1: | 2,561.0 |
| Noise: | 0.2 | | |

**Peak table for sample 2 : lib jackie i25 rerun**

| 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 | 80 | 72.80 | 1,372.4 | | 48.73 |
| 3 | 298 | 338.90 | 1,720.5 | | 69.38 |
| 4 | 314 | 90.72 | 438.4 | | 70.61 |
| 5 | 354 | 127.67 | 545.7 | | 73.92 |
| 6 | 371 | 56.19 | 229.5 | | 75.26 |
| 7 | 392 | 113.17 | 437.0 | | 76.99 |
| 8 | 478 | 514.76 | 1,631.1 | | 82.08 |
| 9 | 491 | 102.34 | 315.7 | | 82.82 |
| 10 | 504 | 182.81 | 549.6 | | 83.51 |
| 11 | 533 | 102.13 | 290.3 | | 84.84 |
| 12 | 591 | 162.83 | 417.2 | | 87.51 |
| 13 | 626 | 91.48 | 221.4 | | 88.74 |
| 14 | 672 | 145.08 | 326.9 | | 90.23 |
| 15 | 695 | 146.04 | 318.2 | | 90.97 |
| 16 | 734 | 123.38 | 254.7 | | 91.56 |
| 17 | 982 | 590.23 | 910.6 | | 94.82 |
| 18 | 1,108 | 834.21 | 1,140.7 | | 95.76 |
| 19 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

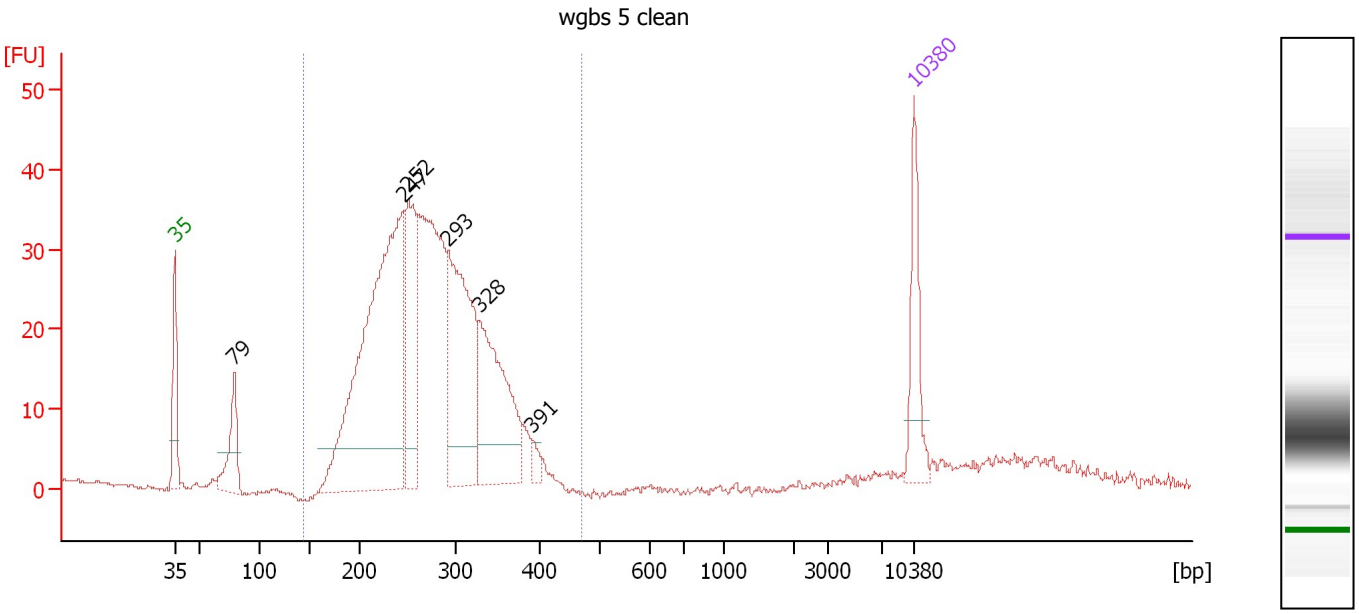
**Region table for sample 2 : lib jackie i25 rerun**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 223 | 2,043 | 753 | 2,561.0 | 13,323.8 | 4,660.42 | 96 | 51.9 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 3 : wgbs 5 clean**

| | | | |
|---|---|---|---|
| Number of peaks found: | 6 | Corr. Area 1: | 622.9 |
| Noise: | 0.3 | | |

**Peak table for sample 3 : wgbs 5 clean**

| 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 | 79 | 105.57 | 2,018.0 | | 48.61 |
| 3 | 247 | 765.66 | 4,701.1 | | 64.67 |
| 4 | 252 | 220.80 | 1,328.8 | | 65.12 |
| 5 | 293 | 343.76 | 1,779.3 | | 68.86 |
| 6 | 328 | 262.22 | 1,211.2 | | 71.79 |
| 7 | 391 | 16.42 | 63.7 | | 76.84 |
| 8 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

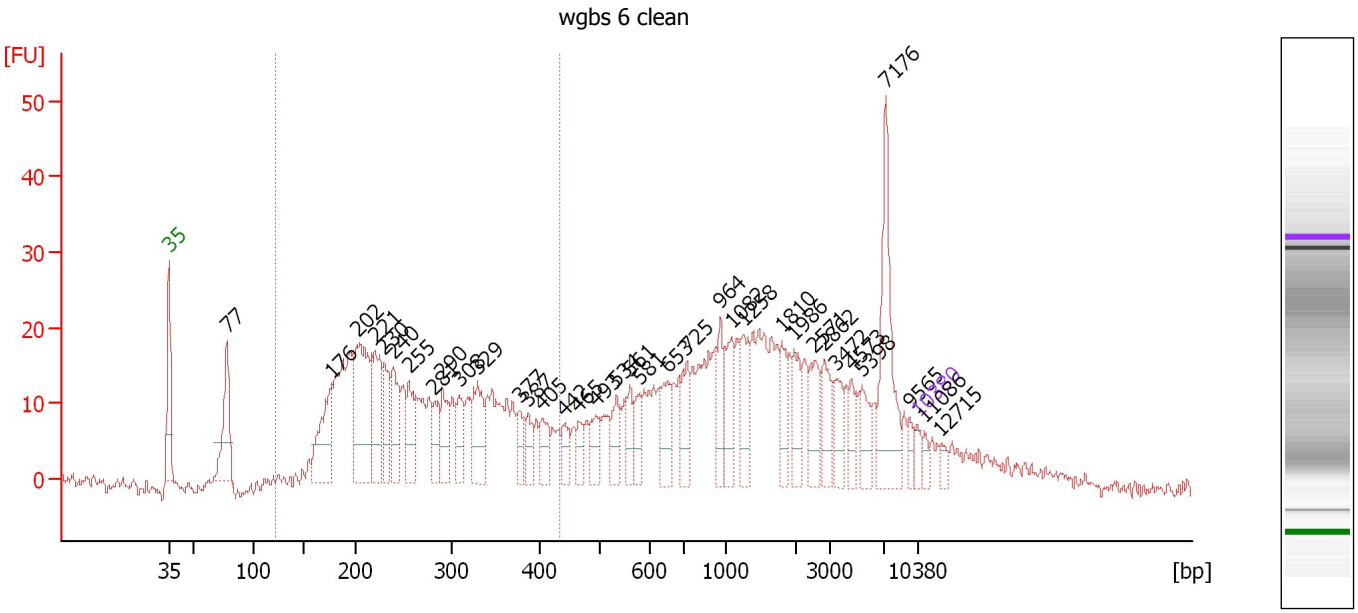
**Region table for sample 3 : wgbs 5 clean**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 145 | 468 | 275 | 622.9 | 11,851.7 | 2,062.62 | 90 | 18.7 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 4 : wgbs 6 clean**

| | | | |
|---|---|---|---|
| Number of peaks found: | 36 | Corr. Area 1: | 411.4 |
| Noise: | 1.0 | | |

**Peak table for sample 4 : wgbs 6 clean**

| 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 | 77 | 776.41 | 15,212.8 | | 48.39 |
| 3 | 176 | 745.76 | 6,405.6 | | 58.17 |
| 4 | 202 | 1,254.64 | 9,396.2 | | 60.61 |
| 5 | 221 | 667.28 | 4,576.6 | | 62.31 |
| 6 | 230 | 414.09 | 2,725.4 | | 63.16 |
| 7 | 240 | 479.93 | 3,036.0 | | 64.00 |
| 8 | 255 | 377.91 | 2,242.1 | | 65.45 |
| 9 | 281 | 238.78 | 1,287.1 | | 67.80 |
| 10 | 290 | 319.65 | 1,670.9 | | 68.60 |
| 11 | 308 | 284.49 | 1,400.9 | | 70.14 |
| 12 | 329 | 462.63 | 2,132.7 | | 71.84 |
| 13 | 377 | 166.87 | 669.9 | | 75.78 |
| 14 | 387 | 161.79 | 633.0 | | 76.58 |
| 15 | 405 | 220.40 | 825.1 | | 77.88 |
| 16 | 442 | 153.58 | 526.2 | | 80.02 |
| 17 | 465 | 130.19 | 424.3 | | 81.32 |
| 18 | 493 | 204.95 | 630.1 | | 82.91 |
| 19 | 534 | 229.61 | 652.1 | | 84.86 |
| 20 | 561 | 172.33 | 465.7 | | 86.11 |
| 21 | 581 | 177.14 | 461.6 | | 87.06 |
| 22 | 653 | 269.93 | 626.5 | | 89.60 |
| 23 | 725 | 284.63 | 594.5 | | 91.45 |
| 24 | 964 | 248.95 | 391.1 | | 94.59 |
| 25 | 1,082 | 315.55 | 442.0 | | 95.59 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**

**... Peak table for sample 4 : wgbs 6 clean**

| Peak | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|
| 26 | 1,258 | 331.15 | 398.9 | | 96.73 |
| 27 | 1,810 | 209.65 | 175.5 | | 100.33 |
| 28 | 1,986 | 228.73 | 174.5 | | 101.47 |
| 29 | 2,571 | 269.01 | 158.5 | | 103.42 |
| 30 | 2,862 | 223.16 | 118.1 | | 104.37 |
| 31 | 3,472 | 189.97 | 82.9 | | 105.42 |
| 32 | 4,573 | 144.03 | 47.7 | | 106.81 |
| 33 | 5,398 | 198.29 | 55.7 | | 107.86 |
| 34 | 7,176 | 759.80 | 160.4 | | 110.06 |
| 35 | 9,565 | 80.08 | 12.7 | | 112.25 |
| 36 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |
| 37 | 11,086 | 0.00 | 0.0 | | 113.65 |
| 38 | 12,715 | 0.00 | 0.0 | | 115.15 |

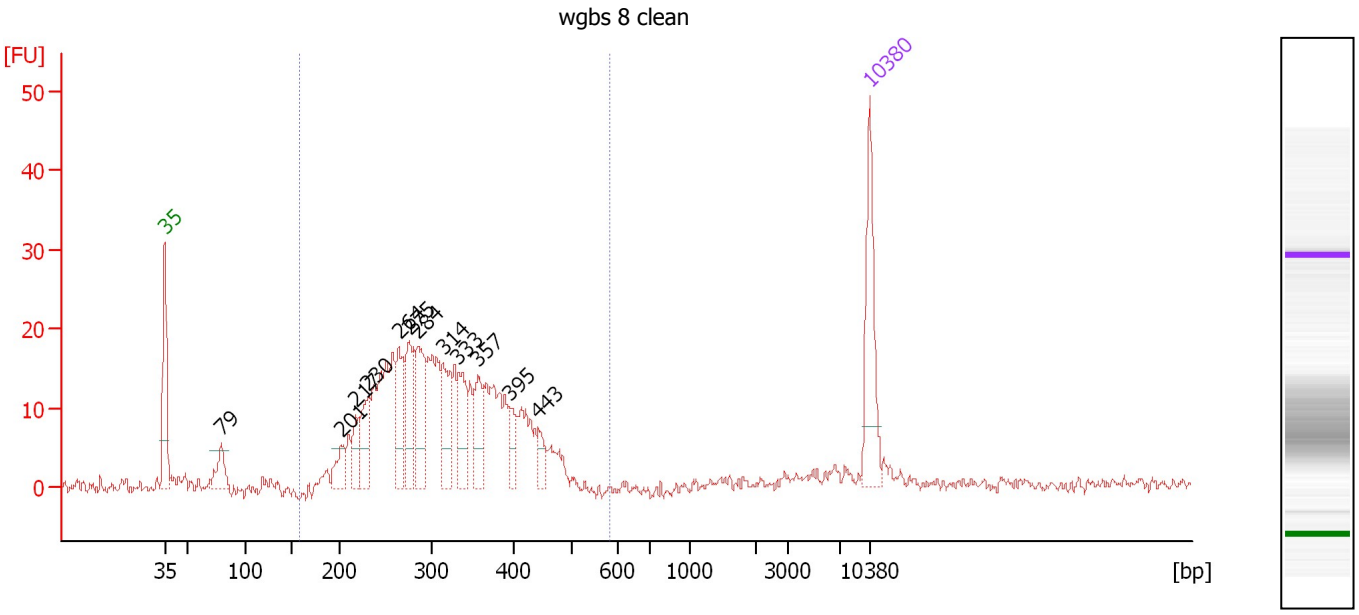
**Region table for sample 4 : wgbs 6 clean**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 121 | 435 | 273 | 411.4 | 60,116.9 | 9,769.64 | 42 | 26.9 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 5 : wgbs 8 clean**

| | | | |
|---|---|---|---|
| Number of peaks found: | 12 | Corr. Area 1: | 360.6 |
| Noise: | 0.9 | | |

**Peak table for sample 5 : wgbs 8 clean**

| 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 | 79 | 41.88 | 800.4 | | 48.61 |
| 3 | 201 | 31.58 | 238.5 | | 60.46 |
| 4 | 217 | 30.60 | 213.8 | | 61.94 |
| 5 | 230 | 55.09 | 363.5 | | 63.11 |
| 6 | 264 | 55.52 | 318.8 | | 66.23 |
| 7 | 275 | 69.81 | 384.8 | | 67.23 |
| 8 | 284 | 79.08 | 422.5 | | 68.03 |
| 9 | 314 | 56.93 | 275.1 | | 70.62 |
| 10 | 333 | 53.88 | 245.5 | | 72.15 |
| 11 | 357 | 51.01 | 216.6 | | 74.11 |
| 12 | 395 | 25.82 | 99.1 | | 77.18 |
| 13 | 443 | 15.93 | 54.4 | | 80.09 |
| 14 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

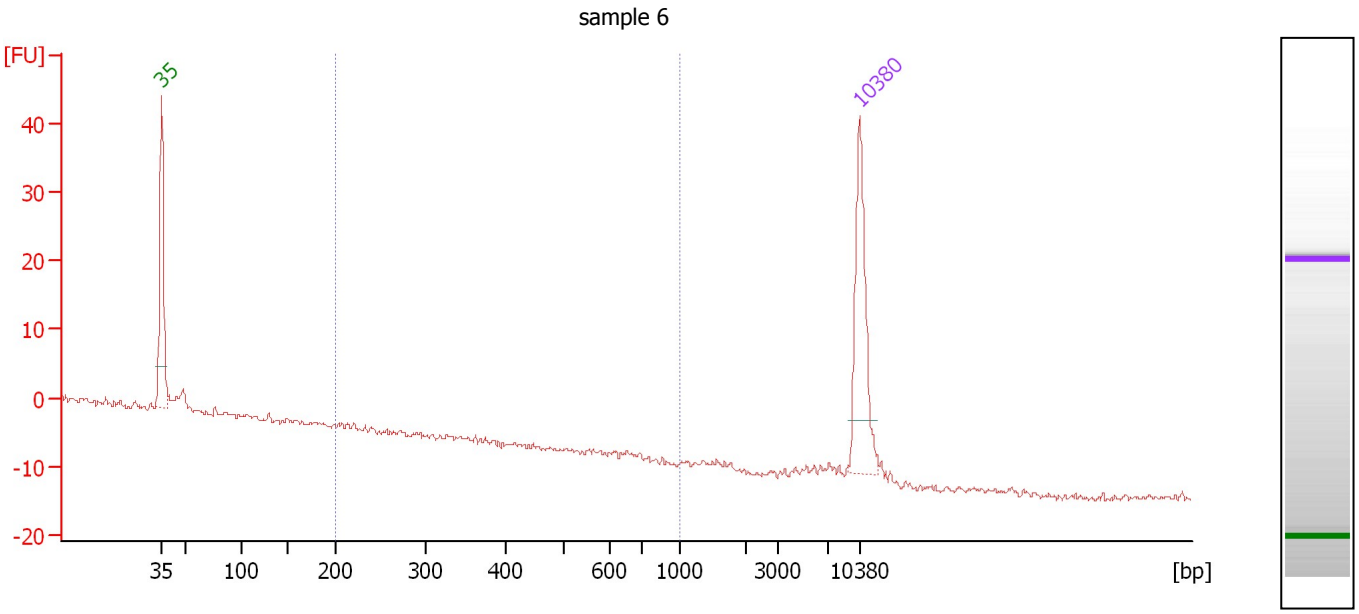
**Region table for sample 5 : wgbs 8 clean**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 156 | 584 | 315 | 360.6 | 5,674.7 | 1,108.33 | 93 | 21.7 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Electropherogram Summary Continued ...**




**Overall Results for sample 6 : sample 6**

| | | | |
|---|---|---|---|
| Number of peaks found: | 0 | Corr. Area 1: | 0.0 |
| Noise: | 0.4 | | |

**Peak table for sample 6 : sample 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 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

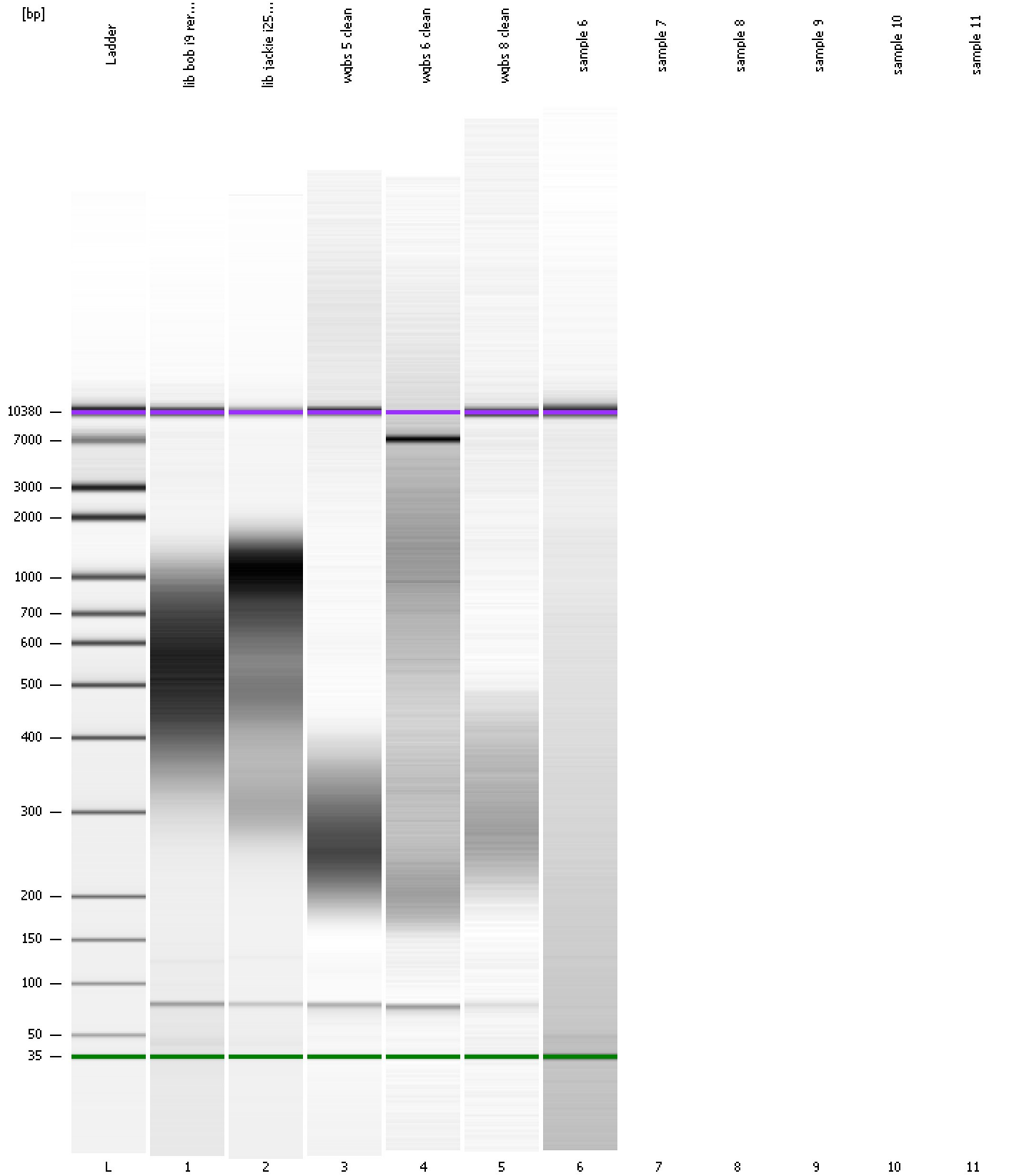
**Region table for sample 6 : sample 6**

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 200 | 1,000 | 220 | 0.0 | 0.0 | 0.01 | 0 | 1.1 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

**Gel Image**



Assay Class: High Sensitivity DNA Assay Created: 2/25/2016 3:00:57 PM
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad Modified: 2/25/2016 3:27:58 PM

**Invalid Samples**

Sample 7 has not been run, no results available.

Sample 8 has not been run, no results available.

Sample 9 has not been run, no results available.

Sample 10 has not been run, no results available.

Sample 11 has not been run, no results available.

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...ents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad

Created: 2/25/2016 3:00:57 PM
Modified: 2/25/2016 3:27:58 PM

## Run Logbook

| Description | Number | Source | Category | Sub Category | Time | Time Zone | User | Host |
|---|---|---|---|---|---|---|---|---|
| Run ended on port 1 (Number of wells acquired: 7) | | Instrument | Run | | 2/25/2016 3:27:57 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Run started on port 1 (File: C:\Documents and Settings\Bioanalyzer\2016-02-25\2016-02-25_002.xad) | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Product Number : G2938B | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Name : | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Vendor : Agilent Technologies | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Serial# : DE13701086 | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Firmware : C.01.069 | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Cartridge : Electrode | | Instrument | Run | | 2/25/2016 3:01:03 PM | (GMT --08:00) Pacific Standard Time | UC Davis | D8XSMGH1 |