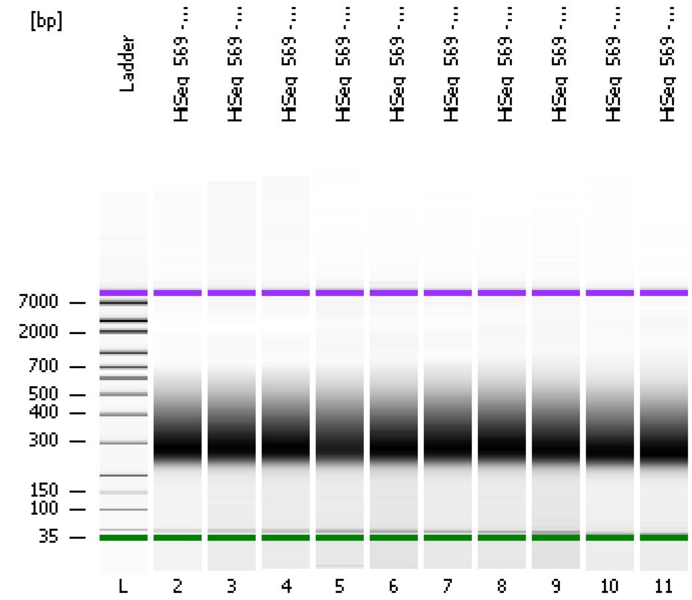
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad
Created: 8/25/2016 11:49:16 AM
Modified: 8/25/2016 4:25:37 PM

## 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

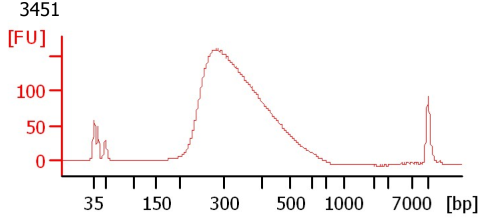
Chip Information:

Chip Lot #:

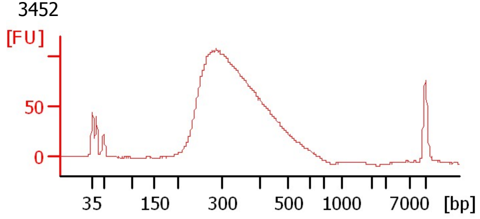
Reagent Kit Lot #:

Chip Comments:

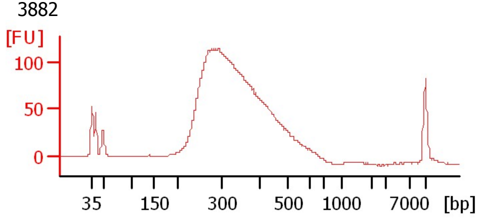
**HiSeq_569 - 1 Library**



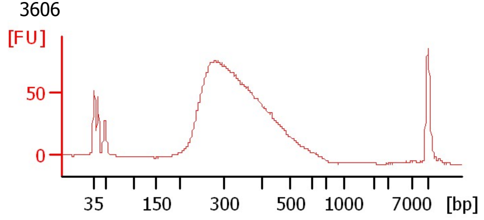
**HiSeq_569 - 2 Library**



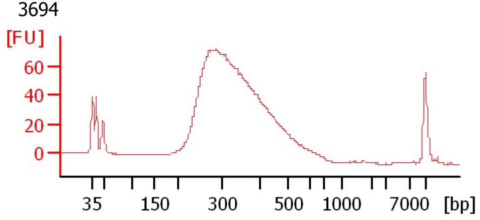
**HiSeq_569 - 3 Library**



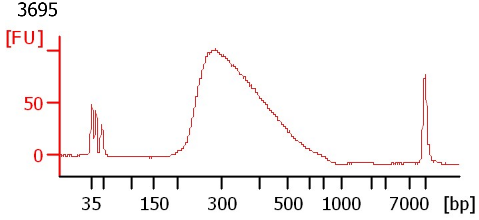
**HiSeq_569 - 4 Library**



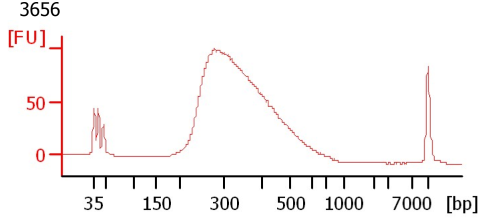
**HiSeq_569 - 5 Library**



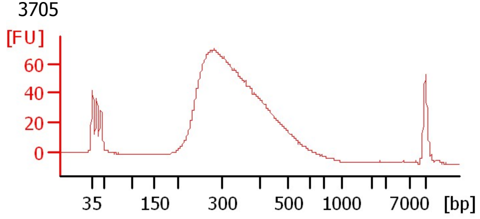
**HiSeq_569 - 6 Library**



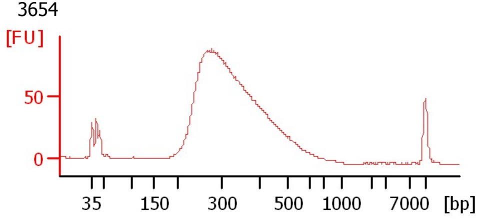
**HiSeq_569 - 7 Library**



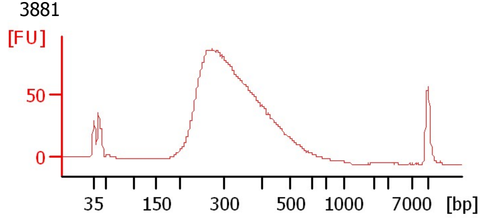
**HiSeq_569 - 8 Library**



**HiSeq_569 - 9 Library**



**HiSeq_569 - 10 Library**



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad
Created: 8/25/2016 11:49:16 AM
Modified: 8/25/2016 4:25:37 PM

## Electrophoresis File Run Summary (Chip Summary)

| **Sample Name** | **Sample Comment** | **Rest. Digest** | **Status** | **Observation** | **Result Label** | **Result Color** |
|---|---|---|---|---|---|---|
| HiSeq_569 - 1 Library | 3451 | ☐ | ✓ | | | |
| HiSeq_569 - 2 Library | 3452 | ☐ | ✓ | | | |
| HiSeq_569 - 3 Library | 3882 | ☐ | ✓ | | | |
| HiSeq_569 - 4 Library | 3606 | ☐ | ✓ | | | |
| HiSeq_569 - 5 Library | 3694 | ☐ | ✓ | | | |
| HiSeq_569 - 6 Library | 3695 | ☐ | ✓ | | | |
| HiSeq_569 - 7 Library | 3656 | ☐ | ✓ | | | |
| HiSeq_569 - 8 Library | 3705 | ☐ | ✓ | | | |
| HiSeq_569 - 9 Library | 3654 | ☐ | ✓ | | | |
| HiSeq_569 - 10 Library | 3881 | ☐ | ✓ | | | |
| 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

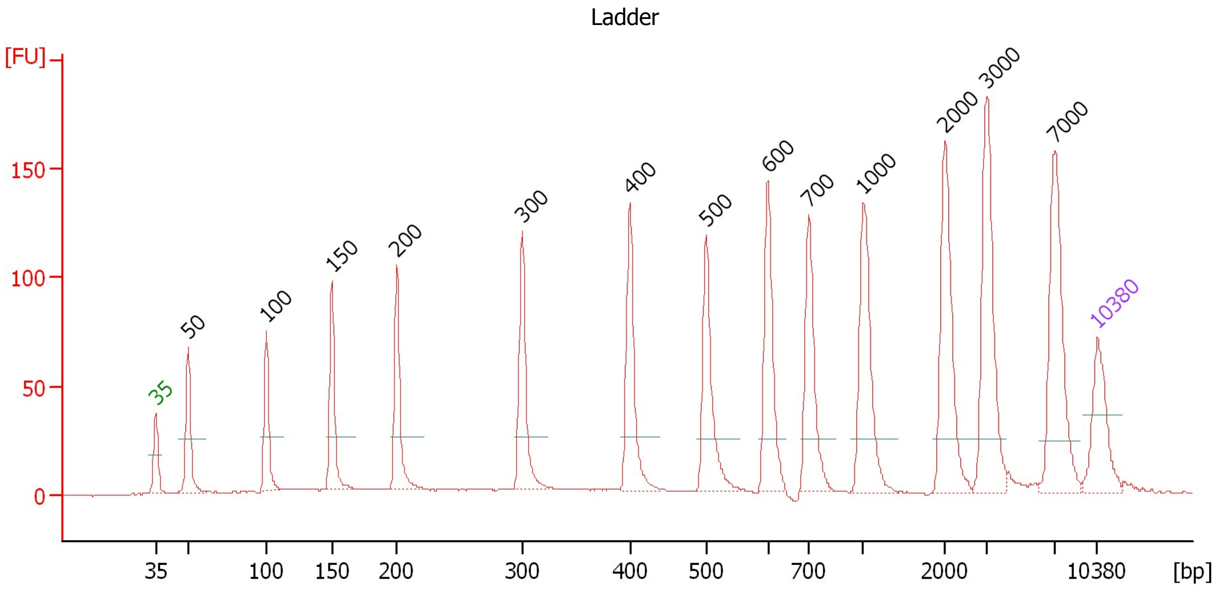
### Filter Settings

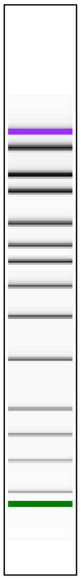
Filter Width [s] : 0.5
Polynomial Order : 4

### 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 |

## Electropherogram Summary





## Overall Results for Ladder

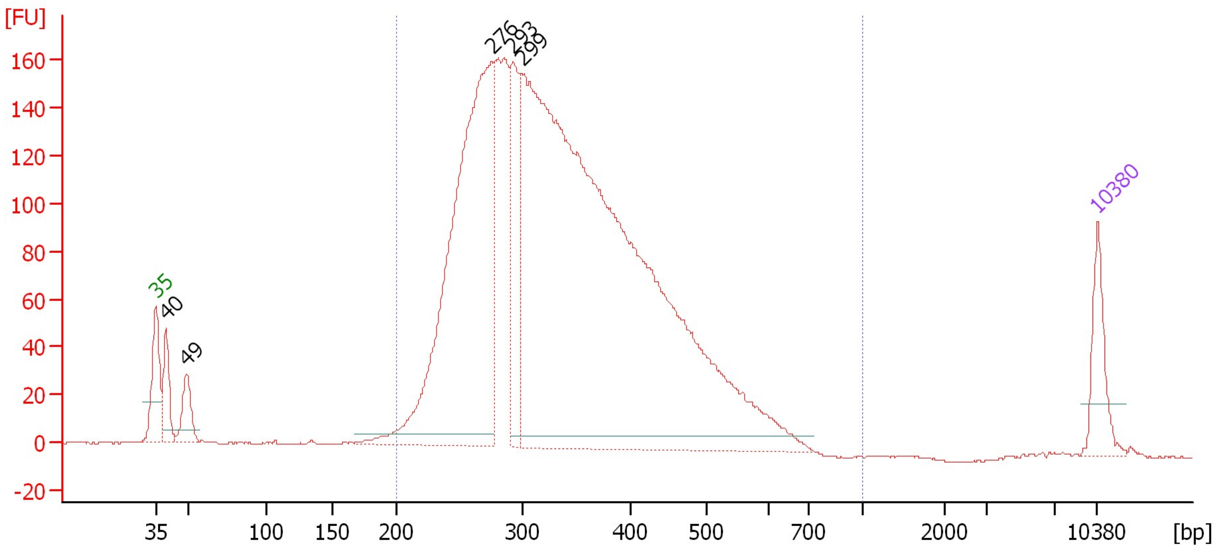
Noise: 0.3

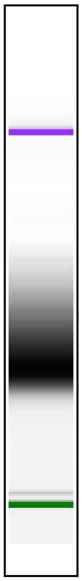
## Peak table for Ladder

| 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 | L | 50 | 150.00 | 4,545.5 | Ladder Peak | 45.45 |
| 3 | L | 100 | 150.00 | 2,272.7 | Ladder Peak | 51.23 |
| 4 | L | 150 | 150.00 | 1,515.2 | Ladder Peak | 56.09 |
| 5 | L | 200 | 150.00 | 1,136.4 | Ladder Peak | 60.95 |
| 6 | L | 300 | 150.00 | 757.6 | Ladder Peak | 70.25 |
| 7 | L | 400 | 150.00 | 568.2 | Ladder Peak | 78.23 |
| 8 | L | 500 | 150.00 | 454.5 | Ladder Peak | 83.91 |
| 9 | L | 600 | 150.00 | 378.8 | Ladder Peak | 88.51 |
| 10 | L | 700 | 150.00 | 324.7 | Ladder Peak | 91.52 |
| 11 | L | 1,000 | 150.00 | 227.3 | Ladder Peak | 95.62 |
| 12 | L | 2,000 | 150.00 | 113.6 | Ladder Peak | 101.65 |
| 13 | L | 3,000 | 150.00 | 75.8 | Ladder Peak | 104.77 |
| 14 | L | 7,000 | 150.00 | 32.5 | Ladder Peak | 109.83 |
| 15 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

## Electropherogram Summary Continued ...

HiSeq_569 - 1 Library [ 3451 ]





**Overall Results for sample 2 :** **HiSeq_569 - 1 Library**

| | | | |
|---|---|---|---|
| Number of peaks found: | 5 | Corr. Area 1: | 3,324.9 |
| Noise: | 0.3 | | |

**Peak table for sample 2 :** **HiSeq_569 - 1 Library**

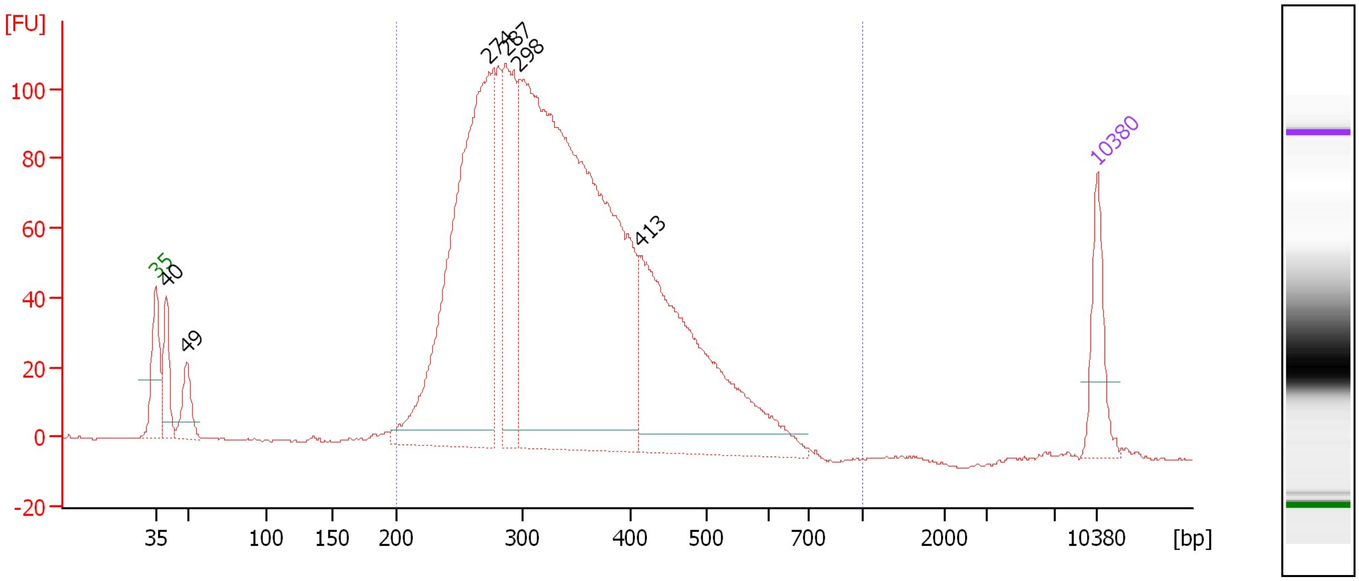
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 97.17 | 3,677.2 | | 43.82 |
| 3 | | 49 | 83.84 | 2,583.7 | | 45.32 |
| 4 | | 276 | 1,195.50 | 6,572.7 | | 67.98 |
| 5 | | 293 | 240.67 | 1,245.6 | | 69.58 |
| 6 | | 299 | 2,881.48 | 14,582.7 | | 70.20 |
| 7 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

**Region table for sample 2 :** **HiSeq_569 - 1 Library**

| 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 | 342 | 3,324.9 | 20,520.2 | ■ | 4,305.01 | 96 | 24.7 |

## Electropherogram Summary Continued ...

HiSeq_569 - 2 Library [ 3452 ]



### Overall Results for sample 3 : HiSeq_569 - 2 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 6 | Corr. Area 1: | 2,215.6 |
| Noise: | 0.3 | | |

### Peak table for sample 3 : HiSeq_569 - 2 Library

| 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 | | 40 | 102.89 | 3,889.2 | | 43.83 |
| 3 | | 49 | 82.28 | 2,528.6 | | 45.34 |
| 4 | | 274 | 934.64 | 5,173.8 | | 67.81 |
| 5 | | 287 | 305.97 | 1,614.6 | | 69.05 |
| 6 | | 298 | 1,709.72 | 8,700.5 | | 70.04 |
| 7 | | 413 | 579.81 | 2,125.3 | | 78.99 |
| 8 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

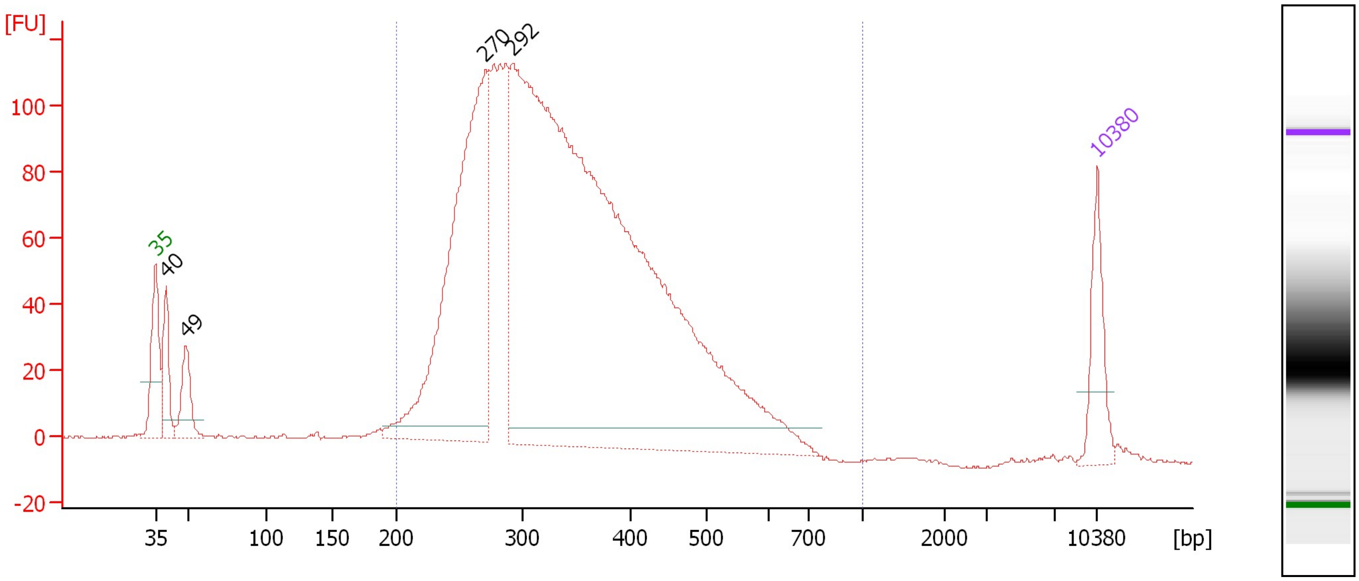
### Region table for sample 3 : HiSeq_569 - 2 Library

| 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 | 342 | 2,215.6 | 16,300.5 | 🟦 | 3,424.12 | 95 | 24.4 |

| | | | |
|---|---|---|---|
| Assay Class: | High Sensitivity DNA Assay | Created: | 8/25/2016 11:49:16 AM |
| Data Path: | C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad | Modified: | 8/25/2016 4:25:37 PM |

## Electropherogram Summary Continued ...

HiSeq_569 - 3 Library [ 3882 ]



### Overall Results for sample 4 : HiSeq_569 - 3 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 4 | Corr. Area 1: | 2,356.4 |
| Noise: | 0.3 | | |

### Peak table for sample 4 : HiSeq_569 - 3 Library

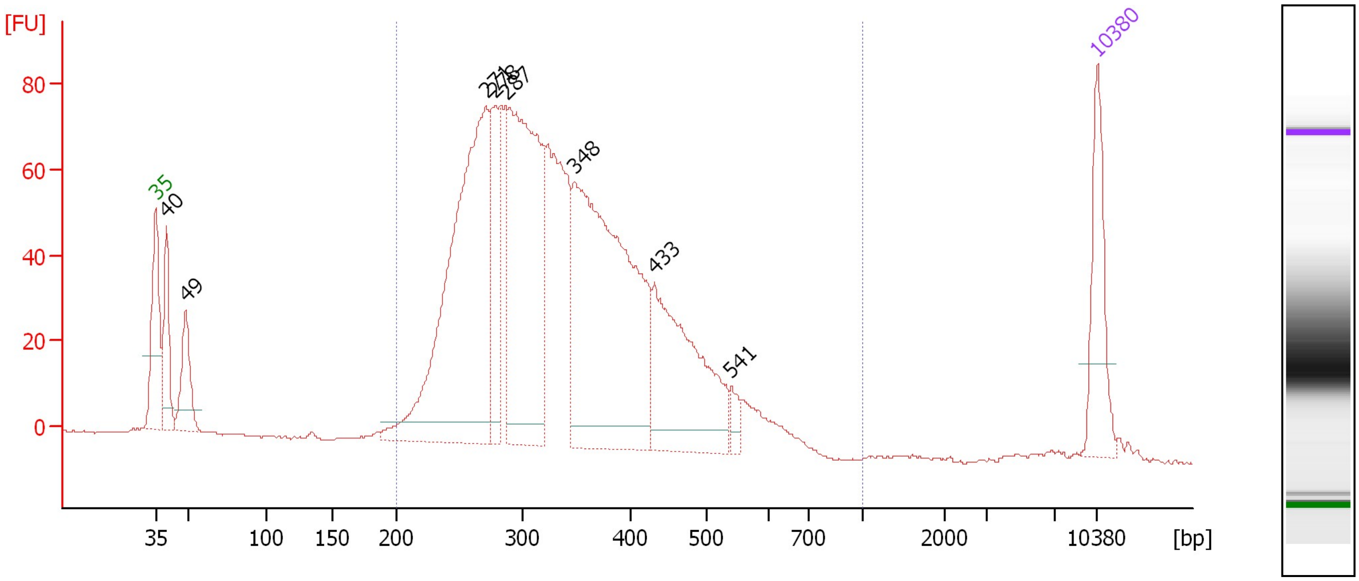
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 101.55 | 3,862.2 | | 43.79 |
| 3 | | 49 | 93.78 | 2,907.5 | | 45.27 |
| 4 | | 270 | 822.74 | 4,610.9 | | 67.49 |
| 5 | | 292 | 2,605.16 | 13,495.7 | | 69.55 |
| 6 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

### Region table for sample 4 : HiSeq_569 - 3 Library

| 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 | 344 | 2,356.4 | 16,043.8 | 🟦 | 3,381.19 | 95 | 24.8 |

## Electropherogram Summary Continued ...

HiSeq_569 - 4 Library [ 3606 ]



### Overall Results for sample 5 : HiSeq_569 - 4 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 8 | Corr. Area 1: | 1,526.1 |
| Noise: | 0.2 | | |

### Peak table for sample 5 : HiSeq_569 - 4 Library

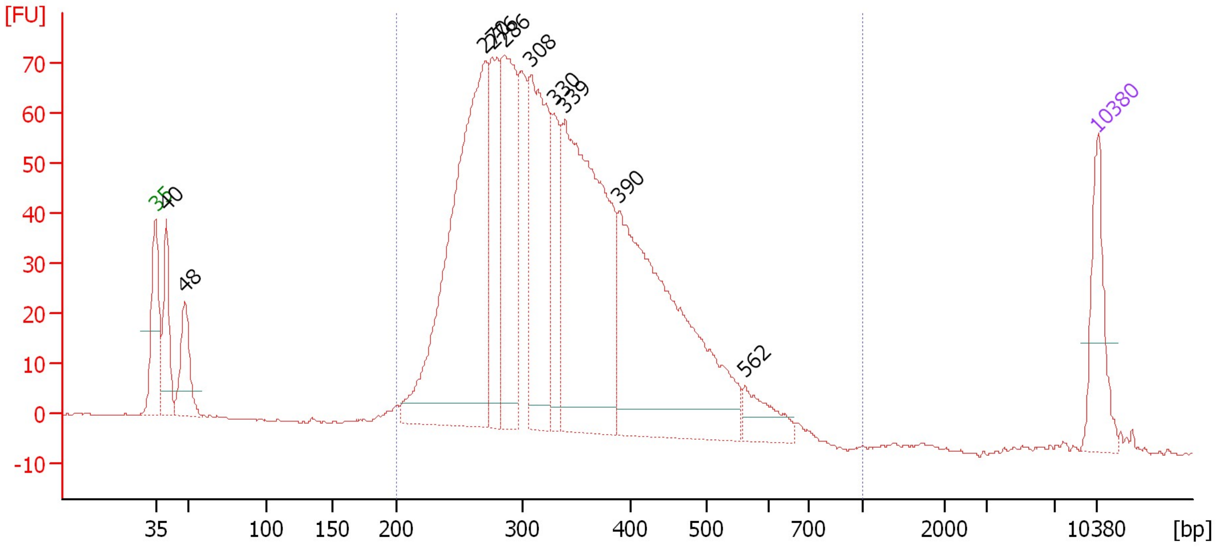
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 99.34 | 3,773.2 | | 43.80 |
| 3 | | 49 | 86.05 | 2,677.3 | | 45.24 |
| 4 | | 271 | 568.39 | 3,179.4 | | 67.54 |
| 5 | | 278 | 123.81 | 674.0 | | 68.24 |
| 6 | | 287 | 436.18 | 2,298.7 | | 69.09 |
| 7 | | 348 | 534.14 | 2,323.7 | | 74.11 |
| 8 | | 433 | 233.79 | 818.8 | | 80.08 |
| 9 | | 541 | 16.80 | 47.1 | | 85.79 |
| 10 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

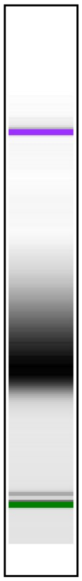
### Region table for sample 5 : HiSeq_569 - 4 Library

| 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 | 341 | 1,526.1 | 9,902.5 | ■ 2,076.89 | 94 | 23.7 |

**Electropherogram Summary Continued ...**

HiSeq_569 - 5 Library [ 3694 ]





## Overall Results for sample 6 : HiSeq_569 - 5 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 10 | Corr. Area 1: | 1,491.5 |
| Noise: | 0.2 | | |

## Peak table for sample 6 : HiSeq_569 - 5 Library

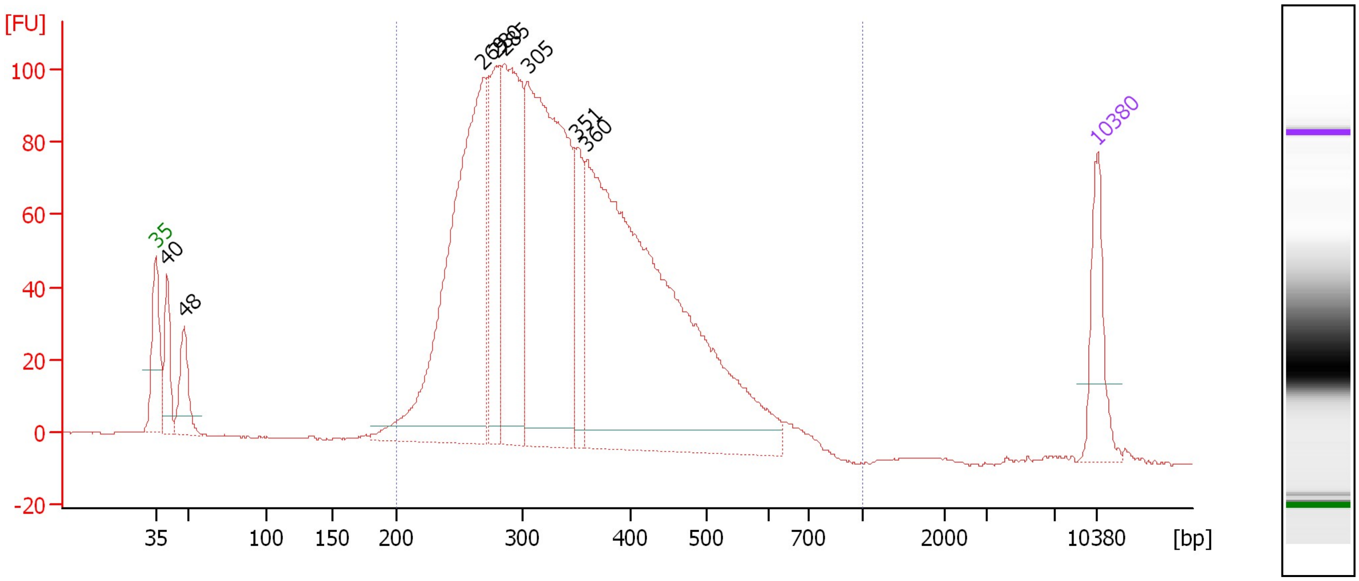
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 120.16 | 4,558.4 | | 43.81 |
| 3 | | 48 | 101.98 | 3,207.5 | | 45.16 |
| 4 | | 270 | 683.15 | 3,833.1 | | 67.46 |
| 5 | | 276 | 173.62 | 951.7 | | 68.06 |
| 6 | | 286 | 281.09 | 1,490.8 | | 68.92 |
| 7 | | 308 | 312.75 | 1,540.5 | | 70.86 |
| 8 | | 330 | 112.44 | 516.4 | | 72.64 |
| 9 | | 339 | 555.23 | 2,479.0 | | 73.39 |
| 10 | | 390 | 548.71 | 2,131.6 | | 77.43 |
| 11 | | 562 | 53.76 | 144.9 | | 86.76 |
| 12 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

## Region table for sample 6 : HiSeq_569 - 5 Library

| 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 | 342 | 1,491.5 | 13,372.5 | 🟦 | 2,801.44 | 94 | 24.6 |

**Electropherogram Summary Continued ...**

HiSeq_569 - 6 Library [ 3695 ]



### Overall Results for sample 7 : HiSeq_569 - 6 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 8 | Corr. Area 1: | 2,173.2 |
| Noise: | 0.2 | | |

### Peak table for sample 7 : HiSeq_569 - 6 Library

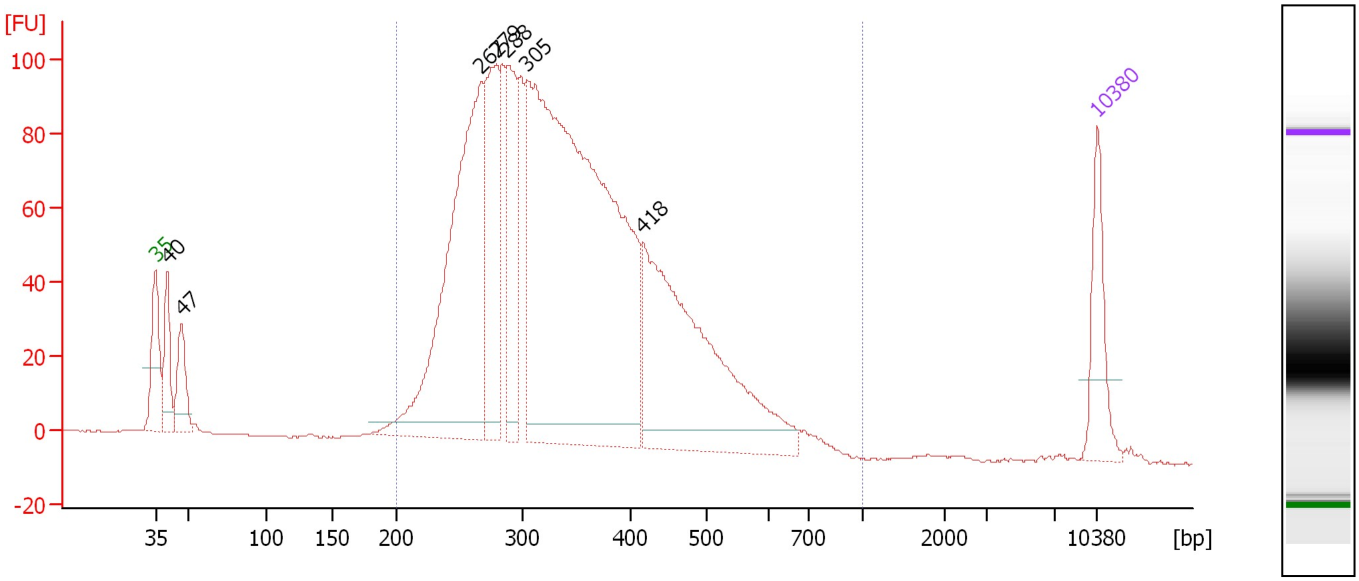
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 94.59 | 3,554.1 | | 43.87 |
| 3 | | 48 | 94.03 | 2,969.2 | | 45.12 |
| 4 | | 269 | 723.27 | 4,076.8 | | 67.35 |
| 5 | | 280 | 209.47 | 1,133.8 | | 68.39 |
| 6 | | 285 | 376.44 | 1,999.9 | | 68.88 |
| 7 | | 305 | 713.37 | 3,540.8 | | 70.67 |
| 8 | | 351 | 107.00 | 461.9 | | 74.32 |
| 9 | | 360 | 1,102.26 | 4,640.5 | | 75.03 |
| 10 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

### Region table for sample 7 : HiSeq_569 - 6 Library

| 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 | 348 | 2,173.2 | 14,658.0 | 🟦 | 3,105.91 | 95 | 25.8 |

**Electropherogram Summary Continued ...**

HiSeq_569 - 7 Library [ 3656 ]



**Overall Results for sample 8 :** **HiSeq_569 - 7 Library**

| | | | |
|---|---|---|---|
| Number of peaks found: | 7 | Corr. Area 1: | 2,122.3 |
| Noise: | 0.2 | | |

**Peak table for sample 8 :** **HiSeq_569 - 7 Library**

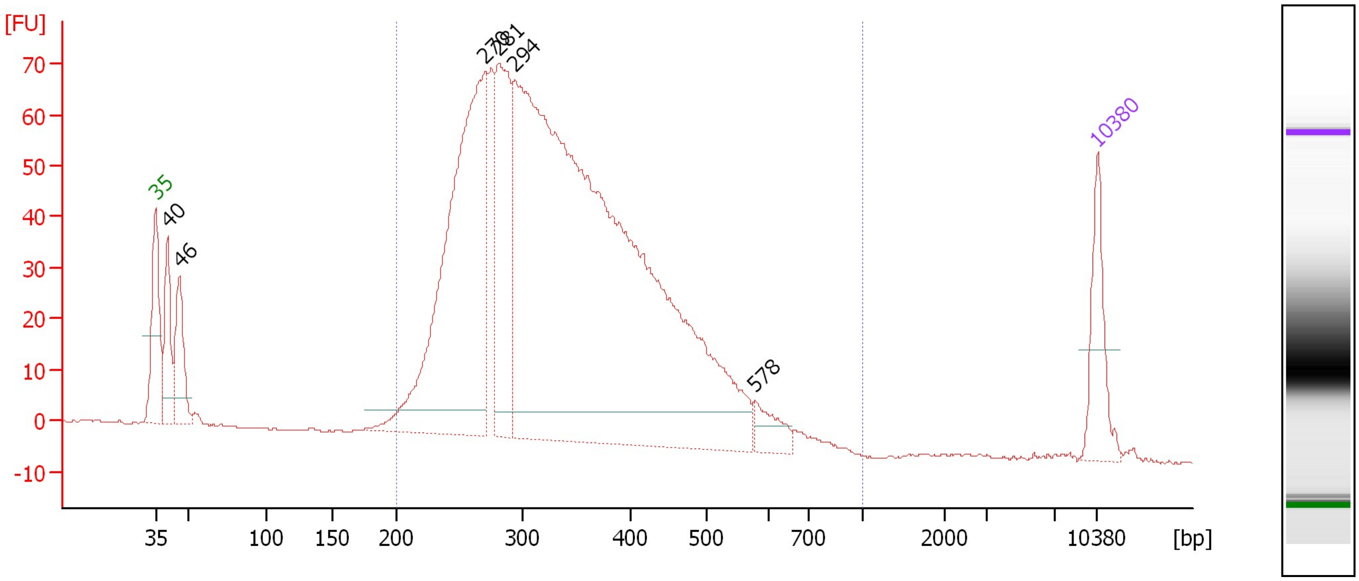
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 40 | 95.19 | 3,570.5 | | 43.88 |
| 3 | | 47 | 89.76 | 2,906.1 | | 44.93 |
| 4 | | 267 | 650.34 | 3,685.5 | | 67.22 |
| 5 | | 279 | 239.82 | 1,304.1 | | 68.26 |
| 6 | | 288 | 187.92 | 990.3 | | 69.09 |
| 7 | | 305 | 1,351.51 | 6,718.4 | | 70.64 |
| 8 | | 418 | 507.73 | 1,841.2 | | 79.24 |
| 9 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

**Region table for sample 8 :** **HiSeq_569 - 7 Library**

| 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 | 348 | 2,122.3 | 14,210.3 | 🟦 | 3,010.90 | 95 | 26.0 |

## Electropherogram Summary Continued ...

HiSeq_569 - 8 Library [ 3705 ]



**Overall Results for sample 9 :** **HiSeq_569 - 8 Library**

| | | | |
|---|---|---|---|
| Number of peaks found: | 6 | Corr. Area 1: | 1,450.7 |
| Noise: | 0.2 | | |

**Peak table for sample 9 :** **HiSeq_569 - 8 Library**

| 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 | | 40 | 125.79 | 4,713.9 | | 43.89 |
| 3 | | 46 | 126.48 | 4,178.4 | | 44.78 |
| 4 | | 270 | 778.76 | 4,363.5 | | 67.50 |
| 5 | | 281 | 289.66 | 1,561.0 | | 68.50 |
| 6 | | 294 | 2,151.15 | 11,075.2 | | 69.72 |
| 7 | | 578 | 40.36 | 105.8 | | 87.50 |
| 8 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

**Region table for sample 9 :** **HiSeq_569 - 8 Library**

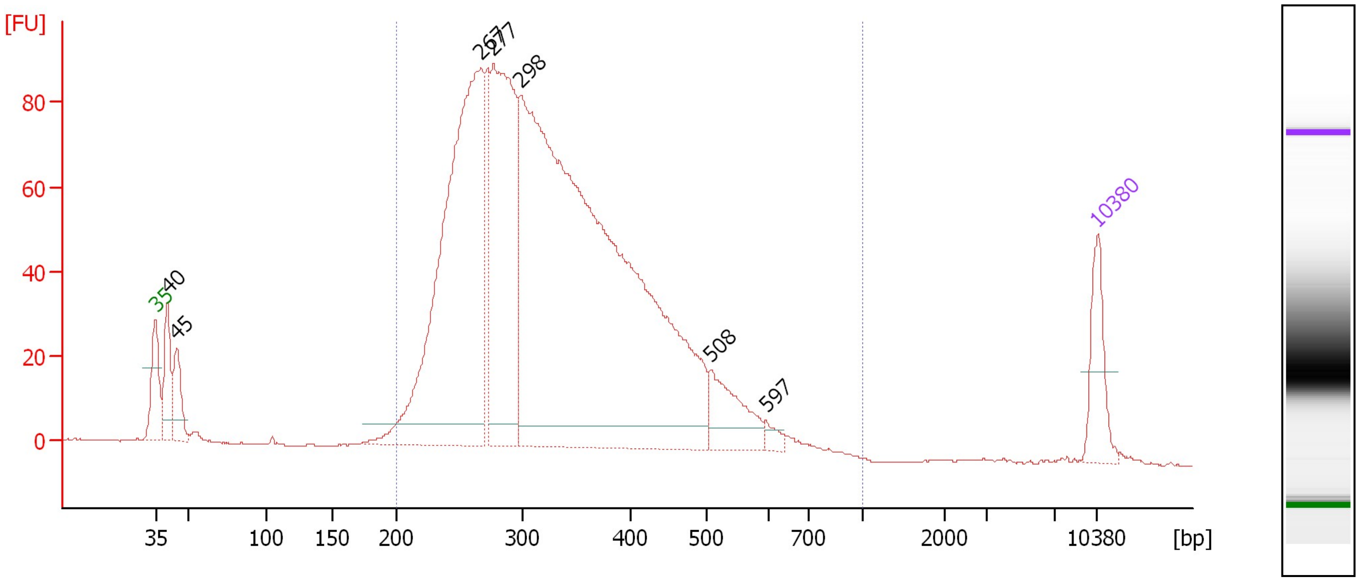
| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 1,000 | 341 | 1,450.7 | 14,560.3 | 🟦 | 3,035.45 | 94 | 25.2 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad

Created: 8/25/2016 11:49:16 AM
Modified: 8/25/2016 4:25:37 PM

## Electropherogram Summary Continued ...

HiSeq_569 - 9 Library [ 3654 ]



### Overall Results for sample 10 : HiSeq_569 - 9 Library

| | | | |
|---|---|---|---|
| Number of peaks found: | 7 | Corr. Area 1: | 1,767.2 |
| Noise: | 0.2 | | |

### Peak table for sample 10 : HiSeq_569 - 9 Library

| 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 | | 40 | 117.24 | 4,388.5 | | 43.90 |
| 3 | | 45 | 89.51 | 3,042.0 | | 44.57 |
| 4 | | 267 | 1,045.06 | 5,941.5 | | 67.14 |
| 5 | | 277 | 606.60 | 3,321.3 | | 68.09 |
| 6 | | 298 | 2,168.05 | 11,008.7 | | 70.10 |
| 7 | | 508 | 116.50 | 347.5 | | 84.27 |
| 8 | | 597 | 15.43 | 39.2 | | 88.36 |
| 9 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

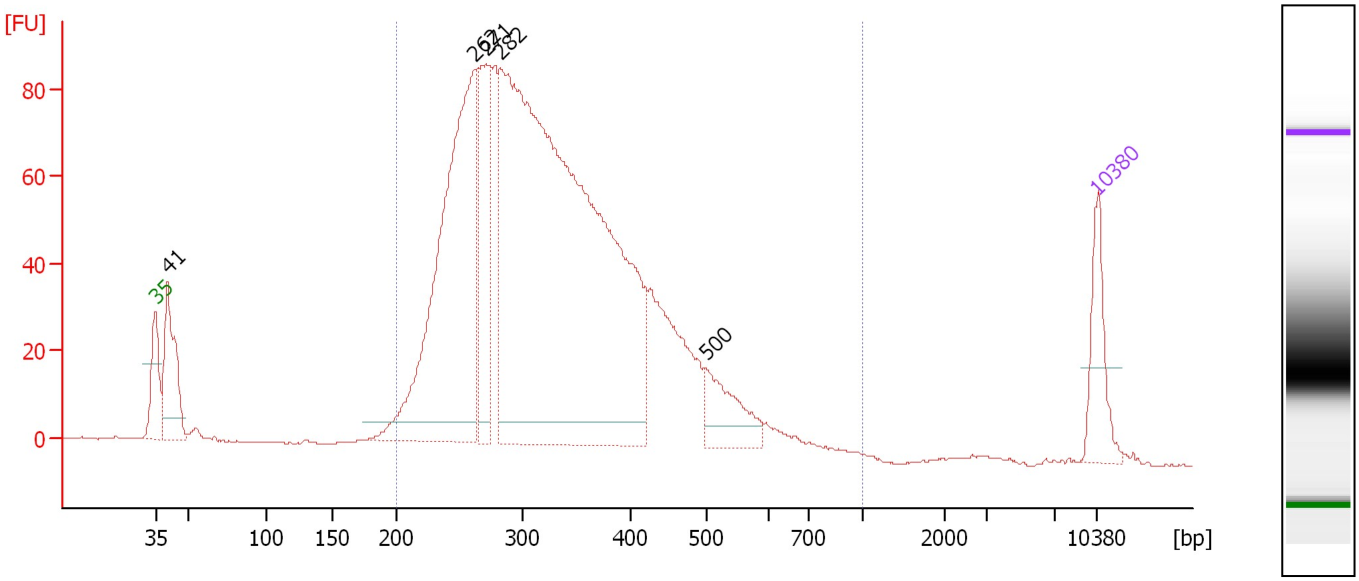
### Region table for sample 10 : HiSeq_569 - 9 Library

| 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 | 1,767.2 | 18,745.5 | 🟦 | 3,840.76 | 95 | 25.8 |

| | | | |
|---|---|---|---|
| Assay Class: | High Sensitivity DNA Assay | Created: | 8/25/2016 11:49:16 AM |
| Data Path: | C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad | Modified: | 8/25/2016 4:25:37 PM |

**Electropherogram Summary Continued ...**

HiSeq_569 - 10 Library [ 3881 ]



**Overall Results for sample 11 :** **HiSeq_569 - 10 Library**

| | | | |
|---|---|---|---|
| Number of peaks found: | 5 | Corr. Area 1: | 1,723.9 |
| Noise: | 0.1 | | |

**Peak table for sample 11 :** **HiSeq_569 - 10 Library**

| 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 | | 41 | 197.67 | 7,389.6 | | 43.90 |
| 3 | | 262 | 814.19 | 4,702.5 | | 66.75 |
| 4 | | 271 | 245.11 | 1,368.1 | | 67.60 |
| 5 | | 282 | 1,934.58 | 10,380.2 | | 68.61 |
| 6 | | 500 | 101.63 | 308.2 | | 83.88 |
| 7 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

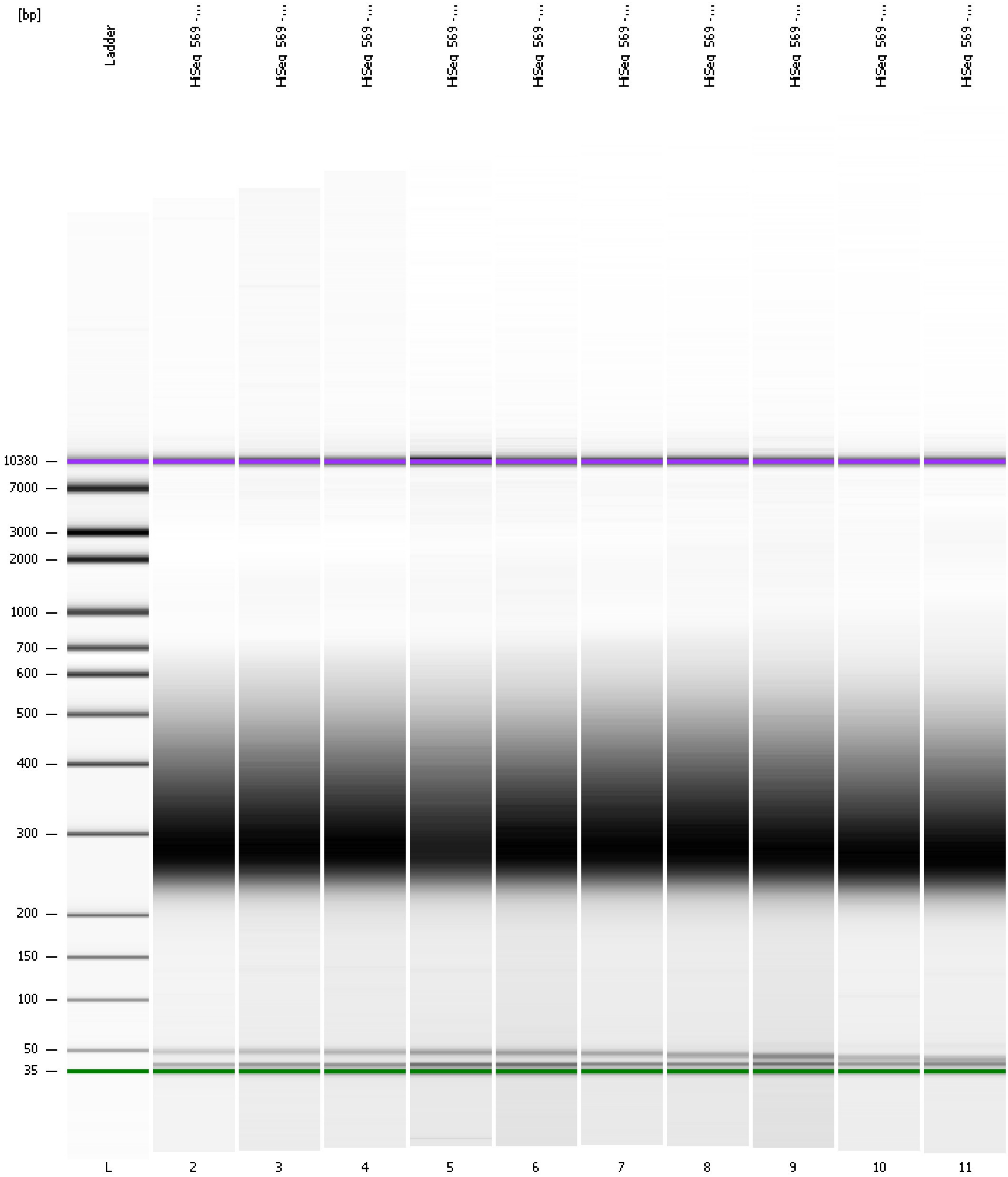
**Region table for sample 11 :** **HiSeq_569 - 10 Library**

| 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 | 335 | 1,723.9 | 16,533.9 | 🟦 | 3,376.36 | 95 | 26.2 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...\data\2016-08-25\2016-08-25_002_HiSeq569_Libraries_1-10.xad

Created: 8/25/2016 11:49:16 AM
Modified: 8/25/2016 4:25:37 PM

**Gel Image**



## 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 | | 8/25/2016 12:29:44 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\2016-08-25\2016-08-25_002.xad) | | Instrument | Run | | 8/25/2016 11:49:22 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Product Number : G2938B | | Instrument | Run | | 8/25/2016 11:49:22 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Name : | | Instrument | Run | | 8/25/2016 11:49:22 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Vendor : Agilent Technologies | | Instrument | Run | | 8/25/2016 11:49:22 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Serial# : DE13701086 | | Instrument | Run | | 8/25/2016 11:49:21 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Firmware : C.01.069 | | Instrument | Run | | 8/25/2016 11:49:21 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |
| Cartridge : Electrode | | Instrument | Run | | 8/25/2016 11:49:21 AM | (GMT --07:00) Pacific Standard Time | UC Davis | D8XSMGH1 |