Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-11-07\2017-11-07_003.xad

Created: 11/7/2017 12:49:41 PM
Modified: 11/7/2017 1:30:59 PM

## Electrophoresis File Run Summary

Instrument Information:

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

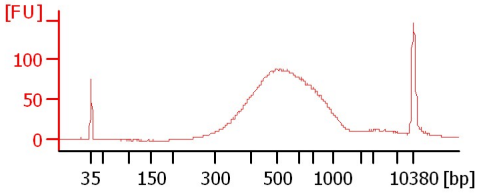
Assay Information:

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

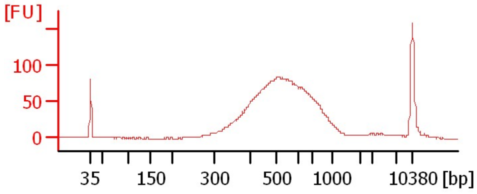
Chip Information:

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

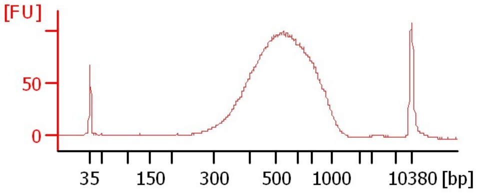
**HiSeq1126 - 3kb MP lib (1:7)**



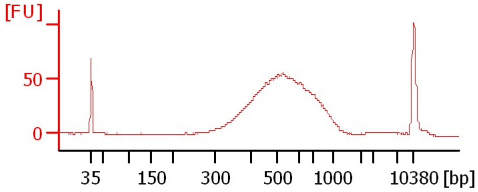
**HiSeq1126 - 6kb MP lib (1:7)**



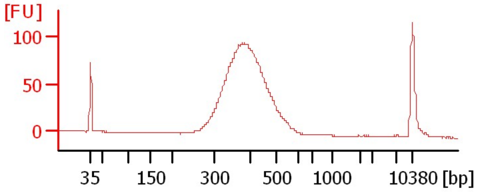
**HiSeq1126 - 8kb MP lib (1:2)**



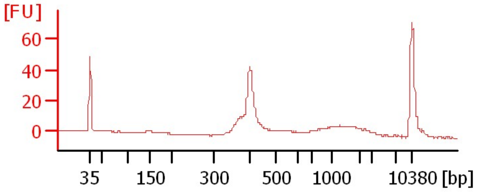
**H1126P (1:4)**



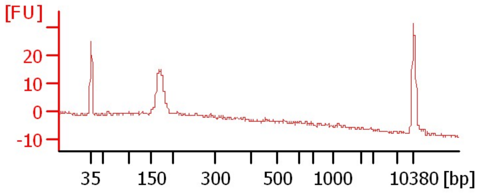
**BMAG053**



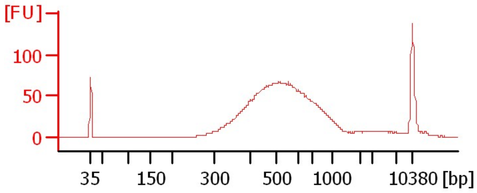
**Igwe sample 1:5**



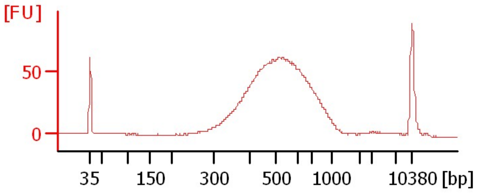
**Bovine smRNA pool**



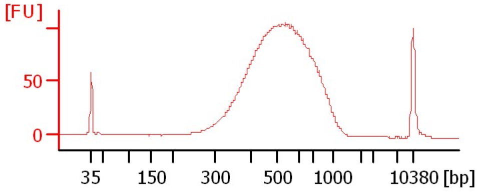
**HiSeq1126 - 3kb MP lib (1:7)**



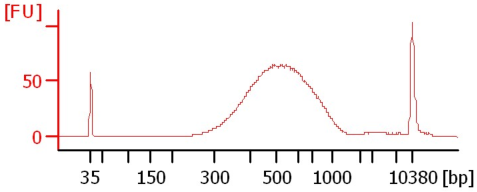
**HiSeq1126 - 6kb MP lib (1:7)**



**HiSeq1126 - 8kb MP lib (1:2)**



**H1126P (1:4)**



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-11-07\2017-11-07_003.xad

Created: 11/7/2017 12:49:41 PM
Modified: 11/7/2017 1:30:59 PM

## Electrophoresis File Run Summary (Chip Summary)

| Sample Name | Sample Comment | Rest. Digest | Status | Observation | Result Label | Result Color |
|---|---|---|---|---|---|---|
| HiSeq1126 - 3kb MP lib (1:7) | | ☐ | ✓ | | | |
| HiSeq1126 - 6kb MP lib (1:7) | | ☐ | ✓ | | | |
| HiSeq1126 - 8kb MP lib (1:2) | | ☐ | ✓ | | | |
| H1126P (1:4) | | ☐ | ✓ | | | |
| BMAG053 | | ☐ | ✓ | | | |
| Igwe sample 1:5 | | ☐ | ✓ | | | |
| Bovine smRNA pool | | ☐ | ✓ | | | |
| HiSeq1126 - 3kb MP lib (1:7) | | ☐ | ✓ | | | |
| HiSeq1126 - 6kb MP lib (1:7) | | ☐ | ✓ | | | |
| HiSeq1126 - 8kb MP lib (1:2) | | ☐ | ✓ | | | |
| H1126P (1:4) | | ☐ | ✓ | | | |
| 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

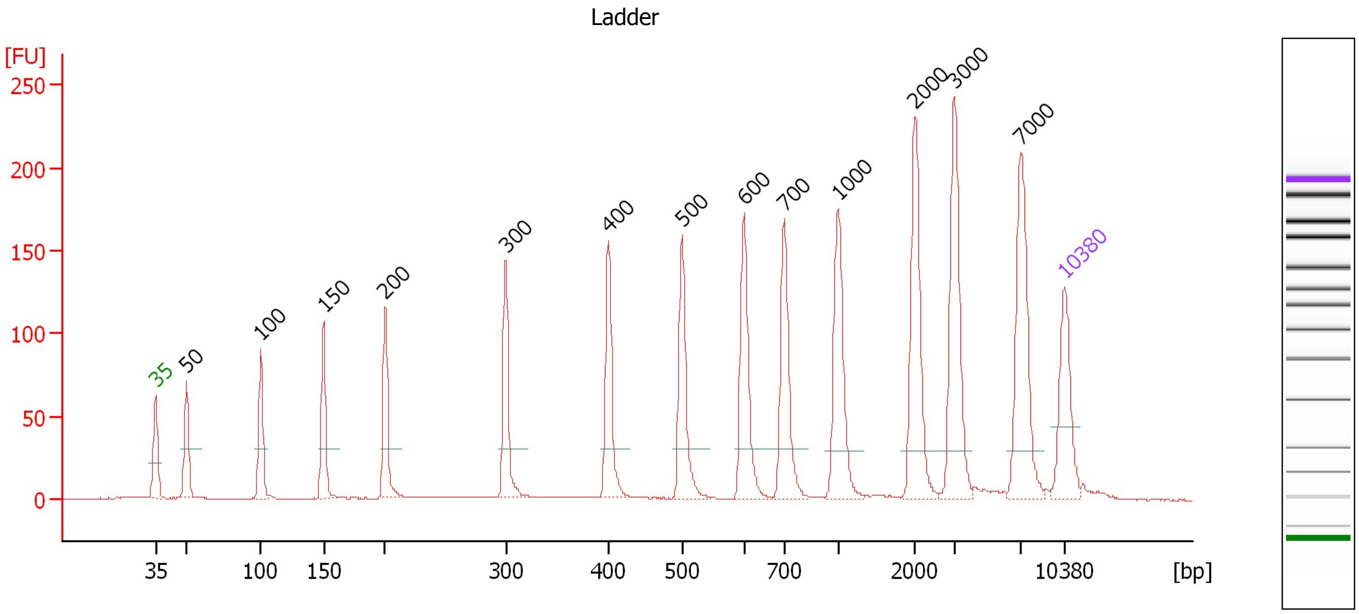
### Ladder

| 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\2017-11-07\2017-11-07_003.xad

Created: 11/7/2017 12:49:41 PM
Modified: 11/7/2017 1:30:59 PM

## Electropherogram Summary



## Overall Results for Ladder

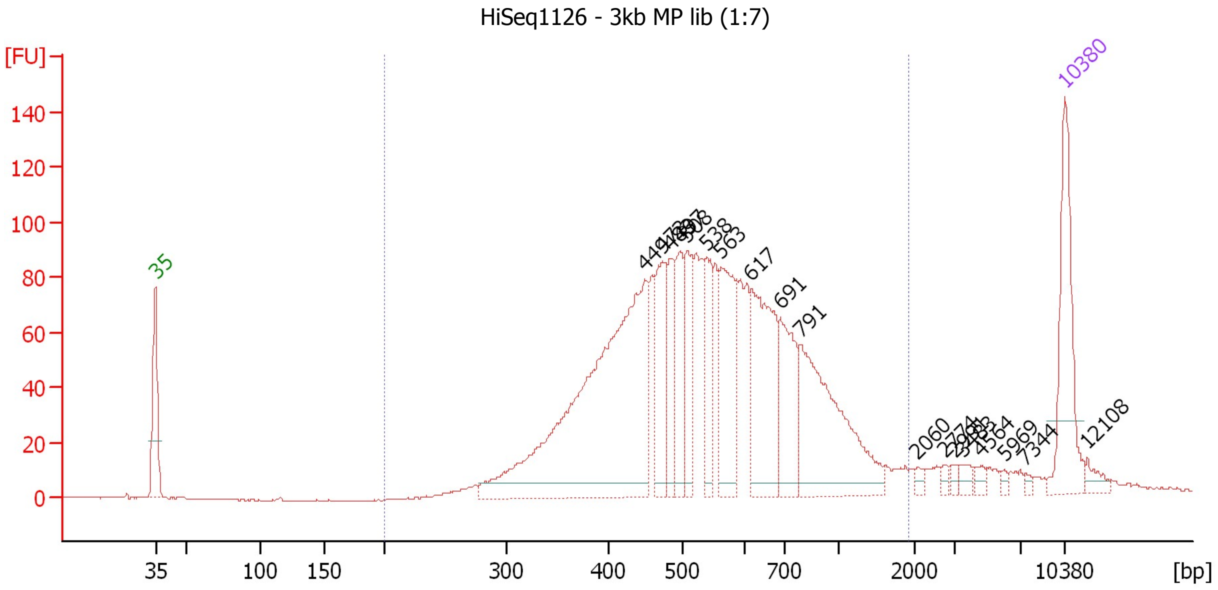
Noise: 0.1

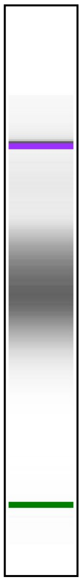
## Peak table for Ladder

| 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 | 45.39 |
| 3 | ∟ | 100 | 150.00 | 2,272.7 | Ladder Peak | 51.10 |
| 4 | ∟ | 150 | 150.00 | 1,515.2 | Ladder Peak | 55.93 |
| 5 | ∟ | 200 | 150.00 | 1,136.4 | Ladder Peak | 60.67 |
| 6 | ∟ | 300 | 150.00 | 757.6 | Ladder Peak | 69.97 |
| 7 | ∟ | 400 | 150.00 | 568.2 | Ladder Peak | 77.88 |
| 8 | ∟ | 500 | 150.00 | 454.5 | Ladder Peak | 83.55 |
| 9 | ∟ | 600 | 150.00 | 378.8 | Ladder Peak | 88.33 |
| 10 | ∟ | 700 | 150.00 | 324.7 | Ladder Peak | 91.42 |
| 11 | ∟ | 1,000 | 150.00 | 227.3 | Ladder Peak | 95.56 |
| 12 | ∟ | 2,000 | 150.00 | 113.6 | Ladder Peak | 101.49 |
| 13 | ∟ | 3,000 | 150.00 | 75.8 | Ladder Peak | 104.49 |
| 14 | ∟ | 7,000 | 150.00 | 32.5 | Ladder Peak | 109.64 |
| 15 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

## Electropherogram Summary Continued ...

HiSeq1126 - 3kb MP lib (1:7)





### Overall Results for sample 1 : HiSeq1126 - 3kb MP lib (1:7)

| | | | |
|---|---|---|---|
| Number of peaks found: | 18 | Corr. Area 1: | 1,935.0 |
| Noise: | 0.2 | | |

### Peak table for sample 1 : HiSeq1126 - 3kb MP lib (1:7)

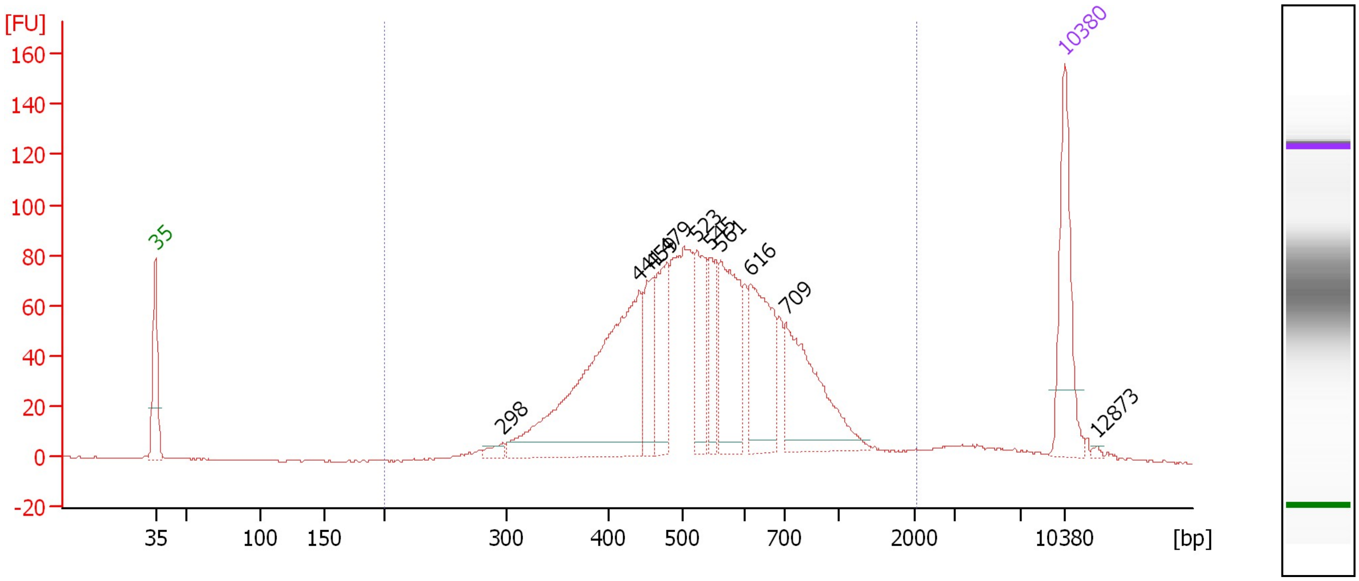
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 449 | 438.70 | 1,481.1 | | 80.65 |
| 3 | | 473 | 71.18 | 227.8 | | 82.04 |
| 4 | | 483 | 49.49 | 155.2 | | 82.60 |
| 5 | | 497 | 61.48 | 187.4 | | 83.38 |
| 6 | | 508 | 53.34 | 159.0 | | 83.94 |
| 7 | | 538 | 56.51 | 159.0 | | 85.38 |
| 8 | | 563 | 96.54 | 260.0 | | 86.54 |
| 9 | | 617 | 120.72 | 296.4 | | 88.86 |
| 10 | | 691 | 72.41 | 158.8 | | 91.14 |
| 11 | | 791 | 157.03 | 300.9 | | 92.67 |
| 12 | | 2,060 | 4.64 | 3.4 | | 101.67 |
| 13 | | 2,774 | 4.11 | 2.2 | | 103.81 |
| 14 | | 2,991 | 3.62 | 1.8 | | 104.46 |
| 15 | | 3,483 | 6.64 | 2.9 | | 105.11 |
| 16 | | 4,564 | 4.94 | 1.6 | | 106.50 |
| 17 | | 5,969 | 2.80 | 0.7 | | 108.31 |
| 18 | | 7,344 | 2.61 | 0.5 | | 109.98 |
| 19 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |
| 20 | | 12,108 | 0.00 | 0.0 | | 114.72 |

### Region table for sample 1 : HiSeq1126 - 3kb MP lib (1:7)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 1,918 | 589 | 1,935.0 | 4,259.7 | 🟦 | 1,417.48 | 93 | 41.7 |

## Electropherogram Summary Continued ...

HiSeq1126 - 6kb MP lib (1:7)



### Overall Results for sample 2 : HiSeq1126 - 6kb MP lib (1:7)

| | | | |
|---|---|---|---|
| Number of peaks found: | 10 | Corr. Area 1: | 1,712.2 |
| Noise: | 0.3 | | |

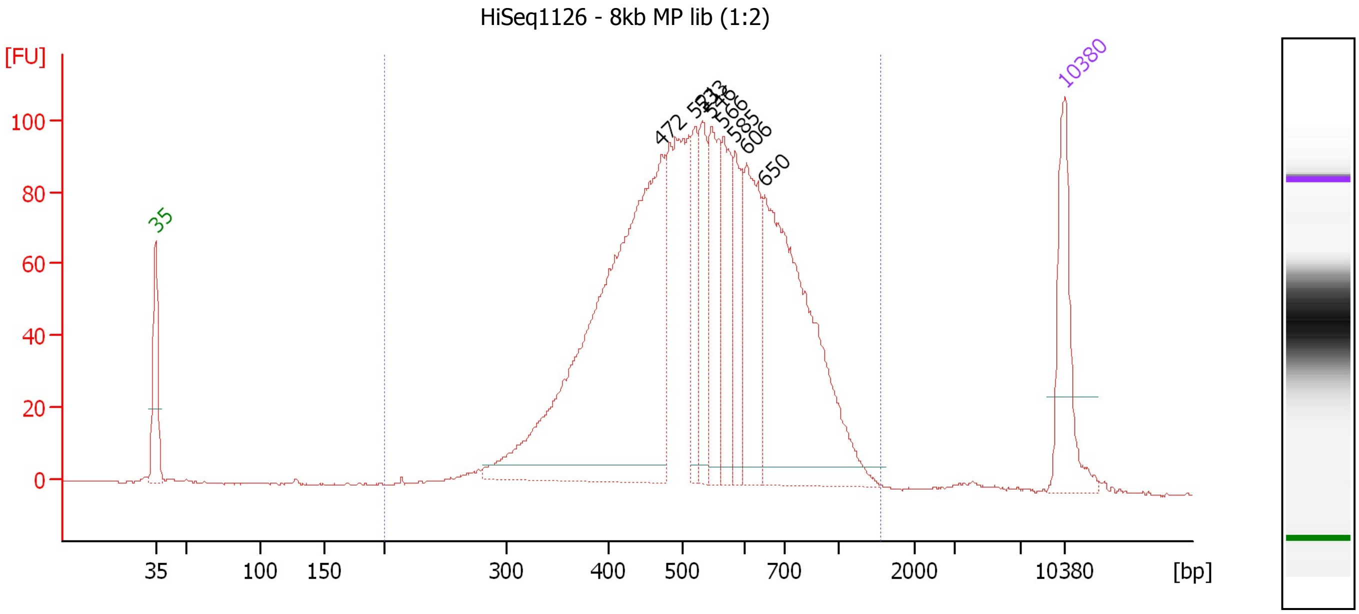
### Peak table for sample 2 : HiSeq1126 - 6kb MP lib (1:7)

| 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 | | 298 | 10.25 | 52.2 | | 69.75 |
| 3 | | 441 | 316.66 | 1,087.3 | | 80.22 |
| 4 | | 459 | 55.00 | 181.4 | | 81.25 |
| 5 | | 479 | 81.21 | 256.7 | | 82.37 |
| 6 | | 523 | 72.77 | 210.7 | | 84.66 |
| 7 | | 545 | 43.71 | 121.6 | | 85.69 |
| 8 | | 561 | 110.20 | 297.4 | | 86.49 |
| 9 | | 616 | 112.16 | 275.9 | | 88.82 |
| 10 | | 709 | 128.30 | 274.3 | | 91.54 |
| 11 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |
| 12 | | 12,873 | 0.00 | 0.0 | | 115.48 |

### Region table for sample 2 : HiSeq1126 - 6kb MP lib (1:7)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 2,057 | 571 | 1,712.2 | 3,758.4 | 🟦 | 1,240.84 | 95 | 38.9 |

## Electropherogram Summary Continued ...



### Overall Results for sample 3 : HiSeq1126 - 8kb MP lib (1:2)

| | | | |
|---|---|---|---|
| Number of peaks found: | 8 | Corr. Area 1: | 2,064.3 |
| Noise: | 0.2 | | |

### Peak table for sample 3 : HiSeq1126 - 8kb MP lib (1:2)

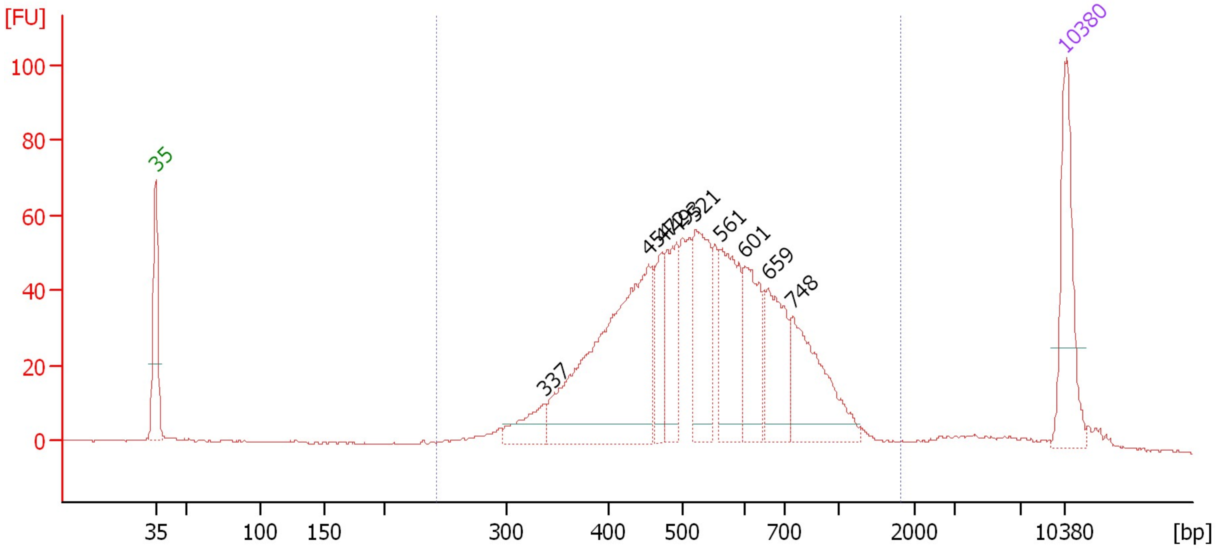
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 472 | 636.53 | 2,044.8 | | 81.94 |
| 3 | | 521 | 70.73 | 205.8 | | 84.54 |
| 4 | | 533 | 74.99 | 213.3 | | 85.10 |
| 5 | | 546 | 100.81 | 279.6 | | 85.76 |
| 6 | | 566 | 85.87 | 229.8 | | 86.71 |
| 7 | | 585 | 71.40 | 185.0 | | 87.61 |
| 8 | | 606 | 120.91 | 302.5 | | 88.50 |
| 9 | | 650 | 343.66 | 801.2 | | 89.87 |
| 10 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

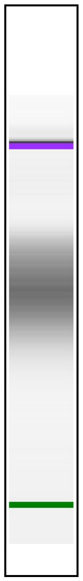
### Region table for sample 3 : HiSeq1126 - 8kb MP lib (1:2)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 1,546 | 555 | 2,064.3 | 5,608.8 | ■ | 1,834.44 | 97 | 31.0 |

**Electropherogram Summary Continued ...**

H1126P (1:4)





## Overall Results for sample 4 : H1126P (1:4)

| | | | |
|---|---|---|---|
| Number of peaks found: | 9 | Corr. Area 1: | 1,163.9 |
| Noise: | 0.2 | | |

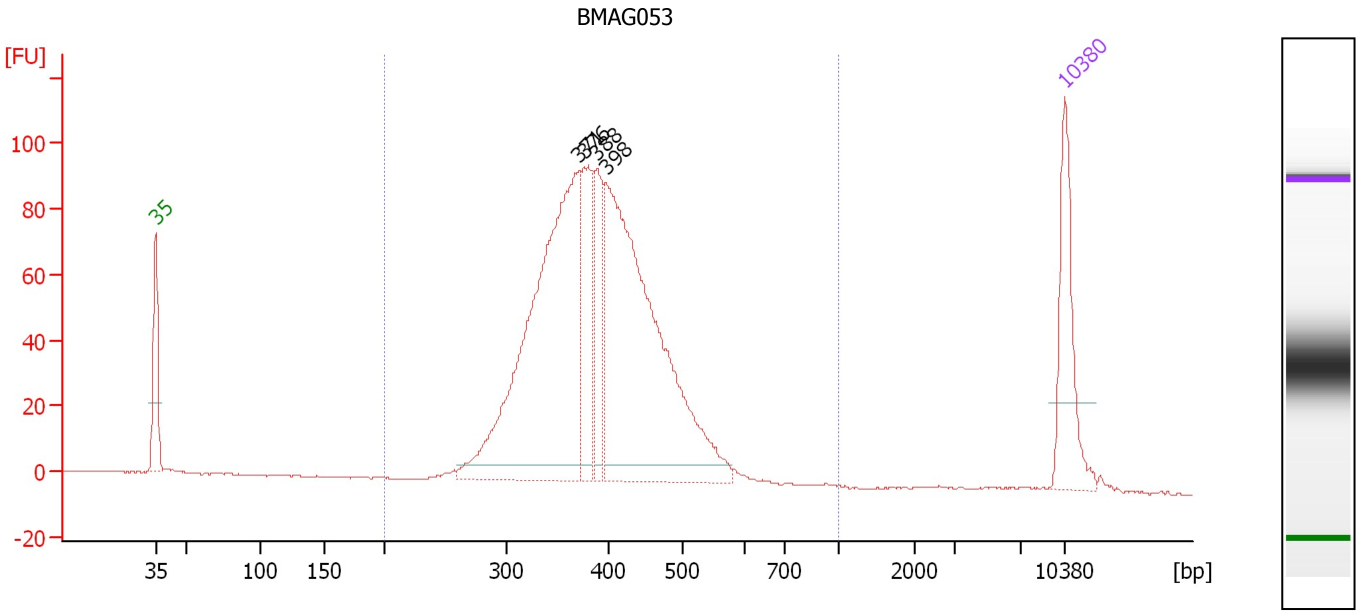
## Peak table for sample 4 : H1126P (1:4)

| 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 | | 337 | 37.26 | 167.3 | | 72.92 |
| 3 | | 454 | 314.24 | 1,048.0 | | 80.96 |
| 4 | | 472 | 50.01 | 160.5 | | 81.97 |
| 5 | | 493 | 74.45 | 229.0 | | 83.12 |
| 6 | | 521 | 108.98 | 316.7 | | 84.57 |
| 7 | | 561 | 103.15 | 278.8 | | 86.44 |
| 8 | | 601 | 80.16 | 202.0 | | 88.37 |
| 9 | | 659 | 83.12 | 191.2 | | 90.15 |
| 10 | | 748 | 110.98 | 224.9 | | 92.07 |
| 11 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

## Region table for sample 4 : H1126P (1:4)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co lor | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 243 | 1,816 | 565 | 1,163.9 | 3,619.8 | 🟦 | 1,188.27 | 91 | 35.5 |

## Electropherogram Summary Continued ...



### Overall Results for sample 5 : BMAG053

| | | | |
|---|---|---|---|
| Number of peaks found: | 4 | Corr. Area 1: | 1,394.7 |
| Noise: | 0.2 | | |

### Peak table for sample 5 : BMAG053

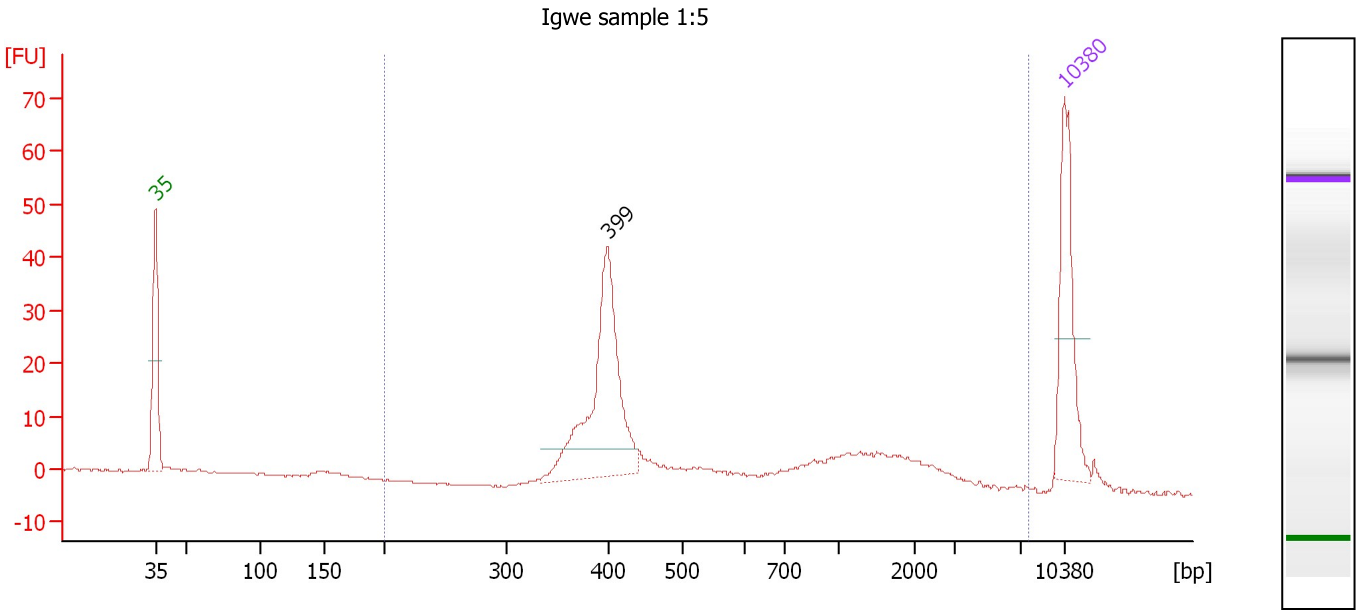
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 371 | 494.14 | 2,017.4 | | 75.60 |
| 3 | | 376 | 105.58 | 425.4 | | 75.99 |
| 4 | | 388 | 74.42 | 290.4 | | 76.96 |
| 5 | | 398 | 481.10 | 1,831.1 | | 77.73 |
| 6 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

### Region table for sample 5 : BMAG053

| 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 | 397 | 1,394.7 | 4,915.7 | ■ | 1,239.60 | 96 | 18.4 |

| | | | |
|---|---|---|---|
| Assay Class: | High Sensitivity DNA Assay | Created: | 11/7/2017 12:49:41 PM |
| Data Path: | C:\... bioanalyzer\2100 expert\data\2017-11-07\2017-11-07_003.xad | Modified: | 11/7/2017 1:30:59 PM |

### Electropherogram Summary Continued ...


Igwe sample 1:5

### Overall Results for sample 6 : Igwe sample 1:5

| | | | |
|---|---|---|---|
| Number of peaks found: | 1 | Corr. Area 1: | 256.9 |
| Noise: | 0.2 | | |

### Peak table for sample 6 : Igwe sample 1:5

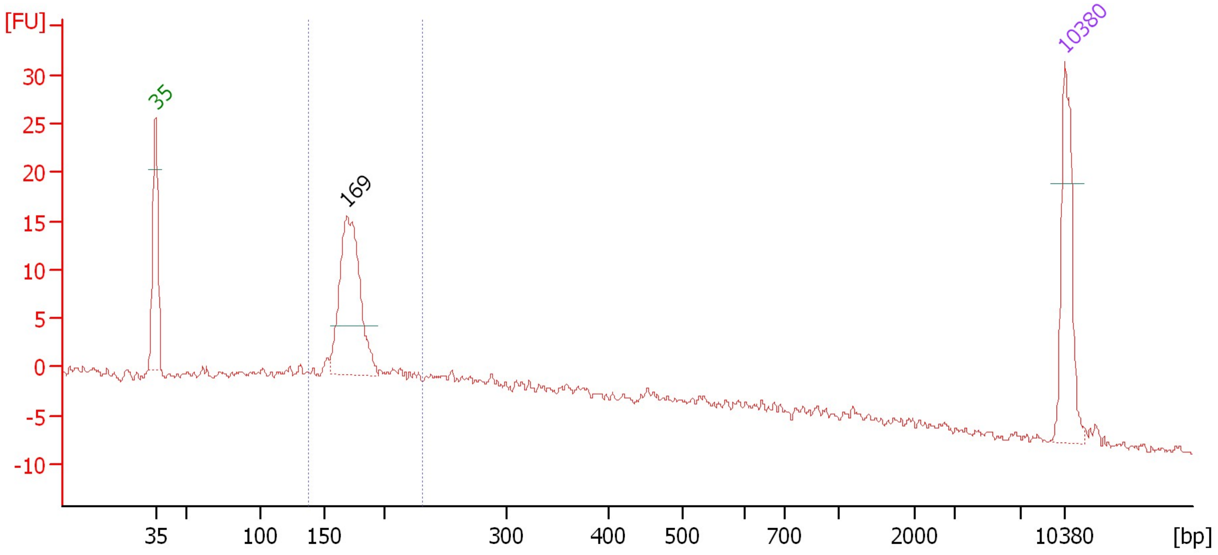
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 399 | 193.94 | 736.5 | | 77.81 |
| 3 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

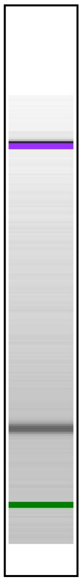
### Region table for sample 6 : Igwe sample 1:5

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 7,581 | 903 | 256.9 | 1,053.6 | 🟦 | 351.25 | 94 | 100.0 |

## Electropherogram Summary Continued ...

Bovine smRNA pool





### Overall Results for sample 7 : Bovine smRNA pool

Number of peaks found: 1
Corr. Area 1: 77.5
Noise: 0.3

### Peak table for sample 7 : Bovine smRNA pool

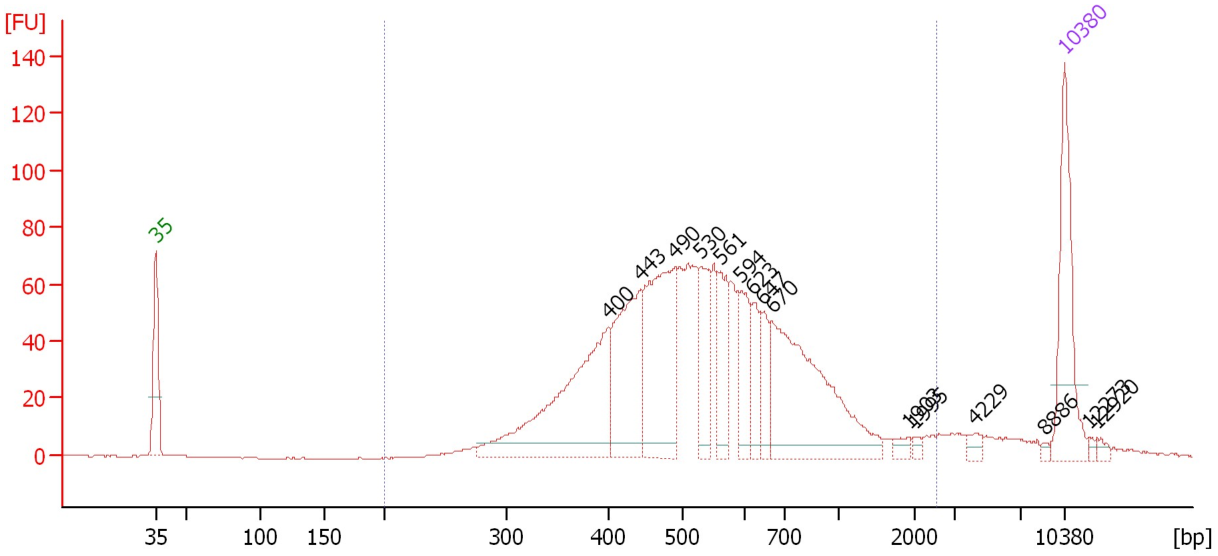
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 169 | 222.34 | 1,989.1 | | 57.77 |
| 3 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

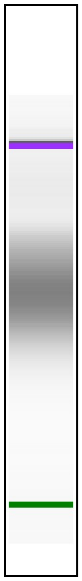
### Region table for sample 7 : Bovine smRNA pool

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 139 | 230 | 176 | 77.5 | 2,757.7 | 🟦 | 317.84 | 49 | 9.9 |

## Electropherogram Summary Continued ...

HiSeq1126 - 3kb MP lib (1:7)





## Overall Results for sample 8 : HiSeq1126 - 3kb MP lib (1:7)

| | | | |
|---|---|---|---|
| Number of peaks found: | 15 | Corr. Area 1: | 1,507.2 |
| Noise: | 0.1 | | |

## Peak table for sample 8 : HiSeq1126 - 3kb MP lib (1:7)

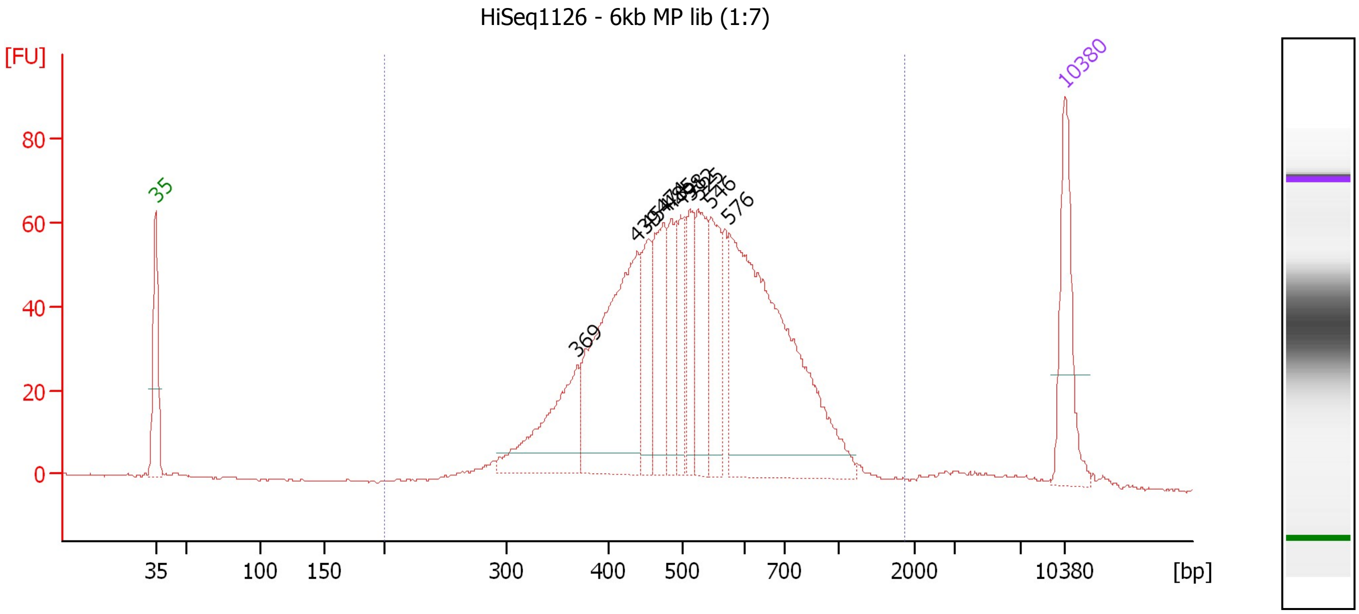
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 400 | 215.60 | 817.5 | | 77.85 |
| 3 | | 443 | 127.78 | 436.9 | | 80.33 |
| 4 | | 490 | 166.21 | 513.6 | | 83.00 |
| 5 | | 530 | 53.17 | 152.0 | | 84.98 |
| 6 | | 561 | 51.57 | 139.3 | | 86.47 |
| 7 | | 594 | 48.85 | 124.6 | | 88.05 |
| 8 | | 623 | 34.05 | 82.8 | | 89.04 |
| 9 | | 647 | 27.70 | 64.9 | | 89.78 |
| 10 | | 670 | 202.16 | 457.5 | | 90.48 |
| 11 | | 1,903 | 6.65 | 5.3 | | 100.92 |
| 12 | | 1,995 | 3.55 | 2.7 | | 101.47 |
| 13 | | 4,229 | 6.29 | 2.3 | | 106.07 |
| 14 | | 8,886 | 2.14 | 0.4 | | 111.51 |
| 15 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |
| 16 | | 12,273 | 0.00 | 0.0 | | 114.88 |
| 17 | | 12,920 | 0.00 | 0.0 | | 115.52 |

## Region table for sample 8 : HiSeq1126 - 3kb MP lib (1:7)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 200 | 2,553 | 602 | 1,507.2 | 3,634.7 | 🟦 1,192.15 | 92 | 52.3 |

## Electropherogram Summary Continued ...

HiSeq1126 - 6kb MP lib (1:7)



### Overall Results for sample 9 : HiSeq1126 - 6kb MP lib (1:7)

| | | | |
|---|---|---|---|
| Number of peaks found: | 10 | Corr. Area 1: | 1,319.7 |
| Noise: | 0.3 | | |

### Peak table for sample 9 : HiSeq1126 - 6kb MP lib (1:7)

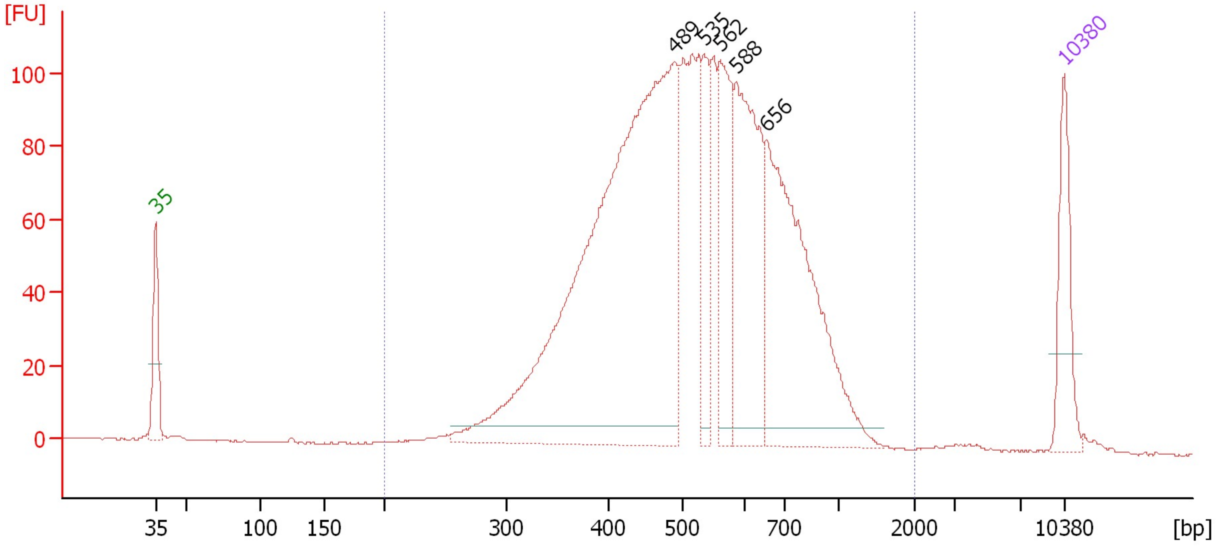
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 369 | 133.86 | 549.3 | | 75.45 |
| 3 | | 439 | 291.87 | 1,006.8 | | 80.11 |
| 4 | | 454 | 71.18 | 237.5 | | 80.95 |
| 5 | | 474 | 100.44 | 320.9 | | 82.09 |
| 6 | | 485 | 62.74 | 196.1 | | 82.68 |
| 7 | | 498 | 58.46 | 177.9 | | 83.42 |
| 8 | | 512 | 67.69 | 200.3 | | 84.12 |
| 9 | | 525 | 83.57 | 241.0 | | 84.76 |
| 10 | | 546 | 82.33 | 228.4 | | 85.75 |
| 11 | | 576 | 410.99 | 1,080.8 | | 87.19 |
| 12 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

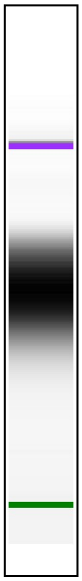
### Region table for sample 9 : HiSeq1126 - 6kb MP lib (1:7)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Color | Conc. [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|---|
| 200 | 1,871 | 547 | 1,319.7 | 4,936.8 | 🟦 | 1,583.29 | 95 | 34.6 |

## Electropherogram Summary Continued ...

HiSeq1126 - 8kb MP lib (1:2)





### Overall Results for sample 10 : HiSeq1126 - 8kb MP lib (1:2)

| | | | |
|---|---|---|---|
| Number of peaks found: | 5 | Corr. Area 1: | 2,222.3 |
| Noise: | 0.1 | | |

### Peak table for sample 10 : HiSeq1126 - 8kb MP lib (1:2)

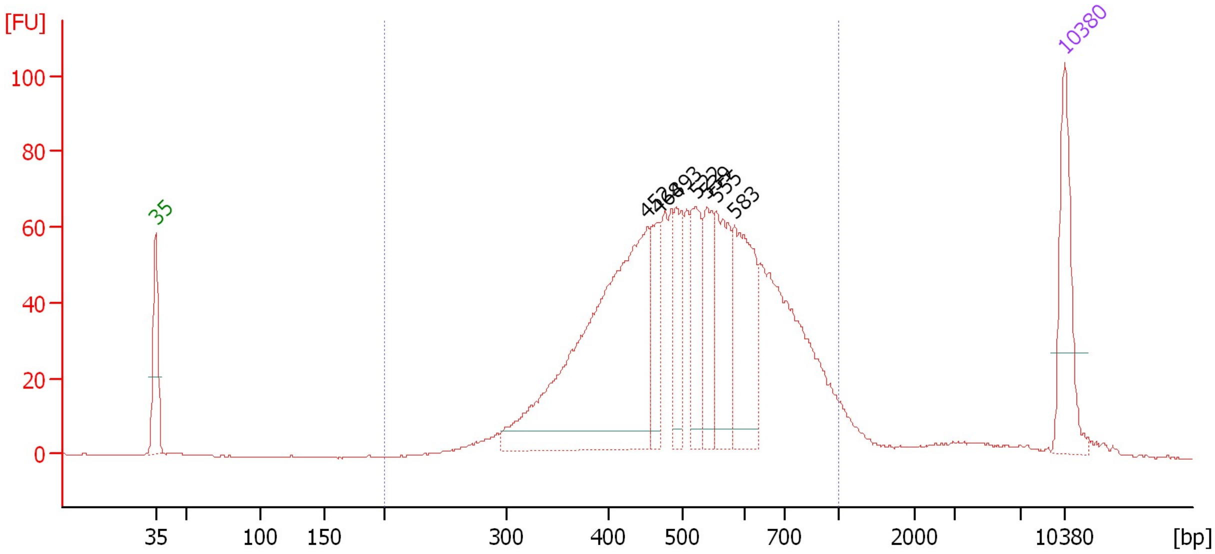
| Peak | | Size [bp] | Conc. [pg/µl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|---|---|---|---|---|---|---|
| 1 | ◀ | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 2 | | 489 | 1,139.80 | 3,530.8 | | 82.93 |
| 3 | | 535 | 97.73 | 276.9 | | 85.21 |
| 4 | | 562 | 155.55 | 419.6 | | 86.50 |
| 5 | | 588 | 269.82 | 695.8 | | 87.73 |
| 6 | | 656 | 411.38 | 950.0 | | 90.06 |
| 7 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

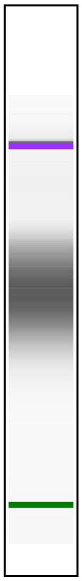
### Region table for sample 10 : HiSeq1126 - 8kb MP lib (1:2)

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/µl] | % of Total | Size distribution in CV [%] |
|---|---|---|---|---|---|---|---|
| 200 | 1,987 | 542 | 2,222.3 | 7,867.1 | ■ 2,521.37 | 99 | 30.8 |

**Electropherogram Summary Continued ...**

H1126P (1:4)





**Overall Results for sample 11 :** **H1126P (1:4)**

| | | | |
|---|---|---|---|
| Number of peaks found: | 7 | Corr. Area 1: | 1,355.9 |
| Noise: | 0.1 | | |

**Peak table for sample 11 :** **H1126P (1:4)**

| 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 | | 452 | 469.05 | 1,571.7 | | 80.84 |
| 3 | | 468 | 61.63 | 199.5 | | 81.73 |
| 4 | | 493 | 60.03 | 184.6 | | 83.13 |
| 5 | | 522 | 78.00 | 226.2 | | 84.62 |
| 6 | | 539 | 71.62 | 201.3 | | 85.42 |
| 7 | | 555 | 101.05 | 276.0 | | 86.17 |
| 8 | | 583 | 137.16 | 356.6 | | 87.51 |
| 9 | ▶ | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

**Region table for sample 11 :** **H1126P (1:4)**

| 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 | 529 | 1,355.9 | 4,757.3 | ■ | 1,505.75 | 93 | 27.2 |

## Gel Image