

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
Modified: 9/14/2017 1:59:02 PM

Electrophoresis File Run Summary

Instrument Information:

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

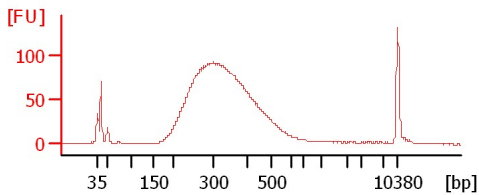
Assay Information:

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

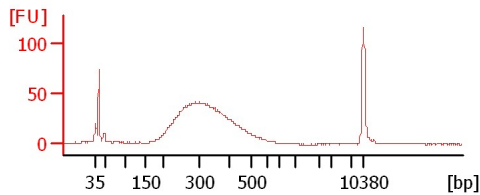
Chip Information:

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

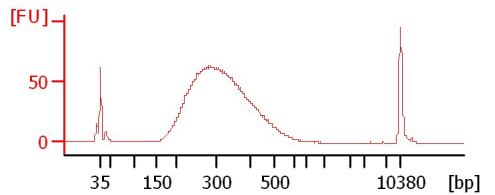
HiSeq1053 - 16 library



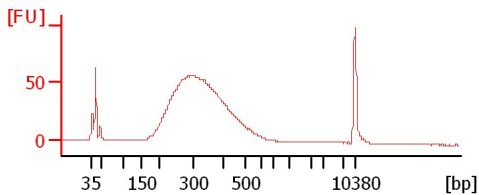
HiSeq1053 - 17 library



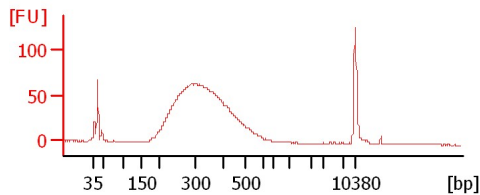
HiSeq1053 - 23 library



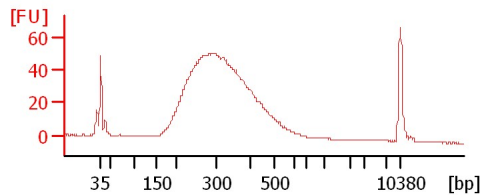
HiSeq1053 - 24 library



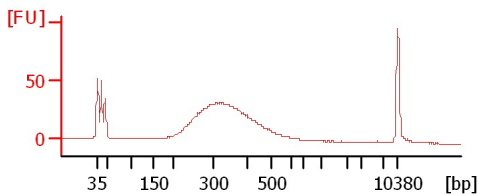
HiSeq1053 - 25 library



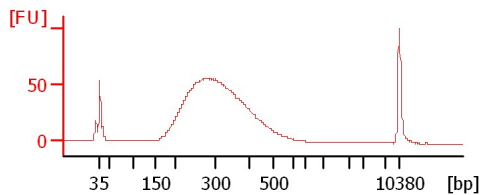
HiSeq1053 - 26 library



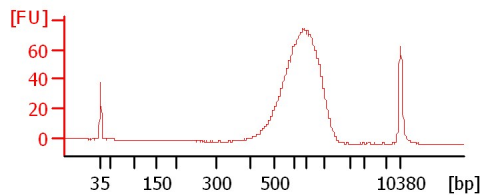
HiSeq1053 - 27 library



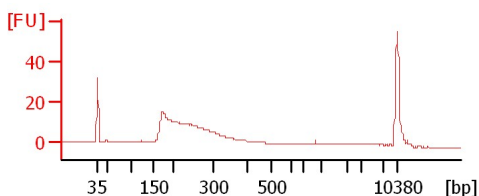
HiSeq1053 - 28 library



M565P 0.6x BC



TL3



Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
Modified: 9/14/2017 1:59:02 PM

Electrophoresis File Run Summary (Chip Summary)

| Sample Name | Sample Comment | Rest. Digest | Status | Observation | Result Label | Result Color |
|------------------------|----------------|--------------------------|--------|-------------|--------------|--------------|
| HiSeq1053 - 16 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 17 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 23 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 24 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 25 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 26 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 27 library | | <input type="checkbox"/> | ✓ | | | |
| HiSeq1053 - 28 library | | <input type="checkbox"/> | ✓ | | | |
| M565P 0.6x BC | | <input type="checkbox"/> | ✓ | | | |
| TL3 | | <input type="checkbox"/> | ✓ | | | |
| sample 11 | | <input type="checkbox"/> | ✓ | | | |
| Ladder | | <input type="checkbox"/> | ✓ | | | |

Chip Lot #

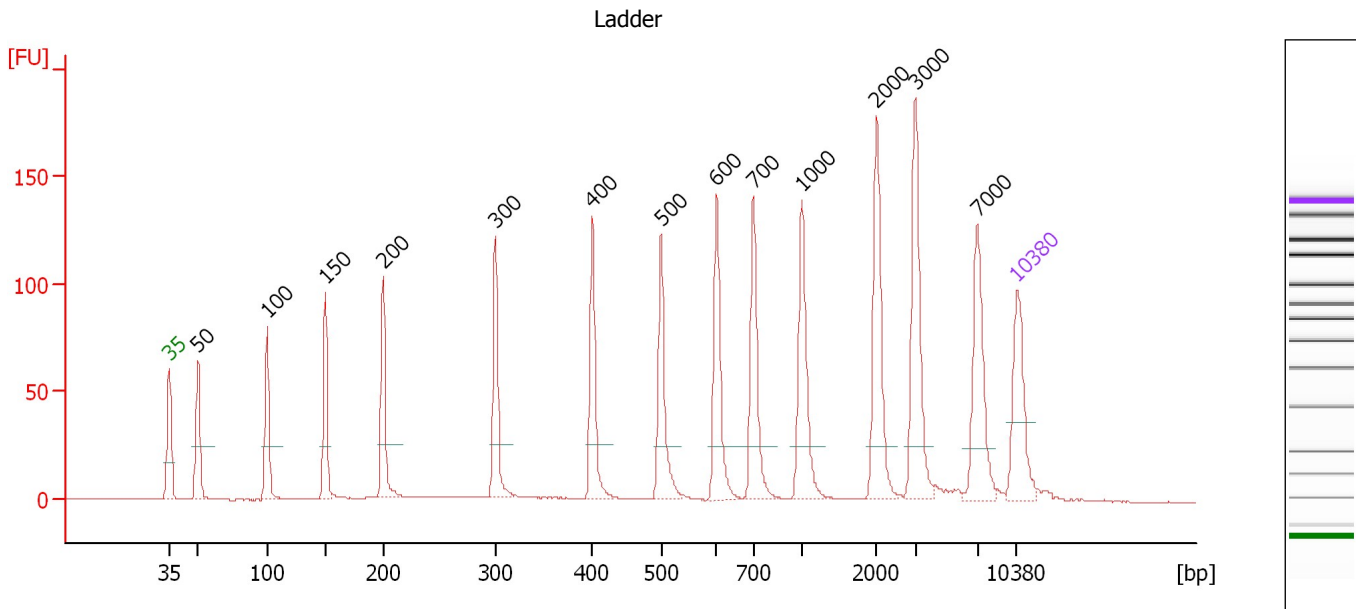
Reagent Kit Lot #

Chip Comments :

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
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Electropherogram Summary



Overall Results for Ladder

Noise: 0.1

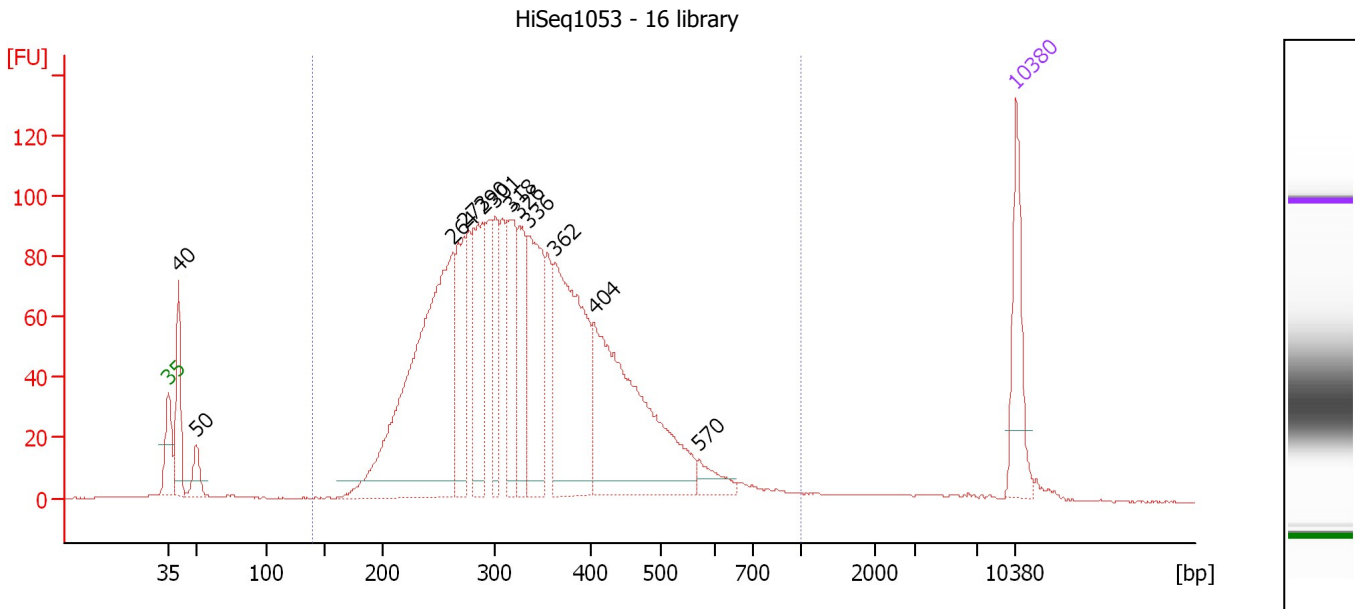
Peak table for Ladder

| 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 | 45.34 |
| 3 | 100 | 150.00 | 2,272.7 | Ladder Peak | 51.05 |
| 4 | 150 | 150.00 | 1,515.2 | Ladder Peak | 55.89 |
| 5 | 200 | 150.00 | 1,136.4 | Ladder Peak | 60.62 |
| 6 | 300 | 150.00 | 757.6 | Ladder Peak | 69.90 |
| 7 | 400 | 150.00 | 568.2 | Ladder Peak | 77.90 |
| 8 | 500 | 150.00 | 454.5 | Ladder Peak | 83.61 |
| 9 | 600 | 150.00 | 378.8 | Ladder Peak | 88.20 |
| 10 | 700 | 150.00 | 324.7 | Ladder Peak | 91.23 |
| 11 | 1,000 | 150.00 | 227.3 | Ladder Peak | 95.23 |
| 12 | 2,000 | 150.00 | 113.6 | Ladder Peak | 101.43 |
| 13 | 3,000 | 150.00 | 75.8 | Ladder Peak | 104.60 |
| 14 | 7,000 | 150.00 | 32.5 | Ladder Peak | 109.73 |
| 15 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 1 : HiSeq1053 - 16 library

Number of peaks found: 12 Corr. Area 1: 2,329.2
 Noise: 0.2

Peak table for sample 1 : HiSeq1053 - 16 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 | 118.64 | 4,458.0 | | 43.83 |
| 3 | 50 | 41.16 | 1,254.2 | | 45.30 |
| 4 | 264 | 616.20 | 3,540.7 | | 66.53 |
| 5 | 273 | 144.05 | 799.0 | | 67.41 |
| 6 | 290 | 178.76 | 933.8 | | 68.97 |
| 7 | 301 | 100.78 | 506.8 | | 70.00 |
| 8 | 318 | 139.96 | 667.3 | | 71.32 |
| 9 | 326 | 112.19 | 521.8 | | 71.96 |
| 10 | 336 | 187.79 | 846.5 | | 72.79 |
| 11 | 362 | 330.11 | 1,382.4 | | 74.84 |
| 12 | 404 | 380.24 | 1,426.6 | | 78.12 |
| 13 | 570 | 26.98 | 71.7 | | 86.83 |
| 14 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

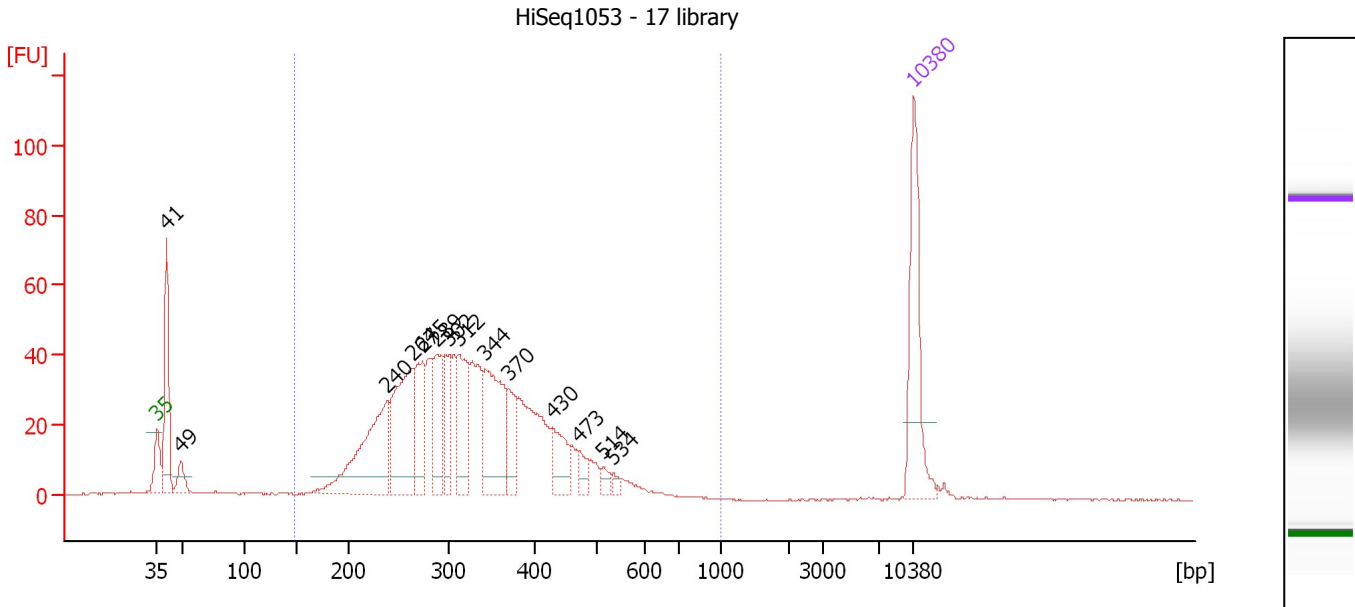
Region table for sample 1 : HiSeq1053 - 16 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|------------------|------------|-----------------------------|
| 141 | 1,000 | 343 | 2,329.2 | 12,829.7 | 2,630.29 | 94 | 29.1 |

Assay Class: High Sensitivity DNA Assay
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Electropherogram Summary Continued ...



Overall Results for sample 2 : HiSeq1053 - 17 library

Number of peaks found: 14 Corr. Area 1: 991.1
 Noise: 0.2

Peak table for sample 2 : HiSeq1053 - 17 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 | 115.92 | 4,317.1 | | 43.89 |
| 3 | 49 | 23.62 | 731.8 | | 45.17 |
| 4 | 240 | 148.14 | 936.1 | | 64.31 |
| 5 | 264 | 134.41 | 770.7 | | 66.58 |
| 6 | 275 | 61.23 | 337.5 | | 67.57 |
| 7 | 289 | 62.93 | 329.6 | | 68.90 |
| 8 | 302 | 45.20 | 227.0 | | 70.03 |
| 9 | 312 | 70.66 | 342.9 | | 70.87 |
| 10 | 344 | 107.33 | 473.3 | | 73.39 |
| 11 | 370 | 38.35 | 157.0 | | 75.51 |
| 12 | 430 | 36.37 | 128.2 | | 79.60 |
| 13 | 473 | 14.64 | 46.9 | | 82.07 |
| 14 | 514 | 8.46 | 24.9 | | 84.24 |
| 15 | 534 | 4.73 | 13.4 | | 85.18 |
| 16 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

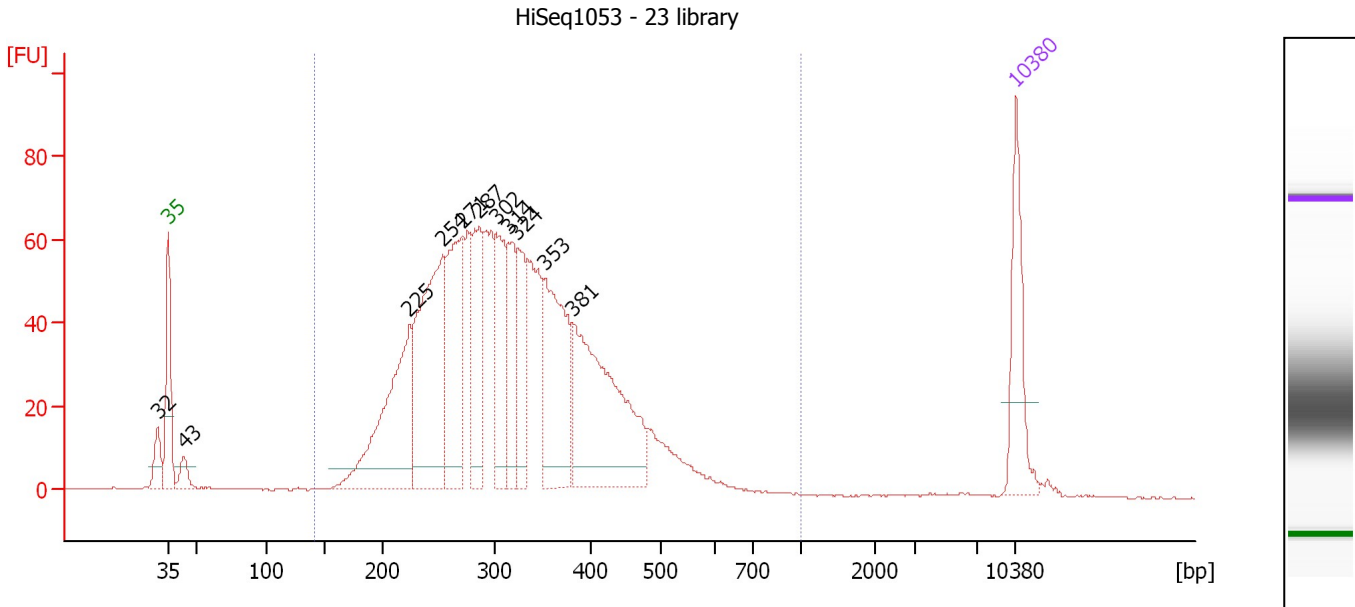
Region table for sample 2 : HiSeq1053 - 17 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|----------------------|------------|-----------------------------|
| 148 | 1,000 | 332 | 991.1 | 5,379.2 | 1,077.97 | 88 | 26.1 |

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Electropherogram Summary Continued ...



Overall Results for sample 3 : HiSeq1053 - 23 library

Number of peaks found: 11 Corr. Area 1: 1,524.2
 Noise: 0.2

Peak table for sample 3 : HiSeq1053 - 23 library

| Peak | Size [bp] | Conc. [pg/μl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|------|-----------|---------------|-------------------|--------------|----------------------------|
| 1 | 32 | 0.00 | 0.0 | | 42.09 |
| 2 | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 3 | 43 | 25.03 | 880.2 | | 44.26 |
| 4 | 225 | 252.20 | 1,701.7 | | 62.90 |
| 5 | 254 | 312.74 | 1,865.9 | | 65.63 |
| 6 | 271 | 186.73 | 1,042.5 | | 67.24 |
| 7 | 287 | 129.50 | 684.5 | | 68.66 |
| 8 | 302 | 114.57 | 574.5 | | 70.07 |
| 9 | 314 | 90.43 | 436.1 | | 71.03 |
| 10 | 324 | 90.74 | 424.0 | | 71.84 |
| 11 | 353 | 194.60 | 836.1 | | 74.11 |
| 12 | 381 | 286.51 | 1,139.3 | | 76.38 |
| 13 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

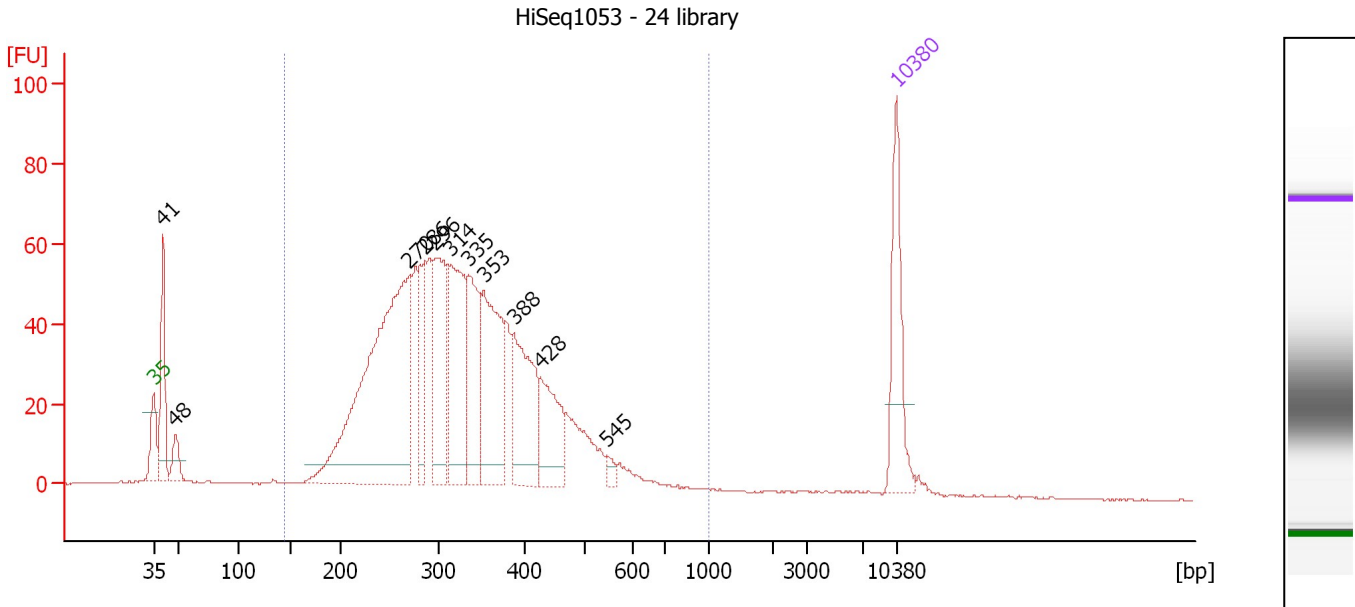
Region table for sample 3 : HiSeq1053 - 23 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|----------------------|------------|-----------------------------|
| 142 | 1,000 | 323 | 1,524.2 | 11,243.3 | 2,191.94 | 96 | 26.9 |

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

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Electropherogram Summary Continued ...



Overall Results for sample 4 : HiSeq1053 - 24 library

Number of peaks found: 11 Corr. Area 1: 1,419.0
 Noise: 0.2

Peak table for sample 4 : HiSeq1053 - 24 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 | 119.96 | 4,456.4 | | 43.90 |
| 3 | 48 | 33.13 | 1,041.8 | | 45.06 |
| 4 | 270 | 513.85 | 2,884.9 | | 67.10 |
| 5 | 286 | 77.72 | 412.3 | | 68.56 |
| 6 | 296 | 154.90 | 791.8 | | 69.56 |
| 7 | 314 | 177.09 | 854.4 | | 71.02 |
| 8 | 335 | 117.61 | 532.3 | | 72.68 |
| 9 | 353 | 164.68 | 707.0 | | 74.13 |
| 10 | 388 | 133.55 | 521.4 | | 76.95 |
| 11 | 428 | 82.03 | 290.3 | | 79.51 |
| 12 | 545 | 8.81 | 24.5 | | 85.68 |
| 13 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

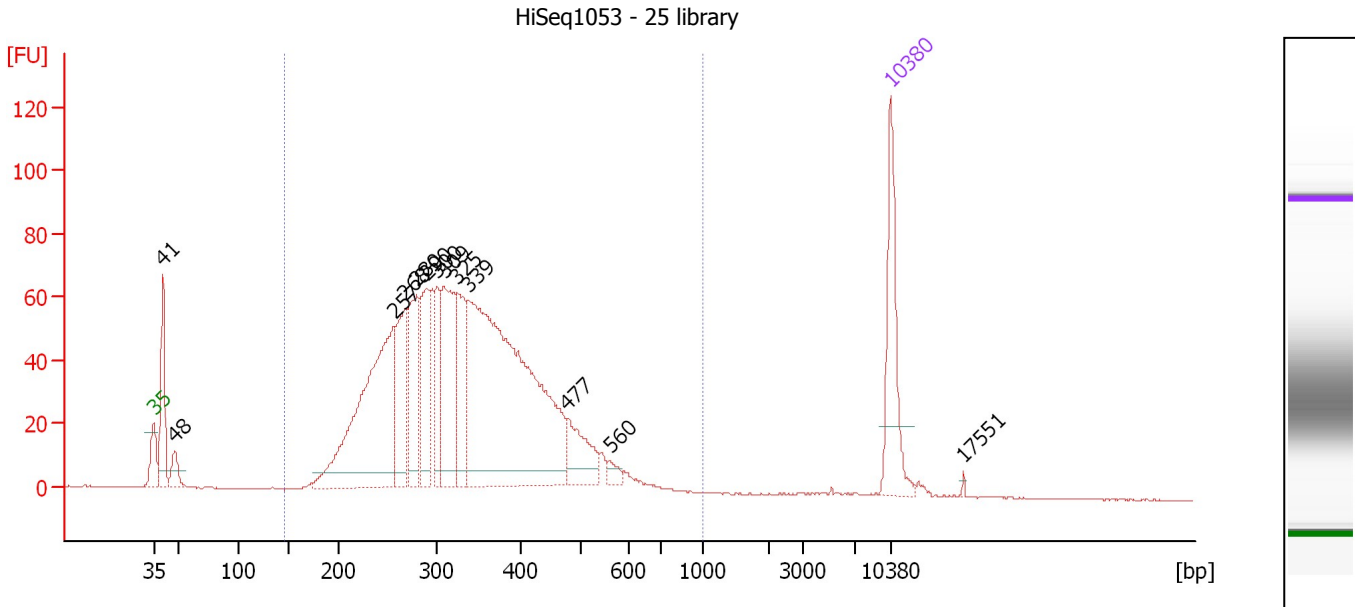
Region table for sample 4 : HiSeq1053 - 24 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|----------------------|------------|-----------------------------|
| 145 | 1,000 | 336 | 1,419.0 | 9,117.7 | 1,831.28 | 91 | 28.6 |

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

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Electropherogram Summary Continued ...



Overall Results for sample 5 : HiSeq1053 - 25 library

Number of peaks found: 13 Corr. Area 1: 1,604.8
 Noise: 0.2

Peak table for sample 5 : HiSeq1053 - 25 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 | 105.29 | 3,937.6 | | 43.86 |
| 3 | 48 | 28.31 | 894.3 | | 45.03 |
| 4 | 257 | 343.95 | 2,029.0 | | 65.89 |
| 5 | 268 | 105.20 | 595.3 | | 66.91 |
| 6 | 280 | 111.24 | 602.4 | | 68.02 |
| 7 | 290 | 92.92 | 486.1 | | 68.93 |
| 8 | 300 | 66.22 | 334.5 | | 69.90 |
| 9 | 309 | 143.18 | 701.0 | | 70.66 |
| 10 | 325 | 83.11 | 387.8 | | 71.87 |
| 11 | 339 | 572.60 | 2,562.4 | | 72.99 |
| 12 | 477 | 56.42 | 179.2 | | 82.31 |
| 13 | 560 | 8.87 | 24.0 | | 86.36 |
| 14 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |
| 15 | 17,551 | 0.00 | 0.0 | | 119.94 |

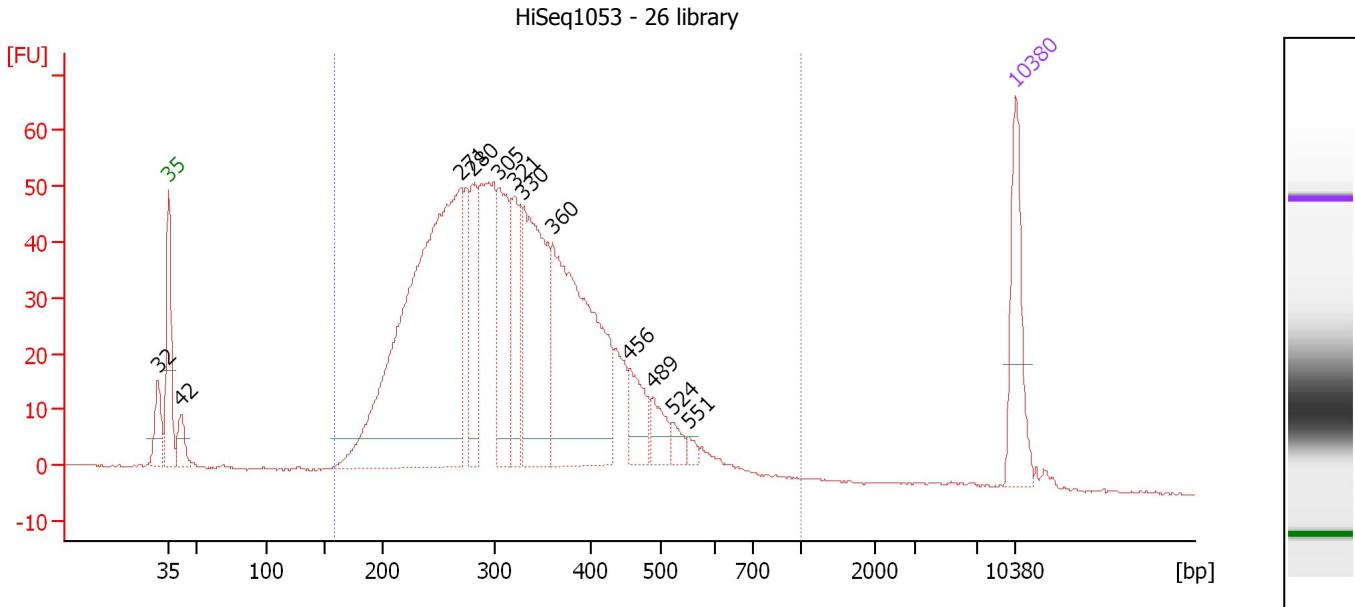
Region table for sample 5 : HiSeq1053 - 25 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|------------------|------------|-----------------------------|
| 146 | 1,000 | 341 | 1,604.8 | 8,337.3 | 1,704.83 | 93 | 27.5 |

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

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Electropherogram Summary Continued ...



Overall Results for sample 6 : HiSeq1053 - 26 library

Number of peaks found: 12 Corr. Area 1: 1,316.5
 Noise: 0.1

Peak table for sample 6 : HiSeq1053 - 26 library

| Peak | Size [bp] | Conc. [pg/μl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|------|-----------|---------------|-------------------|--------------|----------------------------|
| 1 | 32 | 0.00 | 0.0 | | 42.12 |
| 2 | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 3 | 42 | 37.94 | 1,381.8 | | 44.03 |
| 4 | 271 | 762.86 | 4,270.5 | | 67.18 |
| 5 | 280 | 100.97 | 546.2 | | 68.05 |
| 6 | 305 | 138.52 | 689.0 | | 70.27 |
| 7 | 321 | 98.75 | 465.6 | | 71.61 |
| 8 | 330 | 244.94 | 1,125.5 | | 72.28 |
| 9 | 360 | 364.70 | 1,534.9 | | 74.70 |
| 10 | 456 | 50.27 | 167.1 | | 81.09 |
| 11 | 489 | 30.85 | 95.6 | | 83.00 |
| 12 | 524 | 14.01 | 40.5 | | 84.70 |
| 13 | 551 | 7.89 | 21.7 | | 85.94 |
| 14 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

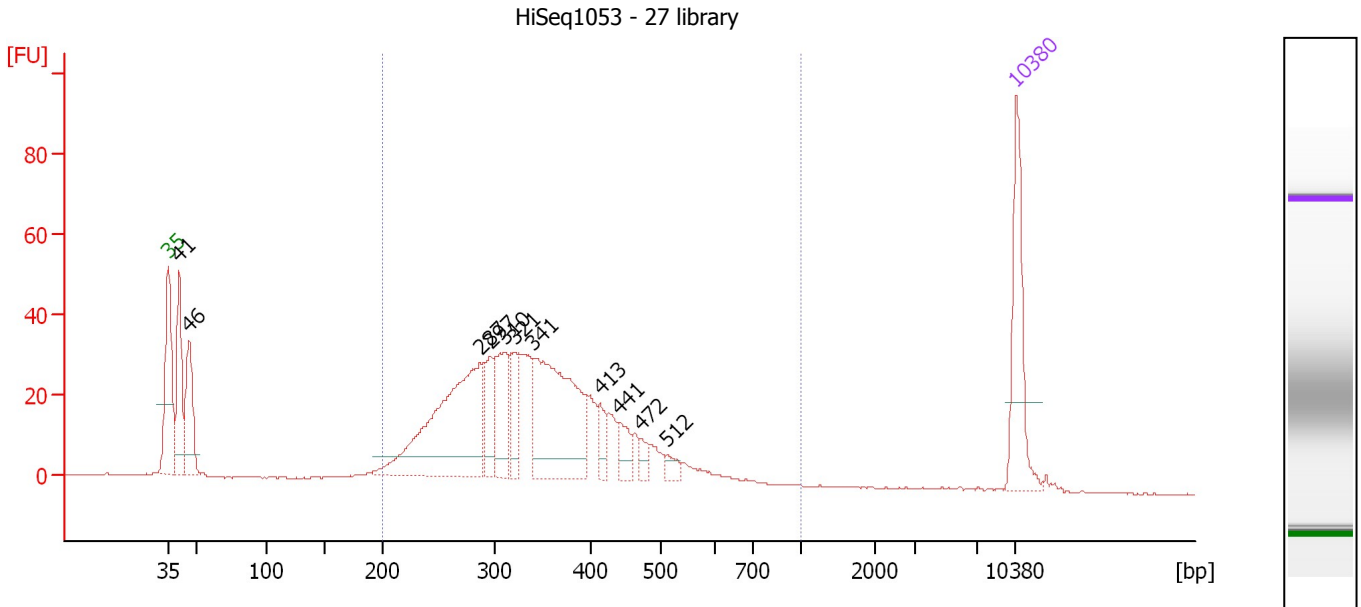
Region table for sample 6 : HiSeq1053 - 26 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|------------------|------------|-----------------------------|
| 159 | 1,000 | 331 | 1,316.5 | 12,130.9 | 2,385.64 | 94 | 29.9 |

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 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

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Electropherogram Summary Continued ...



Overall Results for sample 7 : HiSeq1053 - 27 library

Number of peaks found: 11 Corr. Area 1: 706.2
 Noise: 0.1

Peak table for sample 7 : HiSeq1053 - 27 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 | 110.72 | 4,130.9 | | 43.88 |
| 3 | 46 | 96.85 | 3,197.6 | | 44.70 |
| 4 | 287 | 279.41 | 1,473.4 | | 68.72 |
| 5 | 297 | 52.17 | 266.4 | | 69.60 |
| 6 | 310 | 75.51 | 368.5 | | 70.73 |
| 7 | 321 | 45.37 | 213.9 | | 71.61 |
| 8 | 341 | 222.80 | 990.8 | | 73.15 |
| 9 | 413 | 19.99 | 73.2 | | 78.67 |
| 10 | 441 | 25.64 | 88.2 | | 80.22 |
| 11 | 472 | 12.76 | 41.0 | | 82.02 |
| 12 | 512 | 11.60 | 34.3 | | 84.19 |
| 13 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

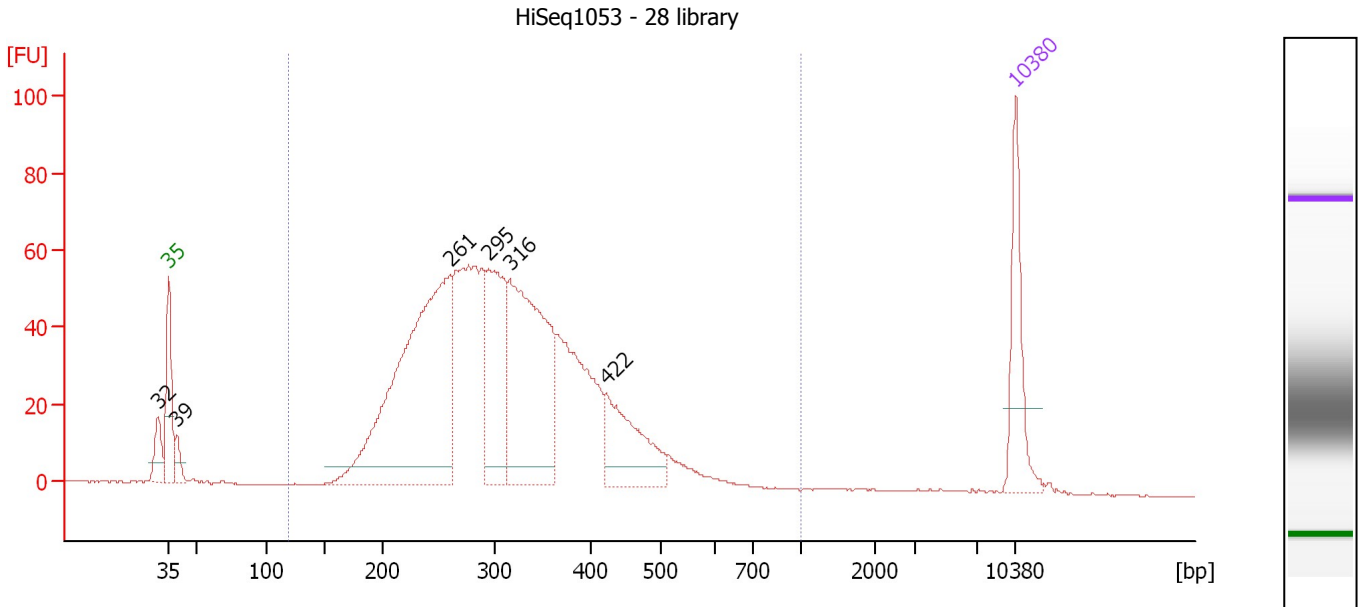
Region table for sample 7 : HiSeq1053 - 27 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|------------------|------------|-----------------------------|
| 200 | 1,000 | 350 | 706.2 | 4,668.7 | 996.82 | 84 | 25.8 |

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Electropherogram Summary Continued ...



Overall Results for sample 8 : HiSeq1053 - 28 library

Number of peaks found: 6 Corr. Area 1: 1,355.9
 Noise: 0.2

Peak table for sample 8 : HiSeq1053 - 28 library

| Peak | Size [bp] | Conc. [pg/μl] | Molarity [pmol/l] | Observations | Aligned Migration Time [s] |
|------|-----------|---------------|-------------------|--------------|----------------------------|
| 1 | 32 | 0.00 | 0.0 | | 42.10 |
| 2 | 35 | 125.00 | 5,411.3 | Lower Marker | 43.00 |
| 3 | 39 | 26.10 | 1,004.2 | | 43.68 |
| 4 | 261 | 572.13 | 3,321.2 | | 66.28 |
| 5 | 295 | 189.45 | 972.7 | | 69.44 |
| 6 | 316 | 355.19 | 1,703.0 | | 71.18 |
| 7 | 422 | 117.39 | 421.9 | | 79.13 |
| 8 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

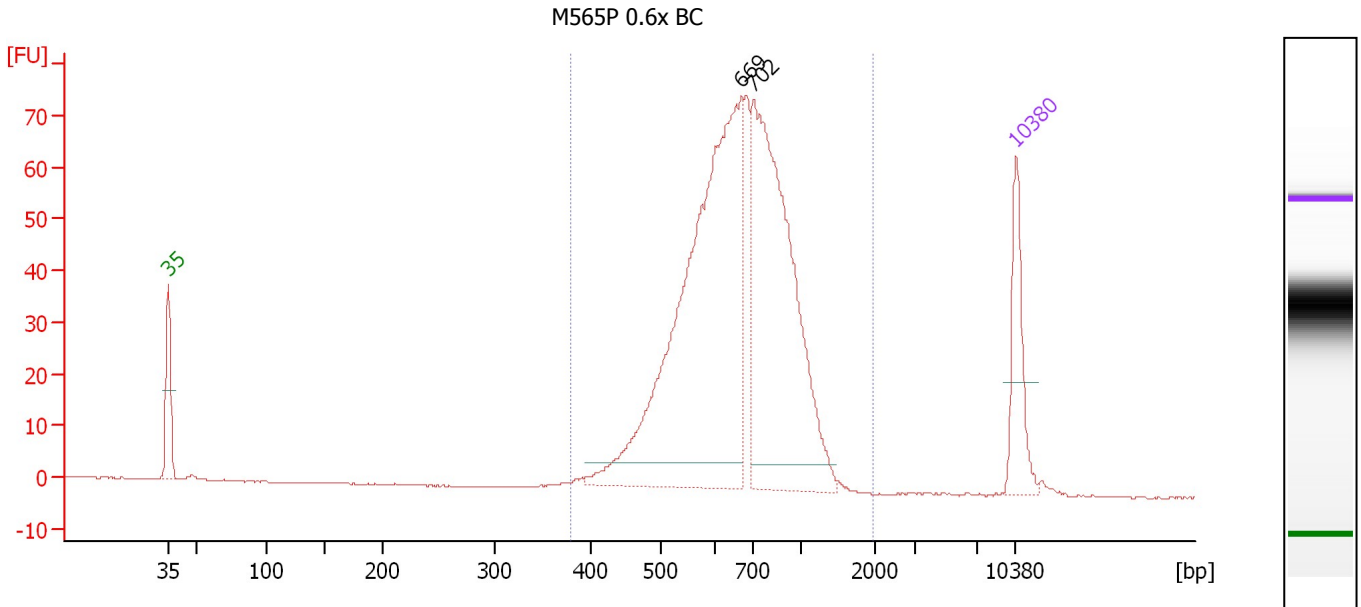
Region table for sample 8 : HiSeq1053 - 28 library

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|------------------|------------|-----------------------------|
| 120 | 1,000 | 319 | 1,355.9 | 9,717.0 | 1,865.04 | 96 | 27.9 |

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

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Electropherogram Summary Continued ...



Overall Results for sample 9 : M565P 0.6x BC

Number of peaks found: 2 Corr. Area 1: 825.5
 Noise: 0.1

Peak table for sample 9 : M565P 0.6x BC

| 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 | 669 | 755.57 | 1,710.0 | | 90.30 |
| 3 | 702 | 531.91 | 1,147.3 | | 91.26 |
| 4 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

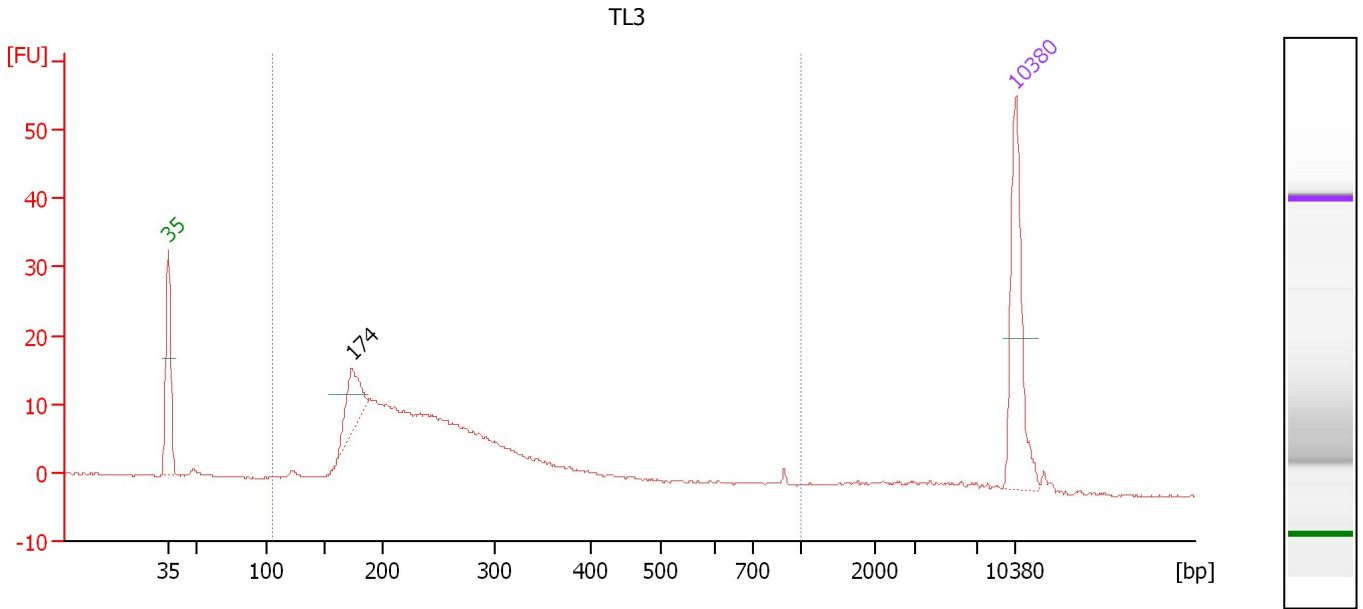
Region table for sample 9 : M565P 0.6x BC

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|----------------------|------------|-----------------------------|
| 379 | 1,974 | 700 | 825.5 | 3,158.2 | 1,363.29 | 99 | 25.5 |

Assay Class: High Sensitivity DNA Assay
 Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
 Modified: 9/14/2017 1:59:02 PM

Electropherogram Summary Continued ...



Overall Results for sample 10 : TL3

Number of peaks found: 1 Corr. Area 1: 244.0
 Noise: 0.1

Peak table for sample 10 : TL3

| 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 | 174 | 51.12 | 444.9 | | 58.17 |
| 3 | 10,380 | 75.00 | 10.9 | Upper Marker | 113.00 |

Region table for sample 10 : TL3

| From [bp] | To [bp] | Average Size [bp] | Corr. Area | Molarity [pmol/l] | Co Conc. lor [pg/μl] | % of Total | Size distribution in CV [%] |
|-----------|---------|-------------------|------------|-------------------|----------------------|------------|-----------------------------|
| 105 | 1,000 | 269 | 244.0 | 3,781.9 | 576.97 | 93 | 43.7 |

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
Modified: 9/14/2017 1:59:02 PM

Gel Image

Assay Class: High Sensitivity DNA Assay
Data Path: C:\... bioanalyzer\2100 expert\data\2017-09-14\2017-09-14_003.xad

Created: 9/14/2017 1:17:35 PM
Modified: 9/14/2017 1:59:02 PM

Invalid Samples

Sample 11 has not been run, no results available.