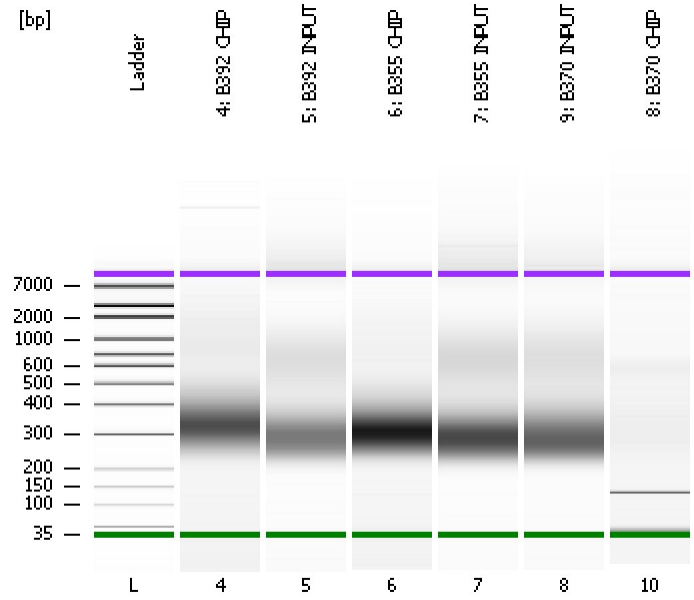
Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electrophoresis File Run Summary



Instrument Information:

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

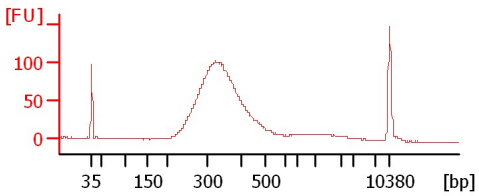
Assay Information:

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

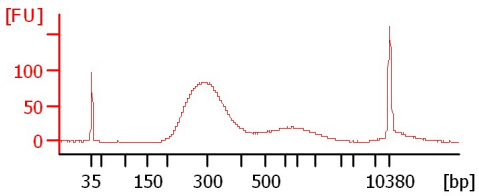
Chip Information:

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

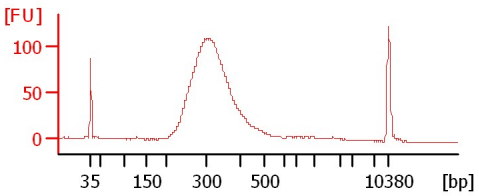
4: B392 CHIP



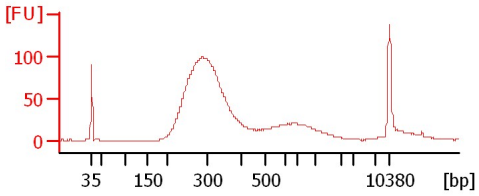
5: B392 INPUT



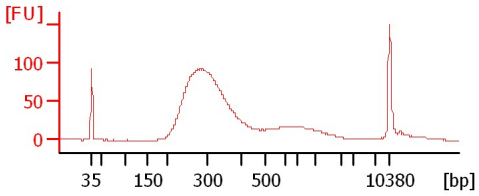
6: B355 CHIP



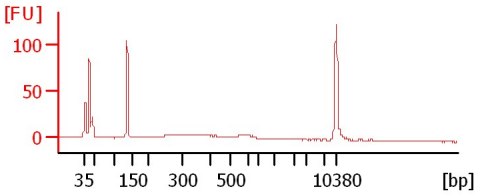
7: B355 INPUT



9: B370 INPUT



8: B370 CHIP



Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electrophoresis File Run Summary (Chip Summary)

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
4: B392 CHIP		☐	✔			
5: B392 INPUT		☐	✔			
6: B355 CHIP		☐	✔			
7: B355 INPUT		☐	✔			
9: B370 INPUT		☐	✔			
8: B370 CHIP		☐	✔			
Ladder		☐	✔			

Chip Lot # **Reagent Kit Lot #**

Chip Comments :

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 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

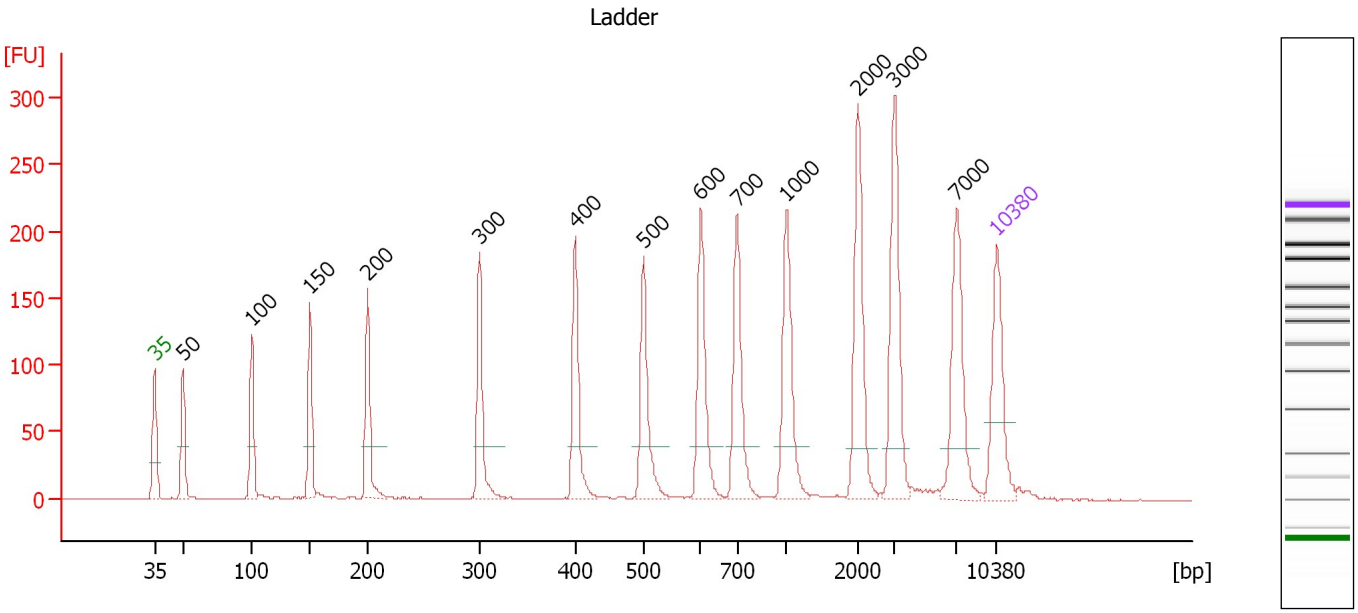
Ladder

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:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary



Overall Results for Ladder

Noise: 0.4

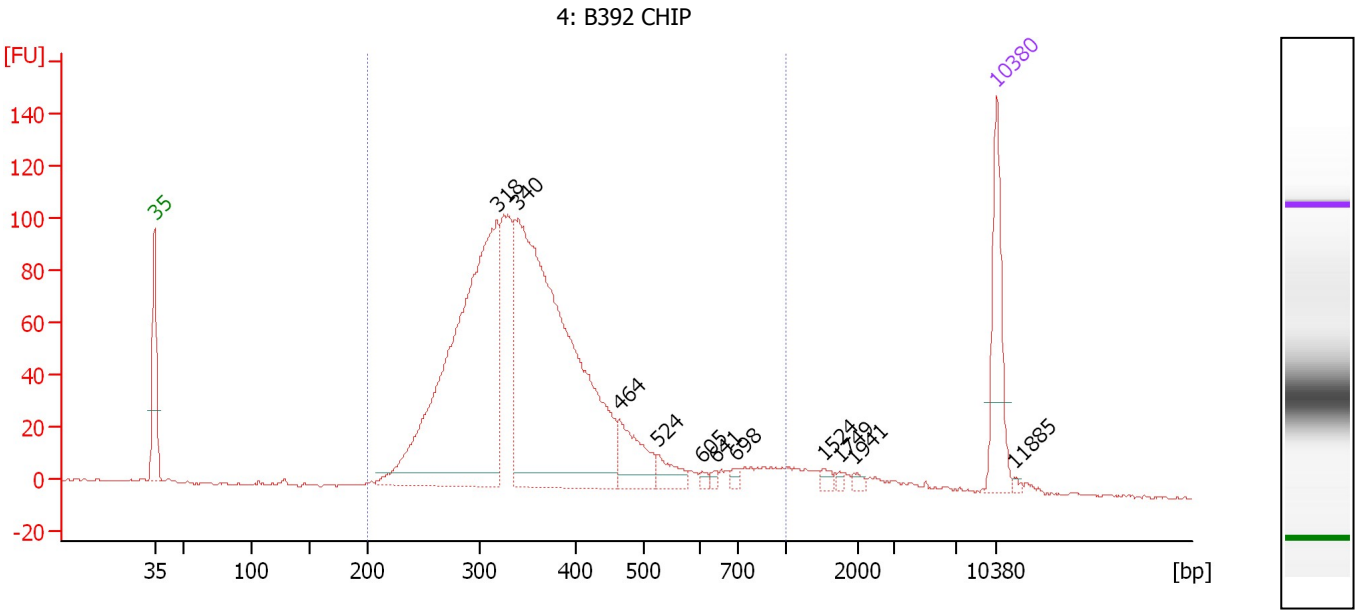
Peak table for Ladder

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	45.36
3		100	150.00	2,272.7	Ladder Peak	51.10
4		150	150.00	1,515.2	Ladder Peak	55.91
5		200	150.00	1,136.4	Ladder Peak	60.72
6		300	150.00	757.6	Ladder Peak	70.02
7		400	150.00	568.2	Ladder Peak	77.98
8		500	150.00	454.5	Ladder Peak	83.62
9		600	150.00	378.8	Ladder Peak	88.39
10		700	150.00	324.7	Ladder Peak	91.39
11		1,000	150.00	227.3	Ladder Peak	95.51
12		2,000	150.00	113.6	Ladder Peak	101.43
13		3,000	150.00	75.8	Ladder Peak	104.49
14		7,000	150.00	32.5	Ladder Peak	109.67
15		10,380	75.00	10.9	Upper Marker	113.00

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 4 : 4: B392 CHIP

Number of peaks found:	11	Corr. Area 1:	1,757.8
Noise:	0.5		

Peak table for sample 4 : 4: B392 CHIP

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	318	642.08	3,056.5		71.47
3	340	704.94	3,141.1		73.20
4	464	62.40	203.6		81.61
5	524	24.66	71.3		84.77
6	605	4.98	12.5		88.53
7	641	3.85	9.1		89.62
8	698	5.59	12.1		91.35
9	1,524	6.27	6.2		98.61
10	1,749	3.22	2.8		99.95
11	1,941	4.99	3.9		101.09
12	10,380	75.00	10.9	Upper Marker	113.00
13	11,885	0.00	0.0		114.48

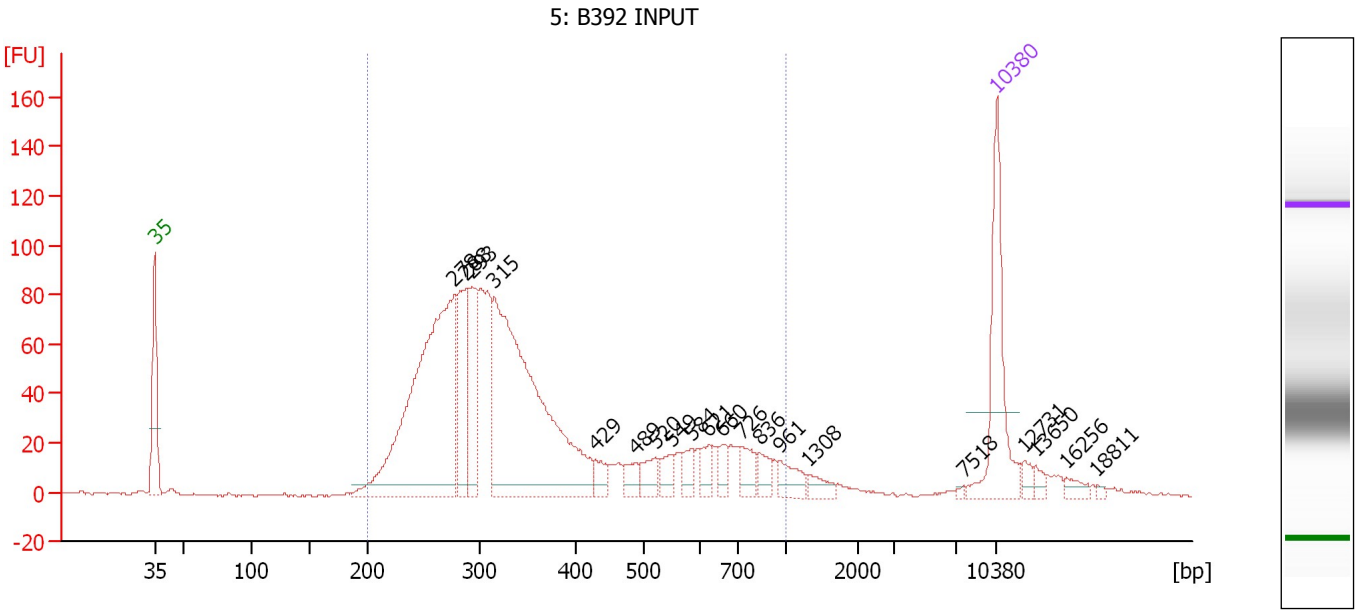
Region table for sample 4 : 4: B392 CHIP

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	369	1,664.48	1,757.8	7,448.7	94	31.0

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 5 : 5: B392 INPUT

Number of peaks found:	20	Corr. Area 1:	1,643.3
Noise:	0.4		

Peak table for sample 5 : 5: B392 INPUT

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	278	373.48	2,039.1		67.93
3	288	84.86	446.8		68.88
4	293	70.82	366.6		69.34
5	315	374.51	1,802.2		71.20
6	429	14.44	51.0		79.61
7	489	13.09	40.6		82.99
8	520	18.53	54.0		84.60
9	549	13.70	37.8		85.96
10	584	13.65	35.4		87.62
11	621	14.42	35.2		89.03
12	660	11.83	27.2		90.19
13	726	17.51	36.6		91.75
14	836	11.48	20.8		93.26
15	961	16.97	26.8		94.97
16	1,308	9.87	11.4		97.34
17	7,518	1.62	0.3		110.18
18	10,380	75.00	10.9	Upper Marker	113.00
19	12,731	0.00	0.0		115.32
20	13,650	0.00	0.0		116.22
21	16,256	0.00	0.0		118.79
22	18,811	0.00	0.0		121.31

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...

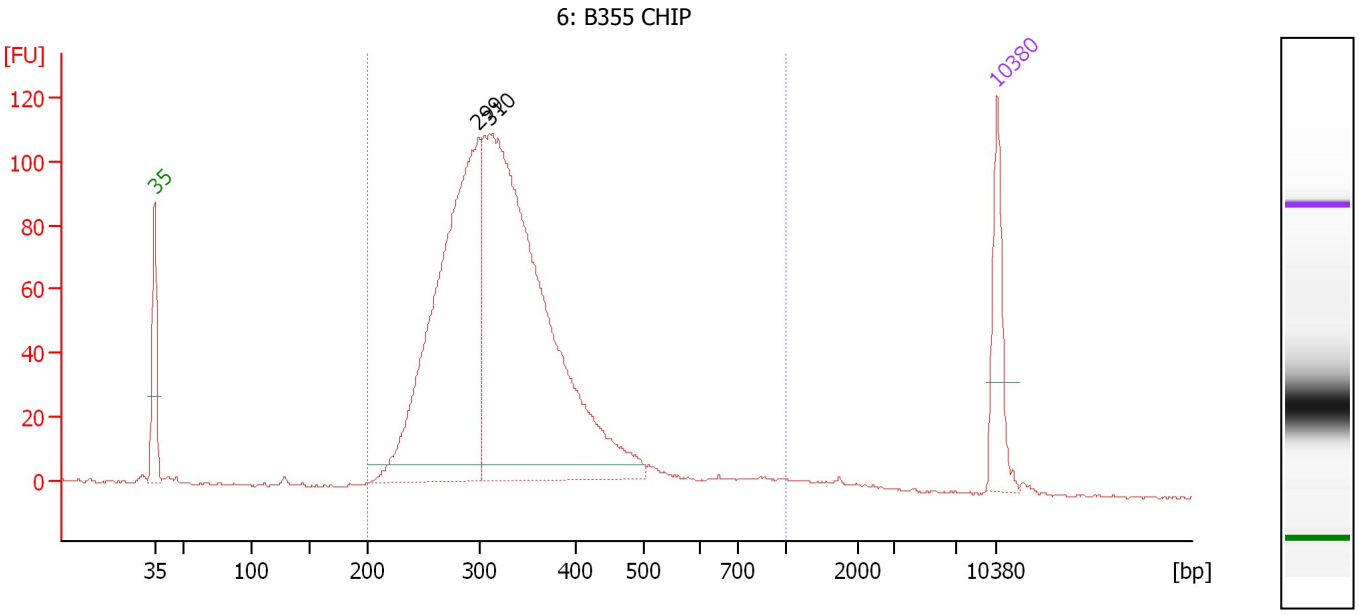
... Region table for sample 5 : 5: B392 INPUT

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	377	1,193.73	1,643.3	5,654.8	92	42.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 6 : 6: B355 CHIP

Number of peaks found:	2	Corr. Area 1:	1,695.2
Noise:	0.3		

Peak table for sample 6 : 6: B355 CHIP

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		299	761.98	3,862.2		69.92
3		310	1,068.60	5,227.3		70.79
4	▶	10,380	75.00	10.9	Upper Marker	113.00

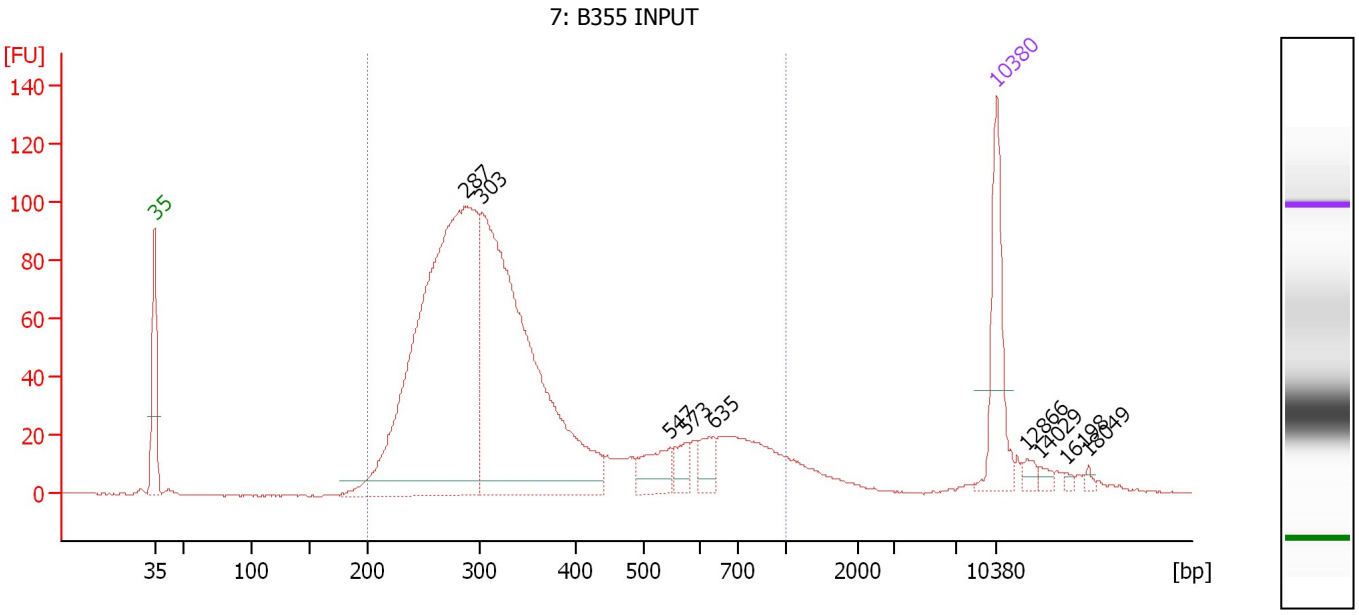
Region table for sample 6 : 6: B355 CHIP

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	337	1,911.36	1,695.2	9,171.8	97	27.5

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 7 : 7: B355 INPUT

Number of peaks found:	9	Corr. Area 1:	1,816.6
Noise:	0.3		

Peak table for sample 7 : 7: B355 INPUT

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	287	806.51	4,259.3		68.80
3	303	655.35	3,276.8		70.26
4	547	41.00	113.6		85.84
5	573	19.03	50.3		87.10
6	635	26.86	64.1		89.44
7	10,380	75.00	10.9	Upper Marker	113.00
8	12,866	0.00	0.0		115.45
9	14,029	0.00	0.0		116.60
10	16,198	0.00	0.0		118.73
11	18,049	0.00	0.0		120.56

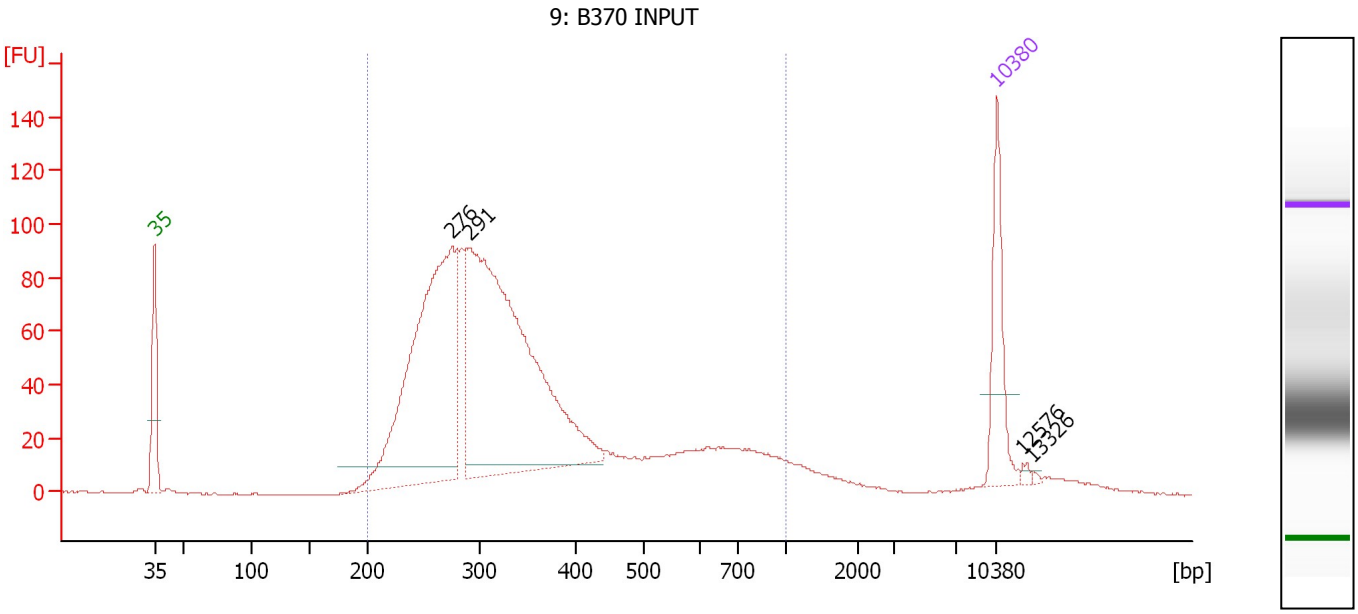
Region table for sample 7 : 7: B355 INPUT

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of Ior Total	Size distribution in CV [%]
200	1,000	369	1,688.04	1,816.6	8,112.4	91	42.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 8 : 9: B370 INPUT

Number of peaks found:	4	Corr. Area 1:	1,797.9
Noise:	0.4		

Peak table for sample 8 : 9: B370 INPUT

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		276	543.51	2,987.0		67.76
3		291	721.84	3,758.1		69.18
4	▶	10,380	75.00	10.9	Upper Marker	113.00
5		12,576	0.00	0.0		115.16
6		13,326	0.00	0.0		115.90

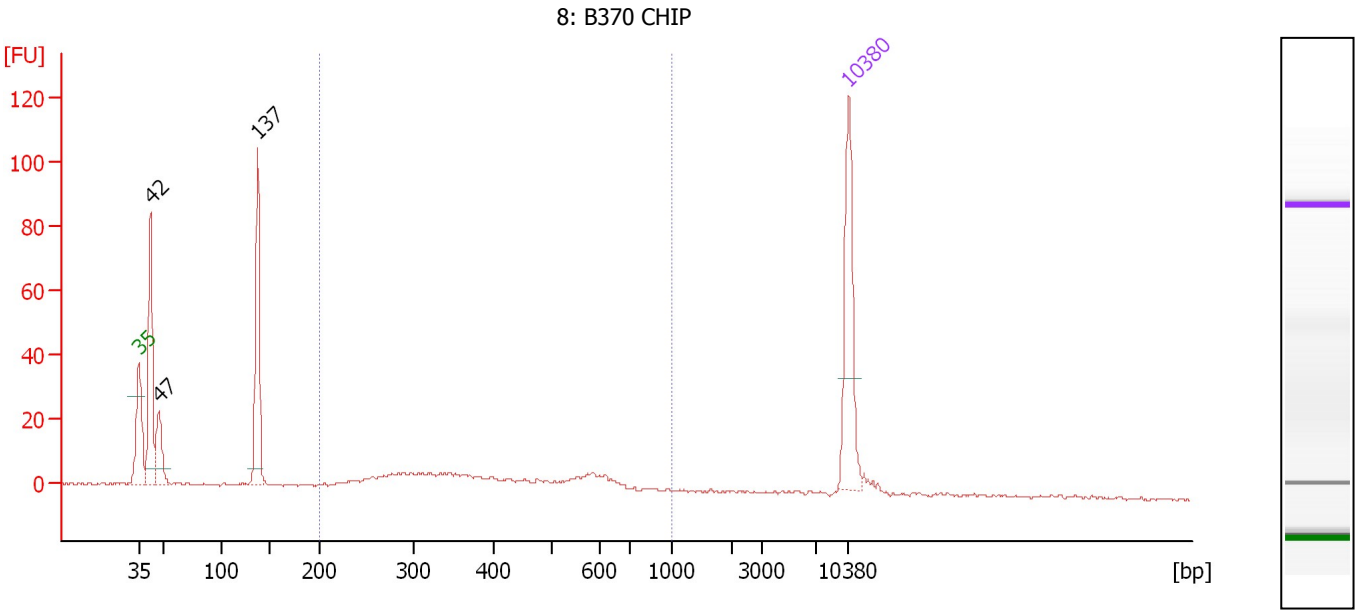
Region table for sample 8 : 9: B370 INPUT

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of Total	Size distribution in CV [%]
200	1,000	366	1,719.71	1,797.9	8,278.2	92	41.4

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

Electropherogram Summary Continued ...



Overall Results for sample 10 : 8: B370 CHIP

Number of peaks found:	3	Corr. Area 1:	135.3
Noise:	0.4		

Peak table for sample 10 : 8: B370 CHIP

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	42	141.40	5,098.6		44.10
3	47	51.02	1,631.9		44.95
4	137	128.22	1,416.1		54.68
5	10,380	75.00	10.9	Upper Marker	113.00

Region table for sample 10 : 8: B370 CHIP

From [bp]	To [bp]	Average Size [bp]	Conc. [pg/µl]	Corr. Area	Molarity [pmol/l]	Co % of lor Total	Size distribution in CV [%]
200	1,000	421	145.01	135.3	610.7	36	34.3

Assay Class: High Sensitivity DNA Assay
Data Path: C:\...rt\data\2018-06-12\2018-06-12_002_NovaSeq_004_Libraries.xad

Created: 6/12/2018 5:27:46 PM
Modified: 6/13/2018 7:54:12 AM

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