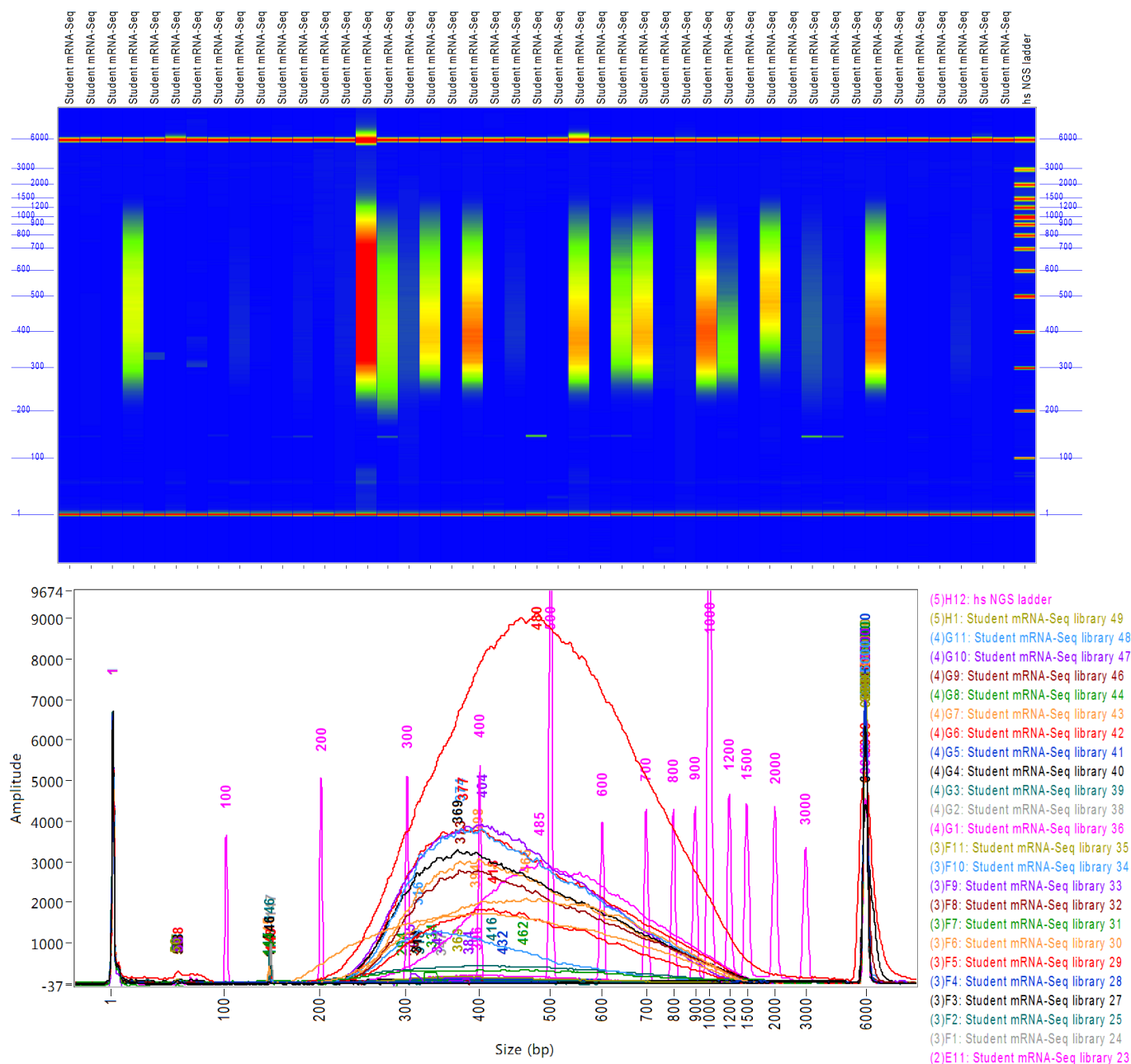


Project Summary:

Data Files: 2019 08 02 17H 40M.raw, 2019 08 02 22H 25M.raw, 2019 08 02 18H 51M.raw, 2019 08 02 20H 02M.raw, 2019 08 02 21H 14M.raw,



Filename and Data Path: C:\AATI\Data\2019 08 02\2019 08 02 Student mRNA-Seq library-1 h
s NGS 17-40-28\2019 08 02 17H 40M.raw

Created: Friday, August 02, 2019 5:56:32 PM

of Capillaries: 12

Array Serial #: 021919-03SFS

Effect Length: 33 cm

Array Usage Count: 236

: 1.2.0.11

Device Serial #: 2730

METHOD INFORMATION

Method Name: DNF-474-33 - HS NGS Fragment 1-6000bp.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 1

Perform Prerun: 6.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: A, # Dips: 1

Sample Injection: 5.0 kV, 30 sec.

Separation: 6.0 kV, 55.0 min.

Tray Name: Tray-1

Analysis Mode: NGS

NOTE

Filename and Data Path: C:\AATI\Data\2019 08 02\2019_08_02_StudentLibs_rowE_hs_NGS 22-2
5-31\2019 08 02 22H 25M.raw

Created: Friday, August 02, 2019 10:41:33 PM

of Capillaries: 12

Array Serial #: 021919-03SFS

Effect Length: 33 cm

Array Usage Count: 240

: 1.2.0.11

Device Serial #: 2730

METHOD INFORMATION

Method Name: DNF-474-33 - HS NGS Fragment 1-6000bp.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 1

Perform Prerun: 6.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: A, # Dips: 1

Sample Injection: 5.0 kV, 30 sec.

Separation: 6.0 kV, 55.0 min.

Tray Name: Tray-1

Analysis Mode: NGS

NOTE

Filename and Data Path: C:\AATI\Data\2019 08 02\2019 08 02 Student mRNA-Seq library-3 h
s NGS 18-51-44\2019 08 02 18H 51M.raw

Created: Friday, August 02, 2019 7:07:47 PM

of Capillaries: 12

Array Serial #: 021919-03SFS

Effect Length: 33 cm

Array Usage Count: 237

: 1.2.0.11

Device Serial #: 2730

METHOD INFORMATION

Method Name: DNF-474-33 - HS NGS Fragment 1-6000bp.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 1

Perform Prerun: 6.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: A, # Dips: 1

Sample Injection: 5.0 kV, 30 sec.

Separation: 6.0 kV, 55.0 min.

Tray Name: Tray-1

Analysis Mode: NGS

NOTE

Filename and Data Path: C:\AATI\Data\2019 08 02\2019 08 02 Student mRNA-Seq library-4 h
s NGS 20-02-59\2019 08 02 20H 02M.raw

Created: Friday, August 02, 2019 8:19:03 PM

of Capillaries: 12

Array Serial #: 021919-03SFS

Effect Length: 33 cm

Array Usage Count: 238

: 1.2.0.11

Device Serial #: 2730

METHOD INFORMATION

Method Name: DNF-474-33 - HS NGS Fragment 1-6000bp.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 1

Perform Prerun: 6.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: A, # Dips: 1

Sample Injection: 5.0 kV, 30 sec.

Separation: 6.0 kV, 55.0 min.

Tray Name: Tray-1

Analysis Mode: NGS

NOTE

Filename and Data Path: C:\AATI\Data\2019 08 02\2019 08 02 Student mRNA-Seq library-5 h
s NGS 21-14-15\2019 08 02 21H 14M.raw

Created: Friday, August 02, 2019 9:30:19 PM

of Capillaries: 12

Array Serial #: 021919-03SFS

Effect Length: 33 cm

Array Usage Count: 239

: 1.2.0.11

Device Serial #: 2730

METHOD INFORMATION

Method Name: DNF-474-33 - HS NGS Fragment 1-6000bp.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 1

Perform Prerun: 6.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: A, # Dips: 1

Sample Injection: 5.0 kV, 30 sec.

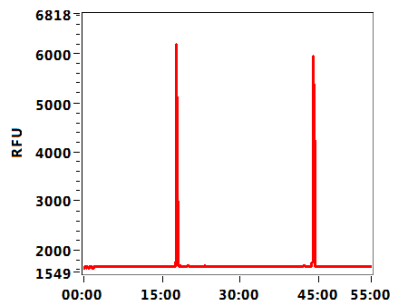
Separation: 6.0 kV, 55.0 min.

Tray Name: Tray-1

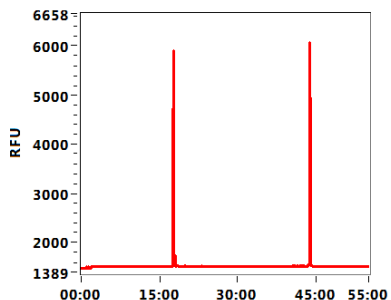
Analysis Mode: NGS

NOTE

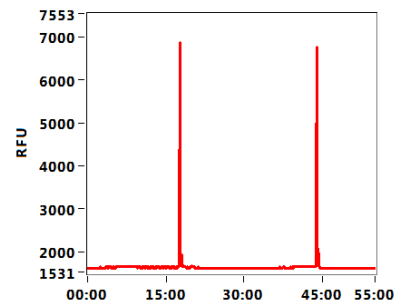
2019 08 02 17H 40M.raw
D1: Student mRNA-Seq library 1



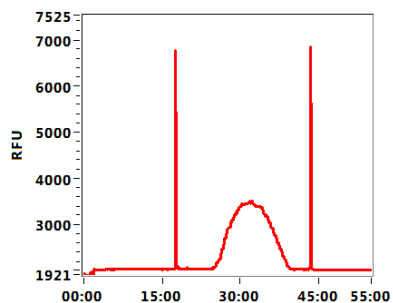
2019 08 02 17H 40M.raw
D2: Student mRNA-Seq library 2



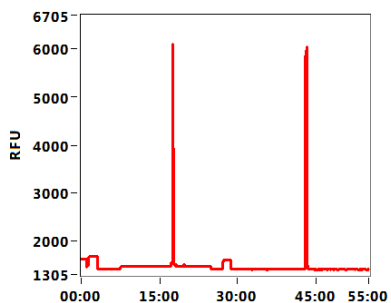
2019 08 02 17H 40M.raw
D3: Student mRNA-Seq library 3 or 7



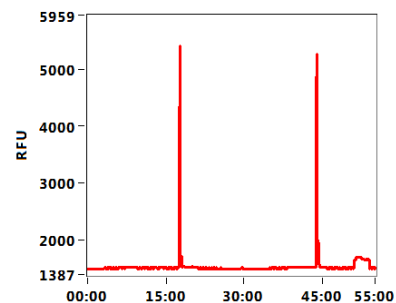
2019 08 02 17H 40M.raw
D4: Student mRNA-Seq library 4



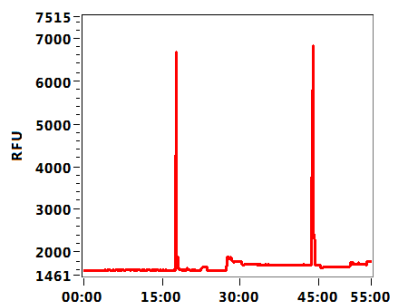
2019 08 02 17H 40M.raw
D5: Student mRNA-Seq library 6



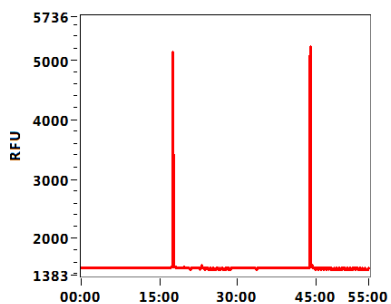
2019 08 02 17H 40M.raw
D6: Student mRNA-Seq library 7 or 3



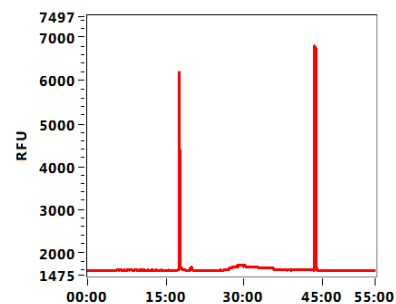
2019 08 02 17H 40M.raw
D7: Student mRNA-Seq library 8



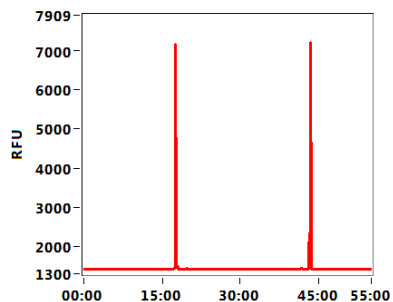
2019 08 02 17H 40M.raw
D8: Student mRNA-Seq library 9



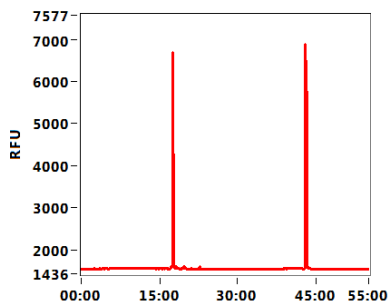
2019 08 02 17H 40M.raw
D9: Student mRNA-Seq library 10



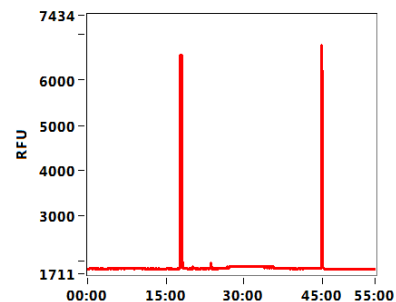
2019 08 02 17H 40M.raw
D10: Student mRNA-Seq library 11



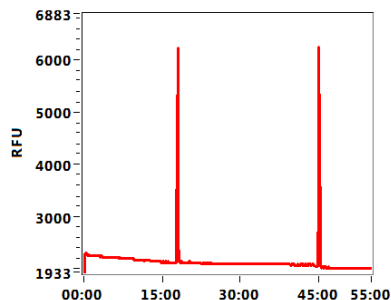
2019 08 02 17H 40M.raw
D11: Student mRNA-Seq library 12



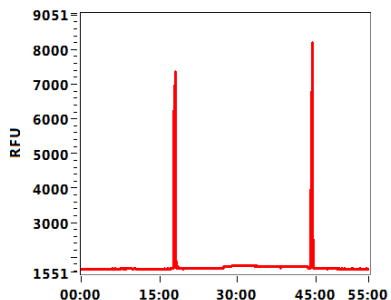
2019 08 02 22H 25M.raw
E1: Student mRNA-Seq library 13



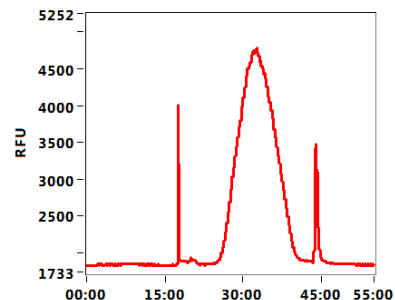
2019 08 02 22H 25M.raw
E2: Student mRNA-Seq library 14



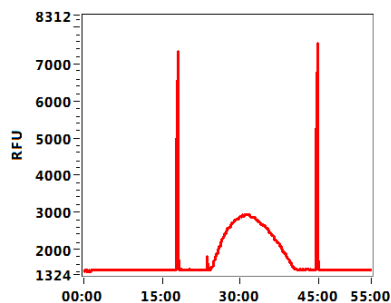
2019 08 02 22H 25M.raw
E3: Student mRNA-Seq library 15



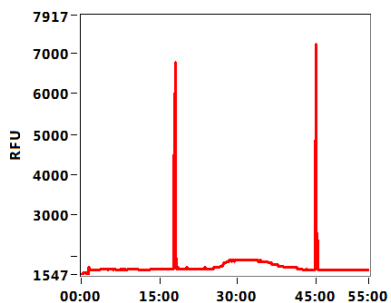
2019 08 02 22H 25M.raw
E4: Student mRNA-Seq library 16



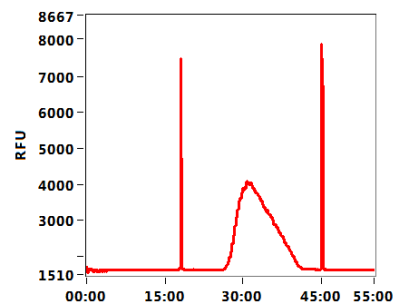
2019 08 02 22H 25M.raw
E5: Student mRNA-Seq library 17



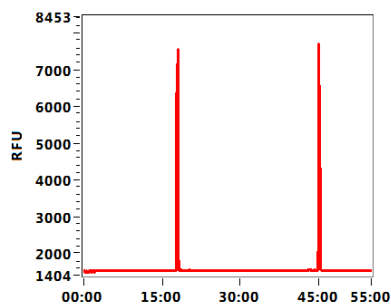
2019 08 02 22H 25M.raw
E6: Student mRNA-Seq library 18



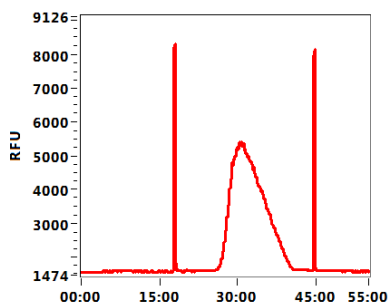
2019 08 02 22H 25M.raw
E7: Student mRNA-Seq library 19



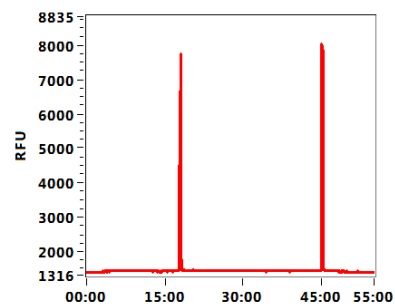
2019 08 02 22H 25M.raw
E8: Student mRNA-Seq library 20



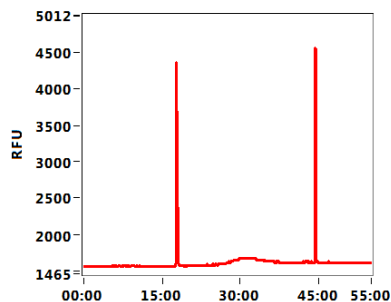
2019 08 02 22H 25M.raw
E9: Student mRNA-Seq library 21



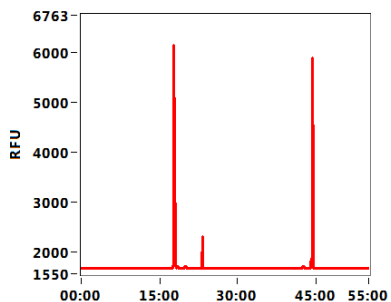
2019 08 02 22H 25M.raw
E10: Student mRNA-Seq library 22



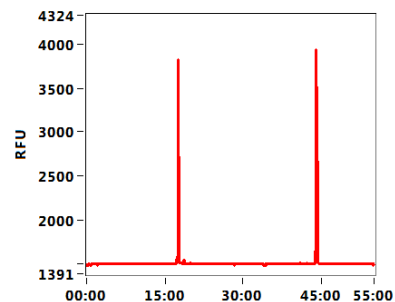
2019 08 02 22H 25M.raw
E11: Student mRNA-Seq library 23



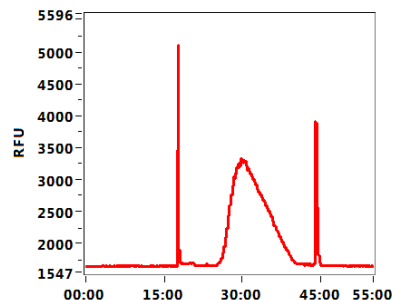
2019 08 02 18H 51M.raw
F1: Student mRNA-Seq library 24



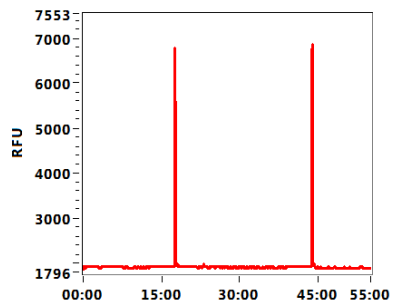
2019 08 02 18H 51M.raw
F2: Student mRNA-Seq library 25



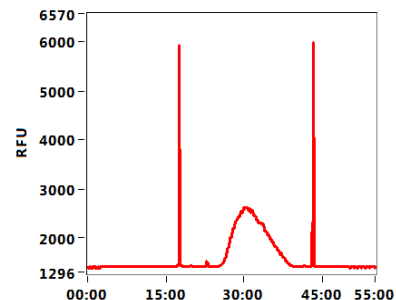
2019 08 02 18H 51M.raw
F3: Student mRNA-Seq library 27



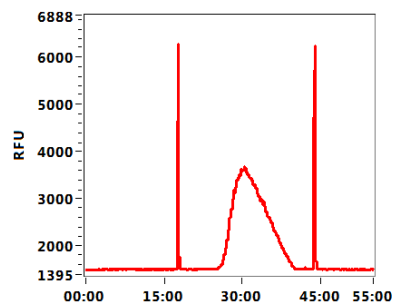
2019 08 02 18H 51M.raw
F4: Student mRNA-Seq library 28



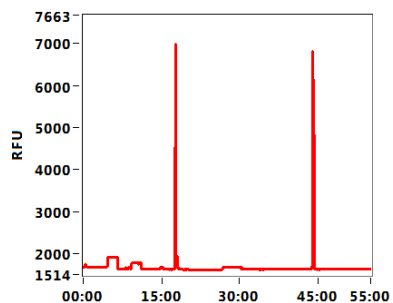
2019 08 02 18H 51M.raw
F5: Student mRNA-Seq library 29



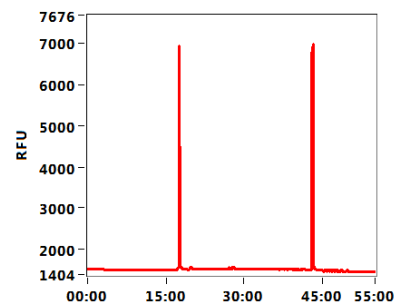
2019 08 02 18H 51M.raw
F6: Student mRNA-Seq library 30



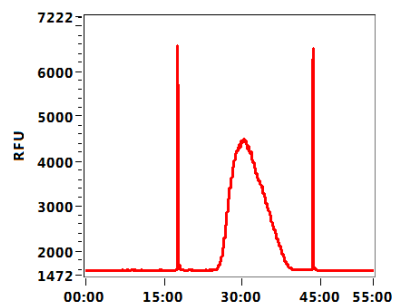
2019 08 02 18H 51M.raw
F7: Student mRNA-Seq library 31



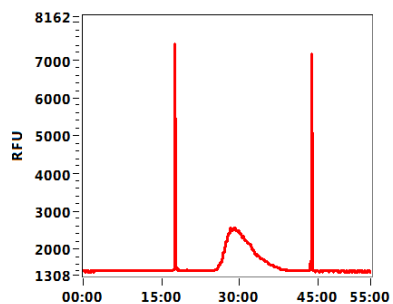
2019 08 02 18H 51M.raw
F8: Student mRNA-Seq library 32



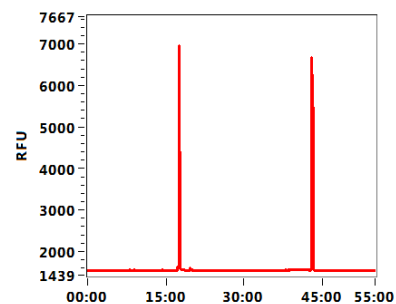
2019 08 02 18H 51M.raw
F9: Student mRNA-Seq library 33



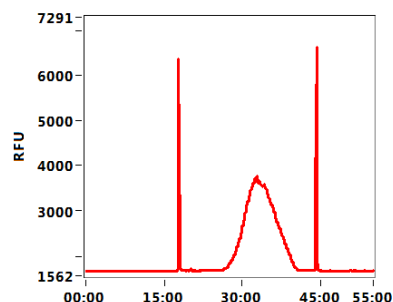
2019 08 02 18H 51M.raw
F10: Student mRNA-Seq library 34



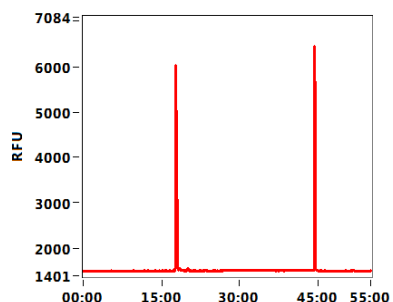
2019 08 02 18H 51M.raw
F11: Student mRNA-Seq library 35



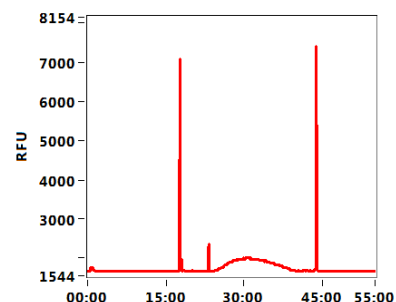
2019 08 02 20H 02M.raw
G1: Student mRNA-Seq library 36



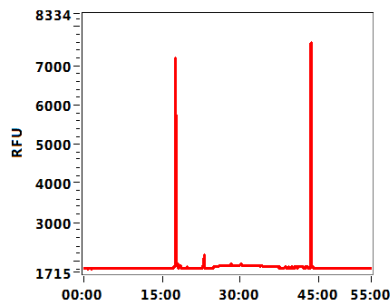
2019 08 02 20H 02M.raw
G2: Student mRNA-Seq library 38



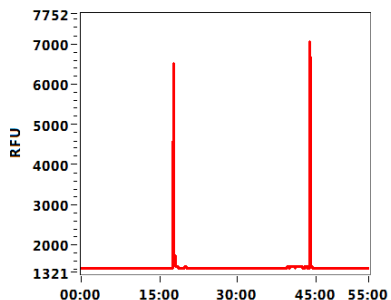
2019 08 02 20H 02M.raw
G3: Student mRNA-Seq library 39



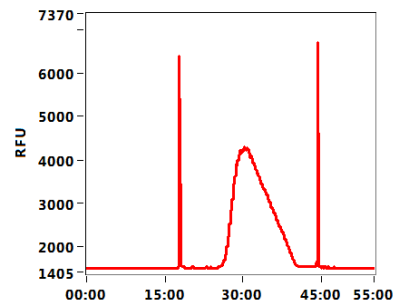
2019 08 02 20H 02M.raw
G4: Student mRNA-Seq library 40



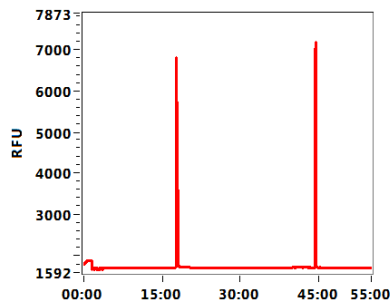
2019 08 02 20H 02M.raw
G5: Student mRNA-Seq library 41



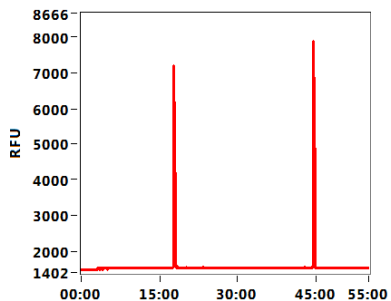
2019 08 02 20H 02M.raw
G6: Student mRNA-Seq library 42



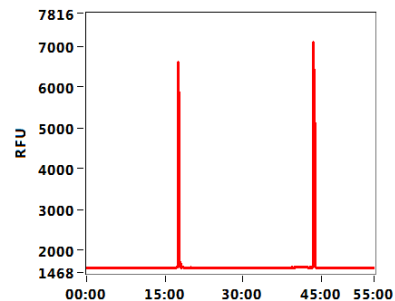
2019 08 02 20H 02M.raw
G7: Student mRNA-Seq library 43



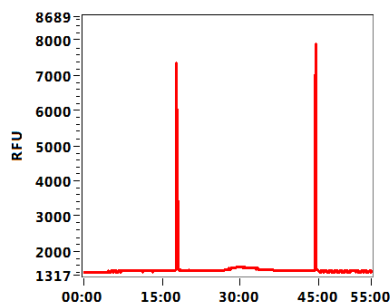
2019 08 02 20H 02M.raw
G8: Student mRNA-Seq library 44



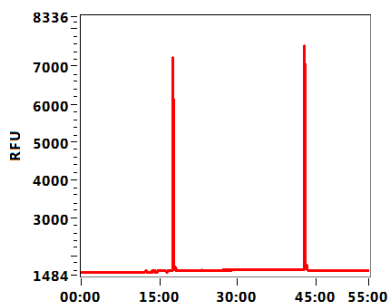
2019 08 02 20H 02M.raw
G9: Student mRNA-Seq library 46



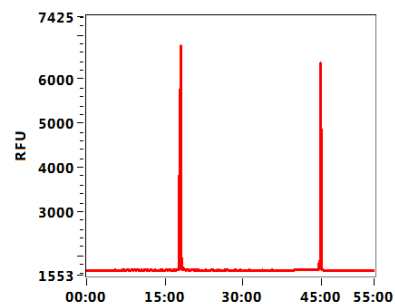
2019 08 02 20H 02M.raw
G10: Student mRNA-Seq library 47



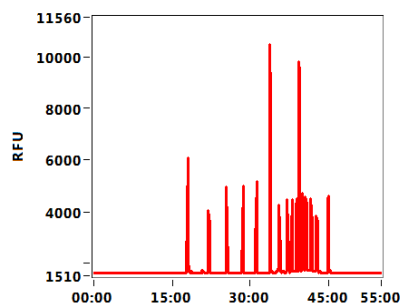
2019 08 02 20H 02M.raw
G11: Student mRNA-Seq library 48



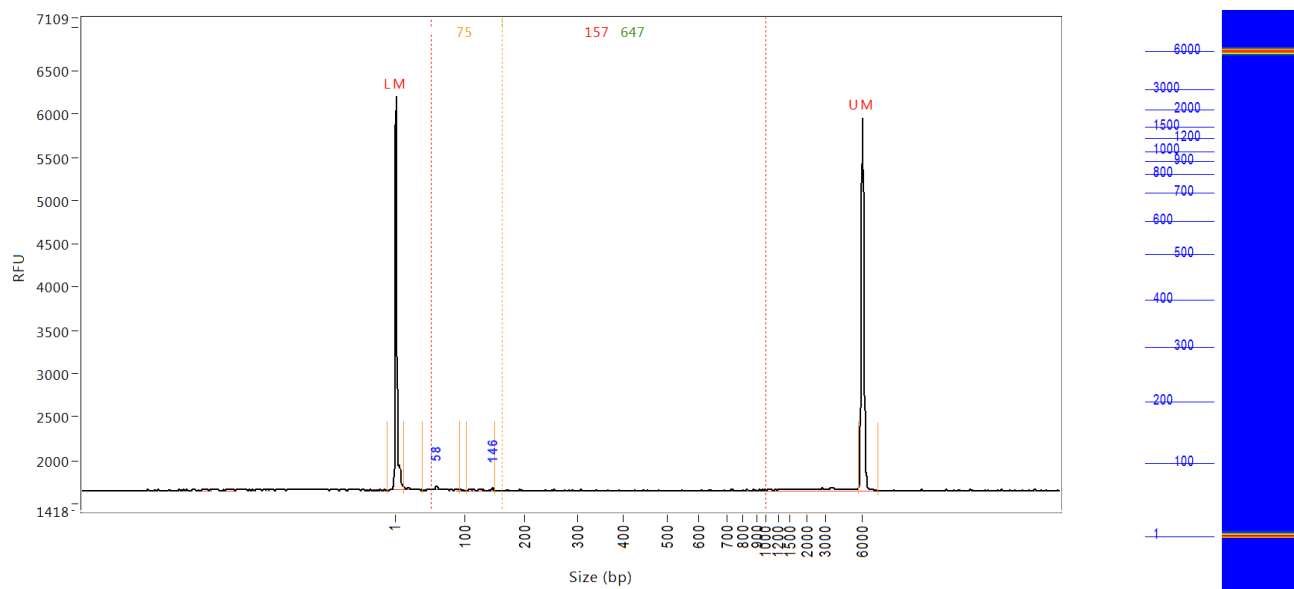
2019 08 02 21H 14M.raw
H1: Student mRNA-Seq library 49



2019 08 02 21H 14M.raw
H12: hs NGS ladder



Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 1
Well Location: D1

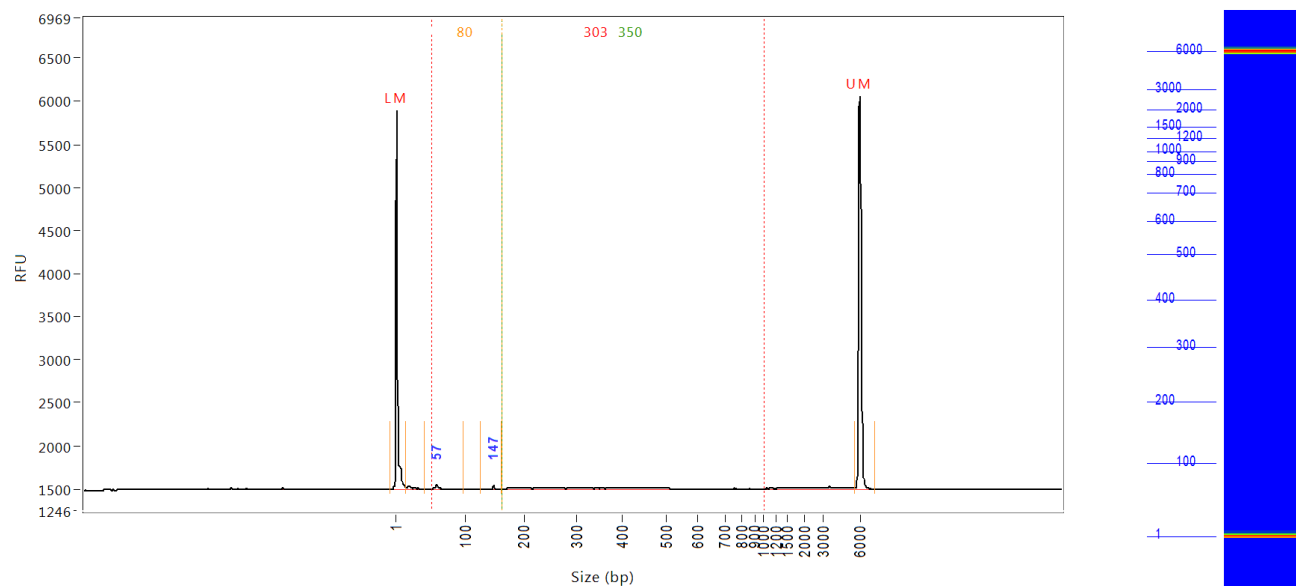


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	182.41	4541	26.474
2	58	0.0025	39	92	61	15.06	43	0.611
3	146	0.0005	101	149	136	10.54	24	0.130
4	6000 (UM)	0.0061	5634	7284	5979	1.92	4297	17.643
	TIC:	0.0031	ng/uL					
	TIM:	0.0746	nmole/L					
	Total Conc.:	0.0112	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0035 ng/ul	31.0 %Total	0.0365 nmole/L	157 Avg. Size (bp)	140.80 %CV
	50 bp to 160 bp	0.0030 ng/ul	26.5 %Total	0.0651 nmole/L	75 Avg. Size (bp)	40.62 %CV
	160 bp to 1000 bp	0.0005 ng/ul	4.4 %Total	0.0013 nmole/L	647 Avg. Size (bp)	36.35 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 2
Well Location: D2

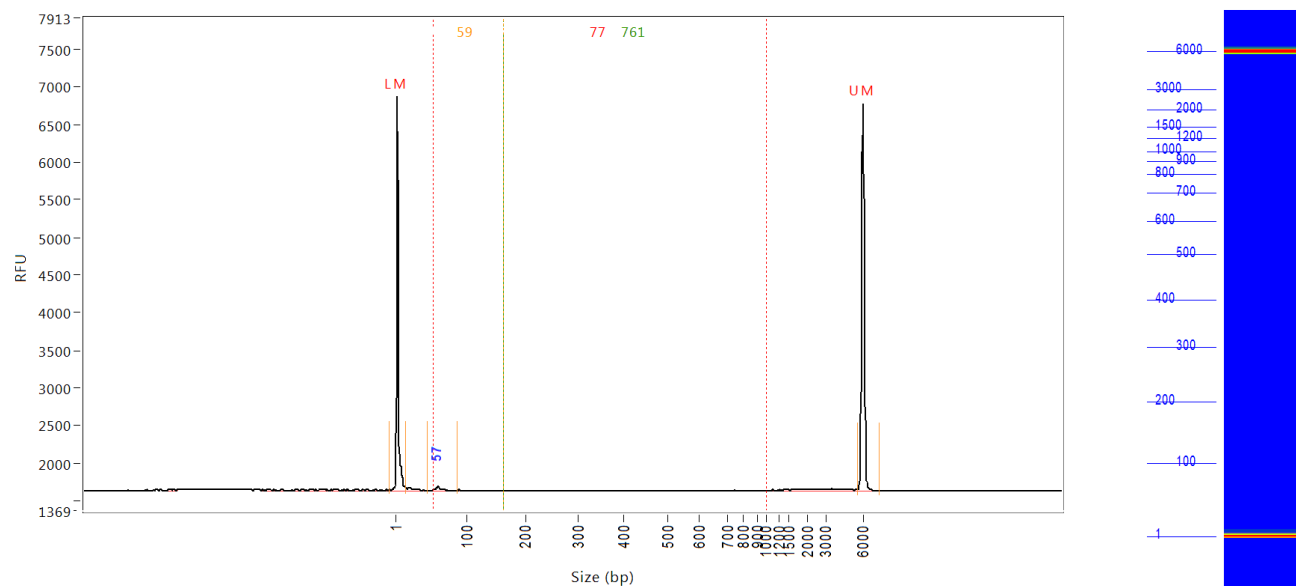


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	199.80	4392	25.880
2	57	0.0026	41	95	59	13.75	44	0.606
3	147	0.0007	125	162	146	2.23	43	0.168
4	6000 (UM)	0.0067	5537	7260	5987	1.95	4555	18.872
TIC:		0.0033	ng/uL					
TIM:		0.0795	nmole/L					
Total Conc.:		0.0285	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0188 ng/ul	66.0 %Total	0.1021 nmole/L	303 Avg. Size (bp)	56.53 %CV
	50 bp to 160 bp	0.0033 ng/ul	11.5 %Total	0.0669 nmole/L	80 Avg. Size (bp)	44.84 %CV
	160 bp to 1000 bp	0.0155 ng/ul	54.5 %Total	0.0731 nmole/L	350 Avg. Size (bp)	43.03 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

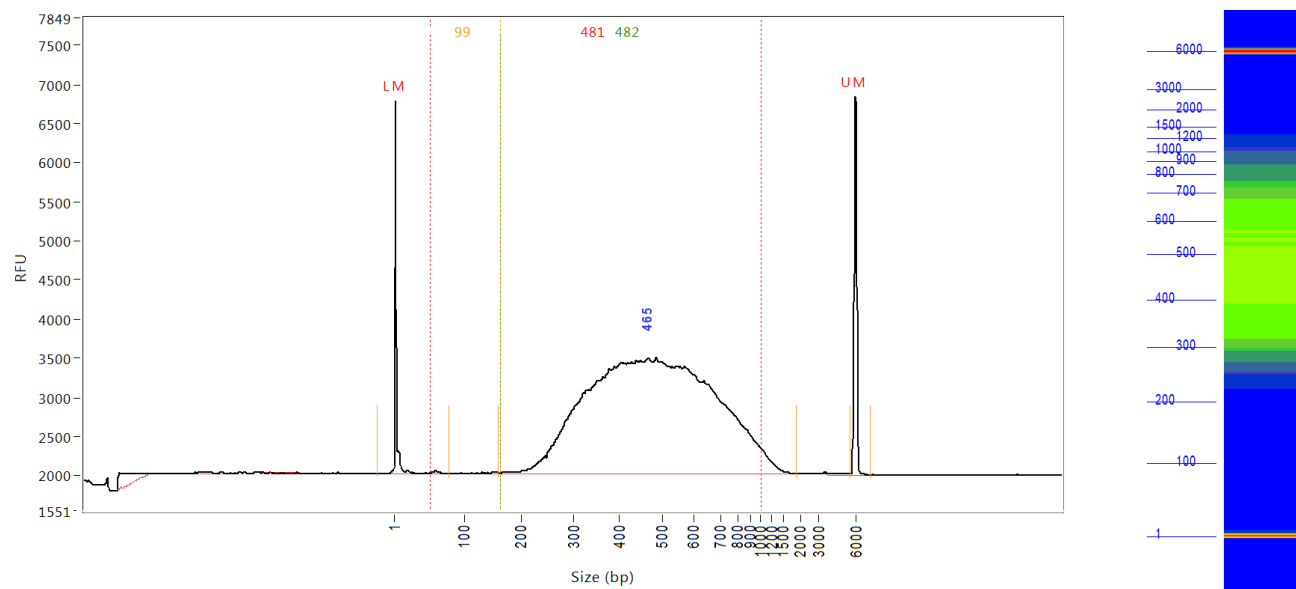
Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 3 or 7
Well Location: D3



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	166.18	5224	30.209
2	57	0.0020	43	87	58	8.64	45	0.543
3	6000 (UM)	0.0064	5634	7357	5992	1.80	5142	20.960
	TIC:	0.0020	ng/uL					
	TIM:	0.0558	nmole/L					
	Total Conc.:	0.0084	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0020 ng/ul	23.9 %Total		0.0427 nmole/L	77 Avg. Size (bp)	147.00 %CV	
	50 bp to 160 bp	0.0020 ng/ul	23.3 %Total		0.0546 nmole/L	59 Avg. Size (bp)	9.22 %CV	
	160 bp to 1000 bp	0.0001 ng/ul	0.6 %Total		0.0001 nmole/L	761 Avg. Size (bp)	12.58 %CV	

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 4
Well Location: D4

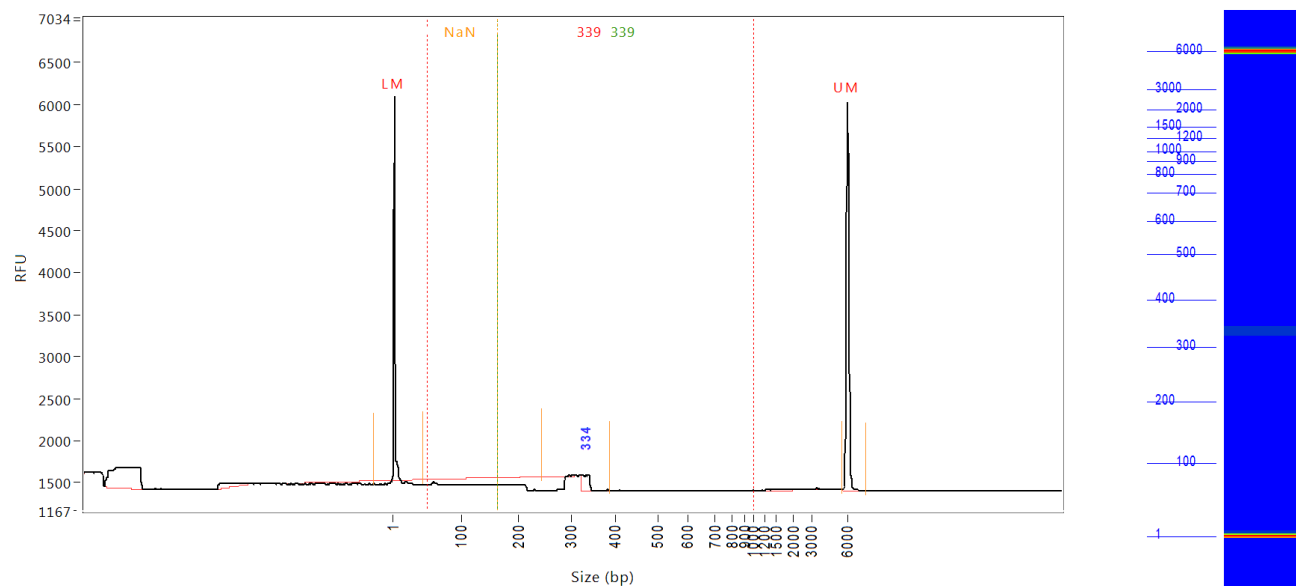


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	78	3	298.24	4752	28.423
2	465	1.6005	161	1921	491	35.45	1484	414.182
3	6000 (UM)	0.0062	5634	7211	5986	1.80	4826	19.233
TIC:		1.6005	ng/uL					
TIM:		5.3638	nmole/L					
Total Conc.:		1.6065	ng/uL					

Smear Analysis	50 bp to 1000 bp	1.5819 ng/ul	98.5 %Total	5.4148 nmole/L	481 Avg. Size (bp)	32.30 %CV
	50 bp to 160 bp	0.0042 ng/ul	0.3 %Total	0.0697 nmole/L	99 Avg. Size (bp)	38.96 %CV
	160 bp to 1000 bp	1.5776 ng/ul	98.2 %Total	5.3889 nmole/L	482 Avg. Size (bp)	32.01 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 6
Well Location: D5



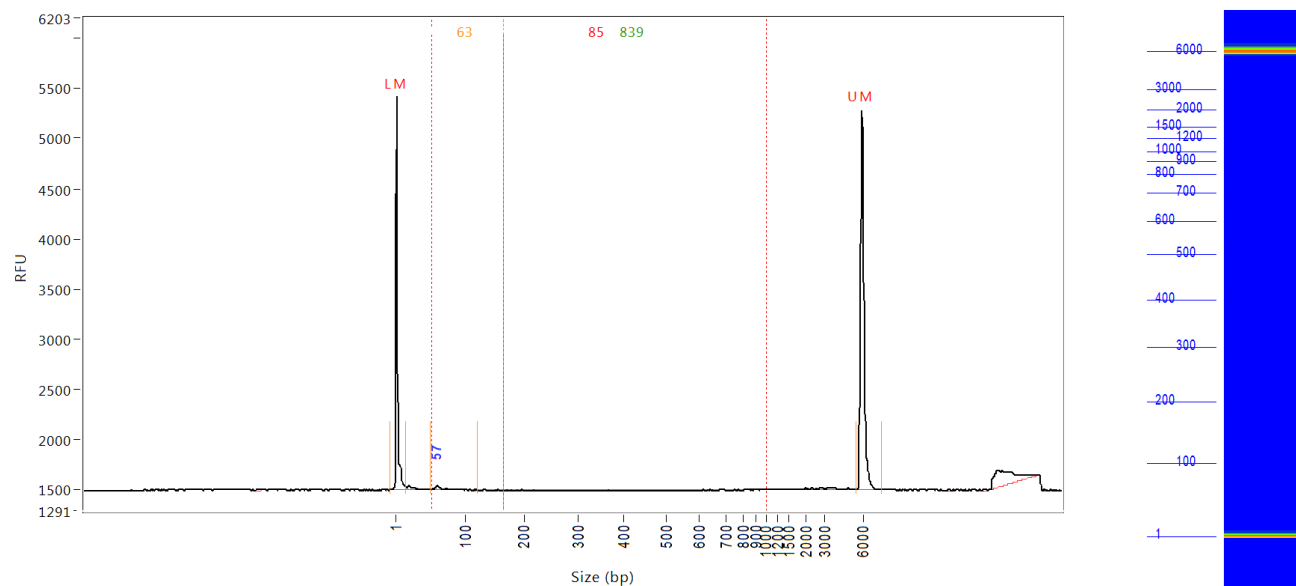
Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	45	1	167.59	4568	24.870
2	334	0.0141	244	387	333	2.55	181	3.199
3	6000 (UM)	0.0069	5610	7526	5997	1.95	4615	18.712

TIC: 0.0141 ng/uL
TIM: 0.0698 nmole/L
Total Conc.: 0.0174 ng/uL

Smear Analysis	50 bp to 1000 bp	0.0143 ng/ul	82.0 %Total	0.0691 nmole/L	339 Avg. Size (bp)	18.54 %CV
	50 bp to 160 bp	0.0000 ng/ul	0.0 %Total	NaN nmole/L	NaN Avg. Size (bp)	NaN %CV
	160 bp to 1000 bp	0.0143 ng/ul	82.0 %Total	0.0691 nmole/L	339 Avg. Size (bp)	18.54 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 28
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 7 or 3
Well Location: D6

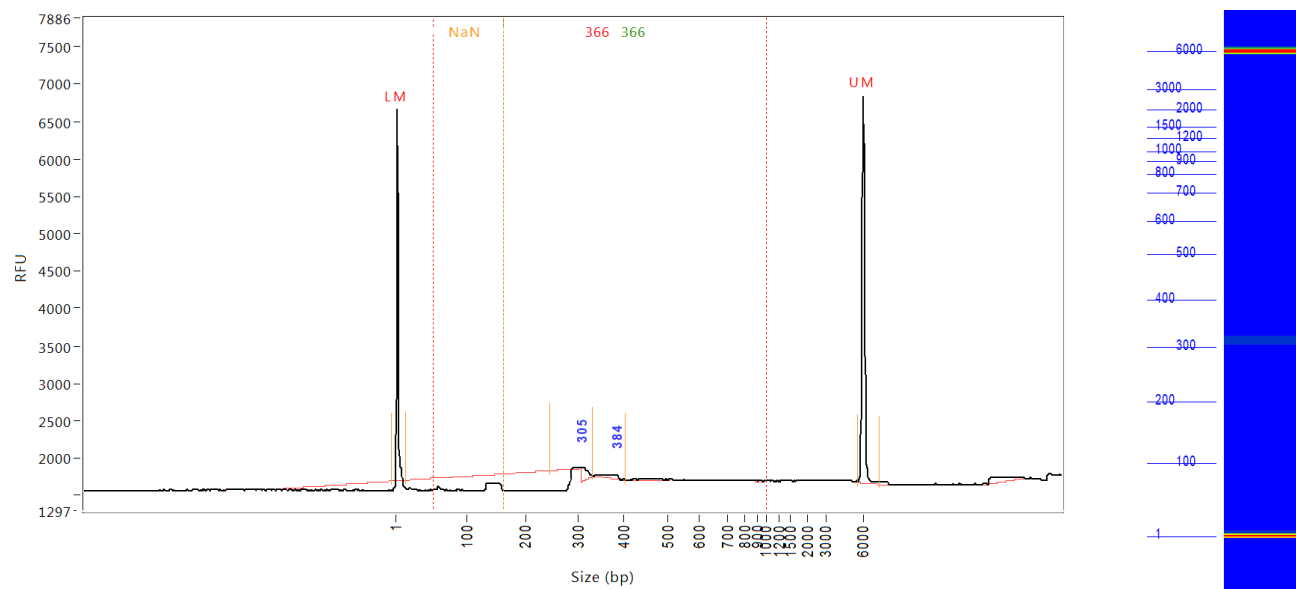


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	193.86	3916	23.063
2	57	0.0040	49	120	63	13.83	42	0.833
3	6000 (UM)	0.0076	5561	7599	6038	3.07	3774	19.178
TIC:		0.0040	ng/uL					
TIM:		0.1032	nmole/L					
Total Conc.:		0.0138	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0041 ng/ul	29.3 %Total	0.0784 nmole/L	85 Avg. Size (bp)	153.45 %CV
	50 bp to 160 bp	0.0039 ng/ul	28.5 %Total	0.1030 nmole/L	63 Avg. Size (bp)	13.76 %CV
	160 bp to 1000 bp	0.0001 ng/ul	0.9 %Total	0.0002 nmole/L	839 Avg. Size (bp)	9.35 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
 Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
 Manual Baseline Start (min): 10 Manual Baseline End (min): 47
 Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
 Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
 Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
 Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 8
Well Location: D7



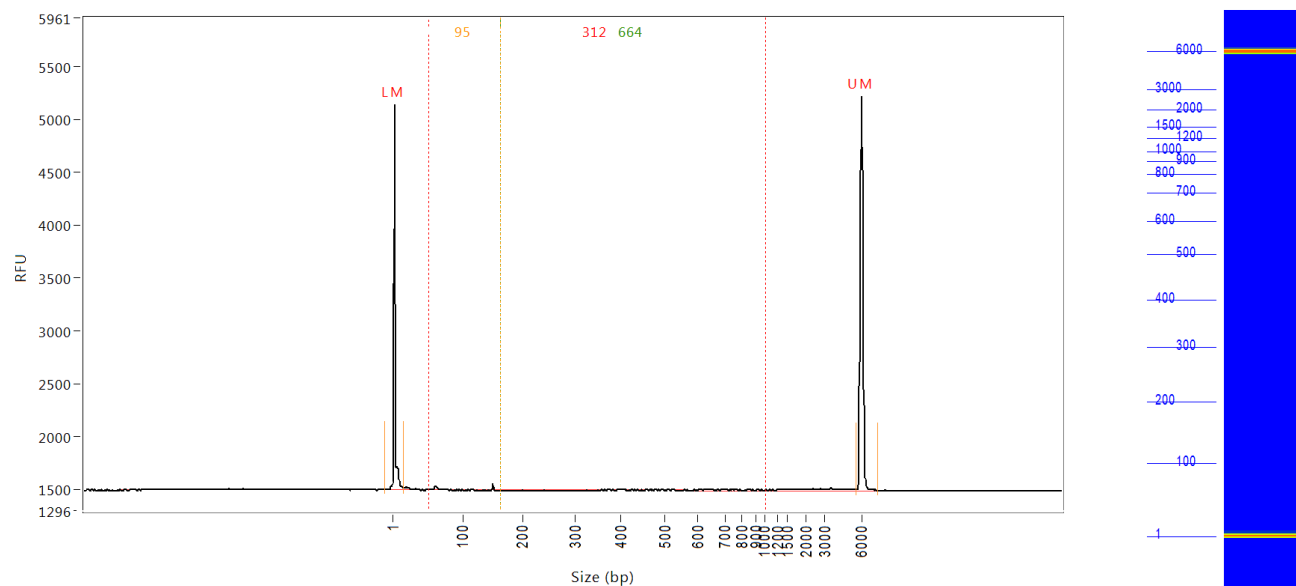
Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	141.46	4971	25.623
2	305	0.0103	245	331	311	2.25	183	2.410
3	384	0.0076	331	405	367	3.86	68	1.772
4	6000 (UM)	0.0078	5610	7284	6009	2.65	5165	21.830

TIC: 0.0179 ng/uL
TIM: 0.0887 nmole/L
Total Conc.: 0.0228 ng/uL

Smear Analysis	50 bp to 1000 bp	0.0214 ng/uL	93.7 %Total	0.0963 nmole/L	366 Avg. Size (bp)	24.37 %CV
	50 bp to 160 bp	0.0000 ng/uL	0.0 %Total	NaN nmole/L	NaN Avg. Size (bp)	NaN %CV
	160 bp to 1000 bp	0.0214 ng/uL	93.7 %Total	0.0963 nmole/L	366 Avg. Size (bp)	24.37 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 28
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

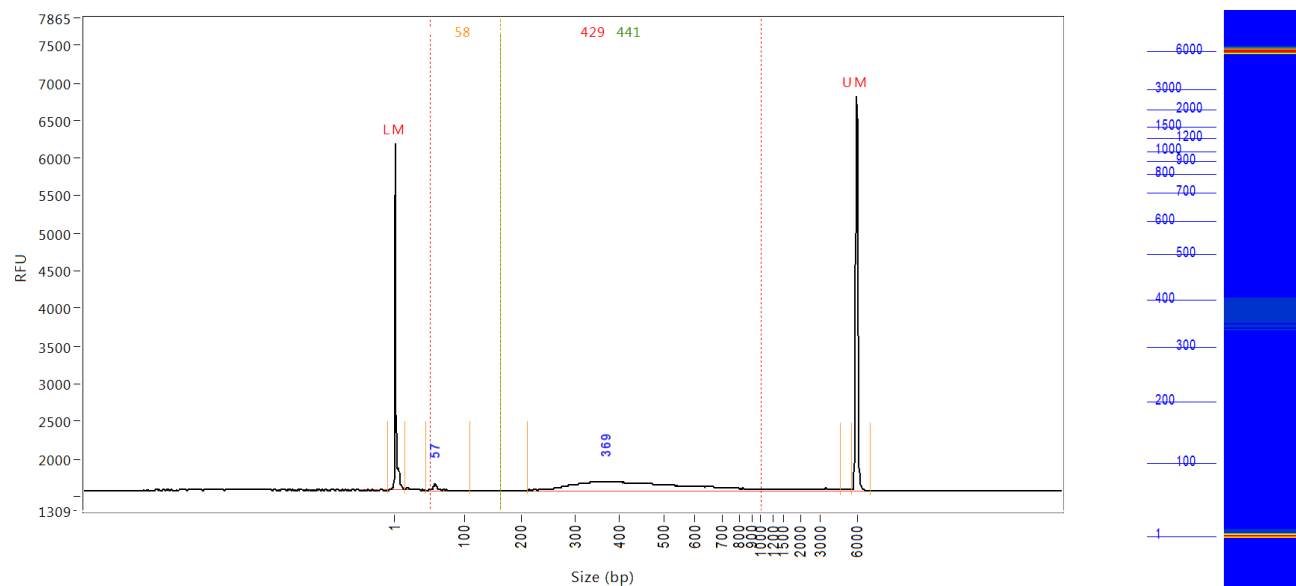
Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 9
Well Location: D8



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	2	149.24	3636	21.586
2	6000 (UM)	0.0065	5586	7260	5981	2.01	3726	15.396
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0109	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0036 ng/ul	33.0 %Total	0.0190 nmole/L	312 Avg. Size (bp)	94.40 %CV		
	50 bp to 160 bp	0.0022 ng/ul	20.4 %Total	0.0385 nmole/L	95 Avg. Size (bp)	46.02 %CV		
	160 bp to 1000 bp	0.0014 ng/ul	12.6 %Total	0.0034 nmole/L	664 Avg. Size (bp)	23.01 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 10
Well Location: D9

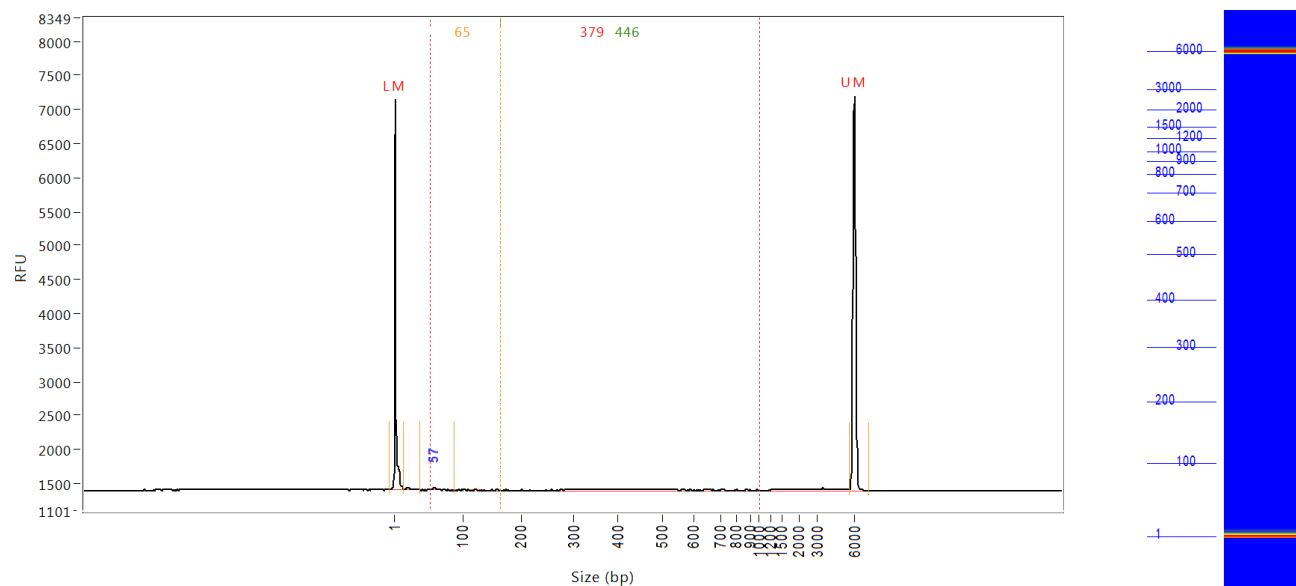


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	156.11	4612	26.502
2	57	0.0034	45	110	58	5.19	78	0.812
3	369	0.1060	209	4659	562	99.34	109	25.567
4	6000 (UM)	0.0072	5610	7115	5994	1.80	5236	20.766
TIC:		0.1093	ng/uL					
TIM:		0.4054	nmole/L					
Total Conc.:		0.1124	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.1031 ng/uL	91.7 %Total	0.3953 nmole/L	429 Avg. Size (bp)	34.93 %CV
	50 bp to 160 bp	0.0033 ng/uL	3.0 %Total	0.0950 nmole/L	58 Avg. Size (bp)	5.04 %CV
	160 bp to 1000 bp	0.0997 ng/uL	88.7 %Total	0.3717 nmole/L	441 Avg. Size (bp)	30.77 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

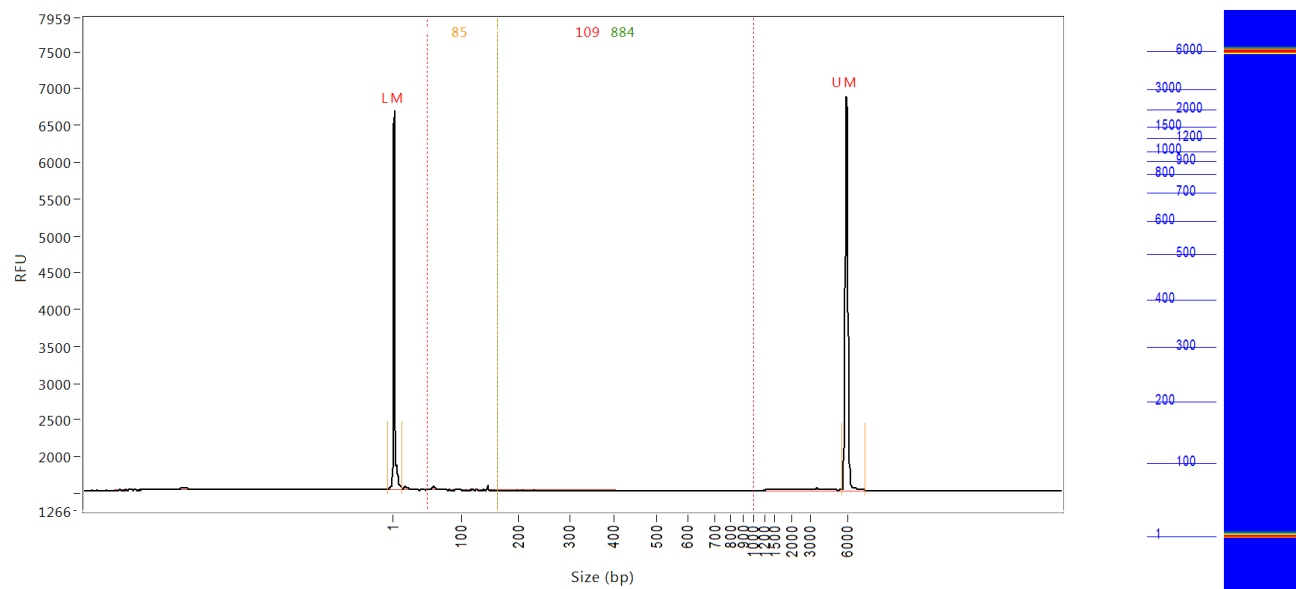
Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 11
Well Location: D10



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	171.46	5749	32.790
2	57	0.0015	38	87	58	6.53	38	0.441
3	6000 (UM)	0.0065	5634	7236	5991	1.80	5789	23.216
	TIC:	0.0015	ng/uL					
	TIM:	0.0417	nmole/L					
	Total Conc.:	0.0163	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0093 ng/ul	56.9 %Total	0.0403 nmole/L	379 Avg. Size (bp)	51.25 %CV		
	50 bp to 160 bp	0.0016 ng/ul	10.0 %Total	0.0416 nmole/L	65 Avg. Size (bp)	32.14 %CV		
	160 bp to 1000 bp	0.0077 ng/ul	46.9 %Total	0.0282 nmole/L	446 Avg. Size (bp)	31.84 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 17H 40M.raw
Sample: Student mRNA-Seq library 12
Well Location: D11

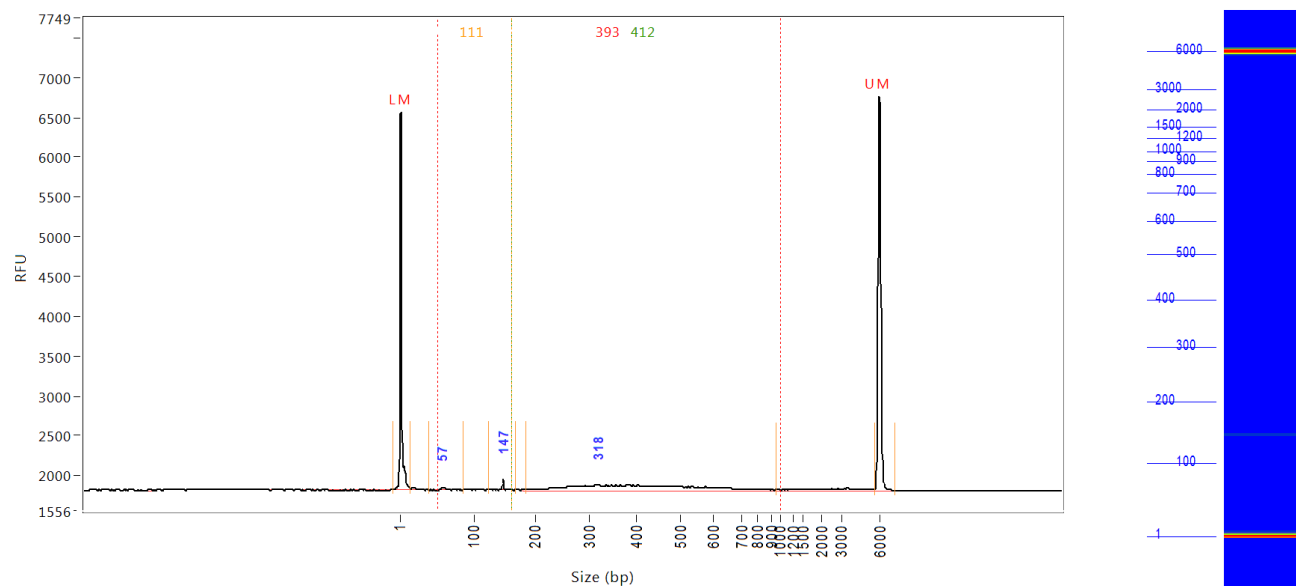


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0092	0	15	1	190.15	5148	30.069
2	6000 (UM)	0.0067	5634	7551	5991	2.54	5348	22.021
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0093	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0024 ng/ul	25.6 %Total	0.0358 nmole/L	109 Avg. Size (bp)	130.73 %CV
	50 bp to 160 bp	0.0023 ng/ul	24.9 %Total	0.0444 nmole/L	85 Avg. Size (bp)	46.43 %CV
	160 bp to 1000 bp	0.0001 ng/ul	0.8 %Total	0.0001 nmole/L	884 Avg. Size (bp)	11.57 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

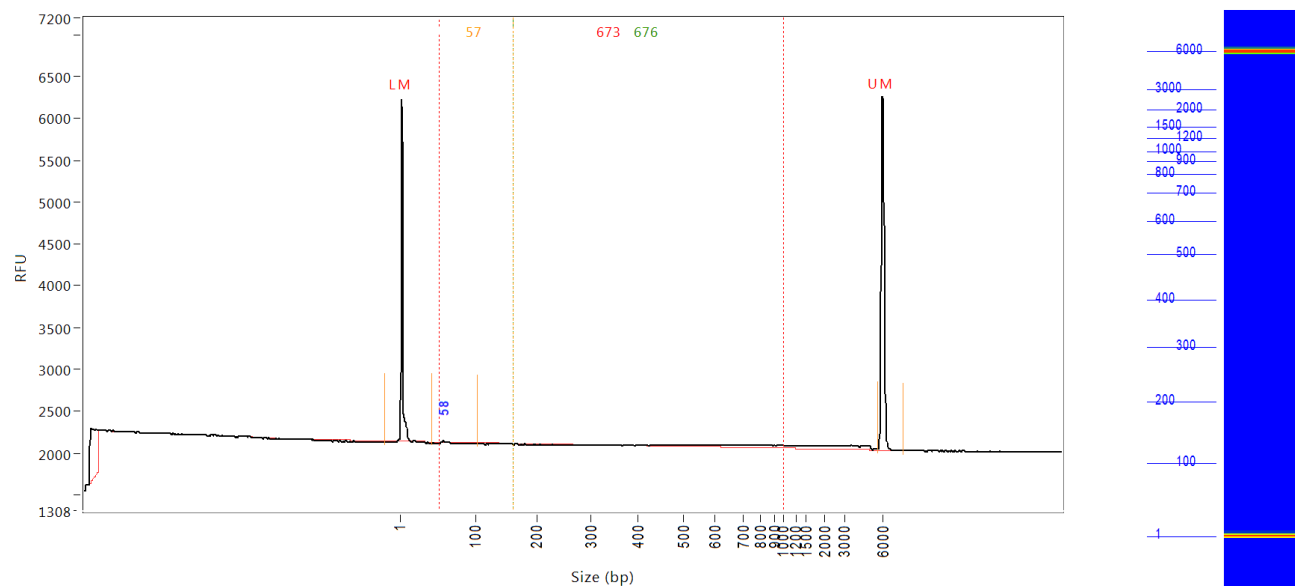
Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 13
Well Location: E1



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	14	1	195.90	4742	28.732
2	57	0.0018	40	84	59	7.72	32	0.395
3	147	0.0035	125	183	149	6.99	139	0.782
4	318	0.0723	169	956	410	33.86	62	16.223
5	6000 (UM)	0.0076	5625	7235	5988	1.96	4947	20.420
TIC:		0.0776	ng/uL					
TIM:		0.3778	nmole/L					
Total Conc.:		0.0876	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0779 ng/ul	7.8 %Total		0.3263 nmole/L	393 Avg. Size (bp)	39.75 %CV	
	50 bp to 160 bp	0.0052 ng/ul	0.5 %Total		0.0774 nmole/L	111 Avg. Size (bp)	36.82 %CV	
	160 bp to 1000 bp	0.0727 ng/ul	7.3 %Total		0.2904 nmole/L	412 Avg. Size (bp)	34.54 %CV	

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 14
Well Location: E2

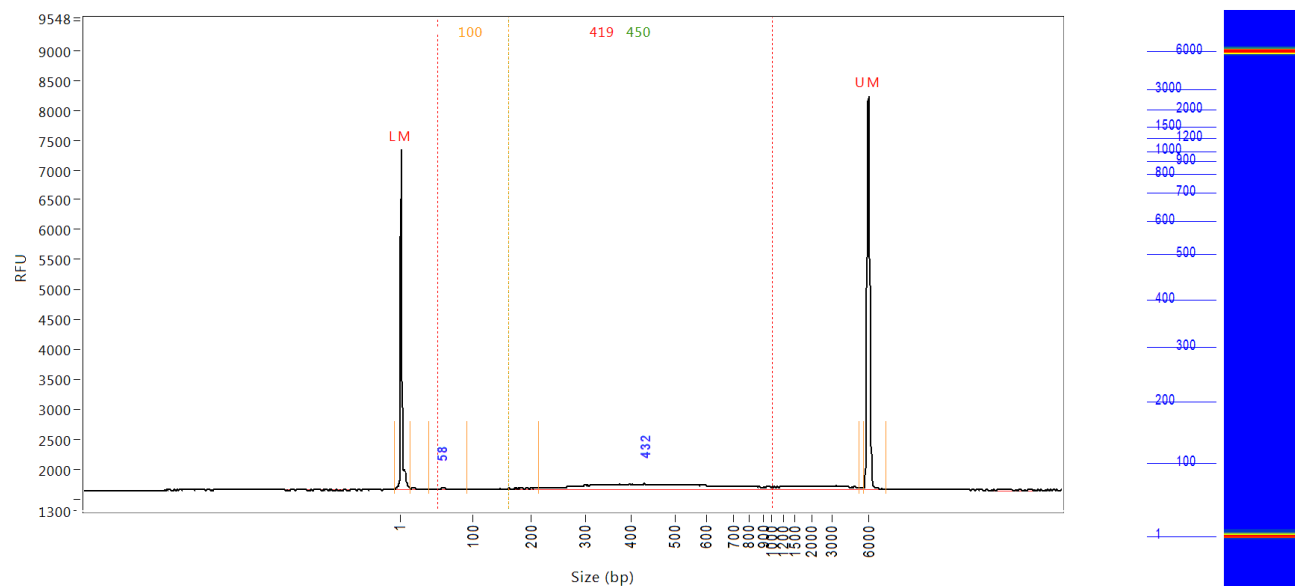


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	41	1	136.40	4087	23.564
2	58	0.0001	41	104	57	1.36	6	0.026
3	6000 (UM)	0.0078	5578	7584	5996	1.81	4226	17.123
TIC:		0.0001	ng/uL					
TIM:		0.0041	nmole/L					
Total Conc.:		0.0477	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0258 ng/ul	54.0 %Total	0.0630 nmole/L	673 Avg. Size (bp)	23.40 %CV
	50 bp to 160 bp	0.0001 ng/ul	0.3 %Total	0.0041 nmole/L	57 Avg. Size (bp)	1.36 %CV
	160 bp to 1000 bp	0.0256 ng/ul	53.7 %Total	0.0624 nmole/L	676 Avg. Size (bp)	22.33 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 15
Well Location: E3

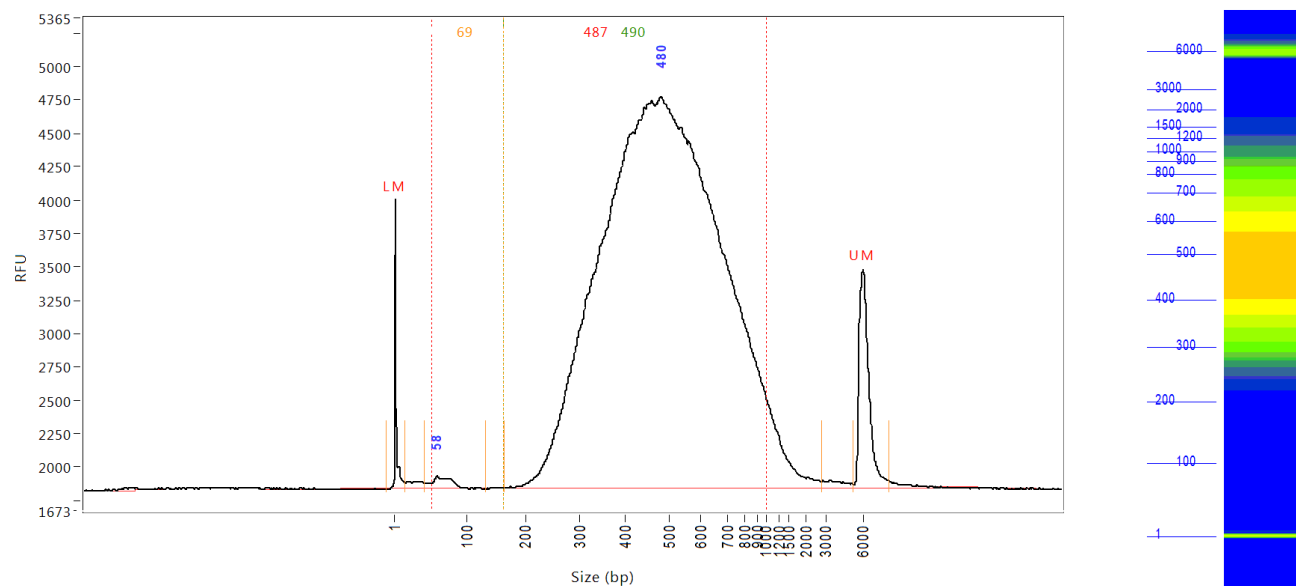


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	188.55	5699	33.646
2	58	0.0057	40	93	66	20.49	42	1.496
3	432	0.1226	213	5250	819	112.41	93	32.193
4	6000 (UM)	0.0084	5649	7421	5990	2.32	6574	26.330
TIC:		0.1283	ng/uL					
TIM:		0.3880	nmole/L					
Total Conc.:		0.1433	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.1166 ng/ul	81.3 %Total	0.4580 nmole/L	419 Avg. Size (bp)	46.30 %CV
	50 bp to 160 bp	0.0105 ng/ul	7.3 %Total	0.1734 nmole/L	100 Avg. Size (bp)	34.52 %CV
	160 bp to 1000 bp	0.1061 ng/ul	74.0 %Total	0.3877 nmole/L	450 Avg. Size (bp)	38.51 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 16
Well Location: E4

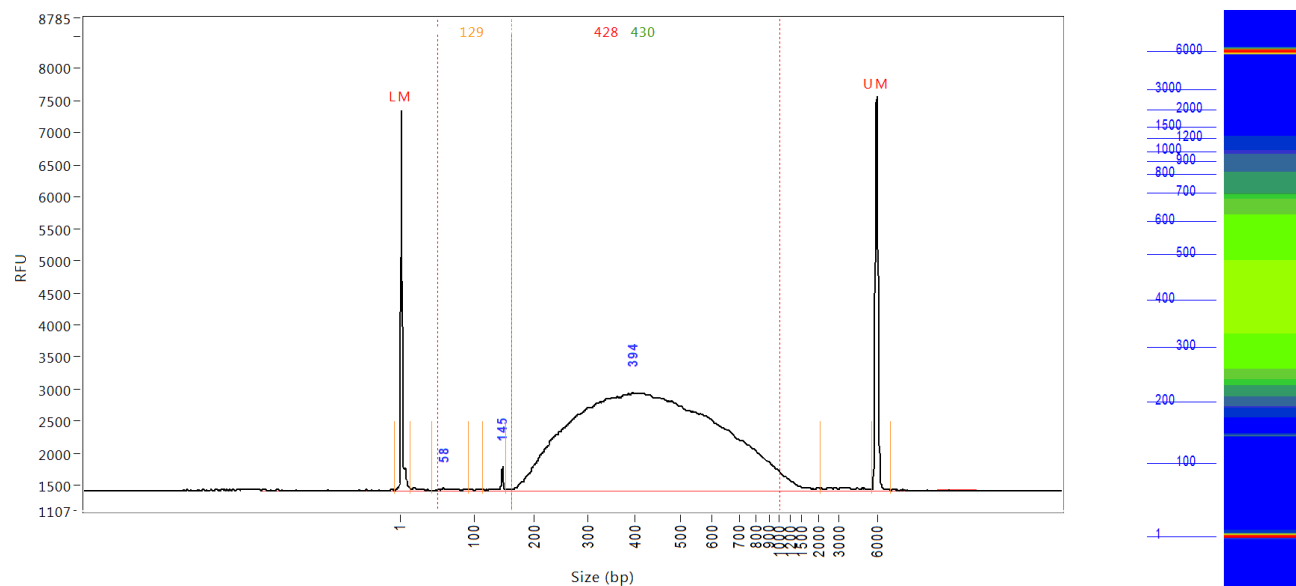


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	2	143.95	2163	13.925
2	58	0.0484	42	133	65	18.60	95	5.257
3	480	6.7923	162	2785	510	39.66	2932	738.180
4	6000 (UM)	0.0182	5203	8096	6155	7.66	1634	23.750
TIC:		6.8407	ng/uL					
TIM:		23.1358	nmole/L					
Total Conc.:		6.8804	ng/uL					

Smear Analysis	50 bp to 1000 bp	6.6774 ng/uL	97.0 %Total	22.5392 nmole/L	487 Avg. Size (bp)	31.28 %CV
	50 bp to 160 bp	0.0433 ng/uL	0.6 %Total	1.0231 nmole/L	69 Avg. Size (bp)	22.61 %CV
	160 bp to 1000 bp	6.6342 ng/uL	96.4 %Total	22.2688 nmole/L	490 Avg. Size (bp)	30.43 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

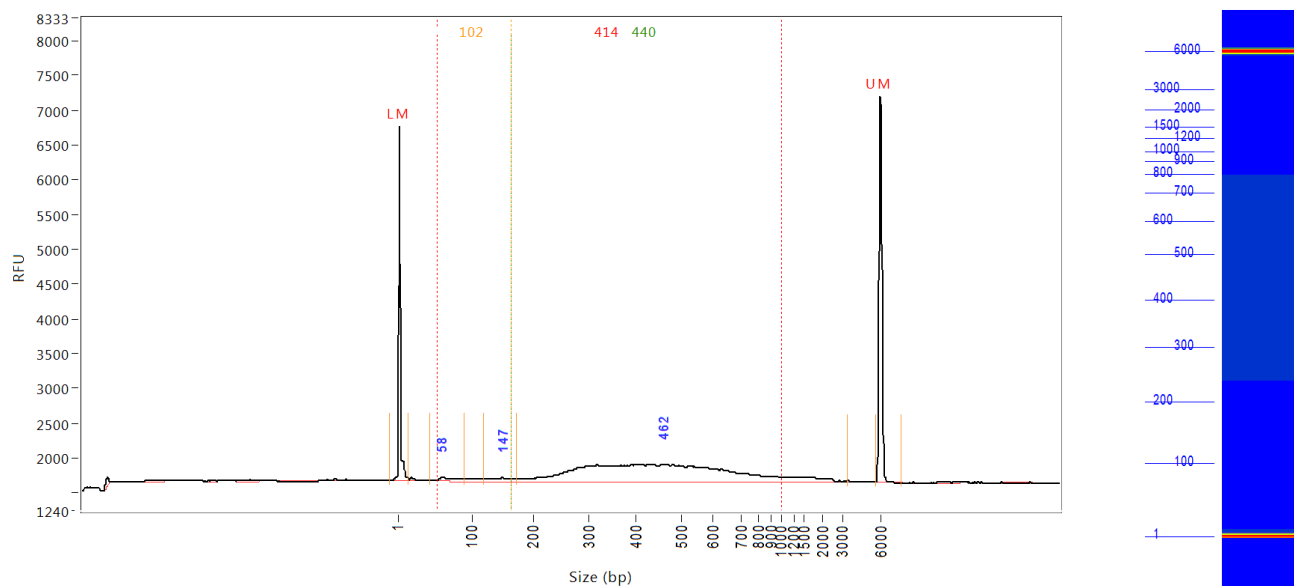
Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 17
Well Location: E5



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	187.09	5899	34.608
2	58	0.0018	43	92	63	15.52	26	0.495
3	145	0.0080	115	152	143	3.54	368	2.163
4	394	1.8045	152	2078	439	41.38	1519	487.380
5	6000 (UM)	0.0075	5625	7118	5985	1.89	6128	24.224
	TIC:	1.8143	ng/uL					
	TIM:	6.9030	nmole/L					
	Total Conc.:	1.8232	ng/uL					
Smear Analysis	50 bp to 1000 bp	1.7935 ng/ul	98.4 %Total	6.8880 nmole/L	428 Avg. Size (bp)	37.57 %CV		
	50 bp to 160 bp	0.0108 ng/ul	0.6 %Total	0.1377 nmole/L	129 Avg. Size (bp)	24.21 %CV		
	160 bp to 1000 bp	1.7827 ng/ul	97.8 %Total	6.8178 nmole/L	430 Avg. Size (bp)	37.12 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 18
Well Location: E6



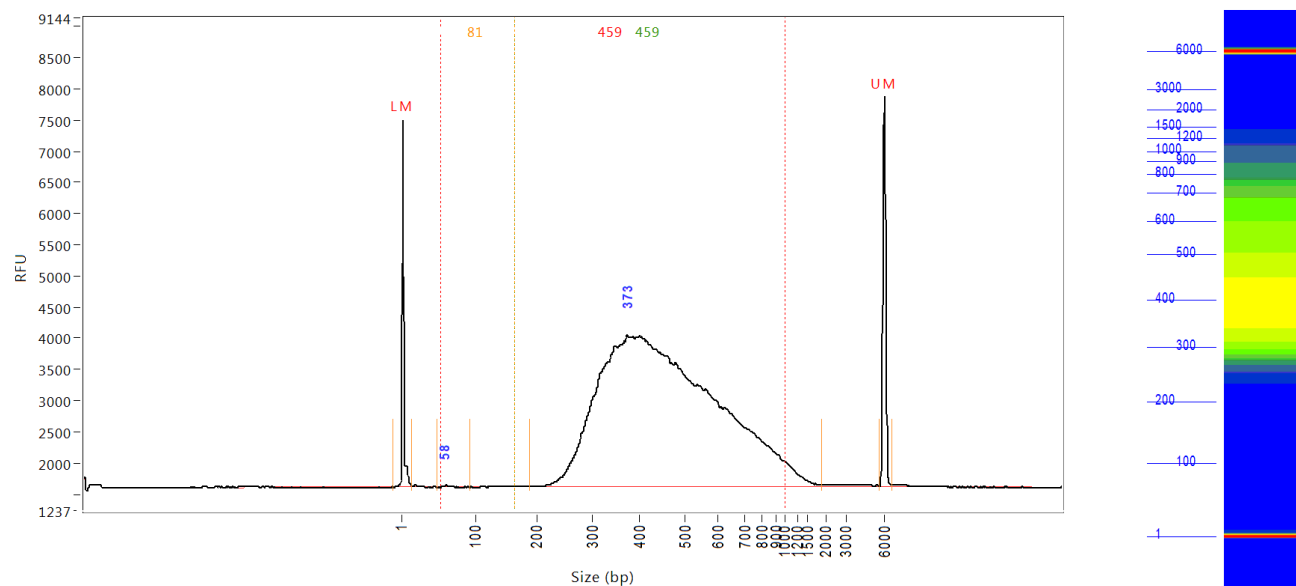
Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	200.32	5108	30.424
2	58	0.0118	42	88	67	17.83	53	2.791
3	147	0.0126	118	172	145	10.48	59	2.991
4	462	0.3489	172	3423	510	67.37	249	82.852
5	6000 (UM)	0.0078	5625	7631	5982	1.80	5556	22.213

TIC: 0.3733 ng/uL
TIM: 1.5563 nmole/L
Total Conc.: 0.3865 ng/uL

Smear Analysis	50 bp to 1000 bp	0.3593 ng/uL	92.9 %Total	1.4289 nmole/L	414 Avg. Size (bp)	43.54 %CV
	50 bp to 160 bp	0.0277 ng/uL	7.2 %Total	0.4439 nmole/L	102 Avg. Size (bp)	31.99 %CV
	160 bp to 1000 bp	0.3317 ng/uL	85.8 %Total	1.2414 nmole/L	440 Avg. Size (bp)	36.89 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 19
Well Location: E7

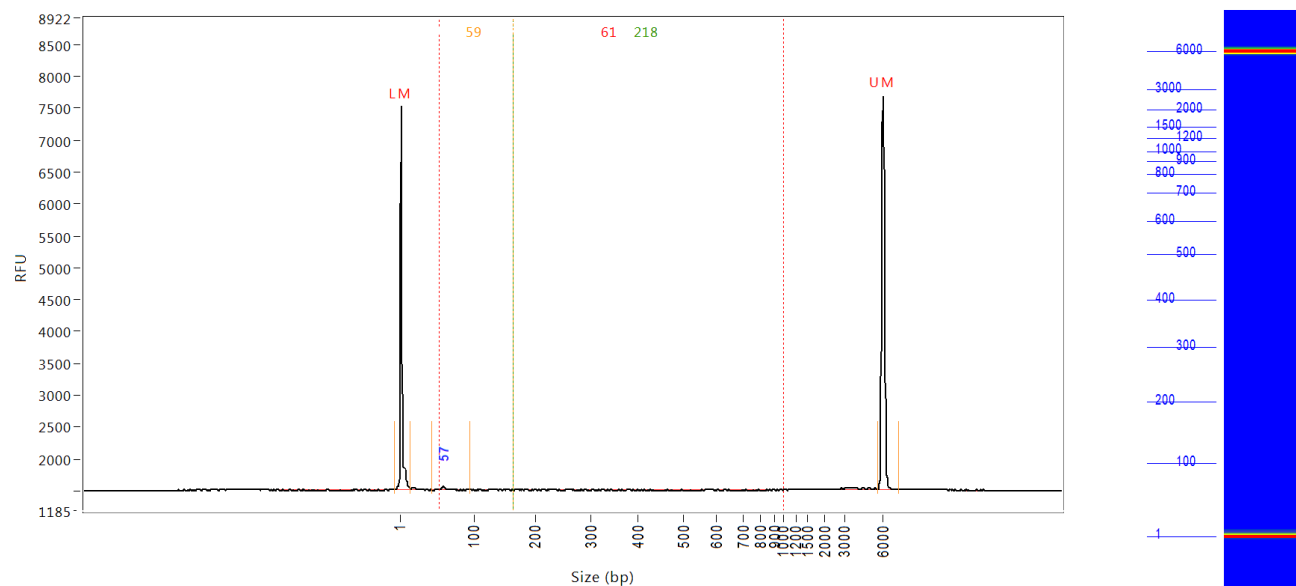


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	184.85	5877	34.671
2	58	0.0012	48	92	59	5.44	29	0.328
3	373	2.1404	188	1882	470	36.10	2439	579.171
4	6000 (UM)	0.0078	5602	6629	5982	1.83	6261	25.351
TIC:		2.1416	ng/uL					
TIM:		7.5271	nmole/L					
Total Conc.:		2.1525	ng/uL					

Smear Analysis	50 bp to 1000 bp	2.1106 ng/ul	98.1 %Total	7.5736 nmole/L	459 Avg. Size (bp)	31.15 %CV
	50 bp to 160 bp	0.0016 ng/ul	0.1 %Total	0.0332 nmole/L	81 Avg. Size (bp)	46.11 %CV
	160 bp to 1000 bp	2.1089 ng/ul	98.0 %Total	7.5629 nmole/L	459 Avg. Size (bp)	31.06 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

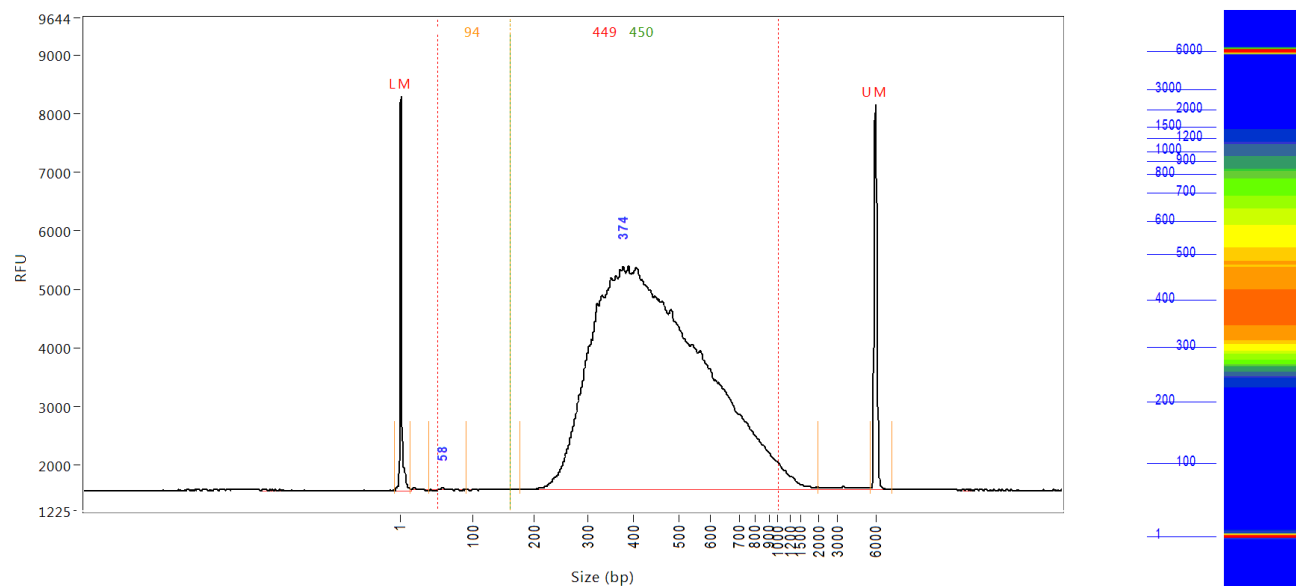
Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 20
Well Location: E8



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	14	1	184.55	6024	35.687
2	57	0.0018	43	94	58	5.49	44	0.500
3	6000 (UM)	0.0076	5602	7235	5981	1.88	6169	25.484
	TIC:	0.0018	ng/uL					
	TIM:	0.0507	nmole/L					
	Total Conc.:	0.0091	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0019 ng/ul	20.5 %Total	0.0501 nmole/L	61 Avg. Size (bp)	32.55 %CV		
	50 bp to 160 bp	0.0018 ng/ul	20.3 %Total	0.0510 nmole/L	59 Avg. Size (bp)	15.66 %CV		
	160 bp to 1000 bp	0.0000 ng/ul	0.2 %Total	0.0002 nmole/L	218 Avg. Size (bp)	24.50 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 21
Well Location: E9

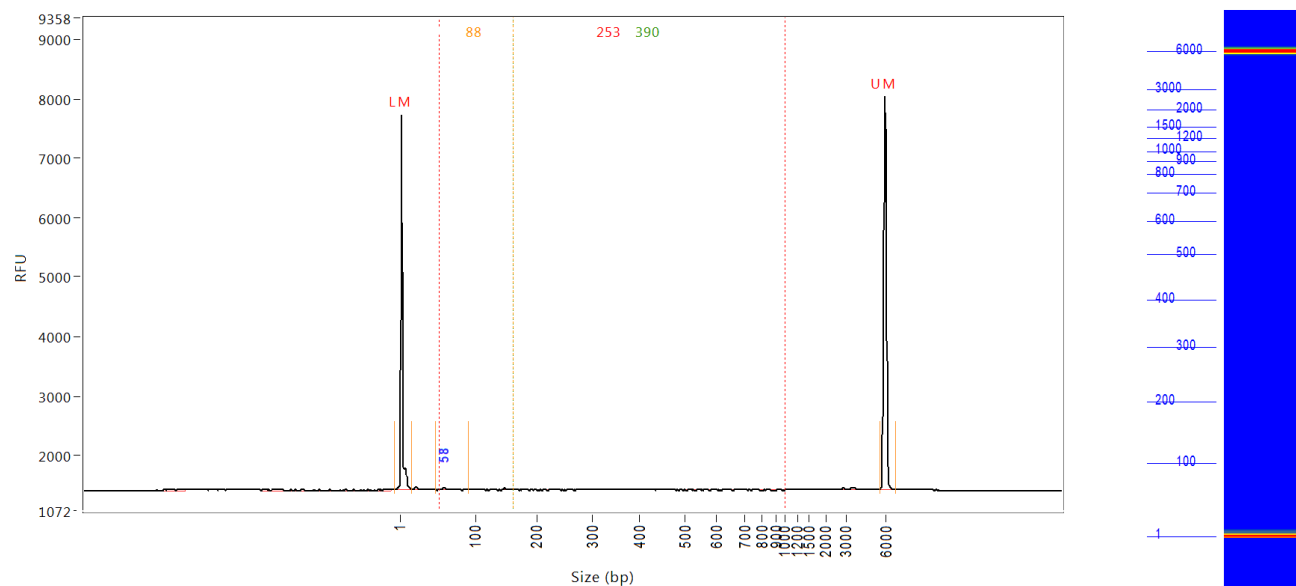


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	191.68	6718	39.872
2	58	0.0020	39	89	60	10.64	46	0.616
3	374	2.8458	178	1975	458	34.75	3814	885.563
4	6000 (UM)	0.0071	5625	7304	5998	2.03	6574	26.381
TIC:		2.8478	ng/uL					
TIM:		10.2781	nmole/L					
Total Conc.:		2.8602	ng/uL					

Smear Analysis	50 bp to 1000 bp	2.8188 ng/ul	98.6 %Total	10.3202 nmole/L	449 Avg. Size (bp)	30.52 %CV
	50 bp to 160 bp	0.0034 ng/ul	0.1 %Total	0.0605 nmole/L	94 Avg. Size (bp)	43.47 %CV
	160 bp to 1000 bp	2.8153 ng/ul	98.4 %Total	10.2976 nmole/L	450 Avg. Size (bp)	30.38 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

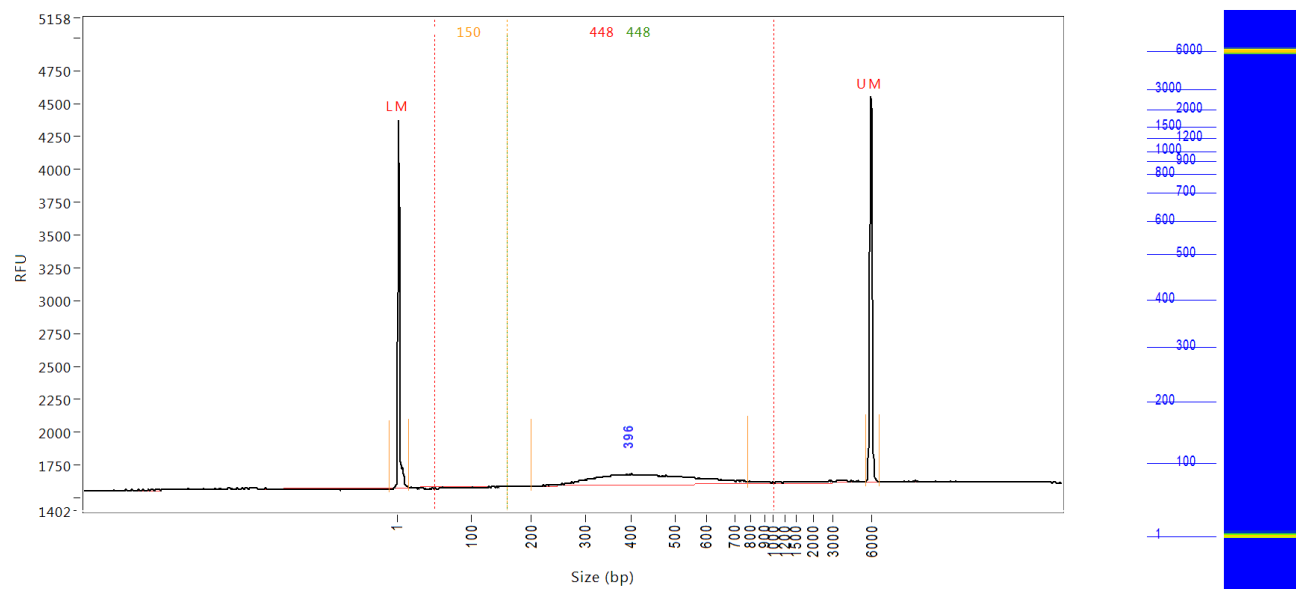
Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 22
Well Location: E10



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	17	1	156.87	6312	37.234
2	58	0.0024	48	91	62	14.45	42	0.702
3	6000 (UM)	0.0075	5625	6908	5986	1.79	6611	26.302
	TIC:	0.0024	ng/uL					
	TIM:	0.0638	nmole/L					
	Total Conc.:	0.0177	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0083 ng/ul	46.6 %Total	0.0537 nmole/L	253 Avg. Size (bp)	76.44 %CV		
	50 bp to 160 bp	0.0037 ng/ul	21.1 %Total	0.0701 nmole/L	88 Avg. Size (bp)	42.07 %CV		
	160 bp to 1000 bp	0.0045 ng/ul	25.5 %Total	0.0190 nmole/L	390 Avg. Size (bp)	41.07 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 22H 25M.raw
Sample: Student mRNA-Seq library 23
Well Location: E11

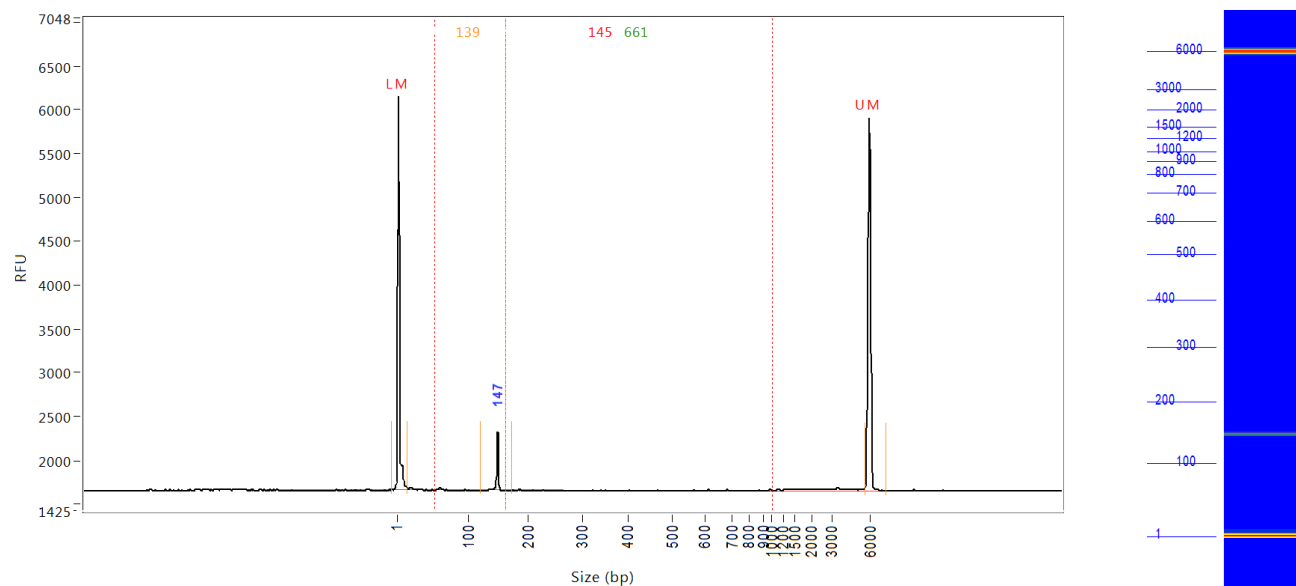


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0107	0	15	1	157.36	2793	16.285
2	396	0.1317	202	787	439	25.31	82	16.741
3	6000 (UM)	0.0081	5625	6699	5997	1.76	2940	12.289
	TIC:	0.1317	ng/uL					
	TIM:	0.4937	nmole/L					
	Total Conc.:	0.1432	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.1347 ng/ul	94.1 %Total	0.4942 nmole/L	448 Avg. Size (bp)	28.28 %CV
	50 bp to 160 bp	0.0000 ng/ul	0.0 %Total	0.0003 nmole/L	150 Avg. Size (bp)	0.44 %CV
	160 bp to 1000 bp	0.1346 ng/ul	94.0 %Total	0.4940 nmole/L	448 Avg. Size (bp)	28.26 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

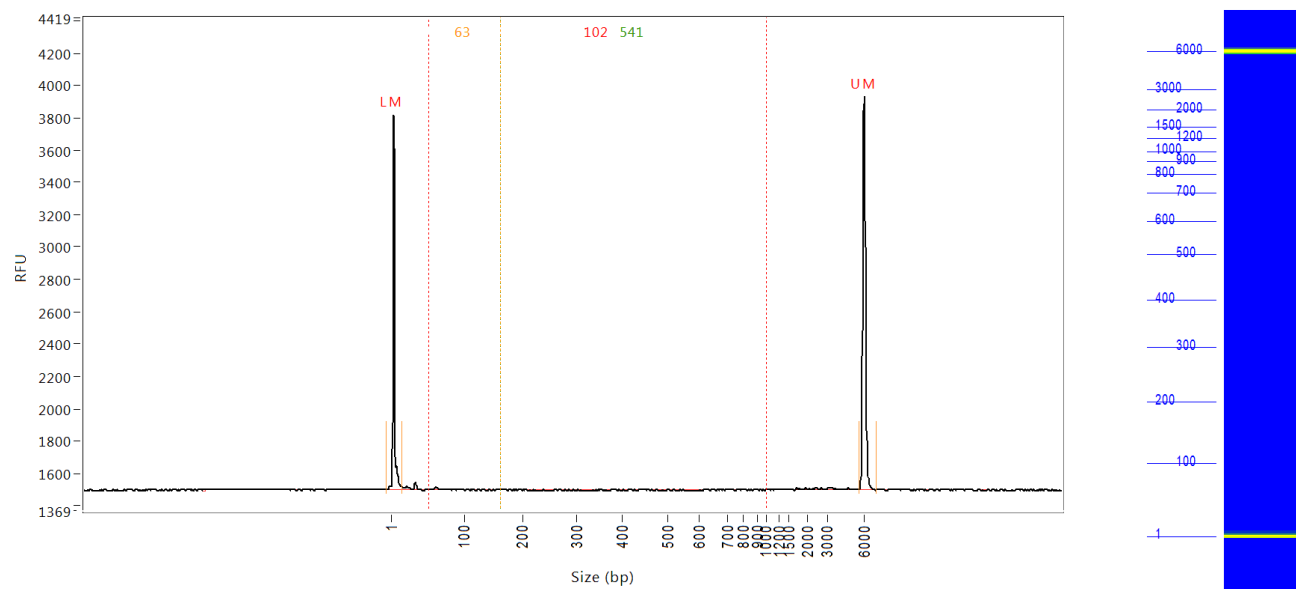
Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 24
Well Location: F1



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	2	143.31	4485	26.756
2	147	0.0110	120	171	146	1.25	654	2.738
3	6000 (UM)	0.0058	5616	7335	5979	1.84	4246	17.339
	TIC:	0.0110	ng/uL					
	TIM:	0.1240	nmole/L					
	Total Conc.:	0.0180	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0121 ng/ul	1.2 %Total	0.1370 nmole/L	145 Avg. Size (bp)	44.43 %CV		
	50 bp to 160 bp	0.0119 ng/ul	1.2 %Total	0.1408 nmole/L	139 Avg. Size (bp)	16.97 %CV		
	160 bp to 1000 bp	0.0001 ng/ul	0.0 %Total	0.0003 nmole/L	661 Avg. Size (bp)	45.42 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 25
Well Location: F2

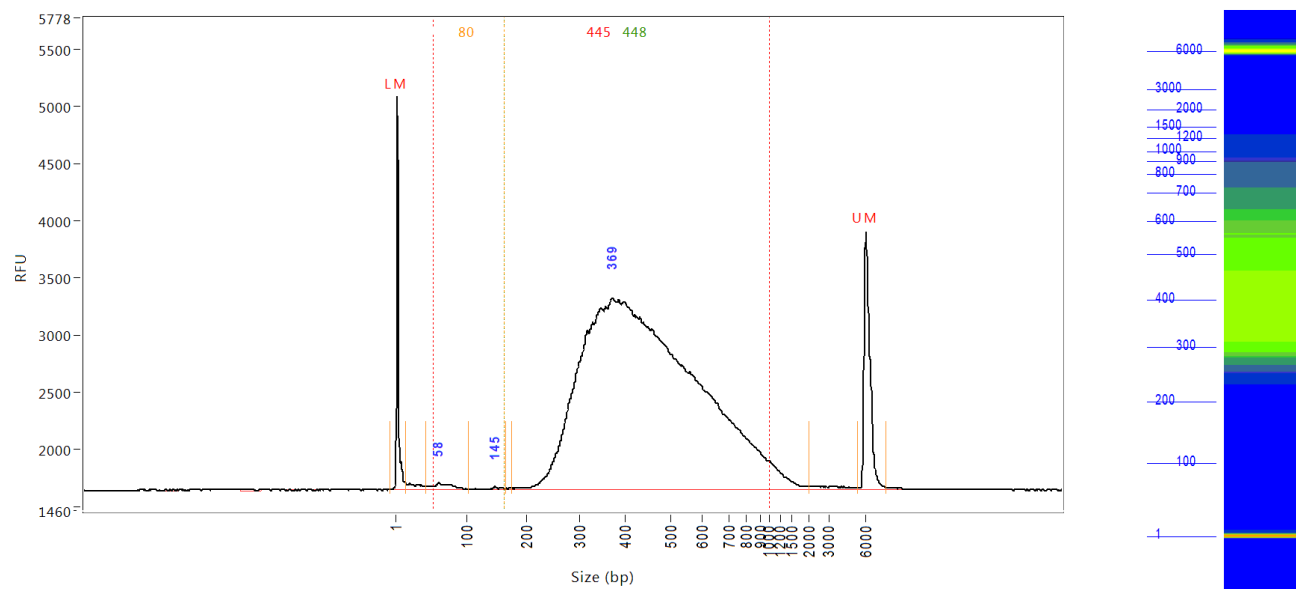


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	202.40	2319	14.225
2	6000 (UM)	0.0064	5592	6954	5991	1.86	2429	10.088
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0083	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0013 ng/ul	15.5 %Total	0.0206 nmole/L	102 Avg. Size (bp)	157.33 %CV
	50 bp to 160 bp	0.0012 ng/ul	14.3 %Total	0.0306 nmole/L	63 Avg. Size (bp)	21.49 %CV
	160 bp to 1000 bp	0.0001 ng/ul	1.3 %Total	0.0003 nmole/L	541 Avg. Size (bp)	59.99 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

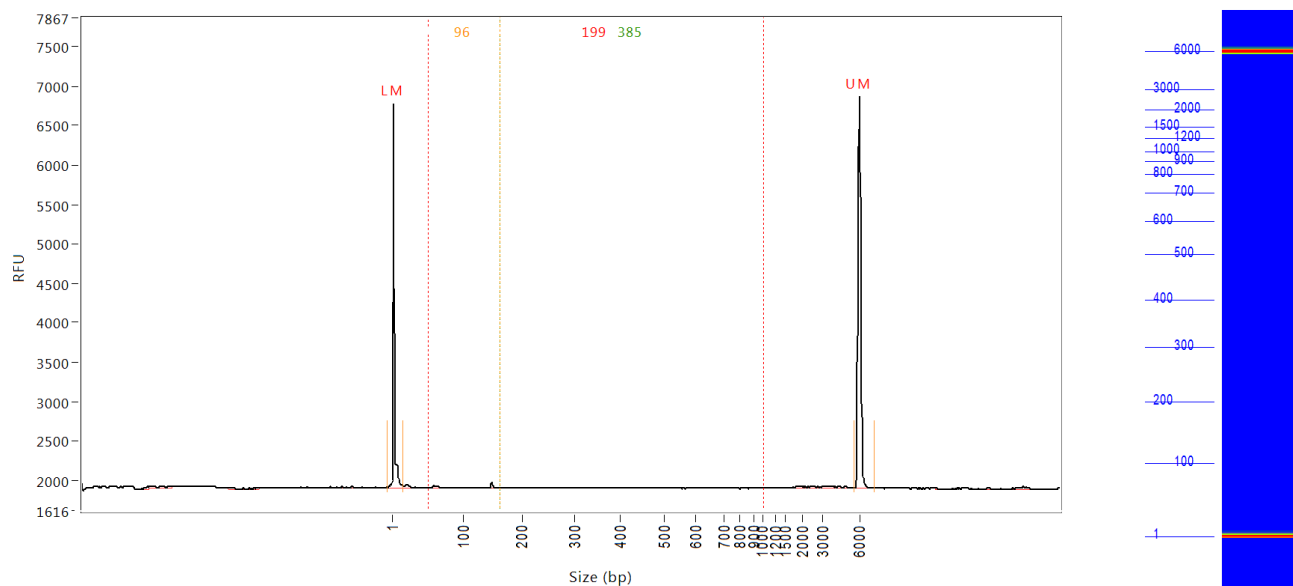
Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 27
Well Location: F3



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	2	152.86	3440	20.867
2	58	0.0157	42	103	65	19.71	58	3.037
3	145	0.0027	103	164	142	10.31	30	0.514
4	369	2.0881	174	2017	459	37.26	1681	404.796
5	6000 (UM)	0.0082	5376	7669	6145	4.69	2251	19.141
	TIC:	2.1064	ng/uL					
	TIM:	7.9114	nmole/L					
	Total Conc.:	2.1225	ng/uL					
Smear Analysis	50 bp to 1000 bp	2.0751 ng/ul	97.8 %Total	7.6680 nmole/L	445 Avg. Size (bp)	32.57 %CV		
	50 bp to 160 bp	0.0161 ng/ul	0.8 %Total	0.3319 nmole/L	80 Avg. Size (bp)	35.96 %CV		
	160 bp to 1000 bp	2.0591 ng/ul	97.0 %Total	7.5604 nmole/L	448 Avg. Size (bp)	31.67 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 28
Well Location: F4

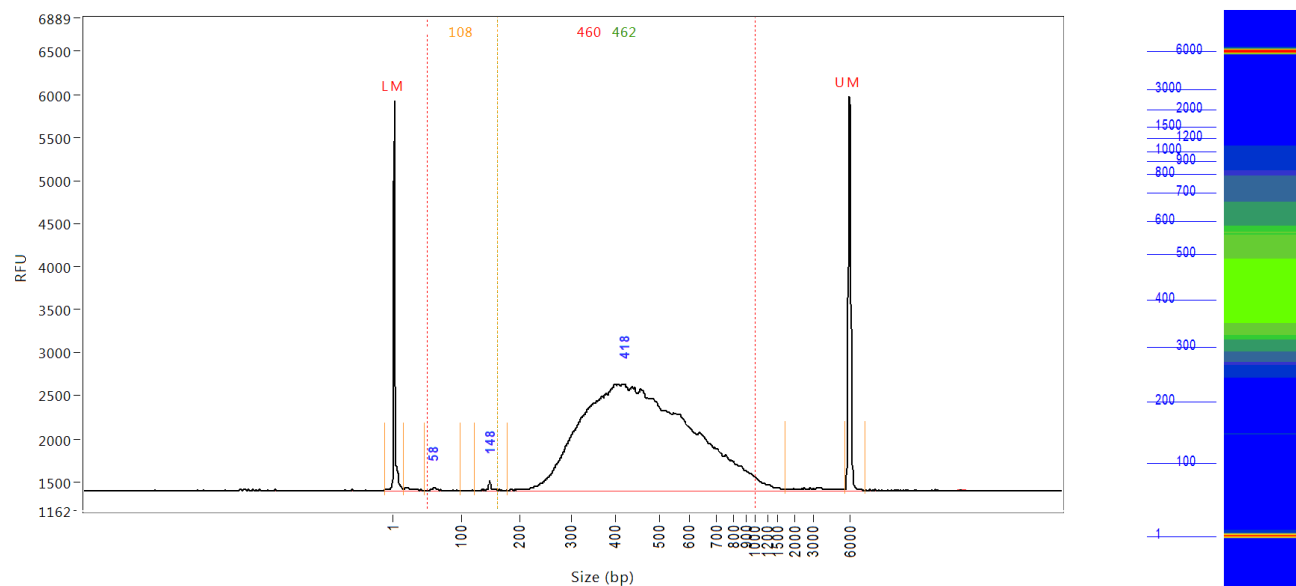


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	205.75	4869	28.855
2	6000 (UM)	0.0064	5616	7240	5995	1.97	4966	20.568
TIC:		0.0000	ng/uL					
TIM:		0.0000	nmole/L					
Total Conc.:		0.0155	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0062 ng/ul	40.0 %Total	0.0511 nmole/L	199 Avg. Size (bp)	94.69 %CV
	50 bp to 160 bp	0.0040 ng/ul	25.7 %Total	0.0680 nmole/L	96 Avg. Size (bp)	41.35 %CV
	160 bp to 1000 bp	0.0022 ng/ul	14.3 %Total	0.0094 nmole/L	385 Avg. Size (bp)	53.88 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

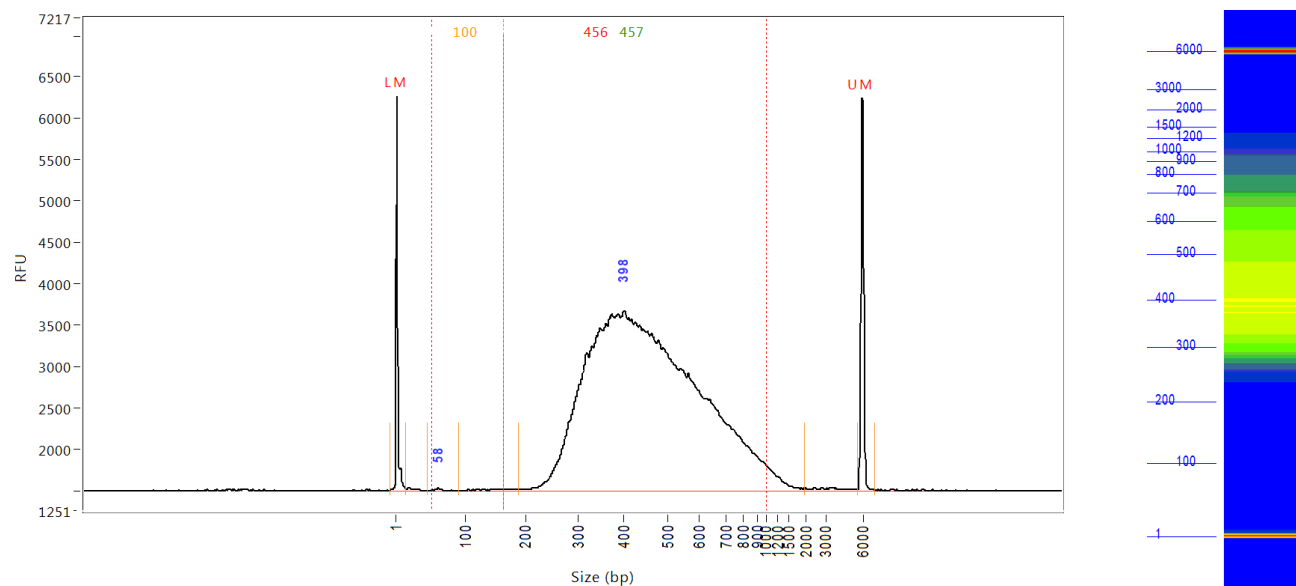
Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 29
Well Location: F5



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	2	150.68	4519	26.764
2	58	0.0019	46	98	61	13.75	34	0.484
3	148	0.0027	122	180	147	5.44	119	0.672
4	418	1.1528	180	1716	468	32.69	1234	286.643
5	6000 (UM)	0.0062	5640	7216	5983	1.84	4571	18.407
	TIC:	1.1575	ng/uL					
	TIM:	4.1358	nmole/L					
	Total Conc.:	1.1652	ng/uL					
Smear Analysis	50 bp to 1000 bp	1.1477 ng/ul	98.5 %Total	4.1031 nmole/L	460 Avg. Size (bp)	30.28 %CV		
	50 bp to 160 bp	0.0045 ng/ul	0.4 %Total	0.0685 nmole/L	108 Avg. Size (bp)	38.67 %CV		
	160 bp to 1000 bp	1.1432 ng/ul	98.1 %Total	4.0746 nmole/L	462 Avg. Size (bp)	29.86 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 30
Well Location: F6

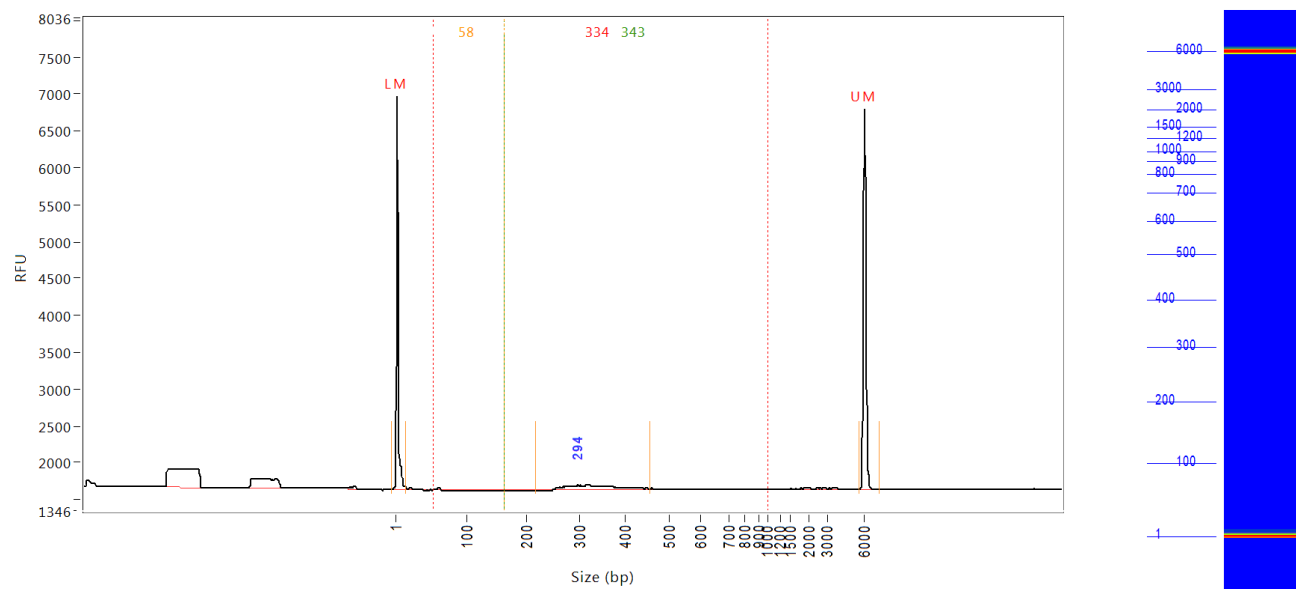


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	160.65	4763	27.366
2	58	0.0014	45	89	59	9.71	27	0.354
3	398	2.0032	189	1966	466	34.89	2180	509.302
4	6000 (UM)	0.0063	5640	7025	5997	1.87	4754	19.338
TIC:		2.0046	ng/uL					
TIM:		7.1120	nmole/L					
Total Conc.:		2.0148	ng/uL					

Smear Analysis	50 bp to 1000 bp	1.9833 ng/ul	98.4 %Total	7.1557 nmole/L	456 Avg. Size (bp)	30.75 %CV
	50 bp to 160 bp	0.0030 ng/ul	0.1 %Total	0.0491 nmole/L	100 Avg. Size (bp)	39.43 %CV
	160 bp to 1000 bp	1.9803 ng/ul	98.3 %Total	7.1366 nmole/L	457 Avg. Size (bp)	30.59 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 31
Well Location: F7



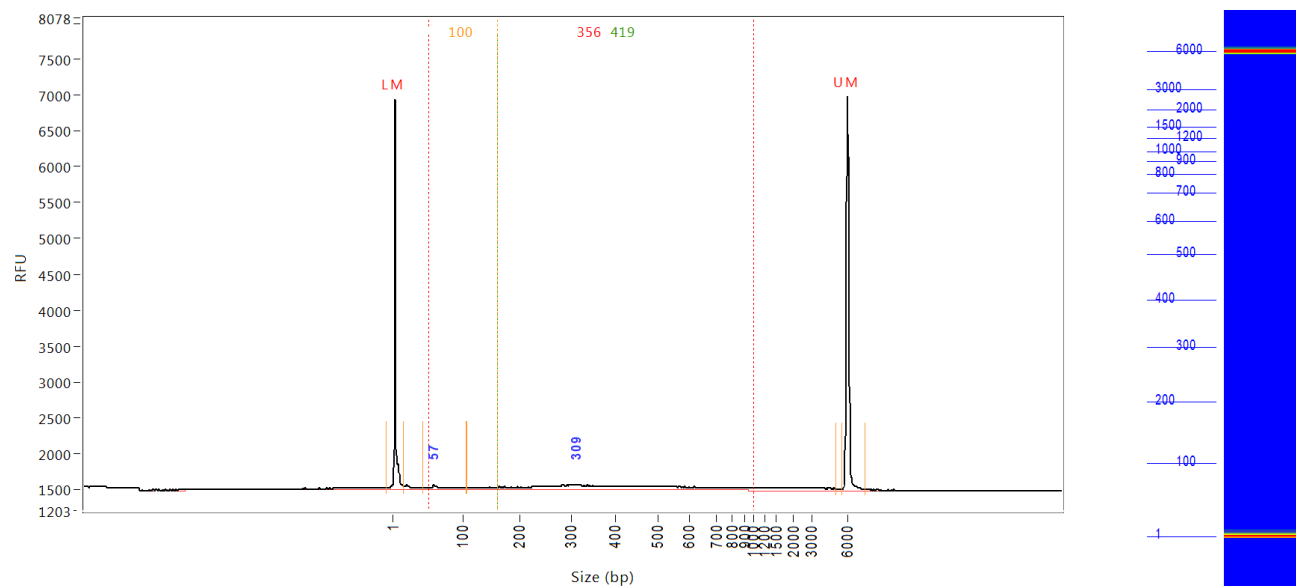
Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	184.34	5334	31.020
2	294	0.0223	218	457	333	15.23	55	6.418
3	6000 (UM)	0.0060	5592	7216	5983	1.74	5159	20.605

TIC: 0.0223 ng/uL
TIM: 0.1100 nmole/L
Total Conc.: 0.0296 ng/uL

Smear Analysis	50 bp to 1000 bp	0.0241 ng/ul	81.5 %Total	0.1190 nmole/L	334 Avg. Size (bp)	27.47 %CV
	50 bp to 160 bp	0.0008 ng/ul	2.7 %Total	0.0231 nmole/L	58 Avg. Size (bp)	2.60 %CV
	160 bp to 1000 bp	0.0233 ng/ul	78.7 %Total	0.1118 nmole/L	343 Avg. Size (bp)	22.49 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 17 Manual Baseline End (min): 47
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 32
Well Location: F8

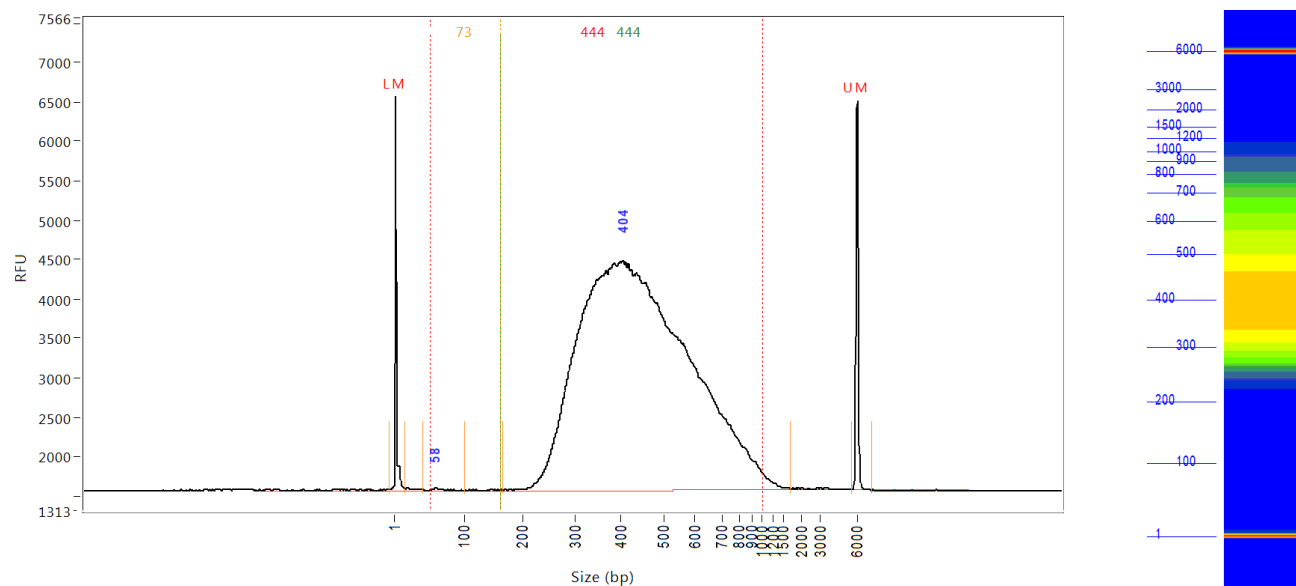


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	188.79	5433	31.869
2	57	0.0105	42	106	72	24.42	55	3.112
3	309	0.0877	108	5112	658	122.25	60	25.957
4	6000 (UM)	0.0063	5592	7502	6013	2.89	5489	22.472
	TIC:	0.0982	ng/uL					
	TIM:	0.4588	nmole/L					
	Total Conc.:	0.1044	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0853 ng/ul	81.7 %Total	0.3943 nmole/L	356 Avg. Size (bp)	59.44 %CV
	50 bp to 160 bp	0.0170 ng/ul	16.3 %Total	0.2775 nmole/L	100 Avg. Size (bp)	32.78 %CV
	160 bp to 1000 bp	0.0684 ng/ul	65.5 %Total	0.2685 nmole/L	419 Avg. Size (bp)	44.86 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 33
Well Location: F9

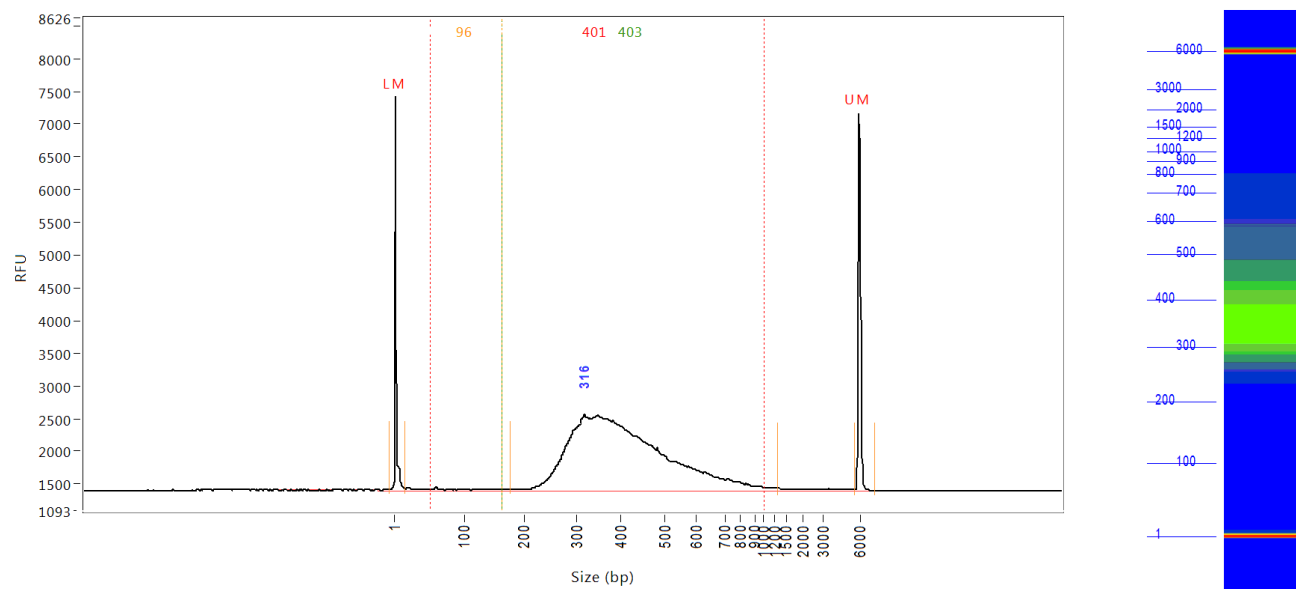


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	14	1	162.11	4991	28.834
2	58	0.0019	41	99	60	13.01	34	0.499
3	404	2.5583	164	1699	448	31.78	2910	685.329
4	6000 (UM)	0.0061	5640	7216	5986	1.80	4943	19.636
TIC:		2.5602	ng/uL					
TIM:		9.4471	nmole/L					
Total Conc.:		2.5678	ng/uL					

Smear Analysis	50 bp to 1000 bp	2.5475 ng/ul	99.2 %Total	9.4422 nmole/L	444 Avg. Size (bp)	30.05 %CV
	50 bp to 160 bp	0.0021 ng/ul	0.1 %Total	0.0480 nmole/L	73 Avg. Size (bp)	38.96 %CV
	160 bp to 1000 bp	2.5454 ng/ul	99.1 %Total	9.4278 nmole/L	444 Avg. Size (bp)	29.94 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 34
Well Location: F10

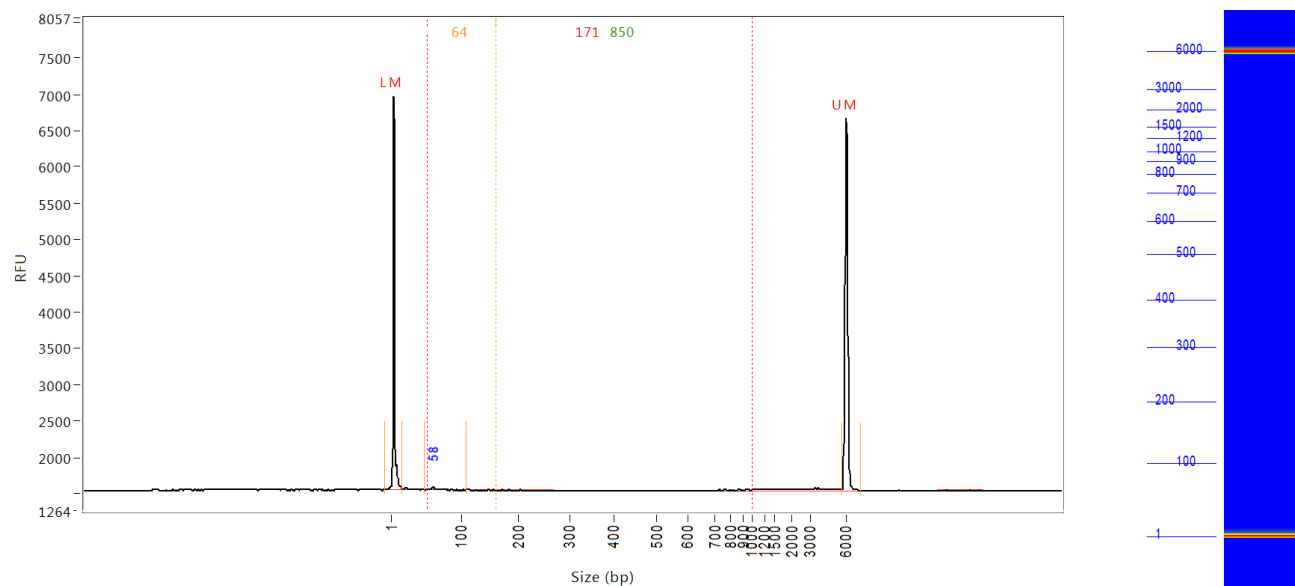


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	174.58	6011	34.954
2	316	0.6945	176	1261	405	30.58	1158	225.534
3	6000 (UM)	0.0059	5640	7216	5991	1.82	5754	23.115
	TIC:	0.6945	ng/uL					
	TIM:	2.8215	nmole/L					
	Total Conc.:	0.7075	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.6970 ng/ul	98.5 %Total	2.8587 nmole/L	401 Avg. Size (bp)	29.86 %CV
	50 bp to 160 bp	0.0041 ng/ul	0.6 %Total	0.0705 nmole/L	96 Avg. Size (bp)	39.78 %CV
	160 bp to 1000 bp	0.6929 ng/ul	97.9 %Total	2.8291 nmole/L	403 Avg. Size (bp)	29.22 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

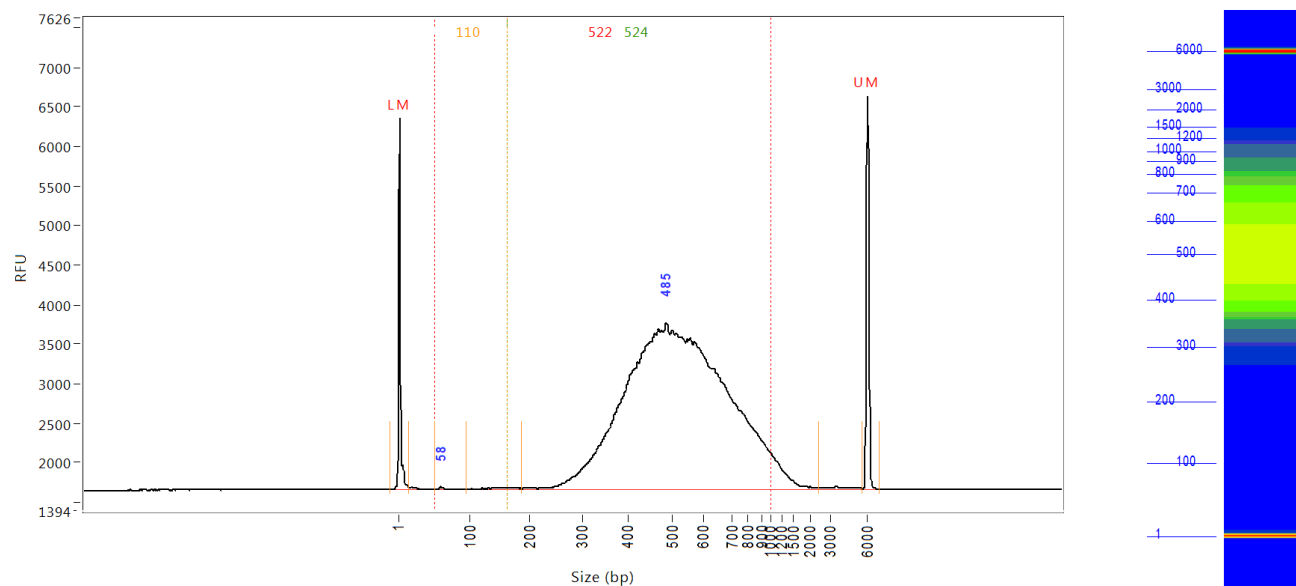
Data File: 2019 08 02 18H 51M.raw
Sample: Student mRNA-Seq library 35
Well Location: F11



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0090	0	15	1	168.96	5419	31.418
2	58	0.0020	46	109	61	14.39	44	0.586
3	6000 (UM)	0.0059	5664	7216	5998	1.81	5128	20.727
	TIC:	0.0020	ng/uL					
	TIM:	0.0539	nmole/L					
	Total Conc.:	0.0095	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0023 ng/ul	24.5 %Total		0.0223 nmole/L	171 Avg. Size (bp)	159.36 %CV	
	50 bp to 160 bp	0.0020 ng/ul	21.2 %Total		0.0518 nmole/L	64 Avg. Size (bp)	22.97 %CV	
	160 bp to 1000 bp	0.0003 ng/ul	3.3 %Total		0.0006 nmole/L	850 Avg. Size (bp)	11.63 %CV	

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 36
Well Location: G1

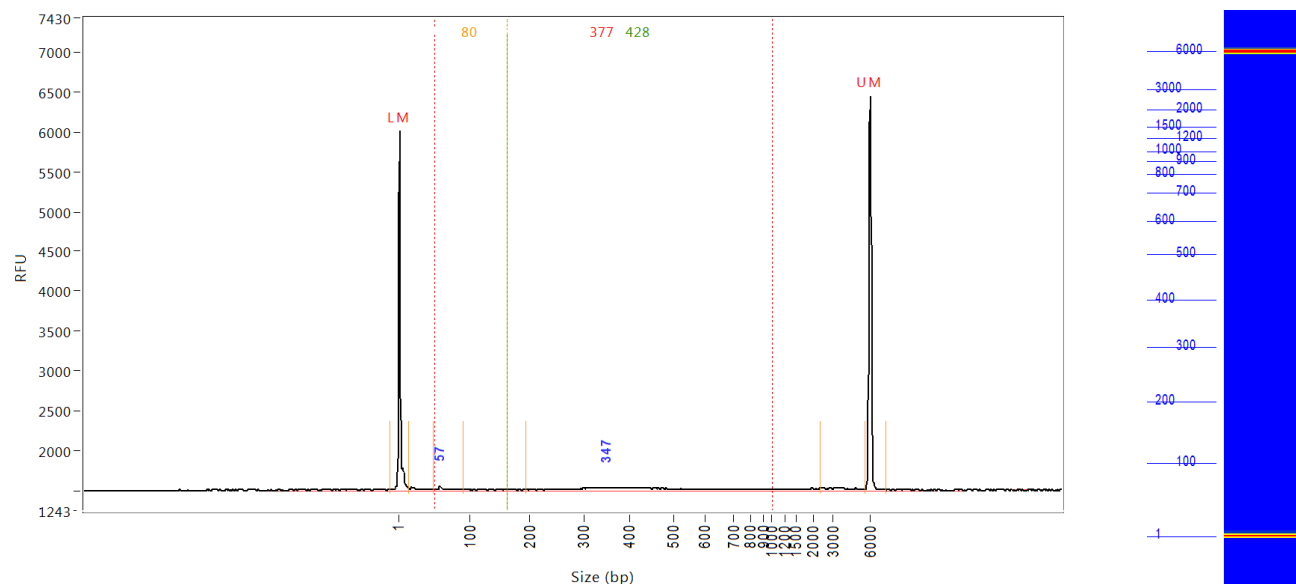


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	2	147.47	4701	28.208
2	58	0.0031	50	93	64	15.93	37	0.701
3	485	1.9030	187	2462	541	33.46	2097	428.858
4	6000 (UM)	0.0068	5628	6994	5999	1.71	4964	18.312
TIC:		1.9061	ng/uL					
TIM:		5.8681	nmole/L					
Total Conc.:		1.9232	ng/uL					

Smear Analysis	50 bp to 1000 bp	1.8697 ng/ul	187.7 %Total	5.8990 nmole/L	522 Avg. Size (bp)	27.50 %CV
	50 bp to 160 bp	0.0088 ng/ul	0.9 %Total	0.1316 nmole/L	110 Avg. Size (bp)	33.90 %CV
	160 bp to 1000 bp	1.8610 ng/ul	186.8 %Total	5.8493 nmole/L	524 Avg. Size (bp)	26.91 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 38
Well Location: G2

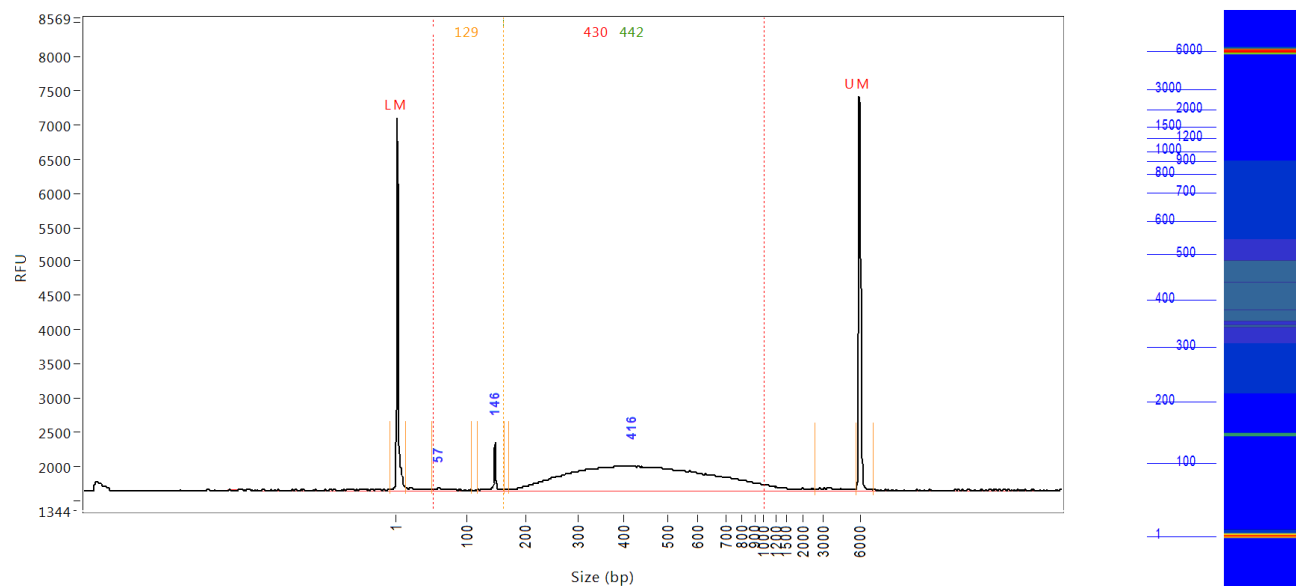


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	2	155.12	4511	26.780
2	57	0.0040	48	89	62	15.71	47	0.864
3	347	0.0356	193	2401	587	77.22	33	7.619
4	6000 (UM)	0.0074	5651	7271	5981	1.87	4938	18.998
TIC:		0.0396	ng/uL					
TIM:		0.2066	nmole/L					
Total Conc.:		0.0514	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0372 ng/ul	72.4 %Total	0.1624 nmole/L	377 Avg. Size (bp)	49.46 %CV
	50 bp to 160 bp	0.0055 ng/ul	10.7 %Total	0.1127 nmole/L	80 Avg. Size (bp)	39.50 %CV
	160 bp to 1000 bp	0.0317 ng/ul	61.7 %Total	0.1217 nmole/L	428 Avg. Size (bp)	35.14 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
 Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
 Manual Baseline Start (min): 10 Manual Baseline End (min): 48
 Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
 Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
 Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
 Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

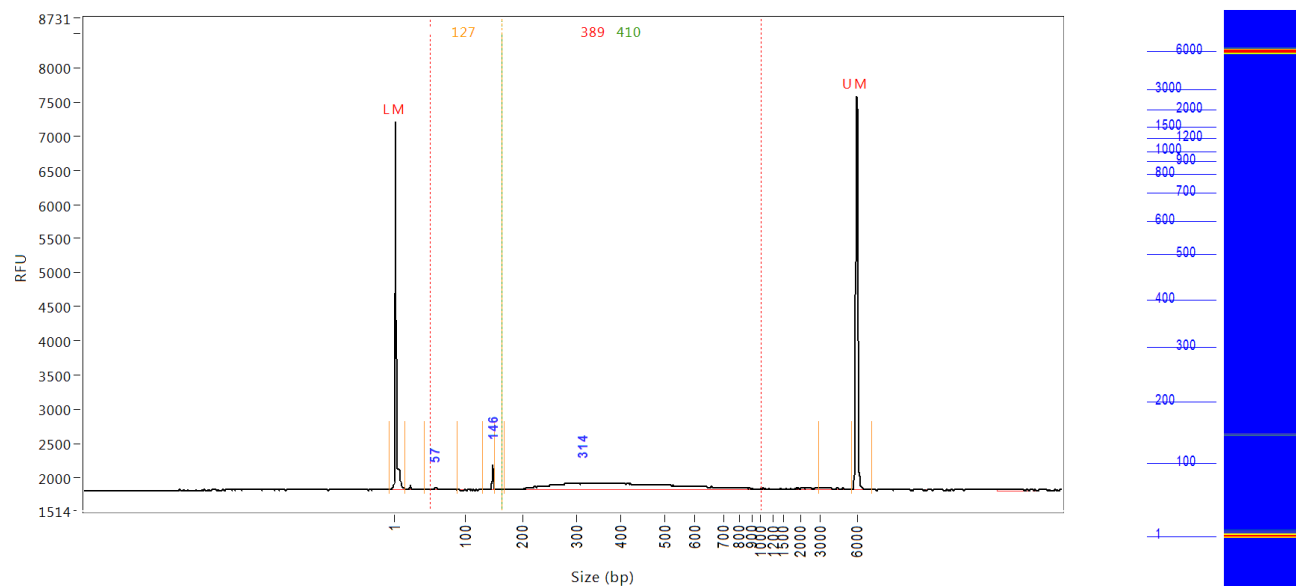
Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 39
Well Location: G3



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	2	156.05	5460	31.947
2	57	0.0033	51	108	66	18.35	38	0.844
3	146	0.0132	116	163	145	3.27	714	3.361
4	416	0.4234	172	2570	464	48.31	354	108.064
5	6000 (UM)	0.0069	5698	7086	5991	1.76	5769	21.184
	TIC:	0.4399	ng/uL					
	TIM:	1.7328	nmole/L					
	Total Conc.:	0.4487	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.4307 ng/ul	96.0 %Total	1.6487 nmole/L	430 Avg. Size (bp)	38.92 %CV		
	50 bp to 160 bp	0.0165 ng/ul	3.7 %Total	0.2101 nmole/L	129 Avg. Size (bp)	25.18 %CV		
	160 bp to 1000 bp	0.4143 ng/ul	92.3 %Total	1.5424 nmole/L	442 Avg. Size (bp)	35.98 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

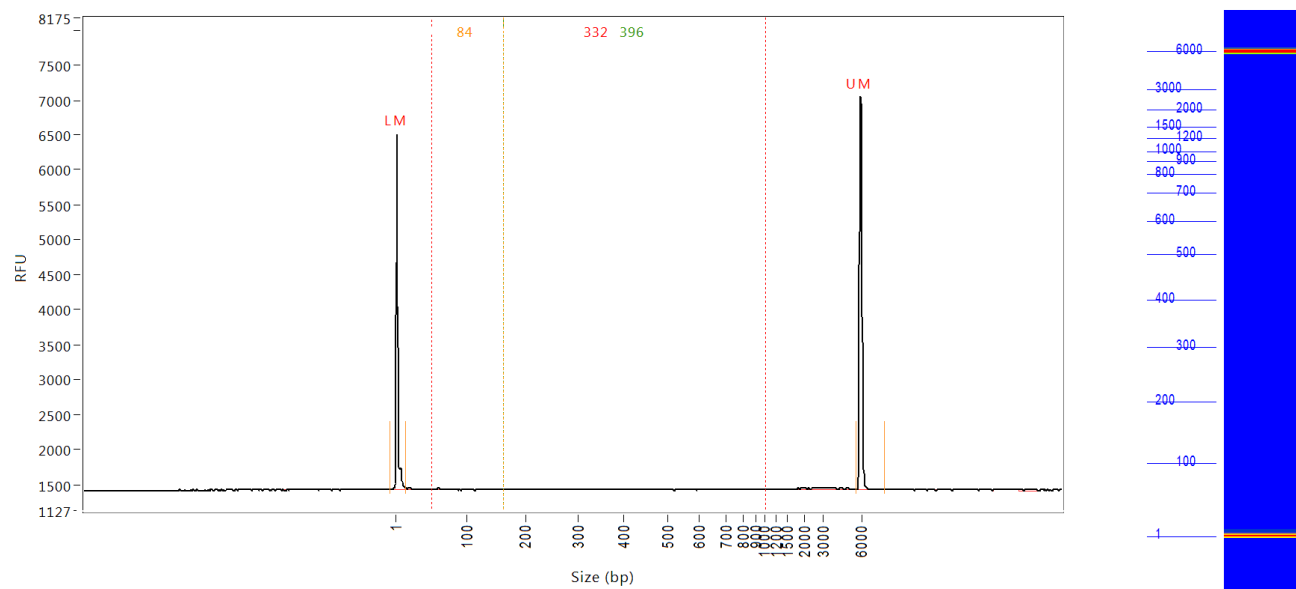
Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 40
Well Location: G4



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	16	2	148.74	5379	31.453
2	57	0.0020	42	89	60	15.33	25	0.513
3	146	0.0065	131	151	145	1.77	367	1.628
4	314	0.1118	166	2985	486	77.55	92	28.103
5	6000 (UM)	0.0071	5651	7294	5977	1.71	5757	21.559
	TIC:	0.1204	ng/uL					
	TIM:	0.5078	nmole/L					
	Total Conc.:	0.1266	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.1145 ng/ul	90.4 %Total	0.4841 nmole/L	389 Avg. Size (bp)	42.13 %CV		
	50 bp to 160 bp	0.0085 ng/ul	6.7 %Total	0.1101 nmole/L	127 Avg. Size (bp)	27.60 %CV		
	160 bp to 1000 bp	0.1060 ng/ul	83.7 %Total	0.4256 nmole/L	410 Avg. Size (bp)	37.02 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 41
Well Location: G5

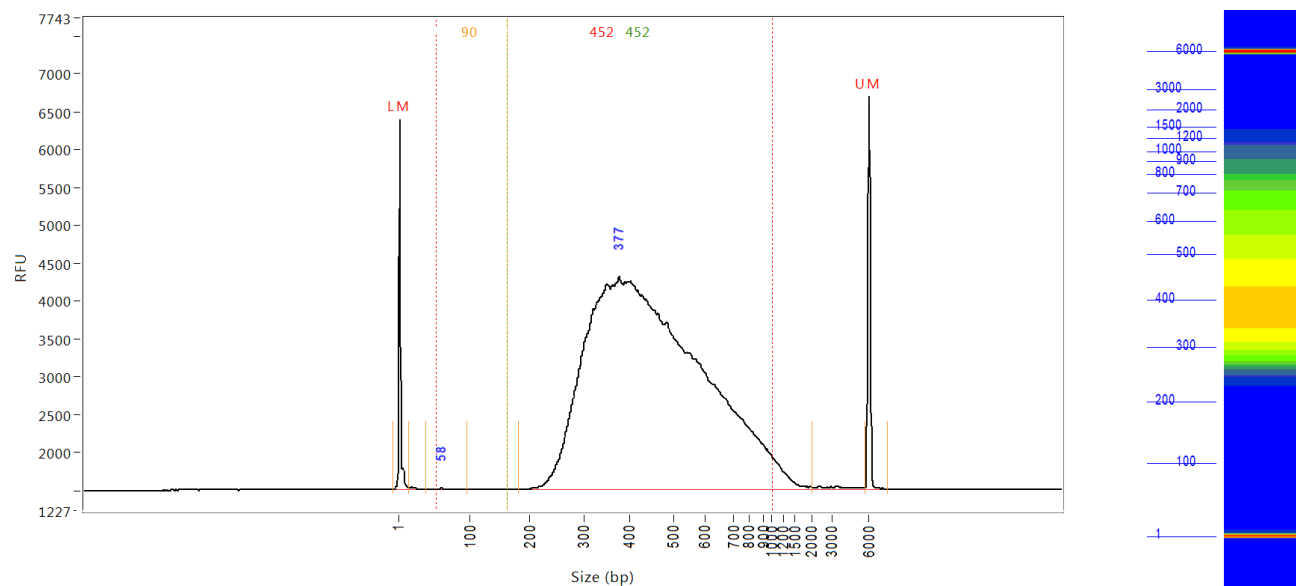


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	2	141.60	5077	30.161
2	6000 (UM)	0.0072	5675	7942	5994	2.22	5623	20.706
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0289	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0156 ng/ul	53.8 %Total	0.0771 nmole/L	332 Avg. Size (bp)	59.60 %CV
	50 bp to 160 bp	0.0032 ng/ul	11.1 %Total	0.0628 nmole/L	84 Avg. Size (bp)	39.77 %CV
	160 bp to 1000 bp	0.0124 ng/ul	42.8 %Total	0.0514 nmole/L	396 Avg. Size (bp)	42.97 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 42
Well Location: G6

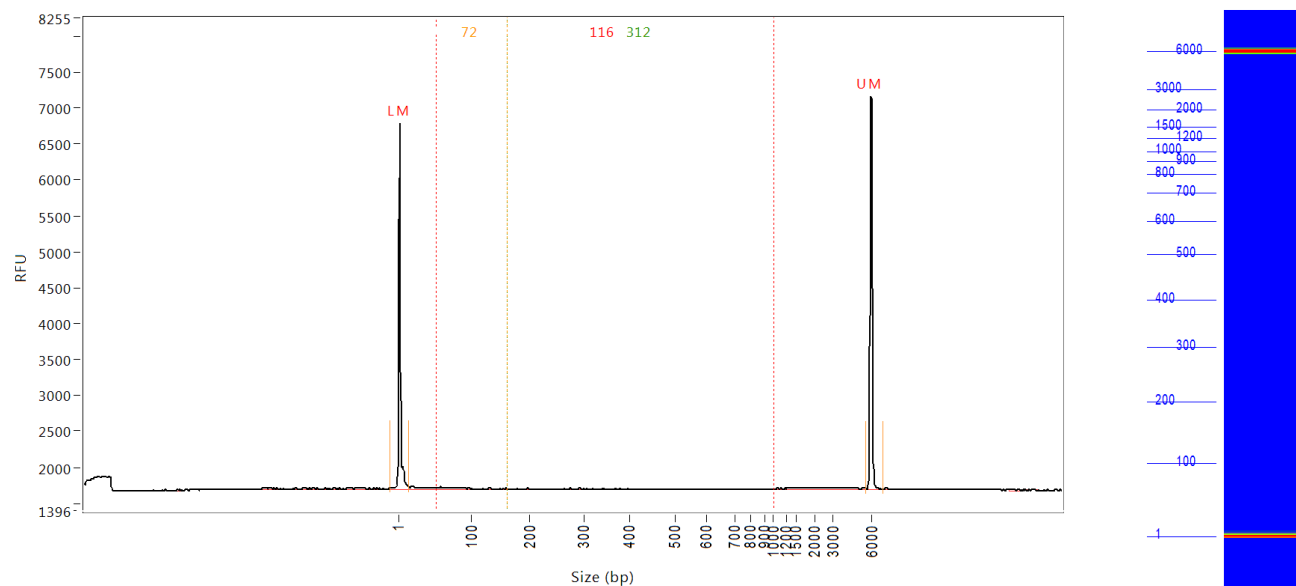


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	1	164.77	4886	28.158
2	58	0.0025	39	95	61	17.06	30	0.562
3	377	2.9934	180	2001	462	36.26	2807	673.391
4	6000 (UM)	0.0070	5675	7479	5990	2.00	5188	19.015
TIC:		2.9959	ng/uL					
TIM:		10.7281	nmole/L					
Total Conc.:		3.0072	ng/uL					

Smear Analysis	50 bp to 1000 bp	2.9569 ng/ul	98.3 %Total	10.7665 nmole/L	452 Avg. Size (bp)	31.61 %CV
	50 bp to 160 bp	0.0036 ng/ul	0.1 %Total	0.0661 nmole/L	90 Avg. Size (bp)	40.92 %CV
	160 bp to 1000 bp	2.9533 ng/ul	98.2 %Total	10.7428 nmole/L	452 Avg. Size (bp)	31.47 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

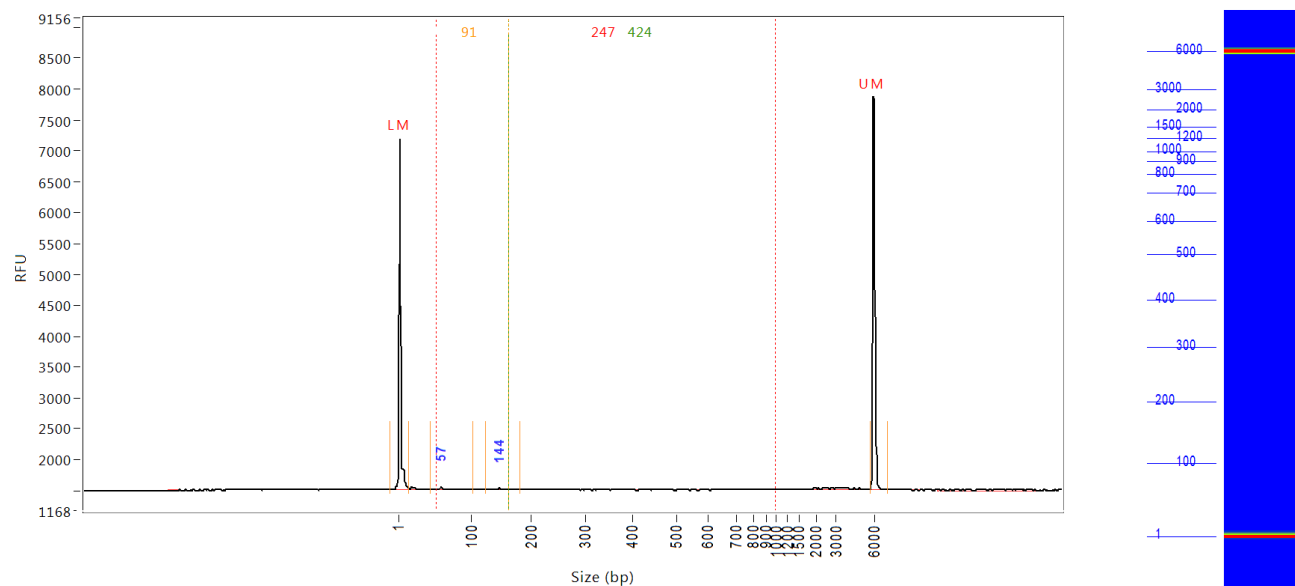
Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 43
Well Location: G7



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	1	191.67	5089	29.846
2	6000 (UM)	0.0070	5698	7040	5995	1.60	5457	20.172
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0139	ng/uL					
Smear Analysis	50 bp to 1000 bp	0.0041 ng/ul	29.4 %Total		0.0579 nmole/L	116 Avg. Size (bp)	94.07 %CV	
	50 bp to 160 bp	0.0033 ng/ul	24.1 %Total		0.0759 nmole/L	72 Avg. Size (bp)	33.84 %CV	
	160 bp to 1000 bp	0.0007 ng/ul	5.3 %Total		0.0039 nmole/L	312 Avg. Size (bp)	40.08 %CV	

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 44
Well Location: G8

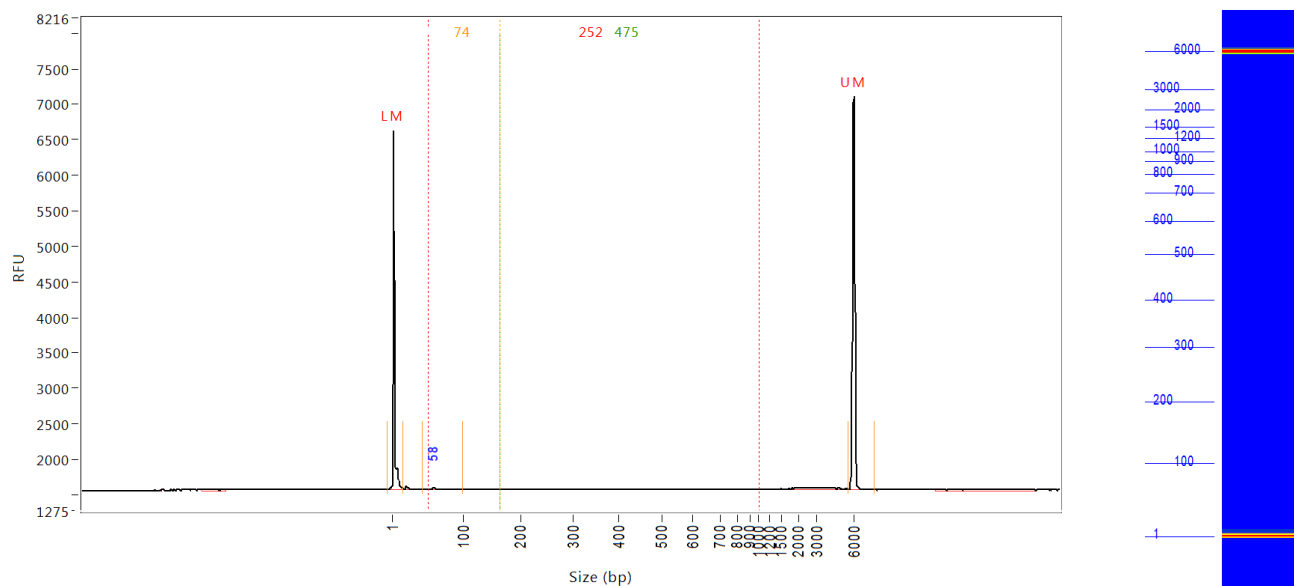


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	14	1	205.37	5681	34.054
2	57	0.0044	44	103	66	21.73	47	1.208
3	144	0.0022	124	181	149	9.45	41	0.599
4	6000 (UM)	0.0073	5698	7156	5996	1.72	6373	23.717
	TIC:	0.0066	ng/uL					
	TIM:	0.1346	nmole/L					
	Total Conc.:	0.0255	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0118 ng/ul	46.4 %Total	0.0789 nmole/L	247 Avg. Size (bp)	99.17 %CV
	50 bp to 160 bp	0.0063 ng/ul	24.8 %Total	0.1139 nmole/L	91 Avg. Size (bp)	39.22 %CV
	160 bp to 1000 bp	0.0055 ng/ul	21.6 %Total	0.0214 nmole/L	424 Avg. Size (bp)	61.28 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 46
Well Location: G9

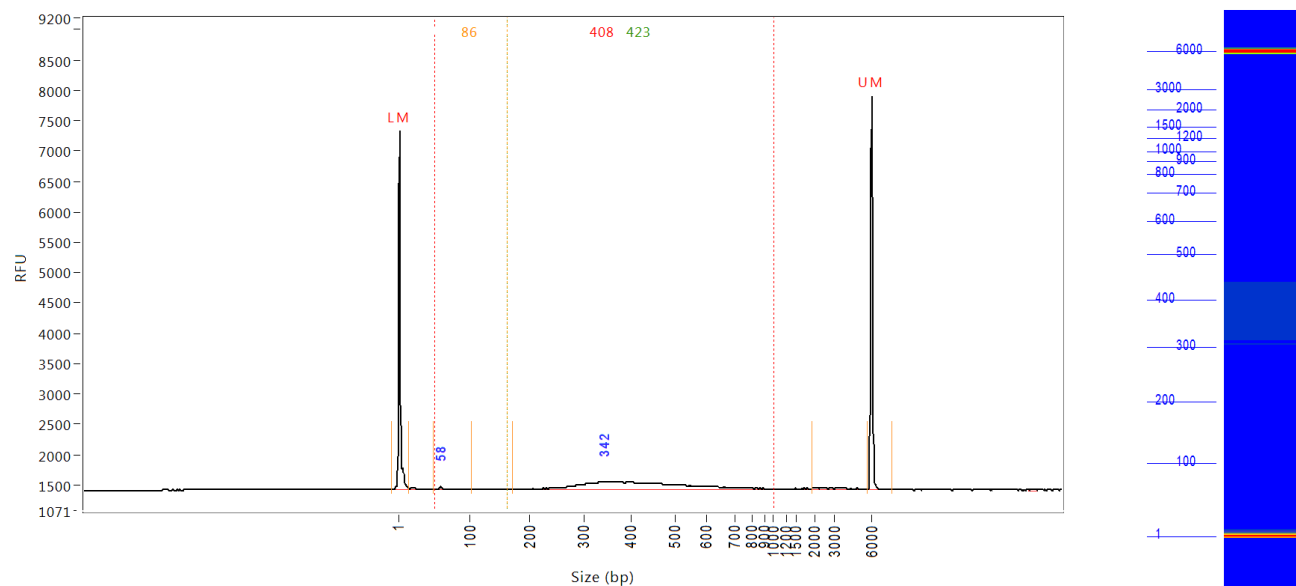


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	2	150.08	5046	29.367
2	58	0.0023	43	98	61	17.03	32	0.545
3	6000 (UM)	0.0072	5628	7710	5980	1.66	5533	20.175
	TIC:	0.0023	ng/uL					
	TIM:	0.0624	nmole/L					
	Total Conc.:	0.0152	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0044 ng/ul	28.9 %Total	0.0286 nmole/L	252 Avg. Size (bp)	102.54 %CV
	50 bp to 160 bp	0.0025 ng/ul	16.2 %Total	0.0543 nmole/L	74 Avg. Size (bp)	39.73 %CV
	160 bp to 1000 bp	0.0019 ng/ul	12.8 %Total	0.0067 nmole/L	475 Avg. Size (bp)	51.71 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 47
Well Location: G10

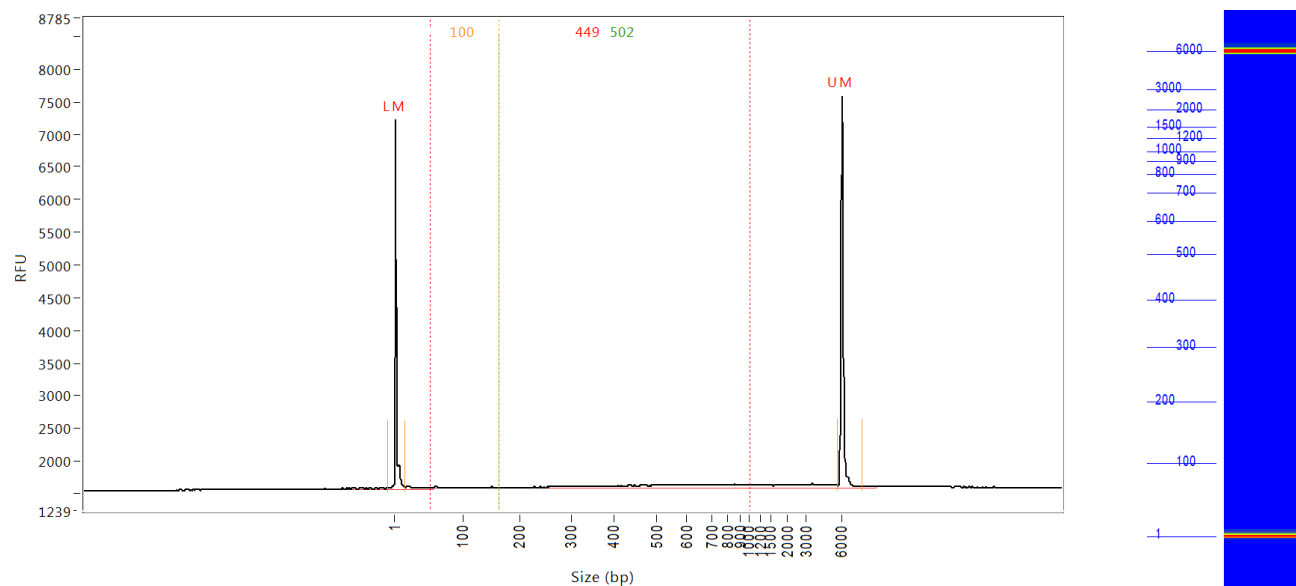


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	1	155.58	5914	34.563
2	58	0.0034	49	101	65	18.93	48	0.940
3	342	0.1080	170	1958	457	51.65	126	29.836
4	6000 (UM)	0.0071	5675	7641	5991	1.81	6484	23.523
TIC:		0.1115	ng/uL					
TIM:		0.4749	nmole/L					
Total Conc.:		0.1225	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.1096 ng/ul	89.4 %Total	0.4419 nmole/L	408 Avg. Size (bp)	37.51 %CV
	50 bp to 160 bp	0.0048 ng/ul	3.9 %Total	0.0917 nmole/L	86 Avg. Size (bp)	40.58 %CV
	160 bp to 1000 bp	0.1047 ng/ul	85.5 %Total	0.4078 nmole/L	423 Avg. Size (bp)	33.00 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 20H 02M.raw
Sample: Student mRNA-Seq library 48
Well Location: G11

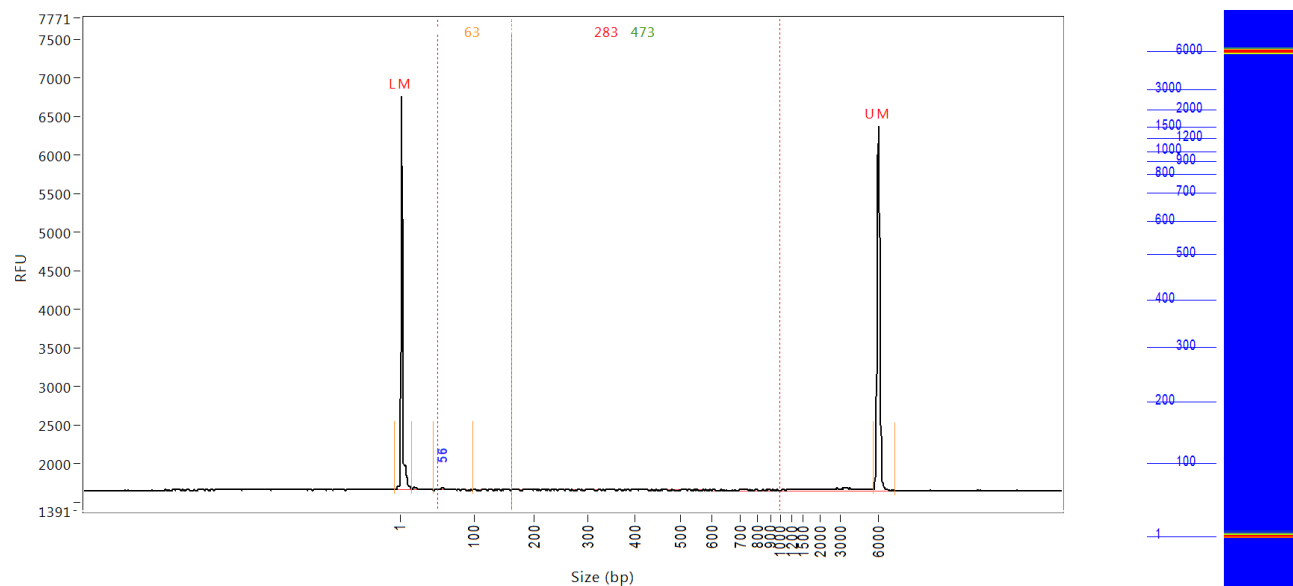


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0104	0	15	1	175.57	5662	32.758
2	6000 (UM)	0.0083	5651	7641	6020	2.67	5980	26.038
	TIC:	0.0000	ng/uL					
	TIM:	0.0000	nmole/L					
	Total Conc.:	0.0803	ng/uL					

Smear Analysis	50 bp to 1000 bp	0.0602 ng/ul	75.0 %Total	0.2209 nmole/L	449 Avg. Size (bp)	52.47 %CV
	50 bp to 160 bp	0.0080 ng/ul	9.9 %Total	0.1304 nmole/L	100 Avg. Size (bp)	34.69 %CV
	160 bp to 1000 bp	0.0523 ng/ul	65.2 %Total	0.1714 nmole/L	502 Avg. Size (bp)	40.91 %CV

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp) 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 21H 14M.raw
Sample: Student mRNA-Seq library 49
Well Location: H1



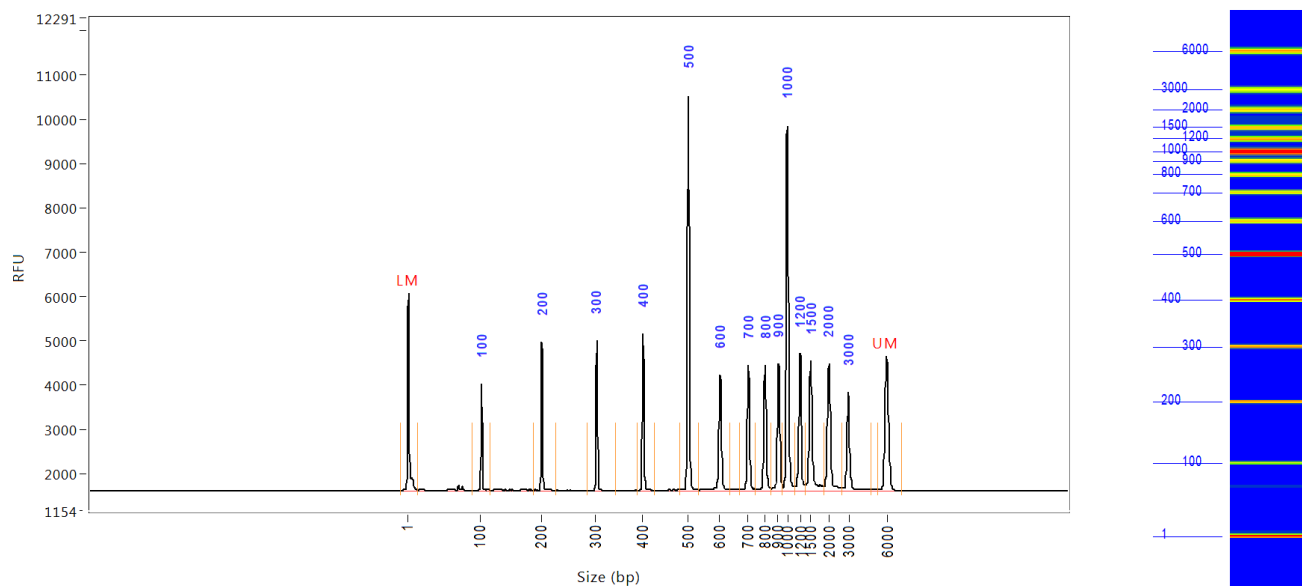
Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0096	0	15	1	187.62	5087	29.804
2	56	0.0010	45	98	58	10.30	21	0.259
3	6000 (UM)	0.0061	5558	7248	5983	1.87	4716	19.081
	TIC:	0.0010	ng/uL					
	TIM:	0.0282	nmole/L					
	Total Conc.:	0.0107	ng/uL					
Smear Analysis								
	50 bp to 1000 bp	0.0023 ng/ul	0.2 %Total	0.0133 nmole/L	283 Avg. Size (bp)	93.25 %CV		
	50 bp to 160 bp	0.0011 ng/ul	0.1 %Total	0.0276 nmole/L	63 Avg. Size (bp)	31.60 %CV		
	160 bp to 1000 bp	0.0012 ng/ul	0.1 %Total	0.0043 nmole/L	473 Avg. Size (bp)	47.97 %CV		

Sample Peak Width (sec): 50 Sample Min Peak Height: 25 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
Manual Baseline Start (min): 10 Manual Baseline End (min): 48
Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0

Data File: 2019 08 02 21H 14M.raw

Sample: hs NGS ladder

Well Location: H12



Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0096	0	15	1	173.62	4449	25.916
2	100	0.0425	87	116	100	1.84	2414	9.592
3	200	0.0534	186	226	200	1.22	3354	12.051
4	300	0.0547	283	344	300	1.07	3380	12.342
5	400	0.0579	387	426	400	0.65	3555	13.051
6	500	0.1533	483	535	500	0.64	8897	34.560
7	600	0.0588	535	634	598	1.61	2618	13.257
8	700	0.0544	673	748	700	1.08	2849	12.258
9	800	0.0544	748	843	798	1.23	2846	12.279
10	900	0.0556	843	949	898	1.41	2883	12.547
11	1000	0.1598	949	1127	999	1.98	8211	36.029
12	1200	0.0620	1127	1363	1202	2.84	3099	13.984
13	1500	0.0667	1363	1850	1512	5.26	2945	15.044
14	2000	0.0629	1850	2677	2024	5.76	2882	14.189
15	3000	0.0493	2677	4745	3042	8.42	2232	11.113
16	6000 (UM)	0.0058	5303	7202	5987	2.38	3032	15.695
TIC:		0.9857	ng/uL					
TIM:		3.1827	nmole/L					
Total Conc.:		0.9960	ng/uL					

Sample Peak Width (sec): 10 Sample Min Peak Height: 100 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
 Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 0
 Manual Baseline Start (min): 10 Manual Baseline End (min): 48
 Marker Peak Width (sec): 5 Marker Min Peak Height: 200 Marker Baseline V to V?: Y Marker Baseline V to V pts: 3
 Lower Marker Selection: First Peak > 200 RFU Upper Marker Selection: Last Peak > 200 RFU
 Ladder Size (bp): 1, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1500, 2000, 3000, 6000
 Quantification Using: Ladder Final Concentration (ng/uL): 0.0830 Dilution Factor: 12.0