Fragment Analyzer Run Summary:

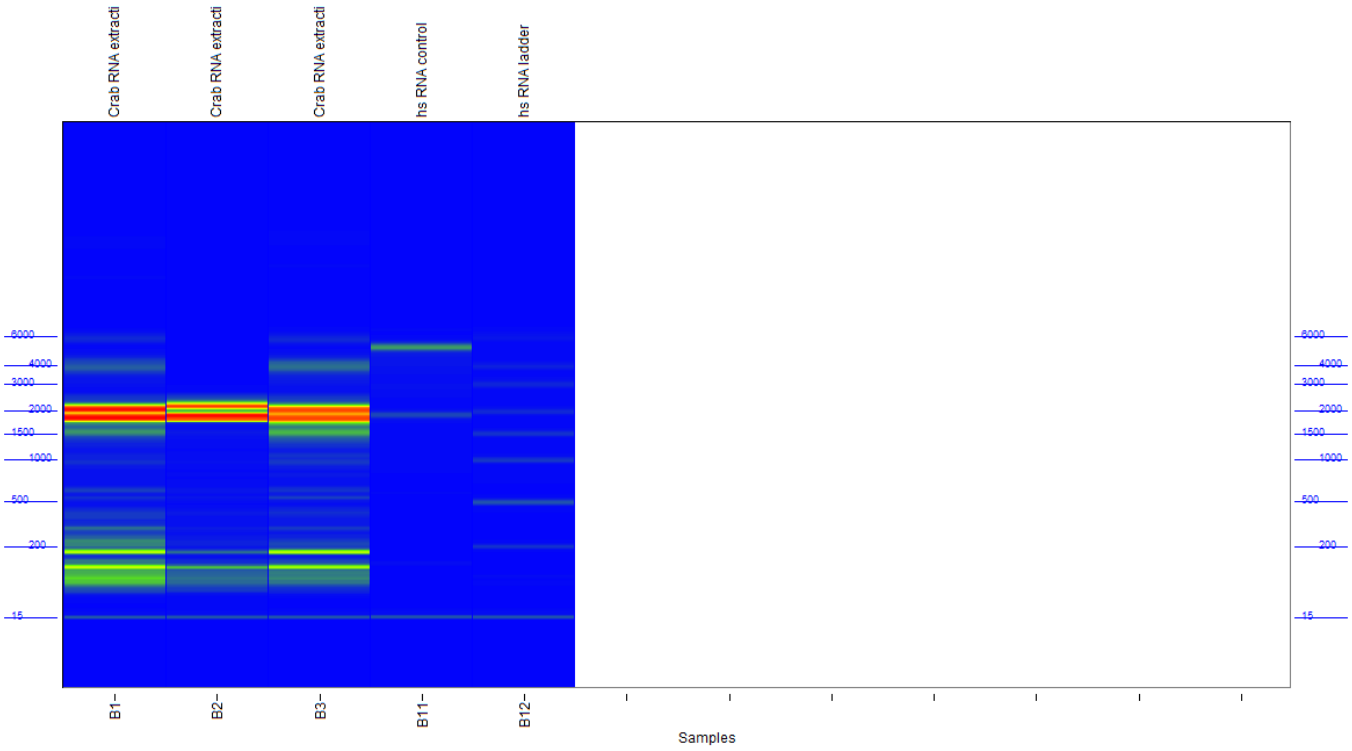
Filename and Data Path: C:\AATI\Data\2019 05 21\2019 05 21 Crab DNase treatment hs RNA 16-34-42\2019 05 21 16H 34M.raw
Created: Tuesday, May 21, 2019 4:56:59 PM
# of Capillaries: 5
Array Serial #: 021919-03SFS
Effect Length: 33 cm
Array Usage Count: 99
FA Version #: 1.2.0.11
Device Serial #: 2730

METHOD INFORMATION
Method Name: DNF-472T33 - HS Total RNA 15nt.mthds
Gel Prime: No
Full Conditioning: Yes
Gel Prime to Buffer: Yes
Gel Selection: Gel 2
Perform Prerun: 8.0 kV, 30 sec.
Rinse: No
Marker 1: No
Rinse: Tray: 3, Row: A, # Dips: 2
Sample Injection: 8.0 kV, 150 sec.
Separation: 8.0 kV, 45.0 min.
Tray Name: Tray-3

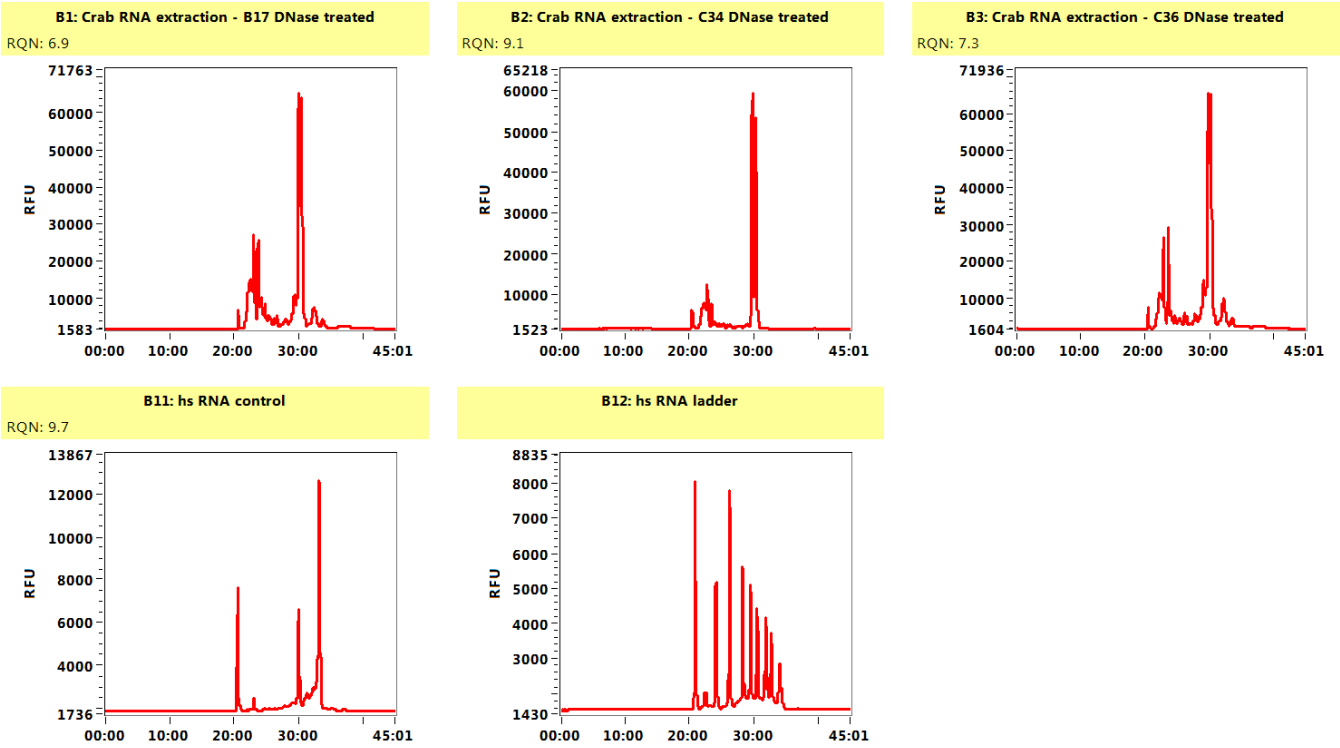
Analysis Mode: RNA (Eukaryotic)

NOTES

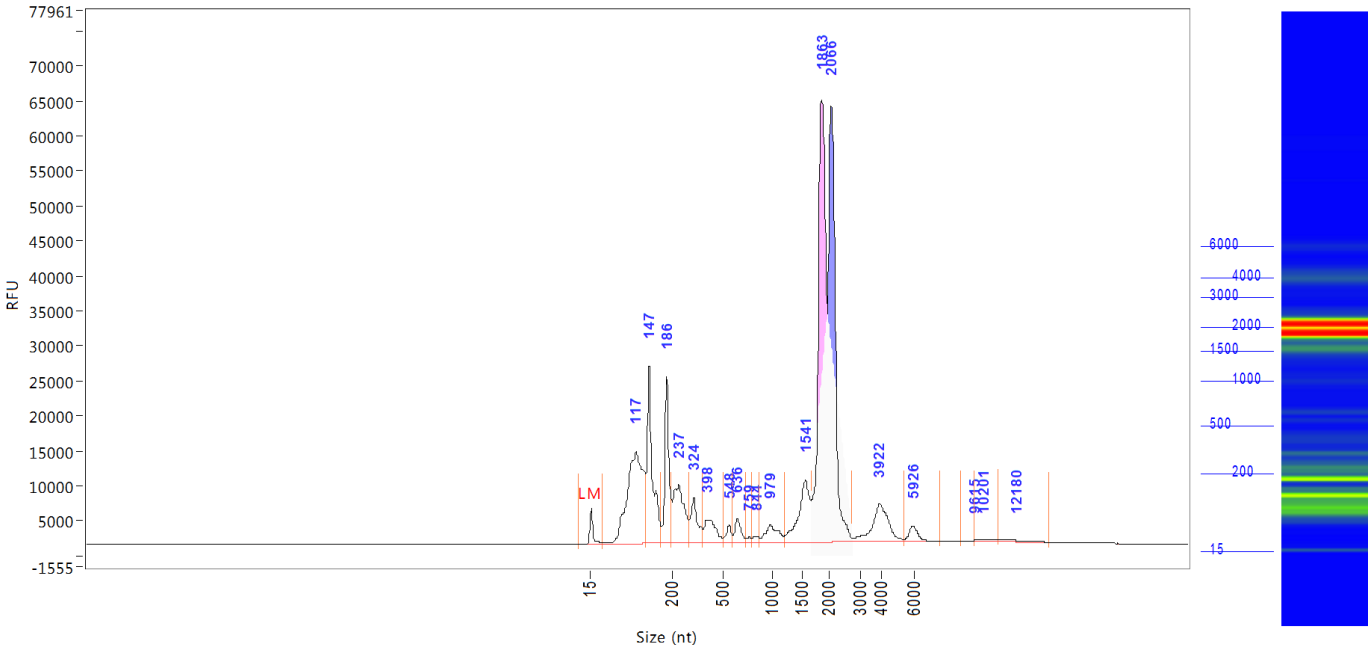
Gel Image



Filename and Data Path: C:\AATI\Data\2019 05 21\2019 05 21 Crab DNase treatment hs RNA 16-34-42\2019 05 21 16H 34M.raw



Sample: Crab RNA extraction - B17 DNase treated
Well Location: B1
Created: Tuesday, May 21, 2019 4:56:59 PM

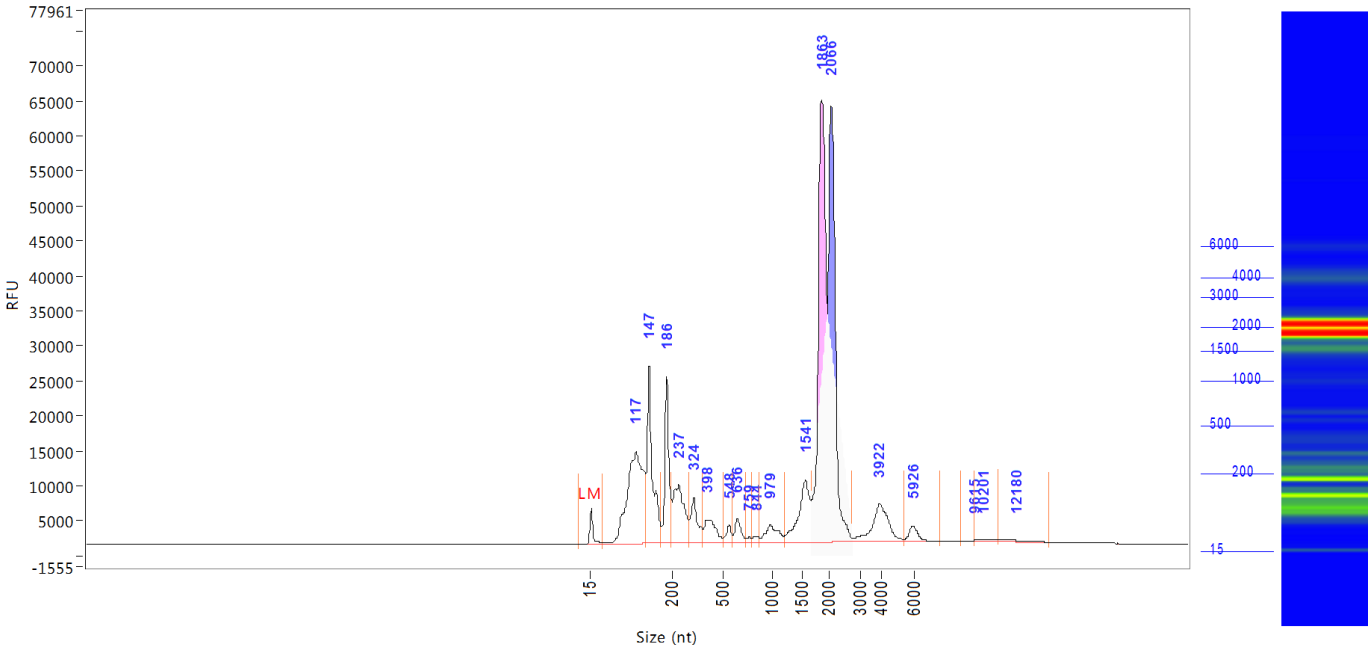


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.0321	0	42	4996
2	117	4.3927	42	139	13212
3	147	2.6994	139	174	25376
4	186	1.9104	174	198	23757
5	237	1.7128	198	294	8331
6	324	0.8449	294	377	6543
7	398	0.6992	377	495	3338
8	548	0.2240	495	590	2564
9	636	0.3726	590	729	3462
10	759	0.0575	729	784	778
11	844	0.0950	784	873	802
12	979	0.5172	873	1187	2478
13	1541	1.5440	1187	1654	8906
14	1863	7.3432	1654	1976	63276
15	2066	6.5655	1976	2766	62388
16	3922	1.2342	2766	5358	5424
17	5926	0.2654	5358	7588	2217
18	9615	0.0010	8809	9640	64
19	10201	0.0257	9640	11081	132
20	12180	0.0455	11081	14134	213

TIC:	30.5501	ng/uL
TIM:	276.5575	nmole/L
Total Conc.:	30.1606	ng/uL

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: Crab RNA extraction - B17 DNase treated
Well Location: B1
Created: Tuesday, May 21, 2019 4:56:59 PM

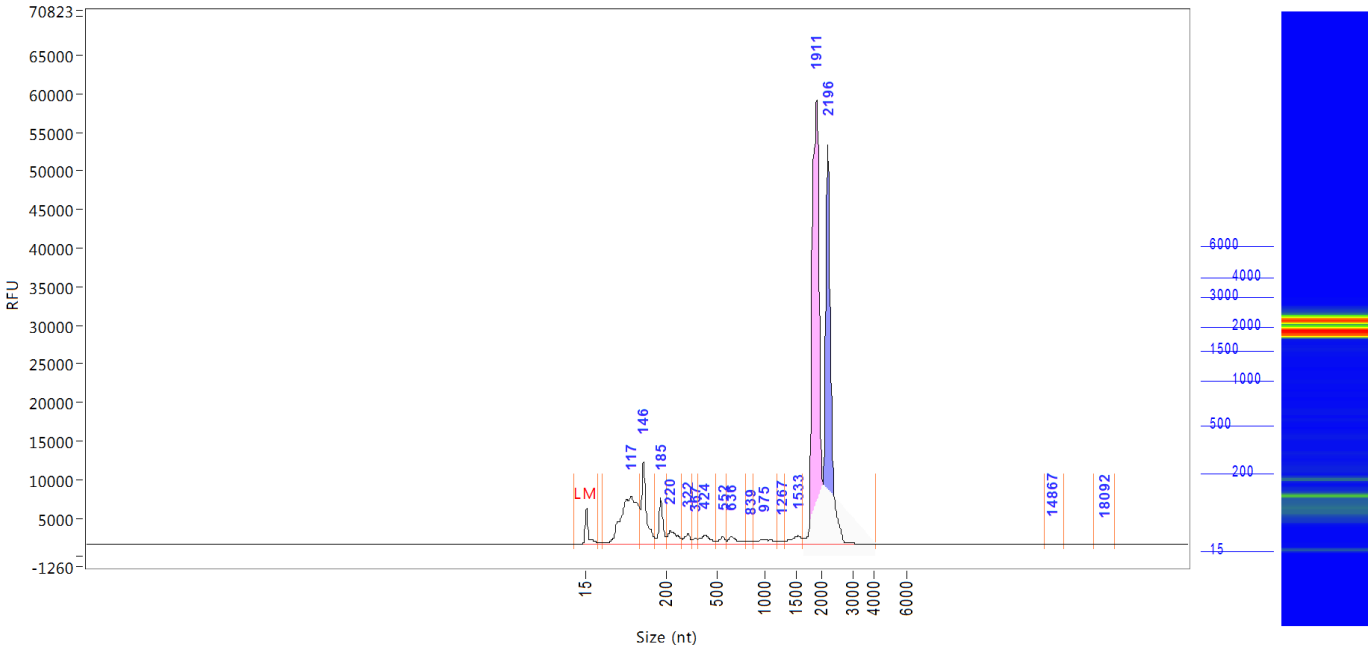


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU

28S/18S:	0.8
RQN	6.9

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: Crab RNA extraction - C34 DNase treated
Well Location: B2
Created: Tuesday, May 21, 2019 4:56:59 PM

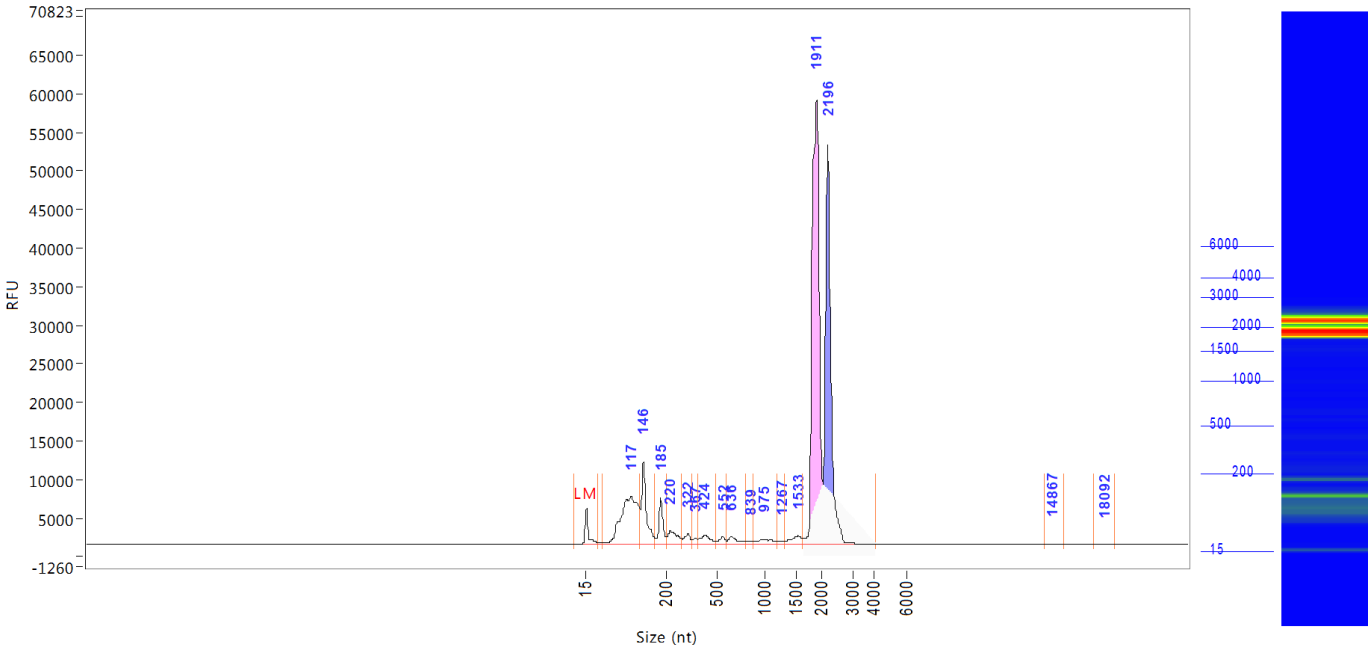


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.0321	0	44	4569
2	117	2.1877	53	138	6190
3	146	1.0418	138	173	10697
4	185	0.4710	173	198	6015
5	220	0.3139	198	289	1651
6	322	0.1455	289	346	1304
7	367	0.0636	346	381	728
8	424	0.2051	381	486	1109
9	552	0.0981	486	586	991
10	636	0.1594	586	789	994
11	839	0.0444	789	877	378
12	975	0.1546	877	1187	634
13	1267	0.0391	1187	1300	436
14	1533	0.1909	1300	1638	1063
15	1911	6.2856	1638	2040	57634
16	2196	4.2884	2040	4100	51766
17	14867	0.0037	14403	15649	108
18	18092	0.0019	17456	18678	55

TIC:	15.6947	ng/uL
TIM:	117.3532	nmole/L
Total Conc.:	15.6045	ng/uL
28S/18S:	0.5	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```

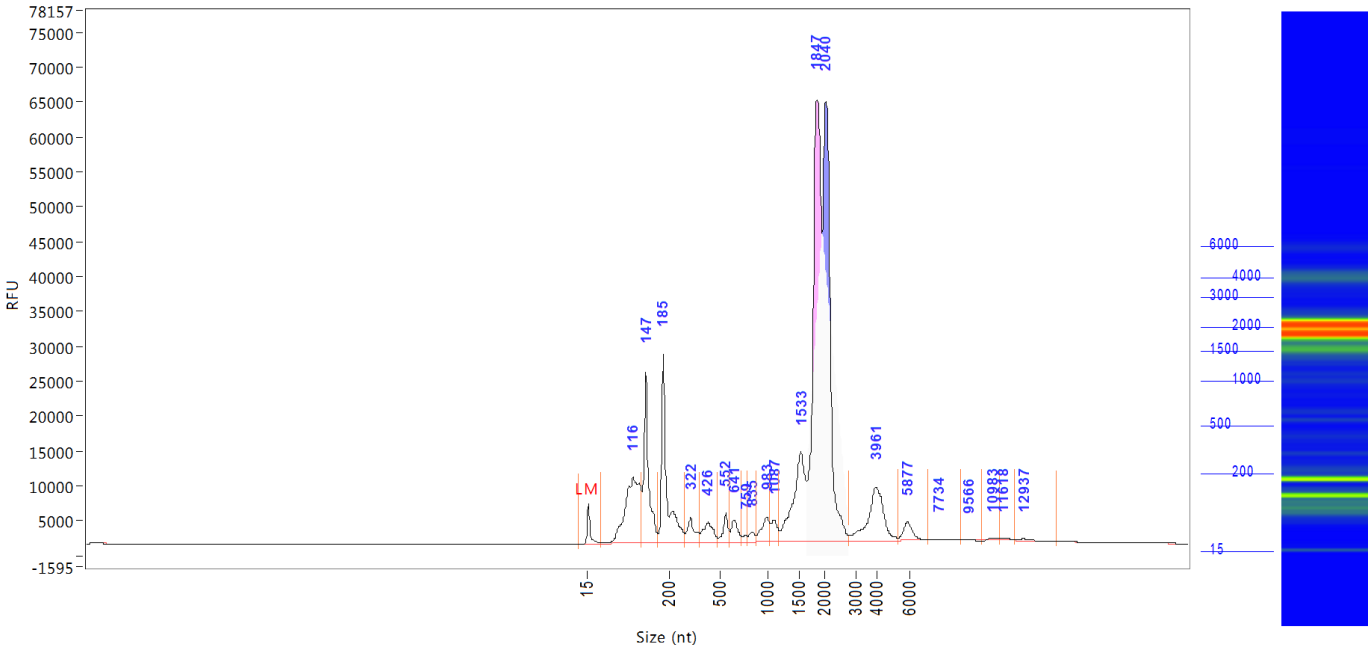

Sample: Crab RNA extraction - C34 DNase treated
Well Location: B2
Created: Tuesday, May 21, 2019 4:56:59 PM



Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
RQN	9.1				

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```

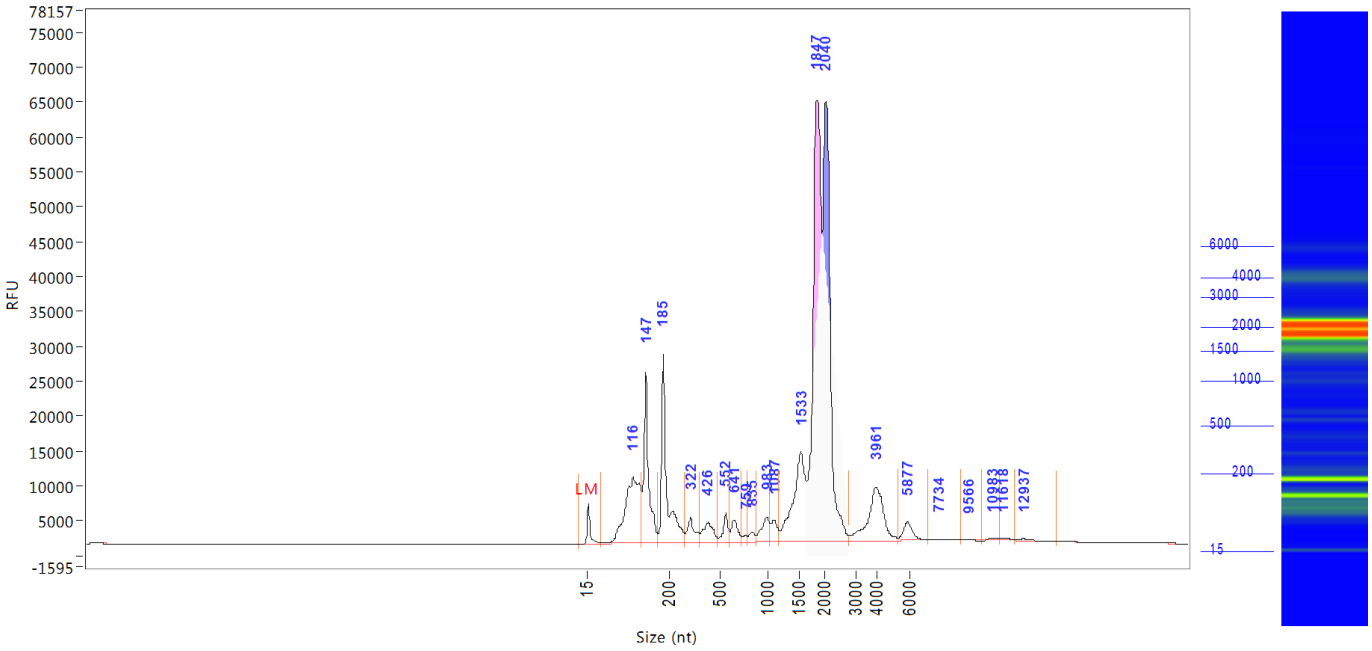

Sample: Crab RNA extraction - C36 DNase treated
Well Location: B3
Created: Tuesday, May 21, 2019 4:56:59 PM



Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.0321	0	43	5759
2	116	2.6192	43	138	9461
3	147	2.0150	138	173	24594
4	185	2.4225	173	291	27089
5	322	0.4159	291	379	3695
6	426	0.4684	379	486	2877
7	552	0.3106	486	598	4132
8	641	0.3227	598	725	3192
9	759	0.0642	725	780	996
10	835	0.1340	780	873	1314
11	983	0.4285	873	1034	3609
12	1087	0.2828	1034	1181	3109
13	1533	2.1076	1181	1646	12807
14	1847	6.8727	1646	1952	63363
15	2040	6.3973	1952	2779	63089
16	3961	1.4833	2779	5284	7678
17	5877	0.2887	5284	7099	2565
18	7734	0.0254	7099	9102	140
19	9566	0.0001	9102	10421	8
20	10983	0.0135	10421	11447	148
21	11618	0.0100	11447	12351	120
22	12937	0.0513	12351	14916	339
	TIC:	26.7336	ng/uL		

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: Crab RNA extraction - C36 DNase treated
Well Location: B3
Created: Tuesday, May 21, 2019 4:56:59 PM

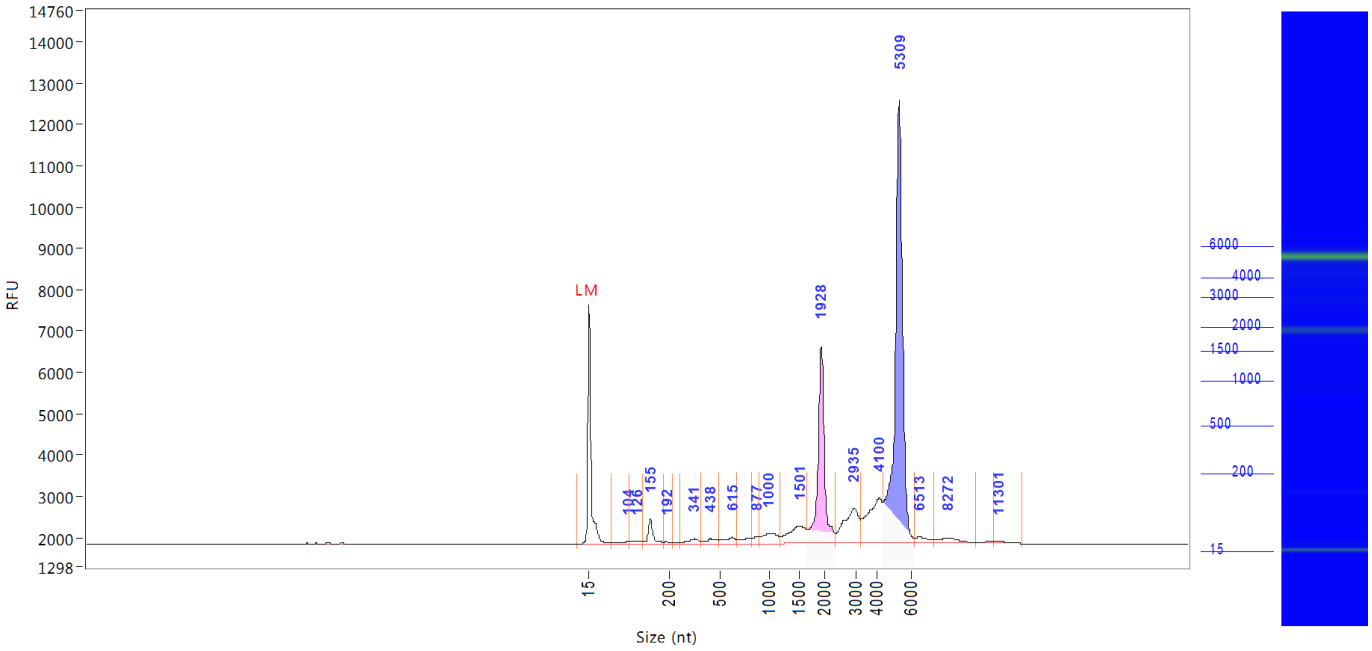


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU

TIM:	192.4043	nmole/L
Total Conc.:	26.3724	ng/uL
28S/18S:	0.7	
RQN	7.3	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: hs RNA control
Well Location: B11
Created: Tuesday, May 21, 2019 4:56:59 PM

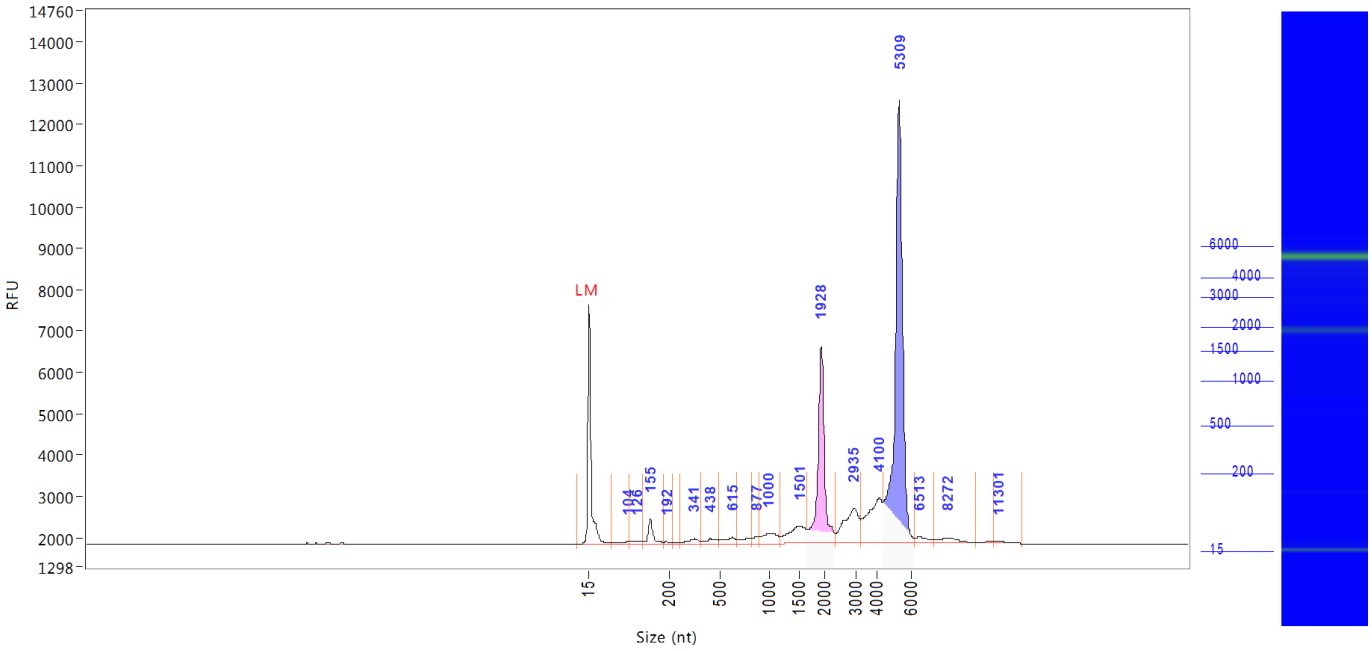


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.0321	0	69	5772
2	104	0.0079	69	110	52
3	126	0.0108	110	140	65
4	155	0.0473	140	186	608
5	192	0.0038	186	213	43
6	341	0.0181	263	384	112
7	438	0.0181	384	488	114
8	615	0.0223	488	662	151
9	877	0.0151	818	903	165
10	1000	0.0491	903	1187	235
11	1501	0.0933	1187	1654	421
12	1928	0.3931	1654	2325	4763
13	2935	0.1528	2325	3197	843
14	4100	0.1852	3197	4322	1093
15	5309	0.9178	4322	6244	10740
16	6513	0.0212	6244	7417	150
17	8272	0.0270	7417	9982	131
18	11301	0.0039	11105	12815	37

TIC:	1.9866	ng/uL
TIM:	3.8713	nmole/L
Total Conc.:	2.0004	ng/uL
28S/18S:	2.4	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```

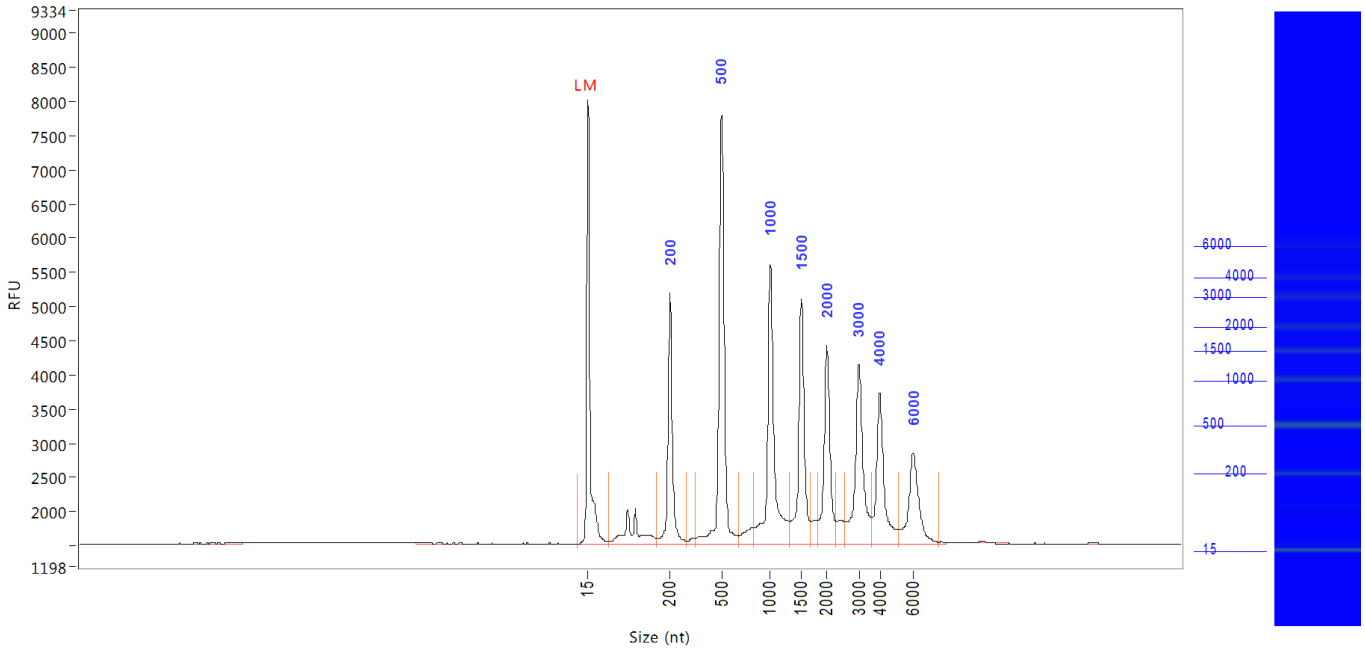

Sample: hs RNA control
Well Location: B11
Created: Tuesday, May 21, 2019 4:56:59 PM



Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
	RQN	9.7			

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 20    Sample Baseline V to V?: Y    Sample Baseline V to V pts: 3
Sample Filter: Binomial       # of Pts for Filter: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: hs RNA ladder
Well Location: B12
Created: Tuesday, May 21, 2019 4:56:59 PM



Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.0321	0	62	6496
2	200	0.2173	170	298	3661
3	500	0.4284	348	674	6274
4	1000	0.3210	839	1320	4089
5	1500	0.2343	1320	1686	3585
6	2000	0.1947	1823	2286	2898
7	3000	0.2215	2585	3628	2607
8	4000	0.1707	3628	5136	2203
9	6000	0.1323	5136	7514	1323

TIC:	1.9202	ng/uL
TIM:	8.1833	nmole/L
Total Conc.:	2.0000	ng/uL

```
Sample Peak Width (sec): 6    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: 9        Sample Start Region (min): 0  Sample End Region (min): 45
Manual Baseline Start (min): 18     Manual Baseline End (min): 38
Marker Peak Width (sec): 6    Marker Min Peak Height: 100   Marker Baseline V to V?: Y    Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 100 RFU                Upper Marker Selection: Last Peak > 100 RFU
Ladder Size (nt)15, 200, 500, 1000, 1500, 2000, 3000, 4000, 6000
Quantification Using: Ladder          Final Concentration (ng/uL): 0.2000          Dilution Factor: 10.0
Min. RFU for Data Processing: 2
```


Sample: hs RNA ladder
Well Location: B12
Created: Tuesday, May 21, 2019 4:56:59 PM
Fit Type: Point to Point