Fragment Analyzer Run Summary:

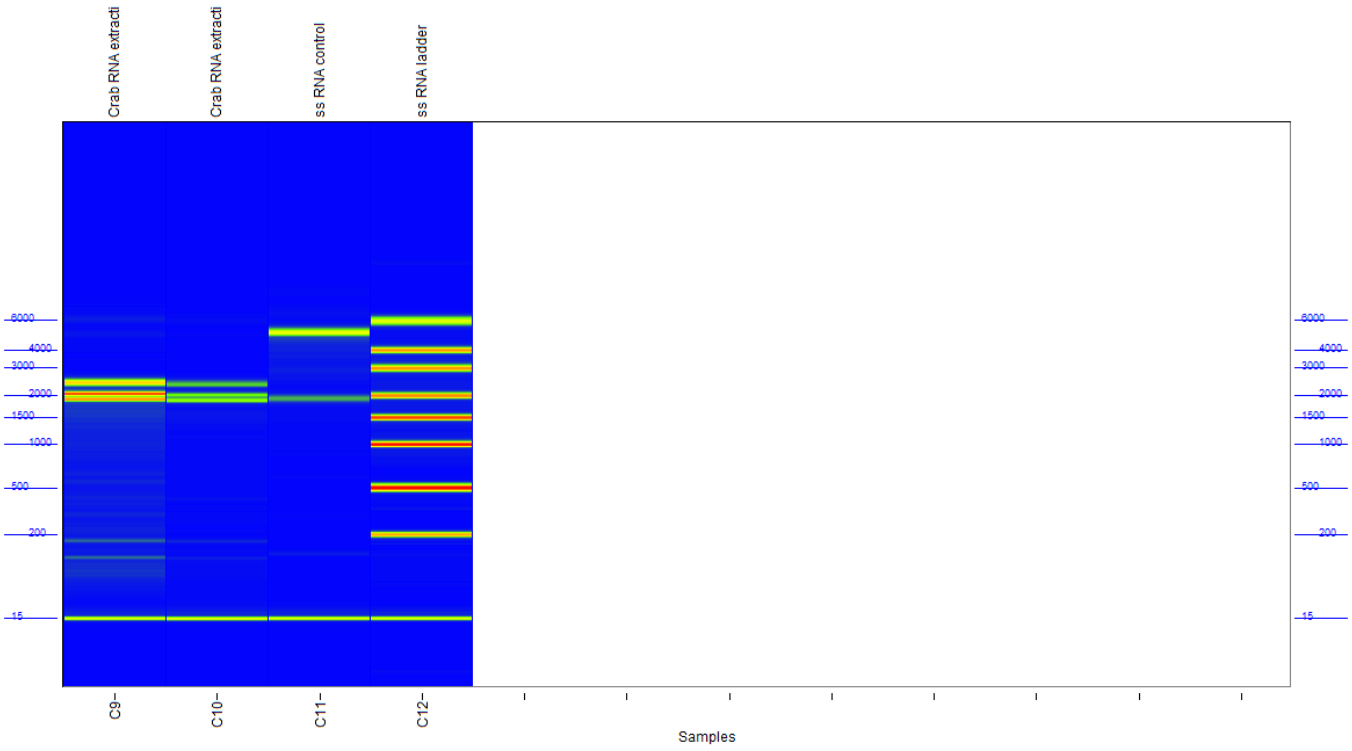
Filename and Data Path: C:\AATI\Data\2019 05 22\2019 05 22 GC3F ss RNA 15-18-27\2019 05 22 15H 18M.raw
Created: Wednesday, May 22, 2019 3:38:21 PM
# of Capillaries: 4
Array Serial #: 021919-03SFS
Effect Length: 33 cm
Array Usage Count: 100
FA Version #: 1.2.0.11
Device Serial #: 2730

METHOD INFORMATION
Method Name: DNF-471-33 - SS Total RNA 15nt-gel2.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: 5.0 kV, 4 sec.
Separation: 8.0 kV, 45.0 min.
Tray Name: Tray-3

Analysis Mode: RNA (Eukaryotic)

NOTES

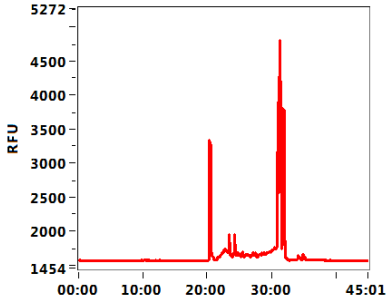
Gel Image



Filename and Data Path: C:\AATI\Data\2019 05 22\2019 05 22 GC3F ss RNA 15-18-27\2019 05 22 15H 18M.raw

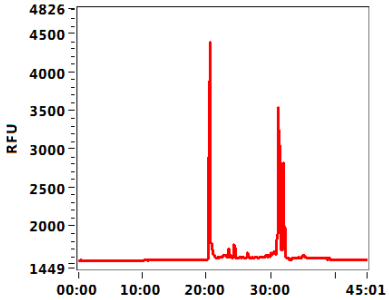
C9: Crab RNA extraction - 44

RQN: 7.5



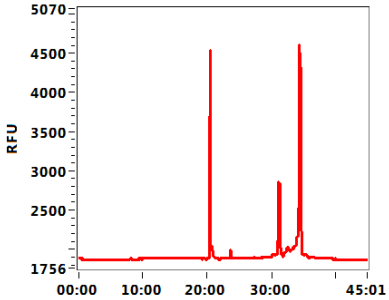
C10: Crab RNA extraction - 45

RQN: 8.7

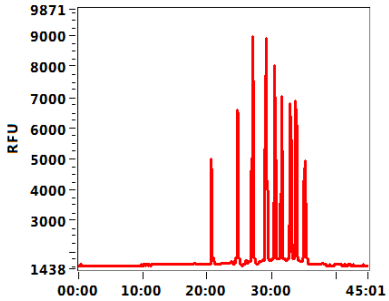


C11: ss RNA control

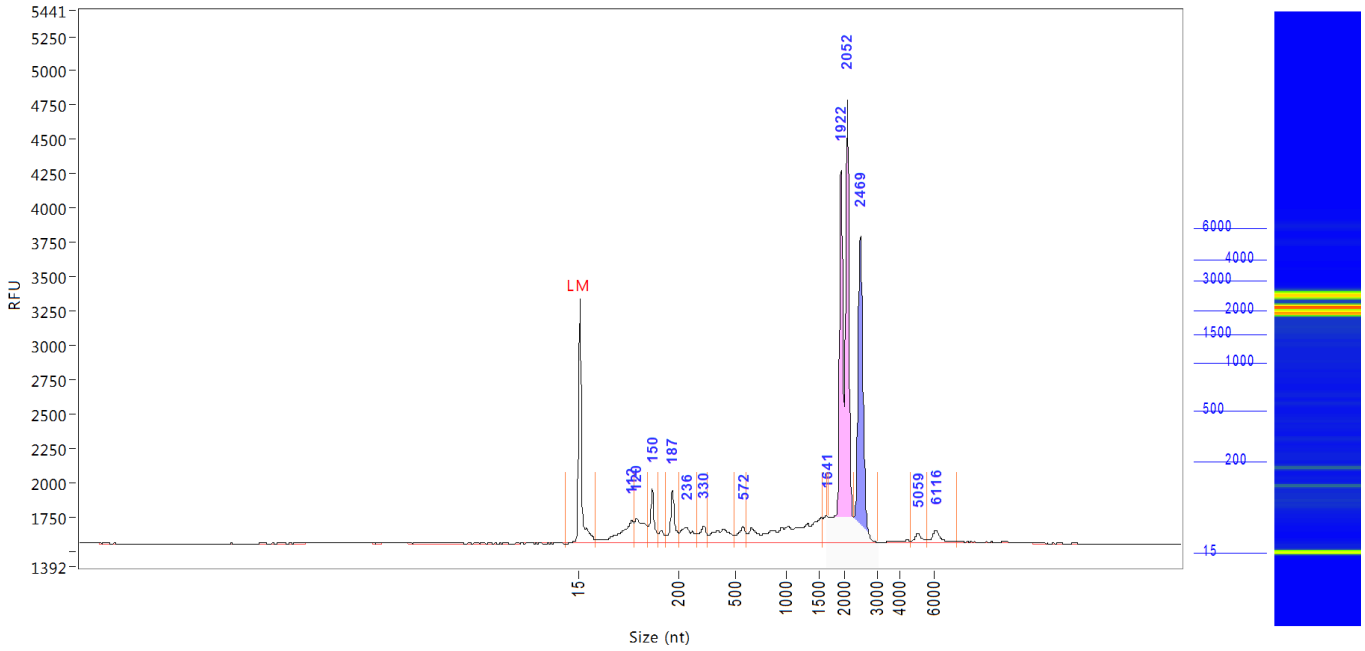
RQN: 10.0



C12: ss RNA ladder



Sample: Crab RNA extraction - 44
Well Location: C9
Created: Wednesday, May 22, 2019 3:38:21 PM

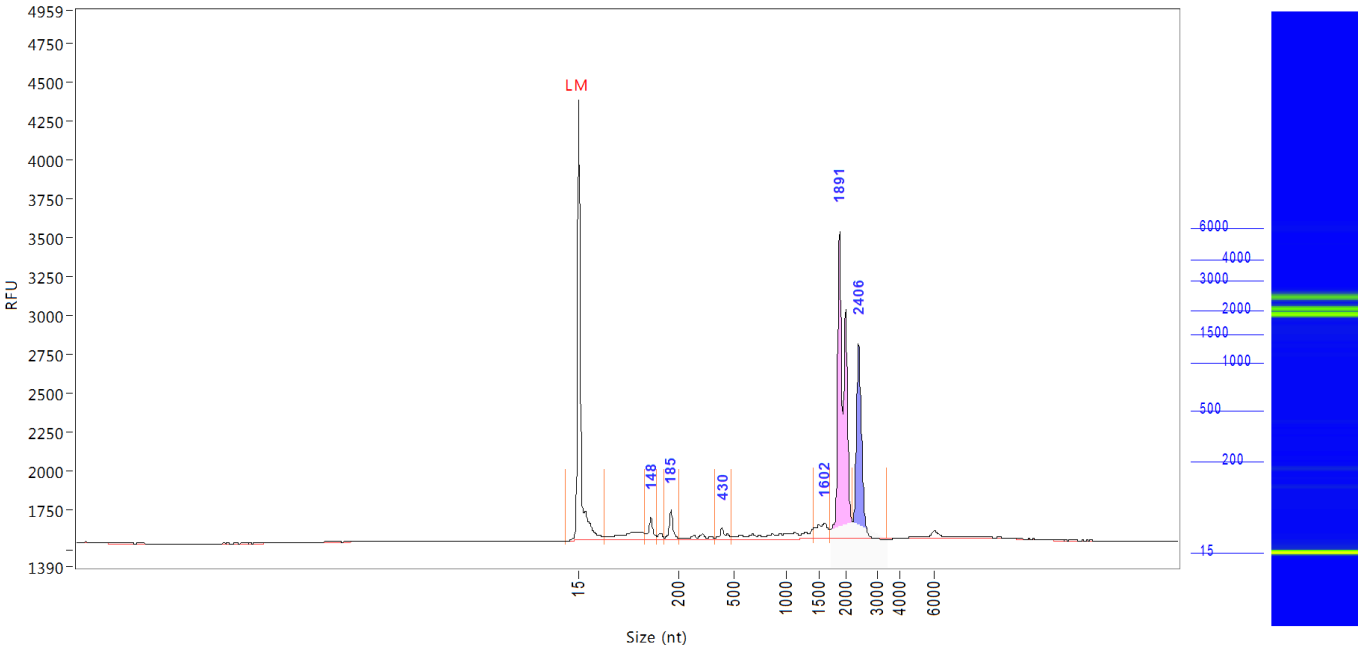


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.5382	0	46	1772
2	112	2.3408	46	115	160
3	120	1.9845	115	143	179
4	150	1.5374	143	160	388
5	187	1.6226	176	199	376
6	236	1.3814	199	299	111
7	330	0.7357	299	354	125
8	572	0.8079	493	611	119
9	1641	0.8708	1571	1696	195
10	1922	8.5894	1696	1984	2705
11	2052	17.5779	1657	2254	3224
12	2469	8.9598	2254	3020	2228
13	5059	0.3129	4636	5624	60
14	6116	0.4713	5624	7305	84

TIC:	47.1925	ng/uL
TIM:	268.8903	nmole/L
Total Conc.:	45.8742	ng/uL
28S/18S:	0.5	
RQN	7.5	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 50    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): 8.0000          Dilution Factor: 12.0
Min. RFU for Data Processing: 2
```


Sample: Crab RNA extraction - 45
Well Location: C10
Created: Wednesday, May 22, 2019 3:38:21 PM

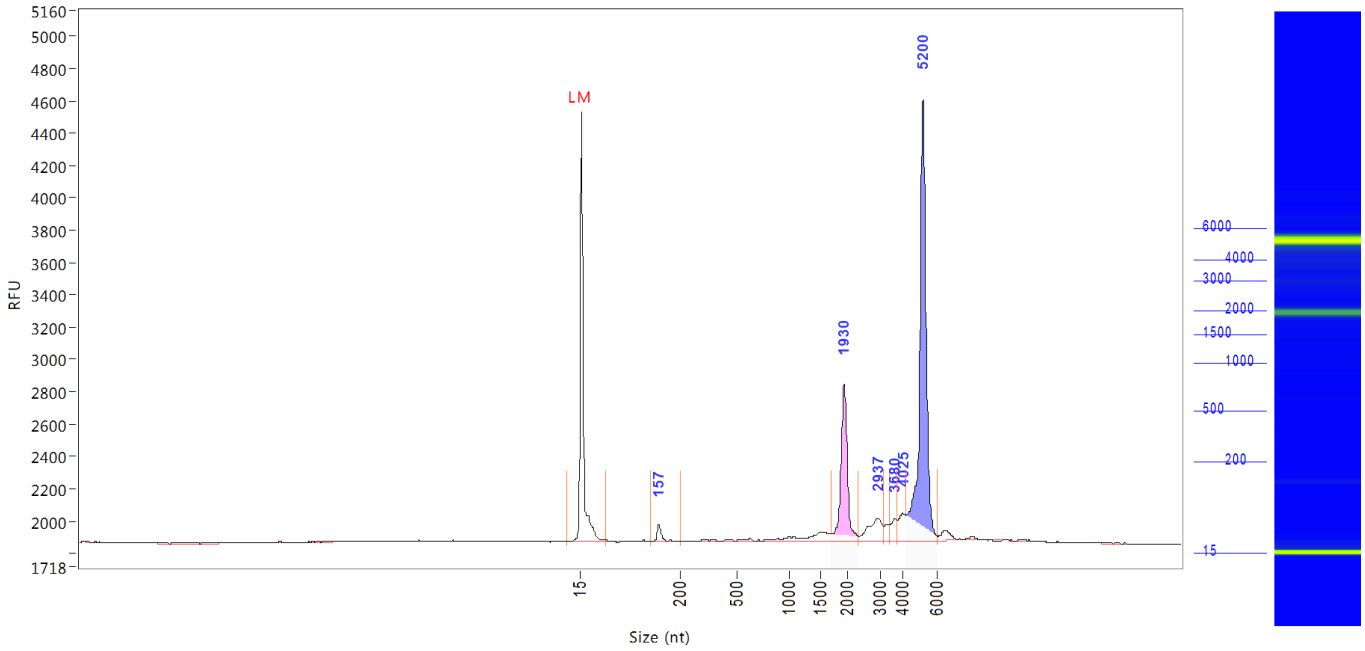


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.5382	0	64	2828
2	148	0.3907	137	159	144
3	185	0.4303	174	200	189
4	430	0.2194	393	480	77
5	1602	0.5506	1410	1719	96
6	1891	6.3080	1719	2229	1968
7	2406	3.0214	2229	3435	1250

TIC:	10.9204	ng/uL
TIM:	32.1941	nmole/L
Total Conc.:	13.2411	ng/uL
28S/18S:	0.5	
RQN	8.7	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 50    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): 8.0000          Dilution Factor: 12.0
Min. RFU for Data Processing: 2
```


Sample: ss RNA control
Well Location: C11
Created: Wednesday, May 22, 2019 3:38:21 PM

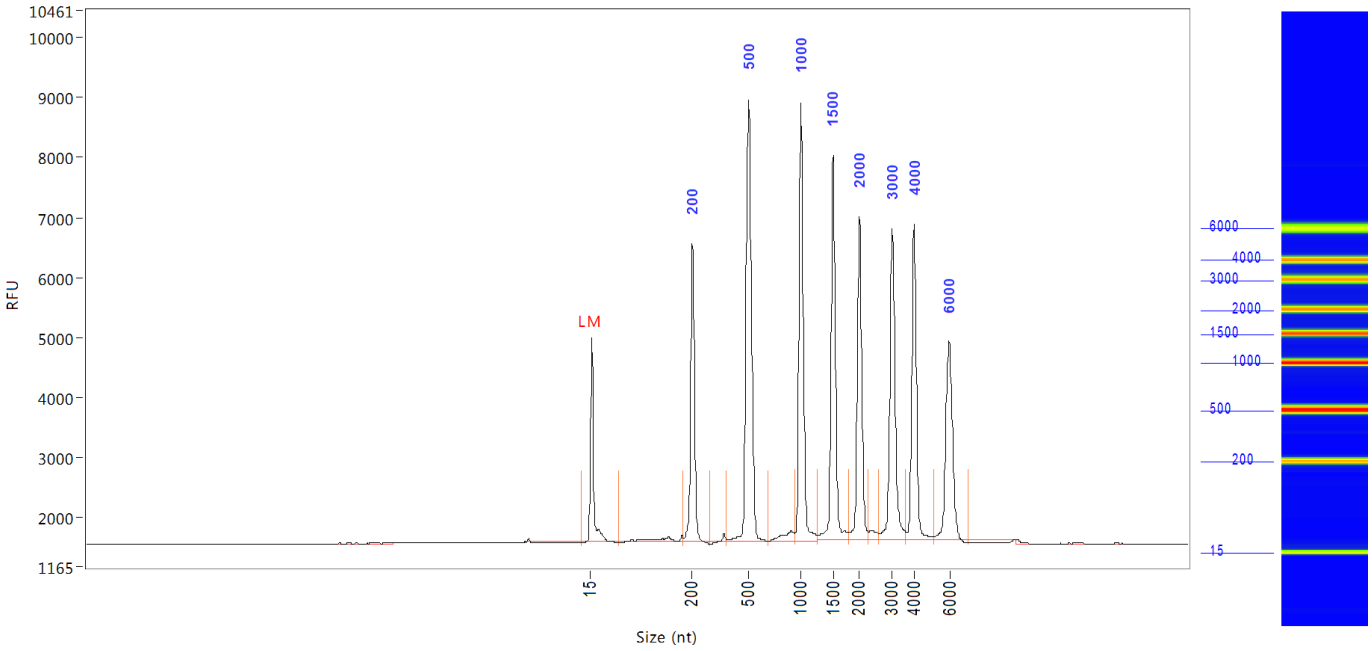


Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.5382	0	60	2658
2	157	0.2844	144	199	103
3	1930	3.2498	1688	2330	971
4	2937	0.9194	2330	3152	137
5	3680	0.4163	3416	3793	132
6	4025	0.5833	3793	4236	166
7	5200	8.4978	4236	6070	2727

TIC:	13.9510	ng/uL
TIM:	17.8106	nmole/L
Total Conc.:	15.3512	ng/uL
28S/18S:	2.6	
RQN	10.0	

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 50    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): 8.0000          Dilution Factor: 12.0
Min. RFU for Data Processing: 2
```


Sample: ss RNA ladder
Well Location: C12
Created: Wednesday, May 22, 2019 3:38:21 PM



Peak	Size (nt)	Conc. (ng/uL)	From (nt)	To (nt)	RFU
1	15 (LM)	0.5382	0	65	3415
2	200	9.9626	184	297	4968
3	500	19.2552	384	682	7375
4	1000	13.9877	941	1263	7312
5	1500	12.3906	1263	1813	6433
6	2000	10.1009	1813	2267	5415
7	3000	11.1280	2595	3642	5213
8	4000	9.4683	3642	5106	5285
9	6000	8.3732	5106	7095	3325

TIC:	94.6664	ng/uL
TIM:	381.8527	nmole/L
Total Conc.:	96.0000	ng/uL

```
Sample Peak Width (sec): 6    Sample Min Peak Height: 200   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): 8.0000          Dilution Factor: 12.0
Min. RFU for Data Processing: 2
```


Sample: ss RNA ladder
Well Location: C12
Created: Wednesday, May 22, 2019 3:38:21 PM
Fit Type: Point to Point