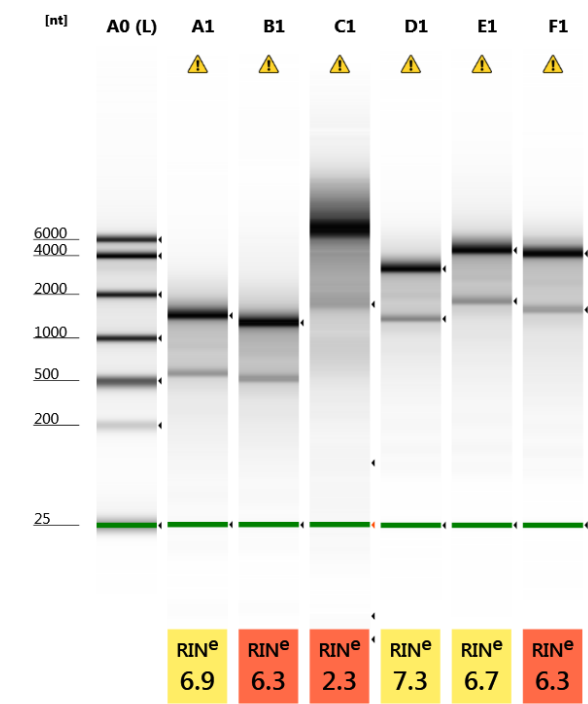
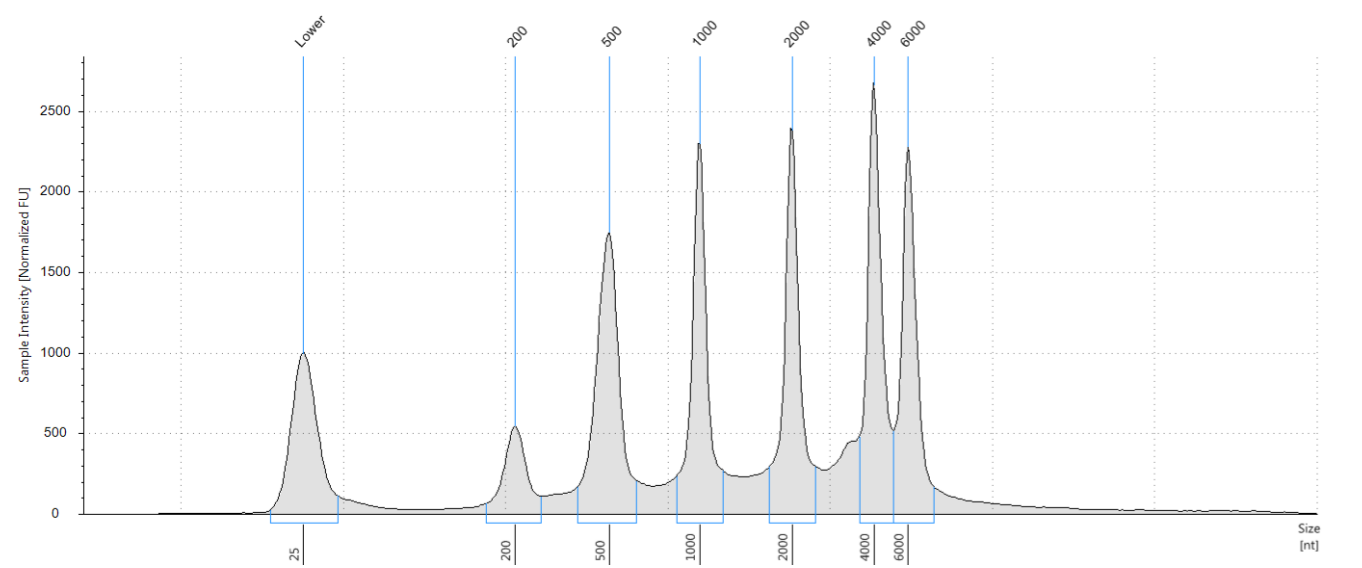


Filename: 2019-12-10-Angilica.HSRNA



Default image (Contrast 50%), Image is Scaled to Sample

A0: Electronic Ladder



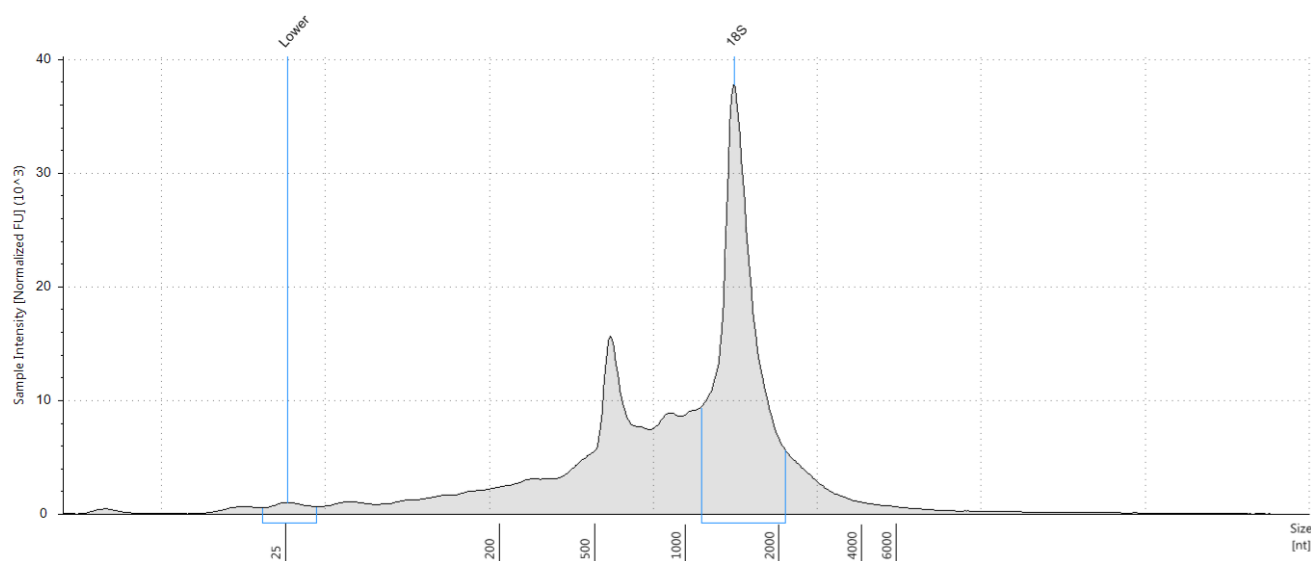
Sample Table

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
A0	-	-	3850	Electronic Ladder		Ladder

Peak Table

Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
200	195	-	2870	6.33		
500	625	-	3680	20.25		
1000	544	-	1600	17.62		
2000	567	-	833	18.36		
4000	614	-	452	19.91		
6000	541	-	265	17.52		

A1: 1

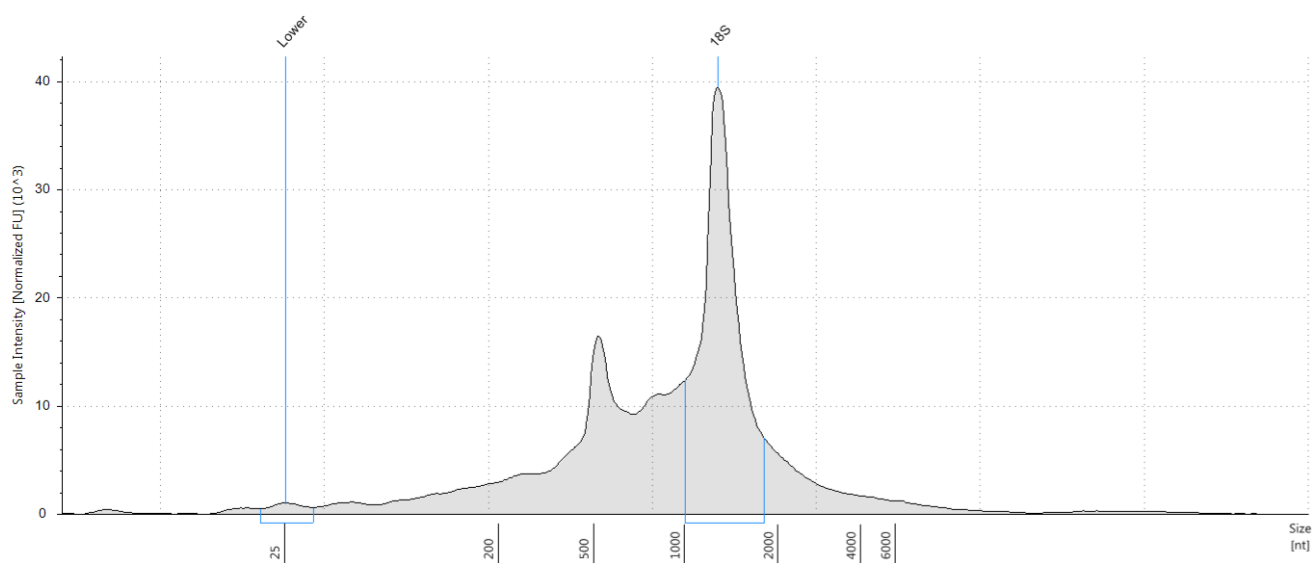


Sample Table

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
A1	6.9	-	16900	1	⚠	Caution! Expired ScreenTape device

Peak Table

Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
1418	7450	-	15500	100.00		18S

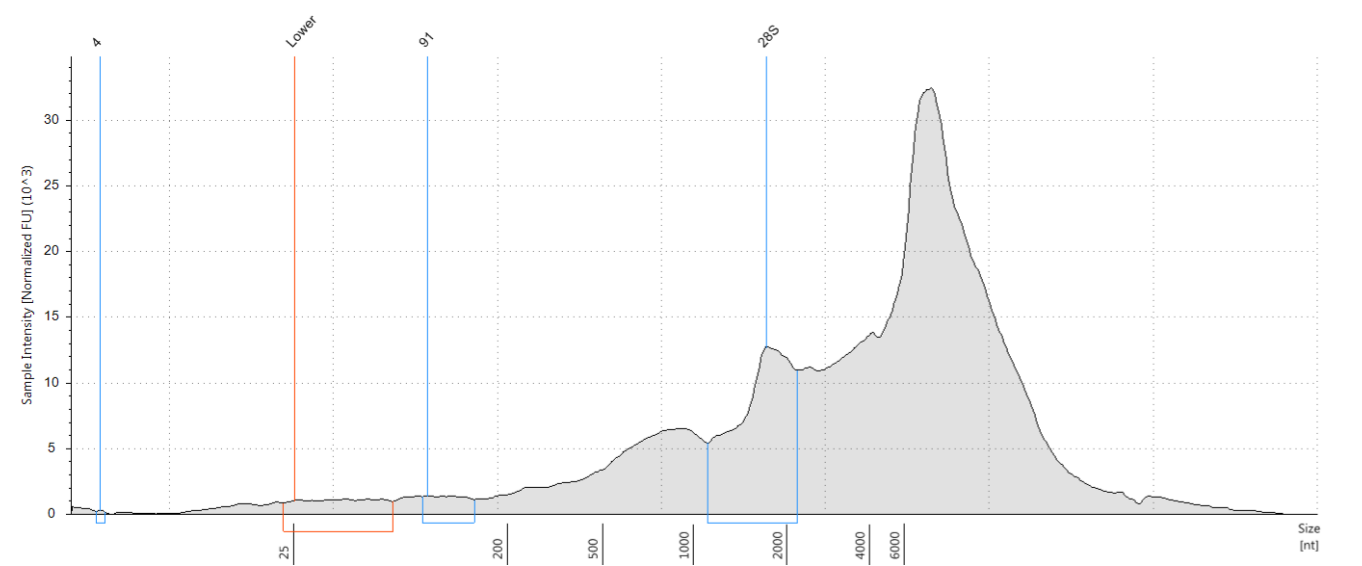
B1: 2**Sample Table**

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
B1	6.3	-	21100	2	⚠	Caution! Expired ScreenTape device

Peak Table

Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
1270	8740	-	20200	100.00		18S

C1: 3

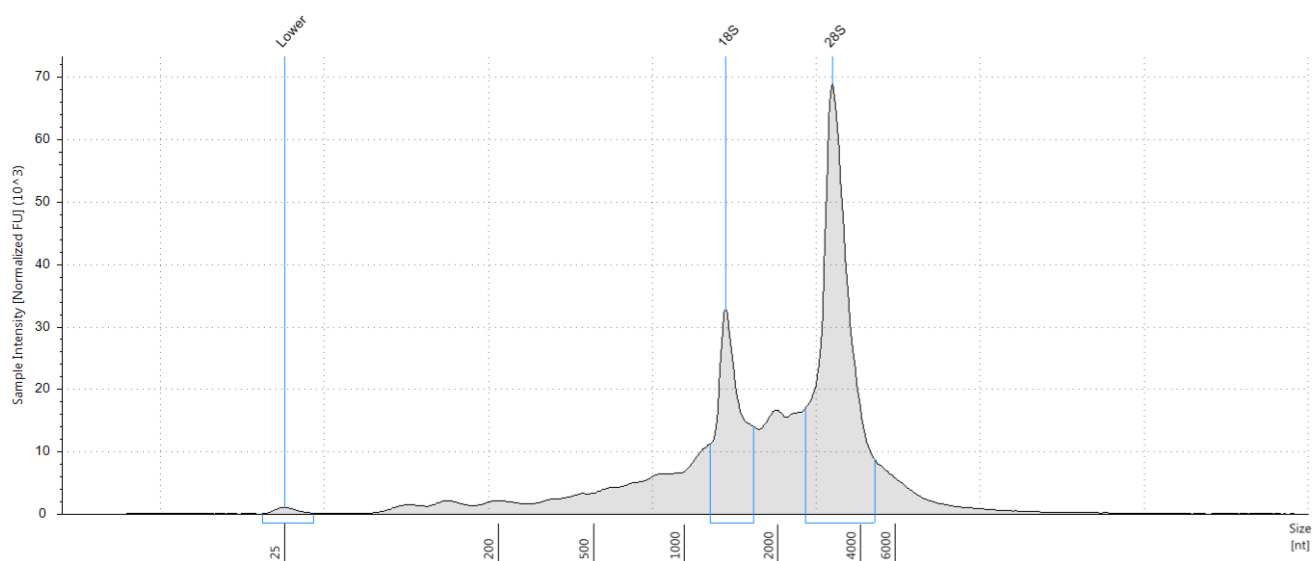


Sample Table

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
C1	2.3	-	12200	3		Caution! Expired ScreenTape device; Markers outside standard running position; RINe edited

Peak Table

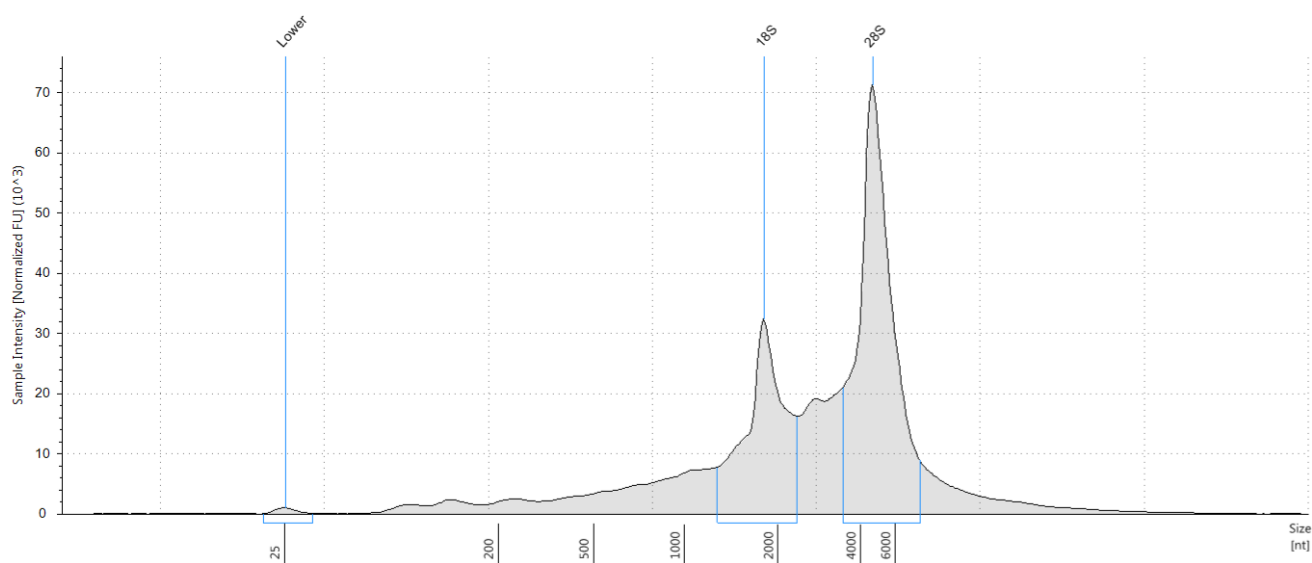
Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
2	41.6	-	53100	2.33		
4	3.56	-	2790	0.20		
25	700	700	82400	-		edited Lower Marker
91	130	-	4200	7.28		
1705	1610	-	2780	90.19		28S

D1: 4**Sample Table**

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
D1	7.3	2.6	46400	4	⚠	Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe

Peak Table

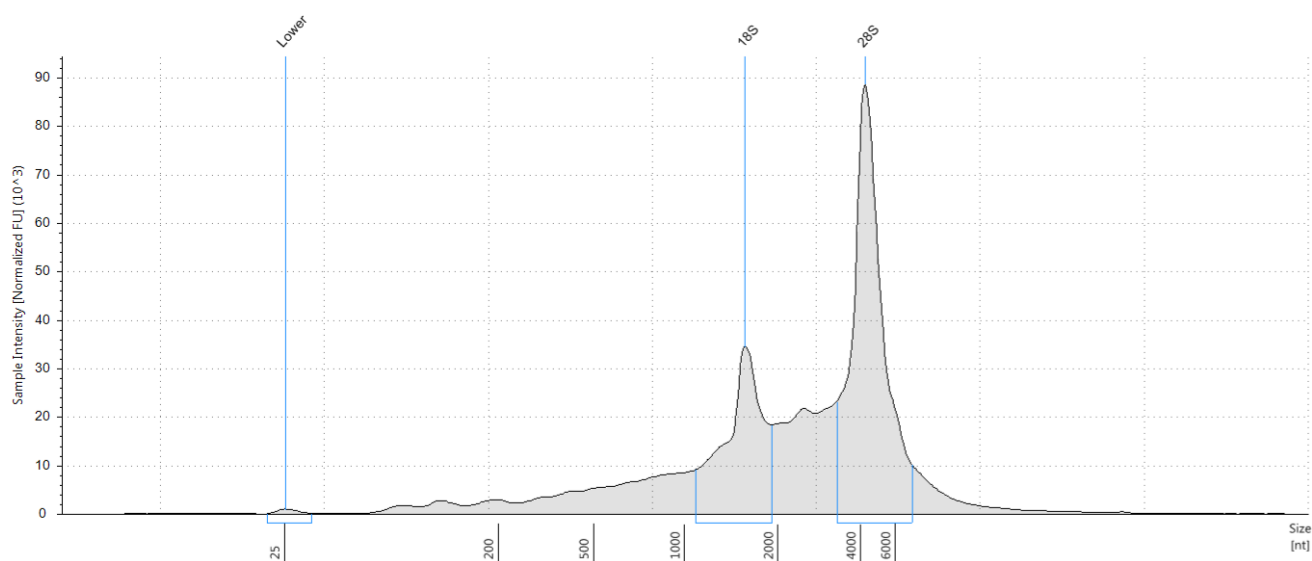
Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
1357	7500	-	16300	27.98		18S
3158	19300	-	18000	72.02		28S

E1: 5**Sample Table**

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
E1	6.7	2.0	59200	5	⚠	Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe

Peak Table

Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
1792	12400	-	20400	33.73		18S
4558	24500	-	15800	66.27		28S

F1: 6**Sample Table**

Well	RINe	28S/18S (Area)	Conc. [pg/μl]	Sample Description	Alert	Observations
F1	6.3	2.1	73000	6	⚠	Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe

Peak Table

Size [nt]	Calibrated Conc. [pg/μl]	Assigned Conc. [pg/μl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	700	700	82400	-		Lower Marker
1562	14100	-	26600	32.28		18S
4208	29700	-	20700	67.72		28S

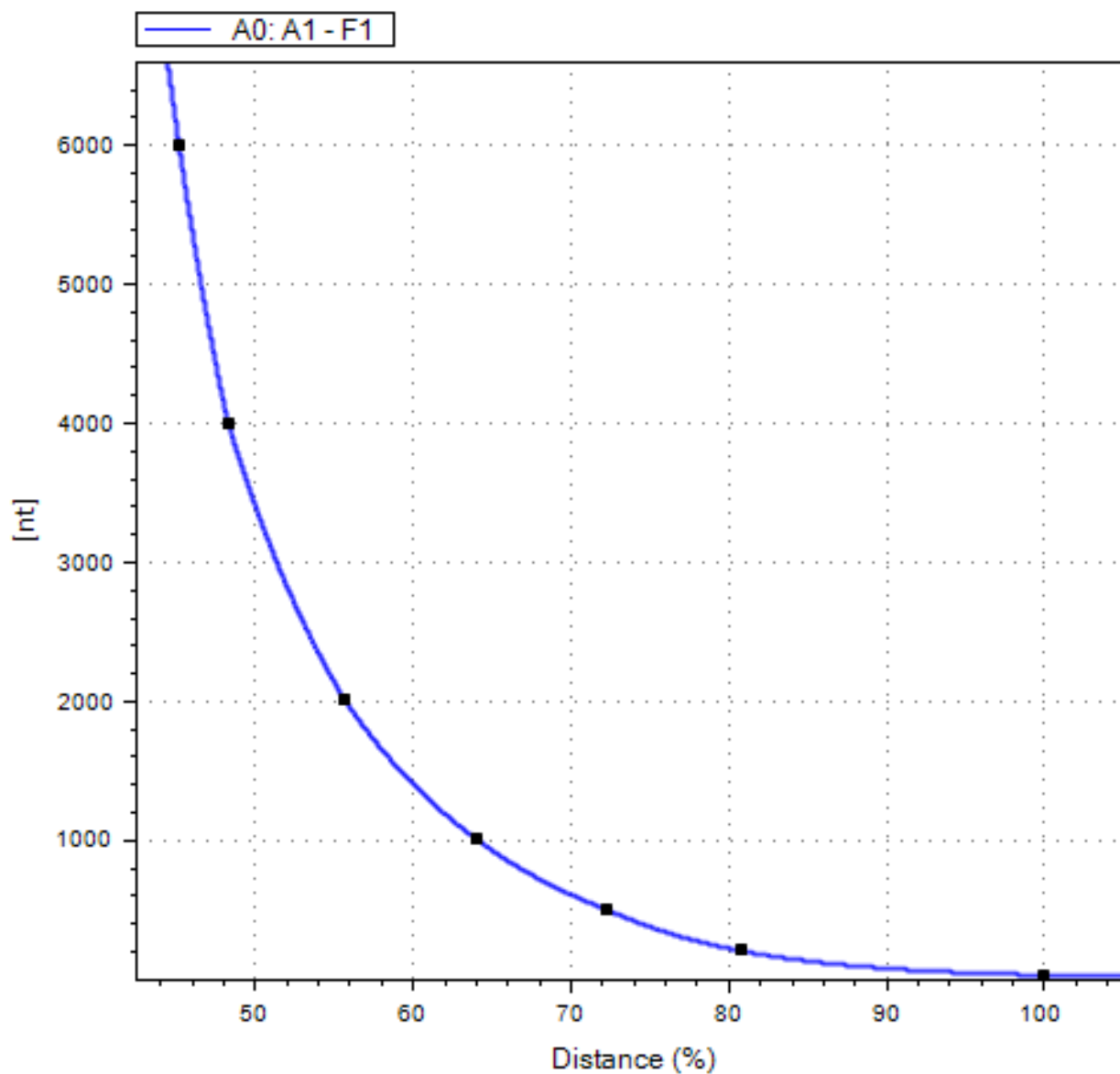
Sample Info

Well	RINe	28S/18S (Area)	Conc. [pg/ul]	Sample Description	Alert	Observations
A0	-	-	3850	Electronic Ladder		Ladder
A1	6.9	-	16900	1		Caution! Expired ScreenTape device
B1	6.3	-	21100	2		Caution! Expired ScreenTape device
C1	2.3	-	12200	3		Caution! Expired ScreenTape device; Markers outside standard running position; RINe edited
D1	7.3	2.6	46400	4		Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe
E1	6.7	2.0	59200	5		Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe
F1	6.3	2.1	73000	6		Caution! Expired ScreenTape device; RNA concentration outside recommended range for RINe

Calibration

Molecular Weight Settings

Fitting type: Log Linear Piecewise
Alignment type: From lower marker



Concentration Settings

Calibration mode: Lower Marker
Normalise peaks from: RNA Bottom Marker Normalisation
Fitting type: Linear Regression