

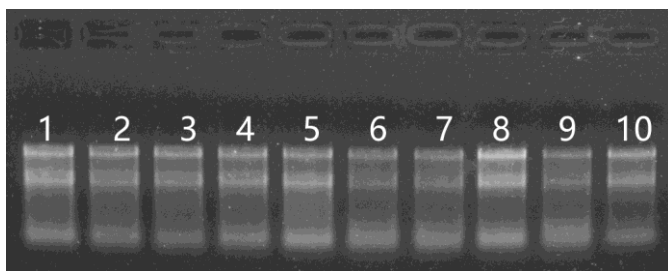
RNA QC EUK

1. RNA Quantification and Quality Assurance by NanoDrop ND-1000

Sample ID	OD260/280 Ratio	OD260/230 Ratio	Conc. (ng/μl)	Volume (μl)	Quantity (ng)	QC Purity Pass or Fail
2018L0071TT	1.98	2.34	1262.29	40	50491.60	Pass
2018L0030TT	1.92	2.24	782.72	30	23481.60	Pass
2018L0121TT	1.94	2.15	756.61	40	30264.40	Pass
2018L0049TT	1.96	2.36	925.98	40	37039.20	Pass
2018L0100TT	1.96	2.29	1061.59	60	63695.40	Pass
2018L0030TN	1.88	2.28	442.38	30	13271.40	Pass
2018L0121TN	1.89	2.23	455.49	20	9109.80	Pass
2018L0071TN	1.88	2.11	611.96	15	9179.40	Pass
2018L0100TN	1.90	2.14	380.99	40	15239.60	Pass
2018L0049TN	1.92	1.97	364.64	30	10939.20	Pass

*For spectrophotometer, the O.D. A260 /A280 ratio should be close to 2.0 for pure RNA (ratios between 1.8 and 2.1 are acceptable). The O.D. A260/A230 ratio should be more than 1.8.

2. RNA Integrity and gDNA contamination test by Denaturing Agarose Gel Electrophoresis



Lane 1: Total RNA of sample 2018L0071TT
 Lane 2: Total RNA of sample 2018L0030TT
 Lane 3: Total RNA of sample 2018L0121TT
 Lane 4: Total RNA of sample 2018L0049TT
 Lane 5: Total RNA of sample 2018L0100TT
 Lane 6: Total RNA of sample 2018L0030TN
 Lane 7: Total RNA of sample 2018L0121TN
 Lane 8: Total RNA of sample 2018L0071TN
 Lane 9: Total RNA of sample 2018L0100TN
 Lane 10: Total RNA of sample 2018L0049TN

*The 28S and 18S ribosomal RNA bands should be fairly sharp, intense bands. The intensity of the upper band should be about twice that of the lower band. Smaller, more diffuse bands representing low molecular weight RNAs (tRNA and 5S ribosomal RNA) may be present. It is normal to see a diffuse smear of ethidium bromide staining material migrating between the 18S and 28S ribosomal bands, probably comprised of mRNA and other heterogeneous RNA species. DNA contamination of the RNA preparation will be evident as a high molecular weight smear or band migrating above the 28S ribosomal RNA band. Degradation of the RNA will be reflected by smearing of ribosomal RNA bands.

Quality Assessment of Sequencing Library

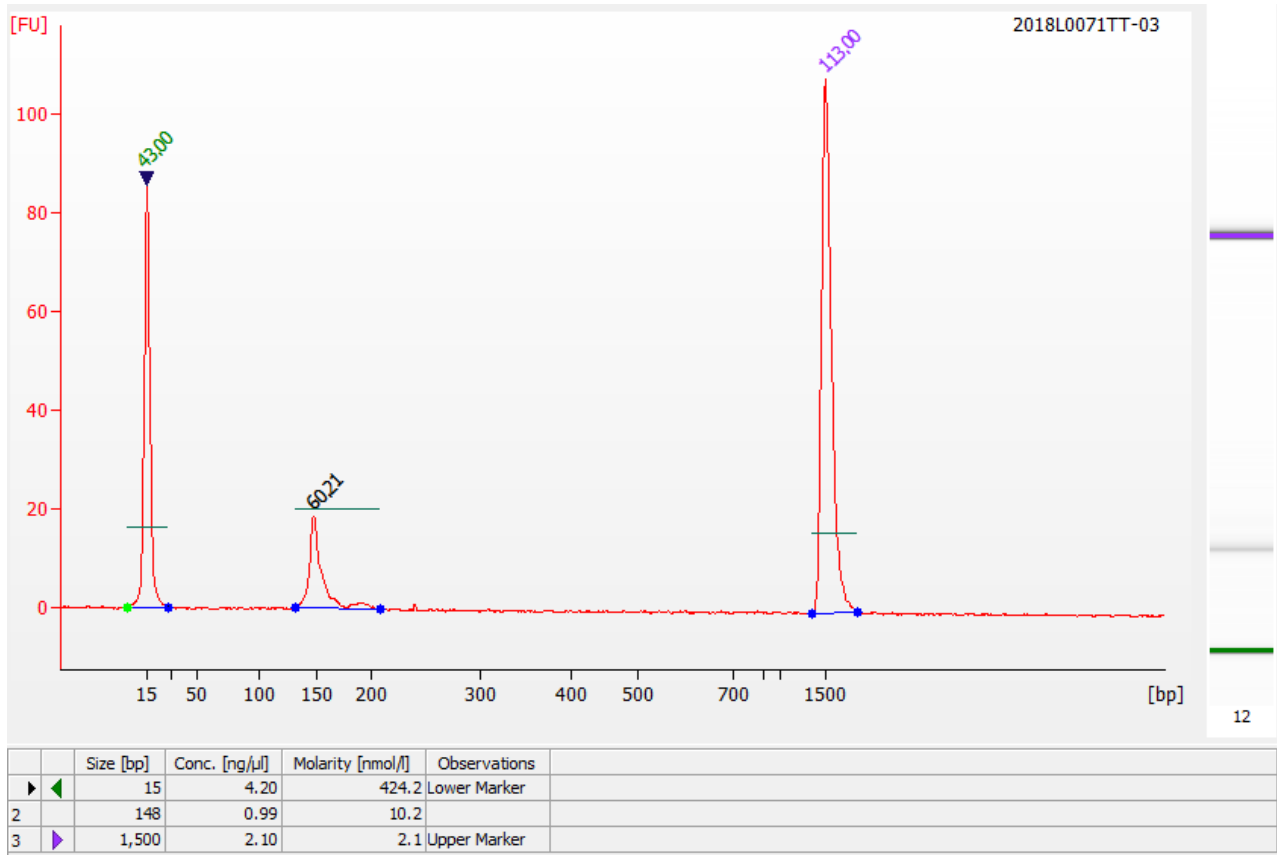
Sequencing library was determined by Agilent 2100 Bioanalyzer using the Agilent DNA 1000 chip kit (Agilent, part # 5067-1504)

Sample Name	Size (bp)	Conc. (ng/μl)	Conc. (nmol/L)	Volume (μl)	Total Amount (ng)
2018L0071TT	148	0.99	10.2	10	9.9
2018L0030TT	148	1.81	18.5	10	18.1
2018L0121TT	147	3.15	32.4	10	31.5
2018L0049TT	151	0.48	4.9	10	4.8
2018L0100TT	157	0.96	9.3	10	9.6
2018L0030TN	148	2.48	25.4	10	24.8
2018L0121TN	147	1.76	18.2	10	17.6
2018L0071TN	147	1.79	18.4	10	17.9
2018L0100TN	147	1.94	19.9	10	19.4
2018L0049TN	148	2.07	21.2	10	20.7

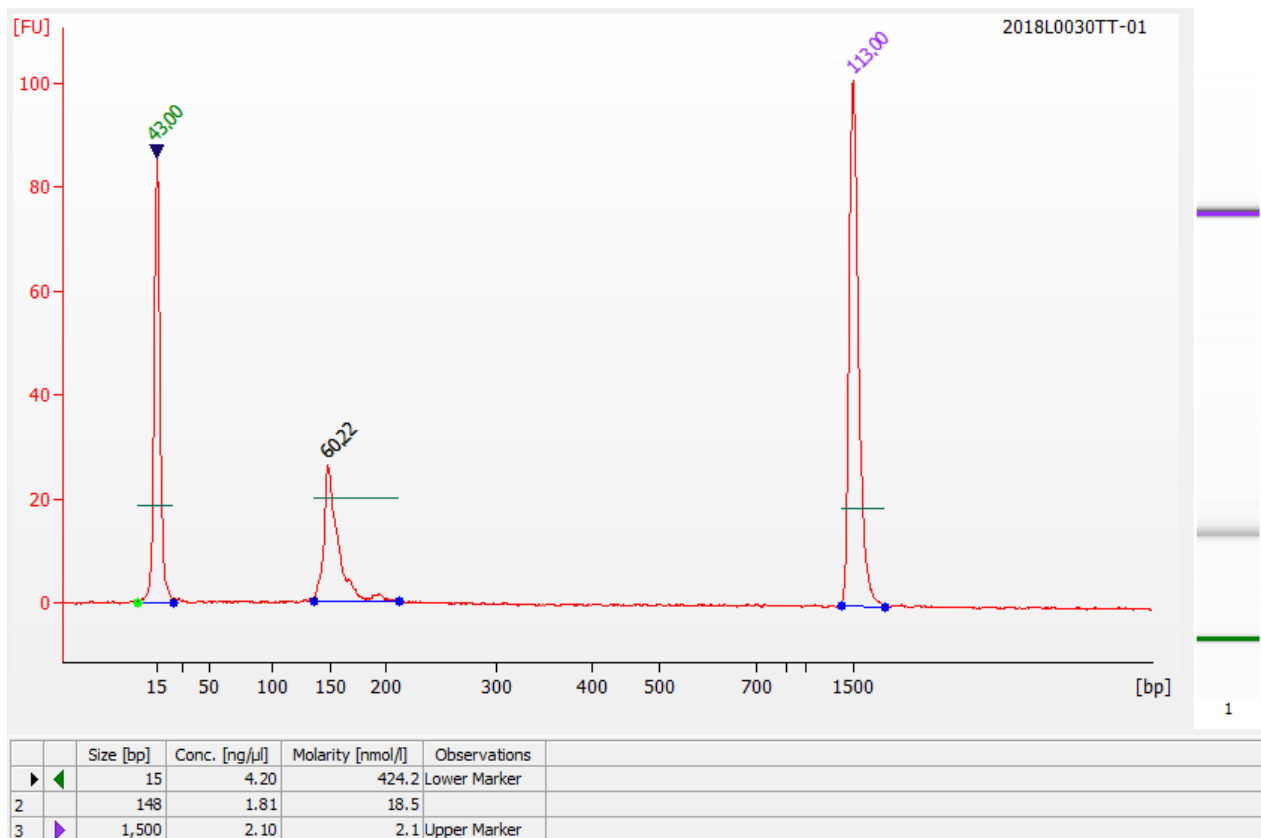
**The libraries were adjusted to 10nM before cluster generation.

Quality control analysis on an Agilent 2100 Bioanalyzer

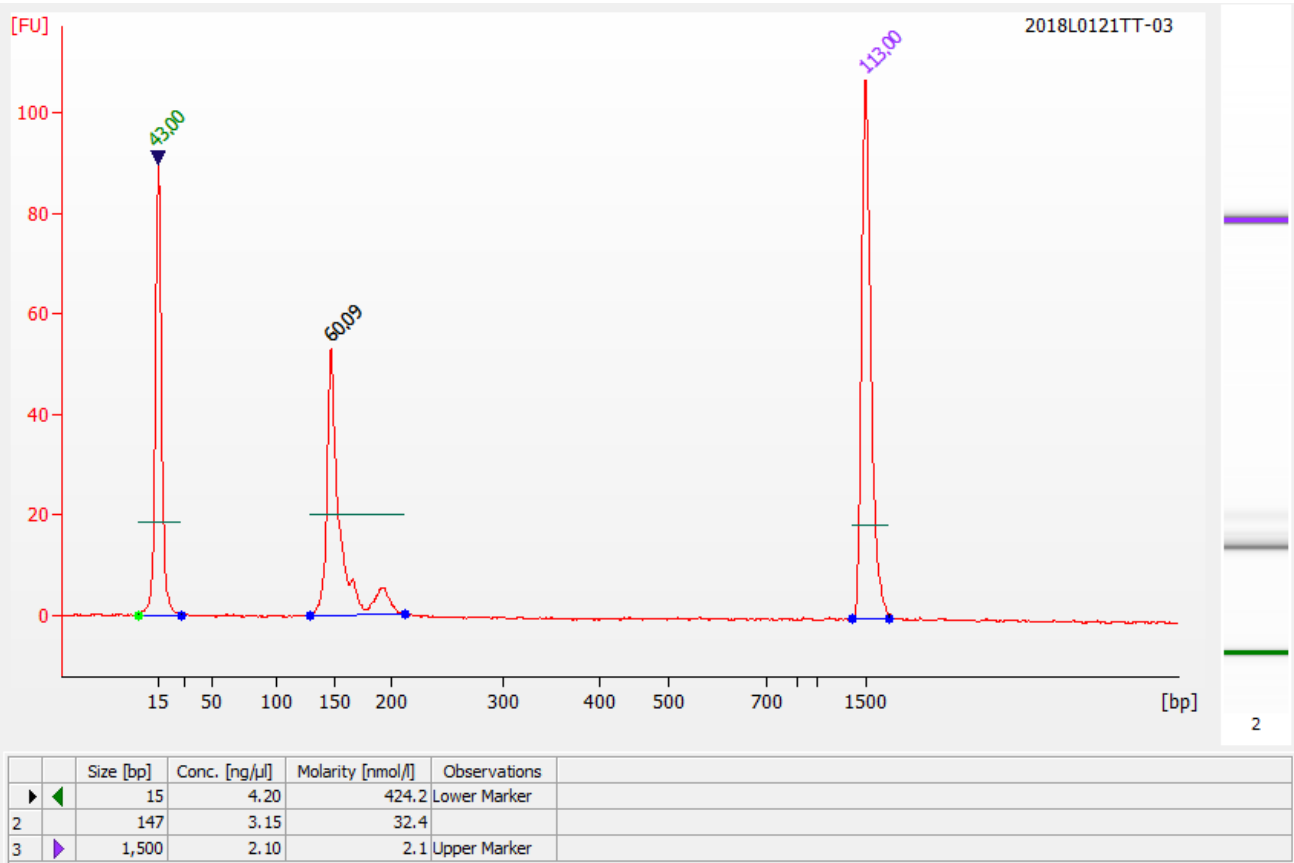
Sample 2018L0071TT:



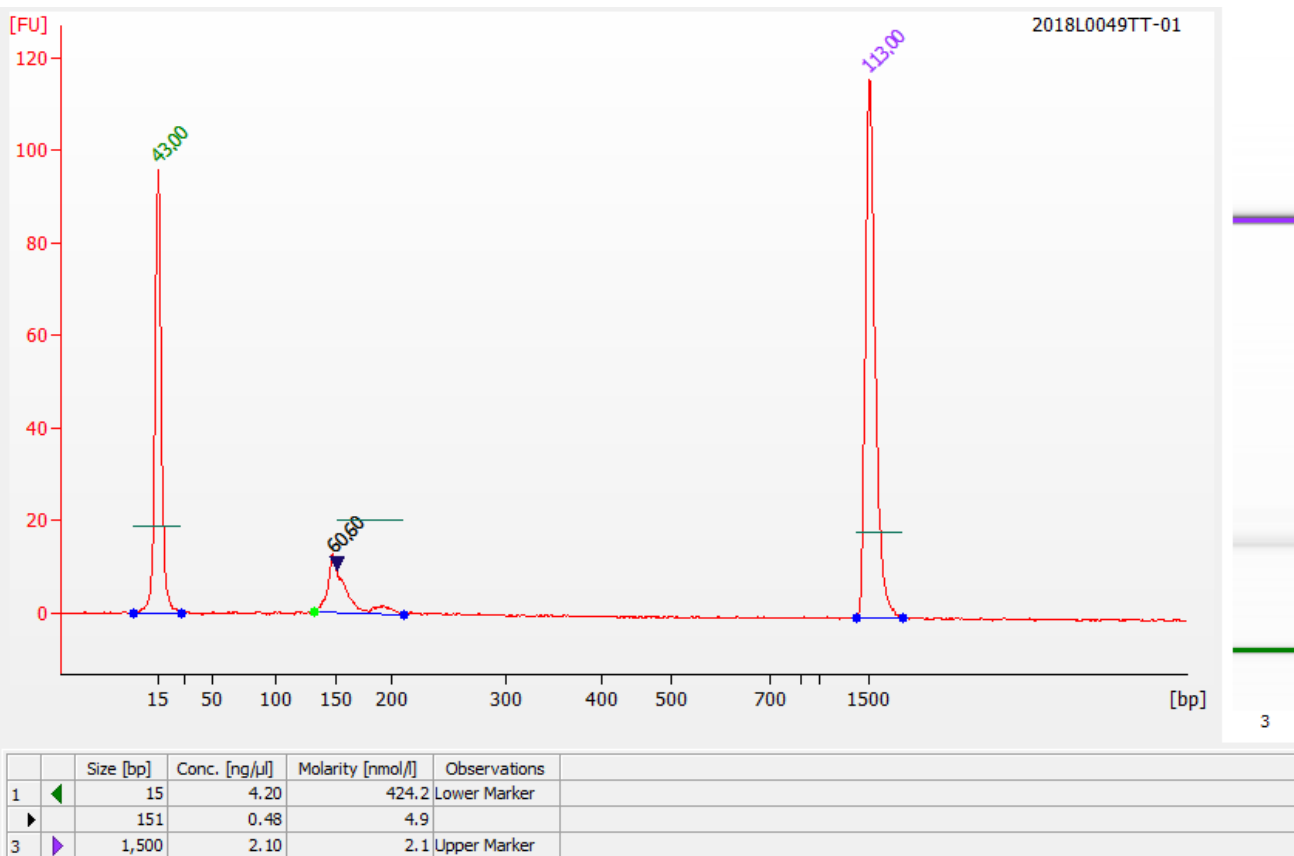
Sample 2018L0030TT:



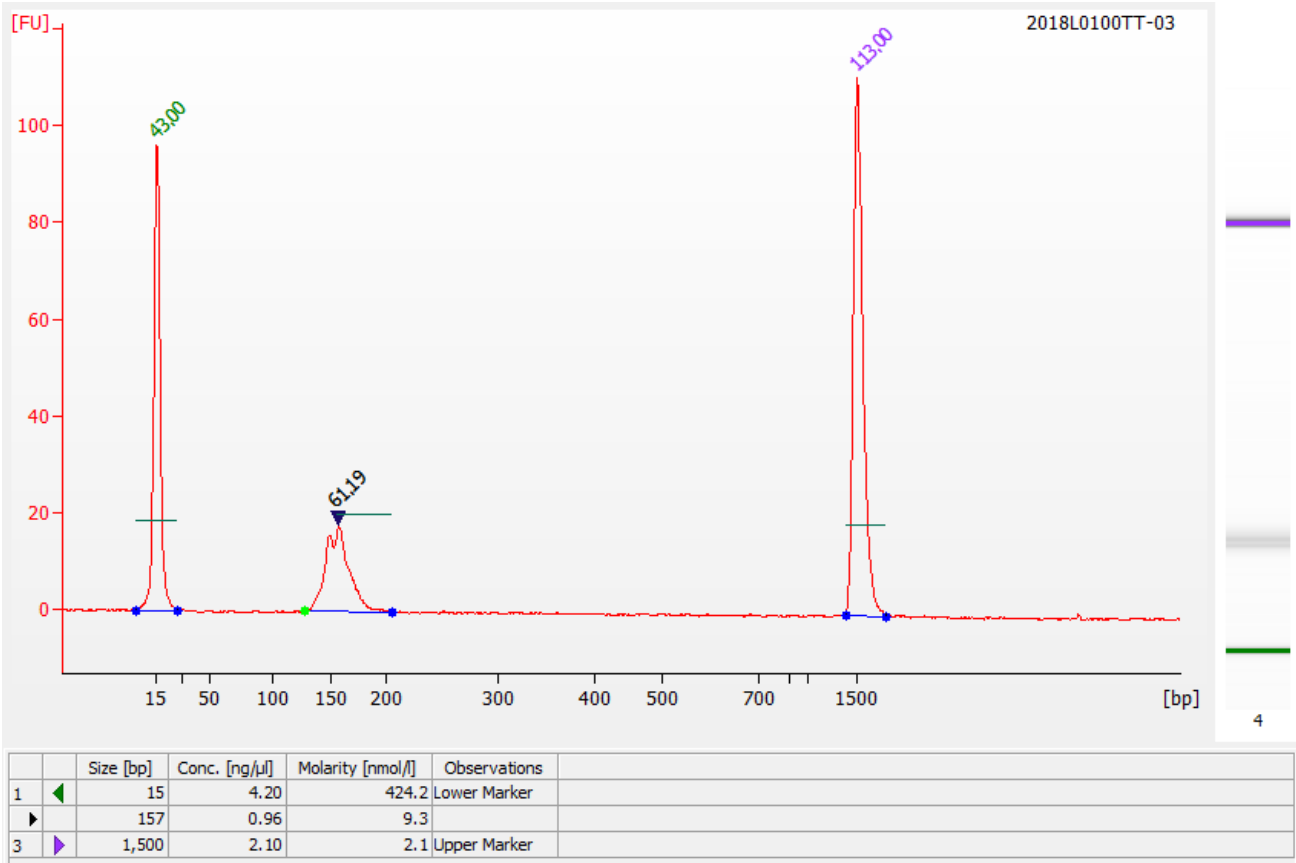
Sample 2018L0121TT:



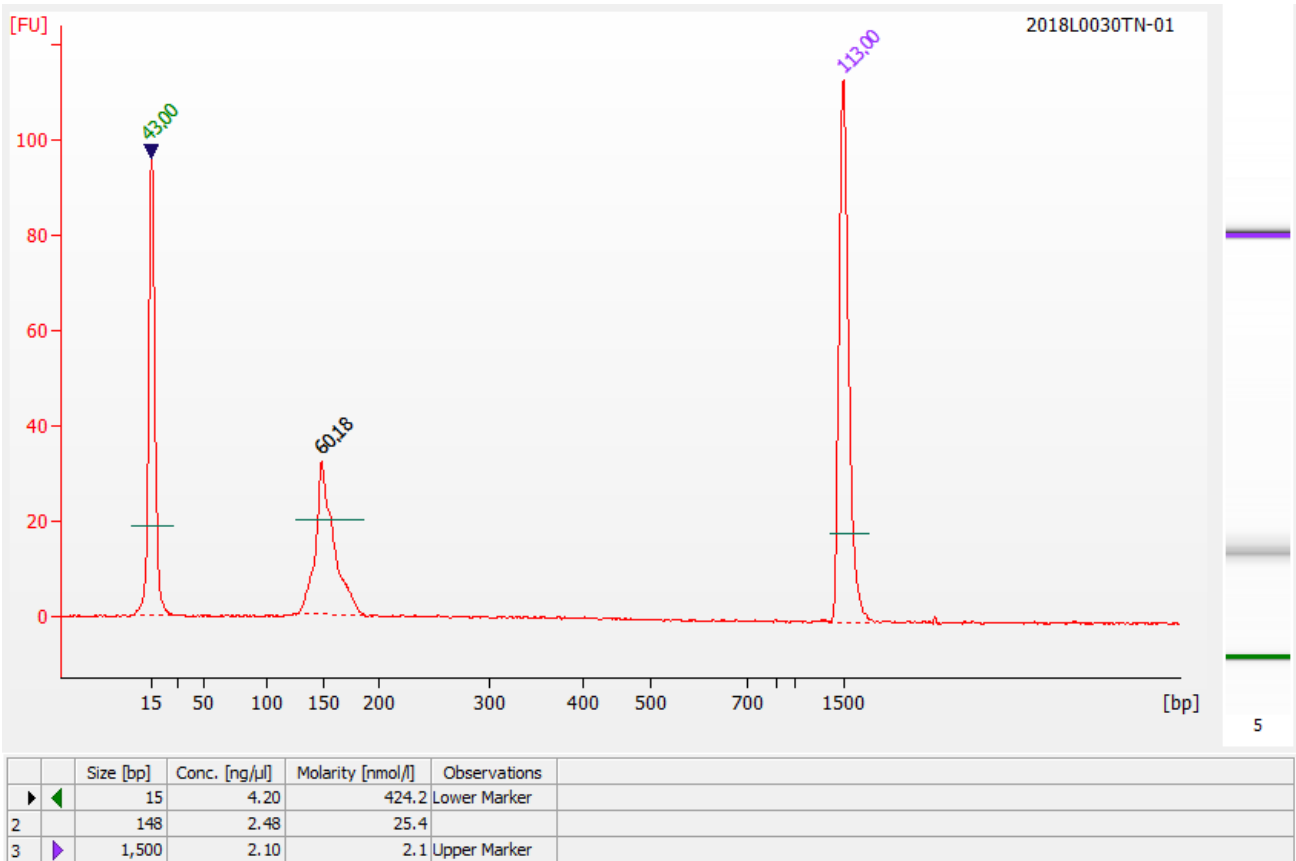
Sample 2018L0049TT:



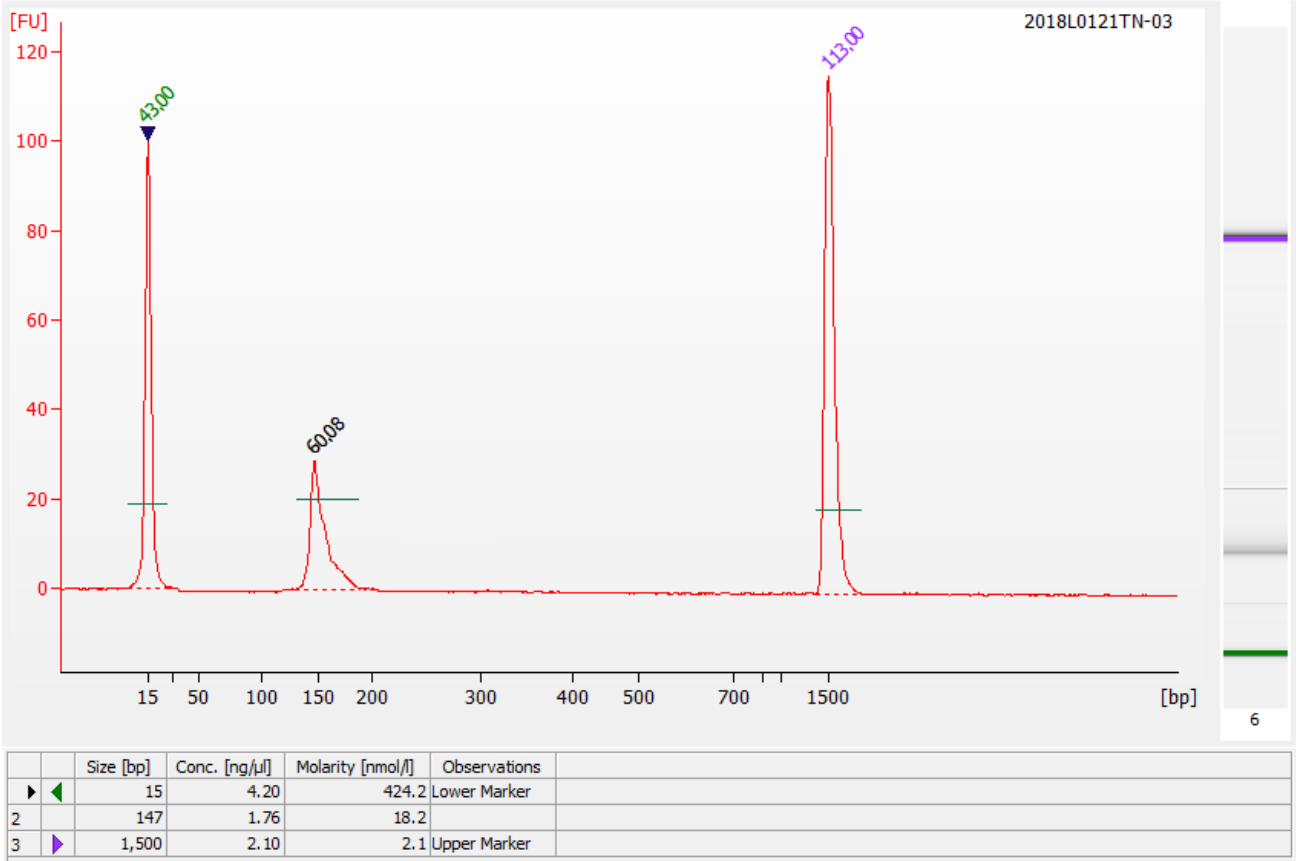
Sample 2018L0100TT:



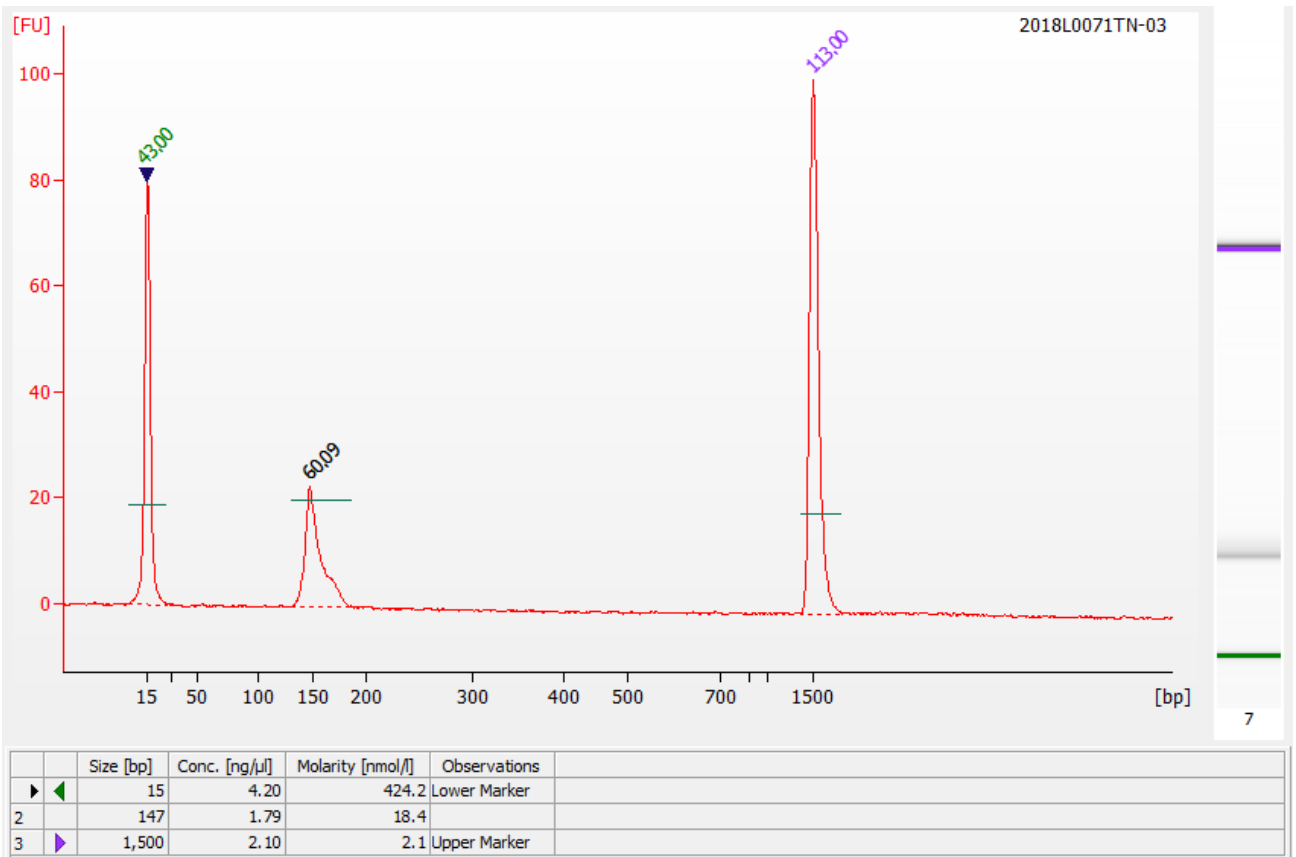
Sample 2018L0030TN:



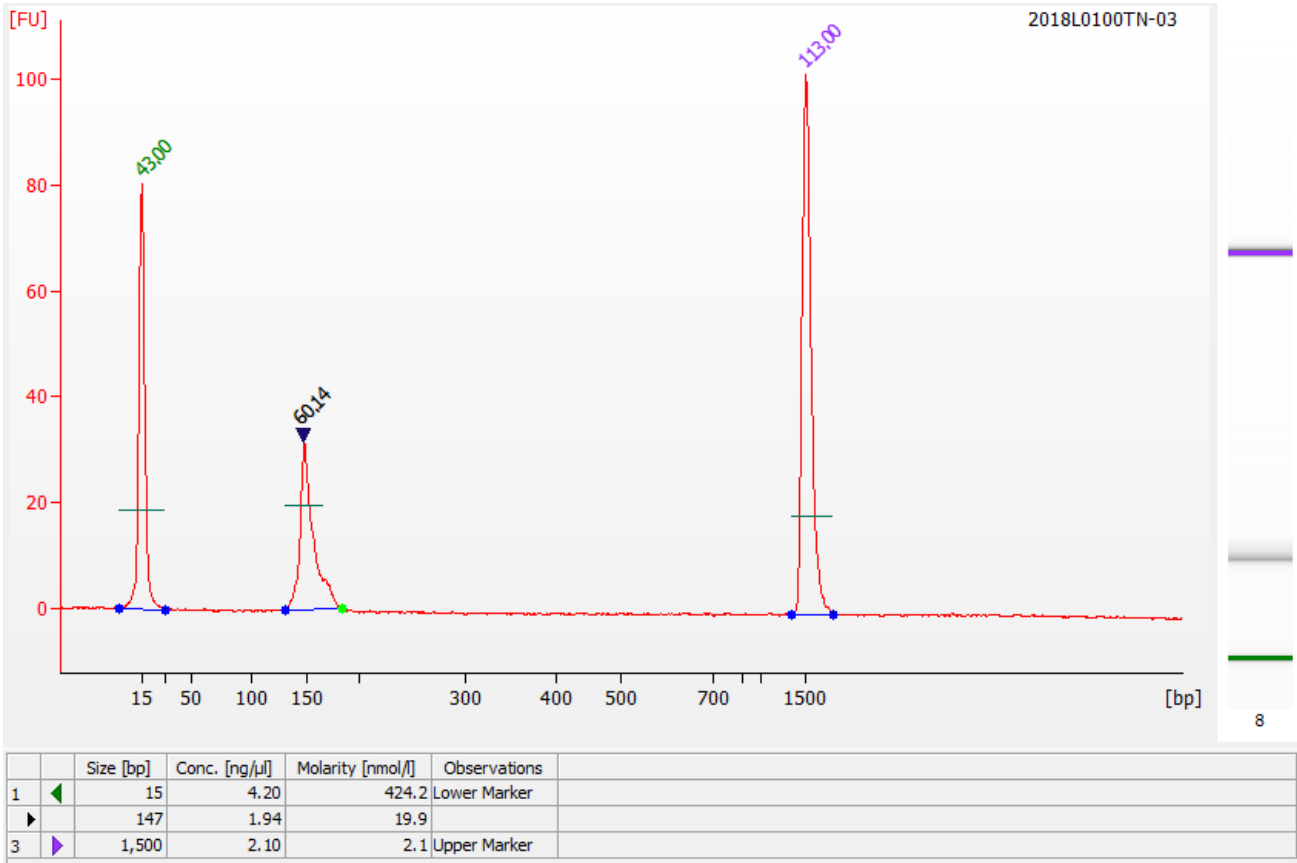
Sample 2018L0121TN:



Sample 2018L0071TN:



Sample 2018L0100TN:



Sample 2018L0049TN:

