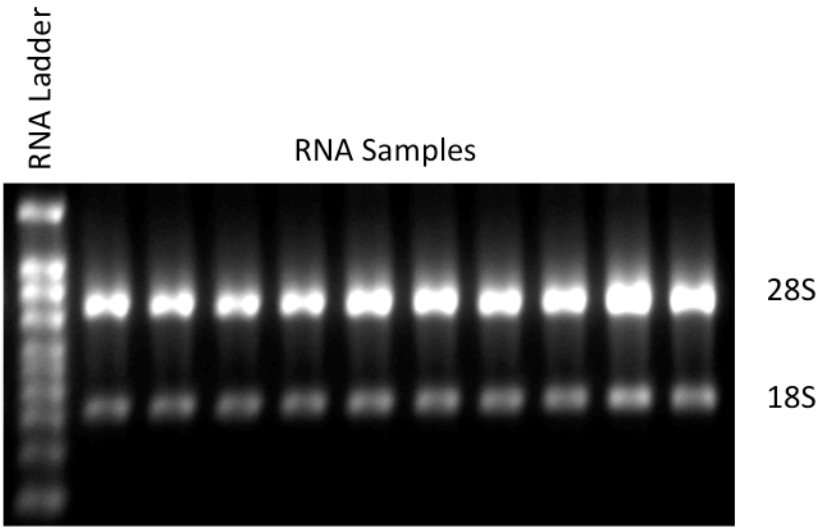

Figure 1. RNA Gel Results showing 28S:18S ratios. (*Image kindly provided by tebu-bio laboratory's RNA extraction and Genomic Profiling Service division*).

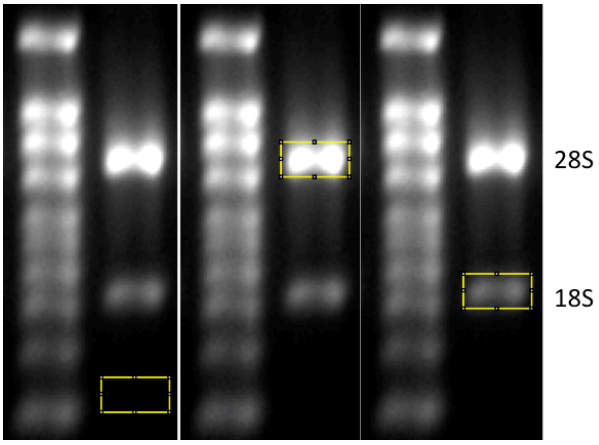

Figure 2. ImageJ quantification of 28S:18S ratio. First measure the background (left), then measure the 28S band (middle), then measure the 18S band (right). Subtract the background from the 28S and 18S values and calculate the ratio.

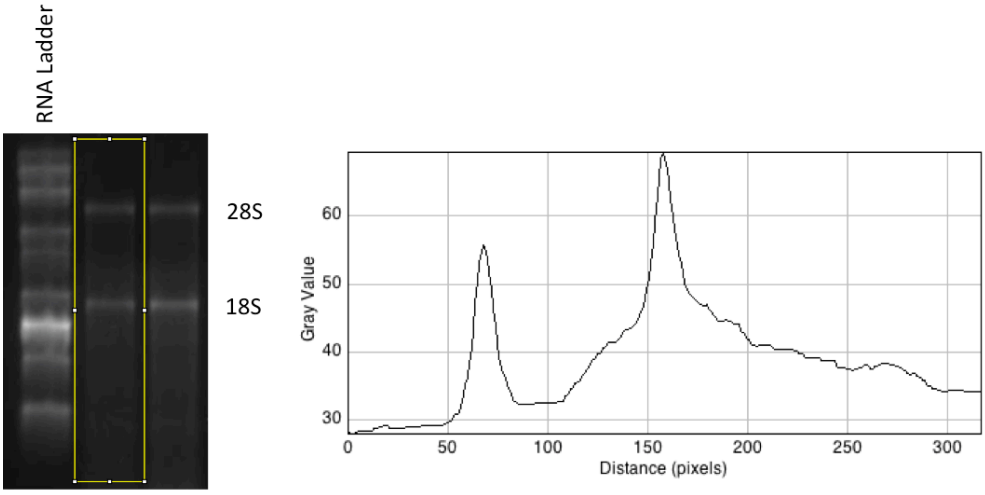

Figure 3. ImageJ Profile Plot assessing RNA quality. Using this RNA gel image found on the internet, the ImageJ (Analyze-Profile Plot Function) was used to draw a histogram, showing a low 28S:18S ratio and significant smearing below the 18S band, indicating poor RNA quality.

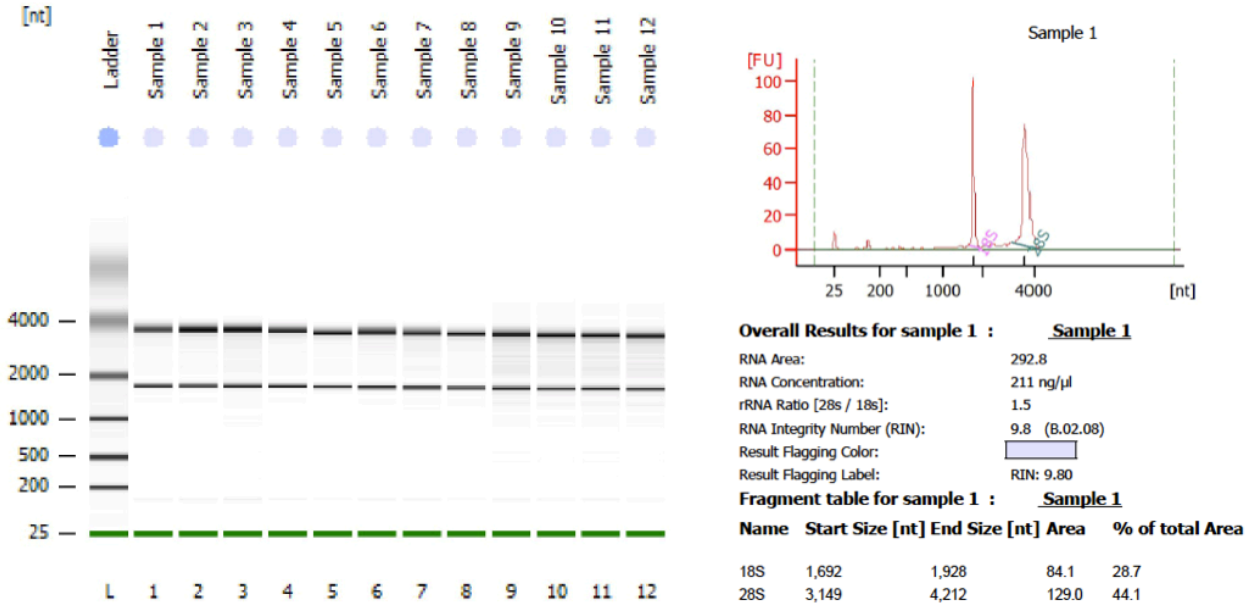

Figure 4. Sample Agilent Bioanalyzer Results. Using a microfluidics approach, the Agilent Bioanalyzer determines the relative abundances of 28S and 18S RNA as well as the degree of degradation. The software creates digital plots that resemble traditional RNA gels (left) and calculates the RNA Integrity Number (RIN) based on the plotted histogram (right).

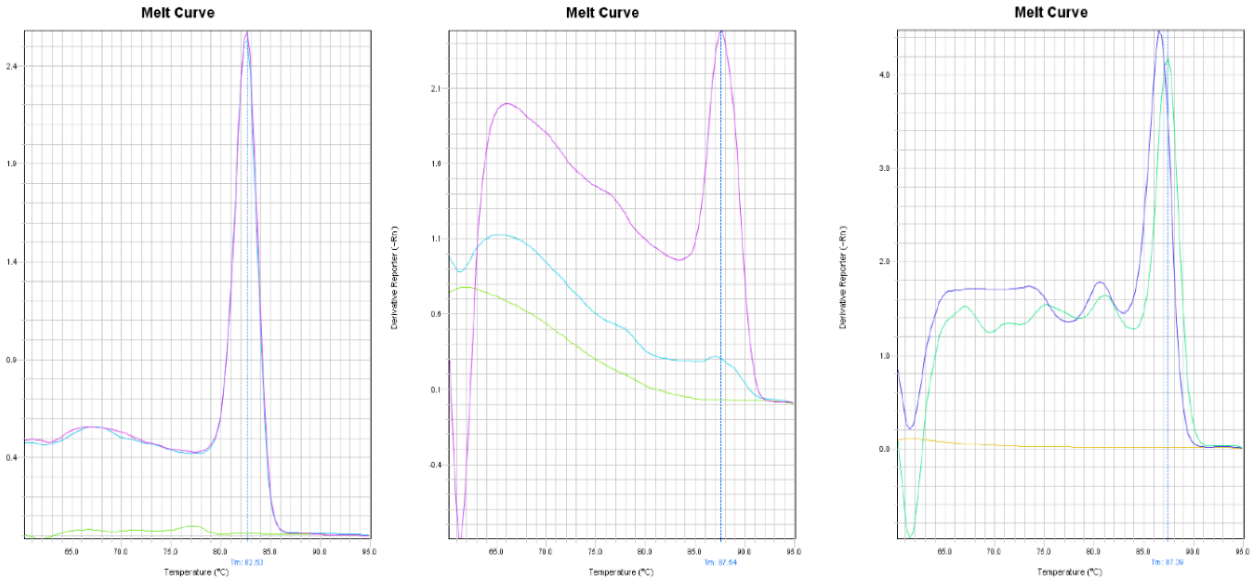

Figure 5. Melting curves. Acceptable melting curves are those showing a melting curve (blue) distinct from the melting curve you get with the negative control (yellow). A good primer pair will give a specific peak (left) while unacceptable primer pairs will yield products with less pure melting curves (middle and right).

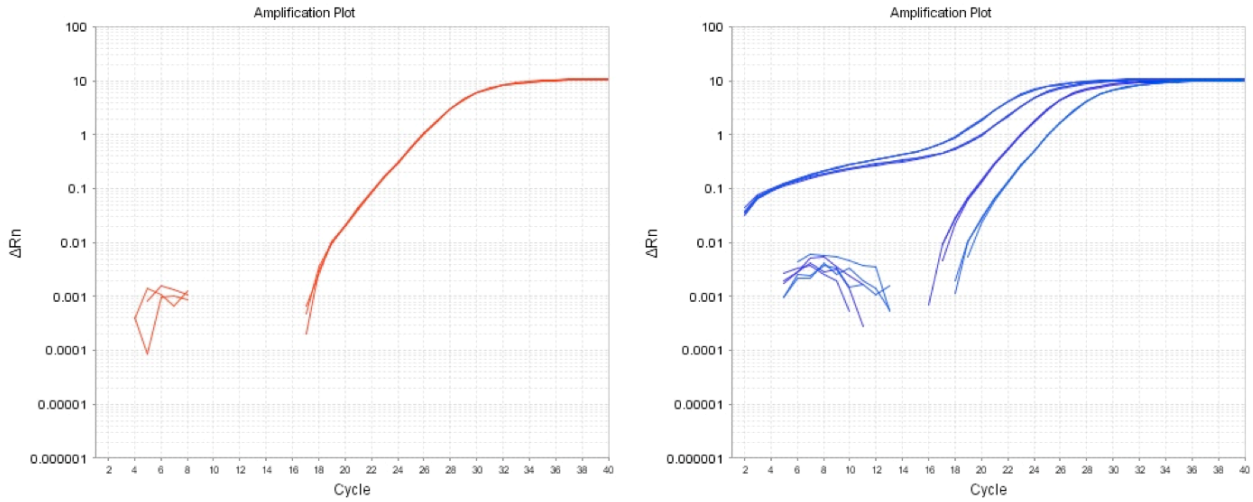

Figure 6. Amplification Curves. Acceptable amplification curves are C-shaped (left). cDNA that is too concentrated may yield an S-shaped curve (right), however further dilution of the sample increase Ct values to the measurable range of 20-30.

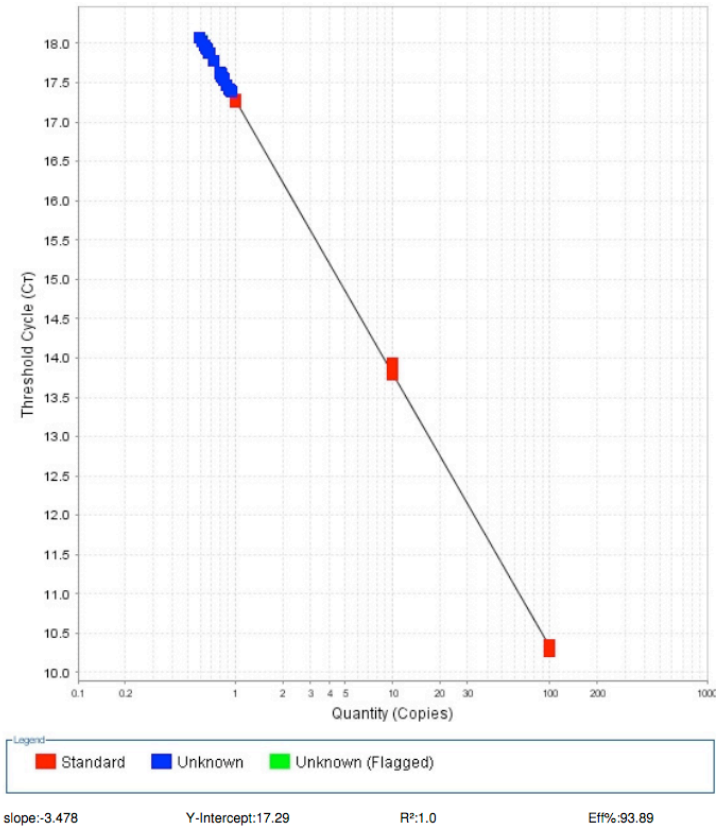

Figure 7. qPCR Standard Curves. Acceptable standard curves will have an R^2 near 1.0 and an Efficiency of 100% or less.