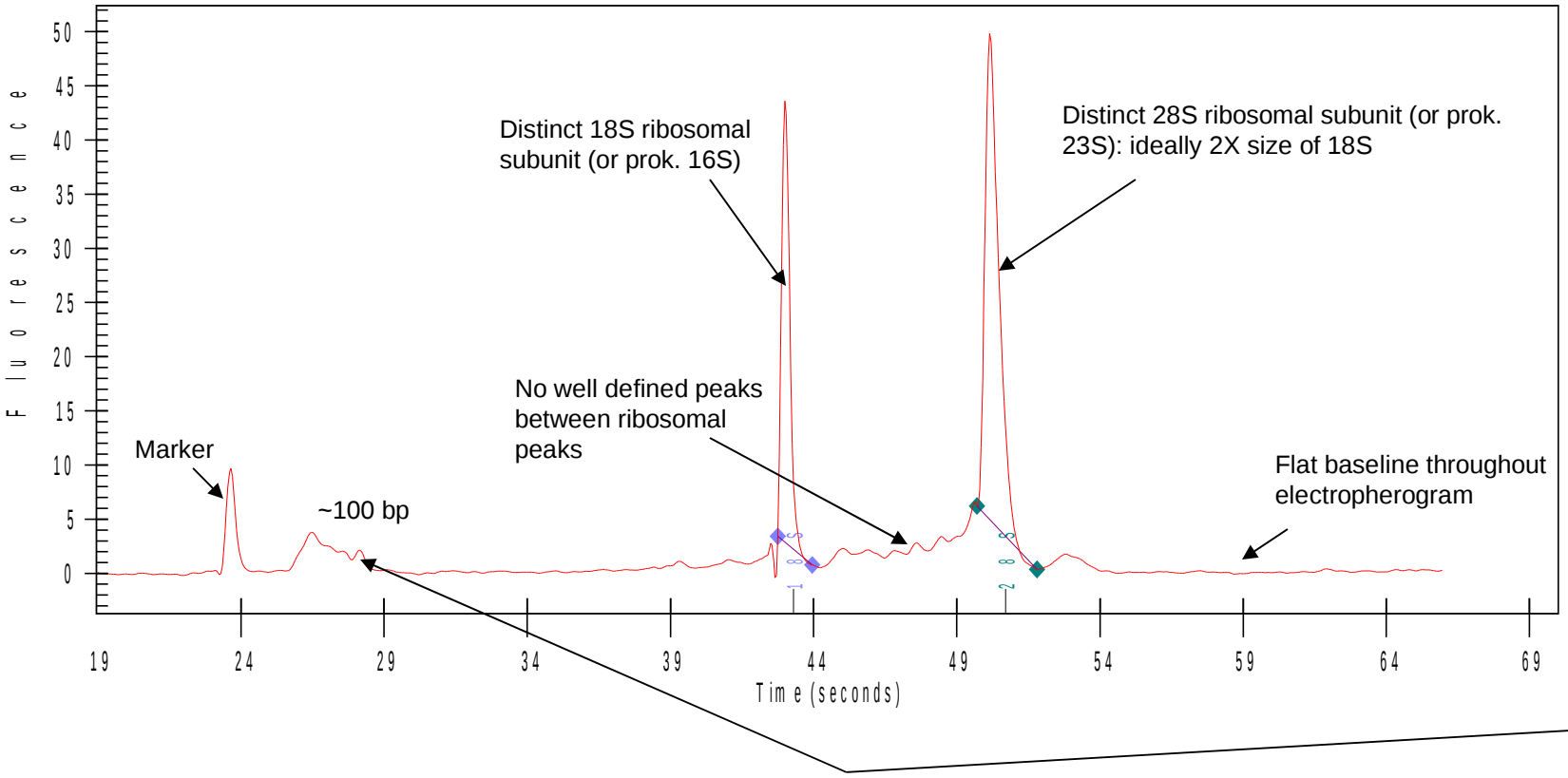
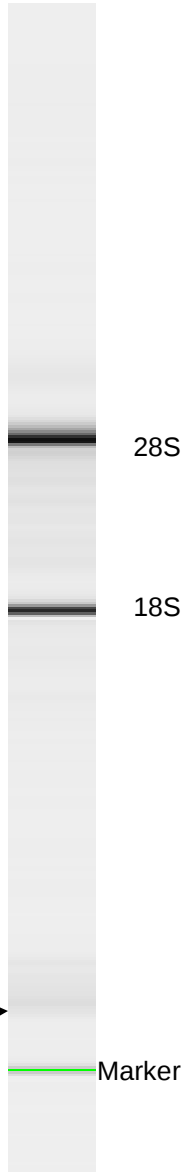
Interpretation of Agilent 2100 Bioanalyzer Data

Intact Total RNA

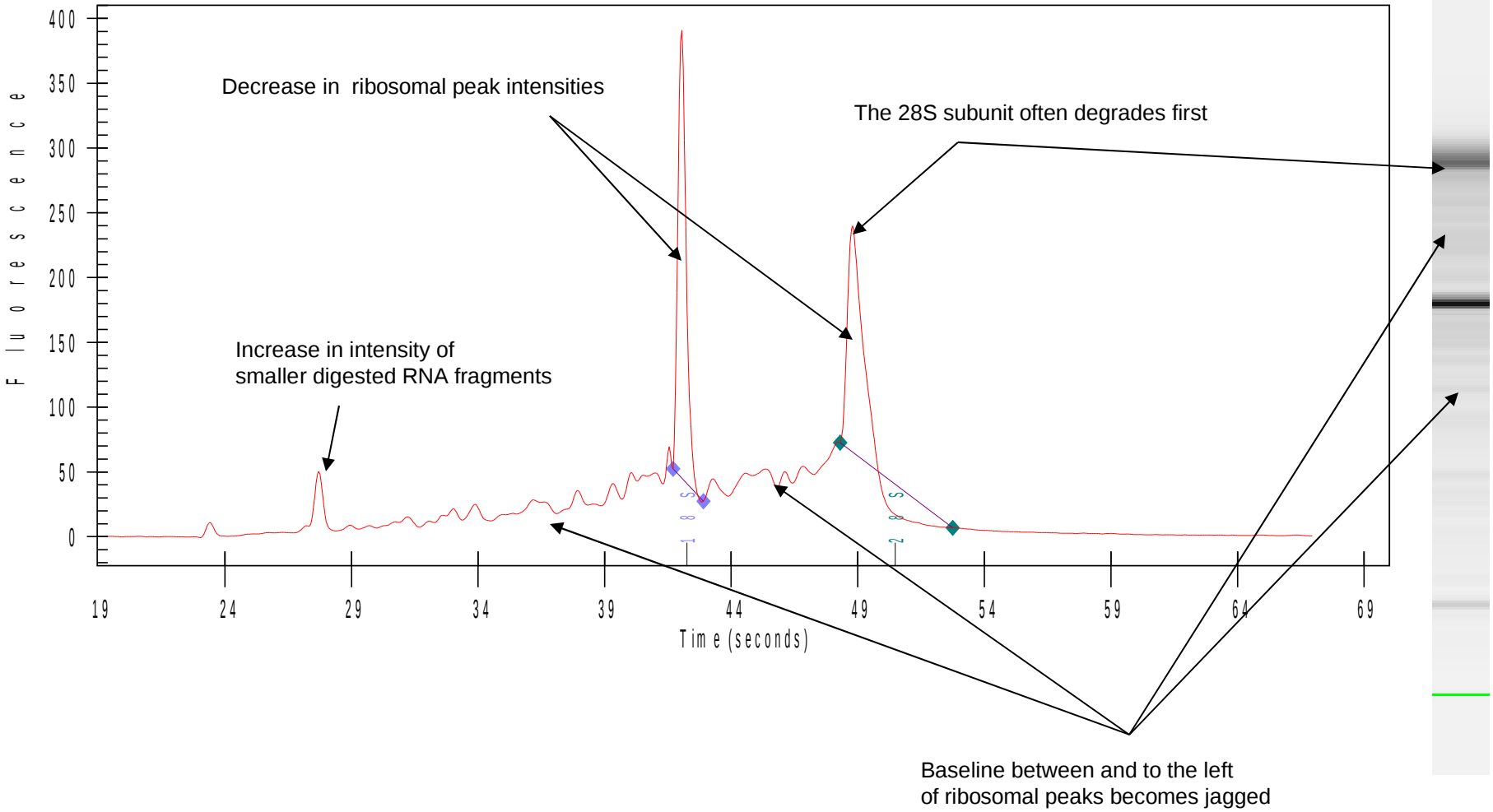




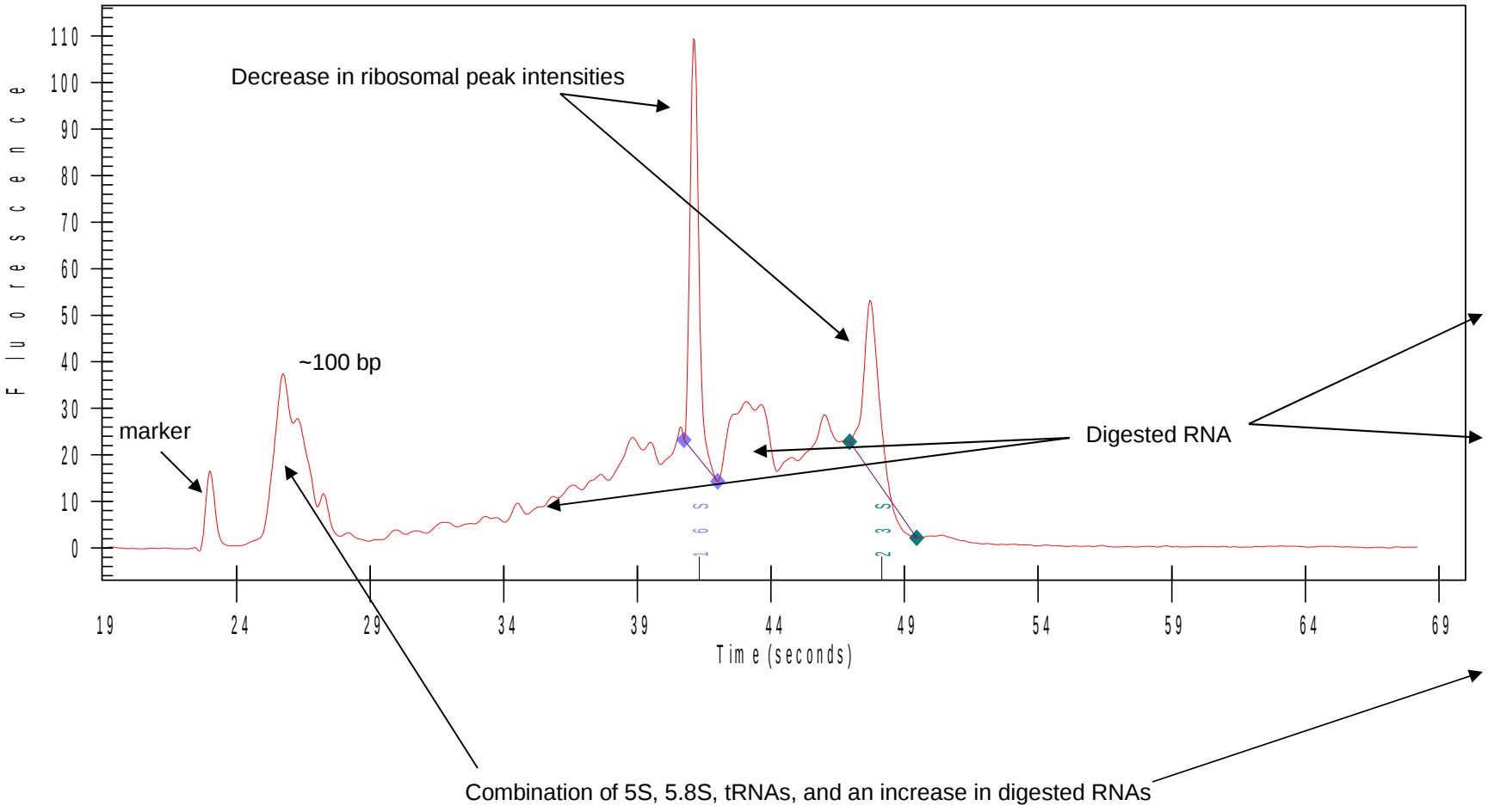
Small peaks are sometimes present after the marker at 24 – 29 seconds. These are represented by 5S and 5.8S subunits, tRNAs, and small RNA fragments about 100bp. These are especially noted when using phenol and trizol extraction methods. They can be removed by treating total RNA through Qiagen columns which removes small RNAs.

Partially Digested Total RNA

Total RNA with images like this are borderline. Re-extraction should be seriously considered.

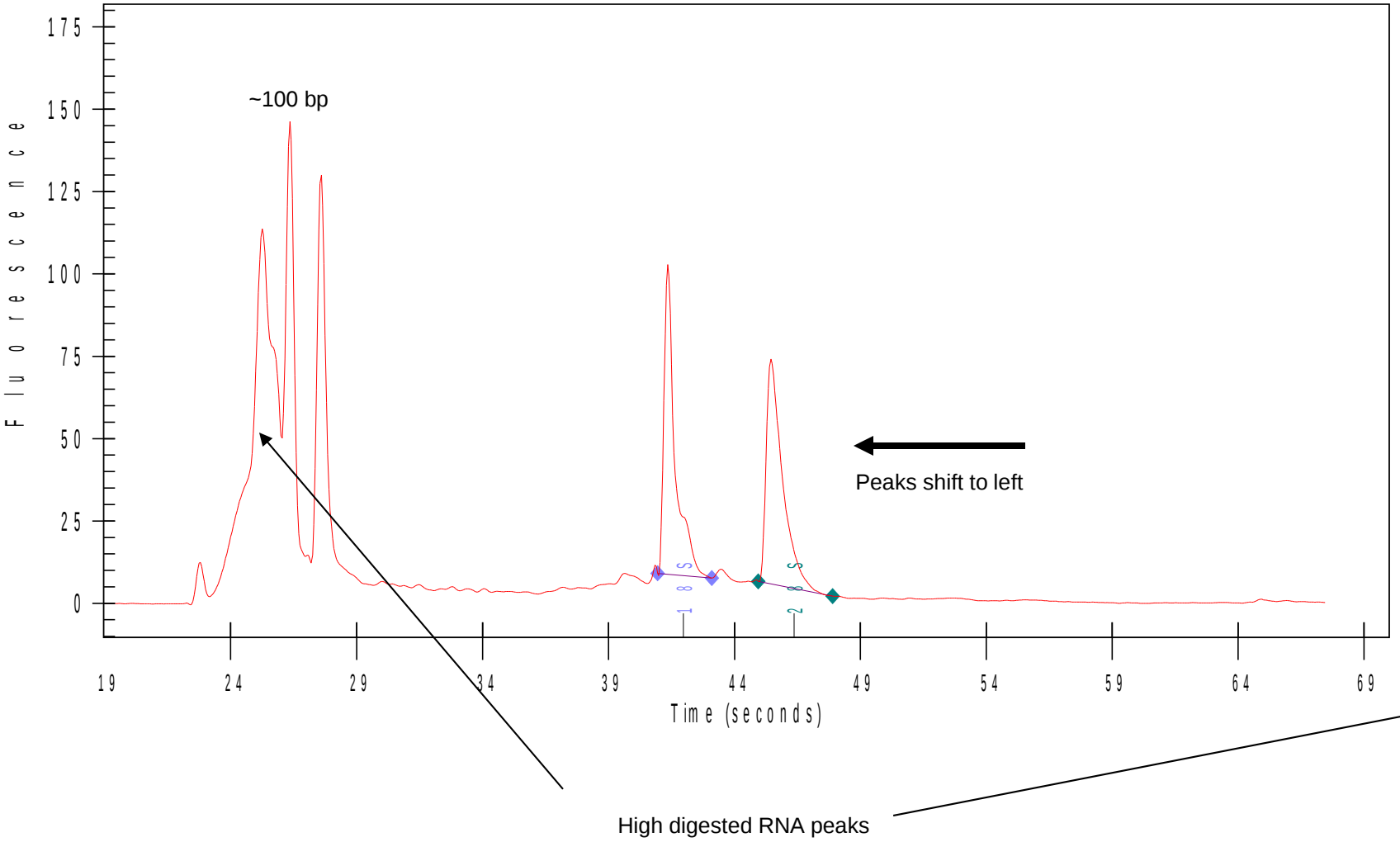


Partially Digested Total RNA Using Trizol Extraction

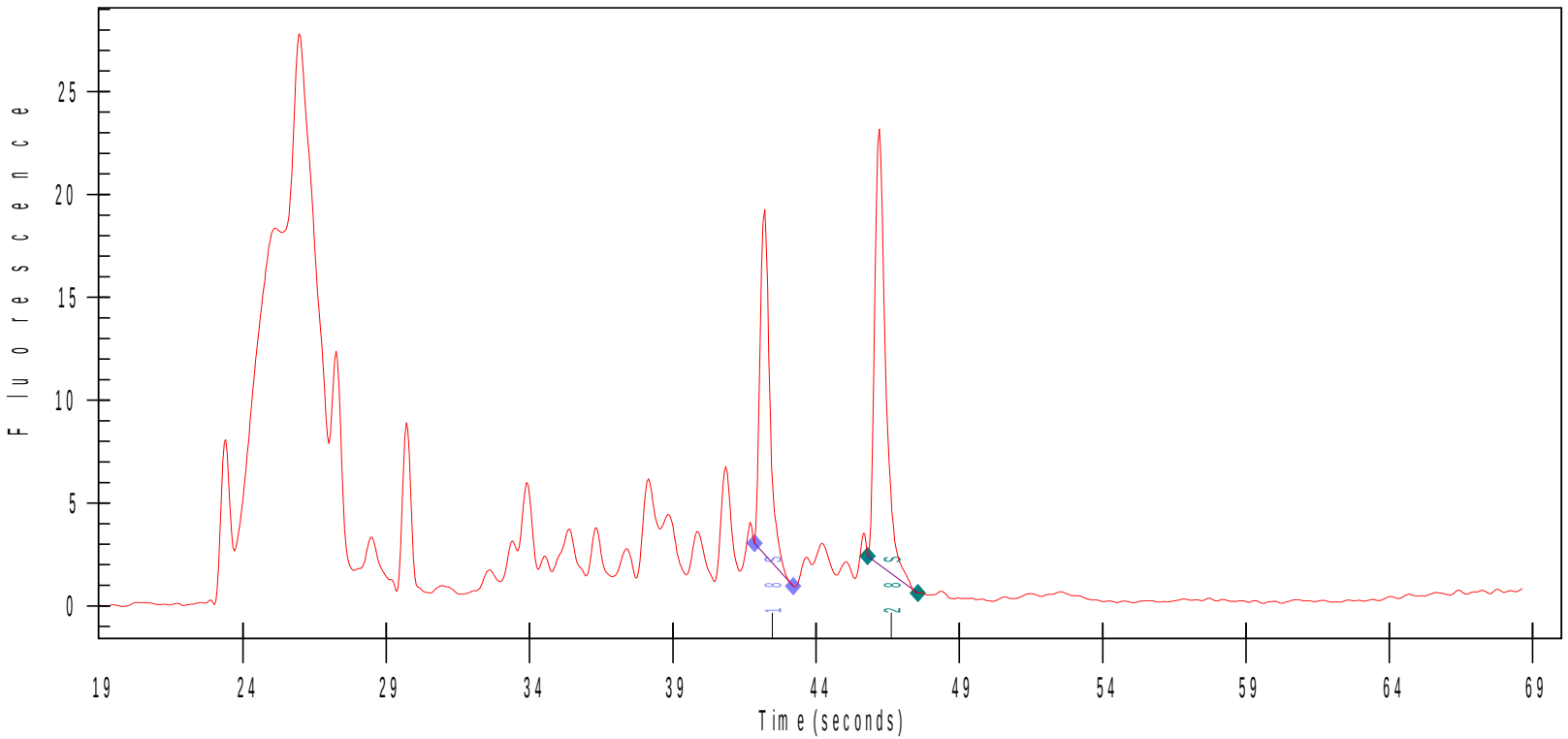


Heavily Digested RNA

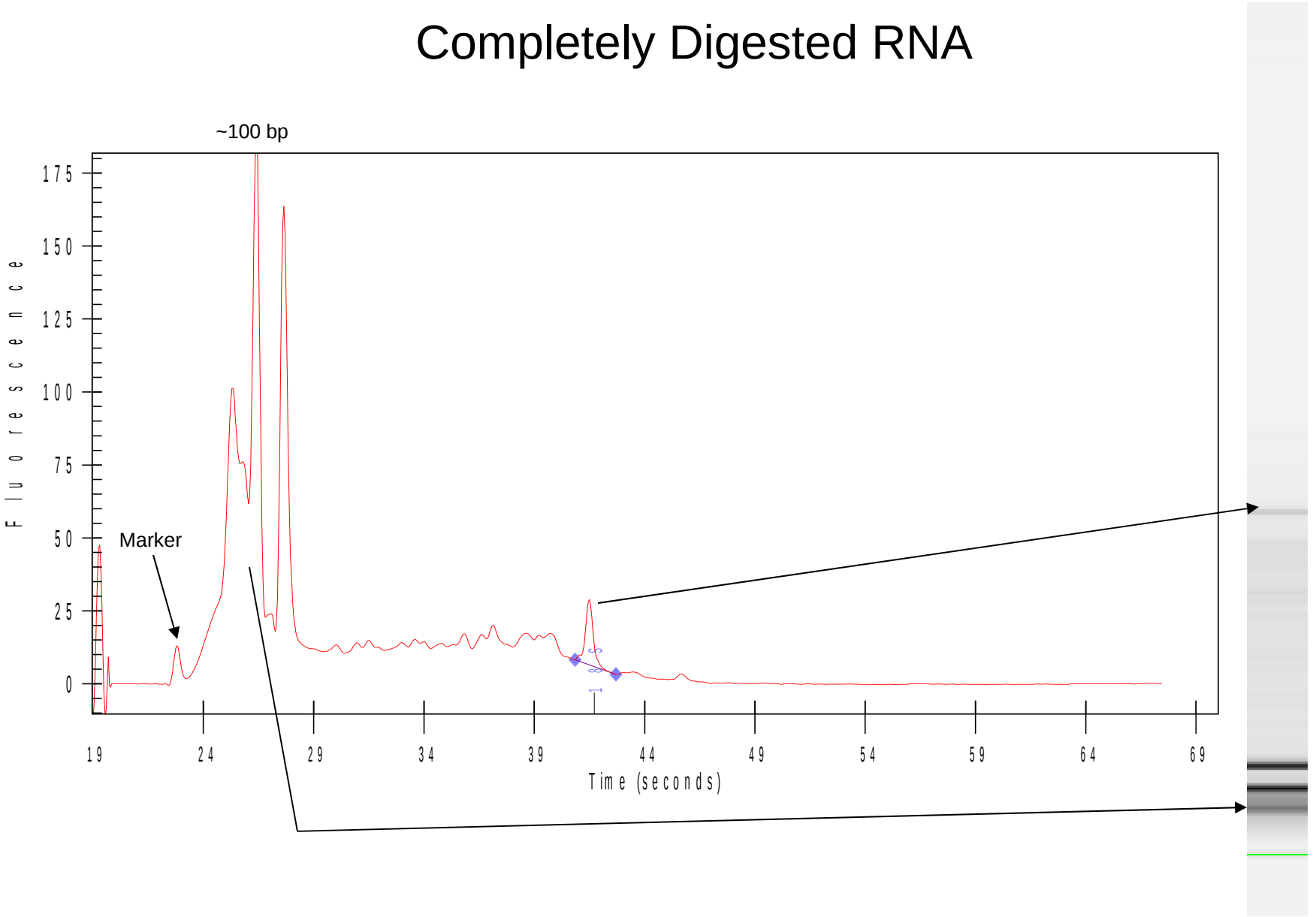
Samples of this quality, if labeled and hybed to a chip, might be in question.



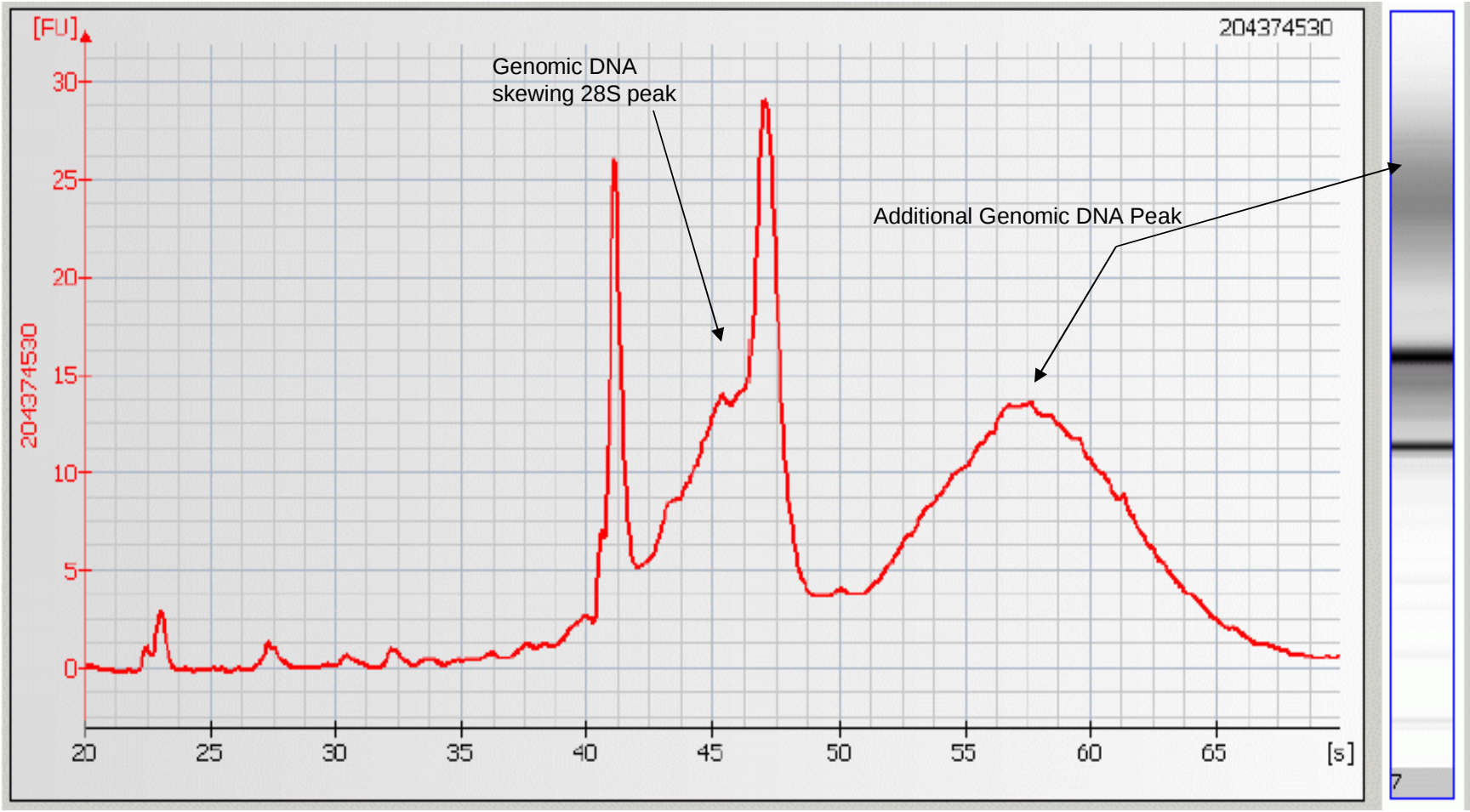
Heavily Digested RNA Using a Hot Phenol with Beads Extraction



Completely Digested RNA

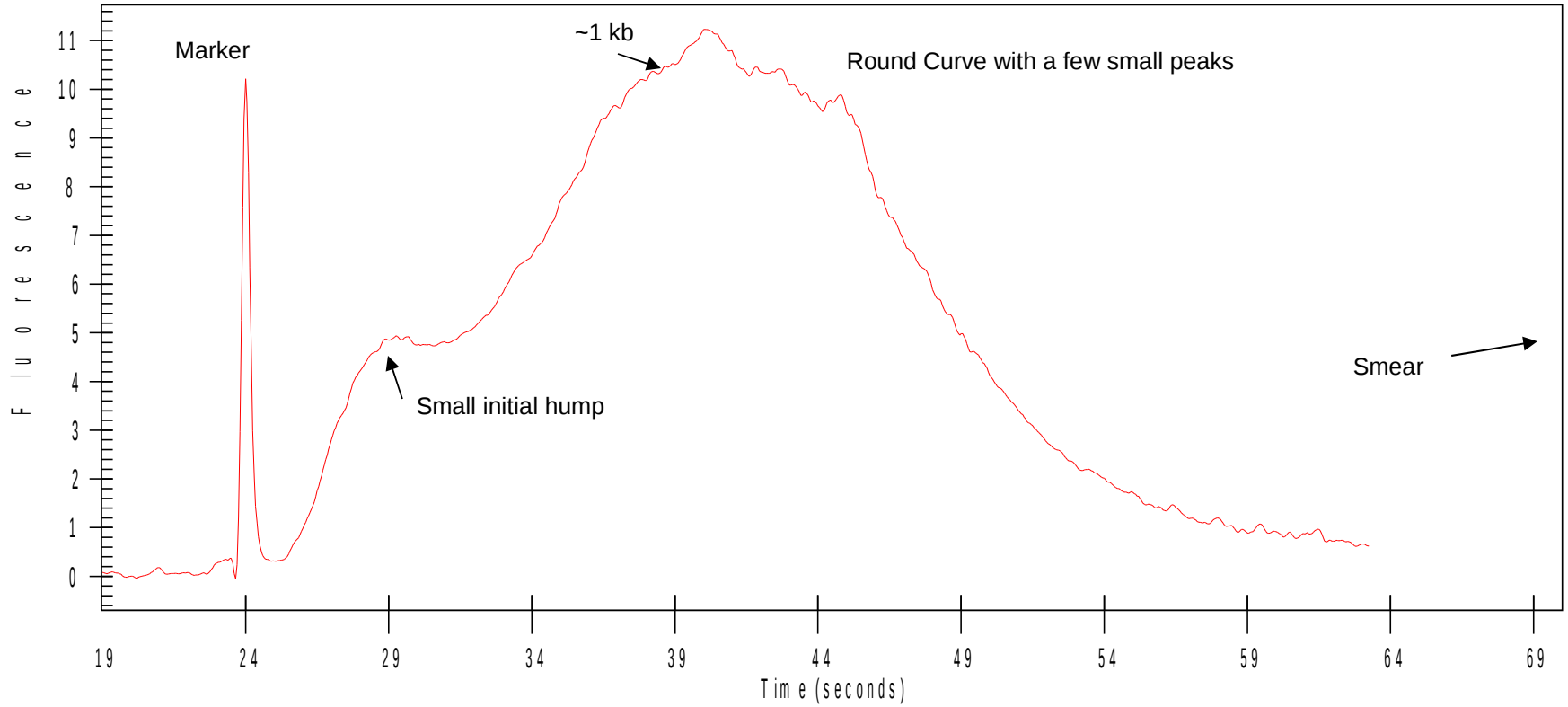


Genomic DNA Contamination



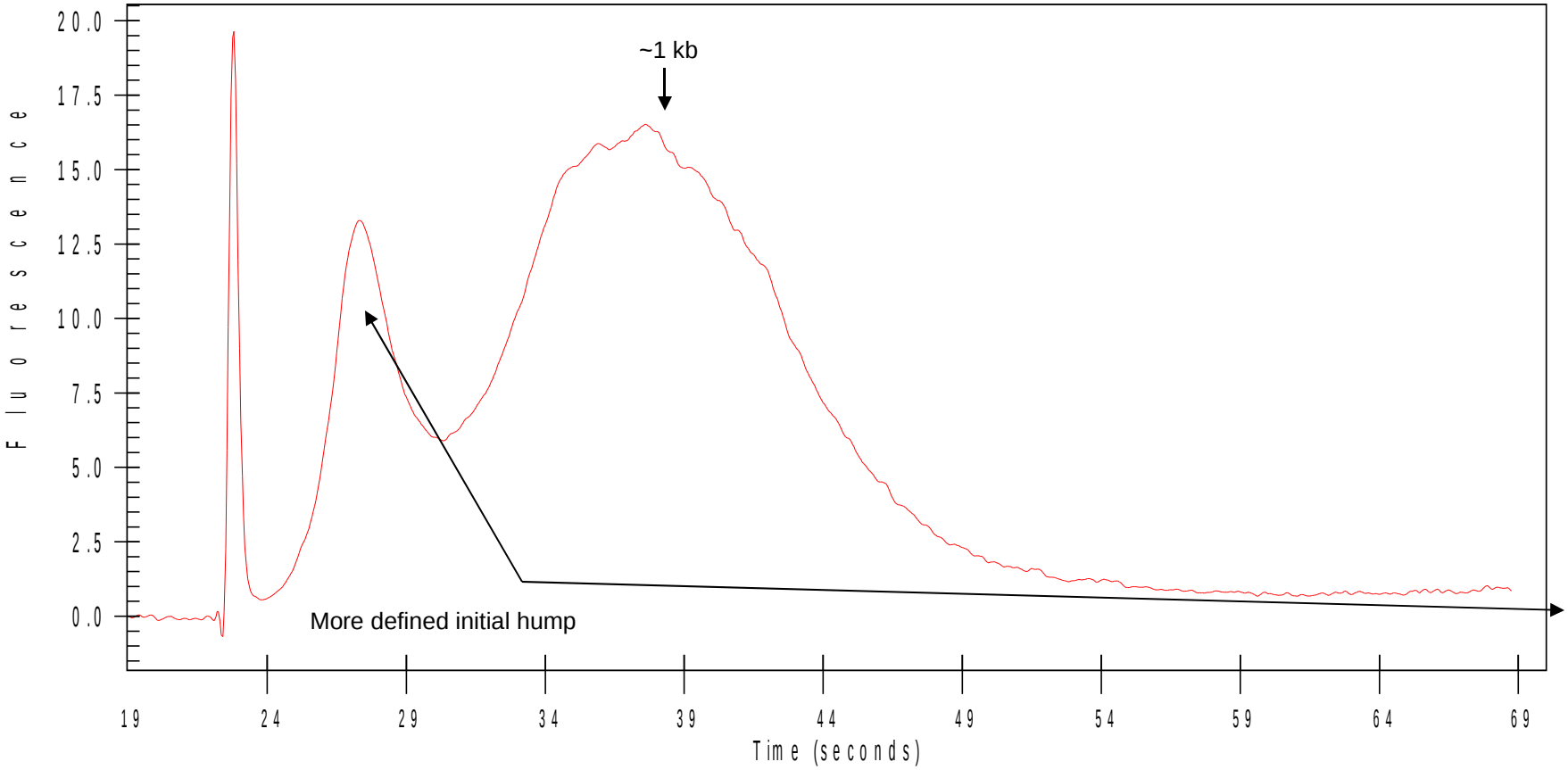
Picture from Agilent Troubleshooting manual

Characteristics of Good Labeled cRNA



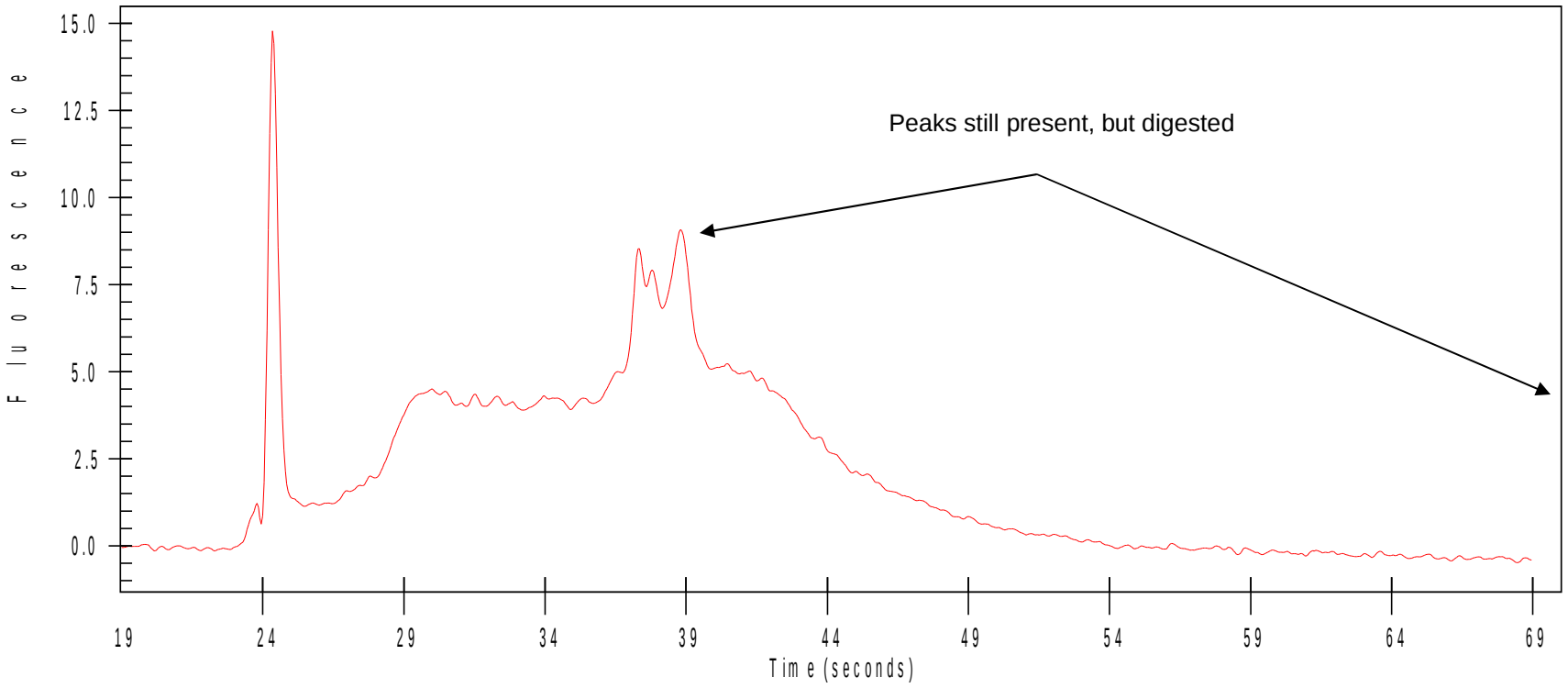
Labeling with Partial Fragmentation

Labeled cRNA with this image are OK to fragment and hyb, but not without risk.



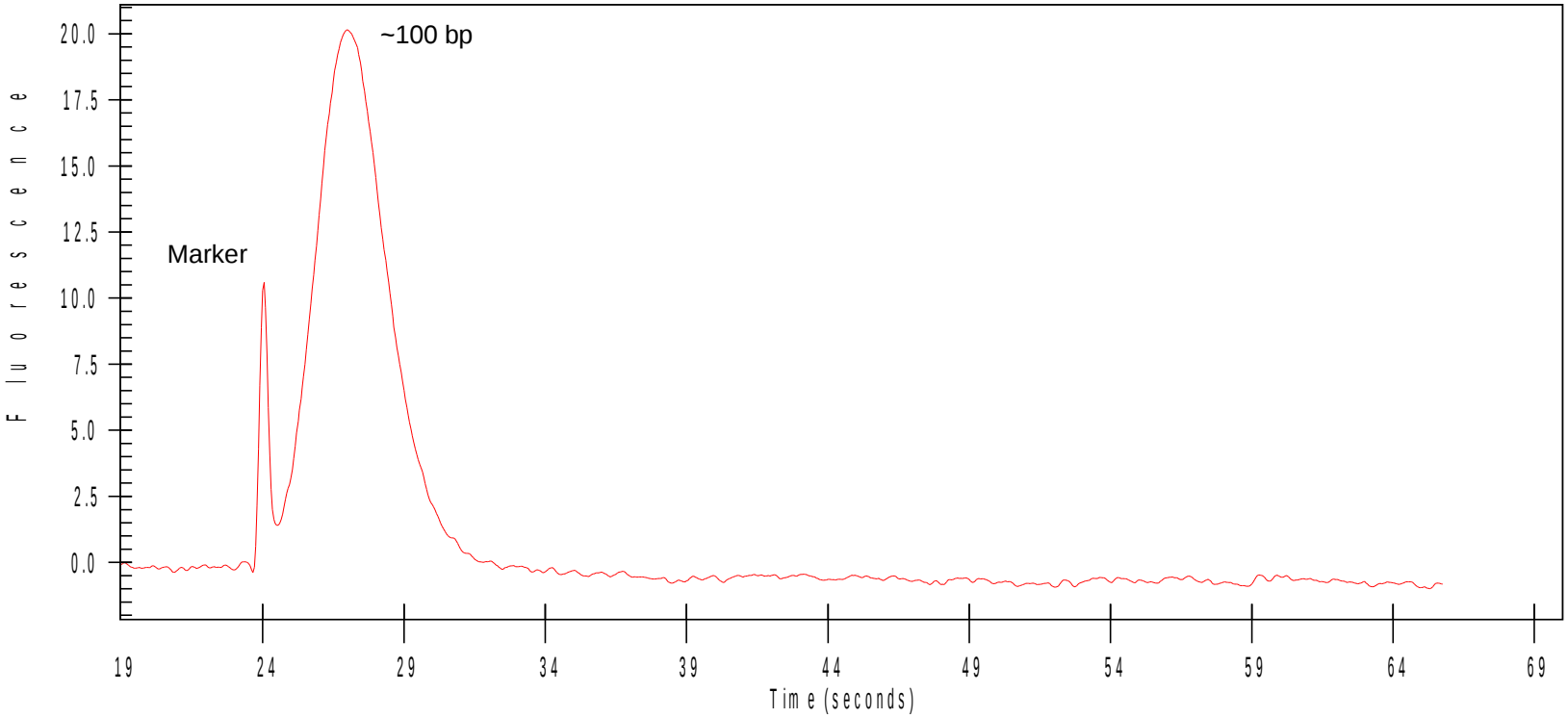
Insufficient Transcription During Labeling

These samples have failed, and are not ready for hybridization.



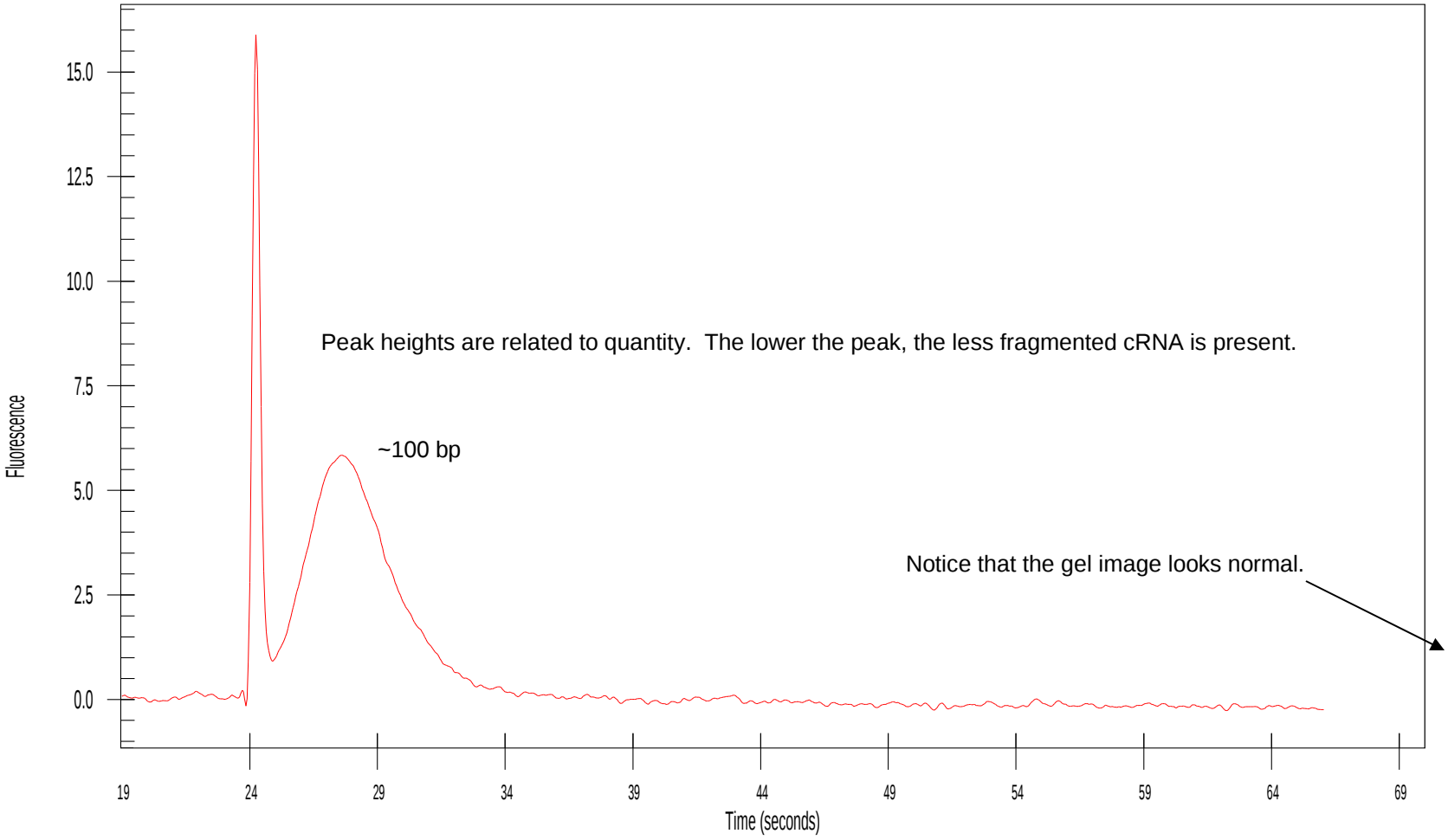
Properly Fragmented cRNA

Fragmented samples with this image are ready for hybridization.



Low Quantities of Fragmented cRNA

This sample may still be OK to hyb, but frequent failures have been reported with cRNA levels this low. It is recommended that the fragmentation be repeated.



Mechanical Spikes

These spikes are due to microparticulates and microbubbles. Dust is a common cause for these. Make sure to quickly load your nanochips and keep your area clean. These do NOT affect the quality of the RNA, labeled cRNA, fragmented cRNA, etc. and are OK to continue processing.