Noise Within Introns

I've been playing with the flux-simulator program for a few days. I've been able to generate simulated FASTQ files for my purposes, but the reads are too nice – after alignment with TopHat or MapSplice there doesn't appear to be any noise to speak of within intron regions.

What parameter settings could I try to increase the amount of noise in non-trascriptomic regions? For example, occasional reads within introns or within intergenic regions as we often see with real RNA-Seq data? These might arise from incompletely spliced transcripts in the sample or from rare intron retention events that may not yet be part of the annotated transcriptome. Is there any way to get flux-simulator to model this?

Many thanks!