Supplementary Figure 4. *Change in abundance estimates of false positive transcript quantifications with introduction of noisy transcription across 30 simulated samples representing 3 simulated tissues. StringTie2 changed from 0.14 median TPM in the absence of noise to 0.13 with intronic noise; 0.15 with splicing noise; 0.14 with intergenic noise; and 0.15 with all noise combined. Salmon changed from 0.4 median TPM in the absence of noise to 0.39 with intronic noise; 0.86 with splicing noise; 0.4 with intergenic noise; and 0.85 with all noise combined. Kallisto changed from 0.19 median TPM in the absence of noise to 0.39 with splicing noise and all sources of noise combined. Abundance estimates reported by Kallisto remained around 0.4 median TPM with introduction of intronic and intergenic noise.*