



Supplementary Figure 5. Simulated abundance of false negative transcript quantifications across 30 simulated samples representing 3 simulated tissues. StringTie2 failed to identify isoforms with median TPM of 0.4 in the absence and presence of all types of noise. Salmon failed to identify isoforms with median 2.02 TPM in the absence of noise and presence of intronic and intergenic noise. Introduction of splicing noise and all sources of noise combined changed the median TPM of expressed transcripts unreported by Salmon to 2.25 TPM. Kallisto failed to identify isoforms with median 1.84 TPM in the absence of noise and presence of intronic and intergenic noise. Introduction of splicing noise and all sources of noise combined changed the median TPM of expressed transcripts unreported by Kallisto to 2.09 TPM.