Supplementary Figure 2. *Number of False Positive transcript quantifications across 30 simulated samples representing 3 simulated tissues. Each method was evaluated separately for each combination of real and noisy reads. StringTie2 changed from 18,844 FPs in the absence of noise to 18,848 with intronic noise; 23,490 with splicing noise; 18,839 with intergenic noise; and 23,494 with all noise combined. Salmon changed from 21,546 FPs in the absence of noise to 21,729 with intronic noise; 36,576 with splicing noise; 21,549 with intergenic noise; and 36,677 with all noise combined. Kallisto changed from 34,316 FPs in the absence of noise to 34,673 with intronic noise; 51,280 with splicing noise; 34,337 with intergenic noise; and 51,478 with all noise combined.*