Supplementary Figure 3. *Number of False Negative 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 2,109 FNs in the absence of noise to 2,112 with intronic noise; 2,086 with splicing noise; 2,111 with intergenic noise; and 2,085 with all noise combined. Salmon changed from 3,061 FNs in the absence of noise to 3,065 with intronic noise; 3,439 with splicing noise; 3,063 with intergenic noise; and 3,439 with all noise combined. Kallisto changed from 1,233 FNs in the absence of noise to 1,234 with intronic noise; 1,740 with splicing noise; 1,233 with intergenic noise; and 1,741 with all noise combined.*