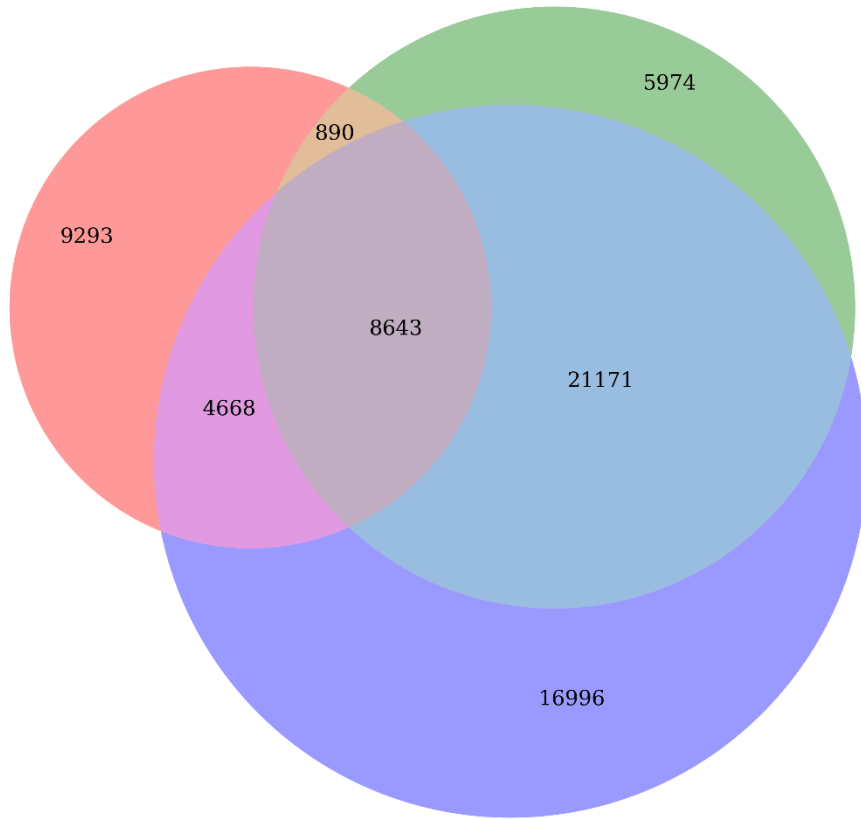
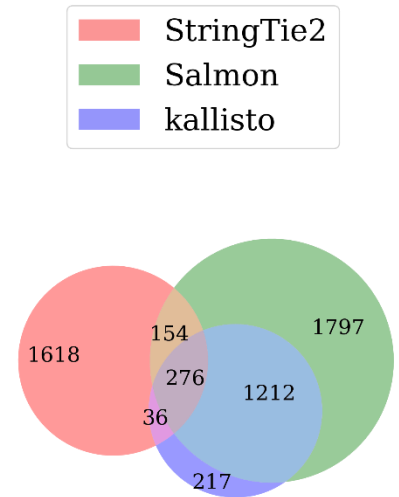


False Positives



False Negatives



Supplementary Figure 9. False transcript predictions. *Overlaps between StringTie2, Salmon and Kallisto in reported FP and FN transcripts in the presence of splicing, intronic and intergenic noise. Average values are reported across 30 simulated experiments.*