Fig. 2: Overview of evaluation for Challenge 1: transcript identification with a reference annotation. transcript identification with a reference annotation. a) Percentage of transcript models fully supported at (left) 5' ends either by reference annotation or same-sample CAGE data, (middle) 3' end either by reference annotation or same-sample Quant-seq data, and (right) splice junctions by short-read coverage or a canonical site. b) Agreement in transcript detection as a function the number of detecting pipelines, c) Performance of tools based on for (top) spliced-short and (bottom) unspliced long SIRVs. d) Performance of tools based on simulated data. e) Performance of tools on known and novel transcripts of 50 genes manually-annotated by GENCODE. f) Summary of performance metrics of tools across all benchmarking datasets. Color scale represents the performance value ranging from worse (dark blue) to better (light yellow). Graphic symbol indicates the raking position of the tool for the metric represented in each row. SJ: Splice Junction, UIC: Unique Intron Chain. LO: Long (reads) Only, LS: Long and Short (reads), Sen_kn: Sensitivity for known transcripts, Pre_kn: Precision for known transcripts, Sen_no: Sensitivity for Novel transcripts, Pre_no: Precision for Novel transcripts, 1/Red: inverse of redundancy. Num: number, SRTM: Supported Reference Transcript Model, SNTM: Supported Novel Transcript Model, Ba: Bambu, FM: Flames, FR: FLAIR, IQ: IsoQuant, IT: IsoTools, IB: Iso_IB, Ly: LyRic, Ma: Mandalorion, TL: TALON-LAPA, Sp: Spectra, ST: StringTie2.