



Extended Data Fig. 23. Percentage of transcript models (TM) with different ranges of sequence coverage by long reads.

a) WTC11. c) H1-mix. c) Mouse ES. Ba: Bambu, FM: FLAMES, FL: FLAIR, IQ: IsoQuant, IT: IsoTools, IB: Iso_IB, Ly: LyRic, Ma: Mandalorion, TL: TALON-LAPA, Sp: Spectra, ST: StringTie2.