Figure S1

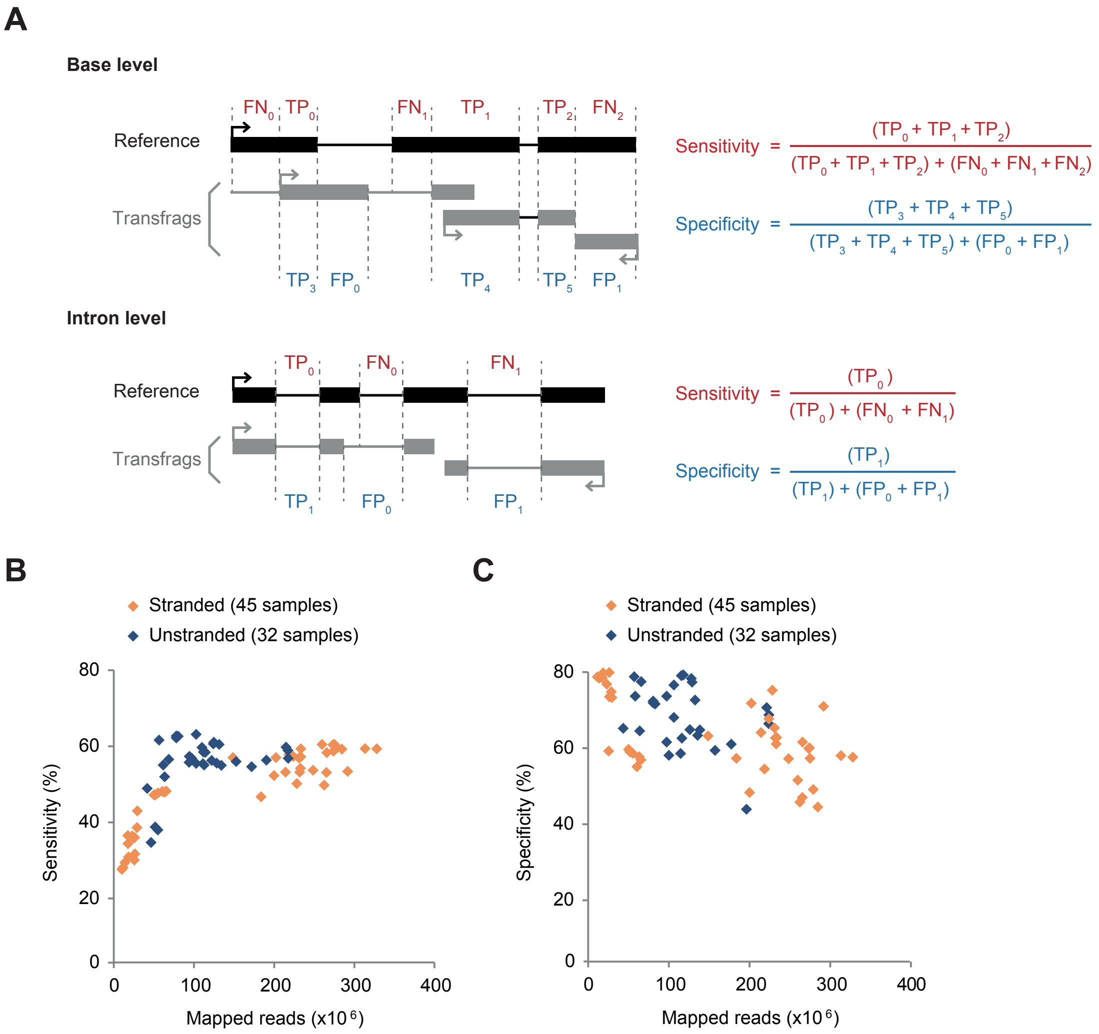

Figure S1. Evaluation of assembled transfrags with or without consideration of their directionality

(A) Evaluation of assembled transfrags at the base and intron level. Resulting transfrags were compared to the reference gene structures and were counted as true positive (TP), false positive (FP), and false negative (FN) at the base (top) and intron level (bottom). Isoforms were combined to create a unified exon model for evaluation. When comparing to the reference in the forward strand, transfrags in the reverse strand were classified as FP when their directionality was considered but as TP when the directionality was not considered. See Methods for more details. (B-C) The sensitivity (B) and specificity (C) of the resulting assemblies produced from the ENCODE dataset. The Cuffcompare analysis was done without considering their directionality during evaluation (default option). The stranded (orange diamond) and unstranded (navy diamond) assemblies were separately evaluated.