Simulation model	Estimation model	MPE	10% EF	FP
theoretical	quality	4.0/10.4/11.8	21.9/51.0/53.8	1.7/4.5/13.6
theoretical	profile	4.1/10.5/11.8	21.9/51.0/53.8	1.8/4.5/13.8
empirical	quality	4.0/10.2/11.6	21.7/50.5/53.2	1.6/4.5/13.7
empirical	profile	4.0/10.2/11.6	21.7/50.5/53.4	1.6/4.6/13.7

Table 1: Accuracy of abundance estimates from RNA-Seq data sets simulated with Ensembl annotations and with different combinations of sequencing error models for simulation and estimation. Values are given as gene/global isoform/within-gene isoform.