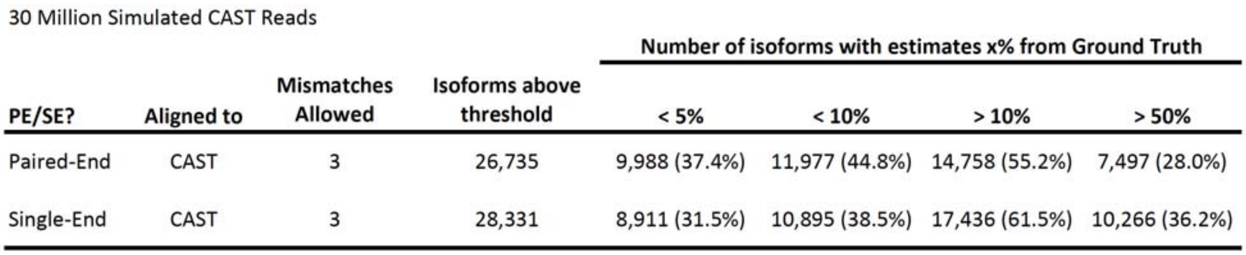
Table S12 Comparison of isoform abundance results in CAST simulation study from using paired-end or single-end sequencing



30 Million Simulated CAST Reads

PE/SE?	Aligned to	Mismatches Allowed	Isoforms above threshold	Number of isoforms with estimates x% from Ground Truth			
				< 5%	< 10%	> 10%	> 50%
Paired-End	CAST	3	26,735	9,988 (37.4%)	11,977 (44.8%)	14,758 (55.2%)	7,497 (28.0%)
Single-End	CAST	3	28,331	8,911 (31.5%)	10,895 (38.5%)	17,436 (61.5%)	10,266 (36.2%)

Paired-end sequencing yields modest improvements in isoform abundance estimation relative to single-end reads. For example, 45% of isoform estimates fall within ten percent of the simulated ground truth value in the analysis of paired-end reads, compared to 39% for single-end reads.