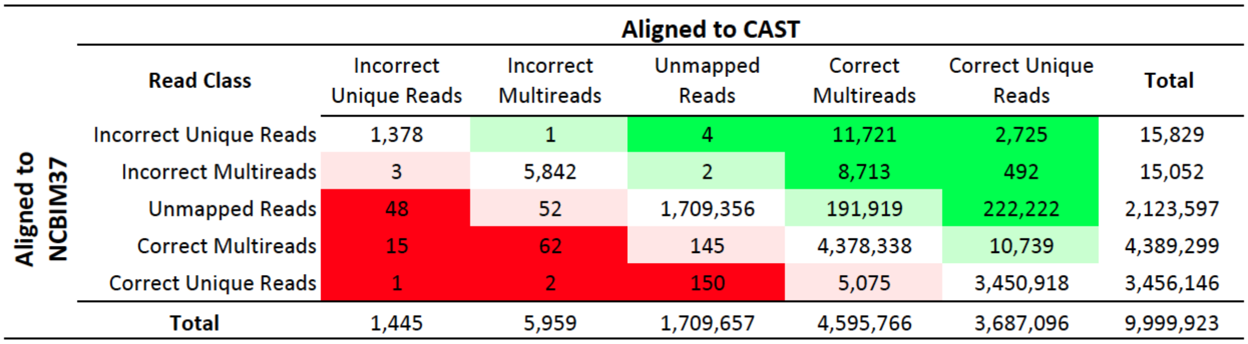
Table S1 Isoform-level summary of read alignment in the simulated CAST data



		Aligned to CAST					
	Read Class	Incorrect Unique Reads	Incorrect Multireads	Unmapped Reads	Correct Multireads	Correct Unique Reads	**Total**
Aligned to NCBIM37	Incorrect Unique Reads	1,378	1	4	11,721	2,725	15,829
	Incorrect Multireads	3	5,842	2	8,713	492	15,052
	Unmapped Reads	48	52	1,709,356	191,919	222,222	2,123,597
	Correct Multireads	15	62	145	4,378,338	10,739	4,389,299
	Correct Unique Reads	1	2	150	5,075	3,450,918	3,456,146
	Total	1,445	5,959	1,709,657	4,595,766	3,687,096	9,999,923

The simulated reads were aligned to the NCBIM37 and CAST transcriptomes. Reads that improve by alignment to CAST are highlighted in green, with those that improve by two or more categories are highlighted in dark green. Reads that improve by alignment to NCBIM37 are highlighted in red, with those that improve by two or more categories highlighted in dark red. Reads on the diagonal align equivalently by both strategies.