**Figure S5**

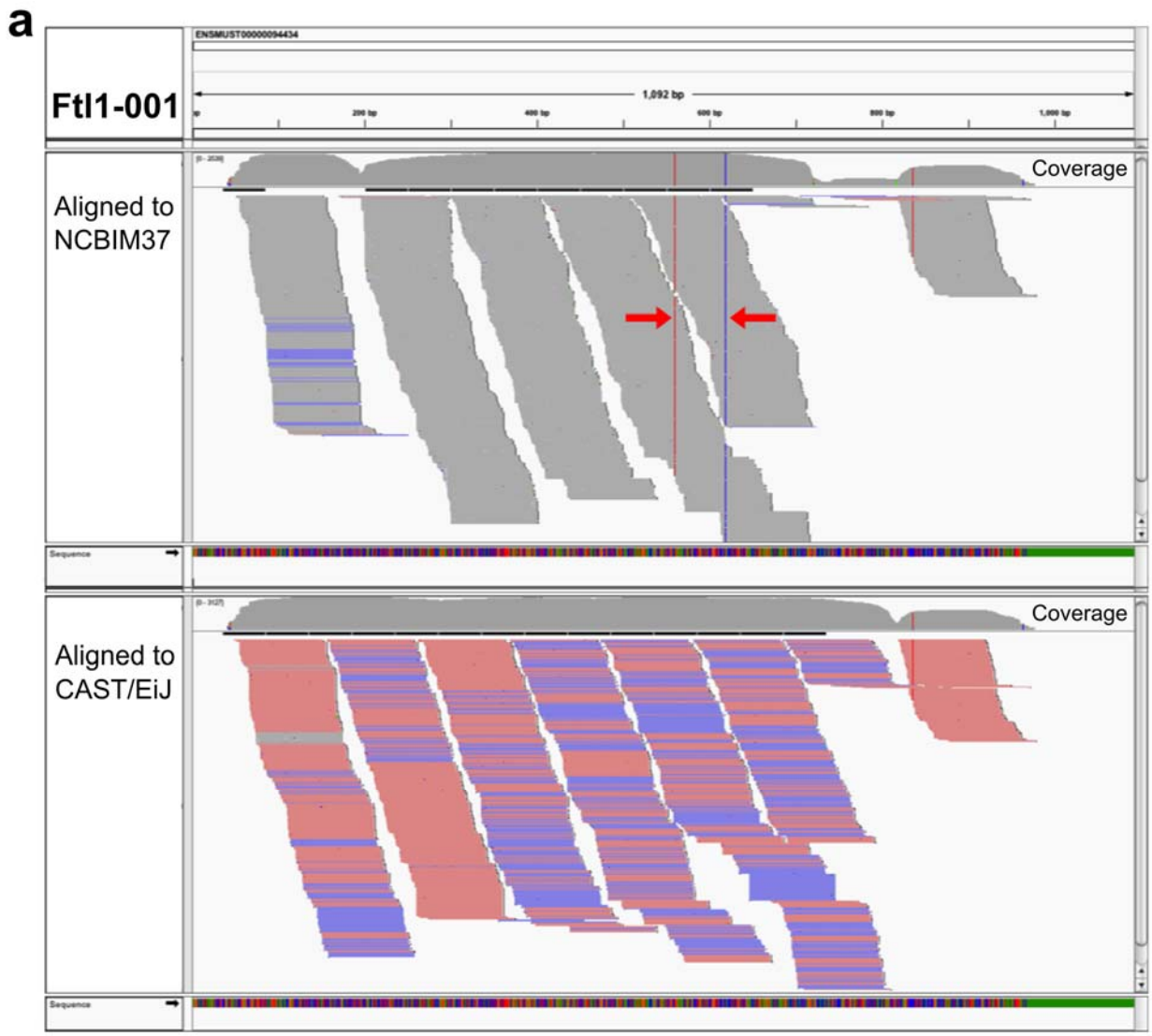
a
Ftl1-001
ENSMUST00000094434
1,092 bp
200 bp
400 bp
600 bp
800 bp
1,000 bp
Aligned to NCBIM37
Coverage
Sequence
Aligned to CAST/EiJ
Coverage
Sequence

**Figure S5 (continued)**

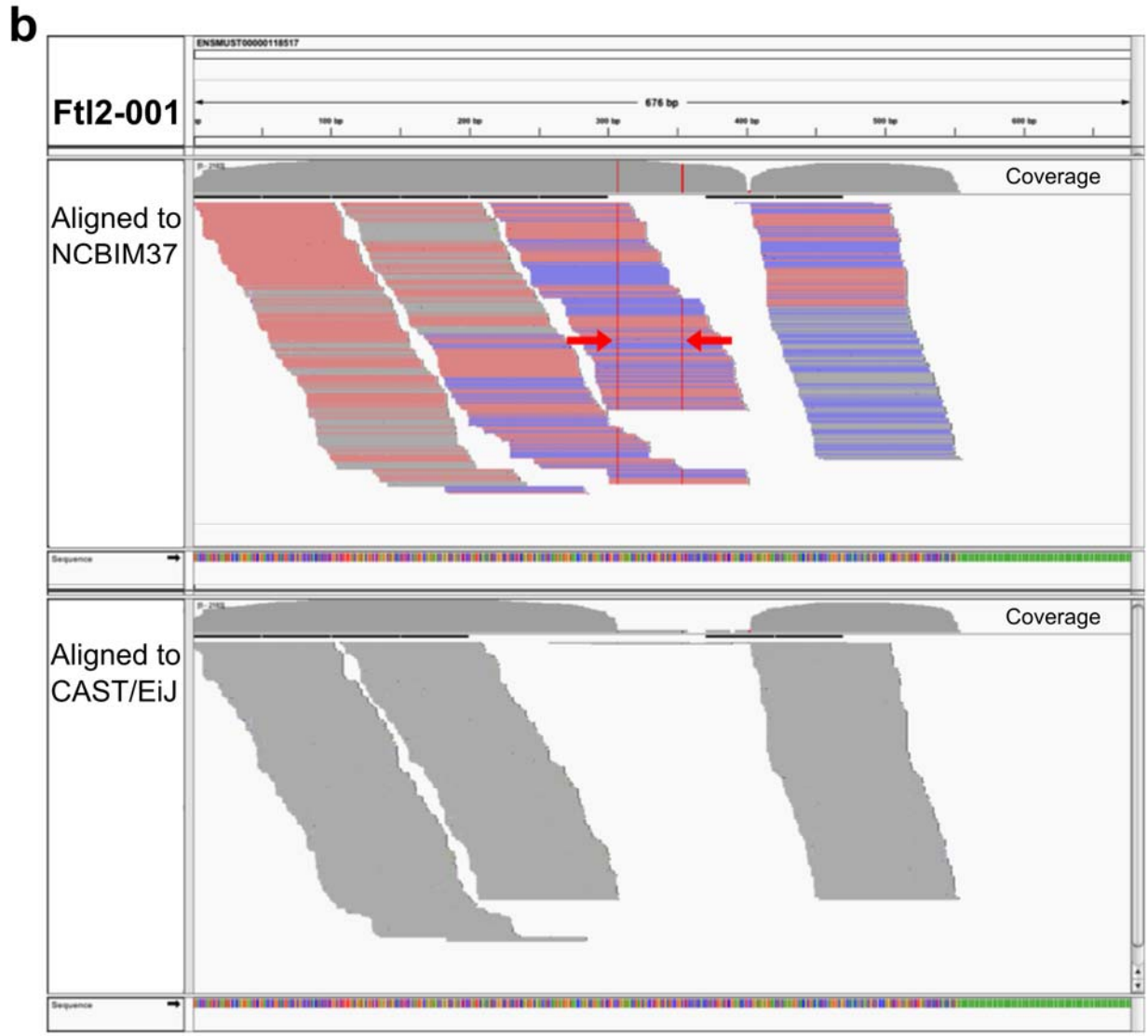


**Figure S5** Coverage of CAST reads to *Ftl1* and *Ftl2* transcript sequences derived from the NCBIM37 reference genome and individualized CAST genome. Coverage plots show the distribution of CAST RNA-seq read alignments to *Ftl1-001* (A) and *Ftl2-001* (B) from alignment to each of the NCBIM37 reference and individualized CAST transcriptomes. Read coverage density (log transformed) is displayed at the top of each panel. For individual aligned reads, read color corresponds to orientation (red = forward strand, blue = reverse strand) and posterior probability. Gray reads have low probability of being transcribed from the aligned transcript location (as estimated by RSEM), while blue/red indicates reads that have been assigned high posterior probabilities. The red arrows point to SNPs in the CAST reads that differ from NCBIM37. Accounting for these CAST SNPs in the alignment diverts many reads from the *Ftl2* pseudogene to the parent protein-coding gene *Ftl1*.