Figure S4

a

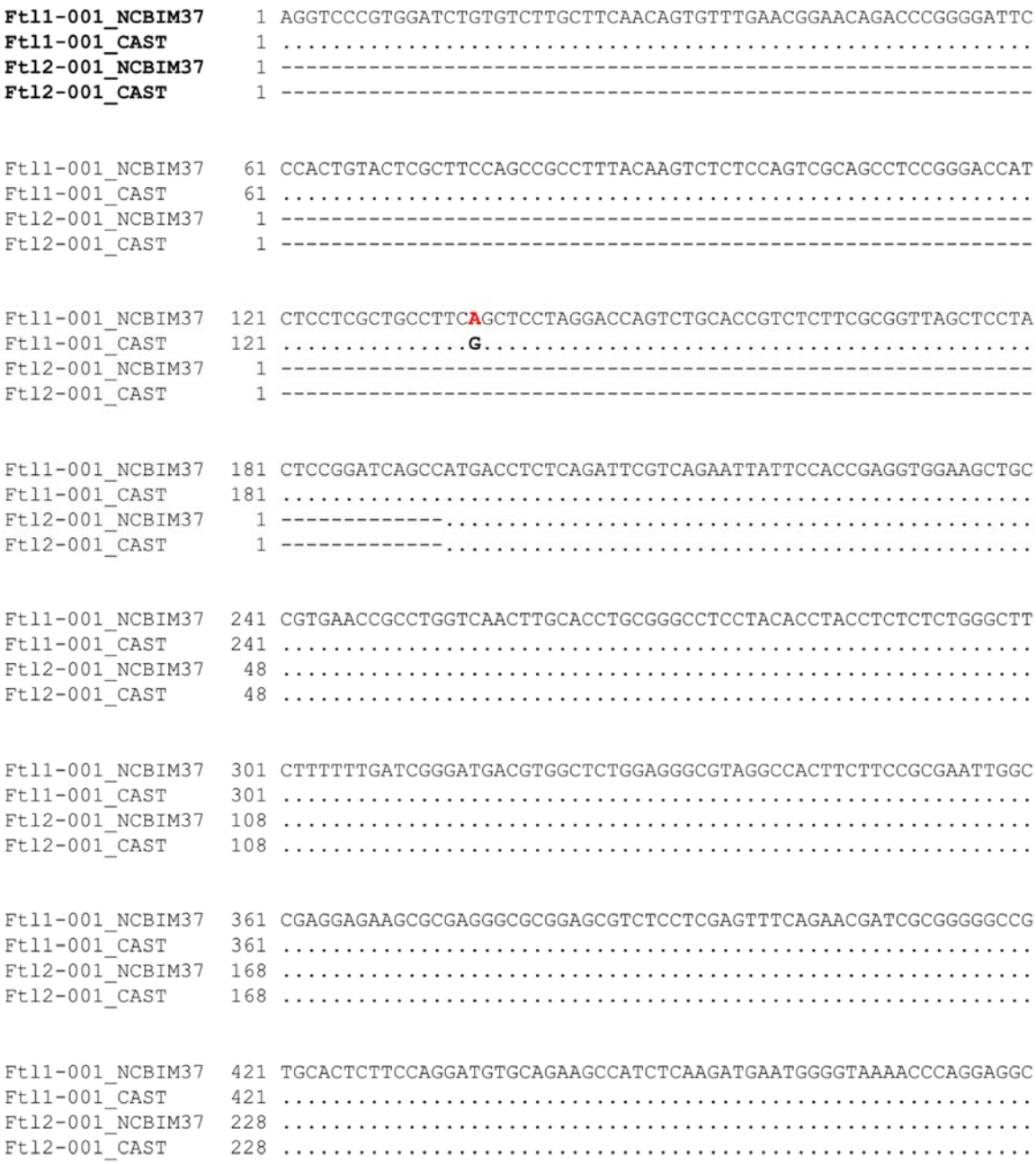
Ftl1-001_NCBIM37 1 AGGTCCCGTGGATCTGTGTCTTGCTTCAACAGTGTTTGAACGGAACAGACCCGGGGATTC
Ftl1-001_CAST 1 .....
Ftl2-001_NCBIM37 1 -----
Ftl2-001_CAST 1 -----
Ftl1-001_NCBIM37 61 CCACTGTACTCGCTTCCAGCCGCCTTTACAAGTCTCTCCAGTCGCAGCCTCCGGGACCAT
Ftl1-001_CAST 61 .....
Ftl2-001_NCBIM37 1 -----
Ftl2-001_CAST 1 -----
Ftl1-001_NCBIM37 121 CTCCTCGCTGCCTTCAGCTCCTAGGACCAGTCTGCACCGTCTCTTCGCGGTTAGCTCCTA
Ftl1-001_CAST 121 .....G.....
Ftl2-001_NCBIM37 1 -----
Ftl2-001_CAST 1 -----
Ftl1-001_NCBIM37 181 CTCCGGATCAGCCATGACCTCTCAGATTCGTCAGAATTATTCCACCGAGGTGGAAGCTGC
Ftl1-001_CAST 181 .....
Ftl2-001_NCBIM37 1 ----------.....
Ftl2-001_CAST 1 ----------.....
Ftl1-001_NCBIM37 241 CGTGAACCGCCTGGTCAACTTGCACCTGCGGGCCTCCTACACCTACCTCTCTCTGGGCTT
Ftl1-001_CAST 241 .....
Ftl2-001_NCBIM37 48 .....
Ftl2-001_CAST 48 .....
Ftl1-001_NCBIM37 301 CTTTTTTGATCGGGATGACGTGGCTCTGGAGGGCGTAGGCCACTTCTTCCGCGAATTGGC
Ftl1-001_CAST 301 .....
Ftl2-001_NCBIM37 108 .....
Ftl2-001_CAST 108 .....
Ftl1-001_NCBIM37 361 CGAGGAGAAGCGCGAGGGCGCGGAGCGTCTCCTCGAGTTTCAGAACGATCGCGGGGGCCG
Ftl1-001_CAST 361 .....
Ftl2-001_NCBIM37 168 .....
Ftl2-001_CAST 168 .....
Ftl1-001_NCBIM37 421 TGCACTCTTCCAGGATGTGCAGAAGCCATCTCAAGATGAATGGGGTAAAACCCAGGAGGC
Ftl1-001_CAST 421 .....
Ftl2-001_NCBIM37 228 .....
Ftl2-001_CAST 228 .....

Figure S4 (continued)

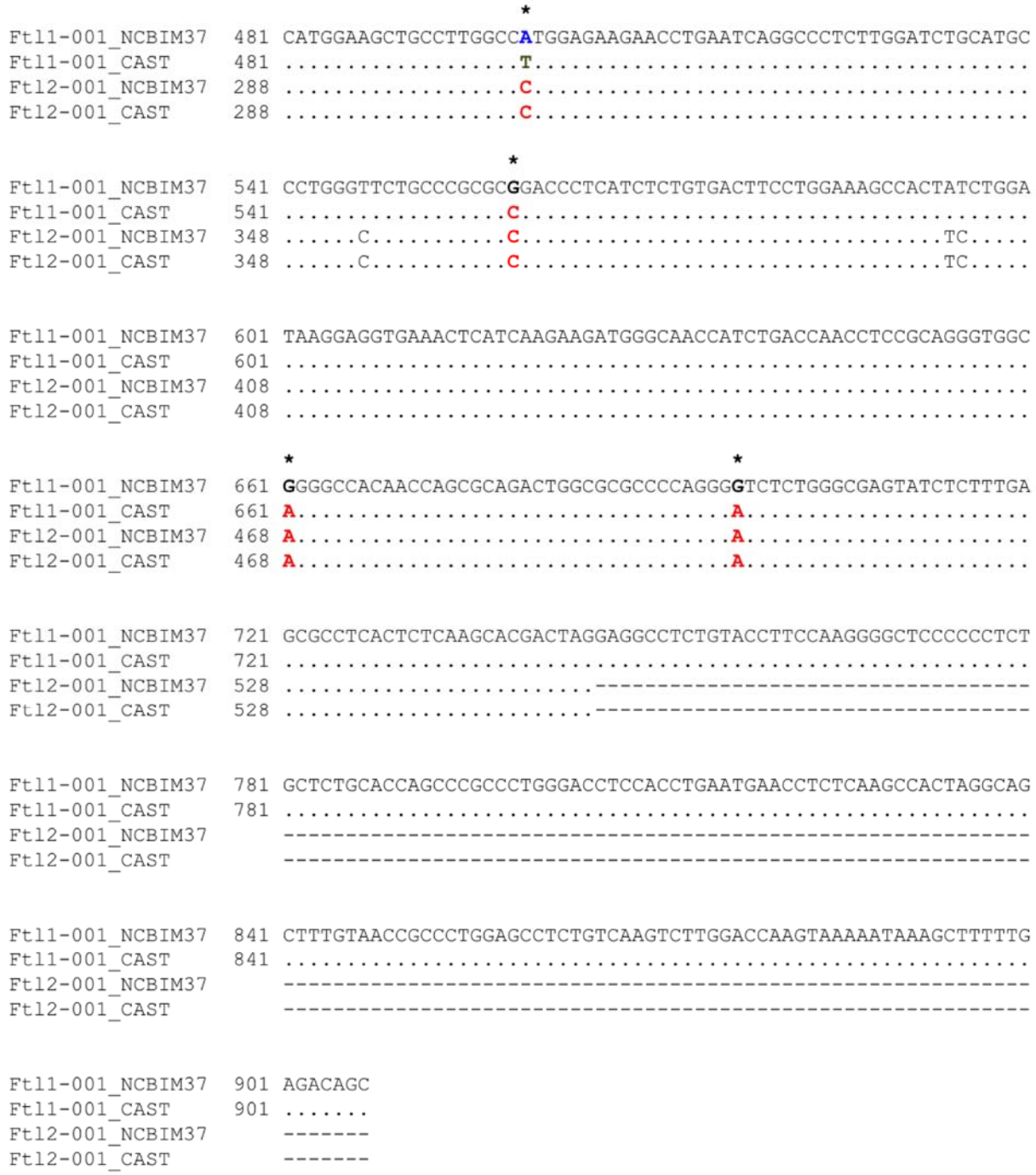

Figure S4 (continued)

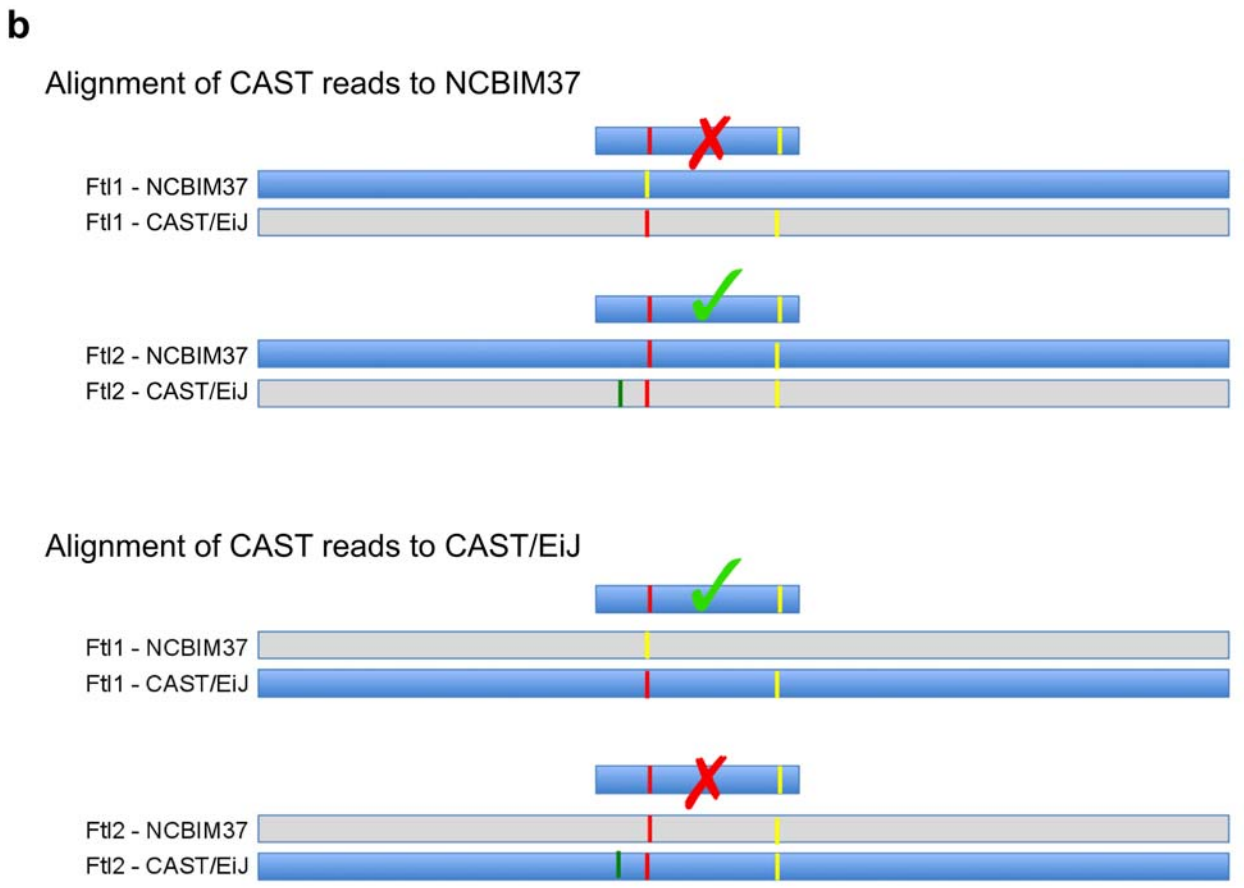

Figure S4 Strain polymorphisms between NCBIM37 and CAST in *Ftl1* and *Ftl2* transcript sequences can bias alignment of CAST-derived *Ftl1* reads. (A) Multiple alignment of *Ftl1-001* and *Ftl2-001* transcript sequences from NCBIM37 and the individualized CAST genomes. Variation in *Ftl1*/*Ftl2* abundance estimates in CAST liver RNA-seq stems mainly from 3-4 SNPs (starred). (B) Schematic showing how CAST polymorphisms in RNA-seq reads can cause misalignments in NCBIM37. CAST *Ftl1* reads that overlap any of these SNPs will align preferentially to *Ftl2* if aligned to NCBIM37 (upper panel). Accounting for CAST strain variation in *Ftl1* reduces spurious alignments to the *Ftl2* pseudogene (lower panel).