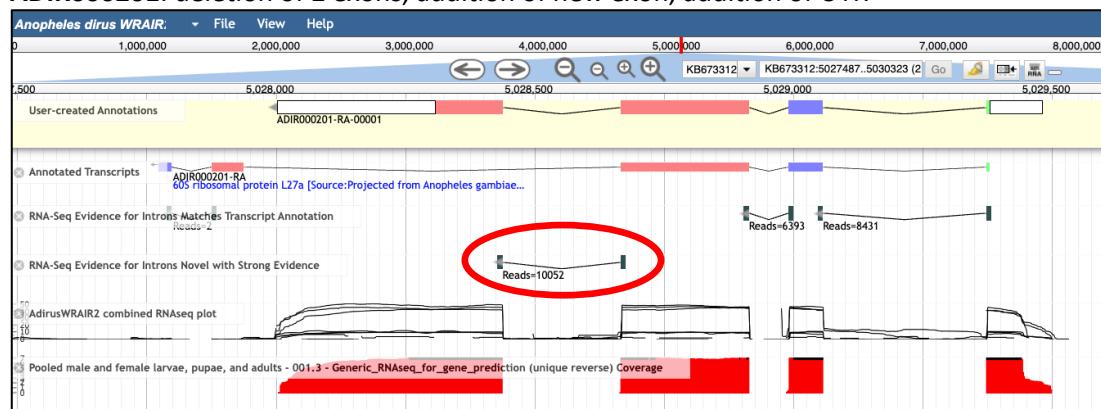


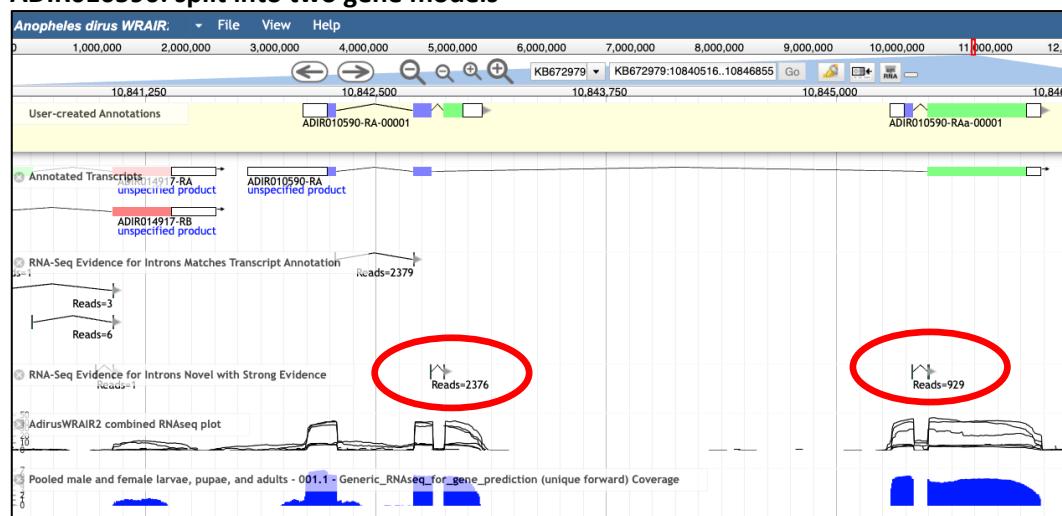
Optional Apollo exercise: answer key

Anopheles dirus WRAIR2

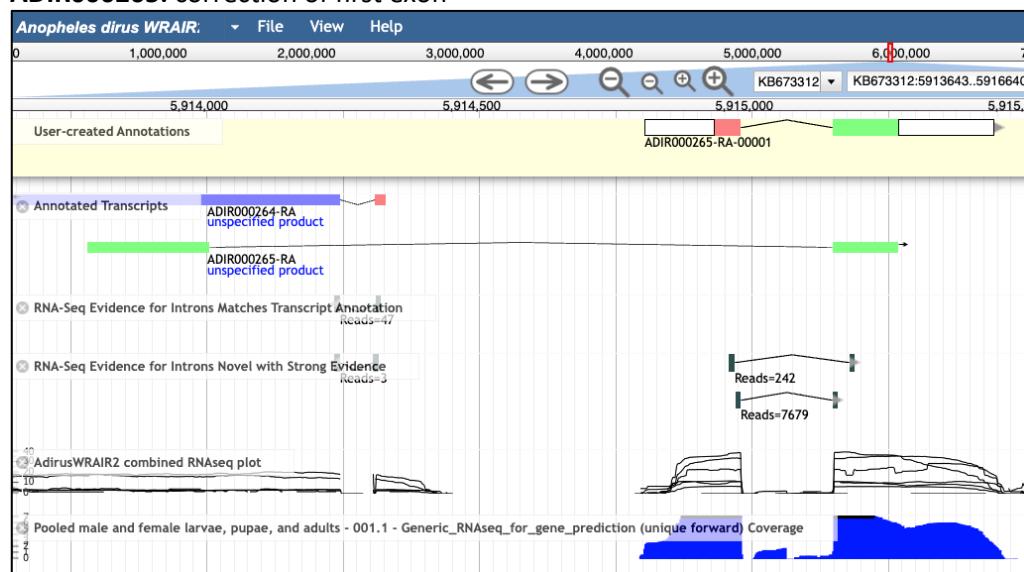
ADIR000201: deletion of 2 exons, addition of new exon, addition of UTR



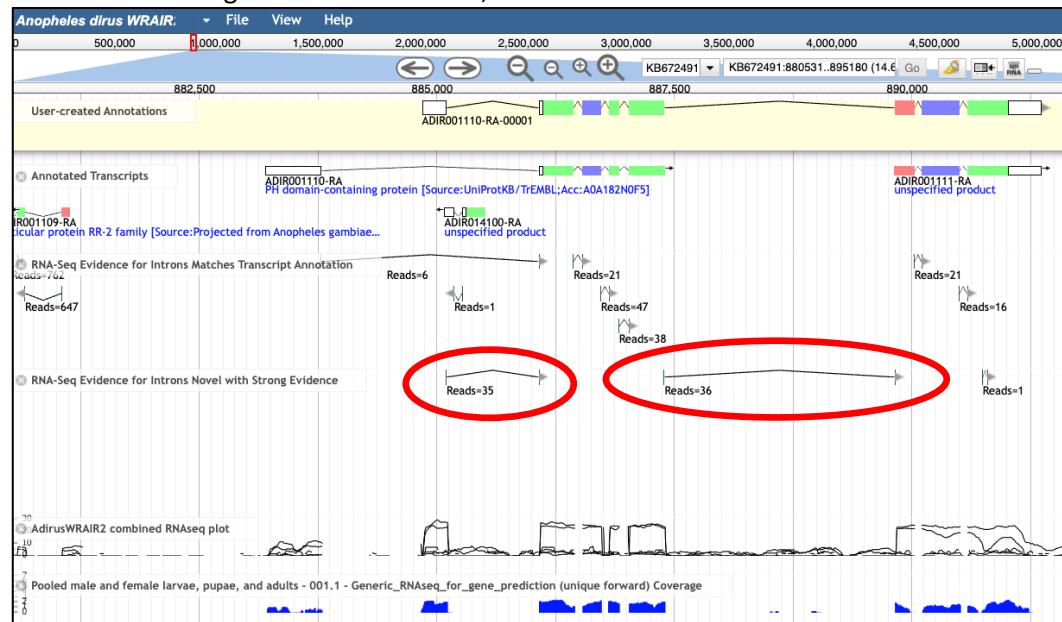
ADIR010590: split into two gene models



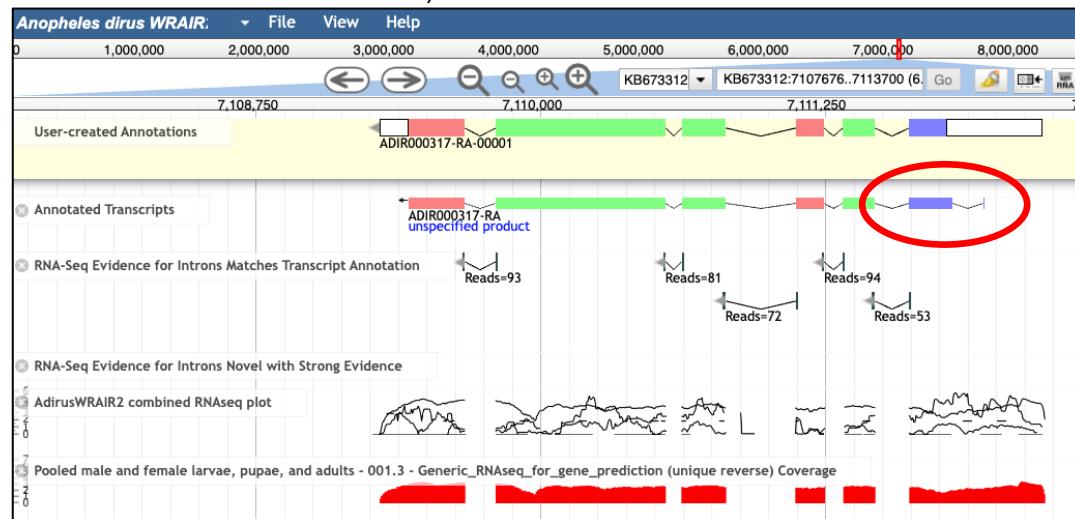
ADIR000265: correction of first exon



ADIR001110: merged with ADIR001111, correction of 5'UTR

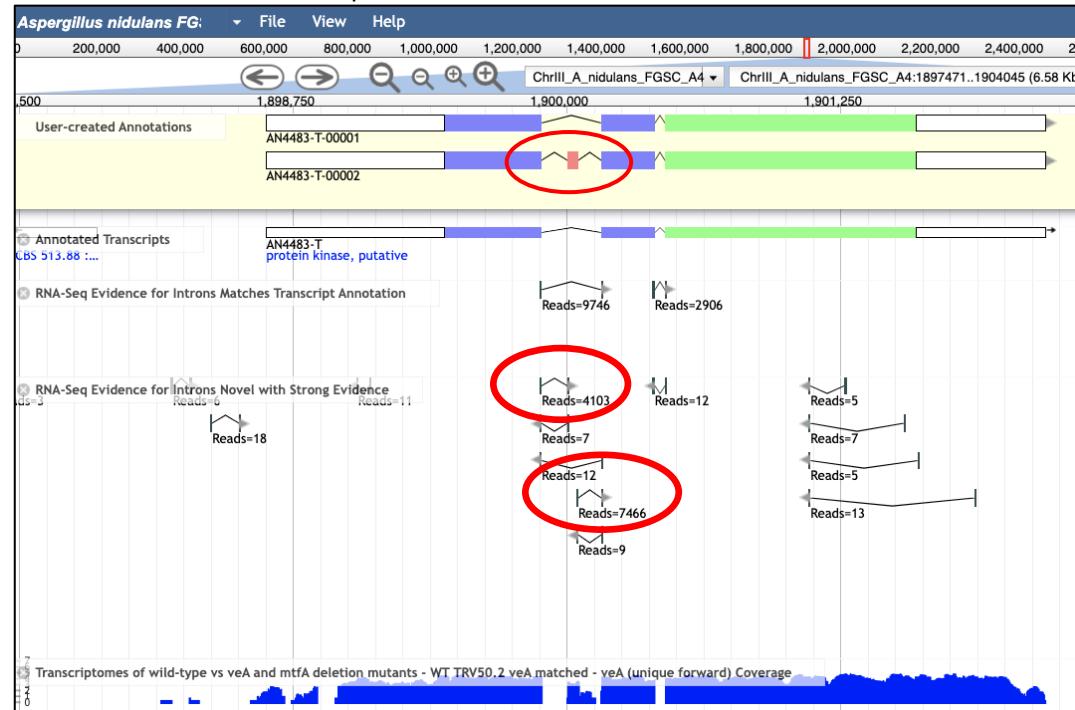


ADIR000317: Deletion of first exon, addition of UTR

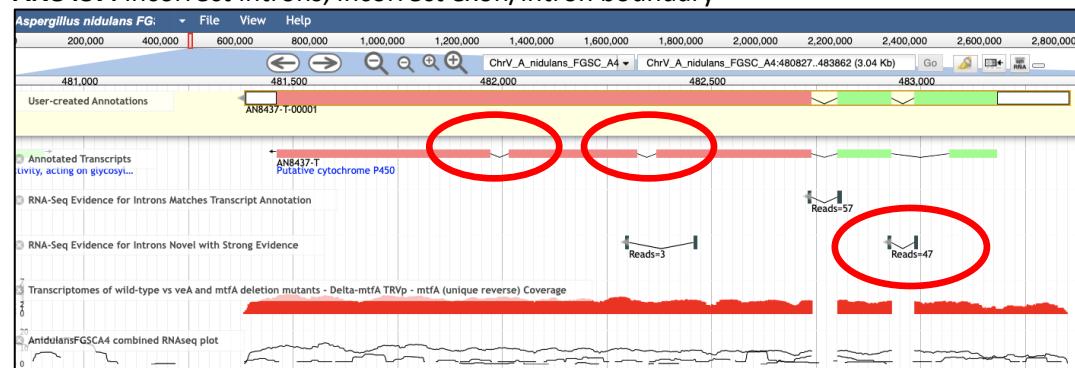


Aspergillus nidulans FGSC A4

AN4483: alternative transcript



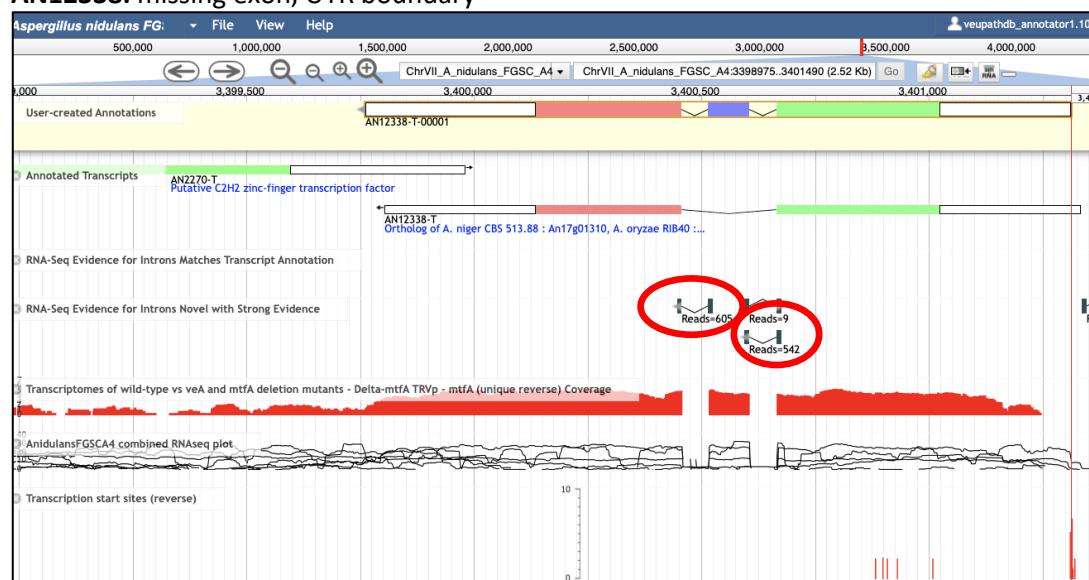
AN8437: incorrect introns, incorrect exon/intron boundary



AN11226: missing exon, 5'UTR

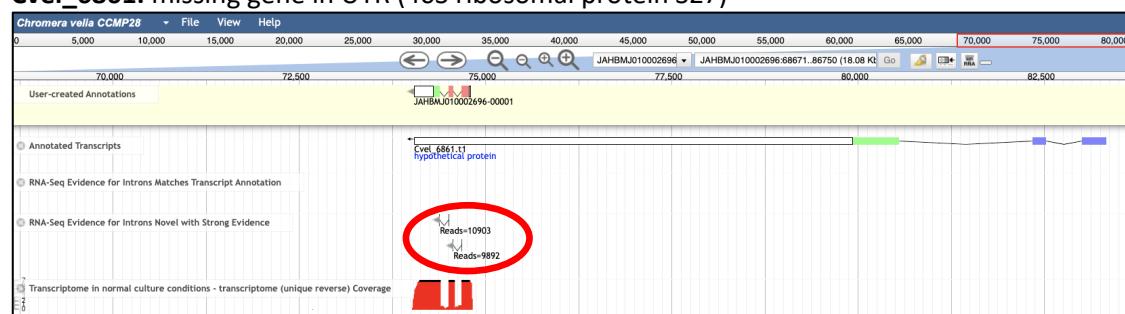


AN12338: missing exon, UTR boundary

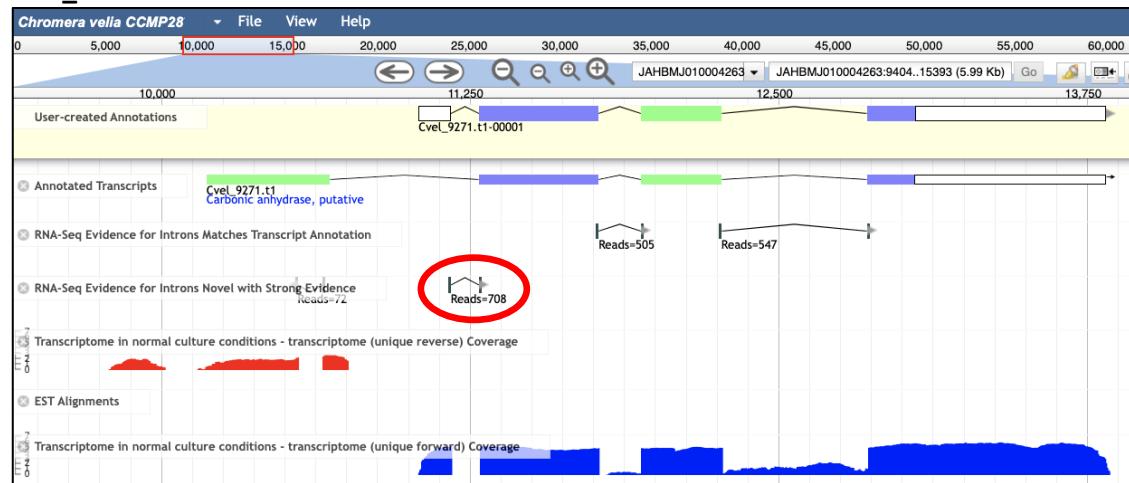


Chromera velia CCMP2878

Cvel_6861: missing gene in UTR (40S ribosomal protein S27)

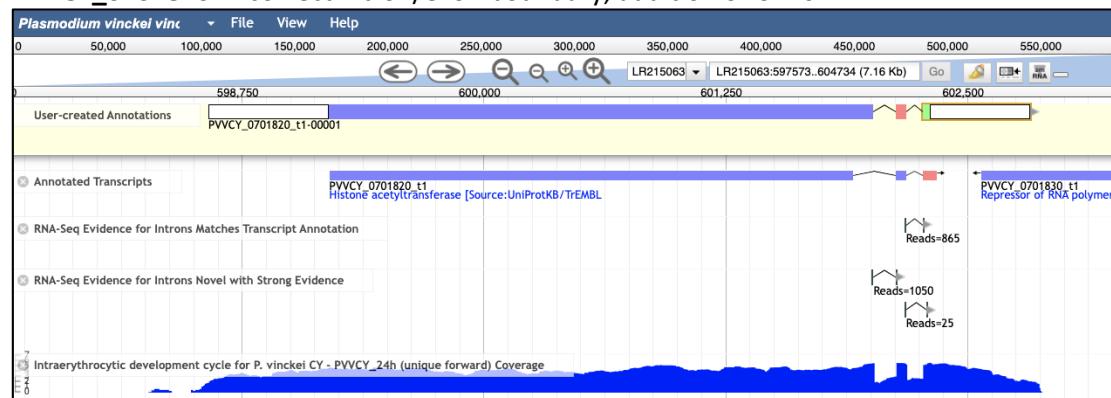


Cvel_9271: incorrect first exon

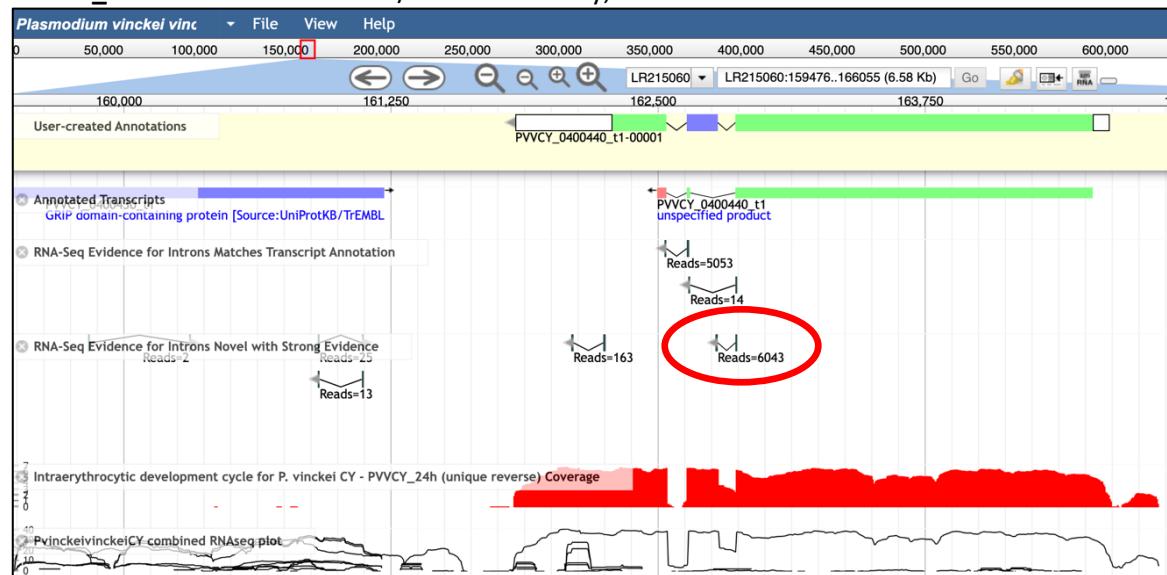


Plasmodium vinckeii vinckeii CY

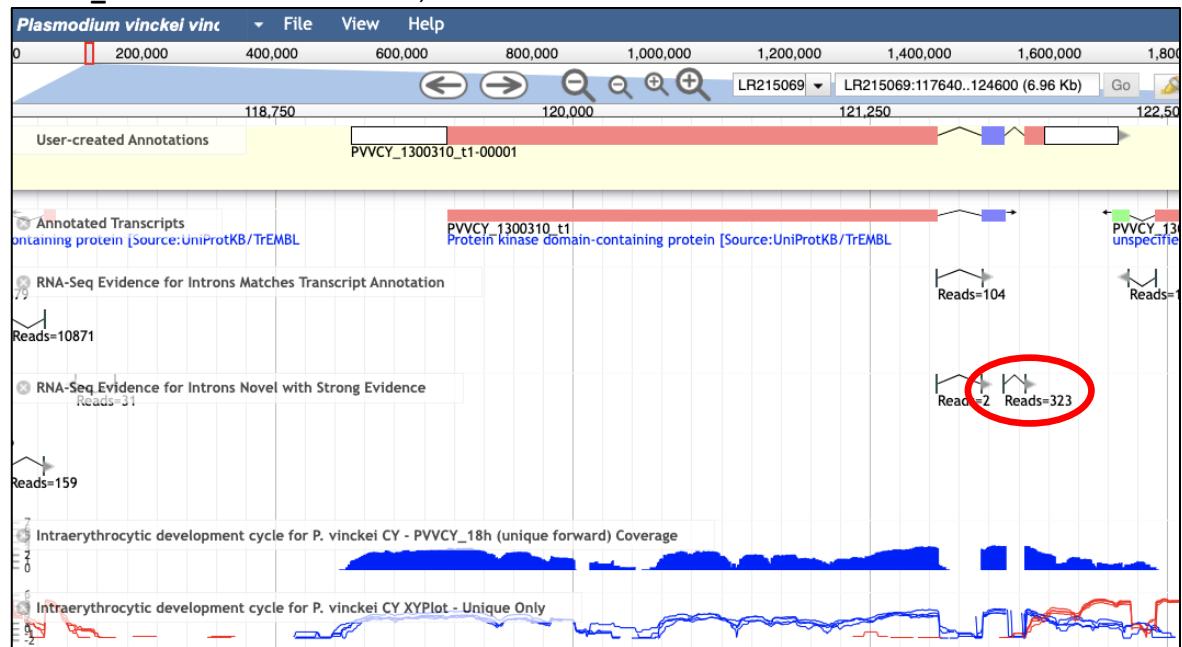
PVVCY_0701820: incorrect intron/exon boundary, addition of UTRs



PVVCY_0400440: incorrect exon/intron boundary, addition of UTRs



PVVCY_1300310: addition of exon, addition of UTR

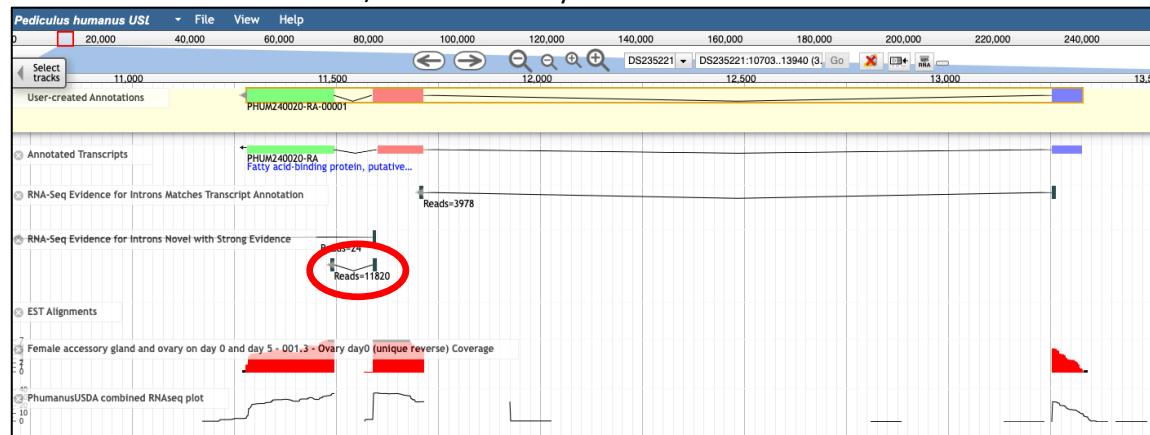


PVVCY_1302110: addition of exon, addition of UTR

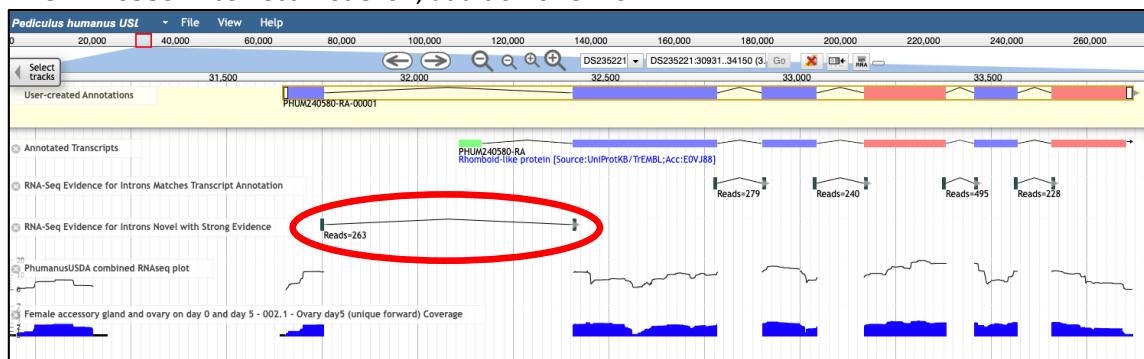


Pediculus humanus USDA

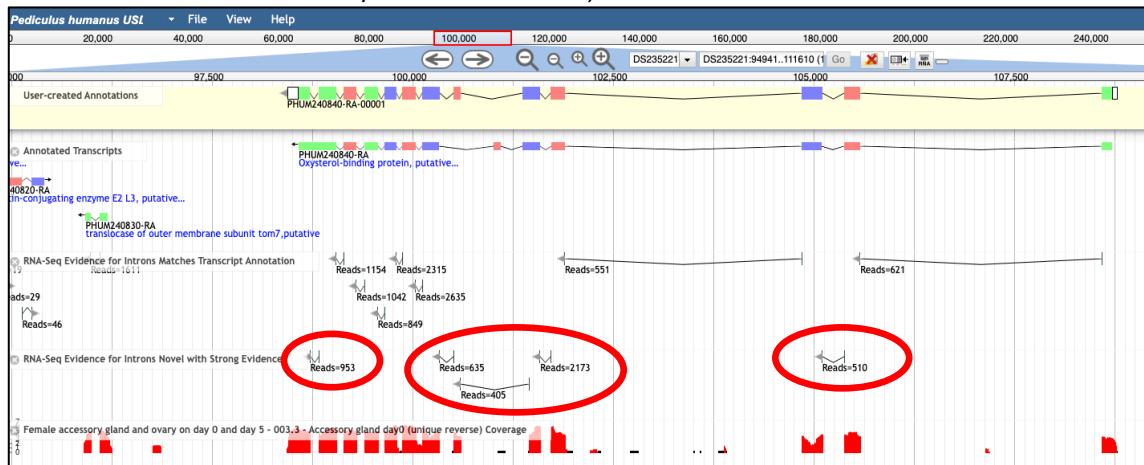
PHUM240020: incorrect exon/intron boundary



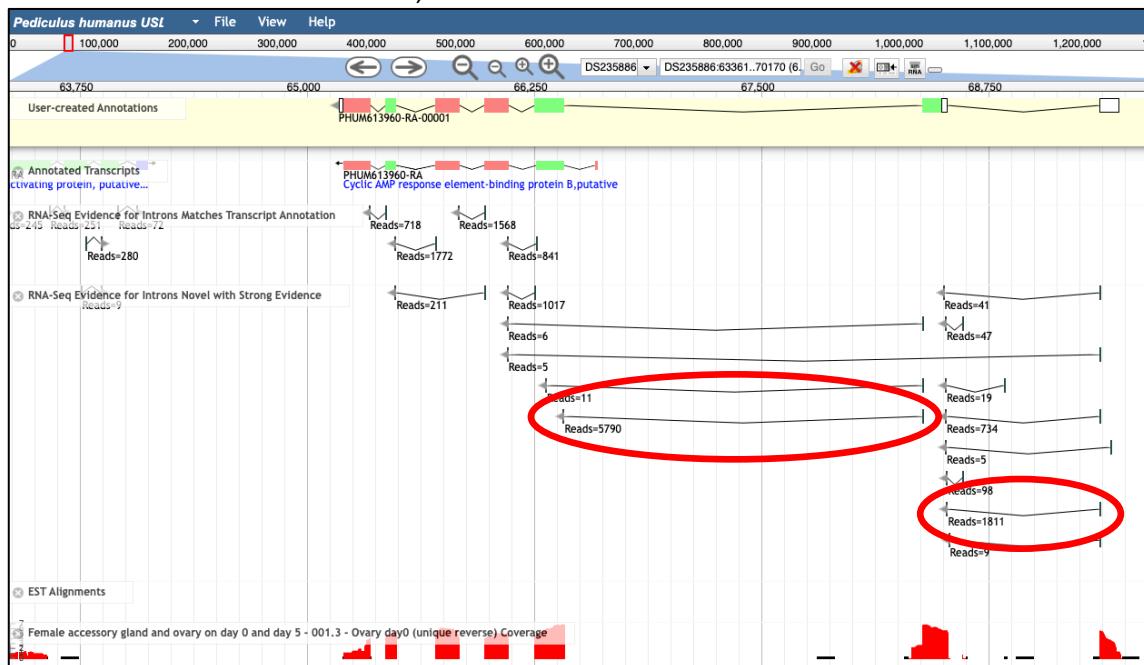
PHUM240580: incorrect first exon, addition of UTRs



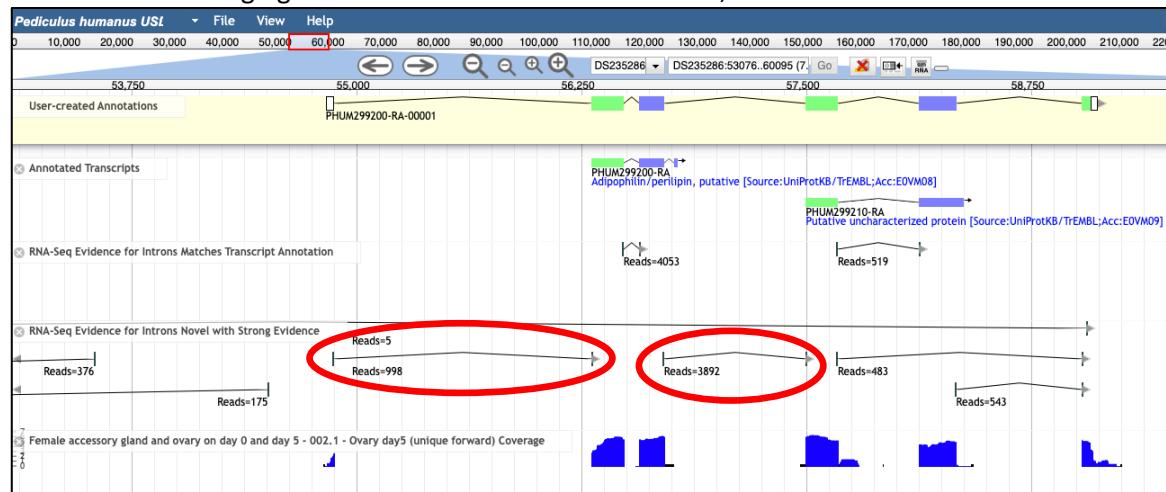
PHUM240840: incorrect exon/intron boundaries, addition of UTRs



PHUM613960: incorrect first exon, addition of UTRs

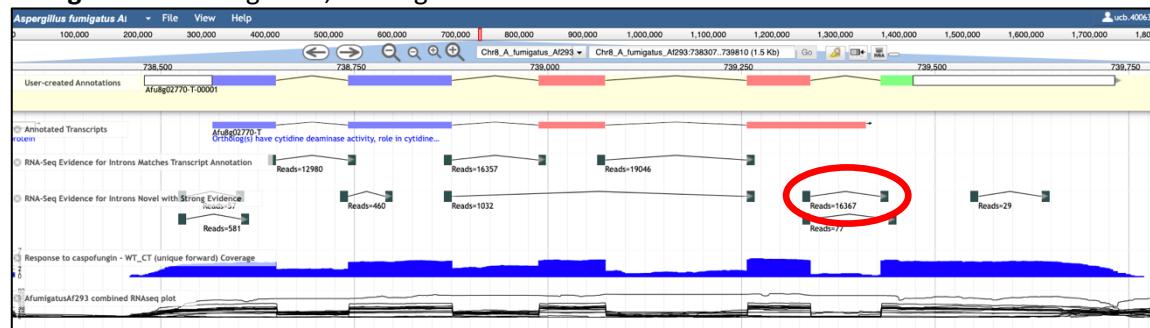


PHUM299200: merging of PHUM299200 and PHUM299210, addition of exon and UTR

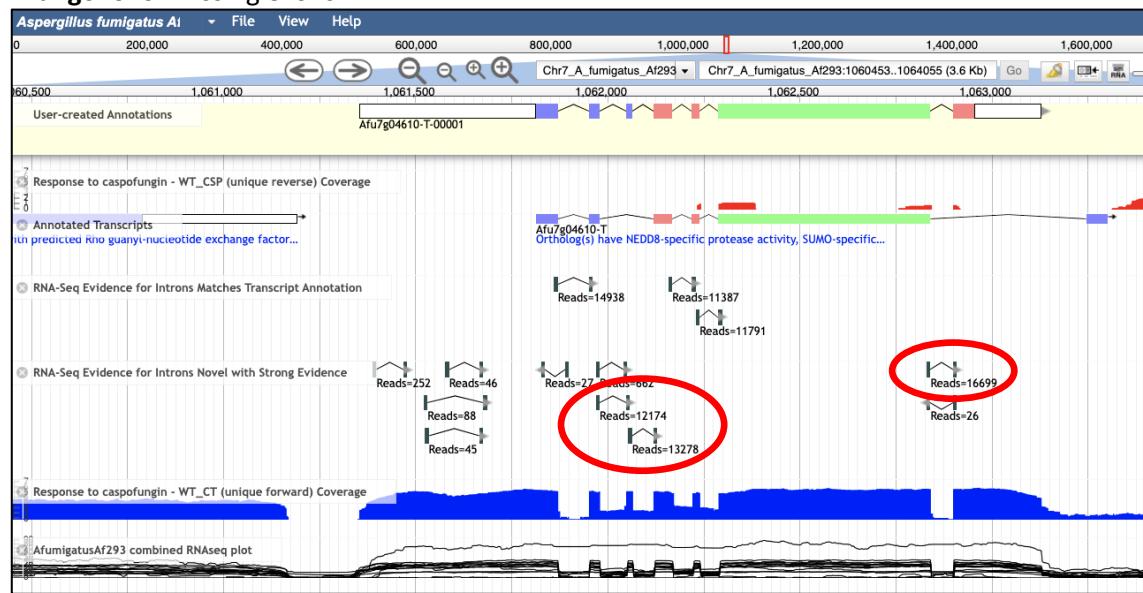


Aspergillus fumigatus Af293

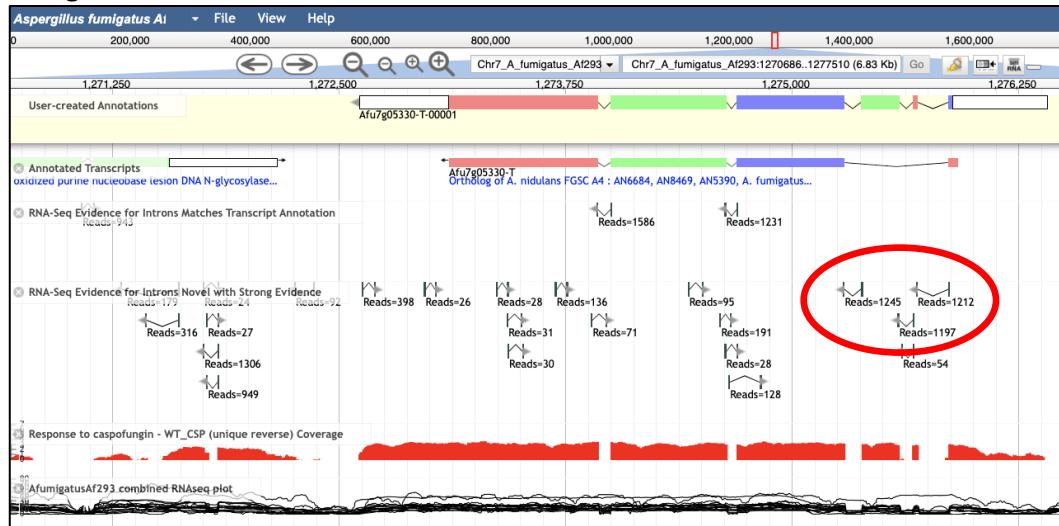
Afu8g02770: missing exon, missing UTRs



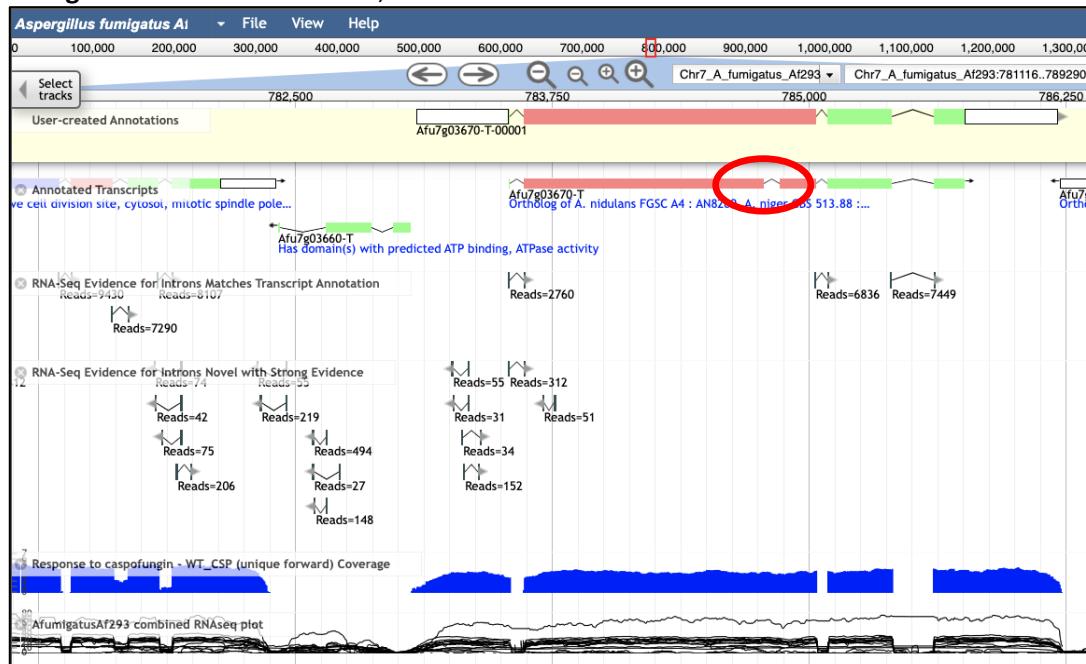
Afu7g04610: missing exons



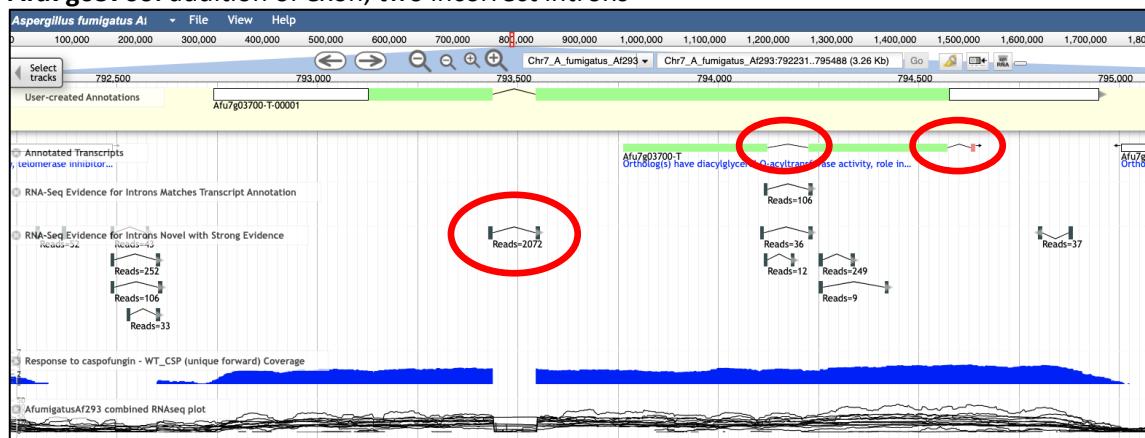
Afu7g05330: addition of exons



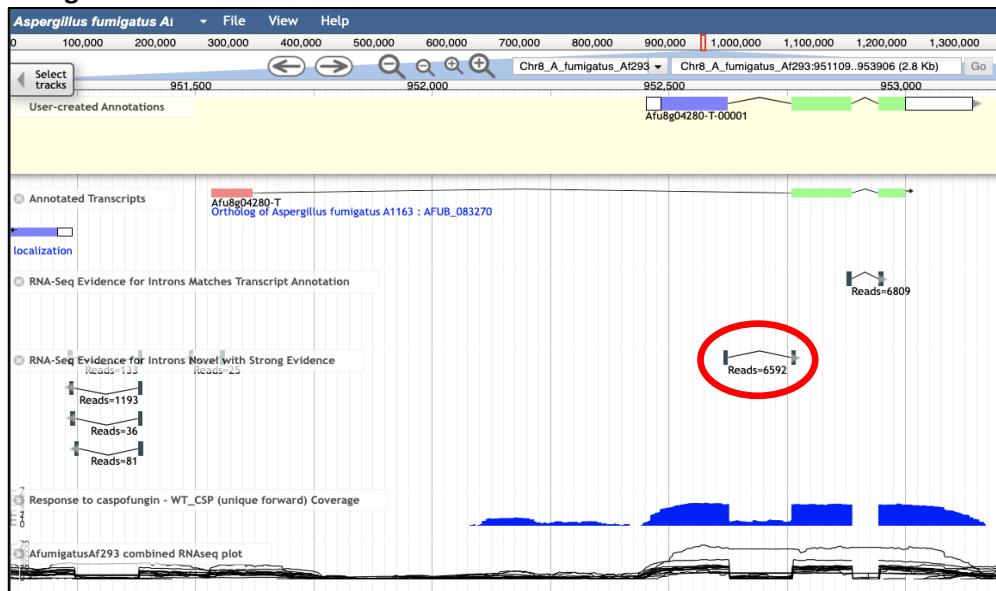
Afu7g03670: deletion of intron, addition of UTRs



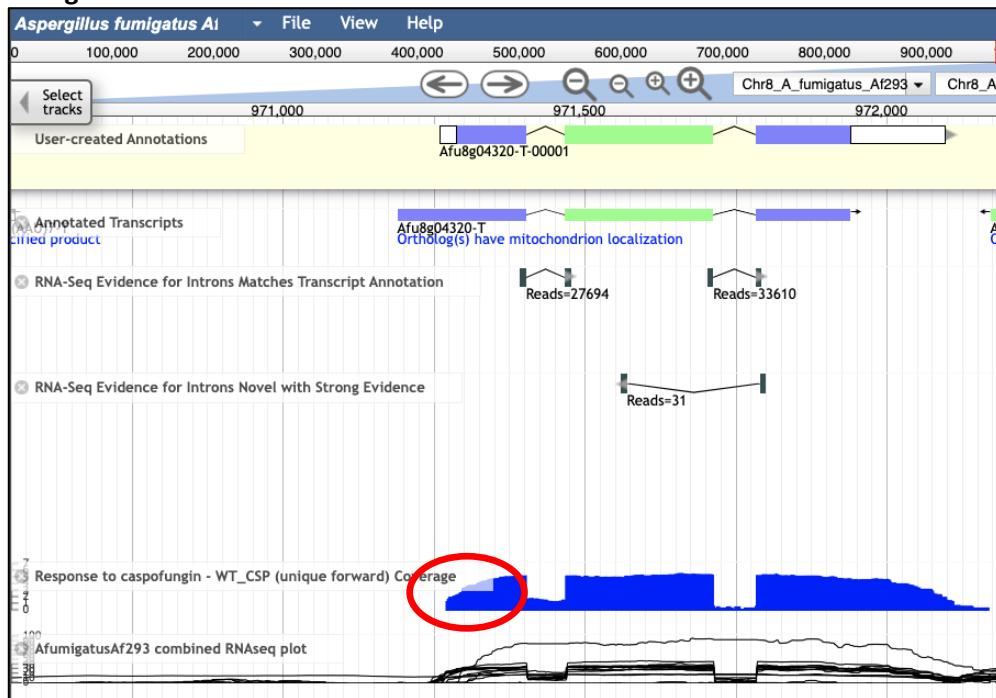
Afu7g03700: addition of exon, two incorrect introns



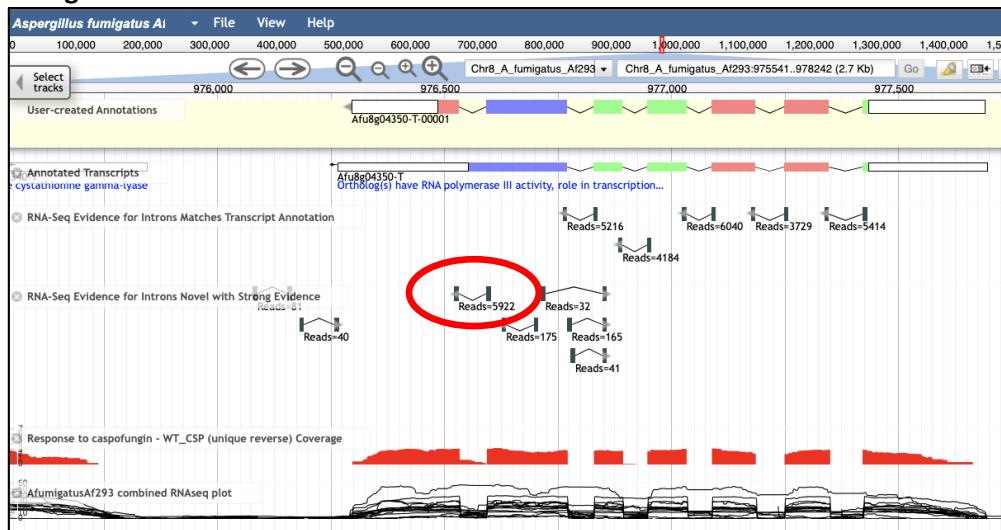
Afu8g04280: incorrect first exon



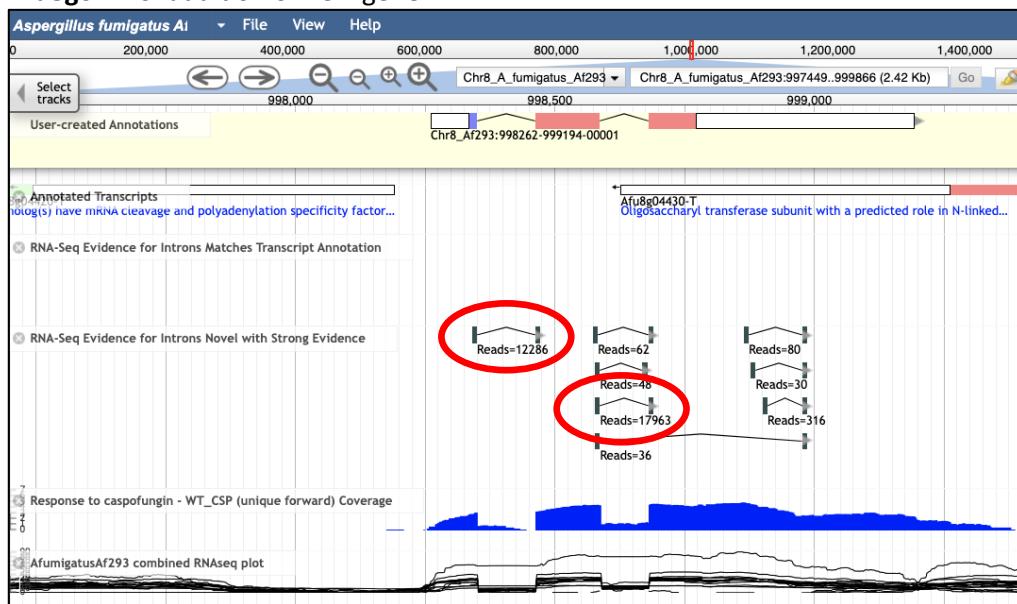
Afu8g04320: incorrect start



Afu8g04350: addition of exon

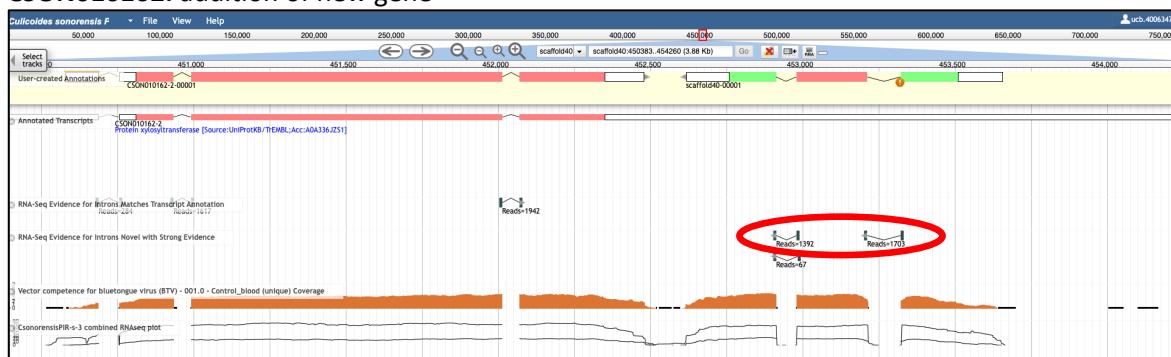


Afu8g04420: addition of new gene

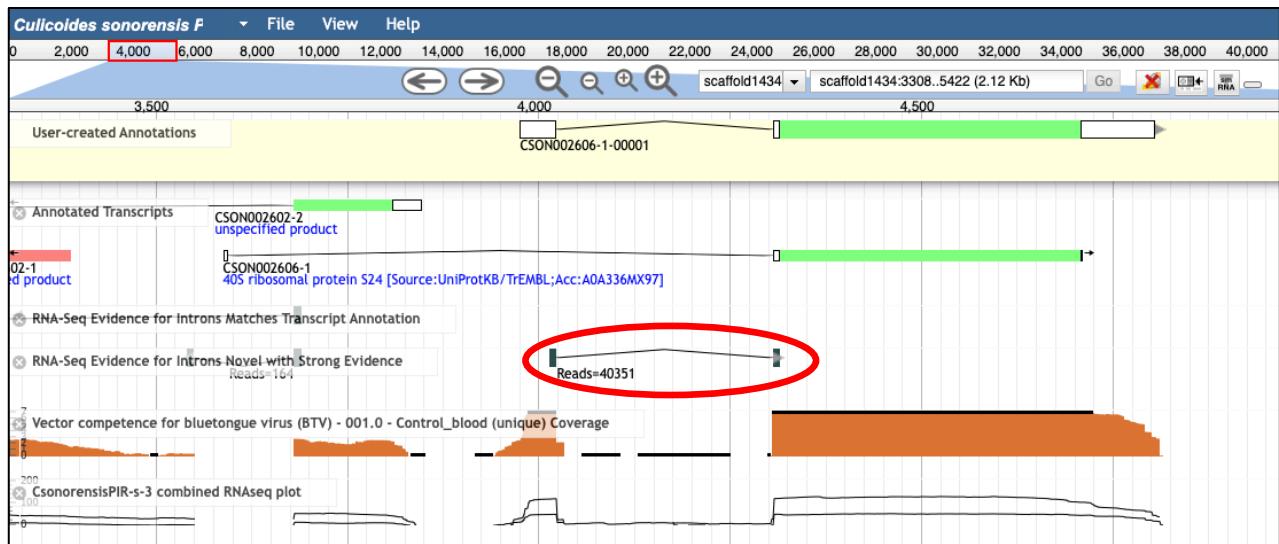


Culicoides sonorensis PIR-s-3

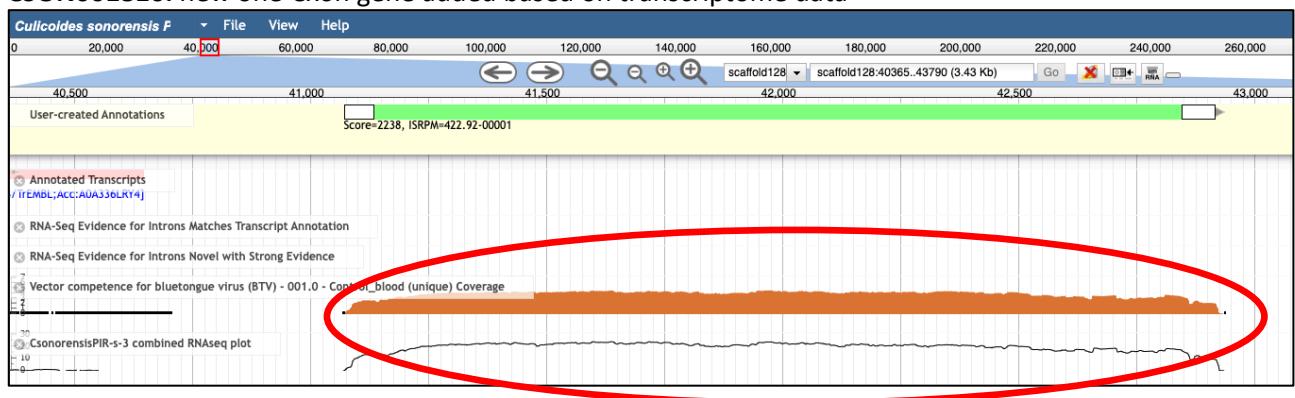
CSON010162: addition of new gene



CSON002606: incorrect UTR



CSON001816: new one-exon gene added based on transcriptome data



CSON009689: addition of exon, change of UTR boundaries

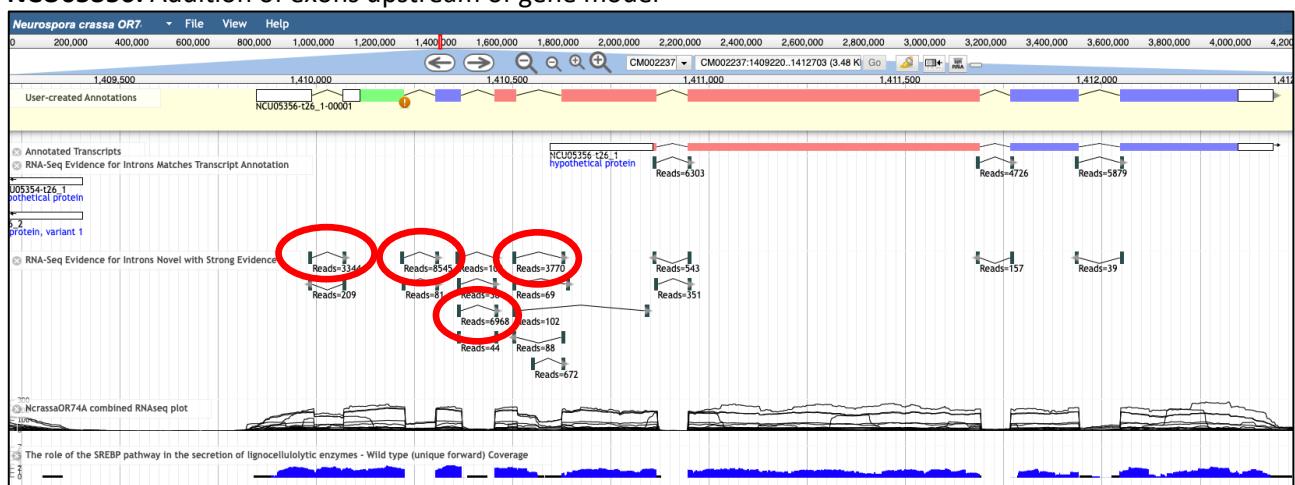


CSON007381: addition of new gene, the new gene is replacing the long UTR of CSON007381

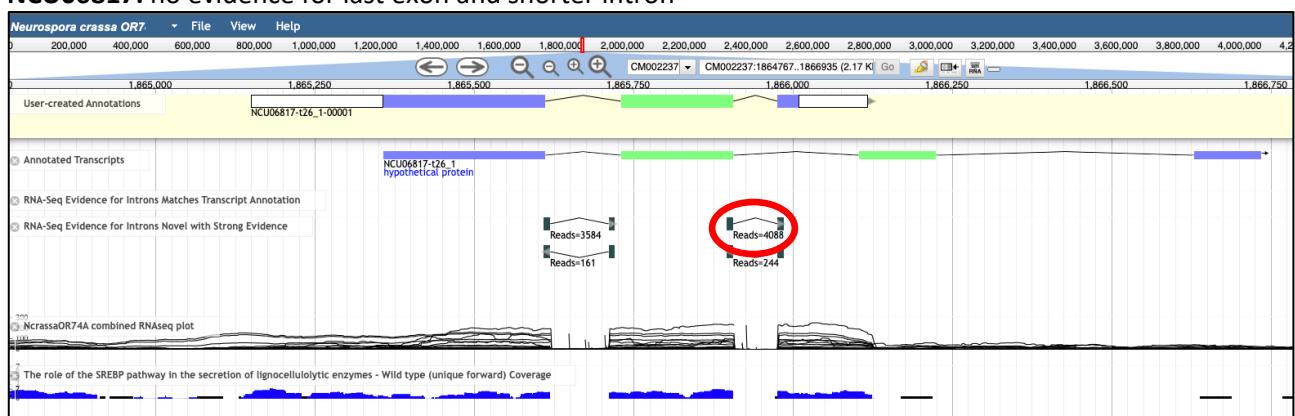


Neurospora crassa OR74A

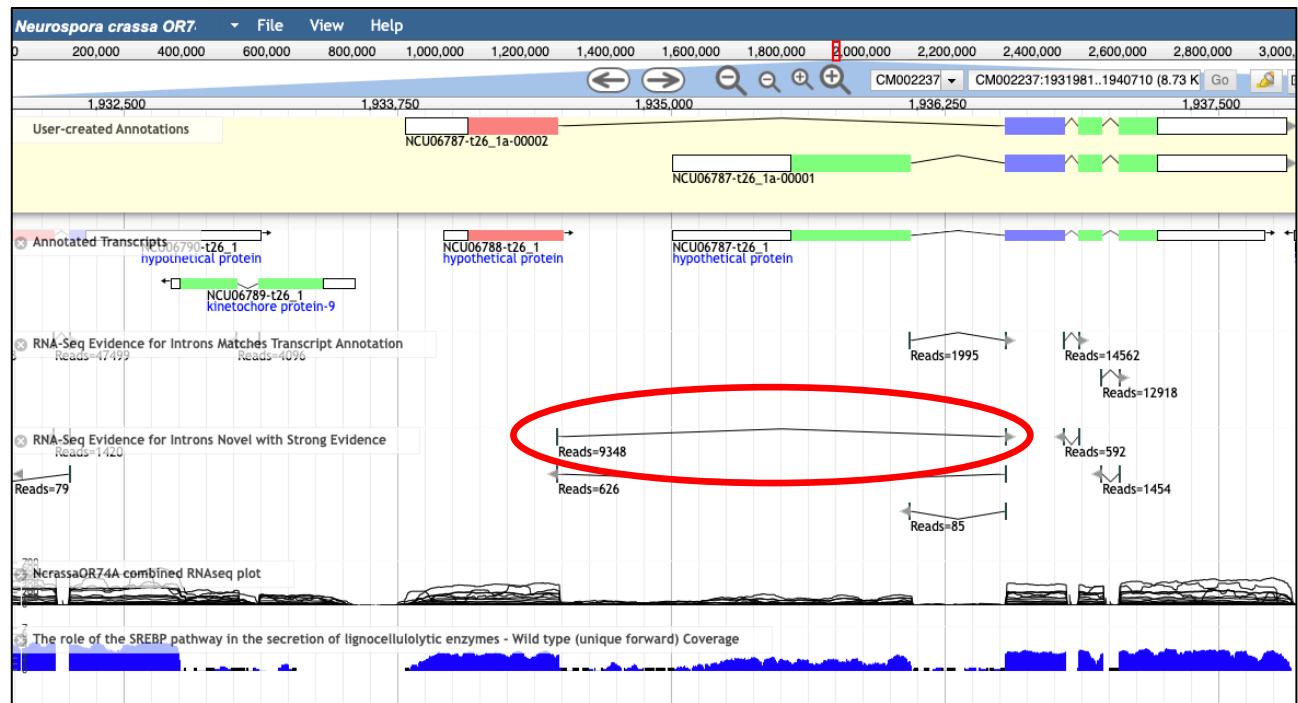
NCU05356: Addition of exons upstream of gene model



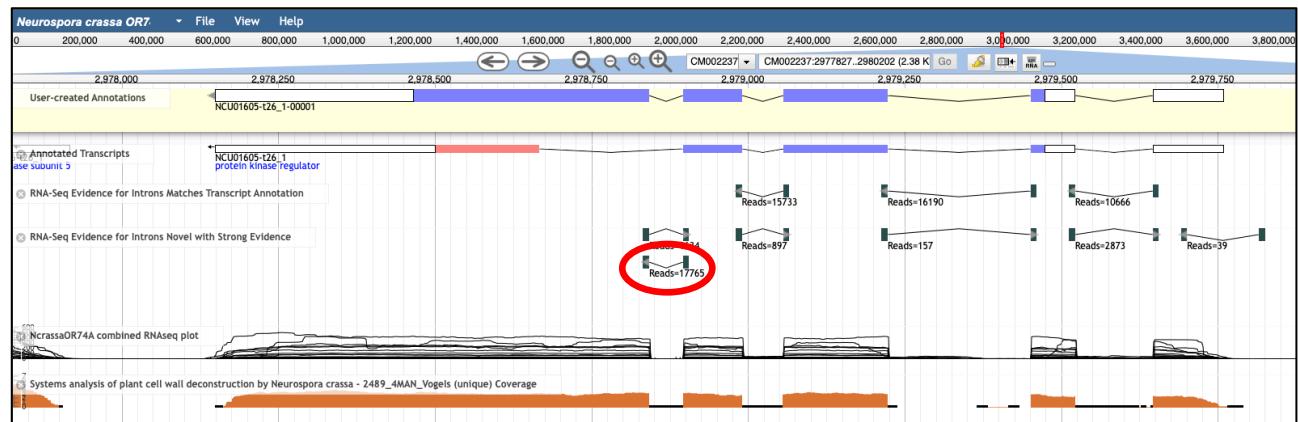
NCU06817: no evidence for last exon and shorter intron



NCU06787: more dominant isoform needs to be created

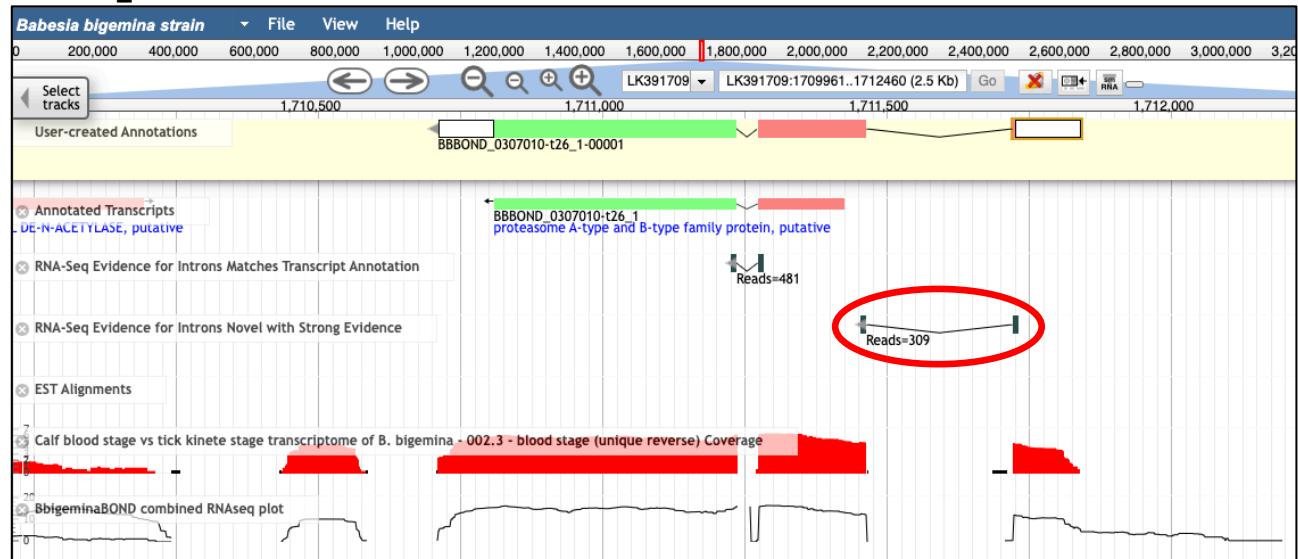


NCU01605: incorrect last exon

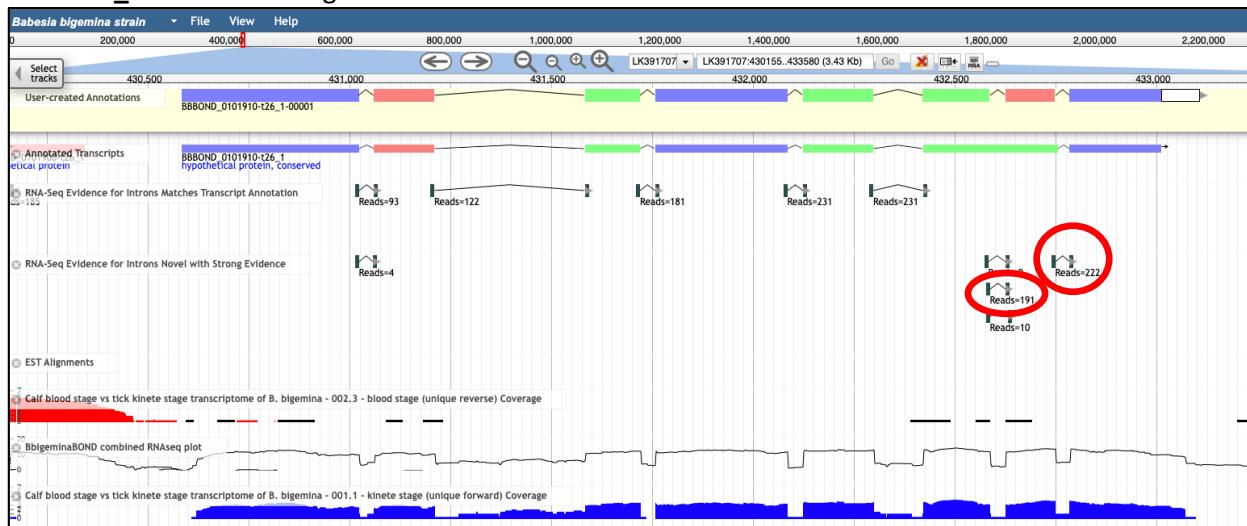


Babesia bigemina strain BOND

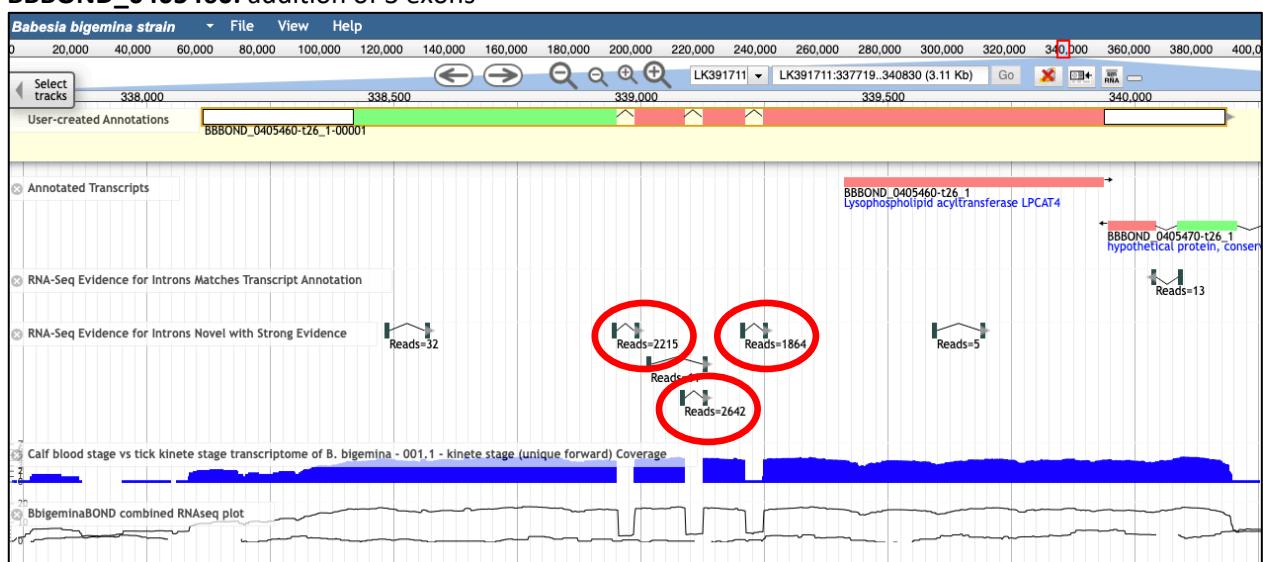
BBBOND_0307010: addition of first exon



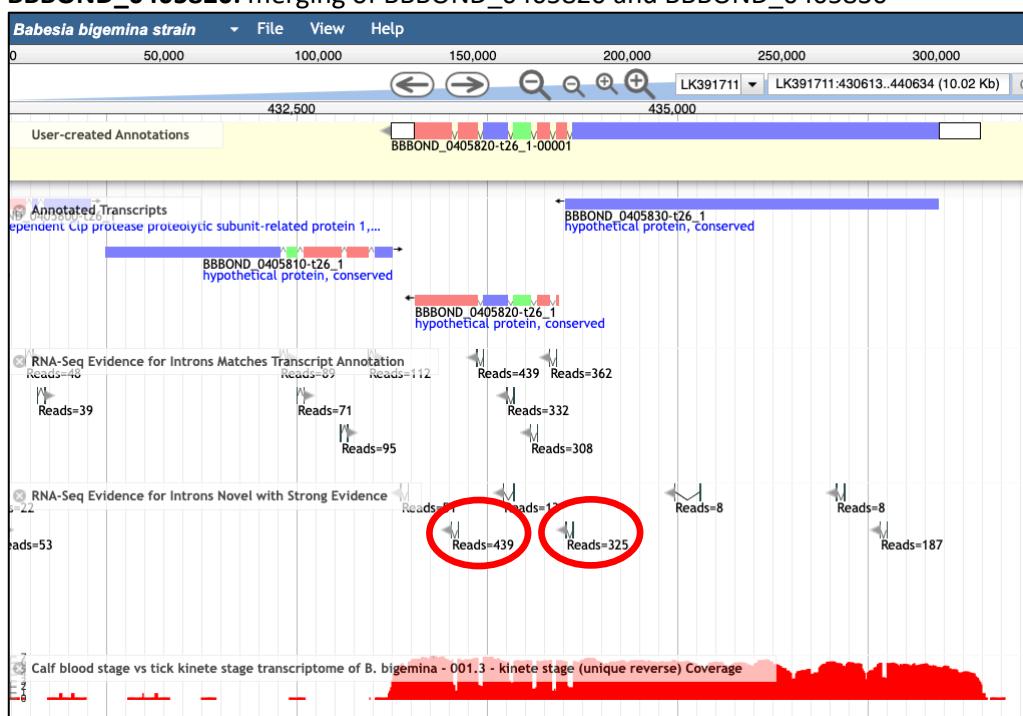
BBBOND_0101910: missing exon



BBBOND_0405460: addition of 3 exons

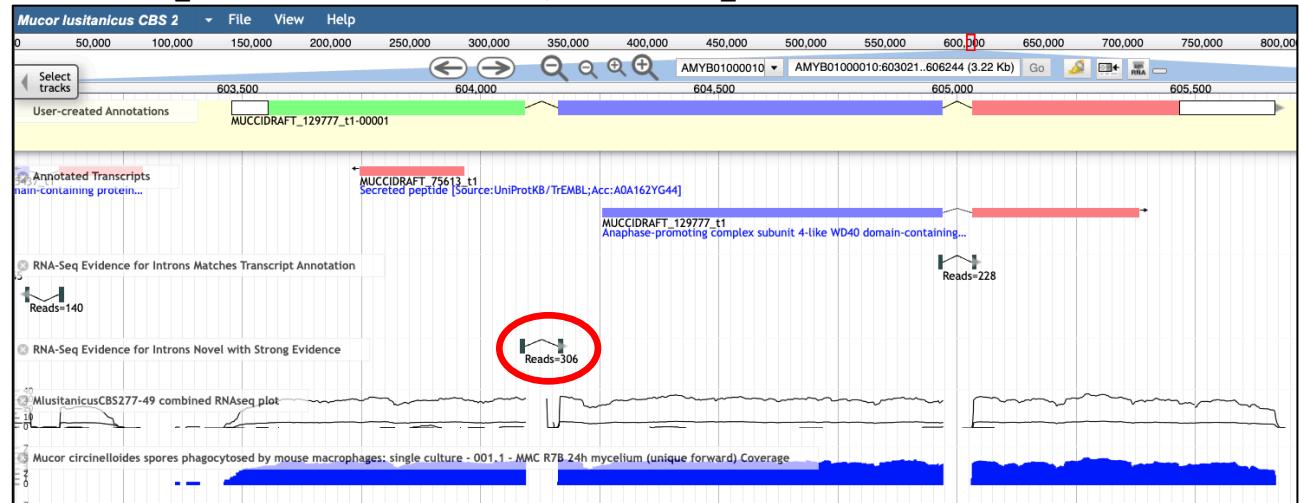


BBBOND_0405820: merging of BBBOND_0405820 and BBBOND_0405830

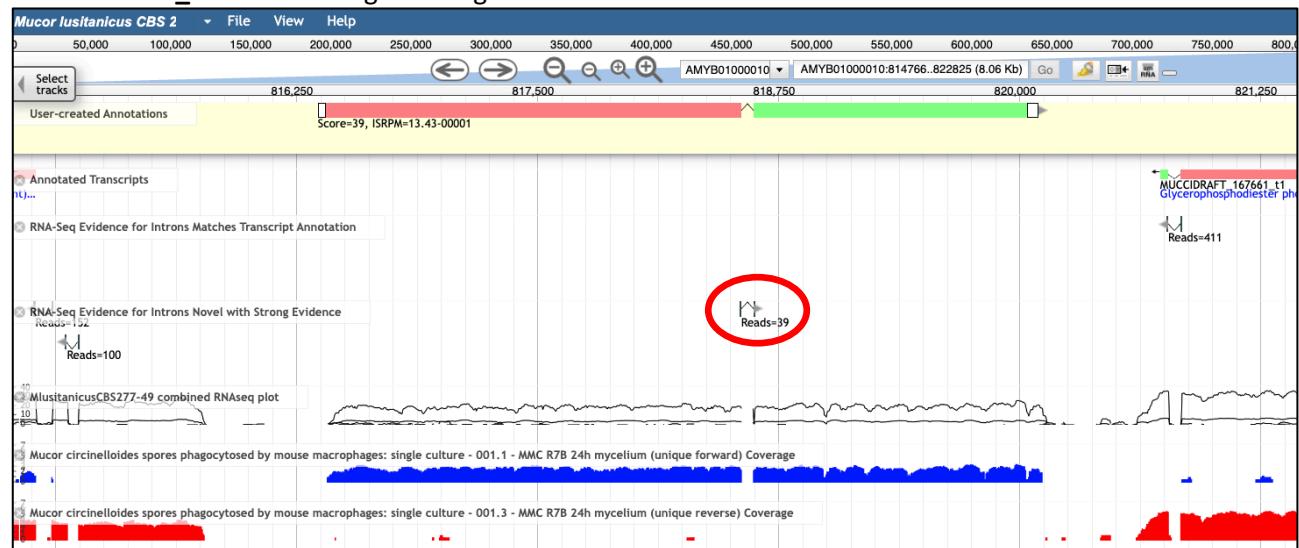


Mucor lusitanicus CBS 277.49

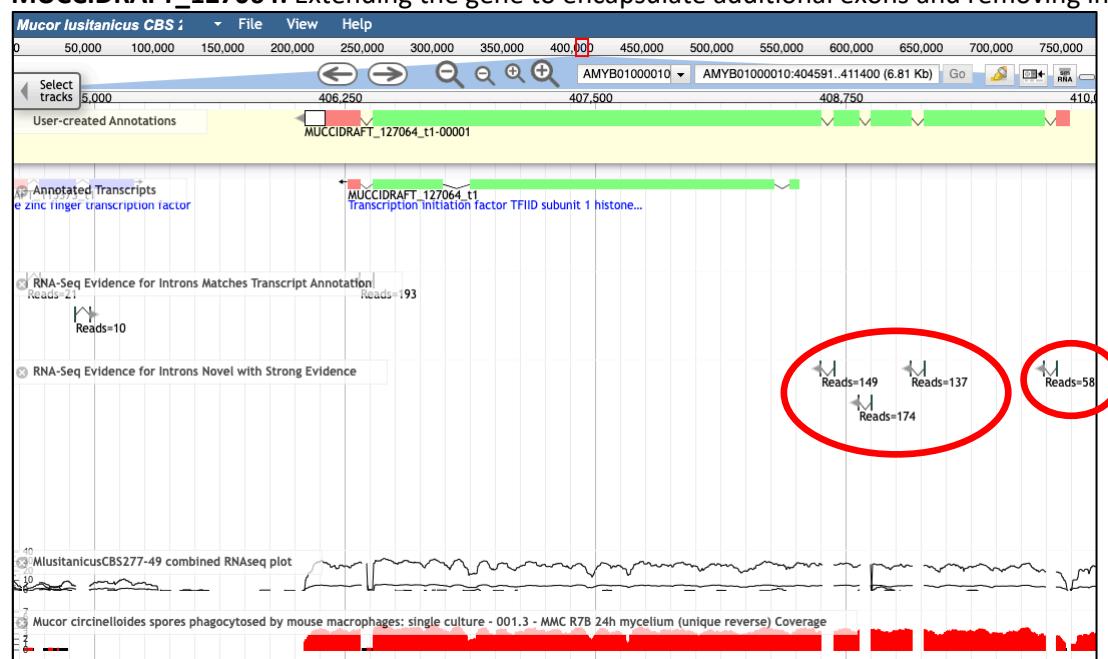
MUCCIDRAFT_129777: Addition of first exon, MUCCIDRAFT_75613 needs to be deleted



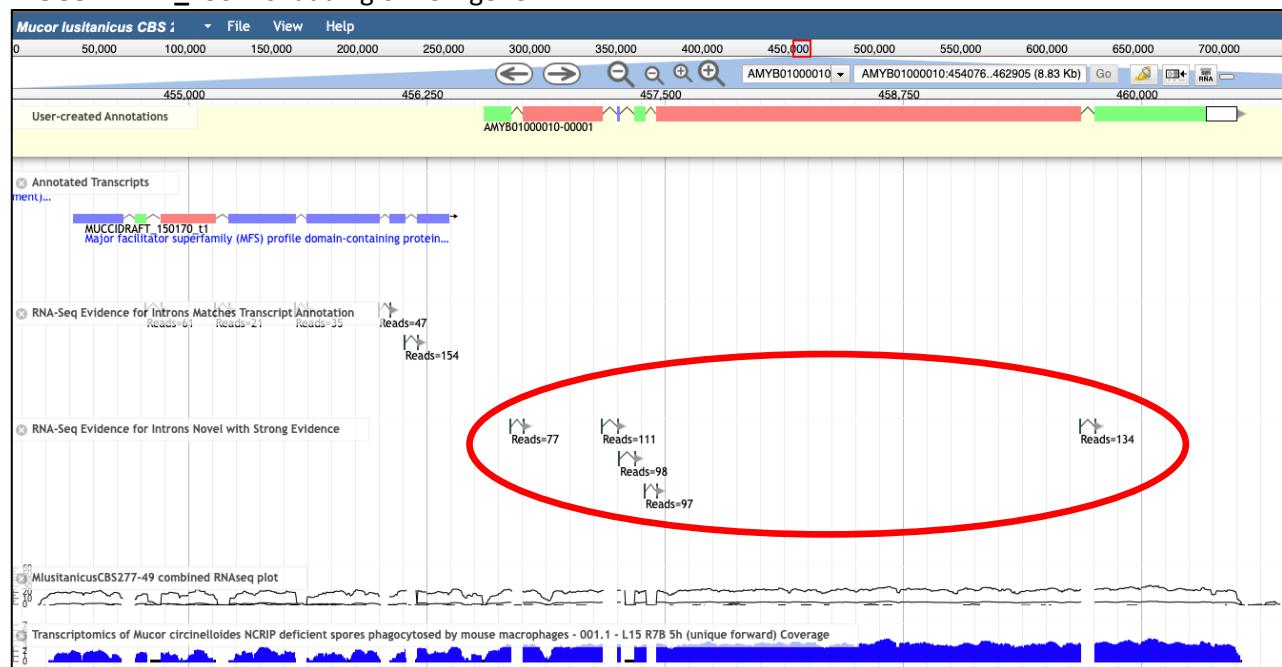
MUCCIDRAFT_167661: Adding of new gene



MUCCIDRAFT_127064: Extending the gene to encapsulate additional exons and removing incorrect introns



MUCCIDRAFT_150170: adding of new gene



MUCCIDRAFT_138180: new exon added

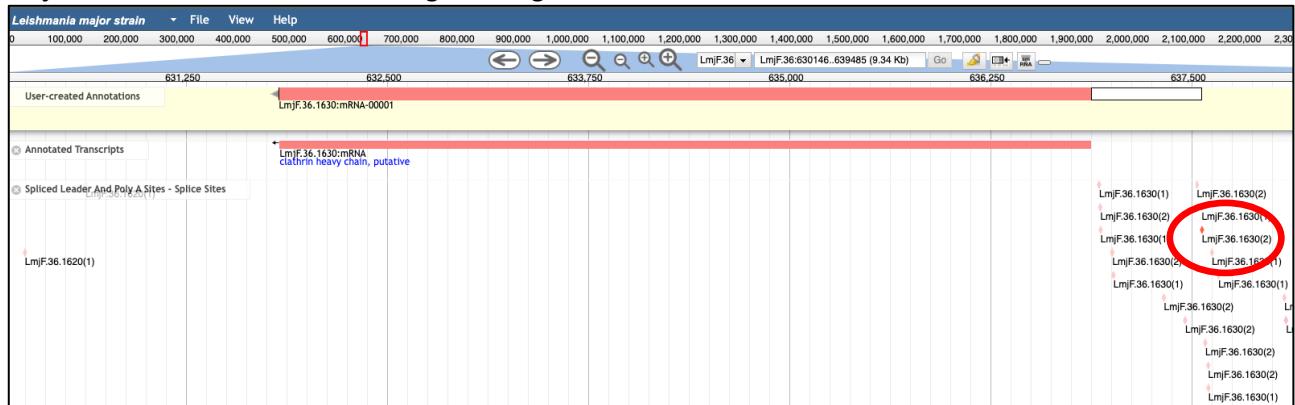


MUCCIDRAFT_126214: addition of 9 exons

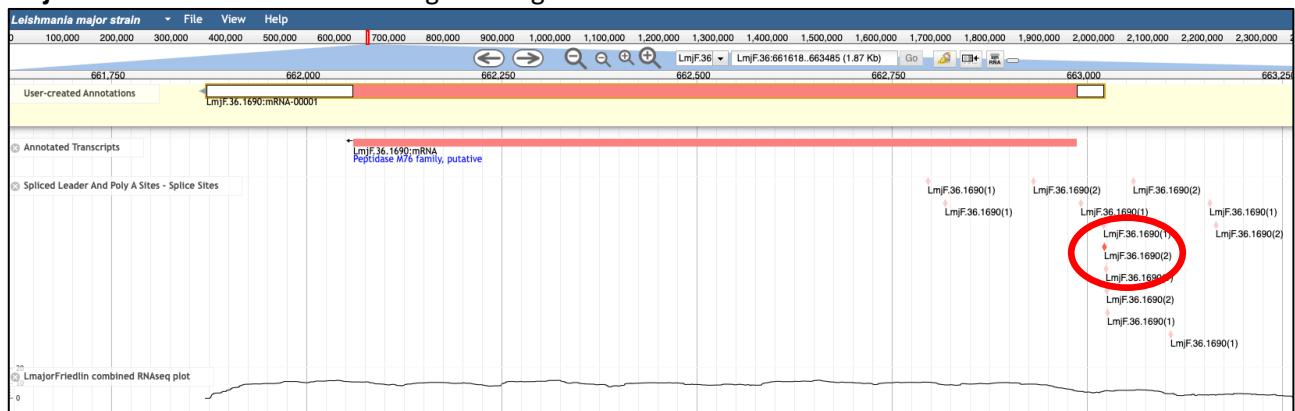


Leishmania major strain Friedlin

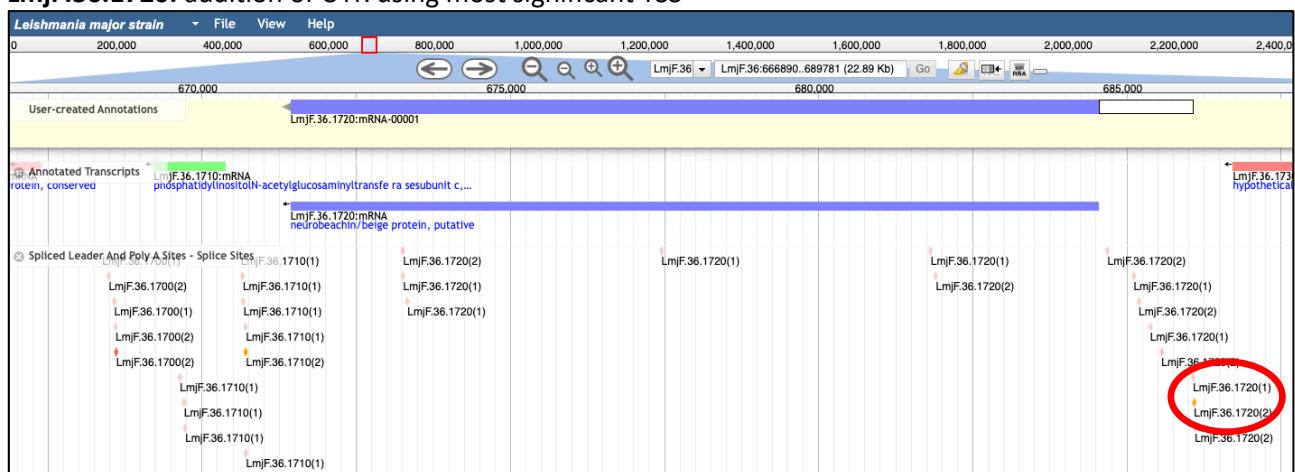
LmjF.36.1630: addition of UTR using most significant TSS



LmjF.36.1690: addition of UTR using most significant TSS



LmjF.36.1720: addition of UTR using most significant TSS



LmjF.36.2070: addition of UTR using most significant TSS

