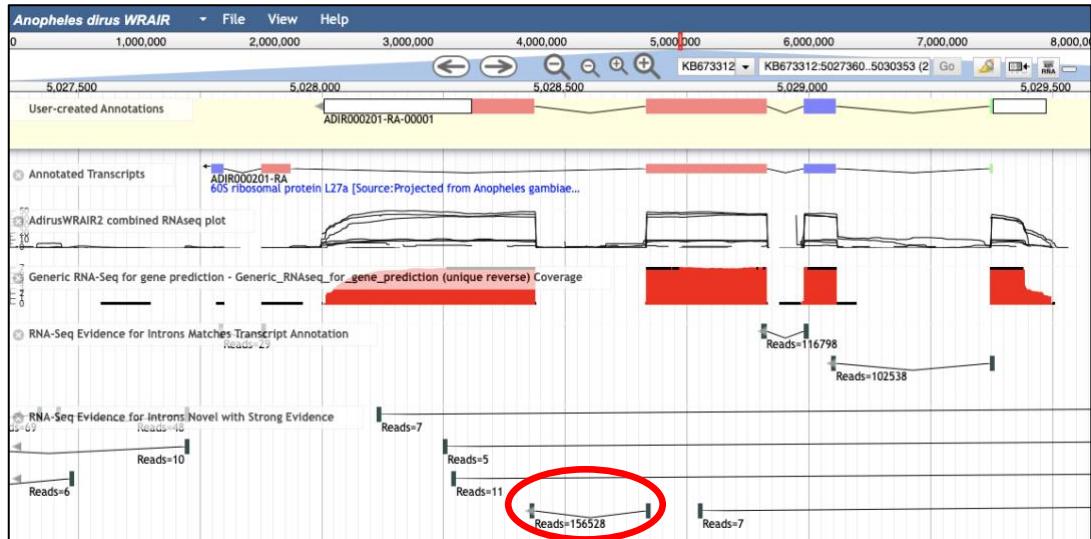


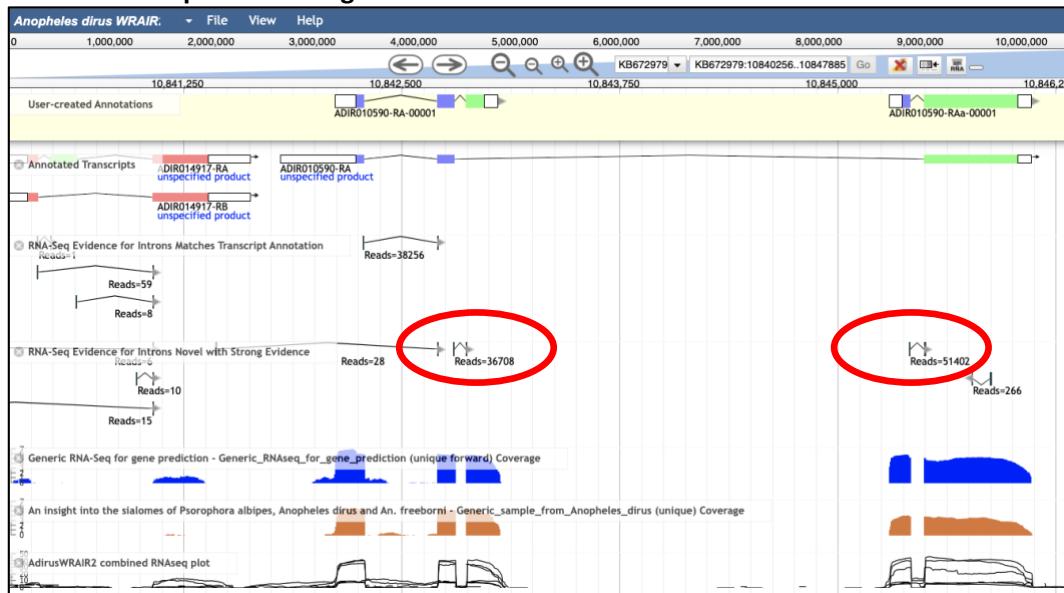
Optional Apollo exercise - answer key

Anopheles dirus WRAIR2

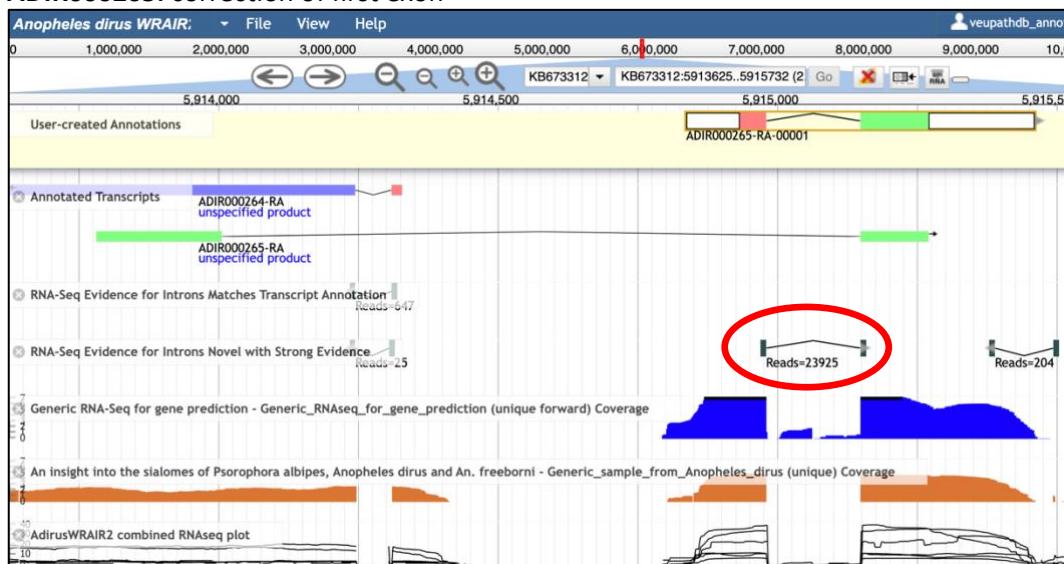
ADIR000201: deletion of 2 exons, addition of new exon, addition of UTR



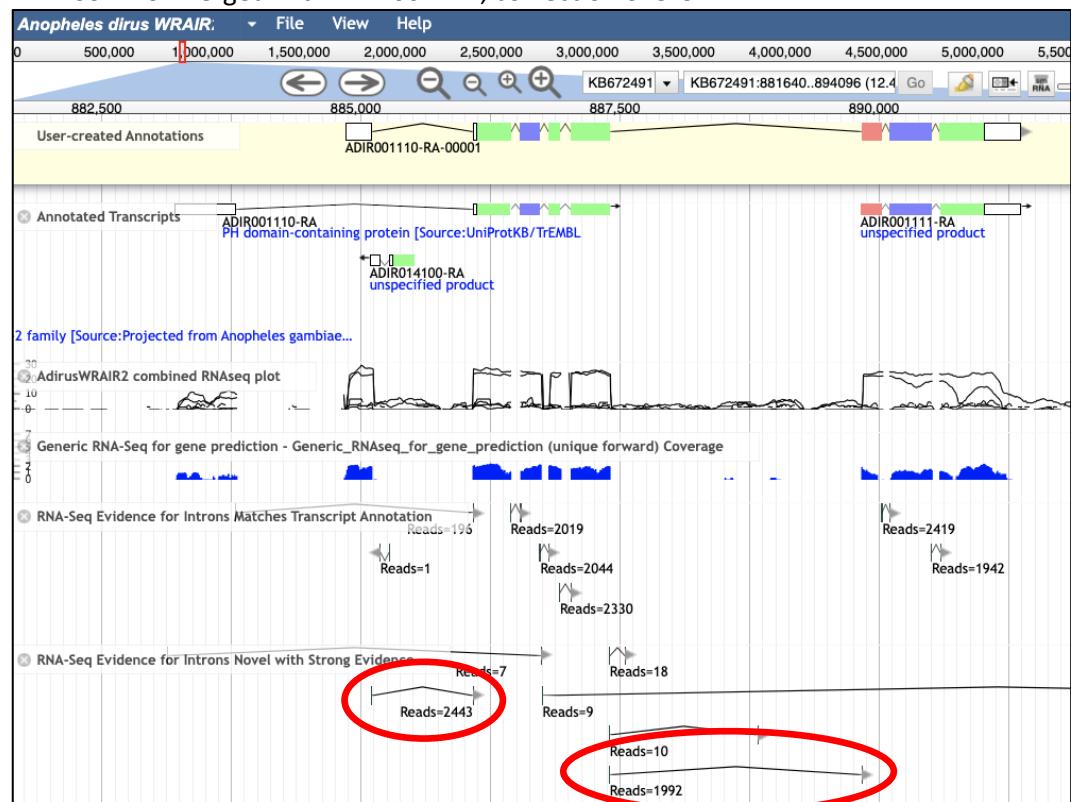
ADIR010590: split into two gene models



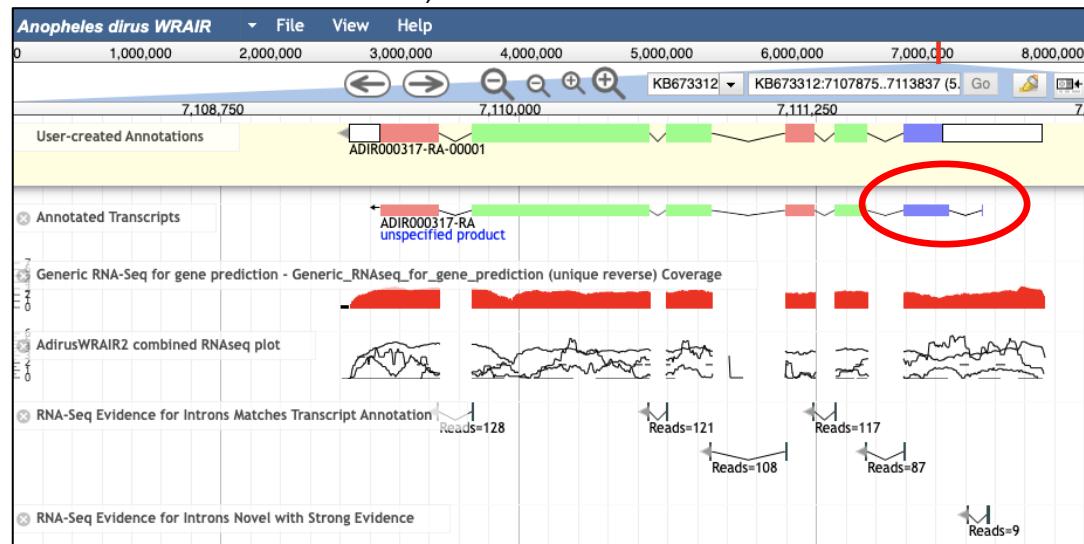
ADIR000265: correction of first exon



ADIR001110: merged with ADIR001111, correction of 5'UTR



ADIR000317: Deletion of first exon, addition of UTR

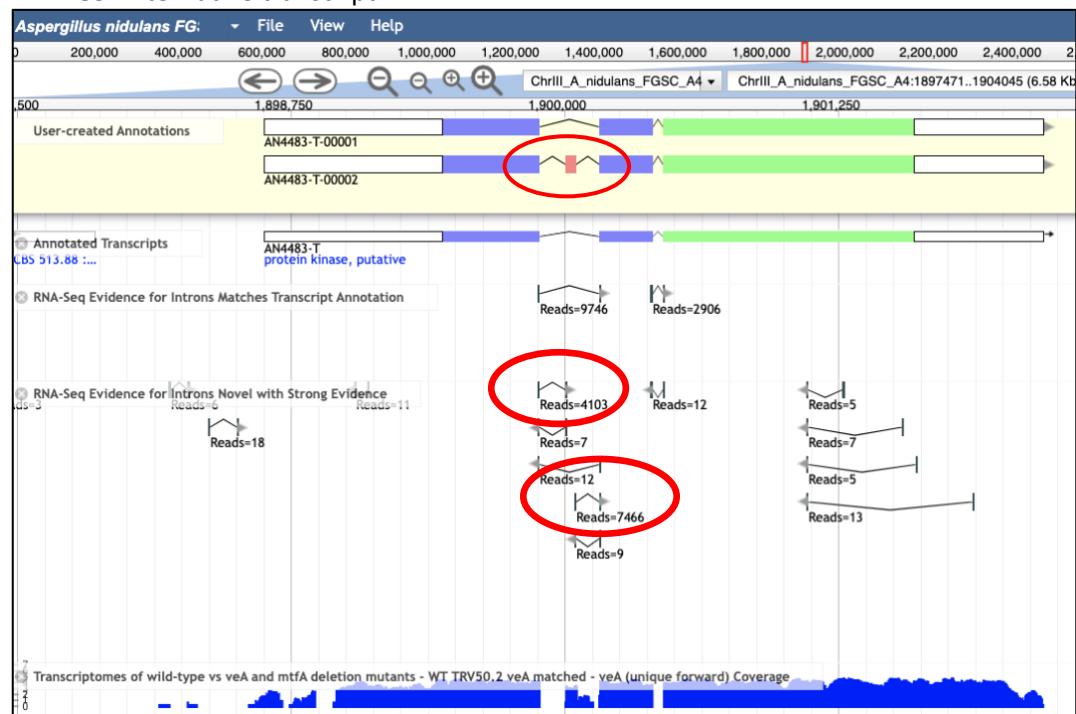


Aspergillus nidulans FGSC A4

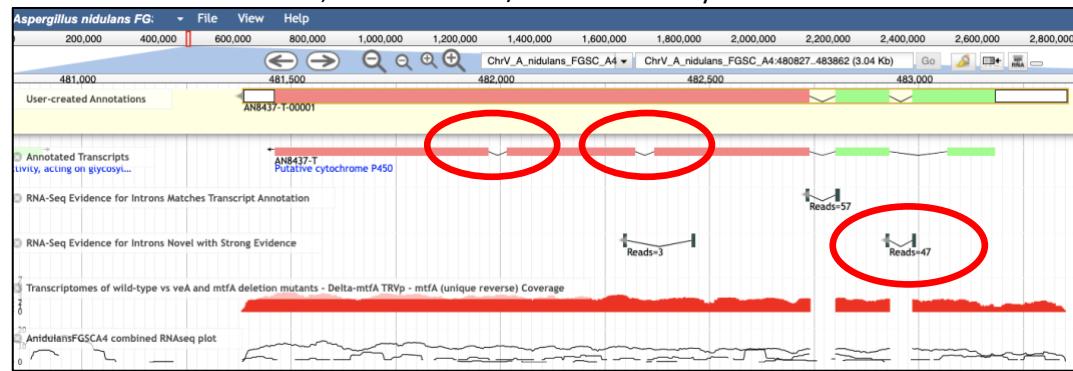
AN10121: Merging with AN10121



AN4483: Alternative transcript



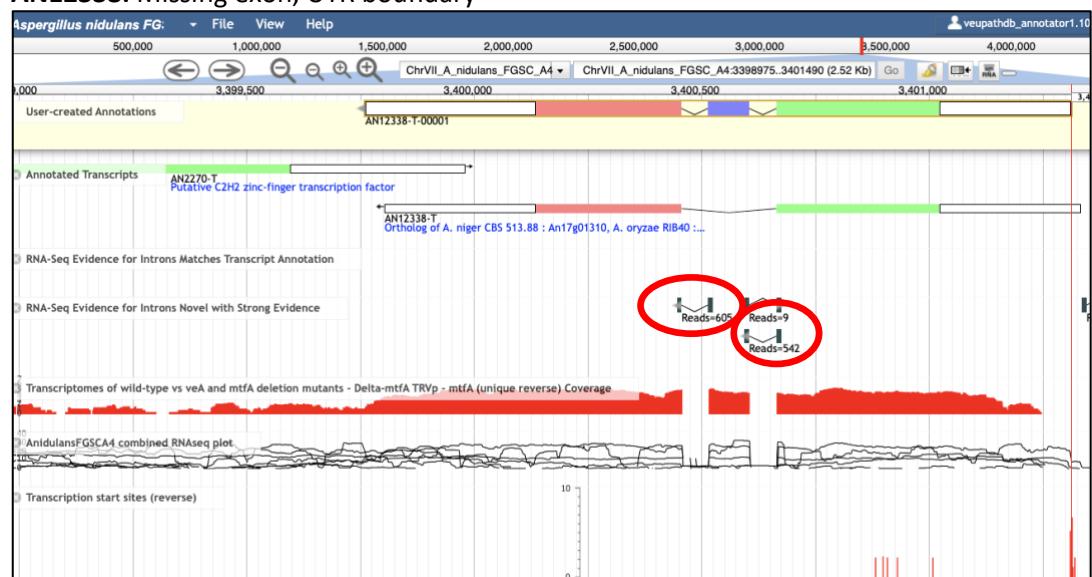
AN8437: Incorrect introns, incorrect exon/intron boundary



AN11226: Missing exon, 5'UTR

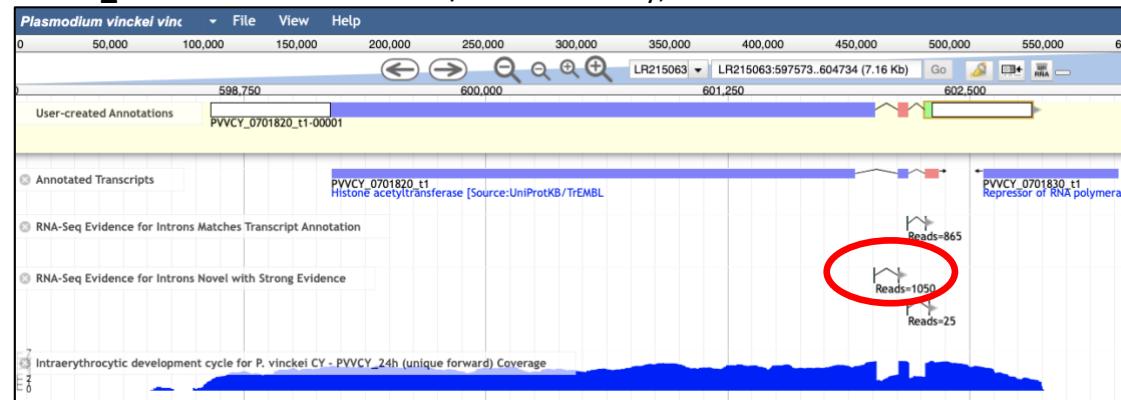


AN12338: Missing exon, UTR boundary

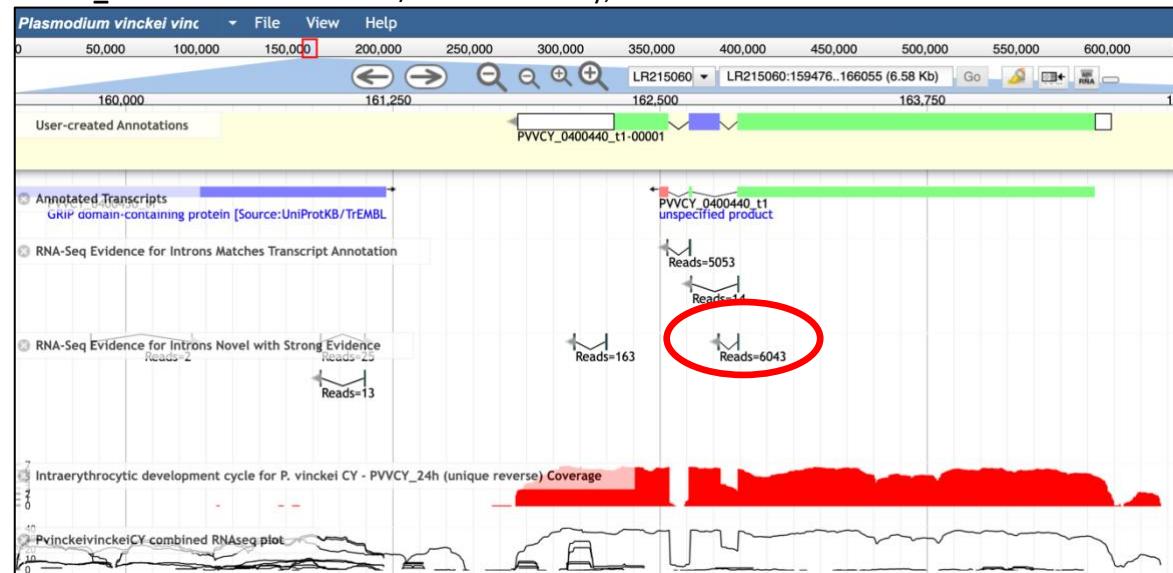


Plasmodium vinckeii vinckeii CY

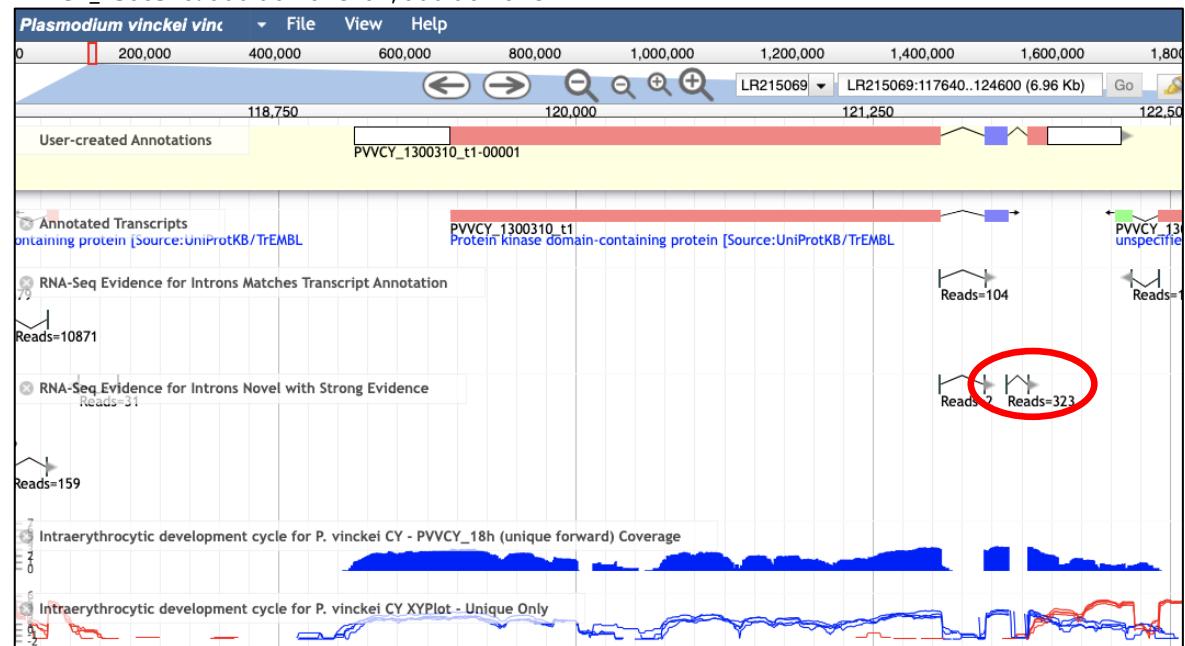
PVVCY_0701820: incorrect intron/exon boundary, addition of UTRs



PVVCY_0400440: incorrect exon/intron boundary, addition of UTRs



PVVCY_1300310: addition of exon, addition of UTR

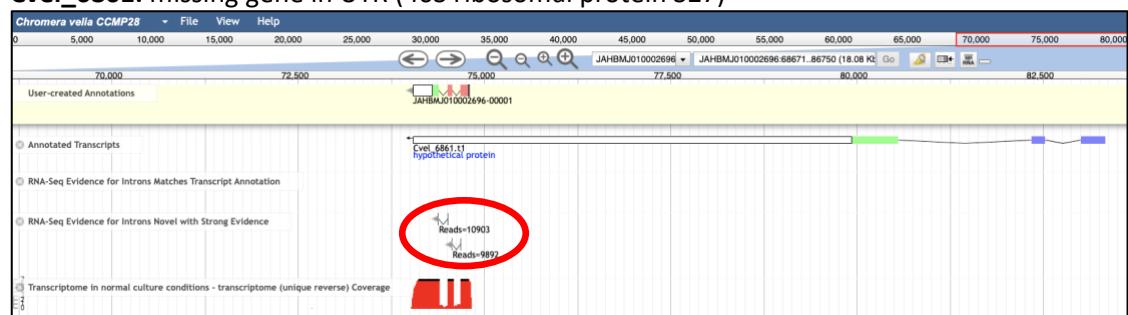


PVVCY_1302110: addition of exon, addition of UTR

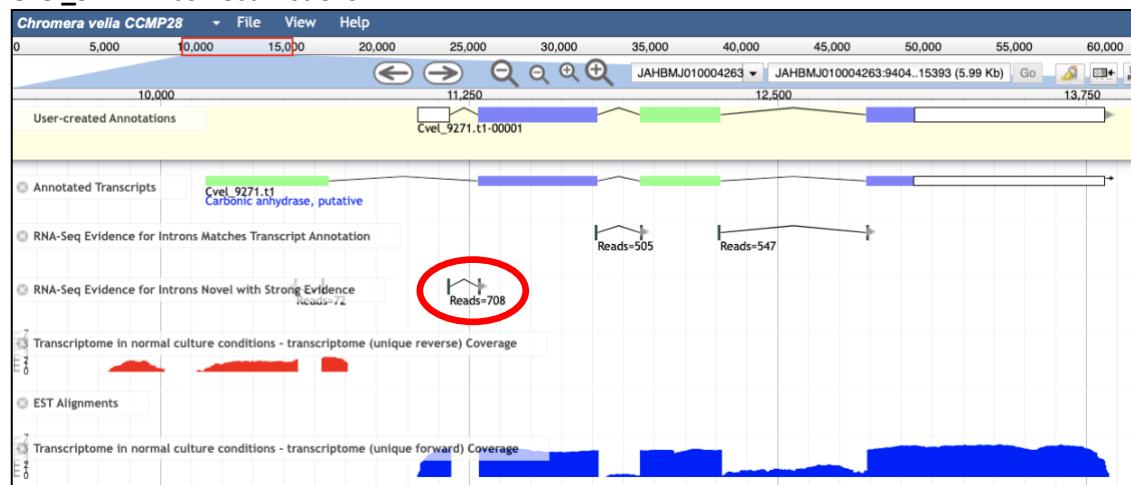


Chromera velia CCMP2878

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

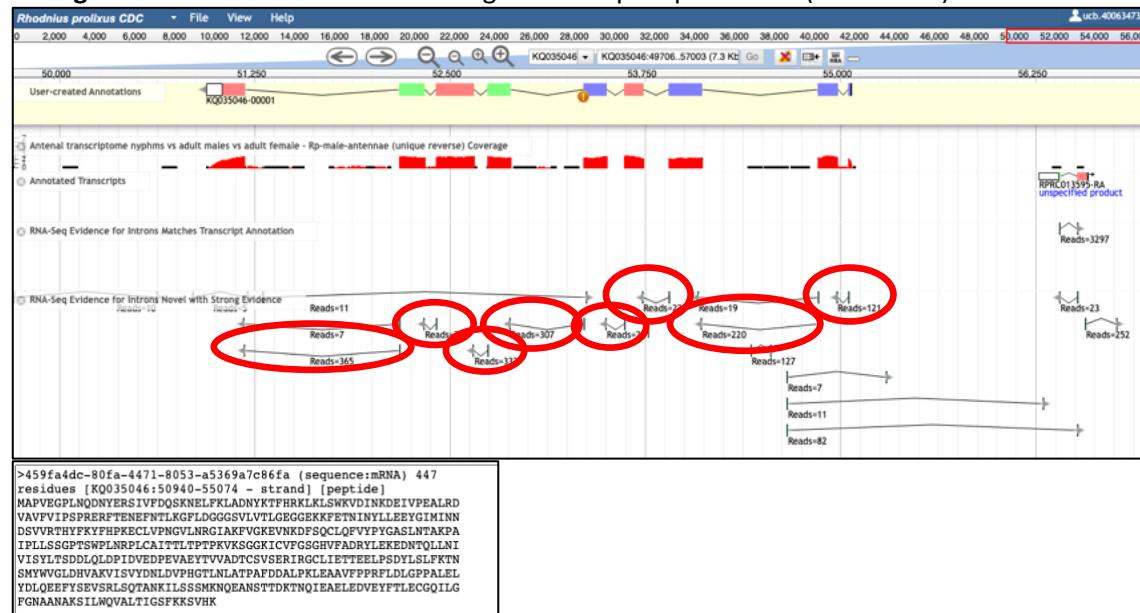


Cvel_9271: incorrect first exon

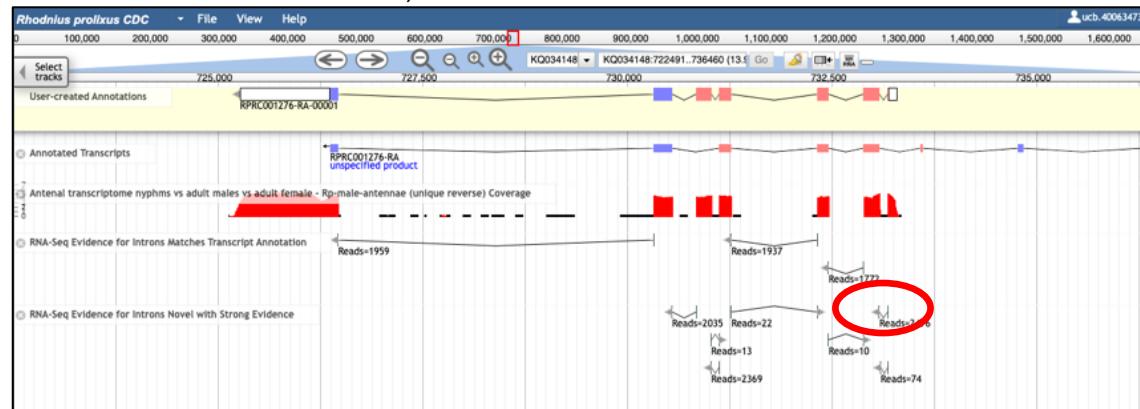


Rhodnius prolixus CDC

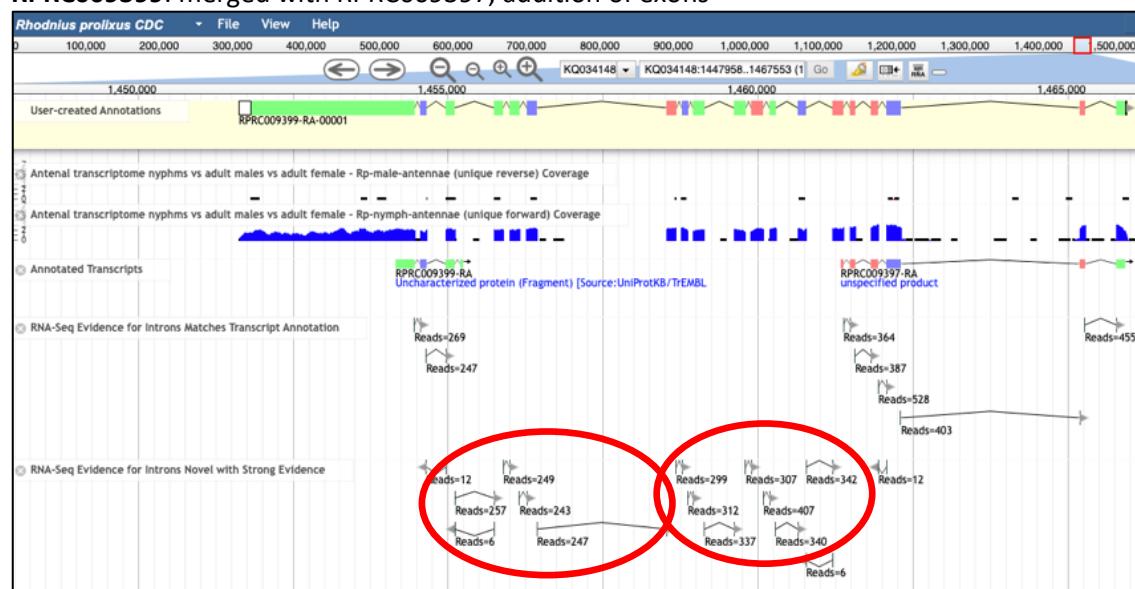
New gene next to RPRC013595: intraflagellar transport protein 52 (IPR039975)



RPRC010556: addition of 2 exons, deletion of 3 exons



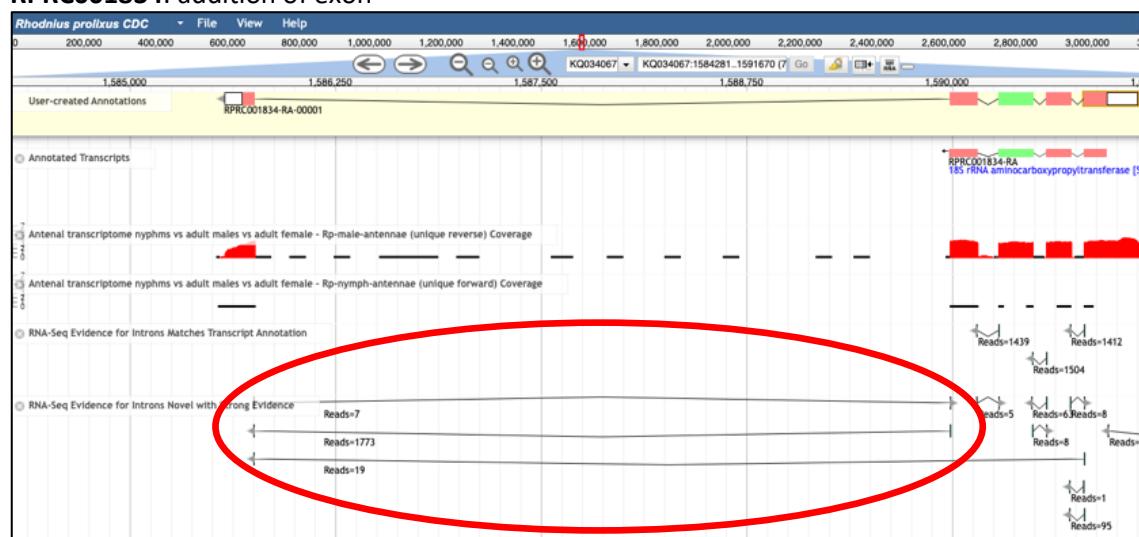
RPRC009399: merged with RPRC009397, addition of exons



New gene next to RPRC006087 (nucleolar protein 11, IPR042859)

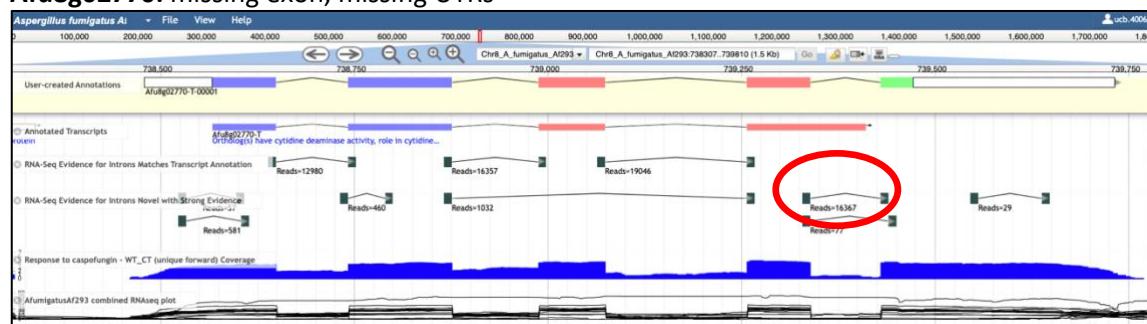


RPRC001834: addition of exon

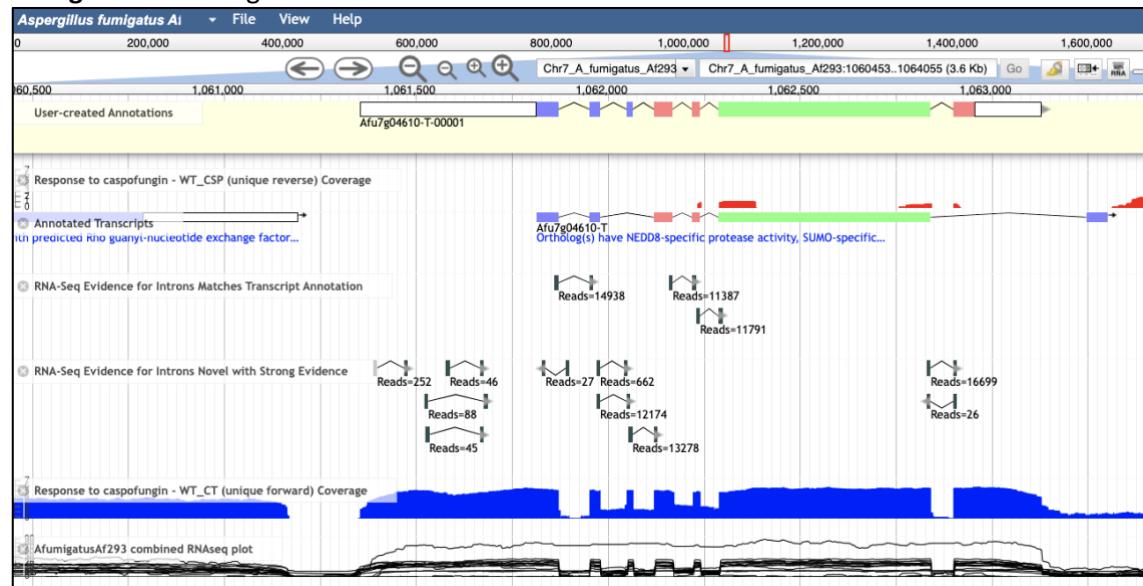


Aspergillus fumigatus Af293

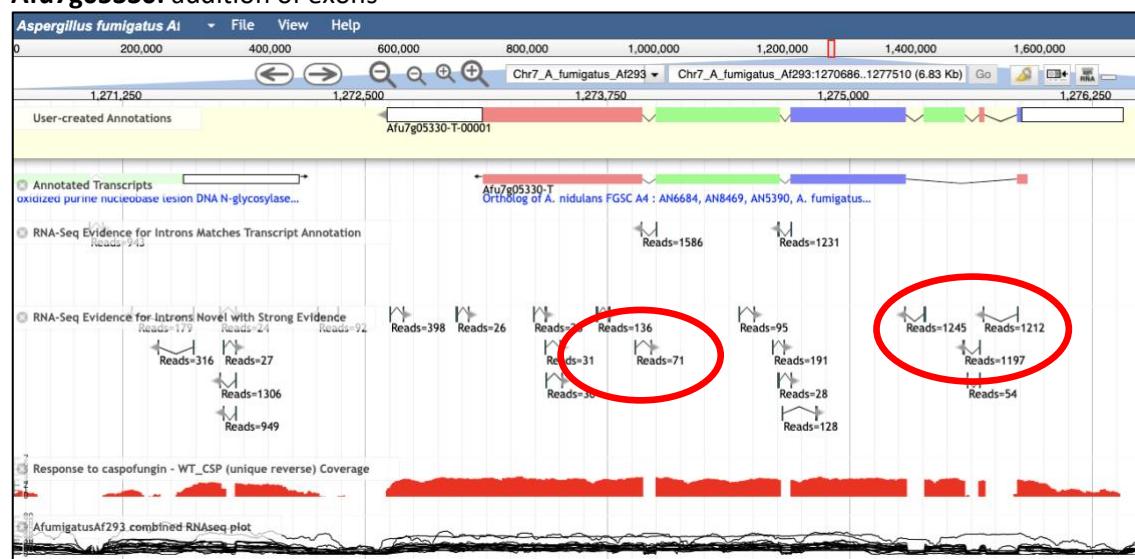
Afu8g02770: missing exon, missing UTRs



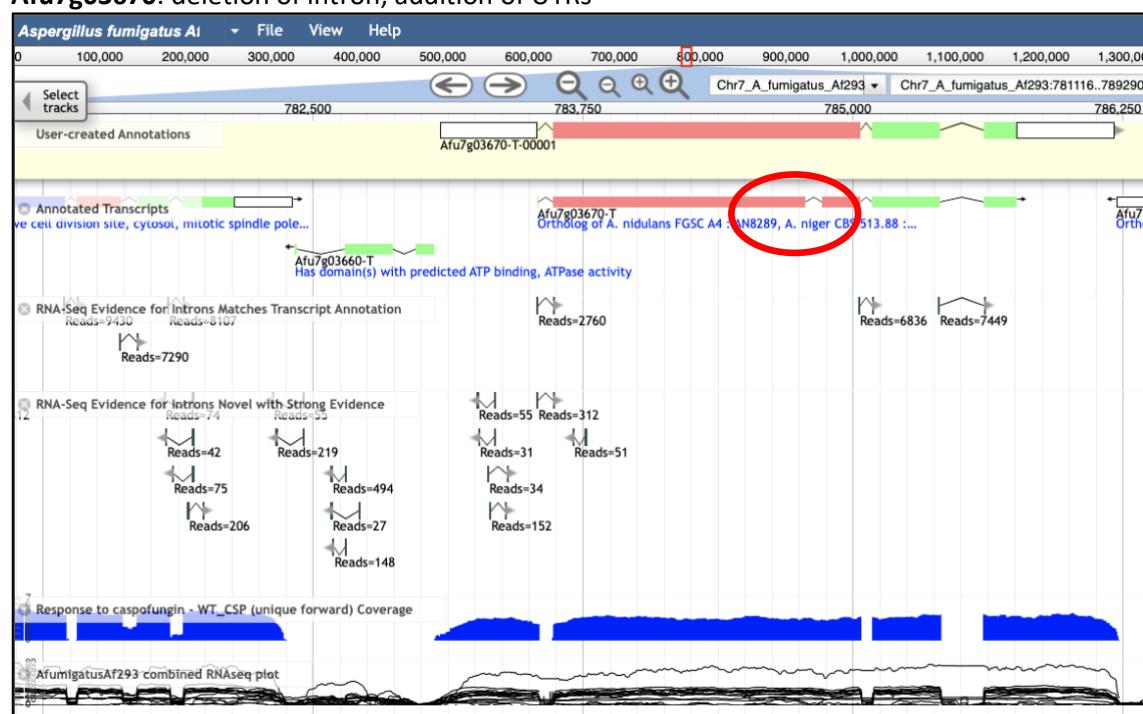
Afu7g04610: missing exons



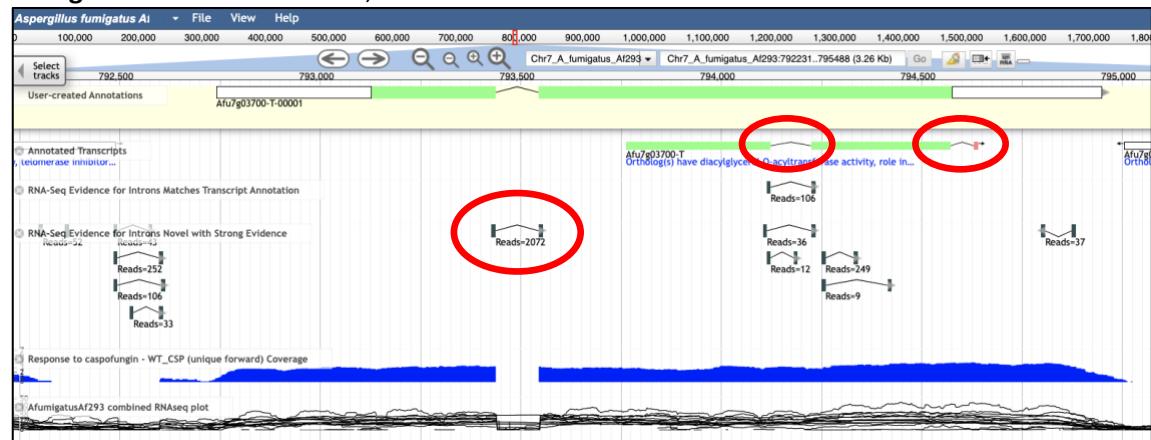
Afu7g05330: addition of exons



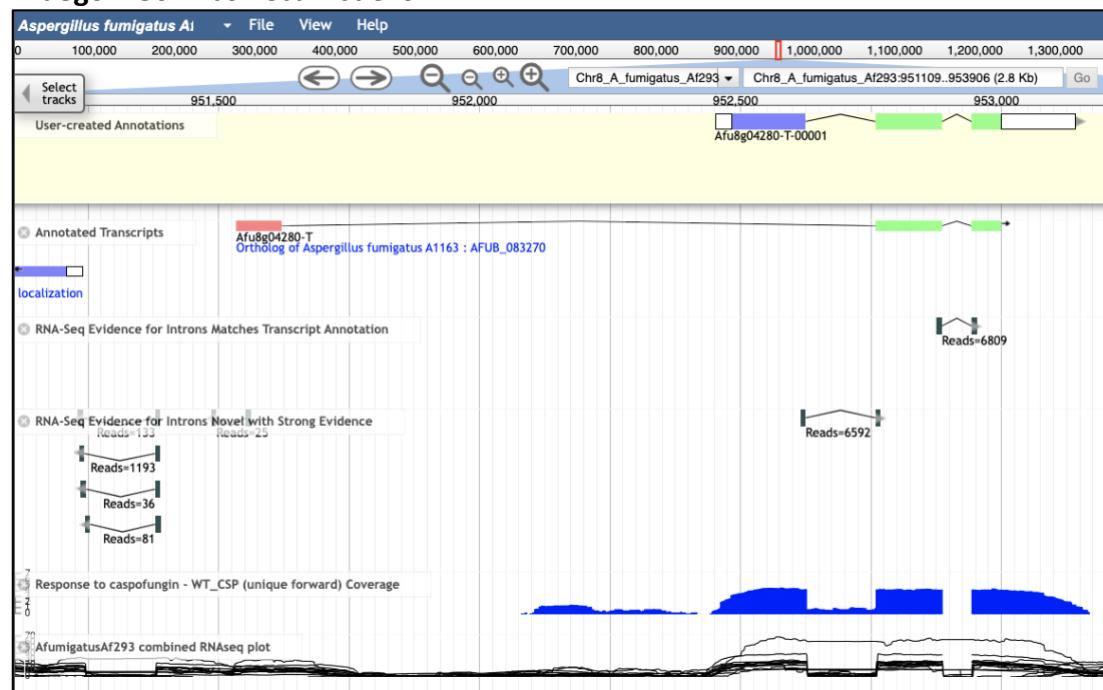
Afu7g03670: deletion of intron, addition of UTRs



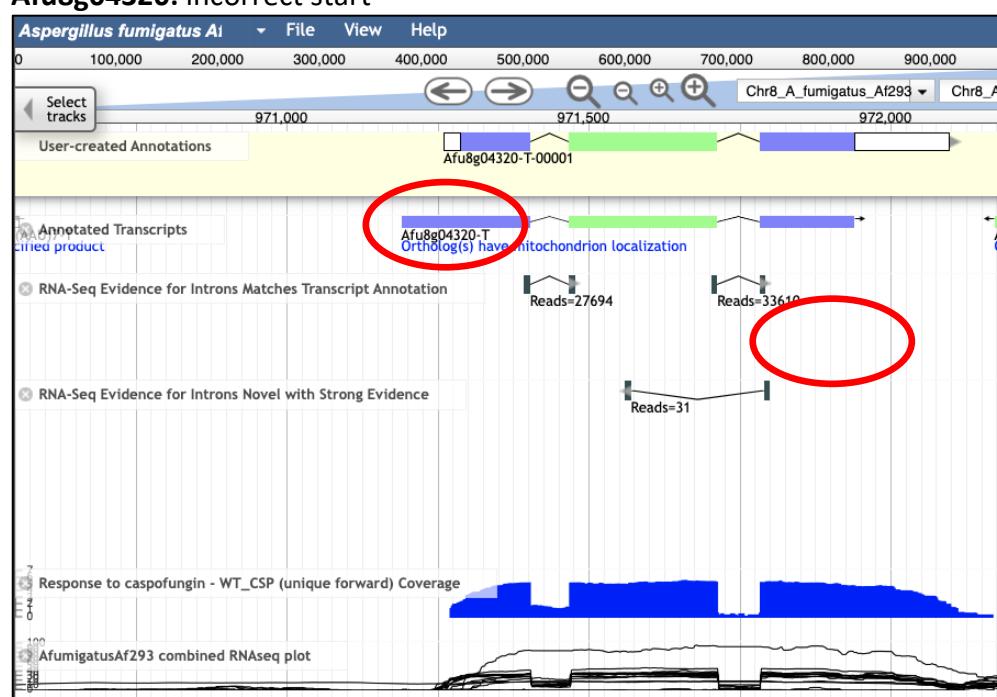
Afu7g03700: addition of exon, two incorrect introns



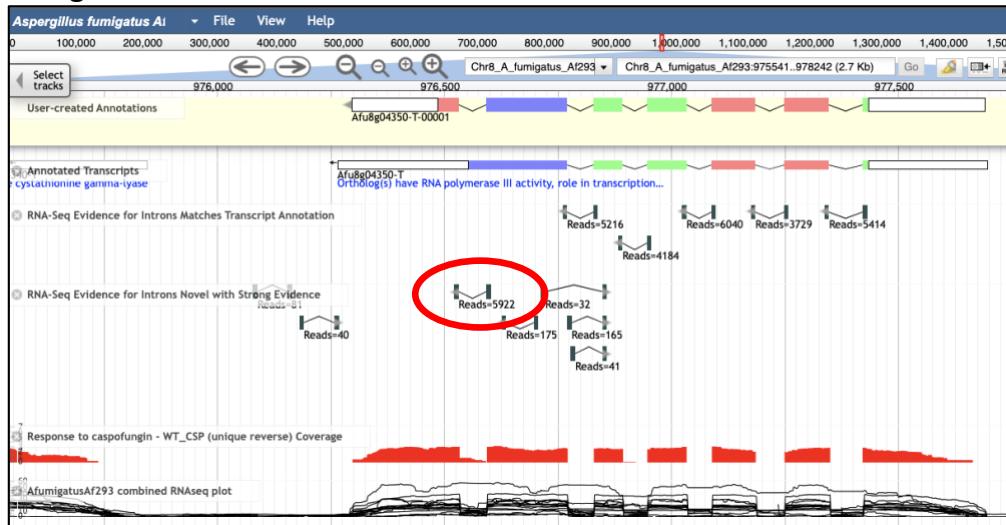
Afu8g04280: incorrect first exon



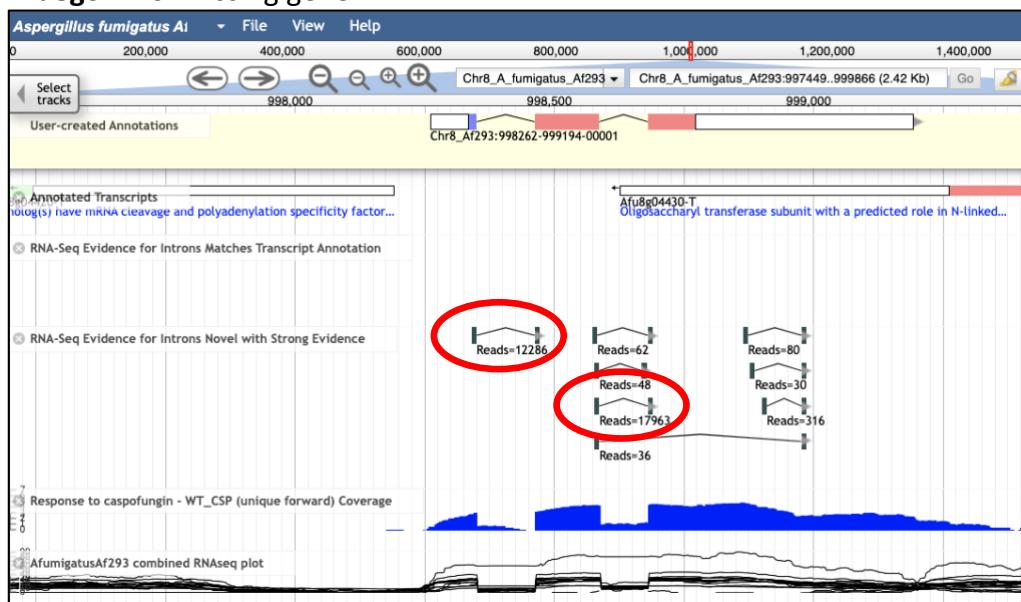
Afu8g04320: incorrect start



Afu8g04350: addition of exon

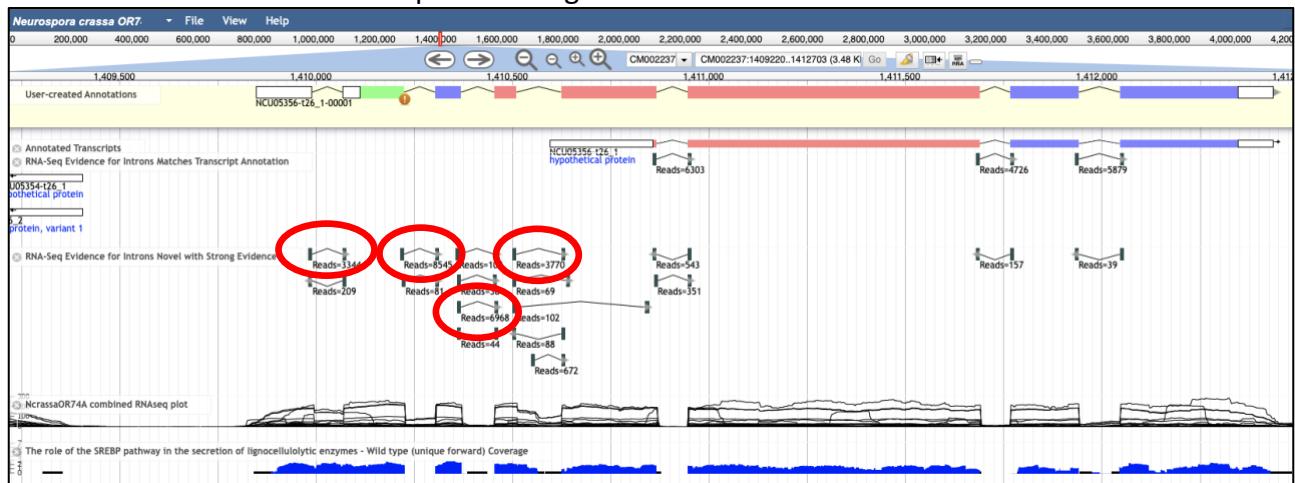


Afu8g04420: missing gene

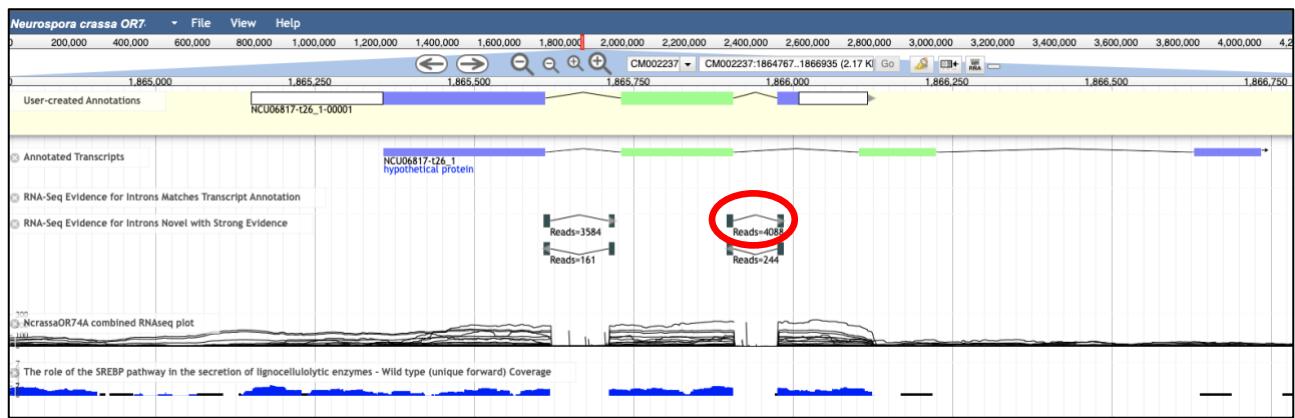


Neurospora crassa OR74A

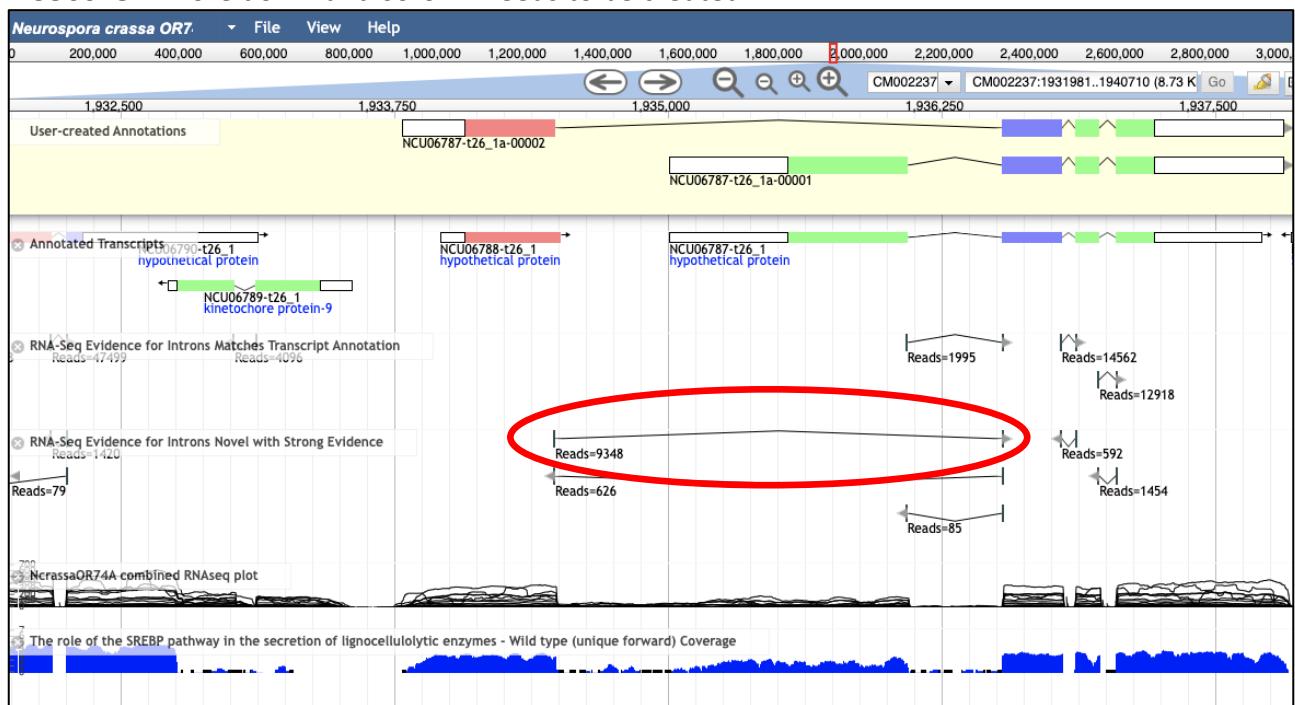
NCU05356: Addition of exons upstream of gene models.



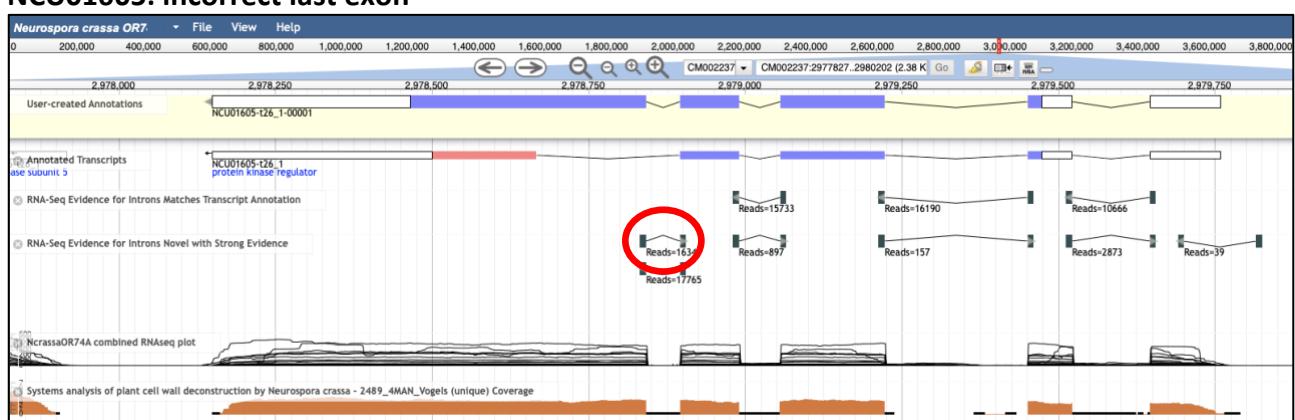
NCU06817: No evidence for last exon and shorter intron.



NCU06787: More dominant isoform needs to be created.

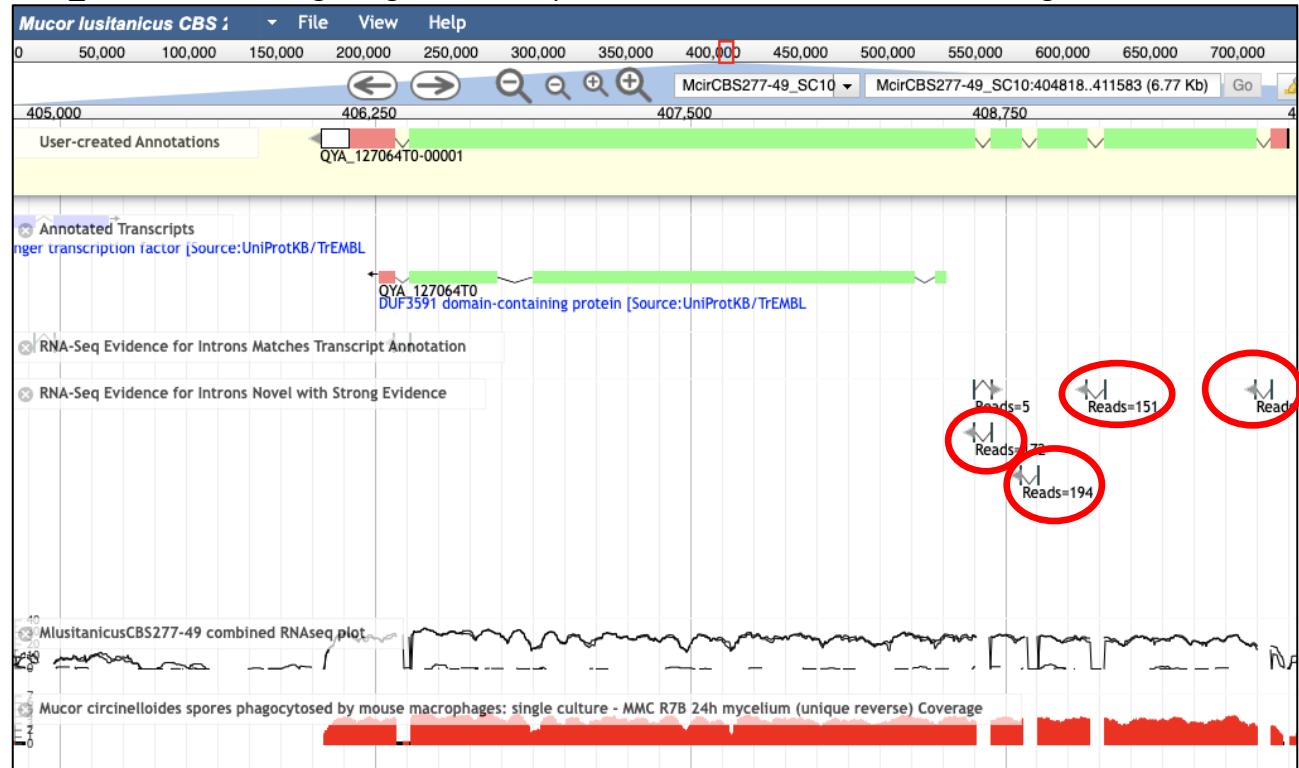


NCU01605: incorrect last exon



Mucor lusitanicus CBS 277.49

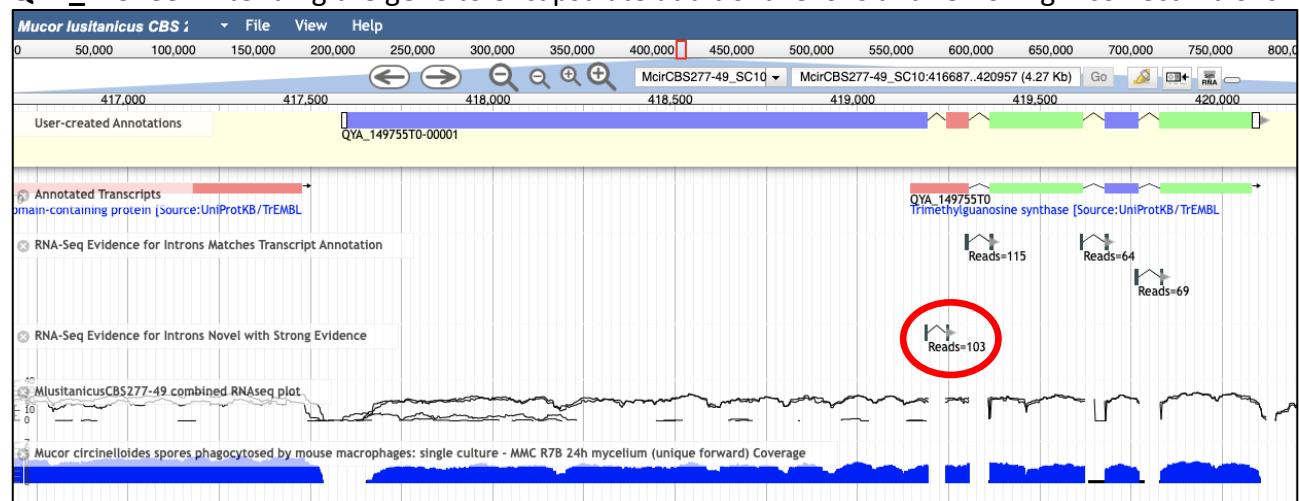
QYA_127064: Extending the gene to encapsulate additional exons and removing incorrect introns



QYA_149865 : Extending the gene to encapsulate additional exons and removing incorrect introns



QYA_149755: Extending the gene to encapsulate additional exons and removing incorrect introns

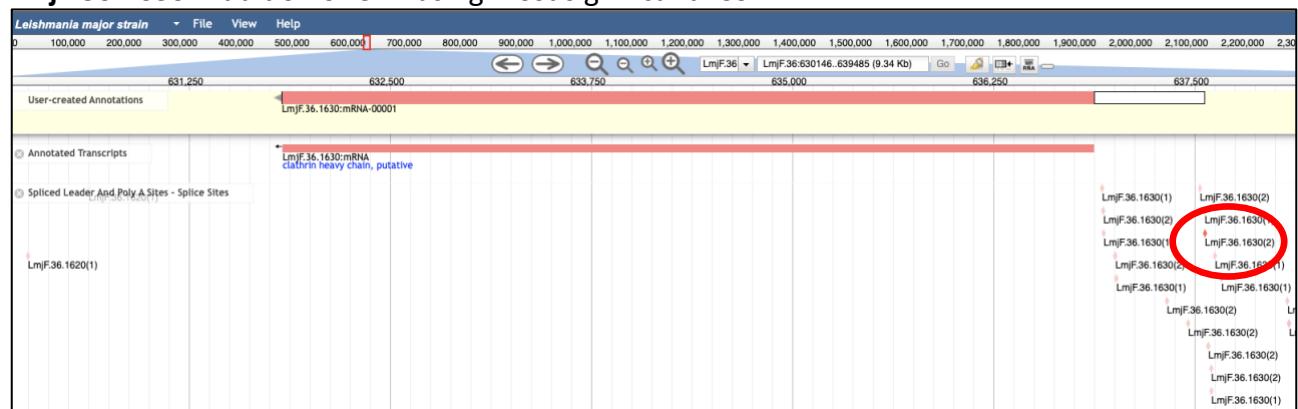


McirCBS277-49_SC10:340541..349710. (coordinates) : Creation of two new genes from the dragable introns.

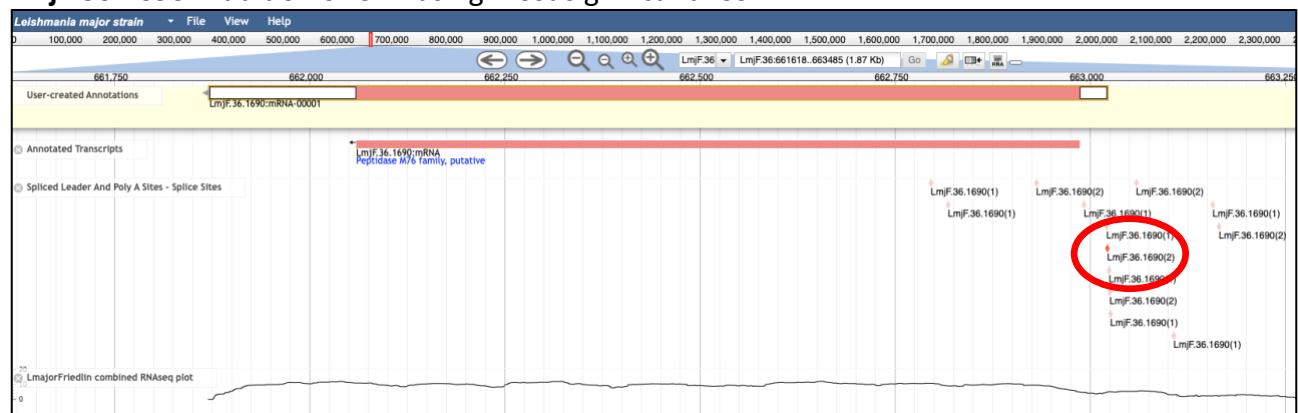


Leishmania major strain Friedlin

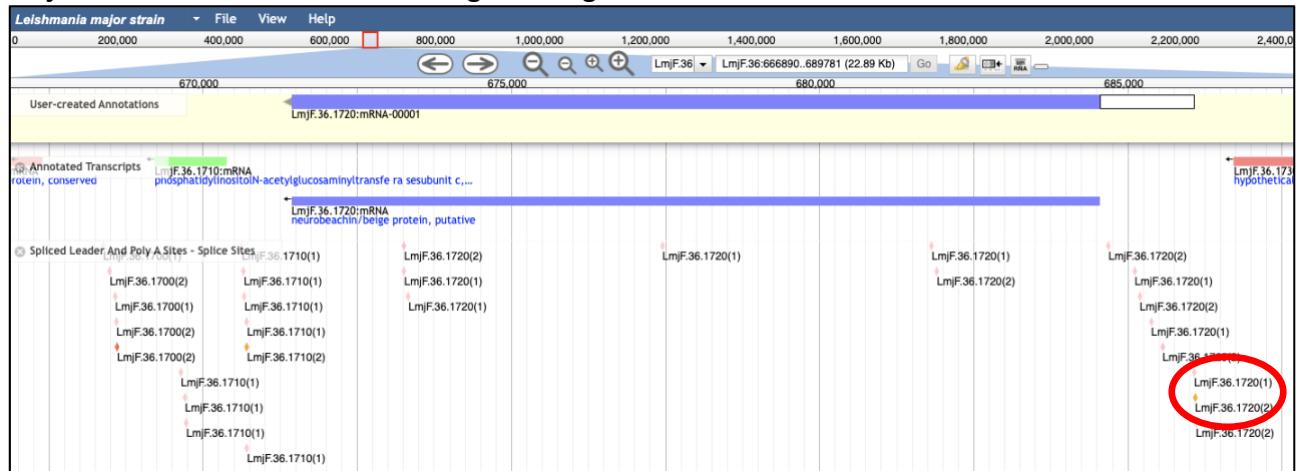
LmjF.36.1630: Addition of UTR using most significant TSS.



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.

