

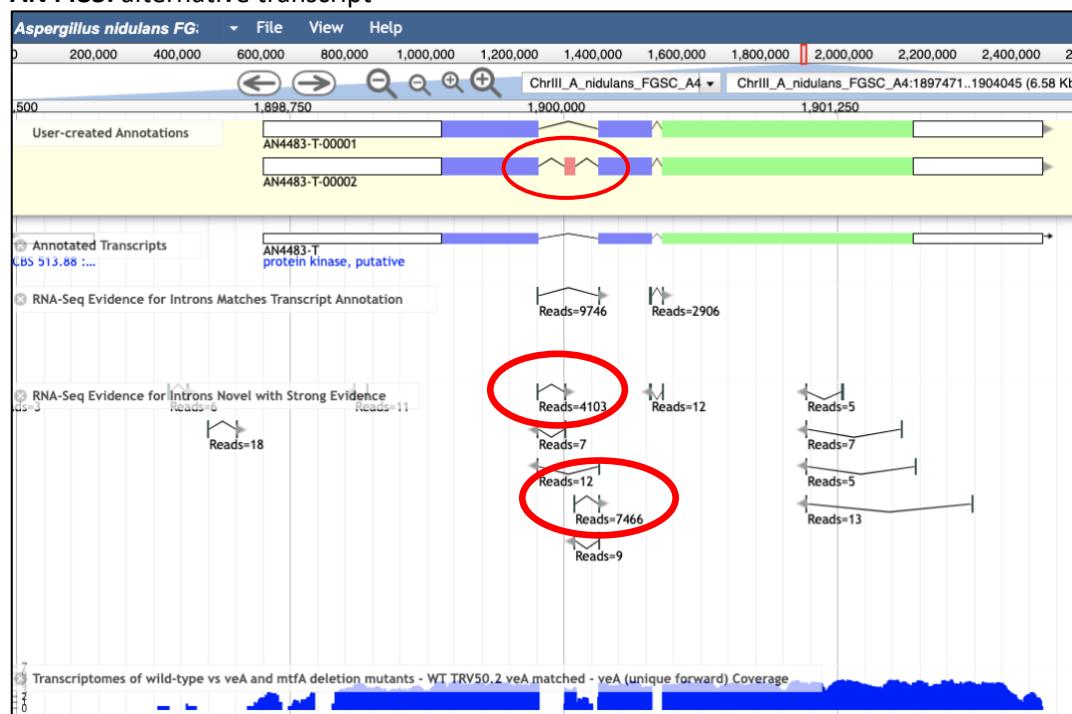
# Optional Apollo exercise: answer key

## *Aspergillus nidulans* FGSC A4

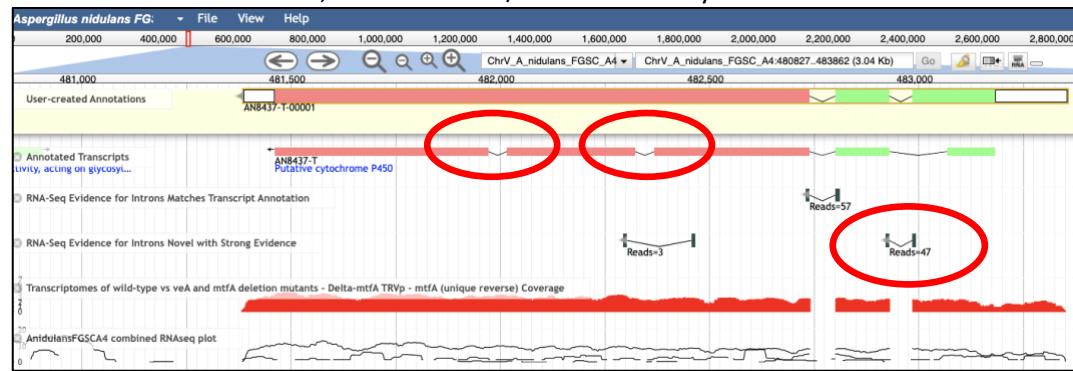
AN10121: merging with AN10119



AN4483: alternative transcript



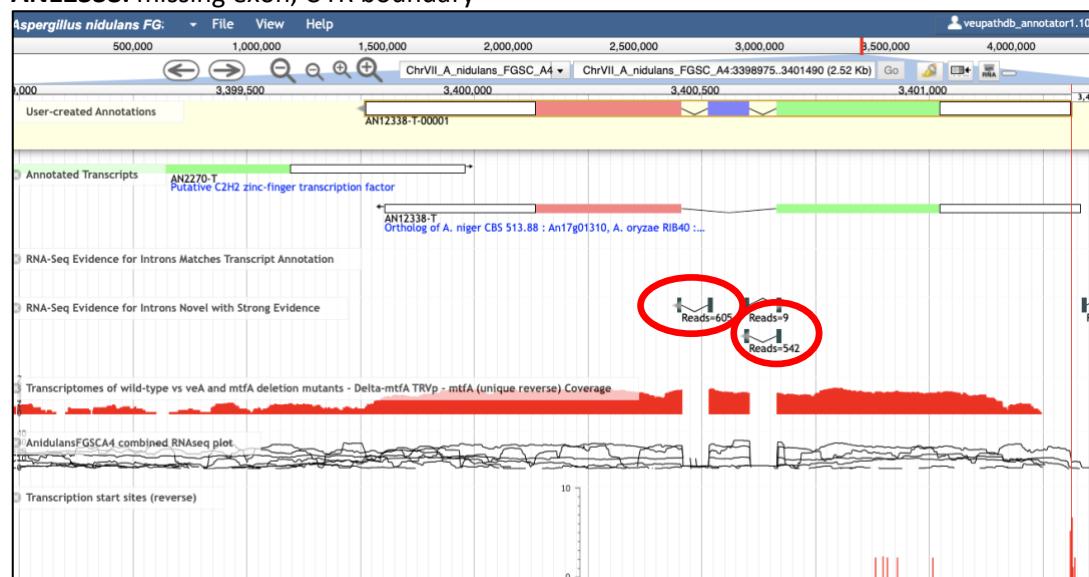
### AN8437: incorrect introns, incorrect exon/intron boundary



### AN11226: missing exon, 5'UTR

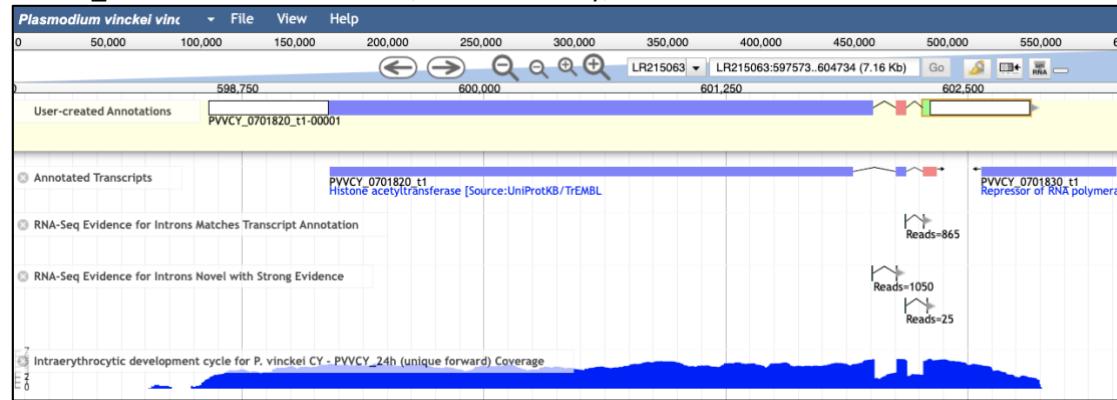


### AN12338: missing exon, UTR boundary

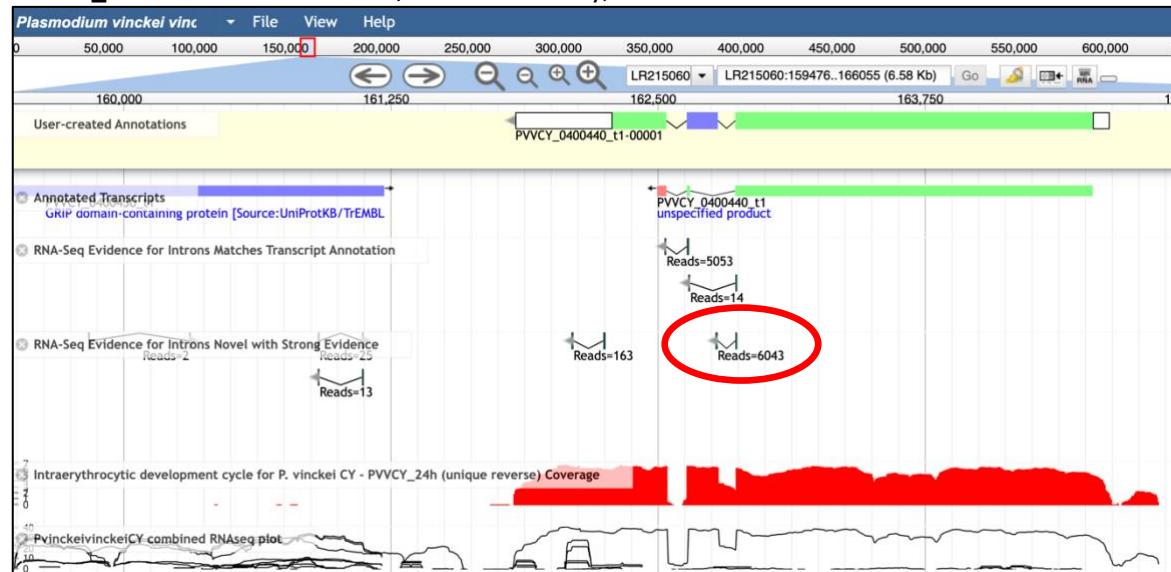


## *Plasmodium vinckeii* vinckeii CY

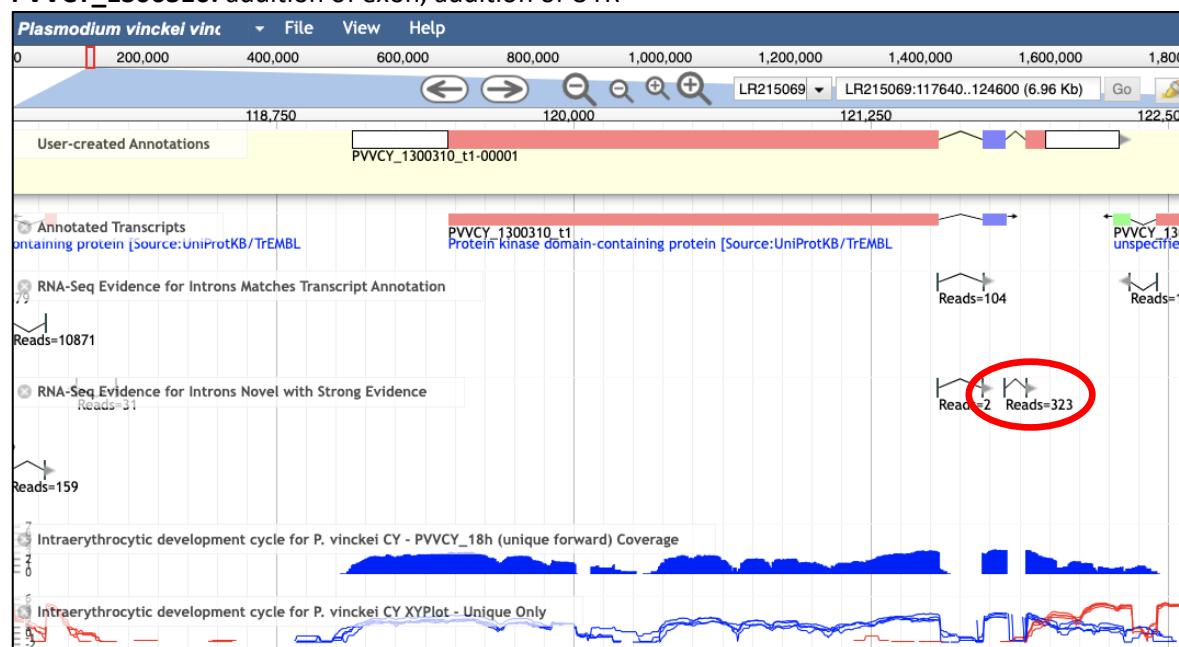
PVVCY\_0701820: incorrect intron/exon boundary, addition of UTRs



PVVCY\_0400440: incorrect exon/intron boundary, addition of UTRs



PVVCY\_1300310: addition of exon, addition of UTR

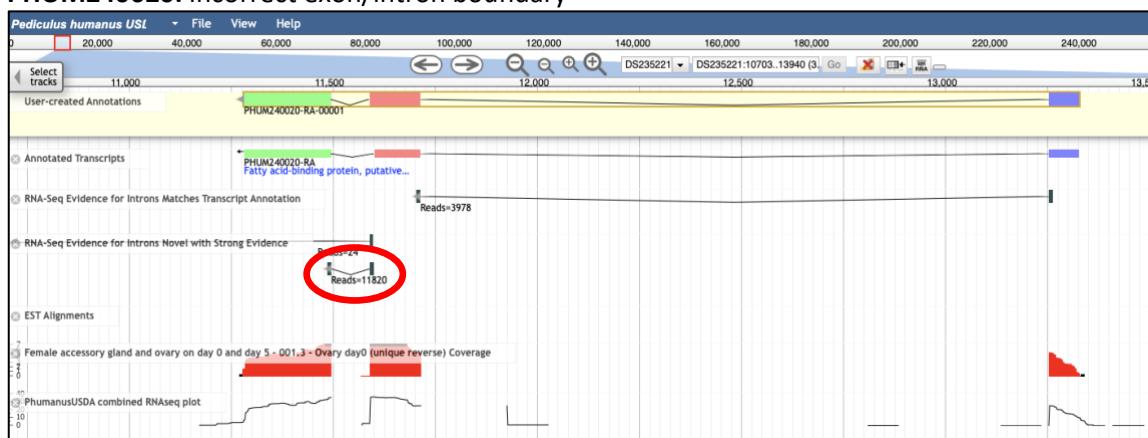


## PVVCY\_1302110: addition of exon, addition of UTR

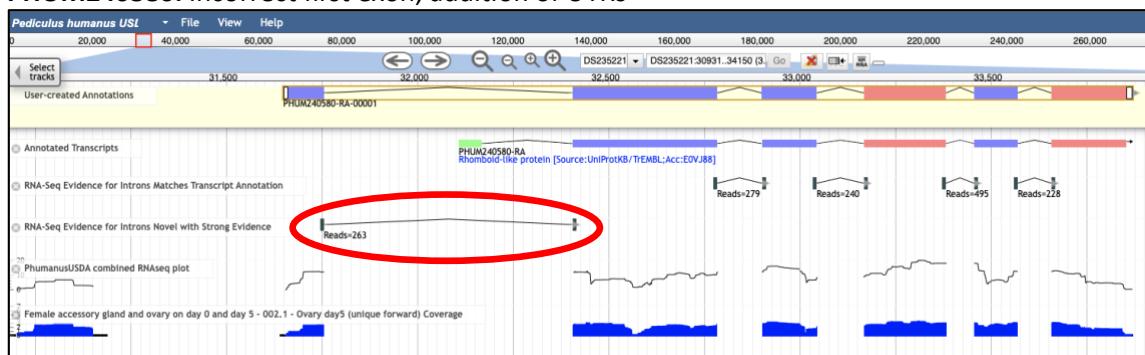


## *Pediculus humanus* USDA

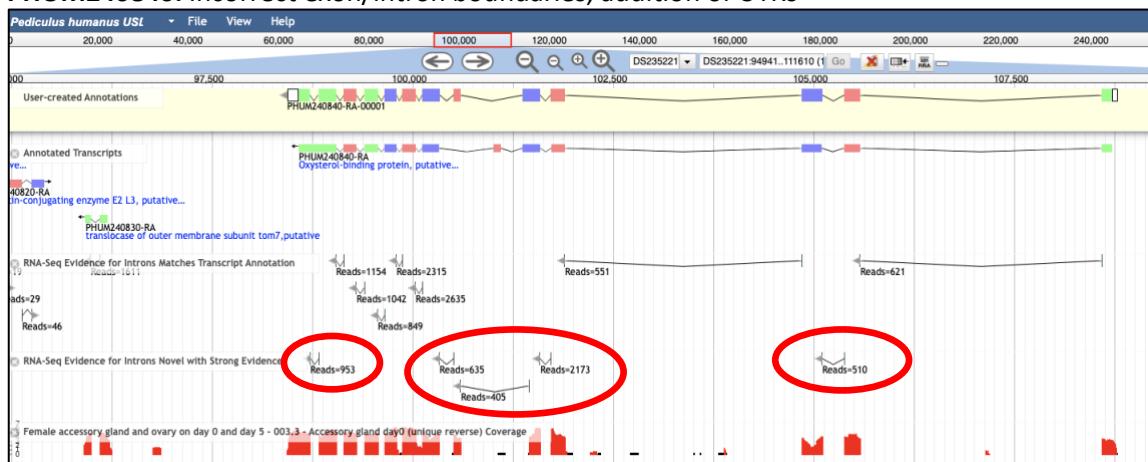
### PHUM240020: incorrect exon/intron boundary



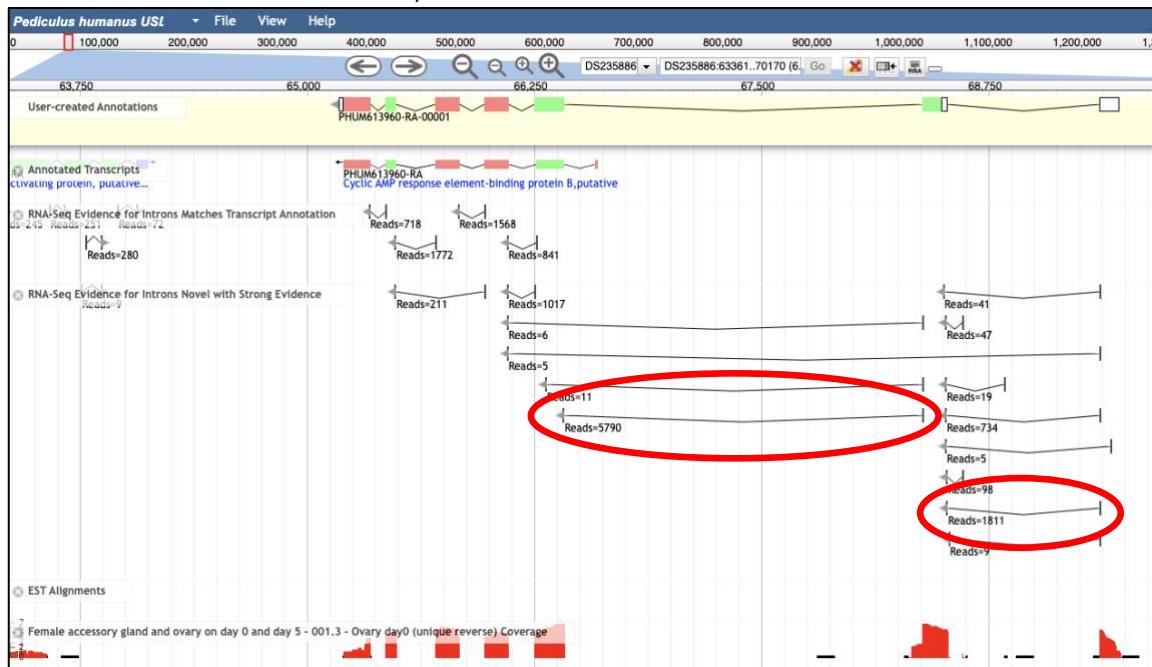
### PHUM240580: incorrect first exon, addition of UTRs



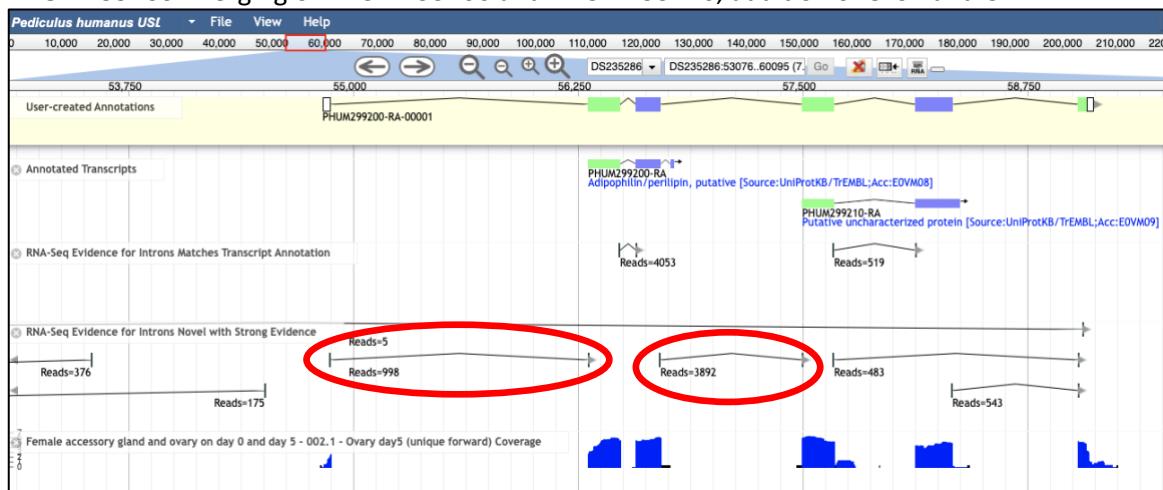
### PHUM240840: incorrect exon/intron boundaries, addition of UTRs



### PHUM613960: incorrect first exon, addition of UTRs

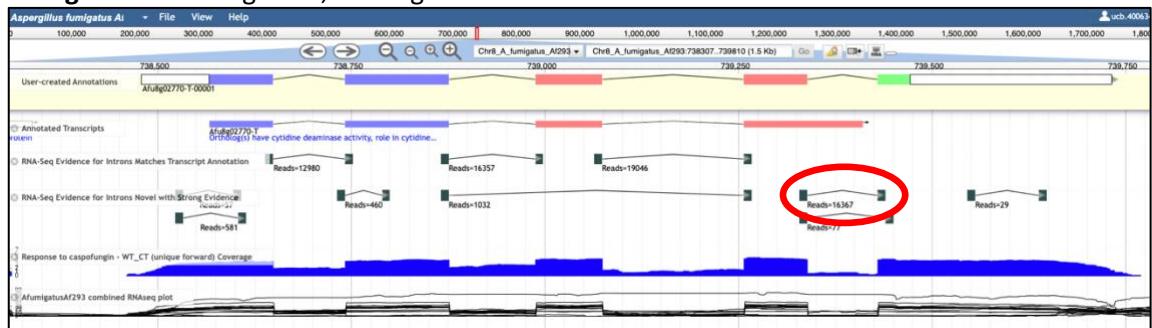


### PHUM299200: merging of PHUM299200 and PHUM299210, addition of exon and UTR

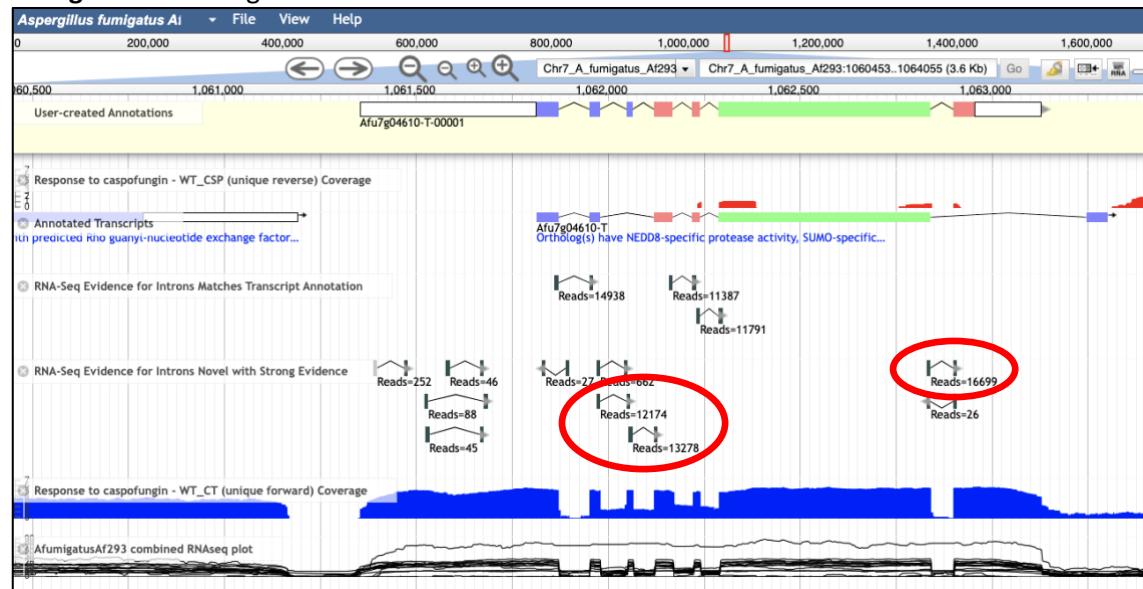


### Aspergillus fumigatus Af293

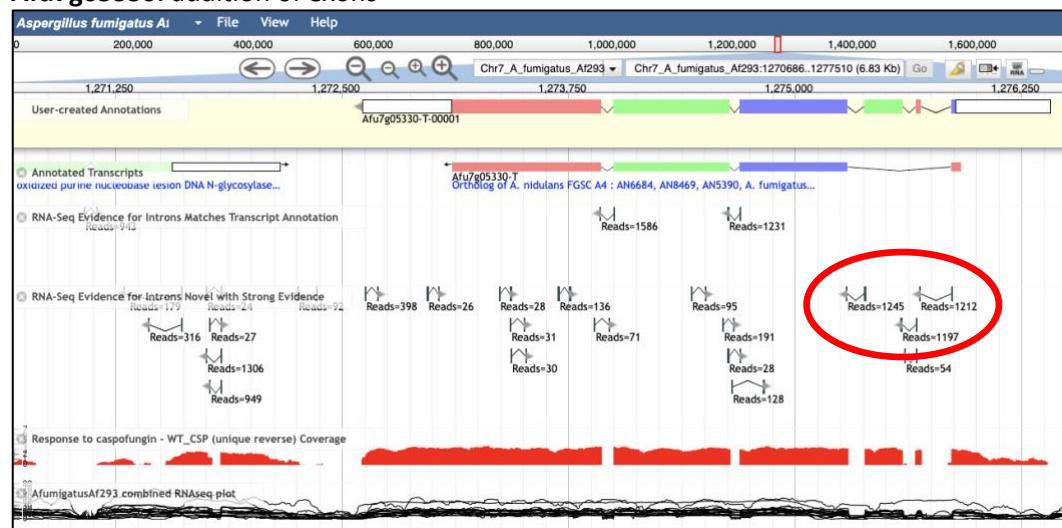
#### Afu8g02770: missing exon, missing UTRs



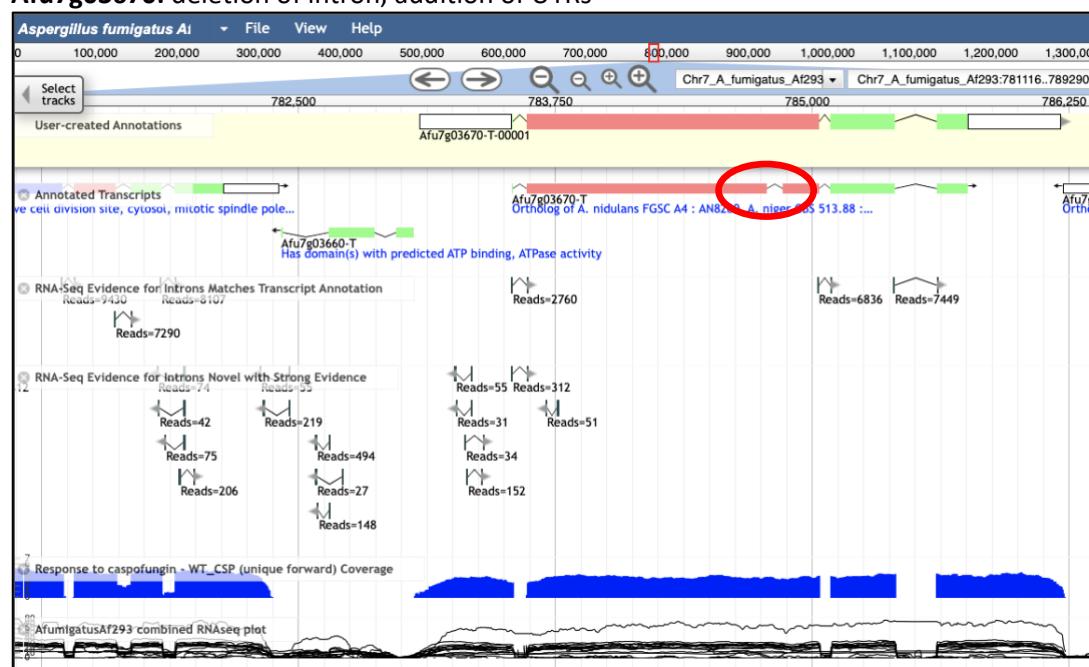
### Afu7g04610: missing exons



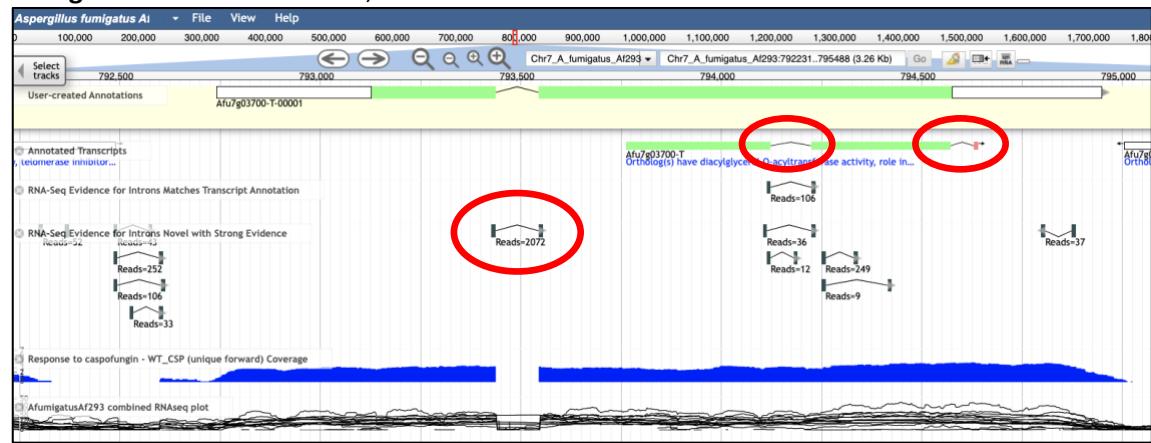
### Afu7g05330: addition of exons



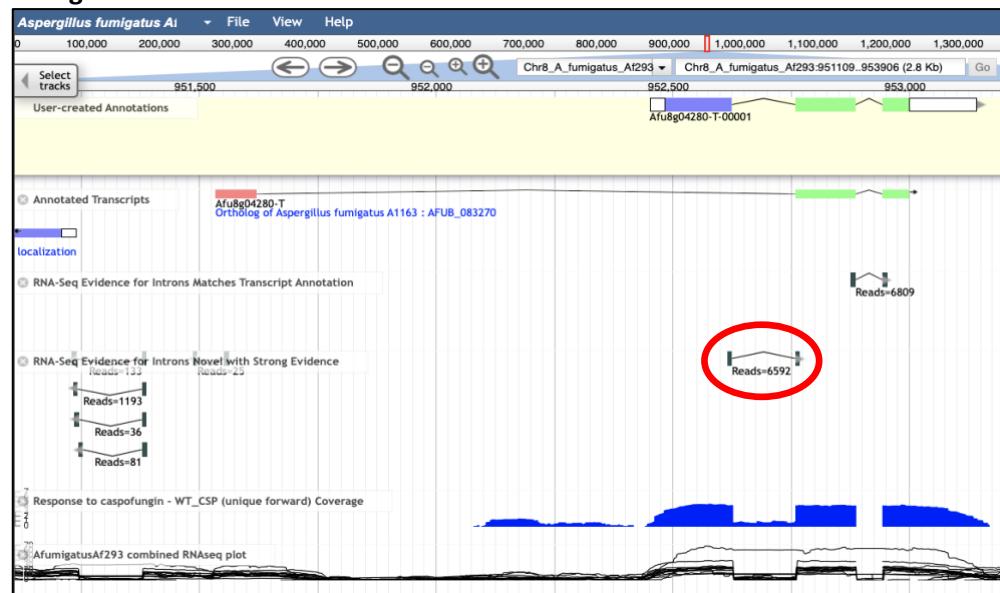
### Afu7g03670: deletion of intron, addition of UTRs



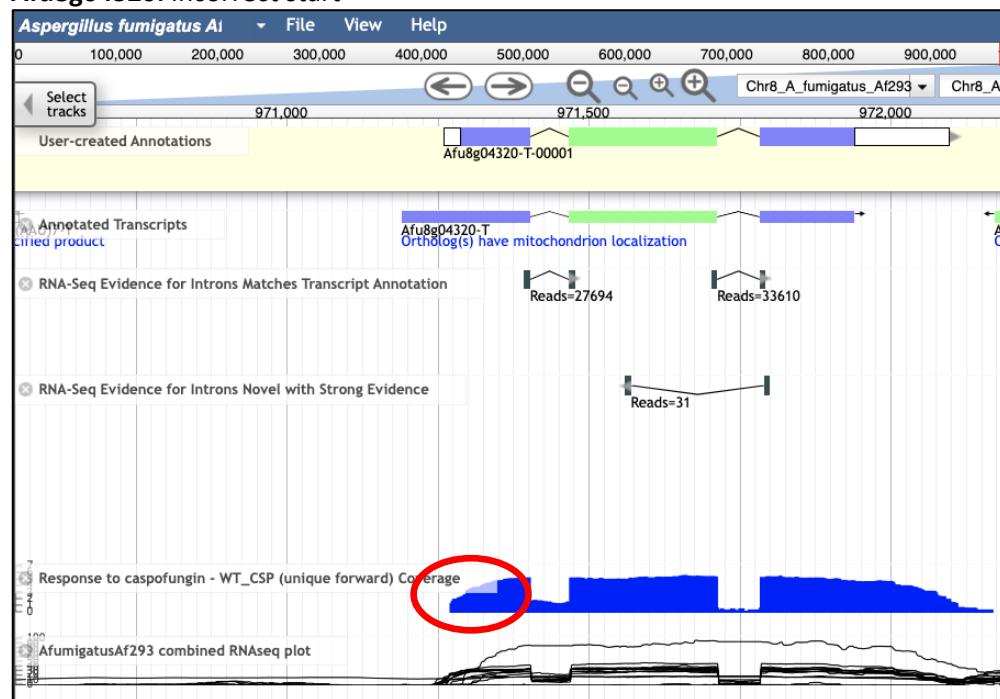
### Afu7g03700: addition of exon, two incorrect introns



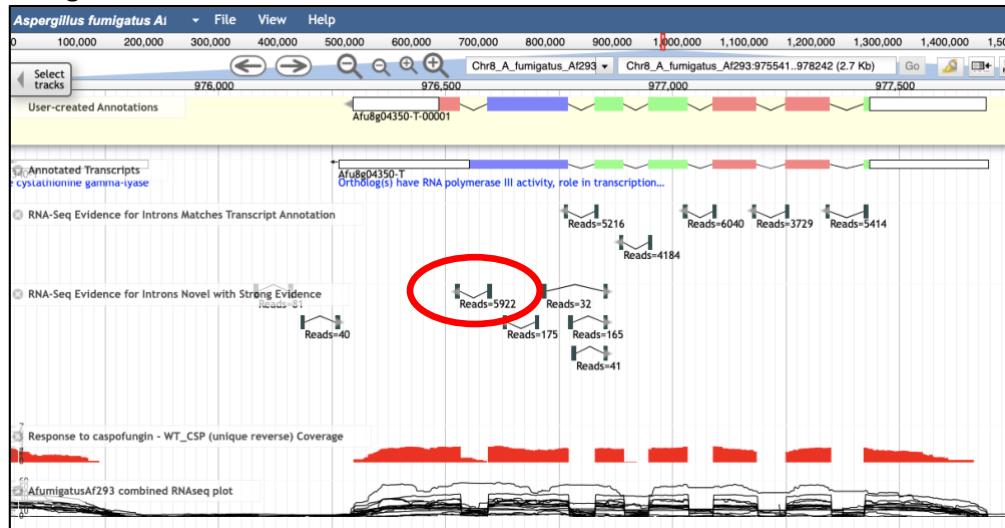
### Afu8g04280: incorrect first exon



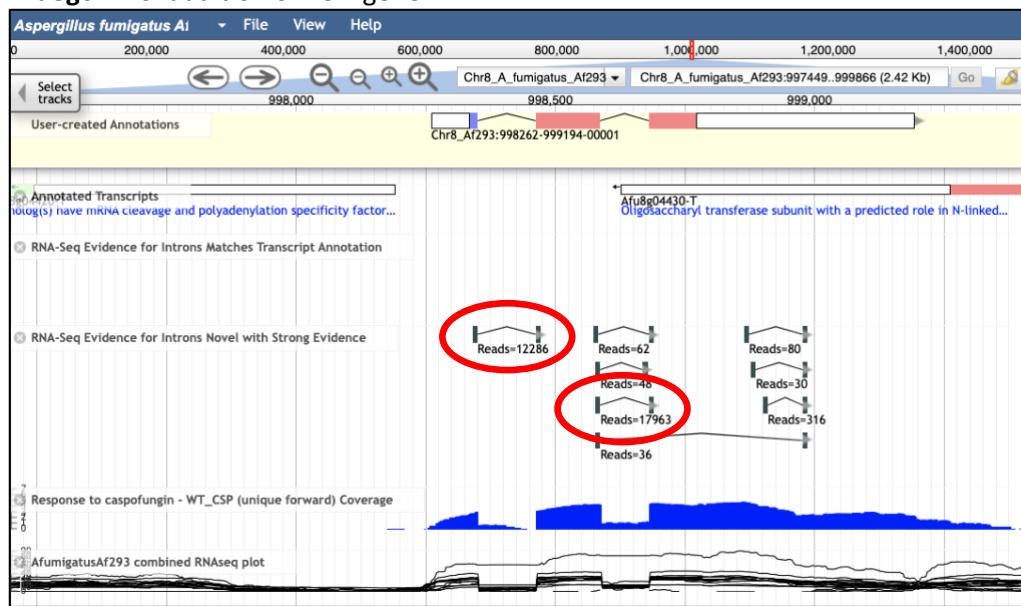
### Afu8g04320: incorrect start



## Afu8g04350: addition of exon

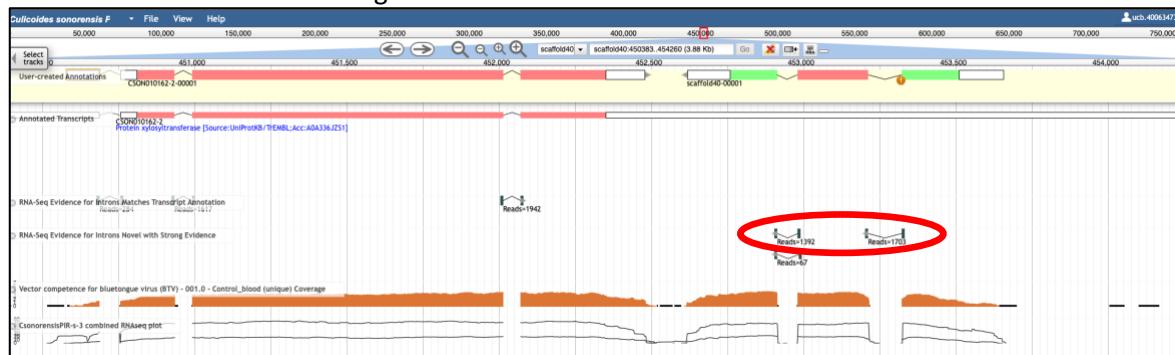


## Afu8g04420: addition of new gene

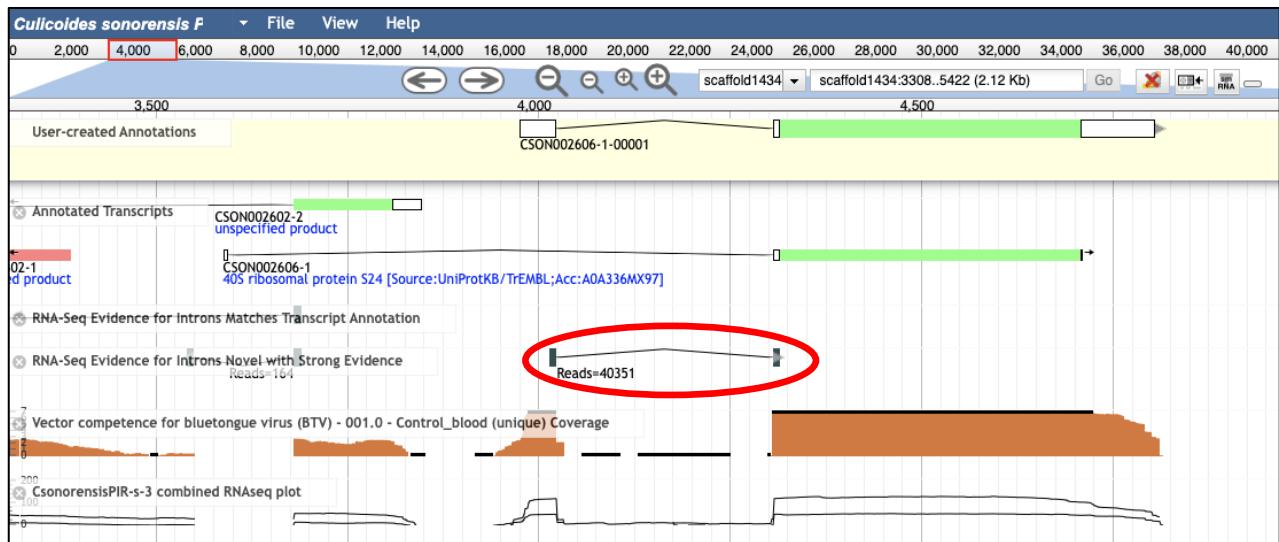


## Culicoides sonorensis PIR-s-3

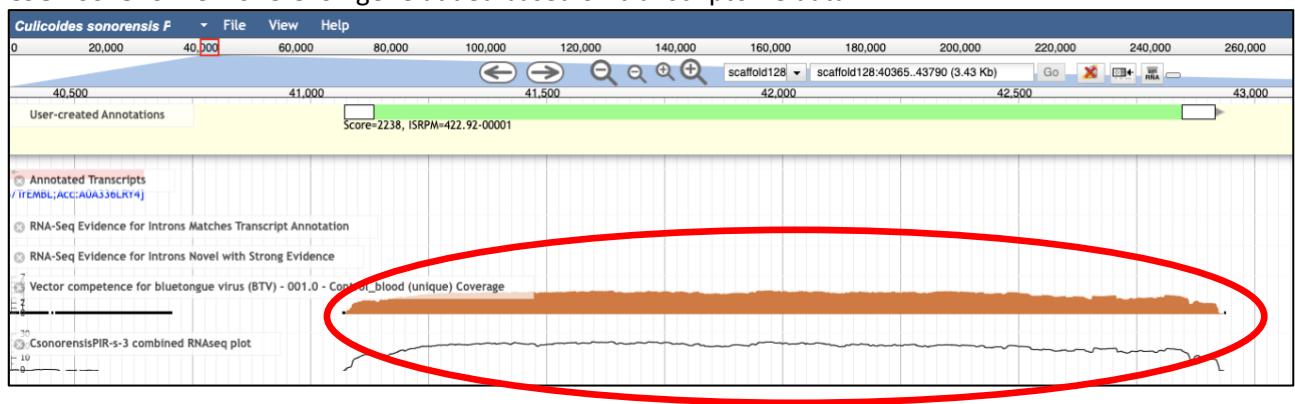
### CSON010162: addition of new gene



### CSON002606: incorrect UTR



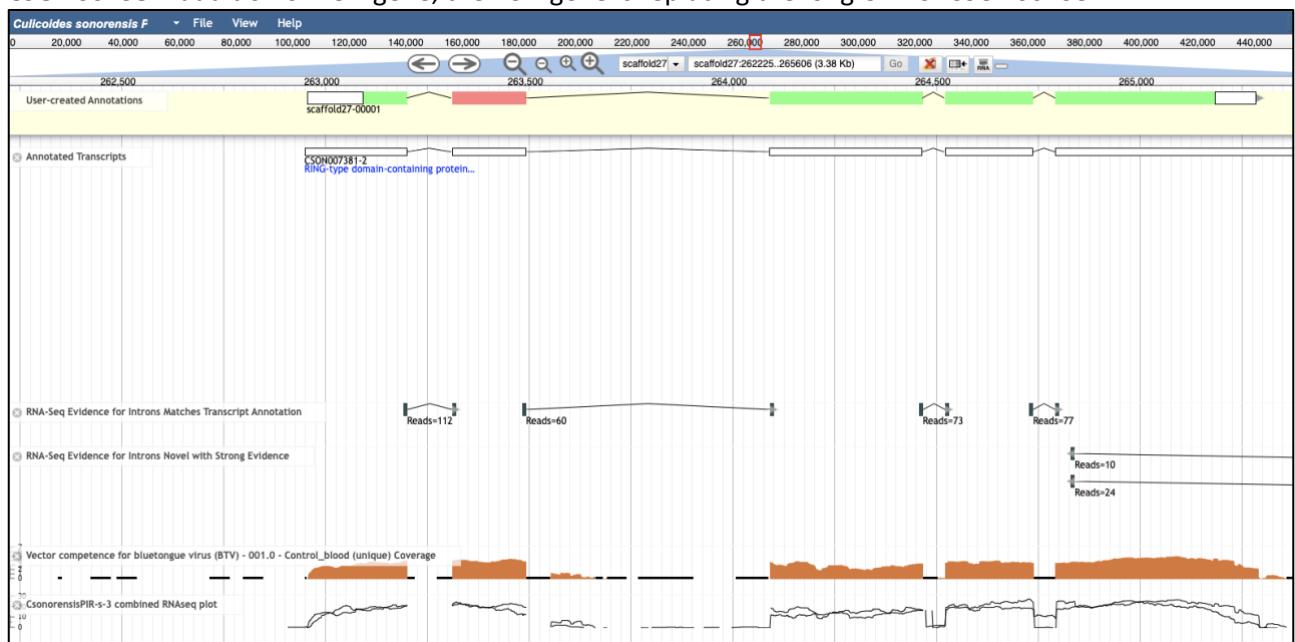
### CSON001816: new one-exon gene added based on transcriptome data



### CSON009689: addition of exon, change of UTR boundaries

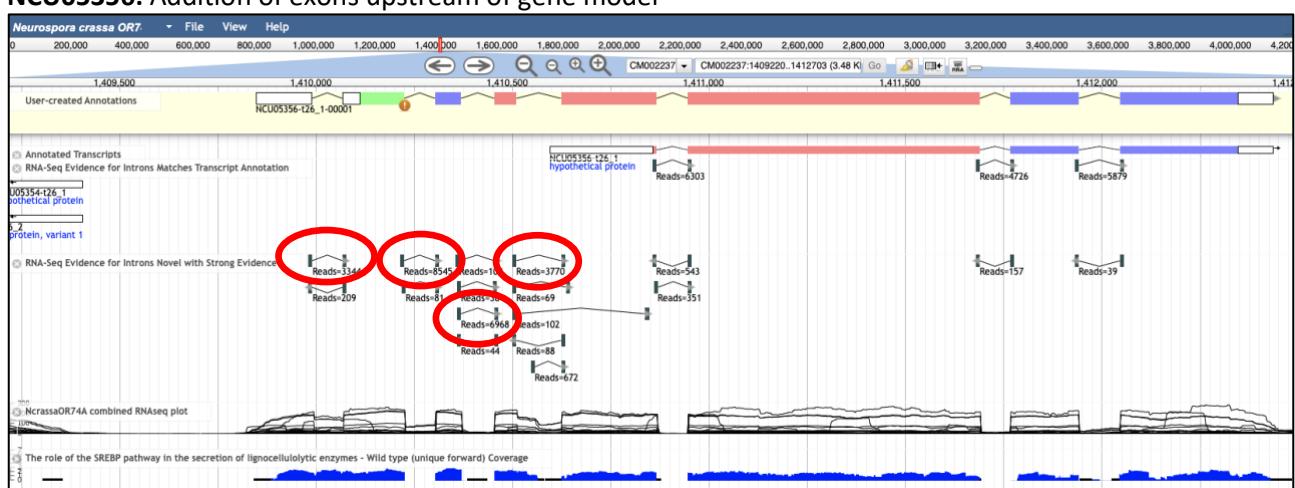


## CSON007381: addition of new gene, the new gene is replacing the long UTR of CSON007381

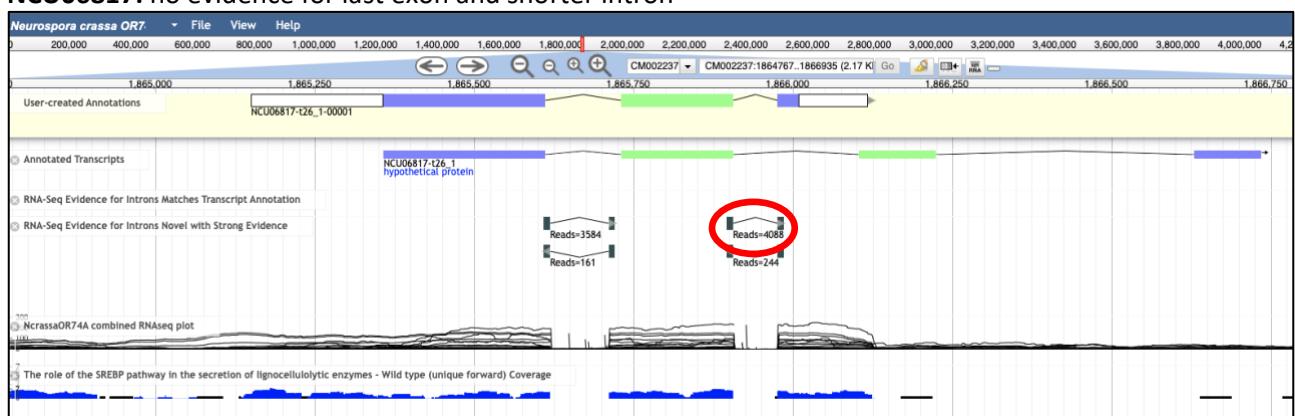


## *Neurospora crassa* OR74A

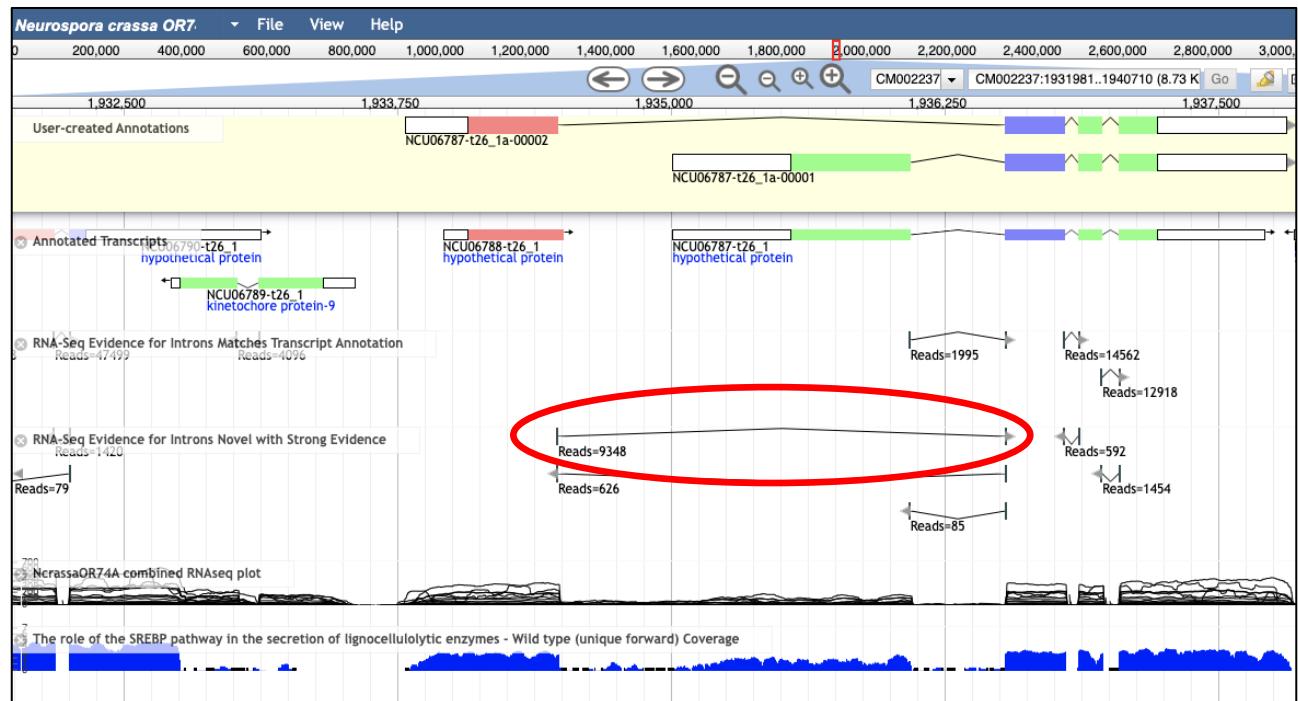
NCU05356: Addition of exons upstream of gene model



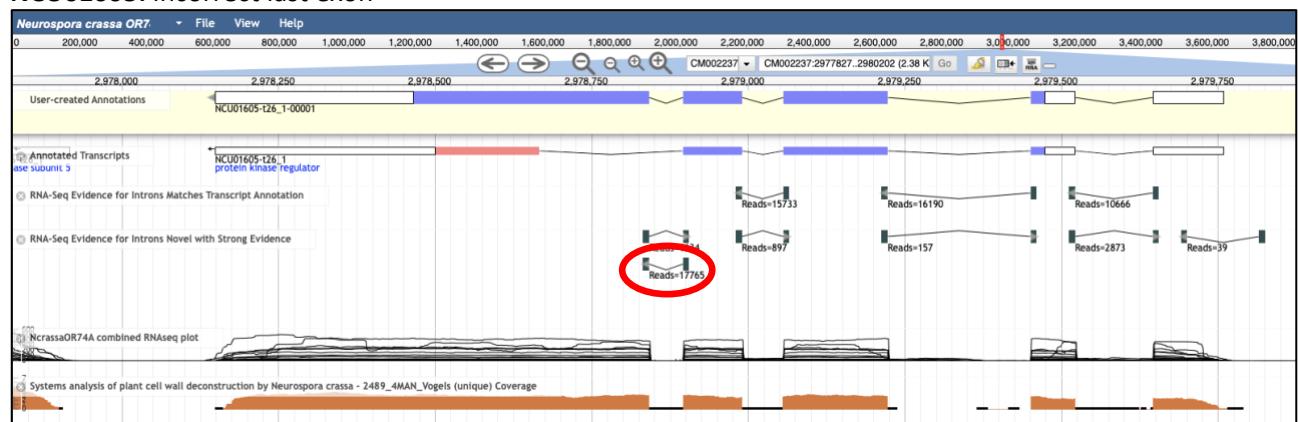
NCU06817: no evidence for last exon and shorter intron



## NCU06787: more dominant isoform needs to be created

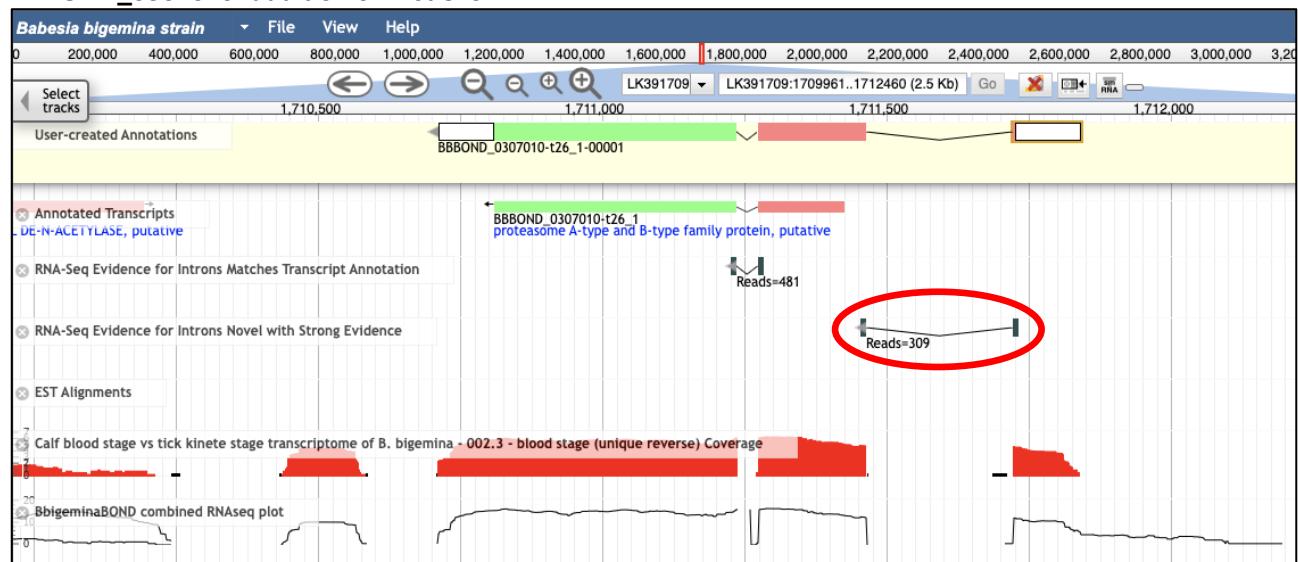


## NCU01605: incorrect last exon

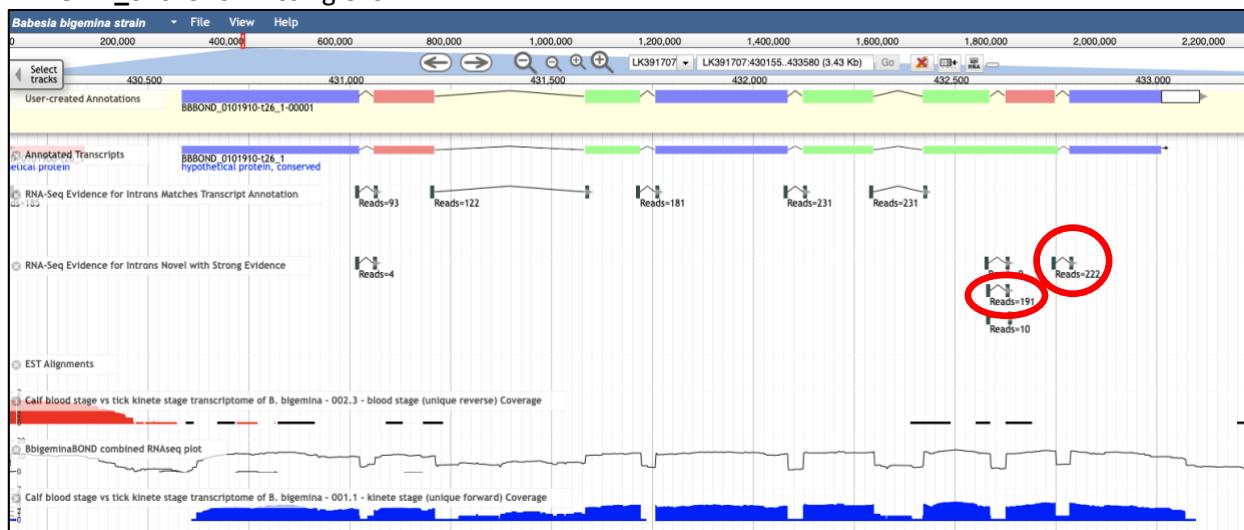


## Babesia bigemina strain BOND

### BBBOND\_0307010: addition of first exon



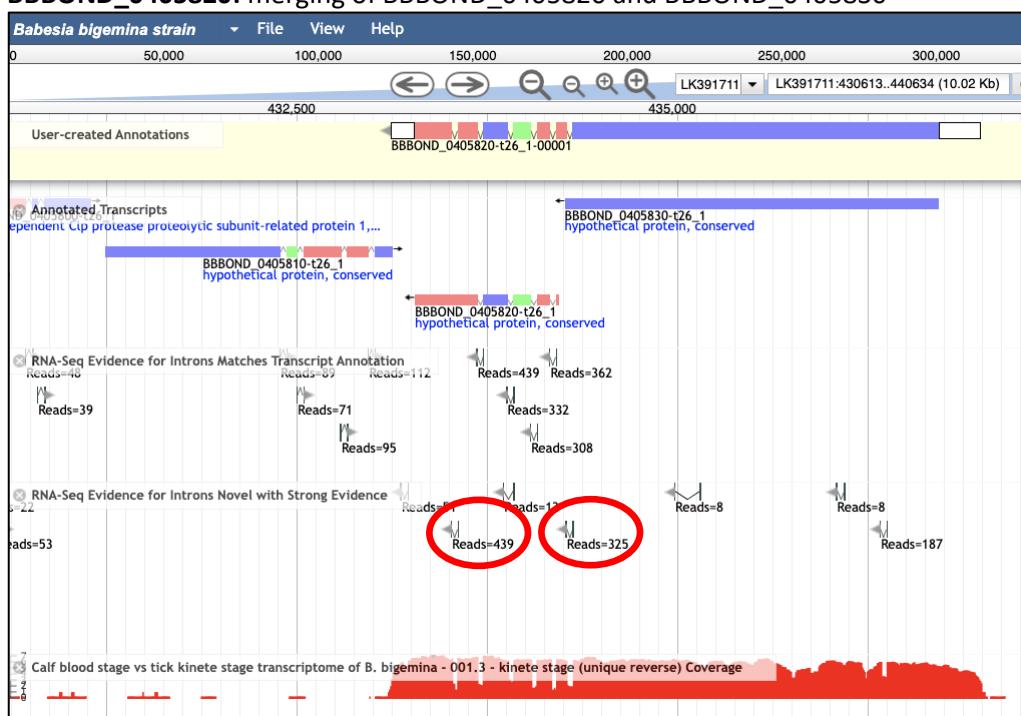
### BBBOND\_0101910: missing exon



### BBBOND\_0405460: addition of 3 exons



### BBBOND\_0405820: merging of BBBOND\_0405820 and BBBOND\_0405830

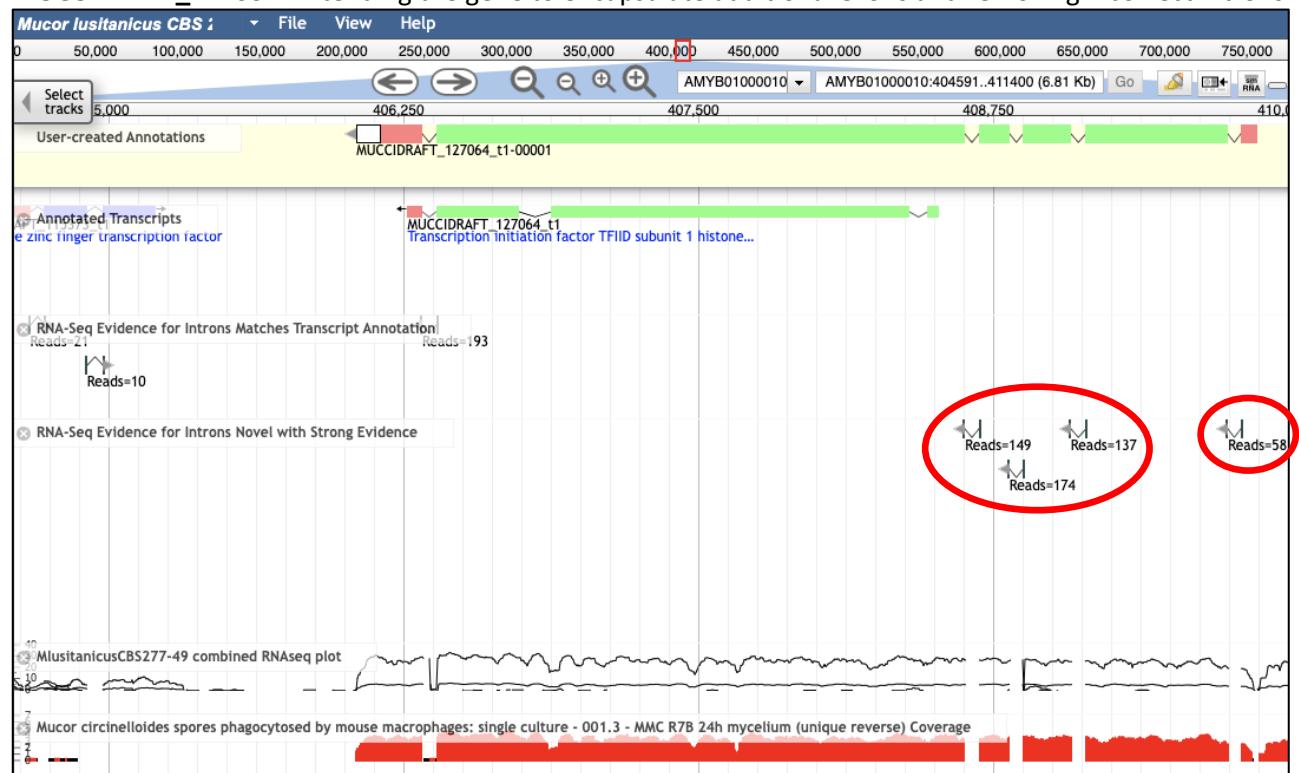


## *Mucor lusitanicus* CBS 277.49

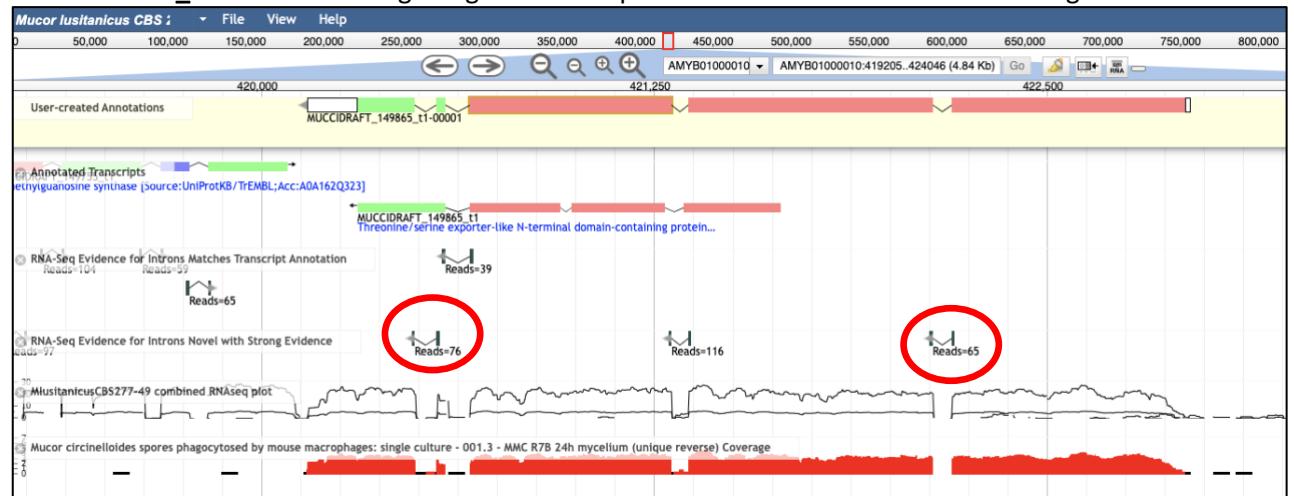
### MUCCIDRAFT\_156881: addition of two exons



### MUCCIDRAFT\_127064: Extending the gene to encapsulate additional exons and removing incorrect introns



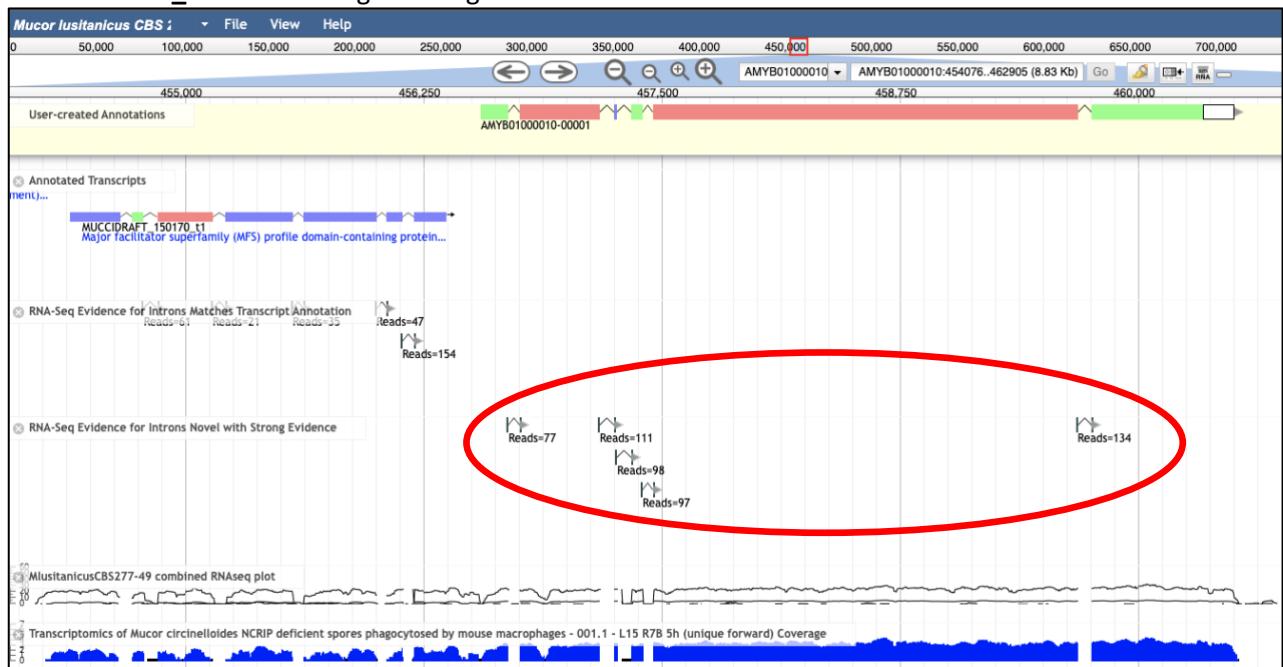
### MUCCIDRAFT\_149865: extending the gene to encapsulate additional exons and removing incorrect introns



## MUCCIDRAFT\_149755: extending the gene to encapsulate additional exons and removing incorrect introns

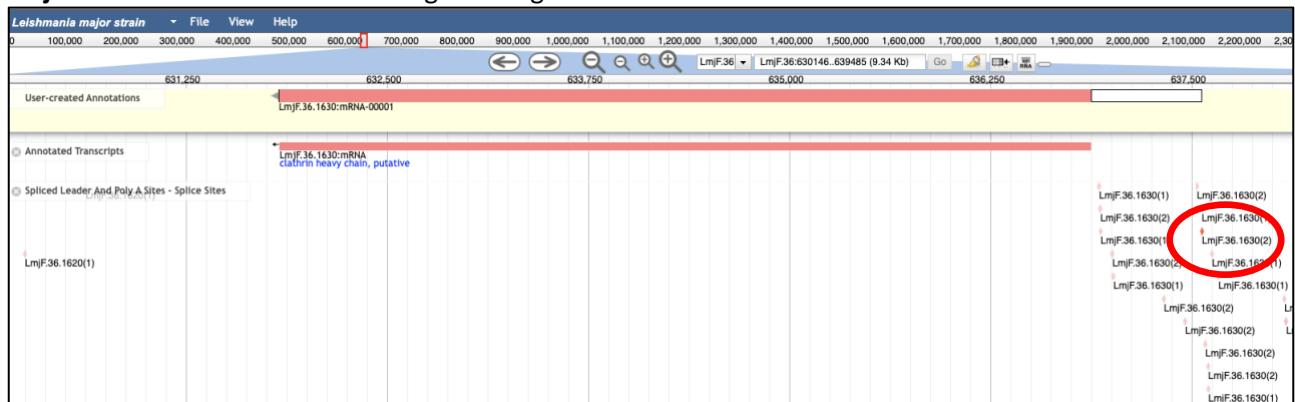


## MUCCIDRAFT\_150170: adding of new gene

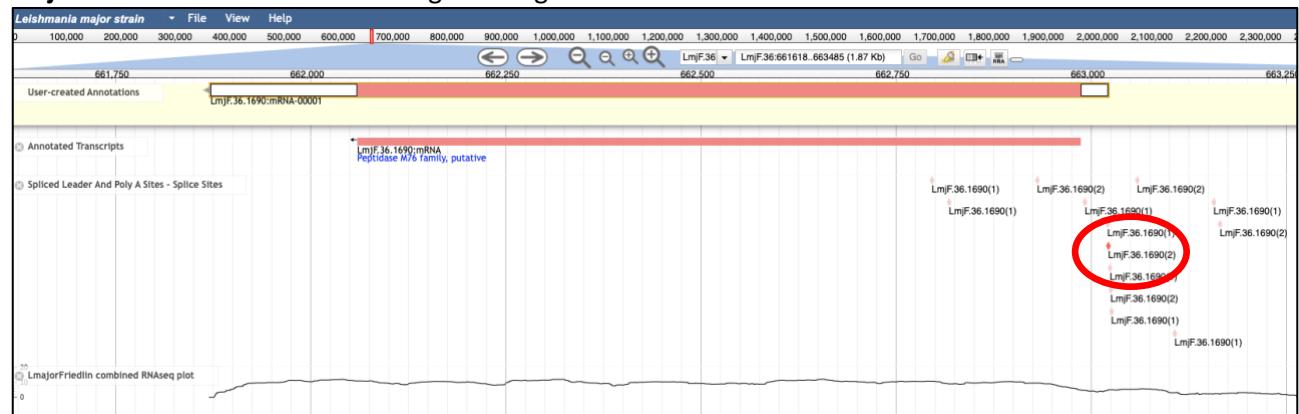


## Leishmania major strain Friedlin

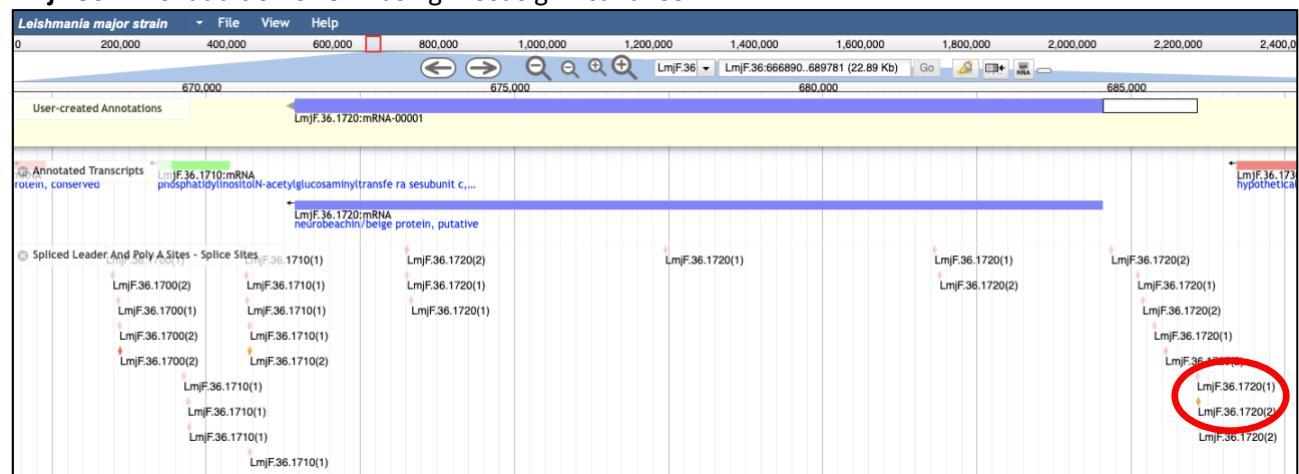
### LmjF.36.1630: addition of UTR using most significant TSS



### 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

