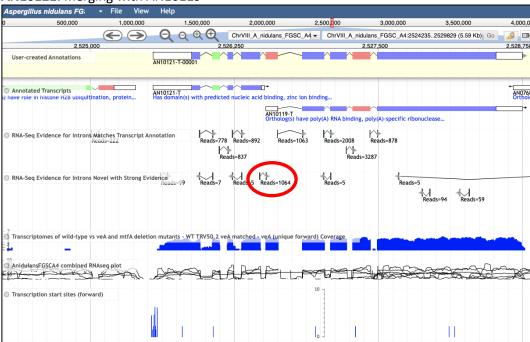
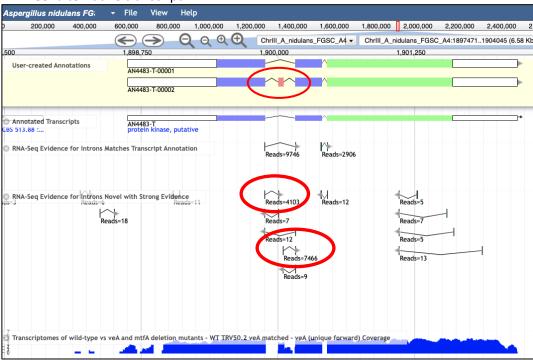
Evaluating gene models (key)

Aspergillus nidulans FGSC A4

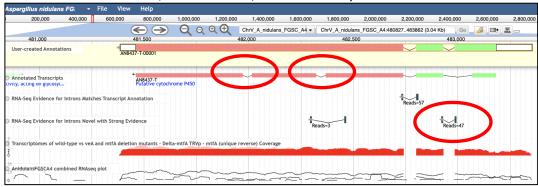
AN10121: merging with AN10119



AN4483: alternative transcript



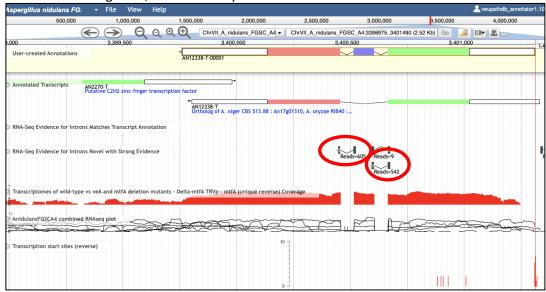
AN8437: incorrect introns, incorrect exon/intron boundary



AN11226: missing exon, 5'UTR



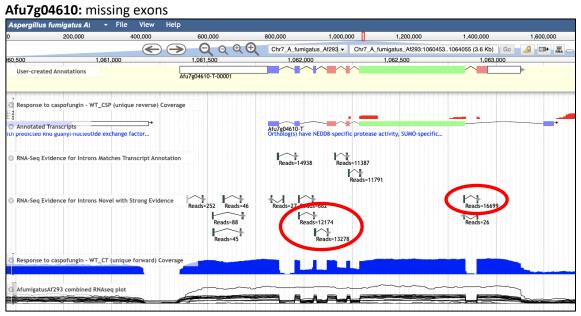
AN12338: missing exon, UTR boundary



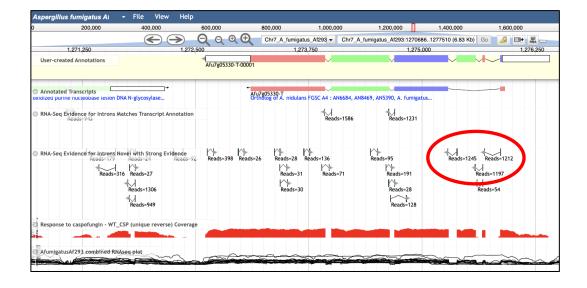
Aspergillus fumigatus Af293

Afu8g02770: missing exon, missing UTRs

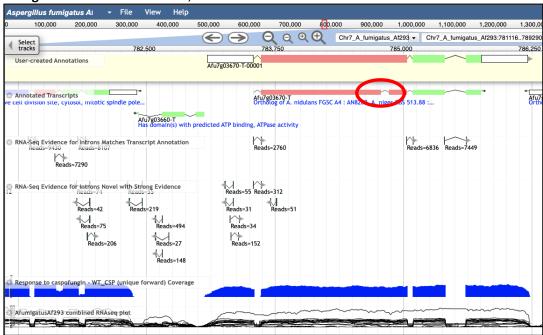




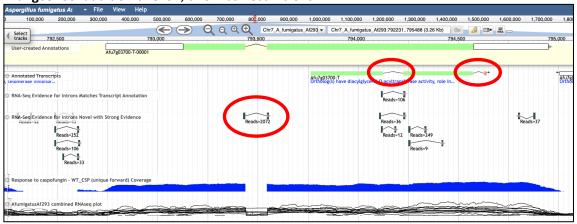
Afu7g05330: addition of exons



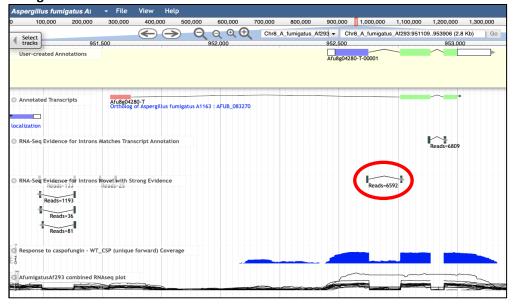
Afu7g03670: deletion of intron, addition of UTRs



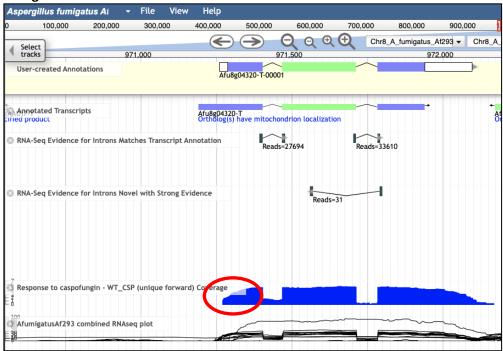
Afu7g03700: addition of exon, two incorrect introns



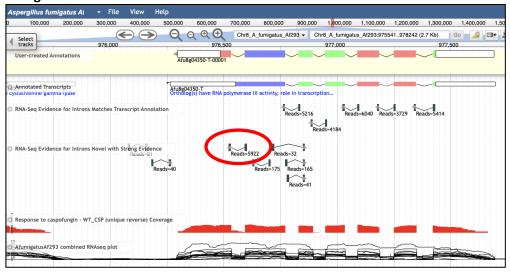
Afu8g04280: incorrect first exon



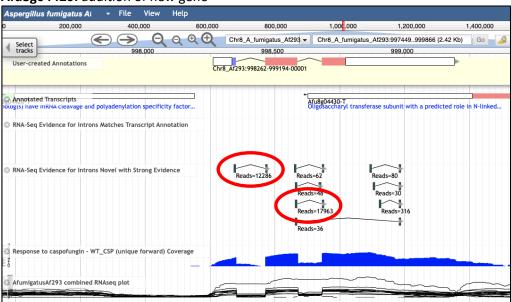
Afu8g04320: incorrect start



Afu8g04350: addition of exon

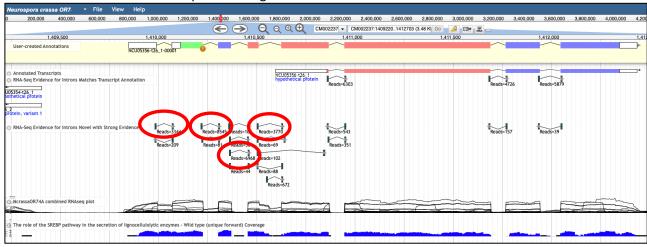


Afu8g04420: addition of new gene

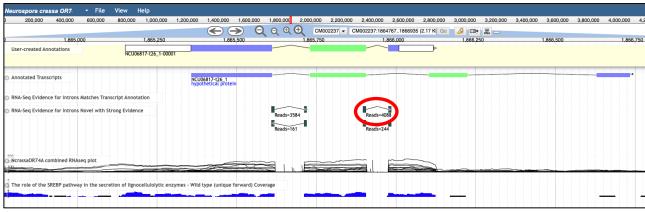


Neurospora crassa OR74A

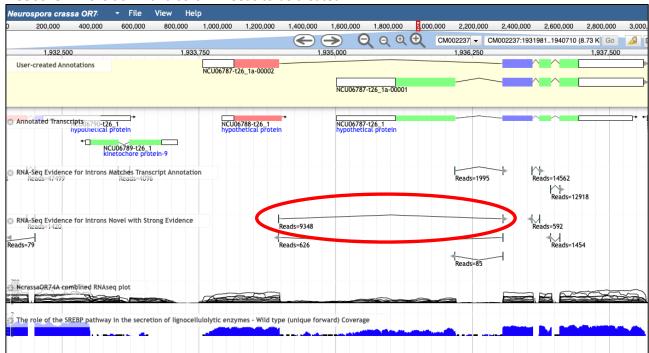
NCU05356: Addition of exons upstream of gene model



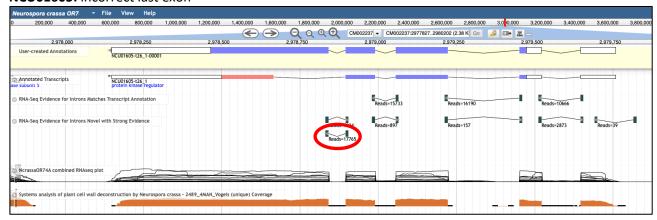
NCU06817: no evidence for last exon and shorter intron



NCU06787: more dominant isoform needs to be created



NCU01605: incorrect last exon

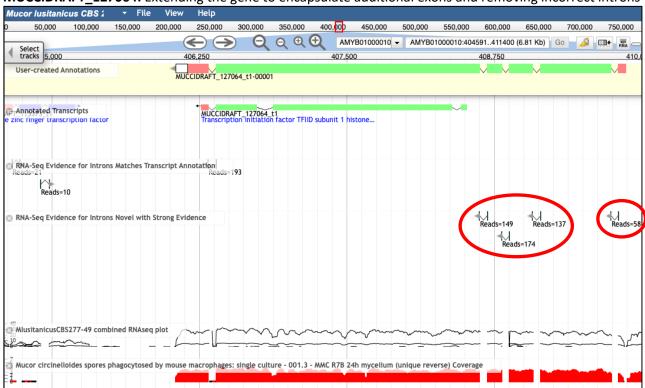


Mucor lusitanicus CBS 277.49

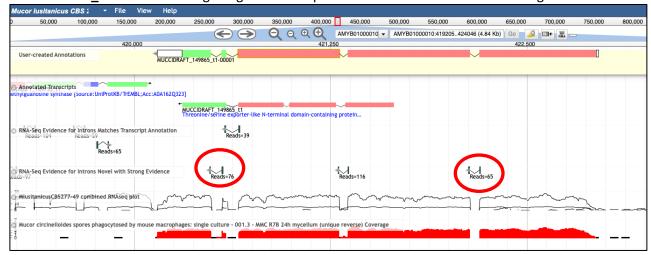
MUCCIDRAFT_156881: addition of two exons



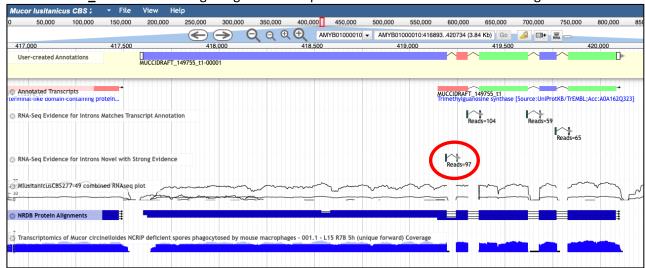
MUCCIDRAFT_127064: Extending the gene to encapsulate additional exons and removing incorrect introns



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

