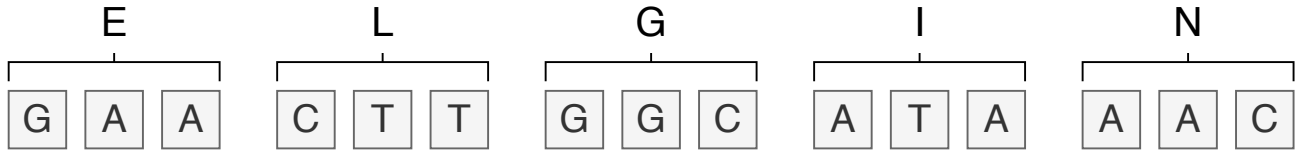
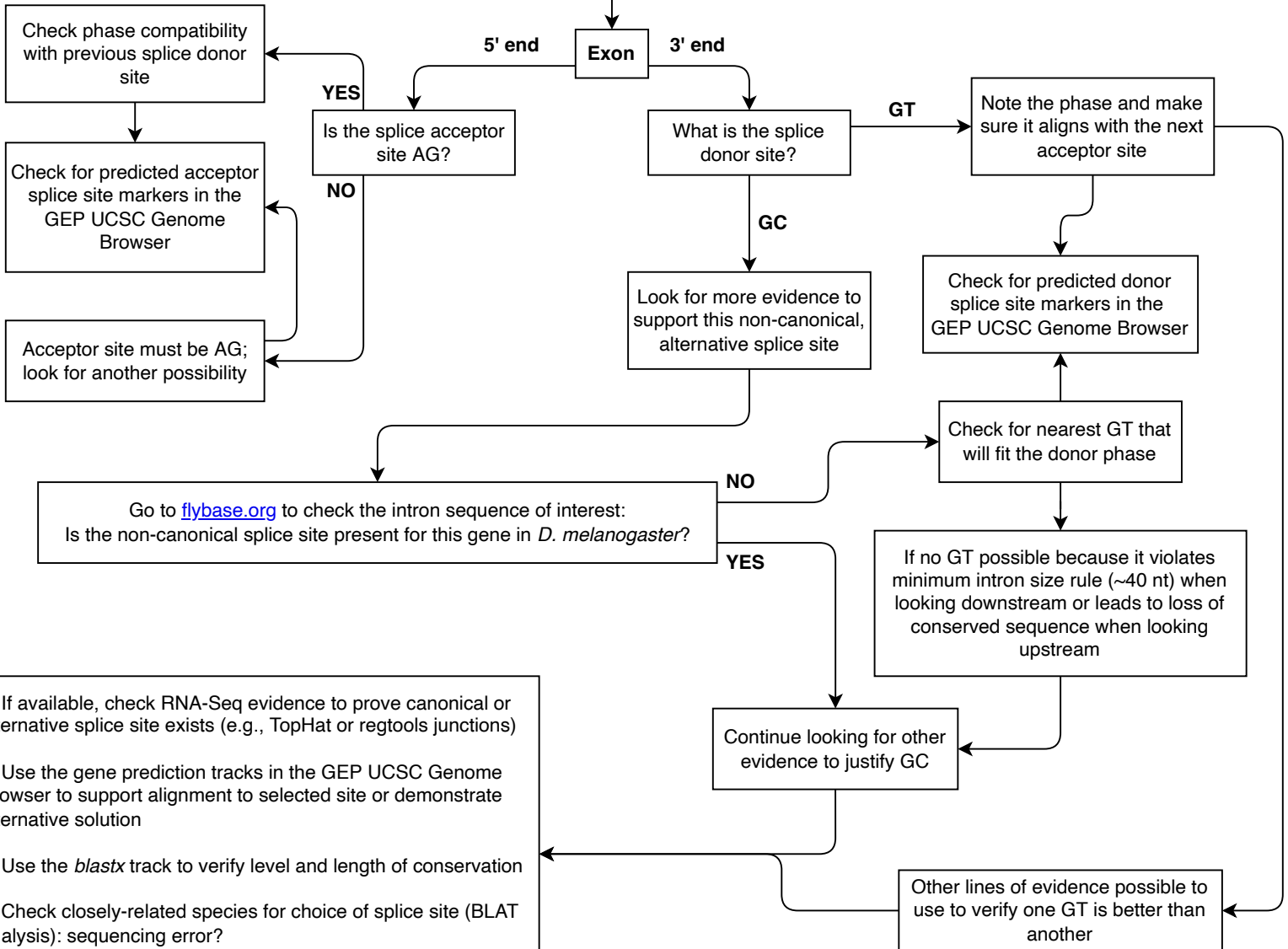


# Determining CDS Coordinates



**tblastn**  
**query** - CDS for *D. melanogaster* exon  
**subject** - nucleotide (nt) sequence of interest (turn off low complexity filter and use no compositional adjustment)

For **highly conserved alignments**: look for splice sites nearest the exon boundaries  
 For **less conserved alignments**: attempt to extend the exon boundaries to include additional sequence from the Open Reading Frame (ORF), while still maintaining correct splice phases; conserve exon size



1. If available, check RNA-Seq evidence to prove canonical or alternative splice site exists (e.g., TopHat or regtools junctions)
2. Use the gene prediction tracks in the GEP UCSC Genome Browser to support alignment to selected site or demonstrate alternative solution
3. Use the *blastx* track to verify level and length of conservation
4. Check closely-related species for choice of splice site (BLAT analysis): sequencing error?
5. Perform Clustal Omega searches to test level of conservation between species