Supplementary Figure 2: Schematic representation of the resolution of several gene models identified in this work. The annotated transcript is represented with a black, with the SL Acceptor sites represented with arrows above, BLAST hits with other genes bellow with colored boxes and the selected chimeric portions with arches. A) In the classical case there is a single SL-ACE that separated two halves with different sets of hits. B) If there are additional SL-ACEs but it is not reflected on changes on the hits it was assumed the SL-ACE was ignored. C) Cases where there are multiple SL-ACEs that separate both sets of hits were used to narrow down the intergenic space by excluding the sequence between them. In an analogous case, if SL-ACEs were D) upstream or E) downstream areas, separating genes with no BLAST hits, those sequences were trimmed down. F) A third gene in the chimeric gene model required that the SL-ACEs separated three discrete areas with their own sets of BLAST Hits. G) Cases where subdivisions where the boundary between genes was unclear were excluded.