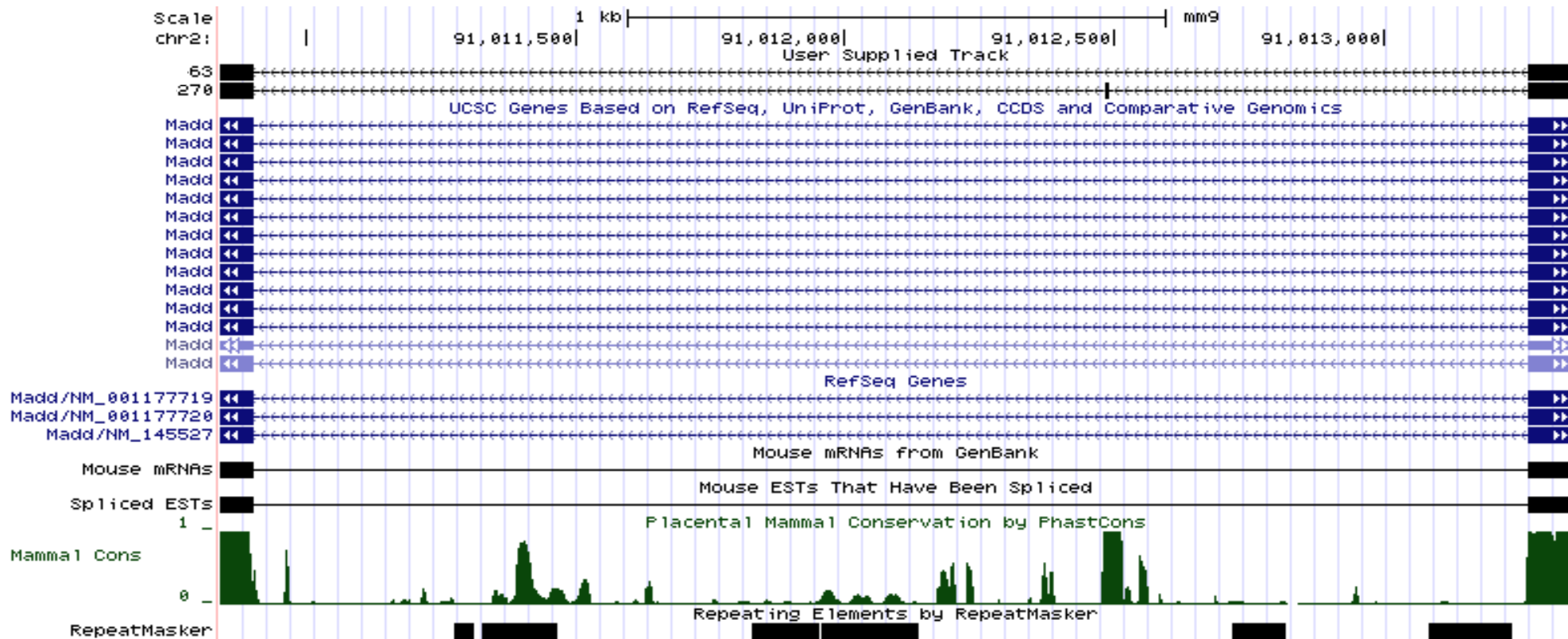


**Supplementary Figure 1:** Number of micro-exons identified by OLEgo and the other three programs.

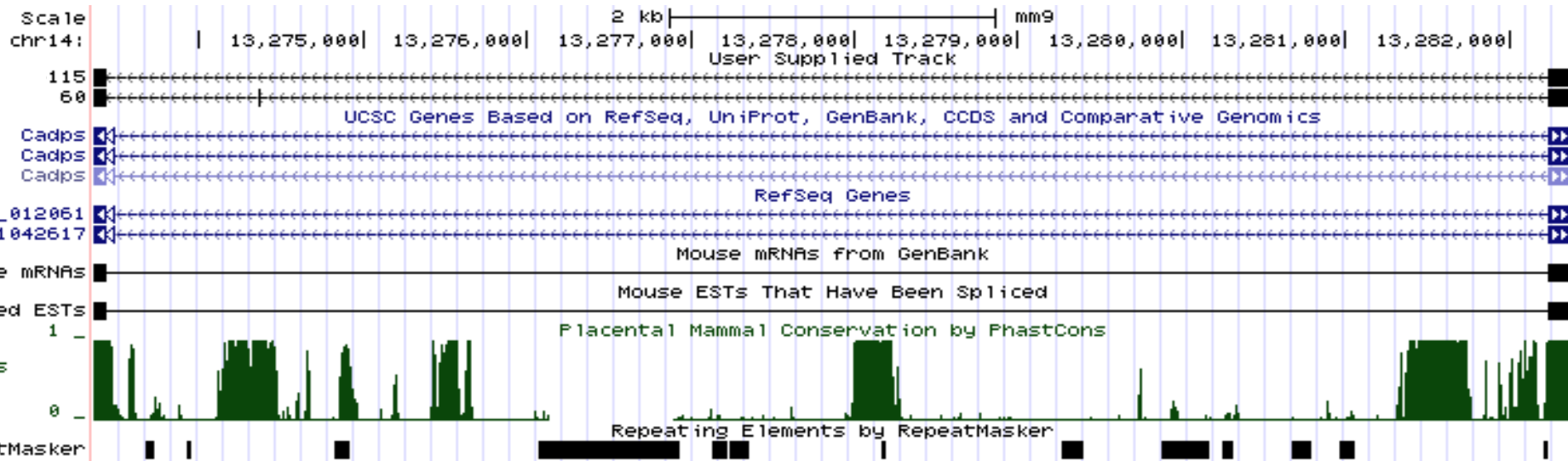
Exons are binned by their sizes (9~27nt), and in each bin, they are classified into three groups: annotated micro-exons in previous gene models (blue), high-confidence novel micro-exons (exons with both flanking constitutive splice sites annotated; green), and other exons (red).

**Supplementary Figure 2: UCSC genome browser screenshots of the validated micro-exons.**

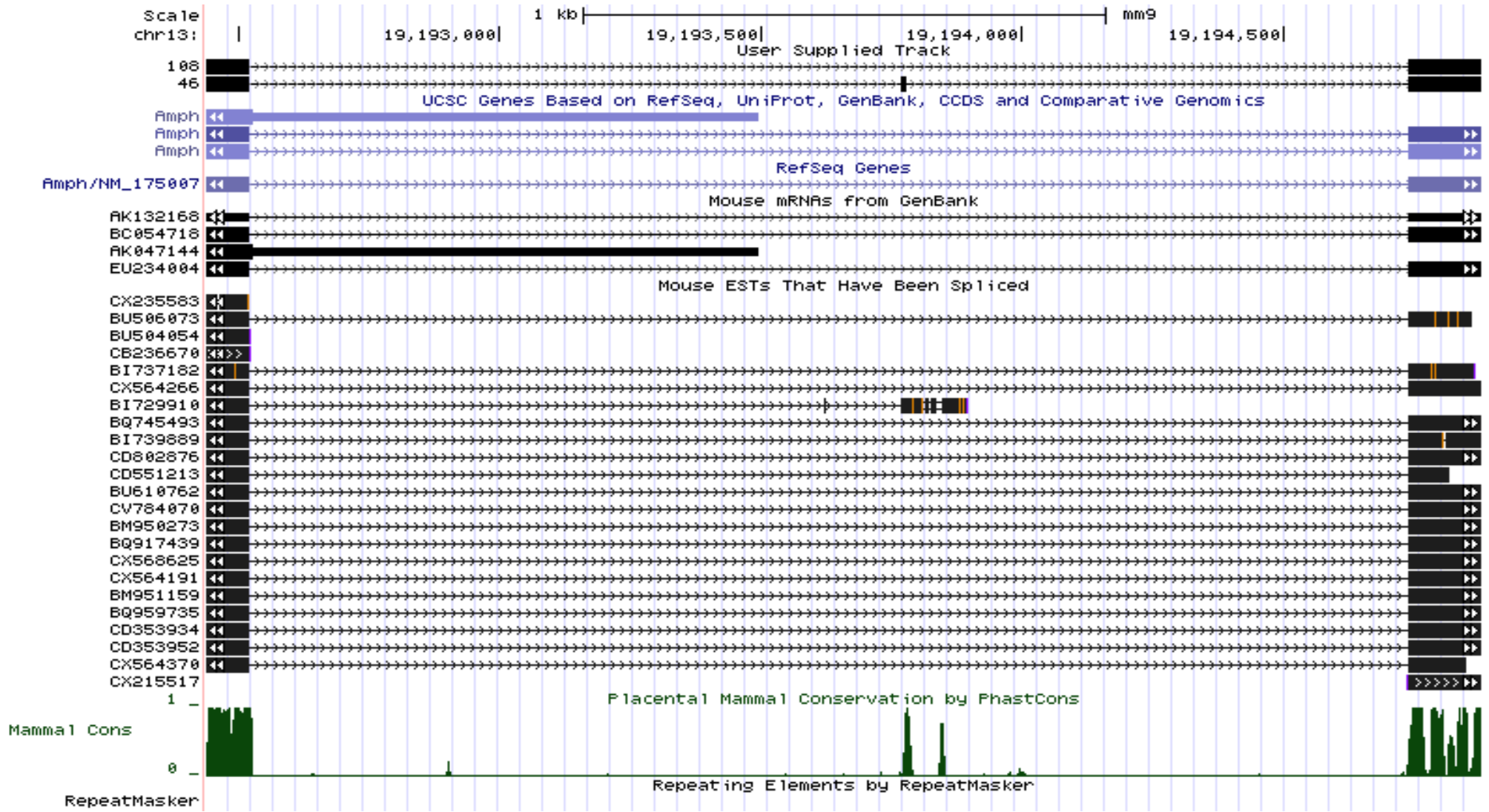
Structures of the inclusion and exclusion isoforms are shown in the user supplied track. The number of supporting reads is indicated to the left of each isoform. Known transcript structures ( UCSC genes, RefSeq genes and ESTs ) are also shown in the screenshots. The micro-exons are in the same order as they are listed in Supplementary Table 2.



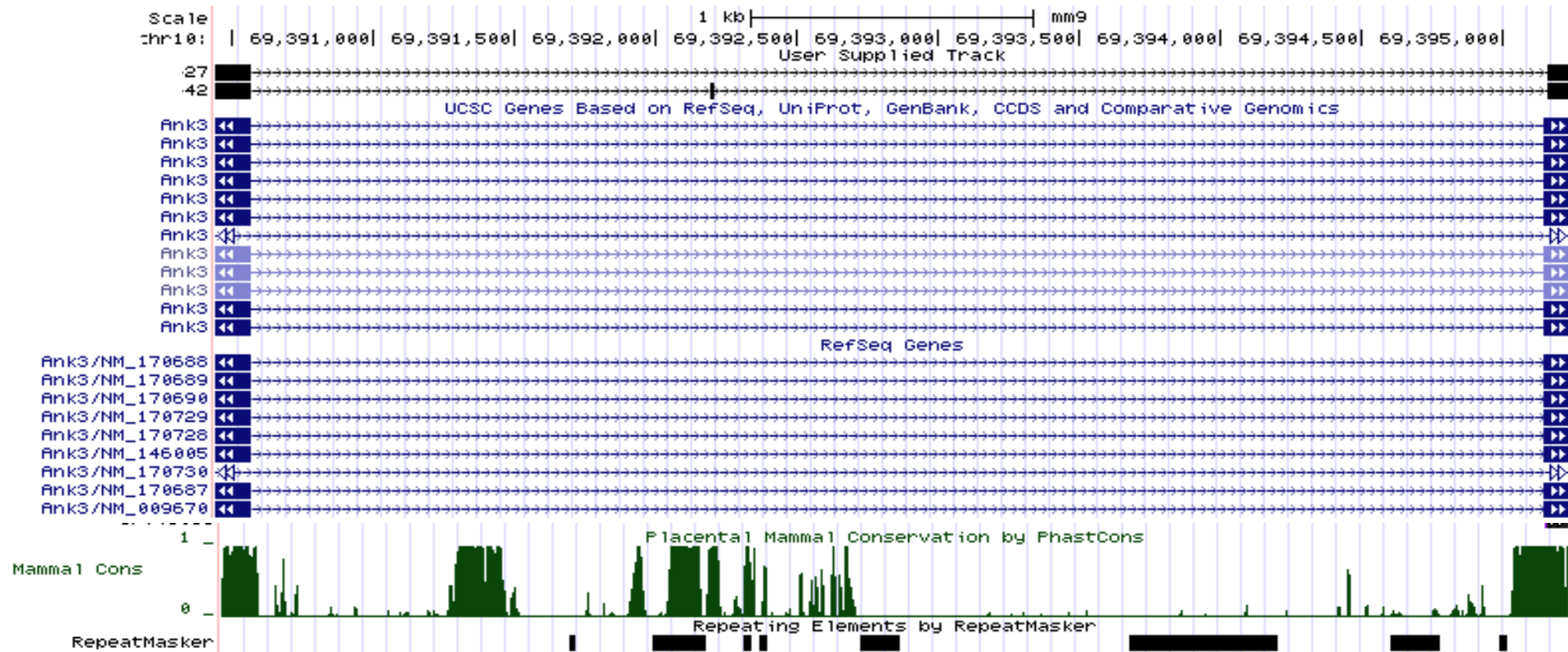
*Madd*



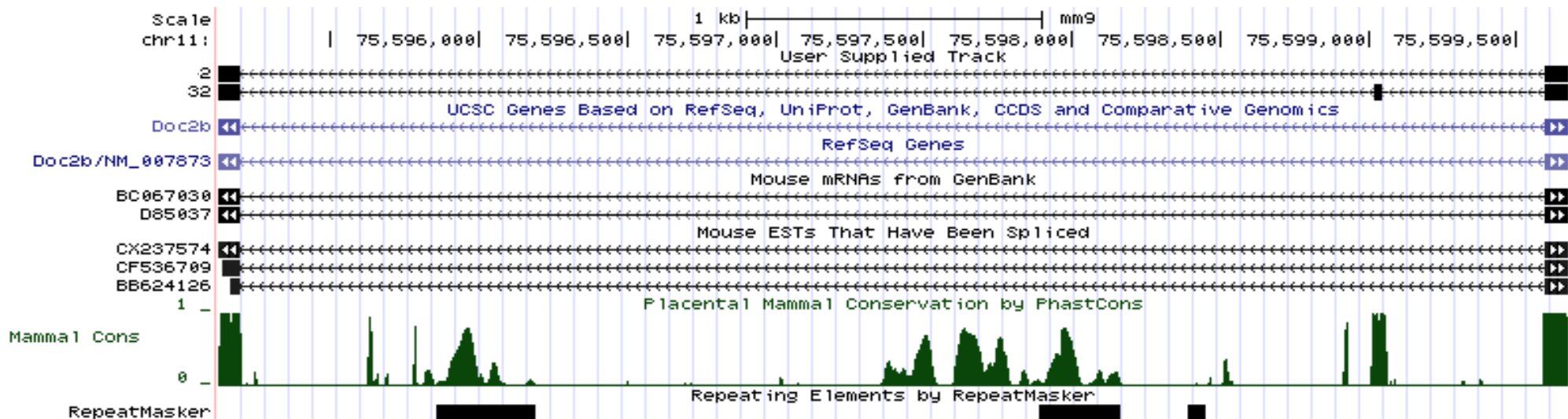
*Cadps*



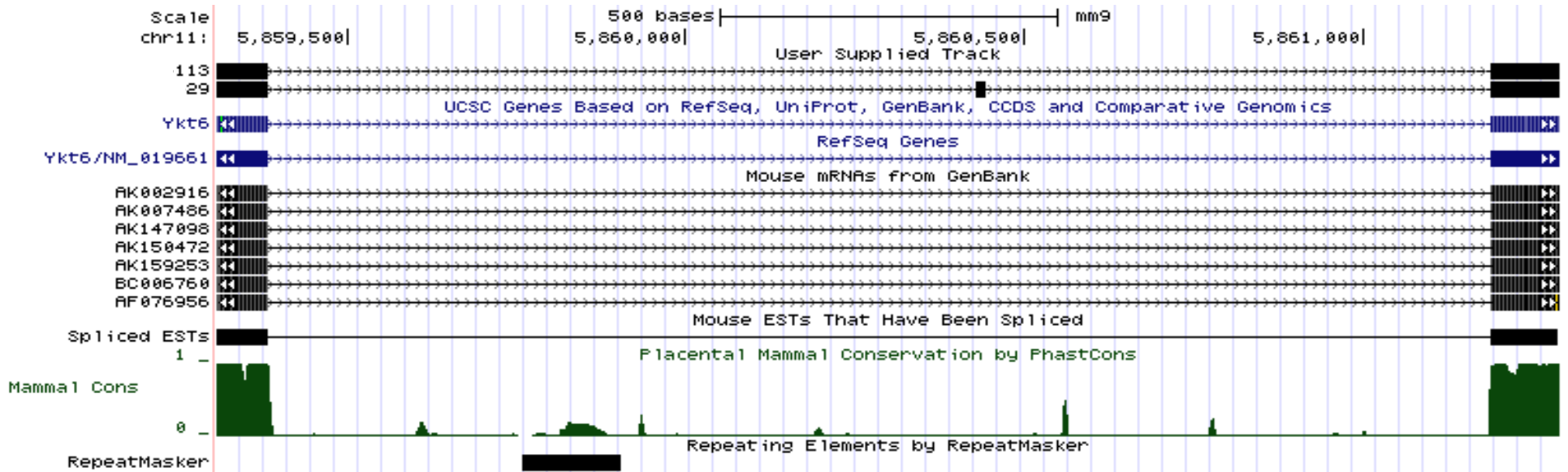
*Amph*



**Ank3**

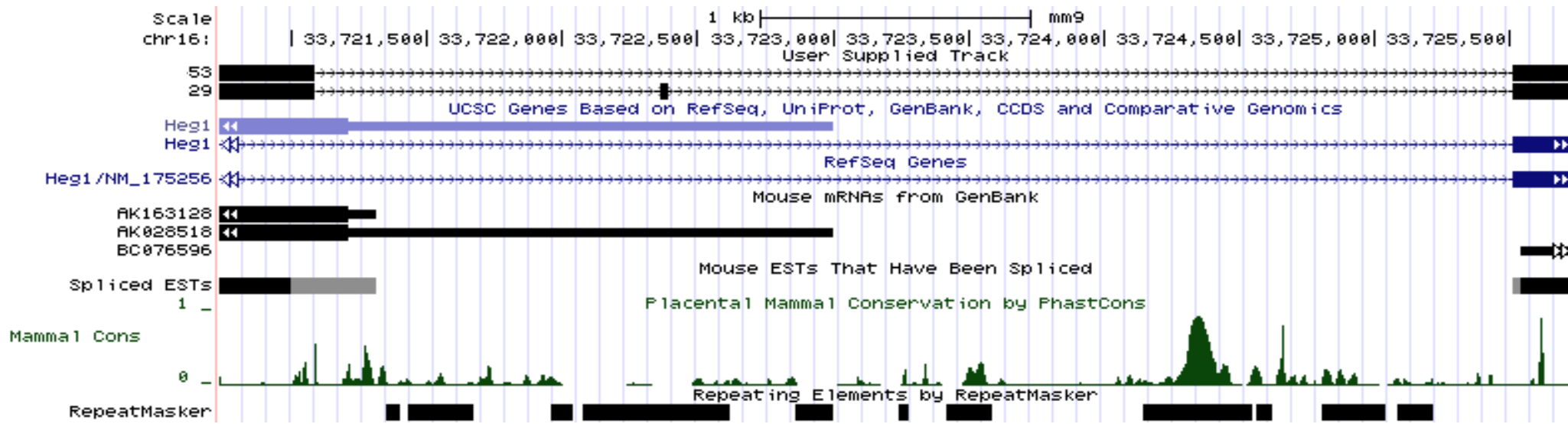


*Doc2b*

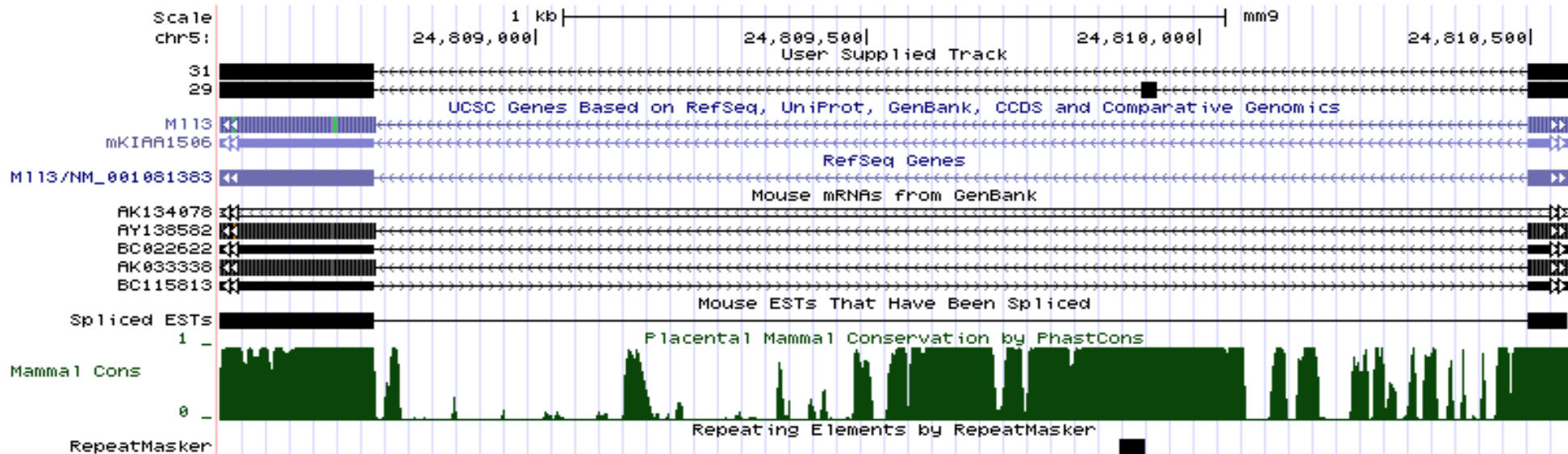


**Ykt6**

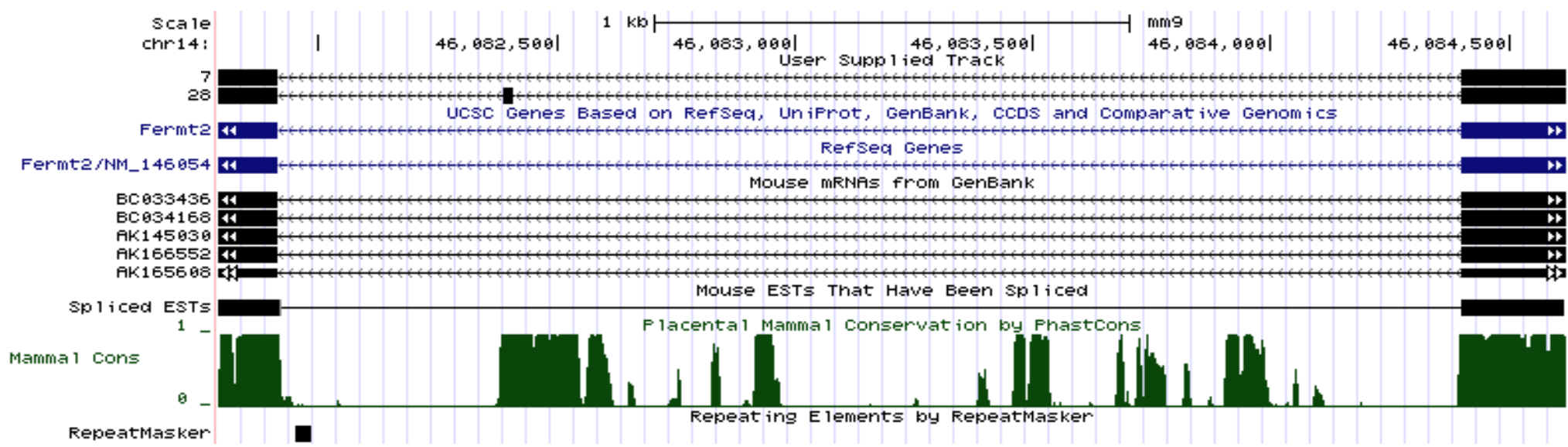




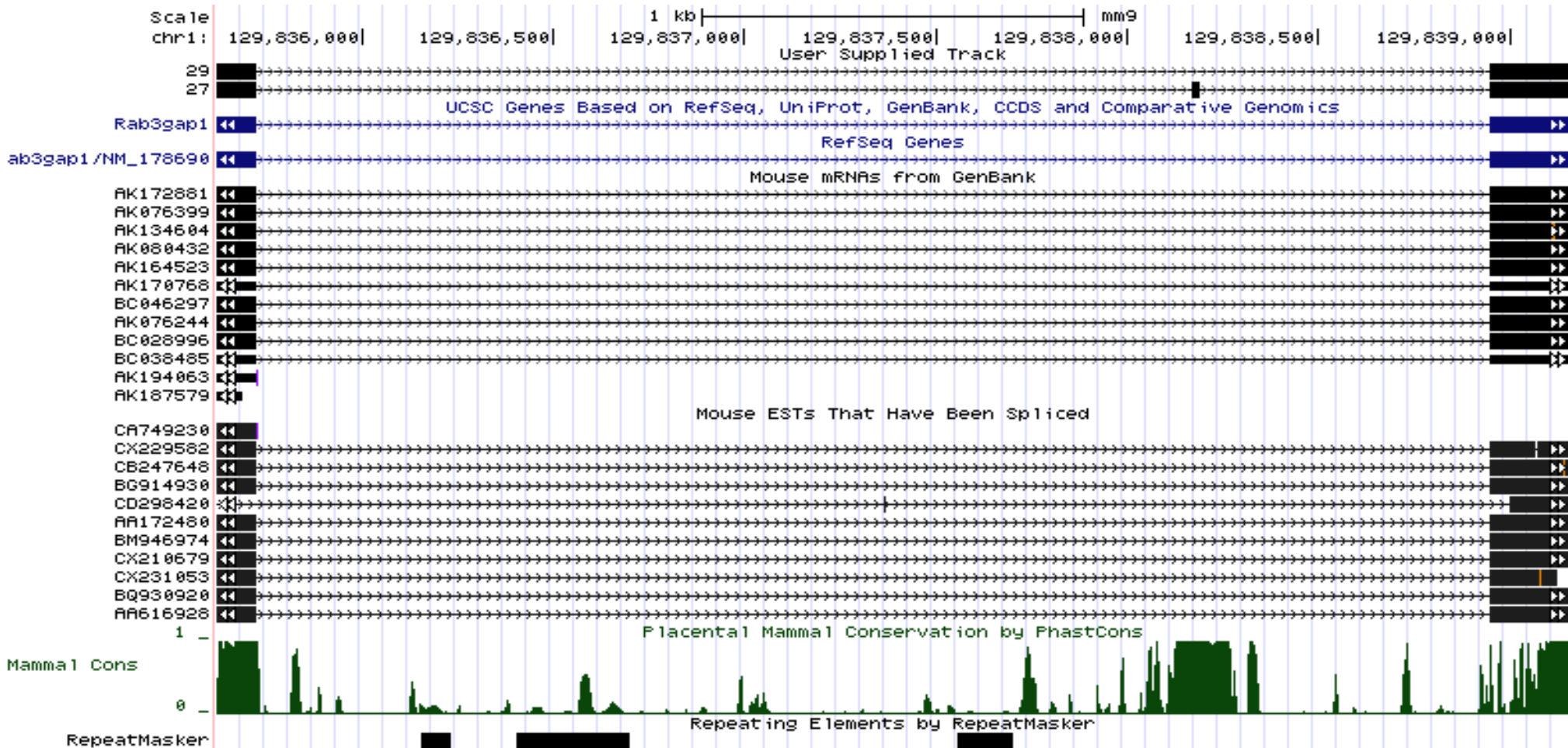
*Heg1*



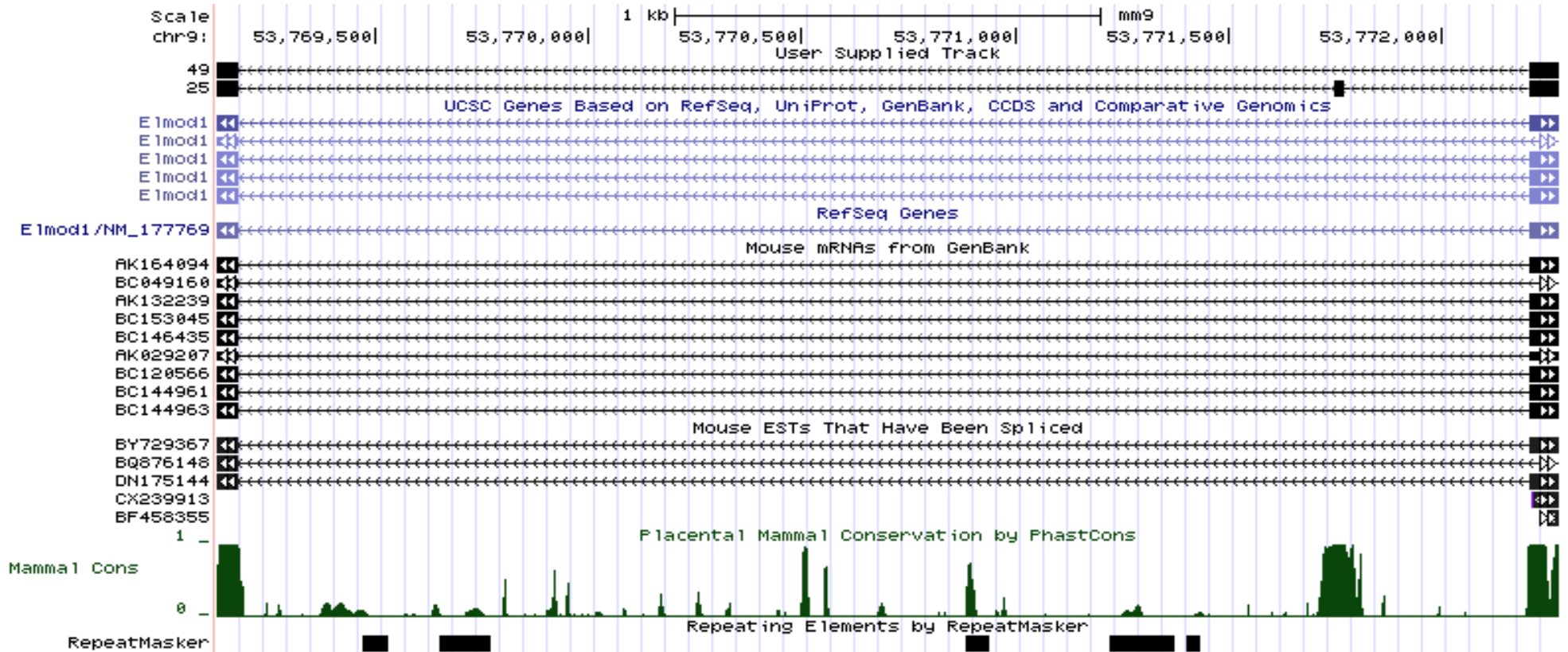
***M113***



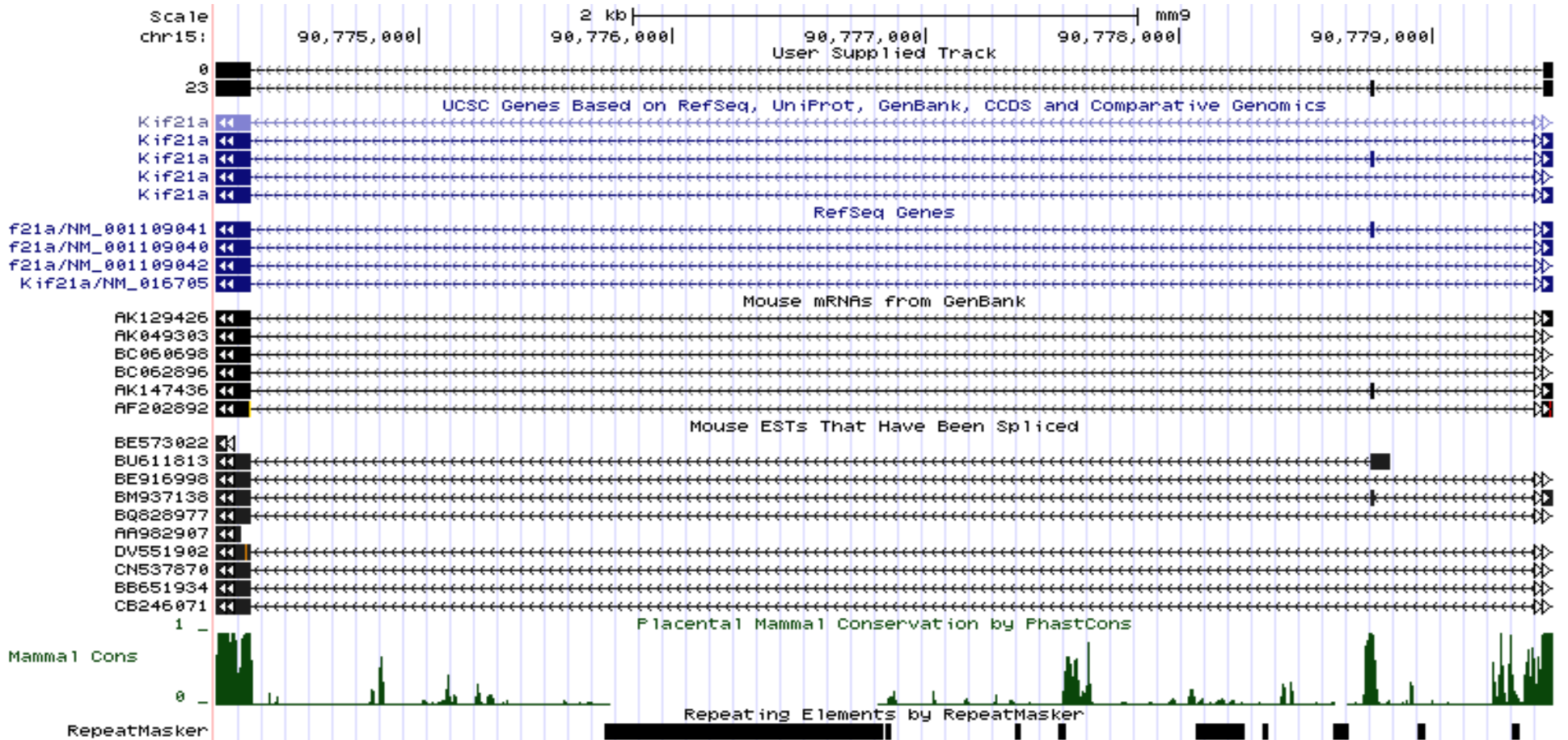
***Fermt2***



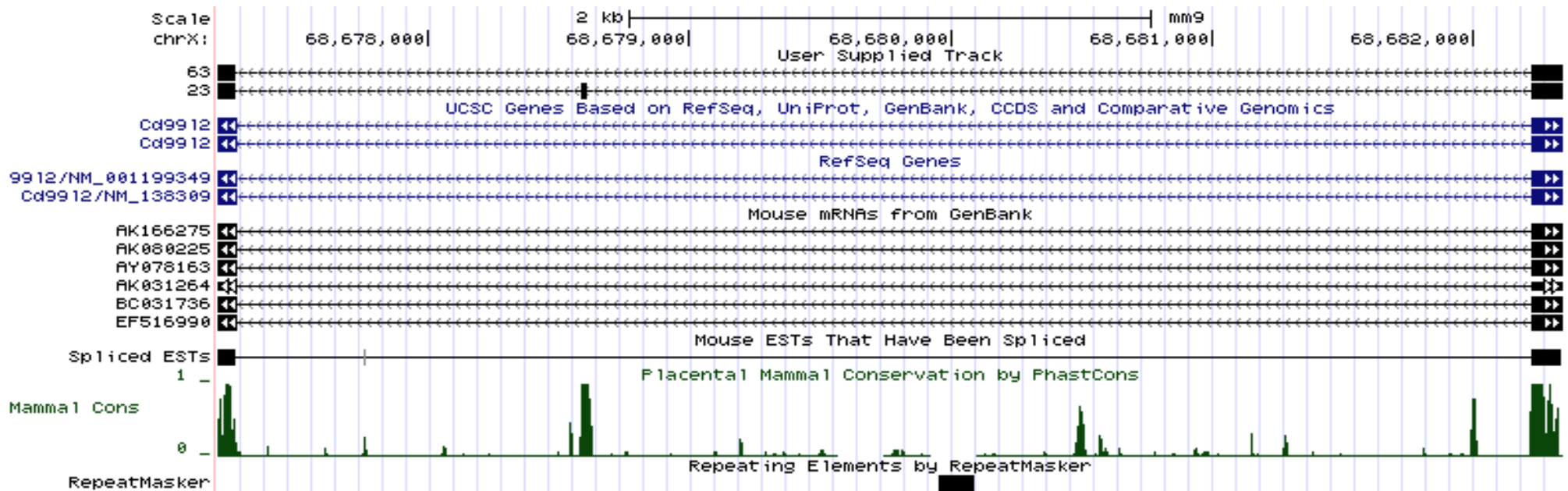
***Rab3gap1***



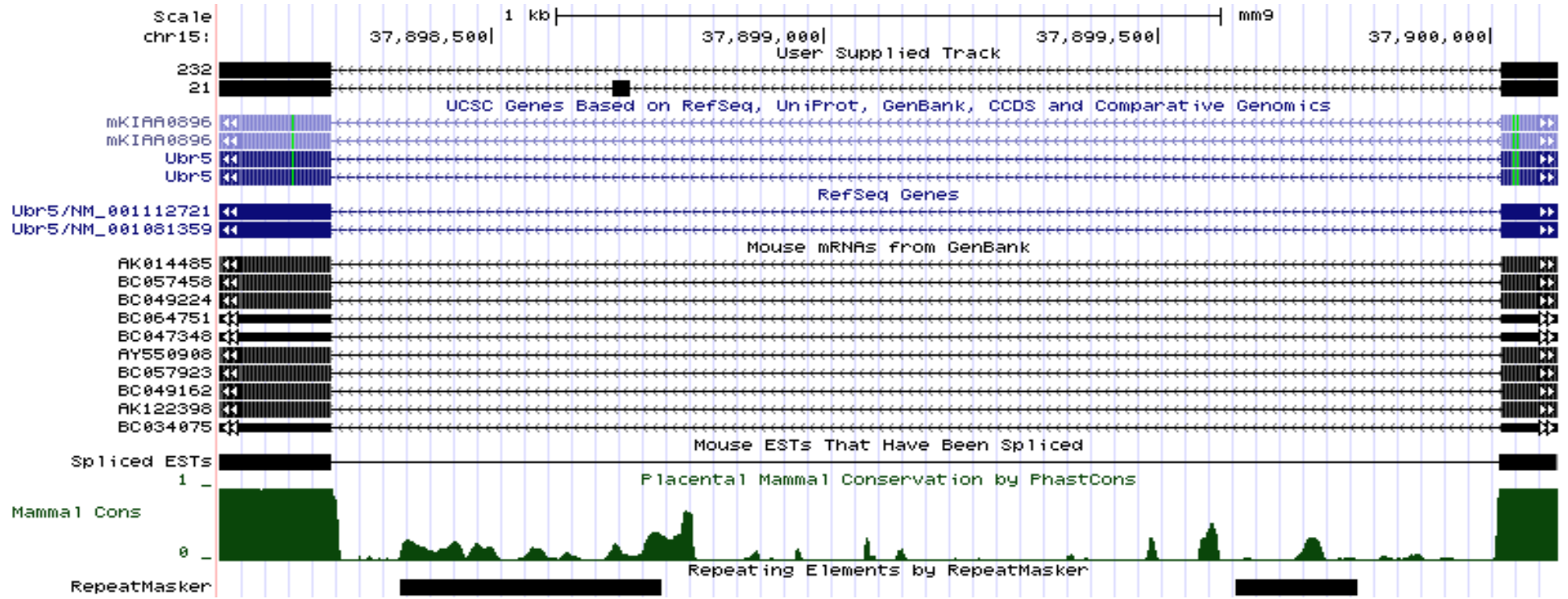
*Elmod1*



***Kif21a***

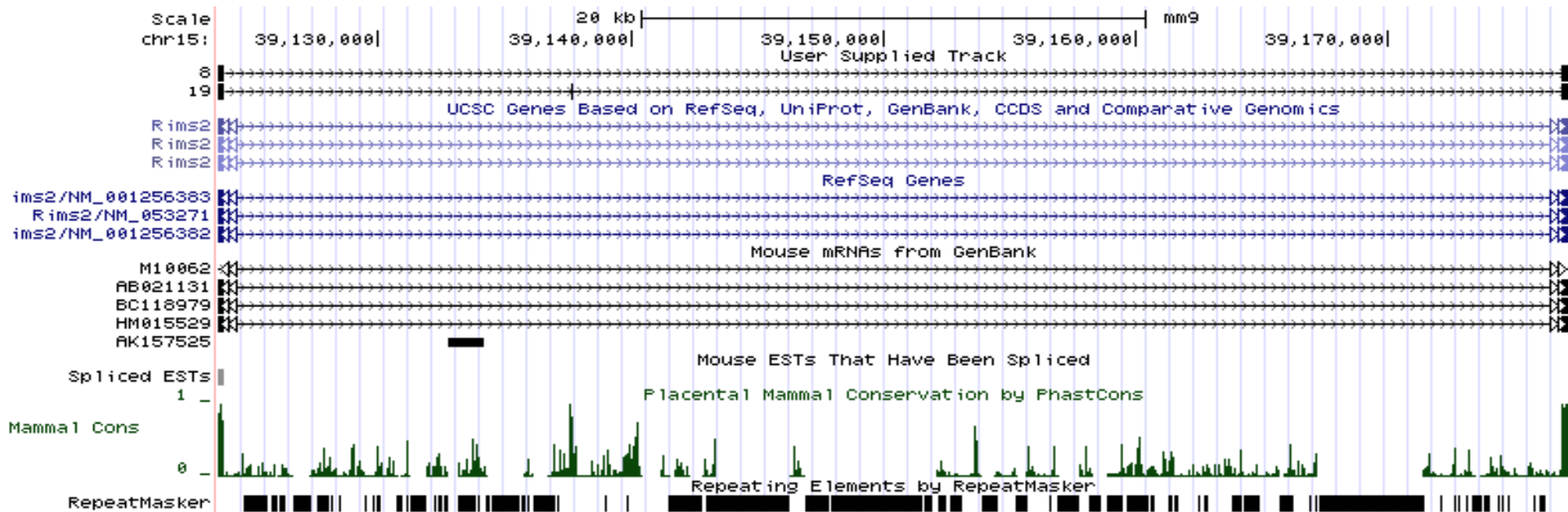


***Cd9912***



***Ubr5***





***Rims2***