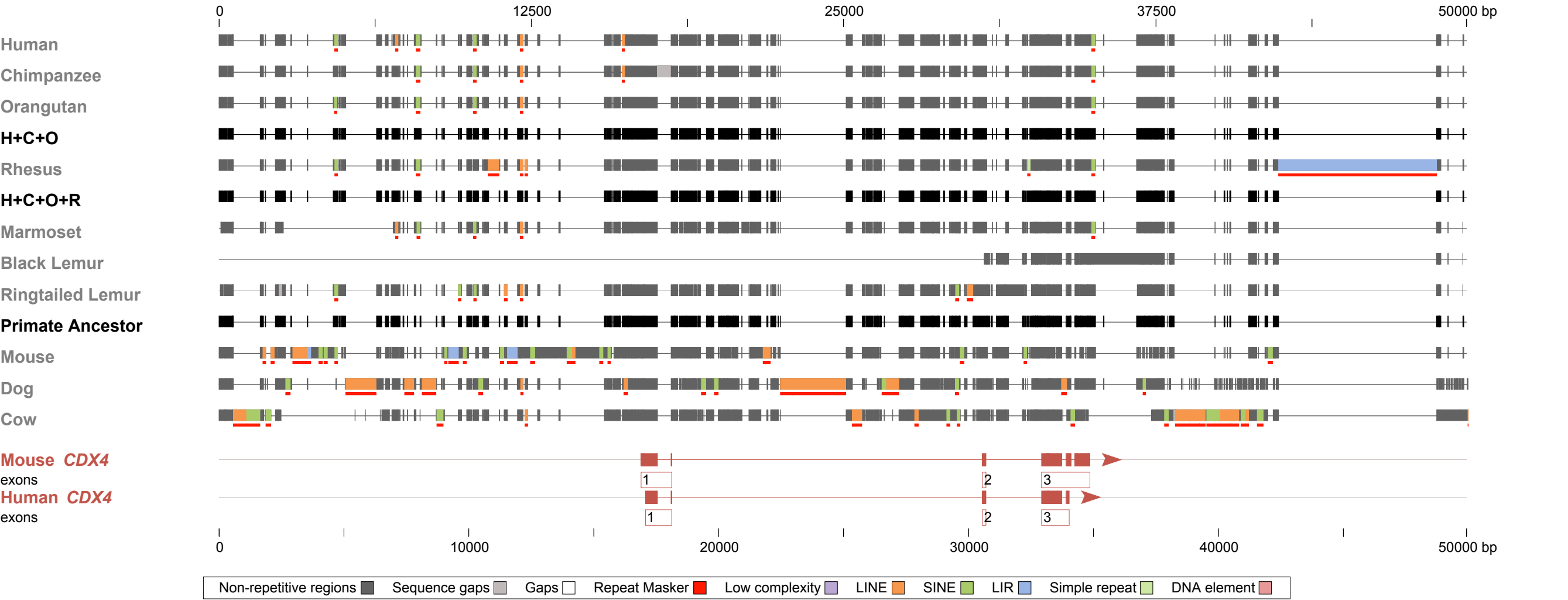
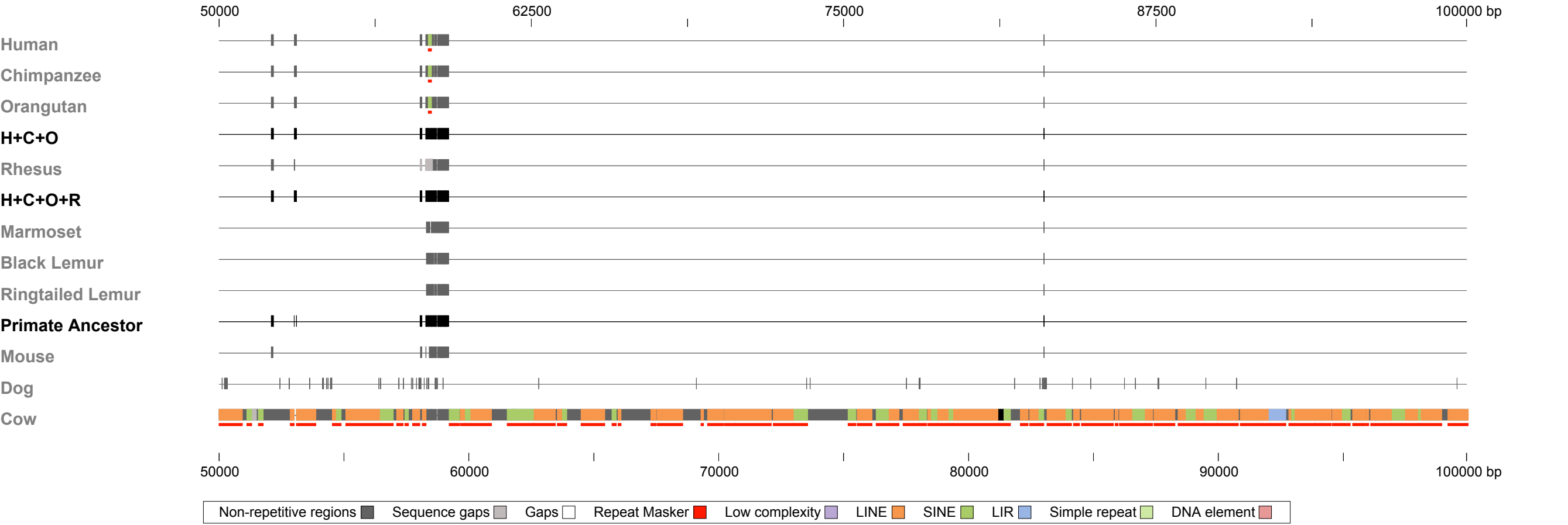
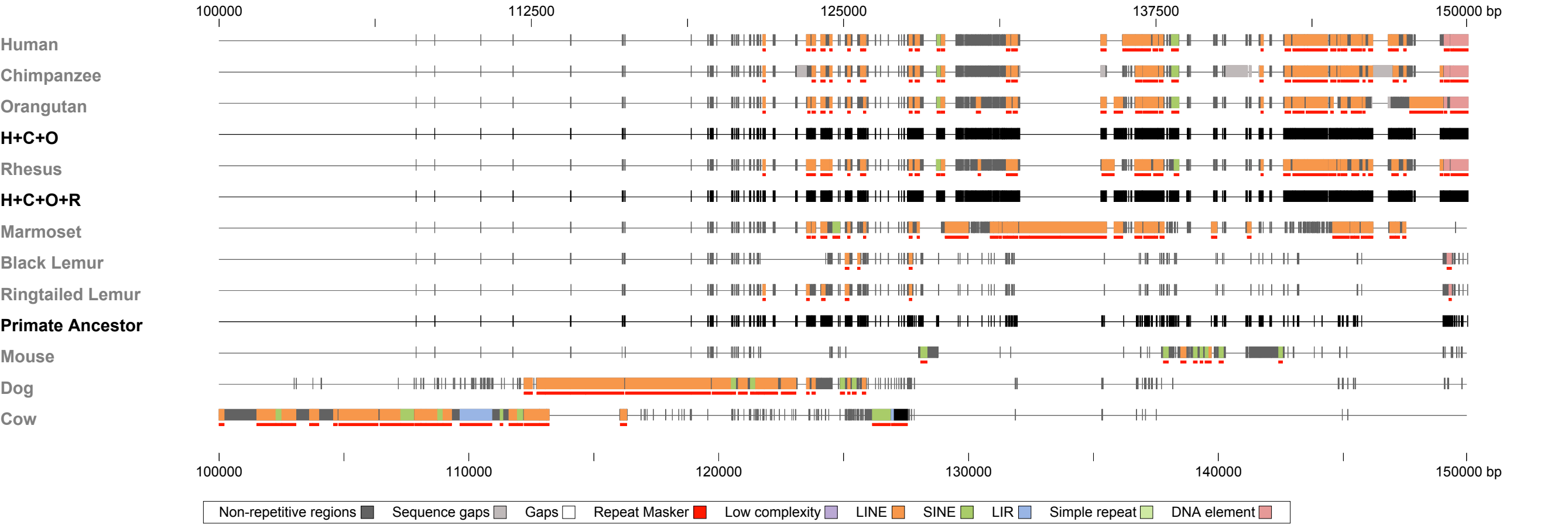
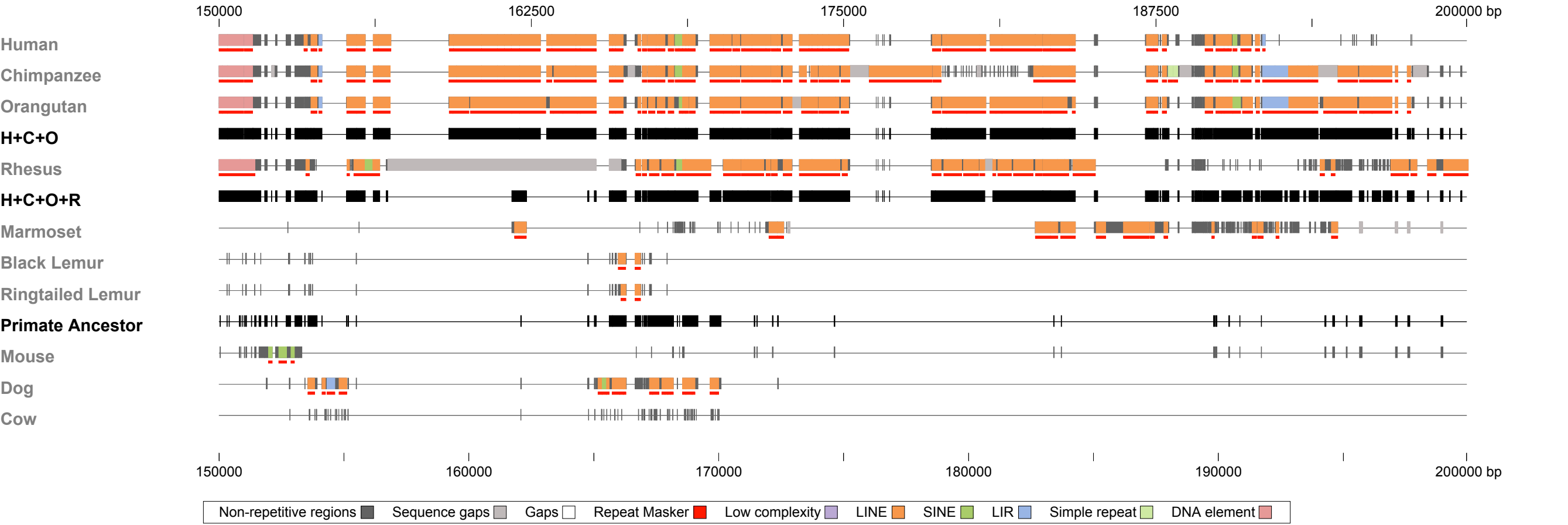


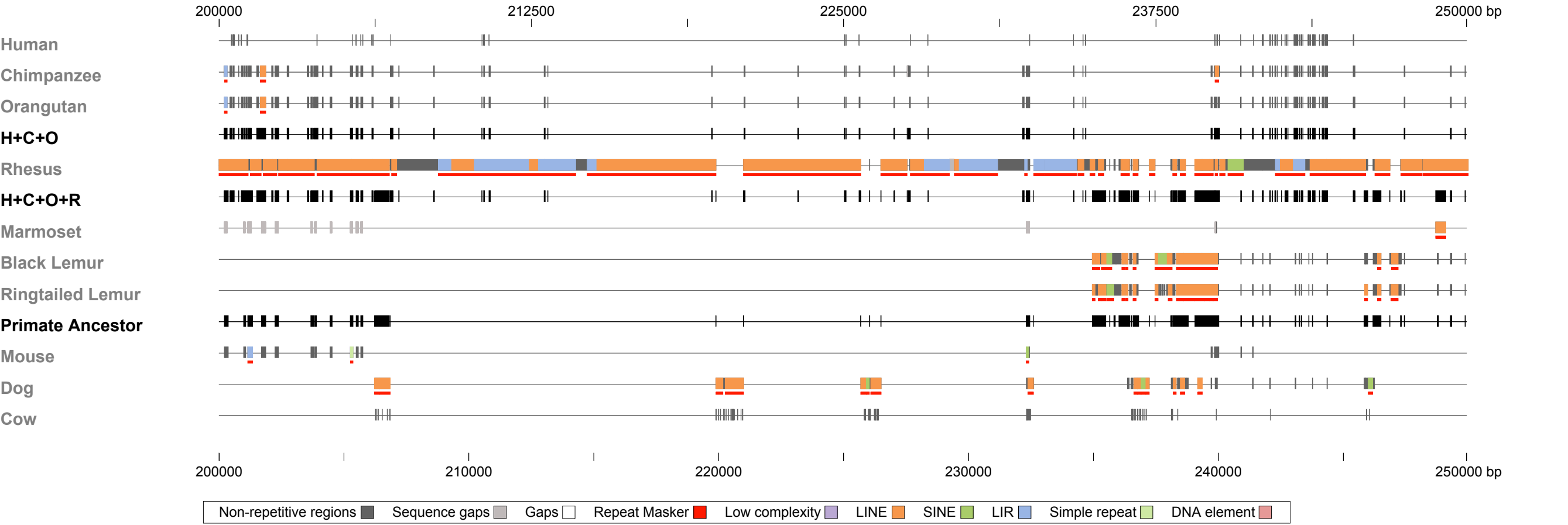


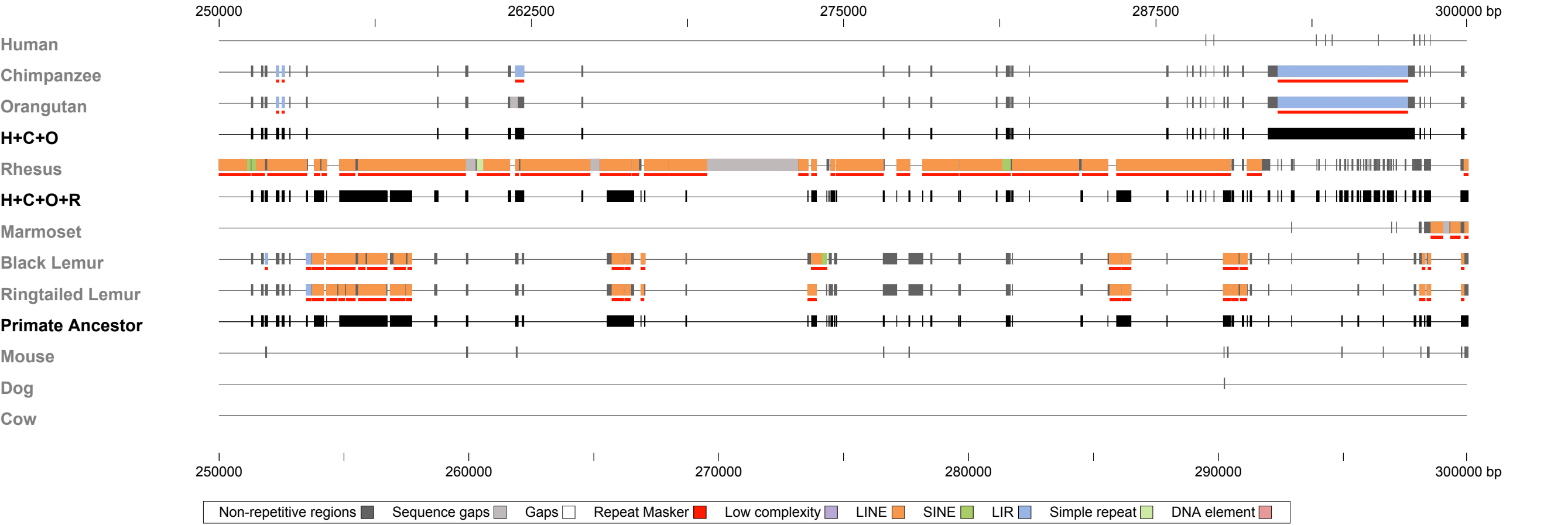
Supplemental Figure 3: Repeat content and alignment across the XIC in 50kb windows
Each page shows a 50kb window across the XIC region, enlarged from Figure 2a. Colored bars representing sequence for each species are shown on a separate horizontal line. The red bars below the sequence indicate repetitive regions identified by RepeatMasker, which are color-coded depending on the repeat identified (see legend). Three ancestrally reconstructed sequences (H+C+O, C+C+O+R and Primate Ancestor) are indicated for comparison of which regions have been gained or lost throughout primate evolution. Below the aligned sequences are the exonic regions annotated based on the human and mouse gene structures.

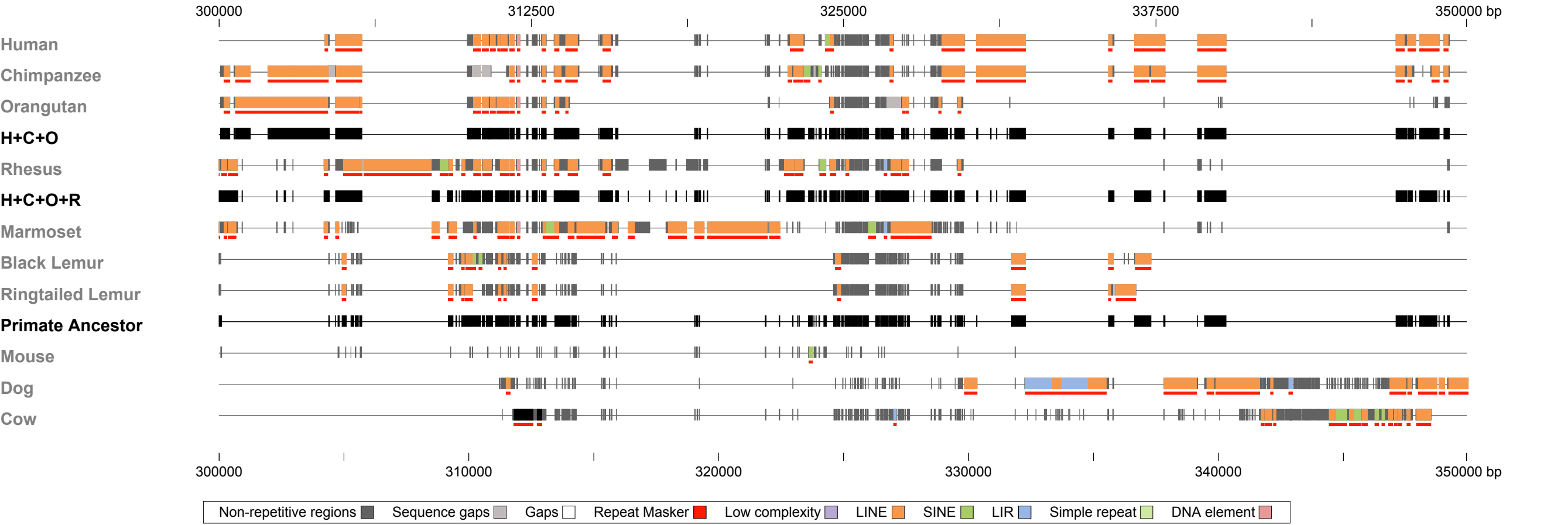


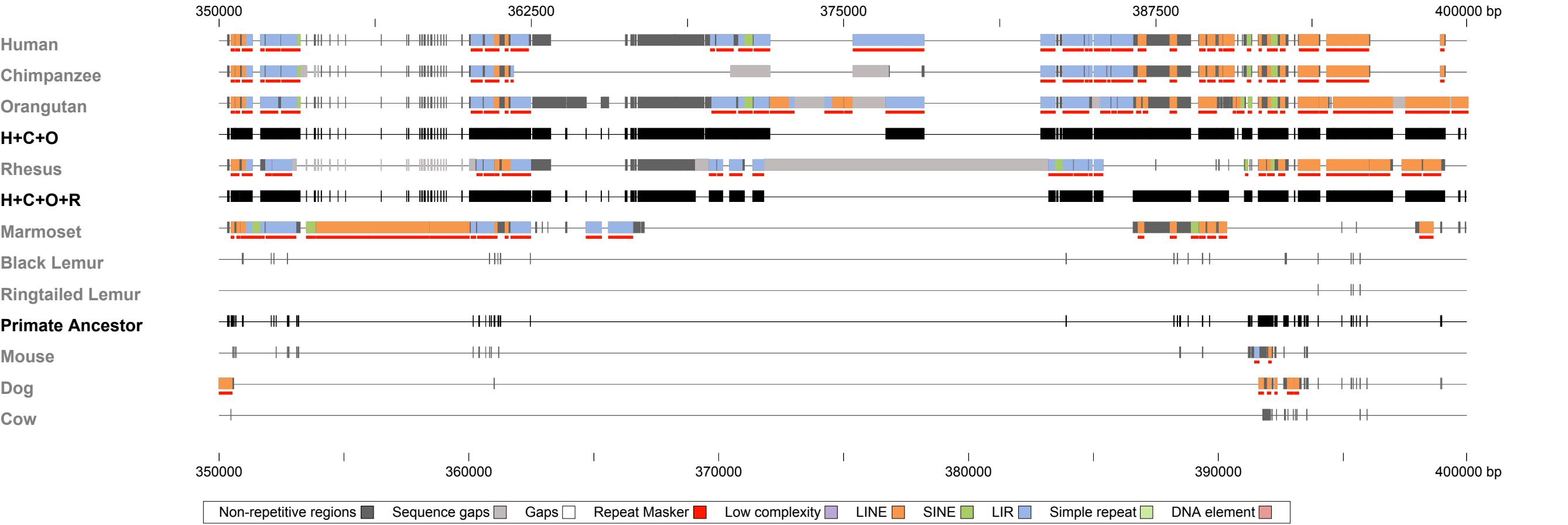


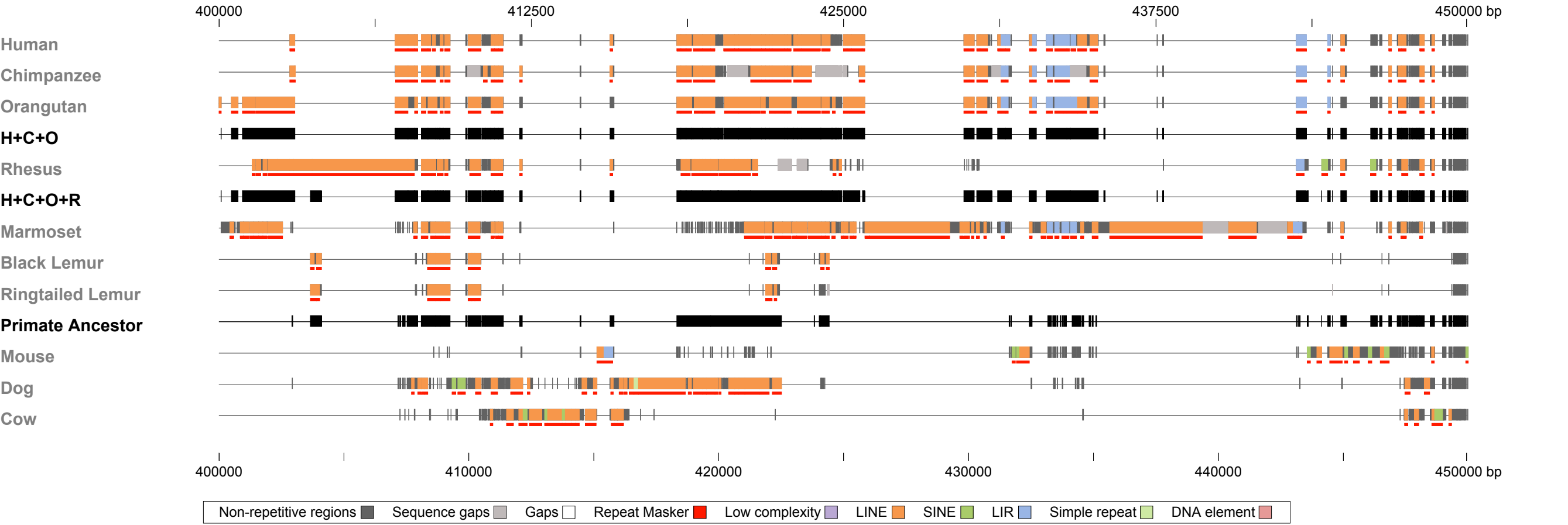


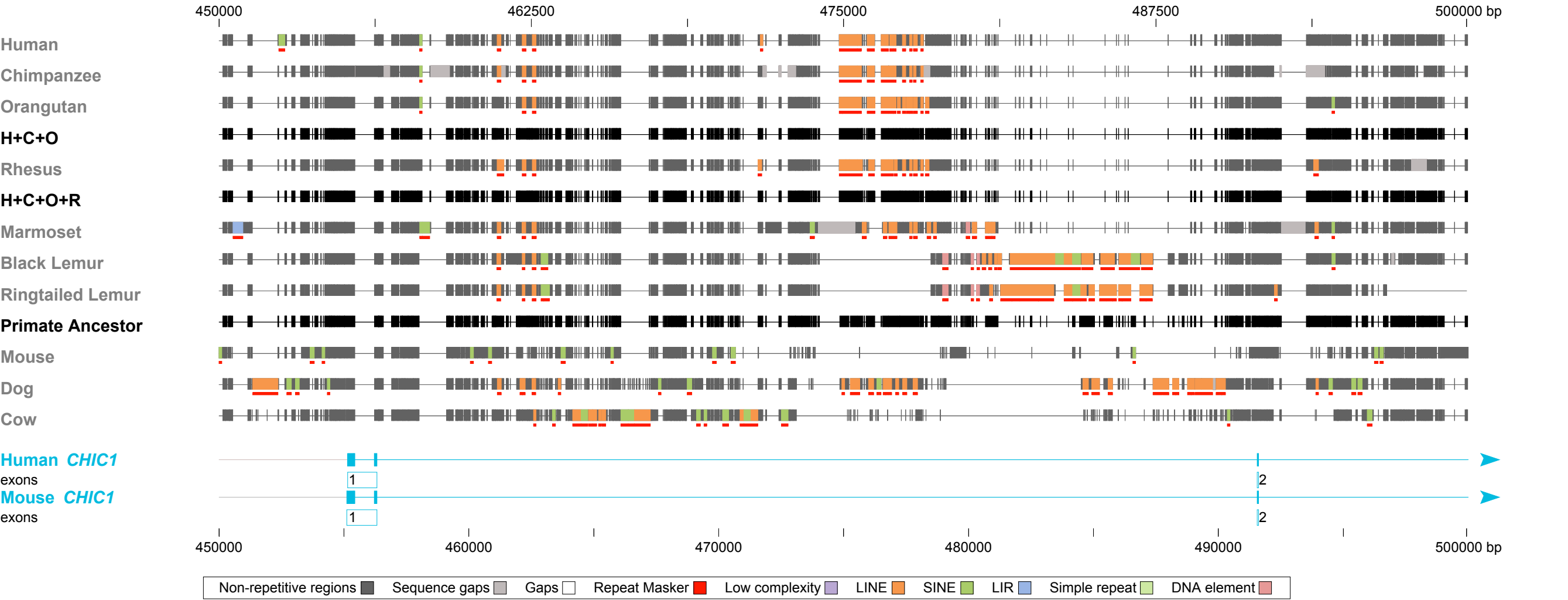


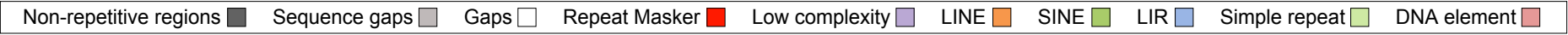
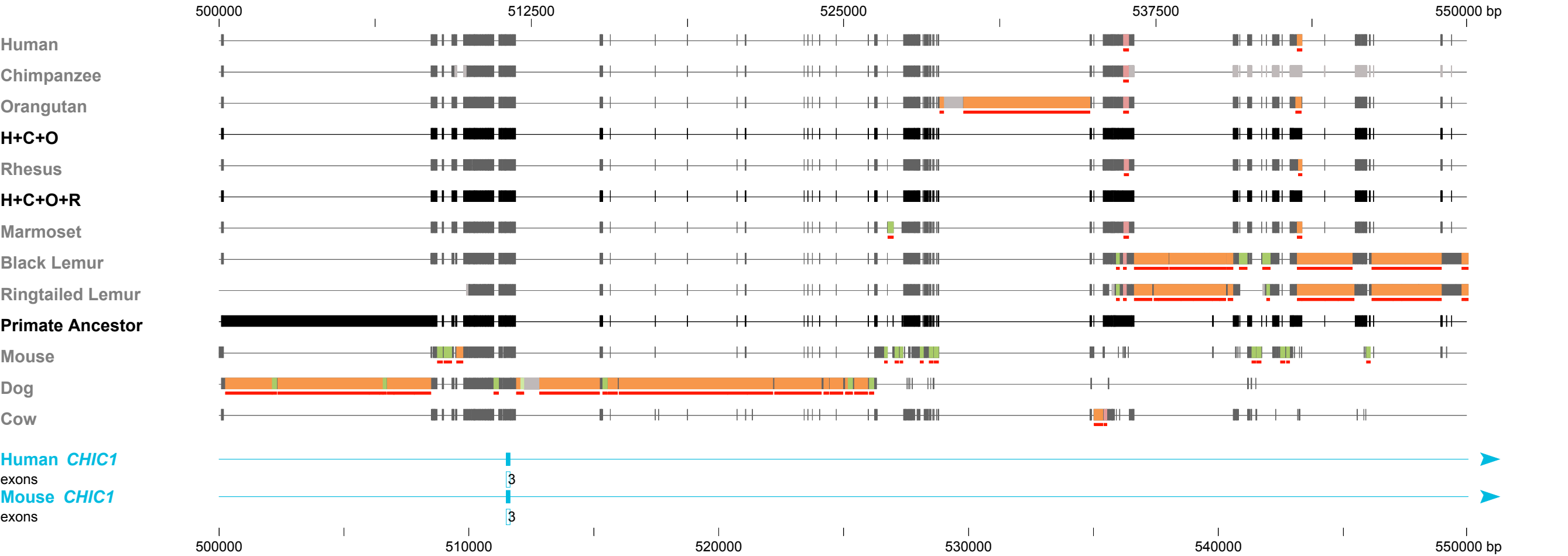




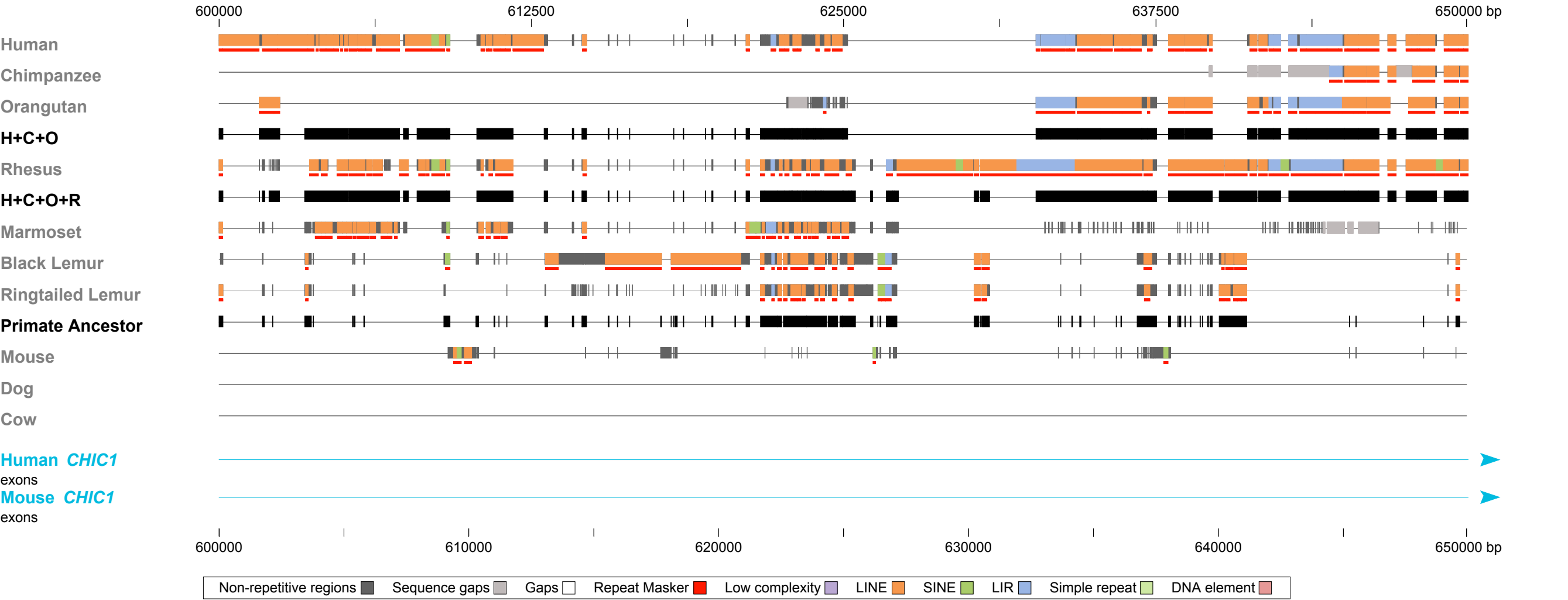


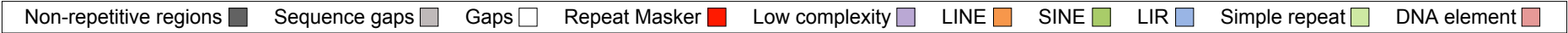
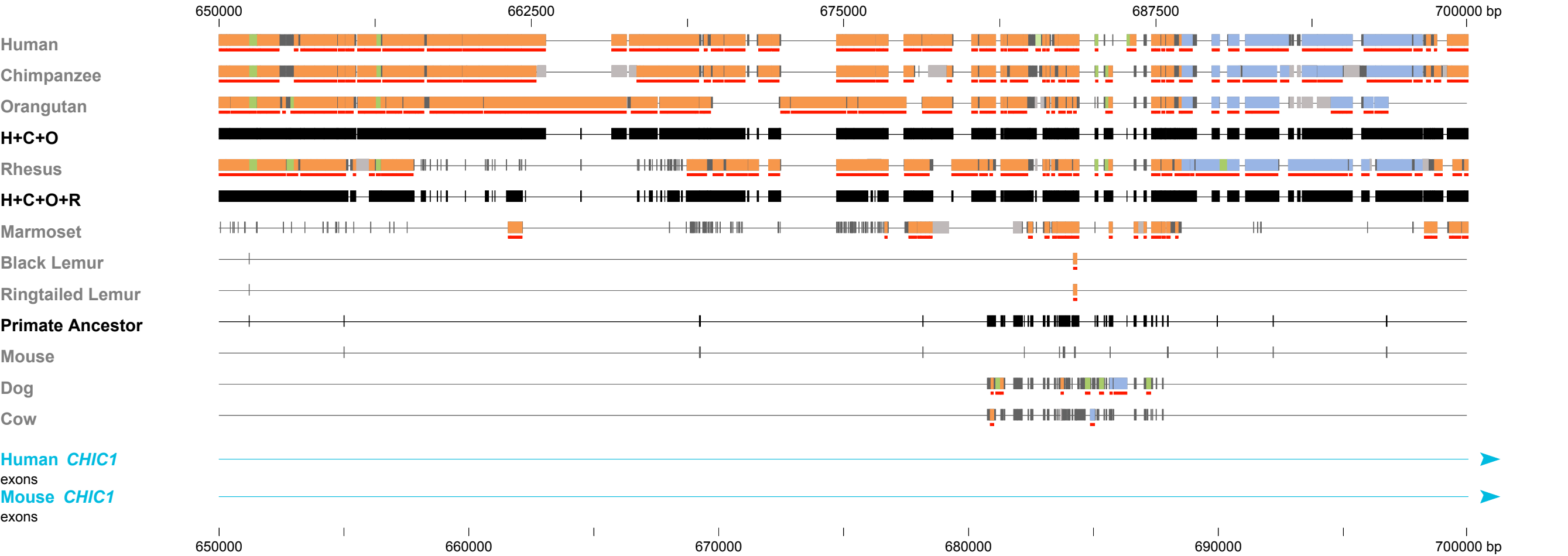


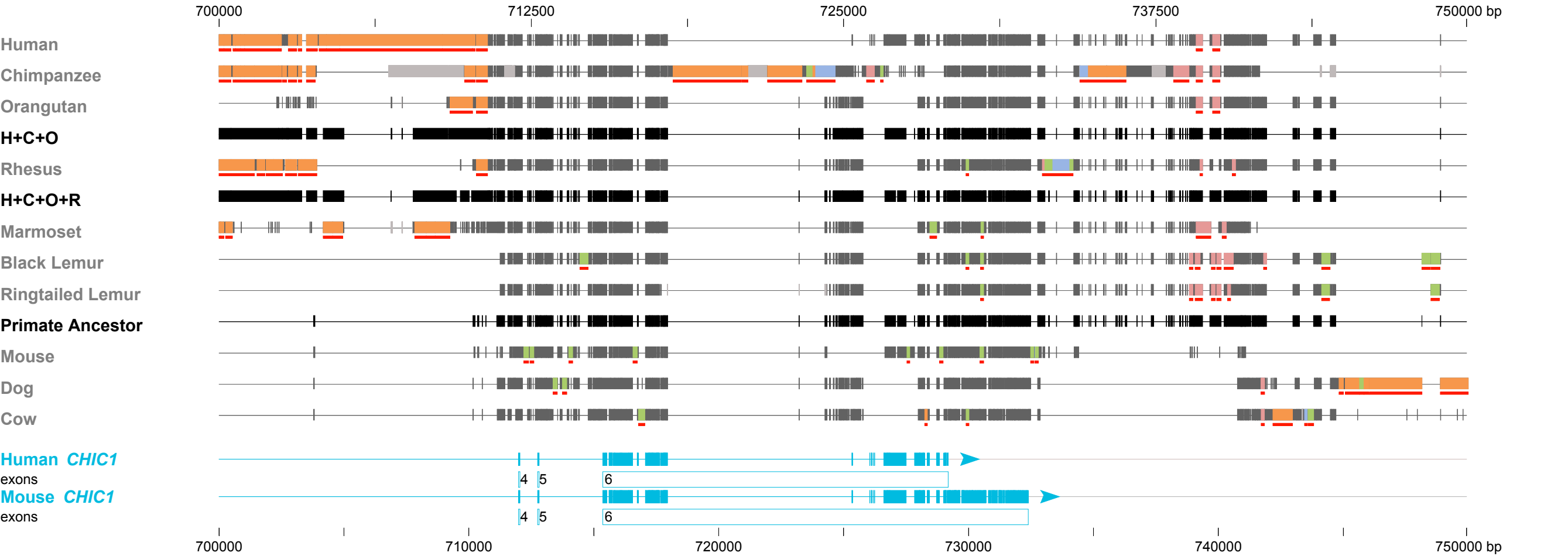




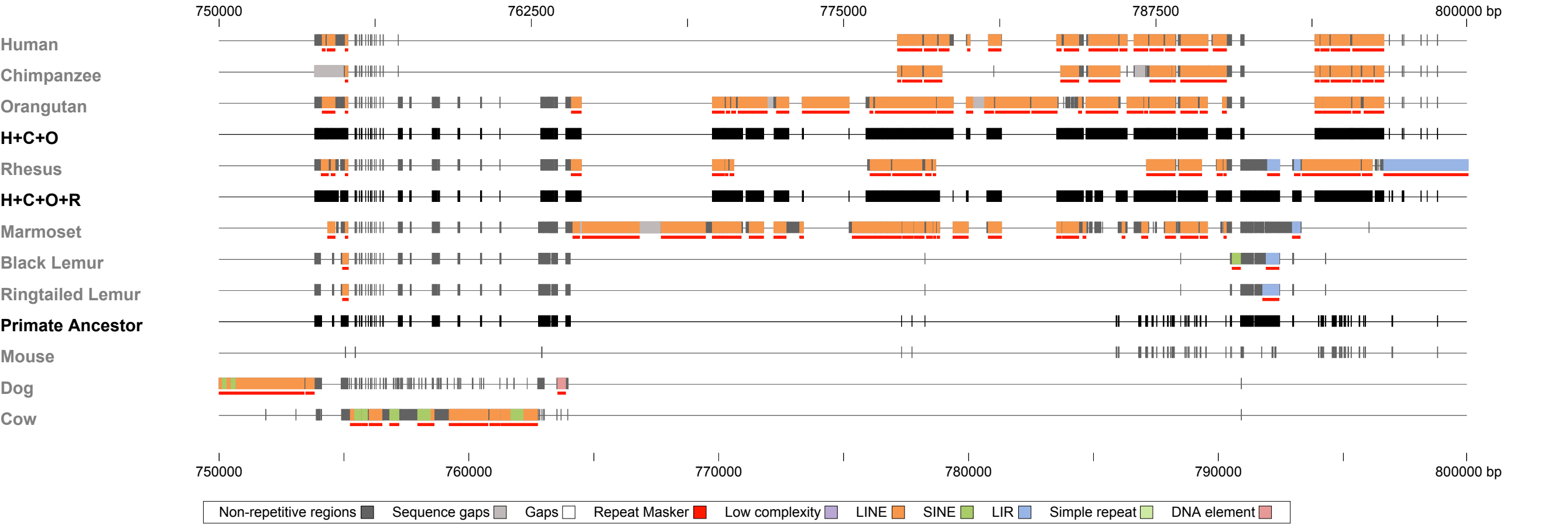


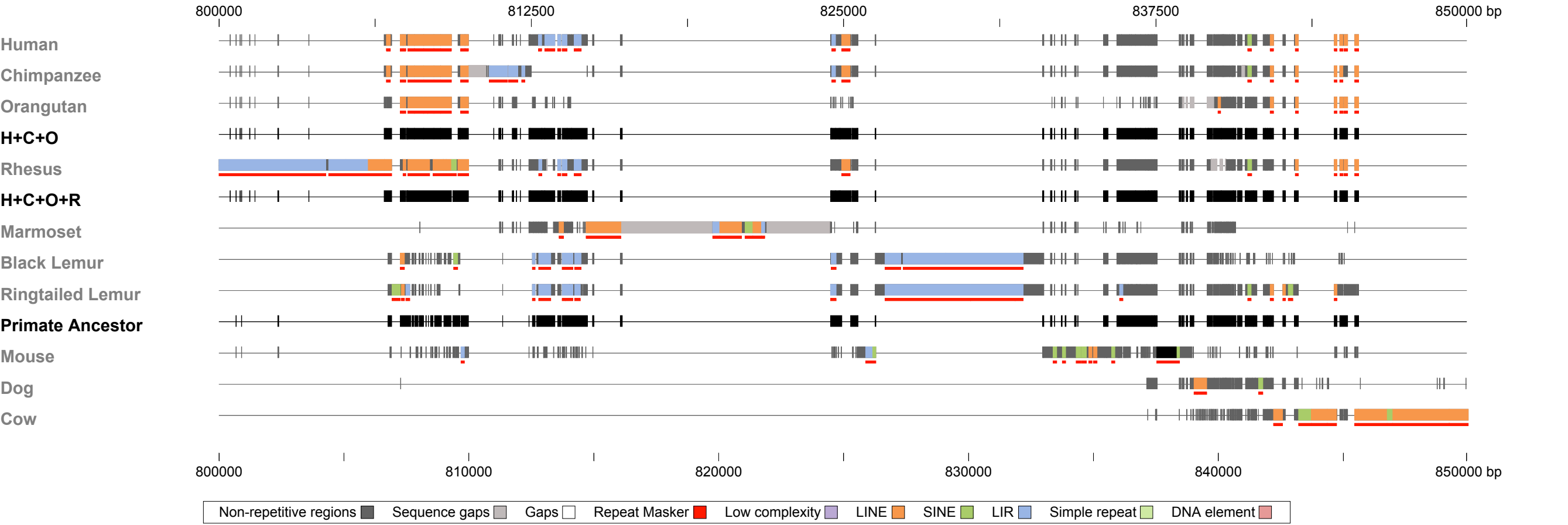


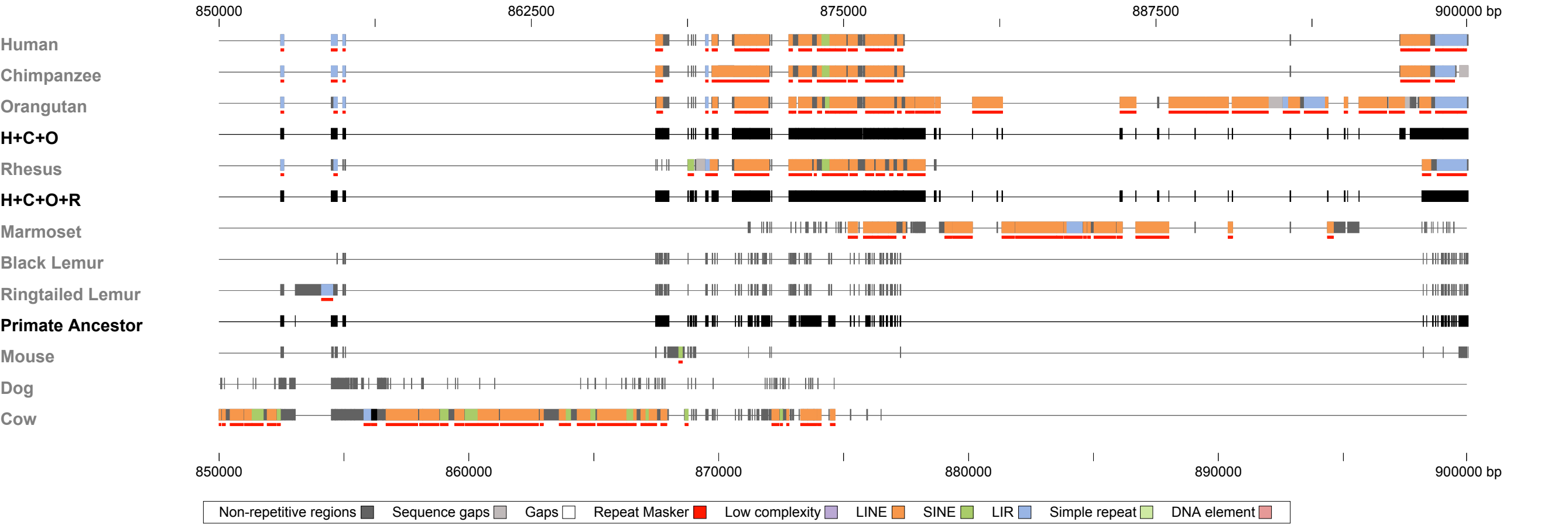


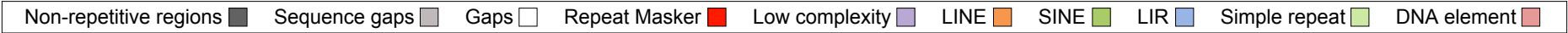
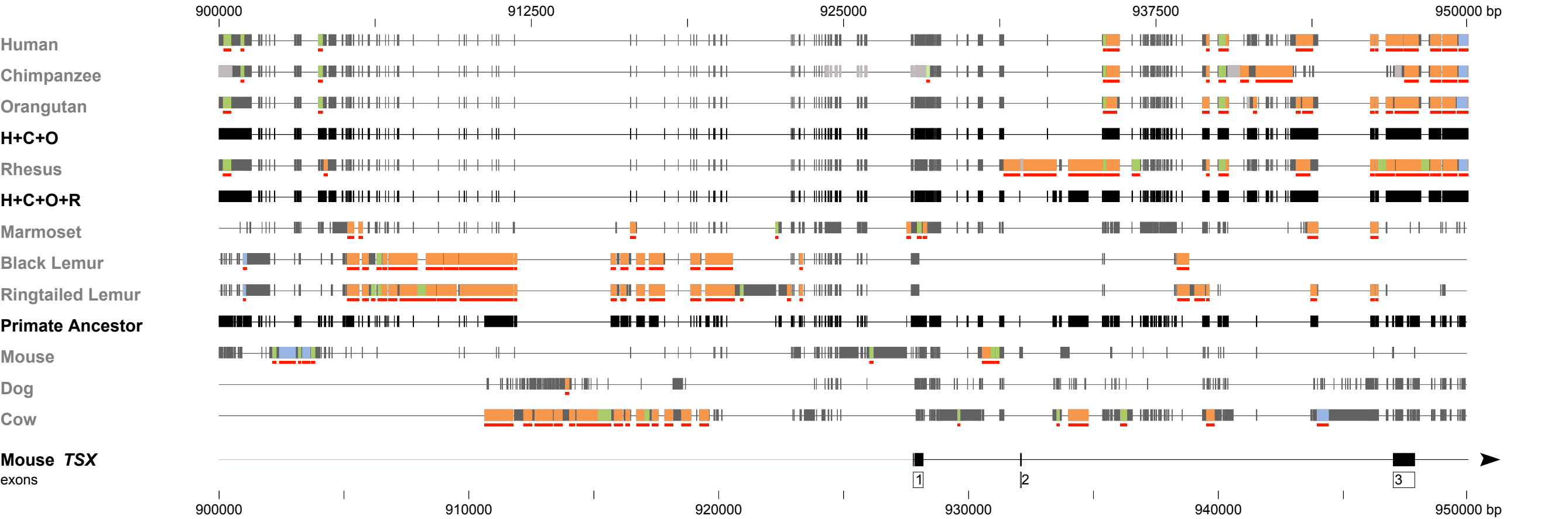


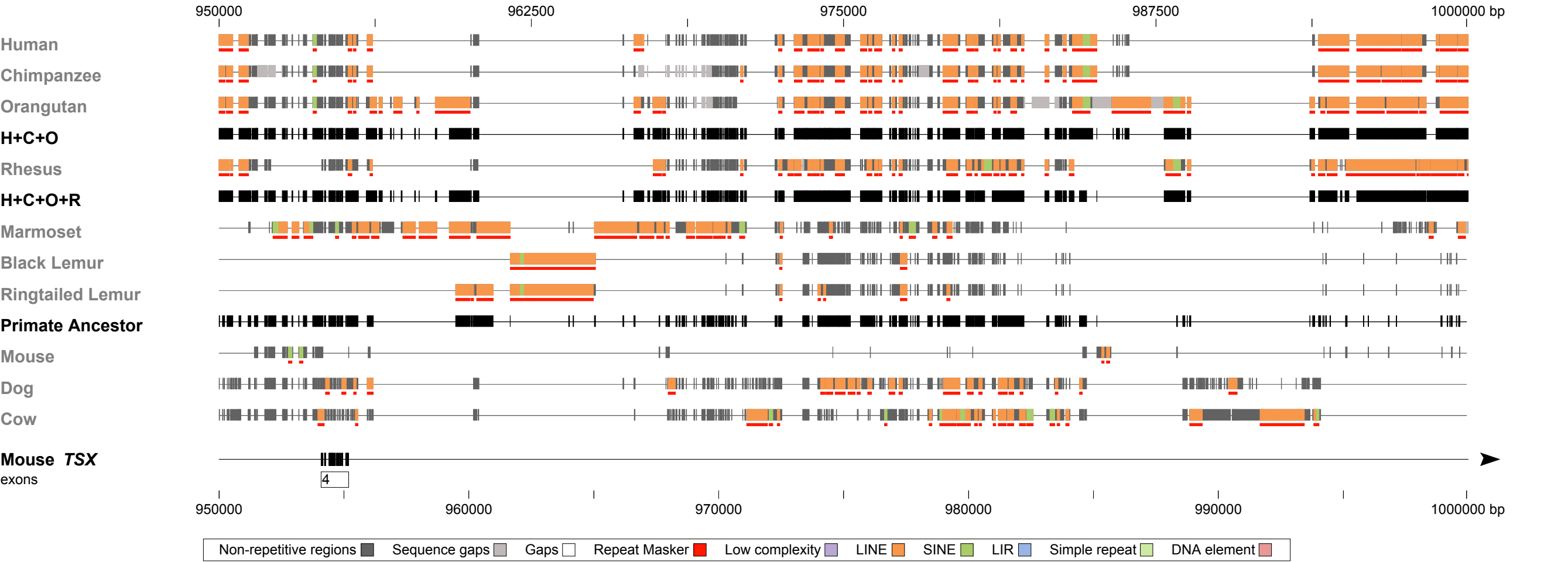
Non-repetitive regions Sequence gaps Gaps Repeat Masker Low complexity LINE SINE LIR Simple repeat DNA element

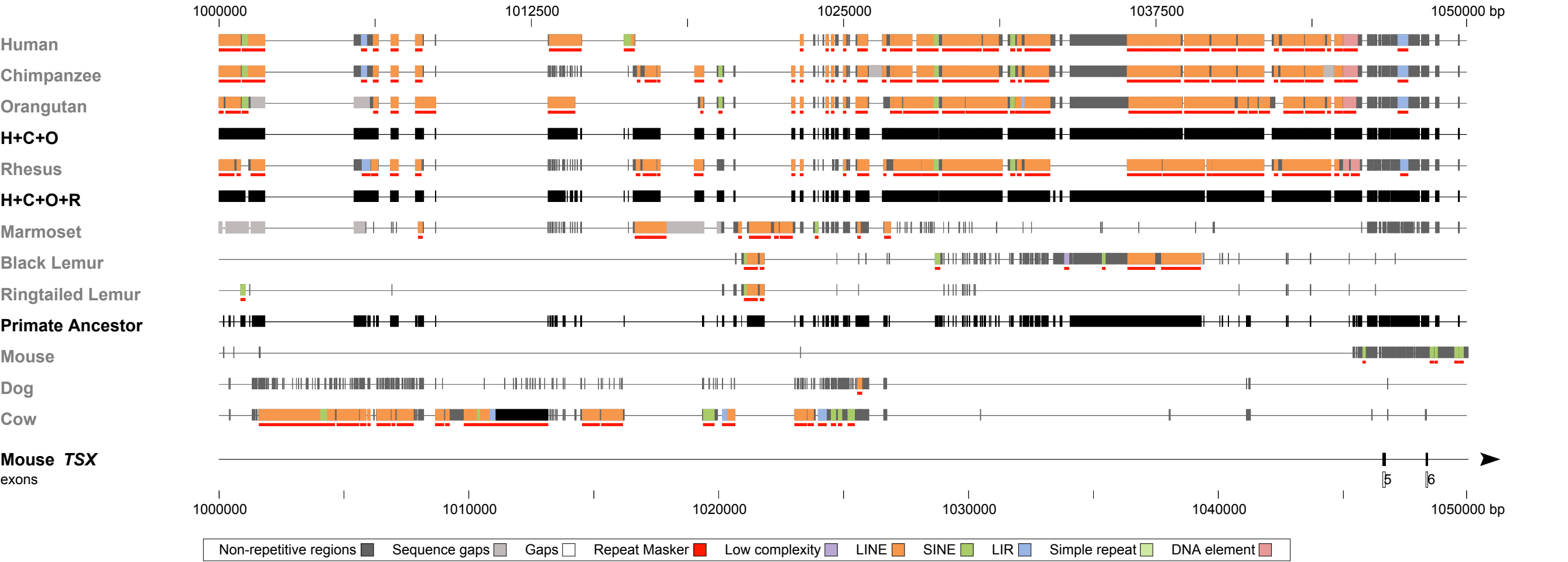


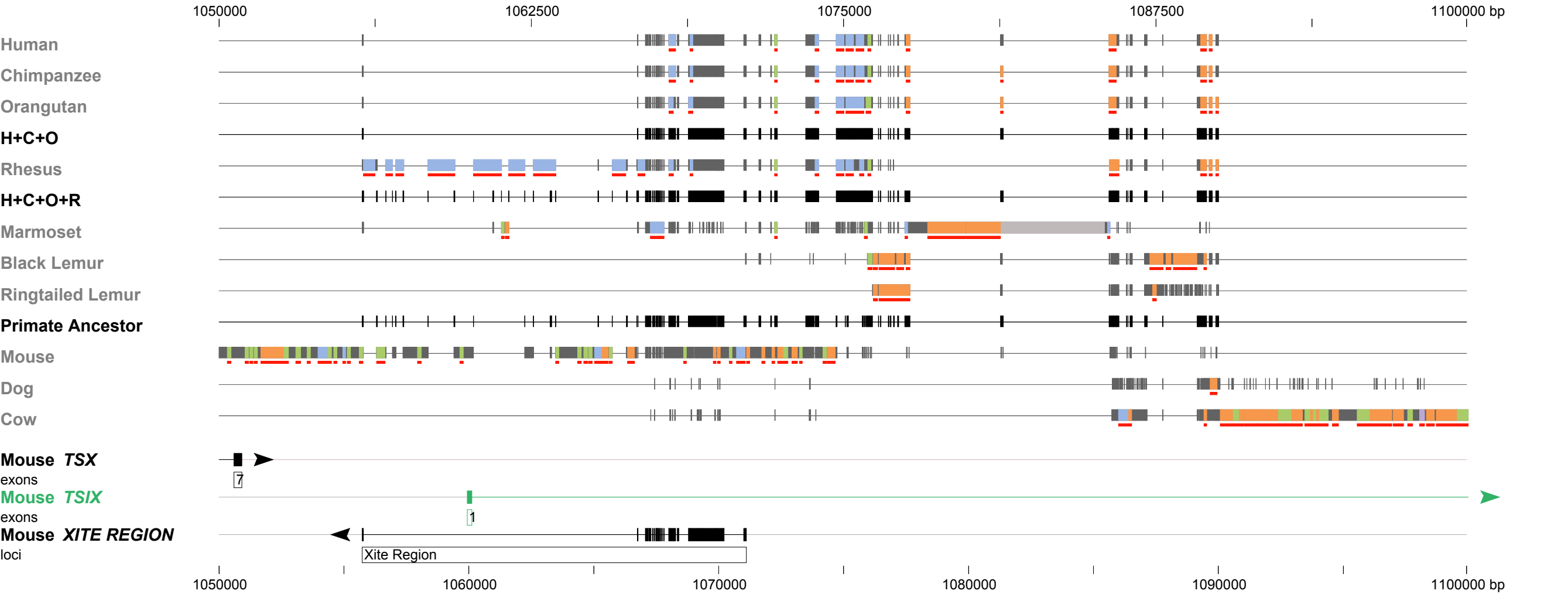


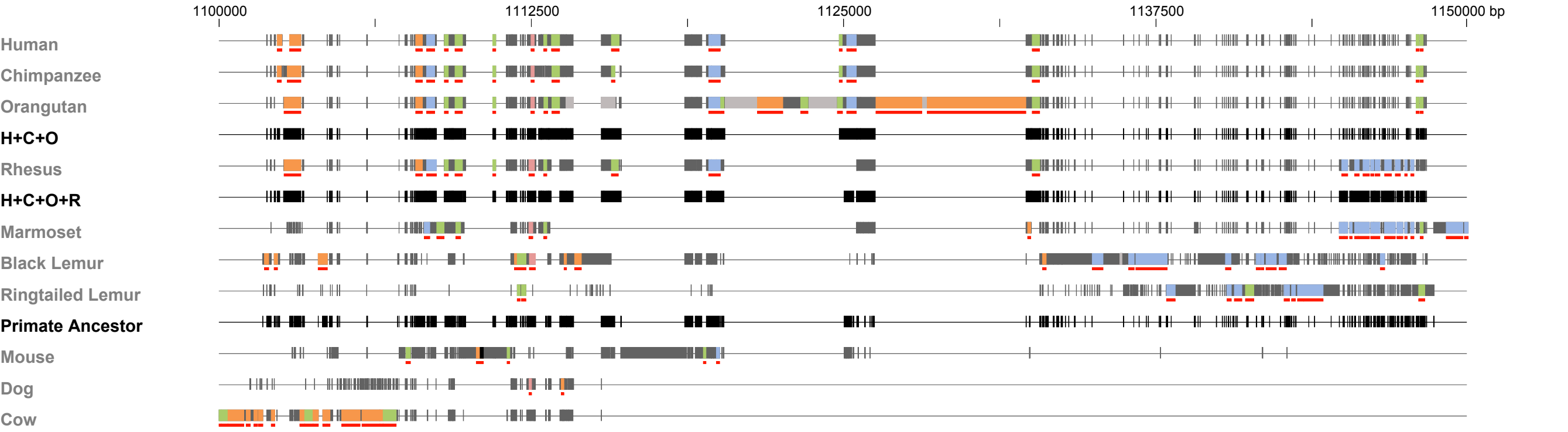












Mouse *DXPAS34* REGION

