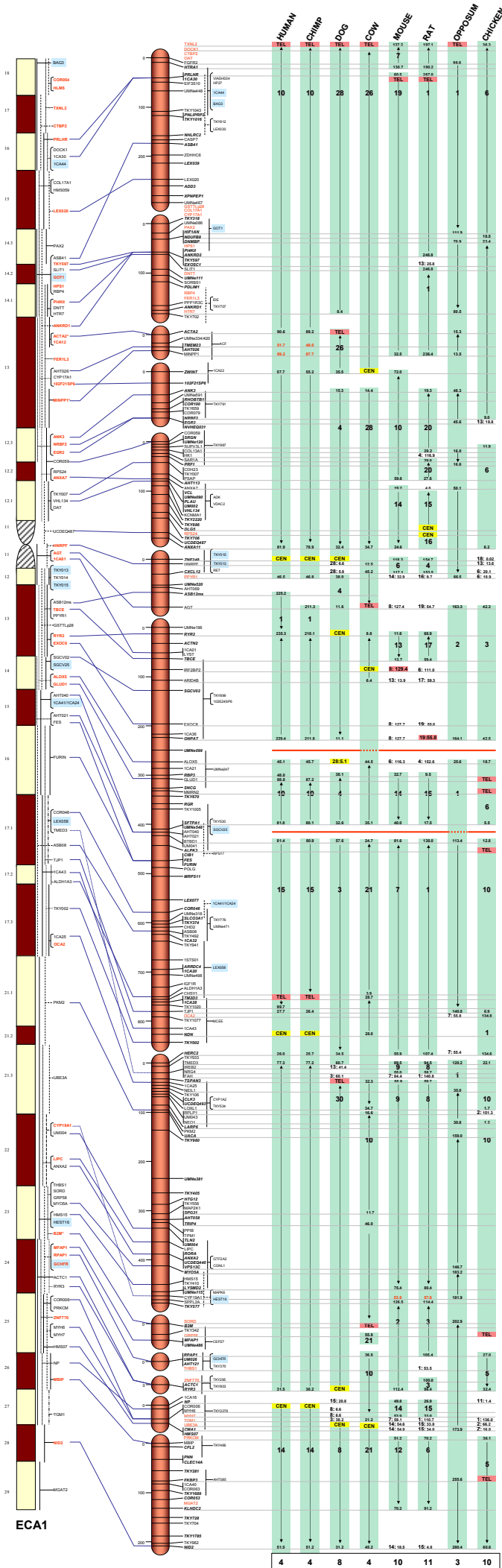
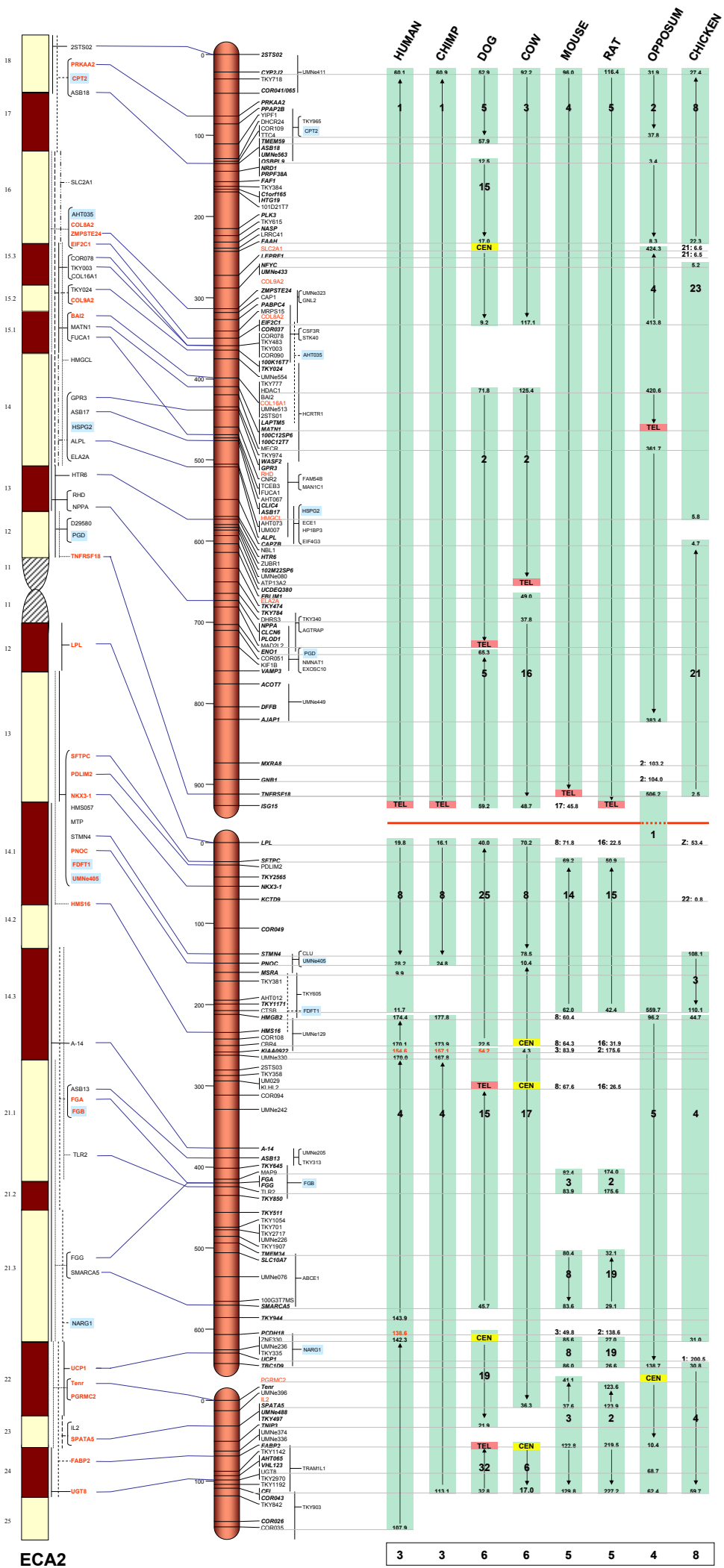


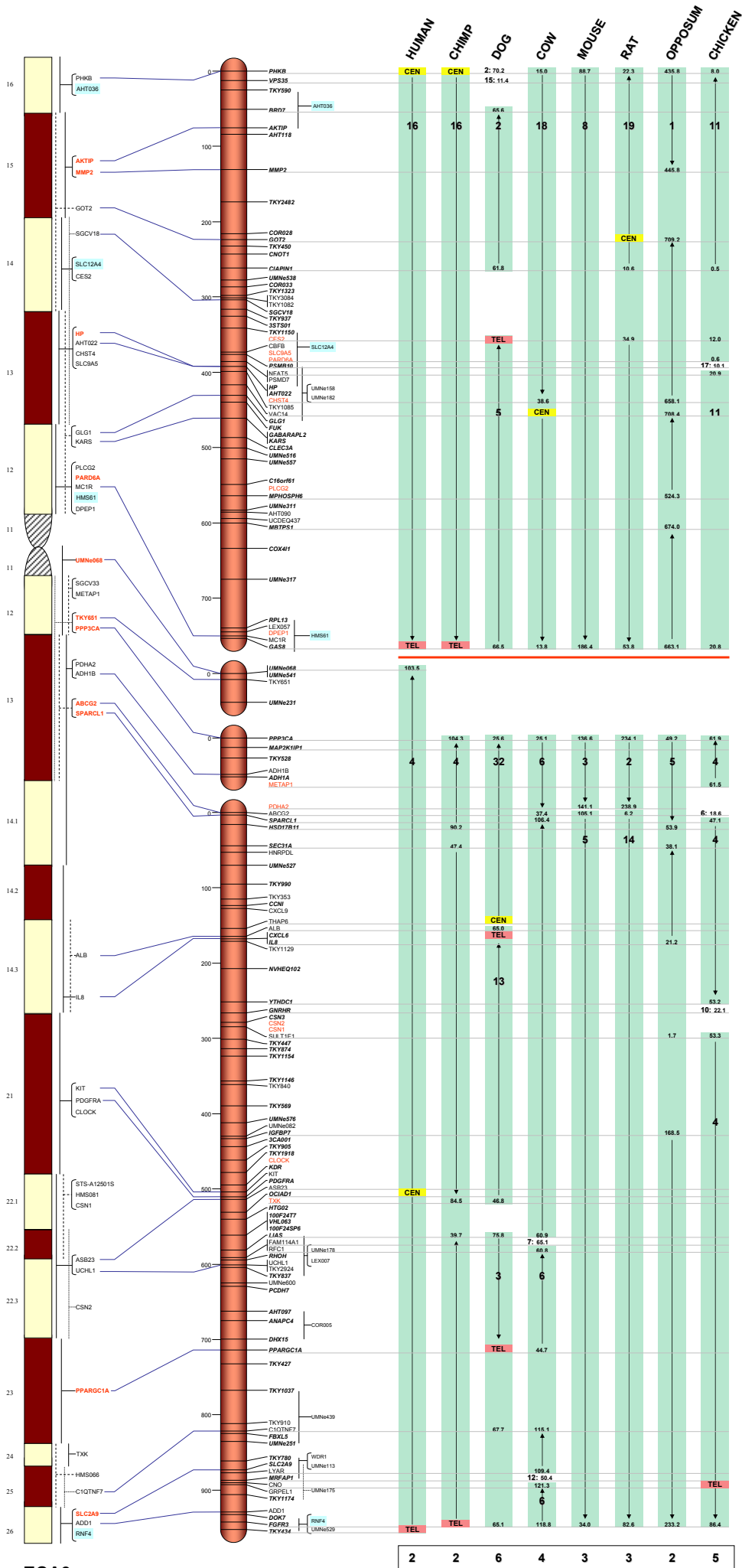
Supplementary Information

Legend for Supplementary Figures 1.1-1.X

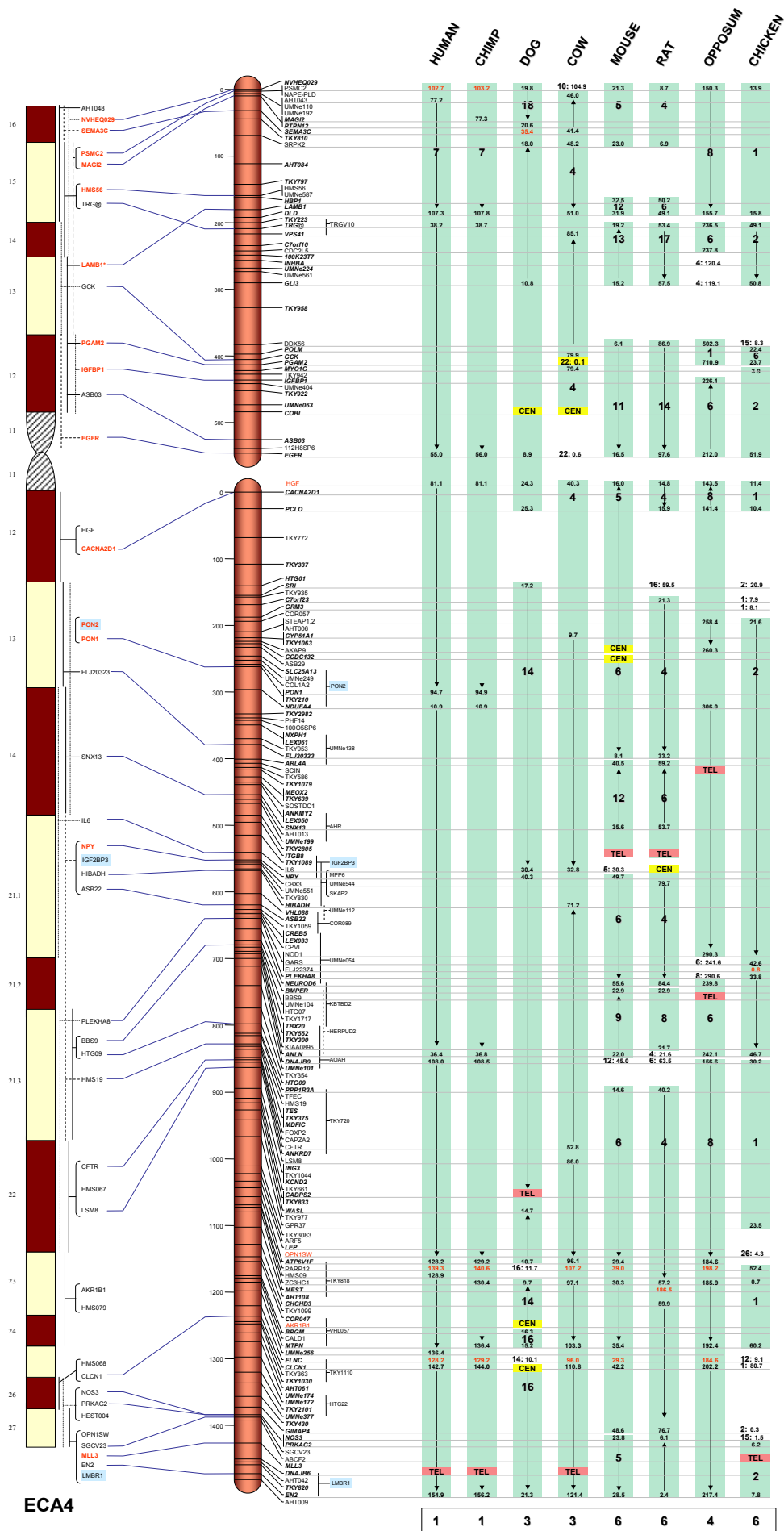
Integrated high-resolution maps for individual horse chromosomes (ECA1-ECAX) containing the second generation radiation hybrid map (RH II; middle), cytogenetic map (left) followed to the right side by a comparative overview in relation to the sequence maps of six eutherian mammals, opossum and chicken. **RH map:** The vertical orange shaded bars depict RH group(s). CentiRay (cR) distances are shown to the left. Loci with a designated RH map position are shown to the right of the vertical bars and are connected to cR positions with horizontal lines. MLE-consensus markers are shown in bold-italics while placed markers are in normal font. Binned markers are shown to the right of RH mapped loci and assigned to a corresponding RH map region with thin vertical lines. Binned markers shown in blue shaded boxes are also present on the FISH map. Markers on the RH map depicted in red font without a connection to cR position are mapped only by FISH and are incorporated into RH map according to their comparative position in humans. **FISH map:** For each horse chromosome, a G-banded ideogram (ISCNH 1997) with band nomenclature is presented. The FISH mapped markers are shown to the right of the ideogram. Markers depicted in red are mapped in this study. Markers connected to the RH map with horizontal lines and those in blue shaded boxes (binned markers) are shared between the RH and FISH maps and represent anchor loci. **Comparative map:** Comparative information for all species was retrieved from the UCSC Genome Bioinformatics website (<http://genome.ucsc.edu>) using the following builds: **human** - NCBI Build 36.1, browser March 2006; **chimp** - panTro2 Build 2 v1, browser March 2006; **dog** - canFam2 v2.0, browser May 2005; **cattle** - Baylor release Btau_4.0, browser September 2007; **mouse** - mm9 NCBI Build 37, browser July 2007; **rat** - rn4 version 3.4, browser November 2004; **opossum** - monDom4, browser January 2006 and **chicken** - galGal3 v2.1 draft assembly, browser May 2006. Light green vertical bars for each species show segments of conserved synteny (consisting of at least two continuous loci) between the horse chromosome and the sequence maps of any of the eight vertebrate species. Numbers within each synteny segment depicted in bold and large font indicate the number of the corresponding chromosome in each species. Sequence map position (in megabases; Mb) of end markers are shown for each syntenic segment. For the ease of alignment, few markers are connected with horizontal lines through the comparative map to the RH map. Single homologous loci are depicted as follows **1:11.1**, where the first number indicates the chromosome and numbers after the colon denotes map Mb position. Sequence map positions in red font indicate observed discrepancies in the otherwise well conserved synteny or linkage. Solid vertical lines within conserved synteny blocks indicate conserved linkages and the arrow at the end of the line indicates the centromere-telomere orientation. Syntenic blocks without vertical lines share no conserved linkage with the horse genome. Horizontal red lines on SI Figs. 1.1, 1.2, 1.3, 1.6, 1.7, 1.8, 1.10, 1.13 and 1.21 indicate evolutionarily conserved synteny breakpoints which are shared by most (all or all but one) of the vertebrate species compared to the horse. Numbers in a box below the comparative map indicate the number of syntenic segments in each species corresponding to the horse chromosome. Putative positions of centromeres and telomeres are indicated by yellow and orange rectangles, respectively.



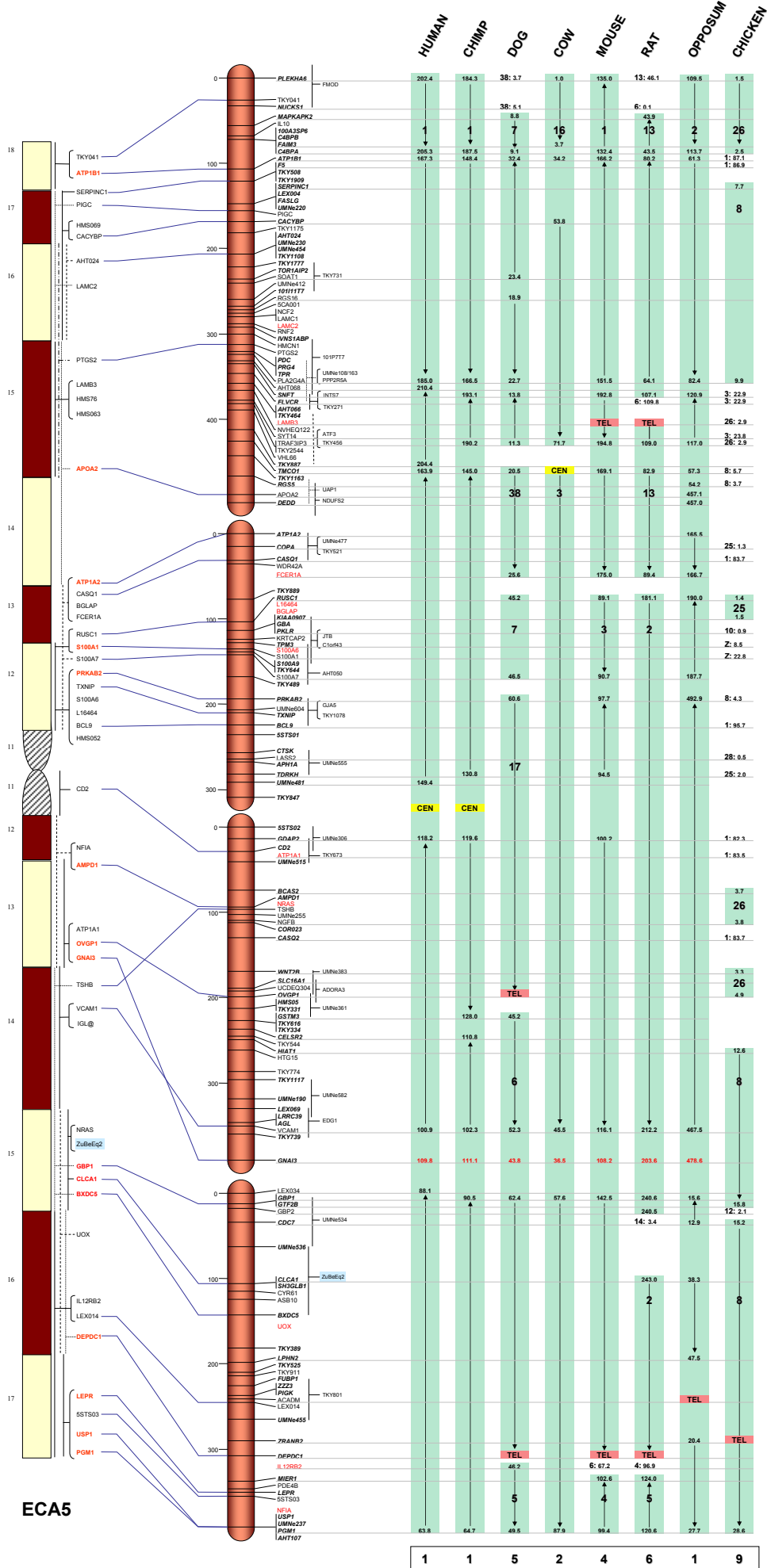


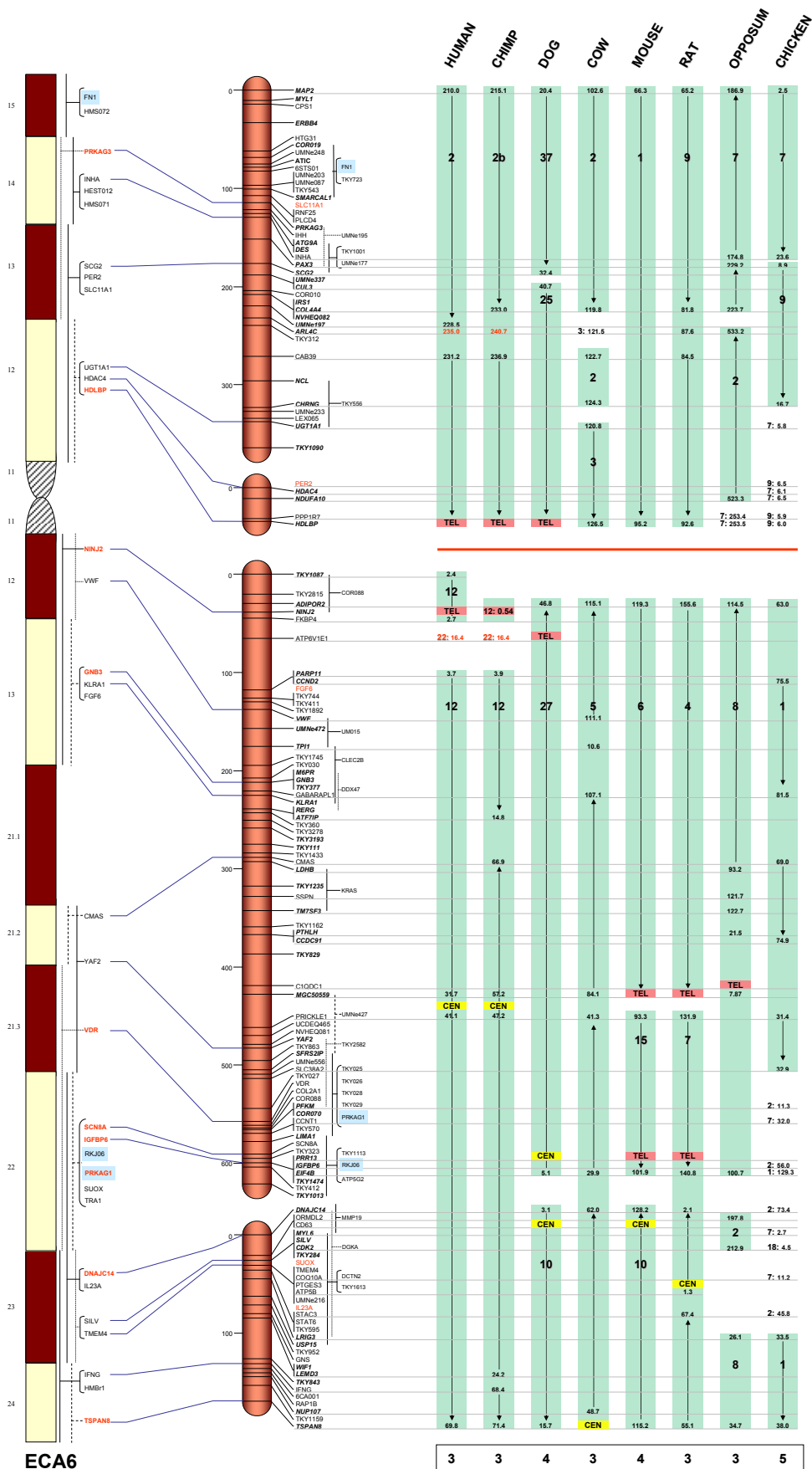


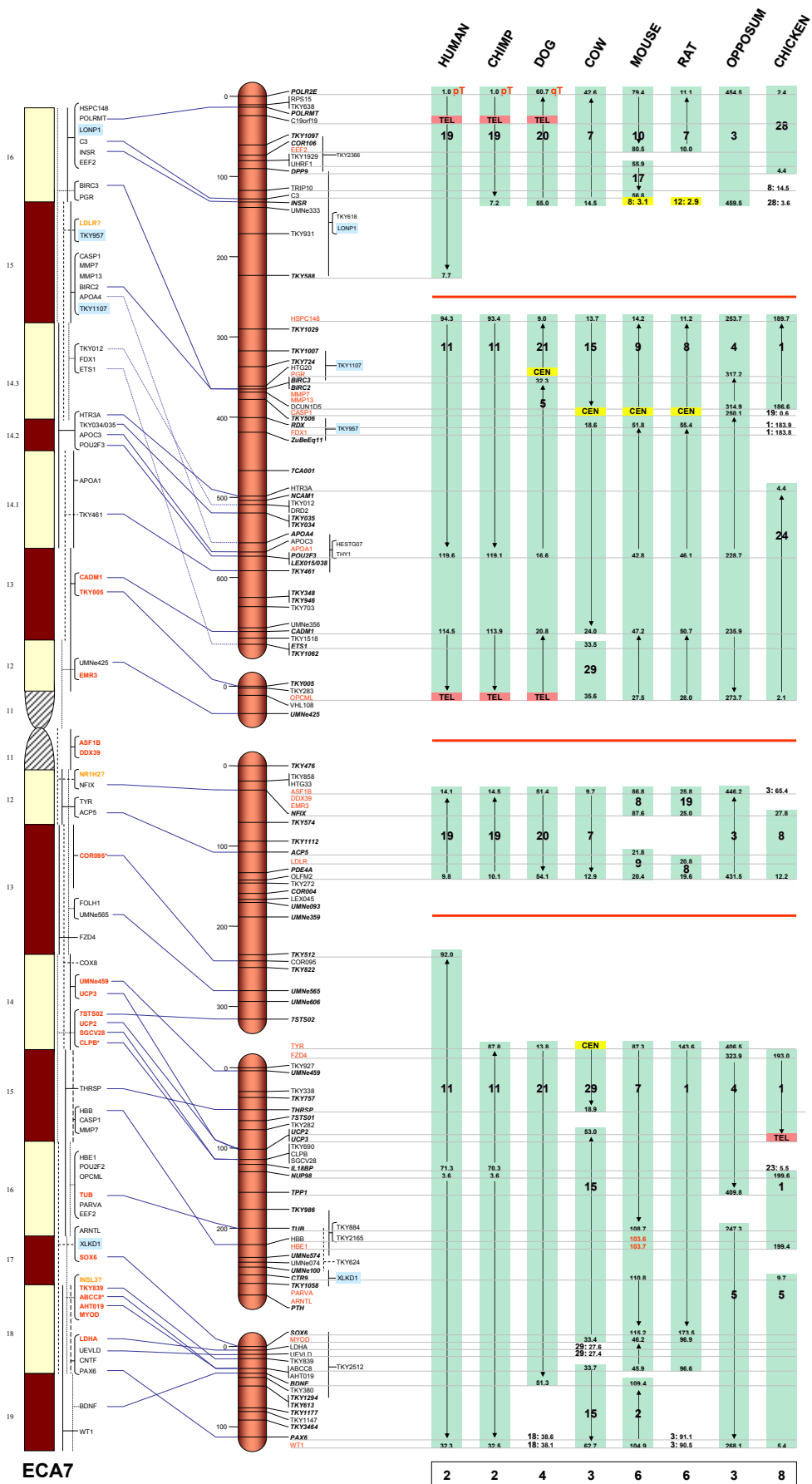
ECA3

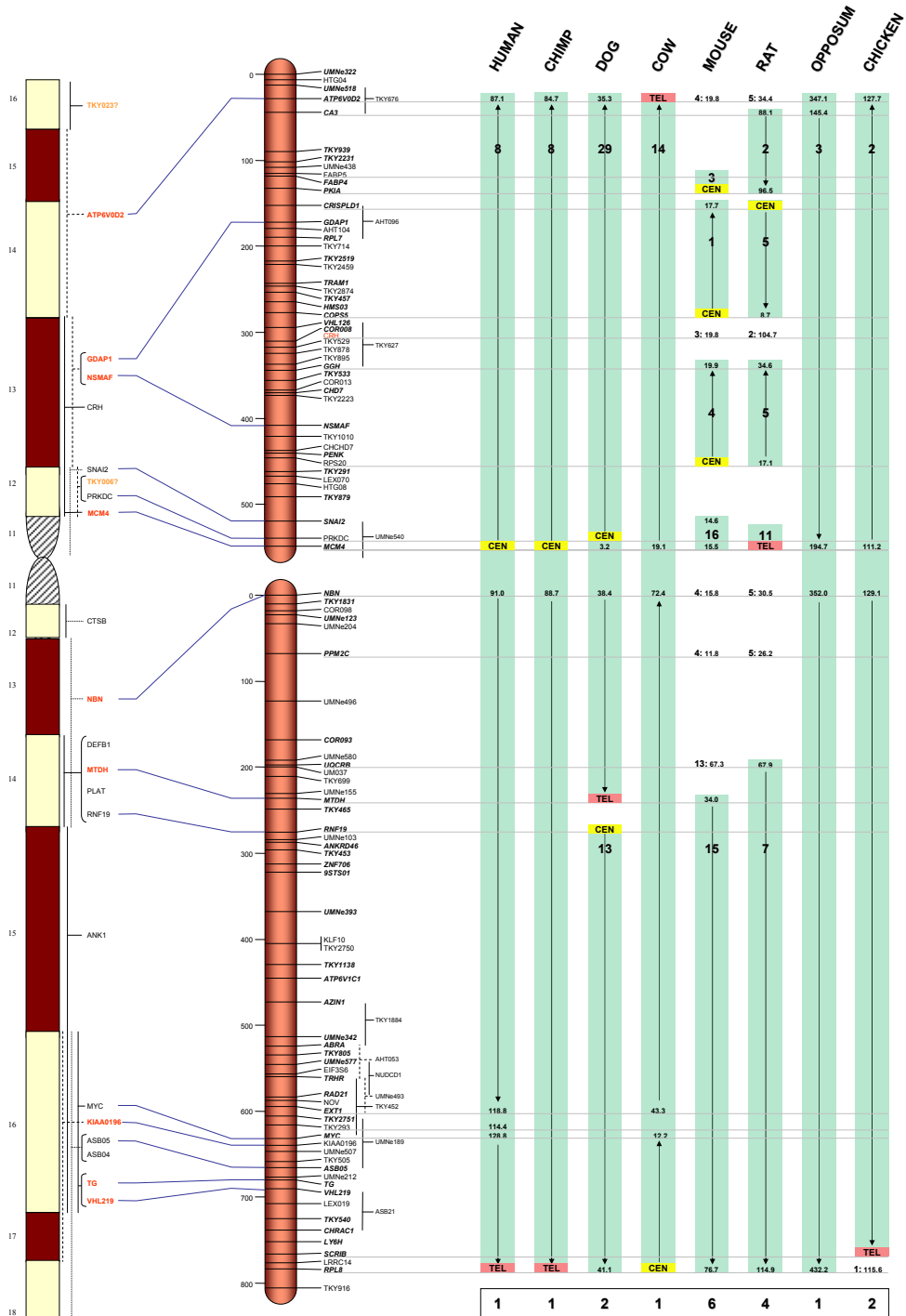


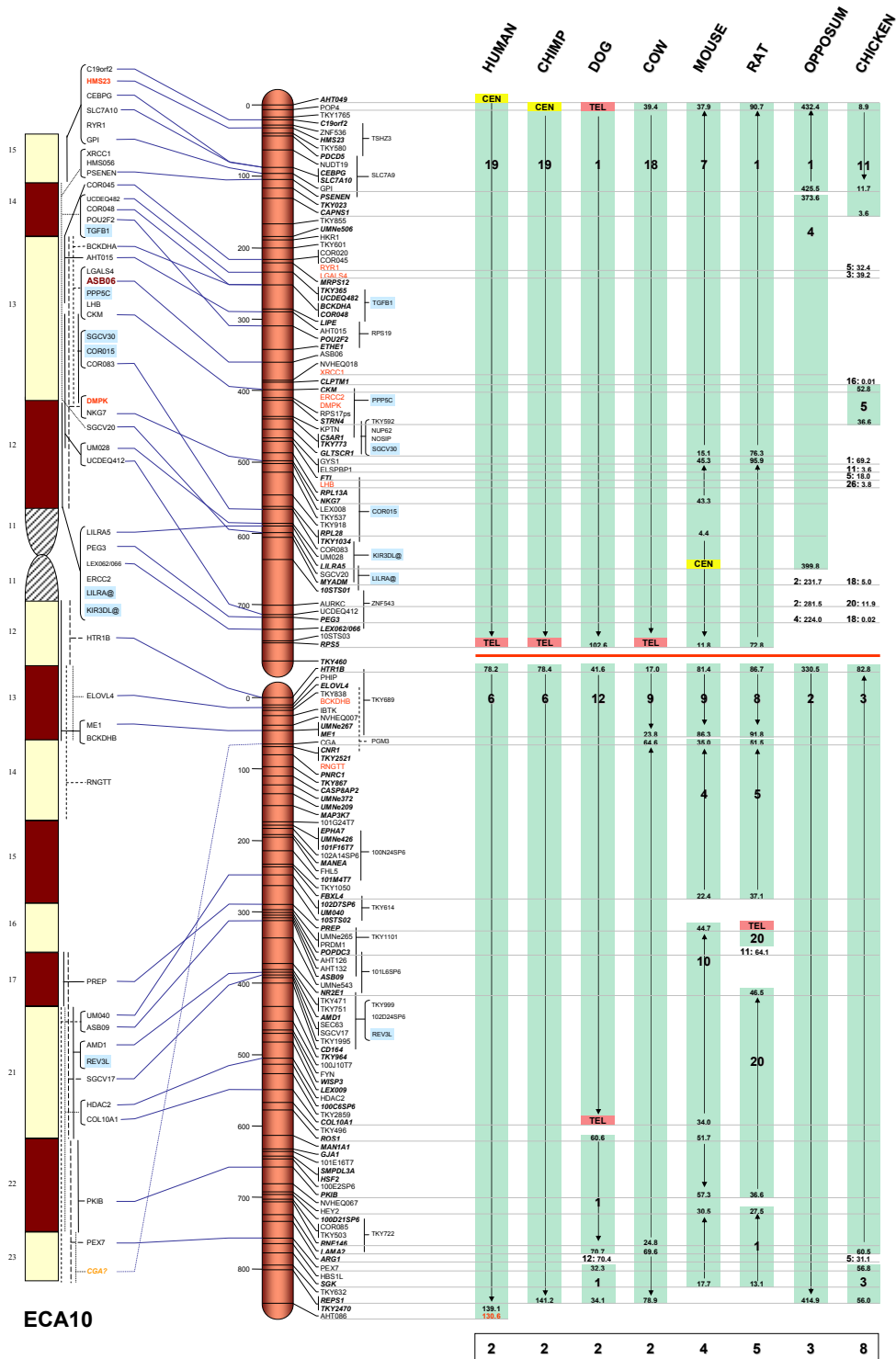
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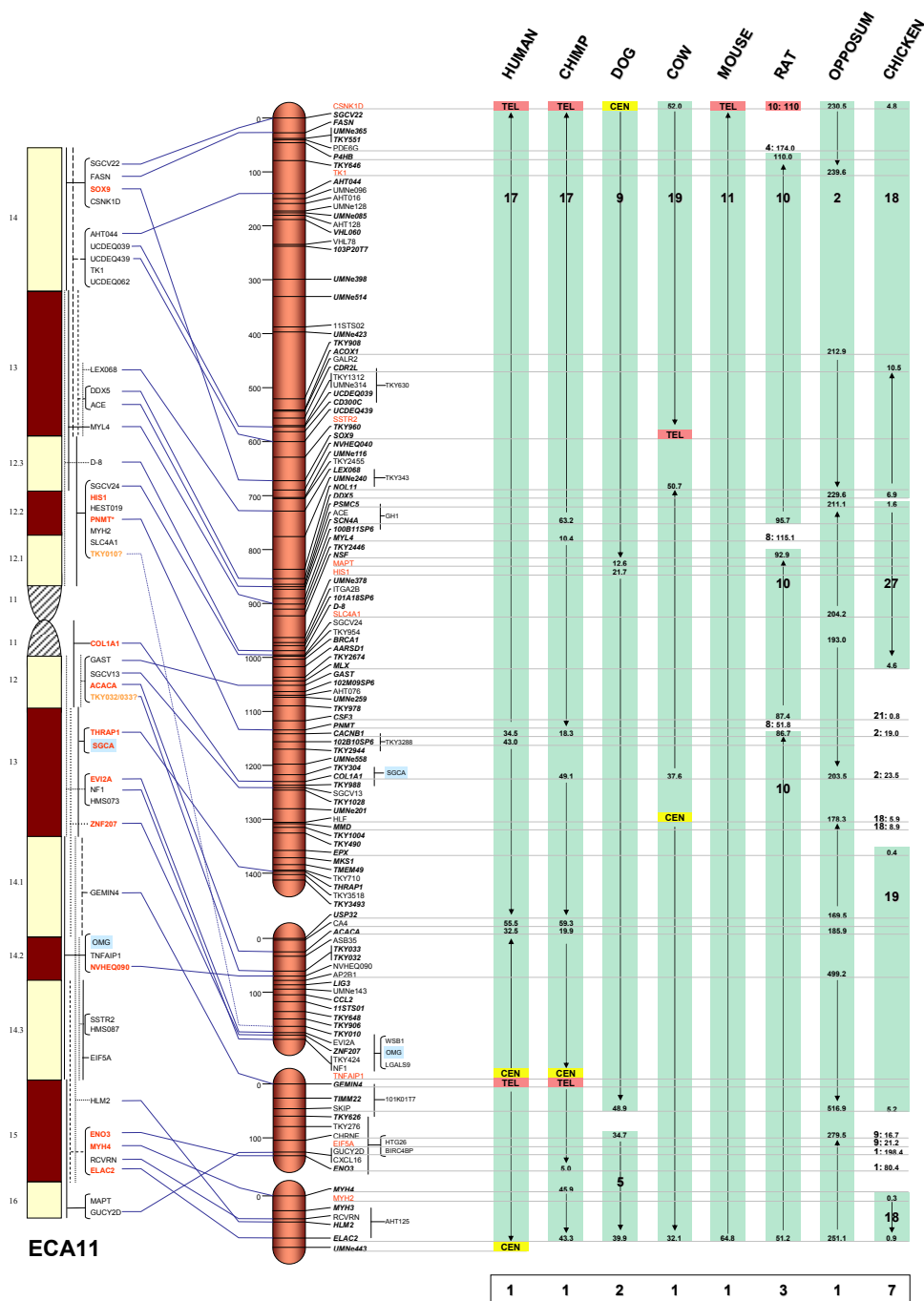


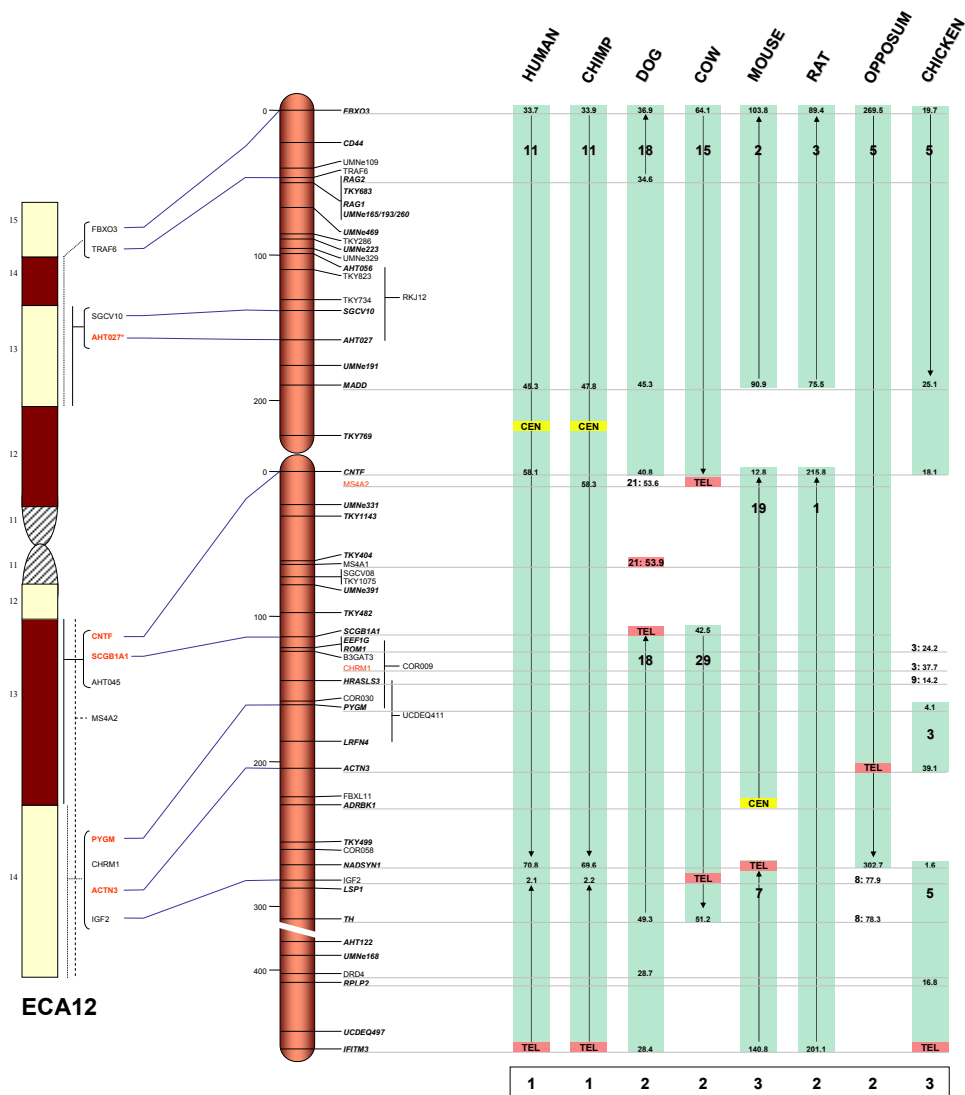


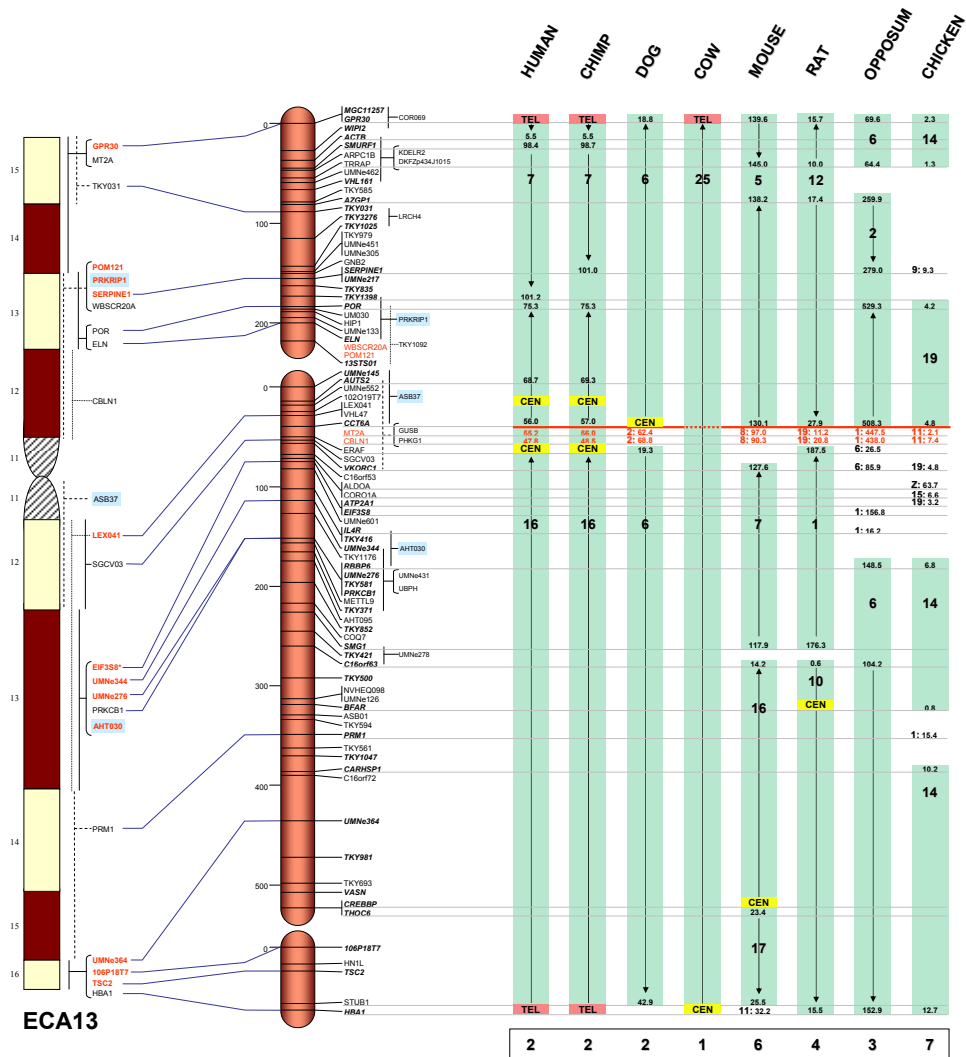


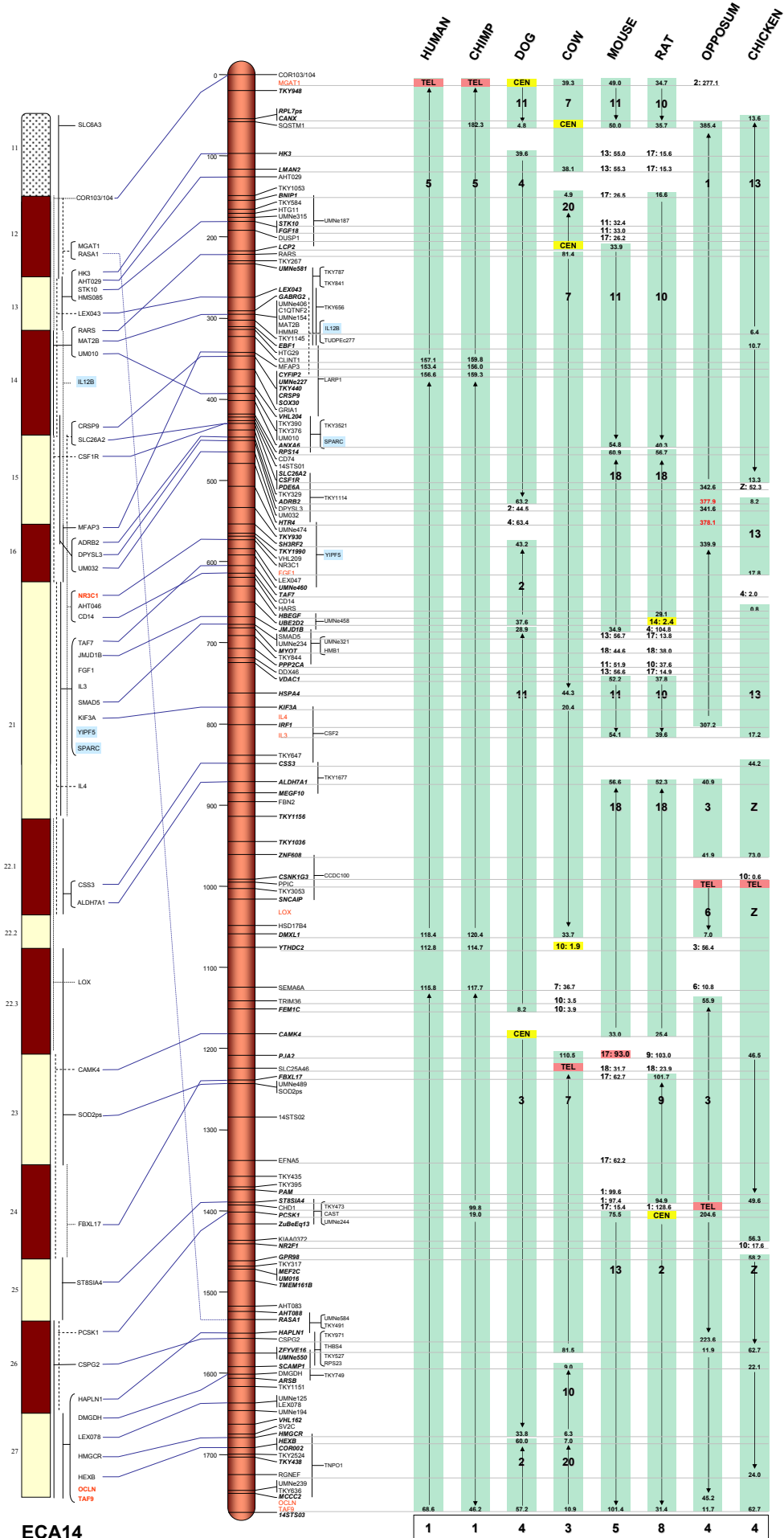




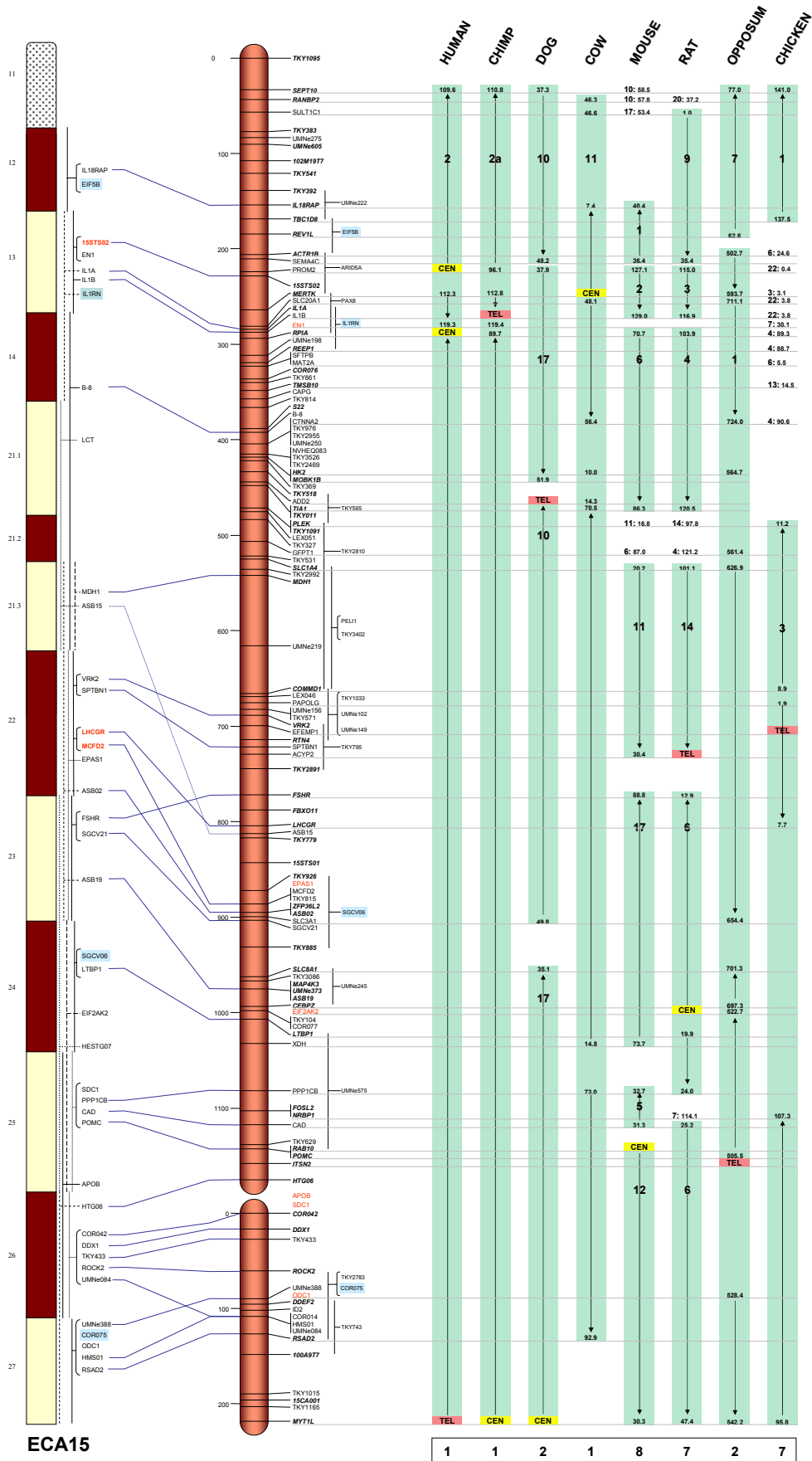


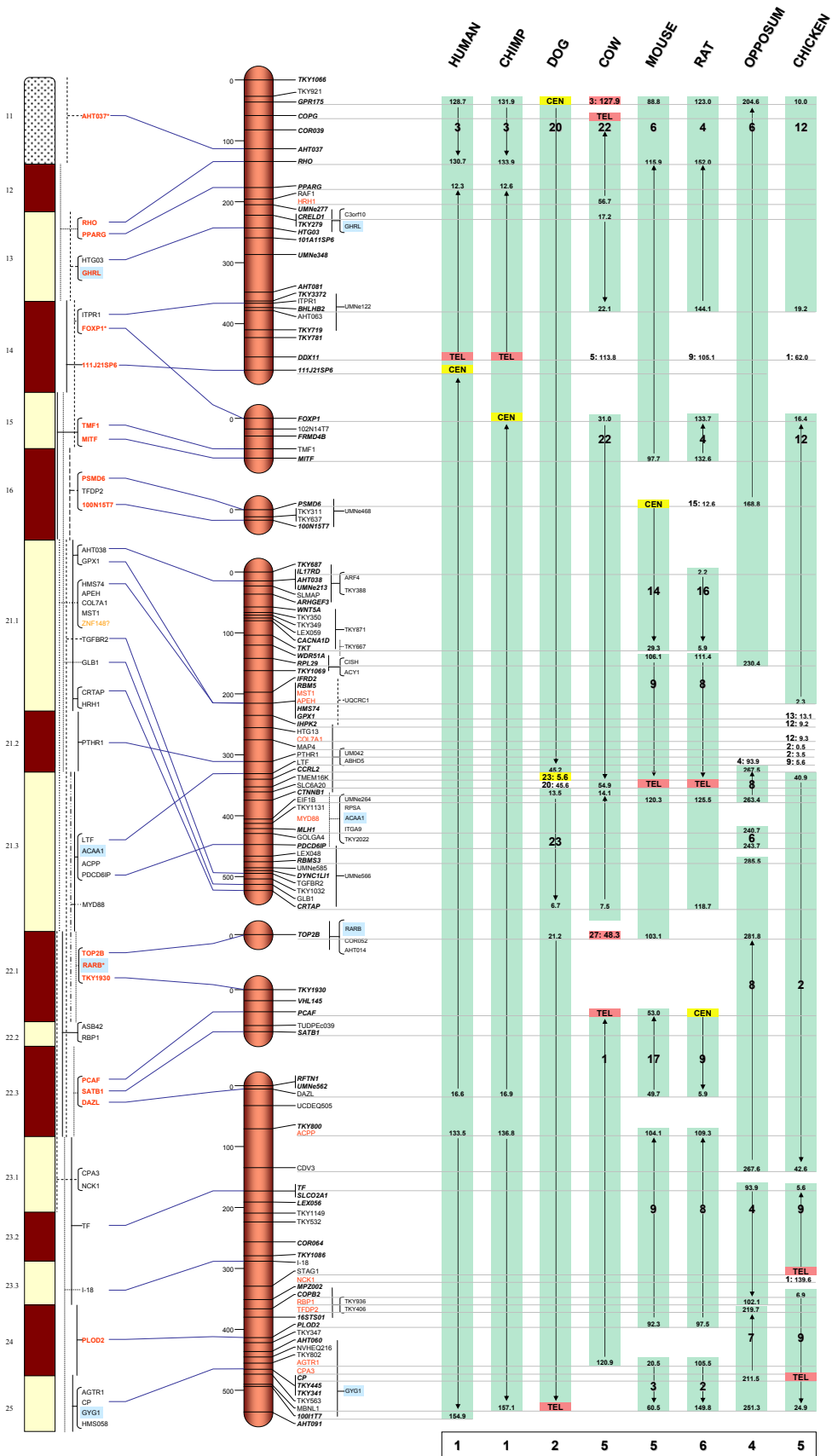




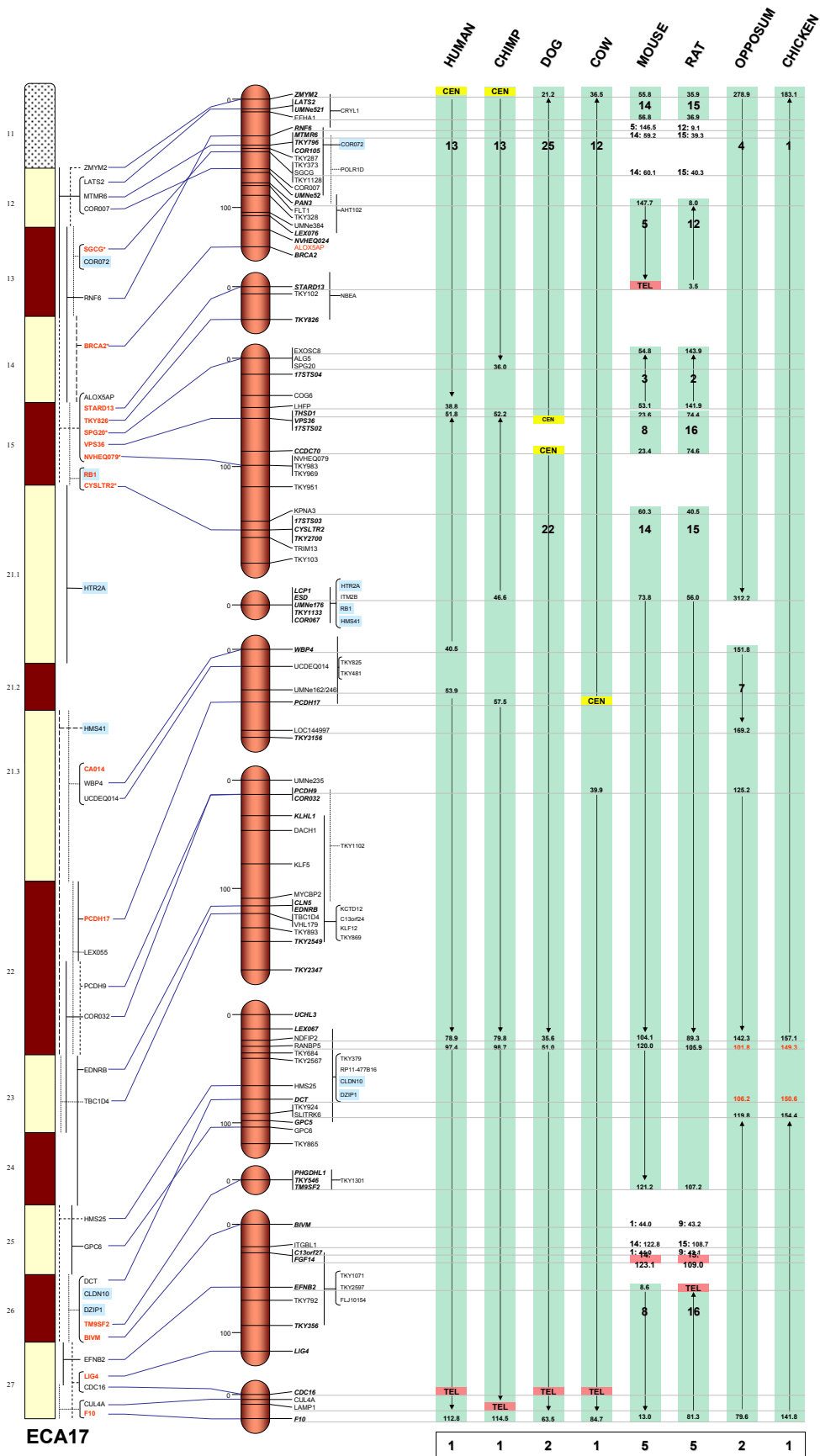


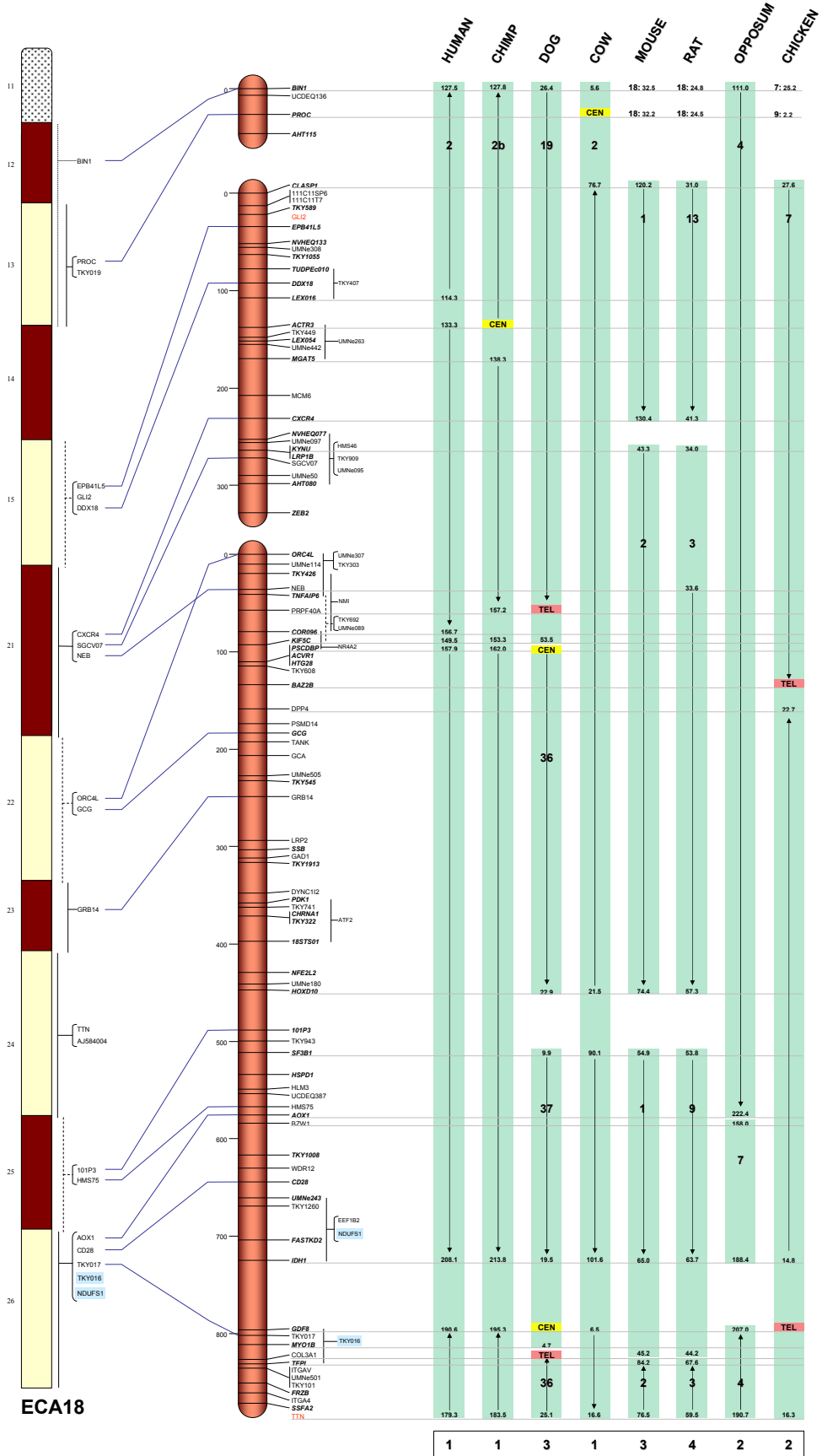
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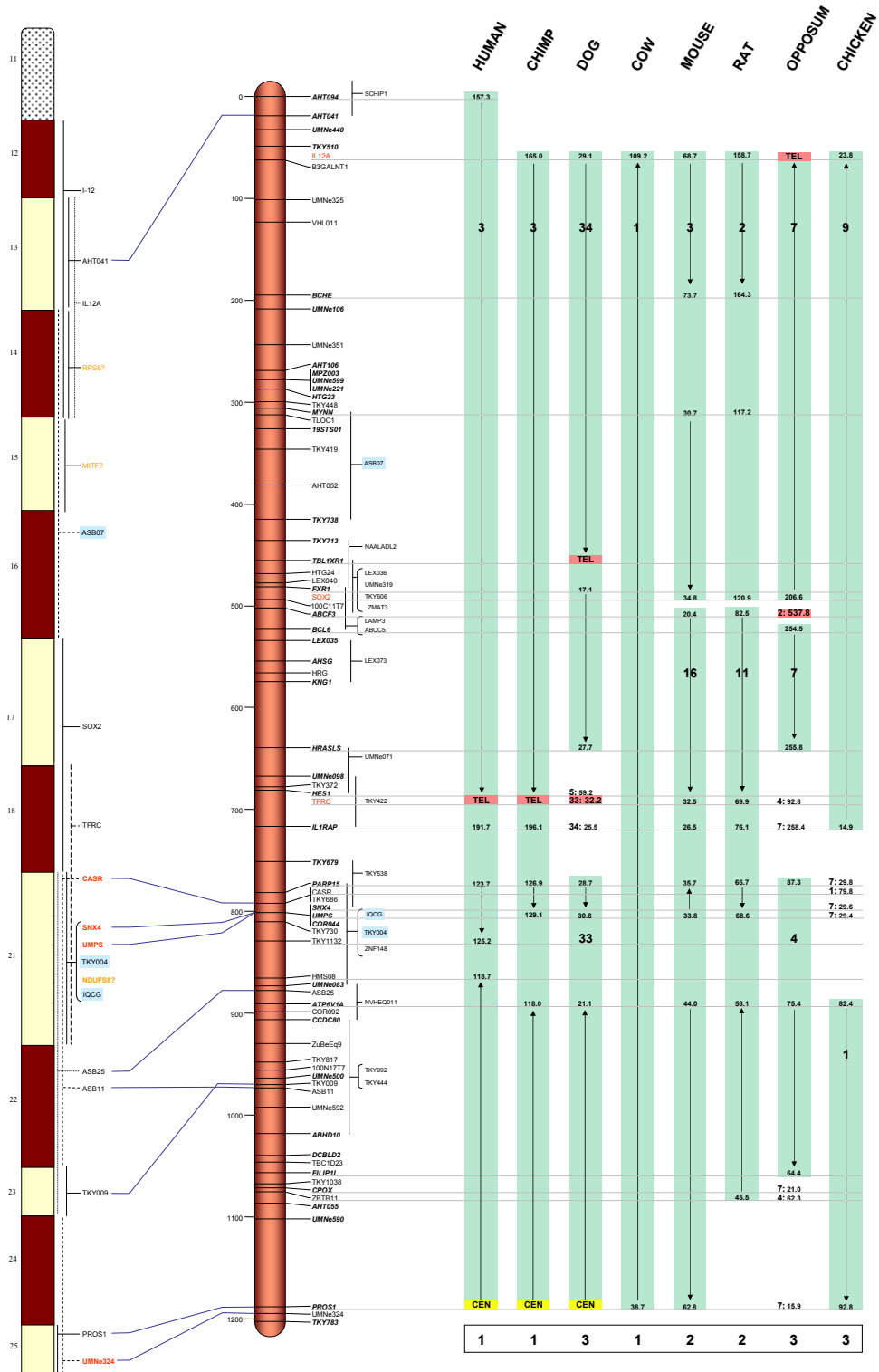




ECA16







ECA19

