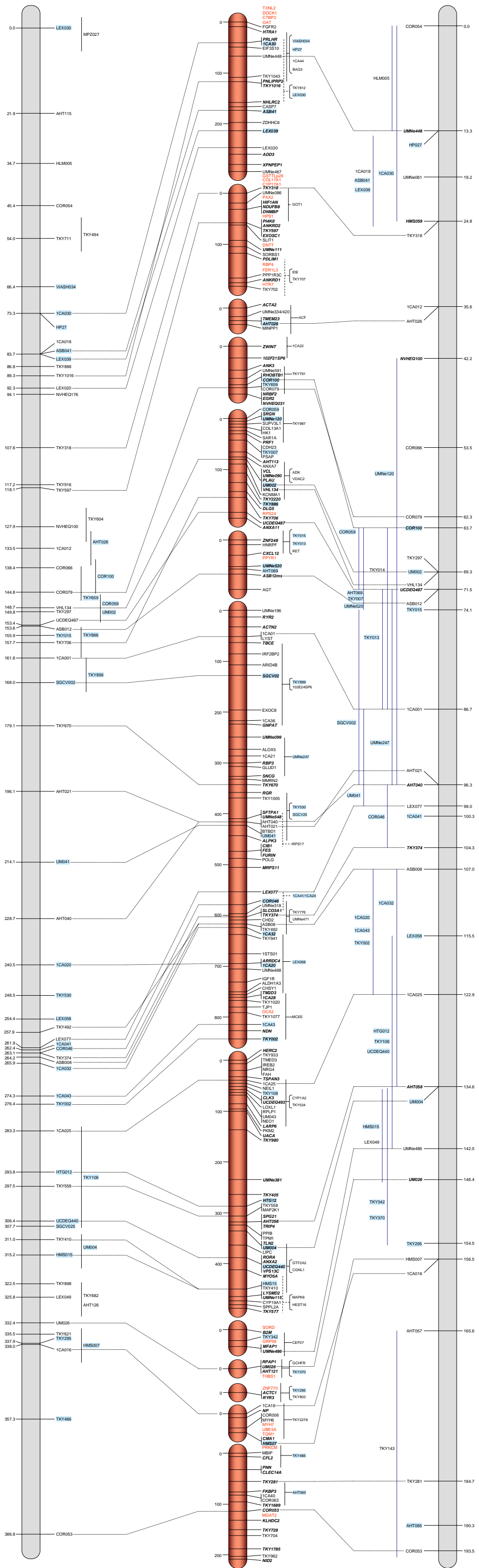


Supplementary Information

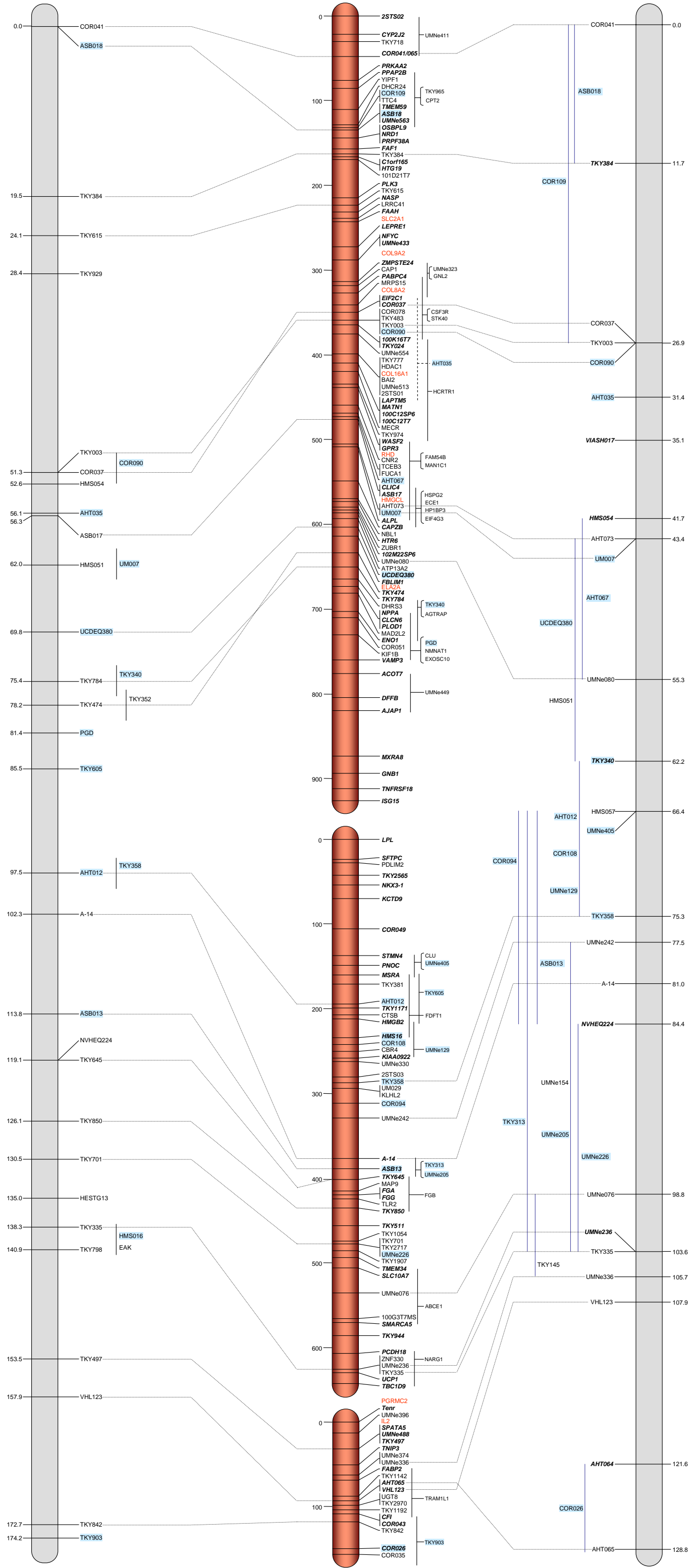
Legend for Supplementary Figures 2.1-2.X

Maps of individual horse chromosomes showing the integration of the second generation radiation hybrid map (RH II; middle) with the two recent whole genome meiotic maps (viz., the IHRFP linkage map - Penedo et al. 2005, to the *left* and the AHT linkage map - Swinburne et al. 2006, to the *right*). The vertical rounded bar(s) represent RH or the meiotic linkage groups. CentiRay (cR) or centiMorgan (cM) distances are shown beside markers of either map. On the RH map (middle), the MLE-consensus markers are depicted in bold-italics while placed markers are in normal font. Binned markers are shown on the side of the RH or linkage maps and are assigned to a map region indicated by thin vertical lines. Markers shared between RH II and the meiotic maps are connected with lines. Markers in blue shaded boxes are binned on at least one of the three maps.

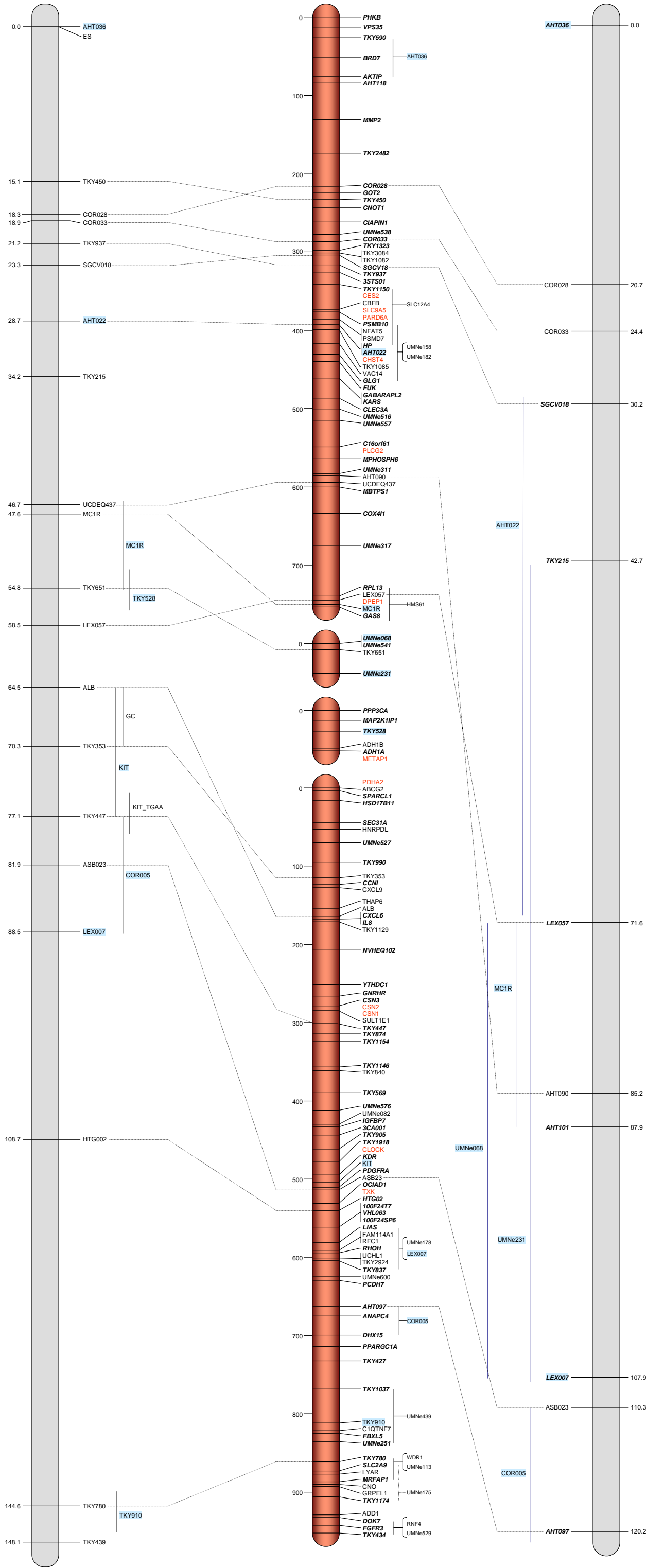
ECA1



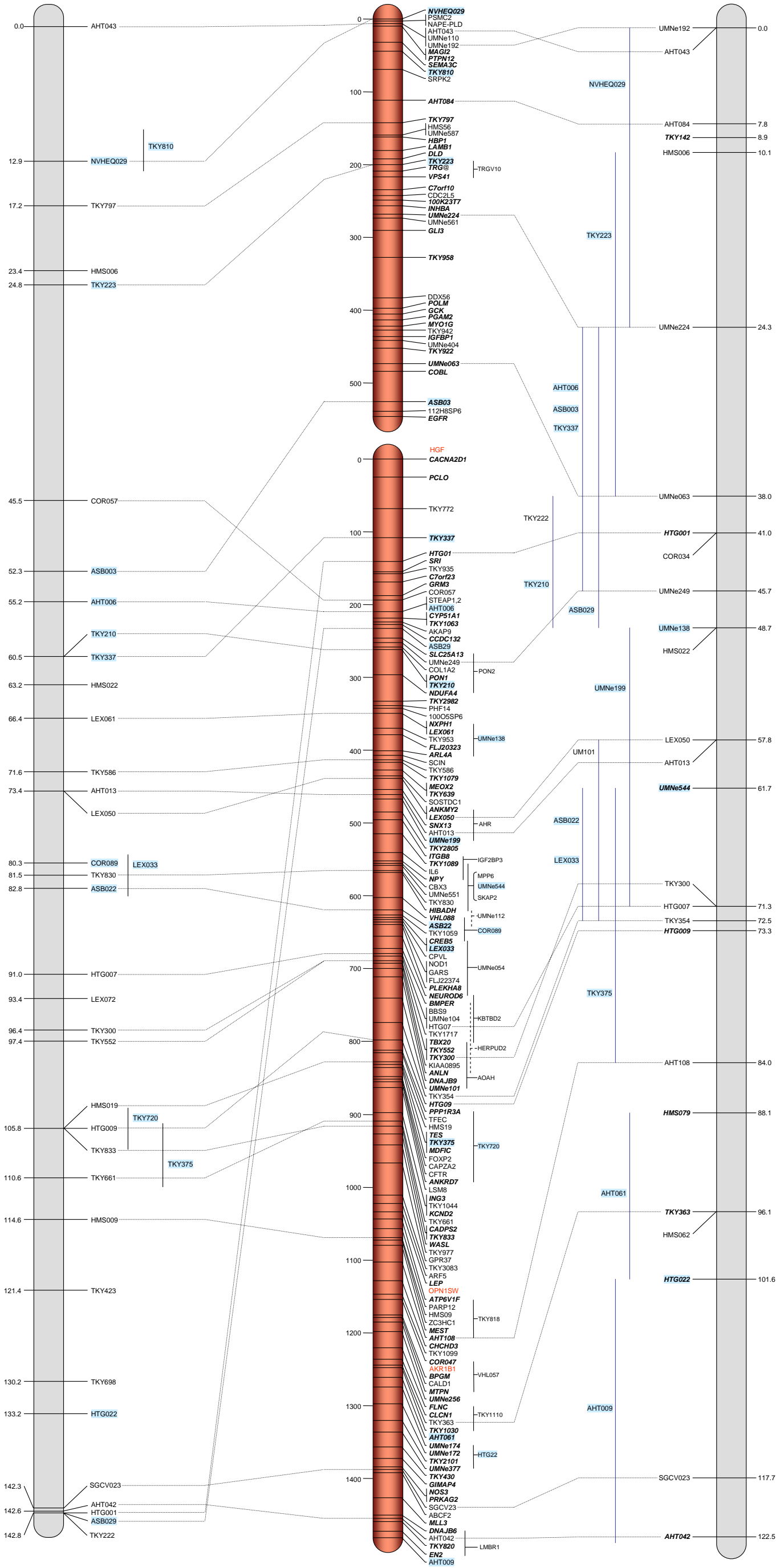
ECA 2



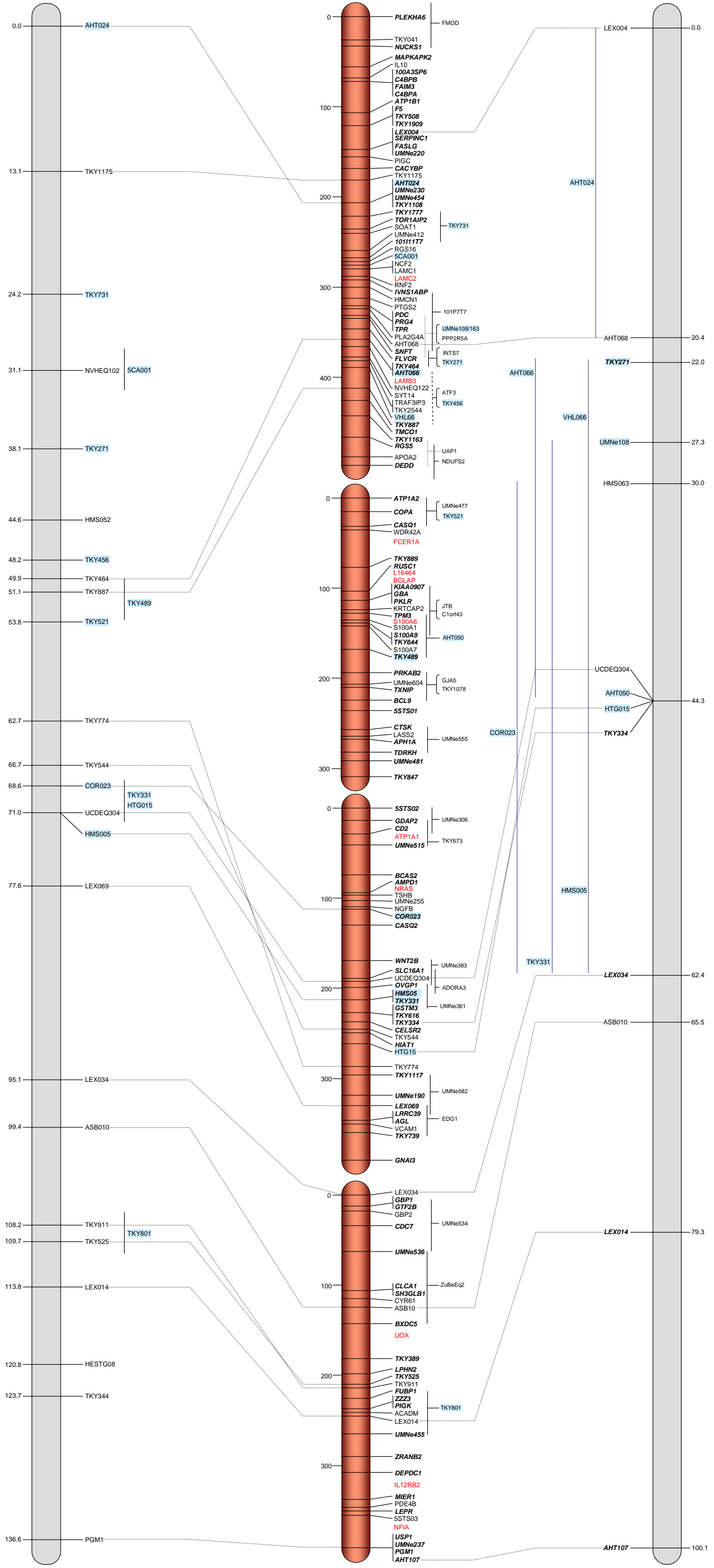
ECA3



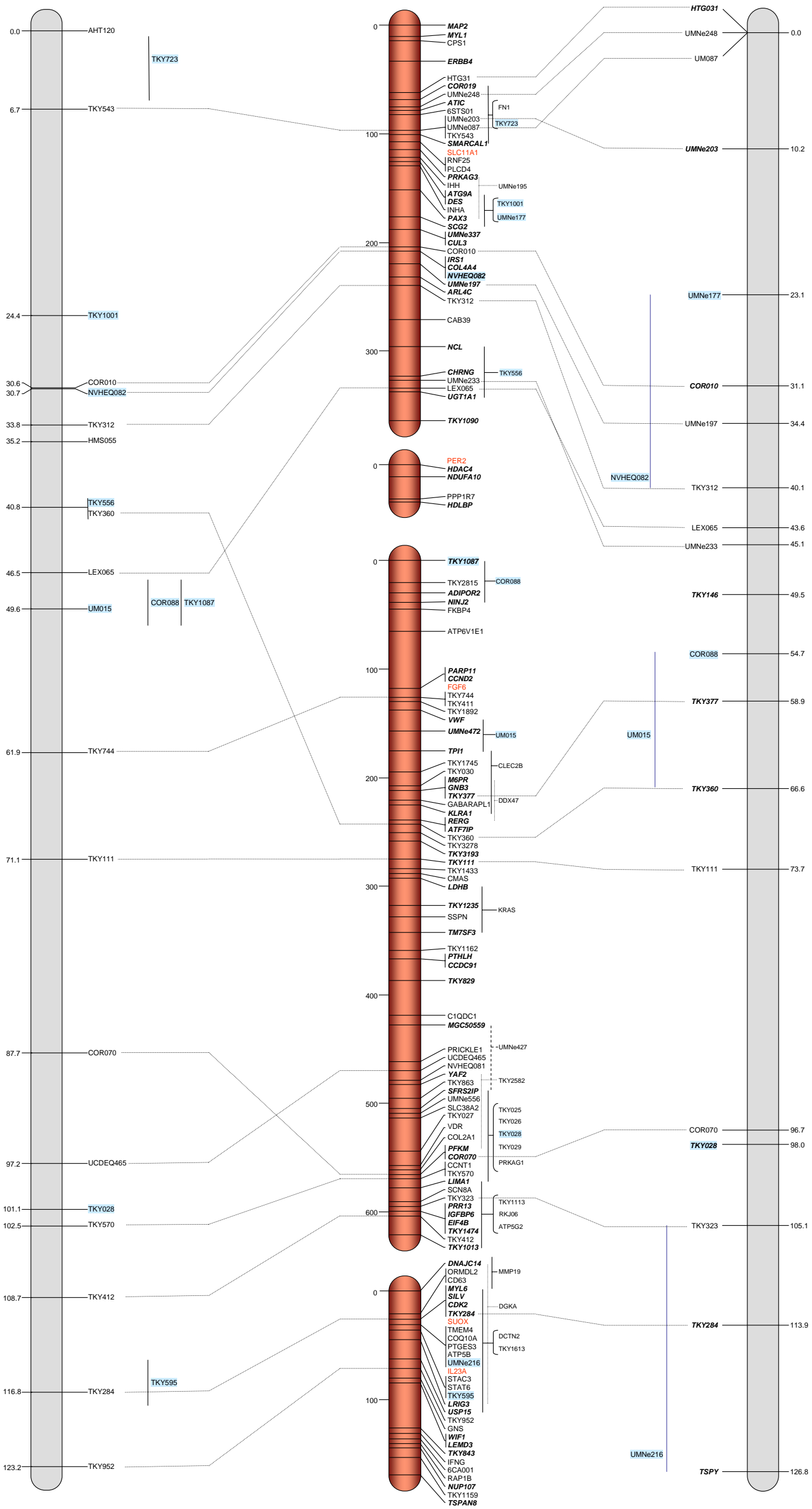
ECA4



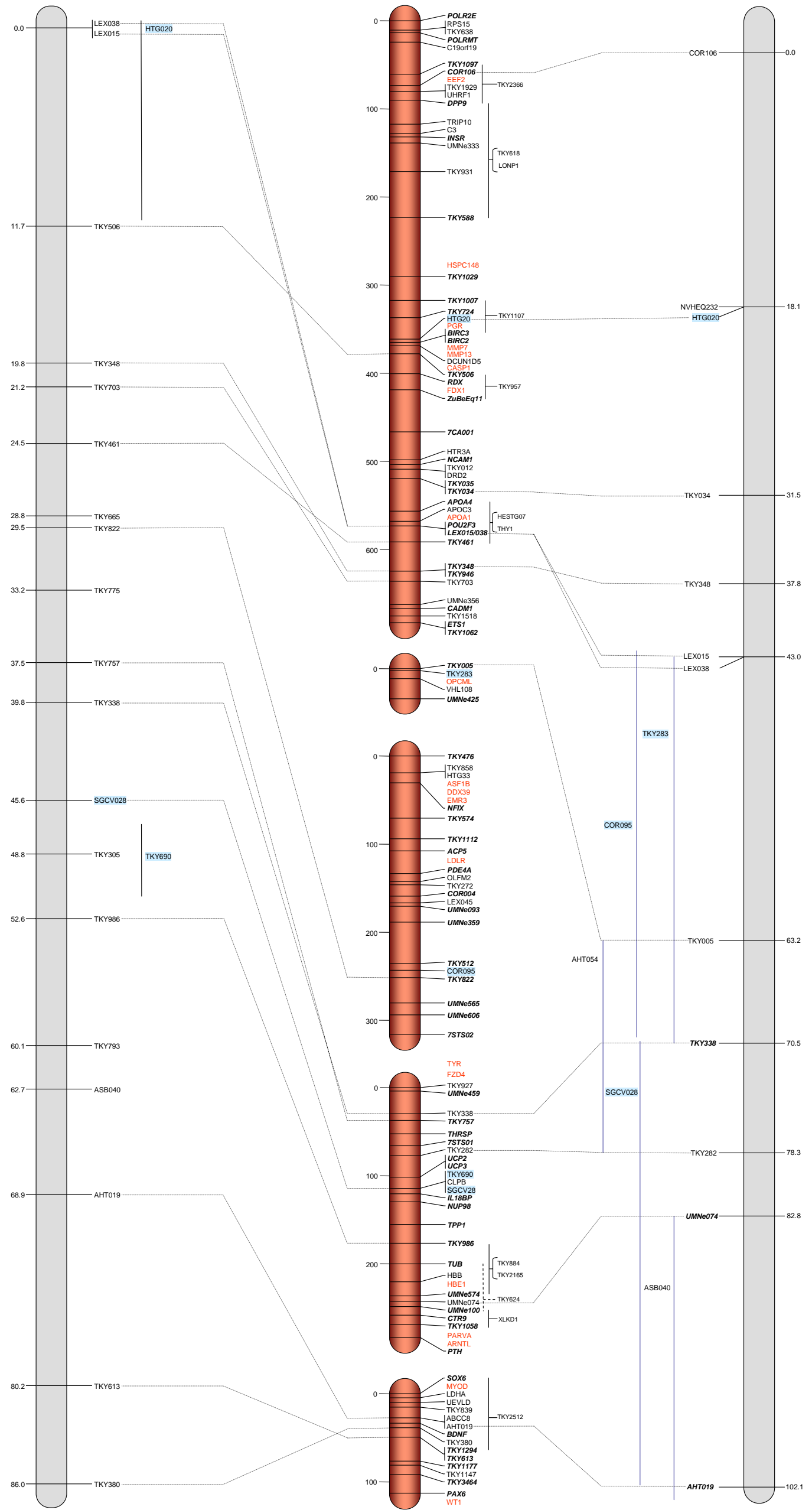
ECA 5



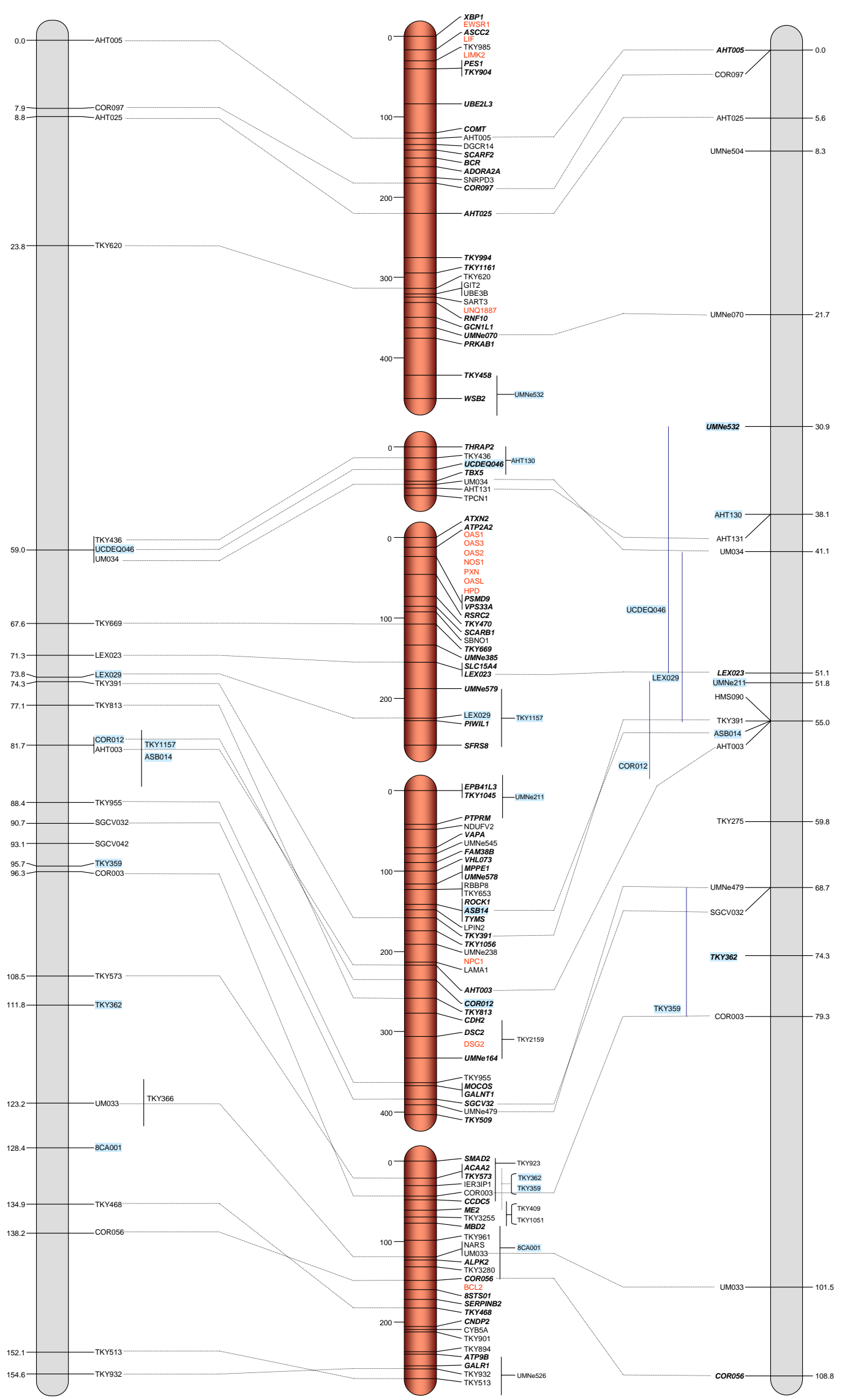
ECA6



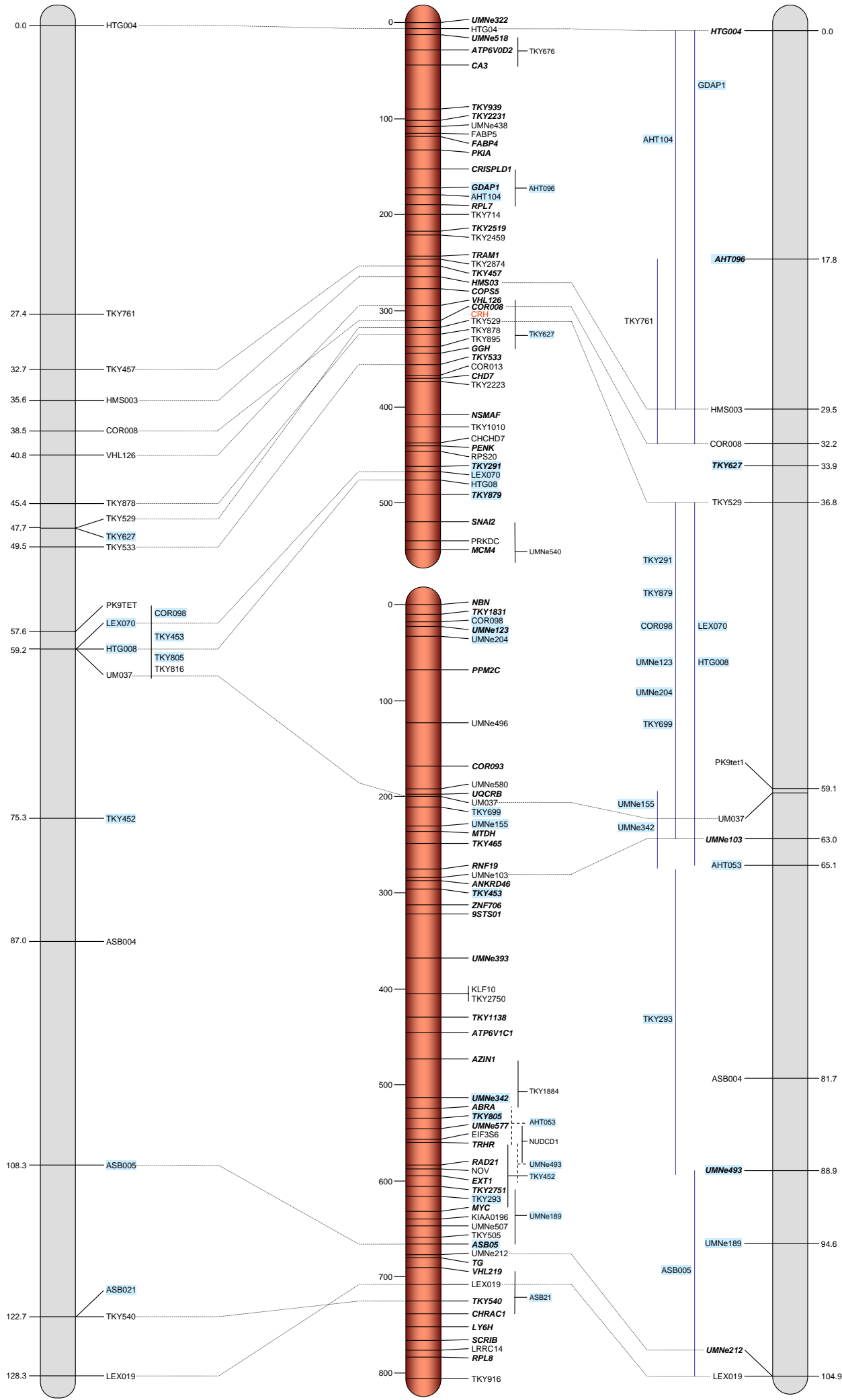
ECA7



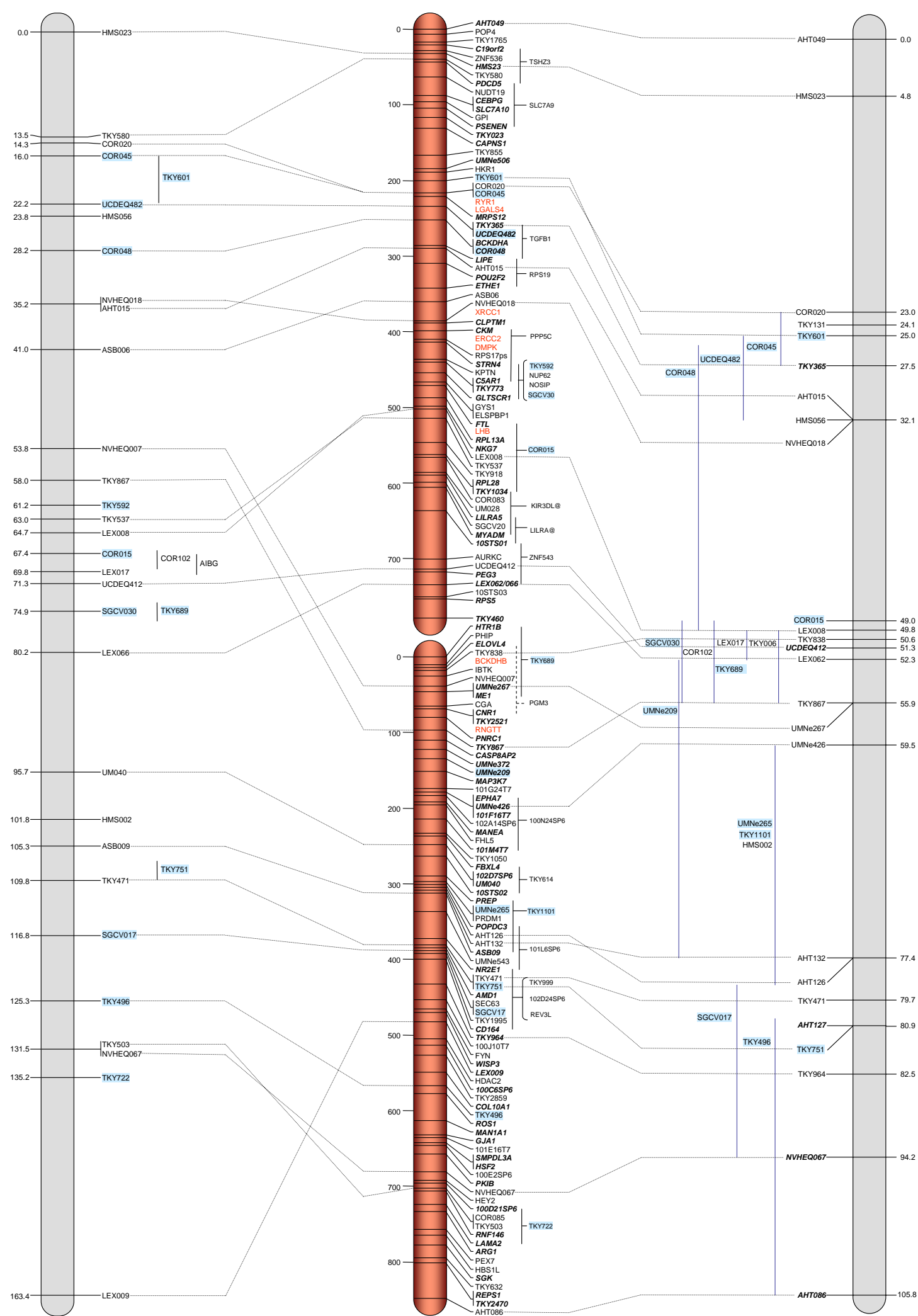
ECA8



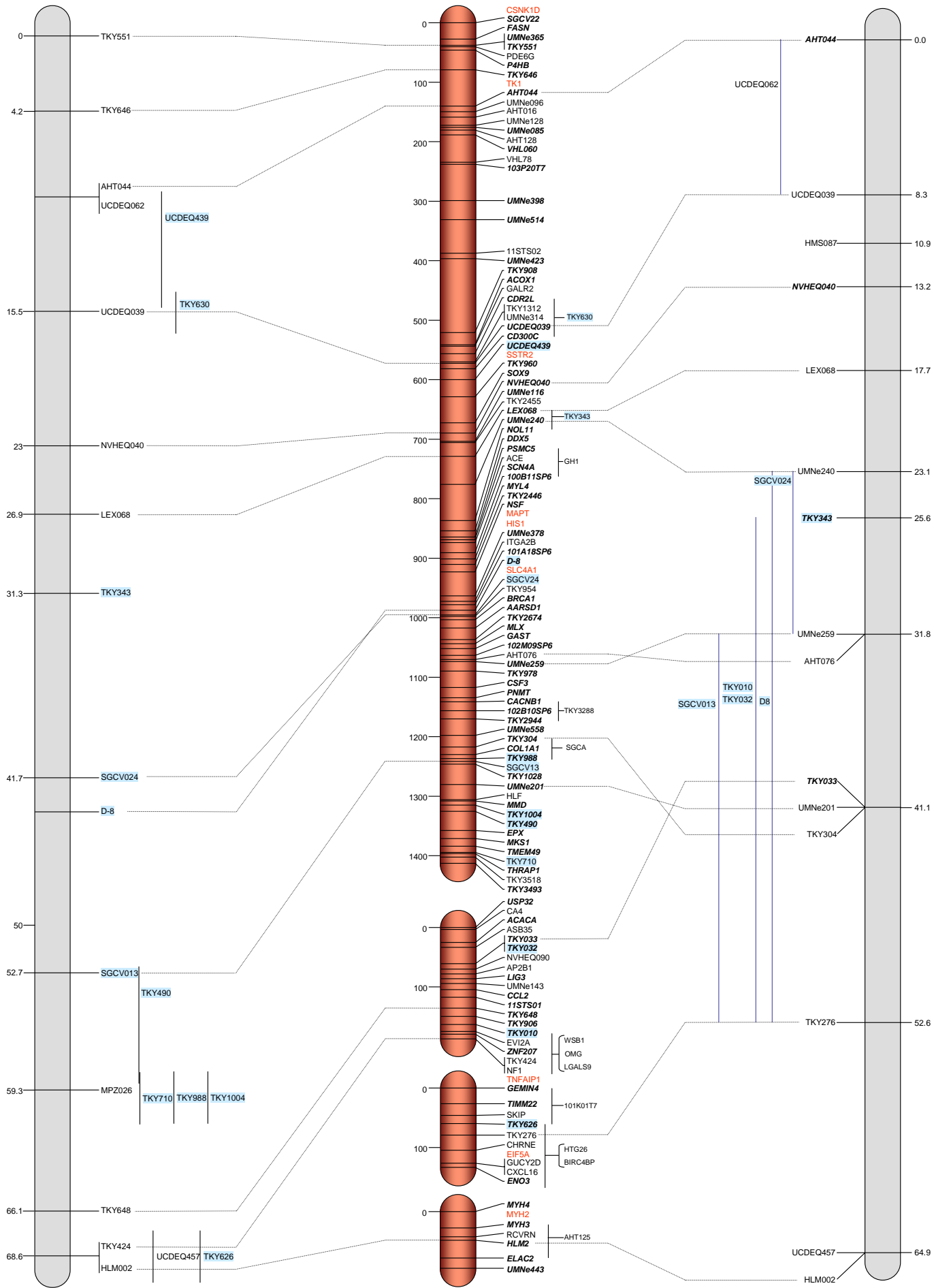
ECA9



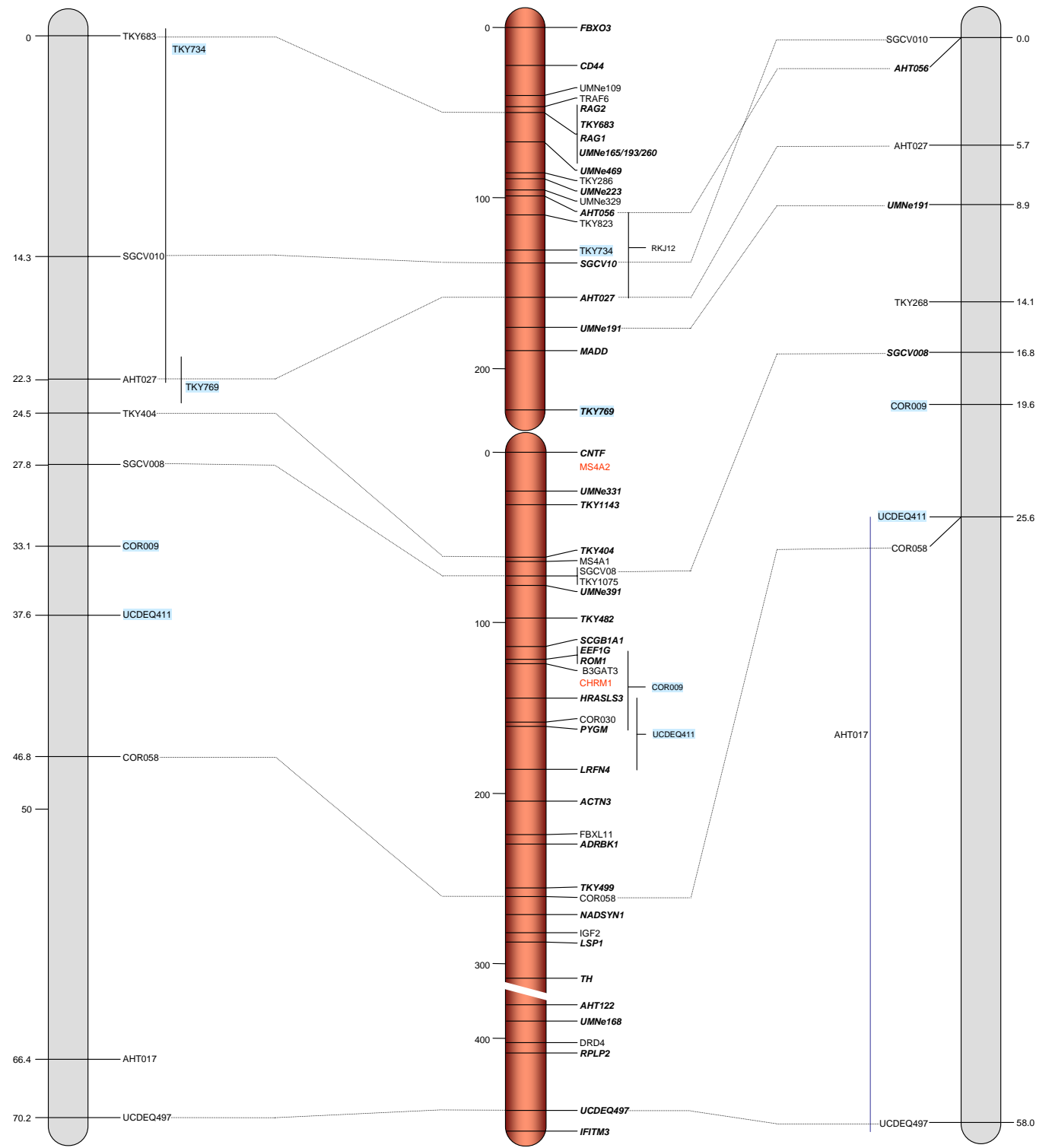
ECA10



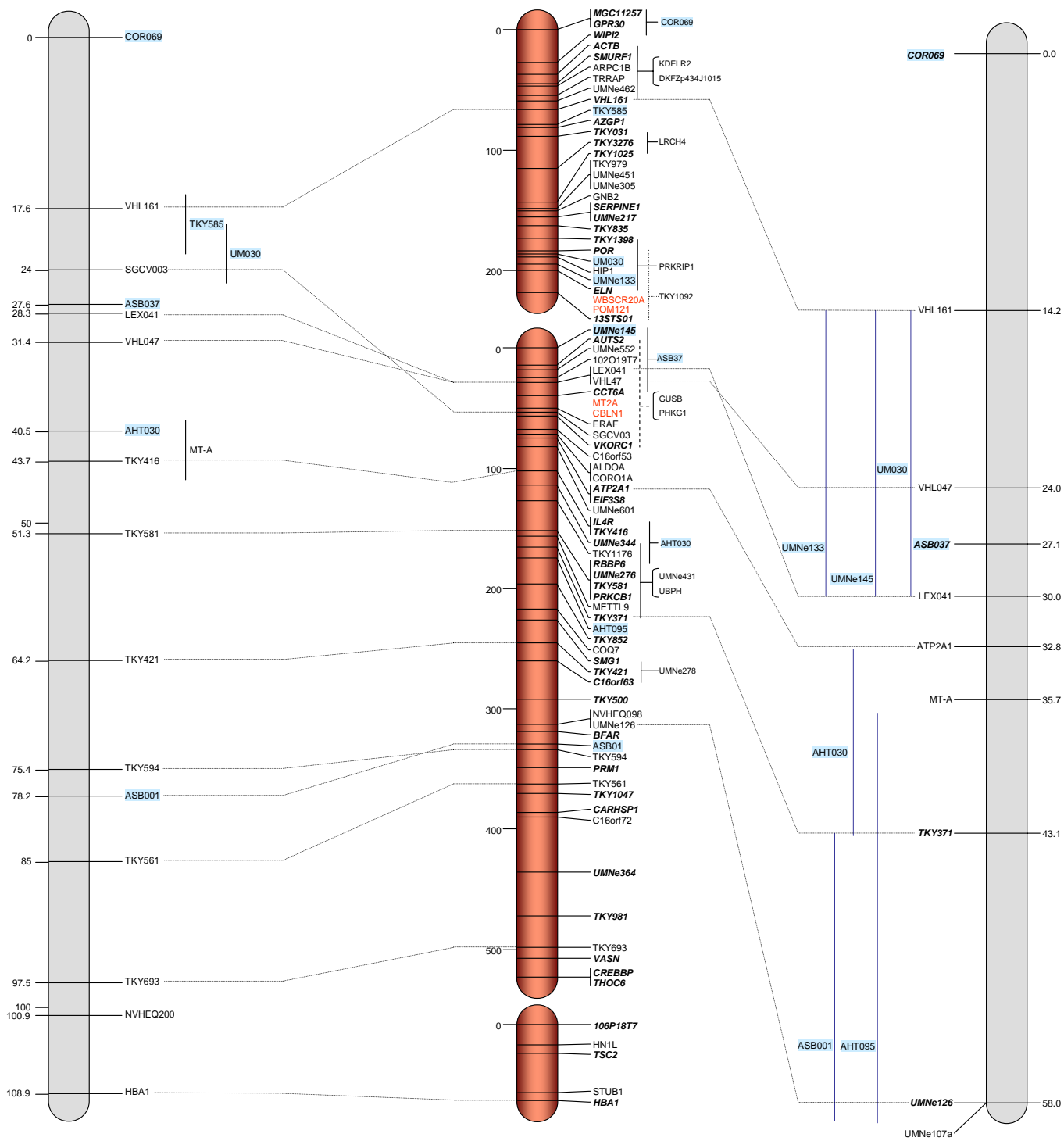
ECA11



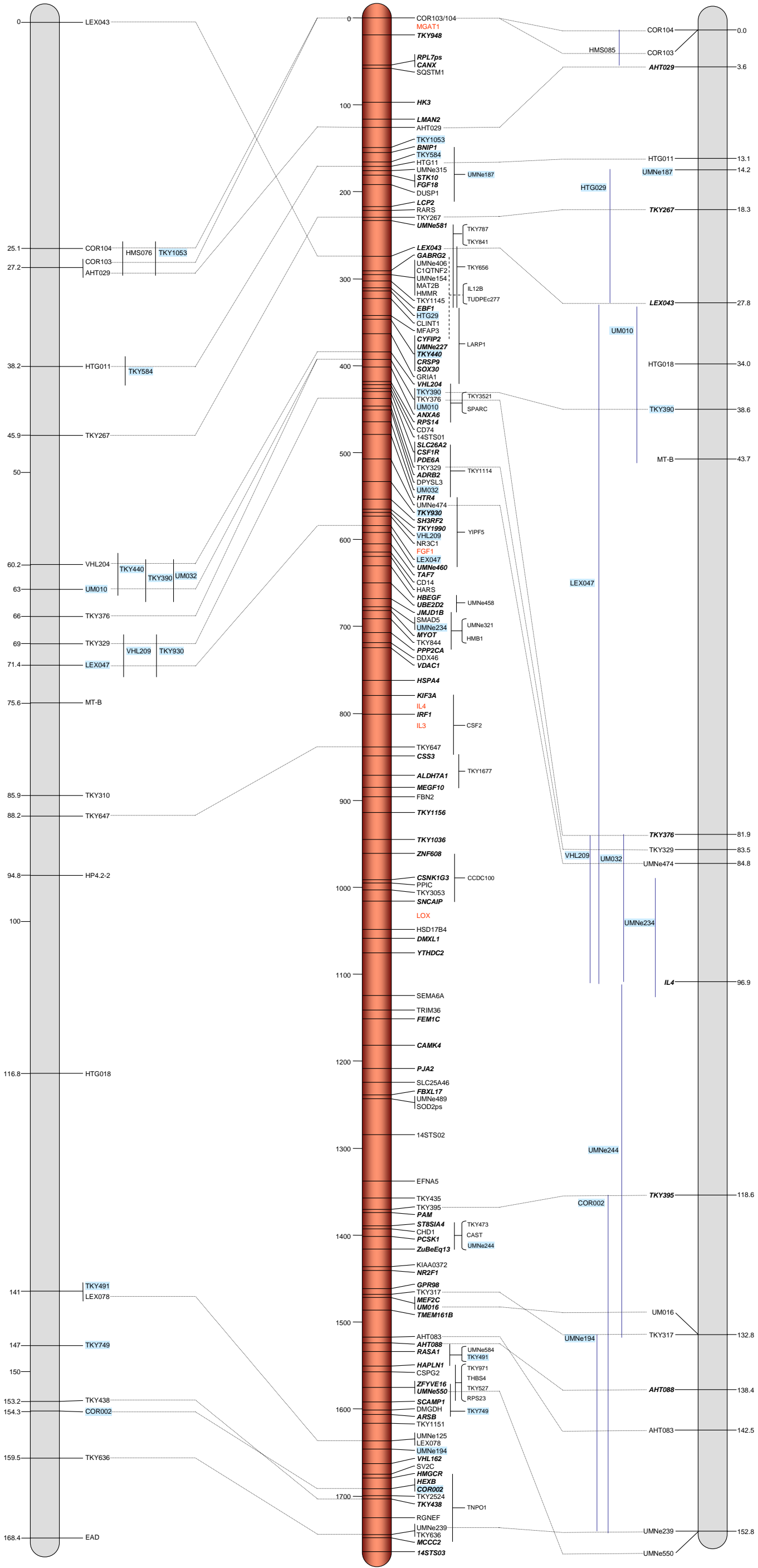
ECA12



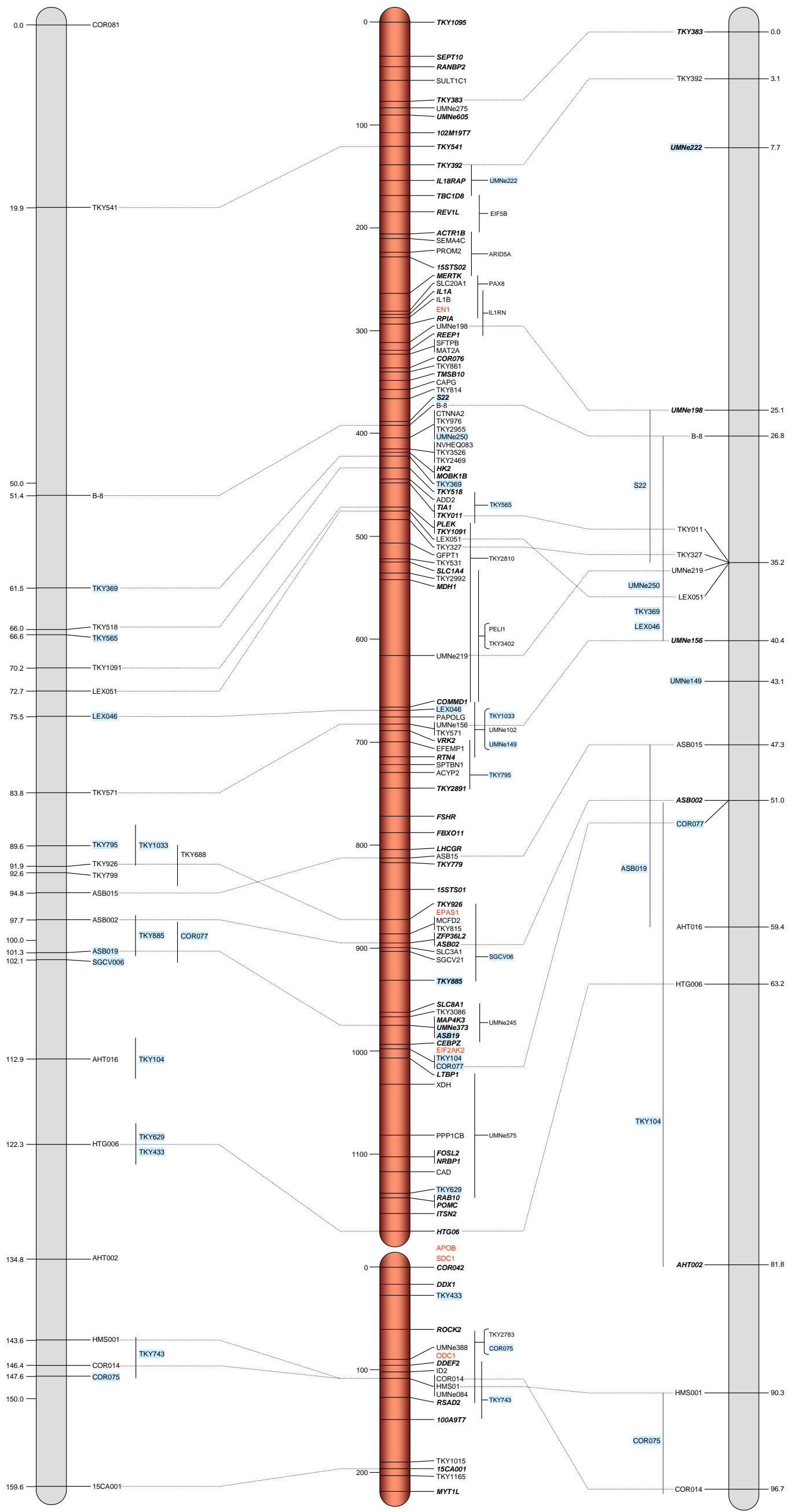
ECA13



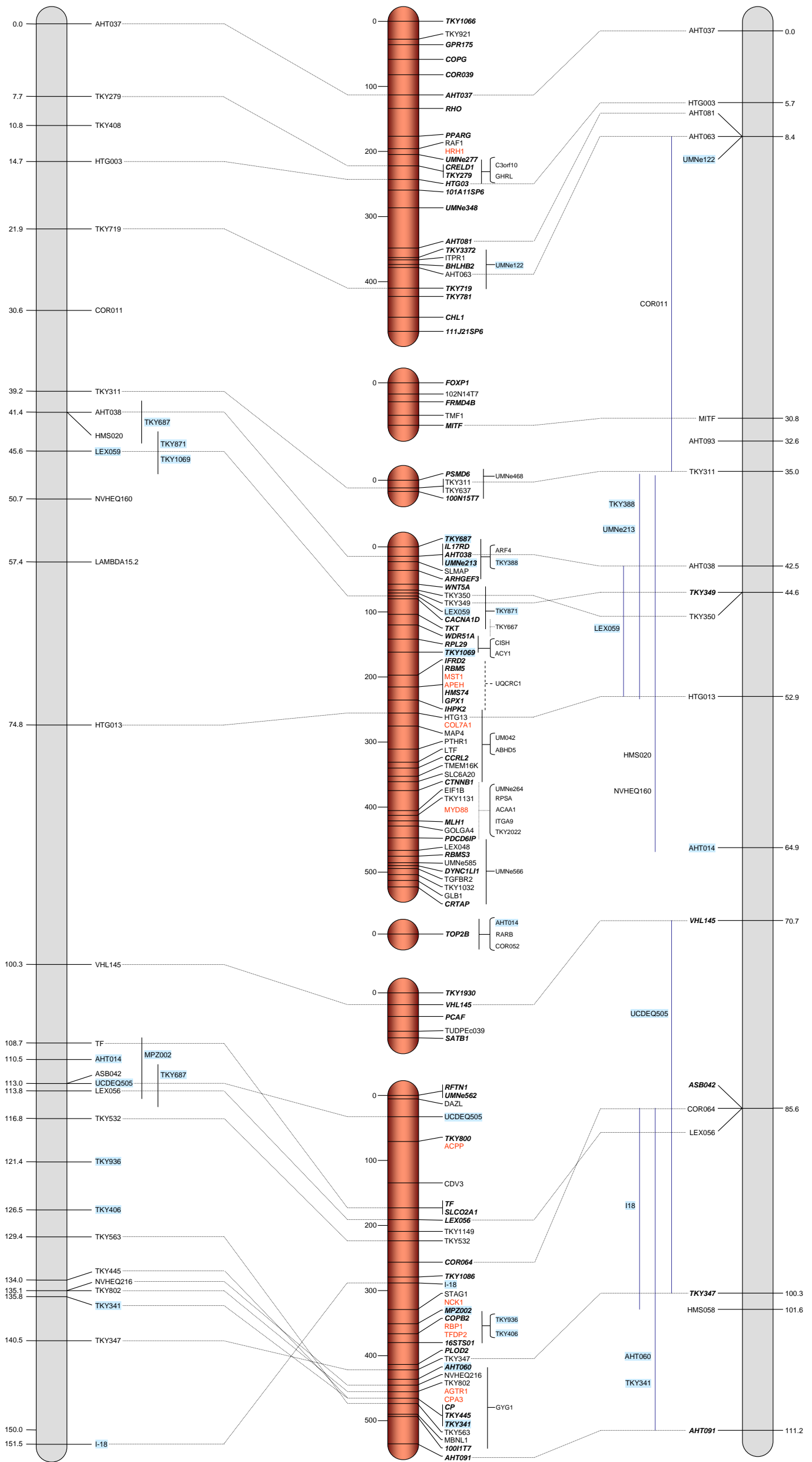
ECA14



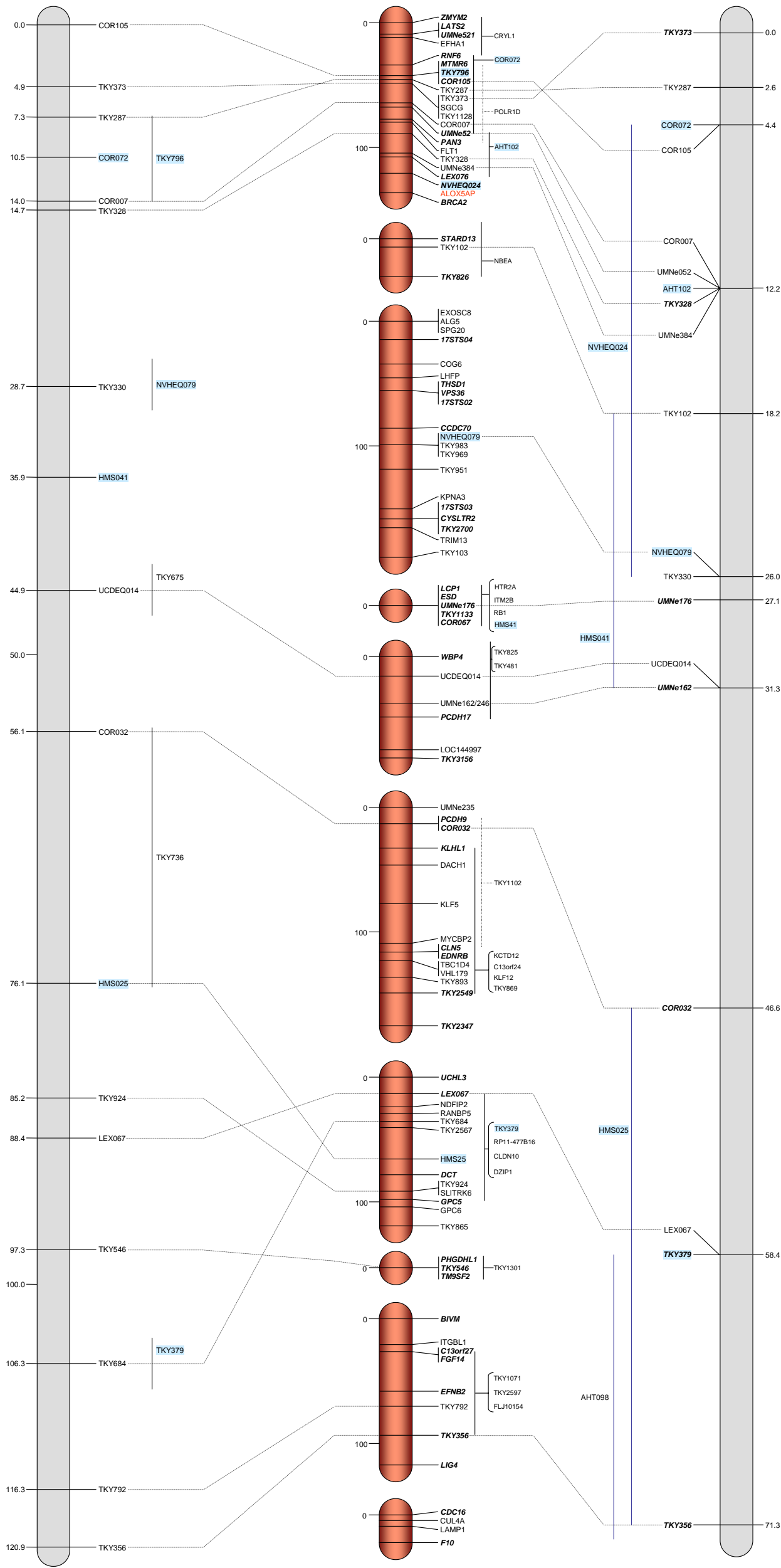
ECA15



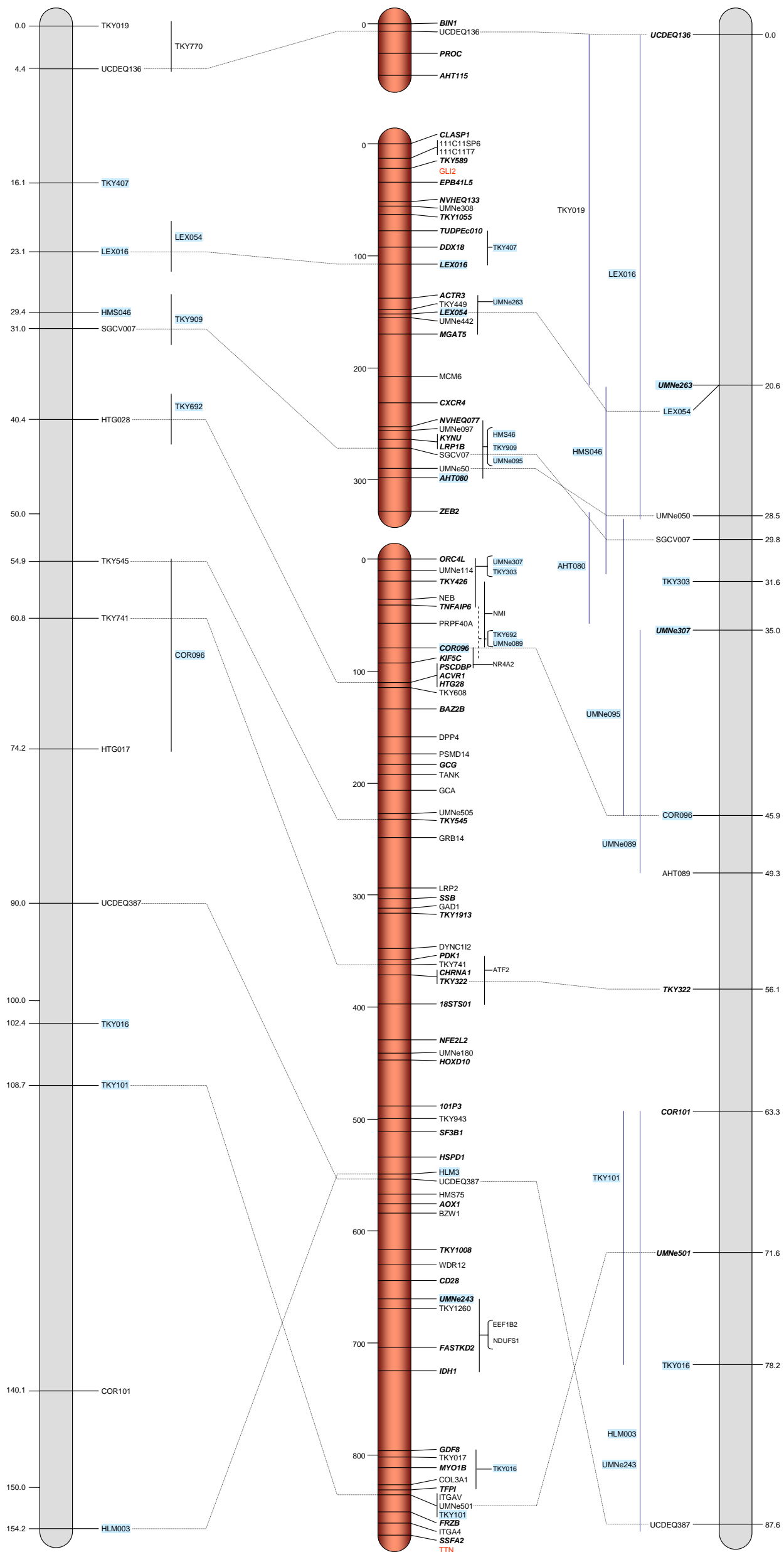
ECA16



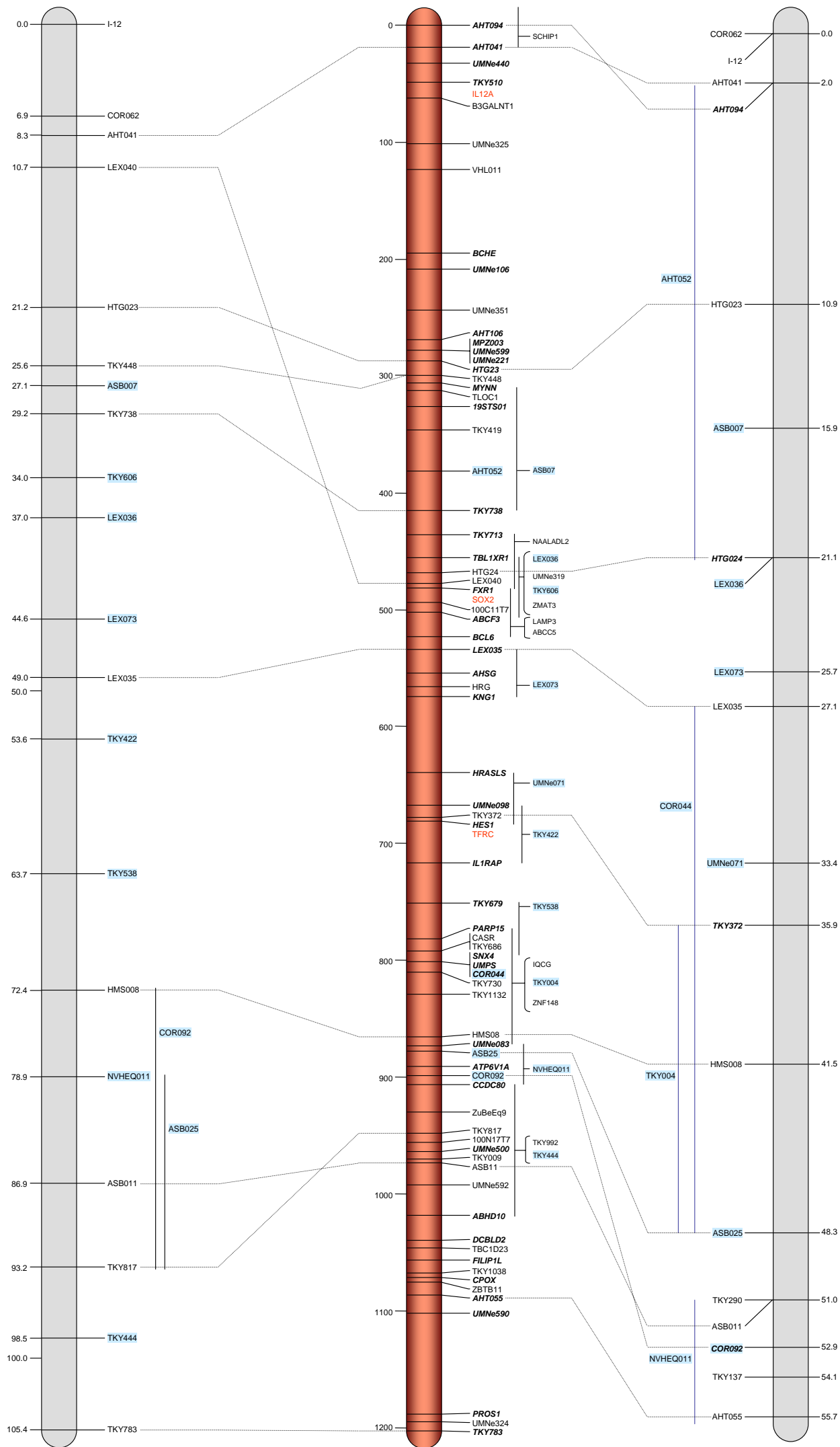
ECA17



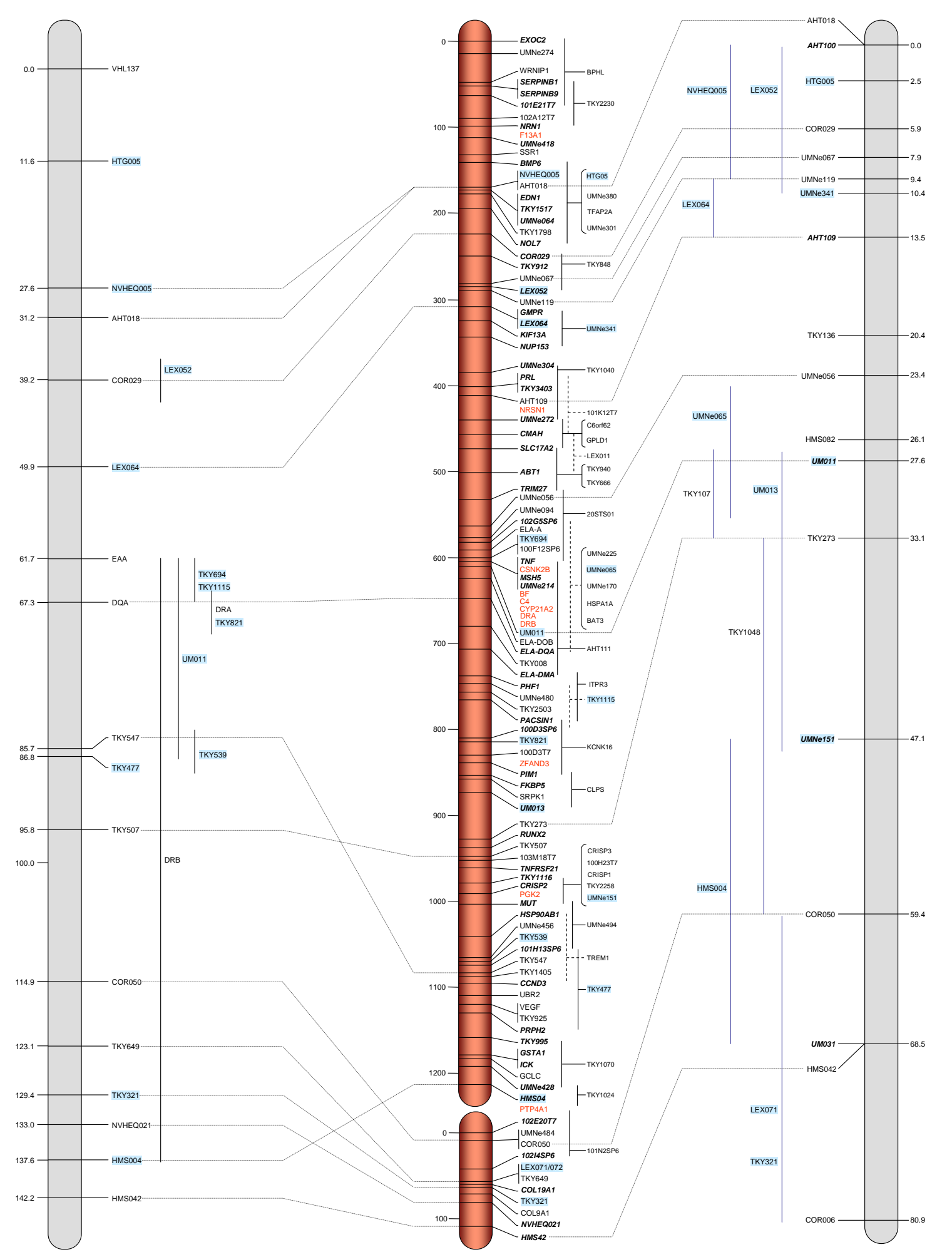
ECA18



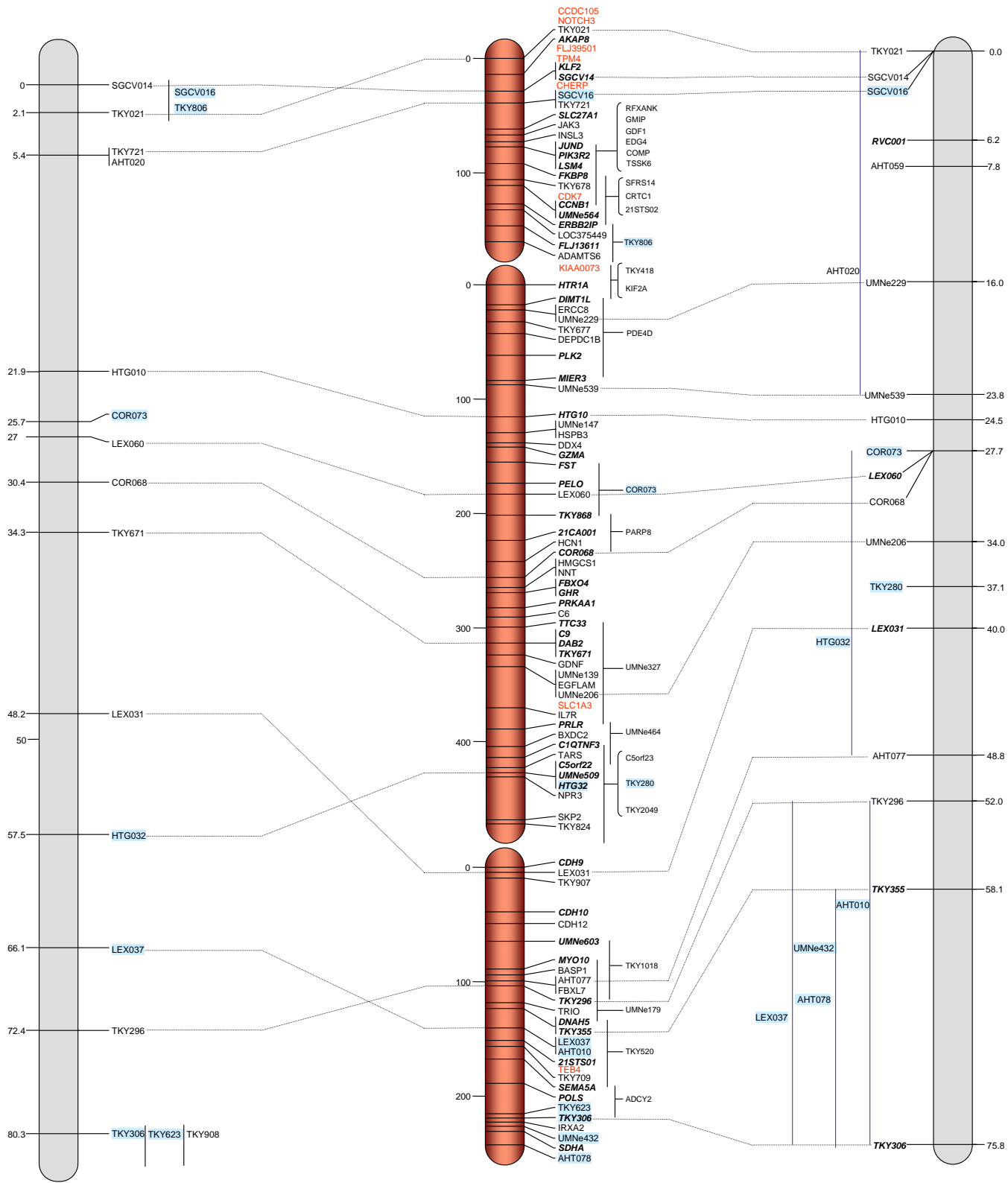
ECA19



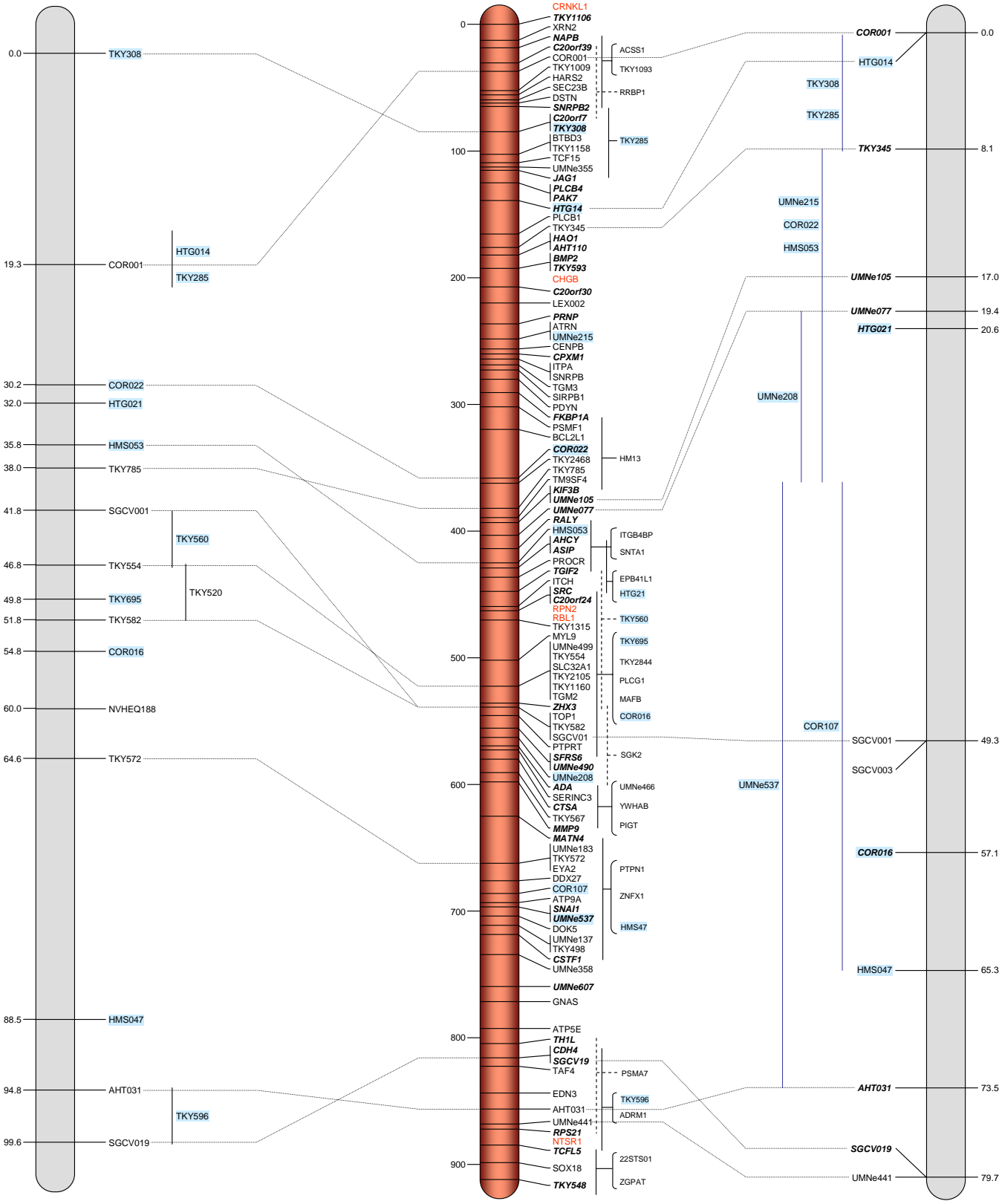
ECA20



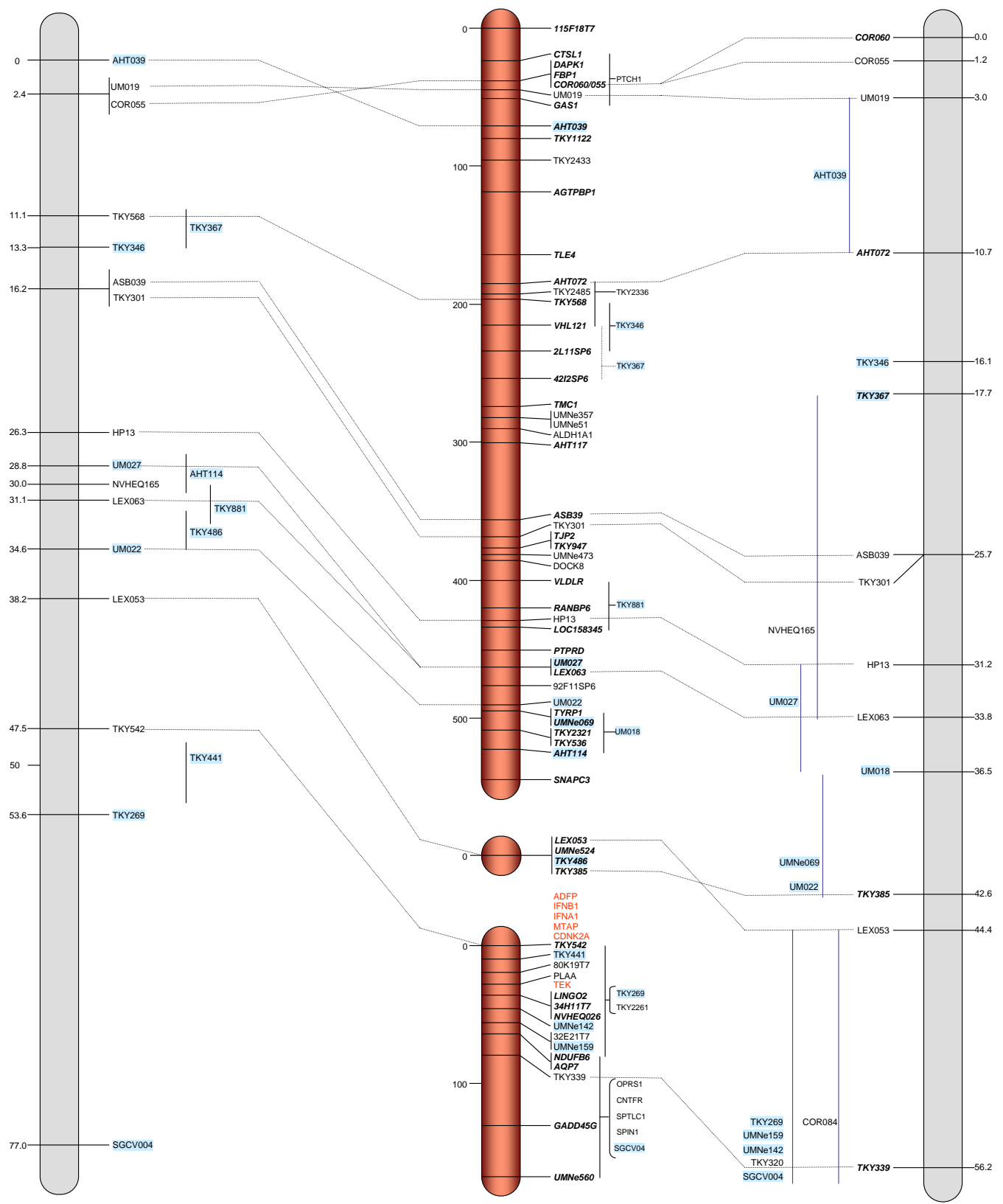
ECA 21



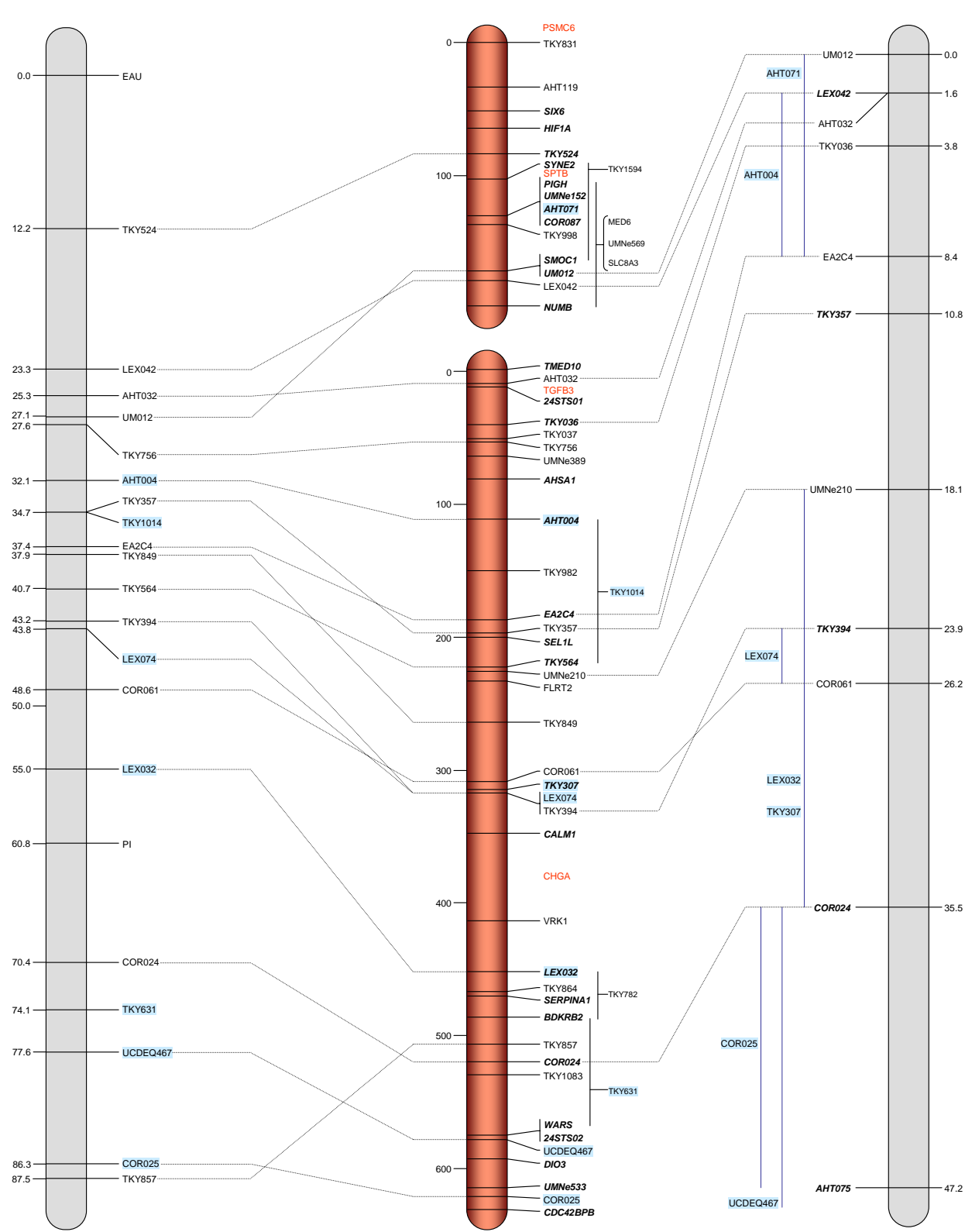
ECA22



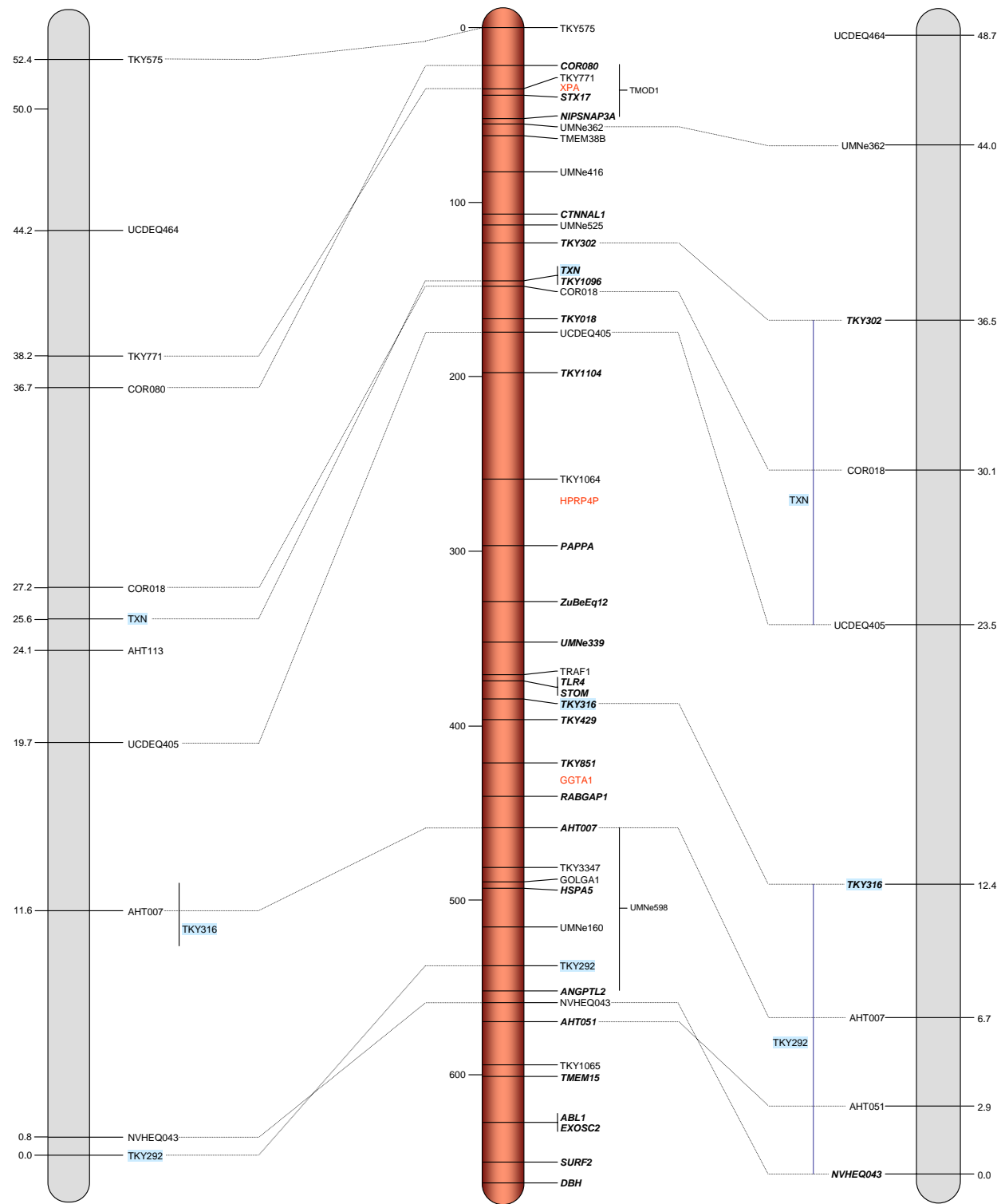
ECA23



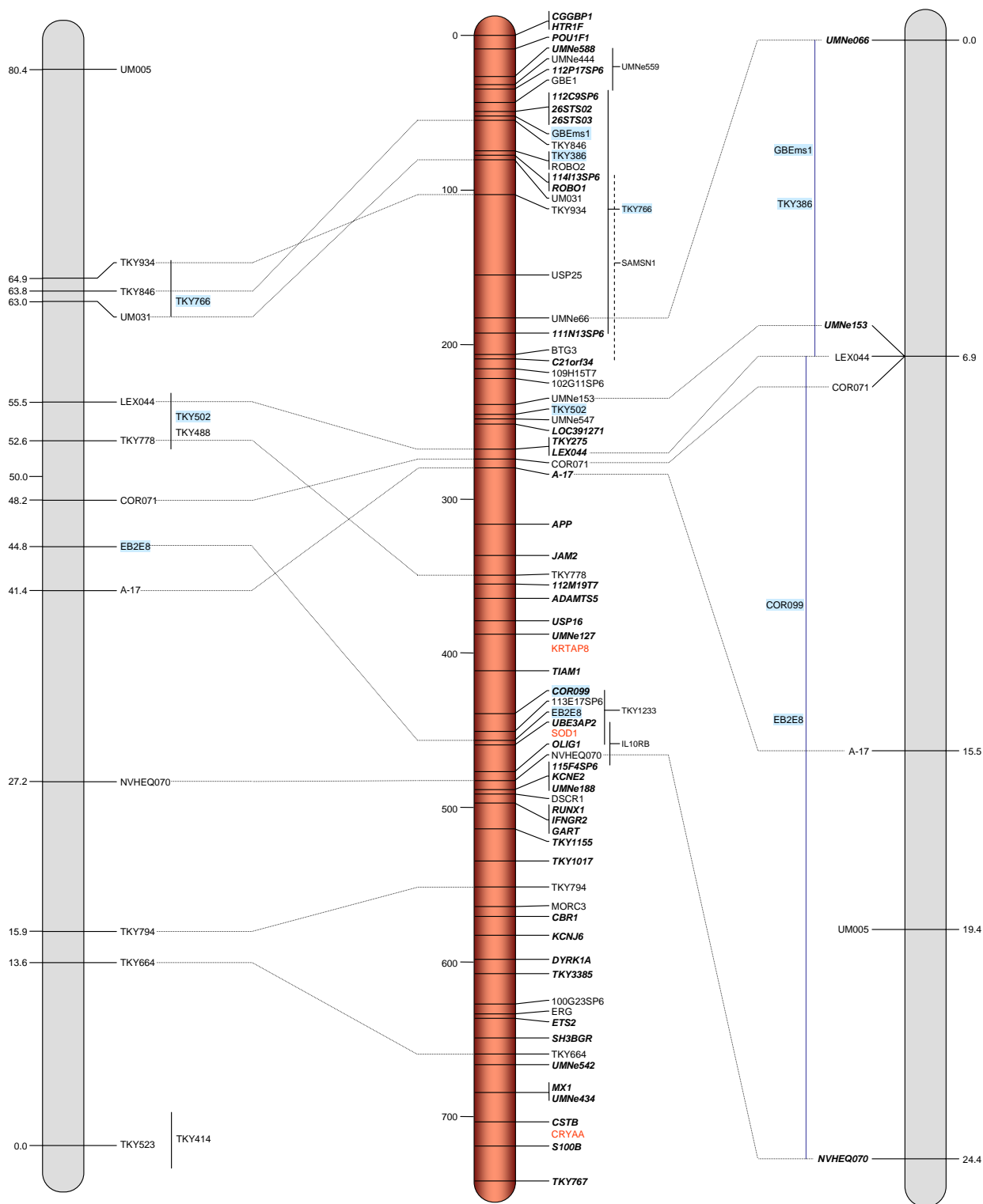
ECA24



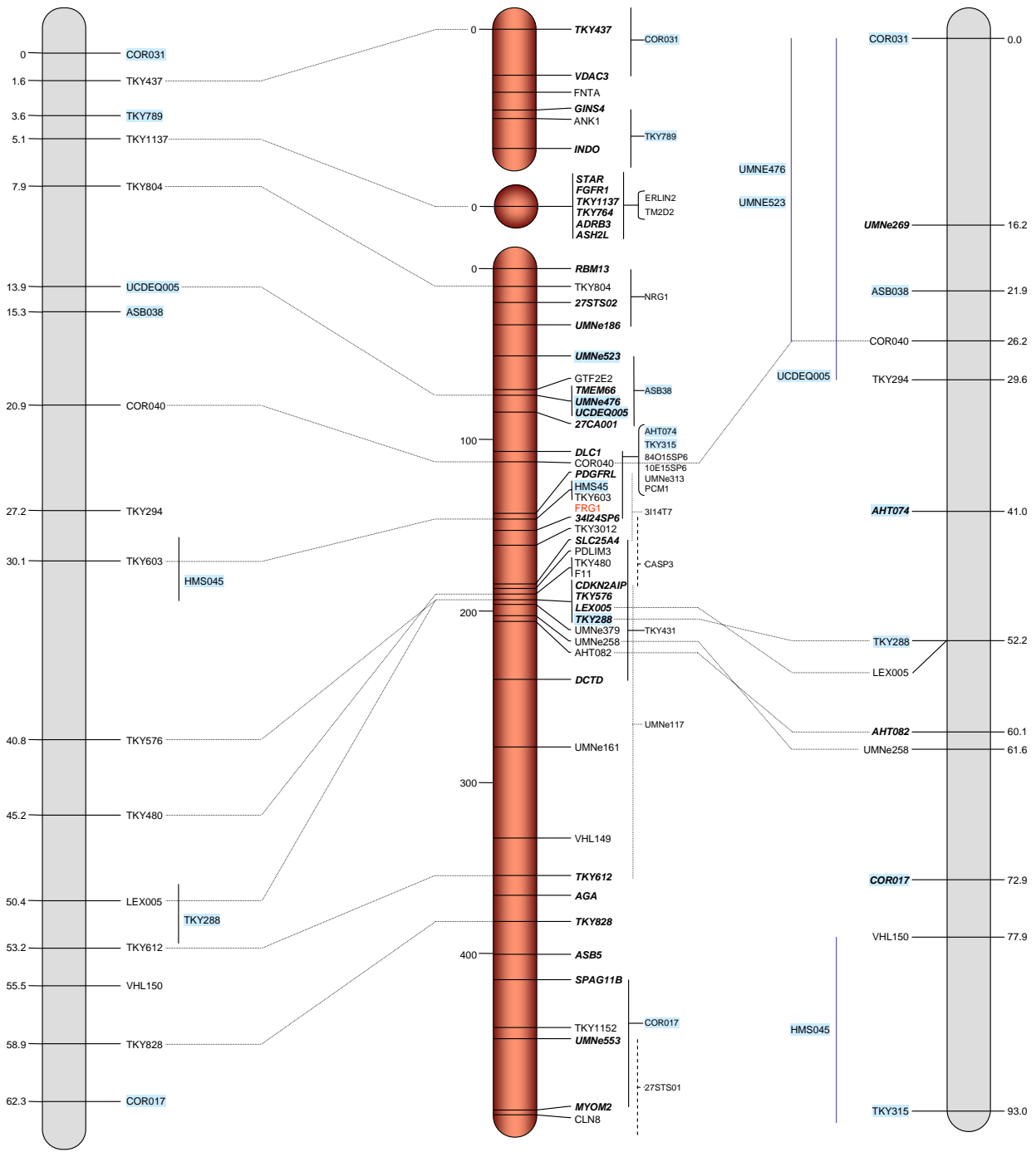
ECA25



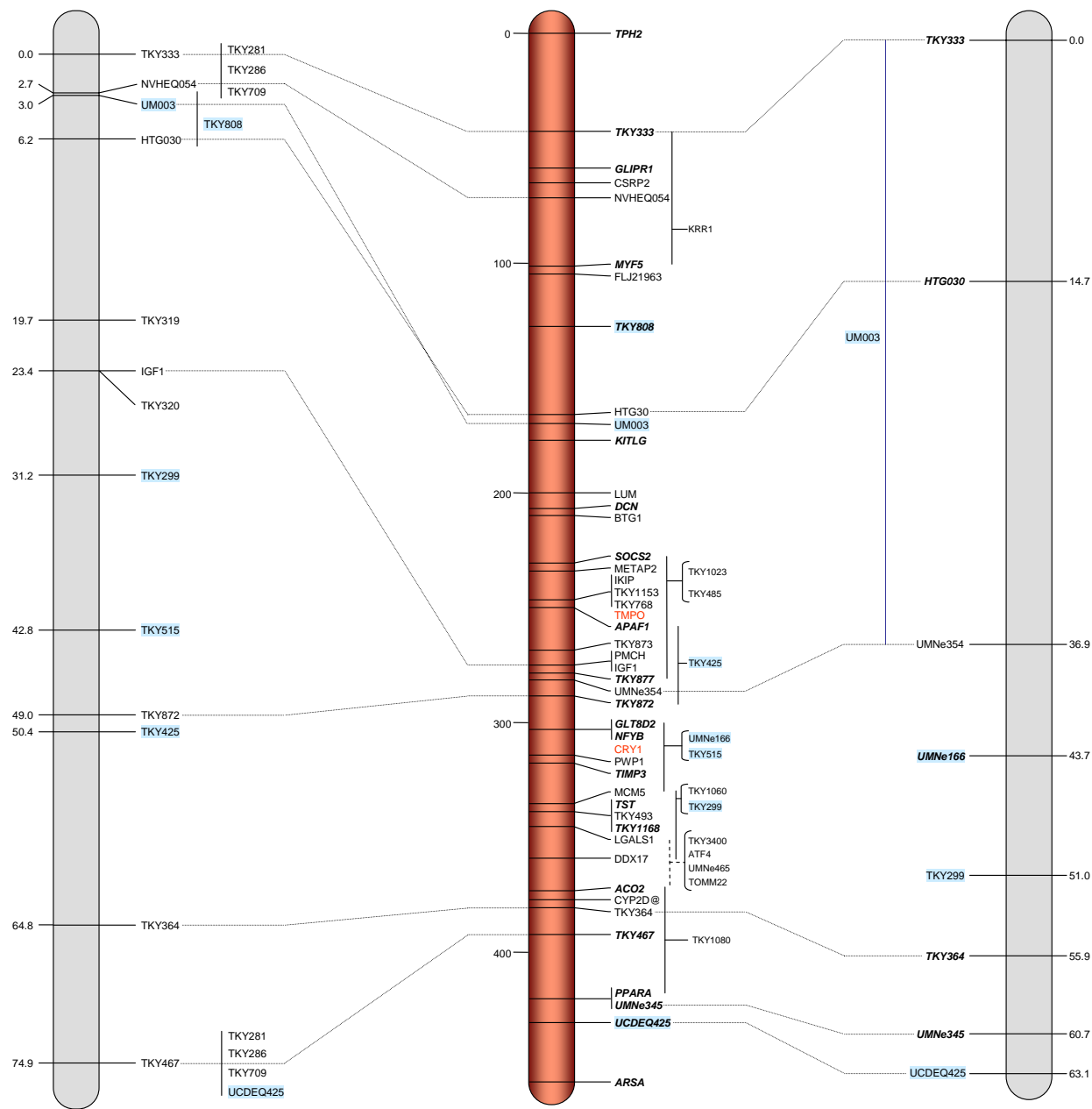
ECA26



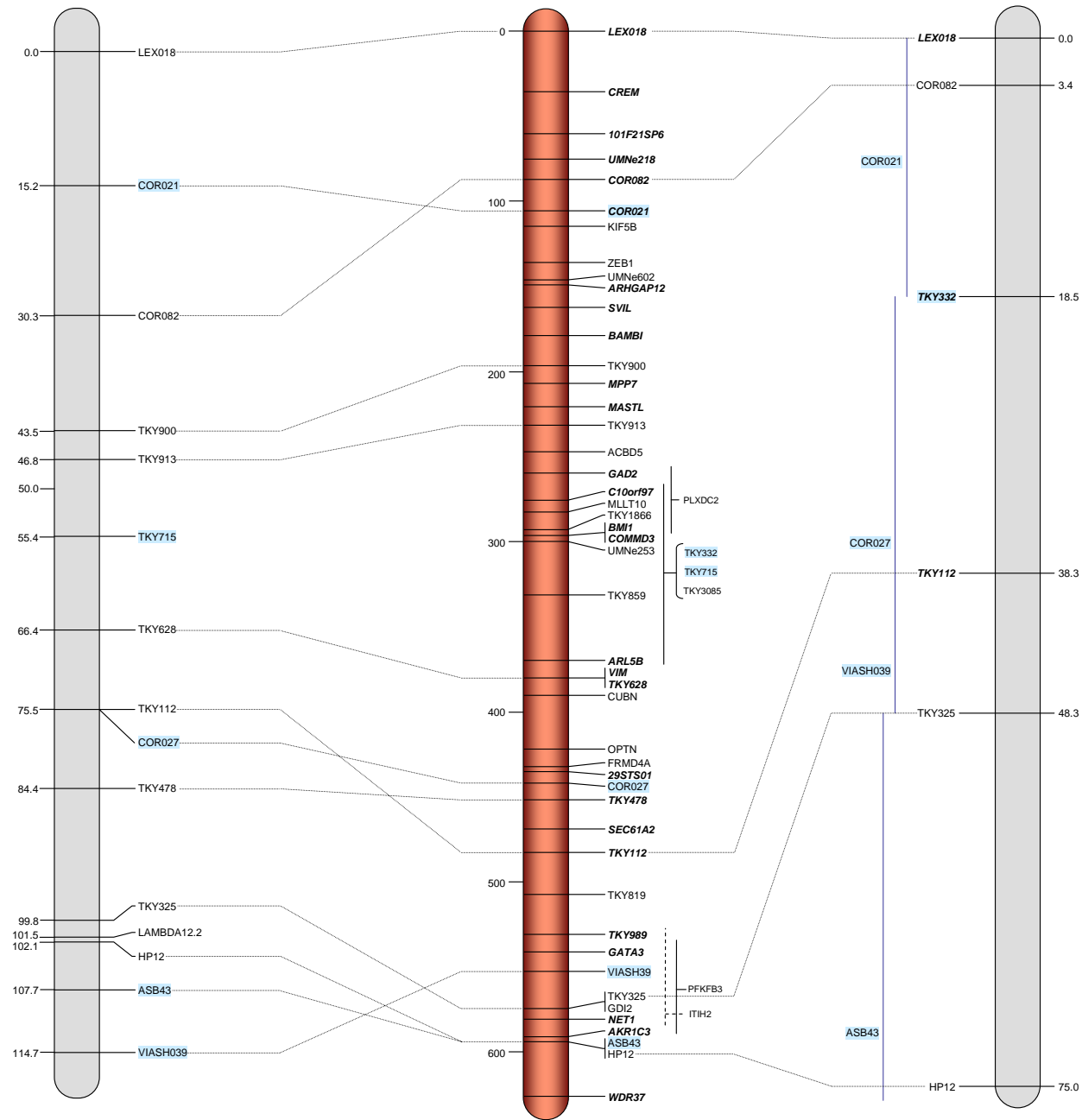
ECA27



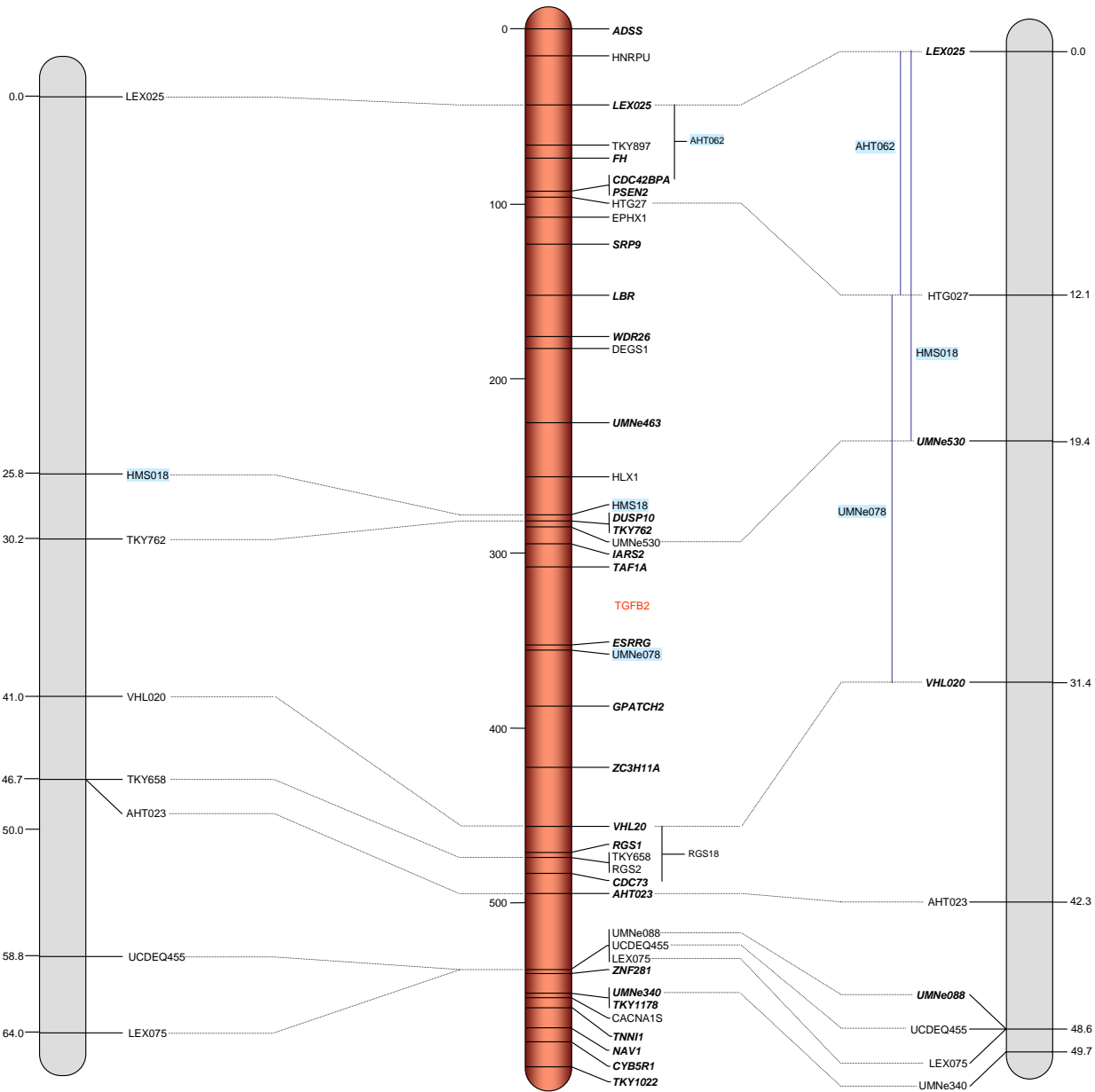
ECA28



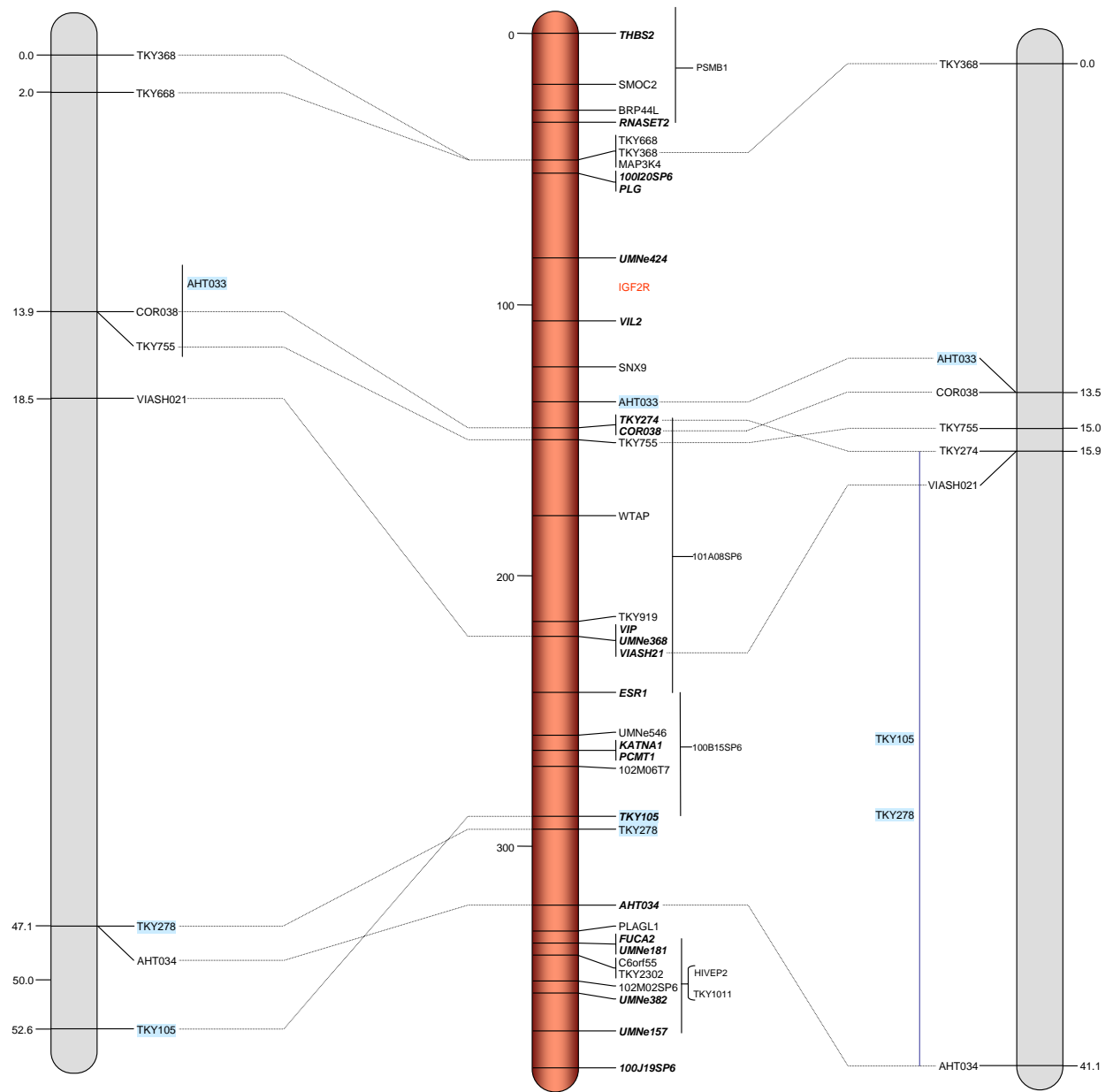
ECA29



ECA30



ECA31



ECAX

