

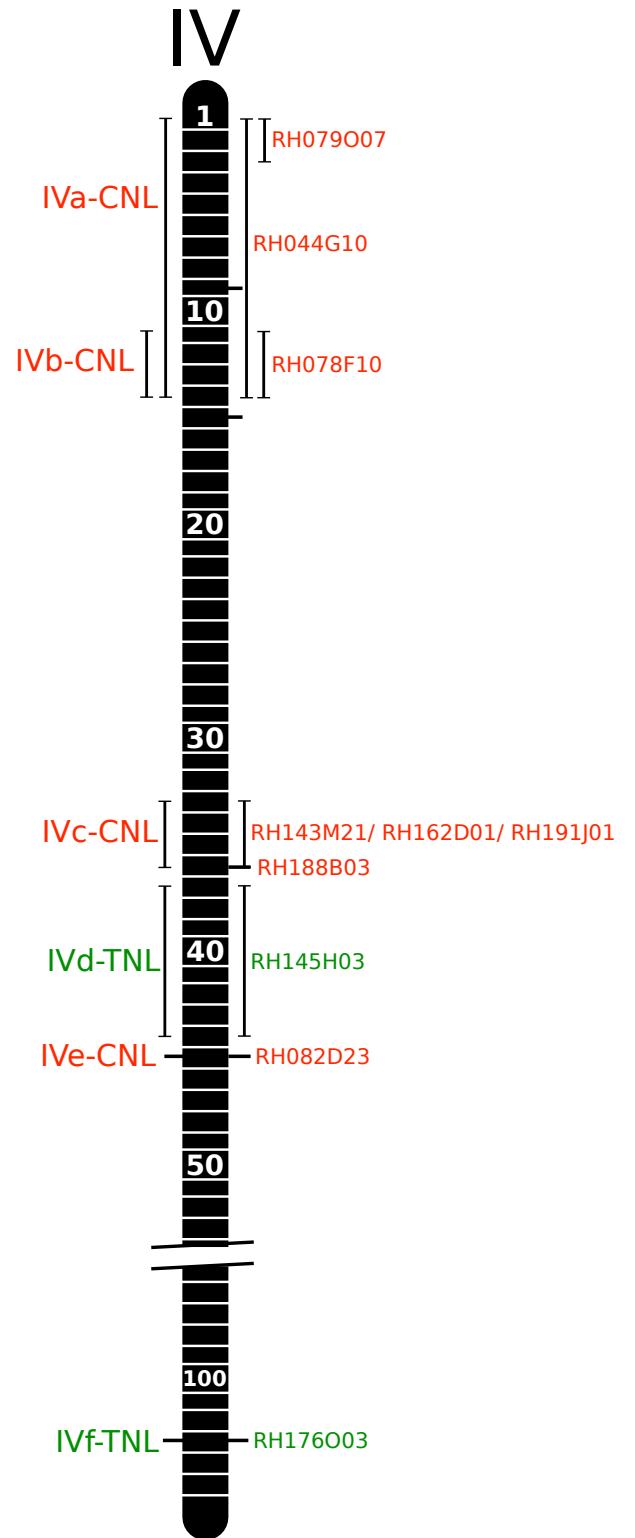
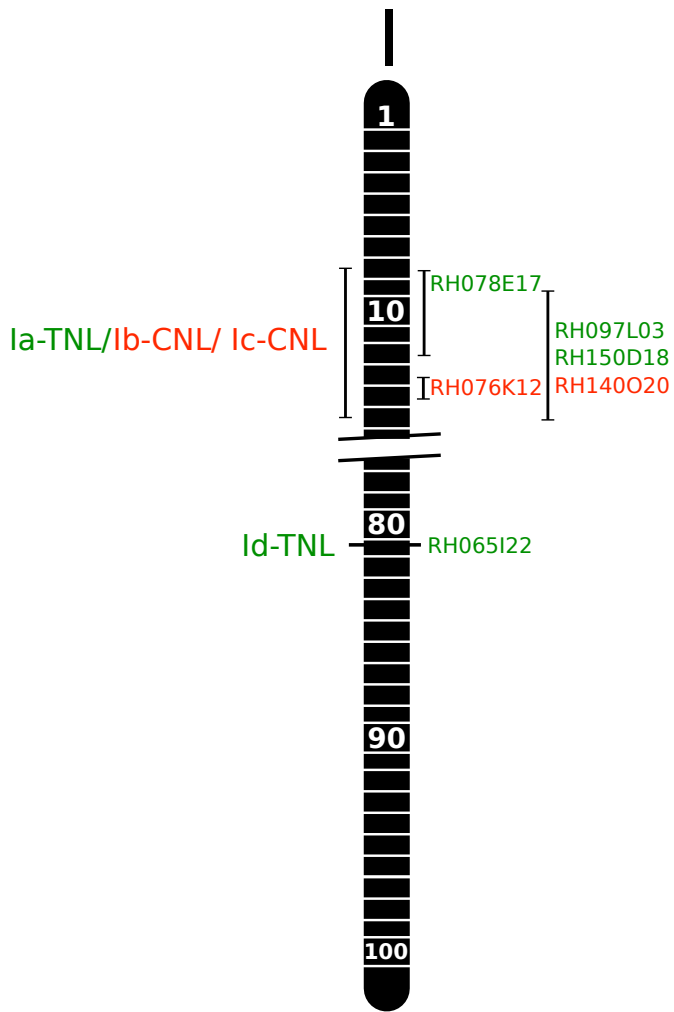
A genome-wide genetic map of NB-LRR disease resistance loci in potato.

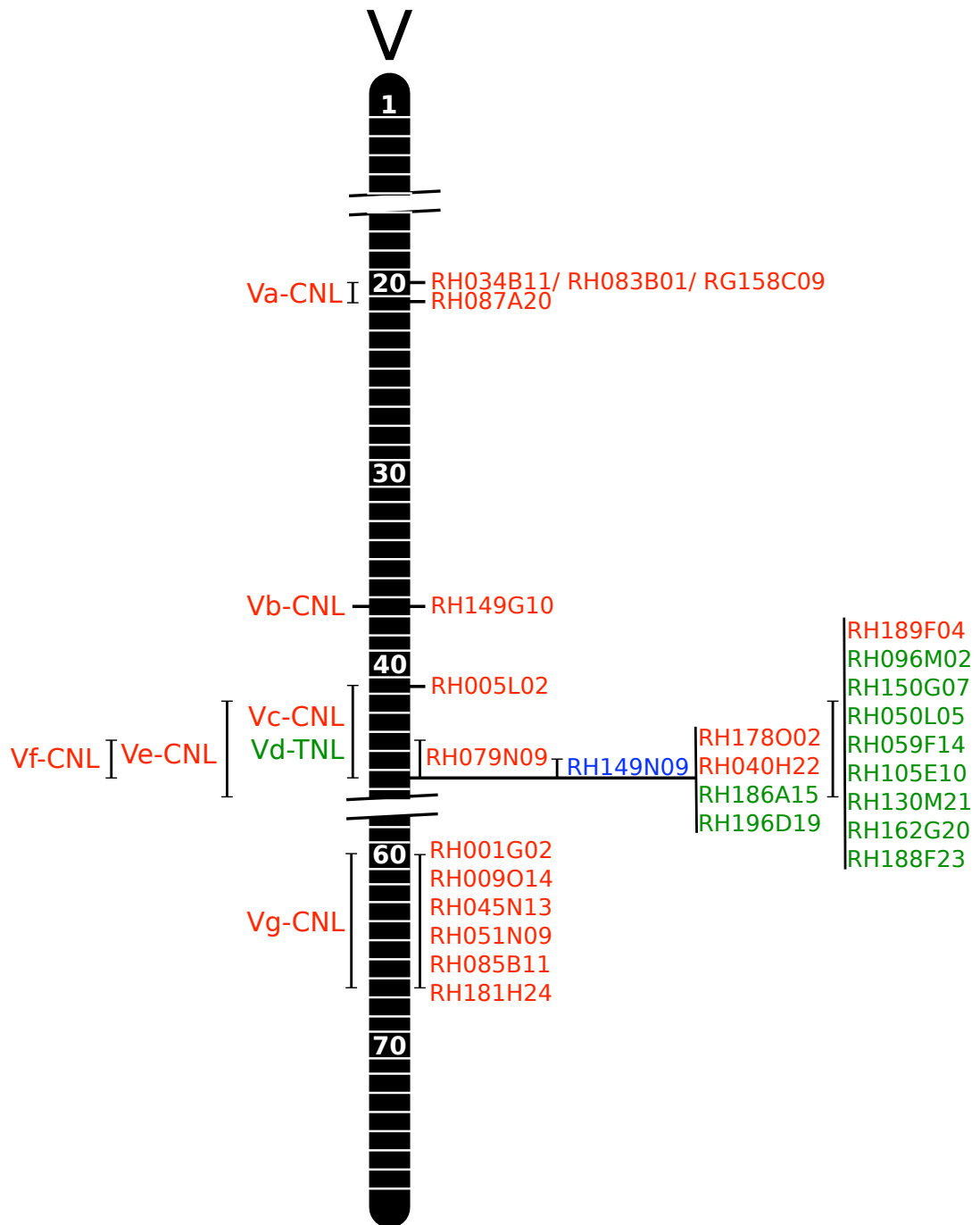
Theoretical and Applied Genetics

Erin Bakker*, Theo Borm, Pjotr Prins, Edwin van der Vossen, Gerda Uenk, Marjon Arens, Jan de Boer, Herman van Eck, Mariëlle Muskens, Jack Vossen, Gerard van der Linden, Roeland van Ham, Rene Klein-Lankhorst, Richard Visser, Geert Smant, Jaap Bakker, Aska Goverse

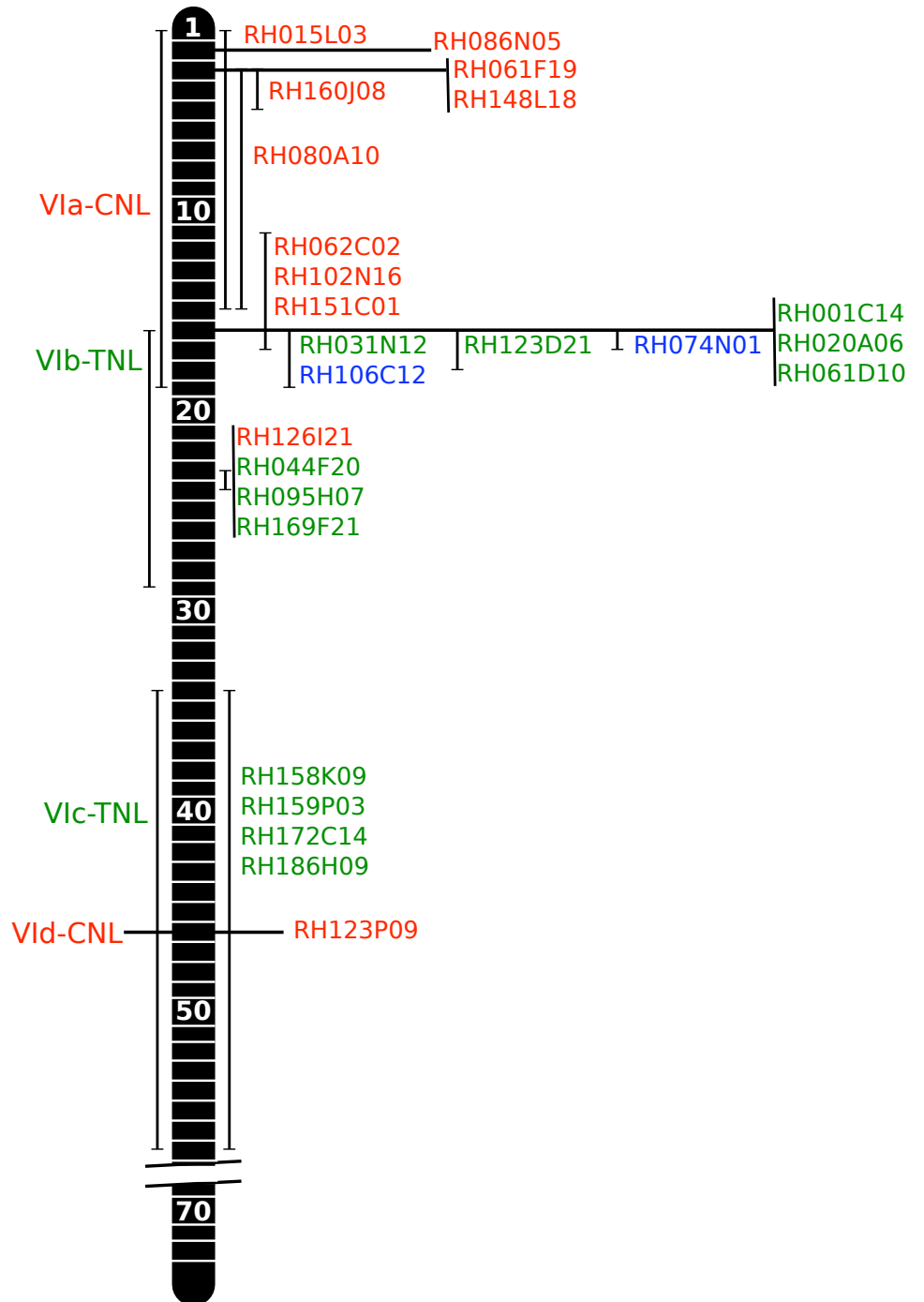
*Laboratory of Nematology, Wageningen University and Research Centre, Droevendaalsesteeg 1, 6708 PB, Wageningen, The Netherlands

Supplemental Fig. 1 Schematic representation of the genetically mapped BACs harbouring RGHs and the defined RGH loci. The broad black vertical bar represents the genetic map with the bin signatures (van Os et al. 2006) separated by white horizontal bars. To the right of the genetic map, the BAC clones that are mapped at this location are presented, with a black horizontal bar to indicate their genetic interval. On the left side, the cluster names, the universal markers and linked cloned *R* genes are indicated, with the interval based on the genetic location of the BAC clones or the bin range of the markers. The red BAC names indicate the presence of CNL RGHs and the absence of TNL RGHs. The green BAC names indicate the presence of TNL RGHs and the absence of CNL RGHs and the blue BAC names indicate the presence of both TNL and CNL RGHs.

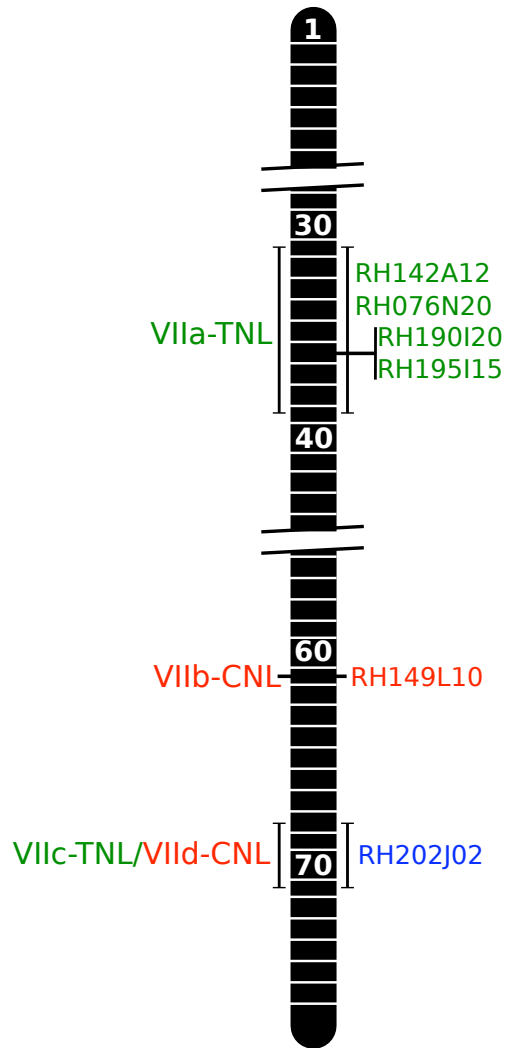




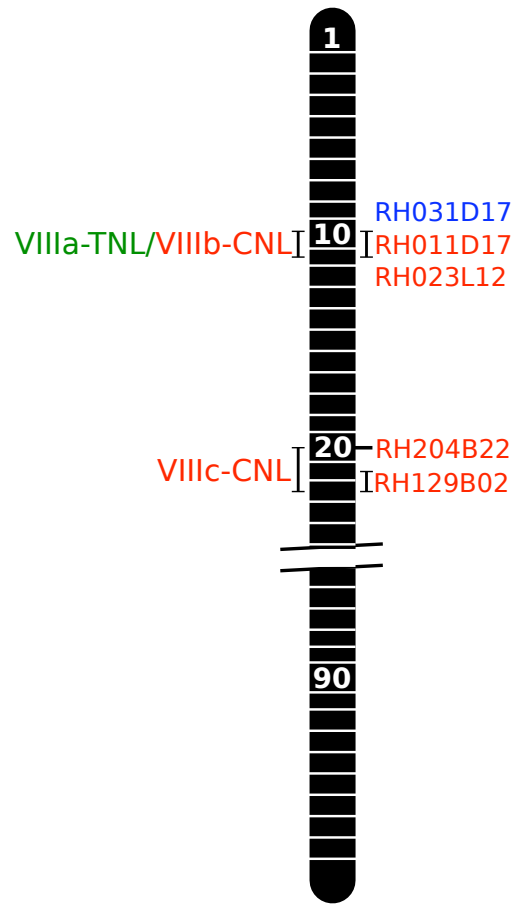
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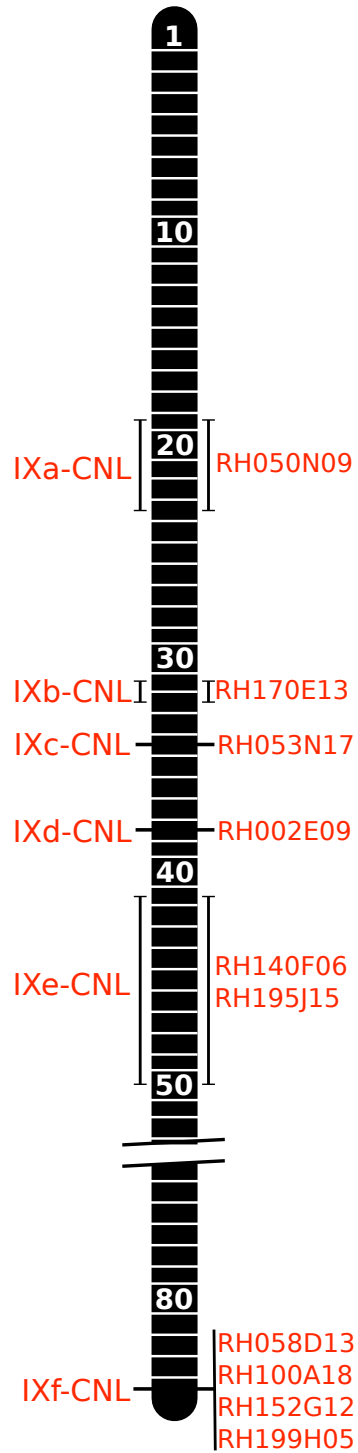
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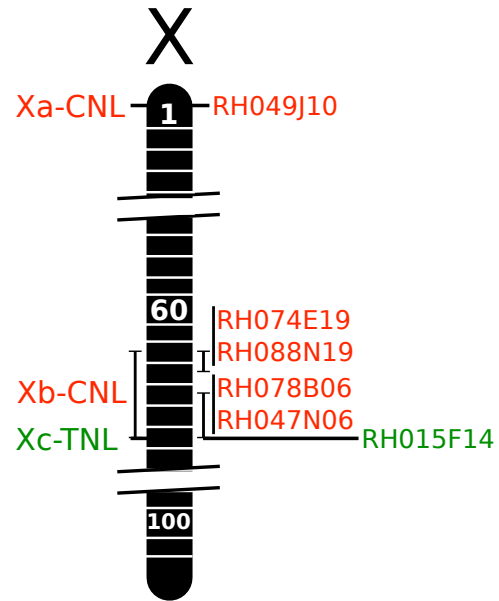


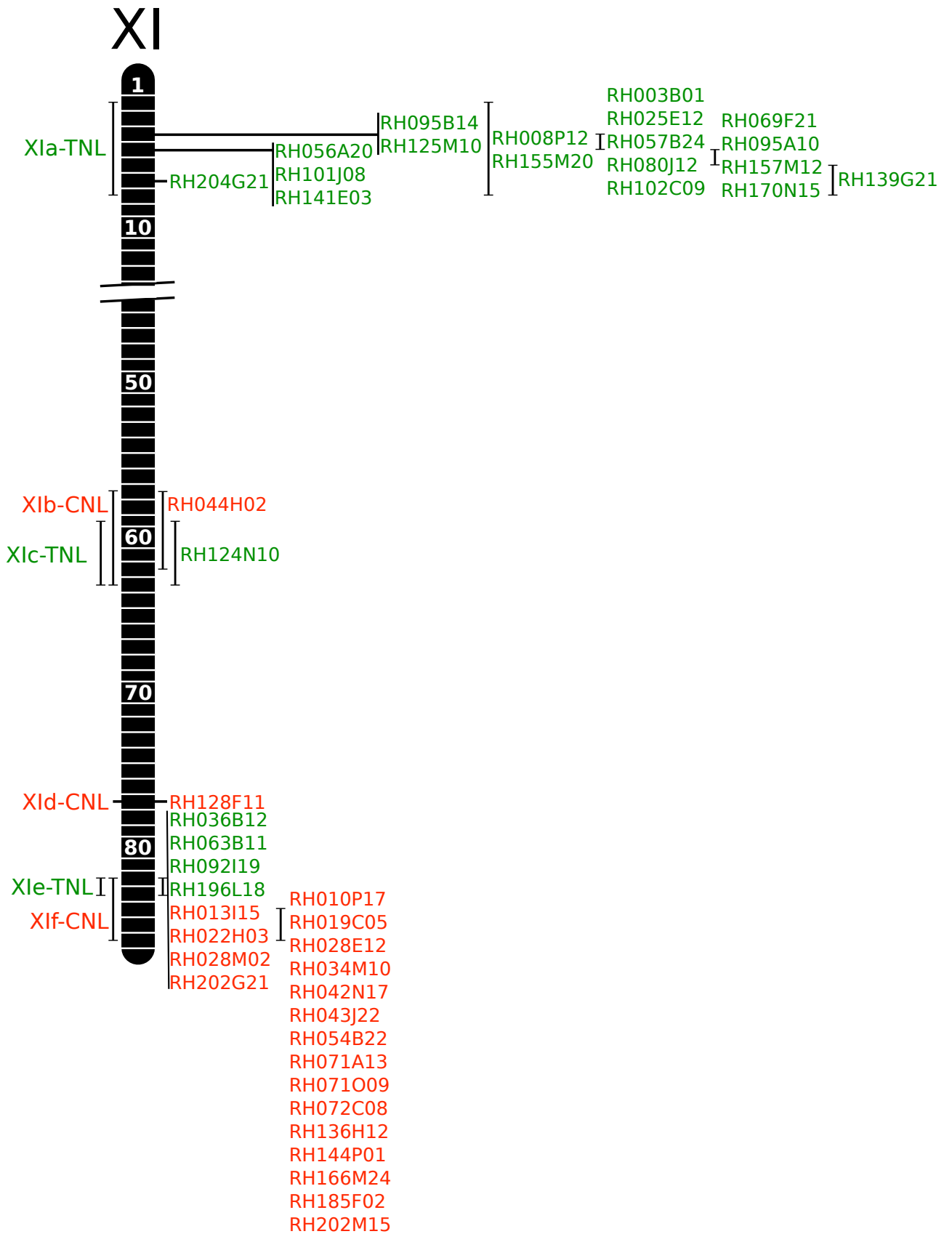
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IX







XII

