Additional file 2 (AF2): Comparison of genomic MHCI regions from selected Salmonids and Northern pike

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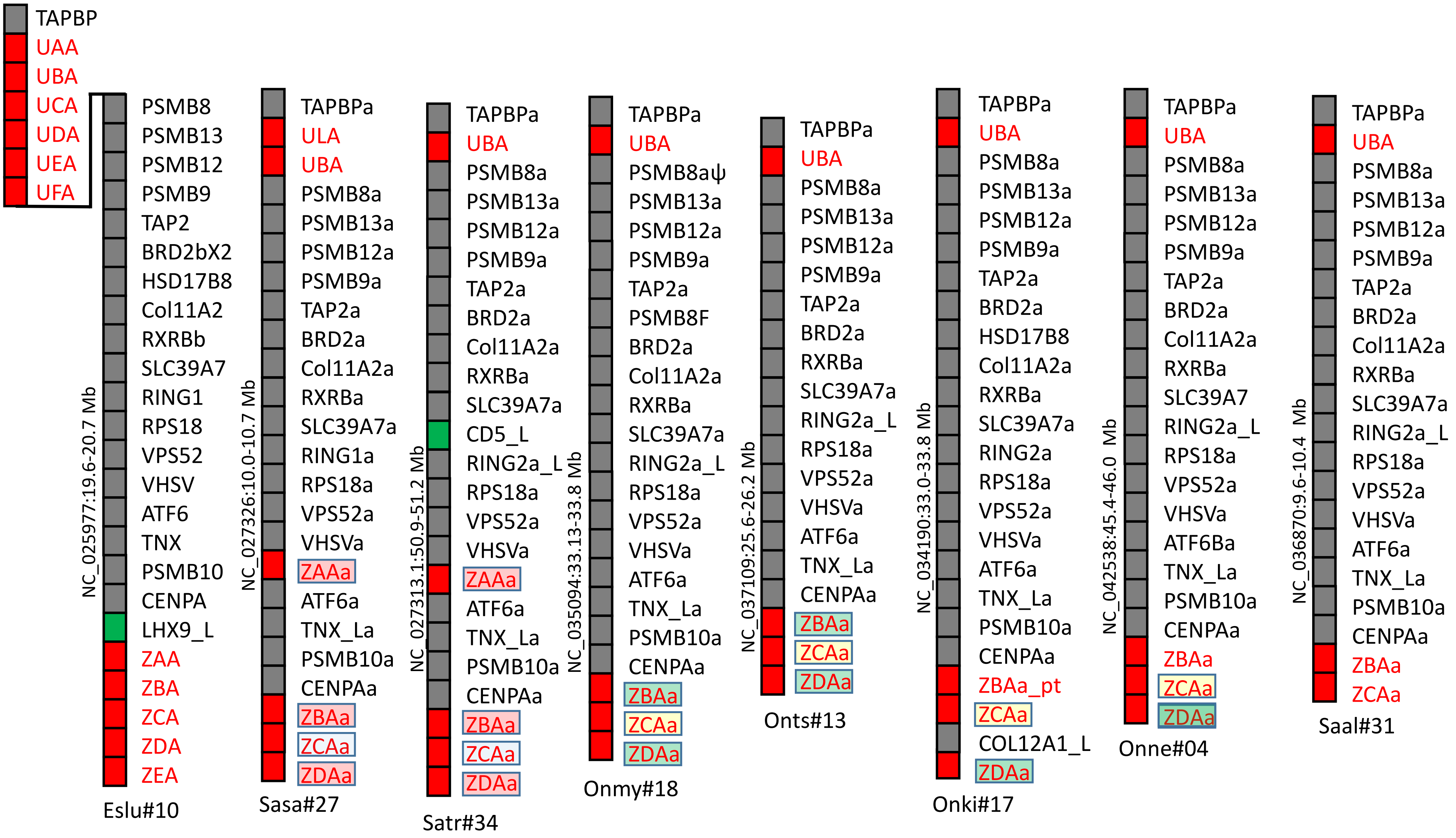
Comparison of genomic regions of MHC class I lineage genes in Salmonids and Northern pike. Genes are depicted as grey boxes apart from MHC class lineage genes are shown as red boxes and in red font. Chromosomal location or unplaced scaffold names are shown below and on the left hand side of each. Scaffolds with MHCI genes only are not shown (see Additional file 4). Typical regional genes are shown using green boxes. Phylogenetic clustering of MHCIa and MHCIb U and Z lineage genes is shown using colored boxes covering the gene names. Arrow in the MHCIb regions indicate direction of the extended MHCIb region shown on page 3 and 4. Large regional gaps are shown using solid black line where gap distance is shown in megabases (Mb). Definite pseudogenes are shown in gene name with a ps extension. Many gene names also have an _L extension for _like as functional verification is needed to define them as orthologs of mammalian molecules. Page 10 * : The single Atlantic salmon S gene region located on Chr. 09 originates from main text reference Lukacs et al.2010, while the six S lineage gene sequences identified in the Atlantic salmon genome all reside on small scaffolds with MHC genes only.

AF2.1. MHC class Ia regions



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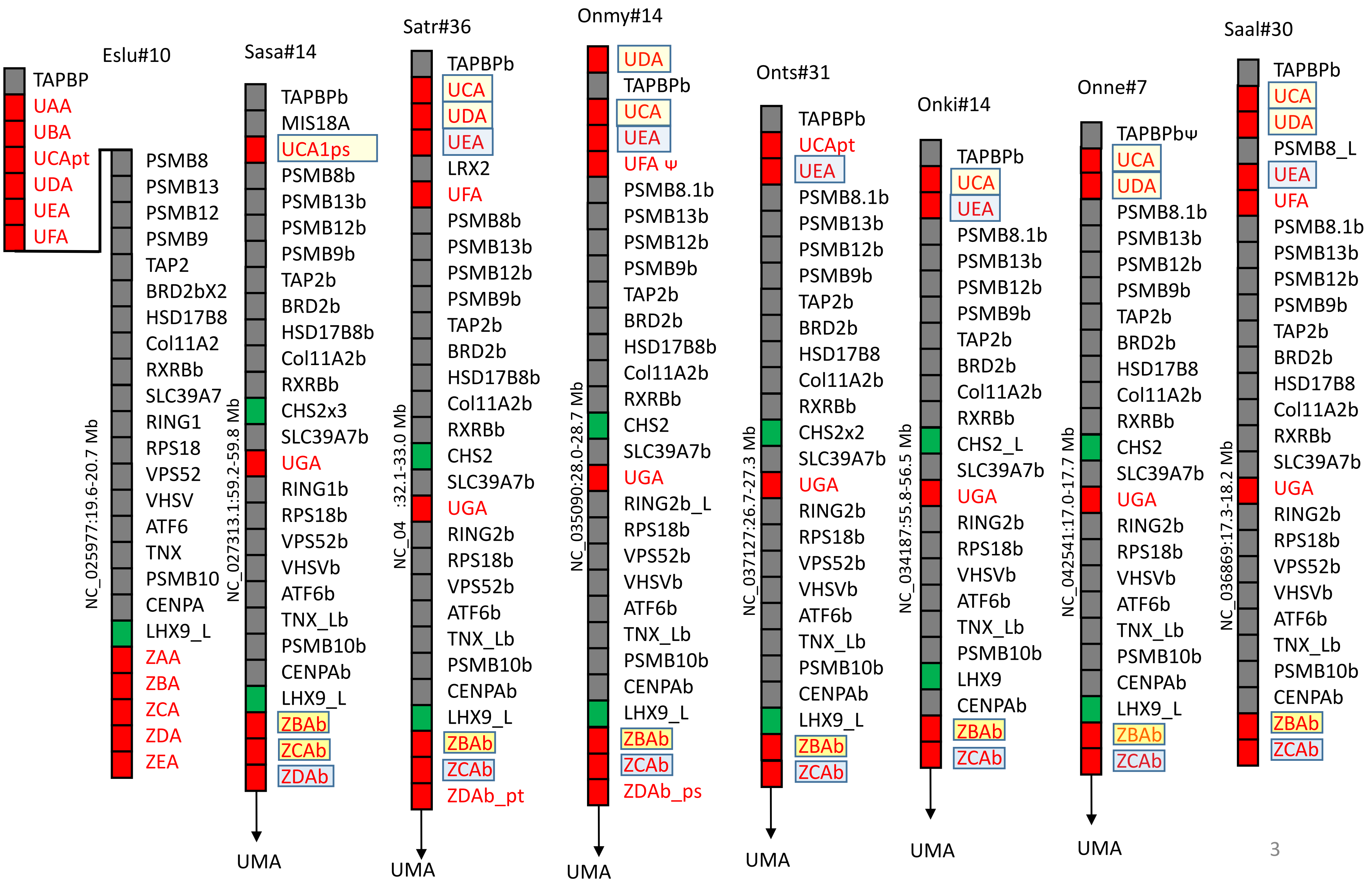

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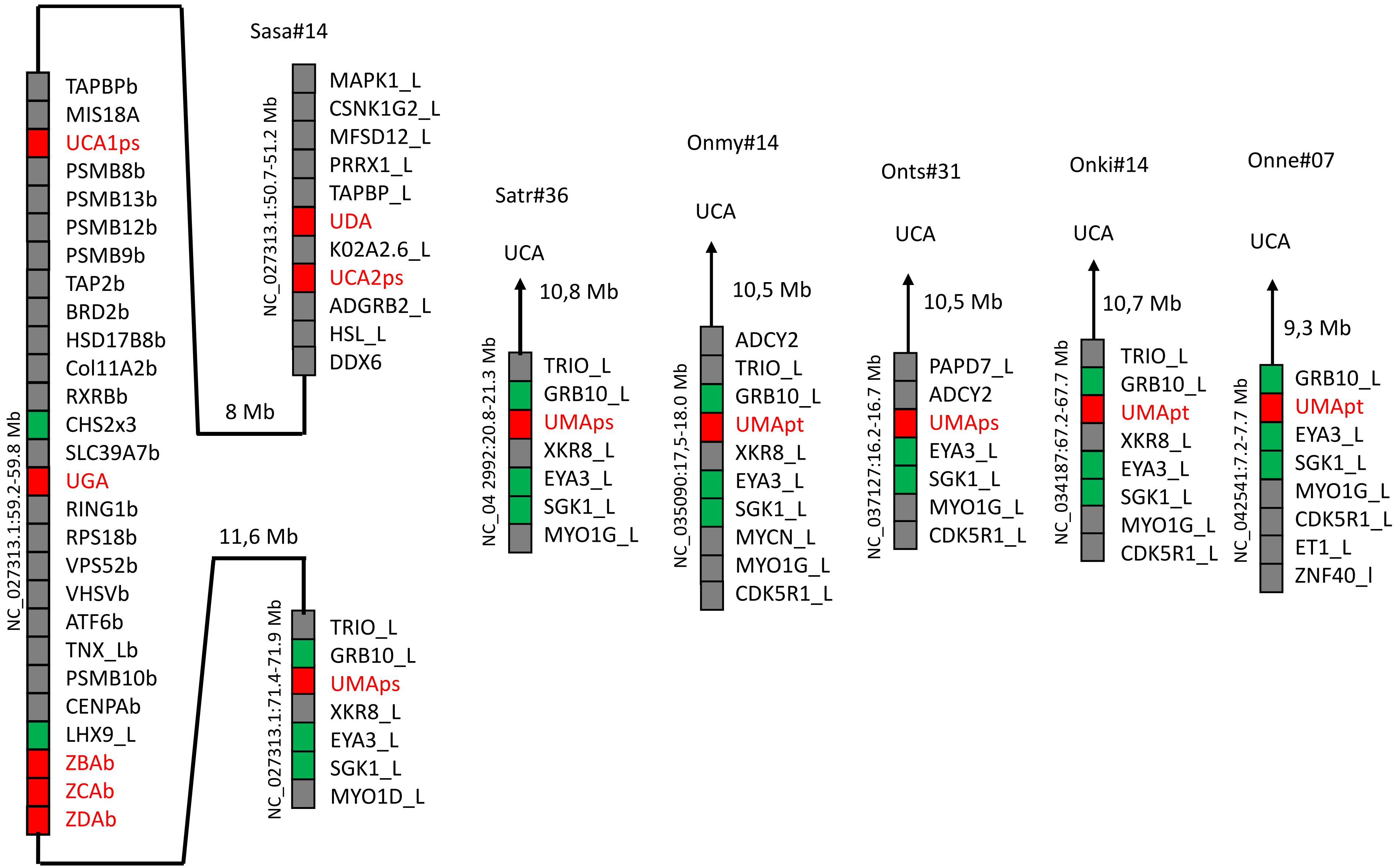
AF2.3. Extended salmonid MHC class Ib regions



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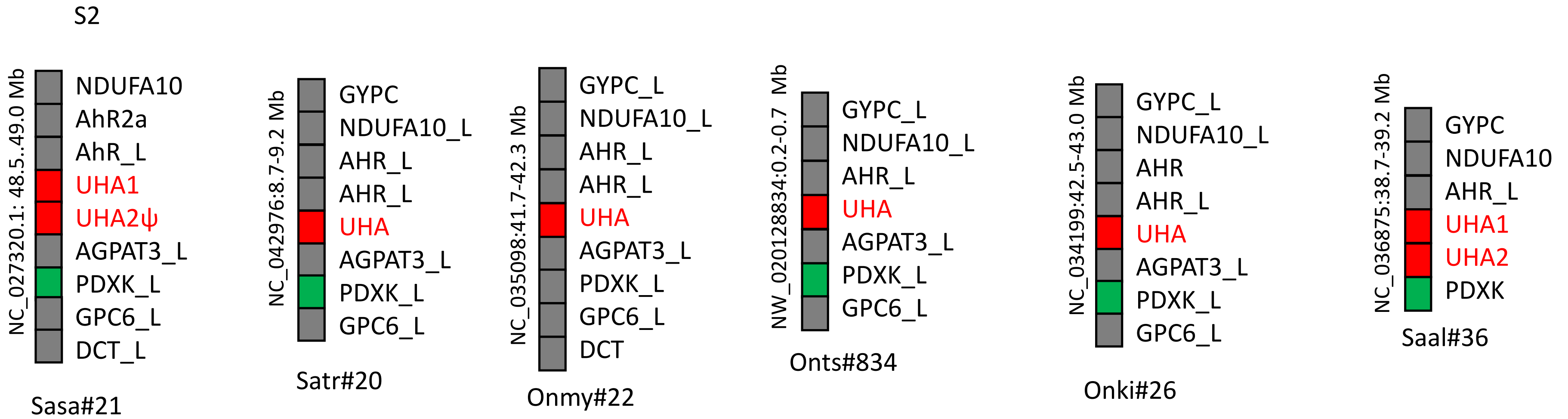

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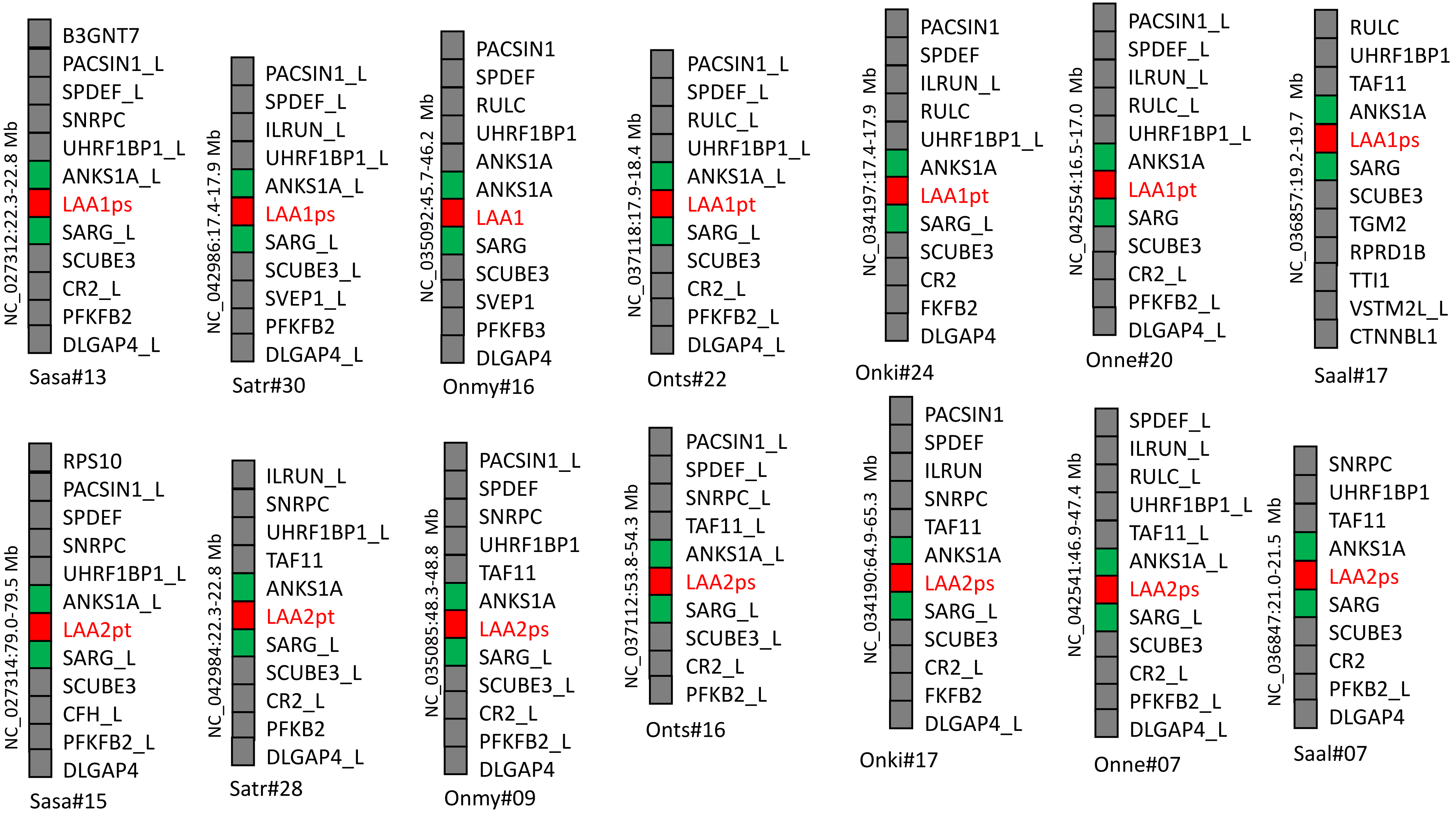

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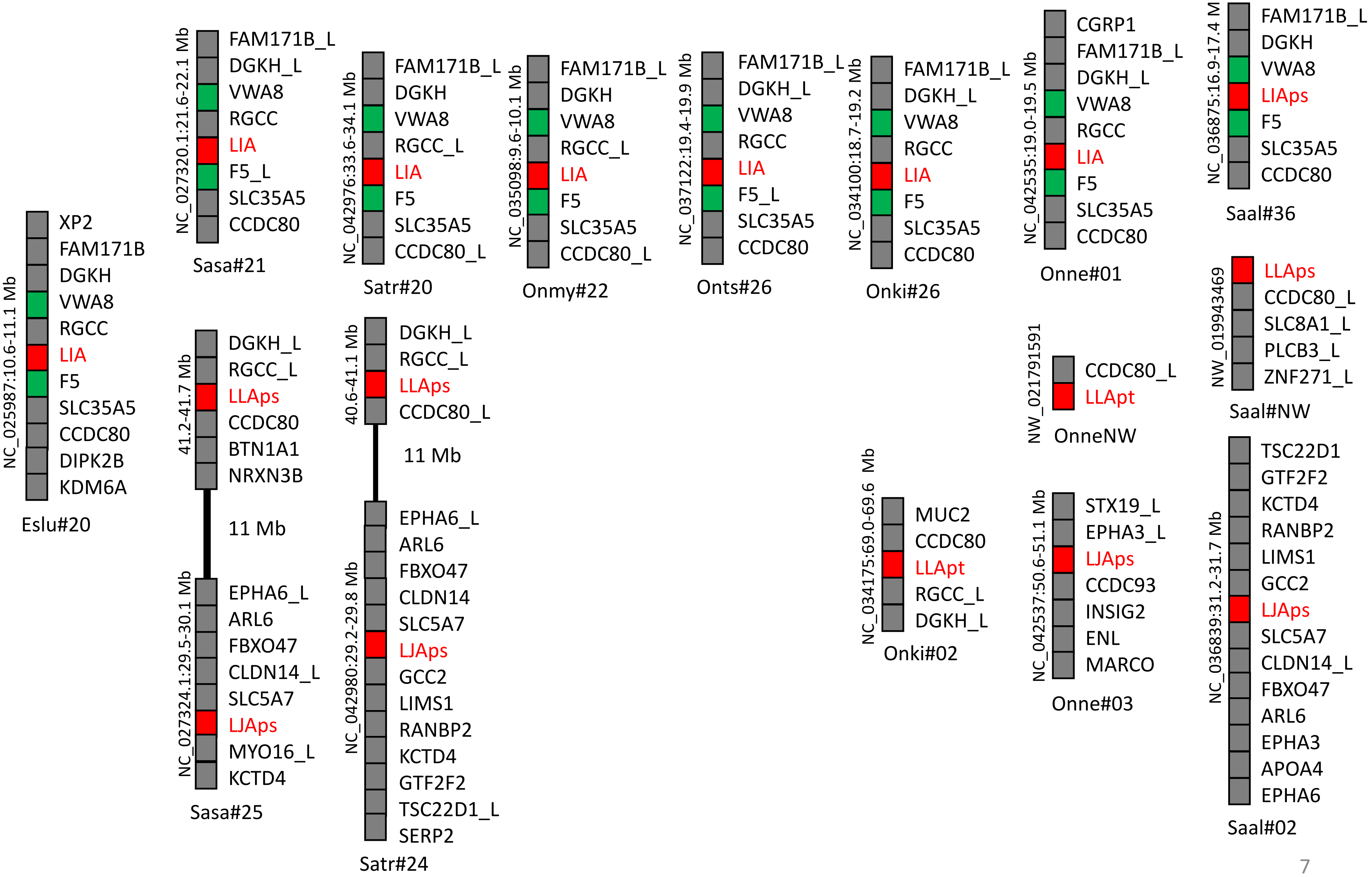

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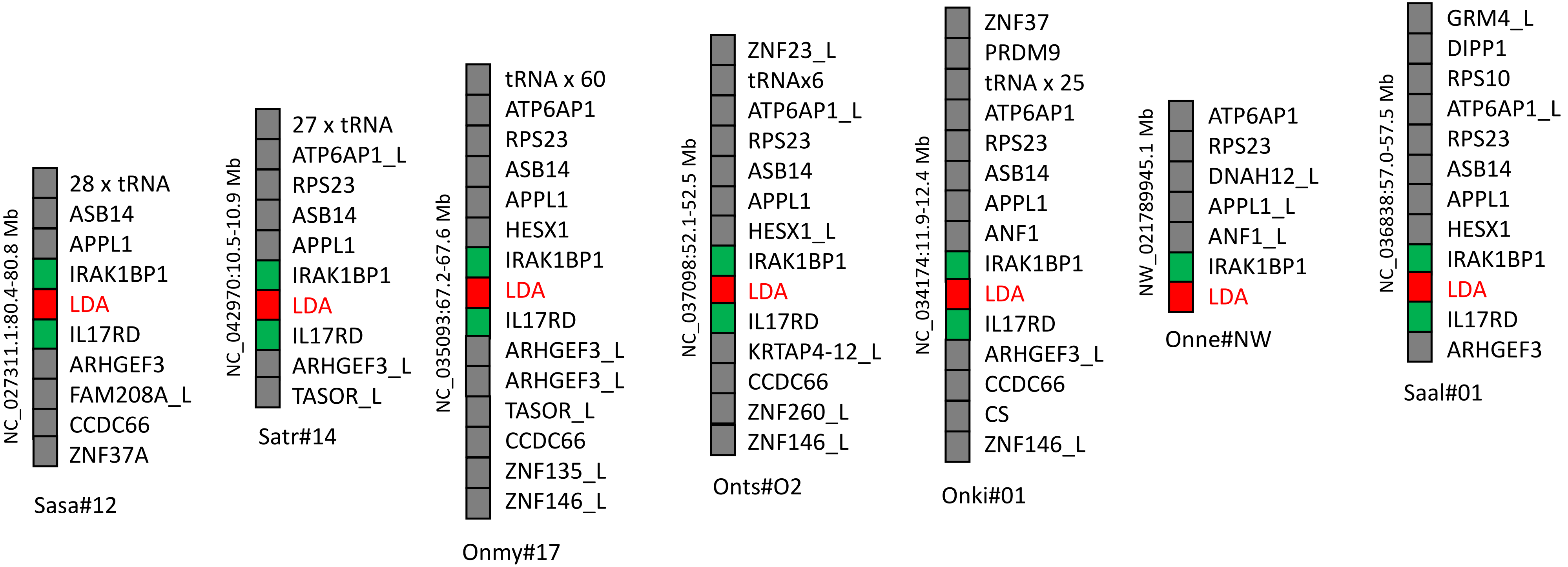

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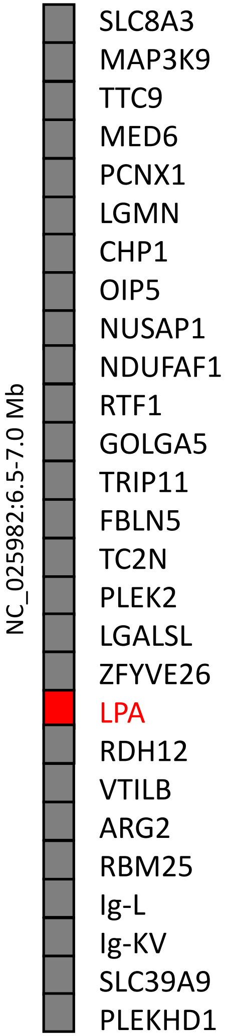

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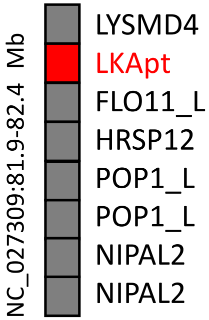

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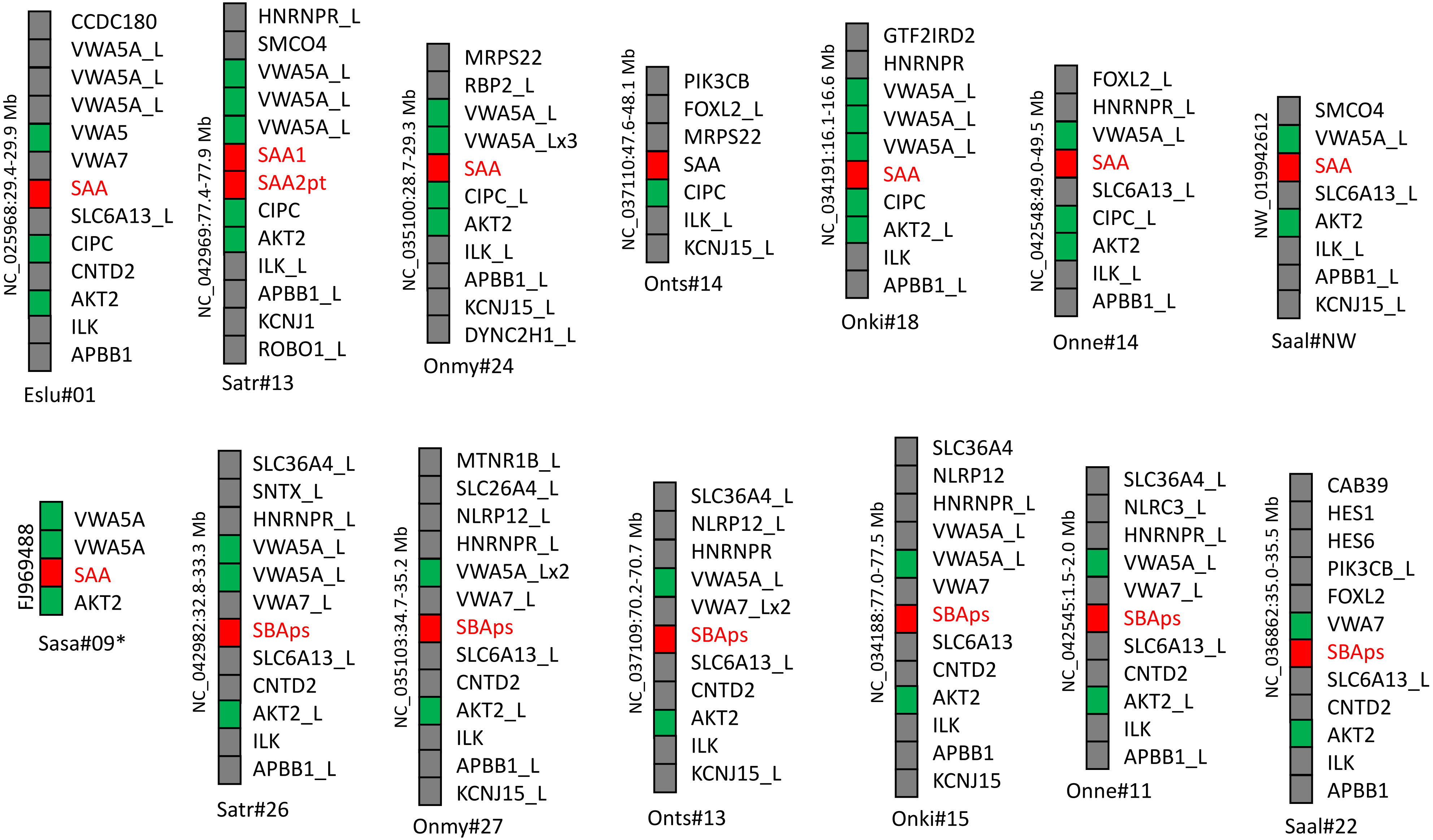

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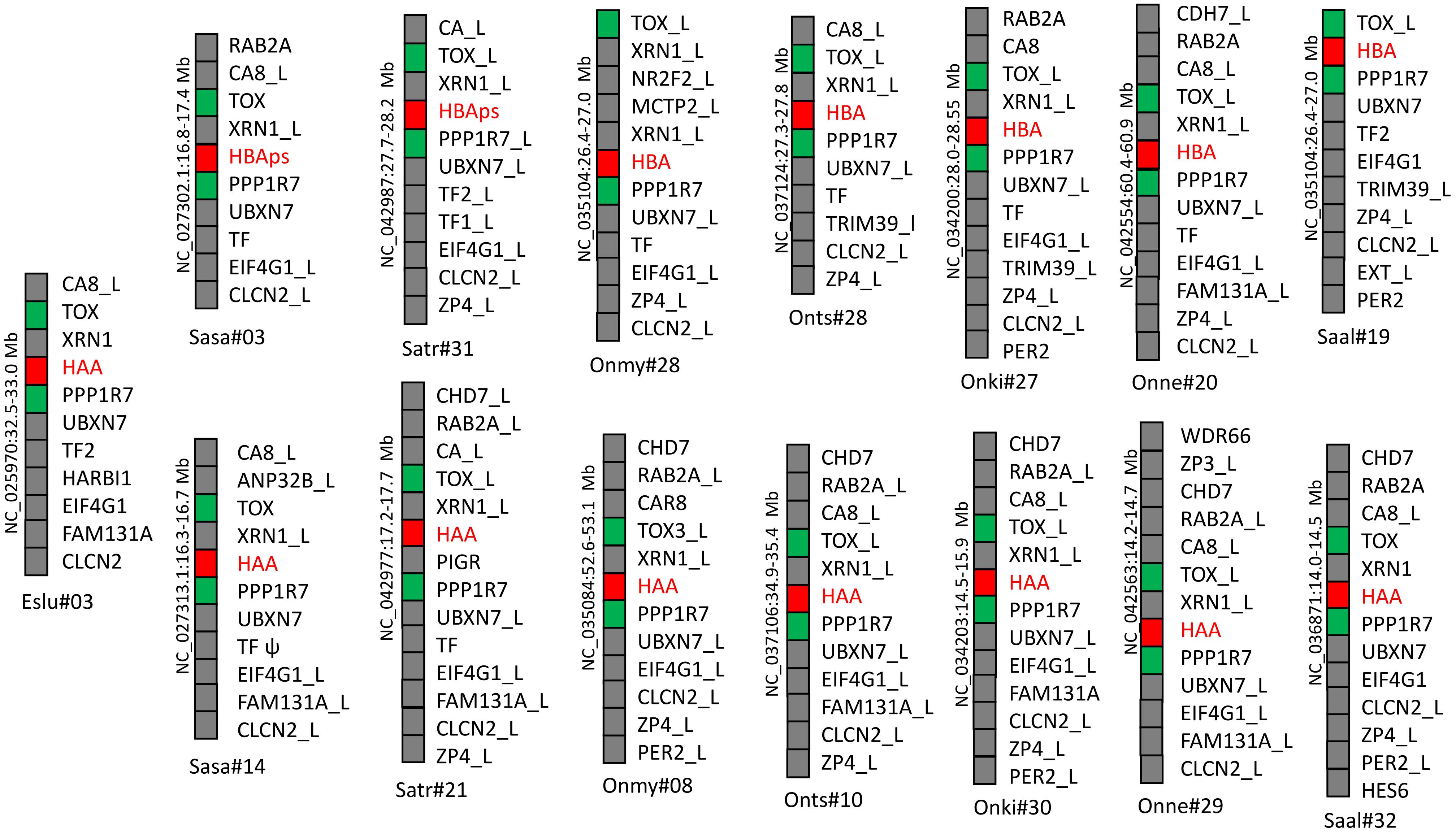
AF2.7. H lineage regions



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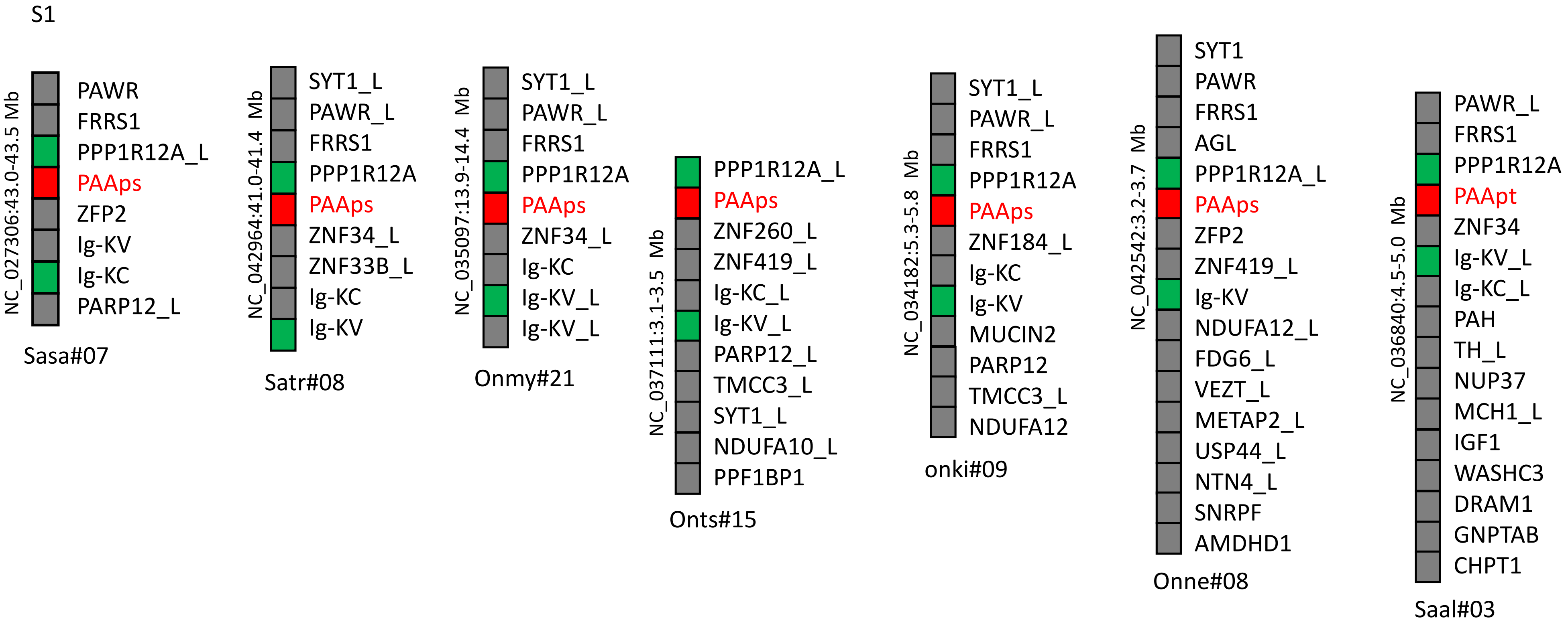
AF2.8. P lineage regions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