Supplementary figure 2 (Fig. S2): Teleost fish and gar MHC class II genomic regions

(Schematic view with details of the scaffolds shown in main text Fig. 2)

Figure legend: The genomic surroundings of MHC class II genes in eight fishes are shown with genes represented by blocks. Data were derived from the Ensembl database, except those of Atlantic salmon (Additional file 8, Text S2). Several genes flanking the MHC class II genes were identified using the Ensembl genome browser and, in some cases, gene prediction software. Identities of all genes without Ensembl annotation were investigated by blasting their deduced products against GenBank. When identity was uncertain, phylogenetic analysis (Neighbor Joining method) was performed. Sequences with low but still convincing sequence identity and members of complex gene families were given the name extension "–like" (_L), while those without convincing match were defined as not determined (n.d.) and sometimes omitted for space purposes. For identifying genes in the depicted Atlantic salmon *Mhc* regions we also compared with previous analyses of this region in trout [main text reference 32] and medaka [main text reference 33]. Names of genomic regions and MHC genes used in this study often are simplified references to species and Ensembl scaffolds/contigs or linkage groups/chromosomes (e.g. O845 A for the MHC class II *A* gene on *Oreochromis niloticus* scaffold GL831845), with details given vertically. For precise location of individual MHC genes see Additional file 5, Table S2. Yellow arrows indicate availability of information on extensions of the depicted region fragments, while green stars indicate absence of such information. Syntenic regions are boxed dark green (synteny group S1), lime green (synteny group S2) or pink (synteny group S3) and individual genes supporting region synteny are depicted by the same color (see also Additional file 4, Table S1). Please be aware that some gene families such as the zinc finger protein family (ZNF) can be extensively dispersed throughout the genome and that their shared presence is not a good indication for region synteny. The tilapia O845 and O18 regions are boxed with a dashed pink line to indicate that more information on surrounding genes is needed to be certain that they belong to the S3 synteny group. The stickleback G131 region is boxed with a dotted pink line because it is syntenic with a region on zebrafish Chr.23 which maps close to the S3 synteny group region (Additional file 4, Table S1). Further colorings of individual genes represent as follows: orange= MHCI class II, red= MHC class I, blue= *Mhc* scaffold genes as found in human, gray= other genes. Obvious pseudogenes are marked with ψ, and names of MHC class II gene with evidence of transcription (Additional file 5, Table S2, and Additional file 8, Text S2) are in red font. On page 11 the sequence of the classical(-like) MHC class I sequence encoded by spotted gar scaffold 501 is shown with residues suggesting classical nature in red font. During our investigations the Ensembl platyfish genome database (XipMac4) was released. Because the platyfish MHC class II data are consistent with the MHC class II situation in the other five investigated neoteleosts, they are not shown in the present article.

Atlantic salmon (*Salmo salar*)

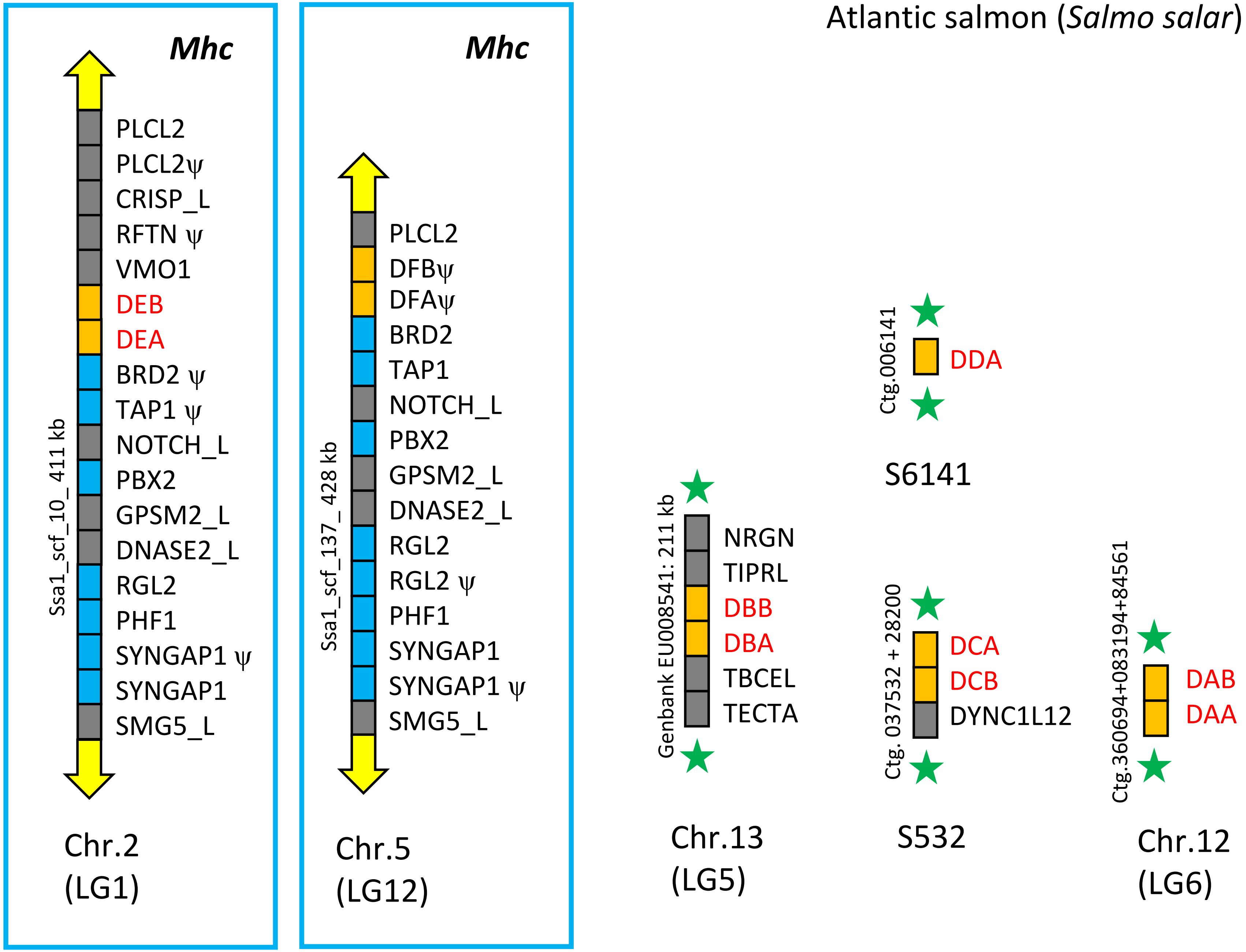


Fig.S2 MHC class II genomic regions

Zebrafish (*Danio rerio*)

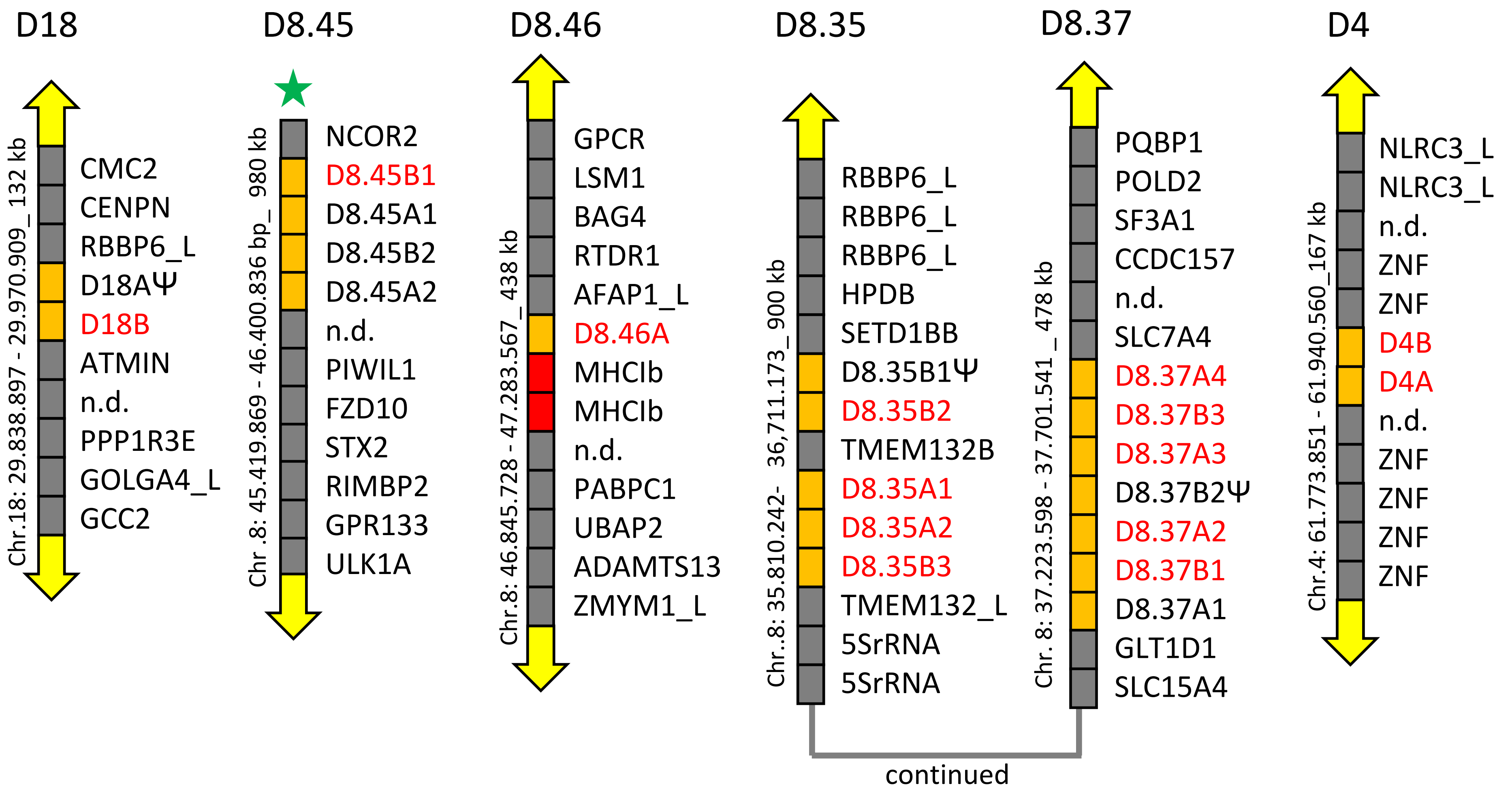


Fig.S2 MHC class II genomic regions

Stickleback (*Gasterosteus aculeatus*)

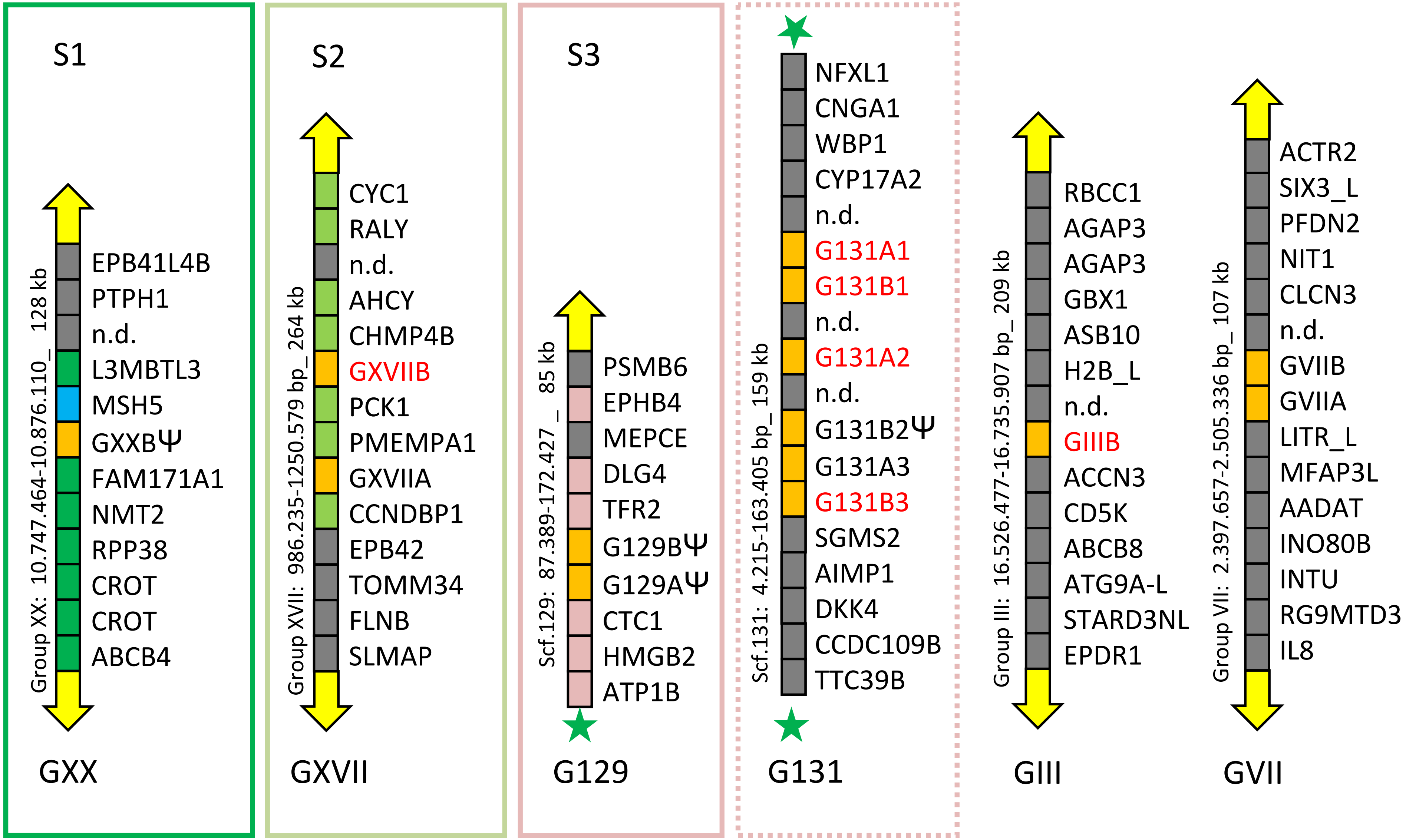


Fig.S2 MHC class II genomic regions

Medaka (*Oryzias latipes*)

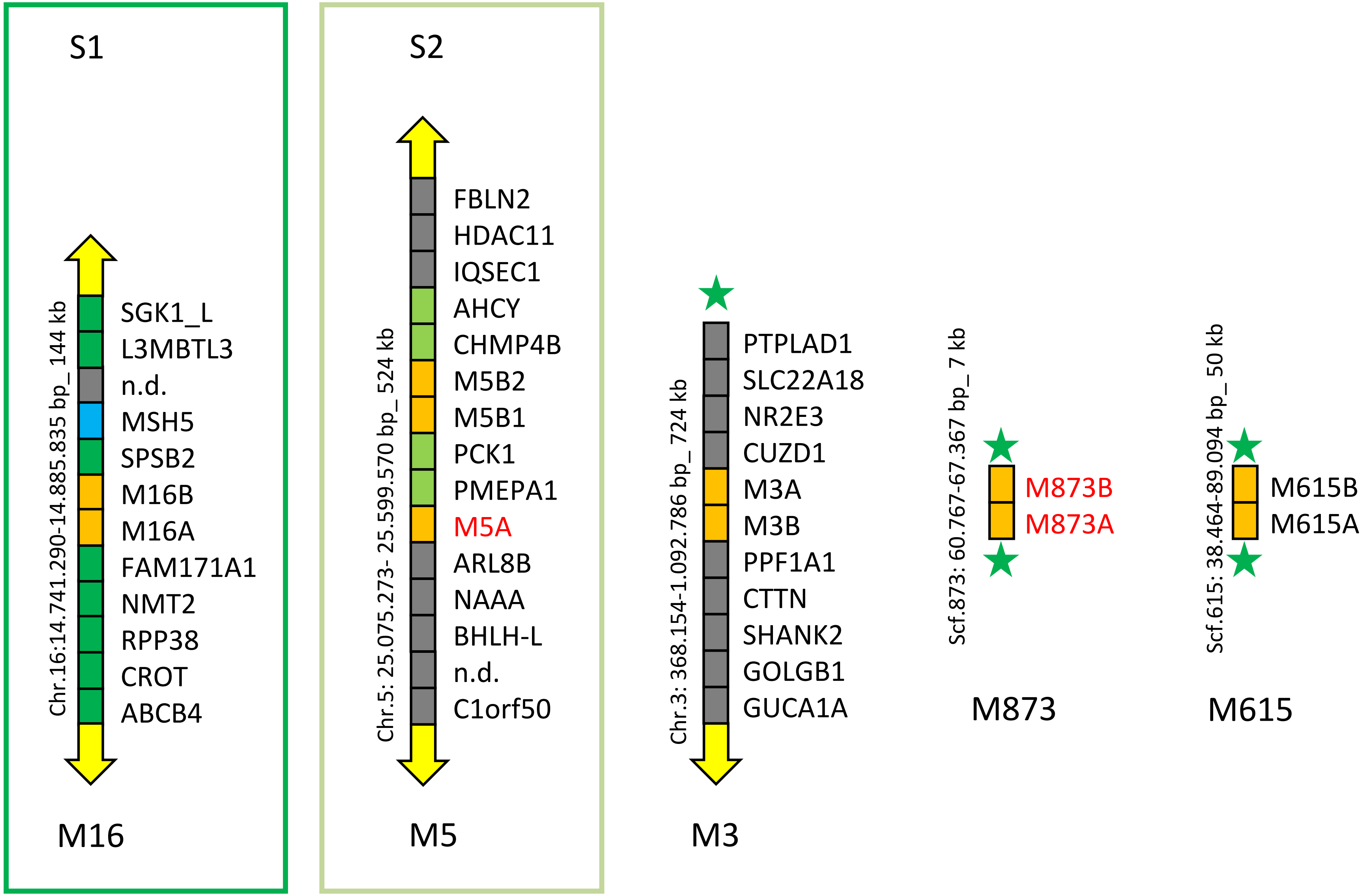


Fig.S2 MHC class II genomic regions

Fugu (*Fugu rubripes*)

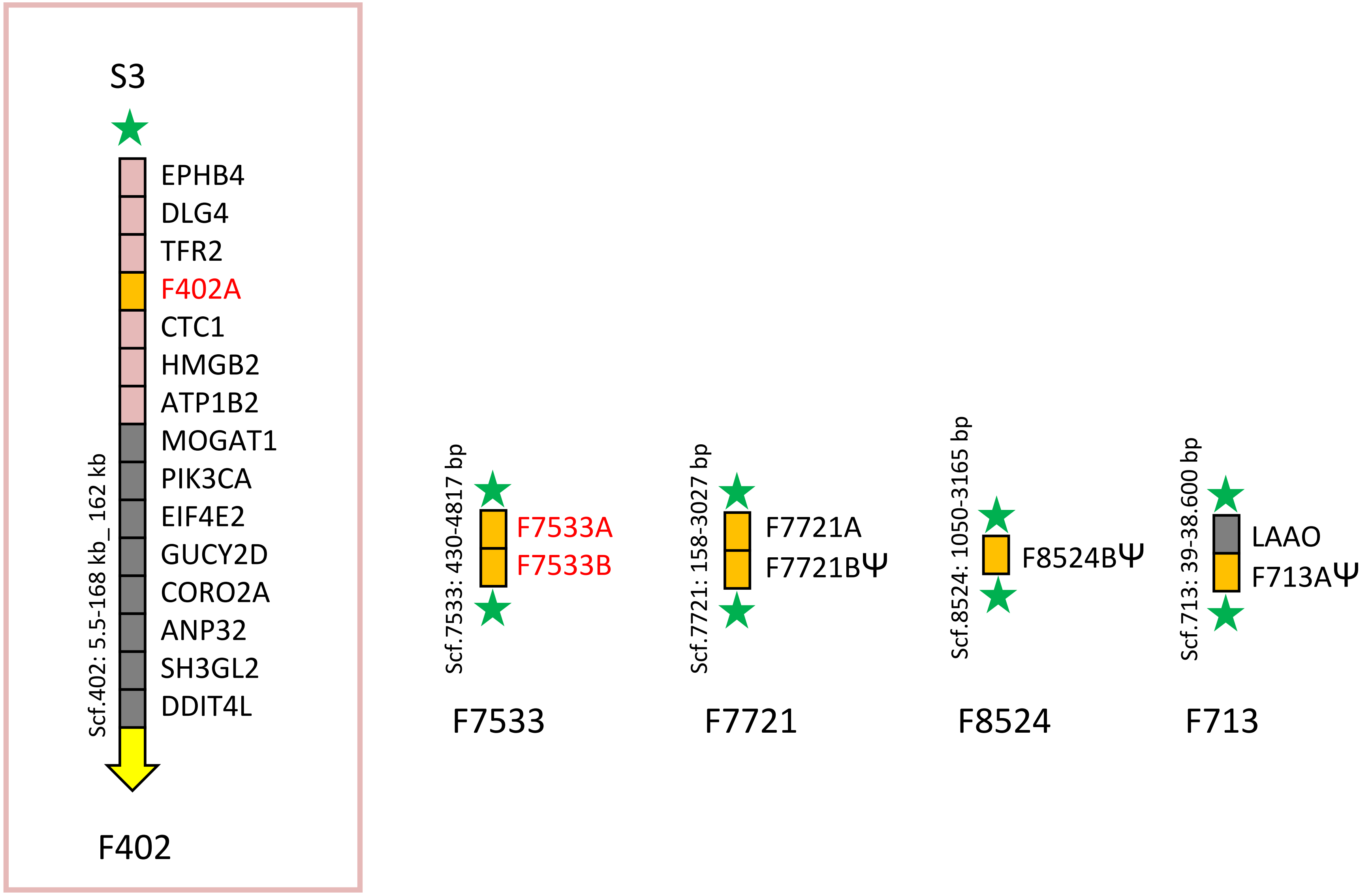
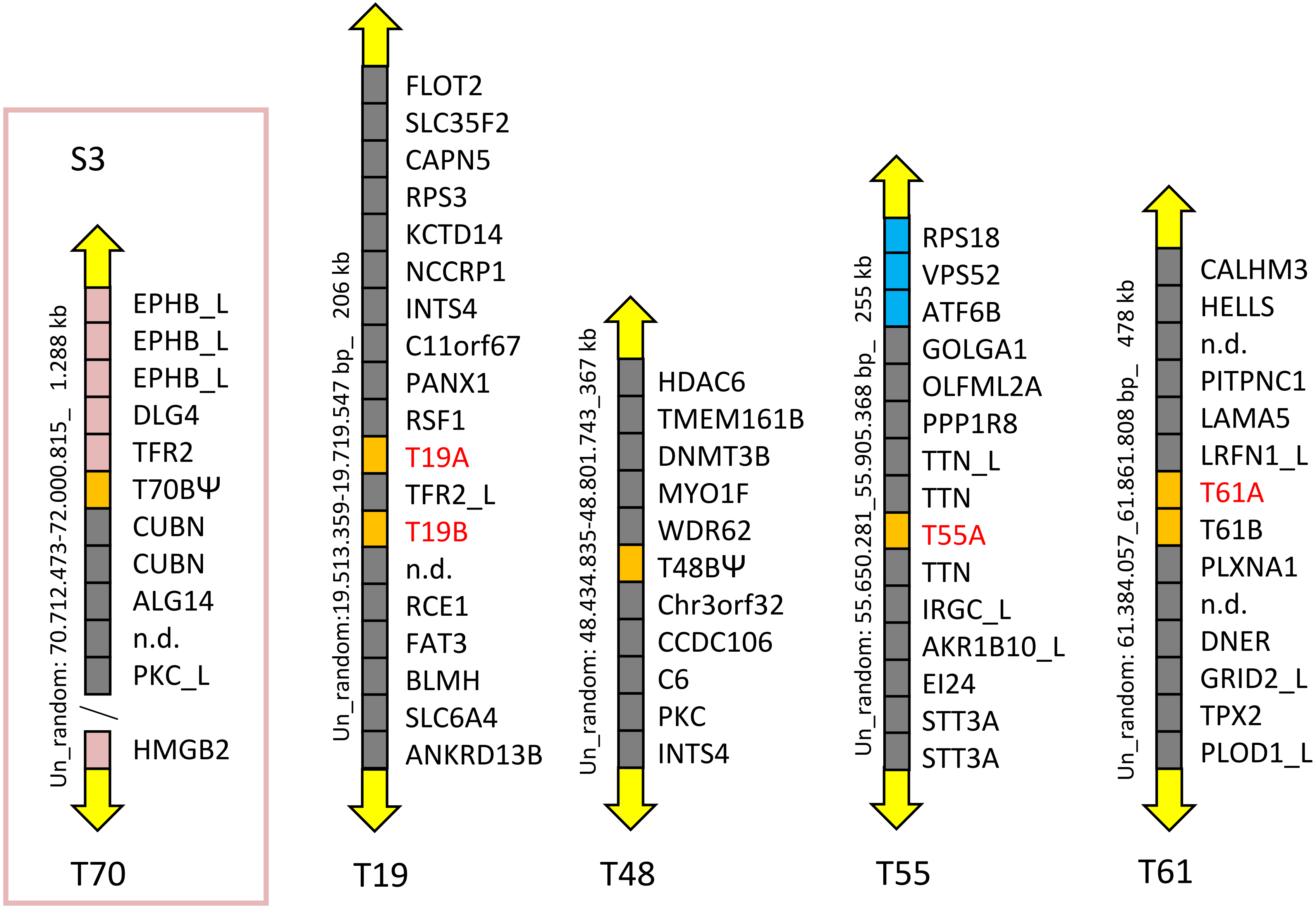


Fig.S2 MHC class II genomic regions

Tetraodon (*Tetraodon nigroviridis*)



Tilapia (*Oreochromis niloticus*)

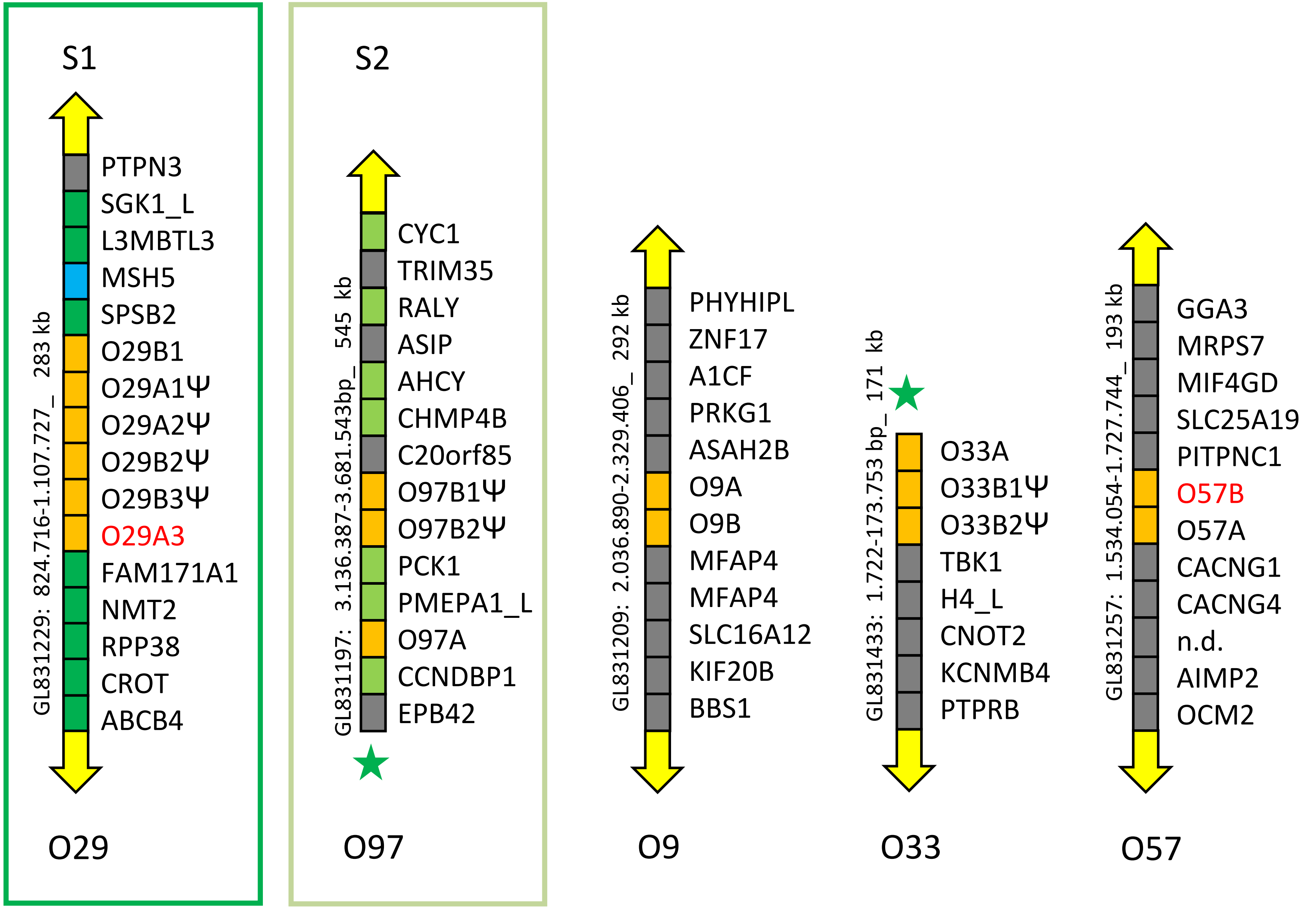


Fig.S2 MHC class II genomic regions

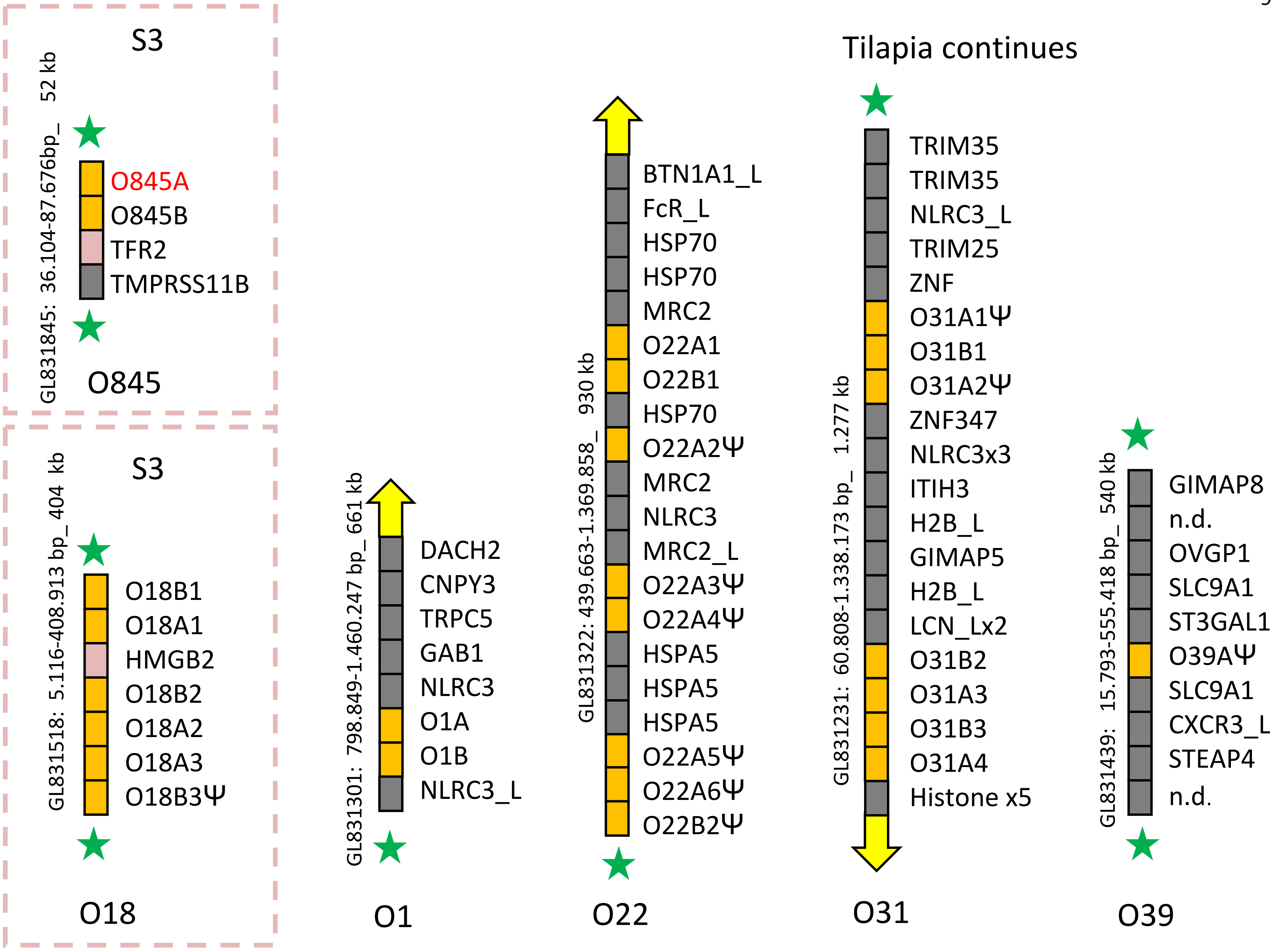


Fig.S2 MHC class II genomic regions

Tilapia continues

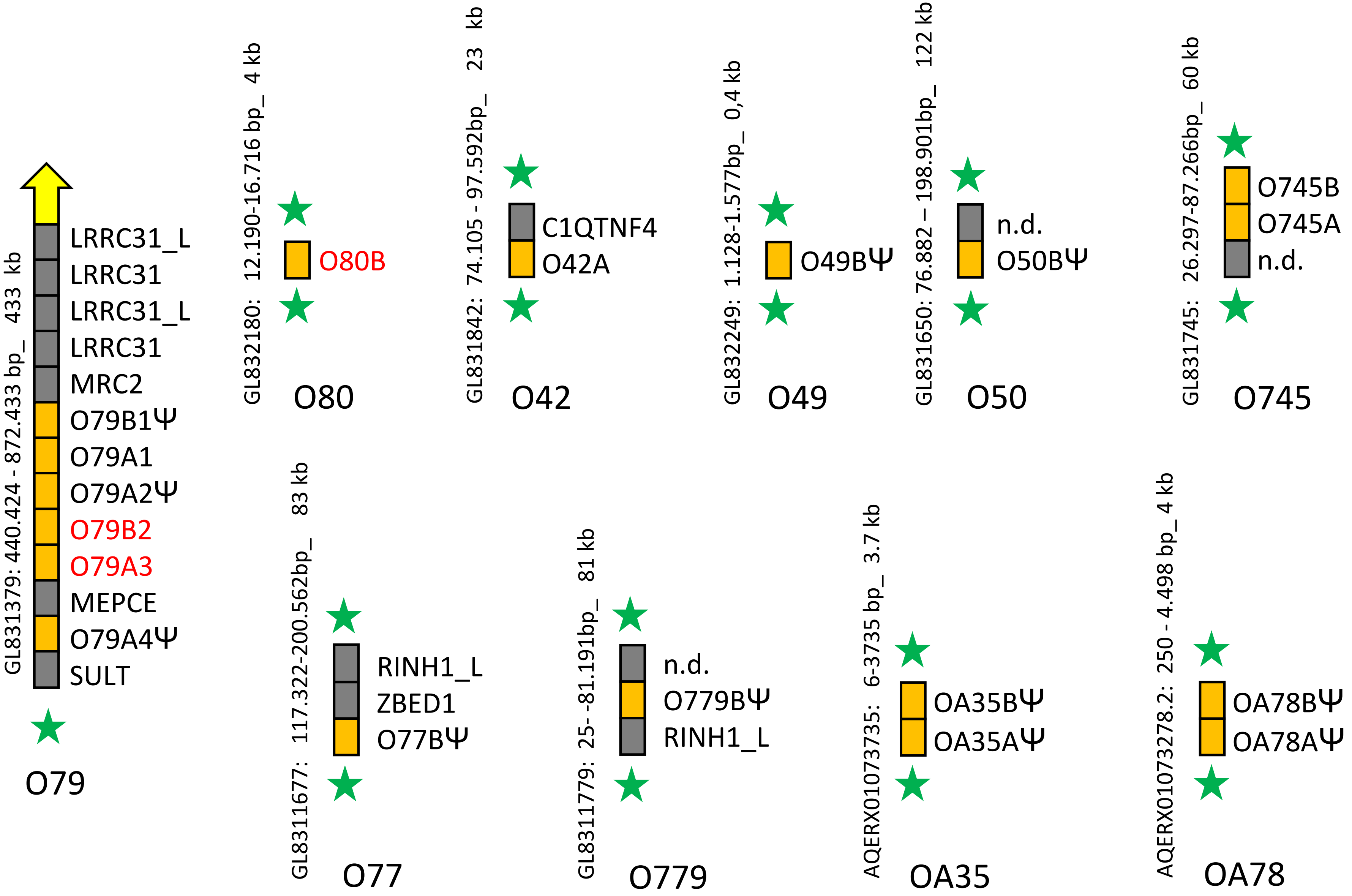
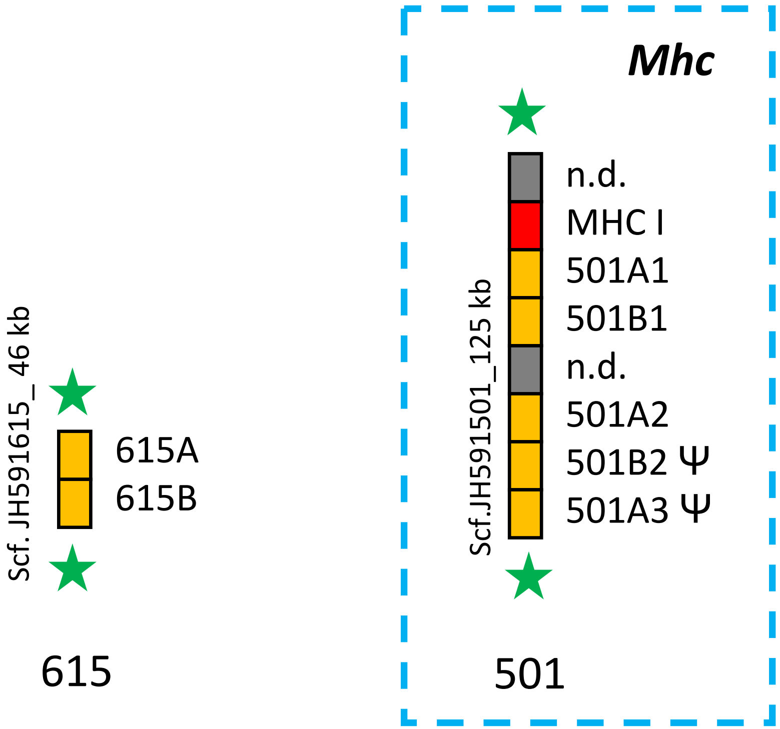


Fig.S2 MHC class II genomic regions

Spotted gar *(Lepisosteus oculatus)*



The MHC class I sequence encoded by scaffold 501 (prediction by GENSCAN software) with the "key amino acids" for binding of peptide termini, which are typical for classical molecules, indicated in red:

MRQGRLPEPPLRYNTFVTHSLR**Y**FYTGVTGVRGFPEFTIVGLVDGQEFVHYDSDIKRMIPKTEWIERNEGKD**Y**WDRQTQILIGAS
QVFKTDLVNLPQ**R**FNQSAGVHTSQSMYGCEWDDEDGTTRGFQQEGYDGEDYLVFDLKTLTWVAPTQRAFL**T**KQN**W**DADRAFNEGK
KN**Y**LTQICIEWLKK**Y**VNYGRETLNRRERPQVSVFHKDSGSGSTELTCLATGFFPRDILVSWWRDGQELHEDVDSGEVVPNGDGSF
QVRKRLRVRAGEEHKYSCRVDHTSLEKTIVQHWEPPSLVPIIAAVCAVVALAVIAVVAVVLVRRRKSSVAVSAFSRRAASDDVIG
ALRTVMAAPCRLVSGRAAIGDQSGYSSLHRSPRFTLLF

Fig.S2 MHC class II genomic regions