**Comparative genome analyses reveal distinct structure in the saltwater crocodile MHC**

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**Figure S4. Amino acid alignment of saltwater crocodile MHC class I genes/pseudogenes identified in the current study and a MHC class I transcript from the American alligator.** Variable positions are relative to sequence variants on the top stretching from leader peptide to cytoplasmic domain. Dots represent identical amino acids to the top variant; asterisks represent stop codons; and numbers above the alignments represent the order of amino acid positions. Sites in boxes indicate amino acid positions that are conserved or have expected functions. These amino acid positions also contain the following additional labels: asterisks, conserved peptide-binding residues of antigen N and C termini, as described in Kaufman et al. [69]; diamonds, salt bridge-forming residues; circles, disulfide bridge-forming cysteines; squares: N-glycosylation site; CD8+, the expected CD8+ binding site. Background colours in the alignments indicate degrees of amino acid identity: 100% in blue; 65-100% in yellow; and below 65% in white