



Supplemental Fig. S2. Oxford Nanopore read coverage for cy0333 complement component C4 duplications

Oxford Nanopore read coverage for the complement 4A (*C4A*) and complement 4B (*C4B*) region in cy0333. Coverage was determined by mapping extracted FASTQ reads against the error-corrected, merged assembly using minimap2. The coverage plot was generated using R. Length is depicted in kb and corresponds to the genomic interval extracted from the full MHC assembly. Coding regions are depicted by black or red boxes on top of or below the assembly. Reads spanning both *C4A* and *C4B* coding regions are highlighted in red.