



Extended Data Figure 4 | *ICAM2* splice junction analysis in *C. atys* and *M. mulatta* by RNA-seq read alignment. **a**, Quantification of observed splicing. Splice site counts for RNA-seq read alignments were added together and sites with more than 100 total reads were compared to find the proportion of reads supporting each splice variant or intronic

retention. **b**, *MmICAM2* splicing analysed by RNA-seq read alignment to the reference genome and visualized in IGV. **c**, *CaICAM2* splicing analysed by RNA-seq read alignment to the reference genome and visualized in IGV.