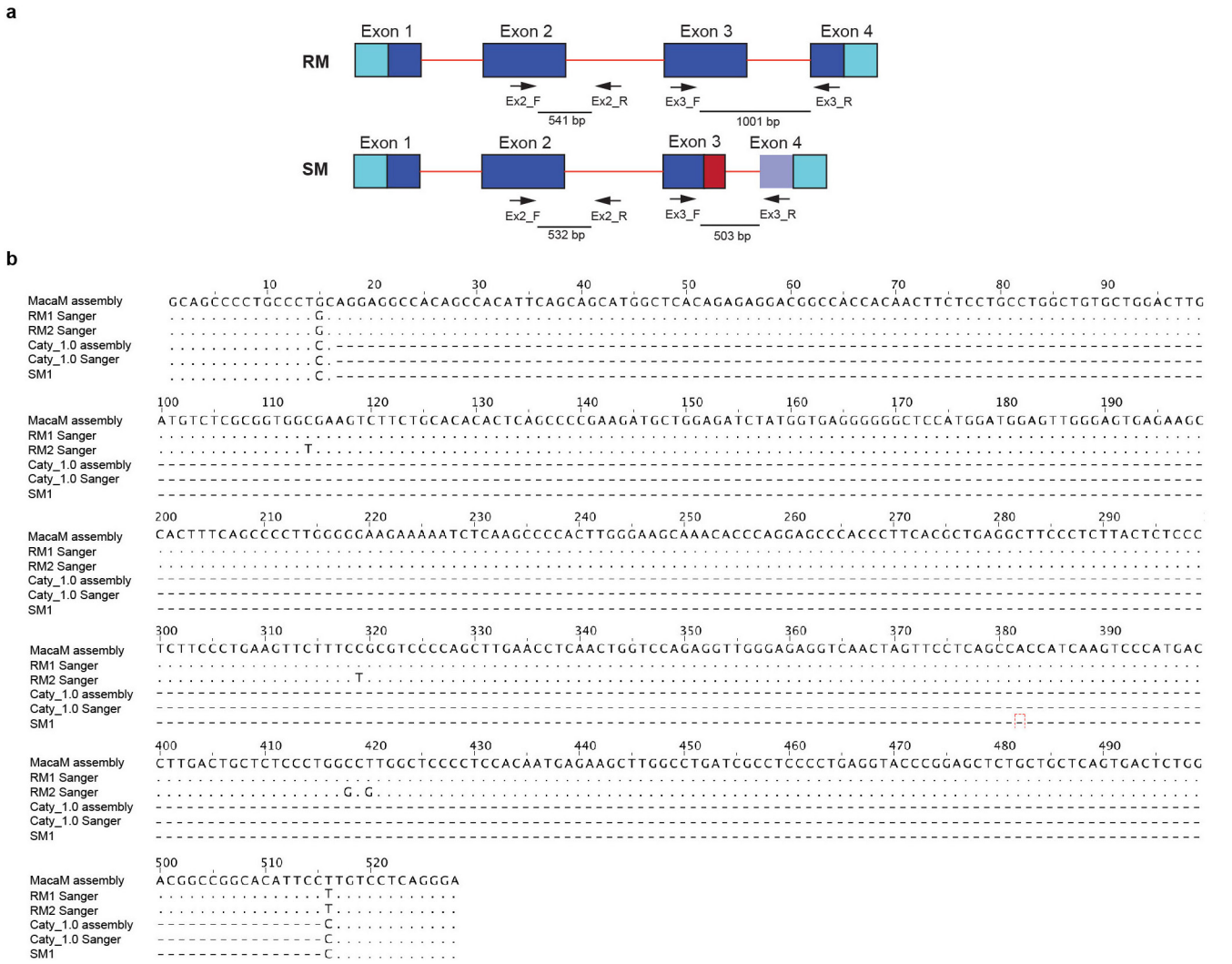

Extended Data Figure 3 | Predicted model of the *ICAM2* gene structure and *ICAM2* genome sequence alignments. a, Predicted model of *ICAM2* gene structure of *M. mulatta* and *C. atys* and the location of PCR primers for Sanger sequencing. Light blue, untranslated region; dark blue, CDS; red lines, intronic sequence; dotted line, exonic and intronic sequences present in human *ICAM2* and Mm*ICAM2* but not in Ca*ICAM2*; red box, the sequence that would be intronic in Mm*ICAM2*, but which is included in the exonic sequence of Ca*ICAM2*; light-purple box for Ca*ICAM2* exon 4 represents the fact that the exon 4 sequence in Mm*ICAM2* is present in Ca*ICAM2* but is not included in the Ca*ICAM2* CDS due to a stop codon in the Ca*ICAM2* exon 3. Primer positions are indicated by arrows. Predicted PCR products are indicated by thick lines. Primers Ex3_F and Ex3_R were designed to amplify a region spanning a putative genomic deletion which includes the 3′ region of Ca*ICAM2* exon 3 and intron 3. **b**, Alignment of *ICAM2* genomic sequences. Sanger sequencing of 2 rhesus macaques and 2 sooty mangabeys (including the Caty_1.0 reference animal) was performed to confirm the *ICAM2* genomic deletion specific to *C. atys*. Starting at Mm*ICAM2* nucleotide position 3166, sequences were aligned using Jalview v.2.9.0. Dashed lines denote the deletion in *C. atys*. RM, rhesus macaque; SM, sooty mangabey.