Electronic Supplementary Material 5. Domain-by-domain phylogenetic analysis of the newly identified *Gogo-B*07* gene. Neighbor-joining trees were constructed from available full-length genomic sequences of *MHC-B* and *-C* genes. Shown in the top left corner is the size of the genomic segments (1-5) which were used for the phylogenetic reconstruction. Black, grey and white circles correspond to bootstrap values of ≥95%, ≥80% or ≥50%, respectively. Black triangles represent compressed *MHC-B* and *-C* sequences of human (*H*), chimpanzee (*C*), gorilla (*G*) and orangutan (*O*) with the total number of sequences given in parentheses. Highlighted in blue are sequences of *Gogo-B*07* alleles. Highlighted in red are sequences of *Gogo-B*03* alleles co-segregating with *Gogo-B*07*. Sequences of other gorilla alleles identified in the present study are highlighted in bold. *HLA*, human; *Patr*, *Pan troglodytes*; *Gogo*, *Gorilla gorilla*; *Gobe*, *Gorilla beringei*; *Popy*, *Pongo pygmaeus*; *Mamu*, *Macaca mulatta*