Supplementary Figure 16 Sliding-window analyses for rhesus-human ancestral gene pairs. For each ancestral gene, translated ORF sequences for rhesus and human were aligned using stretcher (http://emboss.sourceforge.net) with gap-open penalty of 20 and gap-extend penalty of 1. Resulting amino-acid alignments were used to convert corresponding rhesus and human mRNA sequences into codon alignments using PAL2NAL (http://www.bork.embl.de/pal2nal). A custom perl code was used to implement the CODEML program in PAML to calculate dN/dS ratios over a sliding window with a 3-bp step. Coding sequence (CDS) length determined window size: if CDS < 500 bp, window size = 150 bp; if CDS > 500 bp, window size = 300 bp. dN/dS values for each gene as a whole are given in Supplementary Table 3.