



Supplemental Figure S10: Recombination within *TBC1D3* gene model. GARD was run on the codon aligned MSA of expressed *TBC1D3* paralogs to investigate if sites under selection or lineage specific expansions may be explained by gene conversion. **(A)** GARD identified evidence for one breakpoint *TBC1D3* bp 755, corresponding to AA 252, and segmenting the multiple sequence alignment in two subsequences. **(B)** Inferred phylogeny of subsequence 1, the first 755 bp of *TBC1D3*. Green colored lineages illustrate bonobo paralogs nested among human *TBC1D3* copies. **(C)** Inferred phylogeny for the last 1045 bp of *TBC1D3*. For both (B) and (C), species separation is largely maintained, and the inferred breakpoint is not proximal to any sites identified to be undergoing positive selection.