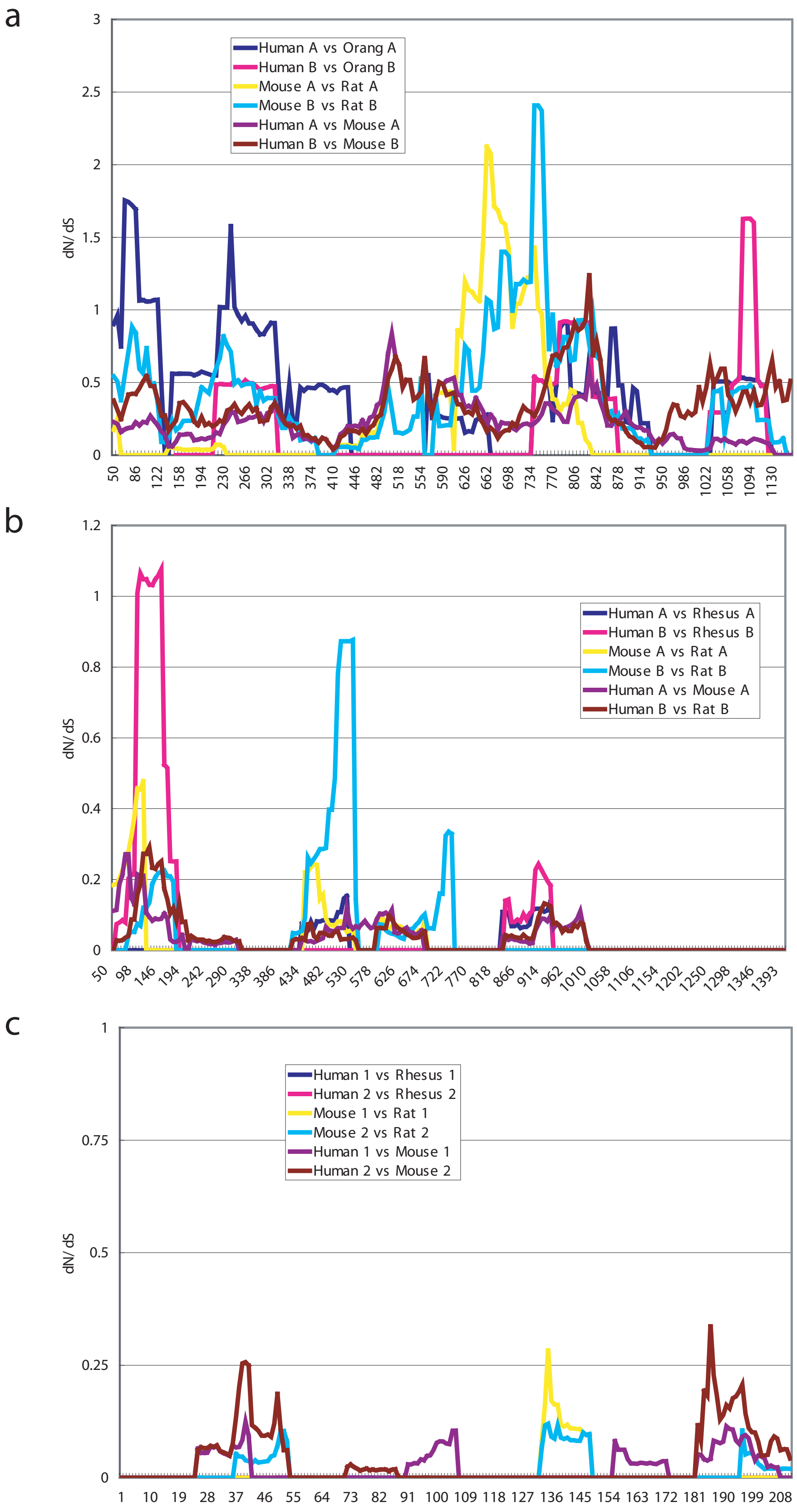

Additional file 8: Sliding window analysis calculating dN/dS between paralogues and orthologues
Sliding windows of 99 bps with a 6 bp step size were used to calculate dN/dS between gene pairs in a) *BMP8A/B*, b) *DDX19A/B* and c) *TUBG1/2*. Values of dN/dS were calculated within the windows using the program K-estimator and plotted across the gene pairs. Primate comparisons were calculated using human-macaque pairs (except in *BMP8A/B* where orangutan was used), while rodent comparisons were calculated using mouse-rat pairs. Although we conducted additional analyses using PAML, no significant evidence of positive selection was found.