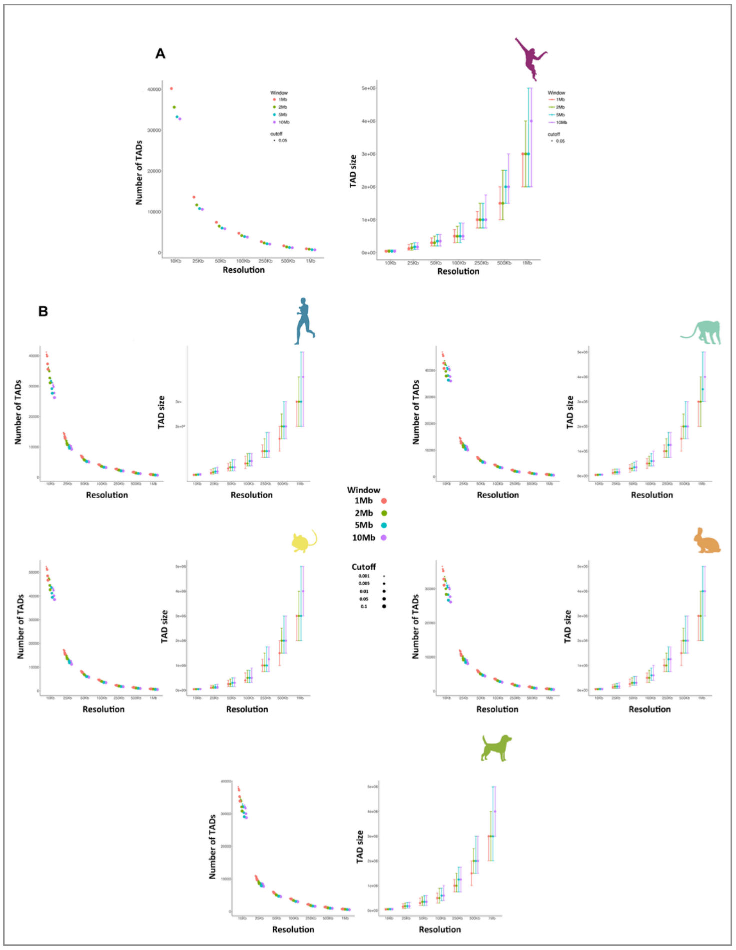
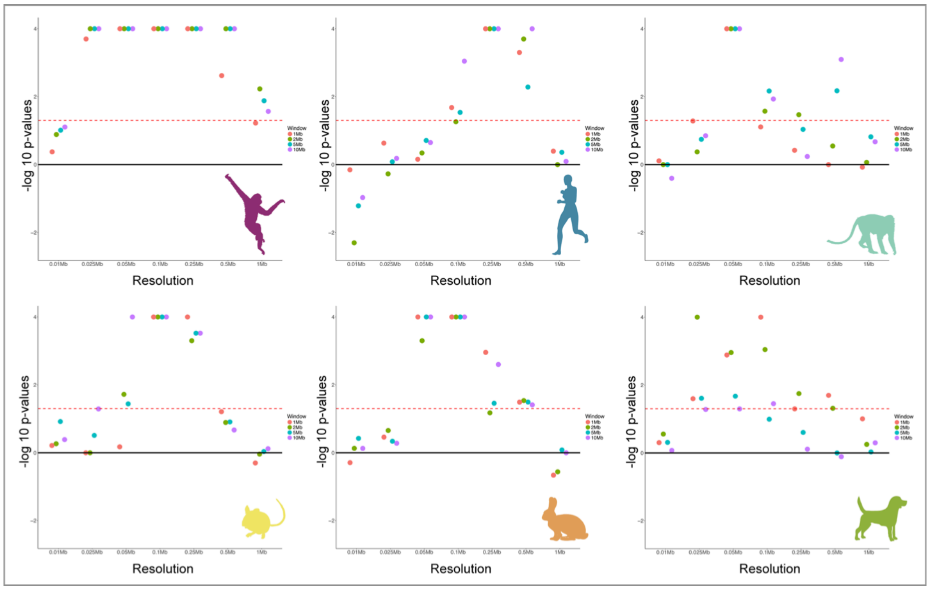


Supplemental Figure S7 - (A) Count and size of gibbon TADs identified using different resolutions (x-axis) and windows (colors) are plotted. A cutoff of 0.05 is represented here and bars show the inter-quartile range. Resolution has the largest impact while cutoff does not seem to have relevant impact. (B) TAD counts and sizes for the other five species included in the study: human, rhesus, mouse, rabbit, and dog. Different Cutoff values are shown for the “Number of TADs” (left panel) and Cutoff of 0.05 is used for the TAD size plots, bars show the inter-quartile range (right panel).



Supplemental Figure S8 - Results of permutation analyses to test association between TAD boundaries and gibbon BOS regions TADs were called using 140 parameter combinations in gibbon and other mammalian species (cutoff 0.05 shown here). A consistent correspondence between TAD boundaries and BOS is evident in gibbon, whereas this correspondence is limited to distinct resolution intervals in the other species. (Dotted line indicates 0.05 significance with no multiple-test correction).