Supplementary Figures and Legends

Supplementary Figure 1 | Genomic architecture of the Alu tested targets in human, chimpanzee and rhesus. The edited Alus are in the center of the screenshot of UCSC genomic browser, with track for the Alus near by. The direction of an Alu is marks by white arrows.

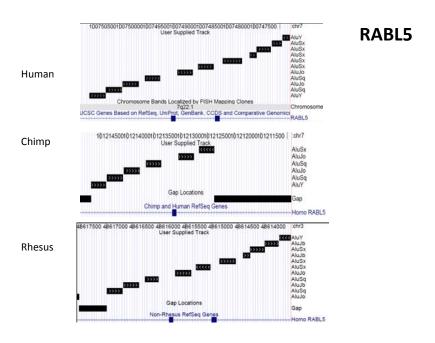
NUP50 43954000 43953500 43953000 43952500 43952000 43951500 43951000 chr22 AluSc AluJb AluSg AluJo Human 44334500 44334000 44333500 44333000 44332500 44332000 44331500 :chr22 AluSc AluJb AluSg AluJo Chimp Gap Locations mp and Human RefSeq Genes Homo NUP50 Homo NUP50 9166000 89165500 89165000 89164500 89164000 89163500 89163500 89162500 chr10 User Supplied Track AluSc AluJb AluSg AluJo Rhesus

Gap Locations

us RefSeq Ge

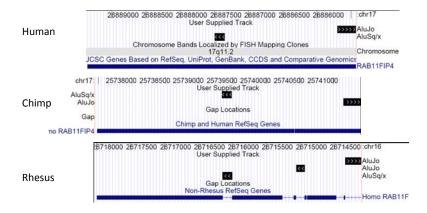
Gap

omo NUP50





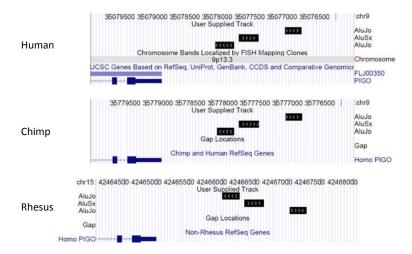
RAB11FIP4



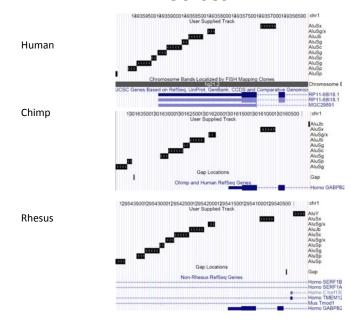
RAB27A



PIGO



MGC29891



MATR3



Supplementary Figure 2 | No significant difference in Alu genomic architecture between

human and monkeys. The analysis was done using UCSC human (hg18 assembly), chimpanzee (panTro2) and rhesus (rheMac2) genome assemblies. For comparison, properties of mouse (mm9) and rat (rn4) Alu-related B1 repeats have been included. **a,** Number of repeats in the genome. Sequences shorter then 50bp and those not mapped into the consensus genome were removed from the analysis. **b,** Repeat element length. **c,** mismatches in sequences as compared to their respective consensus. **d,** Distribution of the different families of Alu sequences (presented only families with 10,000 copies).

