Mobile elements and highly repetitive regions are potent sources of lineage-specific genomic innovation and are integral to the structure and function of eukaryotic cells. Employing long-read sequencing to build gapless (i.e. telomere to telomere, T2T) genome assemblies for humans and non-human primates, we aim to define key genetic, transcriptional and epigenetic features that define centromere maintenance and de novo centromere formation. Using comparative genomics, these studies provide insight into the diversity, distribution and evolution of repetitive regions that not only shape the human genome, but that influence chromosome structure and evolution in species groups experiencing rapid karyotypic change.