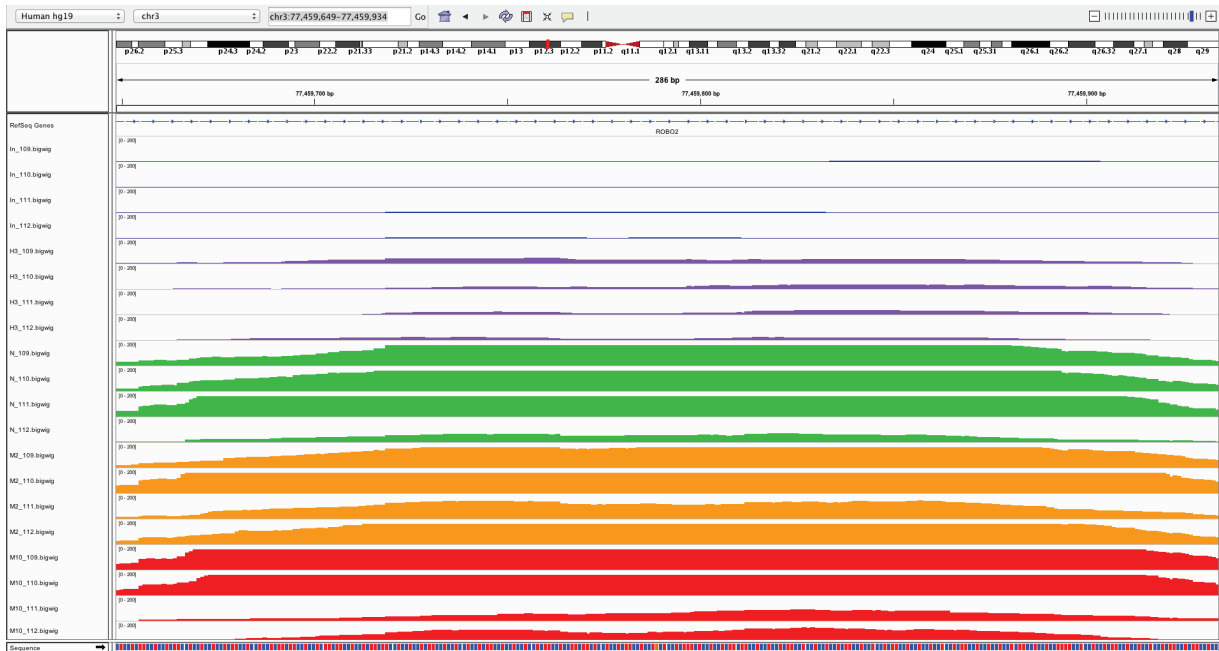
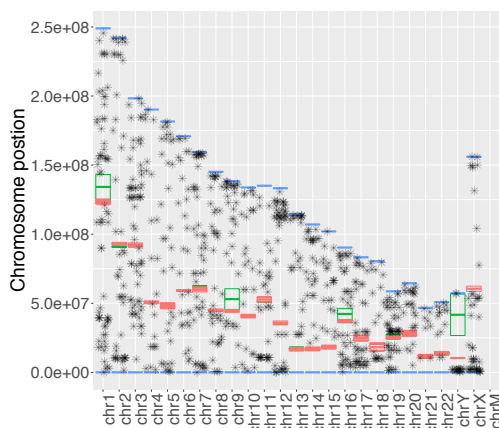


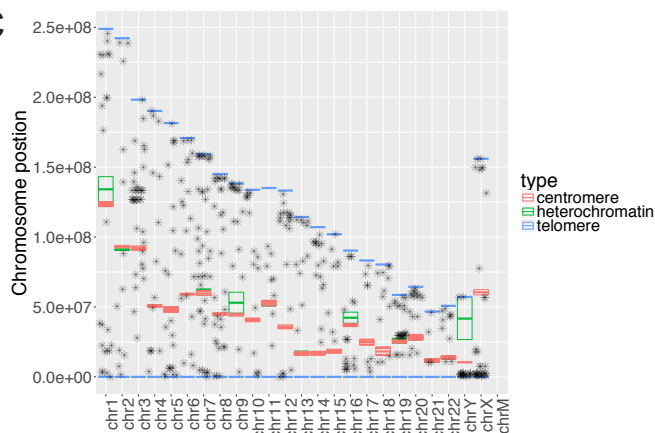
A



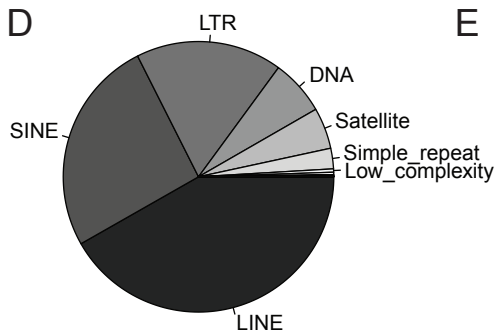
B



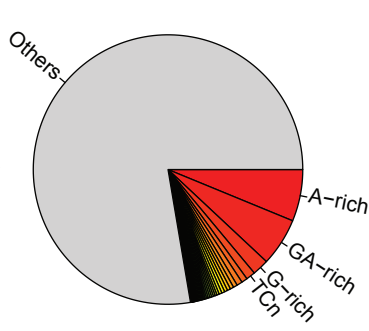
C



D



E



Supplementary Fig. S2 GA-rich repeat RNA enrichment in long RNA-seq and loci analysis A) Example of GA-rich repeat hit from long RNA-seq. Top 4 lines show reads mapping to Input samples, purple to H3 sample, green to Nascent, orange to Mature 2 h and red to Mature 10 h samples. Height on all tracks is set to 200. B) Long hits plotted according to chromosome location. C) Long hits NA and repeats (no genes) plotted according to chromosome location. Base coverage of D) all repeats in genome, total: ~52%, and E) simple repeats and low complexity regions (total: ~1.5%) including colour-coded repeats found in long hits according to relative proportion (total: 0.33% of the genome).