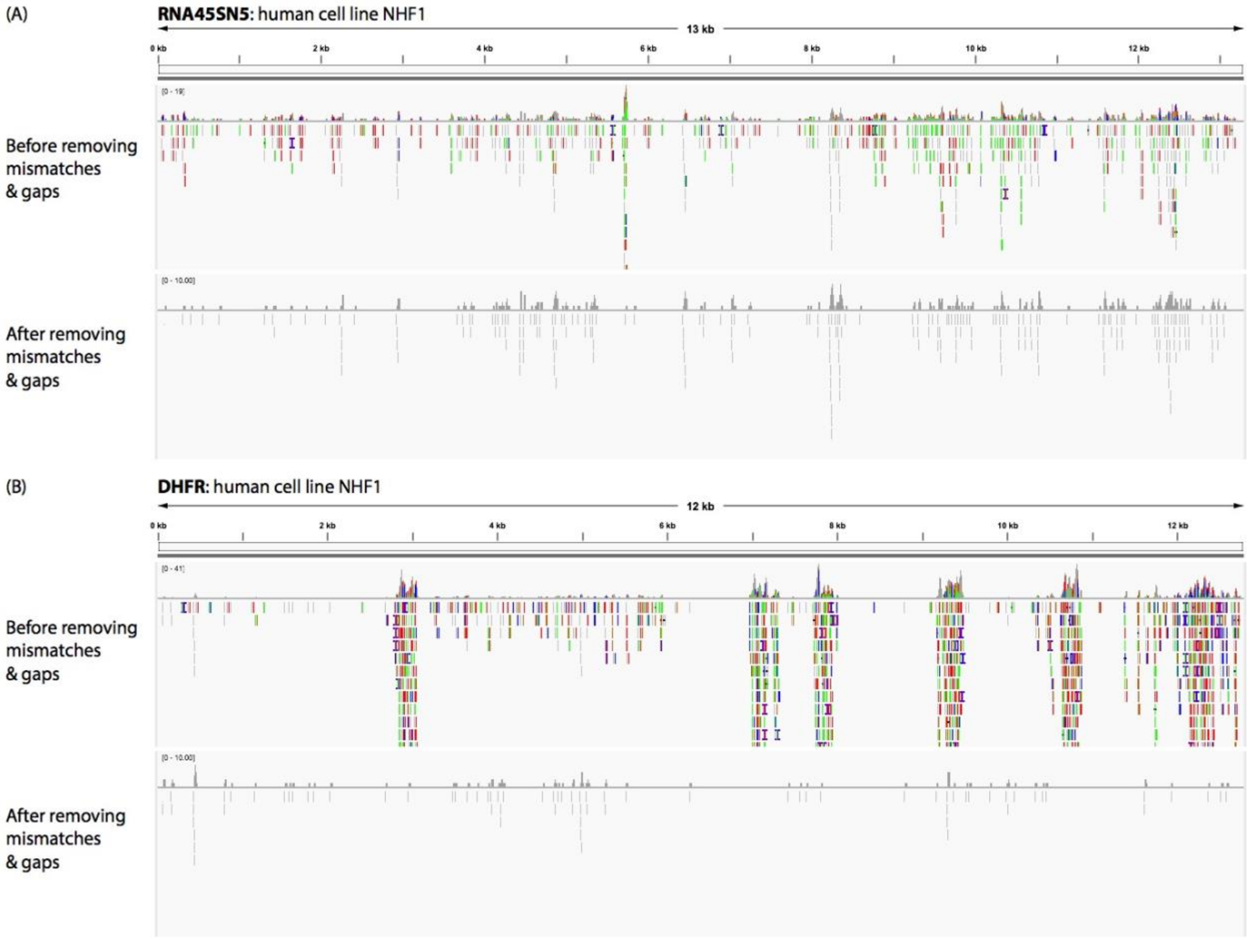
Supporting Information Figure S1. Excision product mapping before and after removing reads with mismatches/gaps. Image shows bam file reads from XR-seq are enriched with lengths around 26 nucleotides. Due to the short-read nature, a great proportion of reads have mismatches/gaps after alignment. We use bamtools to remove such reads. Before and after filtering snapshots are shown for (A) ribosomal gene (rDNA) and (B) *DHFR* for human cell line NHF1.



Supporting Information Figure S2. The GG/CC and AA/TT content in rDNA, *DHFR* and *Dhfr* of humans and mice.