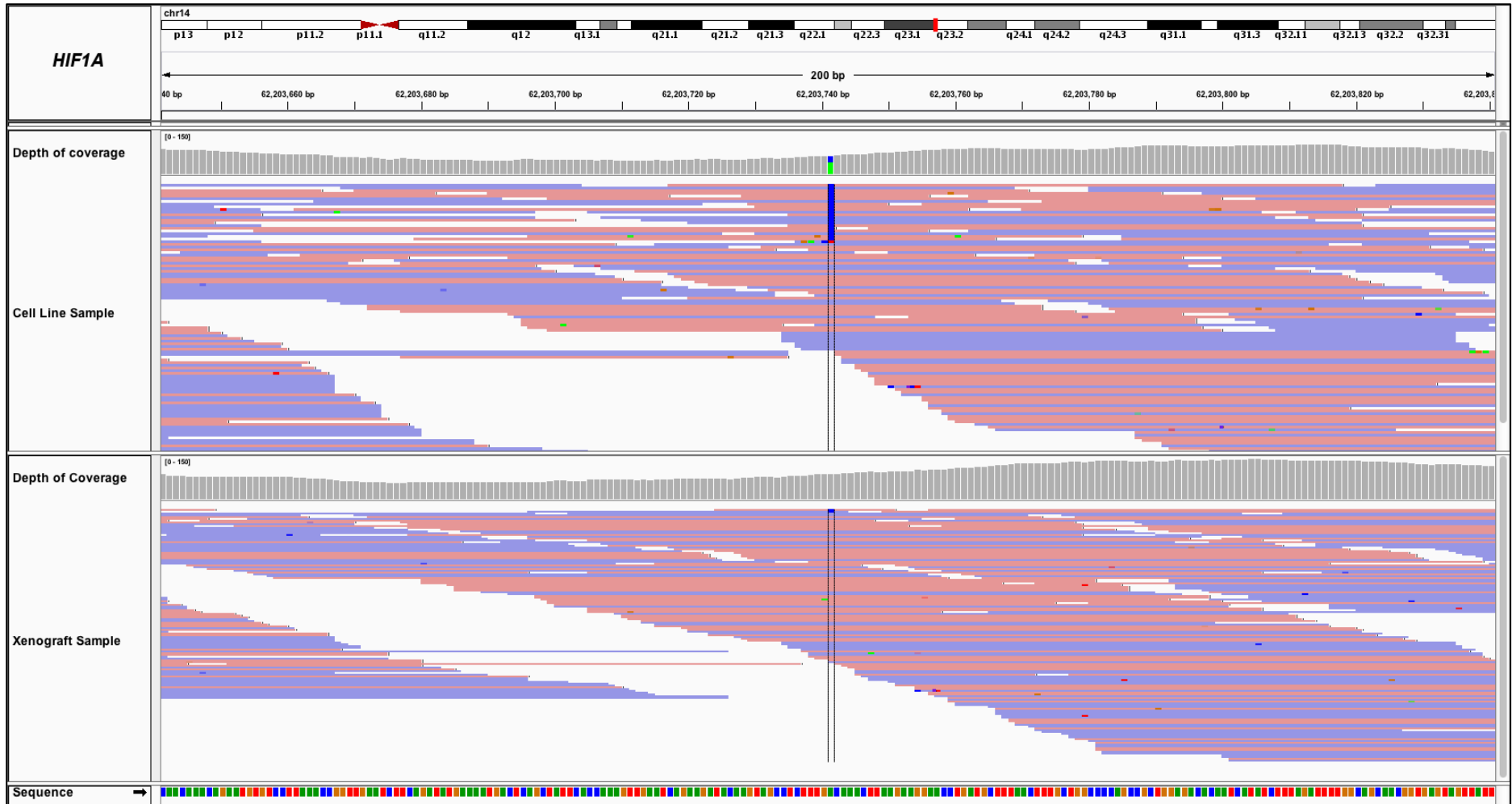
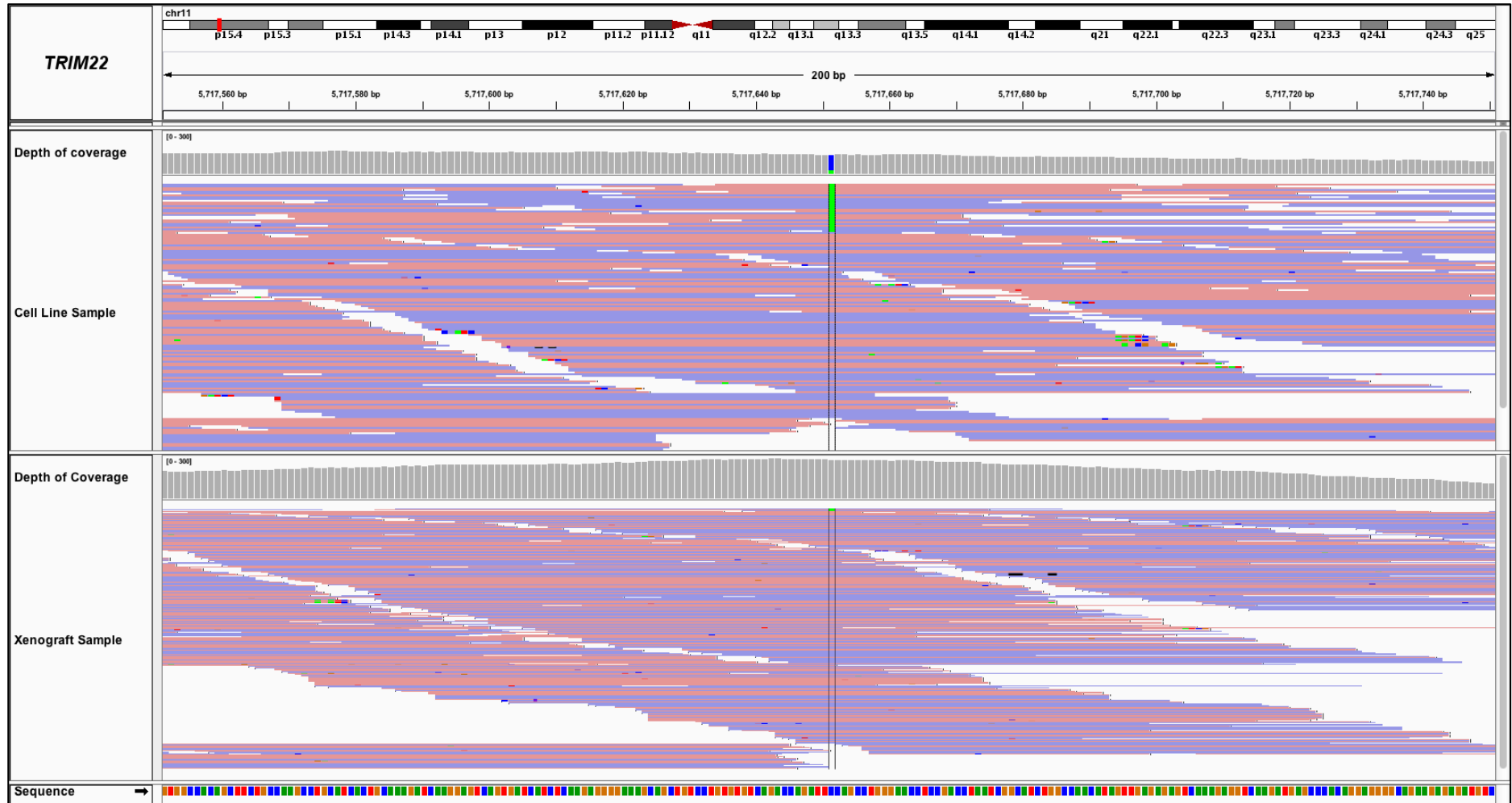


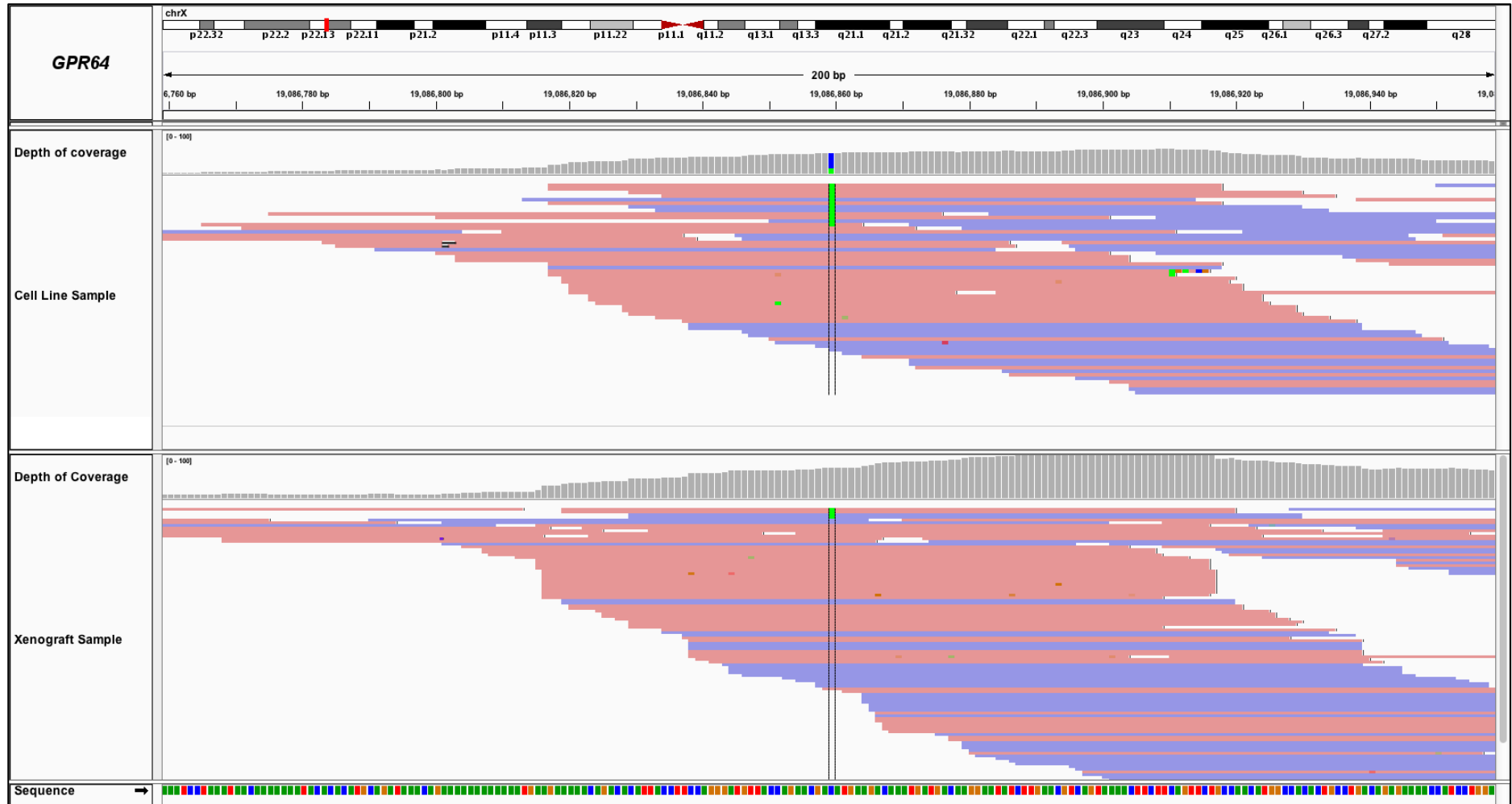
A



B



C



D

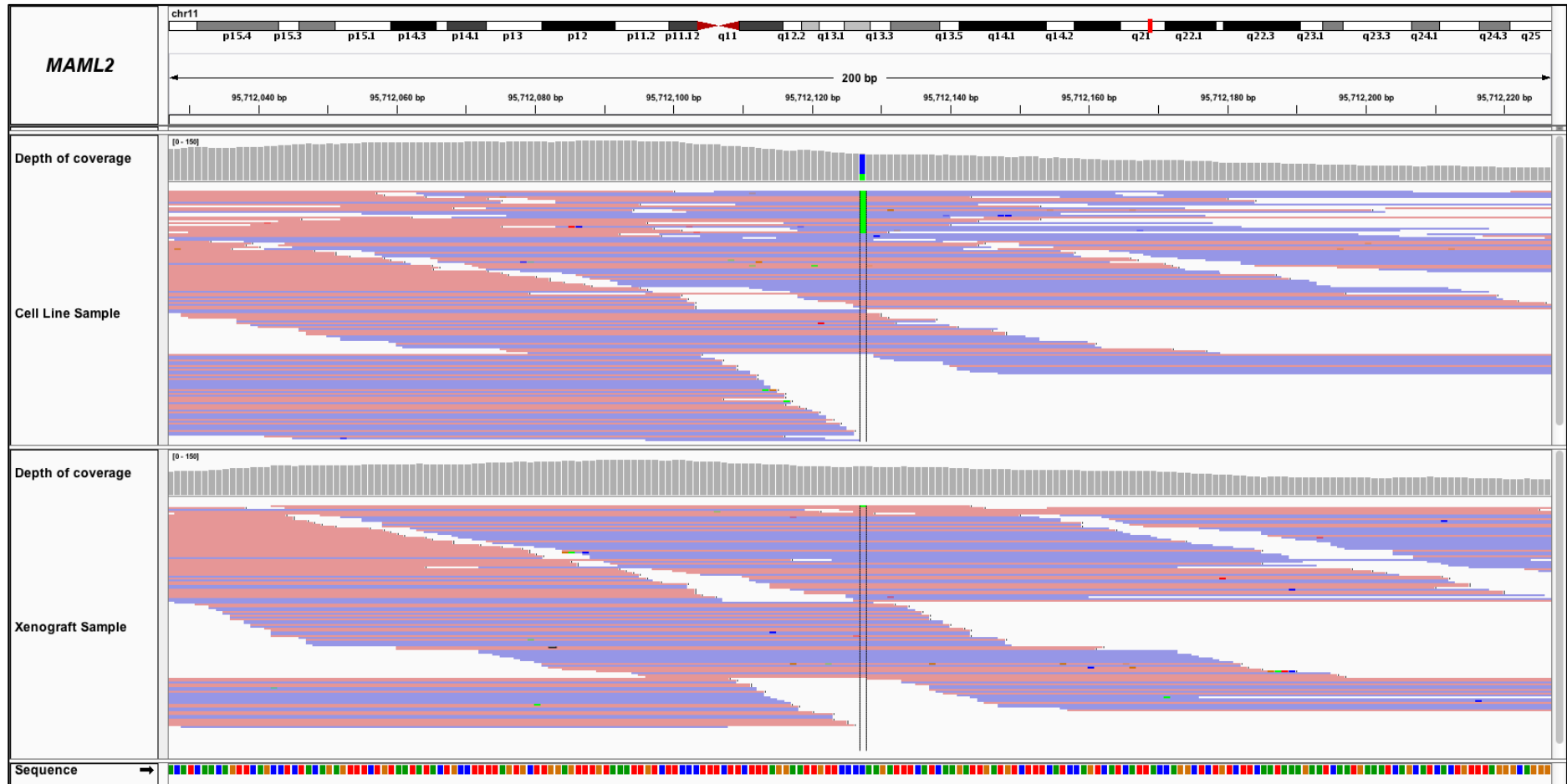


Figure S4. Analysis of cell line-specific variants. Sequence depth of coverage and allele frequency comparisons between the cell line and xenograft samples. Both samples were aligned to the human reference genome hg19. Representative detected variants are shown for *HIF1A* (A), *TRIM22* (B), *GPR64* (C) and *MAML2* (D) genes. Genomic locations for the variants shown are described in supplementary Table 4 A. Variants position is highlighted by black parallel bars. Nucleotide residues are shown in red (thymine), blue (cytosine), green (adenine) and yellow (guanine). Heterozygous variants are indicated in the depth of coverage track and show both reference and alternative alleles. Forward and reverse sequencing reads are shown in pink and blue respectively. Sequence base mismatches are highlighted with its corresponding nucleotide color.