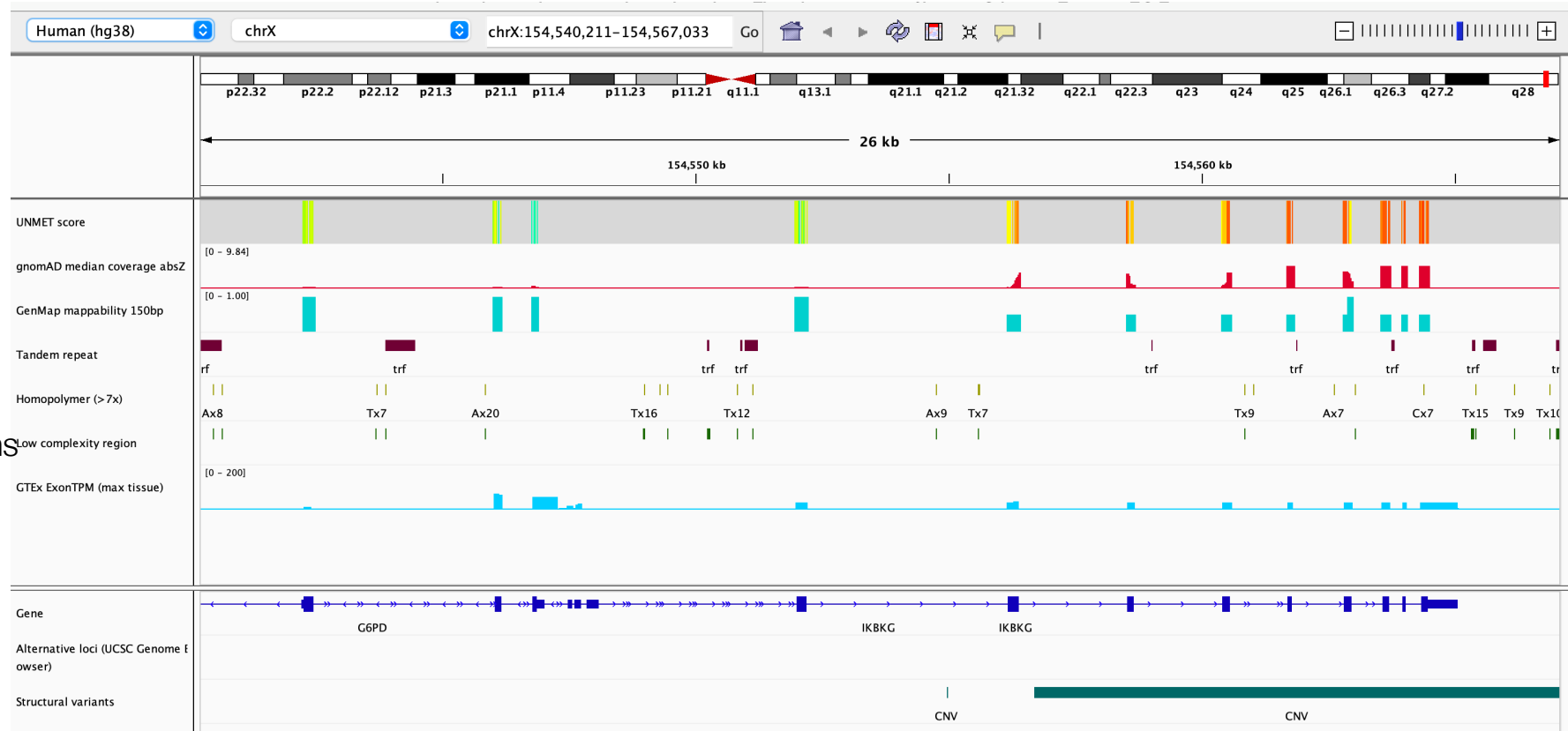


# How to view with the UNMET-igv session file

- When you open the IGV session file, each track view is appeared.
- The UNMET scores are represented by a heatmap (red is high and green is low). The type of view can be switched by the IGV settings.



UNMET score

gnomAD coverage

Mappability

Tandem repeats

Homopolymers

Low complexity regions

Gene expression

Gene

Alternative loci

Structural variants

# Track information

## ➤ UNMET score

A metric for a validity of degree in variant detection for each base in the genome sequence. It ranges 0 to 1 and if it closes to 1, it means a difficulty in detecting variants using solely using short-read type NGS.

## ➤ gnomAD coverage

A standardized median values of genome coverage in the gnomAD v3.1 dataset.

## ➤ Mappability

A measurement to uniquely mapped on the genome sequence. It ranges from 0 to 1. The value of 1 indicates the region is unique in the genome. The values are computed by using the GenMap software, with L (read length) 150bp and E (allowed mis-matches) is 2.

## ➤ Tandem repeats

Tandem repeats computed by using the TandemRepeatFinder software.

## ➤ Homopolymers

Homopolymer tracts with contiguous 7 or more identical bases.

## ➤ Low complexity regions

The LCRs computed by using the Symmetric DUST software.

## ➤ Gene expression

Exon-wise gene expression data obtained from the GTEx v8. The values indicate the largest expression value among the tissues.

## ➤ Alternative loci

Data of the alternative loci obtained from UCSC Genome browser.

## ➤ Structural variants

SV information are obtained from Database of Genomic Variant (DGV).