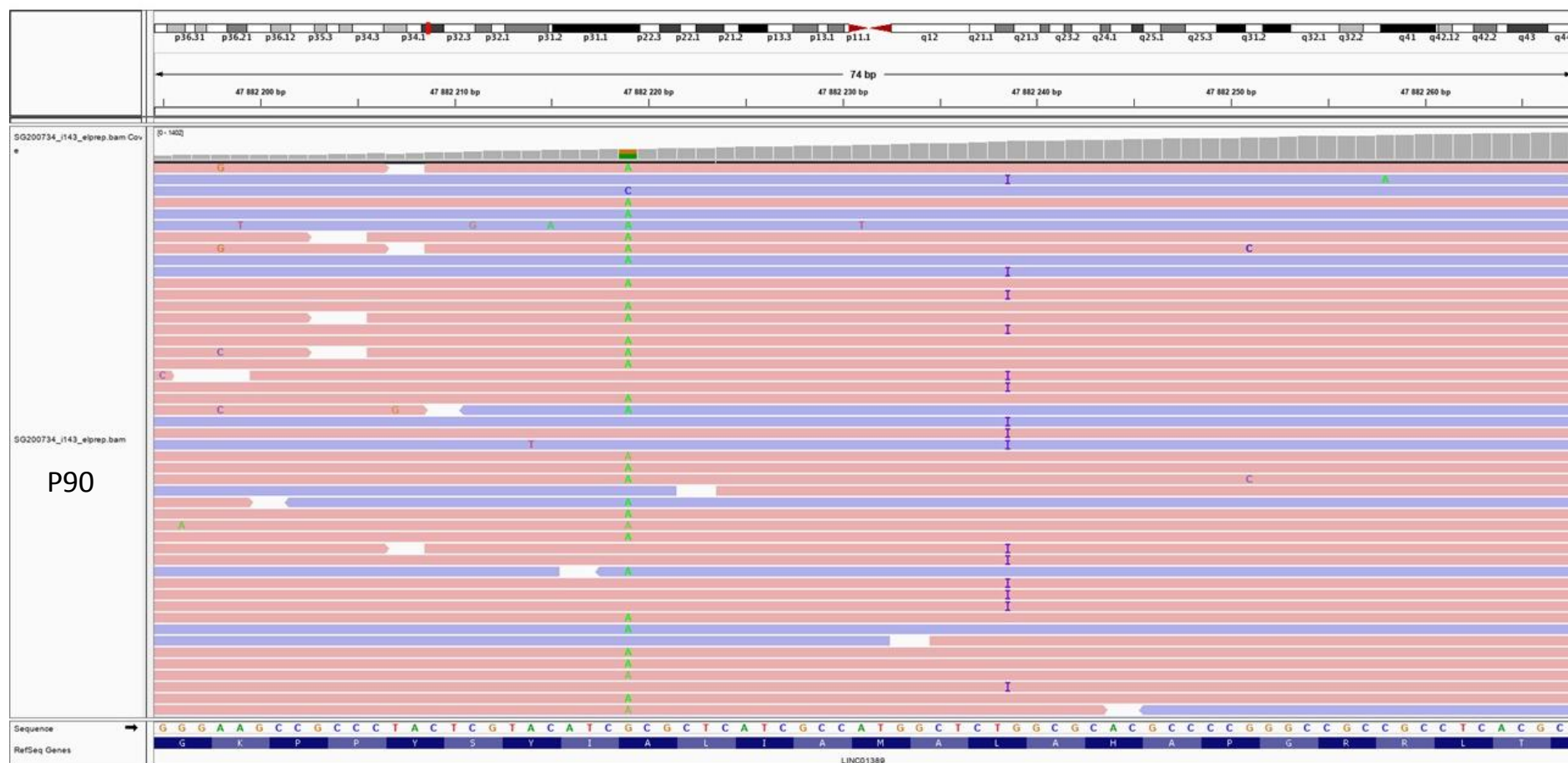


### Supplementary Data 4: P90's BAM visualization of the two *FOXE3* variants using Integrative Genomics Viewer (IGV).

The two pathogenic variants (c.232G>A and c.253dupG) are *in trans* because they are not supported by the same reads.



Integrative Genomics Viewer (IGV): <http://software.broadinstitute.org/software/igv/>