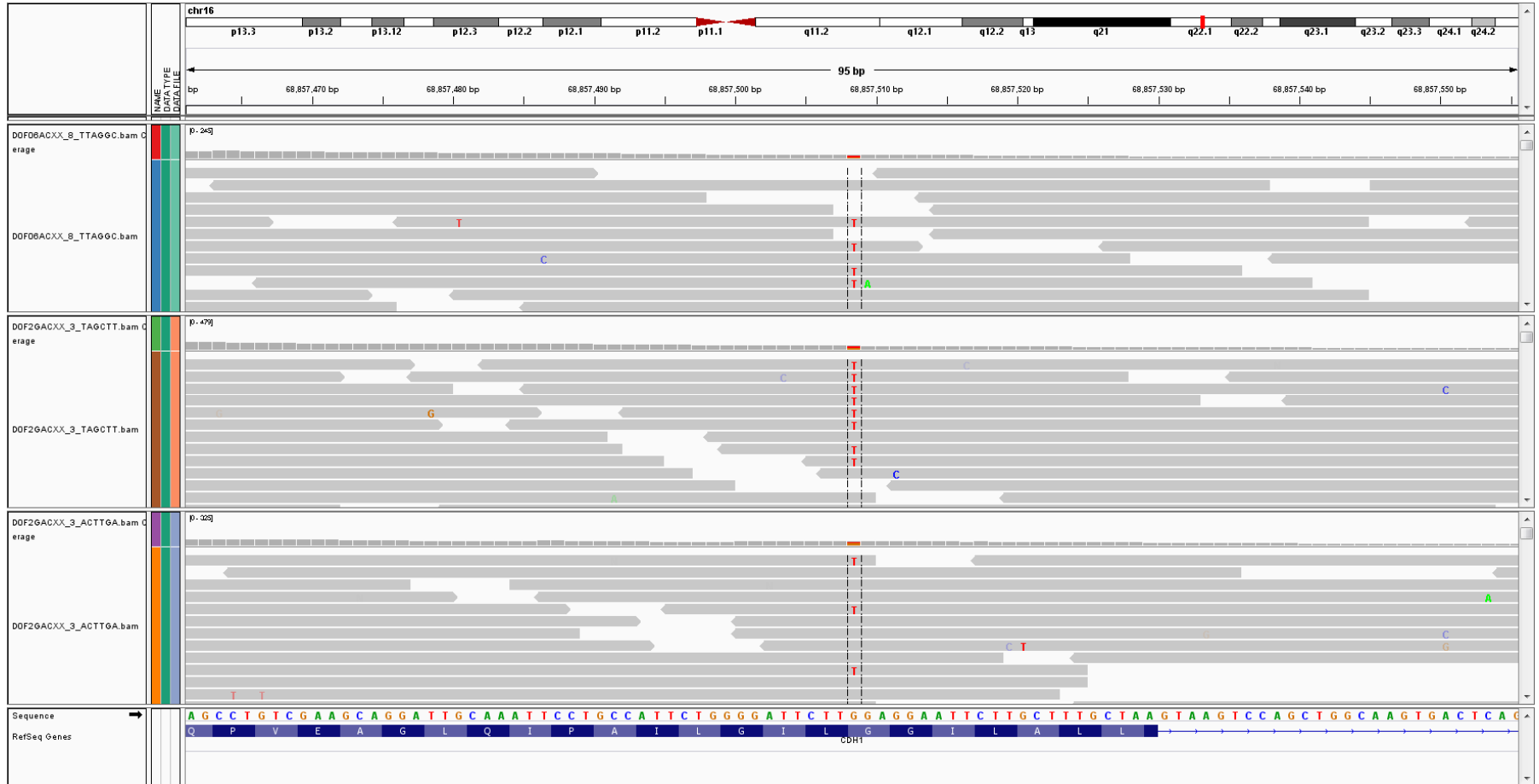
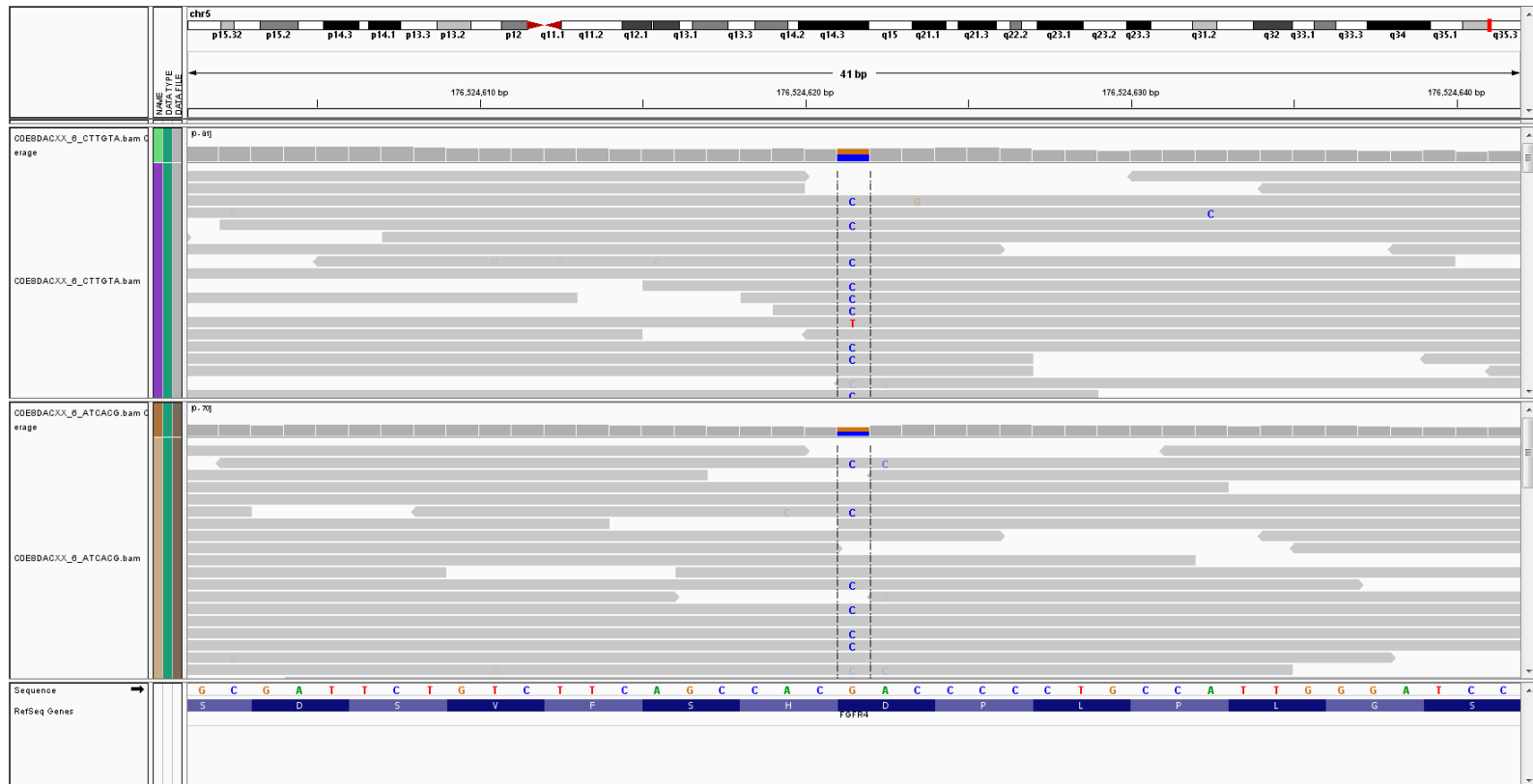


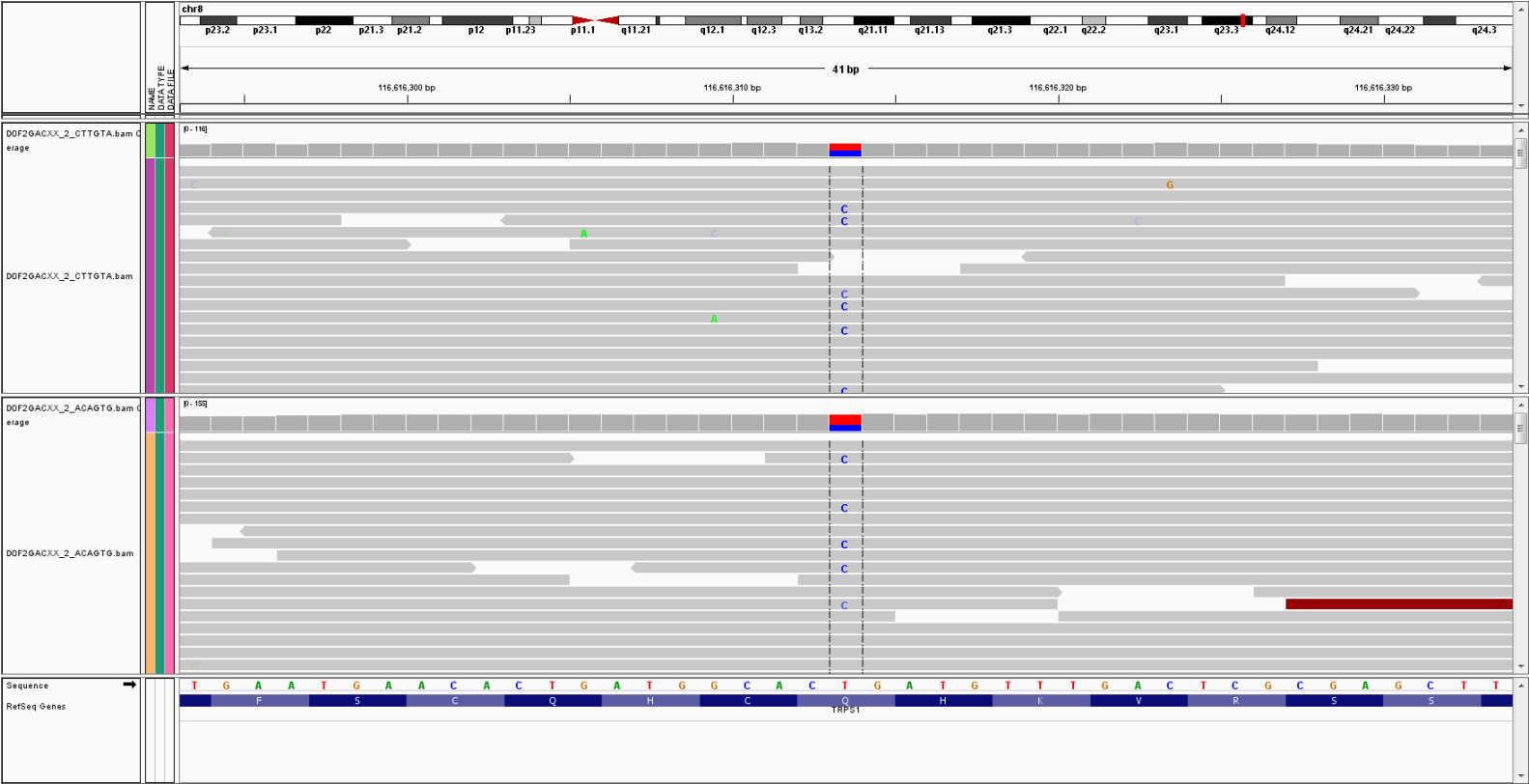
A) Family 15157- CDH1- chromosome 16, position 68857508



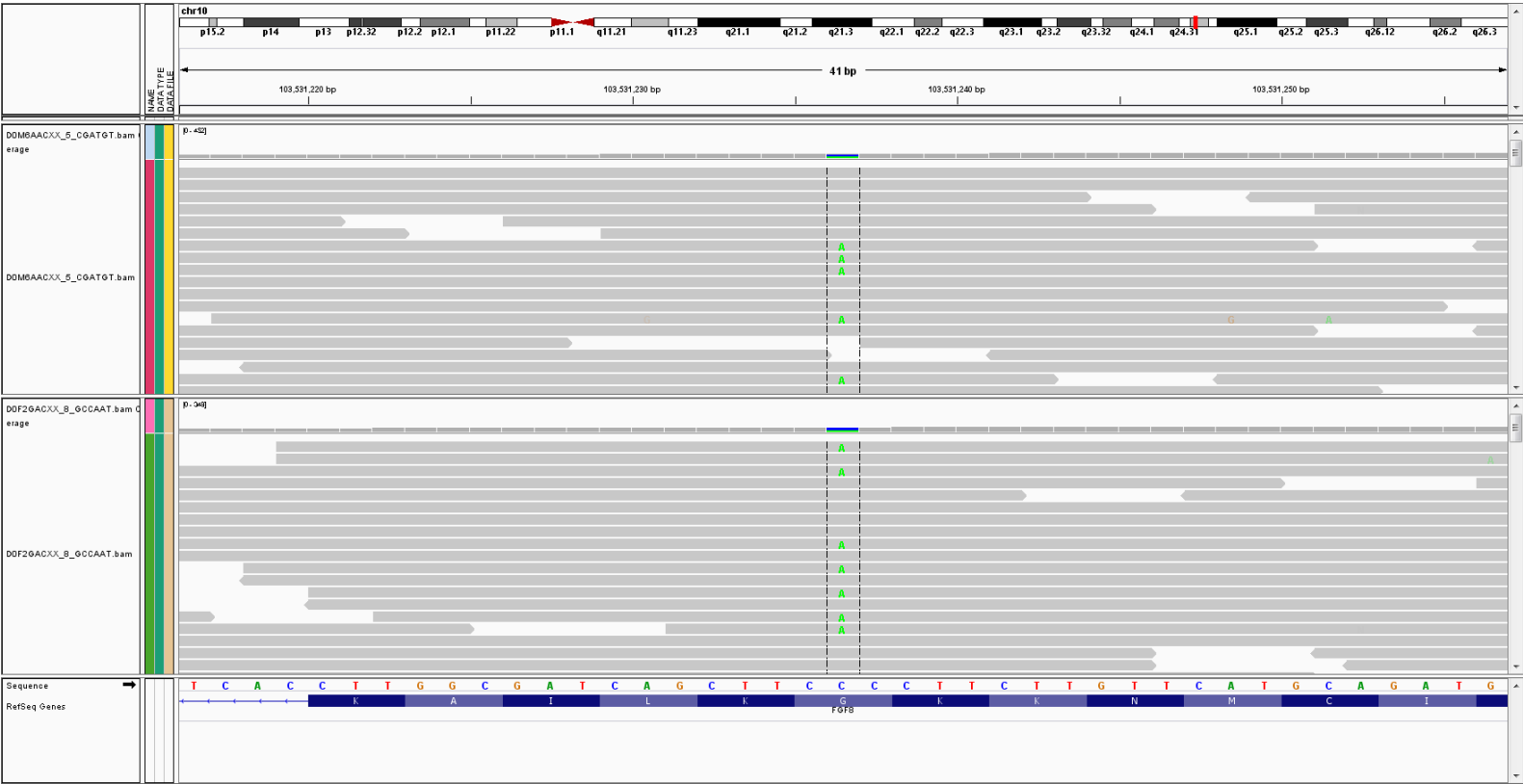
B) Family 15160- FGFR4- chromosome 5, position 176524621



C) Family 17106 – TRPS1 - chromosome 8, position 116616313



D) Family 25324 – FGF8 - chromosome 10, position 103531236



E) Family 28010 – FTCD - chromosome 21, position 47572892

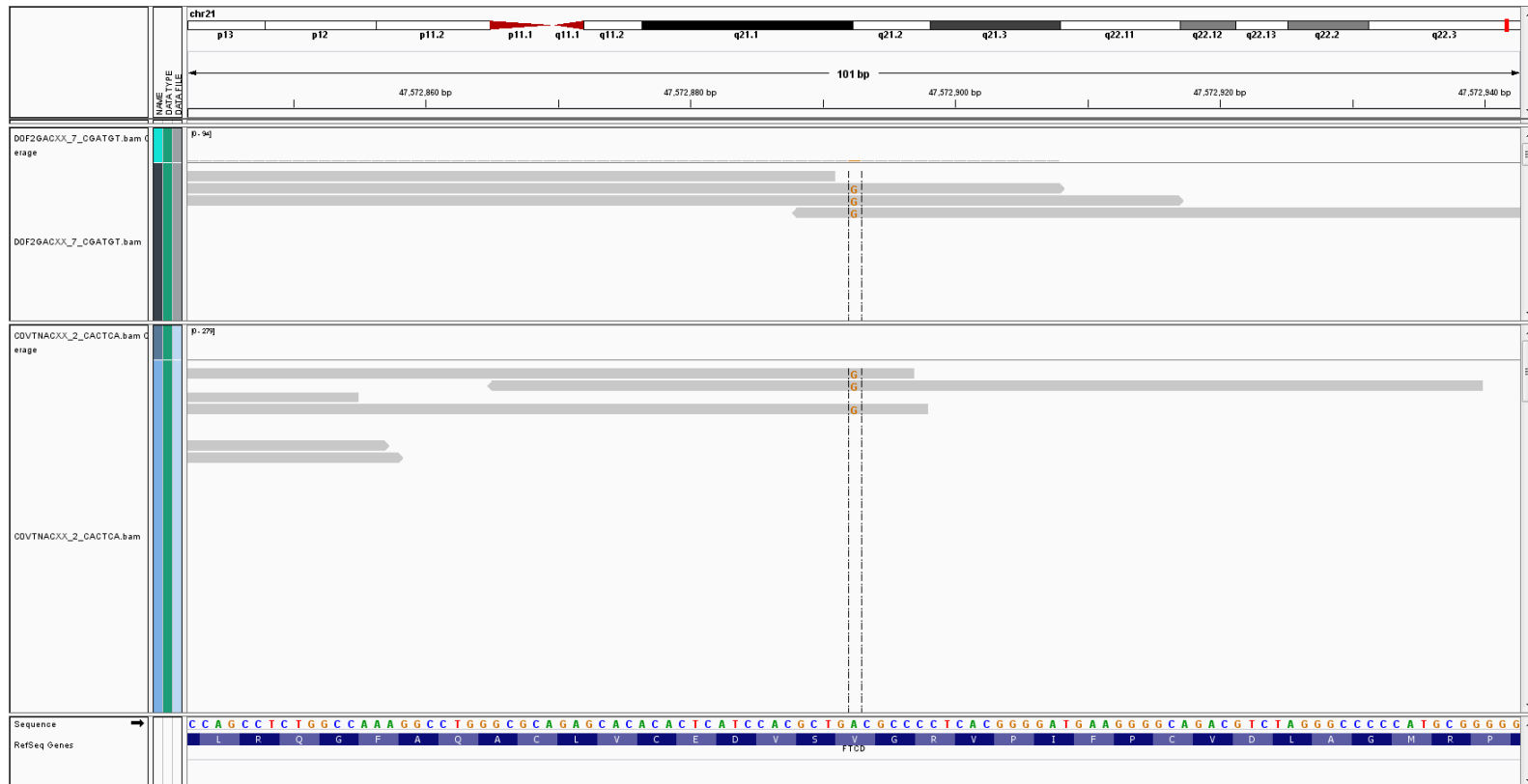


Figure S1 Integrative Genomics Viewer display of the five novel SNVs predicted to be damaging shared by all sequenced affected relatives from the same family as listed in Table 2.