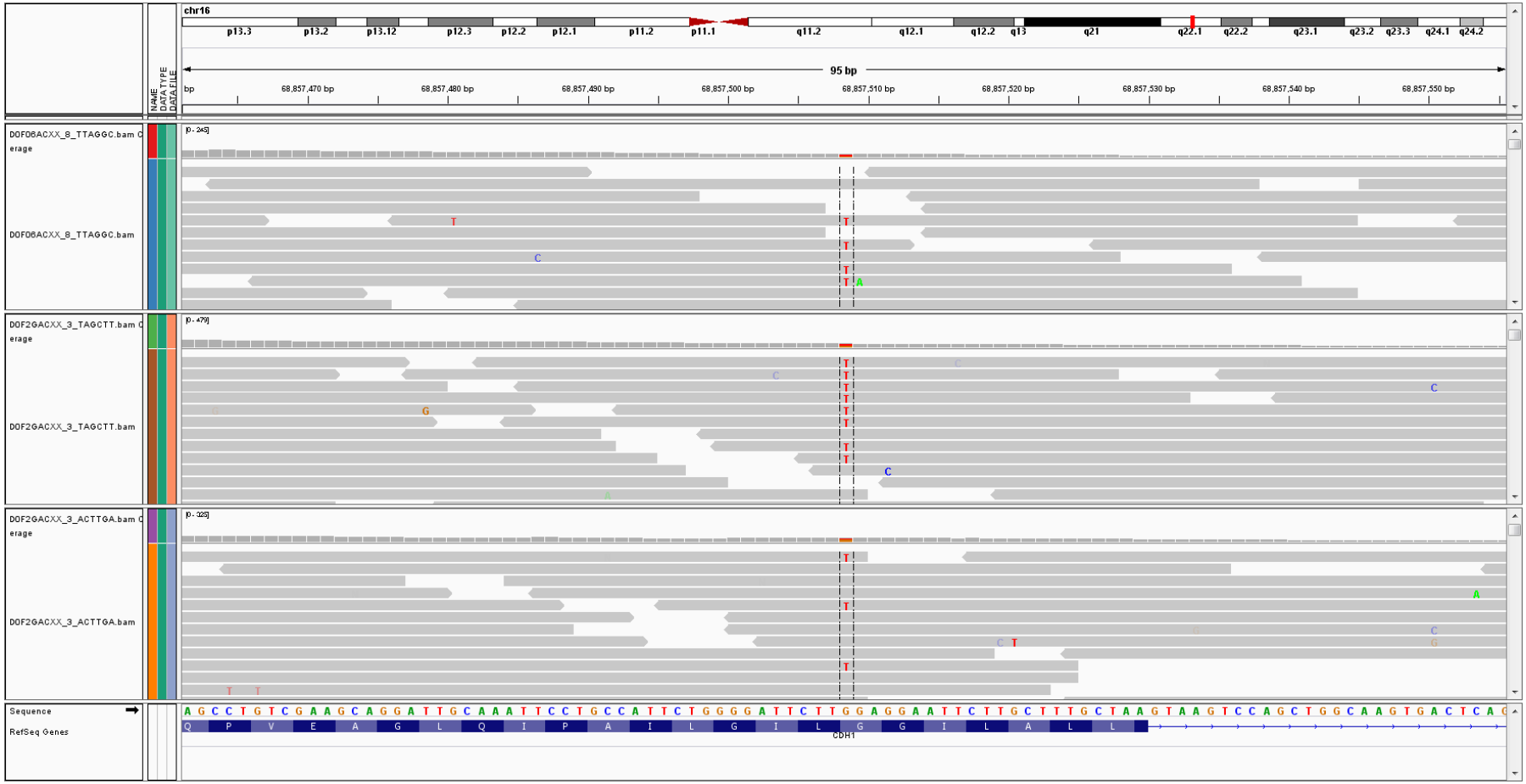
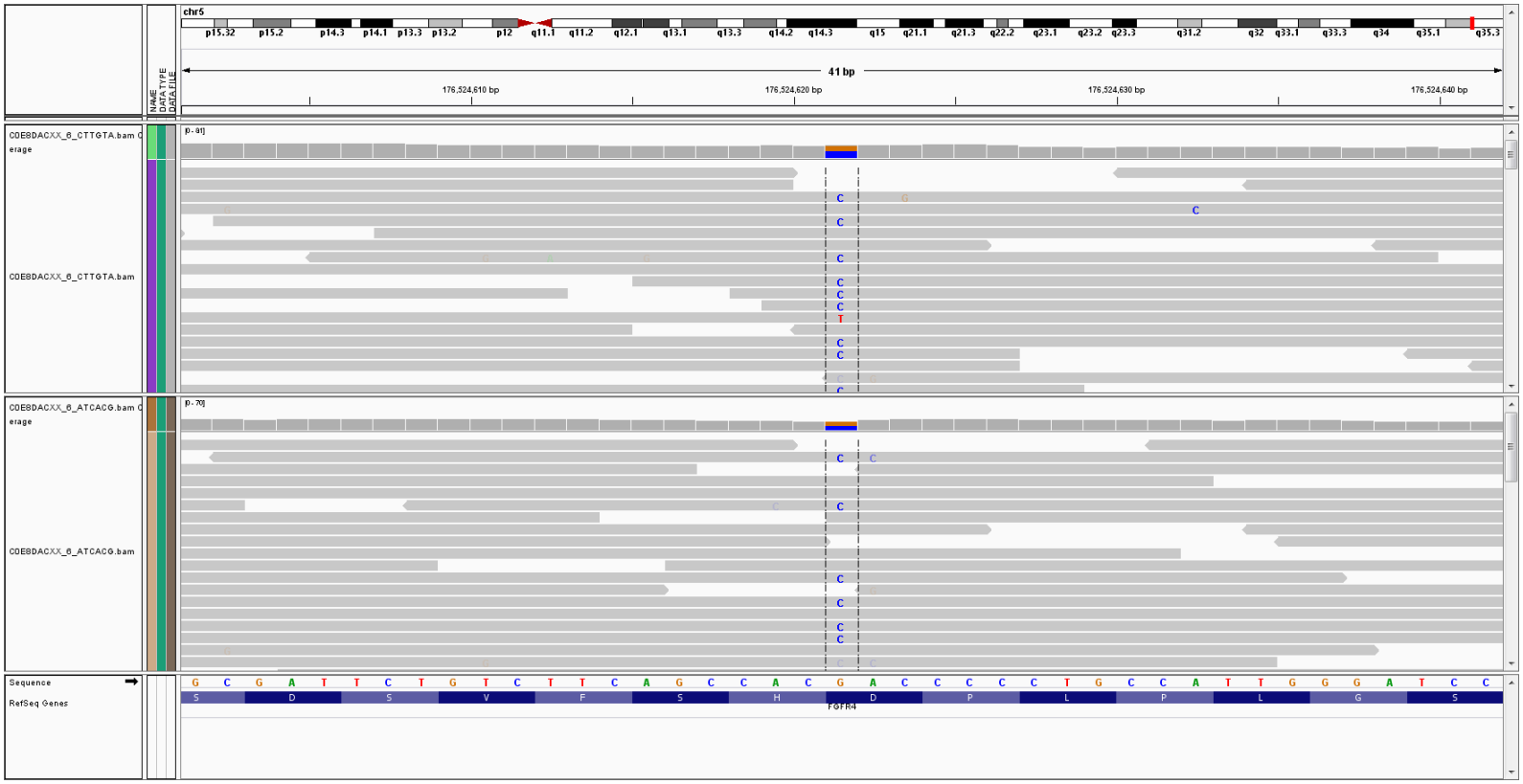
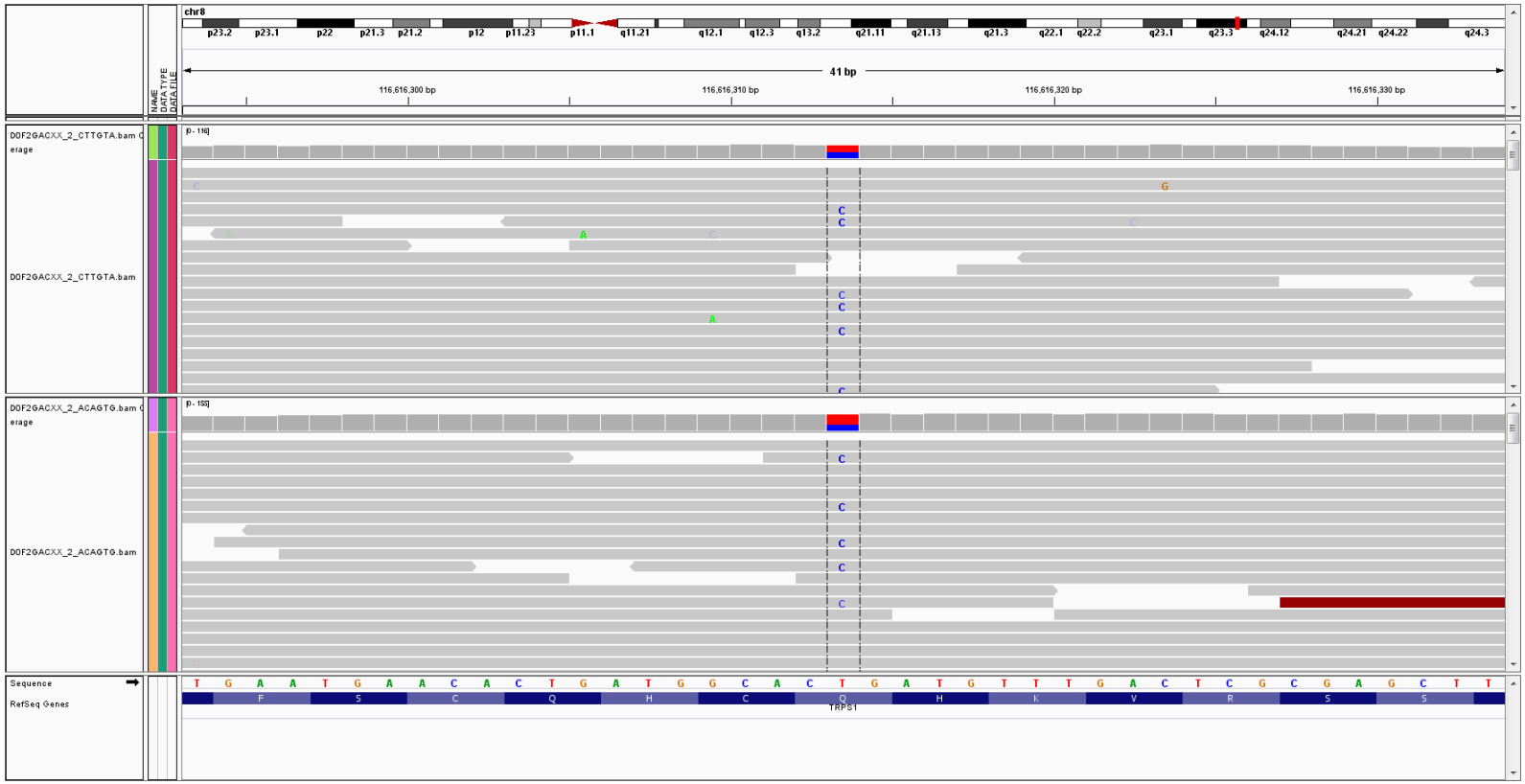
A) Family 15157- CDH1- chromosome 16, position 68857508



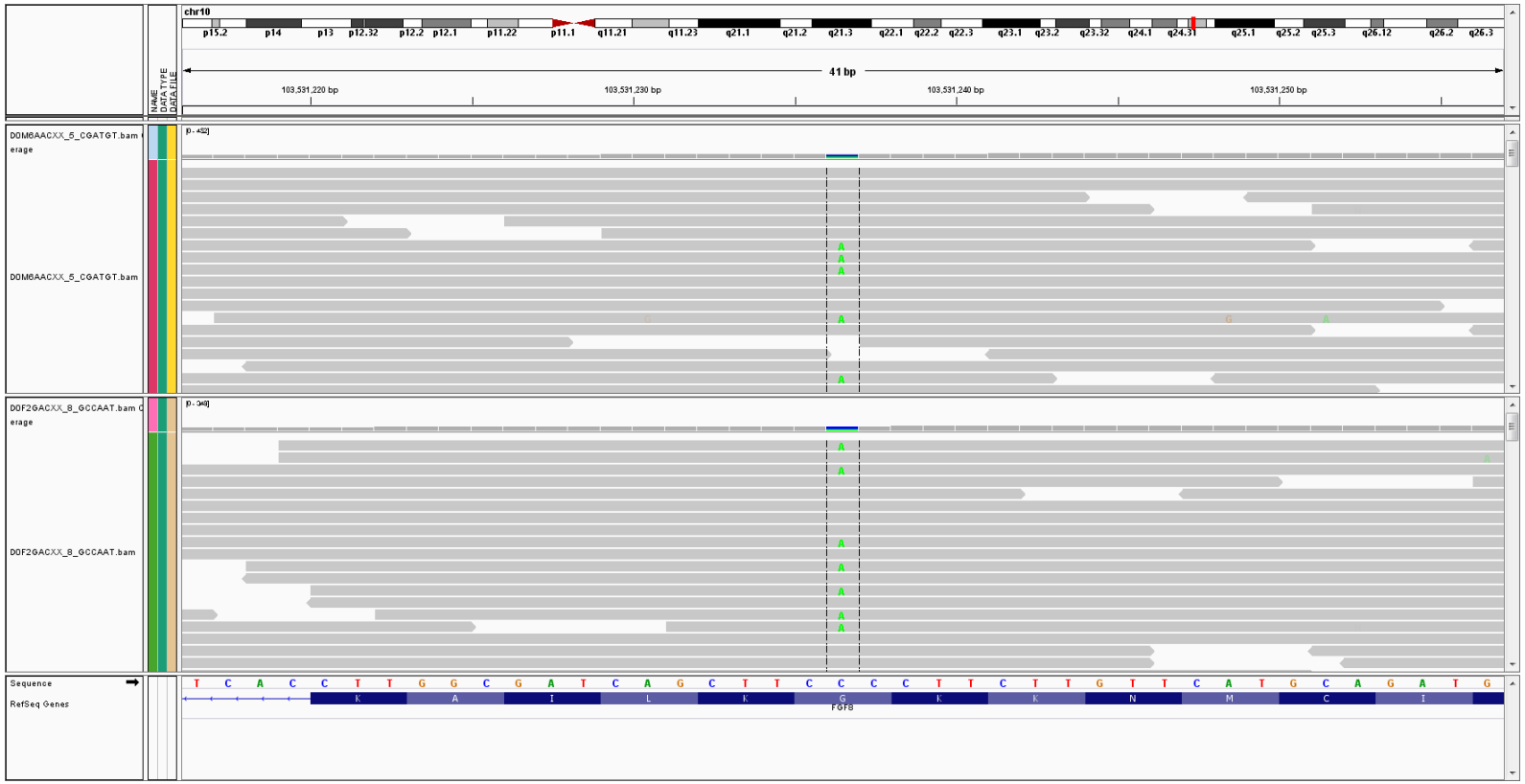
B) Family 15160- FGFR4- chromosome 5, position 176524621



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



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



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

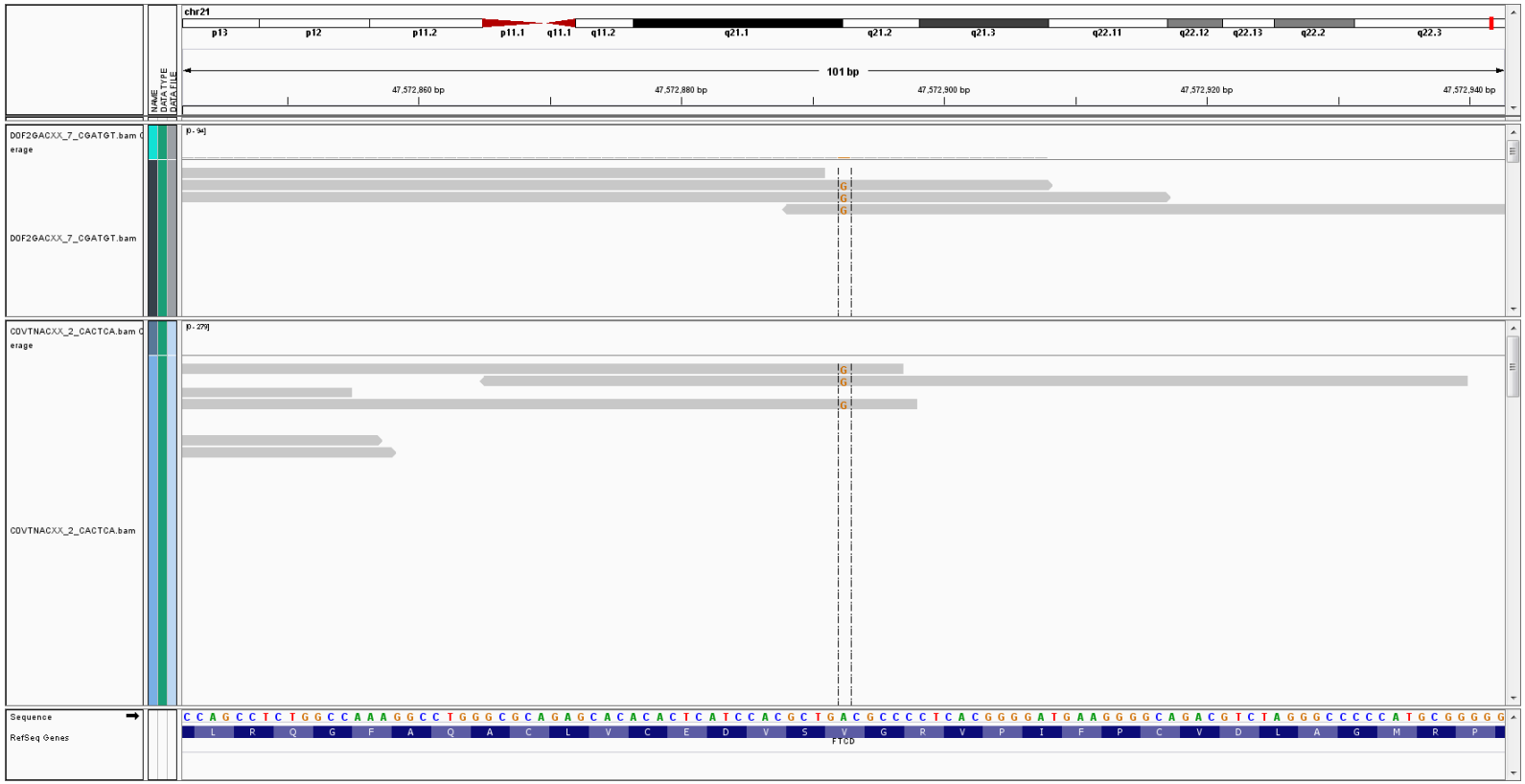


Figure S1 Integrative Genomics Viewer display of the five novel SNVs predicted to be damaging shared by all sequenced affected relatives from the same family as listed in Table 2.

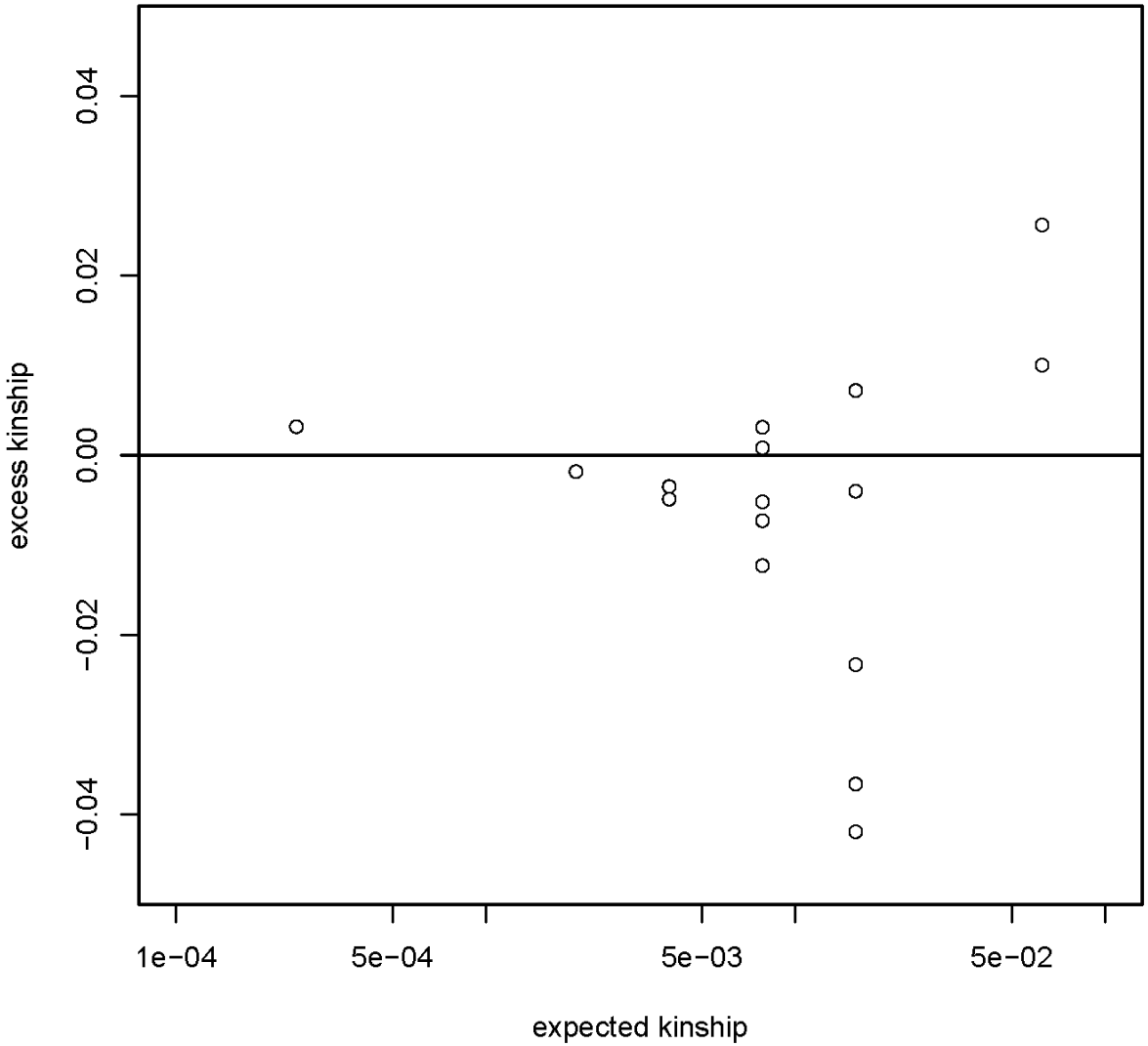


Figure S2 Difference between the robust estimate of kinship coefficient based on genome-wide SNP genotypes and the expected kinship coefficient based on pedigree structure for the affected relative pairs from the Indian family.

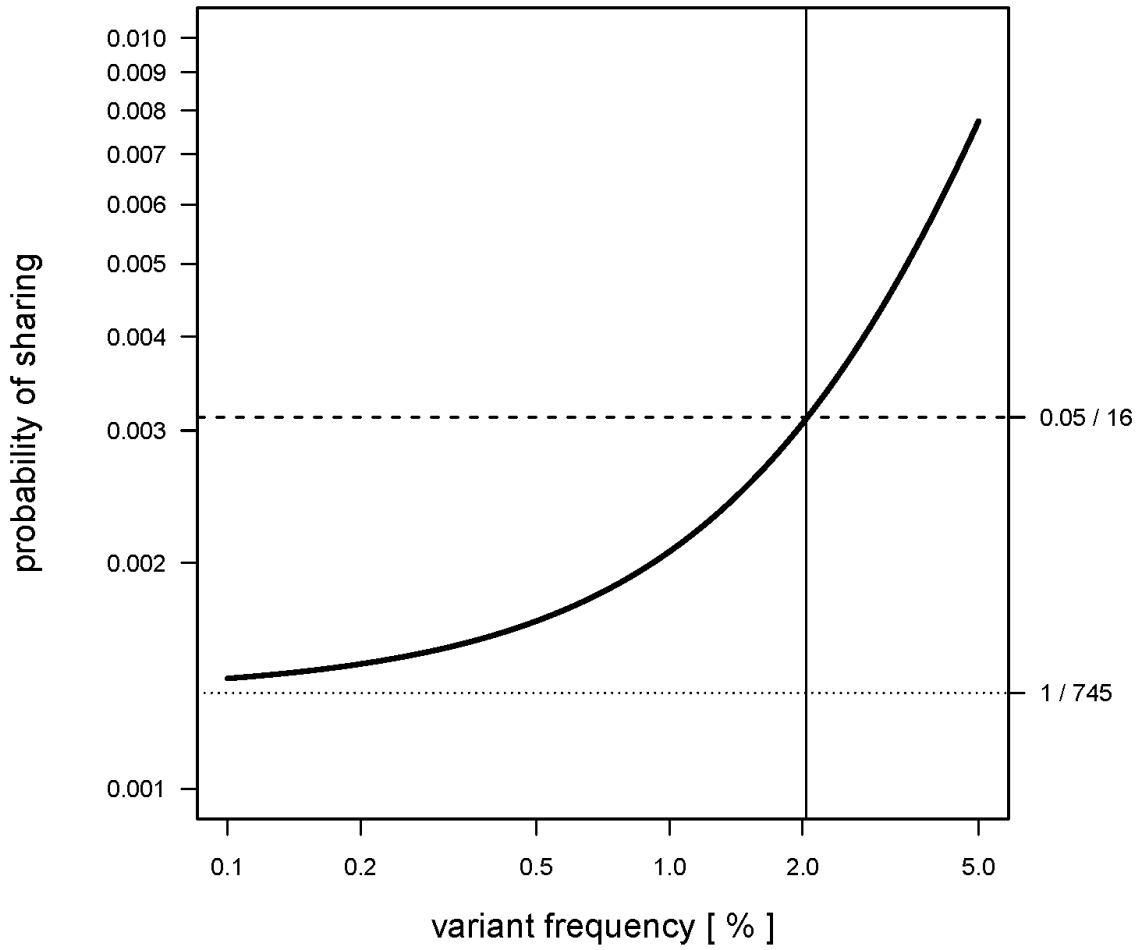


Figure S3 P-value based on IBS sharing. Assuming unrelated founders and Hardy-Weinberg equilibrium, exact IBS sharing probabilities for pedigree members were derived using conditional probabilities under Mendel's laws as a function of variant allele frequency (x-axis). The sharing probabilities calculated under the assumption of no IBS without IBD is 1/745 = 0.0013, indicated by the dotted horizontal line. The multiple comparison corrected significance threshold is 0.05/16 = 0.0031 indicated by the dashed horizontal line.

Tables S1-S2
Available for download as Excel files at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.165225/-/DC1

Table S1 Novel SNVs predicted to be damaging in 348 candidate genes for oral clefts

Table S2 Low frequency exonic and splicee site SNVs