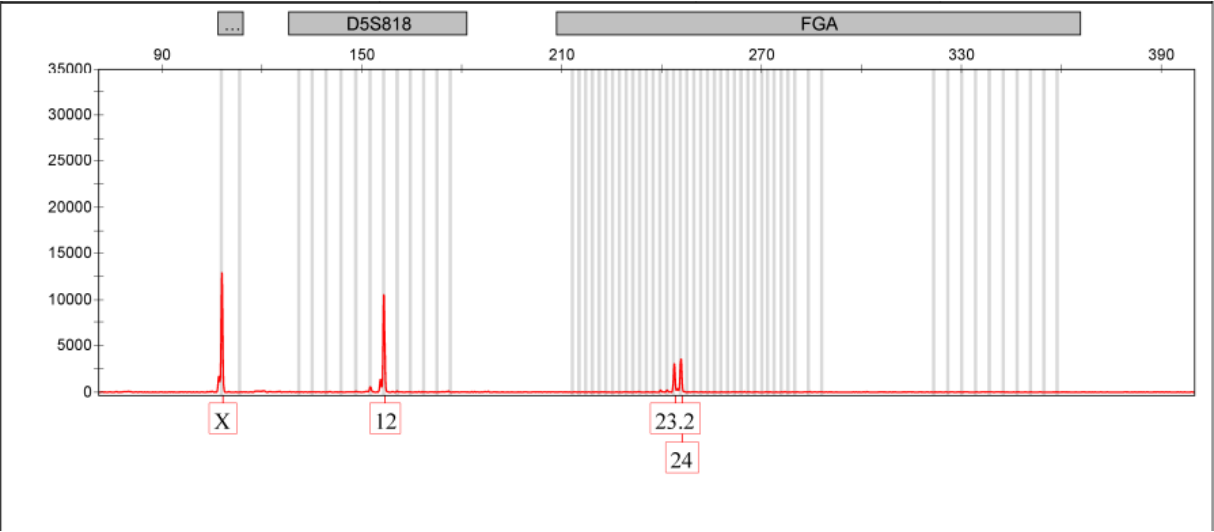
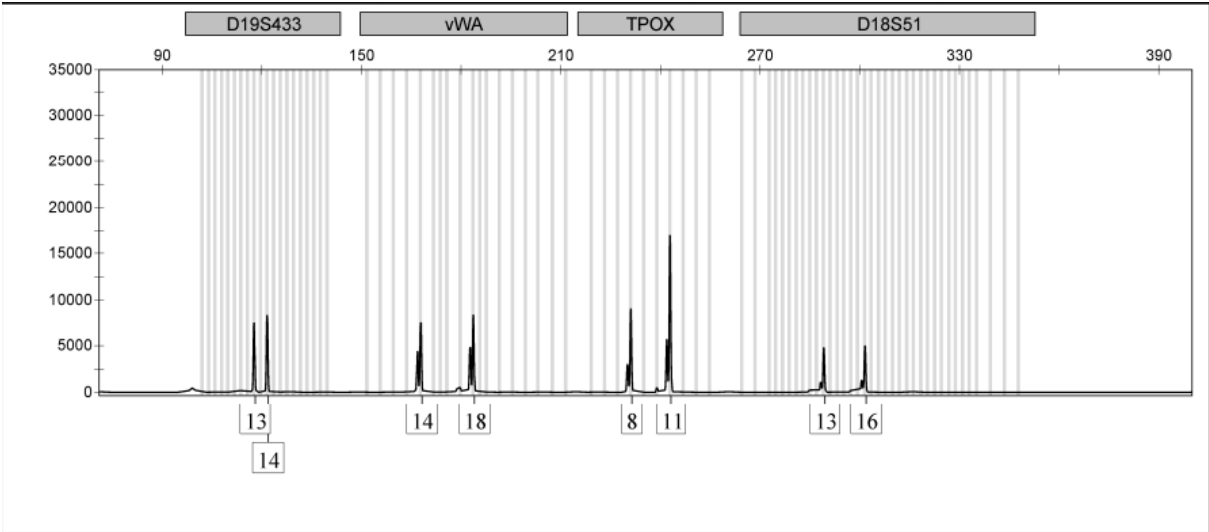
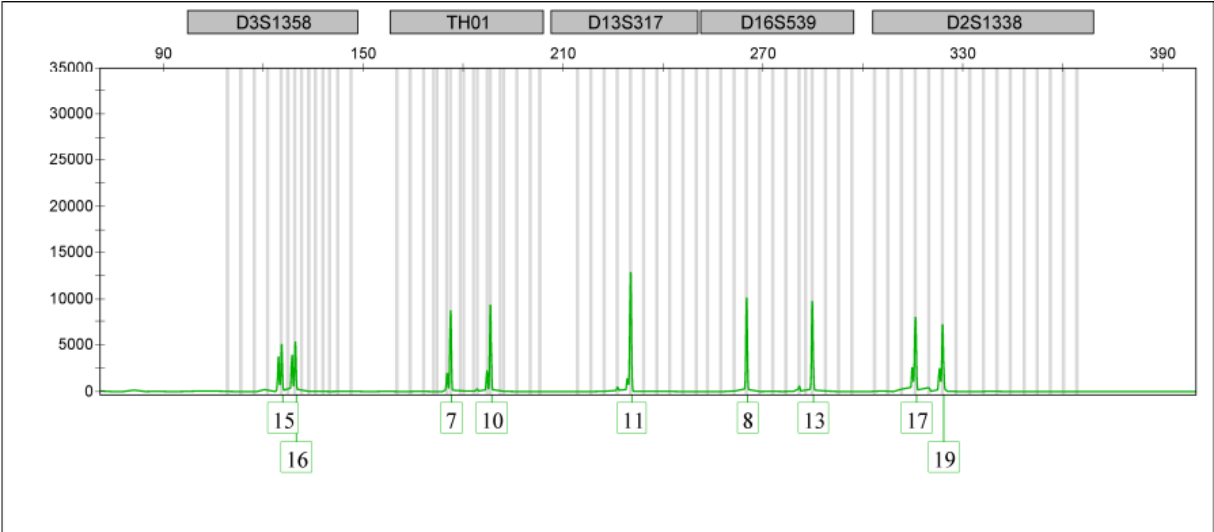
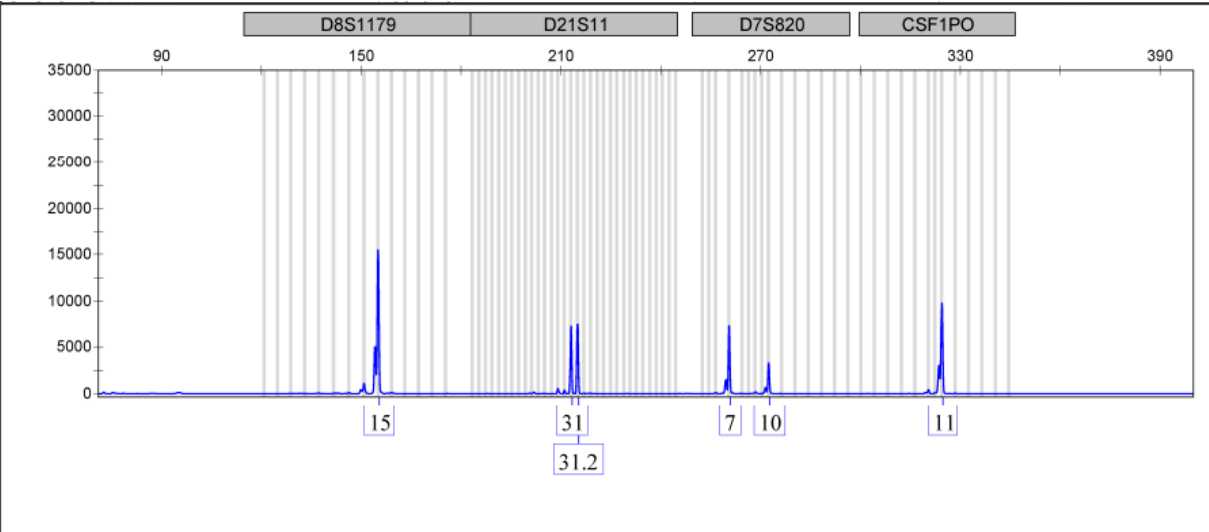


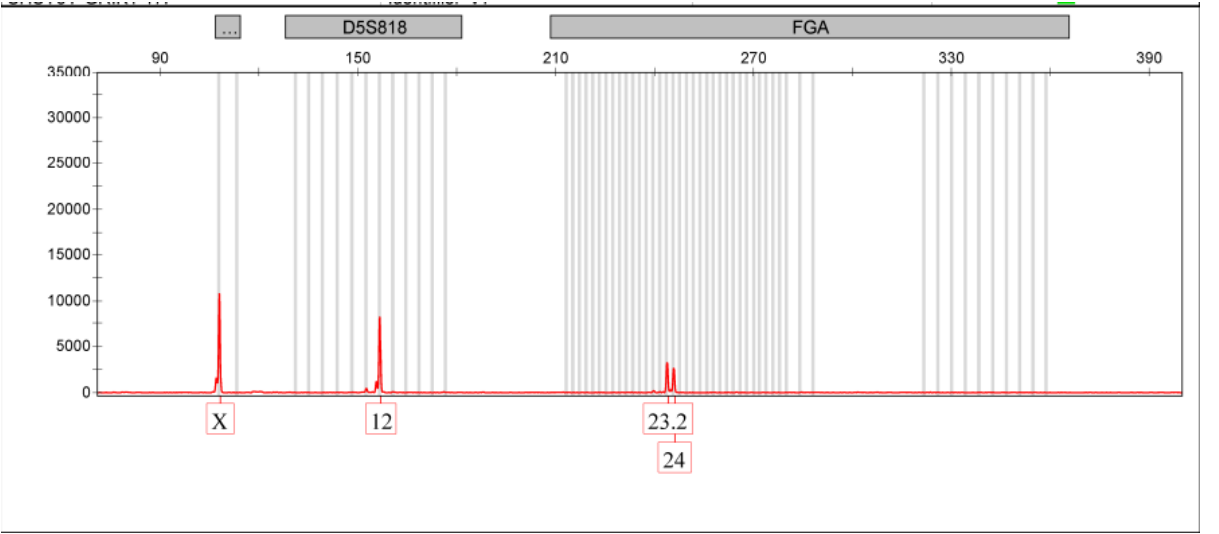
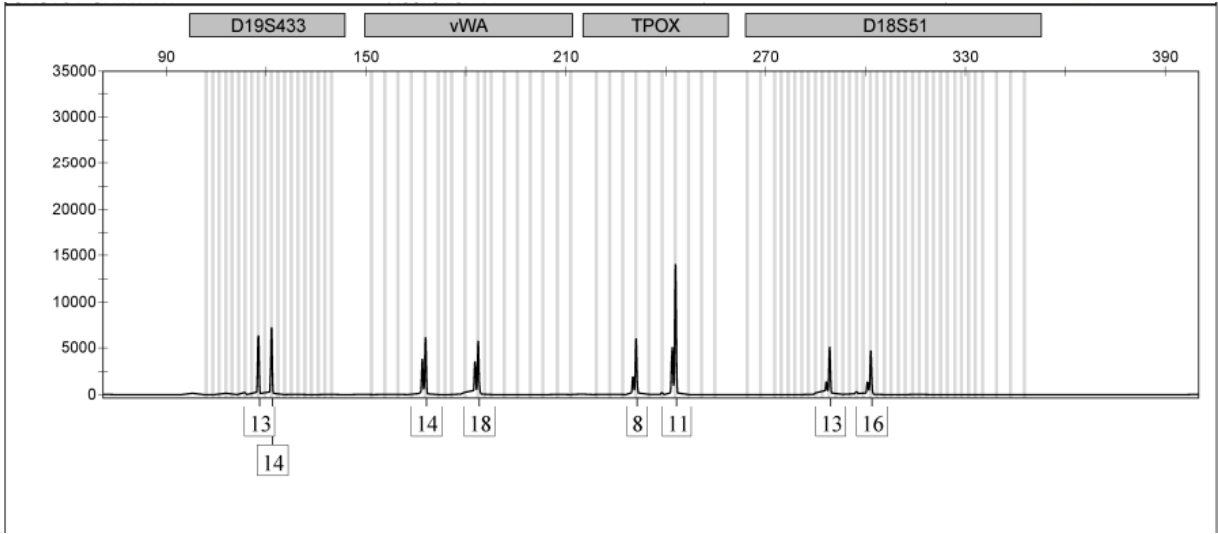
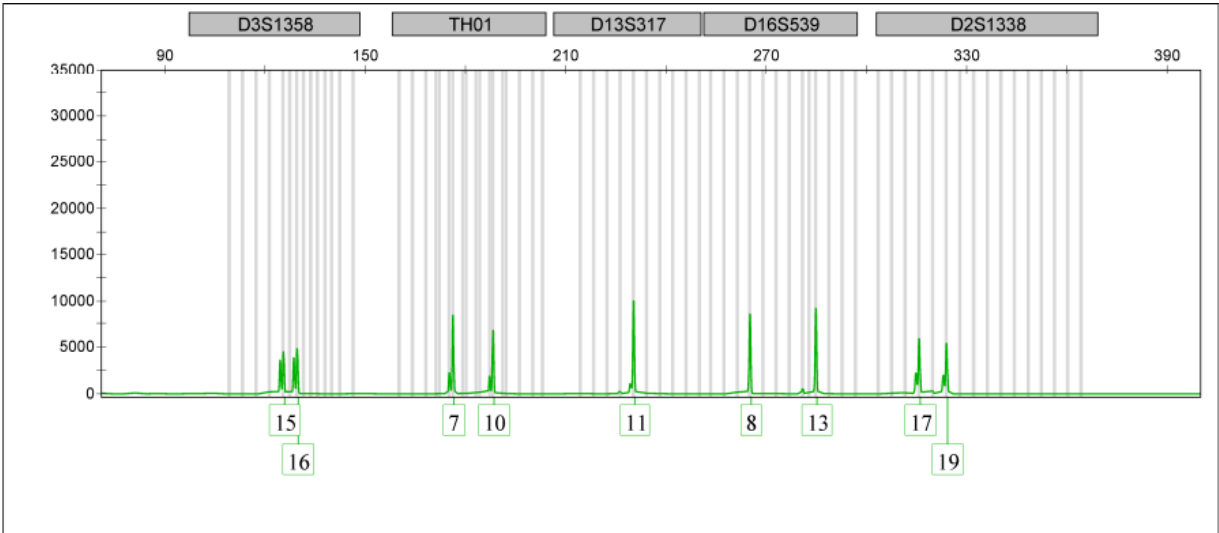
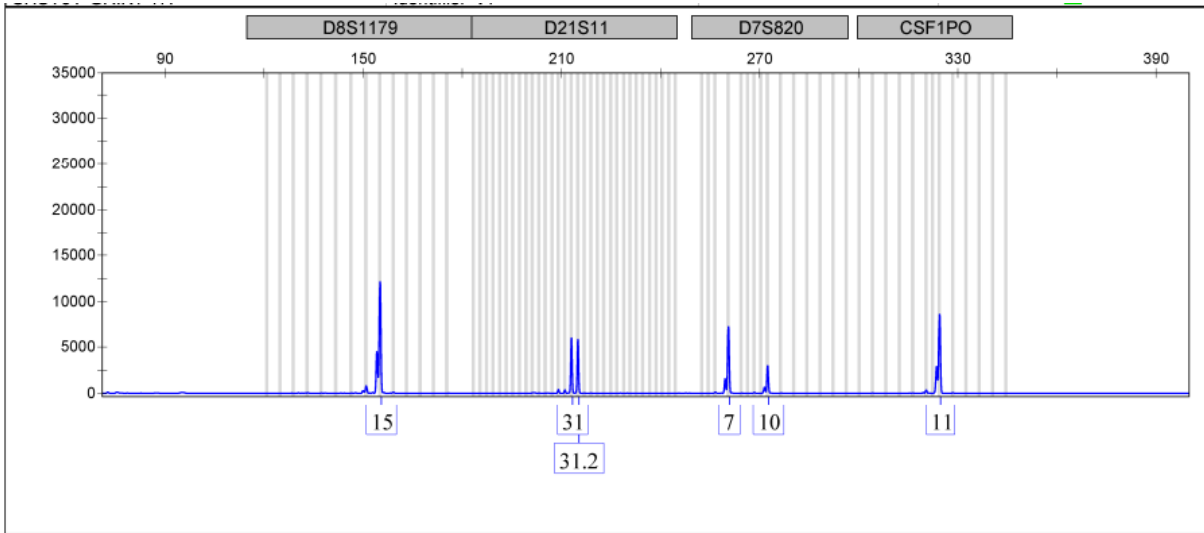
(A)

GRIK1p.L25Pfs\*?/WT



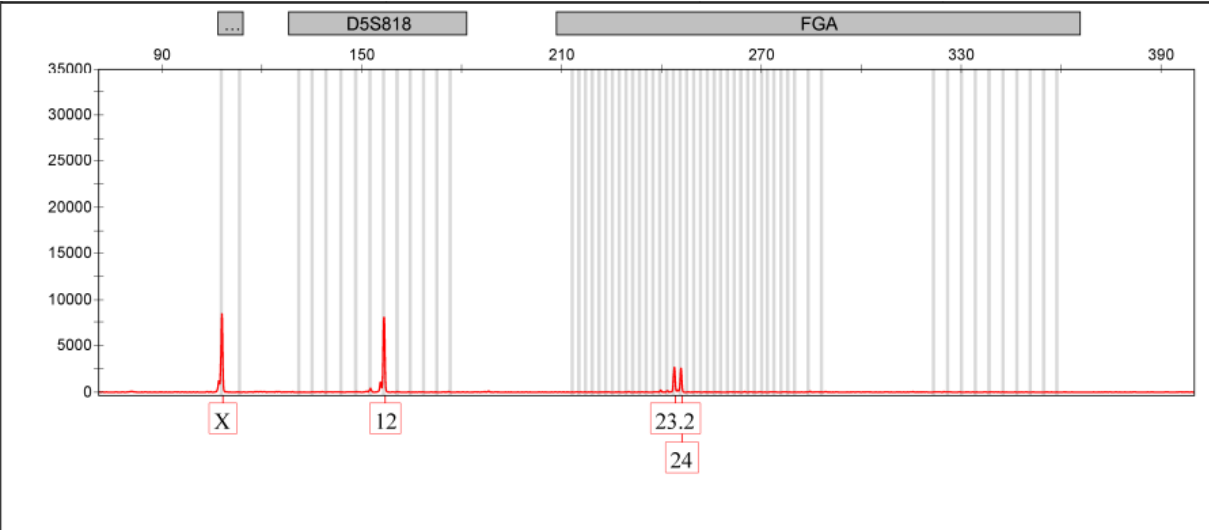
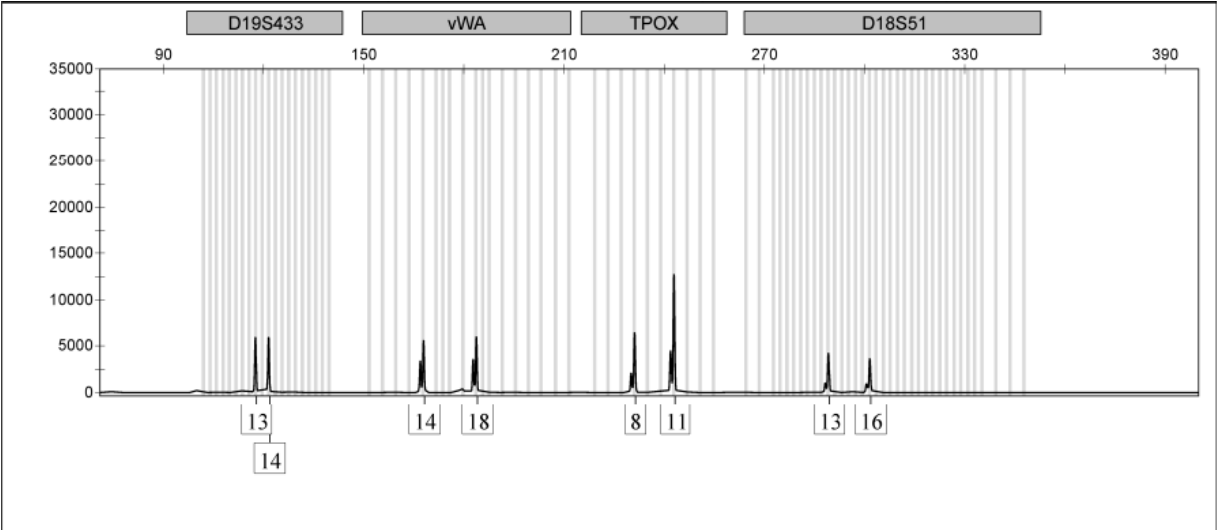
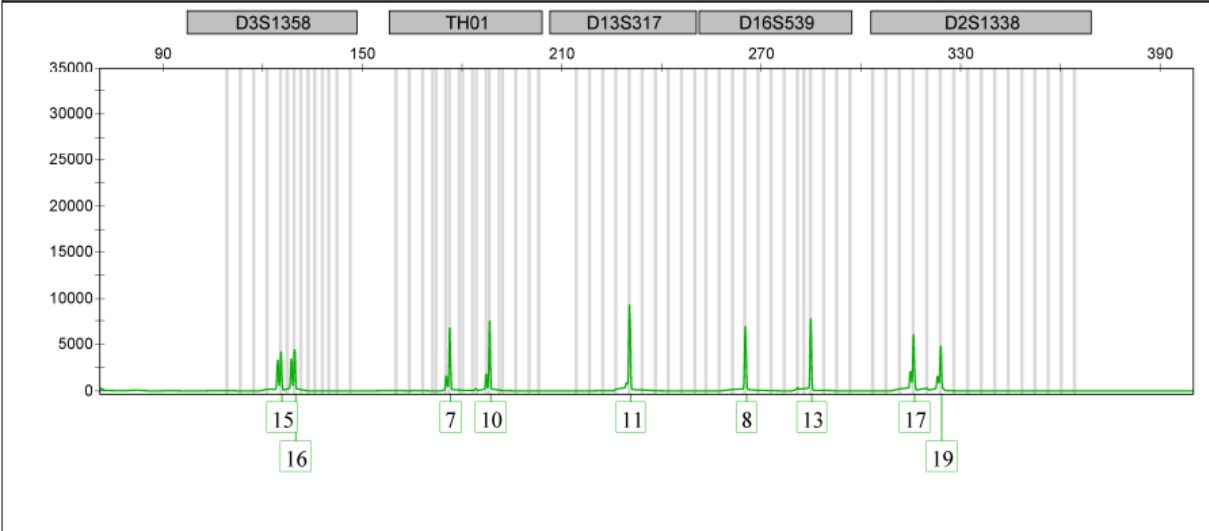
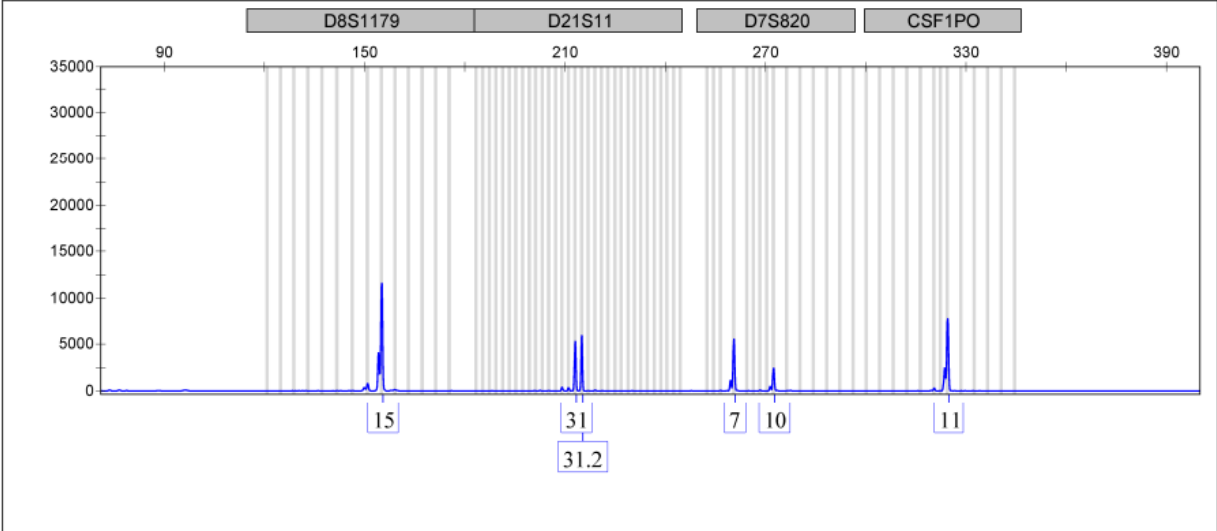
(B)

GRIK1p.L25Pfs\*?/p.L25Pfs\*?



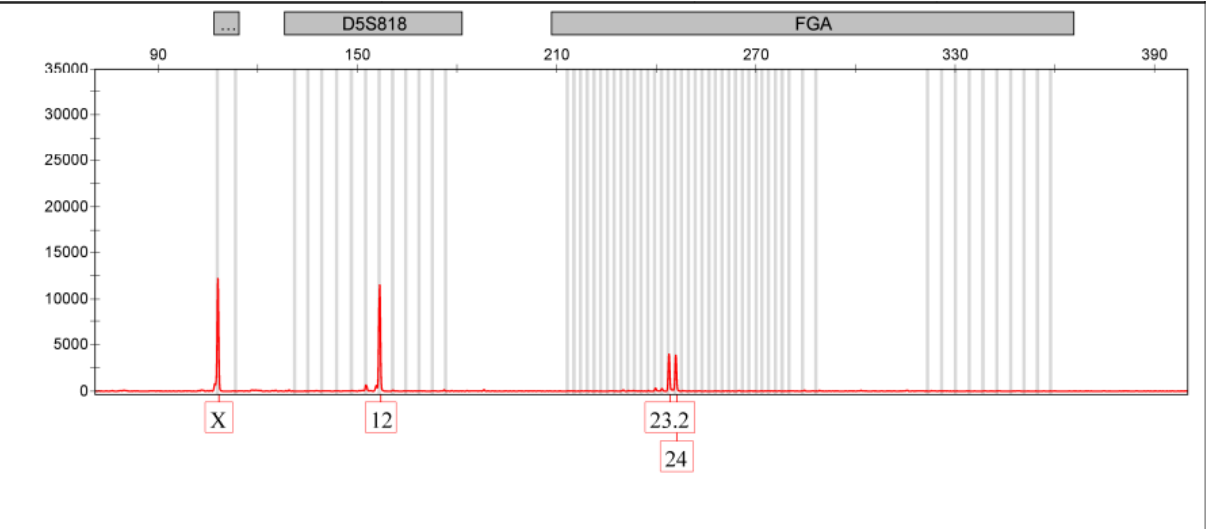
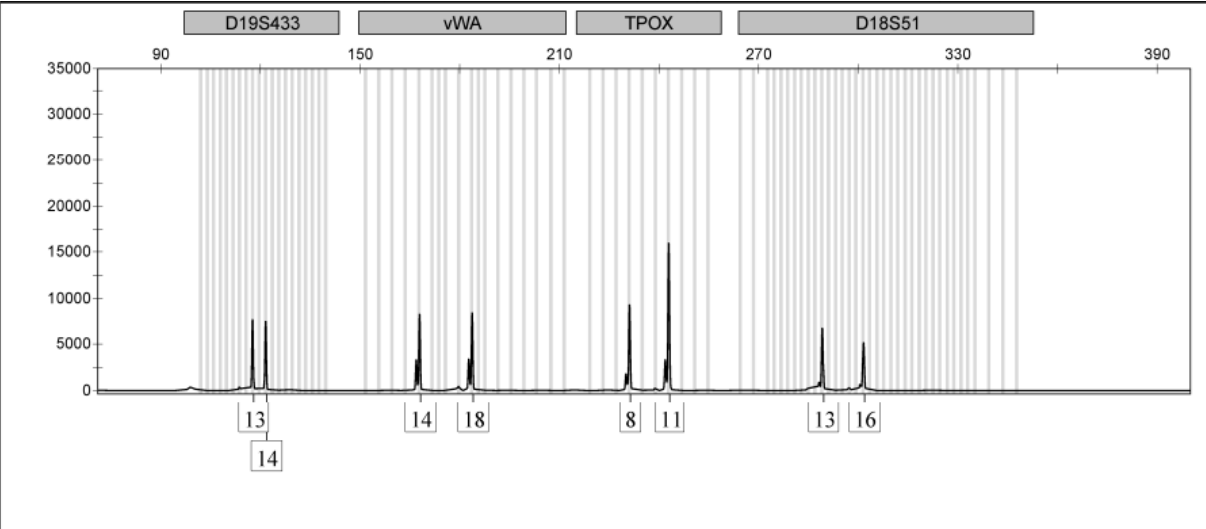
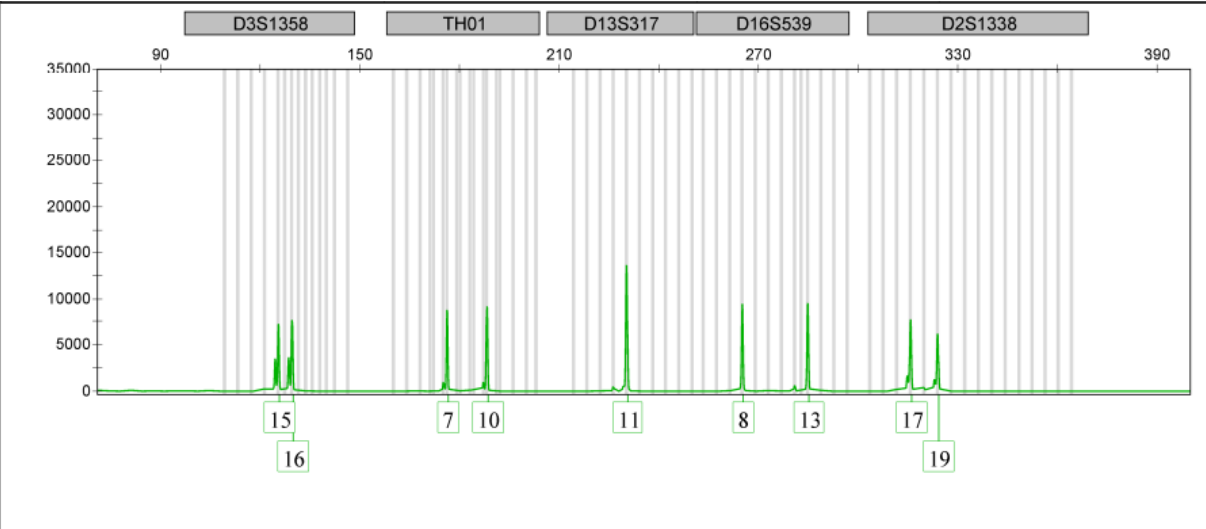
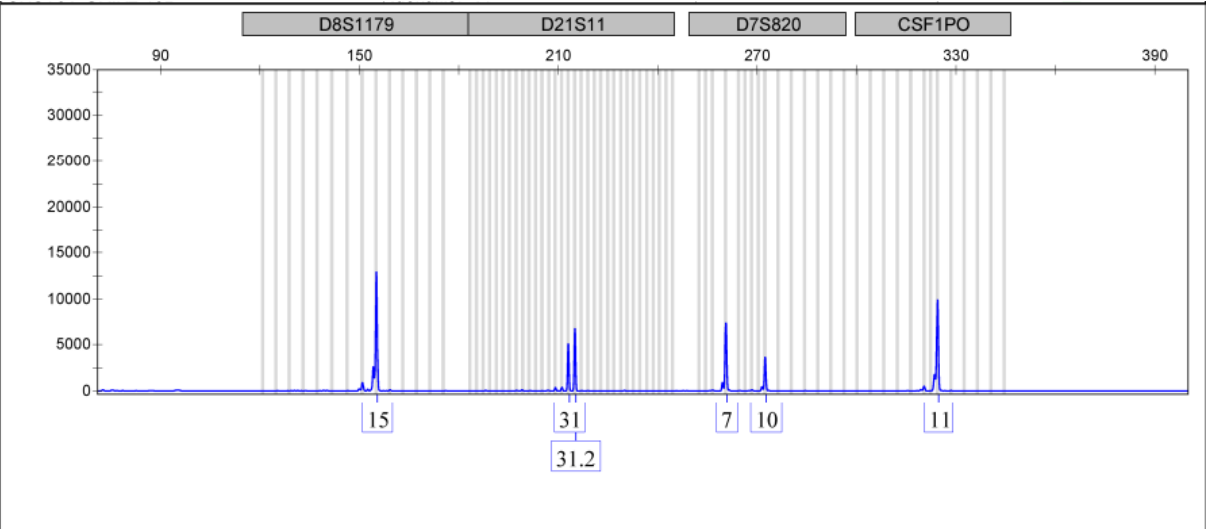
(C)

GRIK2<sup>p.L301Ffs\*/WT</sup>



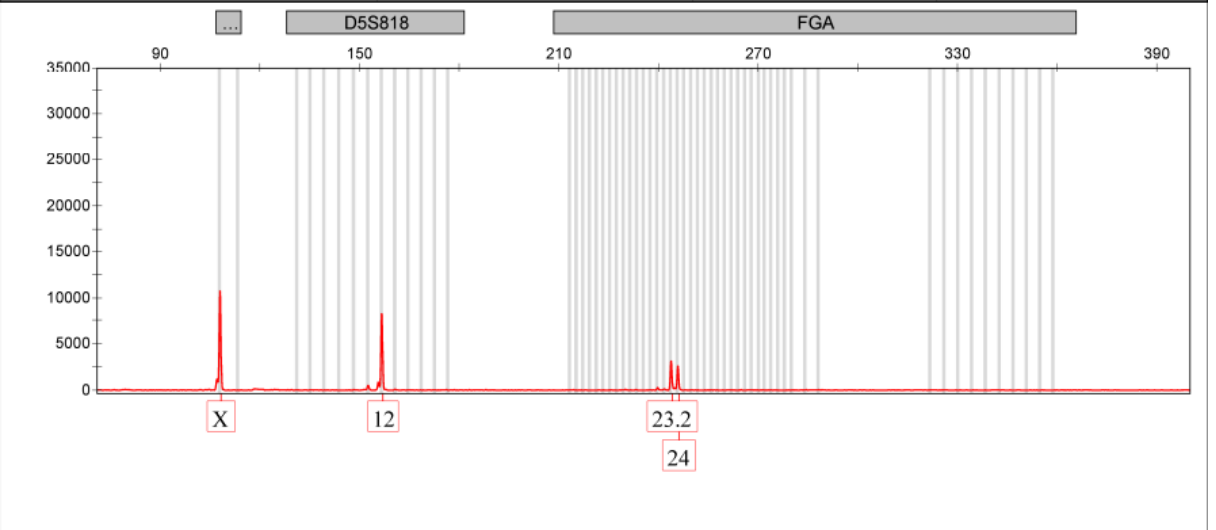
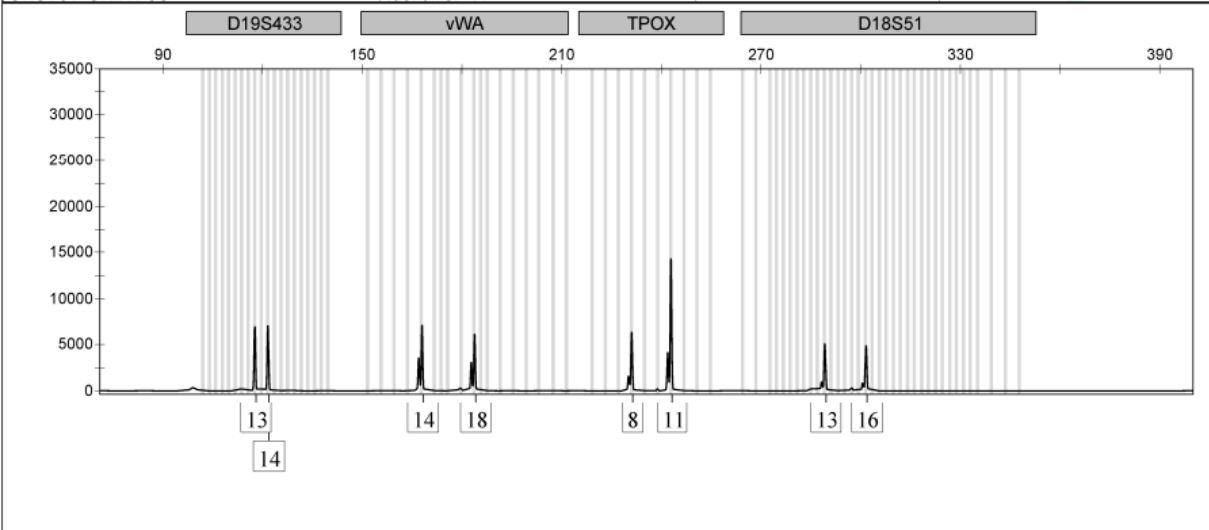
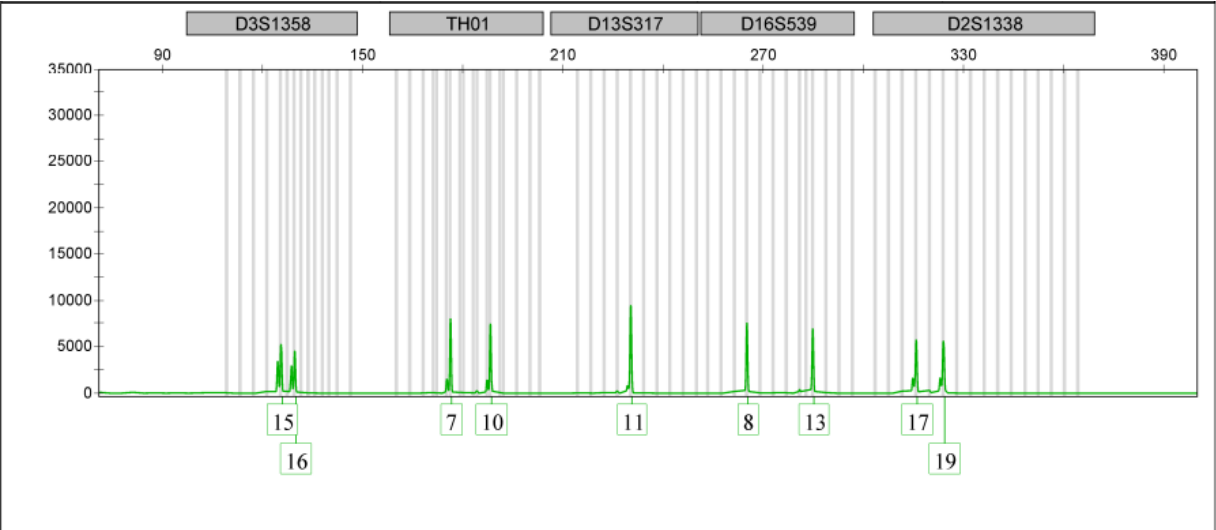
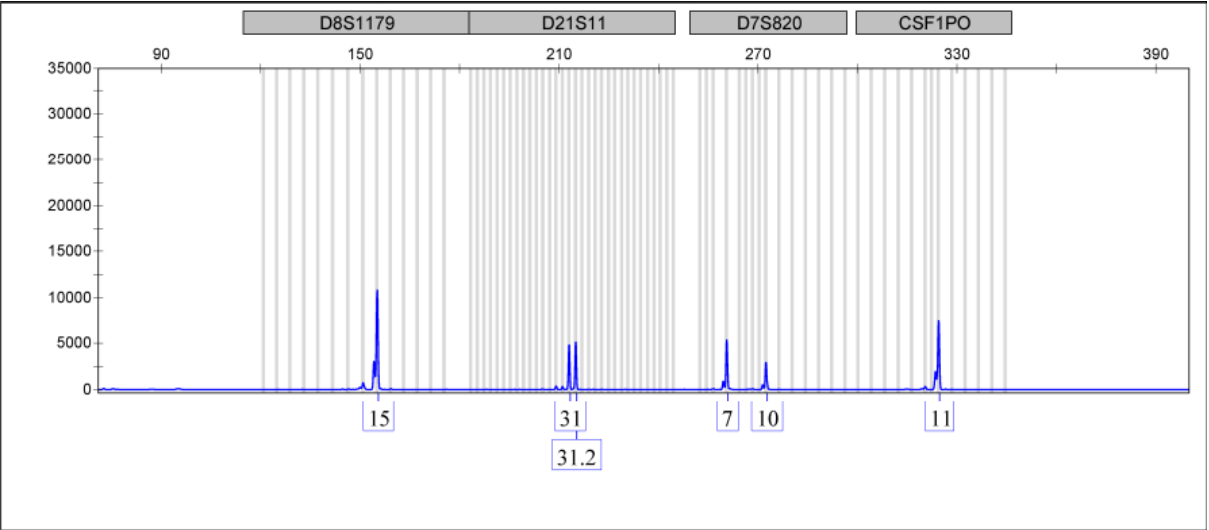
(D)

GRIK2<sup>p.L301Ffs\*?/p.L301Ffs\*?</sup>



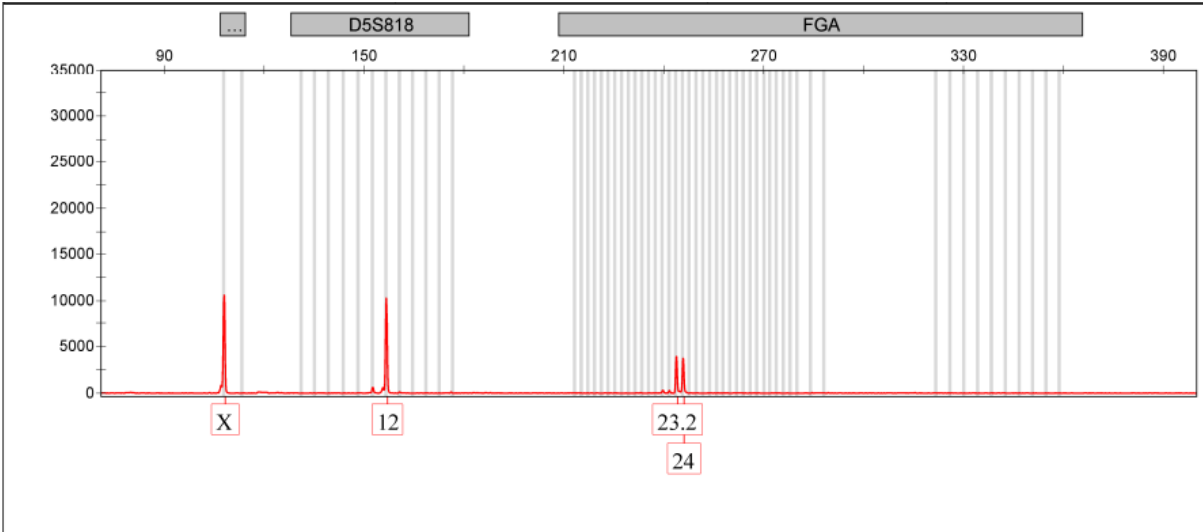
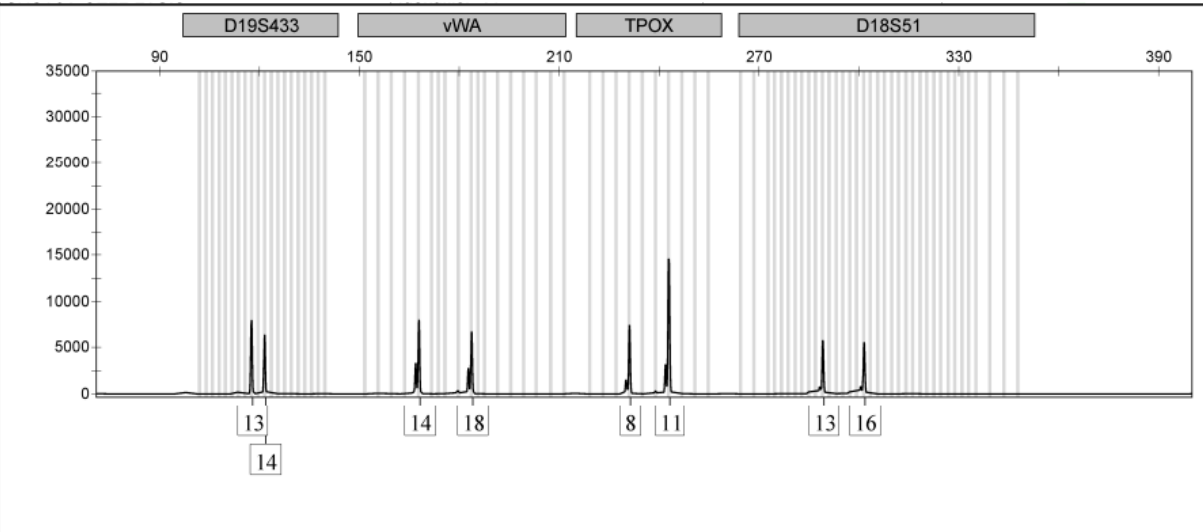
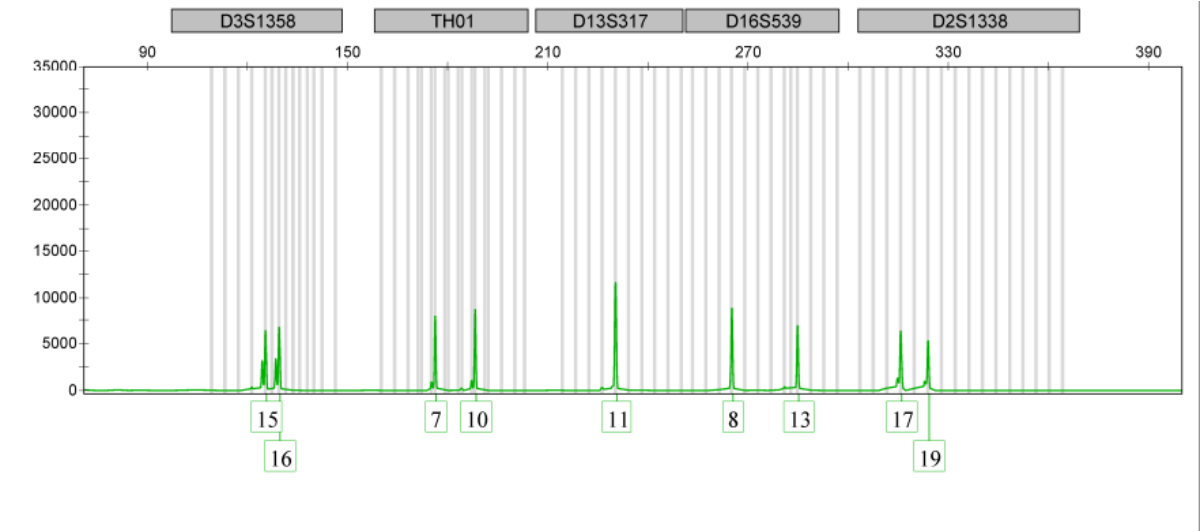
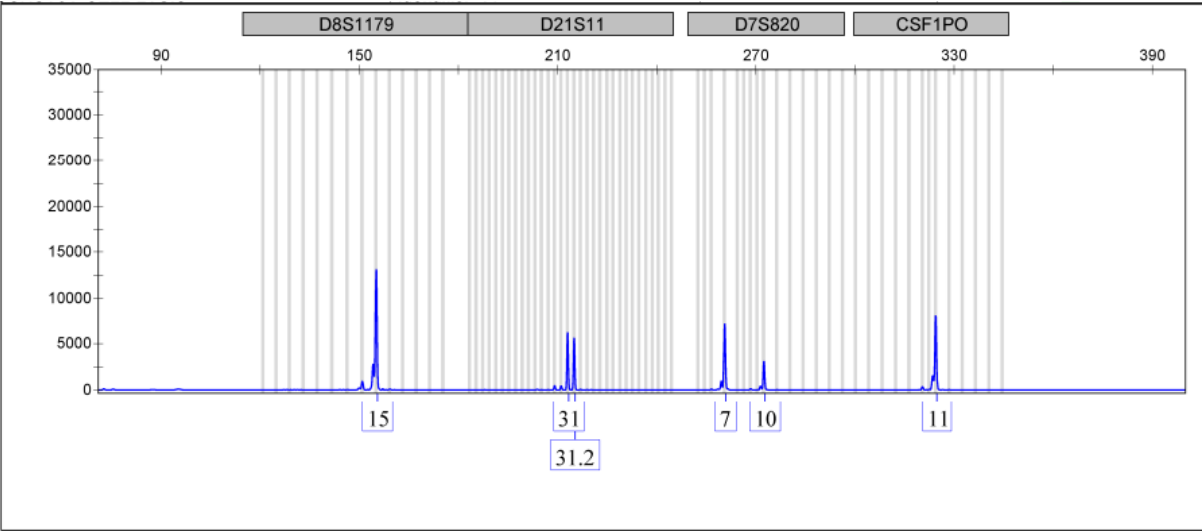
(E)

GRIK4 p.H343Afs\*?/p.H343Afs\*?



(F)

SH-SY5Y wild-type



**Supplementary Figure S2.** GeneMapper Software 4 analyzed 16 STR loci among edited cell lines (A, B, C, D, and E) and SH-SY5Y WT cell (F).