

**Protein sequence:****Wildtype**

MLVTLGLLTSFFSFLYMVAPSIRKFFAGGVCRTNVQLPGKVVVITGANTGIGKETARELASRGARVYIACRDVLKGESAAASEIRVDTKNSQVLVRKLDLSDTKSIRAF AEGFLAEKQLHILINNAGVMMCPYSKTADGFETHLGVNHLGHFLLTYL
 LLERLKVSAPARVVNVSSVAHHIGKIPFHDLQSEKRYSRGFAYCHSKLANVLFTR ELAKRLQGTGVTTYAVHPGVVRSELVRHSSLLCLLWRLFSPFVKTAREGAQTS LHCALAEGLPLSGKYFSDCKRTWVSPRARNNKTAERLWNVSCCELLGI
 RWE (316 amino acids)

Mutant

MLVTLGLLTSFFSFLYMVAPSIRKFFAGGVCRTNVQLPGKVVVITGANTGIGKETARELASRGARVYIACRDVLKGESAAASEIRVDTKNSQVLVRKLDLSDTKSIRAF AEGFLAEKQLHILINNAGVMMCPYSKTADGFETHLGVNHLGHFLLTYL
 LLERLKVSAPARVVNVSSVAHHIGKIPFHDLQSEKRYSRGFAYCHSKLANVLFTR ELAKRLQGTGVTTYAVHPGVVRSELVRHSSLLCLLWRLFSPFSRRHGRGRRPACTAPWLRRAWSP (276 amino acids)

Supplemental File 10. Amino acid sequences of the wild-type and mutant proteins showing the sequence of the c-terminals (wild-type, blue; mutant, red; aa, amino acid).

a) Schematic of the wild-type full length RDH12 protein including the c-terminal amino acid sequence (blue). The unfilled boxes represent the seven coding exons with green boxes representing domains highly conserved in short chain dehydrogenases/reductases, of which RDHs are a subfamily.

These domains are the NADP(H) cofactor binding site at amino acids 46-52 (GANTGIG) and catalytic site at amino acids 200-204 (RDVLK).[8]

b) Schematic of the mutant RDH12 protein predicted to evade NMD resulting from the c.763delG variant in exon 6. The frameshift results in incorporation of a non-native c-terminus (22 amino acid residues, red) and a premature stop codon leading to a truncated protein.