

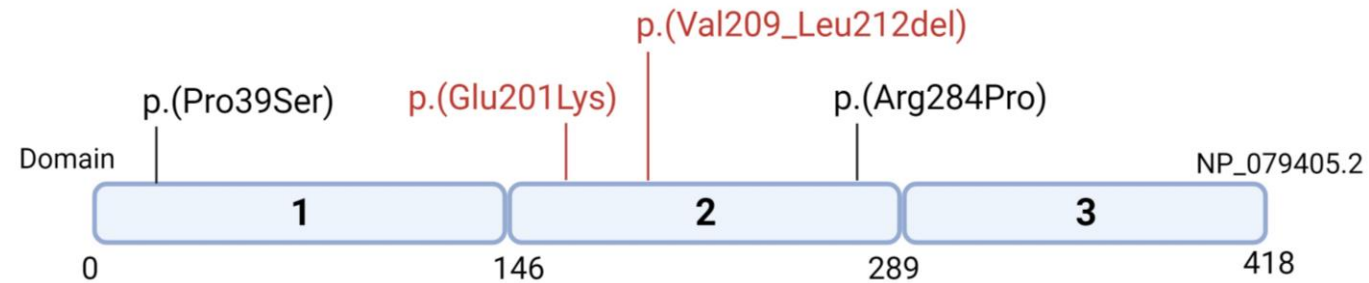
	<b>p.(Glu201Lys)</b>	
Homo sapiens	WW-RLGTFEAVLLPWLVGSLPPQTAR	218
Pan troglodytes	WW-RLGTFEAVLLPWLVGSLPPQTAR	218
Pongo abelii	WW-RLGTFEAVLLPWLVGSLPPQTAR	218
Felis catus	WW-RLGTFEAVLLPWLVGSLPPQAAR	218
Rattus norvegicus	WW-RLGMFEAVLLPWLVGSLPPQAAR	218
Xenopus tropicalis	WW-RLSSQEVMLLCWLVASLAPHSSR	210
Drosophila melanogaster	WW-DLDTRELLLFLLNSS-STMQH	219
Carassius auratus	WWSRLSSQEVVVLVSVLVHSLSGASSC	217
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Supplementary figure 1: Multiple sequence alignment of p.(Glu201Lys) in *FUZ* indicates that glutamine residue at 201 position is conserved among different vertebrates. An asterisk (\*) represents fully conserved residue, colon (: ) represents residues with strongly similar properties, and period (.) represents residues with weakly similar properties.

A)



B)



Supplementary figure 2: A) Cartoon illustration of structure of the gene (*FUZ*) and (B) domains of *FUZ* protein with disease-causing variants identified in individuals with *FUZ* related disorders. Novel biallelic variants identified in this study are coded in red.