

Additional Table 1.

	<b><i>CTNNB1</i>:c.1902dupG p.E634fs</b>
<b>ACMG Classification</b>	Likely pathogenic (LP)
<b>Effect on Protein</b>	Pathogenic Very Strong (PVS1)
<b>Population data</b>	Pathogenic Moderate (PM2)
<b>gnomAD (Exome, Genome, Aggregated), TOPMed Bravo, GME Variome, Iranome, ExAC, 1000 Genomes, ESP 6500, 4.7KJPN, GenomeAsia, Mexican DB, India DB, Turkish Variome</b>	No Observation for this variant
<b>Revel, EVE, Varsity, MUTAssessor, SIFT, Polyphen2, MT, FATHMM, DANN, MetaLR, PrimateAI, BayesDel, CardioBoost ARM, CardioBoost CM, dbscSNV Ada, dbscSNV RF, GERP, GenoCanyon, fitCons, Mitochondrial, MitoTip, APOGEE</b>	N/A