

Supplementary Table 1. In-silico prediction of two novel variants in *EYA3* and *EFTUD2*

Gene name	<i>EYA3</i>	<i>EFTUD2</i>
Transcript ID	NM_001990	NM_001258353
Genomic position	chr1:28365377T>A	chr17:42937346T>C
Nucleotide change	c.197A>T	c.1787A>G
Protein change	p.D66V	p.N596S
ACMG Category	Likely pathogenic (PM1, PM2, PP2, PP3)	Likely pathogenic (PM1, PM2, PP3, PP4, BP1)
SIFT	Damaging	Damaging
Polyphen-2_HDIV	Probably_damaging	Probably_damaging
Polyphen-2_HVAR	Possibly_damaging	Probably_damaging
LRT	Deleterious	Deleterious
MutationTaster	Disease_causing	Disease_causing
MutationAssessor	Low	Medium
FATHMM	Damaging	Tolerable
PROVEAN	Tolerable	Damaging
VEST3	Damaging	Tolerable
MetaSVM	Damaging	Damaging
MetaLR	Damaging	Damaging
M-CAP	Damaging	Damaging
CADD	Damaging	Damaging
DANN	Damaging	Damaging
FATHMM_MKL	Damaging	Damaging
Eigen	Damaging	Damaging
GenoCanyon	Tolerable	Damaging
fitCons	Damaging	Damaging
GERP++	Conserved	Conserved
phyloP	Conserved	Conserved
phastCons	Conserved	Conserved
SiPhy	Conserved	Conserved
REVEL	Damaging	Damaging
ReVe	Damaging	Tolerable
ClinPred	pathogenic	pathogenic
Damaing score	0.83	0.87
gnomAD	None	3.665e-05
dbSNP	None	rs373685919