

Supplemental Figure S2: Conservation analysis of the novel missense variants on *TLL5*

Protein sequence alignment was performed using <https://www.uniprot.org/align/>. The Uniprot entry number is indicated on the left.

				p. (Trp492Arg)	p. (Met505Val)		
Q6EMB2	Homo sapiens	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQD-----	516
G1S3K9	Nomascus leucogenys	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQD-----	516
H2Q8N4	Pan troglodytes	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNPRRSLL-	525
A0A5F7ZXY3	Macaca mulatta	481	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNPRRSLL-	539
Q8CHB8	Mus musculus	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNPRRSLL-	525
D3ZAA1	Rattus norvegicus	369	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNTRRSLL-	427
F1PTL6	Canis lupus familiaris	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNPRRSLL-	525
M3WKA0	Felis catus	467	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRGNPRRSLL-	525
K7GRP4	Sus scrofa	466	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDR-----	516
E1BD55	Bos taurus	438	KVLRRVKEENDRRGGFIRIFPTSET	W	E	IYGSYLEHKTSMNYMLATRLFQDRWRFANLIN-	496
A0A1L1RZ47	Gallus gallus	482	KVLRRVDENERGGFIRIFPTPLT	W	D	LYGSFLEYKTSMNYMLATRLFQDRDKMKGDLI-	540
F7ENG2	Xenopus tropicalis	455	KILRRVQDEYERRGGFVRIFFPRHNT	W	D	LYGSFLEYKTSINNYMLVTHLFPNRAAGNDH---	511
E9P886	Caenorhabditis elegans	543	QIVRKAELEDGRRGDFIRVFPRNGT	W	E	MYSPVMEDLGNEDF--DERLFDDEVVTKKNTKNS	600
Q9VBX5	Drosophila melanogaster	604	RILRNARLQYSRRGGFVRIFFPTDDS	M	D	RYGNFLDSANGIPISTPNVQSQ-----	652