

Supplemental Figure S2: Conservation analysis of the novel missense variants on *TTLL5*

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	WEIYGSYLEHKTS	MNYMLATRLFQD----- 516
G1S3K9	Nomascus leucogenys	467	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQD----- 516
H2Q8N4	Pan troglodytes	467	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNPRRSLL- 525
A0A5F7ZXY3	Macaca mulatta	481	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNPRRSLL- 539
Q8CHB8	Mus musculus	467	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNPRRSLL- 525
D3ZAA1	Rattus norvegicus	369	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNTRRSLL- 427
F1PTL6	Canis lupus familiaris	467	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNPRRSLL- 525
M3WKA0	Felis catus	467	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRGNPRRSLL- 525
K7GRP4	Sus scrofa	466	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDR----- 516
E1BD55	Bos taurus	438	KVLRRVKEENDRRGGFIRIFPTSET	WEIYGSYLEHKTS	MNYMLATRLFQDRWRFANLIN- 496
A0A1L1RZ47	Gallus gallus	482	KVLRRVDENERRGGFIRIFPTPLT	WDLYGSFLEYKTS	MNYMLATRLFQDRDKMKGDLI- 540
F7ENG2	Xenopus tropicalis	455	KILRRVQDEYERRGGFVRIFFPRHN	WDLYGSFLEYKTS	LNMYLVTHLFPNRAAGNDH--- 511
E9P886	Caenorhabditis elegans	543	QIVRKAELEDGRRGDFIRVFPRNGT	WGMYSVMEDLGN	EDF--DERLFDEVVTKKNTKNS 600
Q9VBX5	Drosophila melanogaster	604	RILRNARLQYSRRGGFVRIFFPTDDS	MDRYGNFLDSANG	IPISTPNVQSQ----- 652