Table 2 – Predicting the effects of *PALB2* missense variants on protein function using three *in silico* methods

Nucleotide change	Protein change	Carrier frequency (%)	SIFT [a]	Align GVGD [b]	Polyphen [c]
c.90G>T	p.Lys30Asn	1 (0.1)	Affect protein function; p=0.04	Class C0	Probably damaging 0.999
c.94C>G	p.Leu32Val	1 (0.1)	Tolerated; p=0.37	Class C0	Probably damaging 1.000
c.596A>G	p.Asp219Gly	1 (0.1)	Tolerated; p=0.65	Class C0	Benign 0.000
c.956C>A	p.Ser319Tyr	1 (0.1)	Tolerated; p=0.91	Class C0	Possibly damaging 0.589
c.1010T>C	p.Leu337Ser	25 (3.3)	Tolerated; p=0.59	Class C0	Benign 0.291
c.1475G>T	p.Gly492Val	1 (0.1)	Tolerated; p=0.17	Class C0	Benign 0.161
c.1676A>G	p.Gln559Arg	72 (9.6)	Tolerated; p=0.57	Class C0	Benign 0.000
c.2014G>C	p.Glu672Gln	51 (6.8)	Tolerated; p=0.48	Class C0	Benign 0.225
c.2590C>T	p.Pro864Ser	1 (0.1)	Tolerated; p=0.68	Class C0	Possibly damaging 0.578
c.2993G>A [*]	***p.Gly998Glu***	***17 (0.9)***	***Affect protein function; p=0.00***	***Class C65***	***Probably damaging 1.000***

[*]Predicted to affect protein function by all three programs. [a]Kumar *et al.*(2009) [22]; Ng *et al* (2003) [23]. [b] Tavtigian *et al.* (2006) [24]; Mathe *et al.* (2006) [25]; Tavtigian *et al*. (2008) [26]. [c] Adzhubei *et al.* (2010) [27]