Table S4. *LDLR* variants with negative *in silico* predictions.

Variant	*In silico* analysis			
	SSFL [0-100] WT→ Mutant	MES [0-12] WT→ Mutant	NNSP [0-1] WT→ Mutant	HSF [0-100] WT→ Mutant
Donor				
c.1167G>A	No change for the physiological splice site at c.1186			
c.1977C>A	No change for the physiological splice site at c.1987			
c.2211G>T	— → 75 *(Physiological splice site at c.2311: 82.5)*	5.4 → 10 (+85,2%) *(Physiological splice site at c.2311: 9)*	0.9 → 1 (+4.9%) *(Physiological splice site at c.2311: 1)*	81 → 83 (+2,4%) *(Physiological splice site at c.2311: 85)*
Acceptor				
c.1706-10G>A	74.8 → 74.7 (-0.1%)	7.9 → 7.0 (-11.8%)	— → 0.41	79.7 → 79.6 (-0.1%)
c.2106G>A	No change for the physiological splice site at c.1988			
Donor or Acceptor				
c.1920C>T	No change in neither the physiological acceptor splice site at c.1846 nor the physiological donor splice site at c.1987			