

Supplementary Table 1. The detailed information of EYA1 NM_000503.6:c.1050+4A>G

Data source	Category	Summary
Population database	1000 Genomes	-
	ESP6500	-
	GnomAD	-
	ExAC	-
In silicon data	CADD	2.16
	CADD_Phred	17.23
	MaxEntScan	9.25 (pre-mutation), 7.22 (post-mutation), -21.95% (reduction > 15%)
	dbscSNV_SCORE	0.9995
	Spidex	-35.53
	SpliceAI	0.58
Variant classification (pathogenic)	PVS1 (RNA)	The splicing variant was predicted to be deleterious and verified by multiple experimental evidence.
	PM2	The variant has not been reported in the above population databases.
	PP1	The variant co-segregate in family members with HL