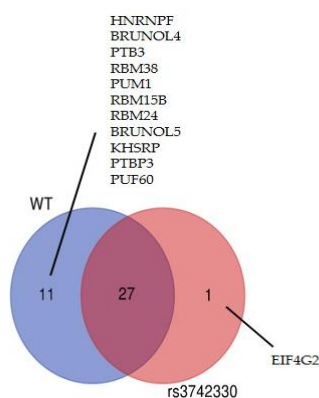


(B)



The binding partners to the 3'UTR reference to 30 nucleotide upstream and downstream of rs3742330 used to predict, the motifs from RBPmap database <http://rbpmap.technion.ac.il/index.html>. Human / Mouse motifs was used as option run the prediction.

(C)

Regulatory motifs altered

Position Weight Matrix ID	Strand	Ref	Alt	Match on: Ref: GTGGGCTCAATCTTGTTAAAGGGATTAGACACCCCTAACAGAGCAAGATCCAATATTT Alt: GTGGCTTCAATCTTGTTAAAGGGATTAGGCACCCCTAACAGAGCAAGATCCAATATTT
Crx_1	+	11.1	11.4	VKVRGATTARDVR
Crx_2	+	11.4	11.5	YBWDGSGGATTADCSR
Dmbx1	+	10.9	12.9	WDEWNVGGATTADKENW
Gsc	+	12.9	13.3	BDHRSGGATTARYDWNW
Obox6	+	12	9.7	MNAWDGSGATTAWHB
Otx2	+	13.4	13.5	NDDRGGGATTAATHDNH
Pitx3	+	12	13.1	VRSRGATTADCKRB5
Smad_1	+	10.5	-1.2	AGACWBNNN

Figure S1: The *in silico* analysis of rs3742330 in *DICER1* showing (A) The genomic region containing the polymorphism on chromosome 14q32.13 and its neighboring features, such as miRNA binding sites, transcription binding sites, regulatory elements, eQTLs, and conservation among species obtained using the UCSC genome browser. (B) The altered RNA binding protein partners predicted using RBP map database. (C) Altered regulatory motifs as detected by HaploReg v4.1.