Pediatric RESEARCH

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IMAGE

Insights Figure for "Susceptibility to congenital heart defects associated with a polymorphism in TBX2 3′ untranslated region in the Han Chinese population"

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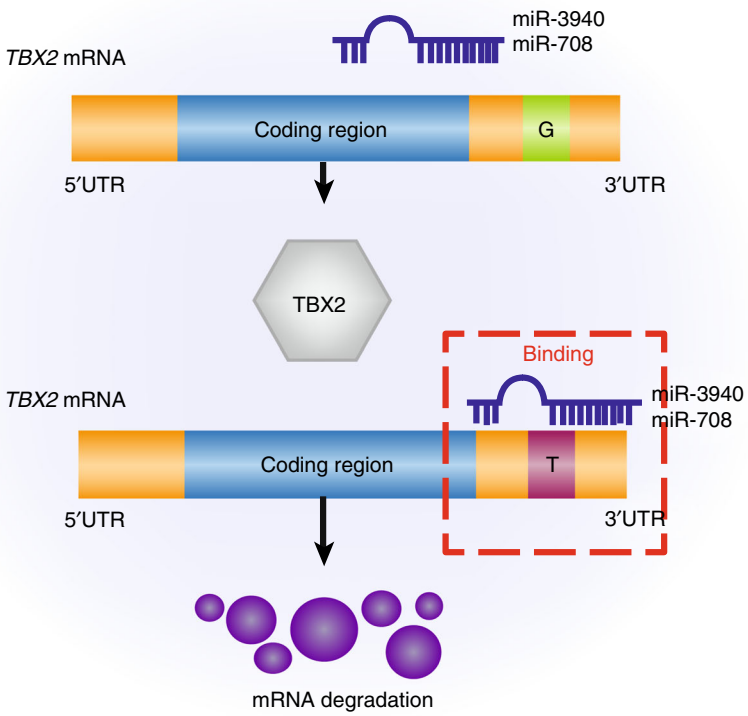
As we found from the association study, the G to T variation of rs59382073 at the 3′ untranslated region of *TBX2* is a significant risk factor to congenital heart defect. This figure depicts the underlying mechanism we discovered. Compared to the G allele, the T allele creates extra miRNAs binding sites for miR-3940 and miR-708, whose binding could degrade the corresponding mRNAs and further decrease TBX2 expression. Since the dosage of Tbx2 is finely regulated during cardiac development, the decreased Tbx2 expression level could lead to a higher risk of heart malformations.

REFERENCE

Wang, J. et al. Susceptibility to congenital heart defects associated with a polymorphism in TBX2 3′untranslated region in the Han Chinese population. *Pediatr Res.* (2018). https://doi.org/10.1038/s41390-018-0181-y



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