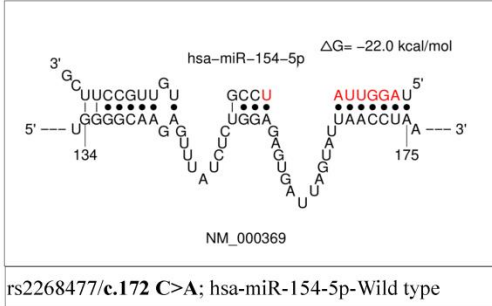


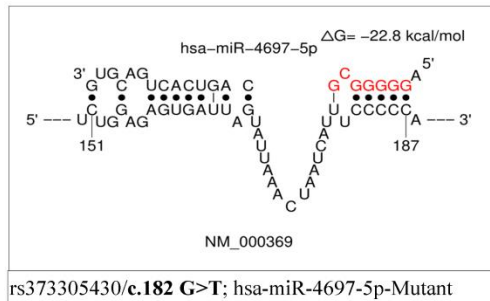
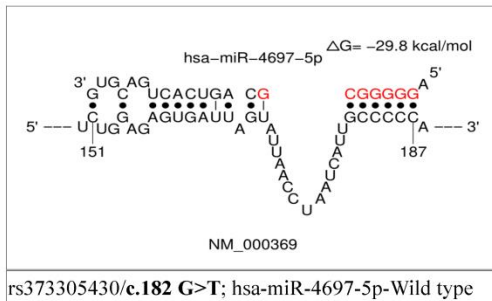
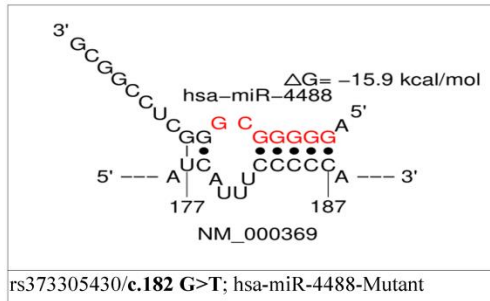
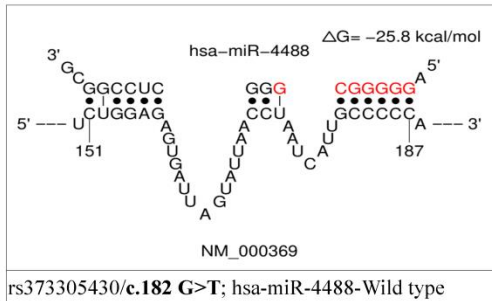
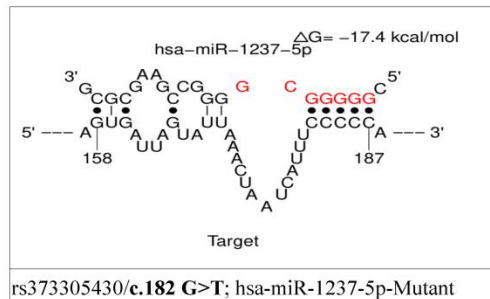
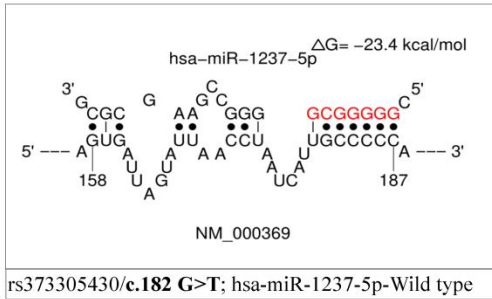
Supplementary Fig. 1.

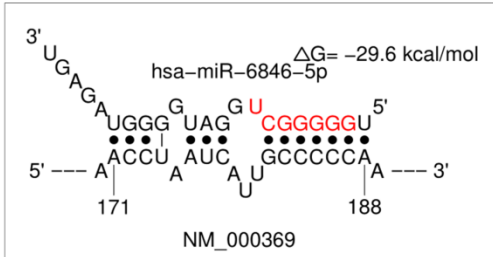
A



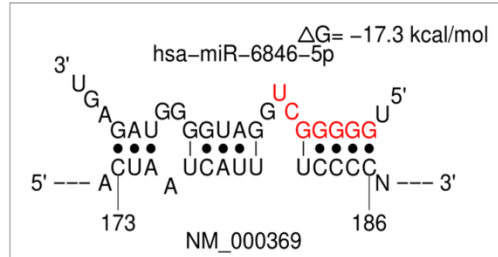
rs2268477/c.172 C>A; hsa-miR-154-5p can disrupt the binding site

B

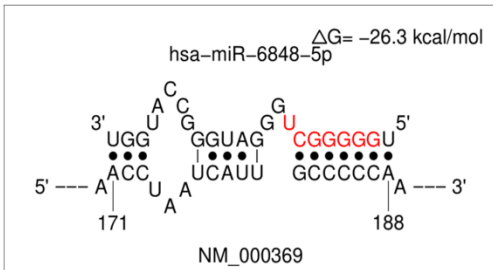




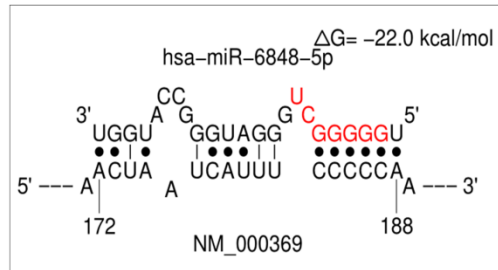
rs373305430/c.182 G>T; hsa-miR-6846-5p-Wild type



rs373305430/c.182 G>T; hsa-miR-6846-5p-Mutant

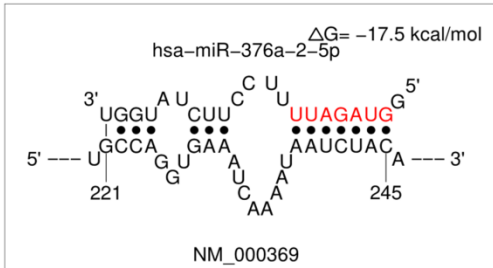


rs373305430/c.182 G>T; hsa-miR-6848-5p-Wild type

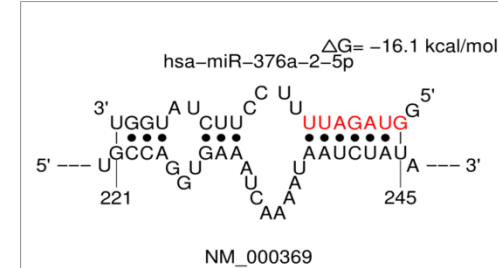


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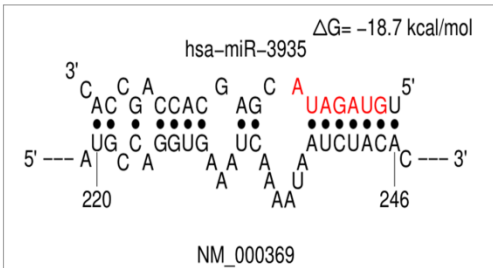
C



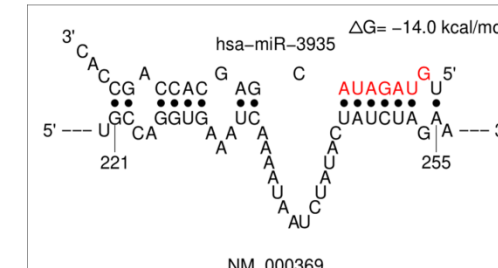
rs7144481/c.245 C>T; hsa-miR-376a-2-5p-Wild type



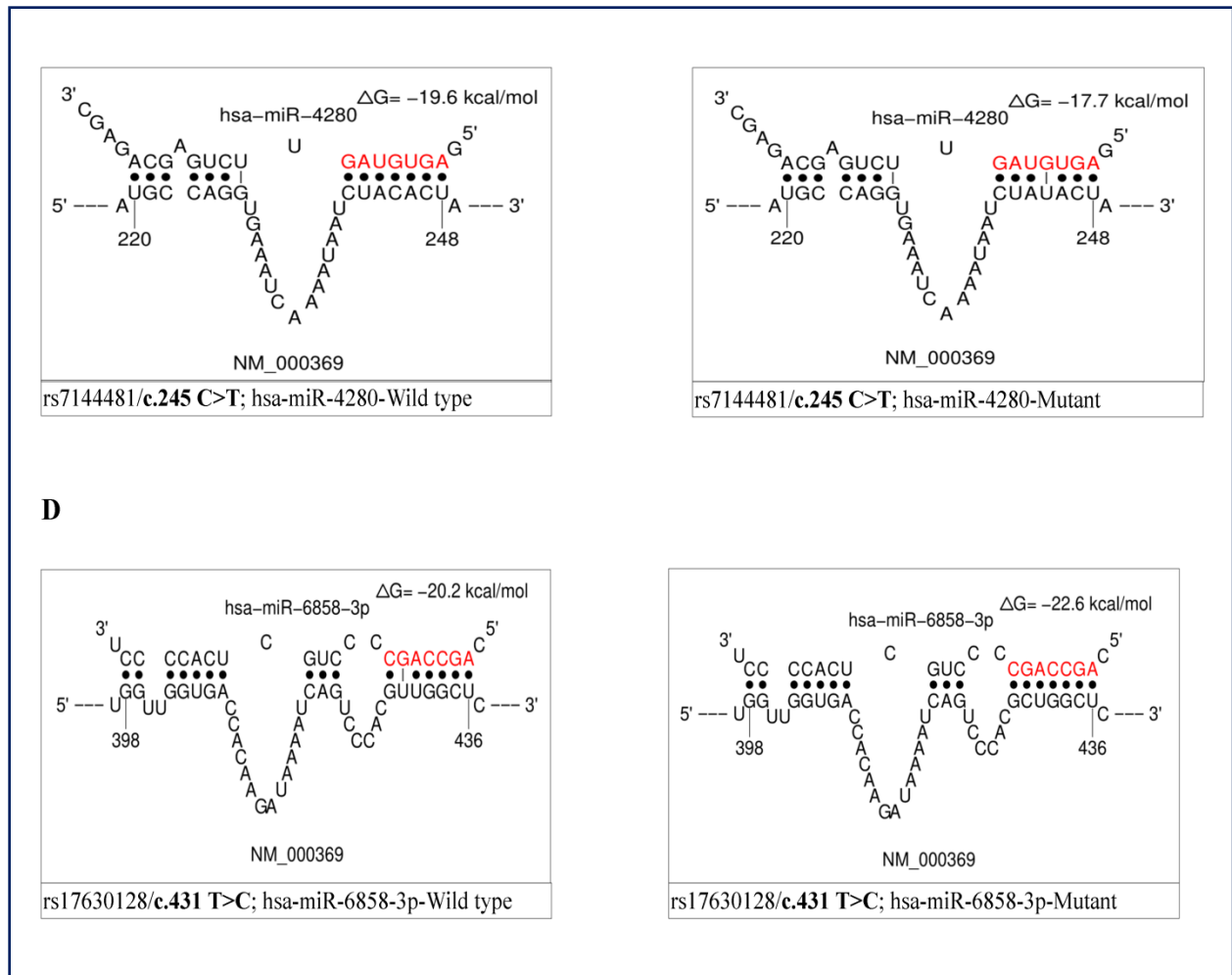
rs7144481/c.245 C>T; hsa-miR-376a-2-5p-Mutant



rs7144481/c.245 C>T; hsa-miR-3935-Wild type



rs7144481/c.245 C>T; hsa-miR-3935-Mutant



Supplementary Fig. 1. Schematic representation of the miRNA binding site on the 3'-UTR variants found in the *TSHR* gene. Hybrid diagram for a seed site (miRNA seed region in red) and hybrid diagram for a seedless (non-canonical) site. (A) rs2268477/c.172 C>A (hsa-miR-154-5p), which can destroy the binding site. (B) rs373305430/c.182 G>T (hsa-miR-1237-5p; hsa-miR-4488; hsa-miR-4697-5p; hsa-miR-6846-5p; hsa-miR-6848-5p). (C) rs7144481/c.245 C>T (hsa-miR-376a-2-5p; hsa-miR-3935; hsa-miR-4280). (D) rs17630128/c.431 T>C (hsa-miR-6858-3p).