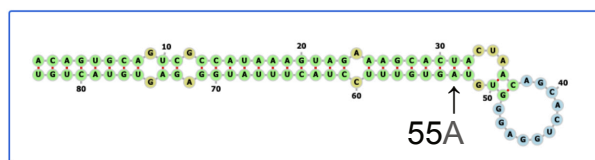# Figure S1 : Predicted hairpin structure of miR-142s and comparison of miR-142s expression

a) miR-142 55A (WT) folding

Start Position: 1, End Position: 83
Sequence Size: 83 nucleotides
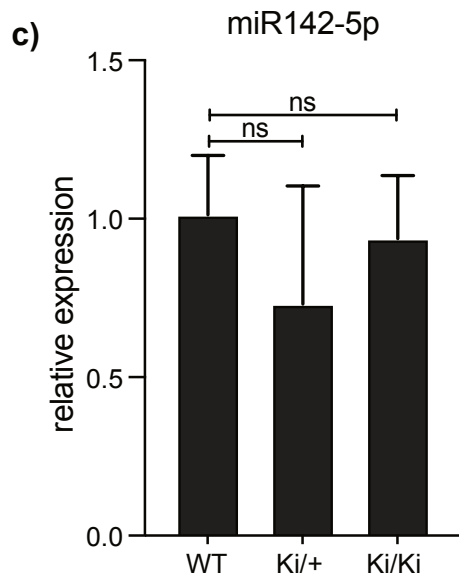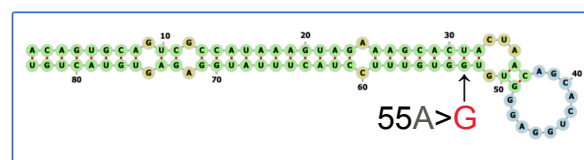Minimum Free Energy: -41.9 kcal/ mol

Sequence:
ACAGUGCAGUCGCCAUAAAGUAGAAAGCACUACUAACAGCUGGAGG
GUGUAGUGUUUCCUACUUUAUGGAGAGUGUACUGU

55A

b) miR-142 55A>G folding

Start Position: 1, End Position: 83
Sequence Size: 83 nucleotides
Minimum Free Energy: -41.6 kcal/ mol

Sequence:
ACAGUGCAGUCGCCAUAAAGUAGAAAGCACUACUAACAGCUGGAGG
GUGUGGUGUUUCCUACUUUAUGGAGAGUGUACUGU

55A>G

c)

miR142-5p

a, b) miRNAFold is the identification of large-scale microRNA precursors in the genome and quickly and sensitively predicts microRNA hairpin structures. The hairpin structure for the miR-142-55A sequence is shown in (a) and the miR-142-55A>G sequence in (b).

c) miR-142-5p expression in bone marrow of 2-month-old mice (n = 3-4).