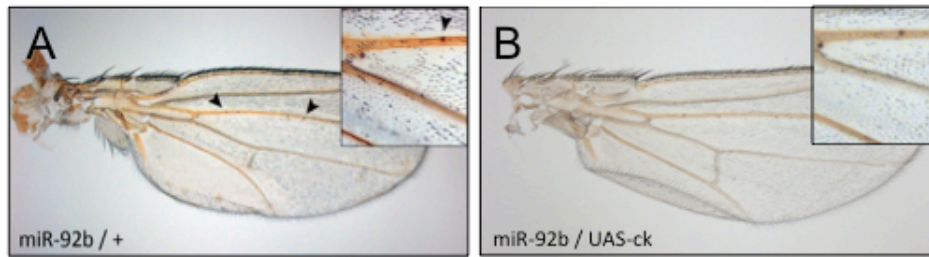


**Figure S1** Expression analysis of the miR-92 family in wing discs. Northern Blot analysis of total RNA from third instar wing imaginal discs of *MS1096-Gal4* driven miRNAs of all six members of the miR-92 family. Reverse complementary DNA oligonucleotides were used as probes. DNA mimics of the indicated miRNAs (5 fmol each) were loaded in lanes 1, 9 and 10 as positive controls and to verify cross hybridization except for *miR-313\**.



**Figure S2** Co-expression of *UAS-ck* with *miR-92b* does not rescue the wing hair defect (A, B). Expression of *UAS-ck* does not rescue the wing hair defect induced by *miR-92b*. Expression of *UAS-ck* causes no effect in a wt-background or in a *miR-312* background (not shown). Both transgenes are driven by one copy of *MS1096-Gal4*. Both wings derived from adult females.

**Table S1** List of all *UAS-miRNA* lines, mature miRNA sequences and the corresponding oligonucleotides (for and rev) that were used for cloning. Phenotypes in the *ey-Gal4* (eye), *MS1096-Gal4* (wing) and *act5C-Gal4* (ubiquitous activation) screens are listed. Phenotypic strength is indicated from weak (+) to strong (+++). Eyes showed size reduction and rough appearance in all cases. Wings showed mostly size reduction, additional defects are indicated.

Available for download at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.145383/-/DC1>.