



*mir-229* secondary structure and expression patterns. (A) Foldback of a 120 nt sequence region around *mir-229* (B) Northern analysis of Dicer influence on precursor accumulation. For both the standard (std.) and enriched (enr.) samples the signal for miR-229 was constant in the wild-type (N2) and mutant (*dcr-1*), while the signal for miR-229-L was 1.6-fold greater in the mutant. (C) Constitutive expression of *mir-229* throughout larval development.