



FIGURE S1: qPCR validation of the expression levels of 22 miRNAs across all samples. The trends of miRNA expression levels and relative abundance across all samples by miRNA-Seq (A) and qPCR (B) are similar for 16 miRNAs. Five additional miRNAs showing differences between miRNA-Seq and qPCR trends in one or more tissues (miR-12, bantam, miR-1013, miR-283, and miR-13a) are denoted with an asterisk. The genome presents several copies of mature miR-13b undistinguishable by qPCR: miR-13b and miR-13b-1 on chr3R, and miR-13b-2 on chrX. MiRNA normalized reads are reported in (A). qPCR assays were performed with at least two independent biological replicates and gave similar trends in (B). M: male ; F: female.