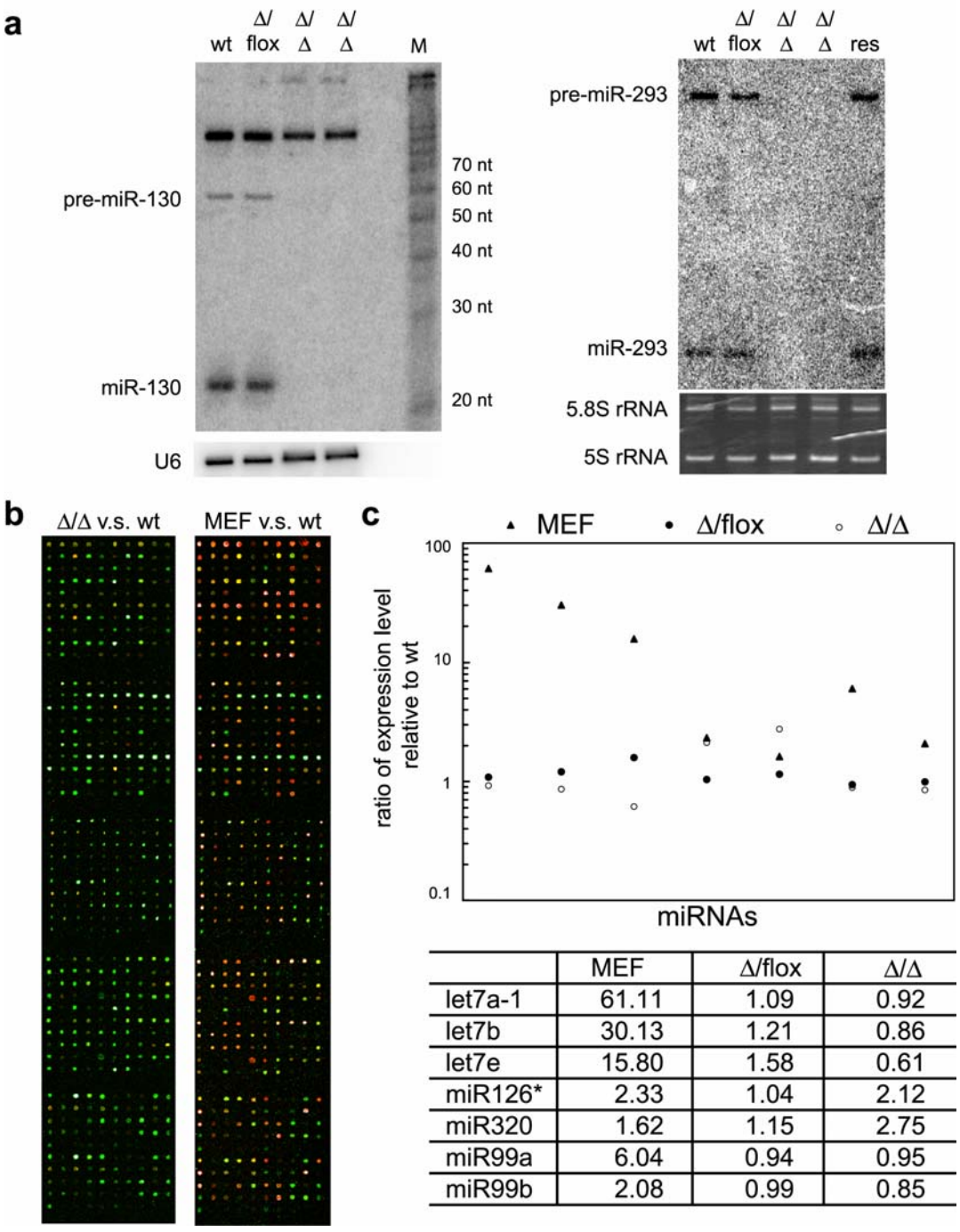

	MEF	Δ/flox	Δ/Δ
let7a-1	61.11	1.09	0.92
let7b	30.13	1.21	0.86
let7e	15.80	1.58	0.61
miR126*	2.33	1.04	2.12
miR320	1.62	1.15	2.75
miR99a	6.04	0.94	0.95
miR99b	2.08	0.99	0.85

Supplemental Figure 1. Northern and microarray analysis of miRNAs. (**a**) Northern Analysis of miR-130 (left panel) and miR-293 (right panel). (**b**) Fluorescence images of microarrays. The left image, DGCR8 knockout vs. wild-type ES cell. The right image, mouse embryonic fibroblasts (MEFs) vs. wild-type ES cell. (**c**) Expression ratios of MEFs, DGCR8 heterozygous and homozygous knockout ES cells relative to wild-type ES cells for 7 miRNAs that have relatively high expression ratios (> 0.2) in homozygous knockout ES cells relative to wild-type ES cells. Signals for four of these seven miRNAs (let7a-1, let7b, let7e and

miR99a) in the DGCR8 knockout ES cell sample appear to be due to contamination from MEF feeder cells. They are highly expressed in the MEF feeder cells compared to wild-type ES cells and their signals diminished with the weaning off MEFs (weaning data not shown). The other three miRNAs (miR-126*, miR-320, miR-99b) showed similar signal levels in MEFs, wild-type, heterozygous and DGCR8 knockout ES cells and did not diminish with weaning of MEFs. These miRNAs may not be processed by the microprocessor complex, or more likely, signals for these miRNAs are due to nonspecific hybridization. Data represent average of two experiments for MEF, average of three experiments for Δ/flox, and average of four experiments (two experiments for each of two independent cell lines) for Δ/Δ, except ratio for miR-126* of MEF is from a single experiment, and ratios for let7a-1 and let7b of Δ/flox are average from two experiments.