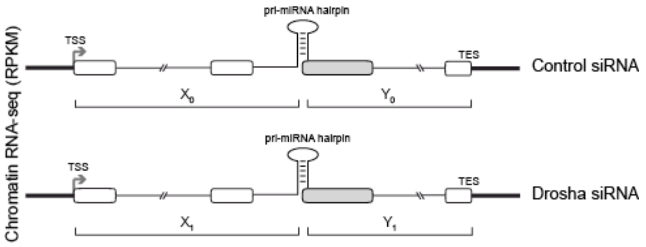

$$\text{Fold increase Drosha siRNA} = \frac{\text{mean } Y_1 / \text{mean } X_1}{\text{mean } Y_0 / \text{mean } X_0}$$

**Supplemental Figure S5. Fold increase of Drosha siRNA-treated cells.**

Analysis of miRNA-containing genes with length ≥2 kb and gene-body RPKM ≥1 resulting from the online available chromatin RNA-seq data of HeLa cells treated with a control siRNA and Drosha siRNA (Dhir et al. 2015). For each gene, average number of reads (normalized to total sequencing depth) spanning from the TSS of the miRNA-containing gene to the start of the pri-miRNA hairpin (mean $X_0$ and mean $X_1$) and from the end of the pri-miRNA hairpin to the TES (mean $Y_0$ and mean $Y_1$) in the control siRNA and Drosha siRNA treated cells were estimated. The ratio between reads mapping downstream and upstream the pri-miRNA hairpin was calculated (mean$Y_0$/mean$X_0$ and mean$Y_1$/mean$X_1$). Then the fold increase of Drosha siRNA-treated cells was calculated as the average number of Drosha siRNA reads over the average number of control siRNA reads, as described in the formula (see also Materials and methods).