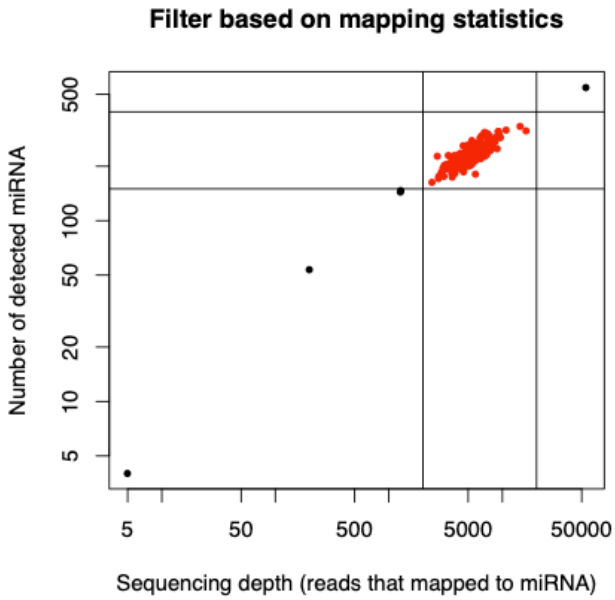
Supplementary Figures

Landscape of microRNA and target expression variation and covariation in single mouse embryonic stem cells

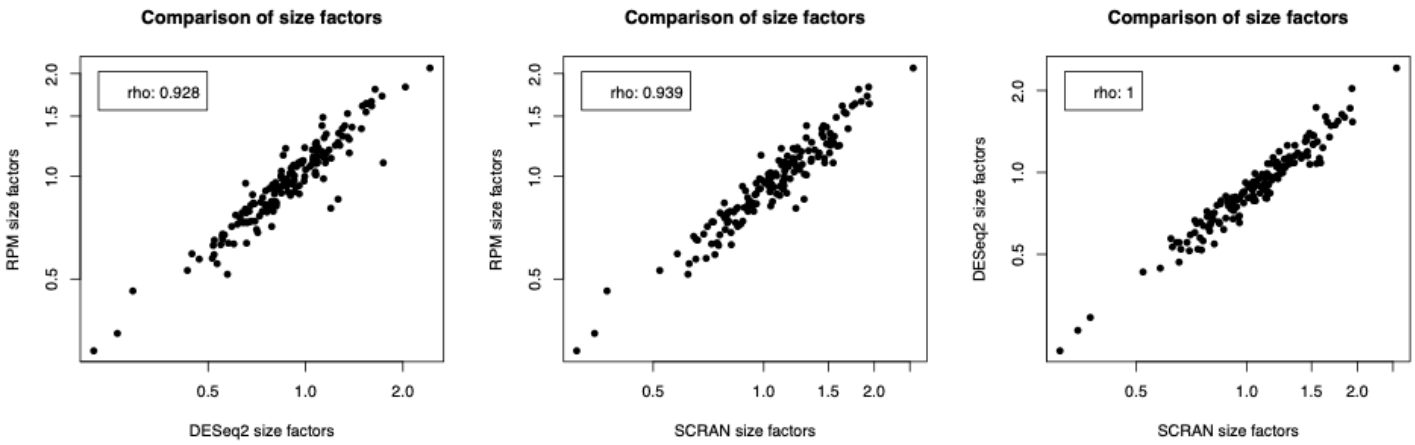
Marcel Tarbier[1,2,‡], Sebastian D. Mackowiak[3], Vaishnovi Sekar[1], Franziska Bonath[1], Etka Yapar[4], Bastian Fromm[5], Omid R. Faridani[6,7], Inna Biryukova[1] and Marc R. Friedländer[1,‡]

[1] Science for Life Laboratory, Department of Molecular Biosciences, The Wenner-Gren Institute, Stockholm University, Stockholm, Sweden
[2] Science for Life Laboratory, Department of Immunology, Genetics and Pathology, Uppsala University, Sweden
[3] Berlin Institute of Health at Charité - Universitätsmedizin Berlin, Center of Digital Health, Berlin, Germany
[4] Department of Biology, Lund University, Lund, Sweden
[5] The Arctic University Museum of Norway, UiT - The Arctic University of Norway, Tromsø, Norway
[6] School of Biomedical Sciences, University of New South Wales, Sydney, Australia
[7] Garvan Institute of Medical Research, Sydney, Australia

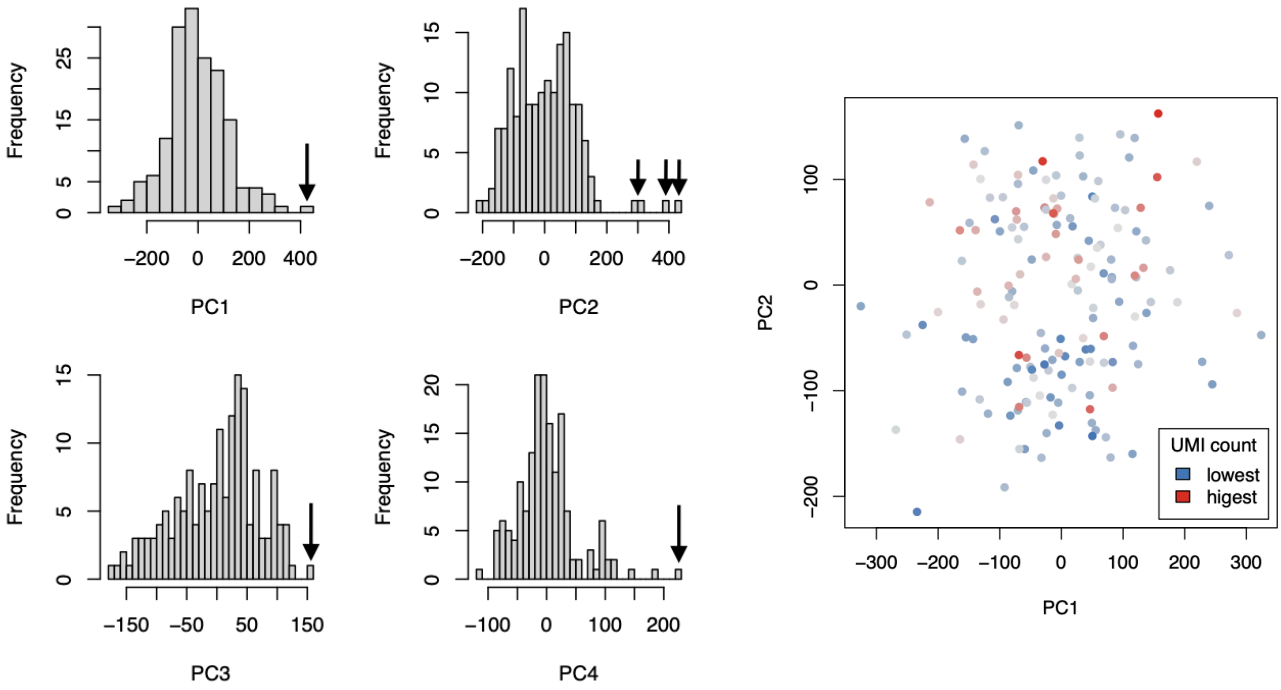
[‡] Correspondence may be addressed to: marcel.tarbier@scilifelab.se, marc.friedlander@scilifelab.se



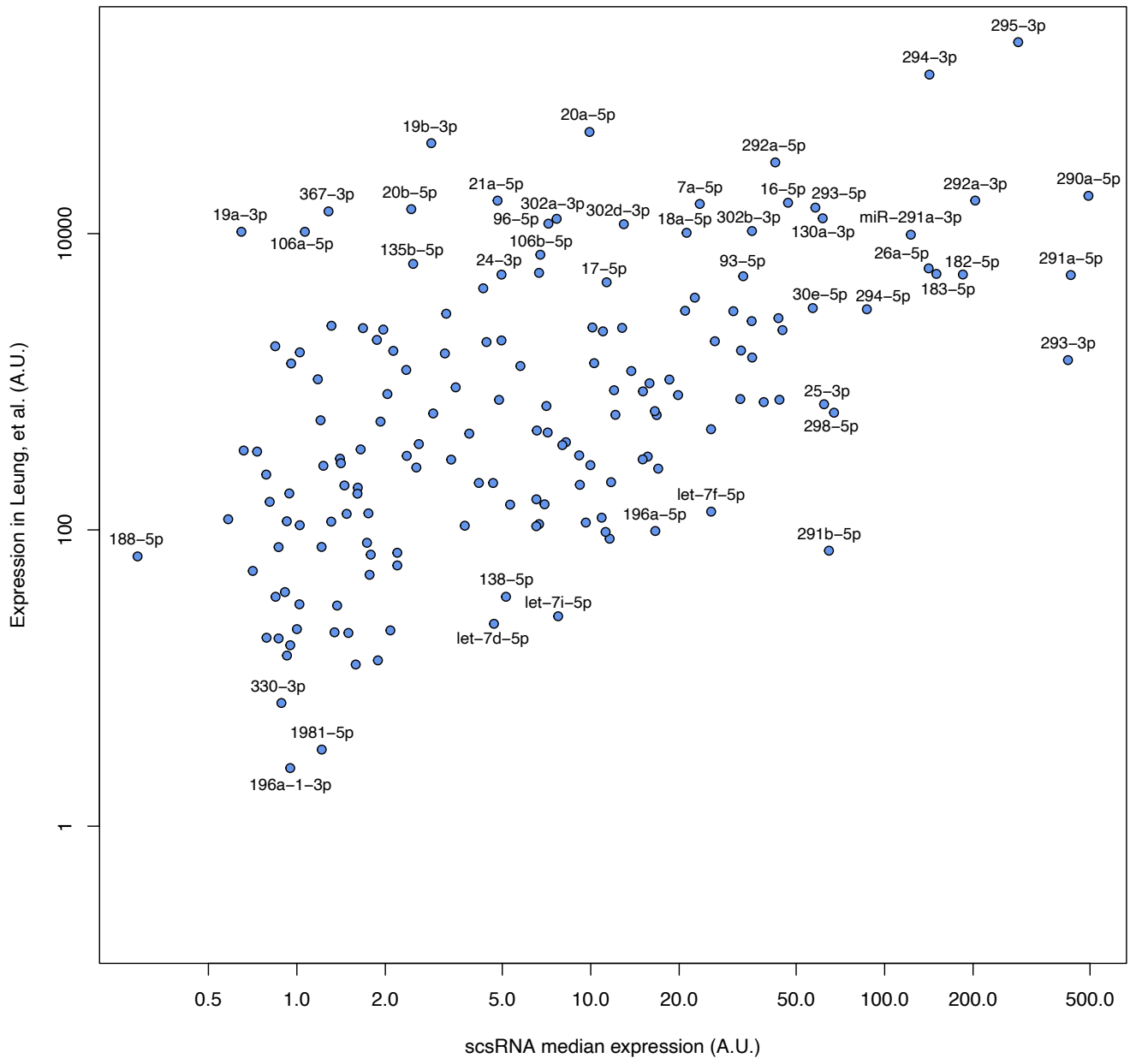
Supplementary Figure S1 – cell filtering according to mapping statistics.



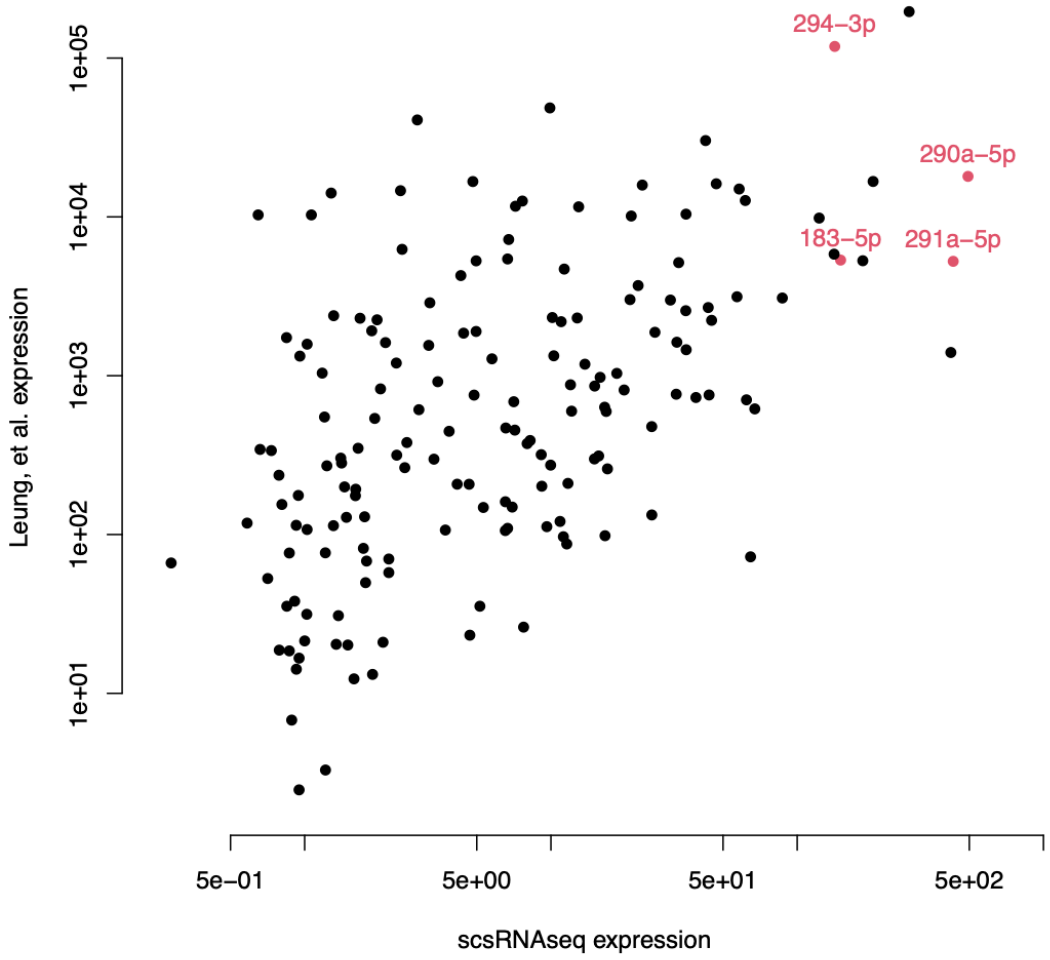
Supplementary Figure S2 – different normalization techniques yield very similar size factors (left: RPM vs. DESeq2, middle: RPM vs. SCRAN, right: DESeq2 vs. SCRAN).



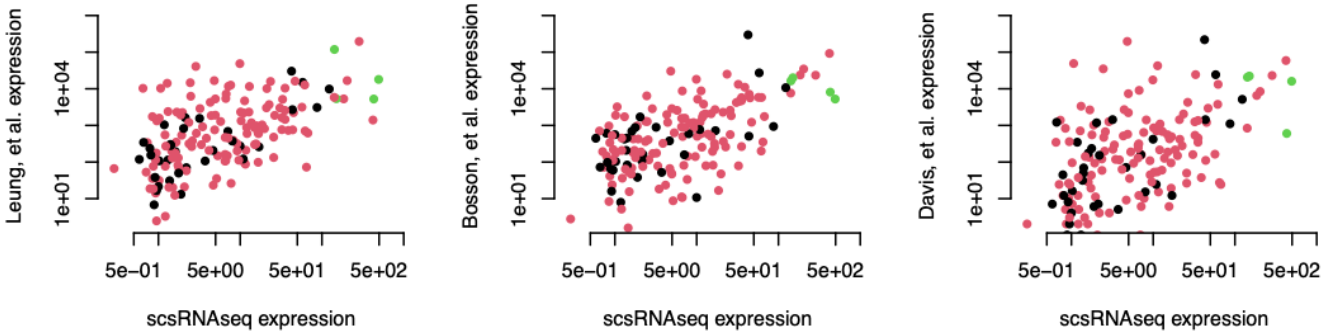
Supplementary Figure S3. Removal of outlier cells (left). In total 7 out of 165 cells were removed because they were outliers in one of the first four principal components (marked by arrows). Following removal of the 7 outlier cells, there was no clear correlation between the UMI count and the first two components (right).



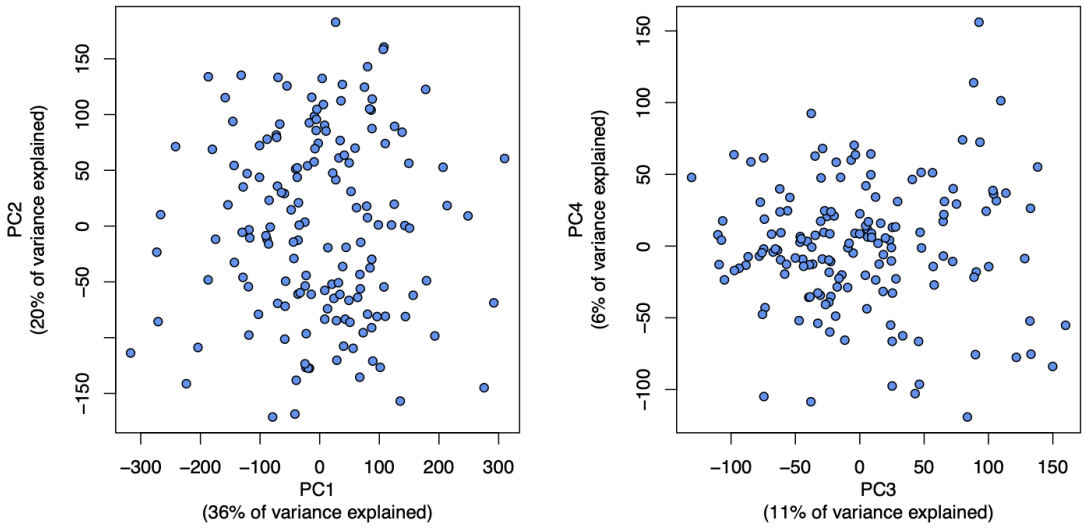
Supplementary Figure S4. Comparison between miRNA expression as profiled by Small-seq (horizontal) and bulk sRNA-seq (vertical).



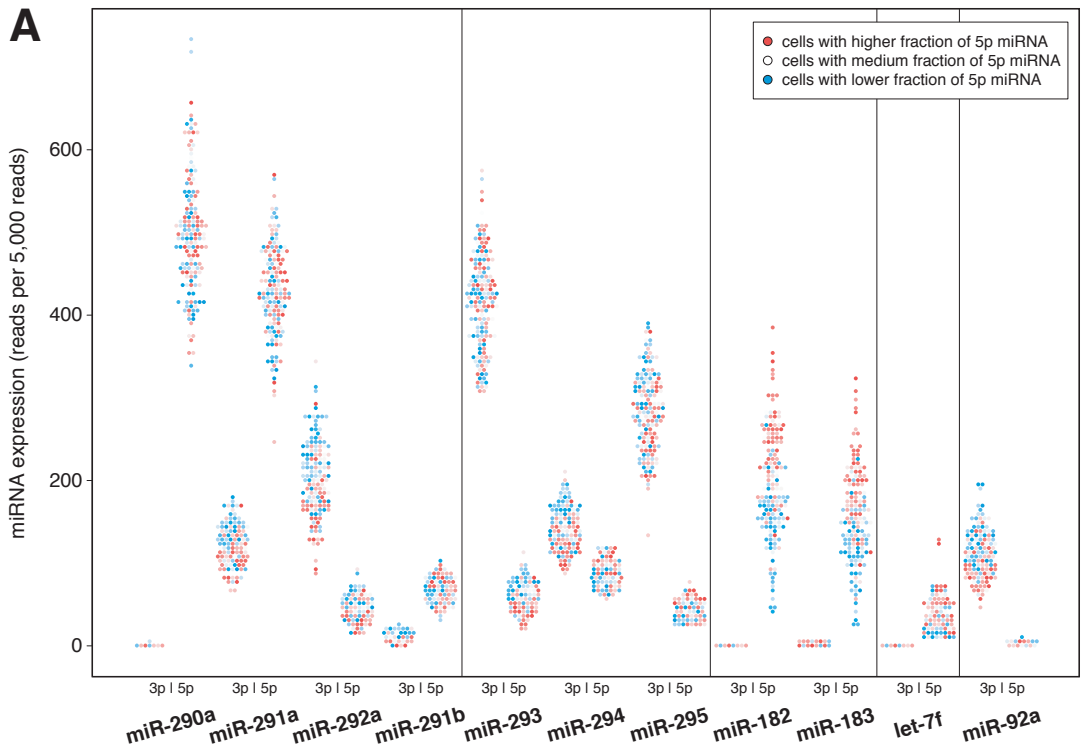
Supplementary Figure S5. Similar to previous Supplementary Figure S4, but miRNAs that are highlighted in this study are marked in red.



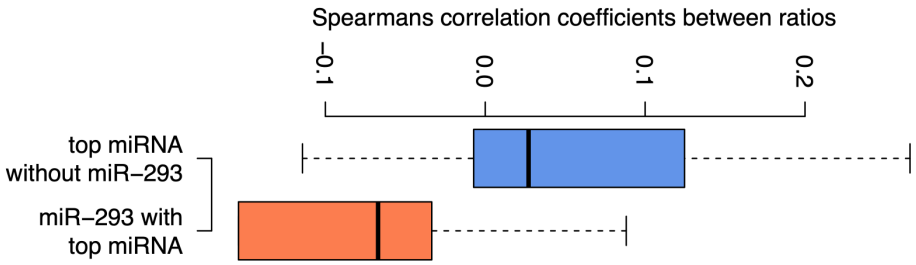
Supplementary Figure S6. MiRNA expression as measured by Small-seq (horizontal axis, this study) and bulk sRNA-seq (vertical, from 3 studies: Leung et al., Bosson et al. and Davis et al.) and). Mature arms are marked in red. miRNAs that are highlighted in this study are marked in green.



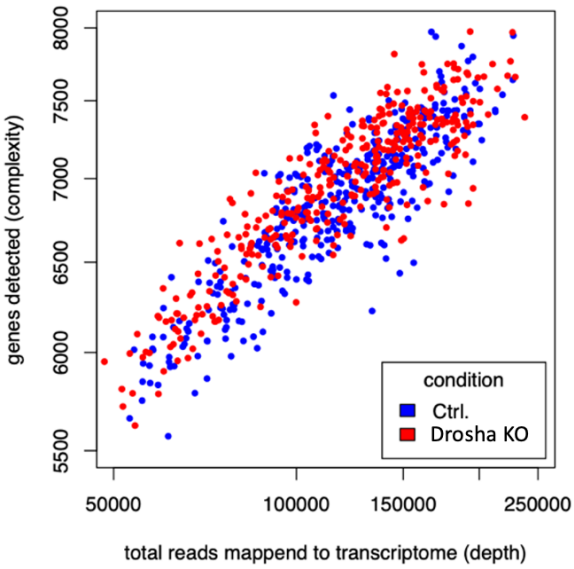
Supplementary Figure S7. PCA of cells, grouped by miRNA expression. The first four principal components are shown in 2D representation.

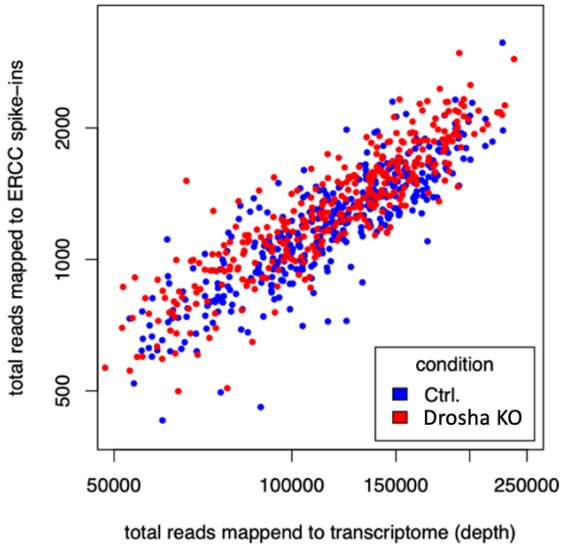


Supplementary Figure S8 – distribution of abundant miRNAs across single cells reflects global 5p bias (each dot represents one cell, color shows cellular 5p bias)

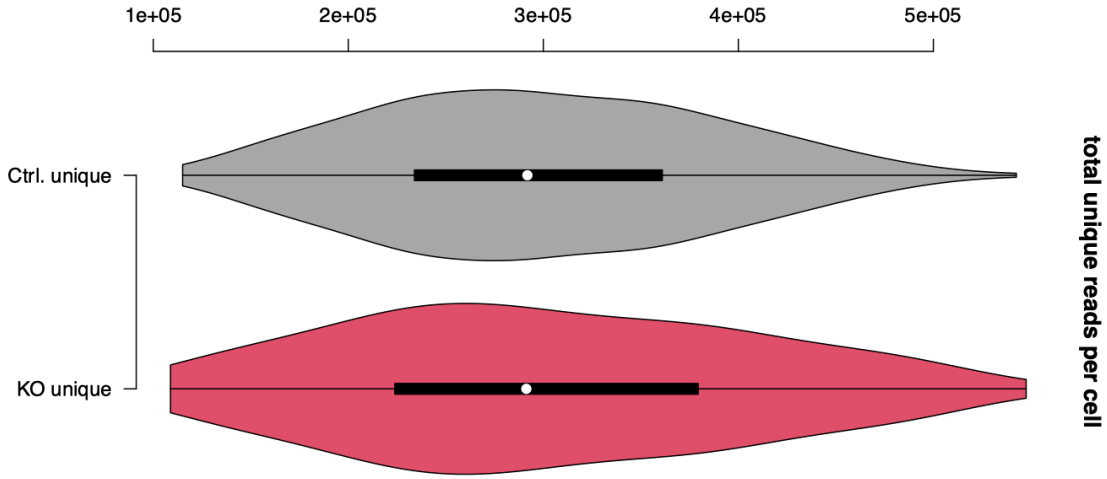


Supplementary Figure S9 – 5p ratio of most miRNAs are positively correlated with each other across single-cells, only miR-293 shows strong anti-correlation with the ratios of all other miRNAs

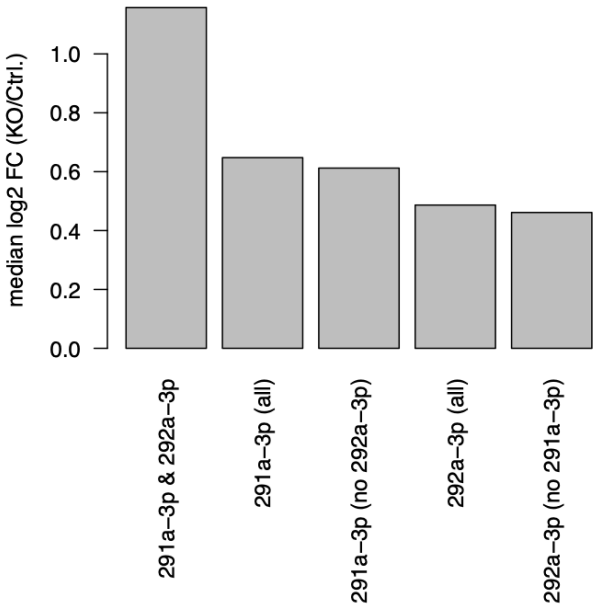




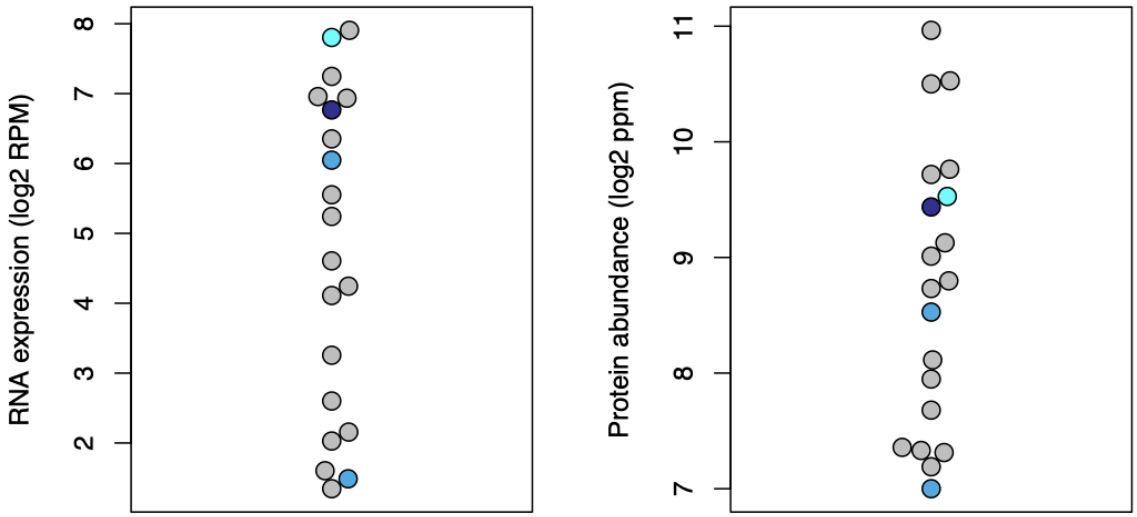
Supplementary Figure S10. Comparison of the total number of reads mapped to the transcriptome vs. the number of genes detected (left) and the total number of reads mapped to the ERCC spike-ins (right). We do not observe any evidence that either *dgcr8* KO or control cells display higher sequence complexity.



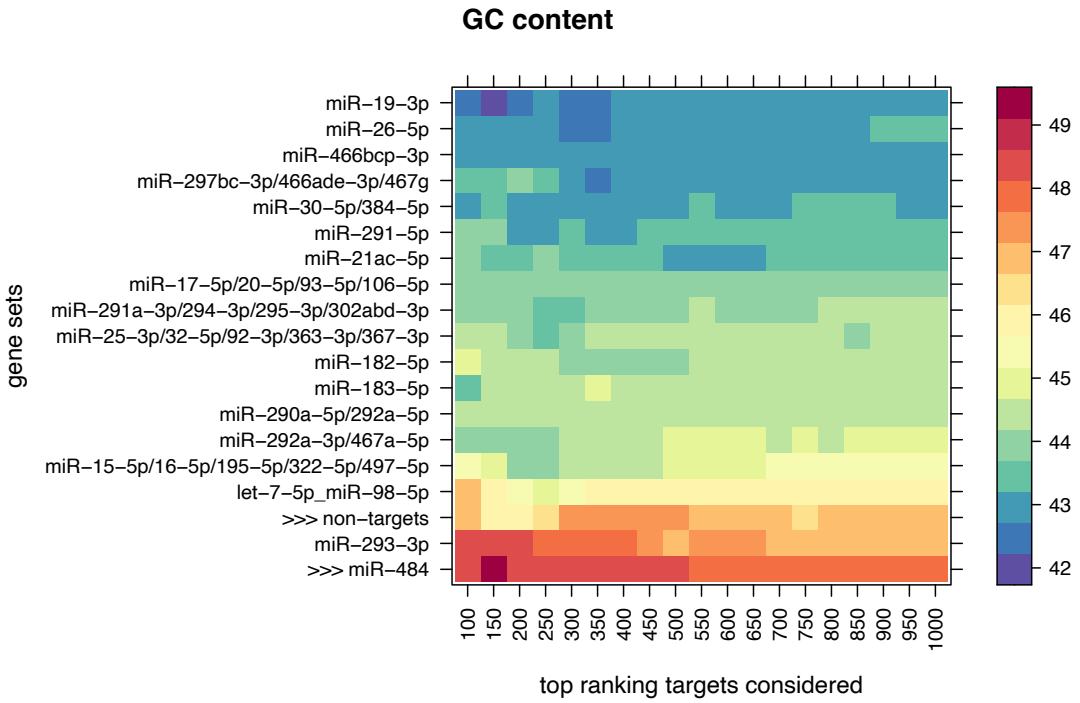
Supplementary Figure S11. Distribution of total unique reads (defined by read start and end) per cell across control cells and *Drosha* KO cells. There is no apparent or statistically significant difference in complexity between the cell types.



Supplementary Figure S12. Expression fold-change for mRNAs that are targeted by both miR-291a-3p and miR-292a-3p; for mRNAs that are targeted of miR-291a-3p (independent of miR-292a-3p targeting); for mRNAs that are targeted by miR-291a-3p but not miR-292a-3p; for mRNAs that are targeted of miR-292a-3p (independent of miR-291a-3p targeting) and for mRNAs that are targeted by miR-292a-3p but not miR-291a-3p.



Supplementary Figure S13. RNA expression data from Reimegård et al. and protein abundance data from PaxDB for the genes shown in figure 6D. Each dot represents one gene. Colors indicate miRNA target predictions (blue: miR-302 targets, turquoise: miR-17 targets, dark blue: targets of both miRNAs, grey: genes that are not targets of either).



Supplementary Figure S14 – GC content (shown by color) of miRNA targets.