

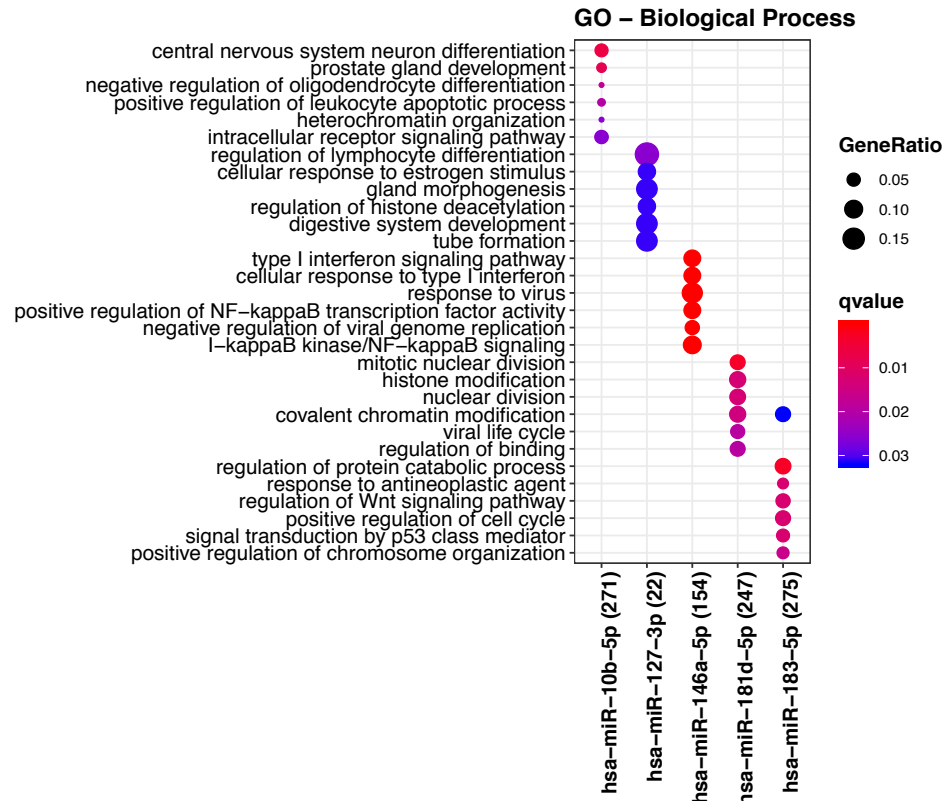
Supplementary Information

Manuscript title: MiR-146a is over-expressed and controls IL-6 production in cystic fibrosis macrophages

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Supplementary Figure S1

A



B

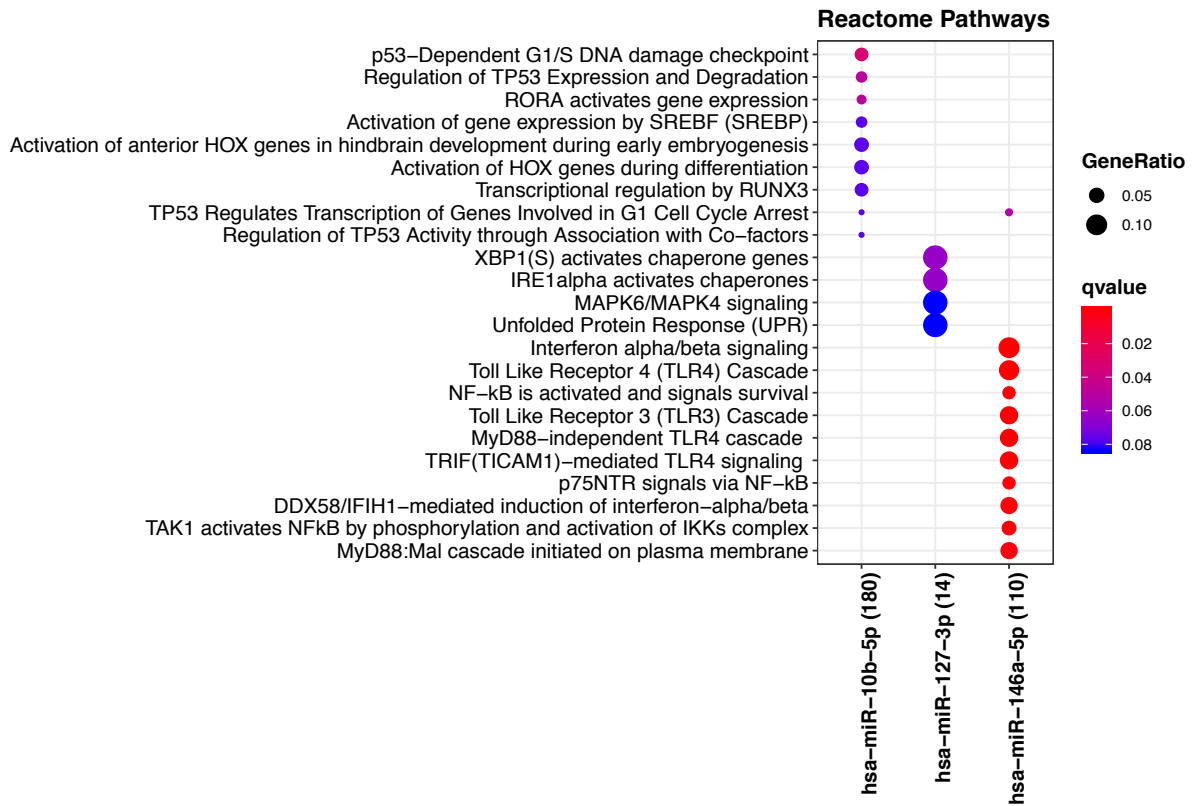
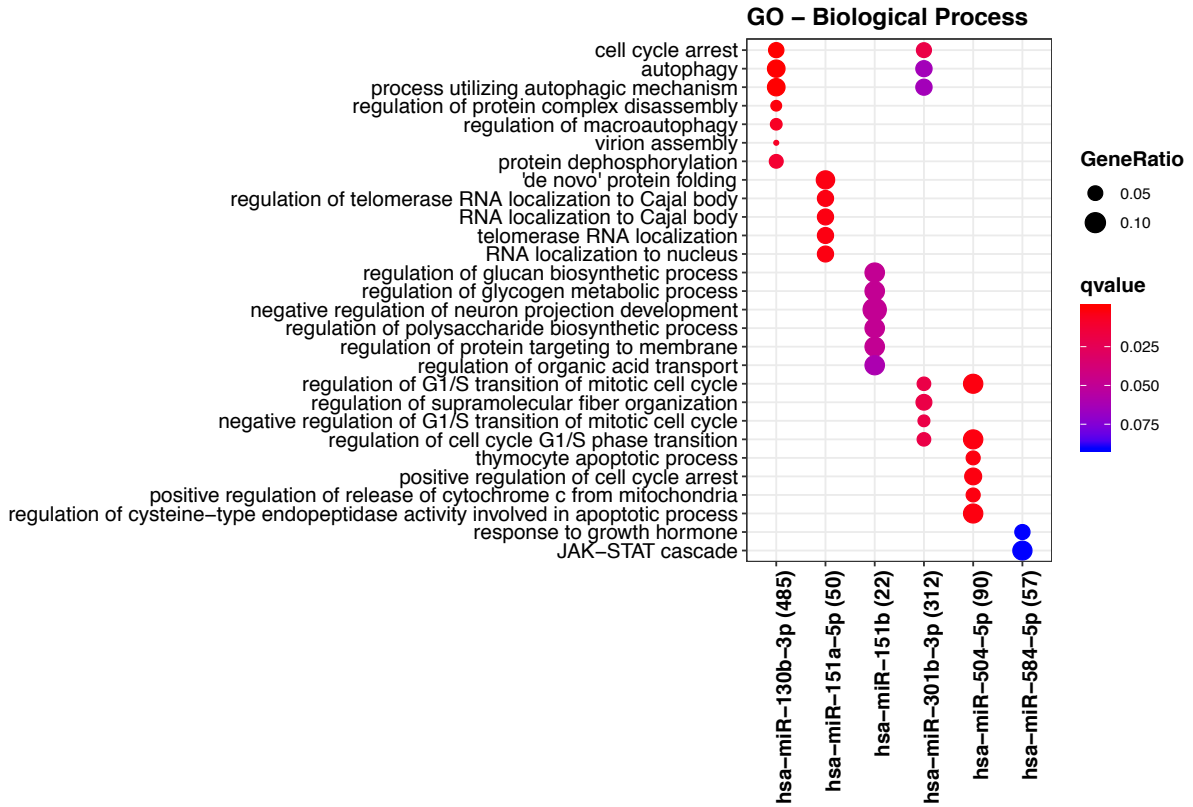


Figure S1. Functional enrichment analysis of genes targeted by upregulated miRNAs.

(A-B) The dotplot shows the top significantly enriched categories of GO biological processes of the differentially upregulated miRNAs target genes. The total number of target genes found in miRTarBase database for each miRNA is reported on x axis labels. Size dots is correlated with the ratio between the total number of target genes and the number of genes that belongs to a GO (A) or Reactome (B) category. Dots are colored according the Benjamini-Hochberg false discovery rate adjusted p-values (q value) from blue (higher q value) to red (lower q value).

Supplementary Figure S2

A



B

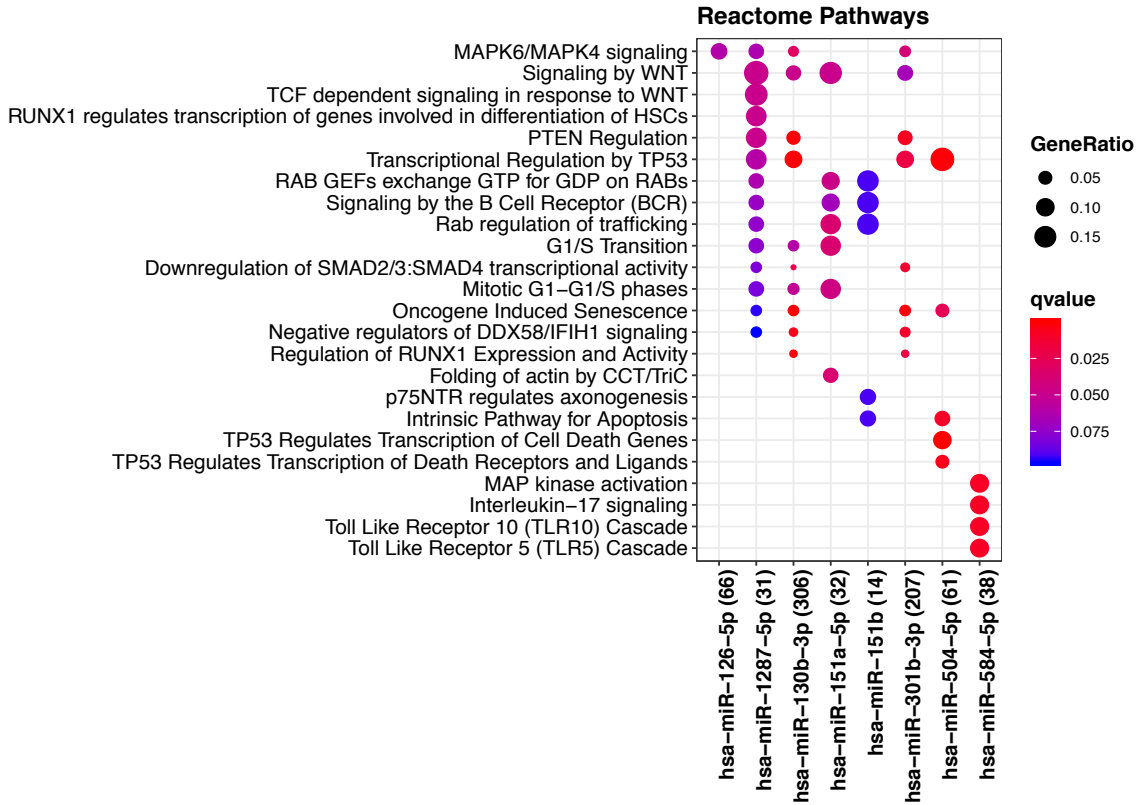


Figure S2. Functional enrichment analysis of genes targeted by downregulated miRNAs.

(A-B) The dotplot shows the top significantly enriched categories of GO biological processes of the differentially downregulated miRNAs target genes. The total number of target genes found in miRTarBase database for each miRNA is reported on x axis labels. Size dots is correlated with the ratio between the total number of target genes and the number of genes that belongs to a GO (A) or Reactome (B) category. Dots are colored according the Benjamini-Hochberg false discovery rate adjusted p-values (q value) from blue (higher q value) to red (lower q value).

Supplementary Figure S3

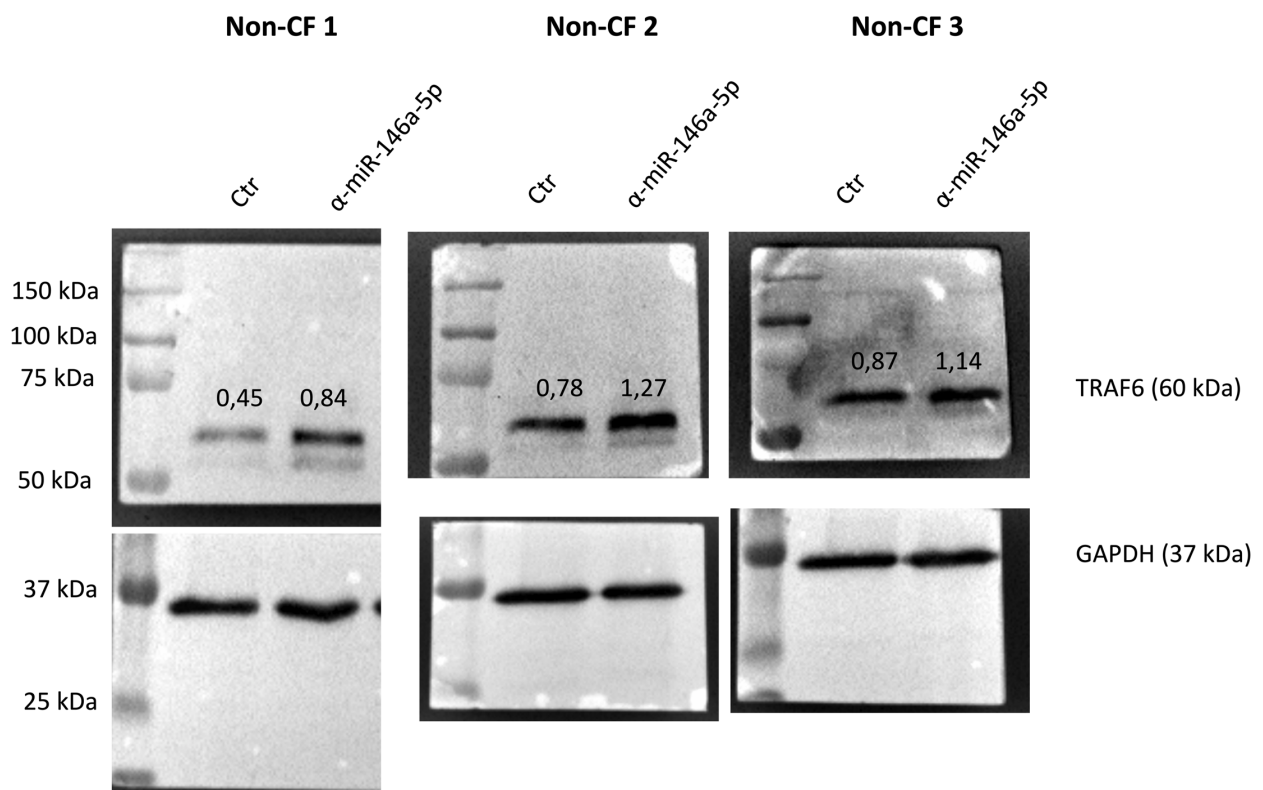


Figure S3. Uncropped western blotting images and quantification data of TRAF6 used for Figure 4b.