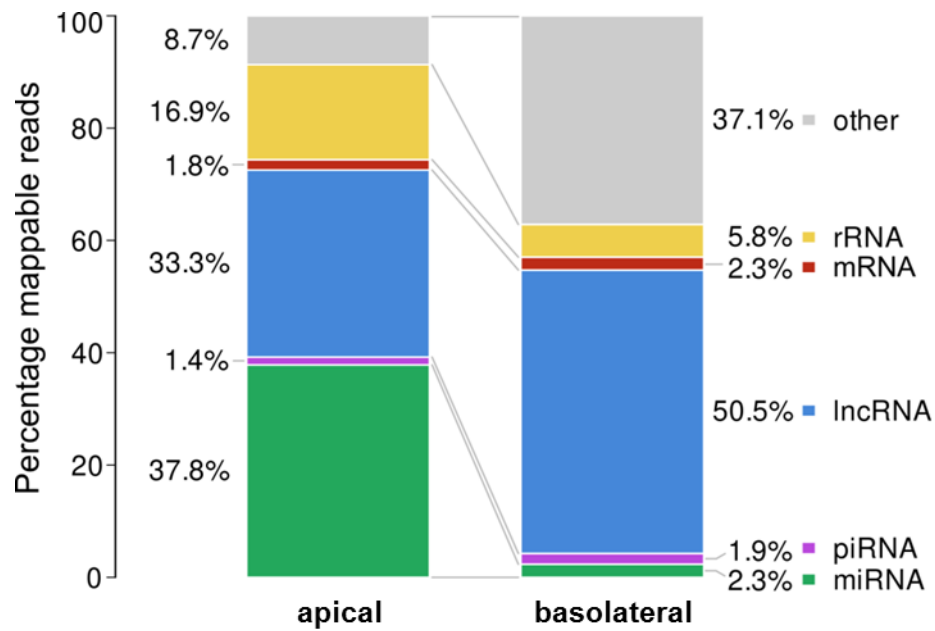
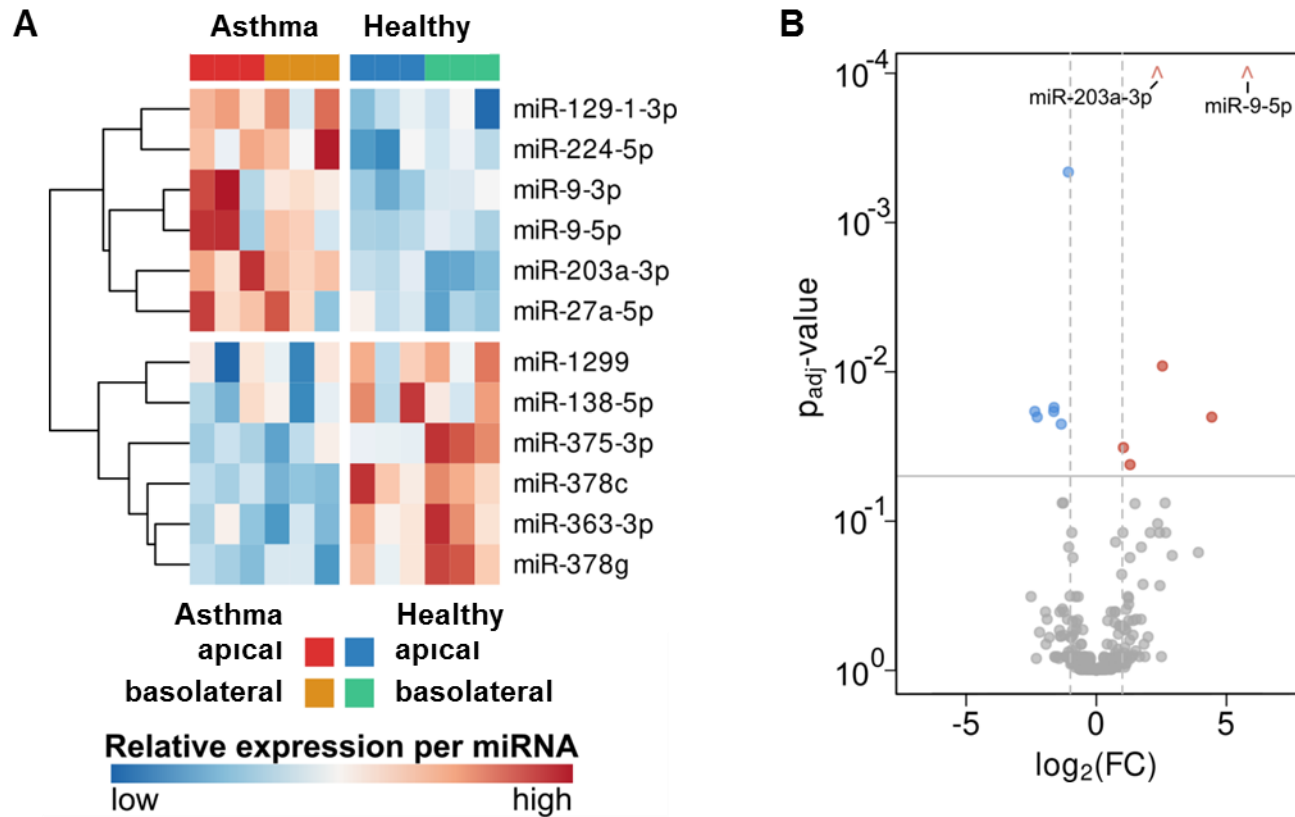


## Supplementary Figure S1



**Supplementary Figure S1.** Comparison of EV total RNA composition between basolateral and apical compartments regardless of disease expression in percentage of reads mapped to indicated RNA species. EV—extracellular vesicle; rRNA—ribosomal RNA; mRNA—messenger RNA; lncRNAs—long-non-coding RNAs; piRNA—PIWI-associated RNAs; miRNA—microRNA.

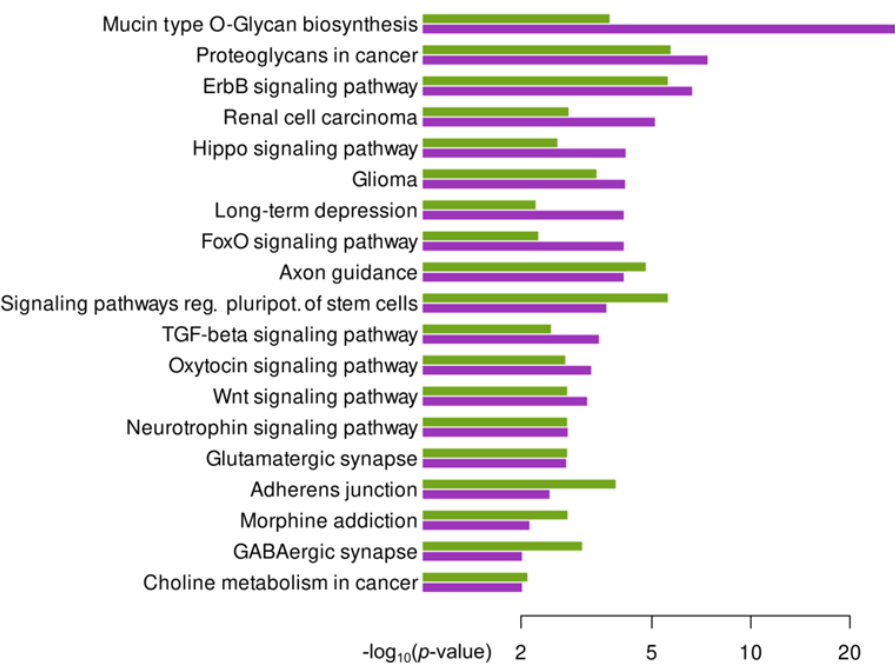
## Supplementary Figure S2



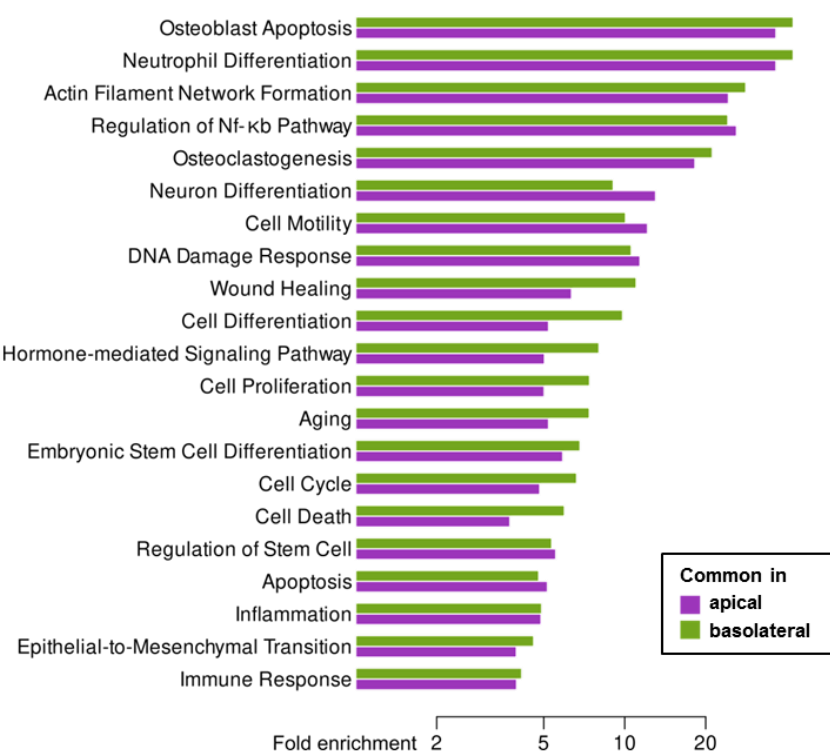
**Supplementary Figure S2.** Differential miRNA expression analysis per disease condition (asthma versus healthy) regardless of compartment (apical and basolateral). (A) Volcano plot and (B) heat map exhibiting the differentially expressed miRNAs of the asthma versus healthy comparison at  $p_{adj} < 0.05$  and  $FC \geq 2$ . miRNA—microRNA; FC—fold change.

# Supplementary Figure S3A & B

## A Enriched KEGG pathways: Asthma vs. Healthy

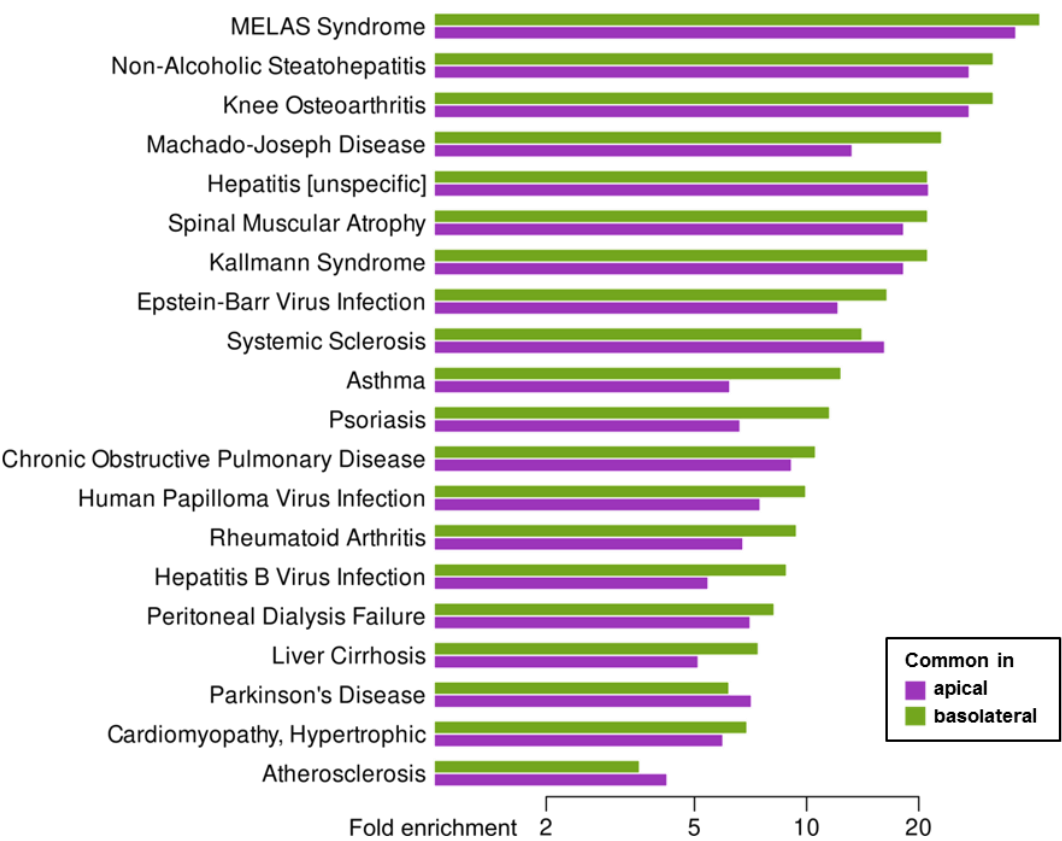


## B Enriched biological functions: Asthma vs. Healthy



Supplementary Figure S3C & D

C Enriched associated diseases: Asthma vs. Healthy



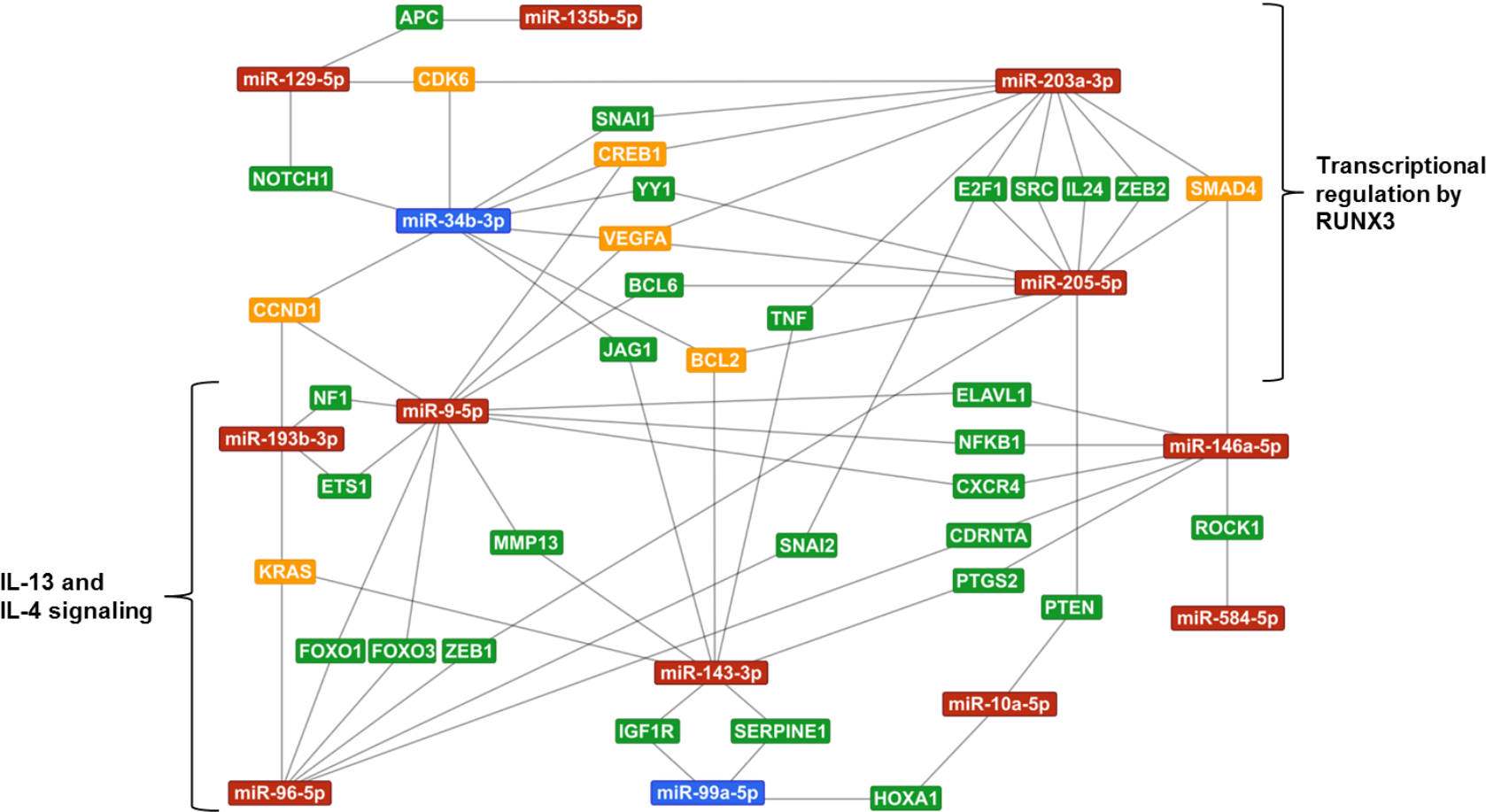
D Enriched target proteins: Asthma vs. Healthy



**Supplementary Figure S3.** Functional analysis of the differentially expressed miRNAs in the asthma versus healthy comparison in each apical and basolateral compartment. (A) KEGG pathway and (B) biological function analyses of differentially expressed vesicular miRNAs of asthma versus healthy in each apical and basolateral compartment, (C) enriched diseases, and (D) target proteins potentially regulated by the differentially expressed miRNAs. miRNA—microRNA.

Supplementary Figure S4A

A



**B**

