SUPPLEMENTAL MATERIAL

Figure S1. Genes related to differentially expressed miRNAs in BS-COPD with an FDR ≤ 0.01, compared to CS-COPD.
Figure S2. Dotplot depicting the activity of biological processes terms.
Figure S3. Enrichment map depicting the association between the enriched biological processes terms;
**Figure S4.** Upstream regulatory network of the differentially expressed miRNAs.

X2K was used to analyse the upstream regulatory network of genes of interest. Enriched transcription factors and kinases were ranked based on hypergeometric p value, and the inferred network was constructed and visualized.