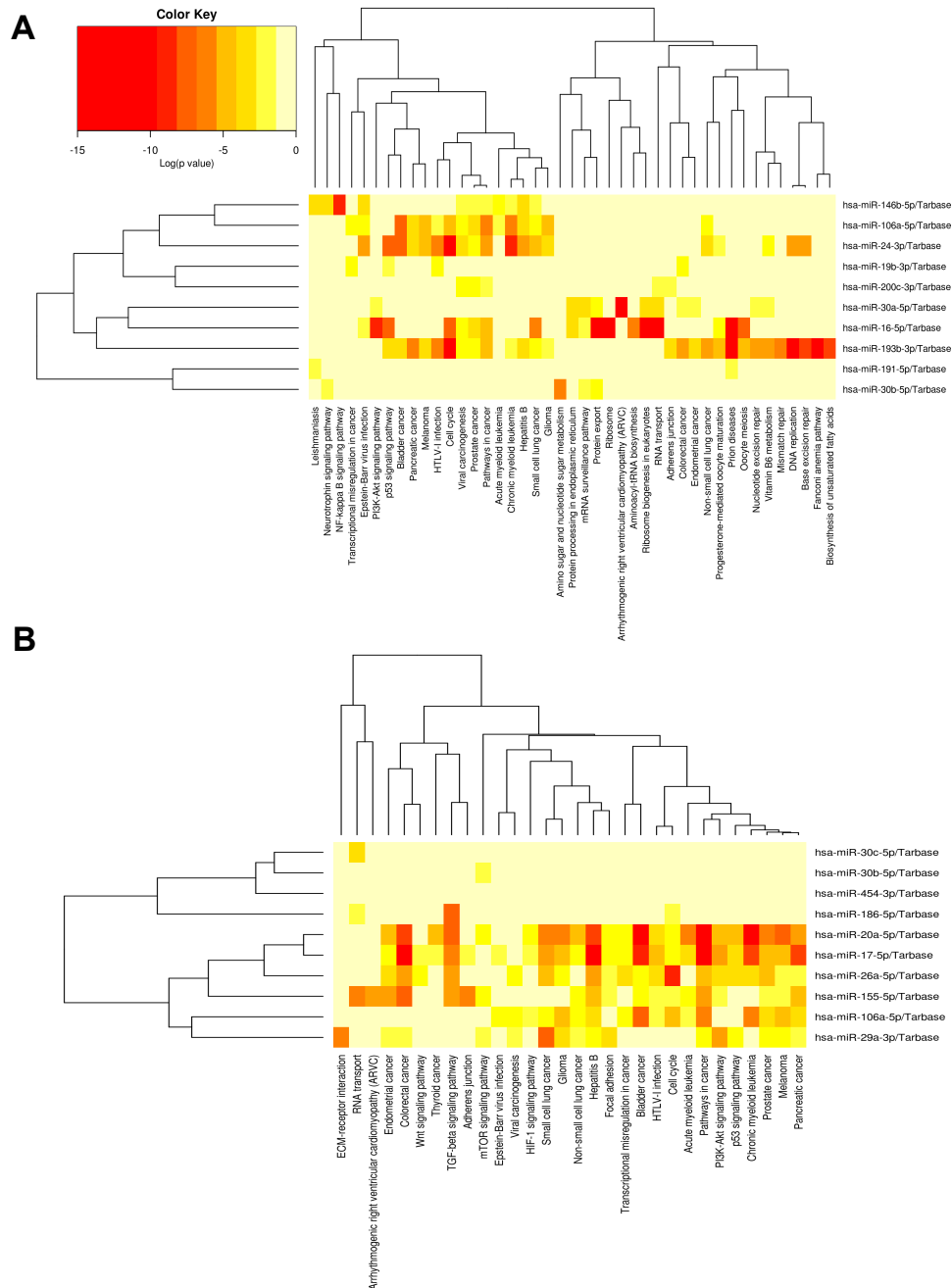


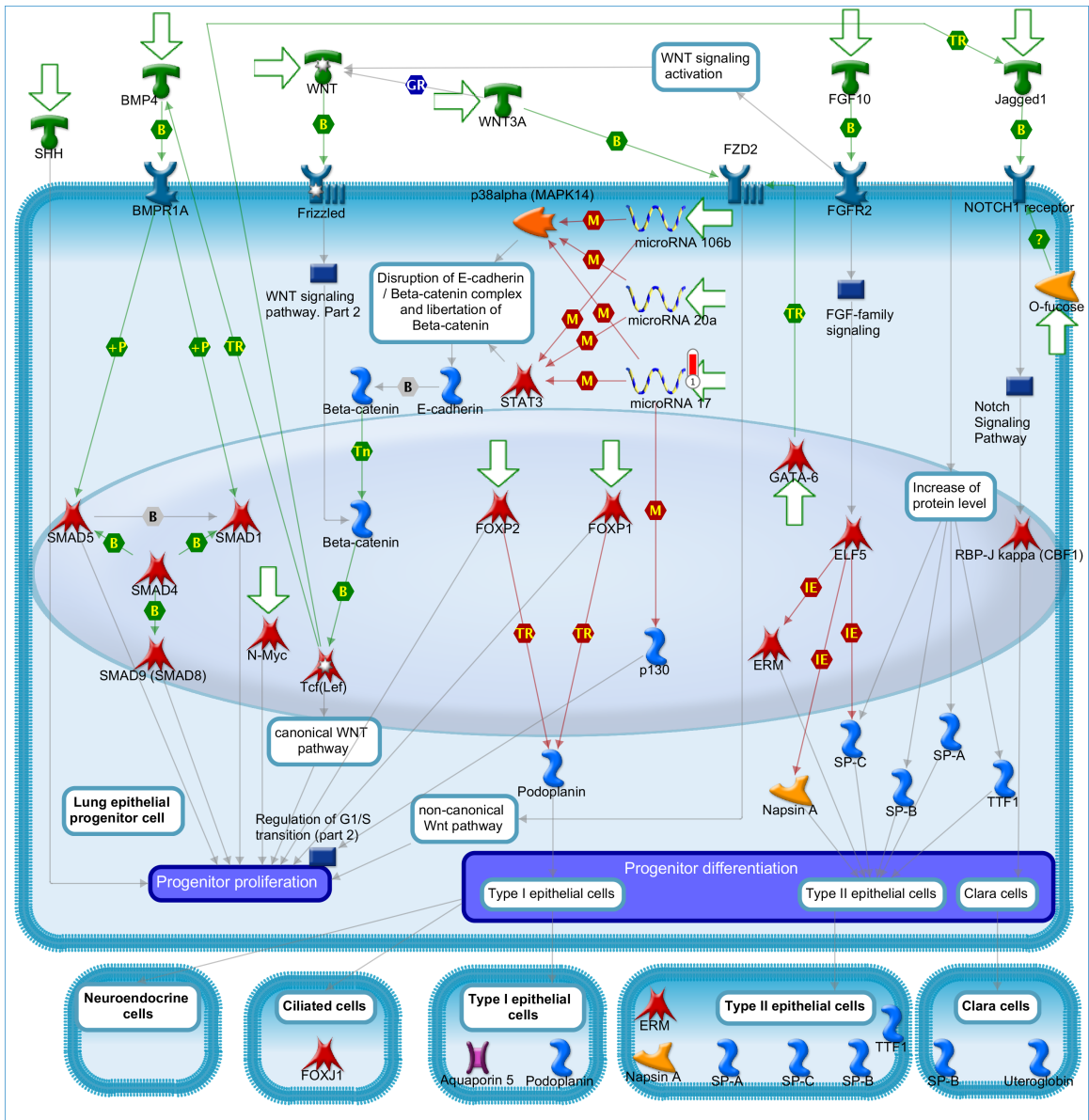
# SUPPLEMENTARY FIGURES

## Human milk miRNAs primarily originate from the mammary gland resulting in unique miRNA profiles of fractionated milk

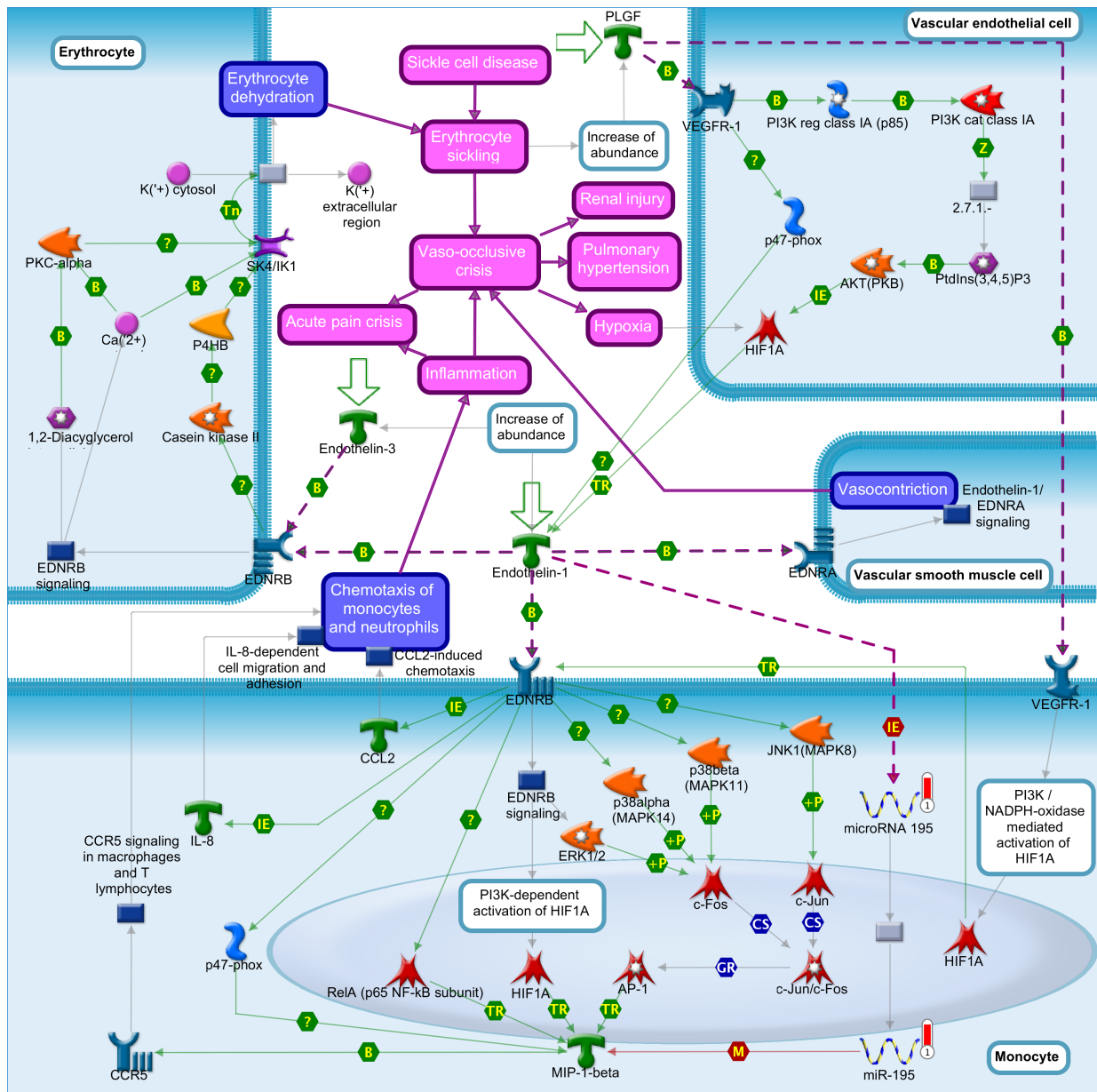
Mohammed Alsaweed, Ching Tat Lai, Peter E. Hartmann, Donna T. Geddes, Foteini Kakulas



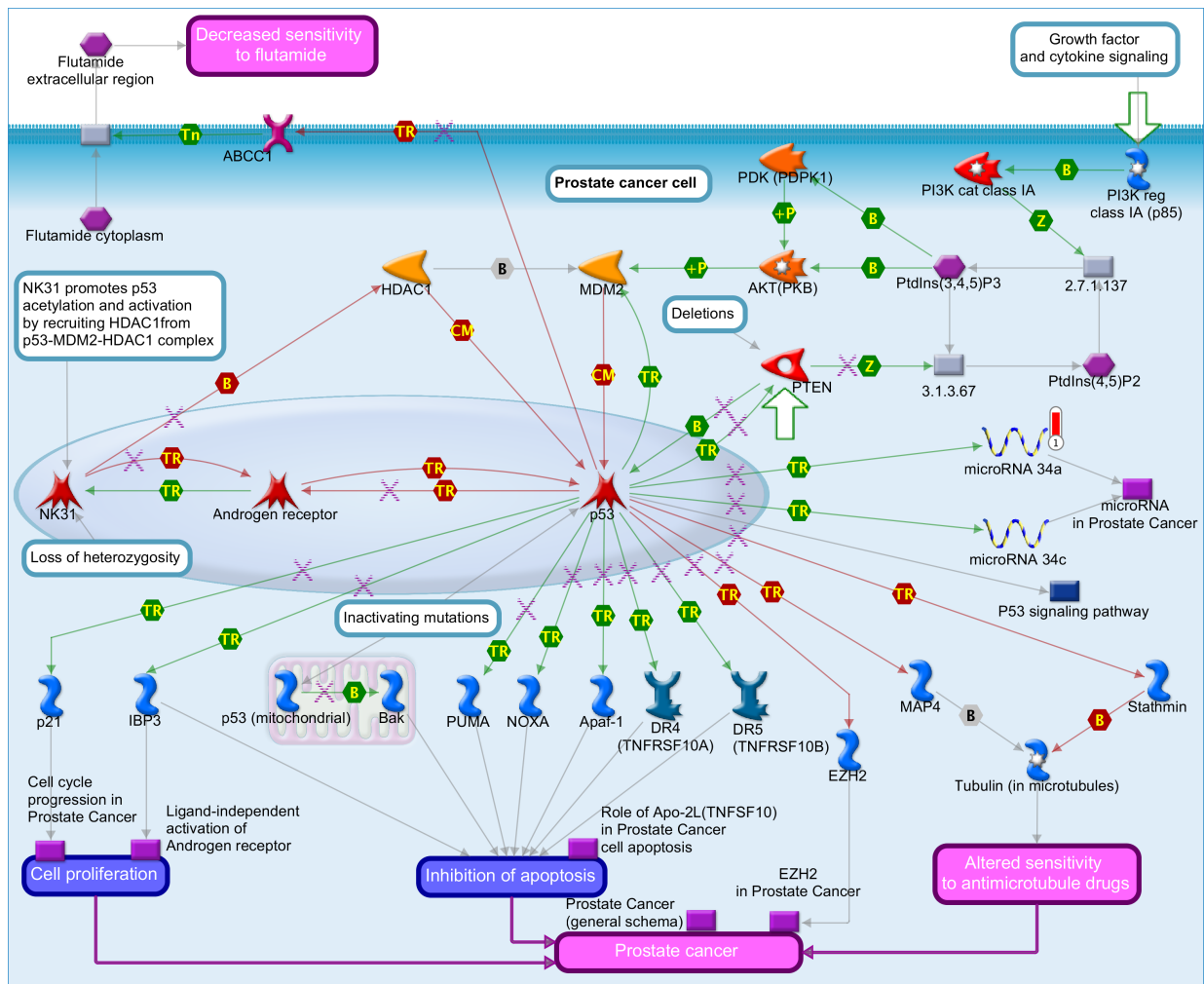
**Figure S1.** Heat maps showing the top 10 most highly expressed miRNAs in **(A)** human milk cells and lipids and **(B)** maternal PBMCs, and their contribution in different signalling and metabolic pathways annotated to mirPath tool<sup>56</sup>.



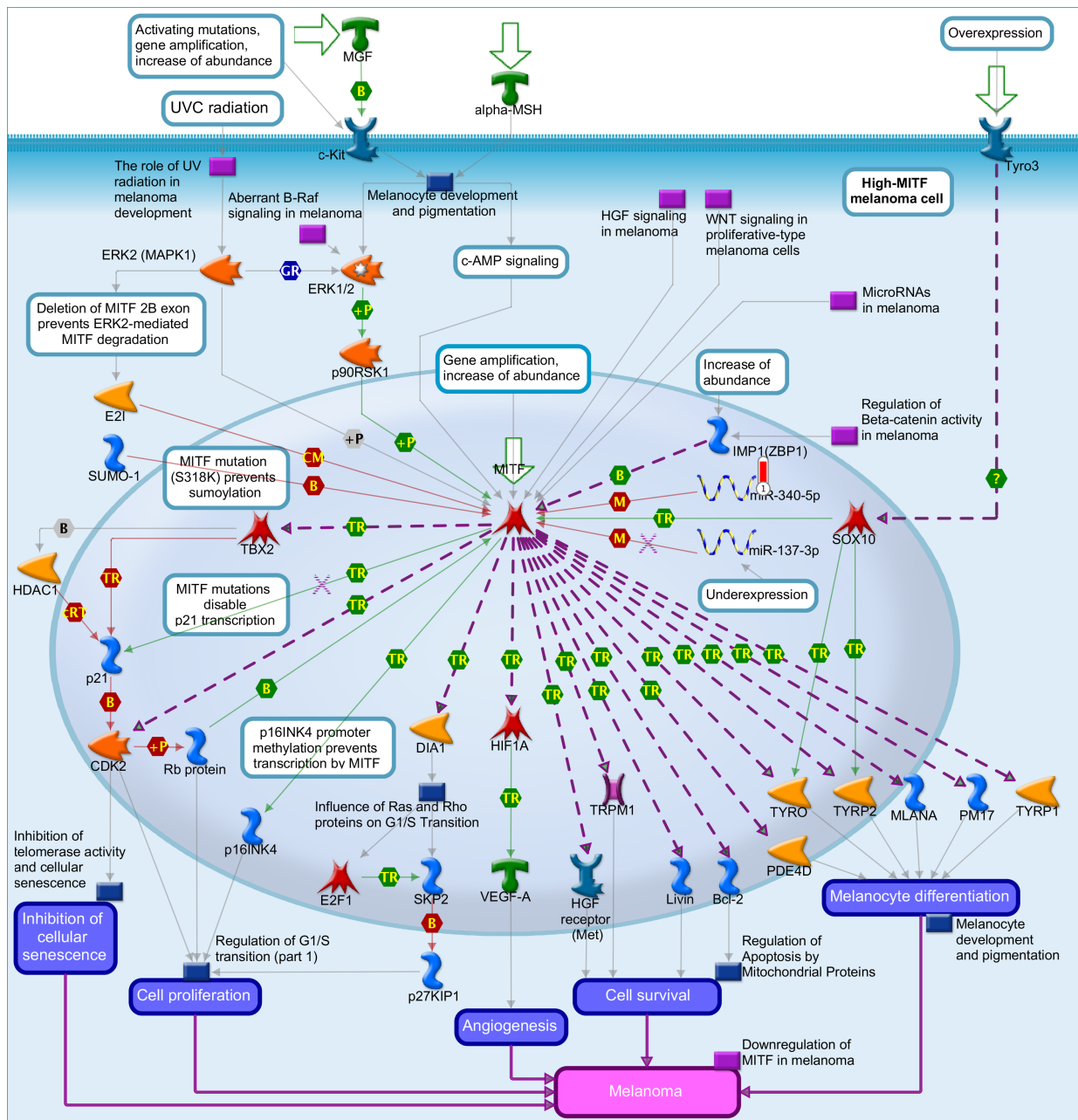
**Figure S2.** Interaction between and roles of reliable miRNAs that were differentially expressed in the regulation of lung epithelial progenitor cell differentiation (MetaCore pathway analysis).



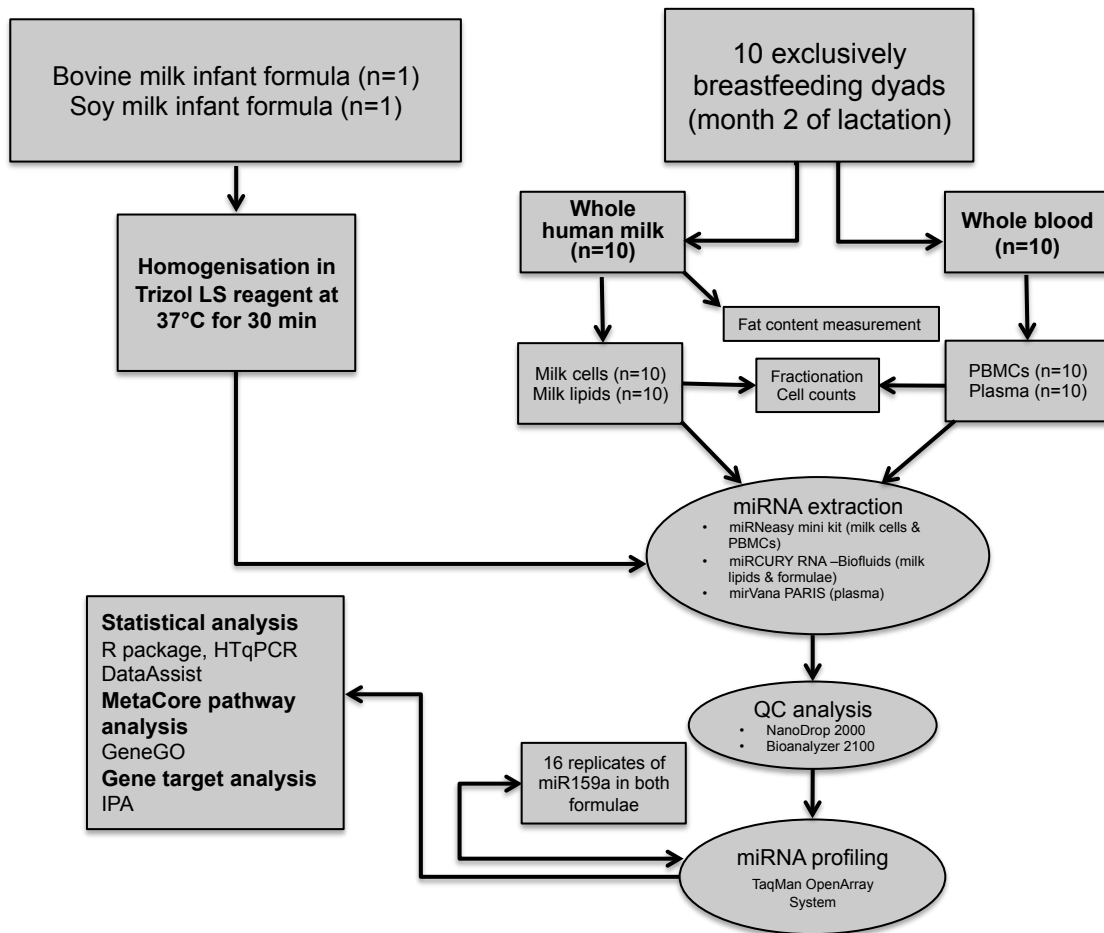
**Figure S3.** Interaction between and roles of reliable miRNAs that were differentially expressed in endothelin-1 pathway of inflammation and vasoconstriction in Sickle cell disease (MetaCore pathway analysis).



**Figure S4.** Interaction between and roles of reliable miRNAs that were differentially expressed in p53 signaling in prostate cancer (MetaCore pathway analysis).



**Figure S5.** Interaction between and roles of reliable miRNAs that were differentially expressed in the upregulation of MTF in melanoma (MetaCore pathway analysis).



**Figure S6.** Flowchart describing the main steps of the study.