

Supplemental Figures

Human milk extracellular vesicle miRNA expression and associations with maternal characteristics in a population-based cohort from the Faroe Islands

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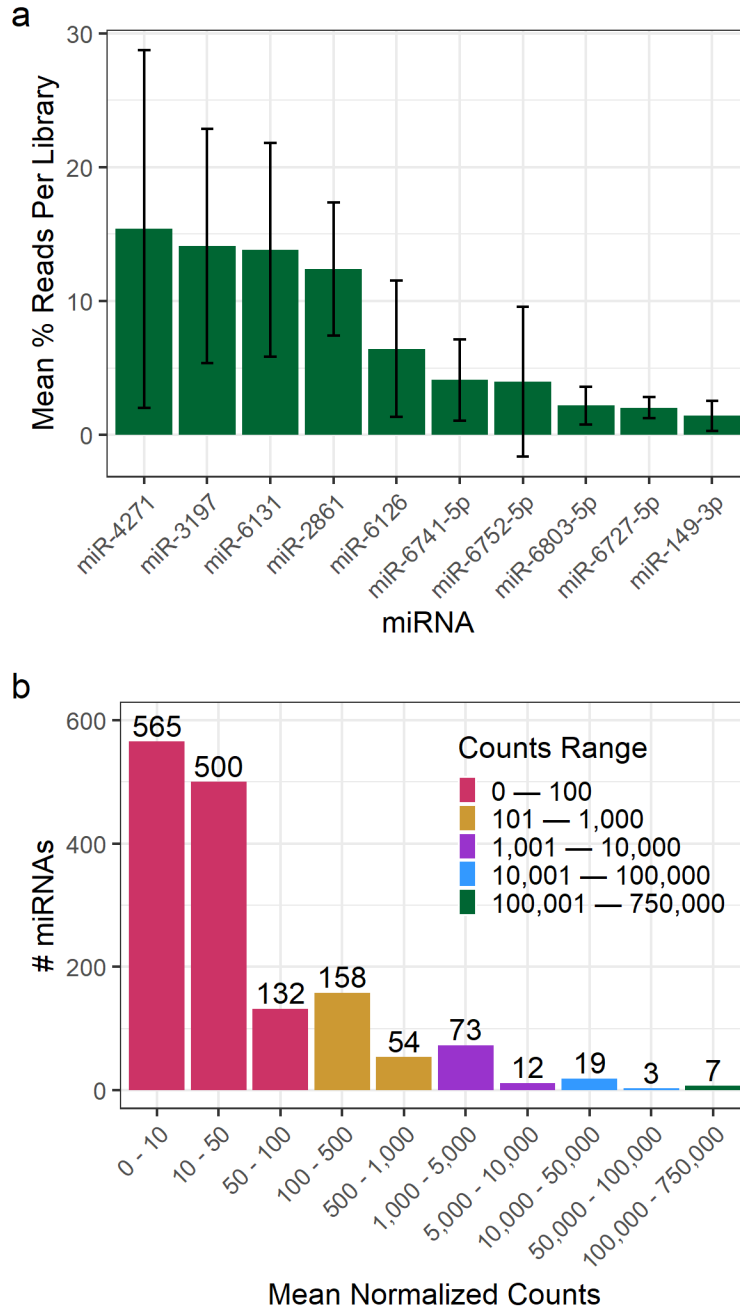
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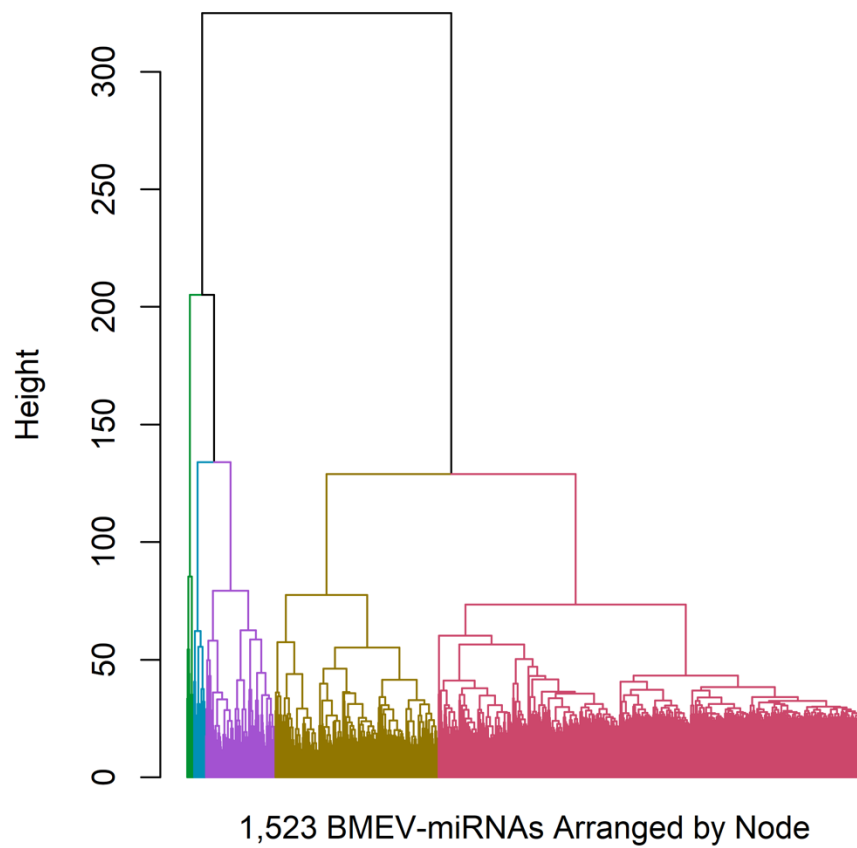
P&S Building Room 16-416

630 W 168th St.

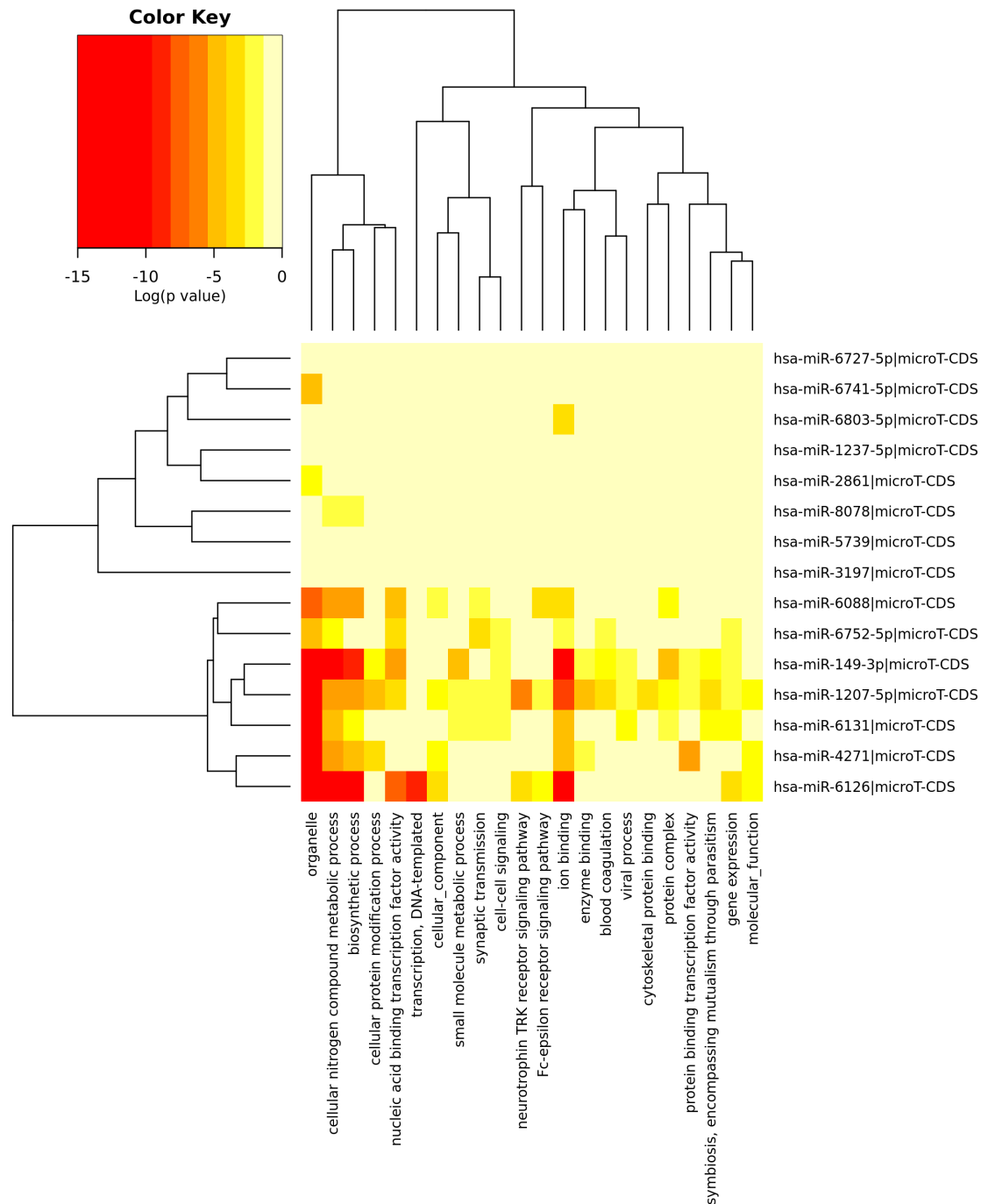
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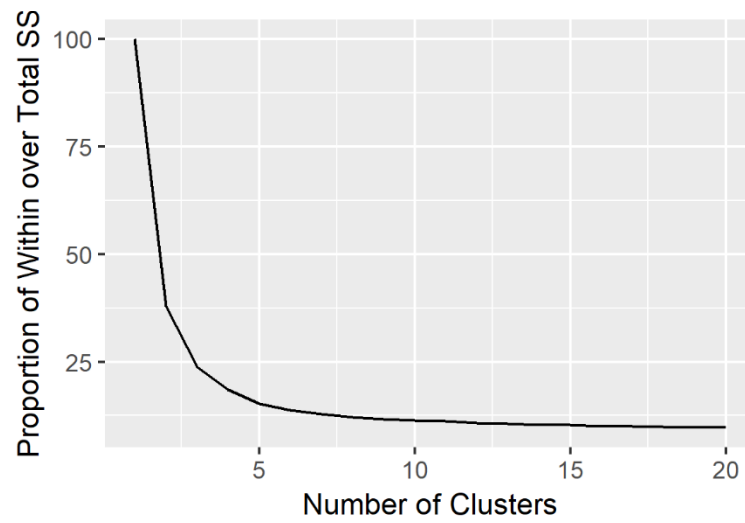
Supplemental Figure S1. Description of human milk extracellular miRNA (BMEV-miRNA) sequencing data (n=364). A) Average $\pm$ standard deviation of percentage reads per sequencing library for top 10 human milk EV-miRNAs. B) Histogram demonstrating the distribution of miRNAs with average expression (as normalized counts) ranging from zero to 750,000 counts per sample. Color indicates range bin: Pink: 0 – 100; Yellow: 101 – 1,000; Purple: 1,001 – 10,000; Blue: 10,001 – 100,000; Green 100,001 – 750,000 average counts.



Supplemental Figure S2. Hierarchical clustering of human milk EV-miRNAs. Hierarchical clustering was performed with Euclidean distance and the complete linkage method to identified optimal miRNA clusters in 1,523 EV-miRNAs from breast milk. miRNAs are on the x-axis arranged by node and Euclidean distance is on the y-axis. Color of branches indicates cluster membership (Green: Cluster 1; Blue: Cluster 2; Purple: Cluster 3; Yellow: Cluster 4; Pink: Cluster 5).



Supplemental Figure S3. Heatmap of False Discovery Rate (FDR) corrected log(p-values) from significant Gene Ontology (GO) categories from miRNAs from cluster 1. Gradient indicates strength of significance. DIANA microT-CDS version 3 (<http://snf-515788.vm.oceanos.grnet.gr/>) was used to predict miRNA mRNA targets and to generate the figure.



Supplemental Figure S4. K-means clustering to identify the optimal number of miRNA clusters in 1,523 BMEV-miRNAs. The proportion of within variance in comparison to the total sum of squares (SS) as the number of miRNA clusters increases.