Excluded samples that had missing exposure or outcome data  
(n = 3)

Excluded non-mature oocytes

(n = 6)

**Supplemental Figure S1**: Flow-chart of exclusion criteria and analyses

**Supplemental Figure S2**: Correlation plot of Pearson’s correlation coefficient among all the metabolites examined. Asterisk denotes a significant correlation (p < 0.05)

KEGG analysis of top Hit EV-miRNAs:

hsa-miR-125b

hsa-miR-15b

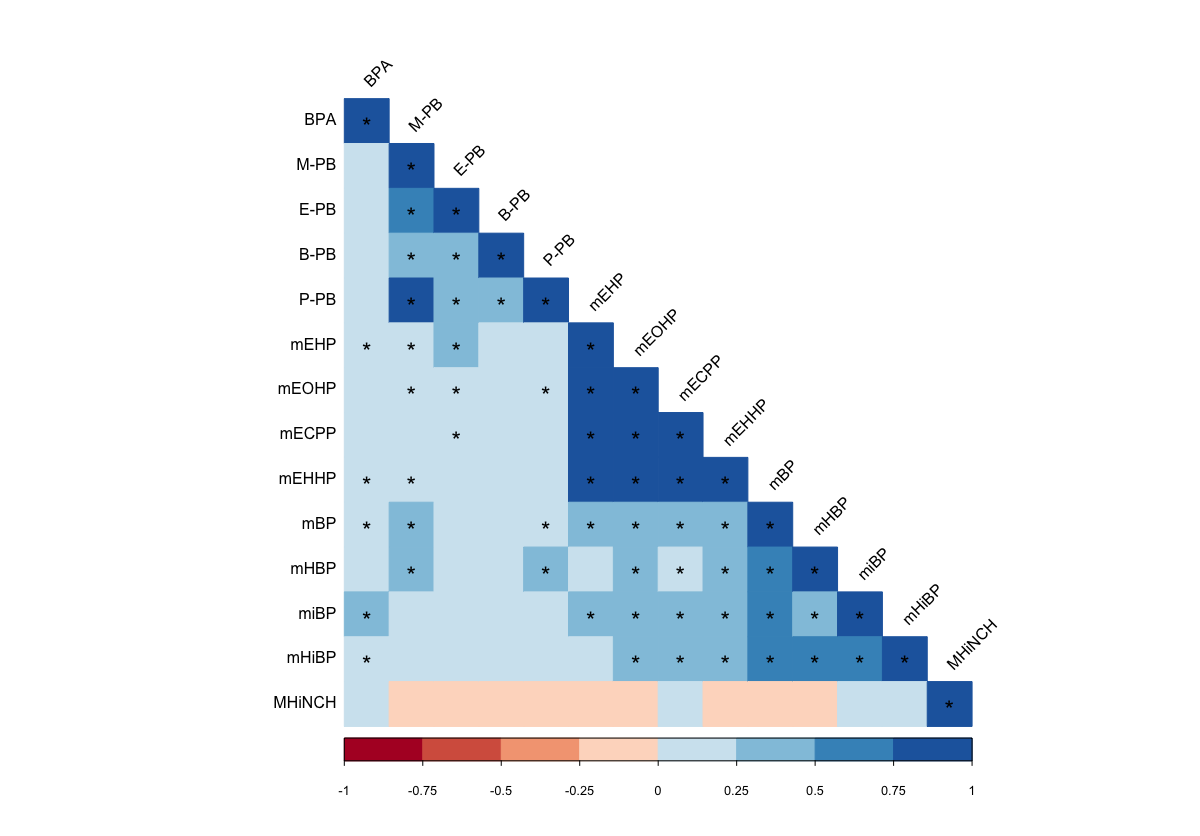
hsa-miR-106b

hsa-miR-374a

hsa-miR-24

*hsa-let-7c*

hsa-miR-19a



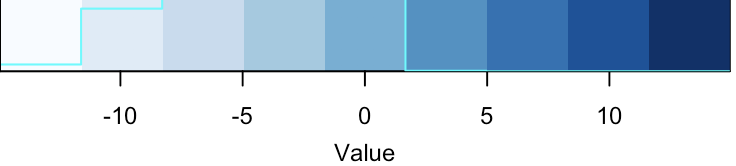
**Supplemental Figure S2**: Correlation plot of Pearson’s correlation coefficient among all the metabolites examined. Asterisk denotes a significant correlation (p < 0.05)



Batch 1

Batch 2

**Supplementary Figure S3:** Heatmap of normalized EV-miRNA expression data. Each row is an individual and each column is an EV-miRNA. Data is sorted by batch as shown on the left-hand side, green is batch 1 and yellow is batch 2. The lighter the blue, the more negative the normalized the expression and the darker the blue, the more positive the normalized expression



-10

-5

0

5

10

Value