**Supplementary Figures**

|  |  |
| --- | --- |
| **(a)** | **(b)** |

**Supplementary Figure S1.** **(a)** qPCR analysis shows that TRMT2A mRNA levels were significantly decreased after TRMT2A silencing (siTRMT2A condition) and significantly increased after ANG silencing (siANG condition), when compared to the control condition (siCTRL). **(b)** Western blotting analysis of TRMT2A protein expression. TRMT2A protein levels were significantly decreased in the siTRMT2A transfected cells and significantly increased after ANG knockdown (siANG condition), when compared to siCTRL, recapitulating the qPCR results. β-tubulin was used as the internal control. All data analysis was done using Student's unpaired t-test, p-value <0.05 (\*\*), p-value <0.001 (\*\*\*), p-value <0.0001 (\*\*\*\*), mean of N=3, error bars reflect standard deviation.

.

|  |
| --- |
| **(a)** |
| **(b)** |

**Supplementary Figure S2. (a) Summary network of GO enrichment analysis based on the BPs of down-regulated DGEs.** Each node represents a cluster of similar GO terms (colored by FDR adjusted *p-value*) and each edge depicts genes shared between the nodes. **(b) Bar plot showing the top 20 KEGG pathways arranged in order of p.adjust value.**  GO enrichment analysis of selected gene sets was performed using clusterProfiler (FDR <0.05) and enrichment maps of the obtained lists of GO terms were constructed using the EnrichmentMap plugin in Cytoscape (FDR <0.05 and edge similarity >0.45). Redundancy was overcome by clustering together and annotating similar terms based on the most frequent words (AutoAnnotate, clusterMaker2, and WordCloud plugins in Cytoscape; clustering algorithm: Markov cluster algorithm - MCL; labeling algorithm: adjacent words with a maximum 3 words per label and an adjacent word bonus of 8).

|  |
| --- |
| **(c)** |
| **(d)** |

**Supplementary Figure S2 (continuation). (c) Summary network of GO enrichment analysis based on the BPs of up-regulated DGEs.** Each node represents a cluster of similar GO terms (colored by FDR adjusted *p-value*) and each edge depicts genes shared between the nodes. **(d) Bar plot showing the 7 KEGG pathways arranged in order of p.adjust value.** GO enrichment analysis of selected gene sets was performed using clusterProfiler (FDR <0.05) and enrichment maps of the obtained lists of GO terms were constructed using the EnrichmentMap plugin in Cytoscape (FDR <0.05 and edge similarity >0.375). Redundancy was overcome by clustering together and annotating similar terms based on the most frequent words (AutoAnnotate, clusterMaker2, and WordCloud plugins in Cytoscape; clustering algorithm: Markov cluster algorithm - MCL; labeling algorithm: adjacent words with a maximum 3 words per label and an adjacent word bonus of 8).

|  |  |
| --- | --- |
| **(a)** | **(b)** |

**Supplementary Figure S3.** **TRMT2A knockdown induces a slightly decrease in the protein synthesis rate and no alterations in cell proliferation.** **(a)** Protein synthesis was accessed by flow cytometry through puromycin incorporation using the SUnSET method. A significant decrease (~20%) of the protein synthesis rate was observed after TRMT2A silencing.  **(b)** Cell proliferation was measured by BrdU incorporation assay. No alterations were observed in the BrDU incorporation after TRMT2A silencing. All data analysis was done using Student's unpaired t-test, p-value <0.05 (\*), mean of N=3, error bars reflect standard deviation.

.