

Description of Additional Supplementary Files

Supplementary Data 1. Dysregulated mRNAs in *Cyfp*^{85.1/+} mutants at night-time period.

RNA-Seq analysis in the whole fly brain from control and *Cyfp* heterozygous flies (n = 3 independent samples, respectively pool of 20 heads,) at ZT16 revealed a total of 1303 differentially dysregulated genes. Moderated t-test with Benjamini-Hochberg method for p-value adjustment (FDR). Genes with $FDR \leq 0.05$ and $|LFC| \geq 0.585$ were considered differentially expressed.

Supplementary Data 2. KEGG enrichment analysis of DEG in *Cyfp*^{85.1/+} flies at ZT16.

Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathway enrichment analysis for up- and down-regulated genes (DEG, differentially expressed genes) between control and *Cyfp* heterozygous flies. Only the pathway with Adj. p value ≤ 0.1 are presented.

Supplementary Data 3. Wakefulness-associated genes are dysregulated in *Cyfp*^{85.1/+}.

Upregulated and downregulated genes ($FDR \leq 0.05$, cut off $|LFC| \geq 0.585$) in *Cyfp*^{85.1/+} flies have been compared to the database for *Drosophila* wakefulness genes¹³.

Supplementary Data 4. Genes shared between the *Cyfp*^{85.1/+} and SREBP overexpression regulon.

Differentially dysregulated genes in *Cyfp* heterozygous flies at ZT16 have been compared with genes dysregulated upon SREBP overexpression^{71, 72, 73}.

Supplementary Data 5. Wakefulness-associated genes (WAG) regulated by SREBP overexpression.

Genes dysregulated upon SREBP overexpression have been compared with database for *Drosophila* wakefulness-associated genes¹³.

Supplementary Data 6. Genotypes and statistics used in this study.

Genotypes, number of independent samples, and descriptive statistics for each figure panel.