A day sleep promoting role of phototransduction in *Drosophila melanogaster*

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Abstract:

The daily sleep-wake cycle is a conserved behaviour defined by locomotion quiescence and

enhanced responsive threshold to sensory stimuli. Both the circadian clock and sleep-homeostasis

determine the daily sleep profile. Environmental light is a major sensory input and also regulates

circadian clock and the balance between sleep and wakefulness. In *Drosophila*, the cellular

mechanism and neural circuitry underlying light-mediated circadian synchronization are well-

established, yet the direct relationship between light/visual input and sleep remains unclear. To

address this knowledge gap, we measured sleep behaviour in *Drosophila* with mutations in genes

involved in phototransduction and downstream neural transmission. We observed consistent day

sleep fragmentation in flies with mutations in multiple phototransduction components. We also

found that mutation that led to hyperpolarised *Drosophila* photoreceptors resulted in shorter day

sleep. We found a severe reduction in locomotor speed in several visual mutants during normal

waking time preventing assessment of their sleep-linked immobility. Taken together, our rigorous

quantification of sleep in phototransduction genetic mutants reveals the key role of visual input in

promoting sleep.

1. Introduction

Sleep is vital for good health. Disruptions to either sleep timing and/or amount has been linked to numerous metabolic and neurological diseases (see reviews, Hartmann and Kempf, 2023; Wulff et al., 2010). Across the animal kingdom, sleep is defined by behavioural quiescence and increased arousal threshold to environmental stimuli such as light or mechanic vibrations. Arousal threshold within a period of sleep varies in stages that are associated with specific electrophysiological signatures in electroencephalogram (EEG) and local field potentials (LFPs) in the brain (Lakhiani et al., 2023). With its versatile genetic toolkit and conserved behavioural and electrophysiological features of sleep (Jagannathan et al., 2024; Shafer and Keene, 2021), the fruit fly *Drosophila melanogaster* has been used for identifying the biological basis and the conserved function of sleep. In parallel to murine investigations, studies in *Drosophila* have demonstrated that neuronal redox status may form a cellular basis of sleep (Hartmann and Kempf, 2023) and sleep stages play roles in synaptic scaling that is important for learning and memory (Dissel et al., 2015; Gilestro et al., 2009; Tainton-Heap et al., 2021; Yap et al., 2017). Recent investigations in *Drosophila* have also shown that sleep is required for effective maintenance of the immune system, gut microbiome, and waste clearance (Alphen et al., 2021; Vaccaro et al., 2020; Vincent et al., 2022).

Daily sleep onset and duration are regulated by two intrinsic mechanisms: the circadian clock and sleep homeostasis. The circadian clock defines the baseline sleep-wake level across 24 hours, whereas sleep homeostasis maintains the overall level of sleep amount. In *Drosophila*, the neural circuits that generate circadian rhythm are composed of 242 clock neurons (Reinhard et al., 2024) that express the core molecular clock mechanism. Whereas the homeostatic control of sleep is distributed across the following neural domains: Pars Intercerebralis (PI), Mushroom Body (MB), Fan-Shaped Body (FSB) and Ellipsoid Body (EB) (Jones et al., 2025; Shafer and Keene, 2021). The circadian clock and sleep homeostasis are likely coordinated, as clock neurons modulate the FSB-mediated sleep homeostat (Hsu et al., 2025).

Light is a prominent environmental stimulus that regulates both circadian clock and sleep homeostasis to maintain an animal's temporal niche and sufficient sleep. The synchronisation between environmental light regime and the neural activity of clock neurons is called circadian photoentrainment. Visual inputs are part of photoentrainment in *Drosophila*. The visual system in the fly is composed of peripheral light sensing neurons: photoreceptors in compound eyes, HB-eyelet and ocelli. Photoreceptors in the eye are subdivided into outer achromatic R1-R6 and inner chromatic R7/R8 neurons, both of which sends their synaptic outputs to downstream visual processing brain areas called the optic lobes and ventrolateral neuropils (Nériec and Desplan, 2016).

Crucially, light signals are converted into depolarisation of the neuronal membrane via a cellular

process called phototransduction in the photoreceptors of the compound eye and HB-eyelet.

Phototransduction requires the light-sensing GPCR Rhodopsins 1-6 (Rh1-6) and their downstream

signal cascades that ultimately activate cation channels depolarising the photoreceptors (Hardie,

2012). Activation of photoreceptors results in synaptic release of histamine or acetylcholine to

communicate with clock neurons either directly or indirectly via a neural network in the optic lobes

(Alejevski et al., 2019; Ogueta et al., 2020, 2018; Rieger et al., 2003; Schlichting et al., 2016; Tang et

al., 2022; Xiao et al., 2023). Apart from via the visual system, *Drosophila* circadian clocks are

entrained by cell autonomous light-sensing mechanisms mediated by *cryptochrome* (*cry*), *quasimodo*

(*qsm*) or *Rhodopsin 7* (*Rh7*) (Chen et al., 2011; Ni et al., 2017; Peschel et al., 2009).

Light can directly regulate sleep by either promoting or supressing sleep via different neural

pathways in the murine system (Altimus et al., 2008; Pilorz et al., 2016). As a crepuscular species,

Drosophila sleep both in the day (light) and in the night (darkness). While current evidence indicates

that distinct neurogenetic networks may control day and night sleep (Chen et al., 2019; Damulewicz

et al., 2020; Hsu et al., 2025; Ishimoto et al., 2012; Lamaze et al., 2018; Mazzotta et al., 2020;

Sengupta et al., 2019), the mechanism underlying light-mediated regulation of the *Drosophila* sleep

homeostat is far from clear. Previous studies indicate that midday sleep (i.e., siesta during six hours

of the midday) can be enhanced by high-intensity light via the HB-eyelet-mediated cholinergic

pathway (Rieger et al., 2007; Schlichting et al., 2019). Separate studies however, have shown

contradictory findings for the role of compound eye photoreceptors in sleep regulation: synaptic

inhibition in these photoreceptors promote sleep (Damulewicz et al., 2020), yet the optogenetic

activation of the same photoreceptors in another investigation did not result in sleep suppression

(Kirszenblat et al., 2019). Moreover, artificial activation of the direct downstream target of eye

photoreceptors, lamina monopolar neuron 2 (L2 LMC), resulted in drastic sleep loss (Muraro and

Ceriani, 2015). This finding contradicts the increased sleep observed in flies with reduced histamine

(Oh et al., 2013), which is the main neurotransmitters released from photoreceptors to inhibit L2

LMC neurons (Pantazis et al., 2008). Furthermore, visual experience in light was recently found to

promote night sleep in *Drosophila* (Kirszenblat et al., 2019), suggesting light and/or vision *per se*

serve as sleep homeostat drivers, similar to in vertebrates (Horne and Walmsley, 1976; Korf et al.,

2017; Miyamoto et al., 2003).

A recent systematic study of mutants with defects in various light input pathways indicate that only

Rh7 is required for shade sleep preference in the day, but the study did not investigate the baseline

sleep level in these mutants (Meyerhof et al., 2024). We therefore investigated the role of light input

pathways in *Drosophila* sleep by focusing on the role of the visual system. Using the conventional

infrared beam-based sleep assay (Chen et al., 2019; Chiu et al., 2010), we surveyed baseline sleep

profiles in three groups of flies: strains with mutations in genes involved in (i) phototransduction

and (ii) downstream histaminergic neurotransmission (Hardie, 2012), and (iii) those with artificial

inhibition of photoreceptors. We also performed electroretinogram (ERG) examine the

phototransduction/neurotransmission defects in these above mutants. By carefully examining sleep

and ERG parameters, we identified a novel role of visual phototransduction in driving sleep.

2. Materials and methods

2.1 Fly husbandry

Drosophila strains were kept in standard fly food (glucose 6.93% w/v, agar 0.5% w/v, cornmeal, 6.3%

w/v, yeast, 4.38% w/v, propionic acid, 0.26% v/v, 0.2% v/v nipagin) at 25°C 12-hour light dark cycle.

Long-term fly stocks are kept in the same food and light regime at 18°C. The Canton S and Oregon R

wildtype strains were obtained from the Kyriacou Lab (University of Leicester, UK), while w^{iso31} (i.e.

iso) control was obtained from the Jepson lab (University College London, UK). The following visual

mutants, Gal4 and UAS transgenic flies were ordered from Bloomington Drosophila Stock Center

(Indiana University, USA) (stock number): trp^1 (5692); trp^{MB} (23636); $trpl^{302}$ (31433); $trpl^{MB}$ (29134);

$ninaE^8$ (2001); $ninaE^5$ (3531); $ninaE^{17}$ (5701); $norpA^{P24}$ (9048); hdc^{MB} (25260); hdc^{JK910} (64203); ort^1

(1133); ort^{attP} (84559); *Rh1-Gal4* (8691); *gmr-Gal4* (1104); *UAS-kir2* (6595); *UAS-TeTxLC* (28837);

UAS-myr-mRFP (7118). All Gal4 and UAS transgenic flies were brought into the w^{iso31} background via

five generation outcrossing following *[w+]* eye colour marker cassette. For *Rh1-Gal4* outcrossing, we

generated *UAS-myr-mRFP/+; Rh1-Gal4/+* flies which expresses RFP in the eyes, we then crossed this

line to w^{iso31} and used this RFP signal as a visible marker under a fluorescent stereoscope to ensure

outcrossing offspring still contained both *UAS-myr-mRFP* and *Rh1-Gal4* transgenes. The final stock

was then established by balancer crossing with w^{iso31C};*Sco/CyO; MKRS/TM6B* and then w^{iso31};*+/+;*

MKRS/TM6B for removing *UAS-myr-mRFP*. Among other lines, hdc^{MB}, ort^{attP}, trp^{MB}, and $trpl^{MB}$

contained either GFP or RFP visible markers, but the rest are classic missense mutations, making

outcrossing without laborious PCR-based sequencing difficult. For simplicity, sleep experiments for

all non-Gal4/UAS mutants were conducted without outcrossing and the only consistent results

among mutant alleles of each gene were interpreted. Following the unexpected but consistent night

sleep among *hdc* mutants, we decided to minimise the genetic background difference among these

lines: since the precise genetic lesion of hdc^{JK910} on the *hdc* loci at the 2nd chromosome is unknown,

only the 1st and 3rd chromosomes of hdc^{JK910} were replaced with those from w^{iso31} stock via the

following successive crossings with balancer lines (gifts from Jepson lab):

P: w^{iso31}/w^{iso31}; *Sco/CyO; MKRS/TM6B*   x   *+/Y;* hdc^{JK910}/hdc^{JK910}; *+/+*

F1: w^{iso31}/w^{iso31}; Sco/CyO; $+^{iso31}/+^{iso31}$.   x w^{iso31}/Y; hdc^{JK910}/CyO; TM6B/+

F2: w^{iso31}/w^{iso31}; hdc^{JK910}/CyO; TM6B/$+^{iso31}$.   x w^{iso31}/Y; hdc^{JK910}/CyO; TM6B/$+^{iso31}$

F3: w^{iso31}/w^{iso31}; hdc^{JK910}/CyO; $+^{iso31}/+^{iso31}$.   x w^{iso31}/Y; hdc^{JK910}/CyO; $+^{iso31}/+^{iso31}$

Separately, hdc^{MB} flies were brought into the w^{iso31} background via five generation outcrossing

following the GFP eye marker.

2.2 Sleep recording and analysis

Drosophila sleep, particularly day time sleep, is highly dependent on by sex, mating and nutrient

status (Dove et al., 2017; Duhart et al., 2023; Isaac et al., 2009; Wu et al., 2018). Typically, mated

females can sleep for as little as 150-200 minutes compared to the 300-400 minutes shown by males

(out of the total 720 minutes of day time). To capture both sleep increase and decrease upon genetic

manipulation, we focused our investigation on virgin male flies. Moreover, by focusing on males, our

data is comparable to the previous decades of photoentrainment investigations of *Drosophila*

circadian research that has been conducted mainly on male visual mutants (e.g. Rieger et al., 2003

and see review in Mazzotta et al., 2020). As such, we would caution against extending our findings to

those of sleep in female flies.

Prior to the sleep experiment, *Drosophila* strains or crossings were reared in food with a richer

recipe (wheat germ 1% w/v, soy 0.8% w/v, glucose/sucrose 3.3%/1.5% w/v, treacle 3% v/v, agar 1%

w/v, cornmeal 1.5% w/v, yeast 3.5% w/v, propionic acid 0.5% v/v, nipagin 0.1% v/v), so as to keep

the rearing conditions consistent with previous experimental conditions (Chen et al., 2019, 2011;

Lamaze et al., 2018). We also note that in general, all strains of flies are less motile or less

reproductively successful in standard fly food (as described above in 2.1). Sleep recordings were

performed as described in (Chen et al., 2019). Three to four day-old virgin adult males were

transferred to typical behaviour tubes containing food (2% w/v agar and 4% w/v sucrose at one end

and cotton wool at the other), and housed in typical Drosophila Activity Monitor (DAM, Trikinetics

Inc.) for 3 days of 12hours light-dark cycle at 25°C in a temperature and light controlled incubator

(MIR-254-PE, PHCbi). The lighting source was a day light fluorescent lamp (FL15D, 6500K) with

intensity between 1.2 and 6.7 w/m^2 depending on the distance to the lamp. With conservative

conversion with luminance surface area between 0.25 to 1 m^2, our light intensity was approximately

equal to 402 to 1608 lux. The locomotion of each fly was recorded as number of infrared beam

crosses per minute. The locomotion data for day 3 was transferred to a previously customised Excel

Calculator (Chen et al., 2019) to calculate all sleep episodes (defined as any period of immobility ≥ 5

minutes) along 24 hours. Additionally, the following parameters were calculated for each fly: **overall**

sleep profile: minutes of sleep per 30 mins across 24 hours; **day sleep**: total minutes of sleep during

12 hours of day; **night sleep**: total minutes of sleep during 12 hours of night; **day average sleep bout**

length: day sleep minutes divided by total number of sleep bout during 12 hours of day; **night**

average sleep bout length: night sleep minutes divided by total number of sleep bout during 12

hours of night; **day waking activity**: number of beam crosses divided by total wake minutes during

12 hours of day**; night waking activity**: number of beam crosses divided by total wake minutes

during 12 hours of night.

2.3 Electroretinogram (ERG)

Three-to-five day-old adult virgin male flies were inserted into a p1000 plastic pipette tip, so that its

head protruded from the narrow ending. The head was fixed using melted honey wax applied

between the thorax and head without blocking the mouthpart and eyes. The pipette tip mounted fly

was kept in the dark for 20 mins and then transferred into the ERG recording rig. Glass electrodes

(Borosilicate) with resistance of ~5 MO and filled with 3 M KCl were inserted into the compound eye

(recording) and head (reference). Each fly was left in the dark for 3 minutes before being exposed to

four light intensities: 0.004, 0.02, 0.1 and 0.5 w/m^2 at 540nm LED green light source (M530L4-C1,

ThorLab). These intensities fall within the liner range of receptor potential response. We stimulated

with 1000 ms exposure to each light intensity and repeated the procedure two further times to

obtain an average value of three presentations at each light intensity for each fly. The potential

difference between the electrodes was amplified 10x, and acquired by Neuroprobe Amplifier model

1600 and 8-channel data acquisition interface DA-8 (A-M systems) using the SciWorks Data

Acquisition & Analysis Suite.

2.4 Data display and statistics

The `ggplot2` package (3.5.2) in R (4.4.2) used to display sleep and ERG data. X-Y plots were used to

display overall sleep profiles for each compared genotype. Boxplots with average values of each

individual were used to display sleep parameters data. We calculated the average voltage change of

on transient, receptor potential and off transient in the ERG profiles of each replicate for each fly

(Figure 1H). The value for each fly was then plotted against light intensity on logarithmic scales by

`ggplot2`. Considering the variability in sleep data (Chen et al., 2019; Lamaze et al., 2018), statistical

significance was identified by Kruskal-Wallis rank sum test for non-parametric multiple comparison

(`kruskal.test`). Pairwise Wilcoxon rank sum exact test with multiple comparison Benjamini-

Hochberg correction (`pairwise.wilcox.test`) was used to specifically identify difference

between pairwise genotypes. Unlike sleep data, ERG voltage changes data were pooled across four

intensities when identifying genotypical difference via Pairwise Wilcoxon rank sum exact test.

Significance level is set at adj.p<0.05. Effect size *r* is calculated by `wilcox_effsize` with magnitude

categories: small; moderate and large assigned. Importantly, while Benjamini-Hochberg correction is

required to correct the p-values, the effect size *r* does not change by multiple comparison, as it is

defined by $Z/\sqrt{n}$. All statistic comparisons, p values, effect size and sample size are listed in Table1 to

Table 6 for the corresponding Figure 1 to Figure 5.

3. Result

3.1 Defects in phototransduction genes caused short day sleep bout

To verify the role of visual phototransduction genes in sleep regulation, we tested eight mutant fly

strains. These strains are mutants of the following four genes: *Rhodopsin 1/ninaE*, *Phospholipase*

C/norpA, and the two cation channels *trp* and t*rpl*. These included both classic missense mutations,

and when available, more recently characterised mutations using P-element insertion. To analyse

the details of sleep-wake profiles under a typical day of 12 hours light-12 hours dark, we examined

three conventional parameters for both day and night period: total sleep, average sleep bout length

and waking activity.

3.1.1 *ninaE*

Upon exposure to light, 11-cis 3-hydroxy-retinal, the chromophore in the Rhodopsin protein

undergoes photoisomerization, transforming Rhodopsin to Metarhodopsin which then triggers a

downstream GPCR signal cascade. Rhodopsin 1/ninaE protein is the main light-sensing GPCR in the

outer photoreceptors R1-R6 of the *Drosophila* compound eye. Reduction or loss of ninaE abolishes

or reduces photoisomerization and therefore blocks the light-induced photoreceptor potential and

transients that are typically measured for R1-R6 in ERG (Hardie, 2012).

Many visual tasks, such as navigation, phototaxis, optomotor and escape, require R1-R6 activity. We

therefore first tested the sleep profile of the class null allele *ninaE[17]* (O'Tousa et al., 1985). During

the day, *ninaE[17]* mutants show a lower midday sleep peak in the sleep profile (Figure 1Ai) but the

amount of total sleep is comparable to the white eye control, w^{iso31} (here after *iso*, Figure 1Di).

However, we found that the average sleep bout length in *ninaE[17]* is shorter than the control,

indicating sleep fragmentation (Figure 1Bi). During the night, we observed increased sleep amount

(Figure 1Gi) while the average sleep bout length is similar to the control (Figure 1Ei). Since sleep

measurements in *Drosophila* depend on locomotion, an increase in sleep can be falsely claimed due

to defects in locomotion. Therefore, "waking activity", i.e., locomotor activity per waking minutes,

was designed as a conventional measure to detangle such a compound scenario (Andretic and Shaw,

2005; Harbison and Sehgal, 2008). We applied this measurement and found that waking activity is

similar between *ninaE[17]* and the control in both day and night (Figure 1Ci,Fi).

ninaE[17] flies contain a secondary *ebony[1]* mutation that impacts sleep-wake cycles (Rossi et al., 2015;

Suh and Jackson, 2007). We therefore tested two other *ninaE* hypomorphs: *ninaE[5]* and *ninaE[8]*

(Scavarda et al., 1983). Both mutants show similar midday sleep peak reductions to those seen in

ninaE[17] flies (Figure 1Aii-iii). This observation is consistent with the significant reduced day sleep

observed in either mutant when compared to the control (Figure 1Dii-iii). Similarly, both mutants

also show shorter average sleep bout length in the day (Figure 1Bii-iii). Intriguingly, the loss of sleep

in the two *ninaE* hypomorphs was observed despite of the loss of waking activity in the day (Figure

1Cii-iii). During the night, *ninaE* hypomorphs both show increased sleep (Figure 1Gii-iii), but only

ninaE^8 mutant shows significant increase of the average sleep bout length compared to control flies

(Figure 1Eii-iii). However, mutants severely reduce their waking activity (Figure 1Fii-iii with effect size

r between 0.67 and 0.82, Table 1). Therefore, the increase in night sleep observed here cannot be

certain, and may simply reflect the loss of locomotor activity. To confirm *ninaE* mutants harbour

phototransduction defects, we measured light-evoked receptor potentials through

Electroretinograms (ERG, Figure 1H). Consistent with previous reports, *ninaE*^{17} and *ninaE*^{8} exhibit

reduced light induction of receptor potential, on and off transients (Figure 1I-J), whereas *ninaE*^{5}

retains certain function (see normal receptor potential and off-transient in *ninaE*^{5}, Figure 1J). Taken

together, our data indicates that the reduction, or loss of, *Drosophila* Rhodopsin 1 (ninaE) protein

results in the reduction of day sleep bout length, and that phototransduction is required to drive day

sleep pressure. However, recent studies show support for a non-visual function of ninaE (Zanini et

al., 2018). To verify if ninaE protein alone or the phototransduction in general regulates day sleep

bout length, we further examined the sleep-regulatory roles for three other key proteins for

phototransduction.

3.1.2 *norpA*

Metarhodopsin triggers Gqα activation and enzymatic reaction of Phospholipase C (PLC) that

produces secondary messengers. The norpA protein is the main PLC in the visual system, and the

classic mutant *norpA*^{p24} exhibits severe visual defects (Gao et al., 2008). The sleep profile of *norpA*^{p24}

shows decline of day sleep from the midday and a secondary dip at midnight compared to the

control (Figure 2A). There is also a phase advance of night sleep in *norpA*^{p24} mutants as compared to

the controls. Such an advance was also noticeable in locomotor profile of another *norpA* allele in a

previous study (Ogueta et al., 2018). The changes in sleep profile coincides with the reduction in day

sleep (Figure 2D) and shorter bout length in both day and night (Figure 2B, 2E). Similar to *ninaE*^{5} and

ninaE^8, the *norpA*^{p24} mutant has low waking activity (Figure 2C, 2F, effect size 0.39/0.75, Table 2). We

also confirmed abnormal ERG profiles in *norpA*^{p24} (Figure 2H).

3.1.3 *trp and trpl*

Activation of the two ion channels, trp and trpl in the last step of phototransduction causes the

crucial cation influx resulting in depolarisation of the photoreceptor. We therefore examined the

sleep profile of four mutant lines, two P-element insertion mediated mutants: *trp*^{MB}, *trpl*^{MB} (Chen et

al., 2015) and two classic null mutants: trp^1, and $trpl^{302}$ (Cosens and Manning, 1969; Leung et al.,

2000; Niemeyer et al., 1996). Except for trp^1, these lines have white eyes, like the $ninaE$ and $norpA$

mutants as described above.

The trp^1 mutant was first isolated from a red eye wild type strain, but the precise background was

not known (Cosens and Manning, 1969), so we compared its sleep profile to two widely used wild

type strains in sleep and vision research: $Canton S$ and $Oregon R$. Significant reductions in day and

night sleep and average sleep bout length are shown in trp^1 mutants as compared to either wild type

flies (Figure 3Ai, 3Bi and 3Ei, effect size: 0.29-0.54, Table 3). The waking activity of trp^1 is comparable

to $Canton S$ but higher than $Oregon R$, and has limited impact to sleep loss (Figure 3Ci and 3Fi). The

sleep profile of trp^{MB} is distinct from trp^1, $norpA$ or $ninaE$ mutants, with day sleep level similar to

controls but a significant night sleep loss (Figure 3Aii, 3Gii). There is no significant change in sleep

bout length detected in trp^{MB} flies (Figure 3Aii and 3Eii). Although, trp^{MB} flies sleep a similar amount

during the day, compared to the control, their waking activity is significantly higher (Figure 3Cii).

This relative normal sleep-wake profile may relate to the less severe reduction in receptor potential

and light on/off transients in the ERG of trp^{MB} as compared to those of the trp^1 null mutant (Figure

3Hi and 3Hii, effect size r = 0.11-0.83 vs 0.78-0.85, Table 3).

On the other hand, both $trpl^{302}$ and $trpl^{MB}$ mutants exhibit day sleep profiles similar to $ninaE$ or

$norpA$ mutants (Figure 3Aiii and 3Aiv), with significant reduced day sleep and average bout length

(Figure 3Biii, 3Biv, 3Diii and 3Div). Night sleep profiles and waking activities for the two $trpl$ mutants

diverged: $trpl^{302}$ sleep more whereas $trpl^{MB}$ sleep less (Figure 3Giii, 3Giv). No significant changes in

night sleep bout length were observed in both mutants as compared to the controls (Figure 3Eiii and

3Eiv). $trpl^{302}$ mutants generally have low waking activity, whereas $trpl^{MB}$ maintains relative normal

waking activity as compared to the controls (Figure 3Ciii, 3Civ, 3Fiii and 3Fiv). $trpl^{302}$ mutant is in cn

and bw mutation background, which may affect the sleep. We therefore tested $w; trpl^{302/MB}$ flies to

reduce the impact of $cn bw$ mutation. Similar to $trpl^{302}$ and $trpl^{MB}$, the $w; trpl^{302/MB}$ transheterozygote

mutant showed shorter day sleep and sleep bout length (Figure 3Biv). As seen in previous reports

(Chen et al., 2015; Leung et al., 2000) both mutants have limited impact on ERG profiles, $trpl^{302}$ flies

show a large reduction of on/off transient (effect size 0.73/0.81, Table 4), whereas $trpl^{MB}$ mutants

maintain normal ERGs, possibly due to synaptic compensatory mechanism (Figure 3Hiii).

Nevertheless, our data indicate the reduced trpl function and expression level cause sleep loss in the

day.

3.2 Divergent sleep function in histaminergic pathway

Drosophila photoreceptors are divided into Rh1-expressing (R1-R6) and non-Rh1-exppressing

neurons (R7/R8). The R1-R6 photoreceptors form synapses onto lamina monopolar neurons (LMC),

while the R7/R8 send their output to the medulla in the optic lobes. Histamine is the primary

neurotransmitter for Rh1-expessing photoreceptors. Therefore, we tested if mutants with defects in

histamine synthesis or postsynaptic reception show altered sleep. Histidine decarboxylase (*hdc*) is

the main histamine synthesis enzyme (Pantazis et al., 2008). We investigated the sleep profiles for

the two *hdc* mutants (*hdc^{JK910}* and *hdc^{MB}*) that were showed to have reduced histamine levels in the

photoreceptors (Burg et al., 1993; Stenesen et al., 2015).

As expected, both mutants selectively reduce on/off transients' levels, the components in ERG that

reflect synaptic transmission between photoreceptors and LMCs (Figure 4Hi). Surprisingly, significant

sleep defects were detected in the night instead of during the day. During the day, increased day

sleep and bout length are found in *hdc^{JK910}* mutants as compared to the controls, whereas *hdc^{MB}* flies

show comparable day sleep and bout length to the controls (Figure 4Bi-ii and 4Di-ii). The waking

activities in the day are similar between *hdc* mutants and controls (Figure 4Ci-ii). During the night,

both *hdc* mutants sleep less with shorter sleep bouts (Figure 4Ei-ii and 4Gi-ii). Only *hdc^{JK910}* mutants

have reduced waking activities compared to the controls at night (Figure 4Fi-ii). Two histamine

receptors, ort and HisCl1, are detected in *Drosophila* CNS, and they are both histamine-gated

chloride channels (Pantazis et al., 2008). Transcriptomic data in *Drosophila* visual system suggests

that ort is expressed selectively in neurons postsynaptic to photoreceptors, whereas HisCl1 is

expressed almost exclusively in photoreceptors as auto-receptors (Davis et al., 2020). We therefore

verified the sleep profile in ort mutants to investigate the role of histamine signal downstream to

photoreceptors.

First, we monitored the sleep profile of the classic *ort^1* mutant against *Canton S*, as they share the

same genetic backgrounds (Inoue et al., 1989). A small but significant day time sleep loss is detected

in *ort^1* flies (Figure 4Dii, effective size 0.27, Table 5). *ort^1* mutants sleep for longer bouts during the

day but have higher day waking activity as compared to *Canton S* (Figure 4Biii and 4Ciii). In contrast

to *hdc* mutants, no night sleep phenotype is detected in *ort^1* flies (Figure 4Eiii-Giii). We also tested

a recent CRISPR-mediated null mutation *ort^{attp}* in the white eye background (Deng et al., 2019). The

sleep profile of *ort^{attp}* is distinct from *ort^1*, showing more sleep as compared to control (Figure 4Div

and 4Giv). However, the waking activities of *ort^{attp}* are severely reduced (Figure 4Civ and 4Fiv,

effective size 0.55/0.60, Table 5) therefore compounding the observed sleep phenotype. Intriguingly,

shorter day sleep bout length and a small reduction of night sleep are detected in *ort$^{attp/+}$*

heterozygotes (Figure 4Biv and 4Giv), accompanying improved waking activity (Figure 4Civ and 4Fiv,

wake activity *ort^{attp}* vs *ort$^{attp/+}$*, Table 5).

Both *ort* mutants exhibit ERG profiles with loss of on/off transients, while *ort[1]* mutants also show

loss of the receptor potential (Figure 4Hii).

3.3. Hyperpolarisation of Rh1-expressing photoreceptor causes short day sleep bout

Our findings so far indicate that seven of the eight phototransduction mutants exhibit day time sleep

defects. However, day sleep loss in *trpl[MB]* mutants do not correlate with ERG phenotypes. Moreover,

norpA[p24], *trp[MB]*, *trpl[MB]*, *ort[attp/+]*, and *hdc* mutants show sleep loss in the night. Thus, we further tested

if direct inhibition of photoreceptor excitability causes sleep defects in the day or night. At first, we

applied the Gal4-UAS system to block synaptic transmission from all photoreceptors by expressing

UAS-TeTxLC (tetanus toxin light chain) with gmr-Gal4 (as seen in Damulewicz et al., 2020). However,

we were not able to obtain viable adult flies even after maintaining the culture in 22°C to reduce the

known overexpression-related toxicity (Rezával et al., 2007; Sweeney et al., 1995). We next used

UAS-Kir2.1 (Baines et al., 2001; Nitabach et al., 2002) crossed with gmr-Gal4 or Rh1-Gal4 to

hyperpolarise all or just Rh1-expressing photoreceptors. Consistent with the finding for *ninaE* and

norpA mutants, *gmr-Gal4>uas-Kir2.1* and *Rh1-Gal4>uas-Kir2.1* flies showed reduced day sleep as

compared to *Gal4>+* or *+>uas-Kir2.1* controls (Figure 5Ai-ii, 5Di-ii), but only *Rh1-Gal4>uas-Kir2.1* flies

exhibit reduced sleep bout length in the day (Figure 5Bi-ii). Night sleep parameters in both *gmr-*

Gal4>uas-Kir2.1 and *Rh1-Gal4>uas-Kir2.1* flies ranges between that of the controls (Figure 5E-G).

This is because the unexpected low sleep exhibited in *+>uas-Kir2.1* controls (*gmr-Gal4>+* vs *+>uas-*

Kir2.1 and *Rh1-Gal4>+* vs *+>uas-Kir2.1*; effect size 0.62/0.74, Table 6). Therefore, we cannot

determine the actual effect of hyperpolarising photoreceptor on night sleep. Kir2.1 expressing flies

had no changes in waking activity (Figure 5C and 5F). Taken together, our data indicates that

phototransduction and the neuronal excitability in the *Drosophila* Rh1-expressing outer

photoreceptors promote day sleep.

4. Discussion

4.1 Primary finding

In this study, we surveyed eight mutants with defects in phototransduction, four mutants with disrupted histaminergic transmission, the main neurotransmitter used by *Drosophila* photoreceptors, and two mutants with hyperpolarised photoreceptors. We observed short or fragmented day sleep in the majority of the phototransduction mutants as well as in mutants with hyperpolarised R1-R6 photoreceptors. This data indicates that R1-R6 photoreceptor neural activities are required for sleep homeostatic drive during the daytime. Importantly, the mutants tested in this study maintain their ability to sense light, as the non-visual pathways such as *cry*, *Rh7* and *qsm* remain intact. Nevertheless, we show robustly that reduced visual phototransduction, or downstream neurotransmission, cause sleep loss and/or sleep fragmentation, indicating a clear role for *Drosophila* photoreceptors R1-R6 in promoting day sleep.

4.2 Contradiction to previous studies

Our data contradicts previous findings. Specifically, it was previously shown that blocking neural transmission for R1-R6 photoreceptors via TeTxLC caused day sleep increase (Damulewicz et al., 2020). As mentioned above, we cannot produce viable adult flies that express TeTxLC in photoreceptors and instead we applied Kir2 channel to hyperpolarise retinal photoreceptors. There may be two factors that explain the data discrepancy between the two studies: Firstly, our Gal4 and UAS lines are outcrossed to the w^{iso31} background, as is standard in the sleep research field, while such outcrossing was not described in Damulewicz et al., (2020). Secondly, vision is important for navigation, and the compromised vision in phototransduction mutants and flies with weakened photoreceptor outputs (i.e., *gmr-Gal4>UAS-kir2* or *gmr-Gal4>UAS-TeTxLC*) can result in reduced waking locomotor activities, which is a major confounding factor in assessing sleep increase. In fact, eight visual mutants in our survey (*ninaE⁵*, *ninaE⁸*, *norpA^{P24}*, *trp¹*, *trpl^{302}*, *hdc^{JK910}*, *ort^{attp}* and *gmr-Gal4>uas-kir2*) showed significant reduced waking activity in either day and/or night. Consequentially, the reduced waking activity prevents us from concluding whether the increased night sleep seen in *ninaE⁸*, *trpl^{302}* and *ort^{attp}* are genuine increases or a reflection of loss of locomotion during wakefulness. Therefore, these night sleep increase phenotypes should be interpreted with caution. The waking activity was not analysed by Damulewicz et al., (2020) preventing direct comparison here.

More surprisingly, the sleep loss identified in *hdc* and *ort* mutants is also opposite to previous findings indicating that histamine is a pro-waking factor (Oh et al., 2013). One major difference

between the current study and Oh et al., (2013) is that we only monitored male sleep to reach a

larger range of sleep dynamics. Importantly, female flies have very low levels of day sleep (see 2.2 in

Materials and method). As mentioned, further investigations of female visual mutants are necessary

before it can be determined if the role of visual input to sleep diverges between male and female

flies. Nevertheless, as shown in our data, two of the four mutants with histaminergic disruption

show lower waking activity, consistent with the proposed arousal promoting role of histamine (Oh et

al., 2013). However, we note that the mentioned previous study (Oh et al., 2013) also did not assess

the impact of waking activity on sleep. Waking activity is a classic, but often ignored, analytical tool

in *Drosophila* sleep research that allows differentiation between sleep and locomotor defects: as we

demonstrate in this study, when the flies exhibit reduced locomotor activity, any increase in sleep

cannot be certain. We therefore recommend that this parameter always be included in any

locomotion-based sleep assay.

4.3 Experimental limitations

The unexpected abnormal low night sleep in *+>uas-Kir2* control flies which is likely due to leaky

expression of Kir2 in other parts of the fly brain, since the *gmr-Gal4* and *UAS-Kir2* lines are

isogenised to w^{iso31} background. Nevertheless, this limits our investigation to day sleep. Future

investigation using gmr-LexA and LexAoP-Kir2 may be required to verify this finding.

The visual mutants tested in this study come with various genetic backgrounds including unknown

white backgrounds and two wild type backgrounds (see Materials and methods). We therefore only

interpreted the consistent phenotypes presented across the alleles. As such, there are allelic specific

night sleep loss phenotypes in in trp^{MB}, $trpl^{MB}$, $ort^{attp/+}$ and $norpA^{p24}$ that is likely due to genetic

background and should be interpreted with caution.

As part of control experiments, we examined the ERG profiles for all the tested gene-specific

mutants. However, the severity of sleep loss phenotype does not directly correlate with ERG defects

except for *trp* mutants: the weakest $ninaE^5$ mutant (only on transient reduction was detected)

showed just as much day sleep fragmentation as $ninaE^8$, $ninaE^{17}$ or $norpA^{p24}$. Moreover, both $trpl^{302}$

and $trpl^{MB}$ exhibit sleep loss, despite minor or no impact of *trpl* mutants on ERG profile. The

divergent sleep phenotypes may be partly due to the various genetic backgrounds that we did not

control for (see Materials and methods). Moreover, it is important to note that ERG only reflects

outer-retina physiology, not downstream optic-lobe integration. Therefore, the inconsistent sleep

phenotypes can also be derived from the expression profile of phototransduction genes in the

central brain beyond the photoreceptors. Future investigation utilising isogenised somatic CRISPR

knockout constructs will be required to verify potential impacts of genetic background on the

identified sleep-controlling role of phototransduction.

4.4 Hypothetical mechanisms underlying day and night sleep

Vision and light-affected sleep are mediated both via circadian clock neurons (eg., LNvs and DN1) as

well as by ring neurons in the EB (Lamaze et al., 2018; Raccuglia et al., 2019; Shang et al., 2008; Singh

et al., 2023). Various neural pathways connect photoreceptors to the wake promoting LNv: R1-R6

photoreceptors propagate the light signal via histamine-mediated inhibition of the downstream LMC

neurons that activates LNvs (Muraro and Ceriani, 2015); on the other hand, R8 has recently been

shown to communicate with LNv via the so-called AMA neurons and cholinergic signalling.

Moreover, sleep promoting signals from photoreceptors may also reach the EB via the Anterior

Visual Pathway through MeTu and TuBu neurons, upon which circadian clock neuron DN1 also

converge (Guo et al., 2018; Lamaze et al., 2018). It is currently unclear which of the above pathways

are required for the photoreceptor mediated day sleep promotion (Figure 6).

Although day sleep loss in ort^1, $ninaE$ mutants and $Rh1$-$Gal4$>uas-$Kir2$ indicates that day sleep

depends on Rh1-positive R1-R6-mediated histaminergic inhibition on LMC neurons, we did not

observe day sleep loss among hdc mutants. Nevertheless, hdc expression is wider than the visual

system (Oh et al., 2013). Moreover, loss of hdc activity does not completely remove histamine

production (eg., Stenesen et al., 2015) and it is not equal to selective blockage of ort-mediated

histamine postsynaptic transmission. However, our findings are consistent with those that previously

found a visually impaired omb mutant showed major sleep loss in both day and night (Kirszenblat et

al., 2019) as well as the finding that activation of L2 LMC neurons cause day sleep lost (Muraro and

Ceriani, 2015). Moreover, our data fit well with previous studies predicting that medium intensity

light convey a day sleep signal via retinal photoreceptors, whereas high intensity light enhances

midday sleep via HB-eyelet (Schlichting et al., 2019). Future orthogonal circuit-manipulation

experimentation is required to verify if the R1-R6 photoreceptors-mediated day sleep depends on L2

LMC and/or LNvs (Figure 6).

Six tested mutants also exhibit night sleep loss (two hdc mutants, $norpA^{p24}$, trp^1, trp^{MB} and $trpl^{MB}$).

Genetic background variation may contribute to this night sleep loss. However, both hdc mutants

exhibit clear night specific sleep loss and hdc^{MB} mutants are in an isogenic w^{iso31} background.

Therefore, this night sleep loss is likely genuine. Day time visual experience influence night sleep in

flies despite there is no or limited vision in the darkness of the night. There are three possible

explanations for night sleep loss in hdc mutants: **1.** Night sleep loss can simply be caused by non-

retinal photoreceptor histaminergic neurons and is mediated by HisCl1 reception instead of ort (Oh

et al., 2013). **2.** Reduction of photoreceptor-mediated histamine results in uneven inhibition among

LMCs to reduce the visual contrast of bright/dark edges and differentially reduce activation of HS/VS

neurons which are known promote night sleep (Kirszenblat et al., 2019). **3.** The *hdc*-mediated night

sleep is related to the reduced histaminergic inhibition in non-LMC neurons mediated by HisCl1 and

is independent of ort. Previous data indicates that HisCl1 is an auto-receptor for all retinal

photoreceptors, and also expresses in glia cells in the optic lobe as well as clock neurons lLNvs (Davis

et al., 2020; Oh et al., 2013; Pantazis et al., 2008). Among retinal photoreceptors, R8 has been

proposed to receive histaminergic inhibition via HisCl1 to regulate its acetylcholine co-release

(Alejevski et al., 2019; Xiao et al., 2023). Loss of this inhibition can result in an ectopic increase in

acetylcholine, which can in turn activate the newly identified AMA (Xiao et al., 2023) and its

downstream wake promoting lLNvs (Shang et al., 2008). Alternatively, R8 can reach sleep/wake

promoting EB-R via anterior visual pathways (Figure 6).

The potential demarcation between achromatic (R1-R6) and chromatic (R8, both blue and green

sensitive) photoreceptors in their control over day and night sleep (Figure 6) bears some

resemblance with the previous finding in mammalian system, where the sleep- vs wake-promoting

effects of green and blue light required proper neural output from rod/cone and the melanopsin

expressing photosensitive retinal ganglion cells (Pilorz et al., 2016). Nevertheless, the revelation of

the potential neural network demarcation of day and night sleep in *Drosophila* require further

investigation to expand our understandings in circuital logic of light-mediated sleep regulation.

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Declaration Of Interests

The authors declare no competing interests.

Figure captions

Figure 1. sleep profile, parameters and ERG quantification for *ninaE* mutants. A. Sleep traces of

average sleep minutes per 30 minutes over 12 hours light-dark cycle. ZT0: light on, ZT12: light off,

ZT24: end of night. Sleep traces of *iso* control and *ninaE* mutants are colour coded in grey and red

shades (i-iii). **B.** Average day sleep bout length (minutes), **C.** Average day wake activity (beam breaks

per waking minutes), **D.** Average day sleep (minutes), E. Average night sleep bout length (minutes),

F. Average night wake activity (beam breaks per waking minutes), and **G.** Average night sleep

(minutes) for *ninaE^{17}* (i), *ninaE^{8}* (ii) and *ninaE^{5}* (iii) compared to iso controls. Average values for each

individual are plotted as filled circles except for those outside scales. **H.** An example ERG profile from

iso control with 1000 ms green light flash that evokes voltage changes of on-transient, receptor

potential and off-transient. **I.** Mean and standard deviation for voltage change (mV) in on transient,

receptor potential and off-transient of ERG upon four light intensity (0.004, 0.02, 0.1 and 0.5 w/m^2)

flash for *ninaE^{17}* and controls. **J.** Mean and standard deviation for voltage change (mV) in on

transient, receptor potential and off-transient of ERG upon four light intensities (0.004, 0.02, 0.1 and

0.5 w/m^2) 1000ms flash for *ninaE^{5}*, *ninaE^{8}* and controls. Plot scales are in either liner (A-G) and

logarithmic (I-J). Asterisk indicates statistical significance (p<0.05) between mutants and iso controls

by pairwise Wilcoxon rank sum exact test without (B-H) and with multiple comparison, Benjamini-

Hochberg correction (I, followed by Kruskal-Wallis rank sum test). See **Table 1** for sample size (n=26-

60 for sleep; n=3-6 for ERG, with 4 replicates for each light intensity), p-values and effect size for

each comparison.

Figure 2. sleep profile, parameters and ERG quantification for *norpA* mutants. A. Sleep traces of

average sleep minutes per 30 minutes over 12 hours light-dark cycle. ZT0: light on, ZT12: light off,

ZT24: end of night. Sleep traces for *iso* control and *norpA^{p24}* mutants are colour coded in grey and

cyan. **B.** Average day sleep bout length (minutes), **C.** Average day wake activity (beam breaks per

waking minutes), **E.** Average night sleep bout length (minutes), **F.** Average night wake activity (beam

breaks per waking minutes), **G.** Average night sleep (minutes) for *norpA^{p24}* compared to iso controls.

Average values for each individual are plotted as filled circles except for those outside scales (B-G).

H. mean and standard deviation for voltage change (mV) in on transient, receptor potential and off-

transient of ERG upon four light intensity (0.004, 0.02, 0.1 and 0.5 w/m^2) flash for *norpA^{p24}* and *iso*

controls. Plot scales are in either liner (A-G) and logarithmic (H). Asterisk indicates statistical

significance (p<0.05) between mutants and iso controls by pairwise Wilcoxon rank sum exact test.

See **Table 2** for sample size (n=21-23 for sleep; n=4 for ERG, with 4 replicates for each light

intensity), p-values and effect size for each comparison.

Figure 3. sleep profile, parameters and ERG quantification for *trp* and *trpl* mutants. A. Sleep traces

of average sleep minutes per 30 minutes over 12 hours light-dark cycle. ZT0: light on, ZT12: light off,

ZT24: end of night. Sleep traces for *Canton S* (i), *Oregon R* (i) and *iso* controls (ii-iv) are coloured

coded in the shades of greys; *trp* (i-ii) and *trpl* (iii-iv) mutants are colour coded in shades of blue and

purples. **B.** Average day sleep bout length (minutes), **C.** Average day wake activity (beam breaks per

waking minutes), **D.** Average day sleep (minutes), **E.** Average night sleep bout length (minutes), **F.**

Average night wake activity (beam breaks per waking minutes), **G.** Average night sleep (minutes) for

trp^1 (i), trp^{MB} (ii), $trpl^{302}$ (iii) and $trpl^{302/MB}$ or $trpl^{MB}$ (iv) compared to controls. Average values for each

individual are plotted as filled circles except for those outside scales. **H.** Mean and standard

deviation for voltage change (mV) in on transient, receptor potential and off-transient of ERG upon

four light intensity (0.004, 0.02, 0.1 and 0.5 w/m^2) flash for trp^1 (i), trp^{MB} (ii), $trpl^{302}$ (iii) and $trpl^{MB}$ (iii)

compared to controls. Plot scales are in either liner (A-G) and logarithmic (H). Asterisk indicates

statistical significance (p<0.05) between mutants and controls by pairwise Wilcoxon rank sum exact

test without (Aii-Gii, Aiii-Giii, Hi and Hii) and with multiple comparison, Benjamini-Hochberg

correction (Ai-Gi, Aiv-Giv, and Hiii followed by Kruskal-Wallis rank sum test). See **Table 3 and Table 4**

for sample size (n=16-53 for sleep; n=3 for ERG, with 4 replicates for each light intensity), p-values

and effect size for each comparison.

Figure 4. sleep profile, parameters and ERG quantification for *hdc* and *ort* mutants. A. Sleep traces

of average sleep minutes per 30 minutes over 12 hours light-dark cycle. ZT0: light on, ZT12: light off,

ZT24: end of night. Sleep traces for *iso* (i-ii, iv) and *Canton S* (iii) controls are coloured coded in the

shades of greys; *hdc* (i-ii) and *ort* (iii-iv) mutants are colour coded in shades of indigos and greens. **B.**

Average day sleep bout length (minutes), **C.** Average day wake activity (beam breaks per waking

minutes), **D.** Average day sleep (minutes), **E.** Average night sleep bout length (minutes), **F.** Average

night wake activity (beam breaks per waking minutes), **G.** Average night sleep (minutes) for *hdc*

mutants (i-ii), ort^1 and $ort^{attp/+}$ or ort^{attp} (iii-iv) compared to controls. Average values for each

individual are plotted as filled circles except for those outside scales (B-G). **H.** Mean and standard

deviation for voltage change (mV) in on transient, receptor potential and off-transient of ERG upon

four light intensity (0.004, 0.02, 0.1 and 0.5 w/m^2) flash for *hdc* (i) and *ort* (ii) mutants compared to

controls. Plot scales are in either liner (A-G) and logarithmic (H). Asterisk indicates statistical

significance (p<0.05) between mutants and controls by pairwise Wilcoxon rank sum exact test

without (Aii-Gii) and with multiple comparison, Benjamini-Hochberg correction (Ai-Hi, Aiii-Giii, and

Hii followed by Kruskal-Wallis rank sum test). See **Table 5** for sample size (n=29-60 for sleep; n=3-5

for ERG, with 4 replicates for each light intensity), p-values and effect size for each comparison.

Figure 5. sleep profile and parameters for flies with hyperpolarised photoreceptors. A. Sleep traces

of average sleep minutes per 30 minutes over 12 hours light-dark cycle. ZT0: light on, ZT12: light off,

ZT24: end of night. Sleep traces for *gmr-Gal4>+* (i), *Rh1-Gal4>+* (ii) and *+>UAS-Kir2* (i-ii) control flies

are coloured coded in the shades of greys; experimental mutants *gmr-Gal4> UAS-kir2* (i) and *Rh1-*

Gal4>UAS-kir2 (ii) are colour coded in light burgundy. **B.** Average day sleep bout length (minutes), **C.**

Average day wake activity (beam breaks per waking minutes), **D.** Average day sleep (minutes), **E.**

Average night sleep bout length (minutes), **F.** Average night wake activity (beam breaks per waking

minutes), **G.** Average night sleep (minutes) for *gmr-Gal4> UAS-kir2* (i) and *Rh1-Gal4>UAS-kir2* (ii)

compared to controls. Average values for each individual are plotted as filled circles except for those

outside scales (B-G). Asterisk indicates statistical significance (p<0.05) between mutants and controls

by pairwise Wilcoxon rank sum exact test with multiple comparison, Benjamini-Hochberg correction

(followed by Kruskal-Wallis rank sum test). See **Table 6** for sample size (n=28-32), p-values and effect

size for each comparison.

Figure 6. Speculative mechanism underlying visually driven day and night sleep. R1-R6

photoreceptors (blue) promote day sleep by inhibiting a subset of wake promoting lamina

monopolar cells (LMC) via histamine release (his, blue text) and ort reception (green text); Night

sleep is controlled by interaction between R1-R6, R7 and R8 (blue/orange) photoreceptors:

Hypothetical histaminergic inhibition (his, blue text) from R1-R6 to R8 is mediated by HisCl1

(magenta text) (Alejevski et al., 2019). Separately R7 and R8 also inhibit each other via histaminergic

signalling (Schnaitmann et al., 2018), these inhibitions maintain a slower suppression of

acetylcholine release (ace, orange text) from R8 and its activation of the AMA neurons (orange) and

downstream waking promoting LNvs (red circle). Alternatively, R8 regulate night sleep by reaching

sleep-regulating EB-Ring neurons (EB-R) via MeTu and TuBu neurons with unknown

neurotransmitters (grey rectangular and arrows).

Reference

Alejevski, F., Saint-Charles, A., Michard-Vanhee, C., Martin, B., Galant, S., Vasiliauskas, D., Rouyer, F.,
2019. The HisCl1 histamine receptor acts in photoreceptors to synchronize Drosophila
behavioral rhythms with light-dark cycles. Nature communications 10, 252.
https://doi.org/10.1038/s41467-018-08116-7
Alphen, B. van, Semenza, E.R., Yap, M., Swinderen, B. van, Allada, R., 2021. A deep sleep stage in
Drosophila with a functional role in waste clearance. Science Advances 7, eabc2999.
https://doi.org/10.1126/sciadv.abc2999
Altimus, C.M., Güler, A.D., Villa, K.L., McNeill, D.S., LeGates, T.A., Hattar, S., 2008. Rods-cones and
melanopsin detect light and dark to modulate sleep independent of image formation.
Proceedings of the National Academy of Sciences 105, 19998–20003.
https://doi.org/10.1073/pnas.0808312105
Andretic, R., Shaw, P.J., 2005. Essentials of Sleep Recordings in *Drosophila:* Moving Beyond Sleep
Time, in: Young, M.W. (Ed.), Methods in Enzymology, Circadian Rhythms. Academic Press,
pp. 759–772. https://doi.org/10.1016/S0076-6879(05)93040-1
Baines, R.A., Uhler, J.P., Thompson, A., Sweeney, S.T., Bate, M., 2001. Altered Electrical Properties in
DrosophilaNeurons Developing without Synaptic Transmission. J. Neurosci. 21, 1523–1531.
https://doi.org/10.1523/JNEUROSCI.21-05-01523.2001
Burg, M.G., Sarthy, P.V., Koliantz, G., Pak, W.L., 1993. Genetic and molecular identification of a
Drosophila histidine decarboxylase gene required in photoreceptor transmitter synthesis.
The EMBO Journal 12, 911–919. https://doi.org/10.1002/j.1460-2075.1993.tb05732.x
Chen, K.F., Lowe, S., Lamaze, A., Kratschmer, P., Jepson, J., 2019. Neurocalcin regulates nighttime
sleep and arousal in Drosophila. eLife 8. https://doi.org/10.7554/eLife.38114
Chen, K.F., Peschel, N., Zavodska, R., Sehadova, H., Stanewsky, R., 2011. QUASIMODO, a Novel GPI-
anchored zona pellucida protein involved in light input to the Drosophila circadian clock.
Current Biology 21, 719–729.
Chen, Z., Chen, H.-C., Montell, C., 2015. TRP and Rhodopsin Transport Depends on Dual XPORT ER
Chaperones Encoded by an Operon. Cell Reports 13, 573–584.
https://doi.org/10.1016/j.celrep.2015.09.018
Chiu, J.C., Low, K.H., Pike, D.H., Yildirim, E., Edery, I., 2010. Assaying Locomotor Activity to Study
Circadian Rhythms and Sleep Parameters in Drosophila. JoVE (Journal of Visualized
Experiments) e2157. https://doi.org/10.3791/2157
Cosens, D.J., Manning, A., 1969. Abnormal Electroretinogram from a Drosophila Mutant. Nature 224,
285–287. https://doi.org/10.1038/224285a0
Damulewicz, M., Ispizua, J.I., Ceriani, M.F., Pyza, E.M., 2020. Communication Among Photoreceptors
and the Central Clock Affects Sleep Profile. Front. Physiol. 11.
https://doi.org/10.3389/fphys.2020.00993
Davis, F.P., Nern, A., Picard, S., Reiser, M.B., Rubin, G.M., Eddy, S.R., Henry, G.L., 2020. A genetic,
genomic, and computational resource for exploring neural circuit function. eLife 9, e50901.
https://doi.org/10.7554/eLife.50901
Deng, B., Li, Q., Liu, X., Cao, Y., Li, B., Qian, Y., Xu, R., Mao, R., Zhou, E., Zhang, W., Huang, J., Rao, Y.,
2019. Chemoconnectomics: Mapping Chemical Transmission in Drosophila. Neuron 101,
876-893.e4. https://doi.org/10.1016/j.neuron.2019.01.045
Dissel, S., Angadi, V., Kirszenblat, L., Suzuki, Y., Donlea, J., Klose, M., Koch, Z., English, D., Winsky-
Sommerer, R., van Swinderen, B., Shaw, P.J., 2015. Sleep Restores Behavioral Plasticity to
Drosophila Mutants. Current Biology 25, 1270–1281.
https://doi.org/10.1016/j.cub.2015.03.027
Dove, A.E., Cook, B.L., Irgebay, Z., Vecsey, C.G., 2017. Mechanisms of sleep plasticity due to sexual
experience in *Drosophila melanogaster*. Physiology & Behavior 180, 146–158.
https://doi.org/10.1016/j.physbeh.2017.08.020

Duhart, J.M., Buchler, J.R., Inami, S., Kennedy, K.J., Jenny, B.P., Afonso, D.J.S., Koh, K., 2023. Modulation and neural correlates of postmating sleep plasticity in Drosophila females. Current Biology 33, 2702-2716.e3. https://doi.org/10.1016/j.cub.2023.05.054

Gao, S., Takemura, S., Ting, C.-Y., Huang, S., Lu, Z., Luan, H., Rister, J., Thum, A.S., Yang, M., Hong, S.-T., Wang, J.W., Odenwald, W.F., White, B.H., Meinertzhagen, I.A., Lee, C.-H., 2008. The Neural Substrate of Spectral Preference in Drosophila. Neuron 60, 328–342. https://doi.org/10.1016/j.neuron.2008.08.010

Gilestro, G.F., Tononi, G., Cirelli, C., 2009. Widespread Changes in Synaptic Markers as a Function of Sleep and Wakefulness in Drosophila. Science 324, 109–112. https://doi.org/10.1126/science.1166673

Guo, F., Holla, M., Díaz, M.M., Rosbash, M., 2018. A Circadian Output Circuit Controls Sleep-Wake Arousal in Drosophila. Neuron 100, 624-635.e4. https://doi.org/10.1016/j.neuron.2018.09.002

Harbison, S.T., Sehgal, A., 2008. Quantitative Genetic Analysis of Sleep in Drosophila melanogaster. Genetics 178, 2341–2360. https://doi.org/10.1534/genetics.107.081232

Hardie, R.C., 2012. Phototransduction mechanisms in Drosophila microvillar photoreceptors. Wiley Interdisciplinary Reviews: Membrane Transport and Signaling 1, 162–187. https://doi.org/10.1002/wmts.20

Hartmann, C., Kempf, A., 2023. Mitochondrial control of sleep. Current Opinion in Neurobiology 81, 102733. https://doi.org/10.1016/j.conb.2023.102733

Horne, J.A., Walmsley, B., 1976. Daytime visual load and the effects upon human sleep. Psychophysiology 13, 115–20.

Hsu, C.T., Guevara, C., Killiany, S.L., Shon, J., Dissel, S., Sehgal, A., 2025. Clock-dependent regulation of a homeostatic sleep center maintains daytime sleep and evening activity. Current Biology 0. https://doi.org/10.1016/j.cub.2025.06.003

Inoue, H., Yoshioka, T., Hotta, Y., 1989. Diacylglycerol Kinase Defect in a *Drosophila* Retinal Degeneration Mutant *rdgA*. Journal of Biological Chemistry 264, 5996–6000. https://doi.org/10.1016/S0021-9258(18)83648-1

Isaac, R.E., Li, C., Leedale, A.E., Shirras, A.D., 2009. Drosophila male sex peptide inhibits siesta sleep and promotes locomotor activity in the post-mated female. Proceedings of the Royal Society of London B: Biological Sciences rspb20091236.

Ishimoto, H., Lark, A., Kitamoto, T., 2012. Factors that differentially affect daytime and nighttime sleep in Drosophila melanogaster. Front Neurol 3, 24.

Jagannathan, S.R., Jeans, T., Van De Poll, M.N., van Swinderen, B., 2024. Multivariate classification of multichannel long-term electrophysiology data identifies different sleep stages in fruit flies. Science Advances 10, eadj4399. https://doi.org/10.1126/sciadv.adj4399

Jones, J.D., Holder, B.L., Montgomery, A.C., McAdams, C.V., He, E., Burns, A.E., Eiken, K.R., Vogt, A., Velarde, A.I., Elder, A.J., McEllin, J.A., Dissel, S., 2025. The dorsal fan-shaped body is a neurochemically heterogeneous sleep-regulating center in Drosophila. PLOS Biology 23, e3003014. https://doi.org/10.1371/journal.pbio.3003014

Kirszenblat, L., Yaun, R., van Swinderen, B., 2019. Visual experience drives sleep need in Drosophila. Sleep 42. https://doi.org/10.1093/sleep/zsz102

Korf, E.M., Mölle, M., Born, J., Ngo, H.-V.V., 2017. Blindfolding during wakefulness causes decrease in sleep slow wave activity. Physiological Reports 5, e13239. https://doi.org/10.14814/phy2.13239

Lakhiani, R., Shanavas, S., Melnattur, K., 2023. Comparative biology of sleep in diverse animals. J Exp Biol 226. https://doi.org/10.1242/jeb.245677

Lamaze, A., Krätschmer, P., Chen, K.-F., Lowe, S., Jepson, J.E.C., 2018. A Wake-Promoting Circadian Output Circuit in Drosophila. Current Biology 28, 3098-3105.e3. https://doi.org/10.1016/j.cub.2018.07.024

Leung, H.-T., Geng, C., Pak, W.L., 2000. Phenotypes of trpl Mutants and Interactions between the
Transient Receptor Potential (TRP) and TRP-Like Channels inDrosophila. J. Neurosci. 20,
6797–6803. https://doi.org/10.1523/JNEUROSCI.20-18-06797.2000
Mazzotta, G.M., Damulewicz, M., Cusumano, P., 2020. Better Sleep at Night: How Light Influences
Sleep in Drosophila. Front. Physiol. 11. https://doi.org/10.3389/fphys.2020.00997
Meyerhof, G.T., Easwaran, S., Bontempo, A.E., Montell, C., Montell, D.J., 2024. Altered circadian
rhythm, sleep, and rhodopsin 7–dependent shade preference during diapause in Drosophila
melanogaster. Proceedings of the National Academy of Sciences 121, e2400964121.
https://doi.org/10.1073/pnas.2400964121
Miyamoto, H., Katagiri, H., Hensch, T., 2003. Experience-dependent slow-wave sleep development.
Nat Neurosci 6, 553–554. https://doi.org/10.1038/nn1064
Muraro, N.I., Ceriani, M.F., 2015. Acetylcholine from visual circuits modulates the activity of arousal
neurons in Drosophila. Journal of Neuroscience 35, 16315–16327.
Nériec, N., Desplan, C., 2016. Chapter Fourteen - From the Eye to the Brain: Development of the
Drosophila Visual System, in: Wassarman, P.M. (Ed.), Current Topics in Developmental
Biology, Essays on Developmental Biology, Part A. Academic Press, pp. 247–271.
https://doi.org/10.1016/bs.ctdb.2015.11.032
Ni, J.D., Baik, L.S., Holmes, T.C., Montell, C., 2017. A rhodopsin in the brain functions in circadian
photoentrainment in Drosophila. Nature 545, 340–344.
https://doi.org/10.1038/nature22325
Niemeyer, B.A., Suzuki, E., Scott, K., Jalink, K., Zuker, C.S., 1996. The Drosophila Light-Activated
Conductance Is Composed of the Two Channels TRP and TRPL. Cell 85, 651–659.
https://doi.org/10.1016/S0092-8674(00)81232-5
Nitabach, M.N., Blau, J., Holmes, T.C., 2002. Electrical Silencing of Drosophila Pacemaker Neurons
Stops the Free-Running Circadian Clock. Cell 109, 485–495. https://doi.org/10.1016/S0092-
8674(02)00737-7
Ogueta, M., Hardie, R.C., Stanewsky, R., 2020. Light Sampling via Throttled Visual Phototransduction
Robustly Synchronizes the Drosophila Circadian Clock. Current Biology 30, 2551-2563.e3.
https://doi.org/10.1016/j.cub.2020.04.067
Ogueta, M., Hardie, R.C., Stanewsky, R., 2018. Non-canonical Phototransduction Mediates
Synchronization of the Drosophila melanogaster Circadian Clock and Retinal Light
Responses. Current Biology 28, 1725-1735.e3. https://doi.org/10.1016/j.cub.2018.04.016
Oh, Y., Jang, D., Sonn, J.Y., Choe, J., 2013. Histamine-HisCl1 Receptor Axis Regulates Wake-Promoting
Signals in Drosophila melanogaster. PLoS ONE 8, e68269.
https://doi.org/10.1371/journal.pone.0068269
O'Tousa, J.E., Baehr, W., Martin, R.L., Hirsh, J., Pak, W.L., Applebury, M.L., 1985. The Drosophila
ninaE gene encodes an opsin. Cell 40, 839–850. https://doi.org/10.1016/0092-
8674(85)90343-5
Pantazis, A., Segaran, A., Liu, C.-H., Nikolaev, A., Rister, J., Thum, A.S., Roeder, T., Semenov, E.,
Juusola, M., Hardie, R.C., 2008. Distinct Roles for Two Histamine Receptors (hclA and hclB) at
the Drosophila Photoreceptor Synapse. The Journal of Neuroscience 28, 7250–7259.
https://doi.org/10.1523/jneurosci.1654-08.2008
Peschel, N., Chen, K.F., Szabo, G., Stanewsky, R., 2009. Light-dependent interactions between the
Drosophila circadian clock factors cryptochrome, jetlag, and timeless. Current Biology 19,
241–247.
Pilorz, V., Tam, S.K.E., Hughes, S., Pothecary, C.A., Jagannath, A., Hankins, M.W., Bannerman, D.M.,
Lightman, S.L., Vyazovskiy, V.V., Nolan, P.M., Foster, R.G., Peirson, S.N., 2016. Melanopsin
Regulates Both Sleep-Promoting and Arousal-Promoting Responses to Light. PLOS Biology
14, e1002482. https://doi.org/10.1371/journal.pbio.1002482
Raccuglia, D., Huang, S., Ender, A., Heim, M.M., Laber, D., Suárez-Grimalt, R., Liotta, A., Sigrist, S.J.,
Geiger, J.R.P., Owald, D., 2019. Network-Specific Synchronization of Electrical Slow-Wave

Oscillations Regulates Sleep Drive in Drosophila. Current Biology.
https://doi.org/10.1016/j.cub.2019.08.070
Reinhard, N., Fukuda, A., Manoli, G., Derksen, E., Saito, A., Möller, G., Sekiguchi, M., Rieger, D.,
Helfrich-Förster, C., Yoshii, T., Zandawala, M., 2024. Synaptic connectome of the Drosophila
circadian clock. Nat Commun 15, 10392. https://doi.org/10.1038/s41467-024-54694-0
Rezával, C., Werbajh, S., Ceriani, M.F., 2007. Neuronal death in Drosophila triggered by GAL4
accumulation. European Journal of Neuroscience 25, 683–694.
https://doi.org/10.1111/j.1460-9568.2007.05317.x
Rieger, D., Fraunholz, C., Popp, J., Bichler, D., Dittmann, R., Helfrich-Förster, C., 2007. The Fruit Fly
Drosophila melanogaster Favors Dim Light and Times Its Activity Peaks to Early Dawn and
Late Dusk. J Biol Rhythms 22, 387–399. https://doi.org/10.1177/0748730407306198
Rieger, D., Stanewsky, R., Helfrich-Förster, C., 2003. Cryptochrome, Compound Eyes, Hofbauer-
Buchner Eyelets, and Ocelli Play Different Roles in the Entrainment and Masking Pathway of
the Locomotor Activity Rhythm in the Fruit Fly Drosophila Melanogaster. Journal of
Biological Rhythms 18, 377–391. https://doi.org/10.1177/0748730403256997
Rossi, F.A., Bochicchio, P.A., Quesada-Allué, L.A., Pérez, M.M., 2015. N-β-alanyldopamine
metabolism, locomotor activity and sleep in Drosophila melanogaster ebony and tan
mutants. Physiological Entomology 40, 166–174. https://doi.org/10.1111/phen.12100
Scavarda, N.J., O'Tousa, J., Pak, W.L., 1983. Drosophila locus with gene-dosage effects on rhodopsin.
Proceedings of the National Academy of Sciences 80, 4441–4445.
https://doi.org/10.1073/pnas.80.14.4441
Schlichting, M., Menegazzi, P., Lelito, K.R., Yao, Z., Buhl, E., Benetta, E.D., Bahle, A., Denike, J., Hodge,
J.J., Helfrich-Förster, C., Shafer, O.T., 2016. A Neural Network Underlying Circadian
Entrainment and Photoperiodic Adjustment of Sleep and Activity in Drosophila. J. Neurosci.
36, 9084–9096. https://doi.org/10.1523/JNEUROSCI.0992-16.2016
Schlichting, M., Menegazzi, P., Rosbash, M., Helfrich-Förster, C., 2019. A Distinct Visual Pathway
Mediates High-Intensity Light Adaptation of the Circadian Clock in Drosophila. J. Neurosci.
39, 1621–1630. https://doi.org/10.1523/JNEUROSCI.1497-18.2018
Schnaitmann, C., Haikala, V., Abraham, E., Oberhauser, V., Thestrup, T., Griesbeck, O., Reiff, D.F.,
2018. Color Processing in the Early Visual System of Drosophila. Cell 172, 318-330.e18.
https://doi.org/10.1016/j.cell.2017.12.018
Sengupta, S., Crowe, L.B., You, S., Roberts, M.A., Jackson, F.R., 2019. A Secreted Ig-Domain Protein
Required in Both Astrocytes and Neurons for Regulation of *Drosophila* Night Sleep. Current
Biology 29, 2547-2554.e2. https://doi.org/10.1016/j.cub.2019.06.055
Shafer, O.T., Keene, A.C., 2021. The Regulation of Drosophila Sleep. Current Biology 31, R38–R49.
https://doi.org/10.1016/j.cub.2020.10.082
Shang, Y., Griffith, L.C., Rosbash, M., 2008. Light-arousal and circadian photoreception circuits
intersect at the large PDF cells of the *Drosophila* brain. Proceedings of the National Academy
of Sciences 105, 19587–19594. https://doi.org/10.1073/pnas.0809577105
Singh, P., Aleman, A., Omoto, J.J., Nguyen, B.-C., Kandimalla, P., Hartenstein, V., Donlea, J.M., 2023.
Examining Sleep Modulation by Drosophila Ellipsoid Body Neurons. eNeuro 10.
https://doi.org/10.1523/ENEURO.0281-23.2023
Stenesen, D., Moehlman, A.T., Krämer, H., 2015. The carcinine transporter CarT is required in
Drosophila photoreceptor neurons to sustain histamine recycling. eLife 4, e10972.
https://doi.org/10.7554/eLife.10972
Suh, J., Jackson, F.R., 2007. Drosophila Ebony Activity Is Required in Glia for the Circadian Regulation
of Locomotor Activity. Neuron 55, 435–447. https://doi.org/10.1016/j.neuron.2007.06.038
Sweeney, S.T., Broadie, K., Keane, J., Niemann, H., O'Kane, C.J., 1995. Targeted expression of tetanus
toxin light chain in Drosophila specifically eliminates synaptic transmission and causes
behavioral defects. Neuron 14, 341–351. https://doi.org/10.1016/0896-6273(95)90290-2

Tainton-Heap, L.A.L., Kirszenblat, L.C., Notaras, E.T., Grabowska, M.J., Jeans, R., Feng, K., Shaw, P.J.,
van Swinderen, B., 2021. A Paradoxical Kind of Sleep in Drosophila melanogaster. Current
Biology 31, 578-590.e6. https://doi.org/10.1016/j.cub.2020.10.081
Tang, M., Cao, L.-H., Yang, T., Ma, S.-X., Jing, B.-Y., Xiao, N., Xu, S., Leng, K.-R., Yang, D., Li, M.-T., Luo,
D.-G., 2022. An extra-clock ultradian brain oscillator sustains circadian timekeeping. Science
Advances 8, eabo5506. https://doi.org/10.1126/sciadv.abo5506
Vaccaro, A., Dor, Y.K., Nambara, K., Pollina, E.A., Lin, C., Greenberg, M.E., Rogulja, D., 2020. Sleep
Loss Can Cause Death through Accumulation of Reactive Oxygen Species in the Gut. Cell 0.
https://doi.org/10.1016/j.cell.2020.04.049
Vincent, C.M., Beckwith, E.J., Silva, C.J.S. da, Pearson, W.H., Kierdorf, K., Gilestro, G.F., Dionne, M.S.,
2022. Infection increases activity via Toll dependent and independent mechanisms in
Drosophila melanogaster. PLOS Pathogens 18, e1010826.
https://doi.org/10.1371/journal.ppat.1010826
Wu, B., Ma, L., Zhang, E., Du, J., Liu, S., Price, J., Li, S., Zhao, Z., 2018. Sexual dimorphism of sleep
regulated by juvenile hormone signaling in Drosophila. PLOS Genetics 14, e1007318.
https://doi.org/10.1371/journal.pgen.1007318
Wulff, K., Gatti, S., Wettstein, J.G., Foster, R.G., 2010. Sleep and circadian rhythm disruption in
psychiatric and neurodegenerative disease. Nature Reviews Neuroscience 11, 589–599.
https://doi.org/10.1038/nrn2868
Xiao, N., Xu, S., Li, Z.-K., Tang, M., Mao, R., Yang, T., Ma, S.-X., Wang, P.-H., Li, M.-T., Sunilkumar, A.,
Rouyer, F., Cao, L.-H., Luo, D.-G., 2023. A single photoreceptor splits perception and
entrainment by cotransmission. Nature 623, 562–570. https://doi.org/10.1038/s41586-023-
06681-6
Yap, M.H.W., Grabowska, M.J., Rohrscheib, C., Jeans, R., Troup, M., Paulk, A.C., van Alphen, B., Shaw,
P.J., van Swinderen, B., 2017. Oscillatory brain activity in spontaneous and induced sleep
stages in flies. Nat Commun 8, 1815. https://doi.org/10.1038/s41467-017-02024-y
Zanini, D., Giraldo, D., Warren, B., Katana, R., Andrés, M., Reddy, S., Pauls, S., Schwedhelm-Domeyer,
N., Geurten, B.R.H., Göpfert, M.C., 2018. Proprioceptive Opsin Functions in Drosophila Larval
Locomotion. Neuron 98, 67-74.e4. https://doi.org/10.1016/j.neuron.2018.02.028
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804 Table 1. Statistics of a. sleep and b. ERG parameters for *ninaE* mutants

a. sleep parameter	genotype comparison	p-value	effect size r	n1	n2	significant r magnitude
806 day sleep	*iso* vs *ninaE*[17]	3.50E-01	0.09	60	52	
807 night sleep	*iso* vs *ninaE*[17]	1.00E-07	0.51	60	51	large
808 day sleep bout length	*iso* vs *ninaE*[17]	9.60E-06	0.42	60	52	moderate
809 night sleep bout length	*iso* vs *ninaE*[17]	7.90E-01	0.03	44	35	
810 day wake activity	*iso* vs *ninaE*[17]	5.70E-01	0.05	60	52	
811 night wake activity	*iso* vs *ninaE*[17]	1.30E-01	0.14	60	51	
812 day sleep	*iso* vs *ninaE*[5]	1.40E-03	0.40	32	31	moderate
813 night sleep	*iso* vs *ninaE*[5]	3.20E-02	0.27	32	31	small
814 day sleep bout length	*iso* vs *ninaE*[5]	5.30E-09	0.68	32	31	large
815 night sleep bout length	*iso* vs *ninaE*[5]	7.10E-02	0.23	32	31	
816 day wake activity	*iso* vs *ninaE*[5]	3.90E-13	0.79	32	31	large
817 night wake activity	*iso* vs *ninaE*[5]	1.90E-10	0.72	32	31	large
818 day sleep	*iso* vs *ninaE*[8]	9.30E-05	0.51	32	26	large
819 night sleep	*iso* vs *ninaE*[8]	1.10E-08	0.75	32	26	large
820 day sleep bout length	*iso* vs *ninaE*[8]	6.90E-09	0.76	32	26	large
821 night sleep bout length	*iso* vs *ninaE*[8]	9.60E-02	0.22	32	26	
822 day wake activity	*iso* vs *ninaE*[8]	1.40E-13	0.82	32	26	large
823 night wake activity	*iso* vs *ninaE*[8]	2.90E-07	0.67	32	26	large
824 **b.ERG parameter**	**genotype comparison**	**p-value**	**effect size r**	**n1**	**n2**	**significant r magnitude**
825 receptor potential	*iso* vs *ninaE*[17]	2.50E-06	0.71	6*4	3*4	large
826 on transient	*iso* vs *ninaE*[17]	1.90E-08	0.78	6*4	3*4	large
827 off transient	*iso* vs *ninaE*[17]	1.60E-09	0.81	6*4	3*4	large
828 receptor potential	*iso* vs *ninaE*[5]	4.40E-01	0.17	3*4	3*4	
829 receptor potential	*iso* vs *ninaE*[8]	4.40E-06	0.83	3*4	3*4	large
830 receptor potential	*ninaE*[5] vs *ninaE*[8]	4.40E-06	0.84	3*4	3*4	large
831 on transient	*iso* vs *ninaE*[5]	1.70E-03	0.64	3*4	3*4	large
832 on transient	*iso* vs *ninaE*[8]	4.40E-06	0.84	3*4	3*4	large
833 on transient	*ninaE*[5] vs *ninaE*[8]	5.97E-02	0.39	3*4	3*4	
834 off transient	*iso* vs *ninaE*[5]	1.70E-02	0.48	3*4	3*4	moderate
835 off transient	*iso* vs *ninaE*[8]	1.10E-06	0.85	3*4	3*4	large
836 off transient	*ninaE*[5] vs *ninaE*[8]	1.10E-06	0.85	3*4	3*4	large

837 **n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison; * sample size in
838 ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

841　**Table 2. Statistics of a. sleep and b. ERG parameters for *norpA* mutants**

a. sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
day sleep bout length	*iso* vs *norpA*^{p24}	9.40E-03	0.39	23	21	moderate
night sleep bout length	*iso* vs *norpA*^{p24}	2.50E-06	0.66	23	21	large
day sleep	*iso* vs *norpA*^{p24}	3.20E-02	0.32	23	21	moderate
night sleep	*iso* vs *norpA*^{p24}	1.20E-01	0.23	23	21	
day wake activity	*iso* vs *norpA*^{p24}	9.40E-03	0.39	23	21	moderate
night wake activity	*iso* vs *norpA*^{p24}	1.70E-07	0.72	23	21	large
b.ERG parameter	**genotype comparison**	**p-value**	**effect size *r***	**n1**	**n2**	**significant *r* magnitude**
receptor potential	*iso* vs *norpA*^{p24}	1.50E-06	0.85	4*4	4*4	large
on transient	*iso* vs *norpA*^{p24}	3.30E-09	0.85	4*4	4*4	large
off transient	*iso* vs *norpA*^{p24}	1.50E-06	0.85	4*4	4*4	large

853　**n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison; * sample size in
854　ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

856 **Table 3. Statistics of a. sleep and b. ERG parameters for *trp* mutants**

a. sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
858 day sleep	*Canton S* vs *Oregon R*	5.33E-01	0.07	38	53	
859 day sleep	*Canton S* vs trp^{1}	1.50E-04	0.47	38	30	moderate
860 day sleep	*Oregon R* vs trp^{1}	2.90E-06	0.54	53	30	large
861 night sleep	*Canton S* vs *Oregon R*	1.20E-04	0.41	38	53	moderate
862 night sleep	*Canton S* vs trp^{1}	1.63E-02	0.29	38	30	small
863 night sleep	*Oregon R* vs trp^{1}	2.30E-07	0.59	53	30	large
864 day sleep bout length	*Canton S* vs *Oregon R*	8.66E-01	0.02	38	53	
865 day sleep bout length	*Canton S* vs trp^{1}	1.40E-02	0.32	38	30	moderate
866 day sleep bout length	*Oregon R* vs trp^{1}	1.20E-02	0.32	53	30	moderate
867 night sleep bout length	*Canton S* vs *Oregon R*	6.61E-01	0.05	38	53	
868 night sleep bout length	*Canton S* vs trp^{1}	5.20E-03	0.35	38	30	moderate
869 night sleep bout length	*Oregon R* vs trp^{1}	1.20E-03	0.39	53	30	moderate
870 day wake activity	*Canton S* vs *Oregon R*	8.20E-08	0.58	38	53	large
871 day wake activity	*Canton S* vs trp^{1}	7.70E-01	0.04	38	30	
872 day wake activity	*Oregon R* vs trp^{1}	2.90E-07	0.57	53	30	large
873 night wake activity	*Canton S* vs *Oregon R*	1.20E-07	0.58	38	53	large
874 night wake activity	*Canton S* vs trp^{1}	1.60E-02	0.31	38	30	moderate
875 night wake activity	*Oregon R* vs trp^{1}	6.70E-02	0.20	53	30	
876 day sleep	*iso* vs trp^{MB}	5.80E-01	0.09	16	24	
877 night sleep	*iso* vs trp^{MB}	3.70E-03	0.46	16	24	moderate
878 day sleep bout length	*iso* vs trp^{MB}	3.20E-01	0.16	16	24	
879 night sleep bout length	*iso* vs trp^{MB}	3.90E-01	0.14	16	24	
880 day wake activity	*iso* vs trp^{MB}	1.40E-03	0.49	16	24	moderate
881 night wake activity	*iso* vs trp^{MB}	2.90E-01	0.17	16	24	
882 **b.ERG parameter**	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
883 receptor potential	*iso* vs trp^{1}	7.40E-07	0.85	3*4	3*4	large
884 on transient	*iso* vs trp^{1}	2.20E-05	0.78	3*4	3*4	large
885 off transient	*iso* vs trp^{1}	7.40E-07	0.85	3*4	3*4	large
886 receptor potential	*iso* vs trp^{MB}	4.40E-03	0.53	3*4	4*4	large
887 on transient	*iso* vs trp^{MB}	2.60E-07	0.83	3*4	4*4	large
888 off transient	*iso* vs trp^{MB}	5.70E-01	0.11	3*4	4*4	

889 **n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison; * sample size in
890 ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

892 **Table 4. Statistics of a. sleep and b. ERG parameters for *trpl* mutants**

a. sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
day sleep	*iso* vs $trpl^{302}$	1.40E-02	0.32	30	30	moderate
night sleep	*iso* vs $trpl^{302}$	1.40E-06	0.62	30	30	large
day sleep bout length	*iso* vs $trpl^{302}$	1.40E-06	0.59	30	30	large
night sleep bout length	*iso* vs $trpl^{302}$	6.90E-01	0.05	30	28	
day wake activity	*iso* vs $trpl^{302}$	1.10E-08	0.68	30	30	large
night wake activity	*iso* vs $trpl^{302}$	9.70E-04	0.43	30	28	moderate
day sleep	*iso/iso* vs $trpl^{302}/trpl^{MB}$	3.70E-05	0.63	23	24	large
day sleep	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	3.71E-02	0.32	23	21	moderate
day sleep	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	2.57E-02	0.35	24	21	moderate
night sleep	*iso/iso* vs $trpl^{302}/trpl^{MB}$	7.32E-02	0.28	24	22	
night sleep	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	1.56E-02	0.39	24	23	moderate
night sleep	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	1.52E-01	0.22	22	23	
day sleep bout length	*iso/iso* vs $trpl^{302}/trpl^{MB}$	1.60E-04	0.59	23	23	large
day sleep bout length	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	1.60E-04	0.58	23	21	large
day sleep bout length	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	8.69E-01	0.03	23	21	
night sleep bout length	*iso/iso* vs $trpl^{302}/trpl^{MB}$	2.20E-01	0.23	23	22	
night sleep bout length	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	8.42E-02	0.31	23	21	
night sleep bout length	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	4.82E-01	0.13	22	21	
day wake activity	*iso/iso* vs $trpl^{302}/trpl^{MB}$	1.20E-04	0.58	23	23	large
day wake activity	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	9.63E-01	0.01	23	21	
day wake activity	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	1.04E-03	0.50	23	21	large
night wake activity	*iso/iso* vs $trpl^{302}/trpl^{MB}$	2.91E-01	0.21	23	22	
night wake activity	*iso/iso* vs $trpl^{MB}/trpl^{MB}$	6.31E-01	0.12	23	21	
night wake activity	$trpl^{302}/trpl^{MB}$ vs $trpl^{MB}/trpl^{MB}$	7.10E-01	0.07	22	21	
b.ERG parameter	**genotype comparison**	**p-value**	**effect size *r***	**n1**	**n2**	**significant *r* magnitude**
receptor potential	*iso* vs $trpl^{302}$	2.20E-01	0.26	6*4	3*4	
receptor potential	*iso* vs $trpl^{MB}$	8.60E-01	0.03	6*4	5*4	
receptor potential	$trpl^{302}$ vs $trpl^{MB}$	2.20E-01	0.26	3*4	5*4	
on transient	*iso* vs $trpl^{302}$	2.40E-06	0.73	6*4	3*4	large
on transient	*iso* vs $trpl^{MB}$	1.50E-01	0.22	6*4	5*4	
on transient	$trpl^{302}$ vs $trpl^{MB}$	1.00E-05	0.80	3*4	5*4	large
off transient	*iso* vs $trpl^{302}$	4.80E-09	0.81	6*4	3*4	large
off transient	*iso* vs $trpl^{MB}$	9.90E-01	0.00	6*4	5*4	
off transient	$trpl^{302}$ vs $trpl^{MB}$	5.30E-08	0.81	3*4	5*4	large

928 **n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison; * sample size in
929 ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

932 **Table 4. Statistics of a. sleep and b. ERG parameters for *hdc* mutants**

a. sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
day sleep	hdc^{MB} vs *iso*	1.10E-01	0.29	16	16	
day sleep	hdc^{JK910} vs *iso*	7.30E-05	0.60	24	23	large
night sleep	hdc^{MB} vs *iso*	1.40E-02	0.44	16	16	moderate
night sleep	hdc^{JK910} vs *iso*	4.99E-03	0.42	24	23	moderate
day sleep bout length	hdc^{MB} vs *iso*	4.50E-01	0.14	16	16	
day sleep bout length	hdc^{JK910} vs *iso*	1.08E-01	0.25	24	23	
night sleep bout length	hdc^{MB} vs *iso*	1.50E-02	0.43	16	16	moderate
night sleep bout length	hdc^{JK910} vs *iso*	2.50E-06	0.66	24	23	large
day wake activity	hdc^{MB} vs *iso*	8.70E-01	0.03	16	16	
day wake activity	hdc^{JK910} vs *iso*	2.50E-01	0.19	24	23	
night wake activity	hdc^{MB} vs *iso*	5.60E-01	0.11	16	16	
night wake activity	hdc^{JK910} vs *iso*	1.50E-06	0.68	24	23	large
b.ERG parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
receptor potential	*iso* vs hdc^{JK910}	8.00E-01	0.24	3*4	3*4	
receptor potential	*iso* vs hdc^{MB}	4.00E-01	0.06	3*4	3*4	
receptor potential	hdc^{JK910} vs hdc^{MB}	3.80E-01	0.32	3*4	3*4	
on transient	*iso* vs hdc^{JK910}	4.20E-05	0.72	3*4	3*4	large
on transient	*iso* vs hdc^{MB}	2.20E-04	0.79	3*4	3*4	large
on transient	hdc^{JK910} vs hdc^{MB}	9.32E-01	0.02	3*4	3*4	
off transient	*iso* vs hdc^{JK910}	5.50E-05	0.85	3*4	3*4	large
off transient	*iso* vs hdc^{MB}	2.20E-06	0.85	3*4	3*4	large
off transient	hdc^{JK910} vs hdc^{MB}	4.80E-04	0.72	3*4	3*4	large

956 **n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison; * sample size in
957 ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

959 Table 5. Statistics of a. sleep and b. ERG parameters for *ort* mutants

a. sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
day sleep	*Canton S* vs ort^{1}	5.20E-03	0.27	60	47	small
night sleep	*Canton S* vs ort^{1}	1.00E-01	0.16	60	47	
day sleep bout length	*Canton S* vs ort^{1}	2.60E-04	0.35	60	47	moderate
night sleep bout length	*Canton S* vs ort^{1}	7.30E-01	0.04	60	47	
day wake activity	*Canton S* vs ort^{1}	1.10E-08	0.55	60	47	large
night wake activity	*Canton S* vs ort^{1}	6.60E-01	0.03	60	47	
day sleep	*iso* vs ort^{attp}	4.10E-09	0.68	48	29	large
day sleep	*iso* vs $ort^{attp/+}$	8.30E-01	0.02	48	49	
day sleep	ort^{attp} vs $ort^{attp/+}$	4.50E-10	0.73	29	49	large
night sleep	*iso* vs ort^{attp}	6.10E-09	0.67	48	29	large
night sleep	*iso* vs $ort^{attp/+}$	1.50E-02	0.25	48	49	small
night sleep	ort^{attp} vs $ort^{attp/+}$	5.50E-10	0.72	29	49	large
day sleep bout length	*iso* vs ort^{attp}	6.20E-02	0.21	48	29	
day sleep bout length	*iso* vs $ort^{attp/+}$	1.80E-04	0.39	48	49	moderate
day sleep bout length	ort^{attp} vs $ort^{attp/+}$	9.00E-07	0.55	29	49	large
night sleep bout length	*iso* vs ort^{attp}	1.50E-02	0.32	48	29	moderate
night sleep bout length	*iso* vs $ort^{attp/+}$	7.50E-02	0.20	48	49	
night sleep bout length	ort^{attp} vs $ort^{attp/+}$	3.71E-01	0.10	29	49	
day wake activity	*iso* vs ort^{attp}	9.90E-07	0.55	48	29	large
day wake activity	*iso* vs $ort^{attp/+}$	3.00E-02	0.22	48	49	small
day wake activity	ort^{attp} vs $ort^{attp/+}$	6.70E-05	0.45	29	49	moderate
night wake activity	*iso* vs ort^{attp}	4.70E-08	0.60	48	29	large
night wake activity	*iso* vs $ort^{attp/+}$	4.00E-03	0.29	48	49	small
night wake activity	ort^{attp} vs $ort^{attp/+}$	3.00E-06	0.52	29	49	large
b. ERG parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
receptor potential	*iso* vs ort^{1}	2.70E-08	0.83	5*4	3*4	large
receptor potential	*iso* vs ort^{attp}	9.80E-01	0.01	5*4	3*4	
receptor potential	ort^{1} vs ort^{attp}	1.10E-06	0.85	3*4	3*4	large
on transient	*iso* vs ort^{1}	9.30E-08	0.81	5*4	3*4	large
on transient	*iso* vs ort^{attp}	9.30E-08	0.81	5*4	3*4	large
on transient	ort^{1} vs ort^{attp}	2.20E-01	0.26	3*4	3*4	
off transient	*iso* vs ort^{1}	2.70E-08	0.83	5*4	3*4	large
off transient	*iso* vs ort^{attp}	4.90E-06	0.83	5*4	3*4	large
off transient	ort^{1} vs ort^{attp}	7.90E-01	0.06	3*4	3*4	

995 n1 = sample size for first genotype in genotype comparison; n2 = sample size for first genotype in genotype comparison; * sample size in
996 ERG statistic is actual sample size multiple with four reflecting the values from the four light intensities

Table 6. Statistics of sleep parameters for *gmrGal4>UAS-Kir2 and Rh1Gal4>UAS-Kir2* lines

	sleep parameter	genotype comparison	p-value	effect size *r*	n1	n2	significant *r* magnitude
1000	day sleep	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	6.90E-03	0.36	32	32	moderate
1001	day sleep	gmr-Gal4>+ vs +>UAS-Kir2	1.18E-01	0.20	32	32	
1002	day sleep	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	1.50E-04	0.51	32	32	large
1003	night sleep	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	3.90E-01	0.11	32	32	
1004	night sleep	gmr-Gal4>+ vs +>UAS-Kir2	2.10E-06	0.62	32	32	large
1005	night sleep	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	3.80E-04	0.46	32	32	moderate
1006	day sleep bout length	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	8.80E-01	0.02	32	32	
1007	day sleep bout length	gmr-Gal4>+ vs +>UAS-Kir2	6.00E-01	0.11	32	32	
1008	day sleep bout length	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	6.00E-01	0.12	32	32	
1009	night sleep bout length	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	2.70E-01	0.14	32	32	
1010	night sleep bout length	gmr-Gal4>+ vs +>UAS-Kir2	1.14E-01	0.22	32	32	
1011	night sleep bout length	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	5.50E-02	0.30	32	32	
1012	day wake activity	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	9.73E-01	0.01	32	32	
1013	day wake activity	gmr-Gal4>+ vs +>UAS-Kir2	7.10E-03	0.35	32	32	moderate
1014	day wake activity	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	7.10E-03	0.37	32	32	moderate
1015	night wake activity	gmr-Gal4>+ vs gmr-Gal4>UAS-Kir2	1.10E-04	0.50	32	32	moderate
1016	night wake activity	gmr-Gal4>+ vs +>UAS-Kir2	3.32E-02	0.29	32	32	small
1017	night wake activity	gmr-Gal4>UAS-Kir2 vs +>UAS-Kir2	2.37E-01	0.15	32	32	
1018	day sleep	+>UAS-Kir2 vs Rh1-Gal4>+	2.60E-02	0.29	28	31	small
1019	day sleep	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	1.10E-02	0.36	28	30	moderate
1020	day sleep	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	2.00E-05	0.58	31	30	large
1021	night sleep	+>UAS-Kir2 vs Rh1-Gal4>+	4.90E-08	0.74	28	31	large
1022	night sleep	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	3.99E-03	0.38	28	30	moderate
1023	night sleep	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	9.40E-04	0.44	31	30	moderate
1024	day sleep bout length	+>UAS-Kir2 vs Rh1-Gal4>+	8.74E-01	0.02	28	31	
1025	day sleep bout length	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	6.60E-03	0.37	28	30	moderate
1026	day sleep bout length	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	1.50E-03	0.44	31	30	moderate
1027	night sleep bout length	+>UAS-Kir2 vs Rh1-Gal4>+	6.70E-01	0.07	28	31	
1028	night sleep bout length	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	4.40E-01	0.19	28	30	
1029	night sleep bout length	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	6.70E-01	0.06	31	30	
1030	day wake activity	+>UAS-Kir2 vs Rh1-Gal4>+	3.10E-04	0.48	28	31	moderate
1031	day wake activity	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	4.40E-06	0.63	28	30	large
1032	day wake activity	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	9.60E-01	0.01	31	30	
1033	night wake activity	+>UAS-Kir2 vs Rh1-Gal4>+	4.80E-07	0.62	28	31	large
1034	night wake activity	+>UAS-Kir2 vs Rh1-Gal4>UAS-Kir2	6.90E-08	0.68	28	30	large
1035	night wake activity	Rh1-Gal4>+ vs Rh1-Gal4>UAS-Kir2	2.00E-01	0.17	31	30	

1036   **n1** = sample size for first genotype in genotype comparison; **n2** = sample size for first genotype in genotype comparison

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