Figure S6: **Strain differences in sleep and sleep over time**. Average daytime (A) and nighttime (B) sleep across strain. For each fly, the mean sleep is determined by ShinyR-DAM. ShinyR-DAM uses a sliding five-minute window to determine sleep events, where a sleep event is defined as five continuous minutes with no movement. Each column shows the average of the mean sleep across all flies for each genotype.

(A-B) We examined the impact of mating on sleep in three strains with germline tissue: *white* Canton S (wCS, black bars), Berlin (dark gray bars), and *tud/+* with germline (light gray). For these conditions, wCS females were mated to wCS males. Berlin and *tud/+* females were mated to Berlin males. Error bars are standard error of the mean.

Matching letters are not significantly different from one another. No letter or different letters are significantly different at a minimum $P<0.05$ (Tukey-HSD) cut-off. There was a significant effect of both strain and mating, as well as a significant interaction between strain and mating ($P≤0.0001$ for all, two-way ANOVA).

wCS had a significant post-mating reduction in daytime sleep ($P< 0.0001$, Tukey-HSD). wCS also had a significant, post-mating reduction in nighttime sleep ($P< 0.0001$, Tukey-HSD), whereas it was previously shown to have no difference in nighttime sleep (DOVE et al. 2017).

Berlin exhibited a significant post-mating increase in daytime sleep ($P=0.0482$, Tukey-HSD). All statistical results are presented in Table S5.

(C) Sleep across days. Average sleep for each condition is plotted against ZT time with lights on at 8 and lights off at 20 [H]. The number of days post-mating (PM) are indicated across the top for mated females. The Virgins are aged matched. ShinyR-DAM uses a sliding five-minute window to determine sleep events, where a sleep event is defined as five continuous minutes with no movement. Each line shows the average of the mean sleep across all flies for each genotype.