Supporting Information

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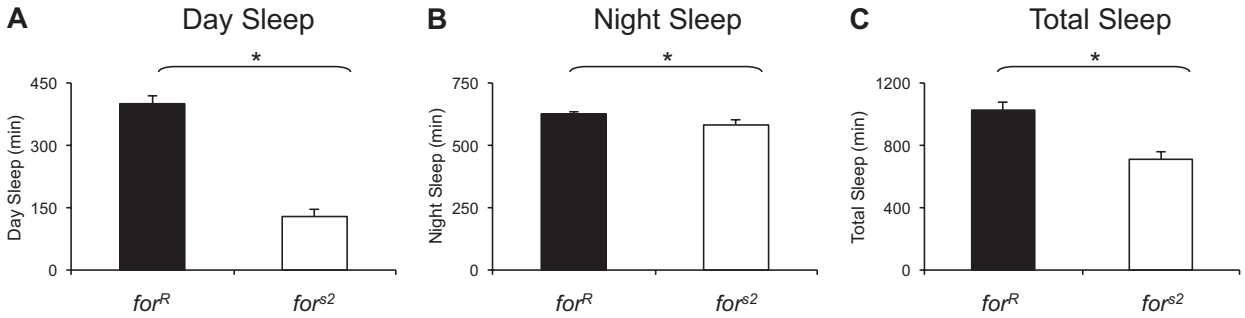

Fig. S1. Polymorphisms at the *foraging* (*for*) locus alter sleep in *Drosophila*. (*A*) for^{s2} mutants show significantly less daytime sleep than *rover* flies (one-tailed *t* test, $P = 0.039$, $n = 30$ each group). (*B*) for^{s2} mutants show significantly less nighttime sleep than *rover* flies (one-tailed *t* test, $P = 4.8 \times 10^{-15}$, $n = 30$ each group). (*C*) for^{s2} mutants show significantly less overall sleep than *rover* (for^R) flies (one-tailed *t* test, $P = 3.58 \times 19^{-14}$, $n = 30$ each group). Data are presented as mean ± SEM.

Table S1. Control metrics consisting of time-to-complete test (TCT), phototaxis index (PI), and quinine sensitivity index (QSI) for each experiment

Genotype	TCT* % control ± SEM	PI† Mean ± SEM (n)	QSI‡ Mean ± SEM (n)
for^R	13.14 ± 0.40	83 ± 4.72 (6)	4:26 ± 0:17 (6)
for^s	13.28 ± 1.38	80 ± 5.16 (6)	4:14 ± 0:20 (6)
for^{s2}	12.14 ± 0.50	93 ± 3.33 (6)	4:28 ± 0:14 (6)
for^s; UAS-*for*T1	12.25 ± 0.25	80 ± 2.58 (6)	4:24 ± 0:20 (6)
for^s; C739	12.12 ± 0.22	75 ± 5.00 (6)	3:51 ± 0:15 (6)
for^s; C739/UAS-*for*T1	13.28 ± 0.52	83 ± 2.10 (10)	4:11 ± 0:22 (6)
for^s; 30y	14.50 ± 0.42	73 ± 4.94 (6)	4:01 ± 0:14 (6)
for^s; 30y/UAS-*for*T1	14.57 ± 0.71	77 ± 5.07 (6)	3:58 ± 0:26 (6)

*TCT represents observed times to complete 16 trials during training. Sample size is therefore the same as for the corresponding figures in the text.
†PI is calculated as the average proportion of visits to the light alley of the T maze during 10 trials in the absence of quinine. The final phototaxis index is the average of the scores ± SEM.
‡QSI was determined by calculating the time in seconds that the fly spent on the dry side of the tube when the other side had been wetted with quinine during a 5-min period.

Table S2. Statistical tests for responses to sleep deprivation and starvation (Fig. 1)

Condition	Statistics
(*A*) Sleep homeostasis (one-way ANOVA for genotype)	$F_{[2,139]} = 10.702$, $P = 7.6 \times 10^{-5}$ $n = 45$–52 each group
(*B*) Short-term memory after sleep deprivation (two-way ANOVA for genotype x condition)	$F_{[2,61]} = 4.065$, $P = 0.022$ $n = 10$ each group (main effect for genotype)
(*C*) Acute starvation (one-way ANOVA for genotype)	$F_{[2,42]} = 12.253$, $P = 1 \times 10^{-18}$ $n = 14$–16 each group
(*D*) Short-term memory after starvation (two-way ANOVA for genotype x condition)	$F_{[2,59]} = 4.552$, $P = 0.015$ $n = 10$ each group (genotype x condition interaction)
(*E*) Short-term memory complementation (for^s/for^{s2}) (one-way ANOVA for condition)	$F_{[2,21]} = 5.167$, $P = 0.015$ $n = 8$ each group (main effect for condition)

Table S3. Statistical tests for social enrichment and long-term courtship memory (Fig. 2)

Condition	Statistics		
(*A*) Social enrichment (one-way ANOVA for genotype)	$F_{[2,44]} = 12.180$, $P = 6.18 \times 10^{-5}$ n = 15–16 each group		
	for^R	for^s	for^{s2}
(*B*) Courtship long-term memory	$F_{[2,48]} = 6.927$, $P = 0.002$ n = 11–26 each group	$F_{[2,77]} = 4.551$, $P = 0.014$ n = 26–27 each group	$P = 0.55$ Two-sample t test

Table S4. Statistical tests for *for* overexpression and RNAi (Fig. 3)

Condition	Statistics
(*A*–*C*) Sleep homeostasis (one-way ANOVA for genotype)	$F_{[6,90]} = 5.841$, $P = 3.5 \times 10^{-5}$ n = 11–16 each group
(*D* and *E*) Short-term memory after sleep deprivation (one-way ANOVA for genotype)	$F_{[1,66]} = 8.866$, $P = 0.004$ n = 6–9 each group
(*F*) Short-term memory with *foraging* RNAi	$F_{[4,59]} = 3.523$, $P = 0.012$ n = 7–9 each group
(*G*–*I*) Courtship long-term memory	$F_{[6,194]} = 16.638$, $P = 1.4 \times 10^{-11}$ n = 9–24

Table S5. Statistical tests for short-term memory after starvation (Fig. 4)

Condition	Statistics
(*A*) c739 overexpression (repeated-measures ANOVA for genotype)	$F_{[142,3440]} = 12.523$, $P = 1.0 \times 10^{-15}$ n = 14–24 each group, genotype x hour interaction
(*B*) 30y overexpression (repeated-measures ANOVA for genotype)	$F_{[142,2982]} = 7.87$, $P = 1.0 \times 10^{-15}$ n = 14–16 each group, genotype x hour interaction
(*C*) 201y overexpression (repeated-measures ANOVA for genotype)	$F_{[71,1775]} = 1.197$, $P = 0.135$ n = 14–15 each group, genotype x hour interaction