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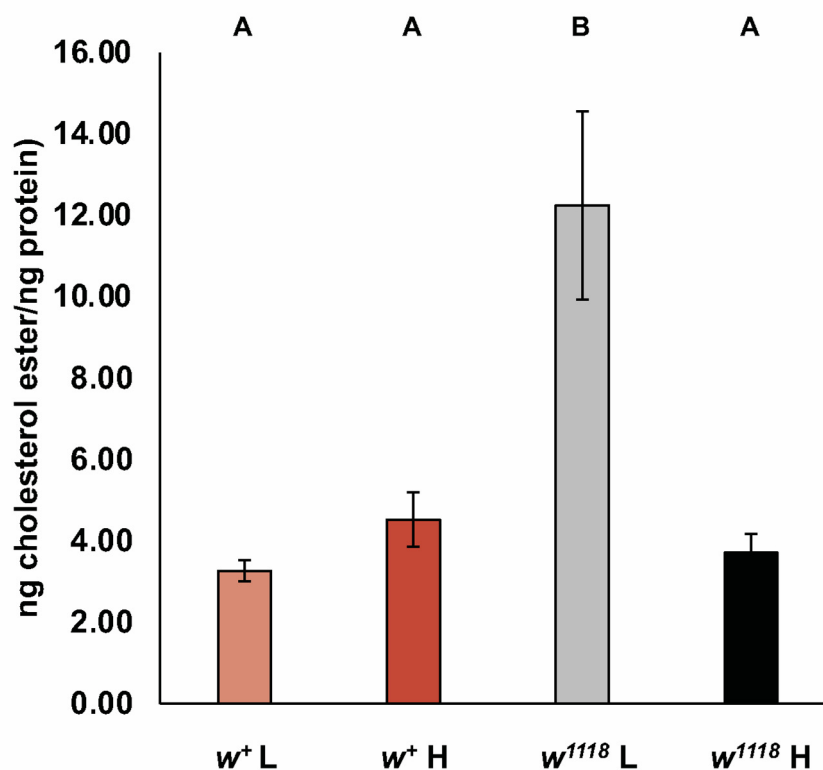
# Mutants of the *white* ABCG Transporter in *Drosophila melanogaster* Have Deficient Olfactory Learning and Cholesterol Homeostasis

## Supplementary Materials

**Table S1.** Odor and Shock Avoidance Controls.

| Experiment   | Genotype   | Shock Avoid-<br>ance | OCT Avoid-<br>ance   | MCH Avoid-<br>ance   |
|--|--|----------------------|----------------------|----------------------|
| 40mM 5-HTP<br>Treatment Ef-<br>fects on Naïve<br>Avoidance                                   | <b>Canton-S (+)</b>  | <b>0.705 ± 0.035</b> | <b>0.462 ± 0.056</b> | <b>0.558 ± 0.062</b> |
|  | Canton-S (+)   | 0.518 ± 0.050*       | 0.482 ± 0.098        | 0.514 ± 0.093        |
|  | + 40mM 5-HTP   |                      |                      |                      |
|  | <i>white</i> <sup>1118</sup>                                       | 0.736 ± 0.023        | 0.247 ± 0.086        | 0.633 ± 0.072        |
|  | <i>white</i> <sup>1118</sup>                                       | 0.659 ± 0.0317       | 0.260 ± 0.111        | 0.594 ± 0.066        |
|  | + 40 mM 5-HTP  | n = 10               | n = 12               | n = 10               |
| L-dopa Treat-<br>ment Effects on<br>Naïve Avoid-<br>ance                                     | <b>Canton-S (+)</b>  | <b>0.755 ± 0.076</b> | <b>0.478 ± 0.050</b> | <b>0.255 ± 0.055</b> |
|  | Canton-S (+)   | 0.743 ± 0.030        | 0.186 ± 0.058*       | 0.226 ± 0.062        |
|  | + 2 mg/ml L-dopa   |                      |                      |                      |
|  | <i>white</i> <sup>1118</sup>                                       | 0.867 ± 0.046        | 0.415 ± 0.029        | 0.259 ± 0.050        |
|  | <i>white</i> <sup>1118</sup>                                       | 0.855 ± 0.025        | 0.430 ± 0.037        | 0.334 ± 0.027        |
|  | + 2 mg/ml L-dopa   | n = 4                | n = 8                | n = 8                |
| Naïve Avoid-<br>ance of ABCG<br>mutants  | <b>Canton-S (+)</b>  | <b>0.751 ± 0.024</b> | <b>0.544 ± 0.069</b> | <b>0.752 ± 0.067</b> |
|  | <i>Atet</i> <sup>MI 01881</sup>                                    | 0.735 ± 0.040        | 0.329 ± 0.052        | 0.194 ± 0.104*       |
|  | <i>CG4822</i> <sup>MI 13074</sup>                                  | 0.824 ± 0.014        | 0.285 ± 0.057*       | 0.316 ± 0.104*       |
|  | <i>CG9663</i> <sup>MI 11447</sup>                                  | 0.852 ± 0.023        | 0.357 ± 0.048        | 0.326 ± 0.113*       |
|  | <i>CG3164</i> <sup>MI 06431</sup>                                  | 0.835 ± 0.022        | 0.297 ± 0.068        | 0.300 ± 0.101*       |
|  | <i>CG3164</i> <sup>MI 10825</sup>                                  | 0.855 ± 0.013        | 0.287 ± 0.067*       | 0.347 ± 0.136*       |
|  | <i>CG17646</i> <sup>MI 04004</sup>                                 | 0.738 ± 0.032        | 0.291 ± 0.095*       | 0.401 ± 0.131        |
|  | <i>w</i> <sup>1118</sup>   | 0.739 ± 0.036        | 0.611 ± 0.578        | 0.730 ± 0.065        |
|  |  | n = 10               | n = 10               | n = 10               |
| Naïve Avoid-<br>ance of<br><i>CG17646</i> and<br><i>w</i> <sup>1118</sup> Heterozy-<br>gotes | <b>Canton-S (+)</b>  | <b>N/A</b>           | <b>0.359 ± 0.070</b> | <b>0.802 ± 0.076</b> |
|  | +; <i>CG17646</i> <sup>MI 04004</sup> /+                           | N/A                  | 0.254 ± 0.076        | 0.803 ± 0.078        |
|  | <i>w</i> <sup>1118</sup> /+; +                                     | N/A                  | 0.399 ± 0.083        | 0.777 ± 0.079        |
|  | <i>w</i> <sup>1118</sup> /+; <i>CG17646</i> <sup>MI 04004</sup> /+ | N/A                  | 0.351 ± 0.083        | 0.743 ± 0.096        |
|  | <i>w</i> <sup>1118</sup> ; +                                       | N/A                  | 0.428 ± 0.083        | 0.803 ± 0.062        |
|  |  |                      | n = 8                | n = 8                |
| Naïve Avoid-<br>ance of <i>CG3164</i><br>and <i>w</i> <sup>1118</sup> Heter-<br>ozygotes     | <b>Canton-S (+)</b>  | <b>N/A</b>           | <b>0.570 ± 0.040</b> | <b>0.729 ± 0.099</b> |
|  | +; <i>CG3164</i> <sup>MI 06431</sup> /+                            | N/A                  | 0.187 ± 0.121*       | 0.467 ± 0.172        |
|  | <i>w</i> <sup>1118</sup> /+; +                                     | N/A                  | 0.377 ± 0.133        | 0.648 ± 0.136        |
|  | <i>w</i> <sup>1118</sup> /+; <i>CG3164</i> <sup>MI 06431</sup> /+  | N/A                  | 0.303 ± 0.107        | 0.475 ± 0.167        |
|  | <i>w</i> <sup>1118</sup> ; +                                       | N/A                  | 0.589 ± 0.039        | 0.692 ± 0.112        |
|  |  |                      | n = 10               | n = 10               |

\*Denotes a significance difference from wildtype Canton-S control in bold (Two-sided Dunnett Analysis of difference between Canton-S wildtype control and experimental genotype with 95% confidence interval).



**Figure S1.** Cholesterol Feeding Differentially Affects Wildtype and  $w^{1118}$  Total Cholesterol Ester Levels. Canton-S ( $w^+$ ) and  $w^{1118}$  flies were reared on a low or high (0.1 mg/mL added) cholesterol containing food.  $w^{1118}$  mutants raised on the low cholesterol diet have greatly increased cholesterol esters compared to wildtype controls and  $w^{1118}$  mutants raised on the high cholesterol diet (Two-way ANOVA, Adj.  $R^2 = 0.747$ ,  $F_{3,8} = 11.829$ ,  $p < 0.003$ ,  $n = 3$ ; Tukey low vs. high cholesterol,  $p < 0.018$ ; Tukey  $w^+$  vs.  $w^{1118}$ ,  $p < 0.010$ ). Groups that do not share letters above the columns are significantly different from each other according to the Tukey post-hoc test ( $p < 0.05$ ).