

Figure S1. Behavioral strategies in anemotaxis in control attP2-attP40>TNT (Related to Figure 2). A. Relative probability of headings during runs. B. Speed versus heading during runs C. Mean heading change in runs D. Turn rate versus heading E. Turn size versus heading F. Distribution of turns from perpendicular direction G. Distribution of head sweeps from perpendicular direction H. Probability of starting a run during a headsweep. A-E Values are mean and s.e.m F-H. In the box plot the median is indicated by the horizontal line. Box boundaries represent first and third quartiles, whiskers extend to the most extreme data points not considered outliers. The outliers are indicated by red +. The outliers are indicated by red +. *: p<0.05, **: p<0.01, ***:<p<0.001 (p-values can be found in Data S1 and the N of animals can be found in Table S2).



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Figure S2. Navigational index in y axis and mean speed in runs of larvae with silenced somatosensory neurons (Related to Figure 3).

A. Navigational index in y axis for the sensory lines and controls B. Mean speed in runs for the inactivated sensory lines and control (*left panel*) 95% confidence interval on the ratio of the inactivated sensory lines mean run speed to the control mean run speed (*right panel*). Bootstrapped values are shown. In the box plot the median is indicated by the horizontal line. Box boundaries represent first and third quartiles, whiskers extend to the most extreme data points not considered outliers. The outliers are indicated by red +. *: p<0.05, **: p<0.01, ***:p<0.001 (p-values can be found in Data S1 and Table S2)



Figure S3. Behavioral inactivation screen (Related to Figure 4).

A Flowchart of the behavioral screen B. Z-score distribution of the tested lines C. Results of 205 tested lines in the anemotaxis assay sorted by performance. Mean navigational indices are shown. The attP2>TNT and attP2-40>TNT controls are shown in blue. The hit lines shown in this paper are shown in red. The chordotonal line is shown in green. Note that some lines that have similar navigational indices as the hit lines were not chosen for follow up, because they had stochastic neuronal expression patterns (The navigational indices can be found in Table S1).



Figure S4. Mean speed in runs and navigational index in y axis of the hit lines (Related to Figure 4). A. Mean speed in runs in non-stimulus conditions (*left panel*). 95% confidence interval on the ratio of the inactivated lines mean run speed to the control mean run speed (*right panel*). For most of the CNS neuron lines (except for *SS00721*, *SS00878*, *SS01948*), the confidence interval includes 1, so we cannot say that the speeds are not the same. B. Navigational index in y axis for the eight hit lines. None of the CNS lines had the navigational index in y axis significantly different than the controls (p-values and N of animals can be found in Data S1 and Table S2). Bootstrapped values are shown. In the box plot the median is indicated by the horizontal line. Box boundaries represent first and third quartiles, whiskers extend to the most extreme data points not considered outliers. The outliers are indicated by red +.



Figure S5. Detailed anatomy of light and electron microscopy images (Related to Figure 5).

A. The left panel depicts a brain with stochastic single-cell expression of SS00886, which morphologically matches its EM correlate (*right panel*). B. The two left panels depict single-cell abdominal and thoracic neurons, which were revealed by multicolor flip-out (MCFO) of the constituent GAL4 parts of *SS01401*. These morphologically match the EM correlate in both x-y and x-z views (right panels). C. The left panel depicts a brain with stochastic single-cell expression of *SS00721*, which matches its EM correlate (*middle panel*). Note that the brain is rotated in a different orientation in LM compared to EM. The right panel displays the axon terminals in the brain with similar brain orientation between LM and EM. D. MCFO of *89G07-GAL4*, a constituent part of *SS00911*. Abdominal single-cell clones morphologically match the EM reconstruction (*middle, right panels*). Scale bars are 50 µm unless indicated as 10 µm.