



Supplementary Figure 1. Evaluation of gene expression from *ins-l* flies placed into a separate genetic background.

A) Schematic of re-selection and back-selection procedures. *ins-l* flies were out-crossed to w^{1118} . After each cross, white-eyed progeny that displayed short-sleep, short sleep bouts and hyperactivity were identified and then crossed again to normal-sleeping w^{1118} flies. This was repeated 5 times creating a new stock, *ins-l^w*. *ins-l^w* flies were then re-selected to obtain insomnia-like flies (left) and back-selected 20 generations to obtain normal sleeping flies (*ns^w*, right). Sleep graph: daily sleep in min/h for 24h for *ins-l^w* (daily sleep: 34 ± 6 min, average nighttime sleep bout duration: 14 ± 6 min, $n=20$) and *ns^w* flies (daily sleep: 825 ± 25 min, average nighttime sleep bout duration 73 ± 8 min, $n=32$). **B)** QPCR confirmation of gene expression changes in *ins-l* flies expressed as % change from Cs flies (*ins-l*/Cs) and *ins-l^w* as a percentage of *ns^w* controls (*ins-l^w*/*ns^w*).