

Supplementary information

Histone methyltransferase G9a is a key regulator of the starvation-induced behaviors in *Drosophila melanogaster*

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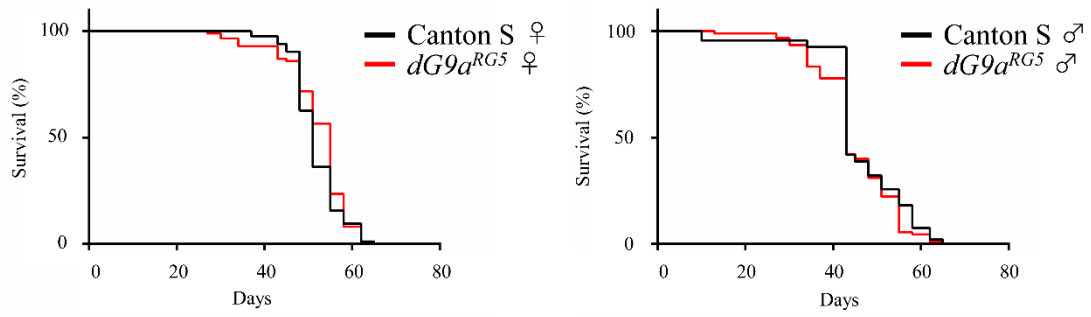


Figure S1 The results of life span assays using males and females of the wild-type (Canton S) (♀; n=83 from 5 independent experiments, ♂; n=93 from 5 independent experiments) and *dG9a* null mutant (*dG9a^{RG5}*) (♀; n=85 from 5 independent experiments, ♂; n=90 from 5 independent experiments). ♀; $P = 0.18$. ♂; $P = 0.09$.

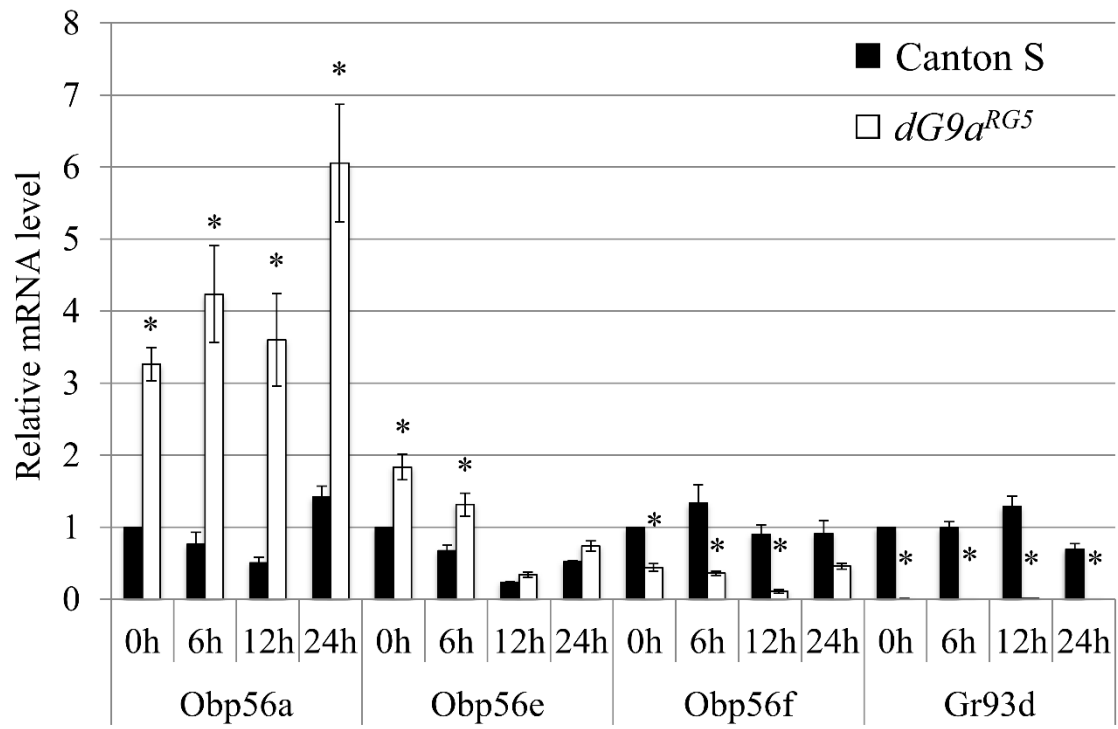


Figure S2 Quantification of mRNA levels by RT-qPCR analyses of *Obp56a*, *Obp56e*, *Obp56f* and *Gr93d* in Canton S and *dG9a^{RG5}* adult flies after 0 h, 6 h, 12 h and 24 h starvation. Error bars represent SE. n=3. * $P < 0.05$.

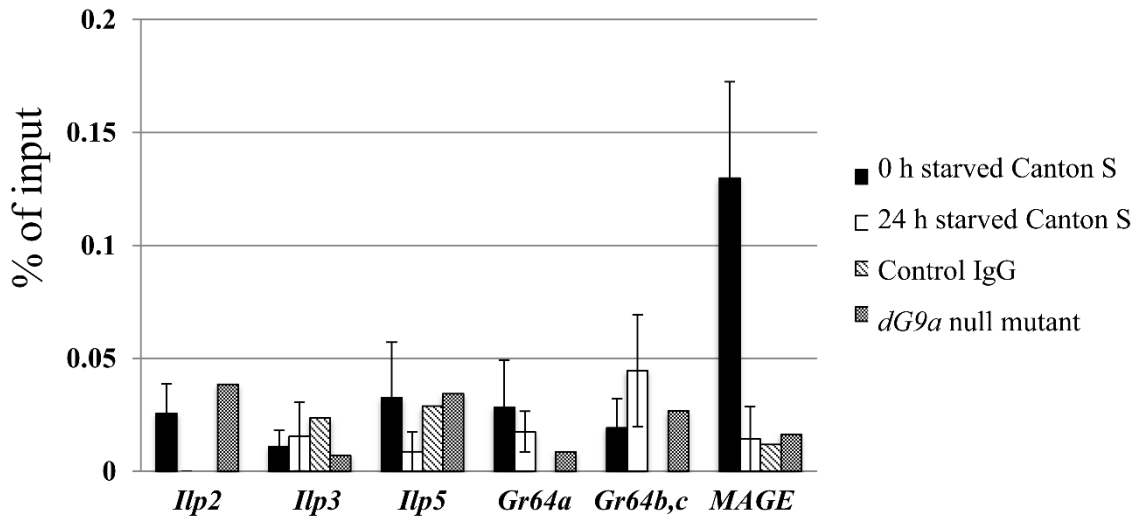


Figure S3 dG9a does not bind to the promoter region of *Ilp* genes and *Gr64* genes. (B) The results of ChIP assays using the anti-dG9a antibody as well as control IgG in Canton S and *dG9a^{RG5}*. Immunoprecipitated DNA was analyzed by RT-qPCR with primers for *Ilp2*, *Ilp3*, *Ilp5*, *Gr64a*, *Gr64b/c* and *Drosophila MAGE*. Results were normalized to inputs and shown as %. *MAGE* is a well-known direct target of G9a in mouse (Tachibana 2006) and *Drosophila* (Shimaji 2015). Canton S: n=3. Control IgG, *dG9a* null mutant: n=1.

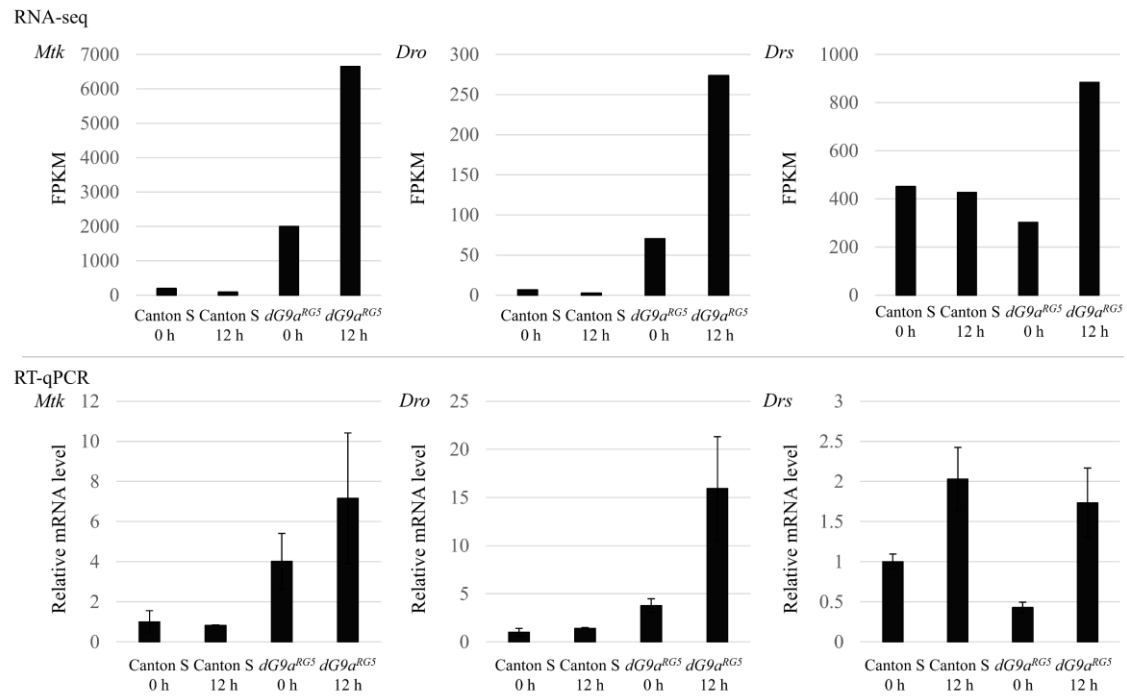


Figure S4 Quantification of mRNA levels by RNA-seq analyses (upper) and RT-qPCR analyses (bottom) of *Mtk*, *Dro* and *Drs* in Canton S and *dG9a^{RG5}* adult flies after 0 h and 12 h starvation. Error bars represent SE. RT-qPCR: n=3.