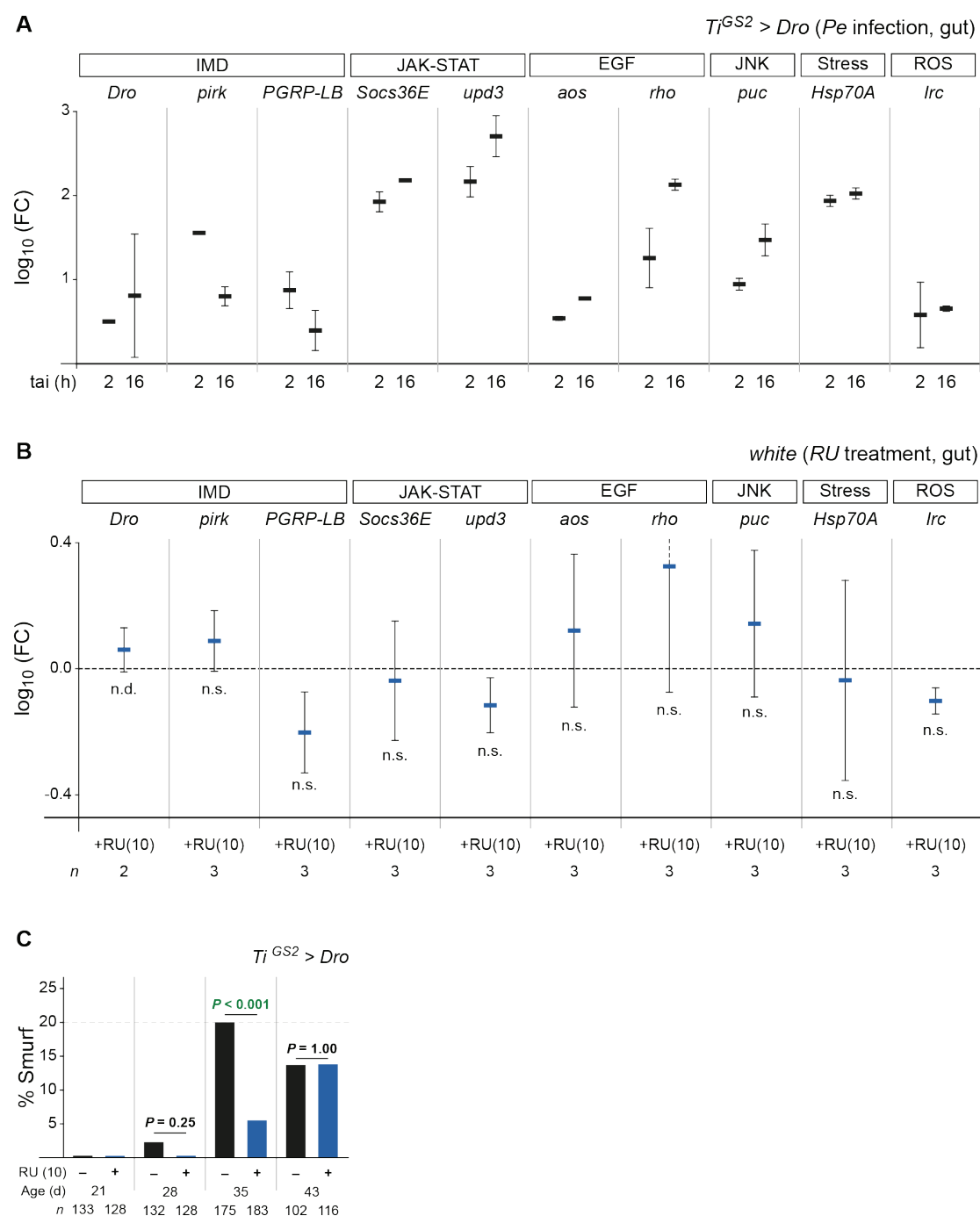




S3 Fig. Control *qPCR* experiments for *Pe* infection and RU treatment, additional Smurf assay. (A) Natural *Pe* infection induces transcription of genes involved in stress response, immune and regeneration activity of the intestinal tract. Transcriptional analysis of different pathways in midguts of female $Ti^{GS2} > Dro$ flies infected for two or 16 hours. (B) RU treatment (with 10 μ g/ml) has no effect on transcription of genes involved in stress response, immune and regeneration activity in the intestinal tract of female *white* flies. Details to the tested genes and pathways see in the main text. (C) *Dro* transcription in the gut reduces intestinal damage. Smurf

analysis of female $Ti^{GS2}>Dro$ flies fed $\pm 10 \mu\text{g/ml}$ RU at different ages. n = number of flies. Statistical tests: (A) not tested, (B) one sample t-tests (except *Dro*) (C) Fisher's exact test. n.s., $P > 0.05$; n.d. not tested. Error bars represent the standard error of the mean. For SEM-, n -, P -values see S1 and S4 Tables. *aos*, *argos*; *Dro*, *Drosocin*; EGF, Epidermal growth factor signaling; *Hsp70A*, *Heat-shock-protein-70A*; IMD, Immune Deficiency pathway; *Irc*, *Immune-regulated catalase*; JAK-STAT, Janus kinase / Signal Transducer and Activator of Transcription pathway; JNK, c-Jun N-terminal kinase signaling; *Pe*, *Pseudomonas entomophila*; *PGRP-LB*, *Peptidoglycan recognition protein LB*; *pirk*, *poor Imd response upon knock-in*; *puc*, *puckered*; *rho*, *rhomboid*; ROS, Reactive oxygen species production; +RU, RU treatment ($\mu\text{g/ml}$); *Socs36E*, *Suppressor of cytokine signaling at 36E*; tai (h), time after infection (in hours); *upd3*, *unpaired 3*.

Genotypes were:

$w/y, w; UAS-Dro/+; TiGS2^{GeneSwitch-gal4/+} (Ti^{GS2}>Dro)$,

$w/w; +/+; +/+$ (*white*).