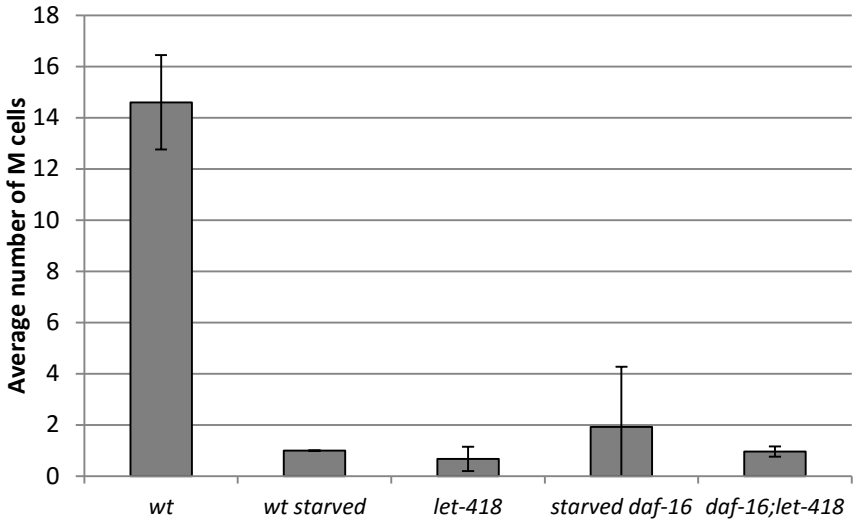
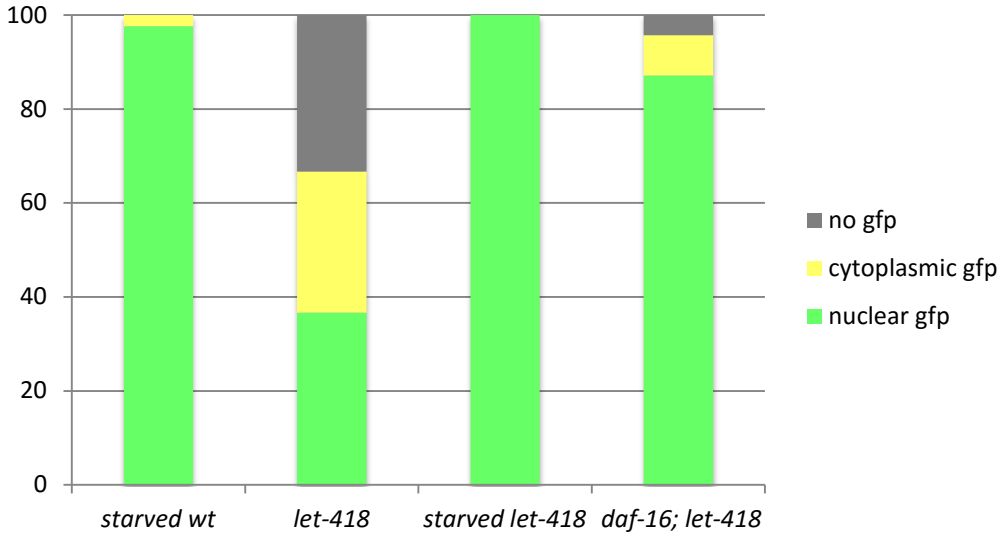
Figure S1 : *daf-16 – let-418* genetic interaction. (A) Number of M cell descendants was scored in the indicated genotypes. (B) *hlh-8::gfp* expression was monitored in the indicated genotypes and the pattern of gfp expression was scored according to the DIC and fluorescent pictures in (C). (D) Survival assay of the indicated genotypes in fed conditions.

A



B



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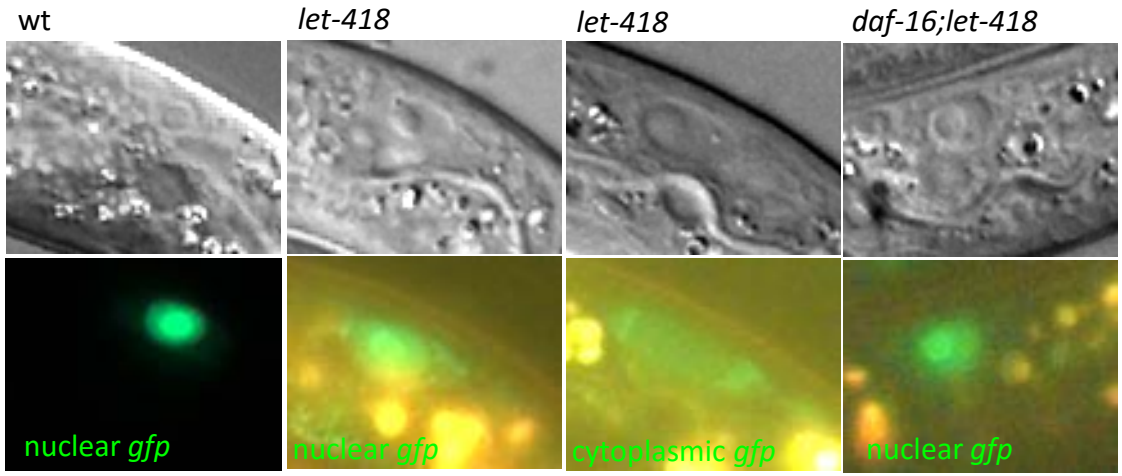


D

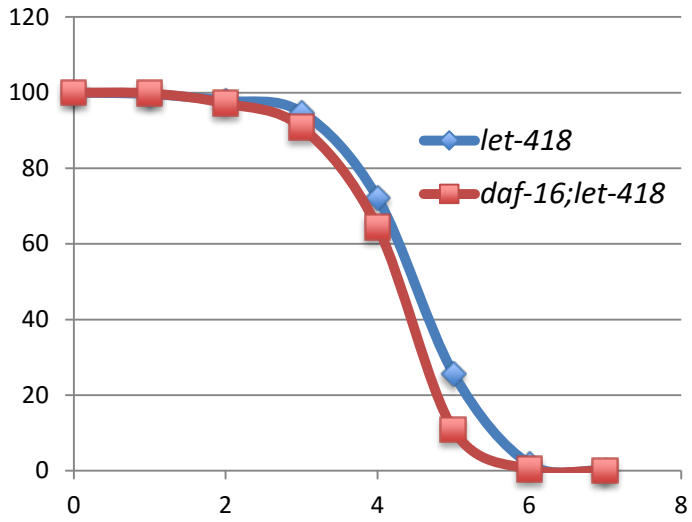


Figure S2: Lack of *set-26* activity suppresses the developmental arrest of *let-418* mutant. *set-26* and *set-9* exhibit 97% sequence identity at the level of the nucleotide sequence. To test if both gene belong to the suppressors, we generated double and triple mutant combinations and we monitored the number of L1 larvae and developing worms in the progeny. Only mutation in *set-26* can suppress the *let-418* developmental arrest. Allele used: *set-26(tm2467), set-9(n4949), let-418(n3536)*.

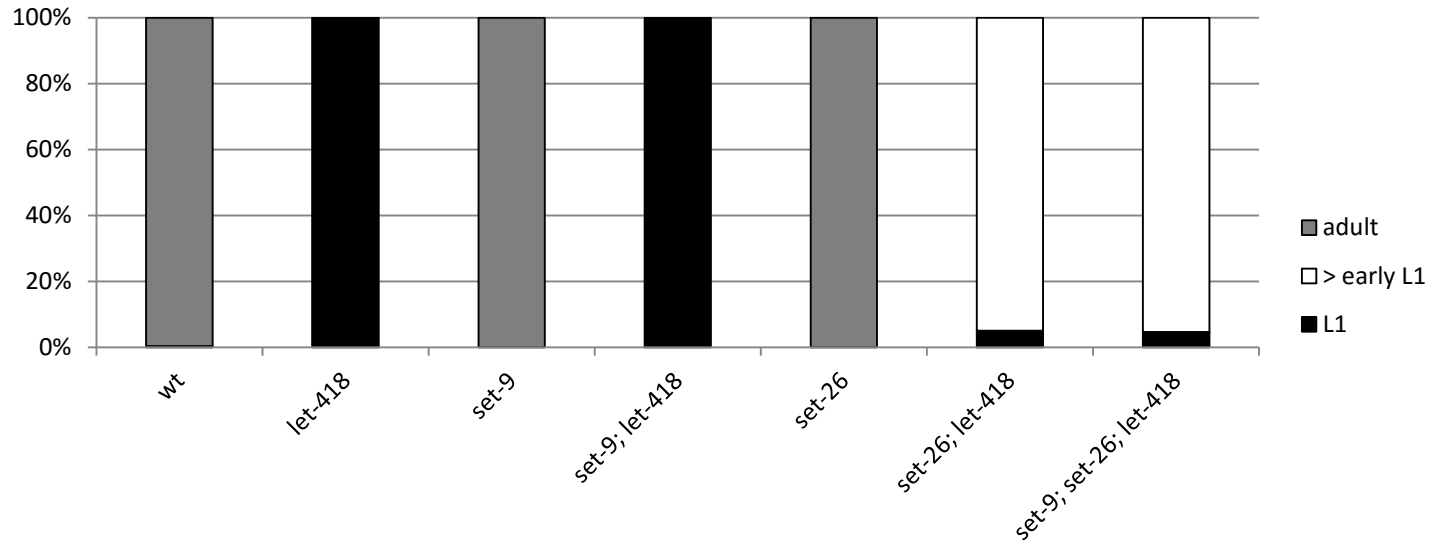


Figure S3: Suppression of *let-418* ectopic P granule expression. All 29 RNAi clones were tested for their ability to suppress *let-418* ectopic P granule expression and all of them except *set-26* show a suppression effect. Y axis: discrete values for P-granule positive cells.

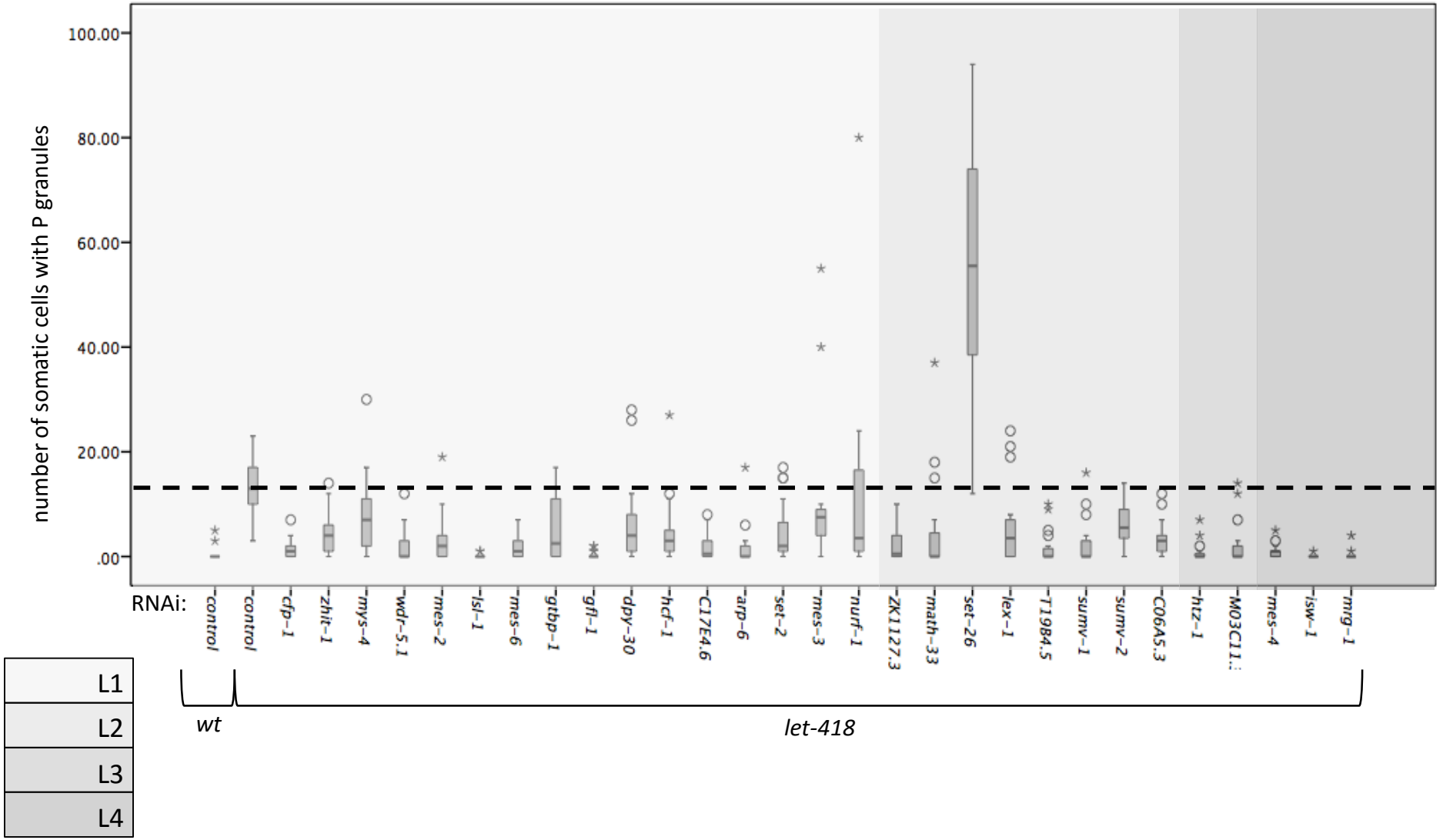


Figure S4: Suppression of *let-418* associated M cell mitotic arrest. All 29 RNAi clones were tested for their ability to suppress M cell mitotic arrest and all them induced M cell mitotic division.

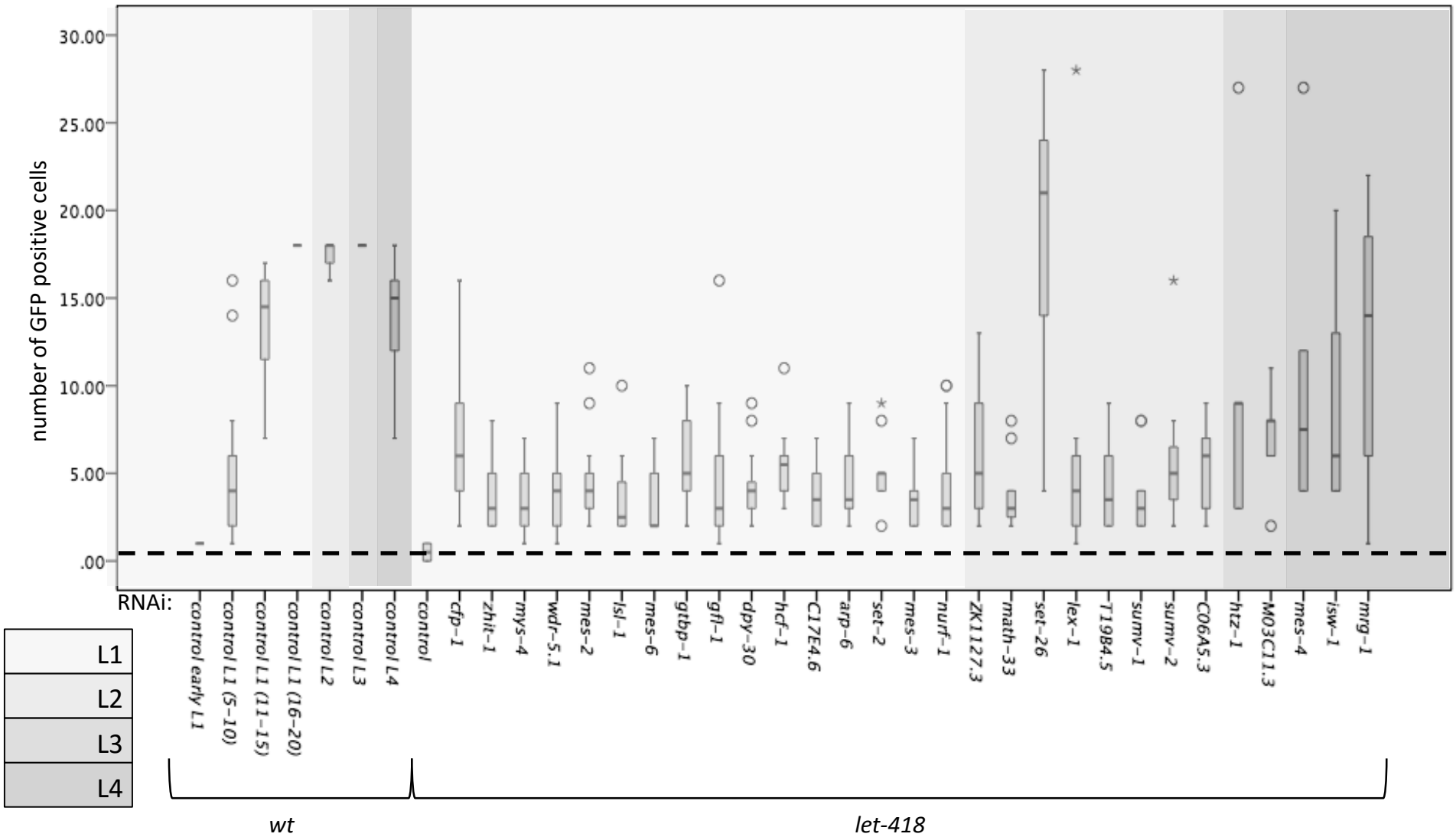


Figure S5: Suppression of *let-418* associated V cell mitotic arrest. All 29 RNAi clones were tested for their ability to suppress V cell mitotic arrest and all them induced V cell mitotic division.

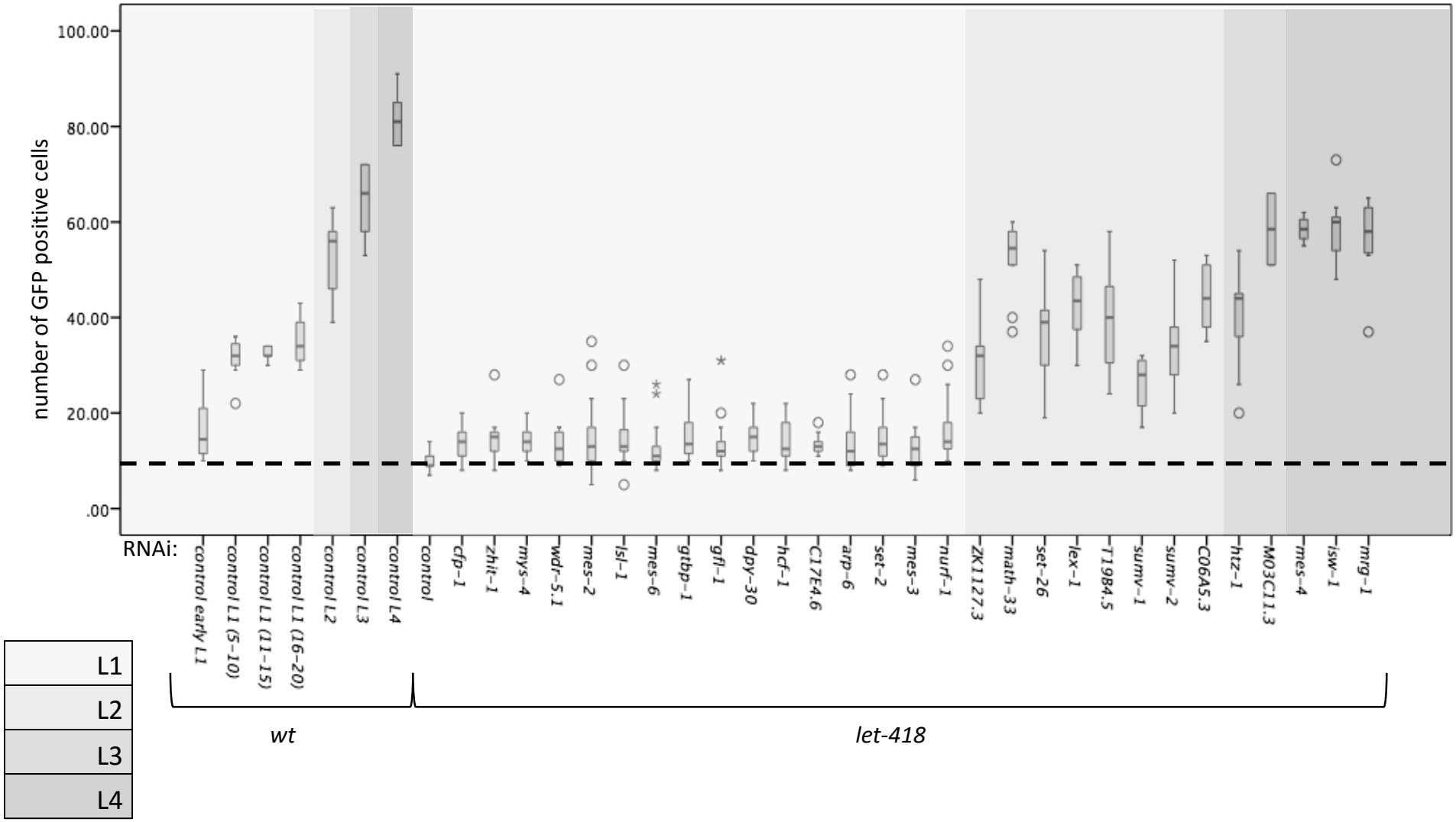
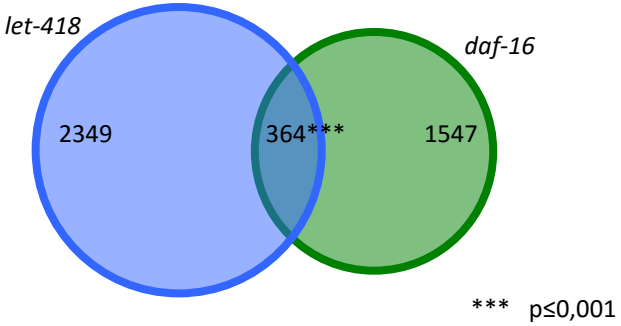


Figure S6 : DAF-16 and LET-418 share common target genes involved in metabolic pathways. Transcriptome analysis of *let-418* and *daf-16* mutants revealed a significant overlap between the 2 sets of target genes. P-values were determined by Fischer's exact test. (B) Go term analysis using the DAVID database indicates that common target genes are involved in various metabolic pathways.

A



B

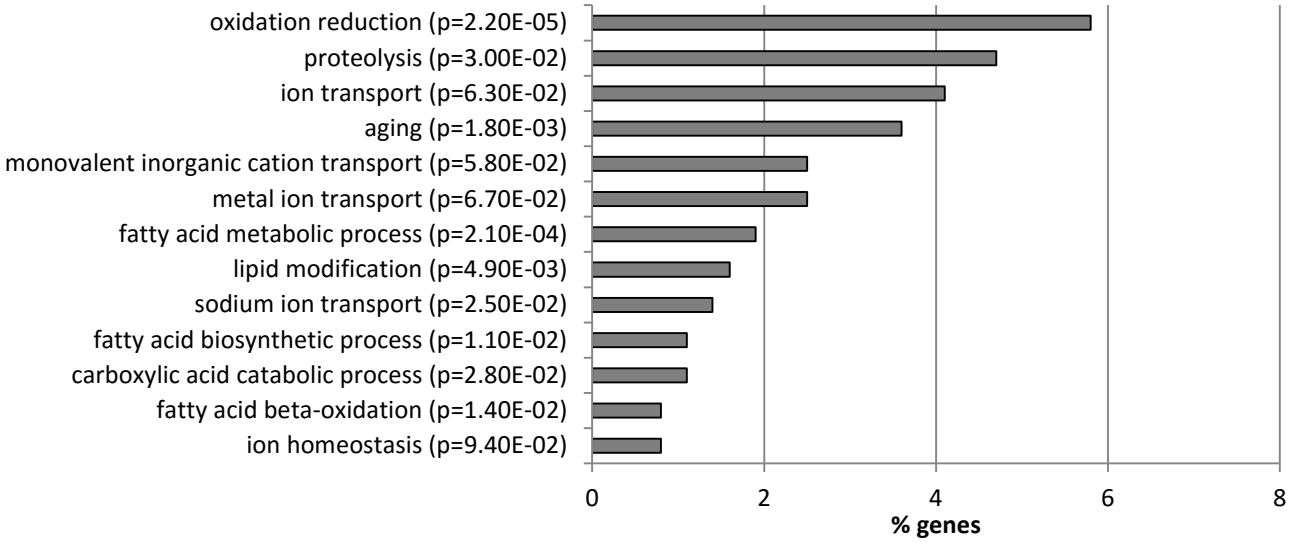


Figure S7: Overexpression of DAF-16 target in *let-418* mutant is only partially dependent on DAF-16. mRNA level of *dct-3*, *W08A12.4* and *fbxa-165* was measured by qRT-PCR and represented as the log10 of fold induction. Total mRNA was isolated from L1 animals of the indicated genotype. *ama-1* was used to normalize.