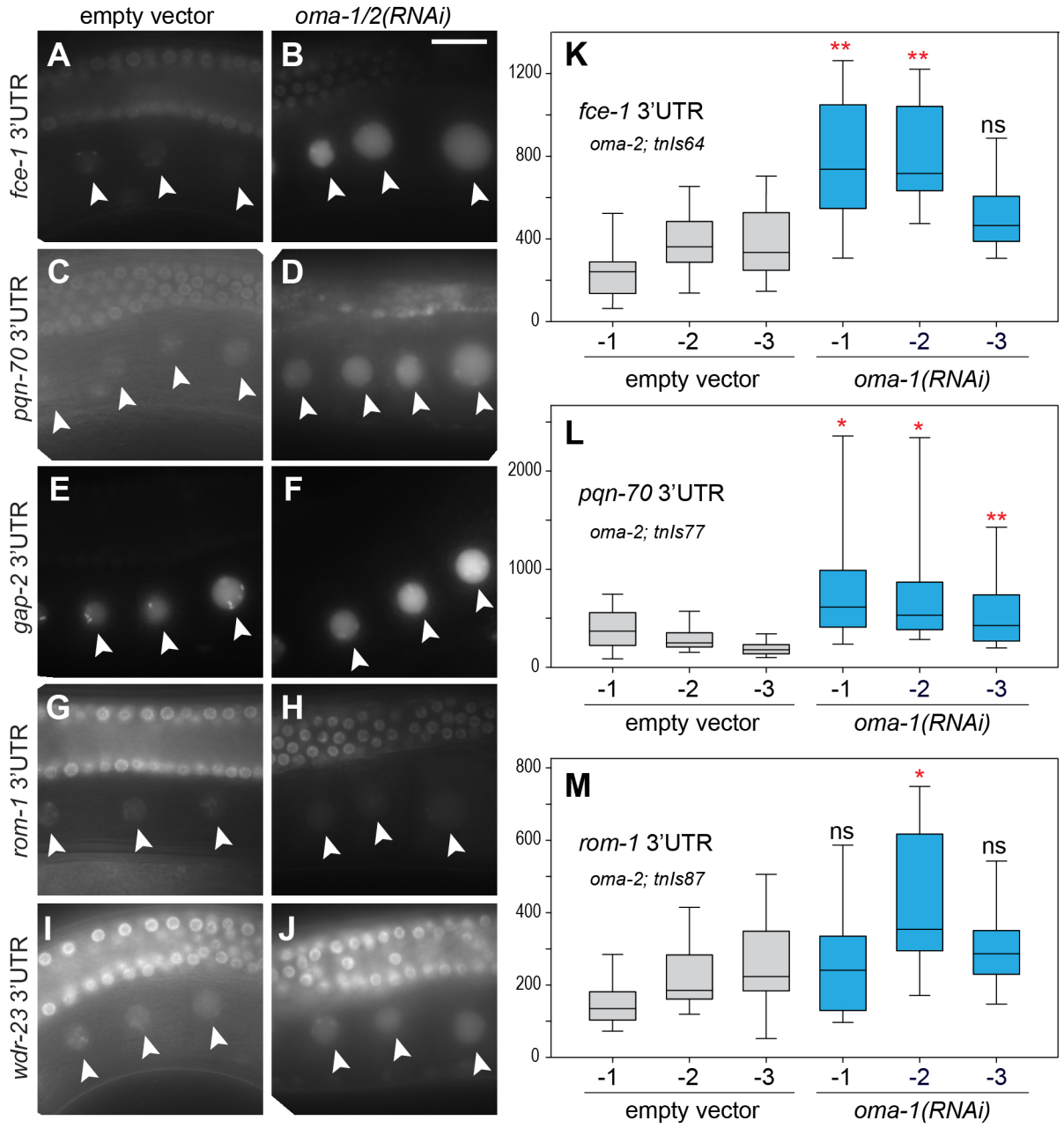

Figure S4 OMA-1-associated 3'UTRs that are weakly repressed or not regulated by OMA-1/2. GFP::Histone 2B (H2B) expression from a reporter transgene containing either the *fce-1* (A, B, K), *pqn-70* (C, D, L) or *gap-2* (E, F) 3' UTR is modestly increased in oocytes after reducing *oma-1/2* function. GFP::H2B expression from a reporter transgene containing either the *rom-1* (G, H, M) or *wdr-23* (I, J) 3'UTR is unaffected. *oma-1/2* function was compromised using *oma-1/2(RNAi)* (B, D, F, H, J) or by combining *oma-1(RNAi)* with a loss-of-function mutation in *oma-2* (K–M). Background-corrected nuclear GFP intensity (in arbitrary fluorescence units, plotted on the y-axis) was measured for the three oocytes closest to the spermatheca (x axis, oocytes –1 to –3) and is significantly increased in *oma-1/2* oocytes as indicated (two asterisks, $P \leq 0.001$; one asterisk, $P<0.05$; ns, not significant, using the Mann-Whitney U-test). Box plots represent the data from 10 oocytes in each position. Box plot whiskers indicate the minimum and maximum background-corrected intensity values. Bar, 20 µm.