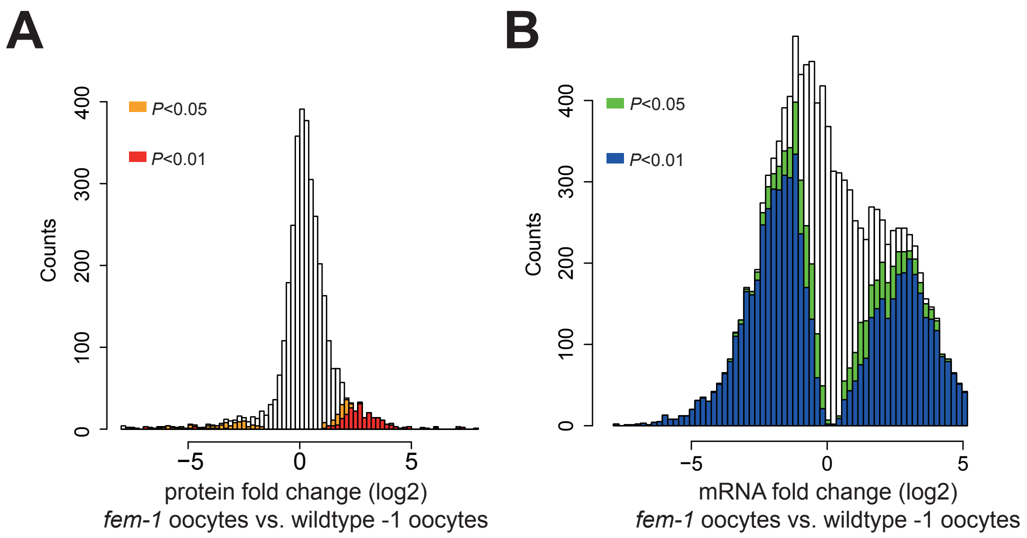
Supplementay Figure S1



Supplementary Figure S1 | Proteome and transcriptome of oocytes accumulating in the gonad of feminized mutants are significantly altered compared to wildtype -1 oocytes.

Previously published studies that isolated *C. elegans* oocytes in biochemical quantities used sterile hermaphrodites (e.g. *fem-1(hc17TS)* or *spe-9(hc88TS)* worms grown at restrictive temperature). Sterile mutant worms accumulate oocytes in their uterus which can thus be easily isolated in large quantities by cutting (or serotonin treatment) and filtration (Aroian *et al*, 1997).

We realized that the transcriptome and proteome of these oocytes (*fem-1* and *spe-9*) are substantially altered compared to wildtype -1 oocytes. In essence, the data suggest that oocytes in sterile hermaphrodites are degrading mRNAs and proteins when they accumulate in the uterus of feminized/sterile mutants. We also observed this when isolating oocytes from very young sterile hermaphrodites and checked for a lack of endoreduplication.

We thus performed all experiments with handpicked -1 wildtype oocytes (Methods) and only used spe-9 oocytes as a heavy labeled reference sample mixed with light-labelled wildtype oocytes and 1-cell stage embryos to compute protein fold-changes with ratio of ratios.

A. Histograms of protein log2-fold changes between oocytes (obtained by standard methods (Aroian *et al*, 1997)) and hand-picked -1 oocytes from wild type hermaphrodites. Significant fold changes are highlighted in orange (*P*<0.05) and red (*P*<0.01).

B. Histograms of mRNA log2-fold changes between oocytes (obtained by standard methods) and hand-picked -1 oocytes from wild type hermaphrodites. Significant fold changes are highlighted in orange (*P*<0.05) and red (*P*<0.01).