

SUPPLEMENTAL FIGURE AND 2 TABLES

Fig. S1. Phenotypes of knockdowns animals showing canal defects at lower frequency

PDF file shows representative affected canals (3x2 Fisher's Exact Test, see Materials & Methods, $p > 1 \times 10^{-6}$) of animals knocked down for: (A) *gst-28*; (B) *gsr-1*; (C) *H09G03.1*; (D) *dhhc-2*; (E) *T19D12.9*; (F) *C09F12.3*. (C', C'') "Million mutation" strains with mutations different mutations in the *H09G03.1* gene. Rare canals with serine substitution for proline 15 showed wide irregular canal with early end (red arrow). Mutation substituting glycine for arginine 67 showed slightly wider slightly irregular canals (diameter of lumen shown by red lines). Inset in (D) is of region posterior to end of lumen, so lumen is not visible inside beads. Red arrows indicate visible large vesicles within cytoplasmic beads in (D).

TABLES:

Table S1. Clones used, genes tested, and effects on canals for RNAi screen

.xlsx file providing list of all clones tested (names from Wormbase) based on data from Miller lab (SPENCER *et al.* 2011), Ahringer Clone IDs (KAMATH *et al.* 2003), and encoded gene if known (from www.Wormbase.org), and the results observed. Clones not tested due to lack of bacterial growth are indicated. New *exc* genes are highlighted in yellow.

Table S2. Number of Excretory Canals Tested for Short Phenotypes During Subsequent RNAi

.xlsx file. Sheet 1 (“Results Summary”) provides summary of canal phenotypic results for secondary tests of the 21 genes tested that provided most significant *p*-values for canals shorter than wild-type.

Sheet 2 (“Data-RNAi”) provides assessed length of all canals examined after RNAi knockdown in the wild-type background, and calculated *p*-values for a 3x2 Fisher exact test of all short canals observed after gene knockdown (vs. wild-type full-length canals)

Sheet 3 (“Graph-RNAi Data”) takes the data from Sheet 2 for the number of short, medium, and full-length canals for each knocked out gene, calculates the percentage of these classes of canals, and presents the data as a stacked bar graph.

Sheet 4 (“Data-MillionMut,Suppressors”) provides length of short canals observed in “million-mutation” strains (vs. wild-type full-length canals), and for tests of knockdown of *suex-1* and *suex-2* to suppress the *Exc-5* short-canal phenotype (vs. *exc-5(rh232)* canals, with calculated *p*-values for a 3x2 Fisher exact test. In addition, the data on knockdowns that suppressed the *exc-5* gene presents the number of animals with canals shorter than halfway (length 2.0, at the vulva); *exc-5* animals never exhibited canals with length longer than 2.0, while knockdown animals in the *exc-5* background predominantly showed such longer canals.

Supplemental References:

- Kamath, R. S., A. G. Fraser, Y. Dong, G. Poulin, R. Durbin *et al.*, 2003 Systematic functional analysis of the *Caenorhabditis elegans* genome using RNAi. *Nature* 421: 231-237.
- Spencer, W. C., G. Zeller, J. D. Watson, S. R. Henz, K. L. Watkins *et al.*, 2011 A spatial and temporal map of *C. elegans* gene expression. *Genome Res* 21: 325-341.