

## SUPPLEMENTAL METHODS

### Large scale culture and isolation of *C. elegans* males

High-density, large scale *C. elegans* culture was carried out using egg plates (A. Skop, K. Van Doren, *pers. comm.*). 300mls LB and 300mls raw egg yolks were heated to 70°C, strained through cheesecloth, and cooled to 35°C before addition of 100mls of concentrated HB101 bacterial suspension. 15mls of egg suspension were poured over solidified 150mm Super NG plates (3g NaCl, 18.75g Bacto Agar, 20g Bacto Peptone, 1ml 15mg/ml cholesterol in ethanol, and 975ml water), then dried to gel consistency over 1-2 days at 20°C.

Spermatogenic samples were isolated from *him-8(e1489)* males. *him-8(e1489)* animals, which produce 37% XO males, were grown on egg plates, rinsed off with 1xM9, subjected to centrifugation at 3000xg for 5 minutes, and resuspended in 1xM9. An equal volume of 60% sucrose solution was added, and the mixture was subjected to centrifugation at 2000xg for 5 minutes at 4°C. Animals were removed from the top of this sucrose float and rinsed over 35mm mesh with 1xM9. For synchronous populations of animals, embryos were collected and hatched overnight in 1xM9. L1 larvae were collected, seeded onto egg plates, and grown at 20°C for 3-4 days on egg plates. Adults were collected by sucrose flotation and rinsed in 1xM9. Filtration through 35mm Nyltex nylon mesh separated male worms from hermaphrodites to over 95% purity as observed by microscopic examination.

**Spermatogenic and oogenic chromatin purification**

Spermatogenic germ cells and germ nuclei were purified as previously described<sup>1</sup> except that male worms were subjected to 20,000 psi for 1 minute 3 times in succession to maximize yield. Spermatogenic material was pelleted by centrifugation at 475xg for 10 minutes, and either used immediately for chromatin preparation or frozen at  $-80^{\circ}\text{C}$ . Using 4',6-diamidino-2-phenylindole (DAPI) staining to observe chromosome cytology, we found 5-20% of spermatogenic cells and nuclei to be in characteristic stages of meiosis, an increase over the 5% of cells in meiosis previously observed<sup>1</sup>. This increase in isolated meiotic nuclei is likely due to the increased force we applied to achieve large-scale isolation of spermatogenic cells and nuclei.

Unfertilized oocytes were purified from *fer-1(hc1)* animals. The *fer-1(hc1)* mutant produces defective sperm at  $25^{\circ}\text{C}$ <sup>2,3</sup>, causing XX animals to be functional females in which some of the oocytes mature, are ovulated but fail to be fertilized and eventually become polyploid through endomitotic duplication (Emo)<sup>4</sup>. Unlike fertilized embryos that have a tough eggshell, oocytes are amenable to the same homogenization procedures used to isolate spermatogenic chromatin and were therefore chosen as the cell type for subtractive analysis.

Synchronous cultures of *fer-1(hc1)* animals were established as described above except L1 animals were grown overnight at  $20^{\circ}\text{C}$ , then shifted to  $25^{\circ}\text{C}$  for 3 days when adults were collected by sucrose filtration. Oocytes were purified as previously described<sup>5</sup>, except animals were disrupted briefly in a Waring blender to release more oocytes from within the body cavity after serotonin treatments. Germ cells in oogenesis after purification were collected by centrifugation at 500xg for 5 minutes at  $4^{\circ}\text{C}$  and used

for chromatin preparation or frozen at  $-80^{\circ}\text{C}$ . Using DAPI staining and cytological examination, we observed 50-70% Emo oocytes, as well as 10-30% of cells in diakinesis, and 20-30% fertilized embryos, indicating that the temperature shift did not completely block fertilization.

Chromatin from both germ cell populations was isolated as follows. Approximately 75-200ml of packed spermatogenic germ cells and nuclei were washed 2x in 50mls Monovalent Free Sperm Medium (MSM)<sup>1</sup> and isolated by centrifugation at 750xg for 5 minutes at  $4^{\circ}\text{C}$ . These spermatogenic cells or 200-750ml of packed oogenic cells were resuspended in 2 mls of Buffer A (250mM sucrose, 10mM Tris HCl pH 8.0, 10mM  $\text{MgCl}_2$ , 1mM EGTA and 1x protease inhibitor cocktail III (PIC) (Boehringer Mannheim). Both spermatogenic and oogenic germ cells were disrupted by homogenization with 100 strokes of a tight fitting pestle. The homogenate was subjected to centrifugation at 4,000xg for 5 minutes. The pellet, containing germ nuclei and chromatin, was resuspended in 2mls Buffer A plus 0.1% Triton X-100, 0.25% NP-40, and 1x PIC. Nuclear membranes were removed by further homogenization of 20 strokes and centrifugation at 40xg for 5 minutes at  $4^{\circ}\text{C}$ . The resulting pellet was extracted 3x in Buffer A. The extracted material and original supernatant were combined and subjected to centrifugation at 4000xg 5 minutes  $4^{\circ}\text{C}$ . The pellet was washed 1x in Tris Buffer (10mM Tris HCl pH 8.0, 0.2mM EDTA) plus 0.1% Triton X-100 1x, 2x in Tris Buffer alone, then resuspended in 1ml Tris Buffer. Chromatin was purified by centrifugation through a sucrose gradient. 0.5mls were layered over 5mls of 1.7M sucrose, 10mM EDTA pH 8.0. The top 1/3 was stirred gently to create a gradient, then subjected to centrifugation at 50,000xg for 1 hour at  $4^{\circ}\text{C}$ . The resulting pellets were resuspended in

1ml Tris Buffer, washed 2x in Tris Buffer, then resuspended in 1ml Tris Buffer.

Chromatin proteins were precipitated with 20% TCA on ice overnight, subjected to centrifugation at 14,000xg for 15 minutes at 4°C, washed 1x in acetone then air-dried. (TCA precipitation was not performed on one spermatogenic and one oogenic chromatin preparation.)

SDS-PAGE and colloidal blue staining (Novex) revealed that core histones were the most abundant proteins in both preparations, suggesting that this procedure results in similar enrichment of chromatin proteins in both sample types (Supplemental Fig. 2). Major sperm proteins (MSPs), the most abundant proteins in sperm cytosol and pseudopods required for amoeboid locomotion of *C. elegans* sperm<sup>6</sup>, were undetectable in our chromatin preparations by colloidal blue staining, indicating that sperm cellular components had been effectively removed. Subsequent tandem mass spectral analysis detected MSP proteins in very low abundance (Supplemental Tables 2 and 3).

### **Multidimensional Protein Identification Technology (MudPIT) identification of chromatin-associated proteins**

A total of eleven 12-step LC/LC/MS/MS experiments were performed: six using spermatogenic chromatin, and five using oogenic chromatin. Precipitated chromatin protein preparations were dissolved in digestion buffer and sequentially digested with Lys-C and trypsin. 50-100 µg of protein were used for each experiment. A digested peptide mixture was loaded onto a biphasic (strong cation exchange/reversed phase) capillary column (0.1 mm ID) and washed with a buffer that contained 95% DDI water, 5% acetonitrile, and 0.1% formic acid. Two-dimensional liquid chromatography (2DLC)

separation and tandem mass spectrometry were used for the analysis<sup>7</sup>. The flow rate at the tip of the biphasic column was  $\sim 300$  nL/min when the mobile phase composition was 95% H<sub>2</sub>O, 5% acetonitrile, and 0.1% formic acid. The ion trap mass spectrometer, ThermoElectron LCQ Deca (Thermo Electron, San Jose, CA) was set to the data-dependent acquisition mode with dynamic exclusion turned on, and maximum ion injection time was set to 100 ms. One MS survey scan, with mass range 400~1400 m/z, was followed by four MS/MS scans. The target value for MS was  $1 \times 10^8$  and for MS/MS was  $7 \times 10^7$ . Roughly 50,000 tandem mass spectra were acquired per experiment. Tandem mass spectra obtained were analyzed by SEQUEST Ver. 27 (rev 9) using the Wormpep database (Ver. wormpep80)<sup>8</sup>. All searches were performed using a precursor mass tolerance of 3 amu calculated using average isotopic masses. Cysteine mass was modified by the addition of 57 amu to represent carboxyamidation. A fragment ion mass tolerance of 1 amu was used. Enzyme cleavage specificity was set to non-specific. The SEQUEST outputs were then analyzed by DTASelect 1.9<sup>9</sup>. The DTASelect filter settings were: XCorr: +1 ions 2.0, +2 ions 2.9, +3 ions 3.8; delta CN: 0.08; only half or full tryptic peptides were considered.

To enhance subtraction of low abundance oogenic factors in later steps, more stringent criteria were adopted for protein identification from spermatogenic germ cells (a minimum of two different peptides per protein per individual preparation) than from oogenic ones (a minimum of two different peptides per protein from all datasets of five preparations combined). Both spermatogenic and oogenic data sets had comparable percentages of proteins in different functional categories (see Supplemental Table 5). Functional categories were determined by using *C. elegans* protein sequences in BLAST

searches of the GenBank database to determine homology/orthology for homologous proteins with E values  $\leq 10^{-10}$  and/or annotations in WormBase ([www.wormbase.org](http://www.wormbase.org) Release 155) and Worm Protein Database (BIOBASE).

### **Subtractive Analysis**

We found subtractive analysis removed appropriate factors. Subtracted proteins included those expected to associate with chromatin in both meiotic cell types, including canonical histone proteins, cohesin proteins SMC-1 and SMC-3 [Structural Maintenance of Chromosomes], the condensin SMC protein MIX-1 (Mitosis and X-associated protein)<sup>10</sup>, and DPY-26 (DumPY) a protein that has roles meiosis as well as dosage compensation<sup>11</sup>. Likely contaminants such as spindle, nuclear envelope/pore, ribosomal, and general housekeeping proteins were also subtracted (Supplemental Table 5).

A unique feature of our approach using abundance measurement is the ability to pinpoint proteins that may have been inappropriately subtracted. A high spermatogenic to oogenic TSC ratio (S/O TSC) (Supplemental Table 1) indicates high enrichment in spermatogenic samples, and can identify bona fide spermatogenesis-enriched proteins that are incorrectly subtracted due to sperm contaminants in oocyte preparations. In such instances, the appropriateness of subtraction can then be assessed by separate means. For example, in our preparations, shared proteins with high S/O TSC included nucleolar residents (e.g. small nucleolar RNA [snoRNA] binding proteins, ribosomal subunits, and FIB-1, *C. elegans* FIBrillarin) as well as components of P-granules, *C. elegans* germ granules (CGH-1 [Conserved Germline Helicase], PGL-1 [P-GranuLe], and GLH-1 [Germ Line Helicase])<sup>12-15</sup>. Antibody staining experiments showed that FIB-1 (nucleolus)

and GLH-1 (P-granule) were similarly localized during both spermatogenesis (Fig. 2f, h) and oogenesis<sup>14,15</sup> but were not associated with mature sperm chromatin, indicating their appropriate subtraction.

### **RNAi analysis**

PCR products corresponding to predicted *C. elegans* genes were synthesized using Ahringer Lab RNAi feeding vectors as templates<sup>16,17</sup>. Primers used to amplify ORFs were: DT7 ForA (TGCGTTATCCCCTGATTCTG) and DT7 RevB (GTAAAACGACGGCCAGTGAG). Alternatively, PCR products were generated by including T7 promoter sequences (TAATACGACTCACTATAG) to the 5' ends of primers designed to each gene. PCR products were verified for yield and size then used as templates for dsRNA synthesis using the Megascript T7 kit from Ambion. RNA was precipitated with a one tenth volume of 3M sodium acetate.

dsRNA corresponding to each gene was injected at 1-4 mg/ml into *him-8(e1489)* L4 hermaphrodites. Animals were plated and transferred to fresh plates after 18 hours, and F1 progeny collected for the next 48 hours. To determine whether low penetrance or subtle defects occurred during gamete formation, the germ cell chromosomes of 50-100 F1 hermaphrodites and males were cytologically observed. After overnight fixation of whole worms in STF (Streck Laboratories), F1 progeny of RNAi-treated animals were rinsed 1x in 1xPBS, 1x in 95% ethanol, 2x in 1xPBS and then stained with 10ng/ml DAPI and mounted using Vectashield (Vector Labs). Germline nuclei in whole animals were visualized using a Zeiss AxioPlanII microscope and OpenLab software (Improvision). Images were captured using an ORCA Hamamatsu CCD camera.

The impact of RNAi on hermaphrodite and male fertility was assessed. F1 hermaphrodites (n=10) were plated individually and serially transferred every 24 hours for 72 hours. The number of embryos and oocytes was counted just after each transfer, and hatched L1 larvae were counted 1 day later to determine number of progeny (the number of viable progeny, dead embryos, and unfertilized oocytes), embryonic lethality (the number of unhatched embryos), and fertilization competence (assessed by the presence of unfertilized oocytes). To assess male fertility, 8 sets of 4 F1 males were mated to either *unc-29(e258)* or *spe-8 dpy-4* hermaphrodites, mating pairs were transferred daily for 4 days, embryos and oocytes counted after transfer, and adult progeny counted after 3 days. Uninjected and mock-injected *him-8(e1489)* F1 male progeny were also scored as controls.

### **Statistical analysis**

To determine statistically meaningful differences in progeny production, numbers of viable progeny, dead embryos, and unfertilized oocytes, F1 hermaphrodite progeny from animals subjected to RNAi (n=10) were compared by a two-tailed T test in each category to a control group from either mock injected or uninjected *him-8(e1489)* animals (n=27). P-values of  $\leq 0.04$  were considered statistically relevant. Because in some cases only 2-3 animals were observed with severely affected fertility (that would be missed by a standard T test), a two-tailed F test was also applied to determine significant variability in numbers of progeny for the ten F1 animals assessed for each experiment. P-values of  $\leq 0.04$  were considered meaningful. We used four categories to assess the extent of sterility (Supplemental Table 6): overall progeny production, variability in progeny



production of individual animals, unfertilized oocyte levels, and embryonic lethality levels. An overall descriptor was also given to each gene to represent the degree of severity and/or penetrance of affected individuals by phenotypic and cytological analysis. High sterility (High Ste) is defined as highly significantly decreased overall progeny number (T-test P value  $\leq 0.00001$ ). High male sterility (High Male Ste) is defined as highly significantly decreased overall progeny number (T-test P value  $\leq 0.00001$ ) not rescued by mating with wild-type N2 males. Moderate sterility (Moderate Ste) is defined as decreased overall progeny number with T-test P values of between 0.00001 and 0.04. Low sterility (Low Ste) have overall progeny numbers that are not statistically different than the control group, but show either significantly increased progeny number variability (F-test P-value  $\leq 0.04$ ), increased unfertilized oocyte levels (T-test P value  $\leq 0.04$ ), embryonic lethality levels (T-test P value  $\leq 0.04$ ), or obvious cytological defects. Fertility defects were also obtained when N2 animals were injected with dsRNA corresponding 10 genes tested (*eft-1*, *hcp-4*, *top-1*, *smz-1*, *smz-1*, *gsp-3*, *gsp-4*, F23B12.7, B0261.6, and F27C8.5).

We found a number of genes (C31H1.1, T28F2.4, C25D7.2, T27E7.1, F32E10.6, F21H7.5, *nex-1* (ZC155.1), and C05B5.5) with increased progeny numbers when compared statistically to the control group. Repeated RNAi analysis against these genes, however, did not show consistently high effects. The variability in the maximum progeny seen, an increase of progeny production of up to 10%, may be due to small changes in environmental factors, such as fluctuations in temperature or levels of food. The following genes showed larval arrest or lethality: B0511.6, C43E11.9, *efk-1* (F42E10A.10), Y48B6A.1, Y54E10A.10, ZK1193.5, *lpd-7* (R13A5.12), Y46E12BL.2.

Y75B8A.7 showed larval arrest and slow growth. C16C8.9 was strongly Egl. The following genes showed no or very slight/low penetrance defects: B0252.5, B0286.3, C05C12.5, *spch-2* (C10G11.9), *ppw-1* (C18E3.7), C25D7.12, C33G3.5, C39E9.6, C39H7.1, C45G9.10, C49C3.12, C52E4.7, *glh-2* (C55B7.1), E03H12.5, F07A5.2, F13E9.10, F18E9.7, F21H7.5, F25B4.5, F25E5.10, F25E5.7, F26A1.12, F26F4.2, F36D3.4, F36F12.5, F36F12.6, F36H12.8, *ifc-2* (F37B4.2), *lec-11* (F38A5.3), F42G9.1, F44G3.2, F46H5.7, *spe-11* (F48C1.7), F49C12.15, F53B6.4, F56A6.1, K01G5.5, K12H6.9, M151.5, R02D3.1, R13H9.5, T08G11.1, T22H6.2, T23B3.5, *qrs-4* (T25C8.3), T26A8.3, *spch-3* (T27A3.4), T27E7.1, *rsp-1* (W02B12.3), Y110A2AL.7, *lys-1* (Y22F5A.4), Y37E11B.10, Y38E10A.17, Y43F8A.2, Y48B6A.12, Y51A2D.8, Y76A2A.1, ZC116.3, ZC204.12, ZK1248.1, *htas-1* (ZK1251.1), ZK354.2, ZK39.8, ZK430.1, ZK512.8, and ZK945.3.

### **Antibodies and immunolocalization**

Anti-GSP-3 (W09C3.6) and GSP-4 (T03F1.5) rabbit (animals 1494 and 1495) and rat (animals 1496 and 1497) antibodies were raised and affinity purified against a C-terminal peptide CTFVMYKPTPKSMRRG. Anti-SPCH-1 (C04G2.8), SPCH-2 (C10G11.9), and SPCH-3 (T27A3.4) rabbit (animals 1338 and 1339) and rat (animals 1340 and 1341) antibodies were raised and affinity purified against the N-terminal peptide MPKSKSQKNKLRPRDSKGRFTPLADADRTV with a C-terminal cysteine linker. Anti-SMZ-1 (C25G4.6) and SMZ-2 (T21G5.4) rabbit antibodies (animals 2256 and 2257) were raised and affinity purified against the C-terminal peptide EQTQTHEIGHDHEGKALRKVK with an N-terminal cysteine-glycine linker. Anti-

HTAS-1 (ZK1251.1) rabbit antibodies (animals 2390 and 2391) were raised and affinity purified against the N-terminal peptide MARLKQRPNRILNTSTKTSSA with a C-terminal cysteine linker. Peptides were coupled to Imject mcKLH (Pierce) for injection and coupled to divinylsulfone (Sigma) for affinity purification. Covance Research Products, Inc. conducted all antibody production. The following antibodies were gifts: anti-SPE-11 from S. Strome<sup>18</sup>, anti-GLH-1 and anti-GLH-2 from K. Bennett<sup>19,20</sup>, anti-TOP-1 from H.-S. Koo<sup>21</sup>, anti-HCP-4<sup>CENP-C</sup>, anti-HCP-3<sup>CENP-A</sup>, and HCP-1 from L. Moore<sup>22-24</sup>. Monoclonal Ab D77, provided by J. Aris, recognizes Nop1p (yeast fibrillarin) and FIB-1 (*C. elegans* fibrillarin)<sup>15,25,26</sup>.

Immunostaining of gonads from wild-type or *him-8(e1489)* gravid hermaphrodites and males was conducted as described previously<sup>27</sup>. An alternative harsher methanol/acetone fixation method<sup>28</sup> was also used to rule out antibody inaccessibility of sperm chromatin. Under these conditions, we observed uniform distribution of histone H1 protein on chromosomes, while HCP-4<sup>CENP-C</sup> remained excluded from inner parts of sperm meiotic chromosomes (data not shown).

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**SUPPLEMENTAL FIGURE LEGENDS****Supplemental Figure 1 | Comparative analysis of spermatogenic and oogenic proteins copurified with chromatin.**

Comparative Analysis: All spermatogenic (1099) and oogenic proteins (812) that copurify with chromatin are compared to identify 132 abundant spermatogenesis-enriched proteins with  $\geq 3$  occurrences (Supplemental Table 1), 427 low abundance spermatogenic proteins with  $\leq 2$  occurrences (Supplemental Table 2) as well as 540 all shared proteins (Supplemental Table 3) and 272 oogenic proteins (Supplemental Table 4).

**Supplemental Figure 2 | Fractionation of spermatogenic and oogenic extracts.**

Purified chromatin from spermatogenic or oogenic germ cells and nuclei was resolved through SDS-PAGE and stained with Colloidal Blue. Molecular weights (MW) correspond to protein size markers (Mark). **a**, Spermatogenic samples. **b**, Oogenic samples. Starting material (Start), supernatant (Sup), chromatin wash (Wash), chromatin (Chrom). Proteins in the chromatin preparations were subsequently analyzed by MudPIT. Brackets delineate core histone proteins. Asterisk marks major sperm proteins.

**Supplemental Figure 3 | HCP-4<sup>CENP-C</sup> associates with mature sperm chromatin.**

**a-c**, Immunolocalization of kinetochore components on mature sperm chromatin. **a**, HCP-4<sup>CENP-C</sup>. **b**, HCP-3<sup>CENP-A</sup>. **c**, HCP-1. DNA is shown in red, antibody (Ab) staining in green. HCP-4<sup>CENP-C</sup>, an inner kinetochore protein, (white arrows) is associated with mature sperm chromatin, unlike the inner kinetochore component HCP-3<sup>CENP-A</sup> and outer kinetochore component HCP-1. This localization illustrates why HCP-4<sup>CENP-C</sup> was identified by mass spectrometric analysis as a sperm-enriched chromatin-associated

protein.

**Supplemental Figure 4 | Spermatogenesis defects caused by RNAi-induced disruption of genes encoding abundant spermatogenesis-enriched chromatin-associated proteins.**

**a**, DAPI-visualized nuclei from a dissected and fixed wild-type male gonad show the progression and maturation of germ cell nuclei. **b**, Schematic of DNA in different sperm meiotic stages numbered for reference in lower panels. **c-e**, DAPI stained nuclei within boxed region shown in **a**. **c**, uninjected control male derived from a *him-8(e1489)* strain. **d**, *gsp-3*(RNAi) and *gsp-4*(RNAi) [*glc seven phosphatase*]; *him-8(e1489)* male. **e**, *smz-1*(RNAi) and *smz-2*(RNAi) [*sperm meiosis pdz domain*]; *him-8(e1489)* male. In **d**, **e**, chromosome segregation defects are apparent (white arrows) as are some normal meiotic figures (circles).

**Supplemental Figure 5 | Defects caused by *top-1*(RNAi) and *rsp-6*(RNAi) are similar.**

**a-c**, Complete adult gonads dissected from wild-type and RNAi-treated hermaphrodites and males that were stained with DAPI. **a**, wild-type, **b**, *top-1*(RNAi) or **c**, *rsp-6*(RNAi) animals. Dotted white lines show outline of gonad. All gonads are at the same magnification. Small arrows indicate oocytes that have undergone endomitotic reduplication (Emo) but have not been ovulated. Regions within yellow boxes are enlarged in insets. Large white arrowheads mark abnormally large sperm nuclei in comparison to normal mature sperm nuclei (small yellow arrows), suggesting

chromosome compaction or segregation defects.

## **SUPPLEMENTAL TABLE LEGENDS**

### **Supplemental Table 6 | Summary of RNAi analysis of abundant spermatogenesis-enriched proteins copurified with chromatin.**

Column headers are defined as follows:

Predicted gene, the predicted Open Reading Frame (ORF) corresponding to each protein from a set of identifying peptides.

*C. elegans* locus, gene name assigned for ORF.

Descriptor, protein description provided in WormBase or Worm Protein Database, (BIOBASE) annotations.

Previous Phenotype, previous RNAi phenotypes observed (see Wormbase).

Sterility Category, is defined by statistically significant variation (P-values are shown in parenthesis) in the following four categories:

% Progeny Production of Control, the average number of viable F2 progeny from 10 F1 progeny of injected animals divided by the average number of F2 progeny from 10 F1 progeny of uninjected animals. Statistically significant differences ( $P \leq 0.04$ ) were determined using a standard T test.

Progeny No. Variability, significantly high variations ( $P \leq 0.04$ ) in number of embryos laid or viable progeny between broods of 10 F1 animals scored as determined by a standard F-test.

% Oocytes, significantly high ( $P \leq 0.04$ ) percentage of oocytes laid as determined by T-test.



% Embryonic Lethality, significantly high ( $P \leq 0.04$ ) percentage of dead embryos produced as determined by T-test.

Cytological Defects, indicates if defects were observed in DAPI stained gonads of progeny of injected animals.

Sex Specificity, indicates if any defects observed were sperm specific.

New Evidence for Fertility Function (this study), indicates new information gained in this study about the function of the predicated gene in fertility.

Overall RNAi Class, degree of severity of RNAi phenotype observed in this study (number of animals exhibiting phenotype and the level of defect observed in each animal).

Complete F1 Lethality, all F1 progeny of injected animals died as embryos (Emb) or embryos and larvae (Emb Lva/Lvl).

Complete F1 Sterility, F1 progeny of injected animals were sterile.

High Ste, F1 progeny produce a significantly low number of embryos or viable progeny with P value  $\leq 0.00001$ .

High Male Ste, F1 progeny produce a significantly low number of embryos or viable progeny with P value  $\leq 0.00001$  and sperm-specific defects.

Moderate Ste, F1 progeny produce a significantly low number of embryos or viable progeny with P value  $\leq 0.00001 > 0.04$

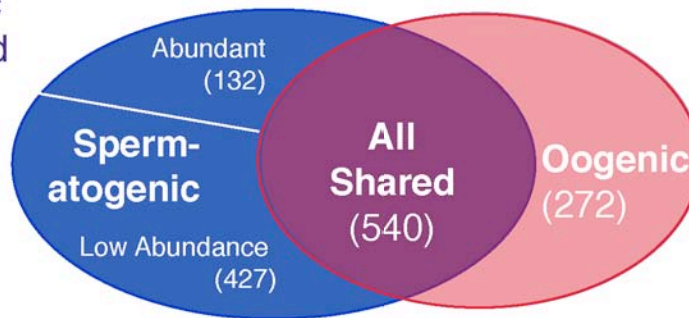
Low Ste, overall F1 progeny production not statistically different than control, but show significant levels of progeny number variability, % oocytes, or % embryonic lethality with P values  $< 0.04$  or consistent cytological defects.

\*, †, § symbols denote highly identical genes whose products may be depleted simultaneously by RNAi. **Bolded text** denotes the new evidence from our study that indicates a role for the protein in fertility. Abbreviations: N/A, not applicable, Ste, sterile; Stp, sterile progeny; Lva, larval arrest; Pvl, protruding vulva; Mul, multi-nuclei in early embryo; Mlt, molting defective; Him, high incidence of males; Rvp, exploded; Gro, slow growth; Dpy, dumpy; Lvl, larval lethal; Emb, embryonic lethal; Sck, sick.

Supplemental Figure 1

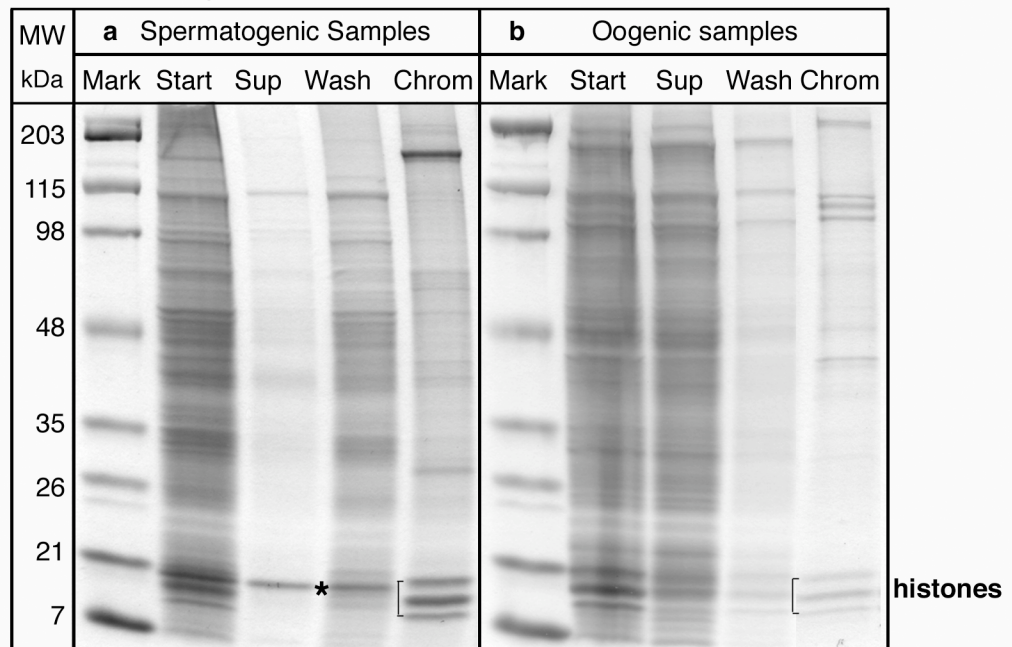
All spermatogenic proteins copurified with chromatin (1099)

### Comparative Analysis

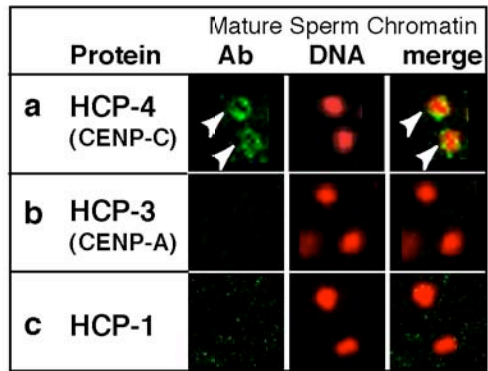


All oogenic proteins copurified with chromatin (812)

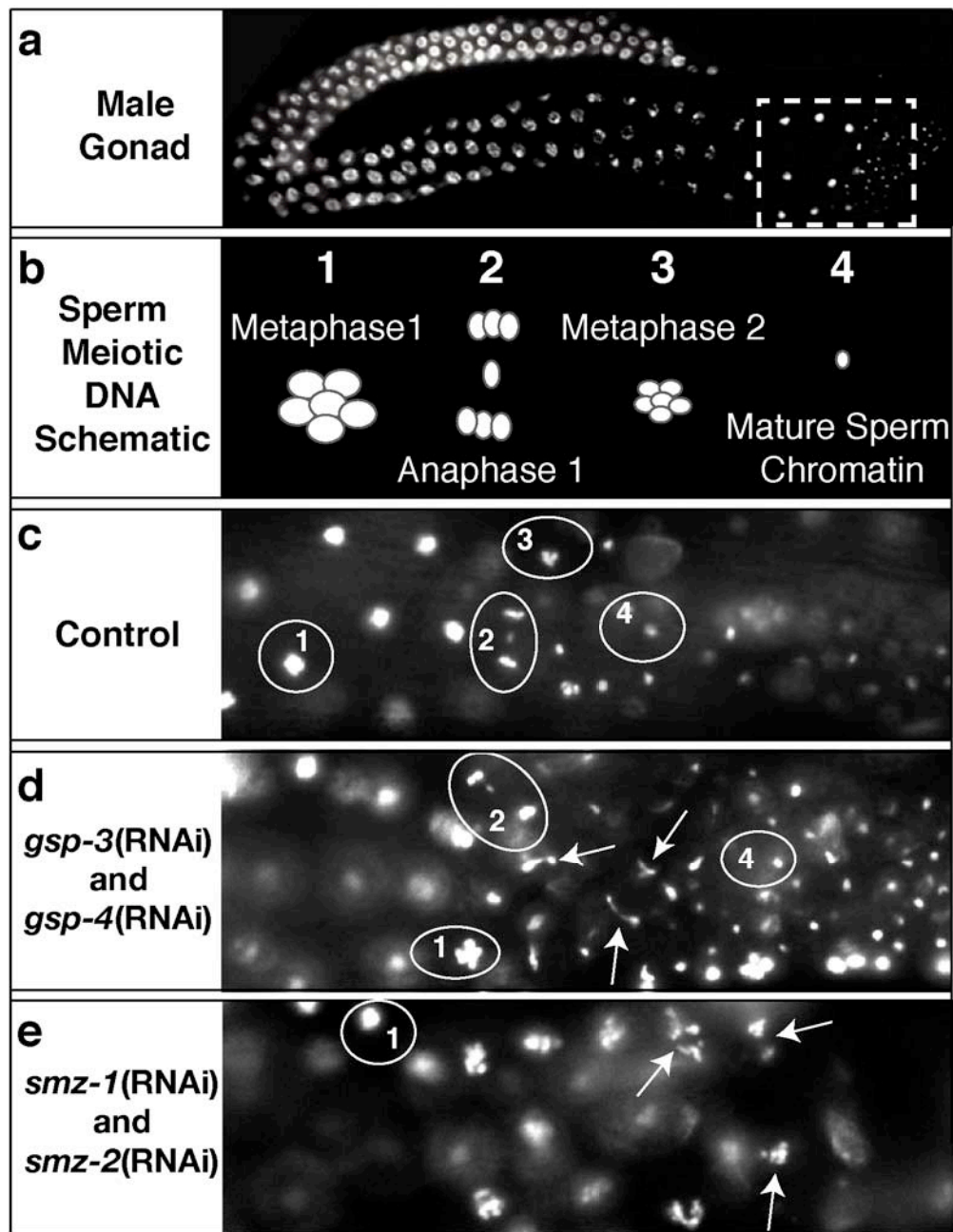
Supplemental Figure 2



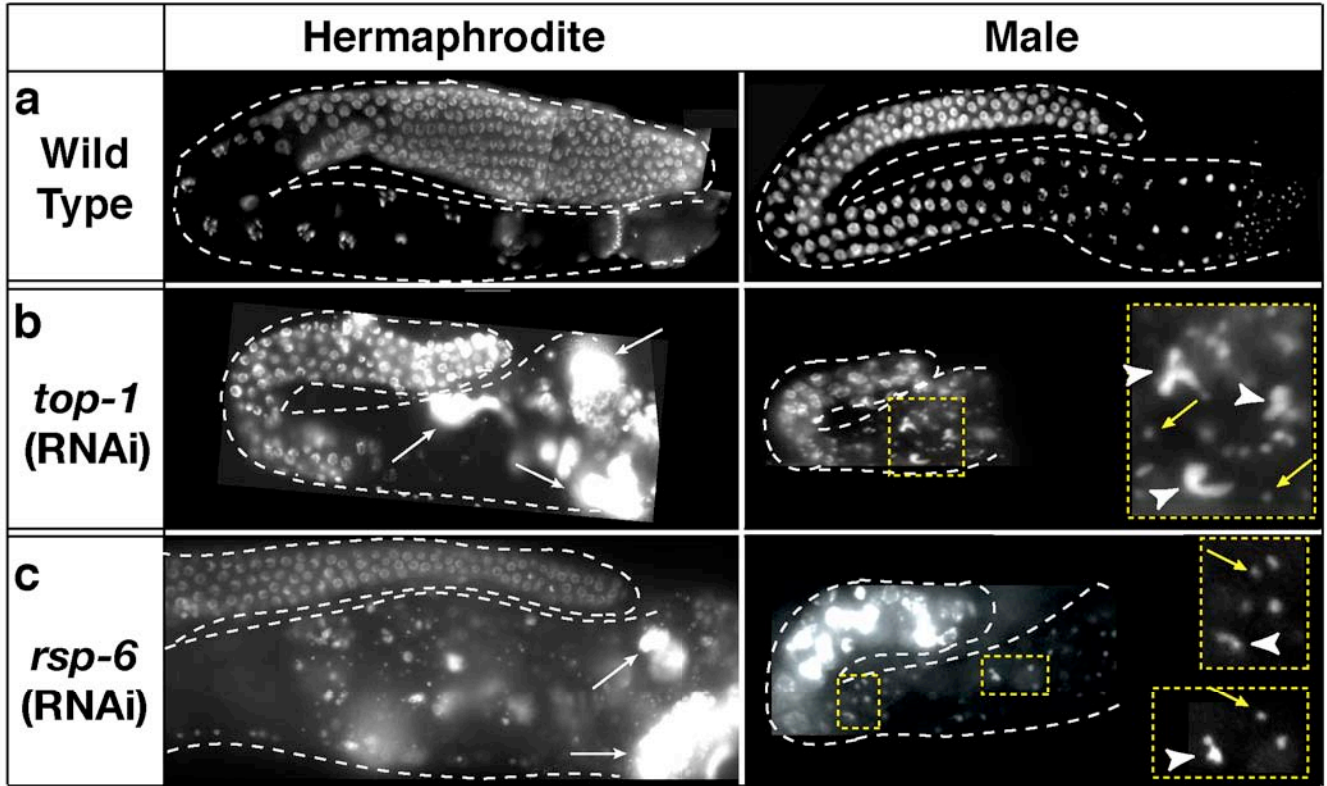
Supplemental Figure 3:



Supplemental Figure 4



Supplemental Figure 5



Supplemental Table 1 Abundant spermatogenesis-enriched proteins copurified with chromatin (132)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans Locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrences	Total Spectrum Count				
DNA	F23B12.7	F23B12.7		V	5	35	13	12.7	953	CCAAT binding factor 1 protein like, txn factor
DNA	C18G1.5	C18G1.5	<i>hil-4</i>	V	5	25	12	15.8	253	Histone H1
DNA	ZK1251.1	ZK1251.1	<i>htas-1</i>	IV	4	31	8	26.2	145	Histone H2A variant
DNA	B0414.3	B0414.3	<i>hil-5</i>	I	3	28	11	19.6	225	Histone H1
DNA	K04C2.2	K04C2.2		III	3	23	8	9.6	990	DNA polymerase V
DNA	ZK1193.5	ZK1193.5		X	3	17	3	10.9	596	Homeobox
DNA	T03F1.9	T03F1.9	<i>hcp-4</i>	I	3	10	7	14.5	866	Centromere protein CENP-C
DNA	M01E5.5	M01E5.5	<i>top-1</i>	I	3	9	4	8.3	806	Topoisomerase I
RNA	K01G5.5	K01G5.5		III	5	70	26	41.8	445	dyskerin, RNA processing
RNA	Y54F10BM.2	Y54F10BM.2		III	5	29	14	13.5	1173	Elongation factor Tu domain 2
RNA	ZK328.2	ZK328.2	<i>eft-1</i>	III	5	22	12	22.3	974	elongation factor 2
RNA	C33H5.12	C33H5.12	<i>rsp-6</i>	IV	5	21	8	25.1	179	RNA binding protein - SR protein
RNA	ZK945.3	ZK945.3		II	5	17	7	13.6	766	pumilio-repeat like domain
RNA	W07E6.1	W07E6.1		II	4	34	17	26.8	664	NOL1/NOP2/sun family ribosomal subunit biogenesis
RNA	JC8.3	JC8.3	<i>rpl-12</i>	IV	4	34	10	45.5	165	Ribosomal protein
RNA	C16A3.3	C16A3.3		III	4	25	19	14.6	1743	spliceosome assembly; in mouse apoptosis
RNA	C55B7.1	C55B7.1	<i>glh-2</i>	I	4	19	15	7.9	974	RNA helicase HAGE testes
RNA	F36A4.7	F36A4.7	<i>ama-1</i>	IV	4	14	10	11.1	1852	RNA polymerase II
RNA	T07A9.9	T07A9.9		IV	4	13	8	17.9	681	Small GTP-binding protein domain (ribosome biogenesis)
RNA	Y48A6B.3	Y48A6B.3		II	3	25	15	65	163	Ribosomal protein, rRNA processing
RNA	Y111B2A.18	Y111B2A.18	<i>rsp-3</i>	III	3	21	5	20.9	235	RNA binding protein - SR protein
RNA	C43E11.9	C43E11.9		I	3	19	10	37.8	180	RNA binding
RNA	Y48B6A.1	Y48B6A.1		II	3	19	10	19.6	674	Ribosomal protein L7Ae
RNA	B0511.6	B0511.6		I	3	16	6	13.2	544	RNA helicase
RNA	C32E8.2	C32E8.2	<i>rpl-13</i>	I	3	16	4	13	207	Ribosomal protein
RNA	Y75B8A.7	Y75B8A.7		III	3	15	8	21.9	648	MPP10, small nucleolar ribonucleoprotein
RNA	C18E3.7	<i>ppw-1/F56A6.1</i>	<i>ppw-1</i>	I	3	14	8	12.5	913	Paz/piwi domain; RNAi
RNA	F56A6.1	<i>ppw-1/F56A6.1</i>		IV	3	14	8	12.9	887	Paz/piwi domain
RNA	K12H4.3	K12H4.3		III	3	14	6	24.1	352	Brix domain-Ribosome biogenesis
RNA	E04A4.8	E04A4.8	<i>rpl-20</i>	IV	3	14	4	19.4	180	Ribosomal protein
RNA	ZK430.1	ZK430.1		II	3	13	9	7.9	1650	HEAT, ARM repeat domain, yeast Nucleolar protein homolog
RNA	D1007.6	D1007.6	<i>rps-10</i>	I	3	13	8	38.9	149	40S ribosomal protein S10
RNA	R13A5.12	R13A5.12	<i>lpd-7</i>	III	3	13	5	16.8	531	Pescadillo, N-terminal, BRCA1 C Terminus,
RNA	W02B12.3	W02B12.3	<i>rsp-1</i>	III	3	12	9	9.3	312	pre-mRNA splicing factor like -SR protein
RNA	F25B4.5	F25B4.5		V	3	11	6	10.7	710	RNA-processing protein, HAT helix
RNA	C18A3.3	C18A3.3		II	3	11	4	16.8	340	rRNA processing
RNA	Y54E10A.10	Y54E10A.10		I	3	10	6	13.8	297	Brix domain-Ribosome biogenesis
RNA	F55F8.2	F55F8.2		I	3	10	5	13.5	746	DEAD box RNA helicase
Housekeeping	K03H1.1	K03H1.1	<i>gln-2</i>	III	6	215	62	61.3	367	Glutamine synthetase, catalytic domain
Housekeeping	T25C8.3	T25C8.3	<i>gln-4</i>	III	6	145	44	46.2	290	glutamine synthetase family
Housekeeping	F44G3.2	F44G3.2		V	5	48	10	13.2	372	arginine kinase
Housekeeping	F07A11.2	F07A11.2		II	5	27	11	25.5	725	glucosamine-fructose-6-phosphate
Housekeeping	C17G10.8	C17G10.8	<i>dhs-6</i>	II	4	45	22	43.1	418	alcohol dehydrogenase
Housekeeping	F54C8.1	F54C8.1		III	4	34	9	25.8	298	3-hydroxyacyl-CoA dehydrogenase
Housekeeping	Y71H10A.1	Y71H10A.1		X	4	12	6	10.3	814	Phosphofructokinase
Housekeeping	F26E4.9	F26E4.9	<i>cco-1</i>	I	3	21	9	54.5	132	cytochrome C oxidase
Housekeeping	R02D3.1	R02D3.1		IV	3	16	11	17.3	934	Saccharopine dehydrogenase
Housekeeping	Y48B6A.12	Y48B6A.12		III	3	16	8	20.2	620	Malic oxidoreductase
Housekeeping	T13A10.11	T13A10.11		IV	3	12	12	37.6	404	S-adenosylmethionine synthetase
Housekeeping	C30F12.7	C30F12.7		I	3	9	9	26.8	373	isocitrate dehydrogenase
Housekeeping	B0286.3	B0286.3		II	3	8	4	4.7	423	SAICAR synthetase
Housekeeping	T22H6.2	T22H6.2		X	3	7	5	9.6	800	1-pyroline-5-carboxylate synthetase
Cytoskeletal	F37B4.2	F37B4.2	<i>ifc-1</i>	V	3	23	11	21.8	500	intermediate filament protein
Signalling	T03F1.5	T03F1.5/W09C3.6	<i>gsp-4</i>	I	5	27	13	40	305	serine/threonine protein phosphatase PP1
Signalling	W09C3.6	T03F1.5/W09C3.6	<i>gsp-3</i>	I	5	27	13	40	305	serine/threonine protein phosphatase PP1
Signalling	C25G4.6	C25G4.6	<i>smz-1</i>	IV	5	18	9	28.5	274	PDZ domain
Signalling	C39H7.1	C39H7.1		IV	4	35	15	26	308	casein kinase
Signalling	Y38H8A.3	Y38H8A.3		IV	4	35	15	26	308	serine/threonine kinase
Signalling	T21G5.4	T21G5.4	<i>smz-2</i>	I	4	16	7	21.2	274	PDZ domain
Signalling	F36H12.8	F36H12.8/R13H9.5		IV	3	20	10	7.4	311	serine/threonine kinase
Signalling	R13H9.5	F36H12.8/R13H9.5		IV	3	20	10	7.4	311	serine/threonine kinase
Signalling	ZK354.2	ZK354.2		IV	3	11	4	20	390	serine/threonine kinase
Signalling	F42G9.1	F42G9.1		III	3	10	7	18.9	491	protein phosphatase 2C gamma
Signalling	F42A10.4	F42A10.4	<i>efk-1</i>	III	3	9	6	9	687	calcium/calmodulin-dependent protein kinase
Major Sperm	F53B6.4	F53B6.4		I	4	125	23	27.8	342	Major Sperm Protein domain
Major Sperm	F21H7.5	F21H7.5		V	4	116	24	35.3	306	Major Sperm Protein domain
Major Sperm	C25D7.12	C25D7.12/C25D7.2		V	4	85	18	12.9	341	Major Sperm Protein domain
Major Sperm	C25D7.2	C25D7.12/C25D7.2		V	4	85	18	15.4	286	Major Sperm Protein domain
Major Sperm	F36D3.4	F36D3.4		V	4	65	19	22.1	285	Major Sperm Protein domain
Extracellular Matrix	C49C3.12	C49C3.12		IV	6	65	18	48.1	214	Lectin C-type domain
Extracellular Matrix	ZK39.8	ZK39.8		I	5	29	11	40.3	226	Lectin C-type domain
Extracellular Matrix	F38A5.3	F38A5.3	<i>lec-11</i>	IV	4	37	14	33.2	232	Lectin
Extracellular Matrix	Y52B11A.5	Y52B11A.5		V	4	15	11	31.5	219	Lectin C-type domain
Extracellular Matrix	F26A1.12	F26A1.12		III	3	28	13	31.2	231	Lectin C-type domain
Extracellular Matrix	C49C3.11	C49C3.11		IV	3	16	9	17.6	404	lectin/insulin IGF
Extracellular Matrix	F36F12.6	F36F12.6		V	3	16	6	36.8	223	Lectin
Extracellular Matrix	C39E9.6	C39E9.6		IV	3	14	5	24.8	210	SCP-like extracellular Proteins
Extracellular Matrix	F36F12.5	F36F12.5		V	3	12	5	32.3	223	Lectin C-type domain
Other	F48C1.7	F48C1.7	<i>spe-11</i>	I	6	49	23	39.1	299	Paternally provided protein essential for embryogenesis
Other	Y51A2D.8	Y51A2D.8		V	4	27	7	19.4	386	Cysteine protease
Other	B0365.3	B0365.3	<i>eat-6</i>	V	4	12	9	9.4	996	Na(+)/K(+) ATPase alpha subunit
Other	ZK1248.1	ZK1248.1		II	4	12	9	11.6	491	Peptidase family M13
Other	F25E5.3	F25E5.3		V	3	57	13	35.8	377	serine protease domain
Other	Y22F5A.4	Y22F5A.4	<i>lys-1</i>	V	3	21	7	31.5	298	LYSozyme gene class
Other	ZC155.1	ZC155.1	<i>nex-1</i>	III	3	15	9	18.9	322	Annexin
Other	F25E5.10	F25E5.10		V	3	14	8	20.9	401	serine proteases
Unknown	M151.5	M151.5		II	6	629	11	16	456	f-box (ub conjugation)
Unknown	B0207.5	B0207.5		I	6	252	119	28.3	3696	SNF2 related N-term domain



Supplemental Table 1 Abundant spermatogenesis-enriched proteins copurified with chromatin (≥3 occurrences)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans Locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrences	Total Spectrum Count				
Unknown	C04G2.8	C04G2.8	<i>spch-1</i>	IV	6	144	14	6.6	197	SNBP-like
Unknown	F49C12.15	F49C12.15		IV	6	129	41	42.1	869	
Unknown	F13E9.10	F13E9.10		IV	6	106	18	45.4	229	
Unknown	F18E9.7	F18E9.7		X	6	67	21	32.2	395	
Unknown	C45G9.10	C45G9.10		III	5	43	15	16.3	971	
Unknown	F14D2.7	F14D2.7		II	5	39	2	5.9	471	
Unknown	Y110A2AL.7	Y110A2AL.7		II	5	34	19	32.1	162	
Unknown	T26A8.3	T26A8.3		IV	5	33	8	36.4	162	Transthyretin-like
Unknown	ZC204.12	ZC204.12		II	5	29	14	18.7	252	BTB POZ domain
Unknown	K12H6.9	K12H6.9		II	5	29	11	44.2	154	
Unknown	C16C8.9	C16C8.9	II	5	22	10	41.4	157		
Unknown	T08G11.1	T08G11.1	I	5	19	13	7.6	3212		
Unknown	K08C9.2	K08C9.2	I	5	16	9	46.4	235		
Unknown	T28F2.4	T28F2.4	I	5	16	9	11.1	748	Cupin domain	
Unknown	C10G11.9	C10G11.9/T27A3.4	<i>spch-2</i>	I	4	79	1	7.4	203	SNBP-like
Unknown	T27A3.4	C10G11.9/T27A3.4		<i>spch-3</i>	I	4	79	1	7.4	203
Unknown	C33G3.5	C33G3.5	X		4	39	9	16.3	435	
Unknown	F27C8.5	F27C8.5	IV	4	23	11	20.5	565	BTB/POZ domain	
Unknown	F36A2.7	F36A2.7	I	4	18	8	30.5	167		
Unknown	E03H12.5	E03H12.5	IV	4	18	8	35.7	210		
Unknown	F26F4.2	F26F4.2	III	4	16	7	39.2	181		
Unknown	F25E5.7	F25E5.7	V	4	10	4	7.3	673	BTB/POZ domain. Serine protease, trypsin family	
Unknown	C05C12.5	C05C12.5	IV	3	33	6	47.7	149		
Unknown	ZK512.8	ZK512.8	III	3	30	14	54.4	171		
Unknown	B0252.5	B0252.5	II	3	29	8	25.9	301		
Unknown	T27E7.1	T27E7.1	IV	3	23	9	34.5	226		
Unknown	T23B3.5	T23B3.5	I	3	19	6	31.8	211		
Unknown	T10E9.4	T10E9.4	I	3	18	9	18.5	693		
Unknown	C14F11.7	C14F11.7	X	3	18	6	35.4	82		
Unknown	Y38E10A.17	Y38E10A.17	II	3	17	11	30.5	586		
Unknown	F07A5.2	F07A5.2	I	3	17	10	14.5	310		
Unknown	Y37E11B.10	Y37E11B.10	IV	3	17	10	21.5	511		
Unknown	F46H5.7	F46H5.7	X	3	17	9	19.9	572		
Unknown	B0261.6	B0261.6	I	3	12	9	16.3	153		
Unknown	C31H1.1	C31H1.1	IV	3	11	7	16.7	693		
Unknown	Y43F8A.2	Y43F8A.2	V	3	11	7	11	502		
Unknown	Y76A2A.1	Y76A2A.1	<i>tag-164</i>	III	3	11	7	24.8	294	
Unknown	C05B5.5	C05B5.5		III	3	11	6	2.7	585	
Unknown	ZC116.3	ZC116.3		V	3	10	9	5.3	3871	CUB domain, EGF-like domain
Unknown	F38A5.6	F38A5.6		IV	3	10	4	31.6	263	
Unknown	ZK809.3	ZK809.3		IV	3	10	6	18.1	210	
Unknown	Y46E12BL.2	Y46E12BL.2		II	3	9	5	3.4	1334	
Unknown	Y45F3A.1	Y45F3A.1		III	3	7	5	29.5	329	
Unknown	C52E4.7	C52E4.7		V	3	7	3	15.5	284	

Functional Category determination is described in Supplemental Methods; Family ID, designation for families of proteins not differentiated by a set of identifying peptides; LG, chromosomal location; Occurrences, the number of preparations in which a protein was identified out of 6 spermatogenic preparations; Total Spectrum Count, the total number of peptides detected for each protein from all preparations; Sequence Count, the number of distinct MS/MS spectra collected from all preparations; Coverage, % of protein represented by uniquely identified peptides; Length, number of amino acids in protein; Descriptor, protein description through homology or provided in WormBase, Worm Protein Database (BIOBASE) annotations.

Supplemental Table 2 Low abundance spermatogenic proteins copurified with chromatin (427)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
DNA	T20B12.8	T20B12.8	<i>hmg-4</i>	III	2	8	13	12.9	697	HMG transcription factor gene class
DNA	F46F11.2	F46F11.2	<i>cey-2</i>	I	2	5	11	33.3	267	cold-shock Y-box DNA binding domain
DNA	Y48E1A.1	Y48E1A.1		II	2	7	8	8.1	1737	DNA-directed RNA polymerase I largest subunit
DNA	Y67D2.3	Y67D2.3		III	2	4	6	23.7	156	Zn Finger
DNA	F55A3.7	F55A3.7		I	2	2	6	6	498	transcription factor
DNA	F14B4.3	F14B4.3		I	2	3	4	6.9	1127	DNA-directed RNA polymerase I
DNA	R166.4	R166.4	<i>pro-1</i>	II	1	4	8	13.4	529	G-protein WD-40 repeat, RCC
DNA	F23H11.1	F23H11.1		III	1	2	6	7	214	Zn finger
DNA	Y39B6A.47	Y39B6A.47		V	1	4	5	5.4	900	nuclear hormone receptor
DNA	F54D5.14	F54D5.14		II	1	2	5	2.6	1130	SMC like protein, RAD18
DNA	F32A11.5	F32A11.5		II	1	2	5	7.6	263	DNA topoisomerase II (N-terminal region) (2 domains)
DNA	F31E3.3	F31E3.3	<i>rfc-4</i>	III	1	2	5	12	334	Replication factor C AAA ATPase
DNA	C24G6.1	C24G6.1	<i>syp-2</i>	V	1	2	5	14.6	213	SynaPsis in meiosis abnormal gene class
DNA	T27F2.1	T27F2.1	<i>skp-1</i>	V	1	3	4	12.5	535	transcriptional regulator, SKIP/SNW domain
DNA	M01E11.5	M01E11.5	<i>cey-3</i>	I	1	3	4	24.5	265	cold-shock DNA binding domain
DNA	F46B6.7	F46B6.7		V	1	3	4	6.5	614	Zinc finger, C2H2 type
DNA	ZK381.1	ZK381.1	<i>him-3</i>	IV	1	2	4	12	291	Meiosis-specific protein
DNA	F27E5.3	F27E5.3		II	1	2	4	7.8	490	homeobox domain
DNA	F27D4.4	F27D4.4		I	1	3	3	9.4	383	Zn Finger
DNA	ZK1128.5	ZK1128.5		III	1	2	3	10.5	446	homolog of Swp73/BAF60, SWI/SNF component
DNA	ZC302.1	ZC302.1	<i>mre-11</i>	V	1	2	3	4.4	772	phosphatase, DNA binding, Human MRE11 protein like
DNA	Y53C10A.12	Y53C10A.12	<i>hsf-1</i>	I	1	2	2	6.3	671	HSF-type DNA binding domain
DNA	T22D1.10	T22D1.10	<i>ruvb-2</i>	IV	1	2	2	10.9	448	RuvB recombination protein homolog
DNA	T20F5.7	T20F5.7		I	1	2	2	11.2	294	Zn finger
DNA	H06O01.2	H06O01.2		I	1	2	2	2.3	1465	chromodomain-helicase-DNA-binding protein
DNA	F41H10.10	F41H10.10	<i>htp-1</i>	IV	1	2	2	3.1	350	DNA binding HORMA
DNA	F40F12.7	F40F12.7		X	1	2	2	9	199	TAZ zinc finger
DNA	D1081.8	D1081.8		I	1	2	2	5.7	755	homeodomain, Myb DNA binding
RNA	C15H11.9	C15H11.9		V	2	6	14	30.6	333	Ribosome biogenesis regulatory protein homolog.
RNA	Y41D4B.5	Y41D4B.5		IV	2	4	12	18.5	65	Ribosomal protein S28e
RNA	C47B2.5	C47B2.5	<i>ief-5</i>	I	2	5	11	16.3	246	Translation Initiation factor (EIF-6)
RNA	F37F2.2	F37F2.2		I	2	3	9	16.5	254	SRP, RNA binding
RNA	C44B7.2	C44B7.2		II	2	3	11	13.9	577	RNA binding
RNA	F10G7.1	F10G7.1		II	2	8	10	12.1	785	RNA processing, ribosome biosynthesis
RNA	T23H2.3	T23H2.3		I	2	6	7	10.5	1009	helicase, RNA polymerase termination factor, SNF2
RNA	Y54E10A.9	Y54E10A.9	<i>vbh-1</i>	I	2	7	10	13.7	641	DEAD and DEAH box helicases
RNA	Y73B3A.18	Y73B3A.18		X	2	6	9	11.1	234	Ribosomal protein L7A
RNA	T04A8.6	T04A8.6		III	2	4	9	17.6	307	RNA recognition motif
RNA	Y65B4A.6	Y65B4A.6		I	2	5	7	12.8	508	DEAD/DEAH box helicase
RNA	F33D11.10	F33D11.10		I	2	5	7	16.3	399	DEAD/DEAH box helicase
RNA	Y39A1A.14	Y39A1A.14		III	2	3	7	23.8	231	Suppressor Mra1 (ribosome biogenesis)
RNA	C24H12.4	C24H12.4		II	2	2	6	3.9	634	helicase DDX25 testes expression
RNA	W02D3.11	W02D3.11		I	2	4	5	9.1	549	RNA recognition motif
RNA	ZK1290.6	ZK1290.6		II	2	3	5	8.2	477	RNAse H
RNA	Y46G5A.13	Y46G5A.13		II	2	2	5	10.4	434	RNA rec motif
RNA	F28C6.3	F28C6.3	<i>cpl-1</i>	II	2	4	4	4.9	430	cleavage and polyadenylation factor
RNA	F55F8.3	F55F8.3		I	2	4	5	8	910	WD40-repeat subunit of 18S rRNA processing complex
RNA	C47E12.7	C47E12.7		IV	2	3	4	12.1	397	Yeast YD78, similarity to human NNP-1/NOP52
RNA	Y66H1A.4	Y66H1A.4		IV	1	5	25	31.9	276	nucleolar protein required for pre-rRNA splicing
RNA	F53F4.11	F53F4.11		V	1	6	10	16.9	543	ribosomal protein
RNA	R11D1.8	R11D1.8	<i>rpl-28</i>	V	1	3	9	7.9	126	ribosomal protein L28 l
RNA	C25A1.6	C25A1.6		I	1	3	9	25	64	Nucleolar RNA-binding protein, Nop10p family
RNA	F58A4.5	F58A4.5		III	1	5	8	6	1222	Reverse transcriptase
RNA	Y94H6A.5	Y94H6A.5		IV	1	4	8	3.9	853	DEAD and DEAH box helicases
RNA	F32E10.4	F32E10.4	<i>ima-3</i>	IV	1	3	7	8.9	514	serine-rich RNA polymerase I suppressor protein (SRP1)
RNA	C25A1.10	C25A1.10	<i>dao-5</i>	I	1	3	3	3.3	971	SRP40, C-terminal domain
RNA	Y71G12B.8	Y71G12B.8		I	1	5	6	10.6	763	DEAD box RNA helicase
RNA	F55D10.2	F55D10.2	<i>rpl-25.1</i>	X	1	4	6	25.2	147	Ribosomal protein L23
RNA	W02B12.2	W02B12.2	<i>rsp-2</i>	II	1	3	6	12.5	281	pre-mRNA splicing factor like protein
RNA	Y47G6A.10	Y47G6A.10		I	1	4	5	3.2	852	ATPase, RNA binding
RNA	R09B3.5	R09B3.5	<i>mag-1</i>	I	1	4	5	24.3	152	MAGO NASHI PROTEIN
RNA	K08E4.1	K08E4.1	<i>spt-5</i>	I	1	4	5	4.3	1208	translation initiation protein SPT5 like
RNA	C43E11.1	C43E11.1		I	1	4	5	13.1	580	RNA recognition motif
RNA	T13H5.5	T13H5.5		II	1	3	5	15.5	238	ribosomal protein S18
RNA	ZK512.2	ZK512.2		III	1	2	5	4.5	578	RNA helicase
RNA	W04D2.6	W04D2.6		V	1	2	5	6	712	RNA recognition motif. (aka RRM, RBD, or RNP domain)
RNA	F59A2.3	F59A2.3		III	1	2	5	11.9	236	Splicing factor-associated
RNA	D1007.12	D1007.12	<i>rpl-24.1</i>	I	1	2	5	8.2	159	60S ribosomal protein L24
RNA	C03D6.8	C03D6.8	<i>rpl-24.2</i>	I	1	2	5	19.1	162	ribosomal protein
RNA	Y110A7A.18	Y110A7A.18		I	1	4	4	8.1	975	Piwi/PAZ
RNA	T23D8.4	T23D8.4	<i>eif-3.C</i>	I	1	4	4	7.1	898	Translation initiation factor, proteasome component
RNA	R05D11.4	R05D11.4		V	1	4	4	10	581	ATP dependent RNA helicase
RNA	F55H2.6	F55H2.6	<i>clu-1</i>	III	1	4	4	6.6	1247	associated with eIF-3 and mitochondria
RNA	C37C3.2	C37C3.2		V	1	4	4	9.9	436	eIF4-gamma/eIF5/eIF2-epsilon
RNA	Y92C3B.2	Y92C3B.2	<i>uaf-1</i>	III	1	3	4	10.5	496	Large subunit of splicing factor U2AF
RNA	Y51H7C.11	Y51H7C.11		I	1	3	4	5.5	1085	nucleolar RNA-associated proteins (Nrap)
RNA	F58A4.9	F58A4.9		III	1	3	4	21.5	144	RNA Pol I/III 16Kd polypeptide
RNA	C42C1.14	C42C1.14	<i>rpl-34</i>	IV	1	3	4	18.2	110	large ribosomal subunit L34 protein
RNA	Y23H5B.6	Y23H5B.6		I	1	2	4	5.3	732	DEAD box helicase
RNA	Y116A8C.34	Y116A8C.34	<i>cyp-13</i>	IV	1	2	4	12.1	331	RNA binding region
RNA	T08A11.2	T08A11.2		III	1	2	4	2.6	1322	U2-snRNP associated splicing factor
RNA	Y53C12B.2	Y53C12B.2		II	1	3	3	14.1	277	KH domain
RNA	C05C8.2	C05C8.2		V	1	3	3	10.8	370	KH domain
RNA	ZK430.7	ZK430.7		II	1	2	3	5	444	ribosomal processing protein
RNA	Y59A8B.6	Y59A8B.6		V	1	2	3	3.2	968	RNA processing HAT
RNA	H27M09.1	H27M09.1		I	1	2	3	6.5	630	helicase
RNA	F11C1.5	F11C1.5		X	1	2	3	1.8	1767	Ribosomal protein L30, AAA ATPase, von Weillebrand
RNA	C03D6.3	C03D6.3	<i>cel-1</i>	I	1	2	3	5	585	mRNA capping enzyme
RNA	Y37D8A.18	Y37D8A.18		III	1	2	2	21.8	156	Ribosomal protein S10
RNA	W09D10.3	W09D10.3		III	1	2	2	14.5	173	ribosomal protein L7VL12 mitochondrial
RNA	T23B12.3	T23B12.3		V	1	2	2	17.8	264	ribosomal protein
RNA	F27C1.6	F27C1.6		I	1	2	2	5.7	647	Utp14 protein-component of ribonucleoprotein complex
RNA	F18H3.3	F18H3.3	<i>pab-2</i>	X	1	2	2	5.9	692	Poly-adenylate binding protein, unique domain

Supplemental Table 2 Low abundance spermatogenic proteins copurified with chromatin (≤2 occurrences)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
RNA	C25A1.4	C25A1.4		I	1	2	2	7.3	454	RNA binding protein
RNA	B0513.3	B0513.3	<i>rpl-29</i>	IV	1	2	2	11.3	62	60S ribosomal protein L29
Housekeeping	F54D8.2	F54D8.2		III	2	6	14	34.4	128	Cytochrome C oxidase
Housekeeping	R12C12.1	R12C12.1		II	2	9	12	9.1	979	Glycine dehydrogenase
Housekeeping	C29E4.8	C29E4.8		IV	2	6	12	24.7	251	Adenylate kinase
Housekeeping	K02F3.10	K02F3.10		III	2	5	12	44.8	201	Aminoacyl-tRNA synthetase class I
Housekeeping	C18E9.6	C18E9.6		II	2	10	11	29.2	301	mito porin
Housekeeping	C09H10.3	C09H10.3	<i>nuo-1</i>	II	2	8	11	30.1	479	NADH-ubiquinone oxidoreductase
Housekeeping	T20H4.5	T20H4.5		III	2	3	11	35.4	212	Mitochondrial complex I 23K chain
Housekeeping	K02D10.1	K02D10.1		III	2	7	9	15	526	4-NITROPHENYLPHOSPHATASE
Housekeeping	Y51H1A.3	Y51H1A.3		II	2	6	9	32.7	199	NADH-ubiquinone oxidoreductase ASH1 subunit
Housekeeping	T10B10.2	T10B10.2		X	2	6	9	15.6	422	ubiquinol-cytochrome c reductase complex core protein 2
Housekeeping	Y50D7A.7	Y50D7A.7		III	2	5	9	13.9	597	FAD linked oxidase
Housekeeping	T22D1.3	T22D1.3		IV	2	7	8	10.3	534	inosine monophosphate dehydrogenase
Housekeeping	C06E7.3	C06E7.3		IV	2	7	8	31.7	404	S-adenosylmethionine synthetase
Housekeeping	C49F5.1	C49F5.1		X	2	5	8	28.5	403	s-adenosylmethionine synthetase
Housekeeping	C02B10.1	C02B10.1		IV	2	4	8	16.7	419	acyl-CoA dehydrogenase
Housekeeping	Y57A10C.6	Y57A10C.6		II	2	3	8	13.6	412	3-keto-acyl-CoA thiolase
Housekeeping	F54F2.8	F54F2.8	<i>prx-19</i>	III	2	3	8	27	282	PEROXISOMAL FARNESYLATED PROTEIN
Housekeeping	H06I04.3	H06I04.3		III	2	7	7	9.5	833	FtsJ-like methyltransferase
Housekeeping	T26A5.3	T26A5.3		III	2	5	7	16.9	474	NADH-ubiquinone oxidoreductase
Housekeeping	F56B3.5	F56B3.5		IV	2	5	7	11.6	284	enoyl-CoA hydratase
Housekeeping	C28D4.3	C28D4.3	<i>gln-6</i>	III	2	5	7	14.7	368	glutamine synthase
Housekeeping	Y105C5B.12	Y105C5B.12		IV	2	5	6	25.4	351	S-adenosylmethionine synthetase
Housekeeping	ZK669.4	ZK669.4		II	2	3	6	10.9	448	lipoamide acyltransferase
Housekeeping	W10D9.5	W10D9.5		II	2	3	6	41.3	109	mito?
Housekeeping	F57C2.5	F57C2.5		II	2	3	6	15	387	strictosidine synthase
Housekeeping	B0464.1	B0464.1	<i>drs-1</i>	III	2	4	5	8.5	531	drs-1 Aspartyl-tRNA synthetase
Housekeeping	F25B4.1	F25B4.1		V	2	3	5	7.7	402	aminomethyltransferase
Housekeeping	F08C6.6	F08C6.6		X	2	4	4	16.1	355	apyrase
Housekeeping	D1005.1	D1005.1		X	2	4	4	6.2	1106	ATP citrate lyase
Housekeeping	C06E7.1	C06E7.1		IV	2	4	4	40.4	404	S-adenosylmethionine synthetase
Housekeeping	C16A3.5	C16A3.5		III	1	8	19	48.5	163	NADH-ubiquinone oxidoreductase B22
Housekeeping	W09C5.8	W09C5.8		I	1	10	18	36.6	175	cytochrome C oxidase
Housekeeping	F45H10.3	F45H10.3		II	1	7	14	32.7	168	NADH-ubiquinone oxidoreductase subunit
Housekeeping	F59C6.5	F59C6.5		I	1	7	8	28.8	260	NADH ubiquinone oxidoreductase
Housekeeping	Y54F10AM.5	Y54F10AM.5		III	1	5	8	33.2	205	CHCH
Housekeeping	Y56A3A.32	Y56A3A.32	<i>wah-1</i>	III	1	6	7	10.6	643	FAD-dependent pyridine
Housekeeping	F55A12.8	F55A12.8		I	1	6	7	9.1	1043	ATPase, GNC-5 related N-acetyltransferase
Housekeeping	F26D10.10	F26D10.10		IV	1	5	7	15.7	369	Carbamoyl-phosphate synthase
Housekeeping	Y110A7A.12	Y110A7A.12		I	1	4	7	11.8	501	ATP synthase
Housekeeping	C31E10.7	C31E10.7		X	1	3	7	31.2	138	cytochrome b5
Housekeeping	C56G2.6	C56G2.6	<i>let-767</i>	III	1	2	7	10.4	316	Alcohol/other dehydrogenases, short chain type)
Housekeeping	ZK973.10	ZK973.10	<i>lpd-5</i>	I	1	5	6	35.2	199	ETC complex
Housekeeping	F28F8.2	F28F8.2		V	1	5	6	17.2	618	long-chain-fatty-acid-CoA ligase
Housekeeping	Y57G11C.12	Y57G11C.12		IV	1	4	6	29.8	131	NADH-ubiquinone oxidoreductase
Housekeeping	R03H10.4	R03H10.4		II	1	4	6	21.1	147	cytochrome
Housekeeping	K12G11.3	K12G11.3		V	1	4	6	21.8	349	alcohol dehydrogenase
Housekeeping	F08A8.1	F08A8.1		I	1	4	6	10.2	674	ACYL-COENZYME A OXIDASE, PEROXISOMAL
Housekeeping	F53F4.10	F53F4.10		V	1	3	6	10.9	239	NADH-ubiquinone dehydrogenase 24 KD subunit
Housekeeping	F53C11.3	F53C11.3		V	1	3	6	17.9	313	2,4-dienoyl-CoA reductase
Housekeeping	F22D6.4	F22D6.4		I	1	3	6	40	140	NADH_ubiquinone oxidoreductase subunit
Housekeeping	F14H8.1	F14H8.1		V	1	3	6	8.9	471	oxysterol-binding protein
Housekeeping	T27E9.2	T27E9.2		III	1	2	6	45.3	75	ubiquinol-cytochrome c reductase complex
Housekeeping	K10H10.2	K10H10.2		II	1	2	6	14.5	337	beta-synthase
Housekeeping	F02A9.4	F02A9.4		II	1	5	5	20.4	608	Hydratase-dehydrogenase-epimerase
Housekeeping	R04F11.2	R04F11.2		II	1	4	5	31.8	107	ATP synthase E
Housekeeping	F37C12.7	F37C12.7		III	1	4	5	7.5	731	AMP-dependent synthetase and ligase
Housekeeping	B0272.4	B0272.4		X	1	4	5	9	255	enoyl-CoA hydratase/isomerase
Housekeeping	T26C5.1	T26C5.1		II	1	3	5	11.1	208	glutathione S-transferase
Housekeeping	F55A11.6	F55A11.6		V	1	2	5	4.9	629	Glutathione S-transferase
Housekeeping	F02E8.1	F02E8.1	<i>asb-2</i>	X	1	4	4	14.4	305	ATP synthase B chain homeodomain like
Housekeeping	C16A3.10	C16A3.10		III	1	4	4	4.3	422	Aminotransferases class-III pyridoxal-phosphate
Housekeeping	Y94H6A.8	Y94H6A.8		IV	1	3	4	12.8	187	NADH:ubiquinone oxidoreductase 17.2 kD subunit
Housekeeping	T08B2.9	T08B2.9	<i>frs-1</i>	I	1	3	4	12.9	552	phenylalanyl-tRNA synthetase
Housekeeping	T05H4.13	T05H4.13		II	1	3	4	10.5	493	aldehyde dehydrogenase
Housekeeping	D2030.5	D2030.5		I	1	3	4	28.4	162	Glyoxalase/Bleomycin resistance/Dioxygenase superfamily
Housekeeping	D2030.4	D2030.4		I	1	3	4	31.7	123	NADH:CoQ oxidoreductase subunit B18
Housekeeping	F37C12.3	F37C12.3		III	1	2	4	17.9	156	acyl carrier
Housekeeping	Y56A3A.19	Y56A3A.19		III	1	3	3	24.8	133	acyl-carrier protein , fatty acid synthase
Housekeeping	W01C9.4	W01C9.4		II	1	3	3	11.3	309	2,4-dienoyl-CoA reductase
Housekeeping	M03A8.1	M03A8.1	<i>dhs-28</i>	X	1	3	3	15.4	436	alcohol dehydrogenase; non-specific lipid transfer protein
Housekeeping	K02B2.1	K02B2.1		IV	1	3	3	10.7	457	6-phosphofructo-2-kinase
Housekeeping	H32C10.1	H32C10.1		IV	1	3	3	12.8	405	hydrolase
Housekeeping	F23H12.2	F23H12.2		V	1	3	3	16.5	188	mitochondrial precursor receptor
Housekeeping	F02E9.3	F02E9.3		I	1	3	3	11.1	289	ubiquitin carboxyl-terminal hydrolase
Housekeeping	E04F6.3	E04F6.3		II	1	3	3	16.1	298	Hydratase-dehydrogenase-epimerase
Housekeeping	C37A2.3	C37A2.3		I	1	3	3	6.1	442	acyl-CoA dehydrogenase
Housekeeping	C25H3.7	C25H3.7		II	1	3	3	23.4	175	Glutathione S-transferases
Housekeeping	Y63D3A.7	Y63D3A.7		I	1	2	3	18.8	117	mito ribosome
Housekeeping	Y53F4B.39	Y53F4B.39		II	1	2	3	16.3	295	beta lactamase
Housekeeping	Y18H1A.8	Y18H1A.8		I	1	2	3	23.8	151	pectinesterase
Housekeeping	T28B4.3	T28B4.3		X	1	2	3	31.9	141	Transthyretin-like
Housekeeping	T25G3.4	T25G3.4		I	1	2	3	6.4	722	mitochondrial glycerol-3-phosphate dehydrogenase
Housekeeping	T09A5.11	T09A5.11		I	1	2	3	10.1	445	N-oligosaccharyl transferase 48kd subunit
Housekeeping	T05H4.5	T05H4.5		V	1	2	3	14.2	309	NADH-cytochrome B5 reductase
Housekeeping	K02A4.1	K02A4.1	<i>eca-39</i>	X	1	2	3	13.5	415	tw1 like protein
Housekeeping	F46E10.10	F46E10.10		V	1	2	3	6.8	336	lactate dehydrogenase
Housekeeping	F40G9.5	F40G9.5		III	1	2	3	5.3	488	cytochrom P450
Housekeeping	F35G2.4	F35G2.4	<i>phy-2</i>	IV	1	2	3	9.6	539	prolyl 4-hydroxylase alpha subunit
Housekeeping	ZK836.2	ZK836.2		V	1	2	2	4	906	2-oxoglutarate dehydrogenase
Housekeeping	ZK550.6	ZK550.6		IV	1	2	2	8	312	phytanoyl-CoA dioxygenase
Housekeeping	ZK54.2	ZK54.2	<i>tps-1</i>	X	1	2	2	1.5	1294	trehalose phosphate synthase
Housekeeping	Y45F3A.3	Y45F3A.3		III	1	2	2	6.8	617	Acyl-CoA dehydrogenase

Supplemental Table 2 Low abundance spermatogenic proteins copurified with chromatin (≤2 occurrences)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
Housekeeping	Y23H5A.7	Y23H5A.7	<i>crs-1</i>	I	1	2	2	3.4	909	aminoacyl-tRNA synthetase
Housekeeping	K07E3.4	K07E3.4		X	1	2	2	7.8	640	tetrahydrofolate synthase
Housekeeping	F53F8.5	F53F8.5		V	1	2	2	9.8	368	SAM
Housekeeping	F09F7.4	F09F7.4		III	1	2	2	10.6	386	Enoyl-CoA hydratase
Housekeeping	C25H3.9	C25H3.9		II	1	2	2	17.8	180	NADH dehydrogenase
Housekeeping	C15H11.4	C15H11.4	<i>dhs-22</i>	V	1	2	2	6.3	333	dehydrogenase
Cytoskeletal	T06G6.9	T06G6.9	<i>vbp-1</i>	I	1	2	2	27	185	Human VHL binding protein like
Cytoskeletal	T02C12.1	T02C12.1		III	1	2	2	3	1017	hum-5 myosin IA
Signalling	F37E3.3	F37E3.3		I	2	6	12	24.1	419	Protein kinase
Signalling	F36H12.10	F36H12.10/R13H9.6		IV	2	5	12	20.9	398	Protein-tyrosine-phosphatase
Signalling	R13H9.6	F36H12.10/R13H9.6		IV	2	3	7	14.5	380	Protein kinase
Signalling	C02B10.6	C02B10.6		IV	2	5	12	20.9	398	Protein tyrosine phosphatase
Signalling	F55F8.5	F55F8.5		I	2	4	10	14.6	439	WD domain, G-beta repeats
Signalling	F49D11.9	F49D11.9		I	2	5	9	7.4	1017	WD domain, G-beta repeats
Signalling	C55B7.3	C55B7.3		IV	2	6	8	15.3	346	Protein-tyrosine-phosphatase
Signalling	F35C11.2	F35C11.2		II	2	6	7	18.9	397	Protein-tyrosine-phosphatase
Signalling	Y23H5B.5	Y23H5B.5		I	2	5	7	16.3	547	G-protein beta WD-40 repeat
Signalling	F36H12.9	F36H12.9		IV	2	3	7	14.5	380	Protein kinase
Signalling	Y66D12A.20	Y66D12A.20	<i>spe-6</i>	III	2	5	6	15	379	protein kinase required for sperm meiosis and spermiogenesis
Signalling	T01G9.6	T01G9.6	<i>kin-10</i>	I	2	5	6	26.5	234	kin-10 KIN-10 casein kinase
Signalling	C55C3.4	C55C3.4/F10G8.1		IV	2	4	6	14.8	431	Tyrosine-protein kinase
Signalling	F10G8.1	C55C3.4/F10G8.1		I	2	6	8	15.1	352	Tyrosine-protein kinase
Signalling	F38H4.4	F38H4.4		IV	2	4	6	4	501	Tyrosine-protein kinase
Signalling	C35E7.10	C35E7.10		I	2	4	6	14.9	430	Protein kinase
Signalling	H05L14.1	H05L14.1		I	2	4	5	9.9	794	casein kinase
Signalling	ZK973.3	ZK973.3		I	2	3	5	13.7	451	Protein phosphatase
Signalling	C08C3.4	C08C3.4		III	2	3	5	17.9	262	BTB/POZ domain
Signalling	F25D1.1	F25D1.1		V	2	3	5	7.7	468	Protein phosphatase
Signalling	M05D6.3	M05D6.3		II	2	4	4	13.9	397	Protein-tyrosine-phosphatase
Signalling	B0280.9	B0280.9		III	1	5	9	12.8	429	WD domain, G-beta repeats
Signalling	W01B6.2	W01B6.2		IV	1	5	7	12.8	366	Serine/threonine kinase
Signalling	K01C8.9	K01C8.9		II	1	5	7	8.5	556	GTP-binding protein
Signalling	T19A6.2	T19A6.2	<i>ngp-1</i>	I	1	4	7	9.7	698	Nuclear/nucleolar GTP-binding Protein
Signalling	Y51H4A.3	Y51H4A.3		I	1	2	7	17.7	192	Ras GTPase
Signalling	T05A7.6	T05A7.6		II	1	5	6	9.6	758	casein kinase
Signalling	Y53C12B.1	Y53C12B.1		II	1	5	5	13.5	793	WD domain, G-beta repeats (4 domains)
Signalling	ZK622.1	ZK622.1		II	1	3	5	8.8	419	Tyrosine-protein kinase
Signalling	F09C12.2	F09C12.2		II	1	2	5	4.5	691	Ser/Thr protein kinase
Signalling	R155.2	R155.2		III	1	4	4	5.3	1308	Protein-tyrosine-phosphatase
Signalling	F47B3.6	F47B3.1/F47B3.6		I	1	4	4	13.7	364	Protein-tyrosine phosphatase
Signalling	F47B3.1	F47B3.1/F47B3.6		I	1	4	4	13.8	363	Protein-tyrosine-phosphatase
Signalling	R11E3.1	R11E3.1		IV	1	2	4	6.8	545	Protein kinase
Signalling	C10H11.9	C10H11.9	<i>let-502</i>	I	1	2	4	3	1173	let-502 Rho-associated kinase
Signalling	C08F8.6	C08F8.6		IV	1	2	4	10.3	380	Serine/threonine kinase
Signalling	F13H8.2	F13H8.2		II	1	3	3	2.2	929	Dip2/Utp12 Family; WD domain, G-beta repeat
Signalling	C06A1.3	C06A1.3		II	1	3	3	8.5	364	Serine/threonine protein phosphatase
Signalling	F58G1.3	F58G1.3		I	1	3	3	9.1	341	Protein phosphatase-1 (PP1) (2 domains)
Signalling	Y18H1A.1	Y18H1A.1		I	1	2	3	4.2	425	tyr specific protein
Signalling	R07E4.6	R07E4.6	<i>kin-2</i>	X	1	2	3	6.9	376	Cyclic nucleotide-binding domain
Signalling	K11E8.1	K11E8.1	<i>unc-43</i>	IV	1	2	3	4.5	559	Ca/Calmodulin-dependent Kinase
Signalling	W03F11.4	W03F11.4		I	1	2	2	1.9	1406	protein-tyrosine phosphatase
Signalling	Y45F10D.7	Y45F10D.7		IV	1	2	2	2.8	897	G-protein WD40 repeat
Signalling	C04C11.2	C04C11.2		X	1	2	2	6	584	Arrestin (or S-antigen)
Signalling	C01F6.6	C01F6.6		IV	1	2	2	4.9	597	PDZ domain (Also known as DHR or GLGF)
Signalling	F36H1.3	F36H1.3		IV	1	2	2	4.4	597	Protein-tyrosine-phosphatase
Signalling	C43E11.5	C43E11.5/C50F2.5		I	1	2	2	7.9	368	Protein-tyrosine-phosphatase
Signalling	C50F2.5	C43E11.5/C50F2.5		I	1	2	2	7.9	368	Protein-tyrosine-phosphatase
Major Sperm	F42A9.7	F42A9.7		IV	2	8	13	21	267	Major Sperm Protein Domain
Major Sperm	ZK354.7	ZK354.7		IV	1	3	4	9.8	224	Major Sperm Protein Domain
Major Sperm	T13F2.11	msp	<i>msp-78</i>	IV	1	2	3	22	127	Major Sperm Protein Domain
Major Sperm	F26G1.7	msp	<i>msp-3</i>	II	1	2	3	22	127	Major Sperm Protein Domain
Major Sperm	W03F11.3	W03F11.3		I	1	2	2	22.4	183	Major Sperm Protein Domain
Major Sperm	F36H12.3	F36H12.3		IV	1	2	2	5.7	335	Major Sperm Protein Domain
Extracellular Matrix	W01A11.4	W01A11.4	<i>lec-10</i>	V	2	10	26	61.5	192	lec-10 galactin (S-lectin)
Extracellular Matrix	W09G10.6	W09G10.6		II	2	11	19	20	621	C type Lectin
Extracellular Matrix	F02E11.5	F02E11.5		II	2	5	14	27.1	207	SCP-like extracellular Proteins
Extracellular Matrix	Y46C8AL.1	Y46C8AL.1		IV	2	5	5	14.6	577	Lectin
Extracellular Matrix	F47C12.4	F47C12.4		IV	2	5	5	12.3	575	C-type Lectin
Extracellular Matrix	F54D1.6	F54D1.6		IV	2	3	5	4	1447	AMOP domain (adhesion)
Extracellular Matrix	W02D7.10	W02D7.10		V	1	5	8	10.7	243	lectin
Extracellular Matrix	R07B1.10	R07B1.10	<i>lec-8</i>	X	1	4	7	26.7	180	galactin domain
Extracellular Matrix	F21H7.4	F21H7.4		V	1	3	5	22.7	282	lectin
Extracellular Matrix	K07E12.1	K07E12.1		III	1	3	4	0.4	13055	Fibronectin, Ig, EGF, Sushi, von Willebrand
Extracellular Matrix	Y25C1A.1	Y25C1A.1		II	1	2	2	8.8	578	lectin
Extracellular Matrix	F46A8.8	F46A8.8		I	1	2	2	5.7	298	galectin
Extracellular Matrix	F14B8.5	F14B8.5		X	1	2	2	9.2	535	Legume lectin, beta domain
Heat Shock	T10B5.5	T10B5.5		V	2	6	8	16.6	535	chaperone
Heat Shock	C55B6.2	C55B6.2	<i>dnj-7</i>	X	1	4	6	15.5	491	heat shock protein
Heat Shock	F22B7.5	F22B7.5	<i>dnj-10</i>	III	1	3	4	12.5	456	heat shock
Heat Shock	T24H10.3	T24H10.3	<i>dnj-23</i>	II	1	2	2	20.2	242	DNAJ protein
Heat Shock	Y63D3A.6	Y63D3A.6	<i>dnj-29</i>	I	1				579	prokaryotic heat shock protein
Nuclear Envelope	Y77E11A.13	Y77E11A.13	<i>npp-20</i>	IV	2	3	7	17.3	313	WD protein
Nuclear Envelope	F07A11.3	F07A11.3	<i>npp-5</i>	II	2	4	5	9.7	813	Nuclear Pore complex Protein
Nuclear Envelope	Y41D4B.19	Y41D4B.19		IV	2	2	4	9	411	npp-8 nucleoporin
Nuclear Envelope	M01D7.6	M01D7.6	<i>emr-1</i>	I	2	3	5	17.5	166	emerin (nuclear membrane protein)
Nuclear Envelope	F53F10.5	F53F10.5		I	1	6	10	9.1	805	Nuclear Pore complex Protein gene class
Nuclear Envelope	Y43F4B.4	Y43F4B.4	<i>npp-18</i>	III	1	3	4	14.9	363	WD domain, G-beta repeat (2 domains)
Nuclear Envelope	C03D6.4	C03D6.4	<i>npp-14</i>	I	1	2	2	2.9	1390	nucleoporin

Supplemental Table 2 Low abundance spermatogenic proteins copurified with chromatin (≤2 occurrences)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
Other	ZC250.1	ZC250.1	<i>cyp-17</i>	V	2	4	22	9.5	517	cyclophilin (protein folding)
Other	F45G2.4	F45G2.4		III	2	7	19	32.5	292	Coatomer
Other	F20G2.4	F20G2.4	<i>nas-24</i>	V	2	5	17	11.7	366	zinc metalloprotease
Other	F21D5.7	F21D5.7		IV	2	4	11	13.1	496	signal recognition particle protein (SRP54)
Other	C01G12.8	C01G12.8		II	2	7	9	4.9	1049	sodium/potassium transporting ATPase
Other	CC4.3	CC4.3	<i>smu-1</i>	I	2	4	9	15.1	510	Suppressor of Mec and Unc defects
Other	C28A5.3	C28A5.3	<i>nex-3</i>	III	2	4	6	22.1	317	Annexin
Other	T10D4.4	T10D4.4	<i>ins-31</i>	II	2	4	5	17.4	218	insulin-related peptide beta type family
Other	C17E4.9	C17E4.9		I	2	4	5	20.9	320	Sodium/potassium transporting ATPase beta chain
Other	F40E10.3	F40E10.3	<i>csq-1</i>	X	2	3	5	16.3	417	Calsequestrin-principal calcium-binding protein
Other	T24H7.1	T24H7.1	<i>phb-2</i>	II	1	4	10	15	286	Prohibitin
Other	B0495.7	B0495.7		II	1	3	7	3.8	895	Peptidase family M28
Other	F56A3.4	F56A3.4	<i>spd-5</i>	I	1	4	6	7.4	1198	pronuclear migration is defective
Other	T14G10.5	T14G10.5		IV	1	3	5	3.9	870	gamma subunit of the coatomer (COP1) complex
Other	K08F11.3	K08F11.3		IV	1	3	5	11.8	390	Proteasome component region PCI
Other	K08D12.3	K08D12.3		X	1	3	5	13.2	151	proteasome component
Other	C27D11.1	C27D11.1	<i>egl-45</i>	III	1	4	4	6.3	1076	Domain in proteasome component, COP9-complex and eIF3 (PCI)
Other	Y66D12A.9	Y66D12A.9		III	1	3	3	22.2	248	proteasome activator
Other	Y16B4A.2	Y16B4A.2		X	1	3	3	2.4	2105	serine carboxypeptidase
Other	T25B6.2	T25B6.2		X	1	3	3	8.8	798	zinc metalloprotease
Other	F59E10.2	F59E10.2	<i>cyp-4</i>	II	1	3	3	11.9	523	cyclophilin
Other	ZK546.14	ZK546.14		II	1	2	3	7.4	472	Surfeit locus protein 6
Other	Y49E10.4	Y49E10.4		III	1	2	2	6.2	436	Thioredoxin
Other	Y39B6A.14	Y39B6A.14		V	1	2	2	6.8	548	ARM/SDA1-actin binding
Other	R09B3.4	R09B3.4	<i>ubc-12</i>	I	1	2	2	22.8	180	Ubiquitin-conjugating enzymes
Other	H06I04.4	H06I04.4	<i>ubl-1</i>	III	1	2	2	11.7	163	UBiquitin-Like family gene class
Unknown	C23G10.8	C23G10.8		III	2	4	8	12.5	937	S. pombe adenylyl cyclase-associated protein (weak)
Unknown	Y67H2A.5	Y67H2A.5		IV	2	8	20	40.7	145	
Unknown	R07E5.15	R07E5.15		III	2	6	18	15	253	
Unknown	F59B1.2	F59B1.2		V	2	4	17	42.2	161	
Unknown	W06H3.1	W06H3.1		V	2	14	16	19.3	663	
Unknown	M70.3	M70.3		IV	2	8	16	13.8	915	
Unknown	C34B2.8	C34B2.8		I	2	8	16	46.2	171	GRIM-19 domain
Unknown	Y73B6BL.24	Y73B6BL.24		IV	2	9	13	39.6	381	
Unknown	T23F11.2	T23F11.2		III	2	7	13	15	253	
Unknown	F42G4.6	F42G4.6		II	2	7	10	22.9	279	
Unknown	Y81G3A.1	Y81G3A.1		II	2	6	9	21.4	243	
Unknown	Y53C10A.10	Y53C10A.10		I	2	6	9	4	627	
Unknown	Y1A5A.1	Y1A5A.1		III	2	6	9	23.4	192	LIM domain
Unknown	T16G1.7	T16G1.7		V	2	6	9	13.1	436	
Unknown	F58D5.7	F58D5.7		I	2	5	9	18.2	258	
Unknown	F08D12.1	F08D12.1		II	2	5	9	10.5	694	TPR Repeat, SRP
Unknown	C38C10.3	C38C10.3		III	2	8	8	30.6	301	
Unknown	W05H9.1	W05H9.1		X	2	4	7	4.6	414	
Unknown	F17E9.3	F17E9.3		IV	2	2	7	14.2	155	
Unknown	M70.1	M70.1		IV	2	5	6	7.3	931	
Unknown	F27C1.3	F27C1.3		I	2	5	6	35.9	262	
Unknown	ZK484.3	ZK484.3		I	2	2	6	12	332	
Unknown	Y54E10BR.4	Y54E10BR.4		I	2	5	5	9.1	364	
Unknown	M7.9	M7.9		IV	2	5	5	12.4	170	
Unknown	T16G1.6	T16G1.4/5/6		V	2	4	5	4	446	
Unknown	T16G1.5	T16G1.4/5/6		V	2	4	5	4.1	434	
Unknown	T16G1.4	T16G1.4/5/6		V	2	4	5	4.1	436	
Unknown	F48G7.12	F48G7.12		V	2	4	5	4.1	444	
Unknown	R186.7	R186.7		V	2	3	5	13.1	359	Pinin SDK
Unknown	B0464.6	B0464.6		III	2	3	5	6.6	609	
Unknown	Y110A7A.15	Y110A7A.15		I	2	2	5	9.4	481	
Unknown	ZC412.5	ZC412.5		V	2	4	4	19	168	
Unknown	R10E9.2	R10E9.2		III	2	4	4	23.6	259	
Unknown	T20D3.2	T20D3.2		IV	2	3	4	9	234	
Unknown	F43C11.2	F43C11.2		II	1	10	23	34.9	169	
Unknown	F54A3.5	F54A3.5		II	1	9	14	62.9	105	
Unknown	B0491.5	B0491.5		III	1	8	10	31.5	327	
Unknown	F59B2.12	F59B2.12		III	1	7	10	8.5	918	
Unknown	Y54E10BL.5	Y54E10BL.5		I	1	4	10	46.3	121	
Unknown	W09D6.4	W09D6.4		III	1	2	10	18.9	148	
Unknown	F17C8.3	F17C8.3		III	1	5	9	2.3	973	
Unknown	Y71F9AL.9	Y71F9AL.9		I	1	4	8	18.2	314	
Unknown	Y62H9A.4	Y62H9A.4		X	1	3	8	16.5	212	
Unknown	C12D12.1	C12D12.1		X	1	3	8	6.1	769	
Unknown	Y59E9AL.6	Y59E9AL.6		IV	1	6	7	18.7	214	
Unknown	F20A1.6	F20A1.6		V	1	4	7	27.9	219	
Unknown	W04C9.2	W04C9.2		I	1	3	7	47.1	102	
Unknown	C48B4.12	C48B4.12		III	1	3	7	14.2	190	
Unknown	K01H12.4	K01H12.4		IV	1	2	7	12.5	329	
Unknown	Y37D8A.2	Y37D8A.2		III	1	5	6	12.1	571	EGF
Unknown	T12A2.5	T12A2.5		III	1	4	6	6.4	994	
Unknown	Y111B2A.2	Y111B2A.2		III	1	3	6	32.6	86	
Unknown	M02D8.1	M02D8.1		X	1	3	6	25.4	197	IG
Unknown	F57B1.2	F57B1.2	<i>sun-1</i>	V	1	2	6	8.2	473	unc-84 like
Unknown	T08G11.2	T08G11.2	<i>egl-32</i>	I	1	5	5	25.2	282	SH2 motif
Unknown	F53B6.7	F53B6.7		I	1	5	5	28.9	287	
Unknown	F42G8.10	F42G8.10		IV	1	5	5	34.8	181	
Unknown	Y57G7A.6	Y57G7A.6		II	1	4	5	7.4	883	
Unknown	Y38F1A.1	Y38F1A.1		II	1	4	5	29	241	CRISPR
Unknown	T10B5.3	T10B5.3		V	1	4	5	14.2	295	
Unknown	F44F4.10	F44F4.10		II	1	4	5	15.7	280	
Unknown	C50F4.3	C50F4.3		V	1	4	5	14.7	374	thiol protease
Unknown	C36F7.5	C36F7.5		I	1	4	5	30.7	322	
Unknown	Y73E7A.2	Y73E7A.2		I	1	3	5	8.2	585	
Unknown	Y54E10A.12	Y54E10A.12		I	1	2	5	6.2	547	
Unknown	T25C12.3	T25C12.3		X	1	2	5	2.1	2014	EGF-repeats
Unknown	R102.7	R102.7		IV	1	2	5	5.1	587	
Unknown	F58G6.6	F58G6.6	<i>del-2</i>	IV	1	2	5	7.7	583	

Supplemental Table 2 Low abundance spermatogenic proteins copurified with chromatin (≤2 occurrences)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
Unknown	BE10.1	BE10.1		III	1	2	5	8	324	
Unknown	ZK637.12	ZK637.12		III	1	4	4	16.9	213	
Unknown	Y57G11C.14	Y57G11C.14		IV	1	4	4	18.2	242	
Unknown	Y34B4A.6	Y34B4A.6		X	1	4	4	14.7	231	
Unknown	T25B9.6	T25B9.6		IV	1	4	4	7	610	
Unknown	F32B6.4	F32B6.4		IV	1	4	4	21.5	223	
Unknown	B0205.10	B0205.10		I	1	4	4	15.4	455	Proline-rich extensin
Unknown	Y32H12A.2	Y32H12A.2		III	1	3	4	7.2	610	
Unknown	W08A12.1	W08A12.1		V	1	3	4	7.4	501	
Unknown	T08B6.4	T08B6.4		IV	1	3	4	8.2	661	
Unknown	K05C4.5	K05C4.5		I	1	3	4	4.7	656	
Unknown	F49C12.7	F49C12.7		IV	1	3	4	14.9	444	
Unknown	F22F7.1	F22F7.1		V	1	3	4	10.1	426	
Unknown	C24A11.1	C24A11.1		I	1	3	4	17.8	202	
Unknown	B0273.1	B0273.1		IV	1	3	4	16.6	223	
Unknown	Y48C3A.7	Y48C3A.7	<i>mac-1</i>	II	1	2	4	5	813	ATPase AAA (proteosome?)
Unknown	Y47D3A.13	Y47D3A.13		III	1	2	4	20.6	136	
Unknown	T01B7.5	T01B7.5		II	1	2	4	7.4	407	Sas10/Utp3
Unknown	F44G4.2	F44G4.2		II	1	2	4	11.2	160	
Unknown	F10D2.10	F10D2.10		V	1	2	4	12.7	346	
Unknown	Y57G7A.5	Y57G7A.5		II	1	3	3	17.2	244	
Unknown	Y57A10A.27	Y57A10A.27		II	1	3	3	10.8	388	
Unknown	Y49F6B.2	Y49F6B.2		II	1	3	3	17.1	252	
Unknown	W03D8.3	W03D8.3		I	1	3	3	14.6	130	Thrombospondin type 3 repeat
Unknown	T12D8.9	T12D8.9		III	1	3	3	8.3	971	
Unknown	R07B7.3	R07B7.3	<i>pqn-53</i>	V	1	3	3	8.2	355	
Unknown	R02F2.7	R02F2.7		III	1	3	3	8.7	693	
Unknown	F43C11.1	F43C11.1		II	1	3	3	12.9	171	
Unknown	F32H2.7	F32H2.7		I	1	3	3	16.5	395	
Unknown	C54G4.3	C54G4.3		I	1	3	3	11	245	
Unknown	C34E10.1	C34E10.1	<i>gap-3</i>	III	1	3	3	11.3	434	Surface antigen
Unknown	C18E9.4	C18E9.4		II	1	3	3	22.3	103	
Unknown	C16C8.8	C16C8.8		II	1	3	3	14.4	139	
Unknown	B0240.2	B0240.2		V	1	3	3	2.7	1247	
Unknown	Y71G10AR.2	Y71G10AR.2		IV	1	2	3	19.5	231	
Unknown	Y45G5AM.7	Y45G5AM.7		V	1	2	3	6.5	433	
Unknown	T19B10.4	T19B10.4	<i>pqn-70</i>	V	1	2	3	15.2	243	
Unknown	M162.7	M162.7		V	1	2	3	3.9	690	
Unknown	K07G5.6	K07G5.6		I	1	2	3	11.8	374	
Unknown	K04F10.7	K04F10.7		I	1	2	3	6.5	293	
Unknown	F57B9.5	F57B9.5	<i>byn-1</i>	III	1	2	3	8.2	449	bystin
Unknown	F47B3.5	F47B3.5/F47B3.4		I	1	2	3	10.1	199	
Unknown	F47B3.4	F47B3.5/F47B3.4		I	1	2	3	7.1	281	
Unknown	F44E5.1	F44E5.1		II	1	2	3	16.7	78	
Unknown	F29C4.2	F29C4.2		IV	1	2	3	24.4	90	
Unknown	C41G7.3	C41G7.3		I	1	2	3	8	553	TspO/MBR family
Unknown	R05F9.10	R05F9.10		I	1	2	2	8	337	TPR domain repeats
Unknown	M01A10.5	M01A10.5	<i>pqn-52</i>	I	1	2	2	8.2	282	
Unknown	K11D12.6	K11D12.6		V	1	2	2	12.4	186	
Unknown	F58D2.2	F58D2.2		IV	1	2	2	3.3	610	
Unknown	F31E8.5	F31E8.5		II	1	2	2	8.9	461	
Unknown	F28B1.2	F28B1.2		V	1	2	2	5.2	973	
Unknown	F02C9.4	F02C9.4		V	1	2	2	15.3	202	Epidermal growth-factor receptor (EGFR), L domain
Unknown	C24D10.6	C24D10.6		IV	1	2	2	19.3	161	
Unknown	C15H9.9	C15H9.9		X	1	2	2	30.7	137	
Unknown	C14A4.14	C14A4.14		II	1	2	2	8.4	418	
Unknown	C03C11.1	C03C11.1		I	1	2	2	28.1	199	
Unknown	B0207.11	B0207.11		I	1	2	2	11.4	273	SH2 motif

Functional Category determination is described in Supplemental Methods; Family ID, designation for families of proteins not differentiated by a set of identifying peptides; LG, chromosomal location; Occurrences, the number of preparations in which a protein was identified out of 6 spermatogenic preparations; Total Spectrum Count, the total number of peptides detected for each protein from all preparations; Sequence Count, the number of distinct MS/MS spectra collected from all preparations; Coverage, % of protein represented by uniquely identified peptides; Length, number of amino acids in protein; Descriptor, protein description through homology or provided in WormBase, Worm Protein Database (BIOBASE) annotations.

Supplemental Table 3 All shared proteins copurified with spermatogenic and oogenic chromatin (540)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
DNA	ZK131.10	Histone H2A	<i>his-16</i>	II	5	775	59	58.3	6	1680	87	64.6	2.2	127	Histone H2A
DNA	ZK131.6	Histone H2A	<i>his-12</i>	II	5	775	59	58.3	6	1680	87	64.6	2.2	127	Histone H2A
DNA	B0035.7	Histone H2A	<i>his-47</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F07B7.10	Histone H2A	<i>his-51</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F07B7.3	Histone H2A	<i>his-53</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F08G2.2	Histone H2A	<i>his-43</i>	II	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F17E9.13	Histone H2A	<i>his-39</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F35H10.1	Histone H2A	<i>his-30</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F45F2.4	Histone H2A	<i>his-7</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F54E12.5	Histone H2A	<i>his-57</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	F55G1.10	Histone H2A	<i>his-61</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	H0212.7	Histone H2A	<i>his-65</i>	IV	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	K06C4.11	Histone H2A	<i>his-19</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	K06C4.3	Histone H2A	<i>his-21</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	T10C6.12	Histone H2A	<i>his-3</i>	V	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	T23D8.6	Histone H2A	<i>his-68</i>	I	5	773	59	58.3	6	1679	87	64.6	2.2	127	Histone H2A
DNA	C50F4.13	Histone H2A	<i>his-35</i>	V	5	772	58	52.8	6	1678	87	64.6	2.2	127	Histone H2A
DNA	W05B10.1	Histone H3		V	5	122	15	39.7	6	421	22	30.9	3.5	136	Histone H3
DNA	F45E1.6	Histone H3	<i>his-71</i>	X	5	121	14	31.6	6	420	21	23.5	3.5	136	Histone H3
DNA	Y49E10.6	Histone H3	<i>his-72</i>	III	5	122	15	39.7	6	420	21	23.5	3.4	136	Histone H3
DNA	B0035.10	Histone H3	<i>his-45</i>	IV	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F07B7.5	Histone H3	<i>his-49</i>	V	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F08G2.3	Histone H3	<i>his-43</i>	II	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F17E9.10	Histone H3	<i>his-32</i>	IV	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F22B3.2	Histone H3	<i>his-63</i>	IV	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F45F2.13	Histone H3	<i>his-6</i>	V	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F54E12.1	Histone H3	<i>his-55</i>	IV	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	F55G1.2	Histone H3	<i>his-59</i>	IV	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	K06C4.13	Histone H3	<i>his-27</i>	V	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	K06C4.5	Histone H3	<i>his-17</i>	V	5	167	32	32.4	6	357	38	24.3	2.1	136	Histone H3
DNA	T10C6.13	Histone H3	<i>his-2</i>	V	5	168	33	39.7	6	357	38	24.3	2.1	136	Histone H3
DNA	ZK131.2	Histone H3	<i>his-25</i>	II	5	168	33	39.7	6	357	38	24.3	2.1	136	Histone H3
DNA	ZK131.3	Histone H3	<i>his-9</i>	II	5	168	33	39.7	6	357	38	24.3	2.1	136	Histone H3
DNA	ZK131.7	Histone H3	<i>his-13</i>	II	5	168	33	39.7	6	357	38	24.3	2.1	136	Histone H3
DNA	T10C6.11	Histone H2B	<i>his-4</i>	V	5	123	12	29.8	6	227	31	56.7	1.8	141	Histone H2B
DNA	ZK131.5	Histone H2B	<i>his-11</i>	II	5	123	12	34.4	6	226	30	63.1	1.8	122	Histone H2B
DNA	ZK131.9	Histone H2B	<i>his-15</i>	II	5	123	12	34.4	6	226	30	63.1	1.8	122	Histone H2B
DNA	F45F2.12	Histone H2B	<i>his-8</i>	V	5	123	12	34.4	6	225	31	65	1.8	123	Histone H2B
DNA	K06C4.12	Histone H2B	<i>his-22</i>	V	5	123	12	34.4	6	225	31	65	1.8	123	Histone H2B
DNA	K06C4.4	Histone H2B	<i>his-20</i>	V	5	123	12	34.4	6	225	31	65	1.8	123	Histone H2B
DNA	F07B7.11	Histone H2B	<i>his-54</i>	V	5	123	12	29.8	6	224	31	56.7	1.8	141	Histone H2B
DNA	F07B7.4	Histone H2B	<i>his-52</i>	V	5	123	12	29.8	6	224	31	56.7	1.8	141	Histone H2B
DNA	F17E9.9	Histone H2B	<i>his-34</i>	IV	5	123	12	34.4	6	224	30	63.1	1.8	122	Histone H2B
DNA	F35H10.11	Histone H2B	<i>his-29</i>	IV	5	123	12	34.4	6	224	30	63.1	1.8	122	Histone H2B
DNA	C50F4.5	Histone H2B	<i>his-41</i>	V	5	123	12	34.4	6	223	30	52	1.8	123	Histone H2B
DNA	F08G2.1	Histone H2B	<i>his-44</i>	II	5	123	12	34.4	6	223	30	63.1	1.8	122	Histone H2B
DNA	F54E12.4	Histone H2B	<i>his-58</i>	IV	5	123	12	34.4	6	223	29	45.5	1.8	123	Histone H2B
DNA	F55G1.3	Histone H2B	<i>his-62</i>	IV	5	123	12	34.4	6	223	29	45.5	1.8	123	Histone H2B
DNA	H0212.6	Histone H2B	<i>his-66</i>	IV	5	123	12	34.4	6	223	29	45.5	1.8	123	Histone H2B
DNA	B0035.8	Histone H2B	<i>his-48</i>	IV	5	122	12	34.4	6	222	29	45.5	1.8	123	Histone H2B
DNA	B0035.9	Histone H4	<i>his-46</i>	IV	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	C50F4.7	Histone H4	<i>his-37</i>	V	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F07B7.9	Histone H4	<i>his-50</i>	V	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F17E9.12	Histone H4	<i>his-31</i>	IV	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F22B3.1	Histone H4	<i>his-64</i>	IV	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F45F2.3	Histone H4	<i>his-5</i>	V	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F54E12.3	Histone H4	<i>his-56</i>	IV	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F55G1.11	Histone H4	<i>his-60</i>	IV	5	178	27	66.8	6	190	28	53.4	1.1	118	Histone H4
DNA	K03A1.6	Histone H4	<i>his-10 his-38</i>	X	5	178	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	K06C4.10	Histone H4	<i>his-18</i>	V	5	179	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	K06C4.2	Histone H4	<i>his-28</i>	V	5	179	27	65	6	190	28	61.2	1.1	103	Histone H4
DNA	T10C6.14	Histone H4	<i>his-1</i>	V	5	180	28	65	6	190	28	61.2	1.1	103	Histone H4
DNA	T23D8.5	Histone H4	<i>his-67</i>	I	5	180	28	65	6	190	28	61.2	1.1	103	Histone H4
DNA	ZK131.1	Histone H4	<i>his-26</i>	II	5	180	28	65	6	190	28	61.2	1.1	103	Histone H4
DNA	ZK131.4	Histone H4	<i>his-10</i>	II	5	180	28	65	6	190	28	61.2	1.1	103	Histone H4
DNA	ZK131.8	Histone H4	<i>his-14</i>	II	5	180	28	65	6	190	28	61.2	1.1	103	Histone H4
DNA	F45F2.2	F45F2.2	<i>his-39</i>	V	5	102	7	19.6	6	154	20	32.1	1.5	112	Histone H4
DNA	R08C7.3	R08C7.3		IV	5	49	14	48.6	6	142	35	56.4	2.9	140	Histone H2A variant
DNA	ZK1005.1	ZK1005.1	<i>pme-5</i>	V	1	5	5	5.3	6	139	73	32.2	27.8	2276	poly (ADP-ribose) polymerase
DNA	E03A3.3	E03A3.3	<i>his-69</i>	III	4	51	6	23.6	6	96	9	23.6	1.9	127	Histone H3 variant
DNA	D2096.8	D2096.8		IV	3	21	8	40.5	6	66	14	42.4	3.1	316	Nucleosome assembly protein (NAP)
DNA	K12D12.1	K12D12.1		II	4	79	35	16.6	6	59	30	16.8	0.7	1520	DNA topoisomerase II
DNA	F32E10.6	F32E10.6		IV	2	3	2	4.8	6	37	18	44.4	12.3	374	chromodomain
DNA	Y39A1C.3	Y39A1C.3		III	3	22	7	31.3	5	25	12	41.2	1.1	294	Cold-shock' DNA-binding domain
DNA	F28B3.7	F28B3.7	<i>him-1</i>	I	4	18	11	7.8	5	24	8	9.4	1.3	1281	SMC-1 protein
DNA	Y17G7A.1	Y17G7A.1	<i>hmg-12</i>	II	2	6	2	9.2	5	20	12	35.2	3.3	315	HMG (high mobility group) box
DNA	F55A3.3	F55A3.3		I	1	7	3	5.2	5	14	7	10.6	2.0	1030	factor
DNA	E03A3.4	E03A3.4		III	1	11	1	11.1	4	36	7	26.2	3.3	126	Histone H3
DNA	M163.3	M163.3	<i>his-24</i>	X	5	40	8	18.8	4	30	7	22.6	0.8	208	Histone H1
DNA	M04F3.1	M04F3.1		I	3	17	7	20.8	4	20	10	29.5	1.2	288	replication protein A2 32 kDa subunit
DNA	ZK863.6	ZK863.6	<i>dpy-30</i>	V	4	23	15	29.4	4	19	11	29.3	0.8	123	dosage compensation component
DNA	F01G4.1	F01G4.1	<i>psa-4</i>	IV	2	49	5	6.9	3	90	2	3.6	1.8	1474	SNF2alpha like
DNA	B0464.7	B0464.7	<i>baf-1</i>	III	2	11	4	42.7	3	24	3	42.7	2.2	89	BAF domain (DNA binding)
DNA	C32F10.5	C32F10.5	<i>hmg-3</i>	I	1	4	3	7.8	3	14	9	11.8	3.5	689	single-strand recognition
DNA	F32A11.4	F32A11.4		II	3	16	6	8.6	3	12	5	10.9	0.8	654	DNA topoisomerase II (N-terminal region)
DNA	Y47D3A.26	Y47D3A.26	<i>smc-3</i>	III	2	9	6	9	3	11	8	9.1	1.2	1269	SMC
DNA	M106.1	M106.1	<i>mix-1</i>	II	2	6	5	7.4	3	10	6	7.6	1.7	1244	mitotic and X-chromosome
DNA	Y73B6BL.9	Y73B6BL.9	<i>hli-2</i>	IV	1	8	2	8.3	3	9	6	13.7	1.1	241	Histone H1
DNA	C53A5.3	C53A5.3	<i>hda-1</i>	V	2	12	6	22.3	3	9	5	11.1	0.8	461	Yeast RPD3 protein like
DNA	C26D10.1	C26D10.1													

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
DNA	PAR2.1	PAR2.1		III	2	2	2	14.7	1	4	3	30	2.0	170	single strand binding protein
DNA	C25G4.5	C25G4.5	<i>dpy-26</i>	IV	2	6	3	5.3	1	4	3	4.4	0.7	1263	dosage-compensation protein HMG box, Bromodomain (5 domains)
DNA	C26C6.1	C26C6.1		I	4	12	5	4.6	1	3	2	1.9	0.3	1883	Zinc finger
DNA	F54F2.2	F54F2.2	<i>zfp-1</i>	III	1	4	3	7.5	1	2	2	2.5	0.5	867	leucine zipper, PHD finger
DNA	T05A7.4	T05A7.4	<i>hmg-11</i>	II	1	3	2	20.4	1	2	2	9.5	0.7	137	nuclear phosphoprotein, DNA binding
RNA	K07C5.4	K07C5.4		V	3	19	12	27.2	6	262	70	65.8	13.8	486	snoRNA binding domain
RNA	W01B11.3	W01B11.3		X	1	8	3	11.1	6	246	65	66.5	30.8	487	Putative snoRNA binding domain
RNA	F31E3.5	F31E3.5	<i>eft-3</i>	III	5	326	67	51.2	6	186	45	58.1	0.6	463	Elongation factor 1-alpha Translation elongation factor EF-1-alpha
RNA	R03G5.1	eft	<i>eft-4</i>	X	5	326	67	51.2	6	186	45	58.1	0.6	463	alpha
RNA	B0041.4	B0041.4	<i>rpl-4</i>	I	5	66	37	44.9	6	155	57	50.1	2.3	345	ribosomal protein L1
RNA	T01C3.7	T01C3.7	<i>fib-1</i>	V	2	7	6	27.6	6	147	34	51.1	21.0	352	fibrillarlin rRNA metabolism
RNA	F53G12.10	F53G12.10	<i>rpl-7</i>	I	4	55	27	43.9	6	128	50	59.4	2.3	244	Ribosomal protein
RNA	F25H2.10	F25H2.10	<i>rps-0</i>	I	4	34	11	49.4	6	95	26	49.7	2.8	312	60s Acidic ribosomal protein family
RNA	F58E10.3	F58E10.3		V	4	15	9	20.7	6	94	31	44.9	6.3	561	ATP-dependent helicase (DEAD box)
RNA	R13A5.8	R13A5.8	<i>rpl-9</i>	III	4	37	12	48.1	6	74	20	48.1	2.0	189	Ribosomal protein L9
RNA	F25H5.4	F25H5.4	<i>eft-2</i>	I	5	53	29	34.2	6	61	30	31.9	1.2	852	Elongation factor Tu family
RNA	B0250.1	B0250.1	<i>rpl-2</i>	V	4	24	10	35.8	6	59	18	39.2	2.5	260	Ribosomal Proteins L2
RNA	C23G10.3	C23G10.3	<i>rps-3</i>	III	5	30	15	36	6	58	25	42.5	1.9	247	Ribosomal protein S3
RNA	K07H8.10	K07H8.10		IV	3	3	3	5.4	6	51	17	15.7	17.0	798	RNA-binding protein
RNA	Y106G6H.2	Y106G6H.2	<i>pab-1</i>	I	3	14	9	20.6	6	43	20	37.5	3.1	646	RNA recognition motif
RNA	C53H9.1	C53H9.1	<i>rpl-27</i>	I	3	13	6	19.9	6	37	12	26.5	2.8	136	60S ribosomal protein L27
RNA	C14B9.7	C14B9.7	<i>rpl-21</i>	III	2	7	3	26.1	6	29	7	24.2	4.1	161	Ribosomal protein L21
RNA	Y105E8A.16	Y105E8A.16	<i>rps-20</i>	I	3	14	8	21.4	6	28	14	22.2	2.0	117	Ribosomal protein S10p/S20e family
RNA	F54C9.1	F54C9.1	<i>ift-2</i>	II	1	4	4	11.2	5	107	20	55.9	26.8	161	initiation factor 5A
RNA	M28.5	M28.5		II	1	5	3	32.8	5	92	24	61.7	18.4	128	Ribosomal protein
RNA	C49H3.11	C49H3.11	<i>rps-2</i>	IV	5	54	13	30.9	5	84	19	30.9	1.6	272	Ribosomal protein
RNA	Y48G8AL.8	Y48G8AL.8	<i>rpl-17</i>	I	4	30	10	23	5	74	23	36.4	2.5	187	Ribosomal protein
RNA	ZC434.2	ZC434.2	<i>rps-4</i>	I	3	29	5	37.6	5	61	5	33	2.1	194	40S ribosomal protein S7
RNA	F36A2.6	F36A2.6	<i>rps-15</i>	I	3	25	10	46.4	5	48	8	47	1.9	151	40S ribosomal protein S15
RNA	F13B10.2	F13B10.2	<i>rpl-3</i>	III	3	18	3	13	5	41	8	23.9	2.3	401	60S ribosomal protein L3
RNA	B0393.1	B0393.1	<i>rps-0</i>	X	3	12	10	37	5	39	14	47.8	3.3	276	40S ribosomal protein
RNA	Y43B11AR.4	Y43B11AR.4	<i>rps-4</i>	IV	2	28	14	30.1	5	37	20	28.2	1.3	259	Ribosomal family S4e family
RNA	T05E11.1	T05E11.1	<i>rps-5</i>	IV	1	8	4	27.6	5	36	10	41.9	4.5	210	40S ribosomal protein S5
RNA	C50C3.6	C50C3.6	<i>prp-8</i>	III	2	13	7	4.8	5	34	15	8.5	2.6	2329	US SNRNP-SPECIFIC PROTEIN
RNA	F57B9.6	F57B9.6	<i>inf-1</i>	IV	2	10	6	21.6	5	28	16	51	2.8	402	ATPase RNA helicase
RNA	F56F3.5	F56F3.5	<i>rps-1</i>	III	3	13	8	29.2	5	27	10	37	2.1	257	Ribosomal protein S3a (human) homolog
RNA	Y71A12B.1	Y71A12B.1	<i>rps-6</i>	I	1	14	5	17.5	5	27	7	19.9	1.9	246	Bromodomain family
RNA	F53A3.3	F53A3.3	<i>rps-22</i>	III	3	10	3	13.8	5	22	9	40	2.2	130	40S ribosomal
RNA	F10G7.2	F10G7.2	<i>tsn-1</i>	II	4	43	22	28.6	5	20	7	16.8	0.5	914	RISC component, found in RNA binding proteins
RNA	C26D10.2	C26D10.2	<i>hel-1</i>	II	2	20	10	30.4	5	17	14	30.8	0.9	425	translation initiation factor eIF-4A
RNA	F57B9.3	F57B9.3		III	1	4	3	9.9	5	12	5	20.1	3.0	363	ATPase RNA helicase: Euk initiation factor 4A
RNA	Y71F9AL.13	Y71F9AL.13	<i>rpl-1</i>	I	3	20	8	36.1	4	37	11	34.7	1.9	216	large ribosomal subunit L10a protein
RNA	JC8.3	JC8.3	<i>rpl-12</i>	IV	2	13	4	22.4	4	34	10	45.5	2.6	165	Ribosomal protein
RNA	R151.3	R151.3	<i>rpl-6</i>	III	2	21	10	38.7	4	32	9	32.7	1.5	217	Ribosomal protein ML16
RNA	T05G5.10	T05G5.10	<i>ift-1</i>	III	2	6	6	39.1	4	32	16	53.4	5.3	161	Initiation factor 5A
RNA	K11H12.2	K11H12.2	<i>rpl-15</i>	IV	2	14	4	16.7	4	29	9	26.5	2.1	204	60S ribosomal protein L15
RNA	Y46G5A.4	Y46G5A.4		II	1	7	5	3.4	4	29	18	12.5	4.1	2145	RNA DEAD box helicase
RNA	F37C12.9	F37C12.9	<i>rps-14</i>	III	2	12	6	30.3	4	28	8	44.1	2.3	152	Ribosomal protein S14
RNA	T08B2.10	T08B2.10	<i>rps-17</i>	I	1	4	3	19.2	4	24	6	42.3	6.0	130	40S ribosomal protein S17
RNA	T21G5.3	T21G5.3	<i>gln-1</i>	I	1	3	2	5.5	4	23	18	20.8	7.7	763	RNA DEAD box helicase
RNA	F23B2.6	F23B2.6	<i>aly-2</i>	IV	2	3	2	17.6	4	20	5	24.2	6.7	227	Ref/ALY RNA export adaptor family
RNA	F20D12.1	F20D12.1		IV	1	2	2	2.3	4	20	15	18.6	10.0	1030	PAZ piwi domain
RNA	C26E6.4	C26E6.4		III	1	4	4	5.8	4	16	11	12.7	4.0	1193	DNA-directed RNA polymerase II
RNA	Y37E3.10	Y37E3.10		I	2	12	4	20.8	4	12	5	18.1	1.0	342	S1 RNA binding domain
RNA	Y97E10AR.5	Y97E10AR.5		V	2	2	2	13.8	4	12	8	13.8	6.0	167	RNA polymerase
RNA	T05F1.3	T05F1.3	<i>rps-19</i>	III	1	3	2	19.9	4	11	7	37	3.7	146	Ribosomal protein S19e
RNA	Y45F10D.12	Y45F10D.12	<i>rpl-18</i>	IV	1	9	4	13.8	3	38	9	31.9	4.2	188	Eukaryotic ribosomal protein L18
RNA	Y41E3.10	Y41E3.10		IV	5	37	9	36.5	3	36	14	32.3	1.0	285	Elongation factor 1 (beta/delta chain)
RNA	F54C9.5	F54C9.5	<i>rpl-5</i>	II	3	20	11	33.3	3	34	15	42.7	1.7	293	60S ribosomal protein L5
RNA	F17C11.9	F17C11.9		V	5	41	11	27.4	3	33	8	25.4	0.8	398	Elongation factor 1-gamma
RNA	Y62E10A.1	Y62E10A.1	<i>rps-2</i>	IV	1	8	5	80.9	3	33	9	80.9	4.1	110	Acidic ribosomal subunit protein P2
RNA	C07H6.5	C07H6.5	<i>cgh-1</i>	III	3	9	6	7.4	3	29	13	20.5	3.2	430	RNA DEAD box helicase
RNA	F54H12.6	F54H12.6		III	5	32	9	48.4	3	22	6	31.9	0.7	213	Elongation factor RNA polymerases L / 13 to 16 Kd subunit
RNA	W01G7.3	W01G7.3		II	2	10	3	24.6	3	22	3	24.6	2.2	122	large ribosomal subunit
RNA	Y106G6H.3	Y106G6H.3	<i>rpl-30</i>	I	1	6	4	38.1	3	19	4	38.1	3.2	113	60S ribosomal protein
RNA	F52B5.6	F52B5.6	<i>rpl-25.2</i>	I	1	3	2	6.2	3	18	8	39.7	6.0	146	RNA recognition motif. (aka RRM, RBD, or RNP domain)
RNA	M18.7	M18.7	<i>aly-3</i>	IV	2	12	5	9.6	3	17	4	25	1.4	240	ribosomal protein L10 (QM protein)
RNA	F10B5.1	F10B5.1	<i>rpl-10</i>	II	1	17	9	36	3	17	11	29	1.0	214	ribosomal protein S11
RNA	F40F11.1	F40F11.1	<i>rps-11</i>	IV	3	10	6	11.6	3	16	8	18.1	1.6	155	large ribosomal subunit L23 protein
RNA	B0336.10	B0336.10	<i>rpl-23</i>	III	2	13	3	27.1	3	16	5	35	1.2	140	60S ribosomal protein L19
RNA	C09D4.5	C09D4.5	<i>rpl-19</i>	I	1	13	2	13.6	3	16	6	22.2	1.2	198	Ribosomal protein
RNA	F28D1.7	F28D1.7	<i>rps-23</i>	IV	1	10	5	23.8	3	16	7	43.4	1.6	143	lysyl-tRNA synthetase
RNA	T02G5.9	T02G5.9	<i>krs-1</i>	II	3	12	8	16.6	3	13	6	17.5	1.1	572	glutamyl-tRNA synthetase
RNA	ZC434.5	ZC434.5	<i>qrs-3</i>	I	2	17	13	18.8	3	13	7	9.1	0.8	1149	RNA DEAD box helicase
RNA	Y71H2AM.19	Y71H2AM.19		III	1	5	2	4.8	3	13	3	4.8	2.6	463	Ribosomal protein
RNA	T07A9.11	T07A9.11	<i>rps-24</i>	IV	1	4	3	8.5	3	13	2	8.8	3.3	329	RISC component, RNA binding
RNA	F56D12.5	F56D12.5	<i>vig-1</i>	II	2	8	4	17.5	3	12	7	27.5	1.5	378	Ribosomal protein
RNA	F42C5.8	F42C5.8	<i>rps-8</i>	IV	1	23	5	34.6	3	12	7	49	0.5	208	Ribosomal protein
RNA	T24B8.1	T24B8.1	<i>rpl-32</i>	II	1	7	4	17.2	3	12	5	17.2	1.7	134	small nuclear ribonucleoprotein SM D3
RNA	Y116A8C.42	Y116A8C.42	<i>snr-1</i>	IV	1	5	3	35.3	3	12	7	22.8	2.4	136	40S ribosomal protein S16
RNA	T01C3.6	T01C3.6	<i>rps-16</i>	V	2	13	8	10.4	3	11	6	25.7	0.8	144	40S ribosomal protein S13
RNA	C16A3.9	C16A3.9	<i>rps-13</i>	III	2	5	4	23.8	3	11	3	17.9	2.2	151	ribosomal protein
RNA	Y37E3.7	Y37E3.7	<i>rps-1</i>	I	1	7	3	41.4	3	11	6	74.8	1.6	111	Pre-mRNA splicing factor activity
RNA	T13H5.4	T13H5.4		II	1	5	3	9	3	10	3	7.2	2.0	500	emb-5 S1 RNA binding
RNA	T04A8.14	T04A8.14	<i>emb-5</i>	III	3	3	3	4.1	3	9	5	6.5	3.0	1521	RNA binding
RNA	F58D5.1	F58D5.1		I	2	10	6	13.6	3	9	8	20.3	0.9	611	Translation elongation factor Tu 1
RNA	Y71H2AM.23	Y71H2AM.23		III	2	12	9	18.5	3	8	4	11.5	0.7	496	Double-stranded RNA binding motif (2 domains)
RNA	H15N14.1	H15N14.1	<i>adr-1</i>	I	2	7	6	11.9	3	8	5	10.8	1.1	959	tRNA synthetase
RNA	Y41E3.4	Y41E3.4	<i>ers-1</i>	IV	3	20	9	18.3	3	7	4	13.2	0.4	786	



Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
RNA	Y54E2A.11	Y54E2A.11	<i>elf-3.B</i>	II	1	2	2	1.5	3	6	5	9.2	3.0	725	eukaryotic initiation factor
RNA	F40F8.10	F40F8.10	<i>rsp-9</i>	II	1	5	5	21.2	3	5	3	11.6	1.0	189	Ribosomal protein
RNA	Y71H2AM.18	Y71H2AM.18		III	1	3	2	9.5	3	5	5	14.6	1.7	328	RNA DEAD box helicase
RNA	C37A2.7	C37A2.7		I	2	9	3	53.3	2	18	6	61.7	2.0	107	Ribosomal protein
RNA	F54E7.2	F54E7.2	<i>rps-12</i>	III	1	7	4	39.3	2	18	6	52.1	2.6	140	Ribosomal protein
RNA	F37C12.4	F37C12.4	<i>rpl-36</i>	III	1	7	4	21.2	2	15	8	44.2	2.1	104	Ribosomal protein
RNA	Y37E3.8	Y37E3.8		I	1	13	5	29	2	14	6	20.7	1.1	145	Ribosomal protein
RNA	C02B10.4	C02B10.4		IV	1	7	2	15.2	2	9	4	15.6	1.3	211	RNA binding
RNA	F56E10.4	F56E10.4	<i>rps-27</i>	V	3	8	4	31.3	2	8	2	15.7	1.0	83	Ribosomal protein
RNA	T22F3.4	T22F3.4	<i>rpl-11.1</i>	V	2	10	4	16.8	2	8	5	24	0.8	196	60S ribosomal protein L11
RNA	C01F6.5	C01F6.5	<i>atly-1</i>	IV	3	8	4	22.9	2	7	3	22.4	0.9	223	RNA binding RNP-1
RNA	T09B4.5	T09B4.5		I	3	12	7	20.5	2	6	4	18	0.5	327	RNA binding
RNA	Y116A8C.35	Y116A8C.35	<i>uat-2</i>	IV	1	6	3	10.2	2	6	3	17.2	1.0	285	RNA binding
RNA	F10E7.7	F10E7.7	<i>rpl-33</i>	II	1	2	2	21.8	2	6	3	21.8	3.0	124	Ribosomal protein
RNA	Y59A8B.10	Y59A8B.10		V	1	3	3	9.9	2	4	2	9.9	1.3	413	KH domain, RNA binding
RNA	F42A6.7	F42A6.7	<i>hrp-1</i>	IV	1	4	2	9.8	2	3	3	14.5	0.8	346	RNA binding
RNA	F45E4.2	F45E4.2		IV	1	2	2	9.7	2	3	2	13.3	1.5	226	RNA binding or ss DNA binding
RNA	ZK381.4	ZK381.4	<i>pgl-1</i>	IV	2	4	2	5.5	2	7	6	9	1.8	730	RNA binding P-granule component
RNA	C27A2.2	C27A2.2	<i>rpl-22</i>	II	2	34	8	25.4	1	30	9	32.3	0.9	130	Ribosomal protein
RNA	C27A2.2	C27A2.2	<i>rpl-22</i>	II	2	34	8	25.4	1	30	9	32.3	0.9	130	Ribosomal protein
RNA	M01F1.2	M01F1.2	<i>rpl-16</i>	III	1	13	2	11.9	1	16	2	13.4	1.2	202	Ribosomal protein
RNA	B0412.4	B0412.4	<i>rps-29</i>	III	3	3	3	51.8	1	8	4	37.5	2.7	56	40S ribosomal protein
RNA	D2013.7	D2013.7	<i>elf-3.F</i>	I	2	2	2	14.3	1	8	3	14.3	4.0	294	Eukaryotic Initiation Factor
RNA	F28C6.7	F28C6.7	<i>rpl-26</i>	II	2	2	2	16.9	1	7	3	16.9	3.5	142	ribosomal protein L26 like
RNA	F07D10.1	F07D10.1	<i>rpl-11.2</i>	X	2	9	3	12.8	1	6	4	16.8	0.7	196	Ribosomal protein
RNA	H20J04.8	H20J04.8		II	2	2	2	9.9	1	6	3	17.4	3.0	253	RNA processing factor, sap-1 (splicing)
RNA	C12D8.11	C12D8.11	<i>rop-1</i>	V	2	2	2	3.9	1	5	4	11.8	2.5	643	ROP-1 ribonucleoprotein RO
RNA	ZK652.4	ZK652.4	<i>rpl-35</i>	III	1	2	2	7.3	1	5	4	16.3	2.5	123	autoantigen
RNA	Y57G11C.16	Y57G11C.16	<i>rps-18</i>	IV	2	2	2	14.9	1	4	3	20.1	2.0	154	ribosomal protein S13
RNA	F28H1.3	F28H1.3	<i>ars-2</i>	I	2	10	6	10	1	2	2	1.9	0.2	968	aminoacyl-tRNA synthetase
RNA	F22D6.3	F22D6.3	<i>nrs-1</i>	I	1	5	4	13.2	1	2	2	5	0.4	545	tRNA synthetase
RNA	Y24D9A.4	Y24D9A.4	<i>rpl-7</i>	II	2	15	8	29.8	2	42	24	33.6	2.8	265	ribosomal protein
Housekeeping	R05G6.7	R05G6.7		IV	4	56	15	48.4	6	404	41	74.2	7.2	283	Channel Protein (mito)
Housekeeping	T08B2.7	T08B2.7		I	5	50	19	21.5	6	272	67	49.9	5.4	781	3-hydroxyacyl-CoA dehydrogenase (mito)
Housekeeping	C34E10.6	C34E10.6	<i>atp-2</i>	III	5	114	22	54.5	6	204	35	63.8	1.8	538	ATP synthase beta chain (mito)
Housekeeping	B0303.3	B0303.3		III	4	30	17	22.8	6	110	43	41.7	3.7	448	Acetyl-coa acetyltransferase
Housekeeping	W10C8.5	W10C8.5		I	3	10	5	19.5	6	93	27	45.4	9.3	399	ATP transferase (mito)
Housekeeping	F32B5.1	F32B5.1		II	2	9	4	13.8	6	87	23	40	9.7	427	phosphotransferase
Housekeeping	D2023.2	D2023.2	<i>pyc-1</i>	III	3	32	19	22	6	85	49	39.2	2.7	1175	pyruvate carboxylase
Housekeeping	H28O16.1	H28O16.1		I	5	43	15	26.2	6	77	21	34.4	1.8	538	ATP synthase Alpha chain
Housekeeping	C29F3.1	C29F3.1	<i>ech-1</i>	V	3	13	6	10.5	6	38	10	16.7	2.9	755	long-chain enoyl-CoA hydratase
Housekeeping	T02H6.11	T02H6.11		II	1	7	4	34.6	6	37	12	61.5	5.3	130	complex subunit
Housekeeping	T24C4.1	T24C4.1		III	1	3	3	8	6	23	14	21.1	7.7	427	cytochrome c reductase (mito)
Housekeeping	W02F12.5	W02F12.5		V	2	2	2	10	6	22	8	26.8	11.0	452	2-oxo acid dehydrogenases
Housekeeping	C05E4.9	C05E4.9	<i>gei-7</i>	V	5	38	25	30.4	5	89	35	32.5	2.3	968	acetyltransferase
Housekeeping	K04G7.4	K04G7.4		III	2	7	3	12.6	5	38	20	32.6	5.4	436	isocitrate lyase
Housekeeping	C05G5.4	C05G5.4		X	2	6	6	13.7	5	34	12	28.9	5.7	322	NADH dehydrogenase
Housekeeping	T10E9.7	T10E9.7	<i>nuo-2</i>	I	2	7	4	10.2	5	32	11	26.7	4.6	401	succinyl-CoA synthetase
Housekeeping	Y53G8AL.2	Y53G8AL.2		III	2	6	3	9.3	5	30	14	30.2	5.0	431	NADH-ubiquinone oxidoreductase
Housekeeping	T22D1.4	T22D1.4		IV	2	9	7	17.6	5	24	6	15	2.7	608	kd subunit
Housekeeping	F42G8.12	F42G8.12	<i>isp-1</i>	IV	2	7	6	33	5	23	11	39.9	3.3	276	glycotransferase
Housekeeping	F20H11.3	F20H11.3	<i>mdh-1</i>	III	5	71	30	49.6	4	181	47	51.3	2.5	341	ubiquinol-cytochrome C reductase
Housekeeping	T05G5.6	T05G5.6	<i>ech-6</i>	III	1	23	10	45.8	4	125	18	48.6	5.4	288	malate dehydrogenase
Housekeeping	F53A2.7	F53A2.7		III	3	33	14	53.3	4	80	23	52.4	2.4	441	Enoyl-CoA hydratase
Housekeeping	F56D2.1	F56D2.1		III	4	13	6	15.3	4	51	19	36.9	3.9	471	Thiolasases
Housekeeping	C54G4.8	C54G4.8	<i>cyc-1</i>	V	2	10	3	18.9	4	46	13	44.6	4.6	285	Mitochondrial processing protease
Housekeeping	ZC434.8	ZC434.8		I	1	8	4	17.8	4	34	12	29.2	4.3	360	enhancing protein
Housekeeping	E04F6.5	E04F6.5		II	2	2	2	5.5	4	30	14	19.9	15.0	613	cytochrome C1, heme protein
Housekeeping	T21B10.2	T21B10.2		II	4	21	7	33.6	4	26	8	26	1.2	434	arginine kinase (mito)
Housekeeping	C33A12.1	C33A12.1		IV	3	3	3	31.3	4	24	3	31.3	8.0	150	Acyl-CoA dehydrogenase
Housekeeping	R07E5.2	R07E5.2	<i>prdx-3</i>	III	1	5	5	25.7	4	22	14	31.4	4.4	226	enolase
Housekeeping	R11A5.4	R11A5.4		I	3	18	10	18.3	4	21	12	24.2	1.2	654	NADH-ubiquinone oxidoreductase 13
Housekeeping	C07A12.4	C07A12.4	<i>pdi-2</i>	X	1	7	4	14.2	4	20	12	24.3	2.9	493	KD-B subunit
Housekeeping	K02F2.2	K02F2.2	<i>dpy-14</i>	I	4	37	21	40.7	4	17	8	28.4	0.5	437	hydroperoxidase Mer5 (mouse)
Housekeeping	F09E5.2	F09E5.2		II	2	9	7	10.4	4	17	14	14.2	1.9	576	antioxidant
Housekeeping	R06F6.9	R06F6.9	<i>ech-4</i>	II	2	2	2	13	4	17	4	23.1	8.5	385	phosphoenolpyruvate carboxykinase
Housekeeping	C44B7.10	C44B7.10		II	2	8	3	10.2	4	15	7	15.6	1.9	832	protein disulfide isomerase (mito)
Housekeeping	T20G5.2	T20G5.2	<i>cts-1</i>	III	2	10	7	19.7	4	14	10	38.7	1.4	468	S-adenosylhomocysteine hydrolase
Housekeeping	Y69A2AR.18	Y69A2AR.18		IV	2	6	4	16.4	4	10	8	20.7	1.7	299	HPC/TSA protein, Glycosyl transferases
Housekeeping	C04C3.3	C04C3.3		IV	1	3	2	7.7	4	10	5	33.5	3.3	352	enoyl CoA hydratase/isomerase
Housekeeping	Y45G12B.1	Y45G12B.1		V	1	7	5	9.7	3	42	18	37.6	6.0	729	Acetyl-CoA hydratases
Housekeeping	Y46G5A.31	Y46G5A.31	<i>gsy-1</i>	II	3	3	3	9.7	3	28	13	21.4	9.3	672	Citrate synthase (mito)
Housekeeping	F32B6.2	F32B6.2		IV	2	11	8	11.9	3	26	18	14.7	2.4	688	ATP synthase
Housekeeping	C03G5.1	C03G5.1		X	3	7	5	14.7	3	22	13	22.1	3.1	646	pyruvate dehydrogenase
Housekeeping	H06O01.1	H06O01.1	<i>pdi-3</i>	I	1	8	5	9.8	3	22	5	20.5	2.8	488	Respiratory chain (mito)
Housekeeping	F47B10.1	F47B10.1	<i>scb-1</i>	X	1	6	2	4.4	3	21	8	24.1	3.5	435	glycogen synthetase) isoform 1
Housekeeping	T22F3.3	T22F3.3		V	2	5	4	6.8	3	20	11	14.1	4.0	882	carbamoyl-phosphate carboxylase
Housekeeping	W05G11.6	W05G11.6		III	2	17	11	19.2	3	20	9	22.6	1.2	651	succinate dehydrogenase flavoprotein
Housekeeping	F54H12.1	F54H12.1	<i>aco-2</i>	III	2	15	8	17.5	3	17	10	21.4	1.1	777	Thioredoxins Protein disulphide isomerase
Housekeeping	F01G4.6	F01G4.6		IV	1	5	4	12.6	3	17	12	25.6	3.4	340	isomerase
Housekeeping	C08F11.14	C08F11.14		IV	3	12	8	8.6	3	16	5	7.4	1.3	907	succinate-CoA ligase
Housekeeping	C34B2.7	C34B2.7		I	1	3	3	7.7	3	16	6	10.3	5.3	640	Glycogen phosphorylase activity
Housekeeping	F22B3.4	F22B3.4		IV	2	3	2	5.8	3	16	7	15.8	5.3	710	glucosamine-fructose-6-phosphate aminotransferase
Housekeeping	F46H5.3	F46H5.3		X	4	29	14	48.3	3	15	8	23.1	0.5	377	arginine kinase
Housekeeping	F23C8.5	F23C8.5		I	2	8	3	26.7	3	15	10	43.9	1.9	255	electron transfer flavoprotein beta
Housekeeping	B0403.4	B0403.4		X	1	3	3	12.3	3	12	7	17.3	4.0	440	protein disulfide-isomerase
Housekeeping	F27D4.5	F27D4.5	<i>tag-173</i>	I	1	3	3	15	3	11	9	33.3	3.7	366	2-oxoisovalerate dehydrogenase (mito)
Housekeeping	F43G9.1	F43G9.1		I	1	9	4	16.8	3	11	9	18.2	1.2	374	isocitrate dehydrogenase (mito)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
Housekeeping	T05H4.12	T05H4.12		V	1	6	5	17.8	3	11	7	17.8	1.8	129	Mitochondrial ATP synthase coupling factor 6
Housekeeping	ZK829.4	ZK829.4		IV	1	6	2	6.3	3	11	8	17.5	1.8	536	glutamate dehydrogenase
Housekeeping	R07G3.5	R07G3.5		II	1	3	3	17.5	3	10	4	17.5	3.3	269	Phosphoglycerate mutase
Housekeeping	T02G5.8	T02G5.8	<i>kat-1</i>	II	1	8	5	22.1	3	10	7	19.2	1.3	407	acetoacetyl-CoA thiolase (mito)
Housekeeping	C05D11.11	C05D11.11	<i>mel-32</i>	III	3	11	4	10.5	3	9	6	16.3	0.8	484	serine hydroxymethyltransferase
Housekeeping	Y39B6A.20	Y39B6A.20	<i>asp-1</i>	V	2	8	6	30.8	3	9	4	22	1.1	396	aspartyl protease
Housekeeping	F01G4.2	F01G4.2	<i>ard-1</i>	IV	3	3	3	22.5	3	9	5	30.6	3.0	258	short-chain alcohol dehydrogenase
Housekeeping	F25H5.3	F25H5.3		I	2	9	4	16.2	3	8	3	11.2	0.9	562	Pyruvate kinase, alpha/beta domain
															Beta-ketoacyl synthase, C-terminal
Housekeeping	F32H2.5	F32H2.5		I	2	9	6	4.6	3	8	7	5.5	0.9	2586	domain
Housekeeping	F01G10.1	F01G10.1	<i>cct-6</i>	IV	3	13	9	9.9	3	6	5	10.5	0.5	618	transketolase
Housekeeping	K09A9.5	K09A9.5	<i>gas-1</i>	X	1	3	2	6.8	3	6	3	13.1	2.0	482	NADH-ubiquinone oxidoreductase
Housekeeping	F35G12.2	F35G12.2		III	1	3	3	11.1	3	5	4	19.7	1.7	380	Isocitrate dehydrogenase
Housekeeping	K09H11.1	K09H11.1		V	1	2	2	2.3	3	5	3	6.4	2.5	985	Acyl-CoA dehydrogenase
Housekeeping	F27D4.1	F27D4.1		I	2	5	3	14.5	3	4	4	20.5	0.8	332	electron transfer flavoprotein
Housekeeping	K11H3.1	K11H3.1		III	1	2	2	9.4	3	4	4	8.3	2.0	351	Glycerol-3-phosphate
Housekeeping	T08H10.1	T08H10.1		V	1	4	3	14.7	2	15	10	25.5	3.8	333	aldose reductase
Housekeeping	F23H11.3	F23H11.3		III	1	8	5	25.5	2	14	3	17.1	1.8	321	succinyl-CoA ligase
Housekeeping	C06H2.1	C06H2.1		V	1	5	4	28.8	2	13	7	41.4	2.6	191	mitochondrial ATP synthase D chain
Housekeeping	F43E2.7	F43E2.7		II	1	5	2	10.2	2	10	3	18.4	2.0	342	mitochondrial substrate carrier
Housekeeping	H14A12.2	H14A12.2	<i>fum-1</i>	III	2	10	8	23	2	9	5	17.6	0.9	501	fumarase (mito)
Housekeeping	C47D12.6	C47D12.6	<i>trs-1</i>	III	3	18	9	20.1	2	8	6	10.8	0.4	725	t RNA synthetase (mito)
Housekeeping	C05D11.12	C05D11.12	<i>let-721</i>	III	1	5	3	7.4	2	8	6	18.1	1.6	597	electron transfer fibroprotein
Housekeeping	F23B12.5	F23B12.5		V	1	2	2	5.7	2	8	4	9.9	4.0	507	pyruvate dehydrogenase complex
Housekeeping	F57B10.3	F57B10.3		I	1	9	2	7.2	2	8	4	13.5	0.9	539	phosphoglycerate mutase
Housekeeping	F49H12.5	F49H12.5		X	2	7	7	23.7	2	7	5	19.5	1.0	257	thioredoxin, ER targeting sequence
Housekeeping	T05D4.1	T05D4.1		III	2	2	2	13.4	2	7	2	12.6	3.5	365	Fructose-bisphosphate aldolase
Housekeeping	F27D9.5	F27D9.5		X	2	23	11	19.3	2	6	5	13	0.3	724	Propionyl-coA carboxylase
Housekeeping	Y37E3.17	Y37E3.17		I	2	11	7	13	2	6	4	6.5	0.5	830	Glycine cleavage T-protein
Housekeeping	K04D7.3	K04D7.3	<i>gta-1</i>	IV	1	2	2	7.7	2	6	4	18.8	3.0	483	4-aminobutyrate aminotransferase
Housekeeping	T03F1.3	T03F1.3		I	1	2	2	7.7	2	5	3	9.6	2.5	417	phosphoglycerate kinase
Housekeeping	C14F11.1	C14F11.1		X	2	10	5	16.2	2	4	4	15	0.4	414	Aspartate aminotransferase
Housekeeping	C48B4.1	C48B4.1		III	2	7	4	6.7	2	4	3	7.1	0.6	659	Acyl-CoA oxidase I
Housekeeping	F08C6.2	F08C6.2		X	1	3	2	11.8	2	4	3	16.7	1.3	347	cholinephosphate cytidyltransferase
Housekeeping	F35D11.4	F35D11.4		II	1	4	2	16.8	2	4	3	9.1	1.0	197	Adenylyl cyclase
Housekeeping	K10B3.7	K10B3.7/K10B3.8	<i>gpd-3</i>	X	1	20	11	35.2	2	4	3	13.5	0.2	341	Glyceraldehyde 3-phosphate
Housekeeping	K10B3.8	K10B3.7/K10B3.8	<i>gpd-2</i>	X	1	20	11	35.2	2	4	3	13.5	0.2	341	Glyceraldehyde 3-phosphate
Housekeeping	M01A10.3	M01A10.3		I	1	3	2	14.3	2	4	3	14.3	1.3	280	oligosaccharyl transferase
Housekeeping	R07H5.8	R07H5.8		IV	1	3	2	12.3	2	4	4	24.9	1.3	342	adenosine kinase
Housekeeping	T25G12.5	T25G12.5		X	1	5	3	14.3	2	4	3	12.1	0.8	412	acyl-CoA dehydrogenase
Housekeeping	Y39E4A.3	Y39E4A.3		III	1	6	5	18.2	2	3	2	6.9	0.5	478	transketolase
Housekeeping	Y37D8A.14	Y37D8A.14		III	1	5	3	23.6	1	36	11	51.1	7.2	174	Cytochrome c oxidase subunit Va
Housekeeping	Y71H2AM.5	Y71H2AM.5		III	2	2	2	17.4	1	18	12	52.9	9.0	121	cytochrome oxidase
Housekeeping	T22B11.5	T22B11.5		IV	2	13	8	13	1	14	5	8.3	1.1	1029	2-oxoglutarate dehydrogenase
Housekeeping	F38B2.4	F38B2.4		X	2	2	2	20	1	12	4	19.5	6.0	210	adenylyl kinase
Housekeeping	E04A4.7	E04A4.7		IV	2	4	2	19.8	1	7	4	33.3	1.8	111	cytochrome C
Housekeeping	Y57G11C.3	Y57G11C.3		IV	1	3	2	15.2	1	6	4	24.2	2.0	269	phosphate isomerase
Housekeeping	C37E2.1	C37E2.1		X	1	3	2	6.6	1	5	2	9.2	1.7	379	isocitrate dehydrogenase
Housekeeping	F46E10.9	F46E10.9	<i>dpy-11</i>	V	2	3	2	11.4	1	5	3	16.7	1.7	246	thioredoxin
Housekeeping	W07E11.1	W07E11.1		X	1	3	3	2.3	1	4	3	1.6	1.3	2207	glutamate synthase
Housekeeping	T08G2.3	T08G2.3		X	1	12	4	13.7	1	3	2	6.7	0.3	417	acyl-CoA dehydrogenase
Housekeeping	T26C12.1	T26C12.1		IV	1	2	2	4.7	1	2	2	6.6	1.0	640	acetolactate synthase
Housekeeping	Y57A10A.26	Y57A10A.26		II	1	3	3	15.2	1	2	2	11.5	0.7	269	Glutathione S-transferase, C-terminal
Housekeeping	R07H5.2	R07H5.2		IV	2	2	2	4.5	1	2	2	4	1.0	646	camitine palmitoyltransferase II
Cytoskeletal	F11C3.3	F11C3.3	<i>unc-54</i>	I	5	268	98	38.2	6	382	129	35.6	1.4	1963	Myosin heavy chain
Cytoskeletal	F07A5.7	F07A5.7	<i>unc-15</i>	I	5	185	61	45.3	6	178	64	42.9	1.0	872	paramyosin
Cytoskeletal	M03F4.2	M03F4.2	<i>act-4</i>	X	5	212	46	61.7	6	91	21	42.3	0.4	376	Actin
Cytoskeletal	T04C12.4	T04C12.4	<i>act-3</i>	V	5	210	45	61.2	6	90	21	42.3	0.4	376	Actin
Cytoskeletal	T04C12.6	T04C12.6	<i>act-1</i>	V	5	210	45	61.2	6	90	21	42.3	0.4	376	Actin
Cytoskeletal	T25C8.2	T25C8.2	<i>act-5</i>	II	5	72	23	61.1	6	78	22	42.4	1.1	375	Actin
Cytoskeletal	T04C12.5	T04C12.5	<i>act-2</i>	V	5	178	41	61.7	6	69	19	42.3	0.4	376	Actin
Cytoskeletal	R06C7.10	R06C7.10	<i>myo-1 let-75</i>	I	5	52	31	17.5	6	67	35	14.5	1.3	1938	Myosin heavy chain
Cytoskeletal	F10C1.2	F10C1.2	<i>itb-1</i>	II	4	43	13	26	6	41	11	15.9	1.0	558	Intermediate filament protein
Cytoskeletal	F10C1.7	F10C1.7	<i>itb-2</i>	II	5	156	41	50.1	5	627	108	67	4.0	543	Intermediate filament protein
Cytoskeletal	ZK973.6	ZK973.6	<i>anc-1</i>	I	4	181	17	33	5	308	29	5.4	1.7	7659	actin binding, nuclear localization
Cytoskeletal	M6.1	M6.1	<i>itc-2</i>	X	3	19	10	11.7	5	210	52	23.8	11.1	1141	Intermediate filament protein
Cytoskeletal	K10B3.10	K10B3.10	<i>spc-1</i>	X	3	25	18	12.4	5	47	32	19.8	1.9	2427	spectrin alpha chain
Cytoskeletal	C43C3.1	C43C3.1	<i>tlp-1</i>	X	3	17	10	16.8	5	45	23	31.7	2.6	776	Intermediate filament protein
Cytoskeletal	T18D3.4	T18D3.4	<i>myo-2</i>	X	4	42	21	14.5	5	42	23	11.7	1.0	1969	Myosin heavy chain
Cytoskeletal	K11C4.3	K11C4.3	<i>unc-70</i>	V	4	10	5	4.2	5	25	5	12.4	3.5	2287	spectrin beta chain
Cytoskeletal	ZC101.2	ZC101.2	<i>unc-52</i>	II	4	87	48	25.8	5	20	17	8.8	0.2	2482	laminin, Ig domains
Cytoskeletal	F09F7.2	F09F7.2	<i>mlc-3</i>	III	3	49	18	66.7	4	39	15	59.5	0.8	153	myosin light chain
Cytoskeletal	K12F2.1	K12F2.1	<i>myo-3</i>	V	4	56	36	22.7	4	29	20	12.6	0.5	1992	Myosin heavy chain
Cytoskeletal	C38E6.3	C38E6.3	<i>mlc-1</i>	X	1	20	8	33.7	4	24	8	30.4	1.2	270	EF hand, Calcium binding
Cytoskeletal	R31.1	R31.1	<i>sma-1</i>	V	2	9	7	2.5	4	11	9	3.3	1.2	4063	spectrin beta chain
Cytoskeletal	R07G3.3	R07G3.3		II	2	5	4	3.7	4	8	5	3.7	1.6	1976	Myosin heavy chain
Cytoskeletal	C36E6.5	C36E6.5	<i>mlc-2</i>	X	2	22	9	53.5	3	19	9	48.2	0.9	170	Myosin Light Chain gene class cytoplasmic intermediate filament
Cytoskeletal	R04E5.10	R04E5.10	<i>itd-1</i>	X	1	8	5	15	3	18	12	26.6	2.3	575	protein
Cytoskeletal	C46G7.2	C46G7.2		IV	3	13	9	42	3	15	5	34.4	1.2	250	Alpha-filagenin, muscle protein
Cytoskeletal	C25A11.4	C25A11.4	<i>ajm-1</i>	X	2	19	6	7.3	3	9	4	4.1	0.5	1480	apical junction molecular
Cytoskeletal	C47E8.7	C47E8.7	<i>unc-112</i>	V	1	11	8	15.4	3	4	3				

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
Signalling	B0205.7	B0205.7	<i>kin-3</i>	I	2	8	5	18.6	5	25	12	28.6	3.1	360	casein kinase
Signalling	F56C9.1	F56C9.1	<i>gsp-2</i>	III	2	7	4	20.4	5	21	13	40.8	3.0	333	Glc Seven-like Phosphatases
Signalling	F29F11.6	F29F11.6	<i>gsp-1</i>	V	2	5	4	21.9	4	16	9	41	3.2	329	Glc Seven-like Phosphatases
Signalling	F52D10.3	F52D10.3	<i>ftt-2</i>	X	2	15	9	30.6	4	15	3	16.5	1.0	248	14-3-3 protein
Signalling	K04D7.1	K04D7.1		IV	3	20	9	41.2	3	27	10	38.2	1.4	325	G-protein WD-40 repeat protein kinase and KH domain-RNA binding
Signalling	E02D9.1	E02D9.1		I	2	11	6	21.6	3	16	8	21.6	1.5	315	
Signalling	C25F6.2	C25F6.2	<i>dlg-1</i>	X	5	40	26	31.2	3	11	11	19.2	0.3	1064	guanylate kinase, adherens junctions
Signalling	F48E8.5	F48E8.5	<i>paa-1</i>	III	1	14	8	19.7	3	9	5	7.7	0.6	664	protein phosphatase 2A, HEAT repeat
Signalling	F49D11.1	F49D11.1		I	1	2	2	6.2	3	9	3	8.8	4.5	567	WD domain G-beta protein
Signalling	Y76A2B.1	Y76A2B.1	<i>pod-1</i>	III	1	4	3	6.9	2	7	3	7.8	1.8	1057	WD domain G-beta protein
Major Sperm	F33D11.11	F33D11.11		I	1	5	4	29.8	3	4	3	25.7	0.8	245	Major Sperm Protein
Major Sperm	C09B9.6	MSP	<i>msp-55</i>	IV	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	C33F10.9	MSP	<i>msp-40</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	C34F11.4	MSP	<i>msp-50</i>	III	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	C34F11.6	MSP	<i>msp-49</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	F32B6.6	MSP	<i>msp-77</i>	IV	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	F36H12.7	MSP	<i>msp-19</i>	IV	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	F58A6.8	MSP	<i>msp-45</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	K05F1.2	MSP	<i>msp-142</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	K07F5.1	MSP	<i>msp-81</i>	IV	1	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	R05F9.13	MSP	<i>msp-31</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	R05F9.8	MSP	<i>msp-37</i>	II	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	R13H9.2	MSP	<i>msp-57</i>	IV	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	R13H9.4	MSP	<i>msp-53</i>	IV	2	3	2	23.6	1	3	2	22	1.0	127	Major Sperm Protein
Major Sperm	T13F2.10	MSP	<i>msp-79</i>	IV	2	3	2	23.1	1	3	2	21.5	1.0	130	Major Sperm Protein
Major Sperm	Y59E9AR.1	MSP		IV	2	3	2	23.1	1	3	2	21.5	1.0	130	Major Sperm Protein
Extracellular Matrix	K08C7.3	K08C7.3	<i>epi-1</i>	IV	1	13	11	5.3	5	60	40	14.8	4.6	3704	Laminin
Extracellular Matrix	W09H1.6	W09H1.6	<i>lec-1</i>	II	4	13	7	33.7	5	26	10	38	2.0	279	Lectin
Extracellular Matrix	F52H3.7	F52H3.7		II	5	38	15	9	5	25	9	22.3	0.7	278	galactoside-binding lectin
Extracellular Matrix	F52H3.7	F52H3.7		II	5	38	15	9	5	25	9	22.3	0.7	278	galactoside-binding lectin
Extracellular Matrix	C54D1.5	C54D1.5		X	2	11	8	9.1	5	24	14	13	2.2	1557	laminin EGF-like
Extracellular Matrix	W03F8.5	W03F8.5	<i>lam-1</i>	IV	4	16	9	9.2	4	32	25	18.9	2.0	1808	Laminin
Extracellular Matrix	Y55B1AR.1	Y55B1AR.1		III	1	3	3	37.7	4	28	10	56.2	9.3	146	Lectin
Extracellular Matrix	F40F4.6	F40F4.6		X	2	6	3	2.8	3	23	12	9.2	3.8	2214	EGF-like repeats, Lectin
Extracellular Matrix	ZK892.1	ZK892.1	<i>lec-3</i>	II	3	8	3	20.5	3	6	4	16.8	0.8	297	galactoside-binding lectin
Extracellular Matrix	C16H3.2	C16H3.2	<i>lec-9</i>	X	1	5	3	37.1	2	5	3	42.1	1.0	140	sugar-binding protein
Extracellular Matrix	W03F11.1	W03F11.1		I	1	4	2	12.3	2	4	4	16.2	1.0	235	chitin binding
Extracellular Matrix	H19M22.2	H19M22.2	<i>let-805</i>	III	3	66	43	16.4	2	3	3	1.4	0.0	4280	let-805 Putative cell adhesion protein
Extracellular Matrix	H0212.1	H0212.1		IV	5	31	11	12.5	1	4	3	4.6	0.1	1332	chitin binding Protein
Spindle	K01G5.7	K01G5.7	<i>tbb-1</i>	III	5	94	35	53.7	6	122	42	52.1	1.3	449	tubulin beta-chain
Spindle	C54C6.2	C54C6.2	<i>ben-1</i>	III	5	46	20	29.9	6	68	24	34.1	1.5	452	tubulin
Spindle	C47B2.3	C47B2.3	<i>tba-2</i>	I	4	46	13	33.9	6	44	18	33.3	1.0	448	alpha tubulin
Spindle	F26E4.8	F26E4.8	<i>tba-1</i>	I	4	39	12	30.7	6	38	18	33.2	1.0	449	TBA-2 tubulin alpha-2 chain
Spindle	F44F4.11	F44F4.11	<i>tba-4</i>	II	4	31	9	24.1	6	30	15	26.6	1.0	448	tubulin alpha-2 chain
Spindle	T28D6.2	T28D6.2	<i>tba-7</i>	III	3	25	7	15.8	5	25	11	16	1.0	444	tubulin alpha subunit
Spindle	B0272.1	B0272.1	<i>tbb-4</i>	X	2	21	12	25.9	5	18	11	21.4	0.9	444	tubulin beta
Spindle	ZK154.3	ZK154.3	<i>mec-7</i>	X	3	13	6	12.9	3	14	7	20.2	1.1	441	beta tubulin
Spindle	C41C4.8	C41C4.8		II	2	13	9	15.1	3	12	5	10.7	0.9	810	P97 protein AAA ATPases
Spindle	F58A4.8	F58A4.8	<i>tbg-1</i>	III	2	2	2	4.1	1	7	5	23.2	3.5	444	Gamma-like tubulin
Spindle	C44B11.3	C44B11.3	<i>mec-12</i>	III	2	6	2	8.4	1	2	2	4.4	0.3	450	alpha tubulin
Heat Shock	F01F1.8	F01F1.8	<i>cct-6</i>	III	1	5	2	7.1	3	8	5	17.3	1.6	539	eukaryotic cytosolic chaperonin
Heat Shock	C37H5.8	C37H5.8	<i>hsp-6</i>	V	2	14	7	13.2	3	4	4	9.7	0.3	657	Heat shock 70 protein
Heat Shock	K01C8.10	K01C8.10	<i>cct-4</i>	II	3	17	8	22.2	2	25	6	24.6	1.5	540	chaperonin
Heat Shock	T05C12.7	T05C12.7	<i>cct-1</i>	II	1	4	2	7.5	2	22	6	10.7	5.5	549	chaperonin
Heat Shock	T27E4.3	T27E4.3	<i>hsp-16.48</i>	V	2	18	4	54.5	2	11	4	44.8	0.6	143	heat shock protein
Heat Shock	T27E4.9	T27E4.9	<i>hsp-16.49</i>	V	2	18	4	54.5	2	11	4	44.8	0.6	143	heat shock protein
Heat Shock	T05C3.5	T05C3.5	<i>djri-19</i>	V	2	2	2	6.8	2	10	6	10.7	5.0	439	DNAJ-like protein
Heat Shock	C24G6.5	C24G6.5	<i>djri-6</i>	V	2	2	2	9	2	7	5	8.3	3.5	374	DNAJ
Heat Shock	T27E4.2	hsp-16	<i>hsp-16.1</i>	V	2	18	8	37.9	2	3	3	26.2	0.2	145	heat shock protein HSP16-1
Heat Shock	T27E4.8	hsp-16	<i>hsp-16.1</i>	V	2	18	8	37.9	2	3	3	26.2	0.2	145	heat shock protein HSP16-1
Heat Shock	Y46H3A.3	hsp-16	<i>hsp-16.2</i>	V	2	17	7	33.8	2	3	3	26.2	0.2	145	heat shock protein
Heat Shock	C14F11.5	C14F11.5	<i>hsp-43</i>	X	1	4	3	12.2	2	3	3	13.3	0.8	368	Hsp20 or alpha crystallin family
Heat Shock	F54D5.8	F54D5.8	<i>djri-13</i>	II	1	4	2	9.7	2	3	2	6.9	0.8	331	DNAJ
Heat Shock	C07G2.3	C07G2.3	<i>cct-5</i>	III	1	2	2	5	1	3	3	10.9	1.5	542	TCP-1 like chaperonin
Heat Shock	F54A3.3	F54A3.3		X	1	6	4	8.4	1	2	2	4.6	0.3	606	Chaperonin
Vitellogenin	C42D8.2	C42D8.2	<i>vit-2</i>	X	5	301	94	45.6	6	117	47	28.6	0.4	1613	Vitellogenin
Vitellogenin	K07H8.6	K07H8.6	<i>vit-6</i>	IV	4	273	86	45.5	6	69	42	30.7	0.3	1650	Vitellogenin
Vitellogenin	K09F5.2	K09F5.2	<i>vit-1</i>	X	4	153	54	25.6	5	58	22	14.1	0.4	1616	Vitellogenin
Vitellogenin	C04F6.1	C04F6.1	<i>vit-5</i>	X	3	83	41	28.6	4	24	11	12	0.3	1603	Vitellogenin
Vitellogenin	F59D8.1	F59D8.1	<i>vit-3</i>	X	3	52	31	22.9	3	13	7	7.5	0.3	1603	Vitellogenin
Vitellogenin	F59D8.2	F59D8.2	<i>vit-4</i>	X	3	55	31	22.7	3	12	6	6.7	0.2	1603	Vitellogenin
Nuclear Envelope	DY3.2	DY3.2	<i>lmn-1</i>	I	4	51	25	41.5	6	139	61	51.6	2.7	566	nuclear laminin
Nuclear Envelope	T23H2.1	T23H2.1	<i>npp-12</i>	I	3	12	8	7	5	41	20	15.5	3.4	1847	integral membrane protein
Nuclear Envelope	C01G8.5	C01G8.5	<i>erm-1</i>	I	3	9	6	8.3	4	26	11	20.1	2.9	563	membrane protein, ERM family of
Nuclear Envelope	F59A2.1	F59A2.1	<i>npp-9</i>	III	2	18	10	22.1	3	13	7	14.8	0.7	860	Nucleoporin
Nuclear Envelope	Y37E3.15	Y37E3.15	<i>npp-14</i>	I	2	10	7	8.5	3	13	10	17.2	1.3	787	Nucleoporin interacting component
Nuclear Envelope	W01G7.5	W01G7.5	<i>lem-2</i>	II	3	11	7	22.6	3	7	4	16.6	0.6	500	nuclear membrane (LEM domain, lamino associated)
Nuclear Envelope	ZK328.5	ZK328.5	<i>npp-10</i>	II	1	3	3	3.6	3	3	3	6.7	1.0	955	NUCLEOPORIN
Nuclear Envelope	F54B11.3	F54B11.3	<i>unc-84</i>	X	1	8	3	5.1	2	5	3	4.9	0.6	1111	nuclear migration, nuclear envelope
Nuclear Envelope	F26B1.3	F26B1.3	<i>ima-2</i>	I	1	6	3	8.9	2	4	3	10.9	0.7	531	importin
Nuclear Envelope															

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	<i>C. elegans</i> locus	LG	Oogenic				Spermatogenic				Abundance Ratio	Length	Descriptor
					Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)	Occur- renc	Total Spectrum Count	Sequence Count	Cover- age (%)			
Other	B0350.2	B0350.2	<i>unc-44</i>	I	2	6	4	3.2	5	12	10	7.1	2.0	2039	ankryrin-like
Other	Y38A10A.5	Y38A10A.5	<i>cr1-1</i>	V	2	11	5	23	4	35	11	48.4	3.2	395	calreticulin precursor
Other	T20G5.1	T20G5.1		III	2	27	20	17.7	4	26	15	13.6	1.0	1681	Claithrin heavy chain
Other	F27C1.7	F27C1.7		I	2	7	6	25.6	4	22	12	33.8	3.1	207	ATPase (mito)
Other	F20B6.2	F20B6.2	<i>vha-12</i>	X	2	13	8	24.6	4	20	9	18.9	1.5	491	vacuolar ATP synthase
Other	C06A1.1	C06A1.1		II	2	15	11	19.8	4	10	5	13.5	0.7	809	AAA ATPase
Other	VW02B12L.1	VW02B12L.1	<i>vha-6</i>	II	1	4	3	7.6	3	31	16	12.7	7.8	865	vacuolar ATP synthase
Other	T26E3.7	T26E3.7		I	1	8	2	10.4	3	28	7	10.4	3.5	106	ATP synthase alpha and beta
Other	C30F8.2	C30F8.2		I	1	5	3	14.9	3	22	10	39.7	4.4	348	vacuolar ATPase
Other	C14B1.1	C14B1.1	<i>pdi-1</i>	III	1	7	4	12.4	3	19	7	14	2.7	485	protein disulfide isomerase
Other	T27E9.7	T27E9.7		III	1	3	3	9.2	3	13	9	12.7	4.3	622	ABC transporters (2 domains)
Other	Y25C1A.5	Y25C1A.5		II	2	9	5	9.8	3	12	4	8	1.3	971	beta subunit of the coatomer (COPI) 19S regulatory particlesubunit of proteasome
Other	T22D1.9	T22D1.9	<i>rpn-1</i>	IV	2	9	6	9.8	3	10	5	7.6	1.1	981	WD domain, COPI complex component
Other	F38E11.5	F38E11.5		IV	1	5	4	9.1	3	10	6	10.8	2.0	1000	ATPase Proteasome component
Other	F56H1.4	F56H1.4	<i>rpt-5</i>	I	2	4	4	14.4	3	9	6	21.4	2.3	430	protein transport protein SEC61 alpha
Other	Y57G11C.15	Y57G11C.15		IV	1	4	2	4.2	3	6	6	4.2	1.5	473	ATPase
Other	C17H12.14	C17H12.14	<i>vha-8</i>	IV	1	2	2	6.2	3	4	4	16.4	2.0	226	ATPases associated with various cellular activities (AAA)
Other	F54B3.3	F54B3.3		II	1	5	4	5.9	2	15	8	17.9	3.0	610	EF hand, calcium binding
Other	W06H8.1	W06H8.1	<i>rme-1</i>	V	2	8	6	10.1	2	11	4	8.4	1.4	786	sec23/24, gelsolin
Other	Y113G7A.3	Y113G7A.3	<i>sec-23</i>	V	2	2	2	5.4	2	10	7	13.4	5.0	821	ABC transporter
Other	T10H9.5	T10H9.5	<i>pmp-5</i>	V	2	3	2	8	2	6	4	11.4	2.0	598	E1-E2 ATPases
Other	K11D9.2	K11D9.2	<i>sca-1</i>	V	2	9	7	11.3	2	5	3	4.5	0.6	1059	ATP synthase
Other	F58F12.1	F58F12.1		II	1	3	3	39.3	2	5	4	22.1	1.7	163	26S protease regulatory subunit
Other	F56F11.4	F56F11.4		III	2	7	6	13.6	2	3	3	8.3	0.4	411	ATPases associated with various cellular activities (AAA)
Other	Y49E10.1	Y49E10.1	<i>rpt-6</i>	III	2	6	5	9.1	2	3	3	8.2	0.5	416	ubiquitin
Other	F25B5.4	F25B5.4	<i>ubq-1</i>	III	1	22	1	1.1	1	22	1	1.1	1.0	838	Vacuolar H ATPase gene class
Other	Y38F2AL.3	Y38F2AL.3	<i>vha-11</i>	IV	2	6	3	6.8	1	5	2	6.8	0.8	384	Adaptor complexes medium subunit
Other	C13B9.3	C13B9.3		III	2	2	2	4.9	1	5	4	14.8	2.5	515	vacuolar ATPase G subunit
Other	F46F11.5	F46F11.5		I	2	2	2	15.9	1	4	3	15.9	2.0	126	Dynamin
Other	C02C6.1	C02C6.1	<i>dyn-1</i>	X	1	2	2	4.1	1	2	2	2.3	1.0	830	Membrane-associated atpase gamma
Other	F55H2.2	F55H2.2		III	1	3	3	12.5	1	2	2	12.5	0.7	257	proteasome component
Other	R12E2.3	R12E2.3	<i>rpn-8</i>	I	1	3	3	14.9	1	2	2	11	0.7	362	ATPase subunit
Other	T14F9.1	T14F9.1	<i>vha-15</i>	X	1	5	5	9.1	2	7	5	9.1	1.4	470	
Unknown	M01E11.4	M01E11.4	<i>pqn-52</i>	I	4	25	15	34.8	6	65	26	46.7	2.6	244	
Unknown	F29G6.3	F29G6.3		X	3	17	11	7.2	5	72	46	23.3	4.2	1929	
Unknown	Y56A3A.21	Y56A3A.21		III	2	6	5	32.1	5	14	8	22.6	2.3	159	
Unknown	Y66H1B.2	Y66H1B.2		IV	2	8	5	4.3	4	36	30	19.1	4.5	1400	
Unknown	W08E3.3	W08E3.3	<i>tag-210</i>	I	3	39	19	46.1	4	28	13	33.7	0.7	395	GTP-binding protein like
Unknown	C08H9.2	C08H9.2		II	1	9	9	8.8	4	24	14	14.1	2.7	1220	high-density lipoprotein-binding
Unknown	C18B2.5	C18B2.5		X	1	6	5	10.5	4	24	13	26.6	4.0	673	
Unknown	VW06B3R.1	VW06B3R.1		X	2	6	3	14.9	4	23	9	30.7	3.8	410	Insulinase
Unknown	D1054.10	D1054.10		V	5	78	15	40.4	4	20	7	28.7	0.3	188	
Unknown	Y39B6A.1	Y39B6A.1		V	1	3	3	1.5	4	19	12	5.2	6.3	735	
Unknown	Y59A8A.3	Y59A8A.3		V	2	18	8	20.9	4	13	3	9.2	0.7	676	
Unknown	D1054.11	D1054.11		V	5	97	18	28.7	4	10	5	19.9	0.1	317	
Unknown	T05F1.6	T05F1.6	<i>hsr-9</i>	V	2	14	11	14.9	4	10	4	7	0.7	1151	BRCA1 C Terminus (BRCT) domain
Unknown	F54F11.2	F54F11.2		II	2	14	8	10.4	3	23	12	15.6	1.6	1589	Zinc-binding metalloprotease
Unknown	Y65B4BR.5	Y65B4BR.5		I	1	10	4	24.1	3	23	6	23.6	2.3	195	Ubiquitin associated domain, NAC
Unknown	T14G11.3	T14G11.3		X	3	9	4	8	3	22	11	20.6	2.4	727	
Unknown	F42C5.10	F42C5.10		IV	2	3	2	3.8	3	20	14	19.7	6.7	1292	
Unknown	F57F4.3	F57F4.3/F57F4.4	<i>gfi-1</i>	V	1	6	3	3.8	3	18	7	6.6	3.0	2153	ET domain (cys residues of unk fxn)
Unknown	F57F4.4	F57F4.3/F57F4.4		V	1	6	3	3.9	3	18	7	6.8	3.0	2090	ET domain (cys residues of unk fxn)
Unknown	ZC373.2	ZC373.2		X	5	47	8	37.7	3	17	4	36.9	0.4	122	
Unknown	C44B12.5	C44B12.5		IV	3	45	12	29.2	3	17	6	20.4	0.4	397	
Unknown	F37C4.5	F37C4.5		IV	1	2	2	5	3	10	6	14.2	5.0	556	
Unknown	F30A10.5	F30A10.5	<i>stl-1</i>	I	1	3	2	10.8	3	7	4	24.6	2.3	334	erythrocyte band 7 integral
Unknown	C02E11.1	C02E11.1		V	1	5	3	5.6	2	9	5	8.1	1.8	1121	
Unknown	B0238.11	B0238.11		V	1	4	3	17.4	2	8	6	32.5	2.0	317	
Unknown	Y71G10AL.1	Y71G10AL.1		IV	2	4	3	12.7	2	7	4	18.9	1.8	408	
Unknown	ZK180.4	ZK180.4		IV	1	3	2	22.2	2	7	3	29.5	2.3	193	GTP binding
Unknown	F12F6.1	F12F6.1		IV	3	3	3	7.2	2	5	3	5.6	1.7	903	
Unknown	Y80D3A.2	Y80D3A.2		V	1	3	3	4	2	3	3	3.8	1.0	1212	
Unknown	C08F11.12	C08F11.12		IV	1	7	4	53.8	1	6	2	15.4	0.9	117	
Unknown	Y45F10C.2	Y45F10C.2		IV	1	6	3	35	1	6	2	15.4	1.0	117	
Unknown	JC8.8	JC8.8		IV	1	2	2	22.6	1	6	3	27	3.0	159	Transthyretin-like
Unknown	C47E12.5	C47E12.5	<i>uba-1</i>	IV	2	12	8	12.4	1	4	3	5	0.3	1113	ubiquitin-activating enzyme
Unknown	W03F9.10	W03F9.10		V	2	2	2	5.1	1	4	4	5.5	2.0	602	
Unknown	F02A9.2	F02A9.2	<i>far-1</i>	III	1	3	3	20.9	1	2	2	9.9	0.7	182	(fatty acid binding protein)
Unknown	F28B4.3	F28B4.3		X	1	4	3	2.6	1	2	2	2.2	0.5	2229	EGF-like repeat
Unknown	Y57G11C.24	Y57G11C.24	<i>eps-8</i>	IV	2	2	2	4.1	1	2	2	5.5	1.0	732	epidermal growth factor receptor
Unknown	Y71H2AM.4	Y71H2AM.4		III	1	2	2	18	1	6	3	24.5	3.0	139	

Functional Category determination is described in Supplemental Methods; Family ID, designation for families of proteins not differentiated by a set of identifying peptides; LG, chromosomal location; Occurrences, the number of preparations in which a protein was identified out of 6 spermatogenic or 5 oogenic preparations; Total Spectrum Count (TSC), the total number of peptides detected for each protein from all preparations; Sequence Count, the number of distinct MS/MS spectra collected from all preparations; Coverage, % of protein represented by uniquely identified peptides; Abundance Ratio, calculated from Spermatogenic TSC/Oogenic TSC; Length, number of amino acids in protein; Descriptor, protein description through homology or provided in WormBase, Worm Protein Database (BIOBASE) annotations.

Supplemental Table 4 Oogenic proteins copurified with chromatin (272)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
DNA	C50B6.2	C50B6.2		V	2	36	19	30.4	582	Histone binding protein
DNA	F26F12.7	F26F12.7	<i>let-418</i>	V	2	13	13	9.2	1829	DNA helicase
DNA	Y39G10AR.14	Y39G10AR.14	<i>mcm-4</i>	I	2	9	6	13.5	823	DNA replication
DNA	C25D7.6	C25D7.6	<i>mcm-3</i>	V	2	7	5	9.4	812	DNA replication licensing factor MCM3
DNA	Y113G7B.23	Y113G7B.23	<i>psa-1</i>	V	2	7	5	12.3	789	SWI/SNF protein
DNA	ZK1127.7	ZK1127.7		II	2	7	6	8.5	816	DNA gyrase/topoisomerase IV, subunit A
DNA	F37D6.2	F37D6.2		I	2	7	2	7.4	582	C2H2 type zinc finger domain
DNA	F09G2.9	F09G2.9		V	2	6	5	17.6	415	DNA binding Domain (A+T hook)
DNA	R07E5.3	R07E5.3		III	2	4	3	17.8	381	Snf5
DNA	C54G10.2	C54G10.2	<i>rtc-1</i>	III	2	3	2	3.5	839	Replication factor C1
DNA	F57C7.1	F57C7.1		X	2	3	2	3.4	1250	Bromodomain
DNA	C03G6.12	C03G6.12		V	2	2	2	7.4	430	ligand-binding domain of nuclear hormone receptor family
DNA	C36B1.3	C36B1.3		I	2	2	2	7.5	402	DNA directed RNA polymerase II
DNA	F44B9.8	F44B9.8		III	2	2	2	7	388	DNA replication factor C complex
DNA	T04H1.4	T04H1.4	<i>rad-50</i>	V	2	2	2	2.9	1298	Recombination/repair protein Rad50
DNA	Y48E1B.12	Y48E1B.12	<i>csc-1</i>	II	2	2	2	9.6	249	borealin, Aurora B kinase complex member
DNA	Y71H2AM.17	Y71H2AM.17		III	2	2	2	14.3	350	HMG (high mobility group)
DNA	T19D12.4	T19D12.4		II	1	12	4	3.3	1028	bromodomain
DNA	F32D1.10	F32D1.10	<i>mcm-7</i>	V	1	7	6	9.7	730	cell division control
DNA	R10E4.4	R10E4.4	<i>mcm-5</i>	III	1	7	6	10.7	759	MCM protein
DNA	Y17G7B.5	Y17G7B.5	<i>mcm-2</i>	II	1	7	4	5.6	881	AAA ATPase MCM protein (DNA replication initiation)
DNA	C01H6.7	C01H6.7		I	1	5	2	7.1	636	Bromodomain
DNA	F22F1.1	F22F1.1	<i>hil-3</i>	X	1	5	3	9.6	208	Histone h1
DNA	M04B2.1	M04B2.1	<i>mep-1</i>	IV	1	5	4	8.1	853	Zinc finger
DNA	T27C4.4	T27C4.4	<i>egr-1</i>	V	1	5	4	6.9	1022	Bromo, Myb, Zn finger
DNA	C08B11.3	C08B11.3		II	1	4	3	4.2	1244	Zinc finger, C2H2
DNA	F53H1.4	F53H1.4/Y51H4A.12		IV	1	4	3	3.6	1378	PHD finger, Zn finger like
DNA	Y51H4A.12	F53H1.4/Y51H4A.12		IV	1	3	3	3	1645	PHD finger, SET domain
DNA	C38D4.3	C38D4.3		III	1	3	2	2.4	1695	AT-hook motif
DNA	F15E6.1	F15E6.1		IV	1	3	3	3	1655	PHD finger, SET domain
DNA	R01H10.1	R01H10.1	<i>div-1</i>	III	1	3	2	5.3	581	DNA polymerase alpha associated
DNA	R06F6.1	R06F6.1	<i>cdl-1</i>	II	1	3	2	10.6	367	histone RNA processing protein
DNA	ZK632.1	ZK632.1	<i>mcm-6</i>	III	1	3	3	5.2	810	MCM
DNA	C09G9.6	C09G9.6	<i>oma-1</i>	IV	1	2	2	10.6	407	Zinc finger protein
DNA	F36A4.14	F36A4.14	<i>nhr-78</i>	IV	1	2	2	7.8	387	zinc finger, nuclear hormone receptor
DNA	F56F3.1	F56F3.1	<i>pqn-45</i>	III	1	2	2	5	761	txn factor homology
DNA	Y37D8A.9	Y37D8A.9	<i>mrg-1</i>	III	1	2	2	9.6	335	chromodomain
DNA	Y39A1B.3	Y39A1B.3	<i>dpy-28</i>	III	1	2	2	2.7	1260	non SMC condensin subunit
DNA	Y47G6A.11	Y47G6A.11	<i>msh-6</i>	I	1	2	2	3.4	1186	DNA mismatch repair protein
DNA	ZK1055.1	ZK1055.1	<i>hcp-1</i>	V	1	2	2	1.4	1475	centromere protein (CENP)-F homolog
DNA	F58A4.3	F58A4.3	<i>hcp-3</i>	III	2	3	2	9	288	Centromeric histone-H3-like protein
DNA	F20D12.4	F20D12.4	<i>czw-1</i>	IV	1	3	2	4.6	778	Centromere kinetochore Zwi10
RNA	F58B3.5	F58B3.5	<i>mrs-1</i>	IV	3	13	6	10.1	917	methionyl-tRNA synthetase
RNA	Y87G2A.5	Y87G2A.5	<i>vrs-2</i>	I	3	11	7	8.4	1050	class I family of aminoacyl-tRNA synthetases
RNA	F26F4.10	F26F4.10	<i>rrt-1</i>	III	3	10	7	15.1	713	arginyl tRNA synthetase
RNA	R74.1	R74.1	<i>lrs-1</i>	III	2	20	15	22.6	1186	leucyl-tRNA synthetase
RNA	T05H4.6	T05H4.6		V	2	9	5	16.3	443	eukaryotic peptide chain release factor subunit 1
RNA	R11A8.6	R11A8.6	<i>irs-1</i>	IV	2	7	6	8.5	1141	isoleucyl-tRNA synthetase
RNA	T28D9.10	T28D9.10	<i>snr-3</i>	II	2	6	2	15.9	126	Putative core component of the spliceosome
RNA	R10E4.2	R10E4.2		III	2	4	2	8.7	357	RNA recognition motifs
RNA	F18E2.2	F18E2.2		V	2	3	2	6.8	622	ABC transporter domains-ribosome
RNA	ZK1098.8	ZK1098.8	<i>mut-7</i>	III	2	3	2	2.5	910	Putative ribonuclease D (RNase D)
RNA	C28H8.3	C28H8.3		III	2	2	2	2.3	1714	DEAD/DEAH box helicase domain
RNA	K02F2.3	K02F2.3		I	2	2	2	2.4	1220	CPSF A subunit region splicing factor
RNA	M88.5	M88.5		III	2	2	2	4.1	820	KH domain, RNA binding
RNA	Y55F3AM.3	Y55F3AM.3		IV	2	2	2	7.1	580	RNA recognition motifs
RNA	C18G1.4	C18G1.4	<i>pgl-3</i>	V	1	7	4	8.7	693	RNA helix DEAD box
RNA	Y39G10AR.8	Y39G10AR.8		I	1	6	3	9.6	469	elongation factor
RNA	T07D3.7	T07D3.7	<i>alg-2</i>	II	1	5	3	5.2	891	RNA interference
RNA	C23G10.4	C23G10.4	<i>rpn-2</i>	III	1	4	3	6.9	950	proteasome/cyclosome, tRNA processing
RNA	M110.4	M110.4	<i>itg-1</i>	II	1	4	2	2.7	1156	initiation factor G
RNA	Y48B6A.2	Y48B6A.2	<i>rpl-43</i>	II	1	4	2	9.9	91	ribosomal
RNA	C04F12.1	C04F12.1		I	1	3	2	3.7	944	Piwi
RNA	H19N07.1	H19N07.1		V	1	3	3	9.1	573	elongation factor
RNA	Y49E10.15	Y49E10.15	<i>snr-6</i>	III	1	3	3	41.1	90	Putative core component of the spliceosome
RNA	R08D7.3	R08D7.3	<i>elf-3.D</i>	III	1	2	2	6.5	570	euk translation initiation
RNA	Y38C9A.2	Y38C9A.2	<i>cgp-1</i>	V	1	2	2	5.7	613	elongation factor
Housekeeping	F01F1.12	F01F1.12		III	3	15	7	35.2	366	fructose-biphosphate aldolase
Housekeeping	K10D2.6	K10D2.6		III	3	3	3	7.1	662	NADP-cytochrome P450 reductase family
Housekeeping	C07D8.6	C07D8.6		X	2	17	9	42.9	317	Aldehyde reductase
Housekeeping	F49E12.1	F49E12.1		II	2	12	10	15	655	peroxidase
Housekeeping	C04F6.3	C04F6.3	<i>cht-1</i>	X	2	11	4	9.4	617	glycosyl hydrolase (family 18)
Housekeeping	F33H1.2	F33H1.2/T09F3.3	<i>gpd-4</i>	II	2	11	6	18.8	341	glyceraldehyde 3-phosphate dehydrogenase 4
Housekeeping	T09F3.3	F33H1.2/T09F3.3	<i>gpd-1</i>	II	2	11	6	18.8	341	glyceraldehyde 3-phosphate dehydrogenase 1
Housekeeping	D2085.1	D2085.1		II	2	6	4	2.3	2198	glutamine-dependent carbamoyl-phosphate synthase
Housekeeping	T23G5.1	T23G5.1	<i>rrr-1</i>	III	2	5	4	10.4	788	Ribonucleoside-disphosphate reductase large chain
Housekeeping	B0334.3	B0334.3		II	2	4	2	6	634	Thiamine pyrophosphate enzyme, central domain
Housekeeping	C47D12.1	C47D12.1	<i>trr-1</i>	II	2	2	2	0.7	3944	Phosphatidylinositol 3- and 4-kinase; FAT domain; FATC domain
Housekeeping	F52D1.1	F52D1.1		X	2	2	2	4.5	941	Glycosyl hydrolases family 31
Housekeeping	Y47D3B.10	Y47D3B.10	<i>phy-1</i>	III	2	2	2	6.1	559	2OG-Fe(II) oxygenase superfamily
Housekeeping	Y75B12B.2	Y75B12B.2	<i>cyp-7</i>	V	1	9	6	57.9	171	Peptidyl-prolyl cis-trans isomerases
Housekeeping	F52E4.1	F52E4.1		X	1	6	6	22.4	536	Carboxyl transferase domain
Housekeeping	T17E9.2	T17E9.2		III	1	6	2	7.6	450	Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain
Housekeeping	K08E3.5	K08E3.5		III	1	5	4	13.8	509	UTP--glucose-1-phosphate uridylyltransferase
Housekeeping	R05H5.3	R05H5.3		II	1	5	4	40.3	149	thioredoxin
Housekeeping	C36A4.4	C36A4.4		III	1	4	3	14.3	484	UTP-glucose-1-phosphate uridylyltransferase family
Housekeeping	K06A5.6	K06A5.6		I	1	4	3	14.6	419	acyl-coA dehydrogenase
Housekeeping	Y119D3B.15	Y119D3B.15		III	1	4	2	34.9	126	DSS/SEM1
Housekeeping	ZK909.3	ZK909.3		I	1	4	2	17	229	guanosine-3',5'-bis(diphosphate)-pyrophosphohydrolase
Housekeeping	F21D5.1	F21D5.1		IV	1	3	3	9.6	550	phosphoacetylglucosamine mutase
Housekeeping	F35H10.4	F35H10.4	<i>vha-5</i>	IV	1	3	3	9.3	873	hydrogen ion transport
Housekeeping	H24K24.3	H24K24.3		V	1	3	2	6.5	384	alcohol dehydrogenase
Housekeeping	K05F1.3	K05F1.3		II	1	3	2	7	412	acyl-caA dehydrogenase
Housekeeping	M02D8.4	M02D8.4		X	1	3	2	6.3	567	asparagine synthase
Housekeeping	R05F9.6	R05F9.6		II	1	3	3	13	568	phosphoglucosyltransferase
Housekeeping	Y49A3A.5	Y49A3A.5	<i>cyp-1</i>	V	1	3	3	19.8	192	Peptidyl-prolyl cis-trans isomerase
Housekeeping	Y75B12B.5	Y75B12B.5	<i>cyp-3</i>	V	1	3	3	35.3	173	Peptidyl-prolyl cis-trans isomerases
Housekeeping	ZK1058.1	ZK1058.1		III	1	3	3	7.4	744	Methylmalonyl-coA mutase
Housekeeping	C14B9.2	C14B9.2		III	1	2	2	3.1	618	thioredoxin (mito)

Functional Category	Predicted Gene	Family ID (when peptides identify more than 1 protein)	C. elegans locus	LG	Abundance		Sequence Count	Coverage (%)	Length	Descriptor
					Occurrence	Total Spectrum Count				
Housekeeping	C32F10.8	C32F10.8		I	1	2	2	5.8	554	alanine aminotransferase
Housekeeping	F59B8.2	F59B8.2		IV	1	2	2	6.6	412	isocitrate dehydrogenase
Housekeeping	K04G7.3	K04G7.3	<i>oat-1</i>	III	1	2	2	4	1151	O-linked N-acetylglucosamine (O-GlcNAc) transferase (nuclear)
Housekeeping	F07A11.2	F07A11.2		II	1	2	2	5.1	725	glucosamine-fructose-6-phosphate
Cytoskeletal	Y105E8A.6	Y105E8A.6	<i>unc-95</i>	I	2	10	3	14.8	364	LIM domain
Cytoskeletal	Y105E8B.1	Y105E8B.1	<i>av-11 tmy-</i>	I	2	10	7	23.6	284	tropomyosin, an actin-binding contractile structural protein
Cytoskeletal	B0272.5	B0272.5		X	2	9	7	9	1973	endothelial actin-binding protein repeats
Cytoskeletal	T17H7.4	T17H7.4		III	2	7	4	10.9	663	may function in morphogenesis of the hypodermis
Cytoskeletal	C46A5.9	C46A5.9	<i>hcf-1</i>	IV	2	6	4	10.4	782	kelch motif
Cytoskeletal	Y71G12B.11	Y71G12B.11		I	1	9	6	5.2	2553	ILWEG (binds actin), Band 4.1 cytoskeletal
Cytoskeletal	F58B3.9	F58B3.9		IV	1	5	5	22.1	213	Transferrin-like
Cytoskeletal	F21C10.7	F21C10.7		V	1	4	4	4.2	2541	Spectrin repeat, IG like
Cytoskeletal	H27M09.4	H27M09.4	<i>col-59</i>	I	1	4	3	8.1	322	collagen
Cytoskeletal	T05A10.3	T05A10.3		X	1	4	3	9.1	406	Transferrin-like
Cytoskeletal	C36A4.5	C36A4.5		III	1	3	3	4.4	954	claustrin I
Cytoskeletal	F25D7.4	F25D7.4/F32A7.5		I	1	3	3	4.5	932	claustrin like
Cytoskeletal	F32A7.5	F25D7.4/F32A7.5		I	1	4	4	8.1	878	claustrin like
Cytoskeletal	F43G9.9	F43G9.9	<i>cpn-1</i>	I	1	3	2	26	192	smooth muscle protein
Cytoskeletal	T11B7.4	T11B7.4	<i>eat-1</i>	IV	1	3	2	2.9	1424	LIM domains, body wall muscle
Cytoskeletal	VW02B12L.3	VW02B12L.3		II	1	3	3	15.4	299	EB1 like, Calponin like
Cytoskeletal	ZK617.1	ZK617.1	<i>unc-22</i>	IV	1	3	3	1.1	6831	Fibronectin domain, IG domain, Ca/calmodulin dep protein kinase
Cytoskeletal	C56G7.1	C56G7.1	<i>mlc-4</i>	III	1	2	2	12.8	172	myosin regulatory light chain
Cytoskeletal	K03H1.4	K03H1.4		III	1	2	2	23	148	Transferrin-like
Cytoskeletal	K07C5.1	K07C5.1	<i>arx-2</i>	V	1	2	2	8.4	395	high similarity to ARP-2
Cytoskeletal	K10B4.3	K10B4.3		III	1	2	2	7.5	827	plecstrin like (cytoskeletal?)
Cytoskeletal	T10B10.3	T10B10.3		X	1	2	2	7.2	741	plecstrin homolog domain, RUN domain
Cytoskeletal	T21E12.4	T21E12.4	<i>dhc-1</i>	I	1	7	5	2.2	4568	dynein heavy chain
Cytoskeletal	C18A11.7	C18A11.7	<i>dim-1</i>	X	4	24	10	15.9	640	Disorganized Muscle <sup>8</sup>
Cytoskeletal	F08B6.4	F08B6.4	<i>unc-87</i>	I	3	25	10	27.4	565	calponin (smooth muscle)
Cytoskeletal	K07D8.1	K07D8.1	<i>mup-4</i>	III	3	24	15	7.8	2104	required for hypodermis and muscle junctional attachments
Cytoskeletal	F11G11.11	F11G11.11		II	1	2	2	9	345	col-20 collagen
Signalling	C46G7.4	C46G7.4	<i>pan-22</i>	IV	2	15	10	22.1	1175	ZASP PDZ domain that bind actinin
Signalling	K01G5.4	K01G5.4	<i>ran-1</i>	III	2	10	6	27.9	215	GTP-binding protein
Signalling	K07C11.2	K07C11.2	<i>air-1</i>	V	2	6	4	10.1	326	Protein kinase
Signalling	F52B5.2	F52B5.2		I	2	2	2	9.3	301	Protein kinase
Signalling	K07C5.8	K07C5.8		V	2	2	2	5.6	638	WD domains (WD-40 repeat)
Signalling	Y54G9A.6	Y54G9A.6		II	2	2	2	11.4	343	WD domain, G-beta repeat
Signalling	C14B9.4	C14B9.4	<i>plk-1</i>	III	1	6	3	8.2	648	POLO kinase
Signalling	C29F9.7	C29F9.7	<i>pat-4</i>	III	1	5	3	11.2	466	integrin-linked kinase
Signalling	C03C10.1	C03C10.1	<i>kin-19</i>	III	1	4	2	7.9	341	casein kinase
Signalling	F38H4.9	F38H4.9	<i>let-92</i>	IV	1	4	3	10.1	318	Serine/threonine protein phosphatase
Signalling	T05G5.3	T05G5.3	<i>cdk-1</i>	III	1	3	3	16.3	332	Serine/threonine protein phosphatase
Major Sperm	C04G2.4	MSP	<i>mso-36</i>	IV	2	3	2	23.6	127	Major Sperm Protein Domain
Major Sperm	K07F5.2	MSP	<i>mso-10</i>	IV	2	3	2	23.6	127	Major Sperm Protein Domain
Major Sperm	K07F5.3	MSP		IV	2	3	2	23.6	127	Major Sperm Protein Domain
Major Sperm	R05F9.3	MSP	<i>mso-32</i>	II	2	3	2	15.8	190	Major Sperm Protein Domain
Extracellular Matrix	B0280.5	B0280.5		III	2	6	2	8.4	491	chitin binding, gonad expression
Extracellular Matrix	C07G2.1	C07G2.1	<i>cej-1</i>	III	1	7	3	8.2	584	chitin binding
Extracellular Matrix	F25B4.9	F25B4.9		V	1	6	2	22.5	173	Lectin
Extracellular Matrix	ZK1248.16	ZK1248.16	<i>lec-5</i>	II	1	6	3	11.1	314	Lectin
Spindle	C06G3.2	C06G3.2	<i>klp-18</i>	IV	3	3	3	6.1	932	Kinesin-like protein 18
Spindle	C33H5.4	C33H5.4	<i>klp-10</i>	IV	2	2	2	5.4	690	Kinesin-like protein 10
Spindle	T10F2.1	T10F2.1	<i>ars-1</i>	III	2	2	2	4.3	742	required for spindle stability
Spindle	M03D4.1	M03D4.1	<i>zen-4</i>	IV	1	8	5	10.8	775	kinesin
Spindle	K08E3.6	K08E3.6	<i>cyk-4</i>	III	2	6	5	8.7	681	GTPase-activator protein for Rho-like GTPases
Spindle	F22B5.7	F22B5.7	<i>zva-9</i>	II	1	4	4	4.9	1415	XMAP215/ch-TOG/Msps homolog
Heat Shock	K09C4.3	K09C4.3	<i>hsp-2</i>	X	2	20	8	18.1	310	Heat Shock
Heat Shock	R151.7	R151.7	<i>hsp75</i>	III	2	5	2	5.5	657	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
Heat Shock	Y63D3A.6	Y63D3A.6	<i>dni-29</i>	I	2	2	2	5.9	579	prokaryotic heat shock protein
Heat Shock	C30C11.4	C30C11.4		III	1	8	6	12.2	776	Heat Shock 70
Heat Shock	Y46H3A.2	Y46H3A.2		V	1	8	2	25.2	143	Heat Shock
Heat Shock	C17H12.1	C17H12.1	<i>hsp-16.41</i>	IV	1	3	3	6.8	643	WD domain, G-beta repeats
Heat Shock	Y55F3AR.3	Y55F3AR.3		IV	1	2	2	4.4	591	chaperonin
Nuclear Envelope	C53D5.6	C53D5.6	<i>imb-3</i>	I	3	3	3	3.4	1092	importin-beta-like
Nuclear Envelope	W04D2.1	W04D2.1		V	2	19	12	19.8	920	alpha-actinin
Nuclear Envelope	ZK742.1	ZK742.1		V	2	3	2	3.3	1080	Exportin, beta-karyopherin
Nuclear Envelope	R05D11.3	R05D11.3	<i>ran-4</i>	I	2	2	2	30.8	133	Putative nuclear transport factor
Nuclear Envelope	Y54E5A.4	Y54E5A.4	<i>nop-4</i>	I	2	2	2	6.9	538	Nuclear pore protein 4
Nuclear Envelope	C29E4.4	C29E4.4		III	1	3	3	3.1	1212	Nup133 nucleoporin family
Nuclear Envelope	F28B3.8	F28B3.8	<i>imb-1</i>	I	1	3	3	9.7	896	importin B
Other	C25B8.4	C25B8.4		X	2	14	4	27.8	212	asialoglycoprotein receptor
Other	F54F2.1	F54F2.1		III	2	11	10	16.2	1226	Vitronectin receptor alpha subunit
Other	C09D1.1	C09D1.1	<i>unc-89</i>	I	2	9	7	2.2	6632	immunoglobulin-like protein
Other	ZK1290.12	ZK1290.12	<i>wrt-1</i>	II	2	6	4	4.8	484	warthog gene
Other	F23F1.8	F23F1.8	<i>rat-4</i>	II	2	5	3	11.1	406	Putative ATPase subunit of 19S proteasome particle
Other	T01B10.2	T01B10.2	<i>ard-1</i>	X	2	5	3	19.7	289	aroundhoq like/hedqehq like
Other	F26E4.3	F26E4.3		I	2	4	4	10.4	491	cysteine protease
Other	Y38C1AA.2	Y38C1AA.2	<i>csn-3</i>	IV	2	4	4	4.4	724	COP9/signalosome complex
Other	Y57G11C.10	Y57G11C.10	<i>adi-1</i>	IV	2	4	3	13.7	444	GDI-1 GDP dissociation inhibitor
Other	C02A12.4	C02A12.4	<i>lys-7</i>	V	2	3	2	11	283	Lysozyme 7
Other	C30C11.2	C30C11.2	<i>rpn-3</i>	III	2	3	2	5.2	504	Proteasome regulatory particle non-ATPase-like 3
Other	F10G7.8	F10G7.8	<i>rpn-5</i>	II	2	3	2	9.6	490	Proteasome regulatory particle non-ATPase-like 5
Other	F32A5.2	F32A5.2		II	2	2	2	3.3	1000	ShTK domain; Animal haem peroxidases
Other	T03G6.3	T03G6.3		X	2	2	2	7.1	465	Type I phosphodiesterase / nucleotide pyrophosphatase
Other	T13F2.8	T13F2.8	<i>cav-1</i>	IV	2	2	2	13.2	235	Enzyme activator that functions in meiosis
Other	F57B9.10	F57B9.10	<i>rpn-6</i>	III	1	9	4	12.8	438	proteasome component
Other	F40E10.1	F40E10.1	<i>hch-1</i>	X	1	7	6	8.9	605	metalloprotease
Other	F29G9.5	F29G9.5	<i>rat-2</i>	V	1	5	4	16.7	443	AAA ATPase
Other	F21H12.6	F21H12.6		II	1	4	3	5.2	1374	serine protease subtilase
Other	H13N06.6	H13N06.6		X	1	4	3	5.2	633	Copper type II, ascorbate-dependent monooxygenase
Other	T06D8.8	T06D8.8	<i>rpn-9</i>	II	1	4	2	11.9	387	Putative non-ATPase subunit
Other	T12D8.8	T12D8.8		III	1	4	4	19.4	422	TPR heat shock
Other	F23F12.6	F23F12.6	<i>rat-3</i>	III	1	3	3	13.5	414	AAA ATPase, proteasome subunit
Other	F41E6.2	F41E6.2	<i>ard-5</i>	V	1	3	3	21.6	102	predicted secreted protein, aroundhoq family
Other	F44E7.4	F44E7.4		V	1	3	3	3.5	1067	peptidase

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					Occurrence	Total Spectrum Count				
Other	R01H2.6	R01H2.6	<i>unc-116</i>	III	1	3	3	24.8	153	E2 ubiquitin-conjugating enzyme
Other	R05D3.7	R05D3.7	<i>unc-116</i>	III	1	3	3	7.6	815	kinesin heavy chain
Other	R12H7.2	R12H7.2	<i>asp-4</i>	X	1	3	3	11.7	444	aspartyl protease
Other	Y39E4B.1	Y39E4B.1		III	1	3	3	6.6	610	ABC transporter, AAA ATPase, metal binding
Other	Y44E3A.6	Y44E3A.6		I	1	3	3	3	932	serine protease, forkhead associated
Other	C17G1.6	C17G1.6	<i>nas-37</i>	X	1	2	2	4.5	736	zinc metalloprotease
Other	C27H6.2	C27H6.2		V	1	2	2	4.6	458	AAA ATPase
Other	C52E4.4	C52E4.4	<i>rpt-1</i>	V	1	2	2	2.8	435	protease regulatory subunit, AAA ATPase
Other	F21F8.7	F21F8.7	<i>asp-6</i>	III	1	2	2	14.9	389	protease
Other	Y71G12B.10	Y71G12B.10		I	1	2	2	11.3	318	HMG-CoA lyase
Unknown	Y37D8A.19	Y37D8A.19		III	4	23	4	42.6	101	
Unknown	C44B12.1	C44B12.1		IV	3	31	9	28.6	203	
Unknown	C39D10.7	C39D10.7		X	3	13	8	11.3	1185	
Unknown	F54E2.3	F54E2.3	<i>pqn-43</i>	V	2	17	12	6.4	4488	
Unknown	Y18D10A.17	Y18D10A.17		I	2	10	8	24.4	340	
Unknown	C18B2.3	C18B2.3		X	2	9	3	26.3	236	
Unknown	C46C2.5	C46C2.5		IV	2	8	5	14.3	223	
Unknown	Y65B4BR.6	Y65B4BR.6	<i>arl-16</i>	I	2	8	3	9.2	393	groundhog like
Unknown	Y39G10AR.12	Y39G10AR.12		I	2	6	3	10.3	507	
Unknown	ZK84.1	ZK84.1		II	2	6	3	3.6	801	
Unknown	T19H12.2	T19H12.2		V	2	4	4	30.7	225	
Unknown	T06E4.8	T06E4.8		V	2	4	2	22.1	199	
Unknown	AC3.5	AC3.5		V	2	2	2	3.1	1071	M1 peptidase family of aminopeptidases.
Unknown	B0361.3	B0361.3		III	2	2	2	3	1221	
Unknown	C06G1.4	C06G1.4		X	2	2	2	6.7	683	
Unknown	D1081.7	D1081.7		I	2	2	2	4.6	857	
Unknown	F16B12.6	F16B12.6		X	2	2	2	2.2	1417	
Unknown	F42A8.1	F42A8.1		II	2	2	2	6.8	370	
Unknown	K08H2.1	K08H2.1	<i>skr-21</i>	X	2	2	2	23.3	176	Skp1 family dimerization domain
Unknown	Y23H5A.3	Y23H5A.3		I	2	2	2	11.1	307	
Unknown	Y32G9A.8	Y32G9A.8		V	2	2	2	11.6	345	immunoglobulin subtype
Unknown	Y39G10AR.10	Y39G10AR.10		I	2	2	2	5.4	690	involved in embryogenesis
Unknown	ZC123.1	ZC123.1		I	2	2	2	5.8	730	
Unknown	ZK1236.3	ZK1236.3		III	2	2	2	4.3	1000	
Unknown	Y62H9A.5	Y62H9A.5		X	1	19	6	18.7	123	
Unknown	C08F11.11	C08F11.11		IV	1	9	6	60.4	111	
Unknown	F25H2.11	F25H2.11		I	1	8	6	36.5	181	translationally controlled tumor protein
Unknown	Y55F3AM.13	Y55F3AM.13		IV	1	8	4	19.5	354	
Unknown	K07C11.7	K07C11.7		V	1	7	4	19	290	calcineurin-like phosphoesterase
Unknown	W05E7.1	W05E7.1	<i>ard-3</i>	IV	1	7	3	16.2	359	groundhog family
Unknown	F33E11.6	F33E11.6		V	1	6	2	8.9	393	
Unknown	C23F12.1	C23F12.1		X	1	5	4	6.3	1874	
Unknown	C25A8.4	C25A8.4		IV	1	5	2	3.3	1050	
Unknown	C34C12.5	C34C12.5		III	1	5	2	14.9	268	
Unknown	F20D1.3	F20D1.3		X	1	5	4	11.7	478	
Unknown	F25H8.5	F25H8.5	<i>dur-1</i>	IV	1	5	5	7.6	798	dauer upregulated gene
Unknown	F56D3.1	F56D3.1		II	1	5	3	12.7	441	
Unknown	R05D11.8	R05D11.8		I	1	5	2	6.4	566	
Unknown	T06E4.9	T06E4.9		V	1	5	4	33	212	
Unknown	W01A8.1	W01A8.1		I	1	5	3	11.6	415	
Unknown	Y55F3AM.12	Y55F3AM.12		IV	1	5	5	14.5	332	
Unknown	C13B4.2	C13B4.2	<i>usp-14</i>	II	1	4	4	10.2	489	Ubiquitin carboxyl-terminal hydrolases family 2
Unknown	F02A9.3	F02A9.3	<i>far-2</i>	III	1	4	2	19.8	182	fatty acid binding protein
Unknown	T12D8.6	T12D8.6		III	1	4	2	29.6	142	EF hand
Unknown	T14G12.3	T14G12.3		X	1	4	3	16.4	201	
Unknown	Y22D7AR.10	Y22D7AR.10		III	1	4	2	44.9	69	
Unknown	Y77E11A.12	Y77E11A.12		IV	1	4	3	3.6	782	
Unknown	C03E10.6	C03E10.6		V	1	3	2	43.9	98	
Unknown	C56C10.3	C56C10.3		II	1	3	2	18.1	221	
Unknown	F11E6.7	F11E6.7		IV	1	3	2	4	1011	
Unknown	F26F4.1	F26F4.1		III	1	3	3	15.5	362	
Unknown	F42A6.3	F42A6.3		IV	1	3	3	7.2	585	
Unknown	R06C7.7	R06C7.7	<i>lin-61</i>	I	1	3	2	6.3	619	mbt domain found in nuclear proteins
Unknown	T25E4.1	T25E4.1		II	1	3	2	17.7	231	
Unknown	T27A3.2	T27A3.2		I	1	3	3	7.1	789	ubiquitin carboxyl-terminal hydrolase
Unknown	Y62H9A.6	Y62H9A.6		X	1	3	2	6.1	181	
Unknown	B0041.2	B0041.2		I	1	2	2	5.2	706	
Unknown	B0379.1	B0379.1		I	1	2	2	10.8	212	
Unknown	C49G7.3	C49G7.3		V	1	2	2	11.3	248	
Unknown	F10D11.6	F10D11.6		I	1	2	2	6.6	846	lipid binding
Unknown	F11C7.5	F11C7.5		X	1	2	2	19	189	
Unknown	F47B7.7	F47B7.7		X	1	2	2	11.7	350	
Unknown	F48A11.5	F48A11.5		II	1	2	2	6.6	632	UBX
Unknown	R05D11.9	R05D11.9		I	1	2	2	3.8	655	
Unknown	T06E4.7	T06E4.7		V	1	2	2	10	441	nematode 7 TM chemoreceptor
Unknown	T23E7.2	T23E7.2		X	1	2	2	3.2	930	
Unknown	Y116A8A.9	Y116A8A.9		IV	1	2	2	6.8	444	
Unknown	Y57A10A.18	Y57A10A.18	<i>pqn-87</i>	II	1	2	2	2.1	1512	MATH domain

Functional Category determination is described in Supplemental Methods; Family ID, designation for families of proteins not differentiated by a set of identifying peptides; LG, chromosomal location; Occurrences, the number of preparations in which a protein was identified out of 5 oogenic preparations; Total Spectrum Count, the total number of peptides detected for each protein from all preparations; Sequence Count, the number of distinct MS/MS spectra collected from all preparations; Coverage, % of protein represented by uniquely identified peptides; Length, number of amino acids in protein; Descriptor, protein description through homology or provided in WormBase, Worm Protein Database (BIOBASE) annotations.

Supplementary Table 5 **Composition of chromatin samples**

Sample Type Category	a. Sample Composition Before Subtraction % Abundance (TSC) in Sample				b. Sample Composition After Subtraction % of Proteins (No. in Sample)		c. Subtraction Summary per Category % of Proteins (No. in Category)	
	Total	≤2 Occur	≥3 Occur	Oogenic Chromatin Total	Spermatogenesis-Enriched	Subtracted	Spermatogenesis-Enriched	Subtracted
DNA	17.5	0.7	16.8	18.8	6.0 (8)	24.3 (90)	9.1	90.9
RNA	20.7	2.5	18.2	15.6	22.7 (30)	23.5 (87)	25.6	74.3
Housekeeping	18.8	2.9	15.9	11.7	10.6 (14)	19.2 (71)	16.5	83.5
Cytoskeletal	11.4	0.5	10.9	19.2	0.8 (1)	7.3 (27)	3.6	96.4
Signalling	2.7	0.7	2.0	1.9	8.3 (11)	3 (11)	50.0	50.0
MSP	1.9	0.1	1.8	0.1	3.8 (5)	0.3 (1)	16.7	83.3
Extracellular Matrix	2.5	0.3	2.1	2.4	6.8 (9)	2.4 (9)	50.0	50.0
Spindle	1.7	0.0	1.7	3	0 (0)	2.4 (9)	0.0	100.0
Heat Shock	0.6	0.5	0.1	6.5	0 (0)	0.5 (2)	0.0	100.0
Vitellogenin	1.3	0.0	1.3	7.7	0 (0)	1.6 (6)	0.0	100.0
Nuclear Envelope	1.3	0.2	1.1	1.4	0 (0)	1.9 (7)	0.0	100.0
Other	5.0	0.9	4.1	4	6.1 (8)	7.3 (27)	22.9	77.1
Unknown	14.7	2.4	12.3	7.7	34.8 (46)	6.2 (23)	66.1	33.9
<b>Total</b>	100	11.8	88.2	100	100 (132)	100 (370)	26.3	73.7

TSC = Total Spectral Count; % Abundance (TSC) in Sample = (TSC for proteins in each functional category)/(Total TSC in chromatin sample); % of Proteins in Sample = (Number of proteins in functional category)/(Total number of proteins in chromatin sample); % of Proteins in Category = (Number of proteins in sample type)/(Total number of proteins in category)



Supplemental Table 6 RNAi analysis of genes encoding abundant spermatogenesis-enriched proteins copurified with chromatin

Predicted Gene	<i>C. elegans</i> Locus	Descriptor	Previous phenotype	Sterility Category						New Evidence for Fertility Function (this study)	Overall RNAi Class
				% Progeny Production of control (P value)	Progeny No. Variability (P value)	% Oocytes (P value)	% Embryonic Lethality (P value)	Cytological Defects	Sex Specificity		
F55F8.2		DEAD box RNA helicase	Gro Stp	0				yes		Complete F1 Sterility Gro Sck	
M01E5.5	<i>top-1</i>	Topoisomerase I	Ste Mlt Him Rup Gro Dpy Lva Lvl	0				yes		Complete F1 Sterility Gro	
Y48A6B.3		ribosomal protein	Gro	0				yes	Sterility	Complete F1 Sterility Gro	
C25G4.6 *	<i>smz-1</i>	PDZ domain	Male Ste	33% (6e <sup>-10</sup> )		41% (6e <sup>-10</sup> )	13% (2e <sup>-6</sup> )	yes	sperm	High Male Ste	
T21G5.4 *	<i>smz-2</i>	PDZ domain	Stp Lva Pvl	19% (6e <sup>-10</sup> )		67% (6e <sup>-10</sup> )	12% (4e <sup>-6</sup> )	yes	sperm	Male sterility High Male Ste	
T03F1.5 †	<i>gsp-4</i>	glc7/PP1 phosphatase	Ste	57% (6e <sup>-9</sup> )	0.0002		29% (3e <sup>-11</sup> )	yes	sperm	Male sterility High Male Ste	
W09C3.6 †	<i>gsp-3</i>	glc7/PP1 phosphatase	Male Ste	62% (6e <sup>-9</sup> )	0.0003		34% (2e <sup>-12</sup> )	yes	sperm	High Male Ste	
B0261.6		Novel	WT	50% (2e <sup>-11</sup> )		11% (3e <sup>-7</sup> )	10% (5e <sup>-3</sup> )	yes		Sterility High Ste	
F23B12.7		CBF/Mak21 family, CCAAT binding factor 1 protein like	Stp Gro Lva	52% (9e <sup>-7</sup> )	0.0002			yes		High Ste Gro	
K04C2.2		DNA polymerase V	Gro Pch Ste Stp Lvl Sck	63% (6e <sup>-10</sup> )	0.01					High Ste	
B0207.5		Novel	WT	83% (.02)				yes		Sterility Moderate Ste	
C30F12.7		isocitrate dehydrogenase	WT	72% (3e <sup>-4</sup> )						Sterility Moderate Ste	
C33H5.12	<i>rsp-6</i>	SR Protein	WT	82% (.04)	0.0003	8% (3e <sup>-4</sup> )		yes		Sterility Moderate Ste	
F14D2.7		Novel	WT	81% (.01)	0.02		10% (1e <sup>-4</sup> )	yes		Sterility Moderate Ste	
F27C8.5		BTB/POZ domain	WT	87% (.002)		11% (3e <sup>-5</sup> )		yes		Sterility Moderate Ste	
F38A5.6		Novel	WT	87% (.02)	0.04			yes		Sterility Moderate Ste	
F54C8.1		3-hydroxyacyl-CoA dehydrogenase	WT	81% (.01)			10% (0.007)			Sterility Moderate Ste	
K03H1.1		Glutamine synthetase	WT	74% (.008)						Sterility Moderate Ste	
T13A10.11	<i>tag-32</i>	S-adenosylmethionine synthetase	Gro Unc	79% (.03)	0.0005					Sterility Moderate Ste Gro	
Y45F3A.1		Novel	Stp	85% (.01)						Moderate Ste	
Y52B11A.5		C-type lectin	WT	77% (.003)			12% (2e <sup>-4</sup> )			Sterility Moderate Ste	
Y54F10BM.2		Translation initiation factor IF-2	Ste Lva	78% (.007)		6% (0.003)		yes		Moderate Ste	
Y71H10A.1		phosphofructokinase	Emb	79% (.008)	0.01		11% (6e <sup>-6</sup> )			Sterility Moderate Ste	
C04G2.8 §	<i>spch-1</i>	Novel	WT		0.006		18% (1e <sup>-4</sup> )			Sterility Low Ste	
C14F11.7		Novel	WT				8% (0.008)			Sterility Low Ste	
C17G10.8	<i>dhs-6</i>	alcohol dehydrogenase	WT		0.0004					Sterility Low Ste	
C18G1.5	<i>hil-4</i>	Histone H1	Abnormal Gonad				9% (0.008)	yes		Low Ste	
C49C3.11		lectin	Ste		0.0005					Low Ste	

Predicted Gene	<i>C. elegans</i> Locus	Descriptor	Previous phenotype	Sterility Category						New Evidence for Fertility Function (this study)	Overall RNAi Class	
				% Progeny Production of control (P value)	Progeny No. Variability (P value)	% Oocytes (P value)	% Embryonic Lethality (P value)	Cytological Defects	Sex Specificity			
F25E5.3		serine protease	WT		0.0005						Sterility	Low Ste
K08C9.2		Novel	Ste					yes				Low Ste
T10E9.4		DX module	WT			8% (4e <sup>-6</sup> )					Sterility	Low Ste
Y38H8A.3		serine/threonine kinase	WT			5% (0.03)	8% (0.009)				Sterility	Low Ste
D1007.6	<i>rps-10</i>	small ribosomal subunit	Emb Unc Ste Lva	N/A								Complete F1 Lethality (Emb)
E04A4.8	<i>rpl-20</i>	large ribosomal subunit	Emb Ste	N/A								Complete F1 Lethality (Emb)
F07A11.2		Glucosamine 6-phosphate synthetase	Emb Ste	N/A								Complete F1 Lethality (Emb)
F26E4.9	<i>cco-1</i>	Cytochrome c oxidase	Gro Clr Ste Age Lpd	N/A								Complete F1 Lethality (Emb)
F36A4.7	<i>ama-1</i>	RNA polymerase II	Emb Gro	N/A								Complete F1 Lethality (Emb)
JC8.3	<i>rpl-12</i>	ribosomal protein	Emb Ste Gro	N/A								Complete F1 Lethality (Emb)
T03F1.9	<i>hcp-4</i>	centromere component	Emb Mul	N/A								Complete F1 Lethality (Emb)
Y111B2A.18	<i>rsp-3</i>	SR protein splicing factor	Emb Lva	N/A								Complete F1 Lethality (Emb)
ZK328.2	<i>eft-1</i>	Elongation factor	Emb Ste Sck	N/A								Complete F1 Lethality (Emb)
B0365.3	<i>eat-6</i>	Na <sup>(+)</sup> /K <sup>(+)</sup> ATPase alpha subunit	Emb Lva	N/A								Complete F1 Lethality (Emb Lvl/Lva)
C16A3.3		Small GTP-binding protein domain	Gro Emb Egl Gon Lva	N/A								Complete F1 Lethality (Emb Lvl/Lva)
C18A3.3		RNA-processing protein, HAT helix	Emb Lva Pvl Ste	N/A								Complete F1 Lethality (Emb Lvl/Lva)
C32E8.2	<i>rpl-13</i>	large ribosomal subunit	Emb	N/A								Complete F1 Lethality (Emb Lvl/Lva)
F36A2.7		Novel	Emb Gro Sle	N/A								Complete F1 Lethality (Emb Lvl/Lva)
K12H4.3		Brix domain-Ribosome biogenesis	Stp Emb Gro Lva	N/A								Complete F1 Lethality (Emb Lvl/Lva)
T07A9.9		Small GTP-binding protein domain (ribosome biogenesis)	Dpy Emb Gro Sma	N/A								Complete F1 Lethality (Emb Lvl/Lva)
W07E6.1		nucleolar protein	Gro Pch Stp Lon Lva	N/A								Complete F1 Lethality (Emb Lvl/Lva)
ZK809.3		Novel	Emb Gro Lva	N/A								Complete F1 Lethality (Emb Lvl/Lva)

\*, †, § Symbols denote highly identical genes whose products may be depleted simultaneously by RNAi. Sterility categories and Overall RNAi classes are defined in Supplemental Methods and Supplemental Legends. Abbreviations: N/A, not applicable; Ste, sterile; Stp, sterile progeny; Emb, embryonic lethal; Lvl, larval lethal; Lva, larval arrest; Pvl, protruding vulva; Mul, multi-nuclei in early embryo; Mlt, molting defective; Him, high incidence of males; Rvp, exploded; Gro, slow growth; Dpy, dumpy; Lvl, larval lethal; Sck, sick

Supplemental Table 7 Additional *C. elegans* abundant spermatogenesis-enriched chromatin proteins with function in fertility

Gene ID	Gene Name	Descriptor	<i>C. elegans</i>					Mammalian	
			Localization	RNAi Cytological Defects		Phenotype	Sum: New Evidence for Fertility Function	Known Homolog	Fertility Link
				Male	Hermaphrodite				
<b>Category III: Additional proteins with function in fertility in <i>C. elegans</i></b>									
F55F8.2		RNA helicase		abnormal gonad morphology, abnormal progression	abnormal gonad development, disorganized gonad, Emo	Complete F1 Sterility Gro Sck	hermaphrodite sterility, herm and male cytological defects	M, Ddx4 (VASA) ( $3e^{-33}$ ) H, DBY ( $2e^{-29}$ ), DDX4 ( $4e^{-33}$ )	M, Ddx4 KO male infertile H, DBY is frequently deleted in infertile patients
Y48A6B.3		ribosomal protein		Mild/low penetrance abnormal gonad structure	Abnormal gonad structure, Emo	Complete F1 Sterility Gro	hermaphrodite sterility, herm and male cytological defects	M, NADP-dependent malic enzyme ( $1.6e^{-168}$ ) H, NADP-dependent malic enzyme ( $3.4e^{-168}$ )	
B0261.6		Novel		none detected	abnormal gonad structure	High Ste	hermaphrodite sterility, hermaphrodite cytological defects		
C30F12.7		isocitrate dehydrogenase		none detected	abnormal gonad morphology with clumped nuclei	High Ste	hermaphrodite sterility, hermaphrodite cytological defects	M, Isocitrate dehydrogenase ( $1.6e^{-104}$ ) H, Isocitrate dehydrogenase ( $5.9e^{-105}$ )	
F23B12.7		CBF/Mak21 and CCAAT binding factor 1 like		abnormal gonad structure, defective chromosome segregation	abnormal gonad structure, oogenesis arrest or Emo	High Ste Gro	hermaphrodite and male cytological defects	M, C/EBP zeta ( $9.9e^{-114}$ ) H, C/EBP zeta ( $1e^{-115}$ )	
F27C8.5		BTB/POZ domain		none detected	embryos do not form hard eggshells, only a few divisions before arrest	High Ste	hermaphrodite sterility, hermaphrodite cytological defects		
K04C2.2		DNA polymerase V		some animals with abnormal gonad morphology, small or stunted	abnormal gonad structure, Emo	High Ste	hermaphrodite and male cytological defects	M, myb binding protein ( $1.6e^{-12}$ ) H, myb binding protein ( $1.7e^{-08}$ )	
T13A10.11	<i>tag-32</i>	S-adenosyl-methionine synthetase		Mild/low penetrance abnormal gonad structure	abnormal gonad structure	High Ste	hermaphrodite sterility, hermaphrodite and male cytological defects	M, Mat1a ( $1.3e^{-130}$ ) H, ENSP00000303147 ( $3.9e^{-131}$ )	
Y54F10BM.2		Translation initiation factor IF2		abnormal gonad structure	abnormal gonad structure	High Ste Gro	hermaphrodite and male cytological defects	M, Translation initiation factor 5B ( $1e^{-105}$ ) H, Translation initiation factor 5B ( $2.4e^{-169}$ ), NASP ( $4.7e^{-09}$ )	H, NASP is a histone H1 binding protein found in sperm cells
B0207.5		Novel		low penetrance chromosome segregation problems	none detected	Moderate Ste	hermaphrodite sterility, hermaphrodite and male cytological defects	M, KIAA0853 ( $4.4e^{-11}$ ), ATRX ( $5e^{-10}$ ) H, ATRX ( $4.1e^{-13}$ )	
C33H5.12	<i>rsp-6</i>	SR Splicing Regulation Protein		abnormal gonad structure, meiotic problems with large nuclei in later germline	abnormal gonad development, oogenesis arrest or Emo.	Moderate Ste	hermaphrodite sterility, hermaphrodite and male cytological defects	M, Sfrs3 ( $9.9e^{-33}$ ), Rbm3 ( $1.7e^{-12}$ ) H, RBMY1 ( $2.9e^{-12}$ ), CSTF2T42 ( $8.7e^{-09}$ ),	M, Sfrs3 KO Embryonic lethal H, Microdeletions including RBMY correlate with male infertility; CSTF2T associated with male infertility, homologs expressed in male meiosis
F14D2.7		Novel		abnormal gonad structure	abnormal gonad structure, uneven nuclei, clumping.	Moderate Ste	hermaphrodite sterility, hermaphrodite and male cytological defects		
F38A5.6		Novel		none detected	abnormal gonad development	Moderate Ste	hermaphrodite sterility, hermaphrodite cytological defects		
F54C8.1		3-hydroxyacyl-CoA dehydrogenase		none detected	Some animals with abnormal gonad structure; absence of fertilized embryos in some adults	Moderate Ste	hermaphrodite sterility, hermaphrodite cytological defects	M, Short chain 3-hydroxyacyl-CoA dehydrogenase ( $8e^{-76}$ ) H, Short chain 3-hydroxyacyl-CoA dehydrogenase ( $1.7e^{-75}$ )	
K03H1.1		Glutamine synthetase		Slightly disorganized gonad	Disorganized gonad, some Emo	Moderate Ste	hermaphrodite sterility, hermaphrodite and male cytological defects	M, Glutamine synthetase ( $1.4e^{-114}$ ) H, Glutamine synthetase ( $1.4e^{-114}$ )	
T10E9.4		DX module		none noted	none detected	Moderate Ste	hermaphrodite sterility, hermaphrodite cytological defects		

Gene ID	Gene Name	Descriptor	<i>C. elegans</i>					Mammalian	
			Localization	RNAi Cytological Defects		Phenotype	Sum: New Evidence for Fertility Function	Known Homolog	Fertility Link
				Male	Hermaphrodite				
Y52B11A.5		C-type lectin		none detected	abnormal gonad structure (shortened, bulging, twisted)	Moderate Ste	hermaphrodite sterility, hermaphrodite cytological defects		
Y71H10A.1		phosphofructokinase		low level abnormal gonad	abnormal gonad structure (small gonad arms, uneven and clumpy nuclei)	Moderate Ste	hermaphrodite sterility, hermaphrodite and male cytological defects	M, 6-phospho-fructokinase (3.1e <sup>-236</sup> ) H, 6-phospho-fructokinase (3e <sup>-234</sup> )	
C14F11.7		Novel		none detected	Low level abnormal gonad structure (gonad misoriented)	Low Ste	hermaphrodite sterility, hermaphrodite cytological defects		
C17G10.8	<i>dhs-6</i>	alcohol dehydrogenase		none detected	none detected	Low Ste	hermaphrodite sterility	M, HSDL2 (3.5e <sup>-107</sup> ) H, HSDL2 protein (4.6e <sup>-79</sup> )	
C18G1.5	<i>hil-4</i>	Histone H1		low level abnormal gonad and meiotic progression	low level abnormal gonad and meiotic progression	Low Ste	hermaphrodite and male cytological defects	M, Histone H1t (1.9e <sup>-13</sup> ) H, Histone H1t (1.6e <sup>-12</sup> )	M, Histone H1t KO male infertile in combo with other genes
C49C3.11		lectin		none detected	none detected	Low Ste			
F25E5.3		serine protease		none detected	low penetrance abnormal gonad development (shortened)	Low Ste	hermaphrodite sterility, hermaphrodite cytological defects		
K08C9.2		Novel		abnormal gonad structure and low level meiotic problems	none detected	Low Ste	hermaphrodite sterility, male cytological defects		
W02B12.3	<i>rsp-1</i>	splicing factor like		none detected	none detected	Male Ste in combo with other <i>rsp</i> genes <sup>31</sup>		M, Sfrs3 (3.7e <sup>-18</sup> ), Rbm3 (1.7e <sup>-12</sup> ) H, RBMY1 (4.1e <sup>-13</sup> )	M, Sfrs3 KO Embryonic lethal H, microdeletions including RBMY correlate with male infertility
Y38H8A.3		serine/threonine kinase		none detected	none detected	Low Ste	hermaphrodite sterility	M, Tau-tubulin kinase (1.5e <sup>-56</sup> ) H, TTBK2 protein (8.9e <sup>-58</sup> )	
Y45F3A.1		Novel		none detected	none detected	Low Ste			

Degrees of sterility are defined in Supplemental Methods. Symbols (\*, †, §, #, ψ) denote highly identical genes whose products may be depleted simultaneously by RNAi. Mammalian fertility link references are listed in Supplemental Table 8. RNAi resistant = protein product detected by immunolocalization in animals subjected to RNAi of corresponding gene. Emo=Endomitotic Reduplication. M = Mouse homologs, H = Human homologs, KO = mouse knock-out.

Supplemental Table 8 **Abundant *C. elegans* spermatogenesis-enriched chromatin proteins homologous to mammalian fertility factors**

<i>C. elegans</i>			Mammalian		References
Gene ID	Gene Name	Descriptor	Known Homolog	Fertility Link	
W09C3.6*	<i>gsp-3</i>	glc7/PP1 phosphatase	M, Ppp1cc (1e <sup>-102</sup> ) H, PPP1C (1e <sup>-95</sup> )	M, Ppp1cc KO male infertile	M, Ppp1cc: Varmuza, S. et al. Dev. Biol. 205, 98-110 (1999).
T03F1.5*	<i>gsp-4</i>	glc7/PP1 phosphatase	M, Ppp1cc (1e <sup>-102</sup> ) H, PPP1C (1e <sup>-95</sup> )	M, Ppp1cc KO male infertile	M, Ppp1cc: Varmuza, S. et al. Dev. Biol. 205, 98-110 (1999).
ZK1251.1	<i>htas-1</i>	histone H2A variant	M, H2AX (2e <sup>-21</sup> ), macroH2A(3e <sup>-27</sup> ) H, H2AX (3e <sup>-21</sup> ), macroH2A (3e <sup>-27</sup> )	M, H2AX KO male infertile	M, H2AX; Celeste, A. et al. Science 296, 922-7 (2002).
C04G2.8§	<i>spch-1</i>	SNBP-like	M, Histone H1T2 (2.3e <sup>-14</sup> ) H, SON DNA-binding protein (1.3e <sup>-19</sup> )	M, Histone H1T2 KO male infertile	M, Histone H1T2: Martianov, I. et al. Proc. Natl. Acad. Sci. U S A 102, 2808-13 (2005). Tanaka, H. et al. Mol. Cell. Biol. 25, 7107-19 (2005).
C10G11.9§	<i>spch-2</i>	SNBP-like	M, Histone H1T2 (2.3e <sup>-14</sup> ) H, SON DNA-binding protein (1.3e <sup>-19</sup> )	M, Histone H1T2 KO male infertile	M, Histone H1T2: Martianov, I. et al. Proc. Natl. Acad. Sci. U S A 102, 2808-13 (2005). Tanaka, H. et al. Mol. Cell. Biol. 25, 7107-19 (2005).
T27A3.4§	<i>spch-3</i>	SNBP-like	M, Histone H1T2 (2.3e <sup>-14</sup> ) H, SON DNA-binding protein (6.5e <sup>-20</sup> )	M, Histone H1T2 KO male infertile	M, Histone H1T2: Martianov, I. et al. Proc. Natl. Acad. Sci. U S A 102, 2808-13 (2005). Tanaka, H. et al. Mol. Cell. Biol. 25, 7107-19 (2005).
C55B7.1	<i>glh-2</i>	RNA helicase	M, Ddx4 (VASA) (1e <sup>-105</sup> ) H, DBY (1e <sup>-92</sup> ), DDX4 (1e <sup>-105</sup> )	M, Ddx4 KO male infertile H, DBY is frequently deleted in infertile patients	M, Ddx4: Tanaka, S.S. et al. Genes Dev. 14, 841-53 (2000). Foresta, C., Ferlin, A. & Moro, E. H, DBY: Foresta, C., Ferlin, A. & Moro, E. Hum Mol Genet 9, 1161-9 (2000).
F55F8.2		RNA helicase	M, Ddx4 (VASA) (3e <sup>-33</sup> ) H, DBY (2e <sup>-29</sup> ), DDX4 (4e <sup>-33</sup> )	M, Ddx4 KO male infertile H, DBY is frequently deleted in infertile patients	M, Ddx4: Tanaka, S.S. et al. Genes Dev. 14, 841-53 (2000). Foresta, C., Ferlin, A. & Moro, E. H, DBY: Foresta, C., Ferlin, A. & Moro, E. Hum Mol Genet 9, 1161-9 (2000).
B0511.6		RNA helicase	M, Ddx4 (VASA) (1e <sup>-105</sup> ) H, DBY (1e <sup>-92</sup> )	M, Ddx4 KO male infertile H, DBY is frequently deleted in infertile patients	M, Ddx4: Tanaka, S.S. et al. Genes Dev. 14, 841-53 (2000). Foresta, C., Ferlin, A. & Moro, E. H, DBY: Foresta, C., Ferlin, A. & Moro, E. Hum Mol Genet 9, 1161-9 (2000).
F42G9.1		protein phosphatase	M, Ppm1 (2.5e <sup>-09</sup> ) H, PPM1G (1e <sup>-55</sup> )	M, Ppm1 KO male infertile	M, Ppm1: Choi, J. et al. Mol. Cell Biol. 22, 1094-105 (2002).
F56A6.1#		piwi/PAZ domain	M, MILI (1.2e <sup>-11</sup> ) H, PIWIL2 (1.6e <sup>-11</sup> ), PIWIL1 (1e <sup>-08</sup> )	M, MILI KO male infertile	M, MILI: Kuramochi-Miyagawa, S. et al. Development 131, 839-49 (2004).
C18E3.7#	<i>ppw-1</i>	piwi/PAZ domain	M, MILI (7.4e <sup>-12</sup> ) H, PIWIL2 (7.4e <sup>-12</sup> ), PIWIL1 (9e <sup>-08</sup> )	M, MILI KO male infertile	M, MILI: Kuramochi-Miyagawa, S. et al. Development 131, 839-49 (2004).
B0414.3	<i>hil-5</i>	histone H1	M, Histone H1t (8.8e <sup>-16</sup> ) H, Histone H1t (1.4e <sup>-13</sup> )	M, Histone H1t KO male infertile in combo with other genes	M, Histone H1t: Nayernia, K. et al. Mol. Reprod. Dev. 70, 406-16 (2005).
C18G1.5	<i>hil-4</i>	Histone H1	M, Histone H1t (1.9e <sup>-13</sup> ) H, Histone H1t (1.6e <sup>-12</sup> )	M, Histone H1t KO male infertile in combo with other genes	M, Histone H1t: Nayernia, K. et al. Mol. Reprod. Dev. 70, 406-16 (2005).
C33H5.12	<i>rsp-6</i>	SR Splicing Regulation Protein	M, Sfrs3 (9.9e-33), Rbm3 (1.7e <sup>-12</sup> ) H, RBMY1 (2.9e <sup>-12</sup> ), CSTF2T42 (8.7e <sup>-09</sup> ),	M, Sfrs3 KO Embryonic lethal H, Microdeletions including RBMY correlate with male infertility; CSTF2T associated with male infertility, homologs expressed in male meiosis	M, Sfrs3: Jumaa, H., Wei, G. & Nielsen, P.J. Curr. Biol. 9, 899-902 (1999) H, RBMY: Mahadevaiah, S.K. et al. Hum. Mol. Genet. 7, 715-27 (1998). CSTF2T: Dass, B., McDaniel, L., Schultz, R.A., Attaya, E. & MacDonald, C.C. Genomics 80, 509-14 (2002)

<i>C. elegans</i>			Mammalian		References
Gene ID	Gene Name	Descriptor	Known Homolog	Fertility Link	
W02B12.3	<i>rsp-1</i>	splicing factor like	M, Sfrs3 (3.7e <sup>-19</sup> ), Rbm3 (1.7e <sup>-12</sup> ) H, RBMY1 (4.1e <sup>-13</sup> )	M, Sfrs3 KO Embryonic lethal H, microdeletions including RBMY correlate with male infertility	M, Sfrs3: Jumaa, H., Wei, G. & Nielsen, P.J. Curr. Biol. 9, 899-902 (1999) H, RBMY: Mahadevaiah, S.K. et al. Hum. Mol. Genet. 7, 715-27 (1998).
Y54F10BM.2		Translation initiation factor IF2	M, Translation initiation factor 5B (1e <sup>-105</sup> ) H, Translation initiation factor 5B (2.4e <sup>-169</sup> ), NASP (4.7e <sup>-09</sup> )	H, NASP is a histone H1 binding protein found in sperm cells	H, NASP: Lee, Y.H. & O'Rand, M.G. Anat. Rec. 236, 442-8 (1993).
M01E5.5	<i>top-1</i>	Topoisomerase I	M, TOP-1 (3e <sup>-154</sup> ) H, TOP-1 (1e <sup>-156</sup> )	M, TOP-1 KO Embryonic lethal H, Decrease of topo I activity in testes of infertile men with varicocele	M, TOP-1: Morham, S.G., Kluckman, K.D., Voulomanos, N. & Smithies, O. Mol Cell Biol 16, 6804-9 (1996). H, TOP-1: Fujisawa, M., Yoshida, S., Matsumoto, O., Kojima, K. & Kamidono, S. Arch. Androl. 21, 45-50 (1988).
C39E9.6		SCP-like extracellular protein	M, CRISP2 (1e <sup>-08</sup> ) H, CRISP2 (1e <sup>-08</sup> )	H, CRISP2 is testes specific gene, candidate male infertility gene	H, CRISP2: Olesen, C. et al. Mol. Hum. Reprod. 7, 11-20 (2001).
F36H12.8ψ		serine/threonine kinase	M, Vrk2 (8e <sup>-15</sup> ); Tau-Tubulin Kinase (2.5e <sup>-56</sup> ) H, TTBK2 (3e <sup>-57</sup> )	M, Vrk2 KO correlates with germ cell deficiency	M, Vrk2: Lu, B. & Bishop, C.E. Biol. Reprod. 69, 161-8 (2003)
R13H9.5ψ		serine/threonine kinase	M, Vrk2 (8e <sup>-15</sup> ); Tau-Tubulin Kinase (2.5e <sup>-56</sup> ) H, TTBK2 (3e <sup>-57</sup> )	M, Vrk2 KO correlates with germ cell deficiency	M, Vrk2: Lu, B. & Bishop, C.E. Biol. Reprod. 69, 161-8 (2003)

Symbols (\*, †, §, #, ψ) denote highly homologous genes. Mammalian homologs with E values ≤ 10<sup>-09</sup> were found using *C. elegans* protein sequences in BLAST searches of the GenBank database and/or annotations in WormBase (www.wormbase.org Release 155) and Worm Protein Database (BIOBASE). C, *C. elegans*; M, Mouse; H, Human; KO, Mouse Knock-Out.

Supplemental Table 9 Abundant spermatogenesis-enriched chromatin factors with mammalian homologs not yet linked to fertility

Predicted Gene	<i>C. elegans</i> locus	Descriptor	<i>C. elegans</i> RNAi phenotype	Mouse Homolog (E value)	Mouse Knock out phenotype	Human Homolog (E value)	References
K01G5.5		RNA processing, centromere/microtubule binding protein, dyskerin	Stp Lva Gro	Dyskerin (2.1e <sup>-154</sup> )	Embryonic Lethal	Dyskerin (5.2e <sup>-160</sup> )	M, Dyskerin: He, J. et al. Oncogene 21, 7740-4 (2002).
ZC116.3		bone morphogenetic protein 1 like CUB domains; EGF like domain	None detected	Intrinsic factor-B12 receptor precursor (1e <sup>-223</sup> ); Notch2 (4e <sup>-50</sup> )	Embryonic Lethal	Intrinsic factor-B12 receptor (1e <sup>-218</sup> ), CUB and sushi multiple domains protein (1.5e <sup>-53</sup> )	M, Notch: Hamada, Y. et al. Development 126, 3415-24 (1999).
ZK328.2	<i>eft-1</i>	elongation factor 2; U5 snRNP-specific protein	Ste Emb Sck	U5 small nuclear ribonucleoprotein component (0), Sfrs3 (4e <sup>-13</sup> )	Sfrs3 (splicing factors) is embryonic lethal	U5 small nuclear ribonucleoprotein component (0), Elongation factor 2 (3.2e <sup>-150</sup> )	M, Sfrs3: Jumaa, H., Wei, G. & Nielsen, P. J. Curr. Biol. 9, 899-902 (1999).
F44G3.2		arginine kinase	None detected	Creatine kinase (3.5e <sup>-61</sup> )	Tissue Specific Defects	Creatine kinase (3.5e <sup>-61</sup> )	M, Creatine kinase: Nahrendorf, M. et al. Cardiovasc. Res. 65, 419-27 (2005).
Y51A2D.8		Cysteine proteases (2 domains) CTSL2 expressed in testes	None detected	Cathepsin (2e <sup>-30</sup> ), Ctsk (8e <sup>-28</sup> )	Tissue Specific Defects (bone, other)	Cathepsin L precursor (2.7e <sup>-33</sup> )	M, Ctsk: Brachvogel, B. et al. Mol. Cell Biol. 23, 2907-13 (2003).
B0365.3	<i>eat-6</i>	eat-6 Na(+)/K(+) ATPase alpha subunit status	Emb	Na+/K+-transporting ATPase $\alpha$ -4 chain (0)	Tissue Specific Defects (brain, neonate)	Na+/K+-transporting ATPase $\alpha$ -4 chain (0)	M, ATPase: Moseley, A. E. et al. J. Biol. Chem. 278, 5317-24 (2003)
T08G11.1		nucleotide binding protein vps-13 like	None detected	CHAC (0), D330038K10Rik protein (3.6e <sup>-168</sup> )	Tissue Specific Defects (erythrocytes)	Vacuolar protein sorting 13 (0)	M, CHAC, Tomemori, Y. et al. J. Neurochem. 92, 759-66 (2005)
D1007.6	<i>rps-10</i>	40S ribosomal protein S10	Ste Emb Unc Lva	40S ribosomal protein S10 (4.8e <sup>-33</sup> ), Plec1 (1e <sup>-25</sup> )	Tissue Specific Defects (heart, muscle, skin)	40S ribosomal protein S10 (1.6e <sup>-32</sup> )	M, Plec1: Andra, K. et al. Genes Dev. 11, 3143-56 (1997)
T13A10.11	<i>tag-32</i>	S-adenosylmethionine synthetase	High Ste	Mat1a (1.3e <sup>-130</sup> )	Tissue Specific Defects (liver)	ENSP00000303147 (3.9e <sup>-131</sup> )	M, Mat1a: Lu, S. C. et al. Proc. Natl. Acad. Sci. U S A 98, 5560-5 (2001); Martinez-Chantar, M. L. et al. Faseb J 16, 1292-4 (2002).
ZC155.1	<i>nex-1</i>	Annexin family member	None detected	Annexin (4.2e <sup>-61</sup> )	Tissue Specific Defects (varies for different Annexins)	Annexin (4.8e <sup>-62</sup> )	M, Annexin: Brachvogel, B. et al. Mol. Cell Biol. 23, 2907-13 (2003); Roviezzo, F. et al. J. Physiol. Pharmacol. 53, 541-53 (2002).
Y48B6A.12		Malic oxidoreductase	None detected	NADP-dependent malic enzyme (1.6e <sup>-168</sup> )		NADP-dependent malic enzyme, mitochondrial precursor (3.4e <sup>-168</sup> )	
K03H1.1	<i>gln-2</i>	Glutamine synthetase, catalytic domain	None detected	Glutamine synthetase (1.4e <sup>-114</sup> )		Glutamine synthetase (4.8e <sup>-114</sup> )	
T25C8.3	<i>qrs-4</i>	glutamine synthetase family	None detected	GLUL (1e <sup>-89</sup> )		Glutamine synthetase (1e <sup>-89</sup> )	
F49C12.15		Novel	None detected	Msx2-interacting protein (6e <sup>-12</sup> ), Splicing factor (5.9e <sup>-11</sup> )		Hypothetical protein FLJ35170 (4.5e <sup>-11</sup> ), Splicing factor (7.9e <sup>-11</sup> )	
B0207.5		Novel	None detected	KIAA0853 (4.4e <sup>-11</sup> ), ATRX (5e <sup>-10</sup> )		Transcriptional regulator ATRX (4.1e <sup>-13</sup> )	
F23B12.7		CCAAT binding factor 1 protein like, txn factor	Stp Gro lva	CCAAT enhancer binding protein zeta (9.91e <sup>-114</sup> )		CCAAT enhancer binding protein zeta (1e <sup>-115</sup> )	
ZK945.3		Puf family RNA-binding protein	Egl Lva	Pumilio-family RNA binding domains (4.7e <sup>-71</sup> )		OTTHUMP00000020987 (1.6e <sup>-72</sup> )	
F07A11.2		glucosamine-fructose-6-phosphate	Emb Ste	glucosamine-fructose-6-phosphate (1.7e <sup>-225</sup> )		glucosamine-fructose-6-phosphate (4.6e <sup>-225</sup> )	

Predicted Gene	<i>C. elegans</i> locus	Descriptor	<i>C. elegans</i> RNAi phenotype	Mouse Homolog (E value)	Mouse Knock out phenotype	Human Homolog (E value)	References
T28F2.4		Mina like (myc regulator)	None detected	brain cDNA (5.8E <sup>-70</sup> ); Myc induced nuclear antigen (5.6e <sup>-40</sup> )		Myc induced nuclear antigen (5.6e <sup>-40</sup> )	
F36A4.7	<i>ama-1</i>	RNA polymerase II	Ste Emb Gro Sck	RNA pol II (0)		RNA pol II (0)	
C16A3.3		rRNA processing protein	Lva Egl Emb Gon Gro Lva Lvl	MKIAA0185 protein (6.1e <sup>-85</sup> ), Programmed cell death protein 11 (1.5e <sup>-83</sup> )		RRP5 protein homolog (1.8e <sup>-91</sup> )	
JC8.3	<i>rpl-12</i>	ribosomal protein	Ste Gro Sck Emb	60S ribosomal protein L12 (9.5e <sup>-67</sup> )		60S ribosomal protein L12 (3.2e <sup>-66</sup> )	
T07A9.9	<i>phi-58</i>	GTP-binding protein CRFG/NOG1 (ODN superfamily)	Stp Emb Gro Lva Unc	Nucleolar GTP-binding protein (4.6e <sup>-146</sup> )		76 kDa protein (1.2e <sup>-157</sup> )	
W07E6.1		tRNA and rRNA cytosine-C5-methylase (nucleolar protein NOL1/NOP2)	Stp Ste Sle Emb Gro Lva Lon	Nucleolar protein 1 (2.6e <sup>-134</sup> )		Proliferating-cell nucleolar antigen p120 (2.7e <sup>-135</sup> )	
E03H12.5		Novel	None detected	Nucleolin (6e <sup>-21</sup> )		Nucleolin (3.7e <sup>-24</sup> )	
Y38H8A.3		casein kinase	None detected	Tau-tubulin kinase (1.5e <sup>-56</sup> )		TTBK2 protein (8.9e <sup>-58</sup> )	
F38A5.3	<i>lec-11</i>	lectin	None detected	Galectin-9 (2.1e <sup>-07</sup> )		40 kDa protein (3.7e <sup>-10</sup> )	
C17G10.8	<i>dhs-6</i>	alcohol dehydrogenase	None detected	Hydroxysteroid dehydrogenase like 2 (3.5e <sup>-107</sup> )		HSDL2 protein (4.6e <sup>-79</sup> )	
F54C8.1		3-hydroxyacyl-CoA dehydrogenase	None detected	Short chain 3-hydroxyacyl-CoA dehydrogenase (8e <sup>-76</sup> )		Short chain 3-hydroxyacyl-CoA dehydrogenase (1.7e <sup>-75</sup> )	
Y71H10A.1		Phosphofructokinase	Emb	6-phosphofructokinase (3.1e <sup>-236</sup> )		6-phosphofructokinase (3e <sup>-234</sup> )	
F36D3.4		msp domain	None detected	Splicing factor, arginine/serine-rich 4 (6.6e <sup>-08</sup> )		Hypothetical protein FLJ46115 (4.3e <sup>-10</sup> )	
K04C2.2		Predicted MYB-binding protein	Stp Gro Lvl Sck Pvl Pch	myb binding protein (1.6e <sup>-12</sup> )		myb binding protein (1.7e <sup>-08</sup> )	
C32E8.2	<i>rpl-13</i>	ribosomal protein	Emb Lva Ste Sck	Ribosomal protein L13 (2.5e <sup>-59</sup> )		Ribosomal protein L13 (3.2E <sup>-59</sup> )	
C18A3.3		rRNA processing EBP2	Emb Lva	rRNA processing protein EBP2 (2.8e <sup>-36</sup> )		rRNA processing protein EBP2 (7.2e <sup>-45</sup> )	
C43E11.9		RNA binding (interacts with MEX-1)	Gro Lva	60S ribosome subunit biogenesis protein NIP7 homolog (2.2e <sup>-61</sup> )		60S ribosome subunit biogenesis protein NIP7 homolog (5.1e <sup>-62</sup> )	
E04A4.8	<i>rpl-20</i>	ribosomal protein	Ste Sck Emb Gro	60S ribosomal protein L18a (4.4e <sup>-58</sup> )		60S ribosomal protein L18a (2.7e <sup>-58</sup> )	
F25B4.5		RNA-processing protein, HAT helix	None detected	PRP39 pre-mRNA processing factor homolog (1.8e <sup>-59</sup> )		Hypothetical protein (1.8e <sup>-59</sup> )	
K12H4.3		Brix domain	Stp Lva Emb Gro	Ribosome biogenesis protein Brix (1.4e <sup>-63</sup> )		Ribosome biogenesis protein Brix (1.2e <sup>-71</sup> )	
R13A5.12	<i>lpc-7</i>	Pescadillo, N-terminal, BRCA C terminal	Stp Lva Emb Gro Lvl	Pescadillo homolog 1 (3.1e <sup>-118</sup> )		Pescadillo homolog 1 (3.7e <sup>-93</sup> )	



Predicted Gene	<i>C. elegans</i> locus	Descriptor	<i>C. elegans</i> RNAi phenotype	Mouse Homolog (E value)	Mouse Knock out phenotype	Human Homolog (E value)	References
Y48A6B.3		Ribosomal protein	Gro	small nucleolar protein (3.6e <sup>-32</sup> )		Hypothetical protein FLJ20479 (2.8e <sup>-32</sup> )	
Y48B6A.1		Ribosomal protein L7Ae	Sck Gro Pck Lva	Ribosome biogenesis protein BOP1 (3.1e <sup>-162</sup> )		Ribosome biogenesis protein BOP1 (6.3e <sup>-162</sup> )	
Y54E10A.10		Brix domain	Lva Ste	Brix domain containing protein 1 (1.3e <sup>-59</sup> )		Brix domain containing protein 1 (3.2e <sup>-58</sup> )	
Y75B8A.7		Mpp10 protein homolog	Gro Lva lvi	MPHOSPH10 protein (3e <sup>-58</sup> )		U3 small nucleolar ribonucleoprotein protein MPP10 (3.8e <sup>-67</sup> )	
ZK430.1		HEAT repeat	Gro Pch Emb Lvl Prz	cDNA similar to PROTEIN BAP28s (5.7e <sup>-36</sup> )		Protein BAP28 (7.3e <sup>-91</sup> )	
ZK354.2		serine/threonine kinase	None detected	Tau-tubulin kinase (1.5e <sup>-28</sup> ), Vrk1 (3e <sup>-10</sup> )		TTBK2 protein (9e <sup>-27</sup> )	
C39H7.1		serine/threonine kinase	None detected	Tau-tubulin kinase (1.7e <sup>-57</sup> ), Casein kinase I (7e <sup>-27</sup> )		TTBK2 protein (3e <sup>-57</sup> ), Casein kinase I (7e <sup>-27</sup> )	
C30F12.7		isocitrate dehydrogenase	None detected	Isocitrate dehydrogenase (1.6e <sup>-104</sup> )		Isocitrate dehydrogenase (5.9e <sup>-105</sup> )	
F26E4.9	<i>cco-1</i>	cytochrome C oxidase	Clr Emb Gro Age Ste Lpd Lva	Cytochrome c oxidase (3.1e <sup>-13</sup> )		Cytochrome c oxidase (1.1e <sup>-06</sup> )	
R02D3.1		Saccharopine dehydrogenase	Gro	Alpha-aminoadipic semialdehyde synthase (1e <sup>-236</sup> )		Alpha-aminoadipic semialdehyde synthase (1.8e <sup>-239</sup> )	
T22H6.2		Glutamate 5-kinase	None detected	Pyrroline-5-carboxylate synthetase (1.2e <sup>-209</sup> )		Pyrroline-5-carboxylate synthetase (1.6e <sup>-209</sup> )	
B0286.3		SAICAR synthetase	None detected	Phosphoribosylaminoimidazole carboxylase (1.9e <sup>-109</sup> )		Phosphoribosylaminoimidazole carboxylase (1.1e <sup>-115</sup> )	
C52E4.7		Phosphoglycerate/bisphosphoglycerate mutase	None detected	ES cells cDNA (1.3e <sup>-10</sup> )		UBASH3A (3.8e <sup>-10</sup> ), Cbl-interacting protein Sts-1 (5e <sup>-10</sup> )	
F07A5.2		Novel	None detected	MKIAA0324 protein (5.9e <sup>-10</sup> )		RNA binding protein (1e <sup>-9</sup> )	
F46H5.7		Novel	None detected	ENSP0000034440(6e <sup>-10</sup> )		RNA binding protein (6.7e <sup>-9</sup> )	
T23B3.5		Novel	None detected	Nucleolin (3.2e <sup>-20</sup> )		Cylicin-2 (8.9e <sup>-23</sup> ), nucleolin (1.9e <sup>-22</sup> )	
Y38E10A.17		Novel	None detected	Keratin (1.8e <sup>-21</sup> )		T rich interactive domain 1B (SWI1-like) isoform 1 (2e <sup>-15</sup> ), Keratin (2e <sup>-15</sup> )	
Y46E12BL.2		HEAT repeat, Carbohydrate kinase, PfkB	None detected	KIAA0690 (7.1e <sup>-86</sup> )		Expressed sequence AA408556 (2.7e <sup>-115</sup> )	

Mammalian homologs with E values  $\leq 10^{-09}$  were found using *C. elegans* protein sequences in BLAST searches of the GenBank database and/or annotations in WormBase ([www.wormbase.org](http://www.wormbase.org) Release 155) and Worm Protein Database (BIOBASE). M, Mouse.