MRG-1/MRG15 is a barrier for germ cell to neuron reprogramming in *Caenorhabditis elegans*

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Abstract

Chromatin regulators play important roles in the safeguarding of cell identities by opposing the induction of ectopic cell fates and, thereby, preventing forced conversion of cell identities by reprogramming approaches. Our knowledge of chromatin regulators acting as reprogramming barriers in living organisms needs improvement as most studies use tissue culture. We used C. elegans as an in vivo gene discovery model and automated solid-phase RNAi screening, by which we identified 10 chromatin-regulating factors that protect cells against ectopic fate induction. Specifically, the chromodomain protein MRG-1 safeguards germ cells against conversion into neurons. MRG-1 is the ortholog of mammalian MRG15 (MORFrelated gene on chromosome 15) and is required during germline development in C. elegans. However, MRG-1's function as a barrier for germ cell reprogramming has not been revealed previously. Here, we further provide protein-protein and genome interactions of MRG-1 to characterize its molecular functions. Conserved chromatin regulators may have similar functions in higher organisms and, therefore, understanding cell fate protection in C. elegans may also help to facilitate reprogramming of human cells.

Introduction

Epigenetic regulators can act as barriers for cellular reprogramming

To successfully reprogram cellular identities using transcription factors (TFs), the expression of genes that are usually repressed, need to be activated. In some contexts, forced expression of a cell fate-inducing TF is sufficient for the activation of ectopic gene expression. One classic example is the mammalian TF MyoD, which, when misexpressed in fibroblasts, induces muscle gene expression leading to the conversion of fibroblasts into muscle cells (Davis *et al.* 1987). However, aside from fibroblasts, many cell types are less efficiently converted into muscle-like cells due to cell fate safeguarding mechanisms, that prevent ectopic gene expression based on repressive epigenetic signatures (reviewed in (Pasque *et al.* 2011; Gifford and Meissner 2012; Brumbaugh and Hochedlinger 2013; Becker *et al.* 2016)). Epigenetic regulators, including histone modifiers and chromatin remodelers, as well as a variety of different factors such as kinases and RNA-binding proteins, contribute to establishing a repressive chromatin signature and, may therefore act as barriers for cellular reprogramming.

RNAi screens in C. elegans to identify reprogramming barriers

The nematode *C. elegans* allows *in vivo* interrogation of such regulators for their role in safeguarding cellular identities using RNAi-mediated gene expression knockdown (Tursun *et al.* 2011; Kolundzic *et al.* 2018b). In contrast to knocking-out a gene by mutagenesis or gene editing (CRISPR/Cas9), RNAi generally leads to a partial knockdown thereby allowing the assessment of essential genes, which cause lethality when fully depleted. We applied RNAi post-embryonically to avoid early lethality, which limited a previous RNAi screen where we identified the highly conserved histone chaperone LIN-53 (CAF-1^{p48}/RBBP7 in humans) as a barrier for direct reprogramming of germ cells into neurons (Tursun *et al.* 2011).

In this study, we aimed to reveal additional factors acting like LIN-53 and identified the conserved chromodomain-containing factor MRG-1 (MORF-related gene on chromosome 15 = MRG15 in human) (Olgun *et al.* 2005; Takasaki *et al.* 2007) as a novel barrier for TF-induced germ cell conversion. In mammals, MRG15 is required for proliferation of neural precursor cells, regulation of pre-mRNA splicing during spermatogenesis (Chen *et al.* 2009; Iwamori *et al.* 2016), DNA repair and protection against genotoxic stress (Hayakawa *et al.* 2010; Bleuyard *et al.* 2017). In *C. elegans*,

MRG-1 plays a role in chromosome pairing, maintaining genomic integrity, repressing X-linked genes, and regulating proliferation in the germline (Fujita *et al.* 2002; Takasaki *et al.* 2007; Dombecki *et al.* 2011; Xu *et al.* 2012; Gupta *et al.* 2015). While MRG-1's role in germline development and differentiation to produce mature germ cells, are well described (Fujita *et al.* 2002; Takasaki *et al.* 2007; Dombecki *et al.* 2015), its function in safeguarding germ cells against TF-induced conversion was unknown. Furthermore, MRG-1-interacting proteins and its genomic DNA-binding sites in *C. elegans* were not described previously. We performed an in-depth analysis of MRG-1's interactions with proteins and DNA using immunoprecipitations combined with mass spectrometry (IP-MS) and ChIP-seq. Interestingly, MRG-1 interacts with SET-26, which mediates repressive histone H3K9 methylation (Greer *et al.* 2014). Conversely, we found that MRG-1 associates predominantly with genomic loci carrying active histone marks, including H3K36me3 and H3K4me3. Yet, our study indicates that MRG-1 and SET-26 might cooperate to prevent conversion of germ cells into neurons.

Overall, understanding mechanisms that safeguard cell fates in *C. elegans* could help to identify conserved reprogramming barriers, as exemplified by the previously identified reprogramming barriers LIN-53 and FACT in *C. elegans* (Tursun *et al.* 2011; Kolundzic *et al.* 2018a), which could be targeted to facilitate the generation of tissues for future replacement therapies.

Results

Setup for automated chromatin RNAi sub-library screening

To perform RNAi screens for chromatin factors that safeguard cell fates, we used a previously described transgenic strain carrying the *gcy-5p::gfp* reporter, which specifically labels the ASER neuron, and the *hsp::che-1* (heat-shock promoter controlled *che-1*) transgene that allows broad mis-expression of the TF CHE-1. CHE-1 induces the fate of specific neurons termed ASER/L, but its broad overexpression does not lead to reprogramming of other cells in wild-type or control backgrounds (Figure 1A). However, RNAi against the histone chaperone gene *lin-53* allows germ cell reprogramming to ASE neurons upon *che-1* overexpression as previously described (Figure 1A) (Tursun *et al.* 2011; Kolundzic *et al.* 2018a; b). We aimed to screen for more factors that prevent *che-1*-induced reprogramming by exposing

animals to RNAi only after embryonic development (P0 RNAi) (Figure 1A).





Automated RNAi Screen with LP Sampler + BioSorter



Figure 1 Automated RNAi screen for epigenetic reprogramming barriers.

(A) Mis-expression of CHE-1 and F1 RNAi against the histone chaperone gene *lin-53* (Caf1p48/RBBP4/7) on solid worm growth media allows <u>germ cell conversion</u> (GeCo) to ASE neuron-like cells as visualized by gcy-5p::gfp expression in the germline (white arrows). Scale bars = 50 µm. (B) Ubiquitously mis-expressed TF CHE-1 is blocked by reprogramming barriers to induce the glutamatergic ASE neuron fate visualized by the ASE-specific reporter gcy-5p::gfp. P0 RNAi screening to identify epigenetic barrier factors, which block germ cell conversion. (C) A solid media-based automated RNAi screening system by combining the BioSorter with a robotic large-particle sampling system (LP sampler, both Union Biometrica). The LP sampler collects worms from solid RNAi medium by repeated flushing and aspiration and directly transfers worms to the BioSorter for fluorescence-intensity scanning. Detailed analysis of aspiration and sorting efficiency is shown in Table S2. Scale bars = 20 µm.

This strategy allows the assessment of factors that cause embryonic lethality, or developmental arrest, when animals are treated with RNAi during embryogenesis by exposing their mothers to RNAi (F1 RNAi). We generated an RNAi sub-library targeting all known factors (approximately 800) that have been implicated in

chromatin regulation (Cui and Han 2007; Shaye and Greenwald 2011; Lai and Wade 2011; Wenzel *et al.* 2011) including a variety of different protein families (Figure S1A, Table S1). Since germ cell reprogramming efficiency drops significantly in liquid RNAi compared to solid media RNAi (Figure S1B), we had to establish a solid phase-based RNAi screening pipeline by combining a large-particle sorter (BioSorter) with an automated sampling system (LPsampler) (Figure 1C, Figure S2).

A previously described automated RNAi screening procedure from solid media requires manual transfer of worms to the sorting unit (Squiban *et al.* 2012). In contrast, the new setup allows a fully automated transfer of worms, which are then automatically analyzed for changes in the pattern of fluorescence (approx.20 worms/sec) (Figure S2, Table S2). The high sensitivity of this system allows for the detection of increased GFP derived from only one additional cell (Figure S2) thereby making it a sensitive and powerful tool to screen for factors that block induction of ectopic GFP expression.

The chromodomain protein MRG-1 is a barrier for germ cell reprogramming

By performing a P0 RNAi screen to identify factors that prevent germ cell to neuron conversion, in combination with the BioSorter, we detected increased GFP expression derived from the *gcy-5p::gfp* transgene upon RNAi against 10 target genes (Figures 2A-E). Depletion of different target factors create permissiveness for *gcy-5p::gfp* induction by CHE-1 in distinct tissues such as the intestine and epidermis (Figures 2A-E). We focused on the target *mrg-1* because closer examination revealed that RNAi against *mrg-1* yields a phenotype resembling the germ cell to neuron conversion (Figure 2B) as seen before for *lin-53* F1 RNAi (Figure 1A). MRG-1 is orthologous to the mammalian chromodomain-containing MRG15 – a component of the NuA4 histone acetyltransferase (HAT) complex (Chen *et al.* 2009) and has recently been shown to regulate the differentiation of germ cells in *C. elegans* (Gupta *et al.* 2015). Assessment of the ectopic *gcy-5p::gfp* induction in *mrg-1* RNAi animals, revealed that germ cells undergo conversion into neuron-like cells (Figures 3A-B) as previously observed when targeting the Polycomb Repressive Complex 2 (PRC2) genes, including *lin-53*, by RNAi (Patel *et al.* 2012).





(A) Transgenic background *hsp::che-1*, *gcy-5p::gfp* used for screening. RNAi control worms show expression of *gcy-5* only in the ASER head neuron. (B-E) Ectopic induction of *gcy-5p::gfp* is detectable in different tissues including germline (B), gut (C), muscle (D), and epidermis (E) depending on the RNAi target. Only depletion of *mrg-1* encoding a chromodomain-containing protein (orthologous to human Mortality factor 4-like protein 1/MRG15) shows ectopic *gcy-5p::gfp* in the germline. Scale bars = 20 µm.

RNAi against mrg-1 without overexpressing che-1 is not causing any ectopic gcy-5p::gfp induction or loss of germ cell characteristics (Figures S3A-B), which excludes the possibility that germ cells converted due to teratoma formation, as previously described (Ciosk *et al.* 2006). The converted germ cells show morphological changes with neuronal characteristics including projection-like extensions (Figure 3A) and start expressing neuron subtype-specific, as well as pan-neuronal marker genes, such as *ceh-36* (ASE/AWC glutamatergic), *osm-6* (pan-sensory), *rab-3* (pan-neuronal) and *unc-119* (pan-neuronal) (Figure 3C) (Tursun *et al.* 2011; Patel *et al.* 2012). To assess whether the neuronal reporter transgenes reflect expression of transcripts derived from endogenous genes, we performed single molecule fluorescent *in situ* hybridization (smFISH) (Figures 3D-E, Figures S3B-D). smFISH revealed that GFP-positive germ cells turn on endogenous expression of *gcy-5*, *ceh-36*, *rab-3*, the panneuronal RIM homolog *unc-10*, and *unc-119* with comparable levels as authentic neurons (Figure 3D-E, Figures S3B-D). Endogenous expression of these neuronal genes further corroborates that germ cells faithfully converted to neuron-like cells.

Converted germ cells upon mrg-1 RNAi lose germline characteristics

RNAi against mrg-1 permits germ cells to adopt neuronal characteristics by changing their morphological appearance, and turning on expression of neuronal genes upon induction of *che-1* overexpression. However, it is possible that germ cell characteristics are still preserved in cell expressing gcy-5p::gfp. To address this, we assessed expression of the germline-specific *pie-1* reporter (*pie-1::RFP::histone*) (Figure 4A-B) and immunostained for germline-specific P-Granules. Both germ cell-specific characteristics are lost in GFP-positive cells upon conversion (Figure 4A-B). Hence, adoption of neuronal gene expression accompanied by the loss of germ cell fate features further substantiates the notion that germ cells can be reprogrammed into ASE neuron-like cells upon RNAi against mrg-1. Notably, we did not observe expression of genes that belong to other neuronal fates such as interneurons or GABAergic motor neurons (Figure S4A) indicating the specificity of ASE neuron fate induction in reprogrammed germ cells by CHE-1. Hence, germ cells that fail to show gcy-5p::gfp but have lost germ cell characteristics may not express other ectopic cell fates.





(A) RNAi control animals show gcy-5p::gfp expression only in head neurons. RNAi against mrg-1 allows mis-expressed che-1 to induce gcy-5p::gfp expression in the germline. Magnification (white stippled box) reveals that GFP-positive cells adopt neuronal morphology by showing axo-dendritic outgrowths and protrusions (white arrow heads). Scale bars = 20 µm. (B) Quantification of animals that show GFP in the germline when treated with mrg-1 RNAi and che-1 mis-expression. Number of animals (n) quantified are indicated. Error bars represent SEM. (C) RNAi against mrg-1 allows che-1 to induce expression of additional neuronal gene reporters. ceh-36p::rfp is specific for glutamatergic ASE and AWC neurons, osm-6p::gfp is specific to pan-sensory neurons such as ASE, rab-3p::nls::rfp and unc-119p::gfp are pan-neuronally expressed genes. White lines outline areas of the germline with

GeCo. Yellow lines outline worm body. Scale bar = 10 μ m. (D) Single molecule fluorescent in situ hybridizations (smFISH) to detect transcripts derived from endogenous neuronal genes in GFP-positive (*gcy-5p::gfp*) germ cells. mRNA molecules are visible as red dots. Control was incubated with mock hybridization. Scale bars, 2 μ m. (E) Quantification of smFISH detections based on counts of hybridization signals (red dots) per GFP-positive cells. For each condition 20 GFP-positive cells were counted for smFISH-derived transcript detection based on fluorescence signals as exemplified in (D). p-values based on ANOVA with Dunnett's multiple comparison test: p1 = 0,0001; p2 = 0,0003; p3 = 0,0002; p4 = 0,0001; p5 = 0,0001.

MRG-1 safeguards germ cell identity independently of LIN-53 and PRC2

We wondered whether the germ cell conversion in mrg-1 RNAi animals might be due to a loss of the previously identified germ cell reprogramming barrier LIN-53 (Tursun et al. 2011; Kolundzic et al. 2018b). LIN-53 acts with the Polycomb Repressive Complex 2 (PRC2), which represses chromatin by catalyzing methylation of histone H3K27, to counteract CHE-1-induced germ cell conversion (Patel et al. 2012). We examined whether mrg-1 depletion affects lin-53 expression in the germline. However, *mrg-1*-depleted animals with or without *che-1* overexpression, do not show obvious alterations of LIN-53 levels in the germline as assessed by immunostainings (Figure 4D). Interestingly, MRG-1 proteins only partially colocalize with LIN-53 in germ cell nuclei (Figure 4E), indicating that both proteins might have little functional overlap to protect the germline. Furthermore, RNAi against lin-53 and other PRC2 subunits causes global loss of the PRC2-mediated histone modification H3K27me3 in the germline (Patel et al. 2012), which we did not observe upon mrg-1 depletion in whole worms (Figure 4F) or specifically in the germline (Figure 4G). Overall, these findings indicate that mrg-1 safeguards germ cells through mechanisms that are not related to PRC2-mediated regulation. Notably, mrg-1 RNAi animals show a slight increase of the constitutive heterochromatin mark H3K9me3, as well as an increase of H3K14ac (Figures 4F-G), which has been implicated in DNA damage checkpoints in yeast (Wang et al. 2012). However, it is unknown which genomic DNA-binding sites are occupied by MRG-1, and, whether MRG-1 is directly linked to regulating histone modifications.

DNA-binding sites of MRG-1 in the germline and soma

To provide clues as to how MRG-1 contributes to safeguarding germ cells against reprogramming, we sought to reveal the genome-wide DNA-binding patterns of MRG-1 by performing chromatin immunoprecipitation with sequencing (ChIP-Seq).



Figure 4 Changes of germline fate and histone modifications upon mrg-1 RNAi.

(A) Induction of gcy-5p::gfp in mrg-1 RNAi-treated worms leads to loss of germ cell characteristics. Expression of the germline-specific reporter pie-1p::rfp diminishes in cell with ectopic gcy-5p::gfp expression as revealed upon magnification of the germline area with germ cell conversion (white stippled box). The blue stippled boxes highlight a control and a reprogrammed germ cell that has lost the typical fried egg-shaped appearance of the nucleus and now displays a rather speckled nucleus typical for neurons. Scale bars = 50 µm (5 µm in magnification). (B) Quantification of pie-1p::RFP reporter loss in reprogrammed germ cells upon mrg-1 RNAi. 150 animals in triplicate experiments were assessed. Error bars represent SEM. (C) Antibody staining for germline-specific P Granules upon mrg-1 RNAi-mediated conversion of germ cells to ASE neuron-like cells. Scale bars = 5 µm. (D) LIN-53 antibody immunostaining of young adult hermaphrodite germlines from control and mrg-1 RNAi treated animals with and without *che-1* overexpression. Asterisk indicates distal tip of the

gonad. Scale bar = 5 μ m (E) Antibody staining of MRG-1 and LIN-53 proteins in the distal wild-type germline of a young adult hermaphrodite. The magnified germ cell nucleus in the zoom is indicated with a white stipple-line box. Asterisk indicates distal tip of the gonad. Scale bar = 5 μ m (F) Western Blot analysis of whole worm lysates from control and *mrg-1* RNAi treated worms without *che-1* overexpression using the indicated antibodies against specific histone modifications. Detection of histone H3 serves as the loading control. (G) Immunostaining of gonads from control and *mrg-1* RNAi treated worms using the indicated antibodies against specific histone modifications. Staining for LIN-53 (shown as overlay with DAPI) serves as a control for staining efficiency. Scale bars = 5 μ m.

Importantly, MRG-1 proteins can be detected in the germline, as well as in somatic cells including neurons and intestinal cells (Figure 5A, Figure S4B). To distinguish between germline-specific and somatic MRG-1 genome binding sites, we used wild-type animals and *glp-4* temperature-sensitive mutants (*bn2*) which lose the germline when grown at 25°C (Beanan and Strome 1992) (Figure 5B). Subsequent comparison of DNA-binding patterns from these two backgrounds provided information about MRG-1 DNA-binding sites in all tissues versus the germline in a highly reproducible manner (Figure 5C, Figures S5A-B, Table S3).

Overall we identified around 6723 DNA-binding sites for MRG-1 in the genome of the WT (N2) background (Figure 5A, Table S3) of which 1183 are differential peaks when compared to the germline-less *glp-4* background (Figure S5B, Table S3). Gene set enrichment analysis using PANTHER (Mi et al. 2013) revealed that MRG-1 target genes, in the soma and germline, are predominantly involved in the regulation of translation, RNA processing, as well as DNA replication and recombination (Figure 5D). Genes that are bound by MRG-1 exclusively in the germline regulate cell cycle and contribute to DNA metabolic processes (Figure 5D). These enriched biological processes of MRG-1 targets concur with findings from previous studies that have implicated MRG-1 and MRG15 in genome integrity, DNA recombination, mRNA processing, germline regulation and proliferation (Takasaki et al. 2007; Luco et al. 2010; Dombecki et al. 2011; Xu et al. 2012; Gupta et al. 2015; Iwamori et al. 2016). Furthermore, human MRG15 associates with the specific histone modification H3K36me3 (Zhang et al. 2006; Luco et al. 2010), which has also been proposed for MRG-1 in conjunction with the SET domain-containing H3K36 methyltransferase MES-4 in C. elegans (Rechtsteiner et al. 2010). In order to test which histone modifications are enriched at MRG-1 DNA-binding sites in C. elegans we made use of available modENCODE data sets (Gerstein et al. 2010) and analyzed the overlap of



MRG-1 peaks with different histone modifications (Figures 5E-F, Figures S6A-B).



(A) Immunostaining of wild-type young adult hermaphrodite with MRG-1 antibody. MRG-1 proteins are detectable in the germline and predominantly in neurons and the intestine. Costaining for LIN-53 is shown in S5 Figureure. Scale bars = 20 μ m. (B) In order to distinguish genome-wide DNA-bindings sites in the soma and germline, MRG-1 ChIP-seq was performed in WT and the germline-lacking *glp-4 (bn2)* background. (C) Browser-shot of a representative genomic region on Chromosome 1 illustrating MRG-1 ChIP-seq peaks from all three replicates for WT and *glp-4 (bn2)* background. Red boxes mark genes that cannot be detected as MRG-1 bound in the germline-less background. The black box marks an intergenic region that cannot be detected as MRG-1 bound in the germline-less background. (D) GO-Term analysis using PANTHER of gene loci bound by MRG-1. (E) Heatmaps showing enrichment of histone modifications at MRG-1 ChIP-seq peaks overlapping in at least two of the WT samples (5141) and peaks which were only identified in WT but not in glp-4(bn2) background (521). The scale bar is the scaled centered peak score. (F) Meta-region profile showing the overall distribution averaged over all peaks for MRG-1 ChIP-seq peaks overlapping in at least two of the WT samples and peaks which were only identified in WT but not in the glp-4(bn2) background.

Soma and germline-shared MRG-1 binding sites correlate predominantly with H3K36me3, H3K9ac, and H3K4me3 while association with genomic loci carrying the repressive histone modifications H3K9me3 or H3K27me3 is rather low (Figures 5E-F, Figures S6B-C). The correlation pattern does not change drastically for germline-exclusive MRG-1-binding sites except for H3K27me3-carrying loci, which become slightly more pronounced (Figures 5E-F, Figures S6B-C). Such genes bound by MRG-1 carrying H3K9me3 or H3K27me3 may be direct targets of MRG-1 for repression (Table S4). Overall, MRG-1 predominantly binds genomic loci carrying H3K36me3, H3K9ac, and H3K4me3 which are histone modifications that mark active genes (reviewed by (Bannister and Kouzarides 2011; Tessarz and Kouzarides 2014; Hyun *et al.* 2017)), suggesting that MRG-1 might protect germ cells against conversion to neurons, not by acting as a repressive chromatin regulator, but by maintaining the genomic integrity and expression of germline components as previously demonstrated (Wu *et al.* 2012; Xu *et al.* 2012).

Protein interaction network of MRG-1

Next, we asked whether MRG-1 protects the germline fate in complex with other proteins. We therefore investigated the protein interaction network of MRG-1 by performing 'Immunoprecipitations in combination with Mass Spectrometry' (IP-MS). IP-MS was performed in the wild-type background using anti-MRG-1 antibodies and, in order to reduce the identification of false-positive protein interactions, we also generated a CRISPR/Cas9-mediated 3xHA knock-in to perform IP-MS using HA antibodies and compared enriched proteins from both experiments (Figure 6A). IP-MS using anti-MRG-1 yielded 100 enriched proteins while IP-MS with HA antibodies in the *mrg-1::3xHA*^{CRISPR} strain yielded 44 proteins (Figure 6B-C, Table S5). Proteins enriched in both IP-MS experiments, which we considered as the most reliable interacting proteins, were ATHP-1, F54D11.4, F59E12.1, Y14H12B.1,

HECD-1, OGT-1, SET-26, SIN-3, SMO-1, and SUMV2 (Figure 6D, Figure S7, Table S5).



Figure 6 Protein-protein interactions of MRG-1

(A) Co-immunoprecipitations (coIPs) with subsequent mass spectrometry (IP-MS) in order to assess MRG-1 protein interactions. WT (N2) was used with anti-MRG-1 and unspecific antibodies as control IP. Additionally, a strain carrying a CRISPR/Cas9-mediated 3xHA knock-in at the *mrg-1* locus (*mrg-1::3xHA*^{CRISPR}) was used fro coIPs with HA antibodies also from N2 worms (no HA tag) as the corresponding negative control. (B-C) Volcano plots showing statistically significant enrichment of co-precipitated proteins. Statistics: t-test, adjusted p-value of 0.05 as FDR cut-off. (D) Common enriched proteins by anti-MRG-1 and anti-HA antibodies.

Interestingly, components of the repressive chromatin regulator PRC2 or the SET domain-containing H3K36 methyltransferase MES-4 could not be detected in any of the IP-MS experiments. In contrast, the SET domain protein SET-26 co-immunoprecipitated as one of the strongest interacting proteins overall (Figures 6B-C, Suppl. Table S5). Notably, SET-26 has H3K9 methylation activity (Greer *et al.* 2014) and could therefore mediate the chromatin silencing and gene repression activities of MRG-1. Furthermore, the SIN3 family histone deacetylase (HDAC) protein SIN-3 is involved in chromatin repression (Choy *et al.* 2007; Checchi and Engebrecht 2011)

and is predicted to associate with another newly identified MRG-1-interacting protein: the β -linked N-acetylglucosamine (O-GlcNAc) transferase OGT-1 (Yang *et al.* 2002; Choy *et al.* 2007; She *et al.* 2009). OGT-1 is the ortholog of the human O-GlcNAc transferase OGT and plays a role in nutrient sensing and insulin signaling pathways both of which are involved in lifespan regulation in *C. elegans* (Hanover *et al.* 2005; Love *et al.* 2010; Mondoux *et al.* 2011; Radermacher *et al.* 2014). In addition, OGT-1 can be part of histone acetyltransferase-containing protein complexes (Hoe and Nicholas 2014) (reviewed by (Gambetta and Müller 2015)) suggesting a direct involvement in chromatin regulation. In summary, our IP-MS identified novel MRG-1 interactions and excludes the possibility of direct MRG-1 association with PRC2 or MES-4. Since the newly identified interactors SIN-3, SET-26 and OGT-1 mediate chromatin regulation, they could potentially contribute to MRG-1's function in protecting the germ cell fate.

SET-26 and OGT-1 might cooperate with MRG-1 to protect germ cells

To examine whether the protein-protein interactions of SIN-3, SET-26 or OGT-1 with MRG-1 are relevant for MRG-1's function in protecting the germline fate we tested whether the mutant backgrounds sin-3 (tm1276), set-26 (tm2467), and ogt-1 (ok430) affect the mrg-1 RNAi-mediated conversion of germ cells into ASE neuron-like cells (Figure 7A). We quantified the number of gcy-5p::gfp-positive cells in gonads showing germ cell to neuron conversion (Figures 7B-C). While the sin-3 (tm1276) mutant background showed no changes in the number of reprogrammed germ cells when compared to the control wild-type (WT) background, set-26 (tm2467), and ogt-1 (ok430) mutations yielded an increase in reprogramming efficiency upon mrg-1 RNAi. On average, the set-26 (tm2467) mutant background allowed an approximately 2-fold increase in the number of germ cells that convert to neurons, while the quantified increase in the ogt-1 (ok430) background by around 1.5-fold, is less pronounced (Figures 7B-C). These observed enhancements in the number of gcy-*5p::gfp*-positive cells in the reprogrammed germlines of *mrg-1* RNAi animals suggest that the newly identified interaction of MRG-1 with SET-26 and OGT-1 could be relevant for MRG-1's role in protecting germ cells against being converted to neurons (Figure 7D).





(A) Rational for testing animal carrying mutations of newly identified MRG-1 interactors for involvement in MRG-1's role in safeguarding germ cells. (B) The mutant backgrounds of *sin-3 (tm1276), set-26 (tm2467)*, and *ogt-1 (ok430)* were tested for enhancement of *mrg-1* RNAi-mediated germ cell reprogramming. Scale bars = 20 μ m (C) Quantifications of converted germ cells upon *mrg-1* RNAi in *sin-3 (tm1276), set-26 (tm2467)*, and *ogt-1 (ok430)* backgrounds. Number of *gcy-5p::gfp*-positive cells in individual gonads were counted. One-way ANOVA multiple comparison: $p^1 = 0.7083$; $p^2 < 0.0001$; $p^3 < 0.0001$. (D) Model illustrating that MRG-1 associates with SET-26 and OGT-1 to counteract the conversion of germ cells to ASE neuron-like cells by the Zn-finger TF CHE-1.

Discussion

Automated screening with solid-phase RNAi identified new safeguarding factors

In order to identify factors that play a role in protecting *C. elegans* cells against reprogramming to neurons, we aimed to setup an automated RNAi screening system. Because we encountered a decrease in germ cell conversion when depleting LIN-53 in liquid versus solid culture, we established an automated screening pipeline allowing worm growth on solid RNAi media. Compared to a previous procedure described by the Ewbank group (Squiban *et al.* 2012), our setup bypasses the requirement for manual transfer of animals from solid RNAi medium to the screening unit. Using our complemented Chromatin 2.0 library for a P0 RNAi screen, we identified 10 factors that prevent ectopic induction of gcy-5p::gfp. Interestingly, ectopic gcy-5p::gfp induction occurs in distinct tissues suggesting that different cell identities are protected by specific mechanisms. The investigation of such tissue-

specific mechanisms can provide further knowledge about the different modes of cell fate maintenance and protection.

MRG-1 safeguards the germ cell fate independently of PRC2

We focused on examining MRG-1, which allowed a germ cell to neuron conversion upon RNAi as recently described for components of the PRC2 complex. MRG-1 is orthologous to the mammalian Mortality Factor 4 Like 1 (MORF4L1) also known as MRG15 (Yochum and Ayer 2002; Olgun *et al.* 2005; Takasaki *et al.* 2007; Chen *et al.* 2009). We used RNAi to deplete *mrg-1* because animals carrying the *hsp::che-1* (*otIs305*) transgene in combination with balanced *mrg-1* mutants (*ok1262, qa6200,* and *tm1227*) were not viable. Since we previously showed for *lin-53* and *mes-2* (PRC2) that homozygous mutants (M+Z-) derived from heterozygous mothers could not recapitulate the RNAi-based germ cell reprogramming due to maternal rescue effects (Tursun *et al.* 2011; Patel *et al.* 2012),we speculate that such maternal rescue is a likely scenario also for *mrg-1* (M+Z-) mutants.

Recently, MRG-1 was shown to be involved in regulating gene expression and antagonizing the germline fate in the intestine, as well as differentiating the mitotic germline to meiotic and mature germ cells in *C. elegans* (Takasaki *et al.* 2007; Petrella *et al.* 2011; Gupta *et al.* 2015). Additionally, an interplay of MRG-1 with the PRC2 complex during germ cell development has been proposed (Rechtsteiner *et al.* 2010). Since our ChIP-seq results revealed MRG-1 binding to H3K27me3-carrying genes, a cooperation of MRG-1 with PRC2 and LIN-53 could be possible. However, other findings argue against interplay between MRG-1 and PRC2 / LIN-53 in protecting germ cells against reprogramming. MRG-1 showed very limited co-localization with LIN-53 or any of the PRC2 subunits. Furthermore, loss of *lin-53* and other PRC2 subunits causes global H3K27me3 decrease in the germline (Patel *et al.* 2012), which we did not observe upon *mrg-1* depletion. Hence, our findings suggest that MRG-1 safeguards the germ cell fate independently of PRC2 and LIN-53.

MRG-1 and the H3K36 methyltransferase MES-4 do not physically interact

Because MRG-1 preferentially associates with DNA loci that carry the histone modification H3K36me3, which is catalyzed by MES-4 (Rechtsteiner *et al.* 2010), we hypothesized that MRG-1 and MES-4 might directly interact which each other. Interestingly, the MRG-1 ortholog Mrg15 in Drosophila promotes the methylation of H3K36 by reinforcing chromatin association of the methyltransferase Ash1 (Huang *et*

al. 2017) and such an interaction during chromatin recruitment has also been proposed for MRG-1 and MES-4 (Rechtsteiner *et al.* 2010). However, we did not detect an interaction of MES-4 with MRG-1 by any of the IP-MS experiments. Hence, it remains to be determined whether MRG-1 and MES-4 may indirectly cooperate in protecting the germ cell fate. Previously, MRG-1 was found to be required for X-chromosomal silencing and an indirect mechanism for its repressive effect has been suggested (Takasaki *et al.* 2007). It is possible that MRG-1 contributes to repressing chromatin in an indirect manner similar to MES-4, by helping to focus PRC2-mediated methylation of H3K27 (Gaydos *et al.* 2012). Since MRG-1 depletion does not lead to a detectable loss of H3K36me3, we speculate that the genomic distribution of H3K36me3 might be altered upon *mrg-1* RNAi that, in turn, could affect gene repression.

MRG-1 binds to genes that regulate metabolism, replication, and cell cycle

Overall, genes bound by MRG-1 are enriched for functions in DNA metabolism, replication, and cell cycle as well as chromosome segregation which is in line with recent findings that MRG-1 and its ortholog MRG15 are implicated in chromosomal break repair and homologous pairing (Garcia *et al.* 2007; Hayakawa *et al.* 2010; Dombecki *et al.* 2011). Therefore, it is possible that a lack of MRG-1 leads to DNA damage thereby causing the observed increase of H3K14ac in the *mrg-1* RNAi germline - an effect that has previously been shown in yeast and mouse (Kim *et al.* 2008; Wang *et al.* 2012). An increase in H3K14ac might lead to a decreased efficiency of H3K9 methylation, as previously suggested (Alvarez *et al.* 2011), which results in lowering or redistributing repressive chromatin marks in the germline. Nevertheless, how such negative crosstalk between these histone modifications might be regulated remains to be determined.

MRG-1 associates with different chromatin-regulating factors

The interaction of MRG-1 with different chromatin-regulating complexes could provide clues as to how MRG-1 functions at the molecular level. As shown for its mammalian ortholog MRG15 (Yochum and Ayer 2002; Doyon *et al.* 2004; Chen *et al.* 2009), we found an interaction of MRG-1 with SIN-3, the ortholog of the mSin3A histone deacetylase complex (HDAC) subunit. Notably, we also identified the ortholog of the human O-GlcNAc transferase (OGT) OGT-1 as a novel MRG-1-interacting protein. OGT has been shown to interact with Sin3A in mammalian cells and is thereby being recruited to promoters of repressed genes (Yang *et al.* 2002),

indicating that MRG-1 might form a complex with an OGT-1-containing Sin3 HDAC. Yet, the Drosophila ortholog of OGT-1 was initially identified as a member of Polycomb group (PcG) class proteins, which are repressive chromatin regulators (Ingham 1984). Additional studies suggest that OGT-1 can be part of histone acetyltransferase-containing protein complexes (Hoe and Nicholas 2014)(reviewed by (Gambetta and Müller 2015)). As one of the most consistent MRG-1-interacting proteins we identified the H3K9 methyltransferase SET-26 (Greer et al. 2014). SET-26 plays a role in the transgenerational sterility of spr-5 mutants and a set-26 mutation suppresses developmental defects seen in animals lacking the NuRD and MEC complex subunit LET-418 (Mi2) (Greer et al. 2014; Erdelyi et al. 2017). Interestingly, we observed a slight increase in H3K9 methylation in mrg-1 RNAi animals, which has previously been reported for mrg-1 mutants (Xu et al. 2012). This effect is counterintuitive because we assumed that *mrg-1* depletion causes more open chromatin based on the observed permissiveness for reprogramming. Furthermore, association of MRG-1 with H3K9 methylated genomic sites, even though to a limited degree, indicated that SET-26 might be directly involved in MRG-1's role as a barrier for germ cell reprogramming. Interestingly, the set-26 mutant background significantly increased germ cell reprogramming upon mrg-1 RNAi, while a modest enhancement could also be observed for the ogt-1, but not for sin-3, mutant background. Based on the high reproducibility of the protein interaction data we therefore suggest that MRG-1 forms a complex with SET-26 and OGT-1 in order to counteract the conversion of germ cells to neuron-like cells. However, we cannot exclude the possibility that SET-26 and OGT-1 contribute to germ cell protection also in parallel to their interaction with MRG-1.

Overall, we demonstrate the value of enhanced RNAi screens for identifying factors that safeguard cellular identities and the use of *C. elegans* as a gene discovery tool. In light of recent findings illustrating conservation of reprogramming barriers from worms to mammalian tissues (Tursun *et al.* 2011; Cheloufi *et al.* 2015), further genetic screens using different cell fate-inducing backgrounds in *C. elegans* have the potential to identify other context-specific factors that regulate cellular reprogramming, both in *C. elegans* and other species.

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Authors' contributions

MH, SS, GB, and EK conducted the experiments, analyzed the data, and helped with the experimental design. AG used bioinformatics to analyze IP-MS and ChIP-Seq data, GB, MK, NF, and AO conducted experiments, SH conducted experiments and maintained the animals. PM helped with IP-MS experiments. BT conceptualized and designed the project, and finalized the manuscript. All authors read and approved the final manuscript.

Methods

Worm strains

The wild type C. elegans Bristol strain (N2) and strains without heat-shock constructs were maintained according to the standard protocol (Stiernagle 2006) at 20°C. Transgenic lines carrying heat-shock constructs were grown at 15°C unless indicated otherwise. The following strains were used in this study: BAT28 otIs305/hsp-16.2p::che-1::3xHA, rol-6(su1006)] ntIs1[gcy-5p::gfp, lin-15(+)] V, BAT29 otIs284[hsp-16.2p::che-1::3xHA, rol-6(su1006)] ntIs1[gcy-5p::gfp, lin-15(+)] V, BAT30 otIs264[ceh-36p::tagRFP], OH3192 ntIs1[gcy-5p::gfp, lin-15(+)] V, BAT326 otIs263[ceh-36p::tagRFP]; otIs305[hsp-16.2p::che-1::3xHA] ntIs1[gcy-5p::gfp, lin-15(+)] V, BAT483 ogt-1(ok430) III.; otIs305[hsp-16.2p::che-1::3xHA, rol-6(su1006)] ntIs1[gcy-5p::gfp, lin-15(+)] V, BAT522 otIs305[hsp-16.2p::che*rol-6(su1006)] ntIs1[gcy-5p::gfp,* 1::3*xHA*, *lin-15(+)] V;* otIs393[ift-20p::NLS::tagRFP], BAT527 otIs355[rab-3p::NLS::tagRFP] IV?; otIs305[hsp-16.2p::che-1::3xHA, rol-6(su1006)] ntIs1[gcy-5p::gfp, lin-15(+)] V; BAT606 edIs6[unc-119p:GFP, rol-6(su1006)]; otIs305[hsp-16.2p::che-1::3xHA, rol-6(su1006)] V, RB653 ogt-1(ok430) III. (obtained from Gene Knockout project at OMRF); otIs305[hsp-16.2p::che-1::3xHA, rol-6(su1006)] ntIs1[gcy-5p::gfp, lin-15(+)] V; BAT32 glp-1(ar202) III, ntIs1 otIs305 V, BAT1940 sin-3(tm1276); otIs305 ntIs1 V, BAT1939 set-26(tm2467); otIs305 ntIs1 V, BAT483 ogt-1(ok430); otIs305 ntIs1 V, , SS104 glp-4(bn11). BAT2019 mrg-1(bar33[mrg-1::3xHA]) III (CRISPR/Cas9).

Synchronized worm population

Synchronized worms were obtained by two standard techniques: bleaching or harvesting early hatched L1 worms. For bleaching, gravid hermaphrodites were treated with sodium hypochlorite solution as previously described (Ahringer 2006). Household bleach (5% sodium hypochlorite) was mixed with 1M NaOH and water in the 3:2:5 ratio. Worms were washed from NGM plates with M9 buffer containing gelatin (0.05% w/v), incubated in bleaching solution for 5 minutes in a 1:1 ratio, vortexed and following worm lysis, eggs were washed three times with M9 buffer. For harvesting L1 worms, plates containing shortly starved adults and freshly hatched L1 larvae were used. Worms were collected into 1.5-ml tubes by washing twice with 800 μ l of M9 buffer + gelatin. Tubes containing worms were left to stand for 2

minutes to allow the separation of the two stages. Adult stage worms sink faster in a solution compared to larvae because they are heavier. Within 2 minutes, adult worms are pelleted at the bottom of the tube, whereas L1 larvae are still swimming near the surface of the solution. The top two thirds of M9 buffer, containing mostly larvae worms, was transferred into a fresh 1.5-ml tube and L1 larvae were collected by centrifugation at 900 g for 1 minute. Harvested L1 larvae or eggs obtained by bleaching were either applied directly onto RNAi plates or regular NGM plates for further maintenance of synchronized population.

Generating the chromatin RNAi sub-library

Candidate genes for the chromatin RNAi sub-library were chosen based on the presence of characteristic protein domains (http://www.uniprot.org), known function in chromatin modifications and remodeling, and any direct or indirect link to chromatin function. The RNAi sub-library was generated by compiling existing RNAi clones from the Ahringer and Vidal RNAi libraries. The list of RNAi clones in the library can be found in the S1 Table. The identity of all RNAi clones was verified by sequencing. Clones that did not exist in the RNAi libraries or clones for which sequence was incorrect, were replaced by newly built RNAi clones (S1 Table). Primers were designed to amplify a unique sequence for each gene of interest (preferably cDNA). PCR products were cloned into the L4440 vector followed by transformation into HT115 (DE3) bacteria. Resulting clones were verified by sequencing. All RNAi clones were grown on plates containing 12.5 µg/ml tetracycline (selection for presence of T7 polymerase and RNase III mutation) and 50 µg/ml carbenicillin (selection for L4440 plasmid) to ensure RNAi efficiency in future experiments. Correct RNAi clones (730 in total) were compiled into the 96-well-plate format S1 Table. Deep-well plates containing 1 ml of LB medium with 50 µg/ml carbenicillin per well were prepared using an automated dispensing machine (MultidropTM Combi Reagent Dispenser, Thermo Scientific). Inoculated RNAi bacteria were grown by shaking overnight at 37°C. Grown bacterial cultures were mixed with glycerol (13% final concentration) and stored at -80°C for further use.

RNAi screening

We used the strain BAT28 to screen for ectopic expression of the glutamatergic neuronal marker *gcy-5p::gfp* upon induction of the transcription factor CHE-1.

Conditions for both automated and manual RNAi have been optimized for solid media to allow precise and fast control of the right developmental stage for che-1 misexpression. RNAi screening of the chromatin sub-library was performed using the feeding technique, as described previously with slight modifications (Kamath et al. 2001). As indicated in the screen workflow in Figure S2B, we aimed to automate as many steps as possible. L1 worms were grown on solid RNAi medium in 48-well plates at 15°C until the L4 stage and heat shocked for inducing ubiquitous misexpression (Tursun et al. 2011) of the ASE neuron fate-inducing TF CHE-1. 16 h later the BioSorter + Large Particle (LP) sampler setup was used to automatically screen for ectopic gcy-5p::gfp expression. We performed the P0 screen, where synchronized L1 larvae were applied on RNAi plates, and scored adults of the same generation (P0). Standard NGM agar medium, supplemented with 50 µg/ml carbenicillin and 1 mM IPTG, was used to pour 48-well or 6-well RNAi feeding plates. The 6-well RNAi plates were dried overnight at room temperature, and then stored at 4°C until use. Because the 48-well RNAi plates tend to dry out quickly, freshly-poured plates were directly turned upside-down, transferred into a humid chamber (plastic box with wet paper towels) and stored at 4°C. The 96-deep-well plates containing 1.2 ml of LB medium with 50 µg/ml carbenicillin/well were poured using the automated dispensing machine (MultidropTM Combi Reagent Dispenser, Thermo Scientific) and then inoculated with RNAi clones of the sub-library and grown by shaking at 37°C. For the manual screen, bacteria grown for sixteen hours were centrifuged for 5 min at 300 g, 800 µl of the supernatant was removed and the bacterial pellet resuspended in the remaining LB medium. Resuspended bacteria were seeded in duplicates on 6-well-RNAi plates (30 µl/well) and dsRNA synthesis was induced overnight at 37°C. The following day, synchronized worms at the L1 stage were added to RNAi plates (100 - 200 larvae/well) that had been pre-cooled to 15°C to avoid heat shock. To minimize the co-transfer of OP50 bacteria, worms were washed three times with M9 buffer prior to plating. Worms on RNAi plates were kept at 15°C until they reached the L4 stage, at which time they were heat-shocked at 37°C for 26 minutes to induce expression of CHE-1. Following heat shock, RNAi plates were shifted to 25°C and scored approximately sixteen hours later. To check for ectopic expression of the gcy-5p::gfp reporter, we used the Olympus MVX10 and Leica M205 FA dissecting microscopes. For the automated screen, the liquid cultures of RNAi bacteria were centrifuged as described above and the majority of the

supernatant was discarded by quickly inverting the 96-well plates. Bacterial pellets were resuspended by vortexing in the remaining medium and from this suspension, 10 µl was used for seeding the 48-well plates. Seeded 48-well plates were placed under the fume hood for one hour to dry the bacterial lawn. Subsequently, plates were incubated in humid chamber at 37°C overnight. The following day, seeded plates were cooled-down to 15°C before applying synchronized worm populations. If necessary, seeded 48-well plates could be stored at 4°C for maximum three days. The concentration of worm eggs or L1 larvae in M9 medium was adjusted to 100 individuals/5 µl and this volume was pipetted on each well of the RNAi plates. Worms on RNAi plates were incubated under the fume hood for five minutes to let the M9 medium be absorbed. Afterwards, worms on RNAi plates were kept in a humid chamber at 15°C until they reached the L4 stage. For the heat-shock treatment, 48-well plates were sealed in plastic bags and floated with the agar side up in a water bath at 37°C for 8 minutes. After heat shock, worms on RNAi plates were placed back into the humid chamber and kept at 25°C for approximately sixteen hours. The following day, we screened worms for ectopic gcy-5p::gfp signal using the Large Particle (LP) Sampler in combination with the BioSorter Large Particle Flow Cytometer (Union Biometrica). Before BioSorter analysis, RNAi plates were incubated at 4°C for one hour to immobilize worms and straighten their body. This step eliminates artifacts during fluorescence acquisition caused by worm bending and clustering. The LP sampler aspirated worms from each well of the 48-well plates containing solid RNAi media. Worms were individually passed through the BioSorter system. Measurement of axial length and optical density allowed exclusion of young animals from the analysis. Worms were scored positive based on the GFP profile along the body length. Red fluorescence was used to subtract the autofluorescent background of worms. We used FlowPilot software for the BioSorter screen and data analysis. Subsequent data processing was performed using Excel.

Antibody Staining

Antibody staining was performed using a freeze-crack protocol on whole worms (Duerr 2006; Hadwiger *et al.* 2010) (Duerr, 2006). After washing worms were placed between two SuperFrost Plus slides and frozen on dry ice for 30 minutes. Worms were cracked by quickly breaking up the slides and immersed in PFA or ice-cold methanol for 5 minutes at RT. After washing once in PBS, worms were incubated for

30 minutes in blocking solution (1x PBS, 0.25% Triton X-100, 0.2% Gelatine, 0.04% NaN3, ddH2O) at 25°C. Primary antibody incubations were performed at 4°C for 4 h – 12h and secondary antibody incubations for 2 h at room temperature. Primary and secondary antibodies were diluted in PGT (1x PBS, 0.25% Triton X-100, 0.1% Gelatine, 0.04% NaN3, ddH2O). After washing off the secondary antibodies, worms were mounted on glass microscopy slides in DAPI-containing mounting media.

Histone modifications were detected with rabbit polyclonal anti-H3K27me3 antibody (Cat.# 07-449, Milipore), rabbit polyclonal anti-H3K9me3 (Cat.# ab8898, Abcam) rabbit polyclonal anti-H3K4me3 (Cat.# ab8580, Abcam), rabbit polyclonal anti-H3K9ac (Cat.# ab4441, Abcam), rabbit monoclonal anti-H3K14ac (Cat.# ab52946), and mouse monoclonal anti-H3K36me2 (gift from Dr. Hiroshi Kimura; Graduate School of Frontier Biosciences Osaka University). We co-stained with monoclonal guinea pig anti-LIN-53 (Pineda). All primary antibodies were diluted at 1:200.

Secondary antibodies were AlexaFlour488 Goat Anti-Guinea Pig (Cat.# A11073, Mol Probes), AlexaFlour568 Goat Anti-Rabbit (Cat.# A21069, Mol. Probes), and AlexaFlour488 Goat Anti-rabbit (Cat.# A11070, Mol. Probes, All secondary antibodies were diluted at 1:1500.

Single molecule fluorescent in situ hybridizations (smFISH)

smFISH probes against *gcy-5, ceh-36, rab-3, unc-199,* and *unc-10* transcripts were custom ordered from Stellaris and used according to the manual provided by Stellaris for hybridizing FISH probes. smFISH probe set sequences:

gcy-5

catteggatgeteeaagaae; caatteeaactegaagegte; caattggaagagtteeacea; tategeatteggtatattee; teeeactaeaacatetaeat; tattggtateageeaactgg; tgeeaetegateaaattgga; tttaeagtagtettggtegt; ettaaggttgeeteaacate; ateegeaetggatatagate; egatettgttaatgeeteat; taegagetegaetetttaea; ggaecaetaattgegeataa; eeaataeteeteattgteaa; tettteeeaaaettgtttgt; tggagttagteeatttgeaa; etaetgtgaatgaeteeeaa; atttetaaeageateegeaa; tgeeateeegtataagtaaa; tagtaaeeatttgeggeata; geggtagagattttgaeeaa; teatgttaaetagtgeeaet; eegtgaeaattgegaagaeg; egtttttetttttgtggeat; gtgatettegaetatttgge; aettteteeggttatagttg; getatgatgttggtggtta; attteteettettetta; ggteeategatagataatee; gatateetgaagtgateete; aaagtteataeeetetgeaa; ggeaagtagetgaaegtaga; eteeeaateegaaatetgtt; tacgattteeteettttte; aagtattaacteeggtegga; aettgeaaatttgeteaget; gttetgeaacttgttttgga; tetecaattgatteeaett; tgteggtaaceeagaaacae; ggaacettgaagetettaea; geceaetattaatteeaatt; atggatagaeeaaegaeaec; gtateeceaaataggeaata; ttteeattaettteeattet; tgtgeagettetgaeatag; teteetettgaacttgttte; tgttteeattaeaeetttte; gattttgtgteaetgteagt;

ceh-36

gtgtagaagttggtggtcat; ggataagcagtgtagccgag; tgcggcagcaaatgcaaatt; atgtaagactgggtgccgtg; cattgtcgttgagcttgtgg; ttcactgtttggagccattg; ctctgttgaacgaggtacgt; ttttccagctgatcgagttg; gatactgtgtttcgcggaaa; gcttctcttctgtgcacatc; caaattgattgccttcgcca; ttacttgtacccttccatca; cgatttttgaaccaaaccgt; gttgtttctatccttggctc; gatggactccatccattttt; gatcttgatgaagtgcttcc; cgttgtgtggagaaccattg; gtgatttagtatcaggcttt; tgtgcctggtatgtgaattc; cactgtgtgcattgaattcc; gagtttgcctcatatttggc; ttgcagttgactcaagactg; agtcctccagttcacttttt; atttggtatctgcaagtggt; cttgagcctgaggaagaagt; agttgcgtaggatgcatatg; tagttgtacgggtaaggagc; gtttgatgggaagtagctgt; tgcttccatattgttggtag; aggcagtaatatttggggtg;

rab-3

caaagttetgategggttgt; atcaggagettgaacatgta; tecaaetgatgaattteega; cateaeagtaaeggaagagg; gtagagaegaaggeagaagt; caetttgaaategatteega; tttgteteeaeggaaeaeaeg; ggtateeeagatttgaagtt; gatagtaggeggtggtgatg; cagaatgaateeeattgete; actetteattagtgatgtea;geaeeaateetgaaeaetat; ttteeeatgagtatgtettg; eeaaeeaaaaeaeettgage; tteagagteeatateaeatt; ceettaeataagataeaaet; aagttgateageaagttgge; ggetgatgtttegaagaatt; cetttaeattaatgttetee; teteeaeeaaetteteaaaa; tetgeeatettateaeaat; etgtgggteettateeaaae; ttegagettetgteetttg; aattgeeattgeagea; attgegtttggaatttggga; agagetaegegettttagaa; cetagatgttgagagaggga; tttaegateeatatatetgg; taattaaaeeaaetaegeee; ggggaatatgattgaaeggt; getetgggaattgtttggaa; ggegaetatgattagttaga; tgggaaetgggaagteaeta; aateaatettteageggtg; eetegaaaataattteetee

unc-10

taaatccggcatcatcgacg; ttcacgttcttctgcagata; ccgtgatctgtttgtctaac;

27

agatttgacagategegtea; caatteegteegeaaatttg; cagattgeettatttttget; gattttgacteattggetgt; catatteegattgtggetet; tttgteetttgttggttttg; aggegtttgttteatagtte; tettgttgteeatgttgatt; attetetetattetgttgt; teteggaattteeagtgtag; ggttgttttggttetgatte; ggtteaaatggtegteagta; tegaagttgeetatgeaate; egagtttttatgategeeat; atggtgacaaggacagegat; eeetgtteeaaaatgateat; tggetgeagaatttteagtt; gtaatgaatgeaeegagettg; atgtggeattttgeagagae; ttgeagegatgetateatat; gaataegeegagatgaeat; gatggatatgeagatggeae; ggetgattgtgaatgtggta; gatgtegaaegattgegtga; gageaaetgagagttgtega; aaaetggeatgatgtetet; ggtteagtaaggeeattata; tegtaateeeagaeagttag; gteatttggggeaagatgat; tegtegtegteaatgtatte; atgatagatggtageetg; tgttggategtaeatateet; teeateaetataatateeet; eattgtagttggeatgetat; aaaettttetttegeteett; eeteagatetageaaaaeeg; gtgageegatetgaagaeaa; ettgetteagaaagggagga; geaaaettgetgageg; aageaettgaegaeegaeaa; ettttaeatagggagetgga; tttggeaatgeattgttge; tteeataegaeegtaateae; tttgegaaateeceatgaat; cagtttataeeaceetata;

unc-119

cgatcgattgttgttgttgt; catctgagacgggaaggttg; gttatagcctgttcggttac; tgatttttcgcgagaagctc; agagctagcacatcatttgg; gcataggaatccttgagtga; ttatagacgtttgccgatgg; cgaggtcacggatttggaat; gcaatttcgaagagcacgtg; attctcttccgtctcatttt; gatatcggacatatcttgcc; aatgtgtgatcggcacatcg; aagtgccgttcaatcattcg; gcatttcaataaacgatcct; ggcatacagaatccaaattc; tgttcacagttgtttctcga; gttgttgtgaaagttgtgga; attattgatcatgtcgtcca; aatagaagctatcggagcgg; gtgcattacgagcttattct; tgcatcatacgagtagtcgg ;

Western Blot

Control and *mrg-1* RNAi treated worms were washed off, collected in SDS/PAGE Sample buffer and frozen at -20°C. Immediately before loading, samples were boiled for 10 minutes and centrifuged. Histone modifications were detected with rabbit polyclonal anti-H3K27me3 antibody (Cat.# 07-449, Milipore) at a dilution of 1:1000, rabbit polyclonal anti-H3K9me3 (Cat.# ab8898, Abcam) at 1:1000, rabbit polyclonal anti-H3K4me3 (Cat.# ab8580, Abcam) at 1:1000, rabbit polyclonal anti-H3K9ac (Cat.# ab4441, Abcam) at 1:500, and rabbit monoclonal anti-H3K14ac (Cat.# ab52946) at 1:2000.

As a standard loading control, we used the rabbit polyclonal anti-histone 3 (Cat.

#ab1791, Abcam) at 1:5000 dilution and the secondary anti-mouse HRP antibody (Cat.#sc-2005, Santa Cruz) at 1:5.000 dilution or anti-rabbit HRP antibody (Cat.#sc-2357, Santa Cruz). The Lumi Light detection kit (Roche) and the ImageQuant LAS4000 system (GE Healthcare Life Sciences) were used for the signal detection.

Generation of CRISPR alleles. CRISPR engineering was performed by microinjection using a PCR repair template containing the 3xHA tag sequence. The injection mix contained Cas9 protein $(0,3mg/\mu l)$, as well as a crRNA targeting *mrg-1* (100ng/ μ l). Overall, we used a recently described procedure (Dokshin *et al.* 2018). Sequences of the crRNA are: 5'GGATCTCTCGCCGCCGACGA3', 5'GTTCGCTCCAACTCCGTCGT3'.

Immunoprecipitations coupled with Mass Spectrometry (IP-MS)

Each immunoprecipitation was performed in triplicate. L4 staged wild type and mrg-1::3xHA^{CRISPR} worms were collected by M9 buffer, washed 4 times with M9 to get rid of bacteria and concentrated into worm pellet after the last wash. The worms were added into liquid nitrogen, drop-by-drop by paying attention that the resulting "worm beads" did not exceed size of a black pepper to achieve even grinding afterwards. The frozen worms were then cryo-fractured by using a pulverizer. In order to obtain a fine powder, worms were further ground using a mortar and pestle on dry ice. The worm powder was resuspended in 1.5x of lysis buffer (20mM Hepes pH 7.4, 150mM NaCl, 2mM MgCl2, 0.1% Tween20 and protease inhibitors), dounced with tight douncer 30 times and sonicated using a Biorupter (6 times 30 sec ON, 30 sec OFF; high settings) followed by centrifugation at 16,000g at 4°C for 10 min. The supernatant was removed to 2 mL Eppendorf tubes and incubated with following antibodies: N2 lysates with anti-MRG-1 (Novus) or with preimmune serum for control samples; mrg-1::3xHA^{CRISPR} and N2 lysates (negative control) with HA antibodies (Roche) for 30 min on a rotator at 4°C. Next, µMACS ProteinA beads (Milteny Biotec) were added into samples as instructed in the kit and samples were incubated for 30 min at 4°C rotating. Meanwhile, the µMACS columns were placed to magnetic separator to be equilibrated and ready for sample application. Samples were diluted 5x of their volume with lysis buffer before being applied to columns and the columns with bound proteins were washed 3 times with lysis buffer to remove background binders. The proteins were eluted with elution buffer (100mM TrisCl pH 6.8, 4 % SDS, 20mM

DTT) heated at 95°C. Eluted samples were prepared for mass spec measurements by using SP3 (Hughes et al. 2014) before they were analyzed on a Q Exactive Plus (Thermo Scientific) connected to a Proxeon HPLC system (Thermo Scientific). Label-free quantification (LFQ) was performed using Max Quant as described below.

IP-MS Analysis

The raw mass spectrometry data was first analyzed using MaxQuant Software {Cox and Mann:2008; Nature Biotechnology} and the resulting "proteinGroups.txt" was then processed using the Bioconductor R package DEP v1.0.1 following the section "Differential of the vignette (https://bioconductor.org/packages/ analysis" release/bioc/vignettes/DEP/inst/doc/DEP.html#differential-analysis, version from 17 November 2017) with minor adjustments. First we set the random seed to the number 123 in order to receive reproducible results and then we followed the paragraphs on "Loading of the Data" and "Data Preparation" of the vignette to create our raw protein table. Then we extracted the associated UniProt IDs from the raw protein table and queried them on the UniProt ID mapping tool (http://www.uniprot.org/uploadlists/) to generate a mapping from "UniProtKB AC/ID" to "Gene name", which was downloaded as a mapping table in tsv format. The unmapped IDs were manually curated by a search in the UniProt Knowledgebase (UniProtKB) and then appended to the mapping table. This mapping table was loaded into R, were we first removed all rows of the table containing duplicated UniProt IDs, next we created unique gene names by appending to each duplicated gene name its number of occurrence separated by a dot, then we merged the raw protein table with the mapping table based on ID and UniProt ID respectively while keeping all rows of the raw protein table and updated those entries in the names column where a gene name was available in the mapping table. Next we loaded the table specifying the experimental design of the IP-MS analysis {table experimentDesign}, followed the instructions of the paragraph "Generate a SummarizedExperiment object" and "Filter on missing values", where we decided to performed the less stringent filtering approach to keep those proteins that are identified in 2 out of 3 replicates of at least one condition. Then we performed the steps described in the "Normalization" and imputed the missing data using random draws from a manually defined left-shifted Gaussian distribution with a shift of 1.8 and a scale of 0.3 as proposed in the "Impute data for missing values" paragraph. Next we followed the paragraph "Differential

enrichment analysis" to identify proteins being significantly enriched in comparison to the control coIP with a minimum log2 fold change of 2 plus t-test with an adjusted p-value (*alpha*) below 0.05 (see Table S5).

ChIP-seq

The ChIP experiment was carried out as previously described (Seelk et al. 2016). In brief, worms (wt and *glp-4(bn2)*) at L4 stage were washed off plates using M9 buffer and flash-frozen as "worm popcorn" in liquid nitrogen. The popcorn was pulverized using a biopulverizer before further grinding to a fine powder using a mortar. The powder was dissolved in 10 vol 1,1 % formaldehyde in PBS+1 mM PMSF and fixed for 10 min with gentle rocking. Quenching was achieved by adding 2,5 M Glycine to a final concentration of 125 mM and gently rocking for 5 min. After centrifugation the pellet was washed with ice-cold PBS+1 mM PMSF, before it was resuspended in FA-buffer (50 mM HEPES/KOH pH 7,5, 1mM EDTA, 1% Triton X-100, 0,1 % sodium deoxycholate, 150 mM NaCl) + 1 % Sarkosyl + protease inhibitor and sonicated twice using a Bioruptor (15 times, 15 sec ON, 15 sec OFF; high settings) followed by 15 min centrifugation at full speed, 4°C. The supernatant was taken off (approx. 2-4 mg protein) and incubated either with MRG-1 antibody (Novus) or with buffer ON at 4°C on a rotator. Next, samples were incubated with µMACS ProteinA beads (Milteny Biotec) for 1 h on ice before they were applied to µMACS magnetic M columns that were equilibrated using FA buffer. The columns with bound material were washed 2x using FA buffer followed by washing with FA buffer + 1 mM NaCl and FA buffer + 500 mM NaCl. After further washing with TEL buffer (0,25 mM LiCl, 1 % sodium deoxycholate, 1 mM EDTA) and 2x with TE buffer, the samples were eluted using elution buffer (1 % SDS, 250 mM NaCl, 10 mM Tris pH 8,0, 1mM EDTA). The fixation was reverse crosslinked using 2 µl of 10 mg/ml Proteinase K at 50°C for 1 h followed by incubation at 65°C ON. The DNA was purified using the QIAquick PCR purification kit in a final volume of 40 µl. The DNA concentration was measured using Qubit dsDNA HS assay kit and libraries were prepared using the NEXTflex qCHIP-Seq v2 kit according to manufacturer's instructions. After measuring the DNA quality using Bioanalyzer DNA1000 kit and Qubit dsDNA HS Assay, sequencing was carried out at a HighSeq4000 as paired end sequencing 2x75 bp.

ChIP-seq Analysis

Alignment. ChIP-seq reads were mapped using bowtie2 v2.3.2 (Langmead and Salzberg 2012) in paired end mode with default settings (-D 15 -R 2 -N 0 -L 22 -i S,1,1.15) and allowing up to one alignment per read (-k 1) to version ce10 of the worm genome. Resulting Alignment files were converted from SAM to BAM format, sorted and indexed using samtools v1.5. Additional BigWig tracks were generated from the alignment files using bedtools bamtobed v2.25.0 (Quinlan and Hall 2010) and an in-house R script.

Peak Calling and Differential Analysis. Peaks were called for each replicate of both conditions ("glp-4" an wt) using the MACS v2.1.0.20151222 (Zhang *et al.* 2008) module callpeak with genome size set to the worm genome, skipping of model building process and extension of reads in 5' to 3' direction to 300 base pairs (-g ce - keep-dup auto -q 0.05 - nomodel -extsize 300).

The resulting peaks were than analysed using the Bioconductor R package DiffBind v2.66 following the section "Example: Obtaining differentially bound sites" of its vignette (http://bioconductor.org/packages/release/bioc/vignettes/DiffBind/ inst/doc/DiffBind.pdf, Edited: March 27, 2017; Compiled: January 19, 2018). Within R we defined a sample sheet with a similar structure as the example and used the dba() function to load all peaks, count the total number of unique peaks after merging overlapping ones (8226) and the total number of peaks that overlap in at least two of the samples (6723). Then we calculated a binding matrix with scores based on read counts for every sample using the dba.count() function with the summit argument set to 250, leading to centering of the peaks at their point of highest enrichment (summit) and extending them 250bp up- and downstream from there. Next we established the contrast based on the tissue metadata and performed the differential analysis to detect significantly differentially bound peaks with a minimum fold change of 1 and a maximum adjusted p-value of 0.05 (1183).

Gene Annotation. The peaks identified by MACS were annotated by overlapping with the ENSEMBL assembly annotation WBcel215 version 70. The gene tables S4 and S5 were defined by deriving the set of unique gene names of all overlapping genes.

Correlation with Histone Modifications. Wiggle signal data files created from ChIPseq experiments were downloaded for a selection of Histone modifications, that shared experimental conditions, from modEncode database (Gerstein *et al.* 2010). The tool CrossMap v0.2.1 (Zhao *et al.* 2013) was used to perform a liftOver of the wiggle tracks from assembly ce6 to assembly ce10 and exporting to BigWig format on the fly. The module multiBigwigSummary of the software deepTools v2.5.1 (Ramírez *et al.* 2016) was used to calculate the average score for equally sized bins of 10 kb size covering the whole genome for all BigWig tracks of the histone modifications and the BigWig tracks of the wt MRG-1 ChIP-seq alignment. The resulting matrix was then used to calculate the Spearman correlation between the histone modifications and the binding profile of MRG-1 (Figure S7 A).

MRG-1 ChIP-seq Peak Heatmaps. The heatmaps were prepared and plotted using the Bioconductor R package genomation v1.10.0 (Akalin et al. 2015). To define the rows of our heatmap we took the summit centered peaks, fixed the center point and extended them to a total length of 4000bp. Then we used the function ScoreMatrixList() from genomation to create a matrix (ScoreMatrix) for every sample, where we have m rows for m being the number of peaks and n columns for n = 50. The columns are constructed by subsetting every peak into n bins of equal width and calculating the average read count per million (rpm) per bin from the respective BAM files of the sample. Because the scores per row can have a high dynamic range, it is sometimes convenient to scale the matrix before plotting, so we scale and center each matrix using the function scaleScoreMatrixList(). This procedure was performed for all peaks that overlap in at least two of the samples (6723), for all significantly differentially bound ChIP-seq peaks between N2 and glp-4(bn2) background with FDR < 0.05 (1183) and for all differentially bound ChIP-seq peaks between N2 and glp-4(bn2) background with FDR < 0.05 and fold change >2 (409) to create Figureures S6 A,B and C respectively.

Histone Modifications Peak Heatmap. For the peak heatmaps of the modEncodebased histone modifications we created a ScoreMatrixList (explained above) with n =400 bins with the score calculated from the BigWig signal tracks. The "soma + germline" heatmap was based on all peaks that overlap in at least two of the N2 samples (5141) and the "germline specific" heatmap is based on all those peaks which were only identified in N2 background but not in *glp-4(bn2)* background (521). *Meta Region Profile*. The meta region profile of the modEncode-based histone modifications was acquired by plotting the ScoreMatrixList in a histogram representation to show the column-wise average of the centered and scaled ScoreMatrix.

Heatmap of Meta Region Profile. The heat map of the meat region profile represents a set of meta region profiles as a stack of heatmaps.

Genome Browser Shot. The Genome Browser view shows the region " chr10:117,922,301-119,587,630" of the ce10 genome assembly and was created using the Bioconductor R package Gviz (Hahne and Ivanek 2016).

Microscopy

Worms were mounted on freshly made 2% agarose pads for fluorescence and Nomarski imaging. 10 mM tetramizole hydrochloride (2,3,3,6 tetrahydro-6-phenylimidasol) in M9 buffer was used to anesthetize animals. Microscopy analyses were performed using the Axio Imager.M2 (Zeiss) equipped with a sensitive CCD camera (Sensicam qe, PCO Imaging). MicroManager was used for image acquisition and processing (Edelstein *et al.* 2010; 2014).

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Supplemental Figures

Figure S1 RNAi library and comparison of liquid vs. solid media RNAi
Figure S2 Automated solid media-based RNAi screening.
Figure S3 Controls for *mrg-1* RNAi and smFISH.
Figure S4 Controls for reprogramming and anti-MRG-1/LIN-53 immunostainings.
Figure S5 MRG-1 ChIP-seq heatmaps
Figure S6 MRG-1 binding correlation with specific histone modifications sites

Figure S7 MRG-1 immunoprecipitations coupled to mass spectrometry (IP-MS)

Supplemental Tables

Table S1 Chromatin 2.0 Sub-library. This table lists all RNAi clones in the Chromatin 2.0 library. Color coding is according to functional groups of proteins. Source of clones indicated and explained at the end of the table.

Table S2 Efficiency of worm recovery from individual plates by the LP sampler. Strains expressing different levels of *gfp* in the neurons were mixed according to indicated numbers. *gcy-5p::gfp* is expressed in only one neuron while *unc-119p::gfp* is expressed in all neurons. Aspirated worms were analyzed by the BioSorter.

Table S3 ChIP-seq results. Genes assigned to MRG-1 binding sites from all ChIP-seq

 experiment (pooled triplicates) backgrounds.

Table S4 Correlation of MRG-1 ChIP-seq peaks with histone modifications. Genes bound by MRG-1 (ChIP-seq peaks) in WT and *glp-4(bn2)* background that also carry H3K27me3 and H3K9me3 based on modEncode datasets

Table S5 Enriched proteins from IP-MS. Spectral values of all proteins enriched by MRG-1 IP-MS from WT, *glp-4(bn2)* and *mrg-1::3xHA*^{CRISPR} backgrounds.



Figure S1 Chromatin RNAi library and liquid vs. solid media RNAi efficiency.

(A) A detailed breakdown of the targeted factors by the Chromatin RNAi sub-library 2.0 showing that targeted chromatin regulating factors are implicated in a variety of different biological processes. The Chromatin 2.0 sub-library was assembled based on a previously published incomplete collection as described in Tursun et al., 2011. Previously missing clones (82) were generated and added (Table S1). All clones of the Chromatin 2.0 sub-library have been checked by sequencing, corrected and complemented. (B) RNAi against *lin-53* in liquid worm cultures results in a 50% GeCo decrease compared to solid media RNAi. Numbers of animals (n) quantified per condition are indicated below each column. Error bars represent SEM. One-way ANOVA: p1=0.022; p2=0.032.

Α

В

Automated RNAi Screen with LP Sampler + BioSorter **BioSorter** wild-type worm Direct Signa uptake from LP sampler solid NGM Worm length/shape laser Signal RNAi on solid medium in 48-well plate positive worm GFP in head 54. 12 54. 12 56 1 GFP in tail H= Rote 3828 H= Rote 382 R= Rote 382 R= Rote 128 R= Rote 1964 . 14 114 84 11 16 0.4 2200 16 0.4 102 16 0.4 102 16 0.4 102 Signal threshold Min. Time of Flight 375.0 (2) eV 100 (2) 12µ0 GFP in head Edincte Green Yellow East 700 0 400 0 re RNAi bact -well LB and RNAi plate on 6- or 48-w or 48-agar all 37°C n of ch and the second states of the Primary Automated RNAi screen Secondary Manual RNAi screen

Figure S2. Automated solid media-based RNAi screening.

RNAi on solid r in 48-well p

(A) A solid media-based automated RNAi screening system by combining the BioSorter (UnionBiometrica) with a robotic large-particle sampling system (LP sampler, Union Biometrica). The LP sampler collects worms from solid RNAi medium by repeated flushing and aspiration followed by fluorescence-intensity

scanning in the BioSorter. Screenshot of the BioSorter software after scanning for GFP signal intensity (Green peak height) of mixed worm strains either expressing the pan-neuronal reporter *unc-119p::gfp* or the ASE-specific *gcy-5p::gfp* is shown. Each dot in the scatter plot represents a single worm. The fluorometric analysis reveals worms with high GFP signals (green dashed box, *unc-119p::gfp*) versus low (red stippled box, gcy-5p::gfp). The peaks of the green curve reflect GFP intensities along the body axis (blue) of individual worms. Detailed analysis of aspiration and sorting efficiency is shown in S3 Table. Scale bars = $20 \mu m$. (B) Workflow of the automated and manual P0 RNAi screens. The MultidropTM dispenser (Thermo Scientific) is used to prepare LB cultures in 96-deep-well plates and to automatically pour either 6-, 12-, or 48-well RNAi plates. RNAi clones are picked from the 96-well format of the frozen library into the 96-deep-well LB cultures and grown overnight. Concentrated bacteria are seeded on the multi-well RNAi plates where dsRNA synthesis is induced at 37°C overnight. A synchronized worm population (L1 larvae) of a strain carrying *hsp::che-1* and *gcy-5p::gfp* transgenes is applied on seeded RNAi plates. Worms are kept on RNAi plates at 15°C until they reach the L4 larval stage and ubiquitous expression of CHE-1 is induced by heat-shock. Screening for ectopic gcy-5p::gfp expression using the BioSorter Large Particle Flow Cytometer (Union Biometrica) is performed within 16-24 hours after heat-shock treatment by aspiration from the 48well RNAi plates with the Large Particle Sampler. A secondary screen to confirm phenotypes is performed using a fluorescent microscope.





Figure S3. Controls for mrg-1 RNAi and smFISH.

(A) RNAi against *mrg-1* without overexpression of che-1 does not lead to ectopic induction of the neuronal reporter. Scale bars = 20 μ m. (B) Antibody staining for germline-specific P Granules upon *mrg-1* RNAi but without *che-1* overexpression. Scale bars = 5 μ m. (C-D) Quantification of smFISH detections based on counts of hybridization signals (red dots) of (C) endogenous ASER neurons and (D) ventral nerve cord neurons, which do not show expression of the ASE neuron-specific genes *gcy-5* and *ceh-36*. For each condition 20 cells were counted for smFISH-derived transcript detection based on fluorescence signals. p-values based on ANOVA with

Dunnett's multiple comparison test: p1 = 0,0001; p2 = 0,0001; p3 = 0,0001; p4 = 0,0001; p5 = 0,0001; p6 = 0,999; p7 = 0,999; p8 = 0,0001; p9 = 0,0001; p10 = 0,0001. (D) Control for expression of neuronal gene expression by smFISH in germ cells Upon *che-1* overexpression without any RNAi depletion no transcripts of the tested genes can be detected in germ cells. Scale bars = 5 µm.

Figure S4

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Figure S4. Controls for reprogramming and anti-MRG-1/LIN-53 immunostainings. (A) Worms co-expressing together with the ASE neuron fate reporter gcy-5p::gfp reporters for different neuronal identities: glr-1p::rfp (inter neurons), ttx-3p::rfp (cholinergic inter neuron), and ttr-39p::rfp (GABAergic neurons) were tested. Upon germ cell reprogramming by *che*-1 overexpression and *mrg*-1 RNAi no other reporter besides gcy-5p::gfp can be detected in the gonad. Scale bars = 10 µm. (B) Young adult hermaphrodite was co-stained using anti-MRG-1 and anti-LIN-53 antibody.

Figure S5



Figure S5. MRG-1 ChIP-seq heatmaps.

(A) Read counts at highest significant ChIP-seq peaks. Only peaks found in at least two replicates are shown. (B) Heatmap of differential ChIP-seq peaks between N2 and *glp-4(bn2)* background with FDR < 0.05. (C) Heatmap of differential ChIP-seq peaks between N2 and *glp-4(bn2)* background with FDR < 0.05 and fold change >2.







Figure S7





Table S1. Chromatin 2.0 Sub-library

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Plate	Position	Origin	Seq. name	Gene name	Characterization	Category	Domain
MH1	A1	96AL_2A01	F47G6.1	dyb-1	alpha-dystrobrevin	Others	coiled-coil, Zn finger
MH1	AZ	96AL_1A12	153612.5	mex-3	KH domain-containing KNA binding proteins	KNA binding	KH
MH1	A3	96AL 3B10	T28F2.4	imiC-1	copurified with chromatin	chromatin binding	JmiC
MH1	A4	96AL_1C09	R119.6	taf-4	Isoform 1 of Transcription initiation factor TFIID	transcription regulation	
					Isoform A of Protein SON. RNA-binding protein that acts as a mRNA splicing cofactor by		
MH1	A5	96AL_3C03	D1037.1		promoting efficient splicing of transcripts that possess weak splice sites.	RNA binding/ splicing	G-patch
MH1	46	9641 1006	E56A6 1	\$990-7	Argonaute homolog that is partially required for the amplification phase of RNAi responses	RNAi machineny	
IVIIII	AU	JOAL_1000	15040.1	Sugo-2	SET domain-containing protein that is most closely related to the ASH1 group of histone-	invarinderintery	
					lysine N-methyltransferases; Essential protein required to maintain expression of homeotic		
					genes egl-5 and mab-5. May play an analogous role to the trithorax Group (trxG) proteins.		AWS, SET, PHD-type, Zn
MH1	A7	96AL_3D03	T12F5.4	lin-59	Histone methyltransferase	histone modification; DNA methylation	finger
MH1	A8	96AI 4D12	C18F3.7	nnw-1	germline.	RNAi machinery	PA7/PIWI
				<i>pp</i> =	encodes an ortholog of human ACIN1 (OMIM:604562, which induces apoptotic chromatin		
MH1	A9	96AL_4E03	C43E11.1	acin-1	condensation)	NA binding	
					histone methyltransferase; met-1 is required for normal levels of histone H3K36 and H3K9		
MH1	A10	96AL_4E05	C43E11.3	met-1	trimethylation	histone modification; DNA methylation	SET
MH1	AII	96AL_4E12	C43E11.10	сас-ь	origin complex component (CDC6), AT nook	DNA binding	AT NOOK
					Part of the Wnt signaling pathway. HMG box-containing protein that is the sole C. elegans		
MU1	A17	0641 2502	W/10C9 2	non 1	member of the TCF/LEF family of transcription factors; Represses expression of target genes	transcription regulation	HMC box
IVITI	A12	50AL_2102	W10C0.2	<i>pop-1</i>	wants interaction with hoars instone deacetylase.		
MH1	R1	96A1 4F04	C43E11 1	acin-1	encodes an ortholog of human ACIN1 (UMIM:604562, Which induces apoptotic chromatin condensation)	NA binding	
MH1	B2	96AL_2G09	C45E1.4	dem 1	condensationy	others	
		-			Ubiquitin-like protein which can be covalently attached to target lysines as a monomer.		
					Does not seem to be involved in protein degradation and may function as an antagonist of		
					ubiquitin in the degradation process. Plays a role in a number of cellular processes such as		
MH1	B3	96AL_1H07	K12C11.2	smo-1	nuclear transport, DNA replication and repair, mitosis and signal transduction.	ubiquitin machinery	Ubiquitin-like
MH1	B4	96AL 1H09	K12C11.4	dank-1	death-associated protein (DAP) kinase	protein kinase	repeats
MH1	B5	96AL_6A02	F54C1.3	mes-3	member of a Polycomb-like chromatin repressive complex that acts via H3K27 methylation	histone modification; DNA methylation	
MH1	B6	96AL_7A04	T05E8.2	his-8	histone H2B	chromatin/nucleosome structure	
MH1	B7	Supp V-14J8	Y59A8A.2	phf-14	PHD finger family	chromatin binding	PHD finger, Zn finger
MU1	DO	Clanad	COEAE 2		PSIP1 protein ortholog	protein-protein interactions	PWWP domain (Pro-Trp-Trp- Pro motif)
WITT	во	cioneu	C00A3.3		Isoform 1 of Structure-specific endopuclease subunit SIX1. Catalytic subunit of a	protein-protein interactions	TTO MOLITY
					heterodimeric structure-specific endonuclease subdinic SLAT. Catalytic subdinic of a		
MH1	B9	96AL_6D02	F56A3.2	slx-1	generated during DNA repair and recombination.	chromatin structure (nucleases)	SLX1-type Zn finger, GIY-YIG
MH1	B10	96AL_6D09	all his-1 (his-2, his-	5, his-6, his-24)	H4 histone, coded by histone gene cluster HIS1	chromatin/nucleosome structure	
							ARID (AT-rich interaction)
MH1	811	96AL_6E09	C01G8.9	let-526	component of the SWI/SNF complex	DNA binding	domain ARID (AT-rich interaction)
MH1	B12	96AL 6E10	C01G8.8/C01G8.9	let-526	component of the SWI/SNF complex	DNA binding	domain
							N-acetyltransferase; helicase
							· · · ·
MH1	C1	96AL_6G02	F55A12.8	nath-10	N-acetyltransferase 10 homolog	histone modification; DNA methylation	and tRNA binding domain
MH1 MH1	C1	96AL_6G02	F55A12.8	nath-10 lin-35	N-acetyltransferase 10 homolog	histone modification; DNA methylation	and tRNA binding domain Retinoblastoma-associated
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog. HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex atts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and deventioned the dimensioned even histone 1014 UDP, finase for the	histone modification; DNA methylation Others	and tRÌNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2	96AL_6G02 96AL_7G08	F55A12.8 C32F10.2	nath-10 lin-35	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome the subenument promotes the recetabilishment of the nucleosome following	histone modification; DNA methylation Others	and tRNA binding domain Retinoblastoma-associated protein A/B domain
MH1 MH1	C1 C2 C3	96AL_6G02 96AL_7G08 96AL_7G10	F55A12.8 C32F10.2 C32F10.5	nath-10 lin-35 hmg-3	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome flowing the passage of RNA polymerase. II. Binds specifically to double-stranded DNA	histone modification; DNA methylation Others DNA binding	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain
MH1 MH1	C1 C2 C3	96AL_6G02 96AL_7G08 96AL_7G10	F55A12.8 C32F10.2 C32F10.5	nath-10 lin-35 hmg-3	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA	histone modification; DNA methylation Others DNA binding	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes
MH1 MH1 MH1 MH1	C1 C2 C3 C4	96AL_6G02 96AL_7G08 96AL_7G10 96AL_11A02	F55A12.8 C32F10.2 C32F10.5 F22D6.6	nath-10 lin-35 hmg-3 ekl-1	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Krs-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin)	histone modification; DNA methylation Others DNA binding histone binding	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones)
MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6	96AL_6G02 96AL_7G08 96AL_7G10 96AL_11A02 96AL_11A102	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D3200	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wrf-12	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor	histone modification; DNA methylation Others DNA binding histone binding transcription regulation	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones)
MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6	96AL_6G02 96AL_7G08 96AL_7G10 96AL_11A02 96AL_11A11 96AL_12B03	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K10D3.3 D2030.9	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats
MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7	96AL_6G02 96AL_7G08 96AL_7G10 96AL_11A02 96AL_11A11 96AL_12B03 AL I-3D18	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin, putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats
MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8	96AL_6602 96AL_7608 96AL_7610 96AL_711402 96AL_111402 96AL_112803 AL I-3D18 96AL_9204	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 S20F0.6	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality, RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein 32: DDB1- and CUI-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions RNA machinery RNA machinery	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10	96AL_6602 96AL_7608 96AL_7610 96AL_1402 96AL_11402 96AL_1203 AL I-1203 96AL_9204 96AL_9204	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C0146.7	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 gno-2	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the resetablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein 2: DDB1- and CUI4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase Phosphoglucosamine acetyltransferase	histone modification; DNA methylation Others DNA binding bistone binding transcription regulation protein-protein interactions RNAi machinery bistone modification; DNA methylation comparison	and RNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11	96AL_6602 96AL_7608 96AL_7610 96AL_17610 96AL_11A02 96AL_12803 AL I-3D18 96AL_12C03 96AL_12C03 96AL_11C08	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K10D3.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.7	nath-10 lin-35 hmg-3 ekl-1 taf-11.2 wdr-23 ego-1 gno-2 tag-298 = swsn-9	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SWJ/SNF nucleosome remodeling complex component homolog of Habolid germ cell-specific nuclear orotein kinave /naroin)	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions RNAI machinery RNAI machinery histone modification; DNA methylation chromatin remodelling protein inge	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C7 C8 C9 C10 C11 C12	96AL_6602 96AL_7608 96AL_7610 96AL_11A02 96AL_11A02 96AL_1203 96AL_1203 96AL_1203 96AL_1203 96AL_1203 96AL_1203	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.7 C01H6.9 T23H2.3	nath-10 lin-35 ekl-1 taf-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex, a general chromatin factor that acts to reorganize template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RTS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUU4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference SW/SNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription faction factor	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions RNAI machinery RNAI machinery Bistone modification; DNA methylation chromatin remodeling protein kinase chromatin remodeling	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12	96AL_6602 96AL_7608 96AL_7610 96AL_11A10 96AL_11A11 96AL_1203 96AL_203 96AL_1203 96AL_1203 96AL_11203 96AL_11203	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.9 T23H2.3	nath-10 lin-35 kh-1 taf-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag-	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the resetablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein 32: DDB1- and CUI4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SW/SNF nuclesome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription termination factor RNA polymerase II; helicase	histone modification; DNA methylation Others DNA binding DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery RNAi machinery protein kinase chromatin remodelling	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1	96AL_6602 96AL_7608 96AL_7610 96AL_1402 96AL_1402 96AL_1203 96AL_1203 96AL_1203 96AL_1203 96AL_1203 96AL_1203 96AL_1108 96AL_1203 96AL_1203	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.7 C01H6.7 C01H6.7 K02F2.3	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-B. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the resetablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repat-containing protein 2: DDB1- and CUI4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SWI/SNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription termination factor RNA polymerase II; helicase homolog of splicing factor 3b	histone modification; DNA methylation Others DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery histone modification; DNA methylation chromatin remodelling protein interactions splicing	and tRiAA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SINF2-related WD repeats
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1	96AL_6602 96AL_7608 96AL_7610 96AL_11A02 96AL_11A02 96AL_12803 ALI-3D18 96AL_9C04 96AL_12803 96AL_11C10 96AL_11C10 96AL_11C10 96AL_12624 96AL_1302	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K10D3.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.9 T23A2.3 K02F2.3	nath-10 lin-35 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = rmt-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203	N-acetyltransferase 10 homolog retinoblastoma protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin fractor that acts to reorganize nucleosomes. The FACT complex, a general chromatin fractor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Kar-1 Lethality: RTS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference SWI/SNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription termination factor RNA polymerase II; helicase homolog of splicing factor 3b polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H2/DON-01/K (M25 foomabilo noticing to factor in in a torscription factor recombins	histone modification; DNA methylation Others DNA binding DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery RNAi machinery chromatin remodelling protein kinase chromatin remodelling splicing splicing splicing splicing splicing	and RRA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3	96AL_6602 96AL_7608 96AL_7610 96AL_11A02 96AL_11A02 96AL_1203 96AL_1203 96AL_1203 96AL_11C10 96AL_11C10 96AL_11C10 AL I-3624 96AL_11D05	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 tag-298 = swsn-9 tag-4/phi-6/tag- 203 lin-61	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin franscription complex subunit ssrp1-8. Component of the FACT complex a general chromatin fractor that acts to reorganize nucleosomes. The FACT complex k is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex atts as a histone chaperone that both destabilities and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the restablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2: DDB1- and CUI-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosame remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog franscription termination at transcription all recognizes and binds H3K9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing protein	histone modification; DNA methylation Others DNA binding DNA binding histone binding transcription regulation protein-protein interactions RNA machinery RNA machinery RNA machinery RNA machinery splicing splicing splicing chromatin remodelling splicing chromatin remodelling splicing chromatin binding/transcription regulation chromatin remodelling splicing splic	and tRNA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD fineer
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3	96AL_6602 96AL_7608 96AL_7610 96AL_11A10 96AL_11A10 96AL_12R03 96AL_12R03 96AL_12C03 96AL_12C03 96AL_11C10 AL 1-3G19 AL 1-3G19 AL 1-3G24 96AL_11D05 AL 11D05	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 R107.2	nath-10 lin-35 eki-1 taf-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex ats as a histone chaperone that both destabilizes and restores nucleosomes. The ACT complex tasts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the resetabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein 2: DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SW/SNF nucleosome remodeling complex component homolog of palpoid germ cell-specific nuclear protein kinase (haspin) homolog transcription termination factor RNA polymerase II; helicase homolog of splicing factor 3b polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing protein	histone modification; DNA methylation Others Others DNA binding DNA binding DNA binding DNA binding Drotein-protein interactions RNA machinery RNA machinery RNA machinery RNA machinery protein kinase chromatin remodelling splicing/chromatin binding/transcription regulation chromatin remodelling splicing spli	and RRMA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD finger
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4	96AL_6602 96AL_7608 96AL_7608 96AL_11A02 96AL_11A02 96AL_11A02 96AL_12803 ALI-3D18 96AL_12803 96AL_11028 96AL_11028 96AL_11028 96AL_11028 96AL_11028	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K10D3.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.9 C01H6.9 C01H6.9 C01H6.9 C01H6.9 C01H6.9 C01H6.9 F2CH23.3 K02F2.3 R06C7.7 R107.2 F21C3.4	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex statistication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1 and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference SWJKNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription factor 3D polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me.2/8 (MBT domain); protein the germline and proyer chromosome segregation.	histone modification; DNA methylation Others Others DNA binding DNA binding ristone binding ristone binding rotein-protein interactions RNAi machinery RNAi machinery RNAi machinery splicing sp	and RRAA binding domain Retinoblastoma-associated protein A/B domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD finger
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4	96AL_6602 96AL_7608 96AL_7610 96AL_11402 96AL_11402 96AL_11402 96AL_12803 AL I-3018 96AL_12803 AL I-3612 96AL_11C08 96AL_11C08 96AL_1102 96AL_11012	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 R107.2 F21C3.4	nath-10 lin-35 ekl-1 taf-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 tag-298 = swsn-9 tag-298 = swsn-9 tag-203 lin-61 rde-2	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex, a general chromatin factor that acts to reorganize template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex ats as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RTS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SW/JSM nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription factor 3D polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me2/3 (MBT domain); predited to function in a transcriptional regulatory complex RNA iDfective, encoding nematode specific protein required for RNA interference, control of transposon transposition in the germline and proper chromosome segregation.	histone modification; DNA methylation Others Others DNA binding DNA binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery Bistone modification; DNA methylation chromatin remodelling splicing chromatin binding/transcription regulation chromatin binding RNAi machinery R	and RRA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SINF2-related WD repeats MBT repeats PHD finger
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4	96AL_6602 96AL_7610 96AL_7610 96AL_11A102 96AL_11A11 96AL_1203 96AL_1203 96AL_1203 96AL_11203 96AL_11203 96AL_11203 96AL_11203 96AL_11120 96AL_11105 96AL_11105 96AL_11105	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 R107.2 F21C3.4	nath-10 lin-35 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tog-298 = swsn-9 teg-4/phi-6/tog- 203 lin-61 rde-2 dth 3	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex ats as a histone chaperone that both destabilizes and restores nucleosomes. The ACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality, RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein 32: DDB1- and CUI4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference SW/SNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog franscription factor 3D polycomb-like protein; sito acoryte chromatin; regulates splicing; recognizes and binds H3K9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing protein RNA Diffective, encoding nematode specific protein required for RNA interference, control of transposen transposition in the germline and proper chromosome segregation.	histone modification; DNA methylation Others Others DNA binding DNA binding Divisione binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery Ristone modification; DNA methylation chromatin remodelling protein kinase chromatin remodelling chromatin binding/transcription regulation chromatin binding RNAi machinery DNA binding	and RRAA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD finger
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6	96AL_6602 96AL_7608 96AL_7608 96AL_11A02 96AL_11A02 96AL_12803 ALI-3D18 96AL_9C04 96AL_1203 96AL_11008 96AL_11008 96AL_11008 96AL_11002 96AL_11012 96AL_12012	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 R107.2 F21C3.4 D2005.5 F30F8.8	nath-10 lin-35 hmg-3 ekl-1 taf-11.2 wdr-23 ego-1 rde-3 mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2 drh-3 taf-5	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3: Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference SWUSNF nucleosome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog transcription factor 3b polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H3X9me2/8 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing nortein RNAi DEfective, encoding nematode specific protein in auranscription alterference, control of transposition in the germline and proper chromosome segregation. dicer-related helicase, required to maintain chromosome integrity and proper chromosome segregation in the germline; RITS (meiotic/germline H3K9me2 on repetitive chromatin) putative TATA binding protein associated transcription alterof	histone modification; DNA methylation Others Others DNA binding bistone binding transcription regulation protein-protein interactions RNAi machinery histone modification, DNA methylation chromatin remodeling splicing Sp	and RRMA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats SNF2-related WD repeats PHD finger
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MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 D7 D8 D9 D10	96AL_6602 96AL_7608 96AL_7608 96AL_11A02 96AL_11A02 96AL_11A02 96AL_12803 96AL_12803 96AL_12803 96AL_12803 96AL_11008 96AL_11008 96AL_11012 96AL_12012 96AL_12012 96AL_12612 96AL_12612 96AL_11H07	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G11.2 C01H6.7 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 R107.2 F21C3.4 D2005.5 F30F8.8 H06001.2 C54G4.1 C254G4.1 C254G5.5	nath-10 lin-35 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2 drh-3 taf-5 chd-1 rskn-2 pbrm-1 dcp-66	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex ats as a histone chaperone that both destabilizes and restores nucleosomas. The ACT complex tas as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the resetabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality, RITS (meiotic/germline H3K9me2 on repetitive heterochromatin putative TATA binding protein 32: DDB1- and CUI-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase Phosphoglucosamine acetyltransferase Phosphoglucosamine acetyltransferase phomolog of sploid germ cell-specific nuclear protein kinase (haspin) homolog transcription termination factor RNA polymerase II; helicase homolog of sploiding factor 3b polycomb-like protein; binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing protein RNAi DEfective, encoding nematode specific protein required for RNA interference, control of transposen transposition in the germline and proper chromosome segregation. dicer-related helicase, required to maintain chromosome integrity and proper chromosome segregation in the germline; RITG (meiotic/germline H3K9me2 or repetitive chromatin) putative TATA binding protein assoc	histone modification; DNA methylation Others Others DNA binding DNA binding DNA binding DNA binding Transcription regulation protein-protein interactions RNAI machinery RNAI machinery RNAI machinery RNAI machinery DNA binding RNAI machinery DNA binding transcription regulation chromatin remodelling transcription regulation chromatin remodelling transcription regulation chromatin remodelling transcription regulation chromatin remodelling	and RifkA binding domain Retinoblastoma-associated protein A/B domain HMG-box domain Tudor (recognizes methylated histones) WD repeats GNAT domain SNF2-related WD repeats MBT repeats PHD finger WD repeats chromodomain
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 D7 D7 D8 D9 D10 D11 D11	96AL_6602 96AL_7608 96AL_7608 96AL_11A02 96AL_11A02 96AL_11A02 96AL_12803 96AL_12803 96AL_12803 96AL_1108 96AL_1108 96AL_11018 96AL_11012 96AL_11D12 96AL_12D12 96AL_12D12 96AL_12122 96AL_12122 96AL_12122 96AL_12122	F55A12.8 C32F10.2 C32F10.2 F22D6.6 F22D6.7 F22	nath-10 lin-35 hmg-3 ekl-1 tof-11.2 wdr-23 ego-1 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2 drh-3 tof-5 chd-1 rskn-2 pbrm-1 dcp-66 spr-4	N-acetyltransferase 10 homolog retinoblastoma protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Kar-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1- and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference WUstor; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase Nomolog of splicing factor 3b polycomb-like protein; binds to ocyte chromatin; regulates splicing; recognizes and binds H3Sme2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PM-Dringer containing protein RNA DEfective, encoding nematode specific protein required for RNA interference, control of transpoost transposition in the germline and proper chromosome segregation RNA DEfective, encoding nematode specific protein required for RNA interference, control of transpoost transposition in the germline and proper chromosome segregation. dicer-relate helicase, required to maintain chromssome integrity and proper chromosome segregation in the germline; RITS (meiotic/germline H3K9me2 on repetitive chromatin) putative TATA binding protein associated transcription factor (wDD onome) hike protein, bindis to ocyte	histone modification; DNA methylation Others Others DNA binding DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery RNAi machinery splicing splicing splicing splicing chromatin remodelling rotein hinding RNAi machinery DNA binding RNAi machinery DNA binding chromatin remodelling transcription regulation chromatin remodelling transcription regulation chromatin remodelling chromatin remodelling transcription regulation chromatin remodelling transcription regulation chromatin remodelling transcription regulation chromatin remodelling	and RRAA binding domain Retinoblastoma-associated protein A/B domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD finger WD repeats chromodomain HMG box, bromodomain, Zn finger
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 D1 D2 D3 D4 D4 D5 D6 D7 D4 D5 D6 D7 D8 D9 D10 D11 D12	96AL_6602 96AL_7610 96AL_7610 96AL_11402 96AL_11402 96AL_11402 96AL_12803 AL I-3018 96AL_12803 96AL_112803 96AL_112803 96AL_112012 96AL_112012 96AL_112012 96AL_112012 96AL_112012 96AL_112012 96AL_112013 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401 96AL_11401	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23G112 C01H6.7 C01H6.9 T23H2.3 K02F2.3 R06C7.7 F21C3.4 D2005.5 F30F8.8 H06001.2 C54G4.1 C26C6.5 C09H6.1 W06D4.4	nath-10 lin-35 hmg-3 ekl-1 tdc-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tgg-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2 drh-3 tdc-5 chd-1 rskn-2 pbrm-1 dcp-66 spr-4 prmt-7	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin franscription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex, a general chromatin factor that acts to reorganize template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex sits as a histone chaperone that both destabilities and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality: RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein associated transcription factor WD repeat-containing protein associated transcription factor WD repeat-containing protein associated transcription eNutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamine acetyltransferase SWI/SNF nucleosome remodeling complex component homolog of aploid germ cell-specific nuclear protein kinase (haspin) homolog transcription factor 3b polycomb-like protein, binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger containing protein RNAi DEfective, encoding nematode specific protein required for RNA interference, control of transposon transposition in the germline and proper chromosome segregation. dicer-related helicase, required to maintain chromosome integrity and proper chromosome segregation in the germline; RTS (meiotic/germline H3X9me2 on repetitive chromatin) putative TATA binding protein associated transcription factor chromodomin-helicase-DNA-binding protein Pu	histone modification; DNA methylation Others Others DNA binding DNA binding bistone binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery RNAi machinery Bistone modification; DNA methylation chromatin remodelling protein binding transcription regulation chromatin remodelling chromatin remodeling chromatin chromatin chromatin chromatin	and RRAA binding domain Retinoblastoma-associated protein A/B domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats PHD finger WD repeats chromodomain HMG box, bromodomain, Zn finger Zn finger, C2H2-type SAM domain
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D1 D2 D3 D4 D5 D6 D7 D4 D5 D6 D7 D8 D9 D10 D11 D12 Z12 Z12 Z12 Z12 Z12 Z12 Z12 Z12 Z12 Z	96AL_6602 96AL_7610 96AL_7610 96AL_11A02 96AL_11A02 96AL_12013 96AL_12013 96AL_12013 96AL_11201 96AL_112013 96AL_112013 96AL_111012 96AL_112012 96AL_12012 96AL_12012 96AL_12012 96AL_12012 96AL_112013 96AL_12013 9	F55A12.8 C32F10.2 C32F10.5 F22D6.6 K1003.3 D2030.9 F26A3.3 K04F10.6 T23611.2 C01H6.7 C01H6.9 T23H1.2 C01H6.7 C01H6.9 T23H2.3 R06C7.7 R107.2 F21C3.4 D2005.5 F30F8.8 H06C01.2 C54G4.1 C26C6.1 C26C6.5 C09H6.1 W06D4.4 F43G9.12	nath-10 lin-35 eki-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tog-298 = swsn-9 tog-298 = swsn-9 tog-203 lin-61 rde-2 drh-3 tof-5 chd-1 rskn-2 pbrm-1 dcp-66 spr-4 prmt-7	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin franscription complex subunit ssrp1-8. Component of the FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex atts as a histone chaperone that both destabilities and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestabilishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2: DDB1- and CUI-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference Mutator; RNAi defective rde-3; nucleotidyltransferase Phosphoglucosamice acetyltransferase SW/JSM nuclesome remodeling complex component homolog of haploid germ cell-specific nuclear protein kinase (haspin) homolog fangloid germ cell-specific nuclear protein kinase (haspin) homolog of splicing factor 3b polycomb-like protein, binds to oocyte chromatin; regulates splicing; recognizes and binds H3X9me2/3 (MBT domain); predicted to function in a transcriptional regulatory complex PHD-finger creating protein RNAi DEfective, encoding nematode specific protein required for RNA interference, control of transposon transposition in the germline and proper chromosome segregation. dicer-related hilease, ITS (meiotic/germline H3K9me2 or nepetitive chromatin) putative TATA binding protein associated transcription factor chromodomain-helicase. DNA-binding protein RNAi DEfective, encoding nematode specific protein required for RNA interference, cont	histone modification; DNA methylation Others Others DNA binding DNA binding DNA binding DNA binding DNA binding transcription regulation protein-protein interactions RNA machinery RNAI machinery RNAI machinery RNAI machinery RNAI machinery RNAI machinery DNA binding transcription regulation chromatin remodelling Chromatin r	and RRAA binding domain Retinoblastoma-associated protein A/B domain Tudor (recognizes methylated histones) WD repeats GNAT domain SNF2-related WD repeats PHD finger WD repeats PHD finger HMG box, bromodomain, 2n finger 2n finger, C2H2-type SAM domain GCFC domain
MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1 MH1	C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 D7 D7 D8 D9 D10 D11 D11 D12 C5 C6 C1 C12 C12 C12 C12 C12 C12 C12 C12 C12	96AL_6G02 96AL_7G00 96AL_7G10 96AL_11A02 96AL_11A02 96AL_11A02 96AL_12803 ALI-3D18 96AL_9C04 96AL_12803 96AL_12003 96AL_11003 96AL_11003 96AL_11012 96AL_12012 96AL_12012 96AL_12012 96AL_121203 96AL_121203 96AL_121203 96AL_121203 96AL_121203 96AL_121203	F55A12.8 C32F10.2 C32F10.2 F22D6.6 F22D6.6 F22D6.3 T22D6.3 F22D6.3 F22D6.3 F22D6.3 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.4 F22D6.5 F30F8.8 H06001.2 C54G4.1 C25C6.5 C09H6.1 W06D4.4 F43G912	nath-10 lin-35 ekl-1 tof-11.2 wdr-23 ego-1 rde-3 = mut-2 gno-2 tag-298 = swsn-9 teg-4/phi-6/tag- 203 lin-61 rde-2 drh-3 taf-5 chd-1 rskn-2 pbrm-1 dcp-66 spr-4 prmt-7 rad-54	N-acetyltransferase 10 homolog retinoblastoma protein (Rb) ortholog HMG box-containing protein 3; Facilitates chromatin transcription complex subunit ssrp1-8. Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilities and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. Binds specifically to double-stranded DNA Enhancer of Ksr-1 Lethality; RITS (meiotic/germline H3K9me2 on repetitive heterochromatin) putative TATA binding protein associated transcription factor WD repeat-containing protein 2; DDB1 and CUL4-associated factor 11 homolog RNA-directed RNA polymerase related EGO-1; regulates germline development and RNA interference WUstor; RNAi defective rde-3; nucleotidyltransferase PMOShP nucleosome remodeling complex component homolog of splicing factor 3b polycomb-like protein, binds to oocyte chromatin; regulates splicing; recognizes and binds H3K9me.2/a (M8T domain); predicted to function in a transcriptional regulatory complex PHO-finger containing protein R15 (meiotic/germline H3K9me2 on repetitive chromation) putative TATA M8T domain; protein Equiptice functore transcription alter ference, control of transposotion in the germline and proper chromosome segregation.	histone modification; DNA methylation Others Others DNA binding DNA binding histone binding transcription regulation protein-protein interactions RNAi machinery RNAi machinery RNAi machinery RNAi machinery RNAi machinery RNAi machinery protein kinase chromatin remodelling protein kinase chromatin remodelling Chromatin binding/transcription regulation chromatin remodelling DNA binding transcription regulation chromatin remodelling DNA binding transcription regulation chromatin remodelling transcription regulation Chromatin remodelling transcription regulation DNA binding activity, transcription regulation DNA binding activ	and RRAA binding domain Retinoblastoma-associated protein A/B domain Tudor (recognizes methylated histones) WD repeats GNAT domain bromodomain SNF2-related WD repeats MBT repeats PHD finger WD repeats chromodomain HMG box, bromodomain, Zn finger Zn finger, C2H2-type SAM domain GCFC domain SNF2-related
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				protein containing a 7 WD-repeat similar to the mammalian homolog RbAp48; histone		
				binding protein; Core histone-binding subunit that may target chromatin assembly factors, chromatin remodeling factors and histone deacetylases to their histone substrates in a		
MH1 MH1	E4 E5	96AL_16B07 K07A1.12 96AL_13D04 T01G9.6	lin-53 kin-10	manner that is regulated by nucleosomal DNA Casein kinase II subunit beta	histone binding protein kinase	WD repeats
MH1	E6	96AL_13D11 C34B7.1		divergent MYST acetyltransferase	histone modification; DNA methylation	
MH1	E7	96AL_14D12 DY3.2	lmn-1	chromatin; bind to histone H2A	chromatin binding	
MH1 MH1	E8 E9	96AL_13E03 F16D3.2 96AL_15E06 C12C8.3	rsd-6 lin-41	RNAi spreading defective, encoding maternal tudor protein. Ring finger-B box-Coiled coil (RBCC) protein	RNAi machinery protein-protein interactions	Tudor domain RING type Zn finger
MH1	E10	96AL_13F02 F02E9.4	sin-3	ortholog of the SIN3 family of histone deacetylase subunits	histone modification; DNA methylation	
MH1	E11 E12	96AL_15F10 C17E4.6		protein of the YL1 family; DNA-binding and may be transcription factor	transcription regulation	
MH1 MH1	F1 F2	96AL_13G07 D1081.8 96AL 14H02 F32H2 1	aei-1	SANT/Myb-domain containing protein	DNA binding Others	SANT/Myb domain
MH1	F3	AL III-6K7 Y56A3A.16	ger 1	PHD-finger containing protein	chromatin binding	PHD finger
MH1 MH1	F4 F5	96AL_15H05 F30A10.10 96AL_15H06 C41G7.1	usp-48 smn-1	Ubiquitin Specific Protease human Survival Motor Neuron homolog.	ubiquitin machinery RNA binding	Tudor domain
N.41.11	56	-	afi 1	-		ARID (AT-rich interaction)
MH1	F0 F7	96AL_20B12 F15D3.1	dys-1	ortholog of human DMD, which when mutated leads to Duchenne muscular dystrophy	Others	ZZ type Zn finger
MH1	F8	964L 17C05 80379 3	mut-16	Mutator, encoding prion-like Q/N-rich domain protein; role in chromatin organization and/or gene expression	chromatin structure / transcription regulation	
MH1	F9	96AL_18D08 T22A3.4	set-18	ortholog of human SMYD1, SMYD2	protein-protein interactions	MYND-type Zn finger
MH1 MH1	F10 F11	Supp I-10A5 F28D9.2 Supp III-8G7 Y119D3B.11	sri-5 orc-3	Serpentine Receptor, class I PHD-finger containing protein	Others (signalling) chromatin binding	PHD finger
MH1	F12	96AL_18G02 B0205.1		SPK-domain containing protein	DNA binding	SPK domain
MH1	G1	96AL_18G04 B0205.3	rpn-10	is a member of the von Willebrand factor	ubiquitin machinery	
				FACT complex subunit spt-16; Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes.		
				that require DNA as a template such as mRNA elongation, DNA replication and DNA repair.		
				During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA		
				polymerase II and transcription by promoting the dissociation of one histone H2A-H2B		
MH1	G2	AL I-508 F55A3.3	phi-16	nucleosome following the passage of RNA polymerase II	chromatin remodelling	
MH1	63	96AL 17H07 F25D7.3	hlmn-1	a zinc finger and SET domain-containing protein that is the C. elegans BLIMP1 (B lymphocyte induced maturation protein 1) ortholog	- DNA binding	Zn finger: SFT domain
MH1	G4	96AL_20H11 R09B3.4	ubc-12	ubiquitin-conjugating enzyme	ubiquitin machinery	
MH1 MH1	G5 G6	96AL_20H12 R09B3.5 AL X-1G12 C46H3.1	mag-1	Drosophila MAGonashi homolog PHD-finger containing protein	Others chromatin binding	PHD finger
MH1	G7	96AL_22A10 T15D6.8	uha 2	putative methyltransferase	histone modification; DNA methylation	-
MH1	G9	AL X-4D20 C11E4.6	ubu-2	PHD-finger containing protein	chromatin binding	PHD finger
MH1 MH1	G10 G11	96AL_22B01 T15D6.11 96AL_23B01 B0019.2		putative methyltransferase SPK-domain containing protein	histone modification; DNA methylation	SPK domain
MH1	G12	96AL_23B03 Y18D10A.1	attf-6	AT hook Transcription Factor family	transcription regulation	AT hook
MH1 MH1	H1 H2	96AL_24B04 T04D3.5 ALI-6G16 K11D2.1		RCC1 domain-containing protein 1 (regulator of chromosome condensation)	others chromatin structure	
MH1	Н3	96AL_21D11 R05D7.2		SPK-domain containing protein family member	DNA binding	SPK domain
				to mediate chromatin remodeling and transcriptional regulation orthologous to human		
MH1 MH1	H4	96AL_24D01 Y40B1B.6	spr-5 hma-20	histone demethylase LSD1 Isoform 1 of High mobility group protein 200	histone modification; DNA methylation	HMG-box domain
			1111g 20	human TATA-binding protein associated factor TAF1L (TAFII250) that possesses histone		
MH1	H6	AL I-7C7 W04A8.7	taf-1	acetyl transferase (HAT) activity and is a component of the TFIID general transcription factor that recognizes the transcription	transcription regulation / histone modification	bromodomain; Zn finger
MH1	H7	96AL_25C08 F47G4.6	hmg-6	High mobility group box domain	DNA binding	HMG-box domain
				does not contain a SET domain, suggesting the existence of another mechanism for		
MH1 MH1	Н8 Н9	96AL_27C09 Y39G10AR.18	thc-13	methylation of lysine residues of histones	histone modification; DNA methylation	DOT1 domain PHD finger
MH1	H10	96AL_26E08 Y54E5B.4	ubc-16	ubiquitin conjugating enzyme.	ubiquitin machinery	inger
MH1	H11	96AL_27E05 Y39G10AR.8 Y39G10AR.7/		eukaryotic translation initiation factor 2 gamma	Others (translation)	
MH1	H12	96AL_27E10 Y39G10AR.8		eukaryotic translation initiation factor 2 gamma	Others (translation)	
MH2	A1	96AL_26F10 ZK909.2	kin-1	serine/threonine protein kinase that is orthologous to cAMP-dependent protein kinase	protein kinase	
MH2 MH2	A2 A3	Suppl-9E5 Y47G6A.6 ALI-3E21 R06C7.1	pcaf-1 waao-1	C. elegans PCAF/GCN5-like histone acetyltransferase. worm Argonaute protein	histone modification; DNA methylation RNAi machinery	PIWI/PA7
						SET domain; MYND-type Zn
MH2 MH2	A4 A5	96AL_26G11 F33H2.7 96AL_25H03 Y105E8A.17	set-10 ekl-4	protein containing trithorax/polycomb SET domain. DNA methyltransferase 1 associated protein, Enhancer of Ksr-1 Lethality	histone modification; DNA methylation histone modification / chromatin remodelling	finger
MH2	A6	96AL_29E12 Y71G12B.15	ubc-3	E2 ubiquitin-conjugating enzyme orthologous	ubiquitin machinery	SAND domain
WITZ	A/	ALIFIAS COIDIZ.2	gineb-1		Others (closest ortholog but no evidence, no	SAND domain
MH2 MH2	A8 A9	96AL_31A09 C01B12.8 96AL 31A10 F23F1.1	nfvc-1	ortholog of human Forkhead-associated (FHA) phosphopeptide binding domain 1 Nuclear transcription Factor Y. subunit gamma	domain) transcription regulation	
MH2	A10	96AL_34A09 W09B6.2	taf-6.1	TAF (TBP-associated transcription factor) family	transcription regulation	DING 7- 5
MH2	A11	96AL_32C12 W04H10.3	nni-3	PAZ and PIWI-domain containing protein that is a member of the highly conserved		KING Zh finger
	A12	0641 22002 70702 7	ala 2	eukaryotic RDE-1/AGO1/PIWI family of proteins that regulate posttranscriptional gene	RNAi machinony	
MH2	B1	AL I-4G17 F52B5.5	cep-1	transcription factor, p53-like protein	DNA binding	Zn finger
MH2 MH2	B2 B3	96AL_36A05 F52C6.12 Supp II-10H2(7K1240.1		ubiquitin-conjugating enzyme E2-17 kDa like. Zn finger-containing protein	ubiquitin machinery	RING-type 7n finger
MH2	B4	96AL_37A06 ZK1240.2		Zn finger-containing protein	DNA binding	RING-type Zn finger
MH2 MH2	B5 B6	96AL_37AU7 2K1240.3 96AL_36H12 B0281.3		Zn finger-containing protein Zn finger-containing protein	DNA binding DNA binding	RING-type Zn finger
MH2 MH2	B7 B8	96AL_37H07 F34D6.4	set-11	histone H3 lysine-9 methyltransferase ortholog	histone modification; DNA methylation	-
MH2	B9	96AL_42A06 C16A11.3		SPK-domain containing protein	DNA binding	SPK domain
MH2 MH2	B10 B11	AL II-3B14 C16A11.4 96AL 42B11 H20J04.2	athp-2	SPK-domain containing protein AT Hook plus PHD finger transcription factor	DNA binding transcription regulation	SPK domain; Zn finger PHD-finger
MH2	B12	96AL_41E08 Y14H12B.2	<i>p</i> =	SPK-domain containing protein	DNA binding	SPK domain; Zn finger
				non-ALPase subunit of the 195 regulatory complex of the proteasome; Metalloprotease component of the 26S proteasome that specifically cleaves 'Lys-63'-linked polyubiquitin		
мнэ	C1	9641 41F04 K07D4 3	rnn-11	chains. The 26S proteasome is involved in the ATP-dependent degradation of ubiquitinated	ubiquitin machinery	
MH2	C2	96AL_42G06 T05A7.4	hmg-11	High mobility group protein I alpha	DNA binding	HMG box
MH2 MH2	C3 C4	AL II-3P2 F10G7.2 96AL_44A05 F58A6.8	tsn-1 msp-45	component of the RNA-induced silencing complex (RISC); nuclease component Tudor-SN major sperm protein	RNAi machinery Others	Tudor domain
MH2	C5	AL I-5C1 T23D8.7		Argonaute protein	RNAi machinery	PIWI/PAZ
MH2	C0 C7	96AL_44B11 C34F11.6	msp-50 msp-49	major sperm protein	Others	

			pra-1: taraets			
MH2	C8	Supp I-10A8 D2030.6	prg-2 as well	Argonaute protein	RNAi machinery	PIWI/PAZ
					Others (protein phosphatase/cell cycle	
MH2	C9	96AL_45B08 C17G10.4	cdc-14	cell-division-cycle related; dual-specificity phosphatase (tyrosine-protein phosphatase)	regulation)	
MH2	C10	Supp II-11J11 ZK1248.7	wago-5	Argonaute protein	RNAi machinery	PIWI/PAZ
MH2	C11	96AL_46C06 H12I13.1		SPK-domain containing protein family member. Protein kinase	protein kinase	SPK domain
				Retinoblastoma-binding protein homolog 5; a WD40 repeat-containing protein that is the C.		
				elegans homolog of Saccharomyces cerevisiae Swd1; required for di- and trimethylation at		
MH2	C12	96AL_46C08 F21H12.1	roop-5	H3K4	nistone modification; DNA methylation	wD repeats
MH2	D1	96AL 44D05 E09E5 1	nkc-3	6/PAR-3/PKC-3/CDC-42 required for establishing embryonic polarity	protein kinase	
MH2	D2	96AL 43D08 R05F9 3	msn-32	major sperm protein	Others	
MH2	D3	96AL 46D05 C29H12.5	cec-9	C. elegans Chromodomain protein	DNA binding/structure	chromodomain
MH2	D4	96AL 43E01 R05F9.8	msp-33	major sperm protein	Others	
MH2	D5	96AL_43E06 R05F9.13	msp-13	major sperm protein	Others	
MH2	D6	96AL_43E09 ZK546.3		major sperm protein	Others	
MH2	D7	96AL_43E11 ZK546.6	msp-152	major sperm protein	Others	
MH2	D8	AL II-5E23 F18C5.2	wrn-1	Probable Werner syndrome ATP-dependent helicase homolog 1	DNA binding/structure	helicase domains
		0001 40040 00005 F		putative historie H4K20 methyltransferase; SE1-4 is orthologous to Drosophila SUV4-20, and	have a strength of the second strength of the	
MH2	D9 D10	96AL_46G10 C32D5.5	set-4	to numan SUV420H1; H3K20 represents specific tag for epigenetic transcriptional repression	Others	
MH2	D10	96AL 45E05 K05E1 7	mcn-63	major sperm protein	Others	
MH2	D12	96AL 43H11 ZC8.3	set-30	protein containing trithorax/polycomb SET domain: H3K4 methylation	histone modification: DNA methylation	
MH2	E1	AL III-1J2 C14B1.6	nrde-1	putative Argonaute	RNAi machinery	
MH2	E2	96AL_49B04 F32A5.1	ada-2	ADA (histone acetyltransferase complex (subuunit)	histone modification; DNA methylation	SANT/Myb
MH2	E3	96AL_49B10 F32A5.7	lsm-4	Probable U6 snRNA-associated Sm-like protein LSm4	splicing	
MH2	E4	AL III-5E16 ZK757.3	alg-4	Argonaute protein	RNAi machinery	PIWI/PAZ
MH2	E5	AL II-518 ZK1127.3		localized to H3/H2A histone acetyltrasnferase complex	histone modification; DNA methylation	
MH2	E6	96AL_48E08_ZK1127.7	cin-4	Chromosome instability 4	DNA binding/structure	
MH2	E7	Cloned Y18H1A.10		homolog of Serine/Threonine-protein kinase haspin	protein kinase	kinase domain
MH2	E8	AL:II-5I18 ZK1127.7	cin-4	Chromosome instability 4	DNA binding/structure	
MH2	E9	AL: II-5J06 T09A5.8	cec-3	C. elegans Chromodomain protein	DNA binding/structure	chromodomain
MH2	E10	Supp III-8819 C16C10.3	hrde-1	Argonaute protein	RNAi machinery	PIWI/PAZ
MH2	E11 F12	96AL_49E10_D1022.1	UUC-0 rnv-1	43 kDa recentor-associated protein of the synapse homolog	Others	RING-type 7n finger
191174	L.12	JUNE_4/004 C1005./	109-2	histone deacetylase: Probably responsible for the deacetylation of lycine recidues on the M	ouncis	
MH2	F1	9641 50G04 C08B11 2	hda-2	terminal part of the core histories (H2A_H2B_H3 and H4)	histone modification: DNA methylation	
MH2	F2	96AL 50G05 C08B11.3	swsn-7	SWI/SNF nucleosome remodeling complex component	chromatin remodelling	SWI/SNF: ARID
MH2	F3	96AL 50G08 C08B11.6	arp-6	spliceosome-Associated Protein and actin related protein	splicing	
MH2	F4	AL IV-3J8 F45E4.10	nrde-4	putative Argonaute	RNAi machinery	
MH2	F5	AL IV-3011 C01G5.2	prg-2	Argonaute protein	RNAi machinery	PIWI/PAZ
MH2	F6	96AL_51C10 F35C11.4			others	
				Regulator of chromosome condensation; associated with RAN (nuclear import/export)		
MH2	F7	96AL_51D12 C26D10.1	ran-3	function	chromatin structure	
MH2	F8	96AL_53D07 T23G7.1	dpl-1	Transcription factor	transcription regulation	
MH2	F9 E10	96AL_52EU3 101B7.5	lat 10	related to SAS10-chromatin silencing	transcription regulation	
IVIT12	F10	3upp 11-10A24K08F8.0	let-19	TD-dependent DEAD/H box RNA belicase orthologous to human RNA belicase A: Unwinds		
				double-stranded DNA and RNA in a 3' to 5' direction. Transcriptional regulator that controls		
MH2	F11	AL II-6M24 T07D4.3	rha-1	germline mitosis and development via histone modification	Others (helicases)	
MH2	F12	96AL 53G04 D2013.9	ttll-12	Tubulintyrosine ligase-like protein 12	Others	TTL domain
MH2	G1	96AL_52H10 T21B10.5	set-17	Histone-lysine N-methyltransferase PRDM9; H3K4 methyltransferase activity	histone modification; DNA methylation	SET domain
						SET domain; MYND-type Zn
MH2	G2	96AL_57B01 R06F6.4	set-14	SET domain-containing protein 14	histone modification; DNA methylation	finger
	62		nnn 10	Nuclear nore complex protein Nup53	Others (nuclear pore)	
MH2	05	90AL_57B02 R00F0.5	npp-19	Nuclear pore complex protein Nupps		
MH2 MH2	G3 G4	AL II-7/16 R166.1	mab-10	related to transcription repression	transcription regulation	DING 1
MH2 MH2 MH2	G4 G5	96AL_57B02_R06F6.5 AL II-7116 R166.1 96AL_55F07_ZK945.4	mab-10	Victoria por Company protein 1955 related to transcription repression Uncharacterized RING finger protein 7.6 forcer containing perception	transcription regulation DNA binding DNA binding	RING-type Zn finger
MH2 MH2 MH2 MH2 MH2	G4 G5 G6	96AL_57602 R06P6.5 AL II-7116 R166.1 96AL_55F07 ZK945.4 96AL_555G09 F33H1.4	mab-10	Vinction por compression Vincharacterized RING finger protein Zn finger-containing protein ubinuitin convol-termina hydrolase family protein	transcription regulation DNA binding DNA binding binuitin machinery	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8	96AL_57602 R06F0.5 AL II-7116 R166.1 96AL_55F07 ZK945.4 96AL_55G09 F33H1.4 AL II-7N4 F07A11.4 AL II-7N8 F07A11.6	mab-10	Nacted yor complex protein repose related to transcription repression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein D&F-12 Interactinge Protein	transcription regulation DNA binding DNA binding ubiquitin machinery NA binding	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9	90AL_57002 K00F0.5 AL II-7116 R166.1 96AL_55F07 ZK945.4 96AL_55G09 F33H1.4 AL II-7N4 F07A11.4 AL II-7N8 F07A11.6 96AL 58G08 ZK20.5	npp-19 mab-10 din-1 rpn-12	Hacter Jole Comparison Jolean Hopp3 Vancharacterized RING finger protein Zn finger-containing protein Uliquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like	transcription regulation DNA binding DNA binding Disputin machinery NA binding Disputin machinery	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9	SoAL_5/B02 K00F0.5 AL II-7116 R166.1 SoAL_55507 ZK945.4 96AL_55509 F33H1.4 AL II-7N4 F07A11.4 AL II-7N8 F07A11.6 96AL_58G08 ZK20.5	din-1 rpn-12	Racted pole complex protein Rep29 related to transcription repression Uncharacterized RING finger protein Diagnatic arboxyl-terminal hydrolase family protein DAF-12 Interacting Protein Proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK	transcription regulation DNA binding DNA binding DNA binding DNA binding NA binding abiquitin machinery	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9	Jobal_3/B02 Jobal_3/B076.3 AL II-7116 R166.1 96AL_5SF07 ZK945.4 96AL_5SF07 ZK945.4 96AL_5SF07 ZK945.4 AL II-714 F07A11.4 AL II-7N8 F07A11.6 96AL_58G08 ZK20.5	din-1 rpn-12	Hacted pole complex protein Http: related to transcription repression Uncharacterized RING finger protein abiquitin carboxyl-terminal hydrolase family protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase	transcription regulation DNA binding DNA binding Ubiquitin machinery NA binding Delquitin machinery	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10	96AL_57b02 K060-5.3 ALII-71.6 R166.1 96AL_55F07 ZK945.4 96AL_55C09 F33H1.4 ALII-71.4 F07A11.4 96AL_58G08 ZK20.5 96AL_58G10 C47D12.1	hpp-19 mab-10 din-1 rpn-12 trr-1	Recter Joic Compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes	transcription regulation DNA binding DNA binding ubiquitin machinery NA binding ubiquitin machinery protein kinase	RING-type Zn finger C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11	96AL_57b02 R0F0.5 ALII-716 R166.1 96AL_55007 ZK945.4 96AL_55009 F33H1.4 ALII-714 F07A11.4 ALII-718 F07A11.6 96AL_58G08 ZK20.5 96AL_58G10 C47D12.1 96AL_60A10 C50F10.4	din-1 rpn-12 trr-1 sop-2	Recter pole compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2	transcription regulation DNA binding DNA binding DNA binding Ulquith machinery NA binding Ubiquith machinery protein kinase transcription regulation	RING-type Zn finger C2H2-type Zn finger SAM-like
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12	90AL_57b2 NOPOLS ALII-716 R166.1 96AL_5507 ZK954.4 96AL_5508 F3811.4 ALII-714 F07A11.6 96AL_5608 ZK20.5 96AL_5608 ZK21.1 96AL_5608 CK21.1 96AL_5608 C67D12.1 96AL_58010 C50E10.4 96AL_59802 F43G6.11	din-1 rpn-12 trr-1 sop-2 hda-5	Nactor pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein abiquitin carboxyl-terminal hydrolase family protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase	transcription regulation DNA binding DNA binding Ubloutin machinery NA binding ubloutin machinery protein kinase transcription regulation bisone modification, DNA methylation	RING-type Zn finger C2H2-type Zn finger SAM-like
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12	96AL_57b02 R0F0.5 ALII-716 R166.1 96AL_55C07 ZK945.4 96AL_55C07 ZK945.4 96AL_55C07 ZK945.4 96AL_55C07 ZK945.4 96AL_58C08 ZK205.5 96AL_58G10 C47D12.1 96AL_58G10 C47D12.1 96AL_50B02 F4366.11	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hdo-5 olg-3; targets olg	Recter Joic Compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase	transcription regulation DNA binding DNA binding Ubioutitin machinery NA binding Ubiquitin machinery protein kinase transcription regulation Nistone modification; DNA methylation	RING-type Zn finger C2H2-type Zn finger SAM-like
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1	96AL_57b02 R0F6.1 96AL_55R07 ZK945.4 96AL_55G09 F33H1.4 ALII-716 F07A11.4 ALII-718 F07A11.4 ALII-718 F07A11.4 ALII-708 F07A11.6 96AL_58G10 C47D12.1 96AL_58G10 C47D12.1 96AL_58G10 C47D12.1 96AL_59B02 F4366.11 ALIV-6A22 T2283.2 66AL_56D30 C50510.4	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alq-3; targets alg 4 as well	Indecting pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein Zn finger-containing protein Uncharacterized RING finger protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb Potein sop- 2	transcription regulation DNA binding DNA binding DNA binding Ubiquitin machinery NA binding Ubiquitin machinery protein kinase transcription regulation histone modification; DNA methylation RNAI machinery	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM like
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3	90AL_57b2 K00F0.5 4ALII-716 R166.1 96AL_5507 ZK945.4 96AL_5507 ZK945.4 96AL_5806 F33H.1.4 ALII-774 F07A11.6 96AL_5808 ZK70.5 96AL_58010 C47D12.1 96AL_58010 C47D12.1 96AL_59802 F43G6.11 ALIV-6A22 T2283.2 96AL_60C02 C50E10.4 96AL_5020 Z50E10.4	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 ton-2	Nacted pole Compression Uncharacterized RING finger protein Uncharacterized RING finger protein Uncharacterized RING finger protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Piotable DAK tooolsomerase 2	transcription regulation DNA binding DNA binding Ubloutin machinery DNA binding Ubloutin machinery protein kinase transcription regulation Nistone modification, DNA methylation RNAi machinery transcription regulation DNA binding DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4	96AL_57b2 NOF0-5. ALII-716 R166.1 96AL_5507 ZK955.4 96AL_5509 F3811.4 ALII-714 F07A11.4 96AL_5800 ZK975.1 96AL_5800 ZK205.1 96AL_5800 C47D12.1 96AL_60A10 C50F10.4 96AL_5902 F4366.1 ALIV-762 T2283.2 96AL_59002 S0E10.4 96AL_5903 K12D12.1 96AL_5903 Y127A1	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 top-2 top-2	Hactes pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topolsomerase 2 AT hook-containing High Mobility Group orotein	transcription regulation DNA binding DNA binding Ubloutin machinery NA binding Ubloutin machinery protein kinase transcription regulation Natione modification; DNA methylation RNAi machinery transcription regulation DNA binding/structure DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5	96AL_57/b2 R0F0.5 ALII-716 R166.1 96AL_55C07 ZK945.4 96AL_55C07 ZK945.4 96AL_55C07 ZK945.4 96AL_58G10 CA7D11.4 ALII-7N8 F07A11.4 96AL_58G10 C47D12.1 96AL_58G10 C47D12.1 96AL_59B02 F4366.11 96AL_59B02 F4366.11 ALIV-6A22 T2283.2 96AL_59C03 K12D12.1	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 hag-2 hag-2 hag-2 hag-2 hag-2	Recter Join Compression Uncharacterized RING finger protein Uncharacterized RING finger protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein MP Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type	transcription regulation DNA binding DNA binding Ubiquitin machinery NA binding ubiquitin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding/structure DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6	96AL_57/b2 NOPO-0-3 ALII-71/6 R166.1 96AL_5500 ZK945.4 96AL_5500 F381.4 ALII-714 F07A11.6 96AL_5800 ZK20.5 96AL_5800 C47D12.1 96AL_58010 C47D12.1 96AL_6802 F4366.11 96AL_6802 F4366.11 96AL_6002 C50E10.4 96AL_59D03 Y17G7A.1 96AL_59D03 Y1037.4 96AL-59D08 W0309.4 AL-V-FIE1 R9A1.1	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1	Naces por Compression Uncharacterized RING finger protein Uncharacterized RING finger protein Uncharacterized RING finger protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Protable DNA topolsomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein	transcription regulation DNA binding DNA binding Ubloutin machinery DNA binding Ubloutin machinery protein kinase transcription regulation Natione modification, DNA methylation RNAi machinery transcription regulation DNA binding/structure DNA binding transcription regulation RNAi machinery	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7	96AL_57b2 NOFO-5. ALII-716 R166.1 96AL_5507 Z4955.4 96AL_5506 F3811.4 ALII-714 F07A11.4 ALII-718 F07A11.4 ALII-718 F07A11.4 ALII-718 F07A11.4 96AL_58G00 C47D12.1 96AL_60A10 C50E10.4 96AL_59C0 F4366.11 ALIV-6A22 T2283.2 96AL_60C02 C50E10.4 96AL_59C03 Y1G7A.1 96AL_59008 V03C9.4 ALV-1F11 R09A1.1 96AL_62062 Z131.3	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets alg 4 as well sop-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-9	Indector pole compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family	transcription regulation DNA binding DNA binding Ubloutin machinery NA binding ubloutin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding transcription regulation DNA binding transcription regulation RNAi machinery transcription segulation RNAi machinery transcription segulation RNAi machinery transcription structure Chromatin structure	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8	9GAL_57/b2 R0F0.3 ALII-716 R166.1 9GAL_55C07 ZK954.4 9GAL_55C07 ZK945.4 9GAL_55C07 ZK945.4 9GAL_55C07 F33H.1.4 ALII-7N4 F07A11.6 9GAL_58G08 ZK20.5 9GAL_60A10 C50E10.4 9GAL_60C2 Z50E10.4 9GAL_59C02 Z50E10.4 9GAL_59C03 K12D12.1 9GAL_59C03 K12D12.1 9GAL_59D03 W13C9.4 AL IV-1611 R09A1.1 9GAL_62C2 ZK131.3 9GAL_62E10 ZK131.7	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hdro-5 alg-3; targets alg 4 as well sop-2 top-2 top-2 top-2 top-2 lin-29 ergo-1 his-9 his-13	Recter pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topolsomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family	transcription regulation DNA binding DNA binding Ubioutitin machinery NA binding Ubioutitin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding/structure DNA binding transcription regulation RNAi machinery transcription regulation Chromatin structure chromatin structure	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H9	96AL_57/b2 NOFO-5. ALII-71/6 R166.1 96AL_5507 ZK955.4 96AL_55067 ZK955.4 96AL_5608 F381.4 ALII-714 F07A11.6 96AL_5608 ZK20.5 96AL_58610 C47D12.1 96AL_58020 F4366.11 96AL_6020 Z5061.4 96AL_6002 C50610.4 96AL_59D03 Y17G7A.1 96AL_59D03 Y17G7A.1 96AL_5202 ZX13.3 96AL_62205 ZX13.3 96AL_52712 Y57A10A.1	din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13	Naces por Compression Uncharacterized RING finger protein Uncharacterized RING finger protein abiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Probable DAK topolsomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family SPK-domain containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery Ubioutin machinery protein kinase transcription regulation Nationer Nationer Nationery transcription regulation DNA binding Transcription regulation DNA binding transcription regulation ENA binding transcription regulation Chromatin structure DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10	96AL_57b2 NOFO-5 4A.II-716 R166.1 96AL_55F07 Z4955.4 96AL_55B07 Z4955.4 96AL_55B07 Z4955.4 96AL_55B07 F07A11.4 ALII-714 F07A11.4 ALII-718 F07A11.4 ALII-718 F07A11.6 96AL_58G08 C47D12.1 96AL_60A10 C50E10.4 96AL_59002 F4366.11 ALIV-6A22 T22B3.2 96AL_59003 Y167A.1 96AL_5903 Y1673.4 96AL_5903 Y167A.1 96AL_62203 Y167A.1 96AL_62205 X131.3 96AL_62210 Z431.17 96AL_62210 Z4731.17 96AL_62105 Z4731.17 96AL_62105 Z4731.7 96AL_62105 X131.7 96AL_62105 X0911.2 96AL_62105 X0911.2 96AL_62105 X0911.2	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-13 his-73 his-74	Indector pole compression Uncharacterized RING finger protein Zn finger-containing protein main hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family bistone H3 f	transcription regulation DNA binding DNA binding DNA binding Ubioutin machinery NA binding ubioutin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding transcription regulation DNA binding transcription regulation NA imachinery transcription regulation NA imachinery transcription regulation NA imachinery transcription regulation NA imachinery DNA binding transcription regulation NA imachinery Chromatin structure DNA binding transcription regulation NA imachinery chromatin structure DNA binding transcription regulation NA imachinery transcription NA imachinery transcription NA imachinery	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 2	96AL_57/62 R166.1 96AL_55R07 ZK955.4 96AL_55C07 ZK955.4 96AL_55C07 ZK955.4 96AL_55C07 ZK955.4 96AL_55C07 ZK955.4 96AL_55C07 ZK955.4 96AL_58G10 C47D12.1 96AL_58G10 C47D12.1 96AL_60A10 C50E10.4 96AL_59C02 Z50E10.4 96AL_59C02 C50E10.4 96AL_59C03 K12012.1 96AL_59C03 X12012.1 96AL_59C03 X12012.1 96AL_59C03 X12012.1 96AL_59C03 X12012.1 96AL_59C03 X1313.1 96AL_62E10 ZK131.3 96AL_62E10 ZK131.3 96AL_62F03 X0941.1 96AL_62F03 X0941.2 96AL_62F03 X0941.2 96AL_62F03 X0941.2 96AL_62F03 X0941.2 96AL_62F05 F8862.3 96AL_62F05 F8862.3	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-73 his-72 hts-4	Indector pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family Discome TBR-ascoriated family. (TAE)	transcription regulation DNA binding DNA binding DNA binding Disquitin machinery protein kinase transcription regulation Histone modification; DNA methylation RNA imachinery transcription regulation DNA binding/structure DNA binding transcription regulation ENAI machinery Chromatin structure chromatin str	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12	96AL_97/b2 R166.1 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_56/08 F07A11.6 96AL_58/01 C47D12.1 96AL_60/01 C50E10.4 96AL_59/02 F4366.11 ALIV-6A22 T2283.2 96AL_60/02 C50E10.4 96AL_59/03 Y17G7A.1 96AL_59/03 W03(9.4 AL-V-FIE1 R09A.1 96AL_62/203 Y17G7A.1 96AL_61/203 W09H.2 96AL_61/203 W09H.2 96AL_61/203 Y09H.2 96AL_61/207 F15D4.1	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well al sop-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Indector pole compression Uncharacterized RING finger protein Zn finger-containing protein abiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomeras 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family member of the TBP-associated family (TAF)	transcription regulation DNA binding DNA binding Ubioutin machinery NA binding Ubioutin machinery protein kinase transcription regulation Usione modification, DNA methylation RNAI machinery transcription regulation DNA binding KNAI machinery transcription regulation DNA binding transcription regulation Chromatin structure DNA binding chromatin structure Chromatin	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1	96AL_97/b2 R166.1 96AL_55/02 K166.1 96AL_55/07 ZK955.4 96AL_56/07 ZK955.4 96AL_56/07 ZK955.4 96AL_60/07 ZK955.4 96AL_60/07 ZK955.4 96AL_52 Z283.2 96AL_59002 ZK910.4 96AL_59003 X1221.1 96AL_59003 X1221.1 96AL_59003 X1221.1 96AL_52002 ZK131.3 96AL_62003 X121.1 96AL_62005 ZK131.3 96AL_62005 ZK131.7 96AL_62105 ZK131.7 96AL_62105 ZK31.7 96AL_62105 ZK31.7 96AL_62105 ZK31.7 96AL_62105 ZK32.3 96AL_62105 ZK32.3 96AL_62105	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 os well sop-2 top-2 top-2 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Naces pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family histone H3 family histone H3 Pan-3 histone H3 Pan-3 h	transcription regulation DNA binding DNA binding DNA binding Ubioutin machinery NA binding ubioutin machinery protein kinase transcription regulation histone modification; DNA methylation RNA imachinery transcription regulation DNA binding transcription regulation NA imachinery transcription regulation NA imachinery transcription regulation DNA binding transcription regulation NA imachinery chromatin structure DNA binding chromatin structure DNA binding Chromating DNA binding DNA binding DNA binding DNA binding DNA b	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1	96AL_57/b2 NOPCO-5. ALII-716 R166.1 96AL_5507 ZK954.4 96AL_5506 F381.4 ALII-714 F07A11.6 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_58610 C47D12.1 96AL_58608 ZK20.5 96AL_5802 F4366.11 ALIV-6A22 T22B3.2 96AL_60C02 C50E10.4 96AL_59D03 Y17G7A.1 96AL_59D03 Y03C9.4 ALIV-1F11 R09A.1 96AL_62E06 ZK31.3 96AL_62F05 F08G2.3 96AL_62F05 F08G2.3 96AL_61F07 F15D4.1 96AL_61F07 F15D4.1 96AL_62F05 Y57A10A.2 957AL0A.2 Y57A10A.2 957AL0A 957A10A.2	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; torgets alg 4 as well sop-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Naces pole comparison for the post related to transcription repression Uncharacterized RING finger protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein Proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polybo topoismerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family SPK-domain containing protein family member. histone H3 family SPK-domain containing protein family member. histone H3 family SPK-domain containing protein family (TAF) SPK containing protein family member.	transcription regulation DNA binding DNA binding Disputitin machinery Disputitin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding transcription regulation RNAi machinery chromatin structure DNA binding chromatin structure chromatin structure chromatin structure chromatin structure Others (helicase) DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2	96AL_97/b2 R166.1 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_56/08 F07A11.4 ALII-714 F07A11.6 96AL_58/010 C47D12.1 96AL_60A10 C50E10.4 96AL_59/02 F4366.11 ALIV-6A22 T2283.2 96AL_59/03 Y17G7A.1 96AL_59/03 Y17G7A.1 96AL_59/03 Y17G7A.1 96AL_59/03 Y13G7A.1 96AL_62/2003 Y13G7A.1 96AL_61/203 W09H1.2 96AL_61/203 W09H1.2 96AL_61/203 Y57A10A.2 Y57A10A.3 Y57A10A.3 96AL_59/203 Y57A10A.2	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as ways top-2 top-2 top-2 top-2 hmg-12 lin-29 ergo-1 hit:-9 his-13 his-73 his-42 btf-1	Indector pole compression Uncharacterized RING finger protein Zn finger-containing protein abiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle 514, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family (TAF) SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery DNA binding Ubioutin machinery protein kinase transcription regulation lissione modification, DNA methylation RNA imachinery transcription regulation DNA binding transcription regulation EnNai machinery chromatin structure DNA binding chromatin structure Chromatin structure Others (helicases) DNA binding DNA binding DNA binding DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H17 H8 H9 H10 H11 H12 A1 A2	96AL_97/b2 R166.1 96AL_55/02 R166.1 96AL_55/07 Z4955.4 96AL_56/07 Z59602 96AL_60/07 C50510.4 96AL_59002 X1221.1 96AL_59002 Z50510.4 96AL_59003 V1767A.1 96AL_59003 V1767A.1 96AL_62002 Z50510.4 96AL_62003 V1767A.1 96AL_62003 X1212.1 96AL_62005 X131.3 96AL_62005 X131.3 96AL_62005 Z4131.7 96AL_62105 Z4731.1 96AL_62105 F1504.1 96AL_62105 F1504.1 96AL_62050 Y57A10A.2 Y57A10A.3 Y57A10A.3 96AL_59601 Y57A10A.4 Y	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 top-2 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Naces pole compression Uncharacterized RING finger protein DAF-12 Interacting Protein protesione Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family histone H3 Family member of the TBP-associated family (TAF) SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery NA binding ubioutin machinery protein kinase transcription regulation Nistone modification; DNA methylation RNAi machinery transcription regulation DNA binding transcription regulation NA imachinery transcription regulation DNA binding transcription regulation NA imachinery transcription regulation DNA binding transcription regulation NA imachinery transcription regulation DNA binding DNA binding chromatin structure chromatin structure chromatin structure DNA binding chromatin structure DNA binding DNA binding DNA binding DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain
мн2 мн2 мн2 мн2 мн2 мн2 мн2 мн2 мн2 мн2	G4 G4 G5 G6 G7 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3	96AL_57/b2 NOPC 000-05 ALII-716 R166.1 96AL_5507 ZK954.4 96AL_5506 F381.4 ALII-714 F07A11.6 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_5608 ZK20.5 96AL_58010 C47D12.1 96AL_59802 F4366.11 ALIV-6A22 T2283.2 96AL_5003 X12012.1 96AL_59802 K12012.1 96AL_59003 K10212.1 96AL_59003 K10212.1 96AL_59003 K10212.1 96AL_59102 K12012.1 96AL_59103 K737A10A.2 %77A10A.5 Y57A10A.4 %77A10	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-73 his-72 btf-1	Naces pole comparison of the table of the table of the table of the table of table o	transcription regulation DNA binding DNA binding DNA binding Displatitin machinery protein kinase transcription regulation Kistone modification; DNA methylation RNAi machinery transcription regulation DNA binding transcription regulation RNAi machinery chromatin structure DNA binding Chromatin structure DNA binding	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain
MH2 MH3 MH3	G4 G4 G5 G6 G7 G8 G9 H1 H2 H3 H4 H5 H6 H7 H8 H10 H11 H12 H12 A1 A2 A3	96AL_97/b2 R166.1 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_55/07 Z4945.4 96AL_56/08 F07A11.4 ALII-714 F07A11.4 ALII-718 F07A11.6 96AL_58/010 C47D12.1 96AL_60/20 Z4366.11 ALIV-6A22 T2283.2 96AL_60/20 C50E10.4 96AL_59/03 Y17G7A.1 96AL_59/03 W1321.1 96AL_59/03 Y13G7A.1 96AL_59/03 W03(9.4 ALV-FITI R09A1.1 96AL_62/20 Z4313.3 96AL_62/20 Z431.7 96AL_62/20 Z431.7 96AL_61/20 X0391.2 96AL_61/20 X0391.2 96AL_61/20 X0391.2 96AL_61/20 X131.7 96AL_61/20 X0391.2 96AL_61/20 X75A10.3 96AL_59/200 Y57A10A.2 Y57A10A.5 Y57A10A.3 96AL	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as way and a sop-2 top-2 top-2 top-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Hacter pole compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle 514, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protein family member. SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery DNA binding Ubioutin machinery protein kinase transcription regulation Histore modification, DNA methylation RNA imachinery transcription regulation DNA binding transcription regulation EnNai machinery chromatin structure DNA binding chromatin structure Others (helicases) DNA binding DNA binding DNA binding DNA binding	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook CZH2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3	96AL_97/b02 R0F0-3 ALII-71/6 R166.1 96AL_55R07 ZK955.4 96AL_55R07 ZK955.4 96AL_55R07 ZK955.4 96AL_55R07 ZK955.4 96AL_55R07 ZK955.4 96AL_55R07 ZK955.4 96AL_58G10 C47D12.1 96AL_60A10 C50E10.4 96AL_59002 K12012.1 96AL_59003 V1202.1 96AL_59003 V1202.1 96AL_59003 V1202.1 96AL_59003 V1202.1 96AL_59003 V1202.1 96AL_59003 V1202.1 96AL_52003 V1707.1 96AL_52003 V1707.1 96AL_52005 X131.3 96AL_62105 ZK131.7 96AL_62105 ZK131.7 96AL_62105 ZK131.7 96AL_62105 ZK131.7 96AL_62107 F1504.1 96AL_62107 F1504.1 96AL_62107 F1504.1 96AL_59601 Y57A10A.2 Y57A1	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 top-2 lin-29 ergo-1 his-13 his-73 his-42 btf-1	Naces pole compression Uncharacterized RING finger protein Zn finger-containing protein mainly dyrolase family protein DAF-12 Interacting Protein protessome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein SPK-domain containing protein family member. histone H3 family histone H3 family SPK containing protein family member. SPK containing protein family member. SPK containing protein family member. SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery NA binding Ubioutin machinery protein kinase transcription regulation transcription regulation NA binding NA inachinery transcription regulation DNA binding transcription regulation DNA binding transcription regulation DNA binding transcription regulation DNA binding	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook CZH2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4	96AL_57/b2 K0000-3 96AL_55/02 K166.1 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/08 FX20.5 96AL_56/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_59/00 Z501.1 96AL_59/00 Z501.1 96AL_59/00 K12012.1 96AL_59/00 X12012.1 96AL_50/02 Z50510.4 96AL_59/03 Y1767A.1 96AL_59/03 X1377.1 96AL_59/02 ZX13.3 96AL_61/03 Y0941.2 96AL_61/03 Y57A10A.1 96AL_61/03 Y57A10A.2 Y57A10A.3 Y57A10A.3 96AL_59/03 Y57A10A.4 Y57A10A.5 Y57A10A.4 Y57A10A.5 Y57A10A.4 Y57A10A.4 Y57A10A.4 Y57A10A.4 Y57A10A.4 Y5	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Naces pole compression Uncharacterized RING finger protein Uncharacterized RING finger protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Probable DAK topolsomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding DNA binding Display the machinery protein kinase transcription regulation Kistone modification; DNA methylation RNA imachinery transcription regulation DNA binding transcription regulation RNAi machinery chromatin structure Chromatin str	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4	96AL_57/62 NBC NF05. 96AL_55707 Z4945.4 96AL_55707 Z4945.4 96AL_55607 Z4945.4 96AL_5806 F33H.1.4 AL II-71M F07A11.4 F07A11.4 AL II-71N8 F07A11.6 96AL_58008 ZK20.5 96AL_5802 F4366.11 96AL_60A10 C50E10.4 96AL_5902 F4366.11 96AL_59030 Y17G7A.1 96AL_5903 Y1221.1 96AL_59030 Y1221.1 96AL_5903 Y1221.1 96AL_59030 Y1221.1 96AL_5903 Y1221.1 96AL_5903 Y1737A.1 96AL_6210 Z131.3 96AL_6210 Z131.7 96AL_6210 Z131.7 96AL_6163 W09H.2 96AL_6163 W09H.2 96AL_61607 F15D4.1 96AL_59601 Y57A10A.2 Y57A10A.5 Y57A10A.4 Y57A10A.5 Y57A10A.5 96AL_59607 Y57A10A.4 Y57A10A.5 Y57A10A.5 Y57A10A.5 Y57A10A.5 Y57A10A.5 Y57A10A.5	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 top-2 top-2 top-2 top-2 hm-12 lin-29 ergo-1 his-9 his-13 his-73 his-73 his-42 btf-1	Indexemplor Compression Uncharacterized RING finger protein DAF-12 Interacting Protein DAF-12 Interacting Protein Proteasome Regulatory Particle 514, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family histone H3 family member of the TBP-associated family (TAF) SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Ubioutin machinery DNA binding Ubioutin machinery protein kinase transcription regulation Histore modification, DNA methylation RNAI machinery transcription regulation DNA binding transcription regulation ENAI inachinery chromatin structure DNA binding	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook CZH2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4	9GAL_57/62 R166.1 9GAL_55/07 ZK955.4 9GAL_6002 C5010.4 9GAL_59002 X1221.1 9GAL_59003 V1671.1 9GAL_59003 V1673.1 9GAL_59003 V1673.1 9GAL_62002 ZK131.7 9GAL_62205 ZK131.7 9GAL_6107 X7510.1 9GAL_6107 X7510.3 9GAL_6107 Y57410.3 9GAL_59G01 Y57410.4 Y57410.5 Y57410.4 Y57410.7 Y57410.6 9GAL_59G07 Y57410.4 Y57410.6 Y57410.6 Y57410.6 Y57410.6 Y57410.6	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Hacter pole compression Uncharacterized RING finger protein Darharacterized RING finger protein biguitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Probable DNA topoisomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protein family member. SPK containing protein family member. SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding Disquitin machinery Disquitin machinery protein kinase transcription regulation histone:modification; DNA methylation RNA imachinery transcription regulation DNA binding	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain
MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G4 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H10 H11 H12 A1 A2 A3 A4 A5 A6	96AL_97/b2 R0F0-3 ALII-716 R166.1 96AL_55F07 ZK955.4 96AL_55607 ZK955.4 96AL_55607 ZK955.4 96AL_5608 F381.4 ALII-714 F07A11.6 96AL_58610 C47D12.1 96AL_5802 F4366.11 96AL_5802 F4366.11 ALIV-6A22 T2283.2 96AL_6002 C50E10.4 96AL_59D03 Y17G7A.1 96AL_59D03 Y17G7A.1 96AL_59D03 Y17G7A.1 96AL_59D12 Y57A10A.1 96AL_61F03 W091.2 96AL_61F03 W091.2 96AL_61F03 Y57A10A.3 96AL_59G01 Y57A10A.3 96AL_59G03 Y57A10A.3 96AL_59G03 Y57A10A.3 96AL_59G05 Y57A10A.3 96AL_59G07 Y57A10A.4 Y57A10A.5 Y57A10A.4 Y57A10A.5 Y57A10A.5 96AL_59G07 Y57A10A.4 96AL_59G07 Y57A10A.4	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; targets olg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1	Naces pole compression Uncharacterized RING finger protein Lin finger-containing protein abiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Probable DAK topolsomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protein family member.	transcription regulation DNA binding DNA binding DNA binding Display the second	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain
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MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2 MH2	G3 G4 G5 G6 G7 G8 G9 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1	96AL_57/62 NB2 NB2 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_55/07 ZK955.4 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_59/02 ZK20.5 ZK20.5 96AL_59/02 96AL_59/02 ZK20.5 ZK20.5 ZK20.5 96AL_60/02 CS010.4 96AL_59/03 Y17G7A.1 96AL_59/03 Y17G7A.1 96AL_59/02 ZK131.3 96AL_62/20 ZK131.7 96AL_62/20 ZK131.3 96AL_61/60 Y57A10A.1 96AL_59/02 Y57A10A.2 96AL_61/60 Y57A10A.2 Y57A10A.3 96AL_59/03 96AL_59/03 Y57A10A.4 Y57A10A.5 96AL_59/03 96AL_59/04 Y57A10A.4 Y57A10A.5 Y57A10A.5 96AL_59/05 Y57A10A.4 Y57A10A.5 Y57A10A.7 96AL_59/06 Y57A10A.4	http:// mab-10 din-1 rpn-12 trr-1 sop-2 htdo-5 alg-3; targets alg 4 as well sop-2 top-2 htmg-12 lin-29 ergo-1 his-9 his-13 his-73 his-42 btf-1 htdo-10 jmjd-2 ubc-15 wago-10 htmg-11	Hacter pole Compression Uncharacterized RING finger protein DAF-12 Interacting protein DAF-12 Interacting Protein DAF-12 Interacting Protein proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DAK topoisomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family member of the TBP-associated family (TAF) SPK containing protein family member. SPK containing protein family m	transcription regulation DNA binding DNA binding DNA binding DNA binding Displatitin machinery Displatitin machinery protein kinase transcription regulation Kistone modification; DNA methylation RNA imachinery transcription regulation DNA binding Transcription regulation RNA imachinery Chromatin structure Chromatin structure Chromatin structure Chromatin structure Chromatin structure DNA binding DNA	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain
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MH2 MH3 MH3	G4 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A4 A5 A6 A7 A8 A9 A10 A11 C12 H3 H4 H5 H6 H7 H8 H9 H10 H11 H2 H3 H4 H5 H6 H7 H7 H7 H7 H7 H7 H7 H7 H7 H7 H7 H7 H7	96AL_57/62 NE NOPO-3 96AL_55707 2K954.4 96AL_55607 2K954.4 96AL_55607 2K954.4 96AL_55607 2K945.4 96AL_55608 ZK20.5 96AL_5608 ZK20.5 96AL_58610 C47D12.1 96AL_5802 7K20.5 96AL_58008 ZK20.5 96AL_5802 FK366.11 AL II-716 96AL_58020 FK366.11 96AL_59802 FK366.11 AL IV-6A22 T2283.2 96AL_60020 C50E10.4 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59003 X12012.1 96AL_59102 Z5003 X12012.1 96AL_5102 X12012.1 96AL_5102 X12012.1 96AL_59102 X12012.1 96AL_59603 Y1767A1.3 96AL_59603 Y57A10A.5 Y57A10A	http:-13 mab-10 din-1 rpn-12 trr-1 sop-2 htao-5 olg-3; torgets olg 4 as well sop-2 top-2 htm:-12 lin-29 ergo-1 his-3 his-42 btf-1 his-42 btf-1	Hacter pole compared many pole in Hepsol Particle of transcription repression Uncharacterized RING finger protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein Proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DNA topoisomerse 2 AT hook-containing High Mobility Group protein zin finger transcription factor of the C2H2 type Argonaute protein histone H3 family BSPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protei	transcription regulation DNA binding DNA binding DNA binding Disputitin machinery Disputitin machinery protein kinase transcription regulation histone modification; DNA methylation RNA imachinery transcription regulation DNA binding D	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain
MH2 MH3	G3 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 B1 B1 B2 B2	96AL_57/62 NB2 NB2 96AL_55/07 ZK945.4 96AL_55/07 ZK945.4 96AL_55/07 ZK945.4 96AL_55/07 ZK945.4 96AL_56/08 ZK20.5 96AL_56/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_58/08 ZK20.5 96AL_59/08 ZK20.5 96AL_60/12 CZ283.2 96AL_60/02 CS010.4 96AL_59/03 Y17G7A.1 96AL_59/03 Y17G7A.1 96AL_59/03 Y17G7A.1 96AL_62/05 ZK313.7 96AL_62/05 ZK313.7 96AL_61/63 W091.2 96AL_61/63 W07A10.4 Y57A10.0.4 Y57A10.3 96AL_59/03 Y57A10.7 Y57A10.3 Y57A10.5 96AL_59/03 Y57A10.4 Y57A10.5 Y57A10.5 96AL_59/03 Y57A10.4 Y57A10.5 Y57A10.5 96AL_59/04 Y57A10.4 Y57A10.5 Y57A10.7 96AL_59/05 Y57A10.4 Y57A10.5<	http://y mab-10 din-1 rpn-12 trr-1 sop-2 htdo-5 olg-3; targets olg 4 as well sop-2 top-2 htmg-12 lin-29 ergo-1 his-9 his-13 his-42 btf-1 hdo-10 jmjd-2 ubc-15 wago-10 htmg-11 nurf-1	Hacter pole compression Uncharacterized RING finger protein Lincharacterized RING finger protein DAF-12 Interacting Protein protein generation protein generation protein generation protein sopher and protein final set of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DAK topoisomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family histone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing protein fami	transcription regulation DNA binding DNA binding DNA binding DNA binding Divabinding Divabinding Divabinding Comparison DNA binding DNA binding Comparison DNA binding DNA bin	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain SPK domain
MH2 MH3	G4 G4 G5 G6 G7 G8 G9 H1 H2 H3 H4 H5 H6 H7 H8 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A110 A111 A12 B1 B2 B3 B4	9GAL_57/62 RIF6.1 9GAL_55/07 ZK954.4 9GAL_55/07 ZK954.4 9GAL_55/07 ZK954.4 9GAL_55/07 ZK954.4 9GAL_55/07 ZK954.4 9GAL_58/08 ZK20.5 9GAL_58/08 ZK20.5 9GAL_58/08 ZK20.5 9GAL_58/08 ZK20.5 9GAL_58/08 ZK20.5 9GAL_59/08 ZK30.5 9GAL_59/08 ZK30.5 9GAL_59/03 YI7G7A.1 9GAL_59/03 YI7G7A.1 9GAL_59/03 YI7G7A.1 9GAL_59/03 YI7G7A.1 9GAL_59/03 YI7G7A.1 9GAL_59/03 YI7G7A.1 9GAL_51/2 Y57A10A.5 9GAL_62/20 ZK313.7 9GAL_62/20 ZK313.7 9GAL_61/07 F15D4.1 9GAL_59/01 Y57A10A.2 Y57A10A.3 Y57A10A.3 9GAL_59/03 Y57A10A.4 Y57A10A.5 Y57A10A.6 9GAL_59/03 Y57A10A.6	npp-19 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 alg-3; targets alg 4 as well sop-2 top-2 top-2 hmg-12 lin-29 ergo-1 hit-9 his-13 his-42 btf-1 hda-10 jmjd-2 ubc-15 wago-10 hmg-1.1	Indexem pole compression Uncharacterized RING finger protein Zn finger-containing protein ubiquitin carboxyl-terminal hydrolase family protein DAF-12 Interacting Protein proteasome Regulatory Particle 514, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Probable DNA topoisomerase 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family bistone H3 family bistone H3 family SPK-domain containing protein family member. histone H3 family SPK containing protein family member. SPK contain	transcription regulation DNA binding DNA binding DNA binding Biodutin machinery Ibiodutin machinery Iprotein kinase transcription regulation Itiscone modification, DNA methylation INA binding DNA bi	RING-type Zn finger CZH2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook CZH2-type Zn finger PIWI/PAZ SPK domain SPK domain
MH2 MH3	G4 G4 G5 G6 G7 G8 G9 G10 G11 G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A4 A10 A112 B1 B2 B3 B4 B5	96AL_57/62 NE NOPOLS 96AL_55707 ZK955.4 96AL_55607 ZK955.4 96AL_55607 ZK955.4 96AL_55607 ZK955.4 96AL_55608 FK20.5 96AL_5608 ZK20.5 96AL_58610 C47D12.1 96AL_5608 ZK20.5 96AL_58610 C50E10.4 96AL_5608 ZK20.5 96AL_660C2 C50E10.4 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_60C2 C50E10.4 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_59008 XI2012.1 96AL_5912 XF3A10A.1 96AL_5202 ZSF3A10A.4 96AL_5912 YSF3A10A.2 YSF3A10A.5 YSF3A10A.5 96AL_59603 YSF3A10A.5 YSF3A10A.5 YSF3A10A.5 96AL_59603 YSF3A10A.5 YSF3A10A.5 YSF3A10A.5 96AL_59603 YSF3A10A.7 96AL_59607 YSF3A10A.5 96AL_59603 <td< td=""><td>npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; torgets olg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-3 his-13 his-42 btf-1 his-4 btf-1</td><td>Hacter pole compared number related to transcription repression Uncharacterized RING finger protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein Number 2014 Proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK Kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DAK topoisomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family SPK-domain containing protein family member. histone H3 family SPK domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing pro</td><td>transcription regulation DNA binding DNA binding DNA binding Disputitin machinery Disputitin machinery protein kinase transcription regulation Kanscription regulation Nationery transcription regulation DNA binding DNA bind</td><td>RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain</td></td<>	npp-13 mab-10 din-1 rpn-12 trr-1 sop-2 hda-5 olg-3; torgets olg 4 as well sop-2 top-2 hmg-12 lin-29 ergo-1 his-3 his-13 his-42 btf-1 his-4 btf-1	Hacter pole compared number related to transcription repression Uncharacterized RING finger protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein DAF-12 Interacting Protein Number 2014 Proteasome Regulatory Particle S14, Non-ATPase-like proteins with similarity to the atypical protein kinases of the TRAAP subfamily of PIKK Kinases that are found in multisubunit, chromatin-modifying histone acetyltransferase complexes Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Histone Deacetylase Argonaute protein Polycomb protein sop-2 Probable DAK topoisomerse 2 AT hook-containing High Mobility Group protein zinc finger transcription factor of the C2H2 type Argonaute protein histone H3 family SPK-domain containing protein family member. histone H3 family SPK domain containing protein family member. histone H3 family SPK containing protein family member. SPK containing pro	transcription regulation DNA binding DNA binding DNA binding Disputitin machinery Disputitin machinery protein kinase transcription regulation Kanscription regulation Nationery transcription regulation DNA binding DNA bind	RING-type Zn finger C2H2-type Zn finger SAM-like PIWI/PAZ SAM-like AT-hook C2H2-type Zn finger PIWI/PAZ SPK domain SPK domain

MH3 MH3	B6 B7	96AL_67C11 F23H11.1 96AL_68C09_W04B5_1	bra-2	homolog of the human BMP receptor-associated molecule (BRAM1)	transcription regulation	MYND-type Zn finger
MH3	B8	96AL 66D04 F40G9.3	uhc-20	Ubiquitin Conjugating enzyme	ubiquitin machinery	
MH3	B9	GP 2D1/3H3 C14B1.4	wdr-5.1	WD-repeat containing protein GMEB (Glucocorticoid Modulatory Element Binding protein) transcriptional regulator	protein-protein interaction	WD repeats
MH3	B10	96AL_69E12 C44F1.2	gmeb-3	homolog	transcription regulation	SAND domain
MH3	B11	96AL_68F08 H05C05.2		SPK-domain containing protein	DNA binding	SPK domain
MH3	B12	96AL_69F09 R13G10.2	amx-1	Amine oxidase family member 1; H3-K4 demethylation activity	histone modification; DNA methylation	
MH3	C1	96AL_69G07 C36A4.8	brc-1	Breast and ovarian cancer susceptibility protein homolog.	DNA binding/ DNA repair/ubiquitin machinery	RING-type Zn finger; PHD
MH3	C2	96AL_70A11 102C12.3	tftc-5	Transcription Factor ThreeC subunit (GTF3C homolog)	transcription regulation	
MH3	C3	96AL_73A07 C34E10.5	prmt-5	protein arginine metnyitransferase.	histone modification; DNA methylation	potential DNA binding
MH3 MH3	C4	96AL_73A10 C34E10.8 96AL_70B01_E03A3.3	his-69	potential chromatin remodelling protein or helicase	chromatin remodelling	domain
				Probable histone deacetylase complex subunit SAP18: Acts in transcription repression.		
MH3	C6	96AL_70C07 C16C10.4		Involved in the tethering of the SIN3 complex to core histone proteins	histone modification; DNA methylation	
MH3	C7	96AL_70C10 C16C10.7	rnf-5	RING finger protein 5	DNA binding	RING-type Zn finger
				ring finger b-box coiled coil domain containing protein; functions together with CGH-1 and		
	60	0001 70004 50054 7	-112	in association with the miRSC complex to regulate the efficacy of microRNA-target	Diat an alterna	TRIM motif; RING-type Zn
MH3	C8 C0	96AL_72C04 F26F4.7	nhl-2	Interactions	RNAi machinery	finger
MH3	C10	96AL_72C11 C26E6.3	nu-9 set-7	bistone H3K4 methyltransferace	histone modification: DNA methylation	
MH3	C11	Supp III-8E15 C26E6.12	500 2	GTP-binding protein, HSR1-related	Others	GTP1/OBG subdomain
MH3	C12	AL V-4H7 Y38A10A.6	smut-1	helicase	DNA binding/structure	helicase domains
MH3	D1	96AL_71G11 C38D4.3	mel-28	protein required for nuclear envelope assembly	Others (nuclear structure)	
MH3	D2	96AL_70H03 R07E5.3	snfc-5	homolog of SNF5/Ini1, a component of the SWI/SNF complex	chromatin remodelling	
MH3	D3	96AL_70H09 R07E5.10	pdcd-2	PDCD (mammalian ProgrammeD Cell Death protein) homolog	Others	MYND-type Zn finger
MH3	D4	AL III-2P1 K10D2.1		Required for replication-independent chromatin assembly	chromatin structure	WD repeats
MH3	D5 D6	96AL_73H05_C05D2.5	xnd-1	AT hook motif containing protein family member; X chromosome nondisjunction factor	DNA binding	AI hook
MH3	D7	96AL 74A12 B0336 7		zinc finger. C2CH-type family member	DNA hinding	C2H2-type 7n finger
	5,	5012_14112 50550.7		LIN37 is a component of the DREAM (MuvB/DRM) complex, which represses cell cycle- dependent genes in quiescent rells and plays a role in the cell cycle-dependent activation of		chine type Entimper
MH3	D8	96AL 77A04 ZK418.4	lin-37	G2/M genes	Others	
				Chromatin-remodeling complex ATPase chain isw-1; energy-transducing component of a		
				NURF-like (nucleosome-remodeling factor-like) complex, which would catalyze ATP-		
MH3	D9	96AL_76C08 F37A4.8	isw-1	dependent nucleosome sliding and facilitate transcription of chromatin	chromatin remodelling	
MH3	D10	96AL_75D09 F47D12.4	hmg-1.2	High mobility group protein 1.2	DNA binding	HMG box
MH3	D11	GP 2E6 C56G2.1		KH-domain containing protein; A-Kinase Anchor Protein	RNA binding	KH; Tudor
MH3	D12	96AL_75E03 C56G2.1	1.11.4	KH-domain containing protein; A-Kinase Anchor Protein	RNA binding	KH; Tudor
MH3	E1 F2	96AL_74E10_C28H8.9 Supp:III-8120_C56G2_15	арјј-1	DPF (transcription factor) Family	transcription regulation	C2H2-type Zn finger; PHD
WIIIJ	22	50002.15		orthologous to the human gene SWI/SNF-related, matrix-associated, actin-dependent	Instone mouncation, but methylation	
				regulator of chromatin, subfamily A-like protein 1 (SMARCAL1); SMARCAL1 is involved in the		
				remodeling of chromatin; possesses intrinsic ATP-dependent nucleosome-remodeling		
MH3	E3	Supp:III-8E14 C16A3.1		activity	chromatin remodelling	
MH3	E4	Cloned R151.8		serine/threonine rich protein; CRAMP1L ortholog	chromatin binding	
				Probable double-stranded RNA-specific adenosine deaminase; RNA-editing enzymes that		
MH3	E5	96AL_77E07 T20H4.4	adr-2	deaminate adenosines to create inosines in double-stranded RNA (dsRNA)	RNA binding/ RNAi machinery	
						TPR (tetratricopeptide
MH3	E6	96AL_75F01 C16A3.3	let-716	Tetratricopeptide repeat-containing	RNA binding and processing	repeat-containing domain)
MH3	E/	96AL_74F05 F25B5.4	ubq-1	Ubiquitin	ubiquitin machinery	
MH3	E8	96AL_76F01 107E3.3		giutatnione S-transferase kappa 1. ImiC domain containing bistone domothylation protoin 1: Histone domothylace that	Others	
мнз	F9	96AL 75H02 T26A5 5	ihdm-1	specifically demethylates H3K36	histone modification: DNA methylation	
WIIIJ	25	JURE_751102 120R3.5	jiun-1	SET domain-containing protein predicted to function as a histone lysine N-	instone mouncation, one methylation	
MH3	E10	96AL_75H04 T26A5.7	set-1	methyltransferase	histone modification; DNA methylation	
MH3	E11	96AL_75H05 T26A5.8		transcription factor CBF/NF-Y/archaeal histone	transcription regulation	histone-fold
MH3	E12	96AL_77H05 T20B12.8	hmg-4	FACT complex subunit SSRP1	DNA binding/transcriptional regulation	HMG-box
MH3	F1	96AL_76H12 R01H2.6	ubc-18	E2 ubiquitin-conjugating enzyme	ubiquitin machinery	
MH3	F2	96AL_79A05 F44B9.6	lin-36	abnormal cell lineage, encoding synthetic MultiVulva protein with two C2H2 zinc fingers.	DNA binding	C2H2-type Zn finger
14112	53	0641 81404 55452.0		uncharacterized protein; domains typical for transcription factors/chromatin remodeling	observatio binding	DnaJ domain; SAN I/Myb
MH3	F3	96AL 80A10 7K1236 2	cec-1	Chromo domain-containing protein	DNA hinding	chromo domain
MH3	F5	96AL 79B04 K12H4.8	dcr-1	endoribonuclease Involved in cleaving double-stranded RNA in the RNA interference	RNAi machinery	
MH3	F6	AL:III-4C10 C14B9.4	plk-1	Serine/threonine-protein kinase	protein kinase	
				retinoblastoma related pathway actor; component of the DRM complex functioning in		
MH3	F7	96AL_81B04 ZK637.7	lin-9	transcription repression	transcription regulation	
MH3	F8	AL:III-4E8 C14B9.4	plk-1	Serine/threonine-protein kinase	protein kinase	
MH3	F9	96AL_78C06 2K783.4	fit-1	DNA binding protein	DNA binding	bromodomain; PHD finger
мнз	F10	96AL 79C06 C14R9 6	aei-8	corepressor 1	transcription regulation	SANT/Myb domain
	110	50/12_75000 01455.0	gero	B-box type zinc finger protein; might act directly as a transcription factor to inhibit RNA		Si atti i tingo domani
MH3	F11	96AL_78D04 ZK112.2	ncl-1	polymerase I (rRNA) and III (5S RNA) transcription	transcription regulation	B box-type Zn finger
MH3	F12	96AL_78F01 ZK652.6		Zinc finger protein	DNA binding	C2H2-type Zn finger
MH3	G1	AL III-4N12 F54G8.4	nhl-1	RING finger protein	protein-protein interaction	Znf_RING
				E3 ubiquitin-protein ligase that mediates monoubiquitination of 'K117' of histone H2B. H2B		
МНЗ	62	96AL 79H05 R05D3 4	rfn-1	nerequisite for histone H3 'K4' and 'K79' methylation	histone modification: DNA methylation	
WIIIJ	02	50AL_75105 10505.4	1) <i>p</i> -1	Histone methyltransferase which is required for the mono- and dimethylation of H3K9. This	instone mouncation, but methylation	
MH3	G3	96AL 79H12 R05D3.11	met-2	increases the efficiency of set-25-mediated trimethylation of histone H3K9	histone modification; DNA methylation	
MH3	G4	96AL_80H05 K02D10.3		, ,	others	
MH3	G5	96AL_81H06 T23G5.6		AT hook motif contaning protein	DNA binding	AT hook
MH3	G6	96AL_80H09 F54F2.2	zfp-1	Zinc finger protein	DNA binding	Znf; PHD
MH3	G7	96AL_81H07 T02C1.1		RING finger protein	protein-protein interaction	Znf_RING
MH3	G8	96AL_80H10 F54F2.2	zfp-1	Zinc finger protein	DNA binding	Znt; PHD
MH3	G9 G10	GP 2F9 C29E4.5	tag-250	Ludor domain containing protein	histone binding	ludor domain
MHR	G11	AL III-5B2 K01G5 2	hnl-2	Chromo domain-containing protein	DNA binding	chromo domain
WIIIJ	011	ALIII-SD2 KOTOS.2	npr-2	protein containing two dsRNA-binding motifs: during the initiation phase of RNA		
				interference (RNAi), RDE-4 appears to function in recognition and subsequent cleavage of		
MH3	G12	96AL_84A08 T20G5.11	rde-4	long-trigger dsRNA molecules into small, interfering RNAs (siRNAs)	RNAi machinery	
				Histone H3-like variant which exclusively replaces conventional H3 in the nucleosome core		
				of centromeric chromatin at the inner plate of the kinetochore. Required for recruitment		
				and assembly of kinetochore proteins, mitotic progression and chromosome segregation.		
14/12	114	0641 83800 55460 3		way serve as an epigenetic mark that propagates centromere identity through replication	DNA hinding (structure	
мн3	ні	90AL_82809 F54C8.2	cpar-1	and cen division.	DIVA DINGING/STRUCTURE	
				synchese multivuva classib (syniviuvb) protein, syniviuvb proteins are required to repress		
мнз	Н2	96AL 83B12 7K632 13	lin-52	multiprotein DRM complex that repress transcription	transcription regulation	
MH3	НЗ	96AL 85C01 C44B9.4	athp-1	AT Hook plus PHD finger transcription factor.	transcription regulation	AT hook
MH3	H4	96AL_84D02 M03C11.3	*	· •	others	
MH3	H5	96AL_84D03 M03C11.4	hat-1/tag-235	Histone acetyltransferase activity; chromatin silencing at telomers	histone modification; DNA methylation	
			-	SWI SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A		
				containing dead H box 1; DNA helicase that possesses intrinsic ATP-dependent nucleosome-		
IVIH3	нь	supp:III-8C/ M03C11.8		remoteing activity and is both required for DNA repair and heterochromatin organization	Dive binding/structure	

MH3	Н7	AL X-1A17 R04A9.2	nrde-3	Transports small interfering RNAs (siRNAs) from the cytoplasm to the nucleus. Required for RNA interference (RNAi) in nuclei. Histone H3-like variant which exclusively replaces conventional H3 in the nucleosome core of centromeric chromatin at the inner plate of the kinetcohore; may serve as an epigenetic	RNAi machinery	PIWI/PAZ
MH3 MH3	Н8 Н9	96AL_82F05 F58A4.3	hcp-3 ubc-7	mark that propagates centromere identity through replication and cell division	chromatin structure	
мнз	H10	96AL_82G11 C07A9.7	set-3	SET domain-containing protein predicted to function as a histone lysine N- methyltransferase	histone modification; DNA methylation	
MH3 MH3	H11 H12	96AL_83H04 ZK1128.5 96AL_89A01 T28A8.6	swsn-3 = ham-3	chromatin remodeling complex Swp73 SWI/SNF related, actin dependent Regulator of Chromatin, subfamily D (SMARCD3) homolog SRK-containing protein family member.	chromatin remodelling DNA binding	SPK domain
MH4	A1	96AL_86B02 Y47D3B.9	bed-2	BED-type Zn finger Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active genes. Constitutes the needominant form of histone H3 in non-dividing cells and is incorrorated into	DNA binding	Zn finger BED-type
				chromatin independently of DNA synthesis. Deposited at sites of nucleosomal displacement throughout transcribed genes, suggesting that it represents an epigenetic imprint of		
MH4 MH4	A2 A3	96AL_87B10 Y49E10.6 96AL_87B11 Y49E10.7	his-72	transcriptionally active chromatin. pseudogene	chromatin structure pseudogene?	
MH4	A4	96AL_87B12 Y49E10.8		pseudogene	pseudogene?	CET de secto
MH4 MH4	A5 A6	GP 2H4 112D8.1 AL III-6D24 T12D8.7	set-16 taf-9	H3K methyltransferases of the SET1/mixed lineage leukaemia (MLL) family TATA binding protein associated transcription factor	transcription regulation	SET domain
MH4	A7	Supp III-8K22 Y55B1BR.3	cec-8	chromodomain-containing protein	DNA binding	chromodomain
MH4	A8	GP 2H2 Y43F4B.3	set-25	putative histone H3 lysine-9 methyltransferase	histone modification; DNA methylation	SET domain
MH4	A10	AL III-6I14 Y111B2A.11	epc-1	enhancer of PolyComb-like; negative regulator of Ras.	transcription regulation	
MH4	A11	96AL_88E07 F53A2.5	dro-1	DR1 transcription factor related	transcription regulation	
MH4	A12	96AL 87G12 Y37D8A.9	mra-1	mortality factor-related gene; associates to oogenic chromatin, but only to autosomes; represses genes on the X chromosome and promotes germline immortality.	DNA binding	chromodomain
MH4	B1	GP 1E9 Y87G2A.11	2	WD-repeat containing protein ATP-dependent serine protease that mediates the selective degradation of misfolded and	protein-protein interaction	WD repeats
MH4	B2	96AL_86H03 Y75B8A.4		unassembled polypeptides in the peroxisomal matrix	Others (protease)	
MH4	B3	GP 3E3 F17C11.10		WD-repeat containing protein	protein-protein interaction	WD repeats
MH4 MH4	в4 В5	96AL_88H10 128A8.3 96AL 88H11 T28A8.4		SPK containing protein family member. SPK containing protein family member.	DNA binding	SPK domain
MH4	B6	96AL_88H12 T28A8.5		SPK containing protein family member.	DNA binding	SPK domain
				Systemic RNAi-defective; plays a role in RNA-mediated gene silencing by mediating endocytic untake of double-stranded RNA (dsRNA) ingested from the environment into		
MH4	B7	96AL_89C06 ZK520.2	sid-2	intestinal cells from the intestinal lumen.	RNAi machinery	
MH4	B8	96AL_91E03 Y71H2AM.17	swsn-3	HMG box family protein like.	DNA binding	HMG box
MH4	B9 B10	96AL 90G04 Y53G8AR.6		nuclear protein hcc-1.	DNA binding	SAP domain
MH4	B11	96AL_90G05 Y53G8AR.6		nuclear protein hcc-1.	DNA binding	SAP domain
MH4 MH4	B12 C1	96AL_90H06_Y53G8AR.2 AL_IV-1A4 C18H7.9	phf-15 nrmt-4	PHD tinger protein methyltransferase type 11 and methyltransferase type 12.	DNA binding histone modification: DNA methylation	Zn PHD finger
MH4	C2	96AL_95A12 F42A6.5	,,	putative uncharacterized protein	DNA binding/repair	
MH4 MH4	C3	96AL_92B02 B0545.1	tpa-1 pabp-1_1	protein kinase C-like	protein kinase Others	
MH4	C5	96AL_92E07 T07A9.1	pqbp-1.2	PQBP1 (polyglutamine tract-binding neurodegeneration protein) homolog	Others	
MH4	C6	Supp:IV-9D12C50A2.2	cec-2	chromodomain-containing protein 3'-5' evonuclease: RNA evonuclease that acts as a negative regulator of RNA interference	DNA binding	chromodomain
MH4	C7	96AL_92E10 T07A9.5	eri-1	(RNAi). Probably acts by degrading the 3'-overhangs of short interfering RNAs (siRNAs)	RNAi machinery	
MH4	C8	GP 4C9 K07C5.8	cash-1	WD-repeat containing protein	protein-protein interaction	WD repeats
MH4 MH4	C10	96AL_95E05_M57.1 96AL_95E09_B0212.3		SPK containing protein family member. SPK containing protein family member.	DNA binding	SPK domain
MH4	C11	AL IV-104 F53H1.4		zinc finger, PHD-type family member.	DNA binding	Zn PHD finger
MH4 MH4	C12	GP 4E3 R11E3.4 GP 1E3 E39B2 2	set-15	containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET domain
MH4	D2	96AL_108B5 ZK1251.6	msp-76	major sperm protein.	Others	
MH4	D3	AL IV-2C22 R08C7.3	htz-1	Variant histone H2A which replaces conventional H2A in a subset of nucleosomes	DNA structure	ANK report
MH4	D4 D5	96AL 99B06 ZK354.4	msp-113	major sperm protein.	Others	ANK repeat
MH4	D6	96AL_99B07 ZK354.5	msp-51	major sperm protein.	Others	
MH4 MH4	D7 D8	96AL_99B12 2K354.11 96AL 97C06 R08C7.10	msp-59 wapl-1	major sperm protein. cohesin interactor. Wings apart-like (Drosophila): regulates heterochromatin structure	chromatin structure	
MH4	D9	96AL_96C09 C35B1.1	ubc-1	Ubiquitin-conjugating enzyme E2	ubiquitin machinery	
MH4	D10	96AL_99C12 F41H10.6	hda-6	histone deacetylase. Histone demethylase required for nervous system development; specifically demethylates	histone modification; DNA methylation	
MH4	D11	96AL_97E12 F29B9.2	jmjd-1.2	dimethylated H3K9me2 and H3K27me2	histone modification; DNA methylation	WD repeate
MH4	E1	96AL 97F1 F29B9.4	psr-1	Dioxyg96AL se that can both act as a histone arginine demethylase and a lysyl-hydroxylase	histone modification; DNA methylation	wD repeats
MH4	E2	96AL_97F3 F29B9.6	ubc-9	ubiquitin conjugating enzyme.	ubiquitin machinery	WD reports
MH4 MH4	E3 F4	GP 1H9 F33G12.2 96AL 99F4 T12F12.2	cec-6	WD-repeat containing protein chromodomain-containing protein	protein-protein interaction DNA binding	WD repeats chromodomain
MH4	E5	AL IV-205 F15E6.1	set-9	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET domain; PHD Zn finger
MH4 MH4	E6 F7	96AL_100A11C06E7.1 AL IV-3B8 E55G1.2	sams-3 his-59	Probable S-adenosylmethionine synthase 3 histone H3	Others (enzymes)	
				protein containing DnaJ and Myb domains that is orthologous to the mammalian		
MH4 MH4	E8	96AL_101B5 F38A5.13 96AL_101B7 F15B10.2	dnj-11 drb-1	ZRF1/MIDA1/MPP11/DNAJC2 family of ribosome-associated molecular chaperones	chaperones RNAi machinen/	
MH4	E10	96AL_103C12F32E10.2	cec-4	chromodomain-containing protein	DNA binding	chromodomain
MH4	E11	96AL_100D3 B0350.2	unc-44	ankyrin-related protein family member	protein-protein interaction	ankyrin repeats
MH4	F1	ALIV-3H6 F32E10.5	unc-44	tudor-domain protein	binding NA, nucleoprotein complexes	tudor domain
MH4	F2	GP 4E12 F32E10.6	cec-5	chromodomain-containing protein	chromatin remodelling	chromodomain
MH4	F3	96AL_101E3 C1/H12.13	anat-1	N-acetyltransterase activity HMG (high mobility group) box-containing protein; HMG-5 binds to double-stranded	histone modification; DNA methylation	
MH4	F4	96AL_103E3 F45E4.9	hmg-5	telomeric DNA in vitro	DNA binding	HMG box
MH4 MH4	F5 F6	96AL_101F3 T05A12.4 96AL_101F10T05A12.4		SNF2-related and DNA/RNA helicase, C-terminal family member. SNF2-related and DNA/RNA helicase, C-terminal family member.	NA binding	RING Zn finger
мна	F7	96AL 101G107K381 /	nal-1	P granule abnormality protein, encoding constitutive component of the germline specific P	RNA hinding	
1911/14	.,	56.1C_1010102N301.4	pgr-1	encoding host cell factor related; transcriptional regulator that associates with histone		
MH4	F8 F9	96AL_103G4 C46A5.9	hcf-1	modification enzymes and plays a role in cell cycle progression	transcription regulation	WD repeats
MH4	F10	ALIV-4A16 F17E9.10	swu-2.1 his-32	histone H3	chromatin structure	wb repeats
MUA	F11	9641 10527 03000 9	nan. 1	protein related in sequence to the conserved NAP (Nucleosome Assembly Protein) family of	chromatin remodelling	
IVIF14	r11	JUAL_10367 02096.8	nup-1	Argonaute protein required for chromosome segregation, embryonic viability, Slicer activity	un omatim remodelling	
MH4 MH4	F12 61	96AL_104C1 F20D12.1	csr-1 rad-26	induced by secondary siRNAs, and (partially) for germline RNAi belicase	RNAi machinery Others (belicases)	
1911714	31	JUNE_100C3 C2/B/.4	100-20	Caenorhabditis elegans essential complex locus mes-6C, encoding polycomb group silencer		
	C 1	0041 10555 00001 1		embryonic ectoderm development-like, dicistronic, component of histone H3	Nistere medification Distances in the	
MH4	62	90AL_105E5 C09G4.4		WD repeat-containing protein that is orthologous to Drosophila Extra sex combs (Esc): as a	instone modification; UNA methylation	
MH4	G3	96AL_105E6 C09G4.5	mes-6	member of a Polycomb-like chromatin repressive complex with MES-2 and MES-3	histone modification; DNA methylation	
MH4	G4	96AL_105E8 F42A9.2	lin-49	bromodomain protein; regulates expression of homeobox genes; may play an analogous role to the trithorax Group (trxG) proteins	transcription regulation	bromodomain

MH4	G5	96AL_107E2 F56D5.4		pseudogene	pseudogene?	_
MH4	G6	AL IV-4J18 F59B8.2	idh-1	Isocitrate dehydrog96AL_se [NADP]	Others (enzymes)	
MH4	G7	96AL_110A7 R11A8.4	sir-2.1	NAD-dependent protein deacetylase; putative histone H3 deacetylase	histone modification; DNA methylation	
MH4	G8	96AL_109B11C04G2.4	msp-36	major sperm protein.	Others	
MH4	G9	GP 2B1 F28C6.3	cpf-1	WD-repeat containing protein	protein-protein interaction	WD repeats
				Putative RNA polymerase II transcriptional coactivator; General coactivator that functions		
				cooperatively with TAFs and mediates functional interactions between upstream activators		
MH4	G10	96AL_108C8 T13F2.2		and the general transcriptional machinery	transcription regulation	
MH4	G11	96AL_108D4 T13F2.10	msp-79	major sperm protein.	Others	
MH4	G12	GP 2B2 F46C5.9		WD-repeat containing protein	protein-protein interaction	WD repeats
MH4	H1	GP 2B5 D2013.2	wdfy-2	WD40- and FYVE-domain containing protein that is orthologous to mammalian WDFY2	protein-protein interaction	WD repeats
MH4	H2	96AL_111D1CF36H1.2	kdin-1	ankyrin and KAP P-loop family member.	Others	
MH4	H3	96AL_108E2 K07F5.1	msp-81	major sperm protein.	Others	
MH4	H4	96AL_108E3 K07F5.2	msp-10	major sperm protein.	Others	
MH4	H5	96AL_109E3 K08F4.8	msp-38	major sperm protein.	Others	
MH4	H6	96AL_108E4 K07F5.3	msp-56	major sperm protein.	Others	
MH4	H7	AL IV-5J14 M7.1	let-70	Ubiquitin-conjugating enzyme E2	ubiguitin machinery	
MH4	H8	96AL 108F8 F32B6.6	msp-77	major sperm protein.	Others	
MH4	H9	96AL 108G11C47E12.4	рур-1	inorganic Pyrophosphatase.	Others	
MH4	H10	96AL 111G3 F01G4.1	psq-4 = swsn-4	ortholog of SWI2/SNF2, a component of the SWI/SNF complex	chromatin remodelling	bromodomain
		-		protein similar to prefoldin 4 chaperone; Binds specifically to cytosolic chaperonin (c-CPN)		
				and transfers target proteins to it. Binds to nascent polypeptide chain and promotes folding		
MH4	H11	96AL 112B8 B0035.4	nfd-4	in an environment in which there are many competing pathways for nonnative proteins	chaperones	
MH4	H12	96AL 112C9 F54E12.1	his-55	histone H3	DNA structure	
		-				
MH5	A1	96AL 112C10F54E12.2		helicase	Others (helicases)	
MH5	A2	96AL 113D6 C29E6.2	trpa-1	TRPA cation channel homolog.	Others	
MH5	A3	96AL 114D4 F28D1.1	wdr-46	WD repeat protein	protein-protein interaction	WD repeats
MH5	A4	96AL 112E2 F22B3.2	his-63	histone H3	chromatin structure	0
MH5	A5	ALIV-6123 C2564.4	taa-347	SAND family member: early sperm-fate marker	transcription regulation	SAND domain
				zinc-finger protein: Required for fem-3 3'-UTR-mediated repression in the regulation of the		
MH5	A6	96AL 112E5 M04B2.1	men-1	sperm/oocyte switch	RNA binding	C2H2 7n finger
MH5	Δ7	96AL 112F7 M04B2 3	afl-1	GAS41-like: nutative transcription factor: associates with chromatin	chromatin binding: transcription regulation	cene en inger
MH5	A8	96AL 113E12 K08E4.1	snt-5	SPT transcription factor component.	transcription regulation	
		50/12_115/12/1002/11	spro	involved in maintaining euchromatin-beterochromatin boundaries: thought to form a		
				complex that enhances transcription from repetitive DNA sequences by modulating		
MHS	40	96AL 113G6 E11A10.1	lev-1	chromatin structure	chromatin structure: transcription regulation	bromodomain
IVIND	AS	50AL_11300 F11A10.1	164-1	Chiomatin structure	chiomatin structure, transcription regulation	biomodomam
		AL IV 744 COOFO 40		DNA-binding SAP containing protein; The SAP motif is found in a variety of nuclear proteins	Data Madhan	CAD downlin
MH5	A10	ALIV-/AI C39E9.12		involved in transcription, DNA repair, KNA processing or apoptotic chromatin degradation	DNA binding	SAP domain
MH5	A11	96AL_117A8 C08F11.7		SPK containing protein family member.	DNA binding	SPK domain
				Synthetic multivulva class B (synMuvB) protein. SynMuvB proteins are required to repress		
				the induction of vulval development by Ras signaling and probably act by forming the		
MH5	A12	AL IV-7E9 JC8.6	lin-54	multiprotein DRM complex that repress transcription	transcription regulation	
MH5	B1	GP 2B9 T01E8.4	mec-15	F-box protein with WD repeats	ubiquitine machinery	F-box domain; WD repeats
MH5	B2	96AL_117E1 B0513.6		pseudogene	pseudogene	_
MH5	B3	96AL_117E10Y37A1B.1	lst-3	putative cell cycle and apoptosis regulatory protein	Others (cell cycle)	
MH5	B4	96AL_116F11 Y38H8A.3		tyrosine protein kinase.	protein kinase	
MH5	B5	96AL_96AL_1Y38H8A.5	fezf-1	FEZ family zinc finger protein	DNA binding	
MH5	B6	96AL_117G1 F52B11.1	cfp-1	CFP1 (CpG-binding protein, CXXC Finger Protein 1) homolog	DNA binding	0
MH5	B7	96AL_116G7 Y45F10A.5	nlp-17	neuropeptide-Like Protein.	Others	
MH5	B8	AL IV-7P18 Y51H4A.12	set-26	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH5	B9	AL:IV-8A12 F26D10.3	hsp-1	hsp70A, a member of the heat shock family of proteins	chaperones	
MH5	B10	96AL_122A6 Y41D4B.12	set-23	probable histone methyltransferase	histone modification; DNA methylation	SET
		-		Probable histone methyltransferase involved in chromatin modification and/or remodeling		
MH5	B11	96AL 122B8 C26E6.9	set-2	in meiotic germ cells. May act redundantly with mes-3 and mes-4 proteins	histone modification; DNA methylation	SET
MH5	B12	96AL 120D2 Y116A8C.13		RAD54B homolog (DNA repair protein); helicase	Others (helicases)	· · · · · · · · · · · · · · · · · · ·
				protein containing ubiquitin-like (UBL) and ubiquitin-associated (UBA) domains that is a		
MH5	C1	GP 2B12 7K20.3	rad-23	member of the Radiation Sensitivity 23 (RAD23) family of proteasomal ubiquitin recentors	ubiquitine machinery	
MH5	C2	96AL 121F1 Y73B3B.1		SPK containing protein family member.	DNA hinding	SPK domain
MH5	C3	AL:IV-8017 F26D10 3	hsn-1	hsn70A a member of the heat shock family of proteins	chanerones	of it domain
MHS	C4	96AL 128D1(V/6H3C /	hop 1	DNA topoisomerase II family member	chromatin structure	
MH5	C5	GP 2C3 E43G6 6	imid-1 1	PHD and ImiC domain-containing protein	histone modification: DNA methylation	PHD: ImiC
MH5	C6	GP 3C4 T10B5 4	<i>jiiija</i> 1.1	GCN5-related N-acetyltransferase family member	histone modification; DNA methylation	0
MHS	C7	GP 3C5 F59A7 8		SNE2-related and DNA/RNA belicase	DNA binding/structure	0
MH5	C8	96AL 131E5 E37B4 10		zinc-finger protein	DNA hinding	7n finger C2H2
	00	50/12_15125 15/54110		protein with similarity to the KAT8 NI S3 non-enzymatic subunit of the mammalian		Linniger ezitz
MUE	<u></u>	0641 126412554011.2	cumu 7	KATE MOE histone asstultraneforate complex	histone modification: DNA methylation	
IVIND	69	50AL_130A12F34D11.2	Sulliv-2	and of two C closers homology of human MTA1 (motastasis associated protein) part of a	historie modification, DNA metrylation	
MUE	C10	0641 12487 72764 4	lin 40	nucleoscome remodeling and historie deacetulation (NURD) complex	histone modification: DNA methylation	
MALIE	C10	0CAL 13CDC C18C1 5	hil 4	linkes bistone 111.4	ebremetin etrusture	
MDr	C12	96AL 138P11 C24CC C	hno 15	mixer misculle F11.4.	Others	
IVIND	CIZ	96AL_138B11C24G0.0	11p0-15	sperinine oxidase.	others	
				systemic tive interference beleative, Plays a role in RivA-mediated gene silencing by acting		
NAUE	D1	0641 12702 00455 1	cid 1	colle	PNAi machinany	
IVINS	DI	96AL_137C2 C04F5.1	SIU-1	cells.	RNA Hachinery	7. 6
IVIH5	02	JUAL_136D3 CD4./	21111-1	Zine iniger, mi-type. DEAD hav BNA balicator MUT 14 activity is conviced and understitutish its nearly - Convert	Diver billuing	Ziriniger mir-type
	D 2	0641 12856 614611.6		DEAD DOX RIVA HERCase; IND I-14 activity is required redunidantly with its paralog SINO I-1,	DNA: machinen.	
IVIH5	03	JUNL_136ED U14U11.0	mut-14	Ior germine RINAL and endogenous SIRINA TOTMATION	kinter en en diffectione. Di terre di dette	anabularanafar dowod
IVIH5	D4	90AL_137F9 B0238.10		N-acceptualis/erase 12	instone modification; DNA methylation	acetyitransferase domain
	0.5	0041 40057 84000 4		wago-8, Argonaute nomolog that is partially required for the amplification phase of KNAI	Philip and the second	0.47/004/
MH5	D5	96AL_139F7 K12B6.1	sago-1	responses;	RNAi machinery	PAZ/PIWI
				Probable corepressor protein, which probably participates in the transcriptional repression		
				of the presenilin protein hop-1. Probably acts via the formation of a multiprotein complex		
MH5	D6	96AL_144D11D1014.8	spr-1	that deacetylates and demethylates specific sites on histones	histone modification; DNA methylation	
				Probable corepressor protein, which probably participates in the transcriptional repression		
				of the presenilin protein hop-1. Probably acts via the formation of a multiprotein complex		
MH5	D7	96AL_144D12D1014.9	spr-1	that deacetylates and demethylates specific sites on histones	histone modification; DNA methylation	
				MYST family histone acetyltransferase-like; Probable catalytic subunit of the Tip60		
MH5	D8	96AL_141E5 VC5.4	mys-1	chromatin-remodeling complex	histone modification; DNA methylation	
MH5	D9	96AL_144E12 K07C11.2	air-1	Aurora/Ipl1-related protein kinase 1	protein kinase	
MH5	D10	96AL_141G8 F09G2.9	attf-2	AT-hook motif containing protein.	DNA binding	AT hook
MH5	D11	GP 3D4 T23B12.1	phf-30	PHD-finger containing protein	chromatin binding	PHD finger
				guanine nucleotide exchange factor (GEF) that is similar to Drosophila Claret and human		-
MH5	D12	96AL 147B4 F07C3.4	alo-4	RP3; chromosome condensation	chromatin structure	
MH5	E1	96AL 145E3 F45F2 13	his-6	histone H3	chromatin structure	
MHE	F2	964L 148E3 P07PE 0	/sv-17	histone acetyltransferase	histone modification: DNA methylation	
CUIN	62	JUNE_14013 KU/B3.9	159-12	AAA+ ATPace orthologous to the RUV/RU1 family of ATPaces right 1 functions as a	instone moundation, own methylation	
MUF	F3	96AL 148H2 C27UC 2	rande 1	component of the TOP signaling nathway	Others	
NAUE	L.3 E.4	06AL 149013 C2/II0.2	rdo 1	component of the DIMU/STING Argonauto /Zwille /a/52a family of asstaine	PNAi machinony	
IVIH5	E4	JUAL_140H11KU8H1U./	rue-1	memoer of the Privity Thiso/Argonaute/Zwille/elr2C tamily of proteins	histone medification DNA well have	SET domain
IVIH5	E5	90AL_15UA6 Y32F6A.1	set-22	protein containing tritnorax/polycomo SET domain.	nistone modification; DNA methylation	SELOOMAIN
	50	0.001 4500 00000		prome nyaroxylase; EGL-9 functions in a conserved hypoxia-sensing pathway to negatively	01h	
MH5	E6	96AL_150A12F22E12.4	egl-9	regulate HIF-1 (hypoxia inducible factor) by hydroxylating prolyl HIF-1 residues	Others	
MH5	E7	96AL_152A12K03B8.4			?	
MH5	E8	96AL_150B12C35A5.9	hda-11	class 4 histone deacetylase (HDAC)	histone modification; DNA methylation	
MH5	E9	Supp V-14G17ZK856.9	zhit-3	HIT zinc finger family protein like.	DNA binding	Zn finger HIT-type
MH5	E10	96AL_149E9 C12D8.10	akt-1	Serine/threonine-protein kinase	protein kinase	
MH5	E11	96AL_151E4 C06H2.3	jmjd-5	JmjC domain containing protein; encoding GCN5-related N-acetyltransferase	histone modification; DNA methylation	JmjC domain
MH5	E12	GP 2C12 H06I04.4	ubl-1	Ubiquitin-like protein 1-40S ribosomal protein S27a	ubiquitine machinery	

MH5	F1	96AL 152F7	T27F2 1	skn-1	ortholog of the SKI-binding protein (SKIP); skp-1 is predicted to function as a transcriptional cofactor.	transcription regulation	
MH5	F2	96AL 149G4	B0024.12	gna-1	glucosamine 6-phosphate N-acetyltransferases	histone modification; DNA methylation	
MH5	F3	96AL_151H11	F47G9.4	3	Probable RING finger protein 207 homolog	DNA binding	Zn finger RING
MH5	F4	GP 2D6	T10F2.4	prp-19	Pre-mRNA-processing factor 19 homolog; yeast PRP (splicing factor) related	splicing	WD repeats
MH5	F5	96AL_153D3	F57F5.5	pkc-1	serine/threonine protein kinase that is orthologous to mammalian protein kinase C epsilon	protein kinase	C2112 7n finant
MH5	F0 F7	96AL_155E3	F54F3.1	nid-1	C.elegans homolog of the nidogen (entactin) protein	Others	C2H2 ZH Hinger
MH5	F8	96AL 156E7	Y2H9A.1	mes-4	Histone-lysine N-methyltransferase	histone modification; DNA methylation	
MH5	F9	96AL_153G9	ZK863.6	dpy-30	Dosage compensation protein	Others	
MH5	F10	96AL_159C6	C53A5.3	hda-1	Histone deacetylase 1 encodes two isoforms of an F-box and WD-repeat-containing protein that is a component of	histone modification; DNA methylation	
MH5	F11	96AL_157D10	F55B12.3	sel-10	an E3 ubiquitin ligase	ubiquitin machinery	WD repeats
MH5	F12	GP 3E12	C47E8.8	set-5	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET; SPK domain
MULT	C1	0641 16301	52050 7		ELM2 (Egl-27 and MTA1 homology 2) domain is a small domain of unknown function. It is	DNA hinding	CLND domain
MH5	62	96AL_162B1 96AL_163G4	T10C6 13	his-2	histone H3	chromatin structure	ELIVIZ UOITIAITI
MH5	G3	AL V-11G22	Y102A5C.18	efl-1	E2F-like (mammalian transcription factor)	transcription regulation	
MH5	G4	96AL_171C1	C25F9.5		SNF2-related domain	transcription regulation	SNF2-related domain
MH5	G5	96AL_172G1	Y113G7B.14		pseudogene	pseudogene	
MH5	G6	96AL_172G4	Y113G7B.17	prmt-1	protein arginine N-methyltransferase PRMT1.	histone modification; DNA methylation	CDV dawain
MH5 MH5	68	96AL_175A6	Y97E1UAR.4		SPK-domain containing protein family member.	DNA binding	SPK domain
MH5	G9	96AL 173B11	B0250.9	dhcr-7	7-dehvdrocholesterol reductase.	Others (enzymes)	Sincomun
MH5	G10	AL V-1H20	Y46H3C.4		topoisomerase II family member.	chromatin structure	
MH5	G11	96AL_176A12	R04A9.7		serine/threonine protein kinase-related and tyrosine protein kinase and protein kinase	protein kinase	
MH5	G12	AL X-1G3	F13C5.2		bromodomain-containing protein like.	chromatin structure	bromodomain
MH5	H1	AL X-1K/	104G9.1		Al hook motif containing protein.	DNA binding	AI hook
MH5	H3	96AL 177G3	7K402.3		SPK-domain containing protein family member.	DNA binding	SPK domain
MH5	H4	GP 2F9	C29E4.5	tag-250		histone binding	Tudor domain
MH5	H5	96AL_177G6	ZK402.5	-	SPK-domain containing protein family member.	DNA binding	SPK domain
MH5	H6	AL:X-2C18	C12D12.5	sox-2	putative HMG-box transcription factor orthologous to human SOX1, SOX2, and SOX3	transcription regulation	
MULT		0641 18202	F48DC 1	446 11 1	putative TATA binding protein associated transcription factor; transcription initiation from	transmistion constation	
	H/	96AL_182D3	F48D6.1	taj-11.1	RNA polymerase II promoter	chromatic remodalling	
MH5	H9	AL X-2J11	C24A8.3	pan-15	prion-like Q/N-rich domain protein.	Others	
				p q ==	protein containing trithorax/polycomb SET domain; histone methyltransferase activity (H3-		
MH5	H10	96AL_183F4	ZC8.3	set-30	K4 specific)	histone modification; DNA methylation	SET domain
					protein containing trithorax/polycomb SET domain; histone methyltransferase activity (H3-		
MH5	H11	96AL_183F5	ZC8.3	set-30	K4 specific)	histone modification; DNA methylation	SET domain
MH5	H12	96AL_180G5	K09C4.3	hsp-2	heat-shock protein	pseudogene?	
MH6	A1	AL X-206	F47F2.1		putative Ser/Thr-protein kinase	protein kinase	
					zinc finger family member, probable transcriptional regulator; suppressor of presenilin		
MH6	A2	96AL_182H9	C07A12.5	spr-3	defect.	transcription regulation	
MH6	A3	SuppX-8A23	T03G11.1	pqn-62	prion-like Q/N-rich domain protein; SAP motif-containing protein	DNA binding	SAP motif
MH6	A4	96AL_185A1	F49E10.5	ctbp-1	CtBP transcriptional co-repressor homolog.	transcription regulation	
MH6	A5 A6	96AL_187A10	K03A1 1	lam-2 bis-40	laminin gamma-1. histone H3	others (cell. structures)	
MH6	Δ7	96AL 184F11	T22B7 1	eal-13	SOX domain transcription factor: HMG box	transcription regulation	HMG box
MH6	A8	96AL_187E10	C10A4.8	mnm-2	M Neuron Morphology abnormal, encoding zinc finger, C2H2-type.	DNA binding	Zn finger C2H2
MH6	A9	96AL_184F7	T22B7.1	egl-13	SOX domain transcription factor; HMG box	transcription regulation	HMG box
MH6	A10	GP 3G9	W01C8.3	set-19	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH6	A11	96AL_184F9	W01C8.4	set-20	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH6	A12 P1	96AL_187F3	K08A8.2	sox-2	putative HMG-box transcription factor orthologous to human SOX1, SOX2, and SOX3	transcription regulation	HMG box
MH6	B1 B2	96AI 188A17	F1466.5	set-12	protein containing trithorax/polycomb SET domain.	histone modification: DNA methylation	SFT domain
MH6	B3	96AL 190A7	C28G1.1	ubc-23	ubiquitin conjugating enzyme.	ubiquitin machinery	
MH6	B4	AL X-4C5	C47C12.3	ref-2	zinc finger C2H2-type, transcription factor	transcription regulation	Zn finger C2H2
MH6	B5	96AL_190B1	C06E2.3	ubc-21	ubiquitin conjugating enzyme.	ubiquitin machinery	
MH6	B6	96AL_190D6	F47E1.3		zinc finger, C2H2-type. Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active	DNA binding	Zn finger C2H2
MH6	B7	96AL_188E4	F45E1.6	his-71	genes	chromatin structure	
MH6	B8	96AL_189E5	D2021.1	utx-1	putative histone H3 di/trimethyllysine-27 (H3K27me2/me3) demethylase	histone modification; DNA methylation	
MH6	B9	96AL_189F1	F18E9.5	jmjd-3.1	histone H3 trimethyllysine-27 (H3K27me3) demethylase	histone modification; DNA methylation	WD40 research
MH6	B10 B11	964L 18866	E22E1 1	swu-2.2 hil-3	histone H1 3	chromatin structure	WD40 repeats
MH6	B12	96AL 188G8	F22F1.3		transcription cofactor activity	transcription regulation	
MH6	C1	96AL_190G12	E01H11.1	pkc-2	protein kinase C.	protein kinase	
MH6	C2	96AL_195A3	C49F5.5		putative histone acetyltransferase activity	histone modification; DNA methylation	Zn finger
MH6	C3	96AL_192D6	F46F6.2	pkn-1	protein kinase N1.	protein kinase	
MHG	C4	96AL_195E3	WU6D11.4	obf 22	Histone-lysine N-methyltransferase, H3K79-specific	histone modification; DNA methylation	RHD finger
MH6	C6	96AL 194F5	C34E11.1	rsd-3	RNAi Spreading Defective	RNAi machinery	
MH6	C7	96AL_194F8	F54F7.1	taf-7.1	putative TATA binding protein associated transcription factor	transcription regulation	
MH6	C8	96AL_193G3	F38B2.1	ifa-1	Intermediate filament protein	Others (cell. structures)	
MH6	C9	96AL_192G9	F13E6.3	phf-31	PHD finger family	chromatin binding	PHD finger
MH6	C10	96AL_194G2	F54F7.7	andra 1	Histone-lysine N-methyltransferase, H3K79-specific	histone modification; DNA methylation	homoodomain like
MH6	C12	96AL_192H3	T01C1.5	Indr-1	ortholog of the human historie demethylase LSD1	histone modification: DNA methylation	nomeodomain-like
MH6	D1	96AL 194H12	C49F5.2	set-6	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET domain
MH6	D2	96AL_197A1	K09A11.1		zinc finger family member.	DNA binding	Zn finger
MH6	D3	96AL_197A5	K09A11.5	phf-33	PHD-finger family protein like.	chromatin binding	PHD finger
MH6	D4	96AL_198A2	ZK1086.3		putative methyltransferase	histone modification; DNA methylation	Methyltransferase FkbM
MH6	D5	96AL_199A3	F23D12.5	jmja-3.2	putative historie H3 di/trimethyliysine-27 (H3K2/me2/me3) demethylase linker historie H1 1, essential for chromatin silencing and germline development: HIS-24 is	histone modification; DNA methylation	
					retained in granular structures in the cytoplasm and this promotes germline development.		
MH6	D6	96AL_199A6	M163.3	his-24	and influences histone H3 methylation by the polycomb group genes MES-2/3/4/6.	chromatin structure/remodelling	
MH6	D7	96AL_197B5	F46G10.3	sir-2.3	similarity to the Saccharomyces cerevisiae Sir2p NAD-dependent histone deacetylase	histone modification; DNA methylation	
MH6	D8	96AL_197B9	F46G10.7	sir-2.2	similarity to the Saccharomyces cerevisiae Sir2p NAD-dependent histone deacetylase	histone modification; DNA methylation	
MH6	D9	96AL_198B8	+48F7.1	alg-1	Argonaut ortholog	RNA: machinery	PPCT domain
MH6	D10	9641 106C11	113F2.3 T22H6.6	pis-1 aei-3	or money or manimalian Pax transcription activation domain interacting protein PTIP	transcription regulation	HMG box
MH6	D12	96AL 197C11	C29F7.6	jmjd-3.3	putative histone H3 di/trimethyllysine-27 (H3K27me2/me3) demethylase	histone modification; DNA methylation	
MH6	E1	GP 3A11	R13.4	miz-1	Miz-type Zn finger transcription factor	transcription regulation	Zn finger
MH6	E2	96AL_196D1	T14G8.1	chd-3	Chromodomain protein, DNA binding helicase Mi-2 like	chromatin remodelling	chromodomain
MH6	E3	GP 4A5	F02D10.7	set-8	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH6	E4	GP 4F8	D1053.2		Histone-iysine N-methyltransterase, H3 lysine-79 specific	DNA binding	UUI1
MH6	ED F6	96AL_198E5	F2000.4 F54B11.6	bra-1	BMP recentor associated protein	NA/protein binding	Zn finger MYND
MH6	E7	96AL_196H10	K08H2.6	hpl-1	Heterochromatin protein 1 homolog	chromatin structure	bci iiiiiib
MH6	E8	GP 1B12	K06A5.8		protein containing WD40 repeats	protein-protein interaction	WD40 repeats
MH6	E9	Supp I-9F2	ZK973.2	cec-10	C. elegans chromodomain protein	chromatin remodelling	chromodomain
MH6	E10	96AL_201A12	1+53H4.6	F53H4.2	putative helicase	Others (helicases)	
	E 1 1	96AL 202A6	FZ2H10.5		putative killase	protein kinase	

				histone deacetylase; Responsible for the deacetylation of lysine residues on the N-terminal		
MH6 MH6	E12 F1	GP 4B1 C10E2.3	hda-4 ameh-2	part of the core histones (H2A, H2B, H3 and H4) SAND family member	histone modification; DNA methylation transcription regulation	SAND domain
MH6	F2	AL X-4L16 C17G1.4	nra-3	Zn finger, PHD-type	chromatin binding	PHD finger
MH6	F3	AL X-7K21 K09A9.4	usp-33	Ubiquitin carboxyl-terminal hydrolase	ubiquitin machinery	
MH6	F4	96AL S1A3 B0207.4	air-2	Serine/threonine-protein kinase which mediates both meiotic and mitotic chromosome segregation. Required for histone H3 'Ser-10' phosphorylation	methylation	
MH6	F5	96AL_S1A11 Y71F9B.7	plk-2	Ser/Thr-protein kinase	protein kinase	
MH6 MH6	F6 F7	96AL_S1C3 Y47G6A.6	pcaf-1 chaf-2	C. elegans PCAF/GCN5-like histone acetyltransferase.	histone modification; DNA methylation	
WIND	F7	50AL_51C0 1710128.1	chuj-2	BET-family protein that colocalizes with chromosomes; Bet-family proteins are		
MH6	F8	96AL_S1C12 Y119C1B.8	tag-332 = bet-1	evolutionarily conserved, have two bromodomains, which recognize acetylated histone	chromatin binding	bromodomain
MH6	F9	96AL_S2B3 T06D10.2	chaf-1	chromatin assembly like.	chromatin structure	
MH6	F10	96AL S3A1 F26A3.8		RNAi	RNAi machinery	
MH6	F11	96AL_S3A7 C41G7.4	set-32	a divergent histone H3 lysine-9 (H3K9) methyltransferase homolog with a SET domain	histone modification; DNA methylation	SET
MH6	F12	cloned Y43F11A.5	set-24	protein containing trithorax/polycomb SET domain	histone modification; DNA methylation	SET
MH6	G1	96AL_S3C9 Y71A12B.9	usp-3	ubiquitin-specific protease PCOP (REST CO Represent) homelogy similar to co represent of REST RE1 silonsing	ubiquitin machinery	
MH6	G2	96AL S3H3 Y74C9A.4	rcor-1	transcription factor.	transcription regulation	SANT; Zn finger GATA
MH6	G3	96AL_S4B3 B0205.9		SPK-domain containing protein	DNA binding	SPK domain
MH6	G4	96AL_S5C9 Y92H12A.2	tak 0	E3 ubiquitin-protein ligase	ubiquitin machinery	
MH6	G6	Supp:II-10011Y52E8A.2	luj-8	putative TATA binding protein associated transcription factor.	DNA binding	Zn finger RING; PHD finger
MH6	G7	Supp:II-10A1CY48E1B.13	csp-1	caspase	Others (caspase)	
MH6	G8	96AL_S7B3 C13B4.2	usp-14	ubiquitin-specific protease	ubiquitin machinery	
MH6	G9	96AL S7E2 Y17G7B.2	ash-2	c. elegans or tholog of brosophila Ash2, a trithorax group protein that is a member of the conserved H3K4 trimethylation (H3K4me3) complex	histone modification; DNA methylation	
				plant homeodomain-containing protein closely related to human ING3; PHD-type zinc finger		
MH6	G10	96AL_S8B9 Y51H1A.4	ing-3	mediates the binding to H3K4me3	chromatin binding	PHD finger
MH6	G11	96AL 59A8 F10B5.7	rrf-3	resistance to viral infections.	RNAi machinery	
MH6	G12	96AL_S9E1 K12H6.11	set-13	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH6	H1	cloned T07C4.11	jmjd-4	JmjC-domain containing protein	histone modification; DNA methylation	JmjC
		0CN CARADVATDOA 4C		putative ribosomal protein S6 kinase (S6K) required additively with IFG-1 for normally high	and the later of	
MH6 MH6	н2 Н3	96AL_S14B12Y4/D3A.16 96AL_S14D1_Y71H2AM.8	rsкs-1 set-27	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SET
MH6	H4	96AL_\$15C3 BE0003N10	3	putative ubiquitin-protein transferase activity	ubiquitin machinery	
MH6	H5	96AL_S15E6 Y111B2A.16	taf-7.2	putative TATA binding protein associated transcription factor.	transcription regulation	
MH6	нь H7	96AL_S15H2 ¥6/D2.7 96AL_S18A1_F40F12.7		CREB binding protein like family member.	transcription regulation transcription regulation	Zn finger TAZ type
MH6	H8	96AL_\$18H5 K03H1.10	cbp-2	CREB binding protein like family member.	transcription regulation	Zn finger TAZ type
MH6	H9	96AL_S20B6 VT23B5.1		ncRNA	others	
MH6 MH6	H10 H11	96AL_S20C3 Y24D9A.2 Supp:IV-9424Y37F11B.4	set-21 taf-2	protein containing trithorax/polycomb SET domain.	histone modification; DNA methylation	SEI
MH6	H12	Supp:IV-9G04Y55F3AM.14	1	zinc finger C2H2 type protein.	DNA binding	Zn finger C2H2
				Colores attales of the Descentille and exampling CET anticles CDD 2 is and interded to be a		
				member of the SET protein complex that functions in chromatin remodeling, DNA repair, and		
MH7	A1	96AL_S23D3 C27B7.1	spr-2	transcriptional regulation	chromatin remodelling / transcription regulation	
MH7	A2	96AL_S24A6 Y94H6A.6	ubc-8	ubiquitin conjugating enzyme	ubiquitin machinery	
MH7	A3	96AL_\$28A6 F26F12.7	chd-4	(NURD) complex; LET-418 is similar to DNA helicases	histone modification / chromatin remodelling	chromodomain; PHD finger
		-	rpm-1/rpm-3/			
N 41 1 7		0041 0001070	sam-1/sad-	F2kisuitia asataia liasaa	ubicuitie mechinem.	
MH7	A4 A5	Supp:V-14E24Y113G7B.23	5/syu-3 psa-1/swsn-1	SWI3/SNF-related matrix-associated actin-dependent regulator of chromatin-like protein	DNA binding	SANT/Myb domain
MH7	A6	96AL_S30F4 K04A8.6	dre-1	F-box protein	ubiquitin machinery	F-box domain
				thialysine N-(epsilon)-acetyltransferase, belonging to the GCN5-related N-acetyltransferase		
MH7 MH7	A7 48	Supp:V-15E2CD2023.4	suds-3	supertamily SUDS (vertebrate SUppressor of Defective Silencing) homolog	histone modification; DNA methylation	GNAT domain
MH7	A9	96AL_\$38D4 F59A7.4	hil-6	Putative histone H1.6	chromatine structure	
MH7	A10	96AL_S40C6 F55G7.2		DOT1 histone methyltransferase family	histone modification; DNA methylation	DOT1
MH7 MH7	A11 A12	Supp:X-8G5 M163.2 Supp:X-8A4 F28H6.1	akt-2	Linc tinger putative Transcription Factor family homolog of the serine/threonine kinase Akt/PKB	protein kinase	
MH7	B1	96AL_\$42B9 Y40A1A.1		protein kinase	protein kinase	
MH7	B2	Supp:X-8F5 F45B8.4	pag-3	C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1	DNA binding	C2H2-type Zn finger
MH7 MH7	В3 В4	VL_10002-F1180205.7 VL_10012-B5 7K909.2	kin-3 kin-1	ortholog of the catalytic subunit of casein kinase ii alpha; serine/threonine kinase serine/threonine protein kinase	protein kinase	
MH7	B5	VL_10012-G1 ZK909.2	kin-1	serine/threonine protein kinase that is orthologous to cAMP-dependent protein kinase	protein kinase	
MH7	B6	VL_10013-E1:Y51H1A.4	ing-3	Proteins are expected to have molecular functions (NADH dehydrog96AL_se (ubiquinone) ac	tchromatin binding	PHD-finger
MH7 MH7	B7 B8	AL II-9E3 W03H9.1 VL 10018-F9 B0207.4	air-2	Zn finger, PHD-type aurora/Inl1-related serine/threonine protein kinase	chromatin binding protein kinase	PHD-finger
MH7	B9	VL_10018-H5 Y48E1B.13	csp-1	caspase	Others (caspase)	
		V# 40000 CE CADRA 2		ubiquitin-specific protease 14 (Usp14), a highly conserved thiol protease that hydrolyzes the	a la sector de la se	
MH7	в10 B11	vL_10020-C5 C13B4.2 VL 10020-C1:Y48E1B.13	usp-14 csp-1	peptide bond at the C-terminal giftline of ubiquitin caspase	Others (caspase)	
MH7	B12	VL_10021-G6 F09E5.1	pkc-3	atypical protein kinase	protein kinase	
MH7	C1	VL_10022-F1 E01H11.1	pkc-2	protein kinases similar to the classical protein kinase C family	protein kinase	
				ET domain-containing protein that is orthologous to the Drosophila Polycomb group protein Enhancer of zeste [F(7)]: as a member of a Polycomb-like chromatin repressive complex		
MH7	C2	VL_10022-G5 R06A4.7	mes-2	with MES-3 and MES-6	histone modification; DNA methylation	
MH7	C3	AL IV-3G8 C17H12.1	dyci-1	dynein intermediate chain	protein-protein interaction	WD repeats
MH7 MH7	C4	VI 10036 CA VEAC3A 31		ubiquitin conjugating enzyme.	ubiquitin machinery	
MH7	C5	VL_10030-04 13402A.31	ubc-13 ubc-14	nutative ubiquitin conjugating enzyme E2G 2	ubiquitin machinery	
MH7	C5 C6	VL_10030-84 73482A.31 VL_10037-B1 Y87G2A.9 VL_10051-F4 F40F12.7	ubc-13 ubc-14	putative ubiquitin conjugating enzyme E2G 2.	ubiquitin machinery DNA binding	Zn finger
MH7	C5 C6 C7	VL_10030-64 F3462A31 VL_10037-B1 Y87G2A.9 VL_10051-F4 F40F12.7 VL_10114-C8 C15F1.8	ubc-13 ubc-14	putative ubiquitin conjugating enzyme E2G 2.	ubiquitin machinery DNA binding ?	Zn finger
	C5 C6 C7 C8	VL_10030-84 F3402A.51 VL_10037-B1 Y87G2A.9 VL_10051-F4 F40F12.7 VL_10114-C8 C15F1.8 VL_10154-B1:F45B8.4	ubc-13 ubc-14 pag-3	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1	ubiquitin machinery DNA binding ? DNA binding	Zn finger C2H2-type Zn finger
	C5 C6 C7 C8	VL_10037-B1 Y87G2A.9 VL_10051-F4 F40F12.7 VL_10114-C8 C15F1.8 VL_10154-B1:F45B8.4	ubc-13 ubc-14 pag-3	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1	Ubioutin machinery DNA binding ? DNA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein
MH7	C5 C6 C7 C8 C9	VL_1003/54 194224.31 VL_10051-F4 F40F12.7 VL_10154-F40F12.7 VL_10114-C8 C15F1.8 VL_10154-B1:F45B8.4 Supp III-8F21 Y54H5A.1	ubc-13 ubc-14 pag-3	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1	Ubioutin machinery DNA binding ? DNA binding chromatin binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain
MH7 MH7	C5 C6 C7 C8 C9 C10	VL_10037-B1 Y87G2A.9 VL_10037-B1 Y87G2A.9 VL_10151-F4 F40F12.7 VL_10114-C8 C15F1.8 VL_10154-B1:F45B8.4 Supp III-8F21 Y54H5A.1 VL_11002-D3 Y37F11R 4	ubc-13 ubc-14 pag-3 taf-2	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2	Ubiquitin machinery DNA binding ? DNA binding chromatin binding transcription regulation	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain
MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11	VL_1003/04 198762A.9 VL_10051-F4 F40F12.7 VL_1014-C8 C15F1.8 VL_1014-C8 C15F1.8 VL_1014-B1:F45B8.4 Supp III-8F21 Y54H5A.1 VL_11002-D3 Y37E11B.4 VL_11010-D1 Y47D3A.26	ubc-13 ubc-14 pag-3 taf-2 smc-3	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint964_nec of chromosomes) family	Ubiquitin machinery UNA binding PNA binding chromatin binding transcription regulation chromatine structure	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain
MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C11 C12 C14	VL_1003-04 i Y8762A.9 VL_1003-14 Y8762A.9 VL_10151-74 F40F12.7 VL_10114-08 C15F1.8 VL_10154-81:F4588.4 Supp III-8F21 Y54H5A.1 VL_11002-D3 Y37E118.4 VL_11010-19 Y4703A.26 VL_11010-19 Y4703A.16	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL, nec of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family	Ubiquitin machinery DNA binding DNA binding DNA binding transcription regulation chromatine structure protein kinase	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain
MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1	VL_1003-04 F 18762A.91 VL_1003-F4 F49762A.9 VL_10154-68 C15F1.8 VL_10114-68 C15F1.8 VL_10154-B1:F4588.4 VL_1010-03 Y37E118.4 VL_11010-D1 Y47D3A.26 VL_11010-E3 Y47D3A.16 AL IV-3C1 C06E7.3	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL_nce of chromosomes) family putative ribosomal protein 56 kinase (56K); Serine/threonine protein kinase family S-adenosyl methionine synthase	Ubiquitin machinery DNA binding ? DNA binding chromatin binding transcription regulation chromatine structure protein kinase Others	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction)
MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2	VL_1003-04 F 198762A.91 VL_1003-F4 F49762A.91 VL_10154-68 C15F1.8 Supp III-8F21 Y54H5A.1 VL_11010-D3 Y37E11B.4 VL_11010-D1 Y47D3A.26 VL_11010-F3 Y47D3A.16 AL IV-3C1 C06E7.3 VL_11013-D6 C0168.9	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 jet-526	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL_nce of chromosomes) family putative ribosomal protein S6 kinase (56K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex	Ubiquitin machinery DNA binding ? DNA binding chromatin binding transcription regulation chromatine structure protein kinse Others DNA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain
MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2	VL_1003-04 198762A.91 VL_1003-14 198762A.91 VL_10151-F4 F40F12.7 VL_10114-C8 C15F1.8 VL_1014-B1:F45B8.4 VL_11010-D1 Y4703A.16 AL IV-3C1 C06F7.3 VL_11013-D6 C0168.9	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL_nce of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWJ/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown	Ubiquitin machinery UNA binding ? DNA binding chromatin binding transcription regulation chromatine structure protein kinase Others DNA binding	2n finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain
MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D3	VL_1003-04 - 198762A.91 VL_10051-F4 F40F12.7 VL_1011-K2 C15F1.8 VL_101154-B1:F4588.4 Supp III-8F21 Y54H5A.1 VL_11002-D3 Y37E118.4 VL_11010-D1 Y47D3A.26 VL_11010-D1 Y47D3A.26 VL_11010-D1 Y47D3A.16 AL IV-3C1 C06E7.3 VL_11013-D6 C0168.9 GP 264 R10E11.1	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL, nec of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to posses histone acetyltransferase activity DMD forcer receiptione article	Ubiquitin machinery Ubiquitin machinery DNA binding ? DNA binding chromatin binding transcription regulation chromatine structure protein kinase DNA binding bistone modification / transcription regulation chromatine modification / transcription regulation bistone modification bistone modification bistone modification bistone modification bistone modification bistone modification bistone	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5	VL_1003-04 + 198762A.91 VL_1003-14 + 198762A.91 VL_101051-F4 + F40F12.7 VL_10114-C8 C15F1.8 VL_10104-C8 C15F1.8 VL_11010-D3 Y37E118.4 VL_11010-D3 Y37E118.4 VL_11010-E3 Y47D3A.16 AL IV-3C1 C05E7.3 VL_11013-D6 C0168.9 GP 264 R10E11.1 Cloned F57C7.1 VL_1101F47C4.6	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1 bet-2 hma-6	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL, nec of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to possess histone acetyltransferase activity PHD-finger containing protein	Ubiquitin machinery UbA binding ? DNA binding chromatin binding transcription regulation chromatine structure protein kinase Others DNA binding histone modification / transcription regulation chromatine binding DNA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger PHD finger HMG hox
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5	VL_1003-04 F3762A.91 VL_1003-F4 F49762A.9 VL_10154-8C 15F1.8 VL_10114-8C 15F1.8 VL_10114-8C 15F1.8 VL_11002-03 Y37E118.4 VL_11010-D1 Y47D3A.16 VL_11010-E3 Y47D3A.16 AL IV-3C1 C06E7.3 VL_11013-D6 C0168.9 GP 2G4 R10E11.1 Cloned F57C7.1 VL_11014-D1 F47G4.6	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1 bet-2 hmg-6	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL, nec of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to passes histone acety/transferase activity PHD-finger containing protein High mobility group box domain	Ubiquitin machinery UNA binding P DNA binding chromatin binding transcription regulation chromatine structure protein kinase Others DNA binding Nistone modification / transcription regulation chromatine binding DNA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger PHD finger HMG box cold-shock domain; CCHC Zn
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 C7 C9 C10 C11 C12 C12 D1	VL_1003-04 F 198762A.9 VL_1003-14 F 198762A.9 VL_10051-F4 F40F12.7 VL_10114-C8 C15F1.8 Supp III-8F21 Y54H5A.1 VL_11010-D1 Y47D13A.26 VL_11010-E3 Y47D3A.16 AL IV-3C1 C06E7.3 VL_11013-D6 C0168.9 GP 2G4 R10E11.1 Cloned F57C7.1 VL_11014-D1 F47G4.6 VL_11014-G3 F02E9.2	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1 bet-2 hmg-6 lin-28	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL_nce of chromosomes) family putative ribosomal protein 56 kinase (56K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to posses histome acetyltransferase activity PHD-finger containing protein High mobility group box domain heterochronic gene; miRNA interaction incomensentian Tames for the	Ubiquitin machinery Ubiquitin machinery DNA binding ? DNA binding transcription regulation chromatine structure protein kinase Others DNA binding histone modification / transcription regulation chromatin binding DNA binding NA binding NA binding NA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBB4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger PHD finger HMG box cold-shock domain; CCHC Zn finger
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 D7 D8	VL_1003-04 F 198762A.9 VL_1003-14 F 198762A.9 VL_10154-81 F 198762A.9 VL_10114-08 C 15F1.8 Supp III-8F21 Y54H5A.1 VL_11010-01 Y4703A.26 VL_11010-18 Y4703A.16 AL IV-3C1 C 06E7.3 VL_11013-D6 C 0168.9 GP 2G4 R10E11.1 Cloned F57C7.1 VL_11014-01 F47G4.6 VL_11014-63 F02E9.2 VL_11014-63 F02E9.2 VL_11019-C 11 Y54E108R.8	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1 bet-2 hmg-6 lin-28 ztf-23 set-32	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL,nce of chromosomes) family putative ribosomal protein S6 kinase (56K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to posses histone acetyltransferase activity PID-finger containing protein High mobility group box domain heterochronic gene; miRNA interaction Zinc finger putative Transcription Factor family SET-domain containing protein; bistone H3 lysine-0 (H3K9) methyltransferase	Ubiquitin machinery Ubiquitin machinery DNA binding ? DNA binding transcription regulation chromatin binding transcription regulation chromatin binding DNA binding NA binding NA binding NA binding DNA binding D	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger PHD finger HMG box cold-shock domain; CCHC Zn finger C2H2-type Zn finger SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	C5 C6 C7 C8 C9 C10 C11 C12 D1 D2 D3 D4 D5 D6 D7 B8 D9	VL_1003-04.4 198762A.9 VL_1003-14 198762A.9 VL_101051-F4 F40F12.7 VL_10114-C8 C15F1.8 VL_10104-B1:F4588.4 Supp III-8F21 Y54H5A.1 VL_11010-D1 Y47D3A.26 VL_11010-D1 Y47D3A.26 VL_11010-D1 Y47D3A.16 AL IV-3C1 C06E7.3 VL_11013-D6 C0168.9 GP 2G4 R10F1.1 Cloned F57C7.1 VL_11014-D1 F47G4.6 VL_11014-D1 F47G4.6 VL_11014-D1 F47G4.6 VL_11019-G7 C41G7.4 VL_11019-G7 C41G7.4	ubc-13 ubc-14 pag-3 taf-2 smc-3 rsks-1 sams-4 let-526 cbp-1 bet-2 hmg-6 lin-28 ztf-23 set-32 set-10	putative ubiquitin conjugating enzyme E2G 2. C2H2 zinc-finger protein orthologous to Drosophila SENSELESS, and to human GFI1 member of the peptidase M1 family, a predicted aminopeptidase with similarity to human TBP-associated factor 2 SMC (structural maint96AL_nce of chromosomes) family putative ribosomal protein S6 kinase (S6K); Serine/threonine protein kinase family S-adenosyl methionine synthase component of the SWI/SNF complex homolog of the mammalian transcriptional cofactors CBP and p300 that have been shown to posses histone acetyltransferase activity PHD-finger containing protein High mobility group box domain heterochronic gene; miRNA interaction Zinc finger putative Transcription Factor family SET-domain containing protein; histone H3 lysine-9 (H3K9) methyltransferase SET (trithorax/polycomb)-domain containing	Ubiquitin machinery Ubiquitin machinery DNA binding Chromatin binding transcription regulation chromatine structure protein kinase Others DNA binding DNA binding DNA binding NA binding	Zn finger C2H2-type Zn finger WD40, histone-binding protein RBBP4 N-terminal domain ARID (AT-rich interaction) domain bromodomain; Zn finger PHD finger HMG box cold-shock domain; CCHC Zn finger C2H2-type Zn finger SET MYND-type Zn finger

MH7	D10	VL 11021-C3	Y74C9A.4	rcor-1		chromatin binding	SANT/Mvb: Zn finger
MH7	D11	VI 11021-E5	Y47G64 19		metallocarboxynentidase	Others	
NA117	D12	VI 11021-F3	P020E 0		CDK domain containing protein	DNA binding	SBK domain
MH7	D12	VL_11021-He	B0205.9		SPK-domain containing protein	DNA binding	SPK domain
MH7	E1	VL_11022-A2	Y71F9B.7	plk-2	Serine/threonine-protein kinase	protein kinase	
MH7	E2	VL_11022-A1	Y47G6A.6	pcaf-1	C. elegans PCAF/GCN5-like histone acetyltransferase	histone modification; DNA methylation	
MH7	E3	Cloned	C04F12.1	vsr-1	Argonaute protein	RNAi machinery	PIWI
MU7	E A	Cloned	V110A7A 12	chn 1	CHORD containing protain: gormline RNAi	RNAi machinen/	CHORD domain
IVIT17	L4	cioneu	1110A/A.15	cnp-1	CHORD containing protein, germine KNAi	inver indefinitely	CHORD domain
					Mediator of RNA polymerase II transcription subunit 1.1; Component of the Mediator		
					complex, a coactivator involved in the regulated transcription of nearly all RNA polymerase		
MH7	F5	VI 11023-C6	Y71F9B.10	son-3	II-dependent genes.	transcription regulation	
					BET-family protein that colocalizes with chromosomes: Ret-family proteins are		
	50	VII 11022 D1	W440C4D 0	1 222 h 4	be in the protocol that concerns the medematic which see an in construct the back	observation binding	have a state of a second se
MH7	Eb	VL_11023-D1	Y119C1B.8	tag-332 = bet-1	evolutionarily conserved, have two promodomains, which recognize acetylated historie		bromodomain
MH7	E7	Cloned	Y37D8A.11	cec-7	C. elegans Chromodomain protein	histone modification; DNA methylation	chromodomain
MH7	FS	VI 11023-H1	K12C11 /	dank-1	death-associated protein (DAP) kinase	nrotein kinase	ANK repeats
	20	vc_11025111	K12C11.4	dupk-1	acath associated protein (DAT) kinase	history and Proton Diff. and history	Antropeats
MH/	E9	Cloned	K03D10.3	mys-2	MYST acetyltransferase	histone modification; DNA methylation	chromodomain
MH7	E10	VL_11025-B9	K05F1.2	msp-142	major sperm protein	Others	MSP
MH7	F11	Cloned	R06C1 1	hda-3	histone deacetylase	histone modification: DNA methylation	histone-deacetylase domain
141117		cioned	10001.1	1100-5	historie deacetylase	instance modification, brittineen justion	instance dedectylase domain
MH7	E12	VL_11031-H3	Y9D1A.1			others	
					nucleolar phosphoprotein related to Saccharomyces cerevisiae SRP40 and the vertebrate		
					Nonn140 proteins that may play a role in rRNA gene transcription and nucleolar structural		
N 41 1 7	F1	Clanad	C25 41 10	dan F	organization	rBNA related	CDD 40 de maio
IVIN /	F1	Cioned	C25A1.10	uu0-5	organization	TRINA-Telateu	SRP40 domain
					trithorax group protein that is a member of the conserved H3K4 trimethylation (H3K4me3)		
MH7	F2	VL_11036-D6	Y17G7B.2	ash-2	complex	histone modification; DNA methylation	
MH7	E3	Cloned	H15N1/ 1	adr-1	ADAR (adenosine deaminase acting on RNA)	RNAi machinery	
		el	1151414.1	-		Others (call structure)	
MH7	F4	Cloned	C43E11.11	cogc-5	Conserved Oligomeric Golgi (COG) Component	Others (cell. structures)	
					PAZ/PIWI domain-containing protein; mutants are resistant to RNA interference in the		
MH7	F5	Cloned	C18F3.7	nnw-1	germline.	RNAi machinery	PAZ/PIWI domain
				his AF - his FF			
				1115-45 = 1115-55,			
				F54E12.1 + many			
MH7	F6	VL_11040-F5	B0035.10	more	histone 3	chromatine structure	
MH7	F7	Cloned	B0261 1		DNA-binding protein	DNA binding	SANT/Myb domain
		cioneu	00201.1		bit		SANT/NIVE COMMAN
MH7	F8	HR	B0261.1		DNA-binding protein	DNA binding	SANT/Myb domain
MH7	F9	Cloned	Y73B3B.2	set-28	SET-domain containing protein	histone modification; DNA methylation	SET
MHZ	F10	VI 11054 117	Y714128 9	usn-3	Libiquitin Specific Protease	ubiquitin machinery	
WILLY	110	vc_11034-H2		usp-u	euro (euro feurle attende europeante la trans de uno a feno a feno atte	a sequent machinery	
					SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 historie		
MH7	F11	VL_11054-H5	Y111B2A.22	ssl-1	acetyltransferase complex	chromatin remodelling; histone modification	SWI/SNF
MH7	F12	VL_11055-F5	D2023.4		N-acetyltransferase	histone modification; DNA methylation	acetyltransferase domain
MU7	61	Cloned	V110A7A 19	nnw 7	ancoding BAZ/DIM/L domain containing	RNAi machinen/	RAZ/RIM/L domain
IVIT17	01	cioneu	1110A/A.10	ppw-2	encounig FAZ/FIWI domain-containing.	inveringerinery	
MH7	G2	VL_11068-F5	F59A7.4	hil-6	Putative histone H1.6	chromatine structure	
MH7	G3	VL_11071-D1	K04A8.6	dre-1	F-box protein	ubiquitin machinery	F-box domain
MH7	G4	VL 11071-F1	Y113G7B.23	psa-1/swsn-1	SWI3/SNF-related matrix-associated actin-dependent regulator of chromatin-like protein	chromatin remodelling	SANT/Myb domain
MH7	65	VI 11071-HG	F38B7 5	duo-1	deubiquitylating with LISD/LIBD and OTLL domains: ubiquitin specific protease	ubiquitin machinery	LISP domain
	65	VL_11071-115	55567.3	000-1	Ustana haina Narathaltara farra 10 haina 70 anaife	history and Costing DNA south latter	osi domani
MH7	Gb	VL_11077-B9	F55G7.2		Histone-iysine N-metnyitransferase, H3 lysine-79 specific	nistone modification; DNA methylation	
MH7	G7	VL_11081-E2	W10G6.2	sgk-1	serine/threonine protein kinase	protein kinase	
MH7	G8	VL_11201-B2	Y48E1B.13	csp-1	Caspase-related protein 1A	Others (caspase)	SPK domain
MH7	69	VI 11303-F8	Y57A10A.3		SPK-domain containing protein	DNA binding	SPK domain
MH7	610	VI 11304-F2	V57A10A 6			otrbers	
141117	010	VL_11504-L2	137/4104.0		Transaciational regulator ATBY hamalan modifier same supression by offerting shreensting	ormens	1
					manscriptional regulator ATKX homolog; mountes gene expression by anecting chromatin;		
MH7	G11	JAP-MS box2	B0041.7	xnp-1/slr-8	helicase	Others (helicases)	
	643	140 440 1					
MH7	G12	JAP-IVIS DOX2	C25F9.5			DNA binding	SNF2-related
MH7	612	JAP-IVIS DOX2	C25F9.5		encoding SWI2/SNE2 family ATPase: may participate in a TRR-1/MYS-1/EPC-1/SSI-1 histone	DNA binding	SNF2-related
MH7	G12	JAP-IVIS DOX2	C25F9.5	cd 1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone	DNA binding	SNF2-related
MH7 MH7	G12 H1	JAP-MS box2	C25F9.5 Y111B2A.22	ss/-1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex	DNA binding chromatin remodelling	SNF2-related SWI/SNF
MH7 MH7	H1	JAP-INS box2	C25F9.5 Y111B2A.22	ssl-1 let-418/evl-11,	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase	DNA binding chromatin remodelling	SNF2-related SWI/SNF
МН7 МН7 МН7	G12 H1 H2	JAP-MS box2 JAP-MS box2 JAP-MS box2	C25F9.5 Y111B2A.22 F26F12.7	ssl-1 let-418/evl-11, chd-4	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LT-418 is similar to DNA helicases	DNA binding chromatin remodelling histone modification / chromatin remodelling	SNF2-related SWI/SNF chromodomain; PHD finger
MH7 MH7 MH7 MH7	G12 H1 H2 H3	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5	ssl-1 let-418/evl-11, chd-4	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member	DNA binding chromatin remodelling Nistone modification / chromatin remodelling DNA binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related
MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14	ssl-1 let-418/evl-11, chd-4	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LT-418 is similar to DNA helicases transcription factor family member	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3 1	ssl-1 let-418/evl-11, chd-4	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/(/HD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1	ssl-1 let-418/evl-11, chd-4	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LT-1418 is similar to DNA helicases transcription factor family member	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18	ssl-1 let-418/evl-11, chd-4 pme-1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/(/HD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. IET-148 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme)	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding chromatin binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex; LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnm11 (DNA-methyltranferase)	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification, DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5 1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/(/HD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; ET-148 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein acrinione N-methyltransferase.	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding chromatin binding histone modification; DNA methylation bistone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5.1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. ET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5.1 C15H11.5	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/(/HD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex; ET-148 Is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltransferase) protein arginine N-methyltransferase protein catianing trithorax/polycomb SET domain	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5.1 C15H11.5 R07B5.9	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5.1 C15H11.5 R07B5.9 Y2390 E	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/(/HD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex_LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y437B8.14 MO4C3.1 Y71F9AL.18 T21B4.4 T23B5.1 C15H11.5 R07B5.9 ZX380.5	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F19B2.5 Y43F8B.14 M04C3.1 Y71F9AL.18 T21B4.4 T23B5.1 C15H11.5 R07B5.9 ZX380.5	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex, ETI-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y43788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/pso-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-181 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAI-related actim-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12	JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9A.18 T21B4.4 T21B4.4 T21B5.1 C15H11.5 R07B5.9 ZK380.5 ZK366.4	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex, LT-1418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C259.5 Y11182A.22 F26F12.7 F1982.5 Y43788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-20	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWJ/SNF	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling bitone motification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Gloned Gloned Gloned Gloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T2184.4 T2184.4 T2185.1 C15H11.5 R07B5.9 ZX380.5 ZX616.4 Y92H12BR.6	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29	encoding SW12/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex, LT-1418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation chromatin remodelling histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y43788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37E3.15	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of MI-2/CH03, a component of the nucloosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAi machinery chromatin remodelling histone modification; DNA methylation RNAi machinery	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T2184.4 T2184.4 T2385.1 C15H11.5 R07B5.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37G13.15 Y39G10AR.18	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/pso-13 set-29 npp-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NUBD) complex. LT-1418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DD11 LBX79 methyltransferase	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C259.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12/11.1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-2/HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3R79 methyltransferase	DNA binding chromatin remodelling histone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (cell, structures)	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SFC kinase-like
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T2184.4 T2184.4 T2184.4 T2385.1 C15H11.5 R07B5.9 ZX380.5 ZX380.5 ZX616.4 Y92H128R.6 Y37E3.15 Y39G10AR.18 H12113.1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-1418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTLI H3K79 methyltransferase SPK containing protein family member	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding Chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAi machinery chromatin remodelling histone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C259.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12H3.1 Y110A2AR.2	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-2/HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3K79 methyltransferase SPK containing protein family member E zu biquitir-onjugating enzyme	DNA binding chromatin remodelling nistone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAi machinery chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation DNA binding DNA binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T21B4.4 T21B4.4 T23B5.1 C15H11.5 R07B5.9 ZX380.5 ZX380.5 ZX616.4 Y32F3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y10P4B.10	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-1418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lae-2 rortein (Notch lizand)	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation kistone modification; DNA methylation chromatin remodelling chromatin remodelling histone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase ubiquitin machinery Others (signaling)	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DS1: EGF-like
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C259.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y39G10AR.18 Y39G10AR.18 H12H3.1 Y410A2AR.2 Y410A2AR.2	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWJ/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDT1L H3K79 methyltransferase SPK containing protein family member E2 ubiguitin-conjugating enzyme putative delta/Serate1/Lag-2 protein (Notch ligand) corredine SIX containing of the family member	DNA binding chromatin remodelling nistone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation DNA binding / kinase ubiquitin machinery Others (signalling) chromatin lending	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7	JAP-MS DOZ2 JAP-MS box2 IAP-MS box2 Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T21B4.4 T21B4.4 T23B5.1 C15H11.5 R07B5.9 ZX830.5 ZX830.5 ZX636.4 Y32F13.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y41D4B.10 Y45F10C.1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serate/Lag-2 protein (Noth ligand) encoding SPK containing protein family member	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation kistone modification; DNA methylation chromatin remodelling chromatin remodelling histone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase ubiquitn machinery Others (signaling) chromatin binding	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H18 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y32F13.15 Y39G10AR.18 H12H3.1 Y39G10AR.18 H12H3.1 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2	ssl-1 let-418/evl-11, ch-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-2/HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnm11 (DNA-methyltranferase) protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member	DNA binding chromatin remodeling nistone modification / chromatin remodeling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodeling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation DNA binding / kinase UNA	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H11 H11 A1 A2 A3 A4 A5 A6 A7 A8	JAP-MS DOZ2 JAP-MS box2 IAP-MS box2 Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y34788.14 M04C3.1 Y71F9AL.18 T2184.4 T2184.4 T2385.1 C15H11.5 R0785.9 ZK616.4 Y32F128R.6 Y37F3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y4104B.10 Y45F10C.1	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTL H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serate/Lag-2 protein (Noch ligand) encoding SPK containing protein family member regulator of chromosome condensation. RCC1 and PHR	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation chromatin remodelling histone modification; DNA methylation Chromatin remodelling bistone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation DNA binding / kinase ubiquitn machinery Others (signaling) chromatin binding chromatin binding	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y11182A 22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y410A8.10 Y45F10C.1 F07B7.12	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M/2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTLI H3K79 methyltransferase SPK containing protein family member E 2 ubiquitin-onjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a outstive bitcomes Ha bisinea webstransferase	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation bistone modification; DNA methylation DNA binding chromatin remodelling Others (cignalling) chromatin binding chromatin binding chromatin binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H11 H11 A1 A2 A3 A4 A5 A6 A7 A8	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 IAP-MS box2 Cloned Clon	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y34788.14 M04C3.1 Y71F9AL.18 T2184.4 T2184.4 T2385.1 C15H11.5 R0785.9 ZX630.5 ZK616.4 Y92H128R.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y41048.10 Y45F10C.1 F0787.12	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTLI H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serate/Lag- protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (cell, structures) chromatin machinery Others (signaling) chromatin binding chromatin binding chromatin binding	SNF2-related SWI/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Clone	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y32F1.15 Y39610AR.18 H12113.1 Y110A2AR.2 Y410A8.10 Y45F10C.1 F07B7.12 Y108F1.3	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-181 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3K39 methyltransferase SPK containing protein family member E2 ubiquith-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase bart is predicted to function in transcriptionia repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling histone modification; DNA methylation DNA binding / kinase ubiquitin machinery Others (signalling) chromatin binding chromatine remodelling histone modification; DNA methylation	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9	JAP-MS DOX2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 IAP-MS box2 Cloned Clon	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y34788.14 M04C3.1 Y1F9AL.18 T2184.4 T2184.4 T2385.1 C15H11.5 R0785.9 ZK616.4 Y92H128R.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y41048.10 Y45F10C.1 F0787.12 Y108F1.3	ssl-1 chd-4 pme-1 ador-1 prmt-3 sset-31/agr-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2/HD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein ing thindra/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithora/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K79 methyltransferase SFK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SFK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32	DNA binding chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (cell, structures) chromatin machinery Others (signaling) chromatin binding chromatin binding chromatin binding chromatine remodelling histone modification; DNA methylation DNA binding / kinase uliquitum machinery Others (signaling) chromatine remodelling histone modification; DNA methylation DNA binding / kinase luiquitum machinery Others (signaling) chromatine binding chromatine remodelling histone modification; DNA methylation	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related chromodomain, SET Chromodomain, SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (E6AP-type E3
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y4104B.10 Y45F10C.1 F07B7.12 Y108F1.3	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M/2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDT1L H3R/9 methyltransferase SPK containing protein family member E 2 ubiquith-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-5, SET-21, and SET-32 regulator of chromosome condensation and HECT domain inrotein: homolog of phase protein functional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling Nistone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase Uniquitin machinery Others (signalling) chromatin binding chromatin binding histone modification; DNA methylation DNA binding / kinase Uniquitin machinery Others (signalling) chromatin binding chromatine remodelling	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK, kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein lizase1)
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9	JAP-MS DOZ2 JAP-MS box2 IAP-MS box2 Cloned	C25F9.5 Y111B2A.22 F26F12.7 F1982.5 Y43F88.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX630.5 ZK616.4 Y92H128R.6 Y37F3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y41048.10 Y45F10C.1 F07B7.12 Y108F1.3	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 berc-1/hnn-72	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2/CHD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex. LT-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serate/1.ag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ulbinuitio-nortein licase	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding bistone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation kistone modification; DNA methylation bistone modification; DNA methylation bistone modification; DNA methylation bistone modification; DNA methylation Chromatin remodelling bistone modification; DNA methylation DNA binding / kinase ubiquitin machinery Others (signaling) chromatine remodelling bistone modification; DNA methylation DNA binding / kinase ubiquitin machinery Chers (signaling) chromatine remodelling bistone modification; DNA methylation DNA binding / kinase ubiquitin machinery Chers (signaling) chromatine binding chromatine remodelling bistone modification; DNA methylation Chers (signaling) chromatine premodelling bistone modification; DNA methylation Chers (signaling) chromatine binding chromatine remodelling bistone modification; DNA methylation Chers (signaling) chromatine premodelling bistone modification; DNA methylation Chers (SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain
MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y110A2AR.	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M/2/CH03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDT1L H3K79 methyltransferase SPK containing protein family member E 2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling Nistone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase Uniquitin machinery Others (signalling) chromatin binding chromatin binding histone modification; DNA methylation DNA binding / kinase Uniquitin machinery uniquitin machinery uniquitin machinery uniquitin machinery uniquitin machinery	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET Chromodomain, SET DOT1-like domain SPK, kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (E6AP-type E3 ubiquitin-protein ligase) domain
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MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11	JAP-MS DOZ2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZX616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y41048.10 Y45F10C.1 F0787.12 Y108F1.3 Y48G8AL.1 C18E3.2	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 mpp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M/2/CH03, a component of the nucloosome remodeling and histone deacetylase (NURD) complex, LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTLI H3K79 methyltransferase SPK containing protein family member E 2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-5, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling Nistone modification; DNA methylation Others (cell. structures) histone modification; DNA methylation DNA binding / kinase Uniquitin machinery Others (signalling) chromatin binding chromatin binding histone modification; DNA methylation DNA binding / kinase Uniquitin machinery Chromatin binding chromatin binding chromatin binding chromatin remodelling histone modification; DNA methylation Uniquitin machinery chromatin binding chroma	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related Chromodomain, SET Chromodomain, SET SET DOT1-like domain SPK, kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (E6AP-type E3 ubiquitin-protein ligase) domain SWiB chromodomain; helicase
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MH7 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 B2	JAP-MS DO22 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 IAP-MS box2 IAP-MS box2 IAP-MS box2 Cloned Clone Cloned Cloned Cloned Cloned Cloned Cl	C259.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G100AR.18 H12113.1 Y110A2AR.2 Y4104B.10 Y45F10C.1 F0787.12 Y108F1.3 Y48G8AL1 C18E3.2 T04D1.4 Y46H3C.4 Y73B3B.1	ssl-1 chd-4 pme-1 ador-1 prmt-3 set-31/ag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets K08E5.1 and top-2 as well	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2(HD3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-418 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K73 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defla/Serrate(Jag.2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 hysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp 73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding DNA binding the second seco	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related chromodomain, SET ST DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SWIB chromodomain; helicase domain SPK
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MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 B2 B3 B4 B5 B6	JAP-MS DO22 JAP-MS box2 IAP-MS	C259.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y436G16.4 Y92H12BR.6 Y37E3.15 Y436G16.4 Y92H12BR.6 Y37E3.15 Y436G16.4 Y1042.1 Y11042AR.2 Y1048.10 Y45F10C.1 F0787.12 Y108F1.3 Y486G8AL1 C18E3.2 T04D1.4 Y46H3C.4 Y73B38.1 CF7X_3.2 C04A2.3 F15D4.1 T2287.1	ssl-1 chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets K08E5.1 and tap-2 as well egl-27 btf-1 edl-13	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K73 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defta/Serrate/1ag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 hysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp 73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling DNA binding bistone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation bistone modification; DNA methylation DNA binding / kinase ubiquitin machinery Others (sell structures) chromatin remodelling DNA binding / bistone chromatin remodelling DNA binding / bistone chromatin remodelling DNA binding / bistone chromatin remodelling Chromatin remodellin	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SYWB chromodomain; helicase domain SPK Myc motif SANT; Zn finger SQX domain
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MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7 MH7	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 B2 B3 B4 B5 B6 B7	JAP-MS DO22 JAP-MS box2 IAP-MS	C259.5 Y11182A.22 F26F12.7 F1982.5 Y243788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G100AR.18 H12113.1 Y110A2AR.2 Y41048.10 Y45F10C.1 F0787.12 Y108F1.3 Y48G8AL1 C18E3.2 T04D1.4 Y46H3C.4 Y73B38.1 CF7X_3.2 C04A2.3 F1504.1 T2287.1 B0564.11	ssl-1 chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2,2 chd-7/tag-192 targets K08E5.1 and tap-2 as well egl-27 btf-1 egl-13 rde-11	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2/HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3K73 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defta/Serrate/1ag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 hysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp 73/BAF60, a component of the SWI/SNF complex beta-1 of topoisomerase II ortholog of human MTA1, part of an ATP-dependent complex with nucleosome remodelling and histone deacetylation activities member of the TBP-associated family (TAF) transcription factor RNAi-defective	DNA binding chromatin remodelling DNA binding bistone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation bistone modification; DNA methylation bistone modification; DNA methylation bistone modification; DNA methylation DNA binding / Names chromatin remodelling Chromatin remodelling Cheros (call, structures) DNA methylation DNA binding / kinase ubiquitin machinery Cheros (call, structures) bistone modification; DNA methylation DNA binding / kinase ubiquitin machinery Cheros (call, structures) chromatin remodelling chromatin remodelling chromatin remodelling chromatin remodelling chromatin remodelling Cheros (call, structures) Chromatin remodelling Chromati	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET SET DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SVWB chromodomain; helicase domain SPK Myc motif SANT; Zn finger SQX domain Zn finger
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MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A1 A1 A1 A2 A3 A4 A5 A6 A7 A1 A1 A1 A1 A2 B3 B2 B3 B4 B5 B6 B7 B8 B9	JAP-MS DO22 JAP-MS box2 IAP-MS	C259.5 Y11182A.22 F26F12.7 F1982.5 Y243788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G100AR.18 H12113.1 Y110A2AR.2 Y40F10C.1 F0787.12 Y108F1.3 Y48G8AL.1 C18E3.2 T04D1.4 Y46H3C.4 Y73B38.1 CE7X_3.2 C04A2.3 F1504.1 T2287.1 B0564.11 C3487.4 M01E5.6	ssl-1 chd-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets KOBE5.1 and tap-2 as well egi-27 btf-1 egi-13 rde-11 mys-4 set-31	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOT1L H3R79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/18_2 ² protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 kyine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-65, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp 73/BAF60, a component of the SWI/SNF complex beta-1 of topoisomerase II ortholog of human MTA1, part of an ATP-dependent complex with nucleosome remodelling and histone deacetylation activities member of the TBP-associated family (TAF) transcription factor RNAi-defective MYST histone acetyltransferase; component of NuA4-like HAT complex	DNA binding chromatin remodelling DNA binding Chromatin binding DNA binding Chromatin binding Chromatin binding Chromatin binding DNA binding Chromatin remodelling Chromatin remodelling DNA binding Chromatin remodelling Chromati	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET CT DOT1-like domain SPK; kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SYWB chromodomain; helicase domain SPK Myc motif SANT; Zn finger SIX domain Zn finger PHD finger KiX domain
MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 A12 B1 A12 B3 B4 B5 B5 B6 B7 B8 B9 B7 B8 B9 B10	JAP-MS 0022 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 IJAP-MS box2 Cloned	C25F9.5 Y11182A.22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZK616.4 Y92H12BR.6 Y32F3.15 Y39G10AR.18 H12113.1 Y10A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y10A5F1.3 Y48G8AL.1 C18F3.2 T04D1.4 Y46H3C.4 Y73B3B.1 CCFX_3.2 C04A2.3 F15D4.1 T2287.1 B0564.11 C3487.4 M01E5.6 711000 0	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets K08E5.1 and top-2 as well egl-27 btf-1 egl-13 rde-11 mys-4 sepo-1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2(PL03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnm11 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDT1L H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase bat is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation bistone modification; DNA methylation RNAI machinery chromatin remodelling chromatin binding bistone modification; DNA methylation DNA binding / kinase United States (States (SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related Chromodomain, SET Chromodomain, SET SET DOT1-like domain SPK; kinase-like SET, PHD, SPK SET HECT (E6AP-type E3 ubiquitin-protein ligase) domain SWIB chromodomain; helicase domain SPK Myc motif SANT; Zn finger SOX domain Zn finger SOX domain SNG SCA domain
MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 B2 B3 B4 B5 B6 B7 B8 B9 B10	JAP-MS 0022 JAP-MS box2 IAP-MS	C259.5 Y11182A.22 F26F12.7 F1982.5 Y243788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y40F1.2 Y108F1.3 Y48G8AL.1 C18E3.2 T04D1.4 Y46H3C.4 Y73838.1 CE7X_3.2 C04A2.3 F15D4.1 T2287.1 80564.11 C3487.4 M01E5.6 ZK1098.8	ssl-1 cht-418/evl-11, cht-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 cht-7/tag-192 targets KO&E5.1 and tap-2 as well egi-27 btf-1 egi-13 rde-11 mys-4 sepa-1 mut-7	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3R/37 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defta/Serrate/1ag-2 protein (Notch ligand) encoding SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defta/Serrate/1ag-2 protein (Notch ligand) encoding SPK containing protein family member engulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp 73/BAF60, a component of the SWI/SNF complex beta-1 of topoisomerase II ortholog of human MTA1, part of an ATP-dependent complex with nucleosome remodelling and histone deacetylation activities member of the TBP-associated family (TAF) transcription factor RNAi-defective MYST histone acetylransferase; component of NuA4-like HAT complex putative transcription cordactor Exounclease 3'-5' domain-containing protein 3 homolog	DNA binding chromatin remodeling DNA binding Chromatin binding DNA binding Chromatin binding DNA binding Chromatin binding bistone modification; DNA methylation histone modification; DNA methylation Natione modification; DNA methylation DNA binding Chromatin remodeling bistone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (signalling) Chromatin remodeling bistone modification; DNA methylation Chromatin remodeling Chromatin r	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET CT DOT1-like domain SFK kinase-like DDSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SFK Myc motif SANT; Zn finger SOX domain Zn finger PHD finger KIX domain 3-5' exonuclease domain
MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 A12 B1 A12 B3 B4 B5 B5 B6 B7 B8 B5 B6 B7 B8 B5 B6 B11	JAP-MS 0022 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Clone	C25F9.5 Y11182A 22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R07B5.9 ZX380.5 ZK616.4 Y92H12BR.6 Y92H12BR.6 Y92H12BR.6 Y92H12BR.6 Y37F3.15 Y43610AR.18 H12113.1 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y10A5F1.3 Y4868AL.1 C18F3.2 T04D1.4 Y46H3C.4 Y73B3B.1 CCFX_3.2 C04A2.3 F15D4.1 T2287.1 B0564.11 C3487.4 M0155.6 ZX1098.8 Y13F7.9 S467.4 Y13F7.9 S467.4 Y13F7.9 Y10F7.2	ssl-1 let-418/evl-11, chd-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets K08E5.1 and top-2 as well egl-27 btf-1 egl-13 rde-11 mys-4 sepa-1 mut.7	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2(PL03, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDTLI H3K79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase barb is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling bistone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation bistone modification; DNA methylation bistone modification; DNA methylation chromatin remodelling chromatin binding chromatin binding chromatin remodelling DNA binding/helicase chromatin remodelling DNA binding/helicase chromatin remodelling Chromatin remod	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related Chromodomain, SET Chromodomain, SET DOT1-like domain SPK; kinase-like SET, PHD, SPK SET HECT (E6AP-type E3 ubiquitin-protein ligase) domain SWIB chromodomain; helicase domain SWK Myc motif SANT; Zn finger SQX domain Zn finger SQX domain Sh Consultation SPK Kix domain Si-Si exonuclease domain S+D finger Kix domain S+Si exonuclease domain S+
MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A8 A9 A10 A11 A12 B1 B2 B3 B4 B5 B6 B7 B8 B5 B6 B7 B8 B9 B10 B12	JAP-MS DO22 JAP-MS box2 IAP-MS	C259.5 Y11182A.22 F26F12.7 F1982.5 Y243788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZK380.5 ZK616.4 Y92H12BR.6 Y37E3.15 Y39G10AR.18 H12113.1 Y110A2AR.2 Y40F13.1 Y110A2AR.2 Y40F13.1 Y10AF1.3 Y48G8AL.1 C18E3.2 T04D1.4 Y46H3C.4 Y73838.1 CE7X_3.2 C04A2.3 F15D4.1 T2287.1 80564.11 C3487.4 M01E5.6 ZK1098.8 Y132FA.9 S140.7 ZK1092.8	ssl-1 cht-418/evl-11, cht-4 pme-1 ador-1 prmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 npp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 cht-7/tag-192 targets KOBE5.1 and tap-2 as well egi-27 btf-1 egi-13 rde-11 mys-4 sepa-1 saea-1	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of M-1/2/HO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex; LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DOTLI H3R79 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative defta/Serrate/18_2 ² protein (Notch ligand) encoding SPK containing protein family member eregulator of chromosome condensation, RCC1 and PHR a putative histone H3 kyine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-65, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp73/BAF60, a component of the SWI/SNF complex beta-1 of topoisomerase II ortholog of human MTA1, part of an ATP-dependent complex with nucleosome remodelling and histone deacetylation activities member of the TBP-associated family (TAF) transcription factor RNAi-defective MYST histone acetylarinsferase; component of NuA4-like HAT complex putative transcription cofactor Exonuclease 3'-5' domain-containing protein 3 homolog ortholog of human isform 4 of transcription-repeating factor 1 artholog of human isform 4 of transcription-repeating factor 1	DNA binding chromatin remodelling instone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding Chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation Notione modification; DNA methylation Chromatin remodelling histone modification; DNA methylation Others (cell, structures) histone modification; DNA methylation Others (signalling) chromatin remodelling histone modification; DNA methylation Chromatin remodelling chromatin remod	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related chromodomain, SET CT DOT1-like domain SFK, kinase-like DOT1-like domain SPK, kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (EGAP-type E3 ubiquitin-protein ligase) domain SFK Myc motif SANT; Zn finger SOX domain Zn finger PHD finger KIX domain 3'-5' exonuclease domain WD repeats SANT/Wb'-70 finger
MH7 MH8 MH8	G12 H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 A1 A2 A3 A4 A5 A6 A7 A1 A1 A2 A3 A4 A5 A6 A7 A1 A1 A1 A2 B1 B1 B2 B3 B3 B4 B5 B6 B7 B8 B3 B10 B11 B12 C1	JAP-MS 00022 JAP-MS box2 JAP-MS box2 JAP-MS box2 JAP-MS box2 Cloned Clon	C259.5 Y11182A 22 F26F12.7 F1982.5 Y343788.14 M04C3.1 Y71F9AL.18 T2184.4 T2385.1 C15H11.5 R0785.9 ZX380.5 ZK616.4 Y92H12BR.6 Y92H12BR.6 Y92H12BR.6 Y37E3.15 Y43G10AR.18 H12113.1 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y110A2AR.2 Y10A51.3 Y48G8AL.1 C18F3.2 T04D1.4 Y46H3C.4 Y73B3B.1 CE7X_3.2 C04A2.3 F15D4.1 T2287.1 B0564.11 C28487.4 M01E5.6 ZX1098.8 Y73F7A.9 F53H10.2 C146.4 C186.4	ssl-1 let-418/evl-11, cdr-4 pme-1 ador-1 pmt-3 set-31/tag-338 lsy-12/mys-3 swsn-6/psa-13 set-29 mpp-13 ubc-15 dsl-3 targets rpm-1 as well set-33 herc-1/hpo-23 swsn-2.2 chd-7/tag-192 targets K08E5.1 and top-2 as well egl-27 btf-1 egl-13 rde-11 and top-2 as well egl-27 btf-1 egl-13 rde-11 adpr-1 seeg-1 sef-3	encoding SWI2/SNF2 family ATPase; may participate in a TRR-1/MYS-1/EPC-1/SSL-1 histone acetyltransferase complex homolog of Mi-2(PLO3, a component of the nucleosome remodeling and histone deacetylase (NURD) complex, LET-118 is similar to DNA helicases transcription factor family member poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme) adenosine receptor like family member; closest homolog to Dnm11 (DNA-methyltranferase) protein arginine N-methyltransferase protein containing trithorax/polycomb SET domain MYST histone acetyltransferase RNAi-related actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SW/SNF protein containing trithorax/polycomb SET domain encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35 homolog of DDT1L H3R/9 methyltransferase SPK containing protein family member E2 ubiquitin-conjugating enzyme putative delta/Serrate/Lag-2 protein (Notch ligand) encoding SPK containing protein family member regulator of chromosome condensation, RCC1 and PHR a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional repression; SET-33 is paralogous to SET-6, SET-15, SET-21, and SET-32 regulator of chromosome condensation and HECT domain protein; homolog of human E6- AP ubiquitin-protein ligase homolog of Swp73/BAF60, a component of the SWI/SNF complex	DNA binding chromatin remodelling histone modification / chromatin remodelling DNA binding DNA binding DNA binding DNA binding DNA binding Chromatin binding histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation histone modification; DNA methylation RNAI machinery chromatin remodelling chromatin binding histone modification; DNA methylation DNA binding / kinase chromatin binding chromatin chinery chromatin remodelling Chromatin negulation Chromatin remodelling Chromatin negulation Chromatin remodelling Chromatin remodelling Chromatin remodelling Chromatin negulation Chromatin remodelling Chromatin hinding Chromatin hinding Chromatin hinding Chromatin hinding Chromatin remodelling Chromatin remodeling Chromatin remodelling C	SNF2-related SW/SNF chromodomain; PHD finger SNF2-related SNF2-related SNF2-related SNF2-related Chromodomain, SET Chromodomain, SET DOT1-like domain SFK, kinase-like DSL; EGF-like SET, PHD, SPK SET HECT (E6AP-type E3 ubiquitin-protein ligase) domain SWIB chromodomain; helicase domain SWIB SNT; Zn finger SOX domain Chromer SOX domain SN; Sexonuclease domain SN; Borner SANT, WbD repeats SANT, WbD; Zn finger SANT; Zn finger SN;

					FANCL homolog; E3 ubiquitin-protein ligase listerin		
MH8	C2	Cloned	Y54E10A.11	unc 27	transcription factor: transducin-like WD-repeat protein orthologous to Drosophila Groucho	ubiquitin machinery	WD repeats
MH8	C4	Cloned	F59F12.9	unc-37	a anschption ractor, a ansodelimike womepear protein oratiologous to prosophila croacho	others	wb repeats
MH8	C5	Cloned	T01H8.1	rskn-1	Putative ribosomal protein S6 kinase alpha-1; Serine/threonine kinase	transcription regulation	N-acetyltransferase domain
MH8	C6	Cloned	Y49F6A.1	wago-11	Argonaute protein	RNAi machinery	PIWI/PAZ
					Catalytic histone acetyltransferase subunit of the RNA polymerase II elongator complex, which is a component of the RNA polymerase II (POI II) holoenzyme and is involved in transcriptional elongator. Tavy play a role in chromatin remodeling. May also		
MH8	C7	Cloned	ZK863.3	elpc-3	have a methyltransferase activity	transcription regulation	
MH8	C8	Cloned	F55A12.1	wago-2	Argonaute protein	RNAi machinery	PIWI/PAZ
MH8	C9	Cloned	T06A10.4	lsy-13	PHD-finger containing protein	chromatin binding	PHD finger
MH8	C10	Cloned	ZK337.2		Zn finger protein	DNA binding	Zn finger C2H2
MHS	C11 C12	Cloned	F50D12.5	vig-1	SPK-containing protein	DNA binding	SPK
141110	012	cioned	155115.1		Probable 26S proteasome non-ATPase regulatory subunit 9; acts as a chaperone during the	bite bitoling	Si K
MH8	D1	Cloned	C44B7.1	psmd-9	assembly of the 26S proteasome	ubiquitin machinery	
MH8	D2	Cloned	F52G2.2	rsd-2	RNAi Spreading Defective, required for systemic RNAi	RNAi machinery	
MH8	D3	Cloned	Y47G6A.4	rde-10	RNAi defective	RNAi machinery	
MH8	D4	Cloned	C11G6.1	taf-3	putative TATA binding protein associated transcription factor	transcription regulation	Zn PHD finger
MHS	D5	Cloned	147D3A.0	110-1	Sex-determining transformer protein 1	chromatin remodelling	SWIR (SWI/SNE)
MH8	D7	Cloned	Y54F10BM.14	nhf-5	Swib domain-containing protein	chromatin binding	PHD finger
MH8	D8	Cloned	Y56A3A.4	taf-12	TATA binding protein associated transcription factor	transcription regulation	Ű.
MH8	D9	Cloned	C09E10.2	dgk-1	diacylglycerol kinase theta	chromatin binding	kinase-specific; PHD finger
MH8	D10	Cloned	Y75B8A.6		methyltransferase activity retinoblastoma Binding protein Related, demethylase specific for tri-and dimethylated	histone modification; DNA methylation	Xn finger CXXC-type
MH8	D11	Cloned	ZK593.4	rbr-2	lysine 4 on histone 3	histone modification; DNA methylation	JmjC; ARID; PHD
MH8	D12	Cloned	K08F4.2	116.2	Manual Mar Backar (da - Cara andre)	NA binding	7. 6
	E1 E2	Cloned	r54n5.4	KIJ-3	AT book motif containing protein		Zn linger Zn finger
MH8	E2	Cloned	C39F7 2	trim-9	F3 ubiquitin-protein ligase	ubiquitin machinery	Zn RING finger
MH8	F4	Cloned	7C302.2	wdr-5.3	WD repeat-containing protein	protein-protein inetraction	WD repeats
MH8	E5	Cloned	F33E11.6	phf-10	PHD-finger containing protein	chromatin binding	PHD finger
MH8	E6	Cloned	F40E10.2	sox-3	SOX (mammalian SRY box) related protein	DNA binding	HMG domain
MH8	E7	Cloned	K04G11.4	wdr-5.2	WD repeat-containing protein	protein-protein inetraction	WD repeats
MH8	E8	Cloned	T07F8.4	100% hom with F10E7.11	SANT-domain containing protein	chromatin binding	SANT domain
MH8	E9	Cloned	F10E7.11	100% hom with T07F8.4	SANT-domain containing protein	chromatin binding	SANT domain
MH8	E10	AL I-9L05	F02E9.2	lin-28	heterochronic gene; miRNA interaction	NA binding	finger
Overv	iew of all n	ewly genereate	ed RNAi clones:				PWWP domain (Pro-Trp-Trp
MH1	B8	cloned	C06A5.3		PSIP1 protein ortholog	protein-protein interactions	Pro motif)
MH3	E7 F4	cloned	R151 8		serine/threenine rich protein: CRAMP11 ortholog	chromatin binding	kinase uomain
MH6	F12	cloned	Y43F11A.5	set-24	protein containing trithorax/polycomb SET domain	histone modification: DNA methylation	SET
MH6	H1	cloned	T07C4.11	jmjd-4	JmjC-domain containing protein	histone modification; DNA methylation	JmjC
MH7	D4	Cloned	F57C7.1	bet-2	PHD-finger containing protein	chromatin binding	PHD finger
MH7	E3	Cloned	C04F12.1	vsr-1	Argonaute protein	RNAi machinery	PIWI
MH7	E4	Cloned	Y110A7A.13	chp-1	CHORD containing protein; germline RNAi	RNAi machinery	CHORD domain
MH7	E7	Cloned	Y37D8A.11	cec-7	C. elegans Chromodomain protein	histone modification; DNA methylation	chromodomain
MH7	E9	Cloned	K03D10.3	mys-2	MYST acetyltransferase	histone modification; DNA methylation	chromodomain
MH7	EII	Cloned	KU6C1.1	naa-3	nistone deacetyiase nucleolar phosphoprotein related to Saccharomyces cerevisiae SRP40 and the vertebrate Nopp140 proteins that may play a role in rRNA gene transcription and nucleolar structural	nistone modification; JNA methylation	nistone-deacetylase domain
MH7	F1	Cloned	C25A1.10	dao-5	organization	rRNA-related	SRP40 domain
MH7	F3	Cloned	H15N14.1	adr-1	ADAR (adenosine deaminase acting on RNA)	RNAi machinery	
MH7	F4	Cloned	C43E11.11	cogc-5	Conserved Oligomeric Golgi (COG) Component	Others (cell. structures)	
MH7	F5	Cloned	C18F3 7	nnw-1	germline.	RNAi machinery	PA7/PIWI domain
MH7	F7	Cloned	B0261.1	ppm 1	DNA-binding protein	DNA binding	SANT/Myb domain
MH7	F9	Cloned	Y73B3B.2	set-28	SET-domain containing protein	histone modification; DNA methylation	SET
MH7	G1	Cloned	Y110A7A.18	ppw-2	encoding PAZ/PIWI domain-containing.	RNAi machinery	PAZ/PIWI domain
MH7	H6	Cloned	Y71F9AL.18	pme-1	poly(ADP-ribosyl) transferase; homolog of PARP1 (chromatin associated enzyme)	chromatin binding	
MH7	H7	Cloned	T21B4.4	ador-1	adenosine receptor like family member; closest homolog to Dnmt1 (DNA-methyltranferase)	histone modification; DNA methylation	
MH7	H8	Cloned	12385.1	prmt-3	protein arginine N-methyltransferase	histone modification; DNA methylation	chromodor-i- CF
	H9 H10	Cloned	C15H11.5	set-31/tag-338	protein containing tritnorax/polycomb SET domain	histone modification; DNA methylation	chromodomain, sei
MH7	H10	Cloned	7K380 5	159-12/1195-5	RNAi-related	RNAi machinery	
MH7	H12	Cloned	ZK616.4	swsn-6/psa-13	actin-like 6; Actin-related protein 4 (Arp4) is a component of chromatin-remodeling enzyme complexes; SWI/SNF	chromatin remodelling	
MH8	A1	Cloned	Y92H12BR.6	set-29	protein containing trithorax/polycomb SET domain	histone modification; DNA methylation	SET
MH8	A2	Cloned	Y37E3.15	npp-13	encoding nuclear Pore complex Protein nucleoporin 93; closely related to Nup35	Others (cell. structures)	
MH8	A3	Cloned	Y39G10AR.18		homolog of DOT1L H3K79 methyltransferase	histone modification; DNA methylation	DOT1-like domain
MH8	A4	Cloned	H12I13.1		SPK containing protein family member	protein kinase	SPK; kinase-like
MH8	A5	Cloned	Y110A2AR.2	ubc-15	E2 ubiquitin-conjugating enzyme	Others (signalling)	
MH8	A6	Cloned	Y41D4B.10	dsl-3	putative delta/Serrate/Lag-2 protein (Notch ligand)	otners (signalling)	DSL; EGF-like
NALIO	A7	Cloned	F0707.10	targets rpm-1 as	regulates of elementary and elementary includes	chromatine remedalling	3L1, FHD, 3FK
MH8	A8	Cloned	FU7B7.12	well	regulator of chromosome condensation, KCL1 and PHK a putative histone H3 lysine-9 methyltransferase that is predicted to function in transcriptional concernion (ET 23) is paralogous to SET 6. SET 16. SET 31, and SET 23	histore medification. DNA methodation	6F.T.
MH8	A9	cioned	110811.3	38 <u>[-</u> 33	regulator of chromosome condensation and HECT domain protein: homolog of human F6-	instance modification; pNA methylation	SE I HECT (E6AP-type E3 ubiquitin-protein ligase)
MH8	A10	Cloned	Y48G8AL.1	herc-1/hpo-23	AP ubiquitin-protein ligase	ubiquitin machinery	domain
MH8	A11	Cloned	C18E3.2	swsn-2.2	homolog of Swp73/BAF60, a component of the SWI/SNF complex	chromatin remodelling	SWIB
MH8	A12	Cloned	T04D1.4	chd-7/tag-192		chromatin remodelling	chromodomain; helicase domain
		1		taraets KORF5 1			
MH8	B1	Cloned	Y46H3C.4	and top-2 as well	beta-1 of topoisomerase II	chromatin remodelling	
MH8	B2	Cloned	Y73B3B.1		ortholog of human plastin-3 isoform 2	chromatin remodelling	SPK
MH8	B3	Cloned	CE7X_3.2			Others	Myc motif

					homolog of human MTA1, part of an ATP-dependent complex with nucleosome remodelling		
MH8	B4	Cloned	C04A2.3	egl-27	and histone deacetylation activities	chromatin remodelling	SANT; Zn finger
MH8	B5	Cloned	F15D4.1	btf-1	member of the TBP-associated family (TAF)	DNA binding/helicase	
MH8	B6	Cloned	T22B7.1	egl-13	transcription factor	transcription regulation	SOX domain
MH8	B7	Cloned	B0564.11	rde-11	RNAi-defective	RNAi machinery	Zn finger
MH8	B8	Cloned	C34B7.4	mys-4	MYST histone acetyltransferase; component of NuA4-like HAT complex	histone modification; DNA methylation	PHD finger
MH8	B9	Cloned	M01E5.6	sepa-1	putative transcription cofactor	transcription regulation	KIX domain
MH8	B10	Cloned	ZK1098.8	mut-7	Exonuclease 3'-5' domain-containing protein 3 homolog	RNAi machinery	3'-5' exonuclease domain
MH8	B11	Cloned	Y73E7A.9	adpr-1	ortholog of human isoform 1 of WD and tetratricopeptide repeats protein 1	chromatin binding	WD repeats
MH8	B12	Cloned	F53H10.2	saeg-1	ortholog of human isoform 4 of Transcriptional-regulating factor 1	chromatin remodelling	SANT/Myb; Zn finger
MH8	C1	Cloned	F21G4.4	phf-34	PHD-finger containing protein	chromatin binding	PHD finger
					FANCL homolog; E3 ubiquitin-protein ligase listerin		
MH8	C2	Cloned	Y54E10A.11			ubiquitin machinery	
MH8	C3	Cloned	W02D3.9	unc-37	transcription factor; transducin-like WD-repeat protein orthologous to Drosophila Groucho	transcription regulation	WD repeats
MH8	C4	Cloned	F59E12.9			others	_
MH8	C5	Cloned	T01H8.1	rskn-1	Putative ribosomal protein S6 kinase alpha-1; Serine/threonine kinase	transcription regulation	N-acetyltransferase domain
MH8	C6	Cloned	Y49F6A.1	wago-11	Argonaute protein	RNAi machinery	PIWI/PAZ
					Catalytic histone acetyltransferase subunit of the RNA polymerase II elongator complex,		
					which is a component of the RNA polymerase II (Pol II) holoenzyme and is involved in		
	67	Chan and	7/062.2	.1	transcriptional elongation. Elongator may play a role in chromatin remodeling. May also	the second states and the test	
IVINA	C/	cloned	21003.3	eipc-s	have a metry transferase activity		004// (047
MH8	0	Cloned	F55A12.1	wago-2	Argonaute protein	RNAI machinery	PIWI/PAZ
	C10	Cloned	100A10.4	15y-15	7 Ginere protein	Chromatin binding	Za finana C2U2
IVINA	C10	cloned	25337.2		Zit ninger protein	DNA binding	Zh linger CZHZ
MH8	C11 C12	Cloned	F56D12.5	vig-1	RNA-Dinding protein orthologous to Drosophila ViG	RNA binding	CDV
IVINO	CIZ	cioned	F29H2.1		Dechable 265 protocome non ATDece regulatory suburit 0, onto co e change on duving the	DNA binding	JFK
мня	D1	Cloned	C44B7 1	nsmd-9	assembly of the 26S proteasome	ubiquitin machinery	
MHS	D1 D2	Cloned	E52G2.2	rsd-7	RNAi Spreading Defective required for systemic RNAi	RNAi machinen/	
MH8	02	Cloned	Y47G64 4	rde-10	RNAi defective	RNAi machinery	
MH8	D4	Cloned	C1166 1	taf-3	putative TATA binding protein associated transcription factor	transcription regulation	7n PHD finger
MH8	D5	Cloned	Y47D34 6	tra-1	Sex-determining transformer protein 1	transcription regulation	C2H2 Zn finger
MH8	D6	Cloned	T24G10 2	001	SWIB domain-containing protein	chromatin remodelling	SWIR (SWI/SNE)
MH8	D7	Cloned	Y54F10BM.14	nhf-5	Strib domain containing protein	chromatin binding	PHD finger
MH8	D8	Cloned	Y56A3A.4	taf-12	TATA binding protein associated transcription factor	transcription regulation	
MH8	D9	Cloned	C09F10.2	dak-1	diacylelycerol kinase theta	chromatin binding	kinase-specific: PHD finger
MH8	D10	Cloned	Y75B8A.6	-9	methyltransferase activity	histone modification: DNA methylation	Xn finger CXXC-type
					retinoblastoma Binding protein Related, demethylase specific for tri-and dimethylated	,,, _,, _	
MH8	D11	Cloned	ZK593.4	rbr-2	lysine 4 on histone 3	histone modification; DNA methylation	JmjC; ARID; PHD
MH8	D12	Cloned	K08F4.2			NA binding	
MH8	E1	Cloned	F54H5.4	klf-3	Kruppel-Like Factor (zinc finger protein)	transcription regulation	Zn finger
MH8	E2	Cloned	Y116A8C.22	athp-3	AT hook motif containing protein	DNA binding	Zn finger
MH8	E3	Cloned	C39F7.2	trim-9	E3 ubiquitin-protein ligase	ubiquitin machinery	Zn RING finger
MH8	E4	Cloned	ZC302.2	wdr-5.3	WD repeat-containing protein	protein-protein inetraction	WD repeats
MH8	E5	Cloned	F33E11.6	phf-10	PHD-finger containing protein	chromatin binding	PHD finger
MH8	E6	Cloned	F40E10.2	sox-3	SOX (mammalian SRY box) related protein	DNA binding	HMG domain
MH8	E7	Cloned	K04G11.4	wdr-5.2	WD repeat-containing protein	protein-protein inetraction	WD repeats
				100% hom with			
MH8	E8	Cloned	T07F8.4	F10E7.11	SANT-domain containing protein	chromatin binding	SANT domain
				100% hom with			
MH8	E9	Cloned	F10E7.11	T07F8.4	SANT-domain containing protein	chromatin binding	SANT domain

CATEGORIES: histone modification; DNA methylation RNA imachinery transcription regulation DNA/chromatin/histone binding, chromatin structure Chromatin remodelling ubiquitin machinery Protein-protein interactions; protein kinases; chaperones RNA binding/splicing Others (helicases, enzymes, translation, cell. structures, signalling

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	# of gcy-5p::gfp worms # of unc-119p::gfp worms	Mixture A 10 40	Mixture B 20 30	Mixture C 30 20
remainders in well	replicate #1A	1	0	0
after LP sampler	replicate #2A	0	0	0
иртаке	replicate #3A	1	0	2
	average %	1,33	0	1,33
transferred to new	replicate #1B	48	49	42
plate into	replicate #2B	39	40	45
corresponding wen	replicate #3B	48	45	46
	average %	90	89,33	88,67
recovered worms	replicate #1C	10	18	27
after sorting for	replicate #2C	10	18	28
gcy-5::gJp	replicate #3C	7	16	22
	average %	90	86,67	85,56
recovered worms	replicate #1D	31	23	18
after sorting for	replicate #2D	39	28	17
unc-119::gjp	replicate #3D	38	29	16
	average %	90	88,89	85

 Table S2 Efficiency of worm recovery from individual plates by the LPsampler.