

Table S1. Lesions in the seven alleles of *mes-4*

Allele	Nucleotide change*	Predicted protein change	Domain affected	H3K36me2 signal†
<i>bn50</i>	TG ₅₄₀ T→TAT	C147Y	PHD I	Undetectable
<i>bn67</i>	C ₇₆₅ AT→TAT	H206Y	PHD I	Undetectable
<i>bn58</i>	C ₁₃₆₂ GT→TGT	R389C	between PHD III and SET	Weak
<i>bn85</i> ‡	Δnt2418-3540, from within intron 6 to within intron 8	Δaa591-768 (Δexons 7 and 8)	SET and post-SET	Undetectable
<i>bn73</i>	TAT ₂₆₈₇ →TAA	Y594Z	Protein undetectable	Undetectable
<i>bn23</i> §	AG ₃₁₃₀ →AA at 3' end of intron 7	Unknown	Protein undetectable	Undetectable
<i>bn87</i> ¶	Δnt4006-5201, from within exon 10 past the 3'-UTR	Δaa877 onward	Protein undetectable	Undetectable

Lesions in *bn23*, *bn73*, and *bn87* were reported previously (Fong et al., 2002).

*Nucleotide position 1 is the A of the start codon.

†Anti-H3K36me2 antibody signal in early embryos and distal germ lines of adults. As expected, both the chromosomal association of MES-4 and the integrity of the SET domain apparently are required for its HMT activity.

‡*bn85* has an ~1.1 kb deletion that removes the region from the middle of intron 6 to the middle of intron 8. If splicing occurs between the 5' end of intron 6 and the 3' end of intron 8, then only exons 7 and 8 are missing. This in-frame deletion is predicted to produce a protein of 720 amino acids. A truncated MES-4 protein of approximately the expected size (178 amino acids or ~20 kDa smaller than wild type) is seen by western blot analysis of *mes-4(bn85)* worms (S. Boyle and L.B.B., unpublished), and protein accumulation in nuclei is seen by immunofluorescence.

§*bn23* has a point mutation that affects the conserved nucleotides at the 3' end of intron 7. If splicing can occur between the 5' end of intron 7 and the 3' end of intron 8, then an in-frame protein missing only exon 8 (44 amino acids) is predicted. No protein is observed by immunofluorescence, suggesting that an altered splicing pattern produces an unstable mRNA and/or protein.

¶*bn87* has an ~1.2 kb deletion that removes the 3' end of exon 10 and all of the 3'-UTR. The absence of protein product by immunofluorescence suggests that gene products are not synthesized or are not stable.

Table S2. Microarray results for the 71 genes whose accumulation is affected at least 1.8-fold ($P<0.05$)**Genes upregulated in *mes-4* relative to wild type**

Primer pair	WormBase ID (gene name)	Chromosome	Genomic start position	<i>mes-4</i> /wt	P-value
F11A6.2	F11A6.2	I	11,682,352	1.9	0.02
M142.1	M142.1 (unc-119)	III	10,906,347	1.97	0.01
C17B7.11	C17B7.11 (fbxa-65)	V	3,346,310	1.87	0.0093
W09B7.8	W09B7.2	V	8,827,969	2.03	0.015
C18D4.6	C18D4.6	V	17,538,168	2.59	0.021
F25E5.1	F25E5.1	V	7,465,706	1.89	0.0037
C04E7.2	C04E7.2	X	353,620	1.88	0.0025
T04G9.3	T04G9.3 (ile-2)	X	768,594	2.05	0.017
F53H8.1	F53H8.1 (apm-3)	X	954,994	2.16	0.03
T26C11.6	T26C11.6 (ceh-21)	X	1,852,730	1.99	0.000044
F07D10.1	F07D10.1 (rpl-11.2)	X	2,242,613	2.1	0.024
F32E4.8	F52E4.8	X	3,102,150	1.85	0.0036
C15C7.1	C15C7.1	X	3,164,514	1.82	0.0012
F35A5.8	F35A5.8 (erp-1)	X	3,802,751	2.84	0.00031
F02E8.1	F02E8.1 (asb-2)	X	4,469,739	1.81	0.0072
C05E11.1	C05E11.1	X	4,588,738	1.92	0.0027
T13H2.4	T13H2.4 (pqn-65)	X	4,620,394	1.82	0.0012
Y34B4A.F	Y34B4A.2	X	5,279,588	1.94	0.0041
F32A6.3	F32A6.3 (vps-41)	X	5,283,796	2.66	0.0017
C54H2.5	C54H2.5 (sft-4)	X	5,780,680	2.08	0.0029
F46G11.3	F46G11.3	X	5,783,363	2.21	0.00064
R07E4.5	R07E4.5	X	5,953,132	1.86	0.026
C09B8.7	C09B8.7 (pak-1)	X	6,048,568	3.3	0.00016
C45B2.6	C45B2.6	X	6,053,058	2.42	0.00052
T13C5.5	T13C5.5 (bca-1)	X	6,206,433	2.67	0.0003
T13C5.6	T13C5.6	X	6,207,584	2.47	0.00085
C03B1.12	C03B1.12 (lmp-1)	X	6,377,643	1.84	0.0028
C36B7.6	C36B7.6	X	7,100,289	1.97	0.000073
F08C6.6	F08C6.6	X	7,569,666	1.83	0.0092
ZK154.7	ZK154.7 (adm-4)	X	7,798,227	2.03	0.0098
F13B9.8	F13B9.8 (fis-2)	X	8,285,157	1.97	0.0051
R09F10.3	R09F10.3	X	8,294,561	1.97	0.0003
F08F1.7	F08F1.7	X	8,421,993	2.47	0.011
C25A11.1	C25A11.1	X	9,119,846	3.46	0.00014
B0416.5	B0416.5	X	9,270,784	2.31	0.0029
B0416.6	B0416.6 (gly-13)	X	9,296,553	2.25	0.001
T20B5.1	T20B5.1 (apa-2)	X	9,336,750	2.3	0.00042
T09B9.4	T09B9.4	X	9,774,286	2.21	0.0038
F47B10.1	F47B10.1	X	10,900,040	2.72	0.0017
W04G3.5	W04G3.5	X	11,073,581	1.85	0.001
C34F6.4	C34F6.4 (hst-2)	X	11,207,015	1.96	0.016
C35C5.6	C35C5.6	X	11,563,910	1.86	0.00042
F54F7.6	F54F7.6	X	11,865,464	2.33	0.000037
VW06B3R.1	VW06B3R.1	X	12,018,349	1.96	0.012
VF11C1L.1	VF11C1L.1 (ppk-3)	X	12,974,958	1.95	0.005
F54B11.5	F54B11.5	X	13,595,987	2.08	0.0038
Y26E6A.1	Y26E6A.1	X	13,917,091	1.8	0.0018
C31E10.5	C31E10.5	X	13,995,987	1.84	0.0045
F28H6.4	F28H6.4	X	14,127,802	2.01	0.00092
C27C12.1	C27C12.1	X	14,853,672	2.44	0.016
C27C12.4	C27C12.4	X	14,854,072	1.8	0.027
C27C12.3	C27C12.3	X	14,865,762	2.35	0.0092
F31F6.1	F31F6.1	X	14,868,218	2.13	0.03
F20D1.1	F20D1.1	X	14,970,190	2.24	0.016
F20D1.2	F20D1.2	X	14,970,668	2.43	0.00084
F20D1.3	F20D1.3	X	14,976,032	2.52	0.00053
F20D1.6	F20D1.6 (rbg-1)	X	14,983,442	1.84	0.0074
H40L08.1	H40L08.1	X	15,083,879	2.29	0.003
R03A10.4	R03A10.4	X	15,441,648	1.83	0.039
K09A9.5	K09A9.5 (gas-1)	X	15,590,318	2.3	0.011
K09A9.1	K09A9.1	X	15,607,888	2.08	0.0079
ZK678.1	ZK678.1 (lin-15A)	X	15,731,887	2.06	0.034
F59F4.4	F59F4.4 (acl-1)	X	15,849,818	1.93	0.016
F31B9.3	F31B9.3	X	15,923,396	2.05	0.00043
F01G12.2	F01G12.2 (sur-7)	X	16,376,514	2.06	0.007
C33E10.2	C33E10.2 (fbxa-120)	X	17,302,664	2.83	0.00024
H11L12.1	H11L12.1	X	17,711,584	2.21	0.0025

Genes downregulated in *mes-4* relative to wild type

Primer pair	WormBase ID (gene name)	Chromosome	Genomic start position	wt/ <i>mes-4</i>	P-value
C16A3.10	C16A3.10	III	6,396,119	2.23	0.0036
F57G4.4	F57G4.4	V	17,639,720	1.84	0.0061
F57G4.8	F57G4.8	V	17,650,317	2.2	0.0026
F59A1.9	F59A1.9	V	17,655,076	1.95	0.0078

Table S3. Comparison of microarray results and real-time PCR results for 15 genes**Genes upregulated at least 1.8-fold ($P<0.05$) in *mes-4* relative to wild type**

Primer pair	WormBase ID (gene name)	Chromosome	<i>mes-4</i> /wt	P-value	Real-time PCR relative to:	
					ZK381.1	F14B4.2
F11A6.2	F11A6.2	I	1.9	0.02	12.95	11.72
C17B7.11	C17B7.11 (fbxa-65)	V	1.87	0.0093	2.88	2.89
F25E5.1	F25E5.1	V	1.89	0.0037	6.13	6.83
C09B8.7	C09B8.7 (pak-1)	X	3.3	0.00016	10.44	9.79
T13C5.6	T13C5.6	X	2.47	0.00085	7.34	8.19
F08F1.7	F08F1.7	X	2.47	0.011	8.06	8.07
C25A11.1	C25A11.1	X	3.46	0.00014	16.99	18.96
R03A10.4	R03A10.4	X	1.83	0.039	6.3	6.31
H11L12.1	H11L12.1	X	2.21	0.0025	14.69	13.77

Gene downregulated at least 1.8-fold ($P<0.05$) in *mes-4* relative to wild type

Primer pair	WormBase ID (gene name)	Chromosome	wt/ <i>mes-4</i>	P-value	Real-time PCR relative to:	
					ZK381.1	14B4.2
F57G4.8	F57G4.8	V	2.2	0.0026	3.71	3.74

Genes with approximately equivalent accumulation in *mes-4* and wild type

Primer pair	WormBase ID (gene name)	Chromosome	wt/ <i>mes-4</i>	P-value	Real-time PCR relative to:	
					ZK381.1	F14B4.2
F14B4.2	F14B4.2	I	1.15	0.0038	1.01	
F49D11.8	F49D11.8 (cpn-4)	I	1.04	0.0053	1.47	1.84
B0361.8	B0361.8	III	1.04	0.0069	0.92	1.14
ZK381.1	ZK381.1 (him-3)	IV	1.18	0.091		0.99
K07C11.2	K07C11.2 (air-1)	V	0.94	0.032	1.14	1.27

As described in the Materials and methods, RNA was isolated from 50 dissected gonads per genotype. It was not linearly amplified. Real-time PCR was performed in triplicate for each gene indicated, relative to two reference genes (ZK381.1 and F14B4.2).