Table S1. Genetic mapping of the *spe-38* gene

Three-factor mapping

Genotype	Recombinants	Segregation*
spe-38/dpy-5 unc-75	Dpy Non-Unc	26/38 Spe
	Unc Non-Dpy	10/37 Spe

SNP mapping

Type†	Name‡	Genomic position§	Nucleotide change N2 to H¶	Recombinants**	Marker N2††
SNIP SNP	ZC247	1:10246168	A to T	Dpy Non-Spe	8/22
				Unc Non-Spe	1/13
SNIP SNP	C3E57	1:1084422	C to T	Dpy Non-Spe	4/22
				Unc Non-Spe	0/13
SNIP SNP	F49D11	1:10932370	G to A	Dpy Non-Spe	6/6
				Unc Non-Spe	0/1
Sequence SNP	Y52B11A SNP1	1:10949940	T to G	Dpy Non-Spe	1/4
				Unc Non-Spe	0/1
Sequence SNP	Y52B11A SNP2	1:10970913	C to T	Dpy Non-Spe	0/1
				Unc Non-Spe	0/1
Sequence SNP	Y52B11A SNP3	1:11054394	T to G	Dpy Non-Spe	0/4
				Unc Non-Spe	1/1
SNIP SNP	W02B9	1:11085342	T to A	Dpy Non-Spe	0/6
				Unc Non-Spe	1/1
SNIP SNP	ZK39	1:11170085	C to A	Dpy Non-Spe	2/22
				Unc Non-Spe	1/13

Complementation tests to sterile mutants in the *spe-38* region‡‡

Gene	Result
stu-10	Complements
sqv-5	Complements
spe-9	Complements

*Recombinants that segregated sterile progeny in the next generation were scored as Spe.

†Single Nucleotide Polymorphisms (SNPs). SNIP SNPs can be detected with restriction digest. Sequence SNPs can only be detected by DNA sequencing.

‡SNPs are named after the cosmid clone or yeast artificial chromosome (YAC) clone that corresponds to their location in the genome. When more than one SNP is in sequence corresponding to the same clone they are given additional numeric designations.

§Genomic position of SNPs are indicated as follows: chromosome:nucleotide position. SNPs were chosen or identified as the location of *spe-38* was progressively narrowed.

¶Sequence change from *C. elegans* strain N2 (Bristol, England) to CB4856 (H, Hawaii).

**Recombinants were derived from *dpy-5 spe-38* (N2) / + + (H) or *spe-38 unc-75* (N2) / + + (H) hermaphrodites.

††The number of recombinants that had N2 sequence for the indicated SNP / total number of recombinant lines examined.

‡‡In order to determine whether the *eb44* mutation was an allele of *stu-10, sqv-5* or *spe-9*, complementation tests were conducted. Heterozygous *stu-10, sqv-5* or *spe-9* males were crossed to homozygous *spe-38* hermaphrodites. If no sterile progeny were detected in the F1 generation then the gene was considered to complement *eb44*.