Table S1 Detailed results of GATK mutation detection

Position	Found in:	Mutant reads / total reads	# reads of other strain	wild-type sequence	mutant sequence
II: 4101403	*sy740*	4/18	10	CACCT**C$_3$AC$_7$**TC	CACCT**C$_{11}$**TC
III: 8457740	*sy740*	13/23	10	TAGGGGAA**G**TGTATTTG	TAGGGGAA**C**TGTATTTG
IV: 13503822	*sy740*	6/13	3	CCCCCA**A**TTGGA**C**ATCCCC	CCCCCA**G**TTGGA**T**ATCCCC
IV: 13503828		6/15	5		
IV: 8719829	*sy740*	8/14	6	ACAGT$_5$**G$_{13}$AG$_5$**TCTAAC	ACAGT$_5$**G$_{19}$**TCTAAC
X: 17375284	*sy740*	8/36	38	GATTGCGT**G**AAGCAAAG	GATTGCGT**A**AAGCAAAG
V: 13647424-13647432	*sy745*	6/22	15	ATCCT**(TCG)$_9$**TC(TCG)$_5$CG	ATCCT**(TCG)$_6$**TC(TCG)$_5$CG
I: 3075678	*sy745*	8/28	21	GTTTTAATT**A$_{13}$**CTGA$_7$GT	GTTTTAATT**A$_{14}$**CTGA$_7$GT
X: 14728375	*sy745*	5/17	12	CGTTAGA**G$_{14}$AG$_3$**TGAAGA	CGTTAGA**G$_{18}$**TGAAGA

Comparison of the high-throughput sequencing output generated using the GATK pipeline identified 1419 predicted changes between *dpy-11(sy740)* and the *C. elegans* reference genome, and 1441 predicted changes between *dpy-11(sy745)* and the *C. elegans* reference genome. Of these predicted changes, 151 were unique to *dpy-11(sy740)* and 173 to *dpy-11(sy745)*, totaling 324 candidates to be strain-specific changes. Mutations predicted to be unique to either strain were manually curated by inspection of the reads aligned to the reference genome: of 324 predicted mutations, 313 were present in both strains and 3 were observed in neither strain. The remaining 8 are detailed above: the position of each is given, the representation of the mutation among reads from the strain bearing the mutation is given, the number of reads at that site for the other strain is given, and the nature of the mutation is shown, with the affected nucleotide(s) bolded and underlined. Note that none of these sites shows homology to the targeting sequence used in the sgRNA to direct Cas9 nuclease activity, GAGCTGGGCACCATGGAGCA.