TABLE S2

Sequence coverage for each mutant under different WGS conditions

Mutant	Flow cell lanes used	Reads	Average coverage[a]	% of genome covered at least 1x	% of genome covered at least 5x
fp6	2	paired-end	52.2	99.915	99.860
fp6	2	single-end	27.2	99.908	99.753
fp6	1	paired-end	25.8	99.901	99.706
fp6	1	single-end	13.6	99.871	98.054
fp9	2	paired-end	55.3	99.914	99.861
fp9	2	single-end	28.9	99.908	99.741
fp9	1	paired-end	27.7	99.902	99.696
fp9	1	single-end	14.7	99.871	98.041
fp12	2	paired-end	54.1	99.920	99.881
fp12	2	single-end	28.1	99.918	99.827
fp12	1	paired-end	26.8	99.910	99.793
fp12	1	single-end	14.1	99.896	98.918

[a] Average coverage is calculated by the mean number of times every nucleotide of the genome is sequenced. Distribution of coverage for 2-lanes paired sequencing is shown in Figure S1. *C. elegans* genomes size is ~100 Mb.