



Figure S3 Whole genome sequencing of strains obtained in Exp. 1 and 12

(A) Description of the strains used for genome sequencing.

(B) and (C) List of the possible off-targets for the sgRNAs used in Exp. 1 and 12.

(D) and (E) Lists of all variants found in edited strains obtained in Exp.1 and 12. The variants were identified by comparison with sequence obtained from wild-type populations maintained by AP and YW who conducted Exp. 1 and 12. None of the variants map to the predicted off-targets shown in B and C, and none show homology to the ssODNs used in the experiments.

Note that the edited strains were established from single hermaphrodites that underwent at least two sequential rounds of cloning to homozygote the edits. In contrast, the wild-type reference sequences were obtained from populations that were passaged by picking multiple hermaphrodites for several generations between the time of injection and sequencing. The wild-type populations, therefore, may have lost variants present at low frequency in the population on the day of injections.

Gene: name of the gene at the indicated position in the genome. "(dist=)" indicates the genomic position of the closest gene; Position: position in the genome; Reference: sequence in the N2 reference strain; Variant: sequence variation found in the established strain; Hom: homozygous; Het: heterozygous.