**Supplementary Information, Table S1A List of oligonucleotide repair templates used in this study.**

| Oligo name | Sequence 5'-3' |
|---|---|
| ***ben-1*$^{22}$ oligo** | TCATATAACTTCAAAAAGAACTTGGAAAAAATGAGAGAAATT GTTCACGTTTAAGCCGGACAATGTGGTAATCAAATCGGAGCCA AGTTCTGGGAAGTGAT |
| ***ben-1*$^{153}$ oligo (±50nt)** | ACTTATAAGGGAGAAAGTGATTTGCAGTTGGAAAGAATCAAT GTCTACTAGAATGAGGCTAATGGTGAGAAATTTAGCTTTTTTA TTCGATTTTCAGATTC |
| ***ben-1*$^{1340}$ oligo** | TTCAGCCTCTTTTCGAACTACGTCGAGCACATTATCGACAAGTT CGGCTCATTCGGTGTAGTGACCCTTGGCCCAGTTGTTTCCGGCT CCGGATTGTCCGA |
| ***ben-1*$^{1499}$ oligo** | AATTAATCCAACCTTTGGCGACGGAACAACCGAGAAAGAACT CATAATTCAATCTGGATACTCTTCACGGATTTTCGAAATGAGA AGAGTTCCCATTCCAG |
| ***drp-1* oligo** | TCGATGCCGTGCGAAAAGAAATCGAAGATGAAACTGCGCGCG TAACTGGAGTGAATAAAGGAATCTCTCTTCTTCC |
| ***flag::ced-9* oligo** | TCTAGAATGTATATTATGATTATGAAAACGAATAAAAATTTTA GATGGACTACAAGGACGACGATGACAAGACACGCTGCACGGC GGACAACTCGCTGACGAATCCGGCGTATCGGCG |
| ***fis-2* oligo** | GTCGACTTTTGCCTTTGCACATGCCATGATTGGATCCAAGCTTT AACTGGACGTGAAGGAGGGAATCGTGTGTCTTGAGAGTGA |
| ***ubr-1* oligo** | CTAGACGTTCGGAACACAAAGAGCACACTGGAAGCTTAAAAT GGCATTGCCGGAGTTGATCCTGCAAGACGGGG |
| ***ben-1*$^{153}$ oligo (±25nt)** | AGTTGGAAAGAATCAATGTCTACTAGAATGAGGCTAATGGTGA GAAATTTA |
| ***ben-1*$^{153}$ oligo (±20nt)** | GAAAGAATCAATGTCTACTAGAATGAGGCTAATGGTGAGAA |
| ***ben-1*$^{153}$ oligo (±15nt)** | AATCAATGTCTACTAGAATGAGGCTAATGGT |
| ***ben-1*$^{153}$ oligo (±10nt)** | ATGTCTACTAGAATGAGGCTA |
| ***ben-1*$^{136}$ oligo** | ACTTATAAGGGAGAAAGTGATTTGCAGTTGGAATGAATCAATG TCTACTATAATGAGGCTAATGGTGAGAAATTTAGCTTTTTTATT CGATTTTCAGATTC |
| ***ben-1*$^{127}$ oligo** | AACTTATAAGGGAGAAAGTGATTTGTAGTTGGAAAGAATCAAT GTCTACTATAATGAGGCTAATGGTGAGAAATTTAGCTTTTTTAT TCGATTTTCAGATTC |
| ***ben-1*$^{115}$ oligo** | CCAGCCTGATGGAACTTATAAGGGATAAAGTGATTTGCAGTTG GAAAGAATCAATGTCTACTATAATGAGGCTAATGGTGAGAAAT TTAGCTTTTTTATTCGATTTTCAGATTC |

**Supplementary Information, Table S1B List of primers used in this study.**

| Usage | Primer | Sequence (5'-3') |
|---|---|---|
| **Genotyping** | *ben-1* F1 | CCCTGGCTAGTTCAAACGAAGAG |
| | *ben-1* R1 | CCCATAGGTTCCCGTATGTC |
| | *ben-1* F2 | TGCGCATTCGCGCTCTATAGCAACC |
| | *ben-1* R2 | CGTCCACGGAACATTGCAGCTACAG |
| | *drp-1* F | TCCACAGATTGTAGTCGTCG |
| | *drp-1* R | CTTTCAGTGCAGGAAGACAG |
| | *ced-9* F | TTTGCCGTTCGATTTCACCG |
| | *ced-9* R | TGTGCATTTCCAACCGTCCG |
| | *fis-2* F | ACTATTCTCGAGGAACGGAC |
| | *fis-2* R | ACCCGTTCACTTTTGTTCCG |
| | *ubr-1* F | TACGCCAGCTGCTGCTCAAG |
| | *ubr-1* R | CCGTCAAATATTGCTGTGCC |
| **Allele-specific primers** | *ced-9* flag F | TTGTTTTGAAACGCACCGCC |
| | *ced-9* flag R | CATCGTCGTCCTTGTAGTCC |
| | *ced-9* N2 F | CGAATAAAAATTTTAGATGACACGC |
| | *ced-9* N2 R | GTGTTCCTTCCAGTTGTTGC |

To confirm that precise knock-ins occurred at the targeted sites in edited animals, genomic DNA spanning each sgRNA target site was PCR amplified using "genotyping" primers and subjected to sequencing analysis. The *ben-1* F1/R1 primer pair was used to amplify the genomic DNA spanning the *ben-1*$^{22}$ and *ben-1*$^{153}$ positions. The *ben-1* F2/R2 primer pair was used to amplify the genomic DNA spanning *ben-1*$^{1340}$, *ben-1*$^{1499}$ sgRNA target sites. *drp-1* F/R, *ced-9* F/R, *fis-2* F/R and *ubr-1* F/R primer pairs were used to amplify the genomic DNA spanning the *drp-1*, *ced-9*, *fis-2* and *ubr-1* sgRNA target sites, respectively. For *drp-1*, *fis-2* and *ubr-1* editing experiments, the same PCR products were digested with restriction enzymes to identify the knock-in animals. In the *flag::ced-9* editing experiments, we used allele-specific primers to identify *flag::ced-9* knock-in animals (*ced-9* flag F/R) from benomyl$^{R}$ F1 animals and homozygous F2 animals with knock-ins (*ced-9* flag F/R and *ced-9* N2 F/R).