Split Fluorescent Proteins for *C. elegans*

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This project is maintained by Maria Ingaramo in the York lab, and is funded by Calico Life Sciences LLC

Supplementary Text and Figures

Supplementary Materials and Methods

Mammalian cell culture.

HEK293T cells (ATCC # CRL-3216) were cultured in high-glucose DMEM supplemented with 10% FBS, 1 mM glutamine and 100 µg/mL penicillin/streptomycin (Gibco). A split-wrmScarlet$_{1\text{-}10}$ cDNA codon-optimized for mammalian expression was fused to the C-terminus of eGFP and cloned into a pCDH lentiviral expression vector (SFFV GFP-split-wrmScarlet$_{1\text{-}10}$). Lentivirus was prepared using standard protocols [Kamiyama 2016] and used to infect HEK293T cells. A polyclonal population of GFP-mScarlet$_{1\text{-}10}$ positive cells was isolated by FACS (using GFP fluorescence) and served as parental cell line for further experiments. For CLTA-N CRISPR engineering, S. pyogenes Cas9/sgRNA ribonucleoprotein complexes were prepared as in [Leonetti 2016] , mixed with HDR donor templates and electroporated into of GFP-mScarlet$_{1\text{-}10}$ cells by nucleofection.

CLTA-N split-wrmScarlet$_{11}$ donor library.

A cDNA pool of degenerate split-wrmScarlet$_{11}$ sequences was generated by oligonucleotide synthesis (GeneScript) and homology arms for HDR-mediated insertion at CLTA N-terminus were appended by PCR (Supplementary Material – Table S7 for sequences). Library diversity was verified by Illumina MiSeq deep-sequencing.

Supplementary Results

Split mScarlet screening in mammalian cells

We tested the applicability of the split-wrmScarlet$_{1\text{-}10}$ system for mammalian cell engineering but were surprisingly unsuccessful at detecting fluorescence. We designed a human codon-optimized split-wrmScarlet$_{1\text{-}10}$ cDNA and expressed it as a C-terminal GFP fusion in HEK293T cells by lentiviral transduction. Expression of GFP verified the successful expression of the fusion protein (Figure S10A). However, subsequent expression of split-wrmScarlet$_{11}$ fragments did not give rise to detectable red fluorescence despite numerous attempts. We reasoned that the split-wrmScarlet$_{11}$ amino-acid sequence might be sub-optimal for complementation in human cells and synthesized a library of degenerate split-wrmScarlet$_{11}$ sequences covering any possible single and double amino-acid mutants. Using an established assay for CRISPR-based knock-in of sequences at the CLTA N-terminus (a highly expressed gene in HEK293T cells [Leonetti 2016] , neither our original split-wrmScarlet$_{11}$ sequence nor its mutant library enabled detectable complementation (Figure S10B, left panels). By contrast, a control experiment using the GFP$_{1\text{-}10}$/GFP$_{11}$ system showed a high level of knock-in and complementation in HEK293T (Figure S10B, right panels). It is possible that split-wrmScarlet$_{1\text{-}10}$ is expressed in a non-functional form in human cells, or that its binding to split-wrmScarlet$_{11}$ is occluded by competing interactions (with cellular chaperones, for example). In addition, we did not attempt complementation on primary non-transformed cell lines, like WI-38 cells, whose different proteostasis network and chaperones could aid split mScarlet folding. At this point, more experiments will be required to fully test the portability of split-wrmScarlet to mammalian systems.

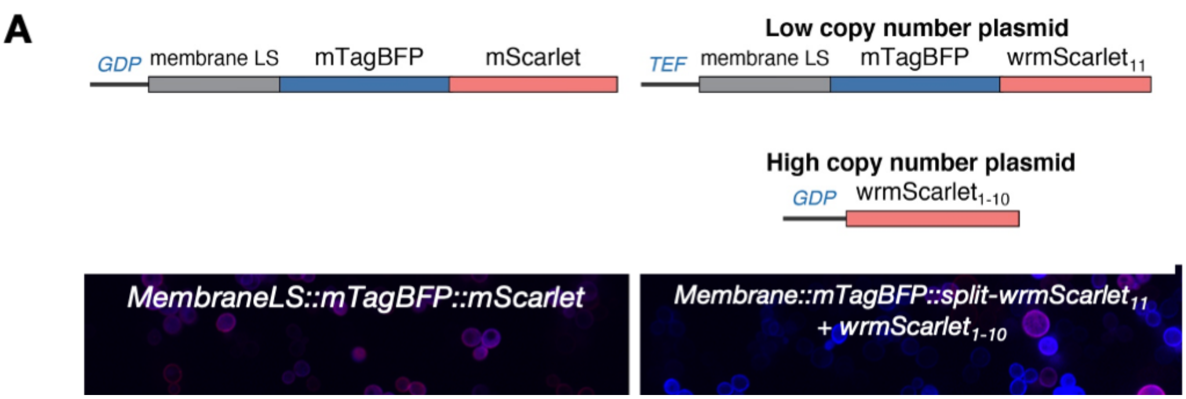
Experiments to investigate whether split-wrmScarlet$_{11}$ functions as a degron in *C. elegans*

After finalizing our experiments, a paper that shows that C-terminal gly-gly sequences might function as degrons in mammalian cells was brought to our attention [Koren 2018]. Since we were unable to obtain non-sterile positive clones of TOMM-20::split-wrmScarlet$_{11}$ that did not have a mutation on the last glycine, and we were also unable to obtain EAT-6 homozygotes, we were concerned that our split-wrmScarlet$_{11}$ might be recognized as a degron. To investigate this, we first labeled HIS-3, EAT-6, and TOMM-20 with the 24 a.a. split-wrmScarlet$_{11(\text{MDELYK})}$, which adds the sequence MDELYK to the C-terminus of split-wrmScarlet$_{11}$. These worms were fertile, and at least as bright as those labeled with split-wrmScarlet$_{11}$ (Figure S6). However, increased fluorescence could be due to increased molecular brightness rather than increased abundance. To address this, we compared the abundance of nuclear HIS-3, HIS-3::split-wrmScarlet$_{11}$, and HIS-3::split-wrmScarlet$_{11(MDELYK)}$ by western blot, and were unable to detect a significant change in abundance (Figure S11). We also could not detect differences in abundance in *S. cerevisiae*, using a p416-GPD plasmid expressing a mTagBFP-mScarlet fusion or the same fusion truncated so that it ends with gly-gly (Figure S12). However, because HIS-3 is a nuclear protein, and expression in yeast was done from an overexpressing plasmid, we cannot exclude that a protein ending with two glycines might be recognized as a degron in other cellular compartments, or at different expression levels, nor that there is no DesCEND degron pathway in yeast and worms. For these reasons, we recommend using the 24 a.a. split-wrmScarlet$_{11(MDELYK)}$ when labeling proteins at their C-termini.

Figure S1. Split-wrmScarlet sequence comparison to mScarlet.

Figure S1: Split-wrmScarlet sequence comparison to mScarlet. (A) Protein sequence alignment of the full-length mScarlet and split-wrmScarlet. The ten amino acid substitutions are highlighted in red, the sequence corresponding to split-wrmScarlet$_{1\text{-}10}$ in light gray and the sequence of split-wrmScarlet$_{11}$ in dark gray. Note that gly-gly sequences at the C-termini of proteins can be degrons in mammalian cells, so when labeling on the C-terminus, we recommend using the 24 a.a. split-wrmScarlet$_{11(MDELYK)}$. (B) Protein structure from split-wrmScarlet generated with Phyre2 and PyMOL. Mutations of split-wrmScarlet relative to mScarlet are highlighted with surface rendering, and the split-wrmScarlet$_{11}$ strand is colored in black.

Figure S2. Split-wrmScarlet brightness in *S. cerevisiae*.



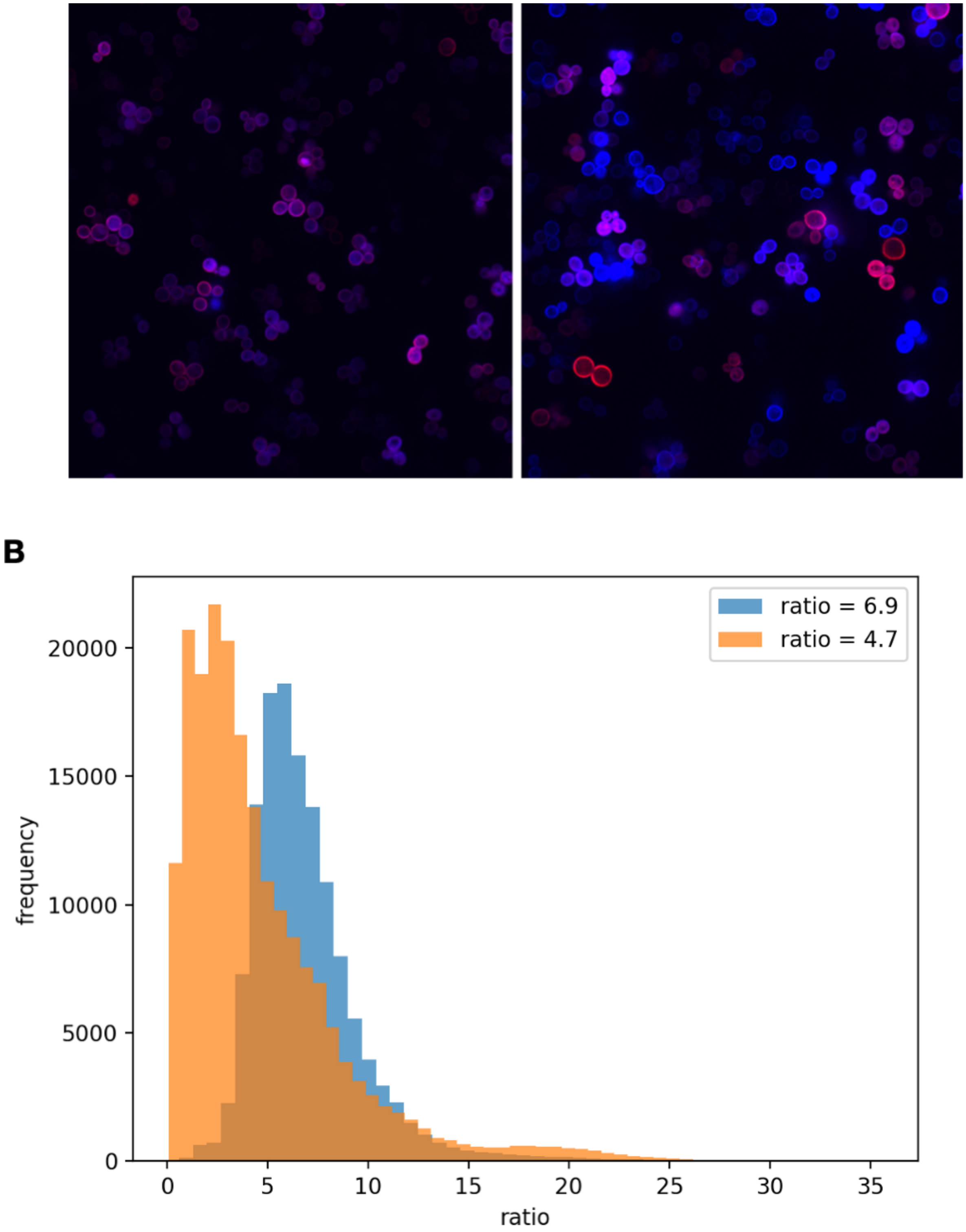


Figure S2: Split-wrmScarlet brightness in *S. cerevisiae*. (A) Composite display of red and blue channels for membrane-localized mTagBFP-mScarlet (wild-type) fusion or split-wrmScarlet$_{1\text{-}10}$ plus membrane localized mTagBFP-split-wrmScarlet$_{11}$ in yeast. Images were acquired and are displayed under identical conditions. Note that the heterogeneity inherent to expression from plasmids is large, but split-wrmScarlet is capable of brightness levels similar to the parent protein. A schematic of the plasmids transformed is presented above each image. (B) Histograms displaying the per-pixel ratio of red to blue fluorescence for background corrected, masked images. mScarlet/mTagBFP ratios are displayed in blue, and split-wrmScarlet/mTagBFP in orange. The inset displays the average red/blue ratio.

Figure S3. Developmental toxicity in worms expressing split-sfCherry3 in somatic nuclei.

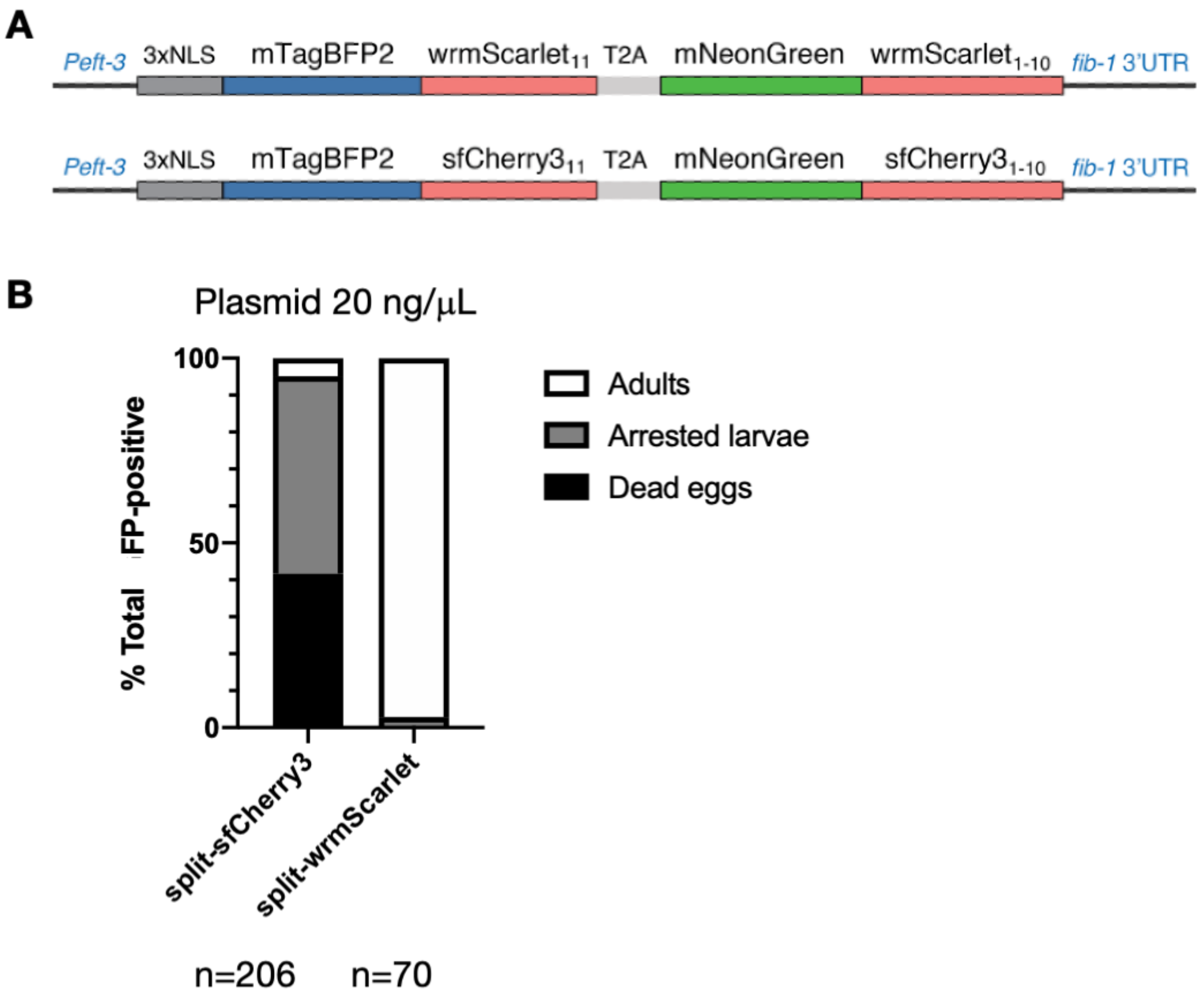


Figure S3: Developmental toxicity in worms expressing split-sfCherry3 in somatic nuclei. (A) Schematic of the plasmids encoding split-wrmScarlet and split-sfCherry3 used for comparison. Each plasmid consists of a large FP_{1-10} fused to mNeonGreen, and the corresponding small FP_{11} fused to mTagBFP2, preceded with three SV40 nuclear localization sequences (NLS). The T2A sequence ensures the separation of NLS::mTagBFP2::FP_{11} and the corresponding mNeonGreen::FP_{1-10}. (B) Quantification of mNeonGreen-positive animals into one of three classes: dead eggs, larvae or adults.

Figure S4. Split-wrmScarlet and split-sfCherry3 comparison.

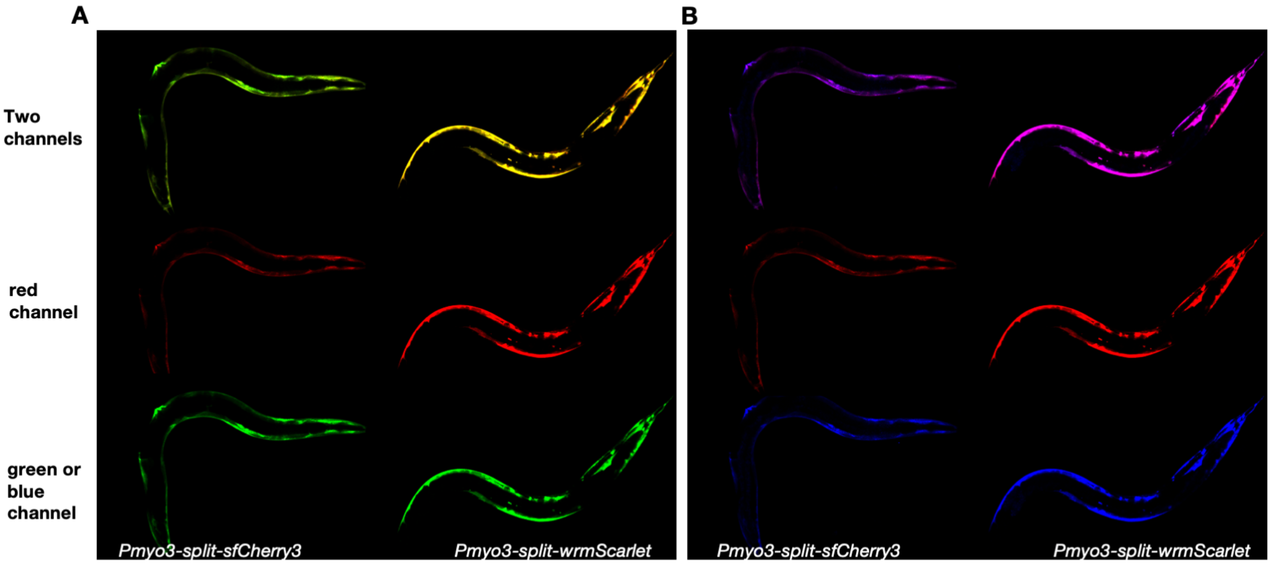


Figure S4: Split-wrmScarlet and split-sfCherry3 comparison. Individual channels and overlays corresponding to the images displayed in Figure 1B.

Figure S5. Brood size and lifespan of split-wrmScarlet$_{1-10}$ and sfGFP$_{1-10}$ lines.

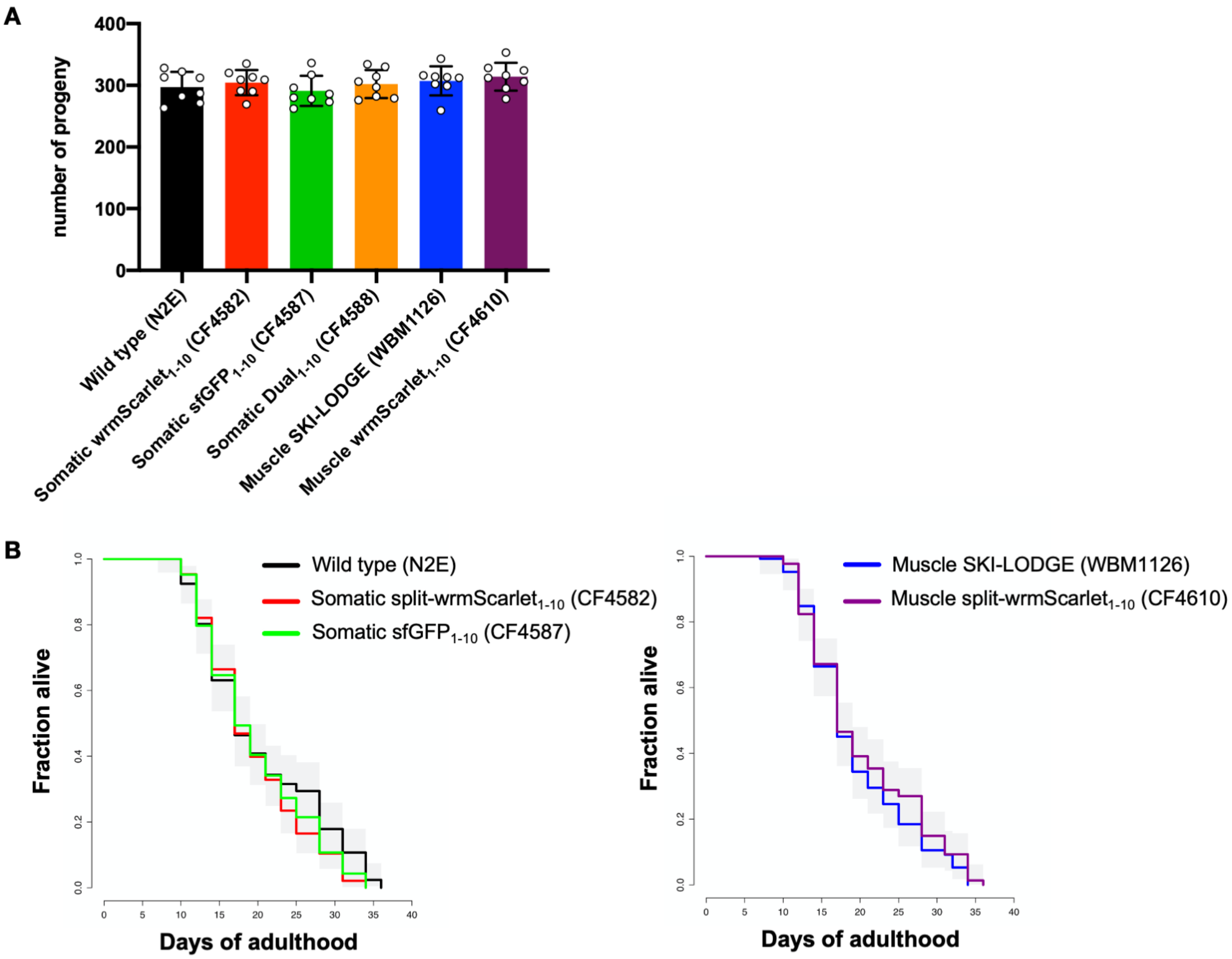


Figure S5: **Brood size and lifespan of split-wrmScarlet$_{1-10}$ and sfGFP$_{1-10}$ lines.** Split-wrmScarlet$_{1-10}$ and split-sfGFP$_{1-10}$ lines produced wild-type numbers of progeny (A) and a wild-type lifespan (B). Genotypes: N2E (wild-type), CF4582 (muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III), CF4587 (muIs253[(Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III), CF4588 (muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)], muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III), CF4610 (muIs257[Pmyo-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR] I) and WBM1126 (wbmIs61[myo-3p::3XFLAG::dpy-10 crRNA::unc-54 3'UTR] I). Supplementary table S6 show survival statistics for all lifespan experiments.

Figure S6. Proteins tagged at their C-terminus with the 24 a.a. split-wrmScarlet$_{11(MDELYK)}$.

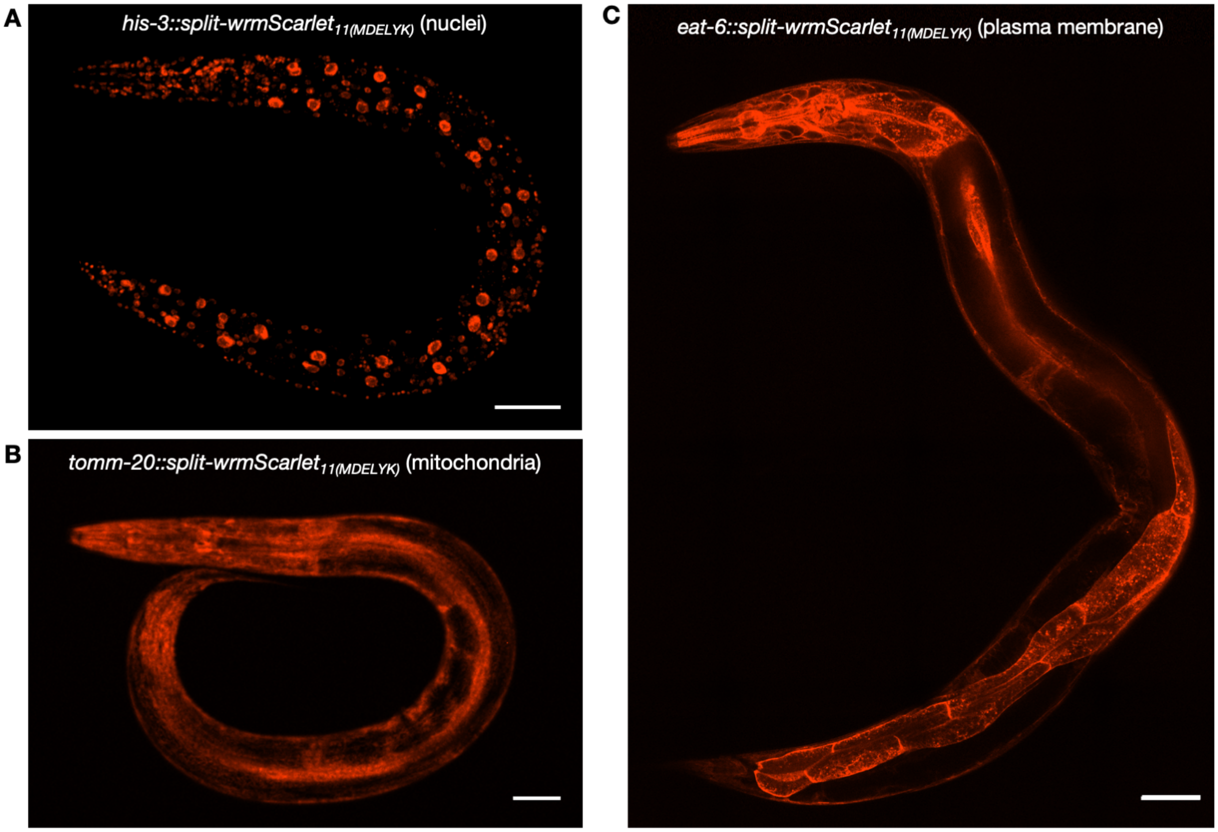


Figure S6: **Proteins tagged at their C-terminus with the 24 a.a. split-wrmScarlet$_{11(MDELYK)}$** Endogenous proteins tagged with split-wrmScarlet$_{11(MDELYK)}$ in animals expressing split-wrmScarlet$_{1-10}$ in somatic tissues. (A-C) Confocal images of worms expressing somatic split-wrmScarlet$_{1-10}$ and (A) HIS-3::split-wrmScarlet$_{11(MDELYK)}$ (nuclei), (B) TOMM-20::split-wrmScarlet$_{11(MDELYK)}$ (mitochondria), or (C) EAT-6::split-wrmScarlet$_{11(MDELYK)}$ (plasma membrane). (A-B) Maximum intensity projections of 3D stacks shown. (C) Single slice shown. Scale bars, 50 μm.

Figure S7. Tissue-specific split-wrmScarlet fluorescence in the germline is undetectable when split-wrmScarlet$_{1-10}$ is integrated using a single-copy transgene via MosSCI.

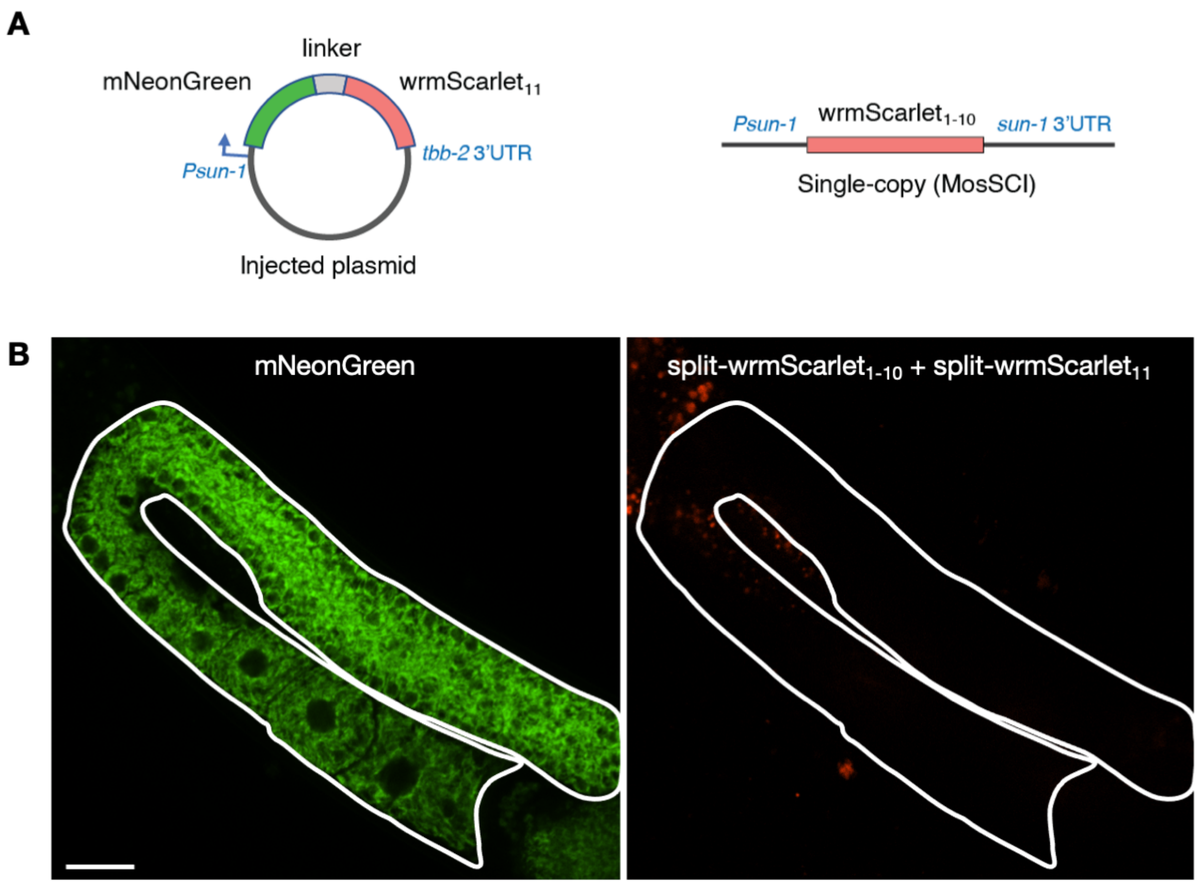


Figure S7: Tissue-specific split-wrmScarlet fluorescence in the germline is undetectable when split-wrmScarlet$_{1-10}$ is integrated using a single-copy transgene via MosSCI. (A) Schematic of the plasmid encoding *Psun-1::mNeonGreen::linker::split-wrmScarlet$_{11}$::tbb-2 3'UTR* (left), which was injected into the MosSCI strain PHX1797 carrying a single, integrated copy of *Psun-1::split-wrmScarlet$_{1-10}$::sun-1 3'UTR* (right). (B) Images of animal expressing mNeonGreen::linker::split-wrmScarlet$_{11}$ and split-wrmScarlet$_{1-10}$ in the germline. Despite detecting mNeonGreen fluorescence, split-wrmScarlet was undetectable in this MosSCI strain, potentially due to compromised expression, folding or maturation of split-wrmScarlet$_{1-10}$. Scale bar, 20 μm.

Figure S8. Generation and validation of germline-specific split-wrmScarlet$_{1-10}$ and sGFP2$_{1-10}$ strains.

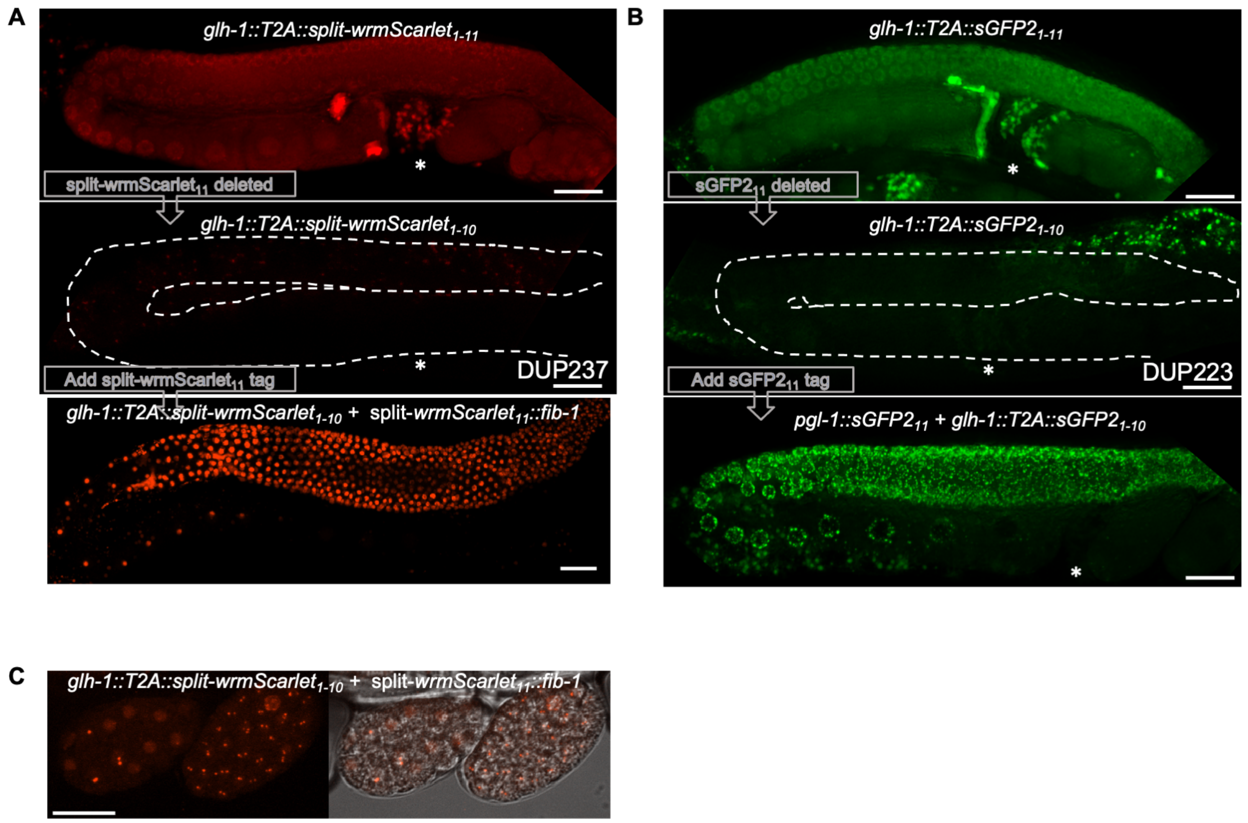


Figure S8: Generation and validation of germline-specific split-wrmScarlet$_{1-10}$ and sGFP2$_{1-10}$ strains. In order to generate germline-specific split-fluorescent strains, we first tagged the C-terminus of glh-1 with T2A::split-wrmScarlet$_{1-11}$ (A) or T2A::sGFP2$_{1-11}$ (B). The T2A separates GLH-1 post-translationally to disperse the fluorophore throughout germ-cell nuclei, syncytium, sperm (*) and early embryos (Upper panels). We then deleted split-wrmScarlet$_{11}$ or sGFP2$_{11}$ to generate the corresponding split-FP$_{1-10}$ strains DUP237 and DUP223 respectively. As expected, these strains were non-fluorescent (Middle panels). Tagging FIB-1 with split-wrmScarlet$_{11}$, or PGL-1 with sGFP2$_{11}$ confirmed that germline-specific labeling with split-wrmScarlet and split-sGFP2 can be successfully achieved using these strains (Lower panels). (C) Split-wrmScarlet$_{11}$::FIB-1 is detectable in early embryos. Scale bars, 20 μm.

Figure S9. Somatic sfGFP$_{11}$ compared to full-length eGFP at the endogenous vha-13 locus.

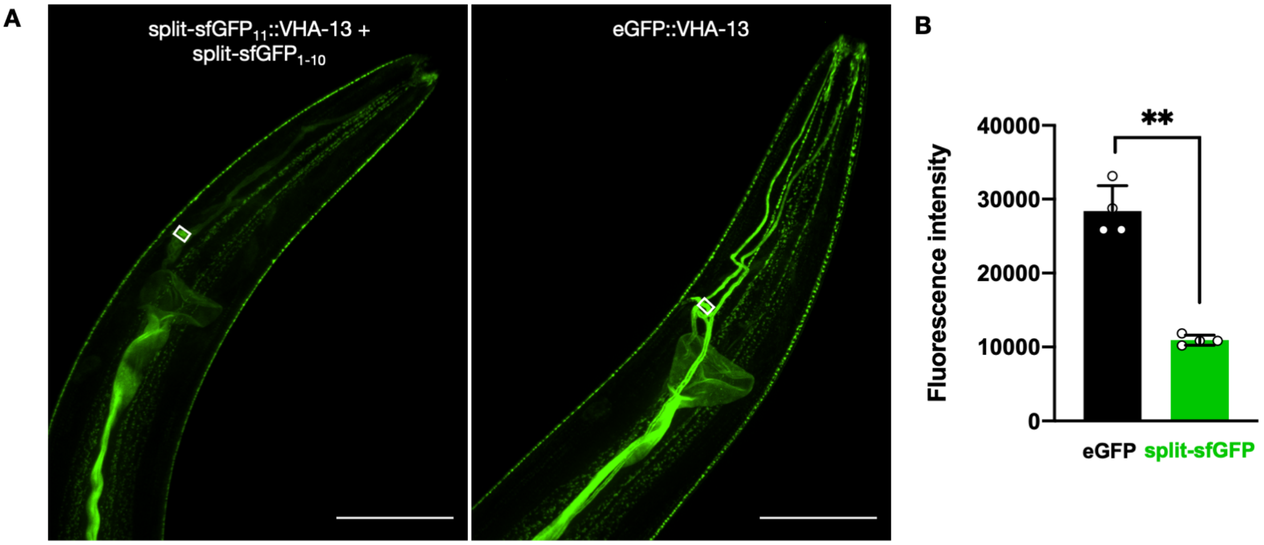


Figure S9: Somatic sfGFP$_{11}$ compared to full-length eGFP at the endogenous vha-13 locus. (A) Representative images of animals expressing sfGFP$_{1-10}$ in somatic tissues with endogenous VHA-13 tagged with sfGFP$_{11}$ (left panel), or endogenous VHA-13 tagged with eGFP in a wild-type background (right panel). Maximum intensity projections of 3D stacks shown. Scale bars, 50 µm. (B) Emission intensities from somatic sfGFP::VHA-13 and eGFP::VHA-13. Quantification was performed in the cell body, as quantifications in the excretory canal had higher variance. Mean ± s.d. Circles are individuals (n=4 for each condition). $^{**}P < 0.005$.

Figure S10. Screen for split-wrmScarlet fluorescence in mammalian cells.

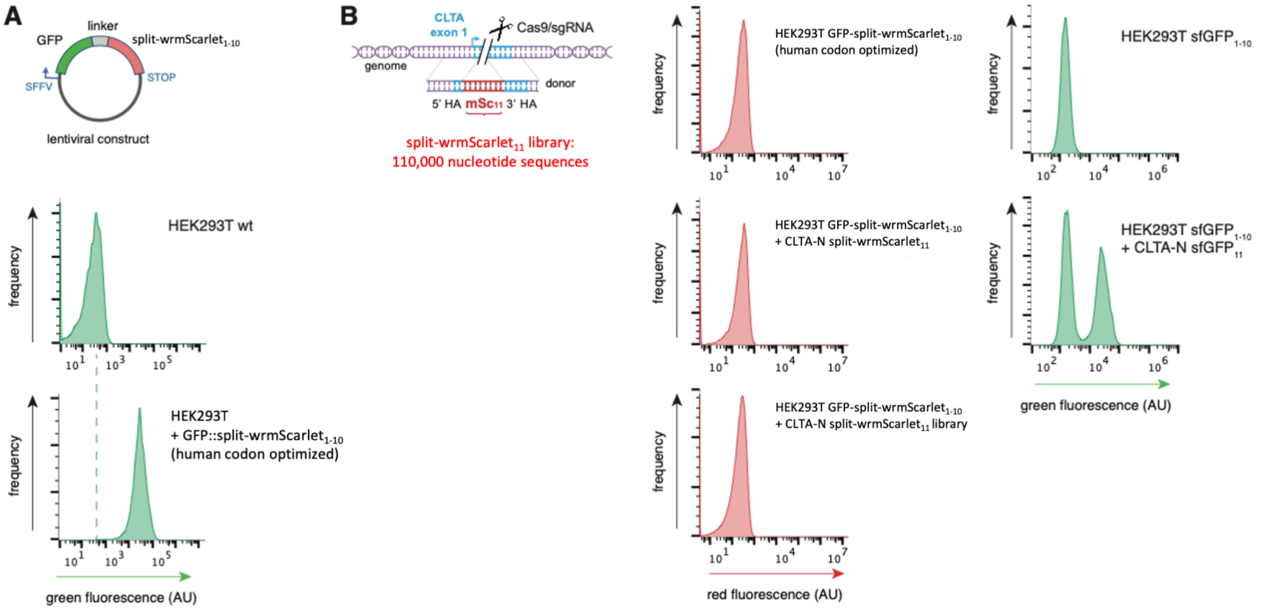


Figure S10: Screen for split-wrmScarlet fluorescence in mammalian cells. (A) FACS histograms of human codon-optimized split-wrmScarlet$_{1-10}$ expressed as a C-terminal GFP fusion. GFP expression verifies successful expression of the fusion protein in HEK293T cells by lentiviral transduction. (B) Schematic of the CRISPR-based knock-in design for screening single and double mutants of split-wrmScarlet$_{11}$. Left panel shows that neither our original split-wrmScarlet$_{11}$ sequence nor its mutant library enabled detectable complementation as detected by FACS. Right panel shows that the control experiment using the sfGFP$_{1-10}$/sfGFP$_{11}$ system displays high levels of knock-in and complementation in HEK293T cells.

Figure S11. Split-wrmScarlet$_{11}$ C-terminal amino acids did not affect H2A abundance.

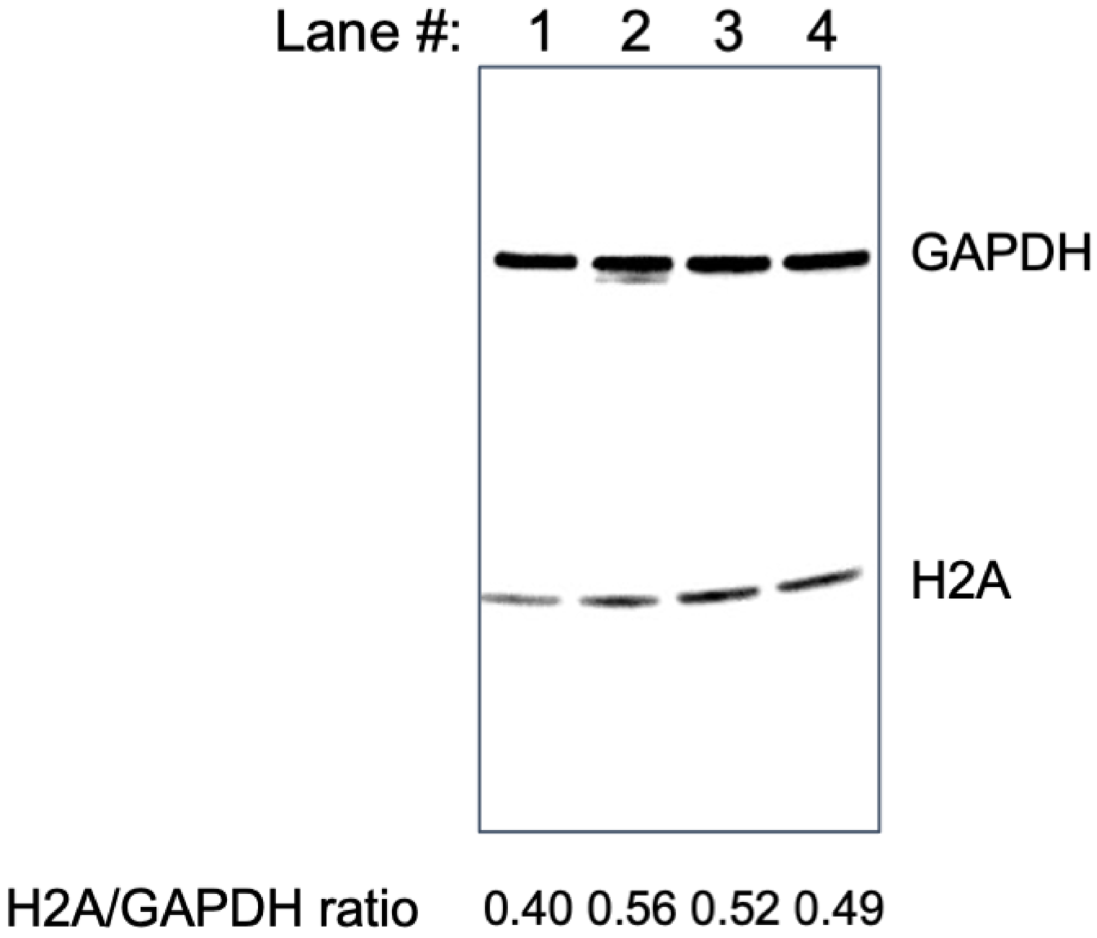


Figure S11: Split-wrmScarlet$_{11}$ C-terminal amino acids did not affect H2A abundance. Western-blot of histone H2A (his-3) with split-wrmScarlet$_{11}$+/- MDELYK. Western blot targeting HIS-3 in wild-type animals (lane 1), somatic split-wrmScarlet$_{1-10}$ expressing animals (lane 2), somatic split-wrmScarlet$_{1-10}$ strain with HIS-3::split-wrmScarlet$_{11}$ ending with two glycines (lane 3), or somatic split-wrmScarlet$_{1-10}$ + HIS-3::split-wrmScarlet$_{11(\mathrm{MDELYK})}$. GAPDH was used as a loading control, and the HIS-3/GAPDH ratios are displayed under each lane.

Figure S12. mScarlet ending with GG or MDELYK yields similar protein abundance in yeast.

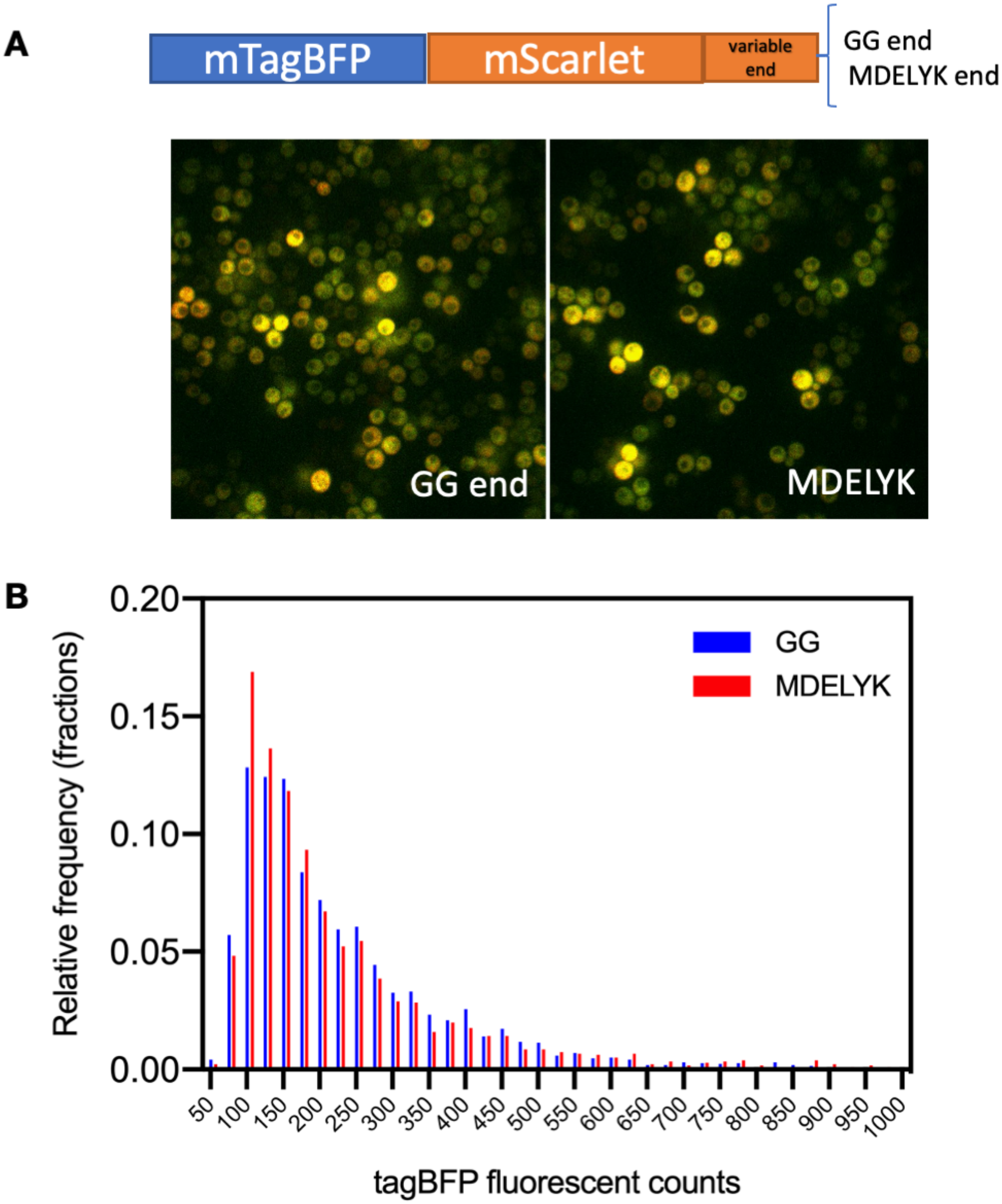


Figure S12: mScarlet ending with GG or MDELYK yields similar protein abundance in yeast. (A) Representative images of yeast expressing mTagBFP::mScarlet fusion truncated to end with gly-gly (GG end) or MDELYK from a p416-GPD promoter plasmid. mTagBFP fluorescence is pseudocolored in green, and mScarlet in red. (B) Histogram of mTagBFP fluorescence from 2556 yeasts expressing the truncation after GG and 1777 yeasts expressing the MDELYK end.

Supplementary Tables

Table S1. DNA Sequences of split-wrmScarlet$_{1-10}$, split-wrmScarlet$_{11}$, sfGFP$_{1-10}$, sfGFP$_{11}$, sGFP2$_{1-10}$ and sGFP2$_{11}$

Gene	DNA sequence
Codon-optimized split-wrmScarlet$_{1-10}$ with 3 introns	ATGGTATCGAAGGGAGAAGCAGTAATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTCATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCAAGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTAC
Codon-optimized split-wrmScarlet$_{11}$	TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA
Codon-optimized split-wrmScarlet$_{11(MDELYK)}$	TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGAATGGATGAGTTATACAAG
Codon-optimized sfGFP$_{1-10}$ with 1 intron	ATGTCTAAGGGAGAAGAGTTATTTACTGGAGTTGTGCCGATCCTCGTCGAGCTCGACGGAGACGTCAACGGACACAAGTTCTCCGTCCGTGGAGAGGGAGAGGGAGACGCCACCATCGGAAAGCTCACCCTCAAGTTCATCTGCACCACCGGAAAGCTCCCAGTCCCATGGCCAACCCTCGTCACCACCCTCACCTACGGAGTCCAATGCTTCTCCCGTTACCCAGACCACATGAAGCGTCACGACTTCTTCAAGTCCGCCATGCCAGAGGGATACGTCCAAGAGCGTACCATCTCCTTCAAGGACGACGGAAAGTACAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagACCCGTGCCGTCGTCAAGTTCGAGGGAGACACCCTCGTCAACCGTATCGAGCTCAAGGGAACCGACTTCAAGGAGGACGGAAACATCCTCGGACACAAGCTCGAGTACAACTTCAACTCCCACAACGTCTACATCACCGCCGACAAGCAAAAGAACGGAATCAAGGCCAACTTCACCGTCCGTCACAACGTCGAGGACGGATCCGTCCAACTCGCCGACCACTACCAACAAAACACCCCAATCGGAGACGGACCAGTCCTCCTCCCAGACAACCACTACCTCTCCACCCAAACCGTCCTCTCCAAGGACCCAAACGAGAAG
Codon-optimized sfGFP$_{11}$	CGTGACCACATGGTCCTTCATGAGTATGTAAATGCTGCTGGGATTACA
Codon-optimized split-wrmScarlet$_{1-10}$ with 1 intron for germline expression	ATGGTTTCCAAGGGAGAGGCTGTTATCAAGGAATTCATGCGCTTCAAGGTTCACATGGAAGGATCTATGAACGGACACGAATTCGAAATCGAAGGAGAAGGAGAAGGACGCCCATACGAGGGAACTCAAACTGCTAAGCTTAAGGTTACTAAAGGAGGACCACTTCCATTCTCTTGGGATATCCTTTCTCCACAGTTCATGTACGGATCTCGCGCTTTCATCAAGCACCCAGCTGATATCCCAGATTACTACAAGCAGTCTTTCCCAGAAGGATTCAAATGGGAGCGCGTTATGAACTTCGAAGATGGAGGAGCTGTTACCGTTACCCAAGATACCTCCCTTGAGGATGGAACCCTTATCTACAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGTTAAGCTTCGCGGAACTAATTTCCCACCAGATGGACCAGTTATGCAGAAGAAGACTATGGGATGGGAAGCTTCTACCGAGCGCCTTTACCCAGAGGATGGAGTCCTTAAGGGAGATATCACCATGGCTCTTCGTCTTAAGGATGGAGGACGTTACCTTGCTGATACCTCTACTACTTACAAGGCTAAGAAGCCAGTTCAGATGCCAGGAGCTTACCTTGTCGATCGTAAGCTTGATATCACTTCTCATAACGAATAC
Codon-optimized sGFP2$_{1-10}$ with 2 intron for germline expression	ATGAGTAAAGGAGAAGAATTGTTCACTGGAGTTGTCCCAATCCTCGTCGAGCTCGACGGAGACGTCAACGGACACAAGTTCTCCGTCCGTGGAGAGGGAGAGGGAGACGCCACCATCGGAAAGCTCACCCTCAAGTTCATCTGCACCACCGGAAAGCTCCCAGTCCCATGGCCAACCCTCGTCACCACCCTCACCTACGGAGTCCAATGCTTCGCCCGTTACCCAGACCACATGAAGCGTCACGACTTCTTCAAGTCCGCCATGCCAGAGGGATACGTCCAAGAGCGTACCATCTCCTTCAAGgtaagtttaaacatatatatactaactactgattatttaaattttcagGACGACGGAAAGTACAAGACCCGTGCCGTCGTCAAGTTCGAGGGAGACACCCTCGTCAACCGTATCGAGCT

	CAAGGGAACCGACTTCAAGGAGGACGGAAACATCCTCGGACACAAGCTCGAGTACAACTTCAACTCCCACAACGTCTACATCACCGCCGACAAGCAAAAGAACGGAATCAAGGCCAACTTCACCgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagACCCGTCACAACGTCGAGGACGGATCCGTCCAACTCGCCGACCACTACCAACAAAACACCCCAATCGGAGACGGACCAGTCCTCCTCCCAGACAACCACTACCTCTCCACCCAAACCGTCCTCTCCAAGGACCCAAACGAGAAG
Codon-optimized sequence of split-wrmScarlet$_{1-10}$ with 3 introns, engineered to avoid piRNA recognition transgene silencing. (Undetectable fluorescence in the MosSCI strain PHX1797)	ATGGTATCGAAGGGAGAAGCAGTCATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTGATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCAAGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTAC

Table S2. C. *elegans* lines expressing single-copy of split-wrmScarlet$_{1-10}$ and/or sfGFP$_{1-10}$

Strain	Genotype	Description	Genomic Position	Genetic Position	Sequence
CF4582	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Somatic split-wrmScarlet$_{1-10}$ (eft-3 promoter)	II: 9.83 MB	II:1.73	gcacctttggtcttttattgtcaacttccattggttcttccattgtttctgttaaattaatgaatttttcataaaataaagacattatacaatataaaaatgaagaatttattgaaaataaactgccagagagaaaaagtatgcaacactcccgccgagagtgtttgaaatggtgtacggtacattttcgtgctaggagttagatgtgcaggcagcaacgagaggggggagagatttttttgggccttgtgaaattaacgtgagttttctggtcatctgactaatcatgttggtttttgttggtttattttgtttttatctttgtttttatccagattaggaaatttaaattttatgaatttataatgaggtcaaacattcagtcccagcgtttttcctgttctcactgtttagtcgaatttttattttaggctttcaacaaatgttctaactgtcttatttgtgacctcactttttatatttttttaatttttaaaaatattagaagtttctaggataatttttcgacttttattctctctaccgtccgcactcttcttacttttaaattaaattgttttttttttcagttgggaaacactttgctcactccgtagcagccATGGTATCGAAGGGAGAAGCAGTAATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTCATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCAAGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTACTAAtaagtccaattactcttcaacatccctacatgctctttctccctgtgctcccacccccctatttttgttattatcaaa

					aaacttctcttaatttctttgttttttagcttcttttaagtcacctctaacaatgaaattgtgtagattcaaaaatagaattaattcgtaataaaaagtcgaaaaaaattgtgctccctccccccattaataataattctatcccaaaatctacacaatgttctgtgtacacttcttatgtttttacttctgataaattttttgaaacatcatagaaaaaaccgcacacaaaataccttatcatatgttacgtttcagtttatgaccgcaatttttatttcttcgcacgtctgggcctctcatgacgtcaaatcatgctcatcgtgaaaaagttttggagtattttggaatttttcaatcaagtgaaagtttatgaaattaattttcctgcttttgctttttggggtttcccctattgtttgtcaagatttcgaggacggcgtttttcttgctaaaatcacaagtattgatgagcacgatgcaagaaagatcggaagaaggtttgggtttgaggctcagtggaaggtgagtagaagttgataatttgaaagtggagtagtgtctatggggtttttgccttaaatgacagaatacattcccaatataccaaacataactgttt
CF4587	muIs253[(Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Somatic sfGFP$_{1-10}$ (eft-3 promoter)	II: 8.42 MB	II:0.77	gcacctttggtcttttattgtcaacttccattggttcttccattgtttctgttaaattaatgaatttttcataaaataaagacattatacaatataaaaatgaagaatttattgaaaataaactgccagagagaaaaagtatgcaacactcccgccgagagtgtttgaaatggtgtacggtacattttcgtgctaggagttagatgtgcaggcagcaacgagaggggagagatttttttggccttgtgaaattaacgtgagttttctggtcatctgactaatcatgttggtttttttgttggtttattttgtttttatctttgtttttatccagattaggaaatttaaattttatgaatttataatgaggtcaaacattcagtcccagcgtttttcctgttctcactgtttagtcgaatttttattttaggctttcaacaaatgttctaactgtcttatttgtgacctcactttttatatttttttaatttttaaaaatattagaagtttctaggataatttttcgacttttattctctctaccgtccgcactcttcttacttttaaattaaattgtttttttttcagttgggaaacactttgctc aaaa ATGTCTAAGGGAGAAGAGTTATTTACTGGAGTTGTGCCGATCCTCGTCGAGCTCGACGGAGACGTCAACGGACACAAGTTCTCCGTCCGTGGAGAGGGAGAGGGAGACGCCACCATCGGAAAGCTCACCCTCAAGTTCATCTGCACCACCGGAAAGCTCCCAGTCCCATGGCCAACCCTCGTCACCACCCTCACCTACGGAGTCCAATGCTTCTCCCGTTACCCAGACCACATGAAGCGTCACGACTTCTTCAAGTCCGCCATGCCAGAGGGATACGTCCAAGAGCGTACCATCTCCTTCAAGGACGACGGAAAGTACAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagACCCGTGCCGTCGTCAAGTTCGAGGGAGACACCCTCGTCAACCGTATCGAGCTCAAGGGAACCGACTTCAAGGAGGACGGAAACATCCTCGGACACAAGCTCGAGTACAACTTCAACTCCCACAACGTCTACATCACCGCCGACAAGCAAAAGAACGGAATCAAGGCCAACTTCACCGTCCGTCACAACGTCGAGGACGGATCCGTCCAACTCGCCGACCACTACCAACAAAACACCCCAATCGGAGACGGACCAGTCCTCCTCCCAGACAACCACTACCTCTCCACCCAAACCGTCCTCTCCAAGGACCCAAACGAGAAGTAA atatccaccgtgctggcgggaggtcgc catctcgcgcccgtgcctctgacttctaagtccaattactcttcaacatccctacatgctctttctccctgtgctcccacccccctatttttgttattatcaaaaaacttctcttaatttctttgttttttagcttcttttaagtcacctctaacaatgaaattgtgtagattcaaaaatagaattaattcgtaataaaaagtcgaaaaaaattgtgctccctccccccattaataataattctatcccaaaatctacacaatgttctgtgtacacttcttatgtttttacttctgataaattttttttgaaacatcatagaaaaaaccgcacacaaaataccttatcatatgttacgtttcagtttatgaccgcaatttttatttcttcgcacgtctgggcctctcatgacgtcaaatcatgctcatcgtgaaaaagttttggagtatttttggaatttttcaatcaagtgaaagtttatgaaattaattttcctgcttttgctttttggggtttcccctattgtttgtcaagatttcgaggacggcgtttttcttgctaaaatcacaagtattgatgagcacgatgcaagaaagatcggaagaaggtttgggtttgaggctcagtggaaggtgagtagaagttgataatttgaaagtggagtagtgtctatggggtttttgccttaaatgacagaatacattcccaatataccaaacataactgttt
CF4588	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)], muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)]	Somatic sfGFP$_{1-10}$ and somatic split-wrmScarlet$_{1-10}$ (eft-3 promoter)	II: 8.42 MB, 9.83 MB	II:0.77, II:1.73	Sequences from CF4582 and CF4587

	II; unc-119(ed3) III				
CF4610	muIs257[Pmyo-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR] I	Muscle split-wrmScarlet$_{1-10}$ (myo-3 promoter)	I: 2.85 MB	I:-5.32	agtgattatagtctctgttttcgttaattttgaattttgcttgataaggctgcaacaaagatcaggttgacatatattttcagtaatttattttaacctgtactctatcactgccggctataataagttcttgaataaaataattttcccgacaaaacatgagtatttctttcgaaaataaaagtgcaggctaattagagattattctgtaattaactgcataatttgtcacgtgccatagttttacattccactacgtcatagttcttaaaatactaatctcctgaaaatagaagtaggtgaagaaagtttaattatcagttctaaaatgacaattgatctttggaatatgttctgaaactaccgatcattgaacagatgctatttgaatgatatagaattgtatatttgcaatttctgaaacgcgttcttaaaggcacacagattaattcaaaagtaagcttctcacaccttttctctcgttatggtggccgattttgagttttgtgtgtgattgctttttcacaatcagtgttttcaggattatgtgatgaactagatcttcaagtttcgttacatttcatatgttttcggaactcacgaagtacatattgggtattgtgctcaaaaaattcagcaatcagcttcgctccgctgactttagaacccaaaaaaatagtatggccaaactgactgtgttacgatcatttcaatttttcaatacatatttaagatttctaagagtaagaaggtcaaaaactgttctggaatacatatatatttttcaggttacaattagtcaaaaagtgcactgaaatatacgttttaatttcacgaataacccaattagttcaatgtatttttggtcaaccaacgttaaagtttggcttccaaccaattatcatttctgatcaaccacaatgtttttctttatctgcaagttaatttttatttttatccagatgtttggcatatttttcaattcttcactagcgcccacttcttgcacttccggcgccctgaatctaatgcatctgttgcaagaattgaaagaccaatcaacacattgttttcttcacgagatactgaagaaaatgaataaaaacagagaaaaagagccatgtgattagtgacaactgttgctaacagataccatagcttggacttggtacgtgatggcaacgtatgggtcaacaaaaatgattgcagagggggtgcaaaacagtcaagtcgagaaaatatgaaaaacagaaaacaaagaacagaaaaatgggtttgagagtcagtataatttataaaagaaaaattgtacatagaaattaaccatttttgtagaagaagttatttttcaagcatcgttaaaaattattcaaagcaccttatttcatatttaattttaaacatggttaaatgaacaacacggtgcgcaatcaggaaaacttgaaatctgaaactgttgttgtgatcttcttcgcaactgttcagatagcactagtgtaatgttaagagtgcgcgaatataatggaatataatggatcacacctcctgccatcaggtaaacgtctctgttatcacatatttccaactattaaatttttaccttttacagttttacattttttgaaaaaagtaactttttgtcttcaaaatccctgacgaaaatatcaaatattttaatcgagactgcagaggaaccgattgatgatttggaaaatccagctttacctgtgtaagaactgaaaagtttcataaccctagggtattcccagttacattccccactggctaacaatagcacccagtttttcatcaccttttcttcaaatttctcggcgatttgttaaaaacaaaatttgtgtcccttctctgatatctctatgtctctaaacacaagttcatcggaaaacgaaggagggtaggtgttggttgggctcccgaagtgaaaatagaagagcaagaatagaatattagagagagagtgcagagagggcgggatagctcccgggattccgttttcttcttctttatcttcaacgatgatgtgtgtgcgtgttgtatagattctgttgctcccccacaactcgctccgaaggctcaatacaattcaattgatattggaggagagcctaccggagtgggaggataagaagaaacataagaagaagaagaagaagaagcatgcttctggtttttgatgctatgaaaacggcacaaaaagatgattgaggtcccttttcaataccttctctcatctttcaaatcccattgaaacctaaaacttctcaccacgctttaccattgttctccaaaaacttatagcaatgtctataactttttatctctgaaaagcagtgttccatttttctttttcctattttatttcaattgtttctcacatttcgtttggattctttgcttgtcaaccagcttcttcttccacttttaccgtctaattttcagggcagggagccatcaaacccacgaccactagatccatATGGTATCGAAGGGAGAAGCAGTAATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTCATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCA

					AGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTACTAAcatctcgcgcccgtgcctctgacttctaagtccaattactcttcaacatccctacatgctctttctccctgtgctcccaccccctatttttgttattatcaaaaaacttctcttaatttctttgttttttagcttcttttaagtcacctctaacaatgaaattgtgtagattcaaaaatagaattaattcgtaataaaaagtcgaaaaaaaattgtgctccctccccccattaataataattctatcccaaaatctacacaatgttctgtgtacacttcttatgtttttacttctgataaattttttgaaacatcatagaaaaaaccgcacacaaaataccttatcatatgttacgtttcagtttatgaccgcaatttttatttcttcgcacgtctgggcctctcatgacgtcaaatcatgctcatcgtgaaaaagttttggagtatttttggaatttttcaatcaagtgaaagtttatgaaattaattttcctgcttttgctttttggggtttcccctattgtttgtcaagatttcgaggacggcgtttttcttgctaaaatcacaagtattgatgagcacgatgcaagaaagatcggaagaaggtttgggtttgaggctcagtggaag
DUP223	glh-1(sam129[glh-1::T2A::sGFP2$_{1-10}$]) I	Germline sGFP2$_{1-10}$	I: 6.85 MB	I: 1.41	gtttcgccacgcgccccaactacagtaacctcgacacactcatctactaaattttgggacagttcctaattctttttgctgttttcaactcaattttctggaaaaatcttaattttctgcgaaaATGTCTGATGGTTGGAGTGATAGCGAAAGTGCTGCTAAGGgtgagttttattttgaactttccaccggttttatttgattaaaaactttatttcagCCAAAACTGGATTCGGTAGTGGAGGCGGTTTCGGTGGTGGTAACAATGGAGGATCTGGGTTTGGTGGTGGTAAAAATGGAGGTACTGGATTCGGTGGAGGAAACACTGGCGGATCTGGATTCGGTGGAGGAACACTGGCGGATCTGGATTCGGTGGAGGAAAGACTGGCGGTTCTGGATTTGGAGGTGGAAATACTTGTGGATCCGGCTTCGGTGGAGGCAGTACAGGAGGATCGCCGTATGGAGGAGCCAGTTCTGGATTCGGTGGTAGTACTGCCACATCTGGATTTGGAAGCGGTGAAAAATCAAGTGCATTTGGAGGATCAGGTGGCTTTGGAGGTAGTGCAACTGGATTCGGAAGTGGAGGAGGATCCTTTGGAGGTGGCAACTCTGGTTTTGGGGAAGGAGGACATGGCGGCGGAGAGAGAAACAATAgttcgtttttttaaattgactttatataattacgtttgtttcagATTGTTTCAATTGCCAACAGCCAGGACATCGATCGAGTGACTGTCCAGAGCCGAGAAAGGAAAGAGAGCCGAGAGgttttattttgatataactttattggcagtaatttgttttattttcagTGTGCTACAATTGCCAGCAACCCCGGGCACACCTCTCGTGAATGTACAGAAGAACGCAAGCCGCGTGAGGGTCGCACTGGTGGATTCGGGGGCGGAGCTGGATTTGGAAACAATGGAGGAAATGACGGTTTCGGTGGGGACGGTGGTTTTGGTGGAGGCGAAGAACGTGGTCCAATGAAATGTTTCAACTGTAAAGGCGAGGGACATCGCTCTGCTGAATGTCCGGAGCCACCCCGTGGATGTTTCAATTGTGGCGAGCAAGGTCATCGCTCGAATGAGTGCCCCAATCCAGCCAAGCCAAGGGAAGGTGTTGAAGGAGAAGGACCTAAGGCGACATACGTGCCAGTCGAAGACAACATGGAGGACGTTTTCAACATGCAGAAAATTTCGGAAGGCCTTATGTTCAACAAGTTTTTCGATGCCGAAGTTAAACTGACTTCATCCGAGAAGACTGTCGGTATCAAACCTTGCAAGACATTCGCGGAAGCTAATCTCACGGAGACCATGCAGAAAAAACGTTGCTCATGCTGGATACTCCAAGACCACTCCAATTCAGCAATATGCTCTTCCACTTGTTCATCAGGGATATGATATCATGGCTTGTGCTCAAACTGGATCAGGAAAAACCGCTGCATTCCTTCTGCCTATCATGACTCGTCTCATTGACGATAATAATCTGAACACTGCCGGAGAAGGCGGTTGCTATCCCCGTTGCATCATCTTGACTCCAACTCGCGAACTCGCTGATCAAATTTACAACGAGGGAAGAAAGTTTGCTTATCAAACAATGATGGAGATCAAACCAGTTTACGGAGGATTGGCTGTCGGTTATAATAAGGGTCAGATCGAAAAGGGAGCCACGATCATTGTCGGAACTGTCGGAAGAATCAAGCACTTCTGTGAAGAGGGTACCATCAAGCTTGACAAATGCCGCTTCTTTGTTCTTGACGAGGCTGATCGTATGATCGATGCTATGGGATTCGGAACTGACATCGAAACTATTGTCAATTATGACAGTATGCCGAGGAAAGAAAATCGCCAGACACTCATGTTCAGTGCCACTTTCCCCGATTCTGTACAGGAAGCAGCTCGCGCTTTTCTCAGAGAAAACTACGTGATGATTGCAA

					TCGACAAGATTGGAGCTGCAAACAAGTGCGTCCTACAGGAATTCGAGAGATGCGAAAGAAGCGAGAAGAAGGACAAACTTCTAGAGCTTCTGGGAATCGATATCGACAGTTACACGACCGAGAAAAgtgagtttttcgttttcttatttgatgaaataaatttcaatatttcagGTGCCGAAGTTTACACAAAGAAAACCATGGTCTTCGTTTCTCAAAGAGCAATGGCTGATACACTGGCTTCAATTTTGTCATCGGCTCAAGTTCCAGCTATCACGgttggtatatttcatttttgaccgctttttaattcaaaatgtacagATCCATGGTGCCCGTGAGCAGAGAGAGCGTTCAGAAGCTTTGAGACAATTCCGAAATGGATCGAAACCTGTTCTTATTGCTACTGCGGTCGCTGAACGTGGACTTGATATCAAAGGAGTGGATCATGTCATCAACTATGACATGCCAGACAACATTGATGACTATATCCATCGTATCGGAAGgtcagttatattttattaatgtttcaataatgcaagcattgttttcagAACTGGAAGAGTTGGAAACTCTGGAAGAGCTACAAGCTTCATCTCGGAGGATTGCAGTCTTCTGTCCGAACTTGTTGGTGTTCTCGCCGACGCACAACAGATTGTTCCAGACTGGATGCAAGGTGCTGCTGGAGGCAATTACGGAGCTAGTGGATTTGGGTCCAGTGTACCAACTCAAGTCCCGCAGGACGAGGAGGGGTGG GGATCGGGA GAGGGACGTGGATCCCTTCTTACCTGCGGAGACGTCGAGGAGAACCCAGGACCA GGAGCATCGGGAGCCTCAGGAGCATCG ATGAGTAAAGGAGAAGAATTGTTCACTGGAGTTGTCCCAATCCTCGTCGAGCTCGACGGAGACGTCAACGGACACAAGTTCTCCGTCCGTGGAGAGGGAGAGGGAGACGCCACCATCGGAAAGCTCACCCTCAAGTTCATCTGCACCACCGGAAAGCTCCCAGTCCCATGGCCAACCCTCGTCACCACCCTCACCTACGGAGTCCAATGCTTCGCCCGTTACCCAGACCACATGAAGCGTCACGACTTCTTCAAGTCCGCCATGCCAGAGGGATACGTCCAAGAGCGTACCATCTCCTTCAAGgtaagtttaaacatatatatactaactactgattatttaaattttcagGACGACGGAAAGTACAAGACCCGTGCCGTCGTCAAGTTCGAGGGAGACACCCTCGTCAACCGTATCGAGCTCAAGGGAACCGACTTCAAGGAGGACGGAAACATCCTCGGACACAAGCTCGAGTACAACTTCAACTCCCACAACGTCTACATCACCGCCGACAAGCAAAAGAACGGAATCAAGGCCAACTTCACCgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagACCCGTCACAACGTCGAGGACGGATCCGTCCAACTCGCCGACCACTACCAACAAAACACCCCAATCGGAGACGGACCAGTCCTCCTCCCAGACAACCACTACCTCTCCACCCAAACCGTCCTCTCCAAGGACCCAAACGAGAAGTAG aaaaccgaccaattgatagtgtttcgcatttattaatgctgtcagttcccccatattttatcctgcccttgttgatttttaattgtatttgttggtgttggttgtcgttatagtcctcgccgcataaactctgttc
DUP237	glh-1(sam140[glh-1::T2A::split-wrmScarlet$_{1-10}$]) I	Germline split-wrmScarlet$_{1-10}$	I: 6.85 MB	I: 1.41	gtttcgccacgcgccccaactacagtaacctcgacacactcatctactaaattttgggacagttcctaattctttttgctgttttcaactcaattttctggaaaaatcttaattttctgcgaaaATGTCTGATGGTTGGAGTGATAGCGAAAGTGCTGCTAAGGgtgagttttattttgaactttccaccggttttattttgattaaaaactttatttcagCCAAAACTGGATTCGGTAGTGGAGGCGGTTTCGGTGGTGGTAACAATGGAGGATCTGGGTTTGGTGGTGGTAAAAATGGAGGTACTGGATTCGGTGGAGGAAACACTGGCGGATCTGGATTCGGTGGAGGAAACACTGGCGGATCTGGATTCGGTGGAGGAAAGACTGGCGGTTCTGGATTTGGAGGTGGAAATACTTGTGGATCCGGCTTCGGTGGAGGCAGTACAGGAGGATCGCCGTATGGAGGAGCCAGTTCTGGATTCGGTGGTAGTACTGCCACATCTGGATTTGGAAGCGGTGAAAAATCAAGTGCATTTGGAGGATCAGGTGGCTTTGGAGGTAGTGCAACTGGATTCGGAAGTGGAGGAGGATCCTTTGGAGGTGGCAACTCTGGTTTTGGGGAAGGAGGACATGGCGGCGGAGAGAGAAACAATAgttcgtttttaaattgactttatataattacgtttgtttcagATTGTTTCAATTGCCAACAGCCAGGACATCGATCGAGTGACTGTCCAGAGCCGAGAAAGGAAAGAGAGCCGAGAGgttttattttgatataactttattggcagtaatttgttttattttcagTGTGCTACAATTGCCAGCAACCCGGGCACAC

					CTCTCGTGAATGTACAGAAGAACGCAAGCCGCGTGAGGGTCGCACTGGTGGATTCGGGGGCGGAGCTGGATTTGGAAACAATGGAGGAAATGACGGTTTCGGTGGGGACGGTGGTTTTGGTGGAGGCGAAGAACGTGGTCCAATGAAATGTTTCAACTGTAAAGGCGAGGGACATCGCTCTGCTGAATGTCCGGAGCCACCCCGTGGATGTTTCAATTGTGGCGAGCAAGGTCATCGCTCGAATGAGTGCCCCAATCCAGCCAAGCCAAGGGAAGGTGTTGAAGGAGAAGGACCTAAGGCGACATACGTGCCAGTCGAAGACAACATGGAGGACGTTTTCAACATGCAGAAAATTTCGGAAGGCCTTATGTTCAACAAGTTTTTCGATGCCGAAGTTAAACTGACTTCATCCGAGAAGACTGTCGGTATCAAACCTTGCAAGACATTCGCGGAAGCTAATCTCACGGAGACCATGCAGAAAAACGTTGCTCATGCTGGATACTCCAAGACCACTCCAATTCAGCAATATGCTCTTCCACTTGTTCATCAGGGATATGATATCATGGCTTGTGCTCAAACTGGATCAGGAAAAACCGCTGCATTCCTTCTGCCTATCATGACTCGTCTCATTGACGATAATAATCTGAACACTGCCGGAGAAGGCGGTTGCTATCCCCGTTGCATCATCTTGACTCCAACTCGCGAACTCGCTGATCAAATTTACAACGAGGGAAGAAAGTTTGCTTATCAAACAATGATGGAGATCAAACCAGTTTACGGAGGATTGGCTGTCGGTTATAATAAGGGTCAGATCGAAAAGGGAGCCACGATCATTGTCGGAACTGTCGGAAGAATCAAGCACTTCTGTGAAGAGGGTACCATCAAGCTTGACAAATGCCGCTTCTTTGTTCTTGACGAGGCTGATCGTATGATCGATGCTATGGGATTCGGAACTGACATCGAAACTATTGTCAATTATGACAGTATGCCGAGGAAAGAAAATCGCCAGACACTCATGTTCAGTGCCACTTTCCCCGATTCTGTACAGGAAGCAGCTCGCGCTTTTCTCAGAGAAAACTACGTGATGATTGCAATCGACAAGATTGGAGCTGCAAACAAGTGCGTCCTACAGGAATTCGAGAGATGCGAAAGAAGCGAGAAGAAGGACAAACTTCTAGAGCTTCTGGGAATCGATATCGACAGTTACACGACCGAGAAAAgtgagtttttcgttttcttatttgatgaaataaatttcaatatttcagGTGCCGAAGTTTACACAAAGAAAACCATGGTCTTCGTTTCTCAAAGAGCAATGGCTGATACACTGGCTTCAATTTTGTCATCGGCTCAAGTTCCAGCTATCACGgttggtatatttcatttttgaccgctttttaattcaaaatgtacagATCCATGGTGCCCCGTGAGCAGAGAGAGCGTTCAGAAGCTTTGAGACAATTCCGAAATGGATCGAAACCTGTTCTTATTGCTACTGCGGTCGCTGAACGTGGACTTGATATCAAAGGAGTGGATCATGTCATCAACTATGACATGCCAGACAACATTGATGACTATATCCATCGTATCGGAAGgtcagttatattttattaatgtttcaataatgcaagcattgttttcagAACTGGAAGAGTTGGAAACTCTGGAAGAGCTACAAGCTTCATCTCGGAGGATTGCAGTCTTCTGTCCGAACTTGTTGGTGTTCTCGCCGACGCACAACAGATTGTTCCAGACTGGATGCAAGGTGCTGCTGGAGGCAATTACGGAGCTAGTGGATTTGGGTCCAGTGTACCAACTCAAGTCCCGCAGGACGAGGAGGGGTGG GGATCGGGA GAGGGACGTGGATCCCTTCTTACCTGCGGAGACGTCGAGGAGAACCCAGGACCA GGAGCATCGGGAGCCTCAGGAGCATCG ATGGTTTCCAAGGGAGAGGCTGTTATCAAGGAATTCATGCGCTTCAAGGTTCACATGGAAGGATCTATGAACGGACACGAATTCGAAATCGAAGGAGAAGGAGAAGGACGCCCATACGAGGGAACTCAAACTGCTAAGCTTAAGGTTACTAAAGGAGGACCACTTCCATTCTCTTGGGATATCCTTTCTCCACAGTTCATGTACGGATCTCGCGCTTTCATCAAGCACCCAGCTGATATCCCAGATTACTACAAGCAGTCTTTCCCAGAAGGATTCAAATGGGAGCGCGTTATGAACTTCGAAGATGGAGGAGCTGTTACCGTTACCCAAGATACCTCCCTTGAGGATGGAACCCTTATCTACAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGTTAAGCTTCGCGGAACTAATTTCCCACCAGATGGACCAGTTATGCAGAAGAAGACTATGGGATGGGAAGCTTCTACCGAGCGCCTTTACCCAGAGGATGGAGTCCTTAAGGGAGATATCACCATGGCTCTTCGTC

					TTAAGGATGGAGGACGTTACCTTGCTGATACCTCTACTACTTACAAGGCTAAGAAGCCAGTTCAGATGCCAGGAGCTTACCTTGTCGATCGTAAGCTTGATATCACTTCTCATAACGAATACTAG aaaaccgaccaattgatagtgtttcgcatttattaatgctgtcagttcccccatattttatcctgcccttgttgatttttaattgtatttgttggtgttggttgtcgttatagtcctcgccgcataaactctgttc

Table S3. *C. elegans* strains, genotypes and sources

Strain	Genotype	Source
N2E	wild type	Kenyon Lab
CF4582	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Kenyon Lab
CF4586	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; vha-13(muIs262[split-wrmScarlet$_{11}$::vha-13]) V	Kenyon Lab
CF4587	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Kenyon Lab
CF4588	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)], muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Kenyon Lab
CF4589	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; vha-13(muIs268[sfGFP$_{11}$::vha-13]) V	Kenyon Lab
CF4592	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; his-3(muIs255[his-3::sfGFP$_{11}$]) V	Kenyon Lab
CF4594	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; his-3(muIs258[his-3::split-wrmScarlet$_{11}$]) V	Kenyon Lab
CF4601	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; fib-1(muIs254[split-wrmScarlet$_{11}$::fib-1]) V	Kenyon Lab
CF4602	muIs253[Peft-3::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)], muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; fib-1(muIs254[split-wrmScarlet$_{11}$::fib-1]), his-3(muIs255[his-3::sfGFP$_{11}$]) V	Kenyon Lab
CF4603	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; eat-6(muIs269[eat-6::split-wrmScarlet$_{11}$]/+) V	Kenyon Lab
CF4608	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; his-3(muIs267[his-3::split-wrmScarlet$_{11}$(x3)]) V	Kenyon Lab
CF4610	muIs257[Pmyo-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR] I	Kenyon Lab
CF4611	muIs257[myo-3p::split-wrmScarlet$_{1-10}$::unc-54 3'UTR] I; fib-1(muIs254[split-wrmScarlet$_{11}$::fib-1]) V	Kenyon Lab
CF4612	muEx690[Pmyo-3::mTagBFP2::sfCherry3$_{11}$::T2A::mNeonGreen::sfCherry3_1-10::fib-1 3'UTR]	Kenyon Lab
CF4613	muEx691[Pmyo-3::mTagBFP2::split-wrmScarlet$_{11}$::T2A::mNeonGreen::split-wrmScarlet$_{1-10}$::fib-1 3'UTR]	Kenyon Lab
CF4614	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; tbb-2(muIs260[split-wrmScarlet$_{11}$::tbb-2]), unc-119(ed3) III	Kenyon Lab
CF4615*	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; tomm-20(muIs261[tomm-20::split-wrmScarlet$_{11}$]) V	Kenyon Lab
CF4616	muIs252[Peft-3::split-wrmScarlet$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III; vha-13(muIs264[split-wrmScarlet$_{11}$(x2)::vha-13]) V	Kenyon Lab
COP1795	knuSi785 [pNU1687(Plet-858::sfGFP$_{1-10}$::unc-54 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	Nemametrix
DUP218	glh-1(sam124[glh-1::T2A::sGFP2$_{1-11}$]) I	Updike Lab
DUP223	glh-1(sam129[glh-1::T2A::sGFP2$_{1-10}$]) I	Updike Lab
DUP225	glh-1(sam129[glh-1::T2A::sGFP2$_{1-10}$]) I; pgl-1(sam126[pgl-1::GFP$_{11}$]) IV	Updike Lab
DUP236	glh-1(sam139[glh-1::T2A::split-wrmScarlet$_{1-11}$]) I	Updike Lab
DUP237	glh-1(sam140[glh-1::T2A::split-wrmScarlet$_{1-10}$]) I	Updike Lab
PHX731	vha-13(syb731[wrmScarlet::vha-13]) V	SunyBiotech
PHX1049	vha-13(syb1049[gfp::vha-13]) V	SunyBiotech
PHX1797	sybSi66[Psun-1::split-wrmScarlet$_{1-10}$::sun-1 3'UTR, Cbr-unc-119(+)] II; unc-119(ed3) III	SunyBiotech

CA1200	ieSi57[eft-3p::TIR1::mRuby::unc-54 3'UTR + Cbr-unc-119(+)] II; unc-119(ed3) III	CGC
WBM1126	wbmIs61[myo-3p::3XFLAG::dpy-10 crRNA::unc-54 3'UTR] I	CGC

* Mutation present - see table S4 for the corresponding sequence

Table S4. crRNAs, HDR templates and oligonucleotide sequences

S4A. Sequences of crRNA and HDR template used for split-wrmScarlet$_{11}$ and sfGFP$_{11}$ knock-in experiments

Gene name	Gene ID	Tagged term	gene-specific crRNA sequence	1x split-wrmScarlet$_{11}$ HDR donor sequence - Ultramer ssDNA (lower case: homology arms; red: split-wrmScarlet$_{11}$; blue: linker)	Sequencing Primer (Forward)	Sequencing Primer (Reverse)
eat-6	B0365.3	C	ACAAGCUGUUCUUUAGUAGU	cgacgagatccgtcgtttcttgattcgcagatatccaggaggatgggtcgagcgtgagacctactac GGAGGAGGATCC TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA taaagaacagcttgtgaatctttgtagaattttctatttttttatcttagttttttattgtttcccat	CCTGGTTCATGTGCTATTGCC	CGACGACAGAAAGTAGCATCAC
fib-1	T01C3.7	N	AUAAUCGAUUUUUGUAGUAU	aatacgaaaaaatcctgaaattcagtttacctccgccgccgccgccacgattgaactctggacgtcc GGATCCTCCTCC TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA catactacaaaaatcgattatttaacaaaaacgaaaagcgaaattacgaaaaatacatacctcagcc	TTCTAGTCGATTCAGATCGACTGG	CGAAACTGCCACGATCACC
his-3	T10C6.12	C	GAAGAAAACCGGAGGAGACA	gattttaaatatttgtggccctaaagagggccgttgggttcggtaaaatgttttaagaaggcatcta TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ttcTttgtctcctccggtCttcttTggcaaaagaacagcttggatatttggaagaactcctccttgg	CCAAGGAGGAGTTCTTCCAAATATC	GATTTTAAATATTTGTGGCCCTAAAG
tbb-2	C36E8.5	N	CGCAUUGUCCGGCUUGCACG	tcttctctatctaaatatagtttttcaattcattacgaccttttcagcaaaaatg TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA GGAGGAGGATCCGGAGGAGGATCCGGAGGAGGATCC agagagatcgtTcacgtgcaagccggacaatgcggaaaccaaatcggatccaaat	CAATATCGACCATGACGTGTTCTC	CTTGAAGGTTCCGTCTGGC
tomm-20	F23H12.2	C	ACACCGACGACUUGGAGUAA	gttggtgaacgaaaaatacgaagaattaaattgaaagttaataaaacttttaaatcattatccatta TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ctccaagtcgtcggtgtcatcgataagctcttggatttgtgctggtggaggtccgtctccgaggtat	GAGCGAAAGCAGATGAGGC	TCCGTGAGGAGGAAAACACC
actual tomm-20 mutation recovered	F23H12.2	C	ACACCGACGACUUGGAGUAA	gttggtgaacgaaaaatacgaagaattaaattgaaagttaataaaacttttaaatcattatccatta T**TA**TCC**AT**TGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ctccaagtcgtcggtgtcatcgataagctcttggatttgtgctggtggaggtccgtctccgaggtat	GAGCGAAAGCAGATGAGGC	TCCGTGAGGAGGAAAACACC
vha-13	Y49A3A.2	N	AUUCUGCGGCCAUCUUUUCC	ggtttattttgattttcttttcgatttccatatagctttctaaattcattcattccaggaaaagatg TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA GGAGGAGGATCC gccgcagaatcttcgtacggattcgtttacggagtgtccggacctgtcgtcacagccgagaagatgg	GGTTTATTTTGATTTTCTTTTCGATTTCC	CCATCTTCTCGGCTGTGAC

Gene name	Gene ID	Tagged term	gene-specific crRNA sequence	1x sfGFP$_{11}$ HDR donor sequence - Ultramer ssDNA (lower case: homology arms; green: sfGFP$_{11}$; blue: linker)	Sequencing Primer (Forward)	Sequencing Primer (Reverse)
his-3	T10C6.12	C	GAAGAAAACCGGAGGAGACA	atagaggattttaaatatttgtggccctaaagagggccgttgggttcggtaaaatgttttaagaaggcatcta GGTGATTCCGGCGGCGTTGACGTACTCGTGGAGGACCATGTGGTCACG TCCTCCTCC ttcTttgtctcctccggtCttcttTggcaaaagaacagcttggatatttggaagaactcctccttgggcg	CCAAGGAGGAGTTCTTCCAAATATC	GATTTTAAATATTTGTGGCCCTAAAG
vha-13	Y49A3A.2	N	AUUCUGCGGCCAUCUUUUCC	ggtttattttgattttcttttcgatttccatatagctttctaaattcattcattccaggaaaagatg CGTGACCACATGGTCCTCCACGAGTACGTCAACGCCGCCGGAATCACC GGAGGAGGATCC gccgcagaatcttcgtacggattcgtttacggagtgtccggacctgtcgtcacagccgagaagatgg	GGTTTATTTTGATTTTCTTTTCGATTTCC	CCATCTTCTCGGCTGTGAC
pgl-1	ZK381.4	C	GGTGGTTACGGGGGTCGTGG	tacggcggagatcgtggacgtggtggttacgggggaagaggaggtagaggtggattt GGAGCATCGGGAGCCTCAGGAGCATCG CGTGACCACATGGTCCTCCACGAGTACGTCAACGCCGCCGGAATCACC taaactccaactattgaatgtttaatttgtttttta	CCAAAGTTGCAAAAGGATTCGGTCAATTTG	CATTTACCGGGAACAAGGAAAAACAGGTTG

Gene name	Gene ID	Tagged term	gene-specific crRNA sequence	1x split-wrmScarlet$_{11(MDELYK)}$ HDR donor sequence - Ultramer ssDNA (lower case: homology arms; red: split-wrmScarlet$_{11(MDELYK)}$; blue: linker)	Sequencing Primer (Forward)	Sequencing Primer (Reverse)
eat-6	B0365.3	C	ACAAGCUGUUCUUUAGUAGU	cgacgagatccgtcgtttcttgattcgcagatatccaggaggatgggtcgagcgtgagacctactac GGAGGAGGATCC TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA**ATGGATGAGTTATACAAG** taaagaacagcttgtgaatctttgtagaattttctattttttatcttagtttttttattgtttcccat	CCTGGTTCATGTGCTATTGCC	CGACGACAGAAAGTAGCATCAC
his-3	T10C6.12	C	GAAGAAAACCGGAGGAGACA	gattttaaatatttgtggccctaaagagggccgttgggttcggtaaaatgttttaagaaggcatcta **CTTGTATAACTCATCCAT**TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ttcTttgtctcctccggtCttcttTggcaaaagaacagcttggatatttggaagaactcctccttgg	CCAAGGAGGAGTTCTTCCAAATATC	GATTTTAAATATTTGTGGCCCTAAAG
tomm-20	F23H12.2	C	ACACCGACGACUUGGAGUAA	gttggtgaacgaaaaatacgaagaattaaattgaaagttaataaaacttttaaatcattatccatta **CTTGTATAACTCATCCAT**TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ctccaagtcgtcggtgtcatcgataagctcttggatttgtgctggtggaggtccgtctccgaggtat	GAGCGAAAGCAGATGAGGC	TCCGTGAGGAGGAAAACACC
actual tomm-20 mutation recovered	F23H12.2	C	ACACCGACGACUUGGAGUAA	gttggtgaacgaaaaatacgaagaattaaattgaaagttaataaaacttttaaatcattatccatta **CTTGTATAACTCATCCAT**TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ctccaagtcgtcggtgtcatcgataagctcttggatttgtgctggtggaggtccgtctccgaggtat	GAGCGAAAGCAGATGAGGC	TCCGTGAGGAGGAAAACACC

S4B DNA template for split-wrmScarlet tandems HDR donor sequence - plasmids

Template name	Tagged term	DNA template for split-wrmScarlet tandems - dsDNA (lower case: homology arms; red: split-wrmScarlet$_{11}$; blue: linkers)
wrmScarlet$_{11}$(x2)::vha-13	N	ggtttattttgattttcttttcgatttccatatagctttctaaattcattcattccaggaaaagatg TACACCGTCGTCGAGCAATACGAGAAGTCCGTCGCCCGTCACTGCACCGGAGGA

		GGTGGCTCTGGAGGT TACACCGTTGTTGAGCAATACGAGAAGTCTGTTGCTCGTCACTGCACCGGAGGC GGAGGAGGATCC gccgcagaatcttcgtacggattcgtttacggagtgtccggacctgtcgtcacagccgagaagatgg
his-3::split-wrmScarlet$_{11}$(x3)	C	gattttaaatatttgtggccctaaagagggccgttgggttcggtaaaatgttttaagaaggcatcta TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA TCCTCCACTACCGCC TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA ACCTCCAGAGCCACC TCCTCCGGTGCAGTGACGGGCGACGGACTTCTCGTATTGCTCGACGACGGTGTA GGATCCTCCTCC ttcTttgtctcctccggtCttcttTggcaaaagaacagcttggatatttggaagaactcctccttgg

S4C. Primers used to PCR split-wrmScarlet tandems HDR donor sequence from plasmid

Primer Name	Sequence of DNA oligo
his-3_F	CCAAGGAGGAGTTCTTCCAAATATC
his-3_R	GATTTTAAATATTTGTGGCCCTAAAG
vha-13_F	GGTTTATTTTGATTTTCTTTTCGATTTCC
vvha-13_R	CCATCTTCTCGGCTGTGAC

S4D. Sequences of crRNA and HDR template used to generate split-wrmScarlet$_{1-10}$ and sfGFP$_{1-10}$ strains

Strain edited -> Final strain	crRNA#1 sequence	crRNA#2 sequence (if applicable)	DNA template - Hybrid PCR amplicon (lower case: homology arms, upper case: insert)
CA1200 -> CF4582	UACUUCUUCUGGAAACGACA	AAGUUCGCUGGACUUGGAGG	tagaagtttctaggataattttttcgacttttattctctctaccgtccgcactcttcttacttttaaattaaattgtttttttttcagttgggaaacactttgctcactccgtagcagccATGGTATCGAAGGGAGAAGCAGTAATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTCATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCAAGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTACTA

			Ataagtccaattactcttcaacatccctacatgctctttctccctgtgctcccaccccctatttttgttattatcaaaaaacttctcttaatttctttgtttttagcttcttttaagtca
COP1795 -> CF4587	GACCAGCUGGGCGCAUAGGG	GCCGCCCCACGAGGGCCAGG	aactcattttcaatttcaactgaaagatttttcattagagaatgtctagaactaggcccgggctacgtaatacgactcacttaaggcctaatttgggtctggctgcatgccaggaggtaGCACCTTTGGTCTTTTATTGTCAACTTCCATTGGTTCTTCCATTGTTTCTGTTAAATTAATGAATTTTTCATAAAATAAAGACATTATACAATATAAAAATGAAGAATTTATTGAAAATAAACTGCCAGAGAGAAAAAGTATGCAACACTCCCGCCGAGAGTGTTTGAAATGGTGTACGGTACATTTTCGTGCTAGGAGTTAGATGTGCAGGCAGCAACGAGAGGGGGAGAGATTTTTTTGGGCCTTGTGAAATTAACGTGAGTTTTCTGGTCATCTGACTAATCATGTTGGTTTTTTGTTGGTTTATTTTGTTTTTATCTTTGTTTTTATCCAGATTAGGAAATTTAAATTTTATGAATTTATAATGAGGTCAAACATTCAGTCCCAGCGTTTTTCCTGTTCTCACTGTTTAGTCGAATTTTTATTTTAGGCTTTCAACAAATGTTCTAACTGTCTTATTTGTGACCTCACTTTTTATATTTTTTTAATTTTTAAAAATATTAGAAGTTTCTAGGATAATTTTTTCGACTTTTATTCTCTCTACCGTCCGCACTCTTCTTACTTTTAAATTAAATTGTTTTTTTTTCAGTTGGGAAACACTTTGCTCaaaaatgtctaagggagaagagttatttactggagttgtgccgatcctcgtcgagctcgacggagacgtcaacggacacaagttctccgtccgtggagagggagagggagacgccaccatcg
WBM1126 -> CF4610	GCUACCAUAGGCACCACGAG		cacttttaccgtctaattttcagggcagggagccatcaaacccacgaccactagatccatATGGTATCGAAGGGAGAAGCAGTAATCAAGGAGTTCATGCGTTTCAAGGTCCACATGGAGGGATCCATGAACGGACACGAGTTCGAGATCGAGGGAGAGGGAGAGGGACGTCCATACGAGGGAACCCAAACCGCCAAGCTCAAGGTCACCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagGGAGGACCACTCCCATTCTCCTGGGACATCCTCTCCCCACAATTCATGTACGGATCCCGTGCCTTCATCAAGCACCCAGCCGACATCCCAGACTACTACAAGCAATCCTTCCCAGAGGGATTCAAGTGGGAGCGTGTCATGAACTTCGAGGACGGAGGAGCCGTCACCGTCACCCAAGACACCTCCCTCGAGGACGGAACCCTCATCTACAAGgtaagtttaaacagttcggtactaactaaccatacatatttaaattttcagGTCAAGCTCCGTGGAACCAACTTCCCACCAGACGGACCAGTCATGCAAAAGAAGACCATGGGATGGGAGGCCTCCACCGAGCGTCTCTACCCAGAGGACGGAGTCCTCAAGgtaagtttaaacatgattttactaactaactaatctgatttaaattttcagGGAGACATCACCATGGCCCTCCGTCTCAAGGACGGAGGACGTTACCTCGCCGACACCTCCACCACCTACAAGGCCAAGAAGCCAGTCCAAATGCCAGGAGCCTACCTCGTCGACCGTAAGCTCGACATCACCTCCCACAACGAGTACTAAcatctcgcgcccgtgcctctgacttctaagtccaattactcttcaacatccctacatgct

S4E. Primers long and short

Primers to mplify split-wrmScarlet for CF4582	Sequence
eft3p_S110(A19)_F	tagaagtttctaggataattttttcgacttttattctctctaccgtccgcactcttcttacttttaaattaaattgtttttttttcagttgggaaacactttgctcactccgtagcagccATGGTATCGAAGGGAGAAGC
unc54_S110(A19)_R	tgacttaaaagaagctaaaaaacaaagaaattaagagaagtttttgataataacaaaaataggggggtgggagcacagggagaaagagcatgtagggatgttgaagagtaattggacTTATTAGTACTCGTTGTGGGAGG

S1-10_A19_F	ATGGTATCGAAGGGAGAAGC
S1-10_A19_R	TTAGTACTCGTTGTGGGAGGTG

Primers to amplify Peft-3 for CF4587	Sequence
E7_eft-3p_F-Long	aactcattttcaatttcaactgaaagattttttcattagagaatgtctagaactaggcccgggctacgtaatacgactcacttaaggcctaatttgggtctggctgcatgccaggaggtaGCACCTTTGGTCTTTTATTGTCAAC
E8_eft-3p_R-Long	cgatggtggcgtctccctctccctctccacggacggagaacttgtgtccgttgacgtctccgtcgagctcgacgaggatcggcacaactccagtaaataactcttctcccttagacattttGAGCAAAGTGTTTCCCAACTG
E5_eft-3p_F	GCACCTTTGGTCTTTTATTGTCAAC
E6_eft-3p_R	GAGCAAAGTGTTTCCCAACTG

Primers to amplify split-wrmScarlet for CF4610	Sequence
PrimerS1-10_myo3F	cacttttaccgtctaattttcagggcagggagccatcaaacccacgaccactagatccatATGGTATCGAAGGGAGAAGC
PrimerS1-10_myo3R	agcatgtagggatgttgaagagtaattggacttagaagtcagaggcacgggcgcgagatgTTAGTACTCGTTGTGGGAGGTG

Table S5. Plasmid sequences

Name	Sequence
Peft-3::3NLS::mTagBFP2::split-wrmScarlet$_{11}$::T2A::mNeonGreen::split-wrmScarlet$_{1-10}$::fib-1 UTR (C. elegans)	gcacctttggtcttttattgtcaacttccattggttcttccattgtttctgttaaattaatgaatttttcataaaataaagacattatacaatataaaaatgaagaatttattgaaaataaactgccagagagaaaaagtatgcaacactcccgccgagagtgtttgaaatggtgtacggtacattttcgtgctaggagttagatgtgcaggcagcaacgagagggggagagatttttttgggccttgtgaaattaacgtgagttttctggtcatctgactaatcatgttggttttttgttggtttattttgtttttatctttgttttatccagattaggaaatttaaattttatgaatttataatgaggtcaaacattcagtcccagcgtttttcctgttctcactgtttagtcgaatttttattttaggctttcaacaaatgttctaactgtcttatttgtgacctcactttttatatttttttaattttaaaaatattagaagtttctaggataattttttcgacttttattctctctaccgtccgcactcttcttacttttaaattaaattgtttttttttcagttgggaaacactttgctcATGCCAAAAAAGAAACGTAAGGTTGATCCGAAGAAAAAGCGAAAAGTTGATCCTAAAAAAAAGCGTAAAGTCGTCTCCAAGGGAGAGGAGCTCATCAAGGAGAACATGCACATGAAGCTCTACATGGAGGGAACCGTCGACAACCACCACTTCAAGTGCACCTCCGAGGGAGAGGGAAAGCCATACGAGGGAACCCAAACCATGCGTATCAAGGTCGTCGAGGGAGGACCACTCCCATTCGCCTTCGACATCCTCGCCACCTCCTTCCTCTACGGCTCCAAGACCTTCATCAACCACACCCAAGGAATCCCAGACTTCTTCAAGCAATCCTTCCCAGAGGGATTCACCTGGGAGCGTGTCACCACCTACGAGGACGGAGGAGTCCTCACCGCCACCCAAGACACCTCCCTCCAAGACGGATGCCTCATCTACAACGTCAAGgtaagtttaaacatatatatactaactaaccctgattatttaaattttcagATCCGTGGAGTCAACTTCACCTCCAACGGACCAGTCATGCAAAAGAAGACCCTCGGATGGGAGGCCTTCACCGAGACCCTCTACCCAGCCGACGGAGGACTGGAGGGACGTAACGACATGGCC

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Peft-3::3NLS::mTagBFP2::sfCherry3$_{11}$::T2A::mNeonGreen::sfCherry31-10::fib-1 UTR (C. elegans)	gcacctttggtcttttattgtcaacttccattggttcttccattgtttctgttaaatt aatgaatttttcataaaataaagacattatacaatataaaaatgaagaatttatt gaaaataaactgccagagagaaaaagtatgcaacactcccgccgagagt gtttgaaatggtgtacggtacattttcgtgctaggagttagatgtgcaggcag caacgagagggggagagatttttttgggccttgtgaaattaacgtgagttttc tggtcatctgactaatcatgttggtttttgttggtttattttgtttttatctttgtttta tccagattaggaaatttaaattttatgaatttataatgaggtcaaacattcagtc ccagcgtttttcctgttctcactgtttagtcgaatttttattttaggctttcaacaa atgttctaactgtcttatttgtgacctcactttttatattttttaatttttaaaaatatt agaagtttctaggataattttttcgacttttattctctctaccgtccgcactcttct tacttttaaattaaattgttttttttcagttgggaaacactttgctcATGCCAA AAAAGAAACGTAAGGTTGATCCGAAGAAAAAGCGAAAA GTTGATCCTAAAAAAAAGCGTAAAGTCGTCTCCAAGGG AGAGGAGCTCATCAAGGAGAACATGCACATGAAGCTC TACATGGAGGGAACCGTCGACAACCACCACTTCAAGT GCACCTCCGAGGGAGAGGGAAAGCCATACGAGGGAA CCCAAACCATGCGTATCAAGGTCGTCGAGGGAGGACC ACTCCCATTCGCCTTCGACATCCTCGCCACCTCCTTC CTCTACGGCTCCAAGACCTTCATCAACCACACCCAAG GAATCCCAGACTTCTTCAAGCAATCCTTCCCAGAGGGA TTCACCTGGGAGCGTGTCACCACCTACGAGGACGGA GGAGTCCTCACCGCCACCCAAGACACCTCCCTCCAA GACGGATGCCTCATCTACAACGTCAAGgtaagtttaaacatat atatactaactaaccctgattatttaaattttcagATCCGTGGAGTCAA CTTCACCTCCAACGGACCAGTCATGCAAAAGAAGACC CTCGGATGGGAGGCCTTCACCGAGACCCTCTACCCA GCCGACGGAGGACTGGAGGGACGTAACGACATGGCC CTCAAGCTCGTCGGAGGTTCCCACCTCATCGCCAACG CCAAGACCACCTACCGTTCCAAGAAGCCAGCCAAGAA CCTCAAGATGCCAGGAGTCTACTACGTCGACTACCGT CTGGAGCGTATCAAGGAGGCCAACAACGAGACCTACG

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Pmyo-3::mTagBFP2::split-wrmScarlet$_{11}$::T2A::mNeonGreen::split-wrmScarlet$_{1-10}$::fib-1 UTR (C. elegans)	taataagttcttgaataaaataattttcccgacaaaacatgagtatttctttcgaaaataaaagtgcaggctaattagagattattctgtaattaactgcataatttgtcacgtgccatagttttacattccactacgtcatagttcttaaaatactaatctcctgaaaatagaagtaggtgaagaaagtttaattatcagttctaaaatgacaattgatctttggaatatgttctgaaactaccgatcattgaacagatgctatttgaatgatatagaattgtatatttgcaatttctgaaacgcgttcttaaaggcacacagattaattcaaaagtaagcttctcacaccttttctctcgttatggtggccgattttgagttttgtgtgtgattgctttttcacaatcagtgttttcaggattatgtgatgaactagatcttcaagtttcgttacatttcatatgttttcggaactcacgaagtacatattgggtattgtgctcaaaaaaattcagcaatcagcttcgctccgctgactttagaacccaaaaaaatagtatggccaaactgactgtgttacgatcatttcaattttcaatacatatttaagatttctaagagtaagaaggtcaaaaactgttctggaatacatatatatttttcaggttacaattagtcaaaaagtgcactgaaatatacgttttaatttcacgaataacccaattagttcaatgtatttttggtcaaccaacgttaaagtttggcttccaaccaattatcatttctgatcaaccacaatgtttttctttatctgcaagttaatttttttatttttatccagatgtttggcatatttttcaattcttcactagcgcccacttcttgcacttccggcgccctgaatctaatgcatctgttgcaagaattgaaagaccaatcaacacattgttttcttcacgagatactgaagaaaatgaataaaaacagagaaaaagagccatgtgattagtgacaactgttgctaacagataccatagcttggacttggtacgtgatggcaacgtatgggtcaacaaaaatgattgcagagggggtgcaaaacagtcaagtcgagaaaatatgaaaaacagaaaacaaagaacagaaaaatgggtttgagagtcagtataatttataaaagaaaaattgtacatagaaattaaccatttttgtagaagaagttatttttcaagcatcgttaaaaattattcaaagcaccttatttcatatttaattttaaacatggttaaatgaacaacacggtgcgcaatcaggaaaacttgaaatctgaaactgttgttgtgatcttcttcgcaactgttcagatagcactagtgtaatgttaagagtgcgcgaatataatggaatataatggatcacacctcctgccatcaggtaaacgtctctgttatcacatatttccaactattaaatttttaccttttacagttttacatttttttgaaaaaaagtaactttttgtcttcaaaatccctgacgaaaatatcaaatatttttaatcgagactgcagaggaaccgattgatgatttggaaaatccagctttacctgtgtaagaactgaaaagtttcataaccctagggtattcccagttacattccccactggctaacaatagcacccagtttttcatcacctttcttcaaatttctcggcgatttgttaaaaacaaaatttgtgtcccttctctgatatctctatgtctctaaacacaagttcatcggaaaacgaaggagggtaggtgttggttgggctcccgaagtgaaaatagaagagcaagaatagaatattagagagagagtgcagagagg

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Pmyo-3::mTagBFP2::sfCherry3$_{11}$::T2A::mNeonGreen::sfCherry31-10::fib-1 UTR (C. elegans)	taataagttcttgaataaaataattttcccgacaaaacatgagtatttctttcgaaaataaaagtgcaggctaattagagattattctgtaattaactgcataatttgtcacgtgccatagttttacattccactacgtcatagttcttaaaatactaatctcctgaaaatagaagtaggtgaagaaagtttaattatcagttctaaaatgacaattgatctttggaatatgttctgaaactaccgatcattgaacagatgctatttgaatgatatagaattgtatatttgcaatttctgaaacgcgttcttaaaggcacacagattaattcaaaagtaagcttctcacaccttttctctcgttatggtggccgatttt

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pD881MR-mtagBFP-split-wrmScarlet$_{11}$	CACCACAATTCAGCAAATTGTGAACATCATCACGTTCATCTTTCCCTGGTTGCCAATGGCCCATTTTCCTGTCAGTAACGAGAAGGTCGCGAATTCAGGCGCTTTTTAGACTGGTCGTAGAGACCATGAAATTCTTTTTAATTAGGTAAAAAATAAAAAATGactagtATGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGGACAACCATCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACTAGCTTCCTCTACGGCAGCAAGACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCACATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTTCACCGAGACGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAACGACATGGCCCTGAAGCTCGTGGGCGGGAGCCATCTGATCGCAAACATCAAGACCACATATAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCTGGCGTCTACTATGTGGACTACAGACTGGAAAGAATCAAGGAGGCCAACAACGAGACCTACGTCGAGCAGCACGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAGCTTAATGGCGGGGGGTCTTATACCGTTGTCGAGCAATATGAAAAGTCAGTGGCGAGGCACTGTACAGGGGGATAAGACGAGCTATATAAGTAActcgagTAGGGTCTCGCGGCCGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCGGGTAACGAATTCAAGCTTGATATCATTCAGGACGAGCCTCAGACTCCAGCGTAACTGGACTGCAATCAACTCACTGGCTCACCTTCACGGGTGGGCCTTTCTTCGGTAGAAGTCTTCTTAATAAGATGATCTTCTTGAGATCGTTTTGGTCTGCGCGTAATCTCTTGCTCTGAAAACGAAAAAACCGCCTTGCAGGGCGGTTTTTCGAAGGTTCTCTGAGCTACCAACTCTTTGAACCGAGGTAACTGGCTTGGAGGAGCGCAGTCACCAAAACTTGTCCTTTCAGTTTAGCCTTAACCGGCGCATGACTTCAAGACTAACTCCTCTAAATCAATTACCAGTGGCTGCTGCCAGTGGTGCTTTTGCATGTCTTTCCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGACTGAACGGGGGGTTCGTGCATACAGTCCAGCTTGGAGCGAACTGCCTACCCGGAACTGAGTGTCAGGCGTGGAATGAGACAAACGCGGCCATAACAGCGGAATGACACCGGTAAACCGAAAGGCAGGAACAGGAGAGCGCACGAGGGAGCCGCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCACTGATTTGAGCGTCAGATTTCGTGATGCTTGTCAGGGGGGCGGAGCCTATGGAAAAACGGCTTTGCCGCGGCCCTCTCACTTCCCTGTTAAGTATCTTCCTGGCATCTTCCAGGAAATCTCCGCCCCGTTCGTAAGCCATTTCCGCTCGCCGCAGTCGAACGACCGAGCGTAGCGAGTCAGTGAGCGAGGAAGCGGAATATATCCTGTATCACATATTCTGCTGACGCACCGGTGCAGCCTTTTTTCTCCTGCCACATGAAGCACTTCACTGACACCCTCATCAGTGCCAACATAGTAAGCCAGTATACACTCCGCTAGCGCAGAAAGGCCCACCCGAAGGTGAGCCAGGTGATTACATTTGGGCCCTCATTAGAAAAACTCATCGAGCATCAAATGAAATTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTAT

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pRSET-split-wrmScarlet$_{1-10}$	GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGTCTCTAAGGGTGAAGCCGTAATTAAGGAGTTCATGAGATTCAAAGTCCACATGGAAGGTTCAATGAACGGACATGAGTTCGAGATAGAAGGAGAGGGGGAGGGGAGACCTTATGAGGGGACCCAGACGGCCAAGTTGAAAGTGACGAAGGGAGGTCCATTGCCCTTTTCCTGGGACATACTGAGTCCCCAATTCATGTATGGAAGCCGTGCGTTTATTAAGCACCCCGCTGATATCCCTGACTACTATAAACAATCTTTCCCGGAAGGCTTCAAGTGGGAAAGAGTGATGAATTTCGAGGACGGCGGGGCGGTTACGGTGACTCAGGACACTTCCCTTGAAGACGGGACCTTAATTTATAAAGTAAAATTGAGGGGGGACGAACTTTCCCCCCGACGGTCCAGTAATGCAAAAAAAAACAATGGGCTGGGAAGCCTCTACTGAAAGGTTGTATCCCGAAGACGGCGTGTTAAAGGGAGATATTACGATGGCTTTAAGGCTAAAGGACGGGGGGGAGGTATCTGGCGGATACGTCTACCACATACAAGGCCAAGAAACCGGTCCAAATGCCGGGCGCTTACCTGGTCGACAGGAAACTTGATATAACAAGTCATAATGAATATTAAGTTGGTGGTGGCGGATCAGAAGCTCGAGATCTGCAGCTGGTACCATGGAATTCGAAGCTTGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAA

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Table S6. Adult lifespans of strains in this study

Strain	Events / n initial	Mean lifespan +/- SEM (Days)	Median lifespan	% mean lifespan change vs. N2	P-value (log-rank) vs. N2
N2E	105 / 134	20.20 +/- 0.74	17		
CF4582	118 / 136	19.27 +/- 0.57	17	-4.60	0.19
CF4587	109 / 129	19.56 +/- 0.64	17	-3.17	0.29
WBM1126	112 / 127	19.31 +/- 0.61	17	-4.41	0.28
CF4610	108 / 128	20.18 +/- 0.69	17	-0.10	0.92

Strain	Events / n initial	Mean lifespan +/- SEM (Days)	Median lifespan	% mean lifespan change vs. WBM1126	P-value (log-rank) vs. N2
WBM1126	112 / 127	19.31 +/- 0.61	17		
CF4610	108 / 128	20.18 +/- 0.69	17	4.51	0.33

Table S7. Mammalian cell screen oligo pool sequences

Sequence
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