GeneWeld: Efficient Targeted Integration Directed by Short Homology in Zebrafish

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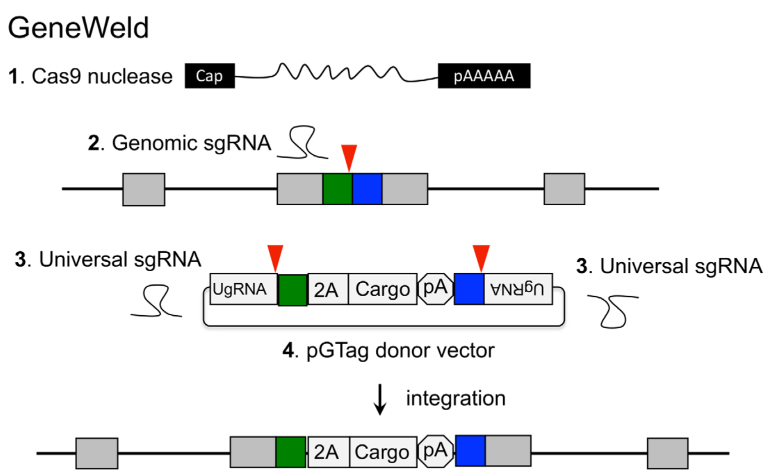
[Abstract] Efficient precision genome engineering requires high frequency and specificity of integration at the genomic target site. Multiple design strategies for zebrafish gene targeting have previously been reported with widely varying frequencies for germline recovery of integration alleles. The GeneWeld protocol and pGTag (plasmids for Gene Tagging) vector series provide a set of resources to streamline precision gene targeting in zebrafish. Our approach uses short homology of 24-48 bp to drive targeted integration of DNA reporter cassettes by homology-mediated end joining (HMEJ) at a CRISPR/Cas induced DNA double strand break. The pGTag vectors contain reporters flanked by a universal CRISPR sgRNA sequence to liberate the targeting cassette *in vivo* and expose homology arms for homology driven integration. Germline transmission rates for precision targeted integration alleles range from 22-100%. Our system provides a streamlined, straightforward and cost-effective approach for high efficiency gene targeting applications in zebrafish.

Keywords: CRISPR/Cas9, Knock-in, Homology mediated-end joining, Targeted integration, Zebrafish,

Graphic abstract:



[Background] Designer nucleases have rapidly expanded the way in which researchers can utilize endogenous DNA repair mechanisms for creating gene knock-outs, reporter gene knock-ins, gene deletions, single nucleotide polymorphisms, and epitope tagged alleles in diverse species ([1-5]. A single dsDNA break in the genome results in increased frequencies of recombination and promotes integration of homologous recombination (HR)-based vectors [6-11]. Additionally, *in vitro* or *in vivo* linearization of targeting vectors stimulates homology-directed repair (HDR) [6-11]. Utilizing HDR or HR at a targeted double-strand break (DSB) allows directional knock-in of exogenous DNA with base pair precision, however, reported frequencies vary widely, and engineering targeting vectors with long homology arms is not straightforward.

Previous work has shown *Xenopus* oocytes have the ability to join or recombine linear DNA molecules that contain short regions of homology at their ends, and this activity is likely mediated by exonuclease activity allowing base pairing of the resected homology [12]. More recently, it was shown in *Xenopus*, silkworm, zebrafish, and mouse cells that a plasmid donor containing short (≤40 bp) regions of homology to a genomic target site can promote precise integration at the genomic cut site when the donor plasmid is cut adjacent to the homology [13-15]. Gene targeting is likely mediated by the alternative-end joining/microhomology-mediated end joining (MMEJ) pathway or by a single strand annealing (SSA) mechanism [16], collectively referred to as a homology mediated end joining (HMEJ). In contrast, in human cell culture, linear donors using a similar strategy with homologous ends have been reported to show inefficient integration until homology domains reach ~600 bp [17], suggesting different repair pathways may predominate depending on cell type. In the initial reports using short regions of homology for *in vivo* gene targeting in zebrafish, the level of mosaicism in F0 injected animals was high, resulting in inefficient recovery of targeted alleles through the germline [13-15,18]. Most recently, studies in Drosophila show efficient integration of exogenous DNA in flies and S2 cells using 100 bp homology arms flanked by a CRISPR target site for *in vivo* homology liberation [19]. Together, these studies suggest a strategy that combines short homology flanked donors with *in vivo* homology arm liberation should lead to efficient precision targeting in zebrafish and mammalian cells.

Here, we present GeneWeld, a HMEJ strategy for targeted integration directed by short homology and demonstrate efficient germline transmission rates for recovery of targeted alleles in zebrafish. We provide a suite of donor vectors, called pGTag, that can be easily engineered with homologous sequences (homology arms) to a gene of interest and a web interface for designing homology arms (Mann et al., 2019; www.genesculpt.org/gtaghd/). 24 or 48 base pairs of homology directly flanking cargo DNA promotes efficient gene targeting in zebrafish with germline transmission rates averaging approximately 50%. The tools and methodology described here provide a tractable solution to creating precise targeted integrations and open the door for more advanced genome editing strategies using short homology.

Materials and Reagents

1. pGTag vectors are available through Addgene (https://www.addgene.org/kits/essner-geneweld/).
2. NEB Stable Competent E. coli, New England Biolabs, C3040I.

3. One Shot TOP10 Chemically Competent E. coli, Thermo Fisher/Invitrogen, C404010.
4. pT3TS-nCas9n expression vector, Addgene, plasmid # 46757.
5. PureYield Plasmid Miniprep System, Promega, A1223.
6. Ambion mMessage Machine T3 Transcription Kit, Thermo Fisher, AM1348.
7. miRNeasy Mini Kit, Qiagen, 217004.
8. NEBNext Ultra II DNA Library Prep Kit for Illumina, New England Biolabs, E7645L.
9. Zebrafish Tg(*miniTol2<14XUAS:mRFP, γcry:GFP>*)^{tl2} (Balcieune et al., 2013).
10. Zebrafish wildtype WIK strain, Zebrafish International Resource Center, ZL84, https://zebrafish.org/home/guide.php.
11. Polystyrene petri dishes, ThermoFisher, FB0875713.
12. Borosilicate Glass Capillaries, World Precision Instruments, 1B100-04.
13. Agarose, Thermo Fisher, BP160-500.
14. Ethidium Bromide, Fisher Scientific, BP1302-10.
15. Ethyl 3-aminobenzoate methanesulfonate (Tricaine, MS-222) $C_9H_{11}NO_2 \cdot CH_4SO_3$, Sigma-Aldrich, 886-86-2.
16. 1-phenyl-2-thiourea $C_7H_8N_2S$, ThermoFisher, AC207250050.
17. Microloader tips, Eppendorf, 920001007.
18. Microcap Microliter Pipets, Drummond Scientific, 1-000-0010.
19. Commercially available molds for injection plates available from https://www.agnthos.se/index.php?id_product=204&controller=product.
20. mMESSAGE mMACHINE T3 Transcription Kit, Invitrogen Life Technologies, AM1348.
21. Kwik-Fill borosilicate glass capillaries, World Precision Instruments, 1B100-4.
22. NorthernMax-Gly Sample Loading Dye, ThermoFisher, AM8551.
23. Decon ElIMINase, Fisher Scientific, 04-355-31.
24. Molecular Grade RNase/DNase-Free water, e.g. Invitrogen, 10977023.
25. ThermoFisher Scientific EasyStrip Plus Tube Strip with Attached Ultra Clear Caps, AB2005.
26. XbaI restriction endonuclease, New England Biolabs, R0145S.
27. BfuAI restriction endonuclease, New England Biolabs, R0701S.
28. BspQI restriction endonuclease, New England Biolabs, R0712S.
29. GoTag Green 2X MasterMix, Promega, M7123.
30. X-Gal solution, ready-to-use, 20mg/ml, ThermoFisher Scientific, R0941.
31. LB Broth, Fisher Scientific, BP9723-500.
32. LB Agar, Fisher Scientific, BP9724-2.
33. SOC Medium, ThermoFisher Scientific, 15544034.
34. Kanamycin, Fisher Scientific, BP9065.
35. T4 Quick Ligase, Rapid DNA Ligation Kit, ThermoFisher Scientific, K1422.
36. Sodium Hydroxide NaOH, Millipore/Sigma Aldrich, 30620.
37. Tris Base, Fisher Scientific, BP152-500.
38. UgRNA 5' GGGAGGCGUUCGGGCCACAG 3' and gene specific sgRNAs ordered from

Synthego.

39. Primers, can be ordered from IDT:

F3'-check	5'-GGCGTTGTCTAGCAAGGAAG -3'
R3' pgtag seq	5'-ATGGCTCATAACACCCCTTG-3'
R-Gal4-5'juncM	5'-GCCTTGATTCCACTTCTGTCA-3'
R-RFP-5'junc	5'-CCTTAATCAGTTCCTCGCCCTTAGA-3'
R-eGFP-5'-junc	5'-GCTGAACTTGTGGCCGTTT-3'
F-Gal4-3'juncM	5'-GCAAACGGCCTTAACTTTCC-3'
F-Gal4-3'junc	5'-CTACGGCGCTCTGGATATGT-3'
F-RFP-3'junc	5'-CGACCTCCCTAGCAAACTGGGG-3'
F-eGFP-3'junc	5'-ACATGGTCCTGCTGGAGTTC-3'

Equipment

1. Flaming/Brown Micropipette Puller, Sutter Instrument, P-97.
2. X-Cite 120W Metal Halide lamp, Excilitas Technologies, X-Cite 120Q.
3. Pico-Injector, Harvard Apparatus, PLI-100.
4. MM-3 Micromanipulator, Narishige, MM-3.
5. Nitrogen gas tank, or, JUN-AIR Oil-lubricated Piston Air Compressor, Cole-Parmer, 1152000.
6. Nanodrop, ThermoFisher Scientific, NanoDrop 2000.
7. iBright FL1500 Imaging System, ThermoFisher Scientific, A44241.
8. Thermo Scientific Shaking Incubator. MaxQ8000.
9. Thermo Scientific Isotemp Standard Laboratory Incubator, e.g. 51-028-065HPM.
10. Thermo Scientific Precision General Purpose Baths, e.g. TSGP02.
11. Eppendorf Thermal Cycler, 6335000020.
12. Zeiss SteREO Discovery.V8 Stereomicroscope or similar and epi-illumination X-Cite 120W metal halide light source with fiber optic cable (Excilitas Technologies).
13. Owl EasyCast B2 Mini Gel Electrophoresis Systems, ThermoFisher Scientific, B2-12.

Software

1. The Gene Sculpt Suite www.genesculpt.org/gtaghd/ (Mann et al., 2019).
2. CRISPRScan http://www.crisprscan.org/ [20].
3. Primer 3 http://biotools.umassmed.edu/bioapps/primer3_www.cgi.
4. Synthego ICE Analysis https://ice.synthego.com/#/.
5. Cas-Analyzer at CRISPR RGEN Tools http://www.rgenome.net/cas-analyzer/#!.
6. GraphPad Prism https://www.graphpad.com/scientific-software/prism/.

Procedure

The GeneWeld protocol is associated with the publication Wierson et al., 2020.

Table of Contents

A. Introduction

The GeneWeld strategy and pGTag vector series are designed for straightforward assembly of vectors containing short homology arms for efficient CRISPR/Cas9 directed recovery of germline precision targeted integration alleles.

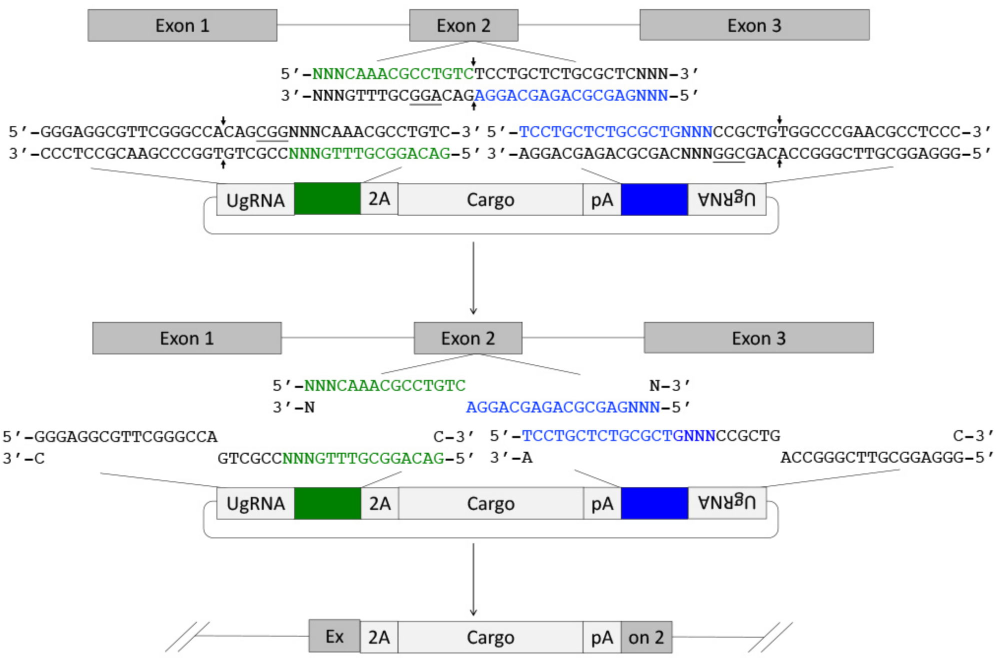


Figure 1. Targeted integration of pGTag vector cargo DNA into a 5' coding exon. Short homology arms complementary to the 5' (green) and 3' (blue) sequences of the genomic target site are cloned on the 5' and 3' sides of the vector cargo DNA. The short homology arm cargo cassette is flanked by two universal guide RNA UgRNA sites. CRISPR/Cas9 simultaneously targets double strand breaks at the sgRNA genomic target site and at the UgRNA sites flanking the cargo on the plasmid donor. Exonuclease end resection liberates single stranded DNA in the vector homology arms that is complementary to the resected strands on the 5' and 3' sides of the genomic double strand break. The complementary sequences direct homology mediated end joining integration of the cargo DNA at the exon target site. PAM sequences are underlined and small black arrows indicate Cas9 cut sites in the genome and vector.

B. Selection of a CRISPR/spCas9 target site in the gene of interest

1. Zebrafish wild type strains in common use are polymorphic. *It is highly recommended to first sequence the target exon in the genomic DNA from your fish strain and use this sequence to design sgRNAs in CRISPRScan.*
2. To identify an sgRNA site for targeting, first, view the gene model on a genome browser, and download the gene sequences.
   a. At <ensembl.org> Search for the gene name of interest for the species of interest and open the Transcript page (Figure 2).

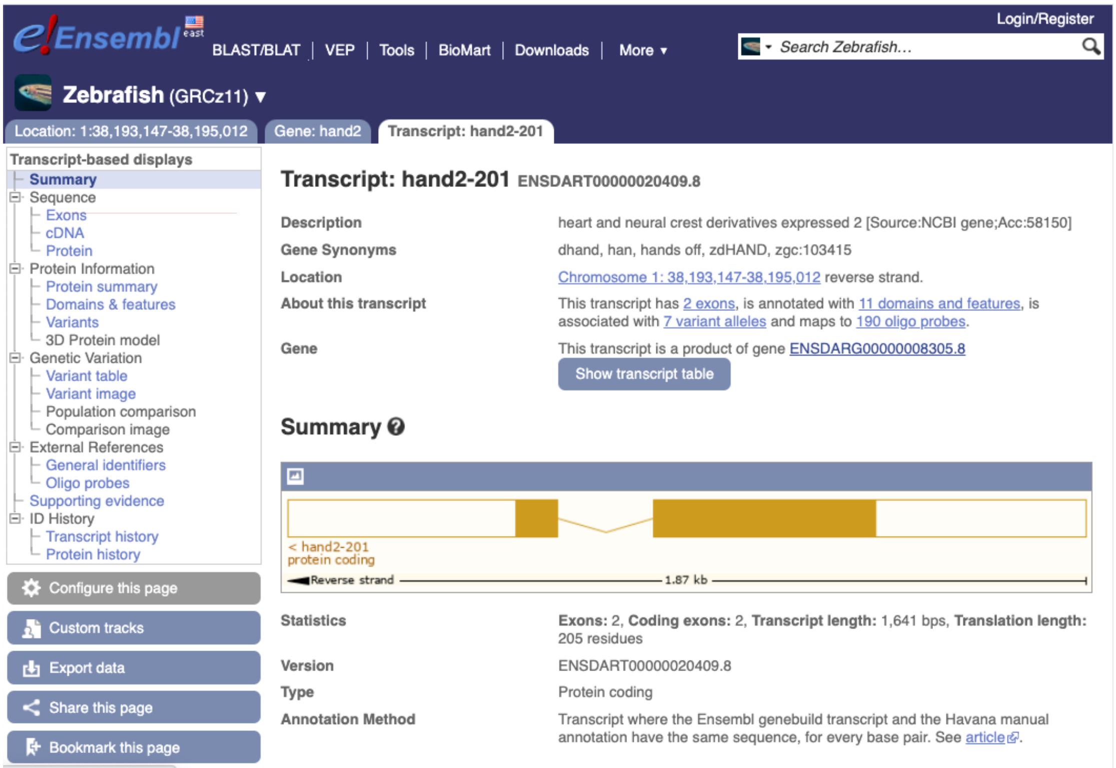


Figure 2. Screenshot of zebrafish *hand2* Transcript page on the ensembl.org genome browser (https://useast.ensembl.org/Danio_rerio/Transcript/Summary?db=core;g=ENSDARG00000008305;r=1:38193147-38195012;t=ENSDART00000020409)

b. In the left-hand side bar click on "Exons" to find the first coding exon and initiation ATG (Figure 3). If there are alternative transcripts for the gene, make sure there are not alternative initiation ATGs. If there are alternative start codons, target the first exon that is conserved in all transcripts to generate a strong loss of function allele.

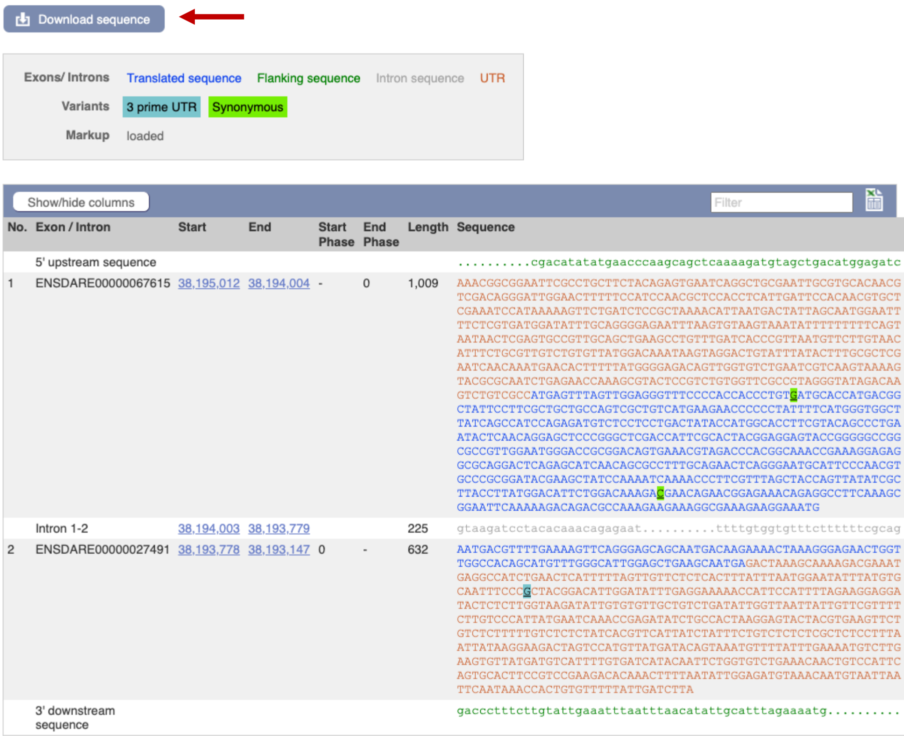


Figure 3. Exon sequences and Download page for zebrafish *hand2* gene on the ensembl.org genome browser.

c. Click on the Download sequence button (Figure 3, red arrow). A list of choices for genomic, coding, untranslated regions, etc sequences is shown. Select the cDNA and target exon and download as separate sequence files.

d. Using ApE <http://biologylabs.utah.edu/jorgensen/wayned/ape/> or SnapGene annotate the coding sequence with the exons.

e. Design primers to amplify the target exon from fin clip genomic DNA and sequence the amplicon. Use this sequence to identify sgRNA sites with CRISPRScan. Select a sgRNA that does not have an in frame ATG downstream of the sgRNA target site. Annotate the selected target sequence and NGG PAM in the cDNA sequence files.

3. sgRNAs can be ordered from Synthego or IDT.

4. Design ~20 bp DNA primers for a PCR amplicon of ~130 bp of DNA surrounding the sgRNA

target site. These primers will be used to amplify genomic DNA from embryos after injection of CRISPR reagents to test for mutagenesis at the target site. The presence of indels at the target site can be detected in the PCR products in multiple ways, including gel electrophoresis to visualize heteroduplex formation, resistance to restriction enzyme digestion at a site overlapping the sgRNA target, or direct sequencing followed by ICE Analysis.

a. User can design primers with Primer 3 http://biotools.umassmed.edu/bioapps/primer3_www.cgi
b. Paste DNA sequence surrounding the target site into the web interface. It is recommended to use 160 – 300 bp of exon sequence centered on the cut site for primer design. Intron sequence can be used, but this often contains polymorphisms that can lead to amplification failure.
c. Locate the target sequence, including the PAM sequence NGG (underlined, Bold in the example below), and predict the cut site (3 bp upstream of the PAM represented here by the 'x'). Mark the targeted exon sequence approximately 65-150 bp on both sides of the cut site by putting [square brackets, highlighted in yellow] around it. Primer3 will design primers outside this sequence. This design allows the primers to be used for both checking of mutagenesis and for junction fragment analysis when checking for integration.

Example:
CGGCCTCGGGATCCACCGGCC[AGAATCGATATACTACGATGAACAGAGCAAATTTGTGTG
TAATACGGTCGCCACCATGGCCTxCCT**CGG**TTTGCTACGATGCATTTGCACCACTCTCTCA
TGTCCGGTTCTGGG]AGGACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGGAGG
GCTCCGTGAAC

d. Set the "Primer Size" variables to Min = 130, Opt = 170, and Max = 300. Everything else can be left at the defaults.
e. Click on "Pick Primers"
f. Select primers from the output. Note the "product size" expected and the "tm" or melting temperature of each primer/pair. Smaller product sizes are easier to visualize mutagenesis.

5. Preparation of SpCas9 mRNA
   a. Digest ~5-10 µg pT3TS-nCas9n plasmid (plasmid Addgene #46757 [21]) with Xba1 to linearize the vector.
   b. Purify linearized DNA with Qiagen PCR cleanup kit or Promega PureYield Plasmid Miniprep System. Elute in RNase Free-water.
   c. Run 100-500 ng on 1.2% agarose gel in 1X TAE to confirm the plasmid is linearized.
   d. Use 100 ng to 1 µg DNA as template for in vitro transcription reaction with the mMESSAGE mMACHINE T3 kit Life Technologies (AM1348). Follow the manufacturer's instructions provided with the kit. Save a 1 ul aliquot of the *in vitro* synthesis reaction.

e. Use the miRNeasy Qiagen kit the purify the nCas9n mRNA according to the manufacturer's instructions.
f. Verify mRNA integrity by running a sample of the *in vitro* synthesized mRNA, before and after miRNeasy Qiagen kit cleanup, on a gel. Mix 1 ul of Cas9 mRNA, 4 ul of Molecular Grade RNase/DNase-Free water, 5 µl glyoxal dye (NorthernMax-Gly Sample Loading Dye, ThermoFisher, AM8551).
g. Heat mixture at 50°C for 30 min in a water bath or thermal cycler, then place on ice.
h. Clean the gel box, comb and tray with Decon ElIMINase, rinse with DI water.
i. Run all 10 µl of RNA mixture on 1.2% agarose gel in 1X TAE at 100 V for 1 h as above. Image gel on iBright FL1500 Imaging System or other gel-documentation imaging system. One band should be visible at ~ 4.5 kb.
j. Determine the concentration of the RNA sample using a Nanodrop. Concentrations between 0.45 and 1 µg/µl are expected.
k. Aliquot and store RNA at -80 °C.

C. Injection of sgRNA and spCas9 mRNA

Deliver 25 pg sgRNA and 300 pg Cas9 mRNA in a 2 nl volume to embryos at the one-cell stage. Below is a step-by-step protocol for zebrafish embryo injection.

A detailed video of zebrafish embryo injection can be found in Rosen et al., 2009[22] in the Journal of Visualized Experiments publication (doi: 10.3791/1115 https://www.jove.com/v/1115/microinjection-of-zebrafish-embryos-to-analyze-gene-function.

1. Cast zebrafish embryo injection trays with custom molds that create 45 degree troughs for lining up and holding embryos (Figure 4A). Molds are also available commercially (for example https://www.agnthos.se/index.php?id_product=204&controller=product).

   Melt 1.2% agarose in 1X E2 Medium (https://wahoo.cns.umass.edu/book/export/html/867) and pour into polystyrene petri dish (Fisher No. FB0875713). The mold is set on top (Figure 4B), and once the plates have set gently remove the mold (Figure 4C). Injection trays can be used multiple times and are stored inverted at 4°C for up to three weeks between use.

A B C

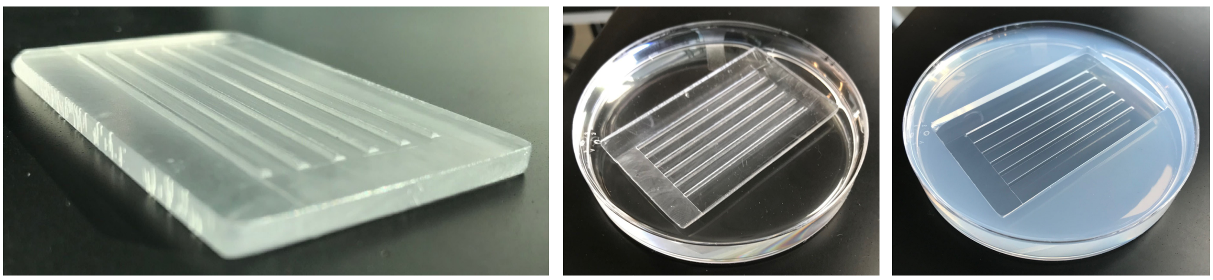


Figure 4. Injection tray mold (A) is set on top of melted 1.2% agarose (B). Solidified injection plate with troughs to hold embryos (C).

2. Before injection, pre-warm injection trays by placing them in a 28.5°C incubator for 20 min.
3. Pull microcapillary glass needles using Kwik-Fill borosilicate glass capillaries (No. 1B100-4) on a Sutter Instrument Flaming/Brown Micropipette Puller (Model P-97).
4. Prepare injection samples containing the following diluted in Molecular Grade RNase/DNase-Free water:
    a. 12.5 ng/µL of genomic sgRNA
    b. 150 ng/µL of mRNA for Cas9

    Keep injection solution on ice.
5. Backload needles with injection solution using microloader pipet tips (Eppendorf), and attach to a micro-manipulator (Narishige). Connect the needle holder tubing to a Harvard Apparatus PLI - 90 Pico-injector. Turn on nitrogen gas or the air compressor to pressurize the system, and set injection pressure to 40 PSI with an injection time of 100-200 msec.
6. Calibrate injection needle by first breaking the end of the tip off with sterile tweezers (Figure 5A, B). Use the pedal to expel 10 droplets and capture each droplet with a 30mm long capillary tube that represents a volume of 1 µl (Drummond No. 1-000-0010) (Figure 5C). Measure the distance from the end of the capillary to the meniscus of the liquid and convert to volume: 1 mm = 30 nl, therefore 2/3 of a mm = 20 nl. The volume of each droplet is adjusted by changing the injection time in order to achieve 2 nl/droplet. There is a linear relationship between volume and time at a set pressure. Avoid injection times less than 100 msec and over 400 msec.
7. Transfer one-cell embryos from collection petri dishes to the troughs on the pre-warmed agarose injection tray (Figure 5D). Each embryo is encased in a chorion. As the embryos near the first cell division at 45 minutes after fertilization, the single cell is clearly visible atop the yolk (Figure 5 D).
8. Use the micro-manipulator to pierce the needle through the chorion and into the embryo. Inject 2 nl of sample at the center of the interface/boundary between the single cell and the yolk (Figure 5E, white arrow points to interface where needle tip is placed). Inject embryos before the first cell division begins.

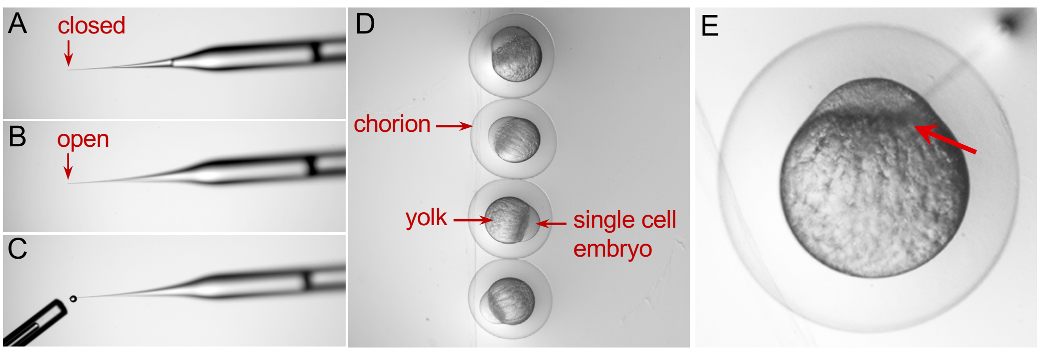


Figure 5. Microinjection needle calibration and zebrafish single cell embryo microinjection. (A) Image of backloaded injection needle with closed tip. (B) A small amount at the tip of the needle is removed using forceps to create an open end. (C) A single droplet of injection solution is expelled by pressing on the injection apparatus pedal. The tip of a 1ul Drummond capillary tube is shown that was used to capture 10 drops. (D) embryos lined up in an injection tray trough with labels indicating the chorion, yolk and single cell embryo. (E) Image of needle inserted through the chorion and into the embryo. The tip of the injection needle is positioned at the membrane interface (white arrow) between the single cell on top and the yolk below. Image in (E) was published in Almeida et al, 2021[23].

9. After embryos have been injected, wash the embryos from the injection tray into a clean petri dish with embryo media.
10. Keep 20-40 embryos separate to use as uninjected controls.
11. At 3-5 h post injection remove any unfertilized or dead embryos from the dishes.

D. Test for sgRNA mutagenesis efficiency and indel production
1. Biallelic inactivation can lead to loss of function phenotypes that may be lethal for essential genes. After injection count and remove dead embryos from the dish of injected embryos. If all of the embryos are defective and unlikely to survive, reduce the amount of guide sgRNA that is injected to 12.5pg. If embryos still fail to survive, reduce the amount of sgRNA further to 6.25pg. As we reported previously, for a ubiquitously expressed, essential gene such as the tumor suppressor *rb1*, the amount of injected sgRNA needs to be reduced to 6.25pg, in order to recover viable juvenile fish that survive to adulthood and transmit germline gene edited alleles [24].
2. Digestion of embryos for isolation of genomic DNA for mutagenesis analysis.
   Extract genomic DNA from zebrafish embryos aged between 1 and 5 dpf, either individual embryos or pools of 5 embryos from the same injection, using the following protocol previously published in [25].
   a. Dechorionate embryos, if they have not emerged from the chorion.
   b. Place embryo into a PCR tube and remove as much of the fish water as possible. Collect at least 3 injected embryos and 1 uninjected control embryo.
   c. Add 20 μl of 50 mM NaOH <u>per embryo</u>.
   d. Heat the embryos at 95°C in a thermocycler for 30 min.
   e. Vortex samples and spin the tubes down. The embryos should be completely dissolved.
   f. Neutralize the samples by adding 1 μl of 1 M Tris pH 8.0 per 10 μl NaOH. Mix by vortexing then spin down.
   g. Genomic DNA is stored at -20°C.
3. Analysis of CRISPR/Cas9 mutagenesis efficiency at targeted gene locus.

a. Remove genomic DNA samples from -20 °C and place on ice to thaw. Keep thawed genomic DNA on ice at all times.

b. Set up the following PCR reactions for each tube of embryo digested genomic DNA using the primers designed at the end of section A, page 10.

µl of 2x GoTaq Mastermix
1 µl of Forward Primer (10 µM)
1 µl of Reverse Primer (10 µM)
1 µl of gDNA template (digested embryos)
9.5 µl of nuclease-free water
25 µl total

c. Flick the tubes to mix and briefly spin down the PCR reactions.

d. Run the following PCR program to amplify the targeted locus.

95 °C 2 min
95 °C 30 s |
55 °C 30 s | x 35 cycles
72 °C 30 s |
72 °C 5 min
4 °C hold

e. Run up to 7 µl of PCR product on a 2.5 to 3% agarose gel, 1X TAE, for 1 h at 80-100V. Image gel on iBright FL1500 Imaging System or other gel-documentation imaging system. An example of sgRNA injection and validation targeted exon 1 of the *hand2* gene (Figure 6A) is shown below. The control uninjected embryo PCR amplicon runs as a single, tight band on the gel (Figure 6B, U). The amplicons from 8 injected embryos show multiple bands, or are diffuse in appearance, in comparison to the control (Figure 6B, 1-8). This indicates heteroduplex formation in the PCR product caused by the presence of indel mutations at the CRISPR target site in the gene of interest.

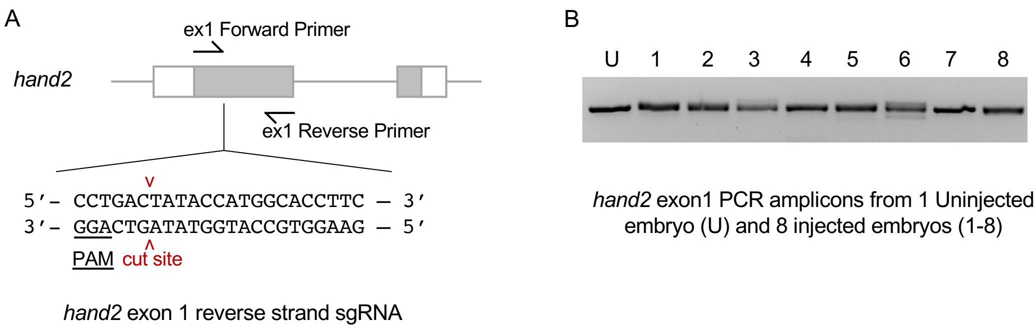


Figure 6. *hand2* exon 1 sgRNA validation. A sequence of hand2 reverse strand sgRNA site located in exon 1. B PCR amplicons with primers flanking the sgRNA target site. Diffuse bands in injected embryos represent heteroduplex DNA caused by indel mutations at the target site.

f. For quantitative analysis of mutagenesis efficiency, Sanger sequence PCR products to verify the presence of indels. % indel formation can be analyzed using Synthego's ICE Analysis https://ice.synthego.com/#/. Alternatively, Illumina MiSeq multiplex next generation sequencing can be used to test the efficiency of multiple gRNAs in parallel.

An example of ICE analysis of amplicons from the *hand2* exon 1 targeted embryos #3 and #6 from Figure 6 is shown below in Figure 7. Embryo #3 and #6 show 84% and 80% indel alleles after targeting, respectively, indicating high mutagenesis efficiency of the sgRNA.

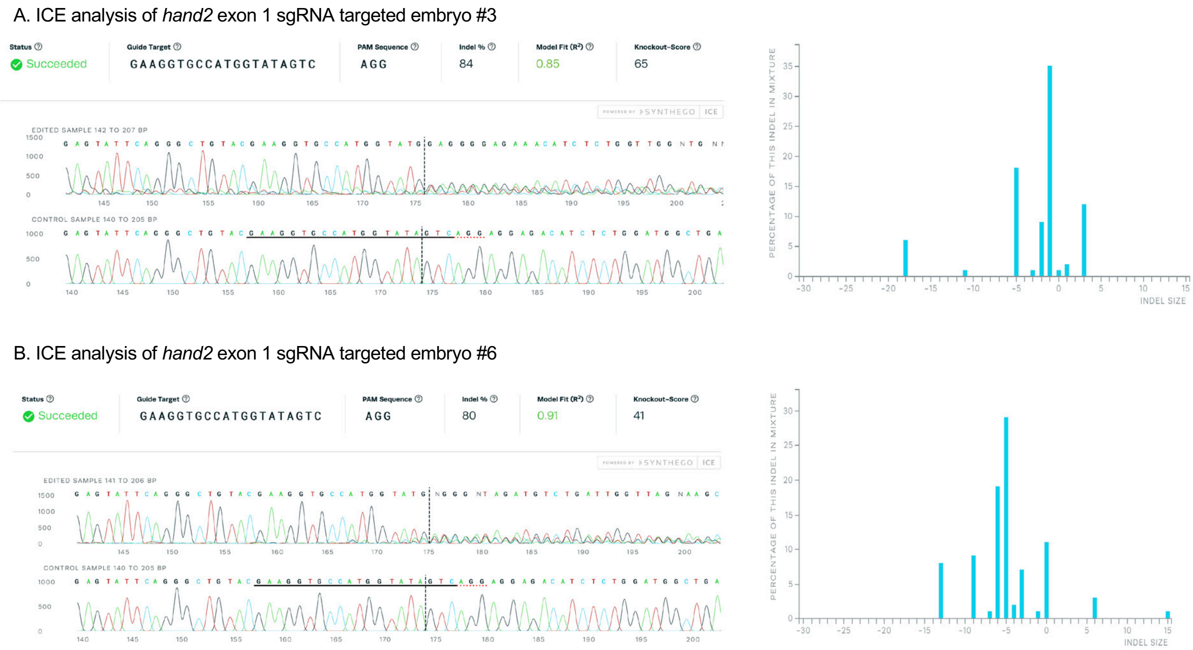


Figure 7. Validation of sgRNA mutagenesis efficiency by ICE analysis. PCR amplicons from *hand2* exon 1 targeted embryos #3 (A) and #6 (B) were Sanger sequenced and the results analyzed with Synthego ICE Analysis, revealing 84% and 80% of sequences contained indel mutations. Plots on the right show the range of indel mutations recovered.

E. Design short homology arms for pGTag targeting vector assembly

Homology directed gene targeting allows the seamless integration of exogenous DNA into the genome with precise repair events at the target site. However, designing and cloning individual targeting vectors and homology arms for each gene of interest can be time consuming. The pGTag vector series and web design tools provide versatility and ease to generate knockout alleles (Figure 7). The vectors contain BfuAI and BspQI type II restriction enzymes for cloning of short homology arms (24 or 48 bp) using Golden Gate cloning. The pGTag vectors require in-frame integration for proper reporter gene function. The reporter gene consists of several parts. A 2A peptide sequence causes translational skipping, allowing the following protein to dissociate from the locus peptide. The eGFP, TagRFP, or Gal4VP16 reporter coding sequences have a number of options for localization signals, including cytosolic (no signal), a nuclear localization signal (NLS), or a membrane localization CAAX sequence. Finally. translation is terminated by one of two different transcription termination polyadenylation (pA) sequences; the 3'UTR region of the zebrafish β-actin gene or the SV40 viral transcription termination sequence.

For many genes, the level of endogenous gene expression is not high enough to produce a detectable fluorescence signal from the integrated reporter gene. The Gal4VP16 pGTag vector in combination with the transgenic Tol2<14XUAS/RFP> reporter line[26] allows for amplification of the signal. The Tol2<14XUAS/RFP> reporter line[26] is available upon request from the lab of Dr. Darius Balciunas, Temple University.

Plasmid sequence maps can be downloaded at www.genesculpt.org/gtaghd/

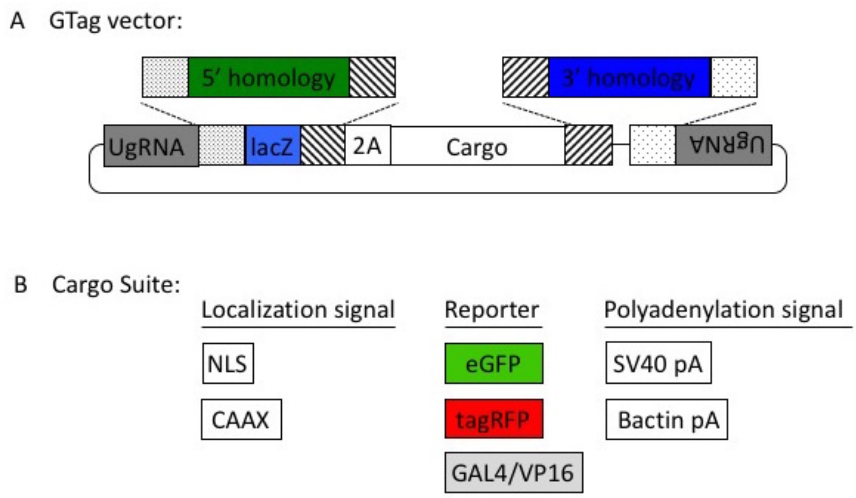


Figure 8. The pGTag vectors allow one step cloning of homology arms.

All vectors (Figure 8) can be obtained through Addgene (www.addgene.org). Because the pGTag plasmids contain repeated sequences, vector recombination can occur in bacteria. We recommend using NEB Stable Competent *E. coli* (New England Biolabs, C3040I). Bacteria should be grown at 30°C to reduce further the possibility of vector recombination.

Homology Arm Design at GTagHD www.genesculpt.org/gtaghd/

The web tool GTagHD www.genesculpt.org/gtaghd/ allows for quick design of oligos to generate short 24 or 48 bp homology arms complementary to the target site in a gene of interest.

Two complementary oligos with overhangs are annealed to generate the double stranded homology arm for cloning into the pGTag vector.

To use the tool, choose the "Submit Single Job" tab. Follow the instructions in the tab.

The sequences of two pairs of complementary oligos will be returned, one pair for the 5' homology arm, the other pair for the 3' homology arm. If there are problems with the sequences and values that were entered, the web page will display the errors and advice on how to fix them. Double check your output as below.

Manual Homology Arm Design

The following protocol describes how to design homology arm oligos manually:

Note：In the following section, orientation of target sites and homology is in the context of the reading frame of the genetic locus of interest. Example: A 5' template strand CRISPR means that the target site for the CRISPR is on the template strand at the locus and is toward the 5' end of the gene. Upstream homology domains are 5' of the CRISPR cut site and downstream homology domains are 3' of the cut site with respect to the gene being targeted.

Also note: Upper case and lower case bases are not specially modified; this is simply a visual marker of the different parts of the homology arms.

Upstream Homology Arm Design

1. Open the sequence file for the gene of interest and identify the CRISPR site. (In this example it is a Reverse CRISPR target in Yellow, the PAM is in Orange, coding sequence is in purple). Copy the 48 bp 5' of the CRISPR cut (the highlighted section below) into a new sequence file; this is the upstream homology.

Figure 9. Screenshot of a targeted gene displayed in ApE, highlighting the target sequence (yellow), PAM (orange), coding sequence (purple), and the gene sequence of the upstream homology arm (highlighted white).

2. Observe the next three bases immediately upstream of the 48 bp of homology, and pick a base not present to be the 3 bp spacer between the homology and the Universal PAM in the vector. (Here the three bases are "GGA" so "ccc" was chosen for the spacer). Add the spacer to the new file 5' (in front) of the homology, see below. The spacer acts as a non-homologous buffer between the homology and the eventual 6 bp flap from the universal guide sequence that will occur when the cassette is liberated and may improve intended integration rates over MMEJ events.

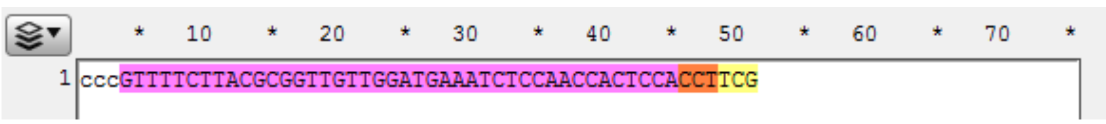


Figure 10. Screenshot of the gene sequence of the upstream homology arm (purple), the PAM (orange), and the remaining target sequence to the cut site (yellow). ccc was added as a spacer with non-homologous sequence.

3. Determine where the last codon is in the homology. Here the 3' G in the homology domain is the first base in the codon cut by this CRISPR target. Complete the codon by adding the remaining bases (called padding on GTagHD) for that codon from your sequence to ensure your integration event will be in frame.

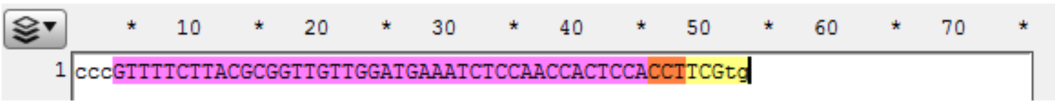


Figure 11. Screenshot of the gene sequence of the upstream homology arm (purple), the PAM (orange), and the remaining target sequence to the cut site with the padding nucleotides (tg) to keep the integration in frame (yellow).

4. Add the BfuAI enzyme overhang sequences for cloning, to the ends of the homology domain. 5'-GCGG and 3'-GGAT. (Here both overhangs are added to prevent errors in copying sequence for the oligos in the next two steps.)

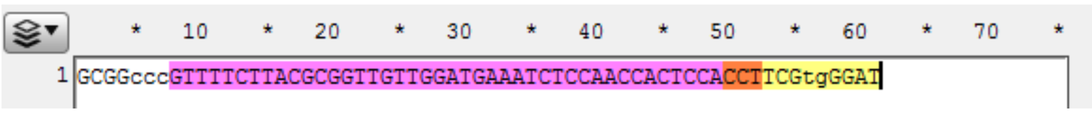


Figure 12. Screenshot of the gene sequence of the upstream homology arm (purple), the PAM (orange), the remaining target sequence to the cut site with the padding nucleotides (tg) to keep the integration in frame (yellow), and the BfuAI sites added to each end.

5. The Upstream Homology Oligo A will be this sequence from the beginning to the end of the last codon (see highlighted below). Copy and paste this sequence into a new file and save it. In this example this oligo sequence is 5'-GCGGcccGTTTTCTTACGCGGTTGTTGGATGAAATCTCCAACCACTCCACCTTCGtg-3'.

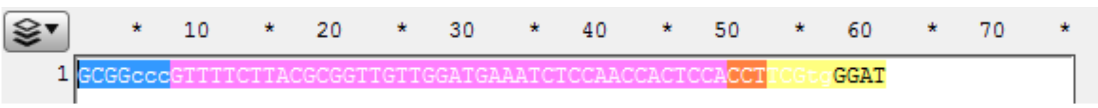


Figure 13. Screenshot of the gene sequence of the upstream homology arm (purple), the PAM (orange), the remaining target sequence to the cut site with the padding nucleotides (tg) to keep the integration in frame (yellow), and the BfuAI sites added to each end. The sequence of Oligo A is highlighted in white.

6. The Upstream Homology Oligo B will be the reverse complement of this sequence from beginning of the spacer to the end of the sequence (see highlighted below in Figure 13). Copy the reverse complement, paste it into a new file, and save it. In this example this oligo sequence is 5'-ATCCcaCGAAGGTGGAGTGGTTGGAGATTTCATCCAACAACCGCGTAAGAAAACggg-3'.

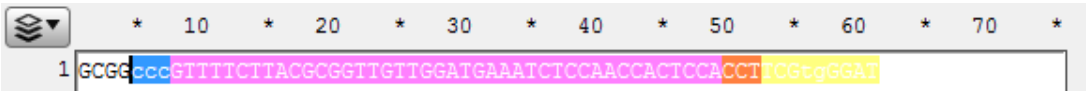


Figure 14. Screenshot of the gene sequence of the upstream homology arm (purple), the PAM (orange), the remaining target sequence to the cut site with the padding nucleotides (tg) to keep the integration in frame (yellow), and the BfuAI sites added to each end. The sequence of Oligo B is highlighted. Use the reverse complement of the highlighted sequence.

Downstream Homology Arm Design

7. Open sequence file for the gene of interest and identify the CRISPR site. (Reverse CRISPR target in Yellow, PAM in Orange, coding sequence is in purple). Copy the 48 bp 3' of the CRISPR cut into a new sequence file; this is the downstream homology.

Figure 15. Screenshot of a targeted gene displayed, highlighting the target sequence (yellow), PAM (orange), coding sequence (purple), and the gene sequence of the downstream homology arm (highlighted white).

8. Observe the next three bases downstream of the 48 bp of homology, and pick a base not present to be the 3 bp spacer between the homology and the Universal PAM in the vector. (Here the bases are "CTG" so "aaa" was chosen for the spacer). Add the spacer to the new file 3' of (after) the homology.

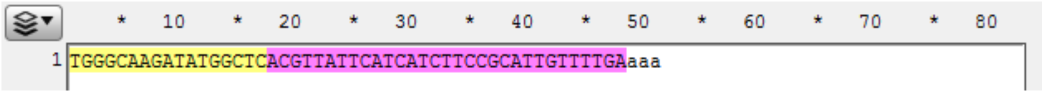


Figure 16. Screenshot of the gene sequence in downstream homology arm from the targeted gene. This comprises part of the target sequence (yellow) and additional 3' coding sequence (purple). aaa was added as padding nucleotides.

9. Add the BspQI enzyme overhang sequences for cloning, to the ends of the homology domain. 5'-AAG and 3'-CCG. (Here both overhangs are added to prevent errors in copying sequence for the oligos in the next two steps.)

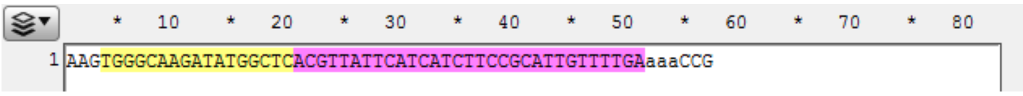


Figure 17. Screenshot of the gene sequence in downstream homology arm from the targeted gene with part of the target sequence (yellow) and additional 3' coding sequence (purple). BspQI enzyme overhang sequences are added to each end.

10. The Downstream Homology Oligo A will be this sequence from the beginning of the sequence to the end of the spacer (see highlighted below). In this example this oligo sequence is 5'-AAGTGGGCAAGATATGGCTCACGTTATTCATCATCTTCCGCATTGTTTTGAaaa-3'.

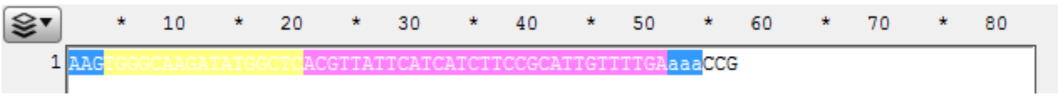


Figure 18. Screenshot of the gene sequence in downstream homology arm from the targeted gene with part of the target sequence (yellow) and additional 3' coding sequence (purple). Sequence for Oligo A is highlighted in white.

11. The Downstream Homology Oligo B (will be the reverse complement of this sequence from the beginning of the homology to the end of the sequence (see highlighted below). In this example this oligo sequence is 5'-CGGtttTCAAAACAATGCGGAAGATGATGAATAACGTGAGCCATATCTTGCCCA-3'

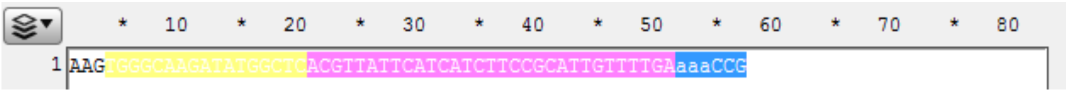


Figure 19. Screenshot of the gene sequence in downstream homology arm from the targeted gene with part of the target sequence (yellow) and additional 3' coding sequence (purple). Sequence for Oligo B is highlighted in white. The reverse complement should be ordered.

F. One Pot Cloning of Homology Arms into pGTag Vectors

Notes:

1. *If the homology arm oligos contain the sequence "5'-ACCTGC-3'" or "5'-GAAGAGC-3'" (or their complements) the cloning reaction will be less efficient.*
2. *If One Plot cloning is unsuccessful, the 5' and 3' homology arms can be cloned sequentially into the vector using gel purified linear plasmids digested with the appropriate enzyme.*

1. Homology Arm Annealing

   Anneal upstream and downstream homology oligo pairs separately:

   4.5 µl oligo A at 10 µM
   4.5 µl olio B at 10 µM
   4 µl 10x Buffer 3.1 from NEB
   27 µl dH20
   40 µl total

   Incubate at 98°C for 4 min, 98°C 45 sec x 90 steps decrementing temp 1°C/cycle, 4°C hold.

   (Alternatively heat in 95-98°C water for 5 minutes, and then remove the boiling beaker from the heat source and allow it to cool to room temp for 2 hours, before placing samples on ice.)

2. 1-Pot Digest

   Assemble the following:

   4.0 µl dH2O
   2 µl Plasmid at 50 ng/ul
   1 µl 10x Buffer 3.1 from NEB
   1 µl 5' annealed homology arm
   1 µl 3' annealed homology arm
   0.5 µl BfuAI enzyme from NEB
   0.5 µl BspQI enzyme from NEB
   10 ul total

   Incubate at 50°C for 1 h, place on ice.

3. Ligation

   Add the following:

3 µl 5x T4 quick ligase buffer
1.5 µl dH2O
0.5 µl T4 quick ligase
15 µl total
Incubate 8-10 min at room temperature (to overnight). Store at -20°C.

4. Transformation – To prevent recombination at repetitive elements in the plasmid, grow transformations and overnight cultures at 30°C. Our standard protocol uses NEB Stable Competent *E. coli* (C3040H) cells for cloning and propagation of the GeneWeld pGTag and pPRISM plasmid series to limit recombination.
    a. On ice, thaw 1 (one) vial competent cells (50 µl) for every 2 ligation reactions. (approx. 5 min).
    b. While cells are thawing, label the microcentrifuge tubes for each ligation and put on ice.
    c. Once the cells have thawed, use a pipette to transfer 25 µl of the competent cells into each labeled tube.
    d. Add 1.5 µl of a ligation reaction into competent cells to transform.
    Amount of ligation reaction added should be less than 5% of volume of competent cells.
    e. Mix by tapping the tube several times or gently mixing with the pipet tip.
    Do NOT mix by pipetting, this will lyse the cells.
    f. Incubate on ice for 5 to 20 min.
    g. Heat shock the cells by submerging the portion of the tube containing the cells in a 42°C water bath for 40 - 50 s.
    h. Incubate cells on ice for 2 min.
    i. Add 125 µl of room temperature LB or SOC to each transformation.
    j. Incubate cells at 30°C for 1-1.5 h in a shaking incubator.
    k. While the transformed cells are recovering, spread 40 µl of X-Gal solution, and 40 µl IPTG 0.8 M on LB Kanamycin selection plates.
    a. X-Gal is lethal to cells while wet, it is recommended to first label the plates and then place them in a 30°C incubator to dry.
    l. After recovery and the X-Gal is dry, Plate 150 µl of each transformation on the corresponding correctly labeled plate.
    m. Incubate plates overnight at 30°C.
5. Growing colonies
    Pick 3 white colonies from each plate and grow in separate glass culture tubes with 3 ml LB/Kanamycin, overnight at 30°C, or to pre-screen colonies by colony PCR:
    a. Pick up to 8 colonies with a pipet tip and resuspend them in separate aliquots of 5 µl dH2O. Place the tip in 3 ml of LB/Kan, label, and store at 4°C.
    b. Make a master mix for your PCR reactions containing the following amounts times the number of colonies you picked.
    7.5 µl 2x GoTaq mastermix

5.5 µl dH_2O

0.5 µl primer at 10 uM "F3'-check" 5'- GGCGTTGTCTAGCAAGGAAG -3'

0.5 µl primer at 10 uM "3'_pgtag_seq"5'-ATGGCTCATAACACCCCTTG-3'

14 µl total

c. Aliquot 14 µl of mixed master mix into separate labeled PCR tubes.

d. Add 1 µl of colony to each reaction as template, or 20 ng purified plasmid as control.

e. Cycle in a thermocycler

95°C 2 min
95°C 30 s |
57°C 30 s | x 35 cycles
72°C 30 s |
72°C 5 min
4°C hold

f. Run 5 µL of PCR product on a 1% agarose gel. Image gel on iBright FL1500 Imaging System or other gel-documentation imaging system. There should be bands that are a different size than the control.

6. Mini Prep Cultures

Follow Qiagen Protocol

7. Sequencing of Plasmids

The 5' homology arm can be sequenced by the 5'_pgtag_seq primer: 5'-GCATGGATGTTTTCCCAGTC-3'.

The 3' homology arm can be sequenced with the "3'_pgtag_seq"primer: 5'-ATGGCTCATAACACCCCTTG-3'.

G. Injection of GeneWeld Reagents (spCas9 mRNA, Universal sgRNA (UgRNA), genomic sgRNA and pGTag homology vector) into 1-cell zebrafish embryos

Prepare and collect the following reagents for injection:

1. Prepare nCas9n mRNA from pT3TS-nCas9n (Addgene #46757 from [21]) as described above in Section B 5.
2. The UgRNA and genomic sgRNA can be directly ordered form IDT or Synthego and resuspended in Molecular Grade RNase/DNase-Free water.
3. The pGTag homology vectors should be purified a second time prior to microinjection under RNase free conditions with the Promega PureYield Plasmid Miniprep System beginning at the endotoxin removal wash. Plasmid DNA is eluted in Molecular Grade RNase/DNase-Free water.
4. Embryo Injections for Integration of pGTag vectors.

Injections are performed into single cell embryos at a volume of 2 nl per embryo containing the following concentration of RNAs and vector:

In injection solution	In embryo
75 pg/nl of nCas9n mRNA	150 pg of nCas9n mRNA

12.5 pg/nl of genomic sgRNA	25 pg of genomic sgRNA
12.5 pg/nl of UgRNA	25 pg of UgRNA
5 pg/nl of pGTag DNA	10 pg of pGTag DNA

H. Test injected embryos for evidence of precision on-target integration.

1. Examine injected embryos for fluorescence under a Zeiss Discovery dissecting microscope with a 1X objective at 70-100X magnification. If weak signals are observed, manually dechorionate the embryos, and view on a glass depression well slide on a standard upright compound microscope with epi-illumination. High resolution confocal live imaging can also be carried out, as shown in Wierson et al., 2020 Figure 3 (Wierson *et al.*, 2020) https://elifesciences.org/articles/53968/figures#fig3.

   The type of light source used for fluorescent protein activation significantly affects the ability to visualize fluorescence signals. The X-Cite 120W metal halide light source with fiber optic cable (Excilitas Technologies) works well to visualize fluorescence after somatic targeting. The TagRFP protein also is shifted in its excitation and filters optimized for this protein are recommended. Filters optimized for GFP and BFP are also recommended. If no or weak signal is observed, integration of pGTag-Gal4VP16 can be used to amplify reporter expression in the 14XUAS-RFP transgenic line [26].

2. Perform junction fragment PCR analysis on positive embryos that display widespread fluorescence in expression domains consistent with the targeted gene. Isolate genomic DNA from individual embryos, and a control embryo, as in Section D. 2 above. PCR amplify the genomic DNA-integrated cassette 5' and 3' junctions fragments. An example of F0 embryo junction analysis is shown in Figure 3s1 in Wierson *et al.*, 2020 https://elifesciences.org/articles/53968/figures#fig3s1).

The following primers are used for junction fragment analysis and must be paired with gene specific primers (5' to 3'):

5' pGTag junctions:

R-Gal4-5'juncM GCCTTGATTCCACTTCTGTCA and a gene specific forward primer
R-RFP-5'junc CCTTAATCAGTTCCTCGCCCTTAGA
R-eGFP-5'-junc GCTGAACTTGTGGCCGTTT

3' pGTag junctions:

F-Gal4-3'juncM GCAAACGGCCTTAACTTTCC and a gene specific reverse primer
F-Gal4-3'junc CTACGGCGCTCTGGATATGT
F-RFP-3'junc CGACCTCCCTAGCAAACTGGGG
F-eGFP-3'junc ACATGGTCCTGCTGGAGTTC

To control for PCR amplification artifacts as described in [27], perform PCR junction analysis on embryos injected with all targeting reagents minus the genomic sgRNA.
The alternate primers F-Gal4-3'juncM and F-Gal4-3'juncJ may increase primer specificity, depending on the target gene.

7.5 µl 2x GoTaq mastermix
5.5 µl dH2O
0.5 µl primer at 10 µM genomic primer
0.5 µl primer at 10 µM pGTag primer
14 µl total

a. Aliquot 14 µl of mixed master mix into separate labeled PCR tubes.
b. Add 1 µl of genomic DNA to each reaction as template.
c. Cycle in a thermocycler with the following steps:
   95 °C 2 min
   95 °C 30 s |
   55 °C 30 s | x 35 cycles
   72 °C 30 s |
   72 °C 5 min
   4 °C hold
d. Run 5 µl of PCR product on a 1.2 % agarose gel in 1X TAE. Image gel on iBright FL1500 Imaging System or other gel-documentation imaging system. Putative junction fragments should give bands that are of predicted size.

I. Establish a new transgenic line of a precision targeted integration allele.

1. Raise to adulthood fluorescence reporter expression F0 siblings of injected embryos that showed positive bands for 5' and 3' junction analysis indicating precision targeted integration. Outcross F0 adults to wild type and examine the progeny for reporter gene fluorescence as above in order to identify F1 embryos that have inherited a stable germline integration allele. For Gal4Vp16 integration alleles, cross the F0 adults to the 14XUAS:RFP reporter line. Silencing of the 14XUAS:RFP reporter may result in mosaic expression patterns in Gal4Vp16 targeted F1 embryos.
2. Test F1 fluorescence positive embryos for precise transgene integration by junction fragment PCR analysis as described above. Raise F1 siblings to adulthood and fin-clip to identify individuals with precise targeted transgene integration as shown in Figure 4s 2-4 in Wierson *et al*., 2020 https://elifesciences.org/articles/53968/figures#fig4s2).
3. Outcross a single positive F1 adults to establish F2 families. F1s can also be sacrificed at 3 weeks post fertilization to the confirm location and precision of targeted integrations by genomic Southern Blot RFLP analysis (Figure 4s1 in Wierson *et al.*, 2020

https://elifesciences.org/articles/53968/figures#fig4s1). Continue to maintain lines by outcrossing to wild type in subsequent generations. Tables 1 and 2 in Wierson *et al.*, 2020 https://elifesciences.org/articles/53968/figures show the range of germline transmission frequencies of precision targeted integration alleles at 8 zebrafish loci.

4. To gain an initial assessment of whether the targeted integration allele causes a loss of function phenotype, F0 and F1 identified fish can be incrossed, or crossed to a known indel allele of the targeted gene.

Data analysis

Links to numerical data in the original article Wierson *et al.*, 2020 are included in the protocol.

Recipes

Zebrafish embryo E2 Medium (https://wahoo.cns.umass.edu/book/export/html/867)

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Competing interests

JJE, MM, and KJC have a financial conflict of interest with Recombinetics, Inc.; JJE and SCE with Immusoft, Inc.; JJE, MM, WAW, KJC and SCE with LifEngine and LifEngine Animal Technologies.

Ethics

All zebrafish experiments described in this protocol were carried out under approved protocols from Iowa State University Animal Care and Use Committee Log#11-06-6252, in compliance with American Veterinary Medical Association and NIH guidelines for the humane use of animals in research.

References

1 Beumer, K. J. *et al.* Efficient gene targeting in Drosophila by direct embryo injection with zinc-finger nucleases. *Proc Natl Acad Sci U S A* **105**, 19821-19826, doi:10.1073/pnas.0810475105 (2008).

2 Geurts, A. M. *et al.* Knockout rats via embryo microinjection of zinc-finger nucleases. *Science* **325**, 433, doi:10.1126/science.1172447 (2009).

3 Yang, H. *et al.* One-step generation of mice carrying reporter and conditional alleles by CRISPR/Cas-mediated genome engineering. *Cell* **154**, 1370-1379, doi:10.1016/j.cell.2013.08.022 (2013).

4 Carlson, D. F. *et al.* Efficient TALEN-mediated gene knockout in livestock. *Proc Natl Acad Sci U S A* **109**, 17382-17387, doi:10.1073/pnas.1211446109 (2012).

5 Bedell, V. M. *et al.* In vivo genome editing using a high-efficiency TALEN system. *Nature* **491**, 114-118, doi:10.1038/nature11537 (2012).

6 Hasty, P., Rivera-Perez, J., Chang, C. & Bradley, A. Target frequency and integration pattern for insertion and replacement vectors in embryonic stem cells. *Mol Cell Biol* **11**, 4509-4517 (1991).

7 Zu, Y. *et al.* TALEN-mediated precise genome modification by homologous recombination in zebrafish. *Nat Methods* **10**, 329-331, doi:10.1038/nmeth.2374 (2013).

8 Hoshijima, K., Jurynec, M. J. & Grunwald, D. J. Precise Editing of the Zebrafish Genome Made Simple and Efficient. *Dev Cell* **36**, 654-667, doi:10.1016/j.devcel.2016.02.015 (2016).

9 Shin, J., Chen, J. & Solnica-Krezel, L. Efficient homologous recombination-mediated genome engineering in zebrafish using TALE nucleases. *Development* **141**, 3807-3818, doi:10.1242/dev.108019 (2014).

10 Orr-Weaver, T. L., Szostak, J. W. & Rothstein, R. J. Yeast transformation: a model system for the study of recombination. *Proc Natl Acad Sci U S A* **78**, 6354-6358 (1981).

11 Rong, Y. S. & Golic, K. G. Gene targeting by homologous recombination in Drosophila. *Science* **288**, 2013-2018 (2000).

12 Grzesiuk, E. & Carroll, D. Recombination of DNAs in Xenopus oocytes based on short homologous overlaps. *Nucleic Acids Res* **15**, 971-985 (1987).

13 Nakade, S. *et al.* Microhomology-mediated end-joining-dependent integration of donor DNA in cells and animals using TALENs and CRISPR/Cas9. *Nat Commun* **5**, 5560, doi:10.1038/ncomms6560 (2014).

14 Hisano, Y. *et al.* Precise in-frame integration of exogenous DNA mediated by CRISPR/Cas9 system in zebrafish. *Scientific reports* **5**, 8841, doi:10.1038/srep08841 (2015).

15 Aida, T. *et al.* Gene cassette knock-in in mammalian cells and zygotes by enhanced MMEJ. *BMC Genomics* **17**, 979, doi:10.1186/s12864-016-3331-9 (2016).

16 Ceccaldi, R., Rondinelli, B. & D'Andrea, A. D. Repair Pathway Choices and Consequences at the Double-Strand Break. *Trends Cell Biol* **26**, 52-64, doi:10.1016/j.tcb.2015.07.009 (2016).

17 Zhang, J. P. *et al.* Efficient precise knockin with a double cut HDR donor after CRISPR/Cas9-mediated double-stranded DNA cleavage. *Genome Biol* **18**, 35, doi:10.1186/s13059-017-1164-8 (2017).

18 Luo, J. J. *et al.* CRISPR/Cas9-based genome engineering of zebrafish using a seamless integration strategy. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology* **32**, 5132-5142, doi:10.1096/fj.201800077RR (2018).

19 Kanca, O. *et al.* An efficient CRISPR-based strategy to insert small and large fragments of DNA using short homology arms. *Elife* **8**, doi:10.7554/eLife.51539 (2019).

20 Moreno-Mateos, M. A. *et al.* CRISPRscan: designing highly efficient sgRNAs for CRISPR-Cas9 targeting in vivo. *Nat Methods* **12**, 982-988, doi:10.1038/nmeth.3543 (2015).

21 Jao, L. E., Wente, S. R. & Chen, W. Efficient multiplex biallelic zebrafish genome editing using a CRISPR nuclease system. *Proc Natl Acad Sci U S A* **110**, 13904-13909, doi:10.1073/pnas.1308335110 (2013).

22 Rosen, J. N., Sweeney, M. F. & Mably, J. D. Microinjection of zebrafish embryos to analyze gene function. *Journal of visualized experiments : JoVE*, doi:10.3791/1115 (2009).

23 Almeida, M. P. *et al.* Endogenous zebrafish proneural Cre drivers generated by CRISPR/Cas9 short homology directed targeted integration. *Scientific Reports* 11(1):1173, doi:10.1038/s41598-021-81239-y (2021).

24 Solin, S. L., Shive, H. R., Woolard, K. D., Essner, J. J. & McGrail, M. Rapid tumor induction in zebrafish by TALEN-mediated somatic inactivation of the retinoblastoma1 tumor suppressor rb1. *Scientific reports* **5**, 13745, doi:10.1038/srep13745 (2015).

25 Wierson, W. A. *et al.* Efficient targeted integration directed by short homology in zebrafish and mammalian cells. *Elife* **9**, doi:10.7554/eLife.53968 (2020).

26 Balciuniene, J. *et al.* Efficient disruption of Zebrafish genes using a Gal4-containing gene trap. *BMC Genomics* **14**, 619, doi:10.1186/1471-2164-14-619 (2013).

27 Won, M. & Dawid, I. B. PCR artifact in testing for homologous recombination in genomic editing in zebrafish. *PLoS One* **12**, e0172802, doi:10.1371/journal.pone.0172802 (2017).