

Tyr
WT CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCA**CCTCCCAGAAAGTCTCCAGTCC**AAACGCTGCTGTCCAGTCTGG
D_143_13 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCACCTCC-----AGTCCAAACGCTGCTGTCCAGTCTGG
D_146_1 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCACCTCC-CAGAAGTCTCCAGTCCAAACGCTGCTGTCCAGTCTGG
D_146_2 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCACCTCC--AGAAGTCTCCAGTCCAAACGCTGCTGTCCAGTCTGG
D_149_2 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCACCTCC--GAAGTCTCCAGTCCAAACGCTGCTGTCCAGTCTGG
D_135_18 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCT-----CTCCAGTCCAAACGCTGCTGTCCAGTCTGG
D_147_9 CAGCTCGTCTCTCCAGCAGTTCCCCCGAGTCTGCACCTCC-----CTCCAGTCCAAACGCTGCTGTCCAGTCTGG

InsrA
WT **CCACGCATTTGTTAGACGAGTGG**GGCTCCAAACAGCCGCCAGACACTGGTCGTGGCAGCACTGGCTGTCTTTAGTGCAG**GCGCGGTGCTTGCA****TGAGGATGG**
D_91_80 CCACGCATTTGTTAGAC-----GGATGG
D_88_3 CCACGCATTTGTTAGAC--GTGGGGCTCCAAACAGCCGCCAGACACTGGTCGTGGCAGCACTGGTTGTCTTTAGTGCAGGCGCGGTGCTTGCA**TGAGGATGG**
D_87_5 CCACGCATTTGTTAGAC---TGGGGCTCCAAACAGCCGCCAGACACTGGTCGTGGCAGCACTGGTTGTCTTTAGTGCAGGCGCGGTGCTTGCA**TGAGGATGG**
D_169_3 CCACGCATTTGTTAGACGAGTGGGGCTCCAAACAGCCGCCAGACACTGGTCGTGGCAGCACTGGTTGTCTTTAGTGCAGGCGCGGTGCTTGCA**TGAGGATGG**
D_90_76 CCACGCATTTGTTAGAC-----ATGAGGATGG

InsrB
WT CCACCGAATCCA**GATCTTGGACCAGTCCA** **GAGTGG**ACAAATAGCACAGGTTTGGGTTCTTCTCGATGCGCA**CCGCTCCCCGCGTGATGTTGGTC**AAACTG
I_111_1 CCACCGAATCCAAGATCTTGGACCAGTCCA**GAGTGG**ACAAATAGCACAGGTTTGGGTTCTTCTCGATGCGCACCGCTCCCCGCGTGATGTTGGTCAA**ACTG**
D_112_48 CCACCGAATCCAAGATCTTGGACCAGTCCA-----CCCGCGTGATGTTGGTCAA**ACTG**
D_106_7 CCACCGAATCCAAGATCTTGGACCAGT-----GGACAAATAGCACAGGTTTGGGTTCTTCTCGATGCGCACCGCTCCCCGCGTGATGTTGGTCAA**ACTG**
D_112_1 CCACCGAATCCAAGATCTTGGACCAGTCCA--AGTGGACAAATAGCACAGGTTTGGGTTCTTCTCGATGCGCACCGCTCCCCGCGTGATGTTGGTCAA**ACTG**
D_100_15 CCACCGAATCCAAGATCTTGGAC-----AAATAGCACAGGTTTGGGTTCTTCTCGATGCGCACCGCTCCCCGCGTGATGTTGGTCAA**ACTG**

Figure S1 Alignment of top 5 alleles of the 3 loci in *Tg(actb2:cas9)*; (*U6x:sgRNA(insra/b)*) fish. The mutant alleles are arranged according to their frequency with the top being the most frequent. Protospacers and PAM are highlighted in yellow and cyan in the wild-type sequence, respectively. Micro-homology pairs are labelled by the same types of underline, or in bold in the wild-type sequence. Red letter in the mutant allele indicates insertion. Dashes in the mutant alleles indicate deletion.

Tables S1-S5

Available for download as Excel files at www.genetics.org/lookup/suppl/doi:10.1534/genetics.115.176917/-/DC1

Table S1. List of primers use in the study.

Table S2. Mutation rates at the three loci calculated based on high throughput sequencing data.

Table S3. Alleles and read counts of *insra* locus identified in the 17 double carriers. “D” denotes deletion. “I” denotes insertion. “C” denotes deletion and insertion. The first number indicates the position at which InDel occurs. The second number is the number of nucleotides of insertion or deletion in the allele.

Table S4. Alleles and read counts of *insrb* locus identified in the 17 double carriers.

Table S5. Alleles and read counts of *tyr* locus identified in the 17 double carriers.

File S1
Supplemental Methods

Construction of U6-based sgRNA expression vectors

1. Order a pair of U6 vector-specific, 23nt targeting primers for each target. For each target (GN19), order a forward primer TTCGN19 for the U6 promoter vectors; order a reverse primer AAACN19. Note that the N19 in the reverse primers is reverse complementary to that in the forward primer.

To order primers compatible with both the pU6x-sgRNA vectors and pT7-gRNA (Addgene plasmid #4675; (JAO *et al.* 2013)), order degenerate primers WTMGGN18 (forward) and AMMCN₁₈C (reverse), where M=A or C, W=A or T. Again, the N18 in the reverse primers is reverse complementary to that in the forward primer.

2. Anneal the two primers (1µl 100µM stock each in a 20µl 1x NEB buffer 2) by incubating the mixture at 95°C for 5 min, ramping down to 50°C at 0.1°C/sec, incubating at 50°C for 10 min, and chilling to 4°C at normal ramp speed.
3. Ligate the annealed oligos to the U6 vector of choice (pU6x-sgRNA #1-#5, see diagrams and plasmid list in the next pages) by mixing the components [1 µl 10x CutSmart buffer, 1 µl T4 DNA ligase buffer, 0.25µl U6 plasmid (about 100ng), 1µl annealed oligos, 0.3 µl T4 DNA ligase, 0.3 µl BsmBI, 0.2µl PstI (optional), 0.2 µl Sall (optional), 5µl H₂O] and incubating 3x(37°C for 20 min, 16°C for 15 min), then 37°C for 10 min, 55°C for 15 min, followed by 80°C for 15 min (optional).
4. The reaction is ready for transformation (use 2 µl of the ligation and plate 10% of the transformants). Transform and spread onto spectinomycin (50µg/ml) plates.

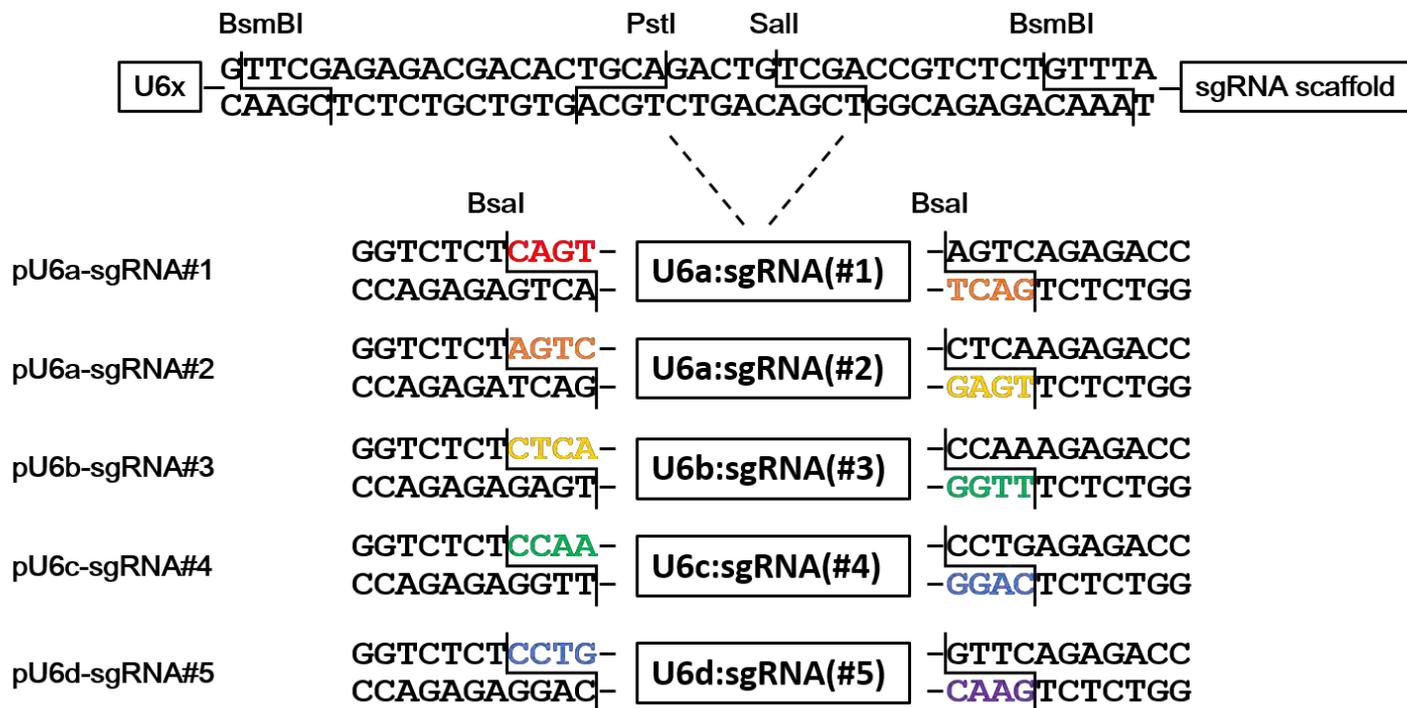
Construction of pGGDestTol2LC-sgRNA vectors

1. Ligate the U6x:sgRNA cassettes into a pGGDestTol2LC vector by mixing the components (2µl 10x CutSmart buffer, 2 µl T4 DNA ligase buffer, 100ng of each pU6x-sgRNA plasmid, 50ng empty pGGDestTol2LC-sgRNA vector of choice (see plasmid list and diagrams), 1µl BsaI, 1µl T4 DNA ligase, adjust volume to 20 µl with H₂O).
2. Incubate mixture 3x(37°C for 20 min, 16°C for 15 min), followed by 80°C for 15 min.
3. The reaction is ready for transformation (use 5 µl of the ligation and plate 50% of the transformants). Transform and spread onto ampicillin (100 µg/ml) plates.

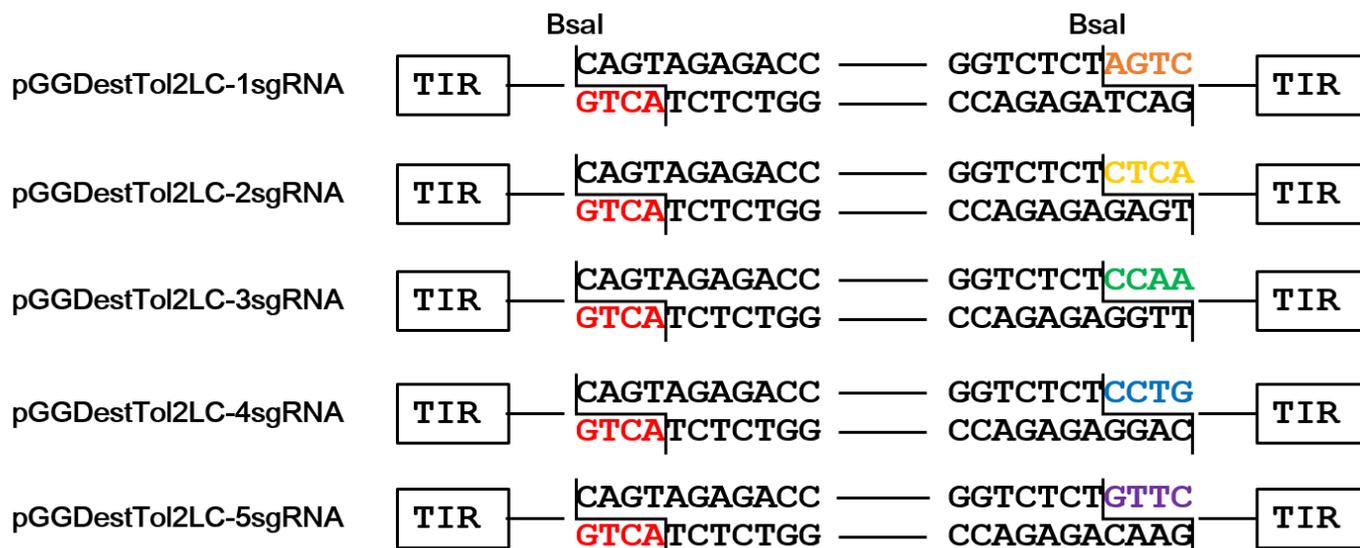
Reference.

JAO, L. E., S. R. WENTE and W. CHEN, 2013 Efficient multiplex biallelic zebrafish genome editing using a CRISPR nuclease system. *Proc Natl Acad Sci U S A* **110**: 13904-13909.

A



B



List of plasmids deposited at Addgene (Deposit 71794)

Plasmid ID	Plasmid Name
64237	pME-Cas9
64239	pGGDestTol2LC-1sgRNA
64240	pGGDestTol2LC-2sgRNA
64241	pGGDestTol2LC-3sgRNA
64242	pGGDestTol2LC-4sgRNA
64243	pGGDestTol2LC-5sgRNA
64245	pU6a:sgRNA#1
64246	pU6a:sgRNA#2
64247	pU6b:sgRNA#3
64248	pU6c:sgRNA#4
64249	pU6d:sgRNA#5
64250	pU6a:sgRNA(tyr)