



## Strain Management- Best Practices

The more information you can provide the better

Submit a new strain for each allele even if your strain is already a compound strain. Once complete, use Cross Strain feature

Please do submit control samples for validation when possible

JAX/MGI ID		Allele	Strain name
N/A	Cre	Conditional Cre	Strain1
030420	Gt(ROSA)26Sortm1(CAG-birA,-EGFP)Joez/J	EGFP transgene (reporter gene)	Strain2
Use 'Cross Strain' function within your account to create compound strain			
N/A	Strain1/Strain2	Strain1 x Strain2	Compound1

## Example of Relevant Data for SIF

**Actb<sup>tm1.1Erv</sup>** Your Input Welcome

Targeted Allele Detail

Nomenclature | Mutation origin | Mutation description | Phenotypes | Find Mice (IMSR) | References

<b>Nomenclature</b>	Symbol: <b>Actb<sup>tm1.1Erv</sup></b> <span style="color: red;">← Construct Name</span>																
	Name: actin, beta; targeted mutation 1.1, James M Ervasti																
	MGI ID: MGI <b>4381824</b> <span style="color: red;">← MGI Database #</span>																
	Synonyms: Actb <sup>Flex</sup>																
	Gene: <b>Actb</b> <span style="color: red;">← Gene Name</span> 42903115-142906754 bp, - strand Genetic Position: Chr5, 81.8 cM																
<b>Mutation origin</b>	Germline Transmission: Earliest citation of germline transmission: J:167543 Parent Cell Line: Not Specified (ES Cell) Strain of Origin: 129S6/SvEvTac																
<b>Mutation description</b>	Allele Type: Targeted (Conditional ready, No functional change) Mutation: Insertion Mutation details: A floxed PGK-neomycin selection cassette in reverse orientation was inserted in intron 1 and a third loxP site was placed in intron 3. The selection cassette was subsequently removed from properly targeted mice by crossing to transgenic mice carrying Tg(Elia-cre)CS379Lmgd. (J:167542) <span style="color: red;">← Description</span>																
<b>Phenotypes</b>	Key: hm homozygous ht heterozygous tg involves transgenes V phenotype observed cn conditional genotype cx complex > 1 genome feature ot (other) hemizygous, indeterminate, ... N normal phenotype																
<b>Genotype/Background</b>	<table border="1"> <thead> <tr> <th>Allelic Composition</th> <th>Genetic Background</th> <th>Cell Line(s)</th> </tr> </thead> <tbody> <tr> <td>cn1 Actb<sup>tm1.1Erv</sup>/Actb<sup>tm1.1Erv</sup> Actg<sup>tm1.2Erv</sup>/Actg<sup>tm1.2Erv</sup> Tg(Atoh1-cre)1Bfrv?</td> <td>involves: 129/Sv * C57BL/6 * CBA * FVB/N</td> <td></td> </tr> <tr> <td>cn2 Actb<sup>tm1.1Erv</sup>/Actb<sup>tm1.1Erv</sup> Foxg1<sup>tm1.1uroDkr</sup>/Foxg1<sup>1</sup></td> <td>involves: 129P2/OlaHsd * 129S6/SvEvTac * C57BL/6 * FVB/N</td> <td></td> </tr> <tr> <td>cn3 Actb<sup>tm1.1Erv</sup>/Actb<sup>tm1.1Erv</sup> Tg(Atoh1-cre)1Bfrv?</td> <td>involves: 129S6/SvEvTac * C57BL/6 * CBA * FVB/N</td> <td></td> </tr> </tbody> </table>	Allelic Composition	Genetic Background	Cell Line(s)	cn1 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Actg <sup>tm1.2Erv</sup> /Actg <sup>tm1.2Erv</sup> Tg(Atoh1-cre)1Bfrv?	involves: 129/Sv * C57BL/6 * CBA * FVB/N		cn2 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Foxg1 <sup>tm1.1uroDkr</sup> /Foxg1 <sup>1</sup>	involves: 129P2/OlaHsd * 129S6/SvEvTac * C57BL/6 * FVB/N		cn3 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Tg(Atoh1-cre)1Bfrv?	involves: 129S6/SvEvTac * C57BL/6 * CBA * FVB/N					
	Allelic Composition	Genetic Background	Cell Line(s)														
cn1 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Actg <sup>tm1.2Erv</sup> /Actg <sup>tm1.2Erv</sup> Tg(Atoh1-cre)1Bfrv?	involves: 129/Sv * C57BL/6 * CBA * FVB/N																
cn2 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Foxg1 <sup>tm1.1uroDkr</sup> /Foxg1 <sup>1</sup>	involves: 129P2/OlaHsd * 129S6/SvEvTac * C57BL/6 * FVB/N																
cn3 Actb <sup>tm1.1Erv</sup> /Actb <sup>tm1.1Erv</sup> Tg(Atoh1-cre)1Bfrv?	involves: 129S6/SvEvTac * C57BL/6 * CBA * FVB/N																
<b>Phenotypes</b>	<table border="1"> <thead> <tr> <th>Affected Systems</th> <th>cn1</th> <th>cn2</th> <th>cn3</th> </tr> </thead> <tbody> <tr> <td>hearing/vestibular/ear</td> <td>✓</td> <td>N</td> <td>✓</td> </tr> <tr> <td>mortality/aging</td> <td></td> <td>✓</td> <td></td> </tr> <tr> <td>nervous system</td> <td>✓</td> <td></td> <td>✓</td> </tr> </tbody> </table> <p>View phenotypes and curated references for all genotypes (concatenated display).</p>	Affected Systems	cn1	cn2	cn3	hearing/vestibular/ear	✓	N	✓	mortality/aging		✓		nervous system	✓		✓
Affected Systems	cn1	cn2	cn3														
hearing/vestibular/ear	✓	N	✓														
mortality/aging		✓															
nervous system	✓		✓														
<b>Find Mice (IMSR)</b>	Mouse strains and cell lines available from the International Mouse Strain Resource (IMSR) Carrying this Mutation: Mouse Strains: 1 strain available <span style="color: red;">← Link to JAX, MMRRC, TAC, KOMP, etc.</span> Carrying any Actb Mutation: 37 strains or lines available																
<b>References</b>	Original: J:167543 Perrin BJ, et al., beta-actin and gamma-actin are each dispensable for auditory hair cell development but required for stereocilia maintenance. PLoS Genet. 2010;6(10):e1001158 <span style="color: red;">← Strain Literature with link</span> All: 5 reference(s)																

JAX Database Name → **B6.129S6(FVB)-Actb<sup>tm1.1Erv</sup>J**

Stock No: **029888** | Actb ← JAX Database #

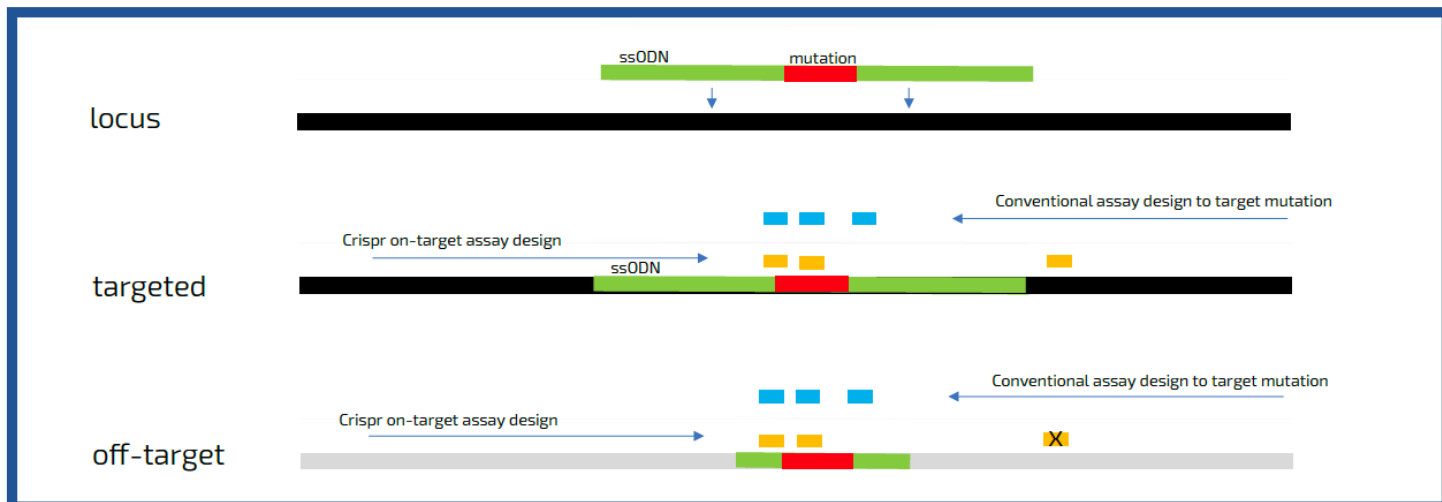
## Submitting a Model Made by CRISPR

Since CRISPR technology often creates many different mutations, which can occur as a mosaic in founder animals, we require that all lines created by CRISPR be fully characterized before Transnetyx can begin developing an assay or genotyping. Characterization means you have sequenced your founders by Sanger or NGS and bred out following questions if you have completed the steps as outlined below:

1. Have you characterized the germline mutation for this CRISPR model?
2. Have you bred your founder animals to wild-type animals to generate G1 animals (animals with inheritable alleles present in the gametes to allow for germline transmission)?
3. Have you bred out off-target allele variants, separating them from the desired mutation of interest?
4. Are you able to provide the exact sequence of the mutation created (should be a result of direct sequencing by Sanger or NGS and not an estimation or reconstruction)?
5. If an ssODN was used, please provide the sequence information. The assay may not be site-specific and could potentially give false positive results if we don't have this information.

Your response may be submitted via the 'Submit Required Information' link on the My Strains homepage or as an email attachment sent to [help@transnetyx.com](mailto:help@transnetyx.com). We understand that the information required to answer the above questions is not always available. In these instances Transnetyx will proceed with assay design, with the customer accepting the associated potential risk of inaccurate results being reported for CRISPR lines where characterization cannot be confirmed.

## Why it is important for us to know if your strain is a CRISPR



## Assay Design and Sequence Data

Shorten your timeline by providing sequence data

**YX** Automated Genotyping

Sequence Data provided in the initial Strain Information Form



Assay Design Process Begins

We send you a Sequencing Request Form (SRF). Strain status: "Requires Sequence Data"



You have the Sequence Data but it was not provided initially



You return the SRF with Sequence Data



Assay Design Process Begins

You don't have the Sequence Data but can provide a sample to be sequenced



You send us a sample for Sequencing purposes and complete the SRF with your sample information



We extract DNA and send it out for sequencing



Sequencing Data Reported



Assay Design Process Begins

Days

Time

Weeks

