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**Mafa<sup>fl/+</sup> or Mafa<sup>lox/w</sup> - Mouse Strain RES228****Mouse Information**

<b>Common Name:</b>	Mafa <sup>fl/+</sup> or Mafa <sup>lox/w</sup>
<b>MGI Official Name:</b>	Mafa <sup>tm1.1Rwst</sup>
<b>Description:</b>	Mafa is a basic leucine-zipper containing member of the large Maf transcription factor family. It is part of the RIPE3b1 activator complex and functions as a key activator of insulin and pdx-1 gene transcription. Mafa <sup>lox</sup> mice may be used to generate both global and cell-specific Mafa null mice, depending on which cre-expressing transgenic mouse is used. Removal of Mafa gene might have a profound effect on beta cell function; thus we can closely monitor the expression of islet hormones, transcription functions and the glucose sensing machinery immunohistochemically. The experiment will provide us with the information about the role of Mafa plays in vivo in islet beta cells and the developing pancreas, thus helping us to understand how transcription activator contribute to the pathogenesis and the treatment of diabetes.
<b>Categories:</b>	None specified.


**Genetic Alterations**

<b>1) Targeted Mutagenesis</b>	
<b>Type of Allele</b>	Conditional Null
<b>Targeted Gene</b>	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian) (Mafa - <a href="#">NCBI GeneID:378435</a> )
<b>Targeted Allele</b>	targeted mutation 1.1 (Mafa <sup>tm1.1(lox)</sup> - <a href="#">MGI:2673307</a> )
<b>Description of Targeting Vector</b>	The targeting vector is FRT.loxP that utilizes both the Cre/Lox and Flpe/FRT recombinase systems. It contains a phosphoglycerol kinase-neomycin (pgk-neo) resistance gene cassette (neoR) for positive ES cell selection, a pgk-thymidine kinase (pgk- <i>tk</i> ) cassette for negative ES cell selection, a 1.723 kb short arm gene fragment, a 4.905 kb long arm fragment, and the 2.354 kb target region (coding sequence plus 1106 bp upstream sequence and 170 bp downstream sequence) in the Mafa gene. Two tandemly oriented loxP sites flank the target region to allow for Cre-recombinase deletion studies; and two tandemly oriented FRT sites flank the neoR for Flpe-recombinase deletion of neoR cassette. The backbone vector is pBluescript KS+. This strain allows for the global and tissue specific knock-out of Mafa gene. For example, crossing the Mafa <sup>lox/lox</sup> mice with an insulin-cre transgenic mouse generates a beta cell specific knock-out of Mafa.
<b>Targeting Vector Genbank File</b>	<a href="#">Maf-A Targeting Vector.gb</a>
<b>Citations</b>	Not Available


**Strain Information**

<b>Strain Type:</b>	Congenic Strain
<b>Chimera/Founder Genetic Background:</b>	129S6/SvEvTac
<b>Current Genetic Background:</b>	C57BL/6J (date recorded: 04/23/2015)
<b>Strain Description:</b>	After achieving germline transmission mice carrying the Mafa <sup>lox</sup> allele were mating to Flpe transgenics

**Access Status**

 This resource is publicly viewable.

**Request this Resource**

 Request from a repository

Primary contributor: [Stein Lab](#)  
Co-contributed by:  

- [BCBC Mouse / ES Cell Core](#)

**Resource Tags**

development, Mafa<sup>fl/+</sup> or Mafa<sup>lox/w</sup>, mESC Core, mouse, mouse strain, pancreas

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**Resource History & Actions**

Approved on Apr 29, 2008  
Last modified on Sep 02, 2008

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**Related resources****BCBC**

No matching resources

**Other Consortia**

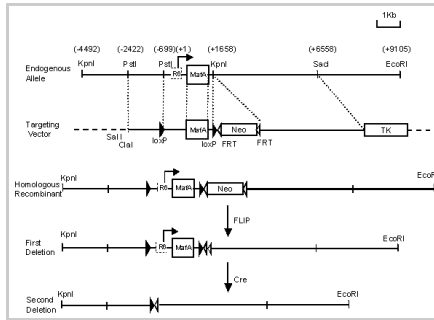
No matching resources

Data courtesy of [dkCOIN](#). Only public resources are displayed.

for the deletion of neoR, and then backcrossed for ten generations into a C57Bl/6J background.

## Associated Images

Image 1



### Description:

Gene targeting and Cre/FLIP deletion events. First is a partial map of the wild type Mafa<sup>W</sup> allele. Second is a map of the Mafa gene targeting vector. Third map from the top is of the recombinant Mafa allele after homologous recombination (HR) carrying a FRT franked Neo cassette and the floxed Mafa coding region. Fourth map from the top is of the mutant Mafa allele after FLIP recombination to have the Neo cassette removed. Fifth map from the top is of the mutant Mafa allele after Cre recombination.

### Reference:

20627934

## Repositories


### MMRRC

 Request via [www.mmrc.org](http://www.mmrc.org) website

Stock #: 029994-UNC

Availability Notes: *Not provided*

### Stein Lab

 Request this resource

Stock #: *Not provided*

Availability Notes: *Not provided*

## Contact Information

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Name	<i>Not provided</i>
Institution	<i>Not provided</i>
Phone	<i>Not provided</i>
Email	<i>Not provided</i>

## Associated Publications

*No publications associated*

## Comments

*There are no comments for this entry.*

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