



Mas1 Cas9-KO Strategy

Designer: Huan Fan

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Project Name

Mas1

Project type

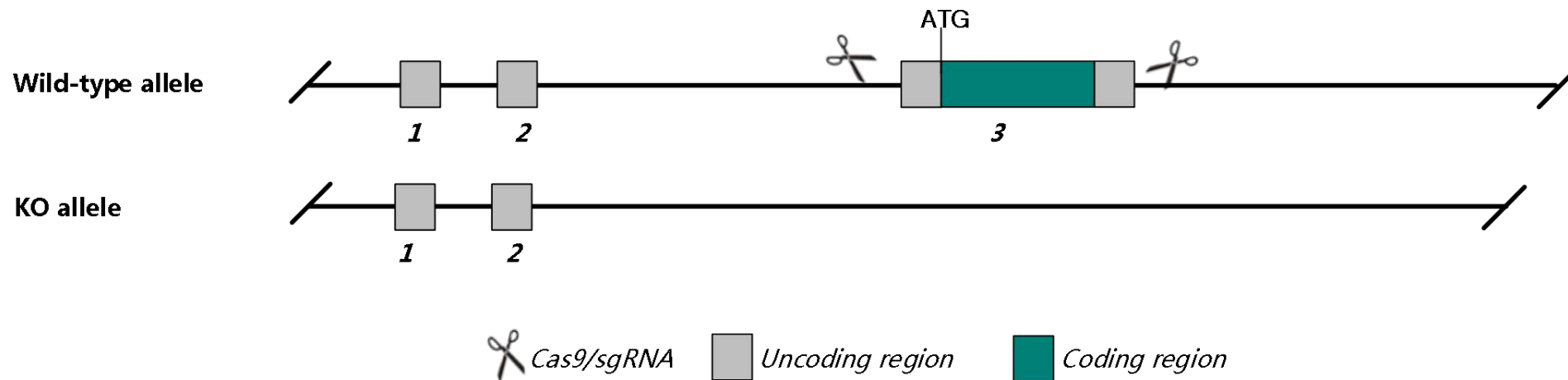
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mas1* gene. The schematic diagram is as follows:



- The *Mas1* gene has 10 transcripts. According to the structure of *Mas1* gene, exon3 of *Mas1*-208 (ENSMUST00000165020.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mas1* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating Positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data Mice homozygous for disruptions in this gene show enhanced long term potentiation and higher levels of anxiety. They are otherwise normal and fertile.
- The *Mas1* gene is located on the Chr17. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Mas1 MAS1 oncogene [*Mus musculus* (house mouse)]

Gene ID: 17171, updated on 14-Aug-2019

Summary



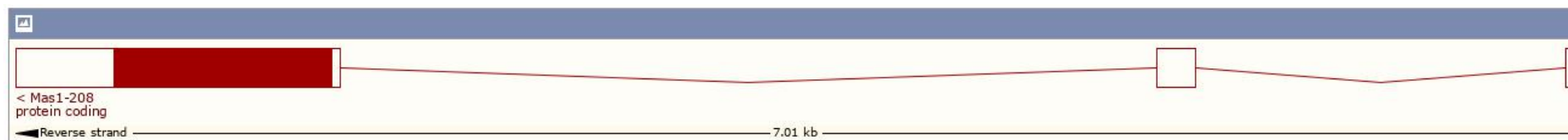
Official Symbol	Mas1 <small>provided by MGI</small>
Official Full Name	MAS1 oncogene <small>provided by MGI</small>
Primary source	MGI:MGI:96918
See related	Ensembl:ENSMUSG00000068037
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MasR; Mgra; Mas-1
Expression	Biased expression in testis adult (RPKM 8.4), cortex adult (RPKM 2.3) and 5 other tissues See more
Orthologs	human all

Transcript information Ensembl

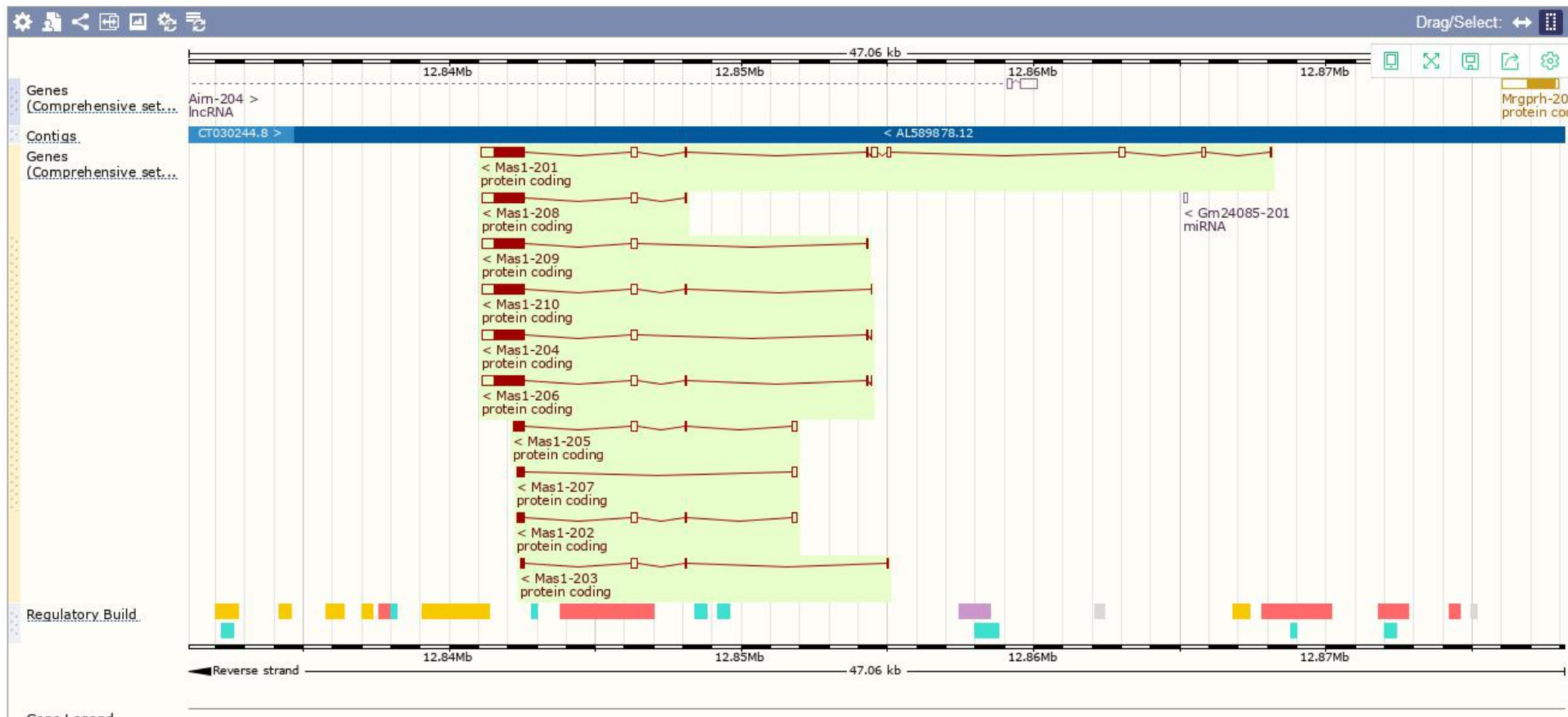
The gene has 10 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Mas1-201	ENSMUST00000089015.9	2401	324aa	ENSMUSP00000086409.3	Protein coding	CCDS28394	P30554 Q0VB49	TSL:1 GENCODE basic APPRIS P1
Mas1-206	ENSMUST00000162333.7	1750	324aa	ENSMUSP00000125108.1	Protein coding	CCDS28394	P30554 Q0VB49	TSL:1 GENCODE basic APPRIS P1
Mas1-210	ENSMUST00000233607.1	1699	324aa	ENSMUSP00000156871.1	Protein coding	CCDS28394	P30554 Q0VB49	GENCODE basic APPRIS P1
Mas1-204	ENSMUST00000161747.7	1687	324aa	ENSMUSP00000123902.1	Protein coding	CCDS28394	P30554 Q0VB49	TSL:1 GENCODE basic APPRIS P1
Mas1-208	ENSMUST00000165020.7	1675	324aa	ENSMUSP00000132300.1	Protein coding	CCDS28394	P30554 Q0VB49	TSL:5 GENCODE basic APPRIS P1
Mas1-209	ENSMUST00000167152.7	1670	324aa	ENSMUSP00000131341.1	Protein coding	CCDS28394	P30554 Q0VB49	TSL:5 GENCODE basic APPRIS P1
Mas1-205	ENSMUST00000162119.7	779	110aa	ENSMUSP00000124952.1	Protein coding	-	E0CX40	CDS 3' incomplete TSL:3
Mas1-202	ENSMUST00000159223.7	684	72aa	ENSMUSP00000124295.1	Protein coding	-	E0CYD1	CDS 3' incomplete TSL:3
Mas1-207	ENSMUST00000162389.1	443	76aa	ENSMUSP00000124879.1	Protein coding	-	E0CX70	CDS 3' incomplete TSL:3
Mas1-203	ENSMUST00000159865.1	409	24aa	ENSMUSP00000124901.1	Protein coding	-	E0CX57	CDS 3' incomplete TSL:1

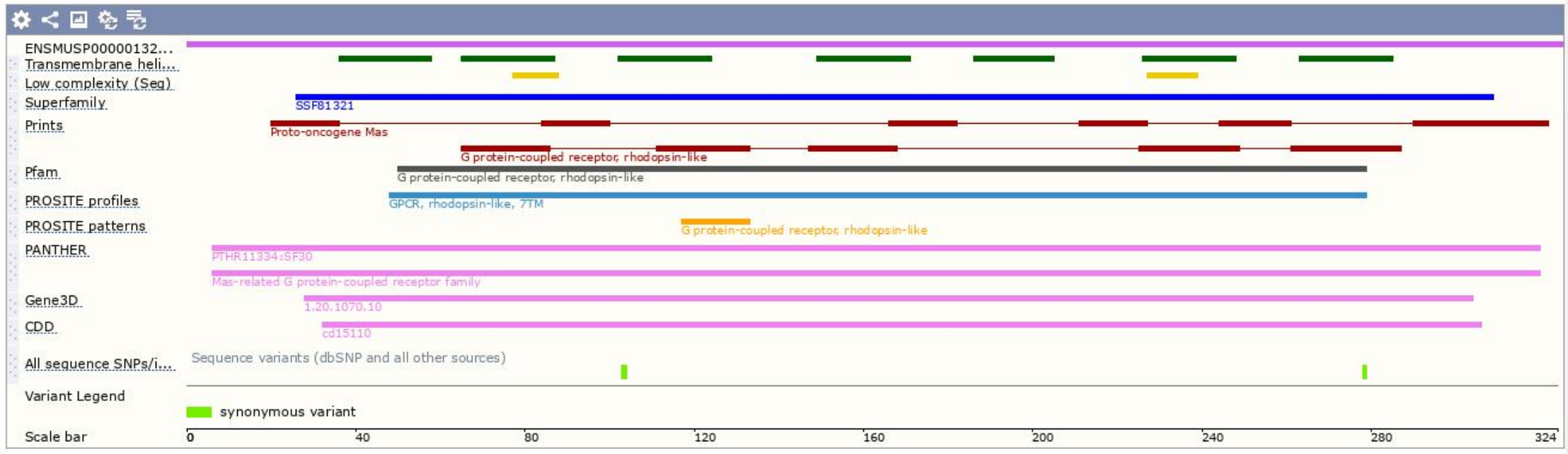
The strategy is based on the design of *Mas1-208* transcript, The transcription is shown below



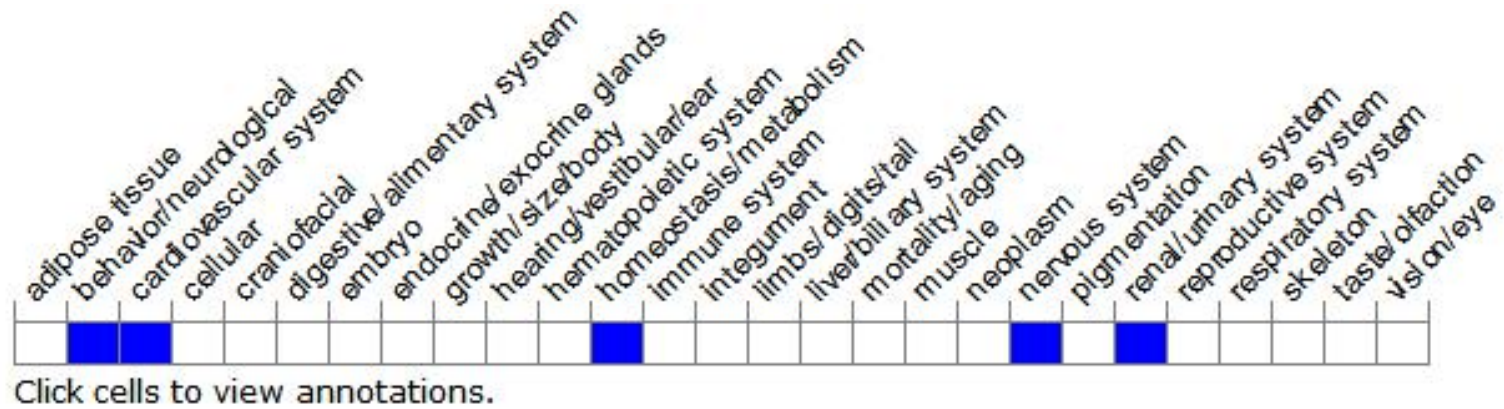
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mutations in this locus affect cell-cycle regulation and apoptosis. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

