Sox1 Cas9-CKO Strategy

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Project Overview

Project Name	***Sox1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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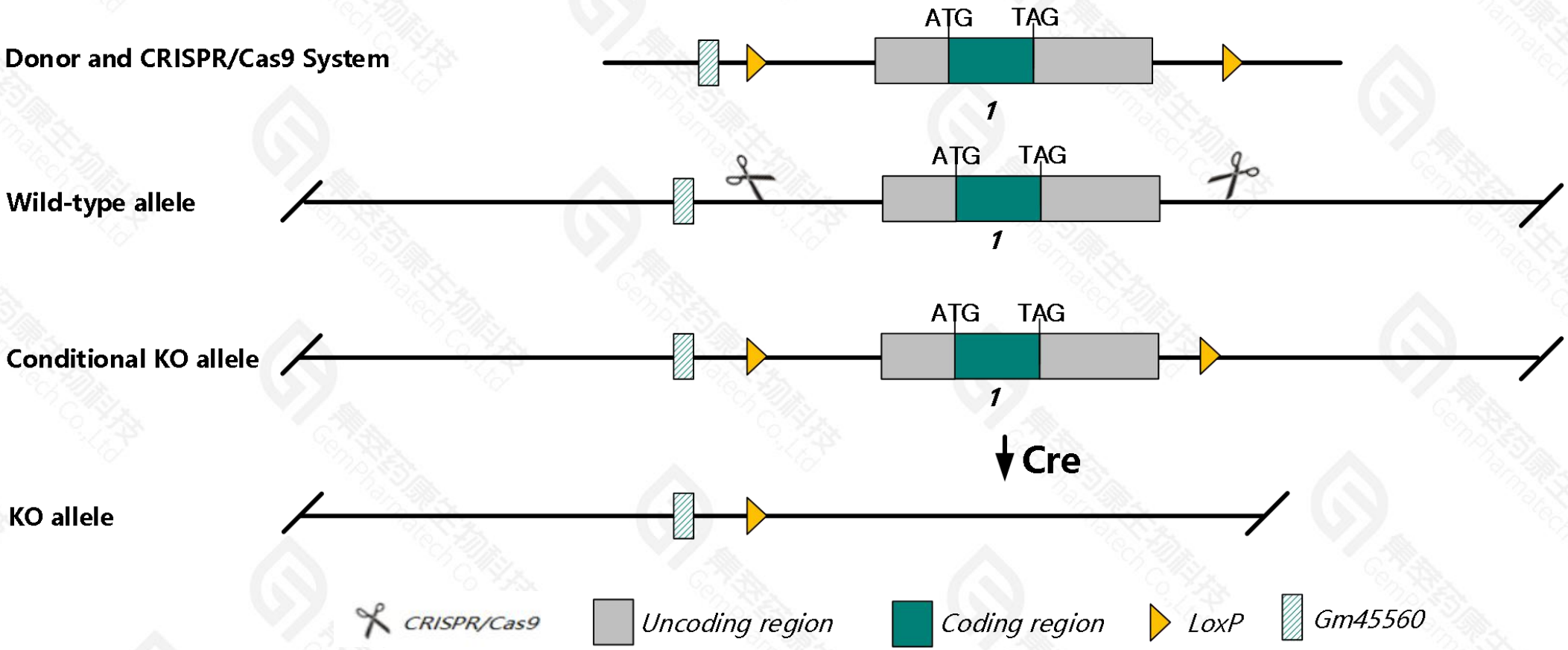
This model will use CRISPR/Cas9 technology to edit the *Sox1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sox1* gene has 1 transcript. According to the structure of *Sox1* gene, exon1 of *Sox1-201*(ENSMUST00000180353.2) 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 *Sox1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.

➢ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ According to the existing MGI data,homozygous null mutants exhibit lens opacity associated with a lack of gamma crystallin expression, microphthalmia, episodic seizures, sexual dysfunction, impaired maternal nurturing, and reduced lifespan.

➢ Insertion sites of loxP are located on both sides of the *Sox1* gene， the insertion of loxP may affect the regulatory function of *Sox1* gene itself.

➢ The KO region contains part of intron of the *Sox1ot* gene. Knockout the region may affect the splicing regulation function of *Sox1ot* gene.

➢ The KO region contains functional region of the *Gm25239* gene. Knockout the region may affect the function of *Gm25239* gene.

➢ The *Sox1* gene is located on the Chr8. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

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Sox1 SRY (sex determining region Y)-box 1 [Mus musculus (house mouse)]

Gene ID: 20664, updated on 13-Mar-2020

Summary

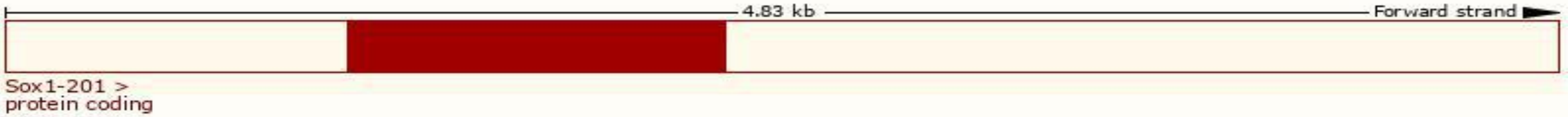
Official Symbol	Sox1 provided by MGI
Official Full Name	SRY (sex determining region Y)-box 1 provided byMGI
Primary source	MGI:MGI:98357
See related	Ensembl:ENSMUSG00000096014
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BB176347, Sox-1
Orthologs	human all

Transcript information（Ensembl）

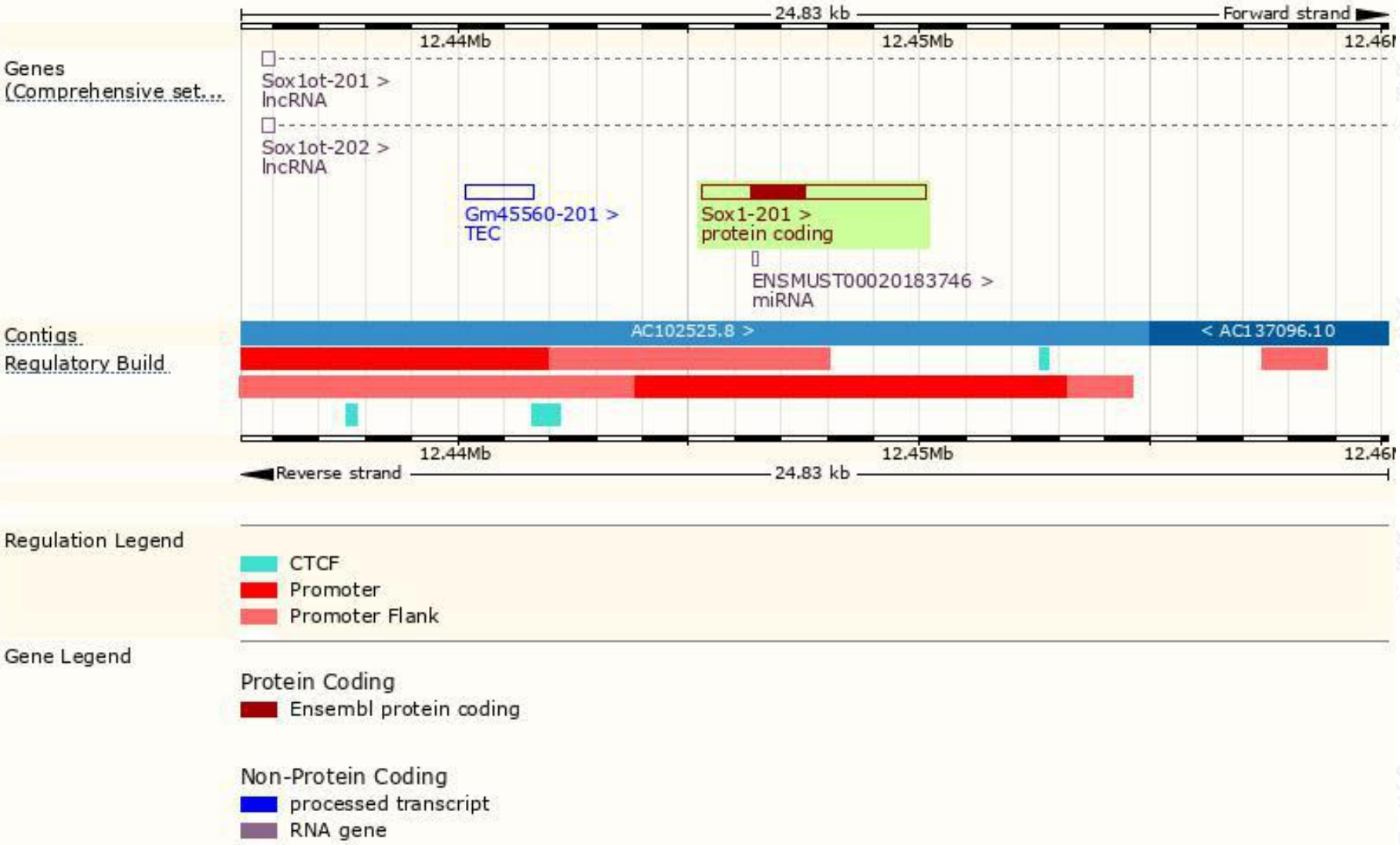
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sox1-201	ENSMUST00000180353.1	4832	391aa	Protein coding	CCDS57605	P53783	TSL:NA GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

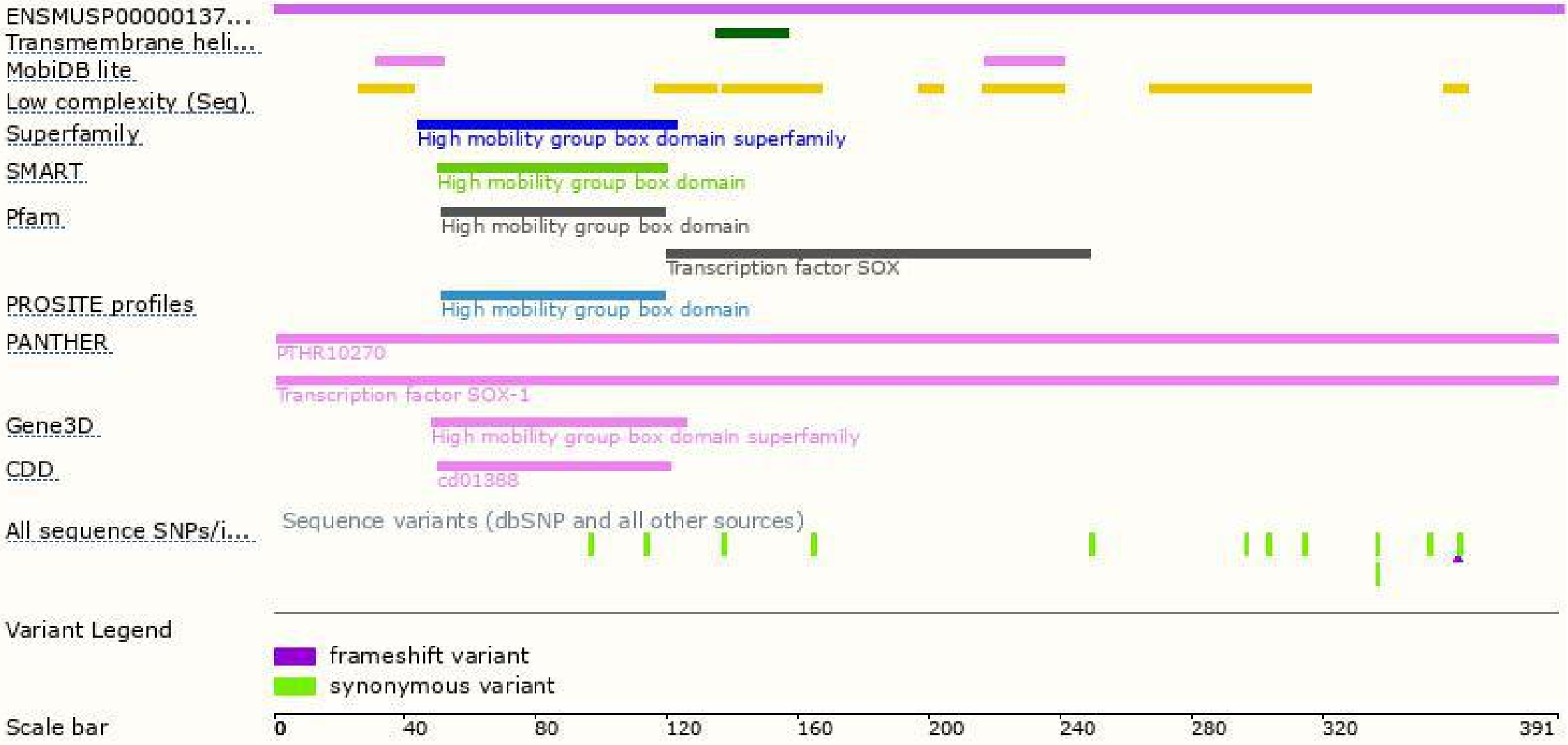
The strategy is based on the design of *Sox1-201* transcript,the transcription is shown below:



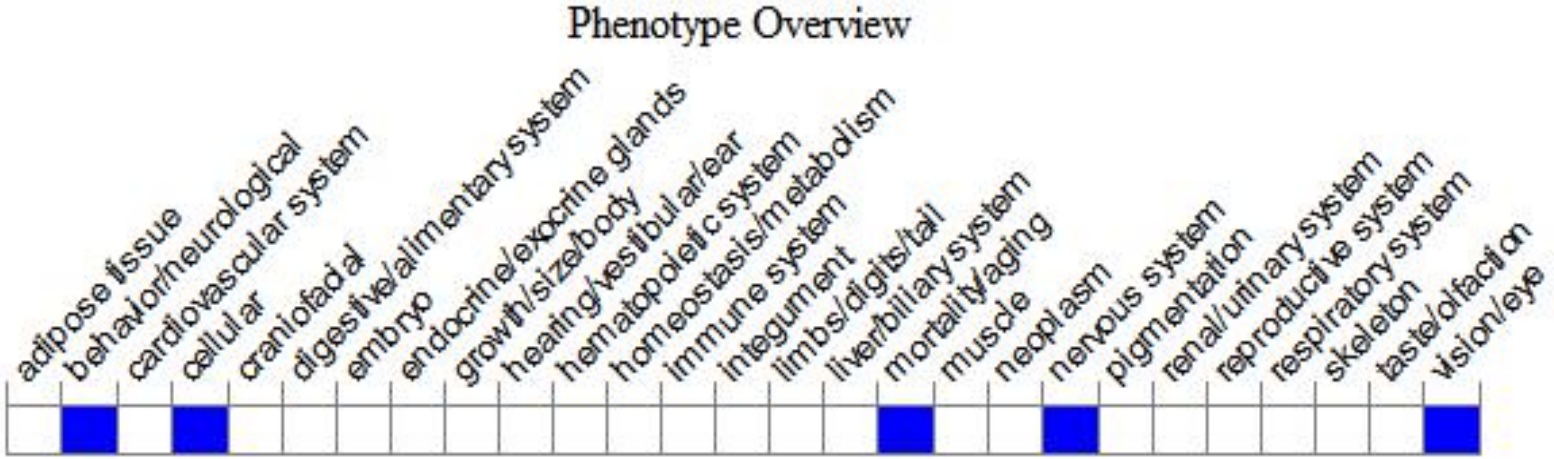
Genomic location distribution



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,homozygous null mutants exhibit lens opacity associated with a lack of gamma crystallin expression, microphthalmia, episodic seizures, sexual dysfunction, impaired maternal nurturing, and reduced lifespan.

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