Bsg Cas9-CKO Strategy

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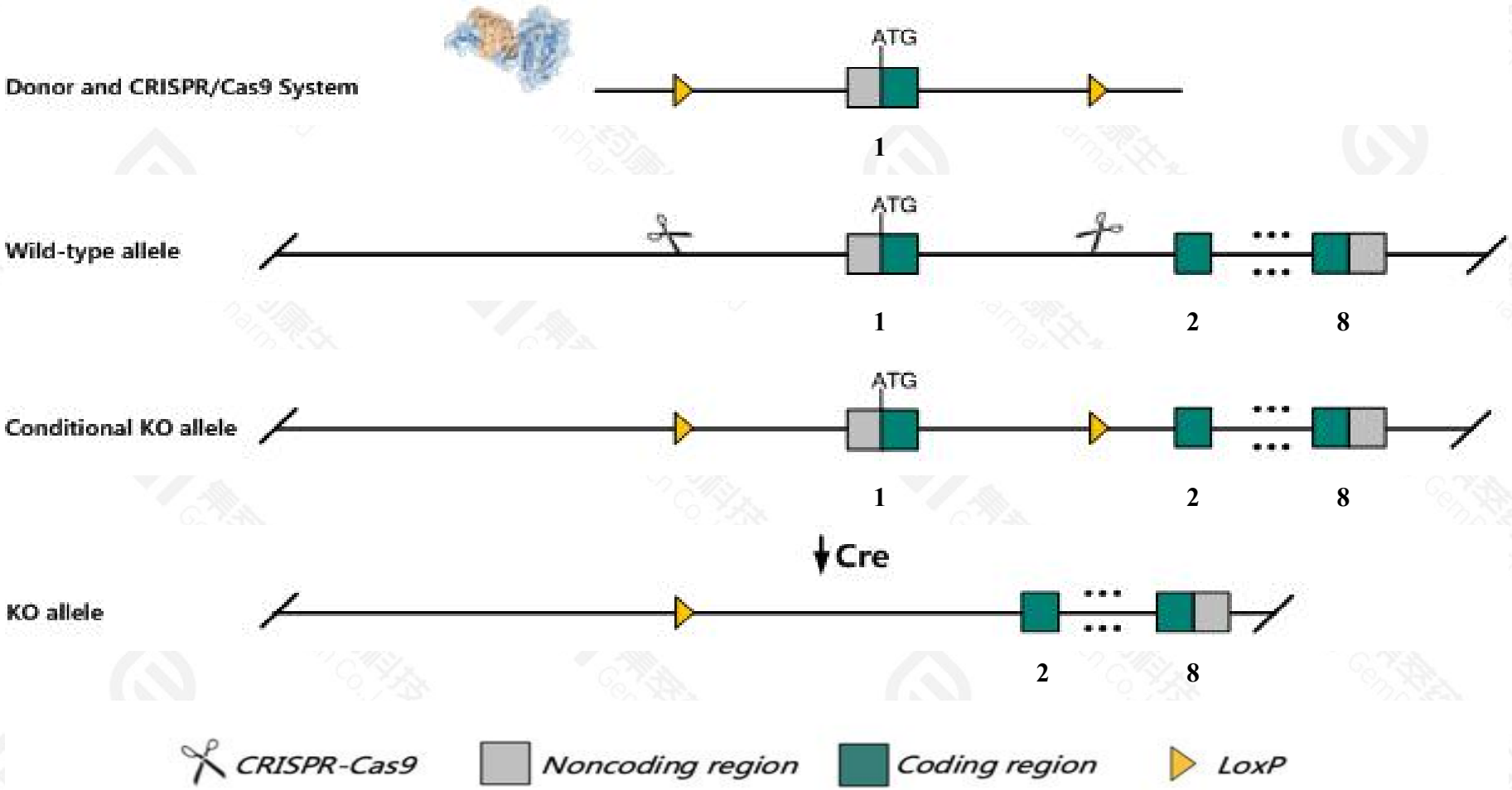
Project Overview

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

Conditional Knockout strategy

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



Technical routes

➢ The *Bsg* gene has 6 transcripts. According to the structure of *Bsg* gene, exon1 of *Bsg-201*(ENSMUST00000067036.12) transcript is recommended as the knockout region.The region contains start codon ATG.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Bsg* 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,most homozygous null mutants die near the time of implantation. Half of the survivors die prior to 1 month of age from interstitial pneumonia. The remaining mice are small, sterile, have retinal abnormalities, and perform poorly in behavioral tests.

➢ The *Bsg*-202 transcript is unaffected and the effect is unknown.

➢ When the target gene is knocked out, the *Gm25794* gene will be destroyed, and the effect is unknown.

➢ The *Bsg* gene is located on the Chr10. 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）

Bsg basigin [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 12215, updated on 10-Apr-2022

Summary

Official Symbol	Bsg provided by MGI
Official Full Name	basigin provided by MGI
Primary source	MGI:MGI:88208
See related	Ensembl:ENSMUSG00000023175 AllianceGenome:MGI:88208
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	HT-7; CD147; EMMPRIN; AI115436; AI325119
Summary	Predicted to enable cell-cell adhesion mediator activity; signaling receptor activity; and virus receptor activity. Involved in neural retina development; photoreceptor cell maintenance; and spermatogenesis. Located in several cellular components, including acrosomal membrane; photoreceptor inner segment; and photoreceptor outer segment. Is expressed in several structures, including alimentary system; brain; early conceptus; reproductive system; and sensory organ. Orthologous to human BSG (basigin (Ok blood group)). [provided by Alliance of Genome Resources, Nov 2021]
Expression	Ubiquitous expression in heart adult (RPKM 307.0), placenta adult (RPKM 296.8) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

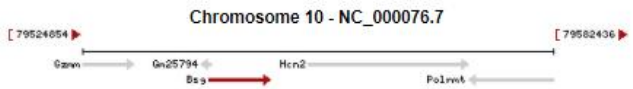
Genomic context

Location: 10 C1; 10 39.72 cM

See Bsg in Genome Data Viewer

Exon count: 8

Annotation release	Status	Assembly	Chr	Location
109	current	GRCm39 (GCF_000001635.27)	10	NC_000076.7 (79540192..79547813)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (79704358..79711979)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (79167103..79174724)

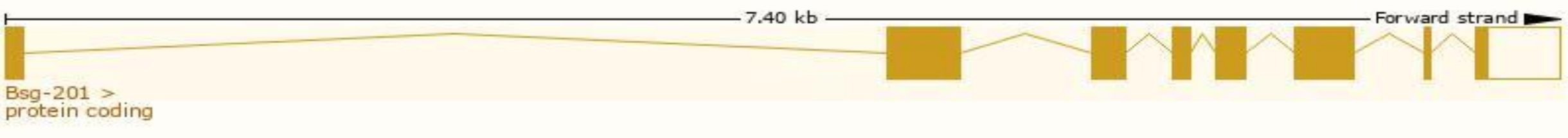


Transcript information（Ensembl）

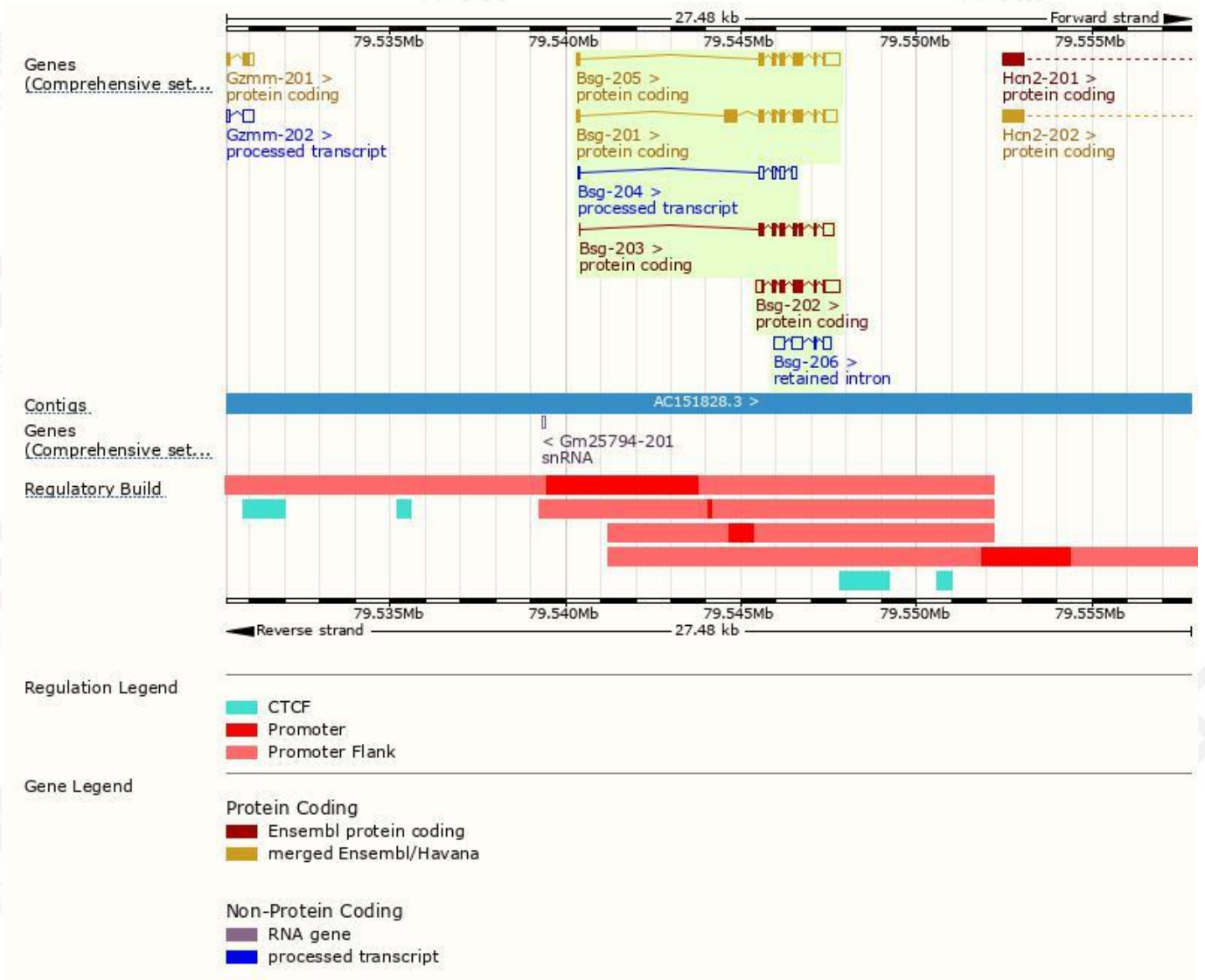
The gene has 6 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000067036.12	Bsg-201	1526	389aa	Protein coding	CCDS23985	P18572-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000179781.8	Bsg-205	1261	273aa	Protein coding	CCDS35967	P18572-2	GENCODE basic TSL:1
ENSMUST00000105381.5	Bsg-202	1240	218aa	Protein coding	-	K3W4Q8	GENCODE basic TSL:1
ENSMUST00000178383.8	Bsg-203	921	197aa	Protein coding	-	J3QP71	TSL:5 CDS 5' incomplete
ENSMUST00000179201.2	Bsg-204	564	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000180235.2	Bsg-206	836	No protein	Retained intron	-	-	TSL:3

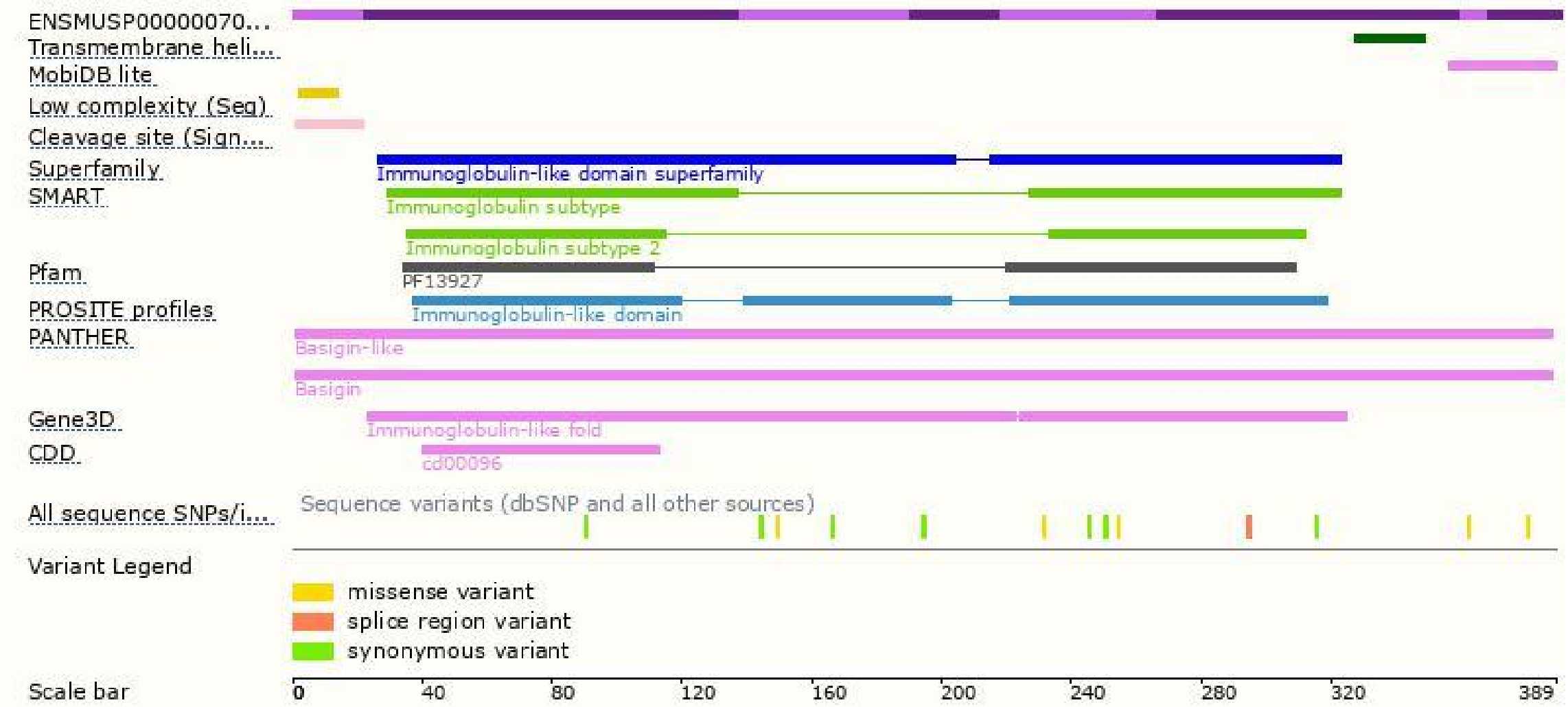
The strategy is based on the design of *Bsg-201* transcript,the transcription is shown below:



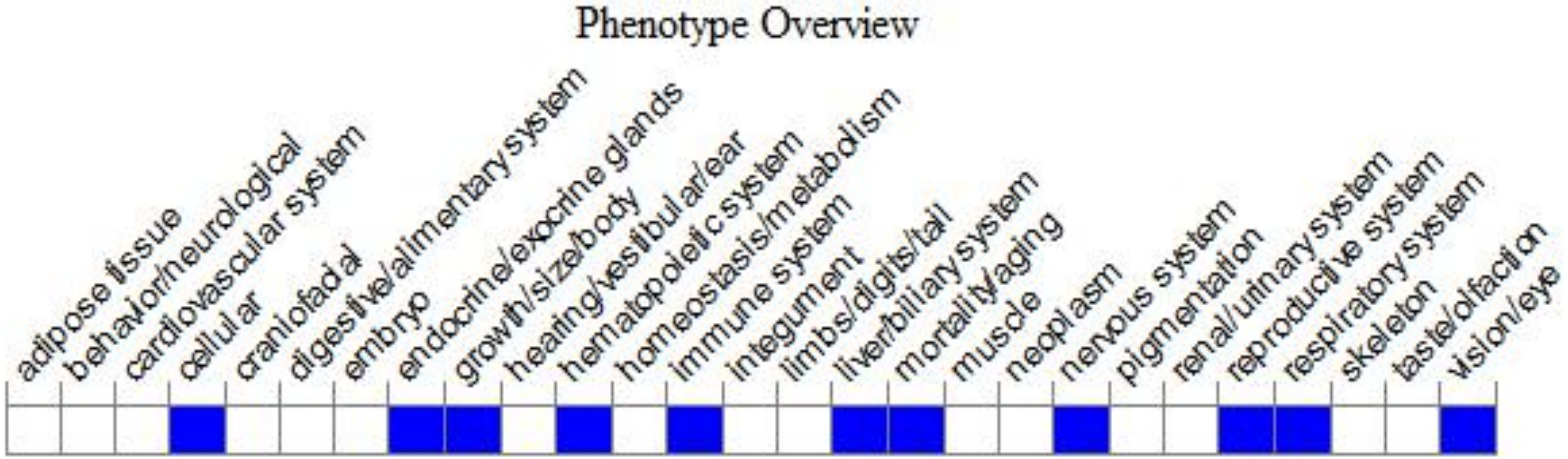
Genomic location distribution



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,most homozygous null mutants die near the time of implantation. Half of the survivors die prior to 1 month of age from interstitial pneumonia. The remaining mice are small, sterile, have retinal abnormalities, and perform poorly in behavioral tests.

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