

Stab2 Cas9-KO Strategy

Designer:

Daohua Xu

Project Overview



Project Name

Stab2

Project type

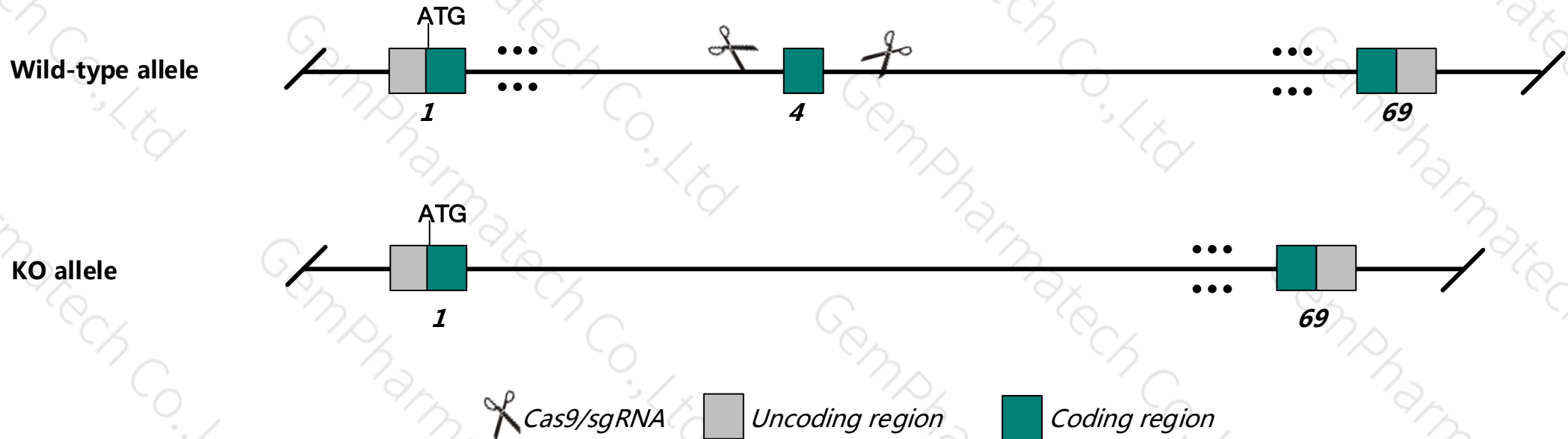
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stab2* gene. The schematic diagram is as follows:



Technical routes

- The *Stab2* gene has 7 transcripts. According to the structure of *Stab2* gene, exon4 of *Stab2*-201 transcript is recommended as the knockout region. The region contains 86bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stab2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Stab2* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Stab2 stabilin 2 [*Mus musculus* (house mouse)]

Gene ID: 192188, updated on 31-Jan-2019

Summary

Official Symbol	Stab2 provided by MGI
Official Full Name	stabilin 2 provided by MGI
Primary source	MGI:MGI:2178743
See related	Ensembl:ENSMUSG00000035459
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FELL; FEEL-2; STAB-2; MFEEL-2
Annotation information	Annotation category: partial on reference assembly
Expression	Biased expression in spleen adult (RPKM 16.0), liver E18 (RPKM 6.2) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

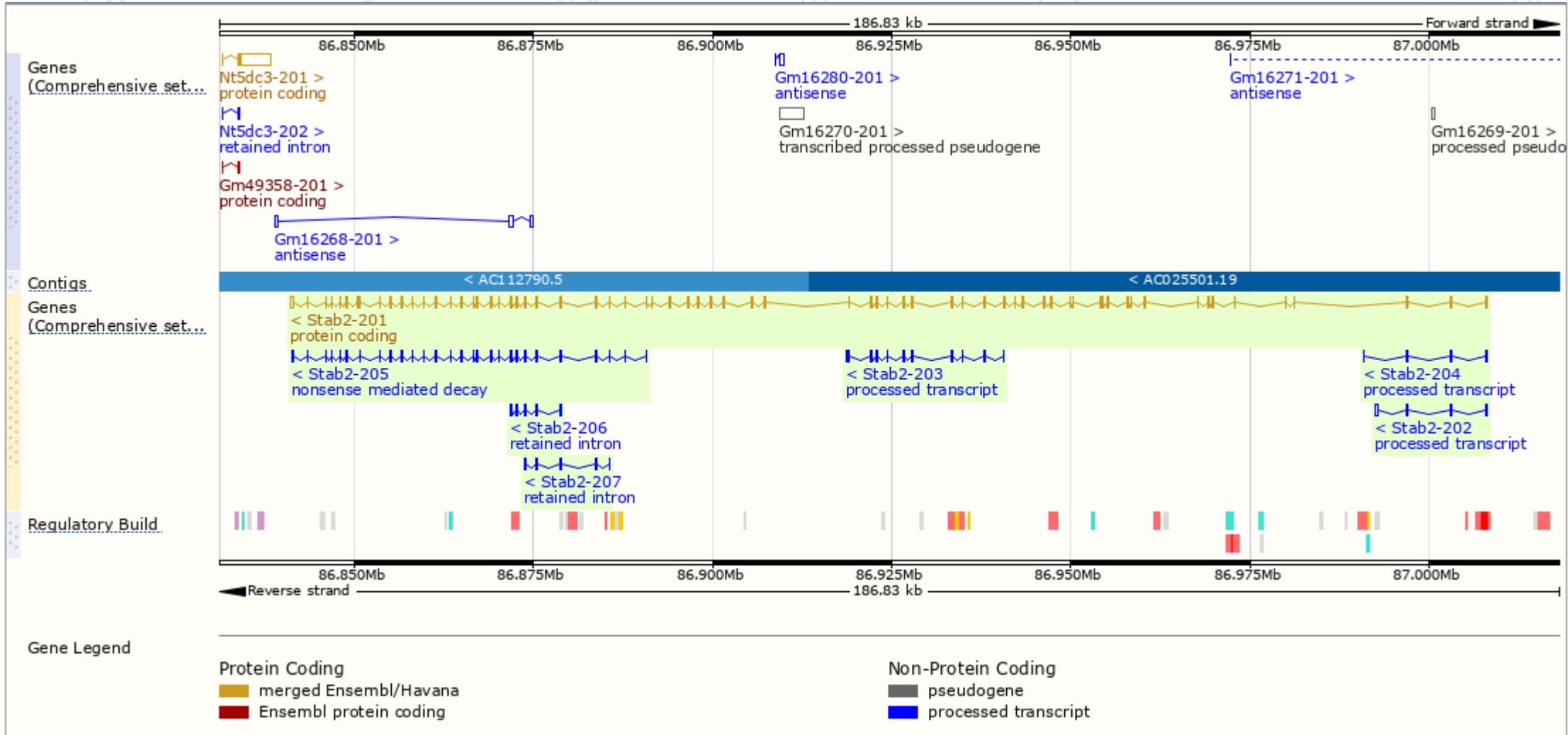
The gene has 7 transcripts, and all transcripts are shown below :

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Stab2-201	ENSMUST00000035288.16	8228	2559aa	Protein coding	CCDS36021	E5RKF9 Q8R4U0	TSL:1	GENCODE basic APPRIS P1
Stab2-205	ENSMUST00000219341.2	3502	870aa	Nonsense mediated decay	-	A0A1W2P6Y4	CDS 5' incomplete	TSL:5
Stab2-203	ENSMUST00000218408.1	1237	No protein	Processed transcript	-	-	TSL:1	
Stab2-202	ENSMUST00000218366.1	720	No protein	Processed transcript	-	-	TSL:1	
Stab2-204	ENSMUST00000219280.1	523	No protein	Processed transcript	-	-	TSL:3	
Stab2-206	ENSMUST00000219612.1	502	No protein	Retained intron	-	-	TSL:3	
Stab2-207	ENSMUST00000219659.1	442	No protein	Retained intron	-	-	TSL:5	

The strategy is based on the design of *Stab2-201* transcript,The transcription is shown below



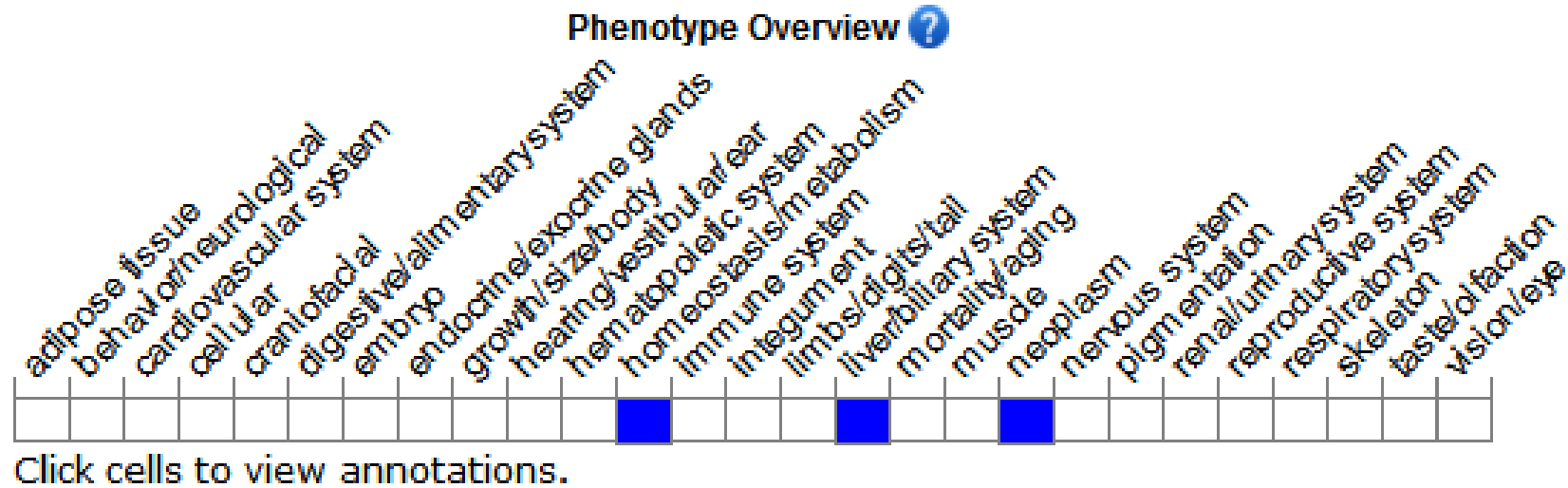
Genomic location distribution



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, Mice homozygous for knock-out alleles exhibit no gross abnormalities.

Mice homozygous for one null allele display elevated serum hyaluronic acid levels and decreased metastasis.

If you have any questions, you are welcome to inquire.
Tel: 025-5864 1534

