

Stam Cas9-KO Strategy

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Project Overview

Project Name

Stam

Project type

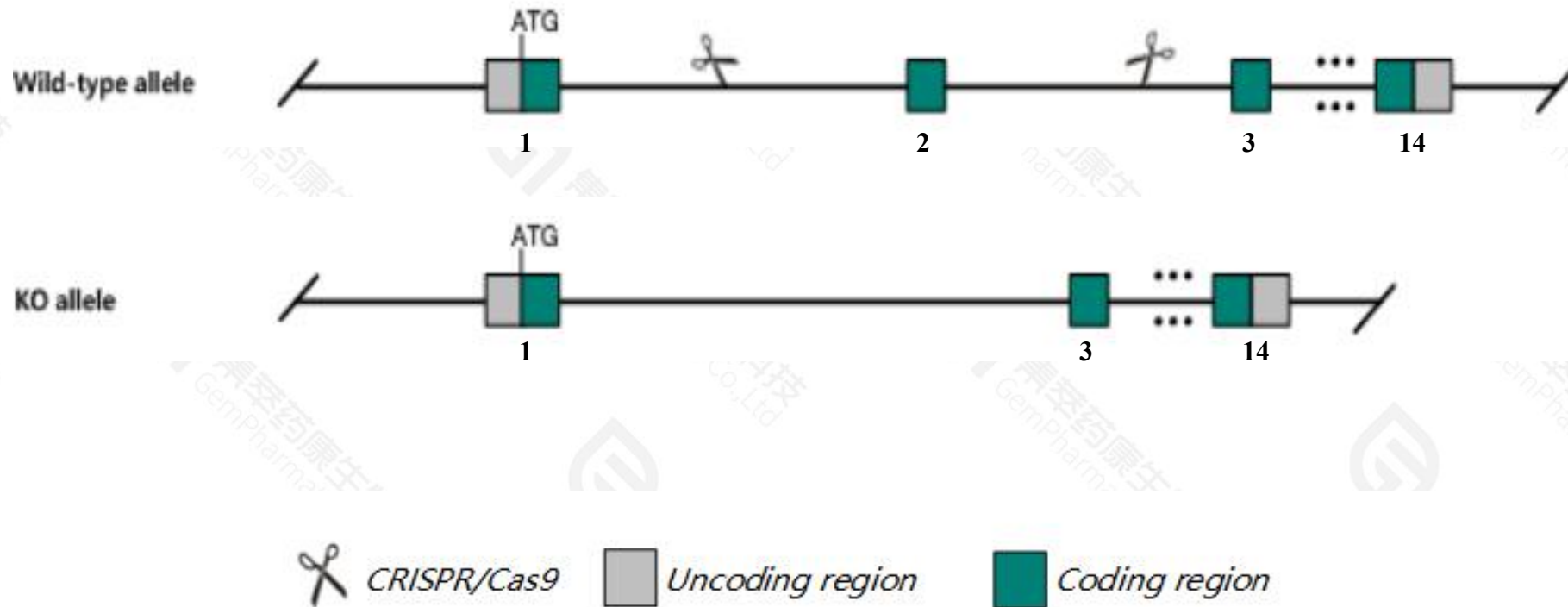
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Stam* gene has 9 transcripts. According to the structure of *Stam* gene, exon2 of *Stam-202*(ENSMUST00000102960.11) transcript is recommended as the knockout region. The region contains 85bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stam* gene. The brief process is as follows: CRISPR/Cas9 system 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 a targeted null mutation exhibit progressive growth retardation, priapism, male infertility, degeneration of hippocapal CA3 pyramidal neurons and premature death, but exhibit normal lymphocyte development, proliferation and responses.
- The *Stam* gene is located on the Chr2. 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.

Stam signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 [Mus musculus (house mouse)]

Gene ID: 20844, updated on 13-Dec-2020

Summary



Official Symbol	Stam provided by MGI
Official Full Name	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 provided by MGI
Primary source	MGI:MGI:1329014
See related	Ensembl:ENSMUSG00000026718
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	STA, STAM1
Expression	Ubiquitous expression in CNS E18 (RPKM 14.5), whole brain E14.5 (RPKM 13.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

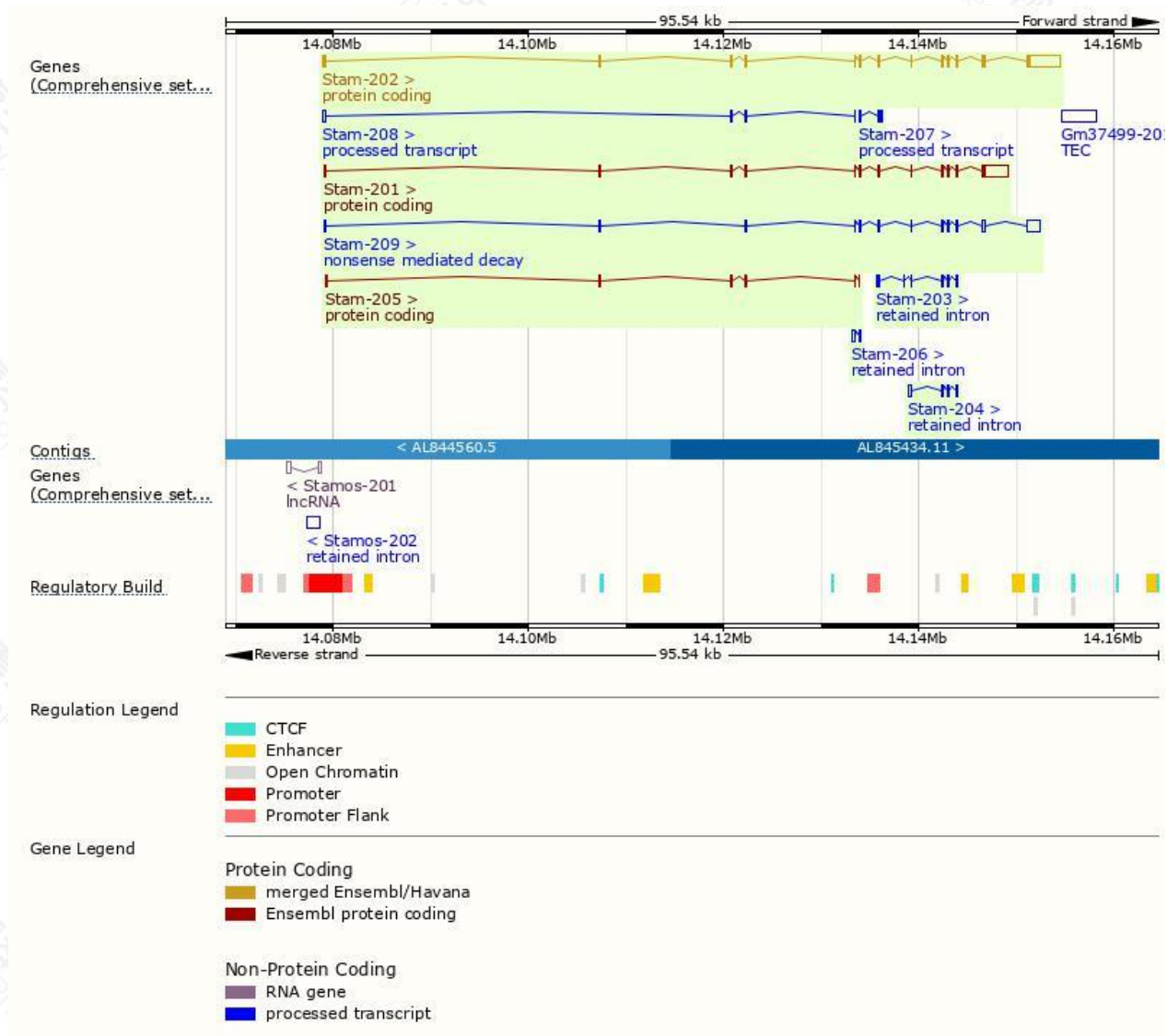
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stam-202	ENSMUST00000102960.11	5000	548aa	Protein coding	CCDS15698		TSL:1 , GENCODE basic , APPRIS P2 ,
Stam-201	ENSMUST00000028050.14	3981	462aa	Protein coding	-		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Stam-205	ENSMUST00000138989.2	711	207aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Stam-209	ENSMUST00000193636.6	2610	50aa	Nonsense mediated decay	-		TSL:5 ,
Stam-208	ENSMUST00000156901.2	616	No protein	Processed transcript	-		TSL:3 ,
Stam-207	ENSMUST00000144944.8	386	No protein	Processed transcript	-		TSL:3 ,
Stam-203	ENSMUST00000128777.7	652	No protein	Retained intron	-		TSL:1 ,
Stam-204	ENSMUST00000131734.3	632	No protein	Retained intron	-		TSL:2 ,
Stam-206	ENSMUST00000140694.2	490	No protein	Retained intron	-		TSL:3 ,

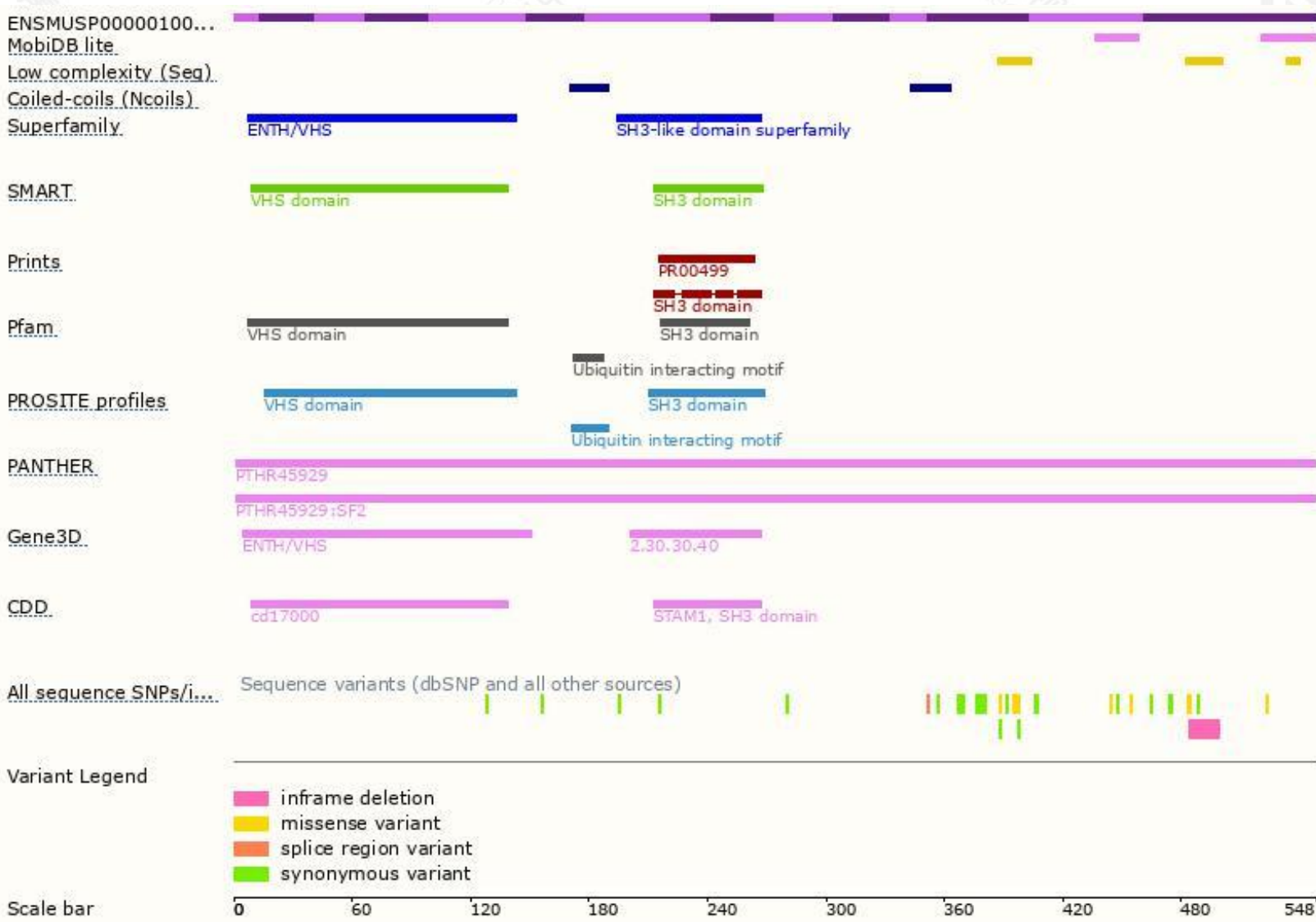
The strategy is based on the design of *Stam-202* transcript,the transcription is shown below:



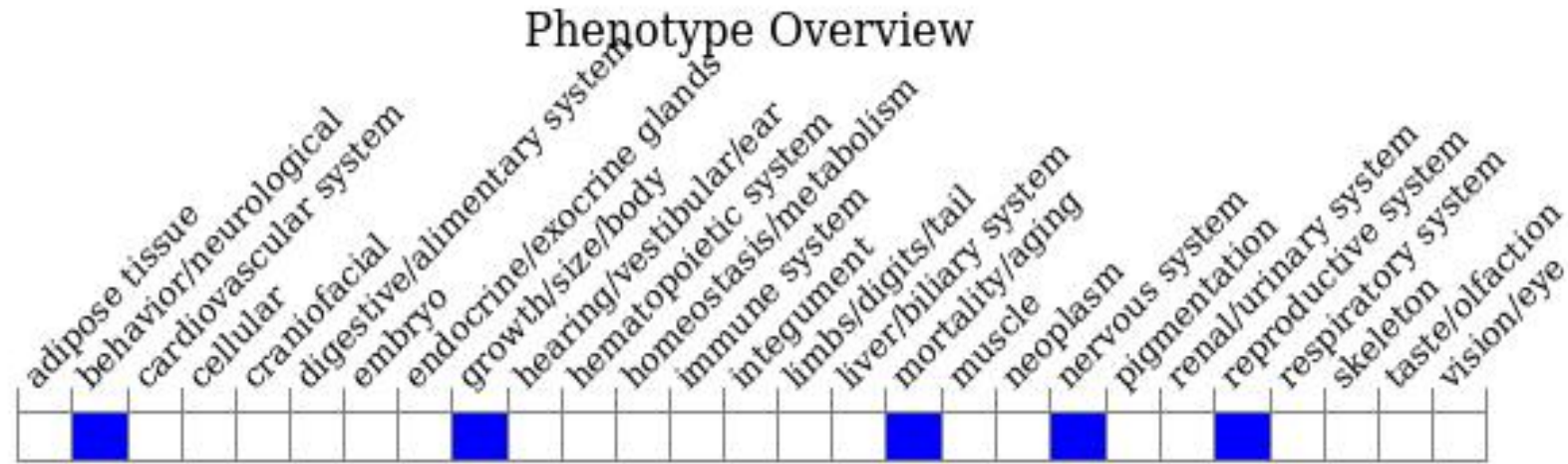
Genomic location distribution



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 a targeted null mutation exhibit progressive growth retardation, priapism, male infertility, degeneration of hippocampal CA3 pyramidal neurons and premature death, but exhibit normal lymphocyte development, proliferation and responses.

If you have any questions, you are welcome to inquire.
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