

Sh3bp2 Cas9-KO Strategy

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Project Overview



Project Name

Sh3bp2

Project type

Cas9-KO

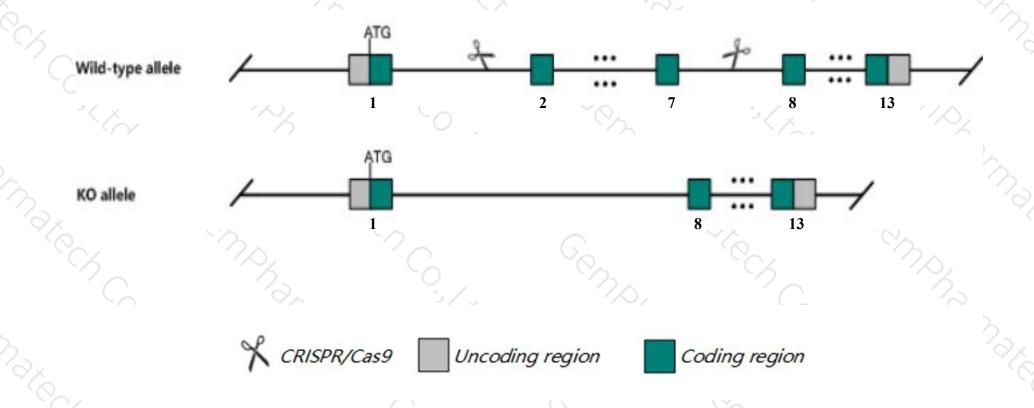
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Sh3bp2 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Sh3bp2* gene has 8 transcripts. According to the structure of *Sh3bp2* gene, exon2-exon7 of *Sh3bp2*-203(ENSMUST00000118545.7) transcript is recommended as the knockout region. The region contains 590bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Sh3bp2* 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.

Notice



- > According to the existing MGI data, nullizygous mutations may lead to higher pre-B cell numbers and impaired B cell receptor signaling or thymus-independent type 2 humoral responses. Homozygosity for a knock-in allele causes premature death, enhanced osteoclast differentiation and TNF production, systemic bone loss and inflammation.
- > The Sh3bp2 gene is located on the Chr5. 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.

Gene information (NCBI)



Sh3bp2 SH3-domain binding protein 2 [Mus musculus (house mouse)]

Gene ID: 24055, updated on 13-Mar-2020





Official Symbol Sh3bp2 provided by MGI

Official Full Name SH3-domain binding protein 2 provided by MGI

Primary source MGI:MGI:1346349

See related <u>Ensembl:ENSMUSG00000054520</u>

Gene type protein coding

RefSeq status VALIDATED

Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as 3BP2

Expression Ubiquitous expression in spleen adult (RPKM 19.5), CNS E14 (RPKM 11.0) and 25 other tissuesSee more

Orthologs <u>human</u> <u>all</u>

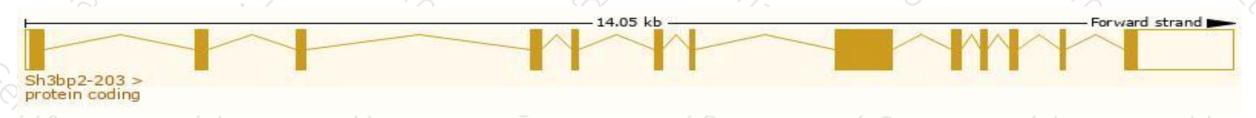
Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

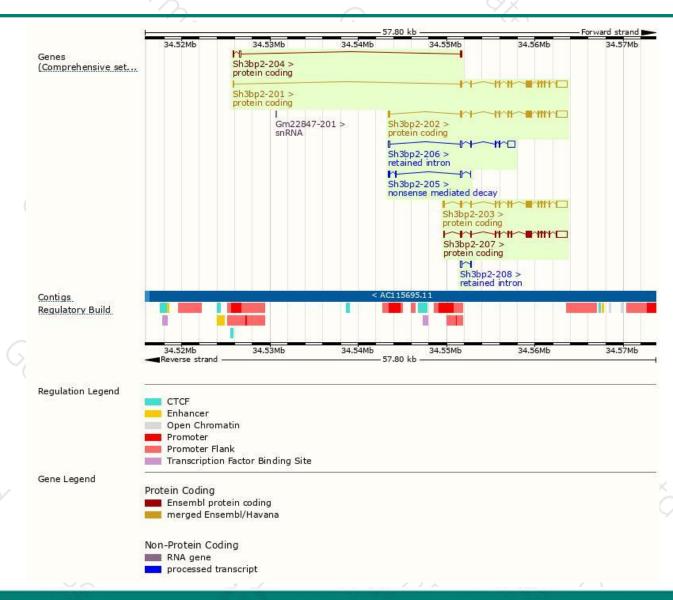
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|-----------------------|------|--------------|-------------------------|-----------|---------|---------------------------------|
| Sh3bp2-203 | ENSMUST00000118545.7 | 3034 | <u>615aa</u> | Protein coding | CCDS51470 | E9QJU7 | TSL:1 GENCODE basic APPRIS ALT2 |
| Sh3bp2-202 | ENSMUST00000101316.9 | 3031 | 603aa | Protein coding | CCDS51469 | Q3UD40 | TSL:1 GENCODE basic APPRIS ALT2 |
| Sh3bp2-207 | ENSMUST00000179943.2 | 2935 | <u>559aa</u> | Protein coding | CCDS19215 | Q5U3L0 | TSL:1 GENCODE basic APPRIS P3 |
| Sh3bp2-201 | ENSMUST00000067638.13 | 2885 | <u>559aa</u> | Protein coding | CCDS19215 | Q5U3L0 | TSL:1 GENCODE basic APPRIS P3 |
| Sh3bp2-204 | ENSMUST00000125817.7 | 416 | <u>45aa</u> | Protein coding | 14 | D3Z107 | CDS 3' incomplete TSL:2 |
| Sh3bp2-205 | ENSMUST00000138912.7 | 431 | <u>46aa</u> | Nonsense mediated decay | | D6RDU0 | TSL:5 |
| Sh3bp2-206 | ENSMUST00000153750.2 | 1481 | No protein | Retained intron | | -2 | TSL:1 |
| Sh3bp2-208 | ENSMUST00000202745.1 | 212 | No protein | Retained intron | _ | 24 | TSL:5 |

The strategy is based on the design of *Sh3bp2-203* transcript, the transcription is shown below:



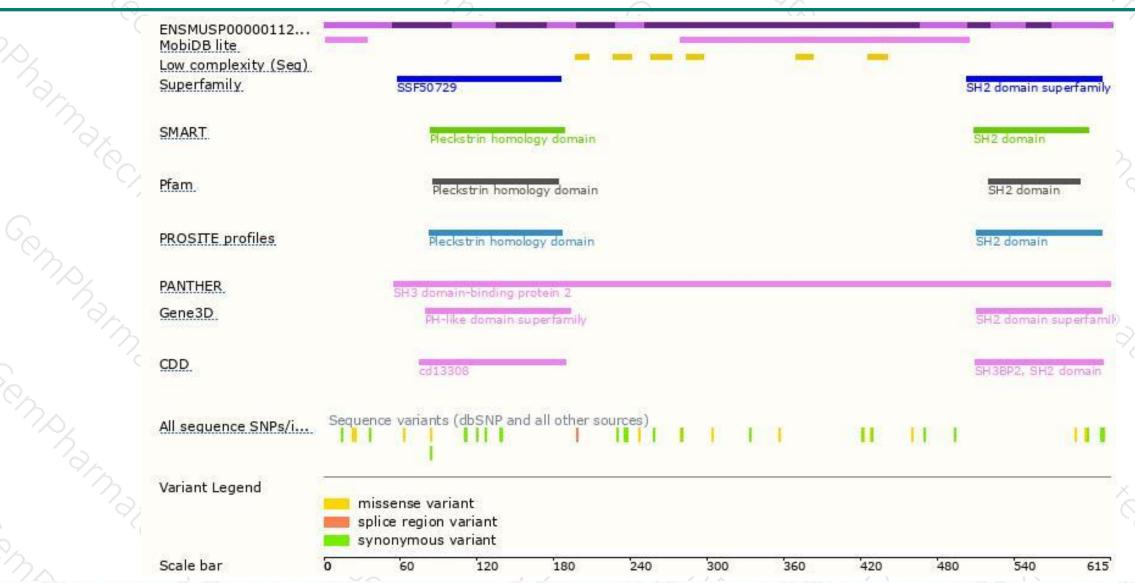
Genomic location distribution





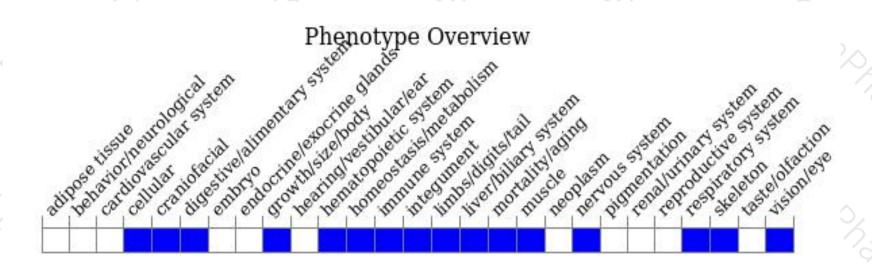
Protein domain





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,nullizygous mutations may lead to higher pre-B cell numbers and impaired B cell receptor signaling or thymus-independent type 2 humoral responses. Homozygosity for a knock-in allele causes premature death, enhanced osteoclast differentiation and TNF production, systemic bone loss and inflammation.



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





