Hspa8 Cas9-KO Strategy

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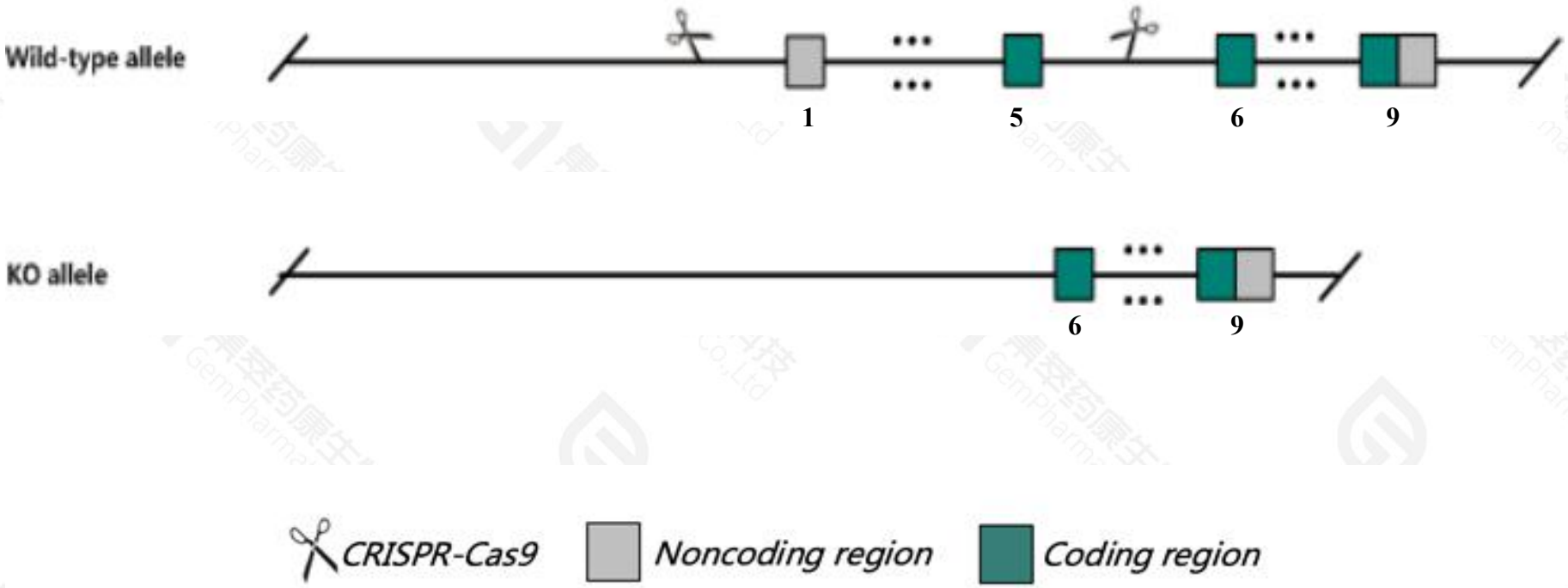
Project Overview

Project Name	***Hspa8***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Hspa8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hspa8* gene has 10 transcripts. According to the structure of *Hspa8* gene, exon1-exon5 of *Hspa8-201*(ENSMUST00000015800.16) 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 *Hspa8* 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

➢ Knockout the region may affect the function *Snord14d-201* gene and destroy *Snord14c* gene.

➢ The *Hspa8* gene is located on the Chr9. 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）

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Hspa8 heat shock protein 8 [Mus musculus (house mouse)]

Gene ID: 15481, updated on 13-Mar-2020

Summary

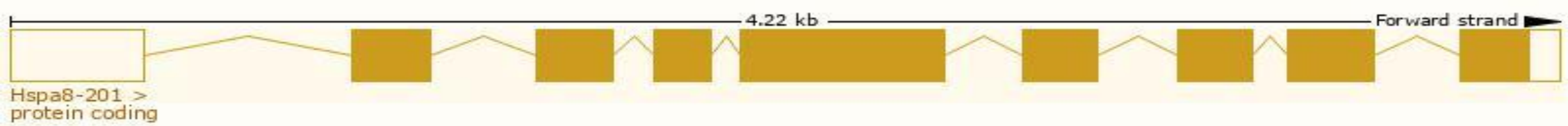
Official Symbol	Hspa8 provided by MGI
Official Full Name	heat shock protein 8 provided by MGI
Primary source	MGI:MGI:105384
See related	Ensembl:ENSMUSG00000015656
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410008N15Rik, Hsc70, Hsc71, Hsc73, Hsp73, Hspa10
Expression	Ubiquitous expression in placenta adult (RPKM 956.1), CNS E11.5 (RPKM 802.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

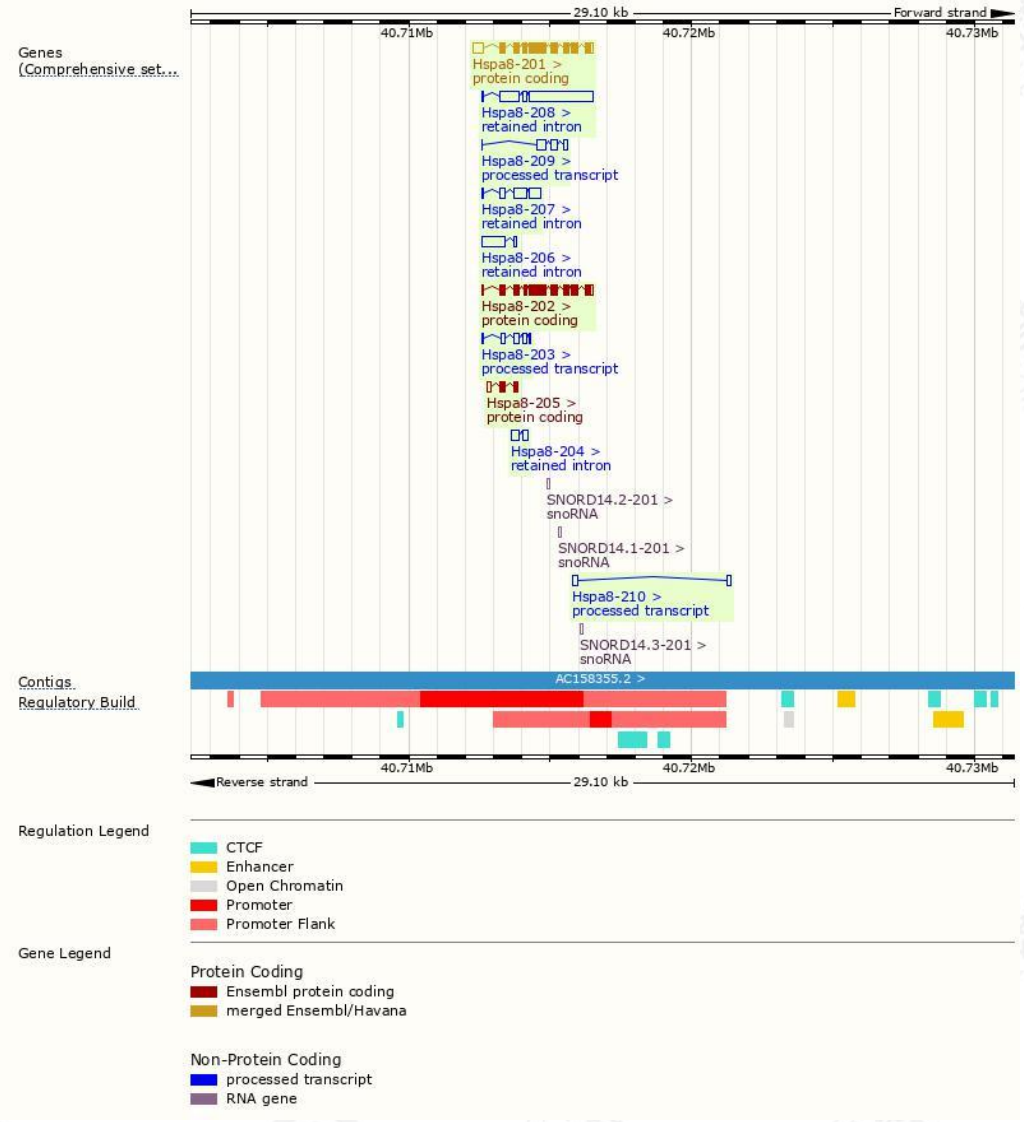
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hspa8-201	ENSMUST00000015800.15	2394	646aa	Protein coding	CCDS23083	P63017	TSL:1 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
Hspa8-202	ENSMUST00000117557.7	2019	627aa	Protein coding	-	Q504P4	TSL:1 GENCODE basic
Hspa8-205	ENSMUST00000133964.1	514	116aa	Protein coding	-	D3Z5E2	CDS 3' incomplete TSL:2
Hspa8-209	ENSMUST00000153847.1	727	No protein	Processed transcript	-	-	TSL:5
Hspa8-203	ENSMUST00000117870.8	598	No protein	Processed transcript	-	-	TSL:3
Hspa8-210	ENSMUST00000215526.1	357	No protein	Processed transcript	-	-	TSL:5
Hspa8-208	ENSMUST00000149936.1	3158	No protein	Retained intron	-	-	TSL:1
Hspa8-207	ENSMUST00000140984.1	1152	No protein	Retained intron	-	-	TSL:5
Hspa8-206	ENSMUST00000138895.1	920	No protein	Retained intron	-	-	TSL:1
Hspa8-204	ENSMUST00000127699.1	456	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Hspa8-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain

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