Hspa12a Cas9-KO Strategy

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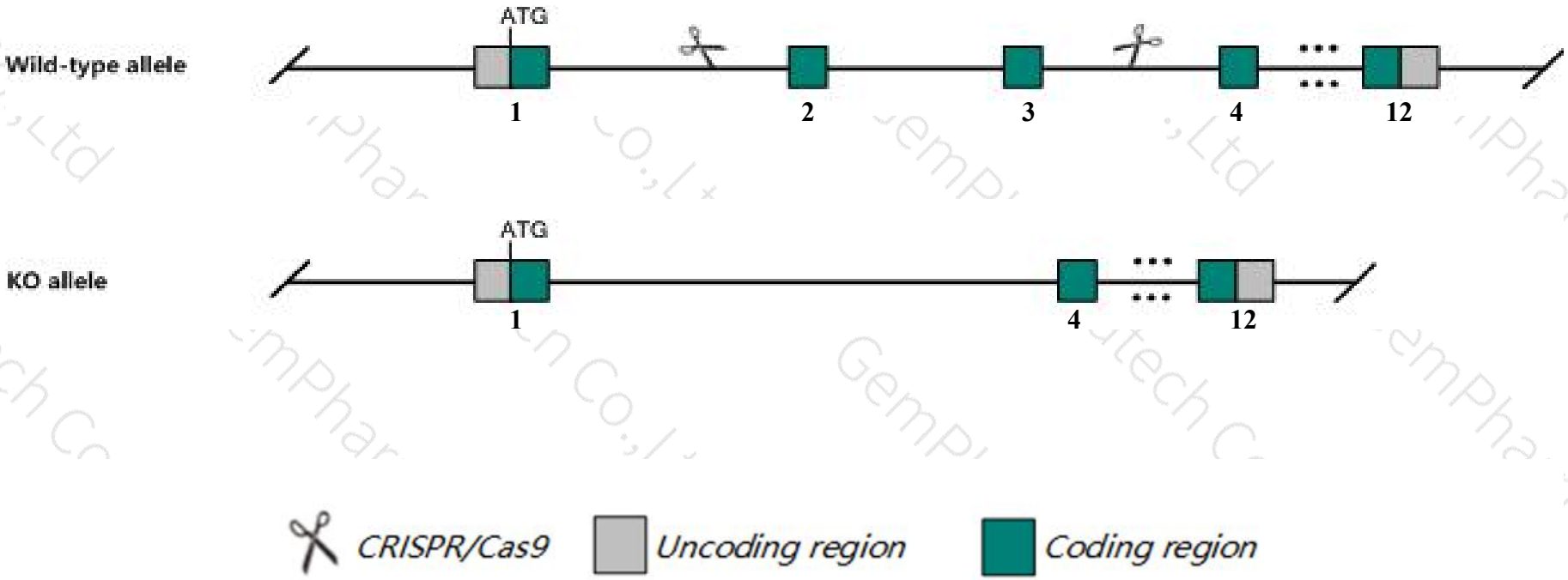
Project Overview

Project Name	***Hspa12a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hspa12a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hspa12a* gene has 10 transcripts. According to the structure of *Hspa12a* gene, exon2-exon3 of *Hspa12a-201* (ENSMUST00000066285.5) transcript is recommended as the knockout region.The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hspa12a* gene. The brief process is as follows: CRISPR/Cas9 syst

Notice

➢ The *Hspa12a* gene is located on the Chr19. 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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Hspa12a heat shock protein 12A [Mus musculus (house mouse)]

Gene ID: 73442, updated on 7-Apr-2019

Summary

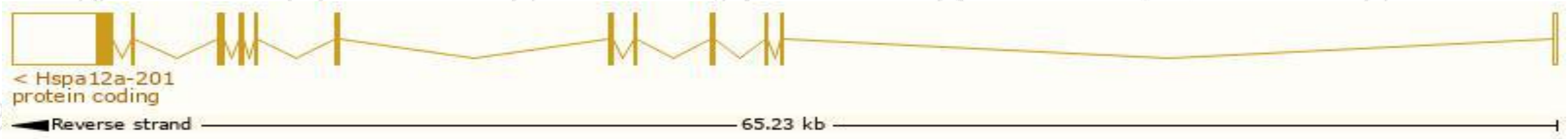
Official Symbol	Hspa12a provided by MGI
Official Full Name	heat shock protein 12A provided byMGI
Primary source	MGI:MGI:1920692
See related	Ensembl:ENSMUSG00000025092
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700063D12Rik, AI118035, AI840429, AW048913, AW556406, D5Mgi40, Gm19925, mKIAA0417
Expression	Broad expression in cortex adult (RPKM 20.3), CNS E18 (RPKM 18.9) and 20 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

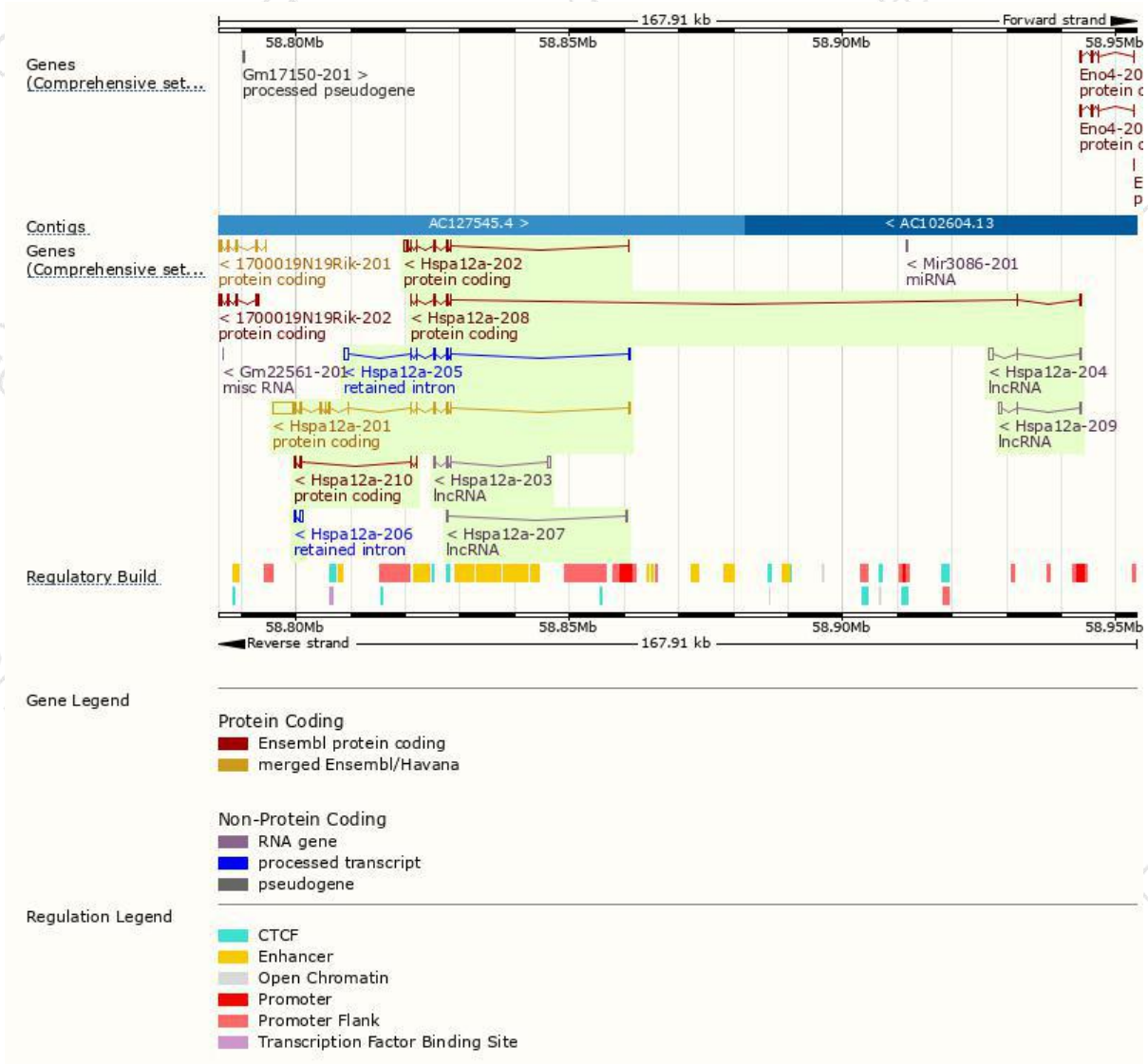
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hspa12a-201	ENSMUST00000066285.5	5734	675aa	Protein coding	CCDS38032	Q8K0U4	TSL:1 GENCODE basic APPRIS P1
Hspa12a-202	ENSMUST00000235263.1	1400	222aa	Protein coding	-	-	GENCODE basic
Hspa12a-208	ENSMUST00000237297.1	877	227aa	Protein coding	-	-	CDS 3' incomplete
Hspa12a-210	ENSMUST00000238055.1	596	199aa	Protein coding	-	-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Hspa12a-205	ENSMUST00000236429.1	1510	No protein	Retained intron	-	-	
Hspa12a-206	ENSMUST00000236453.1	748	No protein	Retained intron	-	-	
Hspa12a-204	ENSMUST00000235791.1	861	No protein	lncRNA	-	-	
Hspa12a-203	ENSMUST00000235662.1	754	No protein	lncRNA	-	-	
Hspa12a-209	ENSMUST00000237786.1	612	No protein	lncRNA	-	-	
Hspa12a-207	ENSMUST00000236839.1	377	No protein	lncRNA	-	-	

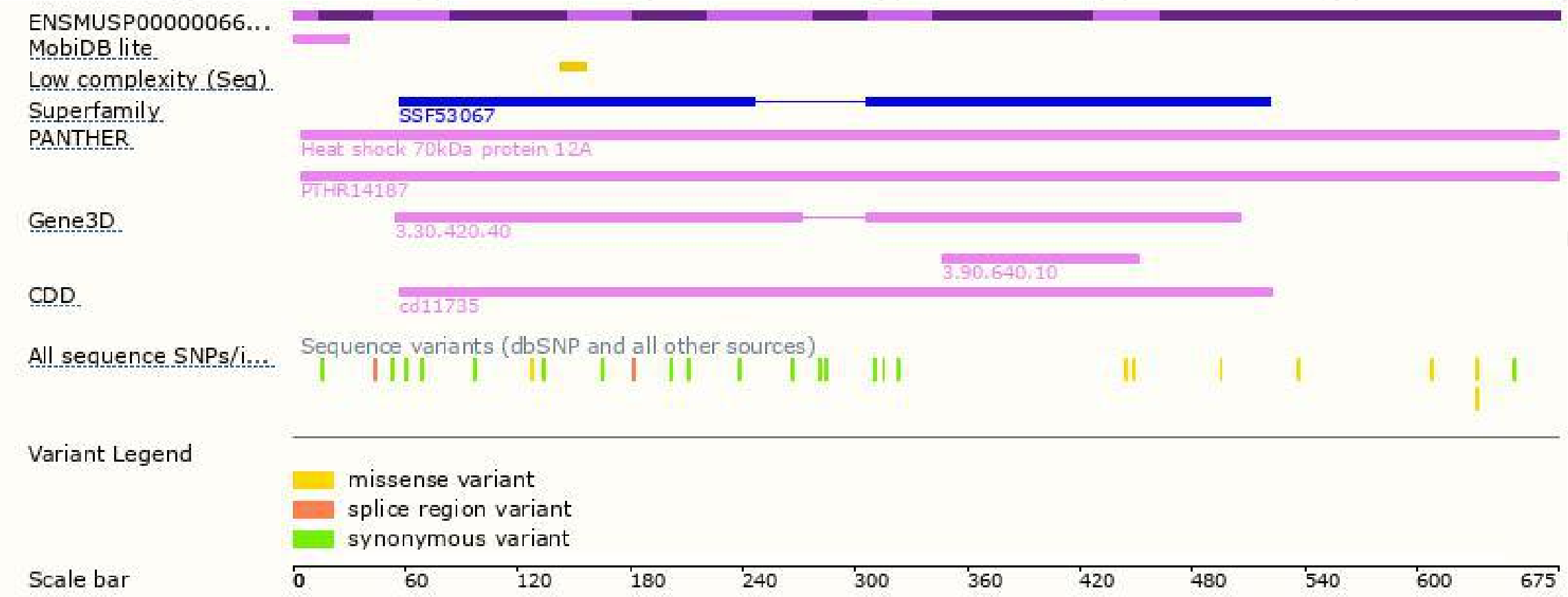
The strategy is based on the design of *Hspa12a-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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