Hspa5 Cas9-KO Strategy

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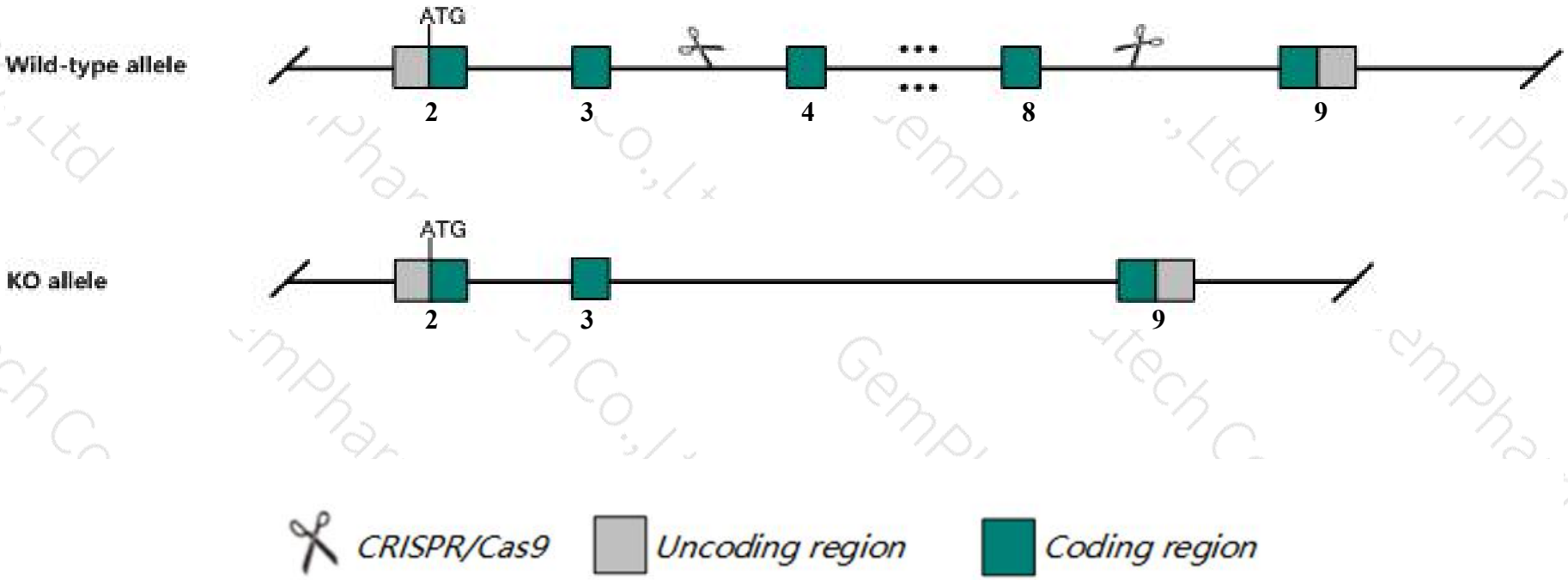
Design Date: 2019-9-30

Project Overview

Project Name	***Hspa5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hspa5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hspa5* gene has 6 transcripts. According to the structure of *Hspa5* gene, exon4-exon8 of *Hspa5-201* (ENSMUST00000028222.12) transcript is recommended as the knockout region.The region contains 1048bp coding sequenc Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hspa5* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Nullizygous embryos die around implantation. Neonates homozygous for a knock-in allele die of respiratory failure. Mice homozygous for an ENU-induced mutation exhibit abnormal thalamocortical axon patterning, small kidneys, cleft palate, respiratory distress, and postnatal lethality.

- The *Hspa5* 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.

Gene information（NCBI）

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Hspa5 heat shock protein 5 [Mus musculus (house mouse)]

Gene ID: 14828, updated on 7-Apr-2019

Summary

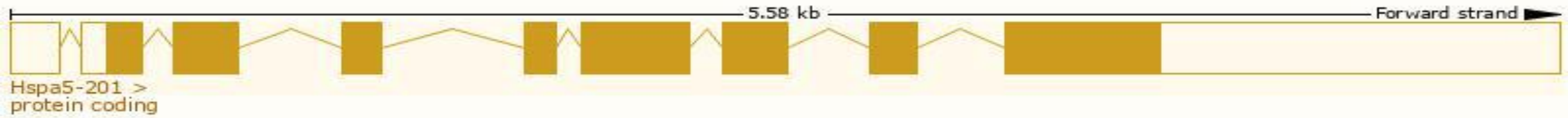
Official Symbol	Hspa5 provided by MGI
Official Full Name	heat shock protein 5 provided by MGI
Primary source	MGI:MGI:95835
See related	Ensembl:ENSMUSG00000026864
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AL022860, AU019543, Bip, D2Wsu141e, D2Wsu17e, Grp78, Hsce70, SEZ-7, Sez7, baffled, mBiP
Expression	Ubiquitous expression in placenta adult (RPKM 321.6), genital fat pad adult (RPKM 154.1) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

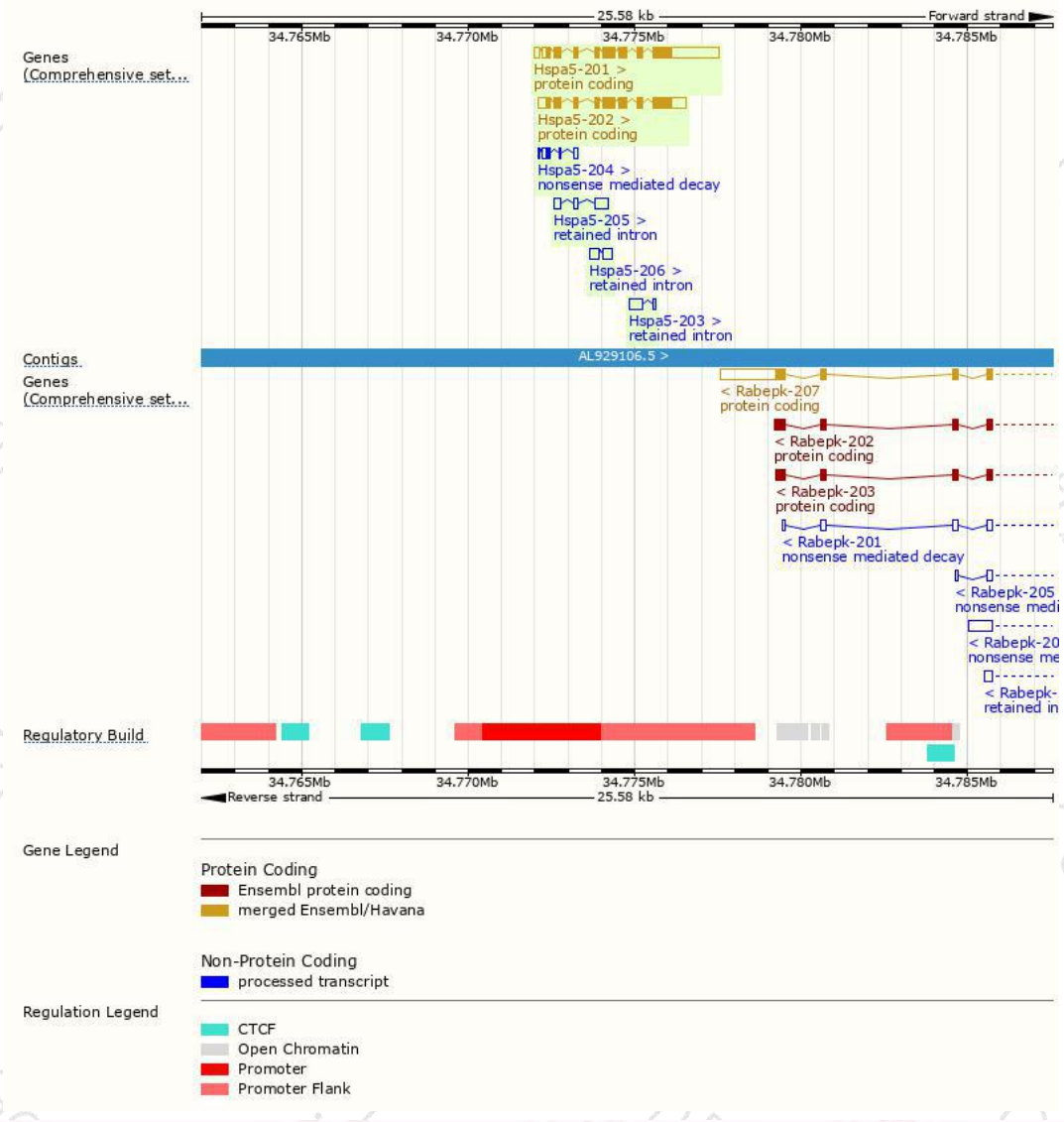
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hspa5-201	ENSMUST00000028222.12	3672	655aa	Protein coding	CCDS15950	P20029	TSL:1 GENCODE basic APPRIS P1
Hspa5-202	ENSMUST00000100171.2	2613	655aa	Protein coding	CCDS15950	P20029	TSL:1 GENCODE basic APPRIS P1
Hspa5-204	ENSMUST00000137145.7	477	42aa	Nonsense mediated decay	-	A0A0A6YXF5	TSL:5
Hspa5-205	ENSMUST00000145466.1	720	No protein	Retained intron	-	-	TSL:1
Hspa5-206	ENSMUST00000155595.1	574	No protein	Retained intron	-	-	TSL:2
Hspa5-203	ENSMUST00000129333.1	452	No protein	Retained intron	-	-	TSL:2

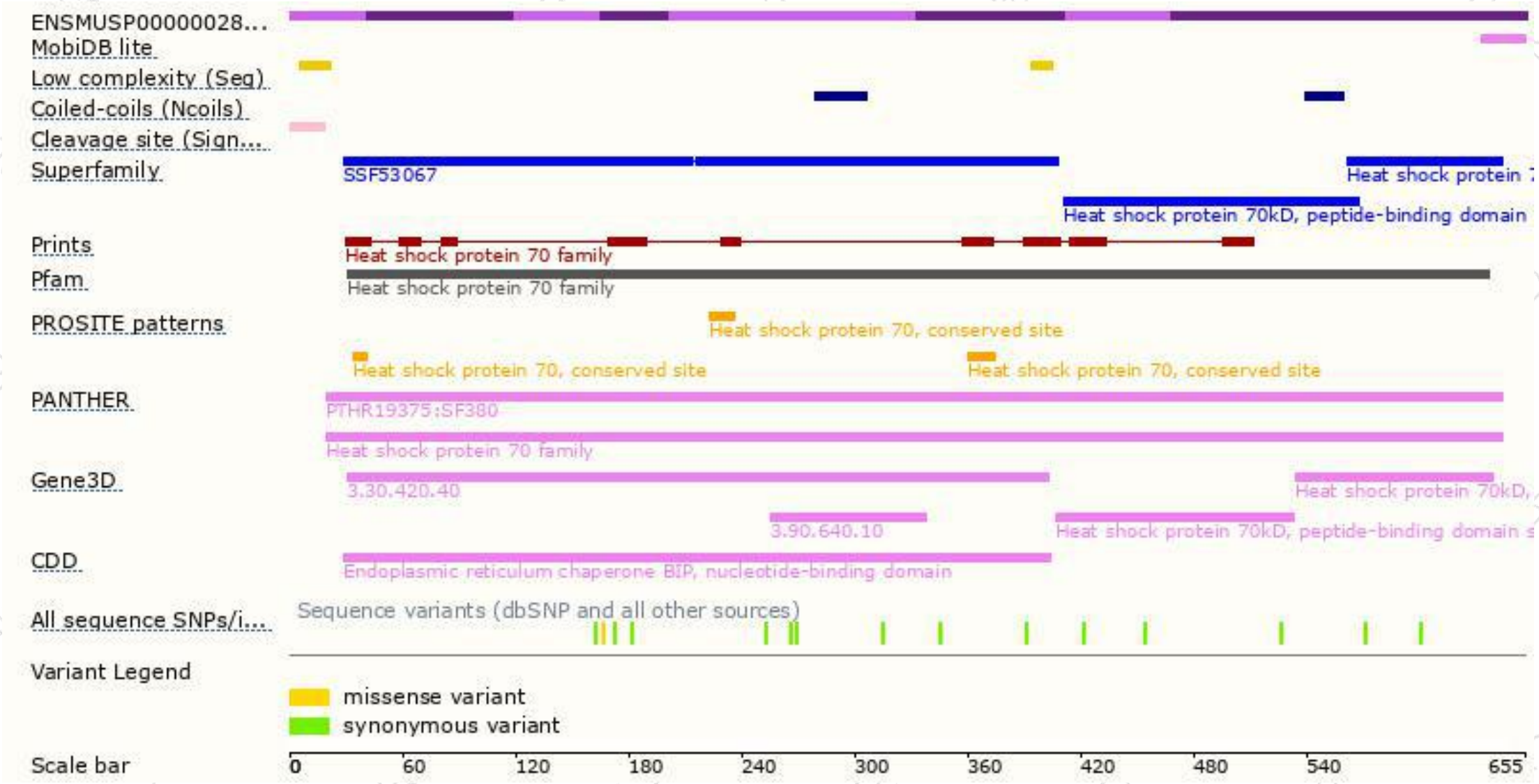
The strategy is based on the design of *Hspa5-201* transcript,The transcription is shown below



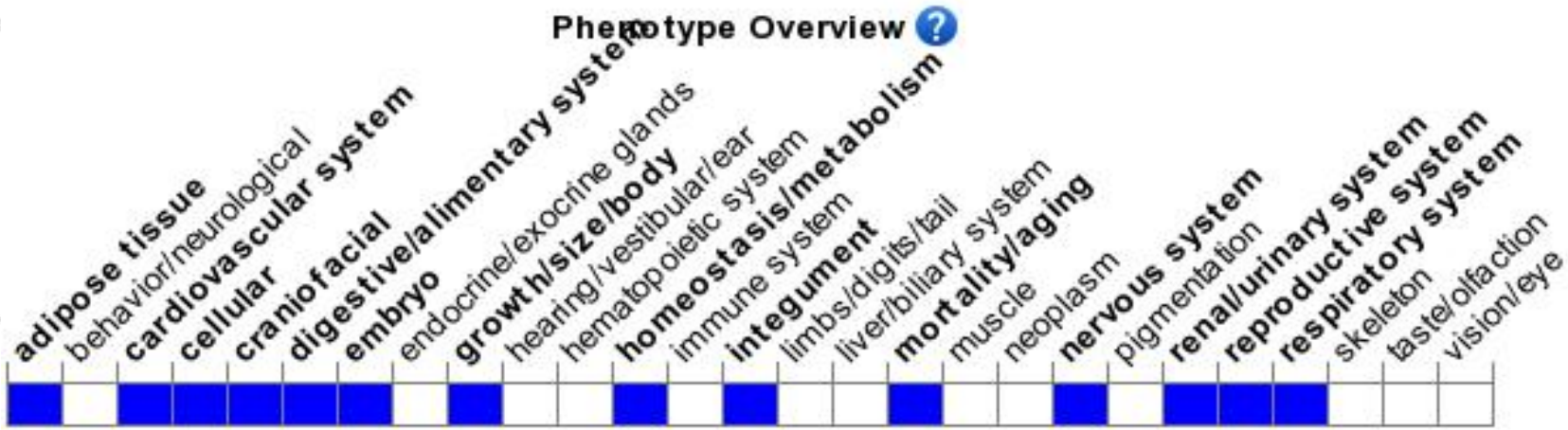
Genomic location distribution



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/).

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

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