Stard7 Cas9-KO Strategy

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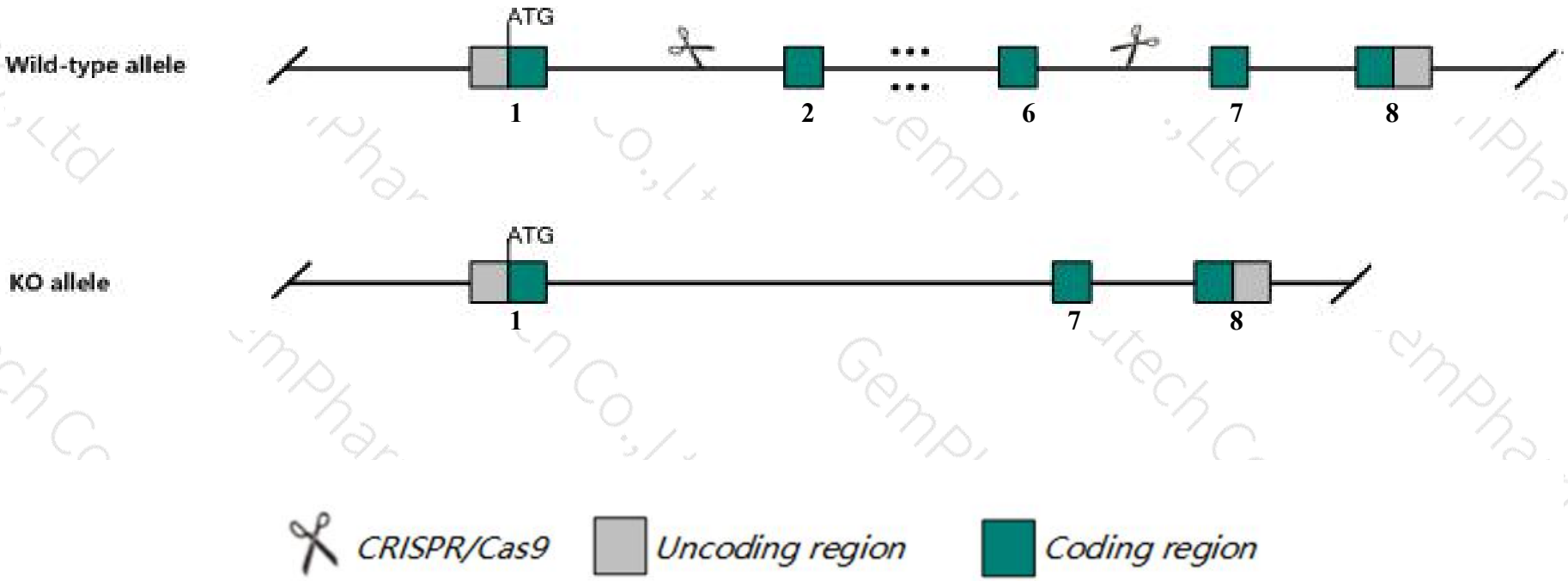
Design Date: 2020-2-26

Project Overview

Project Name	***Stard7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stard7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Stard7* gene has 8 transcripts. According to the structure of *Stard7* gene, exon2-exon6 of *Stard7-202* (ENSMUST00000110375.8) transcript is recommended as the knockout region.The region contains 553bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Stard7* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Heterozygous KO results in exaggerated allergic response (lung inflammation, increased epithelial barrier permeability and airway responsiveness) and atopic dermatitis.

- The *Stard7* 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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Stard7 START domain containing 7 [Mus musculus (house mouse)]

Gene ID: 99138, updated on 31-Jan-2019

Summary

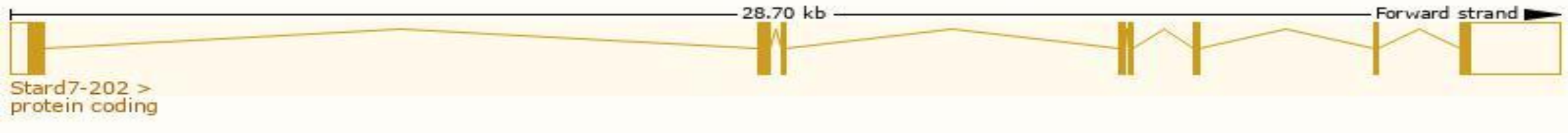
Official Symbol	Stard7 provided by MGI
Official Full Name	START domain containing 7 provided by MGI
Primary source	MGI:MGI:2139090
See related	Ensembl:ENSMUSG00000027367
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI852671, AL022671, AW544915
Expression	Ubiquitous expression in CNS E18 (RPKM 28.6), heart adult (RPKM 28.6) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

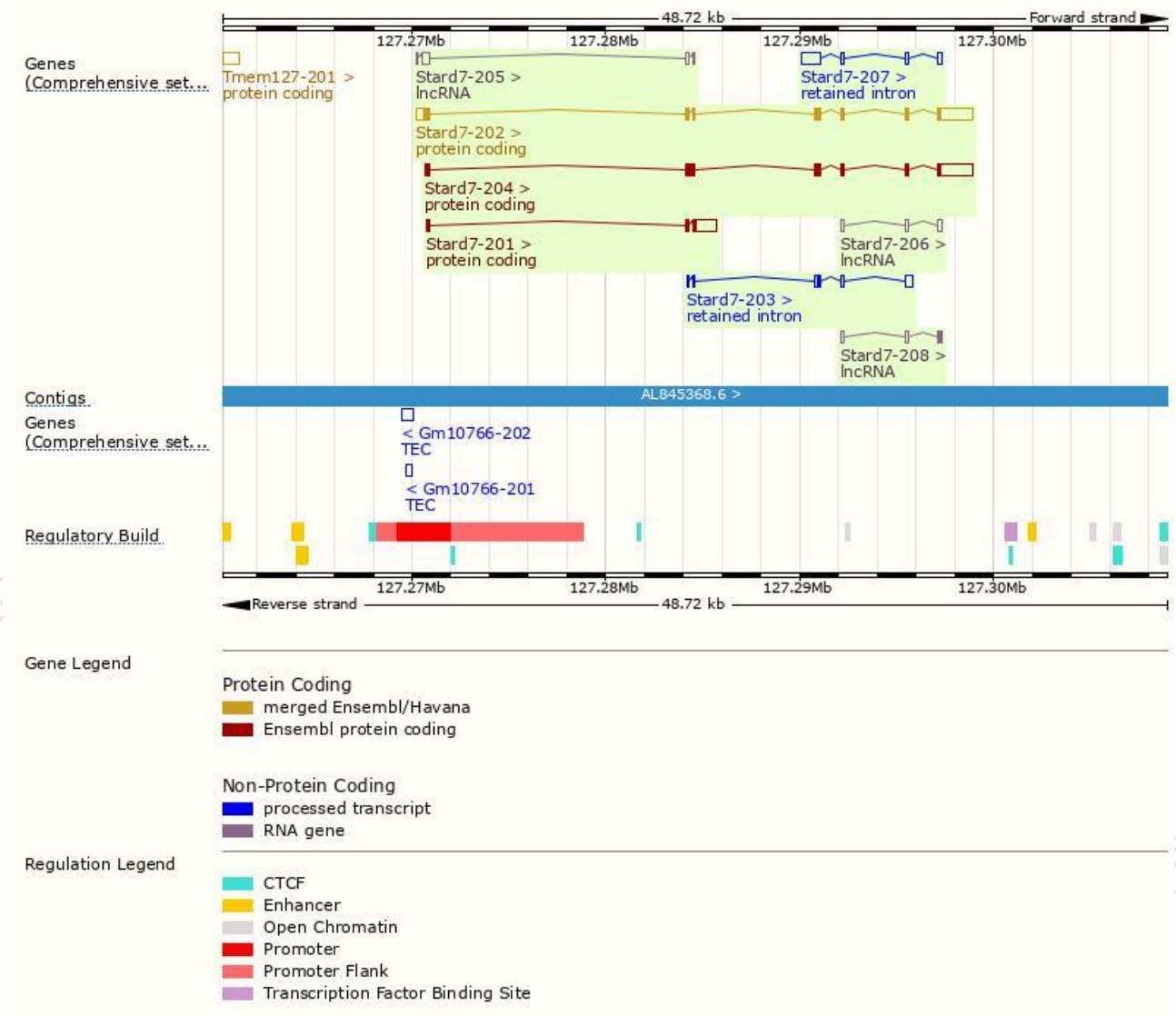
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stard7-202	ENSMUST00000110375.8	3116	373aa	Protein coding	CCDS16698	Q8R1R3	TSL:1 GENCODE basic APPRIS P1
Stard7-204	ENSMUST00000125049.1	2869	409aa	Protein coding	-	F7BBA2	CDS 5' incomplete TSL:2
Stard7-201	ENSMUST00000110374.1	1530	122aa	Protein coding	-	Q8BXP7	TSL:1 GENCODE basic
Stard7-207	ENSMUST00000144687.7	1358	No protein	Retained intron	-	-	TSL:2
Stard7-203	ENSMUST00000123152.7	773	No protein	Retained intron	-	-	TSL:2
Stard7-205	ENSMUST00000131196.1	679	No protein	lncRNA	-	-	TSL:5
Stard7-206	ENSMUST00000135616.7	459	No protein	lncRNA	-	-	TSL:1
Stard7-208	ENSMUST00000154549.1	400	No protein	lncRNA	-	-	TSL:5

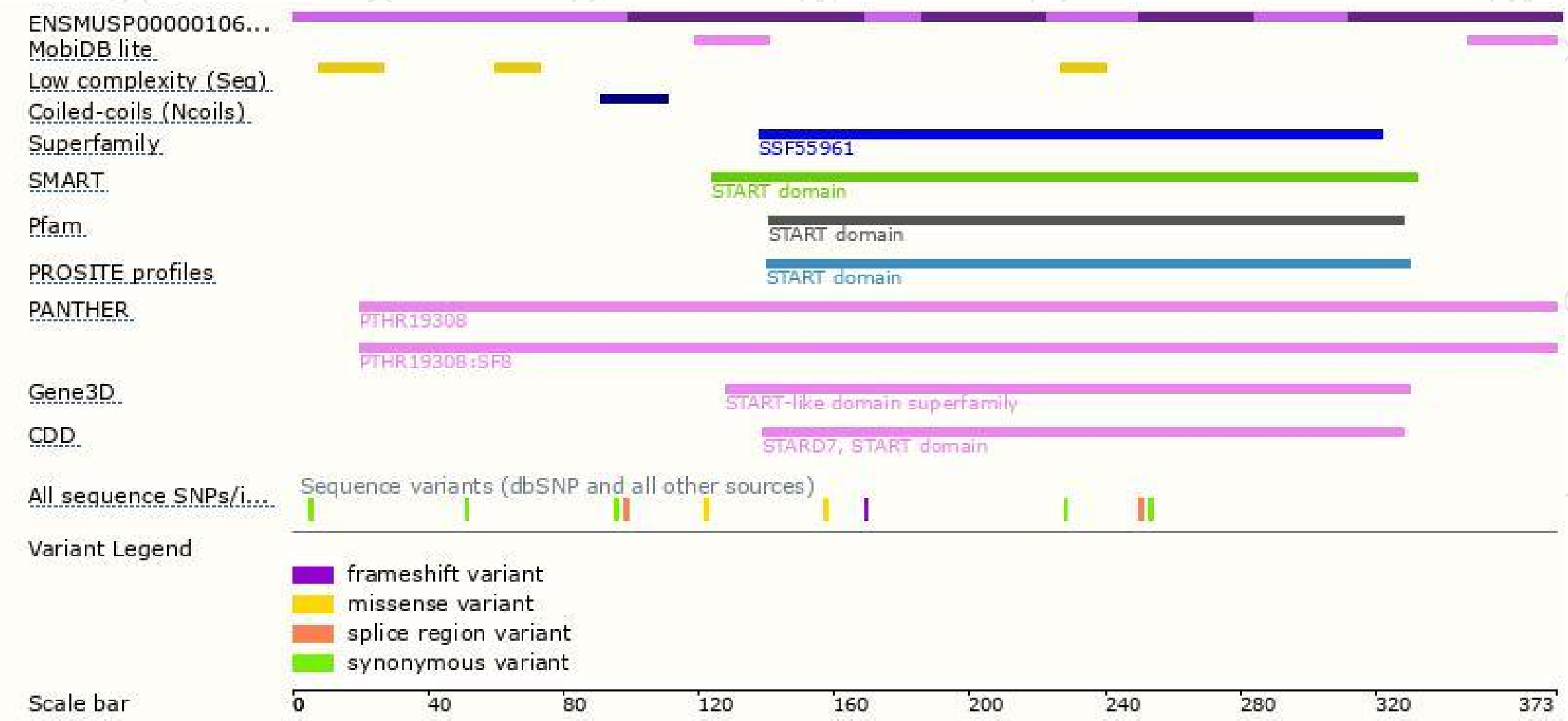
The strategy is based on the design of *Stard7-202* transcript,The transcription is shown below



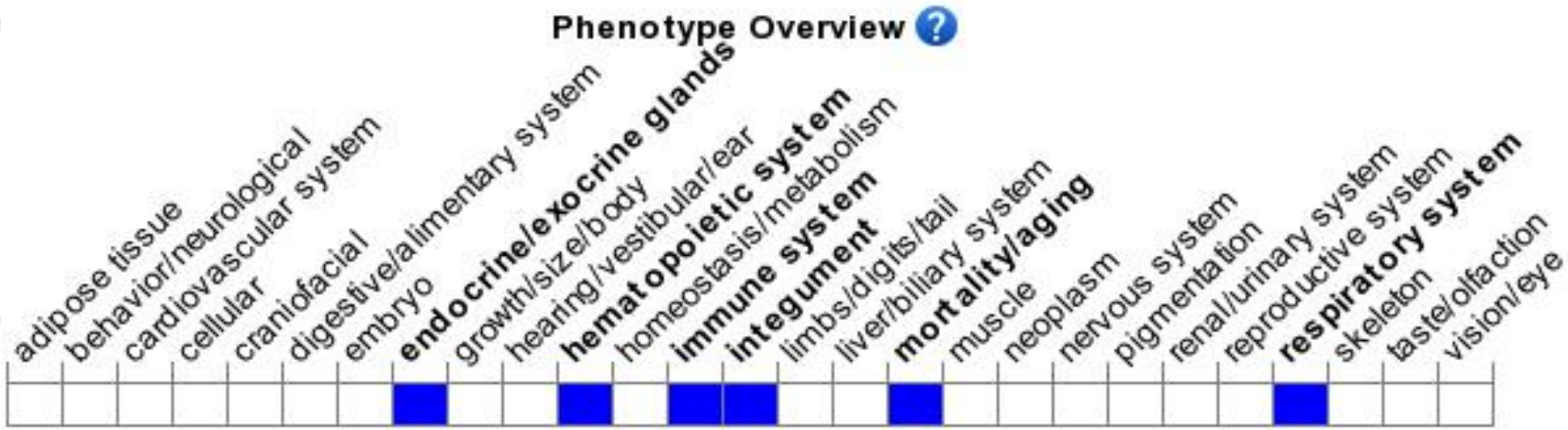
Genomic location distribution



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,Heterozygous KO results in exaggerated allergic response (lung inflammation, increased epithelial barrier permeability and airway responsiveness) and atopic dermatitis.

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

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