

Sdha Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Sdha

Project type

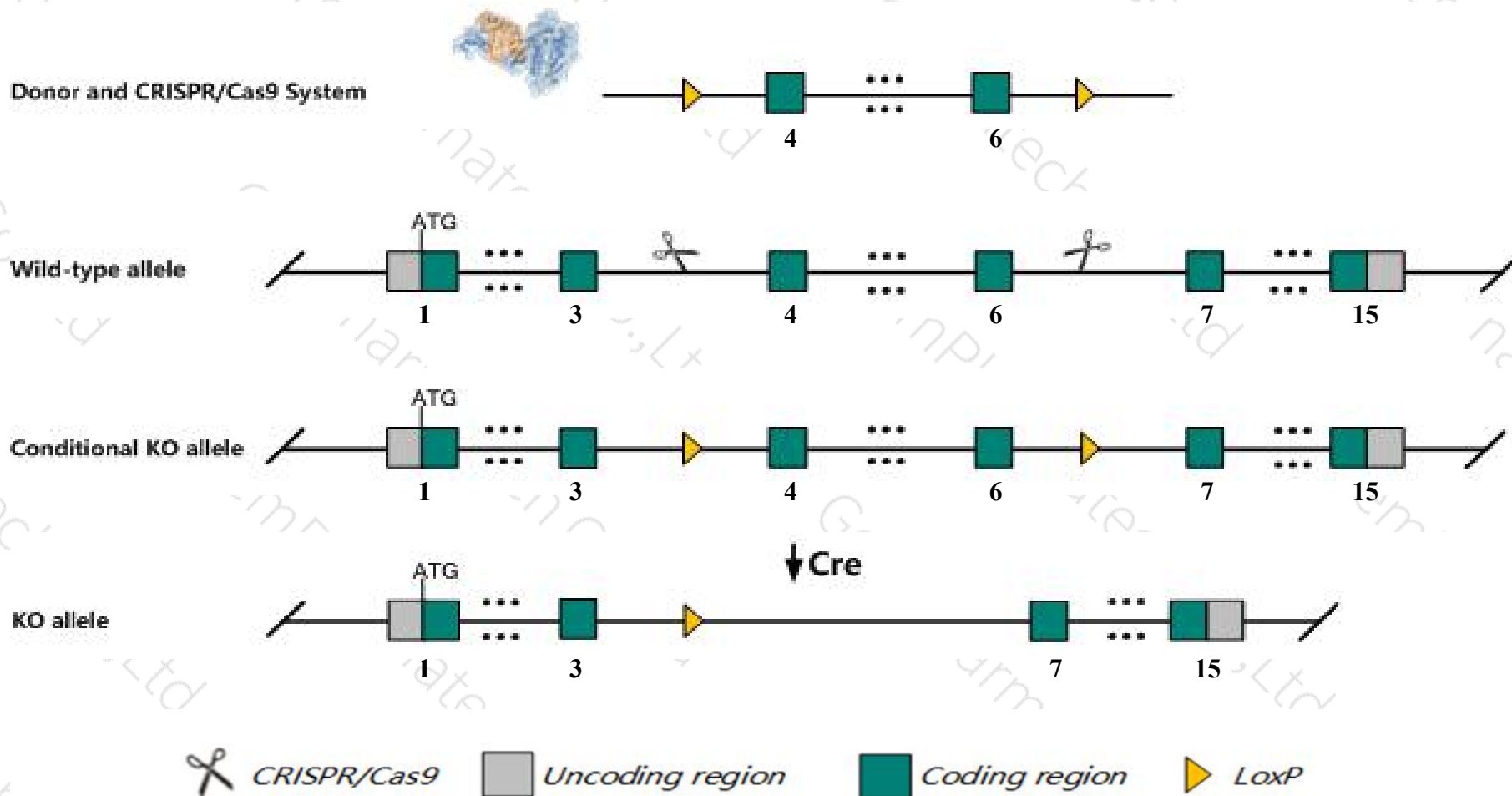
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Sdha* gene has 9 transcripts. According to the structure of *Sdha* gene, exon4-exon6 of *Sdha-201* (ENSMUST00000022062.7) transcript is recommended as the knockout region. The region contains 458bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sdha* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, null homozygotes show embryonic lethality prior to organogenesis.
- The *Sdha* gene is located on the Chr13. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Sdha succinate dehydrogenase complex, subunit A, flavoprotein (Fp) [*Mus musculus* (house mouse)]

Gene ID: 66945, updated on 15-Oct-2019

Summary

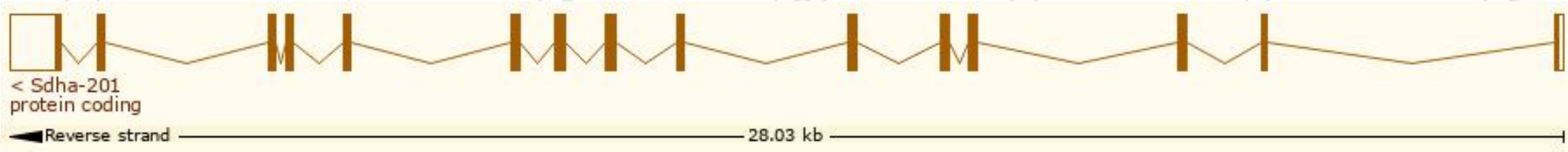
Official Symbol	Sdha provided by MGI
Official Full Name	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) provided by MGI
Primary source	MGI:MGI:1914195
See related	Ensembl:ENSMUSG00000021577
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FP; SDH2; SDHF; C81073; 4921513A11; 1500032O14Rik; 2310034D06Rik
Expression	Ubiquitous expression in heart adult (RPKM 297.9), kidney adult (RPKM 187.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

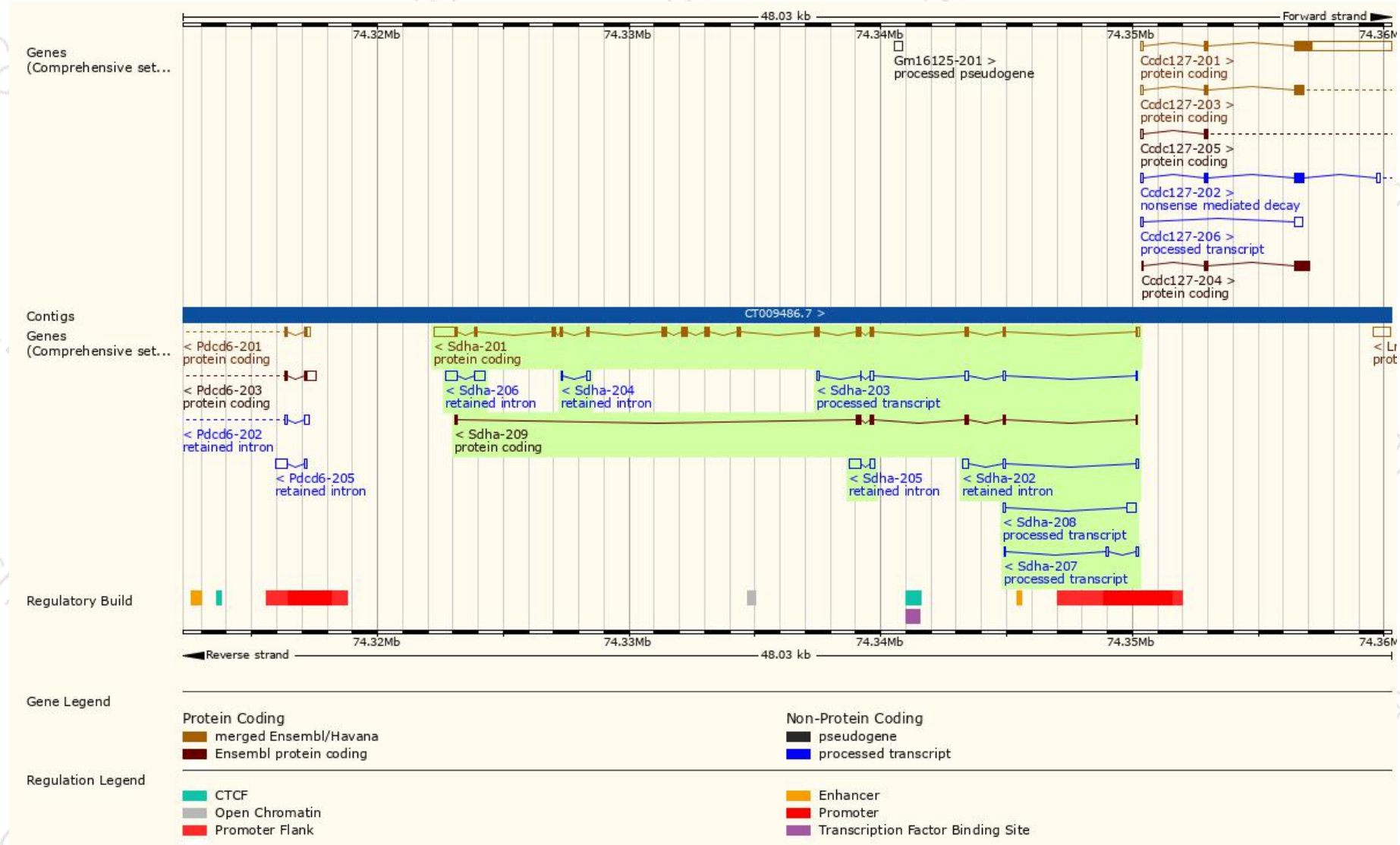
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sdha-206	ENSMUST00000161434.1	858	No protein	Retained intron	-	-	TSL:2
Sdha-205	ENSMUST00000161086.2	647	No protein	Retained intron	-	-	TSL:2
Sdha-202	ENSMUST00000160400.1	438	No protein	Retained intron	-	-	TSL:2
Sdha-204	ENSMUST00000160900.1	239	No protein	Retained intron	-	-	TSL:2
Sdha-201	ENSMUST0000022062.7	2900	664aa	Protein coding	CCDS26643	Q8K2B3	TSL:1 GENCODE basic APPRIS P1
Sdha-209	ENSMUST00000221594.1	722	233aa	Protein coding	-	A0A1Y7VJ55	CDS 5' incomplete TSL:3
Sdha-203	ENSMUST00000160667.7	521	No protein	Processed transcript	-	-	TSL:3
Sdha-208	ENSMUST00000162137.1	420	No protein	Processed transcript	-	-	TSL:3
Sdha-207	ENSMUST00000161456.1	198	No protein	Processed transcript	-	-	TSL:5

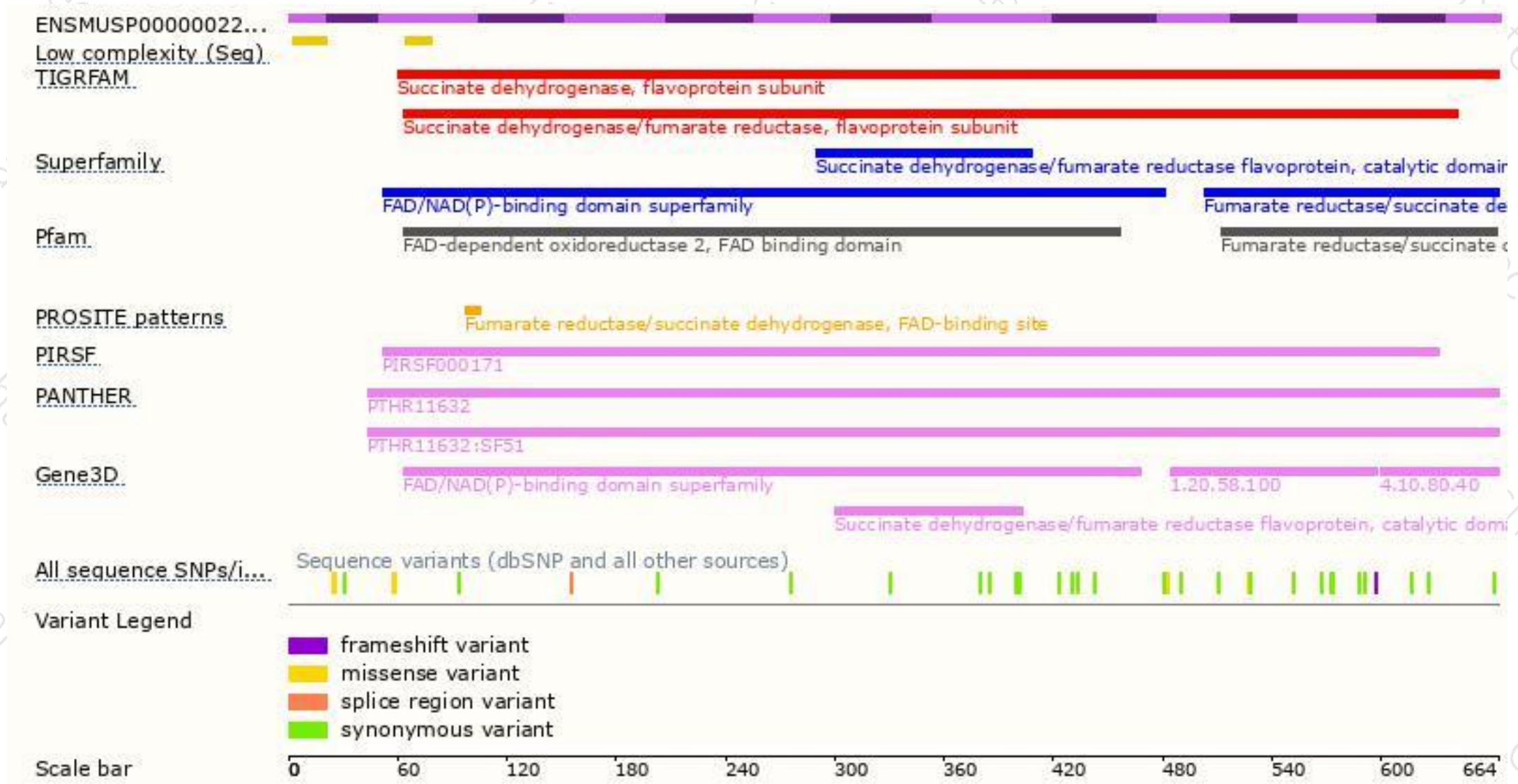
The strategy is based on the design of *Sdha-201* transcript, the transcription is shown below:



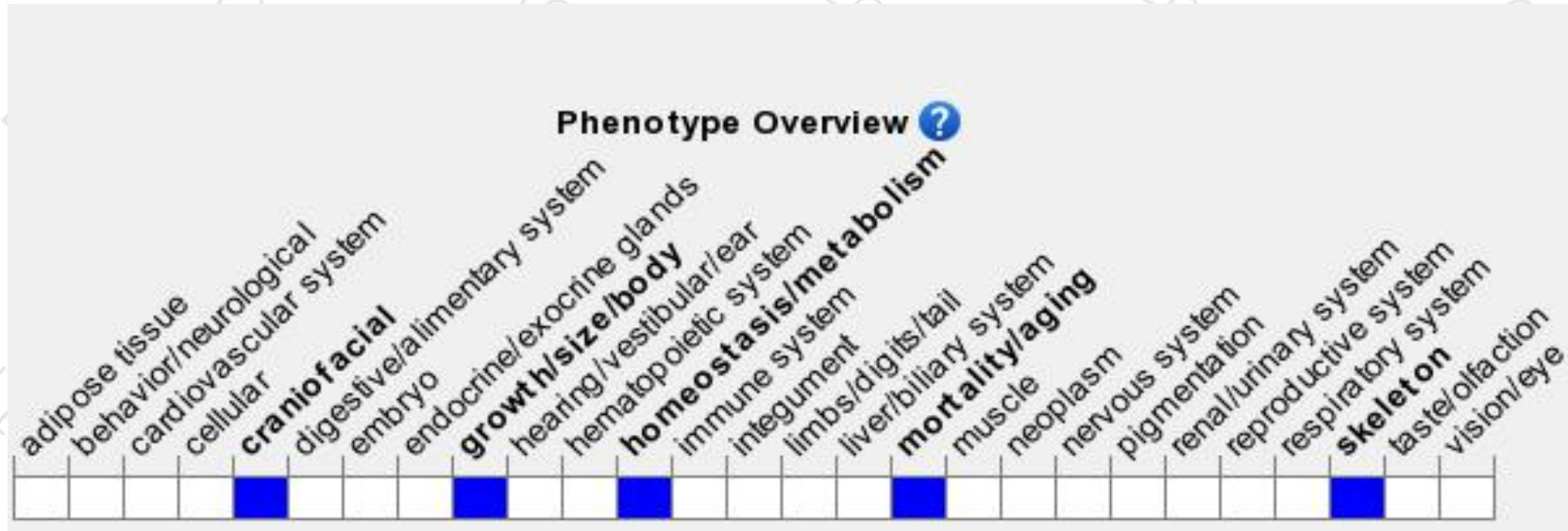
Genomic location distribution



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/>).

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

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