

***Stard10* Cas9-CKO Strategy**

Designer:

Project Overview

Project Name

Stard10

Project type

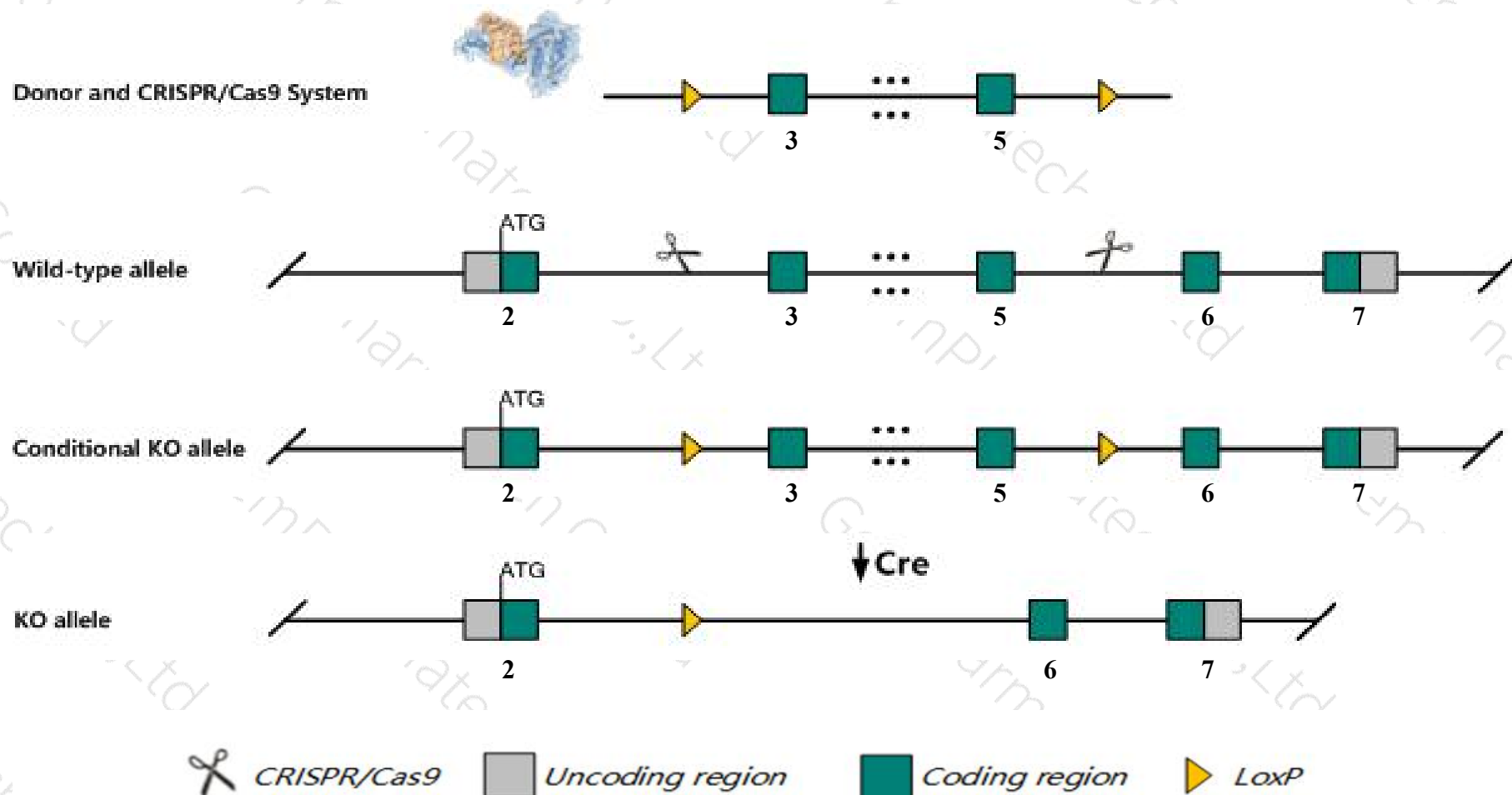
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stard10* gene. The schematic diagram is as follows:



Technical routes

- The *Stard10* gene has 11 transcripts. According to the structure of *Stard10* gene, exon3-exon5 of *Stard10-201* (ENSMUST00000032927.13) transcript is recommended as the knockout region. The region contains 370bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stard10* 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, Mice homozygous for a knock-out allele exhibit altered bile acid homeostasis.
- The *Stard10* gene is located on the Chr7. 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)

Stard10 START domain containing 10 [Mus musculus (house mouse)]

Gene ID: 56018, updated on 31-Jan-2019

Summary



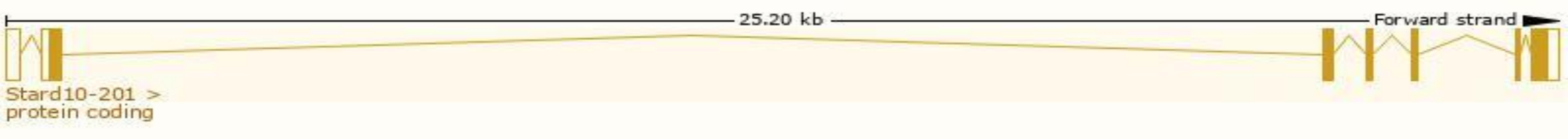
Official Symbol	Stard10 provided by MGI
Official Full Name	START domain containing 10 provided by MGI
Primary source	MGI:MGI:1860093
See related	Ensembl:ENSMUSG00000030688
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV048538, CGI-52, NY-C0-28, PC-TP2, PCTP2, Pctpl, Sdccag28, SdccagG28, TISP-81
Expression	Biased expression in liver adult (RPKM 468.9), colon adult (RPKM 328.7) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

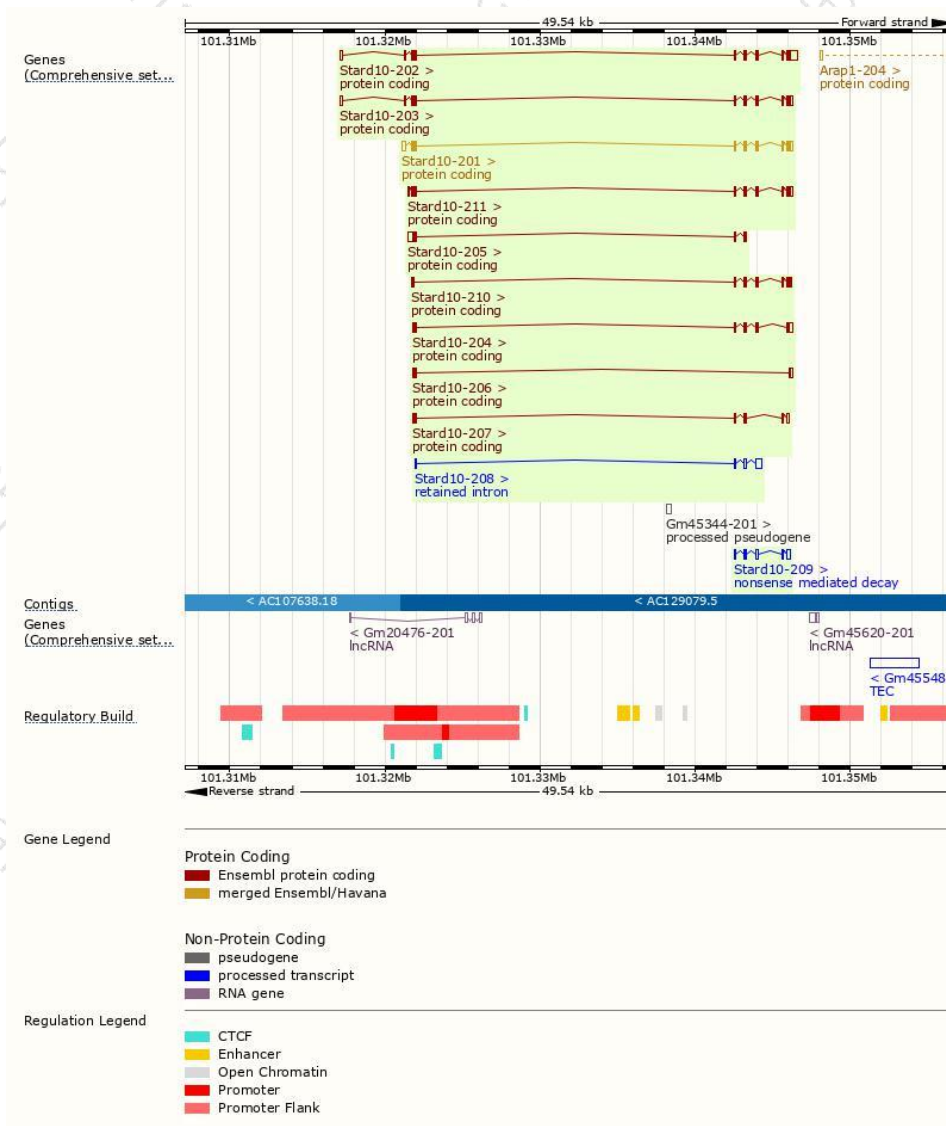
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stard10-201	ENSMUST00000032927.13	1400	291aa	Protein coding	CCDS21509	Q0VG22 Q9JMD3	TSL:1 GENCODE basic APPRIS P1
Stard10-203	ENSMUST00000164479.8	1375	291aa	Protein coding	CCDS21509	Q0VG22 Q9JMD3	TSL:1 GENCODE basic APPRIS P1
Stard10-211	ENSMUST00000210192.1	1258	291aa	Protein coding	CCDS21509	Q0VG22 Q9JMD3	TSL:5 GENCODE basic APPRIS P1
Stard10-202	ENSMUST00000163799.8	1723	364aa	Protein coding	-	E9PVP0	TSL:1 GENCODE basic
Stard10-204	ENSMUST00000167888.8	1049	265aa	Protein coding	-	G3UW37	CDS 5' incomplete TSL:1
Stard10-210	ENSMUST00000174291.7	903	283aa	Protein coding	-	G3UY87	CDS 5' incomplete TSL:5
Stard10-205	ENSMUST00000172630.7	789	150aa	Protein coding	-	G3UYM0	CDS 3' incomplete TSL:2
Stard10-207	ENSMUST00000173270.7	670	160aa	Protein coding	-	G3UY59	TSL:5 GENCODE basic
Stard10-206	ENSMUST00000172662.1	430	87aa	Protein coding	-	G3UYN6	CDS 5' incomplete TSL:1
Stard10-209	ENSMUST00000174140.1	649	49aa	Nonsense mediated decay	-	G3UZB9	CDS 5' incomplete TSL:5
Stard10-208	ENSMUST00000174083.1	731	No protein	Retained intron	-	-	TSL:2

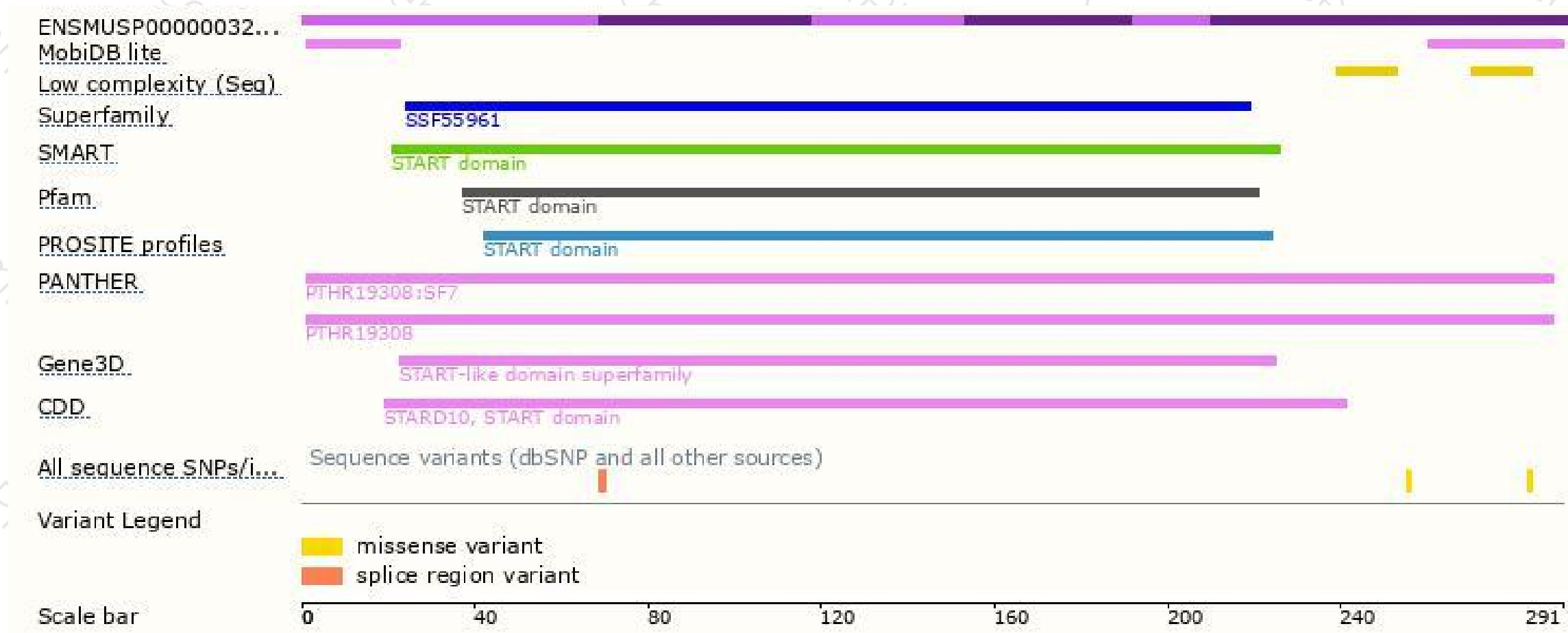
The strategy is based on the design of *Stard10-201* transcript,The transcription is shown below



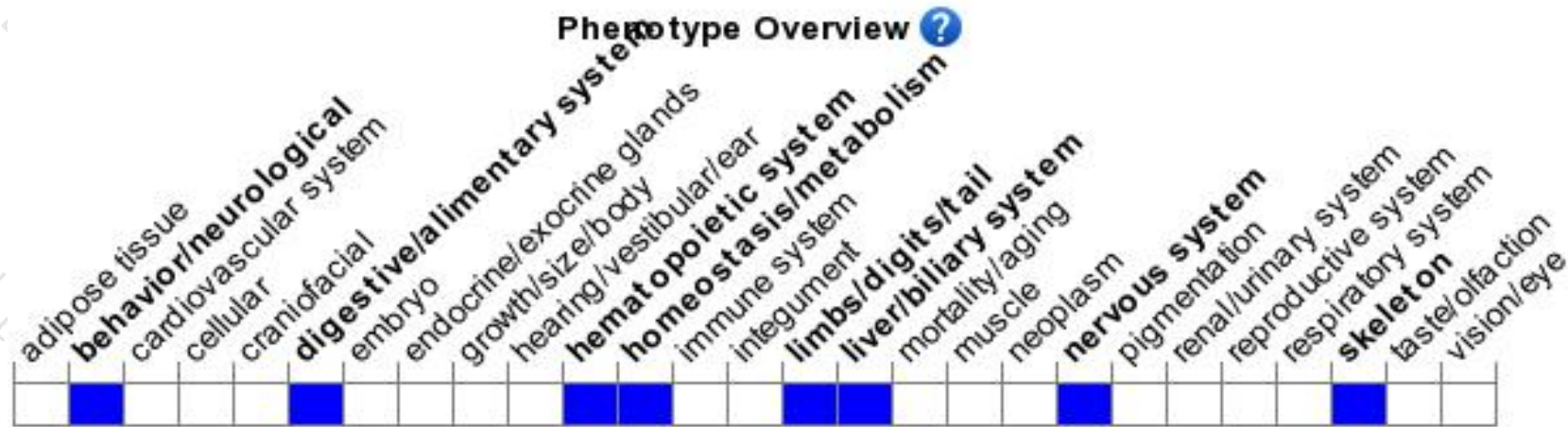
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit altered bile acid homeostasis.

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

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