

***Gar1* Cas9-CKO Strategy**

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Reviewer: JiaYu

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Project Overview

Project Name

Gar1

Project type

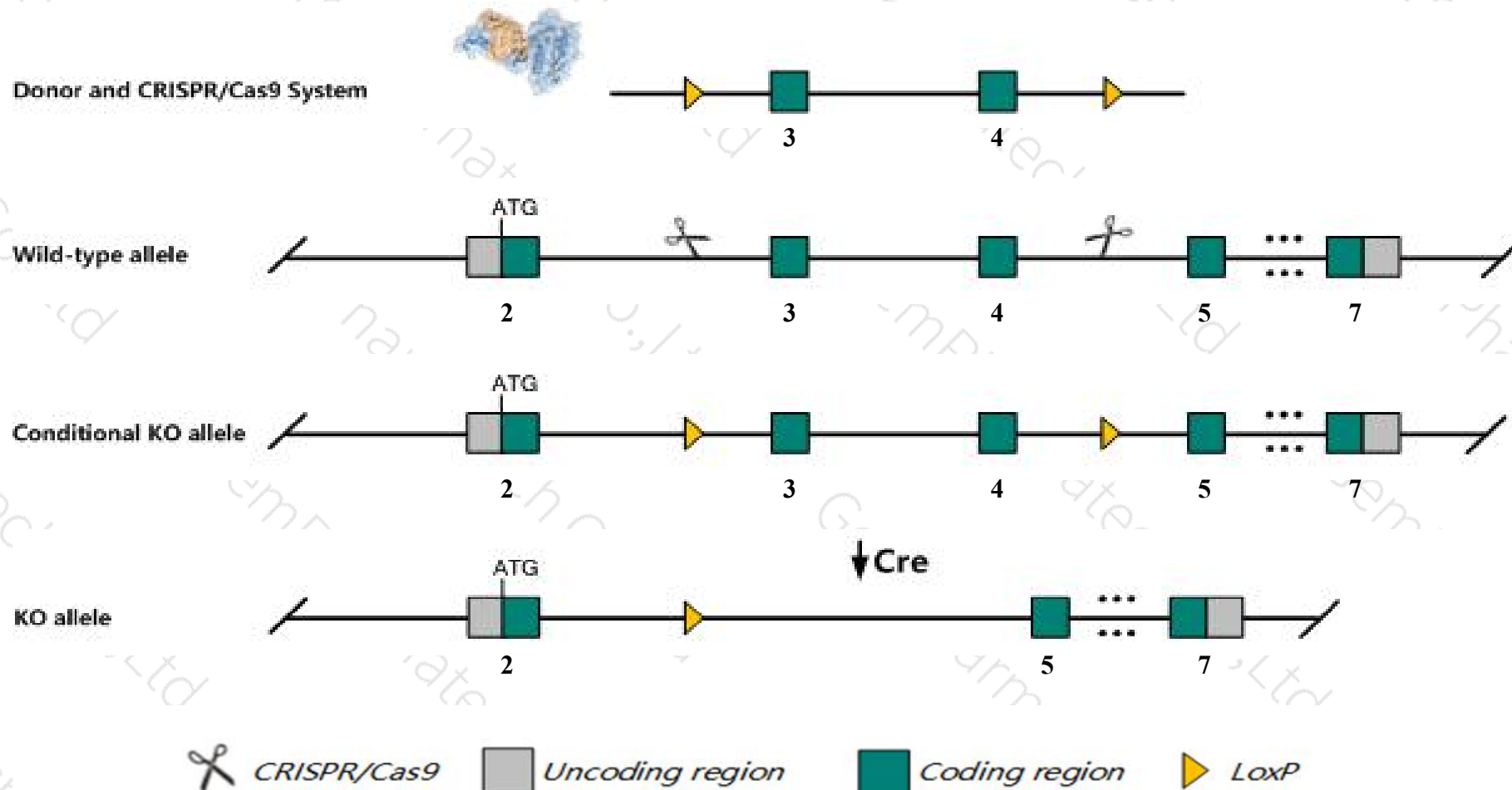
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gar1* gene. The schematic diagram is as follows:



- The *Gar1* gene has 6 transcripts. According to the structure of *Gar1* gene, exon3-exon4 of *Gar1-201* (ENSMUST00000029643.14) transcript is recommended as the knockout region. The region contains 215bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gar1* 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.

Notice

- The *Gar1* gene is located on the Chr3. 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)

Gar1 GAR1 ribonucleoprotein [Mus musculus (house mouse)]

Gene ID: 68147, updated on 13-Mar-2020

Summary



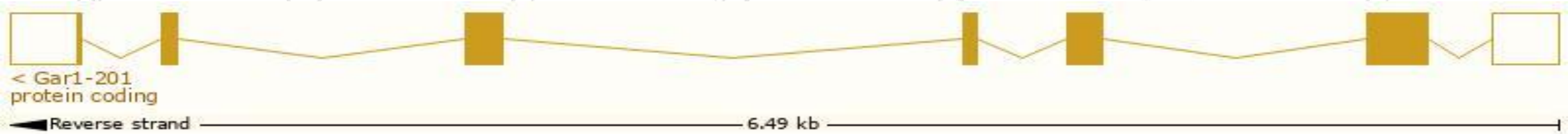
Official Symbol	Gar1 provided by MGI
Official Full Name	GAR1 ribonucleoprotein provided by MGI
Primary source	MGI:MGI:1930948
See related	Ensembl:ENSMUSG00000028010
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA409823, AI326794, C430047J18Rik, Nola1
Expression	Broad expression in liver E14 (RPKM 26.6), CNS E11.5 (RPKM 25.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

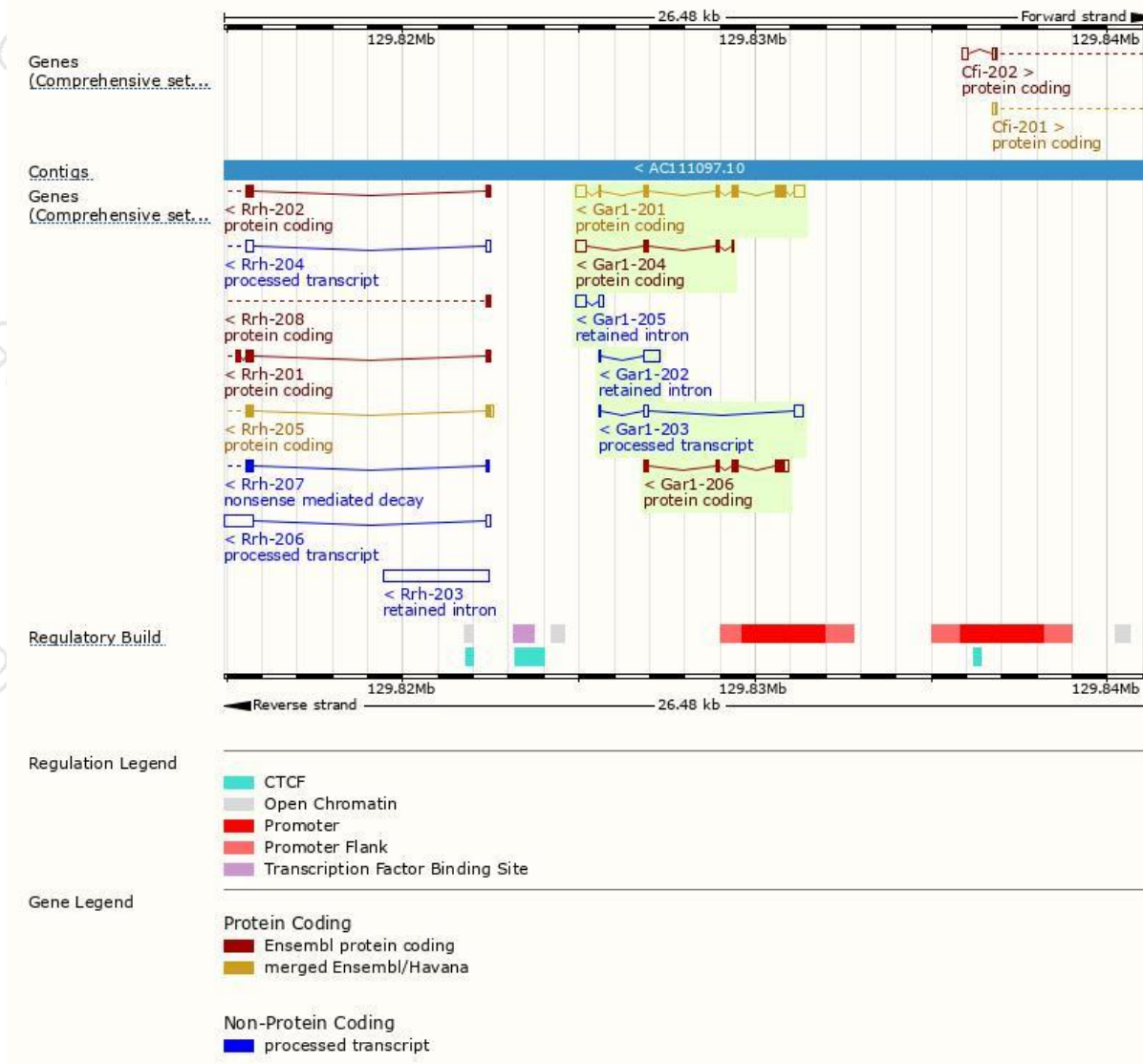
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gar1-201	ENSMUST00000029643.14	1271	231aa	Protein coding	CCDS38634	Q9CY66	TSL:1 GENCODE basic APPRIS P1
Gar1-206	ENSMUST00000149071.1	685	198aa	Protein coding	-	D3YZ09	CDS 3' incomplete TSL:2
Gar1-204	ENSMUST00000134174.7	520	79aa	Protein coding	-	F6SL78	CDS 5' incomplete TSL:2
Gar1-203	ENSMUST00000128441.1	440	No protein	Processed transcript	-	-	TSL:3
Gar1-202	ENSMUST00000127864.1	522	No protein	Retained intron	-	-	TSL:3
Gar1-205	ENSMUST00000143545.1	418	No protein	Retained intron	-	-	TSL:2

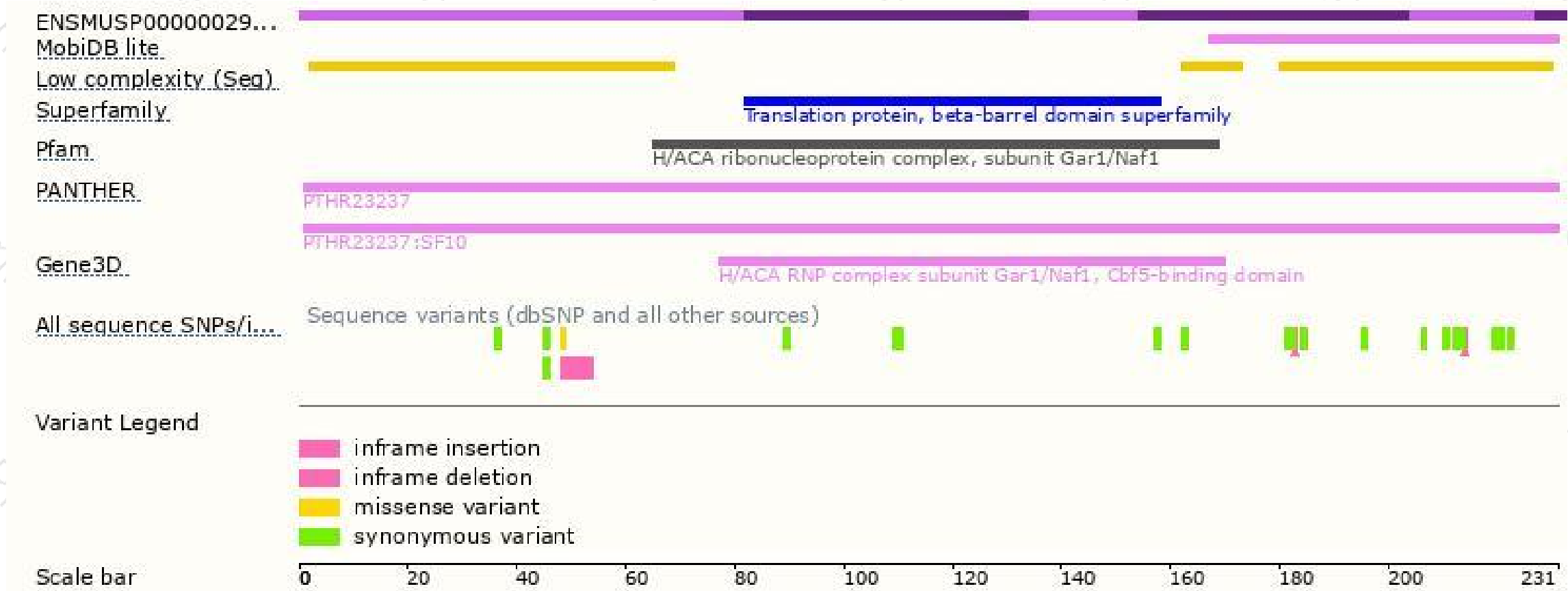
The strategy is based on the design of *Gar1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



Mouse phenotype description(MGI)

Phenotype Overview

adipose tissue	behavior/neurological	cardiovascular system	cellular	craniofacial	digestive/alimentary system	embryo	endocrine/exocrine glands	growth/size/body	hearing/vestibular/ear	hematopoietic system	homeostasis/metabolism	immune system	integument	limbs/digits/tail	liver/biliary system	mortality/aging	muscle	neoplasm	nervous system	pigmentation	renal/urinary system	reproductive system	respiratory system	skeleton	taste/olfaction	vision/eye
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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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