Lin7c Cas9-CKO Strategy

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Project Overview

Project Name	***Lin7c***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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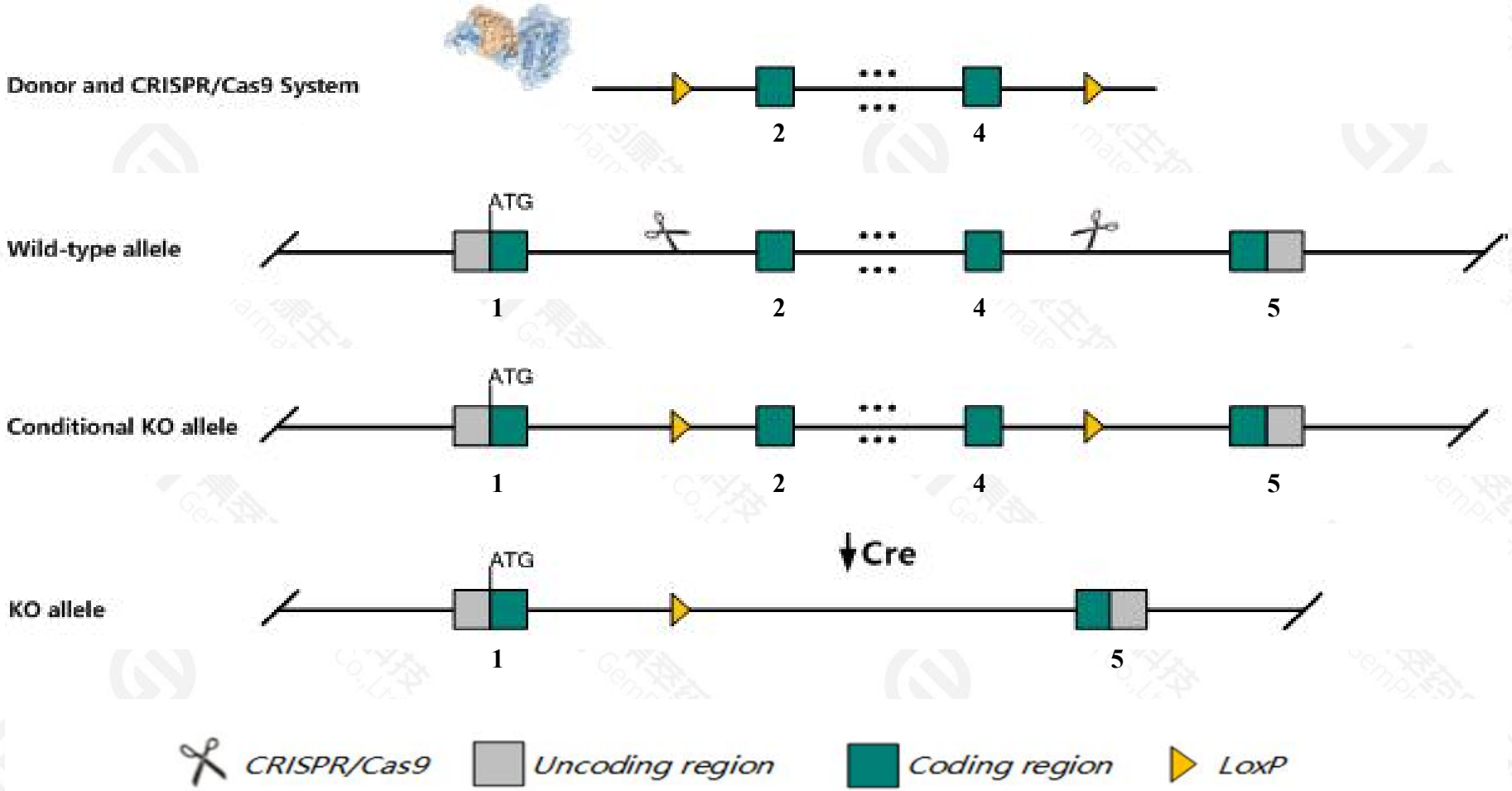
This model will use CRISPR/Cas9 technology to edit the *Lin7c* gene. The schematic diagram is as follows:



Technical routes

➢ The *Lin7c* gene has 2 transcripts. According to the structure of *Lin7c* gene, exon2-exon4 of *Lin7c-201*(ENSMUST00000028583.7) transcript is recommended as the knockout region.The region contains 401bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Lin7c* 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

➢ According to the existing MGI data,targeted disruption of this gene appears to have no phenotype, but when combined with Lin7a or Lin7a and Lin7b results in early postnatal lethality.

➢ The *Lin7c* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

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Lin7c lin-7 homolog C (C. elegans) [Mus musculus (house mouse)]

Gene ID: 22343, updated on 13-Mar-2020

Summary

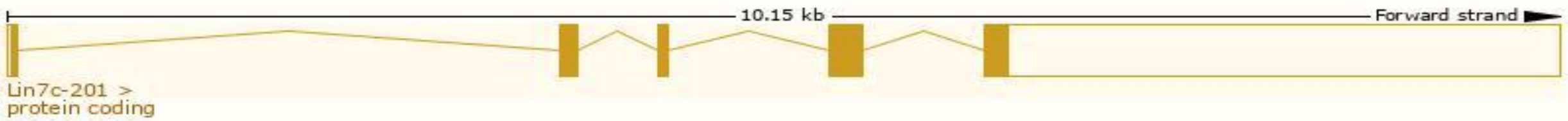
Official Symbol	Lin7c provided by MGI
Official Full Name	lin-7 homolog C (C. elegans) provided byMGI
Primary source	MGI:MGI:1330839
See related	Ensembl:ENSMUSG00000027162
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9130007B12Rik, AI303698, AU019331, AW125731, D2Ertd520e, LIN-7-C, LIN-7C, MALS-3, Veli3
Expression	Broad expression in CNS E18 (RPKM 9.9), whole brain E14.5 (RPKM 7.2) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

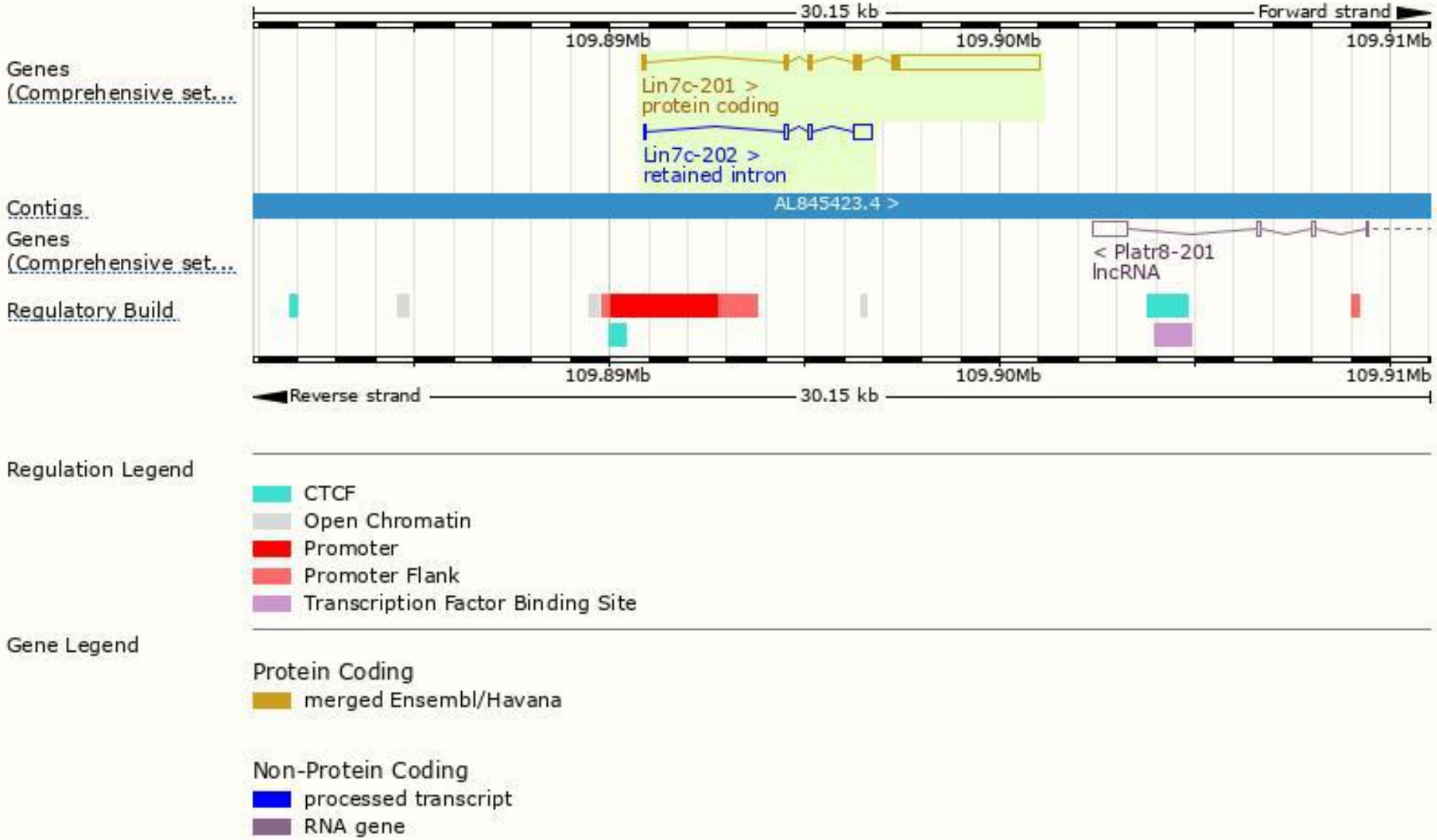
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lin7c-201	ENSMUST00000028583.7	4228	197aa	Protein coding	CCDS16509	O88952	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Lin7c-202	ENSMUST00000151163.1	746	No protein	Retained intron	-	-	TSL:1

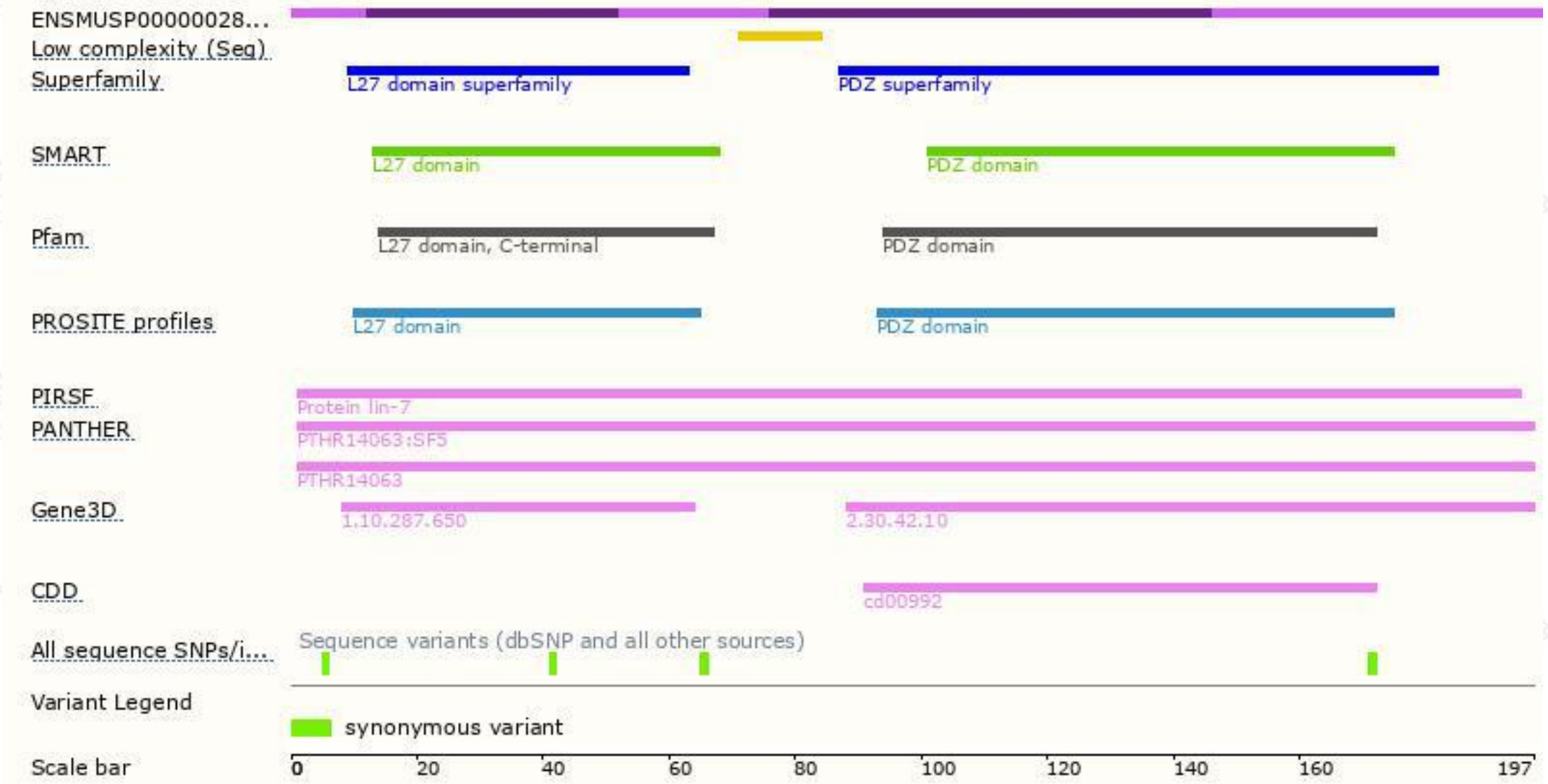
The strategy is based on the design of *Lin7c-201* transcript,the transcription is shown below:



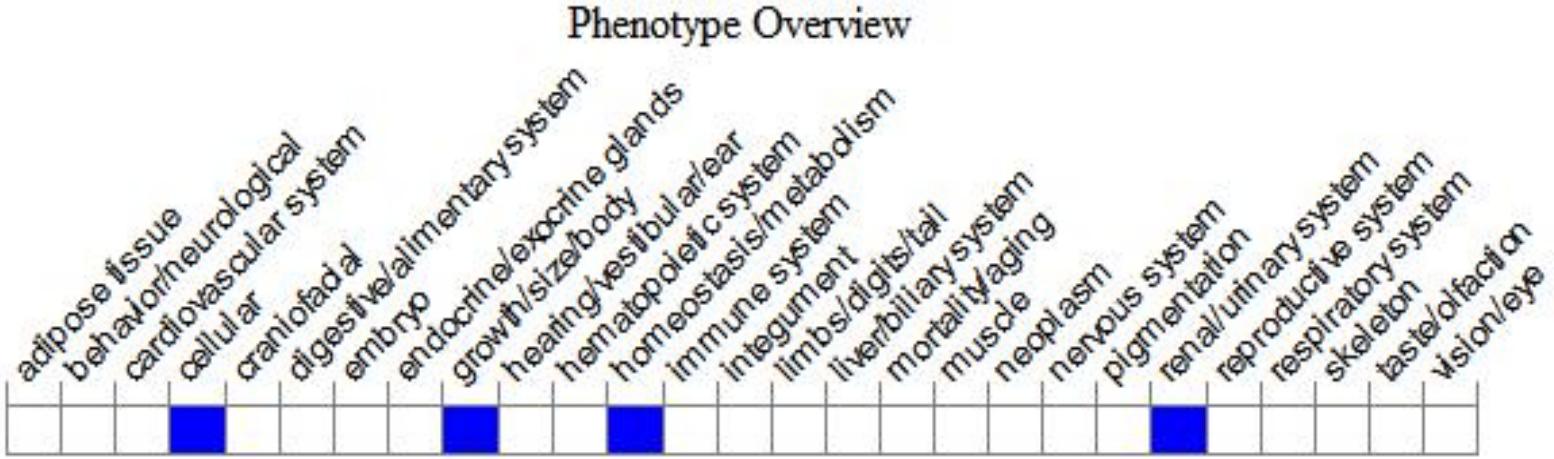
Genomic location distribution



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,targeted disruption of this gene appears to have no phenotype, but when combined with Lin7a or Lin7a and Lin7b results in early postnatal lethality.

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