Lpin3 Cas9-KO Strategy

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Project Overview

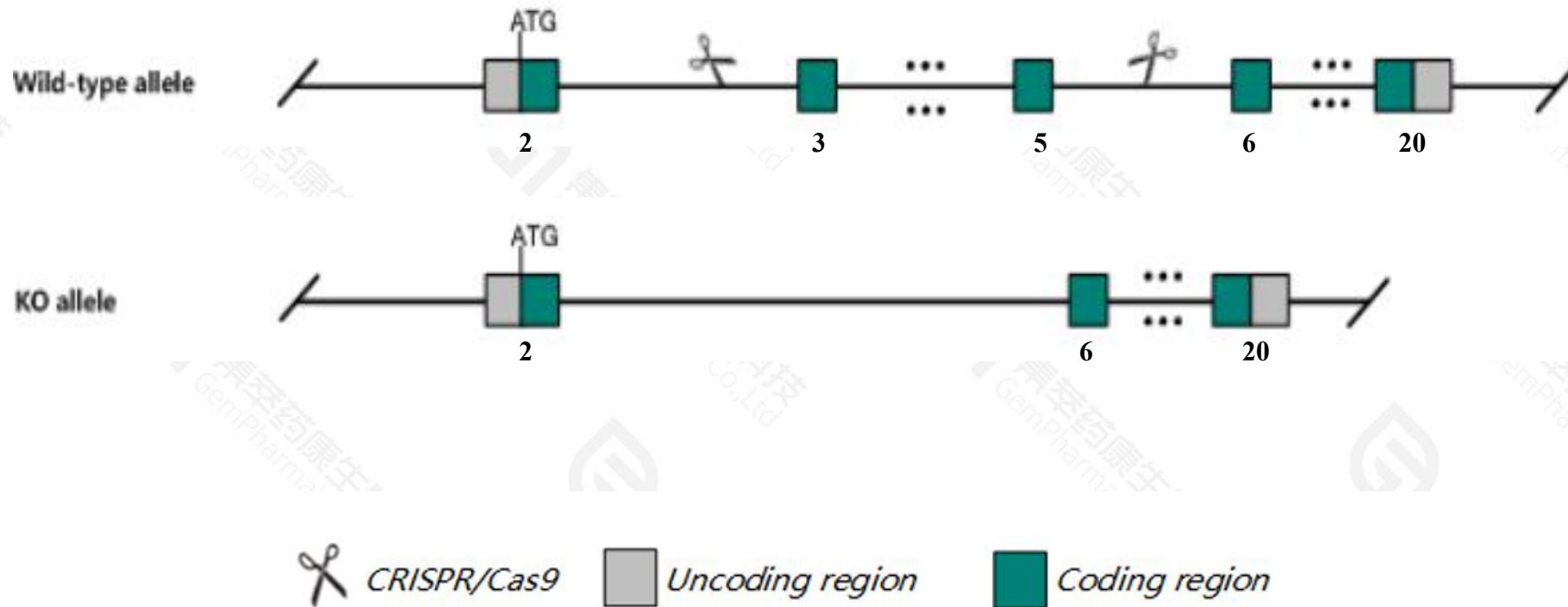|	
Project Name	*Lpin3*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lpin3* gene. The schematic diagram is as follows:

Technical routes

➤ The *Lpin3* gene has 5 transcripts. According to the structure of *Lpin3* gene, exon3-exon5 of *Lpin3-203*(ENSMUST00000109456.8) transcript is recommended as the knockout region.The region contains 428bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Lpin3* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➤ According to the existing MGI data,mice homozygous for a null allele show slightly decreased body weight, especially with age, and abnormal adipogenesis.

➤ The *Lpin3* 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）

Lpin3 lipin 3 [Mus musculus (house mouse)]

Gene ID: 64899, updated on 13-Mar-2020

▲Summary

Official Symbol	Lpin3 provided by MGI
Official Full Name	lipin 3 provided by MGI
Primary source	MGI:MGI:1891342
See related	Ensembl:ENSMUSG00000027412
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	9130206L11Rik, AA438110, AV236139, mKIAA4023
Expression	Broad expression in adrenal adult (RPKM 11.4), large intestine adult (RPKM 11.0) and 18 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lpin3-203	ENSMUST00000109456.8	3470	848aa	Protein coding	CCDS16998	Q149B0 Q99PI4	TSL:1 GENCODE basic APPRIS P2
Lpin3-201	ENSMUST00000040872.12	3458	848aa	Protein coding	CCDS16998	Q149B0 Q99PI4	TSL:1 GENCODE basic APPRIS P2
Lpin3-202	ENSMUST00000109455.8	3365	817aa	Protein coding	-	A2A4B3	TSL:5 GENCODE basic APPRIS ALT2
Lpin3-204	ENSMUST00000109457.2	3215	858aa	Protein coding	-	A2A4B1	TSL:1 GENCODE basic APPRIS ALT2
Lpin3-205	ENSMUST00000124920.1	520	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Lpin3-203* transcript,the transcription is shown below:
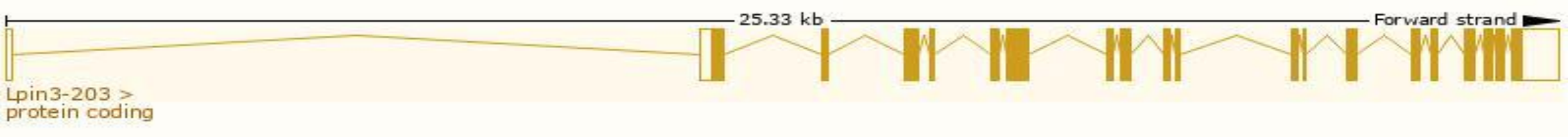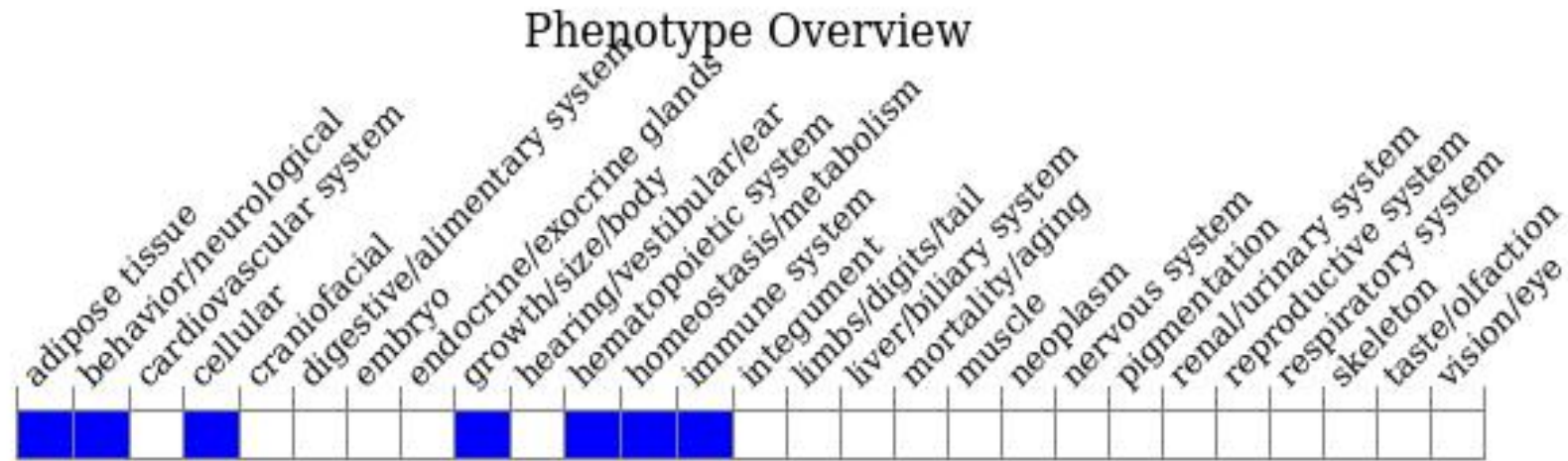
Genomic location distribution

Protein domain
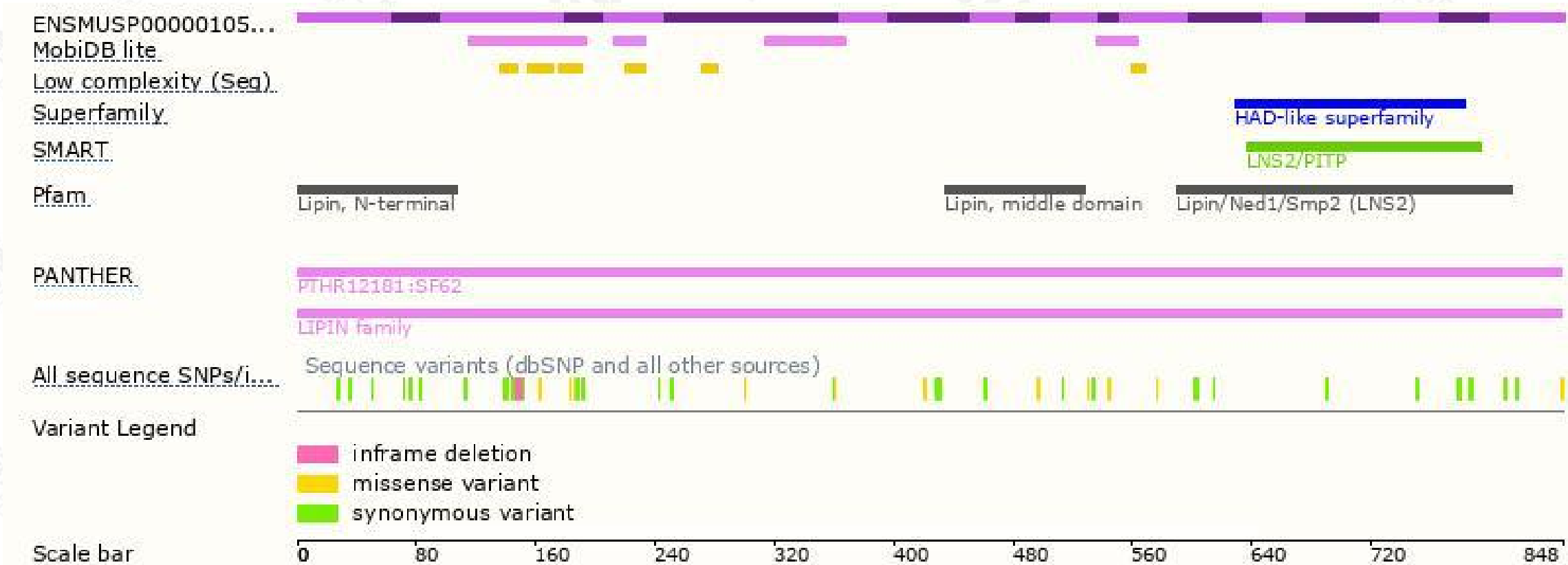
Mouse phenotype description(MGI)

Phenotype Overview

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 null allele show slightly decreased body weight, especially with age, and abnormal adipogenesis.

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