Abca1 Cas9-CKO Strategy

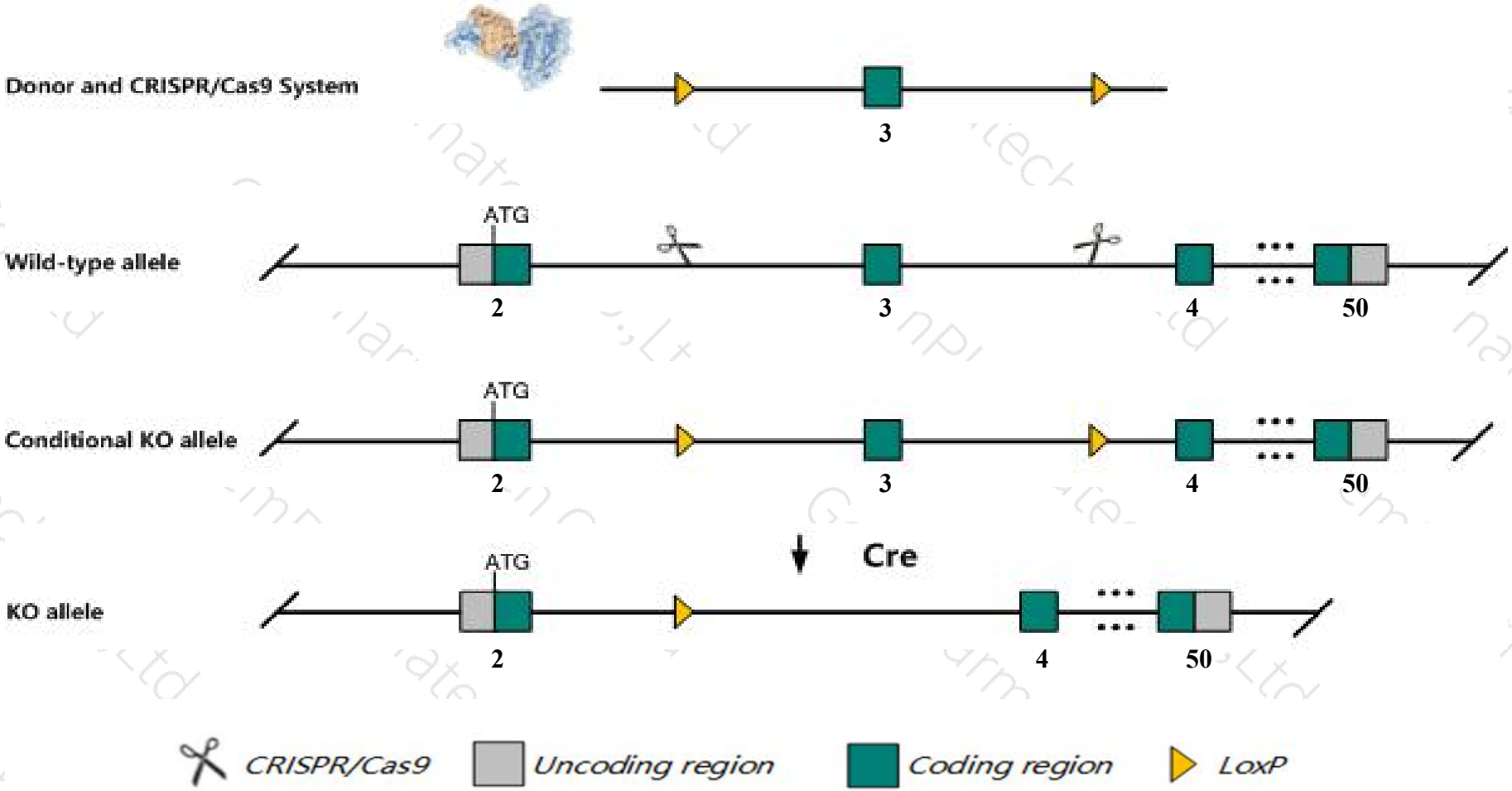
Designer:Lixin LYU

Project Overview

Project Name	***Abca1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abca1* gene. The schematic diagram is as follows:



Technical routes

- The *Abca1* gene has 2 transcripts. According to the structure of *Abca1* gene, exon3 of *Abca1-201* (ENSMUST00000030010.3) transcript is recommended as the knockout region.The region contains 94bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Abca1* 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,Many homozygous null mutants die perinatally with placental defects. Survivors show altered steroidogenesis, defective lipid export in Golgi, low serum cholesterol, lipid accumulation in macrophages and lung, reduced fertility and kidney and heart defects.

➢ The *Abca1* gene is located on the Chr4. 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）

集萃药康 GemPharmatech

Abca1 ATP-binding cassette, sub-family A (ABC1), member 1 [Mus musculus (house mouse)]

Gene ID: 11303, updated on 19-Mar-2019

Summary

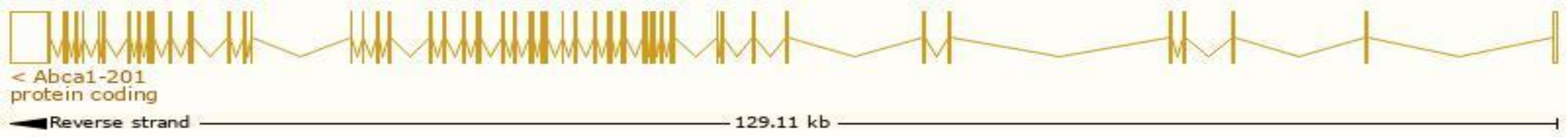
Official Symbol	Abca1 provided by MGI
Official Full Name	ATP-binding cassette, sub-family A (ABC1), member 1 provided by MGI
Primary source	MGI:MGI:99607
See related	Ensembl:ENSMUSG00000015243
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ABC-1, Abc1
Summary	The membrane-associated protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intracellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the ABC1 subfamily. Members of the ABC1 subfamily comprise the only major ABC subfamily found exclusively in multicellular eukaryotes. In humans, this protein functions as a cholesterol efflux pump in the cellular lipid removal pathway. Mutations in the human gene have been associated with Tangier's disease and familial high-density lipoprotein deficiency. [provided by RefSeq, Jul 2008]
Expression	Ubiquitous expression in ovary adult (RPKM 16.1), subcutaneous fat pad adult (RPKM 14.9) and 25 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

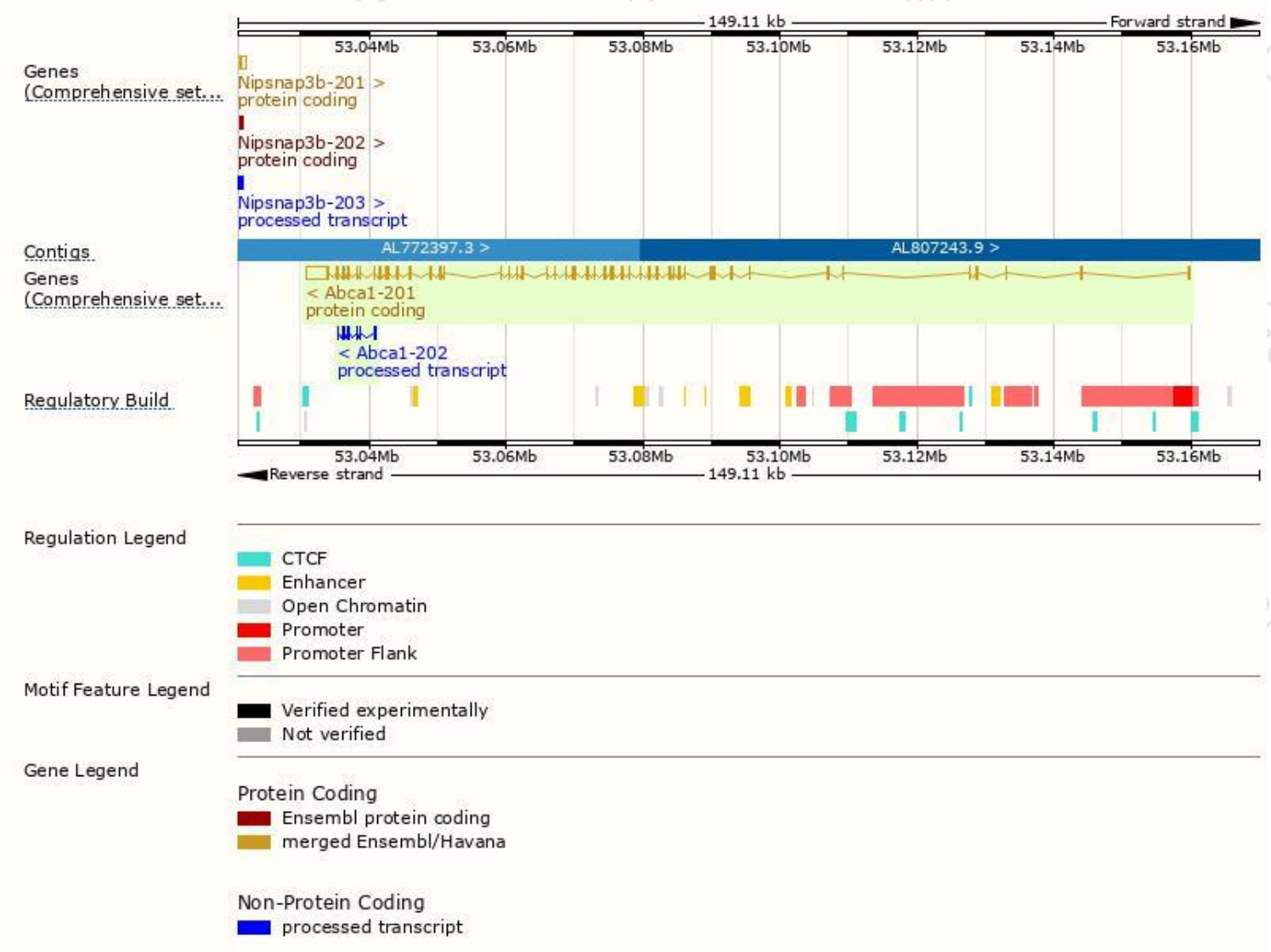
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abca1-201	ENSMUST00000030010.3	10262	2261aa	Protein coding	CCDS18187	P41233	TSL:1 GENCODE basic APPRIS P1
Abca1-202	ENSMUST00000149127.1	775	No protein	Processed transcript	-	-	TSL:5

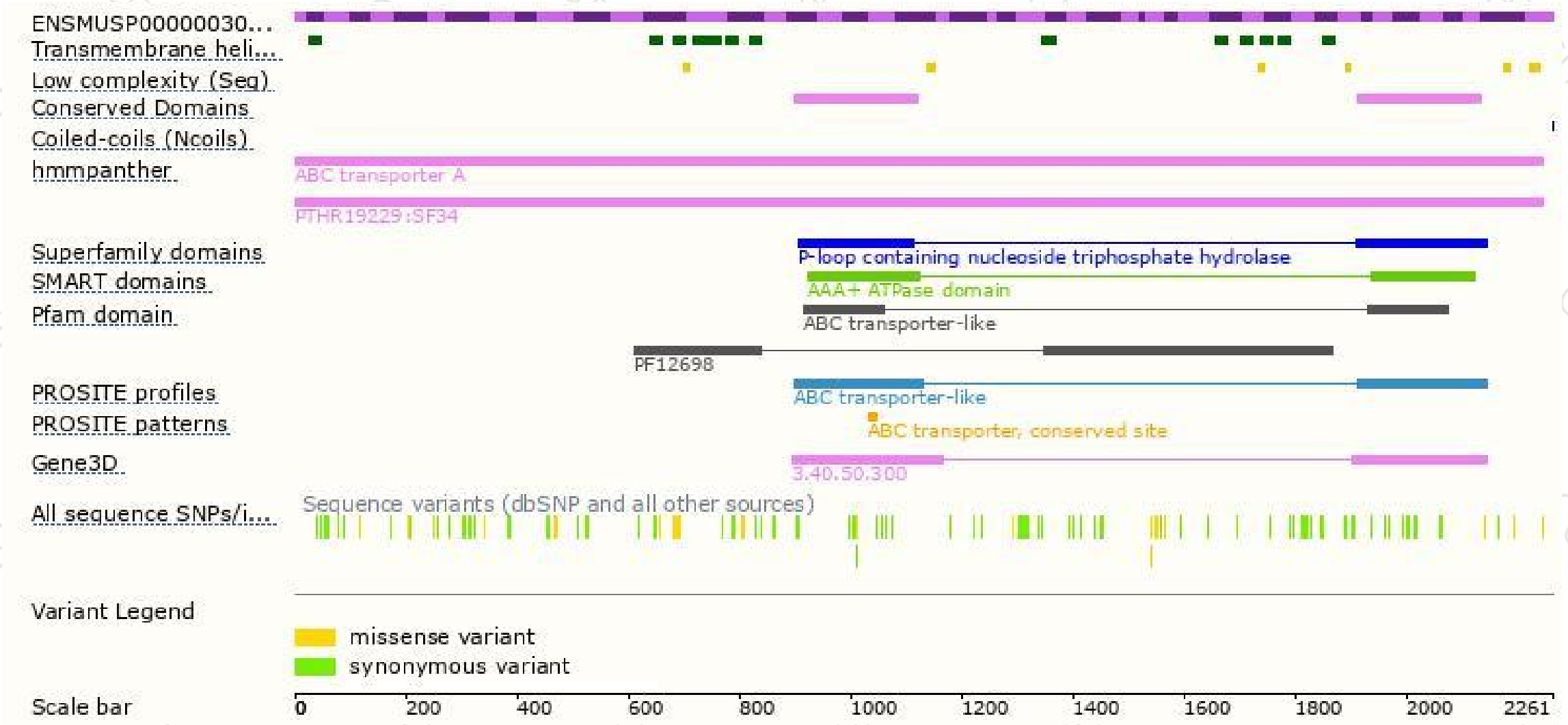
The strategy is based on the design of *Abca1-201* transcript,The transcription is shown below



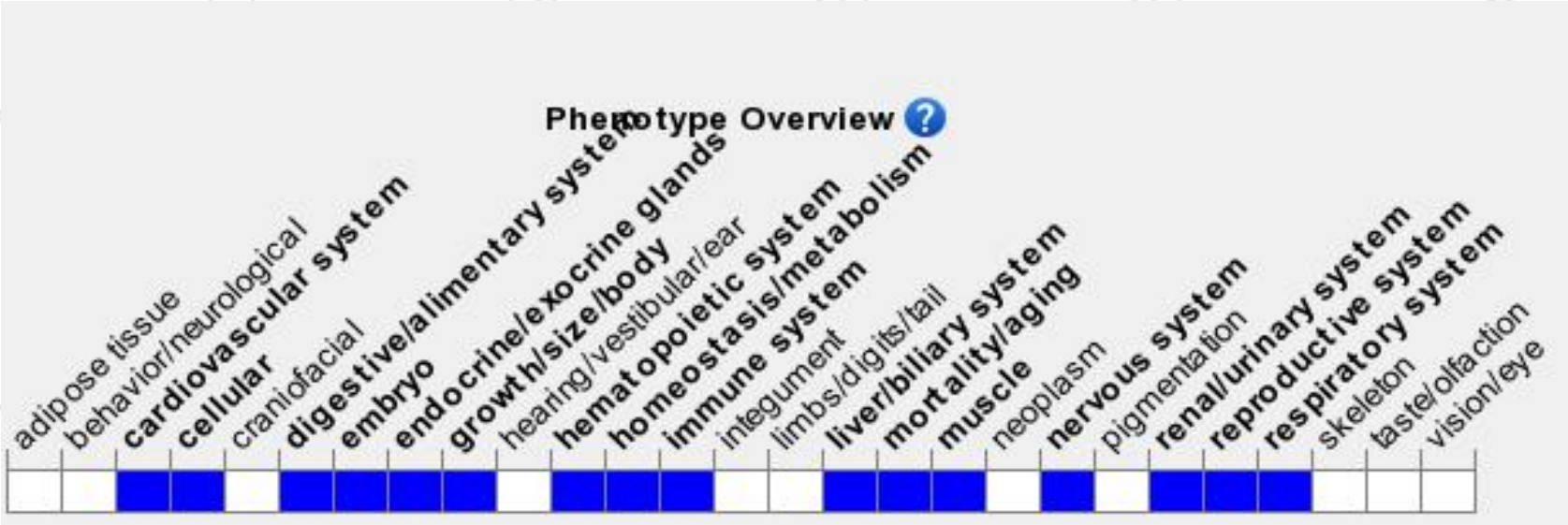
Genomic location distribution



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,Many homozygous null mutants die perinatally with placental defects. Survivors show altered steroidogenesis, defective lipid export in Golgi, low serum cholesterol, lipid accumulation in macrophages and lung, reduced fertility and kidney and heart defects.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd