

Ncoa1 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2019-9-28

Project Overview

Project Name

Ncoa1

Project type

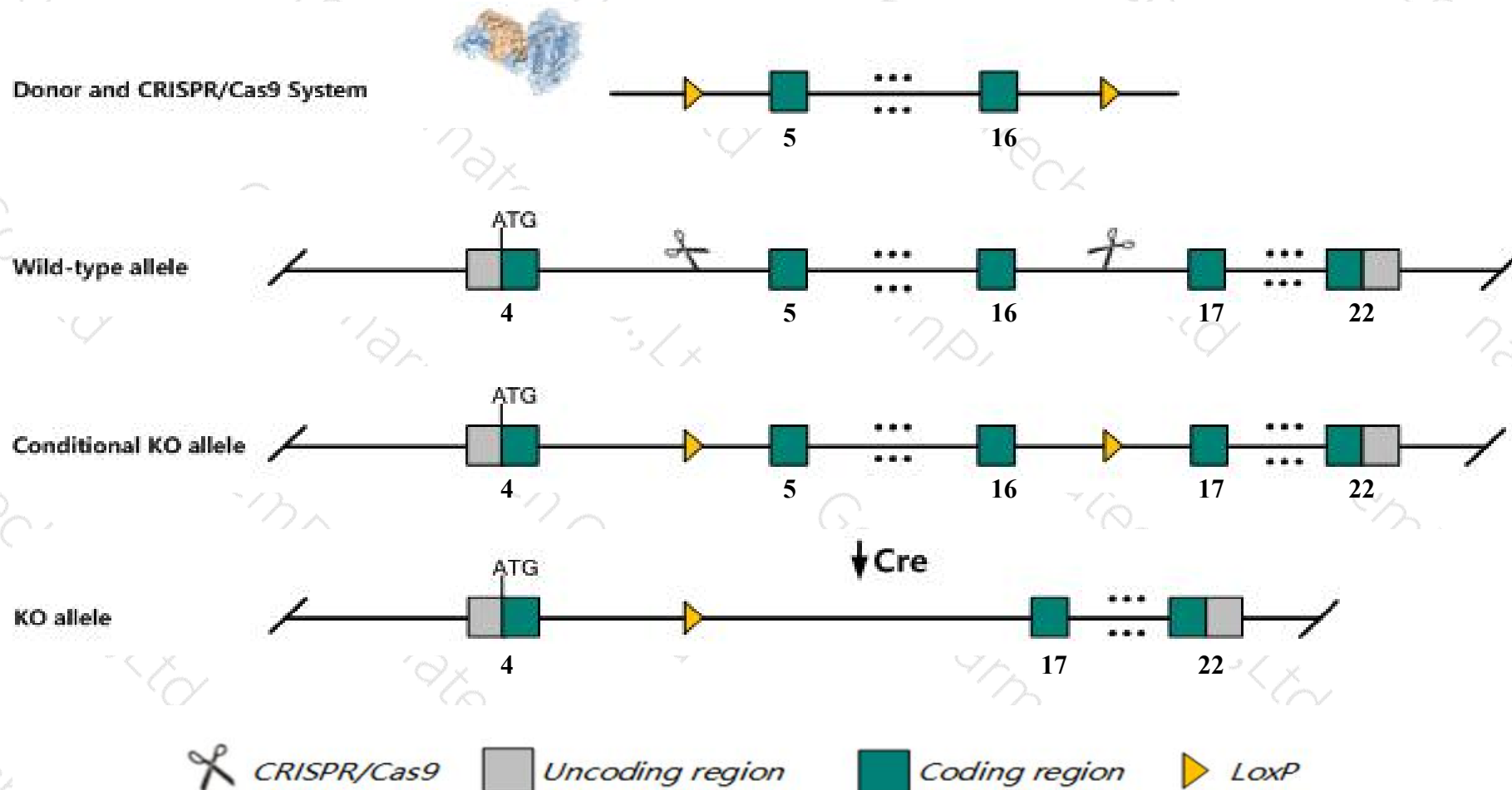
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncoa1* gene. The schematic diagram is as follows:



Technical routes

- The *Ncoa1* gene has 9 transcripts. According to the structure of *Ncoa1* gene, exon5-exon16 of *Ncoa1-201* (ENSMUST00000085814.4) transcript is recommended as the knockout region. The region contains 3130bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ncoa1* 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, Homozygotes for a null allele show osteopenia, increased serum sex hormone levels, altered bone remodeling and skeletal responses to sex hormones, and obesity. Homozygotes for another null allele show thyroid and steroid hormone resistance, delayed Purkinje cell development, and behavioral deficits.
- The *Ncoal* gene is located on the Chr12. 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)

Ncoa1 nuclear receptor coactivator 1 [Mus musculus (house mouse)]

Gene ID: 17977, updated on 31-Jan-2019

Summary



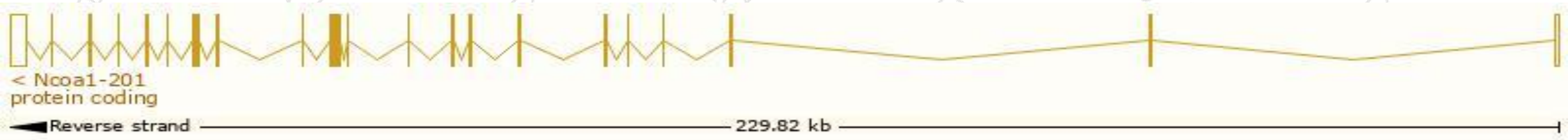
Official Symbol	Ncoa1 provided by MGI
Official Full Name	nuclear receptor coactivator 1 provided by MGI
Primary source	MGI:MGI:1276523
See related	Ensembl:ENSMUSG00000020647
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	KAT13A, NCoA-1, NRC-1, SRC-1, SRC-a, SRC1, bHLHe74, mNRC-1
Expression	Ubiquitous expression in CNS E18 (RPKM 11.3), cerebellum adult (RPKM 11.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

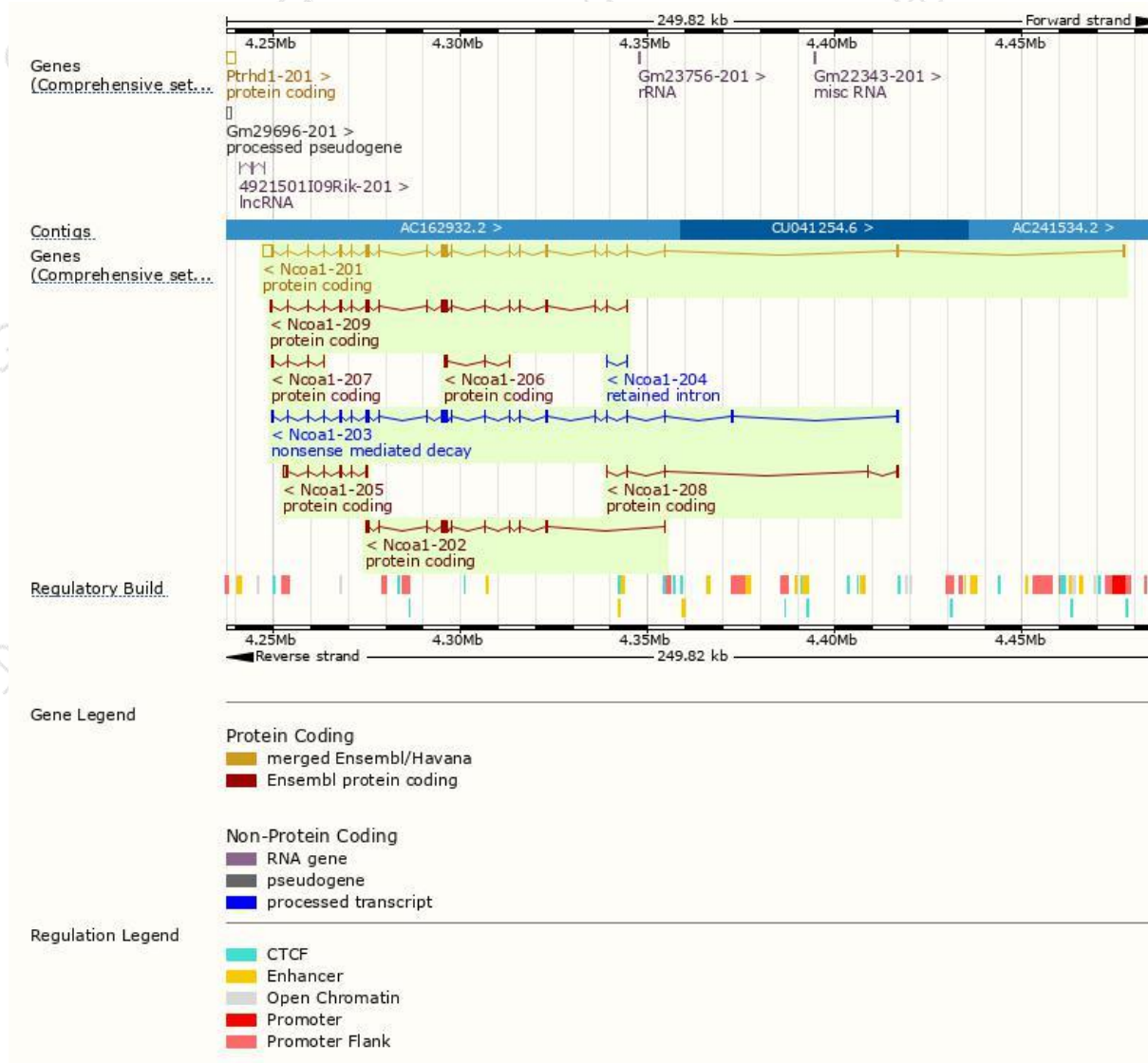
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncoa1-201	ENSMUST00000085814.4	7329	1405aa	Protein coding	CCDS25789	P70365	TSL:1 GENCODE basic APPRIS P2
Ncoa1-209	ENSMUST00000220434.1	4756	1447aa	Protein coding	-	P70365	TSL:1 GENCODE basic APPRIS ALT2
Ncoa1-202	ENSMUST00000217674.1	2822	922aa	Protein coding	-	A0A1W2P7C1	CDS 3' incomplete TSL:5
Ncoa1-205	ENSMUST00000218191.1	2069	430aa	Protein coding	-	A0A1W2P7S6	CDS 5' incomplete TSL:1
Ncoa1-207	ENSMUST00000219373.1	781	154aa	Protein coding	-	A0A1W2P7D7	CDS 5' incomplete TSL:2
Ncoa1-206	ENSMUST00000219275.1	745	99aa	Protein coding	-	A0A1W2P881	CDS 5' incomplete TSL:3
Ncoa1-208	ENSMUST00000219715.1	542	54aa	Protein coding	-	A0A1W2P6K7	CDS 3' incomplete TSL:3
Ncoa1-203	ENSMUST00000217794.1	4917	1330aa	Nonsense mediated decay	-	P70365	TSL:1
Ncoa1-204	ENSMUST00000217822.1	365	No protein	Retained intron	-	-	TSL:3

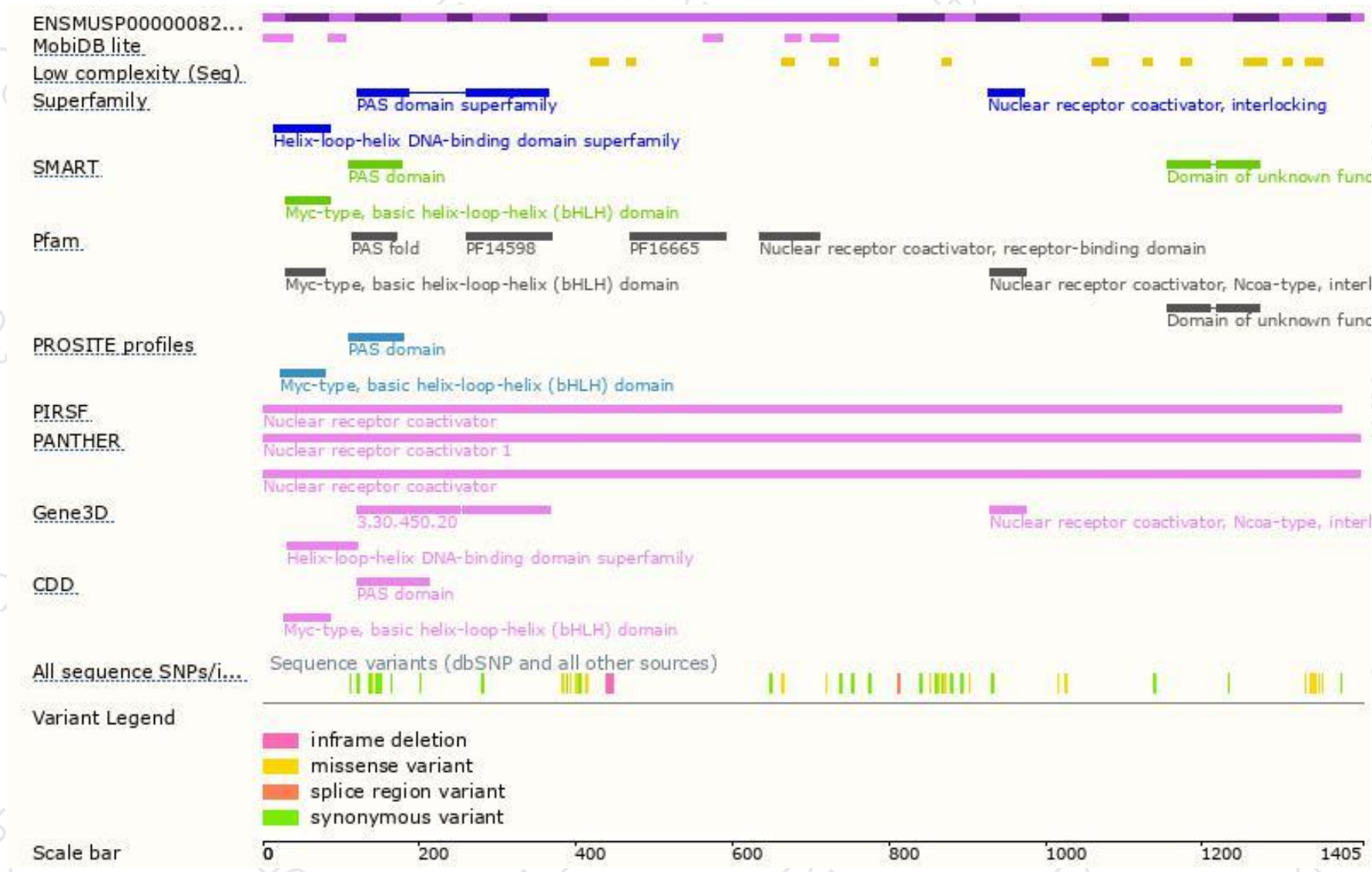
The strategy is based on the design of *Ncoa1-201* transcript,The transcription is shown below



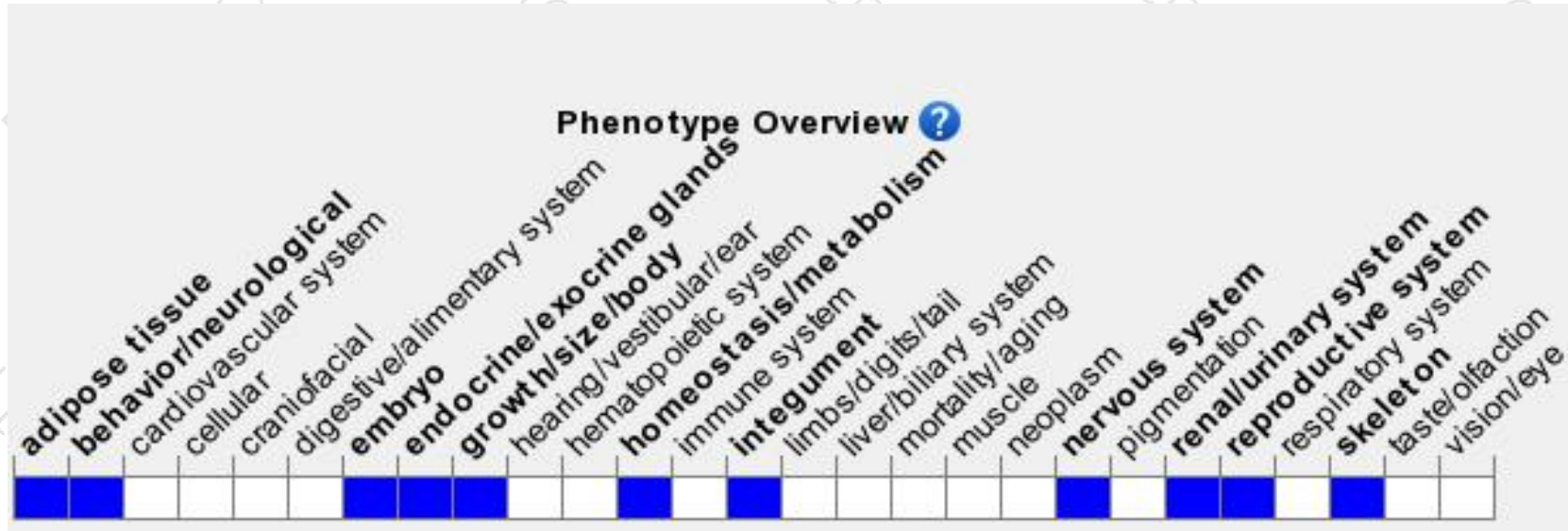
Genomic location distribution



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, Homozygotes for a null allele show osteopenia, increased serum sex hormone levels, altered bone remodeling and skeletal responses to sex hormones, and obesity. Homozygotes for another null allele show thyroid and steroid hormone resistance, delayed Purkinje cell development, and behavioral deficits.

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

Tel: 400-9660890

