Ncoa2 Cas9-CKO Strategy

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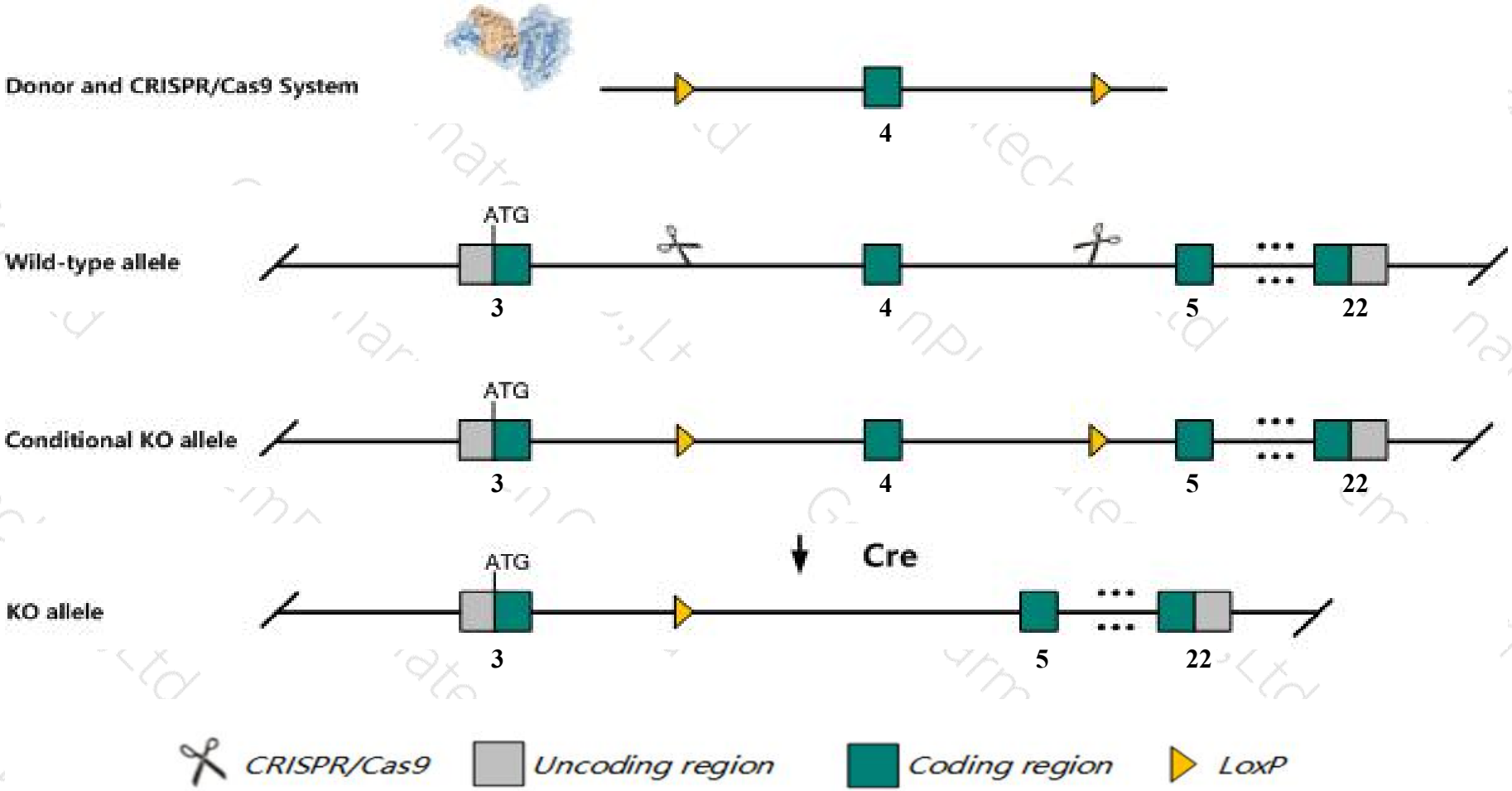
Project Overview

Project Name	***Ncoa2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncoa2* gene. The schematic diagram is as follows:



Technical routes

- The *Ncoa2* gene has 11 transcripts. According to the structure of *Ncoa2* gene, exon4 of *Ncoa2-203* (ENSMUST00000081713.10) transcript is recommended as the knockout region.The region contains 173bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ncoa2* 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,homozygous null mice exhibit a transient postnatal growth deficiency and hypofertility. Male hypofertility is due to defects in spermiogenesis and an age-dependent testicular degeneration preceded by defective lipid metabolism in Sertoli cells. Female hypofertility is due to a placental hypoplasia.

➢ The *Ncoa2* gene is located on the Chr1. 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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Ncoa2 nuclear receptor coactivator 2 [*Mus musculus* (house mouse)]

Gene ID: 17978, updated on 26-Nov-2019

Summary

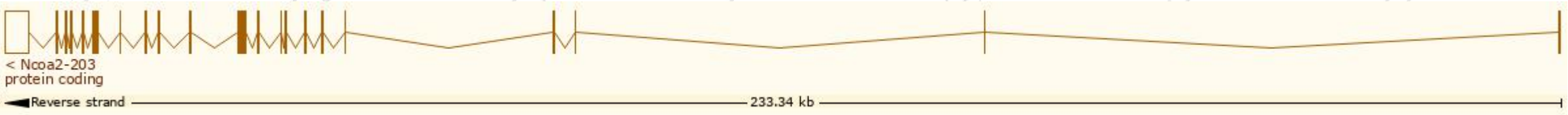
Official Symbol	Ncoa2 provided by MGI
Official Full Name	nuclear receptor coactivator 2 provided by MGI
Primary source	MGI:MGI:1276533
See related	Ensembl:ENSMUSG00000005886
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TIF2; Grip1; SRC-2; GRIP-1; KAT13C; NCoA-2; bHLHe75; D1Ertd433e
Expression	Ubiquitous expression in testis adult (RPKM 10.9), thymus adult (RPKM 8.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

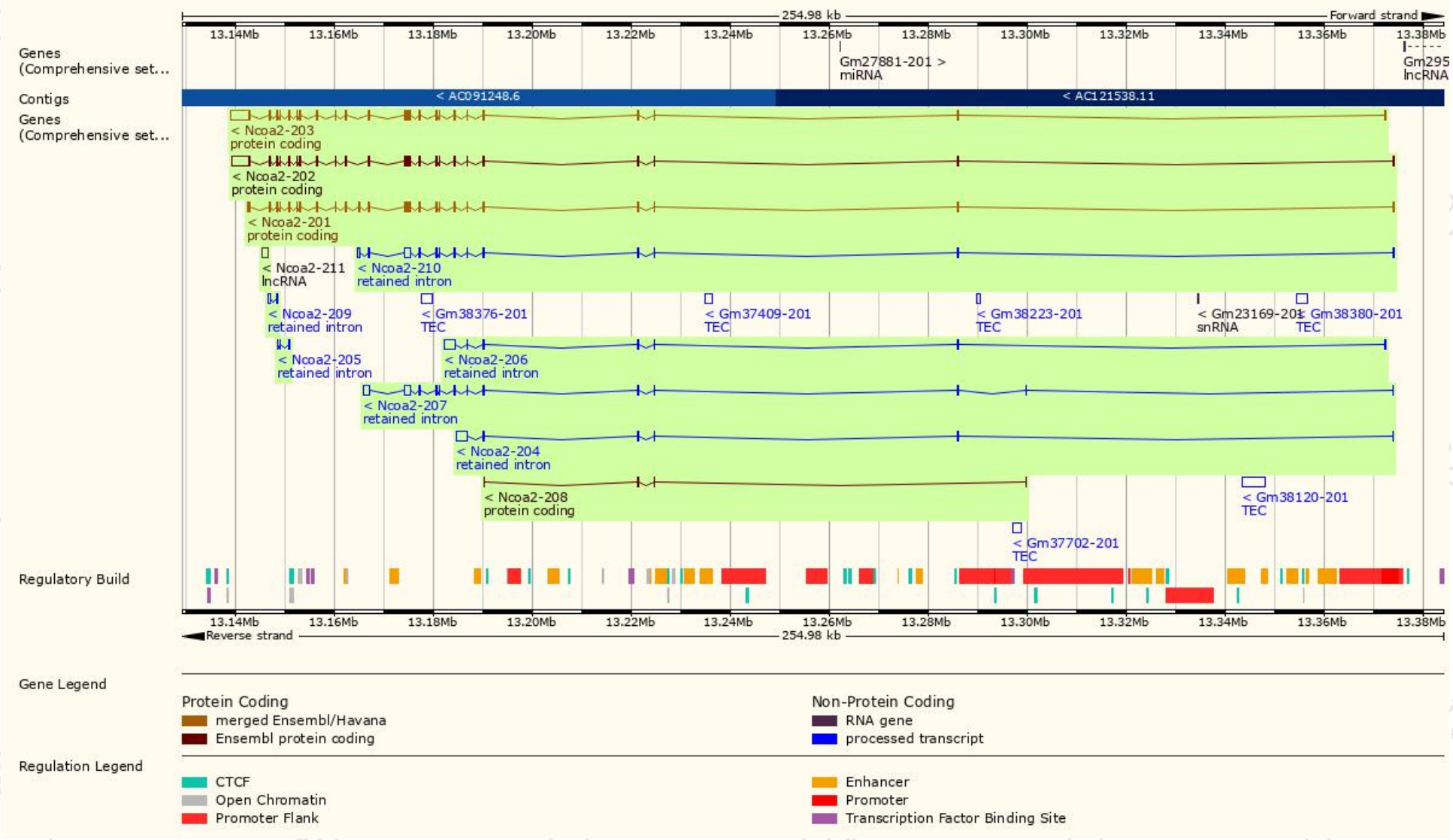
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncoa2-201	ENSMUST00000006037.12	4897	1462aa	Protein coding	CCDS35515	Q61026	TSL:1 GENCODE basic APPRIS P4
Ncoa2-202	ENSMUST00000068304.12	8006	1393aa	Protein coding	CCDS35514	E9PV80	TSL:5 GENCODE basic APPRIS ALT1
Ncoa2-203	ENSMUST00000081713.10	8171	1393aa	Protein coding	CCDS35514	E9PV80	TSL:1 GENCODE basic APPRIS ALT1
Ncoa2-204	ENSMUST00000124088.1	2836	No protein	Retained intron	-	-	TSL:1
Ncoa2-205	ENSMUST00000133232.1	594	No protein	Retained intron	-	-	TSL:2
Ncoa2-206	ENSMUST00000139970.7	2944	No protein	Retained intron	-	-	TSL:1
Ncoa2-207	ENSMUST00000143603.7	3804	No protein	Retained intron	-	-	TSL:1
Ncoa2-208	ENSMUST00000145280.1	423	114aa	Protein coding	-	D3Z4F6	CDS 3' incomplete TSL:3
Ncoa2-209	ENSMUST00000146784.1	557	No protein	Retained intron	-	-	TSL:3
Ncoa2-210	ENSMUST00000147927.7	3429	No protein	Retained intron	-	-	TSL:1
Ncoa2-211	ENSMUST00000185275.1	1330	No protein	lncRNA	-	-	TSL:NA

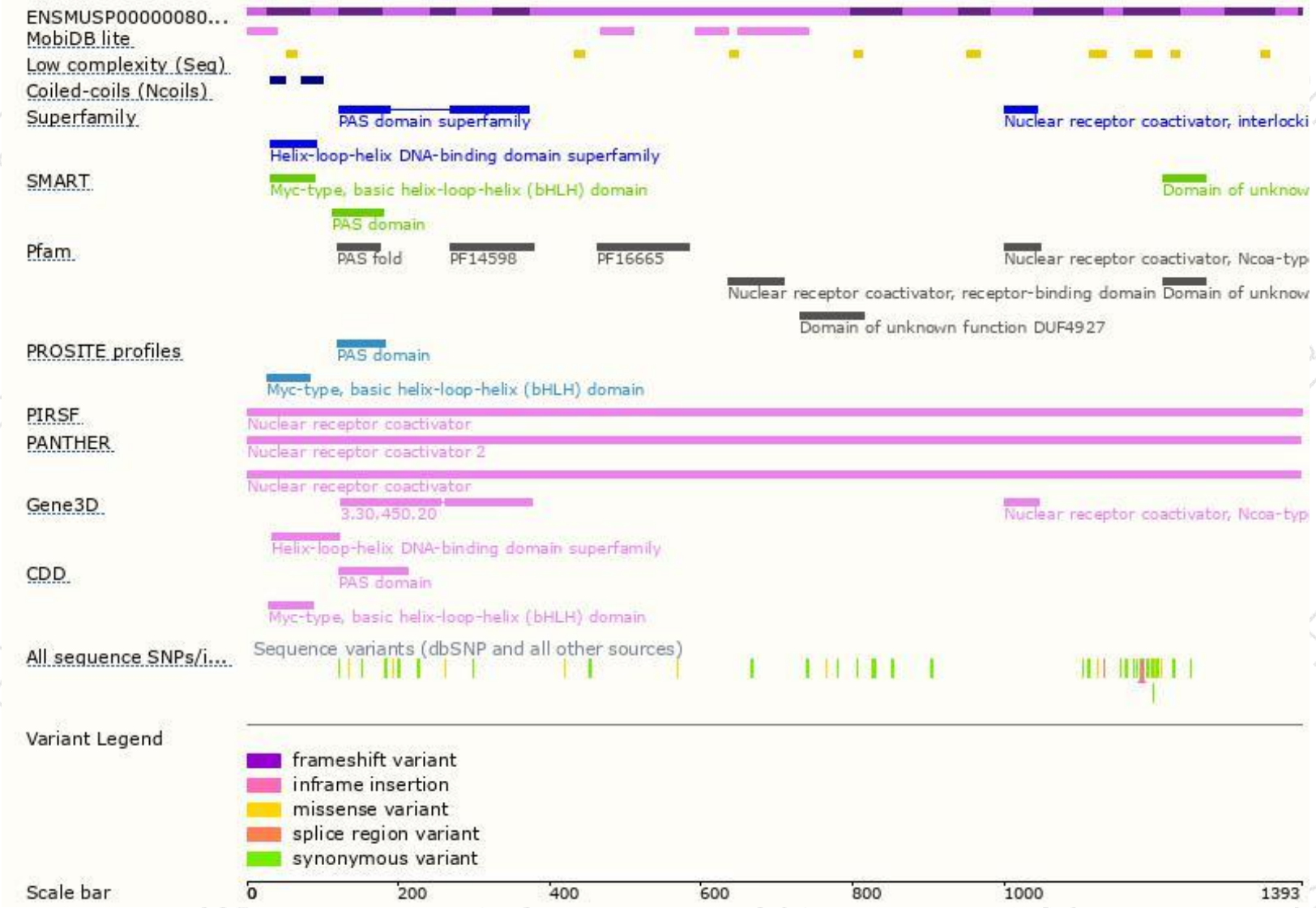
The strategy is based on the design of *Ncoa2-203* transcript,The transcription is shown below:



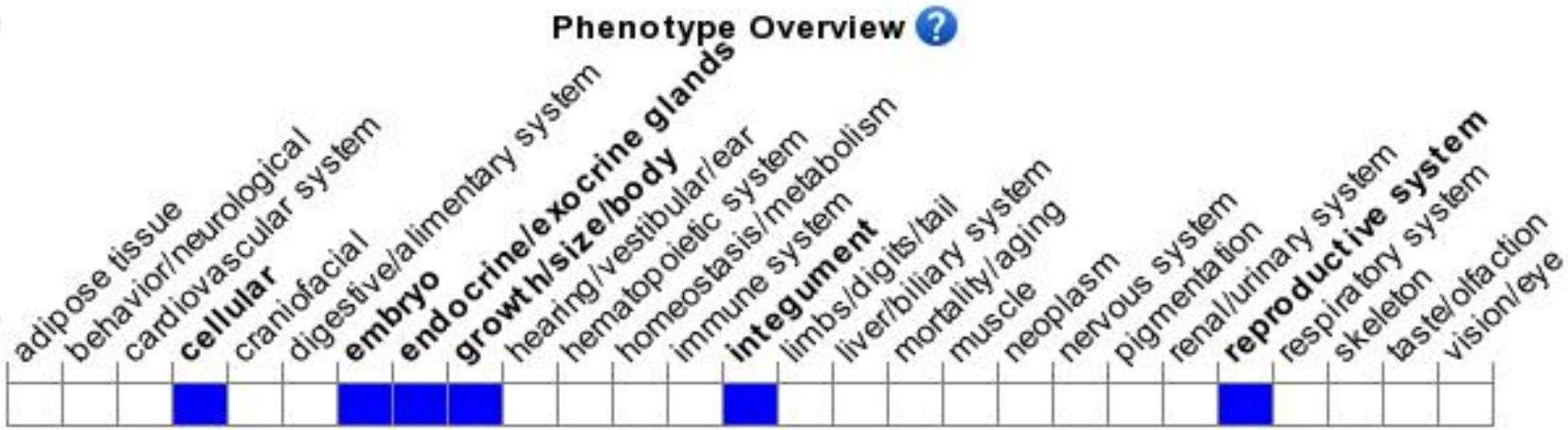
Genomic location distribution



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,Homozygous null mice exhibit a transient postnatal growth deficiency and hypofertility. Male hypofertility is due to defects in spermiogenesis and an age-dependent testicular degeneration preceded by defective lipid metabolism in Sertoli cells. Female hypofertility is due to a placental hypoplasia.

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

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