Ncor1 Cas9-KO Strategy

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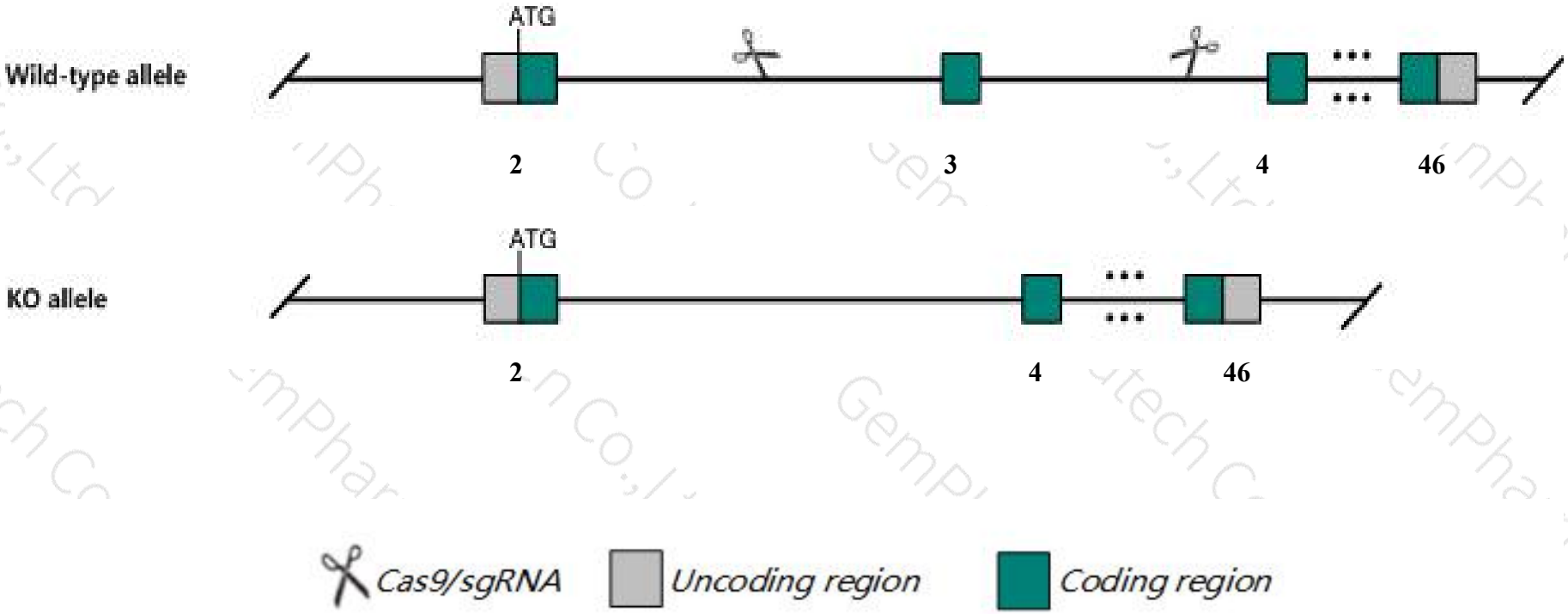
Project Overview

Project Name	***Ncor1***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncor1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ncor1* gene has 25 transcripts. According to the structure of *Ncor1* gene, exon3 of *Ncor1-201* (ENSMUST00000018645.12) transcript is recommended as the knockout region.The region contains 137bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ncor1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

- According to the existing MGI data,Mice homozygous for a targeted mutation in this gene exhibit embryonic lethality with erythrocytic, thymocytic and central nervous system development abnormalities. Mice homozygous for a hypomorphic allele exhibit increased thyroid hormone sensitivity under hypothyroid conditions.

- The *Ncor1* gene is located on the Chr11. 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）

集萃药康 GemPharmatech

Ncor1 nuclear receptor co-repressor 1 [Mus musculus (house mouse)]

Gene ID: 20185, updated on 9-Apr-2019

Summary

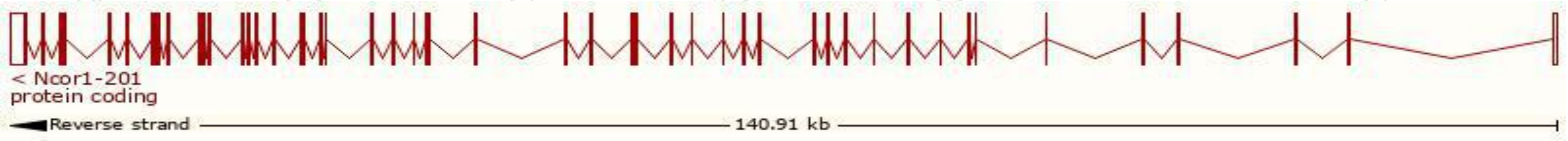
Official Symbol	Ncor1 provided by MGI
Official Full Name	nuclear receptor co-repressor 1 provided byMGI
Primary source	MGI:MGI:1349717
See related	Ensembl:ENSMUSG00000018501
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730405M06Rik, A230020K14Rik, N-CoR, RIP13, Rxrip13, mKIAA1047
Expression	Ubiquitous expression in thymus adult (RPKM 15.4), CNS E14 (RPKM 13.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

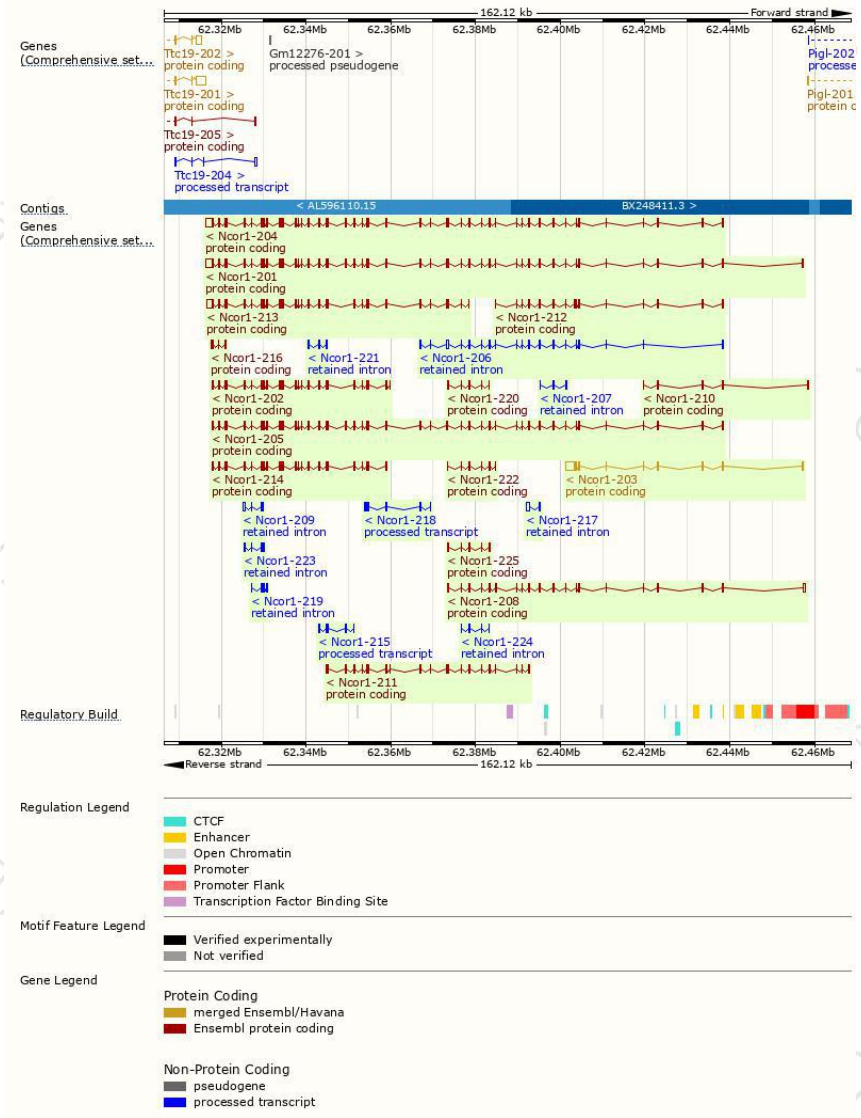
The gene has 25 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncor1-201	ENSMUST00000018645.12	9037	2454aa	Protein coding	CCDS56781	Q5RIM6	TSL:5 GENCODE basic APPRIS P2
Ncor1-204	ENSMUST00000101066.9	8852	2454aa	Protein coding	CCDS56781	Q5RIM6	TSL:5 GENCODE basic APPRIS P2
Ncor1-203	ENSMUST00000069456.10	3171	291aa	Protein coding	CCDS56782	Q8BK32	TSL:1 GENCODE basic
Ncor1-205	ENSMUST00000101067.9	7243	2386aa	Protein coding	-	E9Q2B2	TSL:5 GENCODE basic APPRIS ALT2
Ncor1-213	ENSMUST00000155712.8	6328	1724aa	Protein coding	-	Q8CHB6	CDS 5' incomplete TSL:5
Ncor1-202	ENSMUST00000037575.14	4246	1399aa	Protein coding	-	E9Q9Y2	TSL:1 GENCODE basic
Ncor1-214	ENSMUST00000156740.8	4215	1389aa	Protein coding	-	F7C134	CDS 5' incomplete TSL:5
Ncor1-211	ENSMUST00000151498.8	2979	993aa	Protein coding	-	Q3UV08	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Ncor1-208	ENSMUST00000127471.8	2815	791aa	Protein coding	-	E9Q8K6	CDS 3' incomplete TSL:5
Ncor1-212	ENSMUST00000155486.7	1695	541aa	Protein coding	-	Q5RIN0	CDS 3' incomplete TSL:5
Ncor1-225	ENSMUST00000162236.7	781	261aa	Protein coding	-	F6SFD2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ncor1-222	ENSMUST00000161699.7	762	254aa	Protein coding	-	F6TWR1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ncor1-216	ENSMUST00000159315.1	716	157aa	Protein coding	-	F6TRR6	CDS 5' incomplete TSL:2
Ncor1-220	ENSMUST00000161288.7	649	216aa	Protein coding	-	F6U338	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ncor1-210	ENSMUST00000141447.1	646	163aa	Protein coding	-	E0CYX5	CDS 3' incomplete TSL:5
Ncor1-218	ENSMUST00000161116.2	723	No protein	Processed transcript	-	-	TSL:5
Ncor1-215	ENSMUST00000159224.4	563	No protein	Processed transcript	-	-	TSL:5
Ncor1-206	ENSMUST00000101068.8	2815	No protein	Retained intron	-	-	TSL:5
Ncor1-221	ENSMUST00000161432.1	800	No protein	Retained intron	-	-	TSL:2
Ncor1-209	ENSMUST00000131911.7	793	No protein	Retained intron	-	-	TSL:2
Ncor1-217	ENSMUST00000160171.1	690	No protein	Retained intron	-	-	TSL:5
Ncor1-223	ENSMUST00000161767.7	667	No protein	Retained intron	-	-	TSL:2
Ncor1-219	ENSMUST00000161281.1	643	No protein	Retained intron	-	-	TSL:2
Ncor1-207	ENSMUST00000124027.2	566	No protein	Retained intron	-	-	TSL:5
Ncor1-224	ENSMUST00000162077.1	452	No protein	Retained intron	-	-	TSL:3

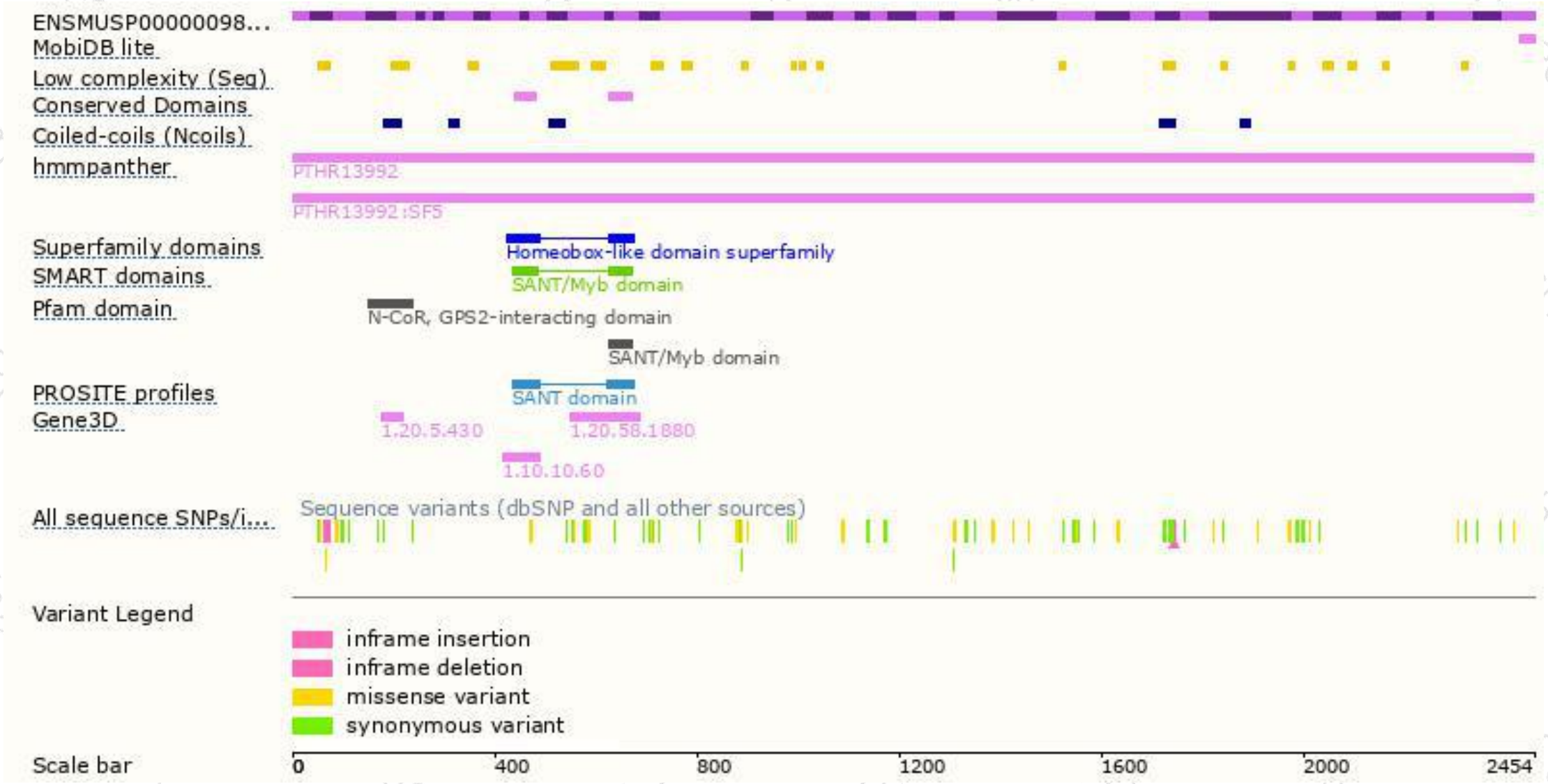
The strategy is based on the design of *Ncor1-201* transcript,The transcription is shown below



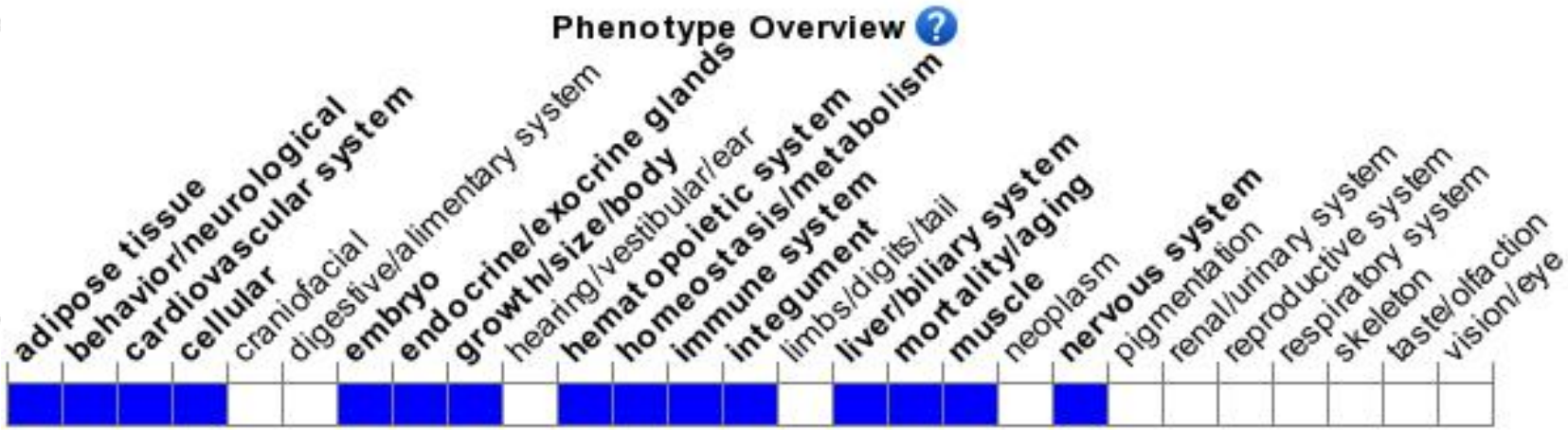
Genomic location distribution



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/).

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