Cecr2 Cas9-CKO Strategy

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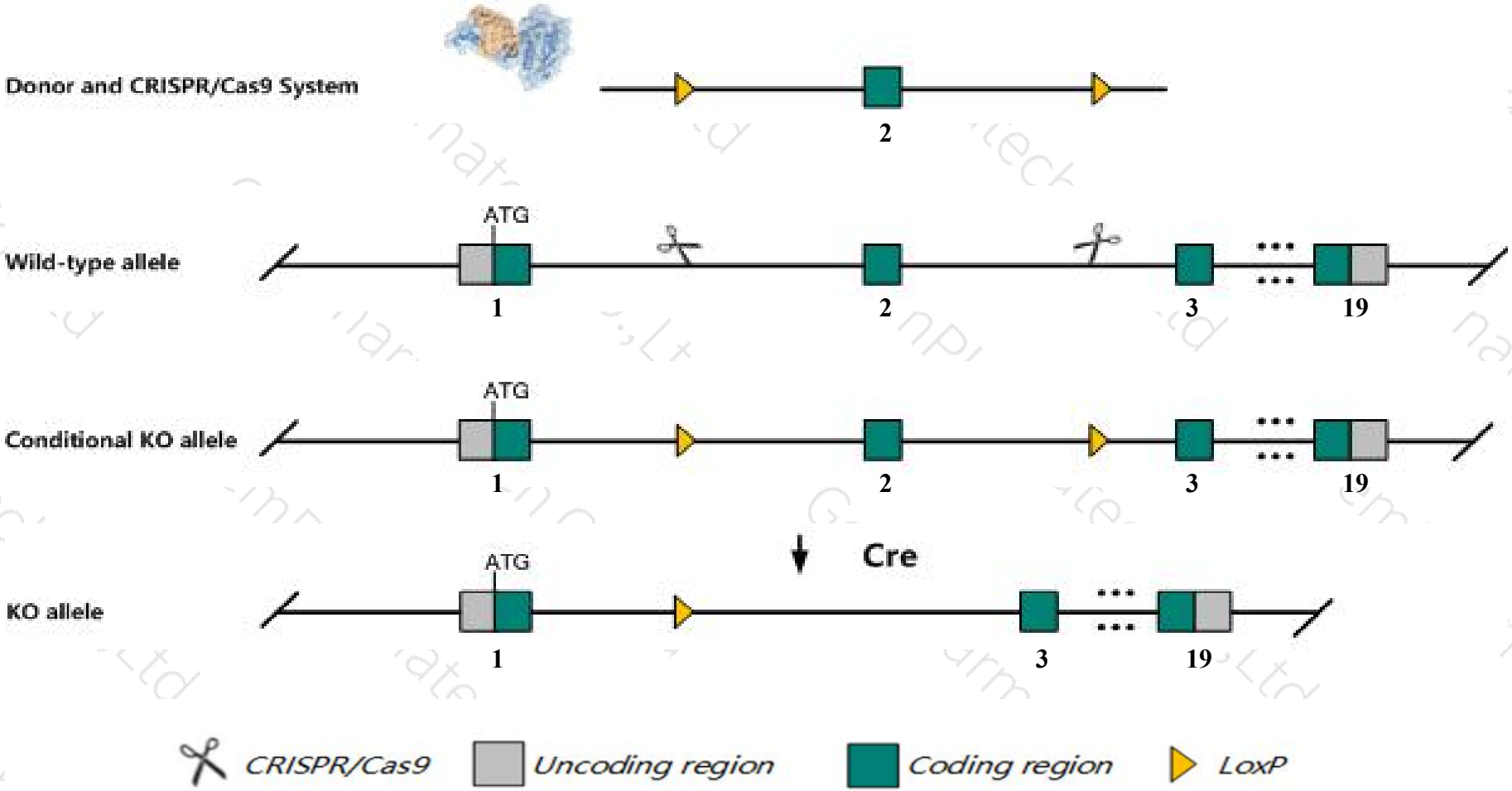
Project Overview

Project Name	***Cecr2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cecr2* gene. The schematic diagram is as follows:



Technical routes

- The *Cecr2* gene has 8 transcripts. According to the structure of *Cecr2* gene, exon2 of *Cecr2-202* (ENSMUST00000112686.7) transcript is recommended as the knockout region.The region contains 95bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cecr2* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 mutant mice display varied penetrance of exencephaly depending on genetic background.

- Transcript *Cecr2-204,206* may not be affected.

- The *Cecr2* gene is located on the Chr6. 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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Cecr2 CECR2, histone acetyl-lysine reader [Mus musculus (house mouse)]

Gene ID: 330409, updated on 21-Feb-2019

Summary

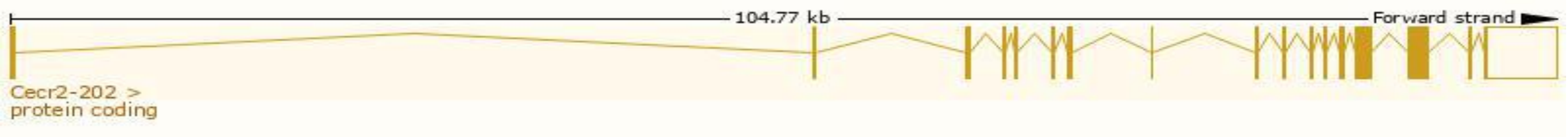
Official Symbol	Cecr2 provided by MGI
Official Full Name	CECR2, histone acetyl-lysine reader provided byMGI
Primary source	MGI:MGI:1923799
See related	Ensembl:ENSMUSG00000071226
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610101O16Rik, 2810409N01Rik, Gtl4
Expression	Ubiquitous expression in testis adult (RPKM 4.5), CNS E11.5 (RPKM 4.0) and 23 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

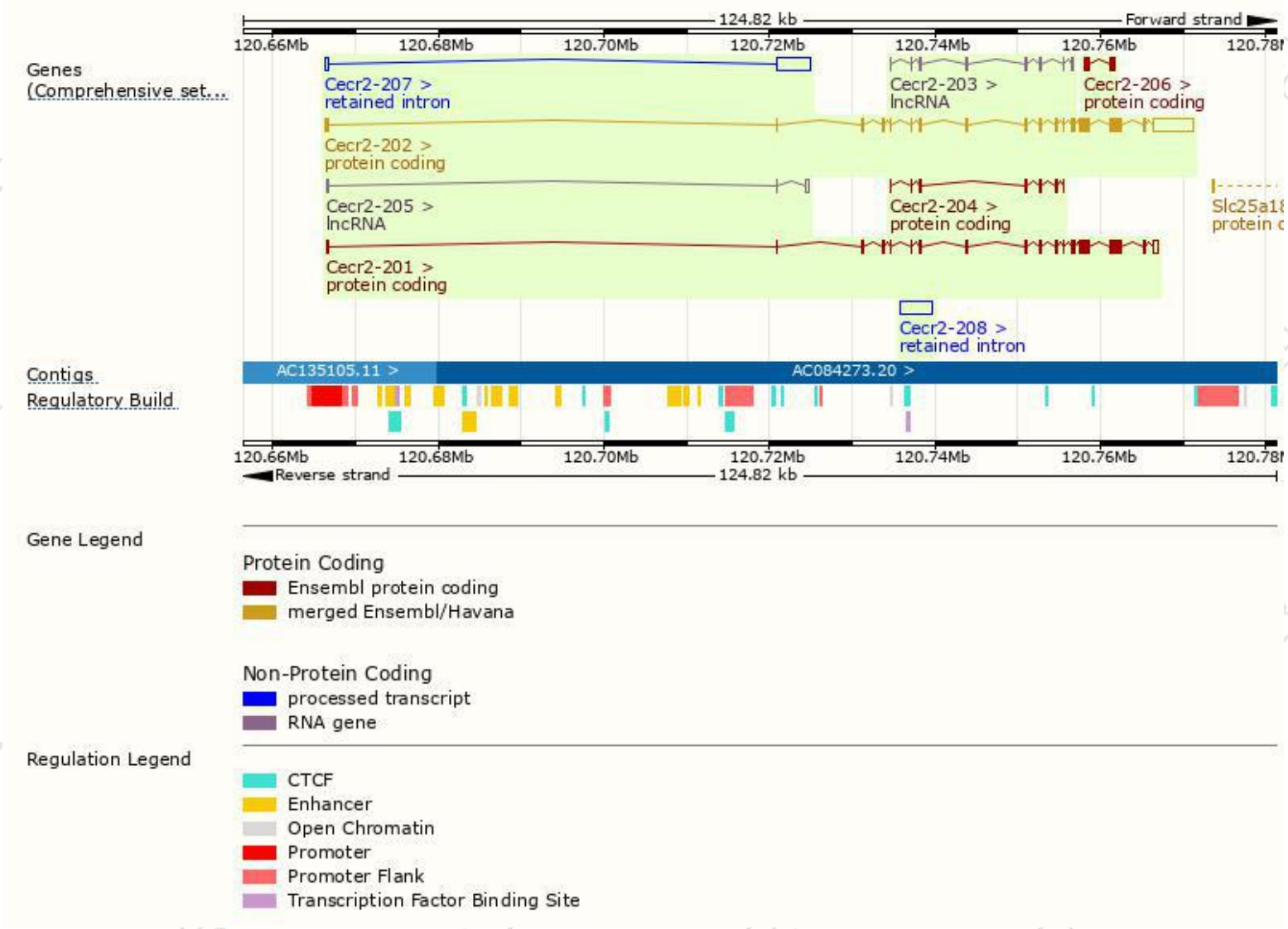
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cecr2-202	ENSMUST00000112686.7	9212	1425aa	Protein coding	CCDS51890	E9Q2Z1	TSL:5 GENCODE basic APPRIS P2
Cecr2-201	ENSMUST00000100993.8	4849	1453aa	Protein coding	-	E9Q2Z1	TSL:5 GENCODE basic APPRIS ALT2
Cecr2-206	ENSMUST00000143563.1	1071	357aa	Protein coding	-	-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Cecr2-204	ENSMUST00000129803.1	704	234aa	Protein coding	-	-	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
Cecr2-207	ENSMUST00000148346.1	4392	No protein	Retained intron	-	-	TSL:1
Cecr2-208	ENSMUST00000204732.1	3996	No protein	Retained intron	-	-	TSL:NA
Cecr2-203	ENSMUST00000124634.1	946	No protein	lncRNA	-	-	TSL:5
Cecr2-205	ENSMUST00000135109.1	641	No protein	lncRNA	-	-	TSL:3

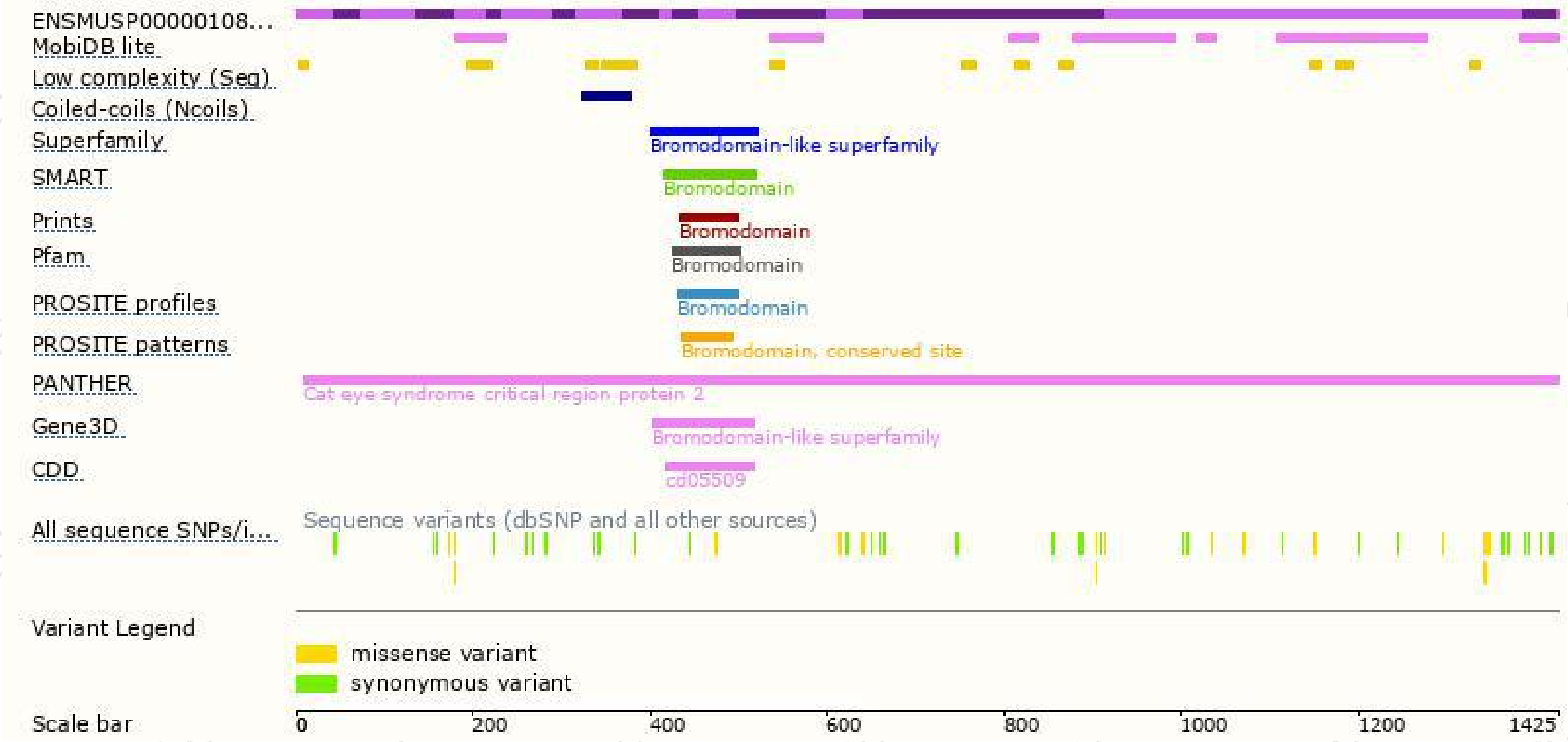
The strategy is based on the design of *Cecr2-202* transcript,The transcription is shown below



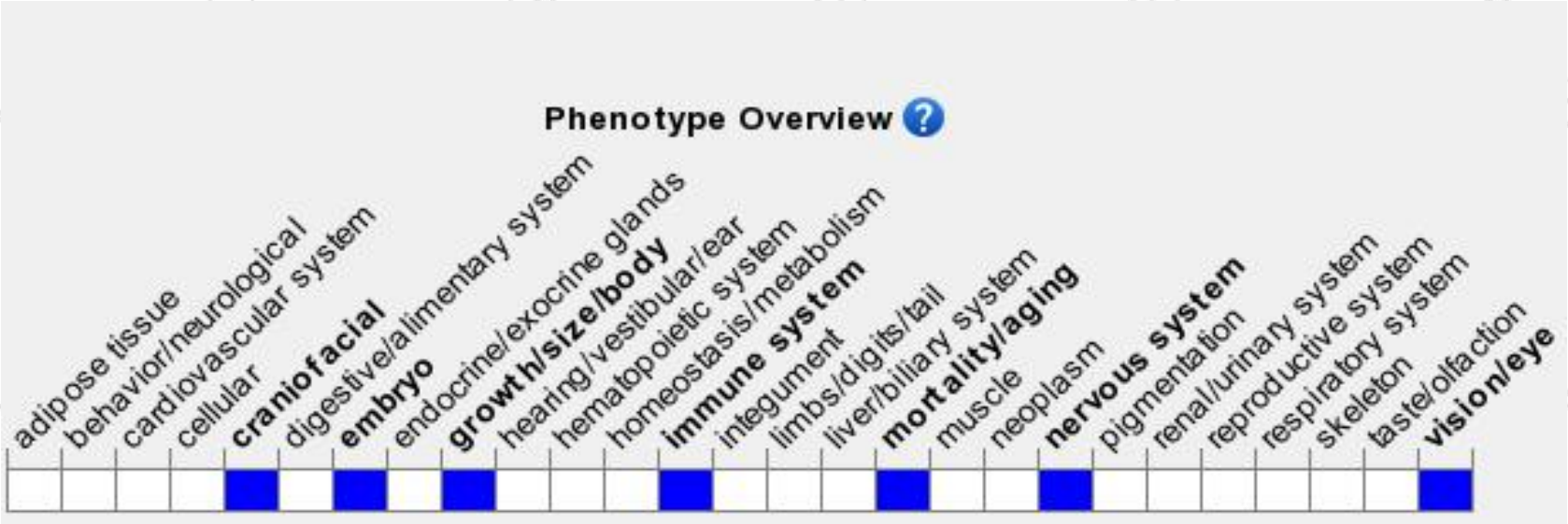
Genomic location distribution



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 mutant mice display varied penetrance of exencephaly depending on genetic background.

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

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