Ywhae Cas9-CKO Strategy

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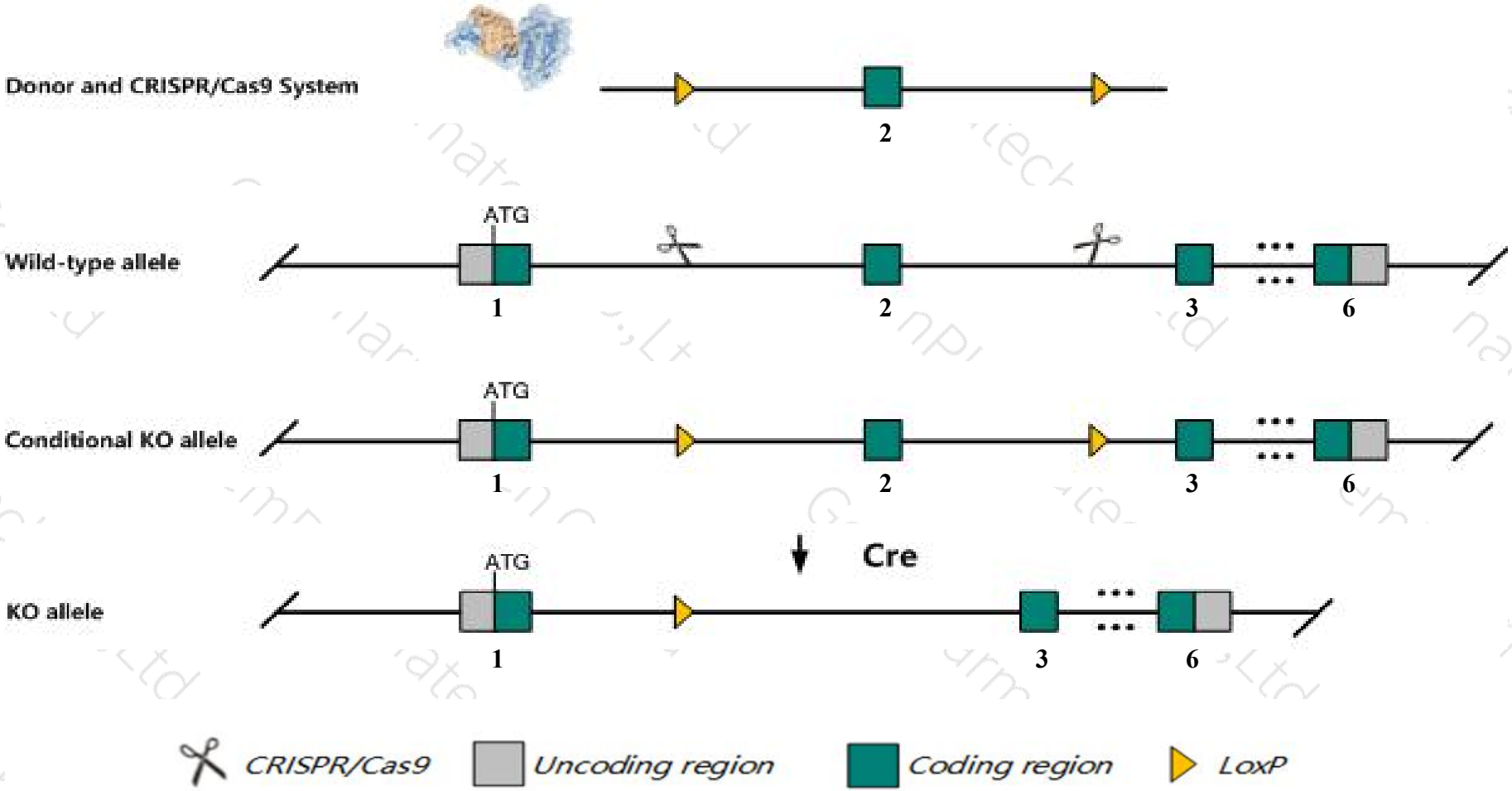
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Ywhae* gene has 5 transcripts. According to the structure of *Ywhae* gene, exon2 of *Ywhae-201* (ENSMUST00000067664.9) transcript is recommended as the knockout region.The region contains 200bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ywhae* 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,Mice homozygous for disruptions of this gene usually die around birth. The small percentage of survivors are small in size and display central nervous system abnormalities including a thinner cortex and a disorganized pyramidal cell layer in the hippocampus.

➢ The *Ywhae* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Ywhae tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus musculus (house mouse)]

Gene ID: 22627, updated on 7-Apr-2019

Summary

Official Symbol	Ywhae provided by MGI
Official Full Name	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide provided by MGI
Primary source	MGI:MGI:894689
See related	Ensembl:ENSMUSG00000020849
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	AU019196
Expression	Broad expression in CNS E11.5 (RPKM 424.9), CNS E18 (RPKM 417.5) and 25 other tissues See more
Orthologs	human all

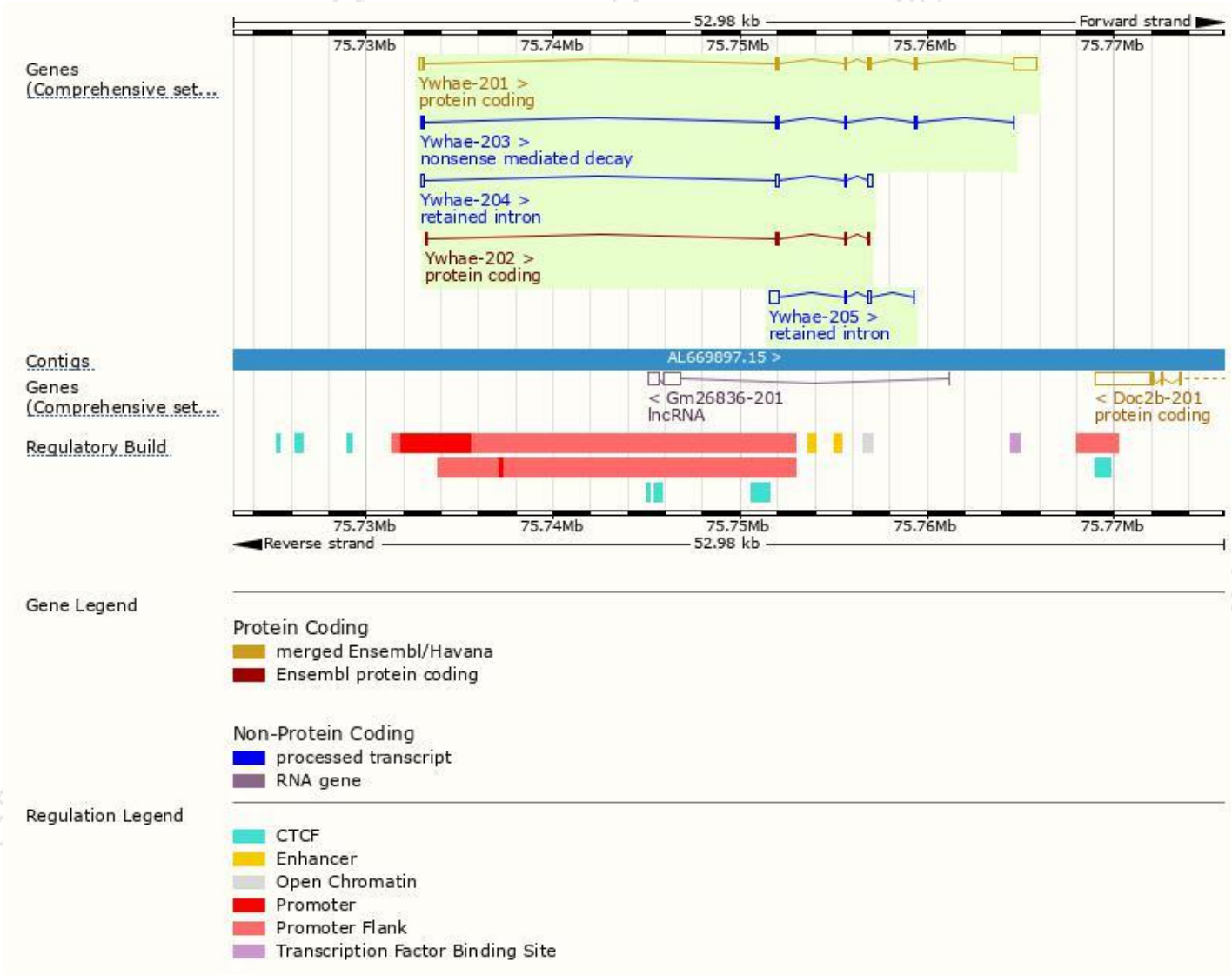
Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ywhae-201	ENSMUST00000067664.9	2100	255aa	Protein coding	CCDS25056	P62259 Q5SS40	TSL:1 GENCODE basic APPRIS P1
Ywhae-202	ENSMUST00000131398.1	461	154aa	Protein coding	-	F6WA09	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
Ywhae-203	ENSMUST00000134745.7	599	130aa	Nonsense mediated decay	-	D6REF3	TSL:1
Ywhae-205	ENSMUST00000155057.1	815	No protein	Retained intron	-	-	TSL:2
Ywhae-204	ENSMUST00000153038.7	738	No protein	Retained intron	-	-	TSL:2

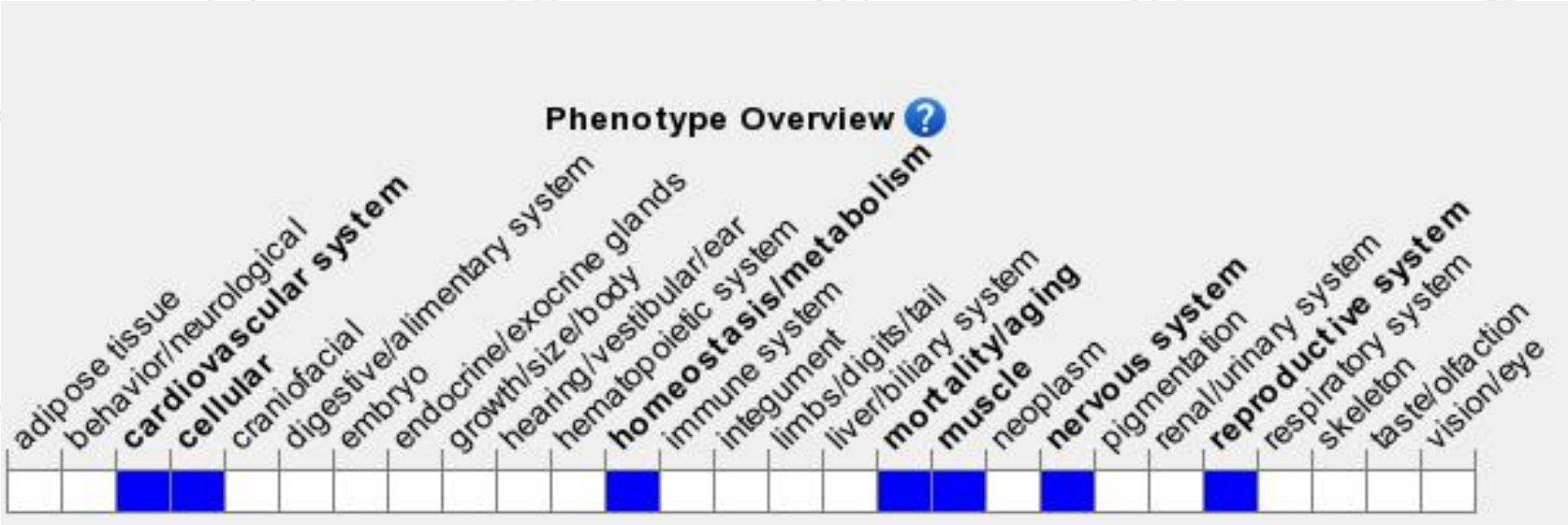
The strategy is based on the design of *Ywhae-201* transcript,The transcription is shown below

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

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