

Wbp2 Cas9-CKO Strategy

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Project Overview

Project Name

Wbp2

Project type

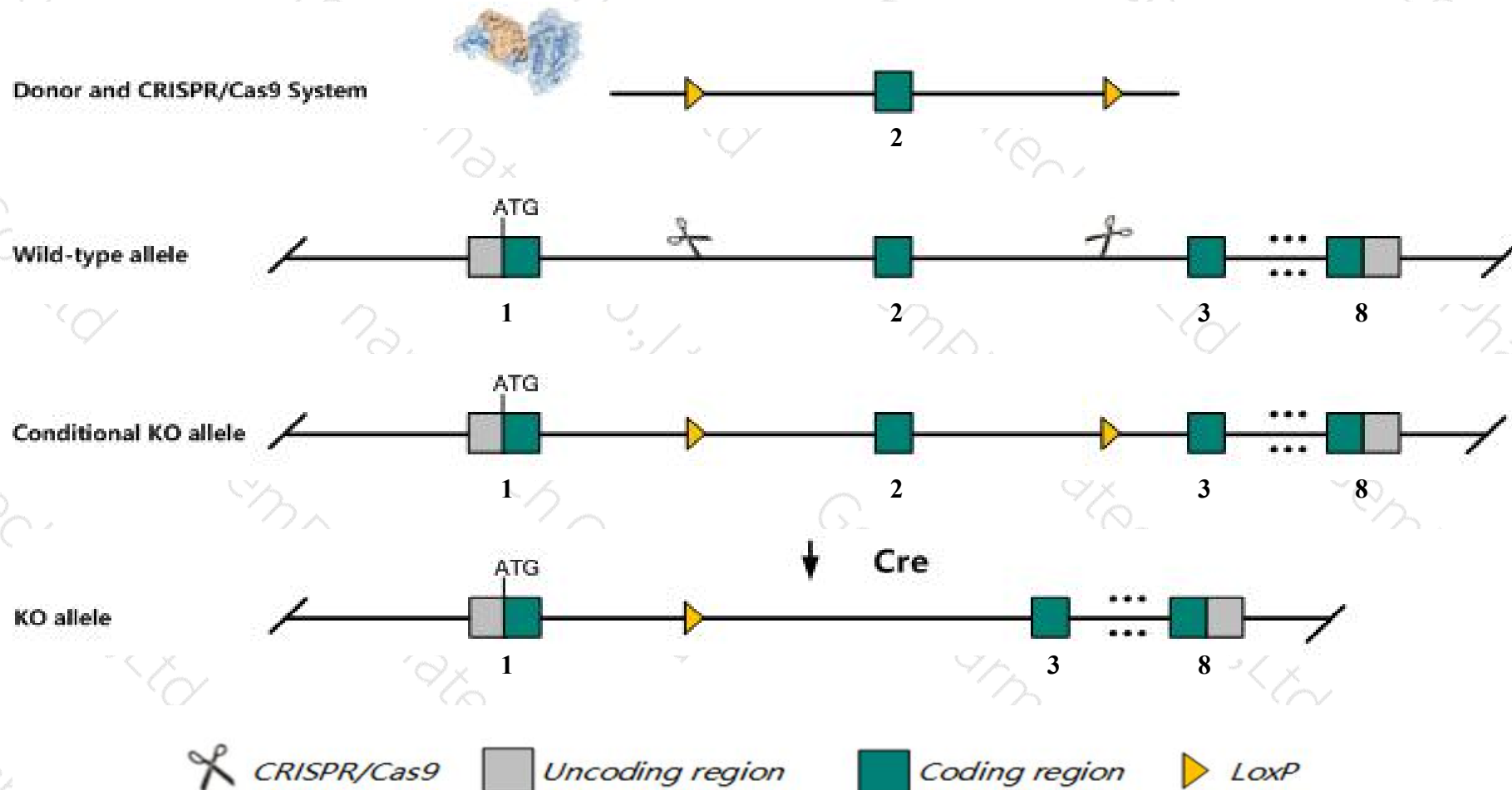
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wbp2* gene. The schematic diagram is as follows:



- The *Wbp2* gene has 5 transcripts. According to the structure of *Wbp2* gene, exon2 of *Wbp2-201* (ENSMUST00000074628.12) transcript is recommended as the knockout region. The region contains 109bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wbp2* 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, Mice homozygous for a null allele show progressive high-frequency hearing loss, raised auditory brainstem response (ABR) thresholds, reduced ABR amplitudes, swelling of afferent terminals, inner hair cell synapse defects, and altered expression of AMPA receptor subunits and post-synaptic proteins.
- The *Wbp2* 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)

Wbp2 WW domain binding protein 2 [Mus musculus (house mouse)]

Gene ID: 22378, updated on 13-Mar-2020

Summary



Official Symbol	Wbp2 provided by MGI
Official Full Name	WW domain binding protein 2 provided by MGI
Primary source	MGI:MGI:104709
See related	Ensembl:ENSMUSG000000034341
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
Expression	Ubiquitous expression in adrenal adult (RPKM 171.5), duodenum adult (RPKM 125.2) and 28 other tissues See more
Orthologs	human all

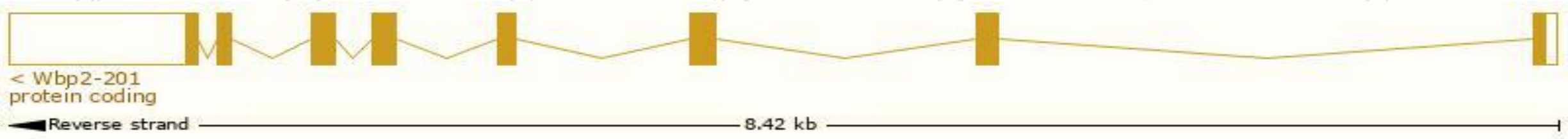
Transcript information (Ensembl)



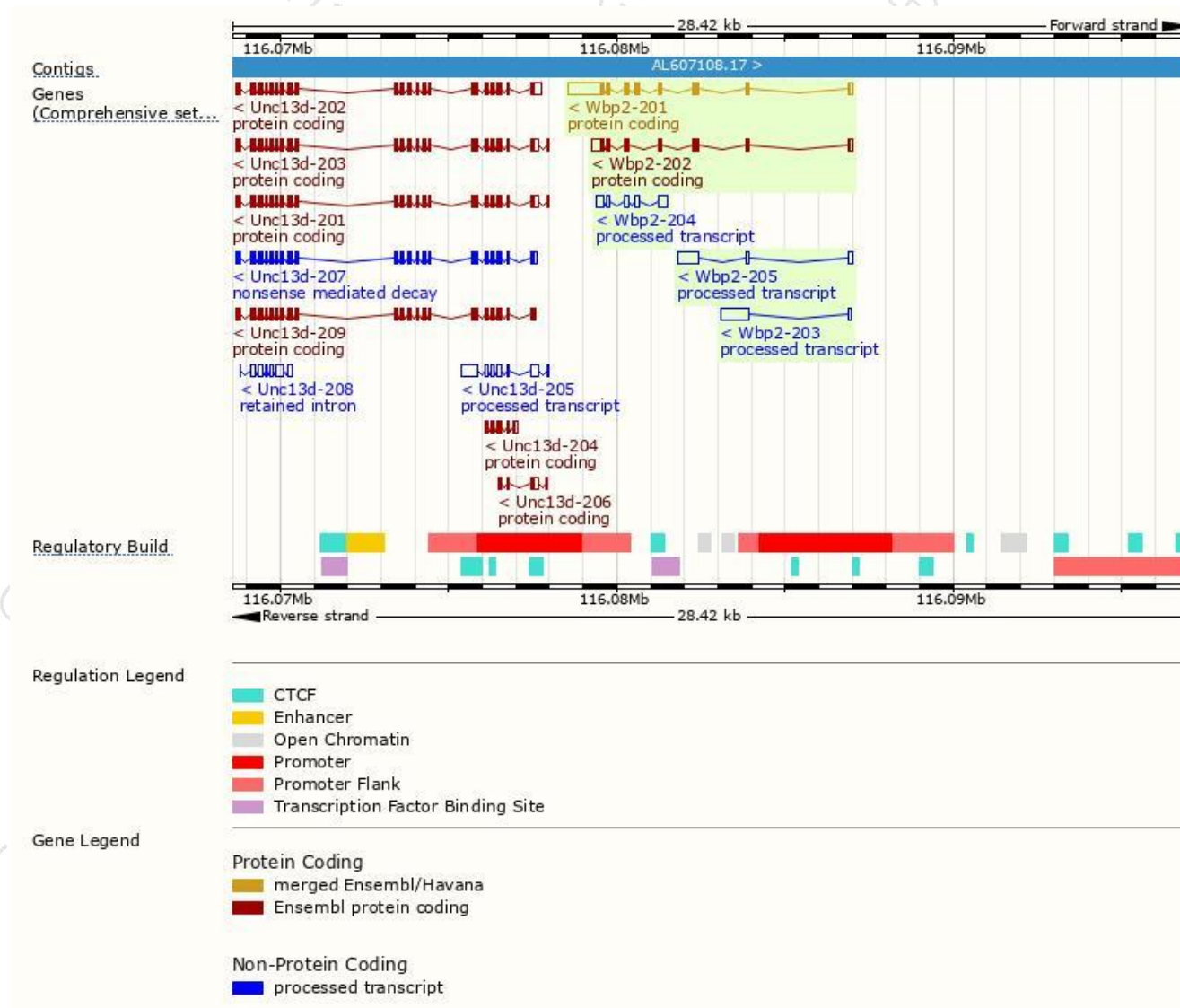
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wbp2-201	ENSMUST00000074628.12	1826	261aa	Protein coding	CCDS25657	P97765_Q544A1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Wbp2-202	ENSMUST00000106444.3	1012	216aa	Protein coding	CCDS83934	P97765	TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT 1
Wbp2-203	ENSMUST00000129532.1	958	No protein	Processed transcript	-	-	TSL:1
Wbp2-205	ENSMUST00000146339.1	821	No protein	Processed transcript	-	-	TSL:2
Wbp2-204	ENSMUST00000145278.1	789	No protein	Processed transcript	-	-	TSL:2

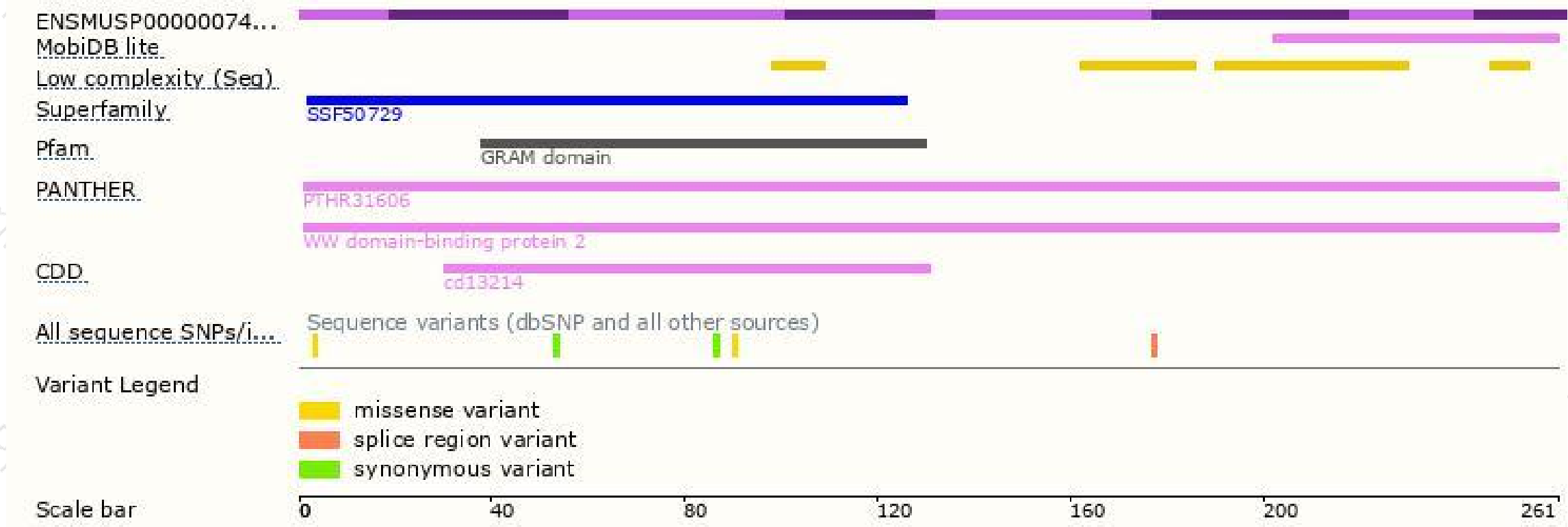
The strategy is based on the design of *Wbp2-201* transcript,The transcription is shown below



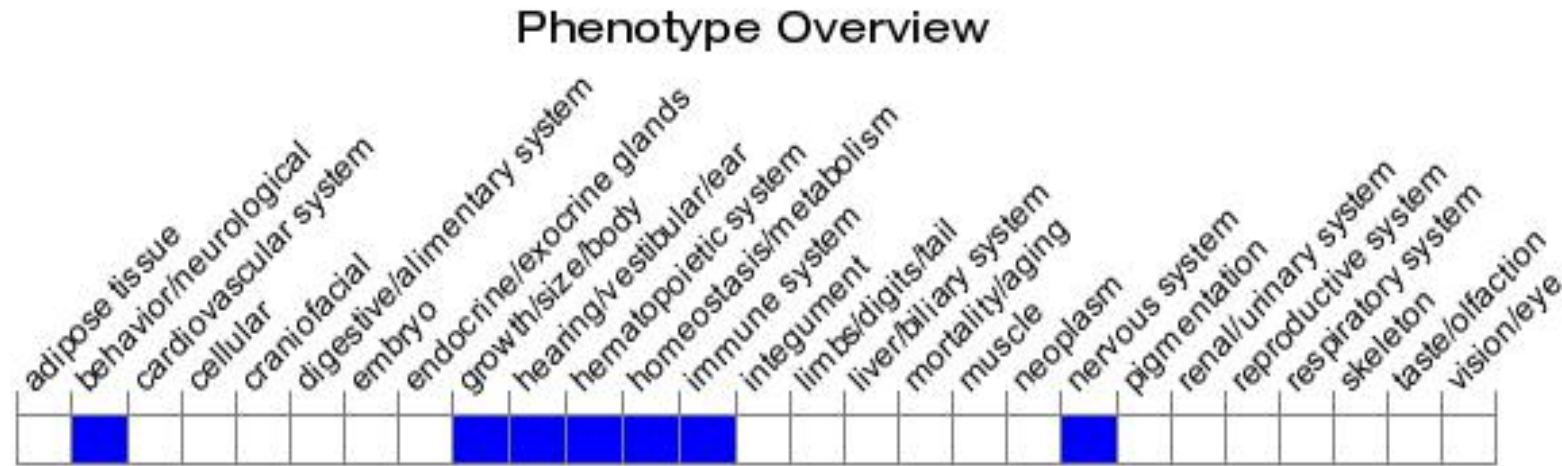
Genomic location distribution



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, Mice homozygous for a null allele show progressive high-frequency hearing loss, raised auditory brainstem response (ABR) thresholds, reduced ABR amplitudes, swelling of afferent terminals, inner hair cell synapse defects, and altered expression of AMPA receptor subunits and post-synaptic proteins.

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

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