

***ErbB4* Cas9-CKO Strategy**

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Project Overview

Project Name

ErbB4

Project type

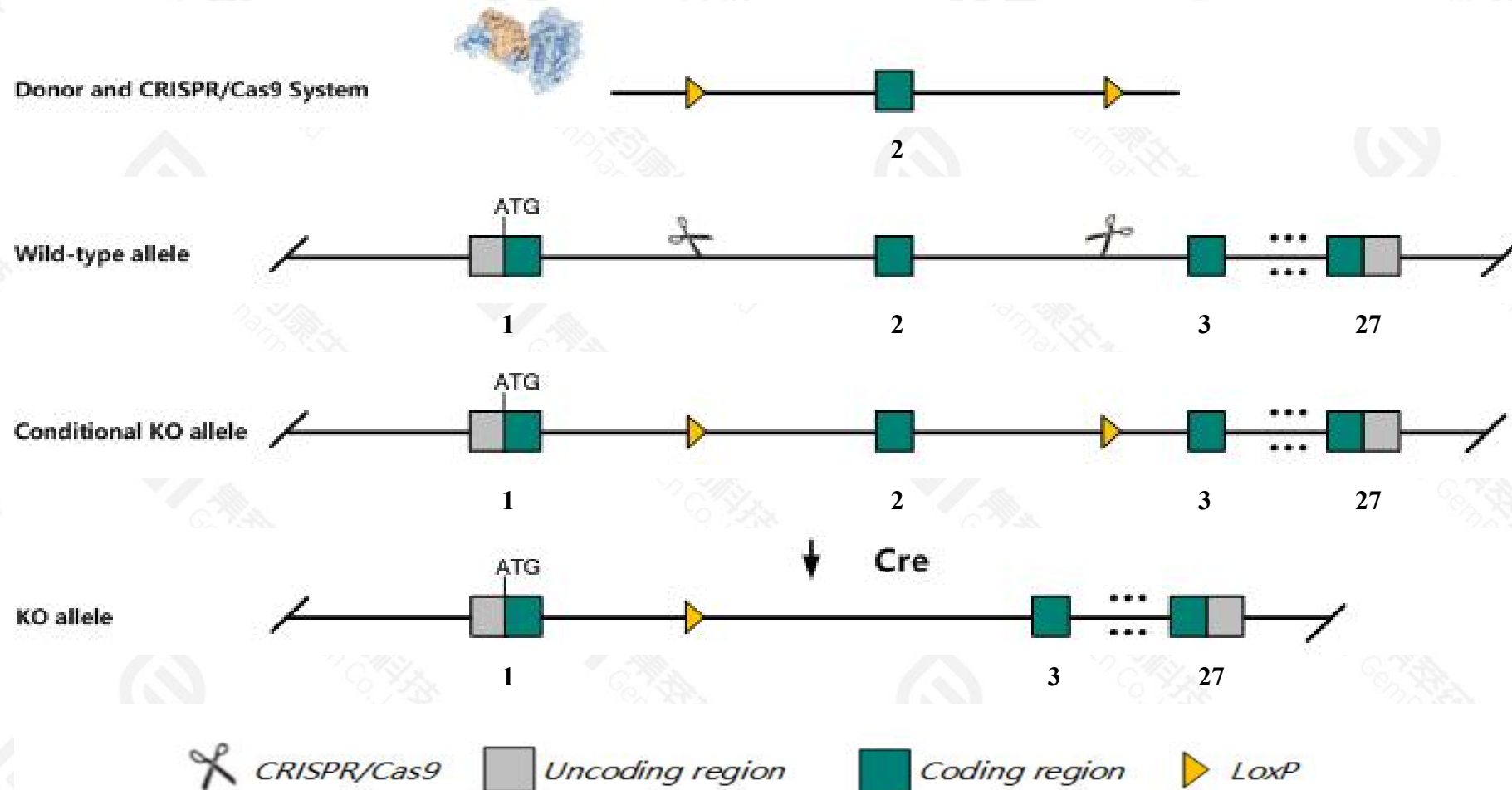
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *ErbB4* gene. The schematic diagram is as follows:



- The *ErbB4* gene has 5 transcripts. According to the structure of *ErbB4* gene, exon2 of *ErbB4*-202(ENSMUST00000121473.8) transcript is recommended as the knockout region. The region contains 152bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *ErbB4* 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, homozygotes for a targeted null mutation exhibit cardiac defects, alterations in hindbrain development, and midgestational lethality. Heterozygotes show schizophrenia-like behavior. Genetically rescued females show mammary defects.
- The *ErbB4* 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)

ErbB4 erb-b2 receptor tyrosine kinase 4 [Mus musculus (house mouse)]

Gene ID: 13869, updated on 22-Mar-2020

Summary

Official Symbol ErbB4 provided by [MGI](#)

Official Full Name erb-b2 receptor tyrosine kinase 4 provided by [MGI](#)

Primary source [MGI:MGI:104771](#)

See related [Ensembl:ENSMUSG00000062209](#)

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 Her4, c-erbB-4

Expression Biased expression in CNS E18 (RPKM 2.3), frontal lobe adult (RPKM 2.1) and 8 other tissues [See more](#)

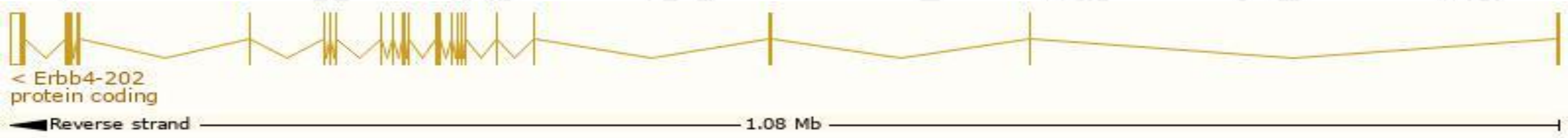
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

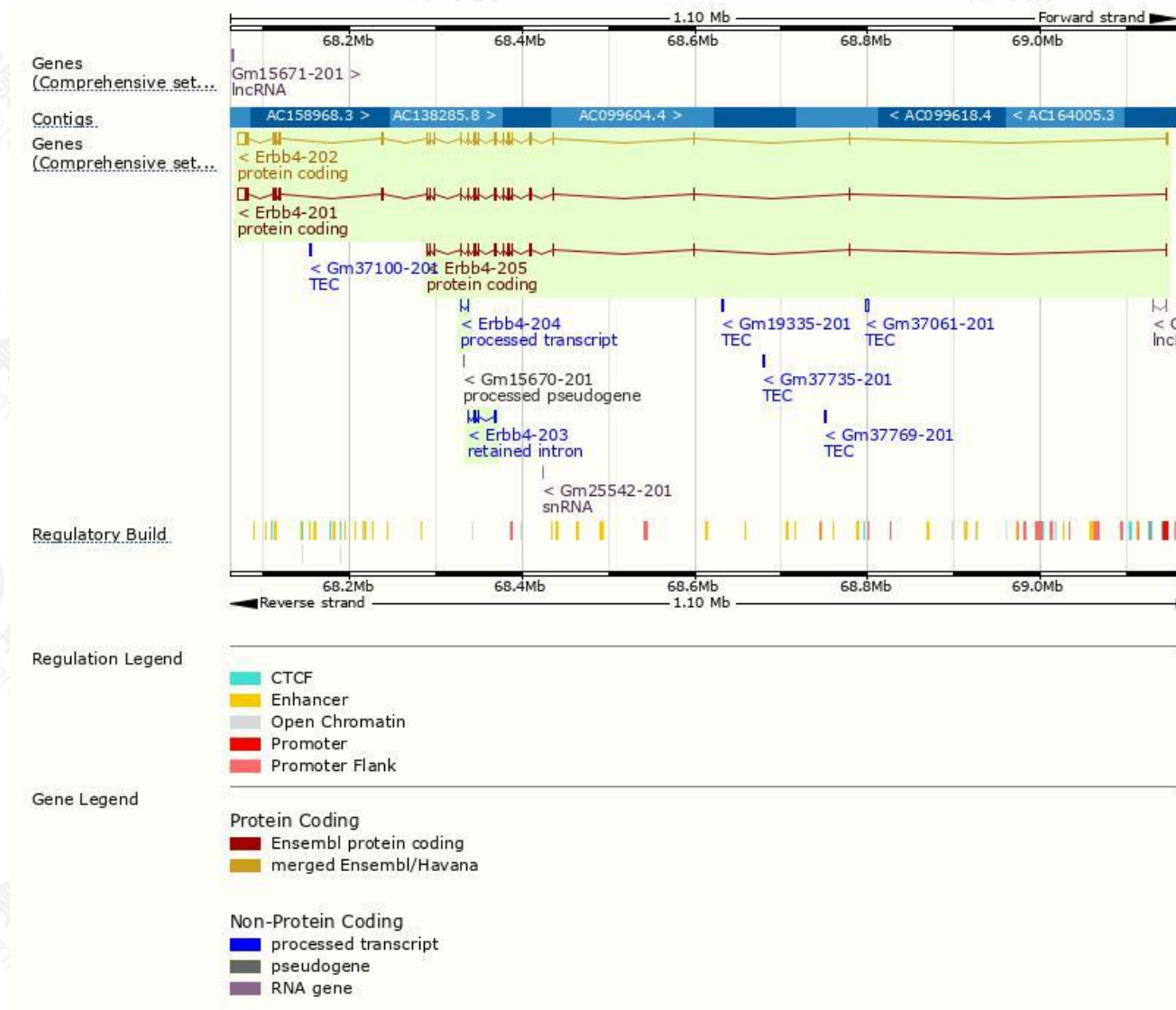
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ErbB4-202	ENSMUST00000121473.7	12037	1292aa	Protein coding	CCDS48285	Q61527	TSL:1 GENCODE basic
ErbB4-201	ENSMUST00000119142.7	11782	1308aa	Protein coding	-	Q61527	TSL:5 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 P1
ErbB4-205	ENSMUST00000153432.1	2196	732aa	Protein coding	-	B2KGF7	CDS 3' incomplete TSL:5
ErbB4-204	ENSMUST00000131148.1	240	No protein	Processed transcript	-	-	TSL:5
ErbB4-203	ENSMUST00000126682.1	744	No protein	Retained intron	-	-	TSL:5

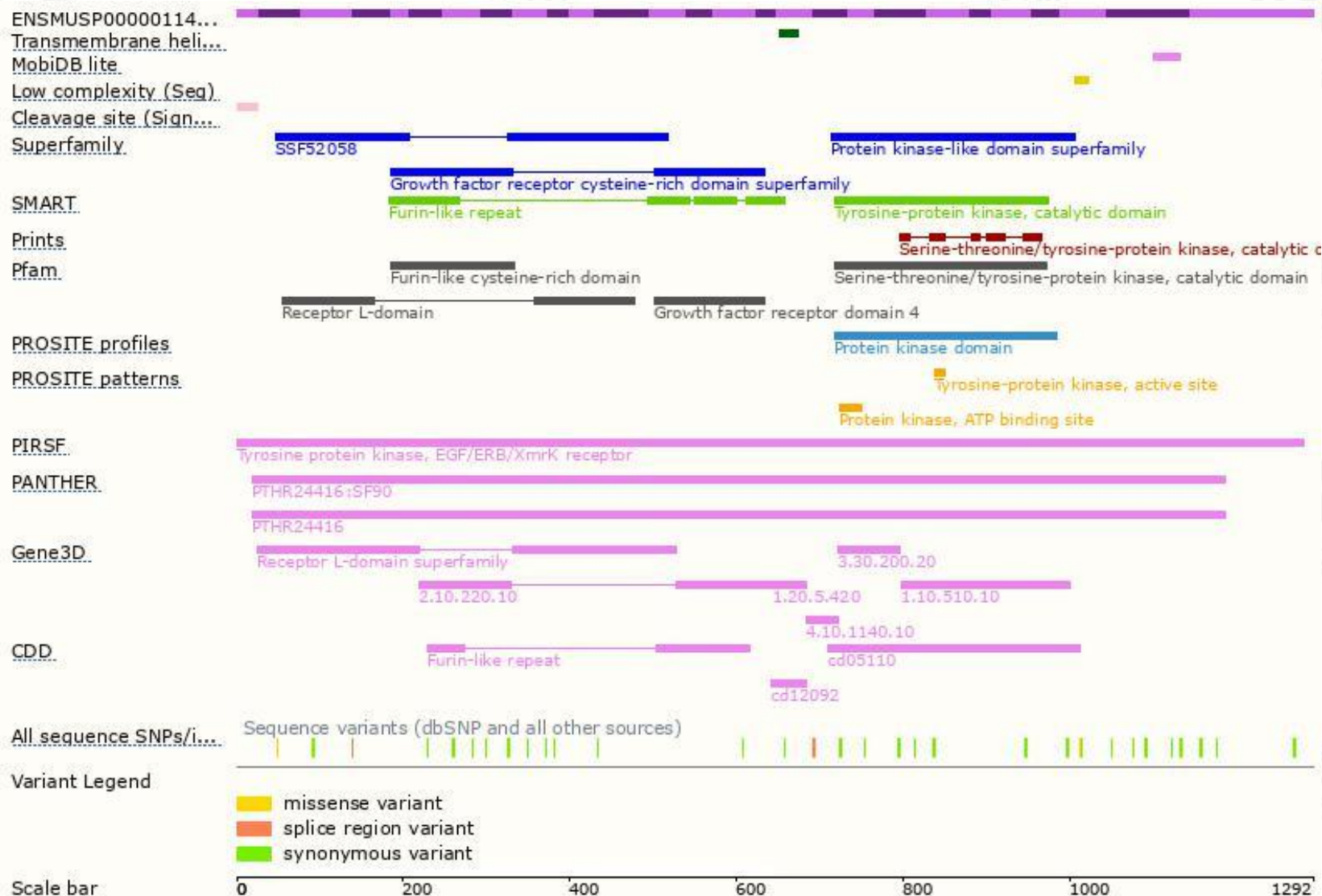
The strategy is based on the design of *ErbB4-202* transcript,the transcription is shown below:



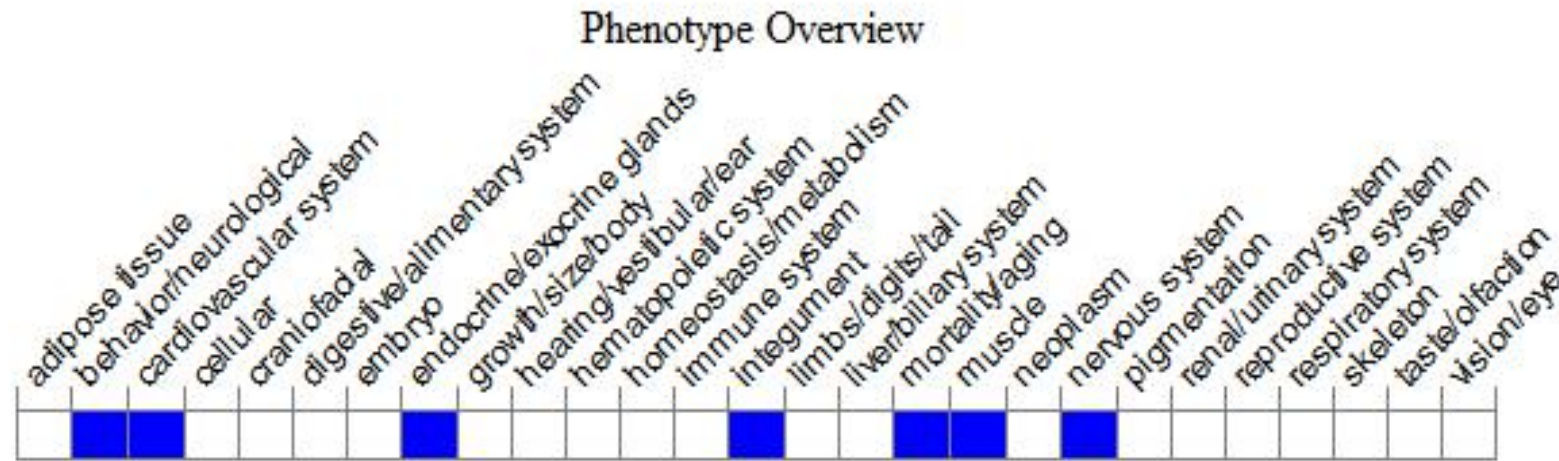
Genomic location distribution



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, homozygotes for a targeted null mutation exhibit cardiac defects, alterations in hindbrain development, and midgestational lethality. Heterozygotes show schizophrenia-like behavior. Genetically rescued females show mammary defects.

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