

Ankfn1 Cas9-CKO Strategy

Designer: Huan Wang

Overview

Target Gene Name

- Ankfn1

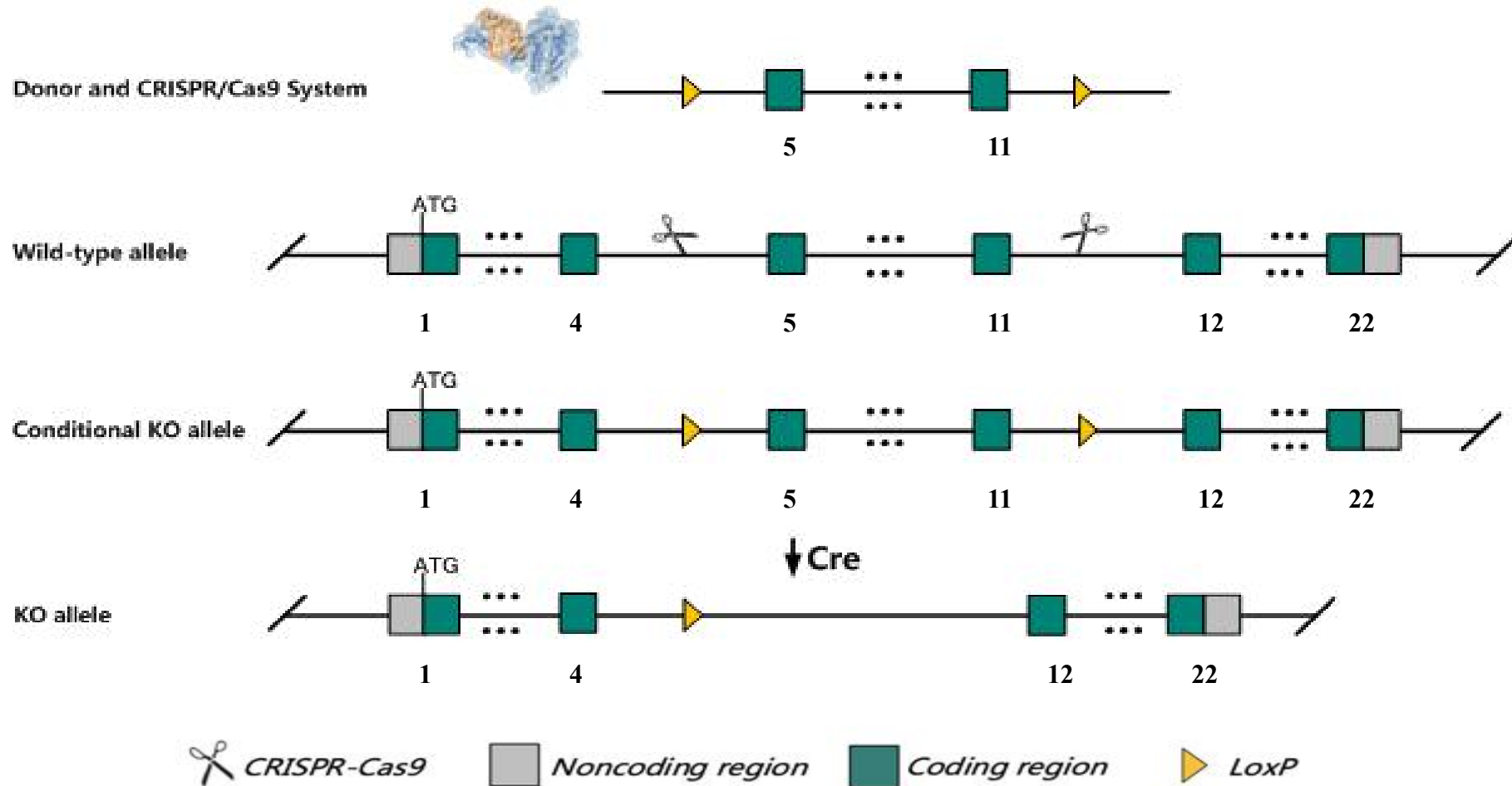
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ankfn1* gene.

Technical Information

- The *Ankfn1* gene has 8 transcripts. According to the structure of *Ankfn1* gene, exon5-exon11 of *Ankfn1*-208 (ENSMUST00000238273.3) transcript is recommended as the knockout region. The region contains 1046bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ankfn1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Ankfn1 ankyrin-repeat and fibronectin type III domain containing 1 [Mus musculus (house mouse)]

Gene ID: 382543, updated on 13-Mar-2020

Summary

| | |
|---------------------------|---|
| Official Symbol | Ankfn1 provided by MGI |
| Official Full Name | ankyrin-repeat and fibronectin type III domain containing 1 provided by MGI |
| Primary source | MGI:MGI:2686021 |
| See related | Ensembl:ENSMUSG00000047773 |
| 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 | 4932411E22Rik, Gm1175, nmf9 |
| Expression | Biased expression in bladder adult (RPKM 7.9), CNS E18 (RPKM 1.0) and 6 other tissues See more |
| Orthologs | human all |

Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

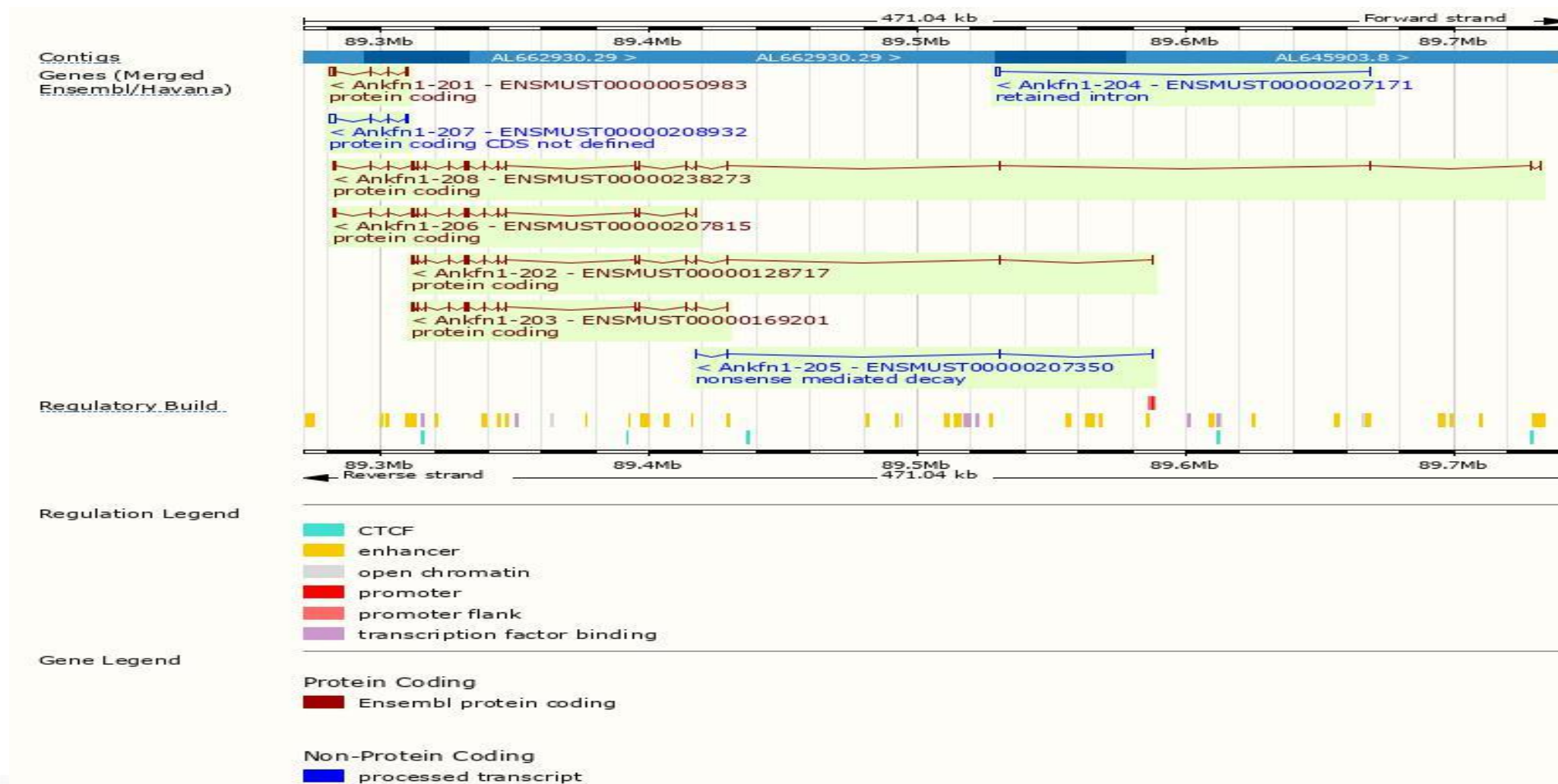
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|--------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|-------------------------------|
| Ankfn1-201 | ENSMUST00000050983.1 | 2665 | 403aa | Protein coding | CCDS25237 | Q8CDJ6 | TSL:1 GENCODE basic |
| Ankfn1-208 | ENSMUST00000238273.2 | 4289 | 1286aa | Protein coding | - | - | GENCODE basic |
| Ankfn1-206 | ENSMUST00000207815.1 | 3250 | 1083aa | Protein coding | - | A0A140LIW7 | CDS 5' incomplete TSL:5 |
| Ankfn1-202 | ENSMUST00000128717.8 | 2391 | 763aa | Protein coding | - | F6RWQ6 | TSL:5 GENCODE basic APPRIS P1 |
| Ankfn1-203 | ENSMUST00000169201.1 | 2232 | 743aa | Protein coding | - | F6X7B3 | TSL:2 GENCODE basic |
| Ankfn1-205 | ENSMUST00000207350.1 | 523 | 48aa | Nonsense mediated decay | - | A0A140LHQ2 | TSL:5 |
| Ankfn1-207 | ENSMUST00000208932.1 | 2665 | No protein | Processed transcript | - | - | TSL:1 |
| Ankfn1-204 | ENSMUST00000207171.1 | 1032 | No protein | Retained intron | - | - | TSL:1 |

The strategy is based on the design of *Ankfn1*-208 transcript, the transcription is shown below:



Source: <https://www.ensembl.org>

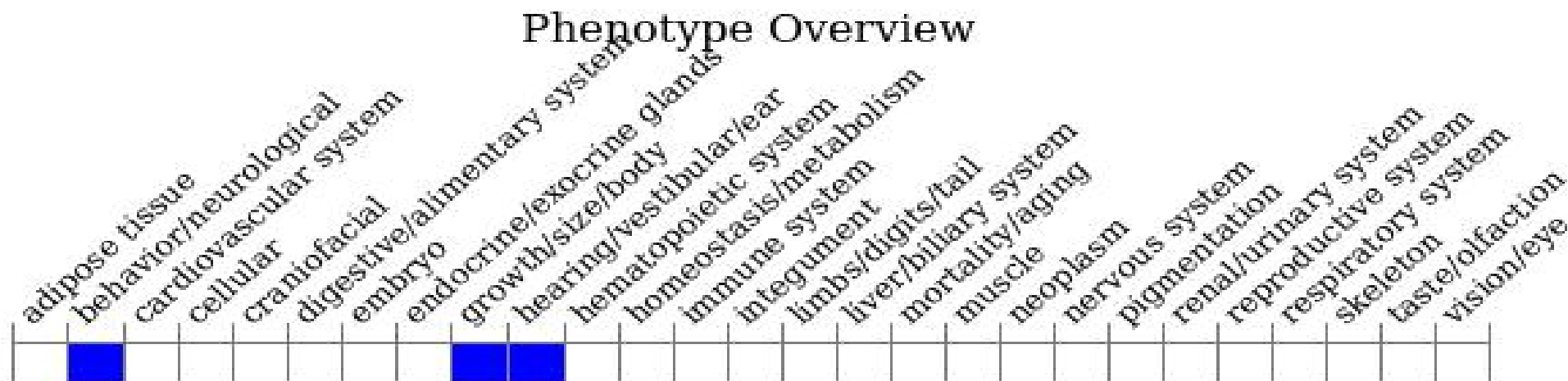
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Mutant mice exhibit a variable and subtle head nodding phenotype.

Important Information

- *Ankfn1* is located on Chr11. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- *Transcript-201* may not be affected.
- 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 the existing technology level.