

Aurka Cas9-CKO Strategy

Designer: Shilei Zhu

Reviewer: Jinlong Zhao

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Project Overview

Project Name

Aurka

Project type

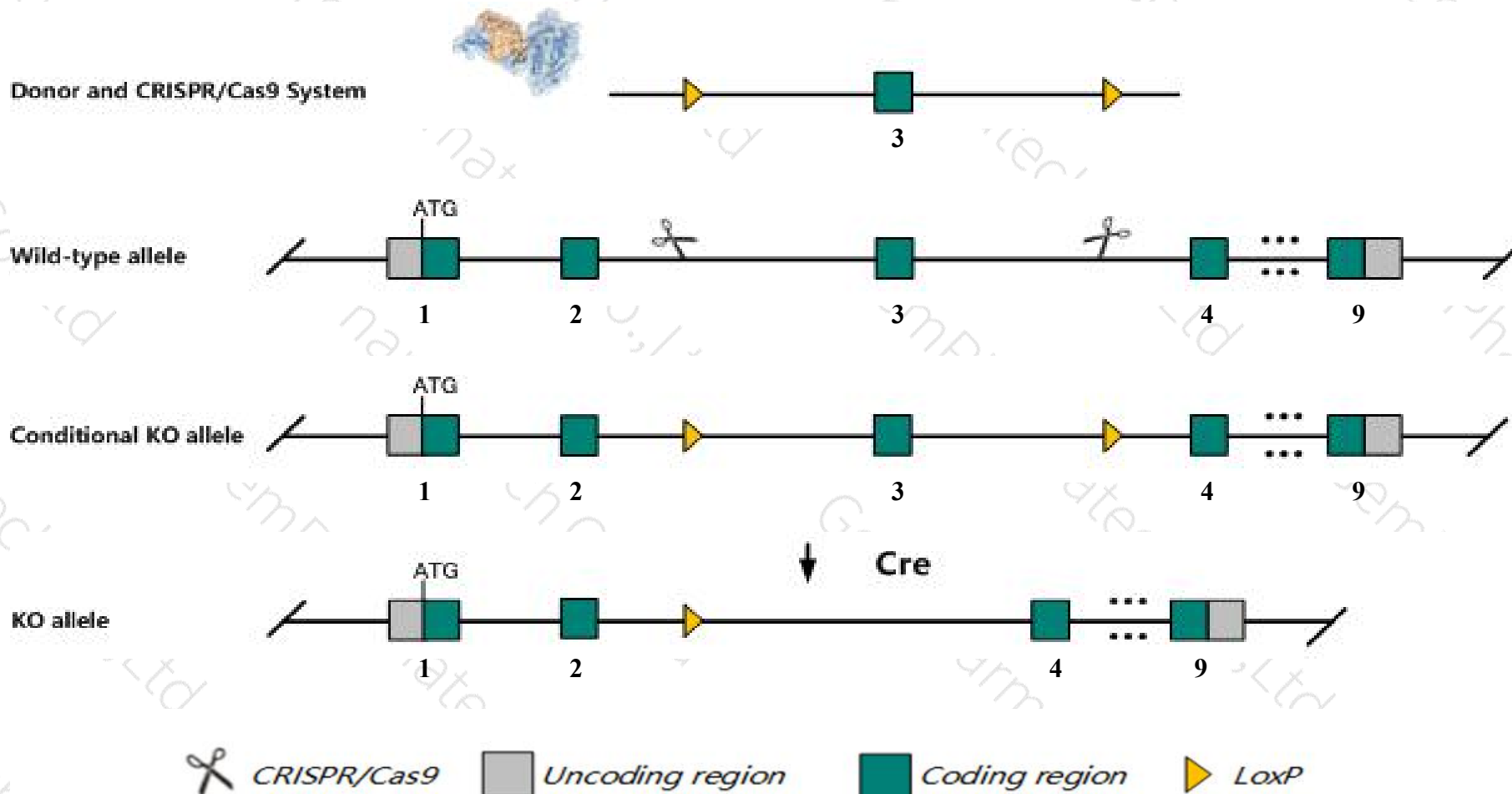
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Aurka* gene has 5 transcripts. According to the structure of *Aurka* gene, exon3 of *Aurka-201* (ENSMUST00000028997.7) transcript is recommended as the knockout region. The region contains 250bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Aurka* 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 display embryonic lethality before implantation, early embryonic growth arrest, and impaired mitosis. heterozygous null mice display increased incidence of tumors primarily lymphomas and chromosomal instability.
- The *Aurka* gene is located on the Chr2. 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.
- 5' loxp was less than 5kb from gene Cstf1.

Gene information (NCBI)

Aurka aurora kinase A [Mus musculus (house mouse)]

Gene ID: 20878, updated on 13-Mar-2020

Summary



Official Symbol Aurka provided by [MGI](#)

Official Full Name aurora kinase A provided by [MGI](#)

Primary source [MGI:MGI:894678](#)

See related [Ensembl:ENSMUSG00000027496](#)

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 AIRK1, ARK-1, AU019385, AW539821, Ark1, Aurora-A, Ayk1, IAK, IAK1, Stk6

Expression Broad expression in liver E14.5 (RPKM 39.2), liver E14 (RPKM 37.7) and 15 other tissues [See more](#)

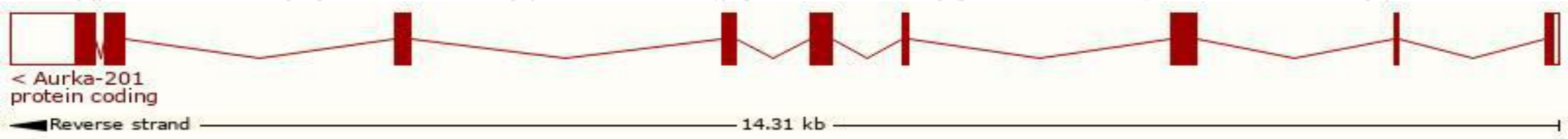
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

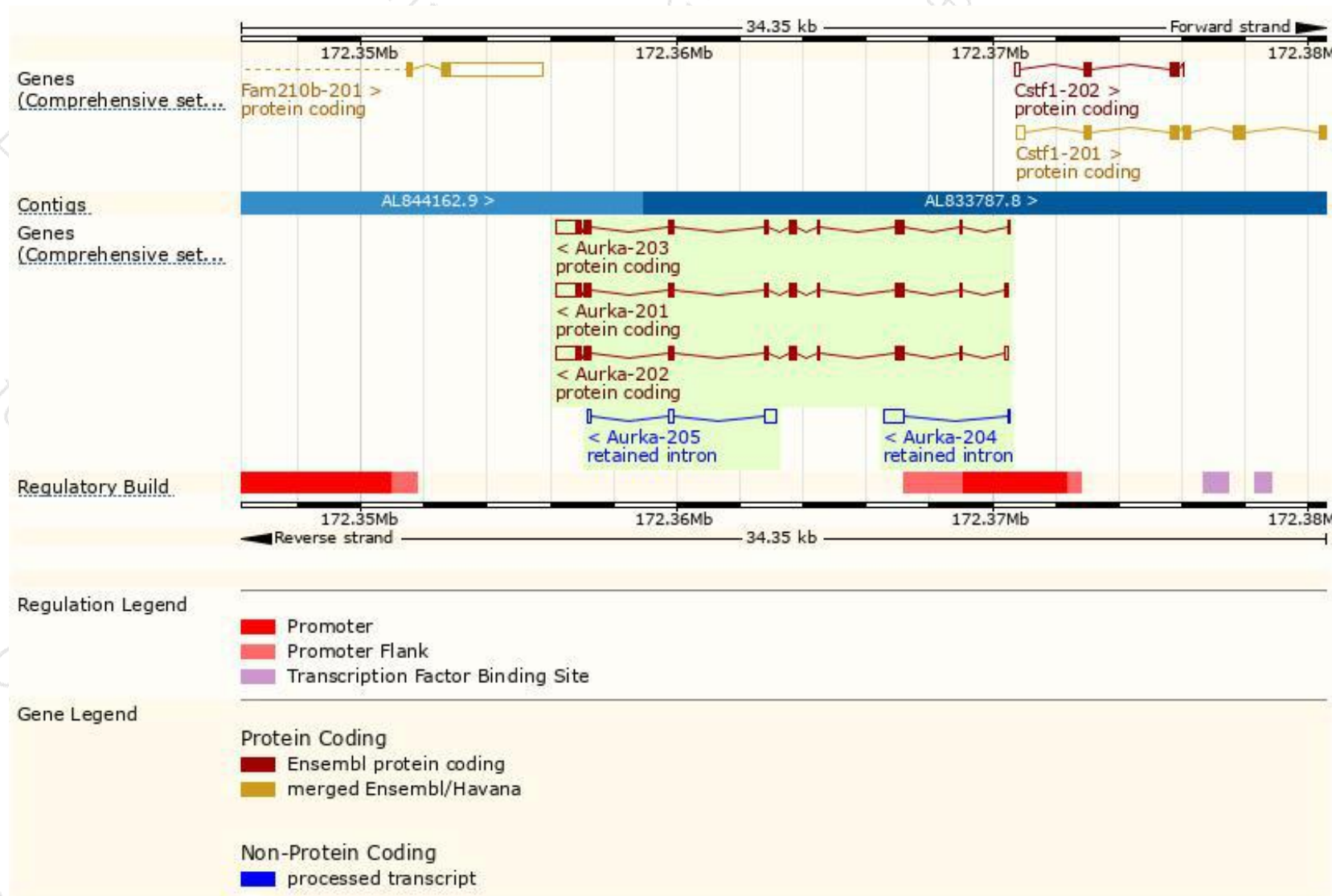
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aurka-201	ENSMUST0000028997.7	1905	417aa	Protein coding	CCDS17129	P97477	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
Aurka-202	ENSMUST00000109139.7	1905	395aa	Protein coding	CCDS71204	P97477_Q3TEY6	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 ALT2
Aurka-203	ENSMUST00000109140.9	1862	395aa	Protein coding	CCDS71204	P97477_Q3TEY6	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 ALT2
Aurka-204	ENSMUST00000126107.1	672	No protein	Retained intron	-	-	TSL:3
Aurka-205	ENSMUST00000128004.1	596	No protein	Retained intron	-	-	TSL:3

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



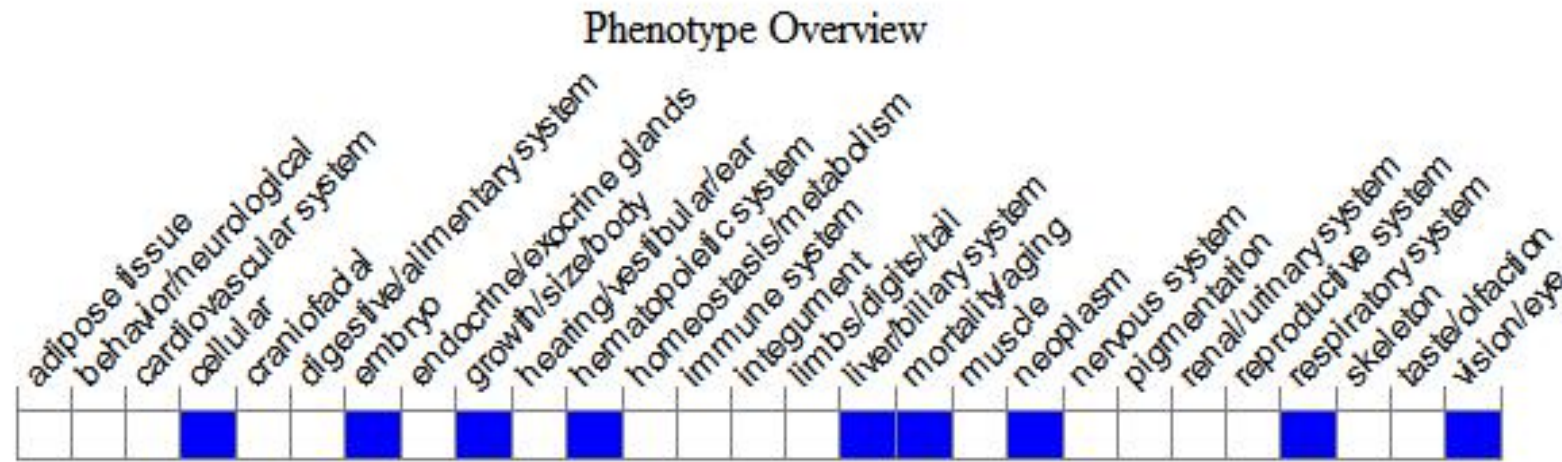
Genomic location distribution



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 display embryonic lethality before implantation, early embryonic growth arrest, and impaired mitosis. Heterozygous null mice display increased incidence of tumors primarily lymphomas and chromosomal instability.

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

Tel: 400-9660890

