

# ***Foxn1* Cas9-CKO Strategy**

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# Project Overview

**Project Name**

***Foxn1***

**Project type**

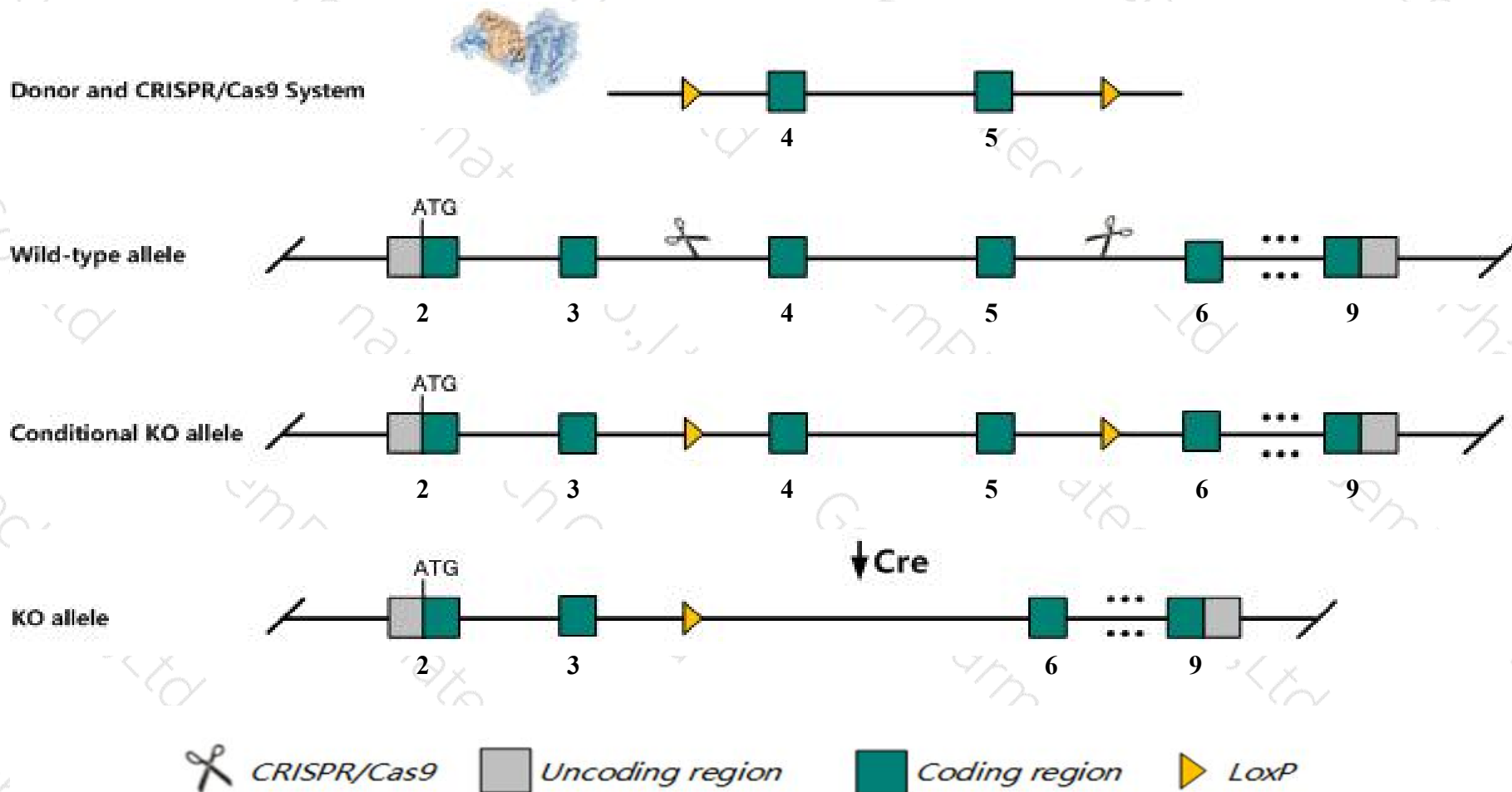
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxn1* gene. The schematic diagram is as follows:



# Technical routes

- The *Foxn1* gene has 1 transcript. According to the structure of *Foxn1* gene, exon4-exon5 of *Foxn1*-201(ENSMUST00000108294.1) transcript is recommended as the knockout region. The region contains 245bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Foxn1* 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 different mutations have in genetically determined absence or loss of hair and failed hair keratinization, premature lethality (differing by genetic background) and absence of thymus, resulting in multiple immune abnormalities. Heterozygotes have enlarged thymuses.
- The *Foxn1* 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)

## Foxn1 forkhead box N1 [Mus musculus (house mouse)]

Gene ID: 15218, updated on 13-Mar-2020

### Summary

**Official Symbol** Foxn1 provided by [MGI](#)

**Official Full Name** forkhead box N1 provided by [MGI](#)

**Primary source** [MGI:MGI:102949](#)

**See related** [Ensembl:ENSMUSG00000002057](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** D11Bhm185e, Fkh19, HFH-11, Hfh11, Whn, nu, nude

**Summary** The protein encoded by this gene is part of the forkhead family or "winged-helix" transcription factors that are important in developmental processes, immune system regulation, metabolism, cancer and aging. This gene family has over 100 members, subdivided into classes (A-Q) based on phylogeny. The encoded protein is proposed to regulate development of the thymus and differentiation of keratinocytes. Mutations in this gene cause severe primary T-cell immunodeficiency and congenital alopecia. In mouse mutations of this gene underlie the phenotype of the nude mouse, which has been widely used as a model system in oncology, immunology, dermatology, and transplantation studies. In humans mutations in this gene have been correlated with T-cell immunodeficiency, the skin disorder congenital alopecia, and nail dystrophy. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Apr 2013]

**Expression** Biased expression in thymus adult (RPKM 7.5), stomach adult (RPKM 0.8) and 1 other tissue [See more](#)

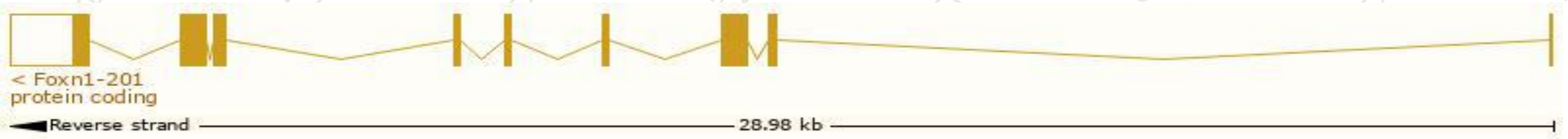
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

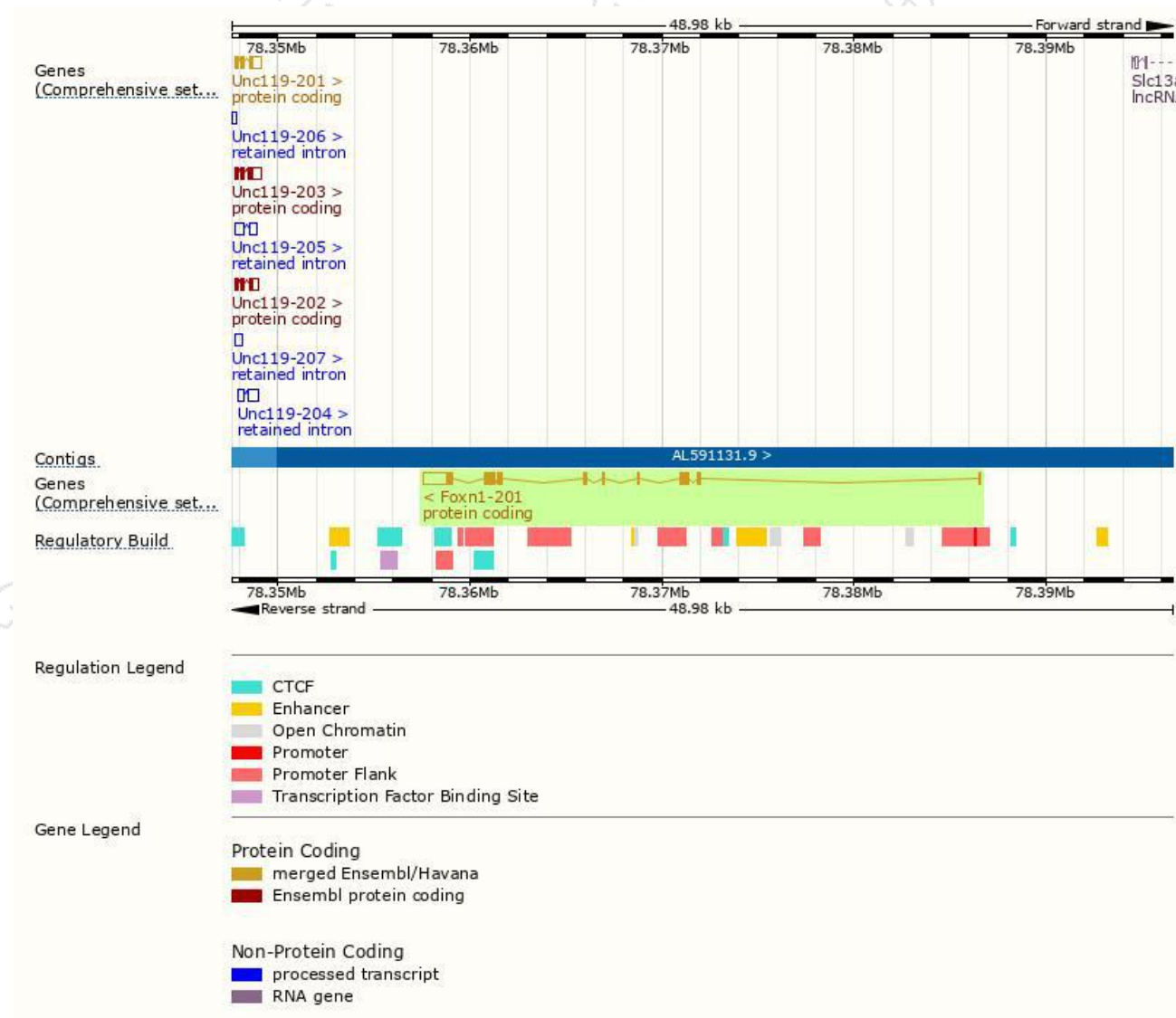
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
<b>Foxn1-201</b>	<a href="#">ENSMUST00000108294.1</a>	3214	<a href="#">648aa</a>	Protein coding	<a href="#">CCDS25102</a>	<a href="#">Q5SYK1</a> <a href="#">Q61575</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Foxn1-201* transcript, the transcription is shown below:



# Genomic location distribution

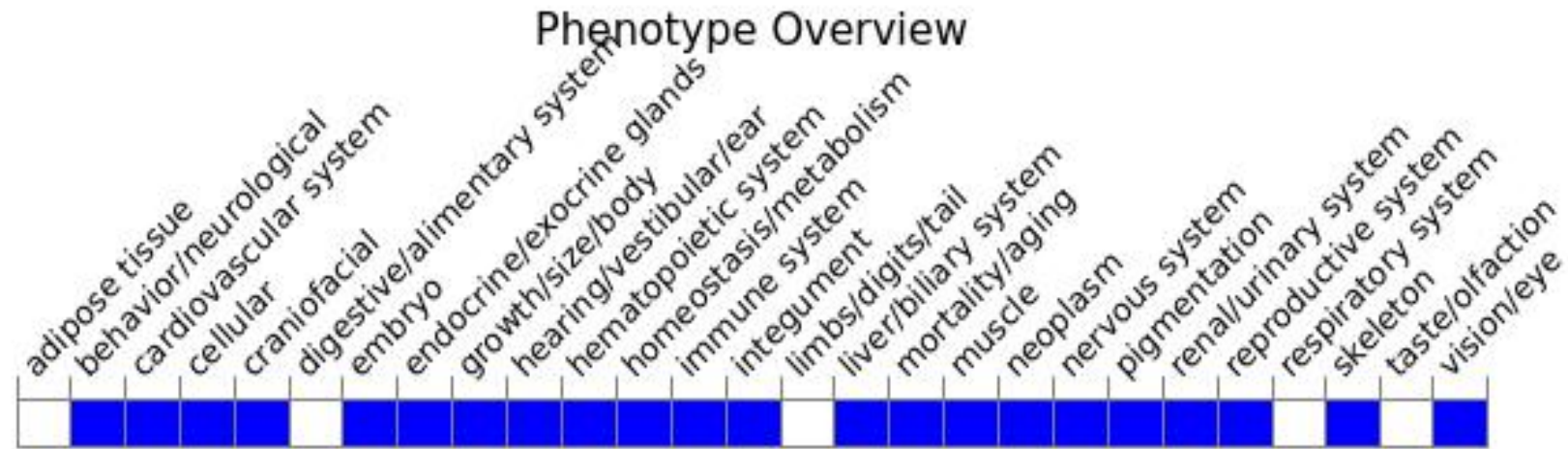




# Protein domain



# 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, homozygotes for different mutations have in genetically determined absence or loss of hair and failed hair keratinization, premature lethality (differing by genetic background) and absence of thymus, resulting in multiple immune abnormalities. Heterozygotes have enlarged thymuses.

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

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