

Foxj1 Cas9-KO Strategy

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Project Overview

Project Name

Foxj1

Project type

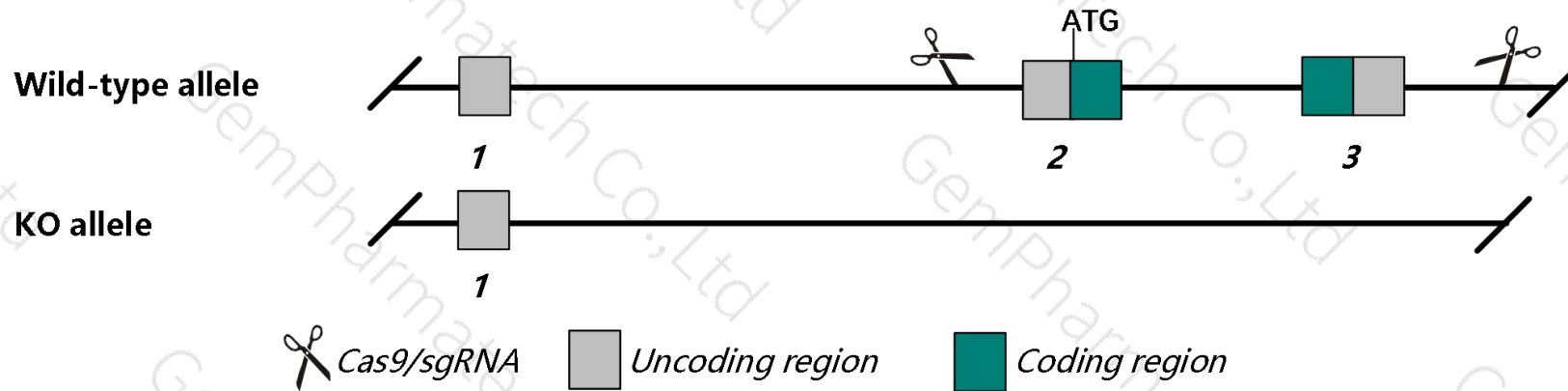
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxj1* gene. The schematic diagram is as follows:



- The *Foxj1* gene has 1 transcript. According to the structure of *Foxj1* gene, exon2-exon3 of *Foxj1-201* (ENSMUST00000036215.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Foxj1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Animals homozygous for targeted mutations in this gene exhibit random determination of left-right asymmetry and defective ciliogenesis.
- The knockout region is near to the N-terminal of *n-R5s74* gene and C-terminal of *Rnfl57* gene, this strategy may influence the regulatory function of the N-terminal of *n-R5s74* gene and C-terminal of *Rnfl57* gene.
- The *Foxj1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Foxj1 forkhead box J1 [*Mus musculus* (house mouse)]

Gene ID: 15223, updated on 22-Oct-2019

Summary

- Official Symbol** Foxj1 provided by [MGI](#)
- Official Full Name** forkhead box J1 provided by [MGI](#)
- Primary source** [MGI:MGI:1347474](#)
- See related** [Ensembl:ENSMUSG00000034227](#)
- 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** Hfh4; HFH-4; FKHL-13
- Expression** Biased expression in ovary adult (RPKM 53.6), lung adult (RPKM 41.4) and 7 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 11 E2; 11 81.16 cM

See Foxj1 in [Genome Data Viewer](#)

Exon count: 3

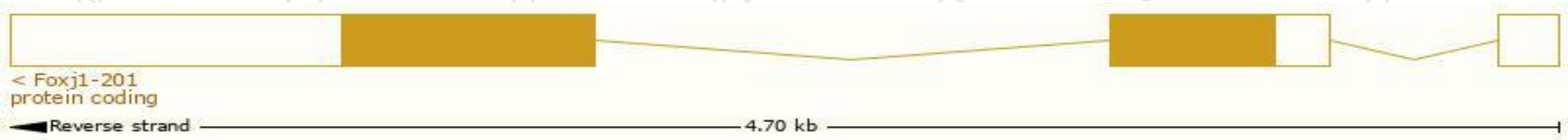
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (116330704..116335499, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (116192018..116196668, complement)

Transcript information (Ensembl)

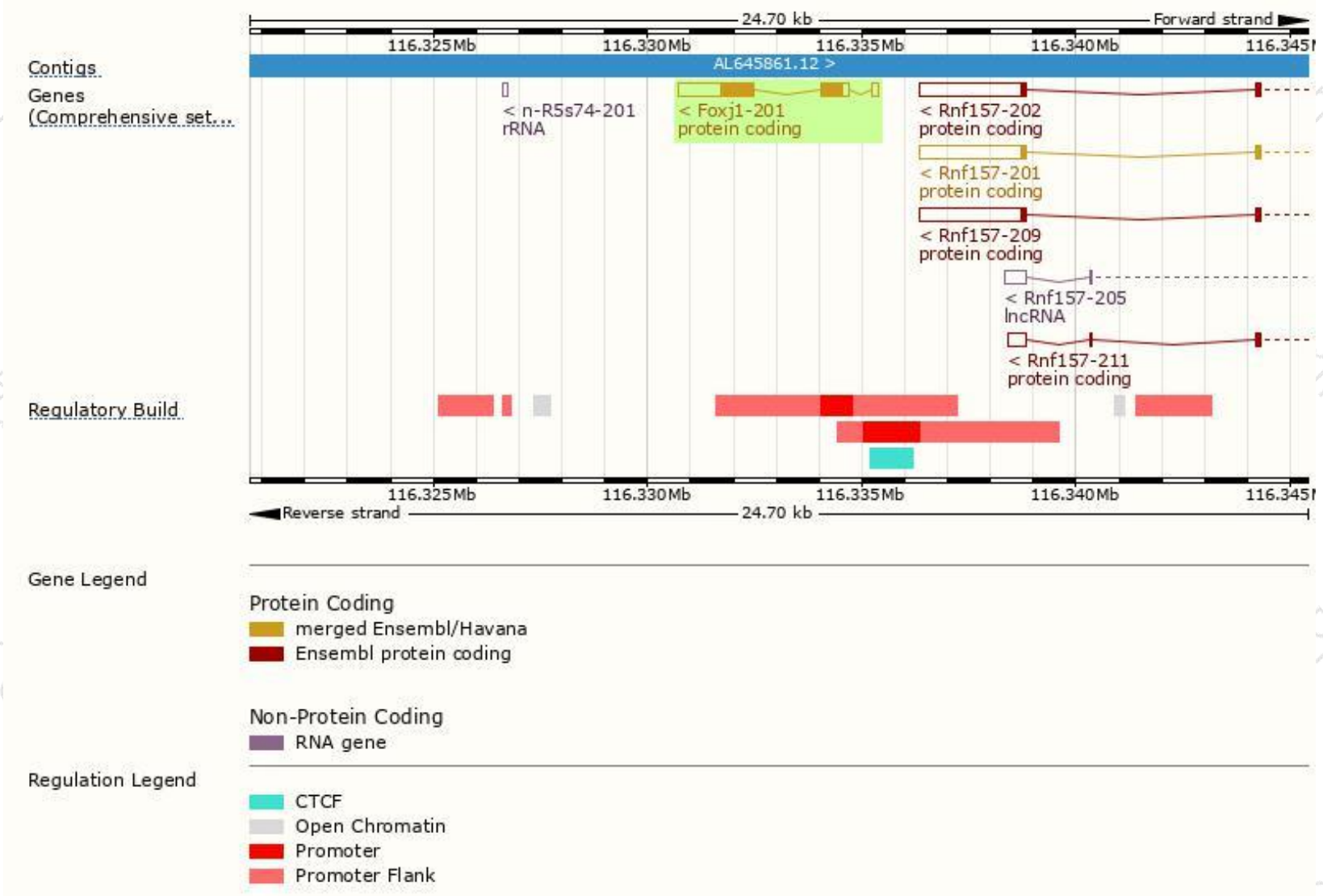
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxj1-201	ENSMUST00000036215.7	2623	421aa	Protein coding	CCDS25665	Q61660	TSL:1 GENCODE basic APPRIS P1

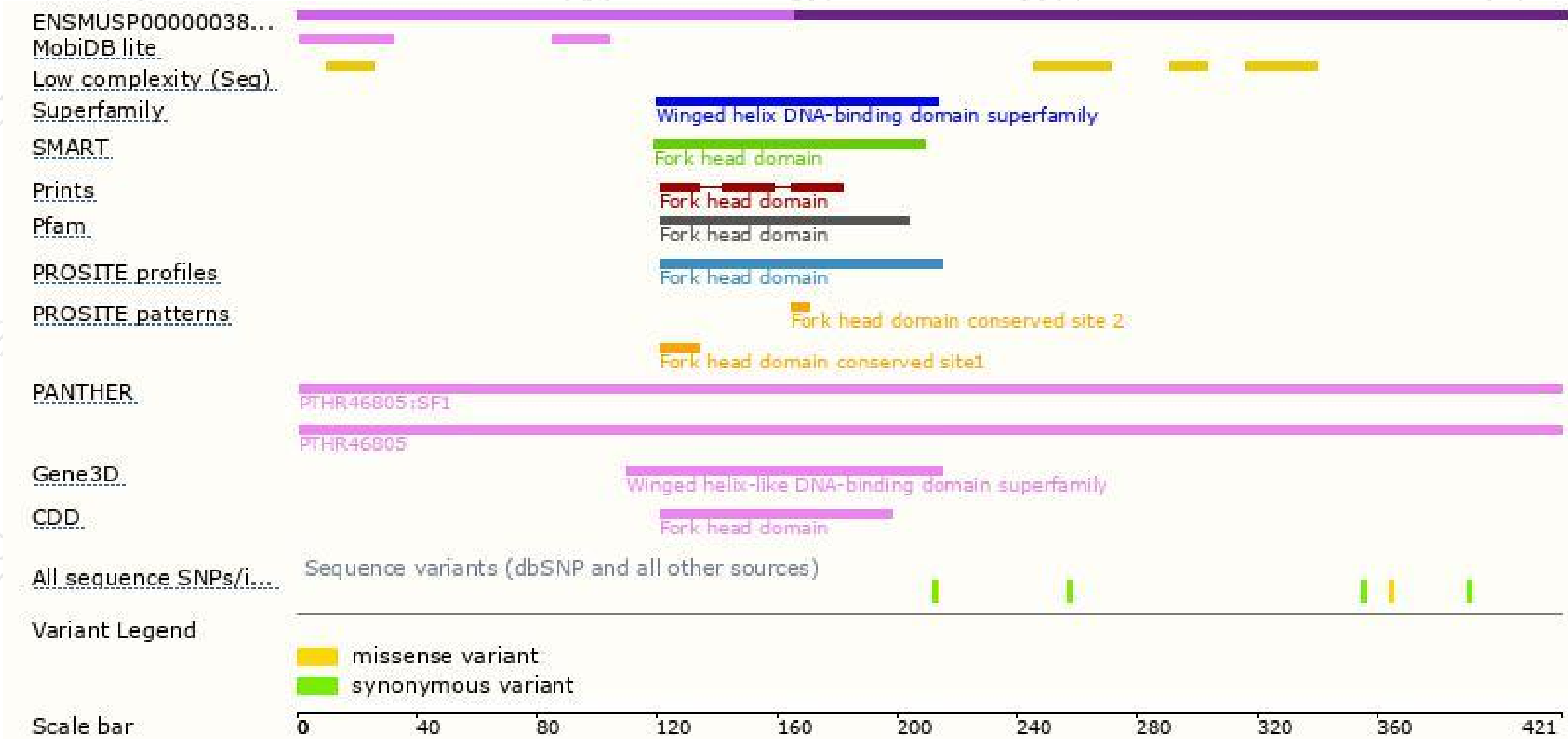
The strategy is based on the design of *Foxj1-201* transcript, The transcription is shown below



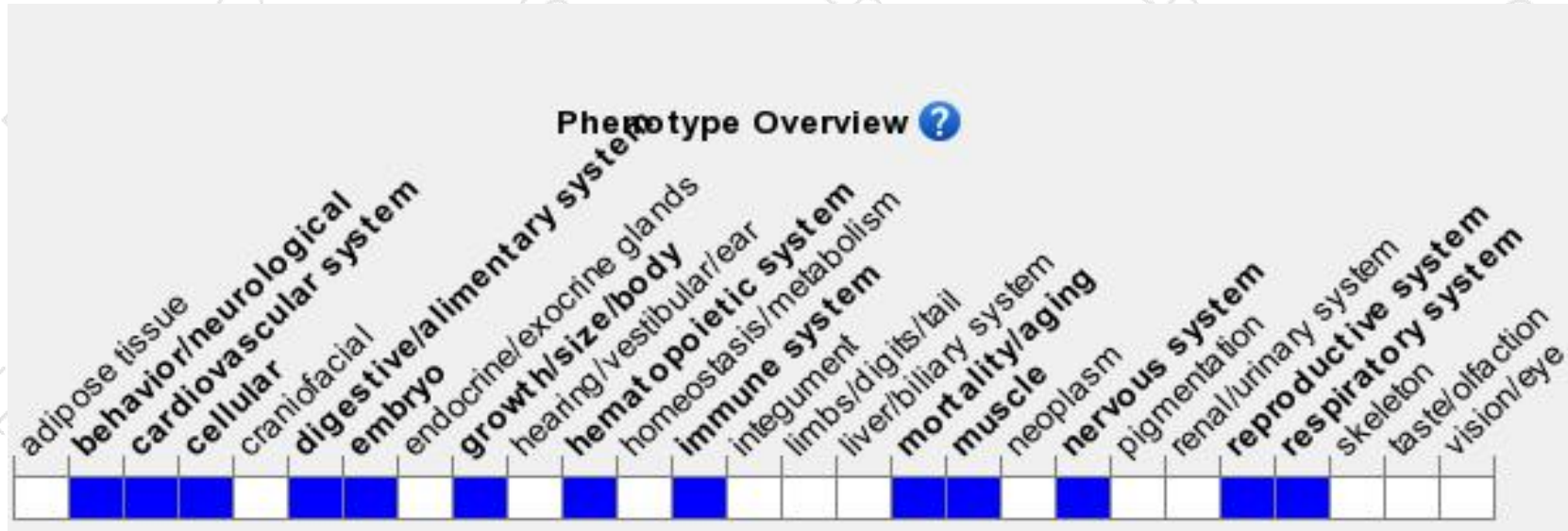
Genomic location distribution



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, Animals homozygous for targeted mutations in this gene exhibit random determination of left-right asymmetry and defective ciliogenesis.

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

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