

***Foxa3* Cas9-KO Strategy**

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Project Overview

Project Name

Foxa3

Project type

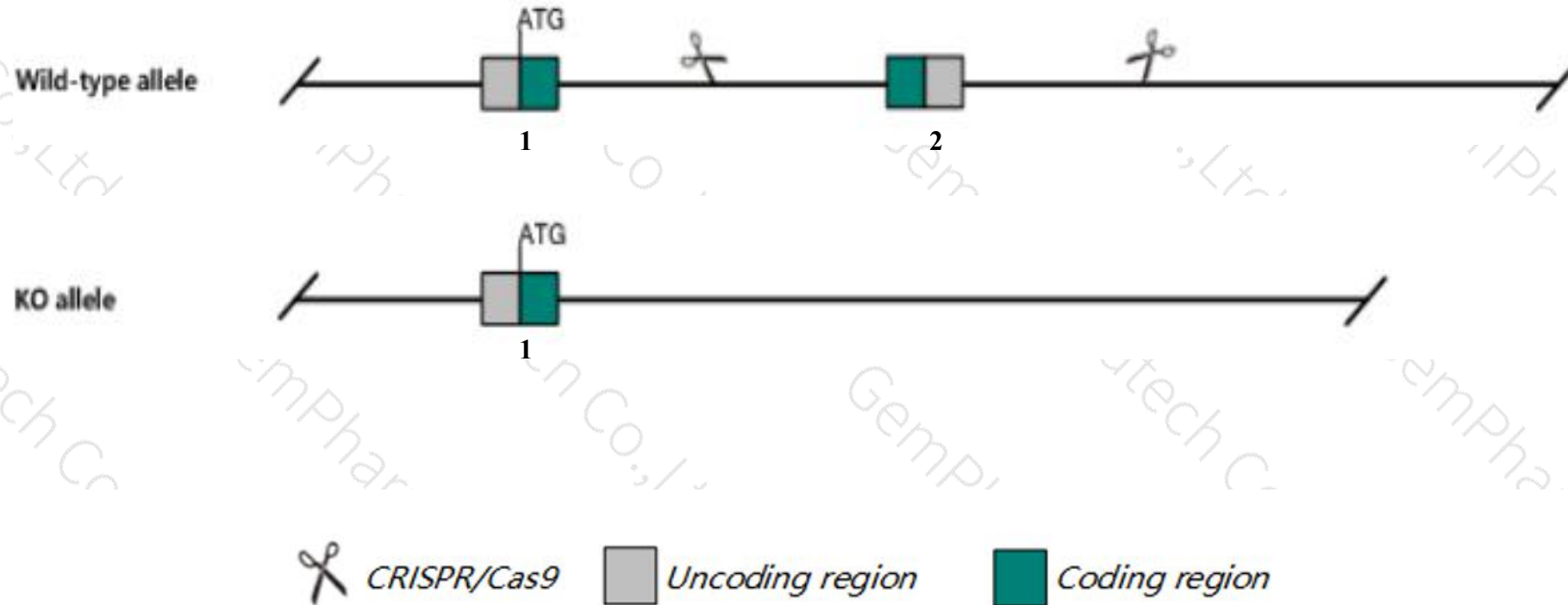
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxa3* gene. The schematic diagram is as follows:



- The *Foxa3* gene has 1 transcript. According to the structure of *Foxa3* gene, exon2 of *Foxa3-201* (ENSMUST00000036018.5) transcript is recommended as the knockout region. The region contains most 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 *Foxa3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygotes for a targeted null mutation exhibit reduced expression of several liver-specific and liver-enriched genes. homozygous mice exhibit abnormal glucose homeostasis and reduced male fertility with abnormal spermatogenesis. mice remodel their fat tissues on high fat diets, store less fat, and burn more energy as they age. mutant mice live significantly longer than controls.
- The *Foxa3* gene is located on the Chr7. 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)

Foxa3 forkhead box A3 [Mus musculus (house mouse)]

Gene ID: 15377, updated on 13-Mar-2020

Summary



Official Symbol Foxa3 provided by [MGI](#)

Official Full Name forkhead box A3 provided by [MGI](#)

Primary source [MGI:MGI:1347477](#)

See related [Ensembl:ENSMUSG00000040891](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

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

Also known as Hnf-3g, Hnf3g, Tcf-3g, Tcf3g

Expression Biased expression in stomach adult (RPKM 32.1), colon adult (RPKM 31.9) and 10 other tissues [See more](#)

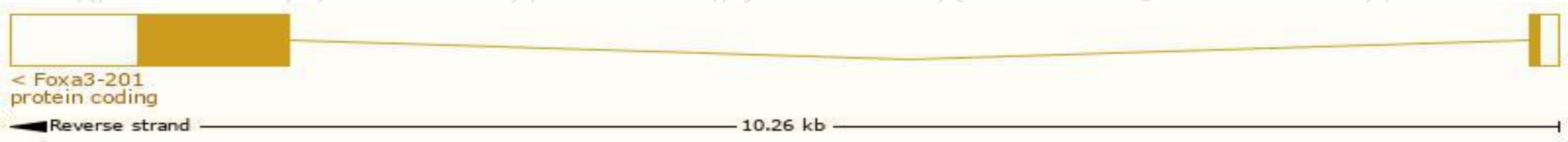
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

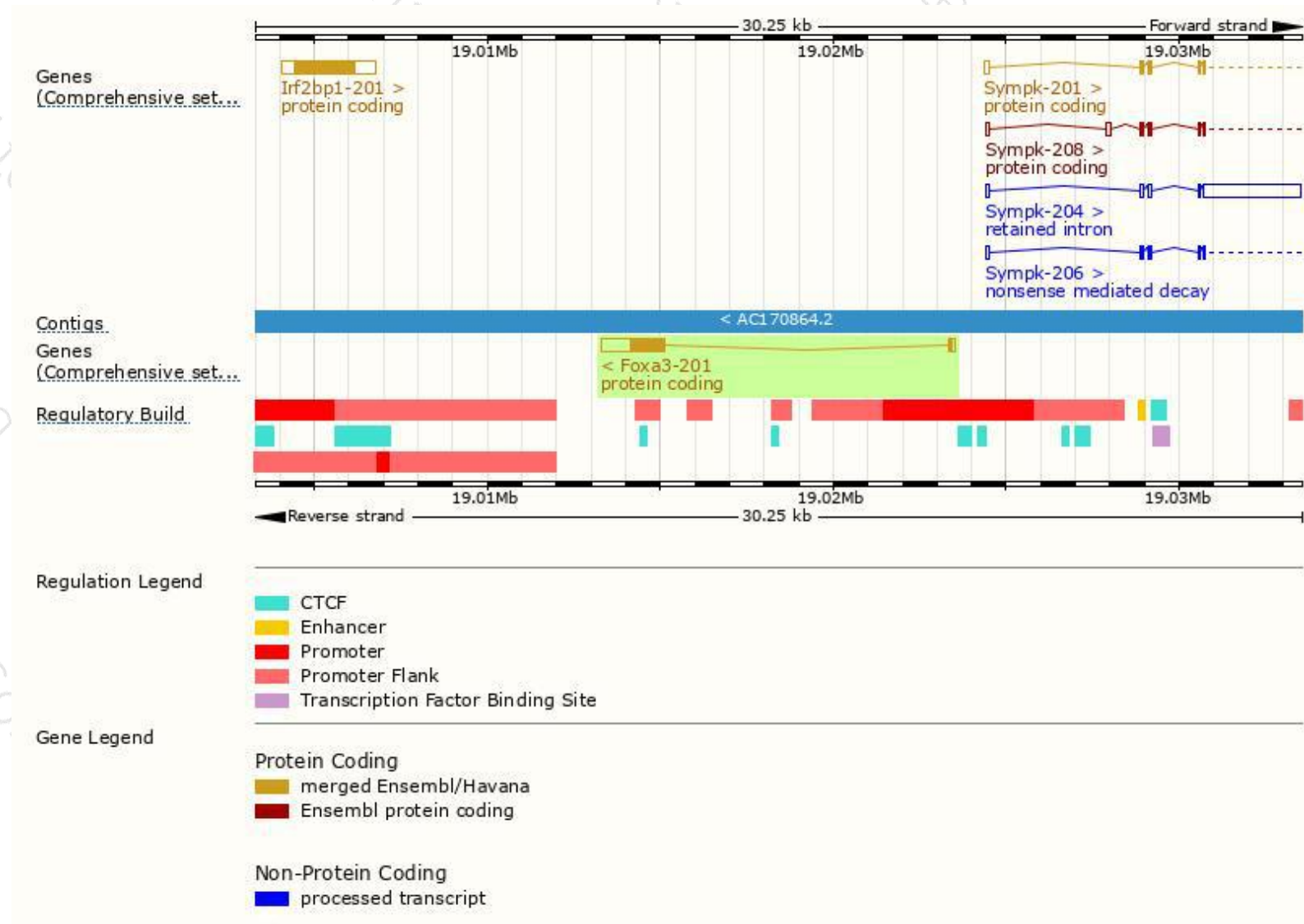
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxa3-201	ENSMUST00000036018.5	2037	353aa	Protein coding	CCDS20886	P35584	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 P1

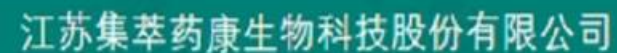
The strategy is based on the design of *Foxa3-201* transcript, the transcription is shown below:



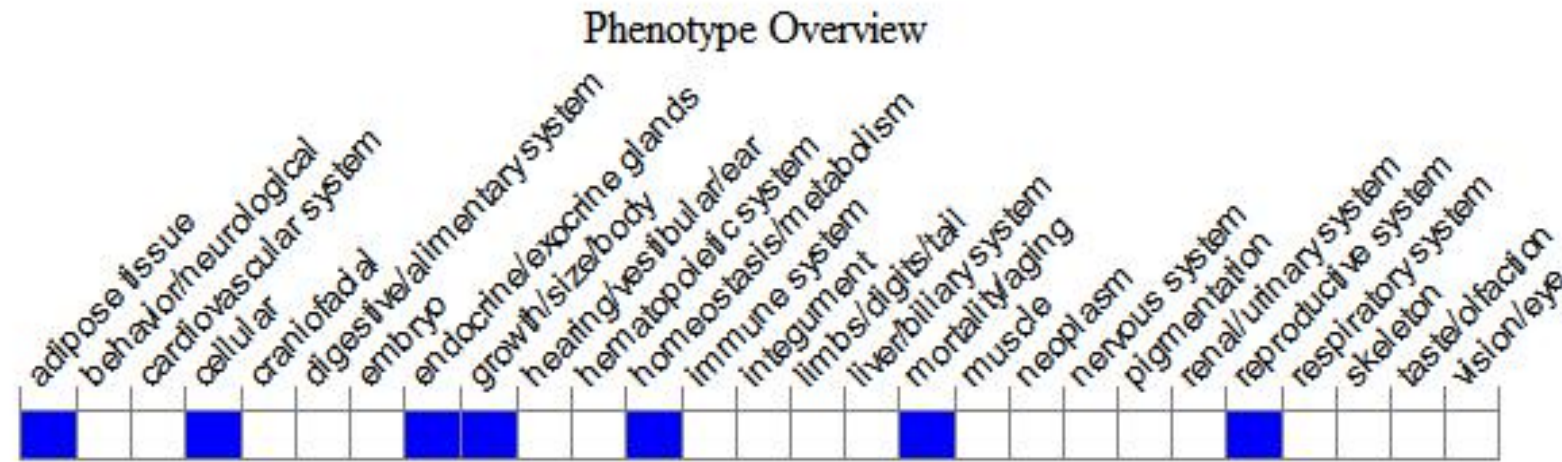
Genomic location distribution



集萃药康
GemPharmatech



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 reduced expression of several liver-specific and liver-enriched genes. Homozygous mice exhibit abnormal glucose homeostasis and reduced male fertility with abnormal spermatogenesis. Mice remodel their fat tissues on high fat diets, store less fat, and burn more energy as they age. Mutant mice live significantly longer than controls.

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

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