Foxe1 Cas9-KO Strategy

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Reviewer: Huimin Su

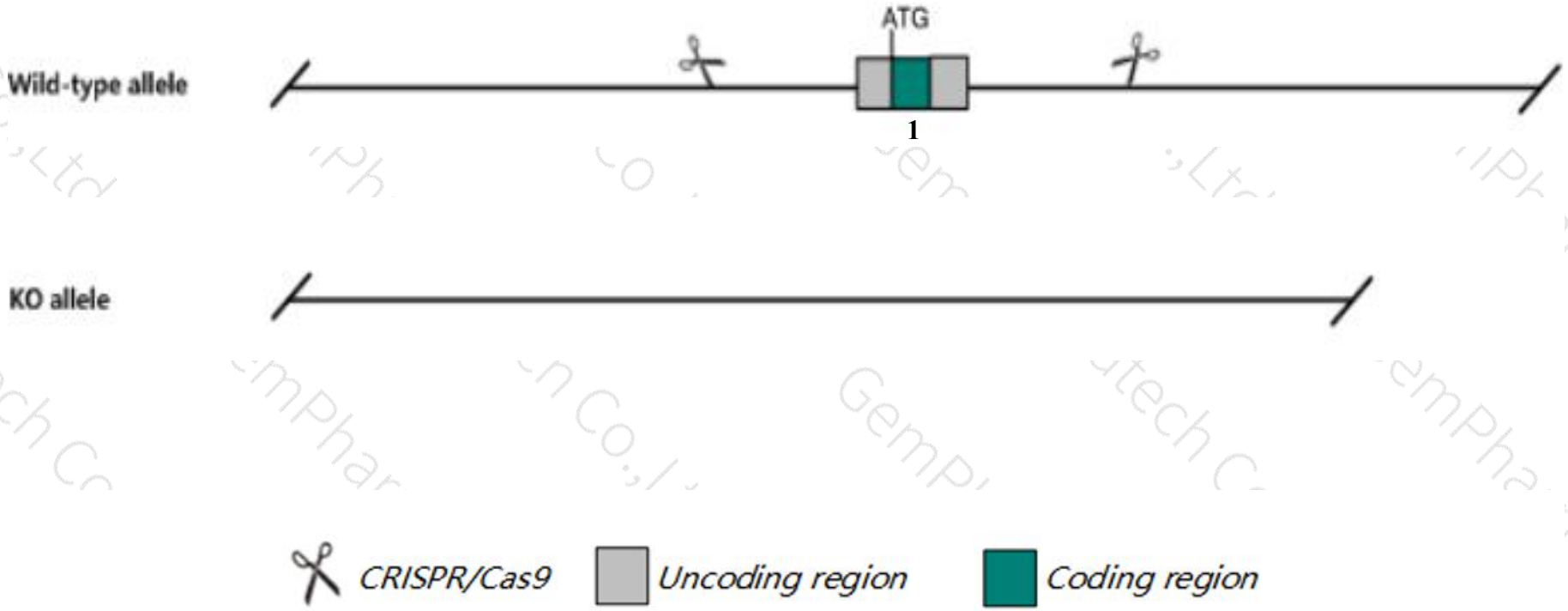
Design Date: 2020-6-15

Project Overview

Project Name	***Foxe1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxe1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Foxe1* gene has 1 transcript. According to the structure of *Foxe1* gene, exon1 of *Foxe1-201* (ENSMUST00000095097.2) 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 *Foxe1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,homozygous null mice die within 48 hours of birth exhibiting cleft palate and a sublingual or absent thyroid gland due to thyroid dysgenesis at the stage of endodermal bud migration. mutant skin grafts display thin, sparse and kinky pelage hairs due to defects in late hair follicle morphogenesis.
- The KO region contains functional region of the *Gm12446* gene.Knockout the region will destroy *Gm12446* gene.
- The *Foxe1* gene is located on the Chr4. 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）

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Foxe1 forkhead box E1 [Mus musculus (house mouse)]

Gene ID: 110805, updated on 13-Mar-2020

Summary

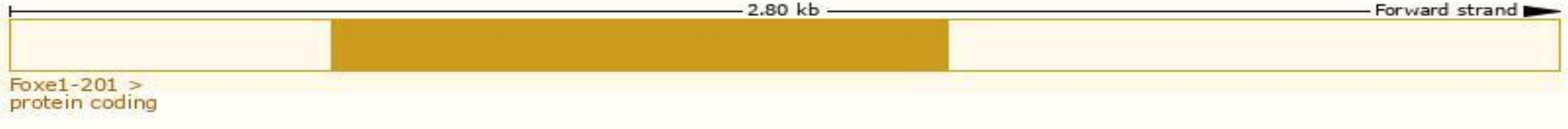
Official Symbol	Foxe1 provided by MGI
Official Full Name	forkhead box E1 provided byMGI
Primary source	MGI:MGI:1353500
See related	Ensembl:ENSMUSG00000070990
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TTF-2, Titf2
Orthologs	human all

Transcript information（Ensembl）

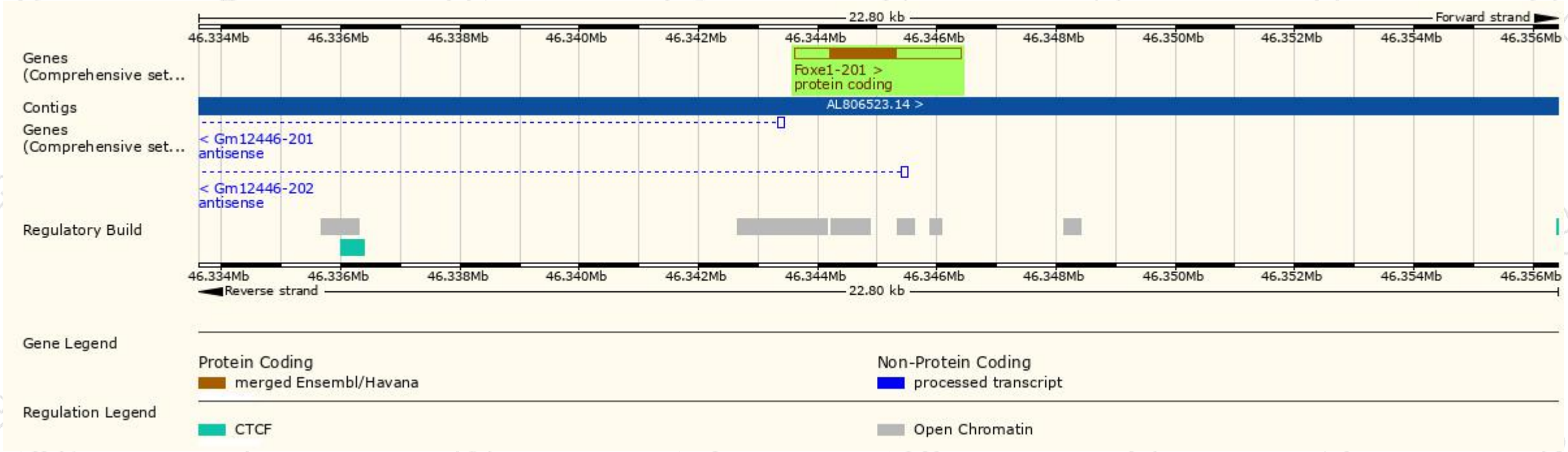
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxe1-201	ENSMUST00000095097.2	2804	371aa	Protein coding	CCDS18147	Q8R2I0	TSL:NA GENCODE basic APPRIS P1

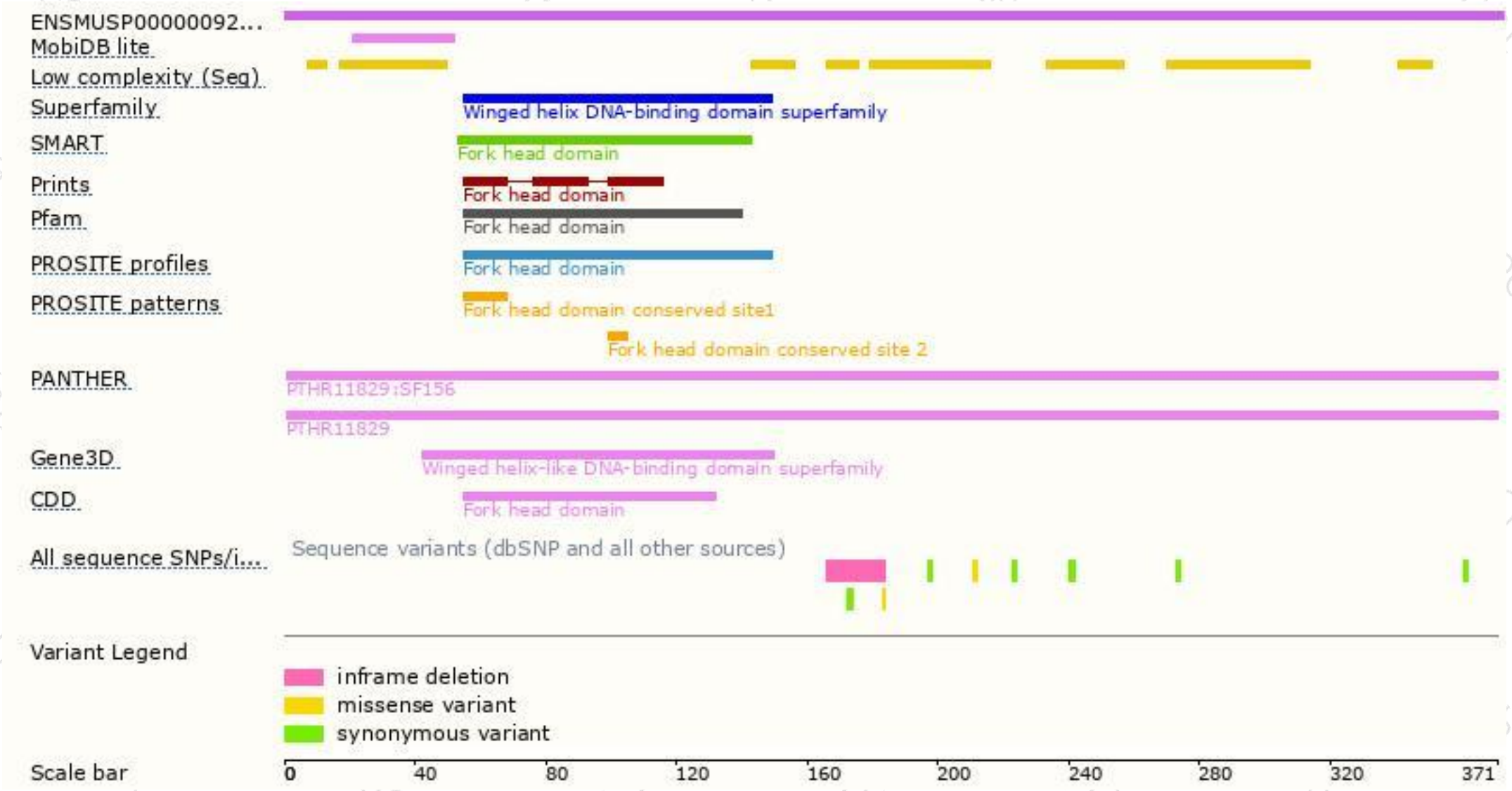
The strategy is based on the design of *Foxe1-201* transcript,the transcription is shown below:



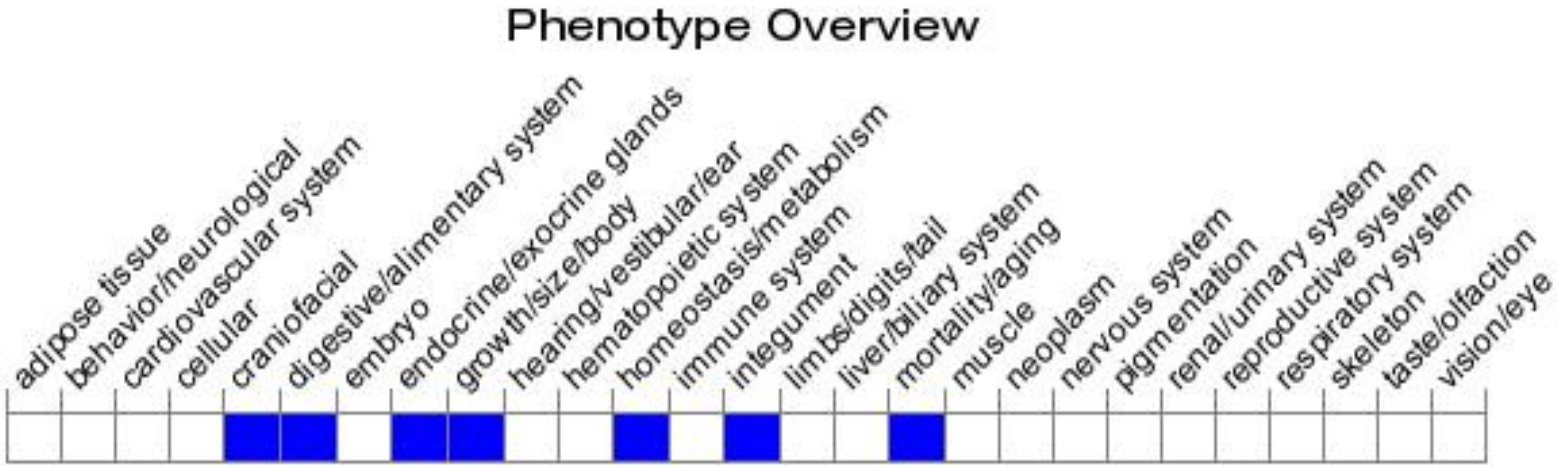
Genomic location distribution



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/).

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

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