Tyro3 Cas9-KO Strategy

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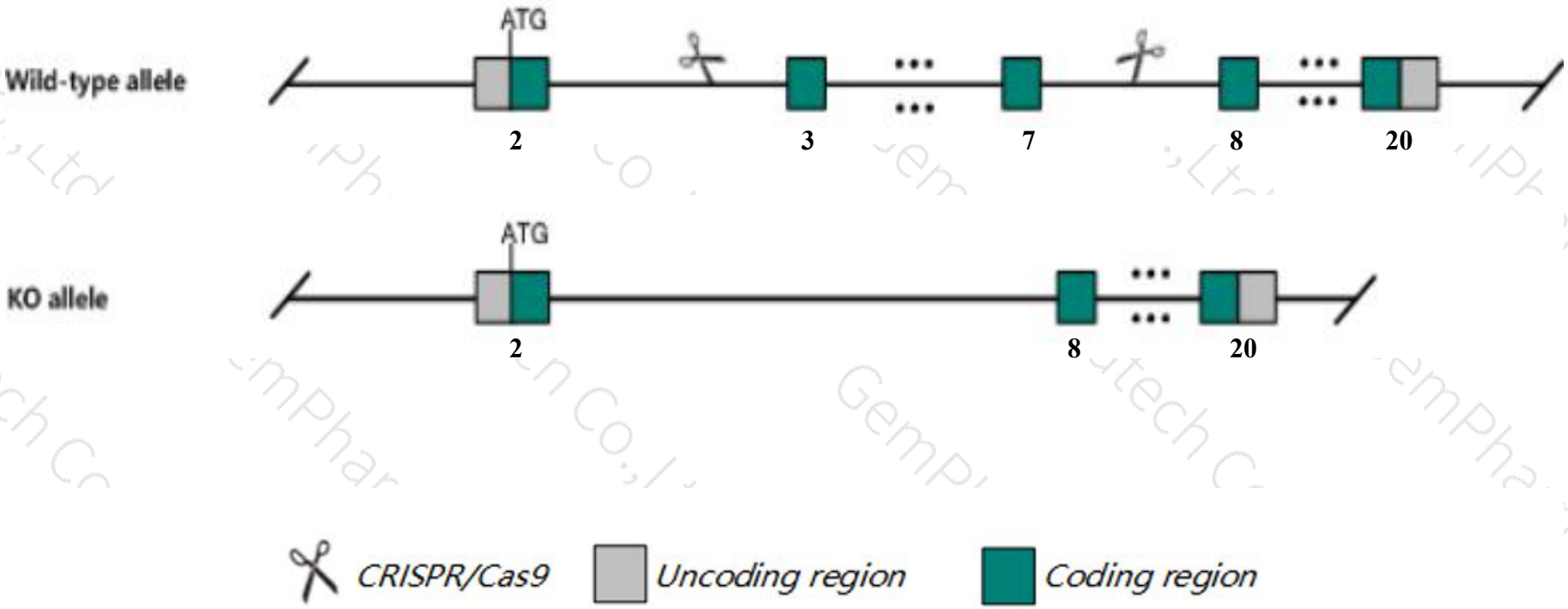
Design Date: 2019-8-20

Project Overview

Project Name	***Tyro3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tyro3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Tyro3* gene has 8 transcripts. According to the structure of *Tyro3* gene, exon3-exon7 of *Tyro3-202*(ENSMUST00000110783.7) transcript is recommended as the knockout region.The region contains 659bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tyro3* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,homozygous mutant mice are phenotypically normal, however in conjunction with mutations in other related receptor tyrosine kinases, mutations of this gene results in fertility defects, autoimmunity, and aberrant apoptosis.

➢ The *Tyro3* 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 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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Tyro3 TYRO3 protein tyrosine kinase 3 [Mus musculus (house mouse)]

Gene ID: 22174, updated on 30-Mar-2019

Summary

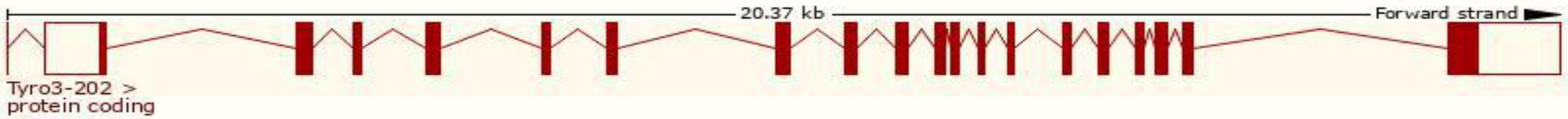
Official Symbol	Tyro3 provided by MGI
Official Full Name	TYRO3 protein tyrosine kinase 3 provided by MGI
Primary source	MGI:MGI:104294
See related	Ensembl:ENSMUSG00000027298
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323366, Brt, Dtk, Etk-2, Rse, Sky, TK19-2, Tif, etk2/tyro3, tk19-1
Expression	Broad expression in cortex adult (RPKM 29.2), cerebellum adult (RPKM 26.7) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

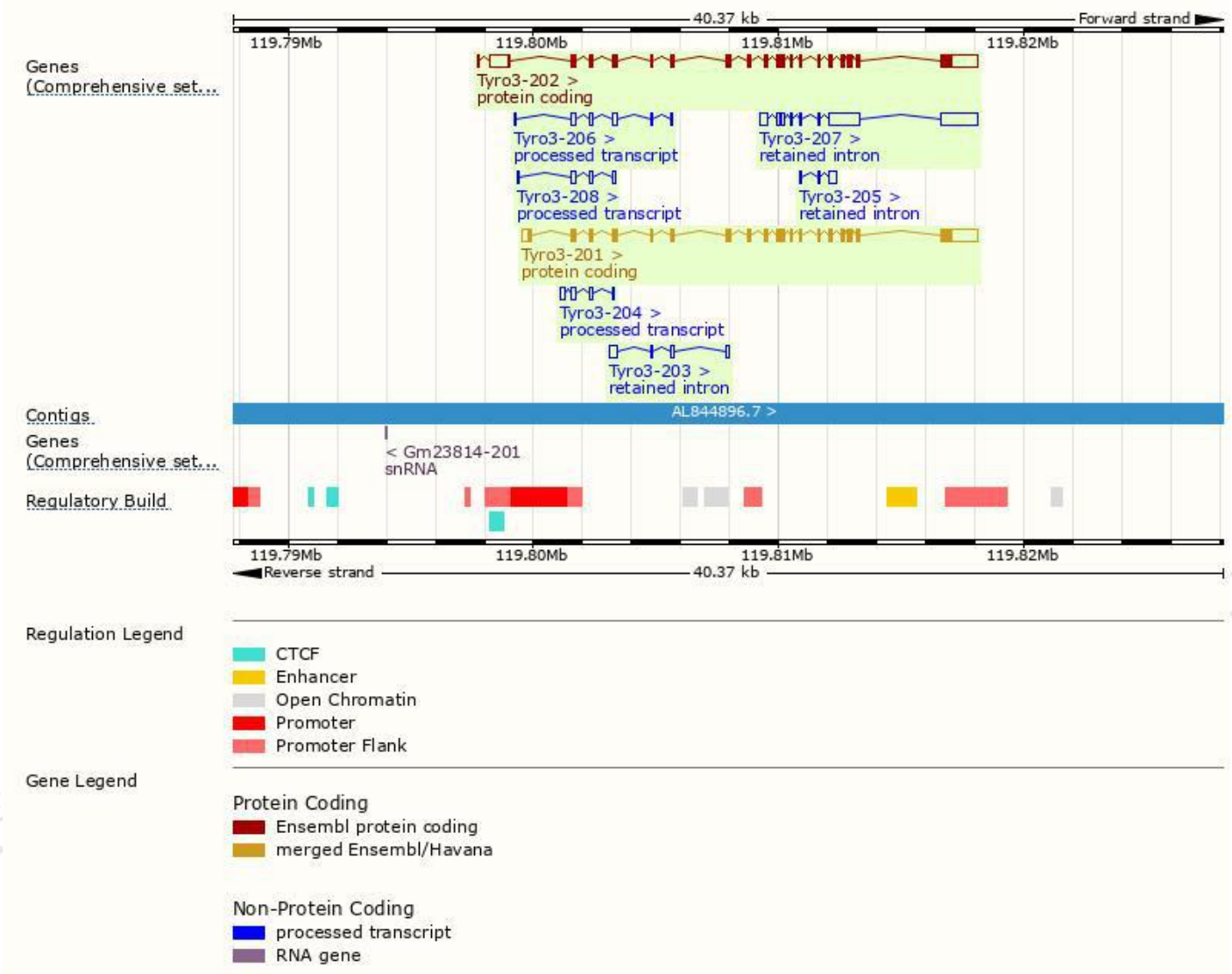
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tyro3-202	ENSMUST00000110783.7	4460	876aa	Protein coding	CCDS71119	P55144	TSL:1 GENCODE basic APPRIS ALT2
Tyro3-201	ENSMUST00000028763.9	3989	880aa	Protein coding	CCDS16611	P55144	TSL:1 GENCODE basic APPRIS P3
Tyro3-206	ENSMUST00000147636.7	643	No protein	Processed transcript	-	-	TSL:3
Tyro3-204	ENSMUST00000135726.1	480	No protein	Processed transcript	-	-	TSL:3
Tyro3-208	ENSMUST00000148343.7	470	No protein	Processed transcript	-	-	TSL:5
Tyro3-207	ENSMUST00000147761.7	3529	No protein	Retained intron	-	-	TSL:2
Tyro3-203	ENSMUST00000130456.1	683	No protein	Retained intron	-	-	TSL:2
Tyro3-205	ENSMUST00000137135.1	521	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Tyro3-202* transcript,the transcription is shown below:

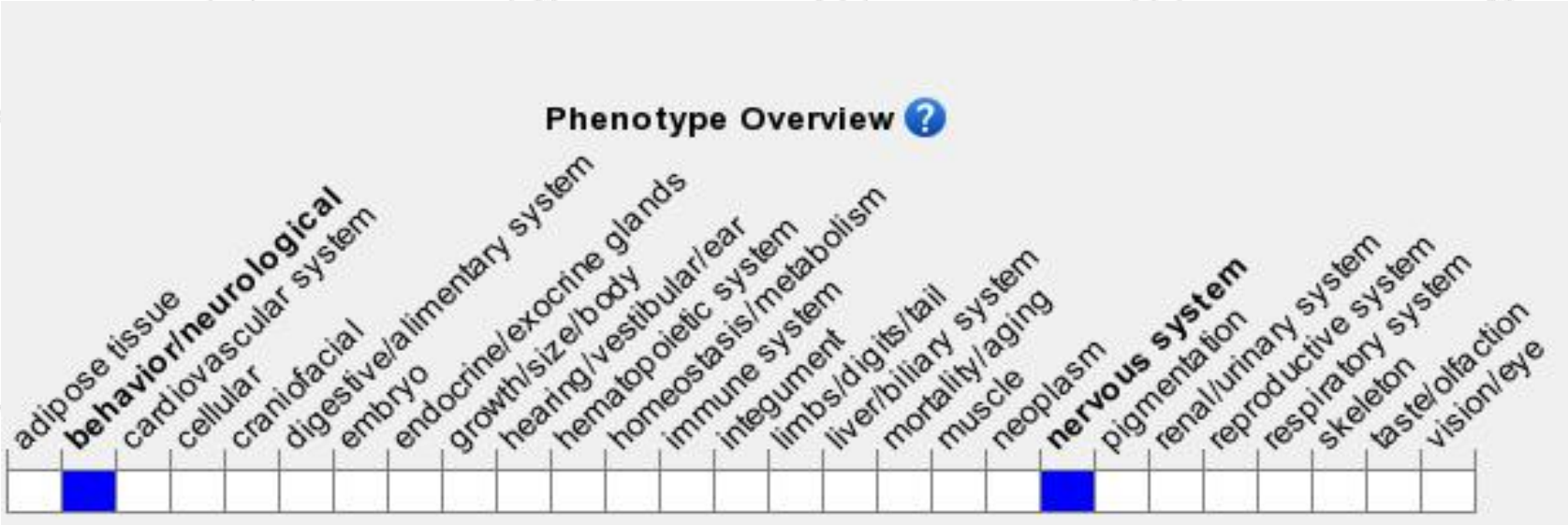


Genomic location distribution



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,homozygous mutant mice are phenotypically normal, however in conjunction with mutations in other related receptor tyrosine kinases, mutations of this gene results in fertility defects, autoimmunity, and aberrant apoptosis.

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

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