Mertk Cas9-CKO Strategy

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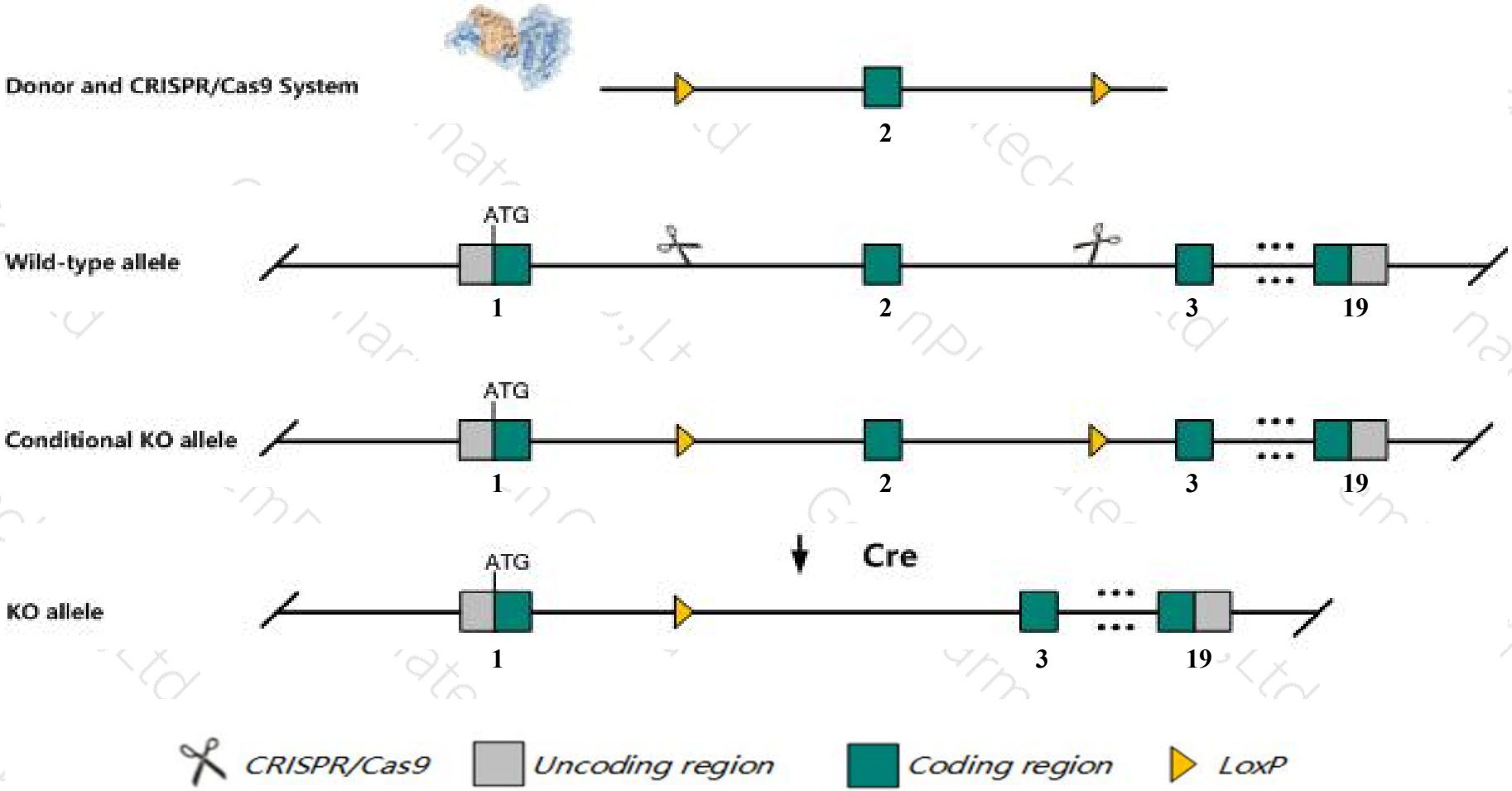
Project Overview

Project Name	***Mertk***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- The *Mertk* gene has 2 transcripts. According to the structure of *Mertk* gene, exon2 of *Mertk-201* (ENSMUST00000014505.4) transcript is recommended as the knockout region.The region contains 409bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Mertk* 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.

Notice

➢ According to the existing MGI data,Homozygotes for targeted null mutations show increased sensitivity to LPS-induced shock, defective phagocytosis of apoptotic cells, lupus-like autoimmunity, degeneration of photoreceptors, decreased platelet aggregation and protection from induced pulmonary thromboembolism and thrombosis.

➢ Transcript *Mertk*-202 may not be affected.

➢ The *Mertk* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Mertk MER proto-oncogene tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 17289, updated on 30-Mar-2019

Summary

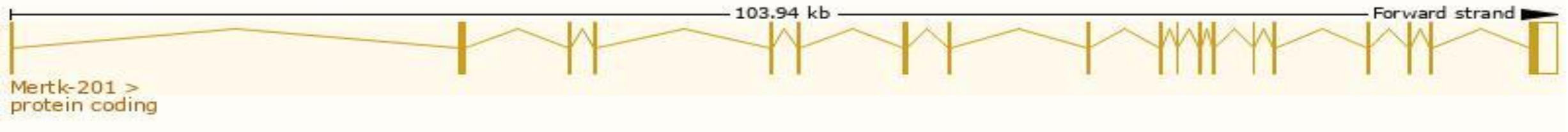
Official Symbol	Mertk provided by MGI
Official Full Name	MER proto-oncogene tyrosine kinase provided by MGI
Primary source	MGI:MGI:96965
See related	Ensembl:ENSMUSG00000014361
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Eyk, Mer, Nyk, nmf12
Expression	Ubiquitous expression in lung adult (RPKM 4.8), kidney adult (RPKM 4.4) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

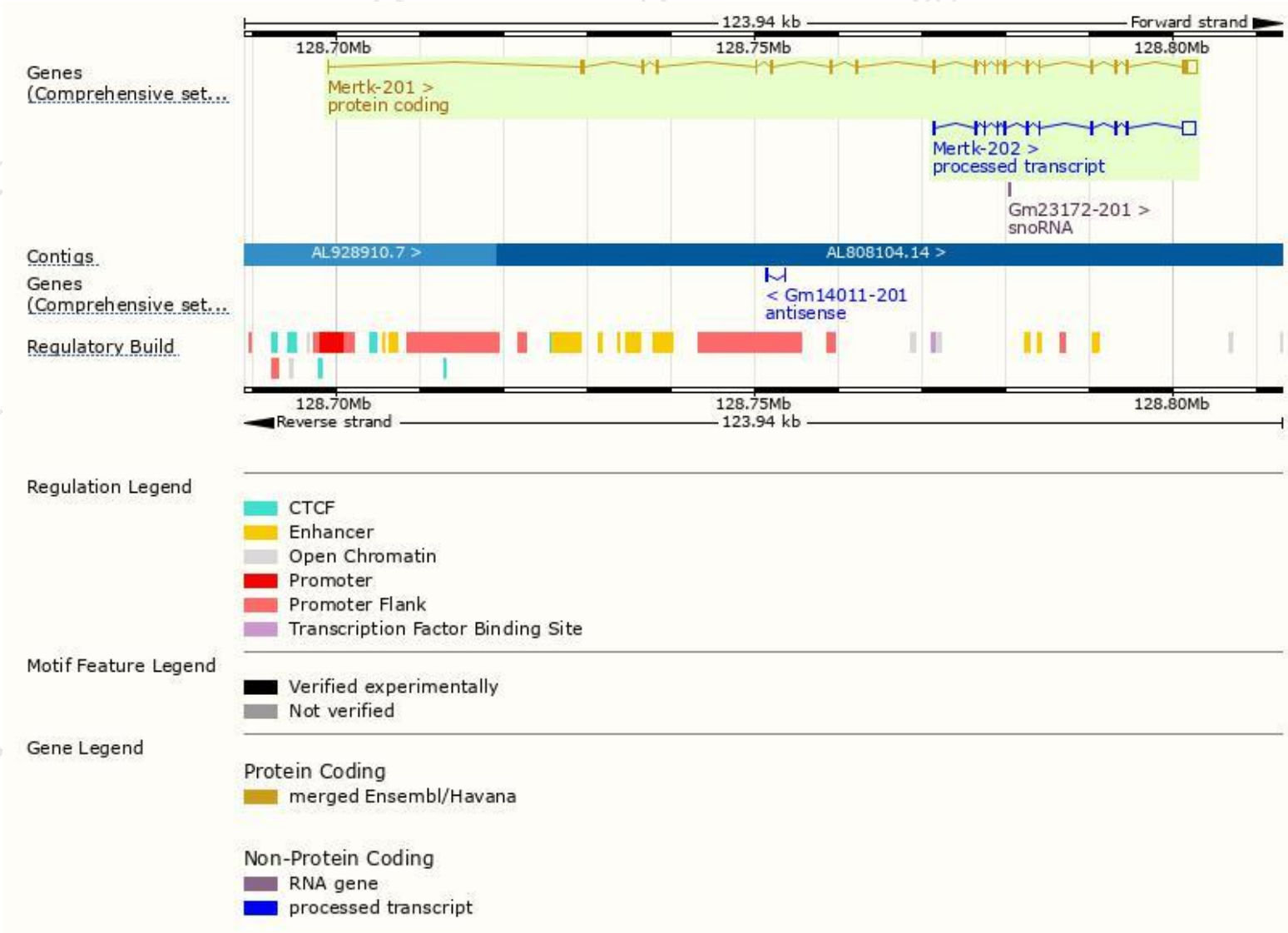
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mertk-201	ENSMUST00000014505.4	4302	994aa	Protein coding	CCDS16716	Q60805	TSL:1 GENCODE basic APPRIS P1
Mertk-202	ENSMUST00000140221.1	2744	No protein	Processed transcript	-	-	TSL:1

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

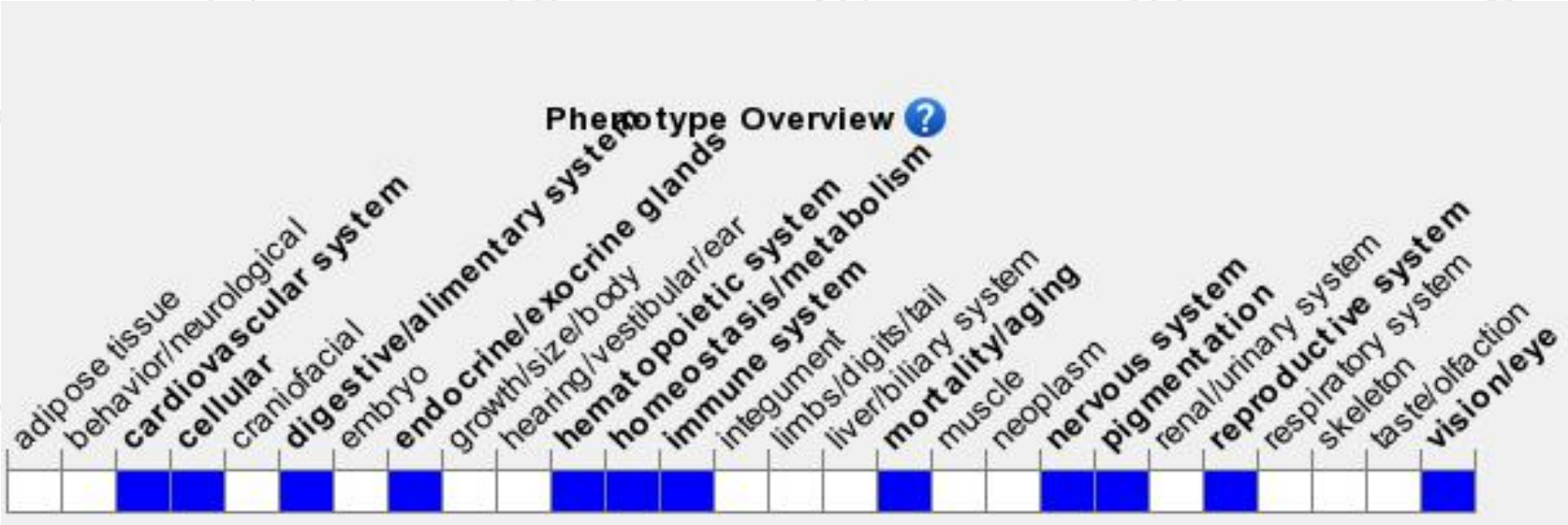


Genomic location distribution



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 targeted null mutations show increased sensitivity to LPS-induced shock, defective phagocytosis of apoptotic cells, lupus-like autoimmunity, degeneration of photoreceptors, decreased platelet aggregation and protection from induced pulmonary thromboembolism and thrombosis.

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

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