Trex1 Cas9-KO Strategy

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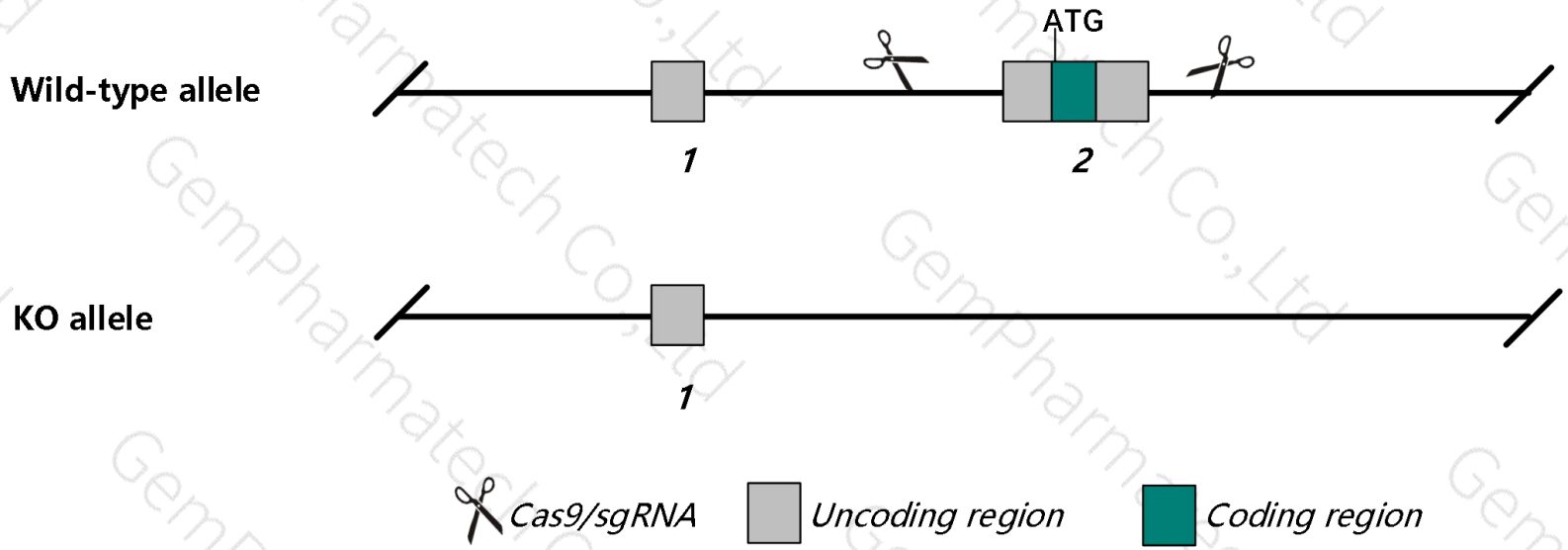
Project Overview

Project Name	***Trex1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trex1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Trex1* gene has 2 transcripts. According to the structure of *Trex1* gene, exon2 of *Trex1-201* (ENSMUST00000061973.4) 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 *Trex1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Nullizygous mice display premature death, cardiomyopathy, myocarditis, atrial thrombosis, and altered spleen morphology. Homozygotes for the D18N allele develop lupus-like disease with systemic inflammation, lymphoid hyperplasia, vasculitis, production of autoantibodies to dsDNA, and renal disease.
- Intron1-2 is small and its effect is unknown.
- The KO region may affect the function of *Shisa5,Atrip* gene.
- The *Trex1* gene is located on the Chr9. 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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Trex1 three prime repair exonuclease 1 [Mus musculus (house mouse)]

Gene ID: 22040, updated on 13-Mar-2020

Summary

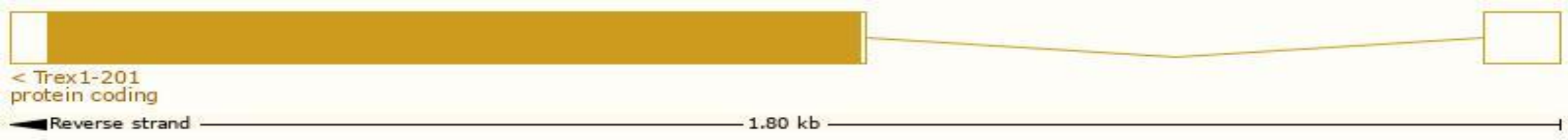
Official Symbol	Trex1 provided by MGI
Official Full Name	three prime repair exonuclease 1 provided by MGI
Primary source	MGI:MGI:1328317
See related	Ensembl:ENSMUSG00000049734
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU041952
Expression	Ubiquitous expression in spleen adult (RPKM 79.9), mammary gland adult (RPKM 65.5) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

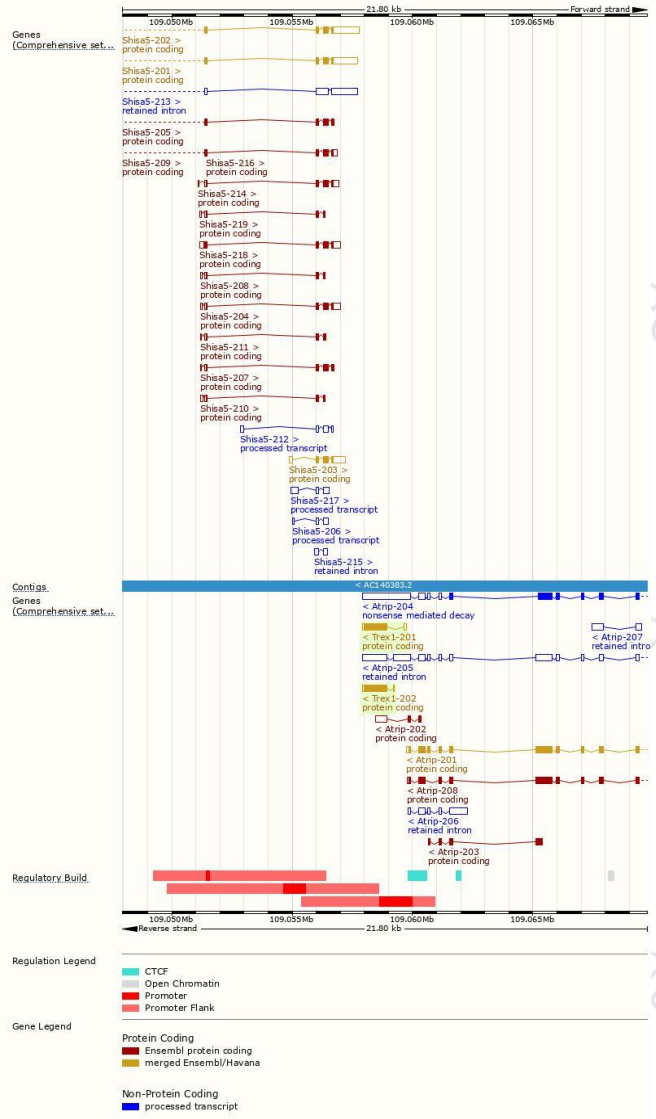
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trex1-201	ENSMUST00000061973.4	1084	314aa	Protein coding	CCDS23544	Q91XB0	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
Trex1-202	ENSMUST00000112053.1	1054	314aa	Protein coding	CCDS23544	Q91XB0	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

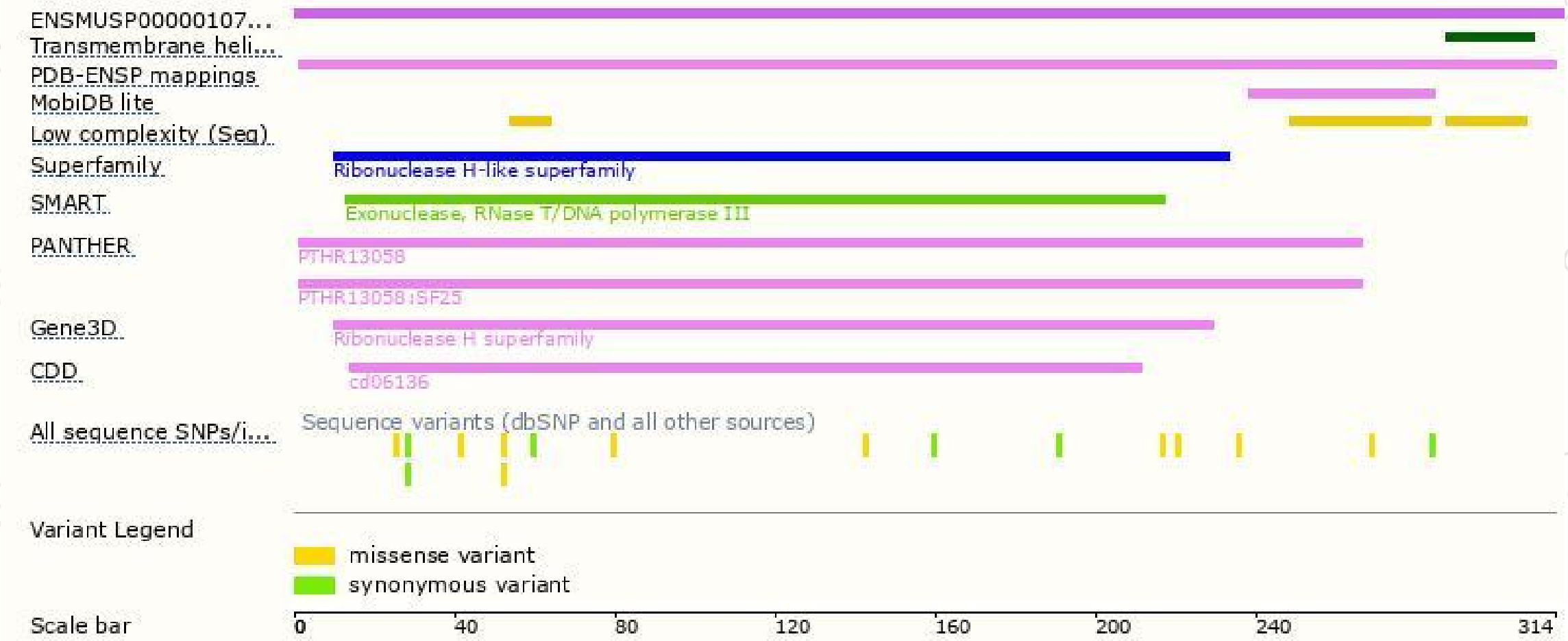
The strategy is based on the design of *Trex1-201* transcript,The transcription is shown below



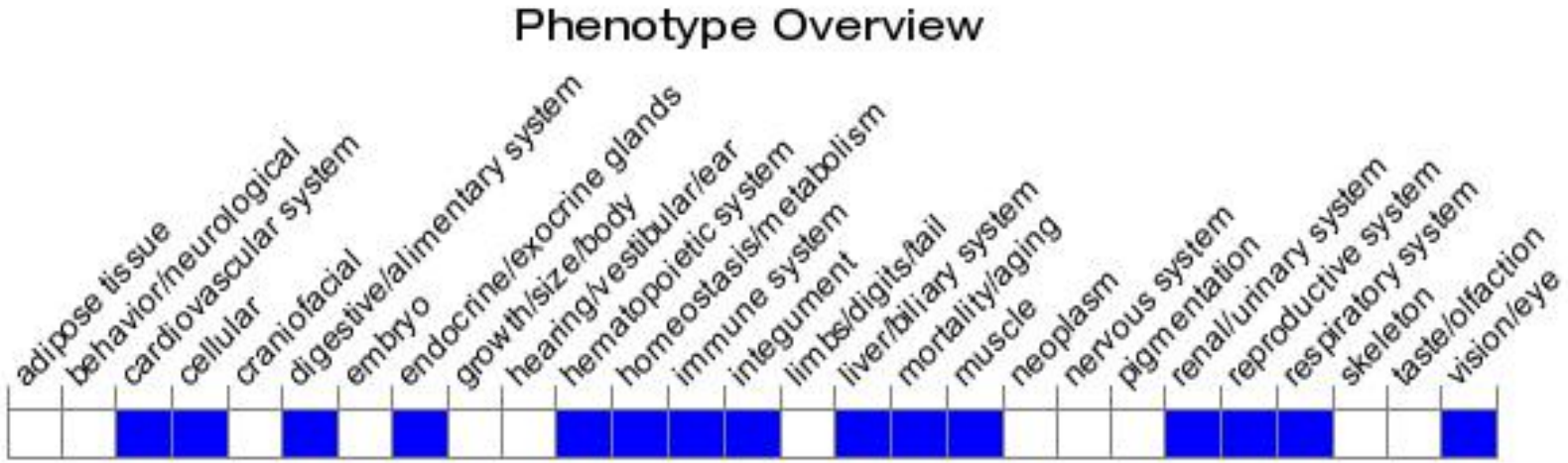
Genomic location distribution



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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