Dtx1 Cas9-KO Strategy

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Reviewer: Xiaojing Li

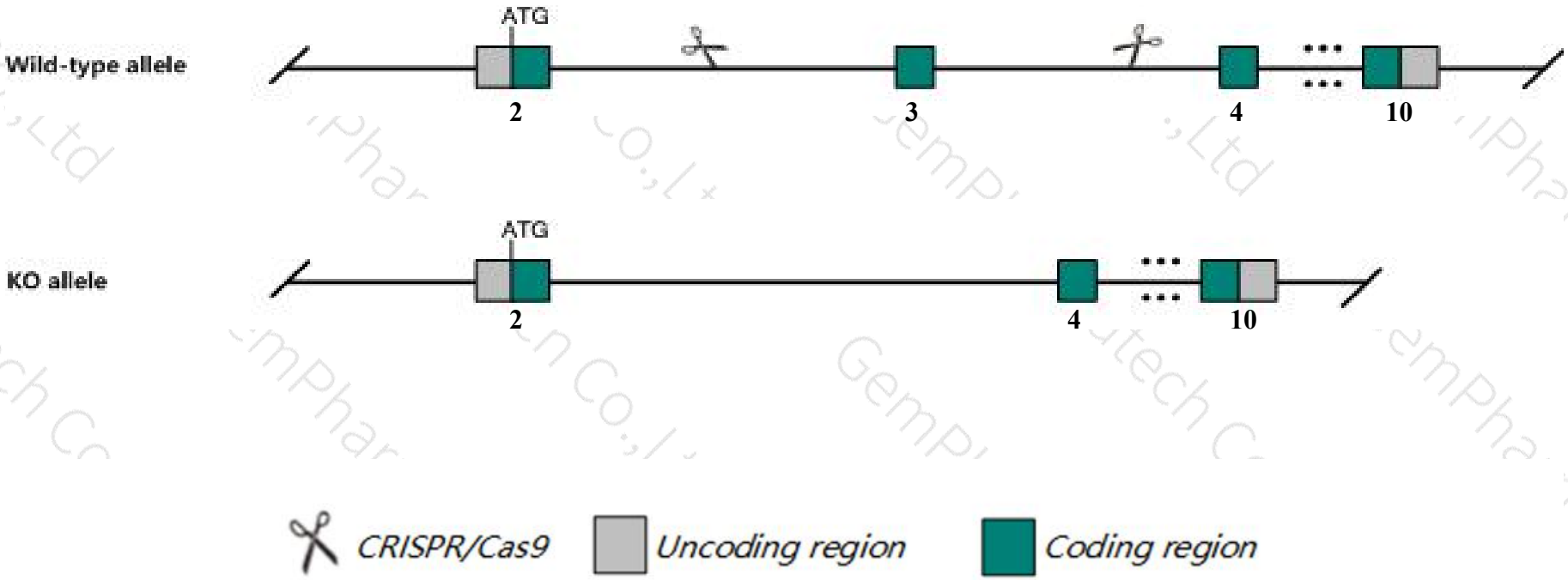
Design Date: 2020-1-20

Project Overview

Project Name	***Dtx1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dtx1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Dtx1* gene has 6 transcripts. According to the structure of *Dtx1* gene, exon3 of *Dtx1-201* (ENSMUST00000031607.6) transcript is recommended as the knockout region.The region contains 703bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Dtx1* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Homozygous mutant mice are viable and fertile with normal B and T cell devlepment and function and no gross abnormalities in any of the major organs.

- The *Dtx1* gene is located on the Chr5. 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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Dtx1 deltex 1, E3 ubiquitin ligase [Mus musculus (house mouse)]

Gene ID: 14357, updated on 31-Jan-2019

Summary

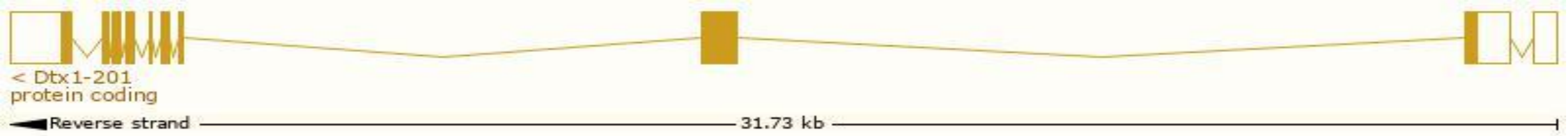
Official Symbol	Dtx1 provided by MGI
Official Full Name	deltex 1, E3 ubiquitin ligase provided byMGI
Primary source	MGI:MGI:1352744
See related	Ensembl:ENSMUSG00000029603
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Fxit1, mKIAA4160
Expression	Biased expression in spleen adult (RPKM 82.7), CNS E18 (RPKM 30.0) and 14 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

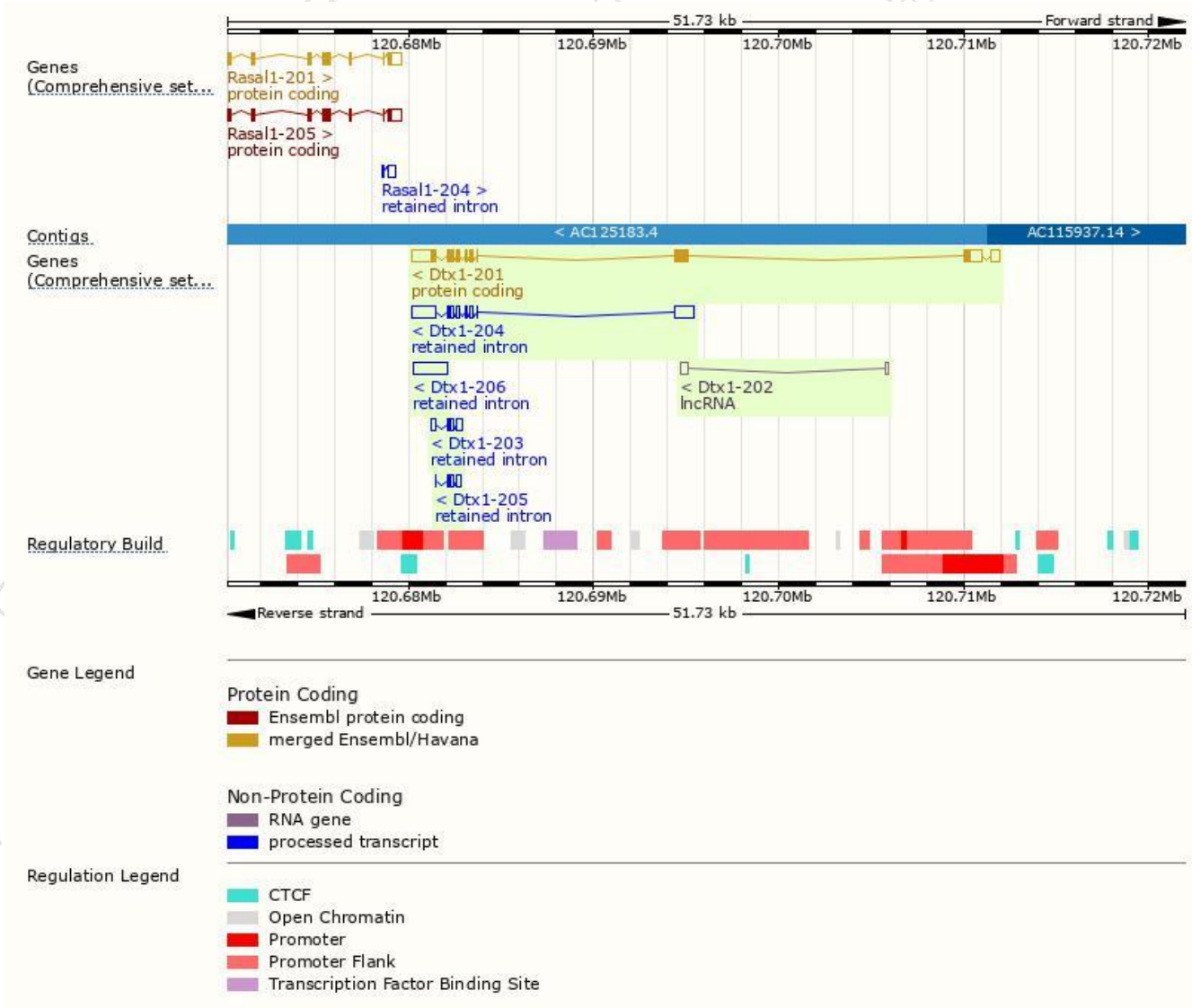
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dtx1-201	ENSMUST00000031607.6	4035	627aa	Protein coding	CCDS19624	Q61010	TSL:1 GENCODE basic APPRIS P1
Dtx1-204	ENSMUST00000145174.7	2961	No protein	Retained intron	-	-	TSL:1
Dtx1-206	ENSMUST00000201264.1	1831	No protein	Retained intron	-	-	TSL:NA
Dtx1-203	ENSMUST00000144889.7	871	No protein	Retained intron	-	-	TSL:3
Dtx1-205	ENSMUST00000151562.1	507	No protein	Retained intron	-	-	TSL:2
Dtx1-202	ENSMUST00000124079.1	540	No protein	lncRNA	-	-	TSL:3

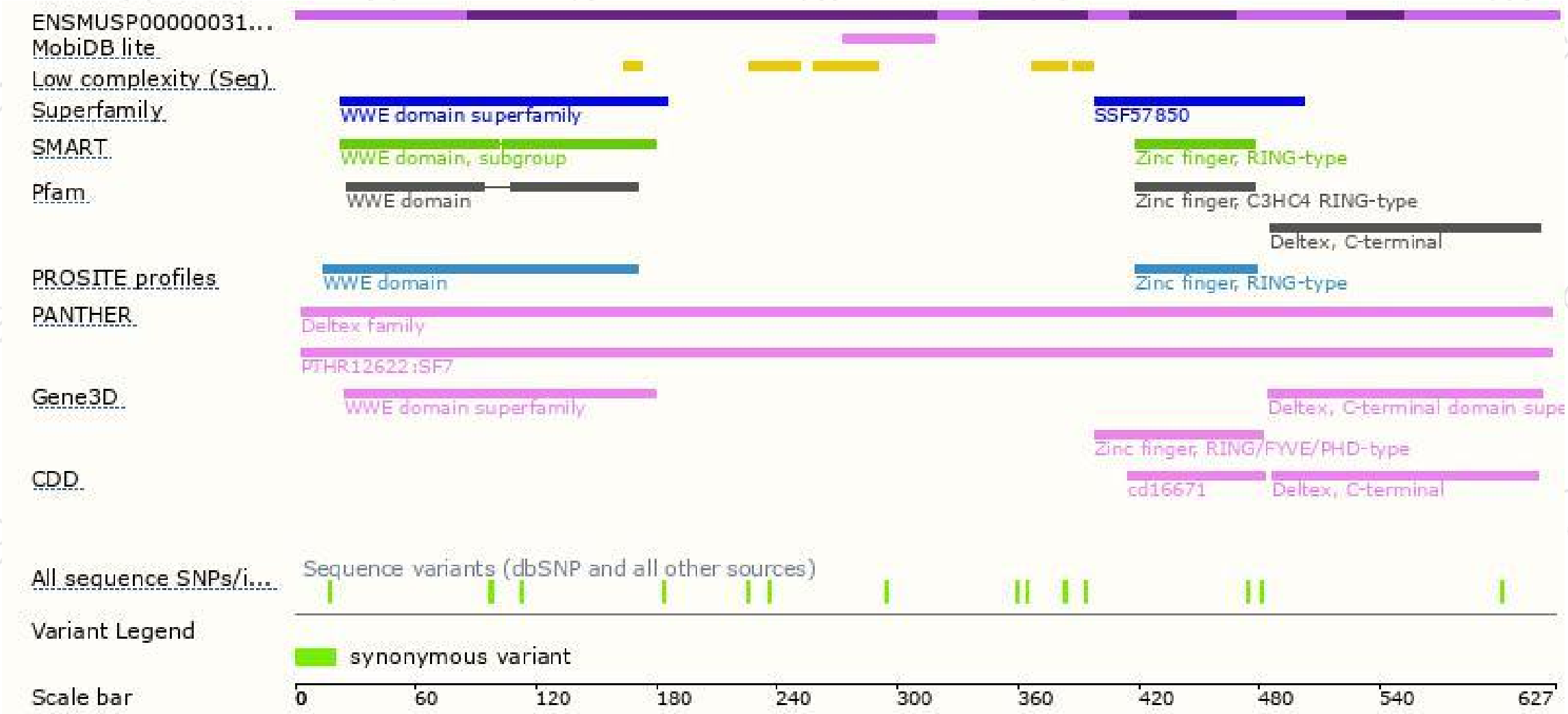
The strategy is based on the design of *Dtx1-201* transcript,The transcription is shown below



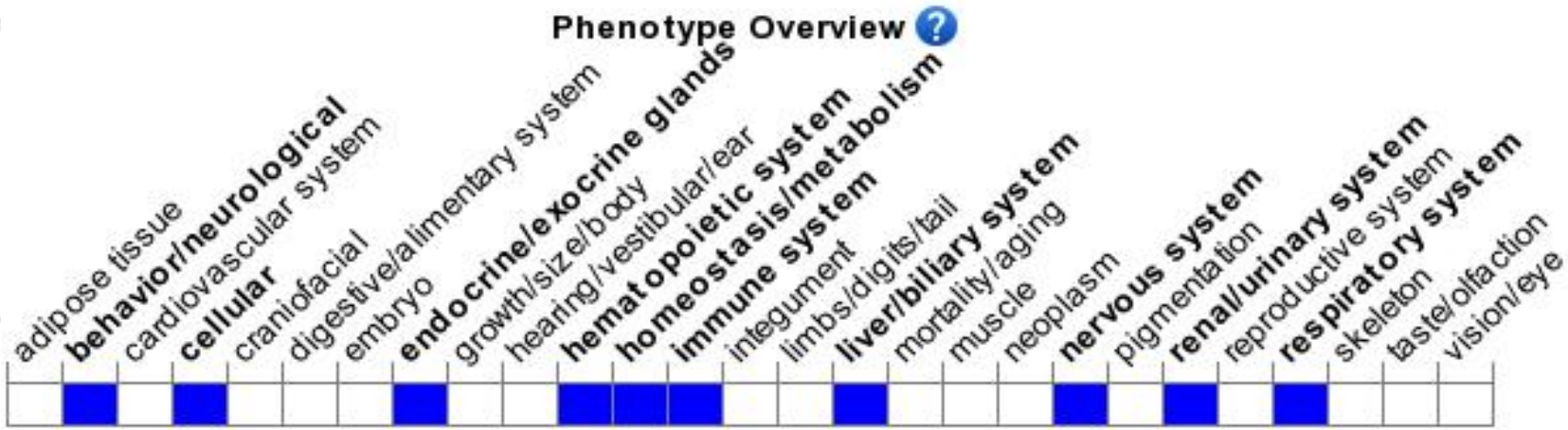
Genomic location distribution



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,Homozygous mutant mice are viable and fertile with normal B and T cell devlepment and function and no gross abnormalities in any of the major organs.

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

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