

Id2 Cas9-KO Strategy

Designer:

Reviewer:

Design Date:

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Project Overview



Project Name Id2

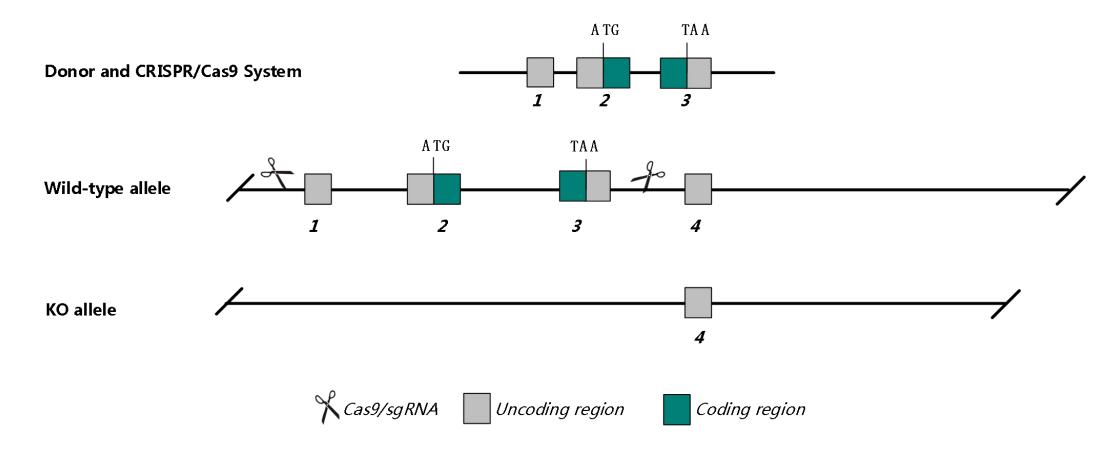
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Id2* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Id2* gene has 3 transcripts. According to the structure of *Id2* gene, exon1-exon3 of *Id2-202* (ENSMUST00000221761.1) transcript is recommended as the knockout region. The region contains most 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 *Id2* gene. The brief process is as follows: CRISPR/Cas9 system we

Notice



- ➤ According to the existing MGI data, Mice homozygous for disruptions in this gene display postnatal lethality with immune system defects. Homozygotes may also have defects in the digestive tract, kidneys, adipose tissue and in mammary gland development.
- > The KO region contains functional region of the Id2 gene.
- The *Id2* gene is located on the Chr12. 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)



Id2 inhibitor of DNA binding 2 [Mus musculus (house mouse)]

Gene ID: 15902, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Id2 provided by MGI

Official Full Name inhibitor of DNA binding 2 provided by MGI

Primary source MGI:MGI:96397

See related Ensembl: ENSMUSG00000020644

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 Al255428, C78922, ldb2, bHLHb26

Expression Ubiquitous expression in kidney adult (RPKM 169.1), adrenal adult (RPKM 168.8) and 26 other tissuesSee more

Orthologs human all

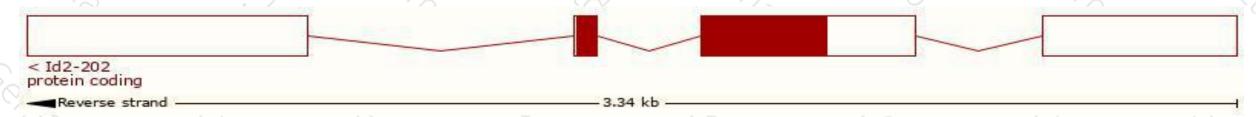
Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

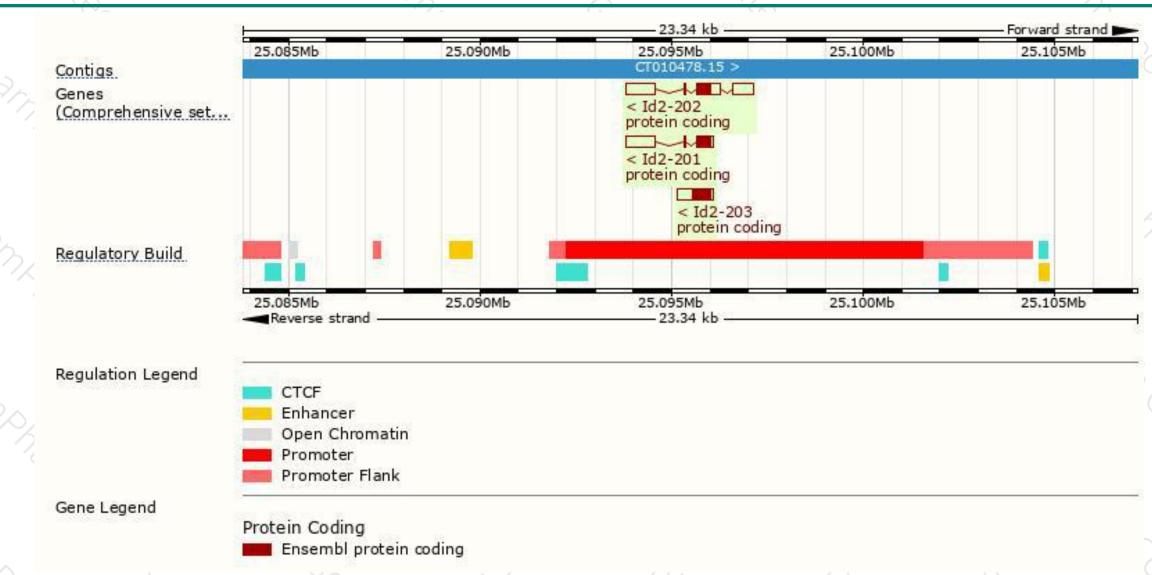
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ld2-202	ENSMUST00000221761.1	1969	<u>134aa</u>	Protein coding	CCDS25846	P41136 Q545T4	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
				×		P41136 Q545T4	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
ld2-203	ENSMUST00000222667.1	958	<u>155aa</u>	Protein coding	=	A0A1Y7VMT3	TSL:NA GENCODE basic

The strategy is based on the design of *Id2-202* transcript, The transcription is shown below



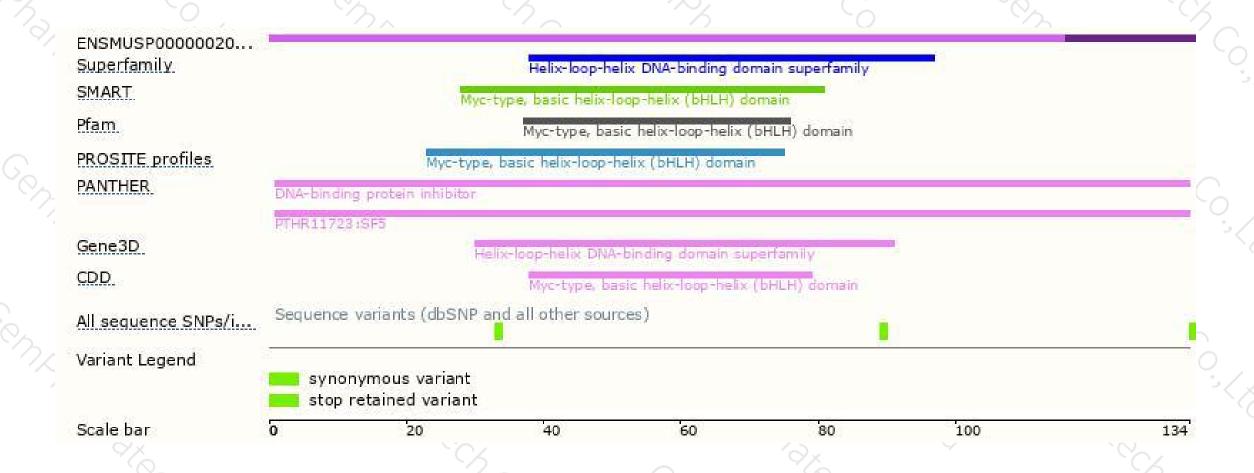
Genomic location distribution





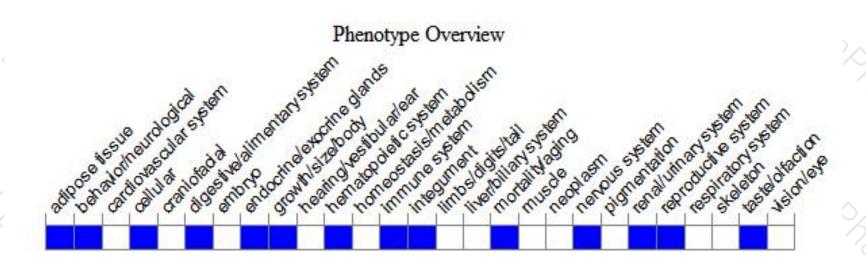
Protein domain





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, Mice homozygous for disruptions in this gene display postnatal lethality with immune system defects. Homozygotes may also have defects in the digestive tract, kidneys, adipose tissue and in mammary gland development.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





