

# ***Mxd3*** Cas9-KO Strategy

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# Project Overview

**Project Name**

***Mxd3***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mxd3* gene. The schematic diagram is as follows:



- The *Mxd3* gene has 4 transcripts. According to the structure of *Mxd3* gene, exon1-exon4 of *Mxd3-201* (ENSMUST00000021941.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mxd3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene have an essentially normal phenotype. They show an increased sensitivity to gamma irradiation.
- The knockout region is near to the N-terminal of *Rab24* gene, this strategy may influence the regulatory function of the N-terminal of *Rab24* gene.
- The *Mxd3* gene is located on the Chr13. 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)

## Mxd3 Max dimerization protein 3 [ *Mus musculus* (house mouse) ]

Gene ID: 17121, updated on 12-Aug-2019

### Summary

Official Symbol	Mxd3 provided by MGI
Official Full Name	Max dimerization protein 3 provided by MGI
Primary source	MGI:MGI:104987
See related	Ensembl:ENSMUSG00000021485
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mad3; bHLHc13; 4631412E13Rik
Expression	Ubiquitous expression in thymus adult (RPKM 35.6), duodenum adult (RPKM 33.9) and 24 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 13 B1; 13 29.8 cM

See Mxd3 in [Genome Data Viewer](#)

Exon count: 6

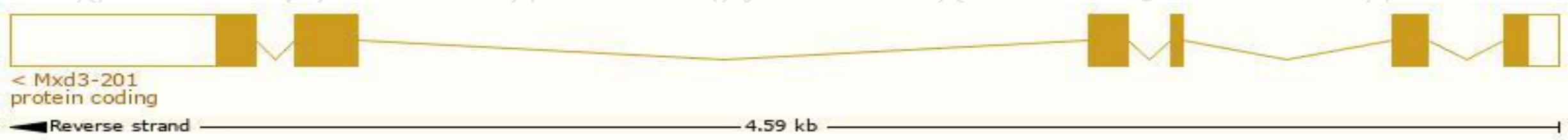
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	13	NC_000079.6 (55325170..55329900, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	13	NC_000079.5 (55426529..55431091, complement)

# Transcript information (Ensembl)

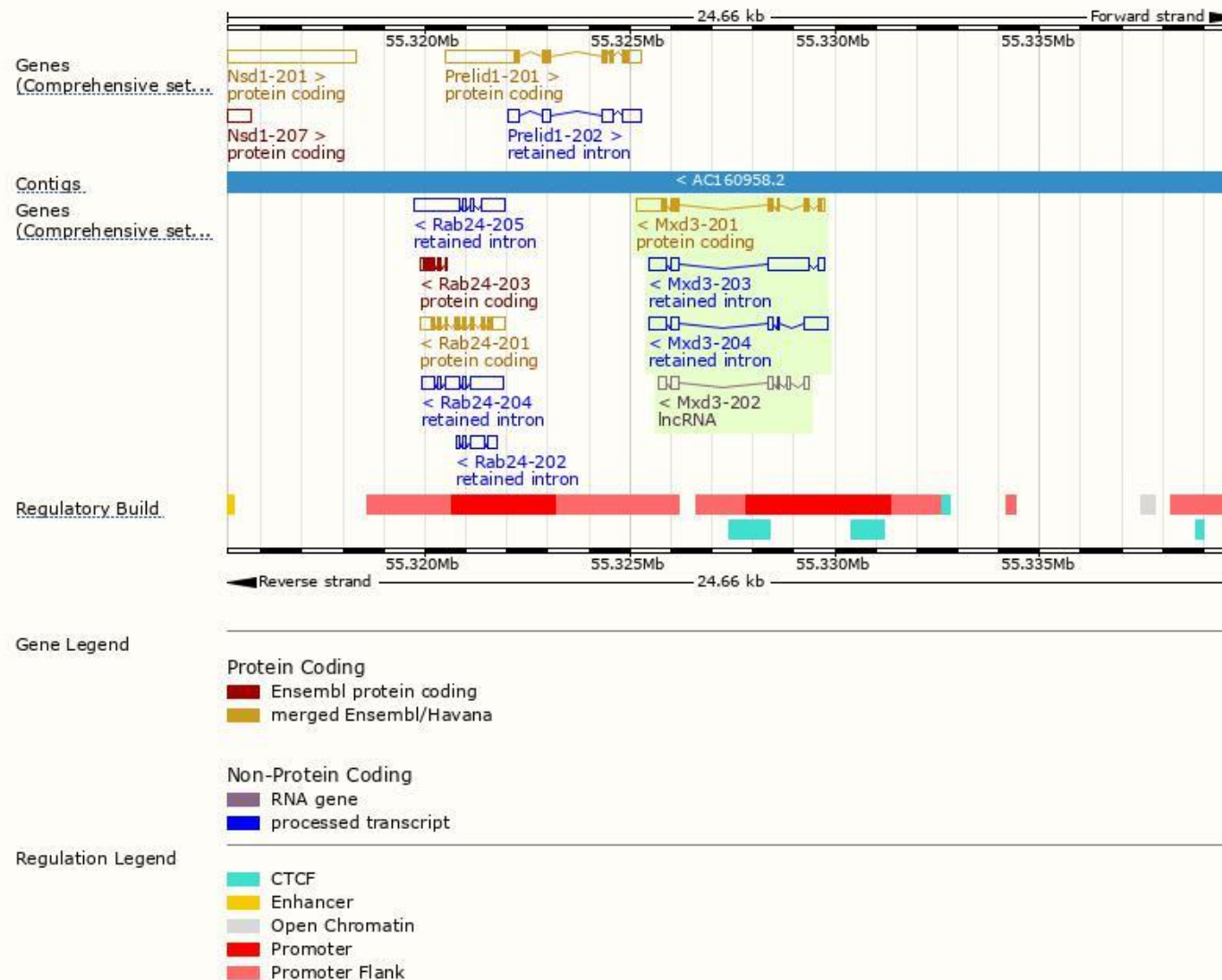
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mxd3-201	<a href="#">ENSMUST00000021941.7</a>	1327	<a href="#">206aa</a>	Protein coding	<a href="#">CCDS26543</a>	<a href="#">Q80US8</a>	TSL:1 GENCODE basic APPRIS P1
Mxd3-203	<a href="#">ENSMUST00000146181.7</a>	1742	No protein	Retained intron	-	-	TSL:2
Mxd3-204	<a href="#">ENSMUST00000225561.1</a>	1296	No protein	Retained intron	-	-	
Mxd3-202	<a href="#">ENSMUST00000141644.1</a>	683	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Mxd3-201* transcript,The transcription is shown below

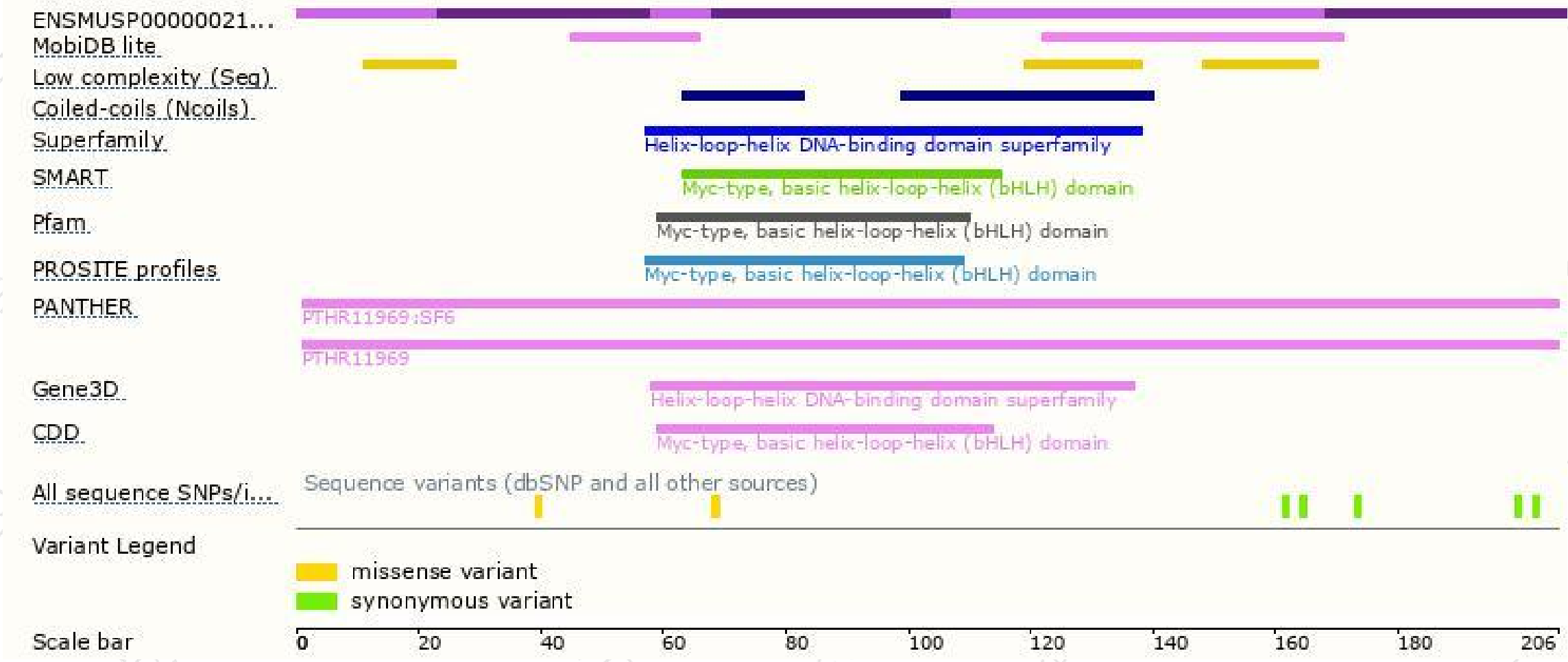


# Genomic location distribution

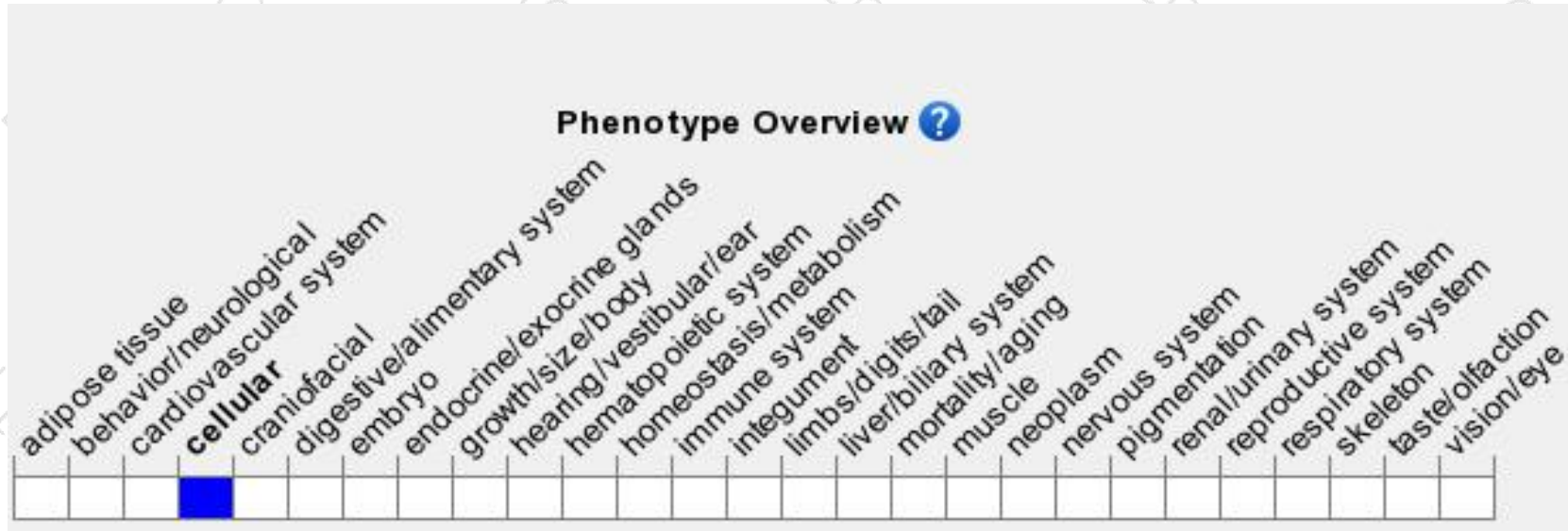




# Protein domain



# 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, Mice homozygous for disruptions in this gene have an essentially normal phenotype.

The show an increased sensitivity to gamma irradiation.

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

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