Mad2l2 Cas9-KO Strategy

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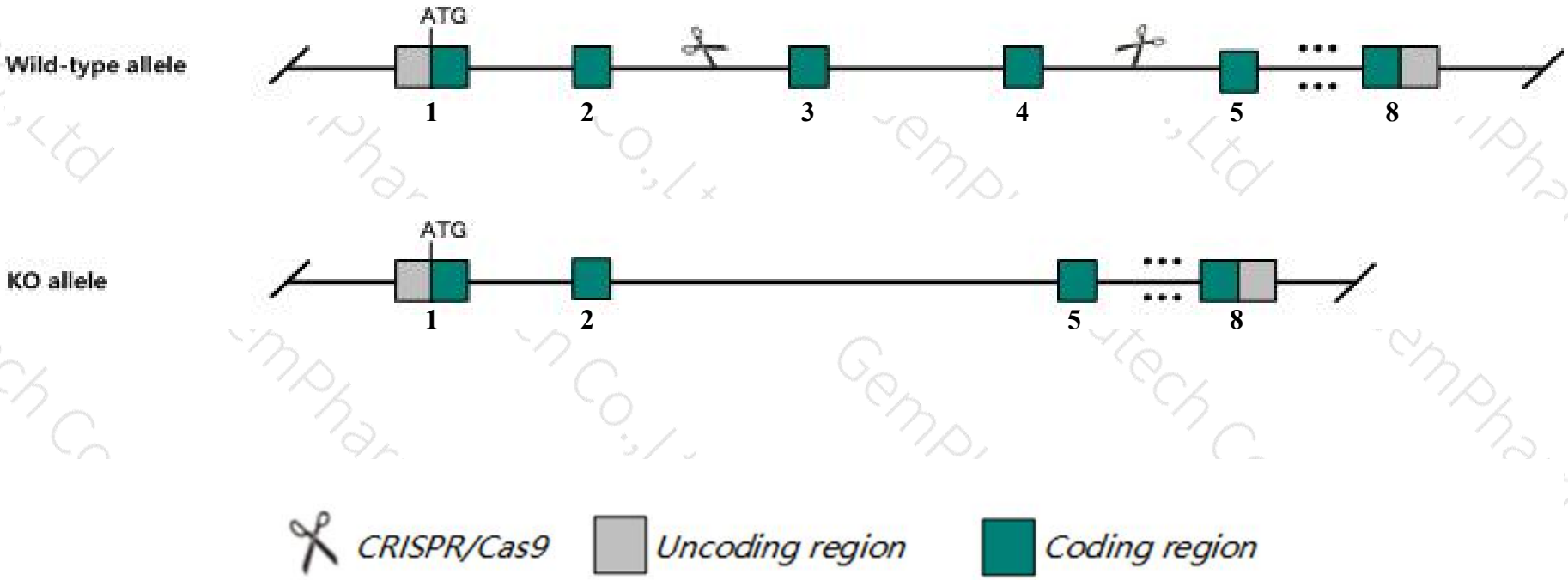
Project Overview

Project Name	***Mad2l2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mad2l2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mad2l2* gene has 8 transcripts. According to the structure of *Mad2l2* gene, exon3-exon4 of *Mad2l2-201* (ENSMUST00000030860.8) transcript is recommended as the knockout region.The region contains 173bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mad2l2* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ According to the existing MGI data,Homozygous disruption of this gene causes partial lethality between E13.5 and weaning, reduced body size, small testes and ovaries, infertility, and abnormal primordial germ cell apoptosis. Homozygotes for a null allele show increased neuroblast apoptosis and accumulation of double strand breaks.

➢Transcript *Mad2l2*-204&205 may not be affected.

➢ The *Mad2l2* gene is located on the Chr4. 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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Mad2l2 MAD2 mitotic arrest deficient-like 2 [Mus musculus (house mouse)]

Gene ID: 71890, updated on 31-Jan-2019

Summary

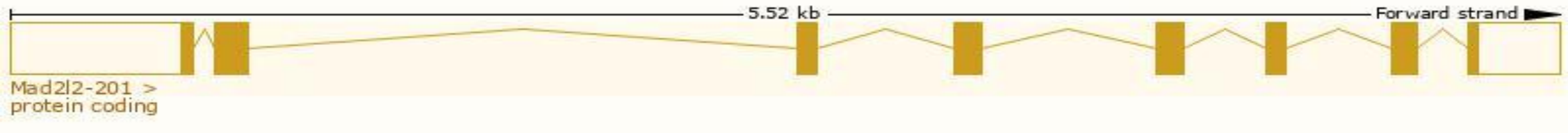
Official Symbol	Mad2l2 provided by MGI
Official Full Name	MAD2 mitotic arrest deficient-like 2 provided by MGI
Primary source	MGI:MGI:1919140
See related	Ensembl:ENSMUSG00000029003
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310033C13Rik, G1-453-4, MAD2B, REV7, repro22
Expression	Broad expression in testis adult (RPKM 68.8), CNS E14 (RPKM 17.7) and 21 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

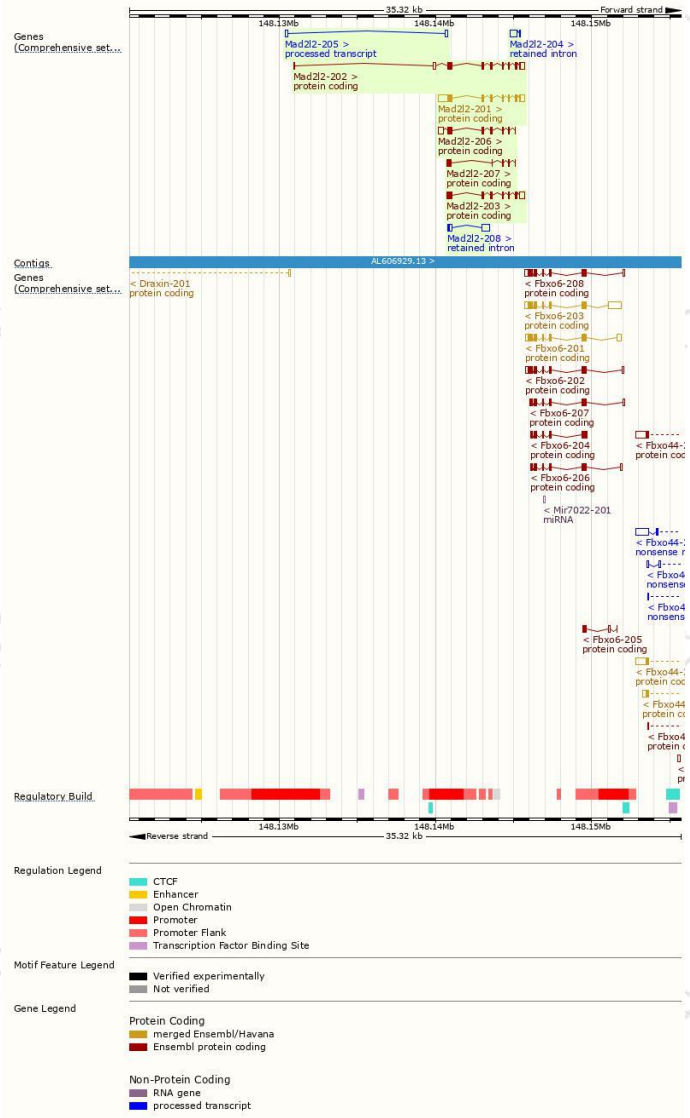
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mad2l2-201	ENSMUST00000030860.8	1535	211aa	Protein coding	CCDS18932	Q9D752	TSL:1 GENCODE basic APPRIS P1
Mad2l2-202	ENSMUST00000084129.8	1162	211aa	Protein coding	CCDS18932	Q9D752	TSL:1 GENCODE basic APPRIS P1
Mad2l2-203	ENSMUST00000105707.1	949	178aa	Protein coding	-	A2A7G7	TSL:3 GENCODE basic
Mad2l2-206	ENSMUST00000132698.7	831	173aa	Protein coding	-	A2A7G6	CDS 3' incomplete TSL:5
Mad2l2-207	ENSMUST00000140049.7	391	106aa	Protein coding	-	A2A7G5	CDS 3' incomplete TSL:3
Mad2l2-205	ENSMUST00000126261.1	339	No protein	Processed transcript	-	-	TSL:3
Mad2l2-208	ENSMUST00000148742.1	667	No protein	Retained intron	-	-	TSL:2
Mad2l2-204	ENSMUST00000105708.2	487	No protein	Retained intron	-	-	TSL:2

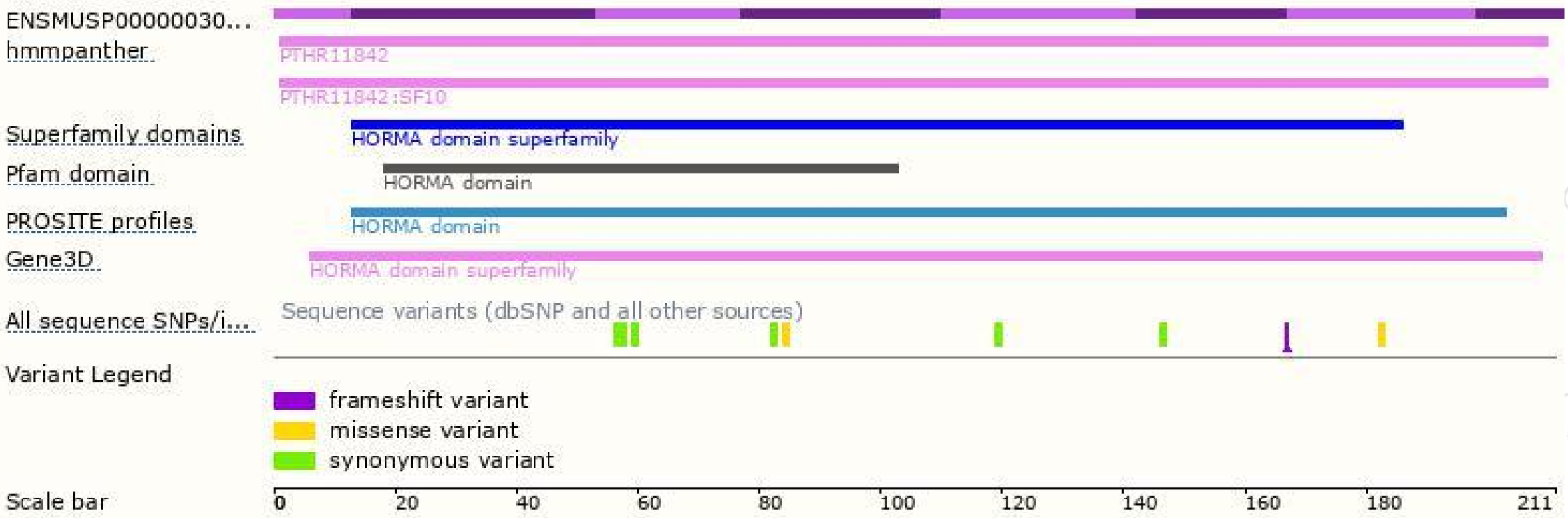
The strategy is based on the design of *Mad2l2-201* transcript,The transcription is shown below



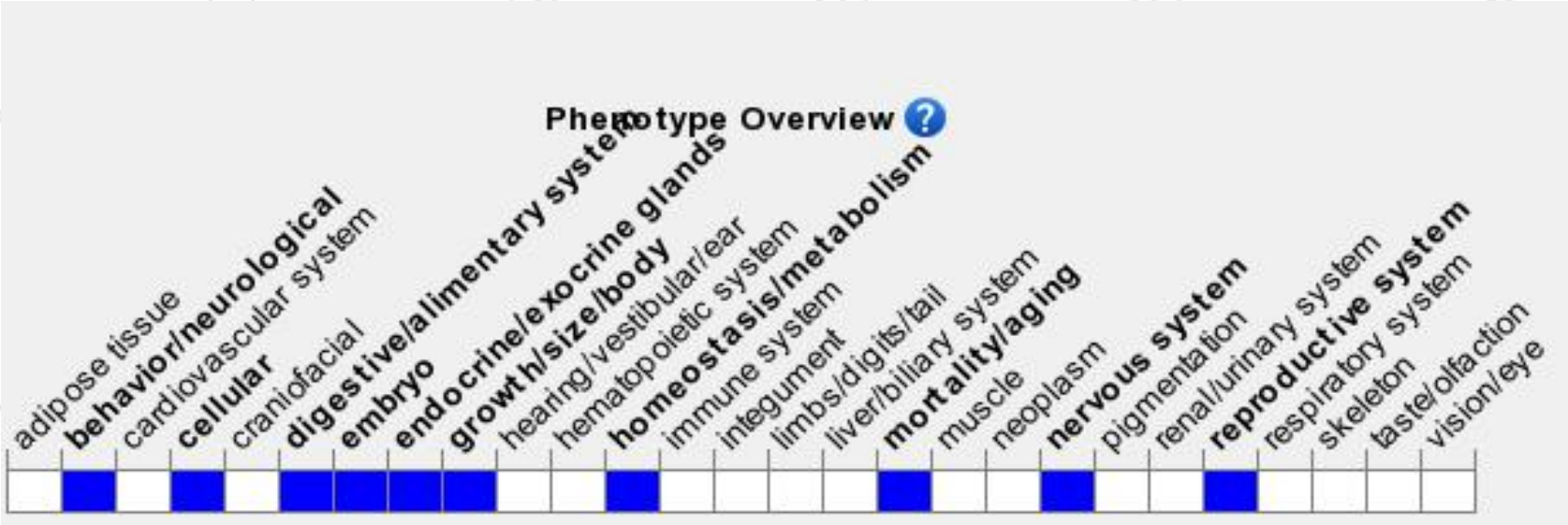
Genomic location distribution



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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