

# *Dpp10* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Dpp10***

**Project type**

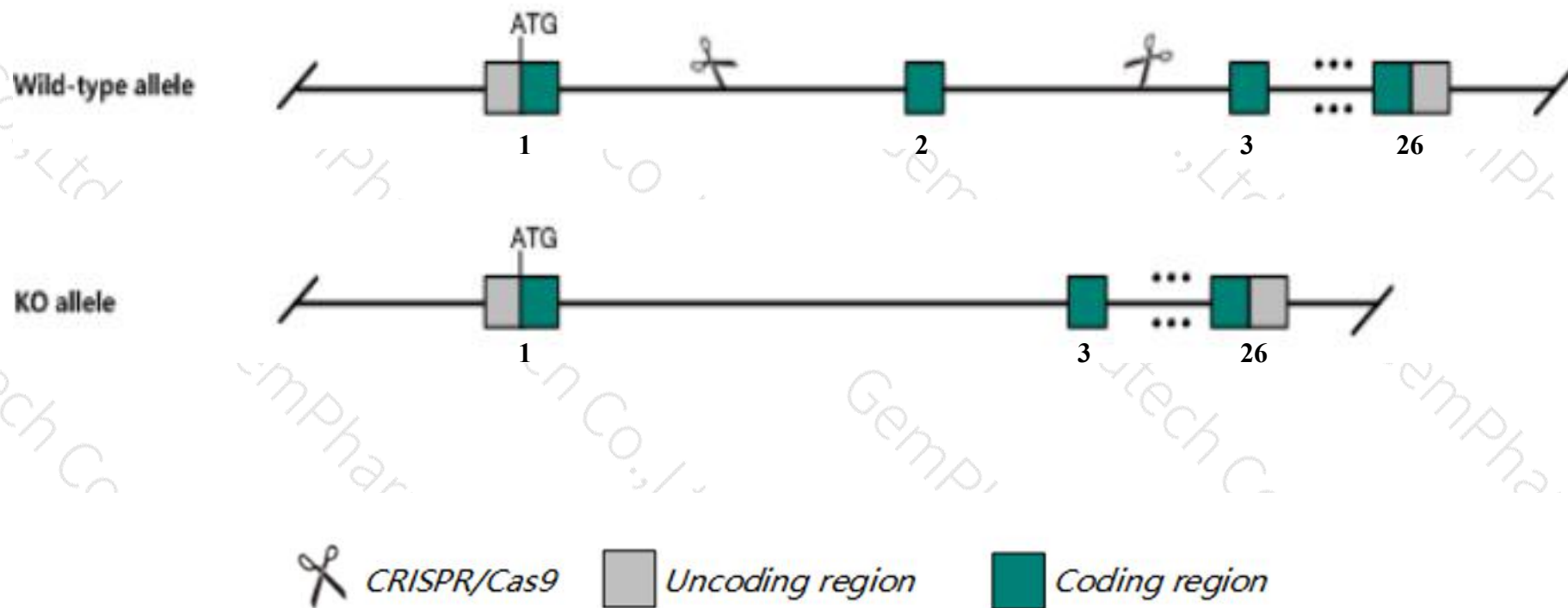
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dpp10* gene. The schematic diagram is as follows:



- The *Dpp10* gene has 6 transcripts. According to the structure of *Dpp10* gene, exon2 of *Dpp10-202* (ENSMUST00000112606.7) transcript is recommended as the knockout region. The region contains 115bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dpp10* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Dpp10* gene is located on the Chr1. 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)

## Dpp10 dipeptidylpeptidase 10 [Mus musculus (house mouse)]

Gene ID: 269109, updated on 13-Mar-2020

### Summary



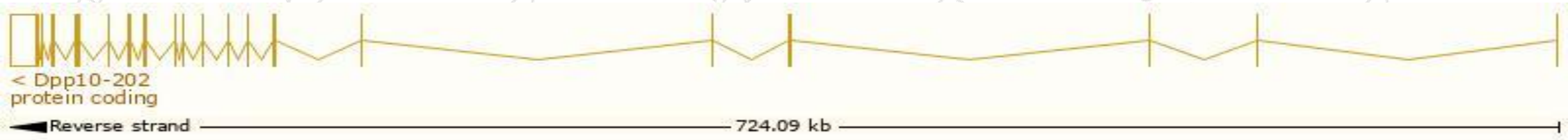
<b>Official Symbol</b>	Dpp10 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	dipeptidylpeptidase 10 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2442409</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000036815</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	6430601K09Rik, DPP X, Dprp3
<b>Expression</b>	Biased expression in frontal lobe adult (RPKM 14.7), cortex adult (RPKM 13.3) and 4 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

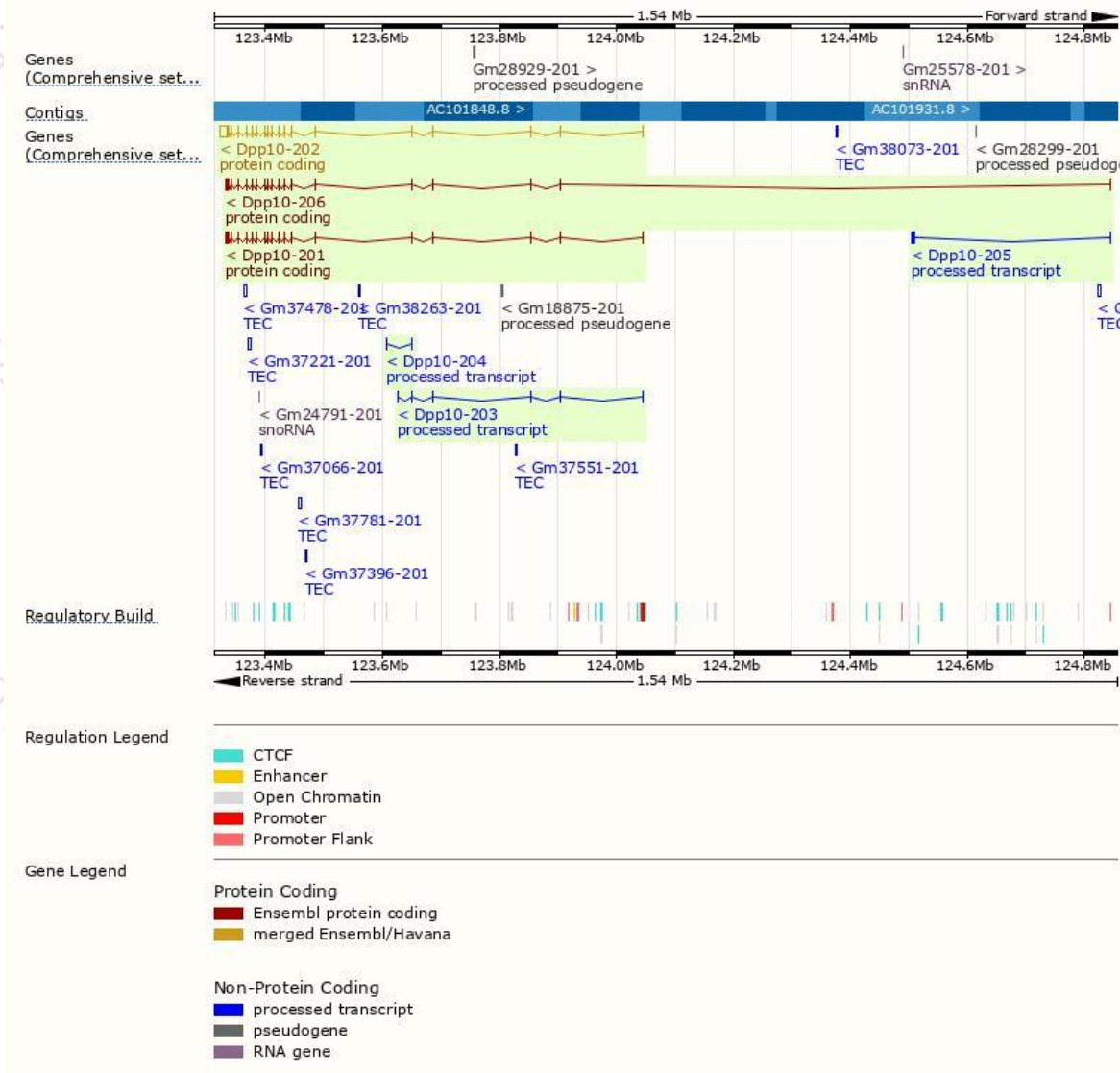
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dpp10-202	<a href="#">ENSMUST00000112606.7</a>	15297	<a href="#">800aa</a>	Protein coding	<a href="#">CCDS15241</a>	<a href="#">E9QN98</a>	TSL:1 GENCODE basic APPRIS P2
Dpp10-206	<a href="#">ENSMUST00000239072.1</a>	4759	<a href="#">796aa</a>	Protein coding	-	-	GENCODE basic APPRIS ALT 1
Dpp10-201	<a href="#">ENSMUST00000112603.3</a>	4477	<a href="#">789aa</a>	Protein coding	-	<a href="#">D3Z5I7</a>	TSL:5 GENCODE basic APPRIS ALT 2
Dpp10-205	<a href="#">ENSMUST00000187286.1</a>	1443	No protein	Processed transcript	-	-	TSL:1
Dpp10-203	<a href="#">ENSMUST00000140361.2</a>	656	No protein	Processed transcript	-	-	TSL:3
Dpp10-204	<a href="#">ENSMUST00000187202.1</a>	285	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Dpp10-202* transcript,the transcription is shown below:

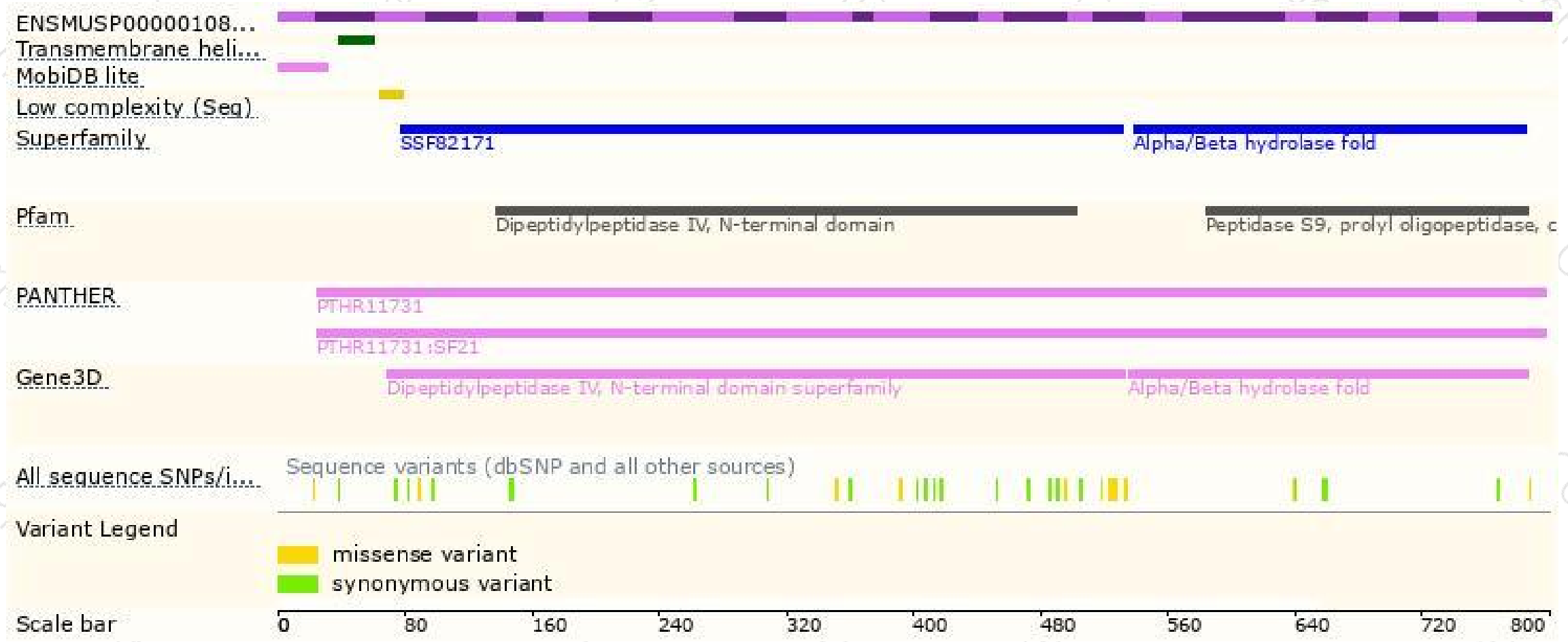


# Genomic location distribution

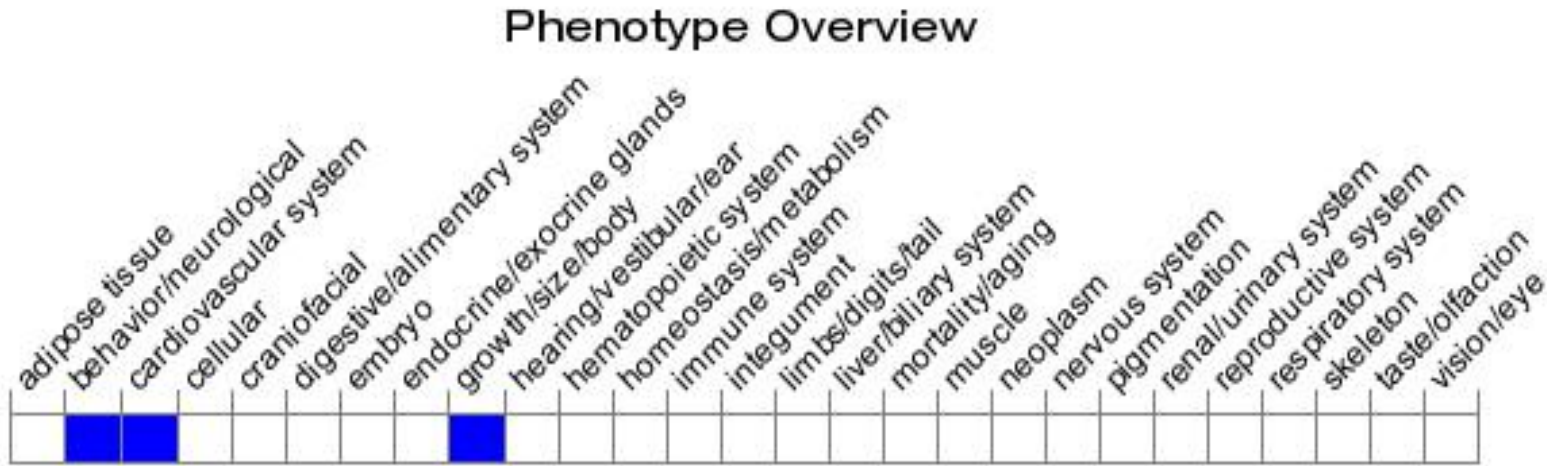




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

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

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