

# *Kmt2d* Cas9-KO Strategy

**Designer:** Huan Wang

**Design Date:** 2019-7-25

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**Project Name**

***Kmt2d***

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**Project type**

**Cas9-KO**

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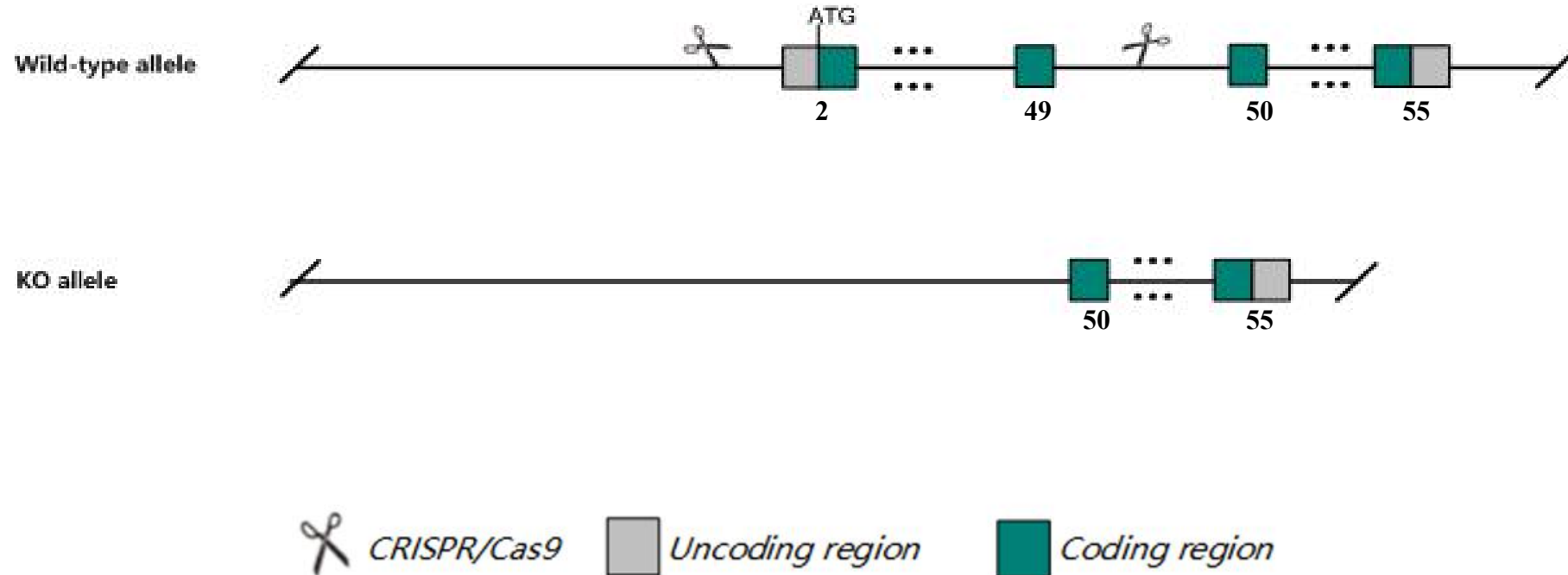
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kmt2d* gene. The schematic diagram is as follows:



The *Kmt2d* gene has 5 transcripts. According to the structure of *Kmt2d* gene, exon2-exon49 of *Kmt2d-201* (ENSMUST00000023741.15) 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 *Kmt2d* gene. The brief process is as follows: CRISPR/Cas9 system

According to the existing MGI data, Mice homozygous for a gene trap allele exhibit embryonic lethality around E9.5. Mice homozygous for a conditional allele activated in different cell-types exhibit impaired adipogenesis, impaired myogenesis, perturbed germinal B cell development and promotion of lymphomagenesis.

The *Kmt2d* gene is located on the Chr15. 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.

## Kmt2d lysine (K)-specific methyltransferase 2D [Mus musculus (house mouse)]

Gene ID: 381022, updated on 2-Apr-2019

### Summary



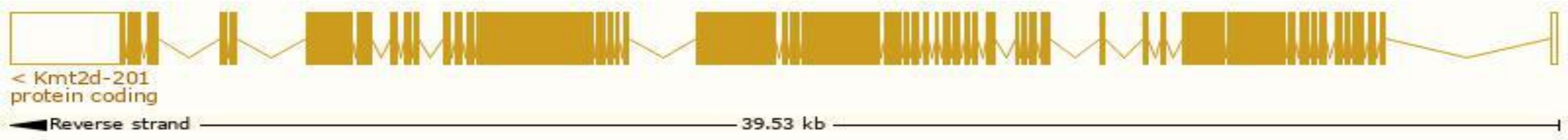
<b>Official Symbol</b>	Kmt2d provided by <a href="#">MGI</a>
<b>Official Full Name</b>	lysine (K)-specific methyltransferase 2D provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2682319</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000048154</a>
<b>Gene type</b>	protein 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>	ALR, BC032281, BC058659, C430014K11Rik, KMT2B, MII2, MII4
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 25.1), spleen adult (RPKM 21.8) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information      Ensembl

The gene has 5 transcripts,all transcripts are shown below:

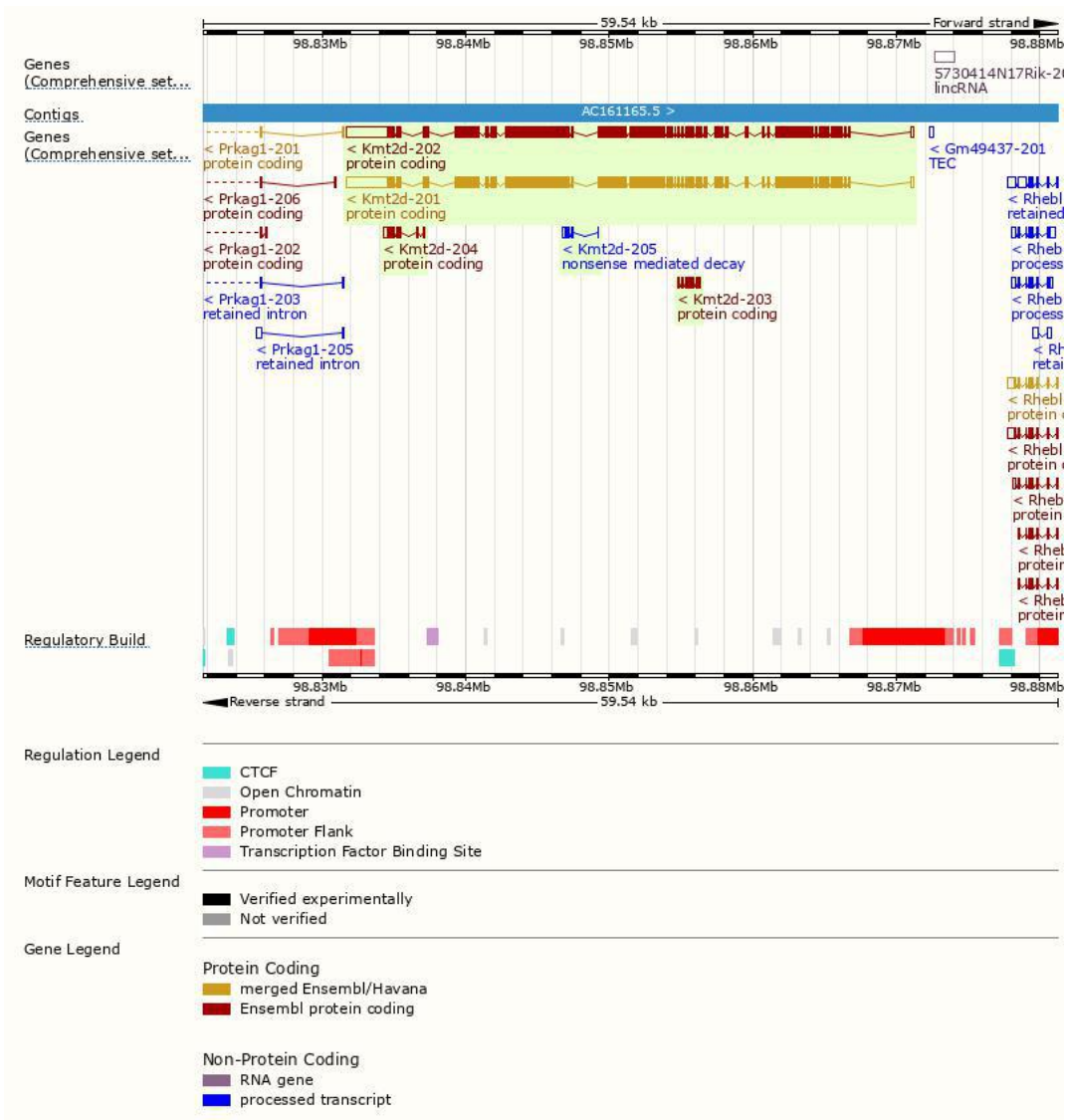
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kmt2d-201	<a href="#">ENSMUST00000023741.15</a>	19823	<a href="#">5588aa</a>	Protein coding	<a href="#">CCDS49725</a>	<a href="#">A0A0A0MQ73</a>	TSL:5 GENCODE basic APPRIS P2
Kmt2d-202	<a href="#">ENSMUST00000178486.8</a>	19805	<a href="#">5588aa</a>	Protein coding	-	<a href="#">Q6PDK2</a>	TSL:5 GENCODE basic APPRIS ALT2
Kmt2d-204	<a href="#">ENSMUST00000191973.2</a>	899	<a href="#">233aa</a>	Protein coding	-	<a href="#">A0A0A6YY77</a>	CDS 5' incomplete TSL:3
Kmt2d-203	<a href="#">ENSMUST00000184363.2</a>	751	<a href="#">250aa</a>	Protein coding	-	<a href="#">V9GX77</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Kmt2d-205	<a href="#">ENSMUST00000229651.1</a>	470	<a href="#">22aa</a>	Nonsense mediated decay	-	<a href="#">A0A2R8VHD4</a>	CDS 5' incomplete

The strategy is based on the design of *Kmt2d-201* transcript,The transcription is shown below





# Genomic location distribution

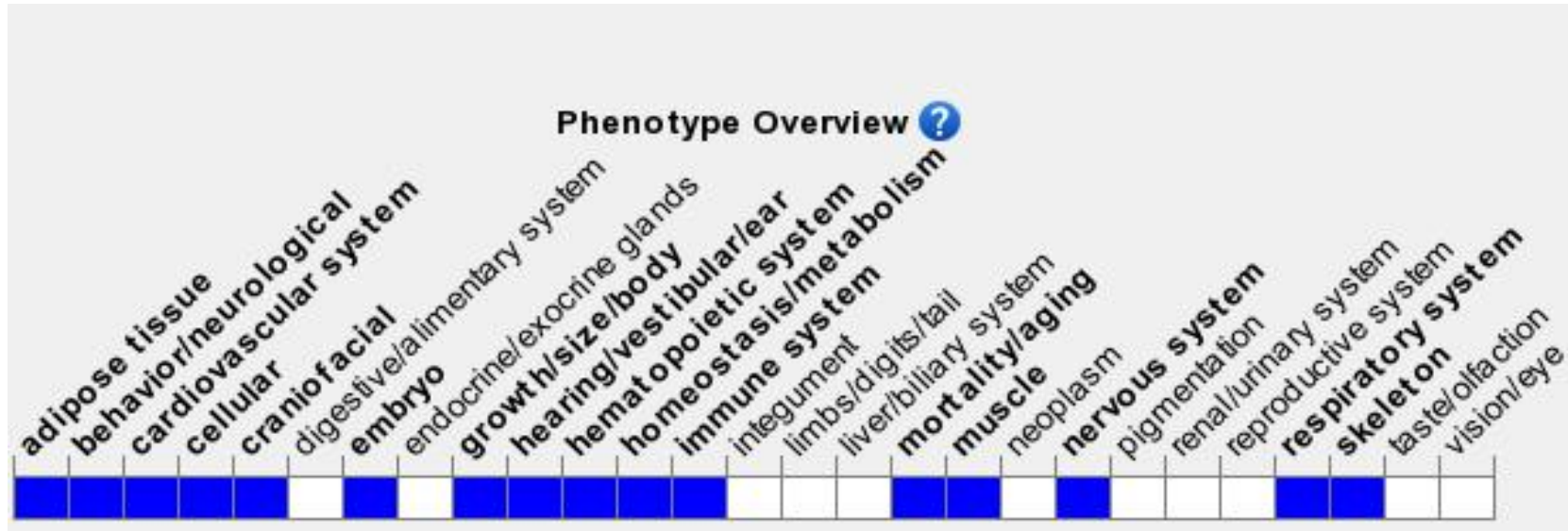




# Protein domain



# 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 a gene trap allele exhibit embryonic lethality around E9.5. Mice homozygous for a conditional allele activated in different cell-types exhibit impaired adipogenesis, impaired myogenesis, perturbed germinal B cell development and promotion of lymphomagenesis.

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