

# Lrrk2 Cas9-KO Strategy

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# **Project Overview**



**Project Name** 

Lrrk2

**Project type** 

Cas9-KO

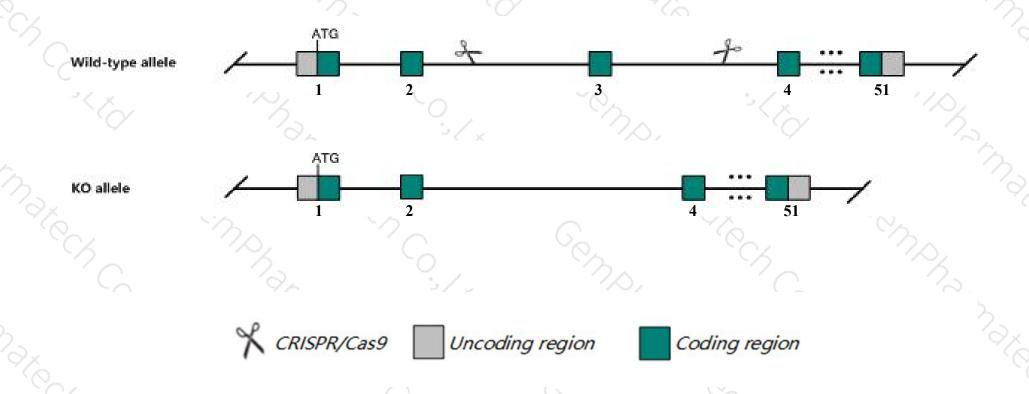
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Lrrk2* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Lrrk2* gene has 6 transcripts. According to the structure of *Lrrk2* gene, exon3 of *Lrrk2-201*(ENSMUST00000060642.6) transcript is recommended as the knockout region. The region contains 110bp coding sequence.

  Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Lrrk2 gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for a knock-in allele exhibit impaired response to dopamine, amphetamine, and quinpirole. Mice homozygous for one knock-out allele exhibit increased neurite growth. Mice homozygous for different knock-out alleles exhibit alopecia due to excessive grooming or kdiney atrophy.
- > The *Lrrk2* 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.

## Gene information (NCBI)



#### Lrrk2 leucine-rich repeat kinase 2 [Mus musculus (house mouse)]

Gene ID: 66725, updated on 9-Apr-2019

#### Summary

☆ ?

Official Symbol Lrrk2 provided by MGI

Official Full Name leucine-rich repeat kinase 2 provided by MGI

Primary source MGI:MGI:1913975

See related Ensembl: ENSMUSG00000036273

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 4921513O20Rik, 9330188B09Rik, AW561911, D630001M17Rik, Gm927, cl-46

Expression Broad expression in kidney adult (RPKM 2.7), lung adult (RPKM 2.3) and 24 other tissuesSee more

Orthologs <u>human all</u>

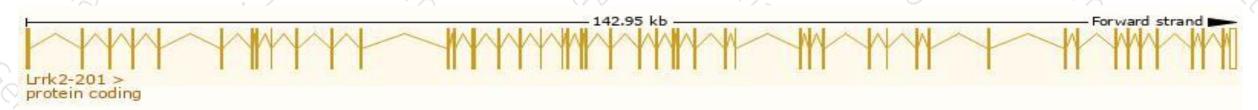
# Transcript information (Ensembl)



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

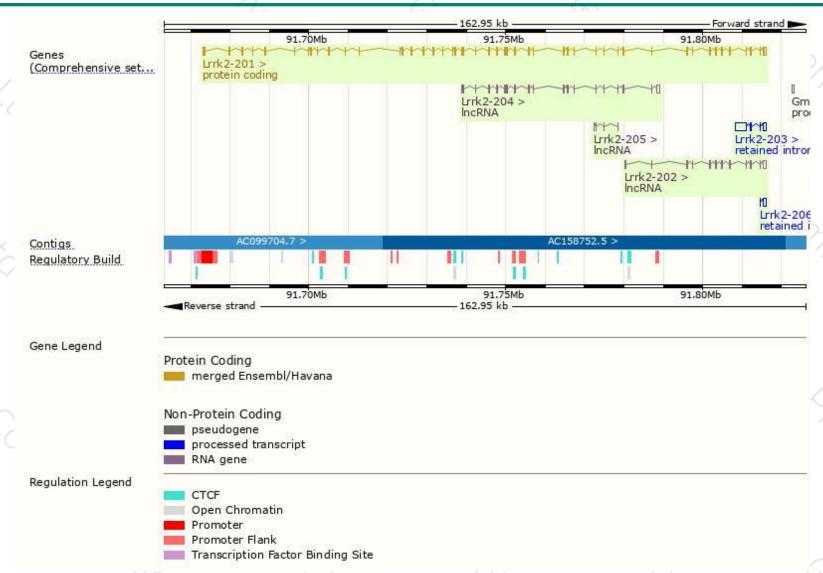
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrrk2-201	ENSMUST00000060642.6	8275	<u>2527aa</u>	Protein coding	CCDS37180	Q5S006	TSL:1 GENCODE basic APPRIS P1
Lrrk2-203	ENSMUST00000137657.1	3801	No protein	Retained intron		(8)	TSL:1
Lrrk2-206	ENSMUST00000172797.1	812	No protein	Retained intron	20	(2)	TSL:1
Lrrk2-204	ENSMUST00000140734.7	3452	No protein	IncRNA	29	120	TSL:1
Lrrk2-202	ENSMUST00000133743.7	2203	No protein	IncRNA	56	-	TSL:1
Lrrk2-205	ENSMUST00000156900.1	438	No protein	IncRNA	-8		TSL:3

The strategy is based on the design of *Lrrk2-201* transcript, The transcription is shown below



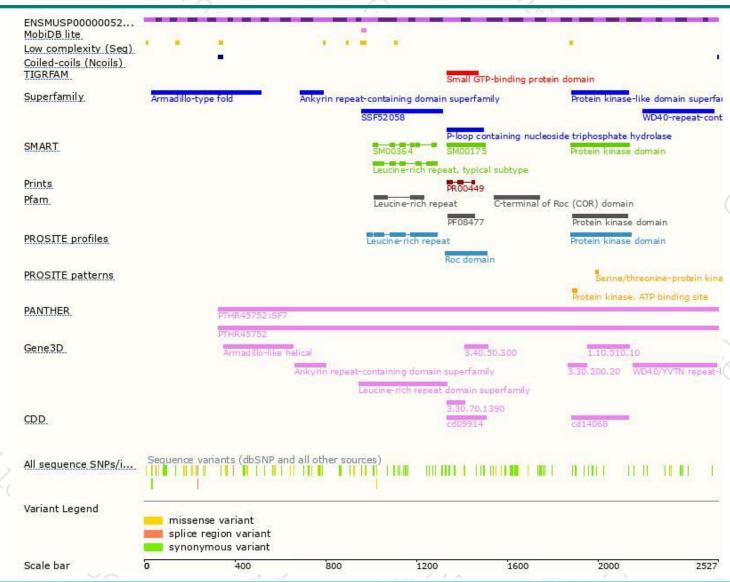
### Genomic location distribution





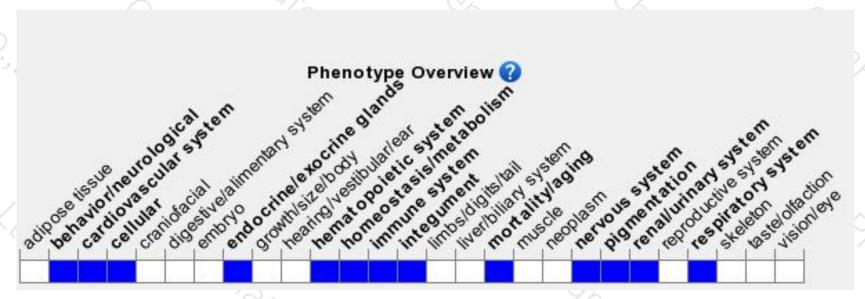
### Protein domain





## 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 knock-in allele exhibit impaired response to dopamine, amphetamine, and quinpirole. Mice homozygous for one knock-out allele exhibit increased neurite growth. Mice homozygous different knock-out alleles exhibit alopecia due to excessive grooming or kdiney atrophy.



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





