

# ***Park7* Cas9-CKO Strategy**

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Design Date: 2019-8-9

# Project Overview

**Project Name**

*Park7*

**Project type**

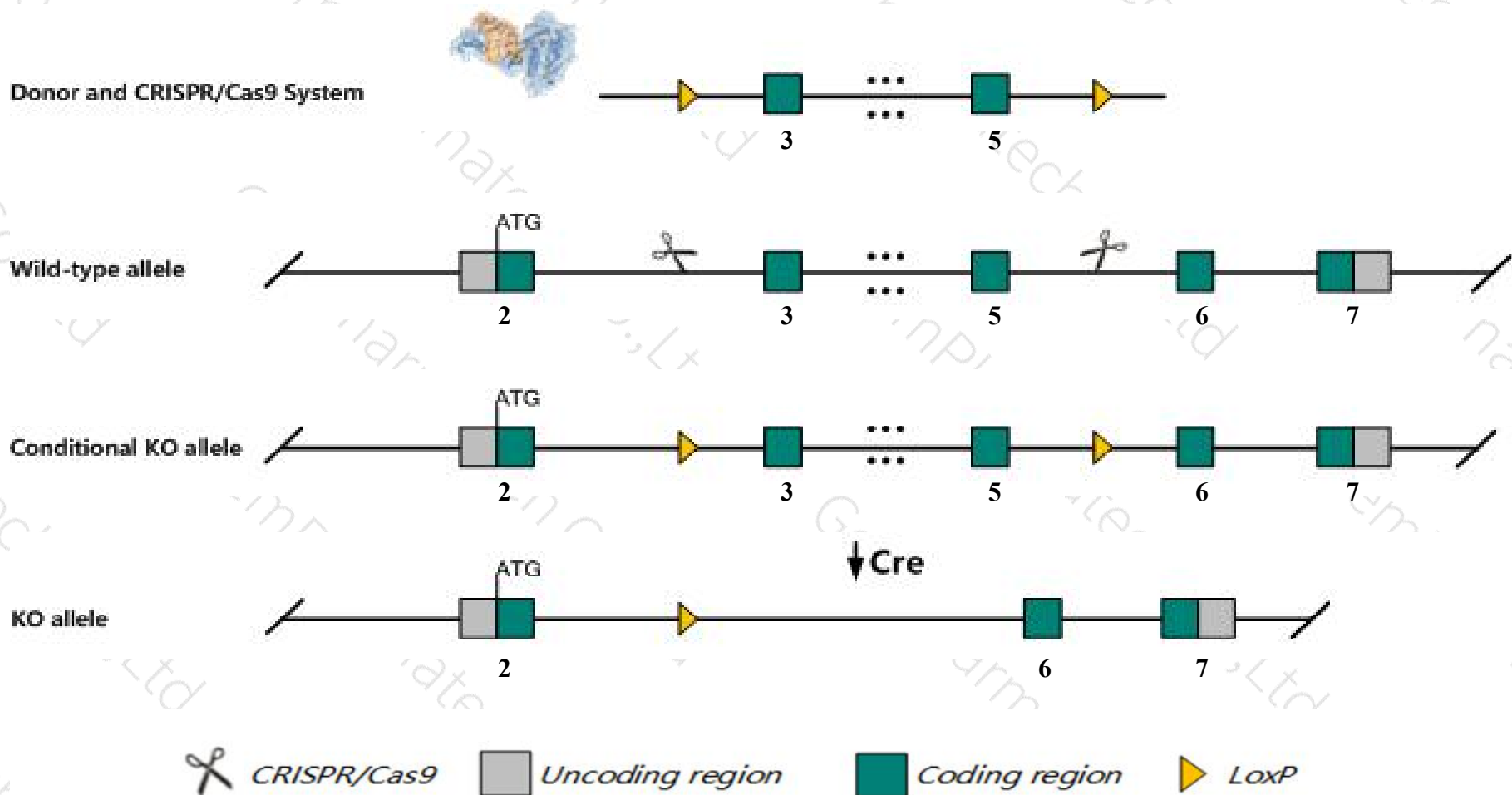
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Park7* gene. The schematic diagram is as follows:



- The *Park7* gene has 10 transcripts. According to the structure of *Park7* gene, exon3-exon5 of *Park7-201* (ENSMUST00000030805.13) transcript is recommended as the knockout region. The region contains 232bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Park7* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous null mice exhibit reduced evoked dopamine overflow in the striatum, resulting primarily from increased dopamine uptake. Mice show hyopactivity, absent long-term depression in medium spiny neurons and decreased sensitivity of nigral neurons to dopamine.
- Transcript *Park7-207* may not be affected .
- The floxed region is near to the N-terminal of *Tnfrsf9* gene, this strategy may influence the regulatory function of the N-terminal of *Tnfrsf9* gene.
- The *Park7* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Park7 Parkinson disease (autosomal recessive, early onset) 7 [Mus musculus (house mouse)]

Gene ID: 57320, updated on 9-Apr-2019

### Summary



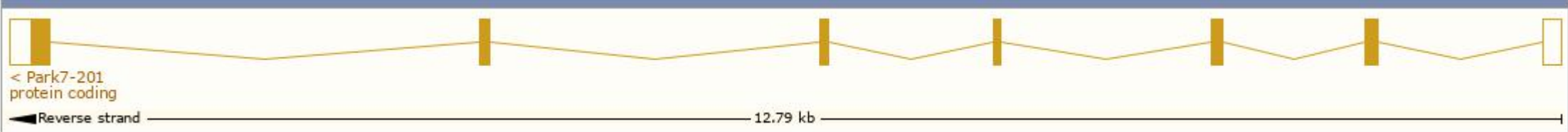
<b>Official Symbol</b>	Park7 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Parkinson disease (autosomal recessive, early onset) 7 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2135637</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000028964</a>
<b>Gene type</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>	DJ-1, Dj1
<b>Expression</b>	Ubiquitous expression in kidney adult (RPKM 117.4), CNS E11.5 (RPKM 109.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

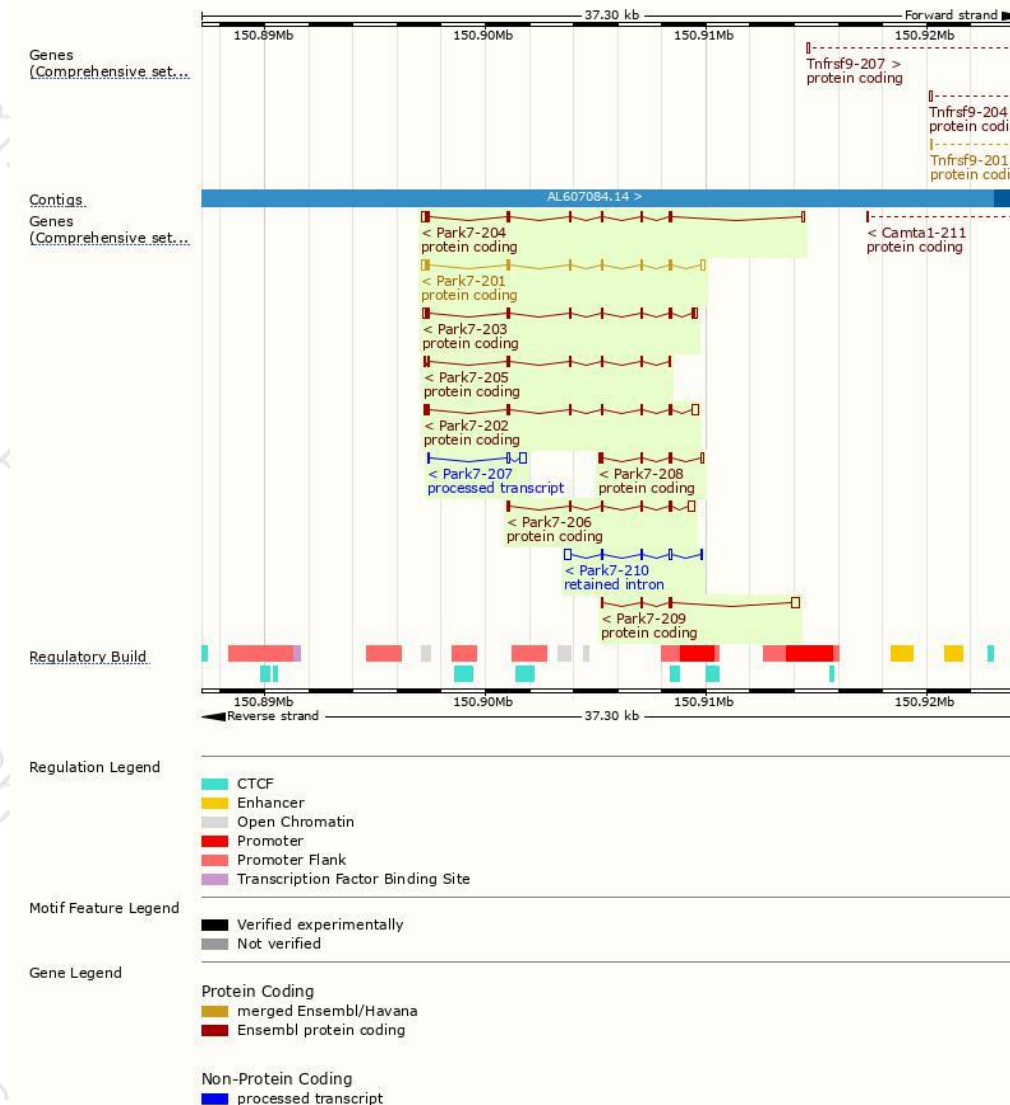
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Park7-203	<a href="#">ENSMUST00000105674.7</a>	937	<a href="#">189aa</a>	Protein coding	<a href="#">CCDS18975</a>	<a href="#">Q99LX0</a>	TSL:5 GENCODE basic APPRIS P1
Park7-202	<a href="#">ENSMUST00000105673.7</a>	919	<a href="#">189aa</a>	Protein coding	<a href="#">CCDS18975</a>	<a href="#">Q99LX0</a>	TSL:5 GENCODE basic APPRIS P1
Park7-201	<a href="#">ENSMUST00000030805.13</a>	908	<a href="#">189aa</a>	Protein coding	<a href="#">CCDS18975</a>	<a href="#">Q99LX0</a>	TSL:1 GENCODE basic APPRIS P1
Park7-204	<a href="#">ENSMUST00000105675.7</a>	882	<a href="#">189aa</a>	Protein coding	<a href="#">CCDS18975</a>	<a href="#">Q99LX0</a>	TSL:5 GENCODE basic APPRIS P1
Park7-206	<a href="#">ENSMUST00000128075.7</a>	715	<a href="#">135aa</a>	Protein coding	-	<a href="#">A2A815</a>	CDS 3' incomplete TSL:5
Park7-209	<a href="#">ENSMUST00000146184.2</a>	584	<a href="#">84aa</a>	Protein coding	-	<a href="#">A2A817</a>	CDS 3' incomplete TSL:5
Park7-205	<a href="#">ENSMUST00000105676.7</a>	582	<a href="#">175aa</a>	Protein coding	-	<a href="#">A2A813</a>	TSL:5 GENCODE basic
Park7-208	<a href="#">ENSMUST00000134751.7</a>	478	<a href="#">125aa</a>	Protein coding	-	<a href="#">A2A816</a>	CDS 3' incomplete TSL:2
Park7-207	<a href="#">ENSMUST00000132265.1</a>	472	No protein	Processed transcript	-	-	TSL:3
Park7-210	<a href="#">ENSMUST00000148626.1</a>	640	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Park7-201* transcript,The transcription is shown below

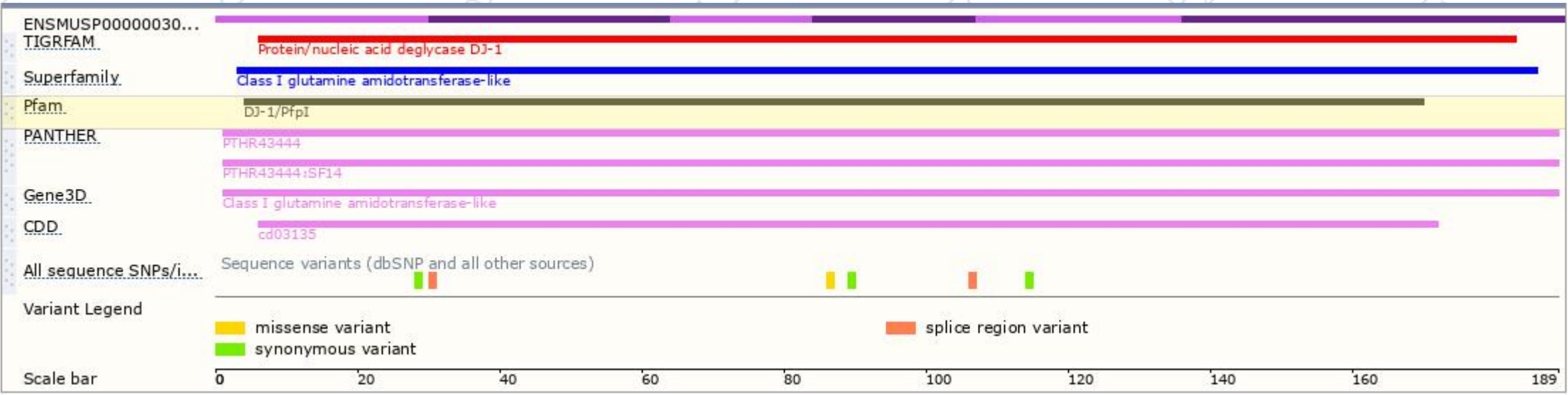


# Genomic location distribution

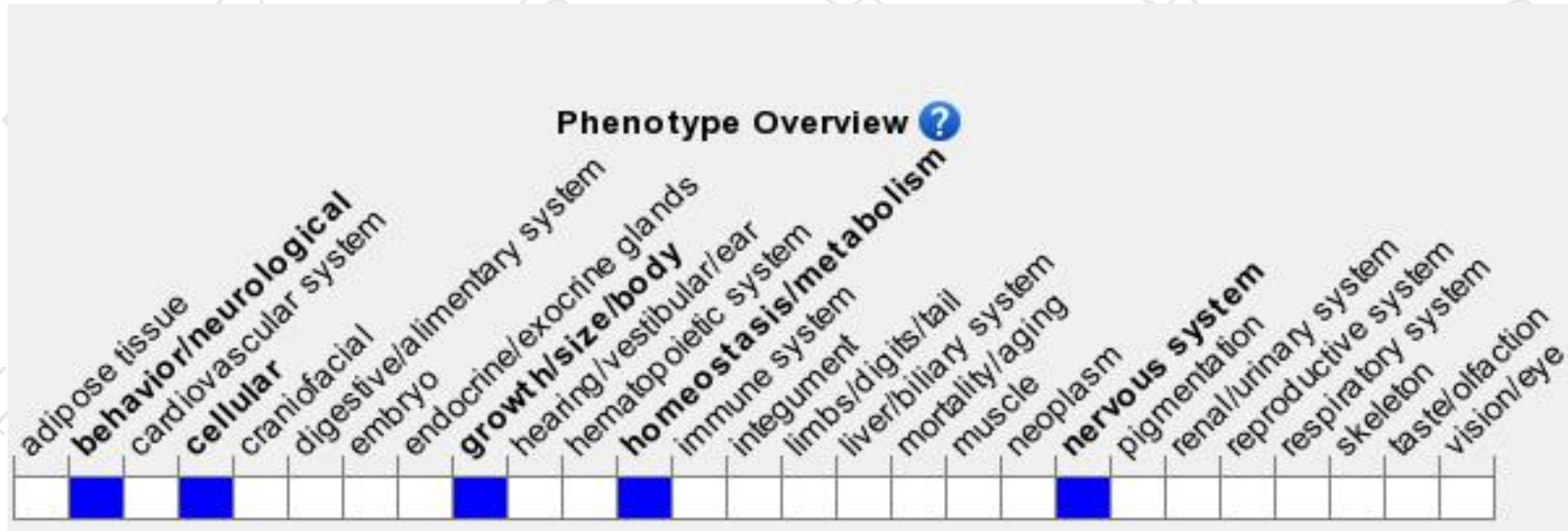




# Protein domain



# 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, Homozygous null mice exhibit reduced evoked dopamine overflow in the striatum, resulting primarily from increased dopamine uptake. Mice show hyopactivity, absent long-term depression in medium spiny neurons and decreased sensitivity of nigral neurons to dopamine.

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

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