

Oprm1 Cas9-CKO Strategy

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Reviewer:

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Date:

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Project Overview

Project Name

Oprm1

Project type

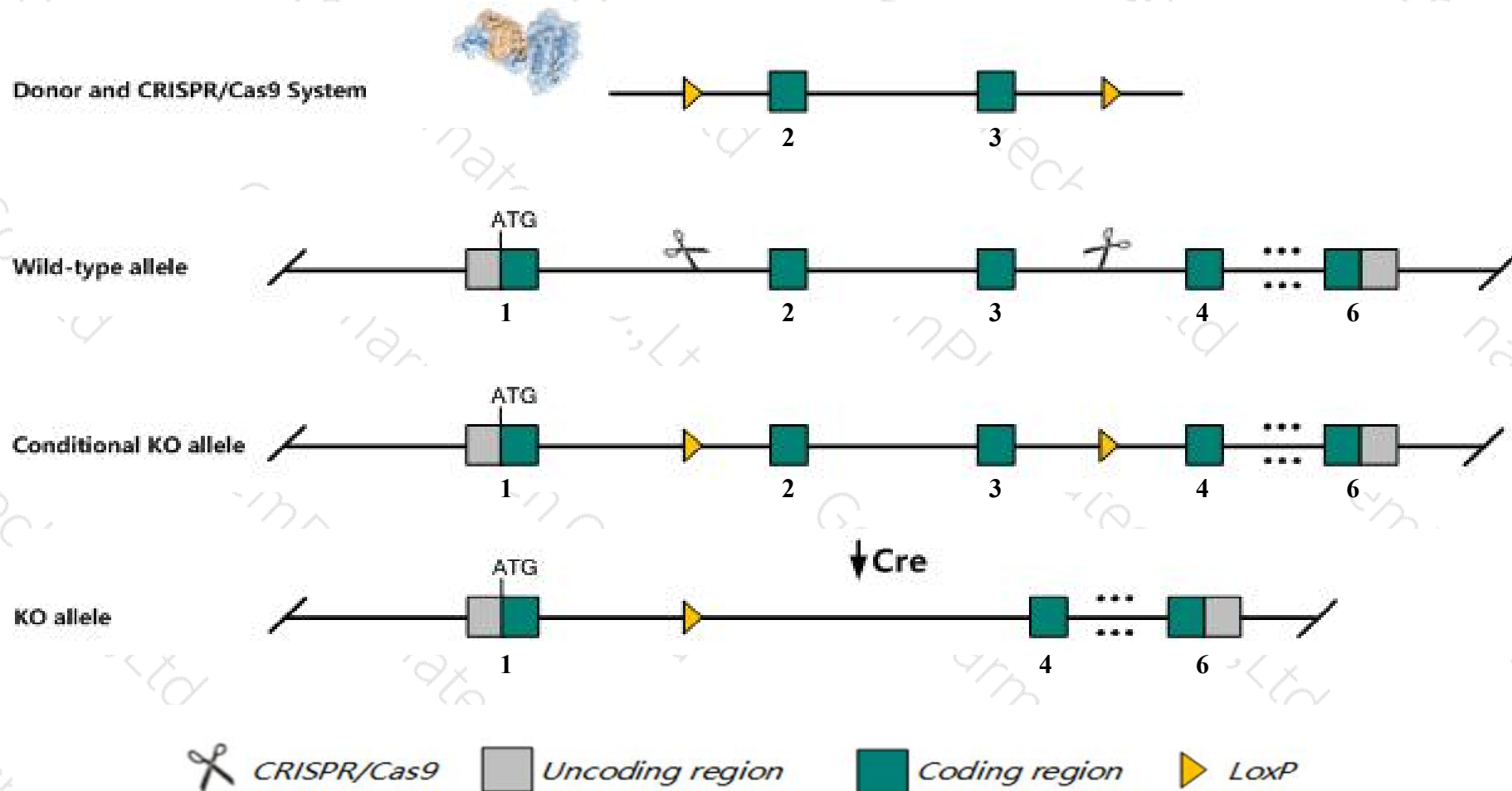
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Oprm1* gene. The schematic diagram is as follows:



- The *Oprm1* gene has 31 transcripts. According to the structure of *Oprm1* gene, exon2-exon3 of *Oprm1-216* (ENSMUST00000105611.7) transcript is recommended as the knockout region. The region contains 874bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Oprm1* gene. The brief process is as follows: CRISPR/Cas9 system 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, Homozygotes for null mutations exhibit isoform dependent loss of behavioral and gastrointestinal opioid responses and may also show impaired spatial memory, heightened nociception, reduced locomotor activity, increased hematopoietic proliferation, and decreased male fertility.
- The *Oprm1* gene is located on the Chr10. 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)

Oprm1 opioid receptor, mu 1 [Mus musculus (house mouse)]

Gene ID: 18390, updated on 19-Mar-2019

Summary



Official Symbol	Oprm1 provided by MGI
Official Full Name	opioid receptor, mu 1 provided by MGI
Primary source	MGI:MGI:97441
See related	Ensembl:ENSMUSG00000000766
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	M-OR-1, MOP-R, MOR-1, MOR-1O, Oprm, mor, muOR
Summary	This gene encodes the mu opioid receptor which is where drugs such as morphine and other opioids have pharmacological effects. Several alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Nov 2014]
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information (Ensembl)

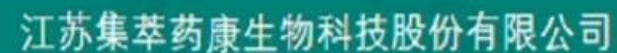
The gene has 31 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Oprm1-216	ENSMUST00000105611.7	2420	428aa	Protein coding	CCDS56687	P42866	TSL1 GENCODE basic
Oprm1-215	ENSMUST00000105607.7	2969	392aa	Protein coding	CCDS78787	P42866	TSL1 GENCODE basic APPRIS P2
Oprm1-230	ENSMUST00000154906.7	2039	409aa	Protein coding	CCDS83672	P42866	TSL1 GENCODE basic
Oprm1-208	ENSMUST00000092734.10	1569	395aa	Protein coding	CCDS78787	P42866	TSL1 GENCODE basic APPRIS P2
Oprm1-214	ENSMUST00000105605.7	1503	391aa	Protein coding	CCDS83673	P42866	TSL1 GENCODE basic
Oprm1-203	ENSMUST00000056385.13	1440	398aa	Protein coding	CCDS78787	P42866	TSL1 GENCODE basic APPRIS P2
Oprm1-204	ENSMUST00000063086.13	1427	325aa	Protein coding	CCDS78785	P42866	TSL1 GENCODE basic
Oprm1-211	ENSMUST00000105602.7	1366	390aa	Protein coding	CCDS83674	P42866	TSL1 GENCODE basic
Oprm1-202	ENSMUST00000052761.13	1334	393aa	Protein coding	CCDS78788	P42866	TSL1 GENCODE basic
Oprm1-217	ENSMUST00000105615.8	1258	370aa	Protein coding	CCDS78784	P42866	TSL1 GENCODE basic
Oprm1-212	ENSMUST00000105603.1	2053	389aa	Protein coding	-	E9Q7D4	TSL5 GENCODE basic
Oprm1-205	ENSMUST00000078634.11	1695	456aa	Protein coding	-	AA09R4J0Z3	TSL1 GENCODE basic
Oprm1-213	ENSMUST00000105604.7	1616	393aa	Protein coding	-	E9Q7D3	TSL5 GENCODE basic APPRIS ALT1
Oprm1-201	ENSMUST00000000783.12	1500	425aa	Protein coding	-	P42866	TSL1 GENCODE basic
Oprm1-222	ENSMUST00000135502.7	1363	416aa	Protein coding	-	P42866	TSL1 GENCODE basic
Oprm1-207	ENSMUST00000092731.10	1332	392aa	Protein coding	-	P42866	TSL1 GENCODE basic
Oprm1-229	ENSMUST00000152674.1	1179	104aa	Protein coding	-	E9Q270	TSL3 GENCODE basic
Oprm1-219	ENSMUST00000128217.7	2205	356aa	Nonsense mediated decay	-	E8FVCI	TSL1
Oprm1-225	ENSMUST00000144264.7	2120	399aa	Nonsense mediated decay	-	P42866	TSL1
Oprm1-220	ENSMUST00000120954.7	1706	448aa	Nonsense mediated decay	-	E9QAG1	TSL1
Oprm1-226	ENSMUST00000147171.7	1570	330aa	Nonsense mediated decay	-	P42866	TSL5
Oprm1-231	ENSMUST00000154941.7	1540	337aa	Nonsense mediated decay	-	E9Q2X5	TSL1
Oprm1-206	ENSMUST00000092729.10	1422	388aa	Nonsense mediated decay	-	P42866	TSL1
Oprm1-228	ENSMUST00000150374.7	1174	411aa	Nonsense mediated decay	-	Q4U2P1	TSL1
Oprm1-210	ENSMUST00000105601.8	1161	222aa	Nonsense mediated decay	-	A1KZ74	TSL1
Oprm1-209	ENSMUST00000105597.7	1133	39aa	Nonsense mediated decay	-	Q4U2P0	TSL1
Oprm1-218	ENSMUST00000123861.7	1020	222aa	Nonsense mediated decay	-	A1KZ74	TSL1
Oprm1-224	ENSMUST00000143875.1	696	84aa	Nonsense mediated decay	-	Q4U2P9	TSL5
Oprm1-223	ENSMUST00000141897.1	1939	No protein	Processed transcript	-	-	TSL5
Oprm1-221	ENSMUST00000133486.1	256	No protein	Processed transcript	-	-	TSL1
Oprm1-227	ENSMUST00000148625.1	242	No protein	Processed transcript	-	-	TSL1

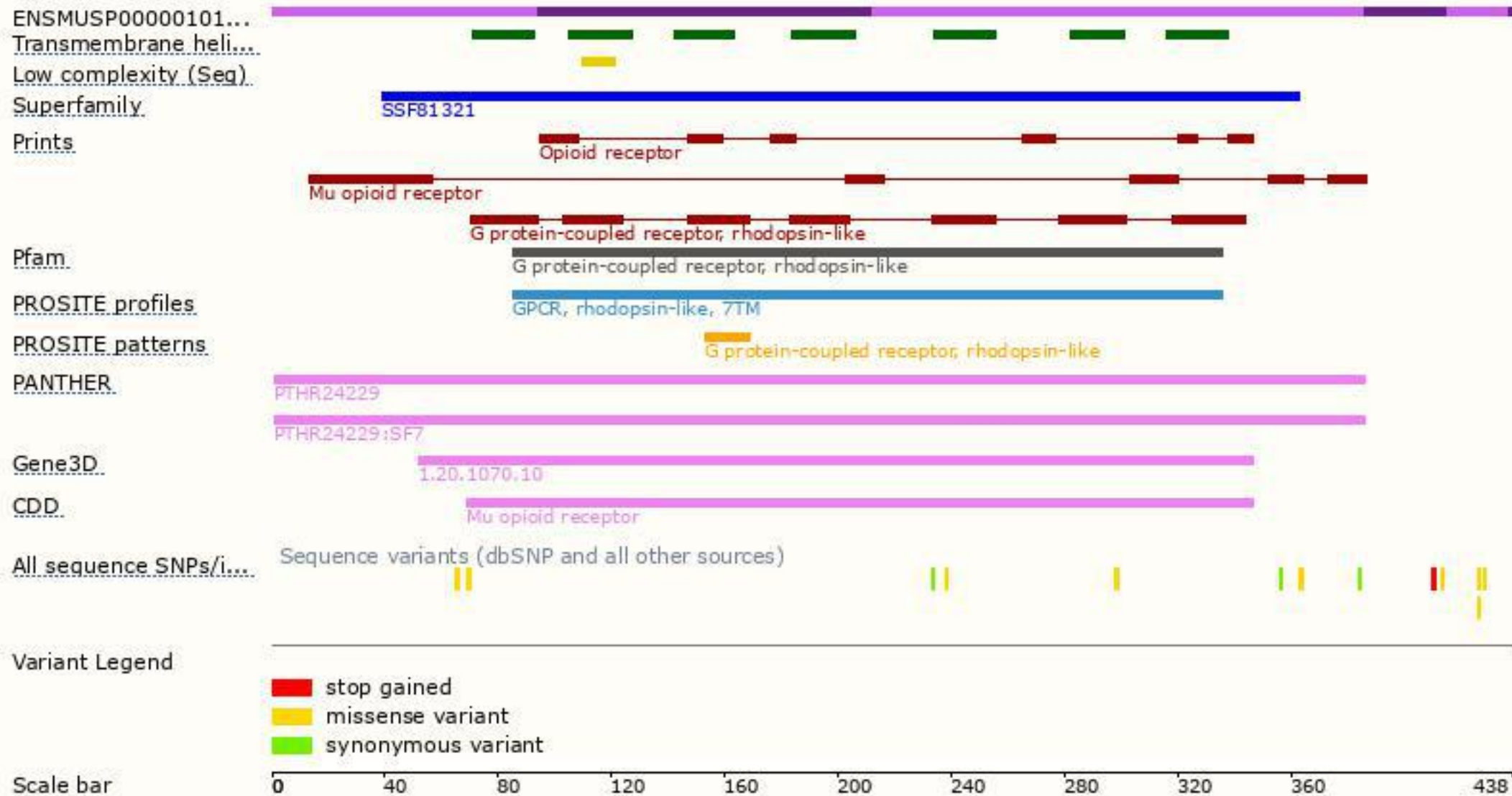
The strategy is based on the design of *Oprm1-216* transcript,The transcription is shown below



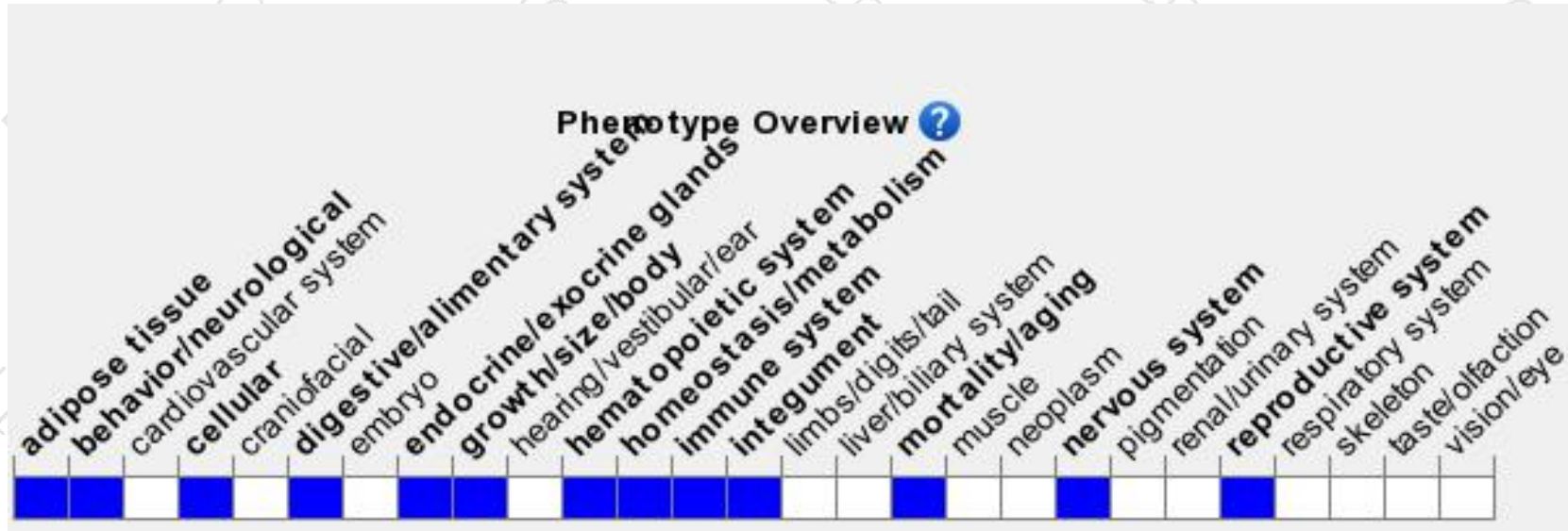
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GemPharmatech



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, Homozygotes for null mutations exhibit isoform dependent loss of behavioral and gastrointestinal opioid responses and may also show impaired spatial memory, heightened nociception, reduced locomotor activity, increased hematopoietic proliferation, and decreased male fertility.

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

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