

# Vipr1 Cas9-CKO Strategy

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**Reviewer:** Yang Zeng

**Design Date: 2018-7-6** 

# **Project Overview**



**Project Name** 

Vipr1

**Project type** 

Cas9-CKO

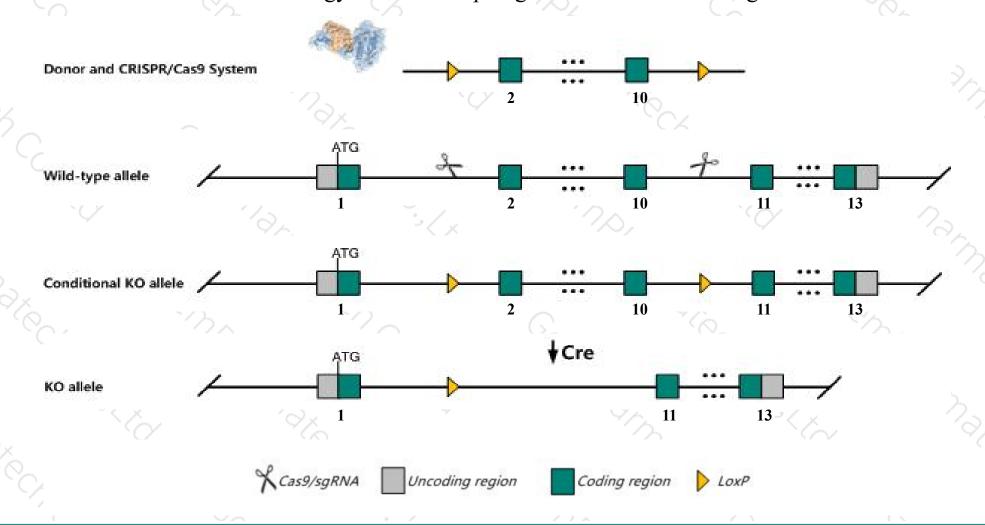
Strain background

C57BL/6JGpt

# Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Vipr1* gene. The schematic diagram is as follows:



### Technical routes



- ➤ The *Vipr1* gene has 5 transcripts. According to the structure of *Vipr1* gene, exon2-exon10 of *Vipr1-201*(ENSMUST00000035115.4) transcript is recommended as the knockout region. The region contains 938bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Vipr1* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was 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.

### **Notice**



- > According to the existing MGI data, Mice homozygous for a knock-out allele exhibit prenatal lethality associated with severe neonatal growth failure, enlarged cecum, intestinal hemorrhage, and enterocyte hyperproliferation in addition to disorganized islets and impaired glucose homeostasisin surviving mice.
- Transcript *Vipr1-204* may not be affected.
- The *Vipr1* gene is located on the Chr9. 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)



#### Vipr1 vasoactive intestinal peptide receptor 1 [Mus musculus (house mouse)]

Gene ID: 22354, updated on 19-Mar-2019

#### Summary

☆ ?

Official Symbol Vipr1 provided by MGI

Official Full Name vasoactive intestinal peptide receptor 1 provided by MGI

Primary source MGI:MGI:109272

See related Ensembl:ENSMUSG00000032528

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 AV071699, VIP-R1, VPAC1

Expression Biased expression in colon adult (RPKM 47.0), small intestine adult (RPKM 34.2) and 8 other tissuesSee more

Orthologs <u>human</u> all

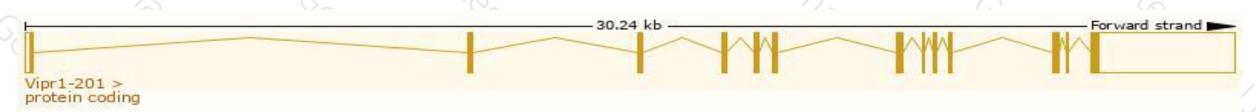
# Transcript information (Ensembl)



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

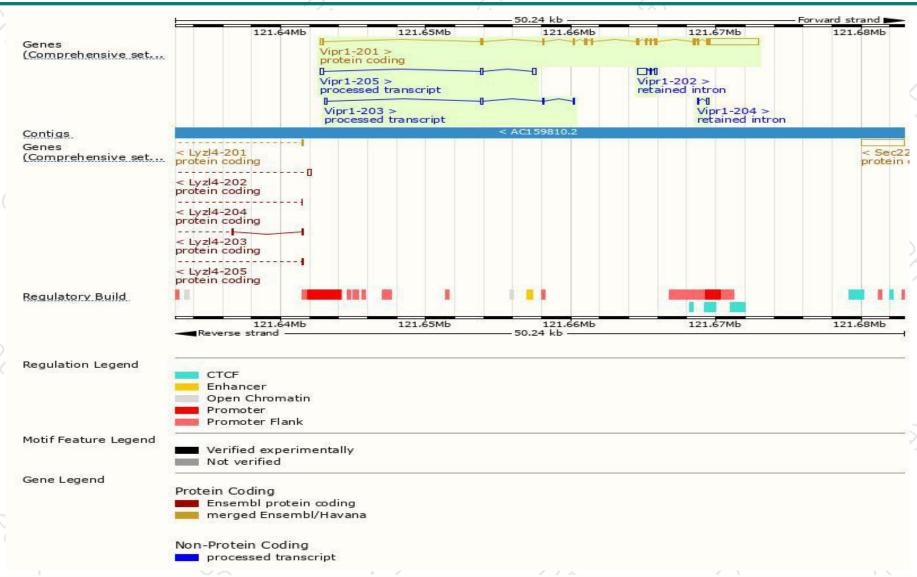
Show/hide columns Filter								
Name A	Transcript ID	bp 🌲	Protein	Translation ID 🔷	Biotype	CCDS	UniProt	Flags 🝦
Vipr1-201	ENSMUST00000035115.4	4902	459aa	ENSMUSP00000035115.4	Protein coding	CCDS23633 ₽	<u>P97751</u> ₽	TSL:1 GENCODE basic APPRIS P1
Vipr1-202	ENSMUST00000129394.1	763	No protein	-	Retained intron	-	9 <del>8</del> 8	TSL:3
Vipr1-203	ENSMUST00000139189.1	412	No protein	-	IncRNA	(=)	(8)	TSL:5
Vipr1-204	ENSMUST00000149959.1	224	No protein	5.	Retained intron	: <del>-</del>	650	TSL:5
Vipr1-205	ENSMUST00000213272.1	508	No protein	5	IncRNA	(450)	0.59	TSL:5

The strategy is based on the design of Vipr1-201 transcript, The transcription is shown below



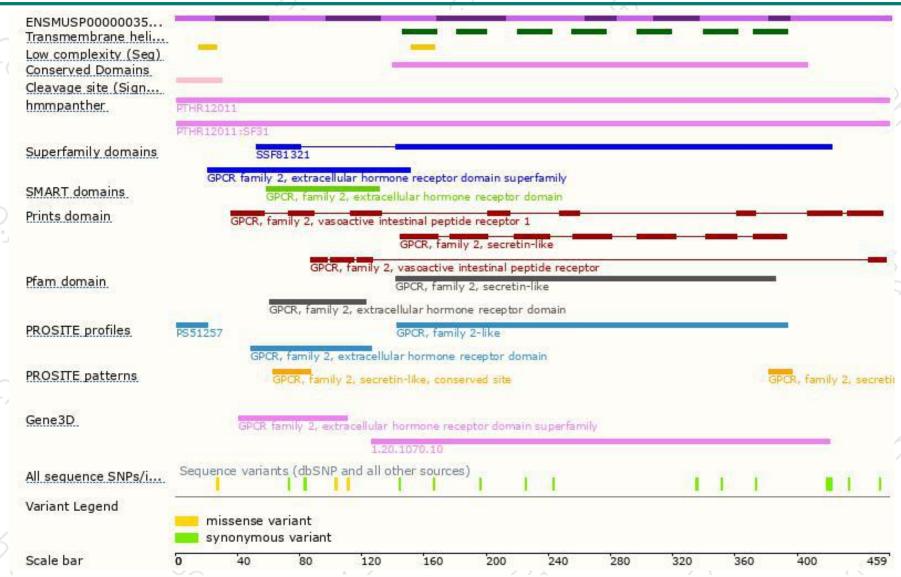
### Genomic location distribution





### Protein domain

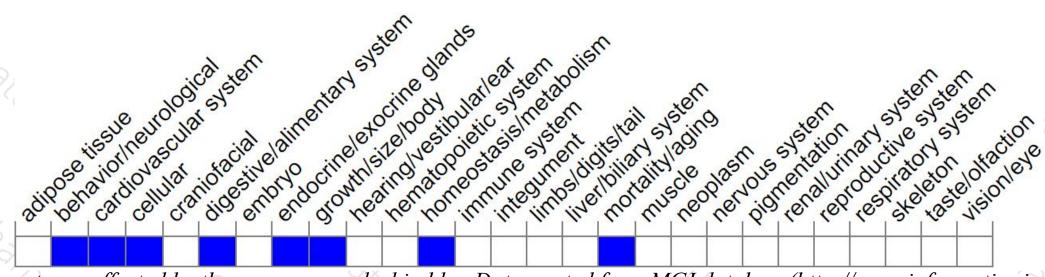




# Mouse phenotype description(MGI)







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-out allele exhibit prenatal lethality associated with severe neonatal growth failure, enlarged cecum, intestinal hemorrhage, and enterocyte hyperproliferation in addition to disorganized islets and impaired glucose homeostasisin surviving mice.



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

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