

Olfr66 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

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Project Overview

Project Name

Olfr66

Project type

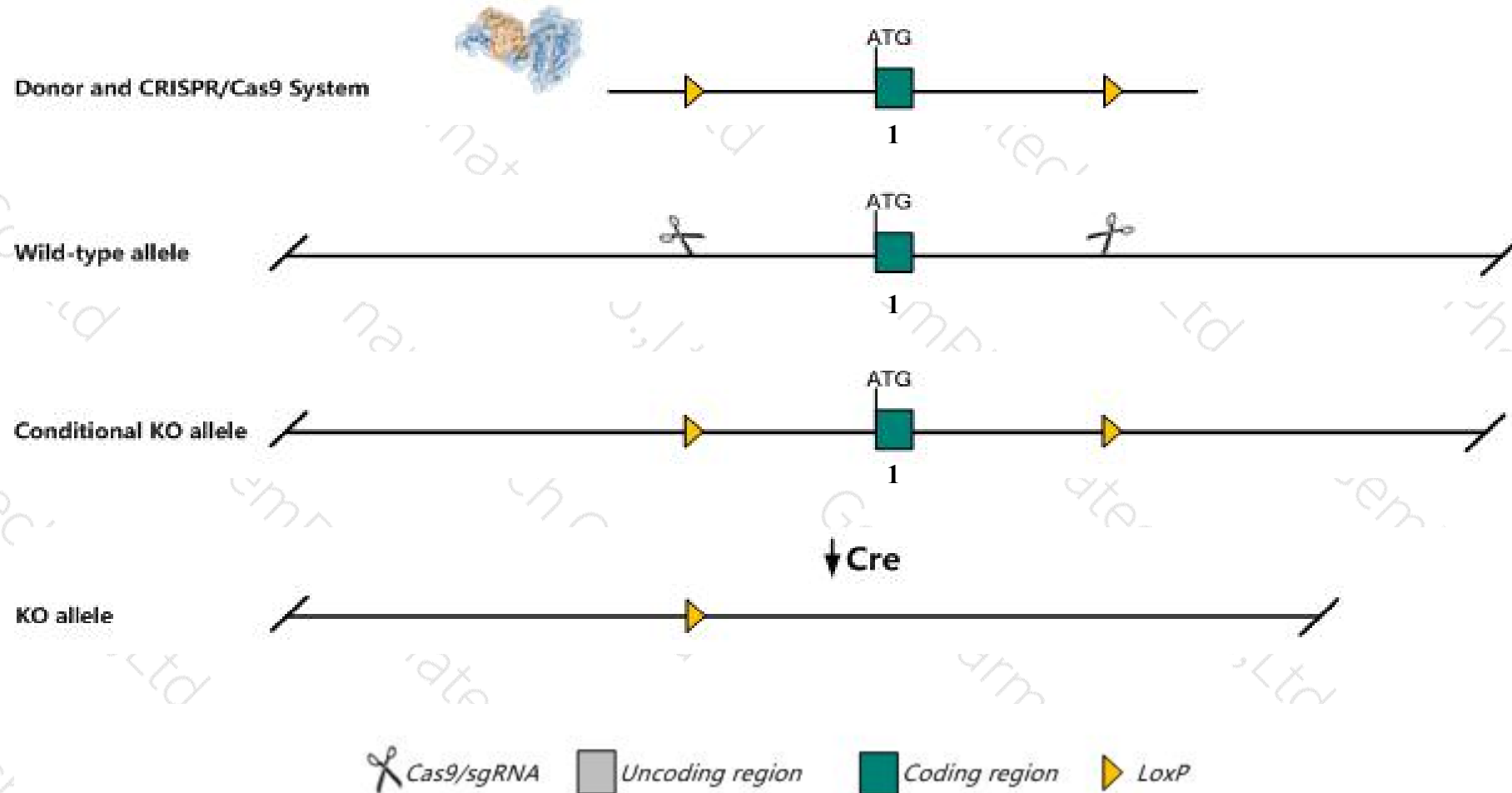
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Olfr66* gene. The schematic diagram is as follows:



Technical routes

- The *Olfr66* gene has 2 transcripts. According to the structure of *Olfr66* gene, exon1 of *Olfr66-201*(ENSMUST00000079117.1) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Olfr66* 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.

- *Dnajc19-ps* gene will be deleted together after Cre recombination in this strategy.
- The *Olfr66* gene is located on the Chr7. 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)

Olfr66 olfactory receptor 66 [Mus musculus (house mouse)]

Gene ID: 18367, updated on 13-Mar-2020

Summary



Official Symbol Olfr66 provided by [MGI](#)

Official Full Name olfactory receptor 66 provided by [MGI](#)

Primary source [MGI:MGI:1341906](#)

See related [Ensembl:ENSMUSG00000058200](#)

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 5'[b]1, 5'beta1, MOR1-3, ORL532

Summary Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms. [provided by RefSeq, Jul 2008]

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

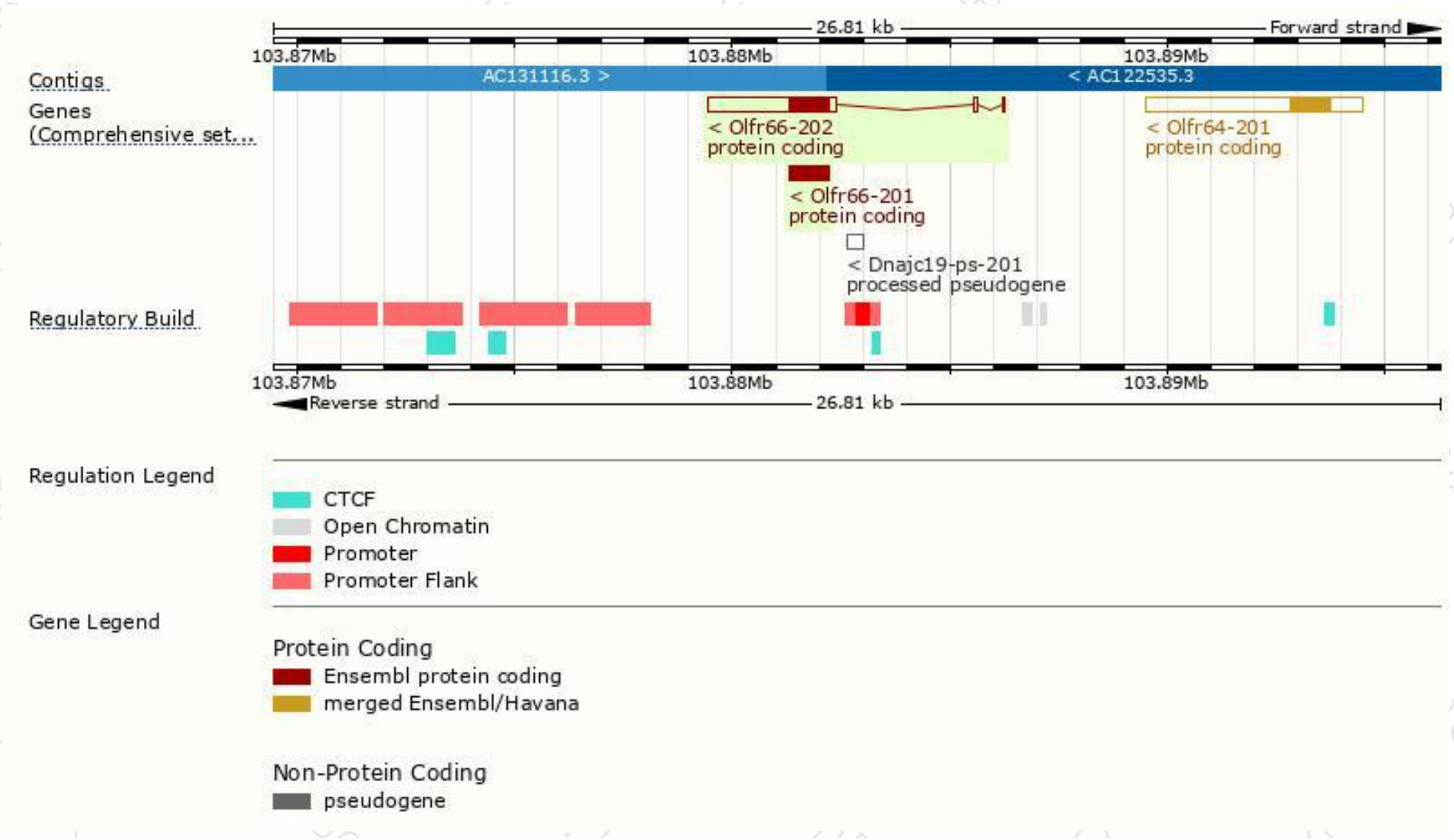
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Olfr66-202	ENSMUST00000216303.1	3080	311aa	Protein coding	CCDS21594	F8VQ01	TSL:5 GENCODE basic APPRIS P1
Olfr66-201	ENSMUST00000079117.1	936	311aa	Protein coding	CCDS21594	F8VQ01	TSL:NA GENCODE basic APPRIS P1

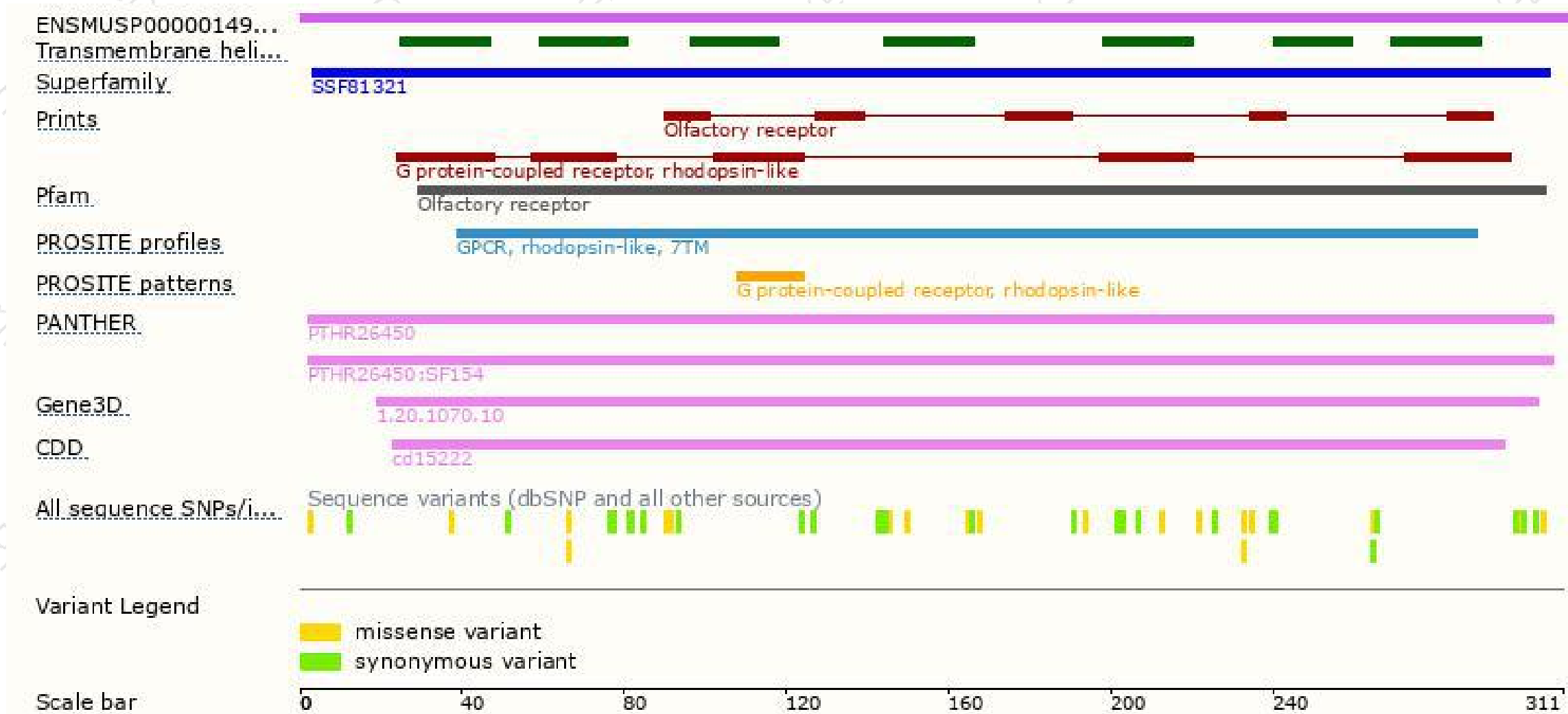
The strategy is based on the design of *Olfr66-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 025-5864 1534

