

# *Olfr17* Cas9-CKO Strategy

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# Project Overview

**Project Name**

***Olfr17***

**Project type**

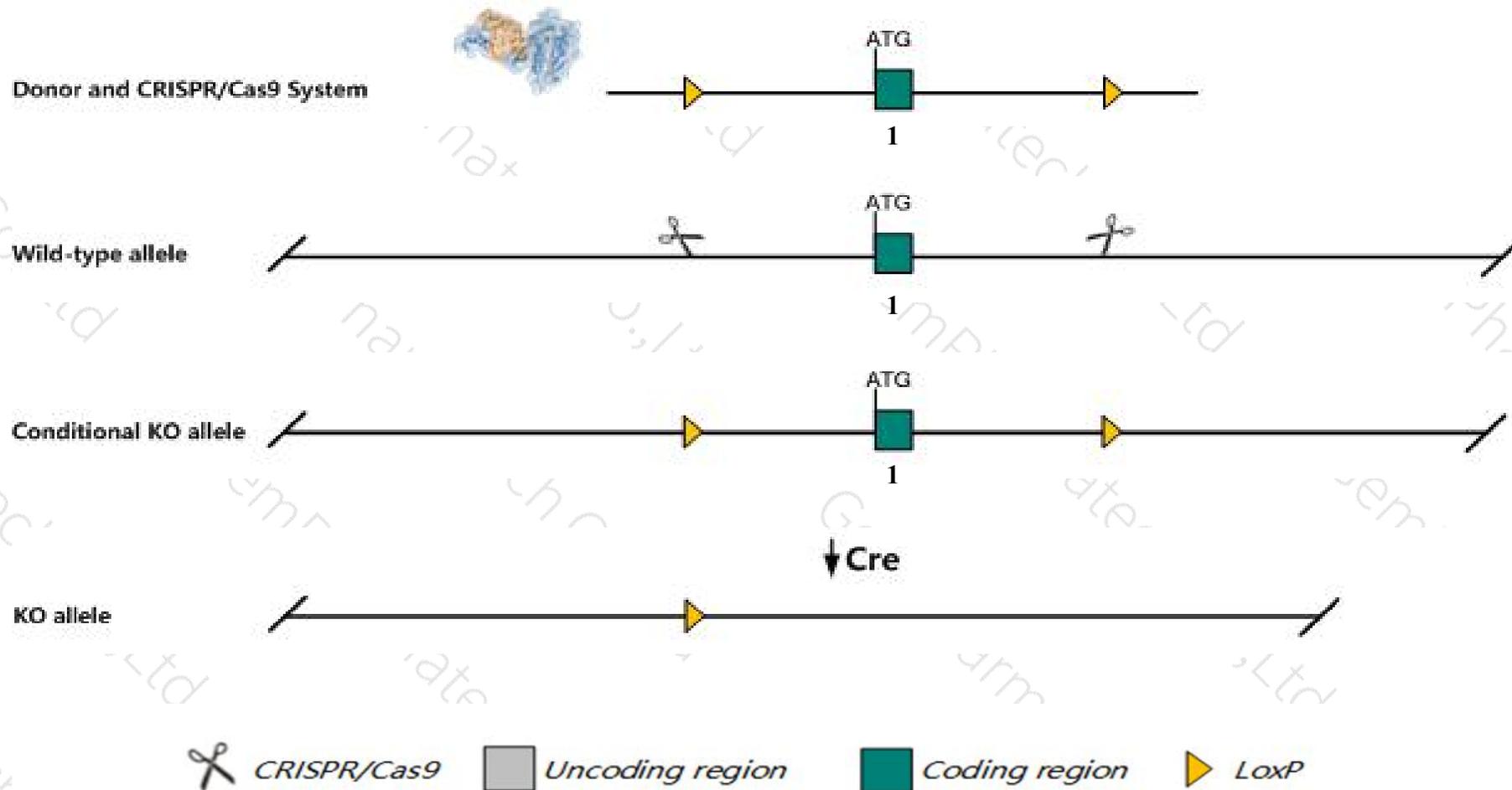
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Olf17* gene. The schematic diagram is as follows:



# Technical routes

- The *Olfr17* gene has 2 transcripts. According to the structure of *Olfr17* gene, exon1 of *Olfr17-201*(ENSMUST00000098138.4) 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 *Olfr17* 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, mice homozygous for disruptions in this gene possess olfactory neurons whose axons fail to project to the appropriate glomeruli in the olfactory bulb.
- The *Olf17* 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)

## Olfr17 olfactory receptor 17 [Mus musculus (house mouse)]

Gene ID: 18314, updated on 13-Mar-2020

### Summary

**Official Symbol** Olfr17 provided by MGI

**Official Full Name** olfactory receptor 17 provided by MGI

**Primary source** [MGI:MGI:109148](#)

**See related** [Ensembl:ENSMUSG00000073897](#)

**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** MOR263-5, P2

**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]

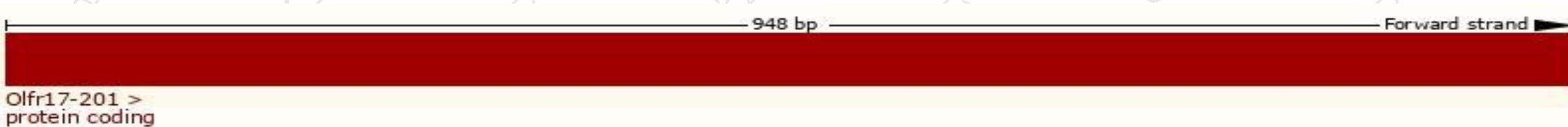
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

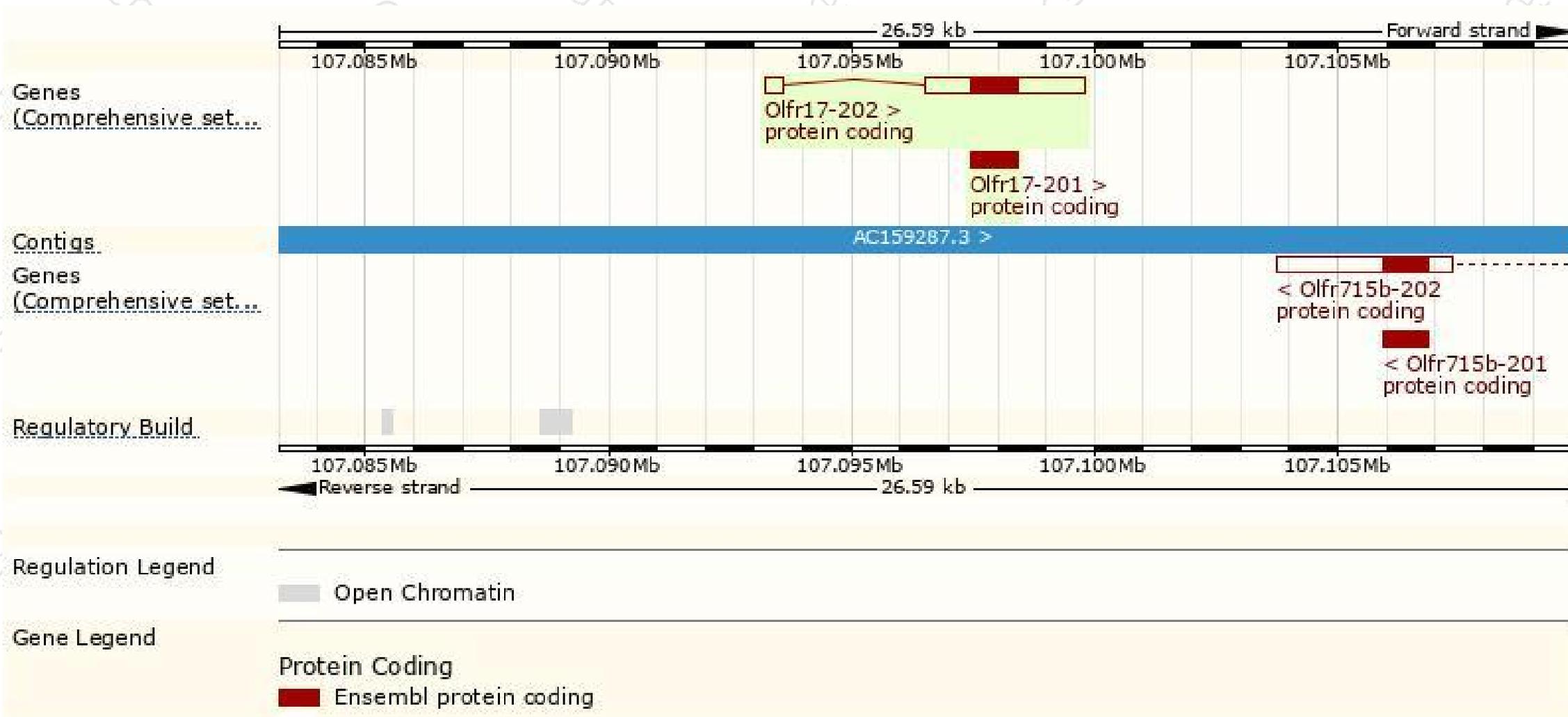
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Olf17-202	<a href="#">ENSMUST00000210568.3</a>	3666	<a href="#">315aa</a>	Protein coding	<a href="#">CCDS57578</a>	<a href="#">Q7TRM9</a>	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Olf17-201	<a href="#">ENSMUST00000098138.4</a>	948	<a href="#">315aa</a>	Protein coding	<a href="#">CCDS57578</a>	<a href="#">Q7TRM9</a>	TSL:NA GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

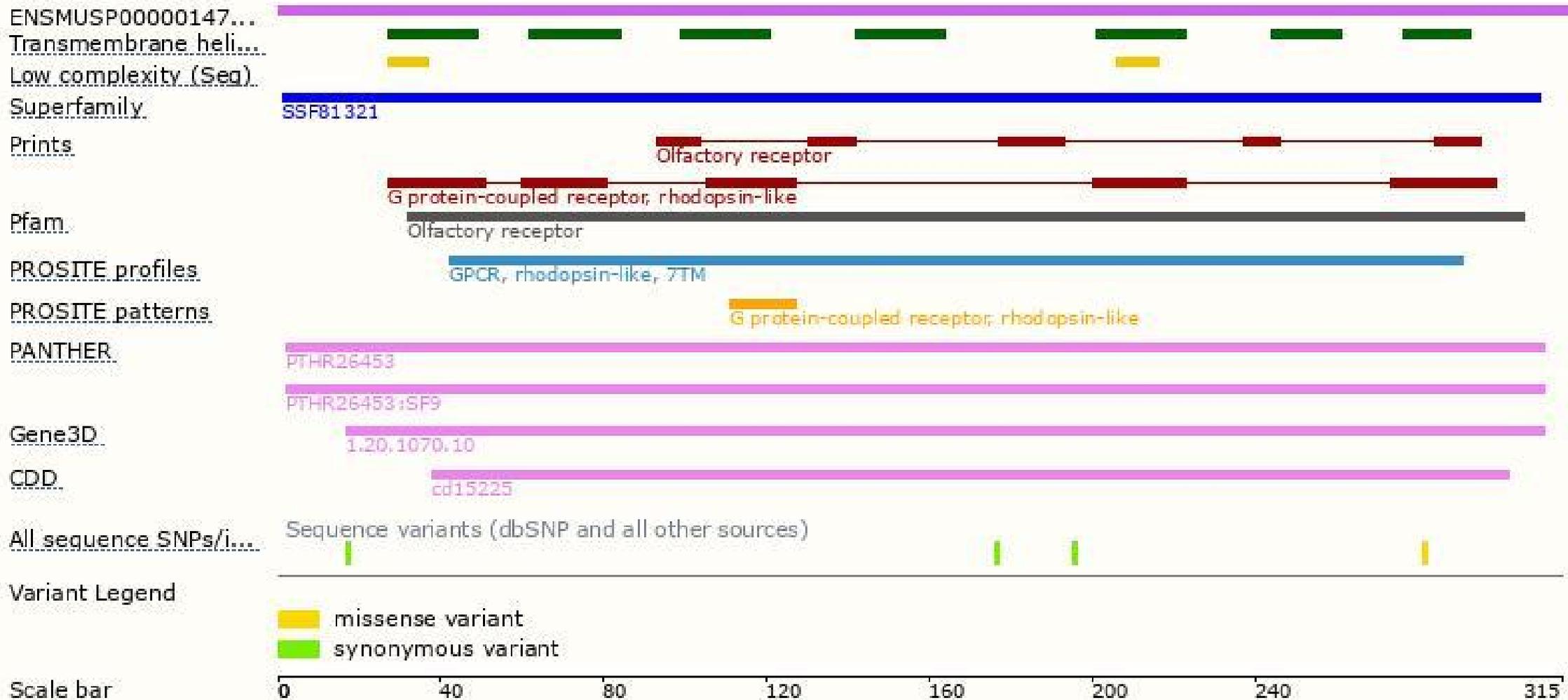
The strategy is based on the design of *Olf17-201* transcript, the transcription is shown below:



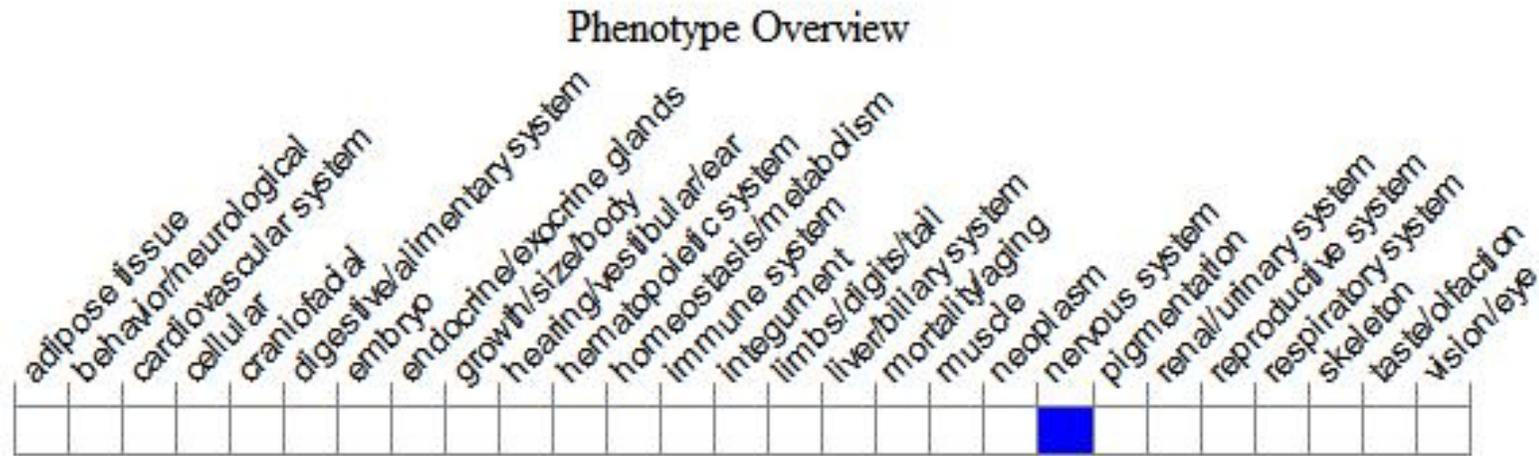
# Genomic location distribution



# 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 disruptions in this gene possess olfactory neurons whose axons fail to project to the appropriate glomeruli in the olfactory bulb.

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

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