GemPharmatech™

Olfr15 Cas9-CKO Strategy

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Design Date: 2023-1-11

Overview

Target Gene Name

- Olfr15

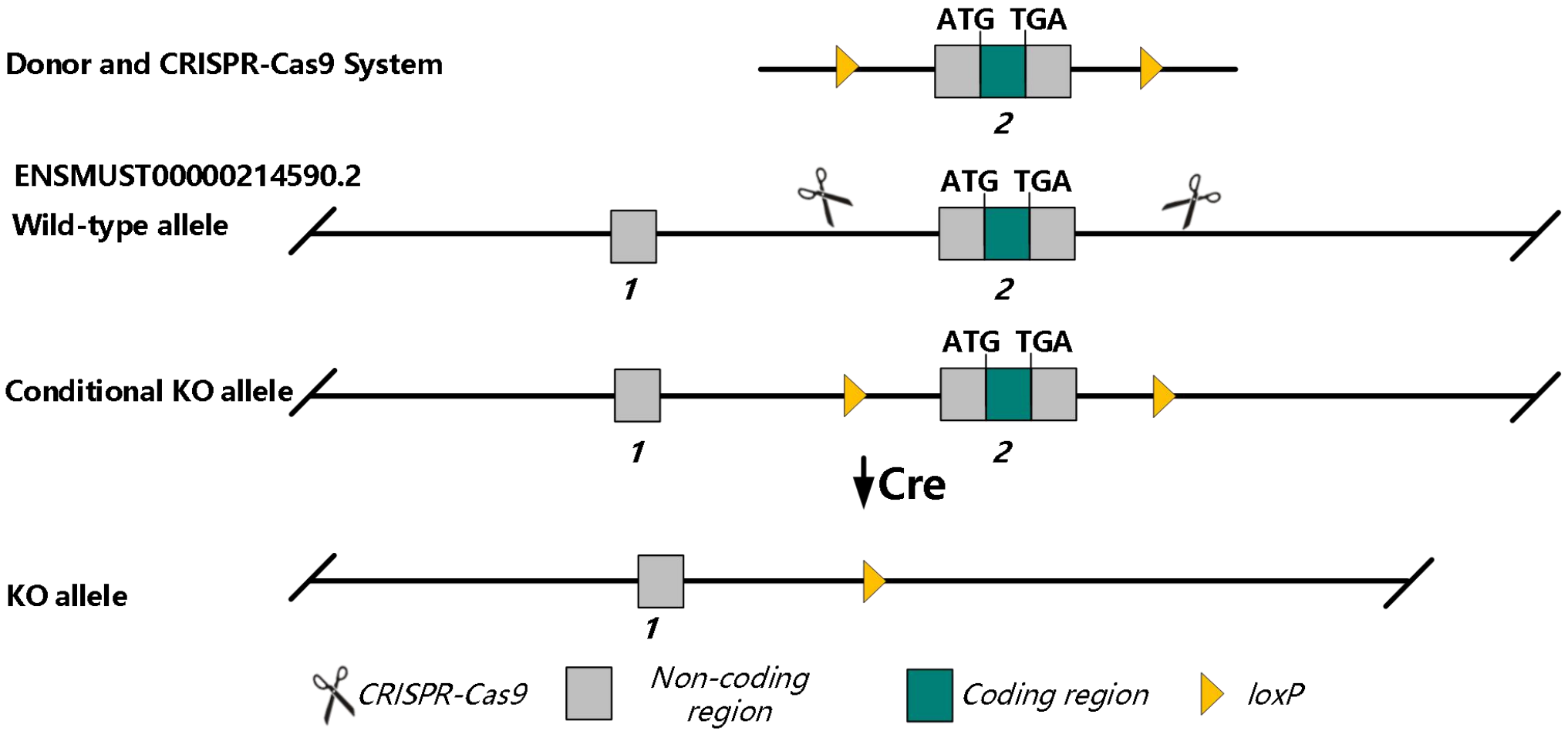
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

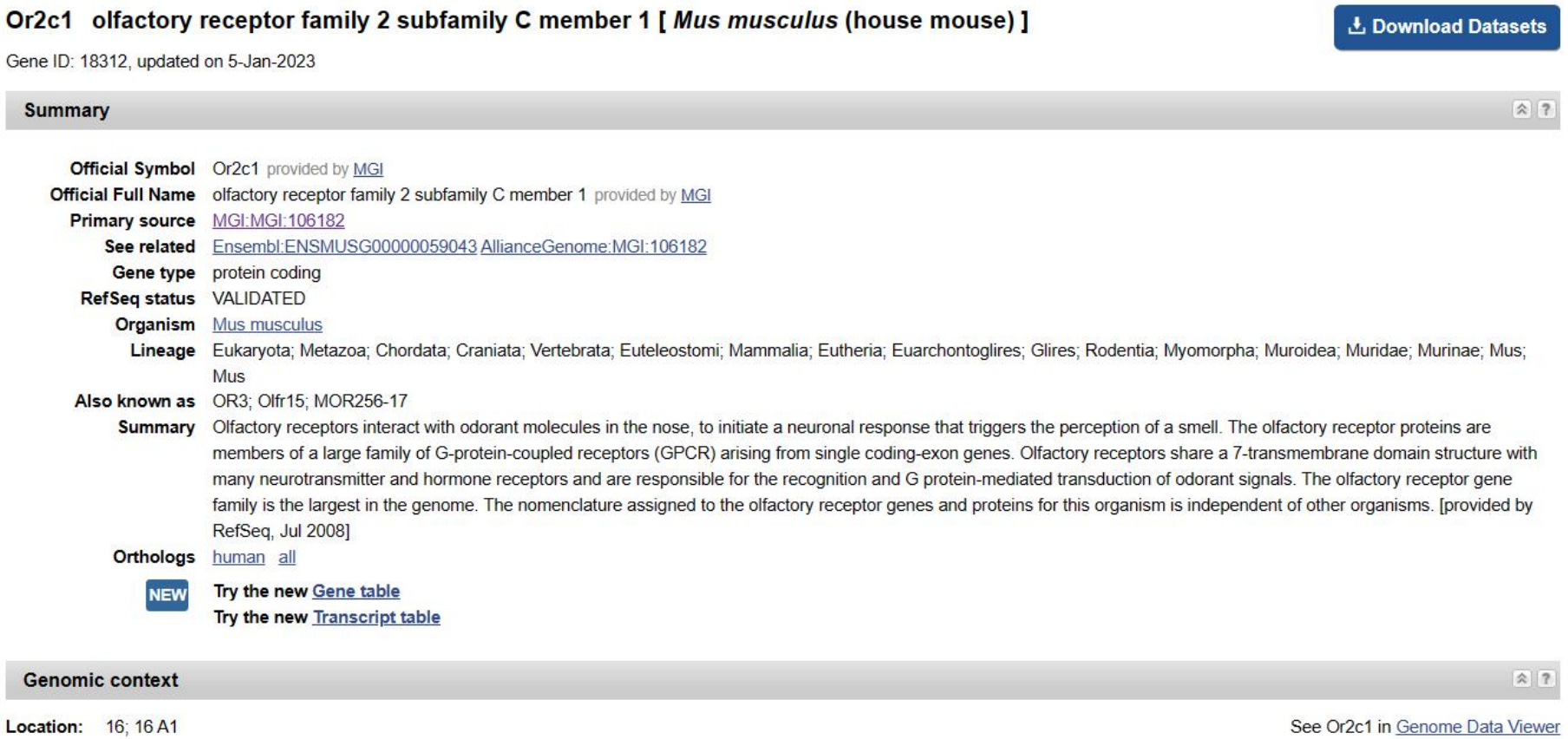


Schematic representation of CRISPR-Cas9 engineering used to edit the *Olfr15* gene.

Technical Information

- The *Olfr15* gene has 3 transcripts. According to the structure of *Olfr15* gene, exon 2 of *Olfr15-203* (ENSMUST00000214590.2) transcript is recommended as the knockout region. The region contains all of the of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Olfr15* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information



Or2c1 olfactory receptor family 2 subfamily C member 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 18312, updated on 5-Jan-2023

Summary

Official Symbol	Or2c1 provided by MGI
Official Full Name	olfactory receptor family 2 subfamily C member 1 provided by MGI
Primary source	MGI:MGI:106182
See related	Ensembl:ENSMUSG00000059043 AllianceGenome:MGI:106182
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	OR3; Olfr15; MOR256-17
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

NEW **Try the new Gene table**
Try the new Transcript table

Genomic context

Location: 16; 16 A1 — See Or2c1 in Genome Data Viewer

Exon count: 1

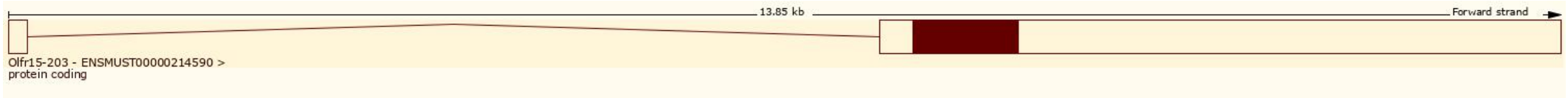
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

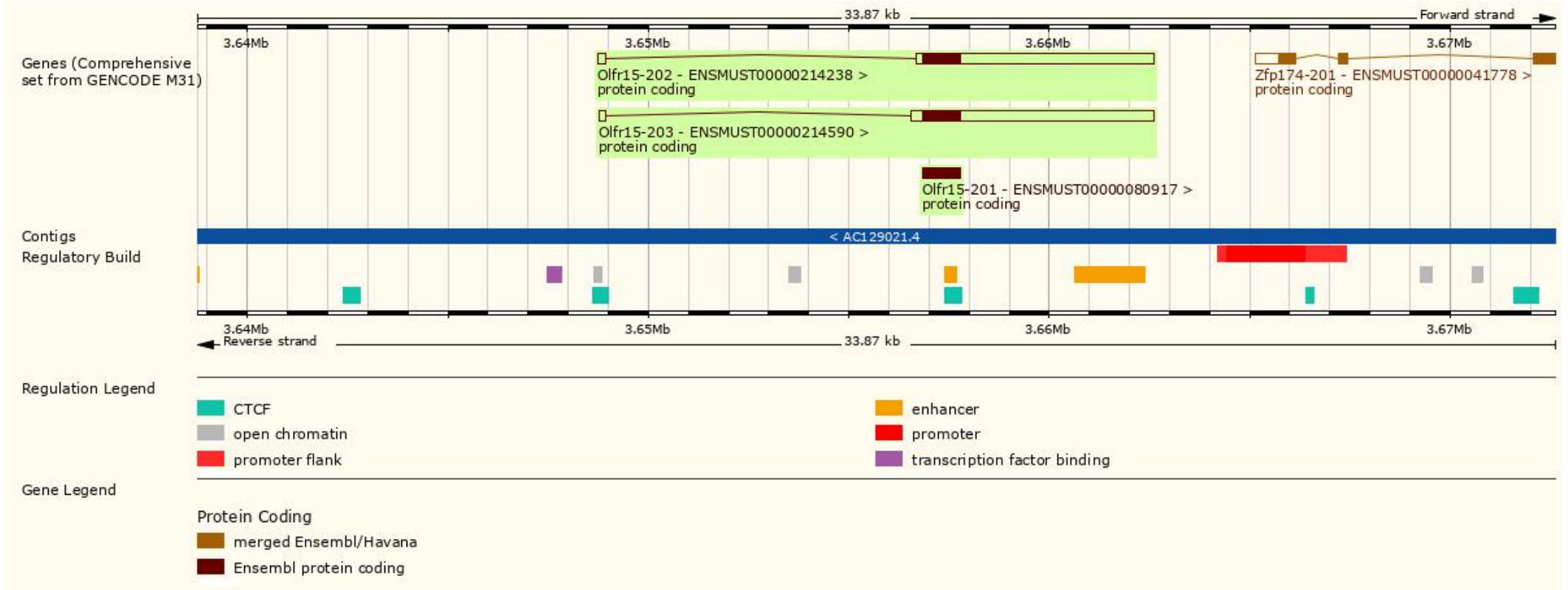
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000214590.2	Olfr15-203	6240	312aa	Protein coding	CCDS27910	P23275	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000214238.2	Olfr15-202	6135	312aa	Protein coding	CCDS27910	P23275	GENCODE basic APPRIS P1 TSL:5
ENSMUST00000080917.2	Olfr15-201	939	312aa	Protein coding	CCDS27910	P23275	GENCODE basic APPRIS P1 TSL:NA

The strategy is based on the design of *Olfr15-203* transcript, the transcription is shown below:



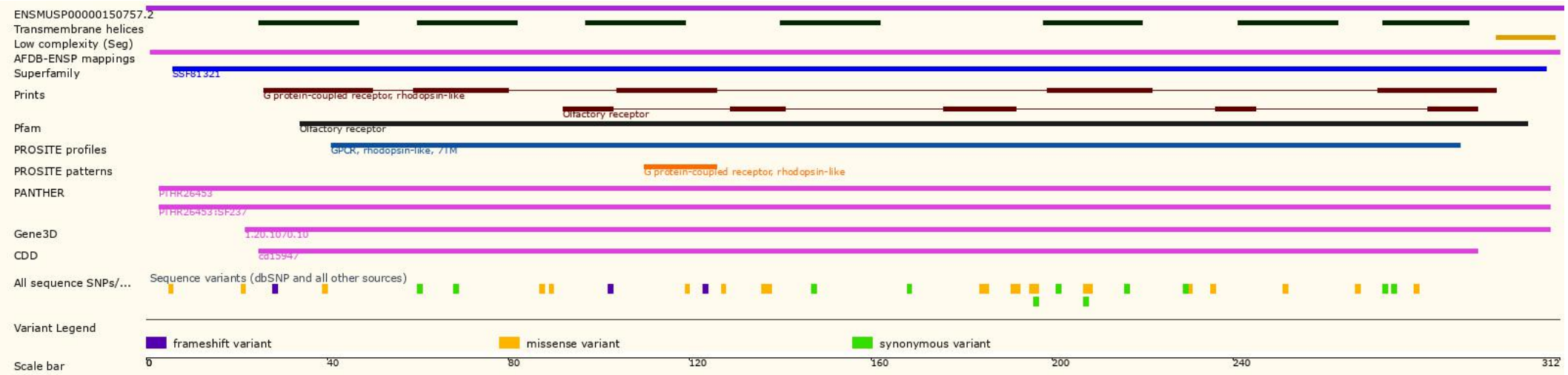
Source: https://www.ensembl.org

Genomic Information



Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Important Information

- The knockout region designed in this strategy is about 2.0 kb away from the 5' end of the *Zfp174* gene, and knockdown of the target gene may affect the regulation of the 5' end of the *Zfp174* gene.
- There are duplicate structures T in the target region, and sequence deletions or mutations may occur during model construction.
- *Olfr15* is located on Chr 16. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.