

Tas1r3 Cas9-CKO Strategy

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Overview

Target Gene Name

- Tas1r3

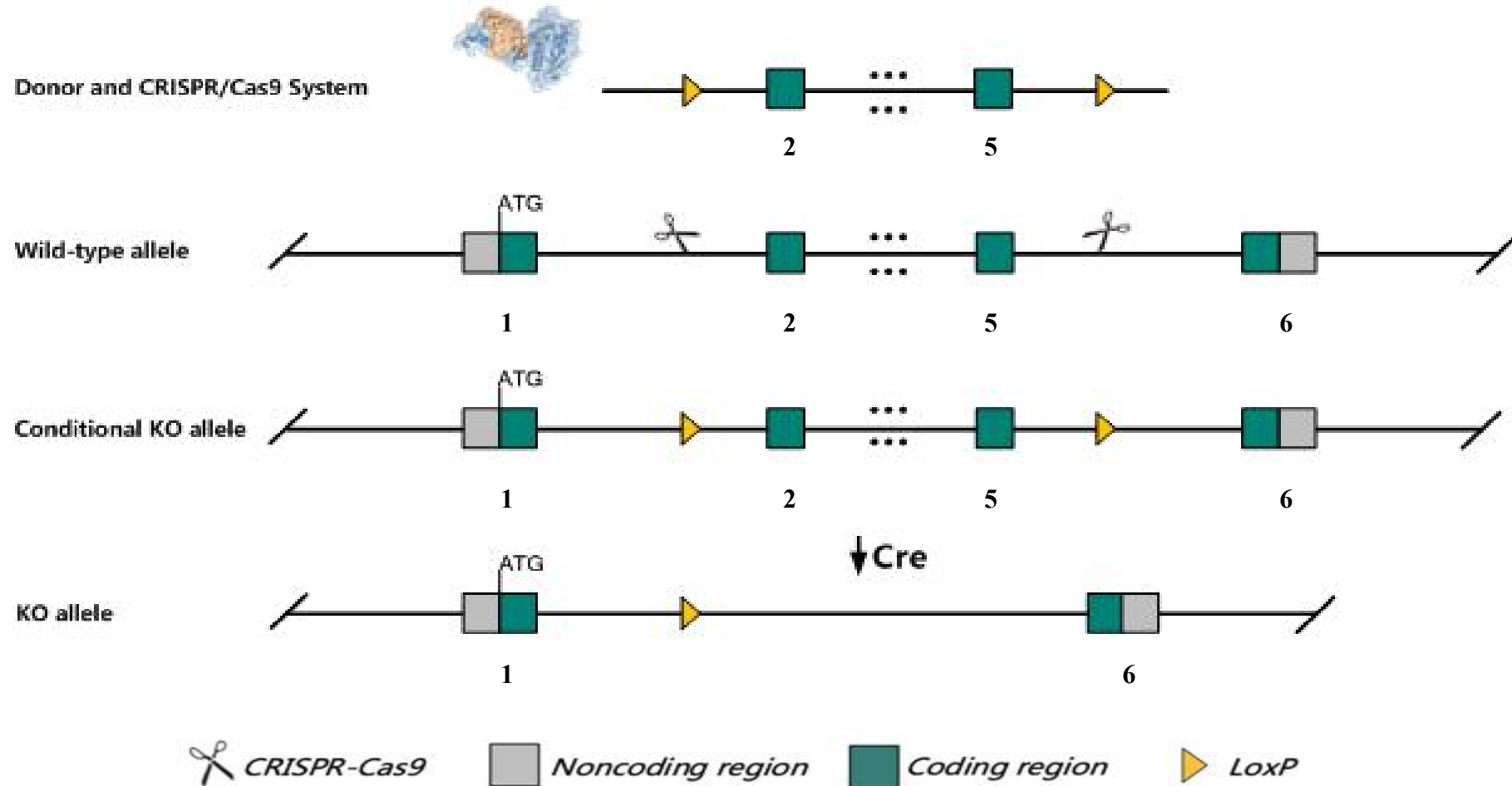
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tas1r3* gene.

Technical Information

- The *Tas1r3* gene has 1 transcript. According to the structure of *Tas1r3* gene, exon2-exon5 of *Tas1r3*-201 (ENSMUST00000030949.4) transcript is recommended as the knockout region. The region contains 1424bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Tas1r3* 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

Tas1r3 taste receptor, type 1, member 3 [Mus musculus (house mouse)]

Gene ID: 83771, updated on 31-May-2023

Summary

Official Symbol	Tas1r3 provided by MGI
Official Full Name	taste receptor, type 1, member 3 provided by MGI
Primary source	MGI:MGI:1933547
See related	Ensembl:ENSMUSG00000029072
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Sac, T1r3
Summary	Predicted to enable G protein-coupled receptor activity. Predicted to contribute to sweet taste receptor activity. Acts upstream of or within sensory perception of sweet taste. Predicted to be located in plasma membrane. Predicted to be integral component of membrane. Predicted to be part of sweet taste receptor complex. Predicted to be integral component of plasma membrane. Is expressed in circumvallate papilla and tongue anterior part. Orthologous to human TAS1R3 (taste 1 receptor member 3). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in testis adult (RPKM 1.6), thymus adult (RPKM 1.4) and 28 other tissues See more
Orthologs	human all

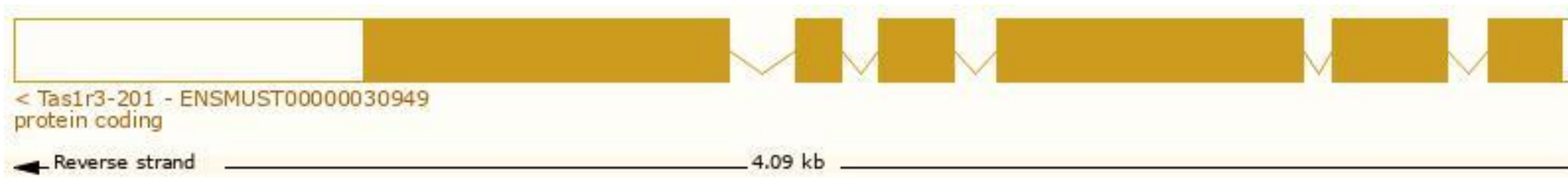
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 1 transcript, and the transcript is shown below:

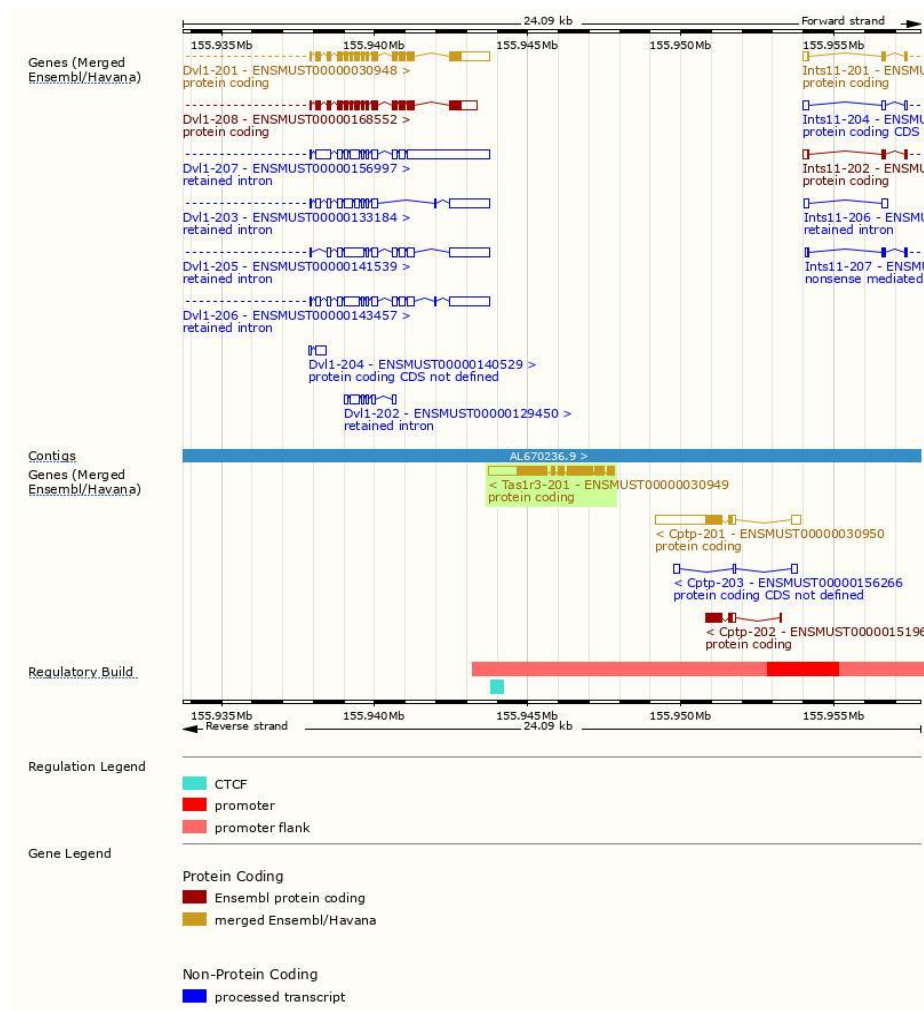
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000030949.4	Tas1r3-201	3523	858aa	Protein coding	CCDS19046	Q925D8	Ensembl Canonical Gencode basic APPRIS P1 TSL:1

The strategy is based on the design of *Tas1r3*-201 transcript, the transcription is shown below:



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

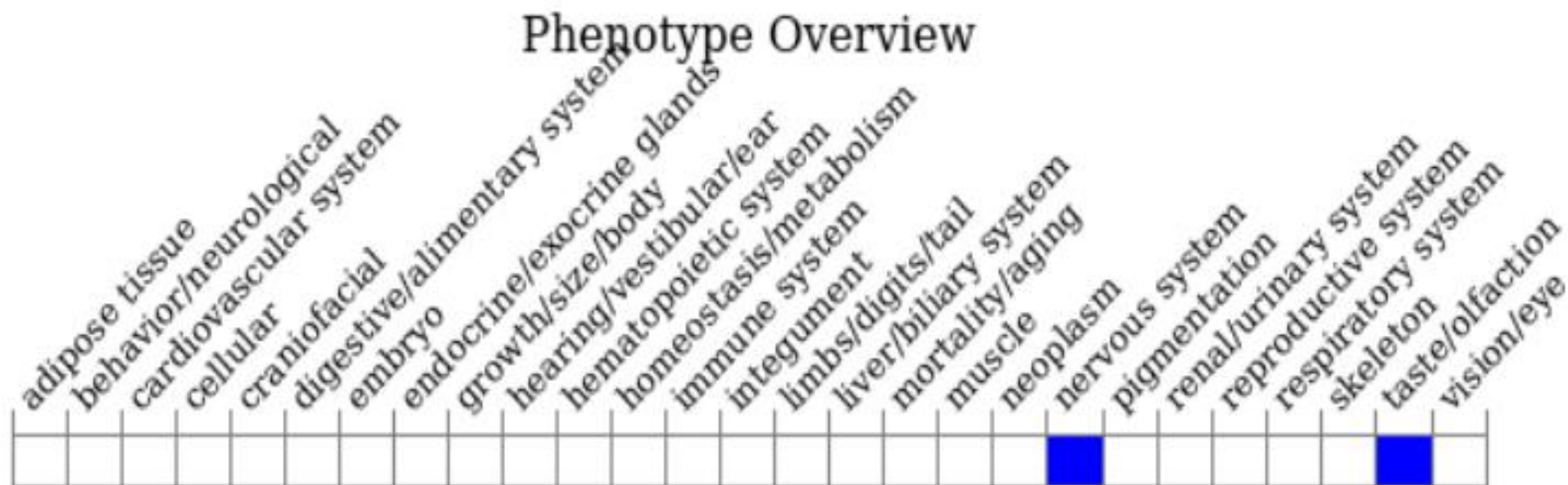
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Mutation of this locus affects taste perception. Complete inactivation results in diminished behavioral and nervous responses to both sweet and umami tastants.

Important Information

- According to the existing MGI data, mutation of this locus affects taste perception. Complete inactivation results in diminished behavioral and nervous responses to both sweet and umami tastants.
- **Because of intron 1-2 and intron 5-6 is very small, the insertion of loxps may influence the splicing of the *Tas1r3* gene before Cre recombinase.**
- The floxed region is near to the C-terminal of *Cptp* gene and *Dvl1* gene, this strategy may influence the regulatory function of the C-terminal of these gene.
- *Tas1r3* is located on Chr4. 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.