

Tas2r138 Cas9-KO Strategy

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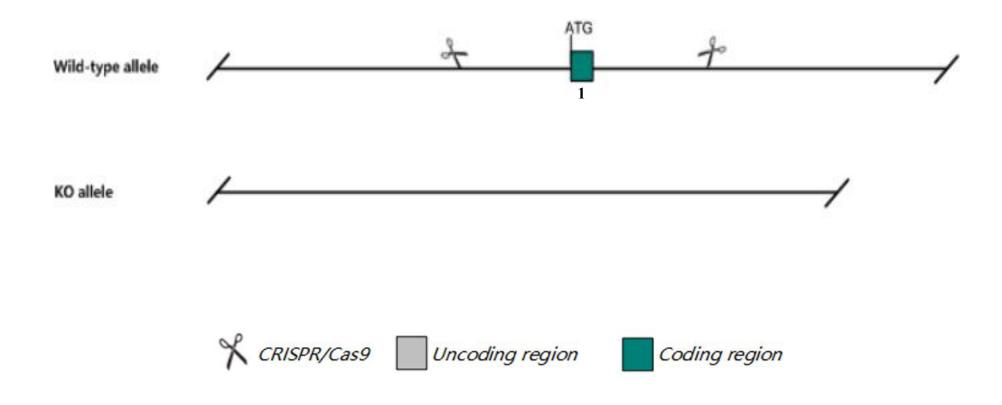


Project Name	Tas2r138
Project type	Cas9-KO
Strain background	C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Tas2r138* gene. The schematic diagram is as follows:





The *Tas2r138* gene has 1 transcript. According to the structure of *Tas2r138* gene, exon1 of *Tas2r138-201* (ENSMUST00000076565.2) 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 Tas2r138 gene. The brief process is as follows: CRISPR/Cas9 syst



The *Tas2r138* gene is located on the Chr6. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

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Gene information NCBI

Tas2r138 taste receptor, type 2, member 138 [Mus musculus (house mouse)]

Gene ID: 387513, updated on 12-Aug-2019

Summary

Official SymbolTas2r138 provided by MGIOfficial Full Nametaste receptor, type 2, member 138 provided by MGIPrimary sourceMGI:MGI:2681306See relatedEnsembl:ENSMUSG00000058250Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Myomorpha; Muroidea; Murinae; Mus; MusAlso known asT2R38; T2R138; mt2r31; Tas2r38Orthologshuman all

Genomic context

Location: 6; 6 B1

Exon count: 1

See Tas2r138 in Genome Data Viewer





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Transcript information Ensembl



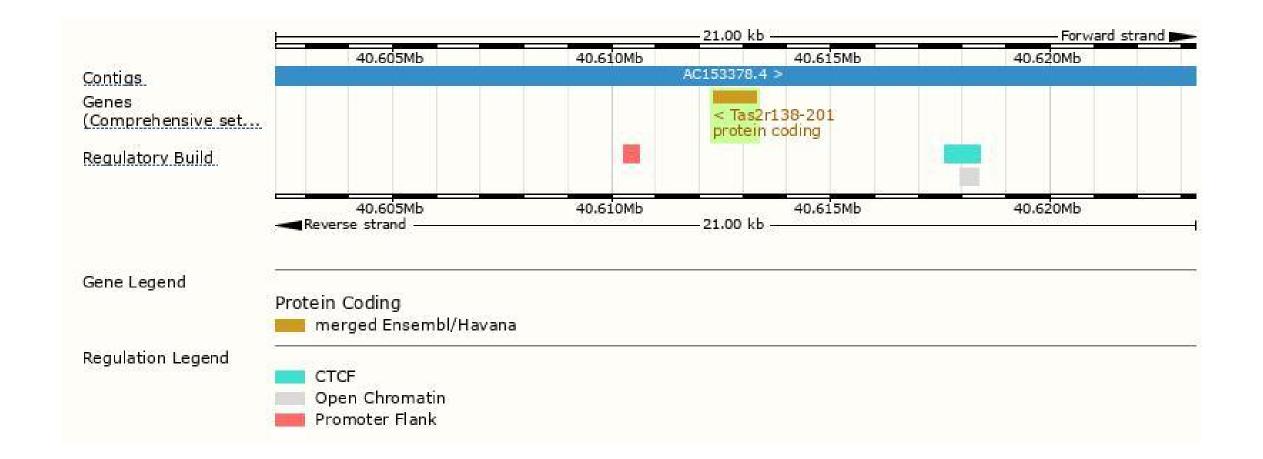
The gene has 1 transcript, and the transcript is shown below:

Name	Name Transcript ID		Protein	Biotype	CCDS	UniProt	Flags
Tas2r138-201	ENSMUST00000076565.2	996	<u>331aa</u>	Protein coding	CCDS20038	Q7TQA6	TSL:NA GENCODE basic APPRIS P1

The strategy is based on the design of *Tas2r138-201* transcript, The transcription is shown below

< Tas2r138-201 protein coding		
Reverse strand	996 bp	1
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Transmembrane heli Low complexity (Seg)									
Superfamily	SSF81	321							
Pfam.	Tast	e receptor type	2						-
PANTHER	Taste rec	eptor type 2 m	ember 38						-
	PTHR113	94							
Gene3D	1.20.1	070.10							
CDD	Tas	te receptor type	2 member 38						
All sequence SNPs/i	Sequenc	e variants (db	SNP and all ot	her sources)	1011	10	11.1	3	1
Variant Legend		sense variant onymous vari							
Scale bar	0	40	80	120	160	200	240	280	331

Protein domain

ENSMUSP0000075...





If you have any questions, you are welcome to inquire. Tel: 400-9660890





