

# ***Htr2a*** Cas9-CKO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Htr2a*

**Project type**

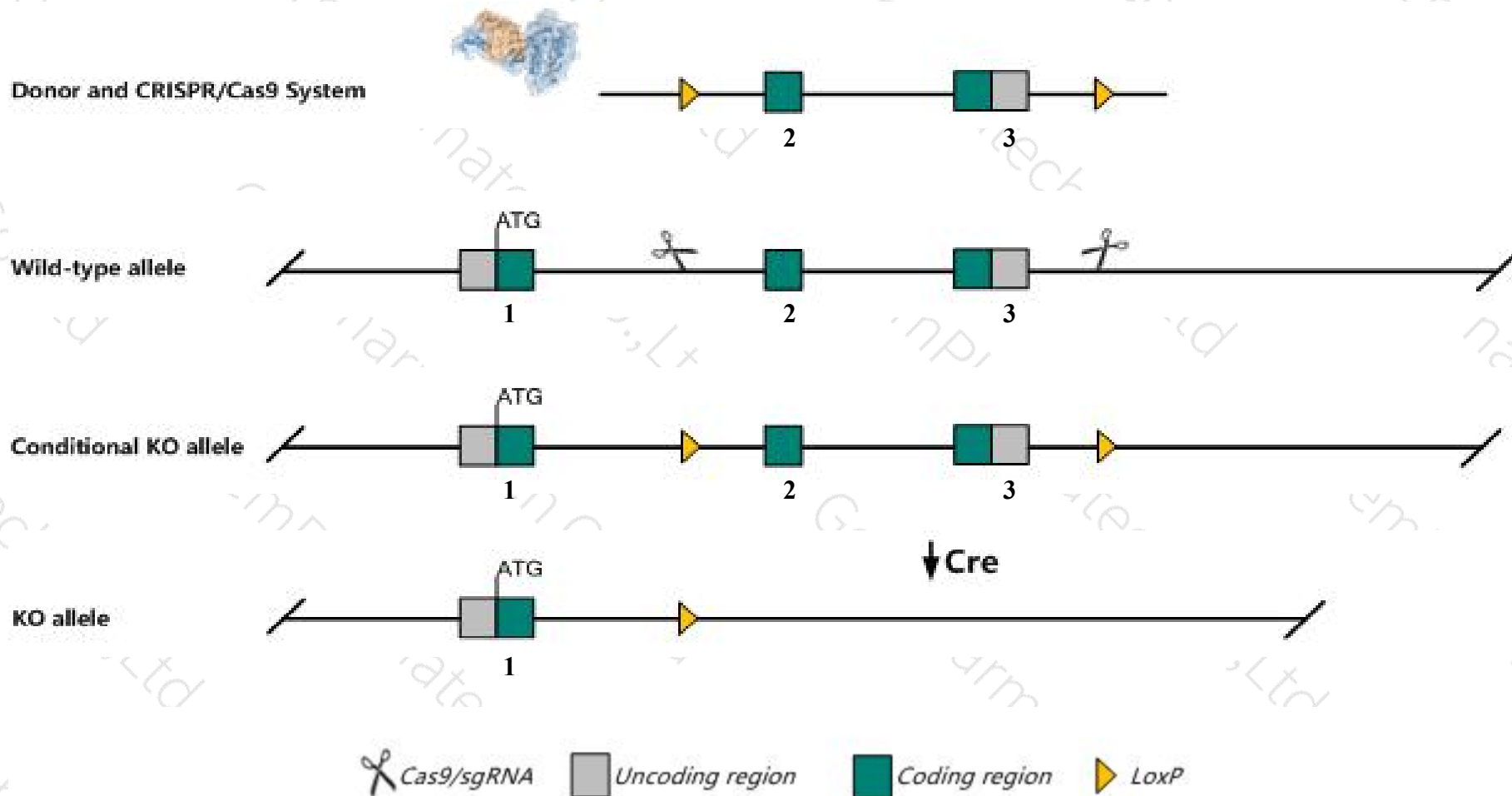
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Htr2a* gene. The schematic diagram is as follows:



- The *Htr2a* gene has 1 transcript. According to the structure of *Htr2a* gene, exon2-exon3 of *Htr2a-201* (ENSMUST00000036653.4) transcript is recommended as the knockout region. The region contains 1004bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Htr2a* 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele show altered anxiety-related responses and increased vertical activity. Mice homozygous for a different knock-out allele exhibit abnormal enterocyte, Paneth cell and smooth muscle morphology.
- The *Htr2a* gene is located on the Chr14. 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)

## Htr2a 5-hydroxytryptamine (serotonin) receptor 2A [Mus musculus (house mouse)]

Gene ID: 15558, updated on 5-Mar-2019

### Summary



<b>Official Symbol</b>	Htr2a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	5-hydroxytryptamine (serotonin) receptor 2A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:109521</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000034997</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	5-HT-2, 5-HT-2A, E030013E04, Htr-2, Htr2
<b>Expression</b>	Biased expression in frontal lobe adult (RPKM 3.5), cortex adult (RPKM 2.6) and 13 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Htr2a-201	<a href="#">ENSMUST00000036653.4</a>	5606	<a href="#">471aa</a>	Protein coding	<a href="#">CCDS27275</a>	<a href="#">P35363 Q543D4</a>	TSL:1 GENCODE basic APPRIS P1

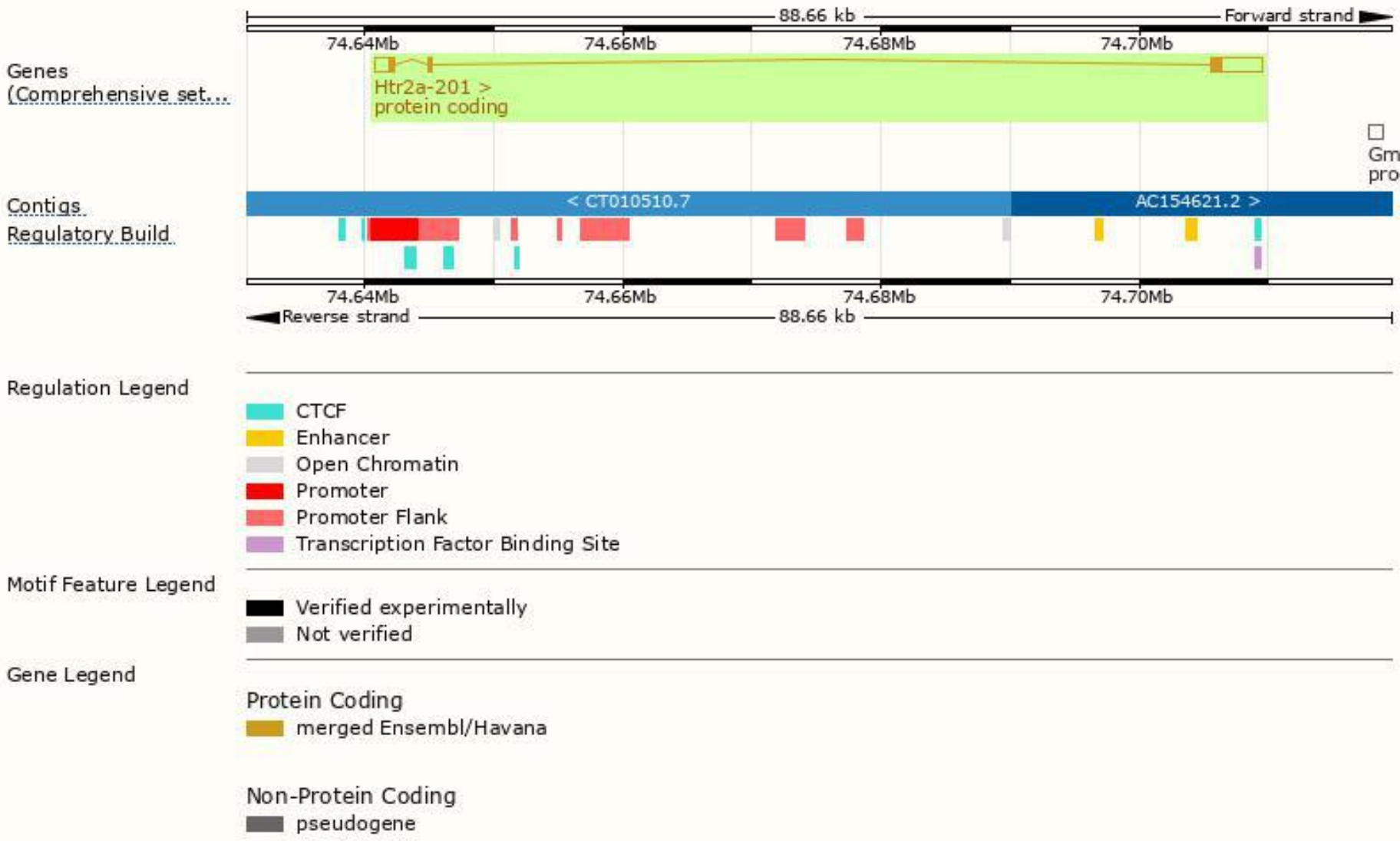
The strategy is based on the design of *Htr2a-201* transcript, The transcription is shown below



# Genomic location distribution



集萃药康  
GemPharmatech





# Protein domain

ENSMUSP00000047...

Transmembrane heli...

Low complexity (Seg)

Conserved Domains

hmmpanther

PTHR24247

5-Hydroxytryptamine 2A receptor

Superfamily domains

SSF81321

SMART domains

G protein-coupled receptor, rhodopsin-like

Prints domain

5-hydroxytryptamine receptor family

G protein-coupled receptor, rhodopsin-like

5-Hydroxytryptamine 2A receptor

Pfam domain

G protein-coupled receptor, rhodopsin-like

PROSITE profiles

GPCR, rhodopsin-like, 7TM

PROSITE patterns

G protein-coupled receptor, rhodopsin-like

Gene3D

1.20.1070.10

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

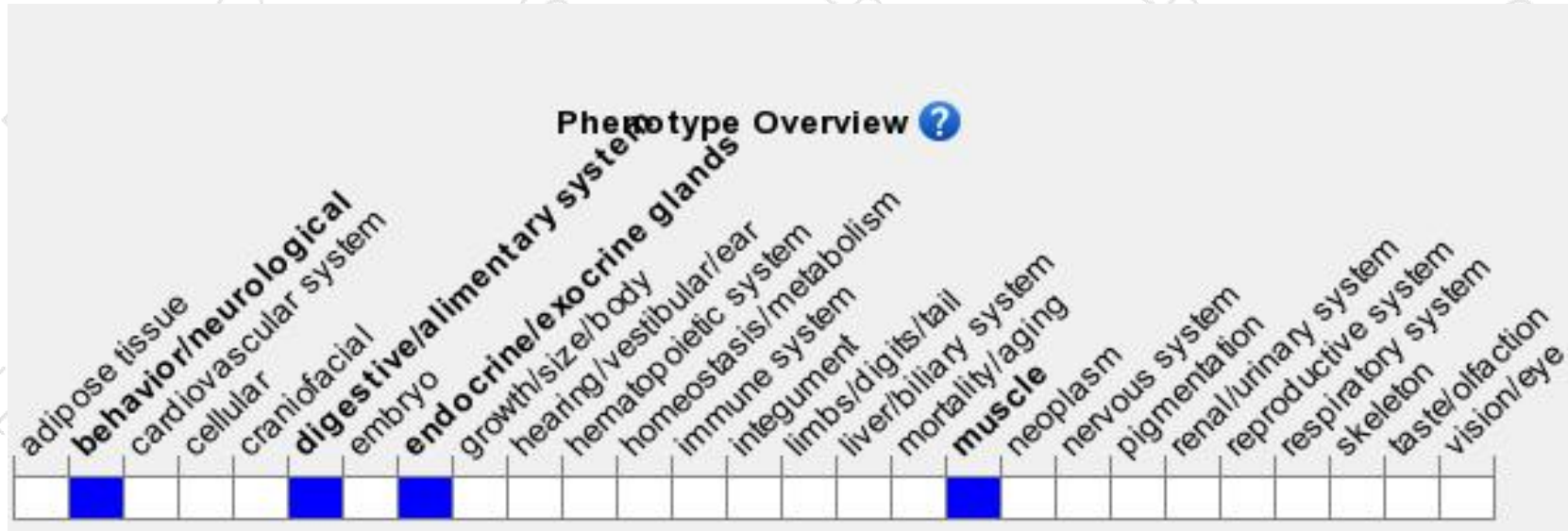
Variant Legend

 synonymous variant

Scale bar

0 40 80 120 160 200 240 280 320 360 400 471

# 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 a knock-out allele show altered anxiety-related responses and increased vertical activity. Mice homozygous for a different knock-out allele exhibit abnormal enterocyte, Paneth cell and smooth muscle morphology.

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

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