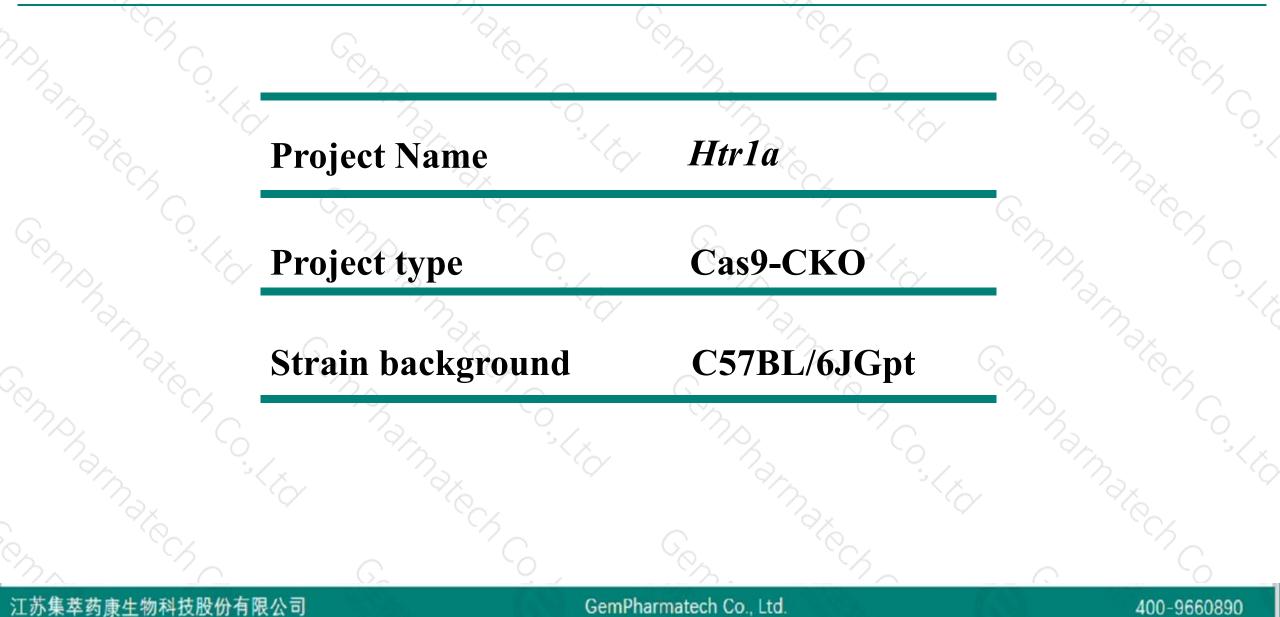
# Htr1a Cas9-CKO Strategy Annak Cherry

**Designer: Design Date:**  Huan Fan 2019-7-25

# **Project Overview**

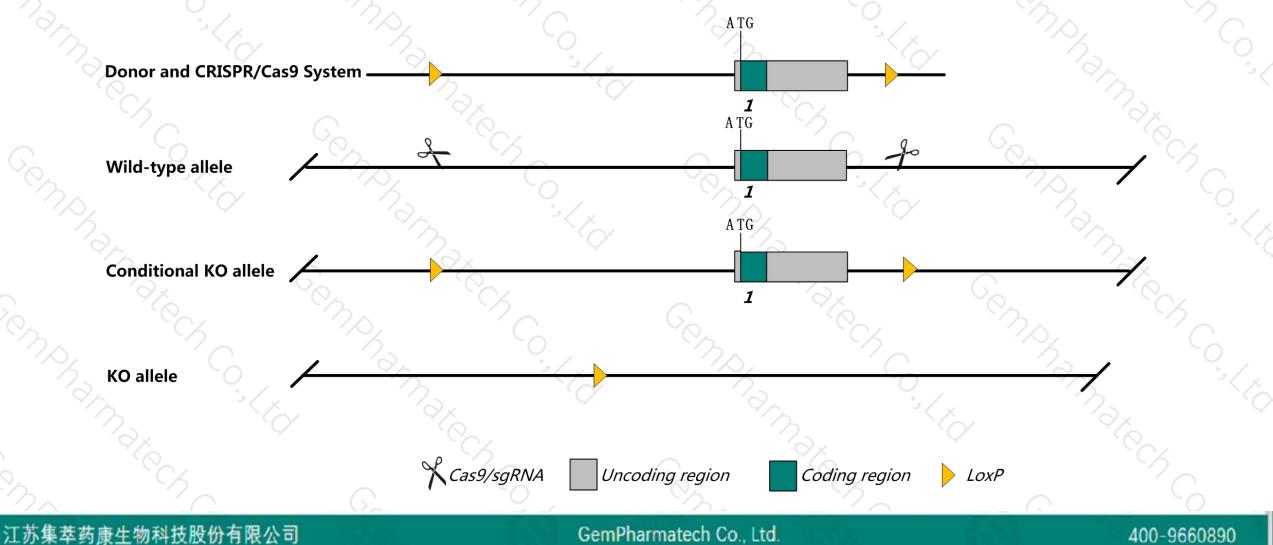




# **Conditional Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Htr1a* gene. The schematic diagram is as follows:





- The *Htr1a* gene has 1 transcript. According to the structure of *Htr1a* gene, exon1 of *Htr1a*-201 transcript is recommended as the knockout region. The region contains start codon ATG coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Htr1a* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 or cell types.

# Notice



- According to the existing MGI data , Homozygotes for targeted null mutations show a common phenotype, including augmented anxious-like behavior in the elevated plus-maze, open-field, and novel object tests, reduced immobility in the forced-swim or tail-suspension test, and changes in density of 5-HTT binding in several brain regions.
   The *Htrla* gene is located on the Chr13. If the knockout mice are crossed with other mice strains to obtain double gene
- The *Htr1a* gene is located on the Chr13. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)



\$ ?

Htr1a 5-hydroxytryptamine (serotonin) receptor 1A [ Mus musculus (house mouse) ]

Gene ID: 15550, updated on 2-Jul-2019

#### Summary

 Official Symbol
 Htr1a provided by MGI

 Official Full Name
 5-hydroxytryptamine (serotonin) receptor 1A provided by MGI

 Primary source
 MGI:MGI:96273

 See related
 Ensembl:ENSMUSG00000021721

 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; Muridae; Murinae; Mus; Mus

 Also known as
 Gpcr18

 Orthologs
 human all

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# **Transcript information (Ensembl)**



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

Show/hi	de columns (1 hidden)					2		Filter	
Name 🖕	Transcript ID	bp 🖕	Protein 🖕	Biotype 💧	CCDS	UniProt 🖕		\$	
Htr1a-201	ENSMUST0000022235.5	4484	<u>421aa</u>	Protein coding	CCDS26756	<u>Q64264</u> &	TSL:NA	GENCODE basic	APPRIS P1

The strategy is based on the design of *Htr1a*-201 transcript, The transcription is shown below

		 P 200. 1	
	4.48 kb —		
Htr1a-201 > protein coding			

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# **Genomic location distribution**



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# Protein domain



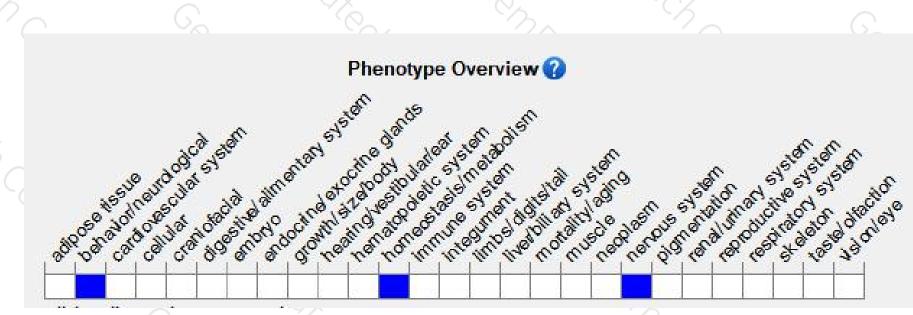
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# Mouse phenotype description(MGI)





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, Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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



