Hgs Cas9-CKO Strategy

Designer:Xueting Zhang
Reviewer:Yanhua Shen
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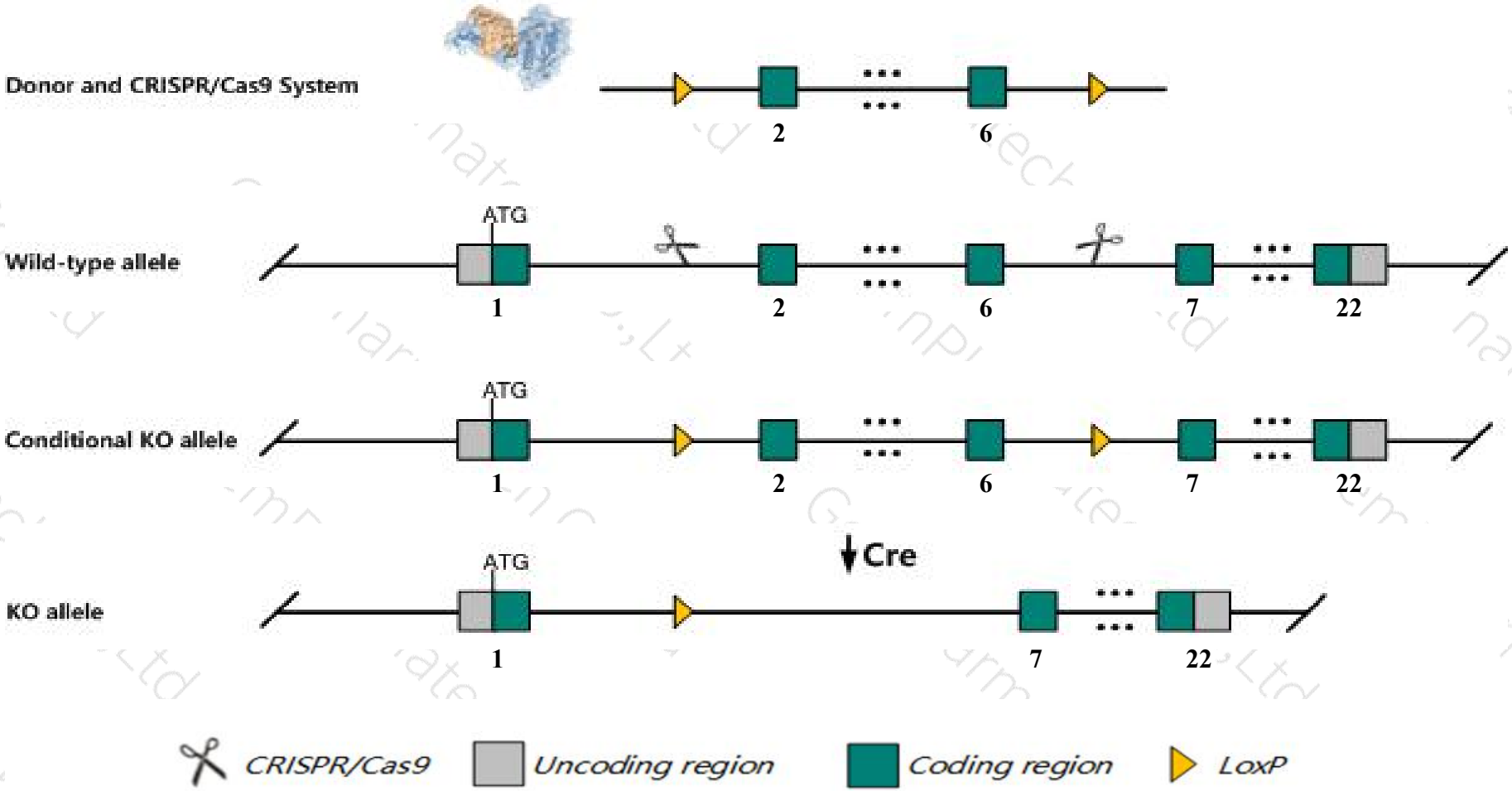
Project Overview

Project Name	***Hgs***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- The *Hgs* gene has 5 transcripts. According to the structure of *Hgs* gene, exon2-exon6 of *Hgs-201* (ENSMUST00000106203.8) transcript is recommended as the knockout region.The region contains 431bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hgs* 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 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 and cell types.

Notice

- According to the existing MGI data,Mice homozygous for disruptions in this gene display embryonic lethality during organogenesis with decreased size and no embryo turning. In addition, one allele shows cardia bifida, no foregut formation, failure of chorioallantoic fusion and neural tube,somite and allantois defects.
- The effect on transcript *Hgs*-203 is unknown.
- The floxed region is near to the N-terminal of *Arl16* gene,this strategy may influence the regulatory function of the N-terminal of *Arl16* gene.
- The *Hgs* gene is located on the Chr11. 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）

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Hgs HGF-regulated tyrosine kinase substrate [*Mus musculus* (house mouse)]

Gene ID: 15239, updated on 12-Aug-2019

Summary

Official Symbol	Hgs provided by MGI
Official Full Name	HGF-regulated tyrosine kinase substrate provided by MGI
Primary source	MGI:MGI:104681
See related	Ensembl:ENSMUSG00000025793
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	tn; Hgr; Hrs; ZFYVE8
Expression	Ubiquitous expression in testis adult (RPKM 102.6), adrenal adult (RPKM 78.0) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 11 E2; 11 84.16 cM

See Hgs in Genome Data Viewer

Exon count: 23

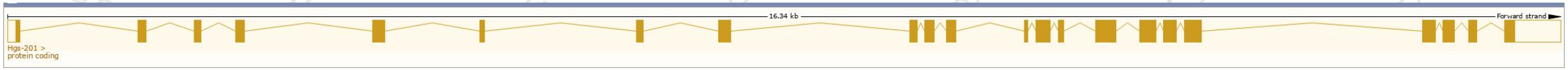
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (120467605..120483984)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (120328949..120345298)

Transcript information（Ensembl）

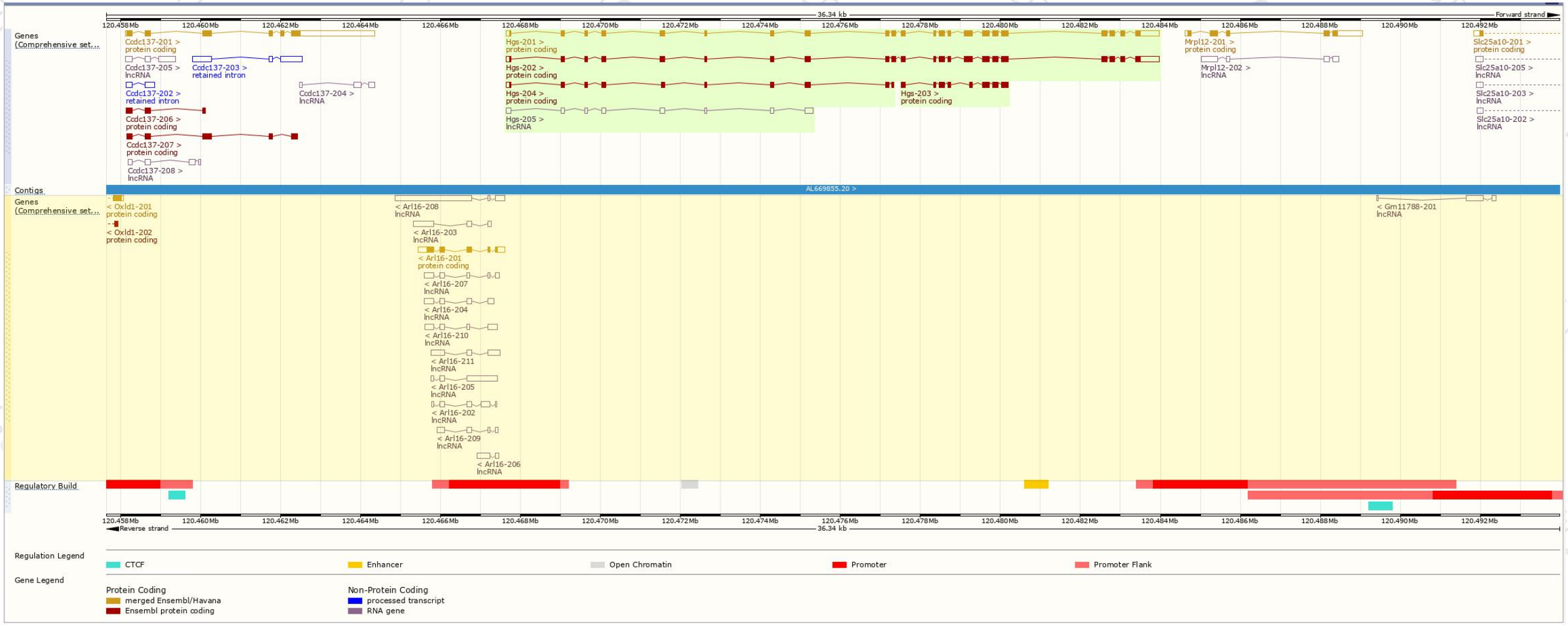
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hgs-201	ENSMUST00000106203.8	2903	776aa	Protein coding	CCDS49005	B1ATZ1 Q3UMA3	TSL:5 GENCODE basic APPRIS P2
Hgs-202	ENSMUST00000106205.8	2900	775aa	Protein coding	-	B1ATZ0 Q99LI8	TSL:5 GENCODE basic APPRIS ALT2
Hgs-203	ENSMUST00000135231.2	882	294aa	Protein coding	-	F6VV02	CDS 5' and 3' incomplete TSL:5
Hgs-204	ENSMUST00000140862.6	829	245aa	Protein coding	-	B1ATY9	CDS 3' incomplete TSL:5
Hgs-205	ENSMUST00000141826.1	829	No protein	lncRNA	-	-	TSL:2

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

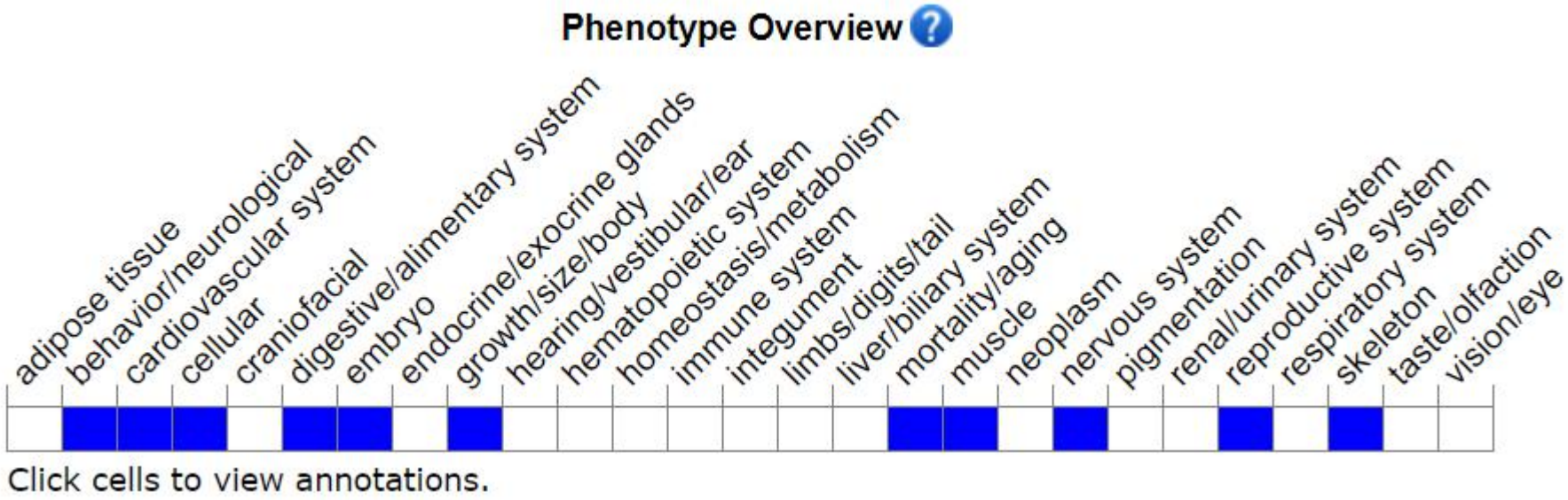


Genomic location distribution



Protein domain

Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd