

# ***Hgs Cas9-KO Strategy***

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# Project Overview

**Project Name**

*Hgs*

**Project type**

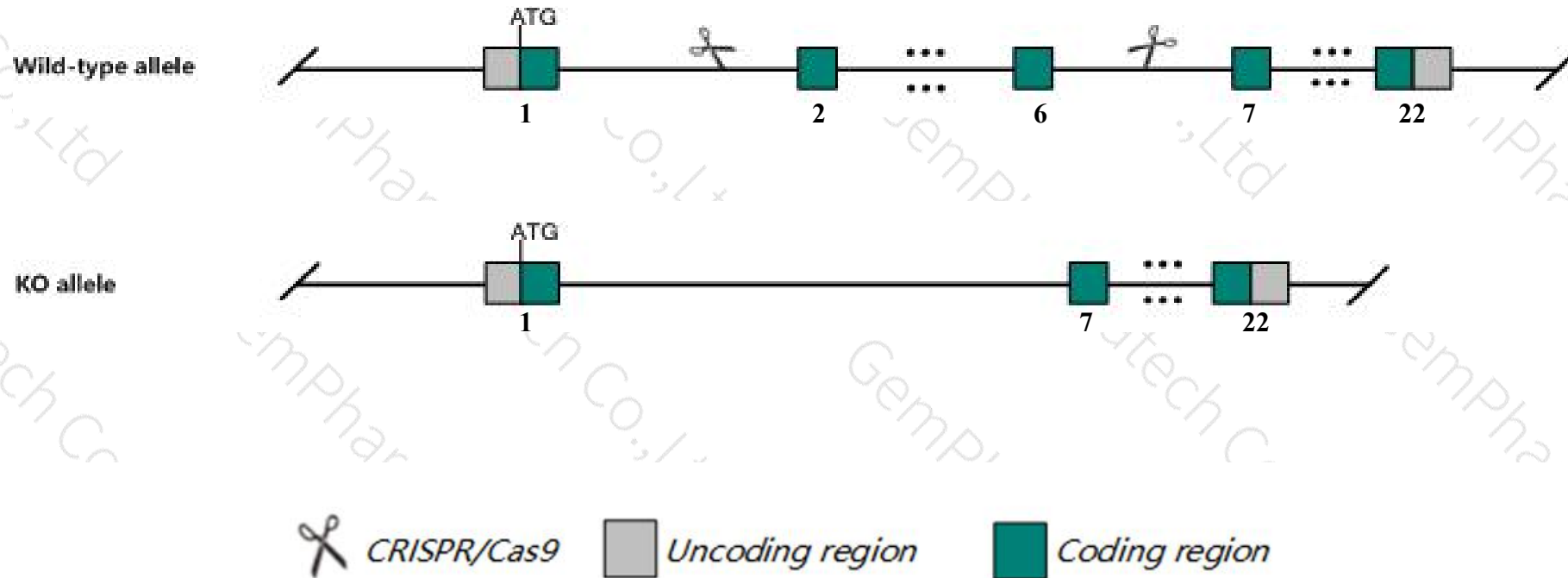
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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 w

- 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 knockout region is near to the N-terminal of *Arl16* gene, this strategy may influence the regulatory function of the N-terminus 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)



## 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:ENSMUSG000000025793
- 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

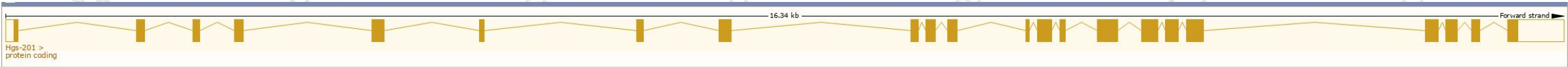
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	11	NC_000077.6 (120467605..120483984)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	11	NC_000077.5 (120328949..120345298)

# Transcript information (Ensembl)

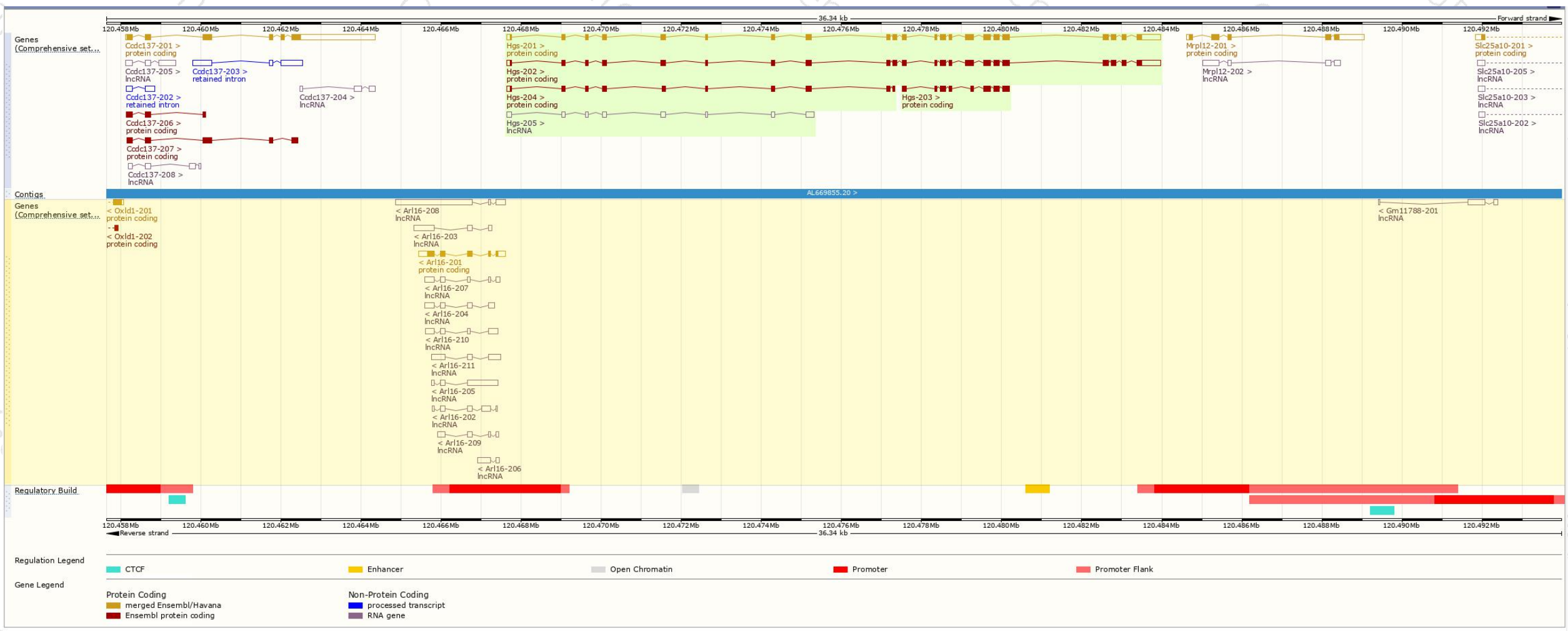
The gene has 5 transcripts,all transcripts are shown below:

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

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

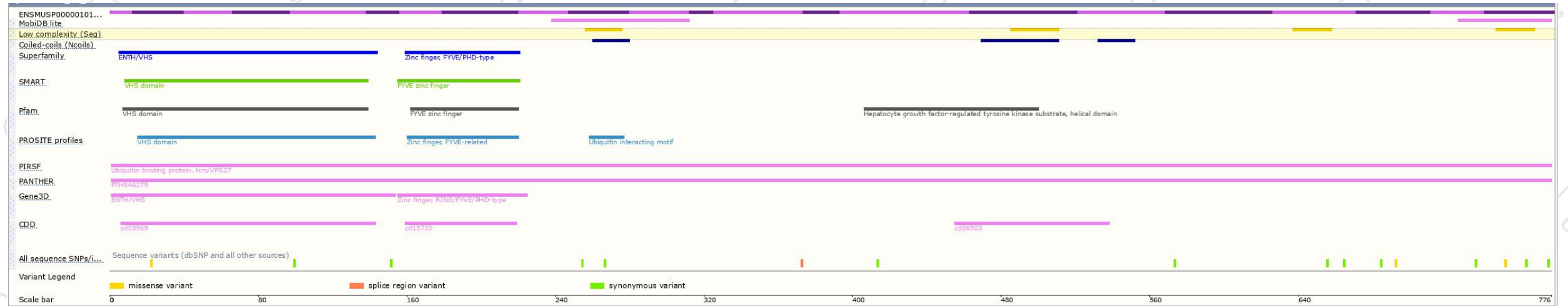


# Genomic location distribution

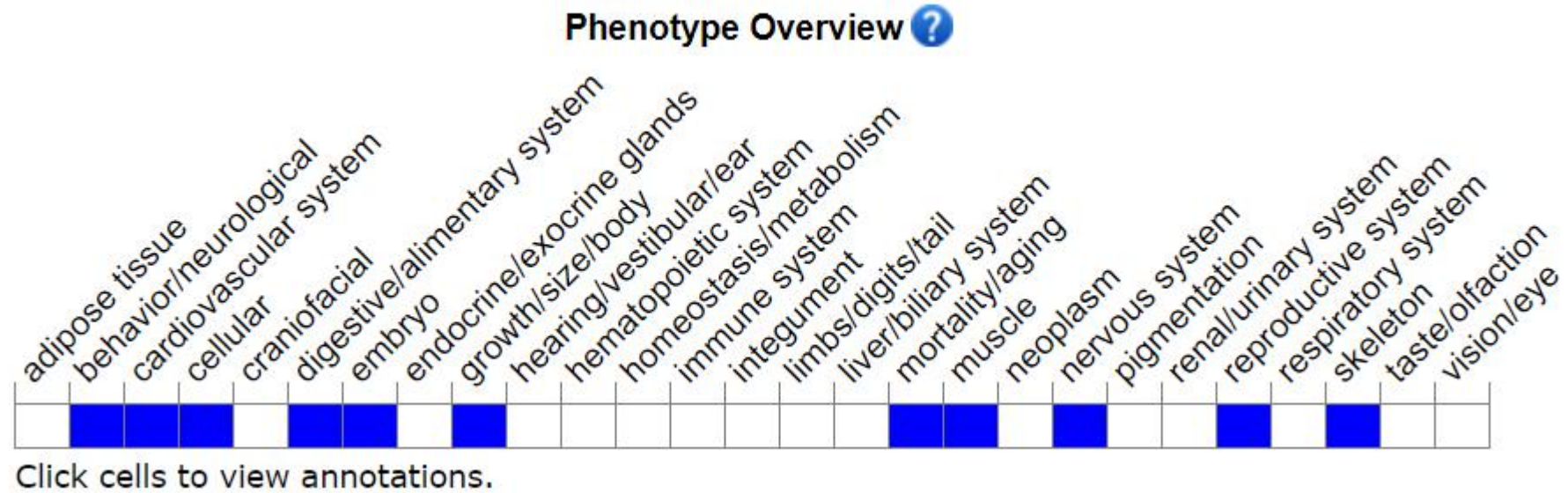




# Protein domain



# Mouse phenotype description(MGI)



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

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.

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

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