

Hmcn1 Cas9-KO Strategy

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Project Overview

Project Name

Hmcn1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmcn1* gene. The schematic diagram is as follows:



- The *Hmcn1* gene has 6 transcripts. According to the structure of *Hmcn1* gene, exon2 of *Hmcn1-201* (ENSMUST00000074783.11) transcript is recommended as the knockout region. The region contains 71bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hmcn1* gene. The brief process is as follows: CRISPR/Cas9 system

- The effect on transcript *Hmcn1*-206 is unknown.
- Transcript *Hmcn1*-203&204 may not be affected.
- The *Hmcn1* gene is located on the Chr1. 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)

Hmcn1 hemicentin 1 [*Mus musculus* (house mouse)]

Gene ID: 545370, updated on 16-Sep-2019

Summary

- Official Symbol** Hmcn1 provided by MGI
- Official Full Name** hemicentin 1 provided by MGI
- Primary source** MGI:MGI:2685047
- See related** Ensembl:ENSMUSG00000066842
- 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** Gm201; FIBL-6; EG545370
- Expression** Broad expression in lung adult (RPKM 6.3), limb E14.5 (RPKM 5.8) and 16 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1; 1 G1

See Hmcn1 in [Genome Data Viewer](#)

Exon count: 108

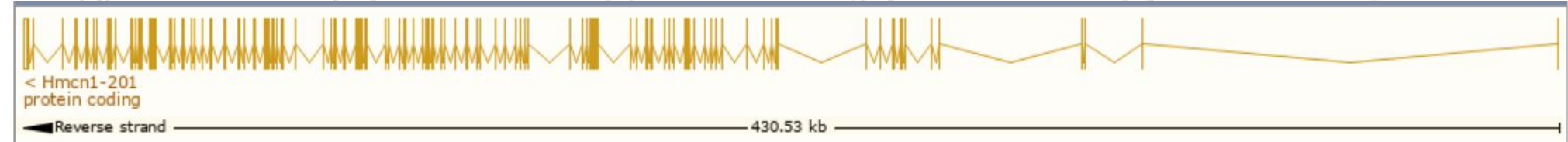
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (150562500..150993652, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (152409630..152840565, complement)

Transcript information (Ensembl)

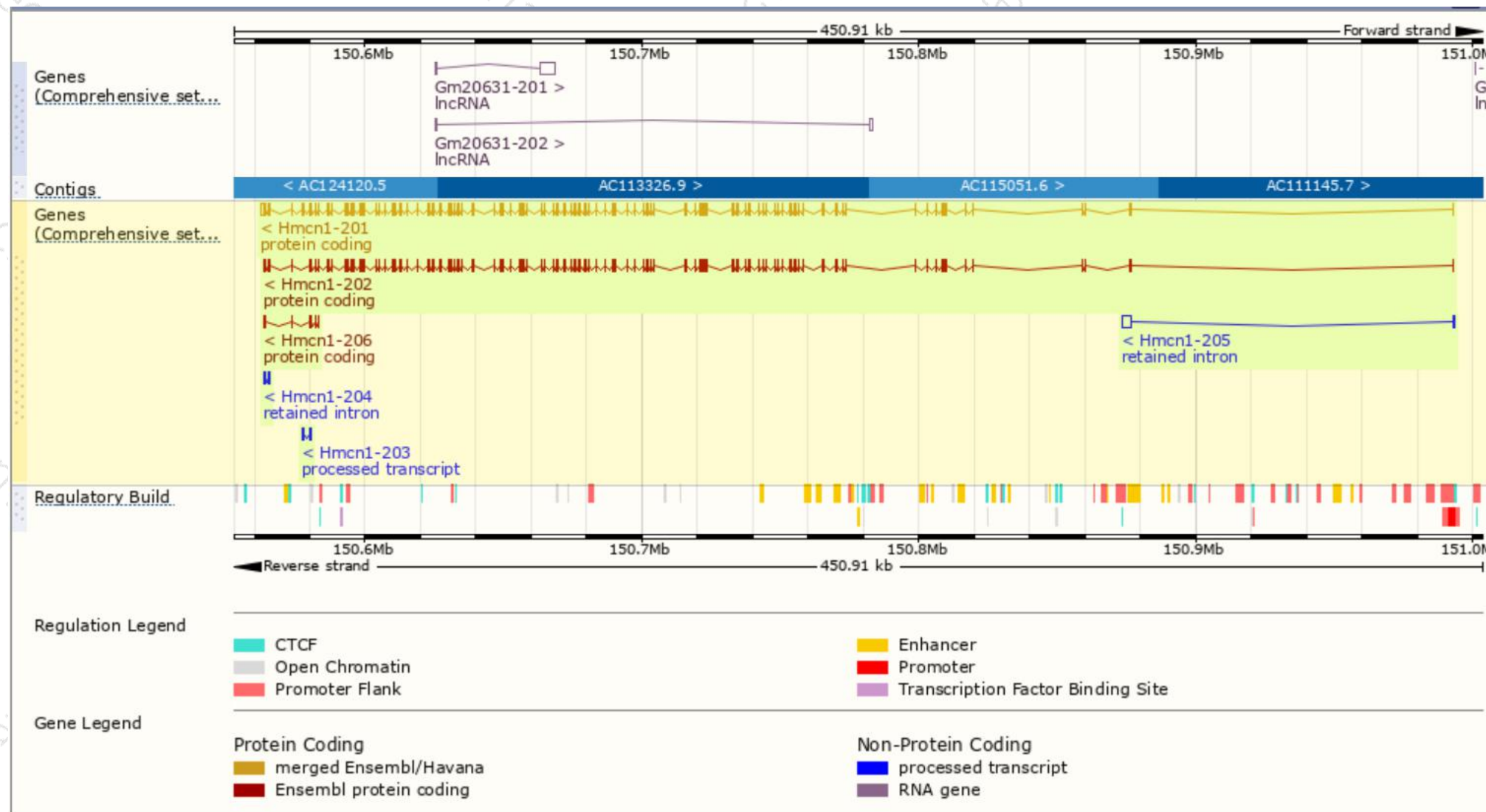
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmcn1-201	ENSMUST00000074783.11	17908	5634aa	Protein coding	CCDS15357	D3YXG0	TSL:5 GENCODE basic APPRIS P2
Hmcn1-202	ENSMUST00000137197.8	16554	5517aa	Protein coding	-	D3YXG0	TSL:5 GENCODE basic APPRIS ALT1
Hmcn1-206	ENSMUST00000177036.1	631	155aa	Protein coding	-	H3BJH2	CDS 5' incomplete TSL:5
Hmcn1-203	ENSMUST00000137909.1	378	No protein	Processed transcript	-	-	TSL:3
Hmcn1-205	ENSMUST00000155715.1	3400	No protein	Retained intron	-	-	TSL:1
Hmcn1-204	ENSMUST00000151899.1	471	No protein	Retained intron	-	-	TSL:2

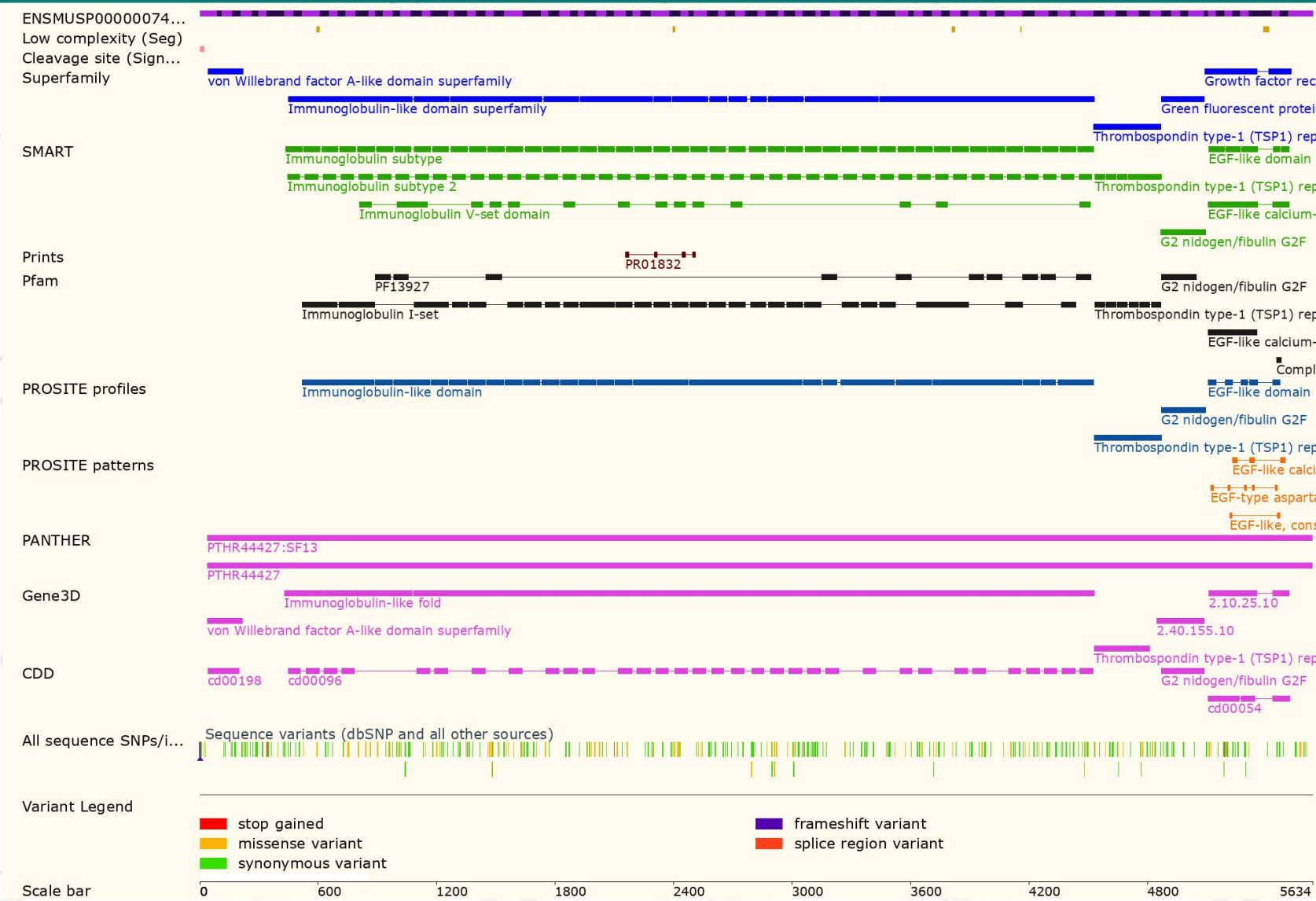
The strategy is based on the design of *Hmcn1-201* transcript,The transcription is shown below



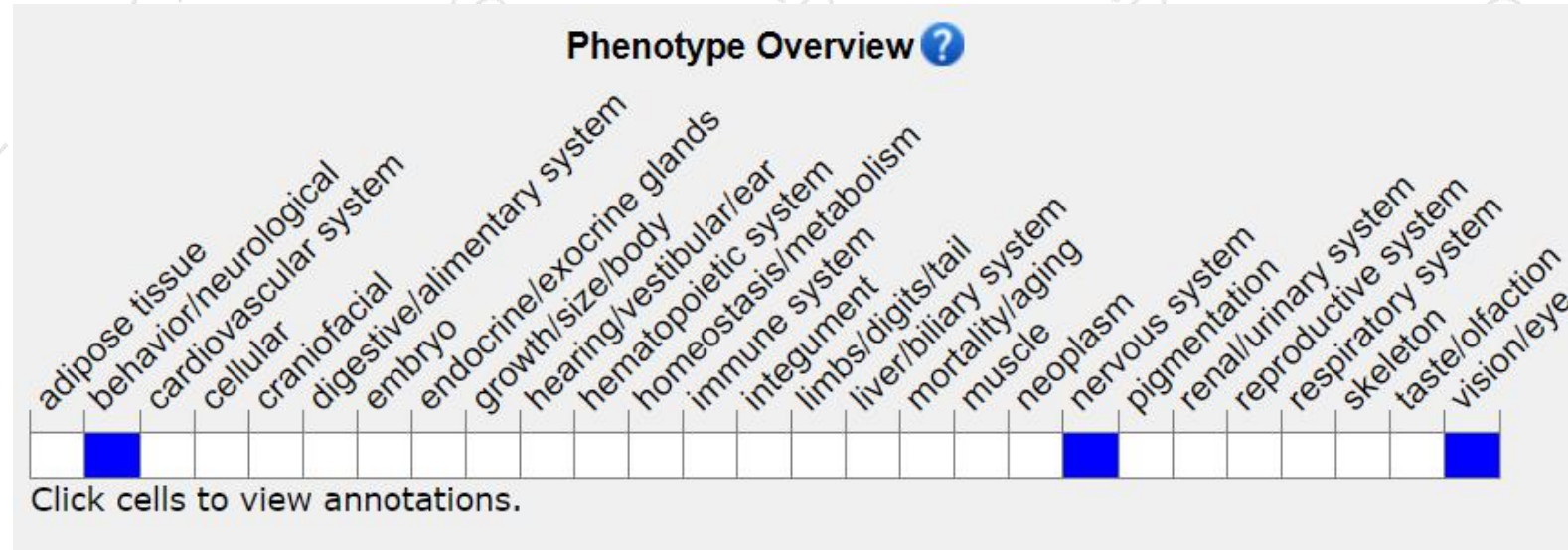
Genomic location distribution



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/>).

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

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