

Mast2 Cas9-KO Strategy

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Project Overview

Project Name

Mast2

Project type

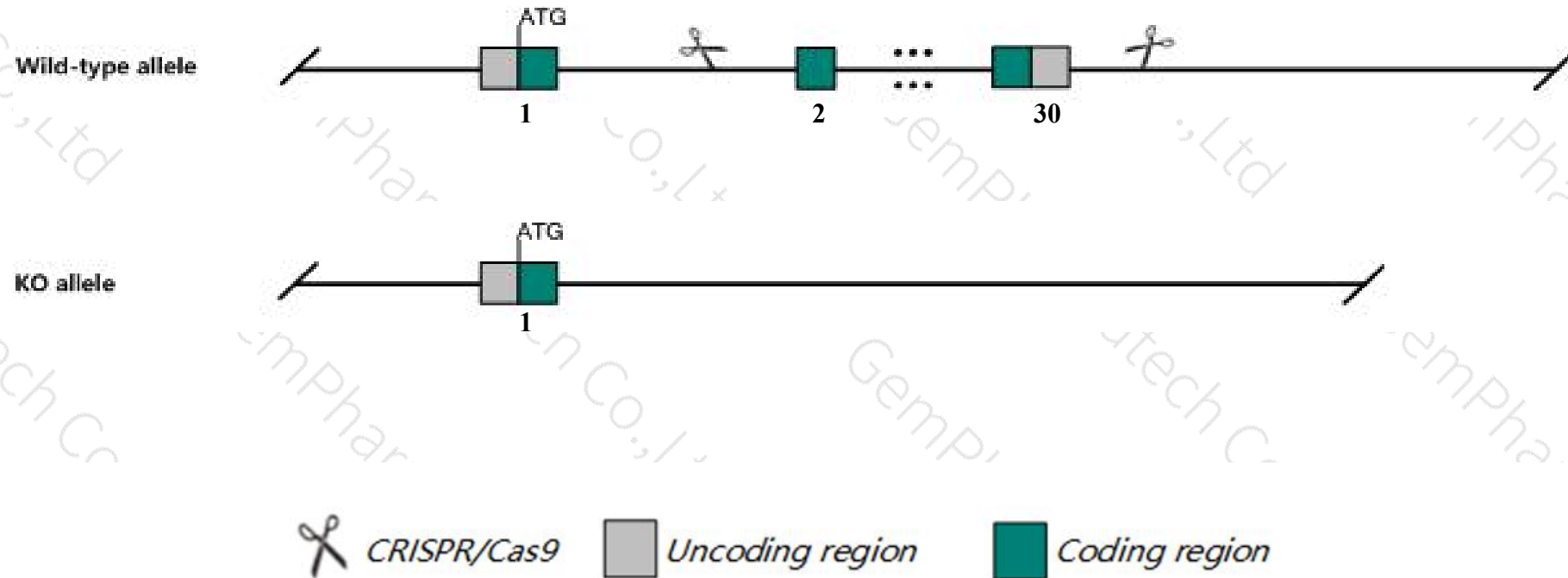
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mast2* gene. The schematic diagram is as follows:



- The *Mast2* gene has 15 transcripts. According to the structure of *Mast2* gene, exon2-exon30 of *Mast2*-204 (ENSMUST00000106486.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mast2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, No phenotype has been reported for a gene trap strain; however, it is not yet known whether the gene trap insertion affects expression of the gene.
- The *Mast2* gene is located on the Chr4. 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)

Mast2 microtubule associated serine/threonine kinase 2 [*Mus musculus* (house mouse)]

Gene ID: 17776, updated on 22-Jan-2020

Summary

- Official Symbol** Mast2 provided by [MGI](#)
- Official Full Name** microtubule associated serine/threonine kinase 2 provided by [MGI](#)
- Primary source** [MGI:MGI:894676](#)
- See related** [Ensembl:ENSMUSG00000003810](#)
- 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** Mtssk; MAST205
- Expression** Ubiquitous expression in testis adult (RPKM 24.2), CNS E18 (RPKM 23.0) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 4; 4 D1

See Mast2 in [Genome Data Viewer](#)

Exon count: 34

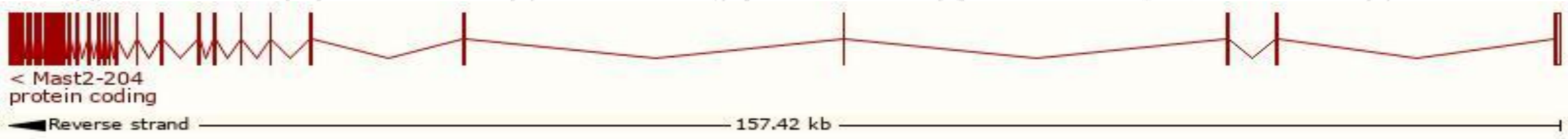
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (116306760..116464223, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (115979367..116136788, complement)

Transcript information (Ensembl)

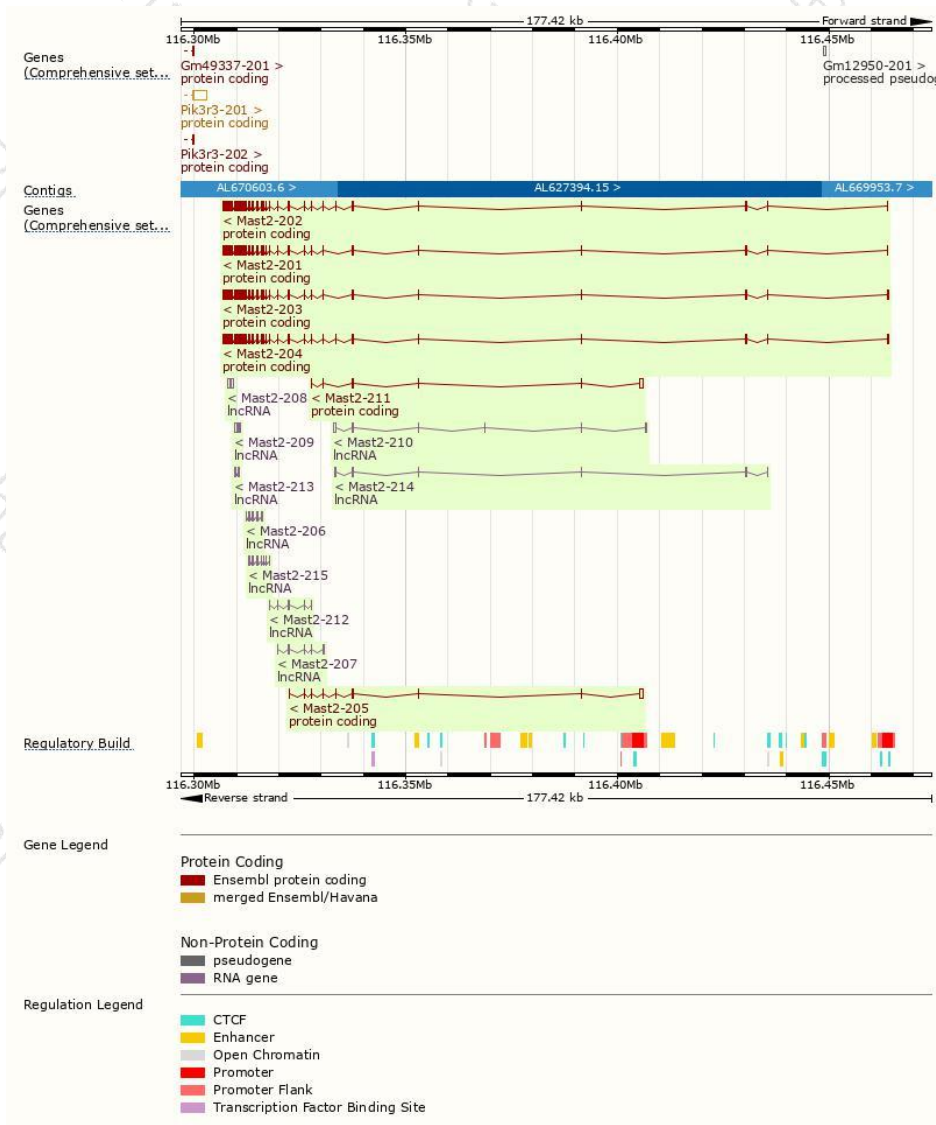
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mast2-204	ENSMUST00000106486.7	5723	1800aa	Protein coding	CCDS38850	E9Q1Q1	TSL:1 GENCODE basic APPRIS P4
Mast2-203	ENSMUST00000106485.7	5705	1794aa	Protein coding	CCDS38849	E9QLW6	TSL:1 GENCODE basic APPRIS ALT2
Mast2-201	ENSMUST0000003908.10	5445	1733aa	Protein coding	-	B1AST8	TSL:1 GENCODE basic APPRIS ALT2
Mast2-202	ENSMUST00000106484.7	5292	1739aa	Protein coding	-	B1AST7	TSL:1 GENCODE basic APPRIS ALT2
Mast2-205	ENSMUST00000123072.7	1195	203aa	Protein coding	-	B1AST5	CDS 3' incomplete TSL:3
Mast2-211	ENSMUST00000144281.1	1033	144aa	Protein coding	-	B1AST6	CDS 3' incomplete TSL:5
Mast2-208	ENSMUST00000128713.1	886	No protein	lncRNA	-	-	TSL:2
Mast2-215	ENSMUST00000156884.1	822	No protein	lncRNA	-	-	TSL:3
Mast2-206	ENSMUST00000123761.7	794	No protein	lncRNA	-	-	TSL:3
Mast2-210	ENSMUST00000134460.7	773	No protein	lncRNA	-	-	TSL:3
Mast2-207	ENSMUST00000128252.1	759	No protein	lncRNA	-	-	TSL:2
Mast2-209	ENSMUST00000131809.1	712	No protein	lncRNA	-	-	TSL:2
Mast2-214	ENSMUST00000151347.1	687	No protein	lncRNA	-	-	TSL:3
Mast2-212	ENSMUST00000147262.7	657	No protein	lncRNA	-	-	TSL:3
Mast2-213	ENSMUST00000147459.1	346	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Mast2-204* transcript,The transcription is shown below



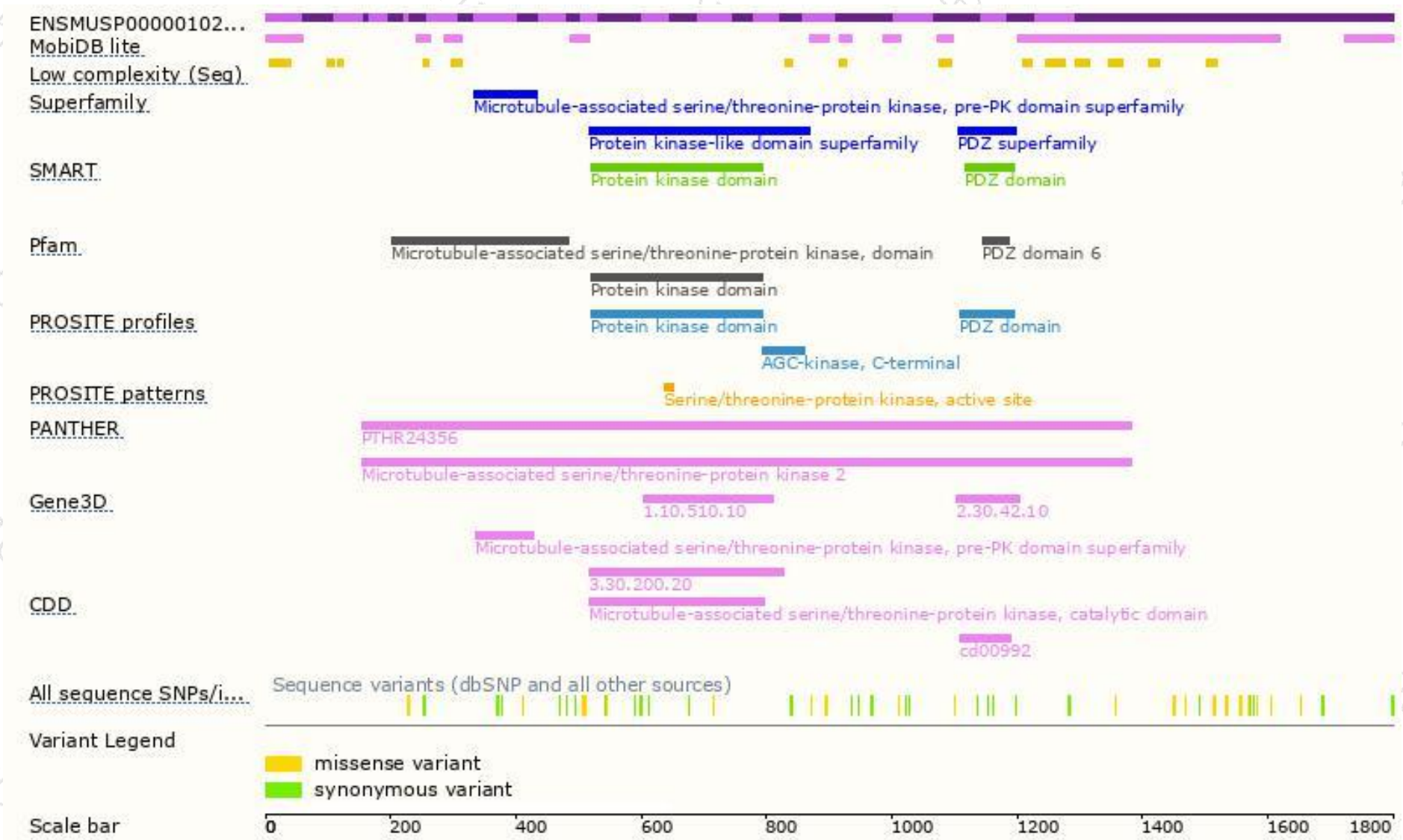
Genomic location distribution



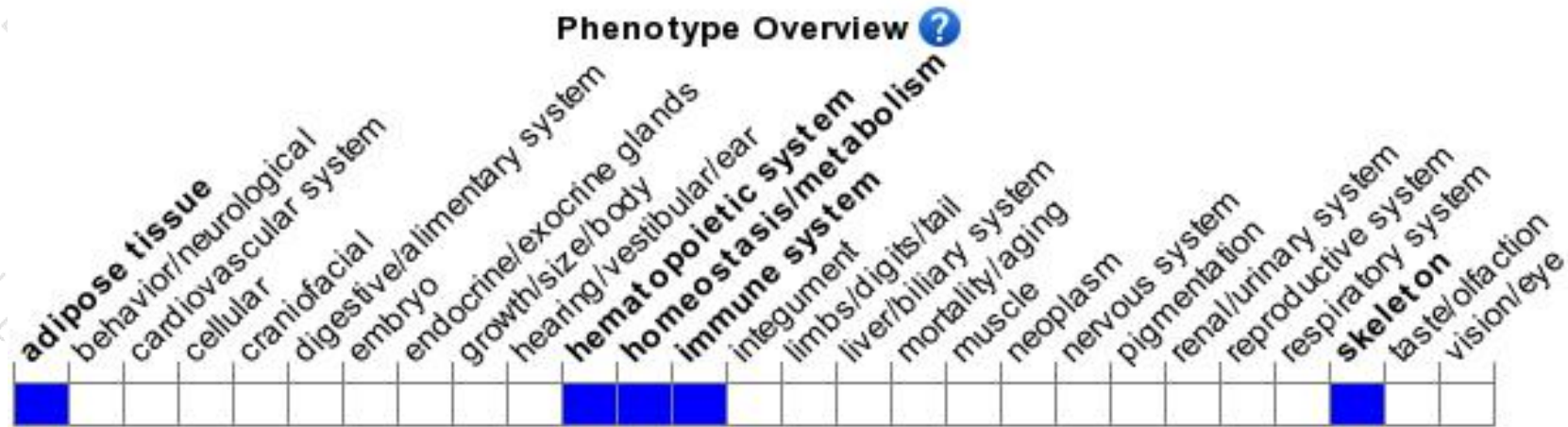
Protein domain



集萃药康
GemPharmatech



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, No phenotype has been reported for a gene trap strain; however, it is not yet known whether the gene trap insertion affects expression of the gene.

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

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