

Mst1r Cas9-KO Strategy

Designer:

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Project Overview



Project Name

Mst1r

Project type

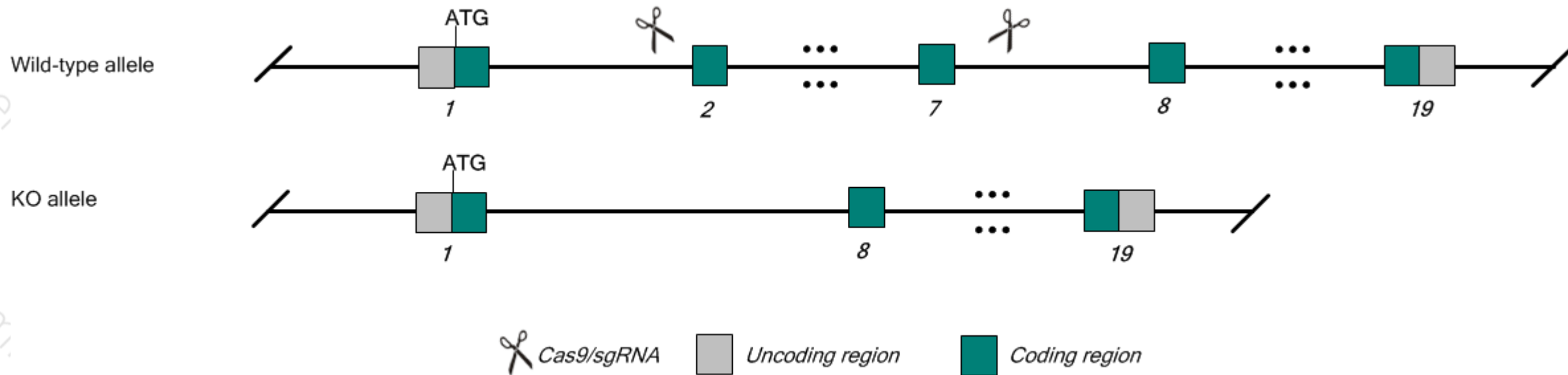
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mst1r* gene. The schematic diagram is as follows:



Technical routes

- The *Mst1r* gene has 4 transcripts, According to the structure of *Mst1r* gene, exon2-7 of *Mst1r-201* transcript is recommended as the knockout region. The region contains the 953bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mst1r* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data , This locus controls susceptibility to splenomegaly or spleen focus formation induced by inoculation with Friend leukemia virus.
- Transcript *Mst1r-202*, *Mst1r-203* may not be affected.
- The *Mst1r* gene is located in the Chr9. 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)

Mst1r macrophage stimulating 1 receptor (c-met-related tyrosine kinase) [*Mus musculus* (house mouse)]

Gene ID: 19882, updated on 31-Jan-2019

Summary

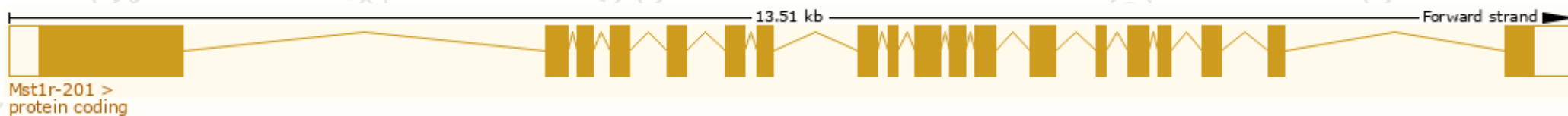
Official Symbol	Mst1r provided by MGI
Official Full Name	macrophage stimulating 1 receptor (c-met-related tyrosine kinase) provided by MGI
Primary source	MGI:MGI:99614
See related	Ensembl:ENSMUSG000000032584
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Fv2; Ron; STK; Fv-2; PTK8; CD136; CDw136
Summary	This gene encodes a precursor protein that is proteolytically cleaved to yield an alpha chain and a beta chain which form a membrane-spanning heterodimer. The encoded protein belongs to a family of cell-surface receptor tyrosine kinases involved in signaling from the cell surface to the intracellular environment. The binding of the encoded protein to its ligand, macrophage-stimulating protein, mediates several biological activities including wound healing, tumor immunity, macrophage activation and hematopoiesis as well as cell growth, motility, survival and adhesion. The protein encoded by this gene also functions in early development and the macrophage-mediated inflammatory response. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Dec 2013]
Expression	Biased expression in stomach adult (RPKM 26.6), colon adult (RPKM 26.4) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

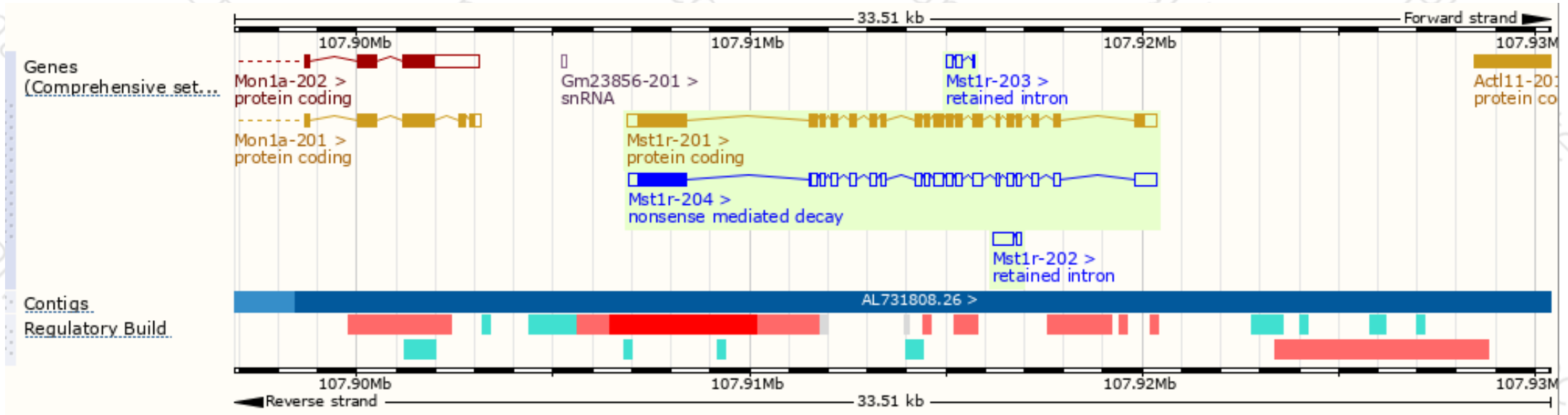
The gene has 4 transcripts, and all transcripts are shown below :

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Mst1r-201	ENSMUST00000035203.8	4722	1378aa	Protein coding	CCDS23509	Q62190	NM_009074 NP_033100	TSL:1 GENCODE basic APPRIS P1
Mst1r-204	ENSMUST00000195617.5	4717	442aa	Nonsense mediated decay	-	A0A0A6YXY9	NR_109782	TSL:1
Mst1r-202	ENSMUST00000194527.1	600	No protein	Retained intron	-	-	-	TSL:3
Mst1r-203	ENSMUST00000195113.1	345	No protein	Retained intron	-	-	-	TSL:3

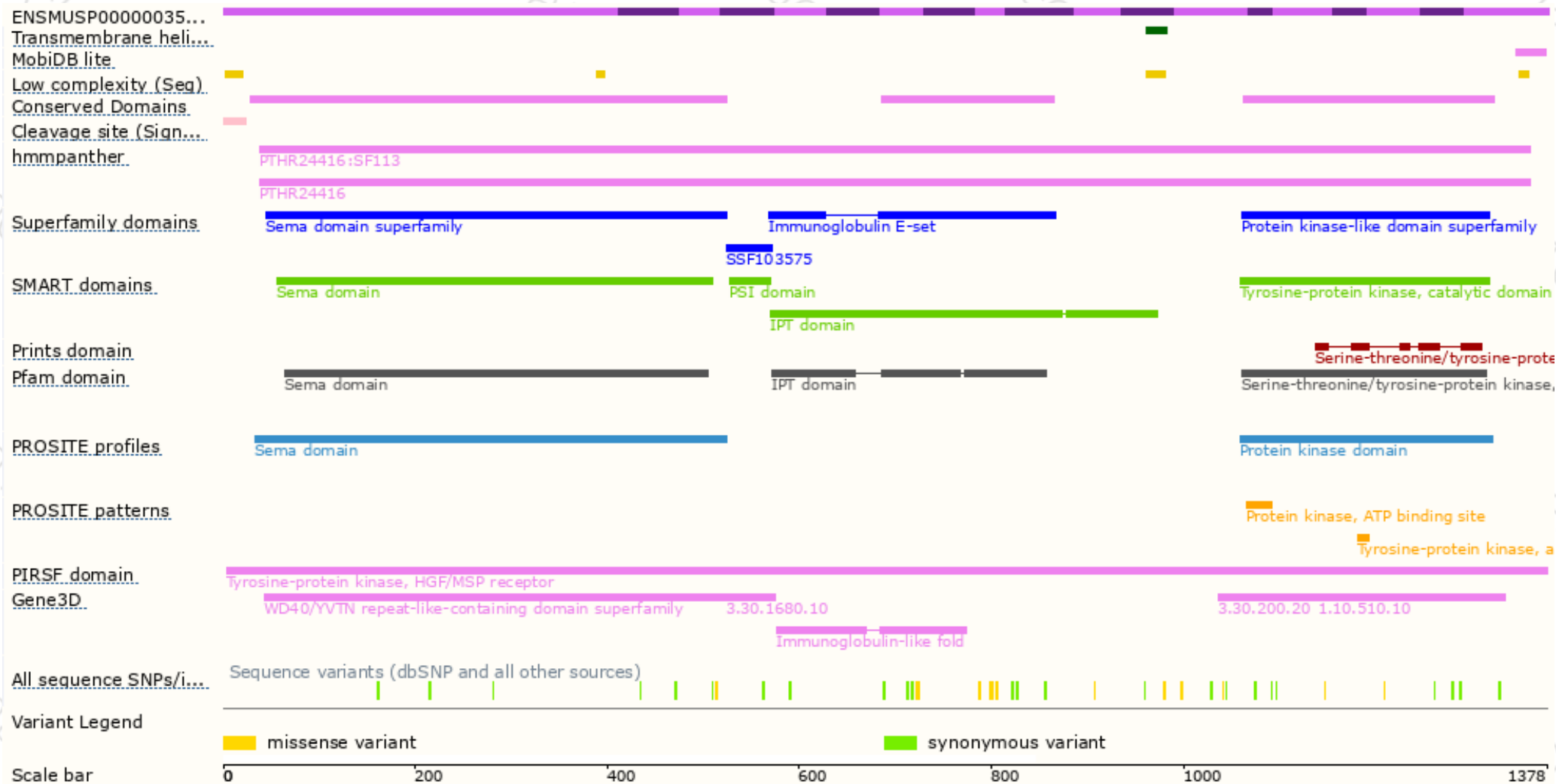
The strategy is based on the design of *Mst1r-201* transcript, The transcription is shown below



Genomic location distribution



Protein domain



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

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