

Malt1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Malt1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Malt1* gene. The schematic diagram is as follows:



- The *Malt1* gene has 13 transcripts. According to the structure of *Malt1* gene, exon2 of *Malt1-201* (ENSMUST00000049248.6) transcript is recommended as the knockout region. The region contains 167bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Malt1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous inactivation of this gene disrupts normal B cell development and leads to impaired cytokine production and T cell and B cell proliferative responses after antigen receptor engagement due to failure of NF-kappaB activation.
- The *Malt1* gene is located on the Chr18. 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)

Malt1 MALT1 paracaspase [*Mus musculus* (house mouse)]

Gene ID: 240354, updated on 13-Jan-2020

Summary

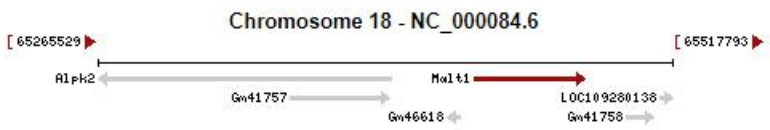
- Official Symbol Malt1 provided by [MGI](#)
- Official Full Name MALT1 paracaspase provided by [MGI](#)
- Primary source [MGI:MGI:2445027](#)
- See related [Ensembl:ENSMUSG00000032688](#)
- Gene type protein coding
- RefSeq status VALIDATED
- Organism [Mus musculus](#)
- Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as Pcas1; A630046N12; D430033E09Rik
- Expression Ubiquitous expression in spleen adult (RPKM 11.3), mammary gland adult (RPKM 4.9) and 27 other tissues [See more](#)
- Orthologs [human](#) [all](#)

Genomic context

Location: 18; 18 E1 See Malt1 in [Genome Data Viewer](#)

Exon count: 18

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (65430939..65478888)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (65590651..65638446)

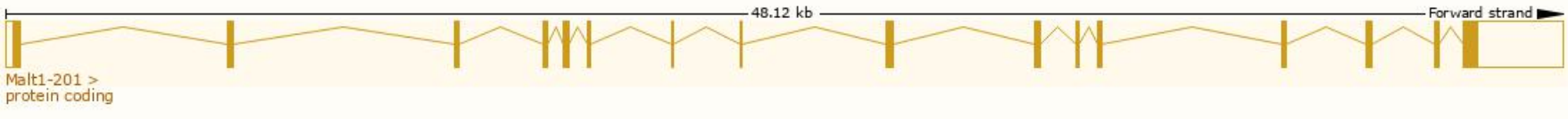


Transcript information (Ensembl)

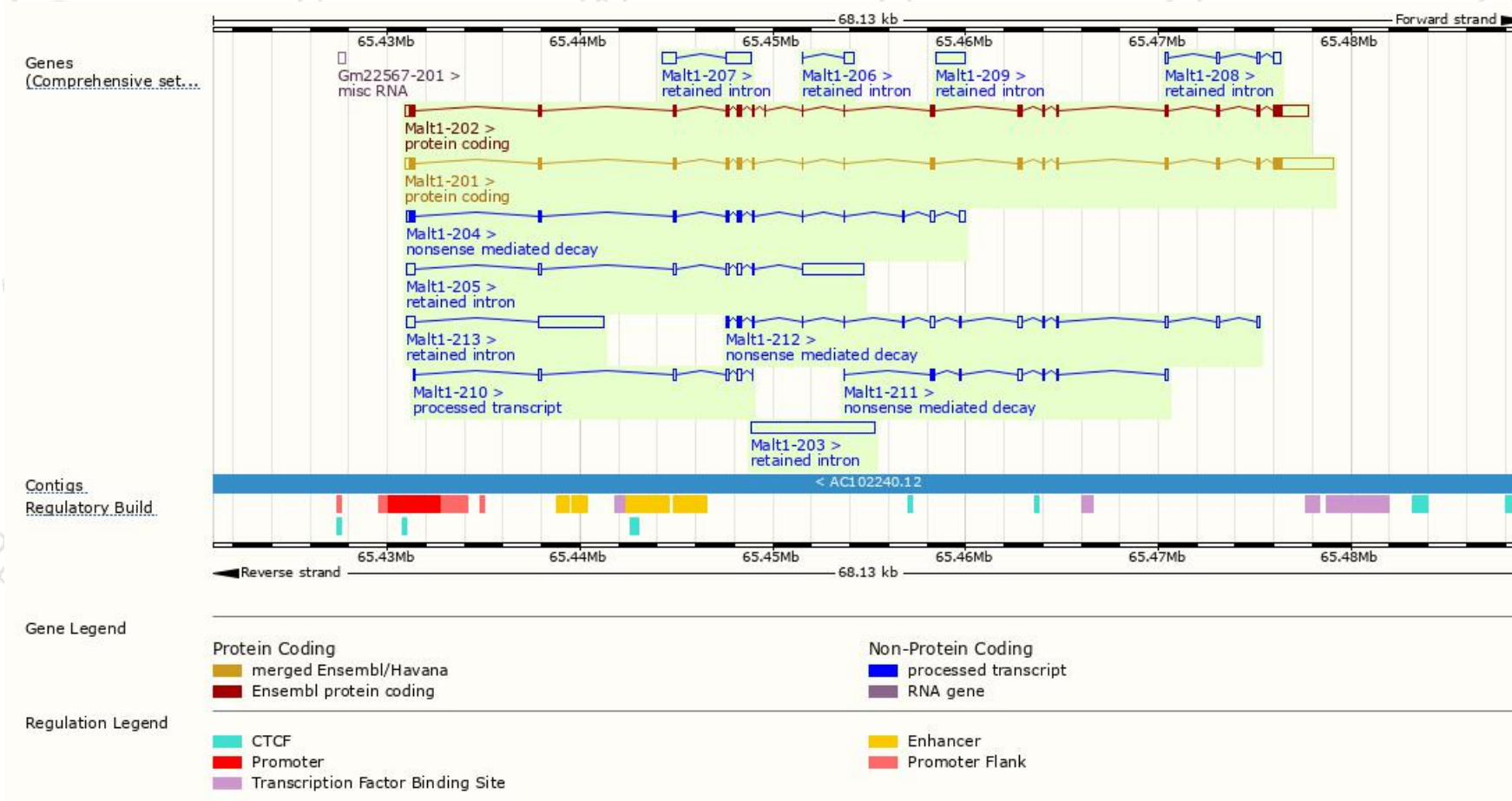
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Malt1-201	ENSMUST00000049248.6	5331	821aa	Protein coding	CCDS29306	Q2TBA3	TSL:1 GENCODE basic APPRIS P2
Malt1-202	ENSMUST000000224056.2	4113	832aa	Protein coding	-	Q2TBA3	GENCODE basic APPRIS ALT2
Malt1-204	ENSMUST000000224265.1	1834	342aa	Nonsense mediated decay	-	A0A494BBJ5	-
Malt1-212	ENSMUST000000237488.1	1649	170aa	Nonsense mediated decay	-	A0A494BAG3	CDS 5' incomplete
Malt1-211	ENSMUST000000236314.1	829	98aa	Nonsense mediated decay	-	A0A494BBB5	CDS 5' incomplete
Malt1-210	ENSMUST000000236284.1	702	No protein	Processed transcript	-	-	-
Malt1-203	ENSMUST000000224229.1	6404	No protein	Retained intron	-	-	-
Malt1-205	ENSMUST000000225085.1	4316	No protein	Retained intron	-	-	-
Malt1-213	ENSMUST000000237739.1	3785	No protein	Retained intron	-	-	-
Malt1-207	ENSMUST000000235209.1	2036	No protein	Retained intron	-	-	-
Malt1-209	ENSMUST000000236050.1	1540	No protein	Retained intron	-	-	-
Malt1-208	ENSMUST000000235999.1	807	No protein	Retained intron	-	-	-
Malt1-206	ENSMUST000000225659.1	556	No protein	Retained intron	-	-	-

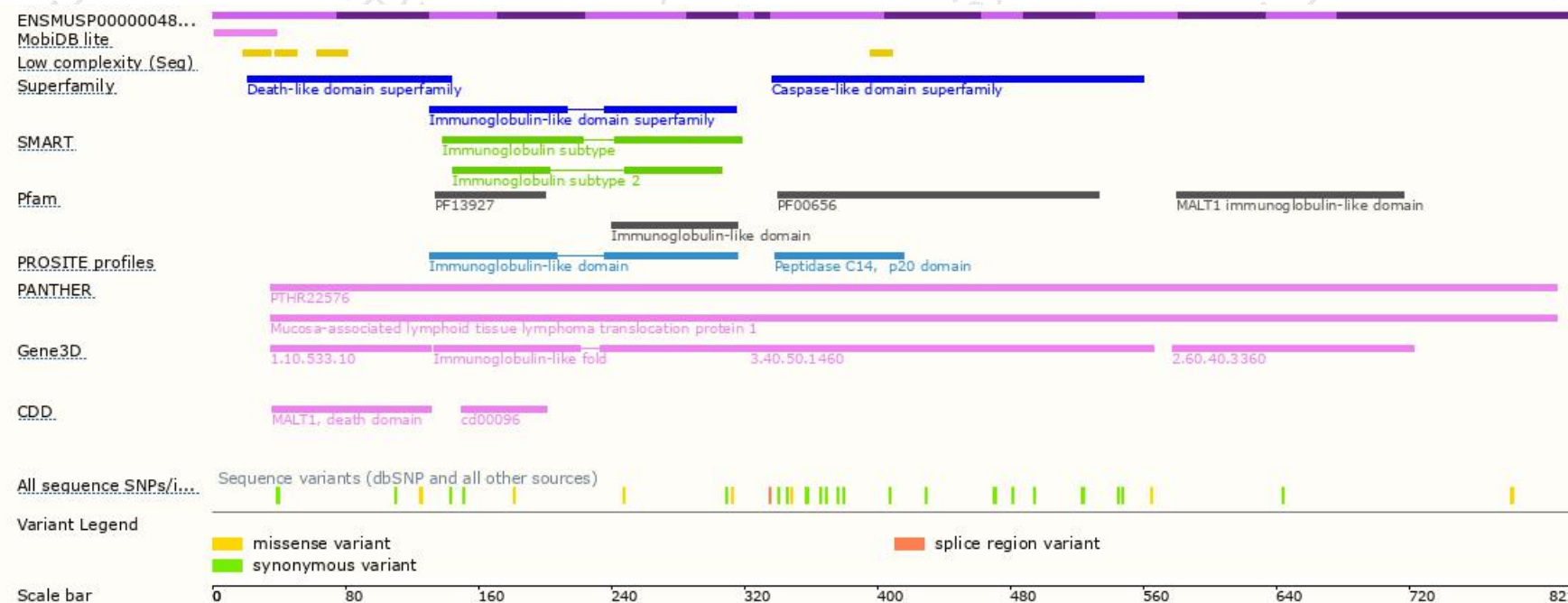
The strategy is based on the design of *Malt1-201* transcript,The transcription is shown below



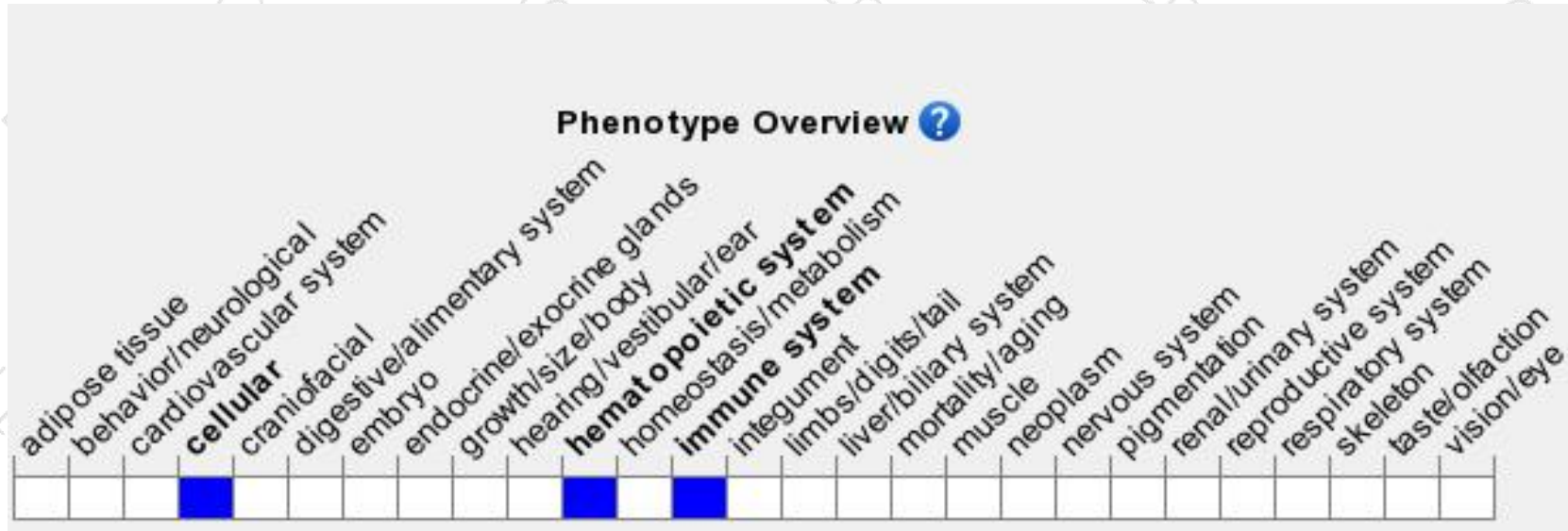
Genomic location distribution



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/>).

According to the existing MGI data, Homozygous inactivation of this gene disrupts normal B cell development and leads to impaired cytokine production and T cell and B cell proliferative responses after antigen receptor engagement due to failure of NF-kappaB activation.

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

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