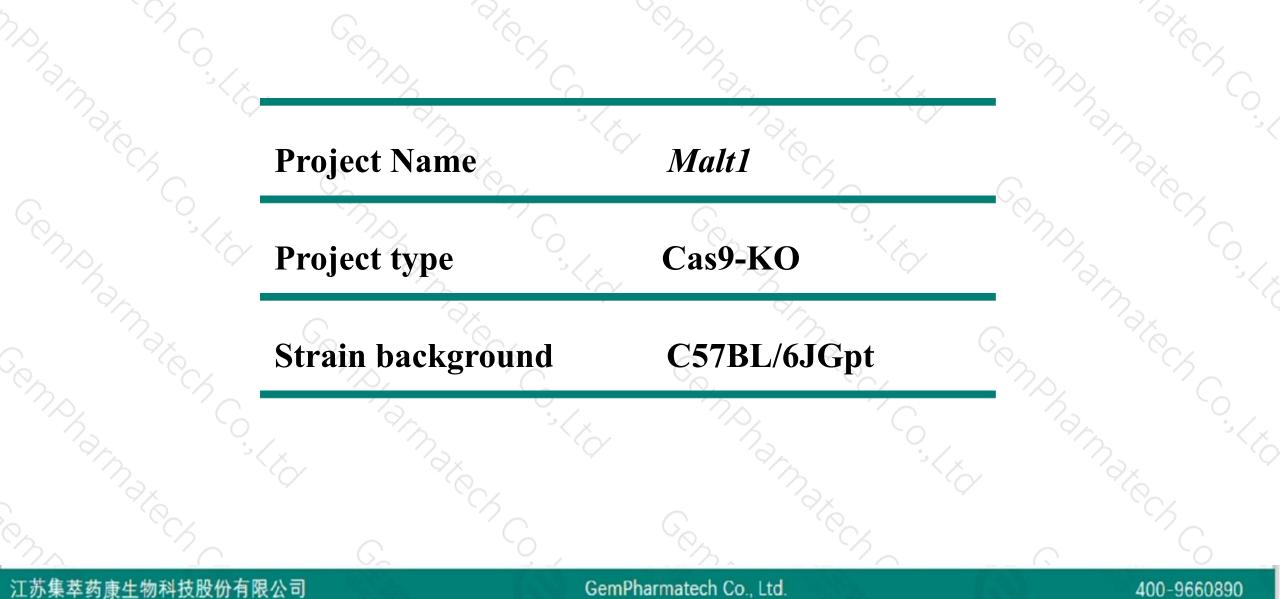


Malt1 Cas9-KO Strategy

Designer: Reviewer: Design Date: Huimin Su Ruirui Zhang 2020-1-22

Project Overview

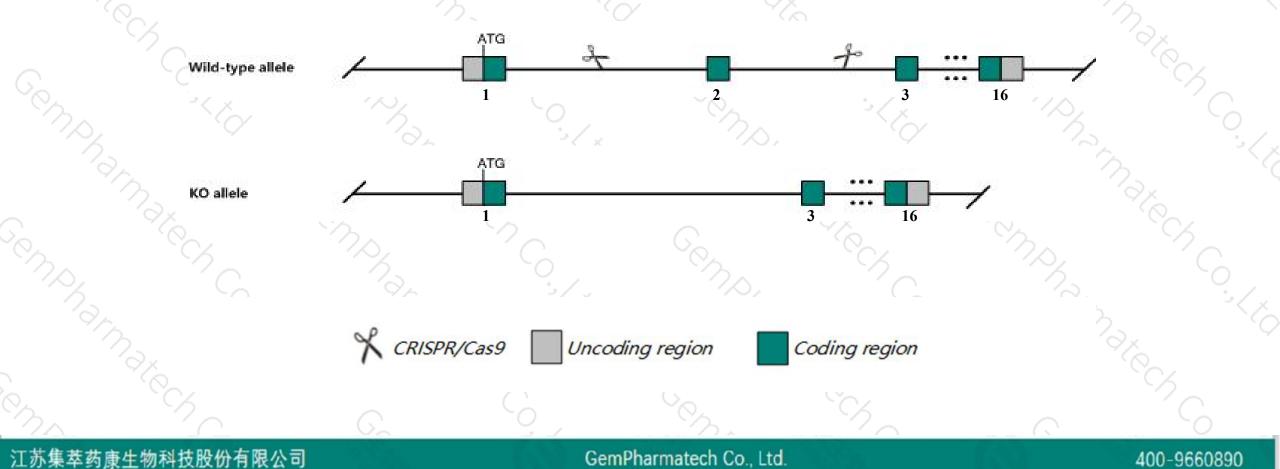




Knockout strategy



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

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- 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.

Notice

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Annotation release

108 Build 37.2

Gene information (NCBI)

Malt1 MALT1 paracaspase [Mus musculus (house mouse)]

Status

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Gene ID: 240354, updated o	n 13-Jan-2020	3
"ann	Summary		12
$\gamma_{\rm Ox}$	Official Symbol	Malt1 provided by MGI	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Official Full Name	MALT1 paracaspase provided by MGI	
Y N	Primary source	MGI:MGI:2445027	
	See related	Ensembl:ENSMUSG00000032688	
	Gene type	protein coding	
	RefSeq status		
G	Organism	Mus musculus	
	Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;	つふ
		Murinae; Mus; Mus	
		Pcasp1; A630046N12; D430033E09Rik	
		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		
0	Location: 18; 18 E1	See Malt1 in Genome Data Viewee	<u>:r</u>
YO_	Exon count: 18		
	21 577 - 05 (1 - 2012)		\sim

[6526	Chromosome 18 - NC_000084.6		65517793 ▶
 previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (6559065165638446)
current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (6543093965478888)

Assembly



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Chr

Location



Transcript information (Ensembl)



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

Name 🍦	Transcript ID	bp 🖕	Protein 💧	Biotype 🖕	CCDS	UniProt	Flags	
Malt1-201	ENSMUST0000049248.6	5331	<u>821aa</u>	Protein coding	<u>CCDS29306</u> 교	Q2TBA3₽	TSL:1 GENCODE basic APPRIS P2	
Malt1-202	ENSMUST00000224056.2	4113	<u>832aa</u>	Protein coding	-	Q2TBA3₫	GENCODE basic APPRIS ALT2	
Malt1-204	ENSMUST00000224265.1	1834	<u>342aa</u>	Nonsense mediated decay	-	A0A494BBJ5@	-	
Malt1-212	ENSMUST00000237488.1	1649	<u>170aa</u>	Nonsense mediated decay	<u> </u>	A0A494BAG3	CDS 5' incomplete	
Malt1-211	ENSMUST00000236314.1	829	<u>98aa</u>	Nonsense mediated decay	2	<u>A0A494BBB5</u> @	CDS 5' incomplete	
Malt1-210	ENSMUST00000236284.1	702	No protein	Processed transcript	23	9 <u>7</u>		
Malt1-203	ENSMUST00000224229.1	6404	No protein	Retained intron	5	a . .	-	
Malt1-205	ENSMUST00000225085.1	4316	No protein	Retained intron	5	5		
Malt1-213	ENSMUST00000237739.1	3785	No protein	Retained intron	70		1 0	
Malt1-207	ENSMUST00000235209.1	2036	No protein	Retained intron	-			
Malt1-209	ENSMUST00000236050.1	1540	No protein	Retained intron	-	-	-	
Malt1-208	ENSMUST00000235999.1	807	No protein	Retained intron	¥:	12	-	
Malt1-206	ENSMUST00000225659.1	556	No protein	Retained intron	2	2	123	
	trage are to							

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

48.12 kb

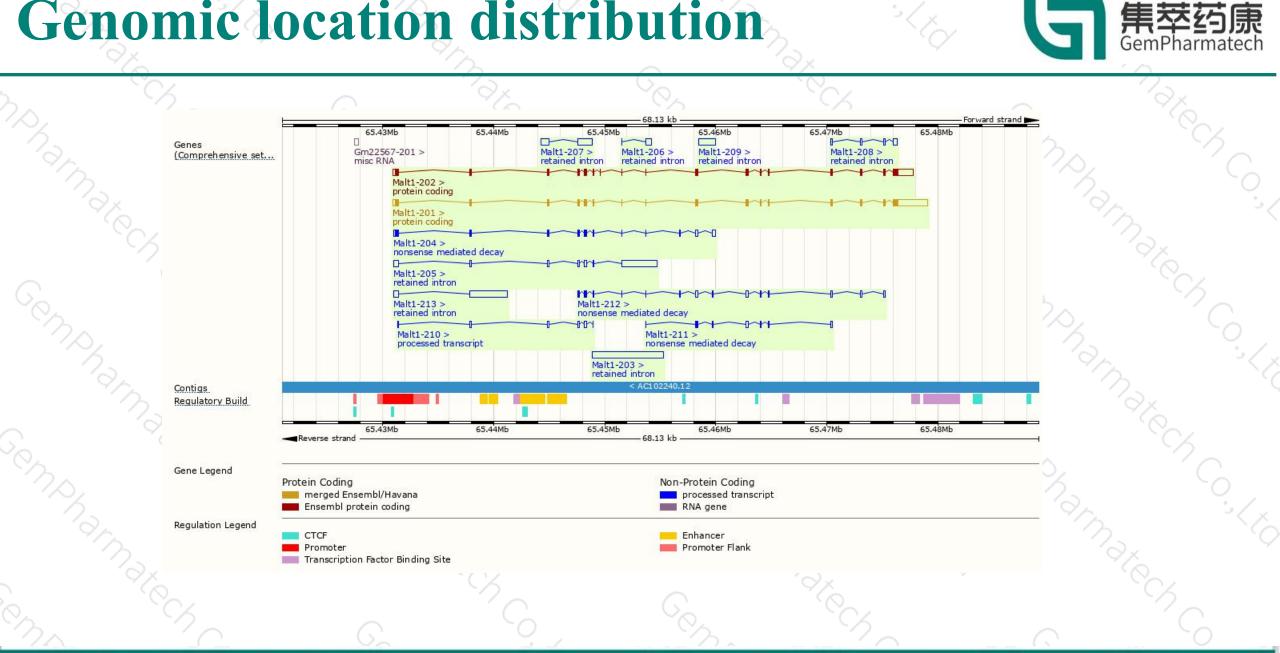
Malt1-201 > protein coding

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Forward stran

Genomic location distribution



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Protein domain



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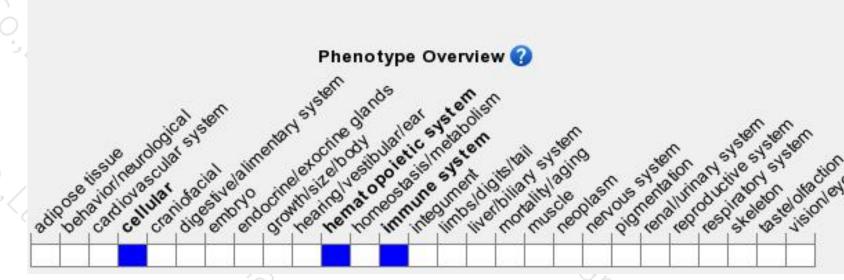
~?				C'AS			Geo	
	ENSMUSP00000048 MobiDB lite Low.complexity (Seg) Superfamily	Death-like domain superfamily		Caspase-like domain superfam	ily		<u></u>	6
, 	SMART	Immuno	obulin-like domain superfamily globulin subtype					Max is a
	Pfam.	Immun PF13927	oglobulin subtype 2 Immunoglobulin-lik	PF00656 ke domain	MALT1	immunoglobulin-like domain		
	PROSITE profiles PANTHER	PTHR22576	obulin-like domain	Peptidase C14, p20 domain				C C
	Gene3D		ue lymphoma translocation protein Iobulin-like fold	3.40.50.1460	2.60.40	.3360	120	. <
	CDD	MALT1, death domain cd000	96					
97	All sequence SNPs/i Variant Legend	Sequence variants (dbSNP and all ot	her sources)	INCOME TO F	III III	1	- X	² CA
		missense variant synonymous variant		splice	region variant			~ C_
	Scale bar	0 80 160	240	320 400	480 560	640 720	821	
×× °C	3	G.	C.	George State		5		° S S

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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.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



