# Ifih1 Cas9-KO Strategy Rondhamater Co-ty

**Designer:** Emphamater Co. 1 to

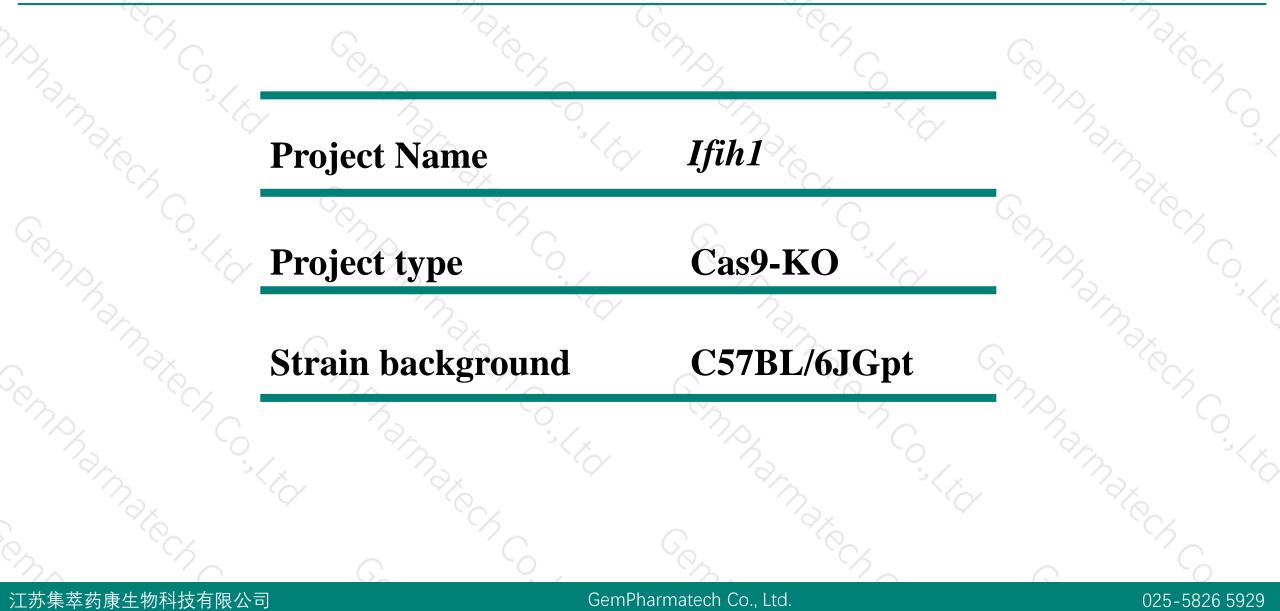
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## **Project Overview**



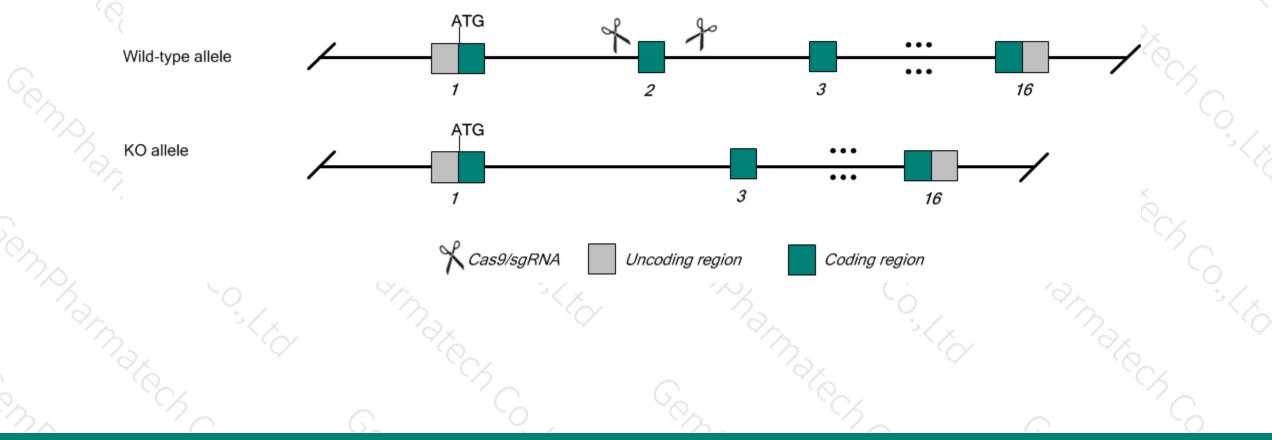


### **Knockout strategy**



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This model will use CRISPR/Cas9 technology to edit the *Ifih1* gene. The schematic diagram is as follows:



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- The Ifih1 gene has 5 transcripts, According to the structure of *Ifih1* gene, exon2 of Ifih1-201 transcript is recommended as the knockout region. The region contains the 169bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ifih1* 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, Mice homozygous for a null allele have increased virus-associated morbidity and mortality, and decreased cytokine response to several viral infection.
- The *Ifih1* gene is located in the Chr2. 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.

Notice

# Gene information (NCBI)



#### Ifih1 interferon induced with helicase C domain 1 [ Mus musculus (house mouse) ]

Gene ID: 71586, updated on 5-Feb-2019

📥 Summary

Official SymbolIfh1 provided by MGIOfficial Full Nameinterferon induced with helicase C domain 1 provided by MGIPrimary sourceMGI:MGI:1918836See relatedEnsembl:ENSMUSG0000026896Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;<br/>Myomorpha; Muroidea; Murinae; Mus; MusAlso known asHIcd; MDA5; RLR-2; Helicard; 9130009C22RikOrthologbuman all

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# Transcript information (Ensembl ) 第譯語

The gene has 5 transcripts, and all transcripts are shown below :

Name 🍦	Transcript ID 🛛 🍦	bp 🖕 Protein 🌲		Biotype 🍦	CCDS 🖕	UniProt 🍦	RefSeq 🍦	Flags 🍦		
lfih1-201	ENSMUST0000028259.11	5470	<u>1025aa</u>	Protein coding	<u>CCDS16068</u> &	<u>D2CGM4</u> @ <u>Q8R5F7</u> ജ	<u>NM_027835</u> <u>NP_082111</u>	TSL:1 GENCODE basic APPRIS P3		
lfih1-202	ENSMUST00000112459.3	3616	<u>976aa</u>	Protein coding	<u>CCDS50594</u> @	<u>Q8R5F7</u> 🗗	<u>NM_001164477</u> ₽ <u>NP_001157949</u> ₽	TSL:1 GENCODE basic APPRIS ALT2		
lfih1-204	ENSMUST00000176388.1	439	No protein	Processed transcript	-	-	-	TSL:3		
lfih1-205	ENSMUST00000176431.7	2904	No protein	Retained intron	-	-	-	TSL:2		
lfih1-203	ENSMUST00000175964.1	2565	No protein	Retained intron	-	-	-	TSL:2		

The strategy is based on the design of *Ifih1-201* transcript, The transcription is shown below



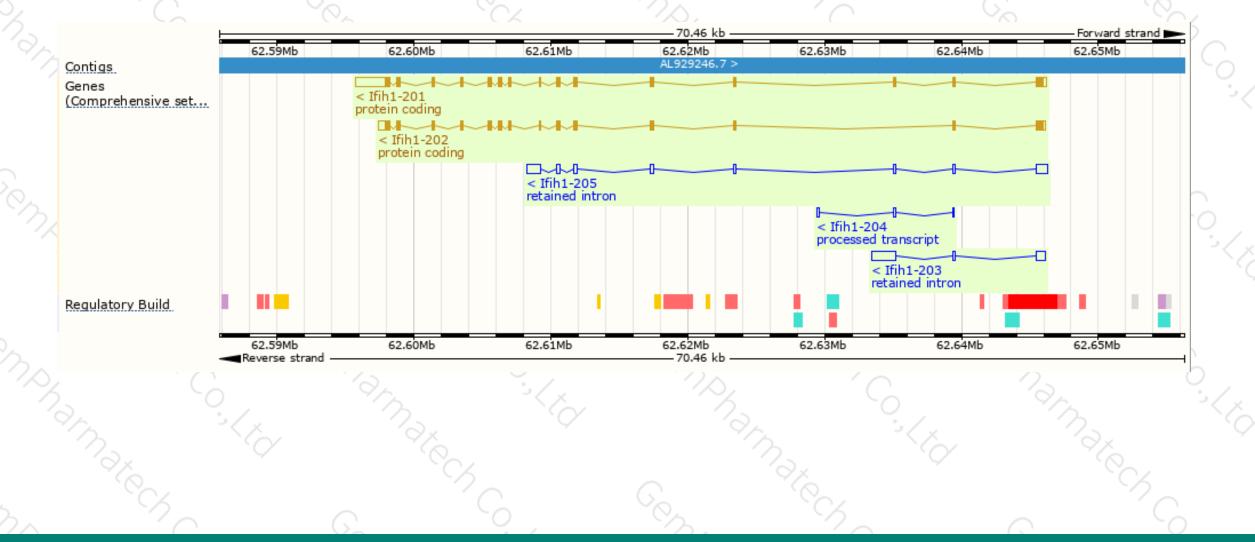
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## **Genomic location distribution**





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# **Protein domain**



	hmmpanther Superfamily domains	PTHR14074:SF14 PTHR14074		omain superfan	ailu	Peloon co	ntaining pus	eoside triv	ohosphate hydrolas					—	و*
	SMART domains				-		ily 1/2, ATP-				licase, C-terminal			(	
	Pfam domain	Caspase recruitn	nent domain	-	Helicase	e/UvrB, N-I	terminal	•		Helicase	, C-terminal	RIG-1	(-like rec	eptor, C	6
2	PROSITE profiles				Helica	se superfa	mily 1/2, AT	P-binding	domain	Helicase,	C-terminal	RIG-I-	ike recej	otor, C-te	34
	Gene3D	1.10.533.10	_		3.40.50	.300			1.20.1320.30			RIG-I-I	ike recep	stor, C-te	
	All sequence SNPs/i Variant Legend	Sequence varia	nts (dbSNP a	and all other so	ources)	- I	1	1 1	1 1 11 1		11			<u> </u>	S
	_		synonymous variant												
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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



