# Cilp2 Cas9-KO Strategy Rondhamater Co.

**Designer:** Emphamater Co. 1 to

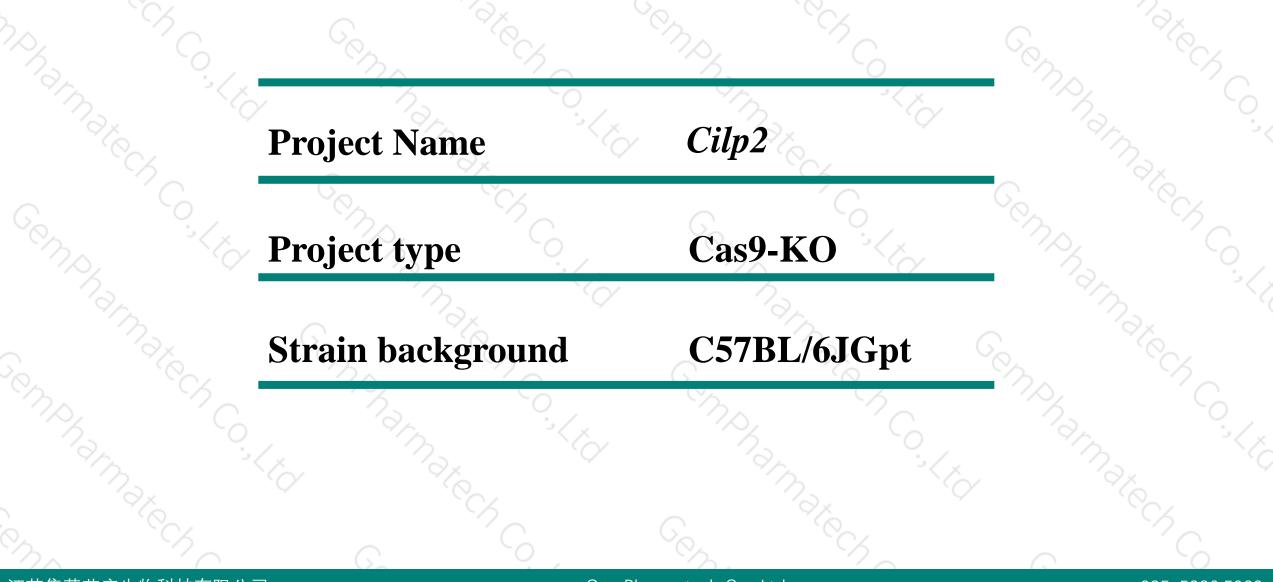
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# **Project Overview**



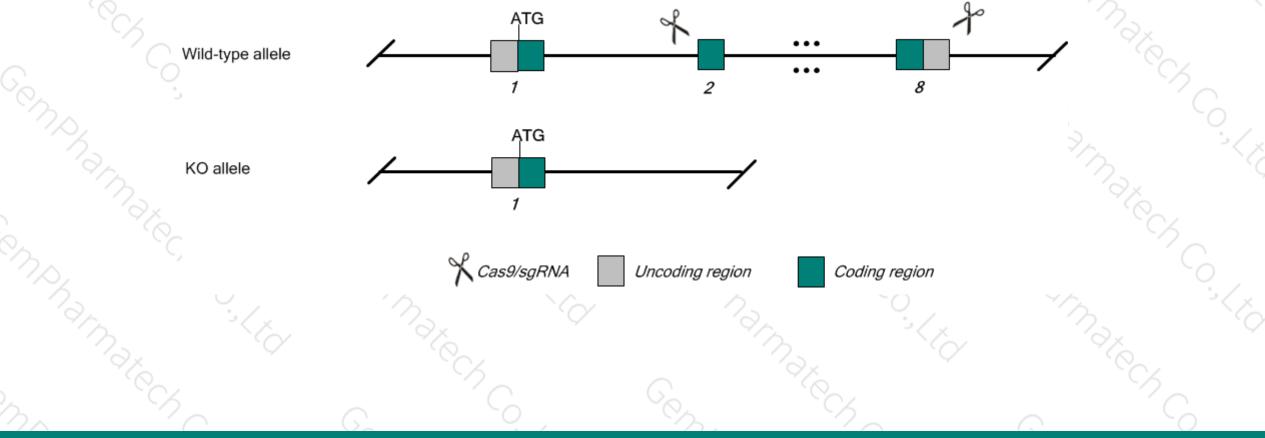


# **Knockout strategy**



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This model will use CRISPR/Cas9 technology to edit the Cilp2 gene. The schematic diagram is as follows:



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- The Cilp2 gene has 1 transcripts, According to the structure of *Cilp2* gene, exon2-8 of Cilp2-201 transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cilp2* 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.

- The *Cilp2* gene is located on the Chr8. 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)



### Cilp2 cartilage intermediate layer protein 2 [ Mus musculus (house mouse) ]

Summary

Official SymbolCilp2 provided by MGIOfficial Full Namecartilage intermediate layer protein 2 provided by MGIPrimary soureMGI:MGI:1915959See relatedEnsembl:ENSMUSG00000044006Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;<br/>Myomorpha; Muroidea; Murinae; Mus; MusAlso known asCLIP-2; AA407300; 1110031k/21RikExpressionBroad expression in heart adult (RPKM 6.0), whole brain E14.5 (RPKM 3.6) and 15 other tissues See more<br/>human all

Gene ID: 68709, updated on 31-Jan-2019

# Transcript information (Ensembl ) 第標語

The gene has 1 transcripts, and the transcript is shown below :

Name 🍦	Transcript ID 🛛 🍦	bp 🌲	Protein 🖕	Biotype 🍦	CCDS 🖕	UniProt 🌲	RefSeq 🍦		Flags	+
Cilp2-201	ENSMUST0000057831.7	4314	<u>1162aa</u>	Protein coding	<u>CCDS40363</u> &	<u>D3Z7H8</u> @	<u>NM_026818</u> ស NP_081094ស	TSL:5	GENCODE basic	APPRIS P1

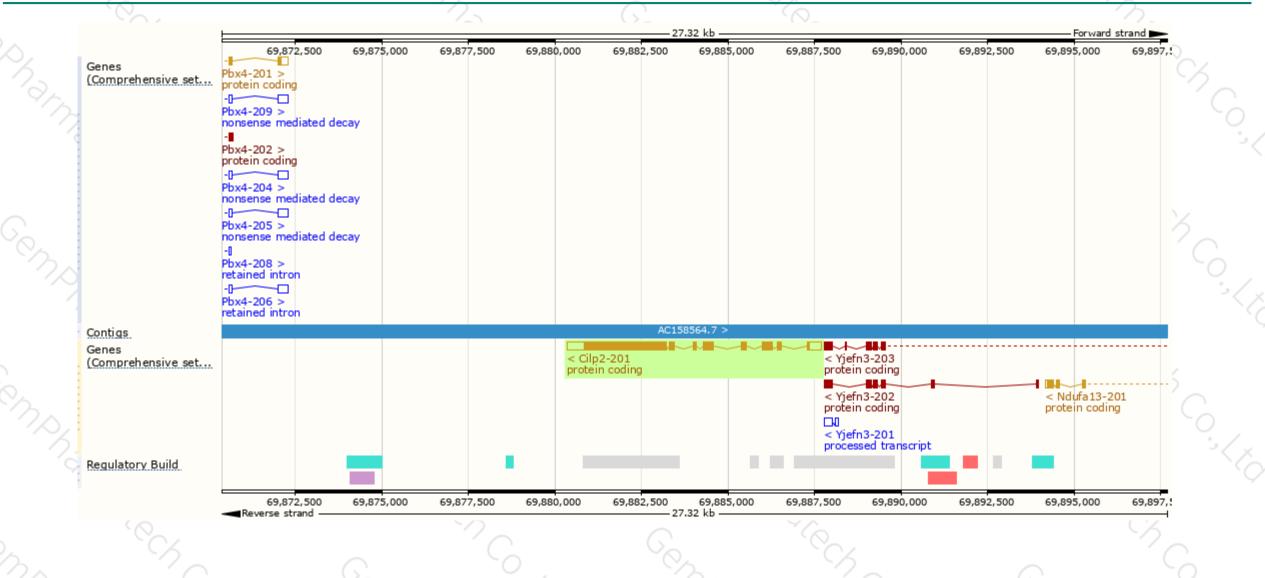
The strategy is based on the design of Cilp2-201 transcript, The transcription is shown below



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# **Genomic location distribution**





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# **Protein domain**



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Superfamily domains	PTHR15031		lobulin-like domai	in superfamily							
SMART domains	Thron										3
Pfam domain	WxxW domain	nbospondin type-1 (TSP1) n PF13620 PF13927									CO.
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PROSITE profiles	-		lobulin-like domai	in							
Gene3D			lobulin-like fold								/
		nbospondin type-1 (TSP1) re	peat superfamily								2
All sequence SNPs/i	Sequence variants (dbSNP	and all other sources)		n i n n		11		1.1	1.1.1	II I	Co
Variant Legend	missense variant splice region variant										3
Scale bar	0 100	200 300	400	500	600	700	800	900	1000	1162	
	6		<u> </u>			/	$\sim$		6		

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



