

# Polr3h Cas9-KO Strategy

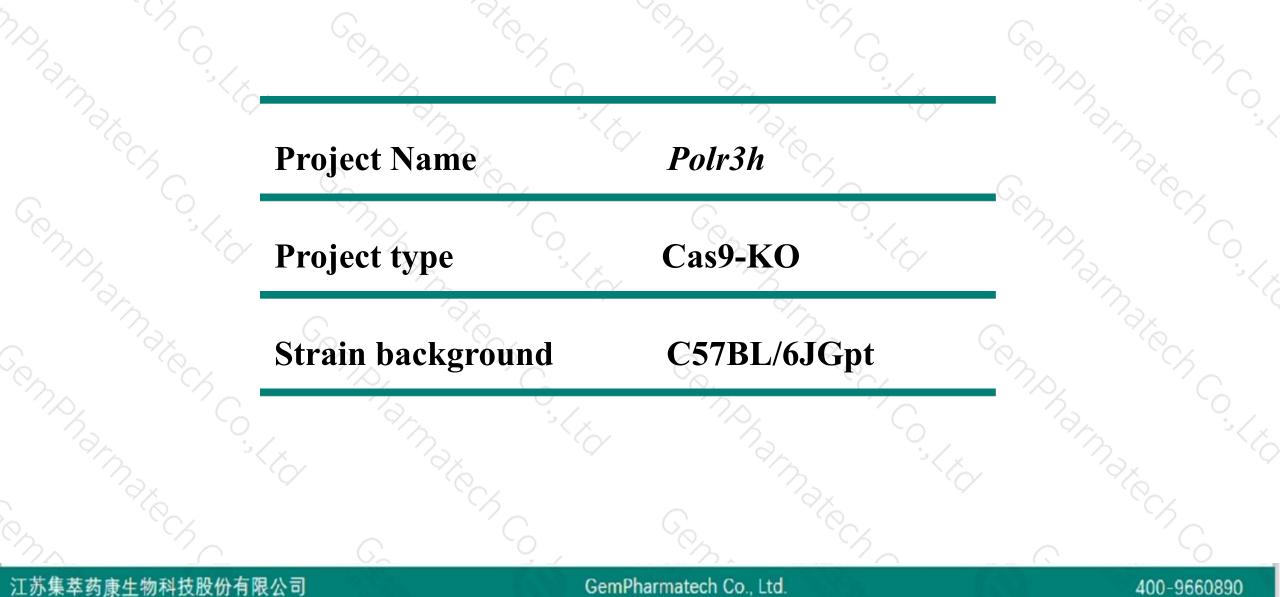
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**Reviewer: Daohua Xu** 

Design Date: 2020-6-17

## **Project Overview**

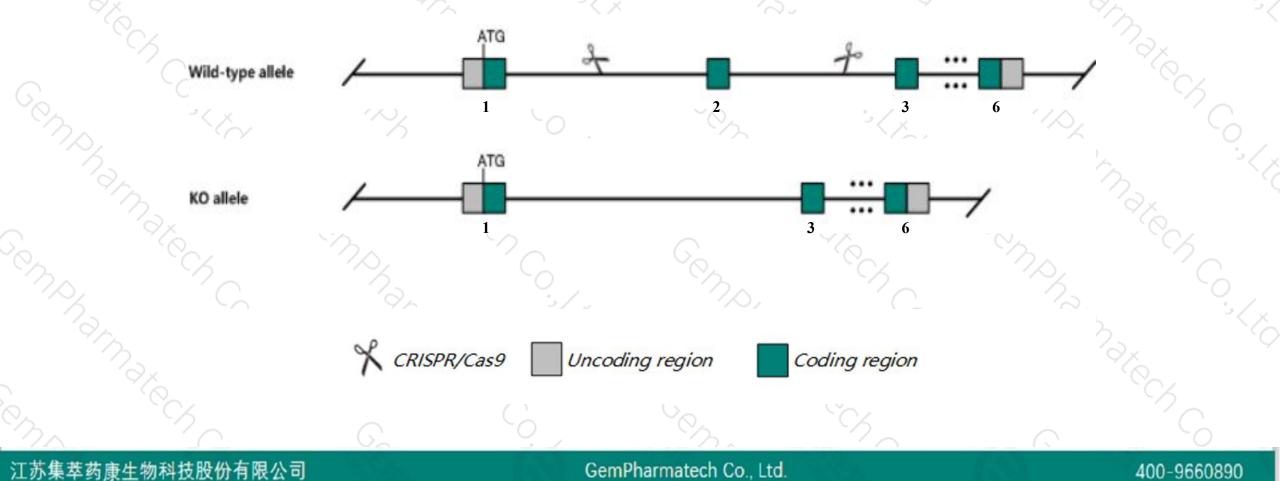




## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Polr3h* gene. The schematic diagram is as follows:





- The *Polr3h* gene has 7 transcripts. According to the structure of *Polr3h* gene, exon2 of *Polr3h-201* (ENSMUST0000023113.6) transcript is recommended as the knockout region. The region contains 97bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Polr3h gene. The brief process is as follows: CRISPR/Cas9 system

- The Polr3h gene is located on the Chr15. 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.
- > Transcript *Polr3h*-204 may not be affected.
- 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

## **Gene information (NCBI)**



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### Polr3h polymerase (RNA) III (DNA directed) polypeptide H [Mus musculus (house mouse)]

Gene ID: 78929, updated on 13-Mar-2020

#### Summary

Official Symbol	Polr3h provided by MGI
Official Full Name	polymerase (RNA) III (DNA directed) polypeptide H provided by MGI
Primary source	MGI:MGI:1926179
See related	Ensembl:ENSMUSG0000022476
Gene type	protein coding
<b>RefSeq status</b>	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
	Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5031409G22Rik, RPC8
Expression	Ubiquitous expression in spleen adult (RPKM 15.6), cortex adult (RPKM 10.0) and 28 other tissues See more
Orthologs	human all

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## **Transcript information (Ensembl)**



### The gene has 7 transcripts, all transcripts are shown below:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Polr3h-201	ENSMUST0000023113.6	2542	<u>204aa</u>	Protein coding	CCDS27676	<u>Q9D2C6</u>	TSL:1 GENCODE basic APPRIS P1	
Polr3h-203	ENSMUST00000230050.1	765	<u>175aa</u>	Protein coding	670	A0A2R8VK29	GENCODE basic	
Polr3h-205	ENSMUST00000230669.1	3030	No protein	Processed transcript	1220	3 <b>1</b>		
Polr3h-206	ENSMUST00000230765.1	1290	No protein	Processed transcript	1.00	<u>82</u>		
Polr3h-207	ENSMUST00000230842.1	498	No protein	Processed transcript	1781	65		
Polr3h-204	ENSMUST00000230066.1	438	No protein	Processed transcript	670	. <del>.</del>		
Polr3h-202	ENSMUST00000229402.1	985	No protein	Retained intron	(127)	84		

The strategy is based on the design of *Polr3h-201* transcript, the transcription is shown below:

#### < Polr3h-201 protein coding

Reverse strand

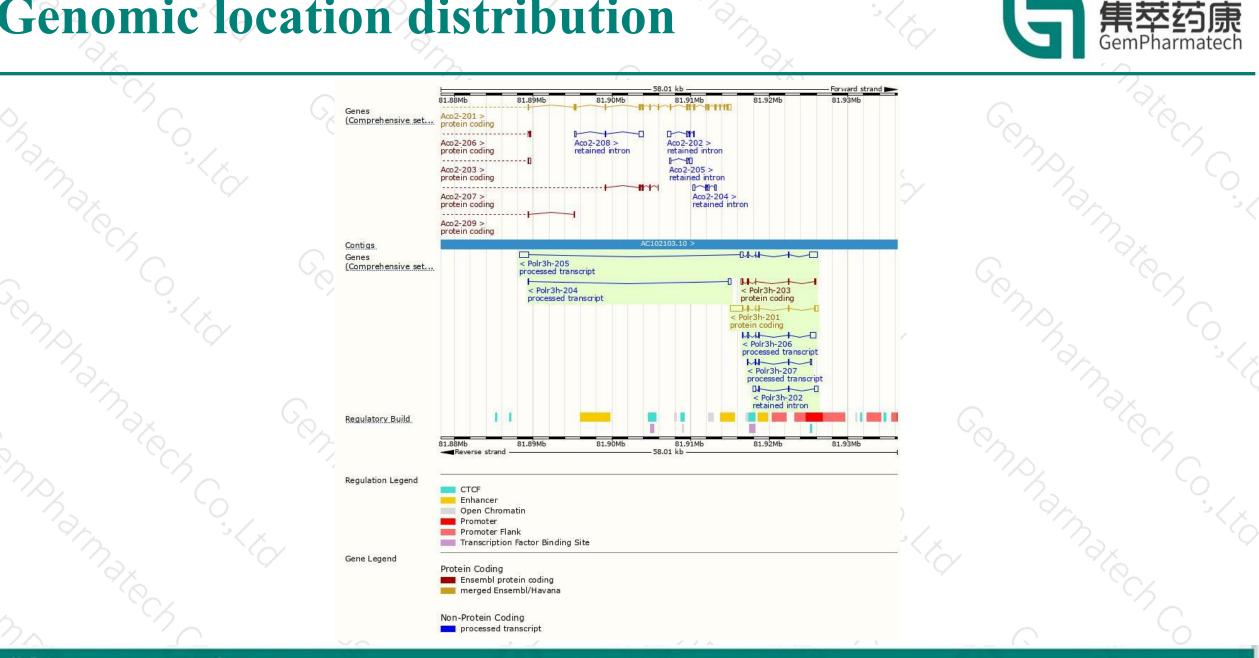
- 11.21 kb ----

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### **Genomic location distribution**



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## **Protein domain**



	° CA	6	2×		<sup>`°</sup> cy		0 <sup>12</sup>	
2	ENSMUSP00000023 Low complexity (Seg) TIGRFAM	DNA-directed RNA	polymerase; subunit E/I	RPC8				× Co
	Superfamily			Nucleic ad	id-binding, OB-fold			
	Pfam.		ob7-like, N-terminal dor se Rpb7-like , N-termin		merase III, subunit R	oc25		
	PANTHER	PTHR12709:SF1						
	Gene3D	PTHR12709 RNA polymerase R	ob7-like, N-terminal dor	main superfamily 2,40,50.1				34
	CDD.	cd04330		2,40,30.	140			
2	All sequence SNPs/i	Sequence variant	s (dbSNP and all oth	er sources)	20	1	1.1	6,/,
	Variant Legend	splice region						
	Scale bar	0 20	40 60	80	100 120	140 1	160 180 204	1
	20	G.	0	~O_	с. А.	Х	- 6	5

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



