

Cenpt Cas9-KO Strategy

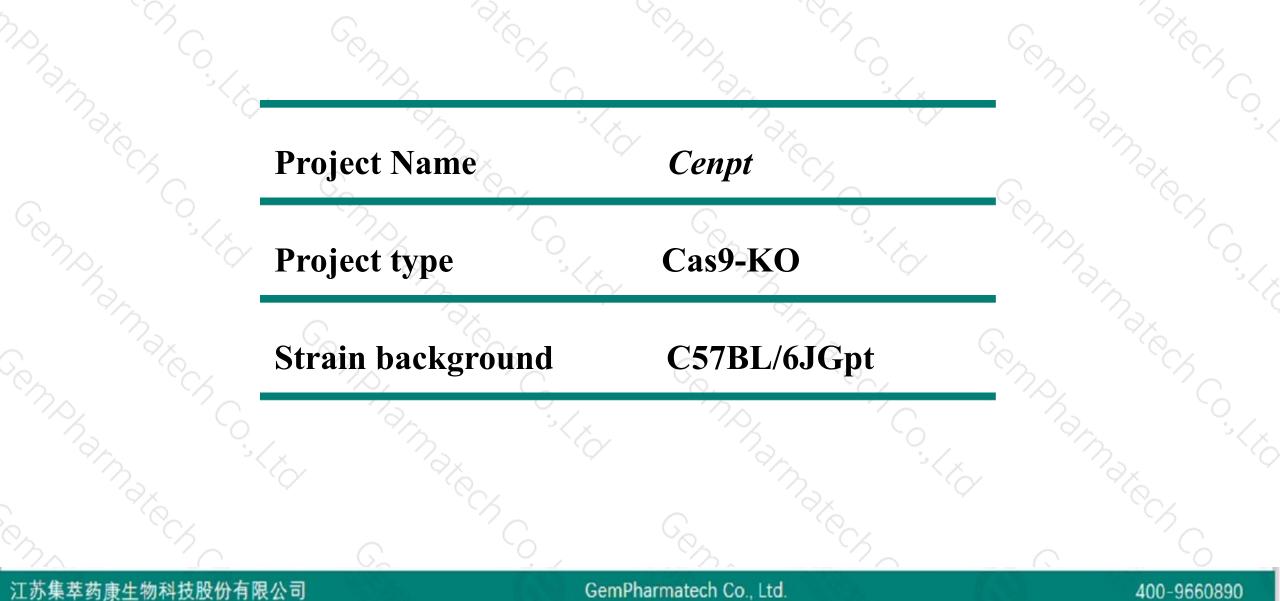
Designer: N Reviewer: S Date: 2

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Yupeng Yang Shilei Zhu 2019/12/4

Project Overview

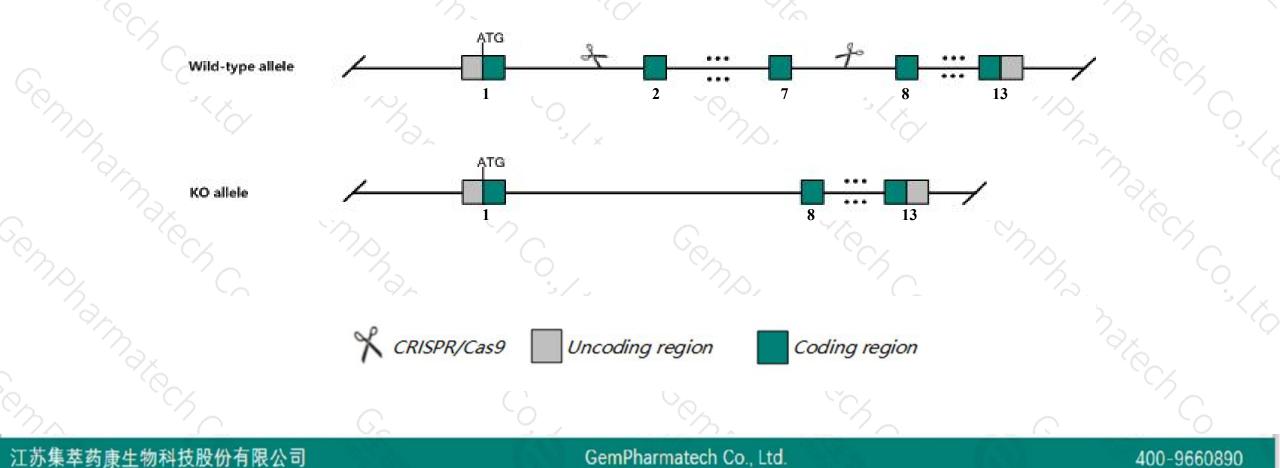




Knockout strategy



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





- The Cenpt gene has 10 transcripts. According to the structure of Cenpt gene, exon2-exon7 of Cenpt-201 (ENSMUST00000040776.5) transcript is recommended as the knockout region. The region contains 605bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Cenpt gene. The brief process is as follows: CRISPR/Cas9 system

- The Cenpt 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Notice

Gene information (NCBI)



☆ ?

Cenpt centromere protein T [Mus musculus (house mouse)]

Gene ID: 320394, updated on 31-Jan-2019

Summary

Official SymbolCenpt provided by MGIOfficial Full Namecentromere protein T provided byMGIPrimary sourceMGI:MGI:2443939See relatedEnsembl:ENSMUSG0000036672Gene typeprotein codingprotein codingPROVISIONALOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muriodea; Murinae; Mus; MusAlso knownasG630055P03RikExpressionUbiquitous expression in CNS E14 (RPKM 19.8), limb E14.5 (RPKM 19.1) and 27 other tissues
See more

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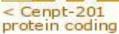
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Cenpt-201	ENSMUST0000040776.5	1814	<u>515aa</u>	Protein coding	CCDS22615	Q3TJM4	TSL:1 GENCODE basic APPRIS	
Cenpt-204	ENSMUST00000212431.1	1762	<u>42aa</u>	Nonsense mediated decay	1.4	A0A1D5RM35	TSL:2	
Cenpt-209	ENSMUST00000212839.1	567	<u>40aa</u>	Nonsense mediated decay	(a)	A0A1D5RLB1	TSL:5	
Cenpt-205	ENSMUST00000212552.1	348	<u>43aa</u>	Nonsense mediated decay	32 <u>4</u> 3	A0A1D5RMD0	TSL:3	
Cenpt-203	ENSMUST00000212357.1	3281	No protein	Retained intron	15	7	TSL:2	
Cenpt-202	ENSMUST00000212204.1	864	No protein	Retained intron	19	÷.	TSL:2	
Cenpt-206	ENSMUST00000212625.1	853	No protein	Retained intron	020	-	TSL:3	
Cenpt-210	ENSMUST00000212873.1	807	No protein	Retained intron	1220	2	TSL:3	
Cenpt-208	ENSMUST00000212803.1	562	No protein	Retained intron	(7)	7	TSL:5	
Cenpt-207	ENSMUST00000212797.1	579	No protein	IncRNA	-	-	TSL:3	

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

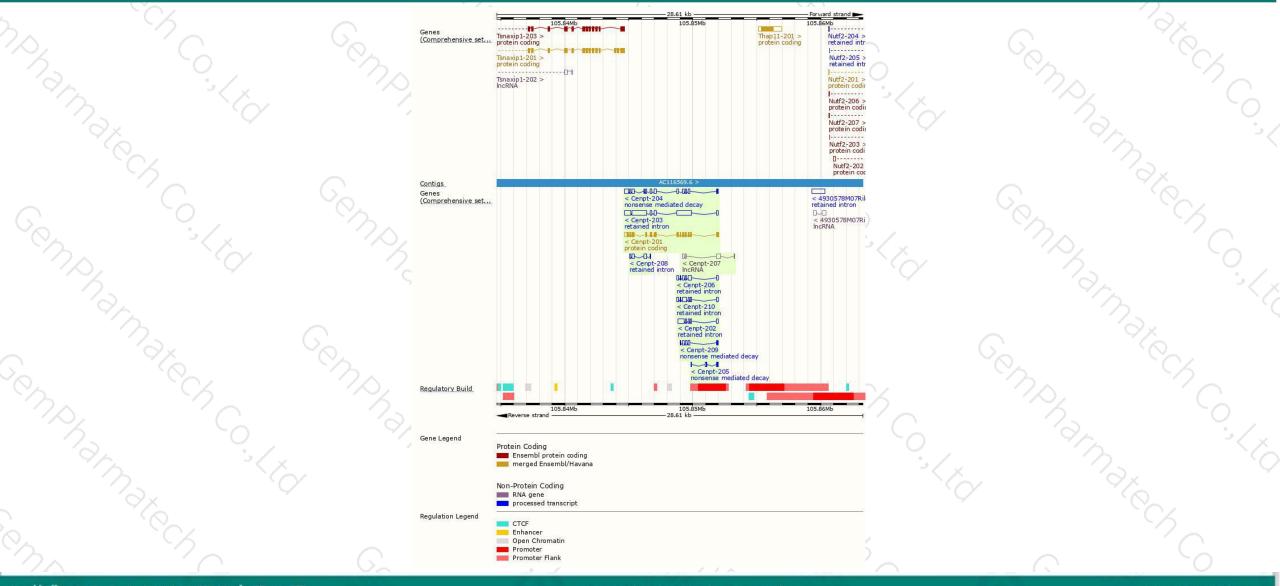


Reverse strand -

-7.38 kb —

Genomic location distribution





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Protein domain



$^{\prime}$			°C/S		$\gamma_{\mathcal{S}_{\mathcal{L}}}$			Coo la	
	ENSMUSP00000038 MobiDB lite Low complexity (Seg) Superfamily			÷			His	stone-fold	
	Pfam.	Centromere kinetocho	re component CEI	NP-T, N-terminal	domain			CENP-T/Histone	e H4, histone
Cen.	PANTHER Gene3D	Centromere protein. T						Histone-fold	
	All sequence SNPs/i	Sequence variants (dbSNP and all o	ther sources)		11.1000.0	11.11	11	
Senz.	Variant Legend	inframe deletic missense varia splice region v synonymous v	int ariant						
	Scale bar	0 60	120	180	240	300	360	420	515
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



