

Atp13a3 Cas9-CKO Strategy

Designer:

Reviewer:

Design Date:

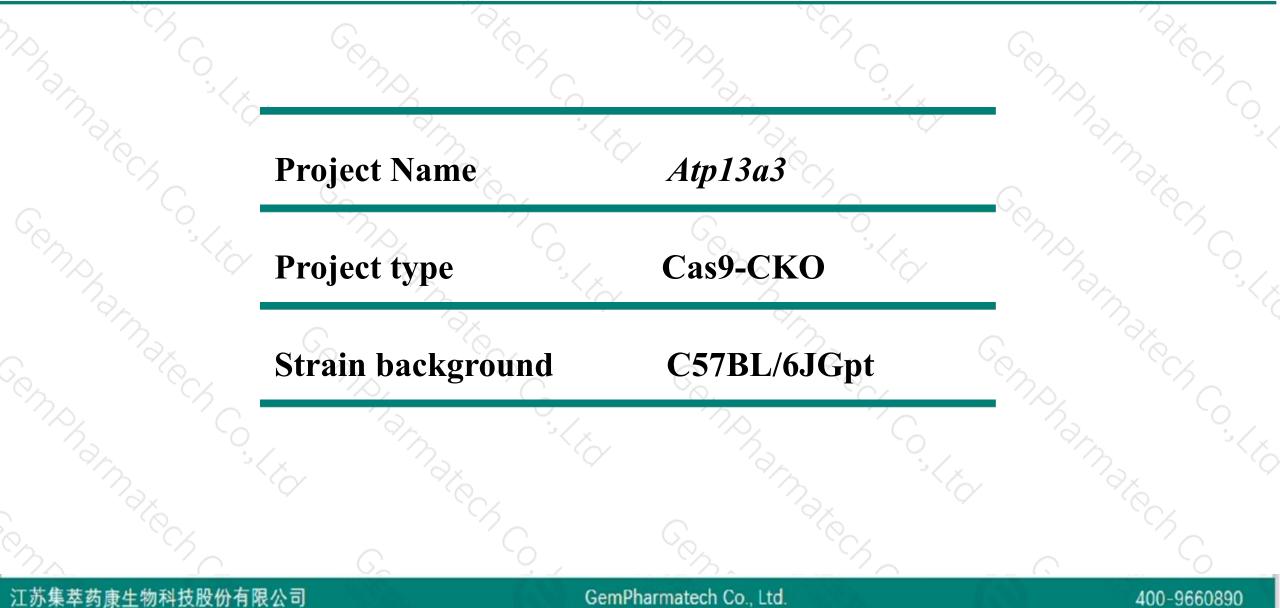
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2020-5-28

Project Overview

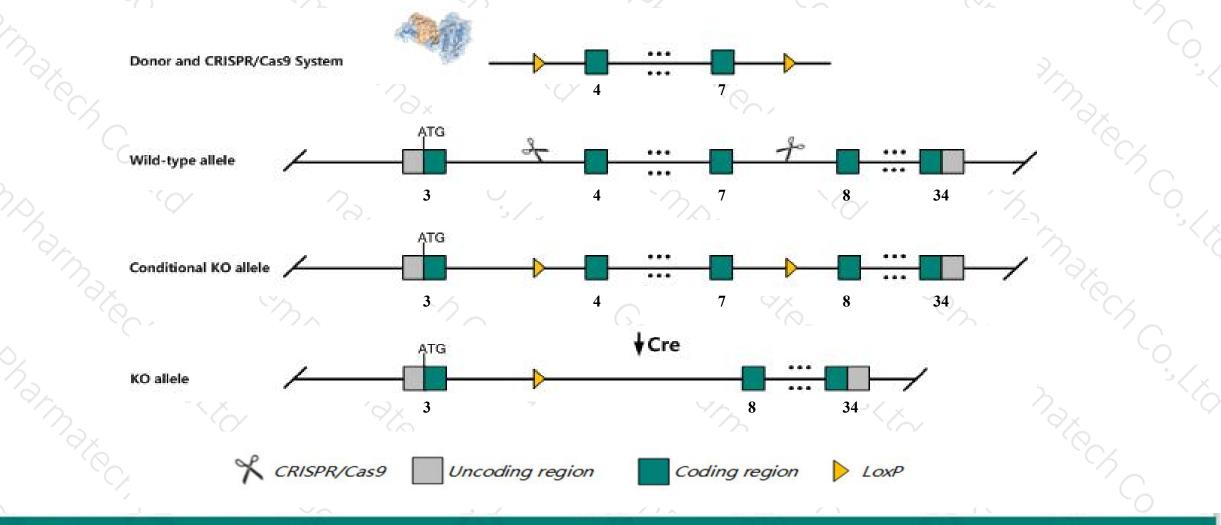




Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Atp13a3* gene. The schematic diagram is as follows:



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The Atp13a3 gene has 8 transcripts. According to the structure of Atp13a3 gene, exon4-exon7 of Atp13a3-202 (ENSMUST00000100013.8) transcript is recommended as the knockout region. The region contains 497bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Atp13a3* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- The Atp13a3 gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



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Atp13a3 ATPase type 13A3 [Mus musculus (house mouse)]

Gene ID: 224088, updated on 13-Mar-2020

Summary

Official Symbol	Atp13a3 provided by MGI
Official Full Name	ATPase type 13A3 provided by MGI
Primary source	MGI:MGI:2685387
See related	Ensembl:ENSMUSG0000022533
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
	Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU022875, Gm1745, Gm541, Gm542
Expression	Ubiquitous expression in bladder adult (RPKM 11.5), placenta adult (RPKM 10.4) and 28 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp13a3-202	ENSMUST00000100013.8	7310	<u>1249aa</u>	Protein coding	CCDS49821	Q5XF89	TSL:5 GENCODE basic APPRIS P4
Atp13a3-201	ENSMUST0000061350.12	7220	<u>1219aa</u>	Protein coding	CCDS49820	Q5XF89	TSL:5 GENCODE basic APPRIS ALT2
Atp13a3-206	ENSMUST00000229503.1	924	<u>259aa</u>	Protein coding	а 1	A0A2R8VI02	CDS 5' incomplete
tp13a3-207	ENSMUST00000229616.1	662	<u>74aa</u>	Protein coding	-	A0A2R8VJX0	CDS 3' incomplete
Atp13a3-208	ENSMUST00000229750.1	825	No protein	Processed transcript	5	1753	
Atp13a3-203	ENSMUST00000136065.1	2250	No protein	Retained intron	-	(3 4	TSL:1
Atp13a3-205	ENSMUST00000153656.1	793	No protein	Retained intron	4	(2)	TSL:2
Atp13a3-204	ENSMUST00000149882.1	310	No protein	Retained intron	2	120	TSL:5

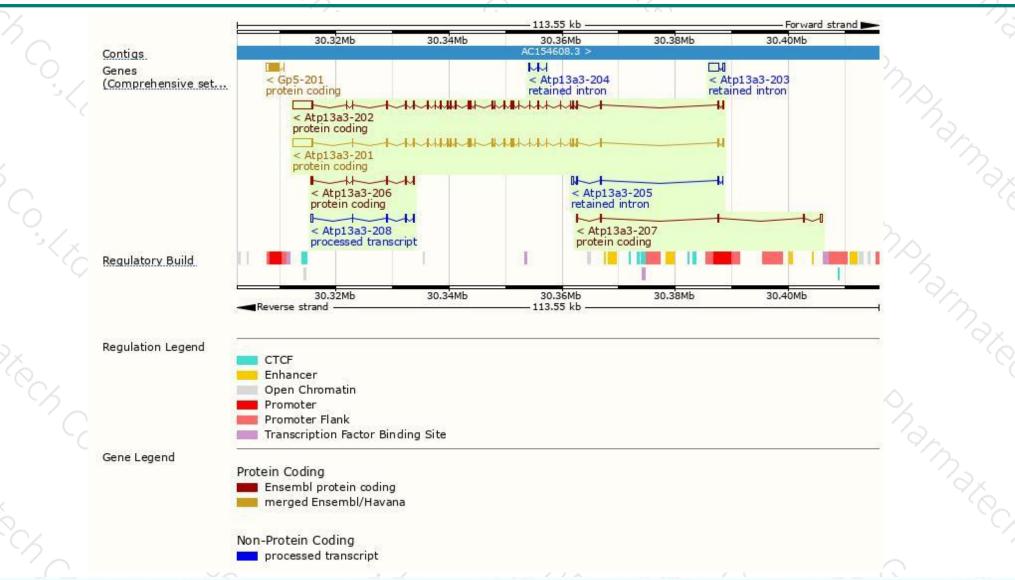
The strategy is based on the design of *Atp13a3-202* transcript, the transcription is shown below:

< Atp13a3-202 protein coding

Reverse strand -

Genomic location distribution





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Protein domain



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		L the unest name	HAD-like superfamily	X	The second	
C C	SFLD.	P-type ATPas	se, A domain superfamily SFLDF00027			
°.3 /	Prints	PR00115	SFLDG00002			~?
	Pfam.		type ATPase, N-terminal	₿ ⁰	2	
×.		P-type ATPase, subfamily V	PF00702		(P)	
And the second	PROSITE patterns	PF00122	P-type ATPase, phospho	endation site	2	
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	CDD.	2.70.150.10 cd07542	P-type ATPa HAD superfamily	se, cytoplasmic domain N	300	
	All sequence SNPs/i	Sequence variants (dbSNP and all ot	ther sources)	The shift is	A A A A A A A A A A A A A A A A A A A	
	Variant Legend	missense variant				3
γ_{c}	Scale bar	0 200	400 600	800 1000	1249	



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



