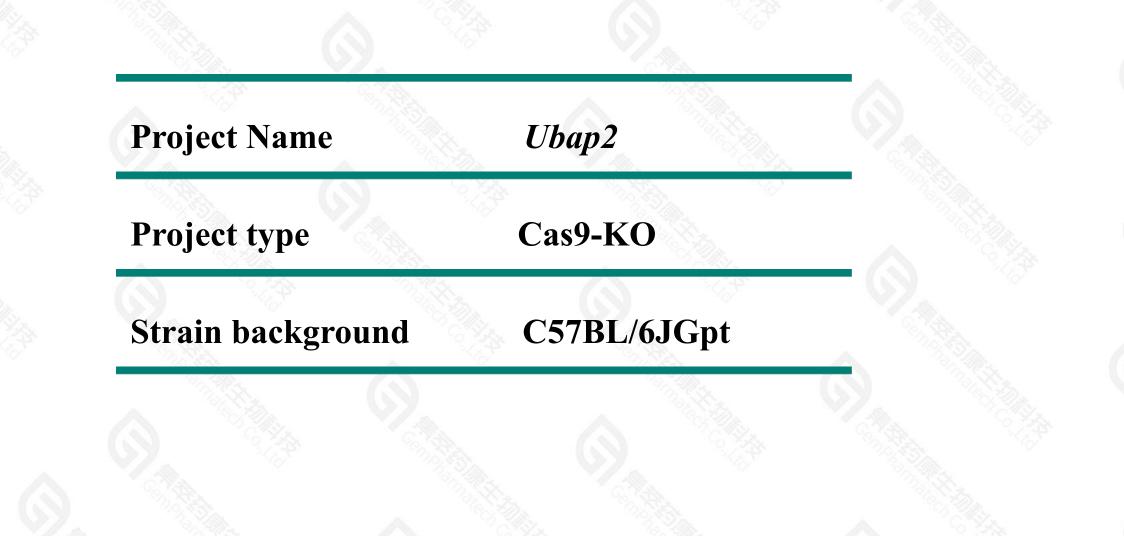


Ubap2 Cas9-KO Strategy

Designer: Daohua Xu

Project Overview





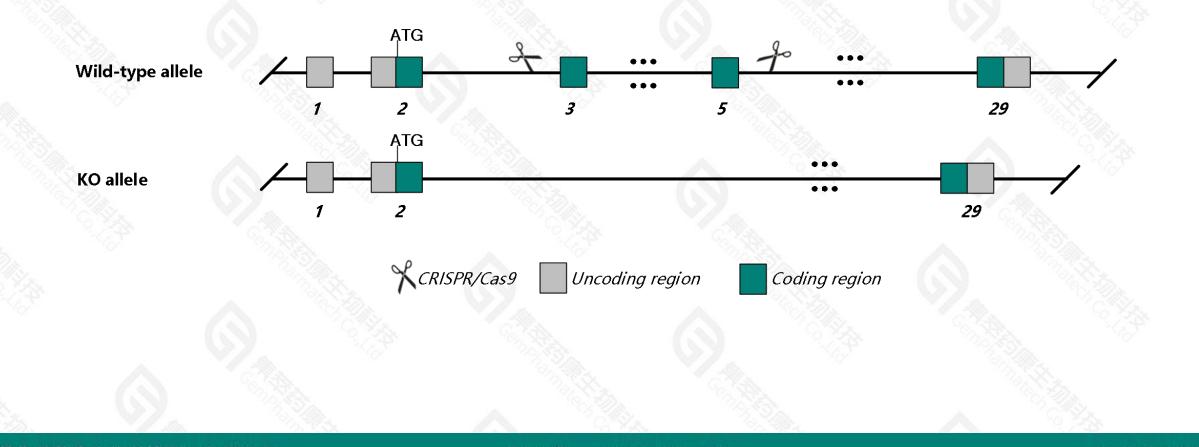
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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Ubap2 gene. The schematic diagram is as follows:



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> The *Ubap2* gene has 8 transcripts. According to the structure of *Ubap2* gene, exon3-exon5 of *Ubap2*-201(ENSMUST00000030143.13) transcript is recommended as the knockout region. The region contains 343bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify Ubap2 gene. The brief process is as follows: CRISPR/Cas9 system 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.



- \succ The *Ubap2* gene is located on the Chr4. 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.

Gene information (NCBI)

Ubap2 ubiquitin-associated protein 2 [Mus musculus (house mouse)]

Gene ID: 68926, updated on 17-Dec-2020

Summary

Official Symbol	Ubap2 provided by MGI
Official Full Name	ubiquitin-associated protein 2 provided by MGI
Primary source	MGI:MGI:1916176
See related	Ensembl:ENSMUSG0000028433
Gene type	protein coding
RefSeq status	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	1190005K07Rik, AA408600, AU045235, UBAP-2, mKIAA1491
Expression	Ubiquitous expression in testis adult (RPKM 65.5), thymus adult (RPKM 28.5) and 28 other tissuesSee more
Orthologs	human all

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¹ armatech

\$?

Transcript information (Ensembl)



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

Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST0000030143.13	4368	<u>1132aa</u>	Protein coding	CCDS18058		TSL:1 , GENCODE basic , APPRIS P2 ,
ENSMUST00000108068.8	4380	<u>1131aa</u>	Protein coding	-		TSL:1 , GENCODE basic , APPRIS ALT2 ,
ENSMUST00000134782.2	735	<u>245aa</u>	Protein coding	82 <u>1</u> 8		CDS 5' and 3' incomplete , TSL:3 ,
ENSMUST00000135323.2	696	<u>227aa</u>	Protein coding			CDS 3' incomplete , TSL:3 ,
ENSMUST00000136057.2	418	<u>140aa</u>	Protein coding	-		CDS 5' and 3' incomplete , TSL:1 ,
ENSMUST00000132499.2	687	No protein	Processed transcript	870		TSL:3,
ENSMUST00000143552.2	502	No protein	Processed transcript	13 - 1		TSL:5 ,
ENSMUST00000140662.2	132	No protein	Processed transcript			TSL:5,
	ENSMUST0000030143.13 ENSMUST0000108068.8 ENSMUST0000134782.2 ENSMUST0000135323.2 ENSMUST0000136057.2 ENSMUST0000132499.2	ENSMUST0000030143.13 4368 ENSMUST0000108068.8 4380 ENSMUST0000134782.2 735 ENSMUST0000135323.2 696 ENSMUST0000136057.2 418 ENSMUST0000132499.2 687 ENSMUST0000143552.2 502	Image: Marcine information Marcine information ENSMUST0000030143.13 4368 1132aa ENSMUST0000108068.8 4380 1131aa ENSMUST0000134782.2 735 245aa ENSMUST0000135323.2 696 227aa ENSMUST0000132499.2 418 140aa ENSMUST0000132499.2 687 No protein	ENSMUST0000030143.1343681132aaProtein codingENSMUST0000108068.843801131aaProtein codingENSMUST0000134782.2735245aaProtein codingENSMUST0000135323.2696227aaProtein codingENSMUST0000136057.2418140aaProtein codingENSMUST0000132499.2687No proteinProtein codingENSMUST0000143552.2502No proteinProtein coding	ENSMUST0000030143.1343681132aaProtein codingCCDS18058ENSMUST0000108068.843801131aaProtein coding-ENSMUST0000134782.2735245aaProtein coding-ENSMUST0000135323.2696227aaProtein coding-ENSMUST0000136057.2418140aaProtein coding-ENSMUST0000132499.2687No proteinProcessed transcript-ENSMUST0000143552.2502No proteinProcessed transcript-	ENSMUST0000030143.1343681132aaProtein codingCCDS18058ENSMUST0000108068.843801131aaProtein coding-ENSMUST0000134782.2735245aaProtein coding-ENSMUST0000135323.2696227aaProtein coding-ENSMUST0000136057.2418140aaProtein coding-ENSMUST0000132499.2687No proteinProcessed transcript-ENSMUST0000143552.2502No proteinProcessed transcript-

The strategy is based on the design of *Ubap2-201* transcript, the transcription is shown below:

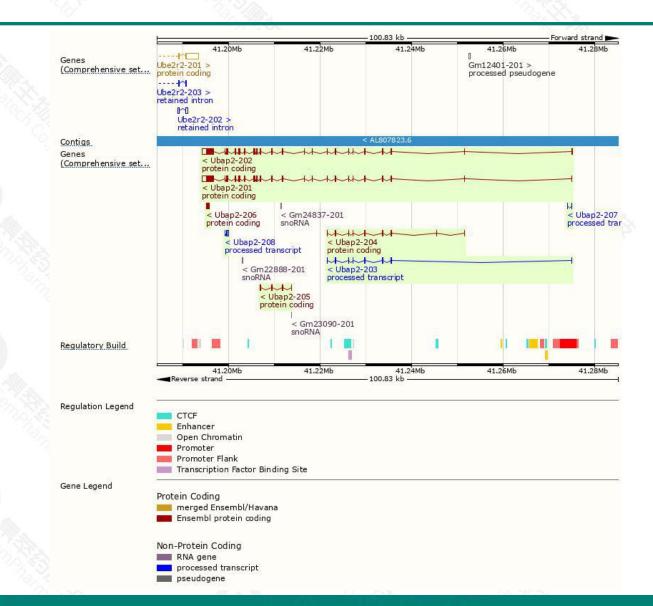


- 80.82 kb

Reverse strand

Genomic location distribution





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Protein domain



ENSMUSP00000030 MobiDB lite Low complexity (Seg) Superfamily SMART	UBA-like superf									
	Ubiquitin-as	sociated domain								
Pfam	UBAP2/protein lingerer									
PANTHER	PTHR16308:SF19									
	PTHR16308									
Gene3D	1.10.8.10									
CDD	cd14277									
All sequence SNPs/i	Sequence variar	nts (dbSNP and a	ll other sources)	1.0.0	111	17	a r	0.0	LE III	1 III
Variant Legend	missense v splice regio synonymou	on variant								
Scale bar	0 100	200 30	00 400	500	600	700	800	900	1000	1132

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



