

Fkbp3 Cas9-KO Strategy

Designer: Reviewer:

Design Date:

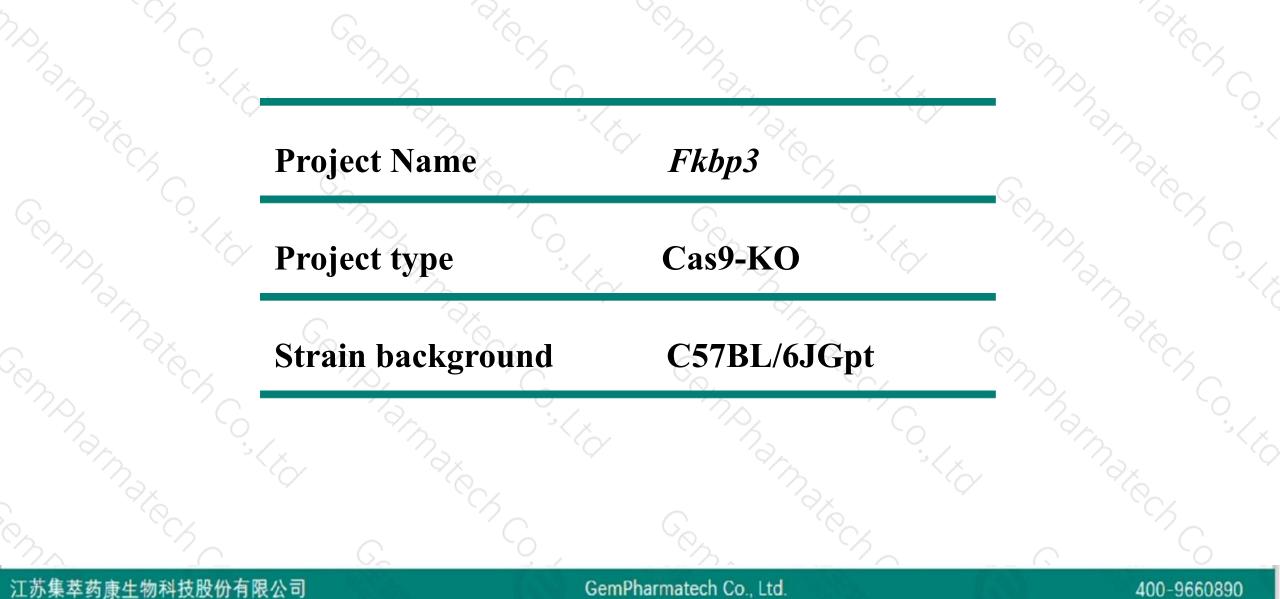
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2020-3-12

Project Overview

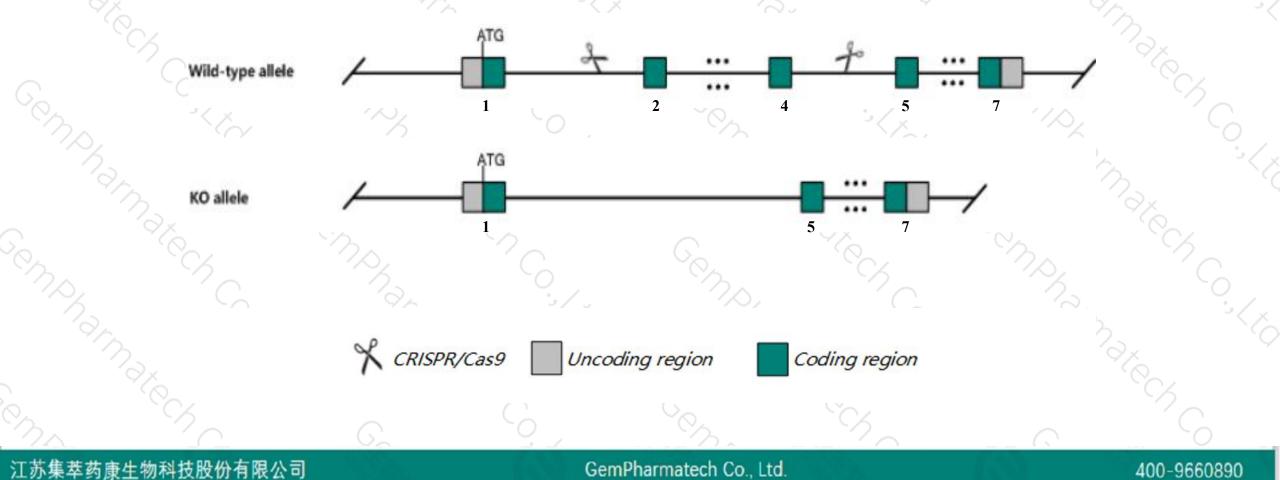




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Fkbp3* gene. The schematic diagram is as follows:





- The *Fkbp3* gene has 12 transcripts. According to the structure of *Fkbp3* gene, exon2-exon4 of *Fkbp3-201* (ENSMUST0000021332.9) transcript is recommended as the knockout region. The region contains 346bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Fkbp3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Fkbp3* gene is located on the Chr12. 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.
- The KO region deletes parts of the coding sequence of *Fkbp3-204* transcript, but does not result in frameshift.
- 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)



Fkbp3 FK506 binding protein 3 [Mus musculus (house mouse)]

Gene ID: 30795, updated on 3-Nov-2019

Summary Image: Constraint of the symbol symbol

Genomic context

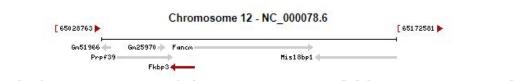
Location: 12; 12 C1

Exon count: 7

See Fkbp3 in Genome Data Viewer

☆ ?

Annotation release Status Assembly Chr Location GRCm38.p6 (GCF_000001635.26) NC_000078.6 (65062432..65073938, complement) 108 12 current NC 000078.5 (66163419..66174925, complement) Build 37.2 previous assembly MGSCv37 (GCF 000001635.18) 12



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Transcript information (Ensembl)



The gene has 12 transcripts, all transcripts are shown below:

Name 🔺	Transcript ID	bp 💧	Protein 💧	Biotype	CCDS A	UniProt	Flags		
	ENSMUST0000021332.9	1022	224aa	Protein coding	CCDS25940	Q3UBU9@Q62446@			
		17.550 7-55	Station Station		<u>CCD320340</u>		TSL:1 GENCODE basic APPRIS P1		
Fkbp3-204	ENSMUST00000220983.1	654	<u>149aa</u>	Protein coding	8 .	A0A1Y7VP01	CDS 5' incomplete TSL:5		
Fkbp3-202	ENSMUST00000220730.1	579	<u>188aa</u>	Protein coding	34	<u>A0A1Y7VLK0</u> 교	TSL:5 GENCODE basic		
Fkbp3-206	ENSMUST00000221608.1	529	<u>88aa</u>	Protein coding	12	<u>A0A1Y7VJ86</u> 교	CDS 5' incomplete TSL:3		
Fkbp3-205	ENSMUST00000221166.1	981	<u>76aa</u>	Nonsense mediated decay	<u>110</u>	<u>A0A1Y7VMJ9</u> @	TSL:5		
Fkbp3-209	ENSMUST00000221913.1	600	<u>82aa</u>	Nonsense mediated decay	5	<u>A0A1Y7VLV3</u> 교	CDS 5' incomplete TSL:3		
Fkbp3-211	ENSMUST00000222684.1	6939	No protein	Retained intron	57	-	TSL:5		
Fkbp3-203	ENSMUST00000220957.1	1910	No protein	Retained intron	10		TSL:2		
Fkbp3-208	ENSMUST00000221710.1	1233	No protein	Retained intron	ii .	-1	TSL:2		
Fkbp3-212	ENSMUST00000223167.1	1109	No protein	Retained intron	1 .	-	TSL:1		
Fkbp3-210	ENSMUST00000222467.1	511	No protein	Retained intron	-	120	TSL:3		
Fkbp3-207	ENSMUST00000221706.1	408	No protein	Retained intron	2. 12	. 2 5	TSL:2		

The strategy is based on the design of Fkbp3-201 transcript, The transcription is shown below

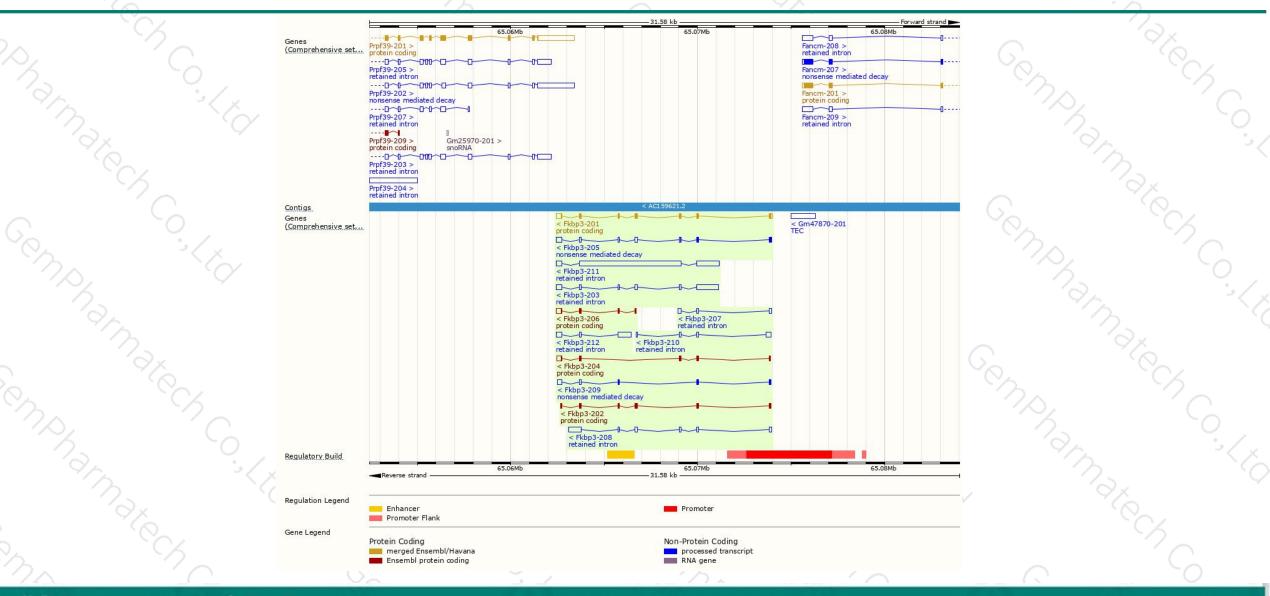
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< Fkbp3-201 protein coding

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Genomic location distribution



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Protein domain



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	ENSMUSP00000021 PDB-ENSP mappings MobiDB lite Low complexity (Seg) Superfamily Pfam	FKBP3, basic tilted	helix bundle domain	ss	F54534	FKBP-type peptidyl-prolyl	cis-trans isomerase domair			~O ~<
Cent	PROSITE profiles PANTHER Gene3D	PTHR46493 1.10.720.80			3,10,50,40	FKBP-type peptidyl-	prolyl cis-trans isomerase d			、) ~人
	All sequence SNPs/i Variant Legend	Sequence variants (d	dbSNP and all other sou	urces)		ynonymous variant	e 11 11			
	Scale bar		40 	60 80 		120 140	160 18	0 ^{'200}	224) *
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



