

Fkbp10 Cas9-CKO Strategy

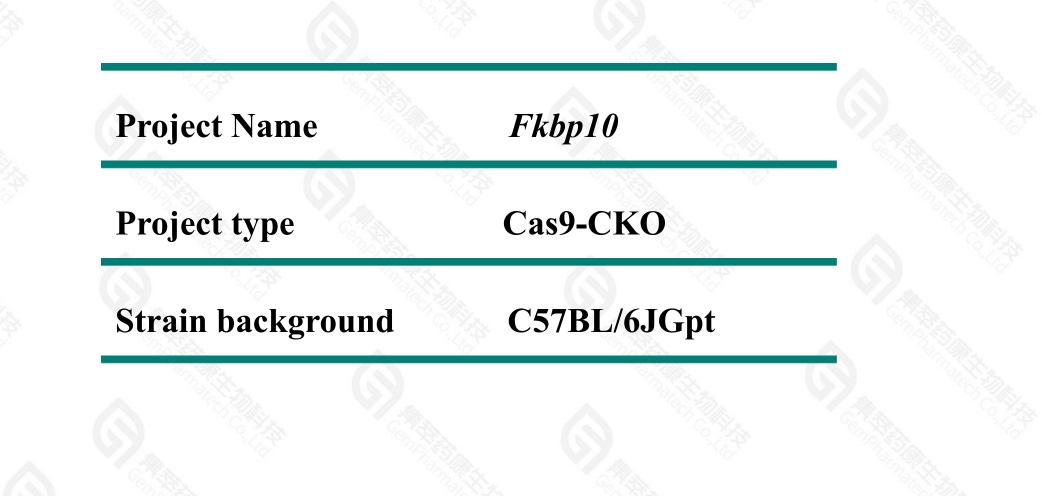
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Reviewer: Yanhua Shen

Design Date: 2022-8-3

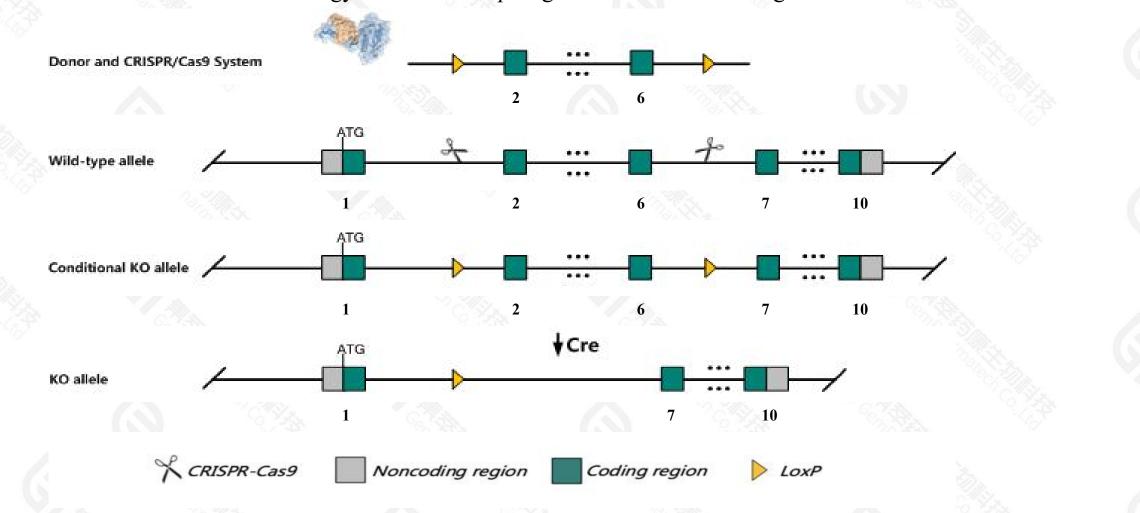
Project Overview





Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Fkbp10* gene. The schematic diagram is as follows:



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Technical routes



> The *Fkbp10* gene has 5 transcripts. According to the structure of *Fkbp10* gene, exon2-exon6 of *Fkbp10-201*(ENSMUST00000001595.10) transcript is recommended as the knockout region. The region contains 818bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR-Cas9 technology to modify Fkbp10 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.



- According to the existing MGI data, homozygous null mice do not survive birth, and embryos exhibit delayed growth, tissue fragility, decreased aorta wall thickness, craniofacial and forelimb anomalies, and connective tissue alterations. Mutant MEFs retain procollagen in the cell layer and show dilated endoplasmic reticulum.
- ➤ The Intron6 is only 536bp,loxp insertion may affect mRNA splicing.
- > This strategy may affect the regulation of the 3-terminal of the Nt5c3b gene.
- > The *Fkbp10* gene is located on the Chr11. 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)



Summary	
Official Symbol	Fkbp10 provided by MGI
Official Full Name	FK506 binding protein 10 provided by MGI
Primary source	MGI:MGI:104769
See related	Ensembl:ENSMUSG0000001555 AllianceGenome:MGI:104769
Gene type	protein coding
RefSeq status	VALIDATED
7.0	Mus musculus
20-200 (20-1) (e Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
	Fkbp6; FKBP65; Fkbprp; FKBP-10; FKBP-65; Al325255; Fkbp-rs1; Fkbp1-rs
Summary	Enables FK506 binding activity and peptidyl-prolyl cis-trans isomerase activity. Acts upstream of or within several processes, including aorta morphogenesis; extracellular matrix organization; and peptidyl-amino acid modific Located in endoplasmic reticulum; membrane; and mitochondrial intermembrane space. Is expressed in several structures, including connective tissue; intestine epithelium; lung; metanephros; and skeleton. Human ortholog gene implicated in osteogenesis imperfecta type 11. Orthologous to human FKBP10 (FKBP prolyl isomerase 10). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in limb E14.5 (RPKM 89.8), ovary adult (RPKM 79.7) and 18 other tissues See more
Orthologs	human all
NEW	Try the new Gene table
	Try the new Transcript table

Annotation release	Status	Assembly	Chr	Location	
109	current	GRCm39 (GCF 000001635.27)	11	NC_000077.7 (100306520100315666)	
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (100415694100424840)	
Build 37.2	previous assembly	MGSCv37 (GCF 000001635.18)	11	NC_000077.5 (100277008100286154)	



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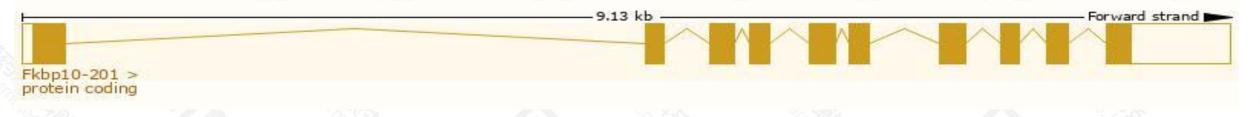
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Transcript information (Ensembl)

The gene has 5 transcripts, all transcripts are shown below:

Transcript ID 🕴 Name 🌒 bp 🌒 Pro		Protein	Protein 🛊 Biotype 💧		UniProt Match	Flags		
ENSMUST0000001595.10	Fkbp10-201	2584	<u>581aa</u>	Protein coding	CCDS25422@	<u>Q61576</u> @	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1	
ENSMUST00000107400.3	Fkbp10-202	1467	<u>469aa</u>	Protein coding		A2A4H9@	GENCODE basic TSL:5	
ENSMUST00000134815.2	Fkbp10-204	853	<u>66aa</u>	Nonsense mediated decay		F6W360@	TSL:5 CDS 5' incomplete	
ENSMUST00000139084.2	Fkbp10-205	815	No protein	Retained intron		-	TSL:2	
ENSMUST00000125616.2	Fkbp10-203	767	No protein	Retained intron		20	TSL-2	

The strategy is based on the design of *Fkbp10-201* transcript, the transcription is shown below:

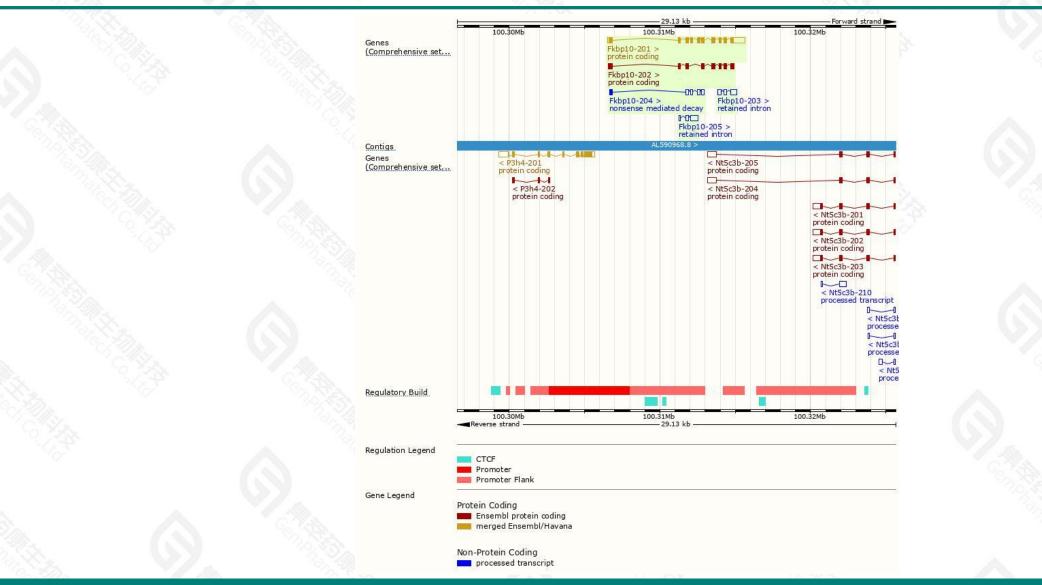


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Genomic location distribution





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Protein domain

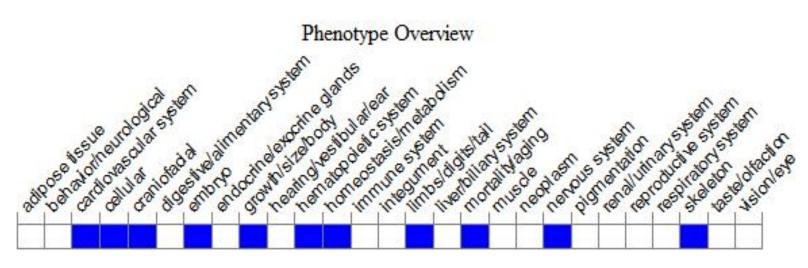


ENSMUSP00000001 MobiDB lite Low complexity (Seg)					
Cleavage site (Sign					
Superfamily	SSF54534				EF-hand domain pair
SMART					EF-hand domain
<u>Pfam</u>	FKBP-type peptidy	/l-prolyl cis-trans isomerase d	main		EF-hand domain
PROSITE profiles	FKBP-type peptic	yl-prolyl cis-trans isomerase (domain		EF-hand domain
PROSITE patterns					EF-Ha
PANTHER	PTHR46046				
	PTHR46046:SF3				
Gene3D	3.10.50:40			38	1,10.238,10
CDD					EF-hand domain
All sequence SNPs/i	Sequence variants (dbSNP	and all other sources)			
			10 1 1 1 1	111.23	<u> 11 11</u>
Variant Legend	missense variant synonymous variant				
Scale bar	0 60 120	0 180 240	300	360 420	480 58:

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Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, homozygous null mice do not survive birth, and embryos exhibit delayed growth, tissue fragility, decreased aorta wall thickness, craniofacial and forelimb anomalies, and connective tissue alterations. Mutant MEFs retain procollagen in the cell layer and show dilated endoplasmic reticulum.

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



