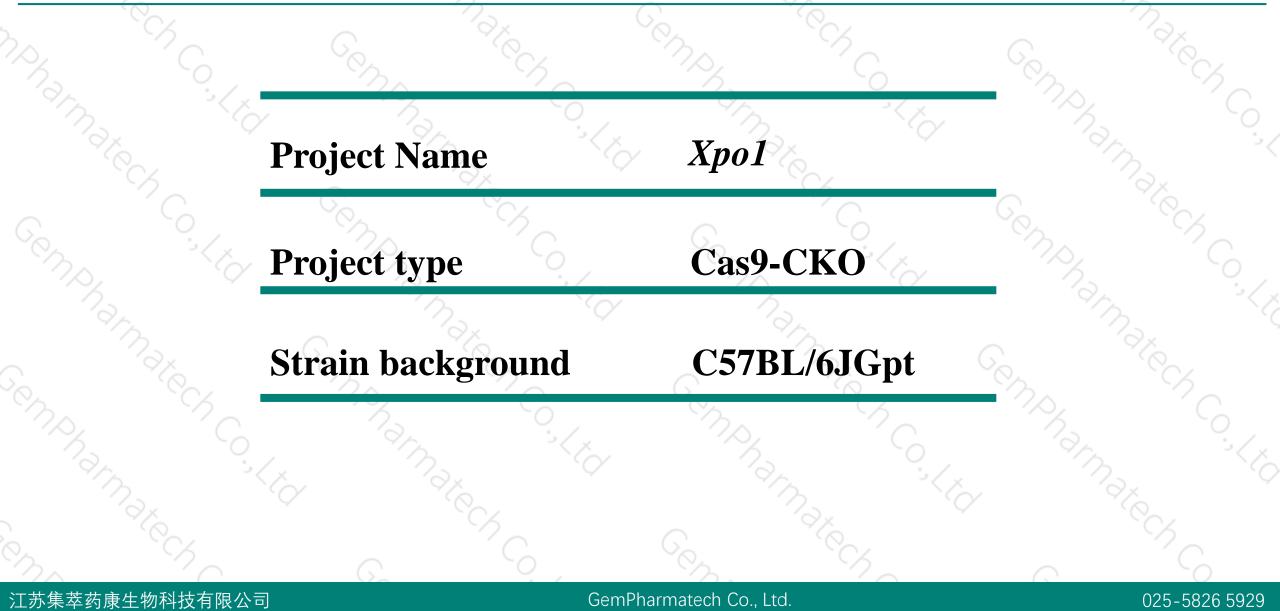
Xpol Cas9-CKO Strategy

Designer: Reviewer: Design Date: Ruirui Zhang Huimin Su 2020-3-24

Project Overview



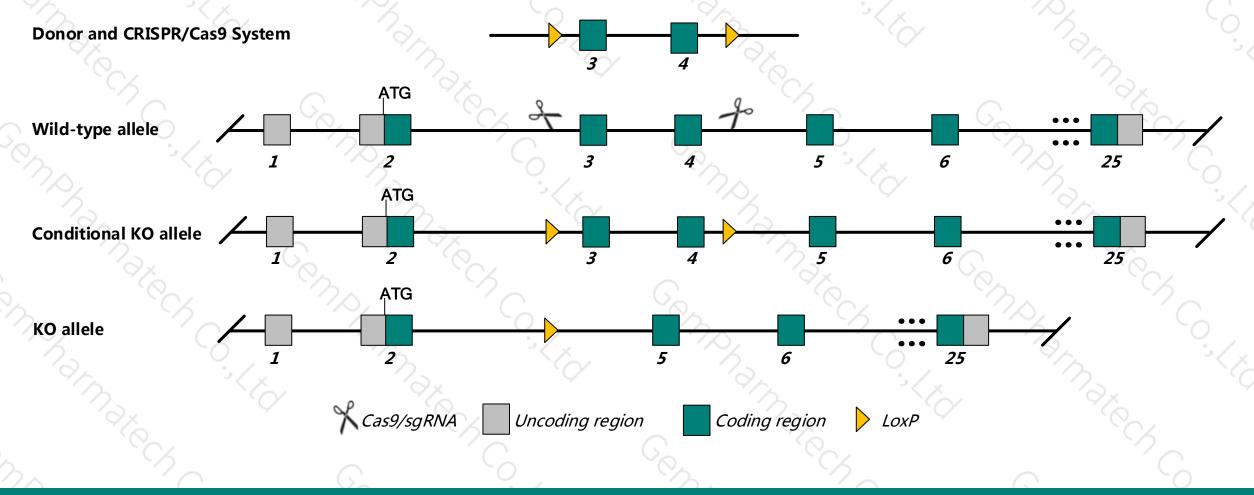


Conditional Knockout strategy



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This model will use CRISPR/Cas9 technology to edit the *Xpo1* gene. The schematic diagram is as follows:



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- The *Xpo1* gene has 7 transcripts. According to the structure of *Xpo1* gene, exon3~exon4 of *Xpo1*-202 (ENSMUST00000102869.7) transcript is recommended as the knockout region. The region contains 175bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Xpo1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- According to the existing MGI data , null homozygotes show complete prenatal lethality prior to heart atrial septation.
 Transcript *Xpo1-207* may not be affected.
- The *Xpo1* 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 the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Notice

Gene information (NCBI)



Xpo1 exportin 1 [Mus musculus (house mouse)]

Gene ID: 103573, updated on 13-Mar-2020

Summary

Official Symbol	Xpo1 provided by MGI
Official Full Name	exportin 1 provided by MGI
Primary source	<u>MGI:MGI:2144013</u>
See related	Ensembl:ENSMUSG0000020290
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	Crm1; Exp1; AA420417
Expression	Broad expression in CNS E11.5 (RPKM 31.7), limb E14.5 (RPKM 25.4) and 23 other tissues See more
Orthologs	human all
Y/2	$\frac{1}{2} \left(\frac{1}{2} \right) = \frac{1}{2} \left(\frac{1}{2} \right) \left(\frac{1}{2} \right) = \frac{1}{2} \left(\frac{1}{2} \right) $

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Transcript information (Ensembl)



The gene has 7 transcripts, and all transcripts are shown below:

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Name 🍦	Transcript ID 🛛 🍦	bp 🖕	Protein 🖕	Biotype 🔺	CCDS 🍦	UniProt 🖕	Flags 🍦
Xpo1-202	ENSMUST00000102869.7	6004	<u>1071aa</u>	Protein coding	<u>CCDS24475</u>	<u>Q6P5F9</u> &	TSL:1 GENCODE basic APPRIS P1
Xpo1-201	ENSMUST0000020538.12	5145	<u>1071aa</u>	Protein coding	<u>CCDS24475</u>	<u>Q6P5F9</u> &	TSL:5 GENCODE basic APPRIS P1
Xpo1-204	ENSMUST00000109551.7	4906	<u>1071aa</u>	Protein coding	<u>CCDS24475</u>	<u>Q6P5F9</u> ₽	TSL:1 GENCODE basic APPRIS P1
Xpo1-203	ENSMUST00000102870.7	3471	<u>1071aa</u>	Protein coding	<u>CCDS24475</u> ₽	<u>Q6P5F9</u> ₽	TSL:5 GENCODE basic APPRIS P1
Xpo1-207	ENSMUST00000150750.2	698	<u>233aa</u>	Protein coding	-	<u>F6YA11</u> &	CDS 5' and 3' incomplete TSL:5
Xpo1-205	ENSMUST00000136235.1	463	<u>59aa</u>	Protein coding	-	<u>A2AKT6</u> ₽	CDS 3' incomplete TSL:3
Xpo1-206	ENSMUST00000149371.1	2902	No protein	Processed transcript	-	-	TSL:5

42.17 kb -

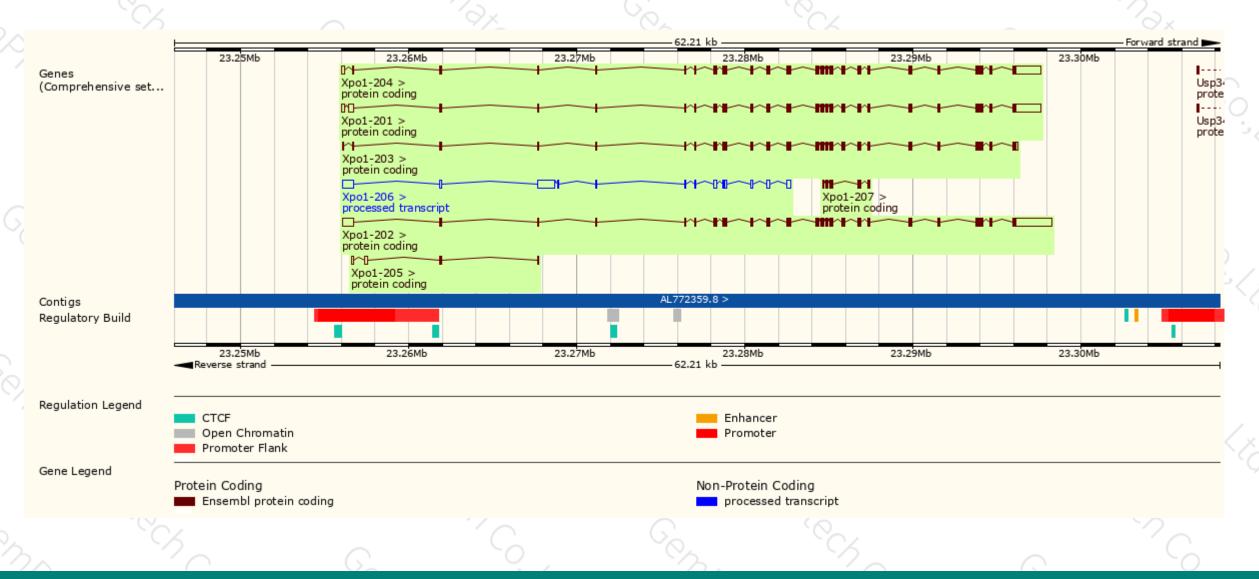
The strategy is based on the design of *Xpo1-202* transcript, the transcription is shown below:

Xpo1-202 > protein coding Forward strand

Genomic location distribution



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Protein domain

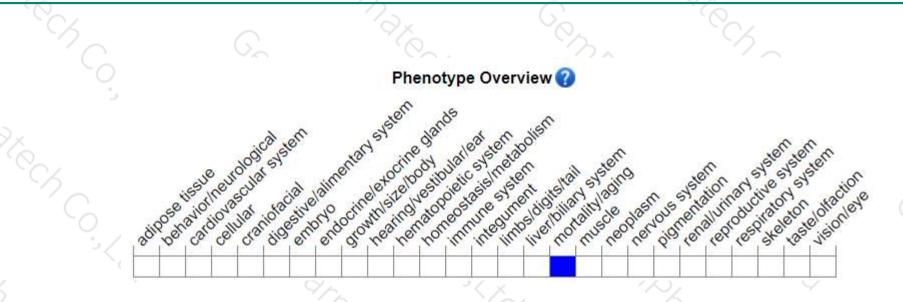


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	ENSMUSP00000099 PDB-ENSP mappings Coiled-coils (Ncoils) Superfamily SMART	Armadillo-type fold Importin-beta, N-t	erminal domain			Exportin-1, C-terr	ninal	- 0.3
	Pfam	Importin-beta, N-t Exp	erminal domain portin-1/Importin-beta-like		n maintenance repeat Exportin-1, repeat 3	Exportin-1, C-terr	ninal	
	PROSITE profiles PANTHER	Importin-beta, N-t	erminal domain	Exporti	n-1, repeat 2			
	PANTHER	PTHR11223 PTHR11223:SF4						
	Gene3D	Armadillo-like helical						
	All sequence SNPs/i	Sequence variants (dbSI	NP and all other sources)	1.1.		н	
	Variant Legend	synonymous variar	nt					
	Scale bar	0 100	200	300 400	500 6	700	800 900	1071
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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, null homozygotes show complete prenatal lethality prior to heart atrial

septation.

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



