

Ect2 Cas9-CKO Strategy

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Project Overview

Project Name

Ect2

Project type

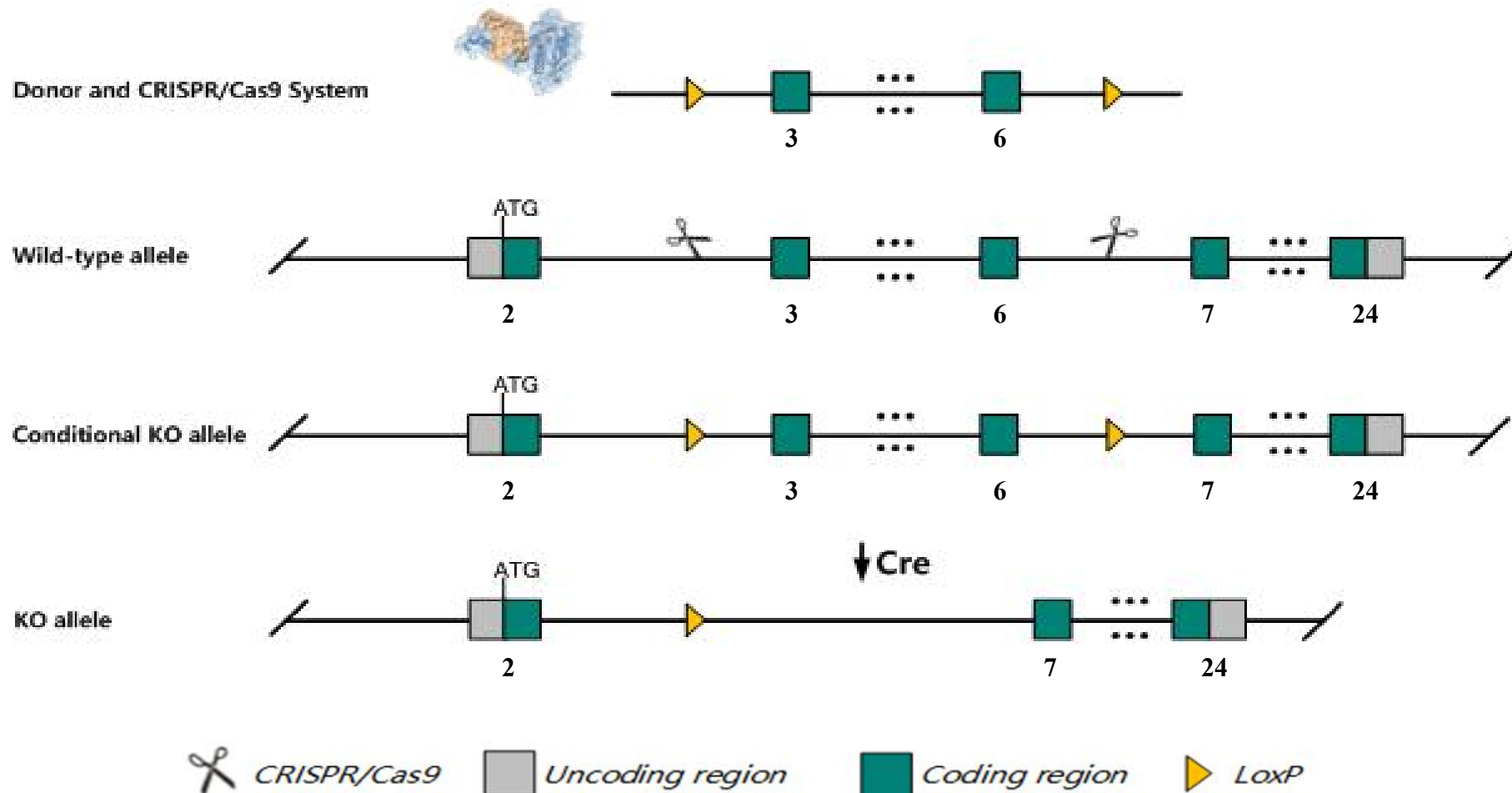
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ect2* gene. The schematic diagram is as follows:



The *Ect2* gene has 13 transcripts. According to the structure of *Ect2* gene, exon3-exon6 of *Ect2*-202(ENSMUST00000108298.8) transcript is recommended as the knockout region. The region contains 461bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Ect2* 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 disruption of this locus is embryonic lethal.

The *Ect2* gene is located on the Chr3. 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.

Ect2 ect2 oncogene [Mus musculus (house mouse)]

Gene ID: 13605, updated on 13-Mar-2020

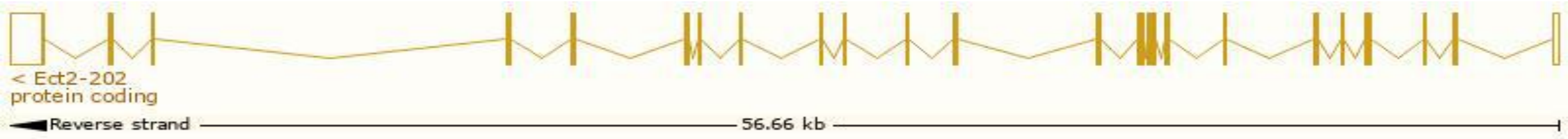
Summary**Official Symbol** Ect2 provided by [MGI](#)**Official Full Name** ect2 oncogene provided by [MGI](#)**Primary source** [MGI:MGI:95281](#)**See related** [Ensembl:ENSMUSG00000027699](#)**Gene type** protein coding**RefSeq status** VALIDATED**Organism** [Mus musculus](#)**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus**Also known as** AI528536**Expression** Biased expression in CNS E11.5 (RPKM 13.0), liver E14 (RPKM 11.1) and 12 other tissues [See more](#)**Orthologs** [human](#) [all](#)

Transcript information Ensembl

The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ect2-203	ENSMUST00000108300.7	4086	913aa	Protein coding	CCDS17270	Q07139	TSL:1 GENCODE basic APPRIS P3
Ect2-202	ENSMUST00000108298.8	4024	882aa	Protein coding	CCDS50875	Q07139	TSL:1 GENCODE basic APPRIS ALT1
Ect2-207	ENSMUST00000176242.8	3985	882aa	Protein coding	CCDS50875	Q07139	TSL:5 GENCODE basic APPRIS ALT1
Ect2-208	ENSMUST00000176535.7	712	188aa	Protein coding	-	H3BL29	CDS 3' incomplete TSL:2
Ect2-209	ENSMUST00000176780.7	683	174aa	Protein coding	-	H3BIZ5	CDS 3' incomplete TSL:3
Ect2-211	ENSMUST00000177055.7	675	181aa	Protein coding	-	H3BIW1	CDS 3' incomplete TSL:3
Ect2-206	ENSMUST00000175857.1	589	167aa	Protein coding	-	H3BK10	CDS 3' incomplete TSL:5
Ect2-212	ENSMUST00000184113.7	3935	133aa	Nonsense mediated decay	-	V9GXV8	TSL:2
Ect2-205	ENSMUST00000150061.1	687	80aa	Nonsense mediated decay	-	H3BL18	CDS 5' incomplete TSL:3
Ect2-201	ENSMUST00000108296.5	2228	No protein	Retained intron	-	-	TSL:1
Ect2-210	ENSMUST00000176908.1	797	No protein	Retained intron	-	-	TSL:3
Ect2-213	ENSMUST00000196926.1	565	No protein	Retained intron	-	-	TSL:2
Ect2-204	ENSMUST00000124727.1	554	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Ect2-202* transcript,the transcription is shown below:



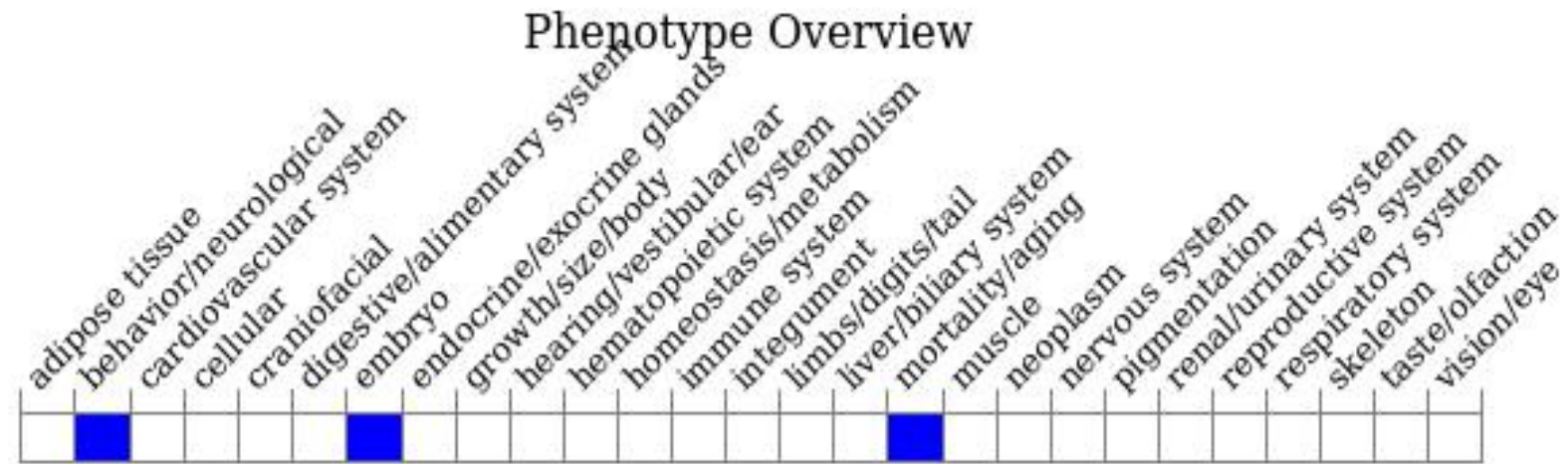
Genomic location distribution



集萃药康
GemPharmatech



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 disruption of this locus is embryonic lethal.

If you have any questions, you are welcome to inquire.
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