

Emsy Cas9-CKO Strategy

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-4-15

Project Overview

Project Name

Emsy

Project type

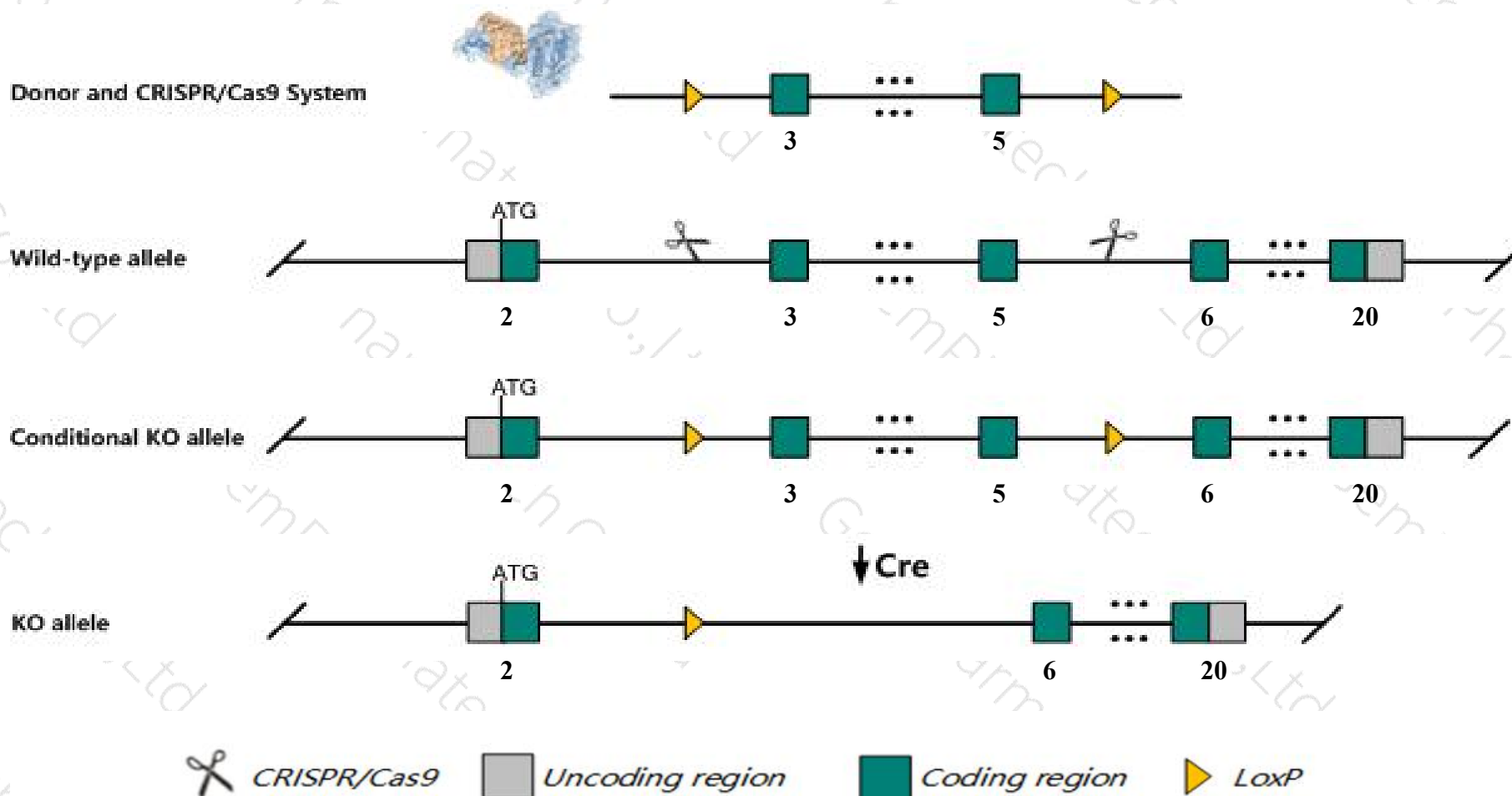
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Emsy* gene has 13 transcripts. According to the structure of *Emsy* gene, exon3-exon5 of *Emsy*-202 (ENSMUST00000205276.1) transcript is recommended as the knockout region. The region contains 217bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Emsy* 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.

- Transcript *Emsy-206* and *Emsy-212* may not be affected.
- The *Emsy* gene is located on the Chr7. 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)

Emsy EMSY, BRCA2-interacting transcriptional repressor [Mus musculus (house mouse)]

Gene ID: 233545, updated on 13-Mar-2020

Summary



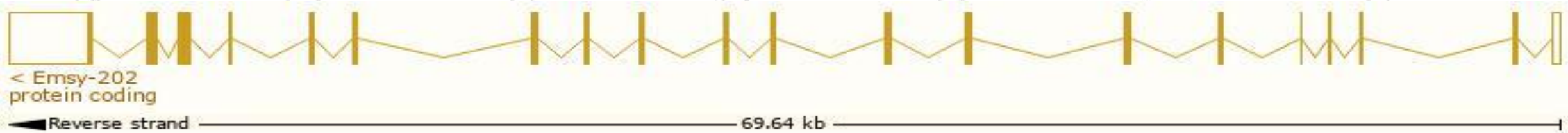
Official Symbol	Emsy provided by MGI
Official Full Name	EMSY, BRCA2-interacting transcriptional repressor provided by MGI
Primary source	MGI:MGI:1924203
See related	Ensembl:ENSMUSG00000035401
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2210018M11Rik, 2310016L09Rik, AU019521, AU019557
Expression	Ubiquitous expression in CNS E11.5 (RPKM 5.9), CNS E14 (RPKM 5.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

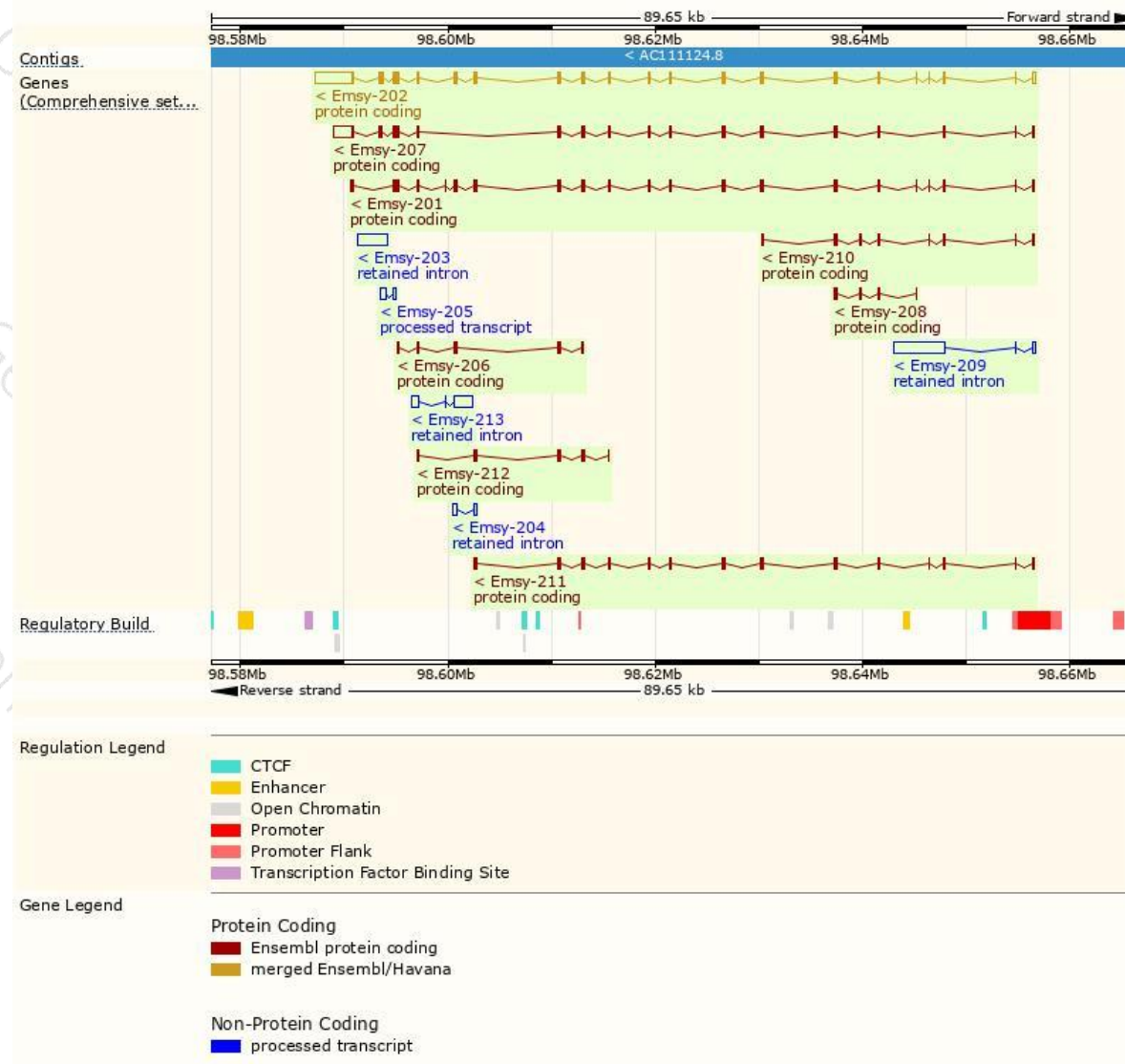
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Emsy-202	ENSMUST00000205276.1	7693	1264aa	Protein coding	CCDS40028	Q8BMB0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Emsy-207	ENSMUST00000205911.1	5079	1070aa	Protein coding	-	A0A0U1RPK1	TSL:5 GENCODE basic
Emsy-201	ENSMUST0000038359.5	3564	1118aa	Protein coding	-	Q8BMB0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Emsy-211	ENSMUST00000206619.1	2368	735aa	Protein coding	-	A0A0U1RPW3	CDS 3' incomplete TSL:1
Emsy-210	ENSMUST00000206611.1	1080	316aa	Protein coding	-	A0A0U1RNN7	CDS 3' incomplete TSL:5
Emsy-212	ENSMUST00000206626.1	740	246aa	Protein coding	-	A0A0U1RQ63	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Emsy-206	ENSMUST00000205886.1	707	235aa	Protein coding	-	A0A0U1RNQ4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Emsy-208	ENSMUST00000206256.1	600	200aa	Protein coding	-	A0A0U1RPN4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Emsy-205	ENSMUST00000205513.1	752	No protein	Processed transcript	-	-	TSL:2
Emsy-209	ENSMUST00000206565.1	5267	No protein	Retained intron	-	-	TSL:1
Emsy-203	ENSMUST00000205331.1	2965	No protein	Retained intron	-	-	TSL:NA
Emsy-213	ENSMUST00000206813.1	2394	No protein	Retained intron	-	-	TSL:1
Emsy-204	ENSMUST00000205485.1	525	No protein	Retained intron	-	-	TSL:3

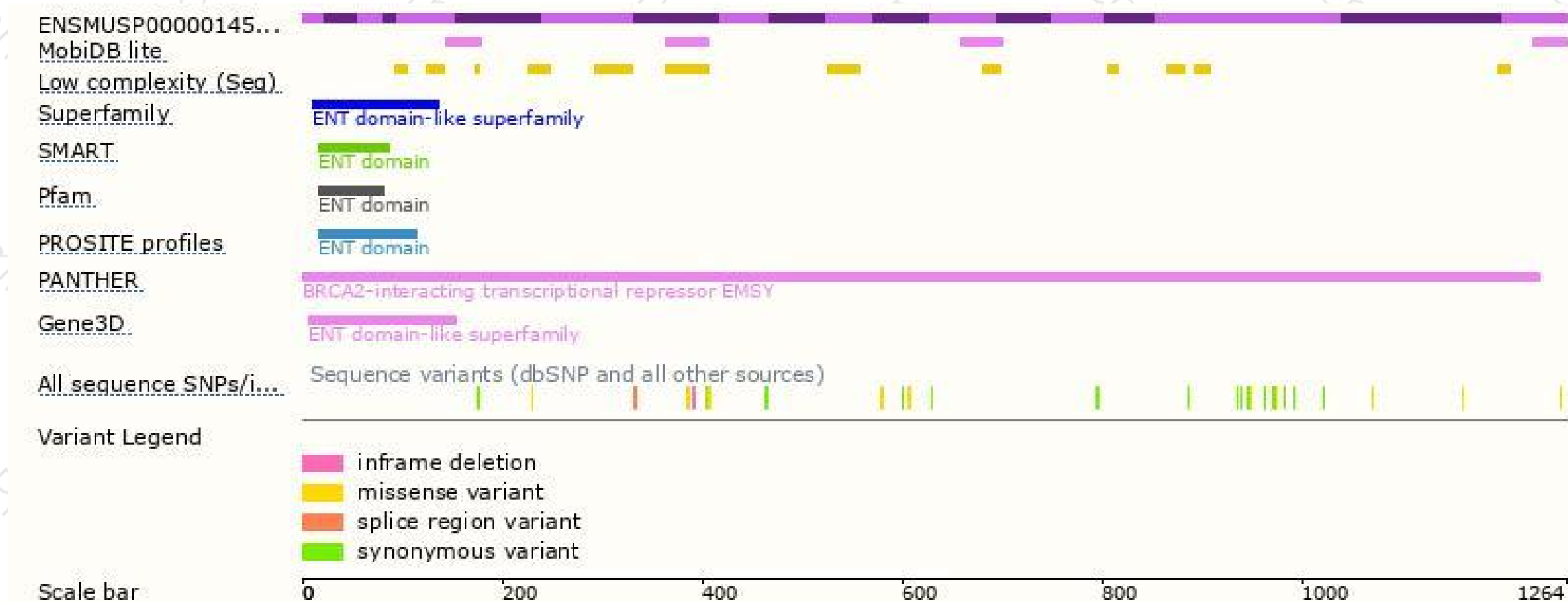
The strategy is based on the design of *Emsy-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

