Suz12 Cas9-CKO Strategy

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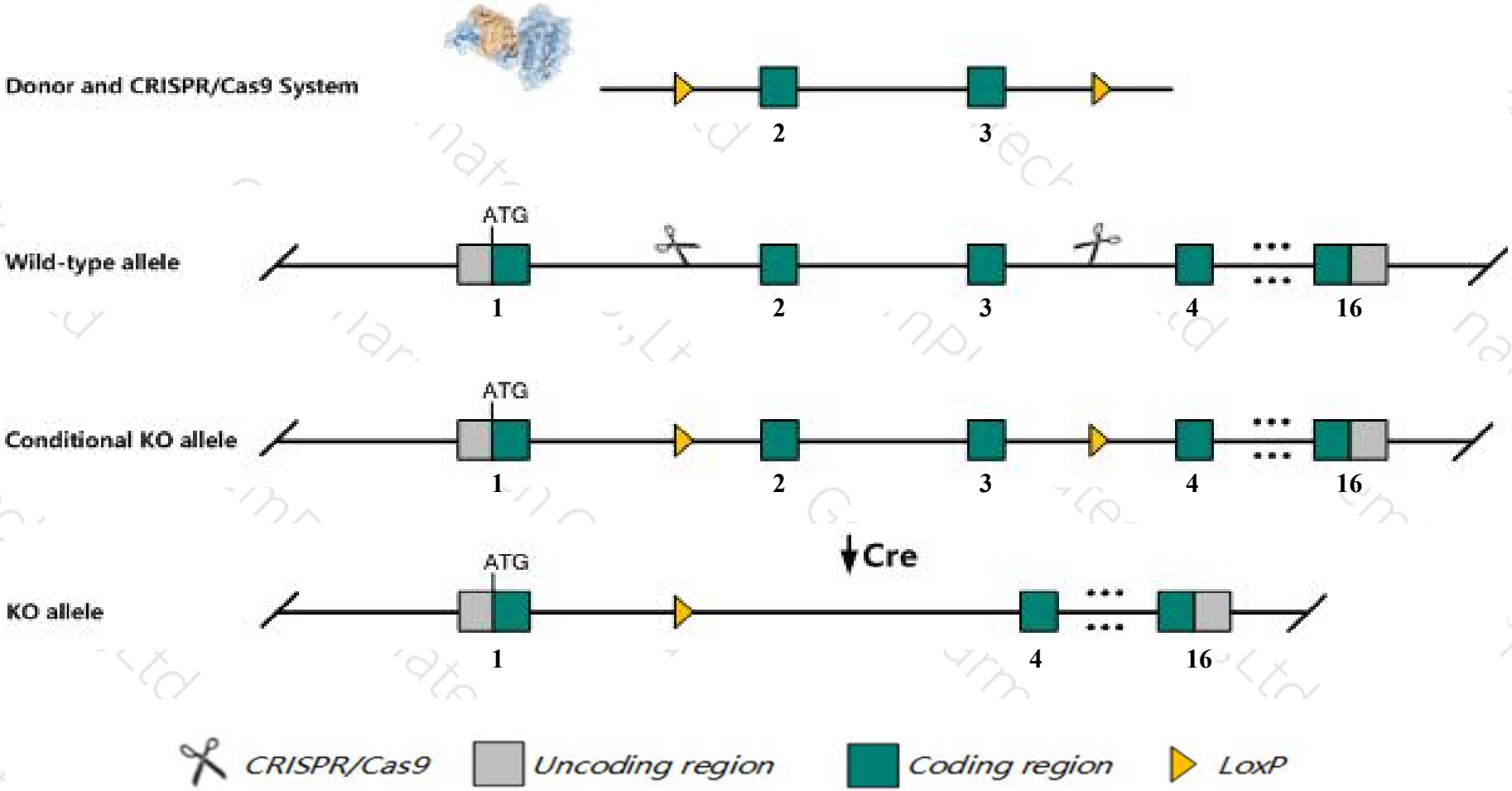
Project Overview

Project Name	***Suz12***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Suz12* gene. The schematic diagram is as follows:



Technical routes

- The *Suz12* gene has 6 transcripts. According to the structure of *Suz12* gene, exon2-exon3 of *Suz12-201* (ENSMUST00000017692.14) transcript is recommended as the knockout region.The region contains 112bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Suz12* 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.

Notice

- According to the existing MGI data,Homozygous null mice die during early postimplantation stages with failure of embryonic and extraembyronic tissues and organogenesis. Mice heterozygous for a knock-out allele exhibit abnormal brain and spinal cord development with varying penetrance.

- The *Suz12* 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）

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Suz12 SUZ12 polycomb repressive complex 2 subunit [Mus musculus (house mouse)]

Gene ID: 52615, updated on 10-Feb-2019

Summary

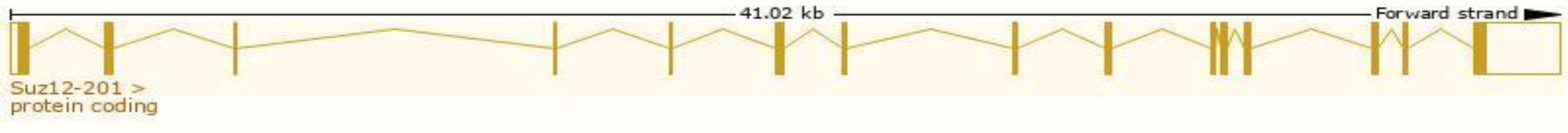
Official Symbol	Suz12 provided by MGI
Official Full Name	SUZ12 polycomb repressive complex 2 subunit provided byMGI
Primary source	MGI:MGI:1261758
See related	Ensembl:ENSMUSG00000017548
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610028O16Rik, AI195385, AU016842, AW536442, D11Ertd530e, mKIAA0160
Summary	This gene encodes a core component of the polycomb repressive complex 2 (PRC2) that also includes, at least, embryonic ectoderm development protein (EED) and enhancer of zeste homolog 1 or 2 (EZH1 or EZH2). Through the methyltransferase activity of EZH1 or EZH2, the PRC2 complex methylates Lys9 and Lys27 of histone 3 and Lys26 of histone 1, leading to recruitment of the PRC1 complex, histone 2A ubiquitylation and transcriptional repression of the target genes. This gene product is essential for the activity and integrity of the PRC2 complex, and is required for X chromosome inactivation, stem cell maintenance and differentiation. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2009]
Expression	Broad expression in liver E14 (RPKM 18.5), CNS E11.5 (RPKM 16.1) and 25 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

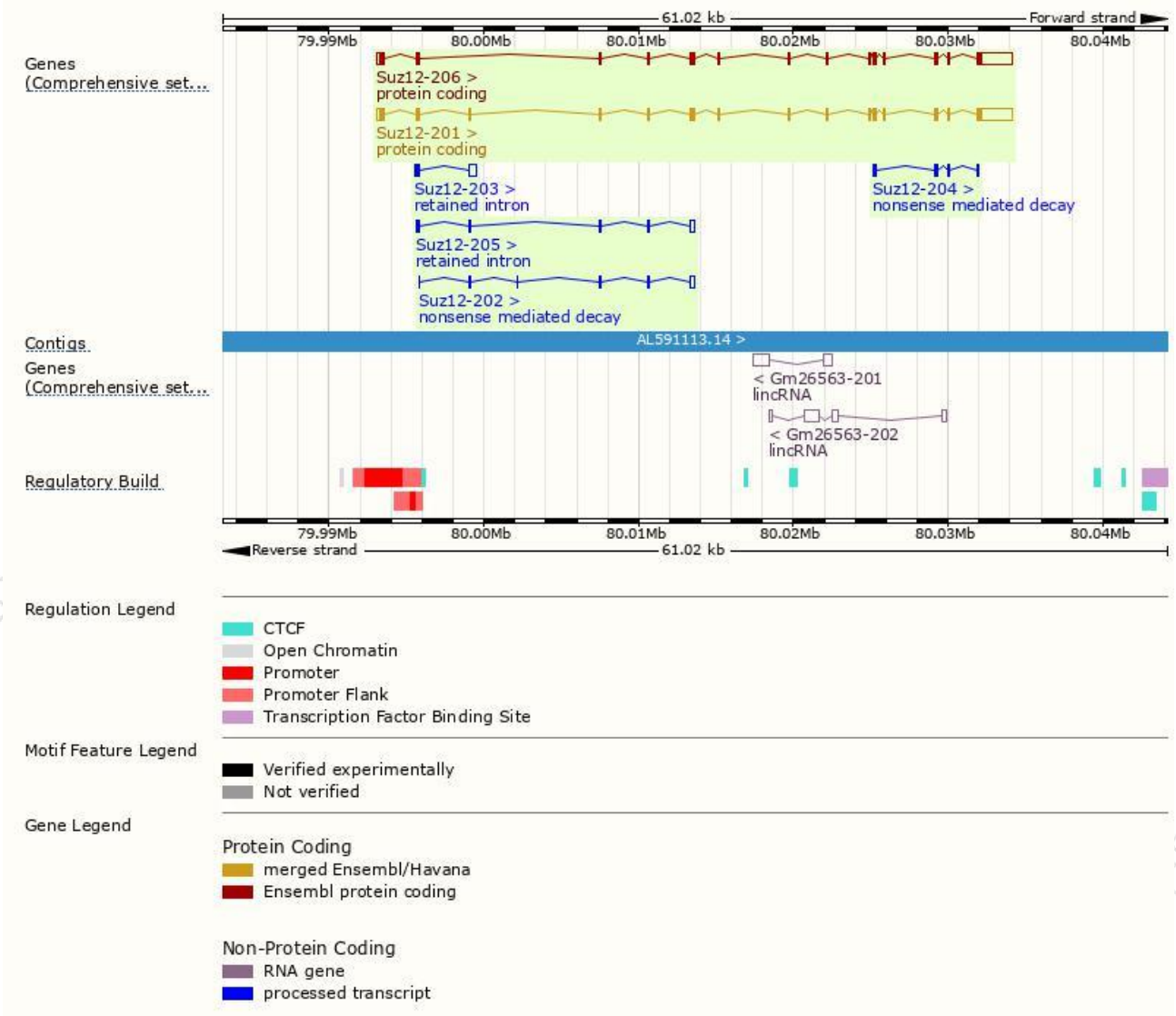
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Suz12-201	ENSMUST00000017692.14	4373	741aa	Protein coding	CCDS25125	Q80U70	TSL:1 GENCODE basic APPRIS P3
Suz12-206	ENSMUST00000163272.1	4303	718aa	Protein coding	CCDS48860	E9PW15	TSL:5 GENCODE basic APPRIS ALT2
Suz12-204	ENSMUST00000144188.1	553	51aa	Nonsense mediated decay	-	F7B7H9	CDS 5' incomplete TSL:3
Suz12-202	ENSMUST00000126091.1	488	59aa	Nonsense mediated decay	-	F6Z494	CDS 5' incomplete TSL:5
Suz12-203	ENSMUST00000132312.7	651	No protein	Retained intron	-	-	TSL:3
Suz12-205	ENSMUST00000148140.1	611	No protein	Retained intron	-	-	TSL:3

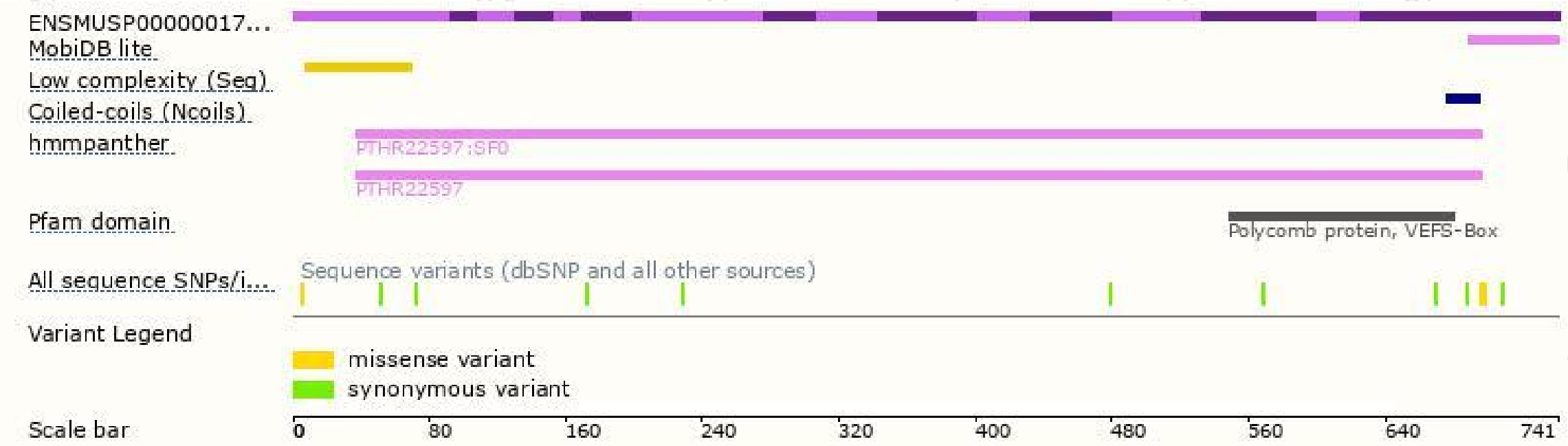
The strategy is based on the design of *Suz12-201* transcript,The transcription is shown below



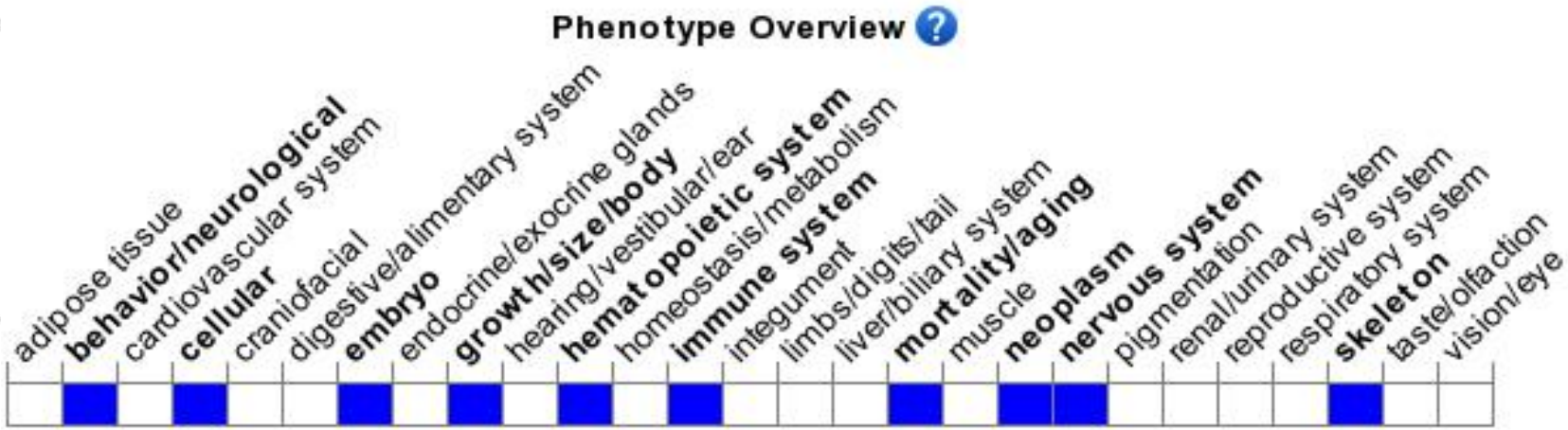
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



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

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

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