

Ess2 Cas9-CKO Strategy

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Project Overview

Project Name

Ess2

Project type

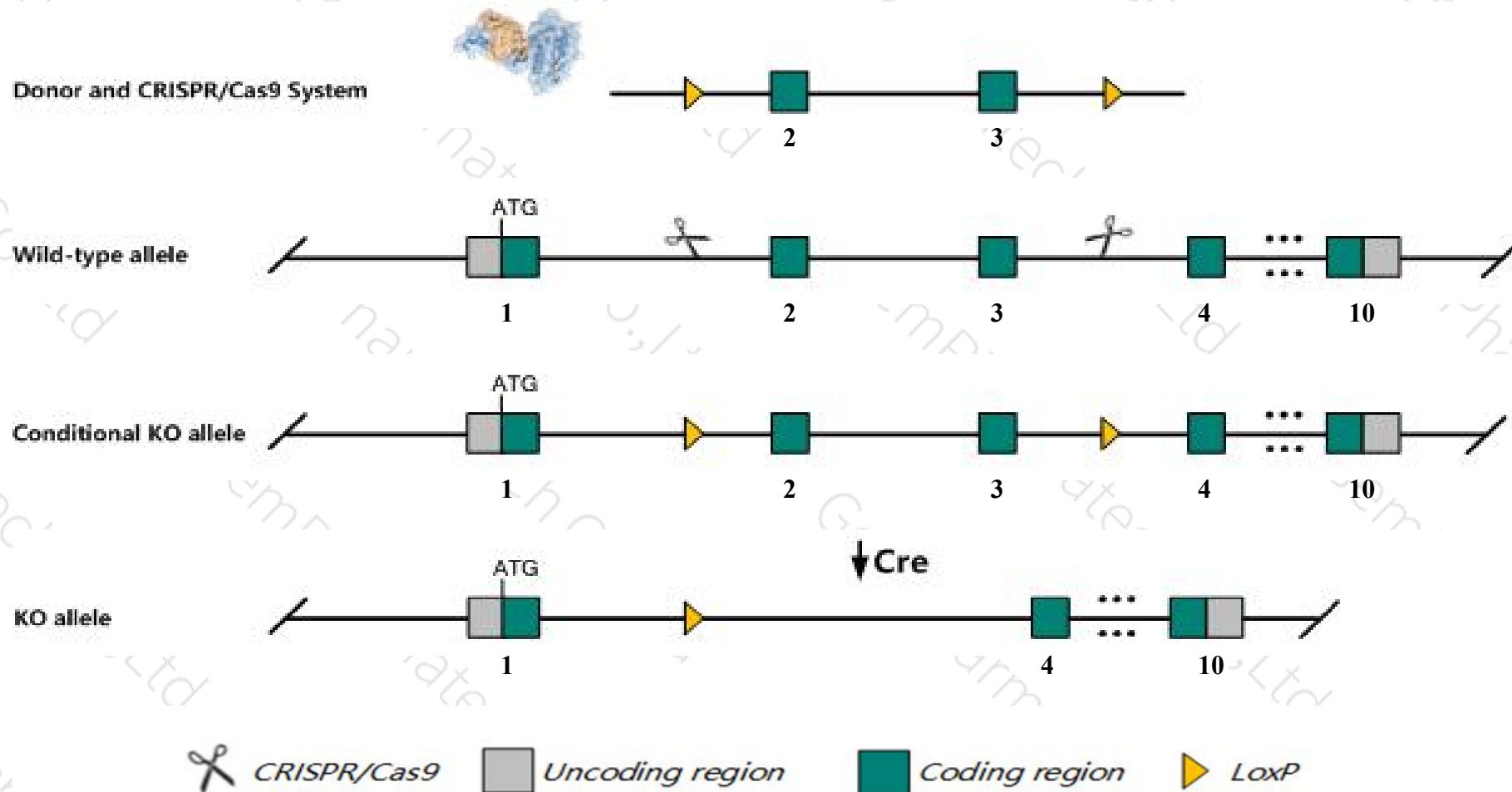
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ess2* gene. The schematic diagram is as follows:



Technical routes

- The *Ess2* gene has 5 transcripts. According to the structure of *Ess2* gene, exon2-exon3 of *Ess2-201* (ENSMUST00000003621.9) transcript is recommended as the knockout region. The region contains 265bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ess2* 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

- The *Ess2* gene is located on the Chr16. 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.
- The transcripts of *Ess2*-202&203&204 may not be affected.
- 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)

Ess2 ess-2 splicing factor [Mus musculus (house mouse)]

Gene ID: 27886, updated on 13-Mar-2020

Summary



Official Symbol Ess2 provided by [MGI](#)

Official Full Name ess-2 splicing factor provided by [MGI](#)

Primary source [MGI:MGI:107854](#)

See related [Ensembl:ENSMUSG000000003527](#)

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 AI462402, D16H22S1269E, Dgcr1, Dgcr14, Dgsi, ES2, Es2el

Summary The human ortholog of this gene is located within the minimal DGS critical region (MDGCR) thought to contain the gene(s) responsible for a group of developmental disorders. These disorders include DiGeorge syndrome, velocardiofacial syndrome, conotruncal anomaly face syndrome, and some familial or sporadic conotruncal cardiac defects which have been associated with microdeletion of human chromosome band 22q11.2. The encoded protein localizes to the nucleus, and the orthologous protein in humans co-purifies with C complex spliceosomes. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Expression Ubiquitous expression in whole brain E14.5 (RPKM 8.4), CNS E14 (RPKM 8.2) and 28 other tissues [See more](#)

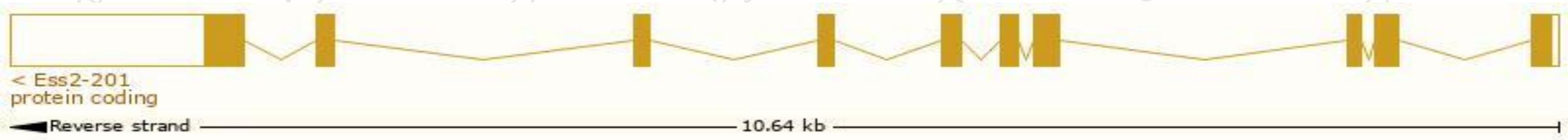
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

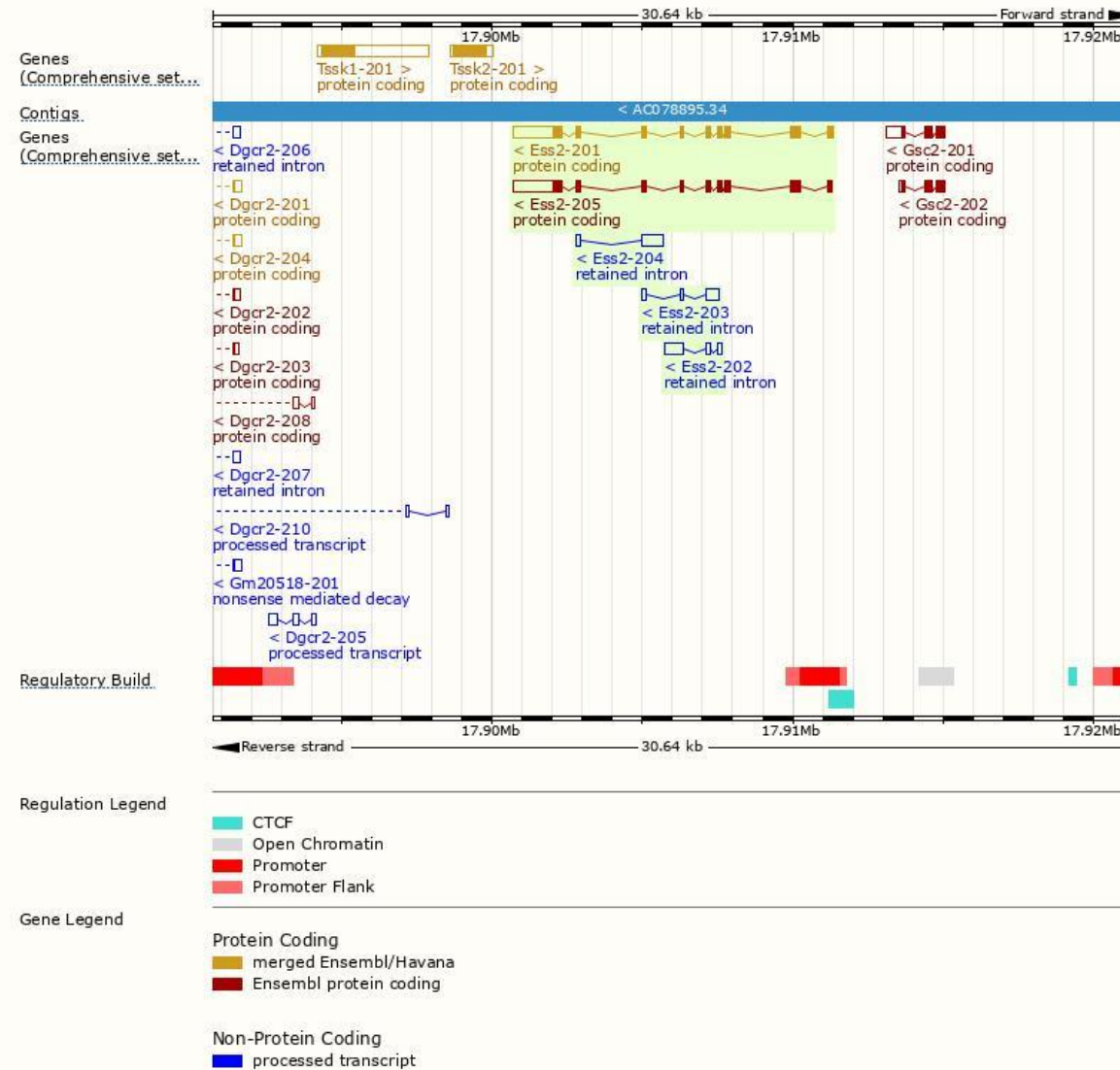
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ess2-201	ENSMUST00000003621.9	2821	480aa	Protein coding	CCDS28013	Q3UFM6	TSL:1 GENCODE basic APPRIS P2
Ess2-205	ENSMUST00000232423.1	2785	479aa	Protein coding	-	O70279	GENCODE basic APPRIS ALT2
Ess2-202	ENSMUST00000231921.1	914	No protein	Retained intron	-	-	
Ess2-204	ENSMUST00000232366.1	800	No protein	Retained intron	-	-	
Ess2-203	ENSMUST00000232111.1	653	No protein	Retained intron	-	-	

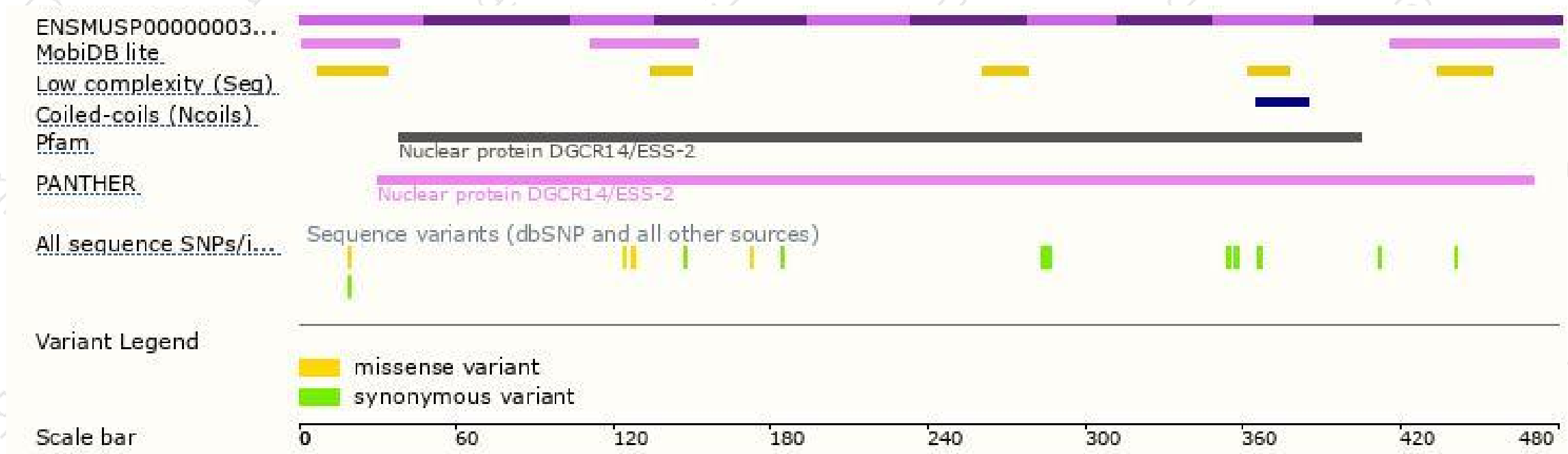
The strategy is based on the design of *Ess2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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