Ess2 Cas9-KO Strategy

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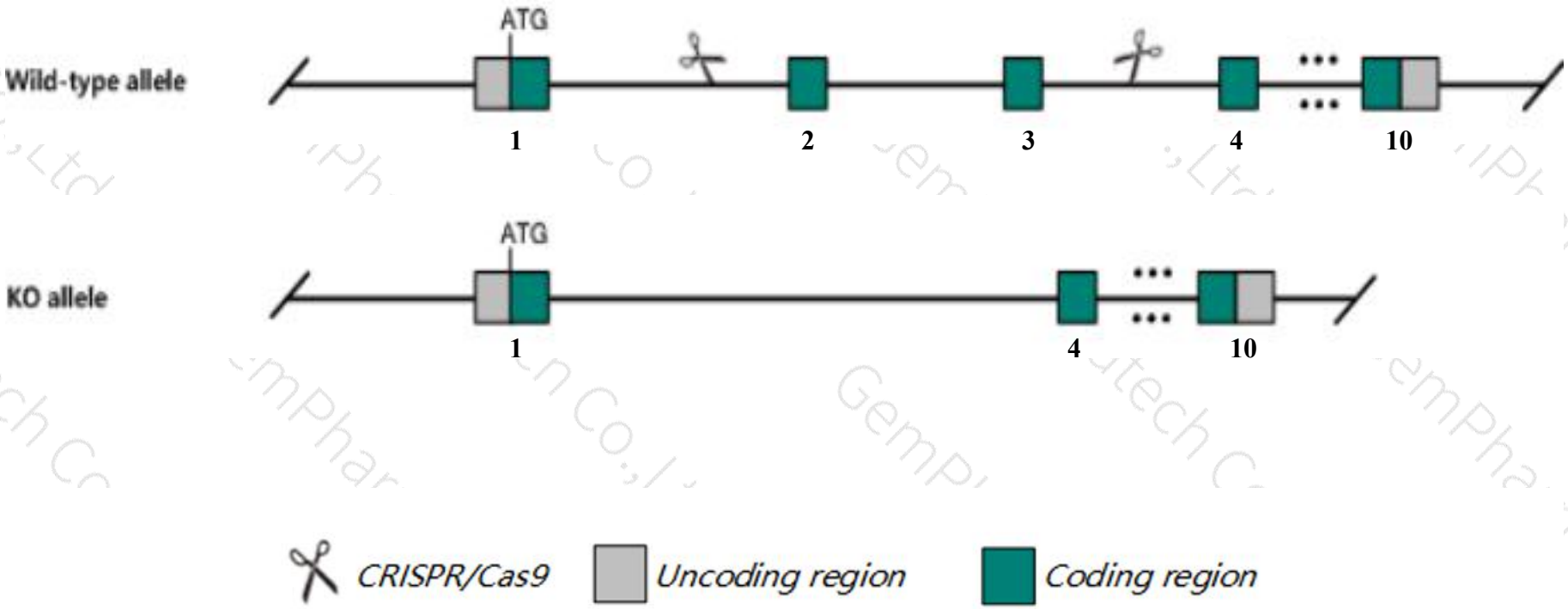
Project Overview

Project Name	***Ess2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

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 v

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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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

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

Summary

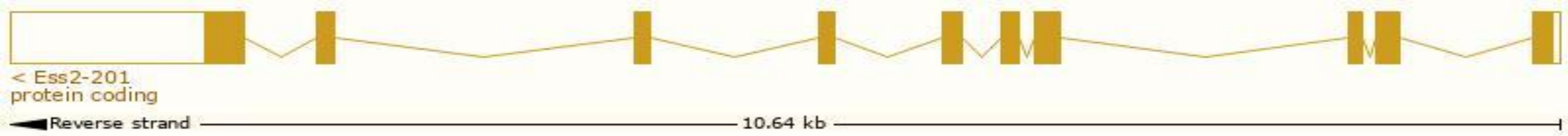
Official Symbol	Ess2 provided by MGI
Official Full Name	ess-2 splicing factor provided by MGI
Primary source	MGI:MGI:107854
See related	Ensembl:ENSMUSG00000003527
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 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 tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

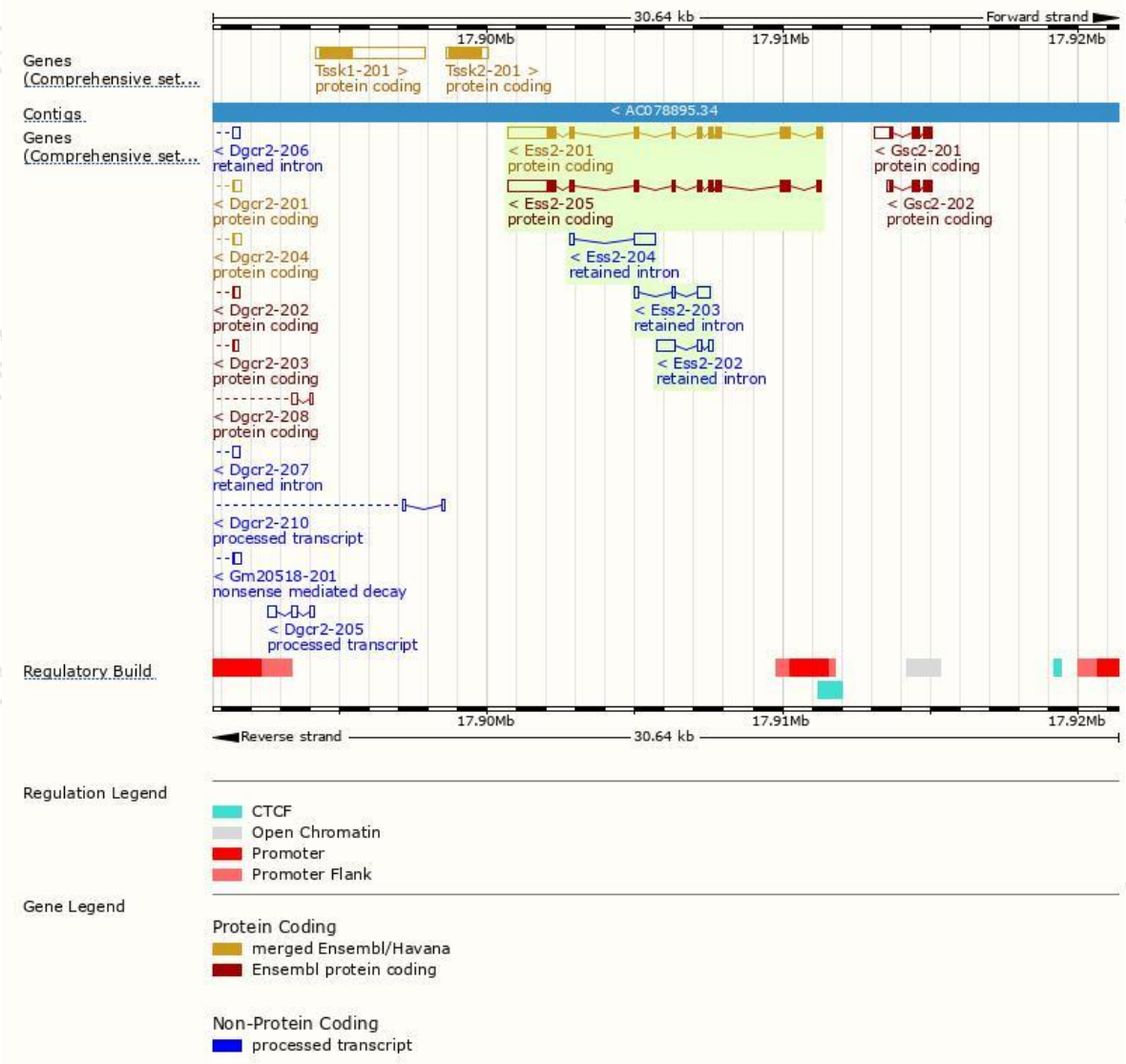
The gene has 5 transcripts,all transcripts are shown below:

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	-	-	

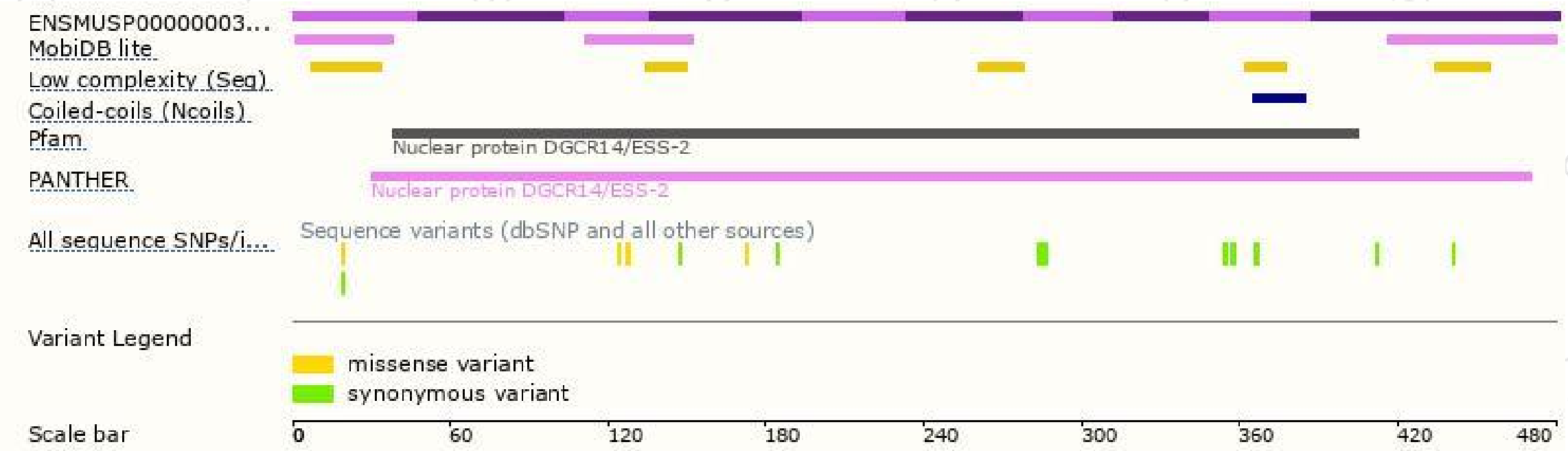
The strategy is based on the design of *Ess2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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