

Spc25 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Spc25

Project type

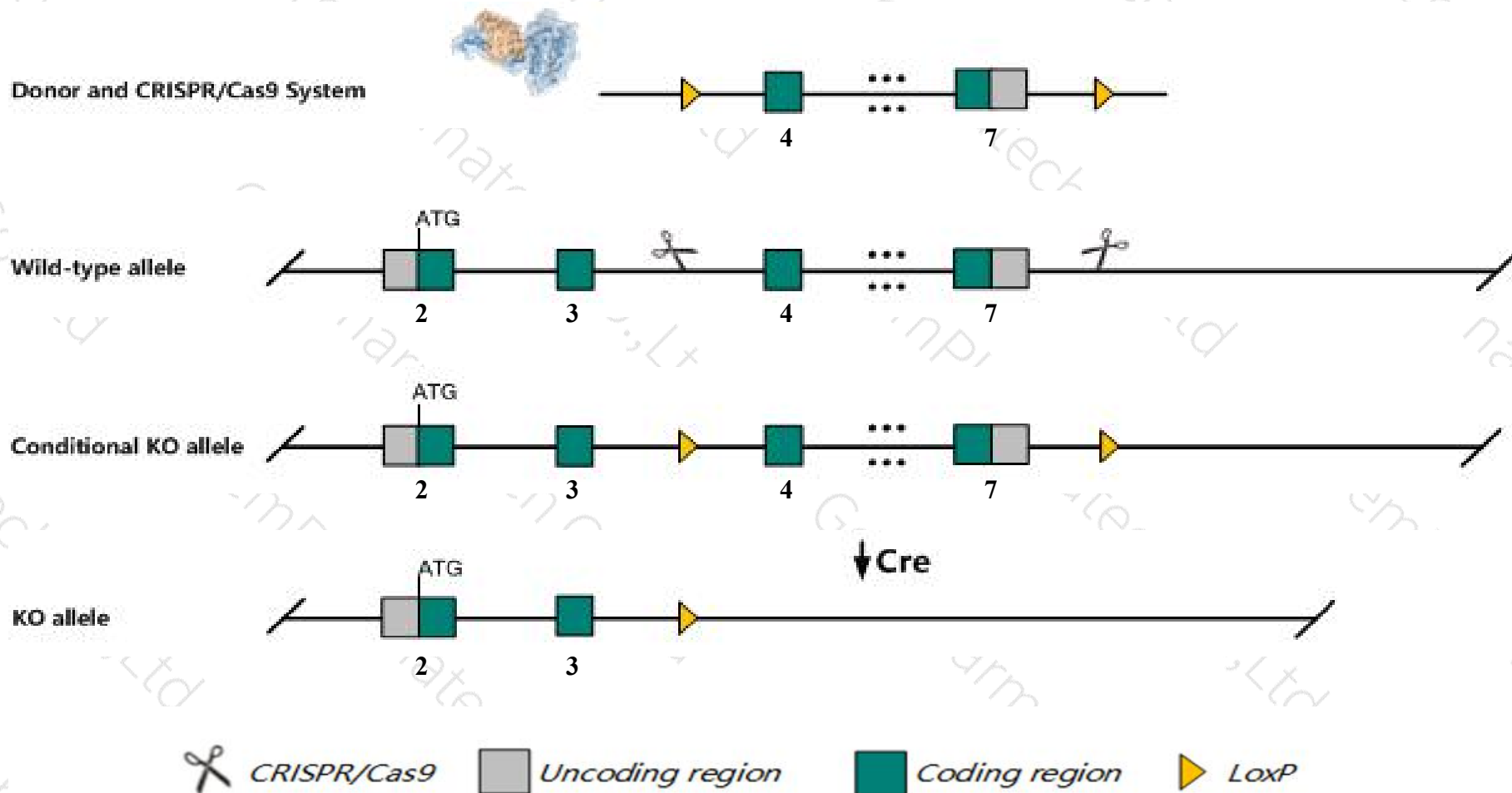
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Spc25* gene. The schematic diagram is as follows:



Technical routes

- The *Spc25* gene has 9 transcripts. According to the structure of *Spc25* gene, exon4-exon7 of *Spc25-202* (ENSMUST00000112320.7) transcript is recommended as the knockout region. The region contains 476bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Spc25* 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 *Spc25* gene is located on the Chr2. 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)

Spc25 SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Mus musculus (house mouse)]

Gene ID: 66442, updated on 31-Jan-2019

Summary



Official Symbol Spc25 provided by [MGI](#)

Official Full Name SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) provided by [MGI](#)

Primary source [MGI:MGI:1913692](#)

See related [Ensembl:ENSMUSG000000005233](#)

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 2600017H08Rik, 2610205L13Rik, Spbc25

Summary This gene encodes a component of the kinetochore-associated NDC80 protein complex, which is required for the mitotic spindle checkpoint and for microtubule-kinetochore attachment. During meiosis in mouse, the protein localizes to the germinal vesicle and then is associated with the chromosomes following germinal vesicle breakdown. Knockdown of this gene in oocytes results in precocious polar body extrusion, chromosome misalignment and aberrant spindle formation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2015]

Expression Biased expression in liver E14 (RPKM 25.3), CNS E11.5 (RPKM 24.7) and 10 other tissues [See more](#)

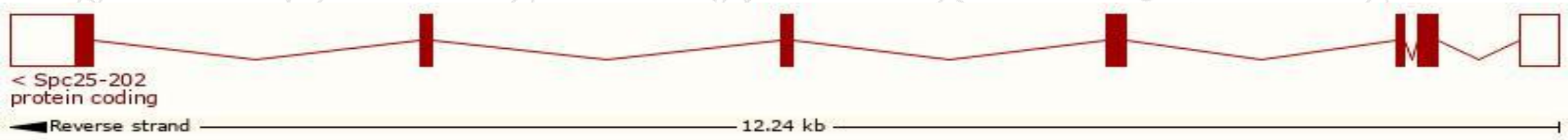
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

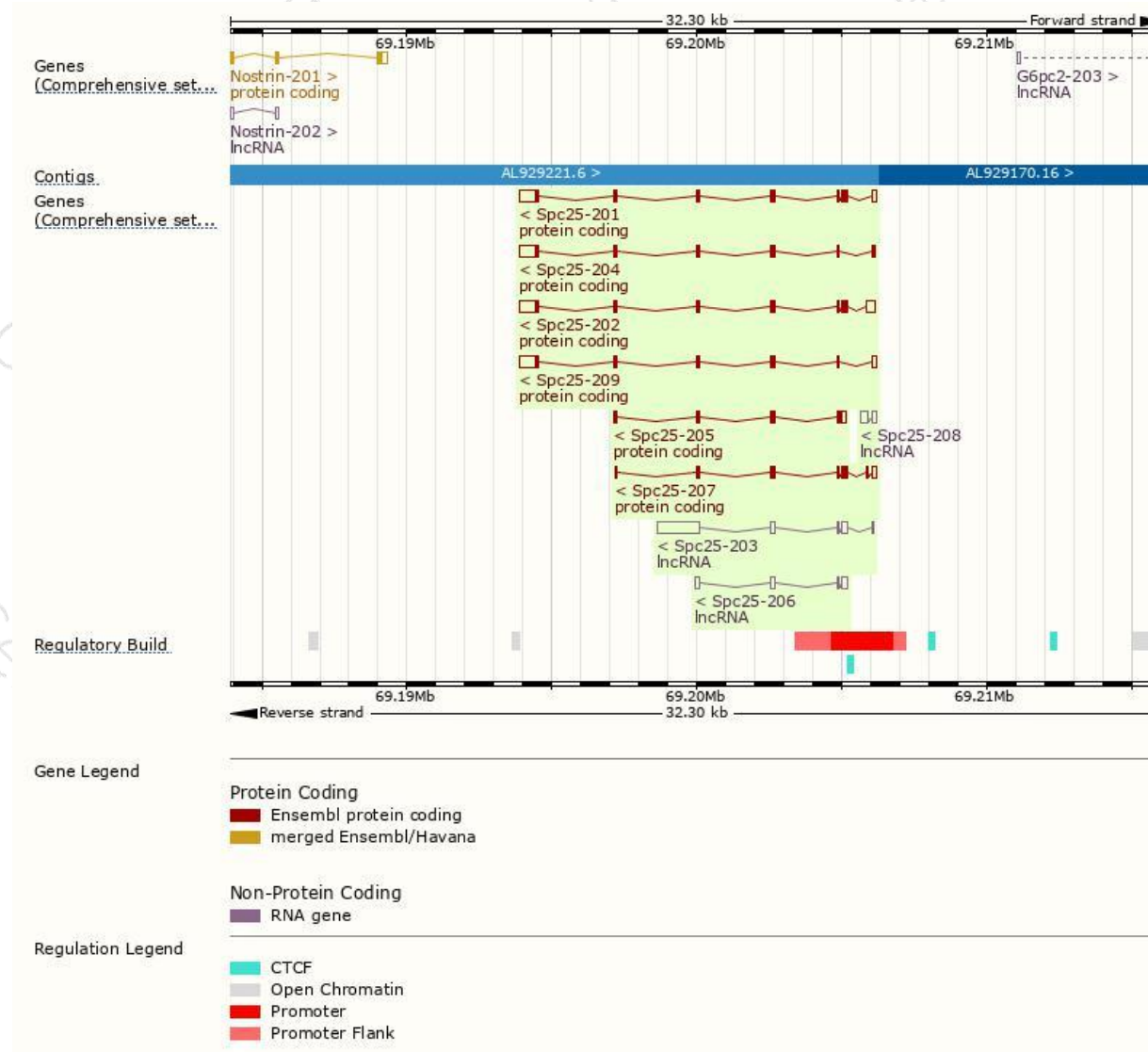
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spc25-202	ENSMUST00000112320.7	1527	226aa	Protein coding	CCDS57174	Q3UA16	TSL:1 GENCODE basic APPRIS ALT2
Spc25-201	ENSMUST00000005365.14	1352	226aa	Protein coding	CCDS57174	Q3UA16	TSL:1 GENCODE basic APPRIS ALT2
Spc25-209	ENSMUST00000167875.8	1194	178aa	Protein coding	CCDS16088	Q3UA16	TSL:1 GENCODE basic APPRIS P3
Spc25-204	ENSMUST00000127243.7	1162	211aa	Protein coding	-	A2AUT4	CDS 5' incomplete TSL:1
Spc25-207	ENSMUST00000149643.1	685	167aa	Protein coding	-	A2AUT3	CDS 3' incomplete TSL:5
Spc25-205	ENSMUST00000149045.7	545	133aa	Protein coding	-	A2AUT1	CDS 3' incomplete TSL:3
Spc25-203	ENSMUST00000126638.7	1869	No protein	lncRNA	-	-	TSL:1
Spc25-206	ENSMUST00000149401.1	570	No protein	lncRNA	-	-	TSL:2
Spc25-208	ENSMUST00000150505.1	361	No protein	lncRNA	-	-	TSL:3

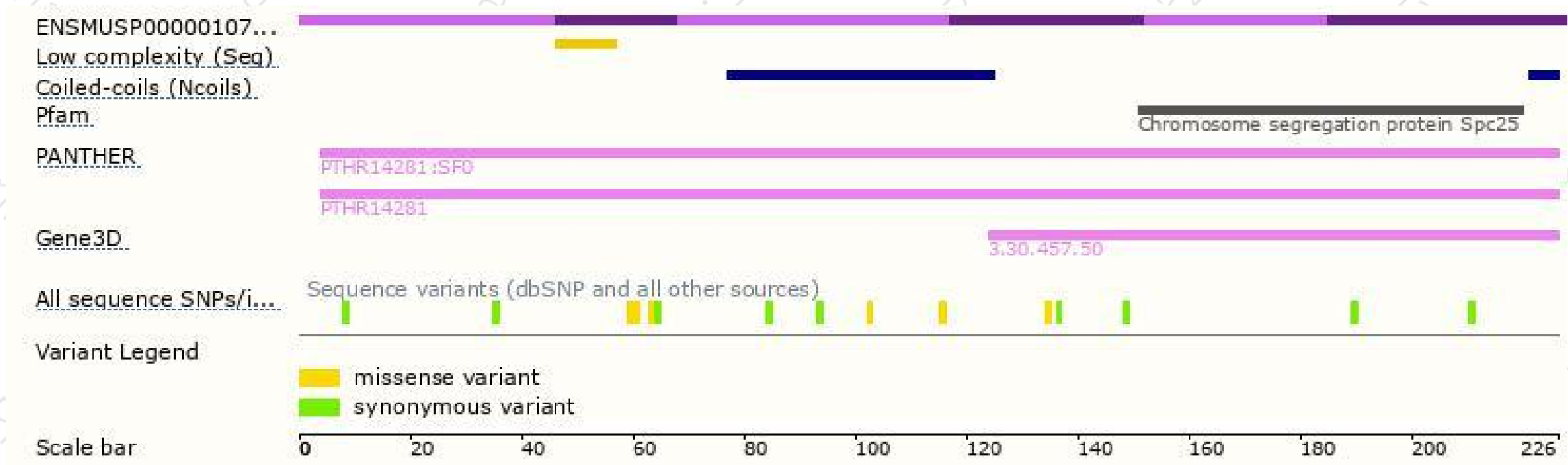
The strategy is based on the design of *Spc25-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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