Sall4 Cas9-KO Strategy

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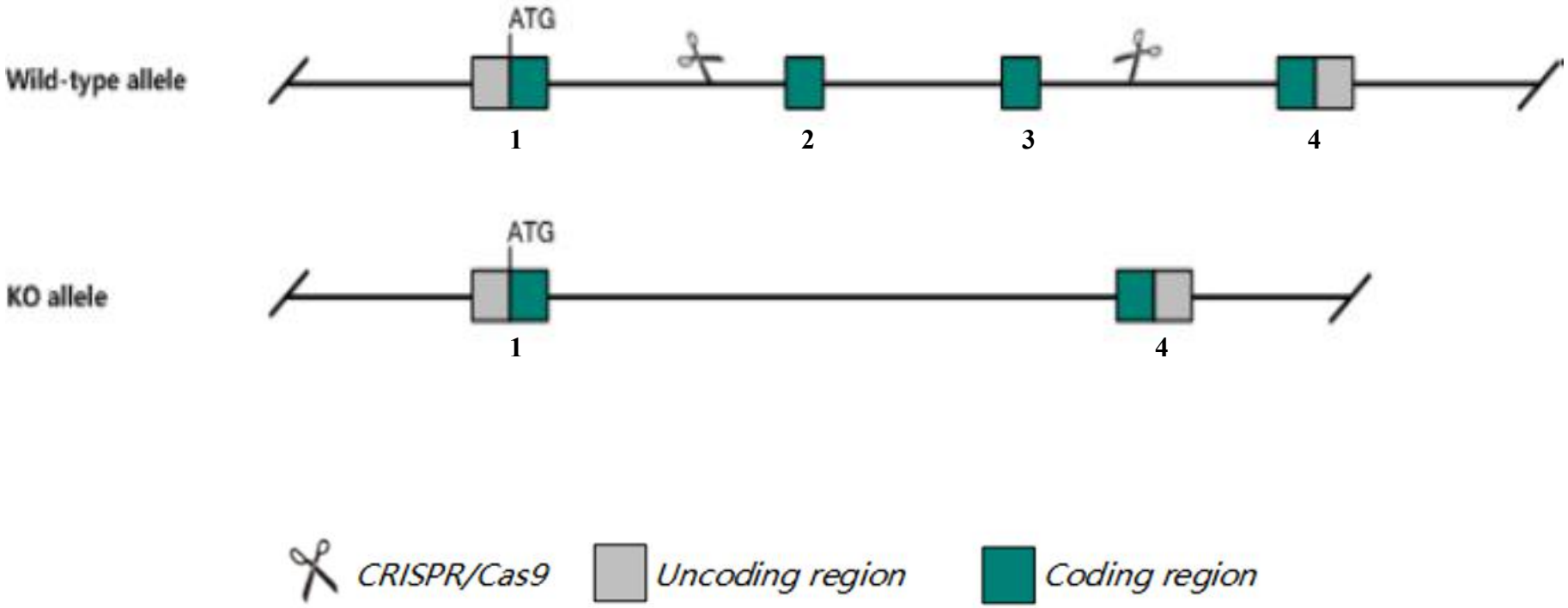
Project Overview

Project Name	***Sall4***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sall4* gene. The schematic diagram is as follows:



Technical routes

The *Sall4* gene has 7 transcripts. According to the structure of *Sall4* gene, exon2-exon3 of *Sall4-201*(ENSMUST00000029061.11) transcript is recommended as the knockout region.The region contains 2654bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Sall4* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

According to the existing MGI data,homozygous mutation of this gene results in early embryonic lethality before somite formation. Heterozygous mutation of this locus causes variable phenotypes, from heart and digit defects to deafness, anogenital tract defects, cranial and carpal bone defects and renal agenesis or hypoplasia.

The *Sall4* 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 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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Sall4 spalt like transcription factor 4 [Mus musculus (house mouse)]

Gene ID: 99377, updated on 13-Mar-2020

Summary

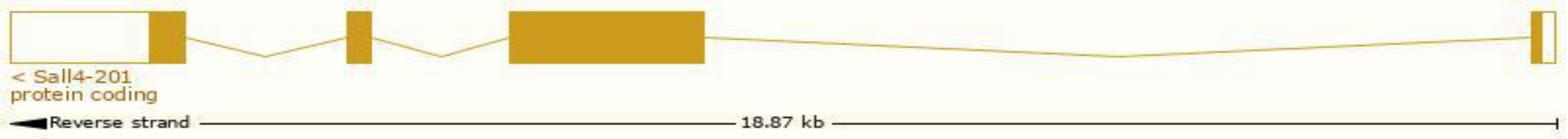
Official Symbol	Sall4 provided by MGI
Official Full Name	spalt like transcription factor 4 provided by MGI
Primary source	MGI:MGI:2139360
See related	Ensembl:ENSMUSG00000027547
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730441M18Rik, AA407717, AL022809, AW536104, C330011P20Rik, C78083, C78563, Tex20
Summary	This gene belongs to the spalt family of zinc finger transcription factors. In mouse, functions for this gene have been described in many embryonic developmental processes, including brain, heart, and limb development. In addition, this gene is an important pluripotency factor that is required for stem cell maintenance. Homozygous mutant mice display embryonic lethality, while conditional knock-out in embryonic germ cells results in failure to establish a robust stem cell population. A pseudogene of this gene is found on chromosome 2. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2015]
Expression	Biased expression in placenta adult (RPKM 3.0), CNS E11.5 (RPKM 2.6) and 8 other tissues See more
Orthologs	human all

Transcript information Ensembl

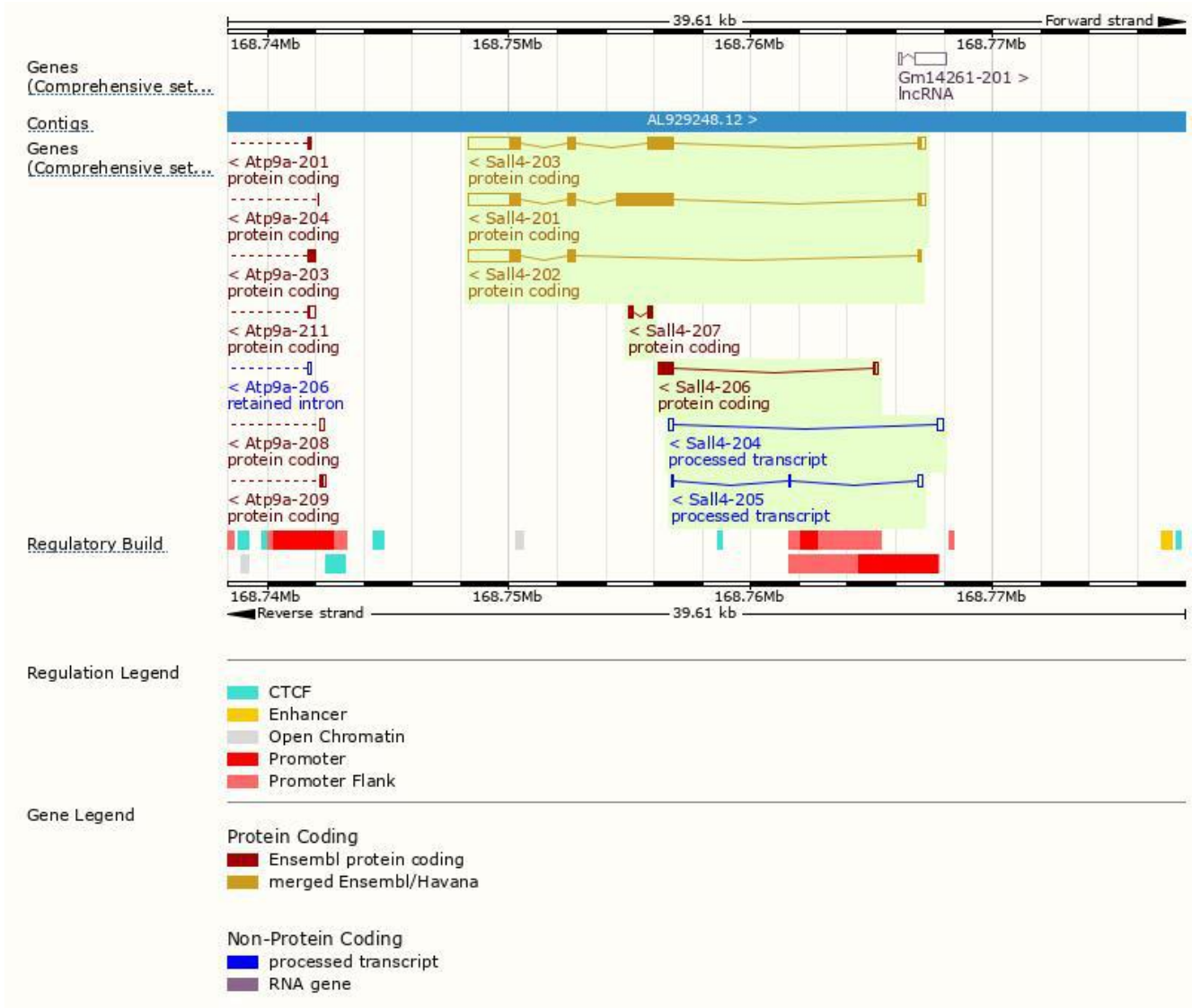
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sall4-201	ENSMUST00000029061.11	5073	1067aa	Protein coding	CCDS17115	Q8BX22	TSL:1 GENCODE basic APPRIS P1
Sall4-203	ENSMUST00000103074.1	3741	623aa	Protein coding	CCDS17116	Q8BX22	TSL:1 GENCODE basic
Sall4-202	ENSMUST00000075044.9	2534	278aa	Protein coding	CCDS17117	Q8BX22	TSL:1 GENCODE basic
Sall4-206	ENSMUST00000137536.1	773	215aa	Protein coding	-	A2AUZ7	CDS 3' incomplete TSL:2
Sall4-207	ENSMUST00000150588.1	393	131aa	Protein coding	-	A2AUZ6	CDS 5' and 3' incomplete TSL:2
Sall4-204	ENSMUST00000125138.1	423	No protein	Processed transcript	-	-	TSL:3
Sall4-205	ENSMUST00000130640.1	328	No protein	Processed transcript	-	-	TSL:3

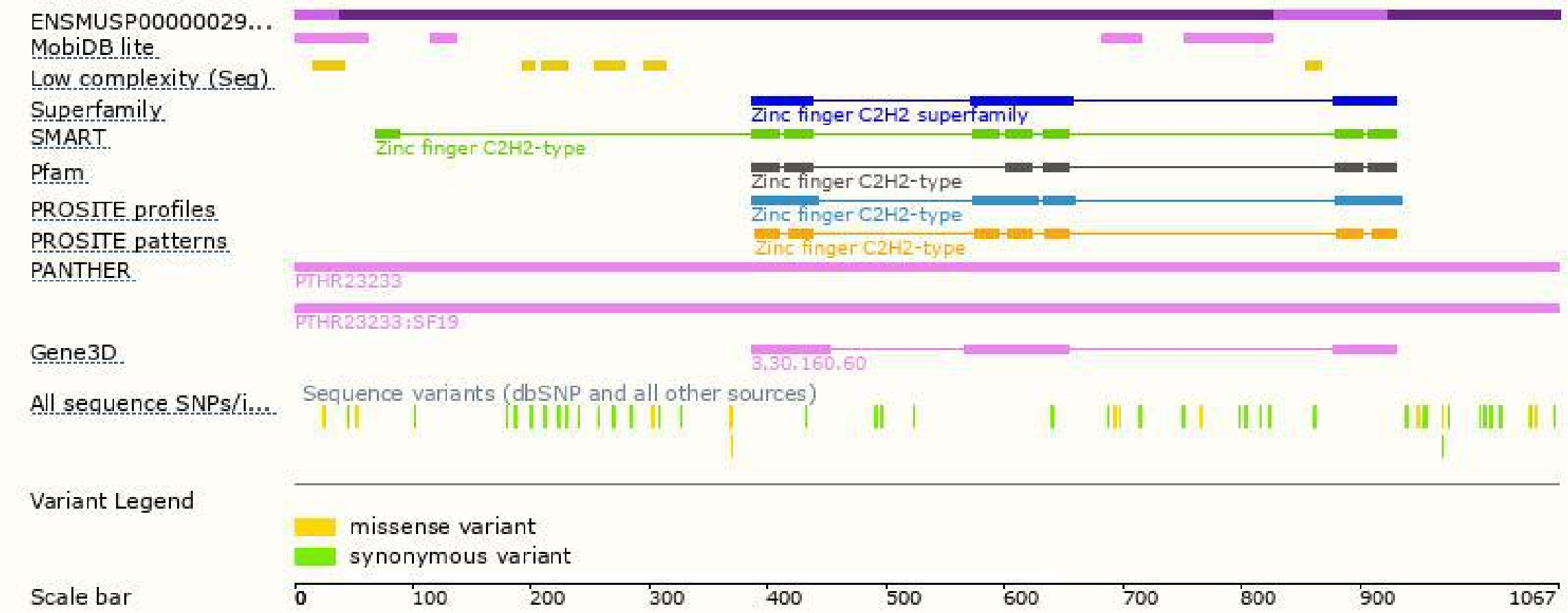
The strategy is based on the design of *Sall4-201* transcript,the transcription is shown below:



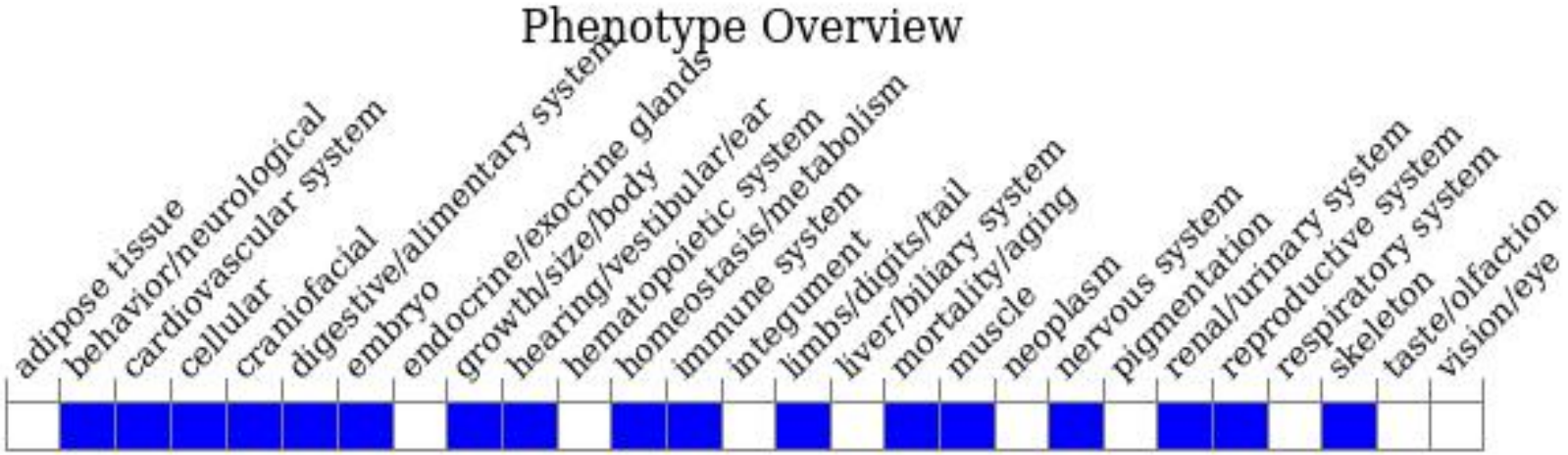
Genomic location distribution



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/).

According to the existing MGI data,homozygous mutation of this gene results in early embryonic lethality before somite formation. Heterozygous mutation of this locus causes variable phenotypes, from heart and digit defects to deafness, anogenital tract defects, cranial and carpal bone defects and renal agenesis or hypoplasia.

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