Sec24c Cas9-CKO Strategy

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Project Overview

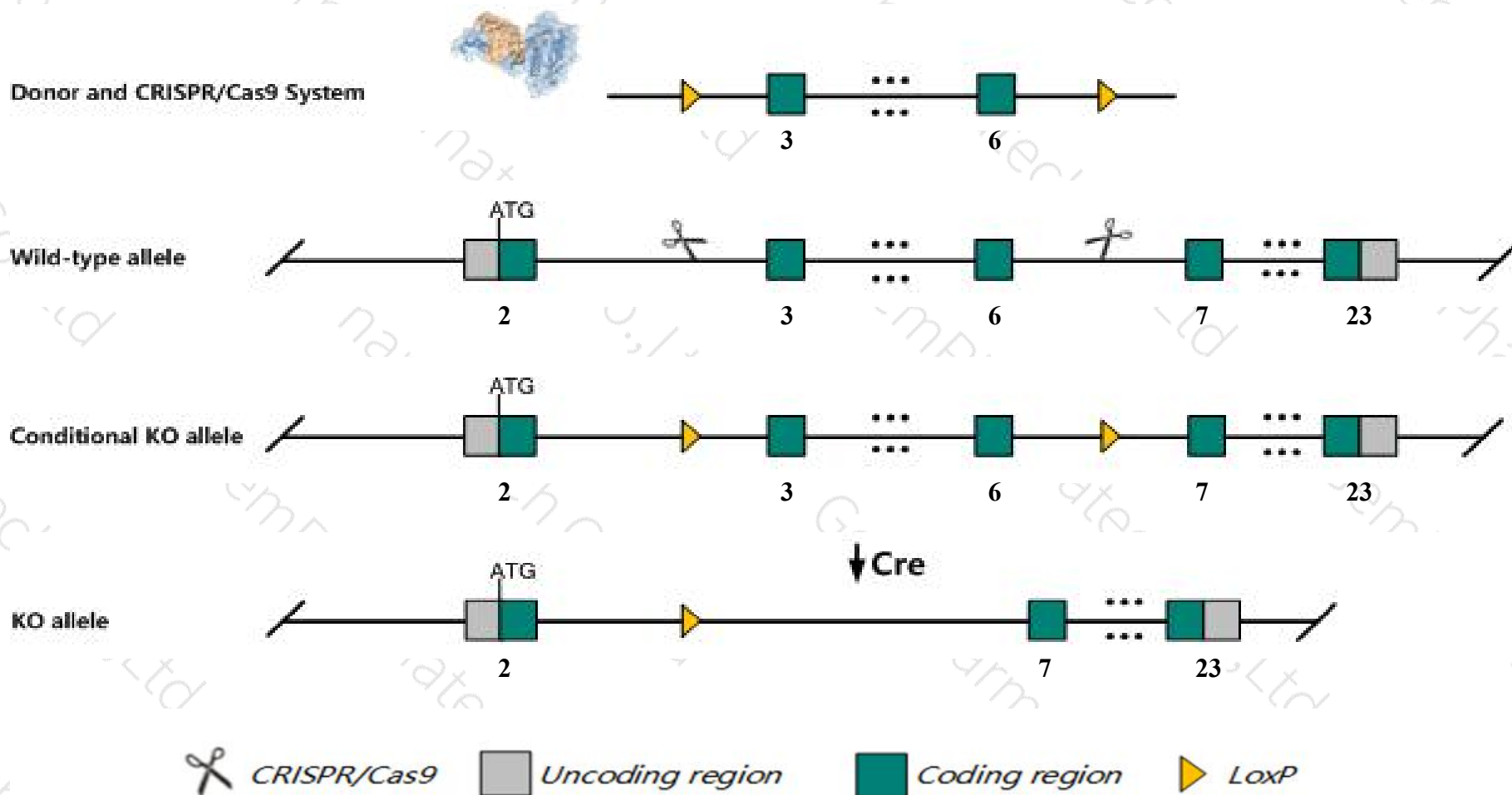|	
Project Name	*Sec24c*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec24c* gene. The schematic diagram is as follows:

Technical routes

➢ The *Sec24c* gene has 15 transcripts. According to the structure of *Sec24c* gene, exon3-exon6 of *Sec24c-201*(ENSMUST00000048657.9) transcript is recommended as the knockout region.The region contains 821bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Sec24c* 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,mice homozygous for a null allele display complete embryonic lethality between implantation and placentation.

➢ Transcript 204、207、212 CDS 3' incomplete the influences is unknown.

➢ Transcript 215 CDS 5' and 3' incomplete the influences is unknown.

➢ The *Sec24c* gene is located on the Chr14. 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）

Sec24c Sec24 related gene family, member C (S. cerevisiae) [Mus musculus (house mouse)]
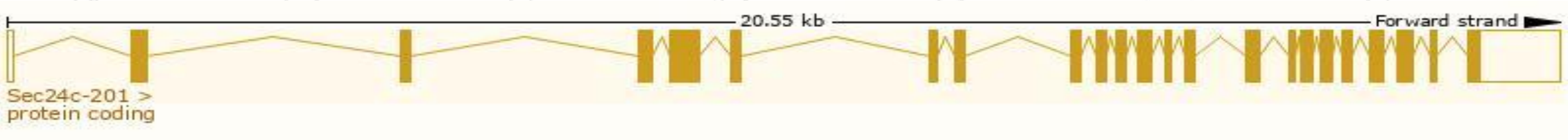
Gene ID: 218811, updated on 13-Mar-2020

Summary

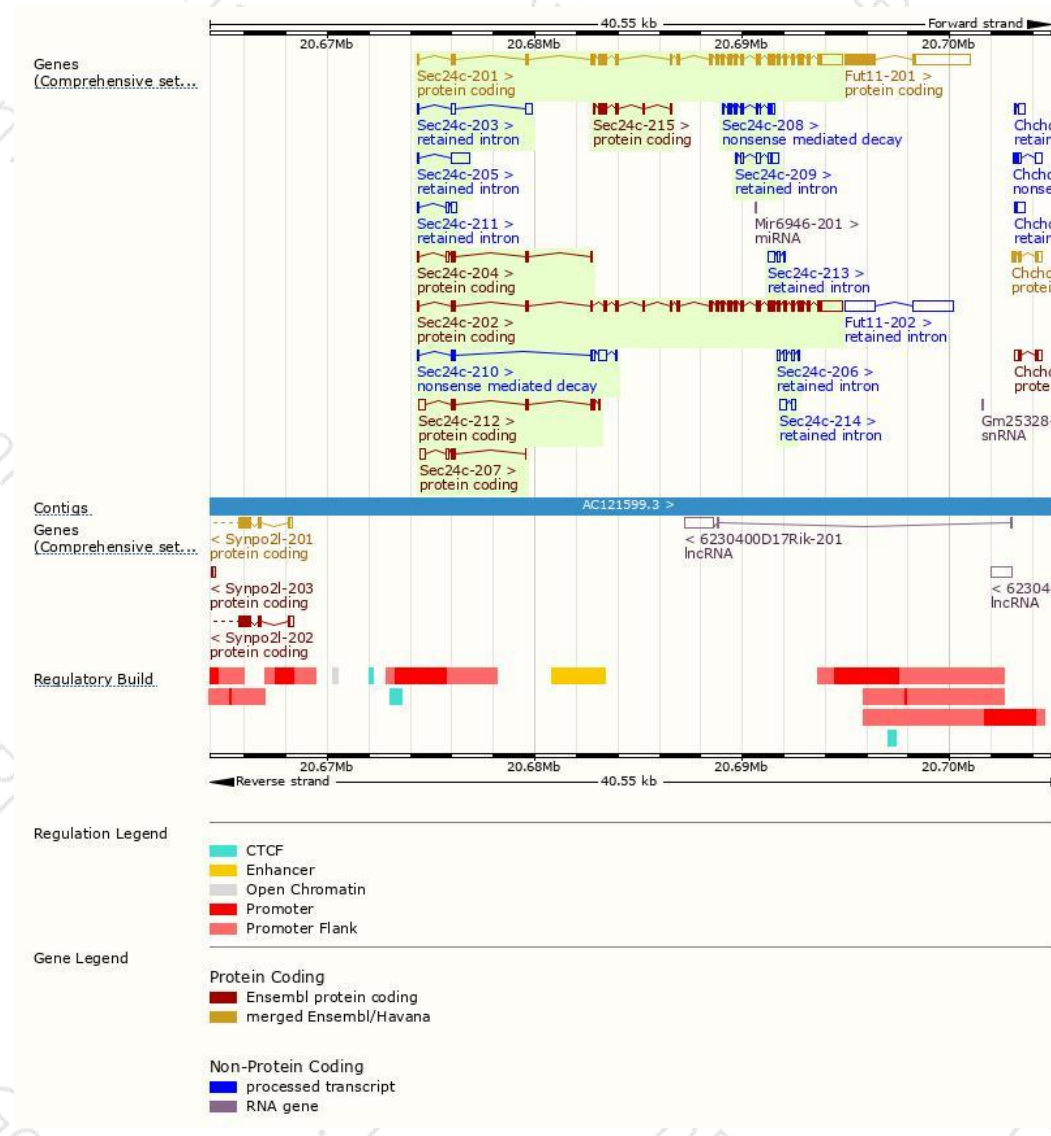|	
Official Symbol	Sec24c provided by MGI
Official Full Name	Sec24 related gene family, member C (S. cerevisiae) provided by MGI
Primary source	MGI:MGI:1919746
See related	Ensembl:ENSMUSG00000039367
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610204K03Rik, mKIAA0079
Expression	Ubiquitous expression in thymus adult (RPKM 52.7), large intestine adult (RPKM 44.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

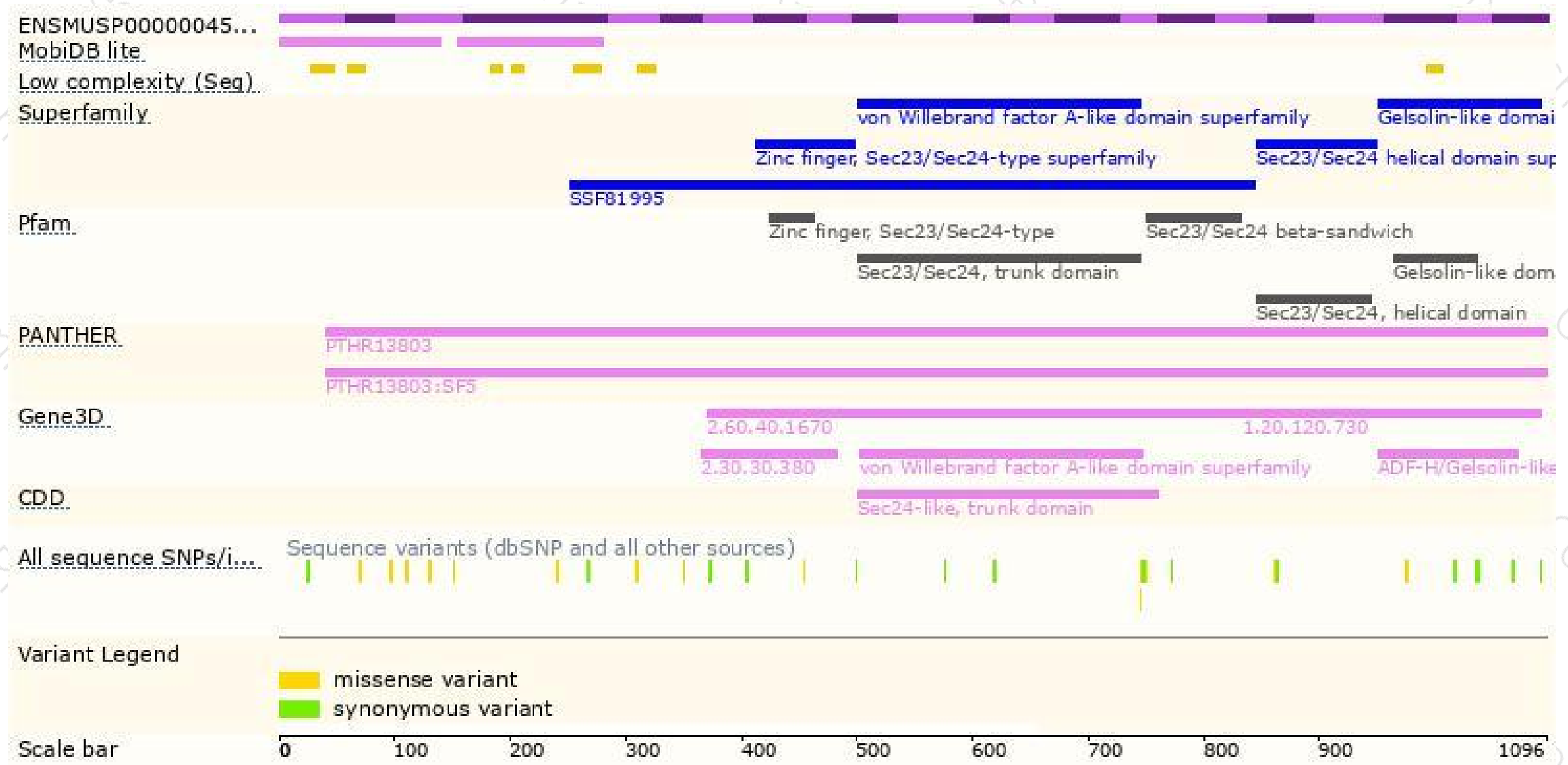| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec24c-201	ENSMUST00000048657.9	4461	1096aa	Protein coding	CCDS26850	G3X972	TSL:1 GENCODE basic APPRIS P1
Sec24c-202	ENSMUST00000223751.1	4196	1020aa	Protein coding	-	A0A286YDI8	GENCODE basic
Sec24c-212	ENSMUST00000225108.1	866	168aa	Protein coding	-	A0A286YCC8	CDS 3' incomplete
Sec24c-215	ENSMUST00000228545.1	715	239aa	Protein coding	-	A0A2I3BQS4	CDS 5' and 3' incomplete
Sec24c-207	ENSMUST00000224754.1	680	71aa	Protein coding	-	A0A286YCX0	CDS 3' incomplete
Sec24c-204	ENSMUST00000224492.1	563	119aa	Protein coding	-	A0A286YDJ8	CDS 3' incomplete
Sec24c-210	ENSMUST00000224876.1	833	90aa	Nonsense mediated decay	-	A0A286YDN4	
Sec24c-208	ENSMUST00000224791.1	724	174aa	Nonsense mediated decay	-	A0A286YD08	CDS 5' incomplete
Sec24c-205	ENSMUST00000224718.1	971	No protein	Retained intron	-	-	
Sec24c-209	ENSMUST00000224793.1	763	No protein	Retained intron	-	-	
Sec24c-203	ENSMUST00000224061.1	605	No protein	Retained intron	-	-	
Sec24c-213	ENSMUST00000225566.1	557	No protein	Retained intron	-	-	
Sec24c-214	ENSMUST00000225903.1	505	No protein	Retained intron	-	-	
Sec24c-206	ENSMUST00000224722.1	472	No protein	Retained intron	-	-	
Sec24c-211	ENSMUST00000224963.1	450	No protein	Retained intron	-	-	

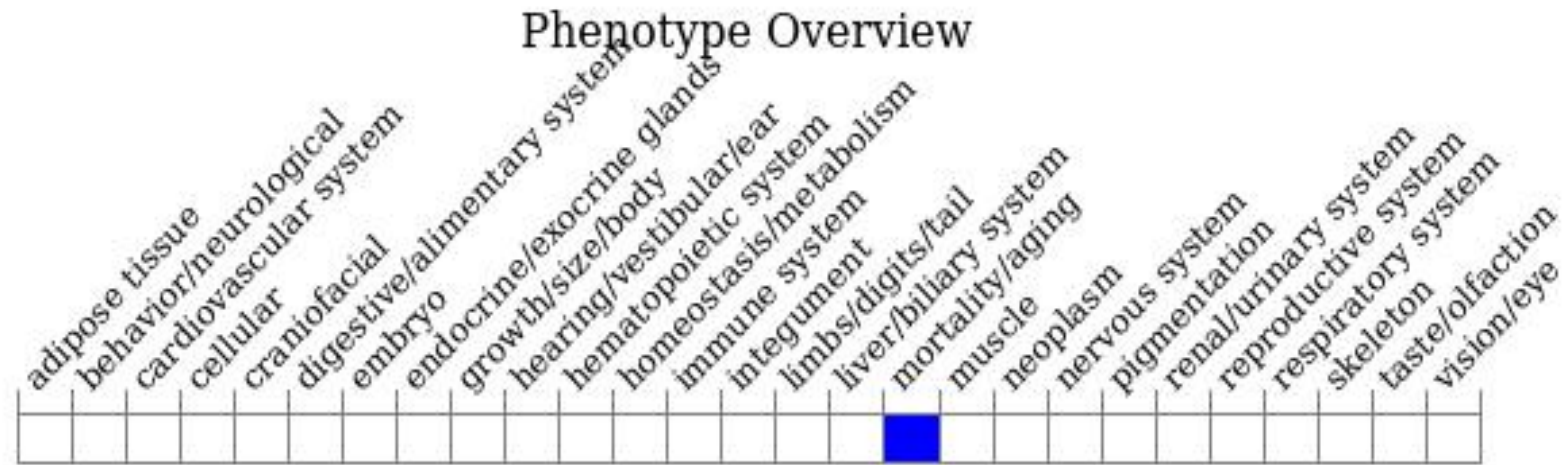The strategy is based on the design of *Sec24c-201* transcript,the transcription is shown below:

Genomic location distribution

Protein domain

ENSMUSP00000045...	
MobiDB lite	
Low complexity (Seg)	
Superfamily	von Willebrand factor A-like domain superfamily, Gelsolin-like domain
	Zinc finger, Sec23/Sec24-type superfamily, Sec23/Sec24 helical domain sup
	SSF81995
Pfam	Zinc finger, Sec23/Sec24-type, Sec23/Sec24 beta-sandwich
	Sec23/Sec24, trunk domain, Gelsolin-like dom
	Sec23/Sec24, helical domain
PANTHER	PTHR13803
	PTHR13803:SF5
Gene3D	2.60.40.1670, 1.20.120.730
	2.30.30.380, von Willebrand factor A-like domain superfamily, ADF-H/Gelsolin-like
CDD	Sec24-like, trunk domain
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend
- ▇ missense variant
- ▇ synonymous variant

Scale bar: 0 100 200 300 400 500 600 700 800 900 1096

Mouse phenotype description(MGI)

Phenotype Overview

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,mice homozygous for a null allele display complete embryonic lethality between implantation and placentation.

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