GemPharmatech™

Sil1 Cas9-CKO Strategy

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Reviewer: Xiaojing Li

Design Date: 2023-05-10

Overview

Target Gene Name

- Sil1

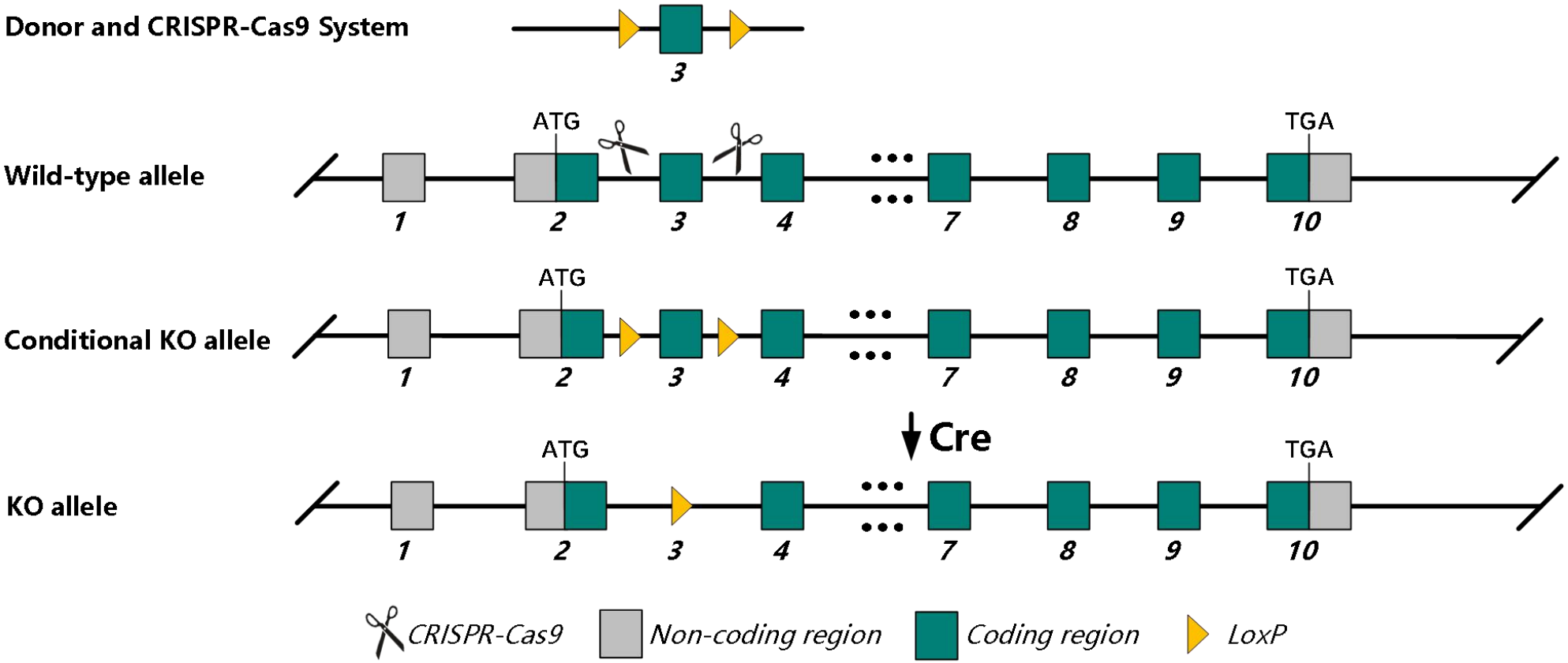
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

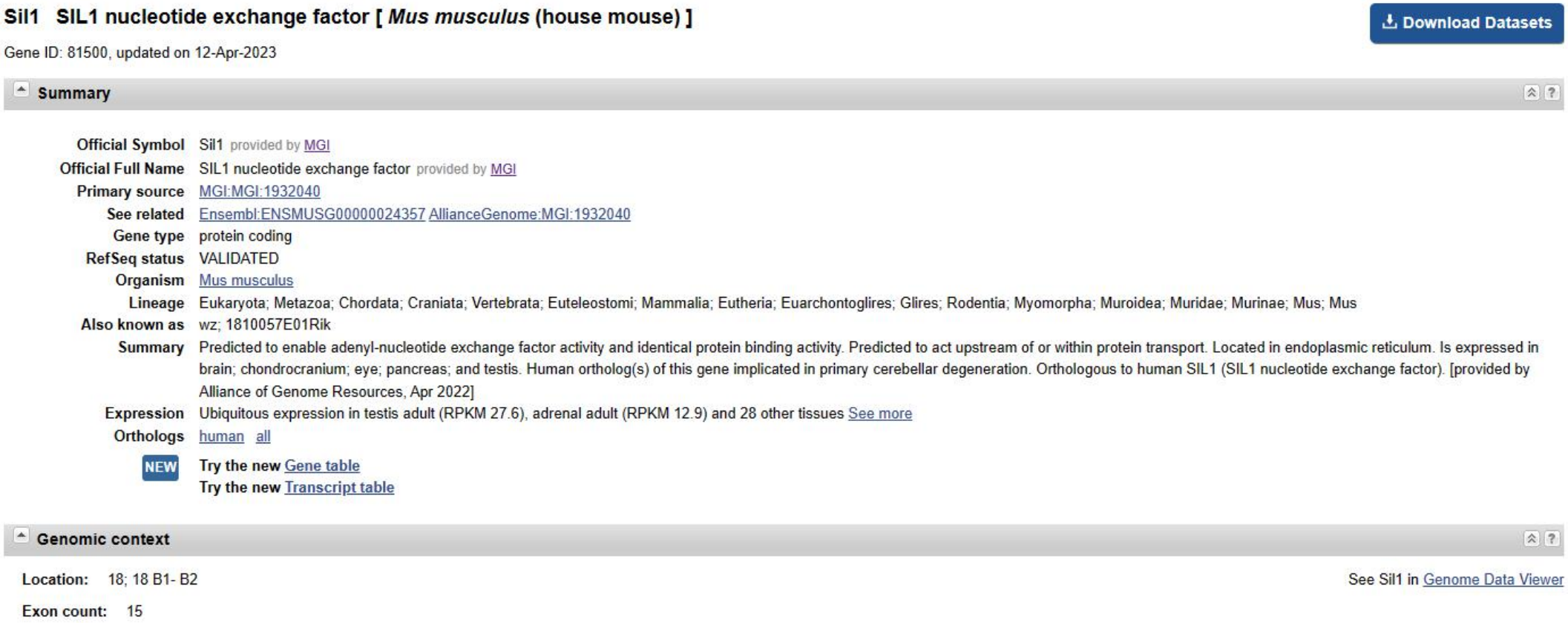


Schematic representation of CRISPR-Cas9 engineering used to edit the *Sil1* gene.

Technical Information

- The *Sil1* gene has 11 transcripts. According to the structure of *Sil1* gene, exon3 of *Sil1*-201 (ENSMUST00000025215.10) transcript is recommended as the knockout region. The region contains 139bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sil1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information



Sil1 SIL1 nucleotide exchange factor [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 81500, updated on 12-Apr-2023

Summary

Official Symbol	Sil1 provided by MGI
Official Full Name	SIL1 nucleotide exchange factor provided by MGI
Primary source	MGI:MGI:1932040
See related	Ensembl:ENSMUSG00000024357 AllianceGenome:MGI:1932040
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	wz; 1810057E01Rik
Summary	Predicted to enable adenyl-nucleotide exchange factor activity and identical protein binding activity. Predicted to act upstream of or within protein transport. Located in endoplasmic reticulum. Is expressed in brain; chondrocranium; eye; pancreas; and testis. Human ortholog(s) of this gene implicated in primary cerebellar degeneration. Orthologous to human SIL1 (SIL1 nucleotide exchange factor). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in testis adult (RPKM 27.6), adrenal adult (RPKM 12.9) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 18; 18 B1- B2 — See Sil1 in Genome Data Viewer

Exon count: 15

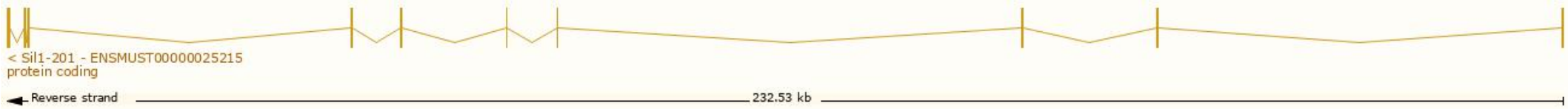
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 11 transcripts, all transcripts are shown below:

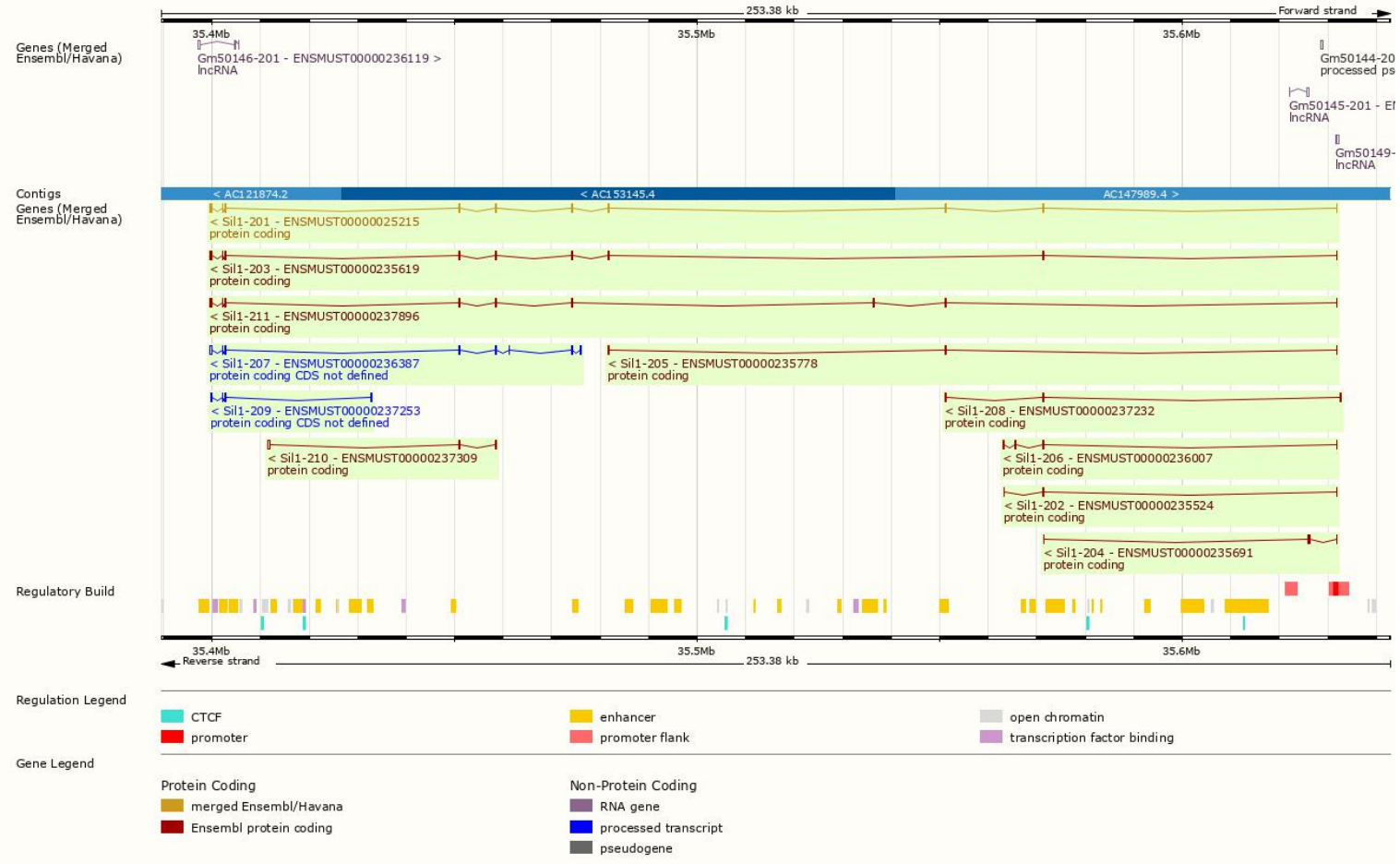
Transcript ID	Name	bp	Protein	Translation ID	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000025215.10	Sil1-201	1703	465aa	ENSMUSP00000025215.9	Protein coding	CCDS29140	Q9EPK6	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000235524.2	Sil1-202	335	38aa	ENSMUSP00000157758.2	Protein coding		A0A494B9U3	GENCODE basic
ENSMUST00000235619.2	Sil1-203	1524	417aa	ENSMUSP00000157636.2	Protein coding		A0A494B9H1	GENCODE basic
ENSMUST00000235691.2	Sil1-204	355	20aa	ENSMUSP00000157444.2	Protein coding		A0A494B950	CDS 3' incomplete
ENSMUST00000235778.2	Sil1-205	342	28aa	ENSMUSP00000157667.2	Protein coding		A0A494B9L8	CDS 3' incomplete
ENSMUST00000236007.2	Sil1-206	538	53aa	ENSMUSP00000157932.2	Protein coding		A0A494BA83	GENCODE basic
ENSMUST00000236387.2	Sil1-207	1532	No protein	-	Protein coding CDS not defined		-	-
ENSMUST00000237232.2	Sil1-208	453	80aa	ENSMUSP00000158247.2	Protein coding		A0A494BAV3	CDS 3' incomplete
ENSMUST00000237253.2	Sil1-209	570	No protein	-	Protein coding CDS not defined		-	-
ENSMUST00000237309.2	Sil1-210	695	119aa	ENSMUSP00000157506.2	Protein coding		A0A494B962	CDS 5' incomplete
ENSMUST00000237896.2	Sil1-211	1501	327aa	ENSMUSP00000157521.2	Protein coding		A0A494B9B2	GENCODE basic

The strategy is based on the design of *Sil1*-201 transcript, the transcription is shown below:



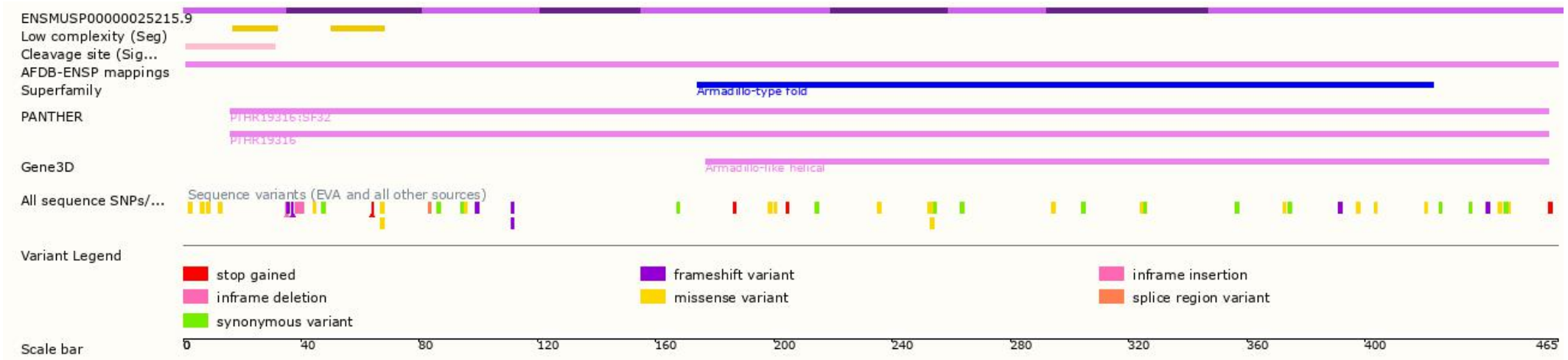
Source: https://www.ensembl.org

Genomic Information



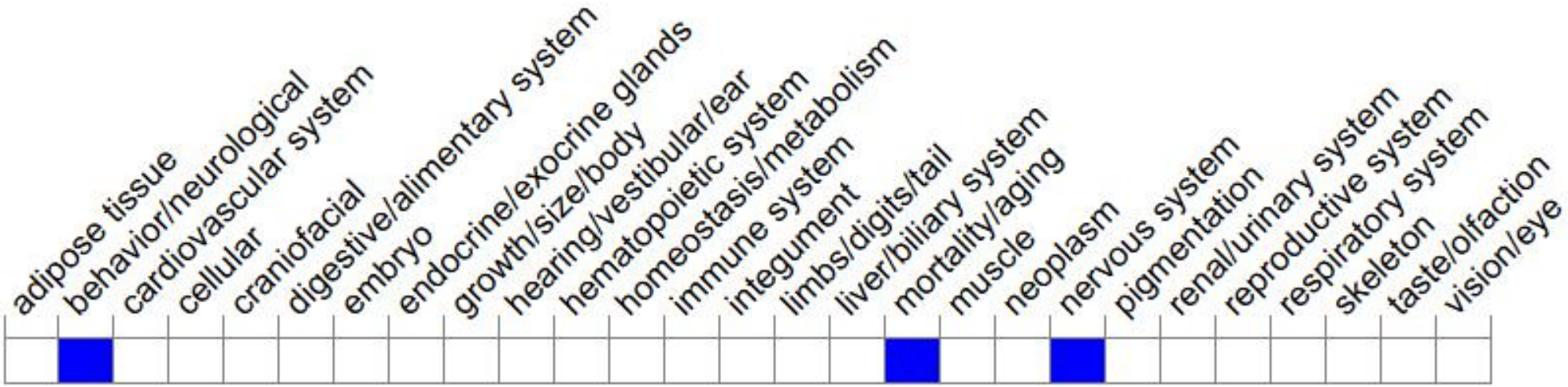
Source: https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Sil1* gene are marked in blue. Mice homozygous for a gene trapped allele or spontaneous mutation exhibit ataxia and Purkinje cell degeneration.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data, mice homozygous for a gene trapped allele or spontaneous mutation exhibit ataxia and Purkinje cell degeneration, and altered hemodynamicsn leading to perinatal lethality.
- The effect of this strategy on the transcript of *Sil1*-202(ENSMUST00000235524.2), *Sil1*-203(ENSMUST00000235619.2), *Sil1*-204(ENSMUST00000235691.2), *Sil1*-206(ENSMUST00000236007.2), *Sil1*-207(ENSMUST00000236387.2), *Sil1*-209(ENSMUST00000237253.2) and *Sil1*-210(ENSMUST00000237309.2) is unknown.
- *Sil1* is located on Chr18. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.