

# *Slc29a1* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Slc29a1*

**Project type**

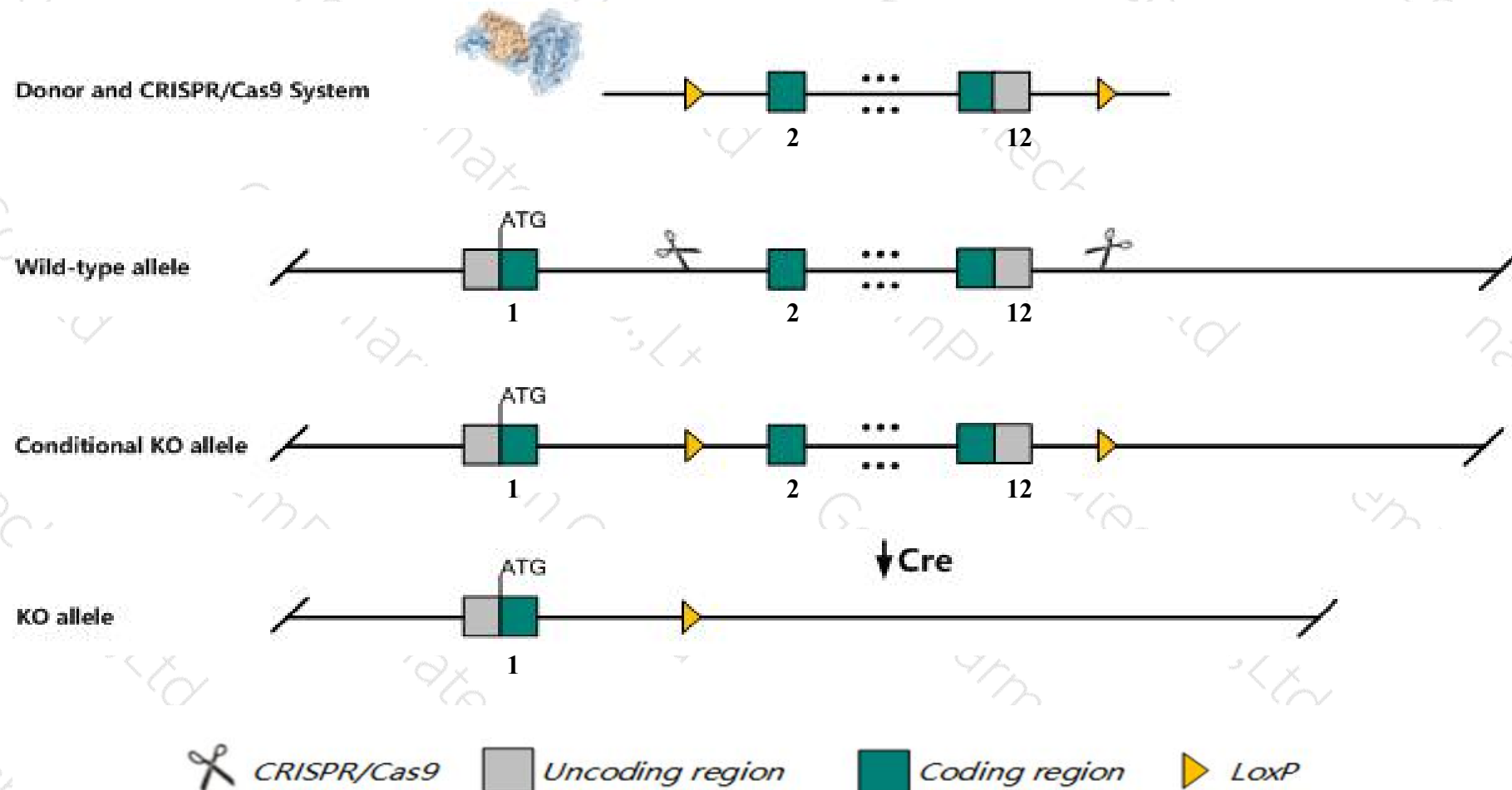
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc29a1* gene. The schematic diagram is as follows:



# Technical routes

- The *Slc29a1* gene has 25 transcripts. According to the structure of *Slc29a1* gene, exon2-exon12 of *Slc29a1*-204 (ENSMUST00000163492.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc29a1* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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.

- According to the existing MGI data, Mice homozygous for a targeted null allele exhibit a slightly decreased body weight, increased alcohol preference and alcohol consumption, and reduced hypnotic and ataxic responses to ethanol associated with a reduction in adenosine tone. Adenosine uptake is almost completely abolished in mice homozygous for a knock-out allele.
- *Gm17080* gene will be deleted together in this strategy.
- The *Slc29a1* gene is located on the Chr17. 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)

## Slc29a1 solute carrier family 29 (nucleoside transporters), member 1 [ *Mus musculus* (house mouse) ]

Gene ID: 63959, updated on 24-Oct-2019

### Summary

Official Symbol	Slc29a1 provided by <a href="#">MGI</a>
Official Full Name	solute carrier family 29 (nucleoside transporters), member 1 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1927073</a>
See related	<a href="#">Ensembl:ENSMUSG00000023942</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ENT1; AA407560; 1200014D21Rik
Expression	Ubiquitous expression in liver adult (RPKM 135.7), adrenal adult (RPKM 95.4) and 26 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 17; 17 B3

See Slc29a1 in [Genome Data Viewer](#)

Exon count: 19

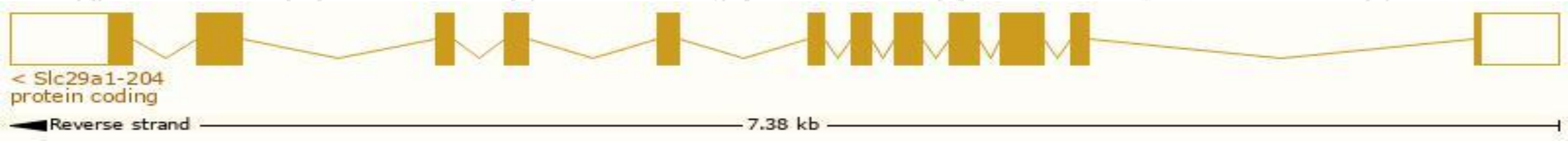
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	17	NC_000083.6 (45585200..45599618, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	17	NC_000083.5 (45722171..45729342, complement)

# Transcript information (Ensembl)

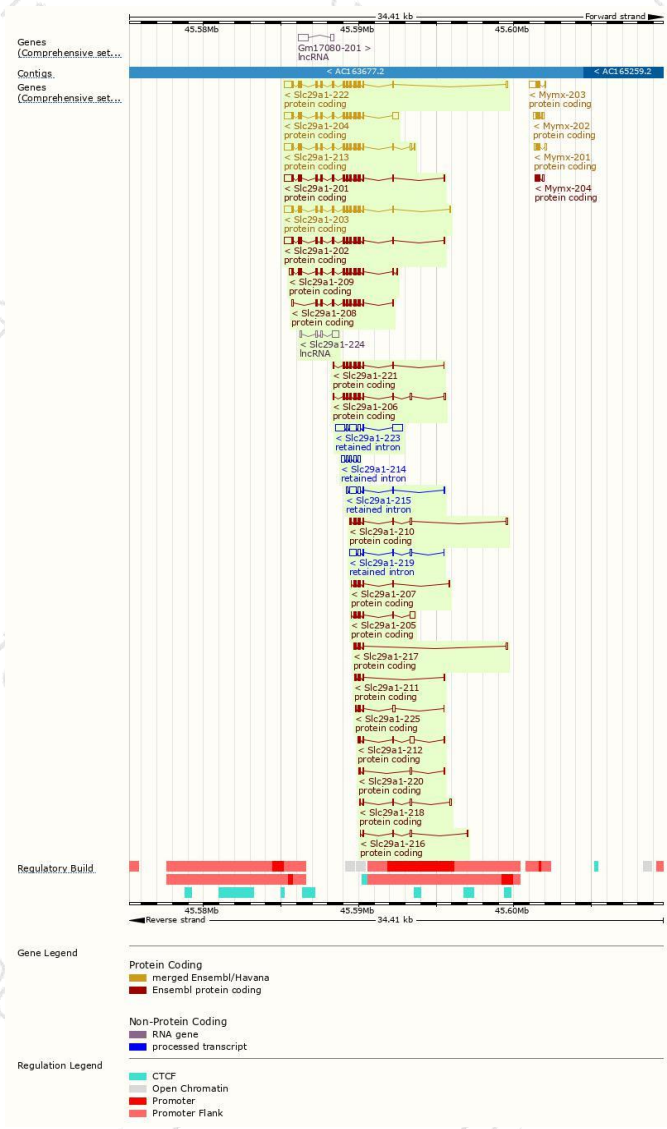
The gene has 25 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc29a1-204	<a href="#">ENSMUST00000163492.7</a>	2216	<a href="#">458aa</a>	Protein coding	<a href="#">CCDS28813</a>	<a href="#">Q3TCZ2_Q9JIM1</a>	TSL1 GENCODE basic APPRIS P3
Slc29a1-213	<a href="#">ENSMUST00000167692.7</a>	2092	<a href="#">460aa</a>	Protein coding	<a href="#">CCDS57096</a>	<a href="#">Q9JIM1</a>	TSL1 GENCODE basic APPRIS ALT2
Slc29a1-222	<a href="#">ENSMUST00000171647.7</a>	2033	<a href="#">458aa</a>	Protein coding	<a href="#">CCDS28813</a>	<a href="#">Q3TCZ2_Q9JIM1</a>	TSL1 GENCODE basic APPRIS P3
Slc29a1-201	<a href="#">ENSMUST00000051574.12</a>	1996	<a href="#">460aa</a>	Protein coding	<a href="#">CCDS57096</a>	<a href="#">Q9JIM1</a>	TSL5 GENCODE basic APPRIS ALT2
Slc29a1-202	<a href="#">ENSMUST00000064889.12</a>	1988	<a href="#">458aa</a>	Protein coding	<a href="#">CCDS28813</a>	<a href="#">Q3TCZ2_Q9JIM1</a>	TSL1 GENCODE basic APPRIS P3
Slc29a1-203	<a href="#">ENSMUST00000097317.9</a>	1931	<a href="#">460aa</a>	Protein coding	<a href="#">CCDS57096</a>	<a href="#">Q9JIM1</a>	TSL1 GENCODE basic APPRIS ALT2
Slc29a1-209	<a href="#">ENSMUST00000166119.7</a>	1598	<a href="#">460aa</a>	Protein coding	<a href="#">CCDS57096</a>	<a href="#">Q9JIM1</a>	TSL5 GENCODE basic APPRIS ALT2
Slc29a1-208	<a href="#">ENSMUST00000164769.7</a>	1226	<a href="#">358aa</a>	Protein coding	-	<a href="#">E9PXM6</a>	TSL1 GENCODE basic
Slc29a1-206	<a href="#">ENSMUST00000164217.7</a>	1062	<a href="#">262aa</a>	Protein coding	-	<a href="#">E9PWY7</a>	CDS 3' incomplete TSL5
Slc29a1-210	<a href="#">ENSMUST00000166633.7</a>	873	<a href="#">195aa</a>	Protein coding	-	<a href="#">E9PXQ6</a>	CDS 3' incomplete TSL3
Slc29a1-221	<a href="#">ENSMUST00000171081.7</a>	862	<a href="#">262aa</a>	Protein coding	-	<a href="#">E9PWY7</a>	CDS 3' incomplete TSL5
Slc29a1-205	<a href="#">ENSMUST00000163905.7</a>	837	<a href="#">160aa</a>	Protein coding	-	<a href="#">E9PZV0</a>	CDS 3' incomplete TSL2
Slc29a1-212	<a href="#">ENSMUST00000167332.7</a>	626	<a href="#">93aa</a>	Protein coding	-	<a href="#">E9Q221</a>	CDS 3' incomplete TSL5
Slc29a1-207	<a href="#">ENSMUST00000164618.7</a>	598	<a href="#">162aa</a>	Protein coding	-	<a href="#">E9PVH9</a>	CDS 3' incomplete TSL3
Slc29a1-217	<a href="#">ENSMUST00000169729.7</a>	543	<a href="#">114aa</a>	Protein coding	-	<a href="#">E9Q3D1</a>	CDS 3' incomplete TSL3
Slc29a1-225	<a href="#">ENSMUST00000172301.7</a>	520	<a href="#">121aa</a>	Protein coding	-	<a href="#">E9PWD6</a>	CDS 3' incomplete TSL5
Slc29a1-211	<a href="#">ENSMUST00000167195.7</a>	459	<a href="#">105aa</a>	Protein coding	-	<a href="#">E9Q503</a>	CDS 3' incomplete TSL3
Slc29a1-218	<a href="#">ENSMUST00000170113.7</a>	403	<a href="#">56aa</a>	Protein coding	-	<a href="#">E9Q5E9</a>	CDS 3' incomplete TSL5
Slc29a1-216	<a href="#">ENSMUST00000168274.1</a>	357	<a href="#">41aa</a>	Protein coding	-	<a href="#">E9Q0Q5</a>	CDS 3' incomplete TSL3
Slc29a1-220	<a href="#">ENSMUST00000170488.7</a>	348	<a href="#">39aa</a>	Protein coding	-	<a href="#">E9Q7R8</a>	CDS 3' incomplete TSL5
Slc29a1-223	<a href="#">ENSMUST00000171876.7</a>	2007	No protein	Retained intron	-	-	TSL5
Slc29a1-215	<a href="#">ENSMUST00000167663.7</a>	944	No protein	Retained intron	-	-	TSL5
Slc29a1-219	<a href="#">ENSMUST00000170425.7</a>	907	No protein	Retained intron	-	-	TSL2
Slc29a1-214	<a href="#">ENSMUST00000167748.1</a>	769	No protein	Retained intron	-	-	TSL1
Slc29a1-224	<a href="#">ENSMUST00000171978.1</a>	736	No protein	lncRNA	-	-	TSL3

The strategy is based on the design of *Slc29a1-204* transcript,The transcription is shown below

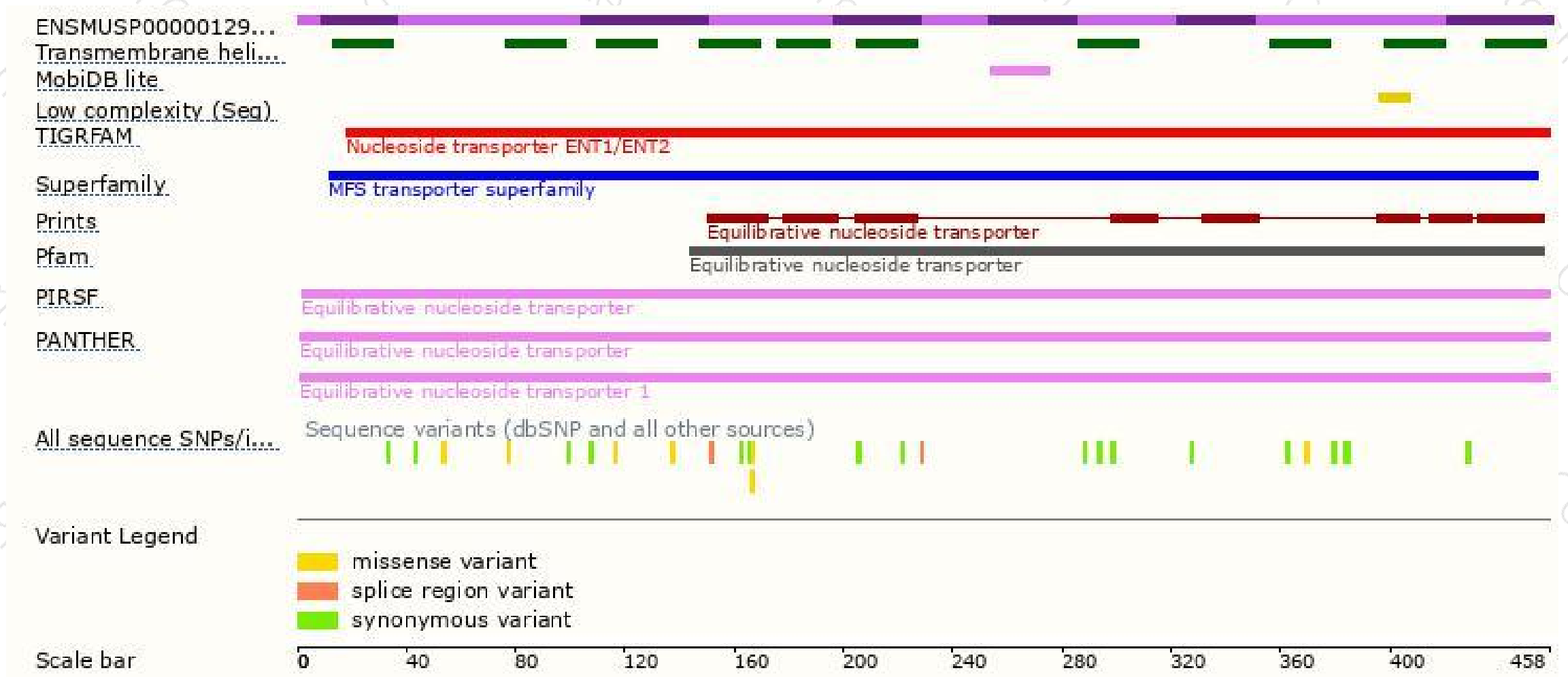


# Genomic location distribution

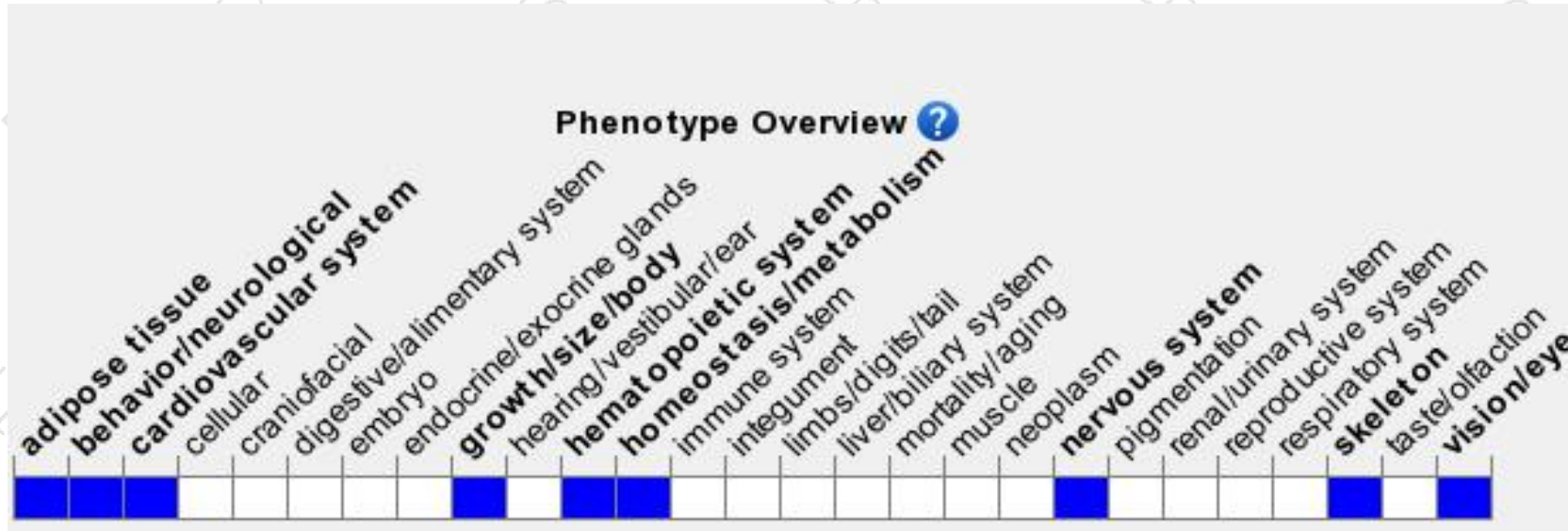




# Protein domain



# 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, Mice homozygous for a targeted null allele exhibit a slightly decreased body weight, increased alcohol preference and alcohol consumption, and reduced hypnotic and ataxic responses to ethanol associated with a reduction in adenosine tone. Adenosine uptake is almost completely abolished in mice homozygous for a knock-out allele.

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

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