

# ***Stk38* Cas9-CKO Strategy**

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**Reviewer:**

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**Design Date:**

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# Project Overview

**Project Name**

***Stk38***

**Project type**

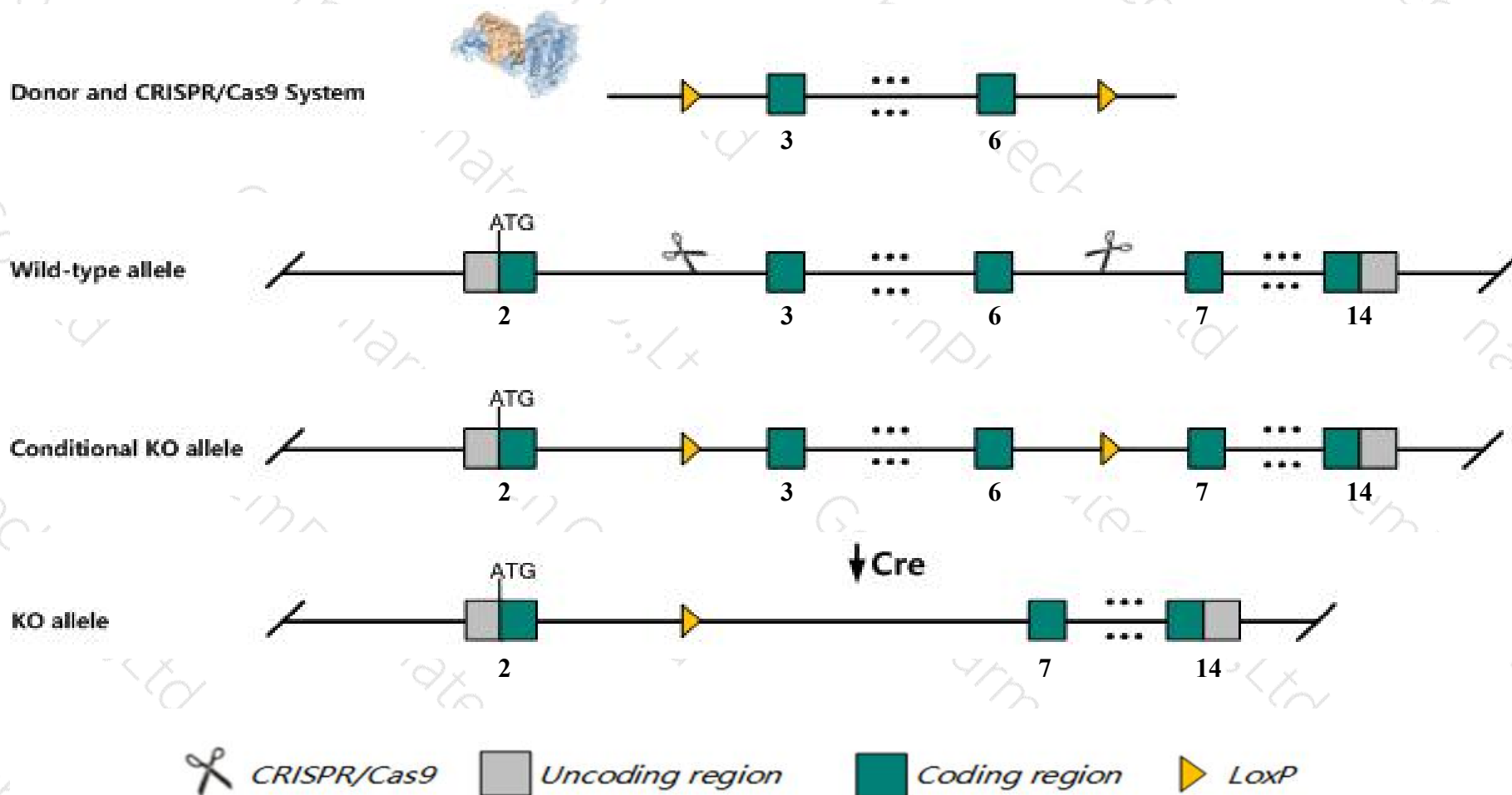
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stk38* gene. The schematic diagram is as follows:



# Technical routes

- The *Stk38* gene has 25 transcripts. According to the structure of *Stk38* gene, exon3-exon6 of *Stk38-202* (ENSMUST00000119274.2) transcript is recommended as the knockout region. The region contains 383bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stk38* 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased susceptibility to bacterial infection and altered TLR9-activated inflammatory responses. Mice homozygous for a different knock-out allele exhibit decreased cellular susceptibility to gamma-irradiation and increased susceptibility to spontaneous and induced tumors.
- Transcript *Stk38-209* and *Stk38-215* may not be affected.
- The KO region contains the *Gm23887* gene. Knockout the region will affect the function of *Gm23887* gene.
- The *Stk38* 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)

## Stk38 serine/threonine kinase 38 [Mus musculus (house mouse)]

Gene ID: 106504, updated on 31-Jan-2019

### Summary



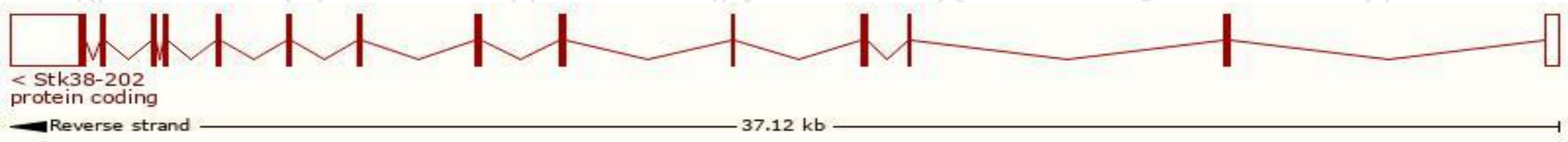
<b>Official Symbol</b>	Stk38 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	serine/threonine kinase 38 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2442572</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000024006</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	5830476G13Rik, 9530097A09Rik, AA617404, Ndr1
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 16.0), thymus adult (RPKM 15.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

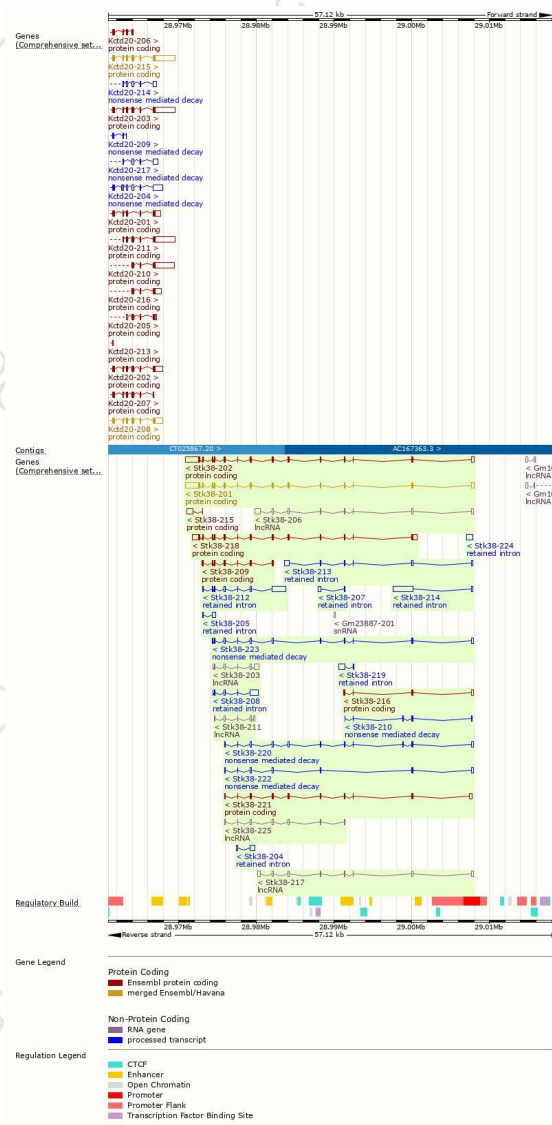
The gene has 25 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stk38-202	<a href="#">ENSMUST00000119274.2</a>	3354	<a href="#">465aa</a>	Protein coding	<a href="#">CCDS28589</a>	<a href="#">Q91VJ4</a>	TSL:1 GENCODE basic APPRIS P1
Stk38-201	<a href="#">ENSMUST00000009138.12</a>	3351	<a href="#">465aa</a>	Protein coding	<a href="#">CCDS28589</a>	<a href="#">Q91VJ4</a>	TSL:1 GENCODE basic APPRIS P1
Stk38-218	<a href="#">ENSMUST00000232836.1</a>	2778	<a href="#">465aa</a>	Protein coding	<a href="#">CCDS28589</a>	<a href="#">Q91VJ4</a>	GENCODE basic APPRIS P1
Stk38-221	<a href="#">ENSMUST00000233441.1</a>	1246	<a href="#">307aa</a>	Protein coding	-	<a href="#">A0A3B2WD34</a>	CDS 3' incomplete
Stk38-215	<a href="#">ENSMUST00000156732.2</a>	880	<a href="#">14aa</a>	Protein coding	-	<a href="#">A0A3B2W7E4</a>	CDS 5' incomplete TSL:3
Stk38-209	<a href="#">ENSMUST00000141431.7</a>	859	<a href="#">281aa</a>	Protein coding	-	<a href="#">A0A3B2W7L2</a>	CDS 5' incomplete TSL:3
Stk38-216	<a href="#">ENSMUST00000232723.1</a>	627	<a href="#">117aa</a>	Protein coding	-	<a href="#">A0A3B2WAZ4</a>	GENCODE basic
Stk38-223	<a href="#">ENSMUST00000233606.1</a>	1276	<a href="#">132aa</a>	Nonsense mediated decay	-	<a href="#">A0A3B2W7T8</a>	
Stk38-220	<a href="#">ENSMUST00000233329.1</a>	1268	<a href="#">61aa</a>	Nonsense mediated decay	-	<a href="#">A0A3B2W7M3</a>	
Stk38-222	<a href="#">ENSMUST00000233510.1</a>	856	<a href="#">58aa</a>	Nonsense mediated decay	-	<a href="#">A0A3B2WD06</a>	
Stk38-210	<a href="#">ENSMUST00000142366.2</a>	335	<a href="#">61aa</a>	Nonsense mediated decay	-	<a href="#">A0A3B2W7M3</a>	TSL:1
Stk38-214	<a href="#">ENSMUST00000145298.1</a>	2767	No protein	Retained intron	-	-	TSL:1
Stk38-212	<a href="#">ENSMUST00000144299.8</a>	2313	No protein	Retained intron	-	-	TSL:2
Stk38-208	<a href="#">ENSMUST00000140355.8</a>	1382	No protein	Retained intron	-	-	TSL:2
Stk38-213	<a href="#">ENSMUST00000144516.8</a>	1186	No protein	Retained intron	-	-	TSL:3
Stk38-219	<a href="#">ENSMUST00000233093.1</a>	897	No protein	Retained intron	-	-	
Stk38-224	<a href="#">ENSMUST00000233723.1</a>	820	No protein	Retained intron	-	-	
Stk38-204	<a href="#">ENSMUST00000126619.1</a>	748	No protein	Retained intron	-	-	TSL:3
Stk38-205	<a href="#">ENSMUST00000126671.1</a>	486	No protein	Retained intron	-	-	TSL:3
Stk38-207	<a href="#">ENSMUST00000129094.2</a>	460	No protein	Retained intron	-	-	TSL:3
Stk38-206	<a href="#">ENSMUST00000126893.7</a>	1663	No protein	lncRNA	-	-	TSL:1
Stk38-217	<a href="#">ENSMUST00000232724.1</a>	1298	No protein	lncRNA	-	-	
Stk38-203	<a href="#">ENSMUST00000125070.8</a>	1052	No protein	lncRNA	-	-	TSL:5
Stk38-225	<a href="#">ENSMUST00000233864.1</a>	694	No protein	lncRNA	-	-	
Stk38-211	<a href="#">ENSMUST00000142923.1</a>	529	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Stk38-202* transcript,The transcription is shown below

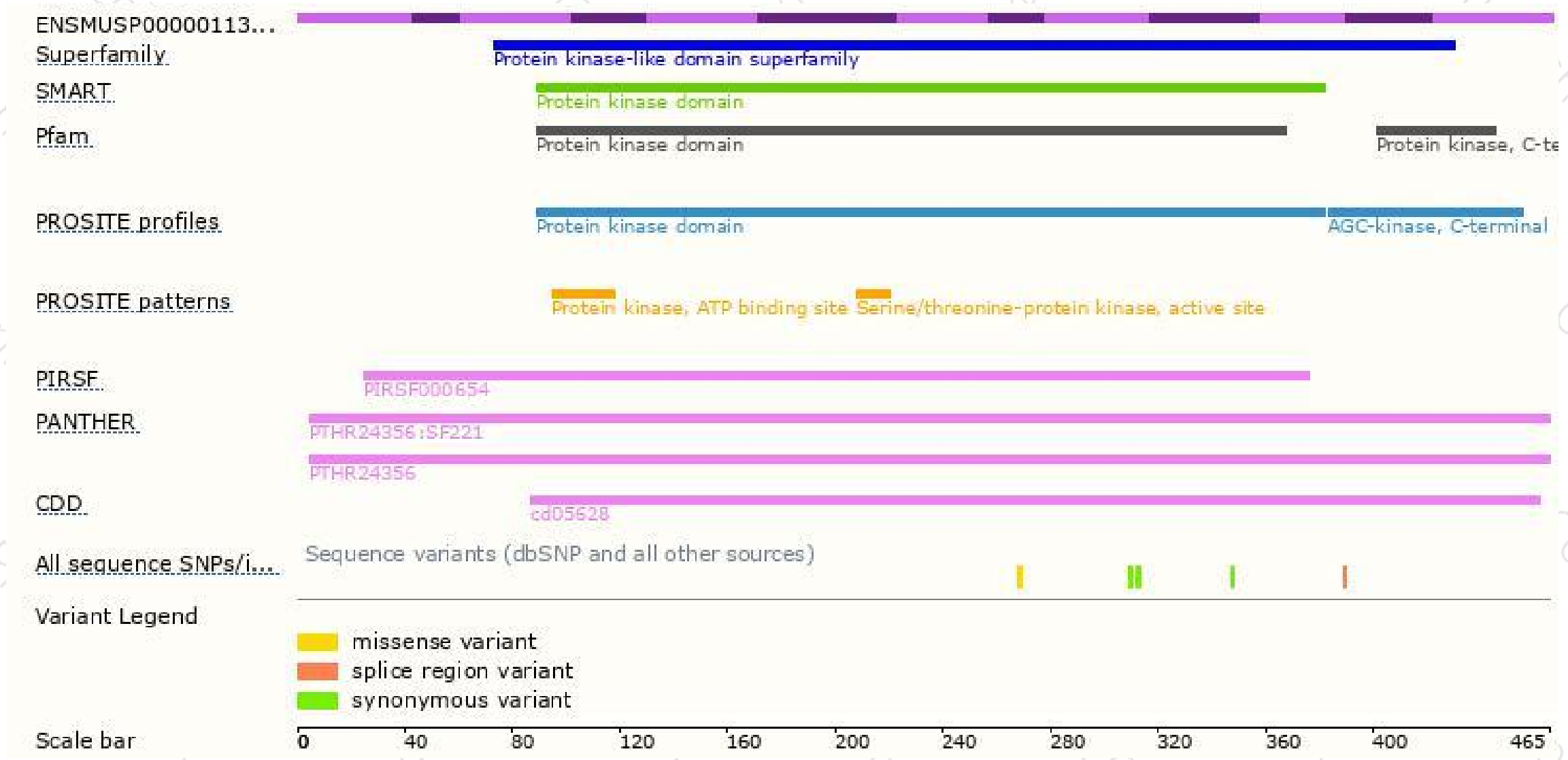


# Genomic location distribution

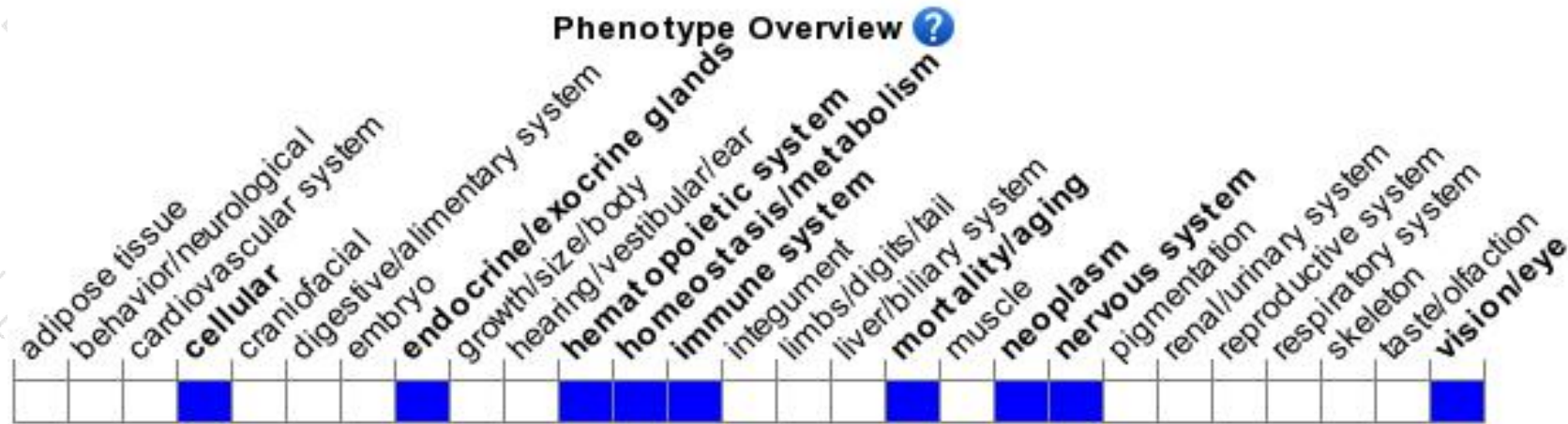




# Protein domain



# 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 knock-out allele exhibit increased susceptibility to bacterial infection and altered TLR9-activated inflammatory responses. Mice homozygous for a different knock-out allele exhibit decreased cellular susceptibility to gamma-irradiation and increased susceptibility to spontaneous and induced tumors.

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

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