

# *Arhgef1* Cas9-CKO Strategy

**Designer: Ruirui Zhang**

**Reviewer: Yanhua Shen**

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# Project Overview

**Project Name**

*Arhgef1*

**Project type**

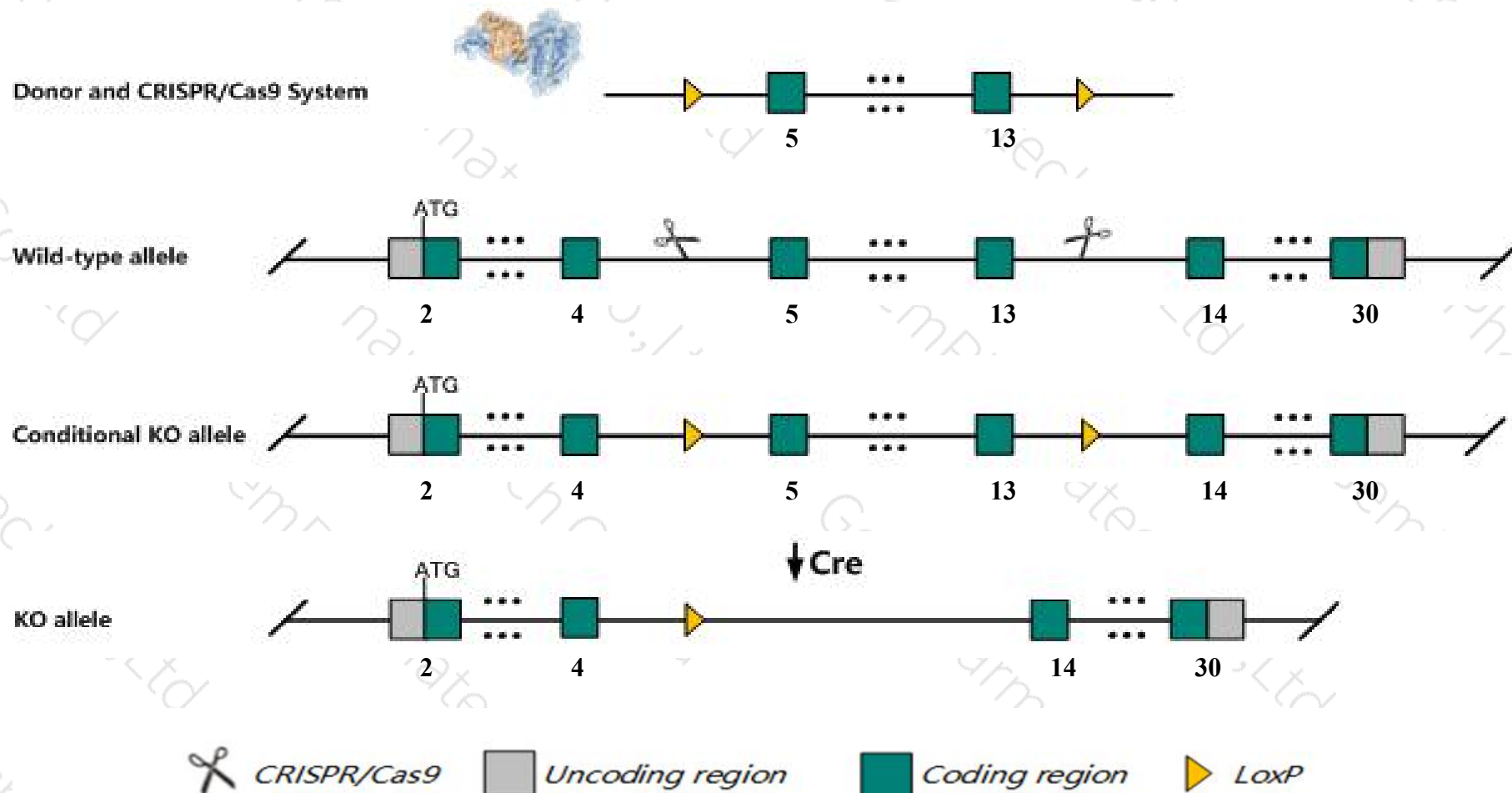
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgef1* gene. The schematic diagram is as follows:



- The *Arhgef1* gene has 19 transcripts. According to the structure of *Arhgef1* gene, exon5-exon13 of *Arhgef1*-204(ENSMUST00000117796.7) transcript is recommended as the knockout region. The region contains 899bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgef1* 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, homozygous mutation of this gene results in impaired humeral immunity, reduced numbers of marginal zone B (MZB) cells, decreased basal T cell proliferation, and reduced basal motility of lymphocytes but enhanced migration of MZB cells after serum activation.
- The *Arhgef1* gene is located on the Chr7. 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)

## Arhgef1 Rho guanine nucleotide exchange factor (GEF) 1 [ *Mus musculus* (house mouse) ]

Gene ID: 16801, updated on 3-Oct-2020

### Summary

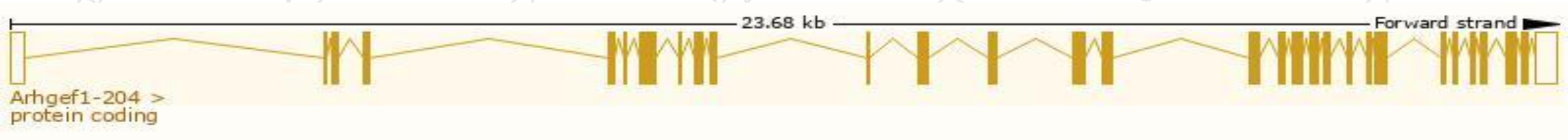
<b>Official Symbol</b>	Arhgef1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Rho guanine nucleotide exchange factor (GEF) 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1353510</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000040940</a>
<b>Gene type</b>	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>	L; Lbc; Lsc; Lbcl2
<b>Expression</b>	Broad expression in thymus adult (RPKM 202.0), spleen adult (RPKM 157.1) and 26 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 19 transcripts,all transcripts are shown below:

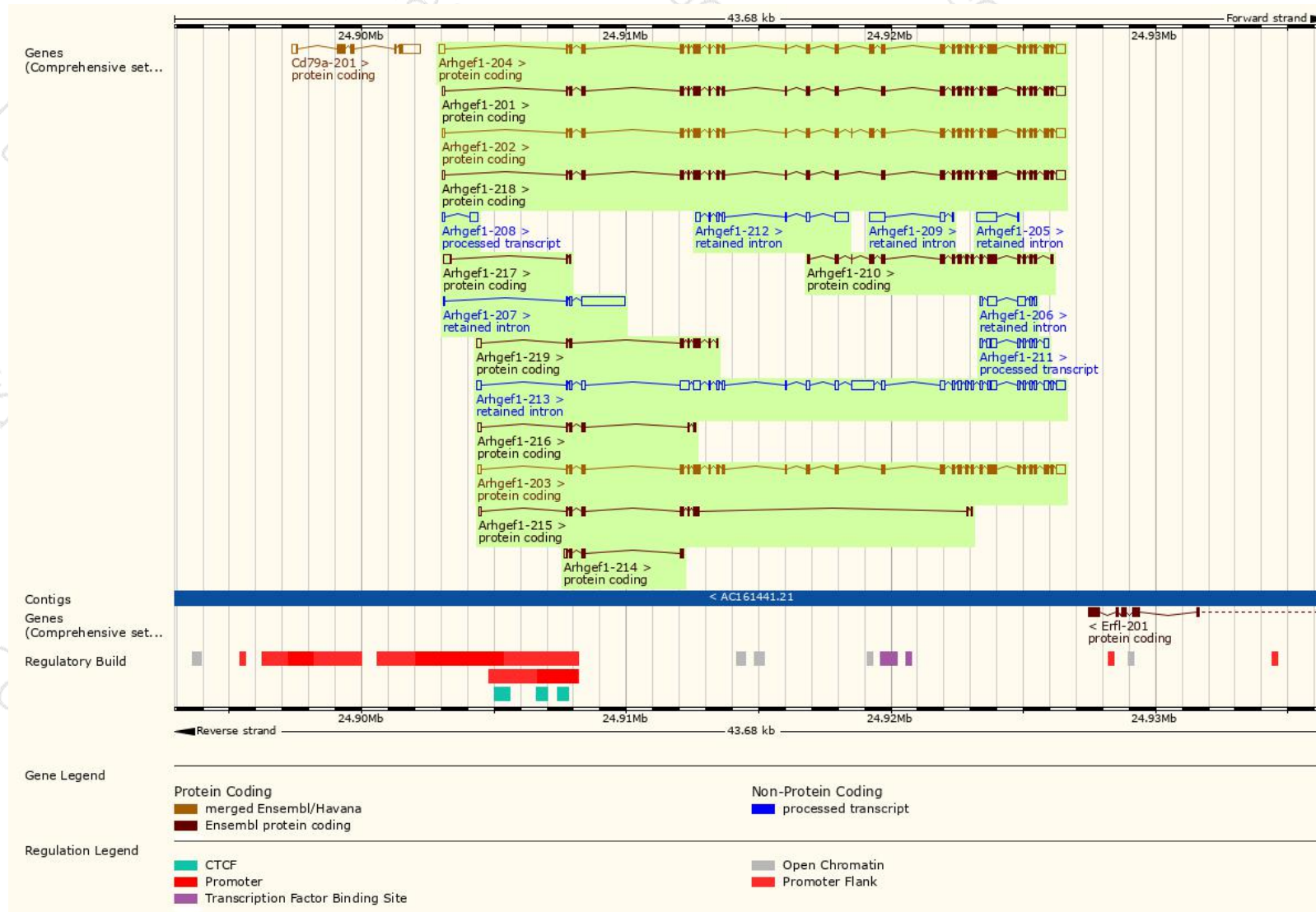
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgef1-213	<a href="#">ENSMUST00000145783.7</a>	4243	No protein	Retained intron	-	-	TSL:5
Arhgef1-207	<a href="#">ENSMUST00000127761.7</a>	1827	No protein	Retained intron	-	-	TSL:2
Arhgef1-212	<a href="#">ENSMUST00000144714.1</a>	1087	No protein	Retained intron	-	-	TSL:3
Arhgef1-206	<a href="#">ENSMUST00000126918.7</a>	821	No protein	Retained intron	-	-	TSL:5
Arhgef1-209	<a href="#">ENSMUST00000129928.1</a>	777	No protein	Retained intron	-	-	TSL:2
Arhgef1-205	<a href="#">ENSMUST00000126484.1</a>	775	No protein	Retained intron	-	-	TSL:1
Arhgef1-204	<a href="#">ENSMUST00000117796.7</a>	3508	976aa	Protein coding	<a href="#">CCDS52140</a>	<a href="#">E9PUF7</a>	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-202	<a href="#">ENSMUST00000098683.10</a>	3375	979aa	Protein coding	<a href="#">CCDS52142</a>	<a href="#">Q61210</a>	TSL:1 GENCODE basic APPRIS P4
Arhgef1-203	<a href="#">ENSMUST00000117419.7</a>	3214	920aa	Protein coding	<a href="#">CCDS52141</a>	<a href="#">Q61210</a>	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-201	<a href="#">ENSMUST00000047873.15</a>	3212	920aa	Protein coding	<a href="#">CCDS52141</a>	<a href="#">Q61210</a>	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-218	<a href="#">ENSMUST00000206508.1</a>	3195	919aa	Protein coding	<a href="#">CCDS85239</a>	<a href="#">Q61210</a>	TSL:1 GENCODE basic APPRIS ALT2
Arhgef1-210	<a href="#">ENSMUST00000132751.1</a>	1851	616aa	Protein coding	-	<a href="#">F6ZN61</a>	CDS 5' incomplete TSL:5
Arhgef1-215	<a href="#">ENSMUST00000205295.1</a>	777	233aa	Protein coding	-	<a href="#">A0A0U1RPN7</a>	CDS 3' incomplete TSL:5
Arhgef1-219	<a href="#">ENSMUST00000206906.1</a>	737	192aa	Protein coding	-	<a href="#">A0A0U1RPP2</a>	CDS 3' incomplete TSL:5
Arhgef1-216	<a href="#">ENSMUST00000206011.1</a>	419	102aa	Protein coding	-	<a href="#">A0A0U1RPH2</a>	CDS 3' incomplete TSL:2
Arhgef1-214	<a href="#">ENSMUST00000151121.1</a>	390	101aa	Protein coding	-	<a href="#">D3YVJ9</a>	CDS 3' incomplete TSL:3
Arhgef1-217	<a href="#">ENSMUST00000206028.1</a>	374	30aa	Protein coding	-	<a href="#">A0A0U1RNQ2</a>	CDS 3' incomplete TSL:3
Arhgef1-211	<a href="#">ENSMUST00000132786.1</a>	832	No protein	Processed transcript	-	-	TSL:5
Arhgef1-208	<a href="#">ENSMUST00000129383.1</a>	351	No protein	Processed transcript	-	-	TSL:2

The strategy is based on the design of *Arhgef1-204* transcript,the transcription is shown below:



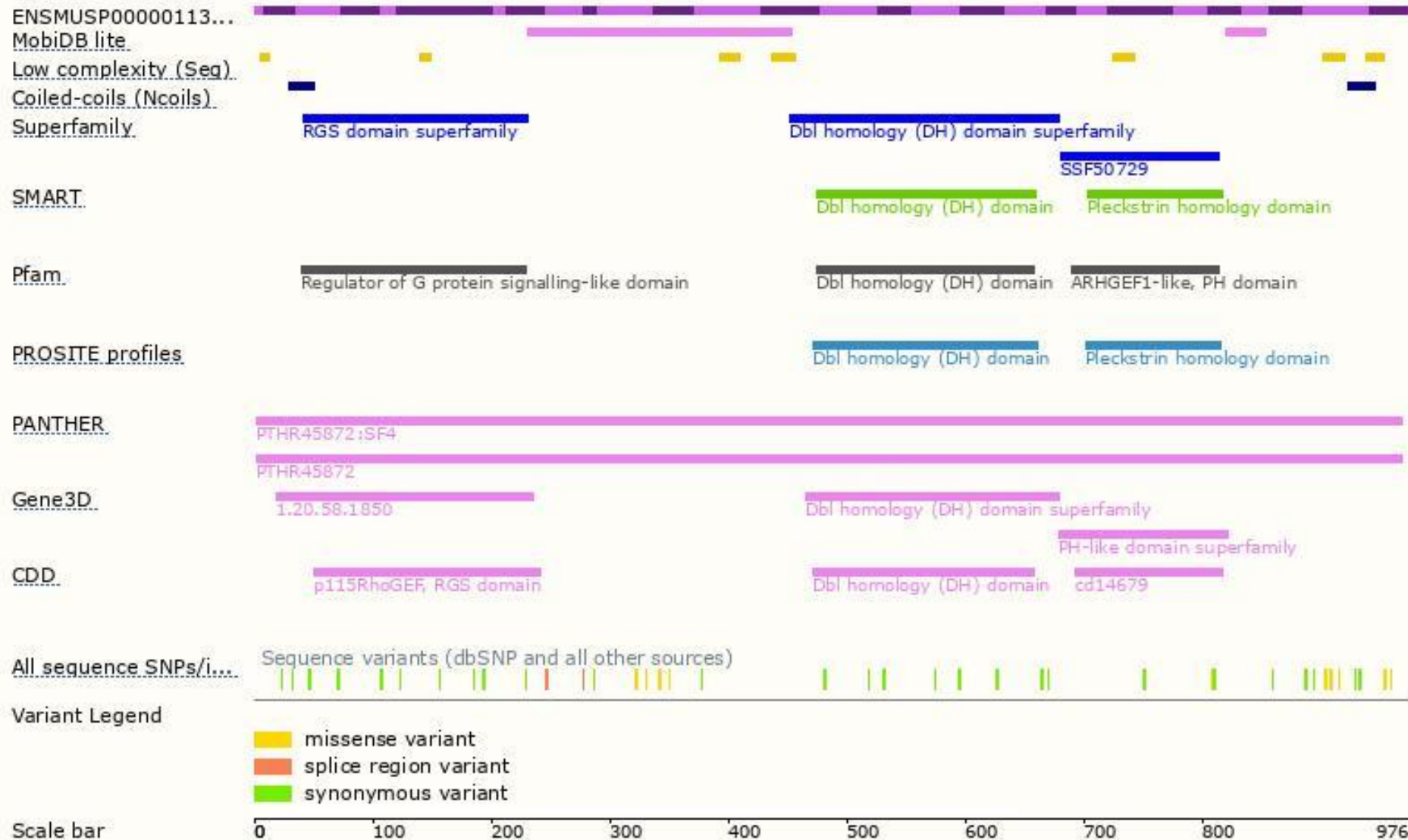


# Genomic location distribution

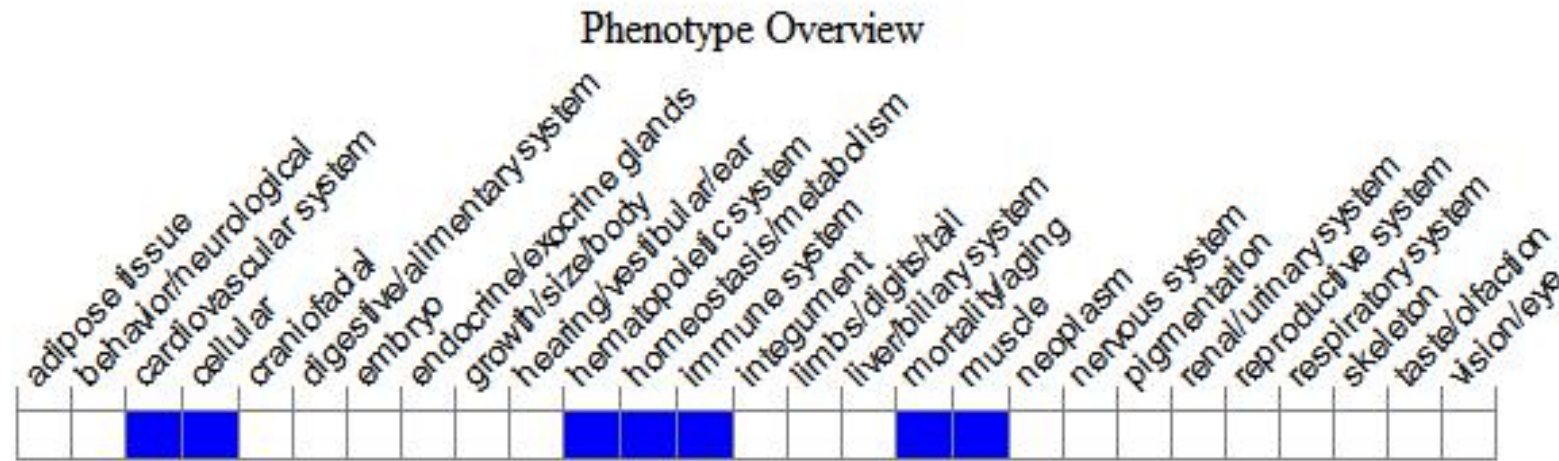




# Protein domain



# 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, homozygous mutation of this gene results in impaired humeral immunity, reduced numbers of marginal zone B (MZB) cells, decreased basal T cell proliferation, and reduced basal motility of lymphocytes but enhanced migration of MZB cells after serum activation.

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

Tel: 400-9660890

