

# *Ago1* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Ago1*

**Project type**

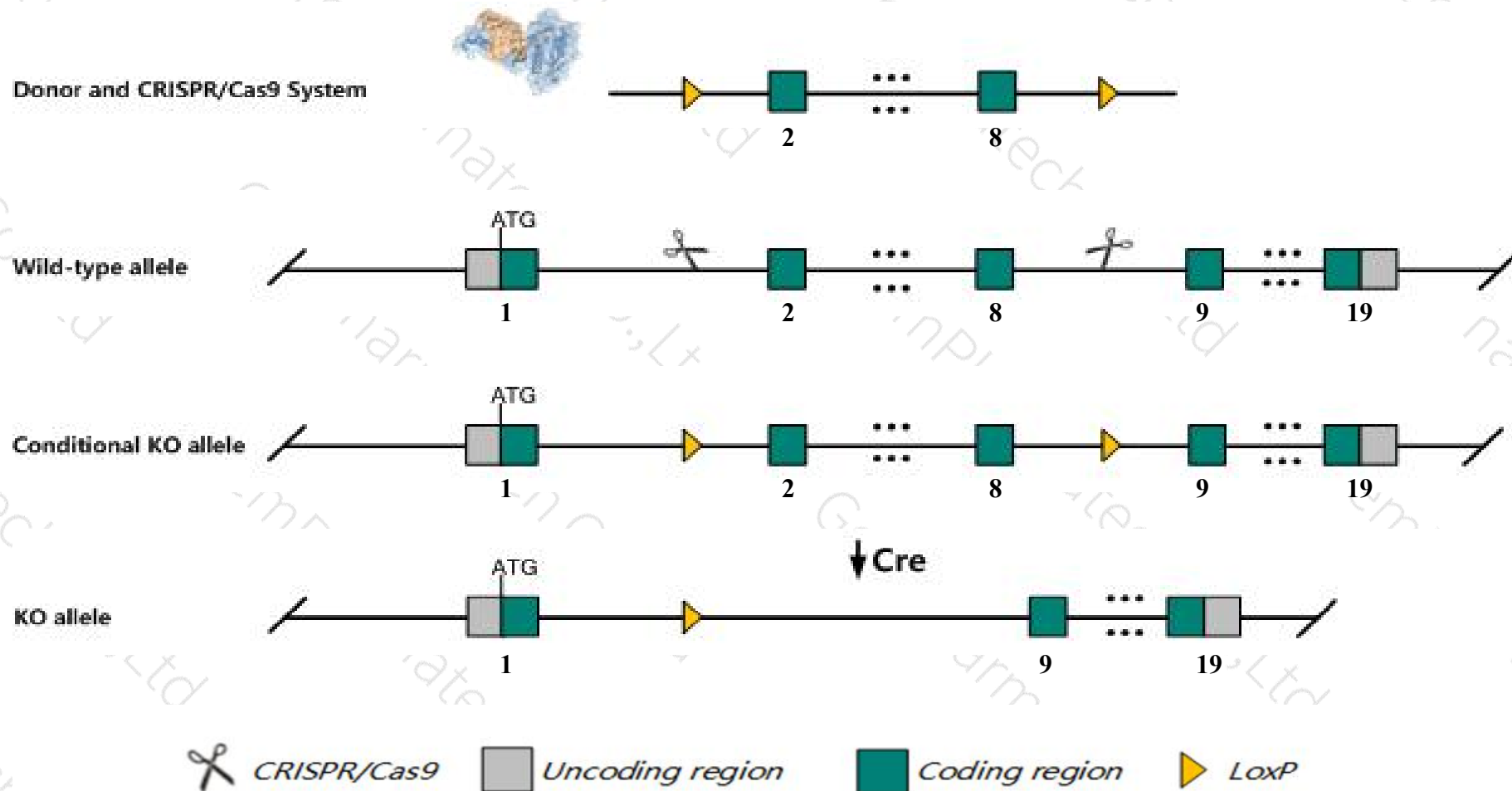
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ago1* gene. The schematic diagram is as follows:



- The *Ago1* gene has 5 transcripts. According to the structure of *Ago1* gene, exon2-exon8 of *Ago1-201* (ENSMUST00000097888.9) transcript is recommended as the knockout region. The region contains 995bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ago1* 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 conditional allele activated in keratinocytes exhibit no abnormal phenotype.
- The *Ago1* gene is located on the Chr4. 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)

## Ago1 argonaute RISC catalytic subunit 1 [Mus musculus (house mouse)]

Gene ID: 236511, updated on 31-Jan-2019

### Summary

**Official Symbol** Ago1 provided by [MGI](#)

**Official Full Name** argonaute RISC catalytic subunit 1 provided by [MGI](#)

**Primary source** [MGI:MGI:2446630](#)

**See related** [Ensembl:ENSMUSG00000041530](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** Eif2c1

**Summary** This gene encodes a member of the argonaute family of proteins, which associate with small RNAs and have important roles in RNA interference (RNAi) and RNA silencing. This protein binds to microRNAs (miRNAs) or small interfering RNAs (siRNAs) and represses translation of mRNAs that are complementary to them. It is also involved in transcriptional gene silencing (TGS) of promoter regions that are complementary to bound short antigenic RNAs (agRNAs), as well as in the degradation of miRNA-bound mRNA targets. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. A recent study showed this gene to be an authentic stop codon readthrough target, and that its mRNA could give rise to an additional C-terminally extended isoform by use of an alternative in-frame translation termination codon. [provided by RefSeq, Nov 2015]

**Expression** Ubiquitous expression in CNS E11.5 (RPKM 22.9), CNS E14 (RPKM 19.3) and 28 other tissues [See more](#)

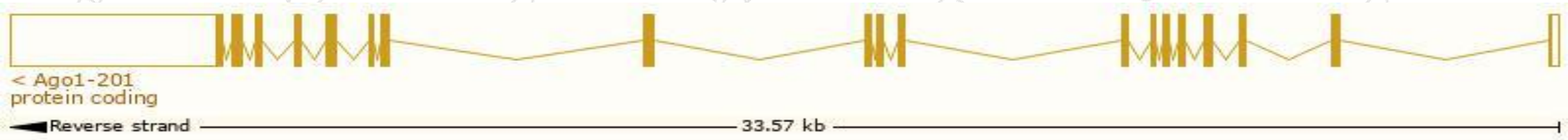
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

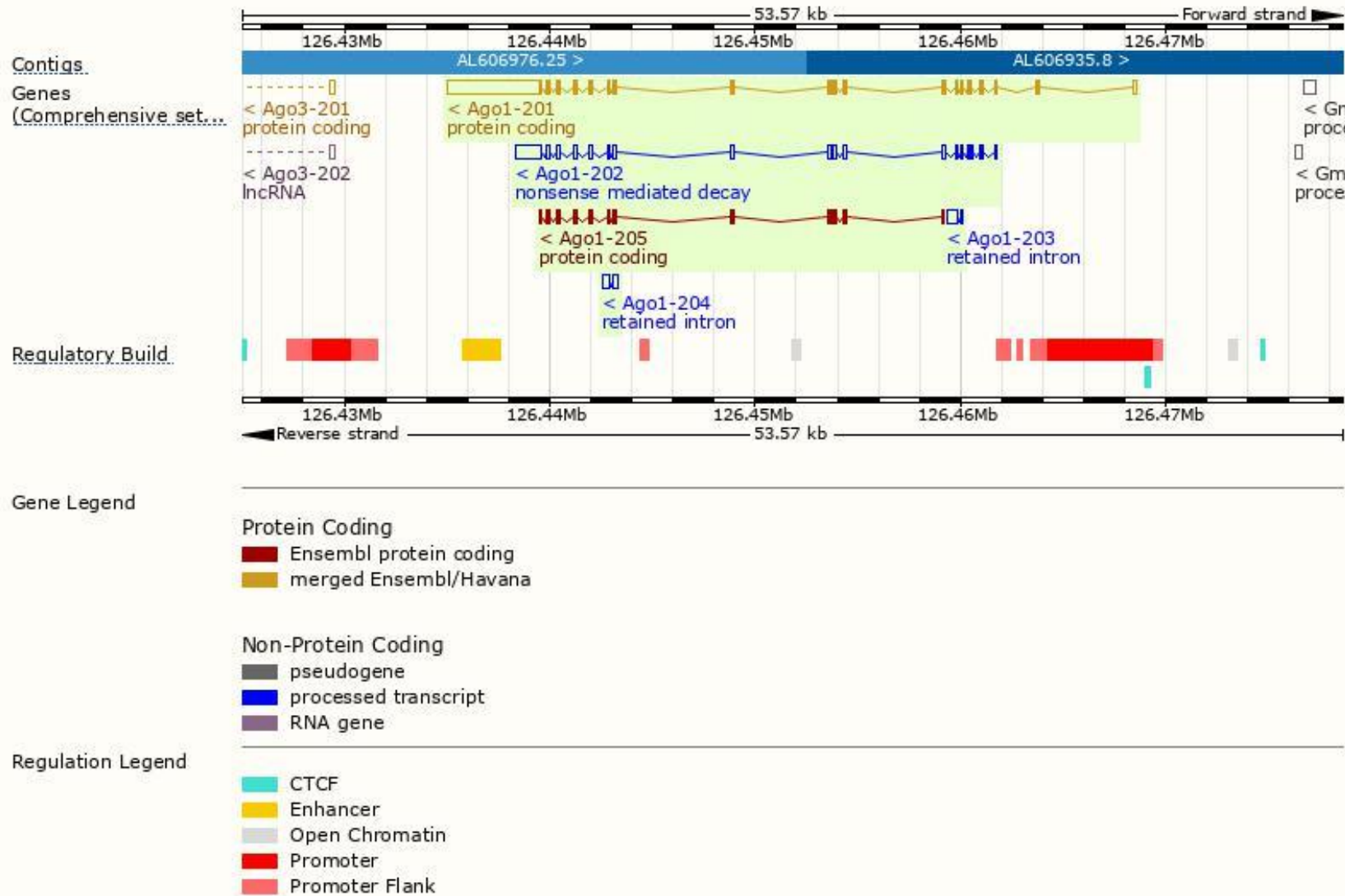
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ago1-201	<a href="#">ENSMUST00000097888.9</a>	7227	<a href="#">857aa</a>	Protein coding	<a href="#">CCDS18653</a>	<a href="#">Q8CJG1</a>	TSL:1 GENCODE basic APPRIS P1
Ago1-205	<a href="#">ENSMUST00000176315.1</a>	1662	<a href="#">553aa</a>	Protein coding	-	<a href="#">H3BJ70</a>	CDS 5' incomplete TSL:5
Ago1-202	<a href="#">ENSMUST00000127800.1</a>	3606	<a href="#">133aa</a>	Nonsense mediated decay	-	<a href="#">H3BL59</a>	CDS 5' incomplete TSL:1
Ago1-203	<a href="#">ENSMUST00000149425.1</a>	678	No protein	Retained intron	-	-	TSL:3
Ago1-204	<a href="#">ENSMUST00000156533.1</a>	588	No protein	Retained intron	-	-	TSL:3

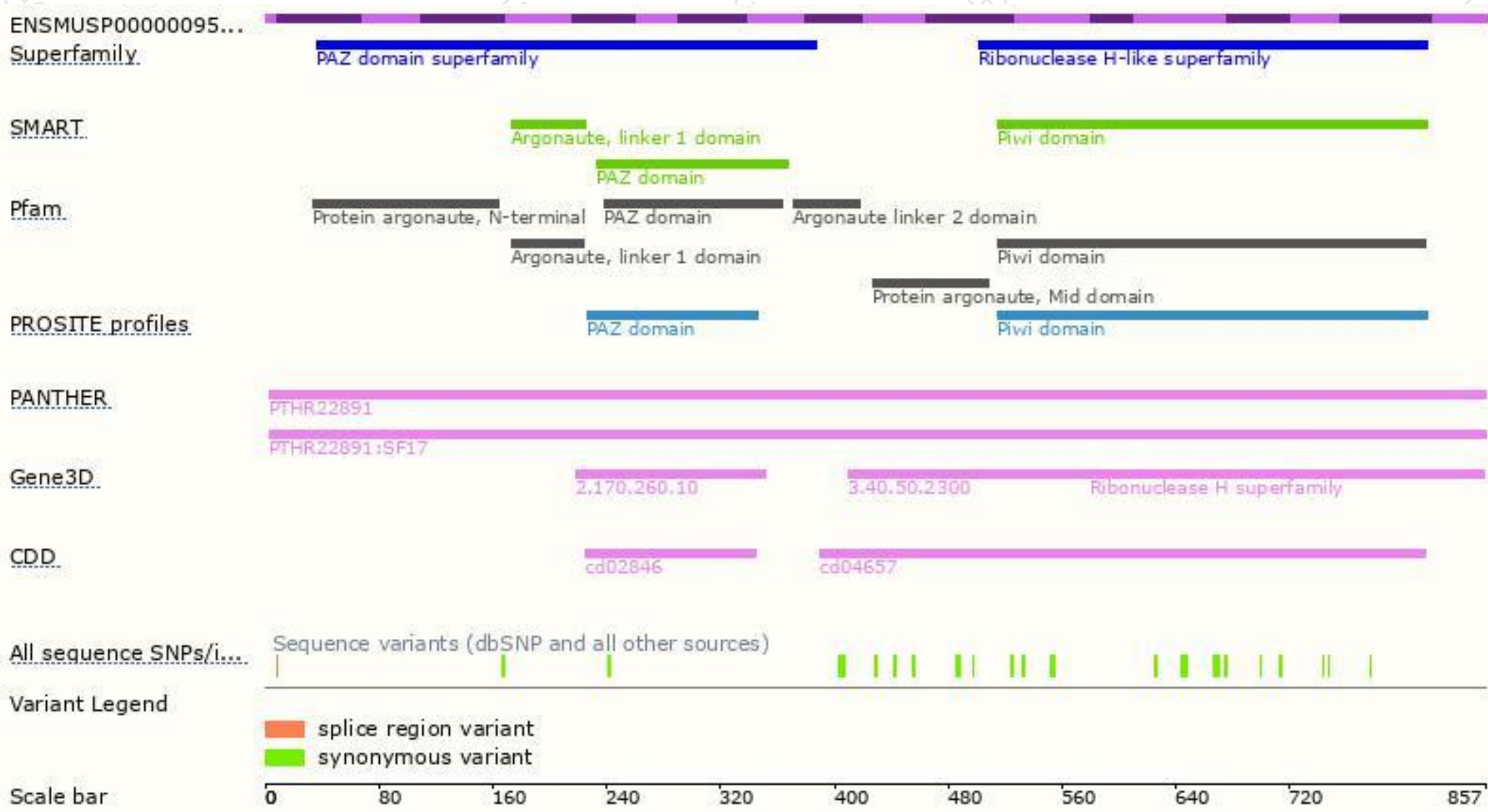
The strategy is based on the design of *Ago1-201* transcript,The transcription is shown below



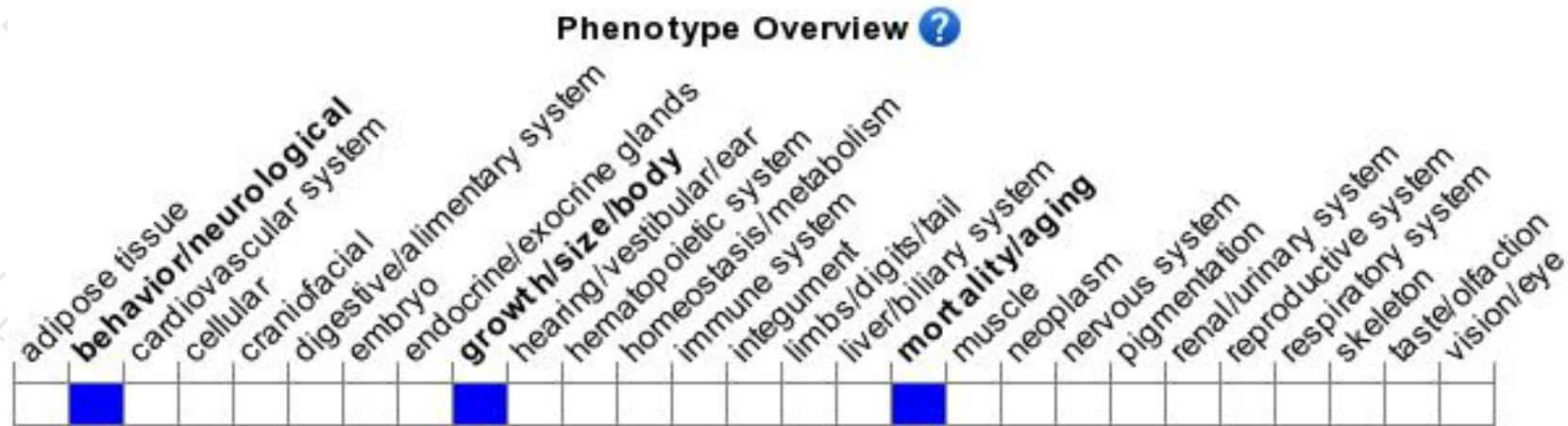
# Genomic location distribution



# 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 conditional allele activated in keratinocytes exhibit no abnormal phenotype.

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

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