

Abraxas2 Cas9-KO Strategy

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Project Overview

Project Name

Abraxas2

Project type

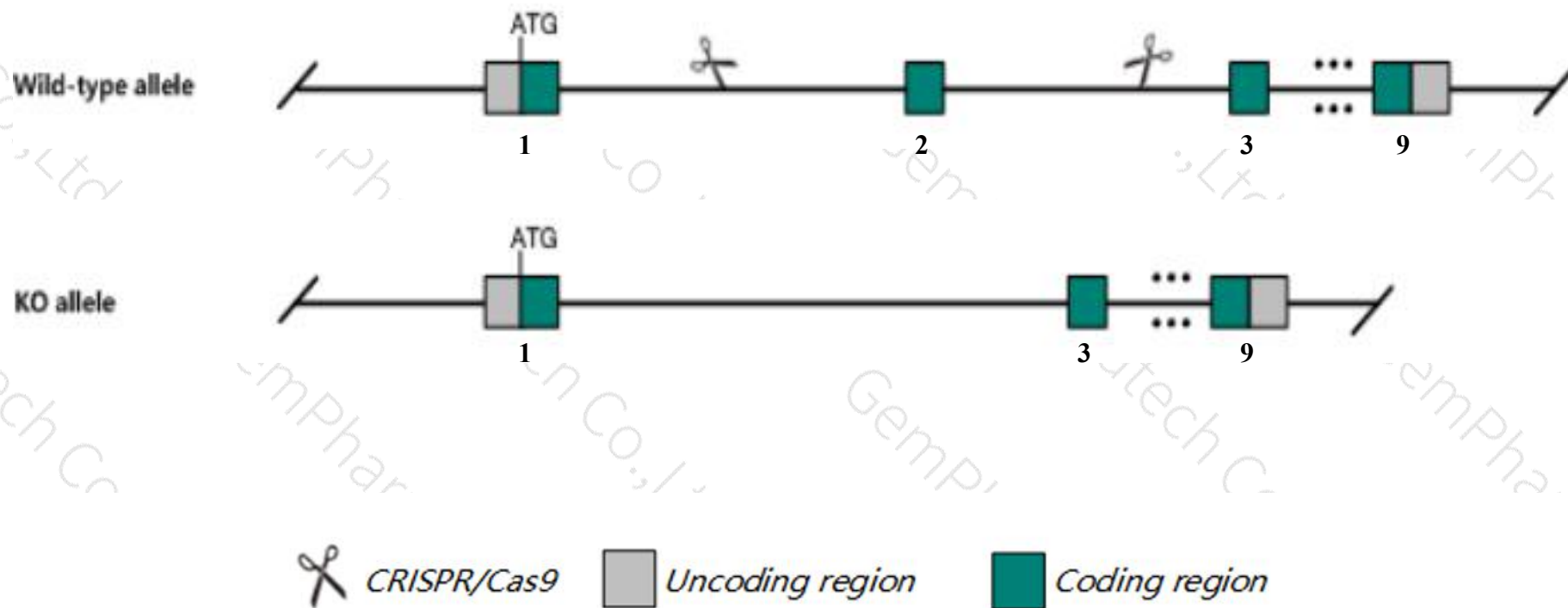
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abraxas2* gene. The schematic diagram is as follows:



- The *Abraxas2* gene has 8 transcripts. According to the structure of *Abraxas2* gene, exon2 of *Abraxas2-201* (ENSMUST00000084497.11) transcript is recommended as the knockout region. The region contains 91bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abraxas2* gene. The brief process is as follows: CRISPR/Cas9 system

- The KO region contains functional region of the *Abraxas2* gene. Knockout the region may affect the function of *Fgfr2* gene.
- The *Abraxas2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Abraxas2 BRISC complex subunit [Mus musculus (house mouse)]

Gene ID: 109359, updated on 13-Mar-2020

Summary



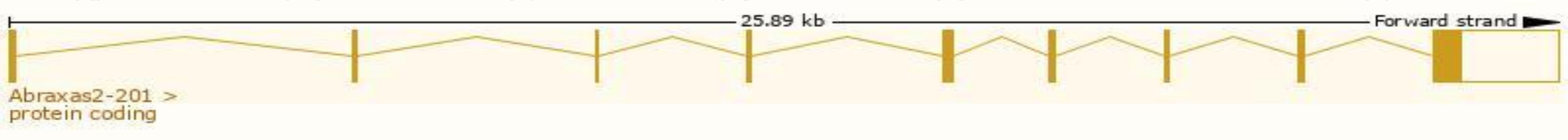
Official Symbol	Abraxas2 provided by MGI
Official Full Name	BRISC complex subunit provided by MGI
Primary source	MGI:MGI:1926116
See related	Ensembl:ENSMUSG00000030965
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA589499, AI853413, Abro1, C430003P19Rik, Fam175b
Expression	Ubiquitous expression in placenta adult (RPKM 10.5), CNS E11.5 (RPKM 9.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

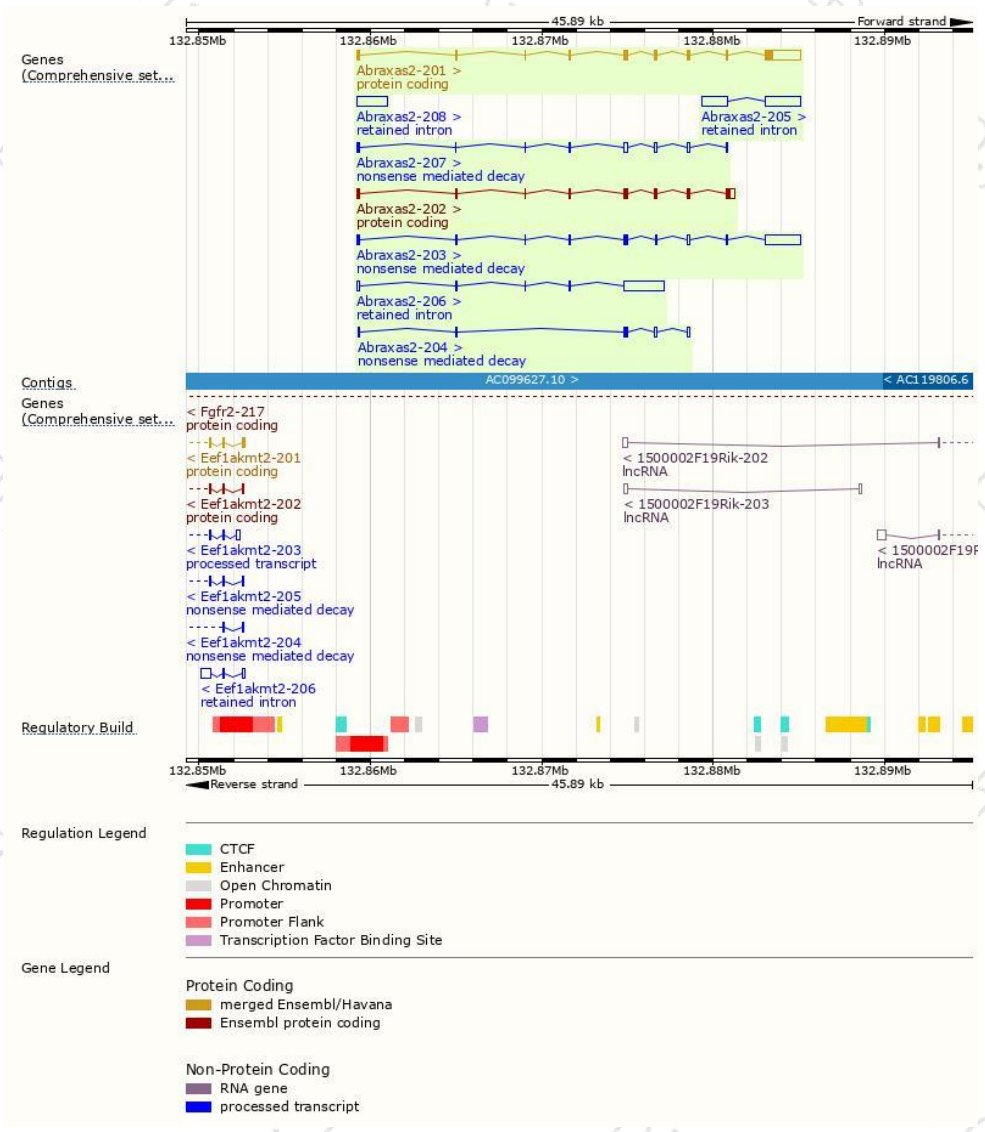
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abraxas2-201	ENSMUST00000084497.11	2892	424aa	Protein coding	CCDS21928	Z4YJY0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Abraxas2-202	ENSMUST00000106161.7	1224	289aa	Protein coding	-	D3Z4D8	CDS 5' incomplete TSL:1
Abraxas2-203	ENSMUST00000129552.1	2827	160aa	Nonsense mediated decay	-	D6RJ39	CDS 5' incomplete TSL:1
Abraxas2-207	ENSMUST00000147786.8	733	60aa	Nonsense mediated decay	-	D6RHR6	CDS 5' incomplete TSL:5
Abraxas2-204	ENSMUST00000134784.1	515	98aa	Nonsense mediated decay	-	A0A1B0GS96	CDS 5' incomplete TSL:3
Abraxas2-205	ENSMUST00000138436.1	3583	No protein	Retained intron	-	-	TSL:2
Abraxas2-206	ENSMUST00000144225.8	2620	No protein	Retained intron	-	-	TSL:2
Abraxas2-208	ENSMUST00000210077.1	1778	No protein	Retained intron	-	-	TSL:NA

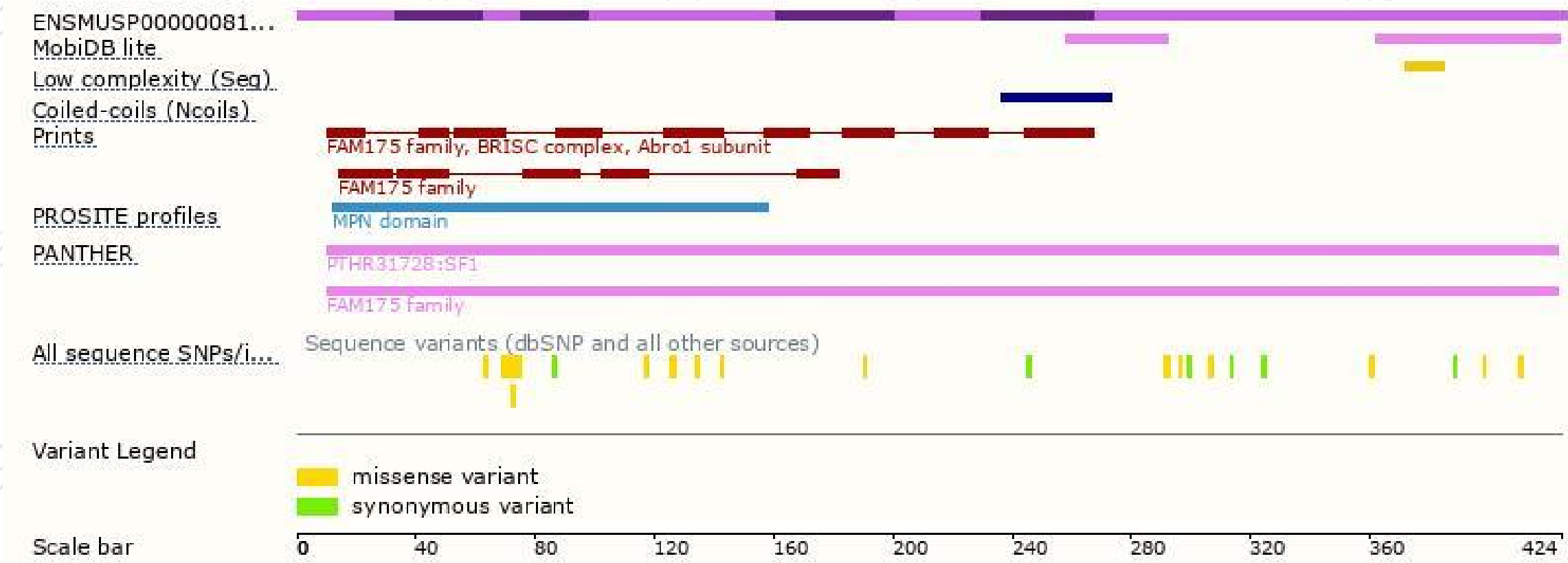
The strategy is based on the design of *Abraxas2-201* transcript,The transcription is shown below



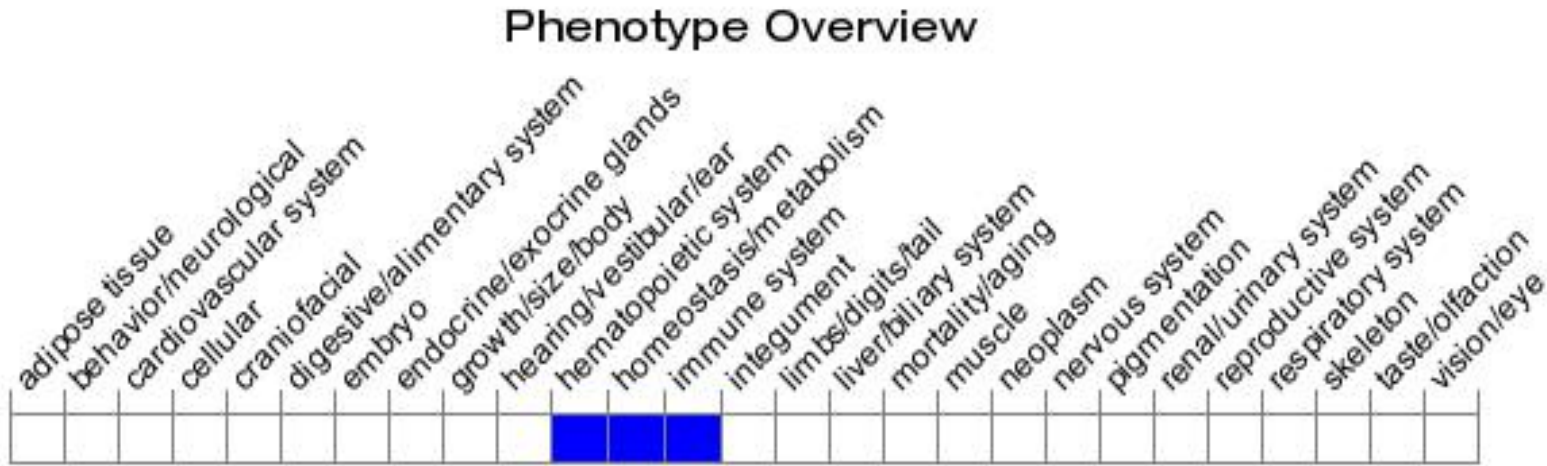
Genomic location distribution



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/>).

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

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