Abraxas1 Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

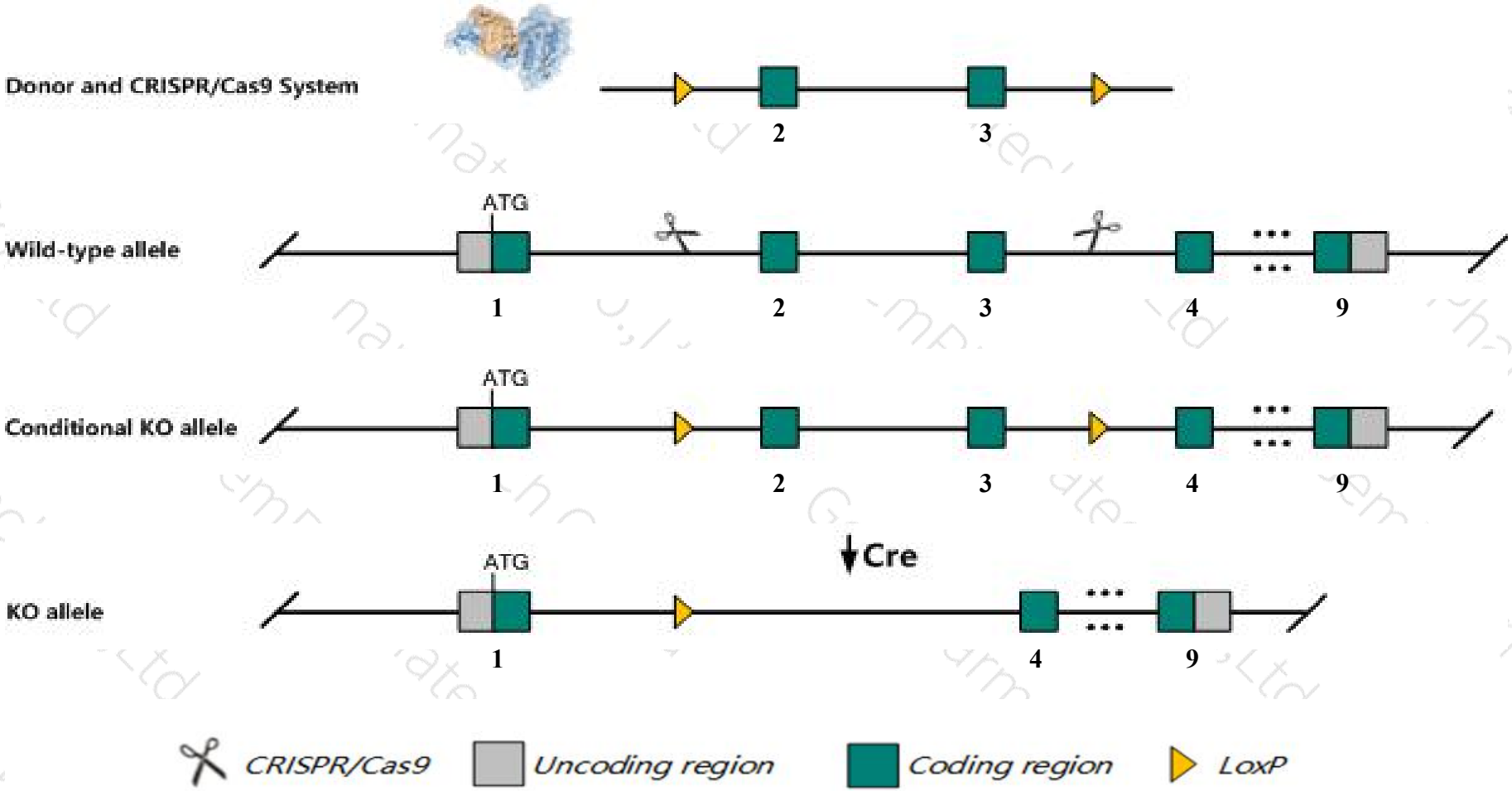
Design Date: 2020-7-14

Project Overview

Project Name	***Abraxas1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abraxas1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Abraxas1* gene has 9 transcripts. According to the structure of *Abraxas1* gene, exon2-exon3 of *Abraxas1-202*(ENSMUST00000055245.12) transcript is recommended as the knockout region.The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Abraxas1* 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 knock-out allele exhibit increased tumor incidence, genetic instability and premature lethality. Mice heterozygous for a knock-out allele exhibit increased tumor incidence and premature death.

➢ Transcript *Abraxas1*-206 may not be affected.

➢ The floxed region is near to the N-terminal of *Gm43513* gene and C-terminal of *Gm43514* gene,this strategy may influence the regulatory function of the N-terminal of *Gm43513* gene and C-terminal of *Gm43514* gene.

➢ The *Abraxas1* gene is located on the Chr5. 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）

Abraxas1 BRCA1 A complex subunit [Mus musculus (house mouse)]

Gene ID: 70681, updated on 13-Mar-2020

Summary

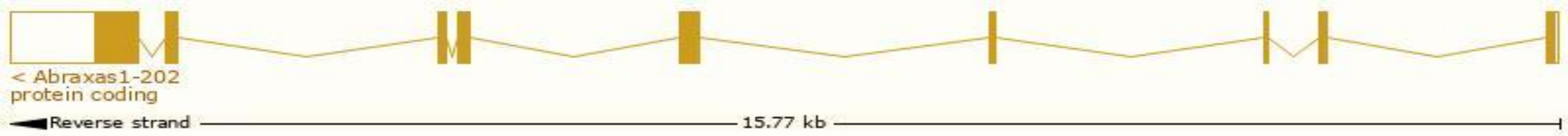
Official Symbol	Abraxas1 provided by MGI
Official Full Name	BRCA1 A complex subunit provided byMGI
Primary source	MGI:MGI:1917931
See related	Ensembl:ENSMUSG00000035234
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3830405G04Rik, 5630400M01Rik, AI506069, AL024423, AV118690, Ccdc98, Fam175a
Expression	Ubiquitous expression in liver E14 (RPKM 4.3), placenta adult (RPKM 4.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

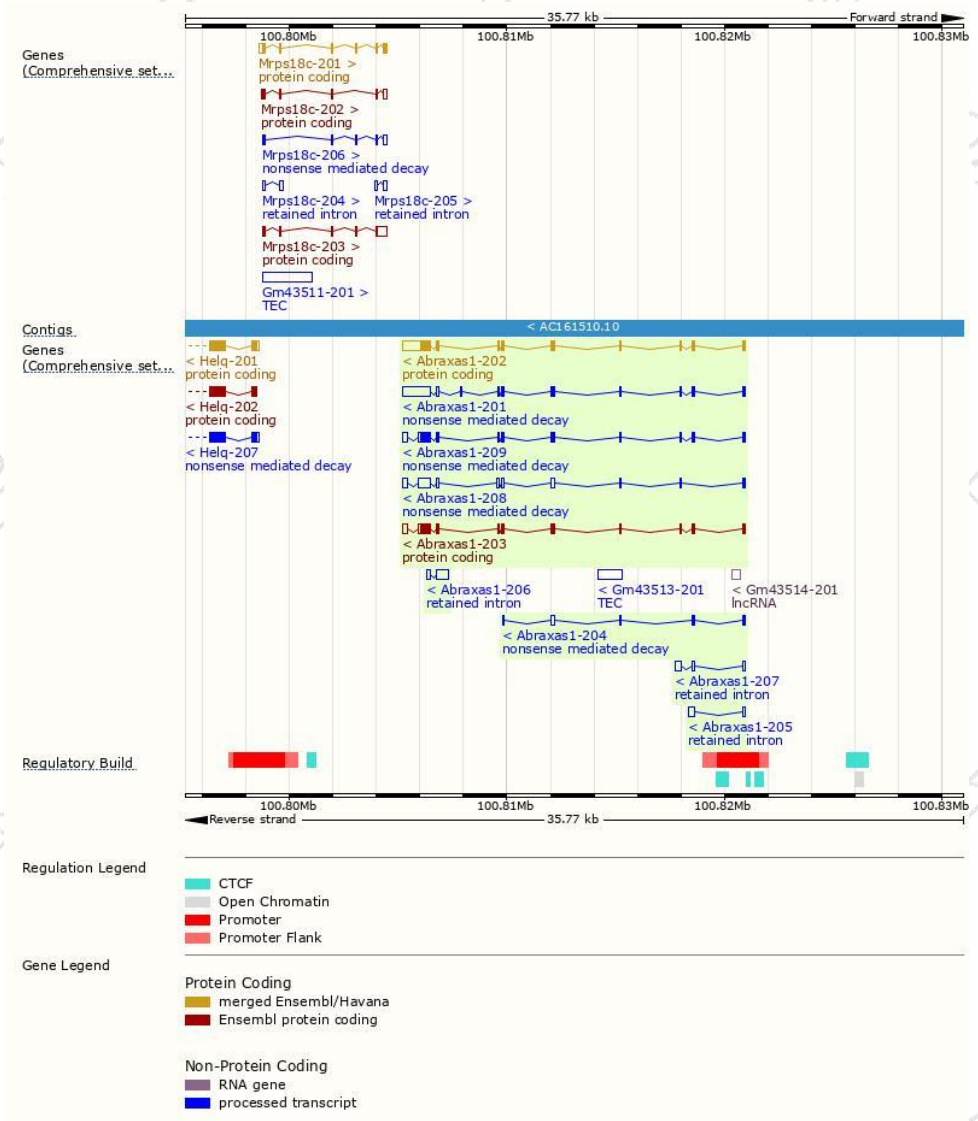
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abraxas1-202	ENSMUST00000055245.12	2139	407aa	Protein coding	CCDS19469	Q8BPZ8	TSL:1 GENCODE basic APPRIS P1
Abraxas1-203	ENSMUST00000117364.7	1657	407aa	Protein coding	CCDS19469	Q8BPZ8	TSL:1 GENCODE basic APPRIS P1
Abraxas1-201	ENSMUST00000044535.13	2182	261aa	Nonsense mediated decay	-	Q8BPZ8	TSL:1
Abraxas1-209	ENSMUST00000200657.4	1668	407aa	Nonsense mediated decay	-	Q8BPZ8	TSL:1
Abraxas1-208	ENSMUST00000153302.7	1582	46aa	Nonsense mediated decay	-	D6RHB0	TSL:1
Abraxas1-204	ENSMUST00000129358.1	545	64aa	Nonsense mediated decay	-	D6RFD4	TSL:3
Abraxas1-206	ENSMUST00000145429.1	701	No protein	Retained intron	-	-	TSL:2
Abraxas1-207	ENSMUST00000145707.1	454	No protein	Retained intron	-	-	TSL:2
Abraxas1-205	ENSMUST00000131857.1	358	No protein	Retained intron	-	-	TSL:3

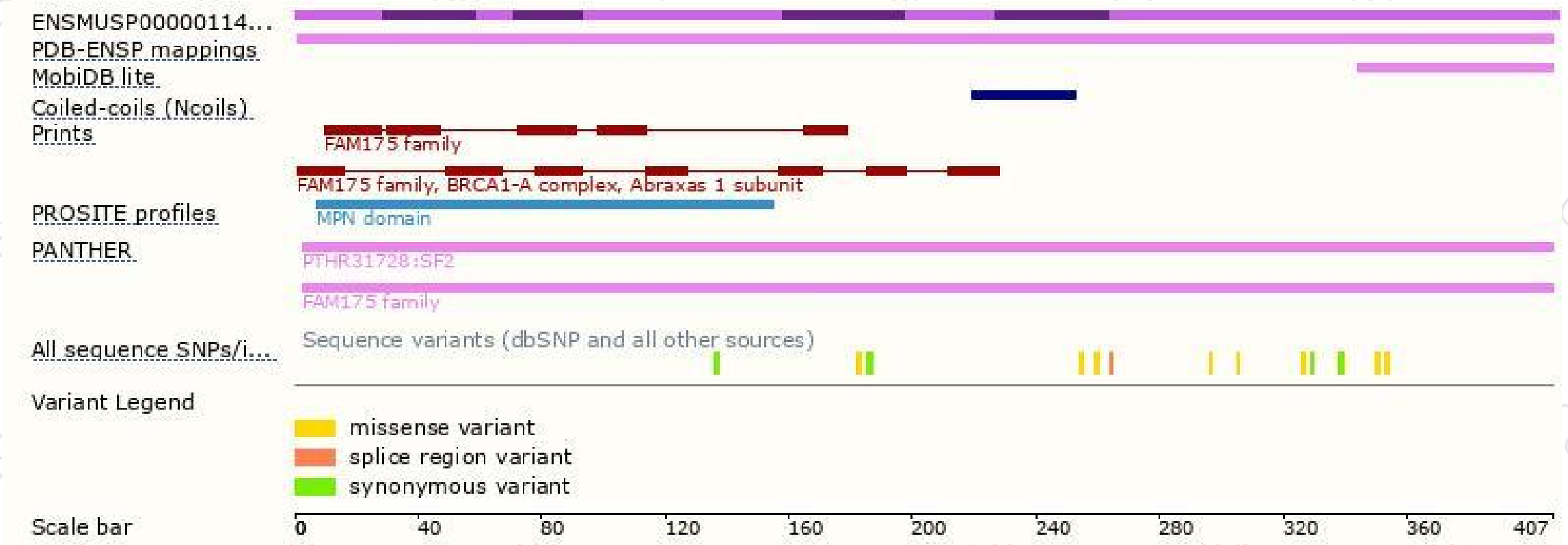
The strategy is based on the design of *Abraxas1-202* transcript,the transcription is shown below:



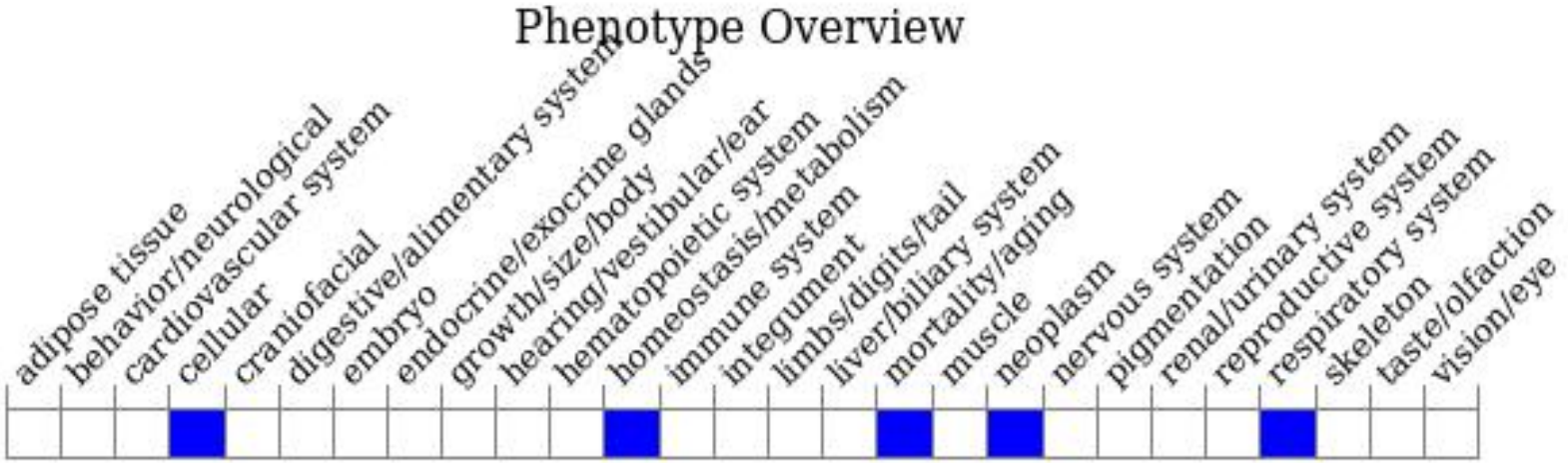
Genomic location distribution



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 tumor incidence, genetic instability and premature lethality. Mice heterozygous for a knock-out allele exhibit increased tumor incidence and premature death.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd