Apba2 Cas9-CKO *Strategy*

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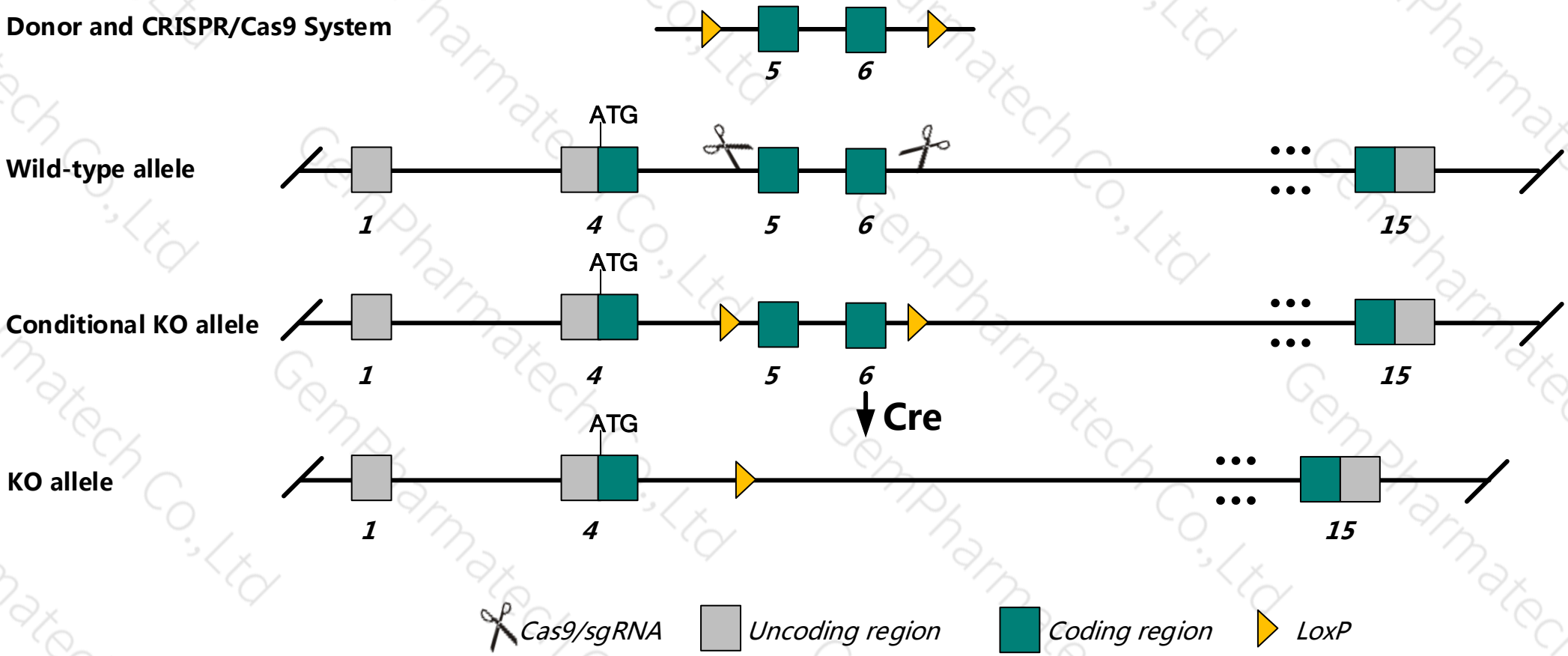
Project Overview

Project Name	***Apba2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Apba2* gene. The schematic diagram is as follows:



Technical routes

- The *Apba2* gene has 7 transcripts.According to the structure of *Apba2* gene, exon5-exon6 of *Apba2*-201 transcript is recommended as the knockout region.The region contains 118bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Apba2* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice

- Transcript *Apba2-203 and Apba2-204* may not be affected.

- The *Apba2* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information （NCBI）

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Apba2 amyloid beta (A4) precursor protein-binding, family A, member 2 [*Mus musculus* (house mouse)]

Gene ID: 11784, updated on 7-May-2019

Summary

Official Symbol	Apba2 provided by MGI
Official Full Name	amyloid beta (A4) precursor protein-binding, family A, member 2 provided by MGI
Primary source	MGI:MGI:1261791
See related	Ensembl:ENSMUSG00000030519
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	X11L; XIIL; mXIIL; X11-like
Expression	Biased expression in CNS E18 (RPKM 37.9), cortex adult (RPKM 35.0) and 7 other tissues See more
Orthologs	human all

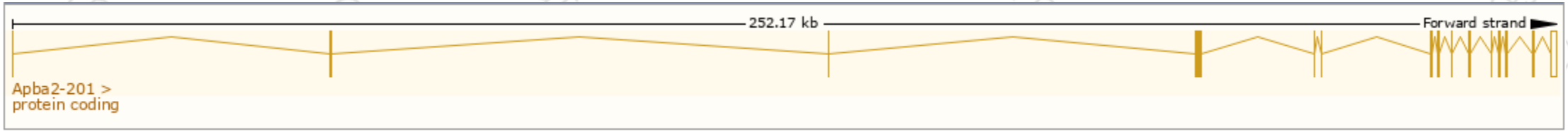
Transcript information（ Ensembl ）

The gene has 7 transcripts, and all transcripts are shown below ：

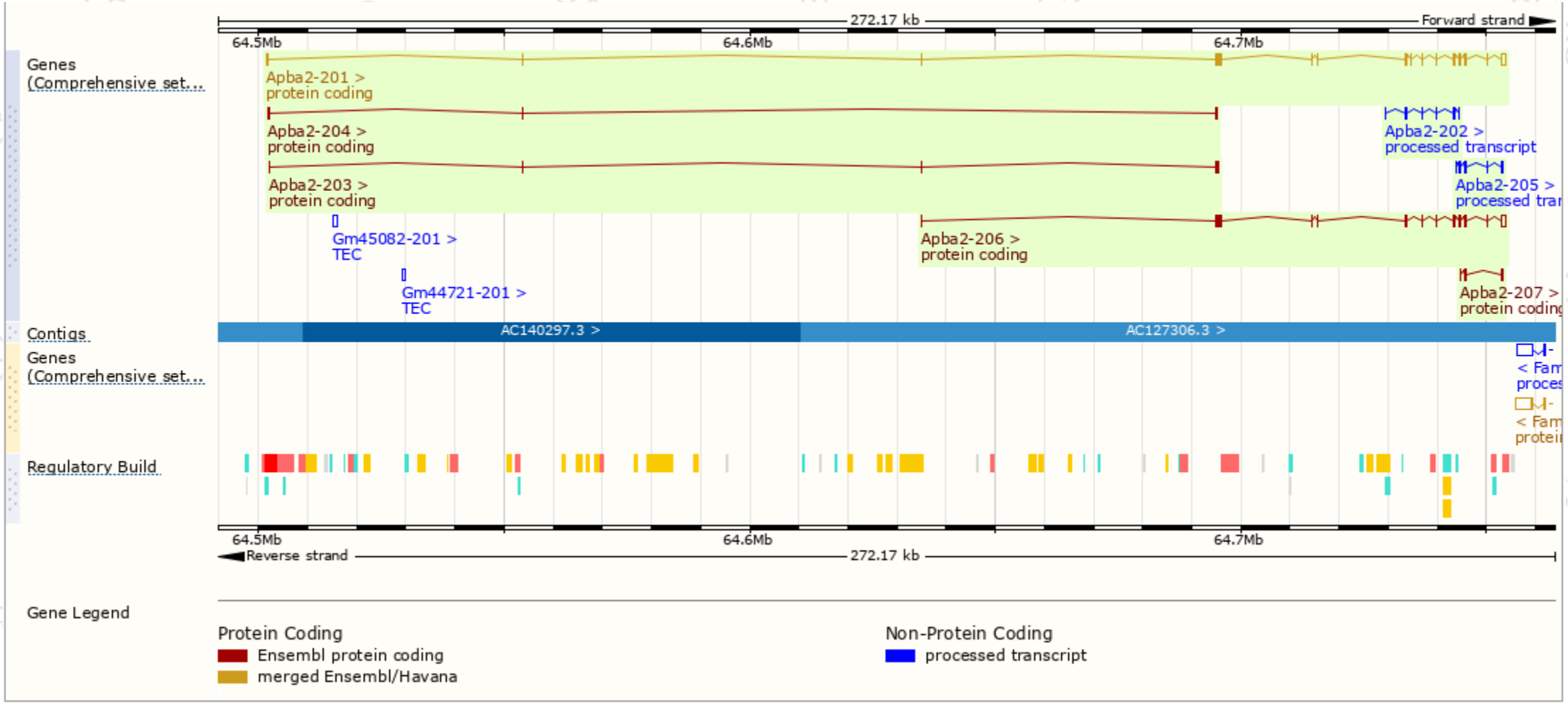
Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Apba2-201	ENSMUST00000032732.14	3321	750aa	Protein coding	CCDS21335	P98084	TSL:1 GENCODE basic APPRIS P2
Apba2-206	ENSMUST00000206246.1	3027	738aa	Protein coding	-	A0A0U1RPM0	TSL:5 GENCODE basic APPRIS ALT2
Apba2-204	ENSMUST00000205613.1	714	81aa	Protein coding	-	A0A0U1RQ68	CDS 3' incomplete TSL:3
Apba2-203	ENSMUST00000205604.1	643	102aa	Protein coding	-	A0A0U1RQ78	CDS 3' incomplete TSL:2
Apba2-207	ENSMUST00000206630.1	501	79aa	Protein coding	-	A0A0U1RPS9	CDS 5' incomplete TSL:3
Apba2-205	ENSMUST00000206061.1	898	No protein	Processed transcript	-	-	TSL:1
Apba2-202	ENSMUST00000205551.1	772	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Apba2-201* transcript,The transcription is shown below

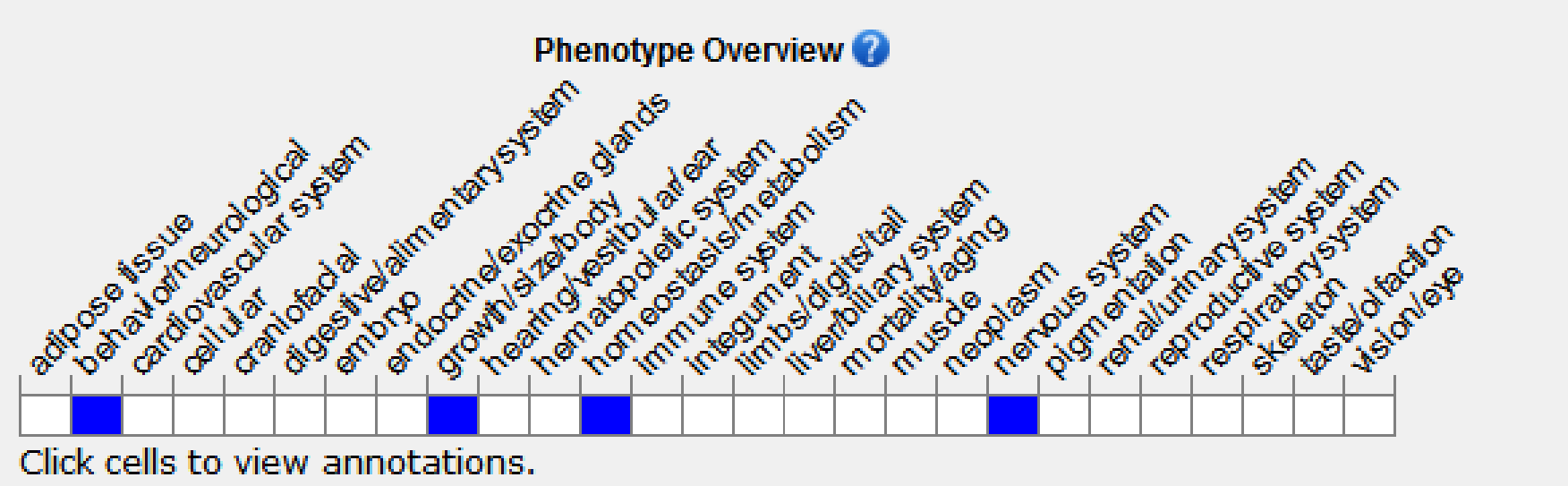


Genomic location distribution



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 disruptions in this gene show a selective deficit in motivated approach behavior, but not in motivated avoidance behavior.

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

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