Cfap69 Cas9-CKO Strategy

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Project Overview

Project Name	***Cfap69***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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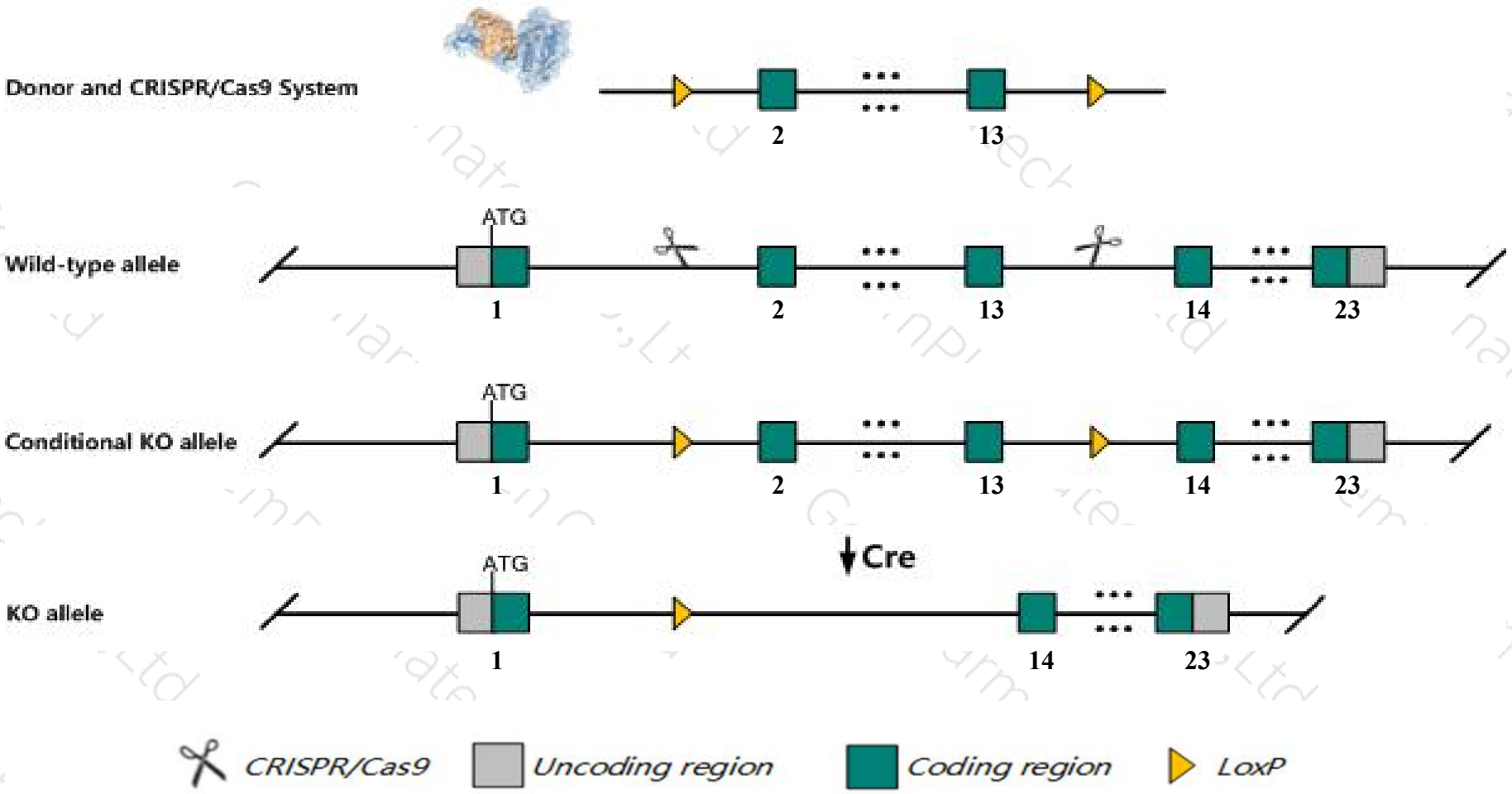
This model will use CRISPR/Cas9 technology to edit the *Cfap69* gene. The schematic diagram is as follows:



Technical routes

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- The *Cfap69* gene has 12 transcripts. According to the structure of *Cfap69* gene, exon2-exon13 of *Cfap69-201* (ENSMUST00000054865.12) transcript is recommended as the knockout region.The region contains 1417bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cfap69* 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 faster response kinetics and stimuli integration to olfactory stimulation and impaired olfaction a buried food pellet test with a background of the same odor.

- The *Cfap69* 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）

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Cfap69 cilia and flagella associated protein 69 [Mus musculus (house mouse)]

Gene ID: 207686, updated on 31-Jan-2019

Summary

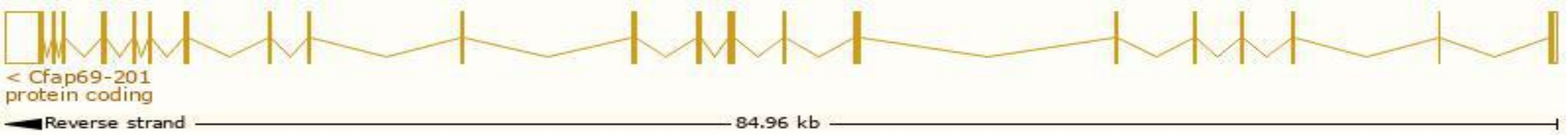
Official Symbol	Cfap69 provided by MGI
Official Full Name	cilia and flagella associated protein 69 provided byMGI
Primary source	MGI:MGI:2443778
See related	Ensembl:ENSMUSG00000040473
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4921525K03, A330021E22Rik, AI427898
Expression	Biased expression in testis adult (RPKM 13.1), frontal lobe adult (RPKM 3.0) and 8 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

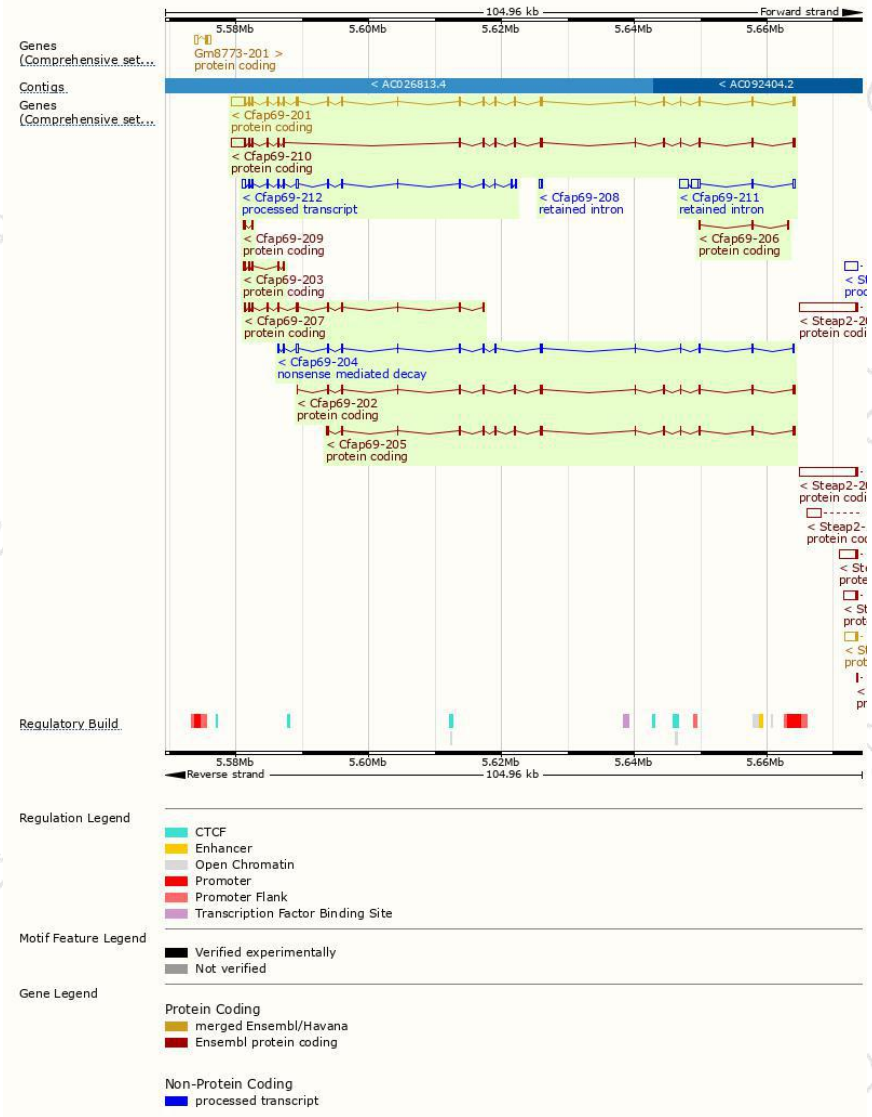
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cfap69-201	ENSMUST00000054865.12	4956	942aa	Protein coding	CCDS19075	Q8BH53	TSL:1 GENCODE basic APPRIS P2
Cfap69-210	ENSMUST00000196165.4	4408	771aa	Protein coding	-	A0A0G2JG21	TSL:1 GENCODE basic APPRIS ALT2
Cfap69-205	ENSMUST00000135252.2	2188	627aa	Protein coding	-	Q8BH53	TSL:1 GENCODE basic APPRIS ALT2
Cfap69-202	ENSMUST00000061008.9	1906	576aa	Protein coding	-	G3X999	CDS 3' incomplete TSL:1
Cfap69-207	ENSMUST00000148347.7	1462	478aa	Protein coding	-	F6S241	CDS 5' incomplete TSL:5
Cfap69-203	ENSMUST00000124734.7	579	170aa	Protein coding	-	F6Q7Y3	CDS 5' incomplete TSL:5
Cfap69-209	ENSMUST00000155048.1	389	76aa	Protein coding	-	F6WCD2	CDS 5' incomplete TSL:5
Cfap69-206	ENSMUST00000148193.1	357	31aa	Protein coding	-	D3YV72	CDS 3' incomplete TSL:3
Cfap69-204	ENSMUST00000132510.7	2080	120aa	Nonsense mediated decay	-	D6RFV9	TSL:5
Cfap69-212	ENSMUST00000199314.4	2189	No protein	Processed transcript	-	-	TSL:1
Cfap69-211	ENSMUST00000198121.1	2920	No protein	Retained intron	-	-	TSL:5
Cfap69-208	ENSMUST00000150140.2	293	No protein	Retained intron	-	-	TSL:5

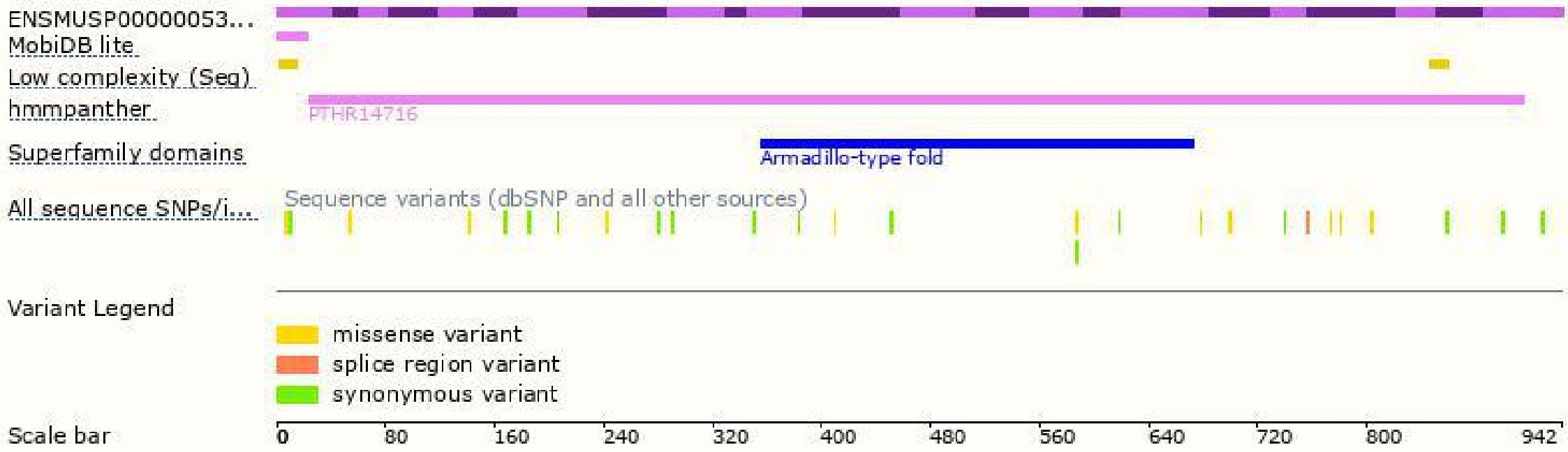
The strategy is based on the design of *Cfap69-201* transcript,The transcription is shown below



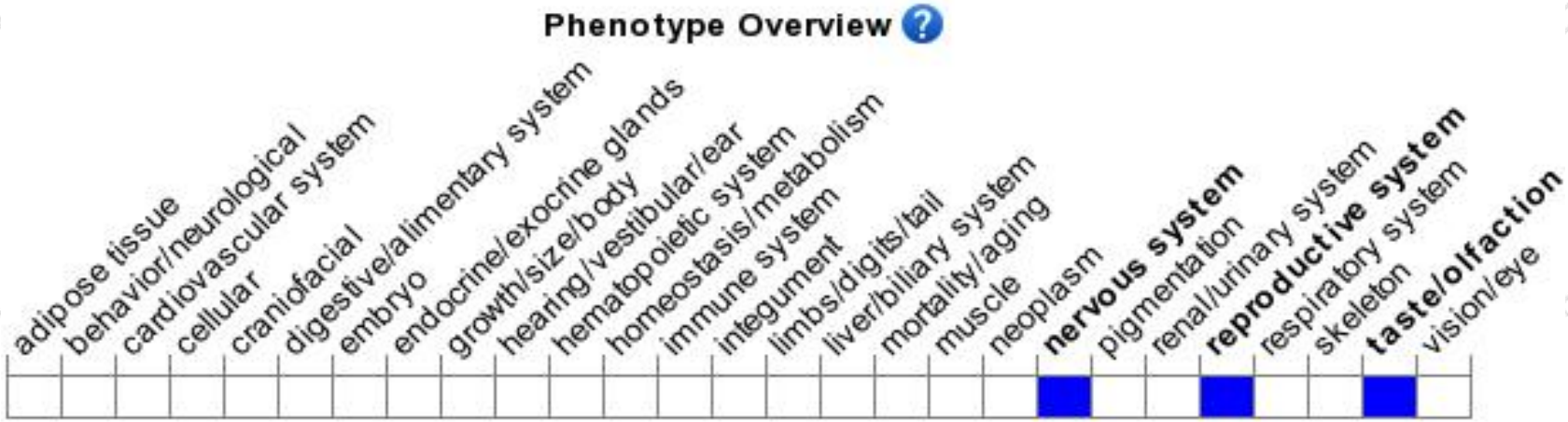
Genomic location distribution



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 knock-out allele exhibit faster response kinetics and stimuli integration to olfactory stimulation and impaired olfaction a buried food pellet test with a background of the same odor.

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

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