Zfp148 Cas9-CKO *Strategy*

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Project Overview

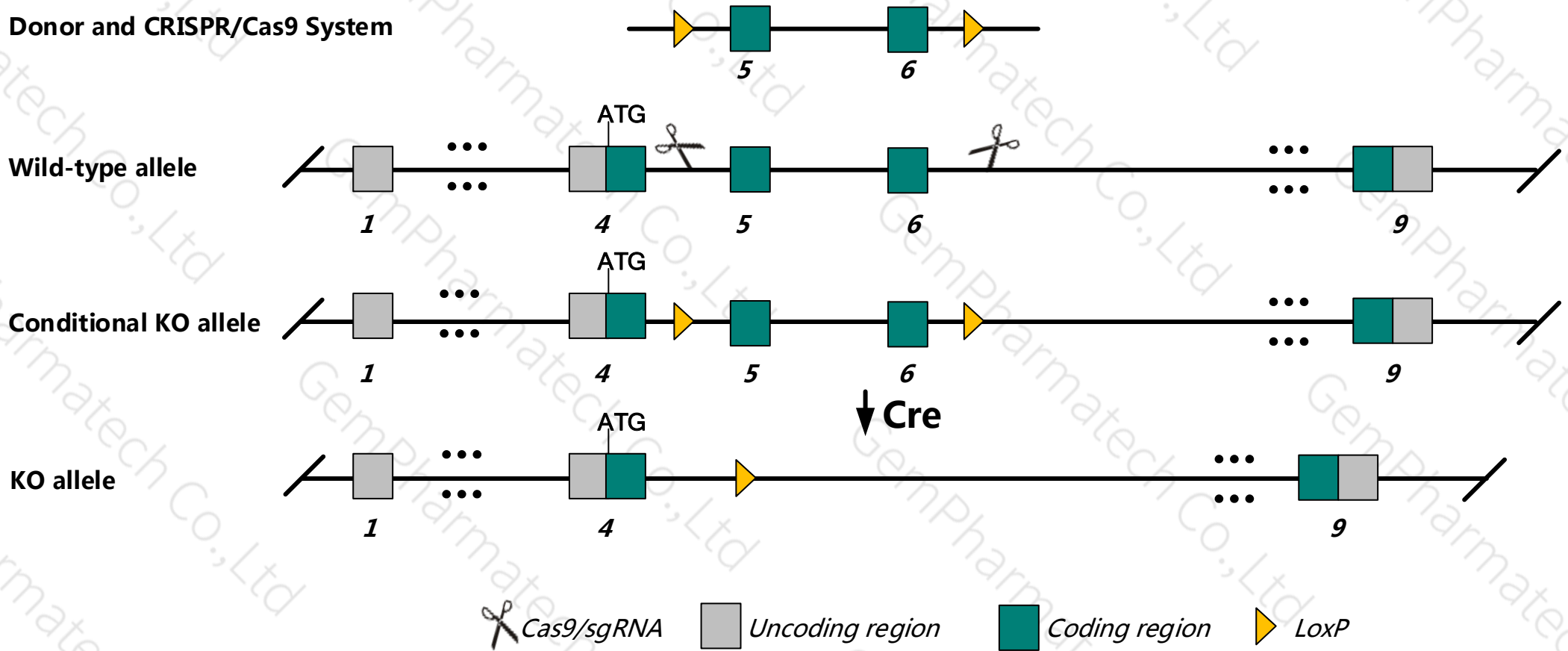|	
Project Name	*Zfp148*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp148* gene. The schematic diagram is as follows:

Cas9/sgRNA | Uncoding region | Coding region | LoxP

Technical routes

- The *Zfp148* gene has 5 transcripts.According to the structure of *Zfp148* gene, exon5-exon6 of *Zfp148*-202 (ENSMUST00000165418.8) transcript is recommended as the knockout region.The region contains 250bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Zfp148* 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

- According to the existing MGI data，Disruption of one allele results in haploinsufficient male infertility in which chimeric males display a loss of germ cells.

- The *Zfp148* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

Zfp148   zinc finger protein 148 [*Mus musculus* (house mouse)]

Gene ID: 22661, updated on 18-Nov-2018

▲ Summary

|	
Official Symbol	Zfp148 provided by MGI
Official Full Name	zinc finger protein 148 provided by MGI
Primary source	MGI:MGI:1332234
See related	Ensembl:ENSMUSG00000022811
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	BERF-1; BFCOL1; ZBP-89; Znf148; AI480666; AW045217; 2210405J08Rik
Expression	Ubiquitous expression in CNS E18 (RPKM 4.4), cortex adult (RPKM 4.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp148-202	ENSMUST00000165418.8	9830	794aa	Protein coding	CCDS28130	Q548L0 Q61624	TSL:1 GENCODE basic APPRIS P1
Zfp148-201	ENSMUST00000089677.6	4032	794aa	Protein coding	CCDS28130	Q548L0 Q61624	TSL:1 GENCODE basic APPRIS P1
Zfp148-205	ENSMUST00000232023.1	2670	752aa	Protein coding	-	A0A338P6K3	GENCODE basic
Zfp148-204	ENSMUST00000231894.1	653	No protein	lncRNA	-	-	-
Zfp148-203	ENSMUST00000231732.1	464	No protein	lncRNA	-	-	-

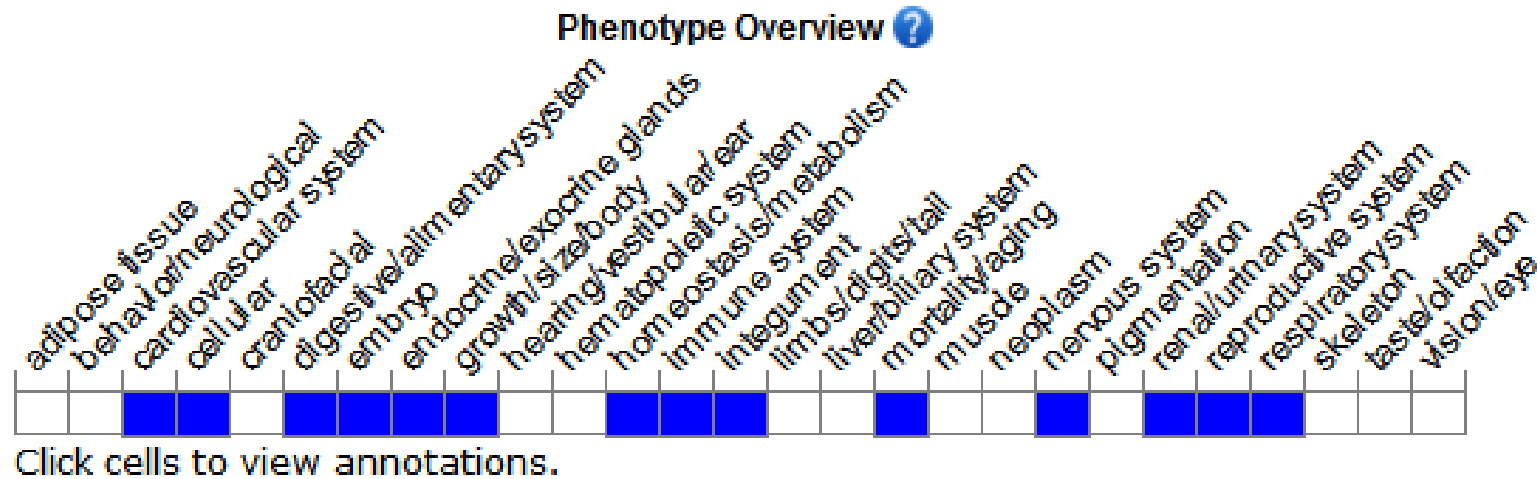The strategy is based on the design of *Zfp148*-202 transcript, The transcription is shown below
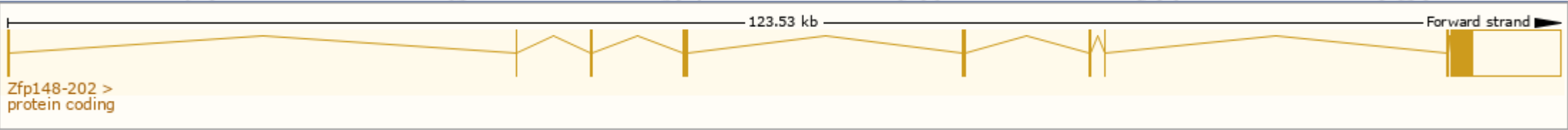
Genomic location distribution
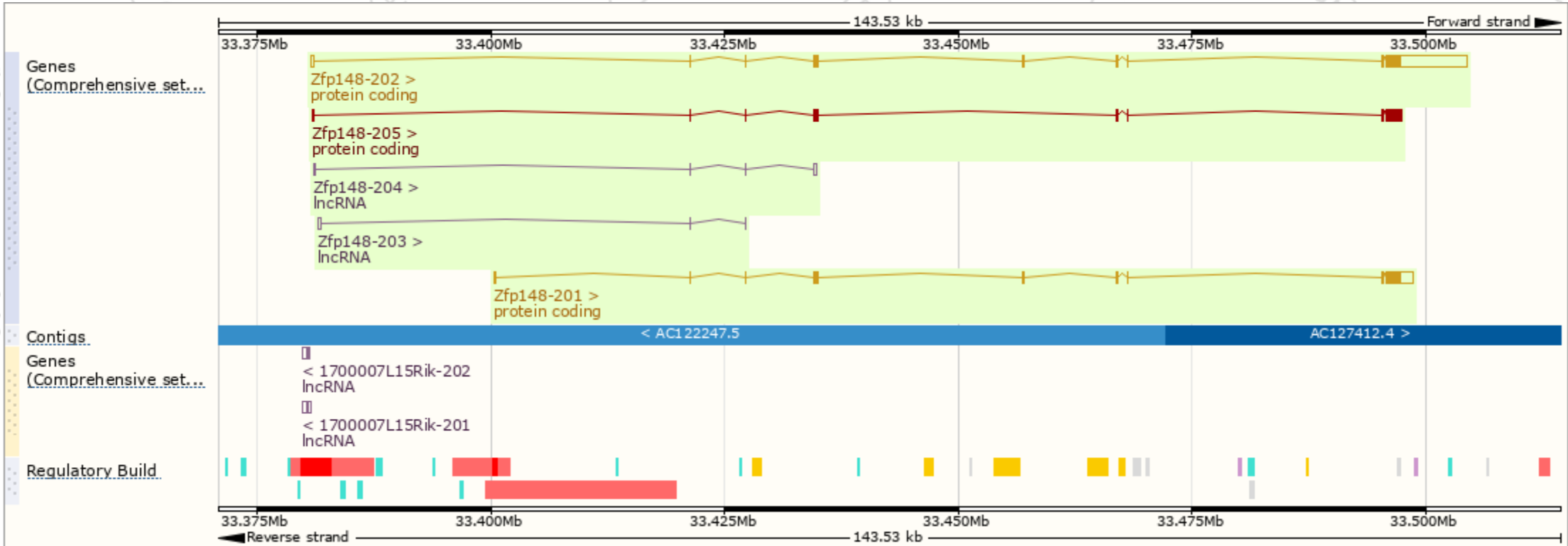
Protein domain
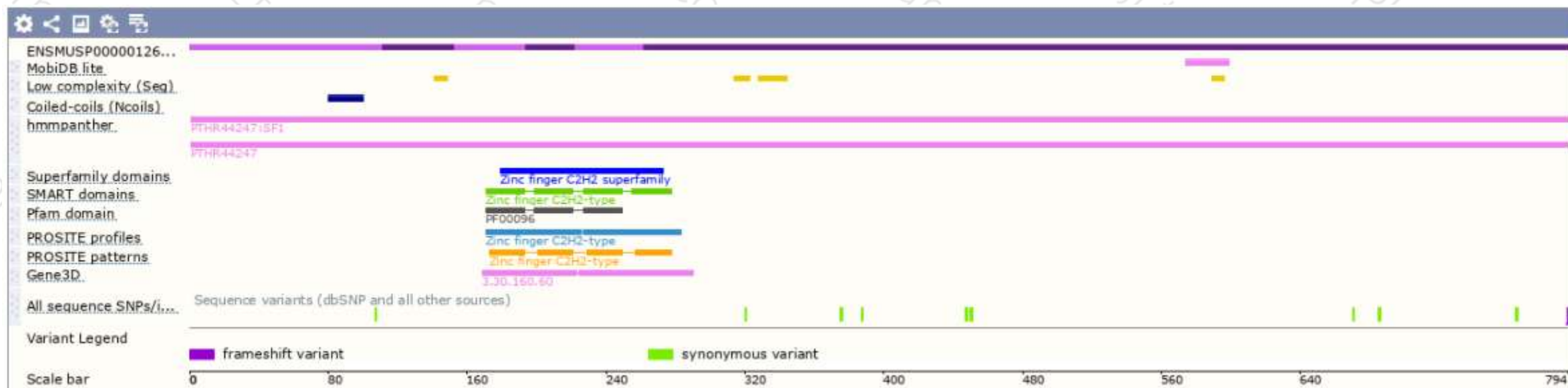
Mouse phenotype description(MGI)

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,Disruption of one allele results in haploinsufficient male infertility in which chimeric males display a loss of germ cells.

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