

Plekha5 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Plekha5

Project type

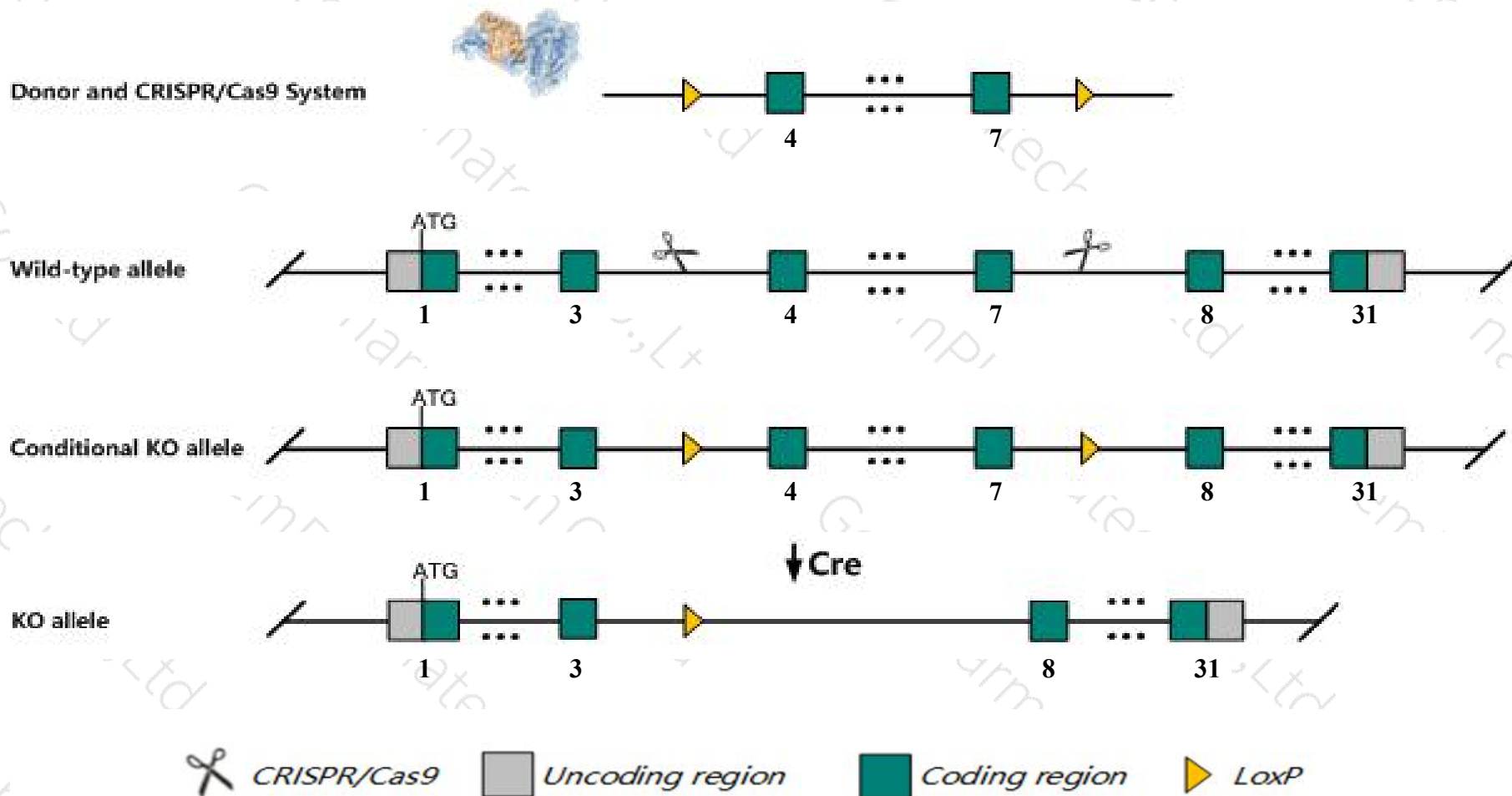
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plekha5* gene. The schematic diagram is as follows:



Technical routes

- The *Plekha5* gene has 16 transcripts. According to the structure of *Plekha5* gene, exon4-exon7 of *Plekha5-201* (ENSMUST00000087622.5) transcript is recommended as the knockout region. The region contains 383bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plekha5* 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.

- The effect on transcripts 202,204,207,214,216 is unknown.
- Transcripts 203,208,210,211,213,215 are unaffected.
- The flox region is about 1.8 kb away from the 3th end of *Gm25780-201*, which may affect the regulation of the 3th end of the gene.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Plekha5* gene is located on the Chr6. 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)

Plekha5 pleckstrin homology domain containing, family A member 5 [*Mus musculus* (house mouse)]

Gene ID: 109135, updated on 22-Oct-2019

Summary

Official Symbol	Plekha5 provided by MGI
Official Full Name	pleckstrin homology domain containing, family A member 5 provided by MGI
Primary source	MGI:MGI:1923802
See related	Ensembl:ENSMUSG00000030231
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	Pepp2; AMH-Cre; Ayu21-9; AI428202; AK129423; 2810431N21Rik; Gt(pU21)9Imeg; Tg(AMH-cre)1Flor
Expression	Ubiquitous expression in frontal lobe adult (RPKM 10.9), CNS E14 (RPKM 9.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

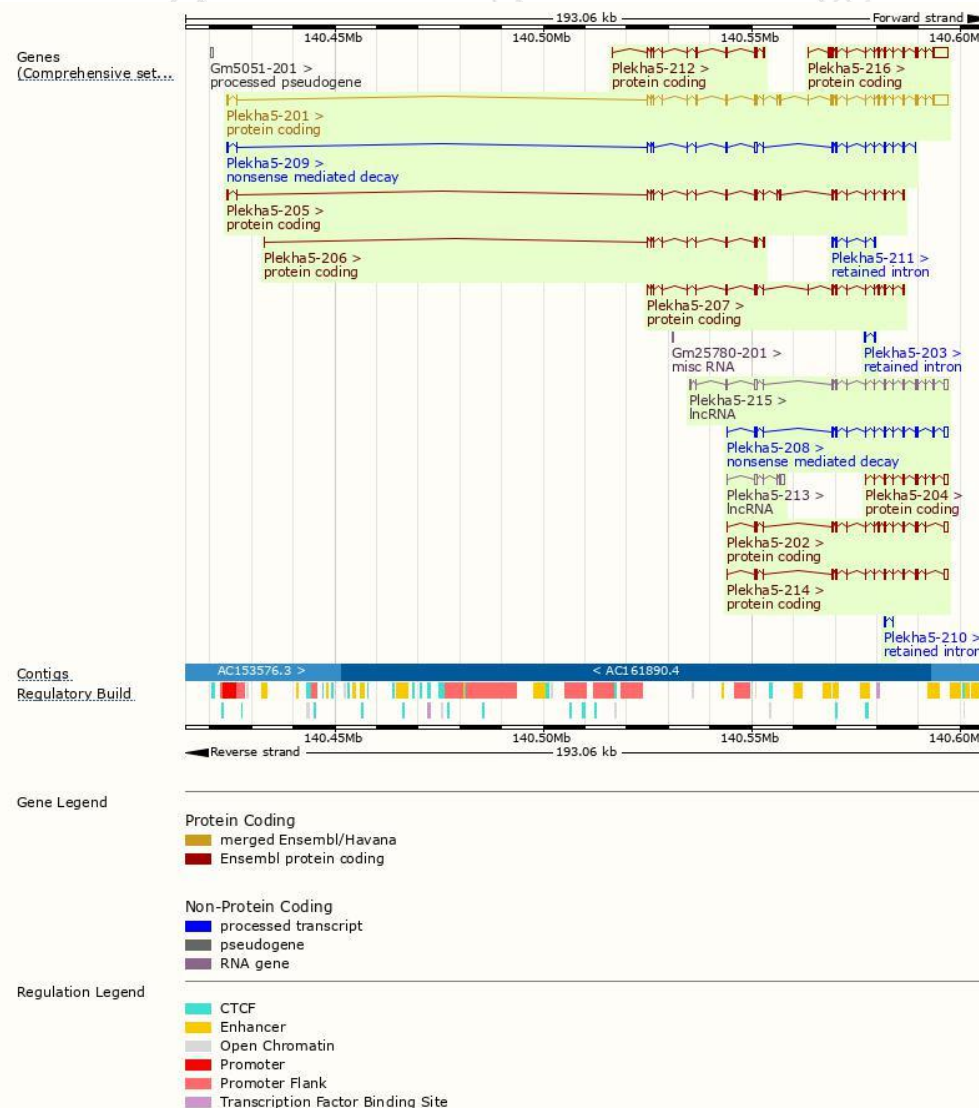
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plekha5-201	ENSMUST00000087622.5	7382	1269aa	Protein coding	CCDS39688	E9Q6H8	TSL:5 GENCODE basic APPRIS P1
Plekha5-216	ENSMUST00000213444.1	5252	596aa	Protein coding	-	A0A1L1SQF5	CDS 5' incomplete TSL:5
Plekha5-202	ENSMUST00000203012.2	3140	770aa	Protein coding	-	A0A0N4SWF5	CDS 5' incomplete TSL:5
Plekha5-205	ENSMUST00000203517.2	3006	1000aa	Protein coding	-	A0A0N4SWD7	CDS 3' incomplete TSL:5
Plekha5-207	ENSMUST00000203955.2	2868	956aa	Protein coding	-	A0A0N4SUU0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Plekha5-214	ENSMUST00000205026.2	2816	662aa	Protein coding	-	A0A0N4SV65	CDS 5' incomplete TSL:5
Plekha5-212	ENSMUST00000204876.2	1928	531aa	Protein coding	-	A0A0N4SW19	TSL:5 GENCODE basic
Plekha5-206	ENSMUST00000203774.2	1912	525aa	Protein coding	-	A0A0N4SUV0	TSL:1 GENCODE basic
Plekha5-204	ENSMUST00000203483.1	1845	324aa	Protein coding	-	A0A0N4SVR9	CDS 5' incomplete TSL:5
Plekha5-208	ENSMUST00000204080.2	2947	668aa	Nonsense mediated decay	-	A0A0N4SUY3	CDS 5' incomplete TSL:5
Plekha5-209	ENSMUST00000204145.2	2902	197aa	Nonsense mediated decay	-	A0A0N4SWC0	TSL:5
Plekha5-211	ENSMUST00000204755.1	777	No protein	Retained intron	-	-	TSL:3
Plekha5-203	ENSMUST00000203315.1	453	No protein	Retained intron	-	-	TSL:3
Plekha5-210	ENSMUST00000204528.1	441	No protein	Retained intron	-	-	TSL:3
Plekha5-215	ENSMUST00000205255.2	3657	No protein	lncRNA	-	-	TSL:5
Plekha5-213	ENSMUST00000205025.1	1768	No protein	lncRNA	-	-	TSL:5

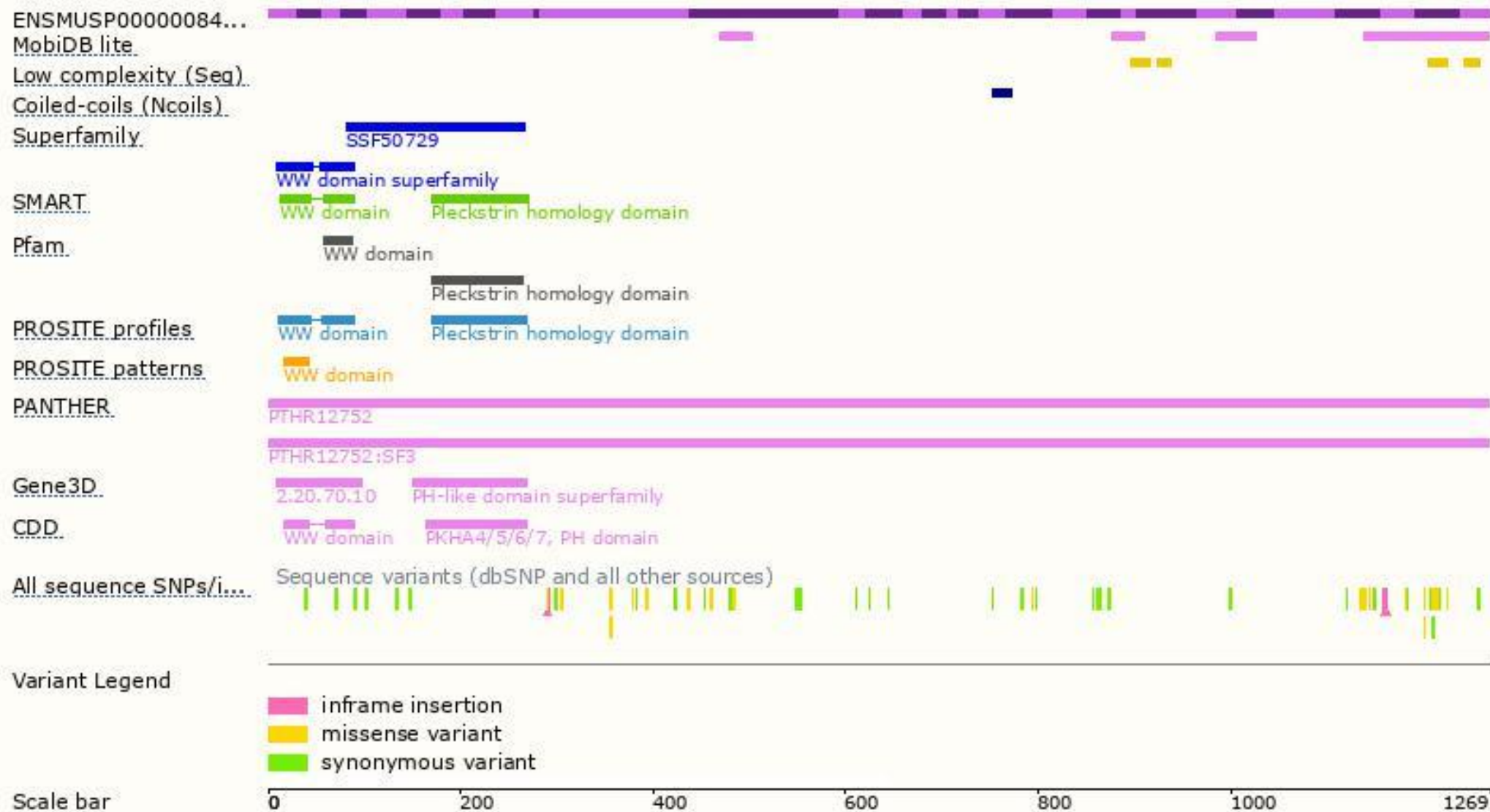
The strategy is based on the design of *Plekha5-201* transcript,The transcription is shown below



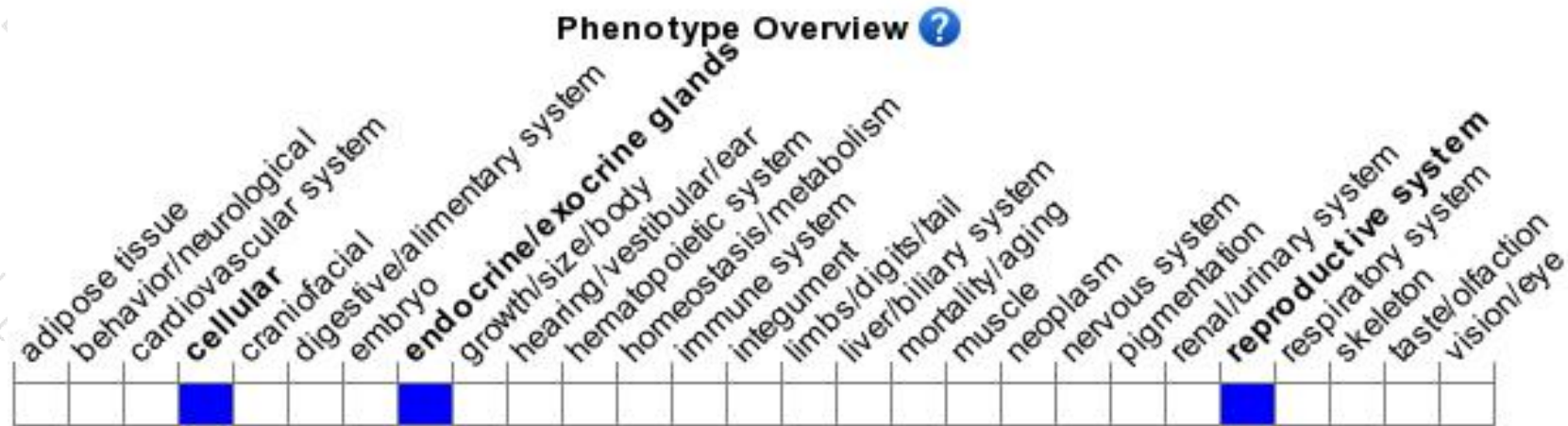
Genomic location distribution



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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