

# *Phlda2* Cas9-CKO Strategy

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# Project Overview

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**Project Name**

***Phlda2***

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**Project type**

**Cas9-CKO**

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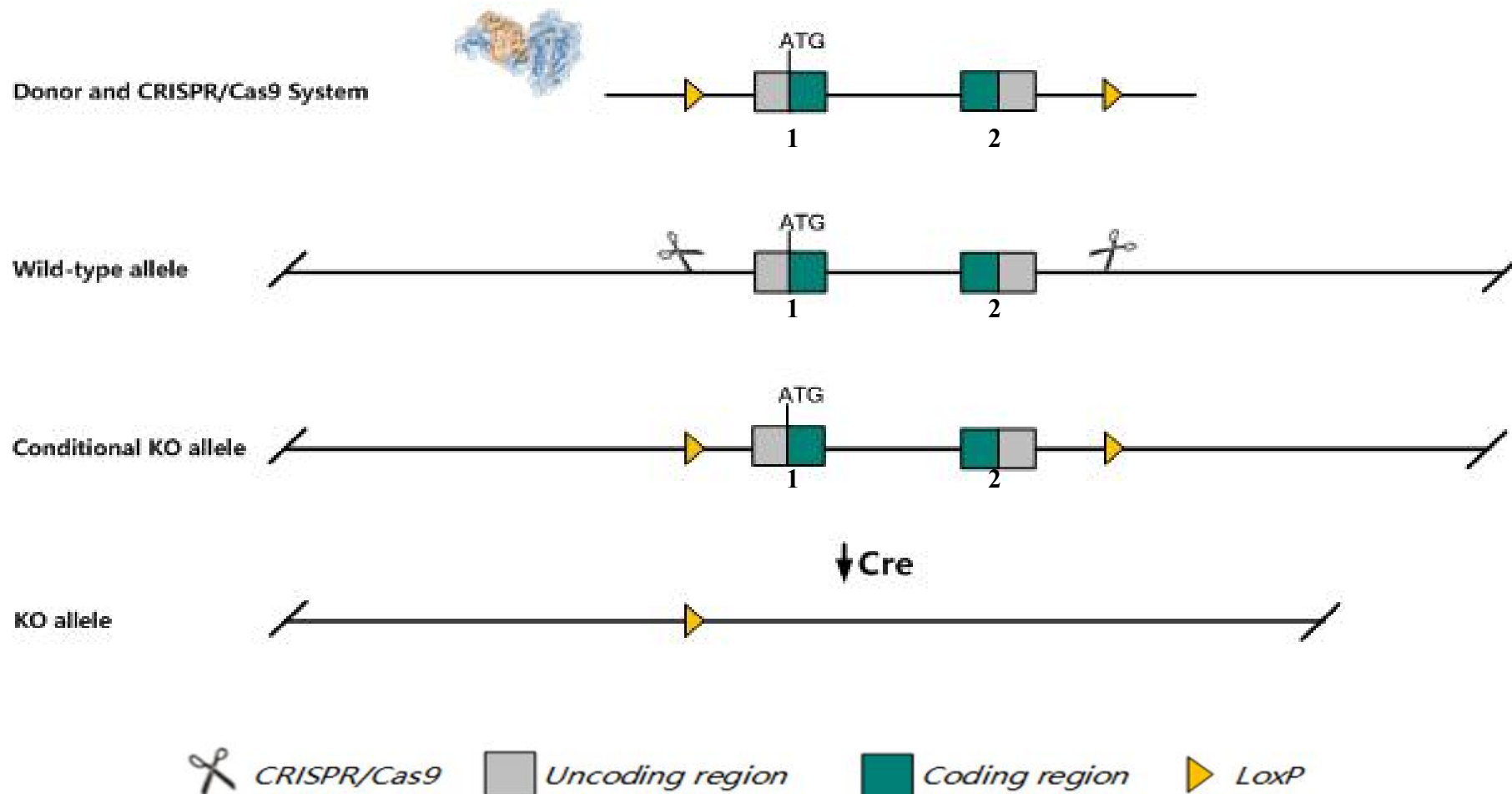
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phlda2* gene. The schematic diagram is as follows:



The *Phlda2* gene has 3 transcripts. According to the structure of *Phlda2* gene, exon1-exon2 of *Phlda2-201* (ENSMUST00000010904.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Phlda2* 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.

According to the existing MGI data, Mice homozygous for disruptions in this gene have enlarged placentas but display little change in fetal weight.

The *Phlda2* 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 biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

## Phlda2 pleckstrin homology like domain, family A, member 2 [Mus musculus (house mouse)]

Gene ID: 22113, updated on 26-Feb-2019

## Summary

**Official Symbol** Phlda2 provided by [MGI](#)**Official Full Name** pleckstrin homology like domain, family A, member 2 provided by [MGI](#)**Primary source** [MGI:MGI:1202307](#)**See related** [Ensembl:ENSMUSG00000010760](#)**Gene type** protein coding**RefSeq status** REVIEWED**Organism** [Mus musculus](#)**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus**Also known as** lpl, Tssc3**Summary** This gene is one of several genes in the imprinted gene domain on chromosome 7. Studies using knockout mice have shown that the product of this gene regulates placental growth. Transcripts from this gene are most abundant in placenta and yolk sac, and are almost entirely transcribed from the maternal allele. [provided by RefSeq, Jul 2008]**Expression** Biased expression in placenta adult (RPKM 163.8), kidney adult (RPKM 10.9) and 1 other tissue [See more](#)**Orthologs** [human](#) [all](#)

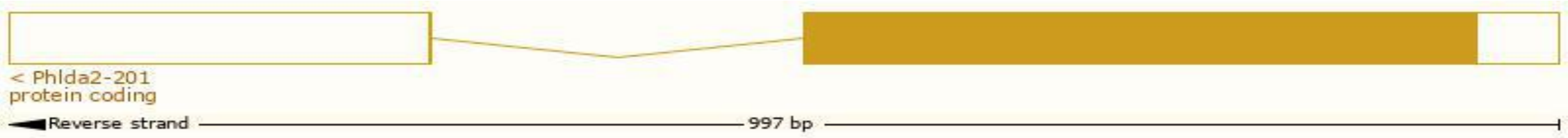
# Transcript information      Ensembl



The gene has 3 transcripts,all transcripts are shown below:

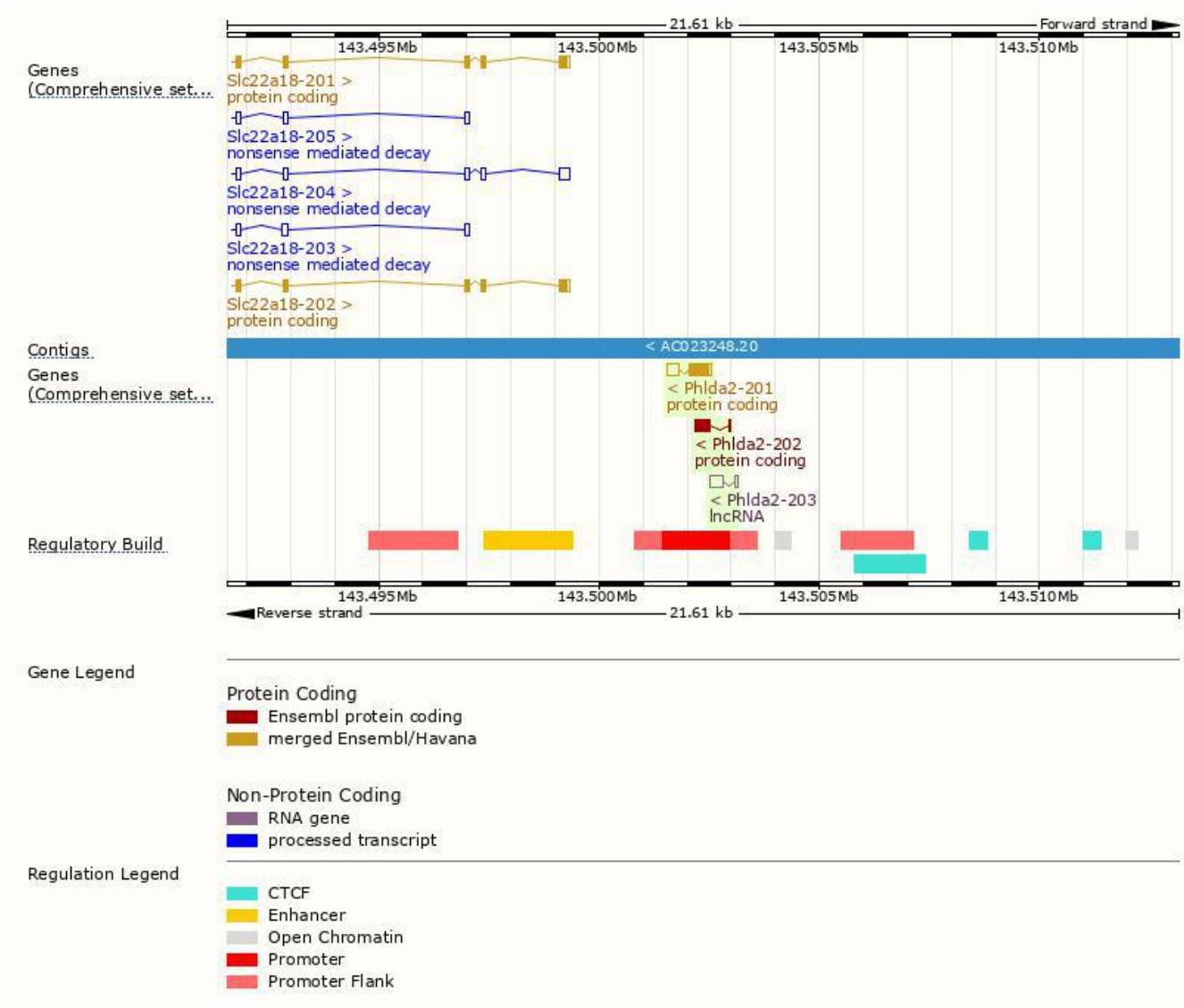
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phlda2-201	<a href="#">ENSMUST00000010904.4</a>	757	<a href="#">144aa</a>	Protein coding	<a href="#">CCDS22042</a>	<a href="#">O08969</a>	TSL:1 GENCODE basic APPRIS P1
Phlda2-202	<a href="#">ENSMUST00000207425.1</a>	376	<a href="#">105aa</a>	Protein coding	-	<a href="#">A0A140LIM7</a>	CDS 3' incomplete TSL:3
Phlda2-203	<a href="#">ENSMUST00000207561.1</a>	363	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Phlda2-201* transcript,The transcription is shown below



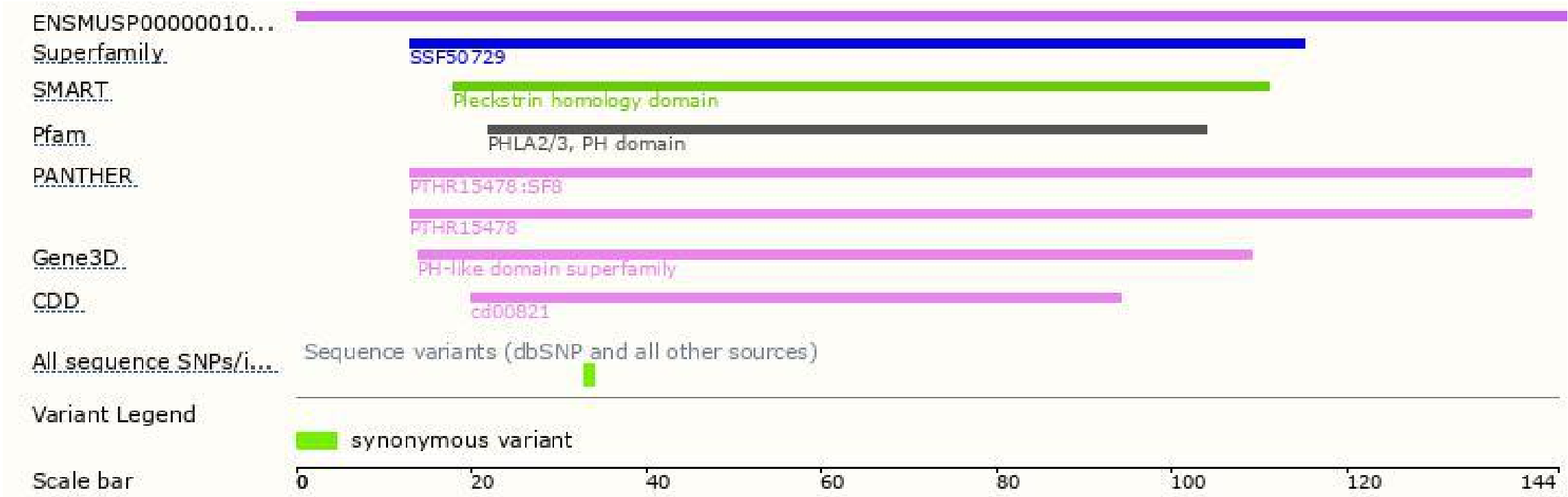


# Genomic location distribution

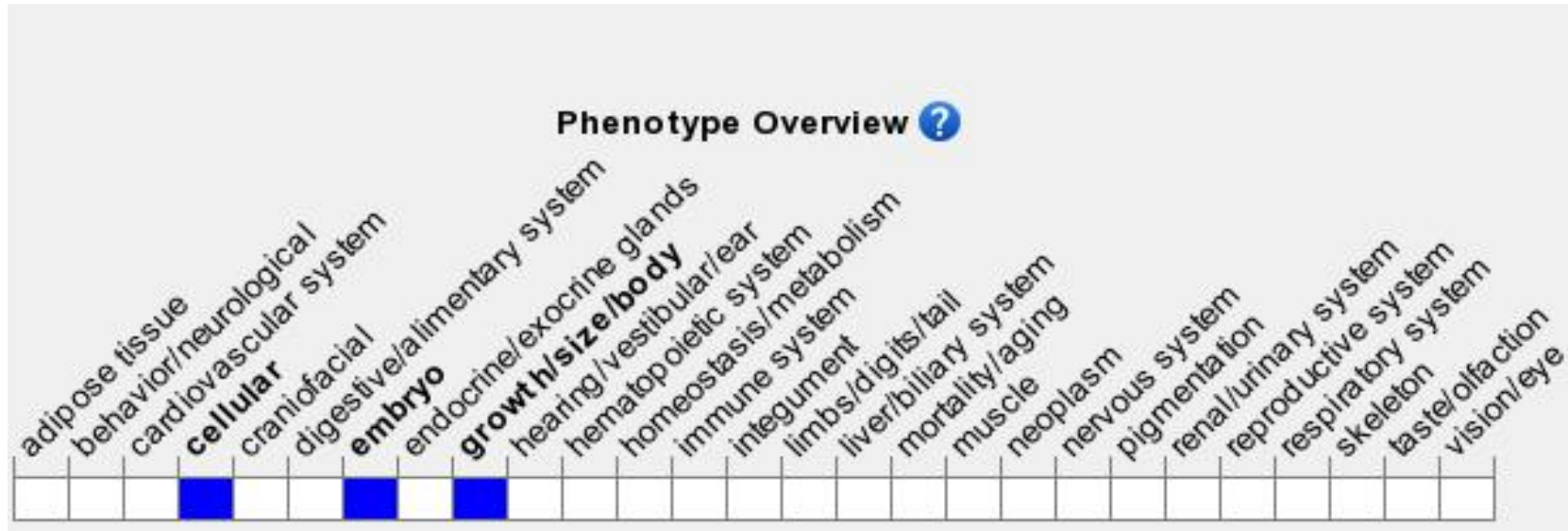




# Protein domain



# 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 have enlarged placentas but display little change in fetal weight.

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