

# *Pdgfra* Cas9-KO Strategy

**Designer:**

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**Design Date:**

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# Project Overview



**Project Name**

***Pdgfra***

**Project type**

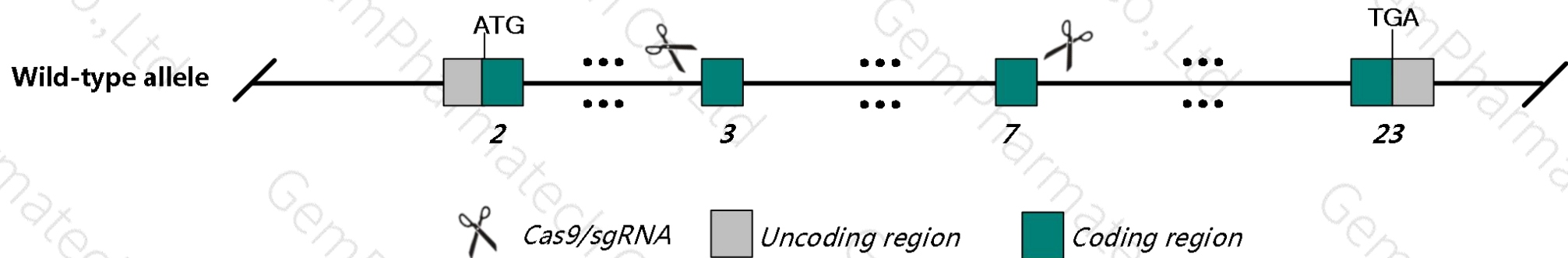
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Pdgfra* gene has 9 transcripts. According to the structure of *Pdgfra* gene, exon3-exon7 of *Pdgfra-202* (ENSMUST00000168162.4) transcript is recommended as the knockout region. The region contains 1072bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pdgfra* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit incomplete cephalic closure, increased apoptosis of neural crest cells, impaired myotome and testis formation, abnormal mucosal linings, thoracic skeletal defects, and midgestational lethality.
- The *Pdgfra* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)

## Pdgfra platelet derived growth factor receptor, alpha polypeptide [Mus musculus (house mouse)]

Gene ID: 18595, updated on 9-Apr-2019

### Summary



**Official Symbol** Pdgfra provided by [MGI](#)

**Official Full Name** platelet derived growth factor receptor, alpha polypeptide provided by [MGI](#)

**Primary source** [MGI:MGI:97530](#)

**See related** [Ensembl:ENSMUSG00000029231](#)

**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** AI115593, CD140a, Pdgfr-2

**Summary** This gene encodes a member of the receptor tyrosine kinase family of proteins. Binding of platelet-derived growth factor protein ligands to this receptor triggers receptor dimerization and autophosphorylation, resulting in the activation of several downstream signaling pathways. Signaling through the encoded receptor plays a role in gastrulation and the development of nearly all organ systems. Mice lacking a functional copy of this gene reportedly exhibit defects in lung, skeleton, testis and the central nervous system, and die soon after birth. Alternative splicing and intronic polyadenylation of gene transcripts have been implicated in muscle regeneration and fibrosis in adult mice. [provided by RefSeq, Jan 2017]

**Expression** Broad expression in limb E14.5 (RPKM 29.6), lung adult (RPKM 20.2) and 19 other tissues [See more](#)

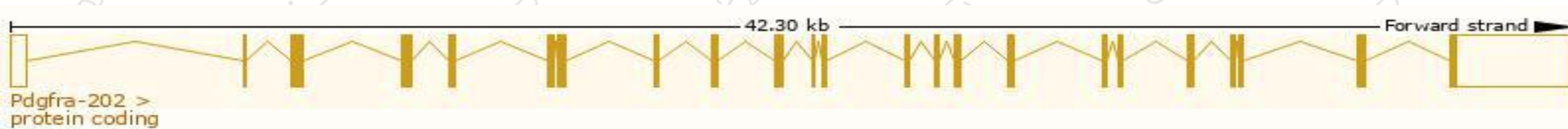
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

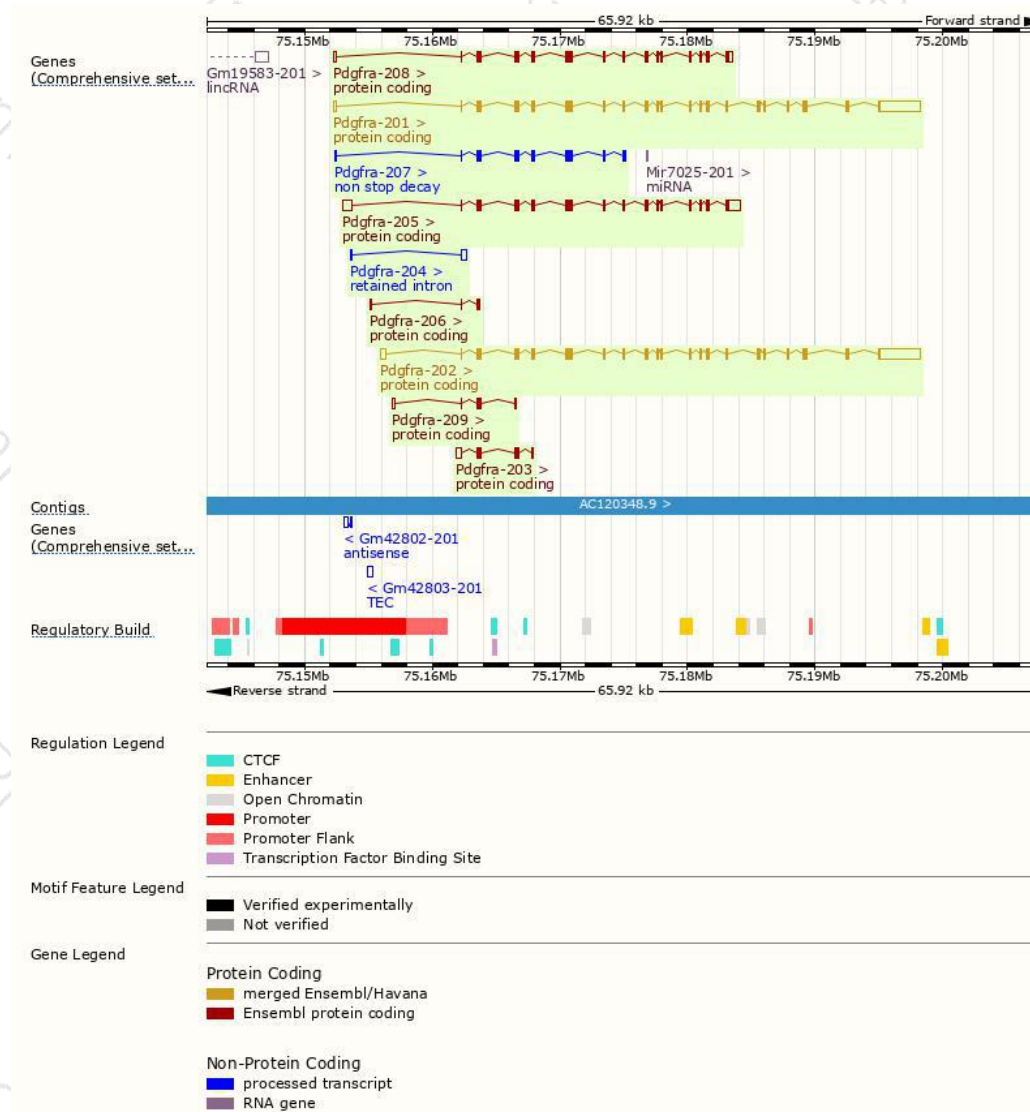
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pdgfra-202	<a href="#">ENSMUST00000168162.4</a>	6834	<a href="#">1089aa</a>	Protein coding	<a href="#">CCDS19351</a>	<a href="#">P26618</a>	TSL:1 GENCODE basic APPRIS P1
Pdgfra-201	<a href="#">ENSMUST00000000476.14</a>	6549	<a href="#">1089aa</a>	Protein coding	<a href="#">CCDS19351</a>	<a href="#">P26618</a>	TSL:1 GENCODE basic APPRIS P1
Pdgfra-205	<a href="#">ENSMUST00000201711.3</a>	4088	<a href="#">790aa</a>	Protein coding	-	<a href="#">P26618</a>	TSL:1 GENCODE basic
Pdgfra-208	<a href="#">ENSMUST00000202681.3</a>	2876	<a href="#">790aa</a>	Protein coding	-	<a href="#">P26618</a>	TSL:1 GENCODE basic
Pdgfra-203	<a href="#">ENSMUST00000200822.1</a>	1138	<a href="#">243aa</a>	Protein coding	-	<a href="#">A0A0J9YVF3</a>	CDS 3' incomplete TSL:5
Pdgfra-209	<a href="#">ENSMUST00000202992.3</a>	615	<a href="#">139aa</a>	Protein coding	-	<a href="#">A0A0J9YUD9</a>	CDS 3' incomplete TSL:3
Pdgfra-206	<a href="#">ENSMUST00000202161.3</a>	442	<a href="#">88aa</a>	Protein coding	-	<a href="#">A0A0J9YV49</a>	CDS 3' incomplete TSL:2
Pdgfra-207	<a href="#">ENSMUST00000202186.3</a>	1561	<a href="#">481aa</a>	Non stop decay	-	<a href="#">A0A0J9YV87</a>	TSL:1
Pdgfra-204	<a href="#">ENSMUST00000201241.1</a>	603	No protein	Retained intron	-	-	TSL:1

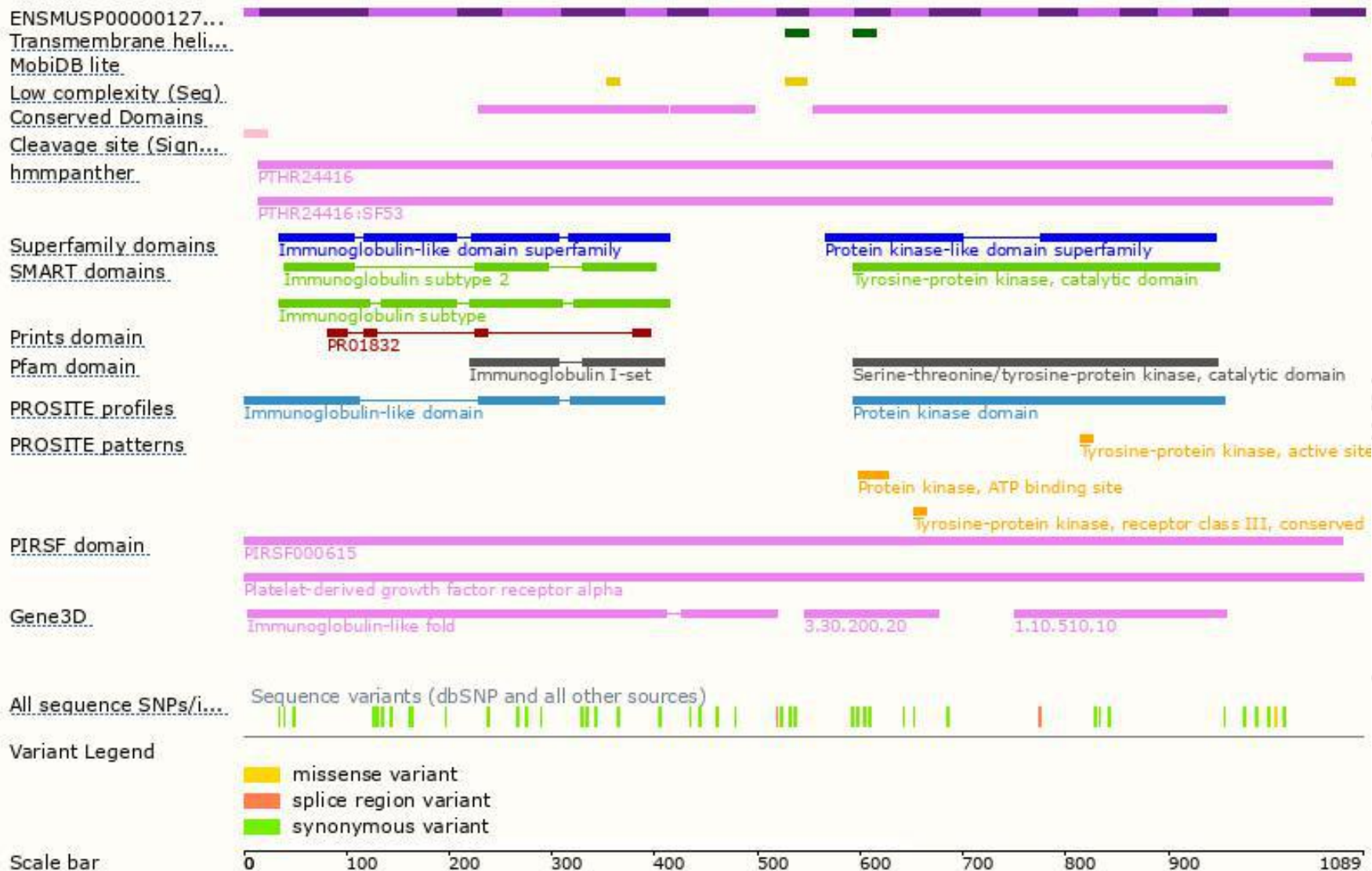
The strategy is based on the design of *Pdgfra-202* transcript, The transcription is shown below



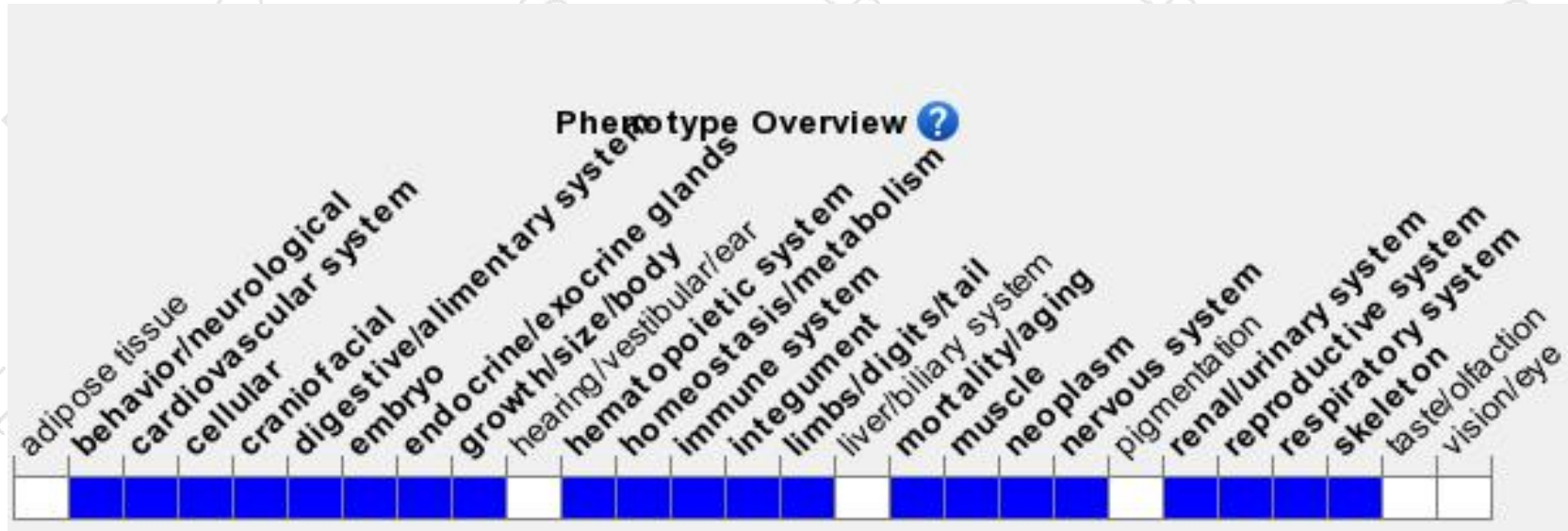
# Genomic location distribution



# 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, Homozygotes for targeted null mutations exhibit incomplete cephalic closure, increased apoptosis of neural crest cells, impaired myotome and testis formation, abnormal mucosal linings, thoracic skeletal defects, and midgestational lethality.

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

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