

# *Med12* Cas9-CKO Strategy

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**Reviewer:**

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**Design Date:**

**2019-10-23**

# Project Overview

**Project Name**

*Med12*

**Project type**

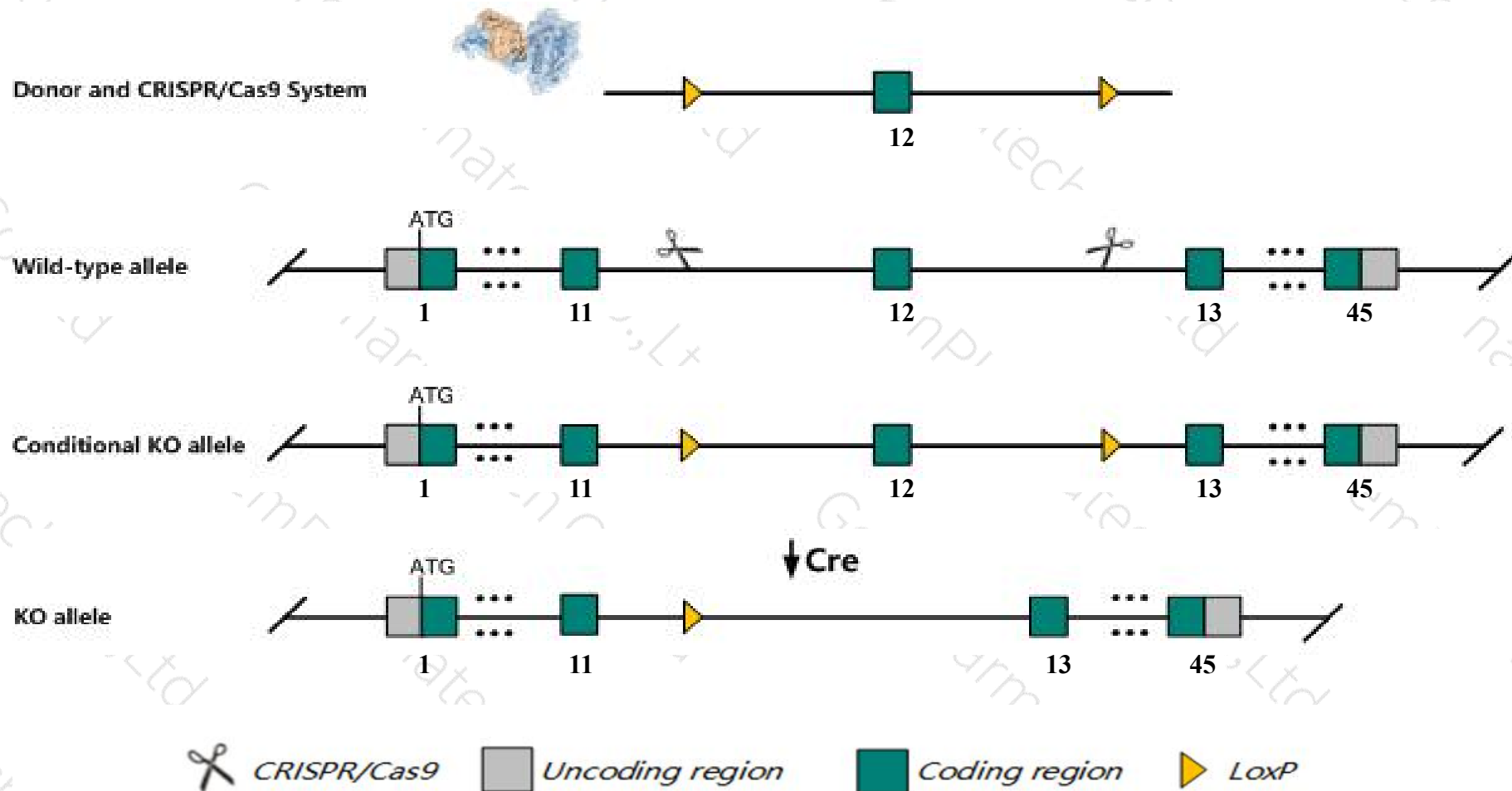
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Med12* gene. The schematic diagram is as follows:



- The *Med12* gene has 9 transcripts. According to the structure of *Med12* gene, exon12 of *Med12-201* (ENSMUST00000087948.10) transcript is recommended as the knockout region. The region contains 127bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Med12* 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, Male chimeras hemizygous for a null allele arrest at E7.5 and lack anterior visceral endoderm. Male chimeras hemizygous for a hypomorphic allele die at E10.5 showing failure of neural crest cell migration and severe defects in neural tube closure, axis elongation, somitogenesis and heart formation.
- The *Med12* gene is located on the ChrX. 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)

## Med12 mediator complex subunit 12 [Mus musculus (house mouse)]

Gene ID: 59024, updated on 3-Feb-2019

### Summary



<b>Official Symbol</b>	Med12 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mediator complex subunit 12 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1926212</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000079487</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	230kDa, Mopa, OPA-1, Tnrc11, Trap230
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 22.1), spleen adult (RPKM 17.5) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

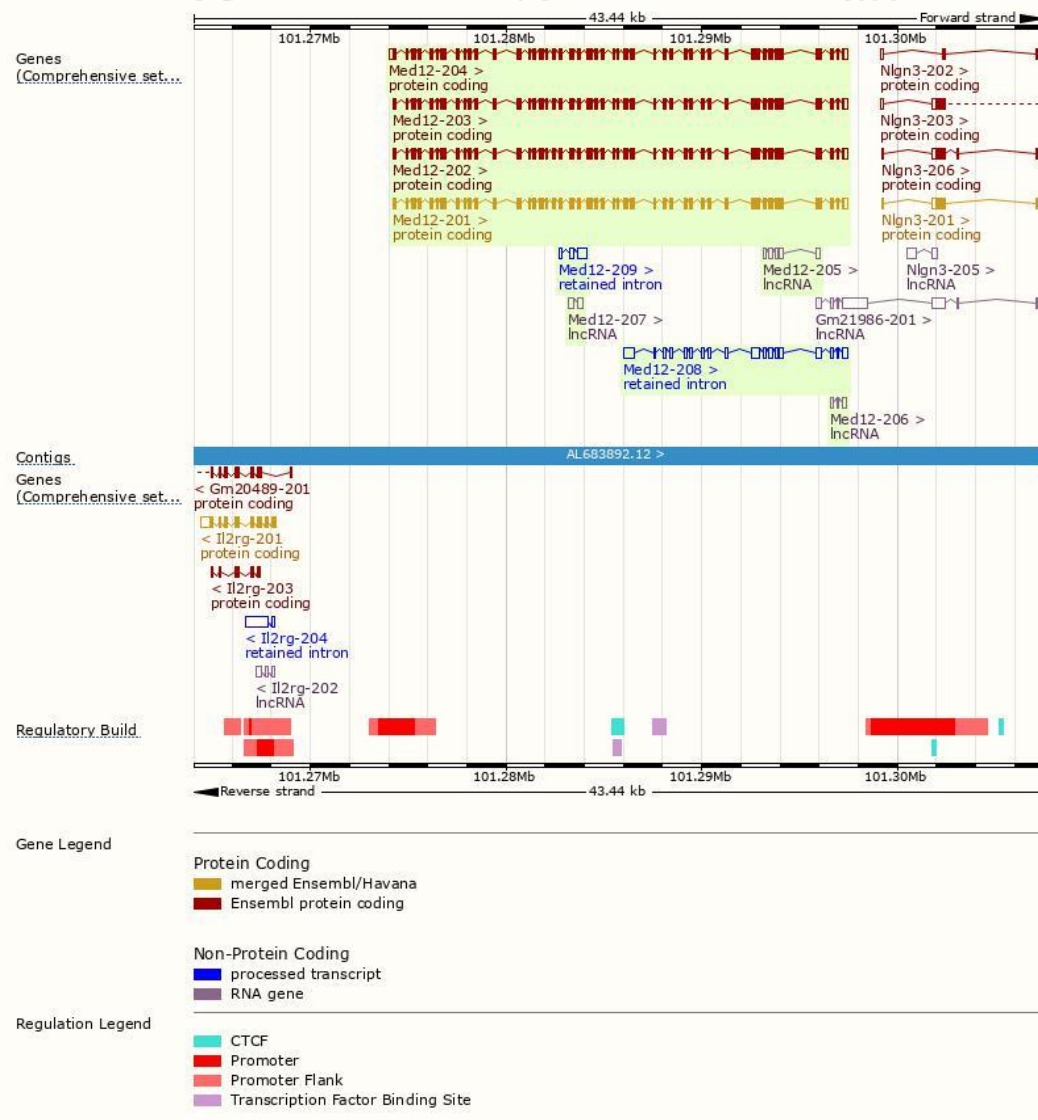
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Med12-201	<a href="#">ENSMUST00000087948.10</a>	6809	<a href="#">2190aa</a>	Protein coding	<a href="#">CCDS41078</a>	<a href="#">A2AGH6</a>	TSL:1 GENCODE basic APPRIS P2
Med12-204	<a href="#">ENSMUST00000117706.7</a>	6940	<a href="#">2157aa</a>	Protein coding	-	<a href="#">A2AGH8</a>	TSL:5 GENCODE basic APPRIS ALT2
Med12-203	<a href="#">ENSMUST00000117203.7</a>	6816	<a href="#">2182aa</a>	Protein coding	-	<a href="#">A2AGH9</a>	TSL:5 GENCODE basic APPRIS ALT2
Med12-202	<a href="#">ENSMUST00000087956.5</a>	6746	<a href="#">2169aa</a>	Protein coding	-	<a href="#">A2AGH6</a>	TSL:5 GENCODE basic APPRIS ALT2
Med12-208	<a href="#">ENSMUST00000148846.7</a>	3273	No protein	Retained intron	-	-	TSL:5
Med12-209	<a href="#">ENSMUST00000156131.1</a>	802	No protein	Retained intron	-	-	TSL:3
Med12-205	<a href="#">ENSMUST00000132269.1</a>	881	No protein	lncRNA	-	-	TSL:5
Med12-207	<a href="#">ENSMUST00000146877.1</a>	521	No protein	lncRNA	-	-	TSL:3
Med12-206	<a href="#">ENSMUST00000137664.1</a>	448	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Med12-201* transcript, The transcription is shown below

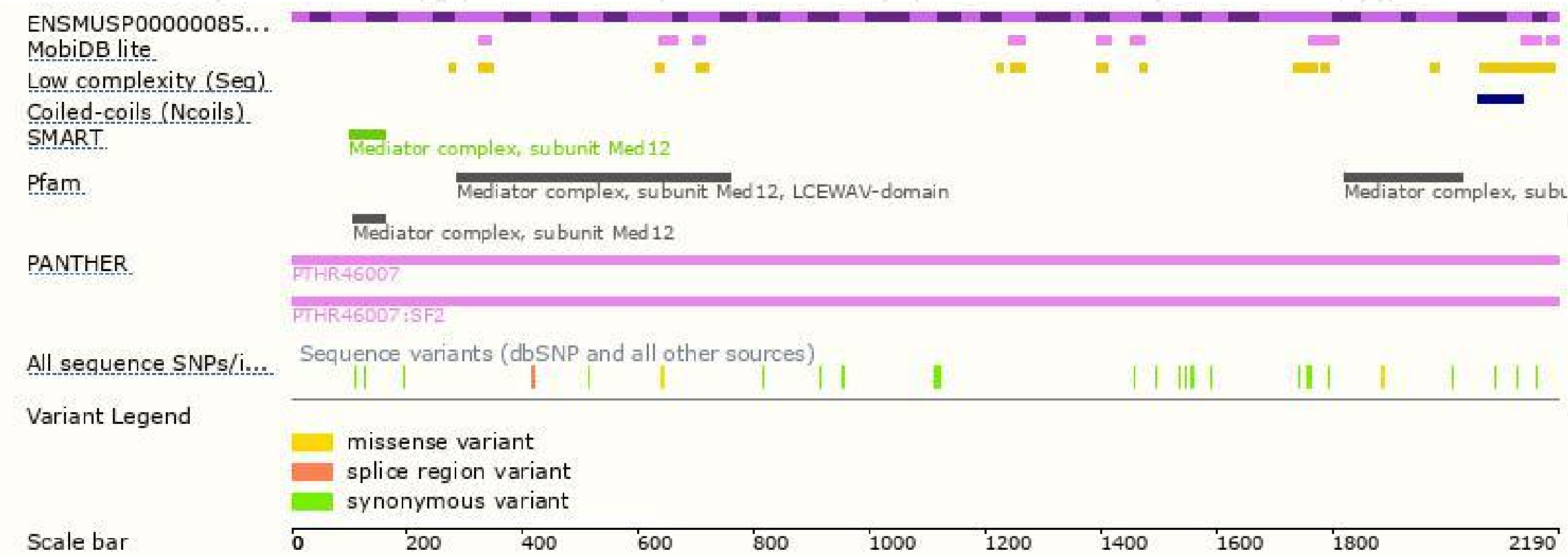


# Genomic location distribution

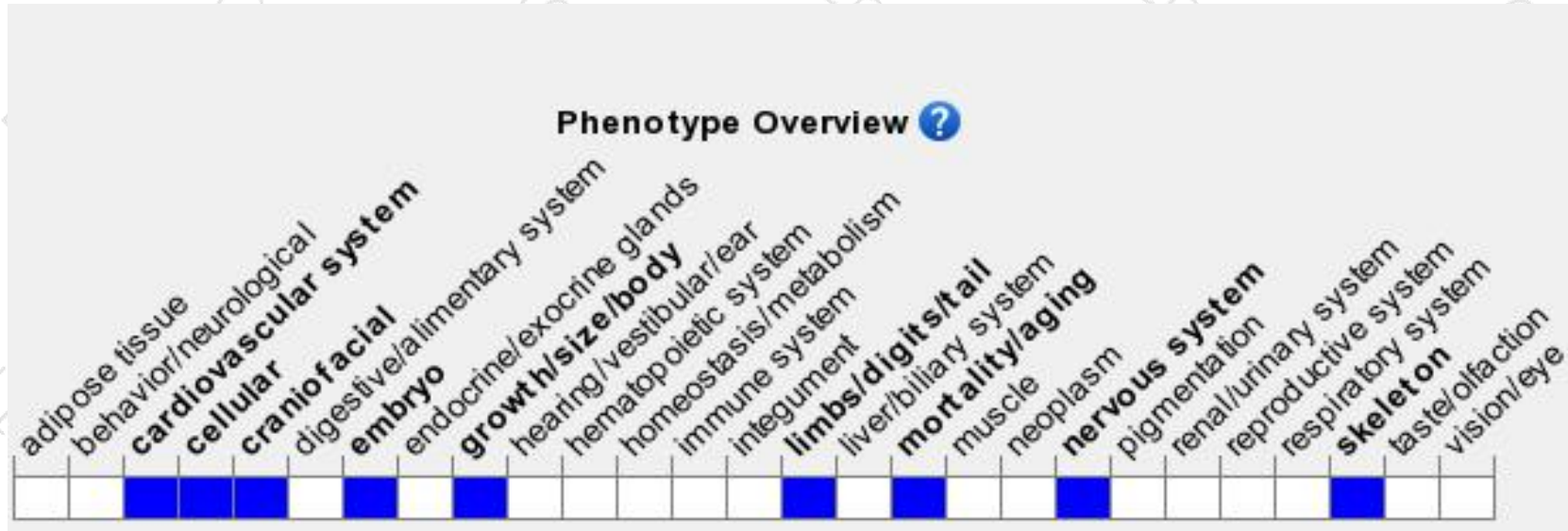




# Protein domain



# 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, Male chimeras hemizygous for a null allele arrest at E7.5 and lack anterior visceral endoderm. Male chimeras hemizygous for a hypomorphic allele die at E10.5 showing failure of neural crest cell migration and severe defects in neural tube closure, axis elongation, somitogenesis and heart formation.

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

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