

# *Med16* Cas9-KO Strategy

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# Project Overview



**Project Name**

***Med16***

**Project type**

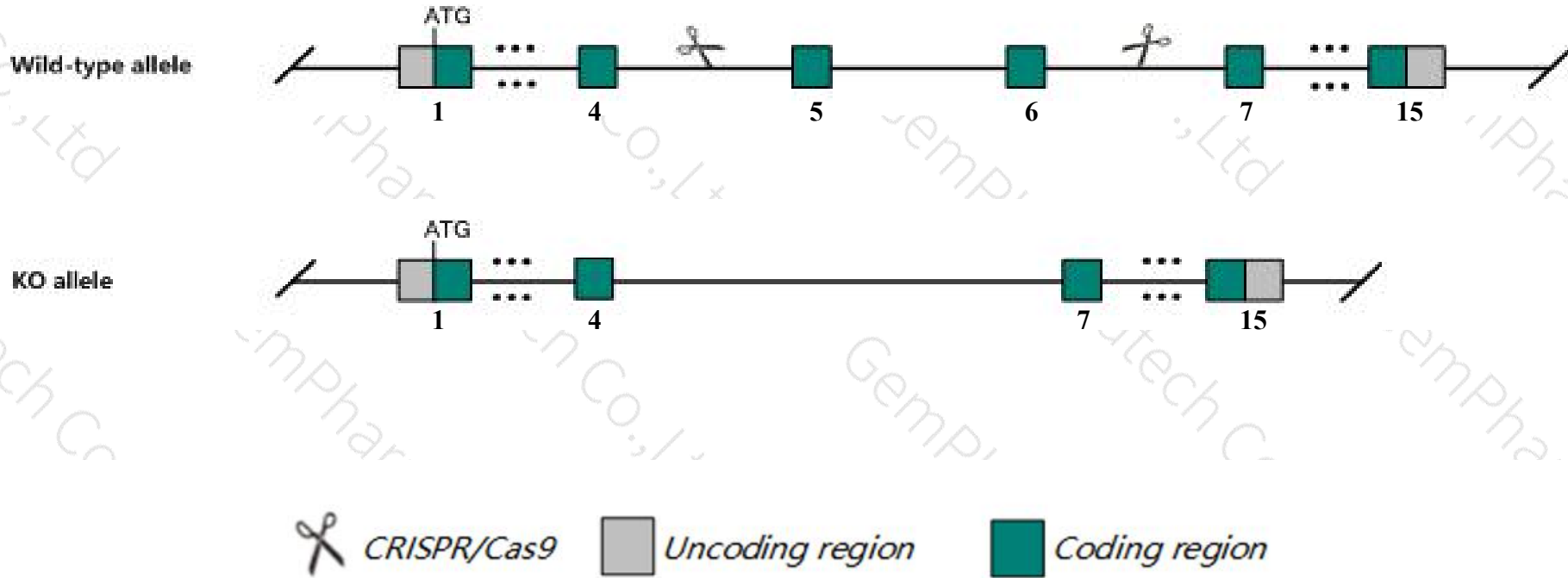
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Med16* gene. The schematic diagram is as follows:



- The *Med16* gene has 7 transcripts. According to the structure of *Med16* gene, exon5-exon6 of *Med16-204* (ENSMUST00000165684.7) transcript is recommended as the knockout region. The region contains 538bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Med16* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 *Med16* gene is located on the Chr10. 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.
- Transcript *Med16-206* may not be affected.
- The N-terminal of *Med16* gene will remain 174aa, it may remain the partial function of *Med16* gene.
- 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)

## Med16 mediator complex subunit 16 [Mus musculus (house mouse)]

Gene ID: 216154, updated on 3-Feb-2019

### Summary



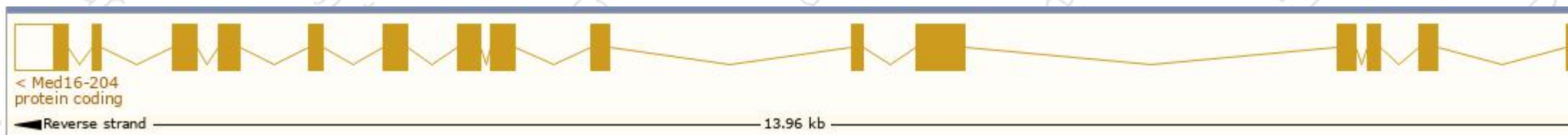
<b>Official Symbol</b>	Med16 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mediator complex subunit 16 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2158394</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000013833</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	95kDa, A630083L04, DRIP92, Thrap5, Trap95
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 63.2), ovary adult (RPKM 52.5) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

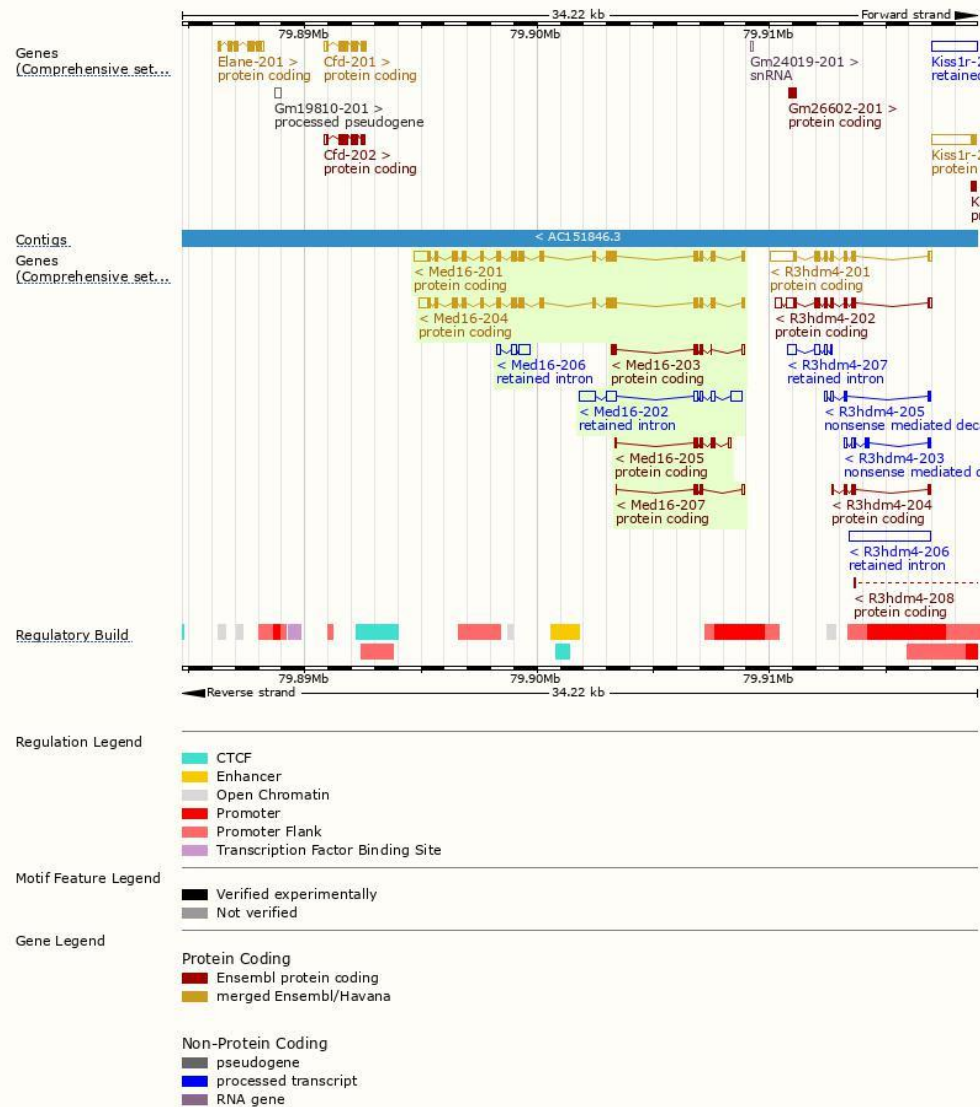
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Med16-201	<a href="#">ENSMUST00000105378.8</a>	3197	<a href="#">864aa</a>	Protein coding	<a href="#">CCDS48623</a>	<a href="#">E9QP84</a>	TSL:1 GENCODE basic APPRIS ALT2
Med16-204	<a href="#">ENSMUST00000165684.7</a>	2950	<a href="#">865aa</a>	Protein coding	<a href="#">CCDS23996</a>	<a href="#">G3UW74</a>	TSL:1 GENCODE basic APPRIS P3
Med16-203	<a href="#">ENSMUST00000164705.7</a>	642	<a href="#">172aa</a>	Protein coding	-	<a href="#">E9PZW4</a>	CDS 3' incomplete TSL:3
Med16-205	<a href="#">ENSMUST00000166964.7</a>	622	<a href="#">162aa</a>	Protein coding	-	<a href="#">E9QAH8</a>	CDS 3' incomplete TSL:3
Med16-207	<a href="#">ENSMUST00000170409.1</a>	431	<a href="#">104aa</a>	Protein coding	-	<a href="#">E9PWX0</a>	CDS 3' incomplete TSL:3
Med16-202	<a href="#">ENSMUST00000163125.1</a>	2065	No protein	Retained intron	-	-	TSL:5
Med16-206	<a href="#">ENSMUST00000170375.1</a>	903	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Med16-204* transcript, The transcription is shown below

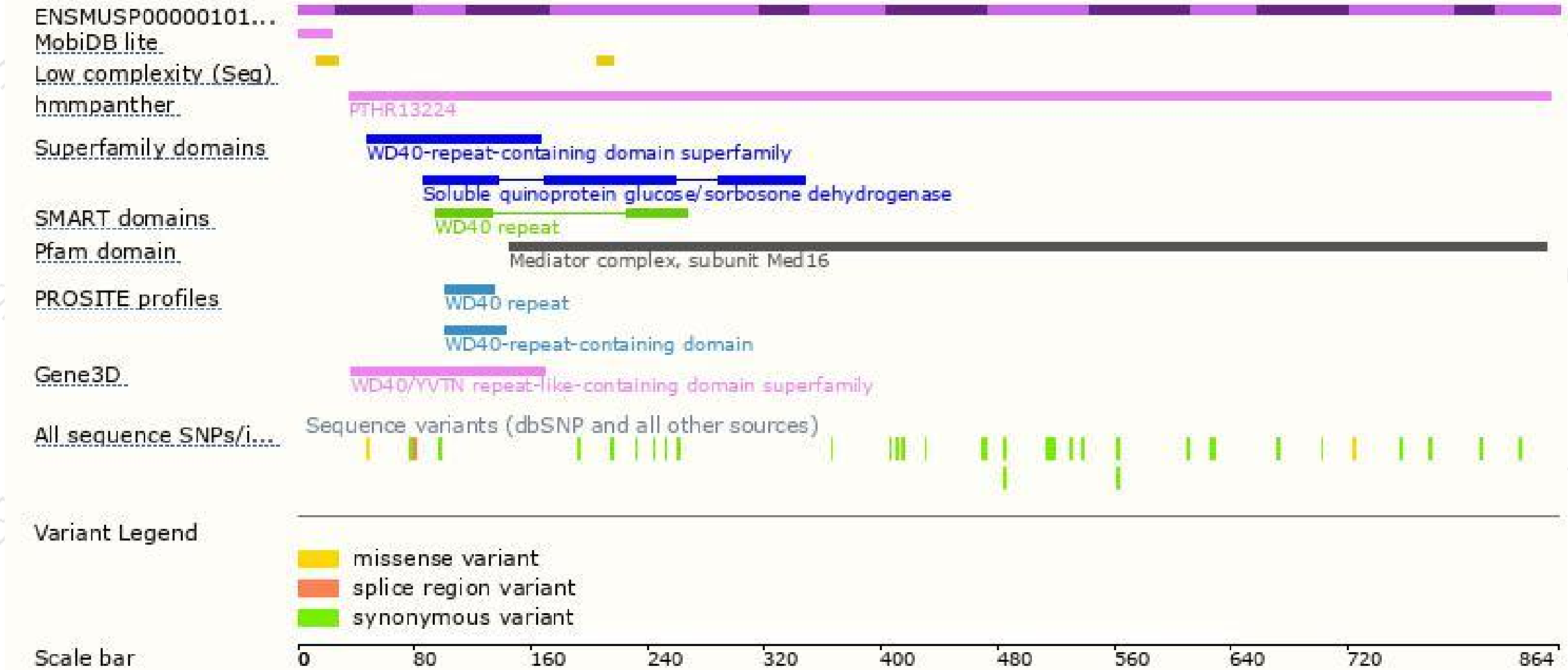


# Genomic location distribution

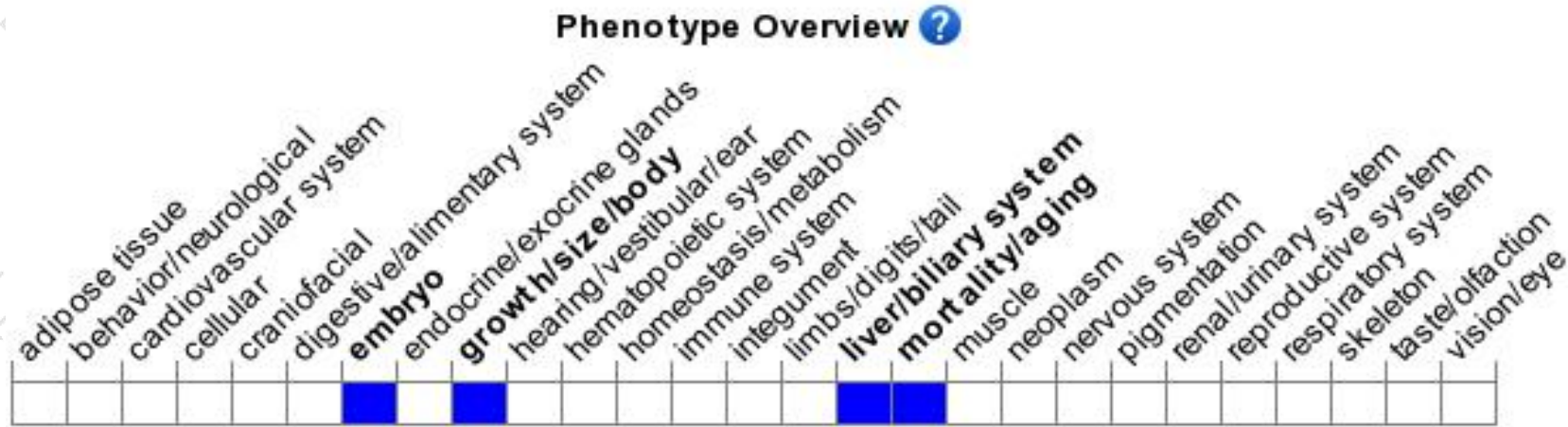




# Protein domain



# 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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