Meis2 Cas9-KO Strategy

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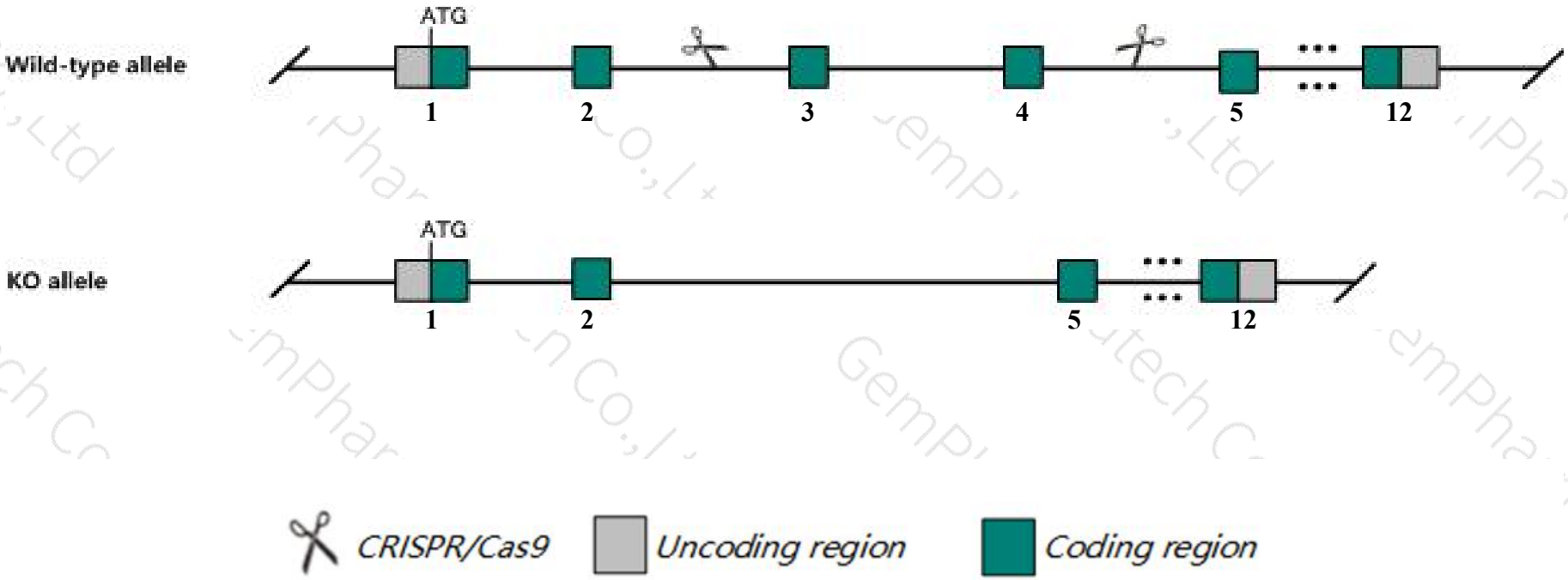
Project Overview

Project Name	***Meis2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Meis2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Meis2* gene has 19 transcripts. According to the structure of *Meis2* gene, exon3-exon4 of *Meis2-205* (ENSMUST00000110907.7) transcript is recommended as the knockout region.The region contains 193bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Meis2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null allele display early fetal lethality with hemorrhaging, persistent truncus arteriosis, absence of cardic valves and defects in other neural crest cell derived tissues.

- The *Meis2* gene is located on the Chr2. 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）

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Meis2 Meis homeobox 2 [Mus musculus (house mouse)]

Gene ID: 17536, updated on 17-Feb-2019

Summary

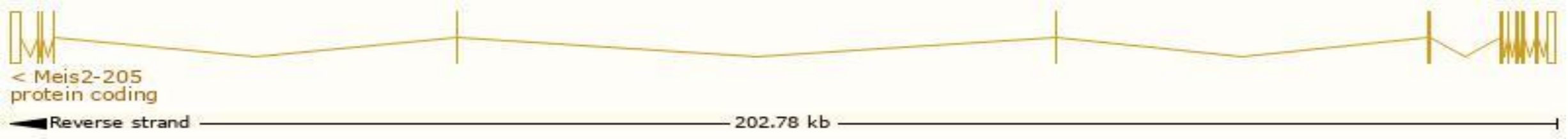
Official Symbol	Meis2 provided by MGI
Official Full Name	Meis homeobox 2 provided by MGI
Primary source	MGI:MGI:108564
See related	Ensembl:ENSMUSG00000027210
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A430109D20Rik, Mrg1, Stra10
Summary	This gene encodes a homeobox protein belonging to the TALE ('three amino acid loop extension') family of homeodomain-containing proteins. TALE homeobox proteins are highly conserved transcriptional regulators and several members have been shown to be essential contributors to developmental programs. In mice, a knock-out of this gene leads to lethality at embryonic day 14, accompanied with hemorrhaging. Embryos lacking this gene show defects in tissues derived from the neural crest, suggesting a critical role of this gene during cranial and cardiac neural crest cell development. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2016]
Expression	Broad expression in frontal lobe adult (RPKM 31.3), CNS E14 (RPKM 21.9) and 17 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

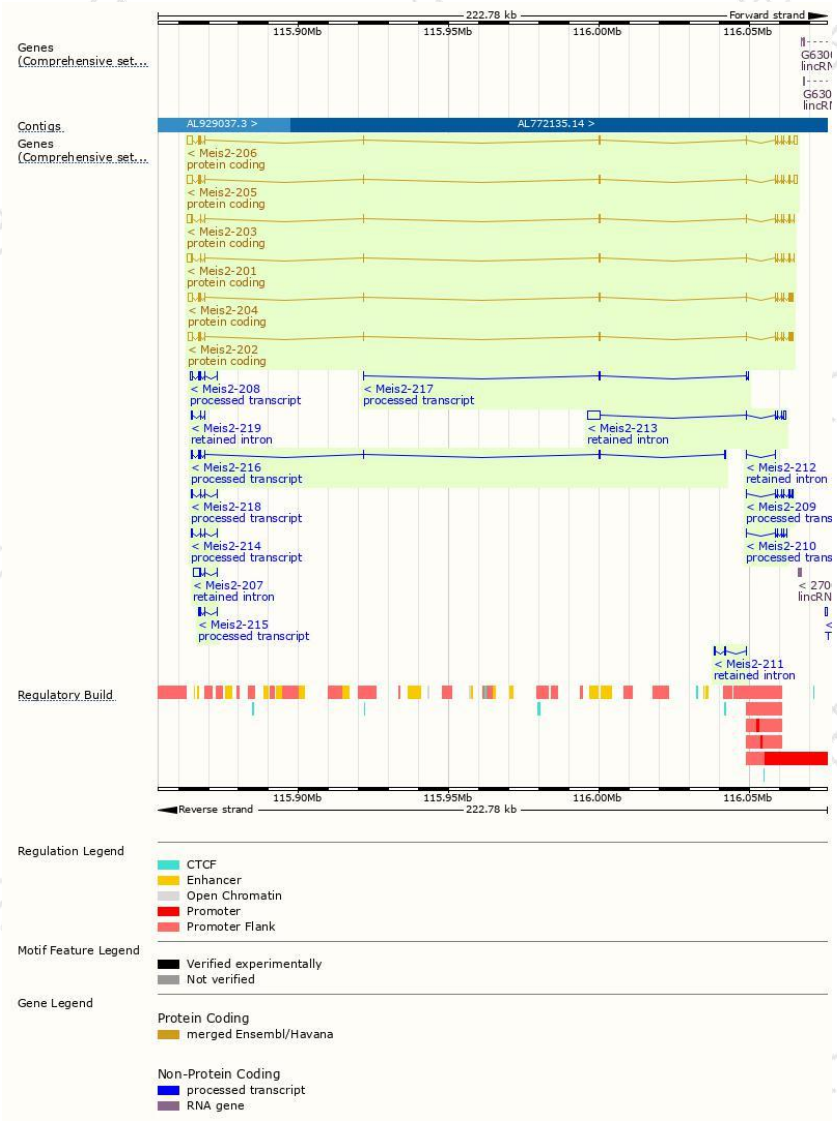
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Meis2-205	ENSMUST00000110907.7	3718	401aa	Protein coding	CCDS50668	P97367	TSL:1 GENCODE basic APPRIS ALT1
Meis2-206	ENSMUST00000110908.8	3697	394aa	Protein coding	CCDS50666	P97367 Q3UJ35	TSL:1 GENCODE basic APPRIS ALT1
Meis2-204	ENSMUST00000110906.8	3229	400aa	Protein coding	CCDS50665	B1AWK4	TSL:2 GENCODE basic APPRIS ALT1
Meis2-202	ENSMUST00000074285.7	2844	393aa	Protein coding	CCDS50664	Q3TYM2	TSL:1 GENCODE basic APPRIS ALT1
Meis2-201	ENSMUST00000028639.12	2831	477aa	Protein coding	CCDS50667	P97367	TSL:1 GENCODE basic APPRIS ALT1
Meis2-203	ENSMUST00000102538.10	2810	470aa	Protein coding	CCDS16568	P97367 Q6GU28	TSL:1 GENCODE basic APPRIS P3
Meis2-208	ENSMUST00000120995.7	1022	No protein	Processed transcript	-	-	TSL:1
Meis2-216	ENSMUST00000151279.7	837	No protein	Processed transcript	-	-	TSL:5
Meis2-209	ENSMUST00000133990.3	804	No protein	Processed transcript	-	-	TSL:5
Meis2-210	ENSMUST00000134314.7	640	No protein	Processed transcript	-	-	TSL:3
Meis2-218	ENSMUST00000177493.7	424	No protein	Processed transcript	-	-	TSL:2
Meis2-214	ENSMUST00000149217.7	393	No protein	Processed transcript	-	-	TSL:2
Meis2-215	ENSMUST00000150477.2	370	No protein	Processed transcript	-	-	TSL:2
Meis2-217	ENSMUST00000154671.7	356	No protein	Processed transcript	-	-	TSL:5
Meis2-213	ENSMUST00000140461.8	5498	No protein	Retained intron	-	-	TSL:2
Meis2-207	ENSMUST00000118654.7	2371	No protein	Retained intron	-	-	TSL:1
Meis2-219	ENSMUST00000189640.6	521	No protein	Retained intron	-	-	TSL:5
Meis2-211	ENSMUST00000135543.2	503	No protein	Retained intron	-	-	TSL:5
Meis2-212	ENSMUST00000138526.1	304	No protein	Retained intron	-	-	TSL:3

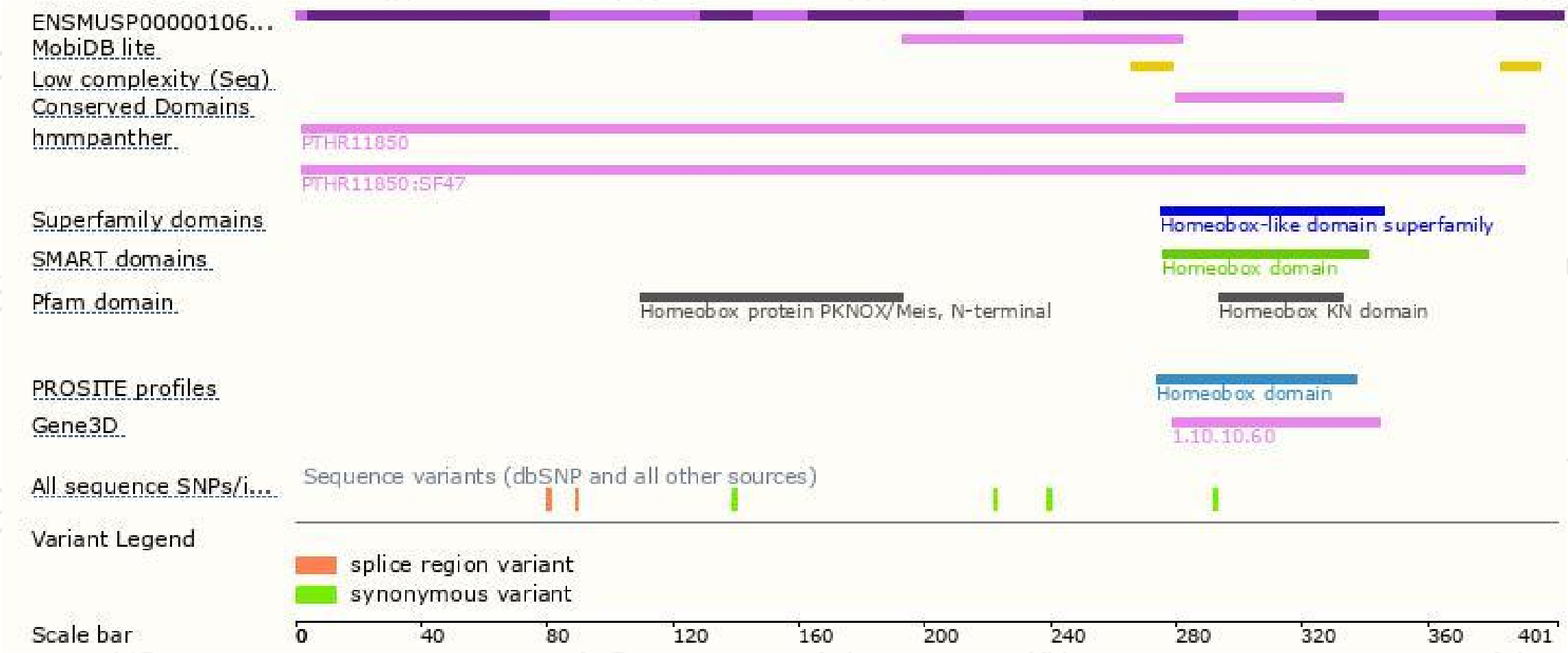
The strategy is based on the design of *Meis2-205* transcript,The transcription is shown below



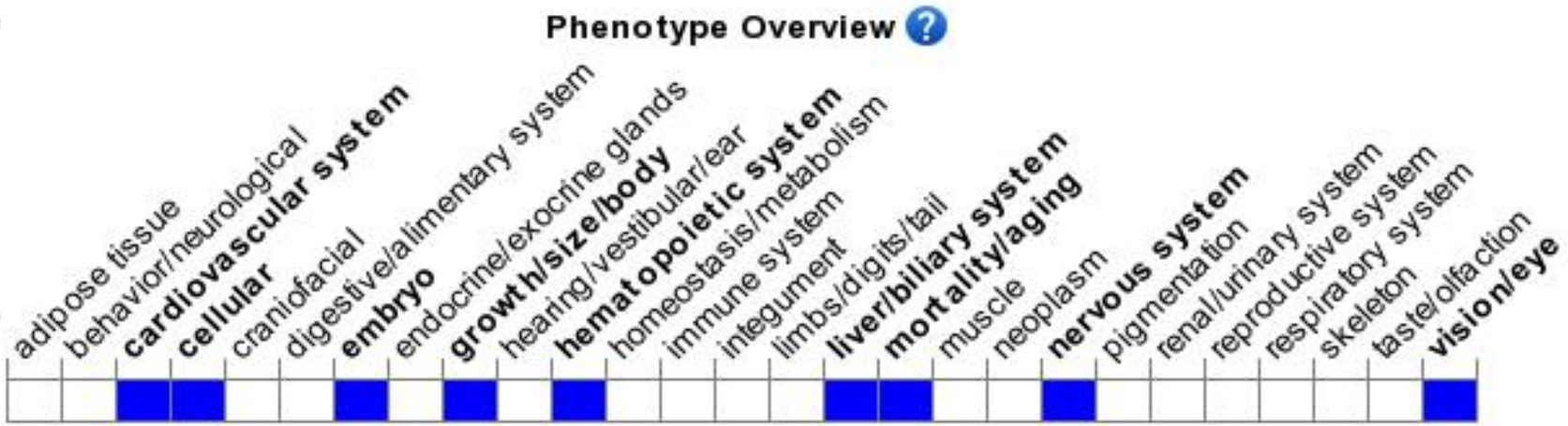
Genomic location distribution



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/).

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

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