Myh11 Cas9-CKO Strategy

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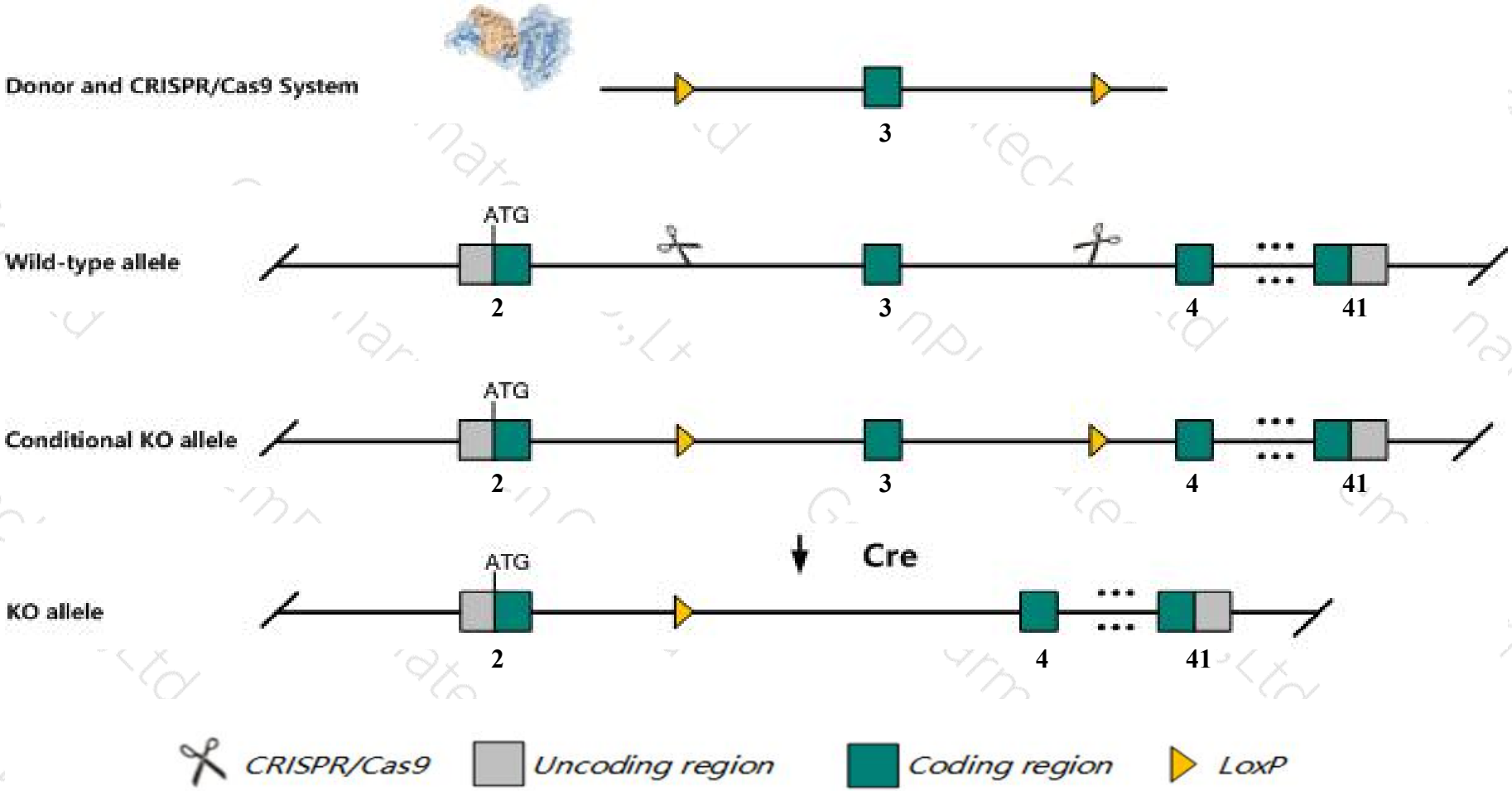
Project Overview

Project Name	***Myh11***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myh11* gene. The schematic diagram is as follows:



Technical routes

- The *Myh11* gene has 4 transcripts. According to the structure of *Myh11* gene, exon3 of *Myh11-202* (ENSMUST00000230397.1) transcript is recommended as the knockout region.The region contains 157bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Myh11* 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.

Notice

- According to the existing MGI data,Homozygous null mice have impaired smooth muscle contractility. They are incapable of urinating, exhibit dilative cardiomyopathy, are growth retarded, and die within 3 days of birth.
- The N-terminal of *Myh11* gene will remain 115aa,it may remain the partial function of *Myh11* gene.
- The *Myh11* gene is located on the Chr16. 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）

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Myh11 myosin, heavy polypeptide 11, smooth muscle [Mus musculus (house mouse)]

Gene ID: 17880, updated on 31-Jan-2019

Summary

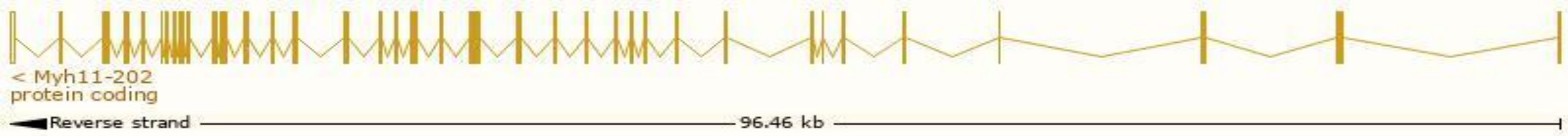
Official Symbol	Myh11 provided by MGI
Official Full Name	myosin, heavy polypeptide 11, smooth muscle provided by MGI
Primary source	MGI:MGI:102643
See related	Ensembl:ENSMUSG00000018830
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV071570, SM1, SM2, smMHC
Expression	Biased expression in bladder adult (RPKM 911.5), colon adult (RPKM 71.0) and 1 other tissue See more
Orthologs	human all

Transcript information（Ensembl）

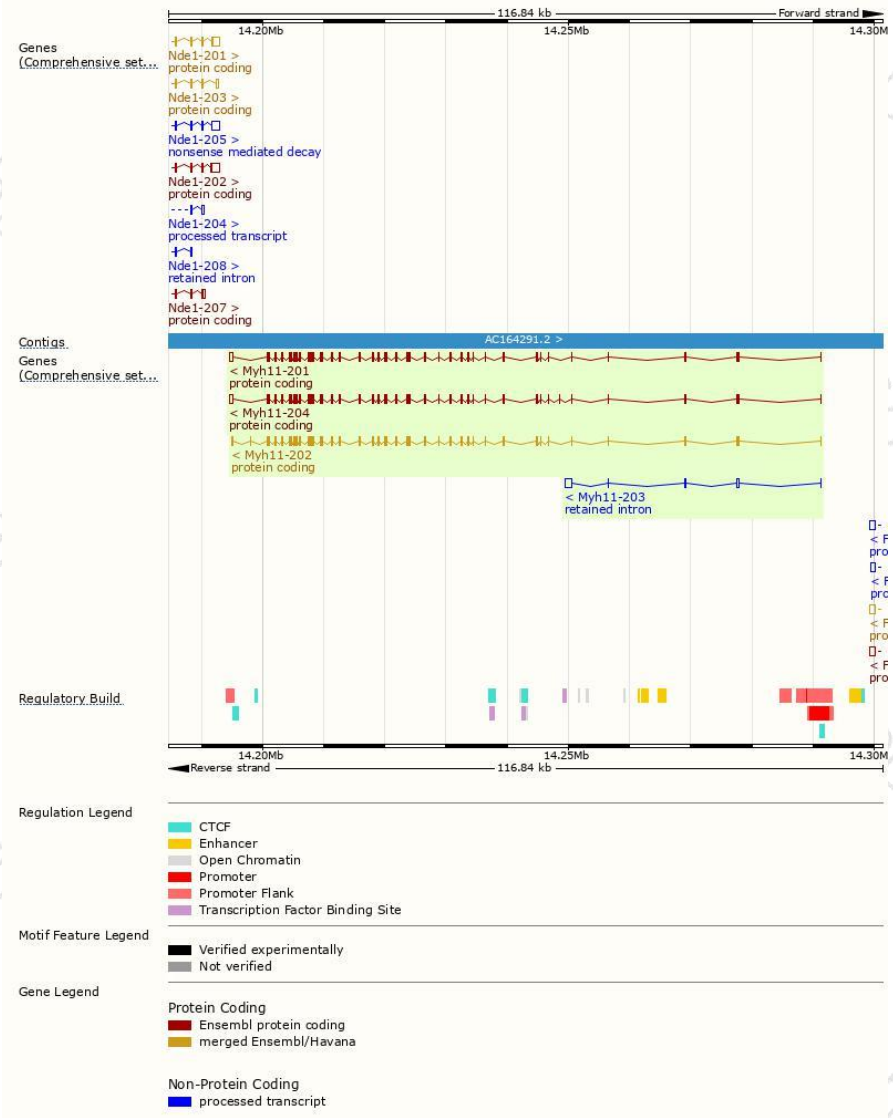
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myh11-202	ENSMUST00000230397.1	6214	1938aa	Protein coding	CCDS27972	A0A2R8VHF9	GENCODE basic
Myh11-201	ENSMUST00000090287.4	6549	1972aa	Protein coding	-	E9QPE7	TSL:1 GENCODE basic APPRIS ALT1
Myh11-204	ENSMUST00000231567.1	6450	1979aa	Protein coding	-	A0A338P6K2	GENCODE basic APPRIS P5
Myh11-203	ENSMUST00000230643.1	1730	No protein	Retained intron	-	-	

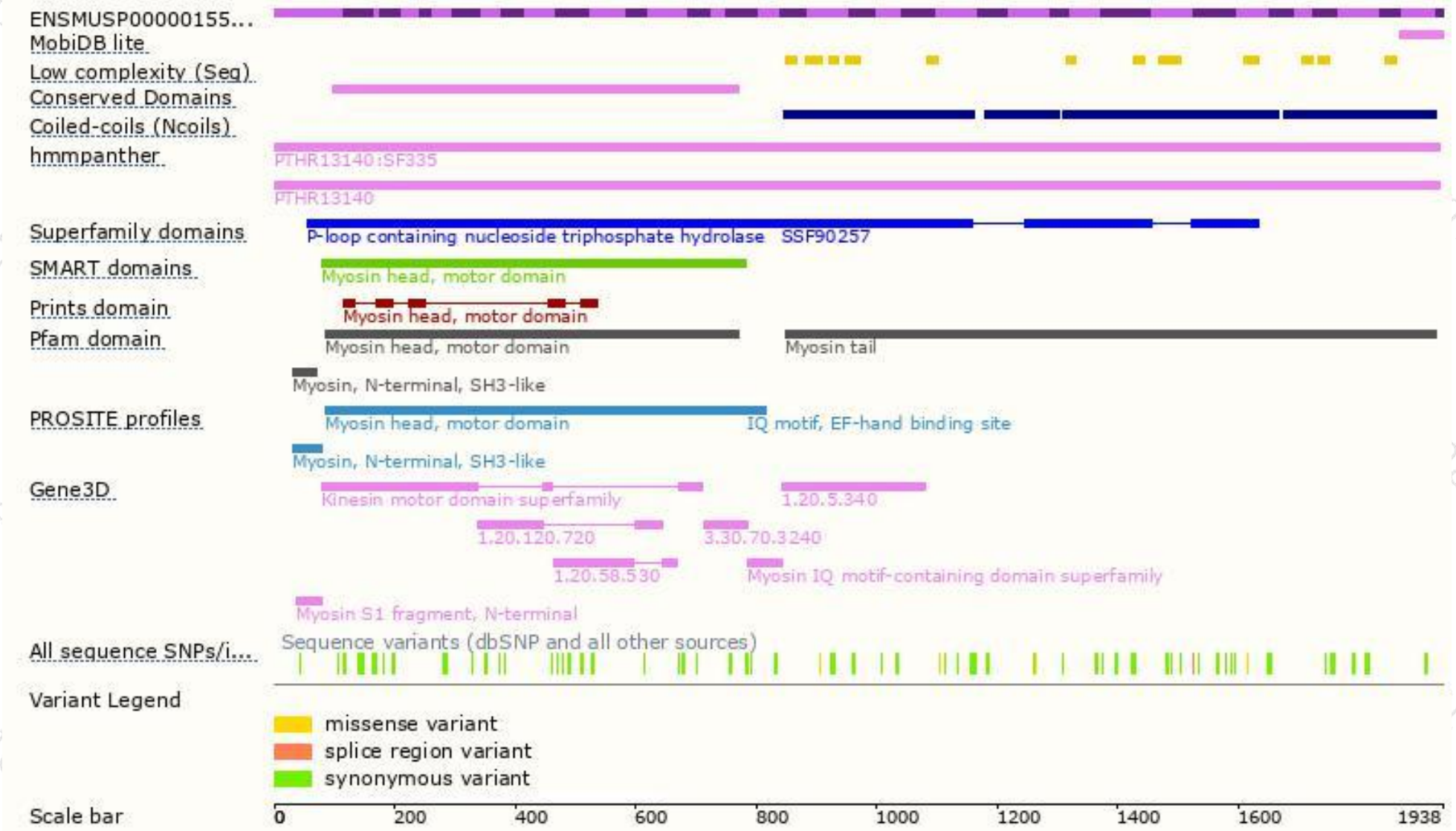
The strategy is based on the design of *Myh11-202* transcript,The transcription is shown below



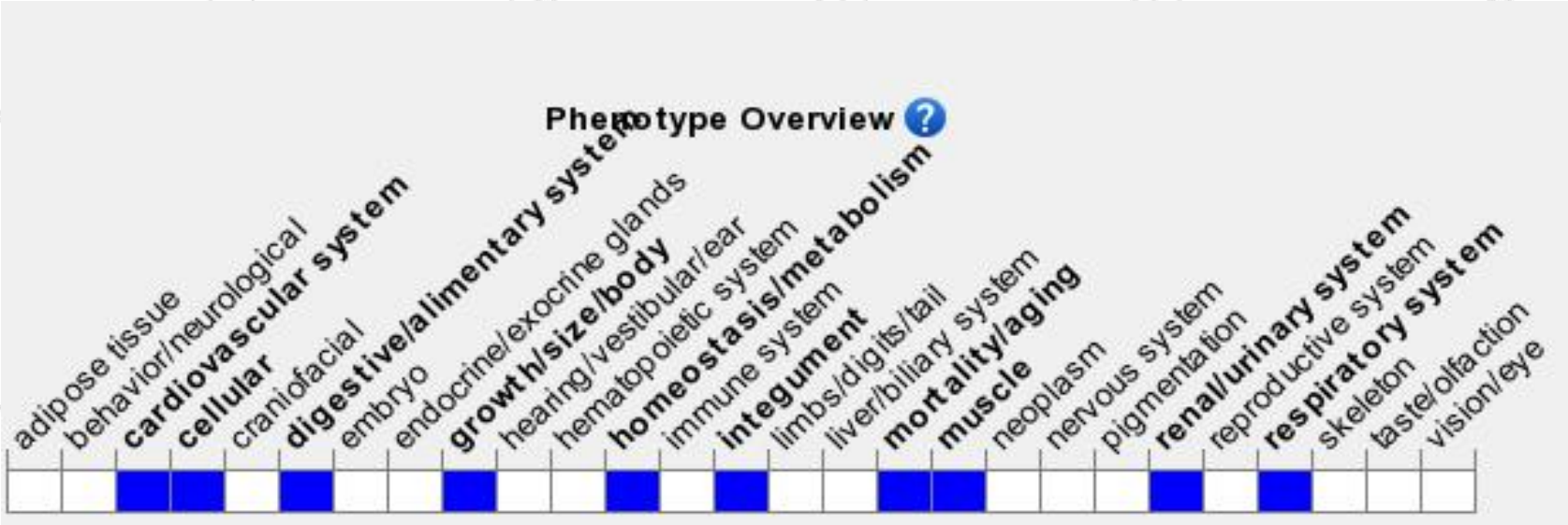
Genomic location distribution



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/).

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

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