Wnt10b Cas9-CKO Strategy

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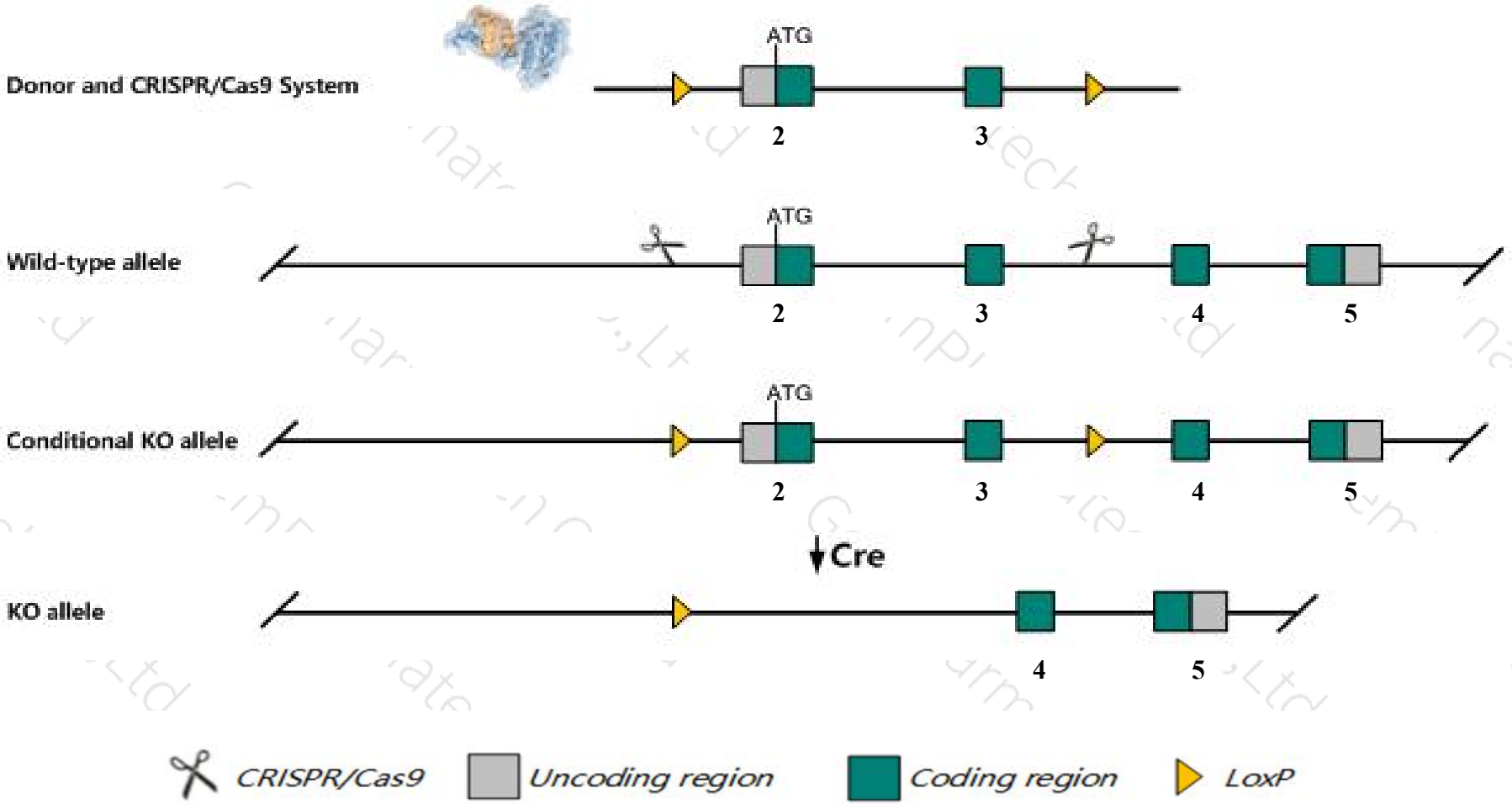
Project Overview

Project Name	***Wnt10b***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wnt10b* gene. The schematic diagram is as follows:



Technical routes

- The *Wnt10b* gene has 7 transcripts. According to the structure of *Wnt10b* gene, exon2-exon3 of *Wnt10b-201* (ENSMUST00000023732.11) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Wnt10b* 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 mutant mice fed a low- or high-fat diet exhibit accelerated myogenic differentiation of myoblasts and those fed a high-fat diet exhibit excessive lipid accumulation in actively regenerating muscle.

- The *Wnt10b* gene is located on the Chr15. 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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Wnt10b wingless-type MMTV integration site family, member 10B [Mus musculus (house mouse)]

Gene ID: 22410, updated on 12-Mar-2019

Summary

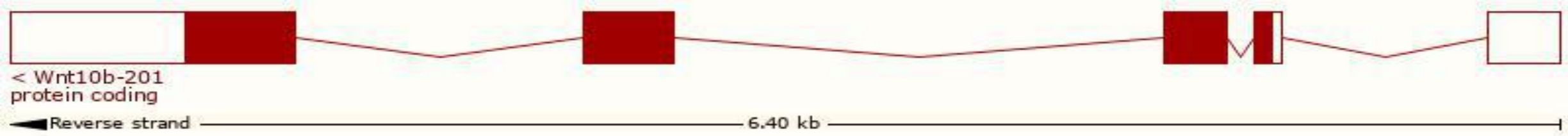
Official Symbol	Wnt10b provided by MGI
Official Full Name	wingless-type MMTV integration site family, member 10B provided by MGI
Primary source	MGI:MGI:108061
See related	Ensembl:ENSMUSG00000022996
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Wnt12
Expression	Biased expression in ovary adult (RPKM 34.8), lung adult (RPKM 7.4) and 1 other tissue See more
Orthologs	human all

Transcript information（Ensembl）

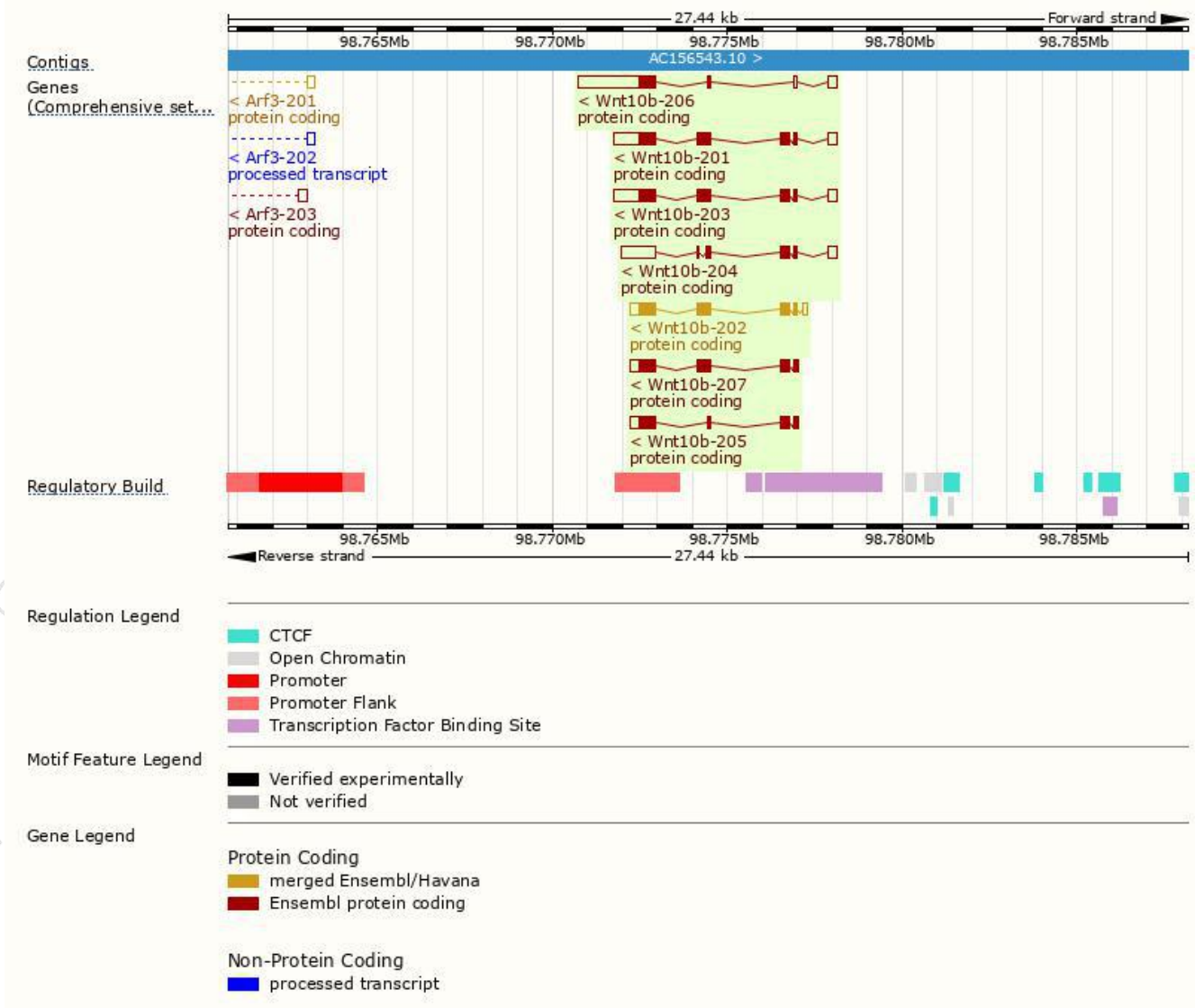
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wnt10b-201	ENSMUST00000023732.11	2226	389aa	Protein coding	CCDS27806	P48614	TSL:5 GENCODE basic APPRIS P1
Wnt10b-203	ENSMUST00000226610.1	2217	389aa	Protein coding	CCDS27806	P48614	GENCODE basic APPRIS P1
Wnt10b-202	ENSMUST00000166022.1	1594	389aa	Protein coding	CCDS27806	P48614	TSL:1 GENCODE basic APPRIS P1
Wnt10b-207	ENSMUST00000228594.1	1510	389aa	Protein coding	CCDS27806	P48614	GENCODE basic APPRIS P1
Wnt10b-206	ENSMUST00000228546.1	2709	171aa	Protein coding	-	A0A2I3BQZ8	GENCODE basic
Wnt10b-204	ENSMUST00000226655.1	1807	173aa	Protein coding	-	Q1RME7	GENCODE basic
Wnt10b-205	ENSMUST00000226846.1	1204	293aa	Protein coding	-	P48614	GENCODE basic

The strategy is based on the design of *Wnt10b-201* transcript,The transcription is shown below

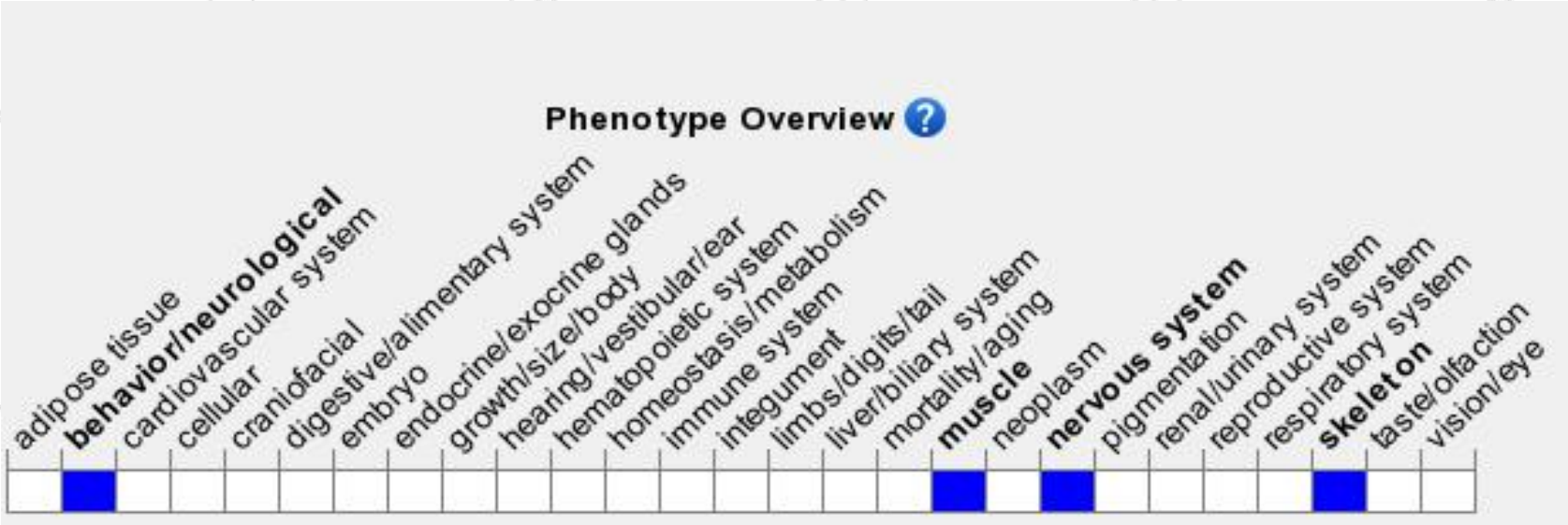


Genomic location distribution



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,Homozygous mutant mice fed a low- or high-fat diet exhibit accelerated myogenic differentiation of myoblasts and those fed a high-fat diet exhibit excessive lipid accumulation in actively regenerating muscle.

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

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