Sox18 Cas9-CKO Strategy

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Project Overview

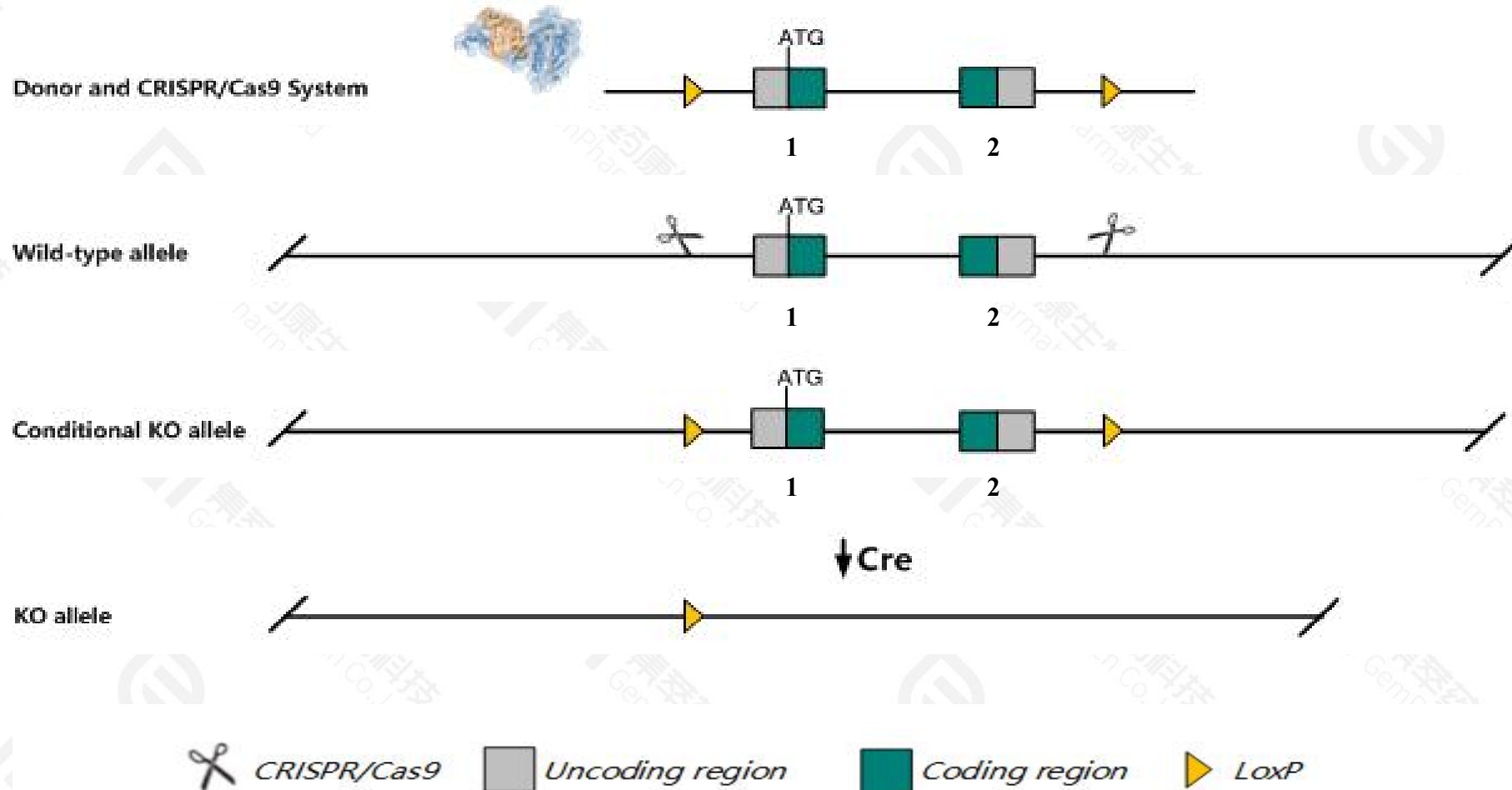|	
Project Name	*Sox18*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sox18* gene. The schematic diagram is as follows:

Technical routes

➤ The *Sox18* gene has 1 transcript. According to the structure of *Sox18* gene, exon1-exon2 of *Sox18-201*(ENSMUST00000054491.6) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Sox18* 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,homozygotes for some mutant alleles show low prenatal viability and cardiovascular defects. Most mutants show darkened coats, reduced zigzag hairs and, depending on the allele, sparse abnormal hair and edema. Heterozygotes show similar or milder defects.

➤ The *Sox18* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Sox18 SRY (sex determining region Y)-box 18 [Mus musculus (house mouse)]

Gene ID: 20672, updated on 13-Mar-2020

Summary

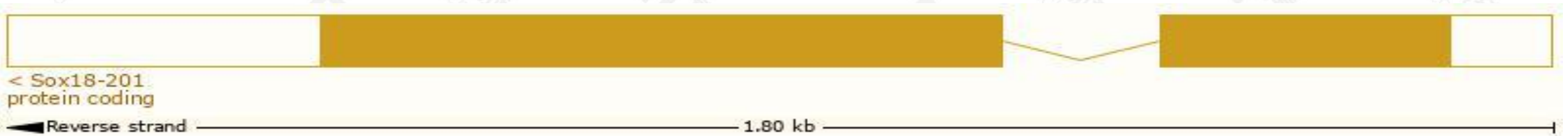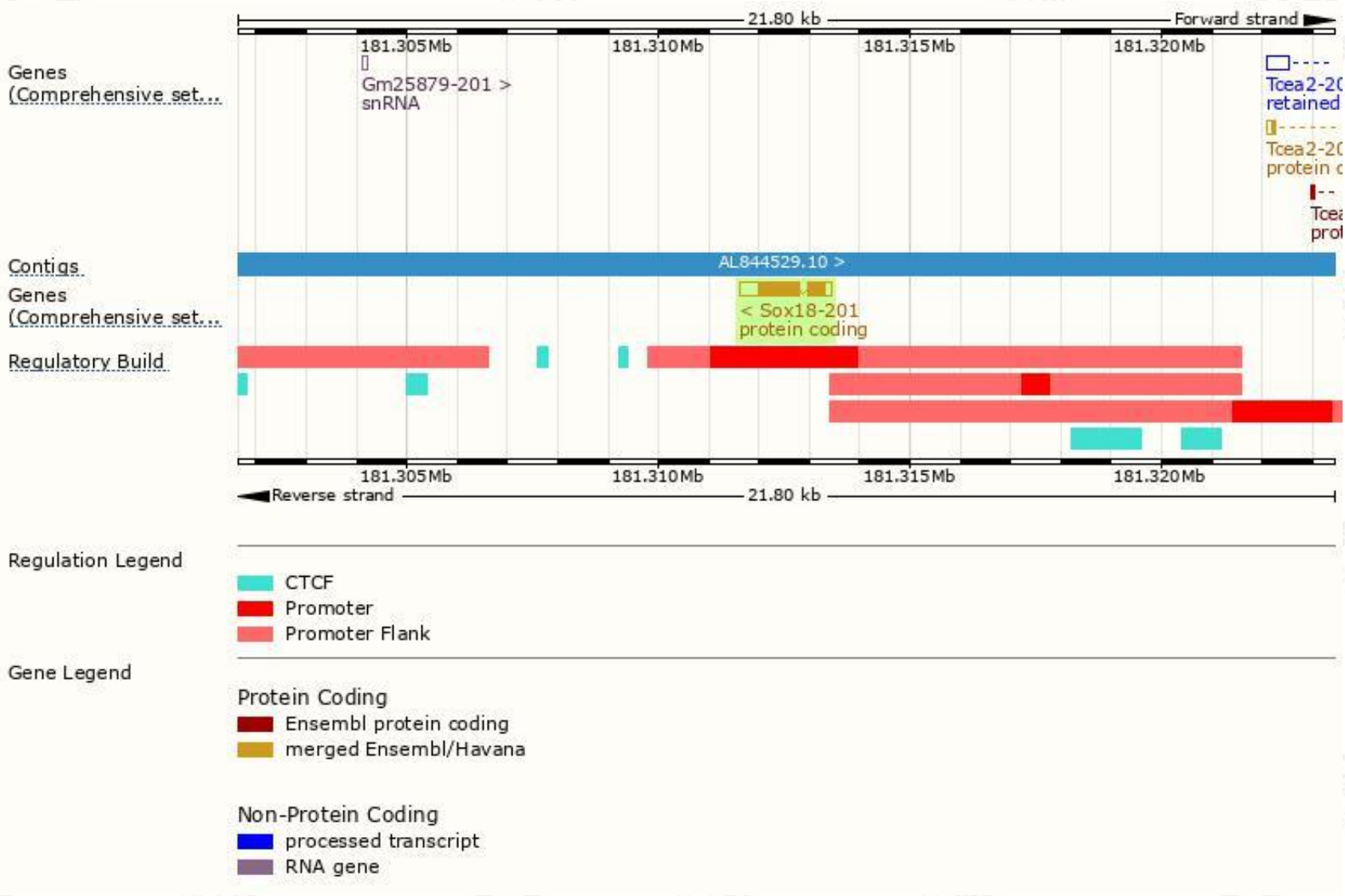|	
Official Symbol	Sox18 provided by MGI
Official Full Name	SRY (sex determining region Y)-box 18 provided by MGI
Primary source	MGI:MGI:103559
See related	Ensembl:ENSMUSG00000046470
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI385749, Ra, Ragl
Expression	Biased expression in lung adult (RPKM 181.7), ovary adult (RPKM 87.7) and 12 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 1 transcript,and the transcript is shown below:

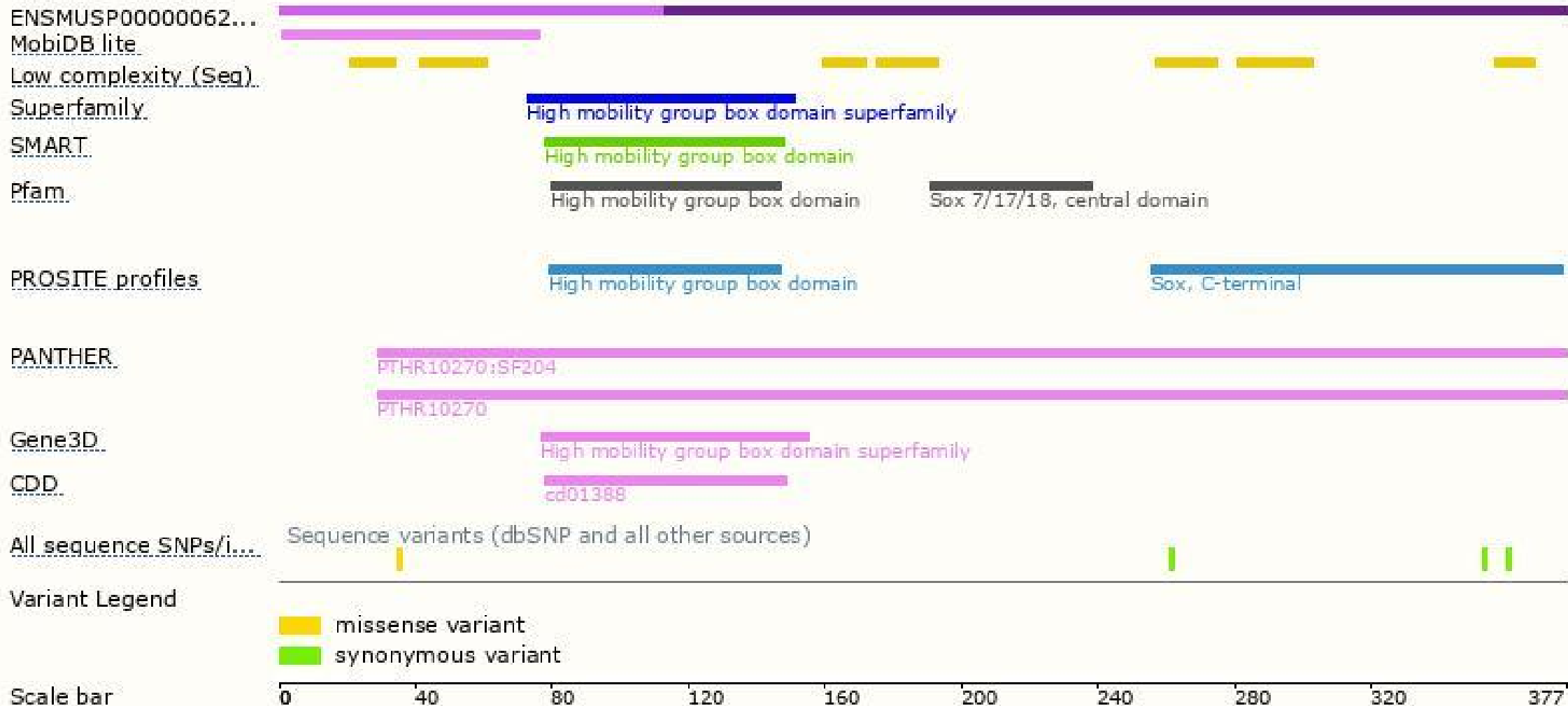| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sox18-201	ENSMUST00000054491.5	1620	377aa	Protein coding	CCDS17218	P43680	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Sox18-201* transcript,the transcription is shown below:
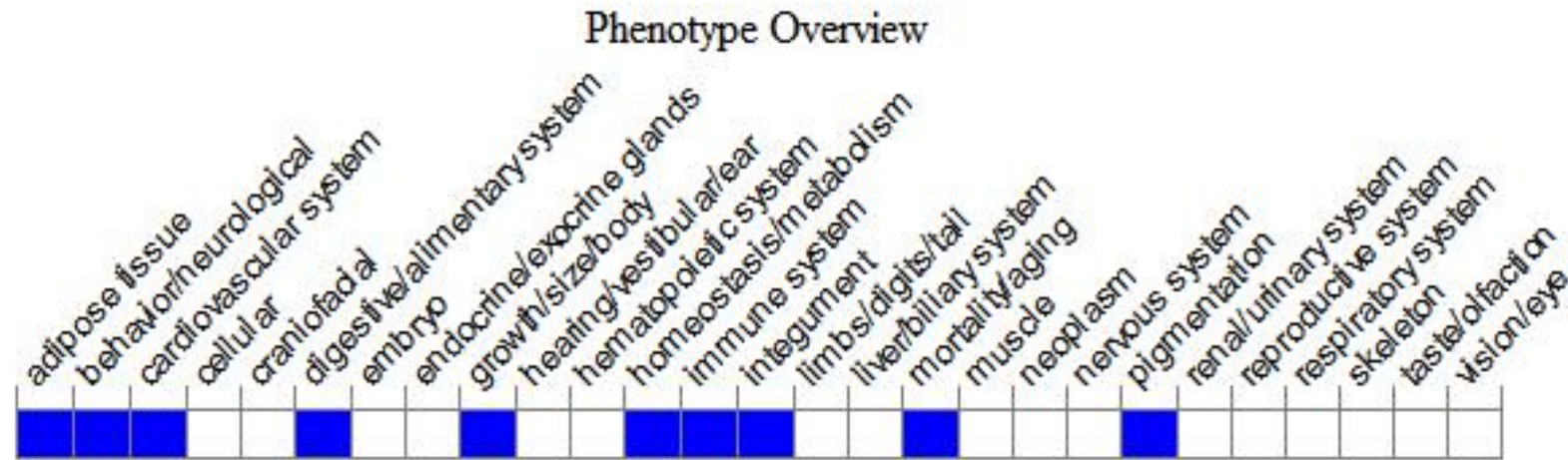

< Sox18-201
protein coding

◄— Reverse strand

1.80 kb

Genomic location distribution

Protein domain

ENSMUSP00000062...				
MobiDB lite				
Low complexity (Seg)				
Superfamily	High mobility group box domain superfamily			
SMART	High mobility group box domain			
Pfam	High mobility group box domain	Sox 7/17/18, central domain		
PROSITE profiles	High mobility group box domain	Sox, C-terminal		
PANTHER	PTHR10270:SF204			
	PTHR10270			
Gene3D	High mobility group box domain superfamily			
CDD	cd01388			
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)			
Variant Legend				

missense variant
synonymous variant

Scale bar: 0 40 80 120 160 200 240 280 320 377

Mouse phenotype description(MGI)

Phenotype Overview

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,homozygotes for some mutant alleles show low prenatal viability and cardiovascular defects.

Most mutants show darkened coats, reduced zigzag hairs and, depending on the allele, sparse abnormal hair and edema.

Heterozygotes show similar or milder defects.

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