Slc30a5 Cas9-KO Strategy

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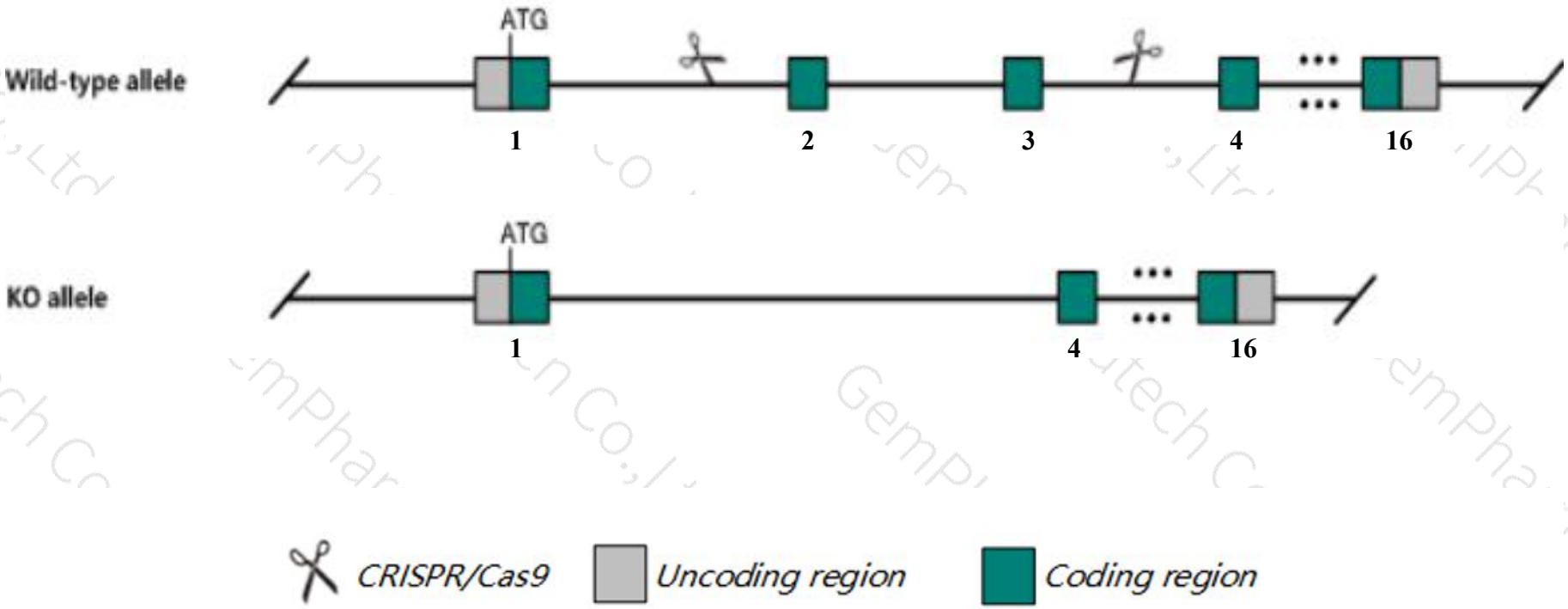
Project Overview

Project Name	***Slc30a5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc30a5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc30a5* gene has 5 transcripts. According to the structure of *Slc30a5* gene, exon2-exon3 of *Slc30a5-201* (ENSMUST00000067246.5) transcript is recommended as the knockout region.The region contains 190bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc30a5* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,homozygous null mice are growth retarded and exhibit skeletal defects including reduced bone density. the majority of mutant male mice die suddenly when they reach reproductive age due to bradyarrhythmia, whereas female mice live a normal term.
- The *Slc30a5* gene is located on the Chr13. 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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Slc30a5 solute carrier family 30 (zinc transporter), member 5 [Mus musculus (house mouse)]

Gene ID: 69048, updated on 13-Mar-2020

Summary

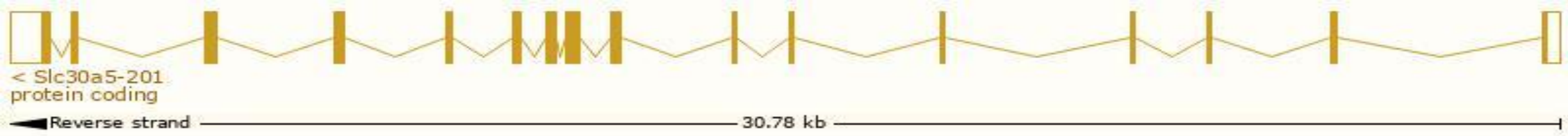
Official Symbol	Slc30a5 provided by MGI
Official Full Name	solute carrier family 30 (zinc transporter), member 5 provided by MGI
Primary source	MGI:MGI:1916298
See related	Ensembl:ENSMUSG00000021629
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810010K08Rik, AF233321, ZNT5, ZTL1, ZnT-5, Zntl1
Expression	Ubiquitous expression in limb E14.5 (RPKM 20.1), large intestine adult (RPKM 17.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

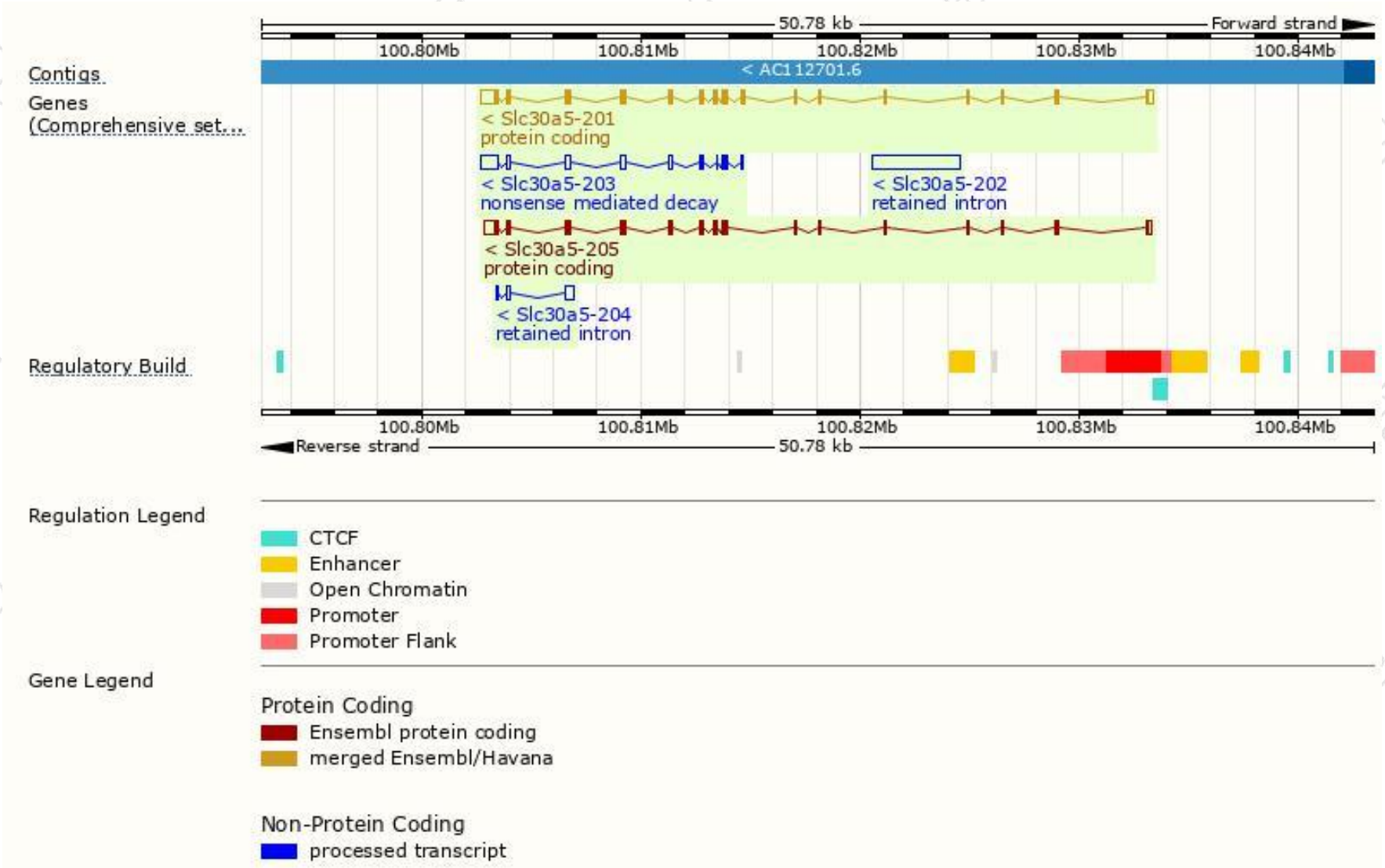
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc30a5-201	ENSMUST00000067246.5	3179	761aa	Protein coding	CCDS26739	Q8R4H9	TSL:1 GENCODE basic APPRIS P2
Slc30a5-205	ENSMUST00000225922.1	2722	704aa	Protein coding	-	A0A286YDV6	GENCODE basic APPRIS ALT2
Slc30a5-203	ENSMUST00000225086.1	2022	153aa	Nonsense mediated decay	-	A0A286YD86	CDS 5' incomplete
Slc30a5-202	ENSMUST00000224177.1	4000	No protein	Retained intron	-	-	
Slc30a5-204	ENSMUST00000225129.1	589	No protein	Retained intron	-	-	

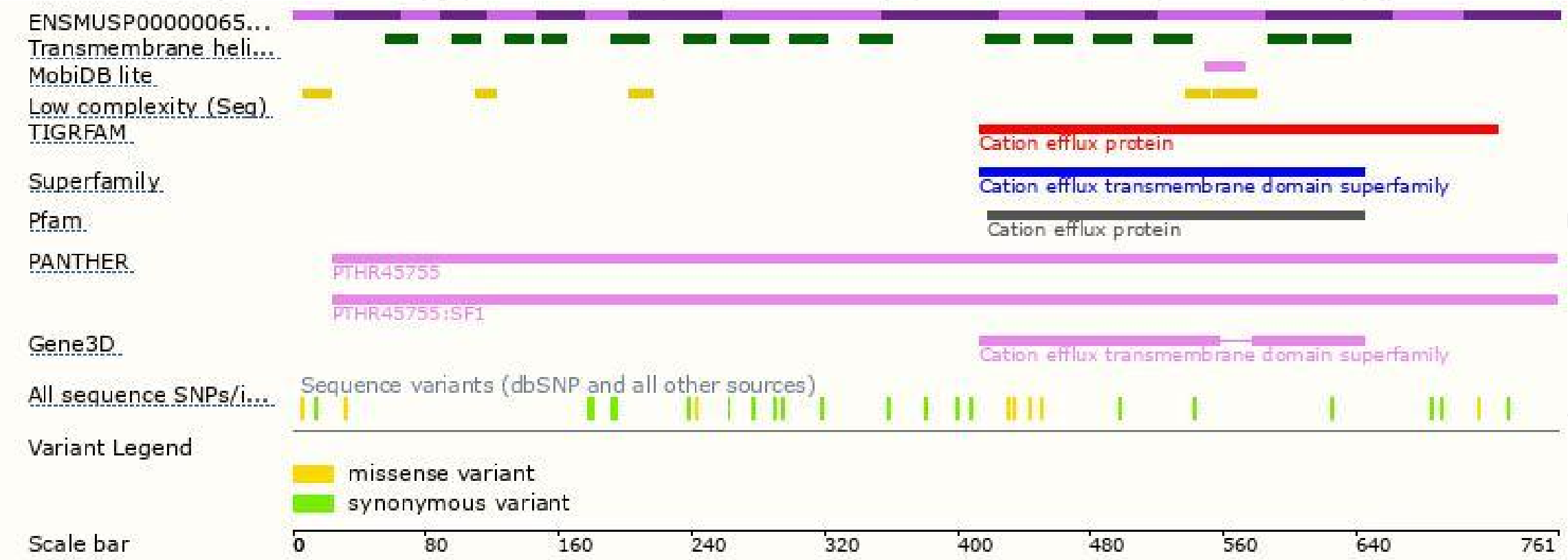
The strategy is based on the design of *Slc30a5-201* transcript,the transcription is shown below:



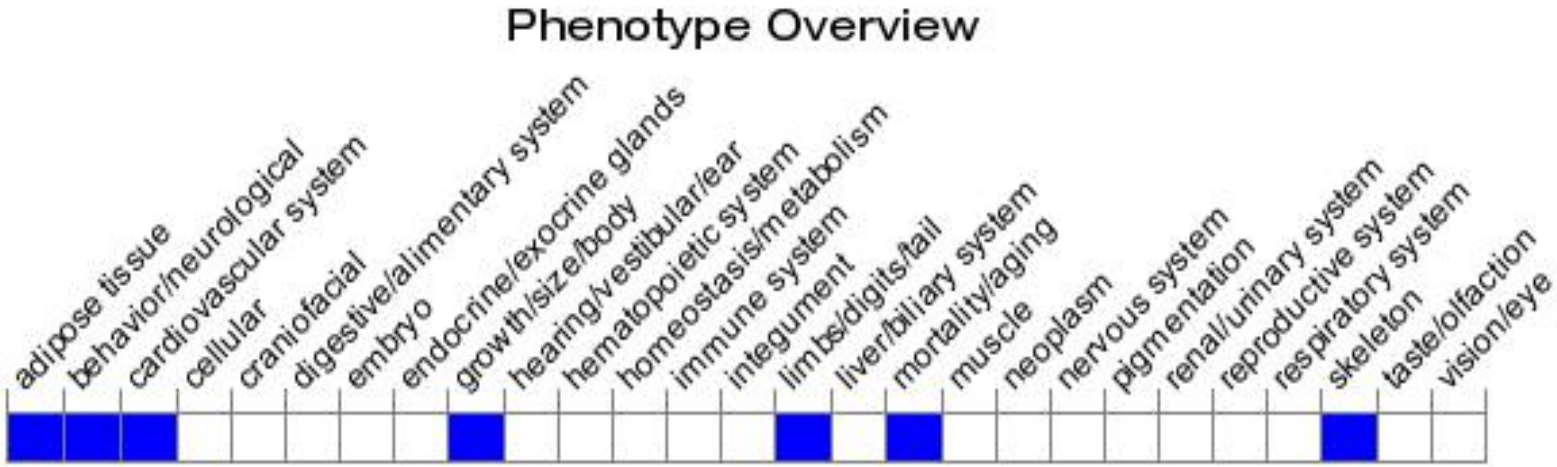
Genomic location distribution



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/).

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

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