

***Sox10-c.32A>T&c.579G insert* Mouse Model Strategy** **-CRISPR/Cas9 technology**

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Project Overview

Project Name

Sox10-c.32A>T&c.579G insert

Project type

cas9-ki(PM)

Strain background

C57BL/6JGpt

Technical Description

- The mouse *Sox10* gene has 4 transcripts.
- This project produced *Sox10-c.32A>T&c.579G insert* point mutation on exon3&exon4 of the transcript of *Sox10-203*(ENSMUST00000230532.1), C. 32A>T mutation was produced in exon3 of mouse *Sox10-203*, and the corresponding amino acid at position 11 was mutated from E to V. After the production of C. 579G by exon4, G base was inserted, resulting in the backward shift mutation of amino acid at position 193.
- In this project, *Sox10* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, sgRNA and donor vectors were constructed. Cas9, sgRNA and donor were injected into the fertilized eggs of C57BL/6JGpt mice for homologous recombination, and obtained positive F0 mice identified by PCR and sequencing analysis. The stable inheritable positive F1 mice model was obtained by mating F0 mice with C57BL/6JGpt mice.

Mutation Site

Before mutation

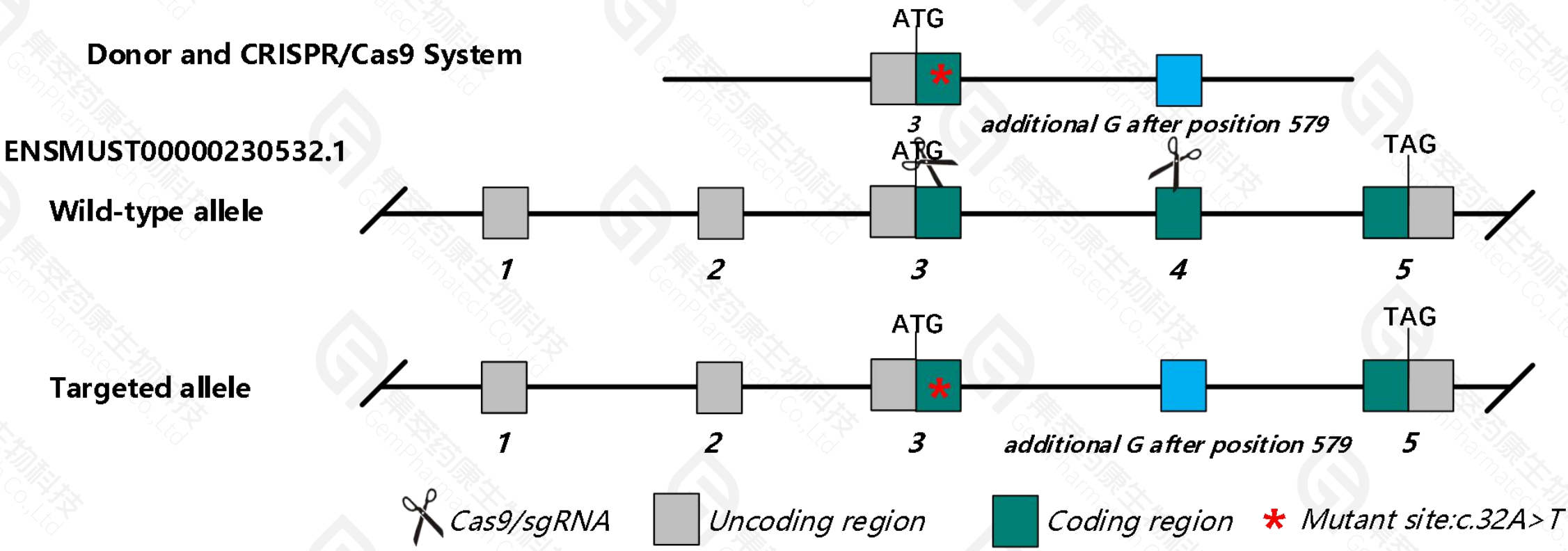
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1 M A E E Q D L S E V E L S P V G S E E P R C L S P G S A P S L G P D ?
1 ATGGCCGAGG AACAGACCT ATCAGAGGTG GAGCTGAGCC CTGTGGGCTC GGAGGAACCC CGTGCCTGT CCCAGGCAG CGGCCCTCG CTGGGACCCG
101 ACGGCGCGG CGGTGGCTCG GGCITGCGAG CCAGCCCGGG GCCCGGTGAA CTGGGCAAGG TCAAGAAGGA ACAGCAGGAC GGCAGGCGG ACGATGACAA
201 GTTCCCGTG TGCAATCCGCG AGGCGGTGAG CCAGGTGCTC AGCGGCTACG ACTGGACGCT GGTGCCCATG CCCGTGCGCG TCAACGGTGC CAGCAAGAGC
301 AAGCCGCAGC TCAAGAGGCC CATGAACGCC TTCATGGTGT GGGCACAGGC GGCACGAGA AAGTAGCCG ACCAGTACCC TCACCTCCAC AATGCTGAGC
401 TCAGCAAGAC ACTAGGCAAG CTCTGGAGGT TGCTGAACGA AAGTGACAAG GCCTCCCTCA TTGAGGAGGC TGAGAGGCTC CGGATGCAGC ACAAAGAAGA
501 CCATCCGGAC TACAAGTACC AACCTCGGCG GCGGAAGAAC GGGAGGCGAC CCCAGGGGGA GGCAGATGC CCAGGCGG G AAGCCGAGCA AGGAGGGGCT
601 GCTGCTATT AGGCTCACTA CAAGAGTGCC CACCTGGACC ACCGGCACCC AGAAGAAGGC TCCCCCATGT CAGATGGGAA CCCAGAGCAC CCCTCAGGCC
701 AGAGCCATGG CCCCAACACC CCTCCAACCA CCCAAAGAC AGAGCTGCAG TCCGGCAAGG CAGACCCCAA AAGGGATGGG GCGTCTTGG GGGAGGGCGG
801 GAAGCCCCAC ATCAGCTTCG GCAACGTGGA CATCGGGGAG ATCAGCCACG AGGTAATGTC CAACATGGAA ACCTTTGATG TGACTGAGCT GGACCAATAC
901 CTGCCACCCA ACGGGCACCC AGGCCATGTG GGTAGCTACT CGGCAGCTGG CTACGGGCTG GGCAGTGCCT TGGCTGTGGC CAGTGGACAC TCTGCCTGGA
1001 TCTCCAAGCC ACCAGGTGTG GCTCTGCCA CGTCTCGCC CCCTGGTGTG GATGCCAAG CCCAGGTGAA GACAGAGACC ACAGGCCCCC AGGGACCCCC
1101 ACACTACACC GACCAGCGT CCACTTCCCA GATCGCTAC ACTTCCCTCA GTCTGCCCA CTACGGCTCC GCTTCCCTT CCACTCTCAG ACCCCAGTTT
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After mutation

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1 M A E E Q D L S E V V L S P V G S E E P R C L S P G S A P S L G P D ?
1 ATGGCCGAGG AACAGACCT ATCAGAGGTG GAGCTGAGCC CTGTGGGCTC GGAGGAACCC CGTGCCTGT CCCAGGCAG CGGCCCTCG CTGGGACCCG
101 ACGGCGCGG CGGTGGCTCG GGCITGCGAG CCAGCCCGGG GCCCGGTGAA CTGGGCAAGG TCAAGAAGGA ACAGCAGGAC GGCAGGCGG ACGATGACAA
201 GTTCCCGTG TGCAATCCGCG AGGCGGTGAG CCAGGTGCTC AGCGGCTACG ACTGGACGCT GGTGCCCATG CCCGTGCGCG TCAACGGTGC CAGCAAGAGC
301 AAGCCGCAGC TCAAGAGGCC CATGAACGCC TTCATGGTGT GGGCACAGGC GGCACGAGA AAGTAGCCG ACCAGTACCC TCACCTCCAC AATGCTGAGC
401 TCAGCAAGAC ACTAGGCAAG CTCTGGAGGT TGCTGAACGA AAGTGACAAG GCCTCCCTCA TTGAGGAGGC TGAGAGGCTC CGGATGCAGC ACAAAGAAGA
501 CCATCCGGAC TACAAGTACC AACCTCGGCG GCGGAAGAAC GGGAGGCGAC CCCAGGGGGA GGCAGATGC CCAGGCGG G AAGCCGAGCA AGGAGGGGCT
601 TGCTGCTATT CAGGCTCACT ACAAGATGTC CCACCTGGAC CACCGGCACC CAGAAGAAGG CTCCTCCATG TCAGATGGGA ACCCAGAGCA CCCCTCAGGC
701 CAGAGCCATG GCCCCAAC CCCTCCAACC ACCCAAGA CAGAGTGCA GTCCGGCAAG GCAGACCCCA AAGGGATGG GCGTCTTGG GGGAGGGCGG
801 GGAAGCCCCA CATCAGCTTC GCAACGTGGA ACATCGGGGA GATCAGCCAC GAGTAATGT CCAACATGGA AACCTTTGAT GTGACTGAGC TGGACCAATA
901 CCTGCCACCC AACGGGCACC CAGGCAATGT GGTAGTACT TCGGCAGCTG GCTACGGGCT GGGCAGTGCC CTGGCTGTGG CCAGTGGACA CTCTGCCTGG
1001 ATCTCCAAGC CACCAAGTGT GGTCTGCCCC ACGTCTCGC CCCTGTGTGT GATGCCCCAA GCCCAGGTGA AGACAGAGAC CACAGGCCCC CAGGAGCCCC
1101 CACACTACAC CGACCAGCGG TCCACTTCCC AGATCGCCTA CACTTCCCTC AGTCTGCCCC ACTACGGCTC CGCTTCCCTT TCACTCTCAC GACCCAGTTT
```

The green region is exon3&exon4 of *Sox10-203*, and the yellow region and red region represents the *c.32A>T*&*c.579G insert* mutation site.

This model uses CRISPR/Cas9 technology to edit the *Sox10* gene and the schematic diagram is as follow:



- According to the data of MGI, Homozygotes for null mutations lack peripheral glial cells, melanocytes, and autonomic and enteric neurons, and die neonatally or sooner. Heterozygotes exhibit white spotting and megacolon.
- Transcript *Sox10-202* and *Sox10-204* may not be affected.
- The phenotype of this model cannot be guaranteed to be completely consistent with that of the reference literature.
- One to two synonymous mutations of amino acids will be introduced on exon3&exon4 of *Sox10*.
- The mutation was located close to the 5' terminal of *GM10863* gene, and its effect on it was unknown.
- Mouse *Sox10* gene is located on Chr15. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr15, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

Gene name and location (NCBI)

Sox10 SRY (sex determining region Y)-box 10 [*Mus musculus* (house mouse)]

Gene ID: 20665, updated on 3-Jan-2021

Summary

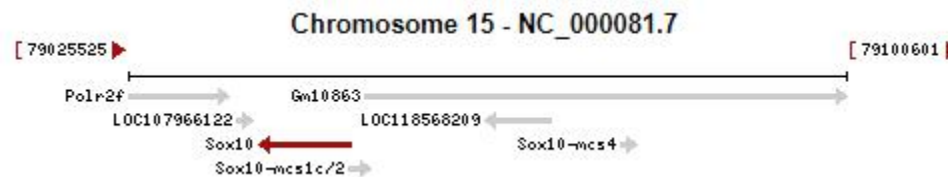
Official Symbol	Sox10 provided by MGI
Official Full Name	SRY (sex determining region Y)-box 10 provided by MGI
Primary source	MGI:MGI:98358
See related	Ensembl:ENSMUSG00000033006
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	gt; Dom; Sox; Sox21
Expression	Biased expression in mammary gland adult (RPKM 22.0), cerebellum adult (RPKM 18.7) and 14 other tissues See more
Orthologs	human all

Genomic context

Location: 15 E1; 15 37.7 cM

Exon count: 4

See Sox10 in [Genome Data Viewer](#)

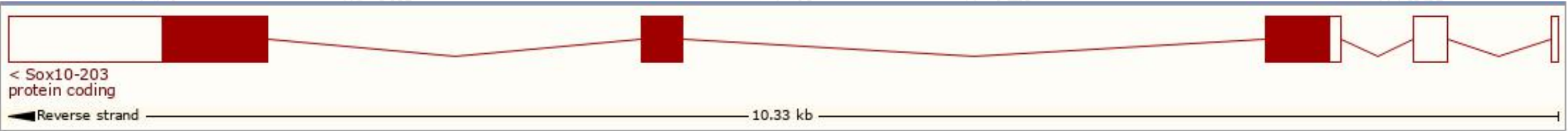


Transcript information (Ensembl)

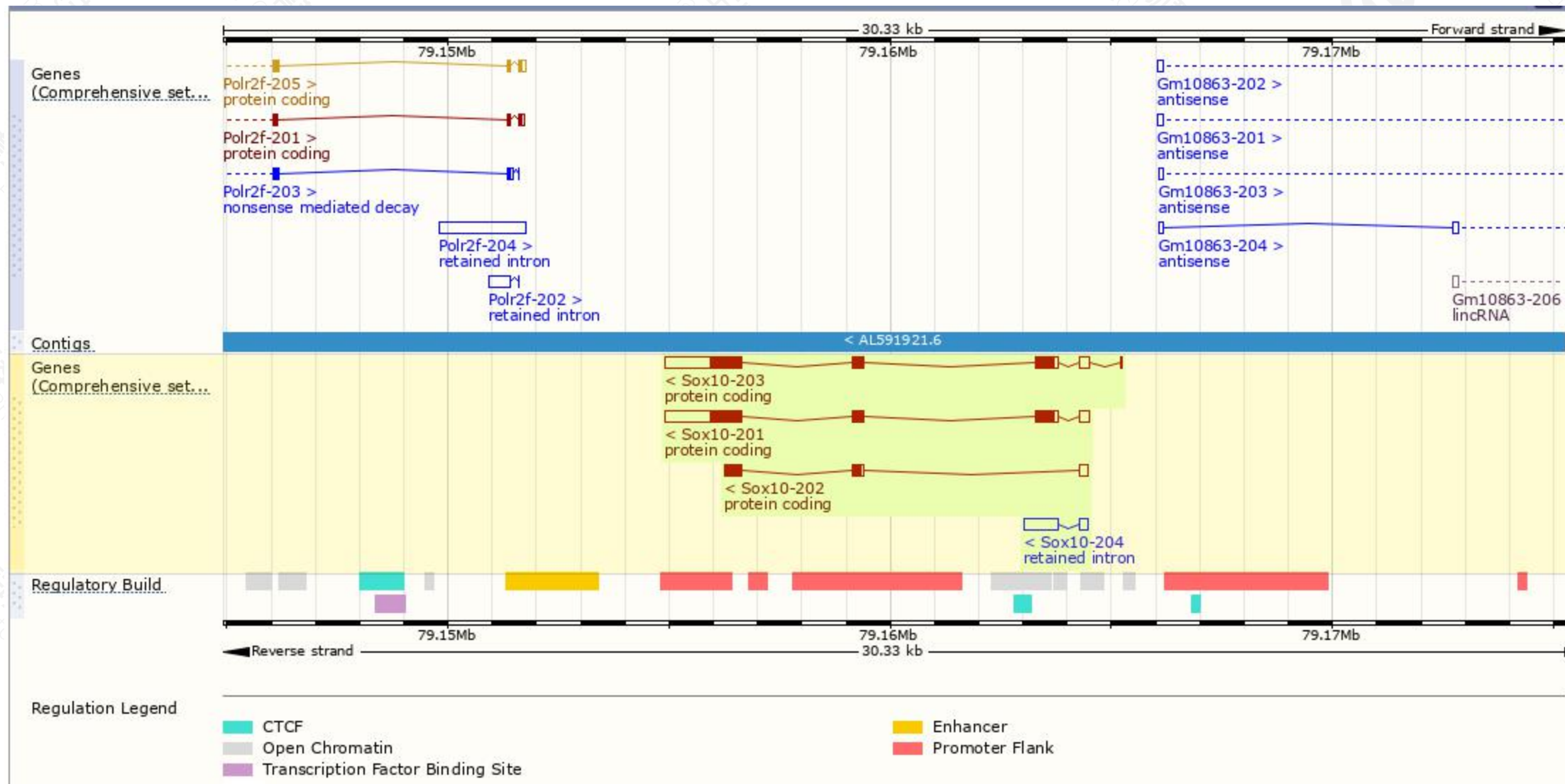
The gene has 4 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt Match	Flags
Sox10-203	ENSMUST00000230532.1	2780	466aa	Protein coding	CCDS49668	Q04888	GENCODE basic APPRIS P1
Sox10-201	ENSMUST00000040019.4	2713	466aa	Protein coding	CCDS49668	Q04888	TSL:1 GENCODE basic APPRIS P1
Sox10-202	ENSMUST00000230261.1	863	205aa	Protein coding	-	A0A2R8VI24	CDS 3' incomplete
Sox10-204	ENSMUST00000230891.1	982	No protein	Retained intron	-	-	-

The strategy is based on the design of *Sox10-203* transcript, the transcription is shown below:



Genomic location distribution



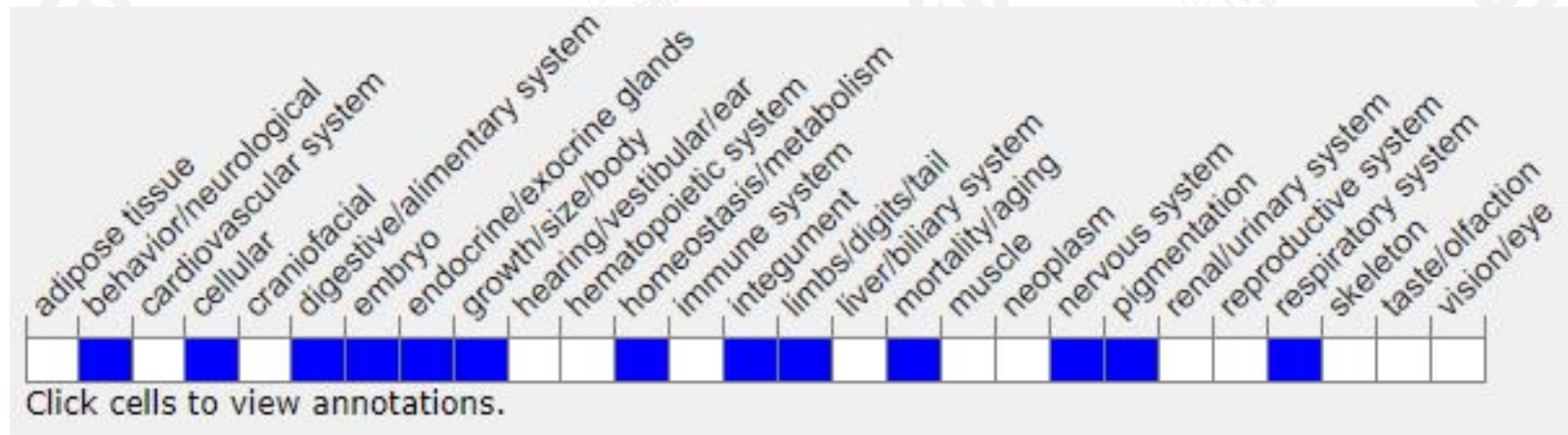
Protein domain



Mouse phenotype description(MGI)

URL link is as follows:

<http://www.informatics.jax.org/marker/MGI:98358>



Homozygotes for null mutations lack peripheral glial cells, melanocytes, and autonomic and enteric neurons, and die neonatally or sooner. Heterozygotes exhibit white spotting and megacolon.

If you have any questions, please feel free to contact us.
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