

Cbfa2t3 Cas9-KO Strategy

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Project Overview

Project Name

Cbfa2t3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cbfa2t3* gene. The schematic diagram is as follows:



- The *Cbfa2t3* gene has 7 transcripts. According to the structure of *Cbfa2t3* gene, exon3-exon5 of *Cbfa2t3-203* (ENSMUST00000127984.8) transcript is recommended as the knockout region. The region contains 410bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cbfa2t3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice that are homozygote null for this gene display skewing of the early myeloid progenitor cells toward the granulocytic/macrophage lineage while reducing the numbers of megakaryocyte-erythroid progenitor cells.
- The *Cbfa2t3* gene is located on the Chr8. 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)

Cbfa2t3 CBFA2/RUNX1 translocation partner 3 [Mus musculus (house mouse)]

Gene ID: 12398, updated on 31-Jan-2019

Summary



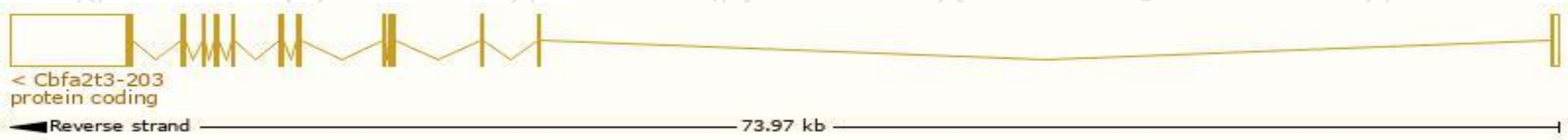
Official Symbol	Cbfa2t3 provided by MGI
Official Full Name	CBFA2/RUNX1 translocation partner 3 provided by MGI
Primary source	MGI:MGI:1338013
See related	Ensembl:ENSMUSG000000006362
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A630044F12Rik, AI465270, AW229127, Cbfa2t3h, ETO-2, Eto2, MTGR2
Expression	Broad expression in lung adult (RPKM 8.3), thymus adult (RPKM 7.0) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

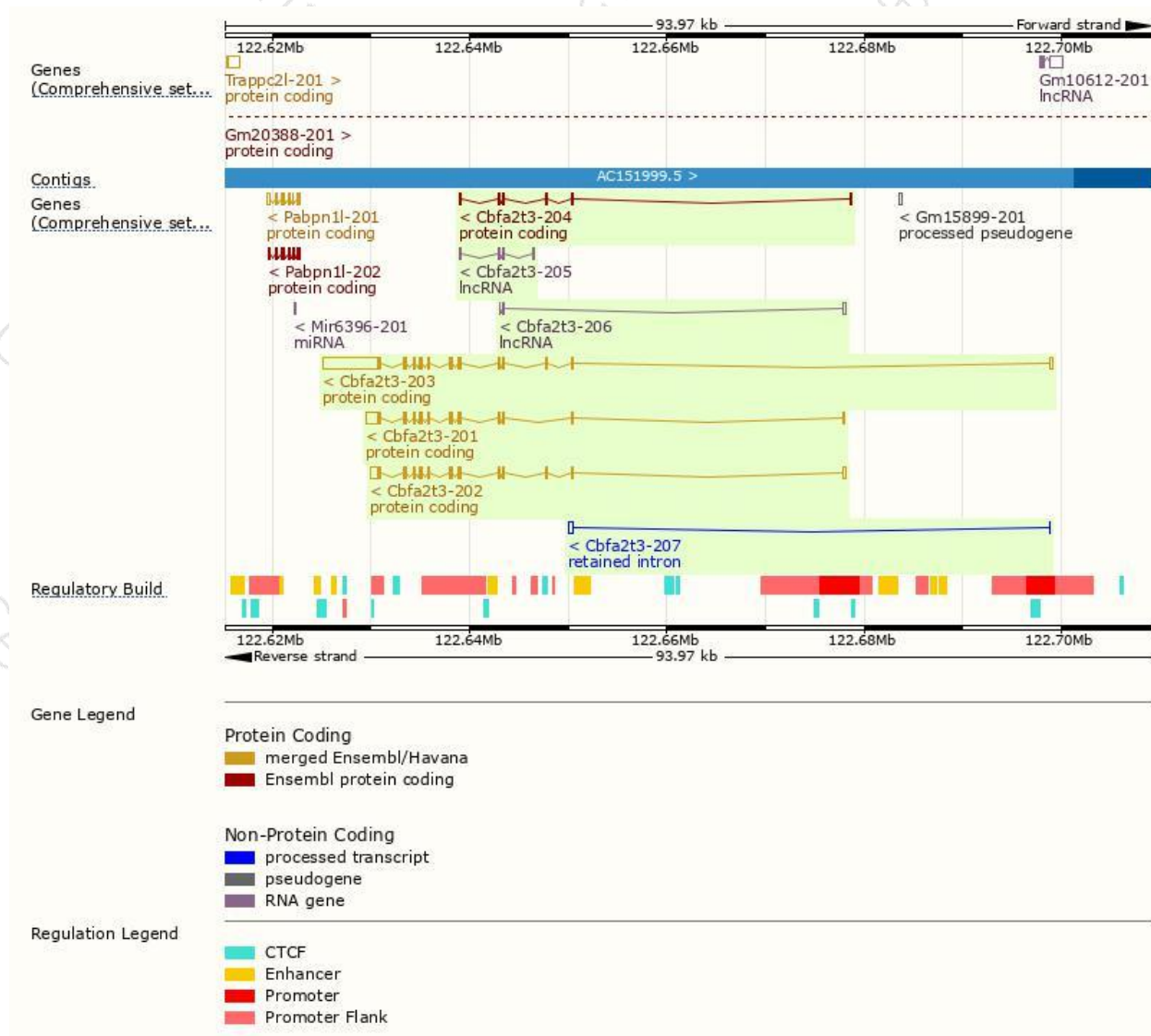
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cbfa2t3-203	ENSMUST00000127984.8	7645	620aa	Protein coding	CCDS22744	B7ZP57	TSL:1 GENCODE basic APPRIS P3
Cbfa2t3-201	ENSMUST00000006525.13	3161	559aa	Protein coding	CCDS52696	O54972	TSL:2 GENCODE basic APPRIS ALT2
Cbfa2t3-202	ENSMUST00000064674.12	2867	585aa	Protein coding	CCDS52697	E9QM80	TSL:1 GENCODE basic APPRIS ALT2
Cbfa2t3-204	ENSMUST00000134045.1	639	185aa	Protein coding	-	D3Z3P7	CDS 3' incomplete TSL:5
Cbfa2t3-207	ENSMUST00000148630.1	537	No protein	Retained intron	-	-	TSL:2
Cbfa2t3-206	ENSMUST00000147374.1	542	No protein	lncRNA	-	-	TSL:3
Cbfa2t3-205	ENSMUST00000142535.7	408	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Cbfa2t3-203* transcript,The transcription is shown below



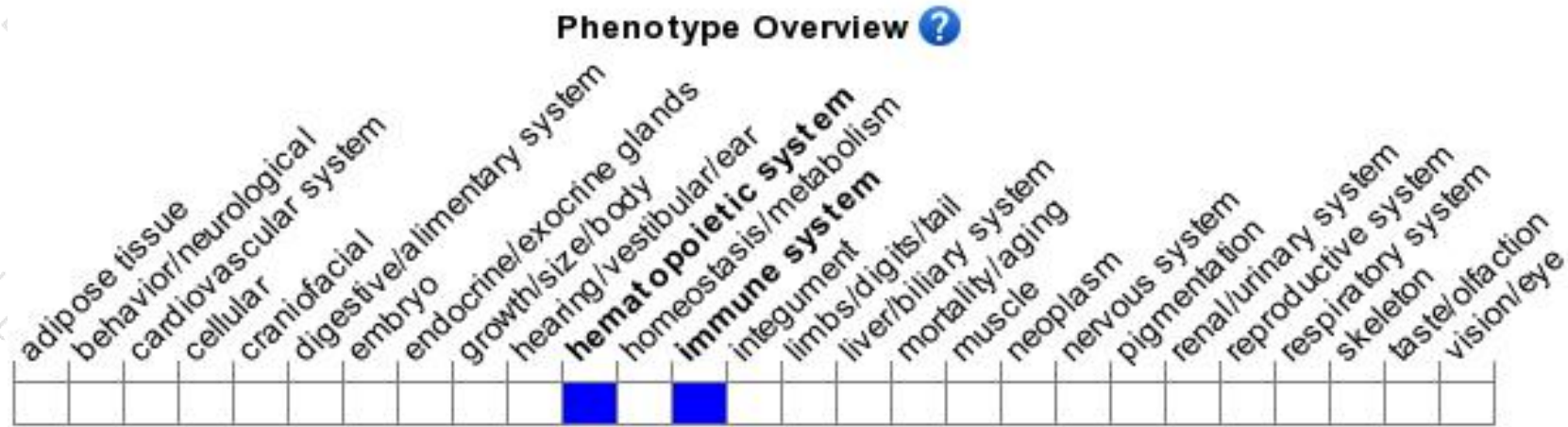
Genomic location distribution



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, Mice that are homozygote null for this gene display skewing of the early myeloid progenitor cells toward the granulocytic/macrophage lineage while reducing the numbers of megakaryocyte-erythroid progenitor cells.

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

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