

Cytip Cas9-KO Strategy

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Design Date: 2020-5-26

Project Overview

Project Name

Cytip

Project type

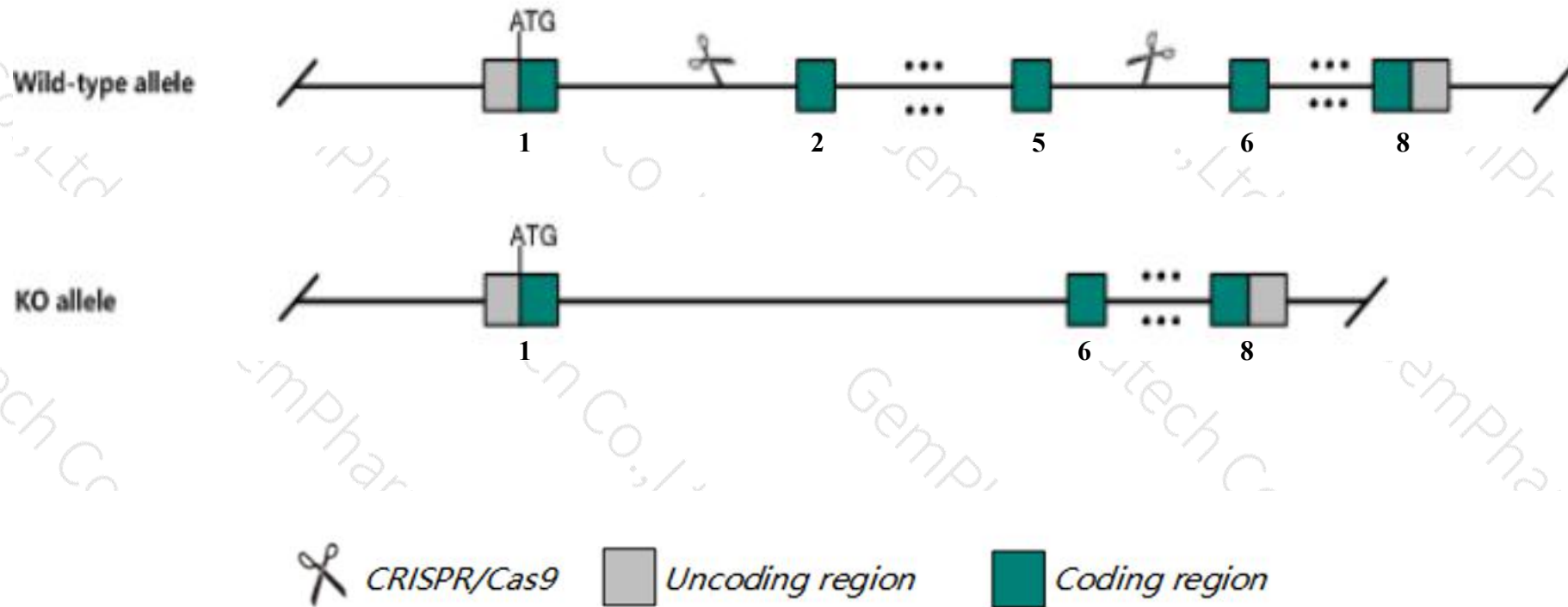
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Cytip* gene has 8 transcripts. According to the structure of *Cytip* gene, exon2-exon5 of *Cytip-201* (ENSMUST00000028175.6) transcript is recommended as the knockout region. The region contains 302bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cytip* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null allele display impaired trafficking and/or cell adhesion of immune system cells. mice homozygous for a reporter allele show normal immune cell development and function; however, mutant hematopoietic stem cells have impaired repopulating activity.
- The *Cytip* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Cytip cytohesin 1 interacting protein [Mus musculus (house mouse)]

Gene ID: 227929, updated on 13-Mar-2020

Summary



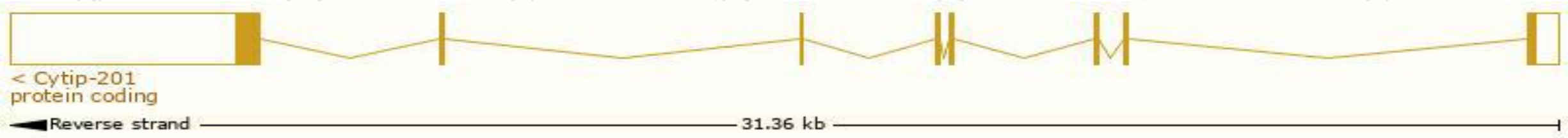
Official Symbol	Cytip provided by MGI
Official Full Name	cytohesin 1 interacting protein provided by MGI
Primary source	MGI:MGI:2183535
See related	Ensembl:ENSMUSG00000026832
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A130053M09Rik, AI462064, C80816, Cbp, Cybr, Pscdbp
Expression	Biased expression in thymus adult (RPKM 15.2), spleen adult (RPKM 14.5) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

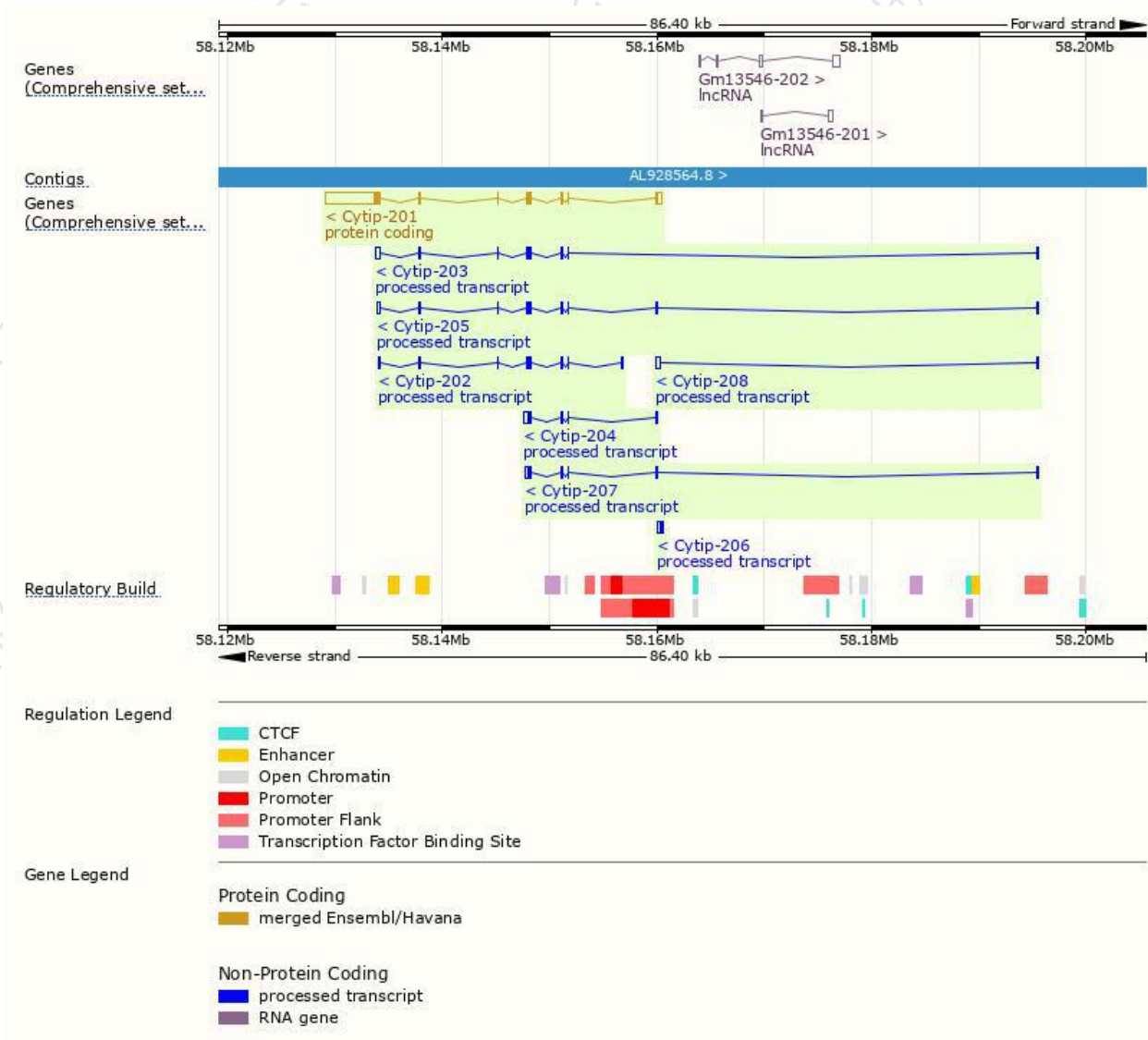
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cytip-201	ENSMUST00000028175.6	6110	359aa	Protein coding	CCDS16048	Q91VY6	TSL:1 GENCODE basic APPRIS P1
Cytip-205	ENSMUST00000148764.7	941	No protein	Processed transcript	-	-	TSL:3
Cytip-203	ENSMUST00000144117.7	856	No protein	Processed transcript	-	-	TSL:2
Cytip-204	ENSMUST00000146545.7	856	No protein	Processed transcript	-	-	TSL:1
Cytip-207	ENSMUST00000151785.1	686	No protein	Processed transcript	-	-	TSL:1
Cytip-202	ENSMUST00000131443.7	641	No protein	Processed transcript	-	-	TSL:5
Cytip-206	ENSMUST00000151169.1	387	No protein	Processed transcript	-	-	TSL:2
Cytip-208	ENSMUST00000153052.1	378	No protein	Processed transcript	-	-	TSL:3

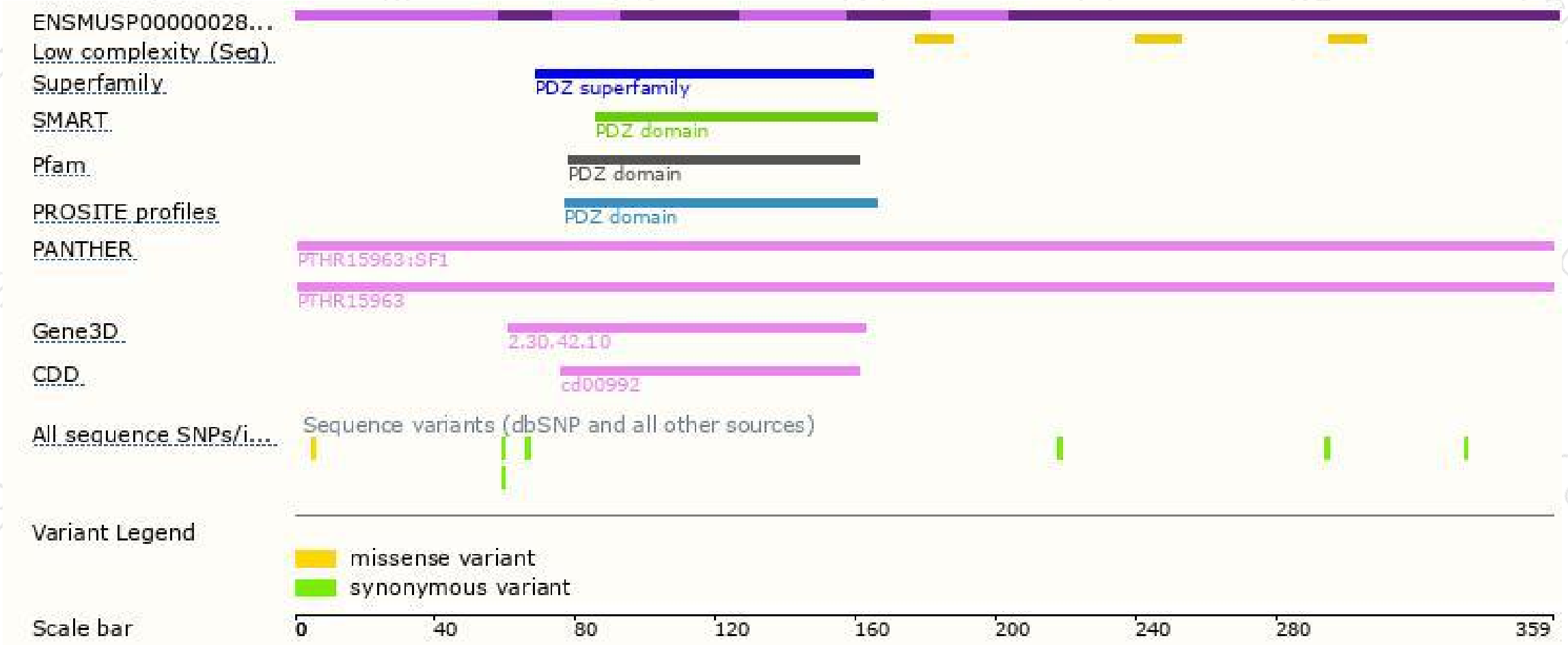
The strategy is based on the design of *Cytip-201* transcript,the transcription is shown below:



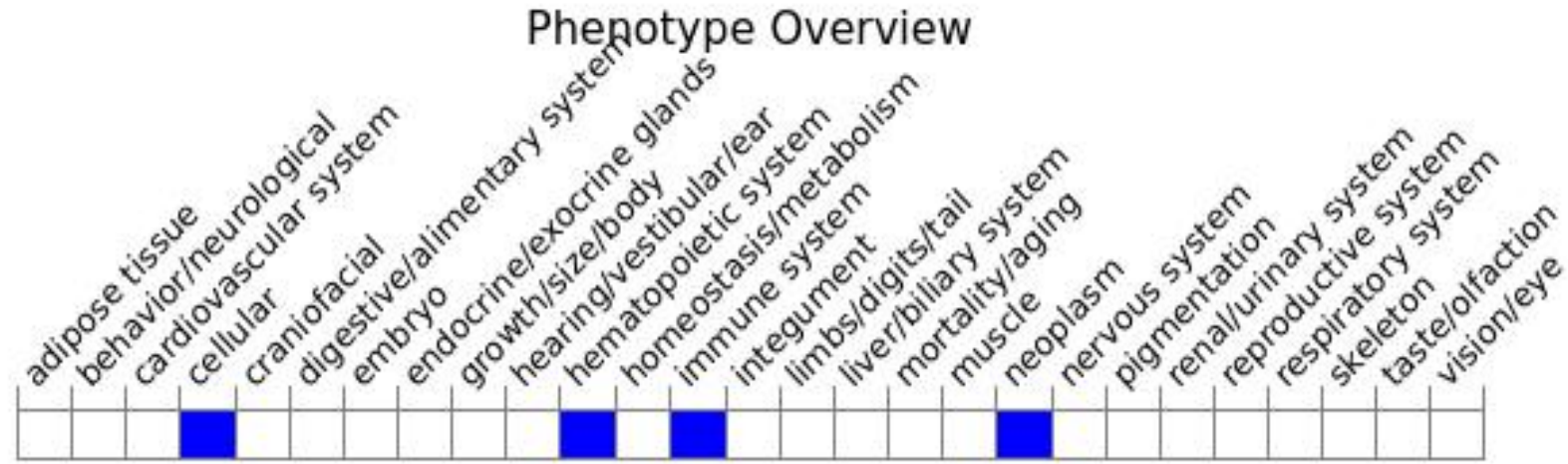
Genomic location distribution



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, mice homozygous for a null allele display impaired trafficking and/or cell adhesion of immune system cells. Mice homozygous for a reporter allele show normal immune cell development and function however, mutant hematopoietic stem cells have impaired repopulating activity.

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

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