

Flt1 Cas9-KO Strategy

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Project Overview

Project Name

Flt1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Flt1* gene. The schematic diagram is as follows:



- The *Flt1* gene has 6 transcripts. According to the structure of *Flt1* gene, exon2-exon4 of *Flt1-202* (ENSMUST00000031653.11) transcript is recommended as the knockout region. The region contains 452bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Flt1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit an excess of hemangioblasts resulting in an overgrowth of endothelial cells, abnormalities of vascular channels and blood islands, and lethality at the mid-somite developmental stage.
- The *Flt1* gene is located on the Chr5. 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)

Flt1 FMS-like tyrosine kinase 1 [Mus musculus (house mouse)]

Gene ID: 14254, updated on 3-Mar-2019

Summary



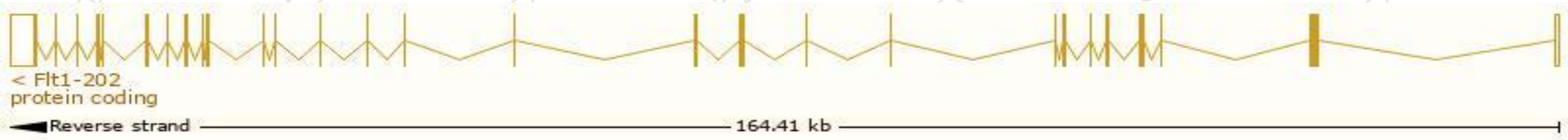
Official Symbol	Flt1 provided by MGI
Official Full Name	FMS-like tyrosine kinase 1 provided by MGI
Primary source	MGI:MGI:95558
See related	Ensembl:ENSMUSG00000029648
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323757, Flt-1, VEGFR-1, VEGFR1, sFlt1
Expression	Biased expression in placenta adult (RPKM 35.7), lung adult (RPKM 11.8) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

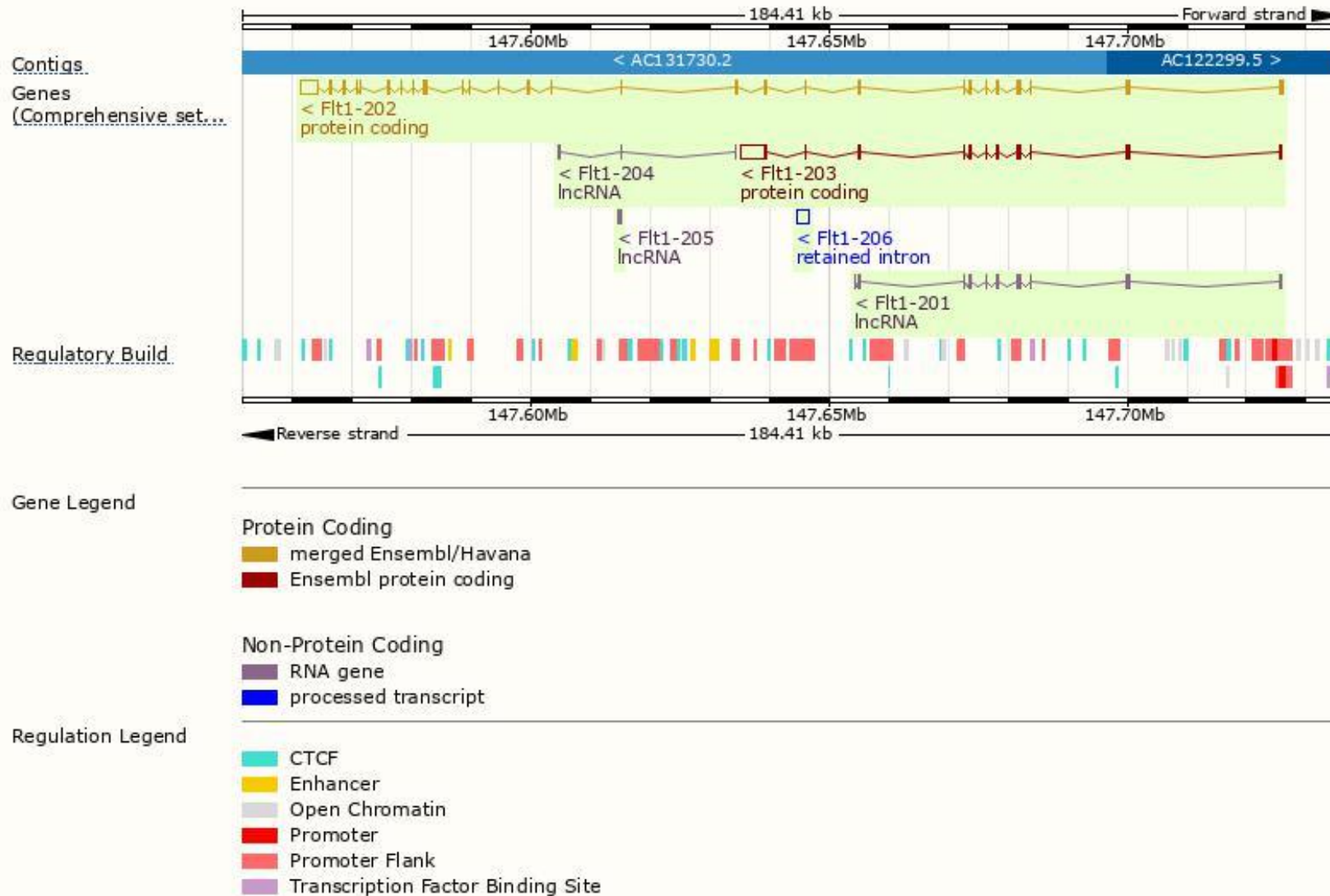
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Flt1-202	ENSMUST00000031653.11	6895	1333aa	Protein coding	CCDS19879	A0A0R4J0A4	TSL:1 GENCODE basic APPRIS P1
Flt1-203	ENSMUST00000110529.5	6292	688aa	Protein coding	-	Q55095	TSL:1 GENCODE basic
Flt1-206	ENSMUST00000200895.1	2030	No protein	Retained intron	-	-	TSL:NA
Flt1-201	ENSMUST00000031652.4	2049	No protein	lncRNA	-	-	TSL:1
Flt1-204	ENSMUST00000125272.1	395	No protein	lncRNA	-	-	TSL:5
Flt1-205	ENSMUST00000142477.1	274	No protein	lncRNA	-	-	TSL:2

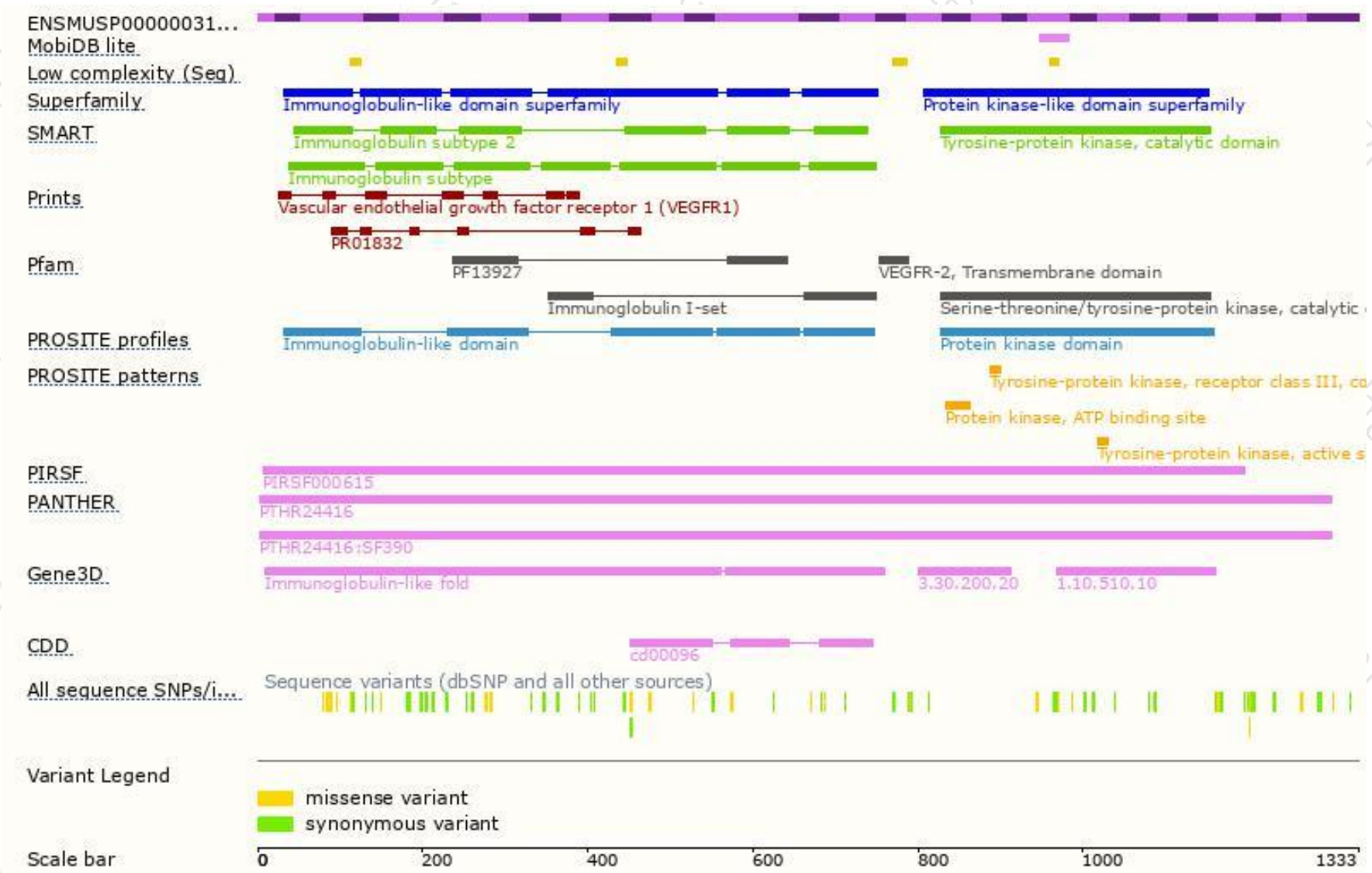
The strategy is based on the design of *Flt1-202* transcript,The transcription is shown below



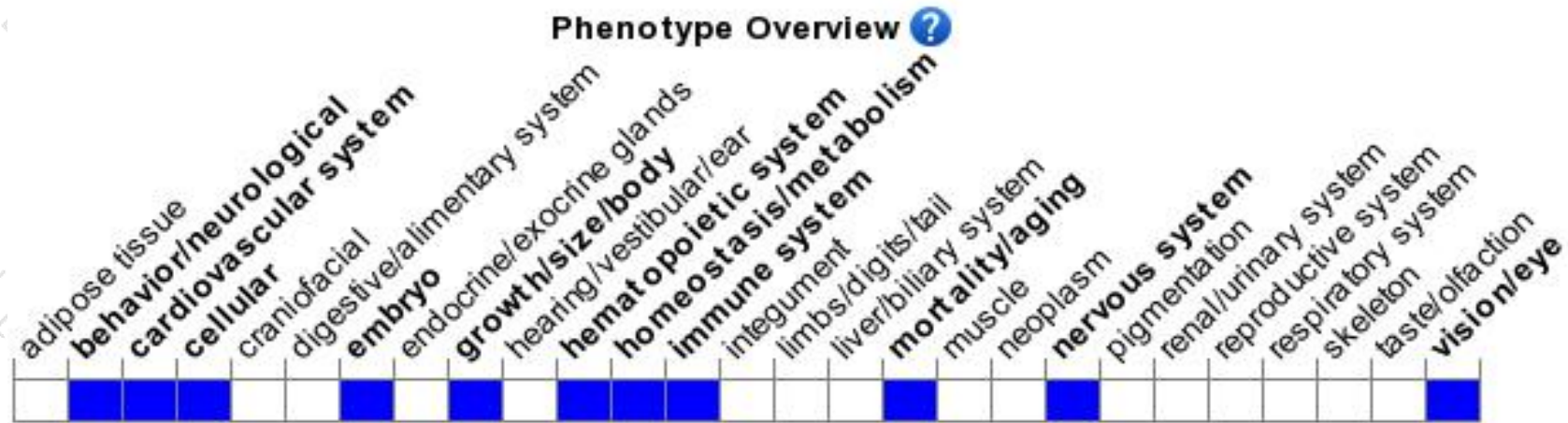
Genomic location distribution



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, Homozygotes for targeted null mutations exhibit an excess of hemangioblasts resulting in an overgrowth of endothelial cells, abnormalities of vascular channels and blood islands, and lethality at the mid-somite developmental stage.

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

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