

Ift140 Cas9-KO Strategy

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Design Date:

2019-12-16

Project Overview

Project Name

Ift140

Project type

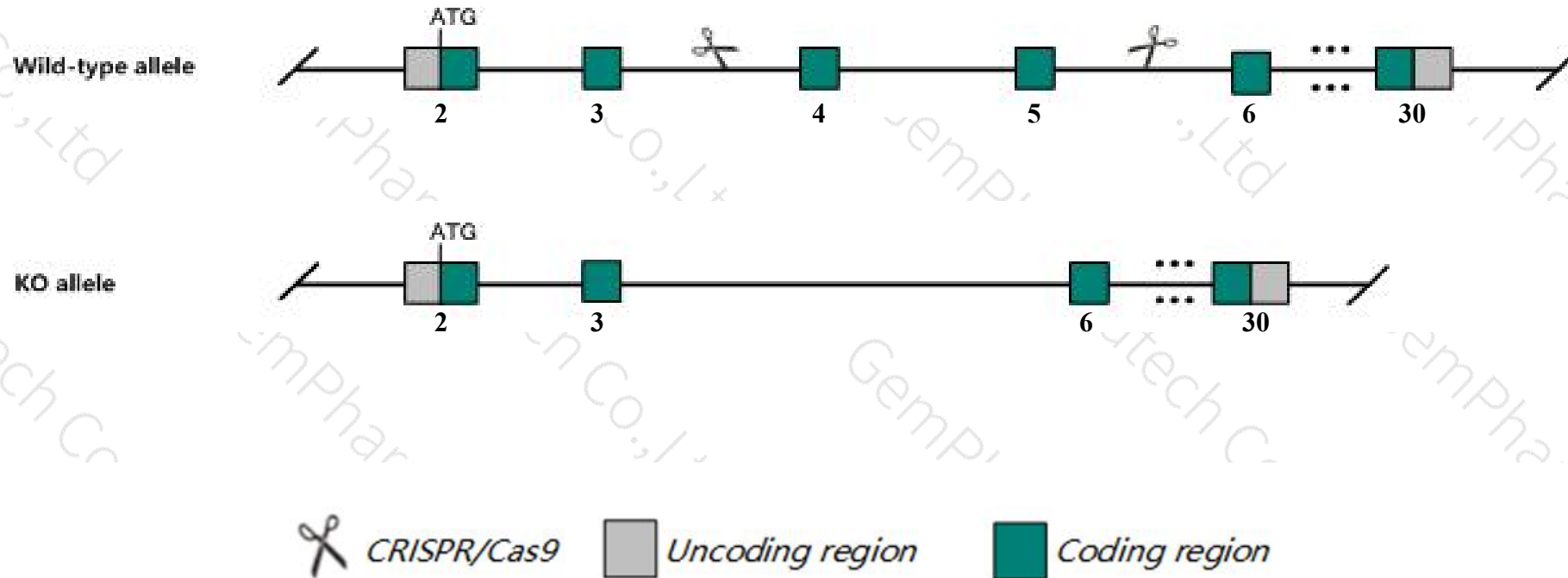
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ift140* gene. The schematic diagram is as follows:



- The *Ift140* gene has 9 transcripts. According to the structure of *Ift140* gene, exon4-exon5 of *Ift140-201* (ENSMUST00000024983.11) transcript is recommended as the knockout region. The region contains 265bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ift140* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a reporter knock-out allele die at mid-gestation. Mice homozygous for an ENU-induced mutation exhibit cardiovascular defects and situs abnormalities.
- The *Ift140* gene is located on the Chr17. 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)

Ift140 intraflagellar transport 140 [Mus musculus (house mouse)]

Gene ID: 106633, updated on 9-Apr-2019

Summary



Official Symbol	Ift140 provided by MGI
Official Full Name	intraflagellar transport 140 provided by MGI
Primary source	MGI:MGI:2146906
See related	Ensembl:ENSMUSG000000024169
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	Al661311, Tce5, Wdtd2, mKIAA0590
Expression	Broad expression in testis adult (RPKM 39.8), liver E14.5 (RPKM 18.4) and 23 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

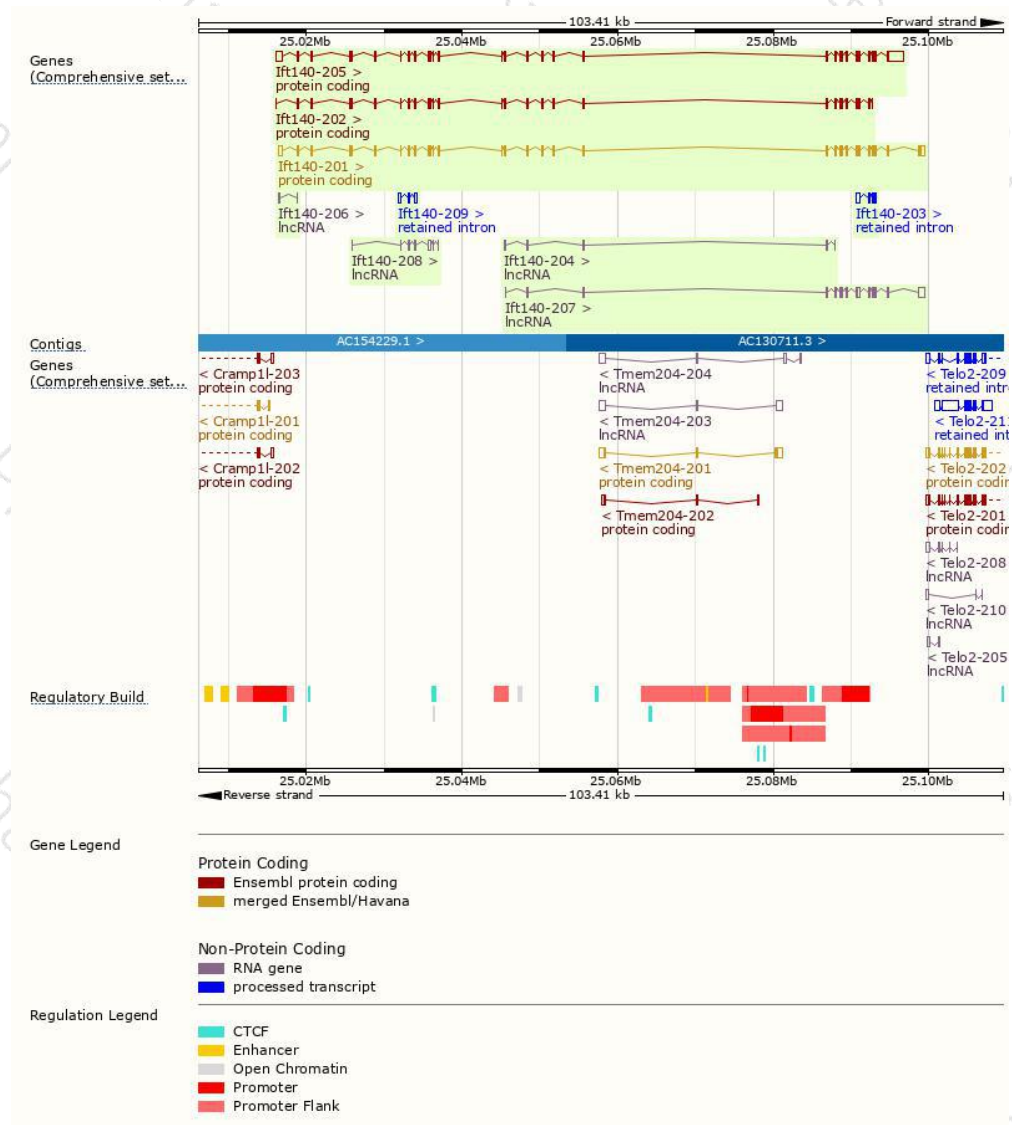
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ift140-201	ENSMUST00000024983.11	5489	1464aa	Protein coding	CCDS28505	E9PY46	TSL:1 GENCODE basic APPRIS P2
Ift140-205	ENSMUST00000142000.8	6942	1421aa	Protein coding	-	A0A3B2W3F6	TSL:1 GENCODE basic APPRIS ALT2
Ift140-202	ENSMUST00000137386.7	3774	1232aa	Protein coding	-	E9Q682	CDS 3' incomplete TSL:5
Ift140-203	ENSMUST00000139300.1	908	No protein	Retained intron	-	-	TSL:3
Ift140-209	ENSMUST00000232788.1	846	No protein	Retained intron	-	-	
Ift140-207	ENSMUST00000153895.7	2938	No protein	lncRNA	-	-	TSL:1
Ift140-208	ENSMUST00000156945.1	740	No protein	lncRNA	-	-	TSL:3
Ift140-204	ENSMUST00000140692.7	734	No protein	lncRNA	-	-	TSL:3
Ift140-206	ENSMUST00000151776.1	343	No protein	lncRNA	-	-	TSL:2

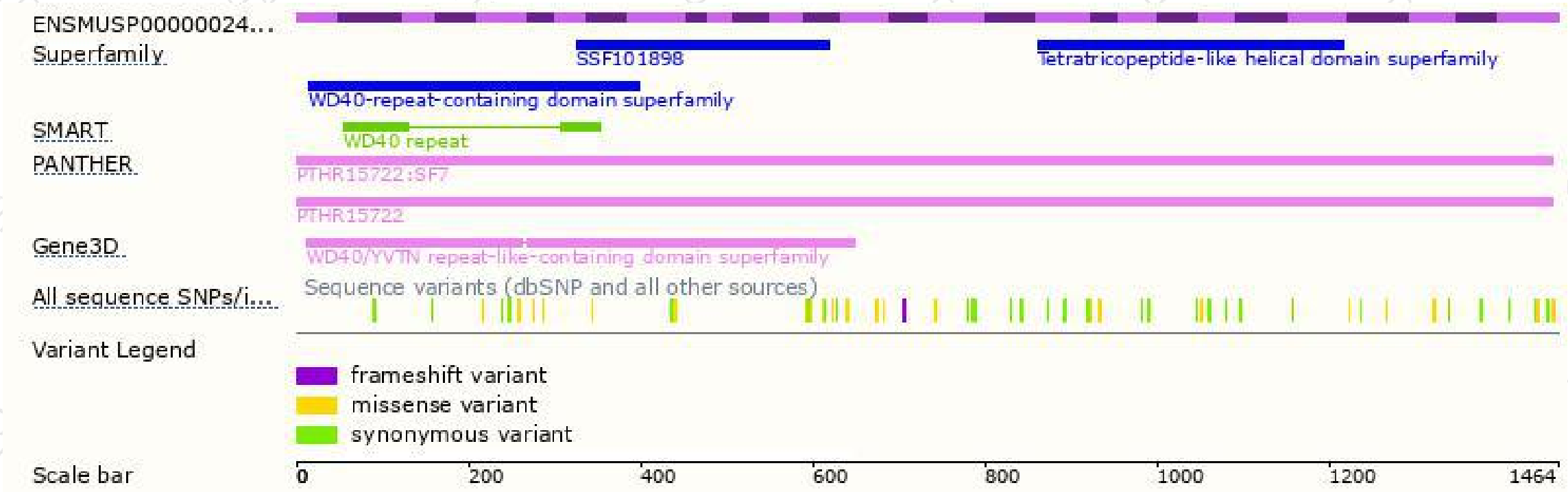
The strategy is based on the design of *Ift140-201* transcript,The transcription is shown below



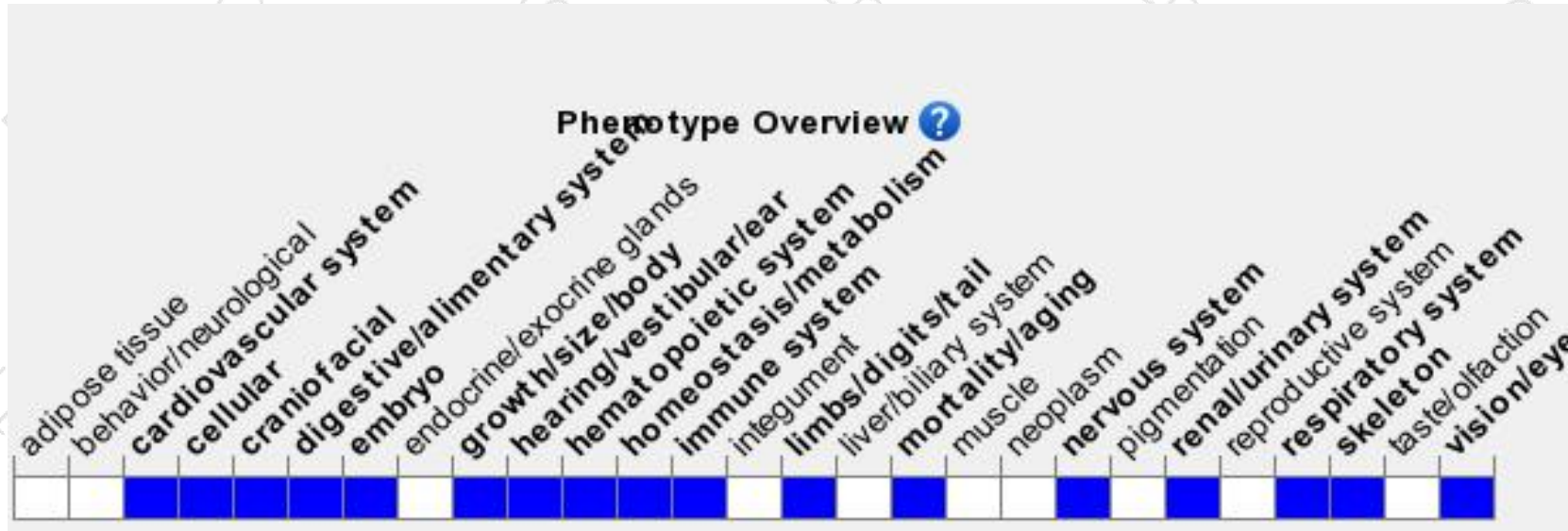
Genomic location distribution



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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