

# *Ift88* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-7-25**

# Project Overview



**Project Name**

***Ift88***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ift88* gene. The schematic diagram is as follows:



- The *Ift88* gene has 5 transcripts. According to the structure of *Ift88* gene, exon8-exon9 of *Ift88-201* (ENSMUST00000122063.7) transcript is recommended as the knockout region. The region contains 196bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ift88* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a null allele display early to mid-gestation lethality, random patterning of the left-right body axis, neural tube defects, pericardial sac expansion, enlarged limb buds, polydactyly, and absent embryonic node cilia.
- The *Ift88* gene is located on the Chr14. 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)

## Ift88 intraflagellar transport 88 [Mus musculus (house mouse)]

Gene ID: 21821, updated on 9-Apr-2019

### Summary



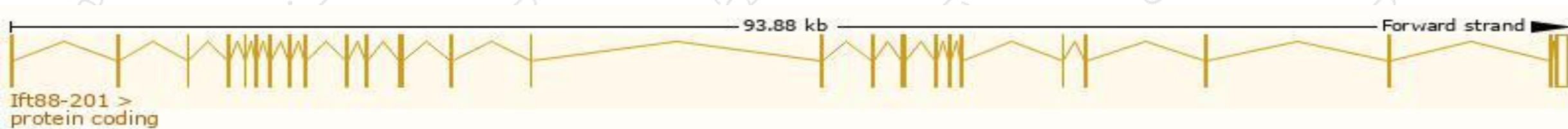
<b>Official Symbol</b>	Ift88 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	intraflagellar transport 88 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:98715</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000040040</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AW552028, Tg737, Tg737Rpw, TgN737Rpw, Ttc10, flexo, fxo, orpk, polaris
<b>Expression</b>	Broad expression in testis adult (RPKM 6.4), CNS E14 (RPKM 4.7) and 23 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

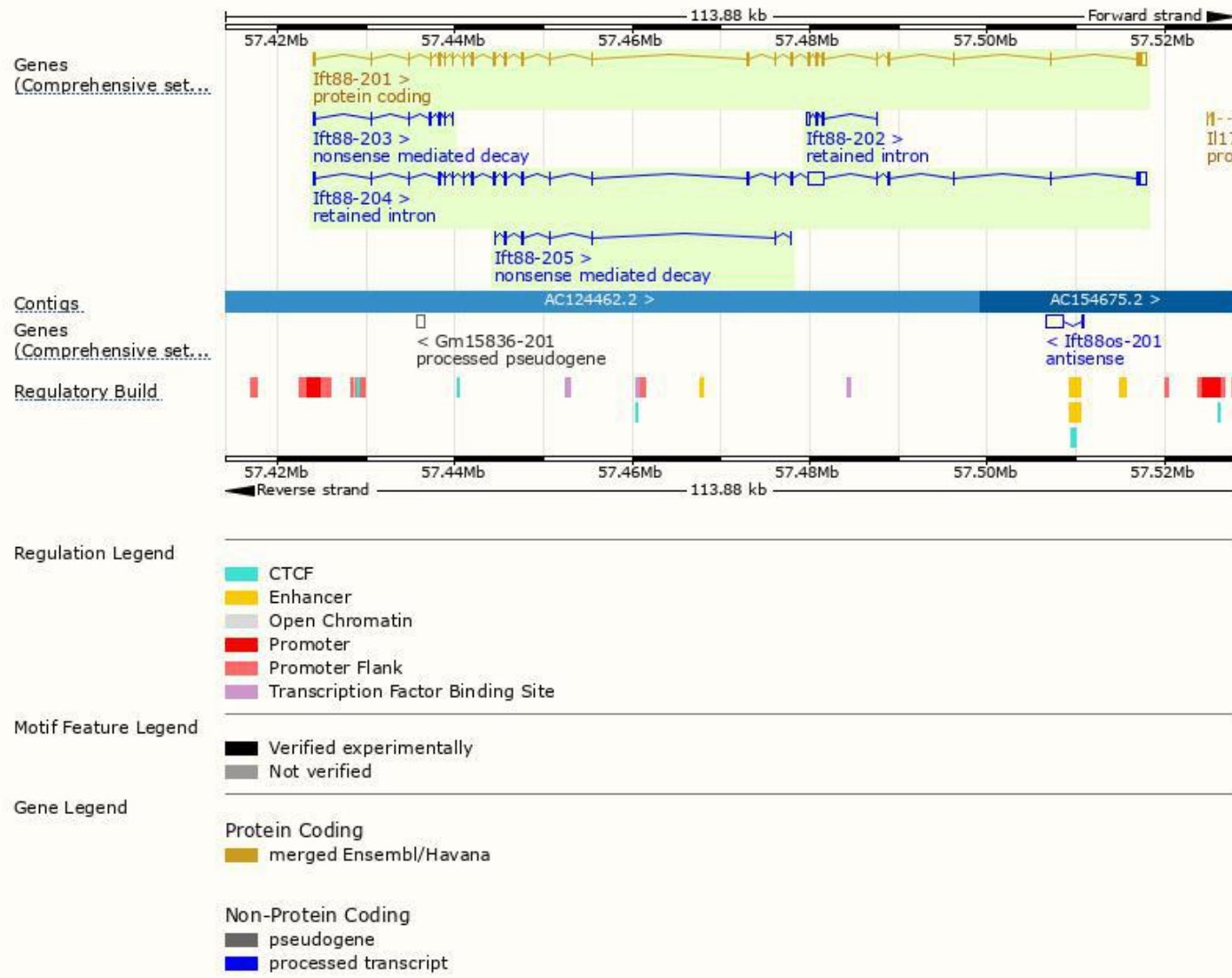
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ift88-201	<a href="#">ENSMUST00000122063.7</a>	3088	<a href="#">825aa</a>	Protein coding	<a href="#">CCDS36937</a>	<a href="#">G3X9Z7</a>	TSL:1 GENCODE basic APPRIS P1
Ift88-205	<a href="#">ENSMUST00000171682.1</a>	686	<a href="#">175aa</a>	Nonsense mediated decay	-	<a href="#">F6QZ23</a>	CDS 5' incomplete TSL:5
Ift88-203	<a href="#">ENSMUST00000150296.7</a>	562	<a href="#">54aa</a>	Nonsense mediated decay	-	<a href="#">D6RJ41</a>	TSL:5
Ift88-204	<a href="#">ENSMUST00000154492.1</a>	4226	No protein	Retained intron	-	-	TSL:2
Ift88-202	<a href="#">ENSMUST00000139943.1</a>	667	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Ift88-201* transcript, The transcription is shown below

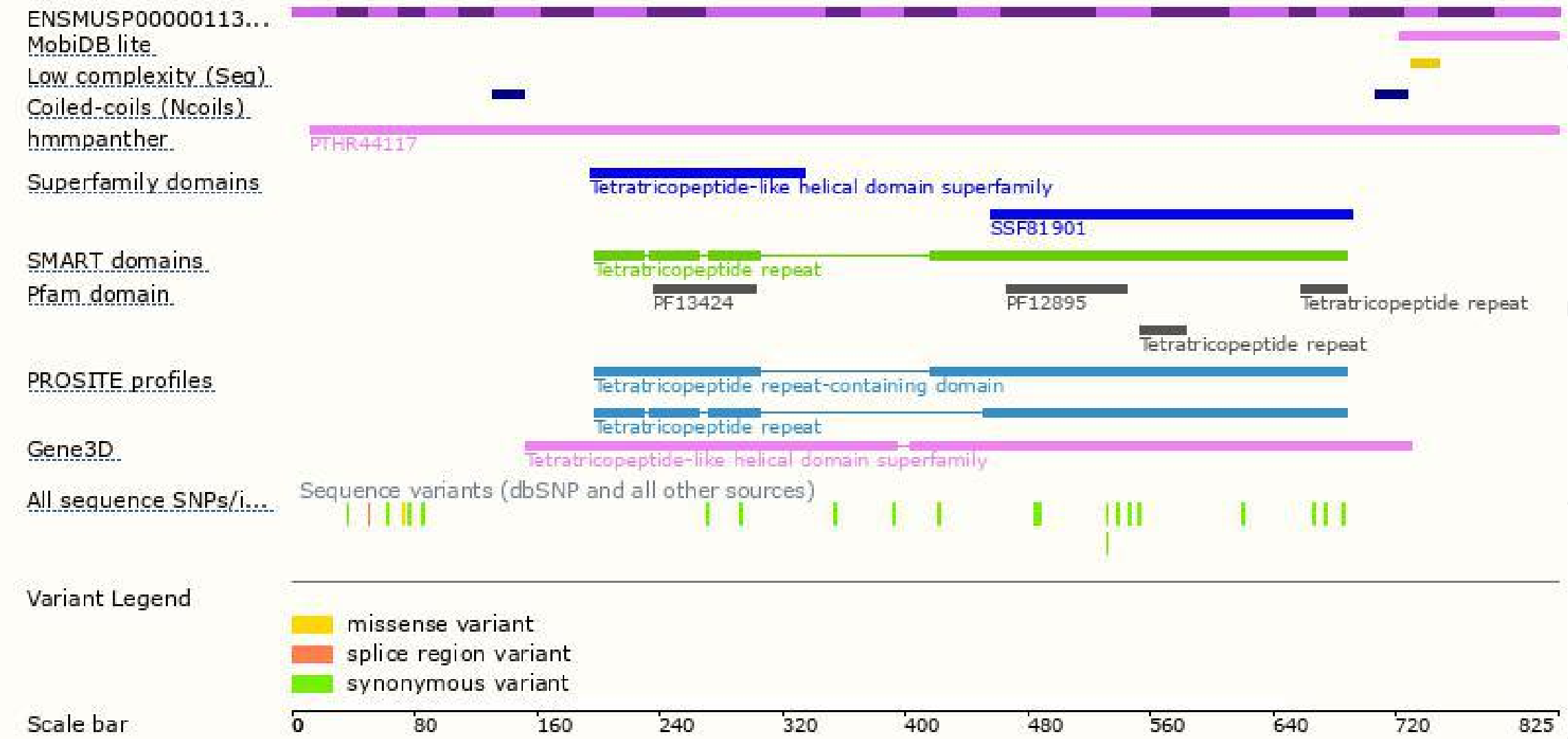


# Genomic location distribution

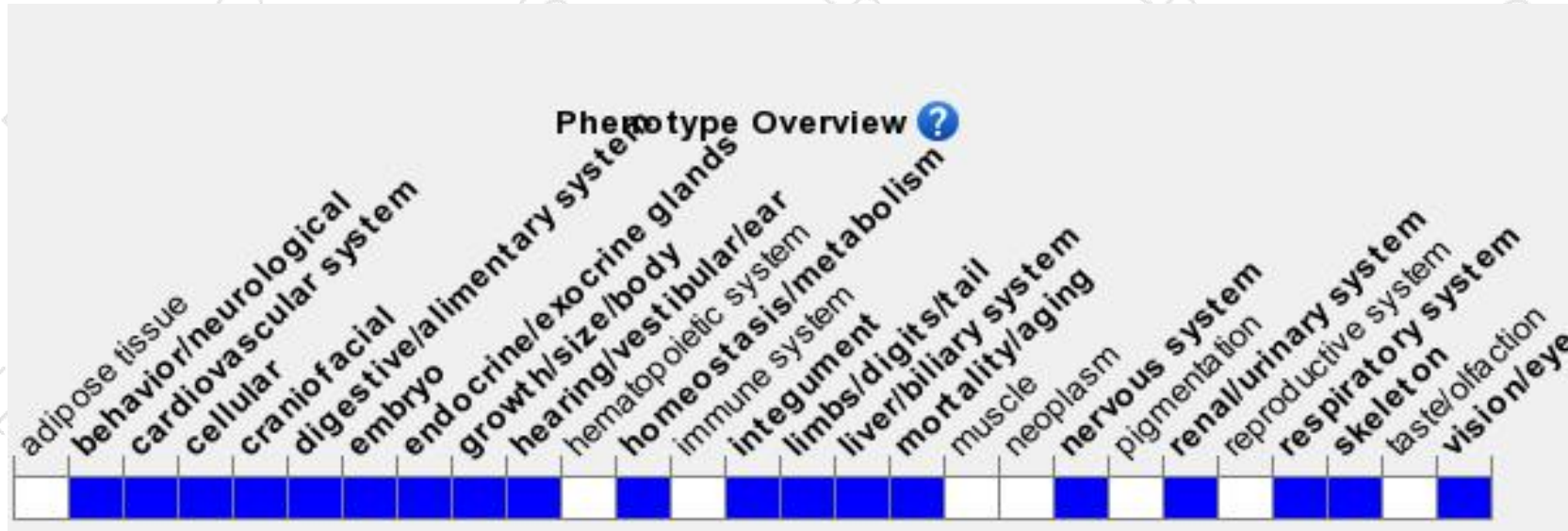




# Protein domain



# 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 early to mid-gestation lethality, random patterning of the left-right body axis, neural tube defects, pericardial sac expansion, enlarged limb buds, polydactyly, and absent embryonic node cilia.

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

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