Intu Cas9-KO Strategy

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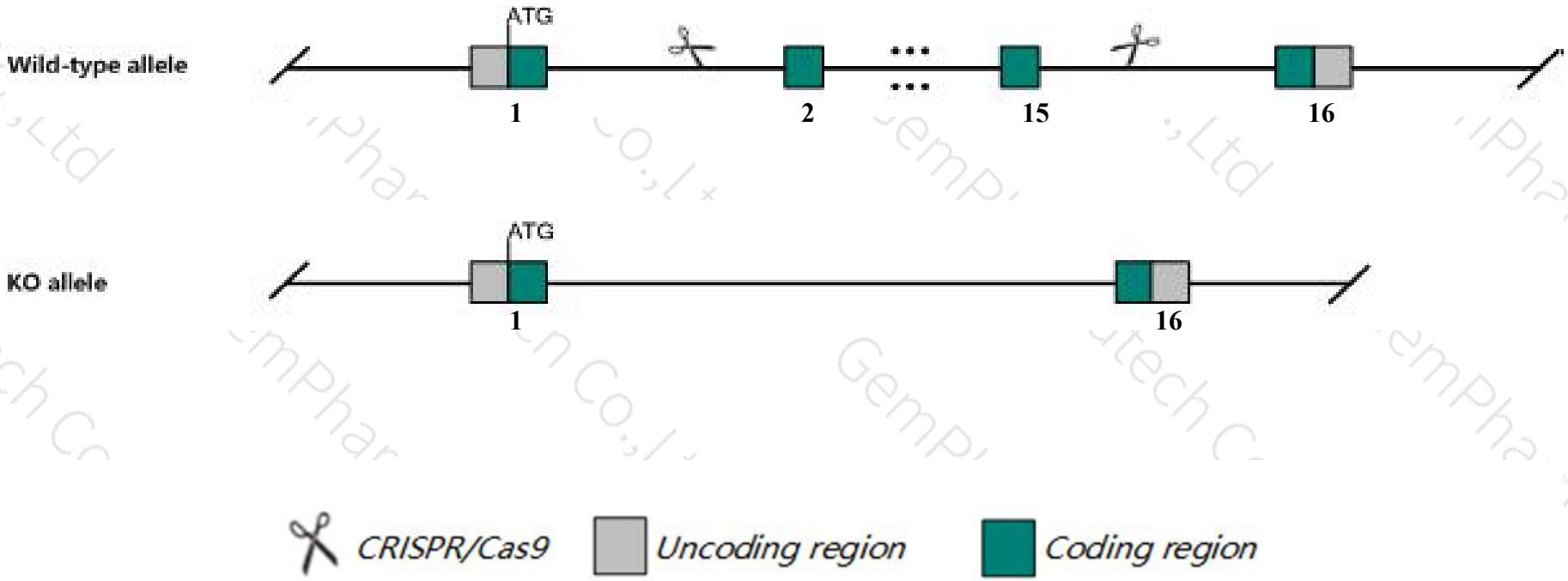
Project Overview

Project Name	***Intu***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Intu* gene has 3 transcripts. According to the structure of *Intu* gene, exon2-exon15 of *Intu-202* (ENSMUST00000091186.6) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Intu* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Homozygous null mice show defective ciliogenesis and neural tube closure, abnormal patterning of the CNS and limbs, polydactyly, edema and death by E16.5. Homozygotes for a hypomorphic allele show defective ciliation and endochondral ossification, stunted growth, polydactyly and postnatal lethality.
- The KO region contains functional region of the *Gm16114* gene.Knockout the region may affect the function of *Gm16114* gene.
- The *Intu* gene is located on the Chr3. 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）

集萃药康 GemPharmatech

Intu inturned planar cell polarity protein [Mus musculus (house mouse)]

Gene ID: 380614, updated on 31-Jan-2019

Summary

Official Symbol	Intu provided by MGI
Official Full Name	inturned planar cell polarity protein provided by MGI
Primary source	MGI:MGI:2443752
See related	Ensembl:ENSMUSG00000060798
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	9230116I04Rik, 9430087H23Rik, Pdzd6, Pdzk6, mKIAA1284
Expression	Broad expression in heart adult (RPKM 2.7), CNS E11.5 (RPKM 2.3) and 26 other tissues See more
Orthologs	human all

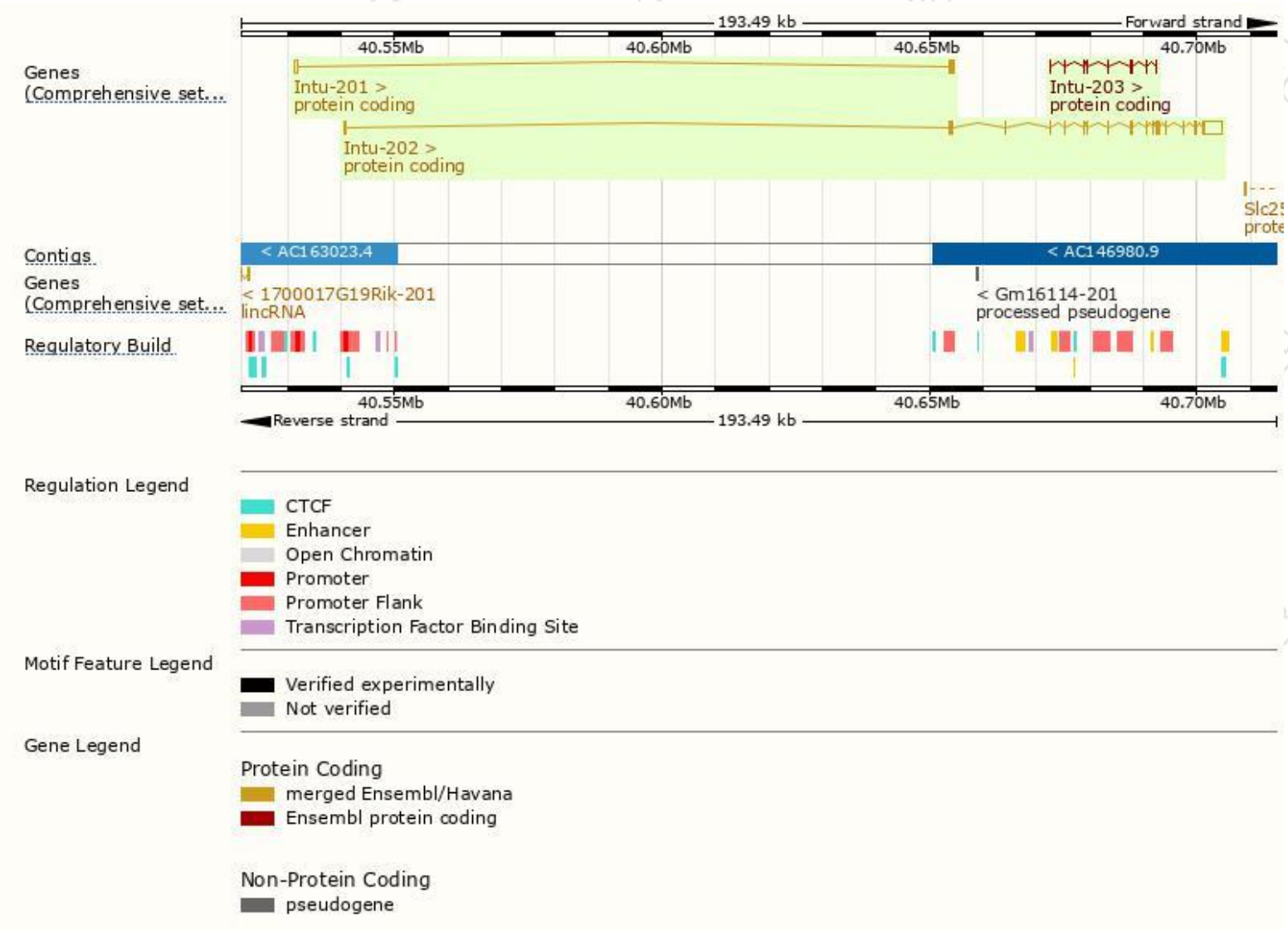
Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

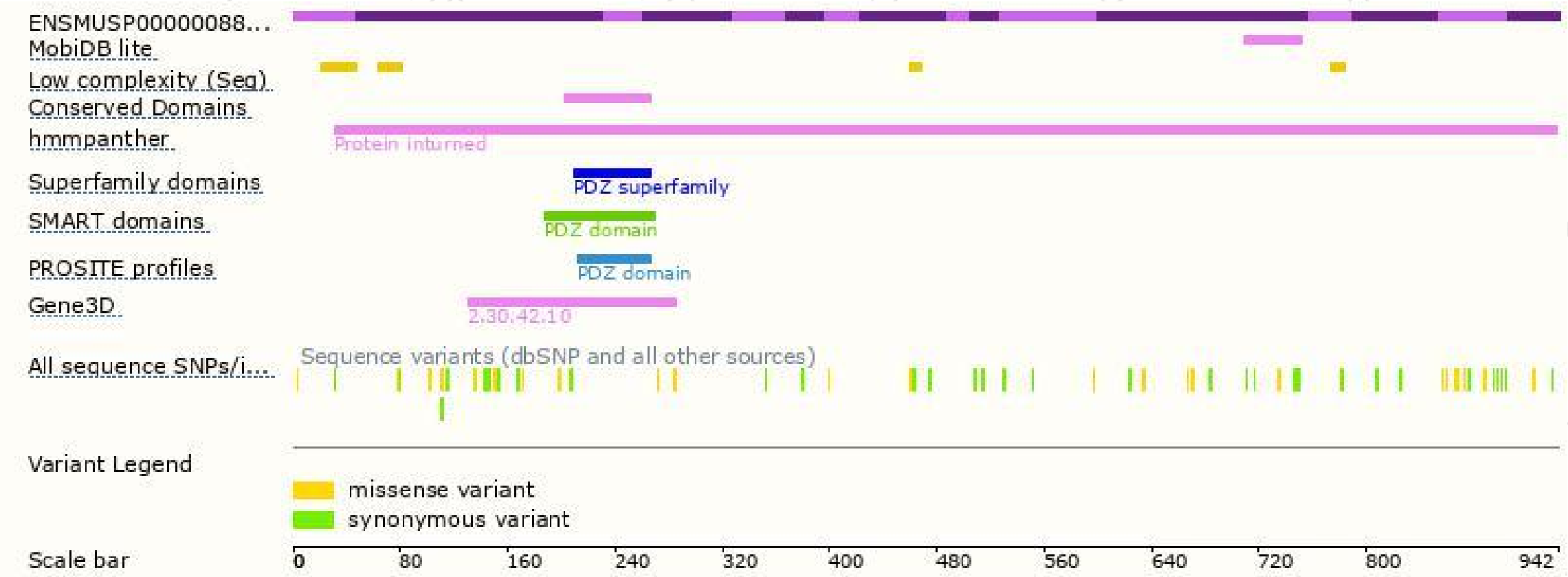
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Intu-202	ENSMUST00000091186.6	6387	942aa	Protein coding	CCDS84619	Q059U7	TSL:1 GENCODE basic APPRIS P2
Intu-201	ENSMUST00000061590.5	1589	229aa	Protein coding	-	Q059U7	TSL:2 GENCODE basic APPRIS ALT2
Intu-203	ENSMUST00000204176.1	774	258aa	Protein coding	-	A0A0N4SUY7	CDS 5' and 3' incomplete TSL:5 APPRIS ALT2

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

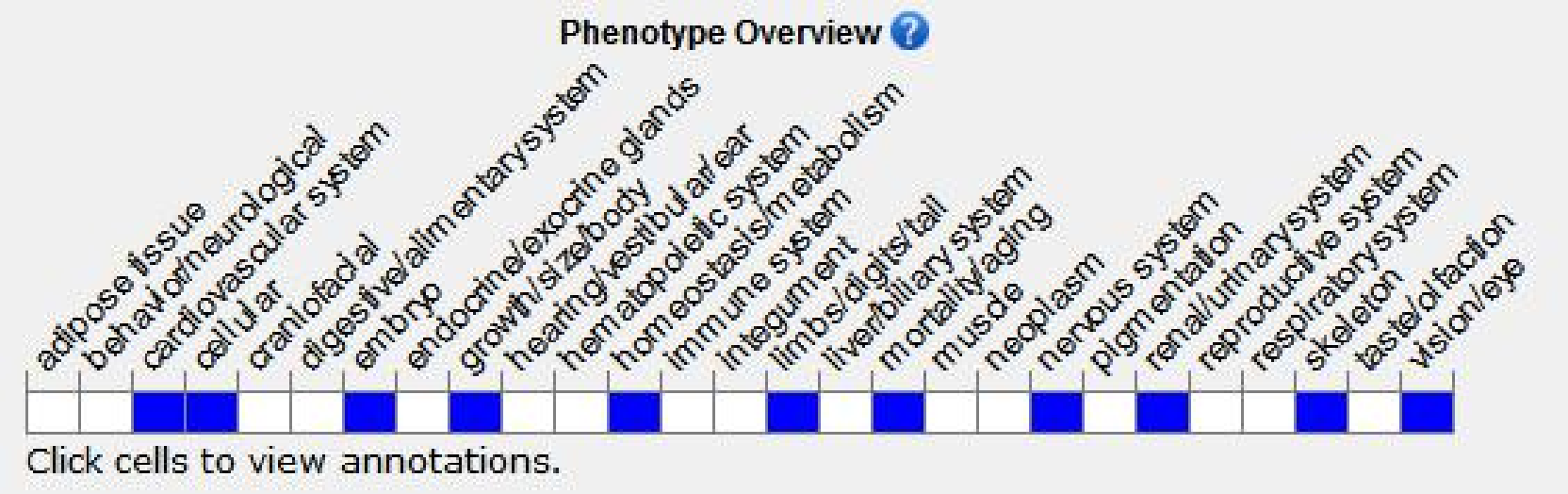
Genomic location distribution



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/).

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

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