Wdr11 Cas9-CKO Strategy

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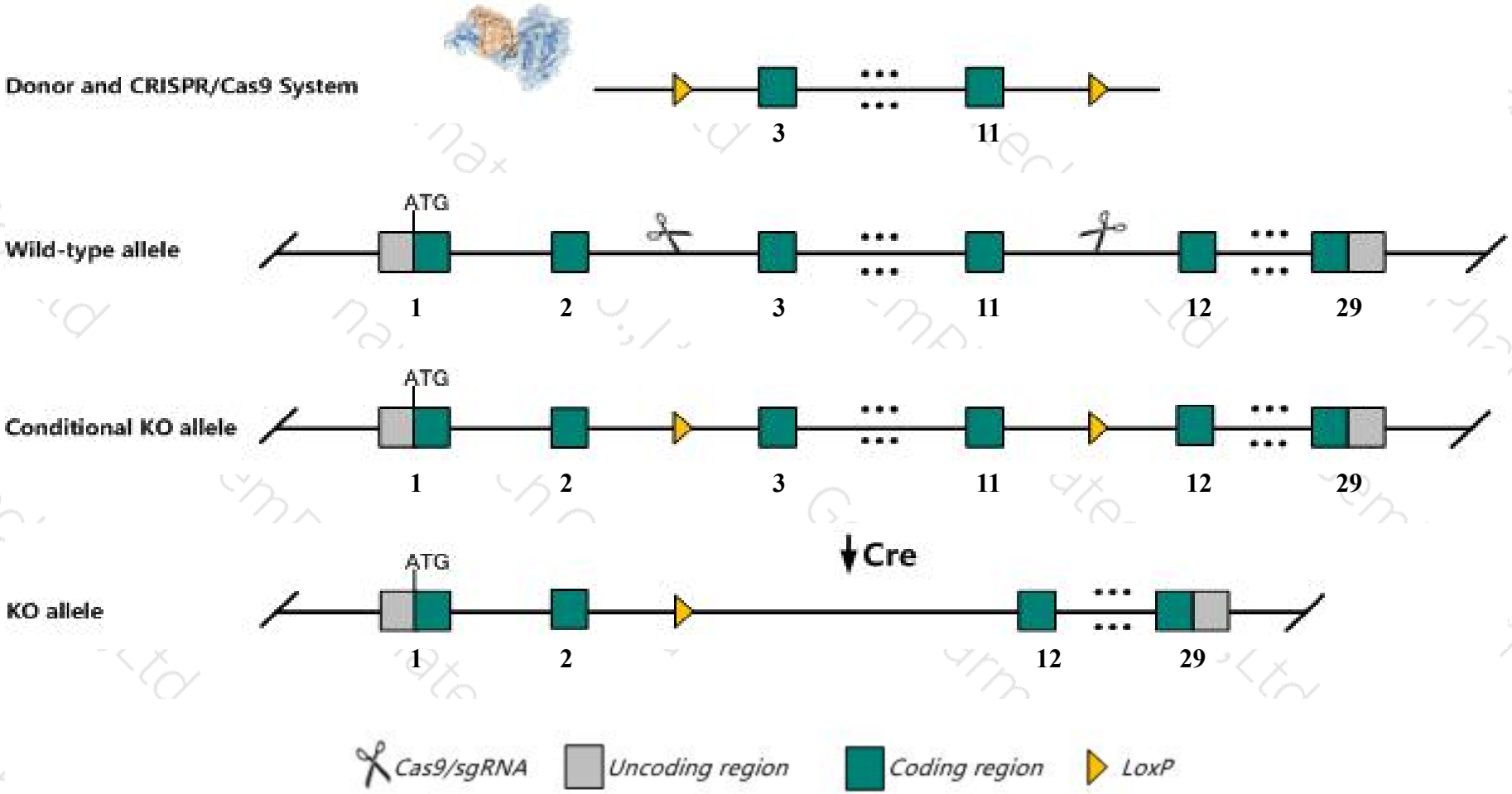
Project Overview

Project Name	***Wdr11***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr11* gene. The schematic diagram is as follows:



Technical routes

➢ The *Wdr11* gene has 9 transcripts. According to the structure of *Wdr11* gene, exon3-exon11 of *Wdr11-201*(ENSMUST00000084519.6) transcript is recommended as the knockout region.The region contains 1355bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Wdr11* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➢ The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ According to the existing MGI data,nullizygous mice show mid-gestational and perinatal lethality and developmental anomalies associated with defective Hh signalling and ciliogenesis, including eye, skeletal, heart and craniofacial defects, holoprosencephaly, pituitary dysgenesis, delayed puberty, reproductive dysfunction and obesity.

➢ Transcript *Wdr11*-202&204 may not be affected.

➢ The effect on transcript *Wdr11*-209 is unknown.

➢ The *Wdr11* gene is located on the Chr7. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Wdr11 WD repeat domain 11 [Mus musculus (house mouse)]

Gene ID: 207425, updated on 13-Mar-2020

Summary

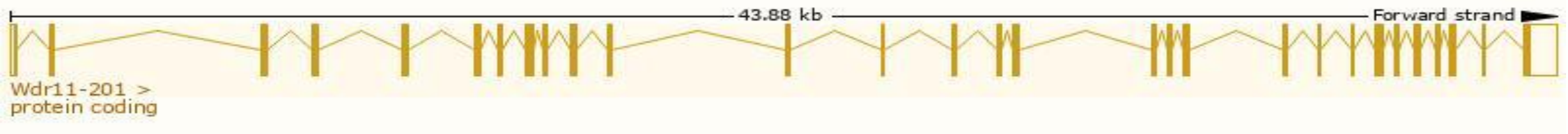
Official Symbol	Wdr11 provided by MGI
Official Full Name	WD repeat domain 11 provided byMGI
Primary source	MGI:MGI:1920230
See related	Ensembl:ENSMUSG00000042055
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900055P10Rik, AW489876, Brwd2, mKIAA1351
Expression	Ubiquitous expression in limb E14.5 (RPKM 10.9), CNS E11.5 (RPKM 9.5) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

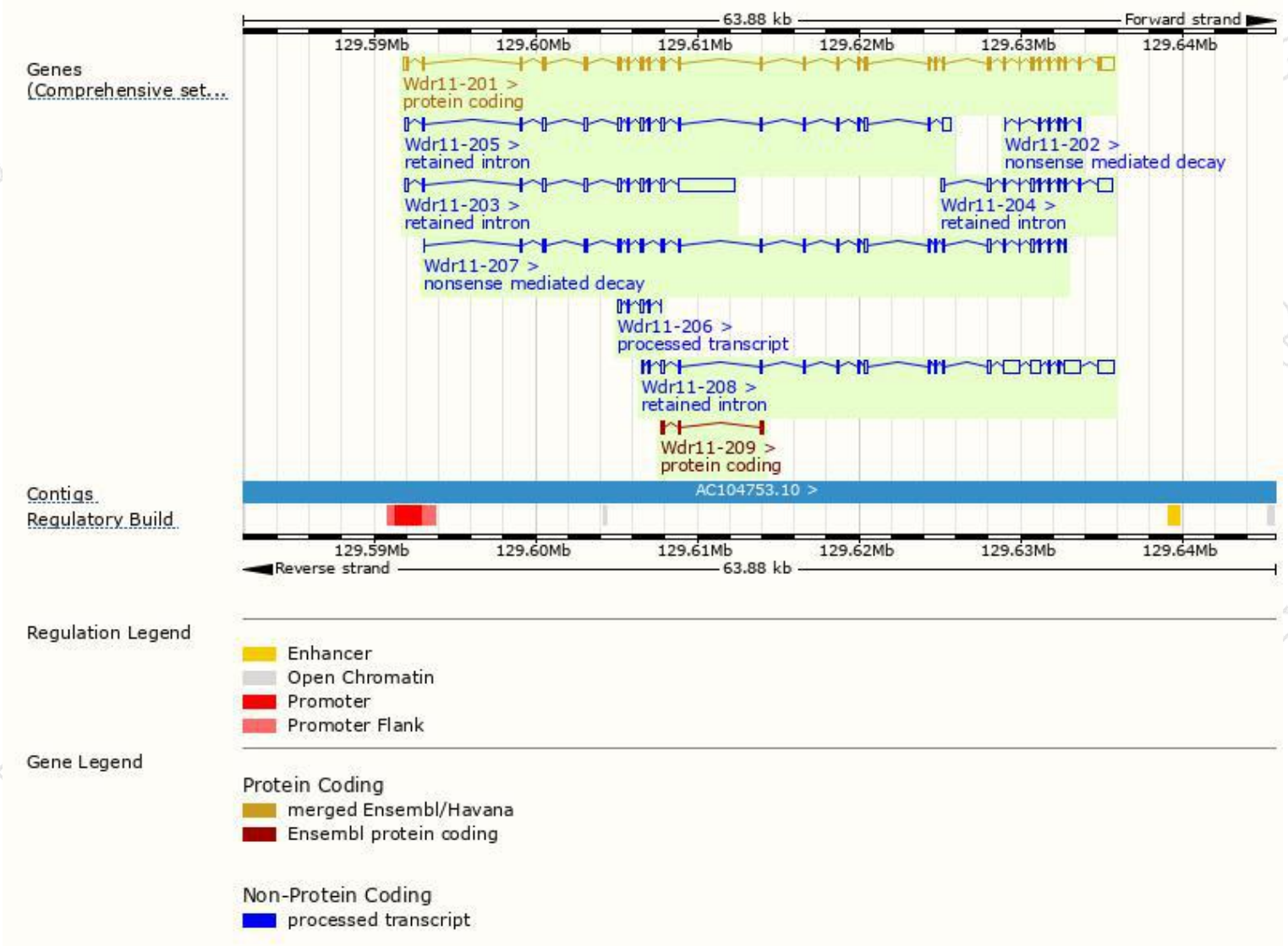
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wdr11-201	ENSMUST00000084519.6	4550	1223aa	Protein coding	CCDS40155	G5E8J3	TSL:1 GENCODE basic APPRIS P1
Wdr11-209	ENSMUST00000206442.1	402	123aa	Protein coding	-	A0A0U1RQ34	CDS 5' incomplete TSL:3
Wdr11-207	ENSMUST00000148752.7	3155	387aa	Nonsense mediated decay	-	A0A0U1RQ40	CDS 5' incomplete TSL:5
Wdr11-202	ENSMUST00000136560.2	618	34aa	Nonsense mediated decay	-	A0A0U1RPD4	CDS 5' incomplete TSL:5
Wdr11-206	ENSMUST00000143849.7	558	No protein	Processed transcript	-	-	TSL:2
Wdr11-208	ENSMUST00000149541.7	5418	No protein	Retained intron	-	-	TSL:2
Wdr11-203	ENSMUST00000136734.7	4989	No protein	Retained intron	-	-	TSL:1
Wdr11-205	ENSMUST00000143422.7	2780	No protein	Retained intron	-	-	TSL:1
Wdr11-204	ENSMUST00000140877.7	2191	No protein	Retained intron	-	-	TSL:1

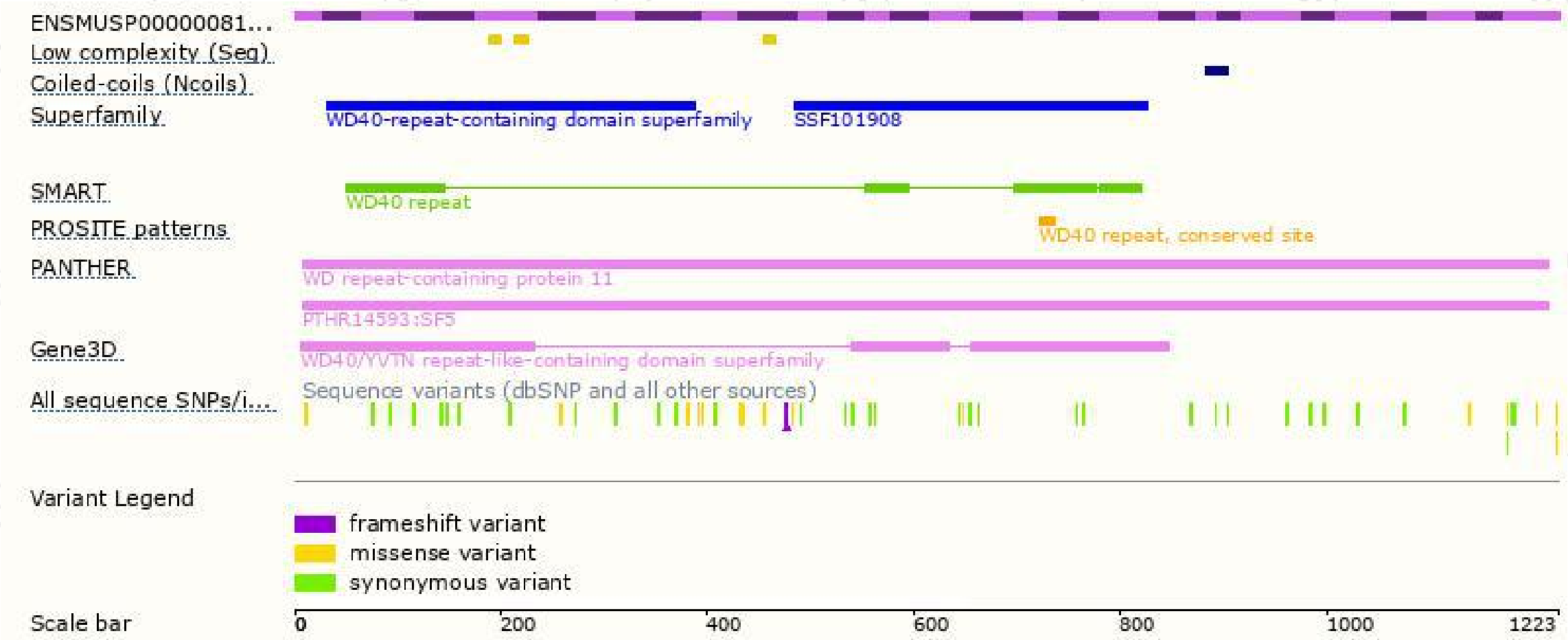
The strategy is based on the design of *Wdr11-201* transcript,the transcription is shown below:



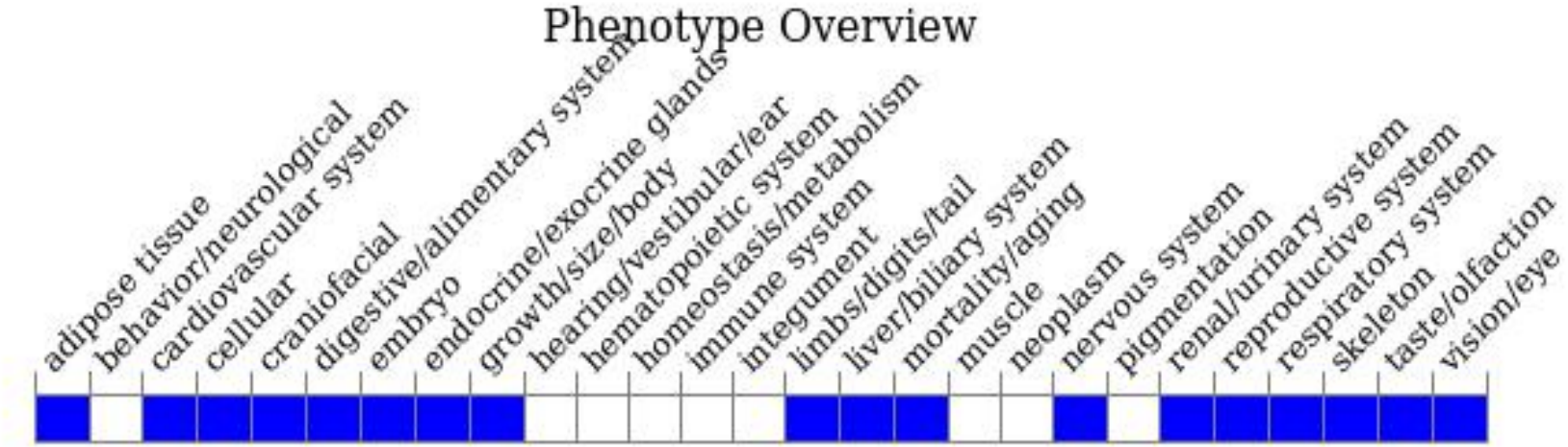
Genomic location distribution



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,nullizygous mice show mid-gestational and perinatal lethality and developmental anomalies associated with defective Hh signalling and ciliogenesis, including eye, skeletal, heart and craniofacial defects, holoprosencephaly, pituitary dysgenesis, delayed puberty, reproductive dysfunction and obesity.

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

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