

Qdpr Cas9-CKO Strategy

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Project Overview

Project Name

Qdpr

Project type

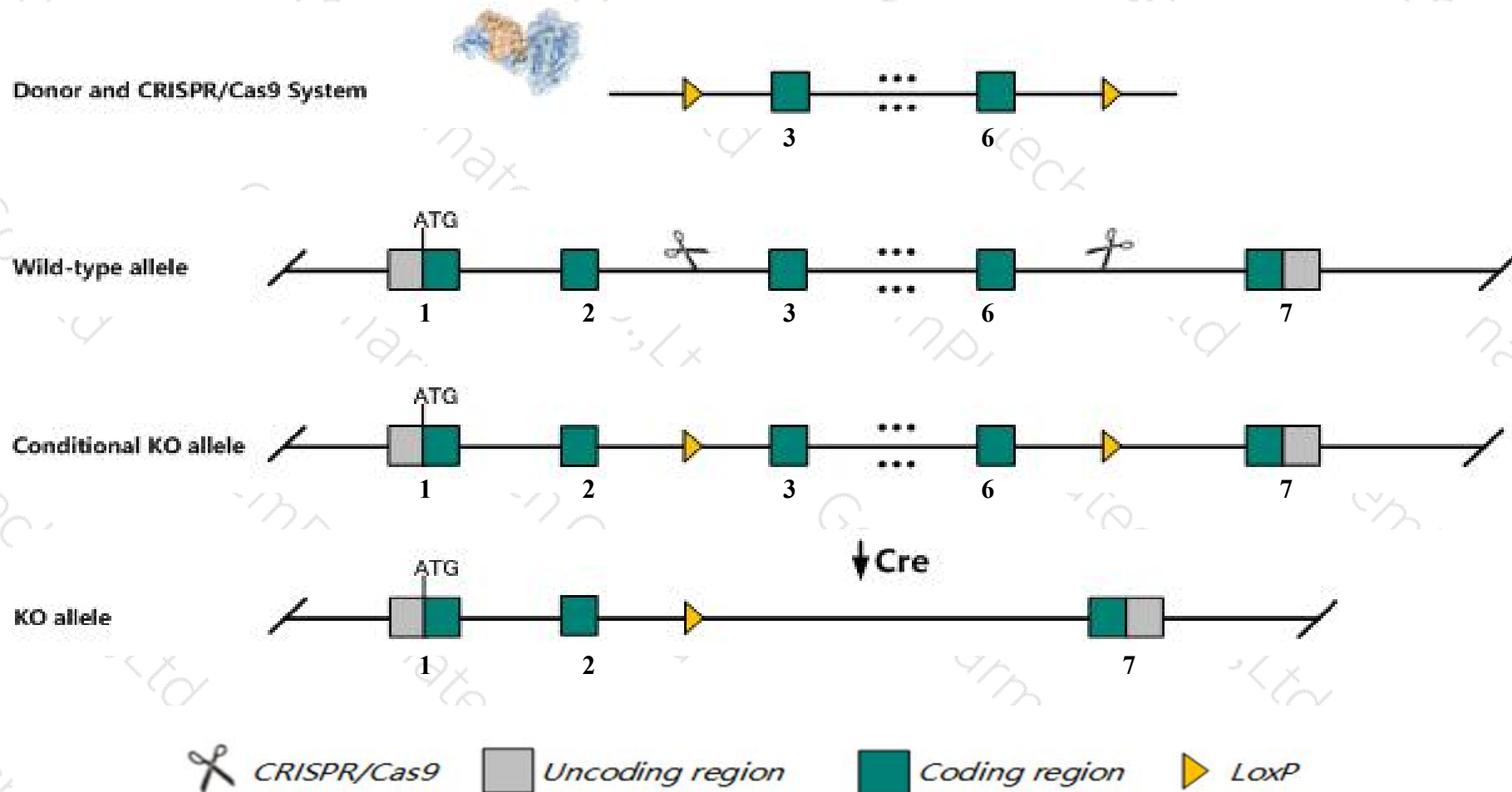
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Qdpr* gene has 10 transcripts. According to the structure of *Qdpr* gene, exon3-exon6 of *Qdpr-201* (ENSMUST00000015950.11) transcript is recommended as the knockout region. The region contains 431bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Qdpr* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be 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.

- According to the existing MGI data, A portion of mice homozygous for a knock-out allele display abnormal rib-sternum attachment, a split xiphoid process, and lumbar vertebral transformation. Another knock-out allele exhibits abnormal folate and bipterin metabolism and oxidative stress in the liver.
- The KO region contains partial intron of the *Gm42413* gene. Knockout the region may affect the function of *Gm42413* gene.
- The *Qdpr* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Qdpr quinoid dihydropteridine reductase [Mus musculus (house mouse)]

Gene ID: 110391, updated on 31-Jan-2019

Summary



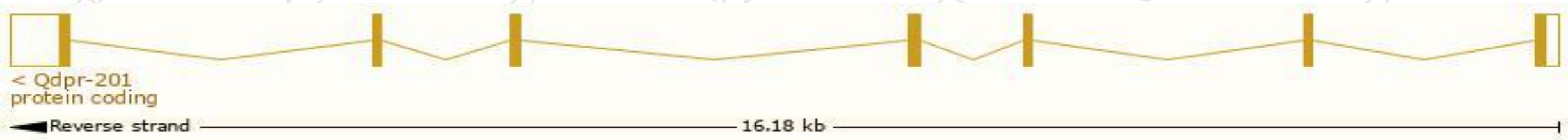
Official Symbol	Qdpr provided by MGI
Official Full Name	quinoid dihydropteridine reductase provided by MGI
Primary source	MGI:MGI:97836
See related	Ensembl:ENSMUSG00000015806
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610008L04Rik, D5Ert371e, Dhpr, PKU2
Expression	Ubiquitous expression in liver adult (RPKM 202.3), cerebellum adult (RPKM 120.9) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

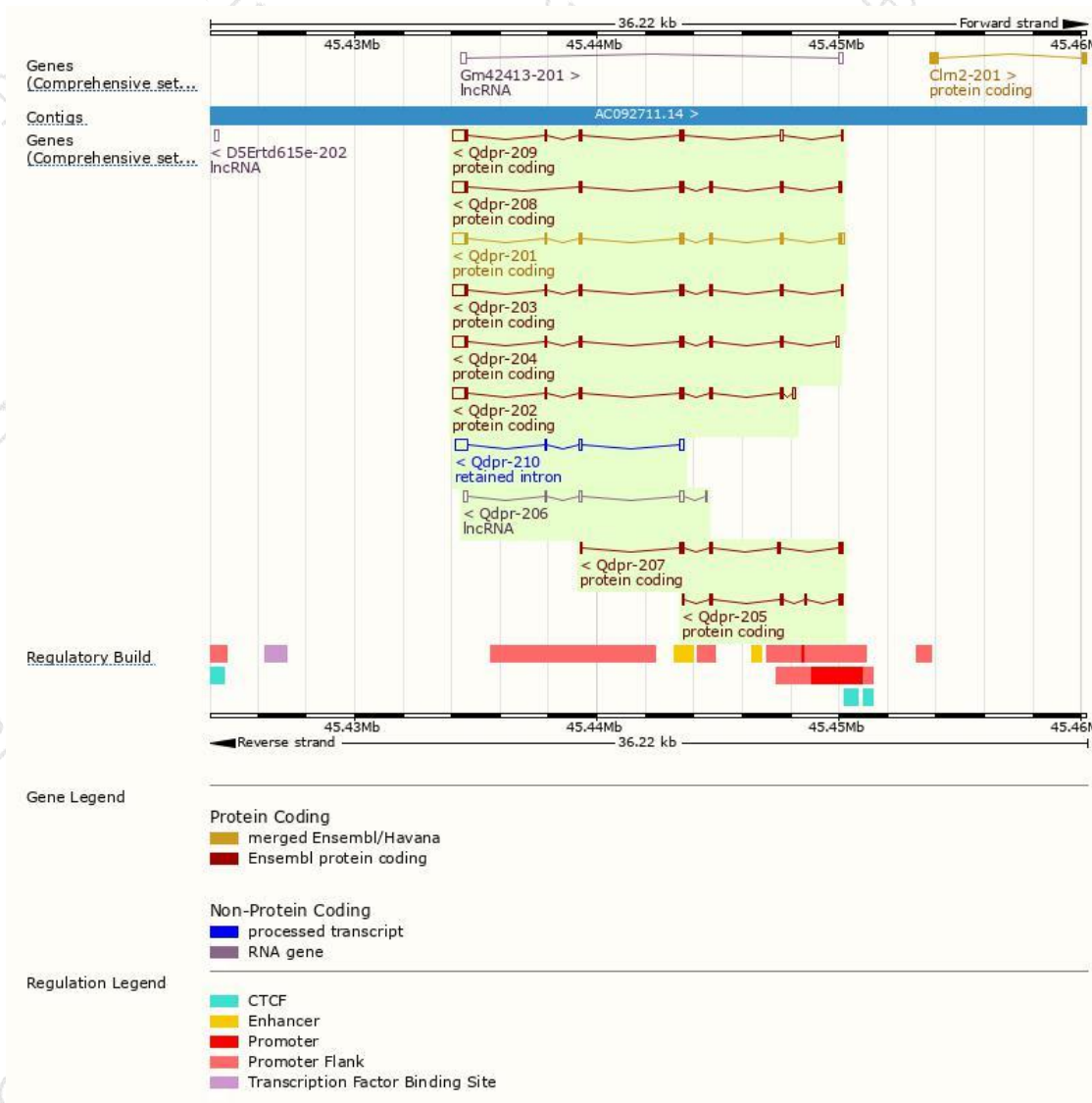
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Qdpr-201	ENSMUST00000015950.11	1380	241aa	Protein coding	CCDS19272	Q8BVI4	TSL:1 GENCODE basic APPRIS P1
Qdpr-204	ENSMUST00000120867.7	1234	189aa	Protein coding	-	D3YWR7	TSL:5 GENCODE basic
Qdpr-203	ENSMUST00000118097.7	1232	189aa	Protein coding	-	D3YWR7	TSL:5 GENCODE basic
Qdpr-202	ENSMUST00000117425.7	1231	189aa	Protein coding	-	D3YWR7	TSL:3 GENCODE basic
Qdpr-208	ENSMUST00000197946.4	1206	213aa	Protein coding	-	A0A0G2JGJ1	TSL:5 GENCODE basic
Qdpr-209	ENSMUST00000198258.4	1172	139aa	Protein coding	-	A0A0G2JGY0	TSL:5 GENCODE basic
Qdpr-207	ENSMUST00000154962.7	530	159aa	Protein coding	-	D3Z1A1	CDS 3' incomplete TSL:3
Qdpr-205	ENSMUST00000127562.2	446	136aa	Protein coding	-	D3Z099	CDS 3' incomplete TSL:5
Qdpr-210	ENSMUST00000200259.4	887	No protein	Retained intron	-	-	TSL:2
Qdpr-206	ENSMUST00000149290.2	561	No protein	lncRNA	-	-	TSL:2

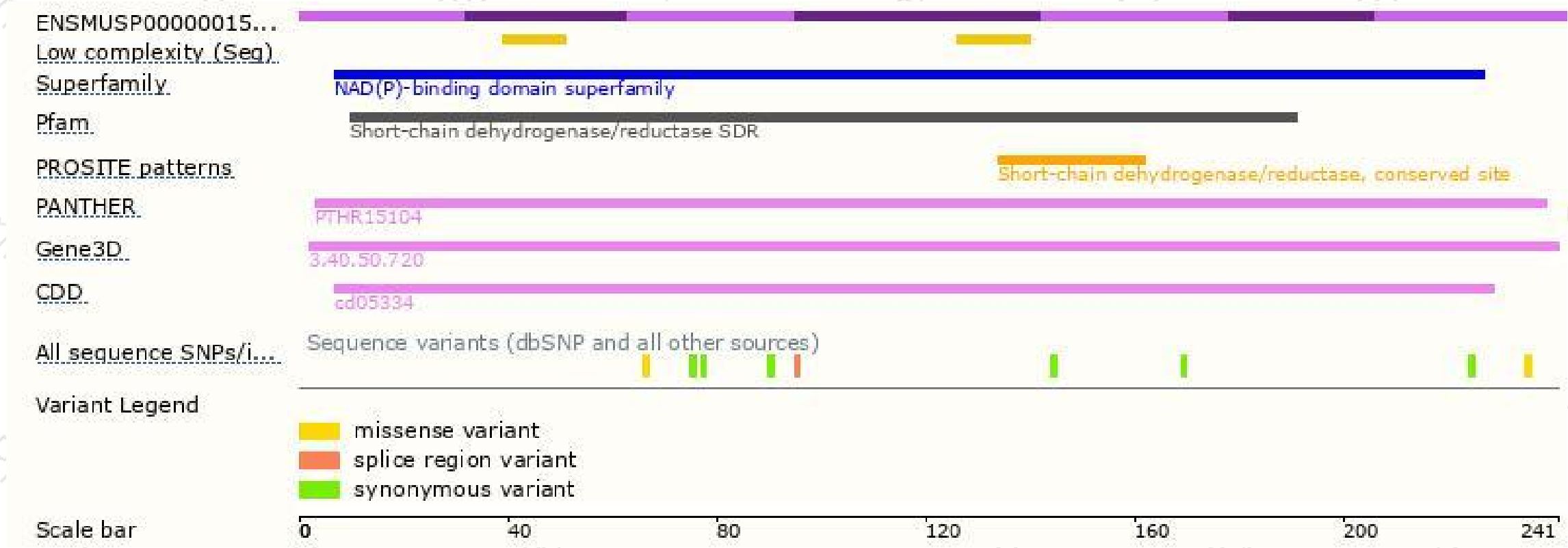
The strategy is based on the design of *Qdpr-201* transcript,The transcription is shown below



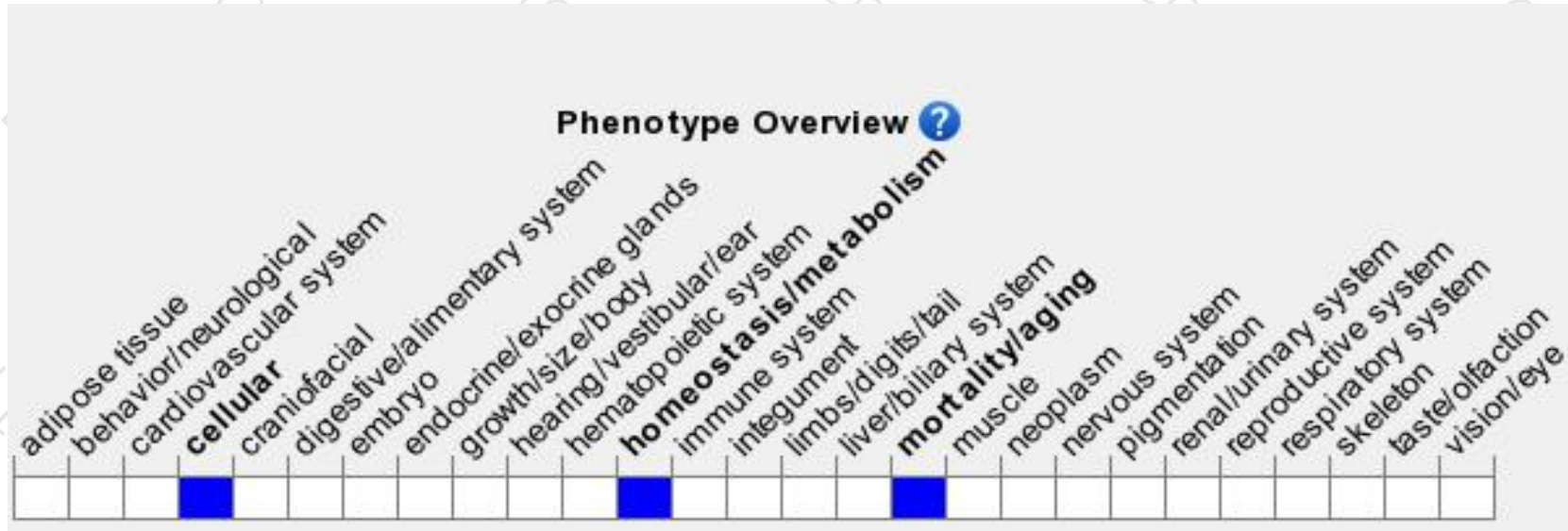
Genomic location distribution



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, A portion of mice homozygous for a knock-out allele display abnormal rib-sternum attachment, a split xiphoid process, and lumbar vertebral transformation. Another knock-out allele exhibits abnormal folate and bipterin metabolism and oxidative stress in the liver.

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

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