

Elf3 Cas9-KO Strategy

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Design Date: 2021-9-27

Project Overview

Project Name

Elf3

Project type

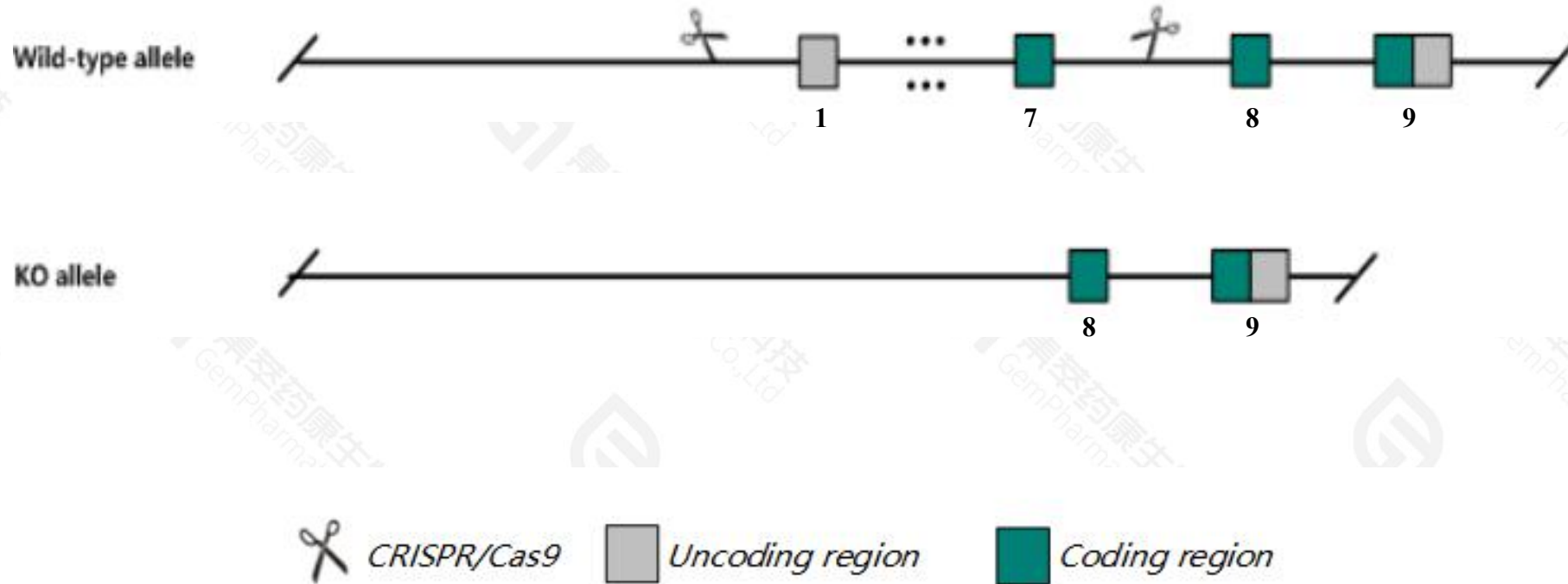
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Elf3* gene. The schematic diagram is as follows:



- The *Elf3* gene has 3 transcripts. According to the structure of *Elf3* gene, exon1-exon7 of *Elf3*-201(ENSMUST00000003135.14) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Elf3* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, about one third of mice homozygous for a reporter allele die at E11.5; over half of those born develop a wasted phenotype, lethargy and watery diarrhea and die during the first few weeks of life exhibiting dysmorphogenesis and altered differentiation of small intestinal epithelium.
- The KO region contains functional region of the *Gm26642* gene. Knockout the region may affect the function of *Gm26642* gene .
- The *Elf3* gene is located on the Chr1. 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)

Elf3 E74-like factor 3 [Mus musculus (house mouse)]

Gene ID: 13710, updated on 13-Mar-2020

Summary



Official Symbol Elf3 provided by [MGI](#)

Official Full Name E74-like factor 3 provided by [MGI](#)

Primary source [MGI:MGI:1101781](#)

See related [Ensembl:ENSMUSG00000003051](#)

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 ESE-1, ESX, jen

Expression Biased expression in colon adult (RPKM 183.3), large intestine adult (RPKM 134.0) and 7 other tissues [See more](#)

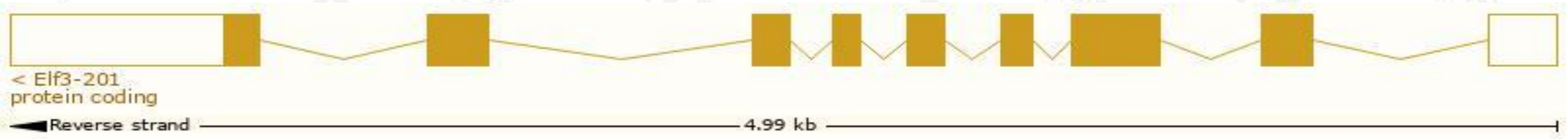
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

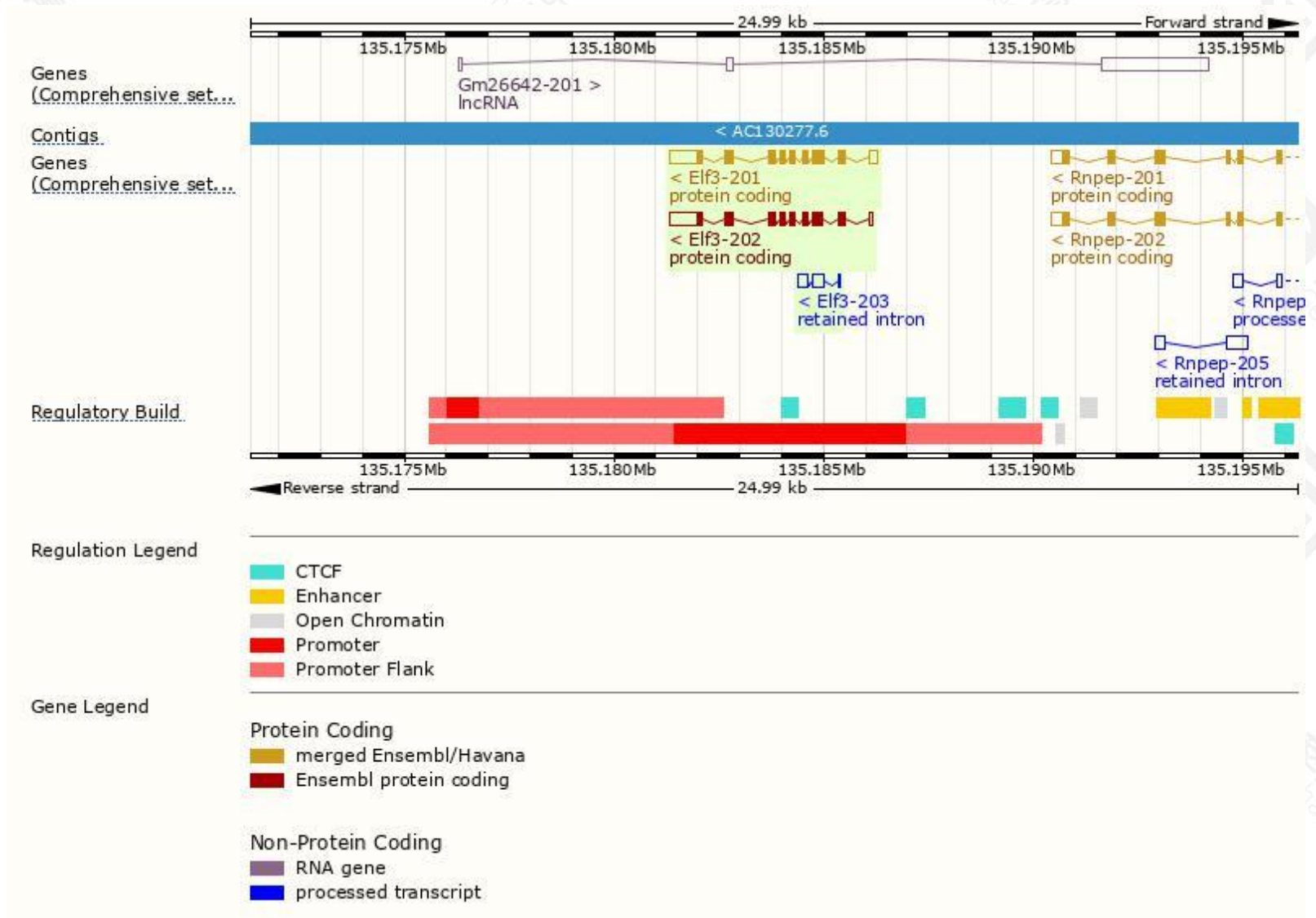
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
EIF3-201	ENSMUST00000003135.13	2095	391aa	Protein coding	CCDS48372	Q3UPW2	TSL:1 GENCODE basic
EIF3-202	ENSMUST00000185752.1	1901	371aa	Protein coding	CCDS78689	Q3UPW2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
EIF3-203	ENSMUST00000188895.1	535	No protein	Retained intron	-	-	TSL:2

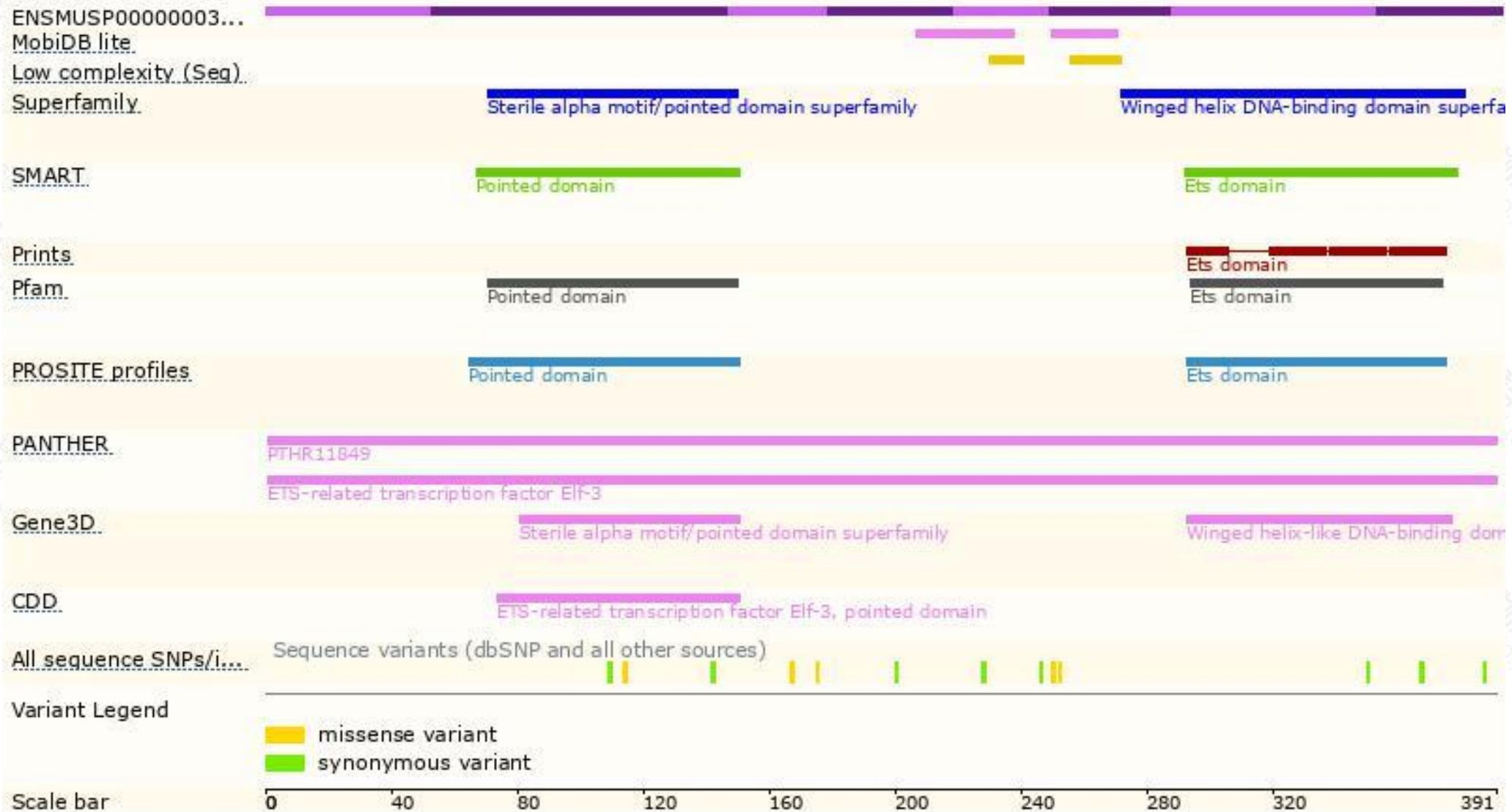
The strategy is based on the design of *Elf3-201* transcript,the transcription is shown below:



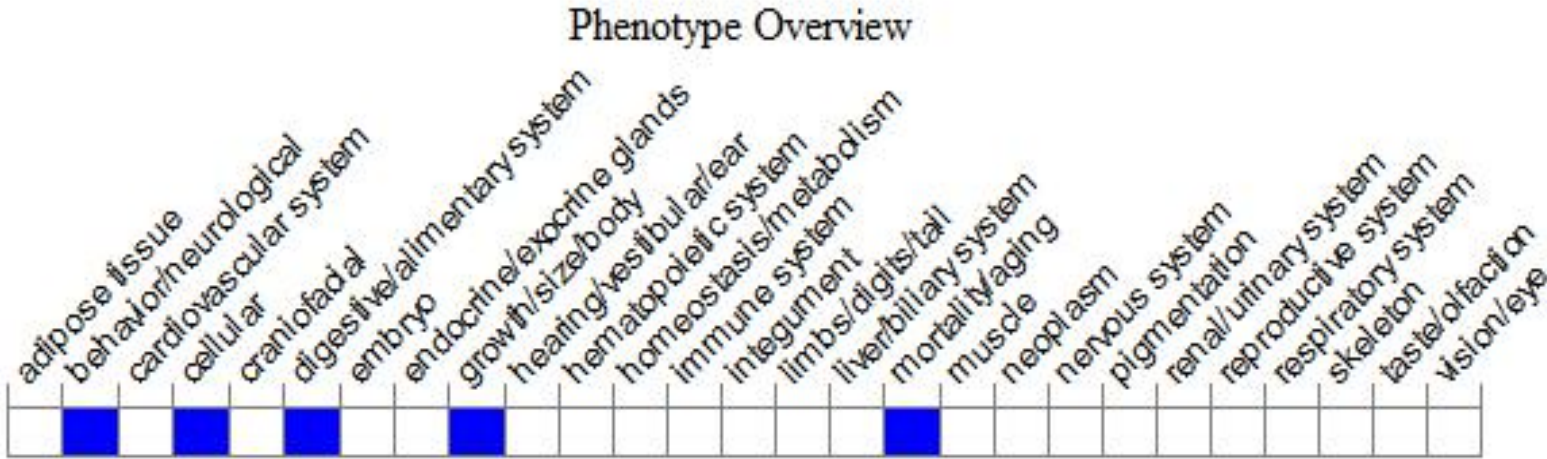
Genomic location distribution



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,about one third of mice homozygous for a reporter allele die at E11.5; over half of those born develop a wasted phenotype, lethargy and watery diarrhea and die during the first few weeks of life exhibiting dysmorphogenesis and altered differentiation of small intestinal epithelium.

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

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