

Glis3 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Glis3

Project type

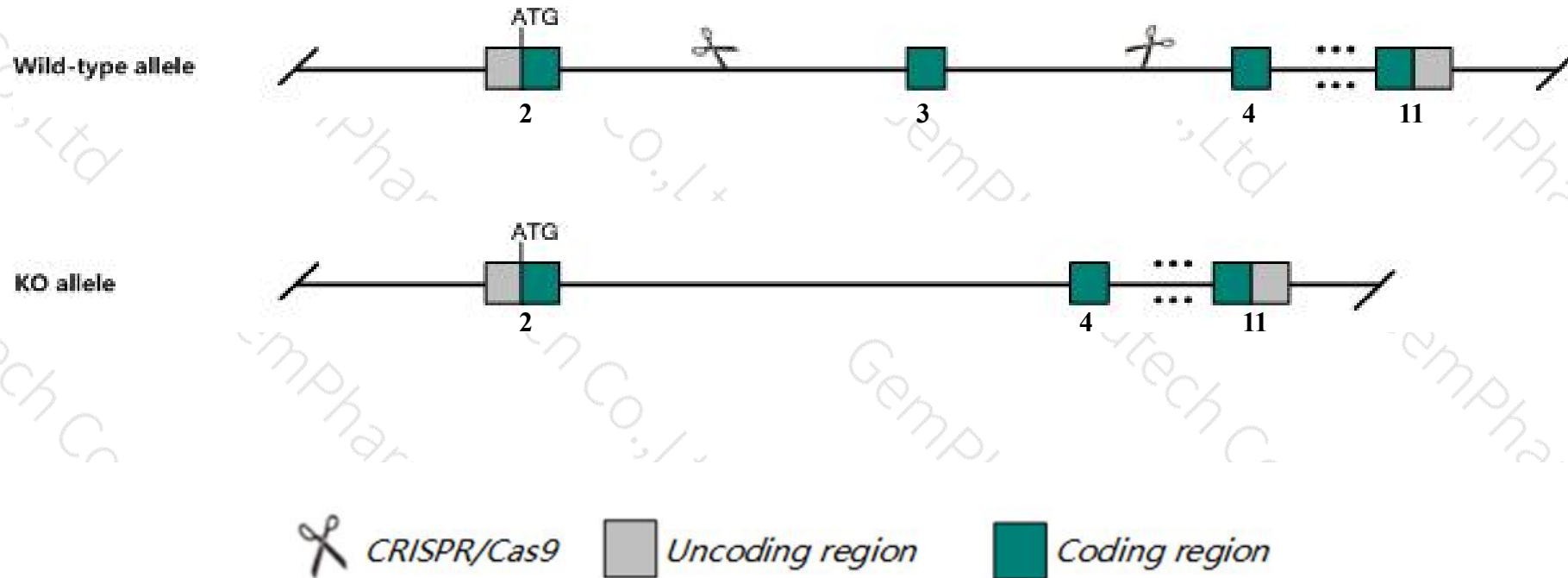
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Glis3* gene. The schematic diagram is as follows:



- The *Glis3* gene has 10 transcripts. According to the structure of *Glis3* gene, exon3 of *Glis3-209* (ENSMUST00000162022.7) transcript is recommended as the knockout region. The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Glis3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for knock-out alleles exhibit postnatal lethality associated with neonatal diabetes and polycystic kidney disease.
- The *Glis3* gene is located on the Chr19. 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)

Glis3 GLIS family zinc finger 3 [Mus musculus (house mouse)]

Gene ID: 226075, updated on 2-Mar-2019

Summary



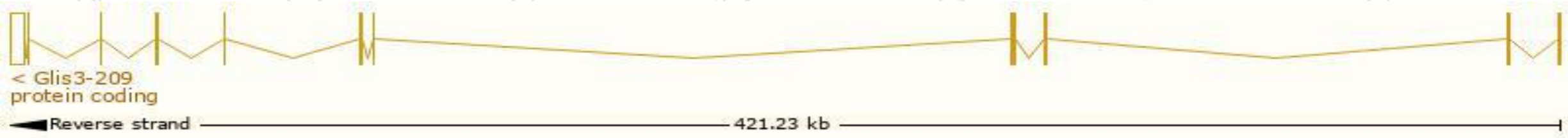
| | |
|---------------------------|--|
| Official Symbol | Glis3 provided by MGI |
| Official Full Name | GLIS family zinc finger 3 provided by MGI |
| Primary source | MGI:MGI:2444289 |
| See related | Ensembl:ENSMUSG00000052942 |
| Gene type | protein coding |
| RefSeq status | REVIEWED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 4833409N03Rik, E330013K21Rik |
| Summary | This gene is a member of the GLI-similar zinc finger protein family and encodes a nuclear protein which contains multiple C2H2-type zinc finger domains. This protein functions as both a repressor and activator of transcription and is specifically involved in the transcriptional regulation of insulin. It is thought to enhance GLI-RE-dependent transcription by binding to the GLI-RE consensus sequence (GACCACCCAC). Mutations in a similar gene in human have been associated with neonatal diabetes and congenital hypothyroidism (NDH). Alternatively spliced transcript variants have been identified. [provided by RefSeq, Mar 2015] |
| Expression | Broad expression in kidney adult (RPKM 6.0), ovary adult (RPKM 1.9) and 18 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

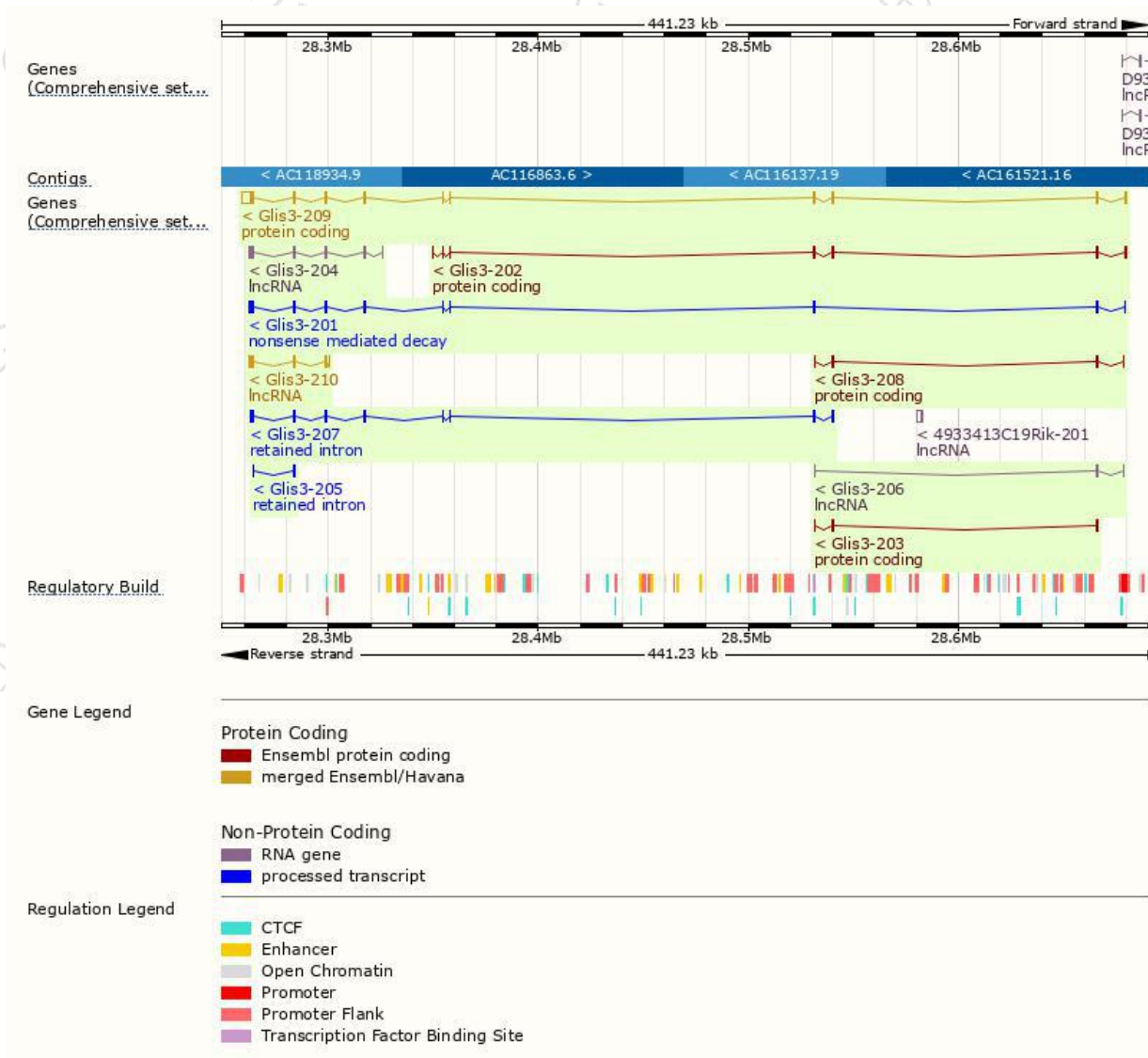
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|---------------------------------|
| Glis3-209 | ENSMUST00000162022.7 | 7514 | 935aa | Protein coding | CCDS37947 | Q0GE24 | TSL:1 GENCODE basic APPRIS P2 |
| Glis3-202 | ENSMUST00000112612.8 | 3016 | 671aa | Protein coding | - | Q6XP49 | TSL:1 GENCODE basic APPRIS ALT2 |
| Glis3-203 | ENSMUST00000159178.1 | 1281 | 245aa | Protein coding | - | E0CX93 | CDS 3' incomplete TSL:5 |
| Glis3-208 | ENSMUST00000161328.7 | 948 | 245aa | Protein coding | - | E0CX93 | CDS 3' incomplete TSL:5 |
| Glis3-201 | ENSMUST00000065113.13 | 3382 | 142aa | Nonsense mediated decay | - | E0CYJ3 | TSL:1 |
| Glis3-207 | ENSMUST00000161026.1 | 2438 | No protein | Retained intron | - | - | TSL:1 |
| Glis3-205 | ENSMUST00000159639.1 | 349 | No protein | Retained intron | - | - | TSL:3 |
| Glis3-204 | ENSMUST00000159520.7 | 1569 | No protein | lncRNA | - | - | TSL:1 |
| Glis3-210 | ENSMUST00000162873.7 | 1323 | No protein | lncRNA | - | - | TSL:1 |
| Glis3-206 | ENSMUST00000160376.7 | 740 | No protein | lncRNA | - | - | TSL:5 |

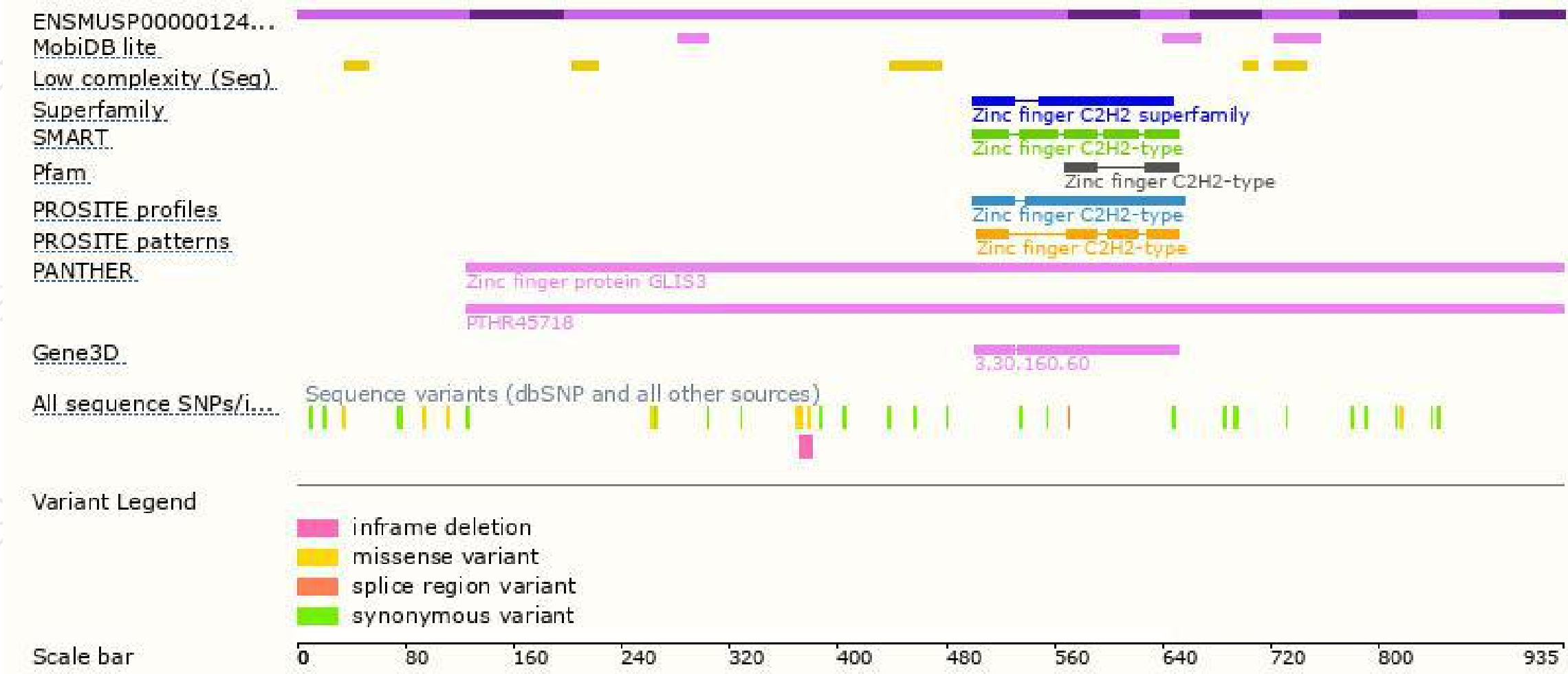
The strategy is based on the design of *Glis3-209* transcript,The transcription is shown below



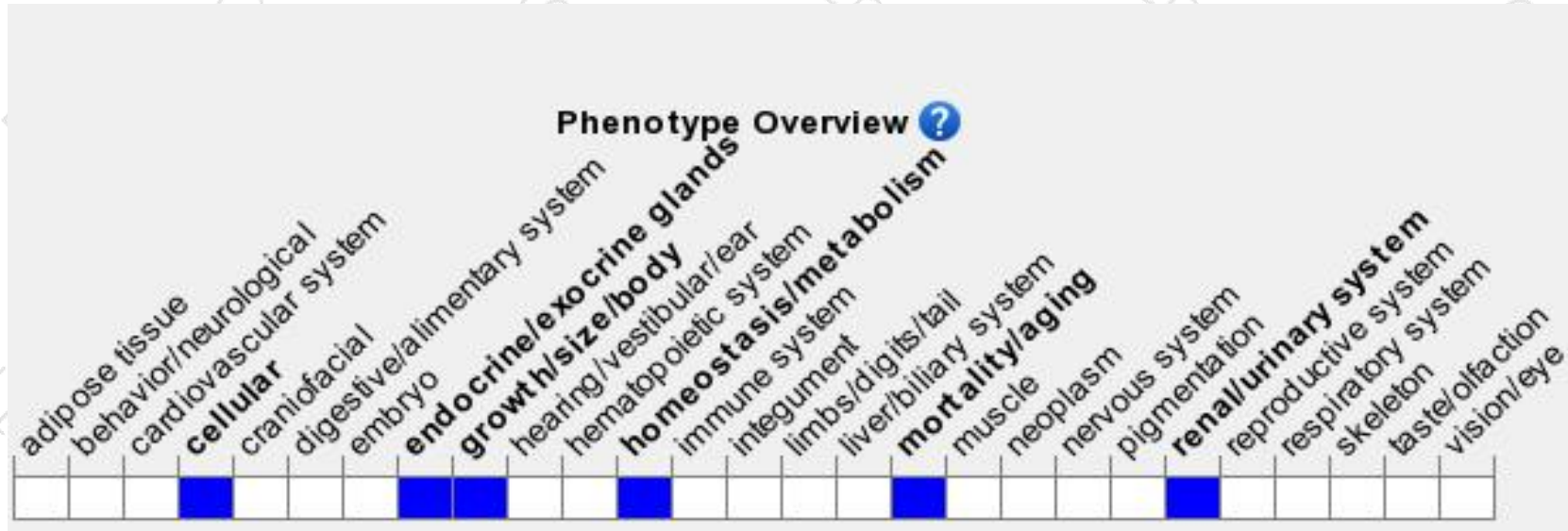
Genomic location distribution



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 knock-out alleles exhibit postnatal lethality associated with neonatal diabetes and polycystic kidney disease.

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

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