

# ***Klf15 Cas9-KO Strategy***

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**Reviewer :**

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**2019-8-28**

# Project Overview



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**Project Name**

***Klf15***

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**Project type**

**Cas9-KO**

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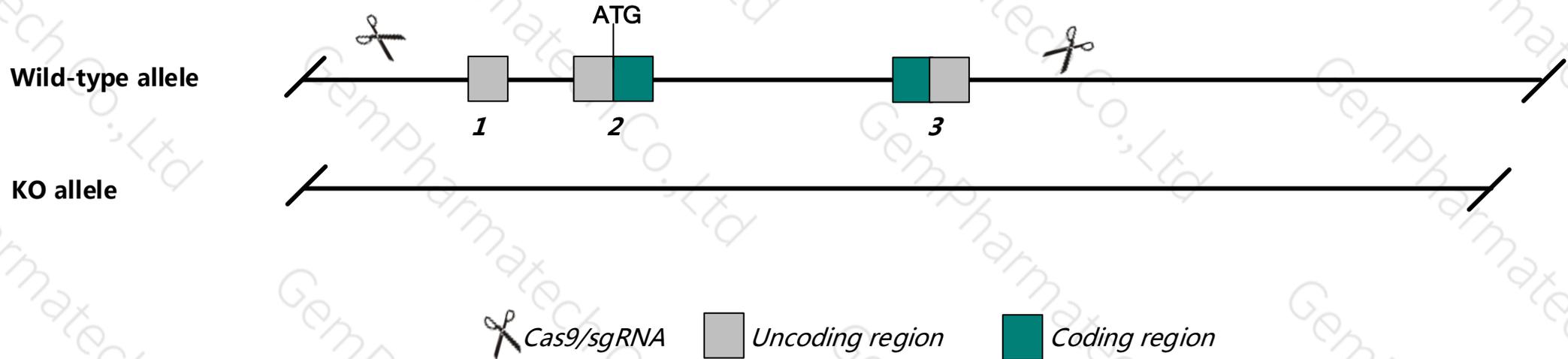
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klf15* gene. The schematic diagram is as follows:



# Technical routes

- The *Klf15* gene has 5 transcripts. According to the structure of *Klf15* gene, exon1-exon3 of *Klf15*-201 (ENSMUST00000203039.2) transcript is recommended as the knockout region. The region contains all coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Klf15* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA 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 , Mice homozygous for a null allele display impaired gluconeogenesis with severe fasting induce hypoglycemia. Homozygotes are also more sensitive to induced cardiac stress and display mild cardiac and aortic abnormalities.
- The KO region contains functional region of the *Gm44117* gene. Knockout the region may affect the function of *Gm44117* gene.
- The *Klf15* gene is located on the Chr6. 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 )



## Klf15 Kruppel-like factor 15 [ *Mus musculus* (house mouse) ]

Gene ID: 66277, updated on 8-Dec-2018

### Summary

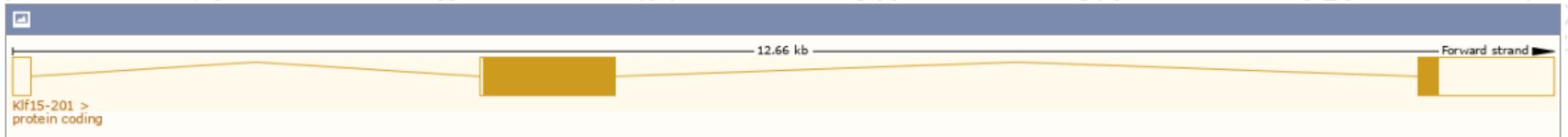
**Official Symbol** Klf15 provided by [MGI](#)  
**Official Full Name** Kruppel-like factor 15 provided by [MGI](#)  
**Primary source** [MGI:MGI:1929988](#)  
**See related** [Ensembl:ENSMUSG00000030087](#)  
**Gene type** protein coding  
**RefSeq status** VALIDATED  
**Organism** [Mus musculus](#)  
**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus  
**Also known as** CKLF; KKLF; AV048136; AW494632; 1810013I09Rik  
**Expression** Broad expression in liver adult (RPKM 36.3), kidney adult (RPKM 26.2) and 20 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)

# Transcript information ( Ensembl )

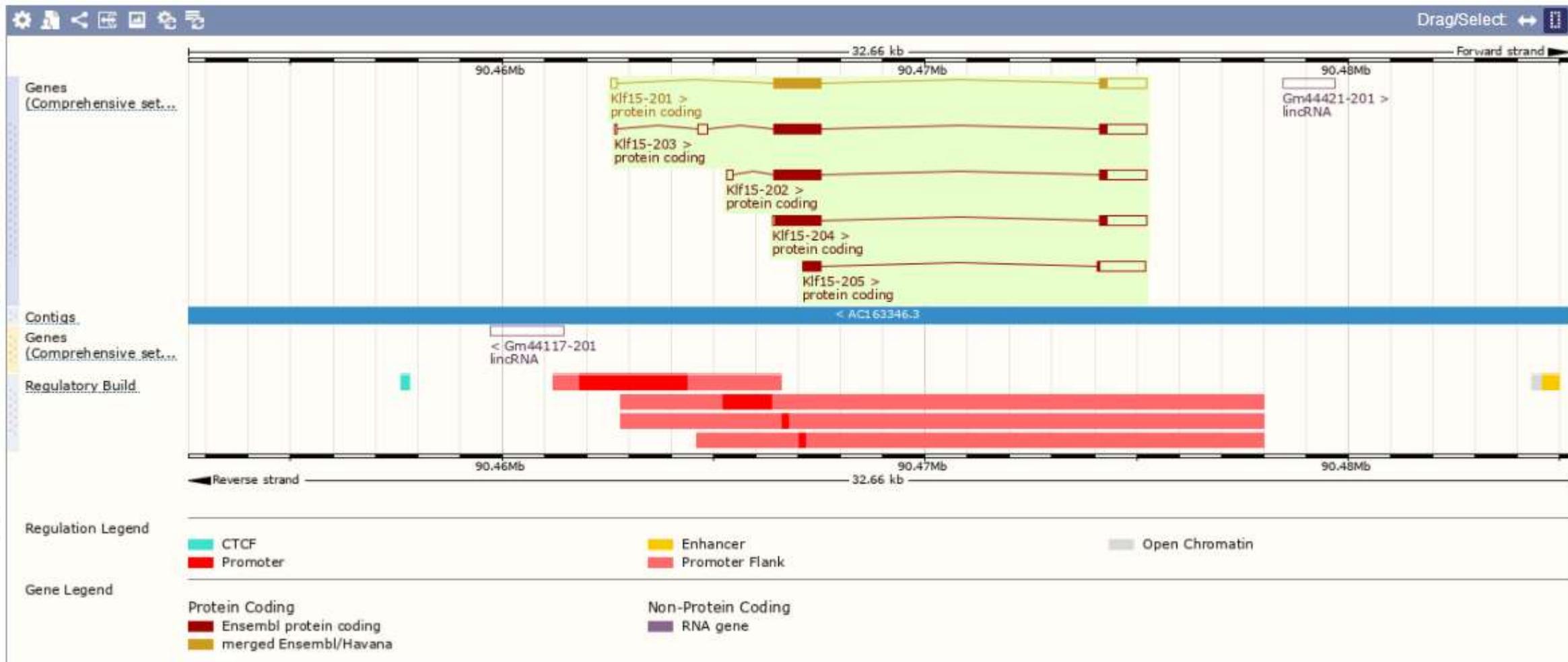
The gene has 5 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)		Filter						
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Klf15-203	<a href="#">ENSMUST00000203039.2</a>	2482	<a href="#">415aa</a>	Protein coding	<a href="#">CCDS20360</a>	<a href="#">Q9EPW2</a>	-	TSL:5 GENCODE basic APPRIS P1
Klf15-202	<a href="#">ENSMUST00000113530.3</a>	2374	<a href="#">415aa</a>	Protein coding	<a href="#">CCDS20360</a>	<a href="#">Q9EPW2</a>	-	TSL:5 GENCODE basic APPRIS P1
Klf15-201	<a href="#">ENSMUST00000032174.11</a>	2373	<a href="#">415aa</a>	Protein coding	<a href="#">CCDS20360</a>	<a href="#">Q9EPW2</a>	<a href="#">NM_023184</a> <a href="#">NP_075673</a>	TSL:1 GENCODE basic APPRIS P1
Klf15-204	<a href="#">ENSMUST00000203607.1</a>	2240	<a href="#">415aa</a>	Protein coding	<a href="#">CCDS20360</a>	<a href="#">Q9EPW2</a>	-	TSL:1 GENCODE basic APPRIS P1
Klf15-205	<a href="#">ENSMUST00000205136.1</a>	1545	<a href="#">153aa</a>	Protein coding	-	<a href="#">A0A0N4SVC6</a>	-	CDS 5' incomplete TSL:1

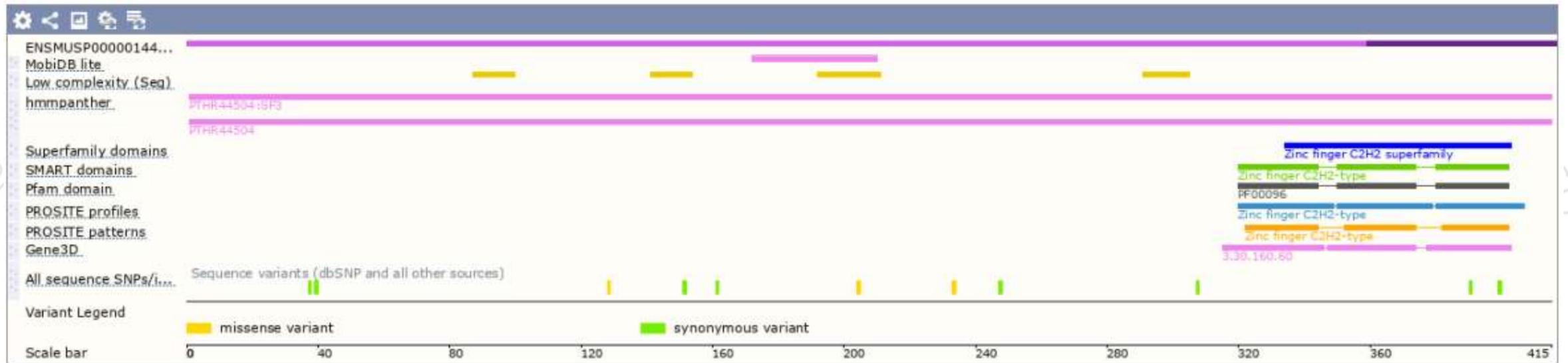
The strategy is based on the design of *Klf15-201* transcript, The transcription is shown below



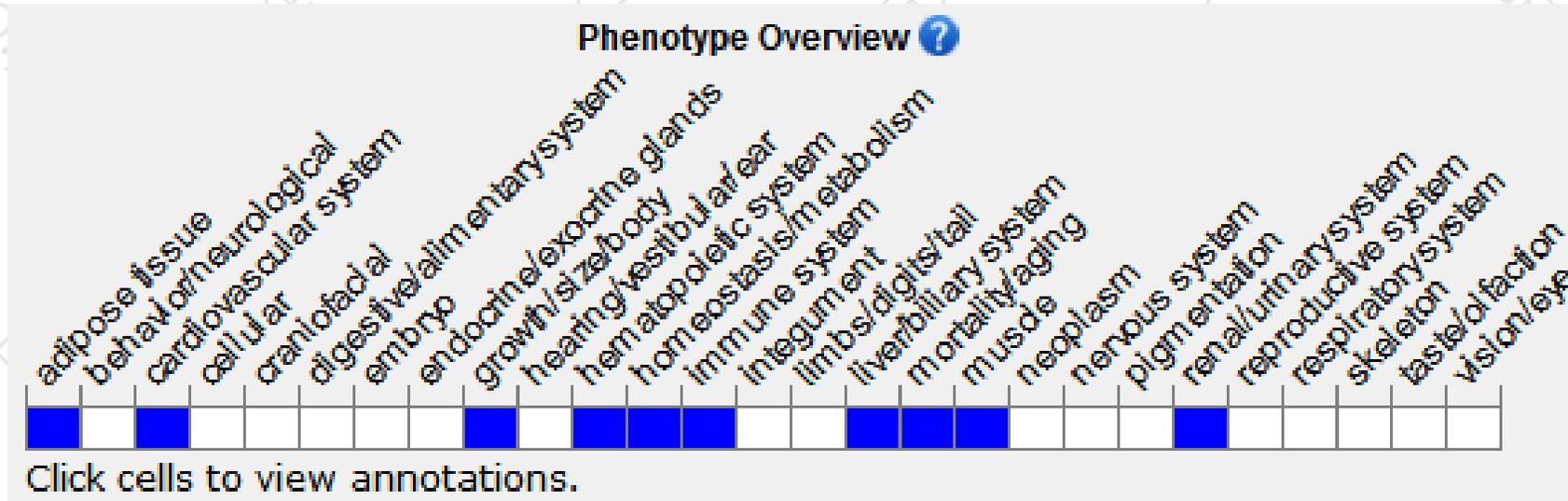
# Genomic location distribution



# 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, Mice homozygous for a null allele display impaired gluconeogenesis with severe fasting induce hypoglycemia. Homozygotes are also more sensitive to induced cardiac stress and display mild cardiac and aortic abnormalities.

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