

# *Gnb1l* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- *Gnb1l*

## Project Type

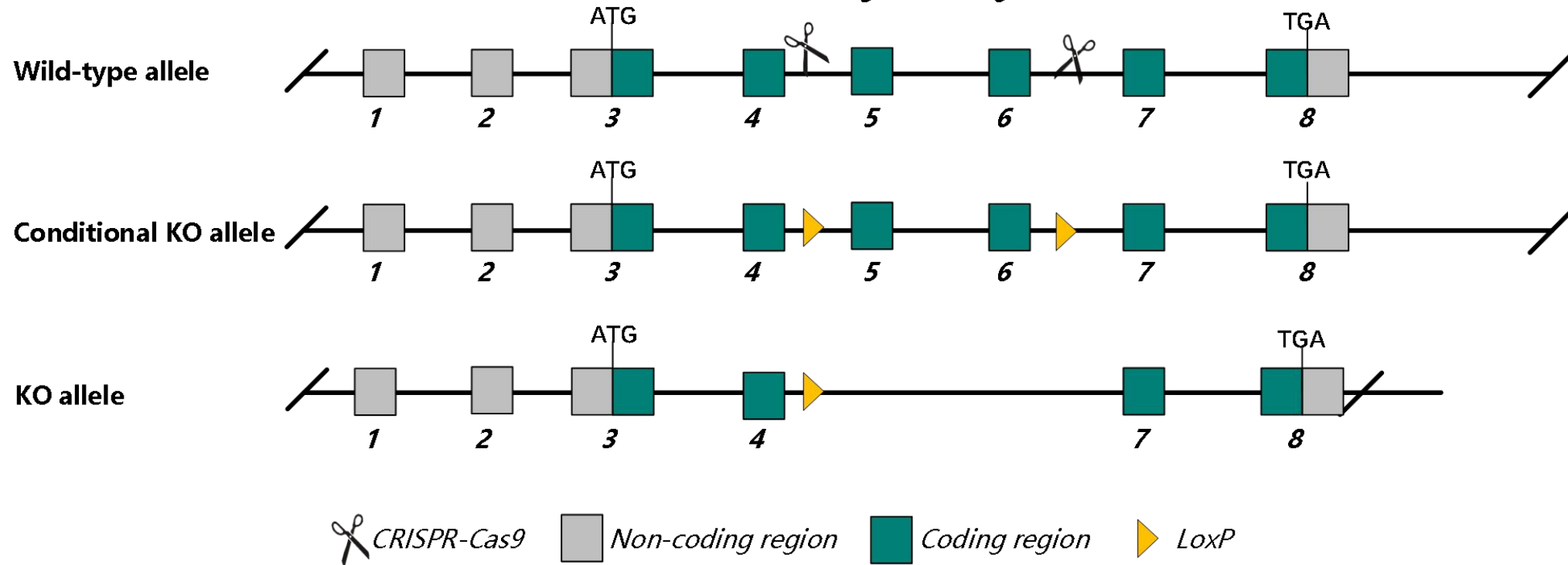
- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy

## Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Gnb1l* gene.

# Technical Information

- The *Gnb1l* gene has 13 transcripts. According to the structure of *Gnb1l* gene, exon5-exon6 of *Gnb1l*-211 (ENSMUST00000167778.9) transcript is recommended as the knockout region. The region contains 256 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Gnb1l* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

# Gene Information

## Gnb1l guanine nucleotide binding protein (G protein), beta polypeptide 1-like [Mus musculus (house mouse)]

Gene ID: 13972, updated on 12-Apr-2023

Summary	
<b>Official Symbol</b>	Gnb1l provided by <a href="#">MGI</a>
<b>Official Full Name</b>	guanine nucleotide binding protein (G protein), beta polypeptide 1-like provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1338057</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000000884</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	ESTM55, Gm16314, Me49f07, Wdr14, Wdvcf
<b>Summary</b>	Acts upstream of or within social behavior. Located in cytoplasm. Is expressed in several structures, including brain; cardiovascular system; forelimb bud; fronto-nasal process; and hemolymphoid system gland. Orthologous to human GNB1L (G protein subunit beta 1 like). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 6.1), thymus adult (RPKM 3.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

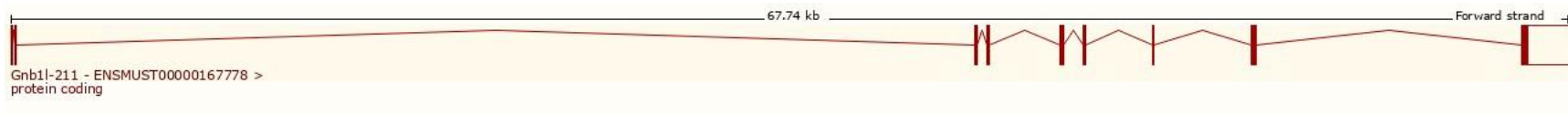
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 13 transcripts, all transcripts are shown below:

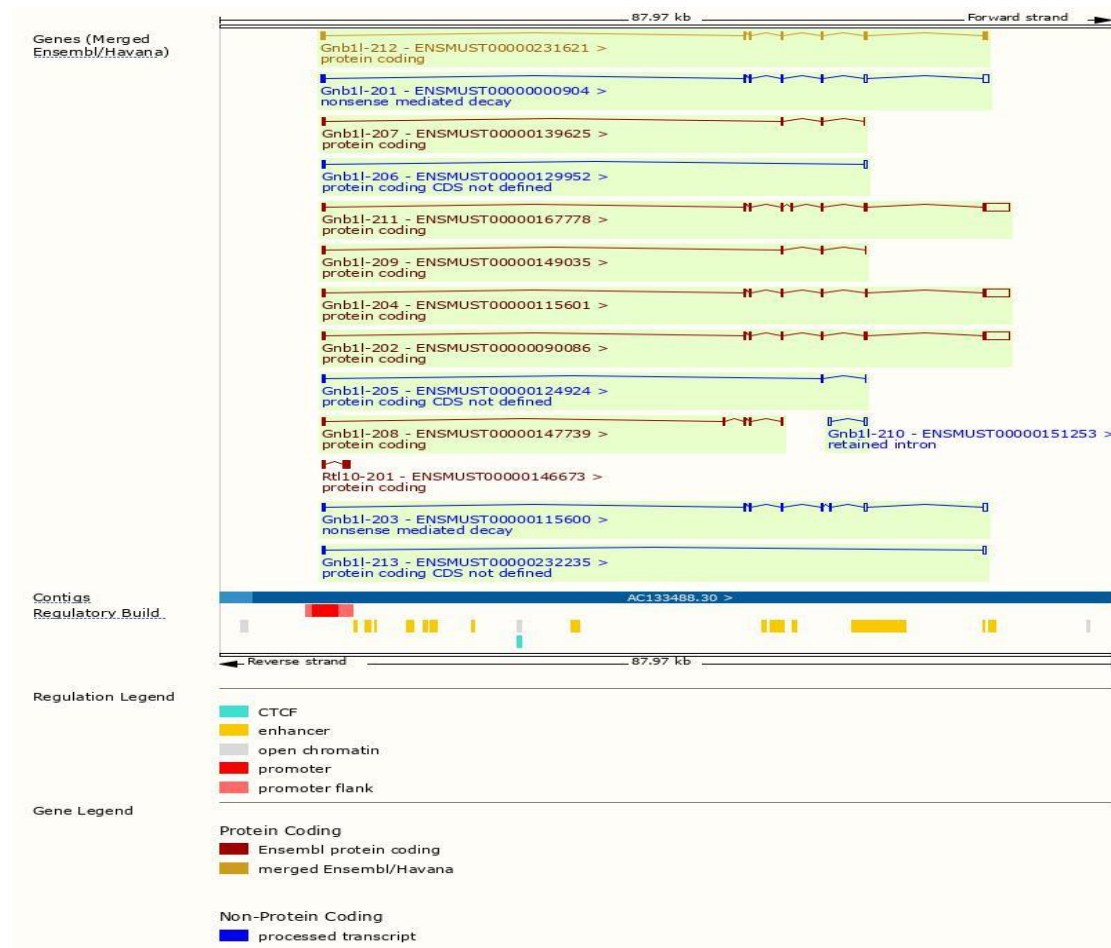
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gnb1l-211	<a href="#">ENSMUST00000167778.9</a>	3592	<a href="#">357aa</a>	Protein coding			A single transcript chosen for a gene which is the most conserved, most highly expressed, has the longest coding sequence and is represented in other key resources, such as NCBI and UniProt. This is defined in detail on <a href="http://www.ensembl.org/info/genome/genebuild/canonical.html">http://www.ensembl.org/info/genome/genebuild/canonical.html</a> Ensembl Canonical, The GENCODE set is the gene set for human and mouse. GENCODE basic, TSL:1,
Gnb1l-202	<a href="#">ENSMUST00000090086.11</a>	3549	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28022</a>		The GENCODE set is the gene set for human and mouse. GENCODE basic, APPRIS P1, TSL:1,
Gnb1l-204	<a href="#">ENSMUST00000115601.8</a>	3507	<a href="#">312aa</a>	Protein coding	<a href="#">CCDS70695</a>		The GENCODE set is the gene set for human and mouse. GENCODE basic, TSL:1,
Gnb1l-212	<a href="#">ENSMUST00000231621.2</a>	1485	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28022</a>		The GENCODE set is the gene set for human and mouse. GENCODE basic, APPRIS P1,
Gnb1l-208	<a href="#">ENSMUST00000147739.8</a>	637	<a href="#">122aa</a>	Protein coding			TSL:3, CDS 3' incomplete,
Gnb1l-209	<a href="#">ENSMUST00000149035.8</a>	453	<a href="#">78aa</a>	Protein coding			TSL:5, CDS 3' incomplete,
Gnb1l-207	<a href="#">ENSMUST00000129625.8</a>	404	<a href="#">75aa</a>	Protein coding			TSL:5, CDS 3' incomplete,
Gnb1l-203	<a href="#">ENSMUST00000115600.4</a>	1519	<a href="#">198aa</a>	Nonsense mediated decay			TSL:1,
Gnb1l-201	<a href="#">ENSMUST0000000904.15</a>	1412	<a href="#">151aa</a>	Nonsense mediated decay			TSL:5,
Gnb1l-213	<a href="#">ENSMUST00000232235.2</a>	455	No protein	Protein coding CDS not defined			
Gnb1l-206	<a href="#">ENSMUST00000129952.8</a>	375	No protein	Protein coding CDS not defined			TSL:2,
Gnb1l-205	<a href="#">ENSMUST00000124924.8</a>	358	No protein	Protein coding CDS not defined			TSL:3,
Gnb1l-210	<a href="#">ENSMUST00000151253.2</a>	535	No protein	Retained intron			TSL:3,

The strategy is based on the design of *Gnb1l*-211 transcript, the transcription is shown below:



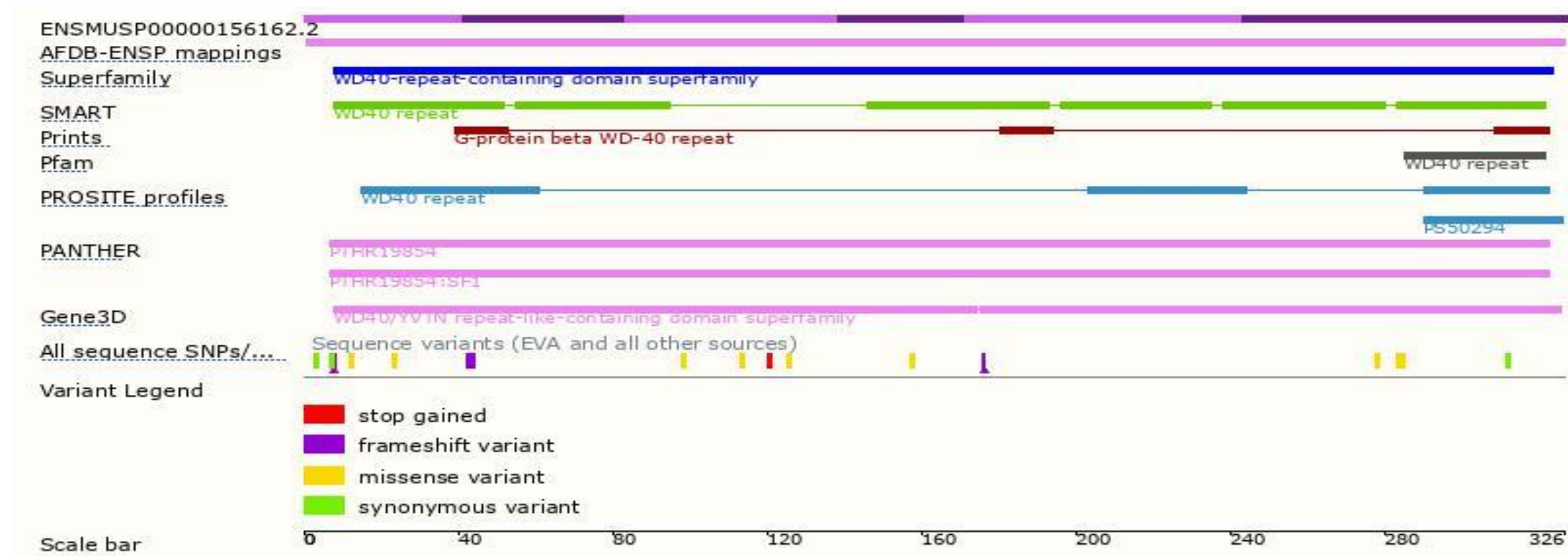
Source: <https://www.ensembl.org>

# Genomic Information



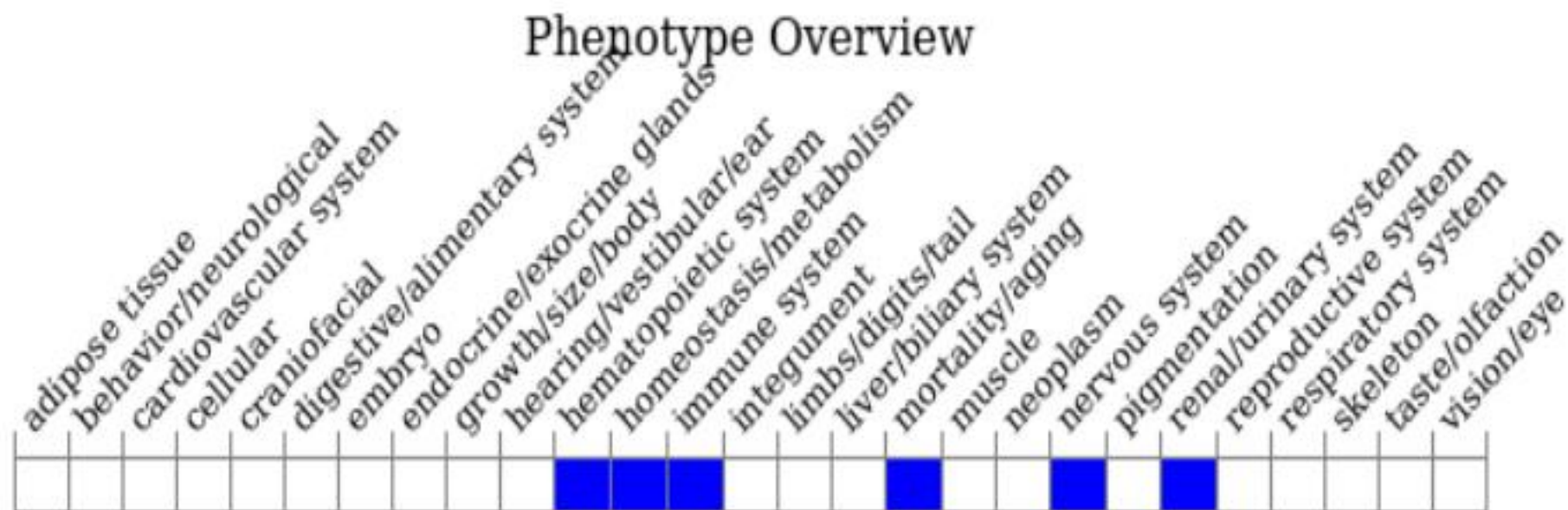


# Protein Information





# Mouse Phenotype Information (MGI)



Mice heterozygous for a gene trapped allele exhibit significantly reduced prepulse inhibition. Homozygotes die during early gestation.

# Important Information

- According to the existing MGI data, mice heterozygous for a gene trapped allele exhibit significantly reduced prepulse inhibition. Homozygotes die during early gestation.
- This strategy may not affect *Gnb1l*-210 transcript.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- *Gnb1l* is located on Chr16. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.