

# *Qars* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Qars*

**Project type**

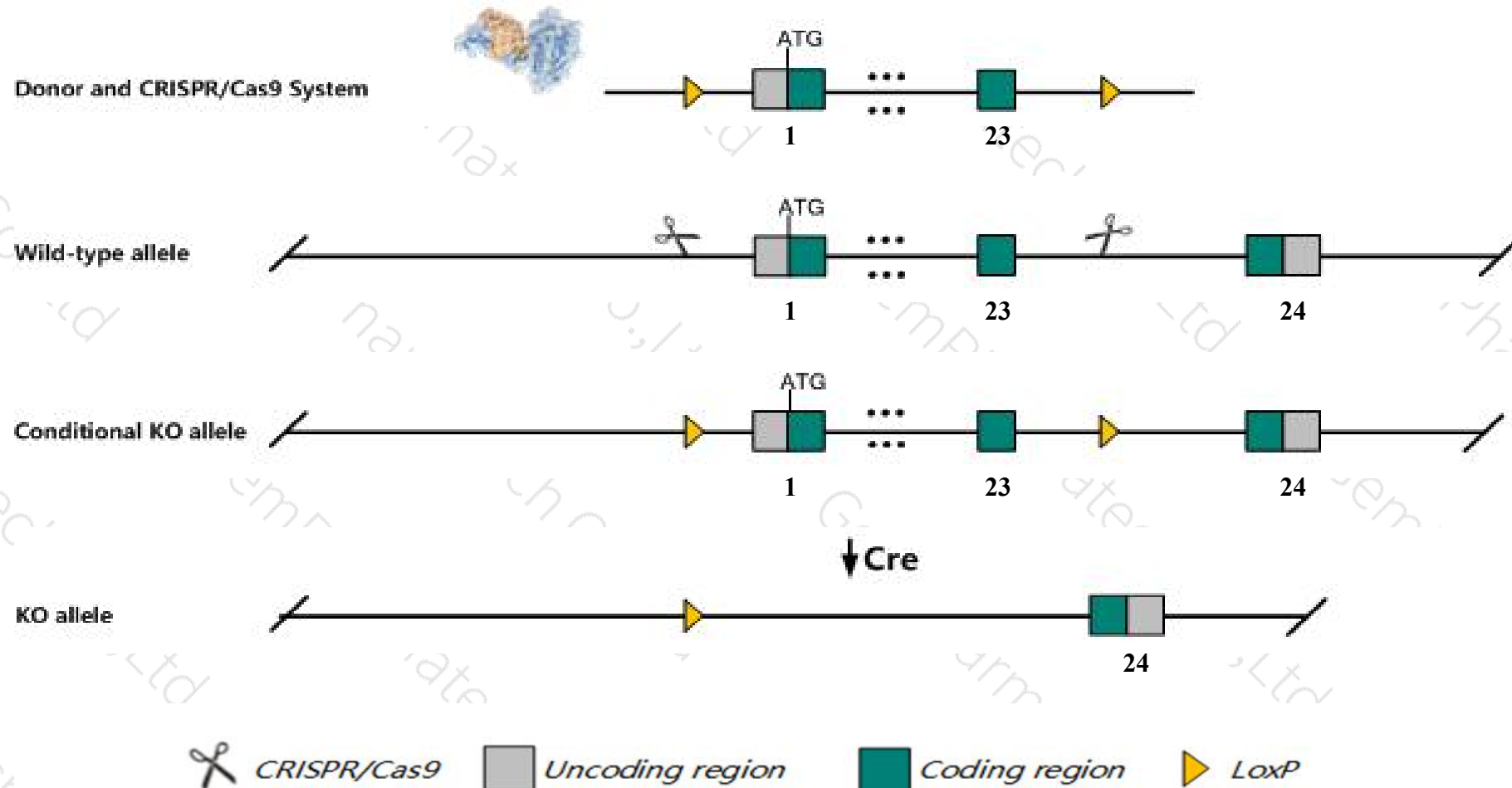
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Qars* gene has 34 transcripts. According to the structure of *Qars* gene, exon1-exon23 of *Qars-201* (ENSMUST00000006838.15) 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 *Qars* 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.

- The KO region may affect the function of *Qrich1* gene.
- Transcript 218 will be destroyed.
- The *Qars* gene is located on the Chr9. 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)

## Qars glutaminyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 97541, updated on 13-Mar-2020

### Summary



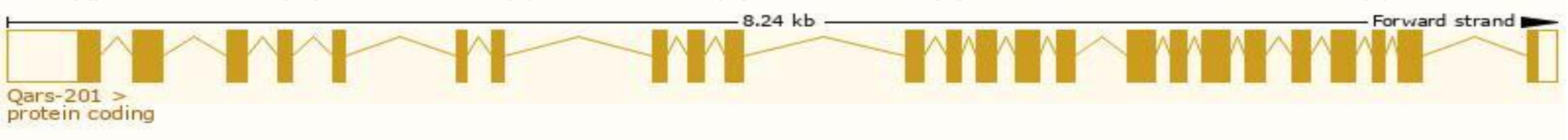
<b>Official Symbol</b>	Qars provided by <a href="#">MGI</a>
<b>Official Full Name</b>	glutaminyl-tRNA synthetase provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1915851</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032604</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	1110018N24Rik, 1200016L19Rik, C80286, GLNRS
<b>Expression</b>	Ubiquitous expression in large intestine adult (RPKM 47.6), placenta adult (RPKM 34.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

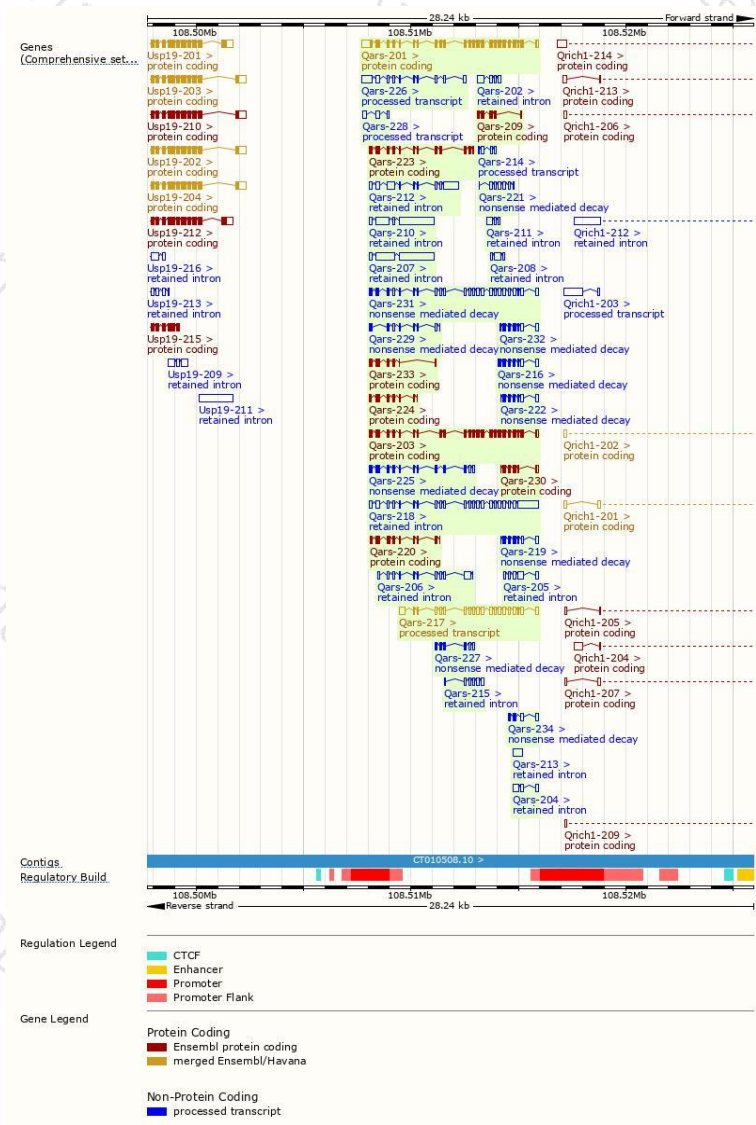
The gene has 34 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Qars-201	ENSMUST00000006936.15	2600	775aa	Protein coding	CCDS22530	Q9BRL6	TSL1 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
Qars-202	ENSMUST00000134939.6	2374	751aa	Protein coding	-	O3Z158	TSL5 GENCODE basic
Qars-223	ENSMUST00000207810.1	1052	341aa	Protein coding	-	A0A140LHZ5	CDS 3' incomplete TSL5
Qars-220	ENSMUST00000207713.1	738	246aa	Protein coding	-	A0A140LHB3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL5
Qars-224	ENSMUST00000207862.1	572	162aa	Protein coding	-	A0A140LJK5	CDS 3' incomplete TSL5
Qars-230	ENSMUST00000208177.1	557	153aa	Protein coding	-	A0A140LD3	CDS 5' incomplete TSL5
Qars-233	ENSMUST00000208561.1	544	173aa	Protein coding	-	A0A140LHJ3	CDS 3' incomplete TSL5
Qars-206	ENSMUST00000141903.3	461	154aa	Protein coding	-	E6TDS3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL5
Qars-231	ENSMUST00000208214.1	2399	100aa	Nonsense mediated decay	-	A0A140LJH1	TSL5
Qars-225	ENSMUST00000207947.1	1087	273aa	Nonsense mediated decay	-	A0A140LJ66	TSL5
Qars-216	ENSMUST00000194045.6	760	152aa	Nonsense mediated decay	-	A0A0ARYY06	CDS 5' incomplete TSL3
Qars-232	ENSMUST00000208506.1	729	160aa	Nonsense mediated decay	-	A0A140LH2	CDS 5' incomplete TSL5
Qars-222	ENSMUST00000207790.1	671	121aa	Nonsense mediated decay	-	A0A140LJ60	CDS 5' incomplete TSL5
Qars-221	ENSMUST00000207734.1	643	12aa	Nonsense mediated decay	-	A0A140LJF6	CDS 5' incomplete TSL5
Qars-219	ENSMUST00000207180.1	639	134aa	Nonsense mediated decay	-	A0A140LJH2	CDS 5' incomplete TSL5
Qars-229	ENSMUST00000208162.1	599	67aa	Nonsense mediated decay	-	A0A140LHC3	TSL5
Qars-227	ENSMUST00000208074.1	520	117aa	Nonsense mediated decay	-	A0A140LJZ4	CDS 5' incomplete TSL5
Qars-234	ENSMUST00000208962.1	486	78aa	Nonsense mediated decay	-	A0A140LJ88	CDS 5' incomplete TSL5
Qars-217	ENSMUST00000207062.1	2150	No protein	Processed transcript	-	-	TSL2
Qars-226	ENSMUST00000208069.1	1314	No protein	Processed transcript	-	-	TSL5
Qars-228	ENSMUST00000208102.1	415	No protein	Processed transcript	-	-	TSL5
Qars-214	ENSMUST00000192627.2	314	No protein	Processed transcript	-	-	TSL5
Qars-218	ENSMUST00000207126.1	3066	No protein	Retained intron	-	-	TSL1
Qars-207	ENSMUST00000141201.6	2615	No protein	Retained intron	-	-	TSL1
Qars-210	ENSMUST00000144253.6	2471	No protein	Retained intron	-	-	TSL1
Qars-212	ENSMUST00000154324.2	1643	No protein	Retained intron	-	-	TSL1
Qars-208	ENSMUST00000137980.2	1022	No protein	Retained intron	-	-	TSL5
Qars-205	ENSMUST00000137655.2	697	No protein	Retained intron	-	-	TSL5
Qars-202	ENSMUST00000131005.7	621	No protein	Retained intron	-	-	TSL2
Qars-215	ENSMUST00000192659.1	600	No protein	Retained intron	-	-	TSL3
Qars-204	ENSMUST00000136292.1	543	No protein	Retained intron	-	-	TSL2
Qars-208	ENSMUST00000141780.1	466	No protein	Retained intron	-	-	TSL3
Qars-212	ENSMUST00000192065.1	448	No protein	Retained intron	-	-	TSLNA
Qars-211	ENSMUST00000154311.1	417	No protein	Retained intron	-	-	TSL3

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

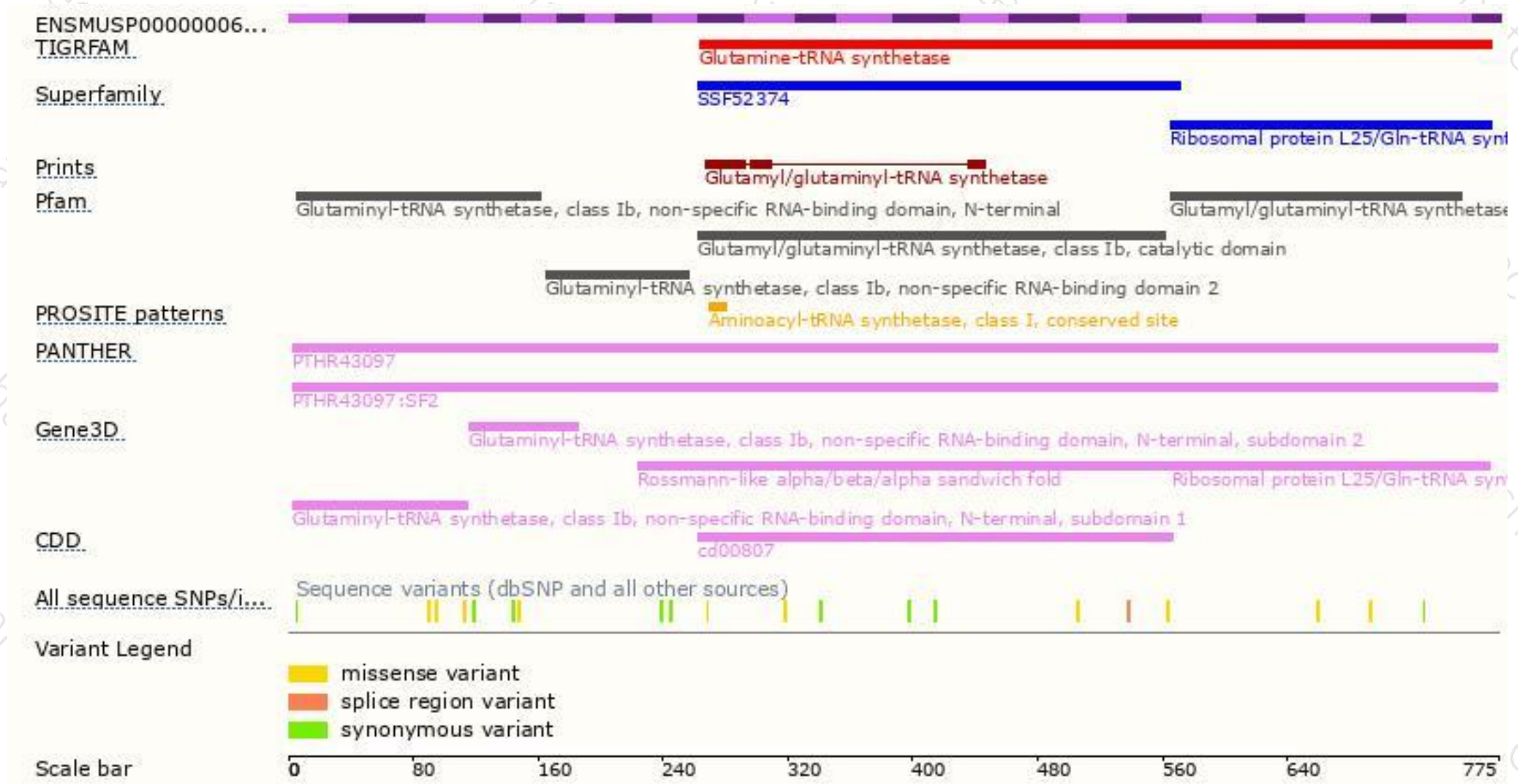


# Genomic location distribution





# Protein domain



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

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