

# *Ube3a* Cas9-CKO Strategy

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**Reviewer: Yanhua Shen**

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# Project Overview

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**Project Name**

*Ube3a*

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**Project type**

**Cas9-CKO**

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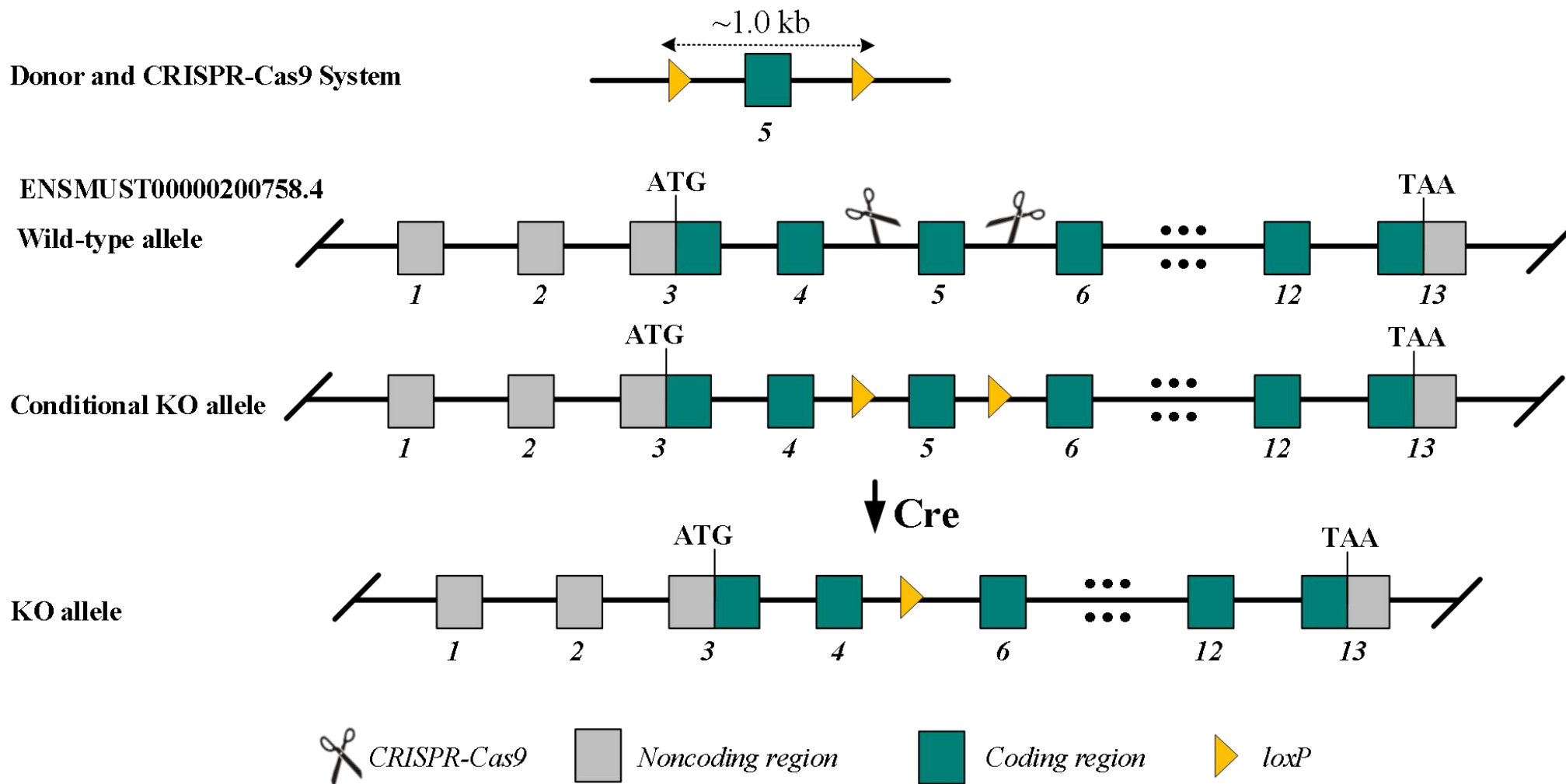
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Ube3a* gene. The schematic diagram is as follows:



- The *Ube3a* gene has 18 transcripts. According to the structure of *Ube3a* gene, exon 5 of *Ube3a-203* (ENSMUST00000200758.4) transcript is recommended as the knockout region. The region contains 290 bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ube3a* 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.

- *Ube3a*, according to the existing MGI data, mice with maternally inherited targeted null mutations exhibit reduced brain weight, impaired motor function, inducible seizures, learning deficits, abnormal hippocampal electroencephalographic recordings, and severely impaired long-term potentiation.
- The effect on the *Ube3a*-202,203, 207,209,211,212,217,218 transcript is unknown.
- The *Ube3a* gene is located on the Chr 7. 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)

## Ube3a ubiquitin protein ligase E3A [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 22215, updated on 3-May-2022

### Summary

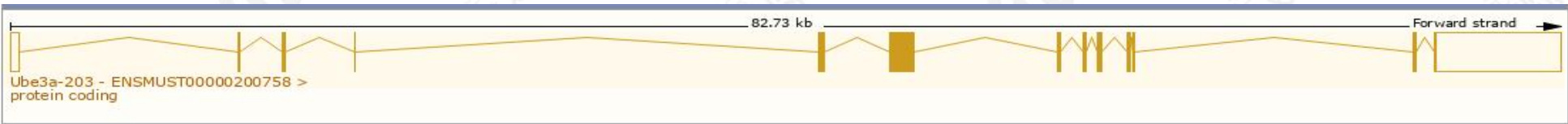
<b>Official Symbol</b>	Ube3a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ubiquitin protein ligase E3A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:105098</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000025326</a> <a href="#">AllianceGenome:MGI:105098</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>	Hpve6a; 4732496B02; 5830462N02Rik; A130086L21Rik
<b>Summary</b>	Enables transcription coactivator activity and ubiquitin protein ligase activity. Involved in positive regulation of Golgi lumen acidification and regulation of circadian rhythm. Acts upstream of or within several processes, including cellular protein metabolic process; positive regulation of phosphatidylinositol 3-kinase signaling; and reproductive structure development. Located in cytosol and nucleus. Is expressed in central nervous system and retina. Used to study Angelman syndrome. Human ortholog(s) of this gene implicated in Angelman syndrome. Orthologous to human UBE3A (ubiquitin protein ligase E3A). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 21.0), ovary adult (RPKM 10.5) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

# Transcript information (Ensembl)

The gene has 18 transcripts,all transcripts are shown below:

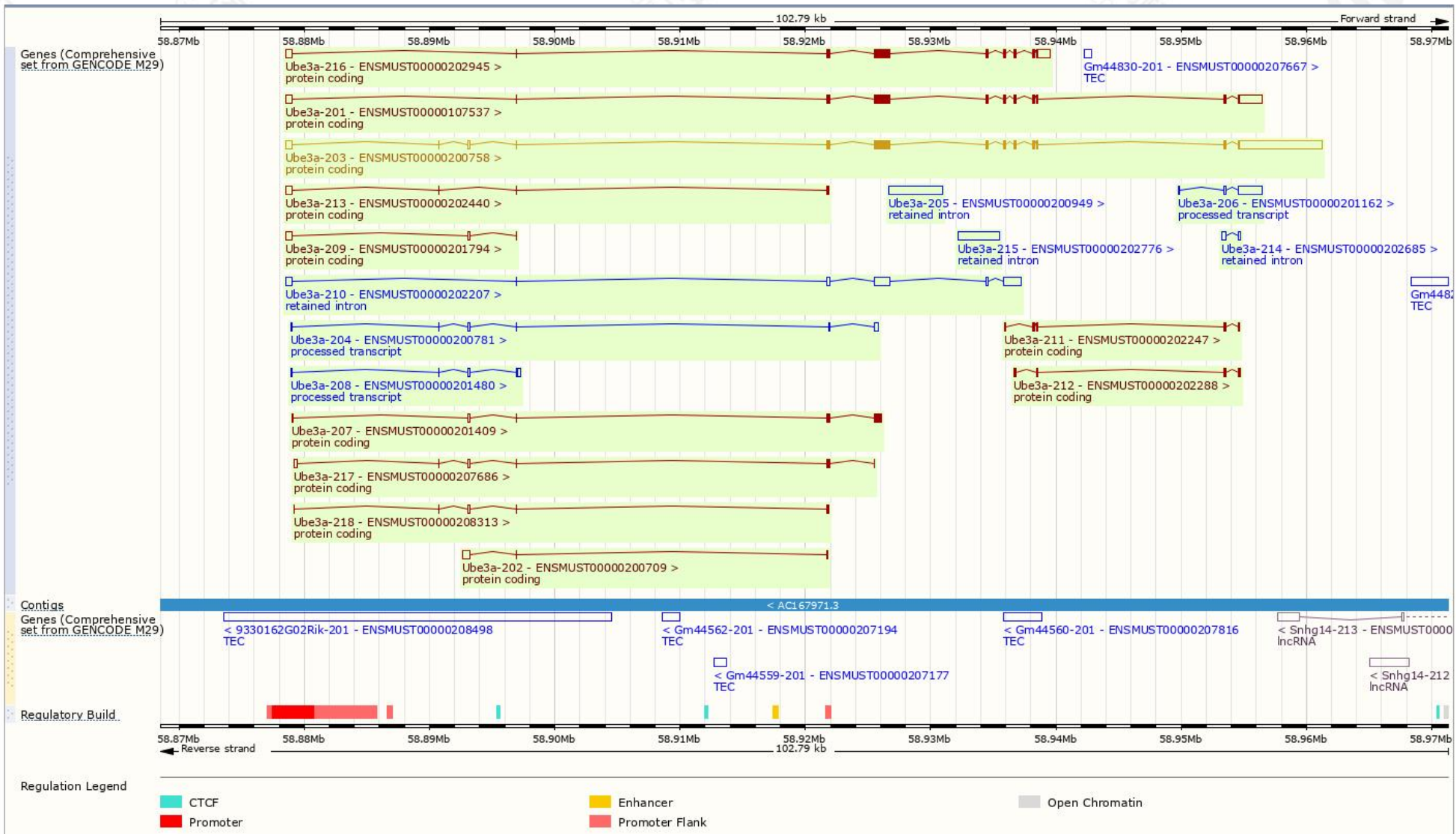
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000200758.4</a>	Ube3a-203	9856	<a href="#">870aa</a>	Protein coding	<a href="#">CCDS39973</a>	<a href="#">O08759-1</a>	Ensembl Canonical Gencode basic APPRIS P4 TSL:1
<a href="#">ENSMUST00000107537.5</a>	Ube3a-201	4911	<a href="#">849aa</a>	Protein coding	<a href="#">CCDS80733</a>	<a href="#">O08759-2</a>	Gencode basic APPRIS ALT1 TSL:1
<a href="#">ENSMUST00000202945.4</a>	Ube3a-216	3889	<a href="#">762aa</a>	Protein coding		<a href="#">O08759-3</a>	Gencode basic TSL:1
<a href="#">ENSMUST00000201409.4</a>	Ube3a-207	1119	<a href="#">313aa</a>	Protein coding		<a href="#">A0A0J9YUK0</a>	TSL:3 CDS 3' incomplete
<a href="#">ENSMUST00000207686.2</a>	Ube3a-217	797	<a href="#">126aa</a>	Protein coding		<a href="#">A0A140LHS2</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000202440.4</a>	Ube3a-213	729	<a href="#">49aa</a>	Protein coding		<a href="#">A0A0J9YTX6</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000200709.2</a>	Ube3a-202	664	<a href="#">40aa</a>	Protein coding		<a href="#">A0A0J9YUF2</a>	TSL:3 CDS 3' incomplete
<a href="#">ENSMUST00000201794.4</a>	Ube3a-209	616	<a href="#">15aa</a>	Protein coding		<a href="#">A0A0J9YV26</a>	TSL:3 CDS 3' incomplete
<a href="#">ENSMUST00000202247.4</a>	Ube3a-211	579	<a href="#">192aa</a>	Protein coding		<a href="#">A0A0J9YUY4</a>	TSL:3 CDS 5' incomplete
<a href="#">ENSMUST00000202288.2</a>	Ube3a-212	442	<a href="#">143aa</a>	Protein coding		<a href="#">A0A0J9YVG1</a>	TSL:5 CDS 5' incomplete
<a href="#">ENSMUST00000208313.2</a>	Ube3a-218	441	<a href="#">78aa</a>	Protein coding		<a href="#">A0A140LI50</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000201162.2</a>	Ube3a-206	2129	No protein	Processed transcript		-	TSL:1
<a href="#">ENSMUST00000200781.4</a>	Ube3a-204	742	No protein	Processed transcript		-	TSL:5
<a href="#">ENSMUST00000201480.2</a>	Ube3a-208	549	No protein	Processed transcript		-	TSL:5
<a href="#">ENSMUST00000200949.2</a>	Ube3a-205	4254	No protein	Retained intron		-	TSL:NA
<a href="#">ENSMUST00000202207.4</a>	Ube3a-210	3586	No protein	Retained intron		-	TSL:1
<a href="#">ENSMUST00000202776.2</a>	Ube3a-215	3348	No protein	Retained intron		-	TSL:NA
<a href="#">ENSMUST00000202685.2</a>	Ube3a-214	436	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Ube3a-203* transcript,the transcription is shown below:



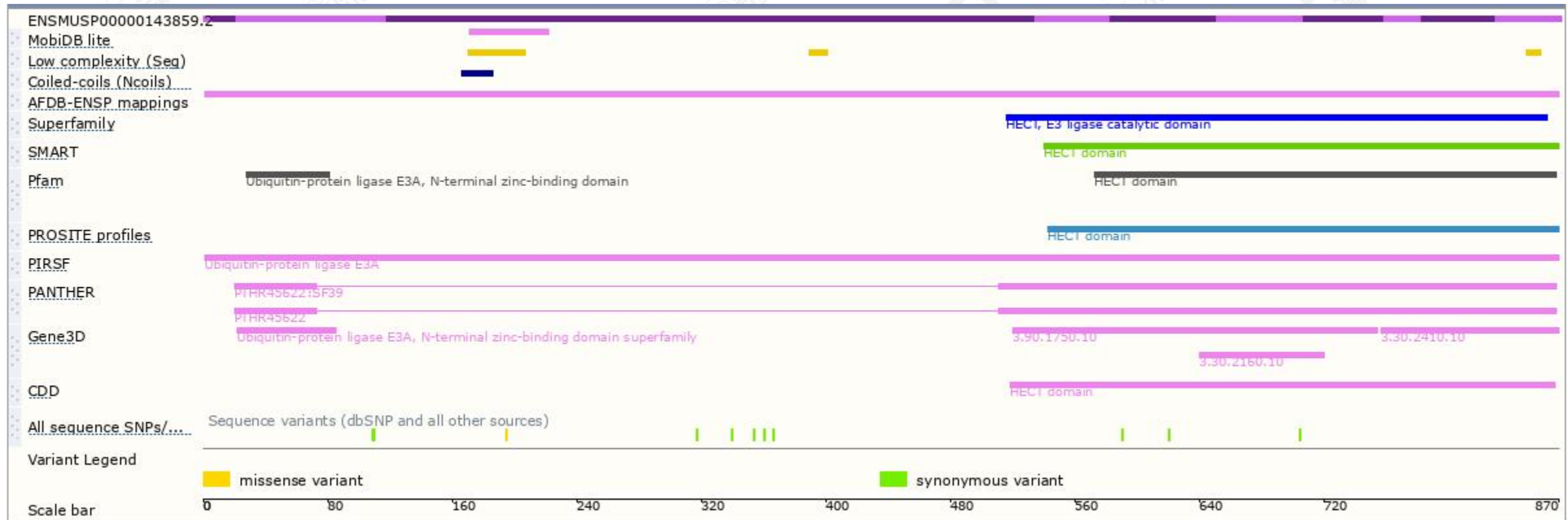


# Genomic location distribution





# Protein domain



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

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