

# *Polh* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Polh*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Polh* gene has 3 transcripts. According to the structure of *Polh* gene, exon3-exon5 of *Polh-201* (ENSMUST00000024749.8) transcript is recommended as the knockout region. The region contains 520bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Polh* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous inactivation of this gene causes increased susceptibility to UV-induced skin tumors and results in reduced immunoglobulin gene mutations at A-T base pairs with a G-C biased mutation pattern.
- The knockout region is near to the N-terminal of *Xpo5* gene, this strategy may influence the regulatory function of the N-terminal of *Xpo5* gene.
- The *Polh* gene is located on the Chr17. 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)

**Polh** polymerase (DNA directed), eta (RAD 30 related) [ *Mus musculus* (house mouse) ]

Gene ID: 80905, updated on 13-Aug-2019

## Summary

**Official Symbol** Polh provided by [MGI](#)  
**Official Full Name** polymerase (DNA directed), eta (RAD 30 related) provided by [MGI](#)  
**Primary source** [MGI:MGI:1891457](#)  
**See related** [Ensembl:ENSMUSG00000023953](#)  
**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** XPV; RAD30A  
**Expression** Ubiquitous expression in liver E14 (RPKM 6.4), liver E14.5 (RPKM 6.3) and 28 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)

## Genomic context

**Location:** 17; 17 C

[See Polh in Genome Data Viewer](#)

**Exon count:** 11

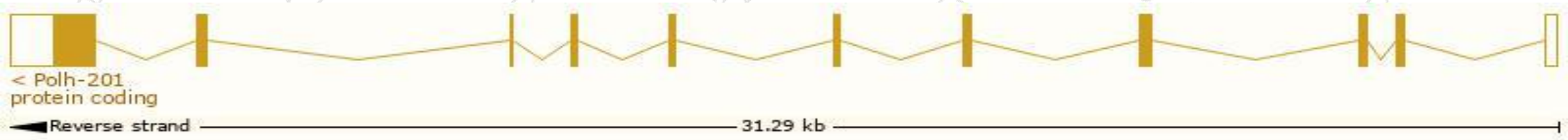
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	17	NC_000083.6 (46171355..46202641, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	17	NC_000083.5 (46308942..46339574, complement)

# Transcript information (Ensembl)

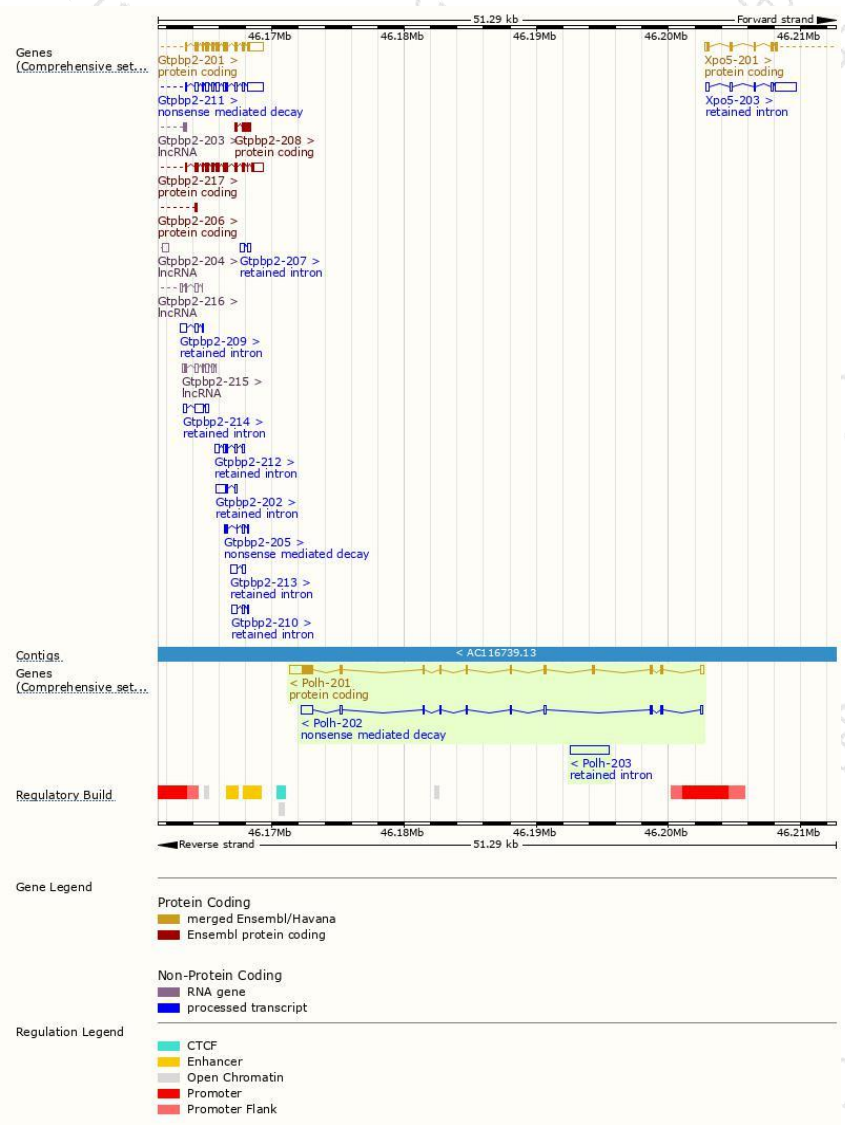
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Polh-201	<a href="#">ENSMUST00000024749.8</a>	3238	<a href="#">694aa</a>	Protein coding	<a href="#">CCDS28822</a>	<a href="#">Q9JJN0</a>	TSL:1 GENCODE basic APPRIS P1
Polh-202	<a href="#">ENSMUST00000233438.1</a>	2130	<a href="#">102aa</a>	Nonsense mediated decay	-	<a href="#">A0A3B2WAL6</a>	
Polh-203	<a href="#">ENSMUST00000233924.1</a>	2927	No protein	Retained intron	-	-	

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

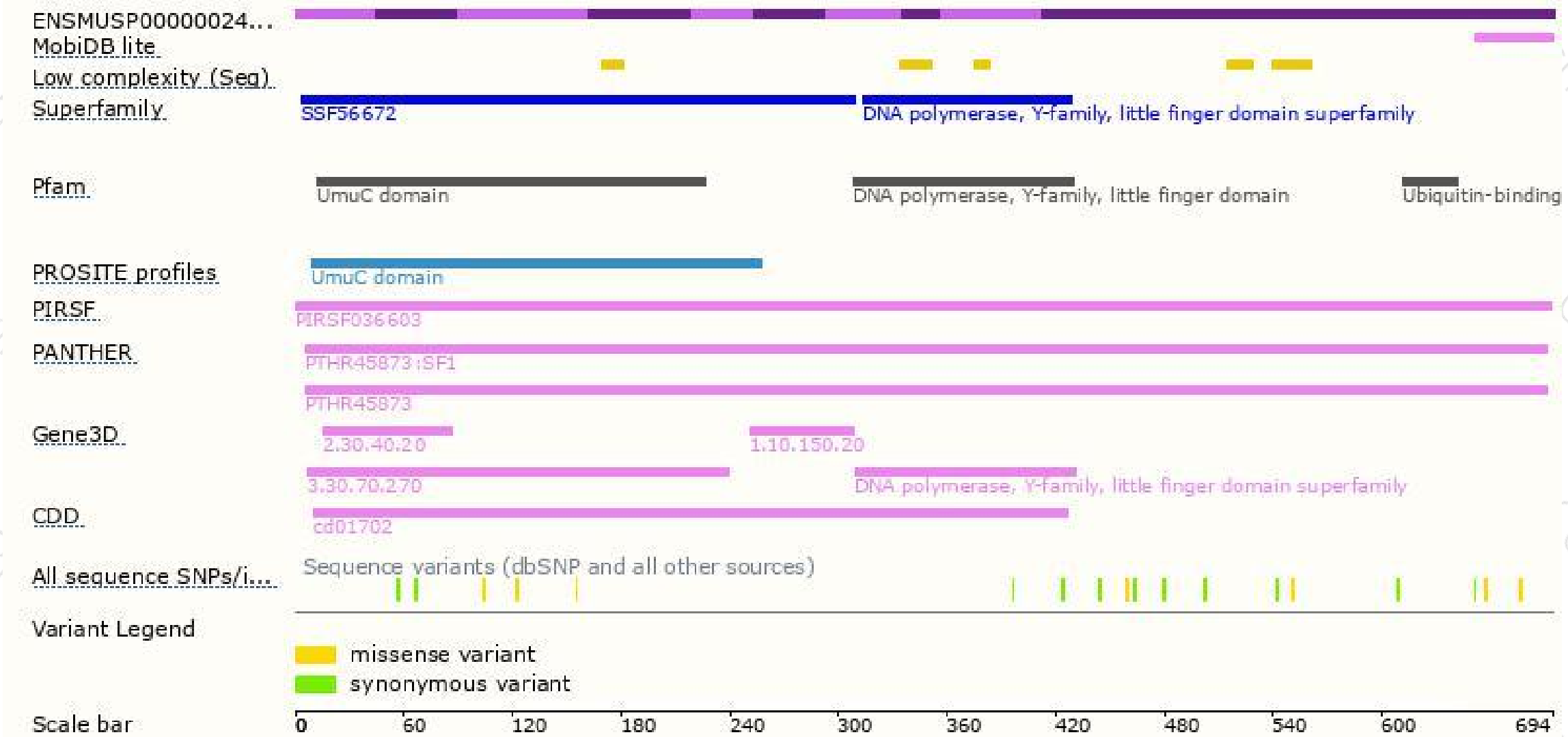


# Genomic location distribution

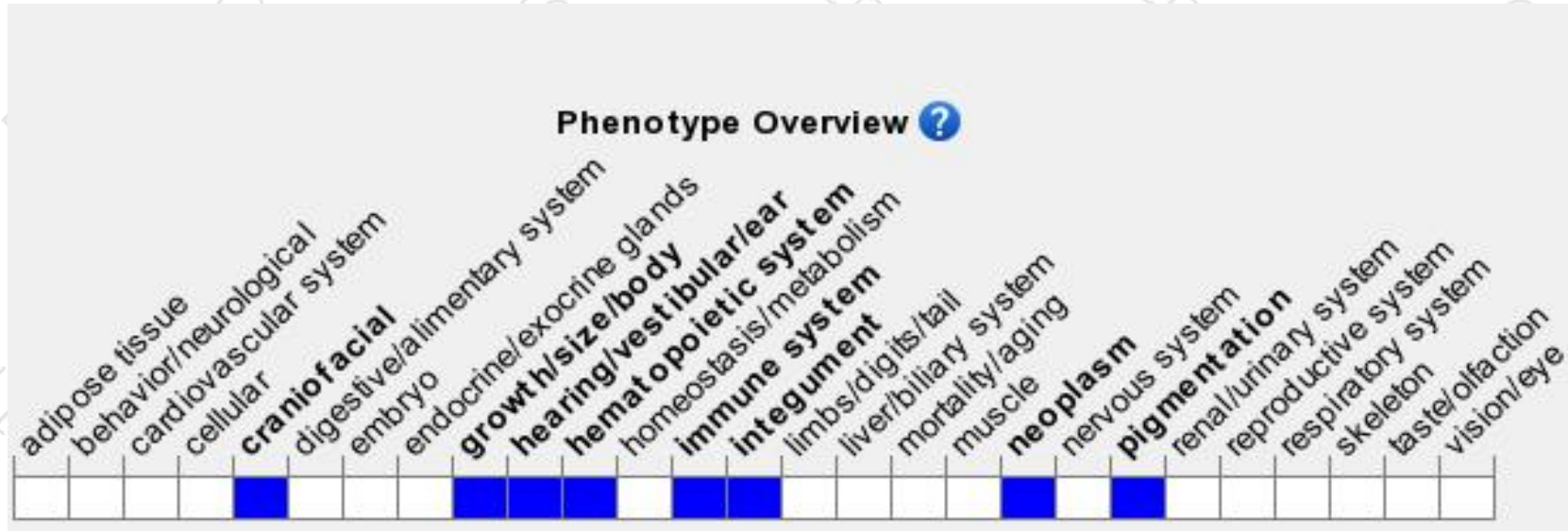




# Protein domain



# 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, Homozygous inactivation of this gene causes increased susceptibility to UV-induced skin tumors and results in reduced immunoglobulin gene mutations at A-T base pairs with a G-C biased mutation pattern.

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

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