

Msh3 Cas9-KO Strategy

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Project Overview

Project Name

Msh3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Msh3* gene. The schematic diagram is as follows:



- The *Msh3* gene has 15 transcripts. According to the structure of *Msh3* gene, exon5-exon8 of *Msh3-202* (ENSMUST00000185852.6) transcript is recommended as the knockout region. The region contains 548bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Msh3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit a partial defect mismatch repair and development of intestinal tumors.
- Transcript *Msh3*-209 may be destroyed directly.
- Transcript *Msh3*-203&207&210&212&213&215 may not be affected.
- The effect on transcript *Msh3*-205&211 is unknown.
- The knockout region is near to the N-terminal of *Dhfr* gene, this strategy may influence the regulatory function of the N-terminal of *Dhfr* gene.
- The N-terminal of *Msh3* gene will remain several amino acids, it may remain the partial function of *Msh3* gene.
- The *Msh3* gene is located on the Chr13. 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)

Msh3 mutS homolog 3 [*Mus musculus* (house mouse)]

Gene ID: 17686, updated on 12-Aug-2019

Summary

- Official Symbol** Msh3 provided by [MGI](#)
- Official Full Name** mutS homolog 3 provided by [MGI](#)
- Primary source** [MGI:MGI:109519](#)
- See related** [Ensembl:ENSMUSG00000014850](#)
- 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** Rep3; Rep-3; D13Em1
- Expression** Ubiquitous expression in CNS E11.5 (RPKM 5.6), CNS E14 (RPKM 4.6) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 13 C3; 13 47.63 cM [See Msh3 in Genome Data Viewer](#)

Exon count: 24

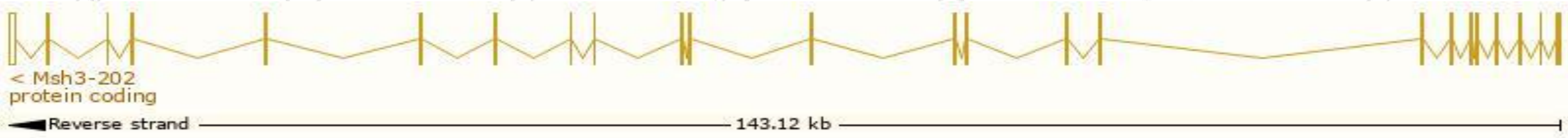
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	13	NC_000079.6 (92211878..92355004, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	13	NC_000079.5 (92981836..93124958, complement)

Transcript information (Ensembl)

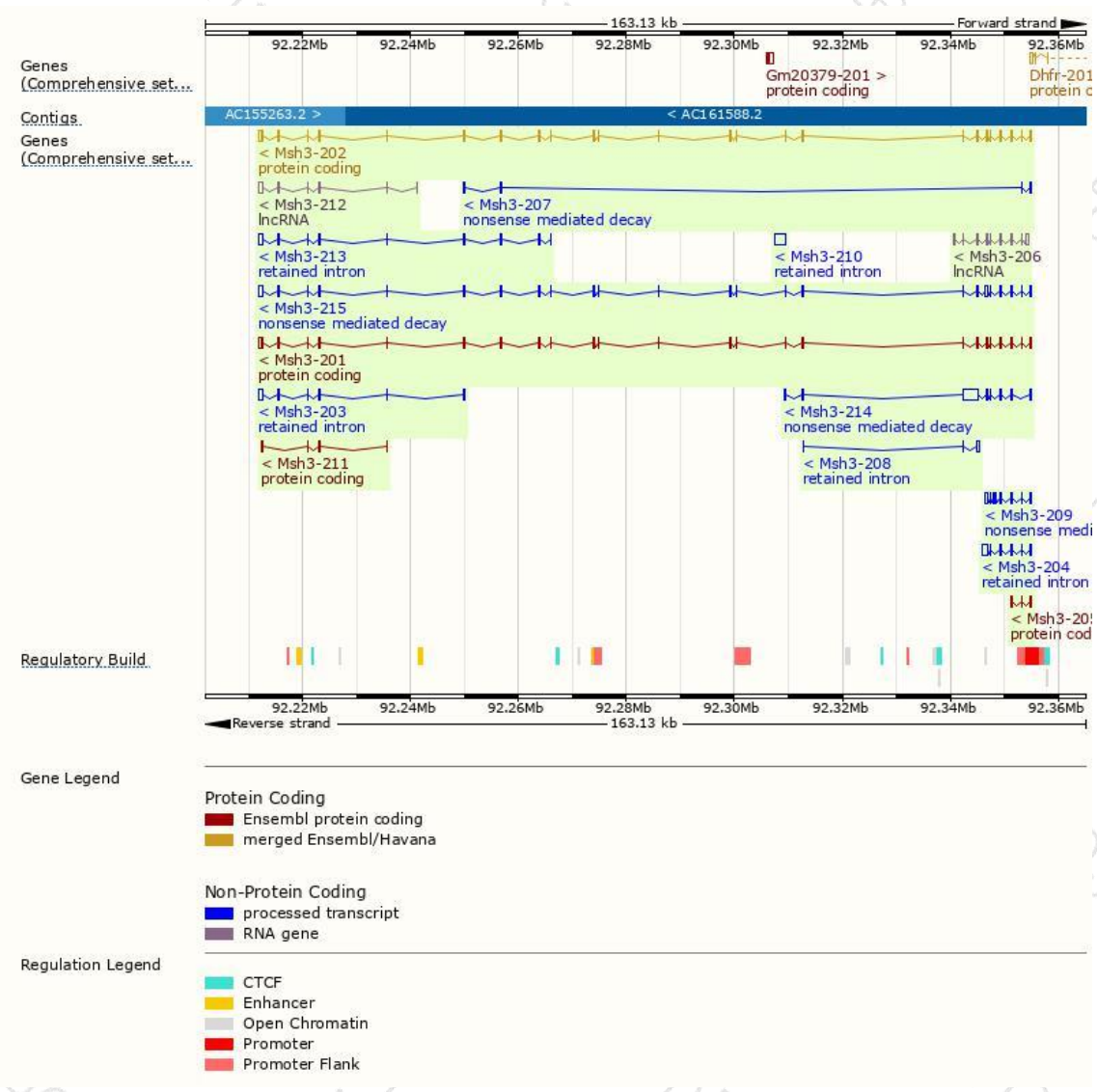
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Msh3-202	ENSMUST00000185852.6	3946	1095aa	Protein coding	CCDS49326	A0A087WQ16	TSL:1 GENCODE basic APPRIS P3
Msh3-201	ENSMUST00000022220.12	3937	1094aa	Protein coding	CCDS79222	E9QPY6	TSL:1 GENCODE basic APPRIS ALT2
Msh3-205	ENSMUST00000187424.1	666	167aa	Protein coding	-	A0A087WP45	TSL:2 GENCODE basic
Msh3-211	ENSMUST00000190761.1	633	129aa	Protein coding	-	A0A087WQZ2	CDS 5' incomplete TSL:5
Msh3-215	ENSMUST00000191550.6	4254	159aa	Nonsense mediated decay	-	A0A087WRJ5	TSL:1
Msh3-214	ENSMUST00000191509.6	4137	56aa	Nonsense mediated decay	-	A0A087WSR8	TSL:1
Msh3-209	ENSMUST00000190393.6	1818	360aa	Nonsense mediated decay	-	A0A087WSS2	TSL:1
Msh3-207	ENSMUST00000187874.6	534	101aa	Nonsense mediated decay	-	A0A087WP43	TSL:5
Msh3-210	ENSMUST00000190462.1	1961	No protein	Retained intron	-	-	TSL:NA
Msh3-204	ENSMUST00000186878.6	1818	No protein	Retained intron	-	-	TSL:1
Msh3-213	ENSMUST00000191304.6	1796	No protein	Retained intron	-	-	TSL:1
Msh3-203	ENSMUST00000186392.1	1555	No protein	Retained intron	-	-	TSL:1
Msh3-208	ENSMUST00000189376.6	625	No protein	Retained intron	-	-	TSL:3
Msh3-206	ENSMUST00000187831.6	1753	No protein	lncRNA	-	-	TSL:1
Msh3-212	ENSMUST00000191242.6	1363	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Msh3-202* transcript,The transcription is shown below



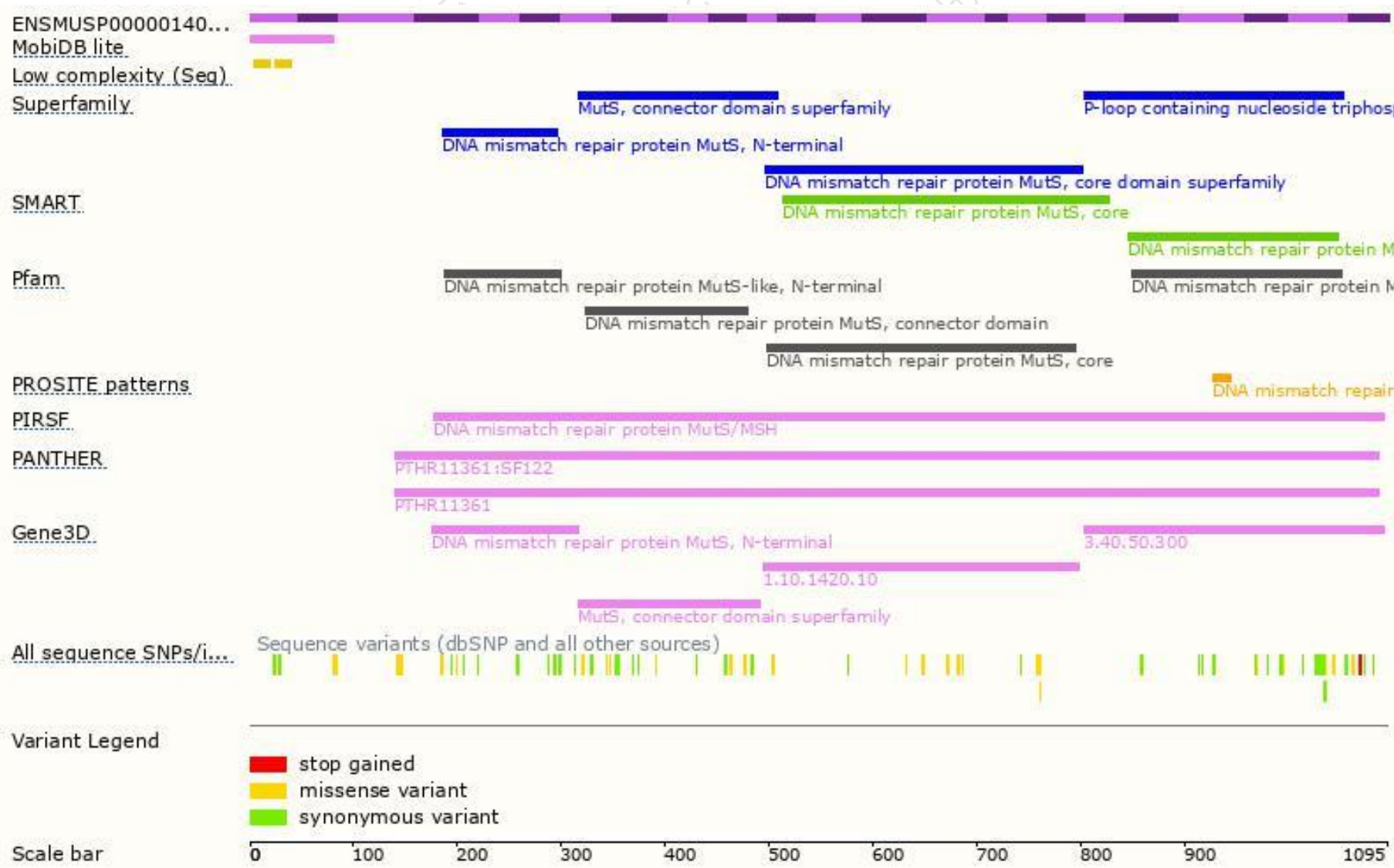
Genomic location distribution



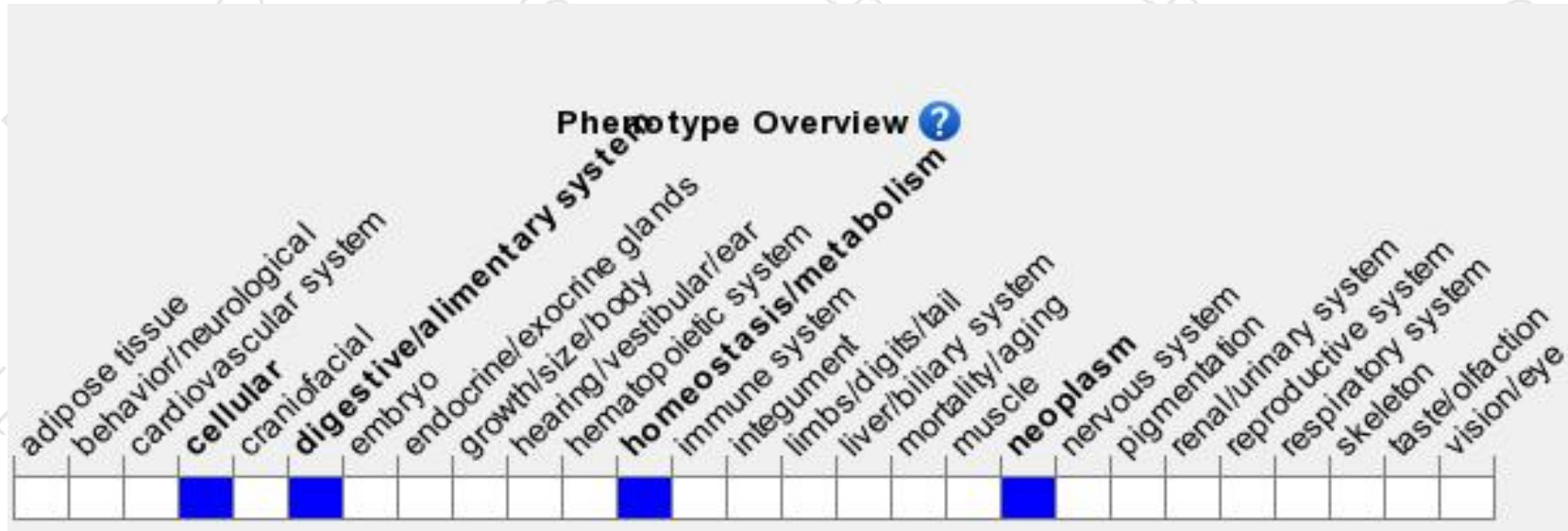
Protein domain



集萃药康
GemPharmatech



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 knock-out allele exhibit a partial defect mismatch repair and development of intestinal tumors.

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

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