

Xpa Cas9-KO Strategy

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Reviewer:

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Design Date:

2020/1/16

Project Overview

Project Name

Xpa

Project type

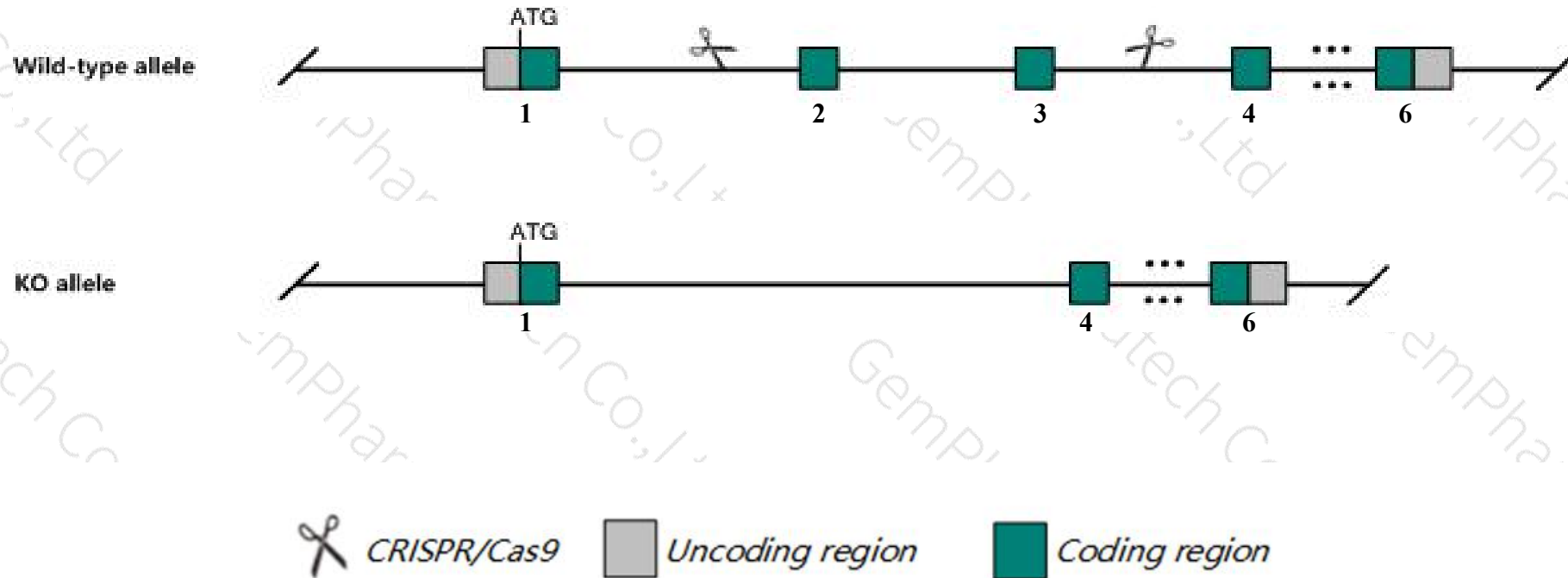
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Xpa* gene has 6 transcripts. According to the structure of *Xpa* gene, exon2-exon3 of *Xpa-201* (ENSMUST00000030013.11) transcript is recommended as the knockout region. The region contains 214bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Xpa* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mutants are highly susceptible to tumors induced by UV (skin and ocular tumors), 7,12-dimethylbenz[a]anthracene (skin tumors), benzo[a]pyrene (pulmonary tumors), 4-nitroquinoline-1-oxide (tongue tumors) and aflatoxin B(1) (liver tumors).
- The *Xpa* gene is located on the Chr4. 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)

Xpa xeroderma pigmentosum, complementation group A [*Mus musculus* (house mouse)]

Gene ID: 22590, updated on 12-Nov-2019

Summary

Official Symbol Xpa provided by [MGI](#)
Official Full Name xeroderma pigmentosum, complementation group A provided by [MGI](#)
Primary source [MGI:MGI:99135](#)
See related [Ensembl:ENSMUSG00000028329](#)
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 Xpac; AI573865
Expression Ubiquitous expression in ovary adult (RPKM 10.5), duodenum adult (RPKM 8.1) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 4 B1; 4 24.49 cM

See Xpa in [Genome Data Viewer](#)

Exon count: 7

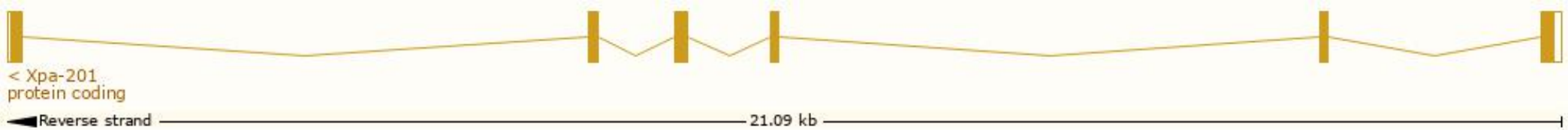
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (46175220..46196344, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (46188094..46209183, complement)

Transcript information (Ensembl)

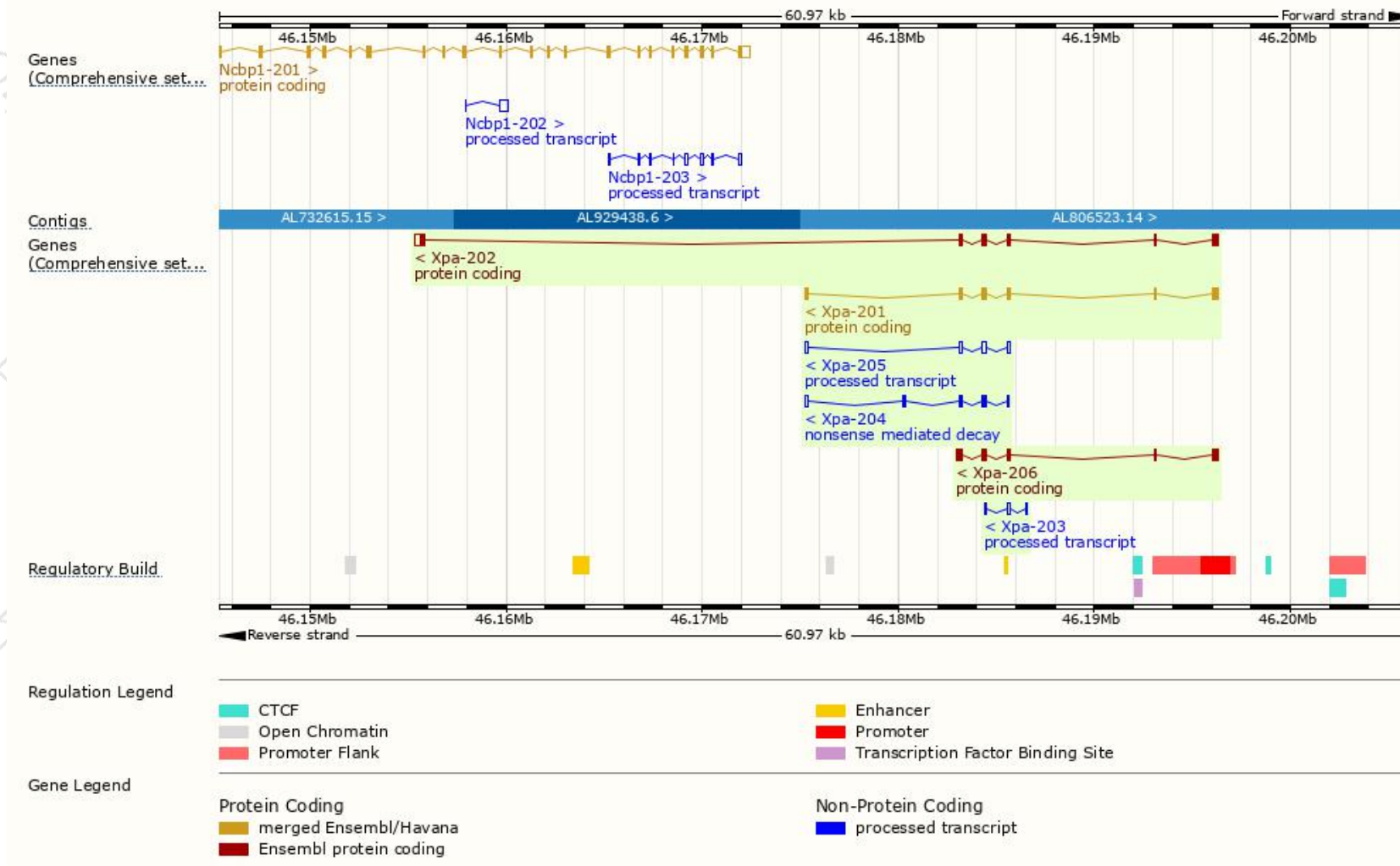
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Xpa-201	ENSMUST00000030013.11	955	272aa	Protein coding	CCDS18146	Q64267	TSL:1 GENCODE basic APPRIS P2
Xpa-202	ENSMUST00000058232.10	1241	279aa	Protein coding	-	Q8K2X7	TSL:1 GENCODE basic APPRIS ALT2
Xpa-206	ENSMUST000000142380.1	903	273aa	Protein coding	-	Q64267	CDS 3' incomplete TSL:1
Xpa-204	ENSMUST000000132358.7	729	134aa	Nonsense mediated decay	-	S4R260	CDS 5' incomplete TSL:5
Xpa-205	ENSMUST000000141318.1	577	No protein	Processed transcript	-	-	TSL:1
Xpa-203	ENSMUST000000130051.1	259	No protein	Processed transcript	-	-	TSL:3

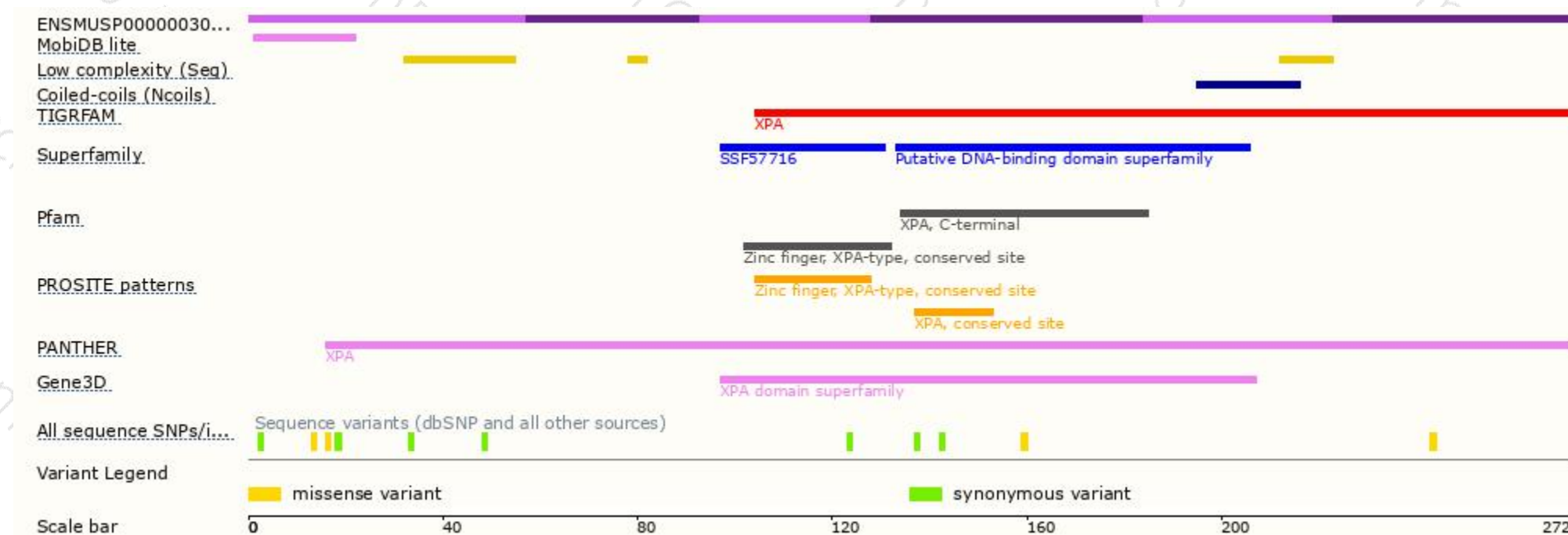
The strategy is based on the design of *Xpa-201* transcript,The transcription is shown below



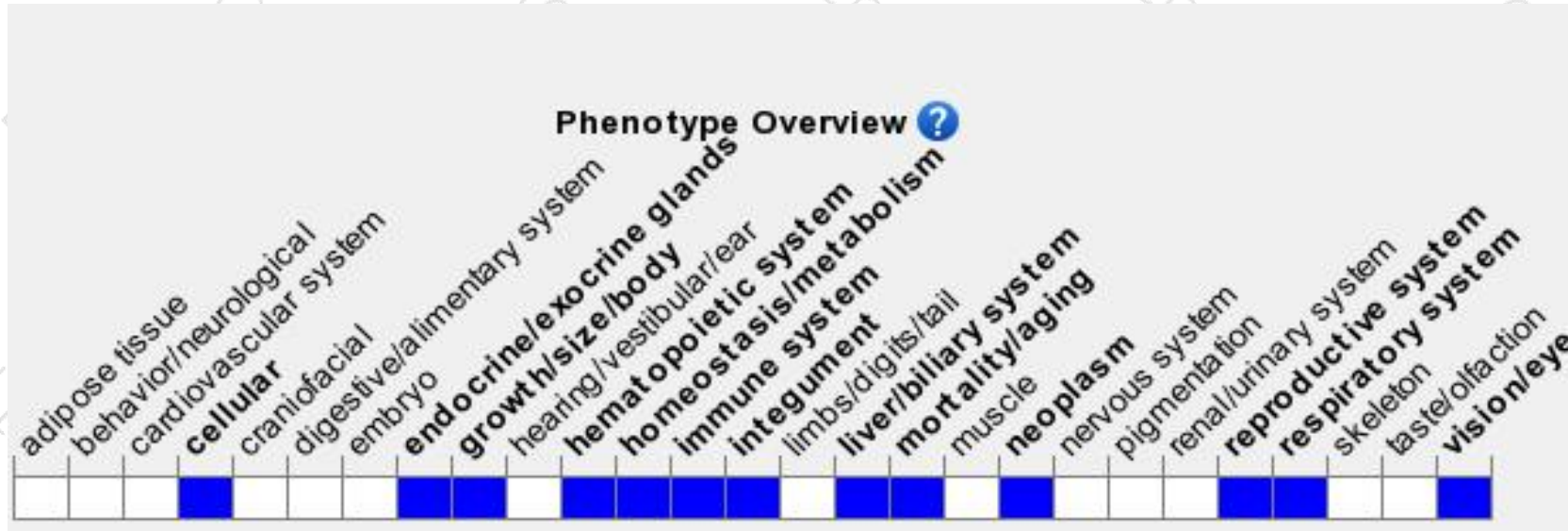
Genomic location distribution



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 null mutants are highly susceptible to tumors induced by UV (skin and ocular tumors), 7,12-dimethylbenz[a]anthracene (skin tumors), benzo[a]pyrene (pulmonary tumors), 4-nitroquinoline-1-oxide (tongue tumors) and aflatoxin B(1) (liver tumors).

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

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