Ahr Cas9-KO Strategy

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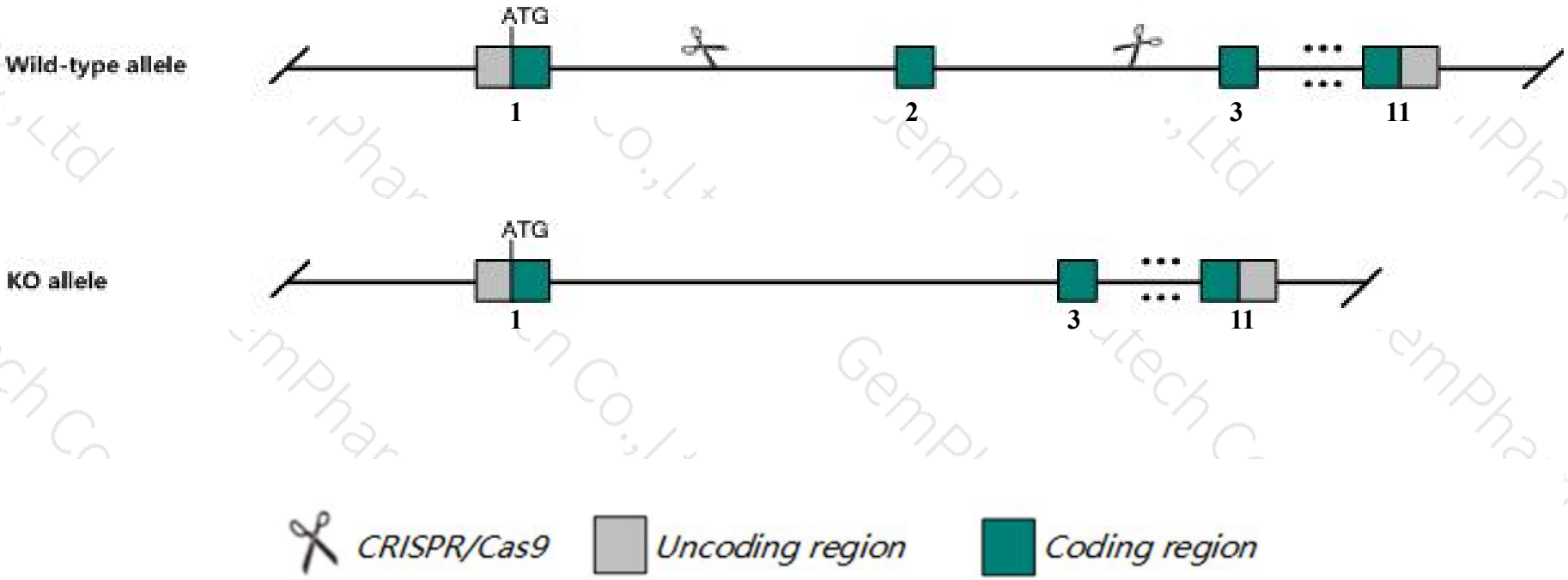
Design Date: 2019-8-6

Project Overview

Project Name	***Ahr***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Ahr* gene has 3 transcripts. According to the structure of *Ahr* gene, exon2 of *Ahr-202* (ENSMUST00000116436.8) transcript is recommended as the knockout region.The region contains 188bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ahr* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Homozygotes for null or hypomorphic alleles do not respond to cyclic compounds (e.g., dioxin) and are resistant to their teratogenic effects. Depending on the allele, null mutants may also have liver defects, impaired female fertility, neonatal or postnatal lethality, and spleen abnormalities. Conditional homozygous KO in the retina leads to retinal degeneration.

- The *Ahr* gene is located on the Chr12. 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）

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Ahr aryl-hydrocarbon receptor [Mus musculus (house mouse)]

Gene ID: 11622, updated on 9-Apr-2019

Summary

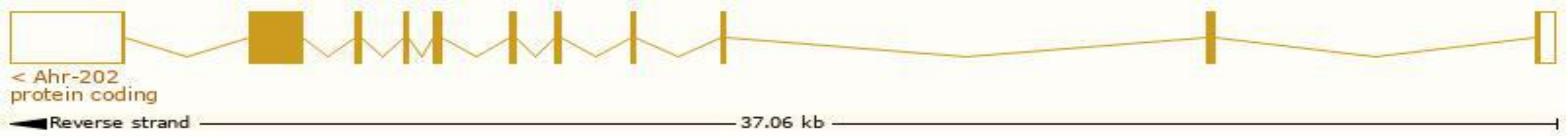
Official Symbol	Ahr provided by MGI
Official Full Name	aryl-hydrocarbon receptor provided by MGI
Primary source	MGI:MGI:105043
See related	Ensembl:ENSMUSG00000019256
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ah, Ahh, Ahre, In, bHLHe76
Summary	The protein encoded by this gene is a ligand-activated helix-loop-helix transcription factor involved in the regulation of biological responses to planar aromatic hydrocarbons. This receptor has been shown to regulate xenobiotic-metabolizing enzymes such as cytochrome P450. Before ligand binding, the encoded protein is sequestered in the cytoplasm; upon ligand binding, this protein moves to the nucleus and stimulates transcription of target genes. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Broad expression in lung adult (RPKM 15.1), bladder adult (RPKM 5.5) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

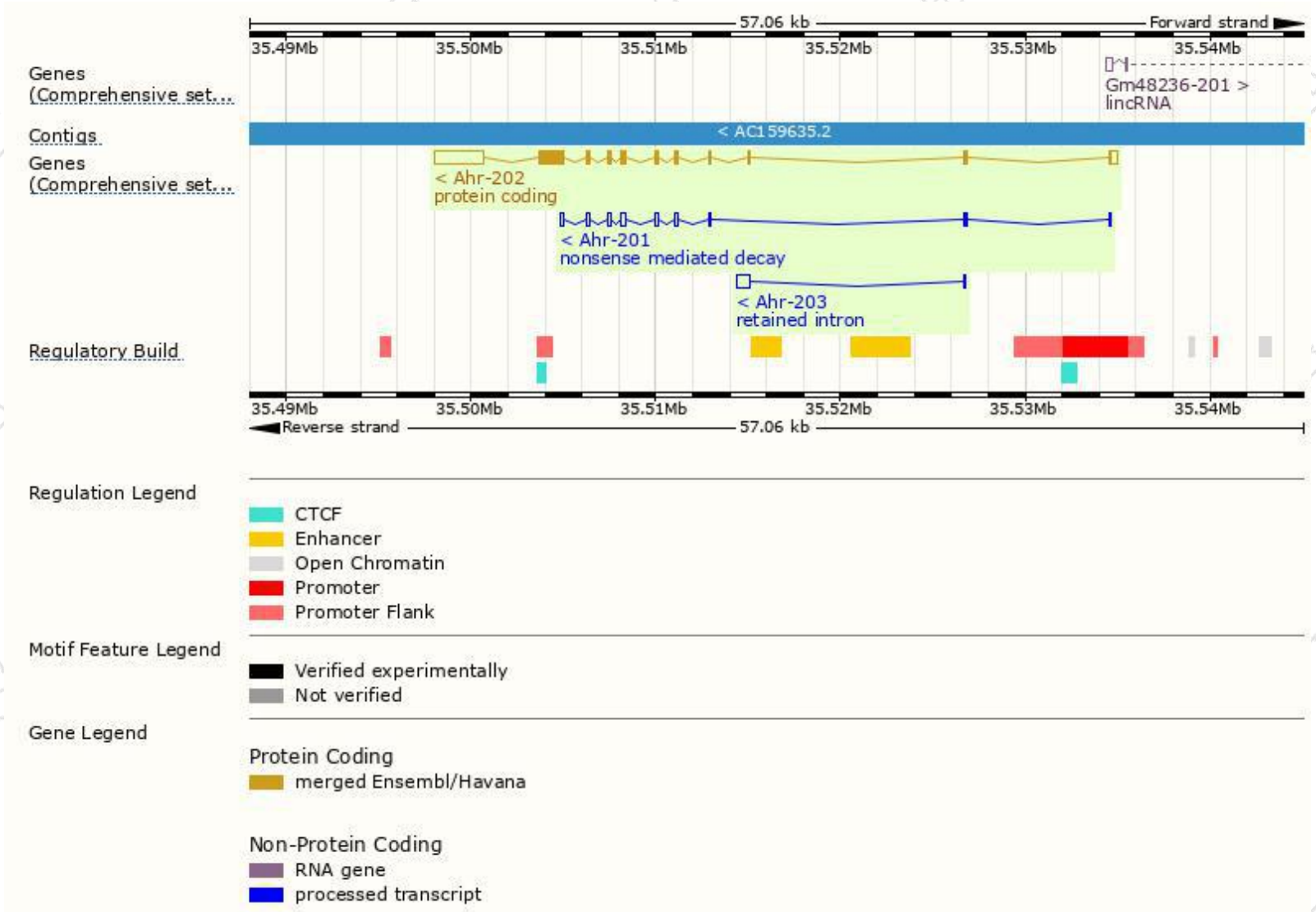
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ahr-202	ENSMUST00000116436.8	5548	805aa	Protein coding	CCDS36434	Q3U5D9	TSL:1 GENCODE basic APPRIS P1
Ahr-201	ENSMUST00000110811.2	1155	114aa	Nonsense mediated decay	-	A0A0B4J1L1	TSL:1
Ahr-203	ENSMUST00000173414.1	818	No protein	Retained intron	-	-	TSL:3

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

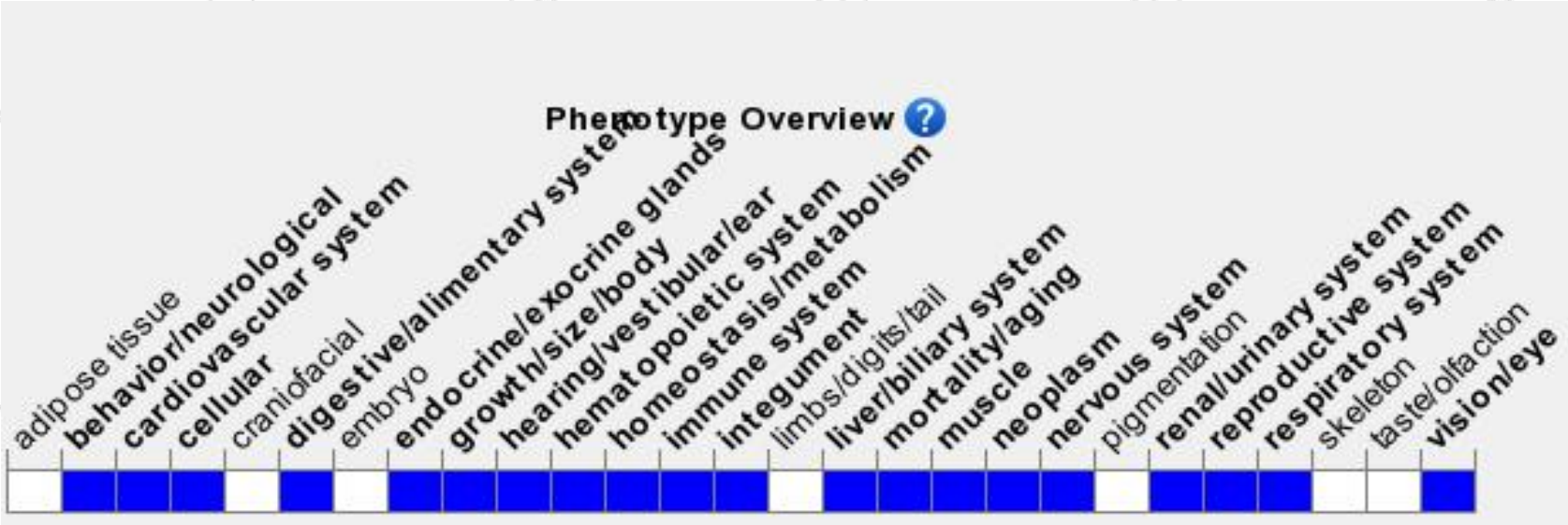


Genomic location distribution



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/).

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

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