Bcr Cas9-KO *Strategy*

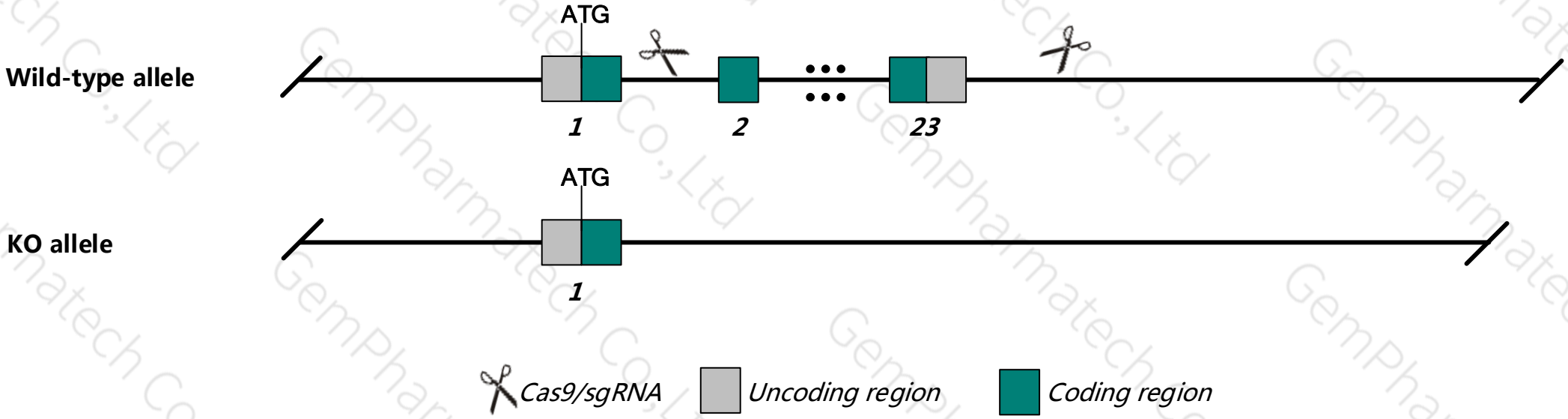
Designer: Daohua Xu

Project Overview

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

Knockout strategy

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



Technical routes

- The *Bcr* gene has 5 transcripts.According to the structure of *Bcr* gene, exon2-exon23 of *Bcr*-201 transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Bcr* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

- The *Bcr* gene is located on the Chr10. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information （NCBI）

Bcr breakpoint cluster region [*Mus musculus* (house mouse)]

Gene ID: 110279, updated on 12-Mar-2019

Summary

Official Symbol	Bcr provided by MGI
Official Full Name	breakpoint cluster region provided by MGI
Primary source	MGI:MGI:88141
See related	Ensembl:ENSMUSG00000009681
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	AI561783; AI853148; mKIAA3017; 5133400C09Rik
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 14.4), lung adult (RPKM 12.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts, and all transcripts are shown below ：

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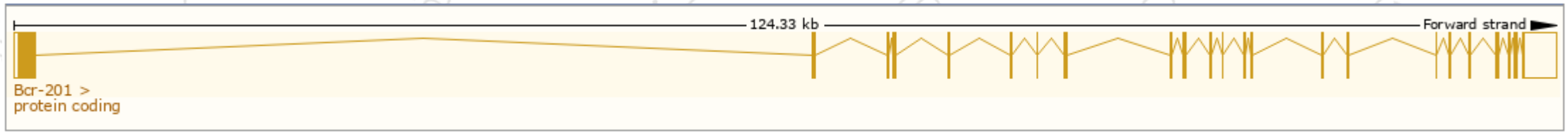
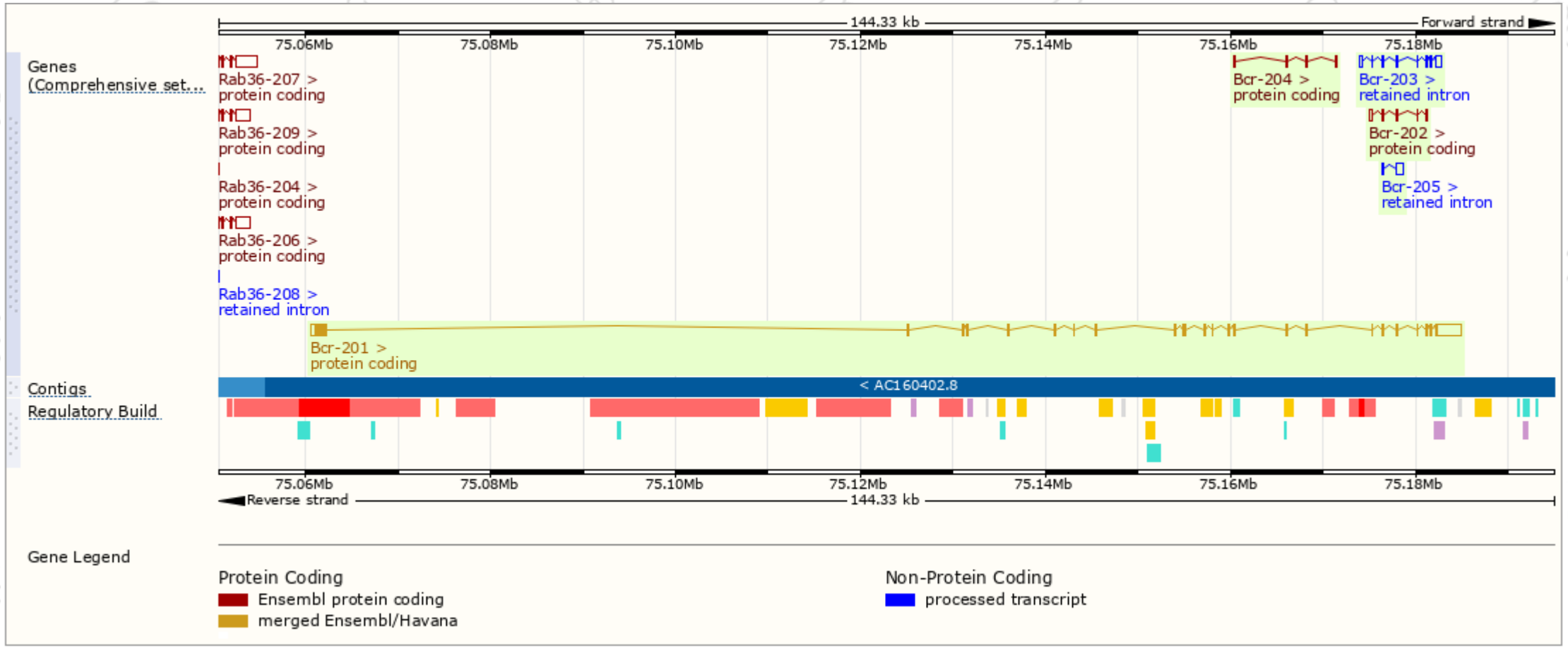
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bcr-201	ENSMUST00000164107.2	6839	1270aa	Protein coding	CCDS35935	Q6PAJ1	TSL:1 GENCODE basic APPRIS P1
Bcr-202	ENSMUST00000218057.1	835	182aa	Protein coding	-	A0A1W2P6I7	CDS 3' incomplete TSL:5
Bcr-204	ENSMUST00000218591.1	489	120aa	Protein coding	-	A0A1W2P6J3	CDS 5' incomplete TSL:5
Bcr-203	ENSMUST00000218465.1	1460	No protein	Retained intron	-	-	TSL:1
Bcr-205	ENSMUST00000219807.1	846	No protein	Retained intron	-	-	TSL:3

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

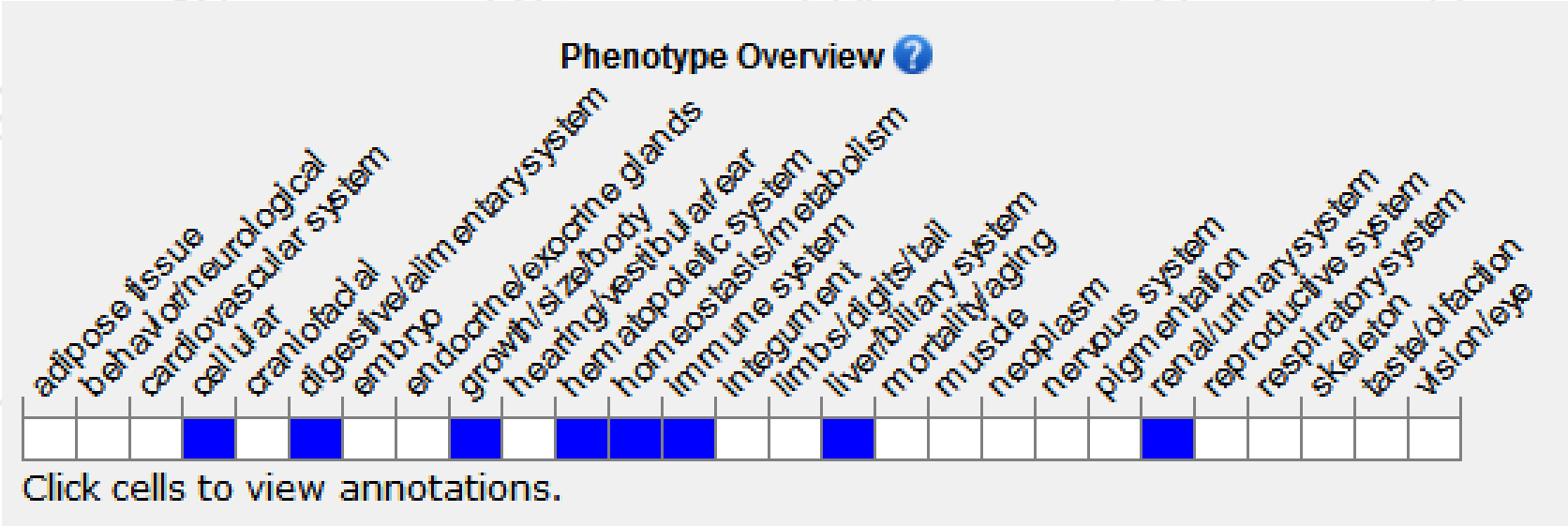


Genomic location distribution



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 defective in hormonal and behavioral stress response regulation and prone to septic shock, whereas chimeric mice carrying a BCR-ABL fusion mutation mimicking human Philadelphia chromosome develop chronic myeloid leukemia.

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

Tel: 025-5864 1534

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