

Cttnbp2 Cas9-CKO Strategy

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Design Date: 2023-9-15

Overview

Target Gene Name

- Ctnnbp2

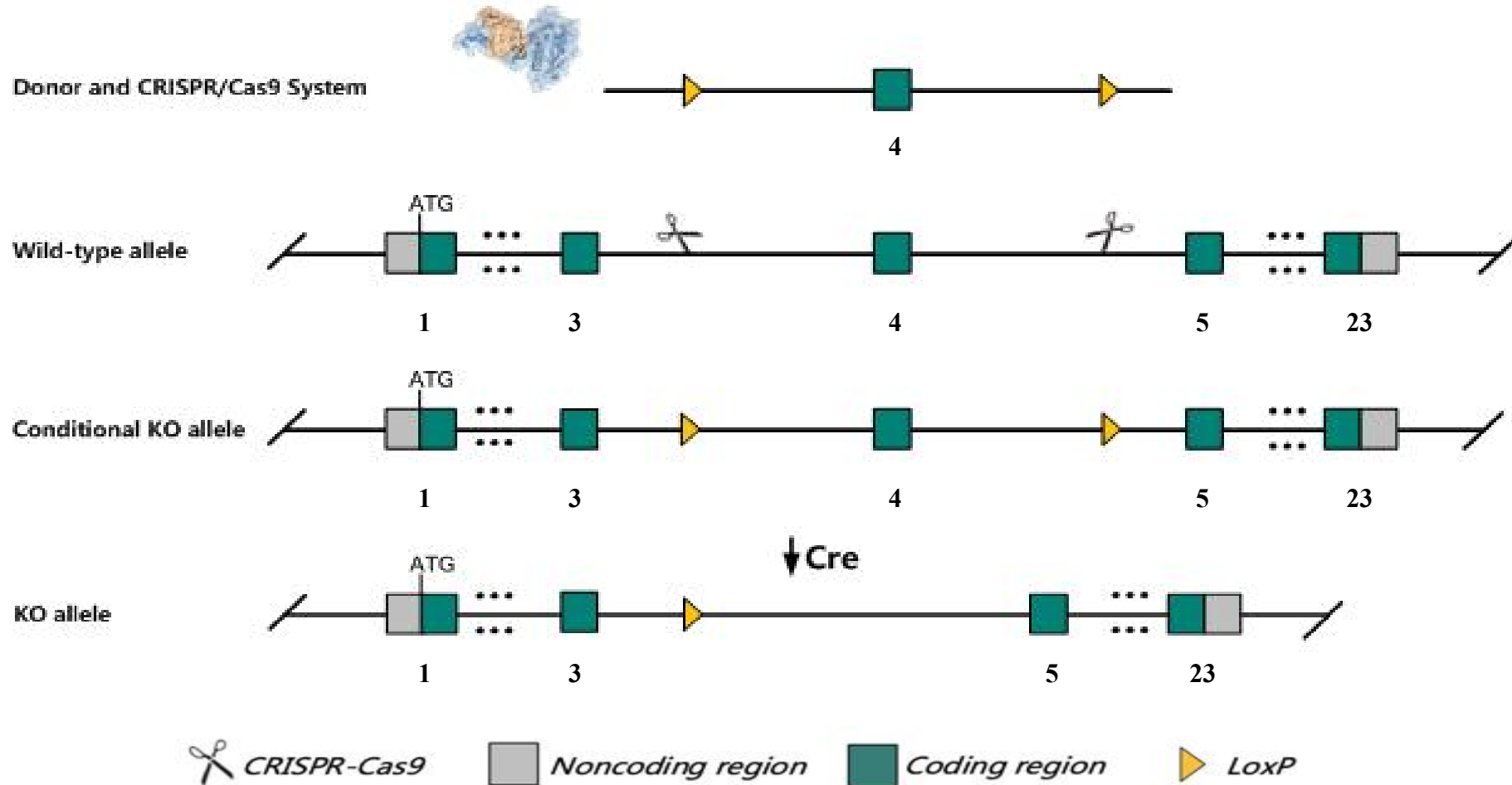
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ctnbp2* gene.

Technical Information

- The *Cttnbp2* gene has 9 transcripts. According to the structure of *Cttnbp2* gene, exon4 of *Cttnbp2*-201 (ENSMUST00000090601.12) transcript is recommended as the knockout region. The region contains 1627bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cttnbp2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Cttnbp2 cortactin binding protein 2 [Mus musculus (house mouse)]

Gene ID: 30785, updated on 13-Mar-2020

Summary

Official Symbol	Cttnbp2 provided by MGI
Official Full Name	cortactin binding protein 2 provided by MGI
Primary source	MGI:MGI:1353467
See related	Ensembl:ENSMUSG00000000416
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	3010022N24Rik, 4732477G22Rik, 6430526E05, 9130022E09Rik, AU040881, Cortbp2, ORF4, mKIAA1758
Expression	Biased expression in frontal lobe adult (RPKM 16.8), cortex adult (RPKM 13.4) and 13 other tissues See more
Orthologs	human all

Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

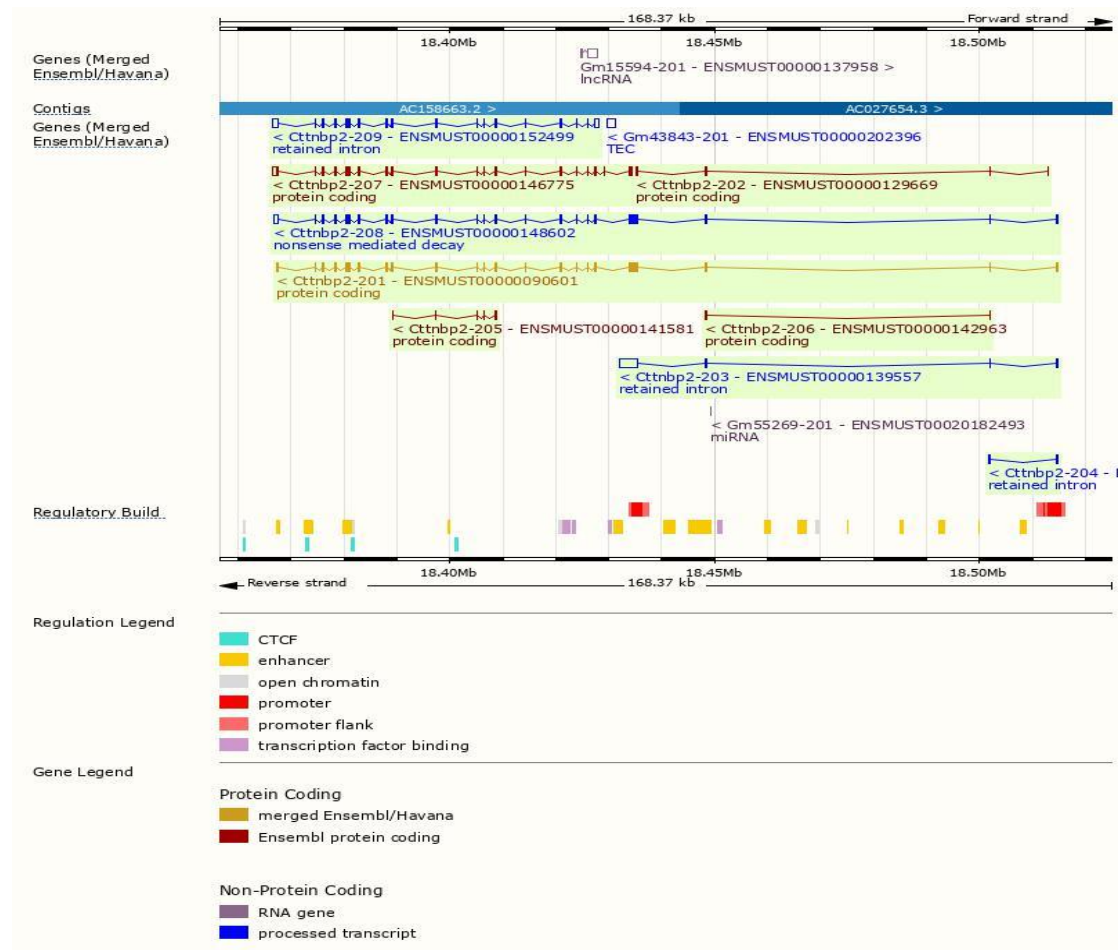
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000090601.12	Cttnbp2-201	5183	1648aa	Protein coding	CCDS39432	B9EJA2-1	Ensembl Canonical Gencode basic APPRIS P1 TSL:1
ENSMUST00000146775.8	Cttnbp2-207	4224	1139aa	Protein coding		F6Q1W8	TSL:1 CDS 5' incomplete
ENSMUST00000141581.2	Cttnbp2-205	580	193aa	Protein coding		F6XSM7	TSL:5 CDS 5' and 3' incomplete
ENSMUST00000129669.8	Cttnbp2-202	575	160aa	Protein coding		D3Z1E3	TSL:5 CDS 3' incomplete
ENSMUST00000142963.3	Cttnbp2-206	328	94aa	Protein coding		D3Z551	TSL:3 CDS 3' incomplete
ENSMUST00000148602.8	Cttnbp2-208	5462	630aa	Nonsense mediated decay		B9EJA2-2	TSL:1
ENSMUST00000152499.8	Cttnbp2-209	4391	No protein	Retained intron		-	TSL:1
ENSMUST00000139557.2	Cttnbp2-203	3982	No protein	Retained intron		-	TSL:1
ENSMUST00000140416.2	Cttnbp2-204	620	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Cttnbp2-201* transcript, the transcription is shown below:

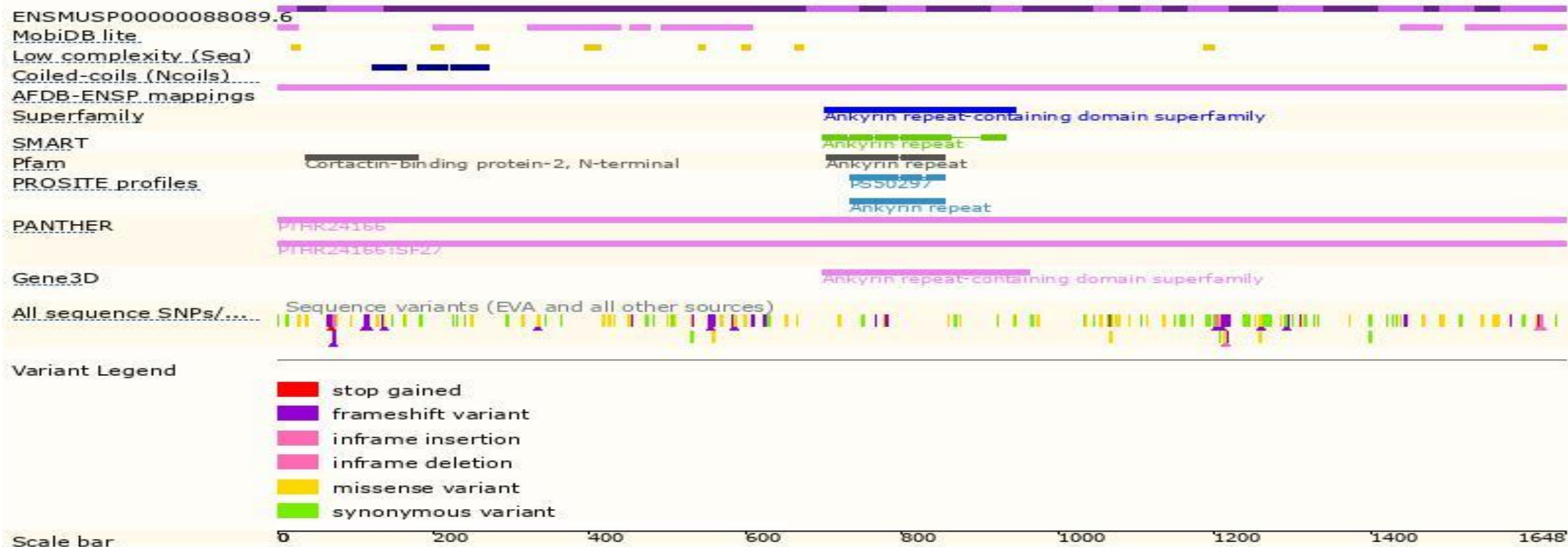


Source: <https://www.ensembl.org>

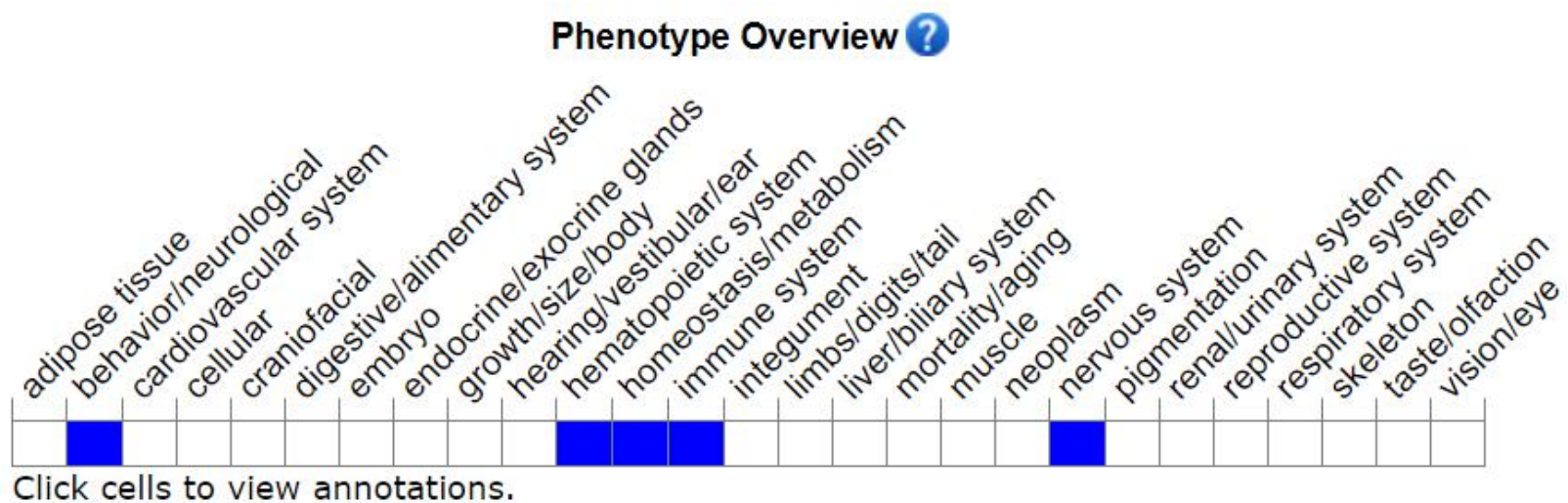
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)

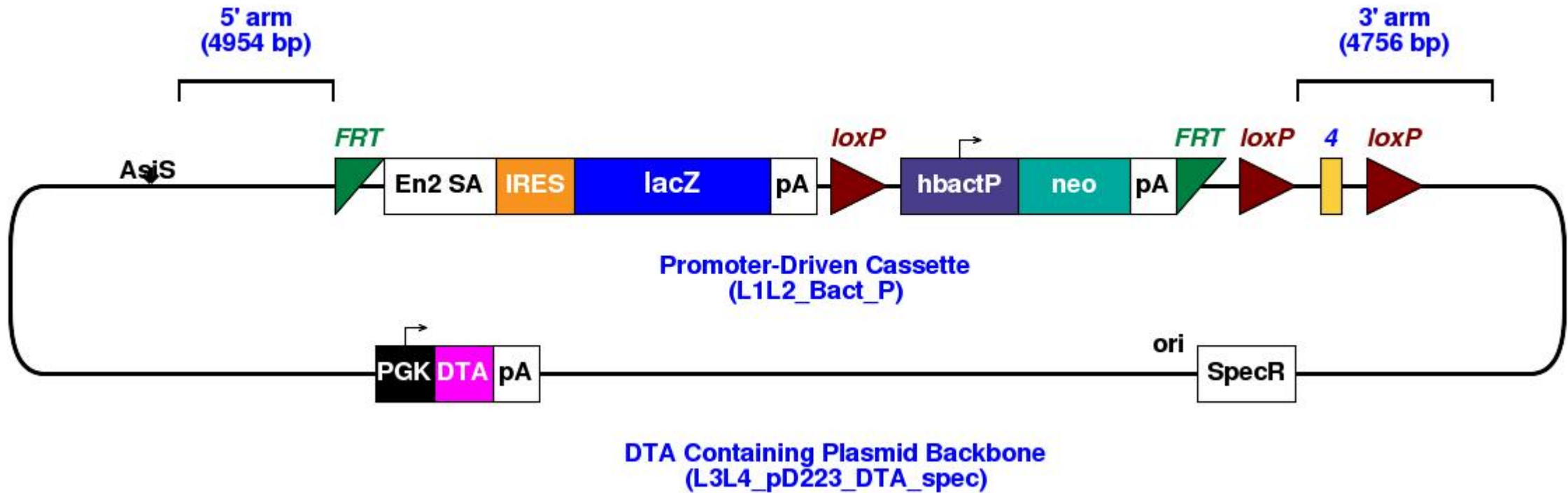


Important Information

- Some amino acids of *Cttnbp2* gene will remain at the N-terminus and some functions may be retained.
- Transcript 207 CDS 5' incomplete the influences is unknown.
- Transcript 202,206 CDS 3' incomplete the influences is unknown.
- Transcript 205 CDS 5' and 3' incomplete the influences is unknown.
- The floxed region is near to the N-terminal of *Gm43843* gene, this strategy may influence the regulatory function of the N-terminal of *Gm43843* gene.
- *Cttnbp2* is located on Chr6. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Reference

MGI Allele	Allele Type	Produced
Ctnbp2^{tm1a(KOMP)Wtsi}	KO first allele (reporter-tagged insertion with conditional potential)	Mice, Targeting vectors, ES Cells



<https://www.mousephenotype.org/data/genes/MGI:1353467>