# *Cdk8* Cas9-CKO Strategy

**Designer:**        **Huan Wang**

**Design Date:**    **2019-7-22**

# Project Overview

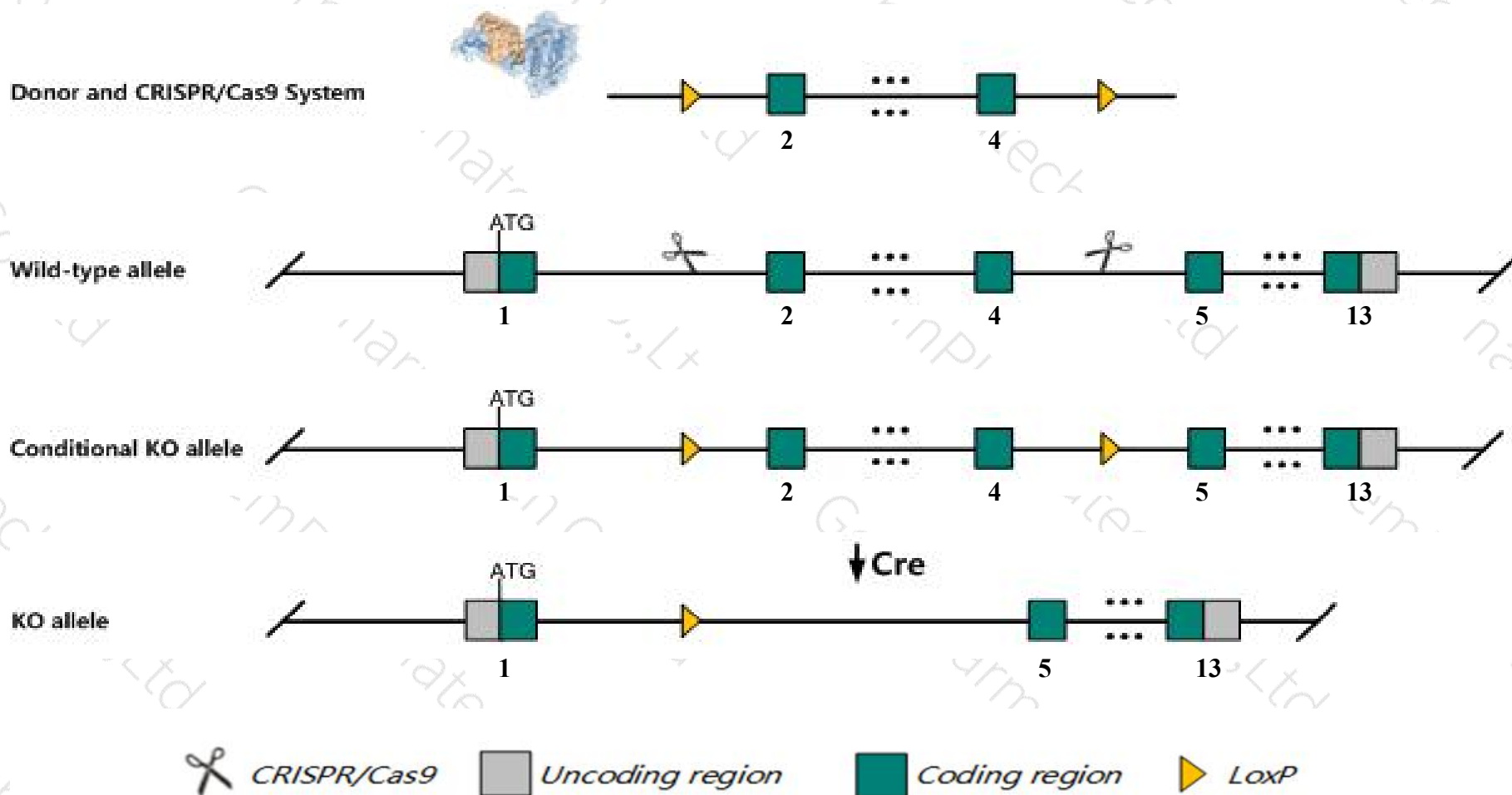| | |
|---|---|
| **Project Name** | *Cdk8* |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdk8* gene. The schematic diagram is as follows:

# Technical routes

➢ The *Cdk8* gene has 9 transcripts. According to the structure of *Cdk8* gene, exon2-exon4 of *Cdk8-201* (ENSMUST00000031640.14) transcript is recommended as the knockout region.The region contains 328bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cdk8* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➢ 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.

# Notice

➢ According to the existing MGI data,Mice homozygous for a gene-trapped allele die prior to implantation exhibiting fragmented blastomeres and failure to undergo compaction.

➢ The *Cdk8* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Gene information （NCBI）

## Cdk8 cyclin-dependent kinase 8 [Mus musculus (house mouse)]
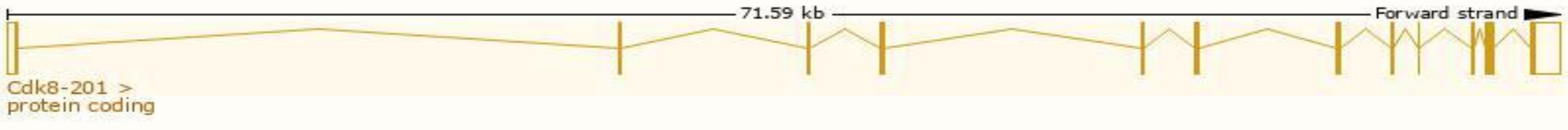
Gene ID: 264064, updated on 5-Mar-2019

### ▲Summary

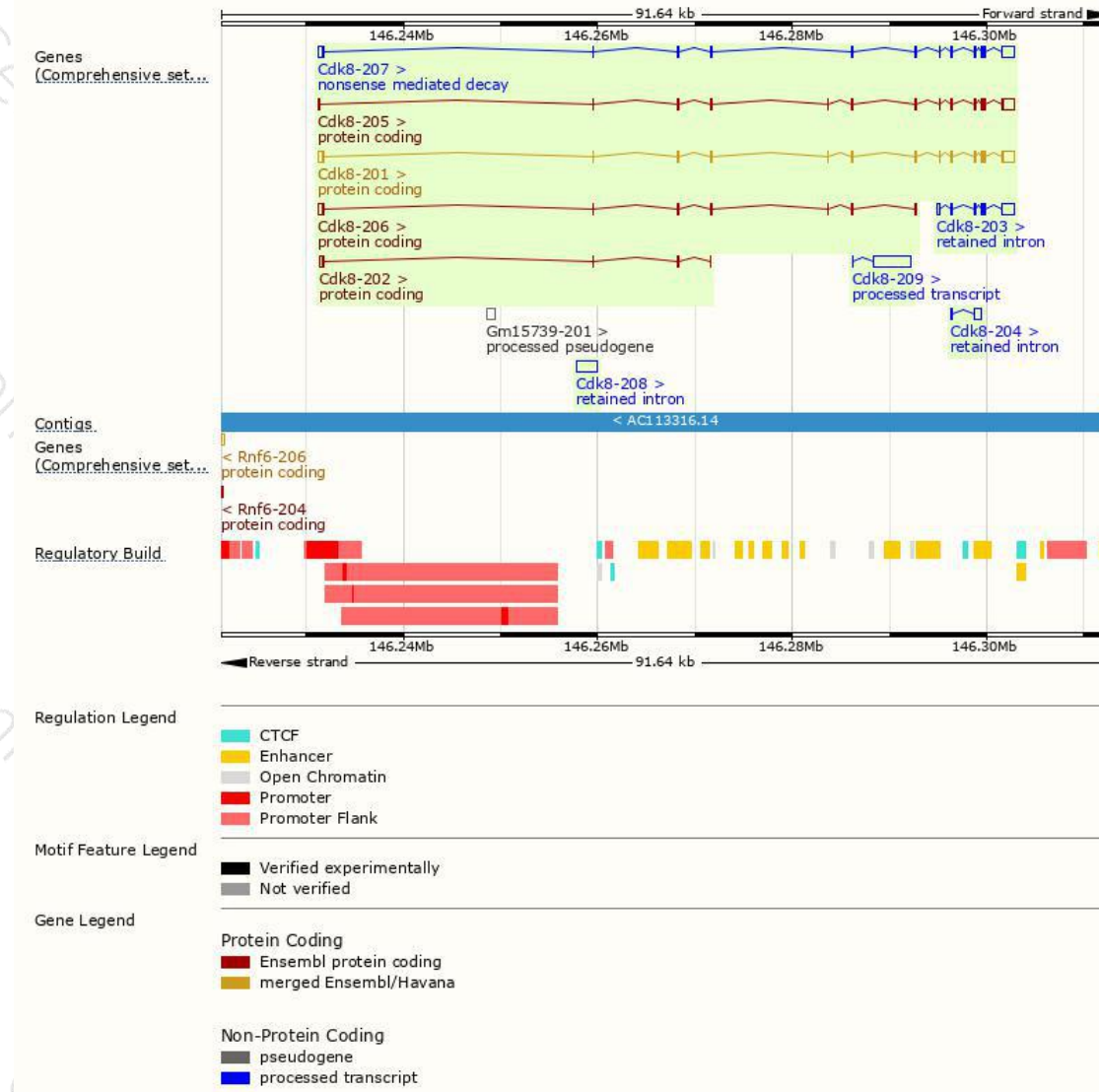| | |
|---|---|
| **Official Symbol** | Cdk8 provided by MGI |
| **Official Full Name** | cyclin-dependent kinase 8 provided by MGI |
| **Primary source** | MGI:MGI:1196224 |
| **See related** | Ensembl:ENSMUSG00000029635 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Expression** | Ubiquitous expression in adrenal adult (RPKM 21.2), ovary adult (RPKM 18.4) and 28 other tissuesSee more |
| **Orthologs** | human  all |

# Transcript information（Ensembl）

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

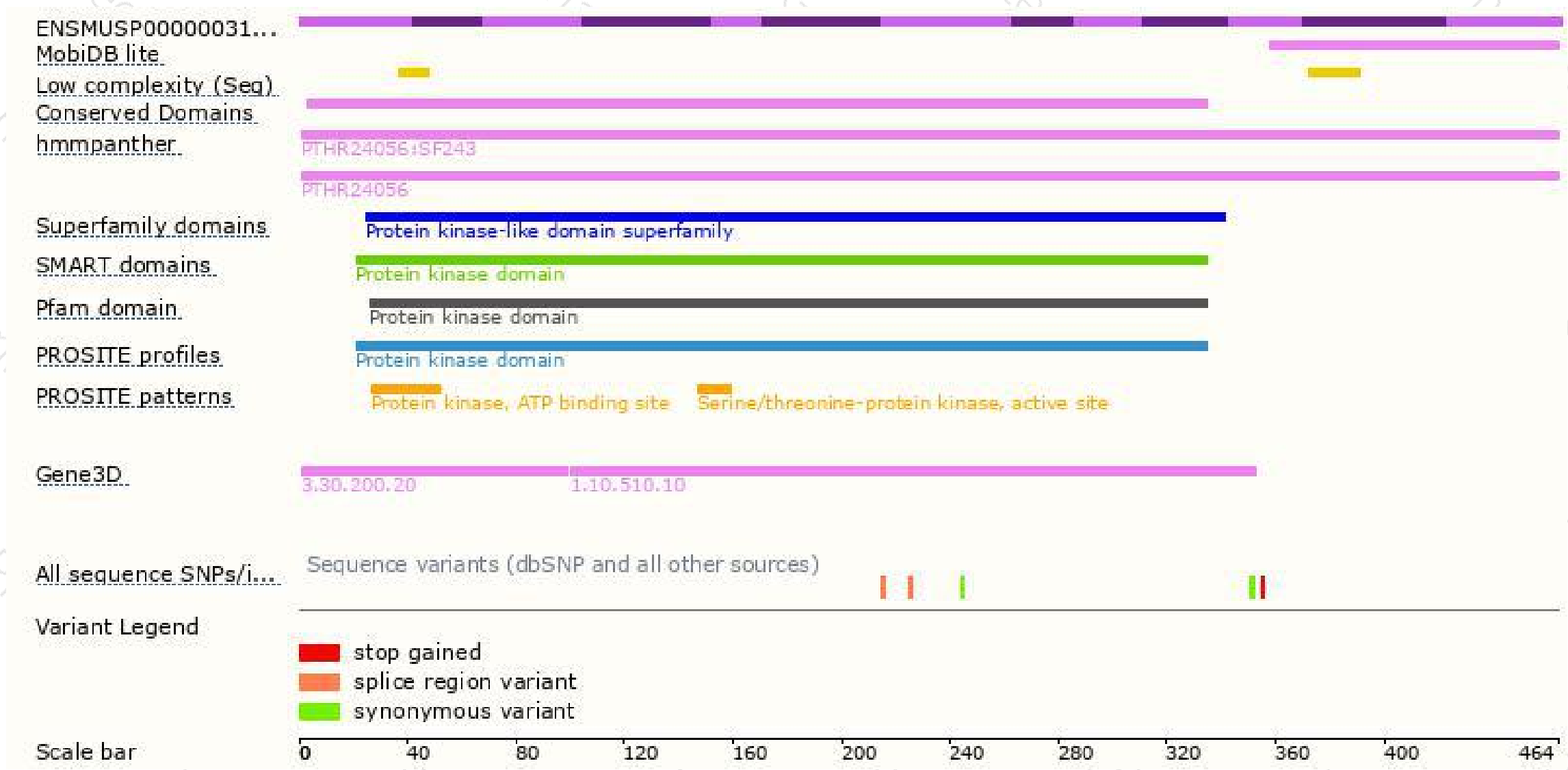| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------|--------------|-----|---------|---------|------|---------|-------|
| Cdk8-201 | ENSMUST00000031640.14 | 2973 | 464aa | Protein coding | CCDS19869 | Q8R3L8 | TSL:2 GENCODE basic APPRIS P1 |
| Cdk8-205 | ENSMUST00000161181.7 | 2467 | 399aa | Protein coding | - | E9Q6E2 | TSL:1 GENCODE basic |
| Cdk8-206 | ENSMUST00000161652.7 | 1142 | 245aa | Protein coding | - | E0CYC4 | CDS 3' incomplete TSL:5 |
| Cdk8-202 | ENSMUST00000159467.1 | 654 | 115aa | Protein coding | - | E0CY29 | CDS 3' incomplete TSL:3 |
| Cdk8-207 | ENSMUST00000162494.7 | 2973 | 164aa | Nonsense mediated decay | - | E0CZC3 | TSL:5 |
| Cdk8-209 | ENSMUST00000198861.1 | 3896 | No protein | Processed transcript | - | - | TSL:5 |
| Cdk8-208 | ENSMUST00000195944.1 | 2195 | No protein | Retained intron | - | - | TSL:NA |
| Cdk8-203 | ENSMUST00000159615.1 | 1976 | No protein | Retained intron | - | - | TSL:1 |
| Cdk8-204 | ENSMUST00000160924.1 | 777 | No protein | Retained intron | - | - | TSL:3 |

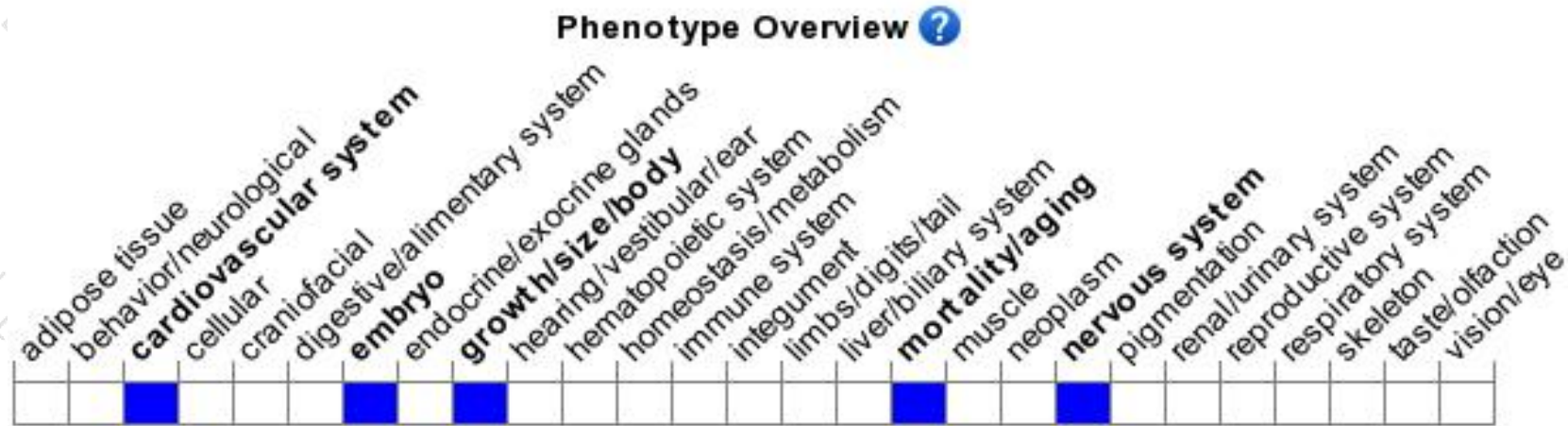The strategy is based on the design of *Cdk8-201* transcript,The transcription is shown below

# Genomic location distribution

# Protein domain



| | | |
|---|---|---|
| ENSMUSP00000031... | | |
| MobiDB lite | | |
| Low complexity (Seg) | | |
| Conserved Domains | | |
| hmmpanther | PTHR24056:SF243 | |
| | PTHR24056 | |
| Superfamily domains | Protein kinase-like domain superfamily | |
| SMART domains | Protein kinase domain | |
| Pfam domain | Protein kinase domain | |
| PROSITE profiles | Protein kinase domain | |
| PROSITE patterns | Protein kinase, ATP binding site    Serine/threonine-protein kinase, active site | |
| Gene3D | 3.30.200.20          1.10.510.10 | |
| All sequence SNPs/i... | Sequence variants (dbSNP and all other sources) | |
| Variant Legend | | |

stop gained
splice region variant
synonymous variant

Scale bar: 0   40   80   120   160   200   240   280   320   360   400   464

# 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 gene-trapped allele die prior to implantation exhibiting fragmented blastomeres and failure to undergo compaction.

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd