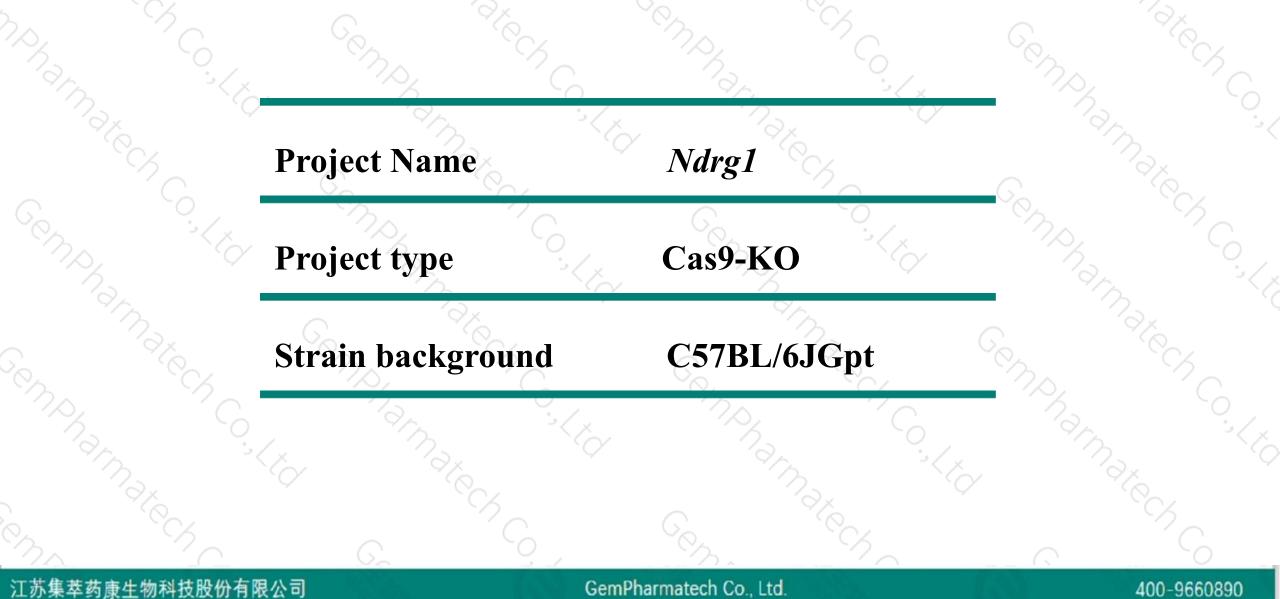


# Ndrg1 Cas9-KO Strategy

Designer: Reviewer: Design Date: Yang Zeng Ruirui Zhang 2019-12-23

### **Project Overview**

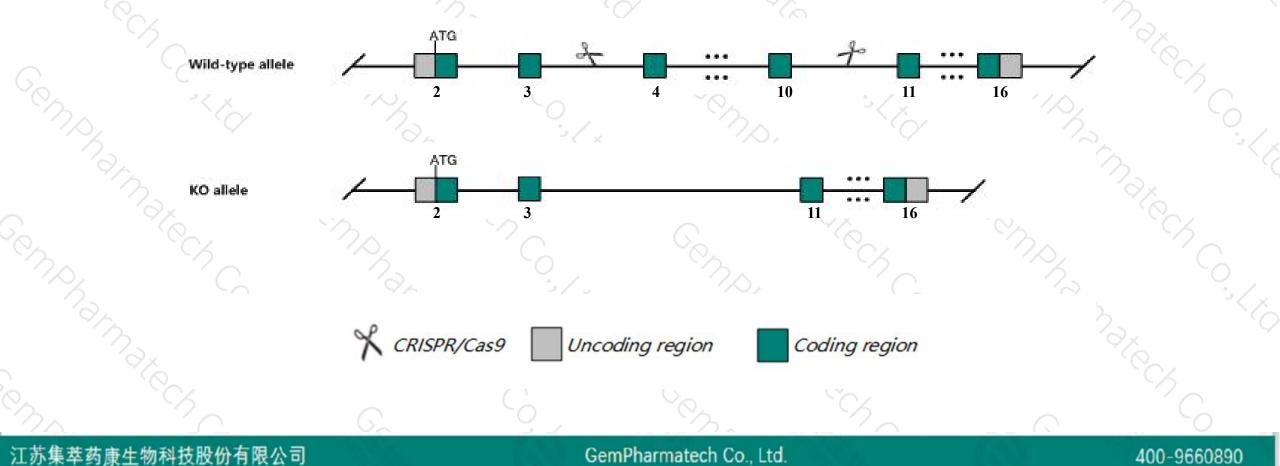




### **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the Ndrg1 gene. The schematic diagram is as follows:





- The Ndrg1 gene has 13 transcripts. According to the structure of Ndrg1 gene, exon4-exon10 of Ndrg1-201 (ENSMUST0000005256.13) transcript is recommended as the knockout region. The region contains 599bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Ndrg1 gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mice exhibit a progressive demyelinating disorder of the peripheral nerves with hindlimb weakness, some mice die between 1 to 10 months.
- The Ndrg1 gene is located on the Chr15. 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.

Notice

### **Gene information (NCBI)**



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Ndrg1 N-myc downstream regulated gene 1 [ Mus musculus (house mouse) ]

Gene ID: 17988, updated on 21-Oct-2019

#### Summary

Official SymbolNdrg1 provided by MGIOfficial Full NameN-myc downstream regulated gene 1 provided by MGIPrimary sourceMGI:MGI:1341799See relatedEnsembl:ENSMUSG0000005125Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;<br/>Muroidea; Muridae; Murinae; Mus; MusAlso known asRTP; DRG1; NMSL; Ndr1; Ndr1; TDD5; CAP43; CMT4D; HMSNL; PROXY1ExpressionBiased expression in kidney adult (RPKM 707.1), liver E18 (RPKM 98.7) and 4 other tissues See more<br/>OrtholosOrtholoshuman all

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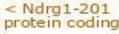
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## **Transcript information (Ensembl)**



Name 🖕	Transcript ID	bp 🖕	Protein 🖕	Translation ID 💧	Biotype 🖕	CCDS 🖕	UniProt 🖕	Flags
Ndrg1-201	ENSMUST0000005256.13	2889	<u>394aa</u>	ENSMUSP0000005256.6	Protein coding	<u>CCDS37092</u>	<u>Q545R3</u> @ <u>Q62433</u> @	TSL:1 GENCODE basic APPRIS P1
drg1-202	ENSMUST00000163496.7	738	<u>155aa</u>	ENSMUSP00000130584.1	Protein coding	-	<u>E9Q518</u> &	CDS 3' incomplete TSL:5
drg1-210	ENSMUST00000170903.7	667	<u>157aa</u>	ENSMUSP00000127302.1	Protein coding	-	<u>E9Q3F9</u> &	CDS 3' incomplete TSL:5
drg1-209	ENSMUST00000168979.7	583	<u>174aa</u>	ENSMUSP00000126985.1	Protein coding	-	<u>E9PVF3</u> &	CDS 3' incomplete TSL:3
drg1-206	ENSMUST00000166420.7	577	<u>141aa</u>	ENSMUSP00000127099.1	Protein coding	-	<u>E9Q514</u> 교	CDS 3' incomplete TSL:3
ldrg1-207	ENSMUST00000167817.7	356	<u>119aa</u>	ENSMUSP00000127075.1	Protein coding	-	F6VLR8	CDS 5' and 3' incomplete TSL:3
ldrg1-203	ENSMUST00000164070.1	316	<u>53aa</u>	ENSMUSP00000126091.1	Protein coding	-	<u>E9Q147</u> 교	CDS 3' incomplete TSL:5
ldrg1-211	ENSMUST00000171266.7	759	<u>39aa</u>	ENSMUSP00000129093.1	Nonsense mediated decay	-	<u>E9Q0J8</u> 료	TSL:5
ldrg1-204	ENSMUST00000164675.7	591	<u>93aa</u>	ENSMUSP00000130150.1	Nonsense mediated decay	-	<u>E9Q7V2</u> &	TSL:3
drg1-208	ENSMUST00000168542.7	473	<u>49aa</u>	ENSMUSP00000127940.1	Nonsense mediated decay	-	E9PZC7	TSL:5
Ndrg1-213	ENSMUST00000172447.7	444	<u>53aa</u>	ENSMUSP00000130281.1	Nonsense mediated decay	-	<u>E9Q7G8</u> &	TSL:5
Ndrg1-212	ENSMUST00000171569.7	4049	No protein	-	Retained intron		-	TSL:1
Ndrg1-205	ENSMUST00000165966.1	849	No protein	*	Retained intron	<u>~</u>	(34)	TSL:2

The strategy is based on the design of Ndrg1-201 transcript, The transcription is shown below



Reverse strand -

- 40.32 kb -

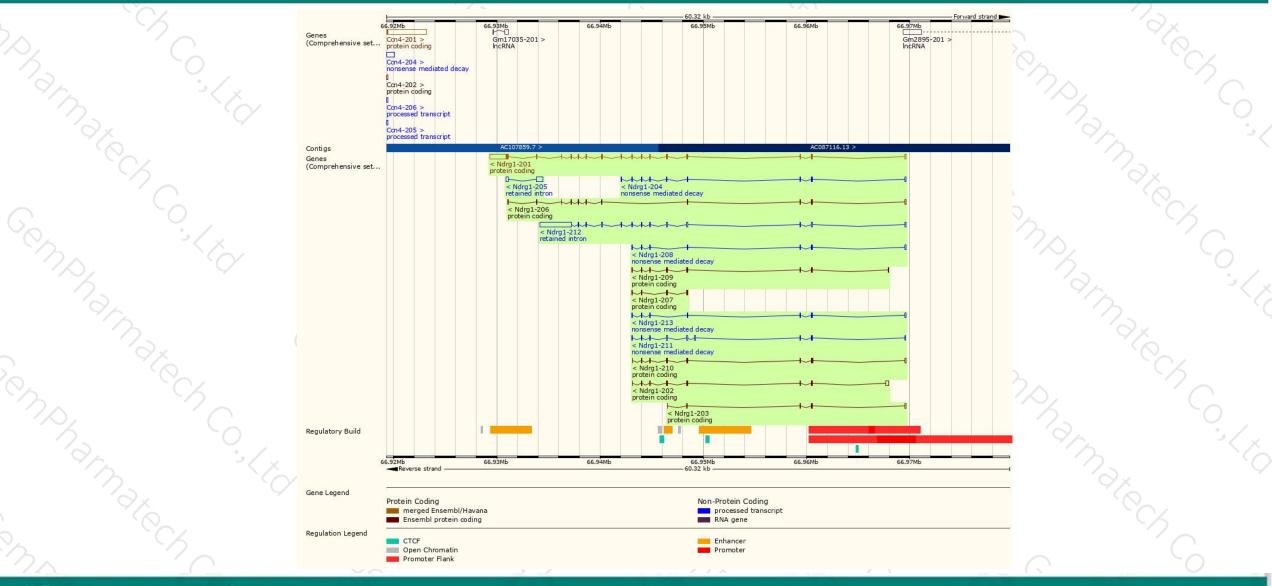
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### **Genomic location distribution**





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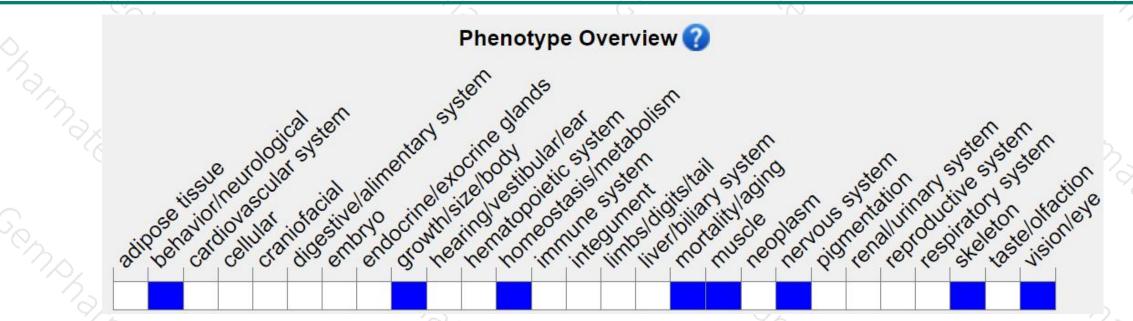
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### **Protein domain**



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	Variant Legend									
	All sequence SNPs/i	Sequence varia	ants (dbSNP and	d all other sou	irces)	1.1.1		110		
	Gene3D	NDRG Alpha/Be	ta hydrolase fold							34
	PANTHER	Protein NDRG1								2
	Pfam.	NDRG								
	ENSMUSP00000005 MobiDB lite Superfamily	Alpha/	Beta hydrolase fo	ld	Aur Jur				-	
	n Kry		K.	8		212	С. С.	la l	75	6 <u> </u>

### 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 mice exhibit a progressive demyelinating disorder of the peripheral nerves with hindlimb weakness, some mice die between 1 to 10 months.



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



