

Wdpcp Cas9-KO Strategy

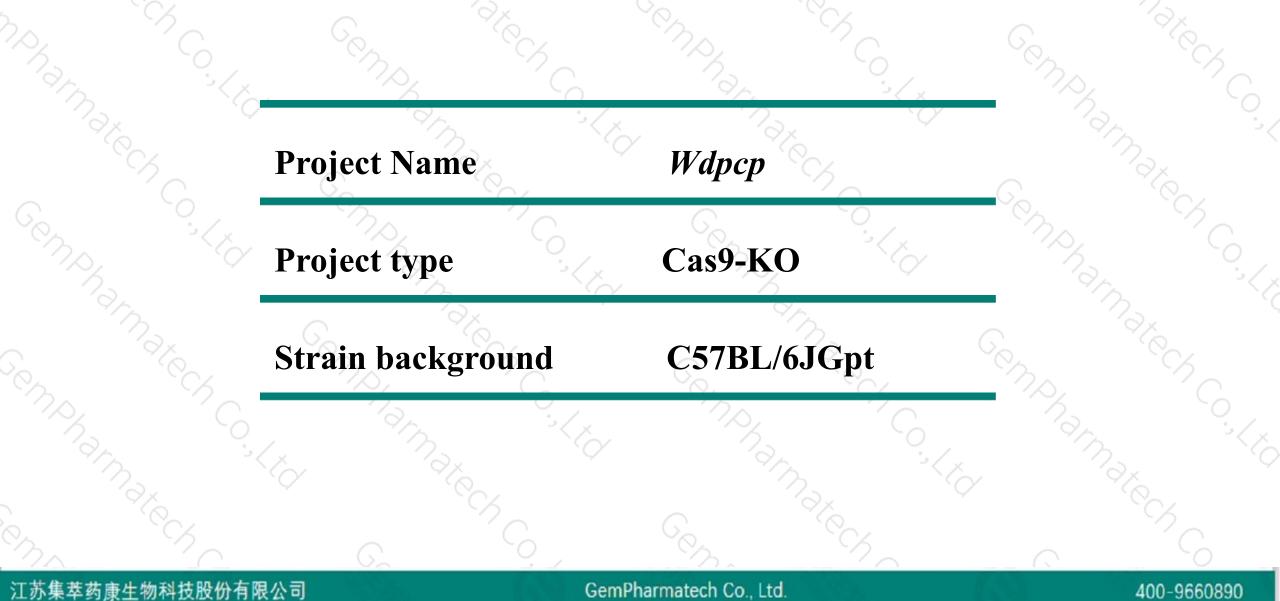
Designer: Reviewer:

Design Date:

Huan Wang Huan Fan 2020-4-23

Project Overview

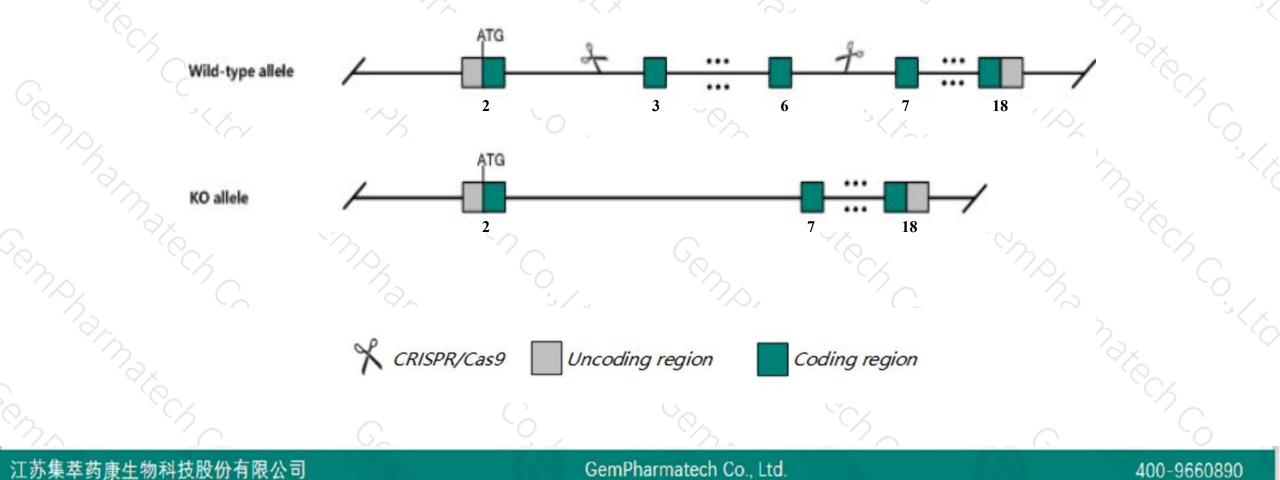




Knockout strategy



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





- The Wdpcp gene has 6 transcripts. According to the structure of Wdpcp gene, exon3-exon6 of Wdpcp-201 (ENSMUST0000020568.9) transcript is recommended as the knockout region. The region contains 230bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Wdpcp gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a null mutation display ciliogenesis defects, anophthalmia, cysts in multiple tissues, central polydactyly, duplex kidney, and septation defects in the outflow tract and cloaca.
- The Wdpcp gene is located on the Chr11. 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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Wdpcp WD repeat containing planar cell polarity effector [Mus musculus (house mouse)]

Gene ID: 216560, updated on 13-Mar-2020

Summary

Official Symbol	Wdpcp provided by MGI
Official Full Name	WD repeat containing planar cell polarity effector provided by MGI
Primary source	MGI:MGI:2144467
See related	Ensembl:ENSMUSG0000020319
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	AV249152, Frtz, homolog-13
Expression	Broad expression in cerebellum adult (RPKM 9.9), testis adult (RPKM 7.2) and 24 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



The gene has 6 transcripts, all transcripts are shown below:

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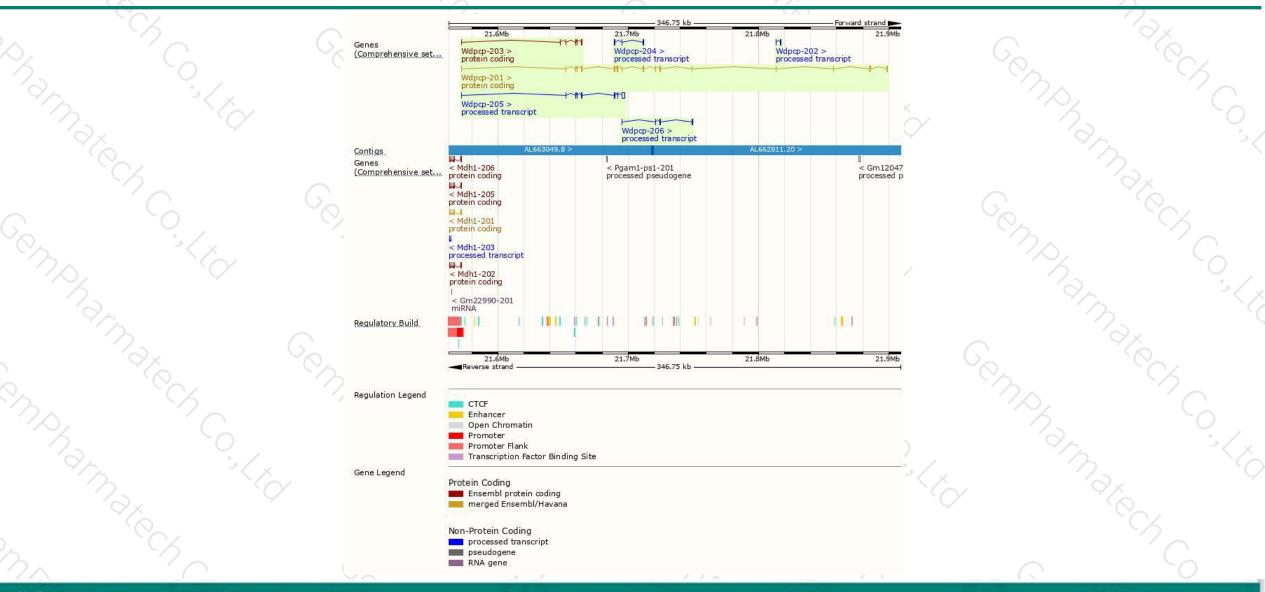
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wdpcp-201	ENSMUST0000020568.9	2792	<u>722aa</u>	Protein coding	CCDS24467	B1ATJ7 Q8C456	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P
Wdpcp-203	ENSMUST00000131135.2	505	<u>97aa</u>	Protein coding	1.0	B1ATQ4	CDS 3' incomplete TSL:3
Wdpcp-205	ENSMUST00000149757.1	3020	No protein	Processed transcript	620	1220	TSL:1
Wdpcp-206	ENSMUST00000156624.1	963	No protein	Processed transcript	724	100	TSL1
Wdpcp-204	ENSMUST00000143608.1	741	No protein	Processed transcript	1.71	151	TSL:2
Wdpcp-202	ENSMUST00000128794.1	480	No protein	Processed transcript	(m)	6,431	TSL:3

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

H M	326.75 kb						
Wdpcp-201 > protein coding	3.1			(x)			

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Genomic location distribution



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Protein domain



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ENSMUSP00000020 MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils)								-		
Superfamily				WD40-repeat	-containing dom	nain superfarr	uly			
<u>Pfam</u>	WD repeat-containing and planar cell polarity effector protein Fritz									
PANTHER	WD repeat-cont	aining and planar ce	l polarity effect	or protein Fritz						
Gene3D	WD40/YVTN repeat-like-containing domain superfamily									
All sequence SNPs/i	Sequence var	iants (dbSNP and a	all other source	ss)	611	1.0	1.706	11,00	10	
Variant Legend	inframe (insertion deletion variant ious variant						111111	0,	
Scale bar	0 8	0 160	240	320	400	480	560	640	722	
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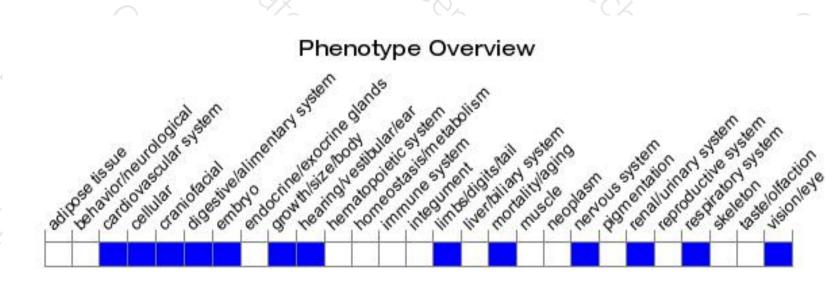
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Mouse phenotype description(MGI)





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 null mutation display ciliogenesis defects, anophthalmia, cysts in multiple tissues, central polydactyly, duplex kidney, and septation defects in the outflow tract and cloaca.



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



