Washc3 Cas9-KO *Strategy*

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Project Overview

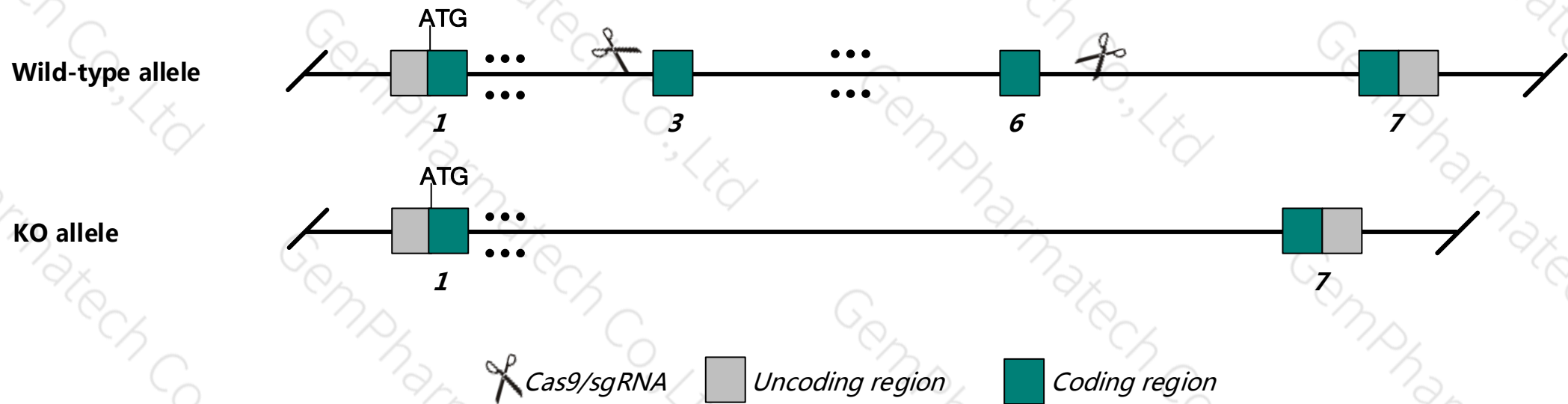|	
Project Name	*Washc3*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Washc3* gene. The schematic diagram is as follows:

Technical routes

➢ The *Washc3* gene has 8 transcripts.According to the structure of *Washc3* gene, exon3-exon6 of *Washc3*-201 (ENSMUST00000020248.15) transcript is recommended as the knockout region.The region contains 350bp coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Washc3* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9, 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 *Washc3* 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 biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Washc3 **WASH complex subunit 3** [*Mus musculus* (house mouse)]

Gene ID: 67282, updated on 9-Sep-2018

▲ Summary

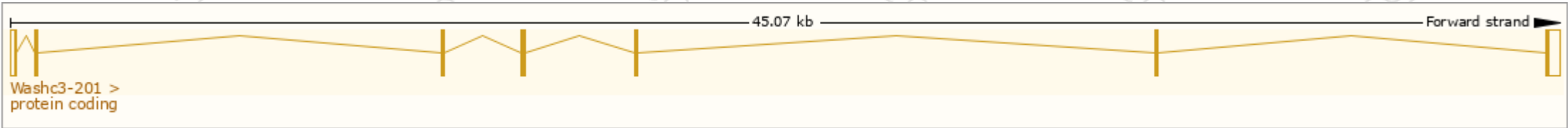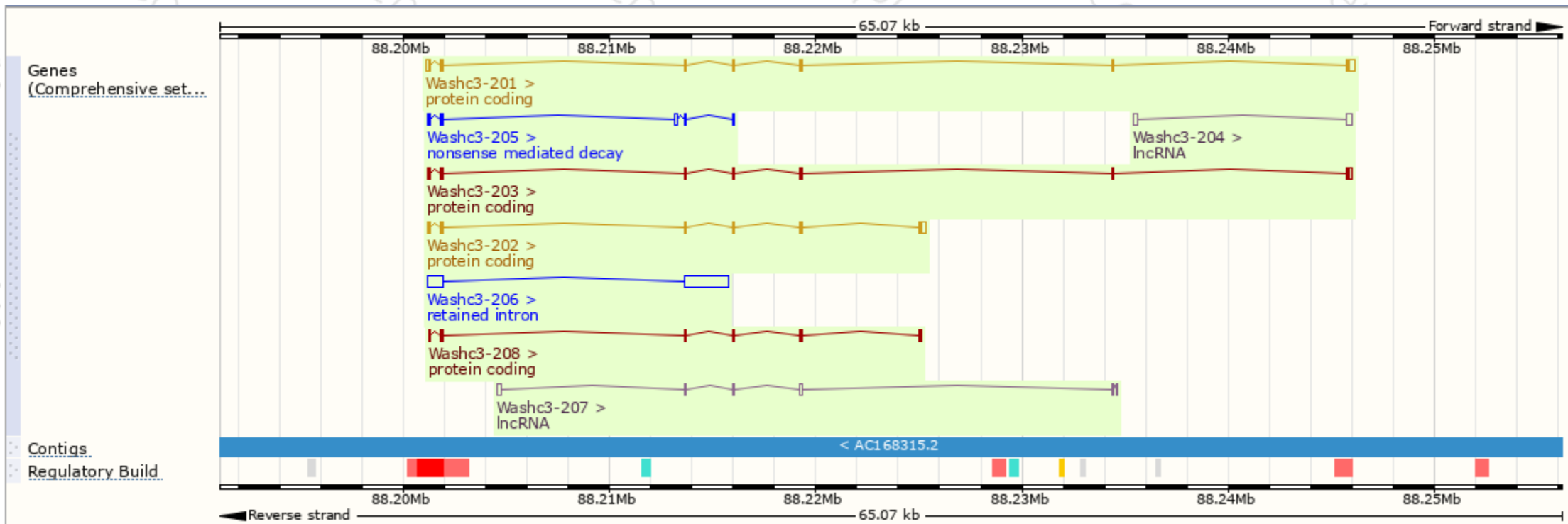|	
Official Symbol	Washc3 provided by MGI
Official Full Name	WASH complex subunit 3 provided by MGI
Primary source	MGI:MGI:1914532
See related	Ensembl:ENSMUSG00000020056 Vega:OTTMUSG00000044399
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ccdc53; 2900091E11Rik; 5730495F03Rik
Expression	Ubiquitous expression in placenta adult (RPKM 9.0), bladder adult (RPKM 8.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 8 transcripts, and all transcripts are shown below:

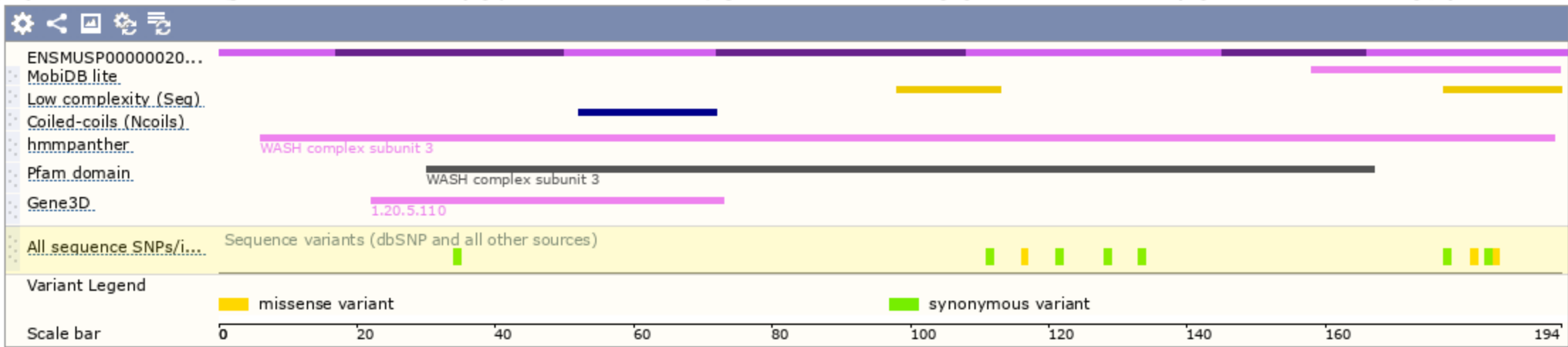| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Washc3-201	ENSMUST00000020248.15	1052	194aa	Protein coding	CCDS24108	Q9CR27	TSL:1 GENCODE basic APPRIS P3
Washc3-203	ENSMUST00000182183.7	838	193aa	Protein coding	CCDS59550	S4R287	TSL:2 GENCODE basic APPRIS ALT2
Washc3-202	ENSMUST00000171151.8	837	179aa	Protein coding	CCDS48664	G3UWG7	TSL:1 GENCODE basic
Washc3-208	ENSMUST00000182619.1	521	171aa	Protein coding	-	S4R1P7	CDS 5' incomplete TSL:5
Washc3-205	ENSMUST00000182299.7	524	50aa	Nonsense mediated decay	-	S4R1K7	TSL:3
Washc3-206	ENSMUST00000182351.1	2848	No protein	Retained intron	-	-	TSL:1
Washc3-207	ENSMUST00000182359.1	639	No protein	lncRNA	-	-	TSL:3
Washc3-204	ENSMUST00000182211.1	413	No protein	lncRNA	-	-	TSL:3

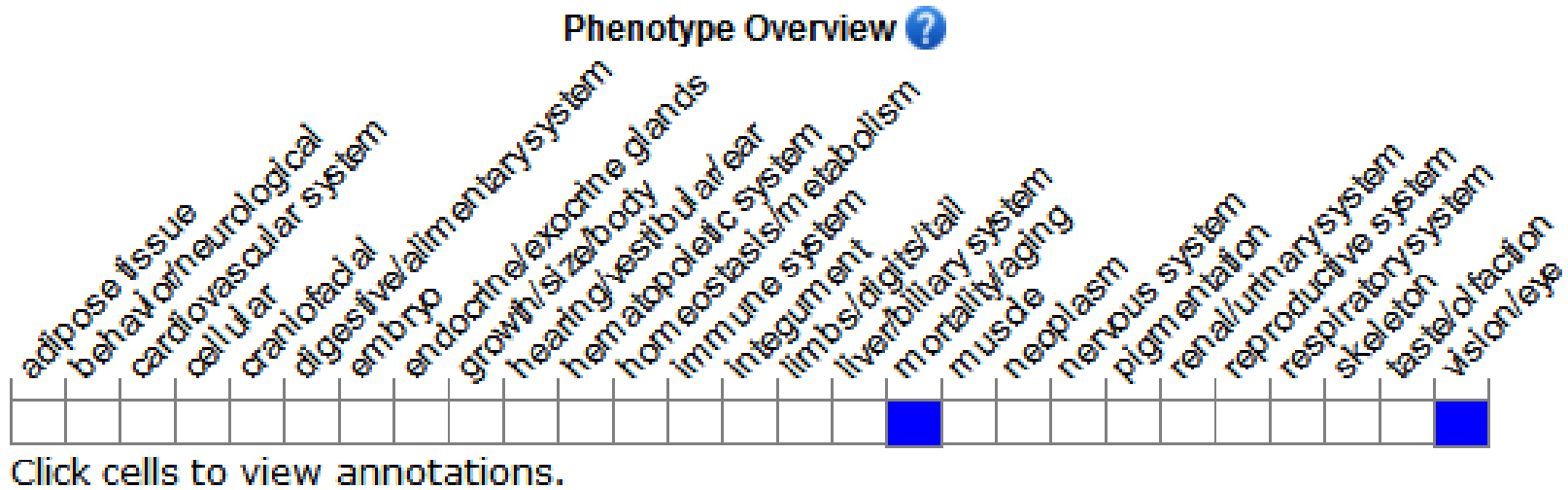The strategy is based on the design of *Washc3*-201 transcript,The transcription is shown below

Genomic location distribution

Protein domain

Mouse phenotype description(MGI)

Phenotype Overview

Click cells to view annotations.

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/) .

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