

Rbm3 Cas9-KO Strategy

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Reviewer :

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Design Date:

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Project Overview

Project Name

Rbm3

Project type

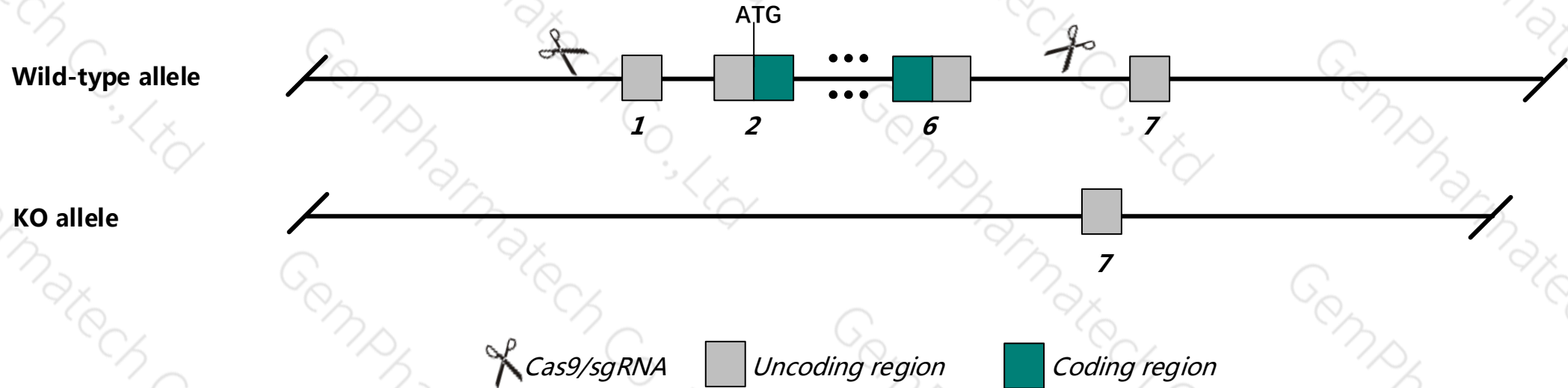
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rbm3* gene. The schematic diagram is as follows:



Technical routes

- The *Rbm3* gene has 11 transcripts. According to the structure of *Rbm3* gene, exon1-exon6 of *Rbm3*-201 (ENSMUST00000040010.9) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rbm3* 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.

- According to the existing MGI data , Mice homozygous for a knock-out allele exhibit decreased cell proliferation in mouse embryonic fibroblasts. This strategy may affect the 5-terminal regulation of the *Mdc1* gene.
- The KO region contains functional region of the *Rbm3os* gene. Knockout the region may affect the function of *Rbm3os* gene.
- The *Rbm3* gene is located on the ChrX. 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.

Gene information (NCBI)

Rbm3 RNA binding motif (RNP1, RRM) protein 3 [*Mus musculus* (house mouse)]

Gene ID: 19652, updated on 4-Jan-2020

Summary

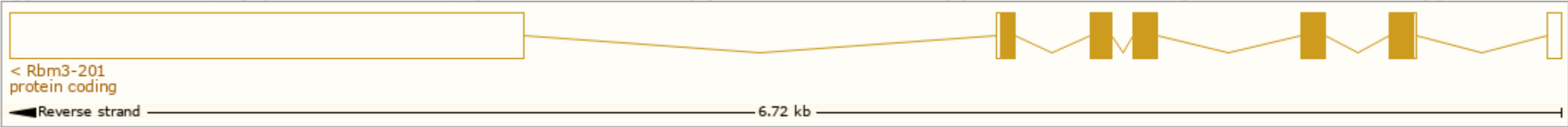
Official Symbol	Rbm3 provided by MGI
Official Full Name	RNA binding motif (RNP1, RRM) protein 3 provided by MGI
Primary source	MGI:MGI:1099460
See related	Ensembl:ENSMUSG00000031167
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2600016C11Rik
Expression	Broad expression in CNS E11.5 (RPKM 50.1), liver E14 (RPKM 45.8) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

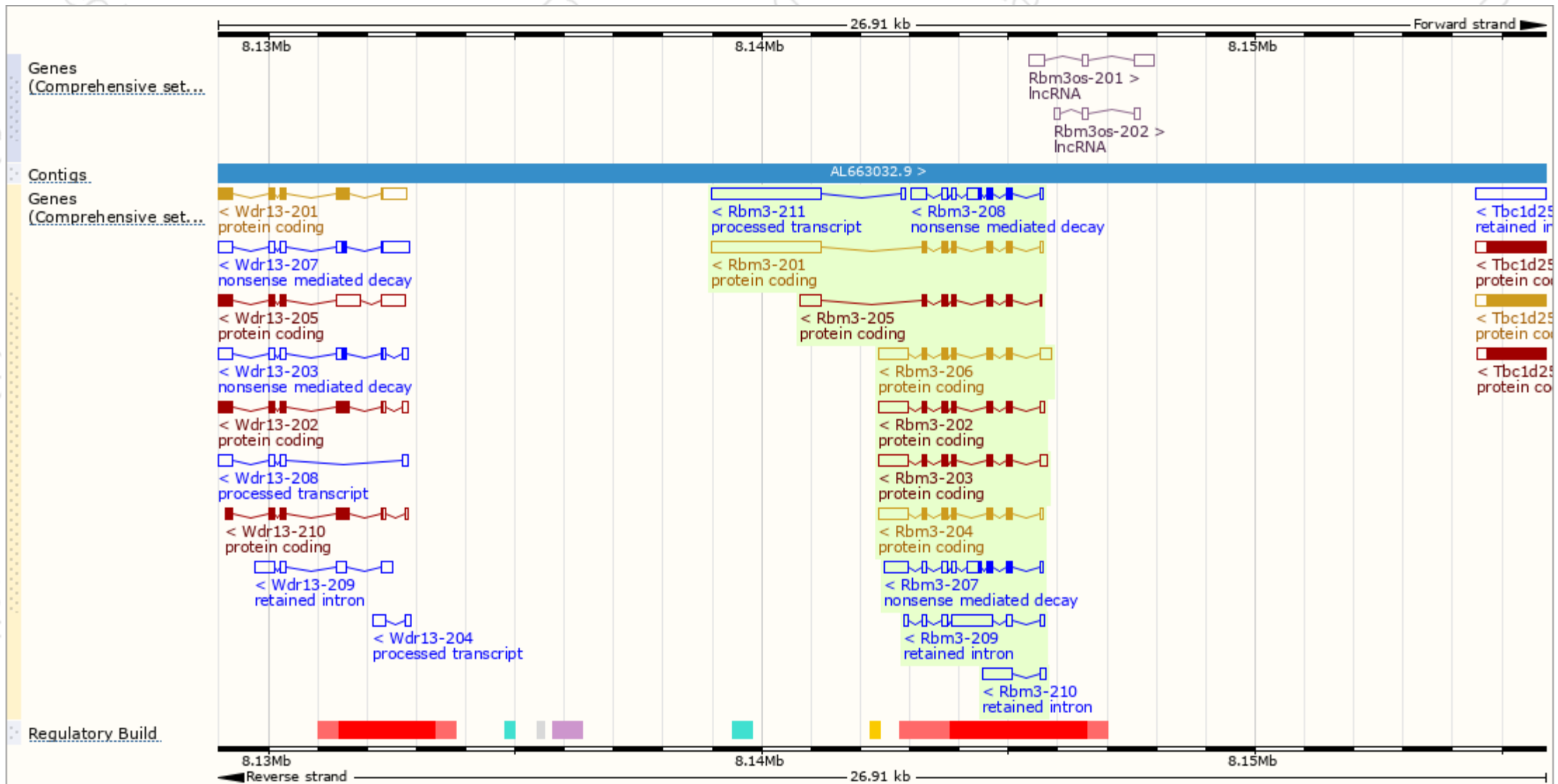
The gene has 11 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rbm3-201	ENSMUST00000040010.9	2792	154aa	Protein coding	CCDS29987	Q8BG13	TSL:1 GENCODE basic APPRIS P3
Rbm3-206	ENSMUST00000115621.8	1338	153aa	Protein coding	CCDS52988	O89086 Q545K5	TSL:1 GENCODE basic APPRIS ALT1
Rbm3-203	ENSMUST00000115616.7	1225	154aa	Protein coding	CCDS29987	Q8BG13	TSL:1 GENCODE basic APPRIS P3
Rbm3-202	ENSMUST00000115615.8	1183	153aa	Protein coding	CCDS52988	O89086 Q545K5	TSL:1 GENCODE basic APPRIS ALT1
Rbm3-204	ENSMUST00000115617.9	1152	154aa	Protein coding	CCDS29987	Q8BG13	TSL:1 GENCODE basic APPRIS P3
Rbm3-205	ENSMUST00000115619.7	969	153aa	Protein coding	CCDS52988	O89086 Q545K5	TSL:3 GENCODE basic APPRIS ALT1
Rbm3-207	ENSMUST00000129947.8	1319	90aa	Nonsense mediated decay	-	S4R2M6	TSL:5
Rbm3-208	ENSMUST00000141629.1	1055	90aa	Nonsense mediated decay	-	S4R2M6	TSL:1
Rbm3-211	ENSMUST00000155599.1	2326	No protein	Processed transcript	-	-	TSL:1
Rbm3-209	ENSMUST00000141925.7	1274	No protein	Retained intron	-	-	TSL:5
Rbm3-210	ENSMUST00000145450.1	721	No protein	Retained intron	-	-	TSL:2

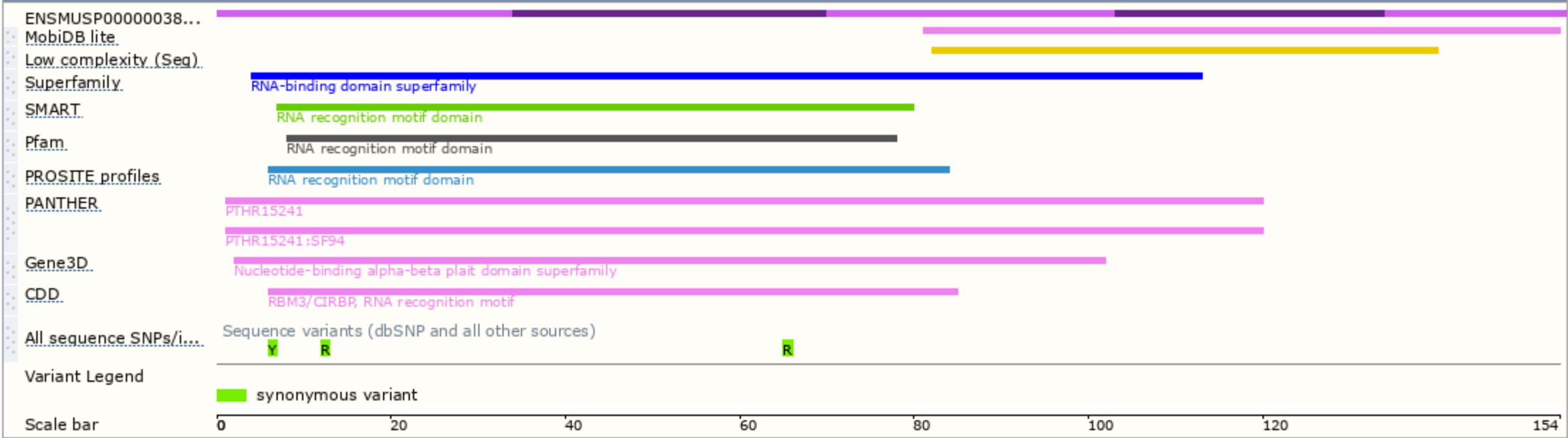
The strategy is based on the design of *Rbm3*-201 transcript, The transcription is shown below



Genomic location distribution

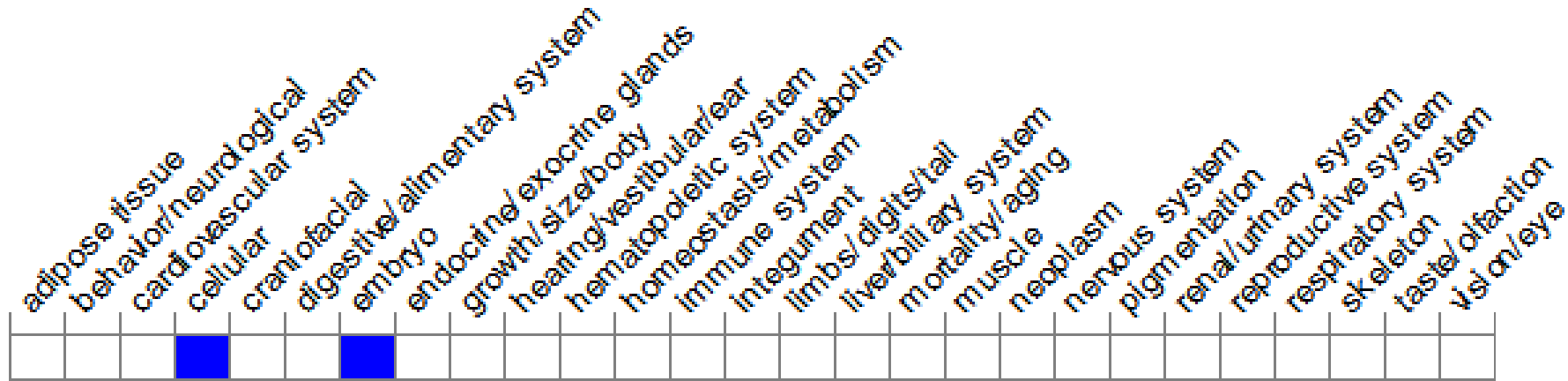


Protein domain



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/>) .

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased cell proliferation in mouse embryonic fibroblasts.

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