

Egfr Cas9-KO Strategy

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Project Overview

Project Name

Egfr

Project type

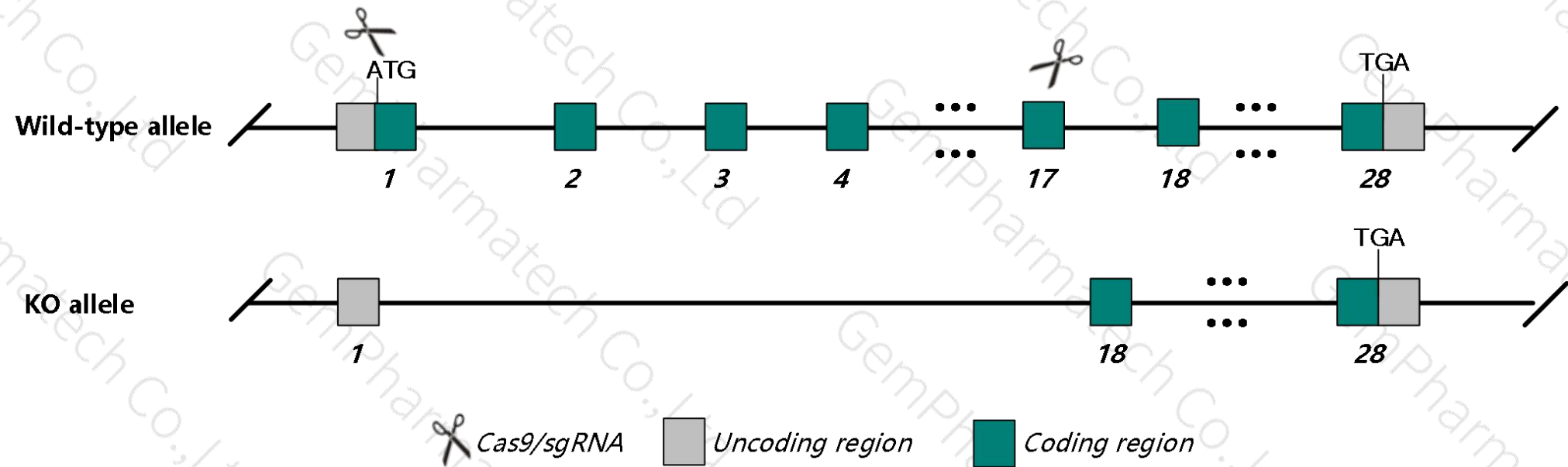
Cas9-KO

Strain background

NCG/Gpt

Knockout strategy

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



- The *Egfr* gene has 5 transcripts. According to the structure of *Egfr* gene, exon1-exon17 of MGP_NODShiLtJ_T0027898.1 transcript is recommended as the knockout region. The region contains 1977bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Egfr* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of NCG 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 NCG mice.

- According to the existing MGI data, mutations widely affect epithelial development. null homozygote survival is strain dependent, with defects observed in skin, eye, brain, viscera, palate, tongue and other tissues. other mutations produce an open eyed, curly whisker phenotype, while a dominant hypermorph yields a thickened epidermis.
- The *Egfr* 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.

Gene information (NCBI)

Egfr epidermal growth factor receptor [*Mus musculus* (house mouse)]

Gene ID: 13649, updated on 10-May-2020

Summary

Official Symbol	Egfr provided by MGI
Official Full Name	epidermal growth factor receptor provided by MGI
Primary source	MGI:MGI:95294
See related	Ensembl:ENSMUSG00000020122
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	Wa5; wa2; Erbb; Errp; wa-2; Errb1; AI552599; 9030024J15Rik
Expression	Broad expression in liver adult (RPKM 26.7), liver E18 (RPKM 8.7) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

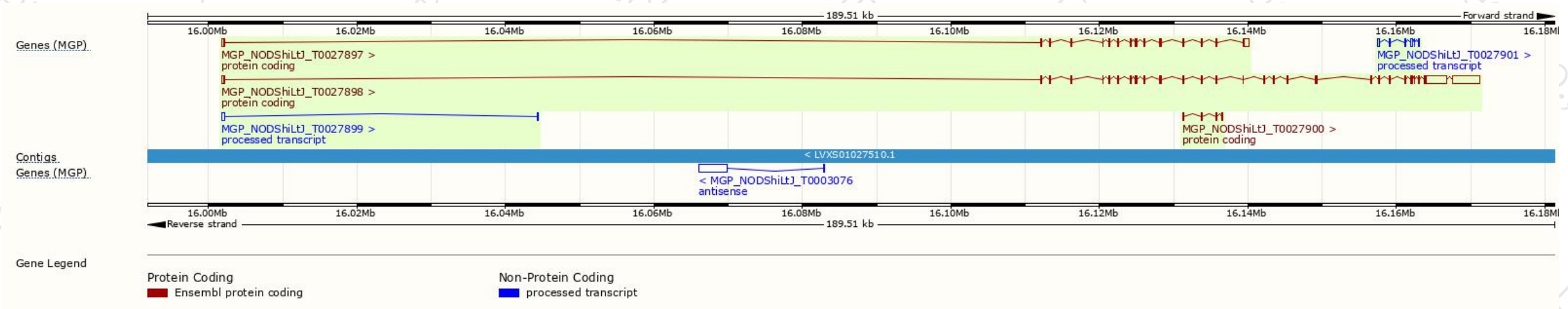
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
-	MGP_NODShiLtJ_T0027897.1	2943	655aa	Protein coding	CCDS24443 , CCDS24444	Q01279 , Q5SVE7 , Q9WVF5	-
-	MGP_NODShiLtJ_T0027898.1	10186	1210aa	Protein coding	-	-	-
-	MGP_NODShiLtJ_T0027900.1	463	136aa	Protein coding	-	-	-
-	MGP_NODShiLtJ_T0027901.1	716	No protein	Processed transcript	-	-	-
-	MGP_NODShiLtJ_T0027899.1	446	No protein	Processed transcript	-	-	-

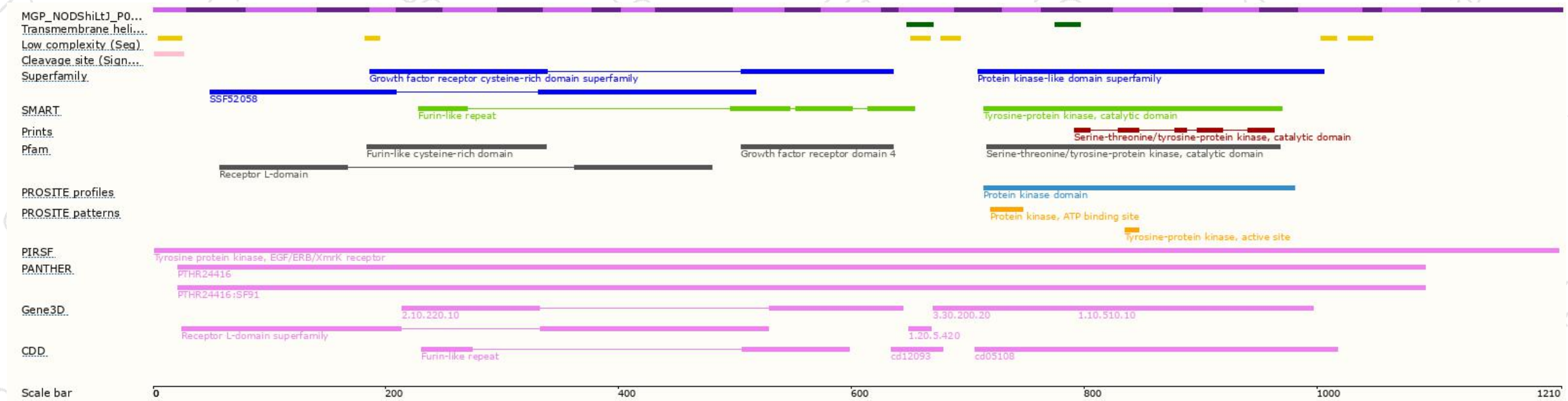
The strategy is based on the design of MGP_NODShiLtJ_T0027898.1 transcript,The transcription is shown below



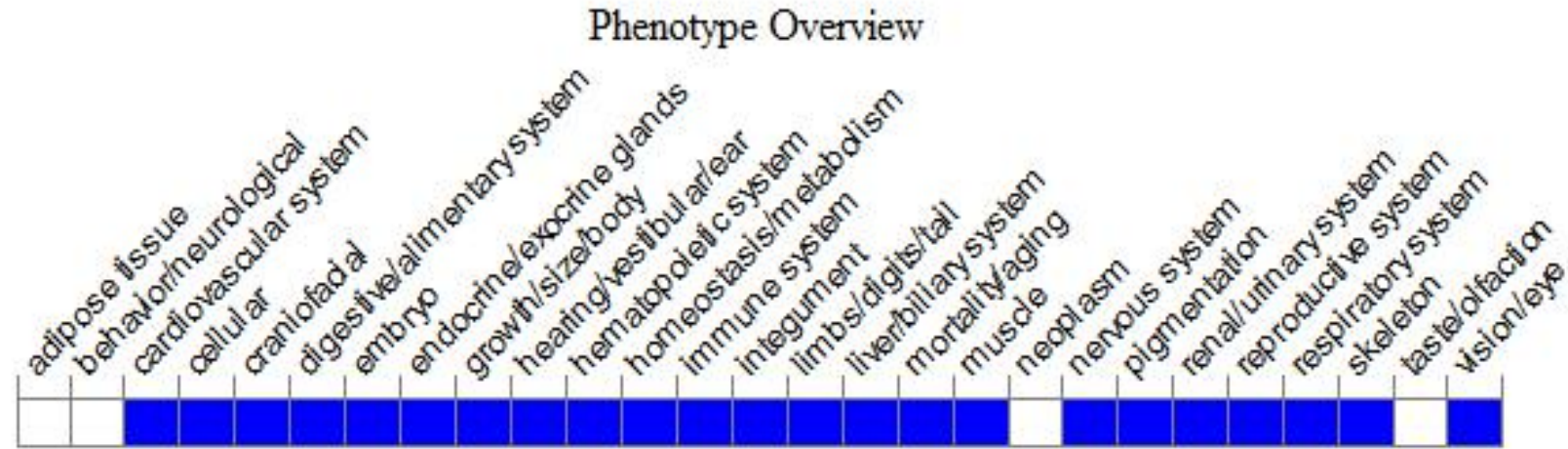
Genomic location distribution



Protein domain



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, Mutations widely affect epithelial development. Null homozygote survival is strain dependent, with defects observed in skin, eye, brain, viscera, palate, tongue and other tissues. Other mutations produce an open eyed, curly whisker phenotype, while a dominant hypermorph yields a thickened epidermis.

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

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