

***Fscn1* Cas9-CKO Strategy**

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Project Overview

Project Name

Fscn1

Project type

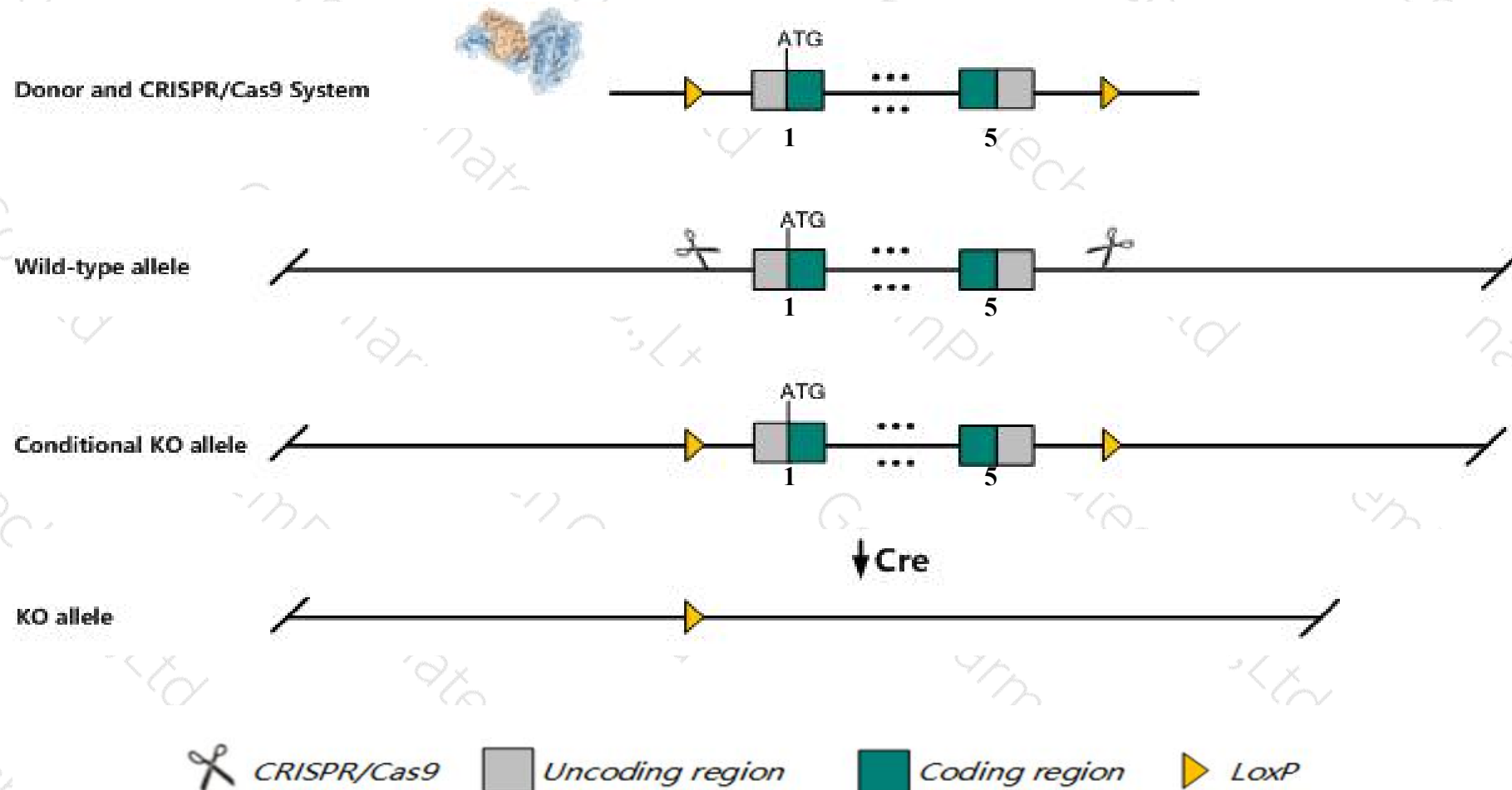
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fscn1* gene. The schematic diagram is as follows:



Technical routes

- The *Fscn1* gene has 7 transcripts. According to the structure of *Fscn1* gene, exon1-exon5 of *Fscn1-201* (ENSMUST00000031565.14) 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 *Fscn1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a gene trap allele show partial neonatal lethality, smaller size, enlarged lateral ventricles, abnormal anterior commissure pars posterior morphology, impaired migration of mature dendritic cells, and hypopigmentation due to migration and cell cycle defects in melanoblasts.
- The *Fscn1* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Fscn1 fascin actin-bundling protein 1 [*Mus musculus* (house mouse)]

Gene ID: 14086, updated on 12-Nov-2019

Summary

Official Symbol	Fscn1 provided by MGI
Official Full Name	fascin actin-bundling protein 1 provided by MGI
Primary source	MGI:MGI:1352745
See related	Ensembl:ENSMUSG00000029581
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	Fan1; AI663989; fascin-1
Expression	Broad expression in whole brain E14.5 (RPKM 192.6), CNS E14 (RPKM 164.7) and 21 other tissues See more
Orthologs	human all

Genomic context

Location: 5 G2; 5 81.84 cM

[See Fscn1 in Genome Data Viewer](#)

Exon count: 5

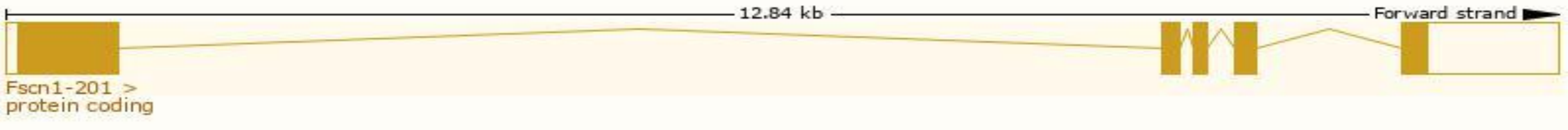
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (142960355..142973189)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (143722034..143734868)

Transcript information (Ensembl)

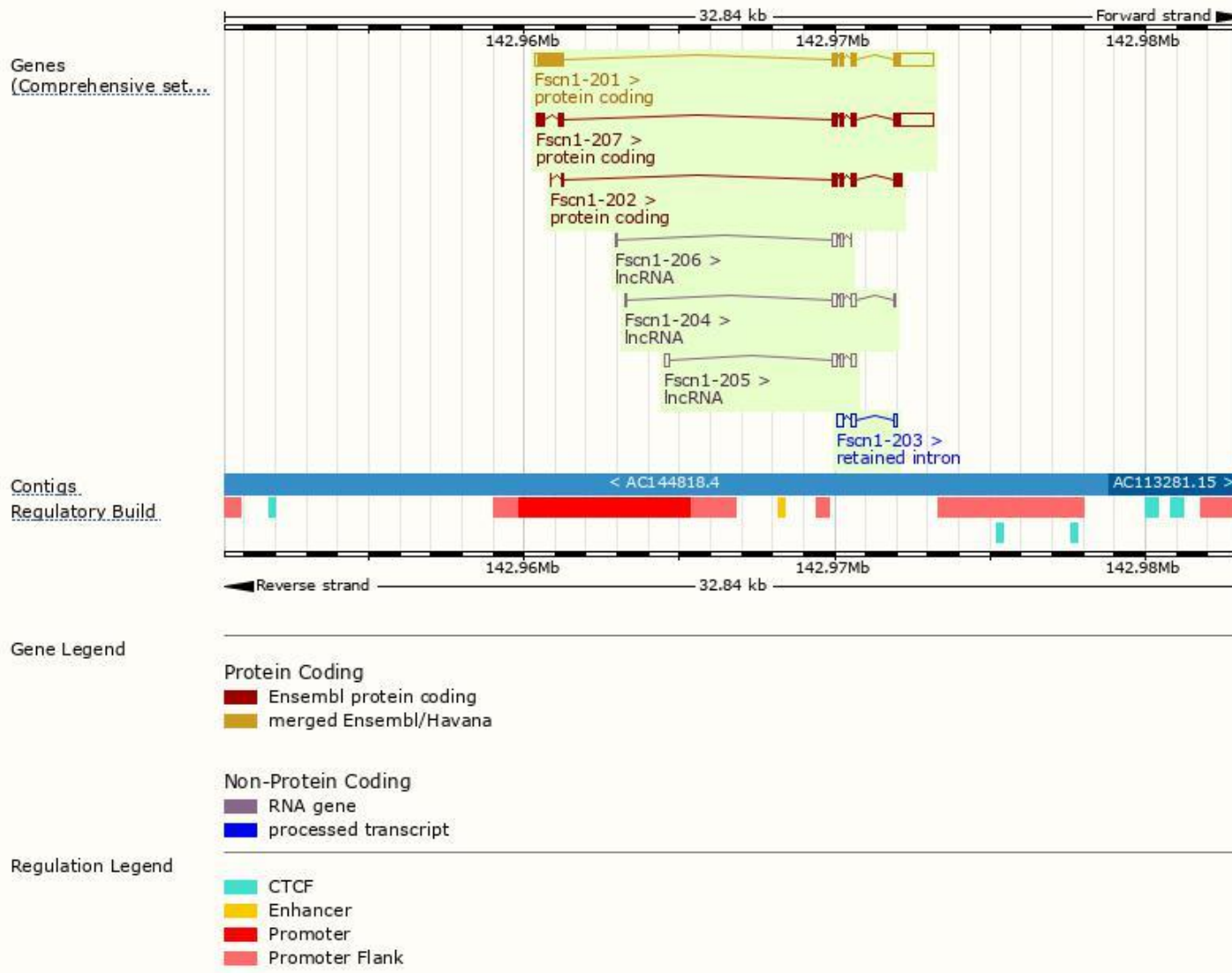
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fscn1-201	ENSMUST00000031565.14	2675	493aa	Protein coding	CCDS19834	Q61553	TSL:1 GENCODE basic APPRIS P1
Fscn1-207	ENSMUST00000198017.4	2157	332aa	Protein coding	-	A0A0G2JDU7	TSL:5 GENCODE basic
Fscn1-202	ENSMUST00000129306.3	797	241aa	Protein coding	-	F7BDR1	CDS 5' incomplete TSL:3
Fscn1-203	ENSMUST00000135293.1	466	No protein	Retained intron	-	-	TSL:2
Fscn1-205	ENSMUST00000139131.2	600	No protein	lncRNA	-	-	TSL:3
Fscn1-204	ENSMUST00000137552.7	566	No protein	lncRNA	-	-	TSL:5
Fscn1-206	ENSMUST00000150622.7	344	No protein	lncRNA	-	-	TSL:3

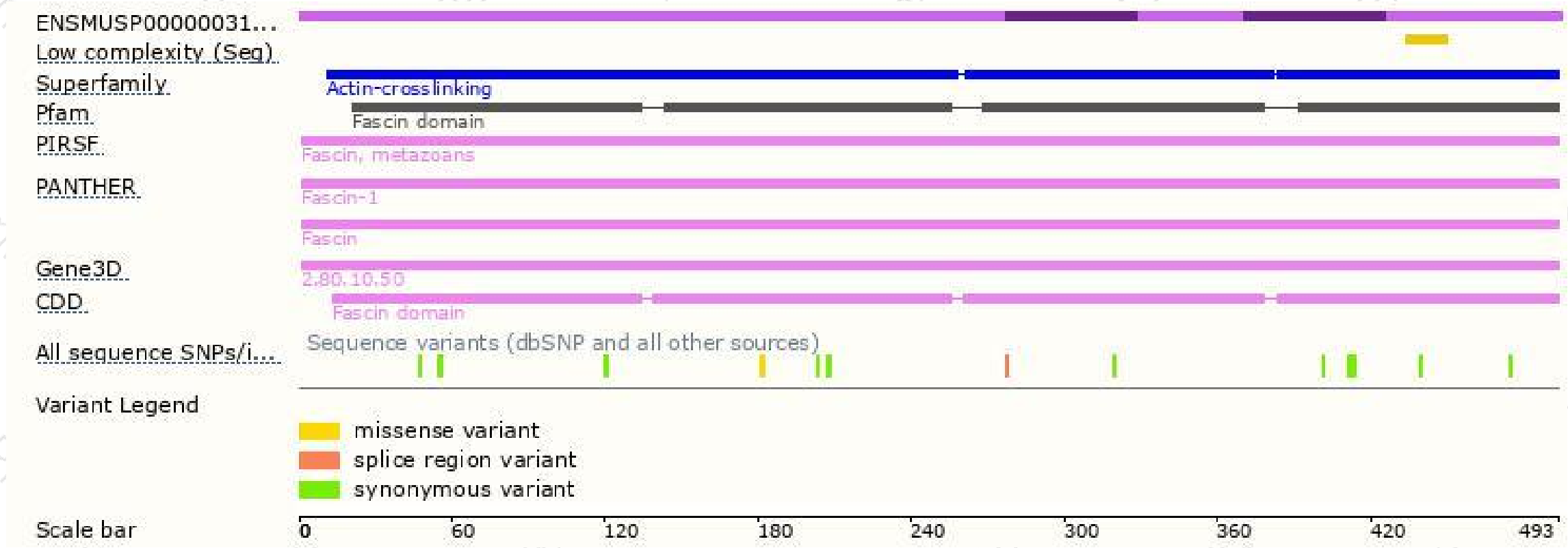
The strategy is based on the design of *Fscn1-201* transcript,The transcription is shown below



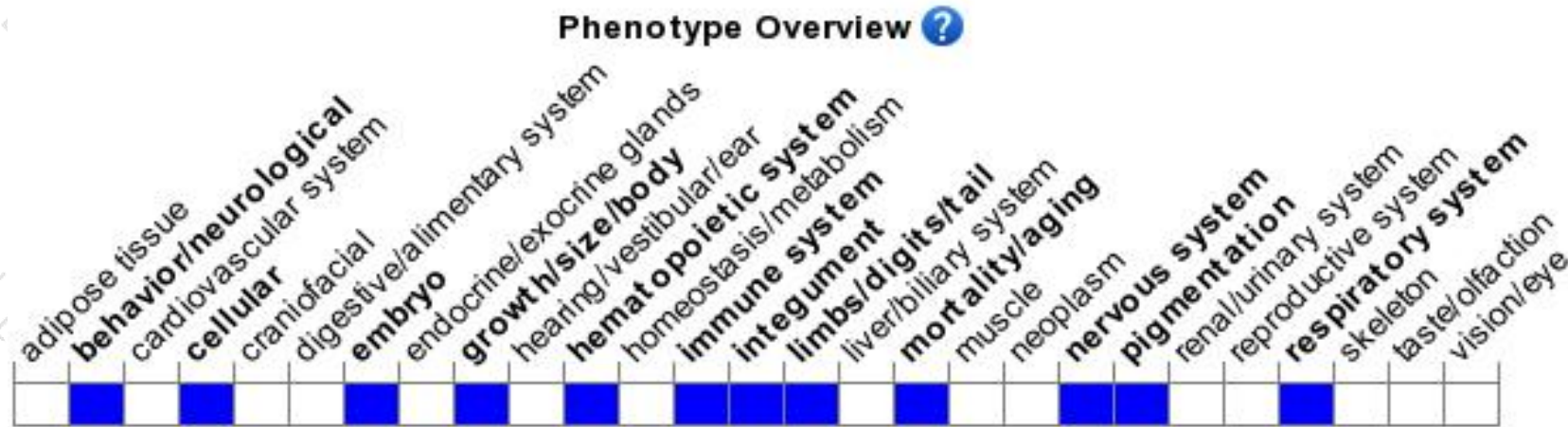
Genomic location distribution



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, Mice homozygous for a gene trap allele show partial neonatal lethality, smaller size, enlarged lateral ventricles, abnormal anterior commissure pars posterior morphology, impaired migration of mature dendritic cells, and hypopigmentation due to migration and cell cycle defects in melanoblasts.

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

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