Ercc6 Cas9-CKO Strategy

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Design Date:	**2020-1-22**

Project Overview

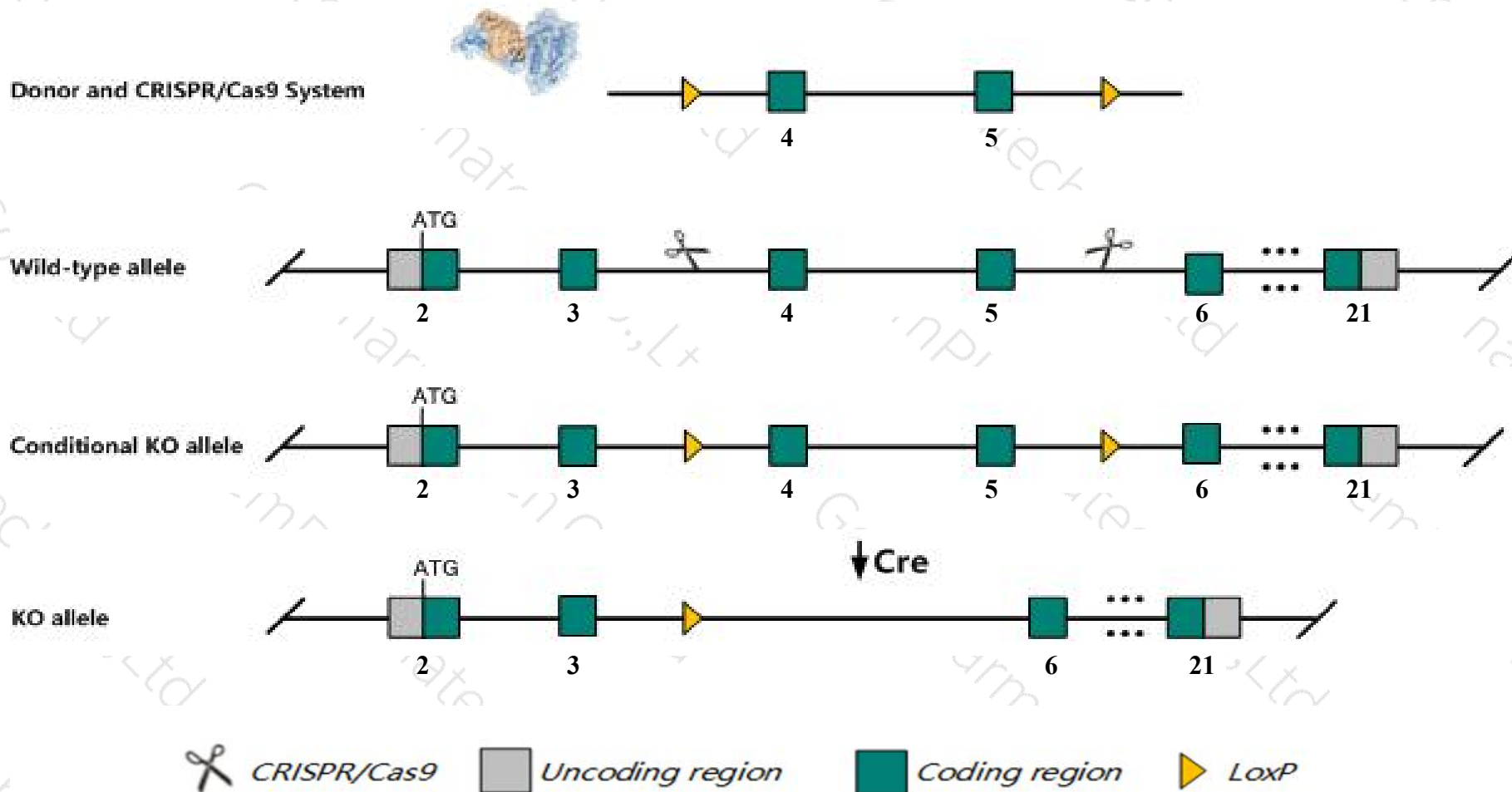|	
Project Name	*Ercc6*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ercc6* gene. The schematic diagram is as follows:

Technical routes

➤ The *Ercc6* gene has 6 transcripts. According to the structure of *Ercc6* gene, exon4-exon5 of *Ercc6-201* (ENSMUST00000066807.7) transcript is recommended as the knockout region.The region contains Ens 842bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Ercc6* 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.

Notice

➢ According to the existing MGI data,Homozygous mutant mice exhibit UV sensitivity, inactivation of transcription-coupled repair, increased incidence of induced skin and eye tumors, circling behavior, impaired coordination and lower body weight.

➢ The *Ercc6* gene is located on the Chr14. 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）

Ercc6 excision repair cross-complementing rodent repair deficiency, complementation group 6 [*Mus musculus* (house mouse)]

Gene ID: 319955, updated on 17-Nov-2019

🔺 Summary

Official Symbol	Ercc6 provided by MGI
Official Full Name	excision repair cross-complementing rodent repair deficiency, complementation group 6 provided by MGI
Primary source	MGI:MGI:1100494
See related	Ensembl:ENSMUSG00000054051
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	CSB; 4732403I04; C130058G22Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 3.9), CNS E14 (RPKM 3.4) and 28 other tissues See more
Orthologs	human all

🔺 Genomic context
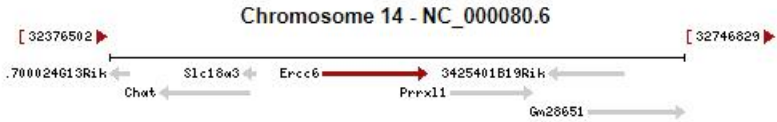
Location: 14; 14 B

See Ercc6 in Genome Data Viewer

Exon count: 24

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	14	NC_000080.6 (32513291..32580990)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (33326707..33394175)

Chromosome 14 - NC_000080.6

[32376502 ▶   [32746829 ▶

.700024G13Rik ◄   Slc18a3 ◄   Ercc6 ▶   3425401B19Rik ◄

Chat ◄   Prrxl1 ◄

Gm28651 ▶

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400-9660890

Transcript information（Ensembl）

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

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Ercc6-201	ENSMUST00000066807.7	8423	1481aa	Protein coding	CCDS36868	F8VPZ5	TSL:5	GENCODE basic	APPRIS P1
Ercc6-206	ENSMUST00000228549.1	2899	48aa	Nonsense mediated decay	-	A0A2I3BQP1		CDS 5' incomplete	
Ercc6-202	ENSMUST00000226285.1	603	No protein	Processed transcript	-	-	-		
Ercc6-205	ENSMUST00000228035.1	473	No protein	Processed transcript	-	-	-		
Ercc6-204	ENSMUST00000228017.1	2991	No protein	Retained intron	-	-	-		
Ercc6-203	ENSMUST00000227434.1	2705	No protein	Retained intron	-	-	-		

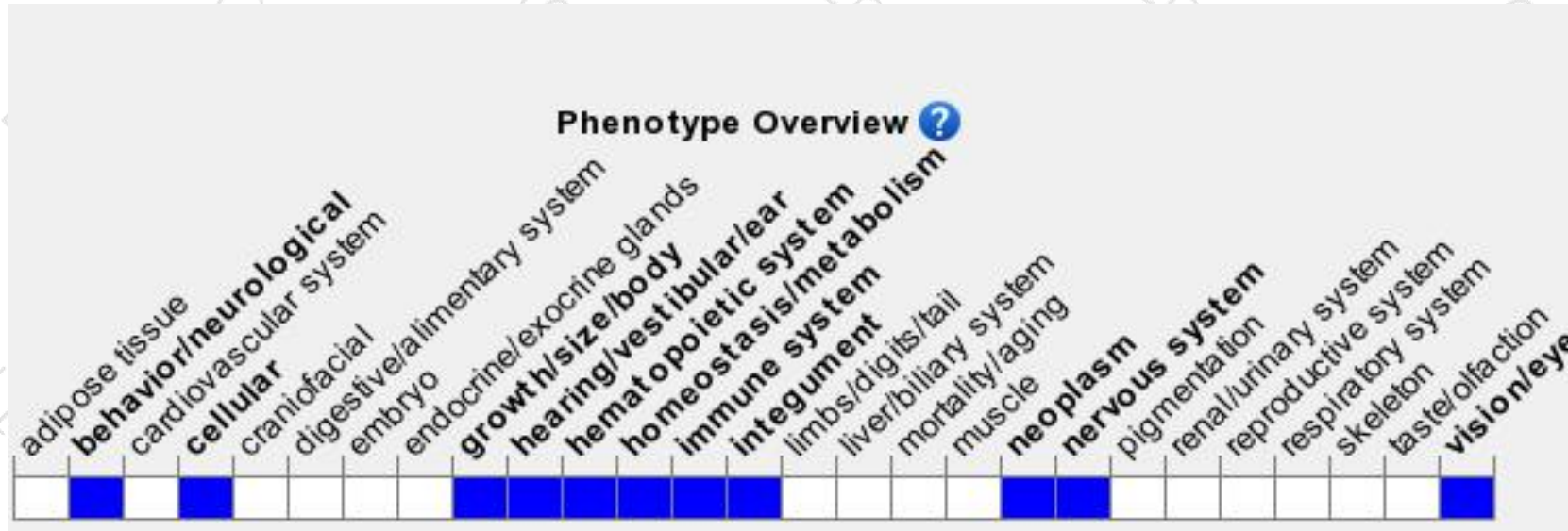The strategy is based on the design of *Ercc6-201* transcript,The transcription is shown below
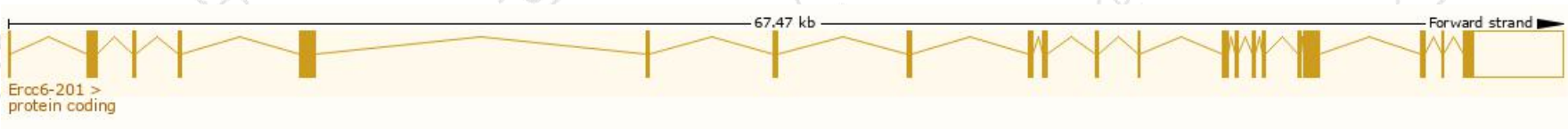
Genomic location distribution
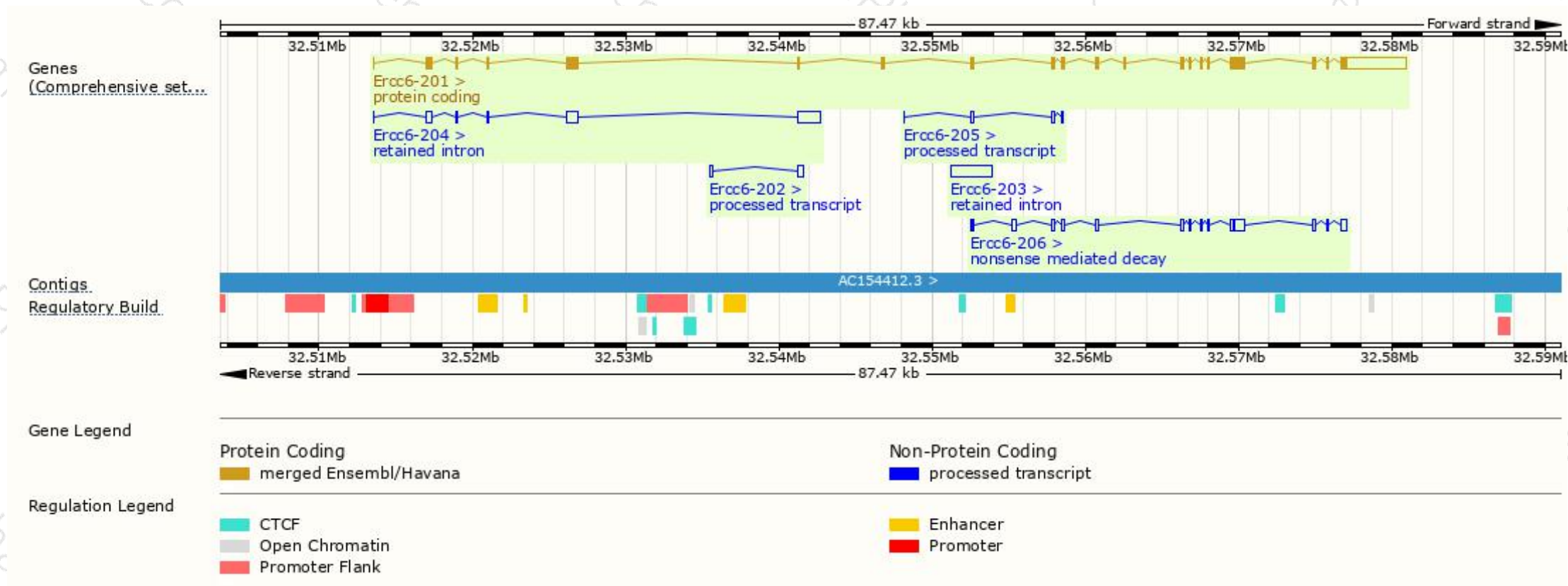
Protein domain
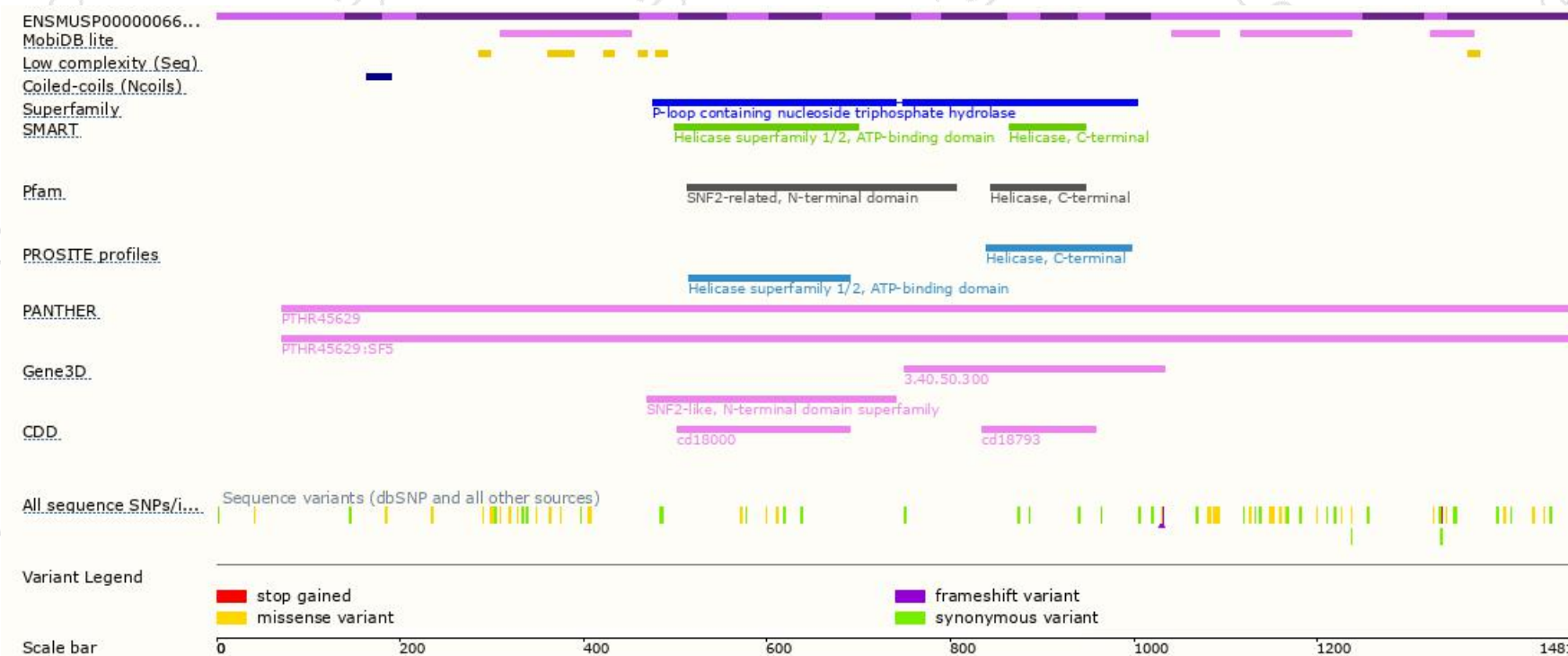
Mouse phenotype description(MGI)

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,Homozygous mutant mice exhibit UV sensitivity, inactivation of transcription-coupled repair, increased incidence of induced skin and eye tumors, circling behavior, impaired coordination and lower body weight.

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