

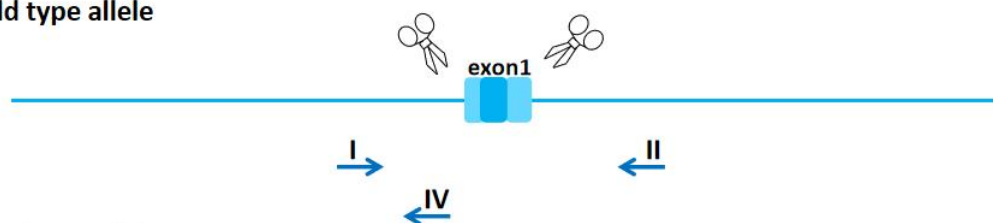
Tas2r108-KO Genotyping Protocol



Common Name	Tas2r108-KO	Cat. NO.	NM-KO-232314
Strain of Origin	C57BL/6J	Version	V1

Genotyping strategy

Wild type allele



knockout allele

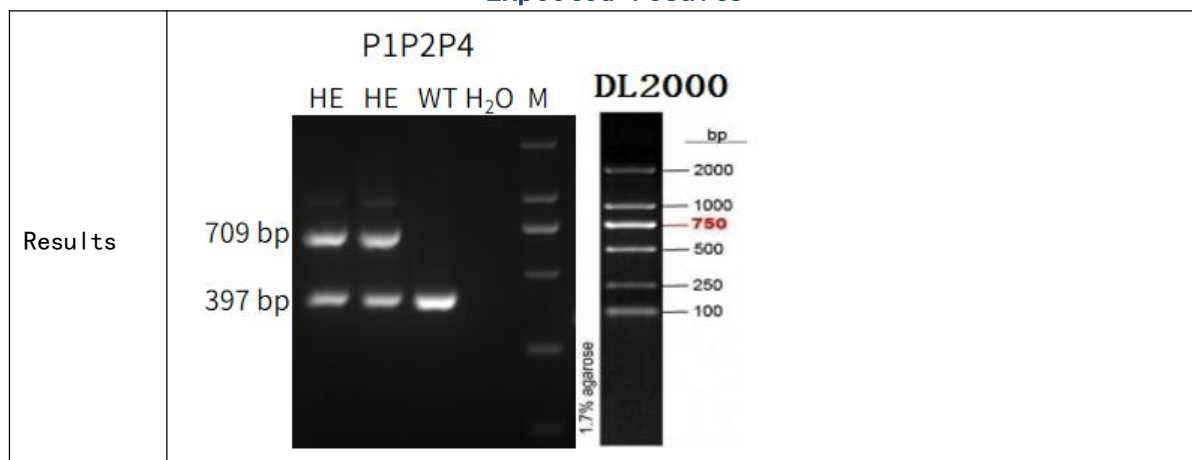


: coding region : uncoding region
 : Cas9/gRNA : mutation
 NHEJ : Non-homologous end joining
 : primer location

Primers

Primer	Sequence (5' → 3')	Primer type
P1	GGTGAACCCCAATGGACTATG	Forward
P2	GGCCTTCCCCTGAACTCTGTAT	Reverse
P4	TGTTCTCCAAGAGCAGAAAGACT	Reverse

Expected results



Genotype	Knockout type: -1580+1bp
	Wild type: P1P4=397 bp
	Heterozygote: P1P2 =709 bp; P1P4=397 bp
	Homozygote: P1P2 =709 bp

Note: In both wild-type and heterozygous mice, whether the P1 and P2 primers can amplify larger bands does not affect the interpretation of the results, because the purpose of designing this pair of primers is to amplify KO band

Reaction &Cycling

PCR Reaction System	Reaction Component			Volume (μl)
	ddH2O			7.5
	2×Taq Plus Master Mix			10.0
	P1 (10 pmol/μl)			0.5
	P2 (10 pmol/μl)			0.5
	P4 (10 pmol/μl)			0.5
	Genomic DNA			1.0
	Total			20
	2×Taq Plus Master Mix from Vazyme (Code Number: P222-1)			
Cycling Reaction	Step	Temp	Time	Note
	1	95° C	5 min	
	2	95° C	20 sec	
	3	60° C	20 sec	
	4	72° C	20 sec	35 repeats to 2
	5	72° C	5 min	
	6	12° C	Hold	