

**Supplementary Table 1** Summary of the results of freeze-thawing in Ayu 8104 mice

Group	Females	Fertility	Frozen	Recovered	Normal
MU (control)	15	152/397 (38.3%)	-	-	-
MF	-	-	80	78 (97.5%)	68 (87.2%)
IUF	9	242/305 (79.3%)	242	222 (91.7%)	135 (60.8%)
IFF	8	135/190 (71.1%)	135	119 (88.1%)	84 (70.6%)

**Supplementary Table 2** Summary of the analyses for *bL* mutant screening

Founders	MU1	MU2	MU3	MU4	MU5	MU6	MU7	MU8	MU9	MU10	
HMA	ND	+	ND	ND*	ND	ND	ND	+ *	+	ND	
RFLP	+	+	+	NT	ND	+	+	NT	NT	ND	
Sequence mutation	+	+	+	+	NT	+	+	+	+	NT	
Genotype	MT	MT	MT	MT		MT	MT	MT	MT		
Founders	MF1	MF2	MF3	MF4	MF5	MF6	MF7	MF8	MF9	MF10	
HMA	ND	ND*	ND	ND	ND	ND*	ND	ND*	ND*	ND	
RFLP	ND	NT	ND	ND	ND	NT	ND	NT	NT	ND	
Sequence mutation	NT	+	NT	NT	NT	+	NT	+	+	NT	
Genotype		MT				MT		MT	MT		
Founders	MF11	MF12	MF13	MF14	MF15	MF16	MF17	MF18	MF19	MF20	MF21
HMA	ND	ND	ND	ND	ND	ND	ND*	ND	ND	ND	ND
RFLP	ND	+	ND	ND	ND	+	NT	ND	ND	ND	ND
Sequence mutation	NT	+	NT	NT	NT	+	+	+/-***	NT	NT	NT
Genotype		MT				MT	MT				
Founders	IUF1	IUF2	IUF3	IUF4	IUF5	IUF6	IUF7	IUF8	IUF9	IUF10	
HMA	ND	+	ND	+	ND	ND	ND	ND*	+	ND	
RFLP	ND	+	+	NT	ND	+	ND	NT	NT	ND	
Sequence mutation	NT	+	+	+	NT	+	NT	+	+	NT	
Genotype		MT	MT	MT		MT		MT	MT		
Founders	IUF11	IUF12	IUF13	IUF14	IUF15	IUF16	IUF17	IUF18	IUF19	IUF20	
HMA	+	ND	ND	ND	ND	ND*	ND	ND	ND*	+	
RFLP	NT	ND	ND	ND	ND	NT	ND	ND	NT	NT	
Sequence mutation	+	NT	NT	NT	NT	+	NT	NT	+	+	
Genotype	MT					MT			MT	MT	
Founders	IFF1	IFF2	IFF3	IFF4	IFF5	IFF6					
HMA	ND	ND	ND	+	ND	ND**					
RFLP	ND	ND	ND	NT	ND	NT					
Sequence mutation	ND	ND	NT	+	NT	+					
Genotype		MT				MT					

\* Smaller amplicon appeared.

\*\* Larger amplicon appeared.

\*\*\* Only single-base substitution was detected.

HMA, heteroduplex mobility assay. RFLP, restriction fragment length polymorphism. ND, not detected. NT, not tested. MT, mutant.

**Supplementary Table 3** Summary of the results of freeze-thawing in C57BL/6N mice

Group	Females	Fertility	Frozen	Recovered	Normal
MUM	20	204/494 (41.3%)	-	-	-
MUI	19	274/577 (47.5%)	-	-	-
MFM	-	-	81	81 (100.0%)	81 (100.0%)
MFI	-	-	150	139 (92.7%)	113 (81.3%)

**Supplementary Table 4** Summary of the analyses for *Clec4b1* mutant screening

Founders	MUM1	MUM2	MUM3	MUM4	MUM5	MUM6	MUM7	MUM8	MUM9	MUM10		
HMA	ND*	ND	+	ND*	ND*	ND	ND*	ND	ND*	ND		
RFLP	NT	+	NT	NT	NT	+	NT	ND	NT	+		
Sequence mutation	+	+	+	+	+	+	+	NT	+	+		
Genotype	MT											
Founders	MUM11	MUM12	MUM13	MUM14	MUM15	MUM16	MUM17	MUM18	MUM19	MUM20		
HMA	ND	+	ND	+	ND*	+	+	+	ND*	ND		
RFLP	+	NT	+	NT	NT	NT	NT	NT	NT	+		
Sequence mutation	+	+	+	+	+	+	+	+	+	+		
Genotype	MT											
Founders	MUI1	MUI2	MUI3	MUI4	MUI5	MUI6	MUI7	MUI8	MUI9	MUI10		
HMA	ND	+	ND	ND*	ND	+*	ND	+	+	+		
RFLP	ND	NT	+	NT	+	NT	+	NT	NT	NT		
Sequence mutation	NT	+	+	+	+	+	+	+	+	+		
Genotype	MT											
Founders	MUI11	MUI12	MUI13	MUI14	MUI15	MUI16	MUI17	MUI18	MUI19	MUI20		
HMA	ND	+	+	+	ND	ND	ND	+	+	ND		
RFLP	+	NT	NT	NT	+	+	+	NT	NT	+		
Sequence mutation	+	+	+	+	+	+	+	+	+	+		
Genotype	MT											
Founders	MFM1	MFM2	MFM3	MFM4	MFM5	MFM6						
HMA	ND	+	ND	ND*	ND*	ND						
RFLP	+	NT	+	NT	+	+						
Sequence mutation	+	+	+	+	+	+						
Genotype	MT	MT	MT	MT	MT	MT						
Founders	MFI1	MFI2	MFI3	MFI4	MFI5	MFI6	MFI7	MFI8	MFI9	MFI10	MFI11	MFI12
HMA	ND	ND*	+	ND	+	ND	ND	ND	+	+	ND	+
RFLP	+	NT	NT	+	NT	+	+	+	NT	NT	+	NT
Sequence mutation	+	+	+	+	+	+	+	+	+	+	+	+
Genotype	MT											

\* Smaller amplicon appeared.

HMA, heteroduplex mobility assay. RFLP, restriction fragment length polymorphism. ND, not detected. NT, not tested. MT, mutant.