

Table S1. Q-PCR primer sequence and product size.

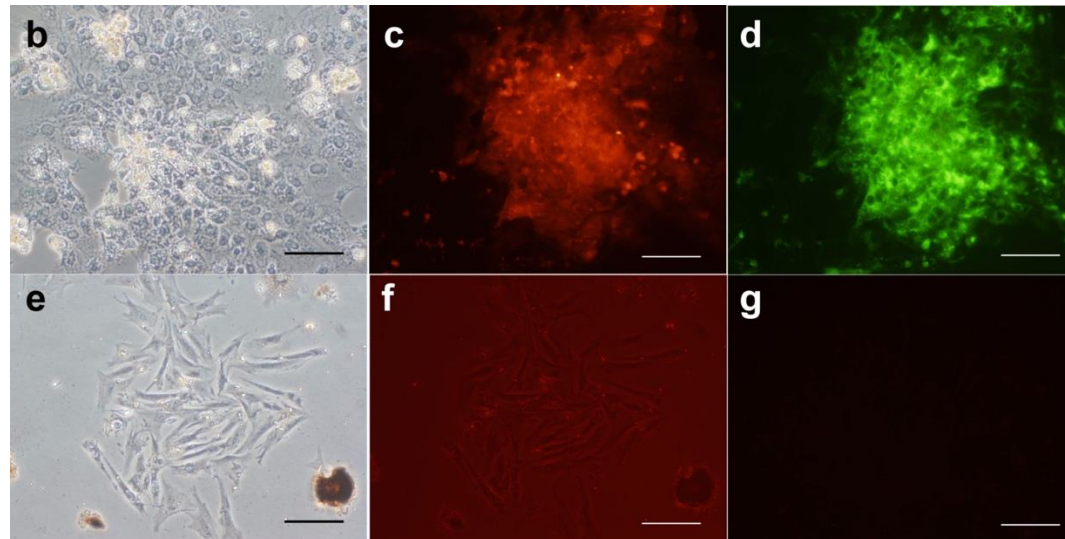
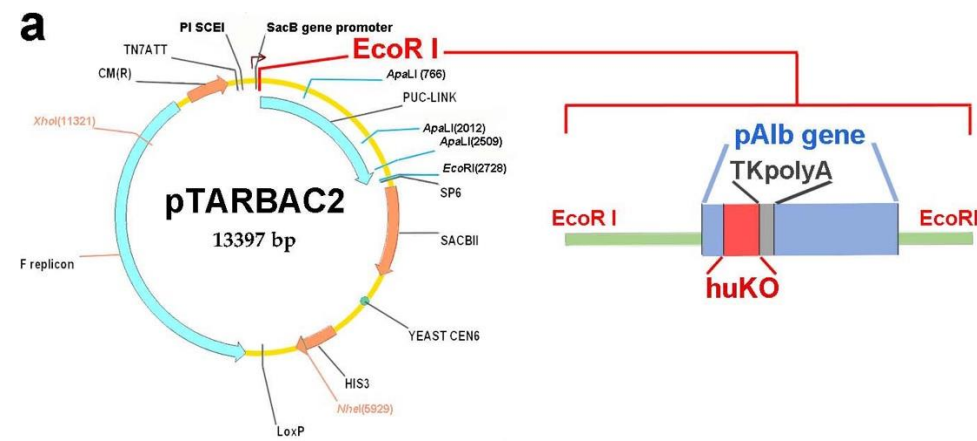
Gene Product	Primer Sequence		Amplicon Size (bp)
	Forward	Reverse	
Albumin	TTTATGCCCCGGAACCTCTTT	AGTCTCTGTTTGGCAGACGAA	148
CYP3A4	AAGTCGCCTCGAAGATACACA	AAGGAGAGAACTGCTCGTG	174
Alpha1-antitrypsin	CCTATAACGTCACCGACCTCG	TGGAAGCATTTCGTGGATCTTG	208
Tyrosine aminotransferase	CTGGACTCGGGCAAATATAATGG	GTCCTTAGCTTCTAGGGGTGC	111
Tryptophan 2, 3-dioxygenase	TCCTCAGGCTATCACTACCTGC	ATCTTCGGTATCCAGTGTCGG	110
Hepatocyte nuclear factor-4 alpha	CGAAGGTCAAGCTATGAGGACA	ATCTGCGATGCTGGCAATCT	141
Cytokeratin 18	GGCATCCAGAACGAGAAGGAG	ATTGTCCACAGTATTTGCGAAGA	216
Carbamoylphosphate synthetase I	TTTAGGGCAATGGCTACAGG	GTTCTGCAAGAGCTGGGTTC	373
Ornithine transcarbamylase	CTGATTACCTCACGCTCC	TCTCCTCTTCTCGTCCCA	308
GAPDH ¹	TGCACCACCAACTGCTTAGC	GGCATGGACTGTGGTCATGAG	87

¹ Glyceraldehyde-3-phosphate dehydrogenase.

Table S2. Primer design and location in genotyping of ornithine transcarbamylase (OTCD) and Severe combined immunodeficiency (SCID) mouse.

Target Gene	Primer Sequence	
	Forward	Reverse
OTCD ¹	ATGTGAGTGATGCTTCTCCTGGGT	TCGATTGAGATAGCTGGTGCAAGTA
Prkdc ²	GAGAAAAGGAGGATCATGGATTCAAGAAATAAATGTAACG	CCTAAGAGTCACCTTTCTCCATTTACACAGTGAAGTGCC
MF	TGGTATCCACAACATAAAATACGCTAA	
WR		TGGCCCCTGCTAACTTTCTCTTAGCA

¹ Primer amplicon includes exon 4 which has a mutation of CAC (¹¹⁷histidine) to GAC (aspartate). After the enzyme digestion (5' CACNN | NNGTG 3'), gel electrophoresis shows a 658 base pair (bp) band (diseased), a 558 bp band (wild type), or 658 and 558 bp bands (heterozygous). Sequence around exon 4: 5'-TTCTCGATTGAGATAGCTGGTGCAAGTACTGATGCCTCATAATTTGGTTAACATTTTAGTTCTTTCGTTTTCCCCTCTCAATACATTCAGTGTCTTTTCTTTTGTCTAGGCTTTGCTCTGCTGGGAGGACACCCTTCCTTTCTTACCACACAAGACATTGACTTGGGTGTGAATGAAAGTCTCACAGACACCGCTCGGTTGTAAACTTTTCTTCCTTCCAAAGTTTATTTCAAACCTCTGATGGGTAGTTTAAAAGAGAAGATGATGCTTCTCCTTAGATAATGGTCTCCCCCTTTTCGGTGTCTTTTGTACCTTCTCCCCCTTACAGGGCTCTTTATTTAATGTTTGAAACGCCTCTCTTTCATTCTGTAGCCCCTTTTTAGTGTCTTACTTTGTTCCCATTTGTTATGATAAAGGCCAAGGTAAAAGCAATTTGGGCAGGAAAGGGTATTTTCATCTTAAAGTCCACATAAAATCCATTTTAAGATGAAATAAACCTTTTCCTAACC AAAGAAAGAAAGCCAGGGCAAGAACTCAAGACAAAAACCAGGATGCAGGAACTCAAGCAGAGGCCATAGAAGAATGGTGTTTAATGGCTTGCTCAAA CTGCCTTCTTAAACCATCCAGGACCACCCACCCAGGAGAAGCATCACTCACATTGAGTGGGGCCCTCTTCTATTGATTGGCAATCAAG -3'. Yellow area indicates exon 4 which includes a mutation of CAC (¹¹⁷histidine) to GAC (aspartate) (double underline). Primer pairs were indicated by under lines. ² According to the polymerase chain reaction using confronting two-pair primers [34]. Gel electrophoresis shows 257 and 180 bp bands (homozygous SCID), 257, 180, and 101 bp bands (heterozygous SCID), and 257 and 101 bp bands (wild type).



Supplementary Figure 1. (a) Construction of transgene used for the establishment of kusabira orange transgenic pig. pAlb gene; promoter of porcine albumin. huKO; humanized kusabira orange gene. Kusabira gene originally from *Fungia concinna* was modified to enhance the expression efficacy by replacing the *Fungia concinna*-specific codons with mammalian ones [19,21]. TKpolyA; HSV-thymidine kinase (TK) promoter. (b–g) Cultured hepatocytes isolated from the pig. (b–d)

Colony of parenchymal hepatocytes at culture day 2. (**e–g**) Colony of non-parenchymal hepatocytes at culture day 3. (**b,e**) Phase contrast micrographs. (**c,f**) Fluorescent micrographs of kusabira orange. (**d,g**) Fluorescent micrographs of albumin staining (FITC). Scale bar: 200 μm .