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Citation	Journal of Heredity, 111(7), 640-645 https://doi.org/10.1093/jhered/esaa054
Issue Date	2020-10
Doc URL	https://hdl.handle.net/2115/82865
Rights	This is a pre-copyedited, author-produced version of an article accepted for publication in "Journal of Heredity" following peer review. The version of record "Journal of Heredity. 111(7), 2020, p.640-645" is available online at: https://doi.org/10.1093/jhered/esaa054
Type	journal article
File Information	J. Hered_v.111(7)_Fig1-3.pdf



**Mouse hair significantly lightened through replacement of the cysteine residue in
the N-terminal domain of Mc1r using the CRISPR/Cas9 system**

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Running head: Genome-edited mouse *Mc1r*

Key words: CRISPR/Cas9, hair color variant, loss of function, melanocortin 1 receptor

Abstract

A loss-of-function mutation in the *melanocortin 1 receptor* gene (*MC1R*), which switches off the eumelanin production, causes yellowish coat color variants in mammals. In a wild population of sables (*Martes zibellina*) in Hokkaido, Japan, the mutation responsible for a bright yellow coat color variant was inferred to be a cysteine replacement at codon 35 of the N-terminal extracellular domain of the Mc1r receptor. In the present study, we validated these findings by applying genome editing on *Mc1r* in mouse strains C3H/HeJ and C57BL/6N, altering the codon for cysteine (Cys33Phe). The resulting single amino acid substitution (Cys33Phe) and unintentionally generated frameshift mutations yielded a color variant exhibiting substantially brighter body color, indicating that the Cys35 replacement produced sufficient MC1R loss of function to confirm that this mutation is responsible for producing the Hokkaido sable yellow color variant. Notably, the yellowish mutant mouse phenotype exhibited brown coloration in subapical hair on the dorsal side in both the C3H/HeJ and C57BL/6N strains, despite the inability of the latter to produce the agouti signaling protein (*Asip*). This darker hair and body coloration was not apparent in the Hokkaido sable variant, implying the presence of an additional genetic system shaping yellowish hair variability.

1 **Introduction**

2 Body color has significant ecological and evolutionary meaning in animals (Rosenblum
3 et al. 2004). In vertebrates, a variety of loci are involved in pigmentation; among these,
4 the melanocortin 1 receptor gene (*Mc1r*) and agouti signaling protein (*Asip*) contribute
5 to the determination of pigmentation patterns (Västermark and Schiöth 2011) and play
6 major roles in evolutionary body color changes (Miller et al. 1995; Hoekstra 2006; Cal
7 et al. 2017). The products of these genes are the receptor and its antagonist, respectively,
8 which regulate pigment production in melanocytes (Rees 2000; Abdel-Malek 2001).
9 The *Mc1r*–*Asip* system functions to create banding patterns on a single hair, termed an
10 agouti pattern. Eumelanin production is generally more intense on the dorsal side of an
11 animal than on the ventral side (Caro and Mallarino 2020), resulting in a contrasting
12 body pattern often called countershading (Ruxton et al. 2004). The molecular system
13 responsible for these patterns lies in the *Asip* promoter regions (Vrieling et al. 1994;
14 Linnen et al. 2013).

15 Mutations on *MC1R* are generally not lethal (Enshell-Seijffers et al. 2010).
16 Gain-of-function *Mc1r* mutations are commonly found in the wild populations and
17 domesticated animals and lead to melanistic phenotype through by single amino acid
18 replacements (Våge et al. 1997; Theron et al. 2001; Kambe et al. 2011) and short amino
19 acid segment deletions (Eizirik et al. 2003; Vidal et al. 2010). Loss-of-function *MC1R*
20 mutations are known to cause yellowish color variants in wild and domestic populations
21 of a number of species such as seals (Peters et al. 2016) and dogs (Everts et al. 2000;
22 Newton et al. 2000; Schmutz et al. 2002). In a recent study, *MC1R* deletion mutant

1 rabbits created by the CRISPR/Cas9 system developed pale yellow coat color (Xiao et al.
2 2019).

3 The bright yellow variant of the sable *Martes zibellina* from Hokkaido, Japan is an
4 example of a pale colored phenotype possibly caused by *MC1R* mutation in a wild
5 population (Hosoda et al. 2005; Ishida et al. 2013; Suzuki 2013). While the yellow sable
6 was found to have two substitutions (Cys35Phe and Asn68Ser) compared to the wild-type
7 individuals (Hosoda et al. 2005), population analyses suggest that replacement of the
8 cysteine residue at codon 35 of the first extracellular domain (Cys35Phe) of MC1R may
9 be responsible for this variant (Ishida et al. 2013).

10 In this study, we applied genome editing techniques to investigate whether a
11 single amino acid replacement of the cysteine residue in the N-terminal domain of Mc1r
12 is sufficient to cause the yellow hair color variant. We also explored the possibility of
13 contrasting color patterns in mice lacking functional Mc1r and Asip genes.

14 15 **Materials and Methods**

16 *Animal experimental procedures*

17 All animal experiments were approved by the Kumamoto University Ethics Committee
18 for Animal Experiments and the Kumamoto University Recombinant DNA Advisory
19 Committee for the generation of *Mc1r* knockout mice. C3H/HeJ and C57BL/6N mice
20 were purchased from Crea-Japan, Tokyo, Japan and housed in a climate-controlled
21 room under a 12-h light/dark cycle. We generated knockout mice by introducing Cas9
22 protein (317-08441; NIPPON GENE, Toyama, Japan), tracrRNA (GE-002; FASMAC,

Kanagawa, Japan), synthetic CRISPR RNA (FASMAC), and a single-strand oligodeoxy nucleotide (ssODN) into fertilized eggs by electroporation, as previously described (Takemoto et al. 2020). For replacement of the targeted cysteine residue at codon 33 of mouse *Mc1r*, we designed CRISPR RNA [ATGGACACATACAGGCACCA (AGG)] and ssODN (CTAGGCTGAGGAAGAGGCCATCTGGGATGGACACATACAGGAACCAAGGCT CTGACTGGTTGGTGGCCAGTCCAAGGTGAGAGG).

F₁ mice were generated by breeding G₀ mice with markedly lighter coat colors, and were subsequently used to generate homozygous F₂ mice.

Genotyping of Mc1r

We determined the nucleotide sequence, targeting the 5' half of the *Mc1r* coding region. Polymerase chain reaction (PCR) was performed using the AmpliTaq Gold 360 DNA Polymerase Kit (Invitrogen, Carlsbad, CA, USA) as previously described (Shimada et al. 2009). We used the primers 5'Mc1r-52 (5'-GCTCATACCACCTGGAGCTGCAGCC-3') and 3'Mc1r+504 (5'-AAGAGGGTGCTGGAGACGATGC TGACC-3').

Measurement of coat color variation

We quantified hair color variation using a spectrophotometer (CM-700d, Konica Minolta Co., Osaka, Japan) with a 3-mm diameter window and the Specular Component

Included option. We used F₂ mice for phenotype characterization to eliminate the mosaic phenotype, which is expected to occur in G₀ mice. For this purpose, we used the CIE L*a*b* colorimetry model, where L* is luminosity from black to white [0, 100], a* encodes the initial color from green to red [-60, 60], and b* encodes the initial color from blue to yellow [-60, 60]. Dorsal and ventral colors were quantified using 10 independent measurements in areas along the midline; we used average values after excluding outlier measurements in which at least one of the quantified values (L*, a*, or b*) exceeded 1.5 times the interquartile range.

The R software (R Development Core Team, 2008) was used to plot dorsal (x-axis) and ventral (y-axis) color values and to perform principal component analysis (PCA). The R 'prcomp' function and the 'ggbiplot' package were used to combine the dorsal and ventral measurement datasets.

Results

Variant Mc1r sequences in genome-edited mice

To test whether single amino acid replacement of Cys35 was sufficient for inducing total dysfunction of Mc1r via the CRIPR/Cas9 system, we targeted the cysteine residue at codon 33 (corresponding to codon 35 in other mammals) in the mouse strains used in this study (Figure 1a). G₀ mice (n = 53) generated in the C3H/HeJ genome-editing experiment showed variable coat color patterns among and within individuals, indicative of appearance of mosaicism (Supplementary Figure S1). Several G₀ mice showed markedly lighter coat color; this phenotype was designated as the yellowish

1 phenotype in contrast to wild-type (WT) mice, which had the original coat color.

2 We explored genotyping of *Mc1r* (Supplementary Table S1) and detected the
3 c.98G>T mutation at the target site and a number of deletion and insertion mutations
4 nearby the target site, including one or more nucleotide (1, 2, 3, and 6 bp) deletions
5 (Figure 1c). Homozygous c.98G>T mice or a combination of c.98G>T and another
6 mutation predicted to cause frameshift mutations had the yellowish phenotype. A
7 non-frameshift mutation caused by the 6-bp deletion, which was expected to lose Cys33,
8 was also found to induce the yellowish phenotype. By contrast, the 3-bp deletion, which
9 resulted in the removal of Trp32 prior to the Cys33 target codon, exhibited the WT
10 phenotype.

11 These results were reproduced in the C57BL/6N experiment, (Supplementary
12 Table S2, Supplementary Figure S2). G₀ mice (n = 28) exhibited a variety of coat color
13 patterns ranging from the yellowish phenotype and a melanistic phenotype caused by the
14 parental strain with the *Asip* null allele (Slominski et al. 2005).

15 We then conducted breeding experiments using representative G₀ c.98G>T, 1-bp
16 deletion, and 2-bp deletion mice of the homozygous C3H/HeJ background. We
17 genotyped 36 F₂ mice with the WT (n = 29) and yellowish (n = 7) phenotypes and
18 found that their coat color phenotypes were those predicted based on the *Mc1r*
19 genotypes. This trend was reproduced in c.98G>T F₂ mice of the B57BL/6N
20 background, as observed among G₀ mice.

21
22 *Hair color phenotypes among Mc1r mutant mice*

We examined the hair color of the yellowish (Figure 2a) and WT phenotypes (Figure 2b) in Mc1r genotyped F₂ mice of the C3H/HeJ background. Hair on both the dorsal and ventral sides exhibited the typical agouti pattern, characterized by black hair color and subapical yellow bands in the WT (Figure 2c, d). In the yellowish phenotype, dorsal hair was creamy pale yellow with darkened tips (Figure 2e) and ventral hair was creamy pale yellow without any apparent banding pattern (Figure 2f).

We quantified hair from both coat color phenotypes in F₂ mice of the C3H/HeJ background (n = 14) using a spectrophotometer. The results showed that lightness (L*) differed substantially between the homozygous or heterozygous WT allele sequence (Cys33) and mice homozygous for c.98G>T (Cys33Phe), and 1-bp and 2-bp deletions in both dorsal and ventral body parts (Figure 3). The results indicated similar trends, particularly in L*, between mice with the homozygous c.98G>T (Phe33) genotype and frameshift mutations that altered the codon sequence including Cys33 (Supplementary Figure S3).

Discussion

The replacement or deletion of the cysteine residue (Cys35) in the extracellular N-terminus of MC1R has been suggested to be a significant driver of bright yellow coat color in sables (Hosoda et al. 2005; Ishida et al. 2013). In the present study, we replaced Cys33 of the first extracellular domain of the murine receptor Mc1r using the CRSPR-Cas9 system. Our results reveal that a single amino acid replacement is sufficient to cause a drastic change in coat color phenotype from WT to the yellowish

1 phenotype, and that this property is shared in mice with frameshift mutations (Figures 2,
2 3). These findings indicate that functional efficiency of the Cys33 replacement or
3 deletion in mouse Mc1r is comparable to a null mutation. This cysteine residue is
4 perfectly conserved in the N-terminus of all melanocortin receptors (Rana et al. 1999;
5 Garcia-Borron et al. 2005) and plays an essential role in guiding MC1R to the plasma
6 membrane, where Cys35 is thought to stabilize the MC1R receptor by mediating
7 dimerization (Zanna et al. 2008). Cys35 substitution has also been reported in humans
8 with red hair (Fargnoli et al. 2003).

9 Substitution or deletion of Cys33 of the Mc1r receptor markedly enhanced the
10 lightness of coat color in mice, as also observed in the Hokkaido sables. However, an
11 interesting difference between the yellowish-phenotype mice and sables is that the
12 yellow hair of the mutant mice had dark brown tips, whereas the variant Hokkaido
13 sables had bright yellow hair on both the dorsal and ventral sides (see photograph in
14 Suzuki 2013). Such dark coloration, which was also reported in yellow-haired mice
15 with a frameshift mutation and stop codon (Robbins et al. 1993), is known as
16 “incomplete yellowing”, suggesting the ability to produce eumelanin in the absence of
17 the MC1R signaling system (Bennett and Lamoreux 2003). Accordingly, several
18 alternative signaling systems have been reported to cause adenylyl cyclase activity on
19 the cell membrane of melanocytes to produce cAMP, possibly regulating melanogenesis
20 independently of MC1R by acting directly on melanosomes (Schallreuter et al. 2008;
21 Kondo and Hearing 2011; Enshell-Seijffers et al. 2010). Alternatively, this apparent
22 difference in yellowish phenotype between mice and sables implies the presence of an

1 additional genetic system adding dark pigmentation. In dogs with the homozygous
2 Mc1r null mutation, lighter hair varies from white to yellow, gold, orange and red
3 (Everts et al. 2000; Newton et al. 2000; Schmutz et al. 2002; Oguro-Okano et al. 2011).
4 The mutant mice created in the present study will facilitate our understanding of the
5 genetic system underlying pigment production and variable yellowish hair color in the
6 genetic background when the MC1R system is lost.

7 In conclusion, we demonstrated that a single amino replacement or deletion was
8 sufficient to cause loss of function of MC1R producing effects comparable to those of a
9 frameshift mutation. We therefore conclude that replacement of Cys35 is the mutation
10 responsible for the bright yellow Hokkaido sable phenotype. Variability in the yellowish
11 coat color between species with homozygous Mc1r null alleles should be examined in
12 future studies.

13 14 **Acknowledgments**

15 We thank all staff members of the KA laboratory for their help in breeding the
16 genome-edited mice used in this study. We would like to thank the editor and 2
17 anonymous reviewers for many helpful suggestions.

18 19 **Data Availability**

20 All relevant data are available in this paper.

21 22 **Funding**

1 This study was conducted with the support of a Japan Society for the Promotion of
2 Science (JSPS) Grant-in-Aid for Scientific Research (B) (17H04604 to H.S.), a JSPS
3 Grant-in-Aid for Scientific Research on Innovative Areas (JS18H05508 to H.S.), and a
4 JSPS KAKENHI grant for Advanced Animal Model Support (JP16H06276 to K.A.).

References

- Abdel-Malek ZA, Scott MC, Furumura M et al. 2001. The melanocortin 1 receptor is the principal mediator of the effects of agouti signaling protein on mammalian melanocytes. *J Cell Sci* 114:1019–1024.
- Bennett DC, Lamoreux ML. 2003. The color loci of mice—a genetic century. *Pigment Cell Res.* 16:333–344.
- Cal L, Suarez-Bregua P, Cerdá-Reverter JM, Braasch I, Rotllant J. 2017. Fish pigmentation and the melanocortin system. *Comp Biochem Physiol A Mol Integr Physiol.* 211:26–33.
- Caro T, Mallarino R. 2020. Coloration in Mammals. *Trend Ecol Evol.* 35:357–366.
- Eizirik E, Yuhki N, Johnson WE, Menotti-Raymond M, Hannah SS, O'Brien SJ. 2003. Molecular genetics and evolution of melanism in the cat family. *Curr Biol.* 13:448–453.
- Enshell-Seijffers D, Lindon C, Wu E, Taketo MM, Morgan BA. 2010. β -Catenin activity in the dermal papilla of the hair follicle regulates pigment-type switching. *Proc Natl Acad Sci.* 107:21564–21569.
- Everts RE, Rothuizen J, Van Oost BA. 2000. Identification of a premature stop codon in the melanocyte-stimulating hormone receptor gene (MC1R) in Labrador and Golden retrievers with yellow coat colour. *Animal Genet.* 31:194–199.
- Fargnoli MC, Chimenti S, Keller G, Hofler H, Peris K. 2003. Identification of four novel melanocortin 1 receptor (MC1R) gene variants in a Mediterranean population. *Hum Mutat.* 21:655.
- Frandberg PA, Doufexis M, Kapas S, Chhajlani V. 2001. Cysteine residues are involved in structure and function of melanocortin 1 receptor: substitution of a cysteine residue in transmembrane segment two converts an agonist to antagonist. *Biochem Biophys Res Commun.* 281:851–857.
- Garcia-Borron JC, Sanchez-Laorden BL, Jimenez-Cervantes C. 2005. Melanocortin-1 receptor structure and functional regulation. *Pigment Cell Res.* 18:393–410.
- Hoekstra HE. 2006. Genetics, development and evolution of adaptive pigmentation in vertebrates. *Heredity.* 97(3):222–234.
- Hosoda T, Sato JJ, Shimada T, Campbell KL, Suzuki H. 2005. Independent nonframeshift deletions in the MC1R gene are not associated with melanistic coat

coloration in three mustelid lineages. *J Hered.* 96:607–613.

Ishida K, Sato JJ, Kinoshita G, Hosoda T, Kryukov AP, Suzuki H. 2013. Evolutionary history of the sable (*Martes zibellina brachyura*) on Hokkaido inferred from mitochondrial *Cytb* and nuclear *Mc1r* and *Tcf25* gene sequences. *Acta Theriol.* 58(1):13–24.

Kambe Y, Tanikawa T, Matsumoto Y, Tomozawa M, Aplin KP, Suzuki, H. 2011. Origin of agouti-melanistic polymorphism in wild Black Rats (*Rattus rattus*) inferred from *Mc1r* gene sequences. *Zool Sci.* 28:560–567.

Kondo T, Hearing VJ. 2011. Update on the regulation of mammalian melanocyte function and skin pigmentation. *Expert Rev Dermatol.* 6(1):97–108.

Linnen CR, Poh YP, Peterson BK, Barrett RD, Larson JG, Jensen JD, Hoekstra HE. 2013. Adaptive evolution of multiple traits through multiple mutations at a single gene. *Science.* 339:1312–1316.

Newton JM, Wilkie AL, He L, Jordan SA, Metallinos DL, Holmes NG et al. 2000. Melanocortin 1 receptor variation in the domestic dog. *Mammal Genome.* 11:24–30.

Oguro-Okano M, Honda M, Yamazaki K, Okano K. 2011. Mutations in the melanocortin 1 receptor, β -defensin103 and agouti signaling protein genes, and their association with coat color phenotypes in Akita-inu dogs. *J Vet Med Sci.* 73:853–858.

Peters L, Humble E, Kröcker N, Fuchs B, Forcada J, Hoffman JI. 2016. Born blonde: a recessive loss-of-function mutation in the melanocortin 1 receptor is associated with cream coat coloration in Antarctic fur seals. *Ecol Evol.* 6:5705–5717.

Rana BK, Hewett-Emmett D, Jin L, Chang BHJ, Sambuughin N, Lin M, Watkins S, Bamshad M, Jorde LB, Ramsay M, et al. 1999. High polymorphism at the human melanocortin 1 receptor locus. *Genetics.* 151(4):1547–1557.

Rees JL 2000. The melanocortin 1 receptor (MC1R): more than just red hair. *Pigment Cell Res.* 13:135–140.

Robbins LS, Nadeau JH, Johnson KR, Kelly MA, Roselli-Rehfuss L, Baack E, et al. 1993. Pigmentation phenotypes of variant extension locus alleles result from point mutations that alter MSH receptor function. *Cell.* 72:827–834.

Rosenblum EB, Hoekstra HE, Nachman MW. 2004. Adaptive reptile color variation and the evolution of the MC1R gene. *Evolution.* 58:1794–1808.

Ruxton GD, Speed MP, Kelly DJ. 2004. What, if anything, is the adaptive function of

countershading?. *Anim Behav.* 68:445–451.

Schallreuter KU, Kothari S, Chavan B, Spencer JD. 2008. Regulation of melanogenesis controversies and new concepts. *Exp Dermatol.* 17:395–404.

Schmutz SM, Berryere TG, Goldfinch AD. 2002. *TYRP1* and *MC1R* genotypes and their effects on coat color in dogs. *Mammal Genome.* 13:380–387.

Shimada T, Sato JJ, Aplin KP, Suzuki H. 2009. Comparative analysis of evolutionary modes in *Mc1r* coat color gene in wild mice and mustelids. *Genes Genet Syst.* 84(3):225–231.

Slominski A, Plonka PM, Pisarchik A, Smart JL, Tolle V, Wortsman J, Low MJ. 2005. Preservation of eumelanin hair pigmentation in proopiomelanocortin-deficient mice on a nonagouti (*a/a*) genetic background. *Endocrinology.* 146:1245–1253.

Suzuki H. 2013. Evolutionary and phylogeographic views on *Mc1r* and *Asip* variation in mammals. *Genes Genet Syst.* 88(3):155–164.

Takemoto K, Tani N, Takada Y, Fujimura S, Tanno N, Yamane M, Okamura K, Sugimoto M, Araki K, Ishiguro KI. 2020. A meiosis-specific factor MRM/C19orf57 modulates localization of RAD51 and DMC1 recombinases to DSBs in mouse meiotic recombination. *bioRxiv.*

Theron E, Hawkins K, Bermingham E, Ricklefs RE, Mundy NI. 2001. The molecular basis of an avian plumage polymorphism in the wild: a melanocortin-1-receptor point mutation is perfectly associated with the melanic plumage morph of the bananaquit, *Coereba flaveola*. *Curr Biol.* 11:550–557.

Våge DI, Lu D, Klungland H, Lien S, Adalsteinsson S, Cone RD. 1997. A non-epistatic interaction of agouti and extension in the fox, *Vulpes vulpes*. *Nat Genet.* 15:311–315.

Västermark A, Schiöth HB. 2011. The early origin of melanocortin receptors, agouti-related peptide, agouti signaling peptide, and melanocortin receptor-accessory proteins, with emphasis on pufferfishes, elephant shark, lampreys, and amphioxus. *Eur J Pharmacol.* 660:61–69.

Vidal O, Araguas RM, Fernández R, Heras S, Sanz N, Pla C. 2010. Melanism in guinea fowl (*Numida meleagris*) is associated with a deletion of Phenylalanine-256 in the *MC1R* gene. *Animal Genet.* 41:656–658.

Vrieling H, Duhl DM, Millar SE, Miller KA, Barsh GS. 1994. Differences in dorsal and ventral pigmentation result from regional expression of the mouse agouti gene.

Figure Captions

Fig. 1 (a) Schematic representation of the mouse G-protein-coupled receptor *Mc1r* with the seven characteristic α -helical transmembrane segments, showing the target amino acid codon (Cys33) produced using the CRIPR/Cas9 genome editing system. (b) Direct sequencing traces (nucleotide positions 85–105 in the coding sequence) showing the mutation from TGC (Cys) to TTC (Phe) at target codon 33. (c) Six sequencing traces representing the (1) wild-type (WT) and (2–6) genome-editing experiment phenotypes, showing characteristic coding variants.

Fig. 2 Mice with (a) WT and (b) yellowish coat colors. Coat color patterns in dorsal and ventral views of F_2 mice with (c, d) WT and (e, f) yellowish coat color, showing banding patterns in small bundles of hair removed from the dorsal and ventral body parts. Scale bar, 5 mm.

Fig. 3 Plots of dorsal (X-axis) and ventral (Y-axis) body color measurements of color traits within CIE Lab color space: lightness (L^*), red/green (a^*), and yellow/blue (b^*). We derived 14 F_2 mice from genome-edited mice with the wild type and altered coat colors. The representative types of the target site of the coat color-related melanocortin 1 receptor gene (*Mc1r*) were those having the cysteine residue at codon 33 (c.98G/c.98G; $n = 2$), a heterozygous target site (c.98G/c.98T; $n = 5$), replacement of the cysteine residue (c.98T/c.98T; $n = 2$), and 1-bp deletion ($n = 3$) and 2-bp deletion ($n = 2$) near the target site.

1

2 **Supplementary Figure S1 (a)** G₀ mice generated in the C3H/HeJ genome-editing
3 experiment targeting the codon 33 (corresponding to codon 35 in other mammals) for
4 the cysteine residue, resulting in variable coat color patterns among and within
5 individuals, indicative of appearance of mosaicism. **(b)** Four G₀ mice showed markedly
6 lighter coat color were subjected to breeding experiments to generate F₂ mice.

7

8 **Supplementary Figure S2 (a)** G₀ mice generated in the C57BL/6N genome-editing
9 experiment targeting the codon 33 (corresponding to codon 35 in other mammals) for
10 the cysteine residue, resulting in variable coat color patterns among and within
11 individuals, indicative of appearance of mosaicism. **(b)** Four G₀ mice showed markedly
12 lighter coat color were subjected to breeding experiments to generate F₂ mice.

13

14 **Supplementary Figure S3** Principal component analysis results for the combined
15 dorsal (d) and ventral (v) L*, a*, and b* measurement datasets.

16

17 **Supplementary Table S1** Supplementary Table S1. Genotyping of Mc1r in G₀ mice in
18 the C3H/HeJ background.

200 fertilized embryos from 10 female mice were subjected to electroporation. After cell culture, 198 injected eggs of the 2-cell stage were transferred to the oviducts of 10 pseudopregnant females, resulting in 53 offsprings.

*Coat color was temporarily categorized into three, yellowish (Y), wild (WT), and intermediate (I) types. See Supplementary Figure S1 for detail.

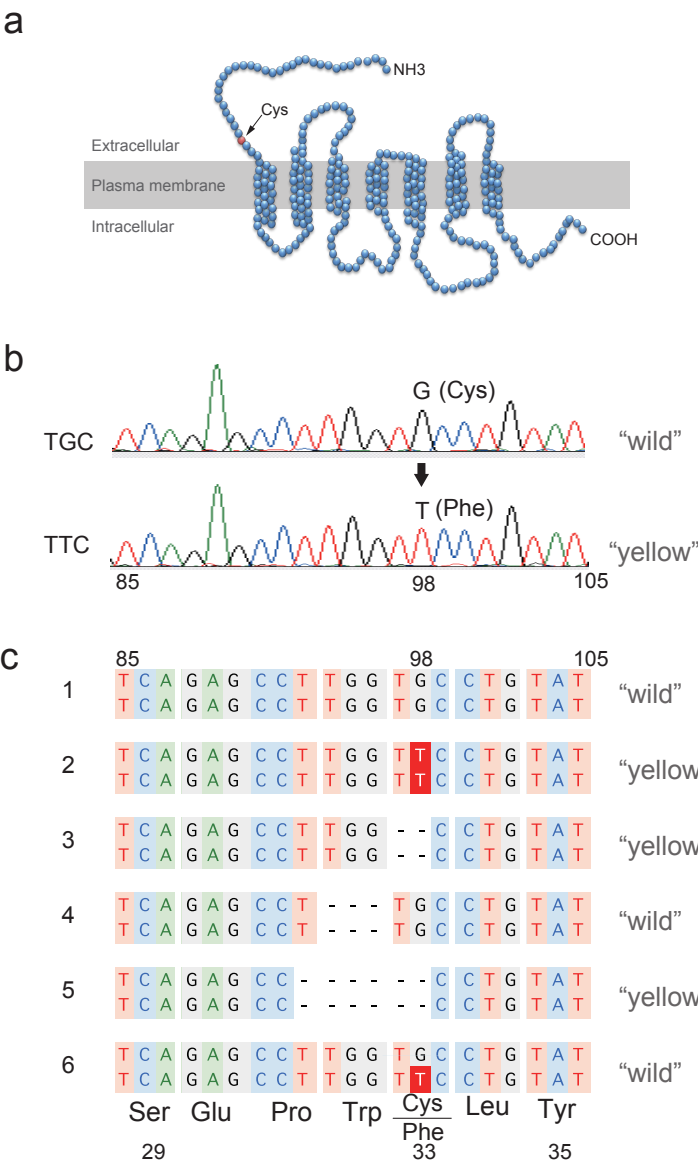
**ND, genotyping was failed to determine because of ambiguous results in the direct sequencing probably due to complex deletion and mosaicism.

Supplementary Table S2 Supplementary Table S1. Genotyping of Mc1r in G₀ mice in the C3H/HeJ background.

100 fertilized embryos from 5 female mice were subjected to electroporation. After cell culture, 99 injected eggs of the 2-cell stage were transferred to the oviducts of 5 pseudopregnant females, resulting in 28 offsprings.

*Coat color was temporarily categorized into three, yellowish (Y), wild (WT), and intermediate (I) types. See Supplementary Figure S1 for detail.

**ND, genotyping was failed to determine because of ambiguous results in the direct sequencing probably due to complex deletion and mosaicism.



Suzuki et al. Fig. 1

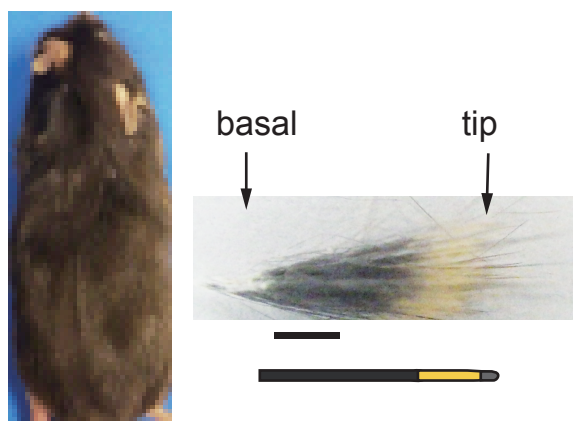
a



b

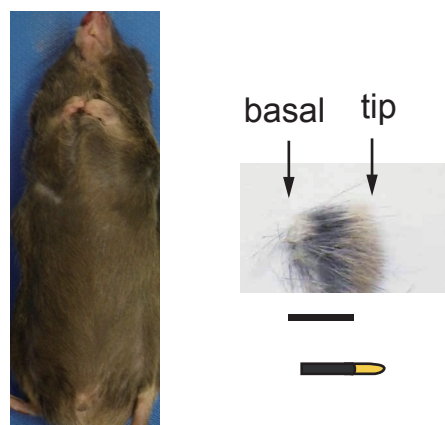


c



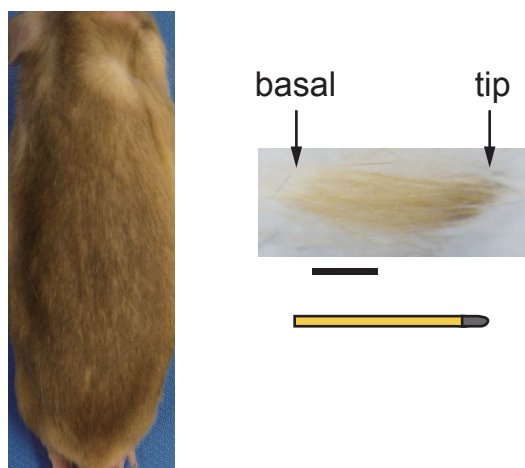
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d



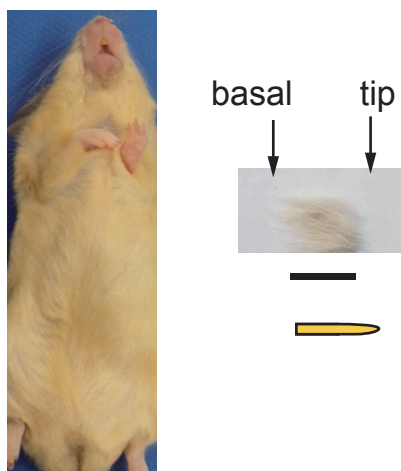
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e



dorsal

f



ventral

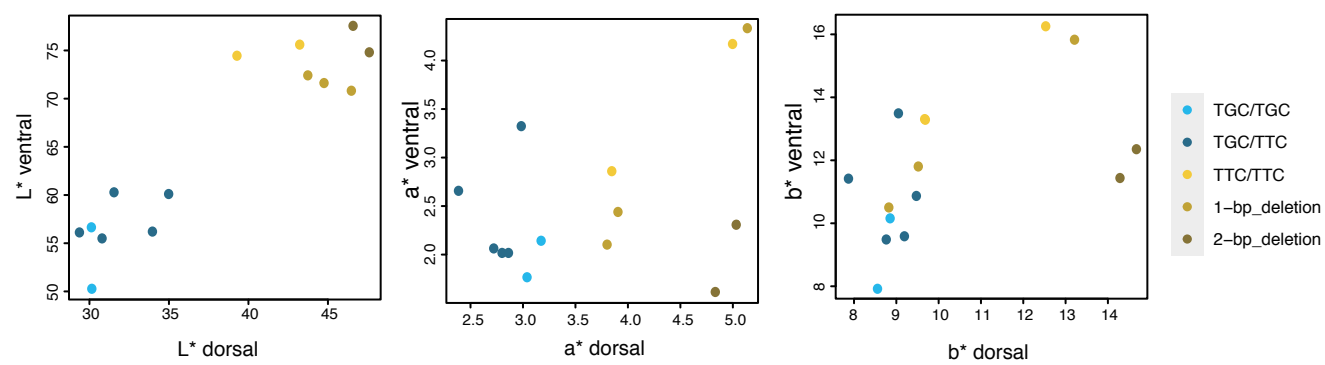


Figure 3.