**Supplementary file 1A.** Shape comparison between *Mitf* mutants and wild-type B6 mice. A Hotelling T2 test was performed to evaluate the difference in mean shape between mutant and wildtype groups; p-value, test statistic, and sample size (N) are shown. The Procrustes distances between mutant and wild type mean shapes are also indicated. \*The comparison between heterozygous and homozygous mice for the *Mitfmi-vga9* mutation is also shown.

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| --- | --- | --- | --- | --- | --- | --- |
|  | *Mitfmi-enu122/ Mitfmi-enu122* | *MitfMi-wh*/*Mitfmi* | *Mitfmi-vga9*/+ | *MitfMi-wh*/*MitfMi-wh* | *Mitfmi-vga9*/ *Mitfmi-vga9* | *Mitfmi-vga9* het vs hom\* |
| Hotelling T2 | p=0.0006 T2(2,12)=20  N=15 | p=0.011 T2(2,7)=9  N=10 | p=0.0042 T2(2,7)=19  N=10 | p=0.0008 T2(2,6)=49  N=9 | p=0.0006 T2(2,7)=56  N=10 | p= 0.0076  T2(2,7)=13  N=10 |
| Procrustes distance | 0.0239 | 0.0253 | 0.0300 | 0.0372 | 0.0466 | 0.0243 |

**Supplementary file 1B.** Missense variants found in the gene *Mitf* of wild mice. 9 populations of wild mice were screened for SNPs causing coding changes in Mitf: *Mus musculus musculus* from Kazakhstan, Check Republic, and Afganistan; *M. m. domesticus* from Iran, Heligoland, France, and Germany; *Mus castaneus;* and *Mus spretus.* Data available in the UCSC browser 🡪 MyData -> Public Sessions -> wildmouse (Harr *et al.* 2016). In addition, 8 hybrids between *M.m.musculus* and *M.m.domesticus* from the German hybrid zone (Turner, Tautz & Harr unpublished data), the same population used in this study, were also screened for coding changes. Reference and variant alleles are shown. nVar = number of chromosomes with the variant allele, n = number of chromosomes per population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Location (mm10)** | **Ref/Var** | **Feature type** | **nVar/n** | **Amino acid change** | **Codon change** | **Species - population** |
| chr6:97941094 | G/A | Transcript | 1/16 | S/N | aGc/aAc | M.m.musculus - Kazakhstan |
| chr6:97941156 | G/C | Transcript | 1/20 | E/Q | Gag/Cag | M.castaneus |
| chr6:97941187 | T/A | Transcript | 2/20 | L/Q | cTg/cAg | M.castaneus |
| chr6:97993296 | G/A | Transcript | 1/20 | S/N | aGc/aAc | M.castaneus |
| chr6:98017825 | G/A | Transcript | 6/16 | G/S | Ggt/Agt | M.spretus |
| chr6:98017984 | A/C | Transcript | 6/16 | M/L | Atg/Ctg | M.spretus |
| chr6:98018168 | C/T | Transcript | 6/16 | A/V | gCg/gTg | M.m.domesticus - Germany |
| chr6:97994441 | C/T | Transcript | 3/16 | H/Y | Cac/Tac | Hybrid mice - Bavaria |

Harr, B., Karakoc, E., et al. (2016). "Genomic resources for wild populations of the house mouse, Mus musculus and its close relative Mus spretus." Sci Data 3: 160075.