# Selective breeding and selection mapping using a novel wild-derived heterogeneous stock of mice revealed two closely-linked loci for tameness

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**Movie S1.** Supplementary movie showing a typical example of a mouse in selected group S2.

**Movie S2.** Supplementary movie showing a typical example of a mouse in control group C1.

**Table S1.** Origins of the WHS founder strains and the 54 strains used in the phylogenic analysis

| Strain | Abbr. | Subspecies group | Place of collection | Year of capture |
|---|---|---|---|---|
| BFM/2Ms | BFM/2 | *M.m.domesticus* | Montpellier, France | 1976 |
| PGN2/Ms | PGN2 | *M.m.domesticus* | Ontario, Canada | 1979 |
| HMI/Ms | HMI | *M.m.castaneus* | Heimei, Taiwan | 1986 |
| BLG2/Ms | BLG2 | *M.m.musculus* | General Toshevo, Bulgaria | 1980 |
| CHD/Ms | CHD | *M.m.musculus* | Chendu, China | 1981 |
| KJR/Ms | KJR | *M.m.musculus* | Kojuri, Korea | 1984 |
| MSM/Ms | MSM | *M.m.musculus* | Mishima, Japan | 1978 |
| NJL/Ms | NJL | *M.m.musculus* | Northern Jutland, Denmark | 1980 |

List of 54 strains used for NJ tree analysis

AEJ/GnLeJ, BFM2/Ms, A/J, AKR/J, BALB/cJ, C3H/HeJ, C57BL/6J, DBA/2J, I/LnJ, RIIIS/J, BLG2/Ms, 129S1/SvImJ, CAST/EiJ, NOD/ShiLtJ, NZO/HILtJ, PWK/PhJ, WSB/EiJ, CHD/Ms, CZECHI/EiJ, CZECHII/EiJ, DDY/Jcl, FVB/NJ, FVB, HMI, JE/LeJ, JF1/Ms, KJR/Ms, KK/HlJ, LEWES/EiJ, LG/J, LP/J, LT/SvEiJ, MOLF/EiJ, MRL/MpJ, MSM/Ms, CBA/CaJ, LP/J, NJL/Ms, NZW/LacJ, P/J, PERC/EiJ, PGN2/Ms, PWD, RBB/DnJ, RBF/DnJ, SF/CamEiJ, SH1/LeJ, SOD1/EiJ, ST/bJ, SWR/J, TIRANO/EiJ, WLA/Pas, WMP/Pas, ZALENDE/EiJ

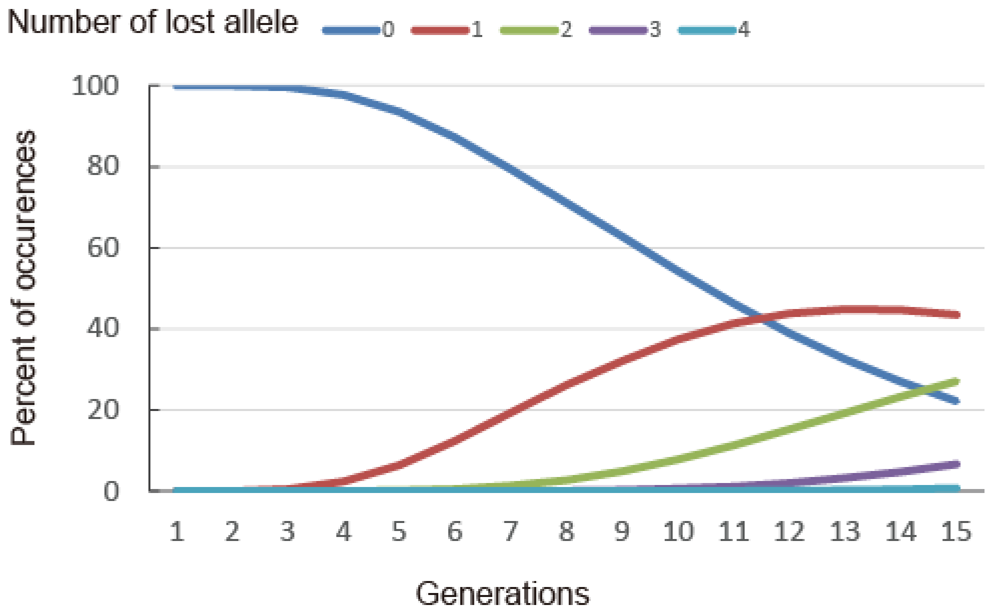
**Table S2.** Threshold for each strain-specific SNP after Bonferroni correction and the observed maximum allele frequencies for the eight founder strains in the four WHS groups

| Strain | | PGN2 | BFM/2 | HMI | BLG2 | CHD | NJL | MSM | KJR |
|---|---|---|---|---|---|---|---|---|---|
| # of SNPs | | 8,109 | 6,038 | 4,533 | 724 | 585 | 275 | 158 | 108 |
| C1 | Threshold | 0.797 | 0.797 | 0.797 | 0.750 | 0.734 | 0.766 | 0.750 | 0.719 |
| | Observed | 0.625 | 0.500 | 0.625 | 0.500 | 0.406 | 0.406 | 0.422 | 0.422 |
| C2 | Threshold | 0.813 | 0.797 | 0.797 | 0.781 | 0.750 | 0.781 | 0.750 | 0.734 |
| | Observed | 0.594 | 0.484 | 0.578 | 0.422 | 0.422 | 0.563 | 0.484 | 0.500 |
| S1 | Threshold | 0.781 | 0.781 | 0.781 | 0.750 | 0.719 | 0.750 | 0.734 | 0.703 |
| | Observed | 0.578 | 0.531 | 0.563 | 0.484 | 0.516 | 0.516 | 0.375 | 0.391 |
| S2 | Threshold | 0.781 | 0.797 | 0.781 | 0.766 | 0.750 | 0.766 | 0.734 | 0.734 |
| | Observed | 0.547 | 0.516 | 0.531 | 0.547 | 0.484 | 0.594 | **0.750** | 0.344 |

**Table S3.** Profiles of 23 mouse genes in the syntenic regions of the dog genome for ATR1 and ATR2 and which are expressed in mouse brain

| | | Start position (bp) | |
|---|---|---|---|
| Region | Gene | Mouse | Dog |
| Ⅰ | *Slc6a4* | 76,812,105 | 47,549,263 |
| Ⅱ | *Zfp207* | 80,196,781 | 43,916,907 |
| Ⅱ | *Psmd11* | 80,242,117 | 43,829,963 |
| Ⅱ | *Cdk5r1* | 80,290,548 | 43,823,095 |
| Ⅲ | *Dhx58* | 100,556,018 | 24,104,700 |
| Ⅲ | *Kat2a* | 100,566,060 | 24,096,480 |
| Ⅲ | *Rab5c* | 100,576,323 | 24,089,152 |
| Ⅲ | *Hcrt* | 100,622,383 | 24,047,856 |
| Ⅲ | *Stat5b* | 100,642,045 | 24,008,792 |
| Ⅲ | *Stat5a* | 100,720,665 | 23,934,905 |
| Ⅲ | *Stat3* | 100,746,412 | 23,899,353 |
| Ⅲ | *Ptrf* | 100,818,047 | 23,828,660 |
| Ⅲ | *Atp6v0a1* | 100,870,766 | 23,740,530 |
| Ⅲ | *Coasy* | 100,943,879 | 23,709,182 |
| Ⅲ | *Fam134c* | 100,957,636 | 23,681,243 |
| Ⅲ | *Ezh1* | 101,052,429 | 23,589,579 |
| Ⅲ | *Ramp2* | 101,107,342 | 23,568,554 |
| Ⅲ | *Becn1* | 101,147,266 | 23,522,490 |
| Ⅲ | *G6pc* | 101,228,875 | 23,450,827 |
| Ⅲ | *Rundc1* | 101,286,399 | 23,390,295 |
| Ⅲ | *Rnd2* | 101,326,313 | 23,355,999 |
| Ⅲ | *Brca1* | 101,350,078 | 23,278,875 |
| Ⅲ | *Nbr1* | 101,413,463 | 23,246,150 |

a. Probabilities of loss of alleles under neutrality



b. Expected distributions of the copy number of an allele under neutrality

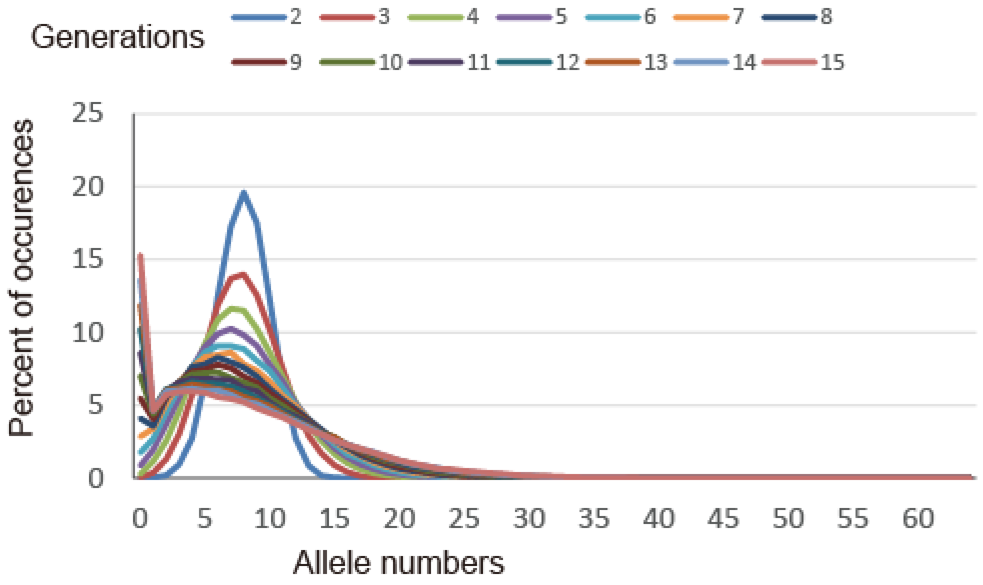


**Figure S1.** Probabilities of changes in the allele frequencies occurring in a colony of 16 pairs of heterogeneous stocks. The stocks were kept using a circle breeding design, and there were initially eight copies of each of the eight alleles at each locus. All data were obtained from 100,000 simulations. (a) Probabilities that alleles were lost under neutrality. (b) Expected distributions of the copy numbers of the 64 alleles (16 pairs of mice) under neutrality.

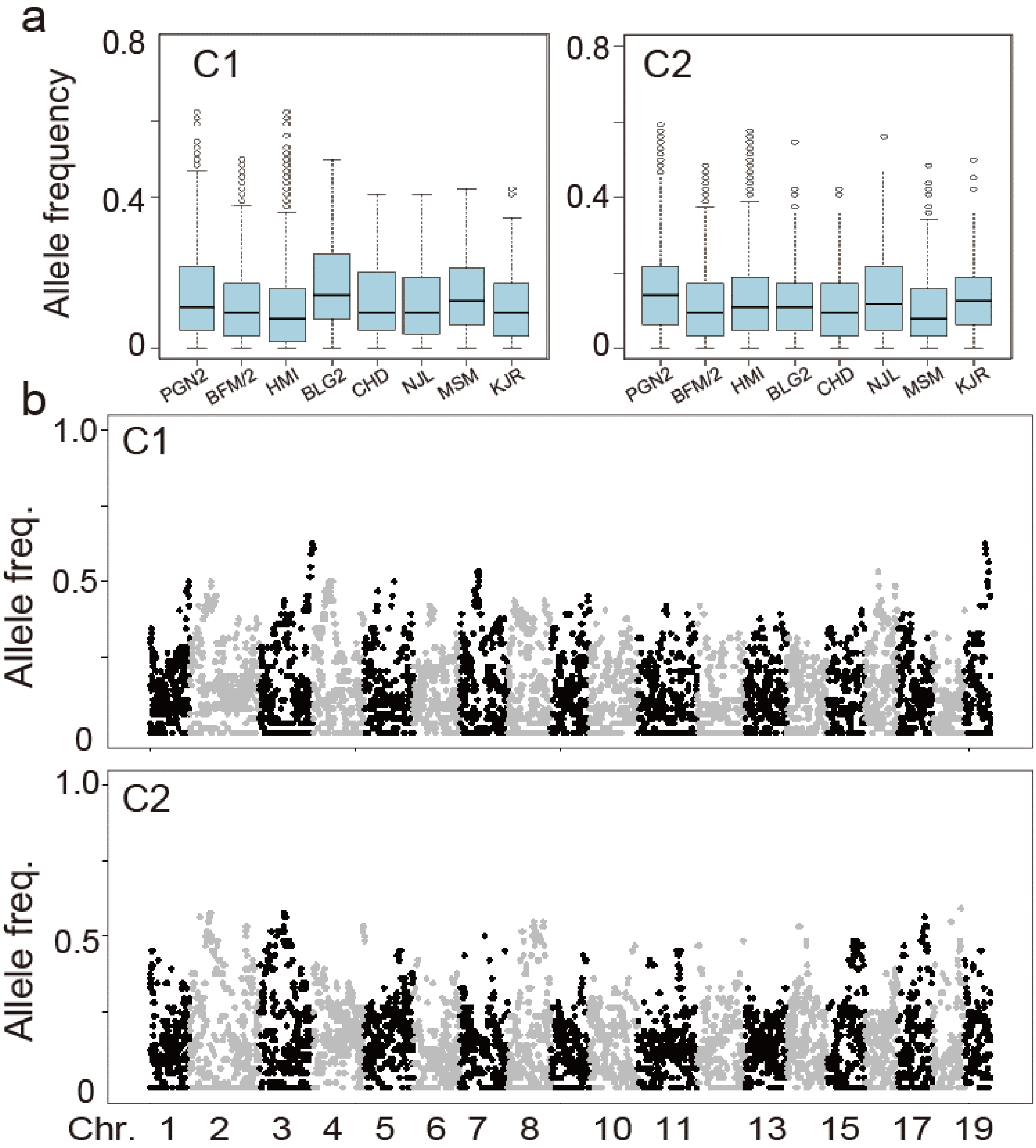


**Figure S2.** Contributions of one-strain-specific SNPs in the WHS and the results of selection mapping for the control groups. (a) Genome-wide average frequencies of 20,530 one-strain-specific SNPs in groups C1 and C2 at generation $G_{12}$. (b) Results of selection mapping in groups C1 and C2. No SNP reached the threshold determined using the computer simulation described in Table S2 in either group C1 or group C2.

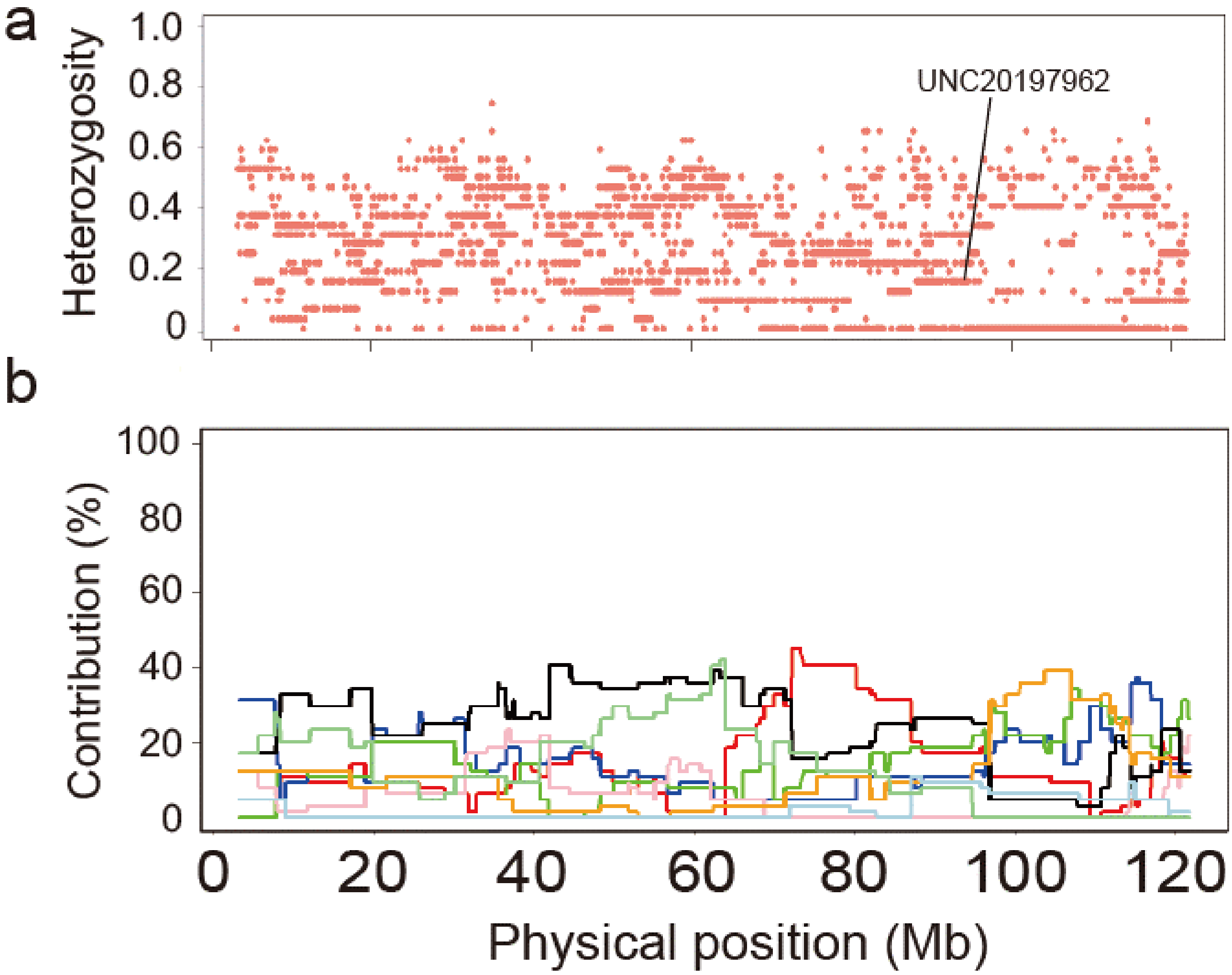


**Figure S3.** The haplotype derived from the MSM strain was not selected in group C1 at generation $G_{12}$. (a) Heterozygosity determined with 100 SNPs sliding windows with 10 SNPs gap. (b) Contributions of inferred haplotypes from the eight founder strains.

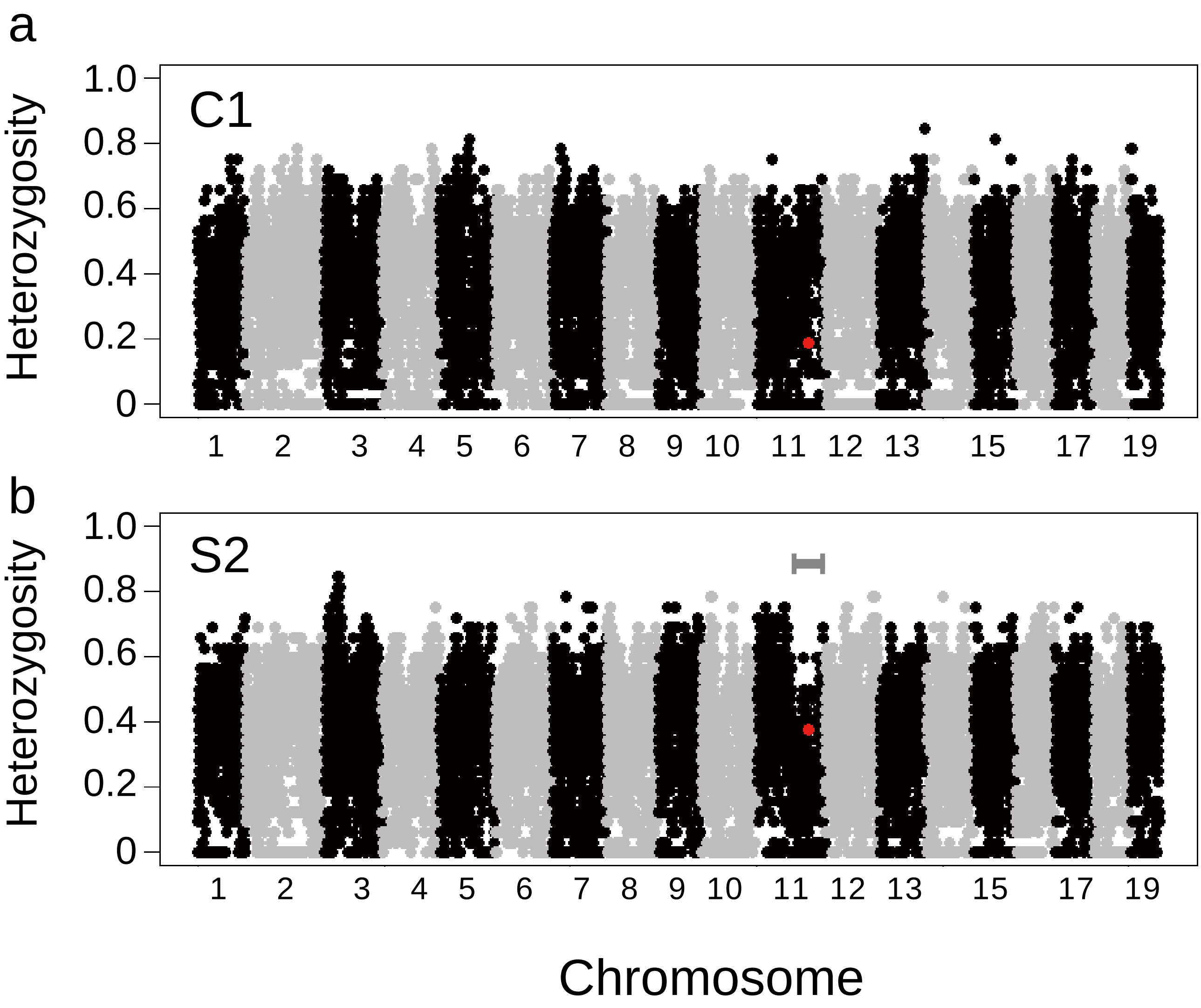


**Figure S4.** Genome-wide heterozygosity in C1 (a) and S2 (b) groups. The red dot on Chromosome 11 indicates detected SNP (UNC20197962) by using the simulation based analysis. The solid horizontal lines indicates the region showing decrease of the heterozygosity. The estimated heterozygosity of the SNP (UNC20197962) was greater in S2 group (H =0.375) than that of C1 group (H =0.1875). This result can be explained by the Hardy-Weinberg equation for considering the allele frequencies of SNP (UNC20197962) for S2 and C1 were 0.75 and 0.188, respectively. Based on the Hardy-Weinberg equation, heterozygosity increase as the allele frequency increase. The heterozygosity will reach the maximum value at the point when allele frequency is 0.5. However, the heterozygosity will decrease when the allele frequency exceeds the 0.5. According to the theory, the allele frequency of UNC20197962 in S2 is 0.75, then the theoretical heterozygosity is 0.375 (and actual heterozygosity is 0.375 in our data). By contrast, the allele frequency in C1 is 0.188, then the theoretical heterozygosity is 0.305 (but actual heterozygosity is 0.188 in our data).