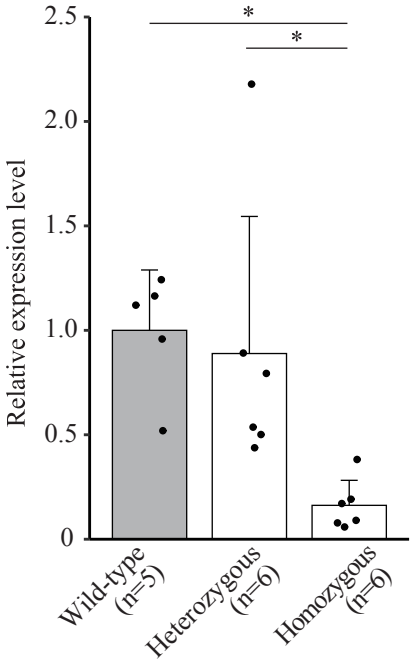


Supplementary Figure 1. *c-Fos* mRNA expression in the *c-Fos* KO rat.
qPCR was performed using the PrimeTime qPCR Probe Assay (Integrated Data Technologies, Inc., USA). Rn.PT.39a.22214838.g and Rn.PT.58.24954639 were used for beta-actin and c-Fos. Bone marrow cells were collected from the femur of *c-Fos* KO rats and stored at –80°C until use. Total RNA was purified from bone marrow cells using a FastGene RNA Premium Kit (FG-81050; Nippon Genetics Co., Ltd., Japan) and reverse-transcribed to cDNA using Rever-Tra Ace® qPCR RT Master Mix with gDNA Remover (FSQ-301; Toyobo Co., Ltd., Japan). We performed qPCR in accordance with the manufacturer's instructions. The error bar indicates the standard deviation, and significant differences were tested using Steel-Dwass test (*$p < 0.05$) (WT rats [n = 5], heterozygous *c-Fos* KO rats [n = 6], and homozygous *c-Fos* KO rats [n = 6]).

| Wild-type | Heterozygous | Homozygous |
|---|---|---|
| 3.57 ± 1.70<br>(30.8% ± 8.4%)** | 5.50 ± 2.07<br>(49.6% ± 12.2%) | 2.14 ± 1.29<br>(19.6% ± 9.8%)** |

n = 14 crossbreedings, Number of pup ± s.d. (% ± s.d.)

Supplementary Table 1. Average number of pups at birth
We crossbred heterozygous *c-Fos* KO rats. The genotyping protocol is reported in the Materials and Methods section. The Wilcoxon rank-sum test was performed to determine whether the expected Mendelian ratio between homozygous *c-Fos* KO and WT rats was equal (**$p<0.01$).