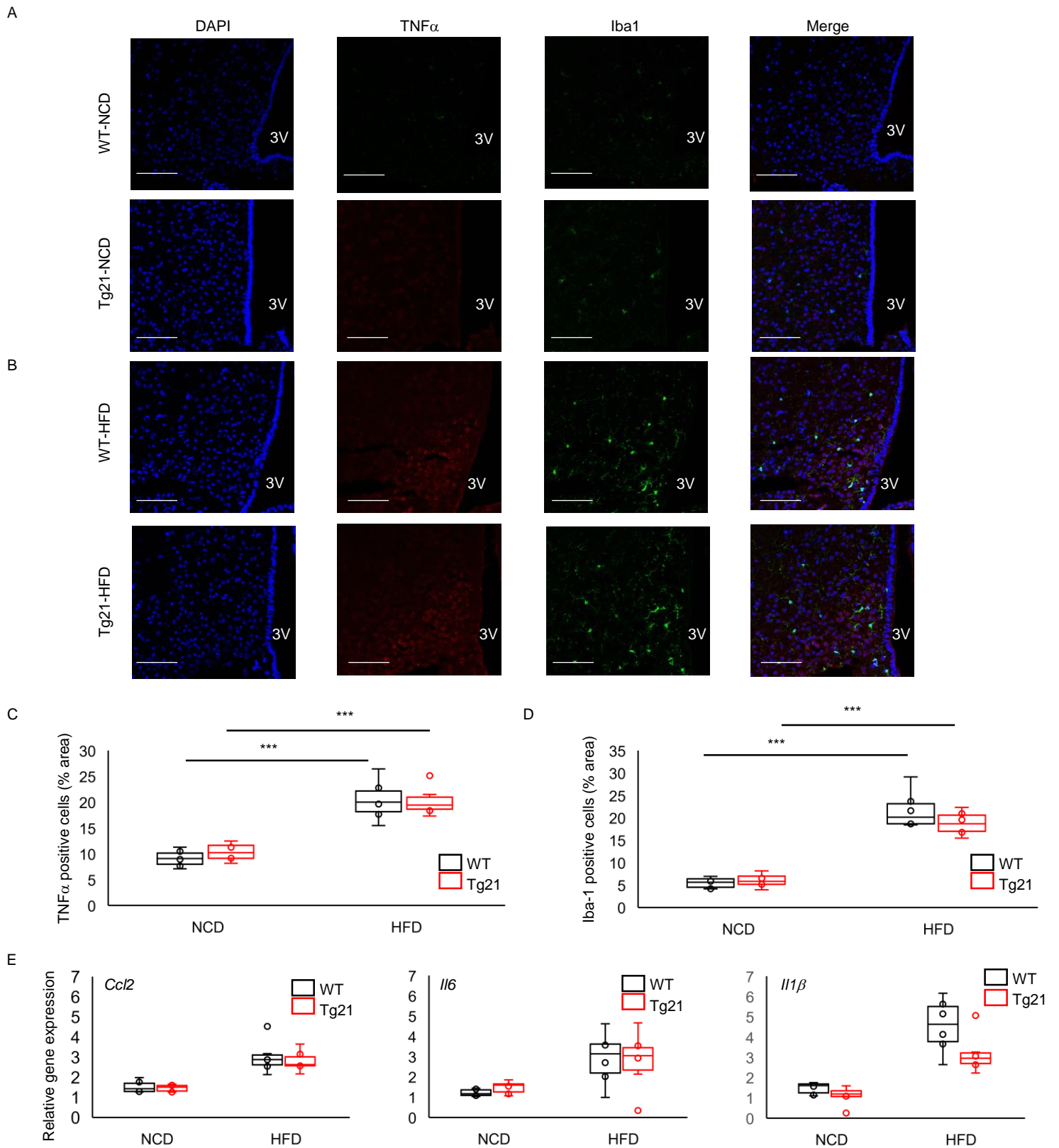


Supplementary Figures:

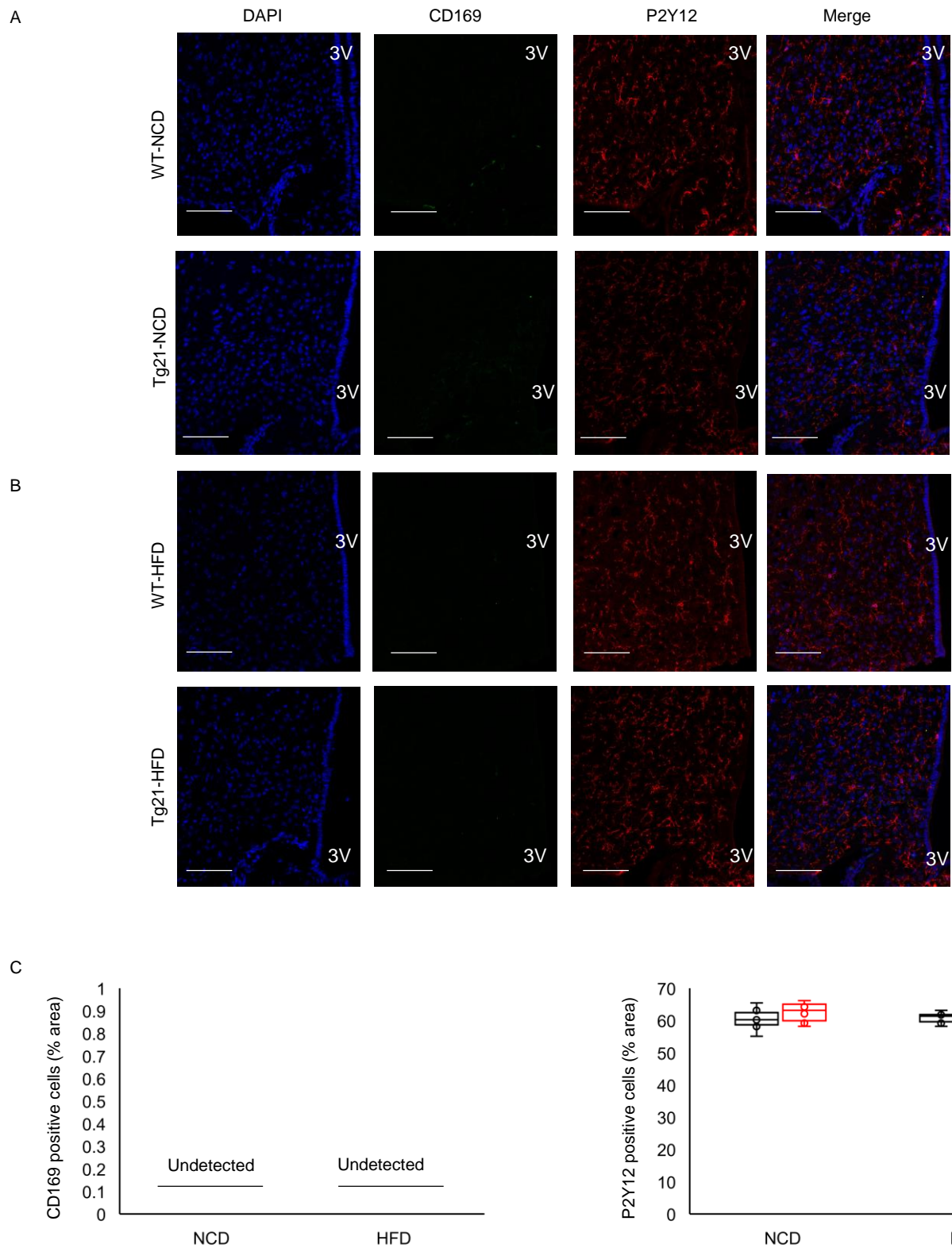
Supplementary Figure 1. Inflammatory and microglial cell response in the hypothalamus of female WT- and *Tg21*-mice are not different on NCD or HFD-feeding. (A, B) Representative hypothalamic sections from age-matched (8 weeks) female *Tg21*- and WT-mice during NCD (A) or after three weeks of HFD-feeding (B) stained for nuclear marker DAPI, inflammatory marker TNF $\alpha$ , and microglial cells marker Iba1 in MBH. (C, D) Quantification of (A) and (B) (E) Gene expression of markers *Ccl2*, *Il6*, and *Il1 $\beta$*  in the hypothalamus of age-matched (8 weeks) female *Tg21*- and WT-mice on NCD or after 3 weeks of HFD determined by quantitative RT-PCR, normalized to WT control mice on NCD, and adjusted to *Gapdh* gene expression. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance is indicated by \*\*\*  $p < 0.001$ , \*\*  $p < 0.01$ , \*  $p < 0.05$  (2-way ANOVA) (n=8-10/group). Scale bar 100 $\mu$ m; magnification 40X, 3V: third ventricle.

Supplementary Figure 2. *Tg21*- and WT-female mice show no difference in P2Y12<sup>+</sup> microglial cells during NCD or HFD-feeding, and no detectable CD169<sup>+</sup> cells in either condition (A) Representative hypothalamic sections from age-matched (8 weeks) female *Tg21*- and WT-mice during NCD (A) or after three weeks of HFD-feeding (B) stained for nuclear marker DAPI, CD169, and P2Y12 in MBH. (C) Quantification of (A) and (B) to measure CD169- and P2Y12-positive cells. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance was tested by 2-way ANOVA (n=6-8/group). Scale bar 100 $\mu$ m; magnification 40X, 3V: third ventricle. Each slide is representative of n=8-10/group.

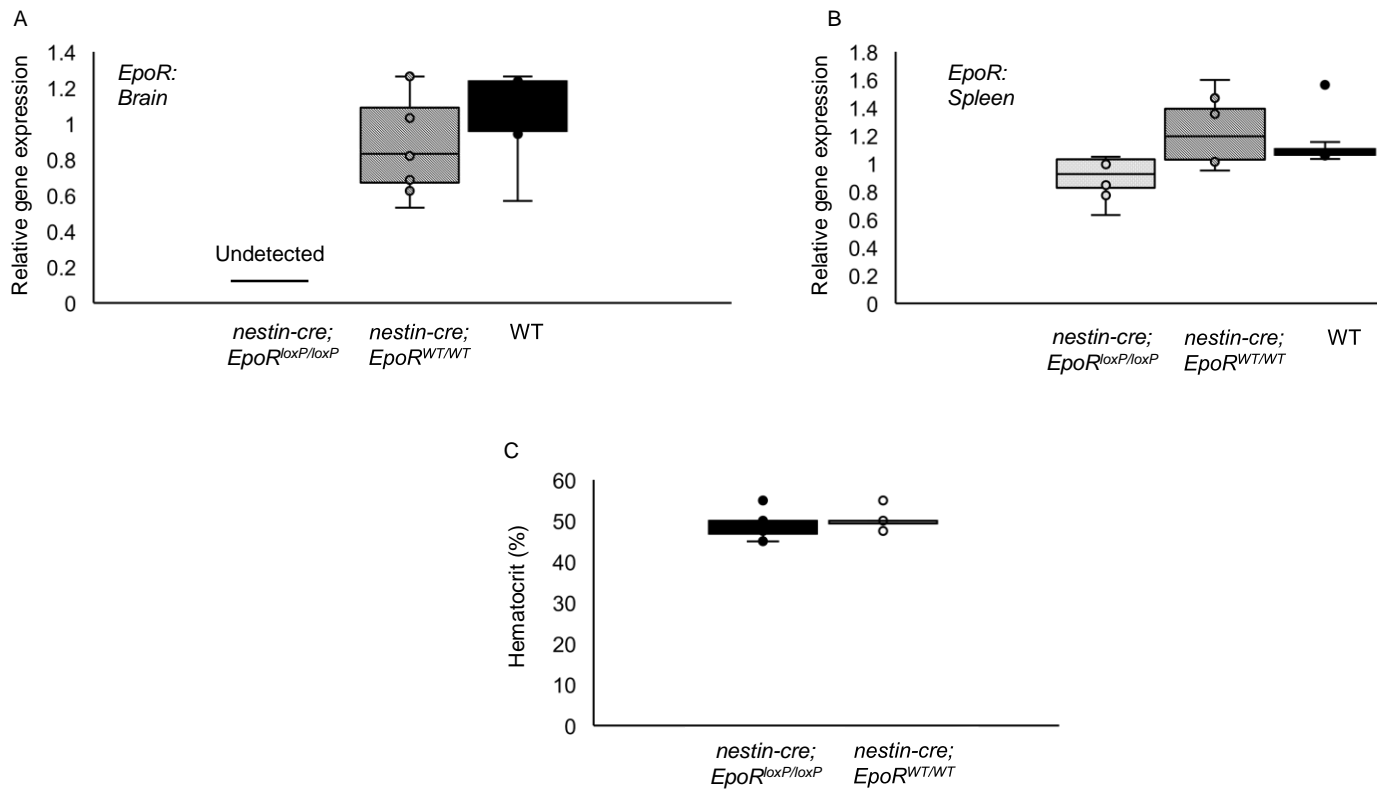
Supplementary Figure 3. *EpoR* gene deletion via *nestin*-promoter driven cre-recombinase expression is specific in the brain and not in the spleen and does not affect hematocrit. (A, B) *EpoR* gene expression in the whole brain and spleen at age 4 weeks of *nestin-cre;EpoR<sup>loxP/loxP</sup>* and *nestin-cre;EpoR<sup>WT/WT</sup>* mice normalized to WT control mice, and adjusted to *Gapdh* gene expression. (C) Hematocrit levels in *nestin-cre;EpoR<sup>loxP/loxP</sup>* and *nestin-cre;EpoR<sup>WT/WT</sup>* mice at age 4 weeks. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance was tested by 2-way ANOVA (n=6-8/group).



Supplementary Figure 1. Inflammatory and microglial cell response in the hypothalamus of female WT- and *Tg21*-mice are not different on NCD or HFD-feeding. (A, B) Representative hypothalamic sections from age-matched (8 weeks) female *Tg21*- and WT-mice during NCD (A) or after three weeks of HFD-feeding (B) stained for nuclear marker DAPI, inflammatory marker TNF $\alpha$ , and microglial cells marker Iba1 in MBH. (C, D) Quantification of (A) and (B) (E) Gene expression of markers *Ccl2*, *Il6*, and *Il1b* in the hypothalamus of age-matched (8 weeks) female *Tg21*- and WT-mice on NCD or after 3 weeks of HFD determined by quantitative RT-PCR, normalized to WT control mice on NCD, and adjusted to *Gapdh* gene expression. For bar graph, each data point represents mean  $\pm$  S.D. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance is indicated by \*\*\*  $p < 0.001$ , \*\*  $p < 0.01$ , \*  $p < 0.05$  (2-way ANOVA) ( $n = 8-10$ /group). Scale bar 100 $\mu$ m; magnification 40X, 3V: third ventricle.



Supplementary Figure 2. *Tg21*- and WT-female mice show no difference in P2Y12<sup>+</sup> microglial cells during NCD or HFD-feeding, and no detectable CD169<sup>+</sup> cells in either condition (A) Representative hypothalamic sections from age-matched (8 weeks) female *Tg21*- and WT-mice during NCD (A) or after three weeks of HFD-feeding (B) stained for nuclear marker DAPI, CD169, and P2Y12 in MBH. (C) Quantification of (A) and (B) to measure CD169- and P2Y12-positive cells. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance was tested by 2-way ANOVA (n=6-8/group). Scale bar 100µm; magnification 40X, 3V: third ventricle. Each slide is representative of n=8-10/group.



Supplementary Figure 3. *EpoR* gene deletion via *nestin*-promoter driven cre-recombinase expression is specific in the brain and not in the spleen and does not affect hematocrit. (A, B) *EpoR* gene expression in the whole brain and spleen at age 4 weeks of *nestin-cre;EpoR<sup>loxP/loxP</sup>* and *nestin-cre;EpoR<sup>WT/WT</sup>* mice normalized to WT control mice, and adjusted to *Gapdh* gene expression. (C) Hematocrit levels in *nestin-cre;EpoR<sup>loxP/loxP</sup>* and *nestin-cre;EpoR<sup>WT/WT</sup>* mice at age 4 weeks. Box and whisker plots denote bounds ranging from 25<sup>th</sup> to 75<sup>th</sup> percentile, line represents the median, whiskers ranging from minimum to maximum values, and includes outliers. Statistical significance was tested by 2-way ANOVA (n=6-8/group).