Supplemental Figure Legends:

Figure S1: Impaired T cell response in C57bl/6 recipient animals reconstituted with Bach1$^{-/-}$ BMCs. (**A**) WT or Bach1$^{-/-}$ BMCs reconstituted C57bl/6 recipients were immunized with OVA/CFA and splenocytes were cultured in the presence or absence of OVA. Splenocytes were subjected to flow cytometric analyses to quantify the percent of CD4^{+} cells that expressed the CD25 T-cell activation marker. (**B, C, D**) Bach1 regulates specific antigen presenting cell numbers upon immunization. Splenocytes from OVA/CFA-immunized animals were subjected to flow cytometric analyses to examine the percent of B cells (**B**), macrophages (**C**), and dendritic cells (**D**). Panels **C** and **D** shows the gating strategy for macrophages and dendritic cells, respectively. (**E**) Total number of splenocytes from age matched adult WT and Bach1$^{-/-}$ animals obtained after red blood cell lyses. The graph represents at least three mice per genotype.

Figure S2: Bach1 regulates steady state development of macrophages and dendritic cells. Splenic white blood cells were subjected to flow cytometric analyses to quantify the percent population of (**A**) T-lymphocytes (CD3ε^{+}), (**B**) non-plasma B-cells (CD19^{+}), (**C**) natural killer cells (NK1.1^{+}, CD49b^{+}), (**D**) erythrocytes (Ter-119^{+}), (**E**) macrophages (F4/80^{+} CD11b^{+} CD11c^{-} MHC II^{+}), (**F**) dendritic cells (CD11c^{+} MHC II^{+}), (**G)** macrophage-committed cells, and (**H**) DC-committed precursors. R1 and R2 is the first and subsequent gated region from flow cytometric analyses, respectively.

Figure S3: Regulation of DC response and antigen presenting activity by Bach1. Equal number of WT or Bach1$^{-/-}$ non-adherent bone-marrow derived dendritic cells (BM-DCs) were treated with LPS (100ng/mL ultrapure LPS) for 24hours. **A**) Supernatant was collected for TNFα ELISA, and **B**) cells were subjected to flow cytometric analyses. The graph shows the geometric mean fluorescent (GMF) of the activation marker MHC II normalized to no treatment of the corresponding genotype. The GMF of MHC II was obtained after CD11c^{+} gating. The graph represents data of BM-DCs derived from 3 WT and 6 Bach1$^{-/-}$ mice. P values (T-test) compare the LPS treated samples.

Figure S4: Genome wide analyses of genes regulated by Bach1. WT or Bach1$^{-/-}$ BMMs were harvested and RNAs were submitted for microarray analyses. Each box corresponds to an individual chromosome and each red dot represents a gene differentially expressed between WT and Bach1$^{-/-}$ BMMs. The data are combined from two separate microarrays with independent biological replicates.

Figure S5: HO-1 regulates APC development. Bone marrow cells from WT or HO-1$^{+/-}$ mice were subjected to flow cytometric analyses after red blood cell lyses to quantify the percent (**A**) macrophages and (**B**) dendritic cells.

Figure S6: Examination of immune cell development in HO-1$^{-/-}$ Bach1$^{-/-}$ mice. Bone marrow from HO-1$^{-/-}$ Bach1$^{-/-}$ and Bach1$^{-/-}$ mice were harvested, red blood cells lyzed, and the remaining white blood cells were subjected to flow cytometric analyses to quantify the percent of (**A**, **B**) T-cells (CD4^{+} CD3ε^{+}, CD8α^{+} CD3ε^{+}), **C**) natural killer cells (NK1.1^{+} GR-1^{-}), (**D**) B-cells (CD19^{+} GR-1^{-}), and (**E**) GR-1^{+} myeloid cells. All plots contain three animals per genotype and graphed with s.e.m.

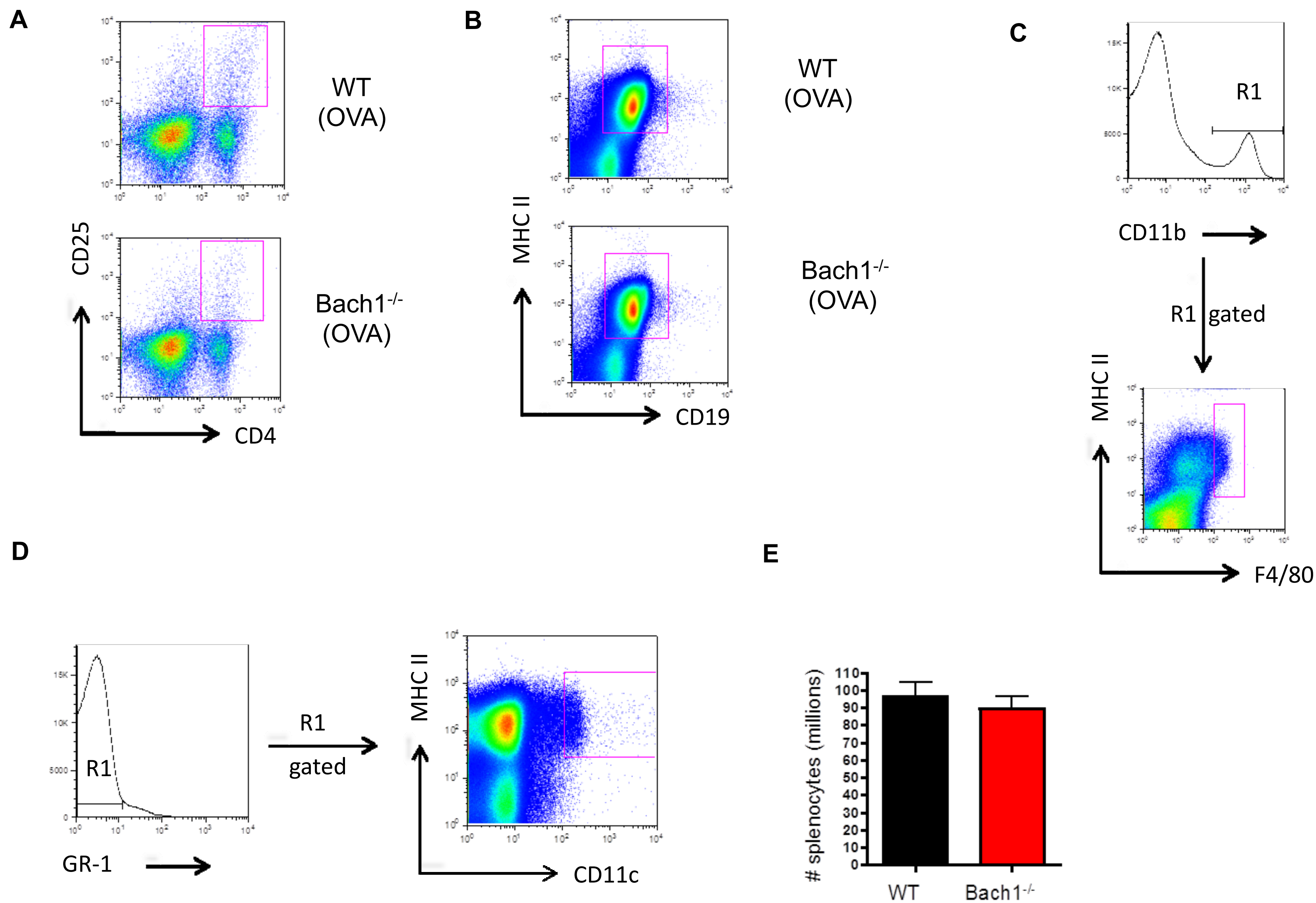


Figure S1:

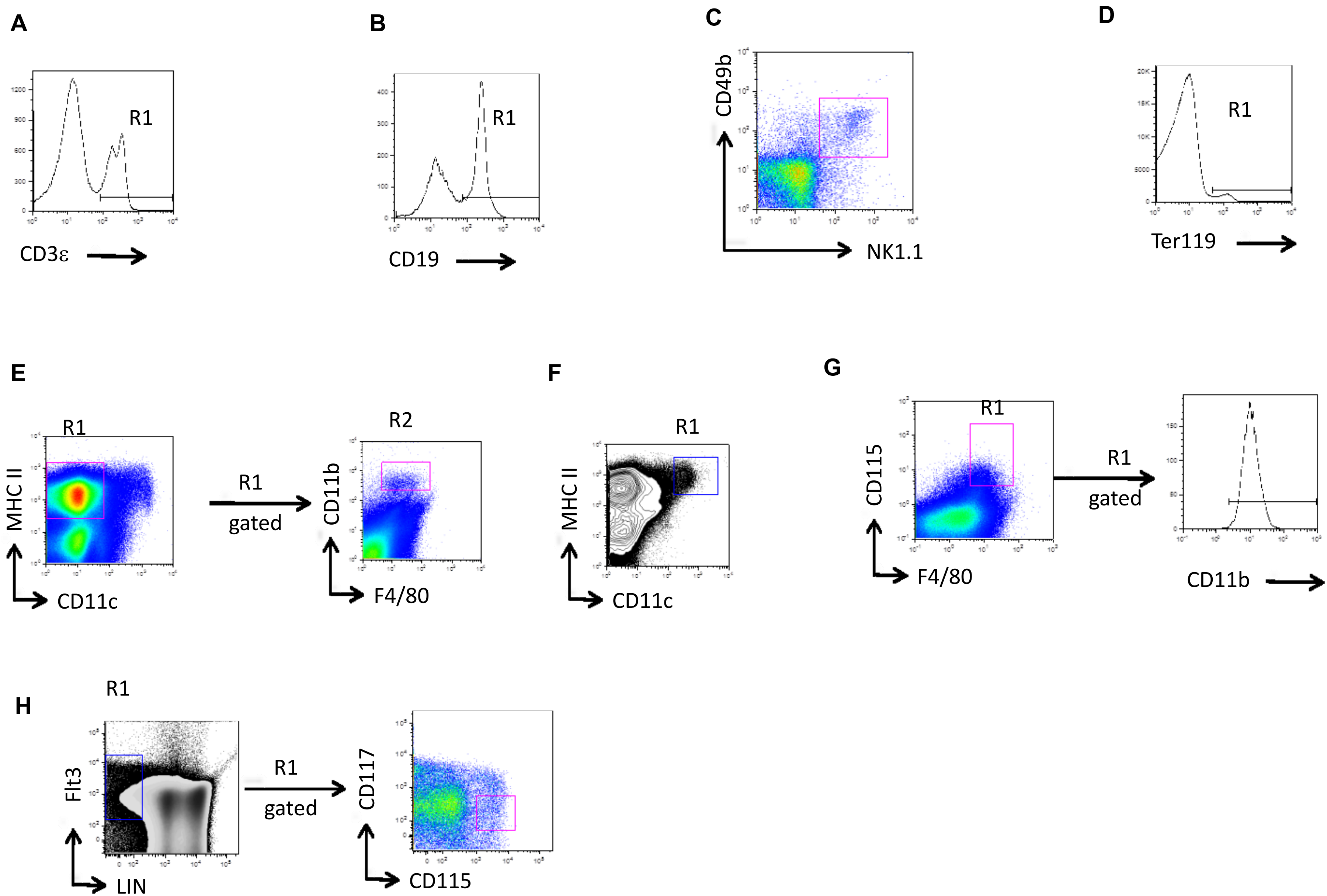
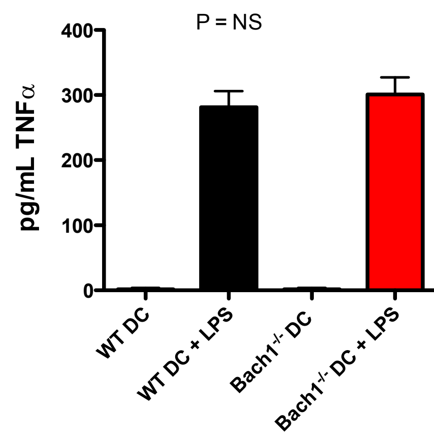


Figure S2:

A



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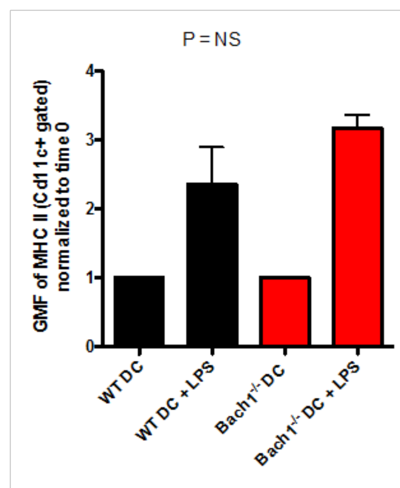

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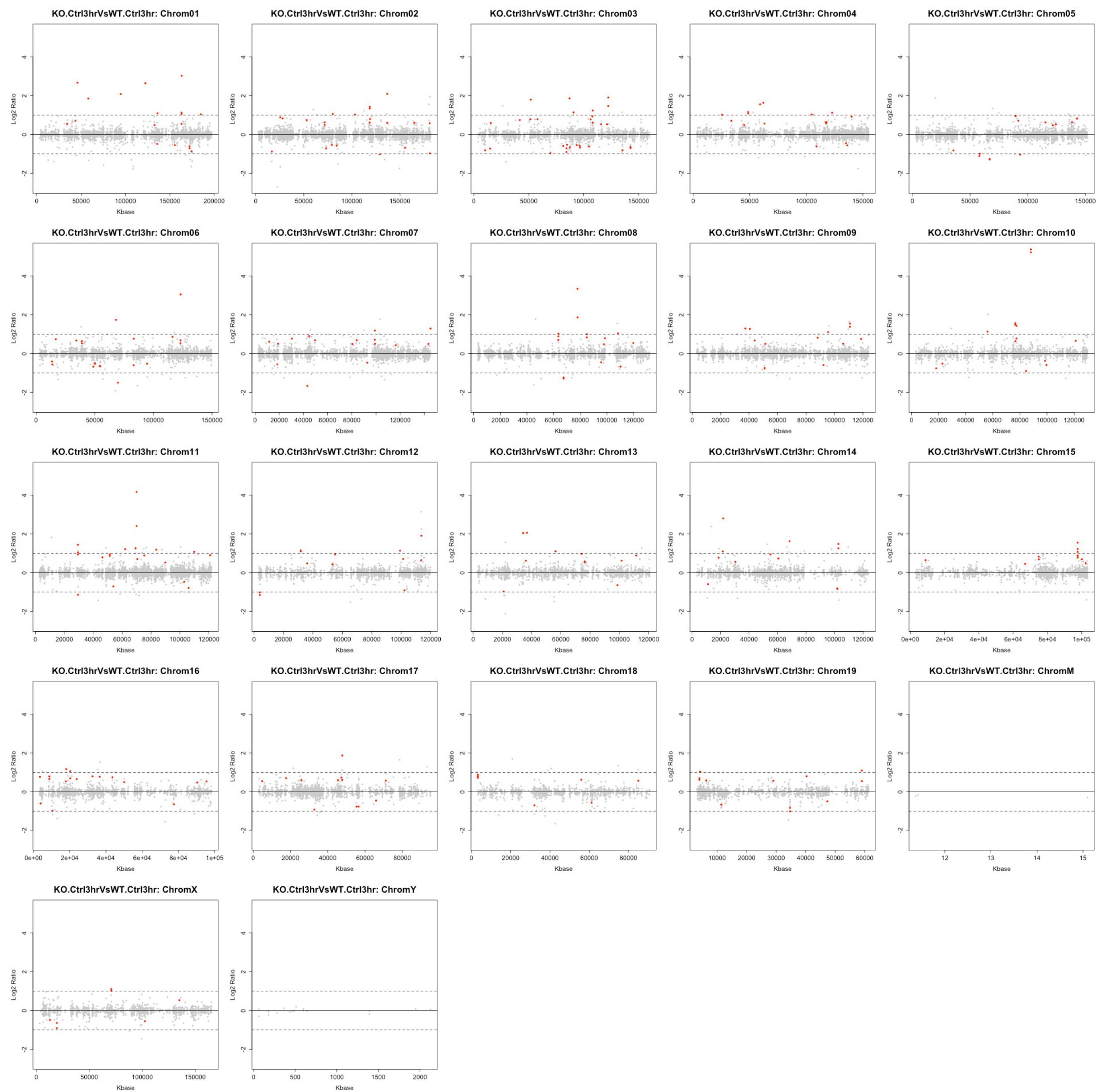
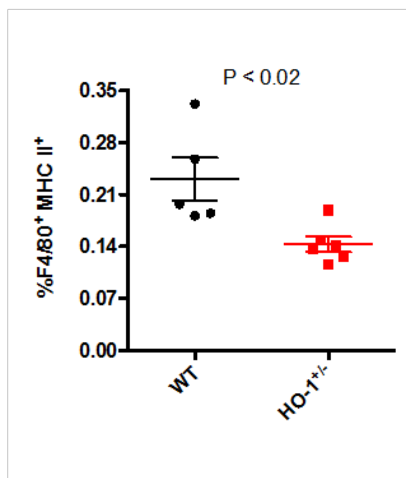


Figure S4:

A



B

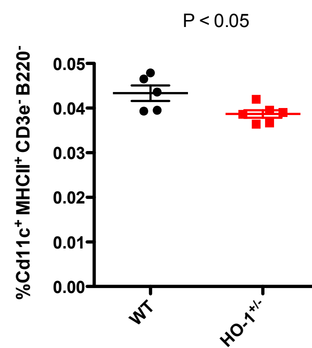


Figure S5:

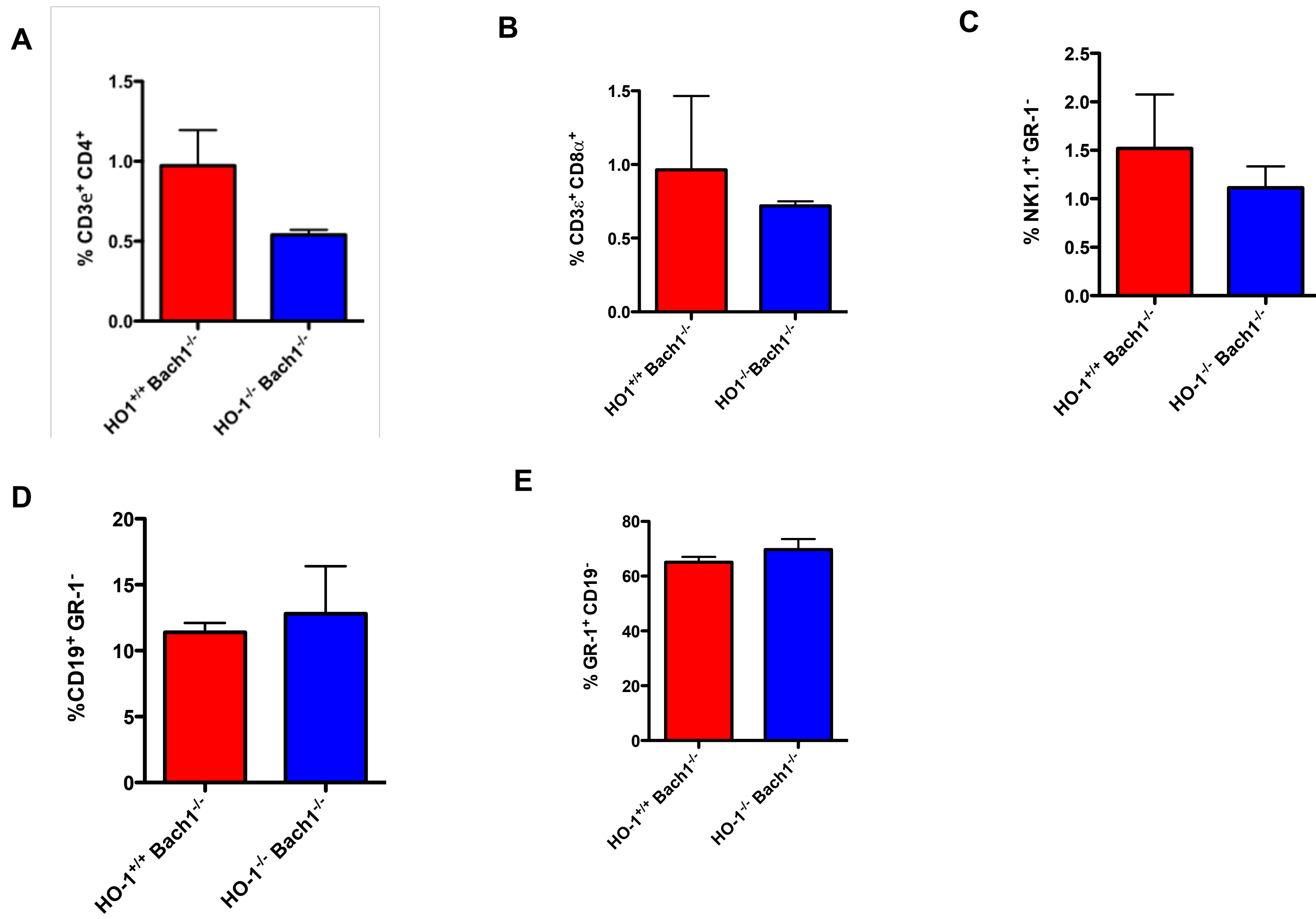


Figure S6: