Figure S1

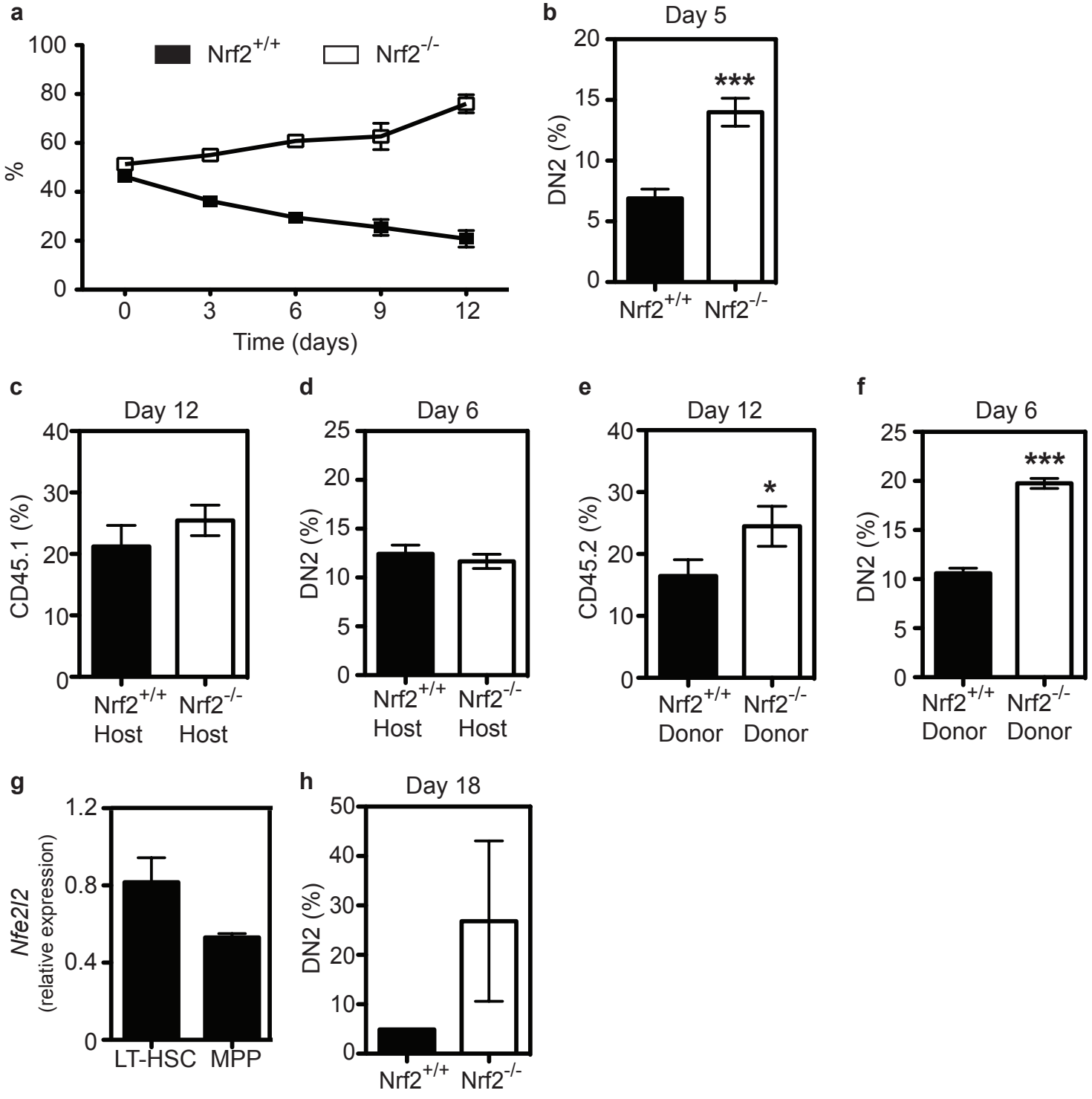
a
Nrf2+/+
Nrf2-/-
%
Time (days)
b
Day 5
DN2 (%)
***
c
Day 12
CD45.1 (%)
d
Day 6
DN2 (%)
e
Day 12
CD45.2 (%)
*
f
Day 6
DN2 (%)
***
Host
Donor
g
Nfe2l2
(relative expression)
LT-HSC
MPP
h
Day 18
DN2 (%)

Figure S1. Nrf2 regulates HSPC Proliferation and Differentiation Intrinsically

(**a**) (Corresponding to Fig. 2a) Relative contribution of WT (CD45.1) and *Nrf2*$^{-/-}$ (CD45.2) sorted BM LSKs co-cultured with OP9-DL1 stromal cells over time. WT:*Nrf2*$^{-/-}$ = 1:1 on day 0. Data represent the mean ± SEM, n = 7 independent observations over 4 experiments.

(**b**) (Corresponding to Fig. 2b) Percentage of LSKs differentiating into DN2 stage on day 5 of OP9-DL1 co-culture. Data represent the mean ± SEM, n = 7 independent observations over 5 experiments.

(**c**) (Corresponding to Fig. 2d) CD45.1^{+} WT LSKs were preconditioned in WT or *Nrf2*$^{-/-}$ BM niche *in vivo* then co-cultured with untransplanted CD45.2^{+} WT LSKs at a 1:1 ratio on day 0 with OP9-DL1 stromal cells. Percentage of distribution from preconditioned WT LSKs determined at day 12 in culture. Data represent the mean ± SEM, n = 5 observations per strain over 2 independent transplant experiments.

(**d**) (Corresponding to Fig. 2e) Percentage of CD45.1^{+} preconditioned WT LSKs differentiating into DN2 stage on day 6 of OP9-DL1 co-culture. Data represent the mean ± SEM, n = 10 observations from WT and 8 from *Nrf2*$^{-/-}$ hosts over 2 independent transplant experiments.

(**e**) (Corresponding to Fig. 2f) CD45.2^{+} WT or *Nrf2*$^{-/-}$ LSKs were preconditioned in CD45.1^{+} WT BM niche *in vivo* then co-cultured with untransplanted CD45.1^{+} WT LSK at 1:1 ratio on day 0 of OP9-DL1 co-culture system. Percentage of distribution from preconditioned LSKs determined at day 12 of culture. Data represent the mean ± SEM, n = 10 observations from WT and 8 from *Nrf2*$^{-/-}$ donors over 2 independent transplant experiments.

(**f**) (Corresponding to Fig. 2g) Percentage of preconditioned CD45.2^{+} WT or *Nrf2*$^{-/-}$ LSKs differentiating into DN2 stage at day 6 of OP9-DL1 co-culture. Data represent the mean ± SEM, n = 9 observations from WT and 8 from *Nrf2*$^{-/-}$ donors over 2 independent transplant experiments.

(**g**) Expression of *Nfe2l2* mRNA transcripts in sorted WT LT-HSC and MPP, presented relative to *Actb* expression. Data represent the mean ± SEM, n = 3 independent experiments.

(**h**) (Corresponding to Fig. 2i) Percentage of LT-HSCs differentiating into DN2 stage at day 18 of OP9-DL1 co-culture. Data represent the mean ± SEM, n = 2 independent observations from WT and 3 from *Nrf2*$^{-/-}$ animals over 2 experiments.

Figure S2

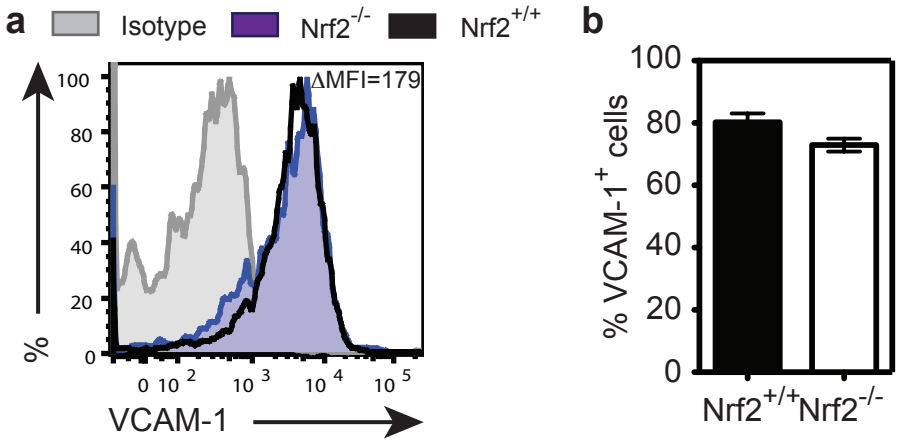

Figure S3

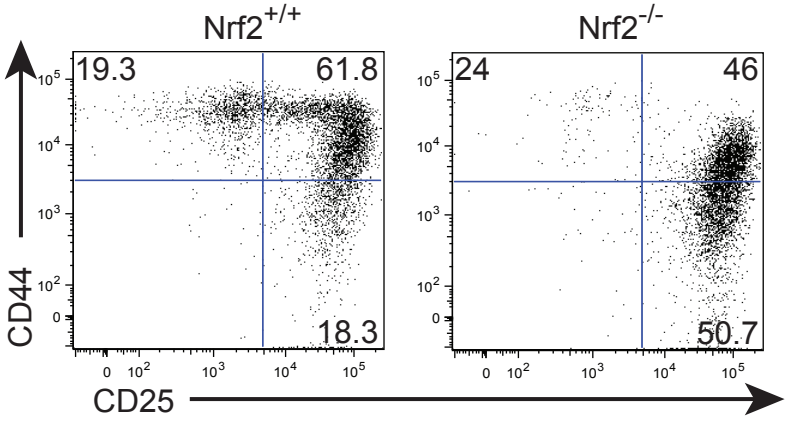

Figure S2. VCAM-1 expression in *Nrf2*$^{-/-}$ HSPCs

(**a**) Representative flow cytometric analysis and (**b**) bar graphs showing the proportion of sorted WT and *Nrf2*$^{-/-}$ BM LSK cells expressing VCAM-1. Δ MFI (Mean fluorescence intensity) = (MFI of WT LSKs) - (MFI of *Nrf2*$^{-/-}$ LSKs). Data represent the mean ± SEM, n = 5 animals per strain.

Figure S3. Differentiation kinetics of *Nrf2*$^{-/-}$ HSPCs transduced with GFP control vector

Representative flow cytometric analysis showing *Nrf2*$^{-/-}$ LSKs transduced with empty GFP control vector differentiated more rapidly into precursor T cells compared to transduced WT LSKs on day 11 of OP9-DL1 culture, n = 3 independent experiments.