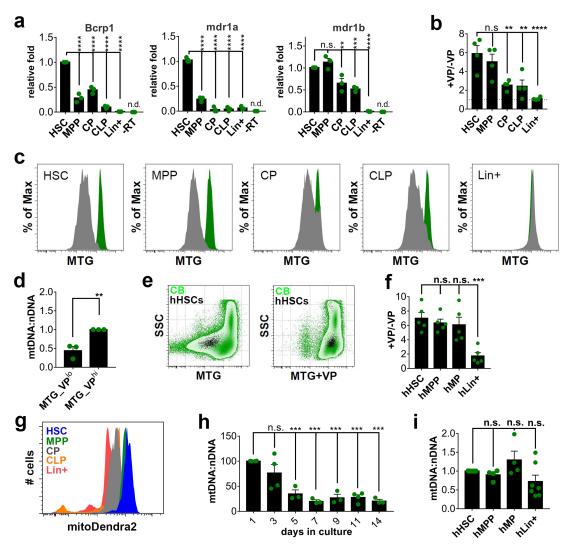


Supplementary Figure 1. Sort and analysis gates, related to Figure 1 and 2. Representative flow cytometric plots showing the gating strategy used to a. isolate mouse hematopoietic populations from adult bone marrow. HSC: hematopoietic stem cell; MPP: multipotential progenitor; CP: committed progenitor (comprising common myeloid, granulocyte-macrophage and megakaryocyte-erythrocyte progenitors), CLP: common lymphoid progenitor and Lin+: lineage positive cells. b. determine donor contribution in the peripheral blood of CD45.2 recipients 16 weeks post competitive transplantation of CD45.1 MTG^{hi} or MTG^{lo} bone marrow donor cells stained with MitoTracker Green (MTG) in the absence (top) or presence (bottom) of VP. c. isolate human hematopoietic populations from cord blood. d. determine donor contribution in the peripheral blood of CD45.2 recipients 16 weeks post competitive transplantation of CD45.2 Dendra2^{hi} or Dendra2^{lo} bone marrow donor cells from mitoDendra2 mice.



Supplementary Figure 2. Mitochondrial mass in hematopoietic cells, related to Figure 1. a. Relative mRNA expression of efflux pumps in hematopoietic populations (mean ± s.e.m., n=3). **b.** Effect of VP on MTG fluorescence in mouse BM hematopoietic populations (mean ± s.e.m., n=4). **c.** Representative MTG fluorescence histograms in the absence (grey) or presence (green) of VP in mouse hematopoietic populations **d.** Relative mtDNA:nDNA ratio within the 10% MTG_VP^{lo} and MTG_VP^{hi} fractions of CPs stained in the presence of VP, normalized to MTG^{hi} (mean ± s.e.m., n=3). **e.** Flow cytometric profile of human CB mononuclear cells (green) and human HSCs (black) stained with MTG in the absence (left) or presence (right) of VP. **f.** Effect of VP on MTG fluorescence in human CB hematopoietic populations (mean ± s.e.m., n=5 from two independent isolations) **g.** Representative fluorescence histograms of BM hematopoietic populations in mitoDendra2 mice. **h.** Relative mtDNA:nDNA ratio of HSCs over time in culture (mean ± s.e.m., n≥3) **i.** Relative mtDNA:nDNA in human CB hematopoietic populations normalized to hHSC (mean ± s.e.m, n≥4 from three independent isolations).