Figure S2. Altered lineage-restricted progenitors and LSK populations in Pias1<sup>−/−</sup> mice. (A) Percentage of T cells (CD4<sup>+</sup> or CD8<sup>+</sup>), B cells (B220<sup>+</sup>), granulocytes/monocytes (Gr1<sup>Mac1</sup>), dendritic cells (CD11c<sup>+</sup>) and erythroids (Ter119<sup>+</sup>) in freshly isolated bone marrow (BM) from 8-12 weeks old WT (Pias1<sup>−/−</sup>) and Pias1<sup>−/−</sup> littermates were assayed by flow cytometry. (B) Same as in A except that frequencies of myeloid-restricted Lin<sup>−</sup> Sca1<sup>−</sup> c-Kit<sup>−</sup> (L<sup>−</sup> S K<sup>−</sup>) populations, common myeloid progenitors (CMP), granulocyte monocyte progenitors (GMP), megakaryocyte erythocyte progenitors (MEP), common lymphoid progenitors (CLP), Pro-B and Pre-B cells as defined in Supplementary Materials and Methods were assayed. (C) Same as in A except that cell numbers of LSK, long-term hematopoietic stem cells (LT-HSC) and short-term multi-potent progenitors (ST/MPP) in total BM as defined in Supplementary Materials and Methods were assayed. (D) Same as in A except that the percentage of Lin<sup>−</sup> population was assayed. (E) Same as in A except that the percentage of dormant hematopoietic stem cells (d-HSCs; Lin<sup>−</sup> Sca1<sup>−</sup> c-Kit<sup>−</sup>CD150<sup>−</sup>CD48<sup>−</sup>CD34<sup>−</sup>) was assayed. Shown in each panel is a pool of 3 independent experiments (n=9-13). Error bars represent SEM. P values were determined by non-paired t-test.