Supplementary information, Figure S1. (A) Relative expression levels of *Lis1* mRNA in control and *Lis1*-deficient LSKs at 12.5 dpc (n=4). (B) Proportions of hematopoietic cells from control and *Lis1*-deficient fetal livers at 14.5 dpc (n=4). (C) Absolute cell number of hematopoietic cells from control and *Lis1*-deficient fetal livers at 14.5 dpc (n=4). (D) Absolute cell number of LKs from control and *Lis1*-deficient fetal livers at different gestational ages (n=2-8 for each genotype for each gestational age). (E-G) Proportions of LKs (E), LSKs (F) and highly purified HSCs (G) from control and *Lis1*-deficient fetal livers at different gestational ages (n=2-8 for each genotype for each gestational age). (H) Representative images of colonies generated from control and *Lis1*-deficient fetal livers at 13.5 dpc. Images were captured at day10. (I) Number of erythroid (BFU-E), myeloid (CFU-GM), multilineage (CFU-GEMM) and total colonies generated by 100 LSKs sorted from control and *Lis1*-deficient fetal livers at 12.5 dpc (n=3). (J) Representative dot plots show the LSK proportions (boxed) of *Lis1*-deficient fetal livers transduced with the Bcl-2 family members. Viable lineage negative cells are shown (n=2). The data are mean $\pm$ S.E.M., for all panels: N.S., no significance; *P < 0.05; **P < 0.001; ***P < 0.0001 by Student's t-*t*est.