

SUPPLEMENTAL MATERIAL

Xu et al., <https://doi.org/10.1084/jem.20160923>

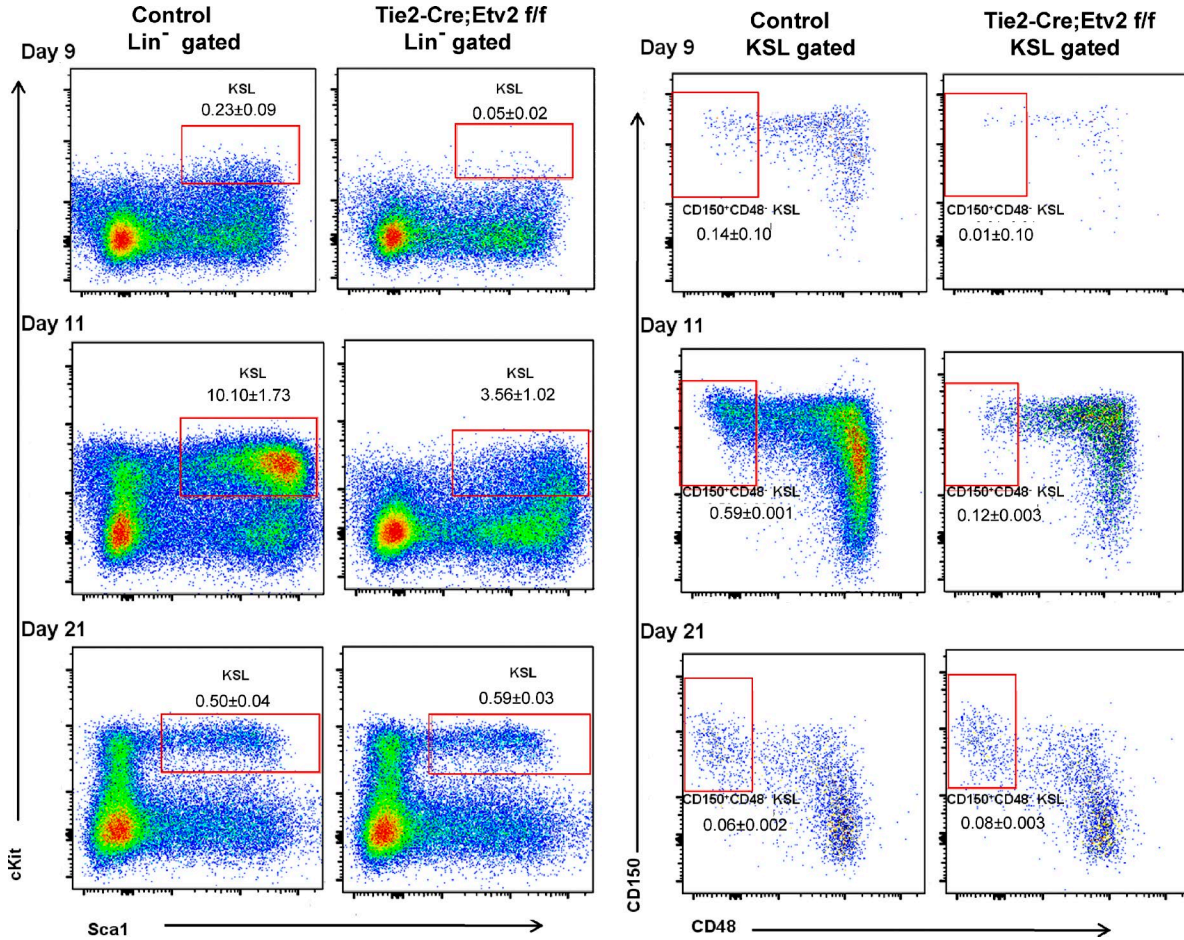


Figure S1. *Etv2* CKO mice display defects in hematopoietic recovery after 5-FU injury (related to Fig. 2). Representative FACS plots of the KSL (c-Kit<sup>+</sup>Sca1<sup>+</sup>Lin<sup>-</sup>) and KSL-SLAM (CD48<sup>-</sup>CD150<sup>+</sup>KSL) analysis in Tie2-Cre;*Etv2* CKO or control mice after 5-FU treatment are shown. Numbers in the boxes indicate the frequency of KSL cells (left) and CD150<sup>+</sup>CD48<sup>-</sup>KSL cells (right).

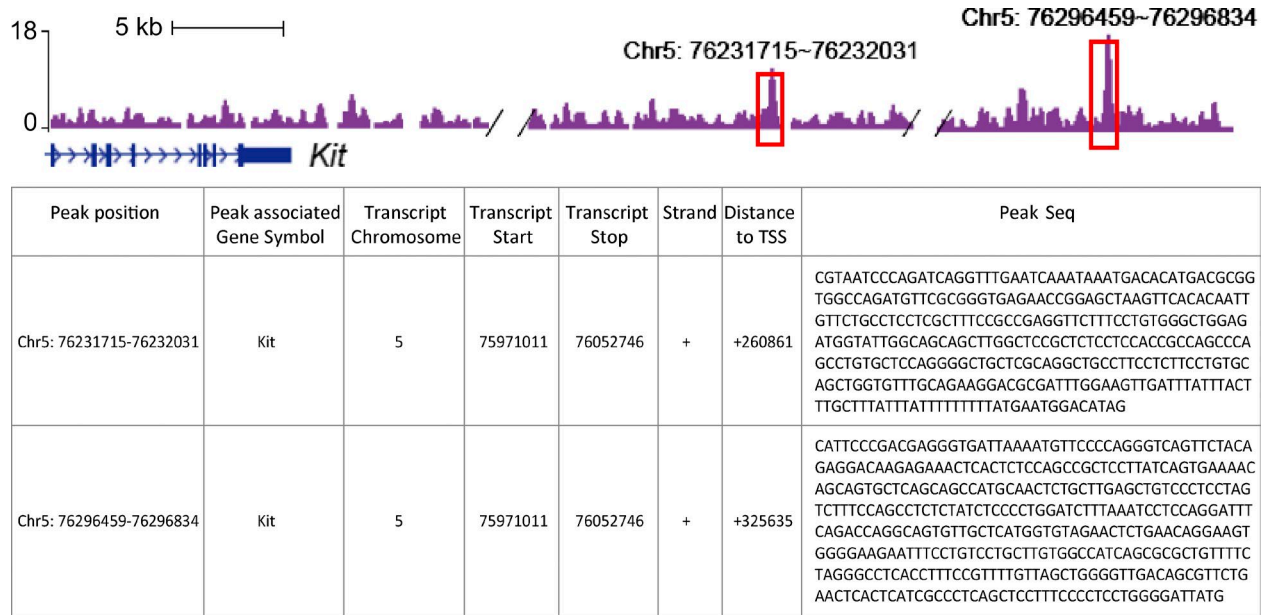


Figure S2. The potential binding sites of ETV2 in the c-Kit locus are shown (related to Fig. 5). Two potential ETV2-binding peaks and the corresponding sequences, identified from the ChIP-Seq analysis, are shown (Liu et al., 2015). TSS, transcription start site.

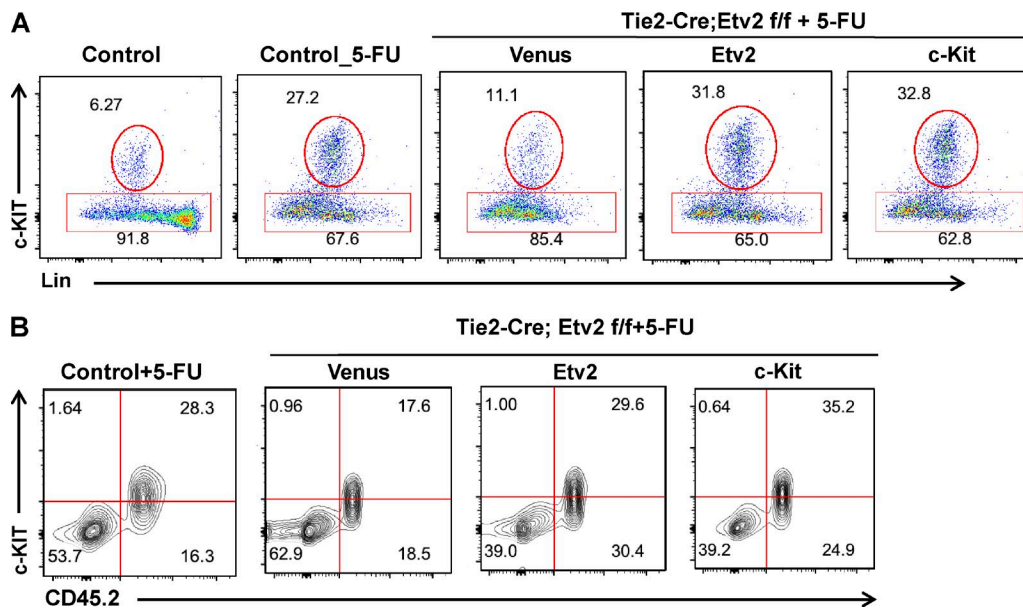


Figure S3. c-Kit is downstream of ETV2 in hematopoietic regeneration (related to Fig. 5). (A) Representative FACS plots showing the percentage of c-KIT<sup>+</sup>Lin<sup>low/-</sup> cells recovered from the culture after infection with lenti-Venus, -Etv2, or -c-Kit virus. (B) Representative FACS plots showing the percentage of donor contribution and CD45.2 and c-KIT<sup>+</sup> cells is shown. BM from Tie2-Cre;Etv2<sup>ff</sup> mice were obtained 7 d after 5-FU injection, infected with lenti-Venus, -Etv2, or -c-Kit, and then competitively transplanted with mock-infected WT BM into 9 Gy-irradiated recipient mice (CD45.1). Littermate control BM was used as the positive control. BM was analyzed 3 d later.