

SUPPLEMENTAL MATERIAL

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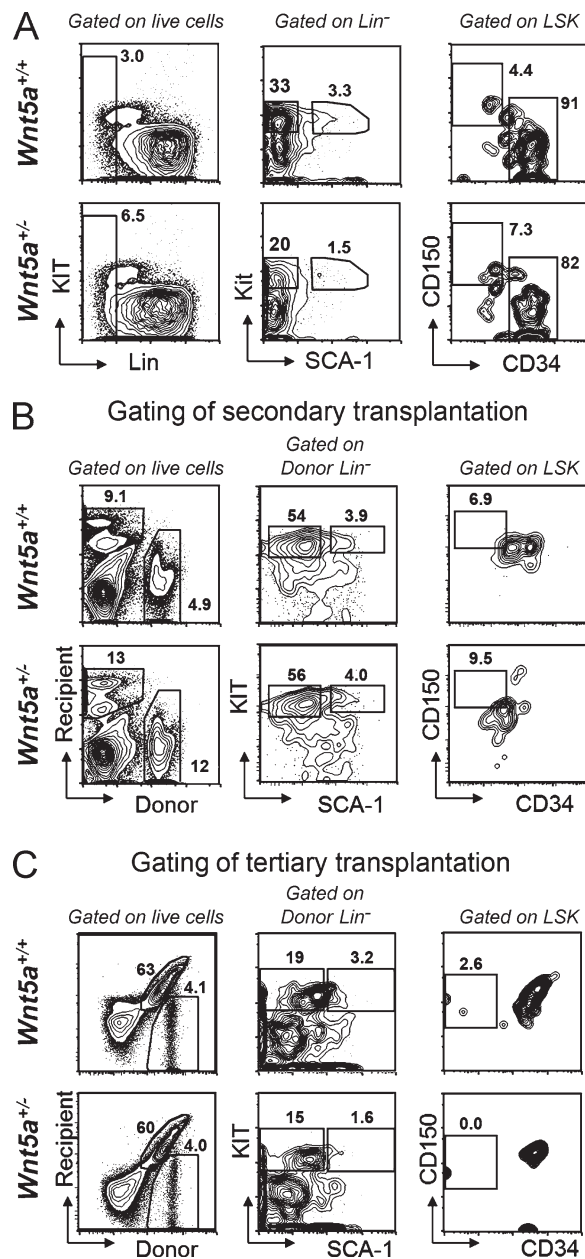


Figure S1. **Gating of BM staining of primary, secondary, and tertiary transplantations (related to Fig. 1).** (A) Representative FACS plots of BM from 1° recipients isolated 16 wk after transplantation. (B) Similar plots from 2° recipients (C) and also for the 3° transplantations.

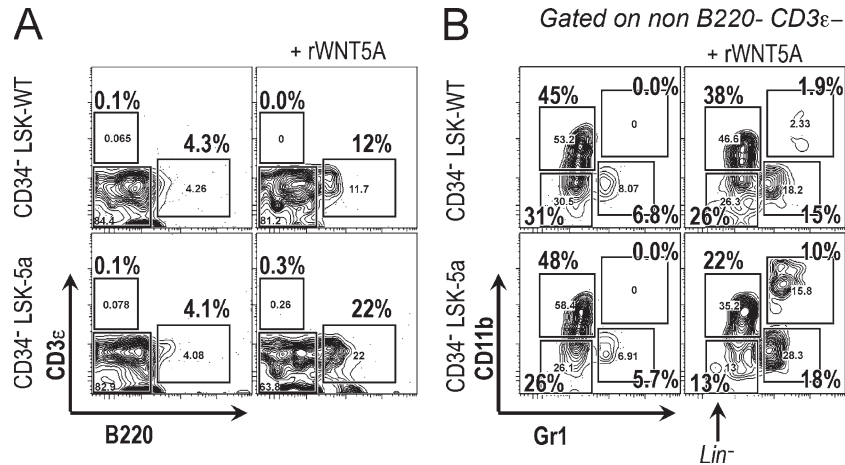


Figure S2. **Gating of single-cell culture of donor CD34⁻ LSK cells isolated from transplanted WT and *Wnt5a*^{+/-} recipients (related to Fig. 5).** Gating strategy of the flow cytometry of CD34⁻ LSK-WT and CD34⁻ LSK-5a cells 6 d after culture in serum-free conditioned medium from UG26-1B6 cells, supplemented with Kitl and IL-11 (open symbols), or with an additional 500 ng/ml rWNT5a. (A) Gating for CD3e⁺ T cells and B220⁺ B-lymphoid populations. (B) The number of granulocytic cells in the nonlymphoid fraction showing the remaining Lin⁻ cells which from which the LSK cells were shown as Fig. 5 L and quantified in Fig. 5 M.

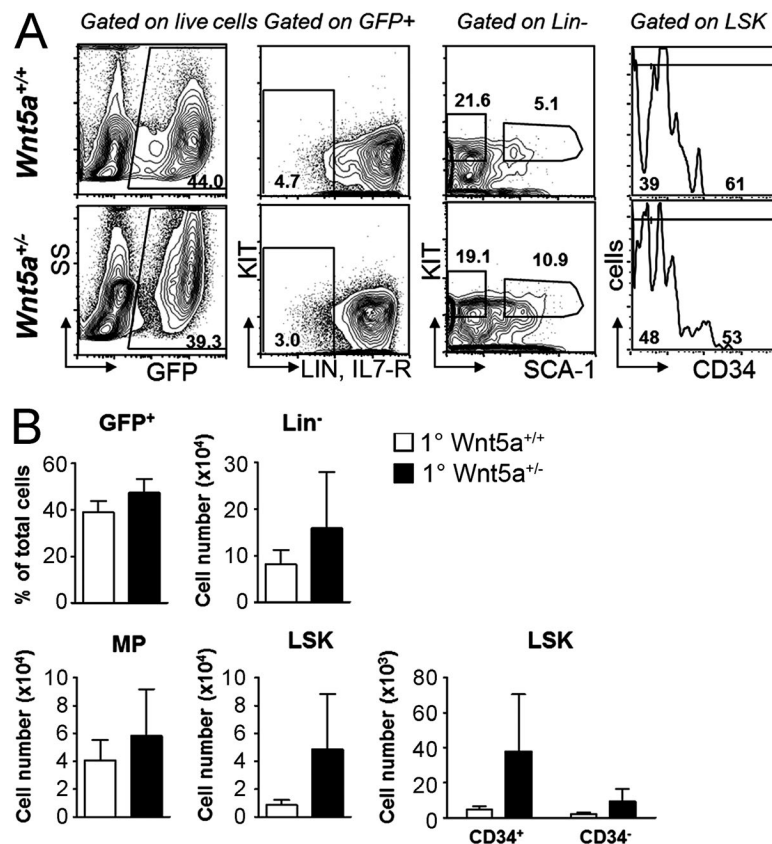


Figure S3. **Flow cytometry of primary BCR-ABL^{p185} Leukemic mice (related to Fig. 7).** (A) Representative FACS plots of BCR-ABL^{p185}GFP⁺ HSCs and progenitors in the BM of 1° recipients. (B) The engraftment BCR-ABL^{p185}GFP⁺ HSCs and progenitors in the BM of 1° recipients. Data represented as mean ± SEM.

Tables S1–S6 are available as Excel files. Table S1 lists primary antibodies used in this study. Table S2 lists secondary reagents and antibodies used in this study. Table S3 is a comparison of mapped RNA sequences from MSC-WT and MSC-5a. Table S4 lists GO enrichment analysis of MSC transcriptomes from transplanted recipients. Table S5 is a comparison of mapped RNA sequences from LSK-WT and LSK-5a. Table S6 lists KEGG pathway enrichment analysis of the genes differentially expressed between LSK-WT and LSK-5a.