Figure S1. The immunophenotype of splenic BCR-ABL1$^+$ leukemic cells. (A) Representative FACS profiles of spleen (SP) cells from a BCR-ABL1$^+$ ALL mouse. GFP$^+$ cells expressed B cell lineage antigen CD19 (bottom panel), and lacked expression of myeloid lineage antigen Gr1 (top panel) and T cell lineage antigen CD3 (middle panel). (B) Scatter plot showing the percentages of Gr1, CD3 and CD19 antigens on GFP$^+$ cells (n=6). Data indicate the means of independent mouse data with the error bars representing the SEM. ***P<0.001; ns, not significant, P>0.05 (Gr1$^+$ vs. CD19$^+$, P<0.001; CD3$^+$ vs. CD19$^+$, P<0.001; Gr1$^+$ vs. CD3$^+$, P=0.269). (C) Representative FACS profiles of SP cells from a *BCR-ABL1*$^+$ ALL mouse. GFP$^+$ cells expressed CD43 and B220 antigens. (D) Scatter plot showing the percentages of CD43+B220$^+$ and CD43-B220$^+$ populations on GFP$^+$ cells from *BCR-ABL1*$^+$ ALL mice (n=6). Data indicate the means of independent mouse data with the error bars representing the SEM. **P<0.01 (CD43$^+$B220$^+$ vs. CD43$^-$B220$^+$, P=0.009).

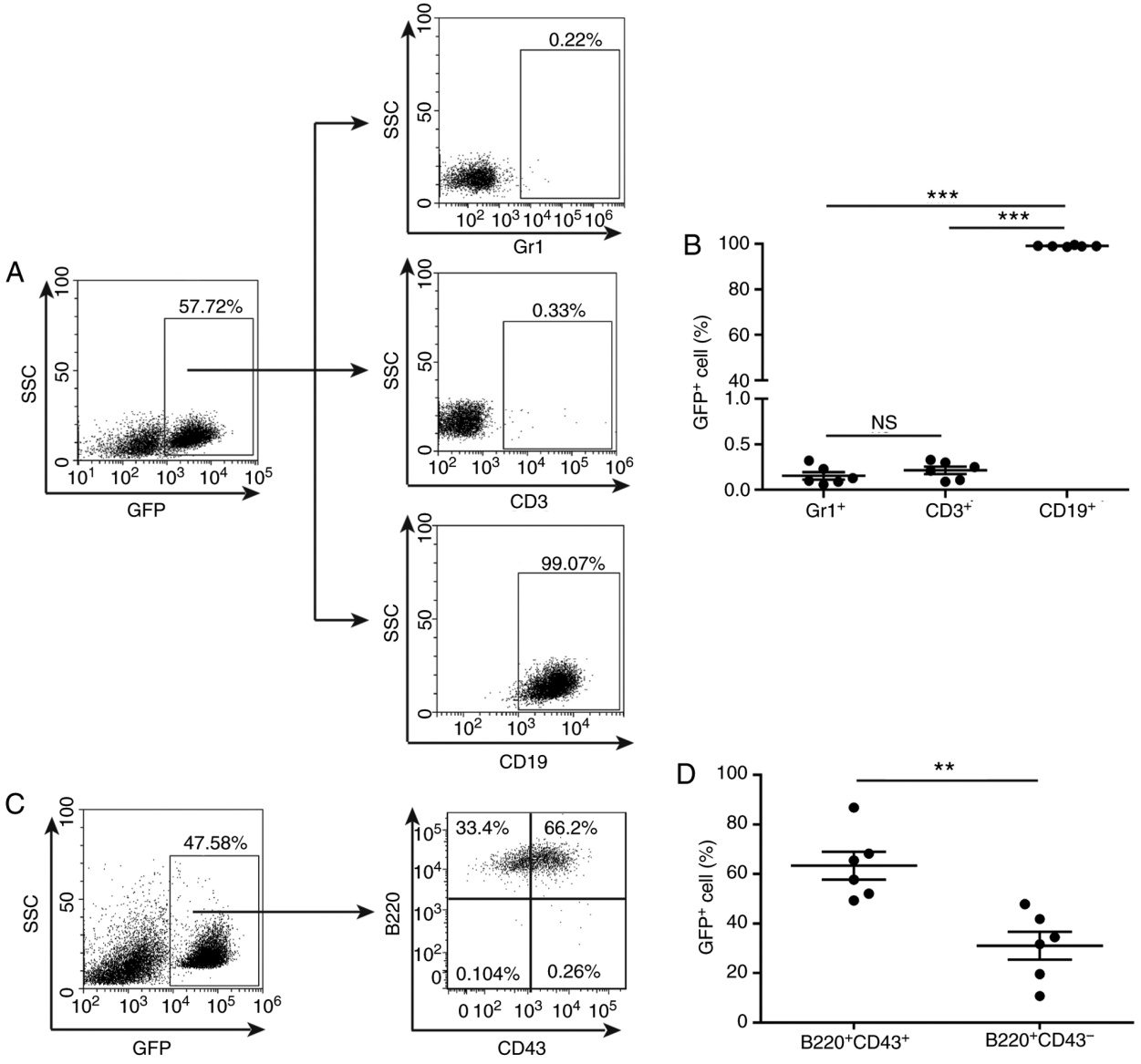

Figure S2. Transcripts of Itga6 and L-selectin genes in bone marrow GFP^+CD19^+ cells from primary B-ALL and secondary B-ALL mice. Transcripts of Itga6 and L-selectin genes were detected in BM GFP^+CD19^+ cells from primary B-ALL mice (n=3) and secondary B-ALL mice (n=3), respectively. Transcripts of Itga6 and L-selectin genes from BM $CD19^+$ cells of healthy mice (n=3) were used as controls. Gene mRNA fold expression values have been normalized to the GAPDH as described in Materials and methods. Data indicate the mean of independent mouse with the error bars representing the SEM; ns, $P>0.05$ and $^*P<0.05$.