Supplementary Figure 1

A. Graph showing CXCR4 relative expression levels for K562, K562LG, and K562LG-CXCR4.86.


C. Graph showing migration percentages for K562, K562LG, and K562LG-CXCR4.86.

D. Flow cytometry data for GFP and CXCR4 expression in K562, K562LG, and K562LG-CXCR4.86.

E. Flow cytometry data for CXCR4 expression in CML CD34+.

F. Flow cytometry data for CXCR7 expression in K562LG and K562LG-CXCR4.86.

G. Bar charts showing viable cell number for K562, K562LG-CXCR4.86, and CML CD34+ at different CXCL12 concentrations.
Supplementary Figure 1. CXCR4 expression and function in K562 and K562LG-CXCR4 cells

(A) CXCR4 mRNA expression was analyzed by qRT-PCR in the wild-type K562 cells, K562-LG (overexpressing the luciferase and GFP genes) and in K562LG-CXCR4 cell line (overexpressing the luciferase and CXCR4-IRES-GFP genes). (B) Flow cytometric analysis of CXCR4 expression in YTS and K562 cells after the transduction with CXCR4-IRES-GFP vector. Cells were stained with anti-CXCR4 antibodies (IgG2a-12G5 PE-conjugated, black- control wild-type cells, gray- transduced cells). (C) Chemotactic ability of wild-type and CXCR4-expressing YTS and K562 cells in response to CXCL12 (500 ng/ml) was measured using trans-well migration assay. (D) Single cell clone with high and stable expression of CXCR4 (K652LG-CXCR4.86) was generated using limiting dilutions method. Relative CXCR4 and GFP expression by the native K562, K562LG and K562LG-CXCR4.86 clone, measured by FACS. (E) CXCR4 surface expression on primary CML CD34+ cells, measured by FACS. (F)CXCR7 surface expression on K562LG and K562LG-CXCR4.86 cells. (G) K562, K562LG-CXCR4.86 or primary CD34+ CML cells were cultured in 24-well plates (4x105 cells per well), in triplicates, in 0.1% FCS medium, in the presence or absence of CXCL12 (50-1000 ng/ml) for 48 hours. Relative number of viable cells was determined by FACS using PI staining. The results represent the average of triplicates ±STDEV (**p<0.01).