SUPPLEMENTAL METHODS

Plasmid Construction

Slug and *c-Kit* were amplified by PCR using Phusion™ high-Fidelity DNA Polymerase (New England Biolabs), and then cloned into pMIGR1 vector. To construct pMig-Slug-2A-c-Kit (Slug/c-Kit), *Slug* and *c-Kit* genes were in-frame linked by T2A sequence and then cloned into pMIGR1 vector.

To construct the c-Kit-LUC luciferase reporter, ~0.8 kb of *c-Kit* promoter region was amplified by PCR using specific primers and cloned in to pGL4.10 vector (Promega). To generate the mutant variants of c-Kit-Luc, point mutations in the four recognition sites were introduced by PCR using specific primers. To construct the Slug-Luc luciferase reporter, ~1.5 kb of *Slug* promoter region was amplified by PCR using specific primers and cloned in to pGL4.10 vector. To construct shRNA targeting mouse c-Kit, we first constructed pLKO.1maxGFP2aPuro vector by cloning maxGFP2aPuro fragment into BamH1 and NsiI sites of pLKO.1 vector. We cloned shRNA control and c-Kit shRNA #1, #2, and #3 into AgeI and EcoR1 sites of pLKO.1maxGFP2aPuro vector. All primers were listed in **Table S3**.

Retroviral and Lentiviral Transduction of Hematopoietic Cells

For generation of retrovirus, 293T cells were transfected with a mixture of DNA containing 1.5 μg of pCL-Eco (IMGENEX), 2.5 μg of pMIGR1 vector only or pMIGR1 expression vectors expressing *Slug*, *c-Kit*, or *Slug/c-Kit* by Fugene HD (Roche) according to the manufacturer's instruction. For preparation of the lentiviruses, 293T cells were transfected with a mixture of DNA containing 2.5 μg of shRNA lentiviral vectors (scramble shRNA control, c-Kit shRNAs or c-Myc shRNAs) and 2.5 μg of the packaging mixture (Genecopoeia, Rockville, MD) by Fugene HD. All Media containing retroviruses or lentiviruses were collected 24 hours after transfection,

and filtered through a 0.45 μm pore-size filter. All shRNAs excluding c-Kit shRNAs were purchased from Sigma and listed in **Table S4**.

To transduce HSPCs, cells were enriched from BM of mice following 5-Fu injection (150 mg/kg body weight). Enriched cells were cultured overnight and were spun at 200 X g. The supernatant was aspirated and replaced with retroviral or lentiviral particles-containing supernatant supplemented with 5 μg/ml polybrene (Sigma), followed by centrifugation (900 x g for 45 min). After two days of transduction, lentivirus-transduced cells were selected by 1 μg/ml puromycin, and then performed for the further experiments.

Flow Cytometric Analysis

BM MNCs were isolated from mouse BM and purified by density gradient centrifugation through Ficoll. For analysis of $Lin^{-}Sca\text{-}1^{+}c\text{-}Kit^{+}$ (LSK) cells, one million of BM MNCs were stained with a mixture of biotinylated antibodies against mouse CD11b, CD3e, CD45R (B220), Ly-6G (Gr-1), and TER-119. Subsequently, the cells were co-stained with streptavidin-FITC, anti-Sca-1-APC, and anti-c-Kit-PE/Cy7.

For sorting and analyzing SP cells, BM MNCs were incubated with 5 μg/ml Hoechst 33342 (Life Technologies) at 37 ^{o}C for 90 mins [1]. For sorting and analyzing SLAM cells, BM MNCs were co-stained with anti-CD150-APC and anti-CD48-PE.

For analysis of peripheral blood, the samples were collected in PBS containing 50 mM EDTA solution via lateral tail vein incision. The peripheral blood MNCs were purified by density gradient centrifugation through Ficoll and then co-stained with anti-CD45.1-PE and anti-CD45.2-Alexa647 antibodies. All antibodies, unless stated, were purchased from Biolegend and eBioscience (**Table S5**). Flow cytometry was performed on a BD LSRFortessa or FACSAria, and all flow cytometric data were analyzed with FlowJo software (TreeStar).

BM Transplantation

6-8-week-old C57BL/6.SJL (CD45.1) mice were given acidified antibiotic water (Sulfamethoxazole and Trimethoprim) for 7 days, and then lethally irradiated with 10 Gy total body irradiation before BM transplantation. HSCs were transduced with retroviral or lentiviral particles for two days, and then transplanted into mice by retro-orbital injection. Adult splenocytes ($1.5x10^6$ cell/ per CD45.1 mouse) were injected as helper cells along with HSCs [2]. Recipient mice were continuously fed with acidified antibiotic water for 1 month to reduce the chance of spontaneous infection. For serial transplantation, $6x10^5$ BM MNCs from the primary recipients were injected into lethally irradiated secondary recipients.

Luciferase Reporter Assay

293T cells or primary BM MNCs were cultured in 24-well plate overnight, and then transfected with 50 ng of luciferase reporter, 400 ng of pMig or pMig-Slug, and 50 ng of pCMV-LacZ using Fugene HD. After 72 hours of transfection, cells were lysed in 250 µl of the passive lysis buffer (Promega) and assayed with a luciferase assay kit (Promega) as directed by the manufacturer. Luciferase activities were expressed as relative luciferase/LacZ activities and normalized to those of control transfections in each experiment.

RNA Extraction, RT-PCR, and Real-time PCR

Total RNA samples were extracted using Quick-RNA MicroPrep Kit (Zymo Research). For real-time PCR, 100 ng of total RNA was reverse-transcribed using SuperScirpt III™ cDNA Synthesis Kit (Invitrogen). *Hprt* or *Gapdh* expression was used as internal control to normalize relative expression of each gene. The list of primers is included in the supplemental Information (**Table S3**).

1. Goodell MA, Brose K, Paradis G, Conner AS, Mulligan RC. Isolation and functional properties of murine hematopoietic stem cells that are replicating in vivo. *The Journal of experimental medicine* 1996 Apr 1; **183**(4)**:** 1797-1806.

2. Stern P, Astrof S, Erkeland SJ, Schustak J, Sharp PA, Hynes RO. A system for Cre-regulated RNA interference in vivo. *Proceedings of the National Academy of Sciences of the United States of America* 2008 Sep 16; **105**(37)**:** 13895-13900.

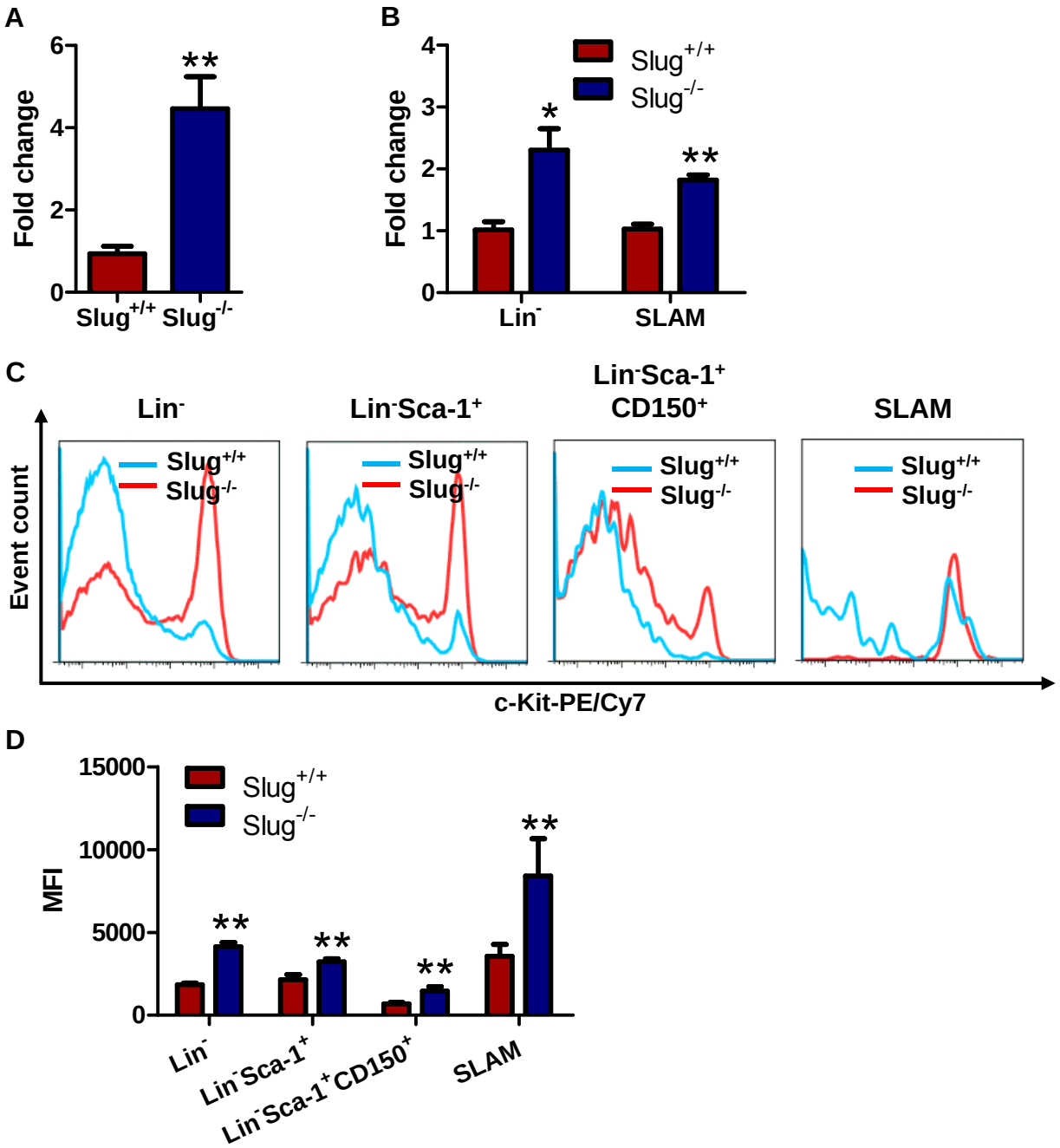

Figure S1. Slug Deficiency Leads to a Higher Expression Level of c-Kit in HSCs

(A) qPCR analysis of *c-Kit* mRNA expression levels in Lin$^-$Sca-1$^+$ HSC subpopulation. Lin$^-$Sca-1$^+$ HSC subpopulation was sorted by FACs from bone marrow of *Slug*$^{+/+}$ and *Slug*$^{-/-}$ mice after 5-FU treatment (n = 3) and followed by RNA extraction and qPCR. Expression levels of *c-Kit* were normalized to *Hprt* levels.

(B) qPCR analysis of *c-Kit* mRNA expression levels in Lin$^-$ subset and SLAM subset. Expression levels of *c-Kit* were normalized to *Hprt* levels.

(C, D) Flow cytometric analysis of c-Kit expression in distinct hematopoietic subsets in BM cells from *Slug*$^{+/+}$ and *Slug*$^{-/-}$ mice (n = 4). The levels of c-Kit were evaluated by flow cytometry. MFI, mean fluorescence intensity. Data are representative of two independent experiments. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (*P < 0.05; **P, < 0.01).

Figure S1

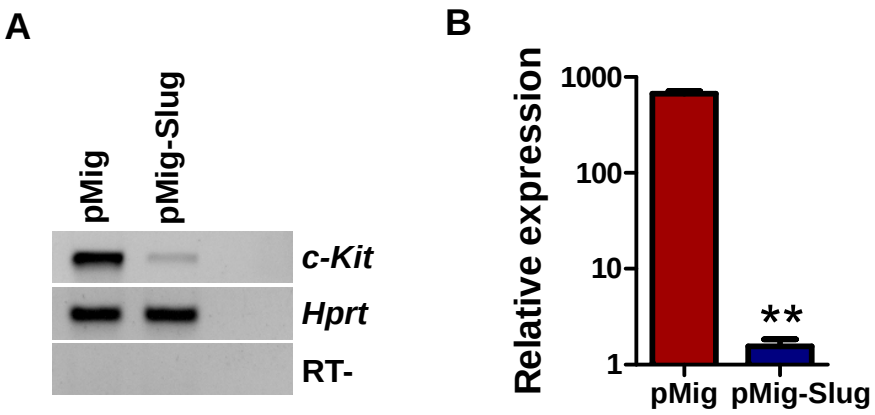

Figure S2. **Semiquantatitive-PCR and qPCR Analysis of c-Kit Transcripts in Primitive Hematopoietic Cells**

(A-B) HSPCs were transduced with pMig or pMig-Slug retroviruses, cultured for three days, and followed by RNA extraction and PCR (A) and qPCR (B) analysis. Data are representative of two independent experiments. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (**$p < 0.01$).

Figure S2

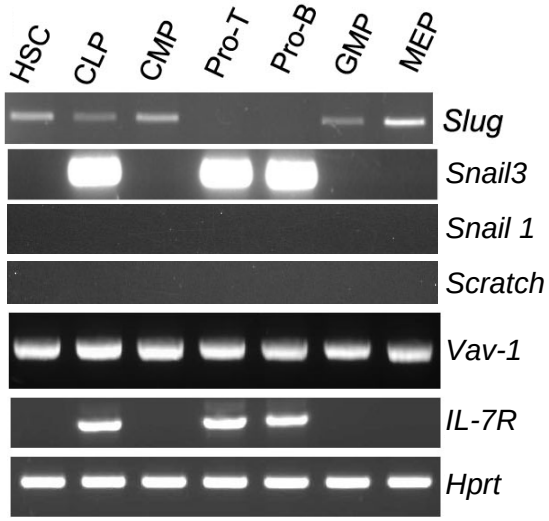

Figure S3. **Expression profiles of Snail Family Members in Different Hematopoietic Cell Lineages**. The indicated subsets of hematopoietic cells were sorted by FACS and analyzed by PCR. HSC: hematopoietic stem cell, CLP: common lymphoid progenitor, CMP: common myeloid progenitor, Pro-T: progenitor T-cell, Pro-B: progenitor B-cell, GMP: granulocyte/macrophage progenitor, MEP: megakaryocyte/erythrocyte progenitor.

.

Figure S3

A

acaagtctcagcaggagcttggctgggtggaggtccacgctggccaataga
aatcagctgtattcttacaggtttcgcag**CAGGTG**gagaaactgagcat
gaaaaattacttaaacgtgggctcggtcttttactgaggtcaggggtgcca
cgatccgtcctcctctaccaacaggaacagaaataaatgttggggacccag
tttcctaatcccttcgcccggcaatcccgactagtaacacctccaccataa
gccgaatatattctccccgctccggagcttgctggagggaccggtggttgt
cctttattgtctagggag**CACCTG**c**CAGGTG**gctggcccgtacctaa
tgcgctcgtggcgctgggcttcacaaagcgcgggcag**CACCTG**cgtggc
cagccagccgcctggactgaaggaccaccgatggagggagagtgctaggag
gaagaggatccagggtggagggcctgtgggggctcctggtcttagagggca
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agcgggagggagtgcgacccgggcgggagaagggaggggcgtggccacgag
ctgggaggagggctggaggaggggctgtcgcgcgccgctagtggctctggg
ggctcggctttgccgcgctcggtgcacttgggcgagagctgtagcagagag
aggagctcagagtctagcgcagccaccgcg**ATG**AGAGGCGCTCGCGGCGC
CTGGGATCTGCTCTGCGTCCTGTTGGTCCTGCTCCGTGGCCAGACAG

Promoter

Exon 1

B

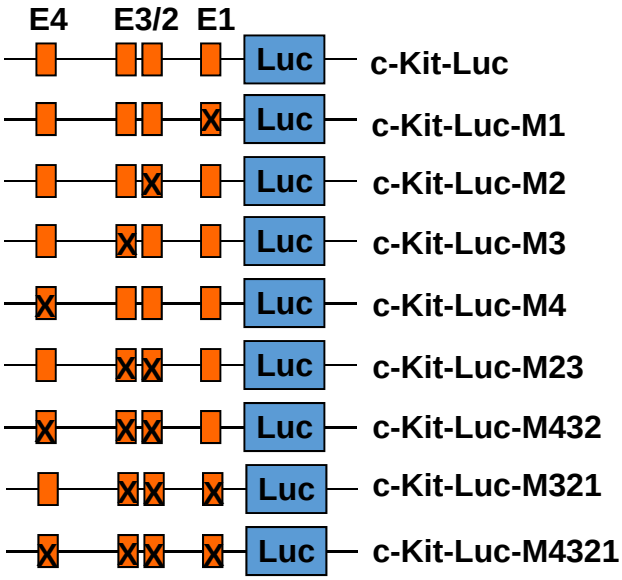


Figure S4. **The sequence of Mouse *c-Kit* Promoter and its Luciferase Report's constructs**
(A) The DNA Sequences of Mouse *c-Kit* Promoter. Potential E-boxes for Slug binding sites (5'-**caggtg**-3') in mouse c-Kit promoter region. The start code (**ATG**) for c-Kit gene is indicated.
(B) Construction diagram of the luciferase reproters for the mutant c-Kit promoters in E-boxes. E, E-box; X, mutant.

Figure S4

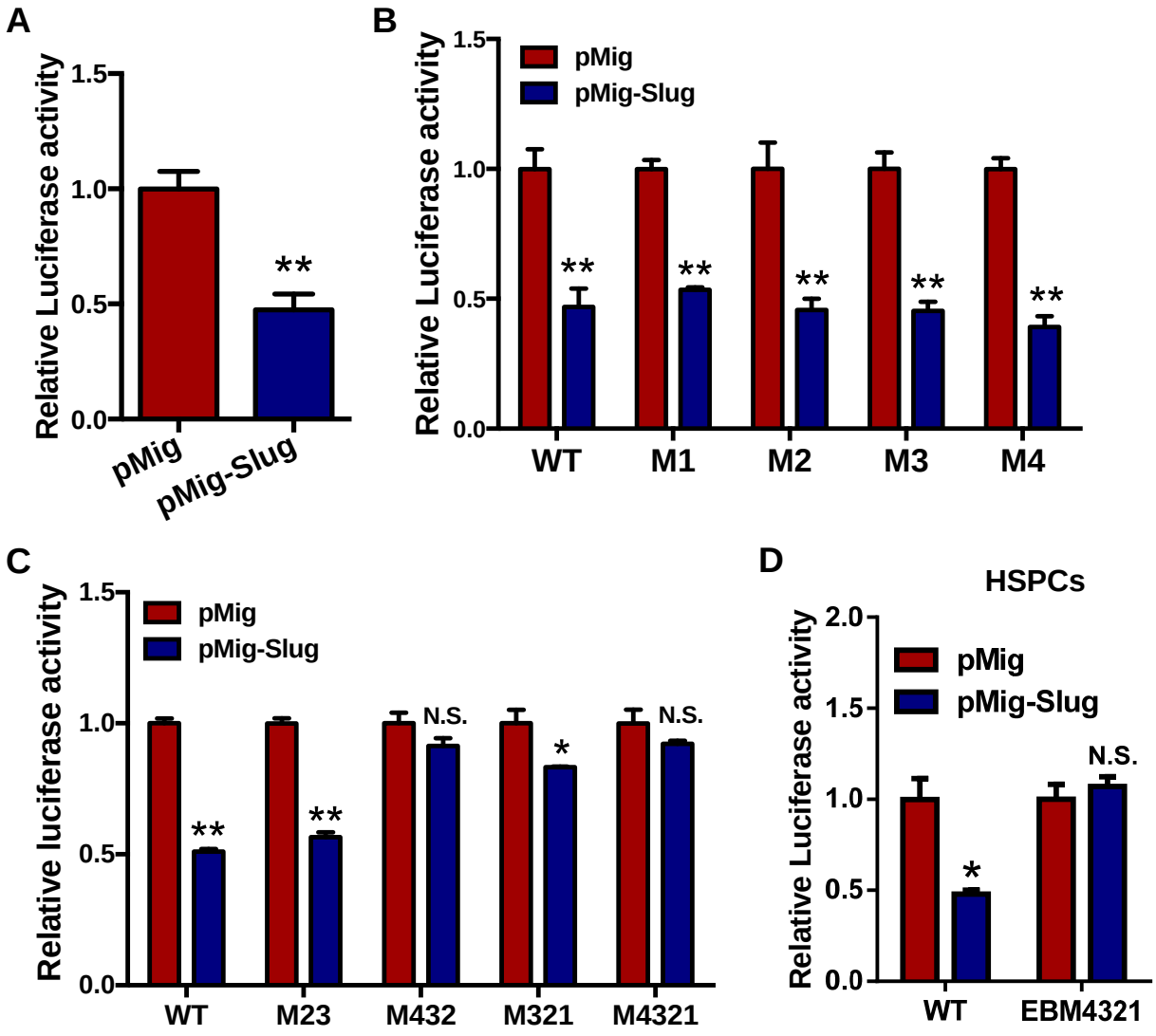


Figure S5. c-Kit luciferase reporter assays in 293T cells and HSPCs

293T cells or primary HSPCs were transfected with the reporter plasmid c-Kit-Luc (A), or its mutants (B, C, D) together with pMig (vector control) or pMig-Slug, then cultured for 72 h before luciferase activity assay. pCMV-LacZ was included in each transfections as an internal control to normalized luciferase activity. Data are representative of three independent experiments. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (*P < 0.05; **p < 0.01; N.S., not significant, P > 0.05).

Figure S5

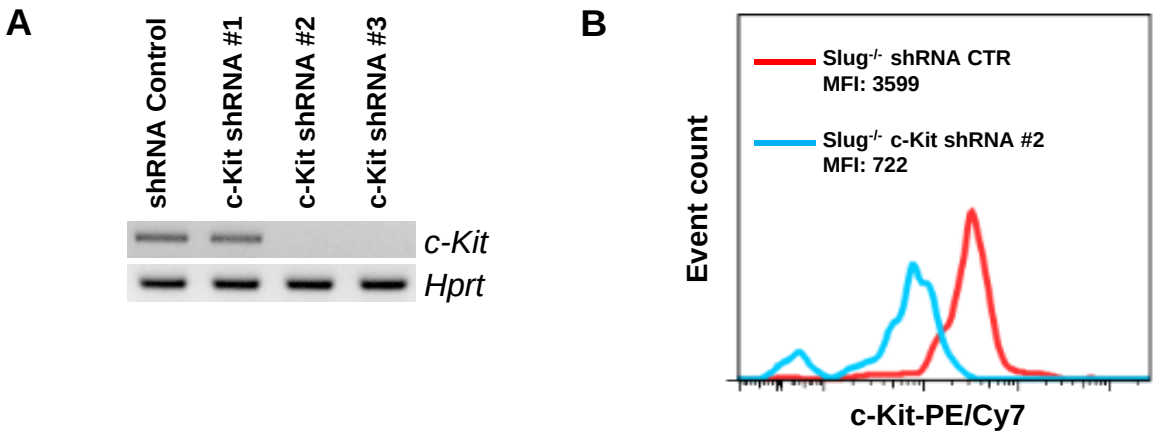


Figure S6. **c-Kit Knockdown by shRNAs**
(A) Semi-quantitative PCR analysis of c-Kit knockdown in primary HSPCs. Transcriptional level of c-Kit was examined by gene-specific, semi-quantitative RT-PCR.
(B) Flow cytometric analysis of c-Kit protein expression in HSPC infected with lentivirus-expressing c-Kit shRNA #2.

Figure S6

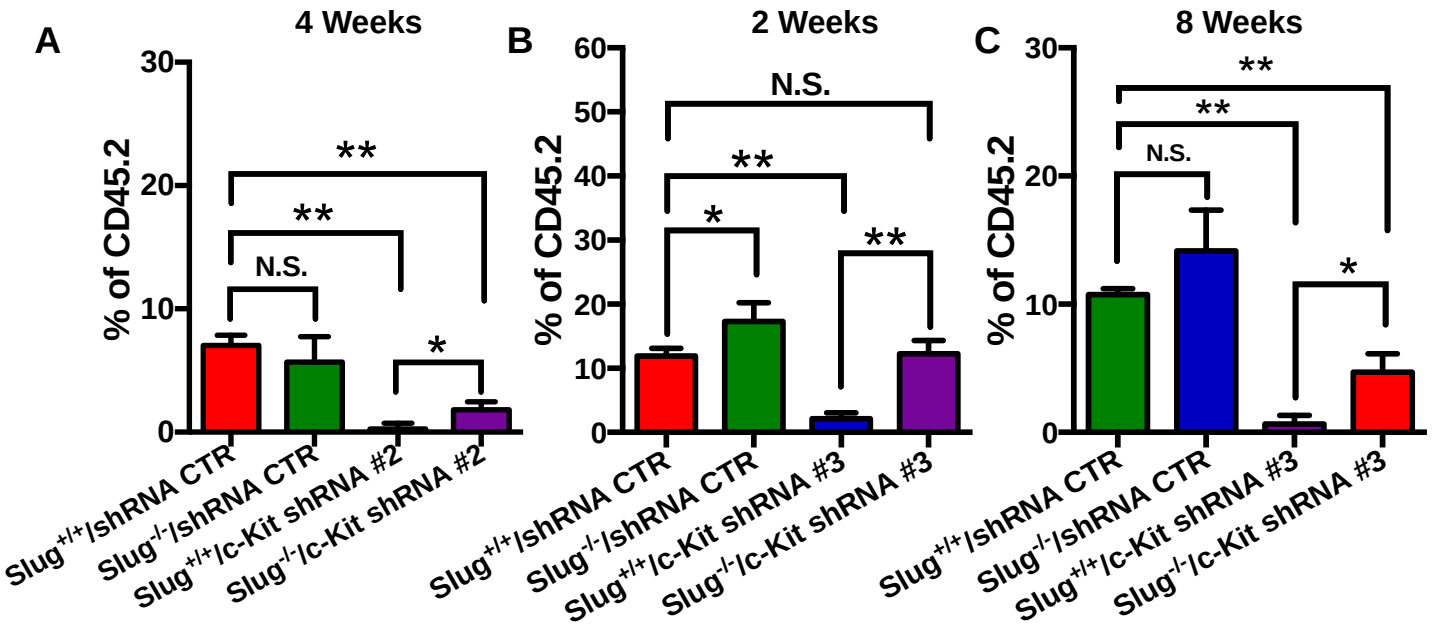


Figure S7. **The Percentage of Donor-derived Cells (CD45.2$^+$) in PB of Recipients**

(A) Percentage of PBMCs in recipients reconstituted with *Slug*$^{+/+}$ or *Slug*$^{-/-}$ infected with shRNA CTR or c-Kit shRNA #2 were evaluated by flow cytometric analysis at 4 weeks after BM transplantation (n = 3 mice).

(B, C) Percentage of PBMCs in recipients reconstituted with *Slug*$^{+/+}$ or *Slug*$^{-/-}$ infected with shRNA CTR or c-Kit shRNA #3 were evaluated by flow cytometric analysis at 2 (B) and 8 (C) weeks after BM transplantation (n = 3-4 mice). Data are representative of two independent experiments. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (*P < 0.05; **p < 0.01; N.S., not significant, P > 0.05).

Figure S7

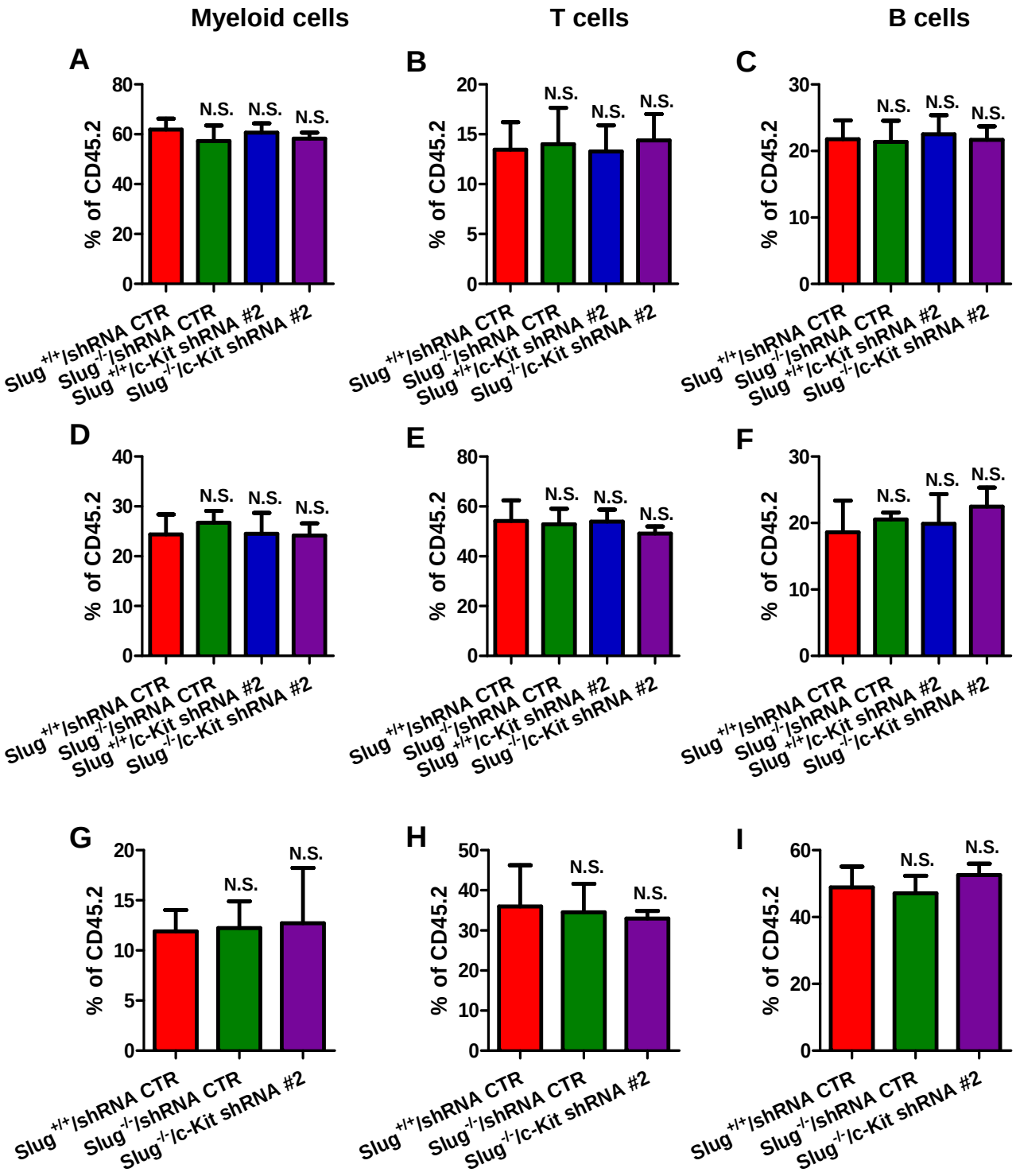


Figure S8. **Analysis of Donor-derived (CD45.2) Hematopoietic Cells in PB of Recipients**. Percentage of myeloid ($CD11b^+$ and $Gr\text{-}1^+$) cells (A, D, G), T cells ($CD3\varepsilon^+$) (B, E, H), and B cells ($B220^+$) (C, F, I) in recipients reconstituted with *Slug*$^{+/+}$ or *Slug*$^{-/-}$ infected with shRNA CTR or c-Kit shRNA#2 were evaluated by flow cytometric analysis at 2 weeks (A-C), 4 weeks (D-F), and 8 weeks (G-I) after BM transplantation (n = 4 mice), respectively. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (not significant, $P > 0.05$).

Figure S8

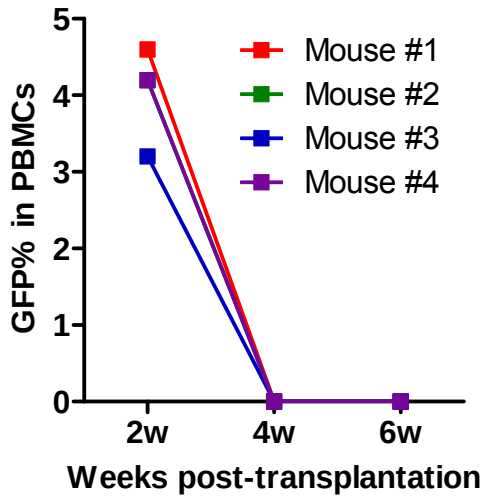


Figure S9. **Analysis of Donor Cells in Peripheral Blood of Recipients**. PBMCs were analyzed by flow cytometry in primary pMig-c-Kit reconstituted mice (n = 4). Data are representative of three independent experiments.

Figure S9

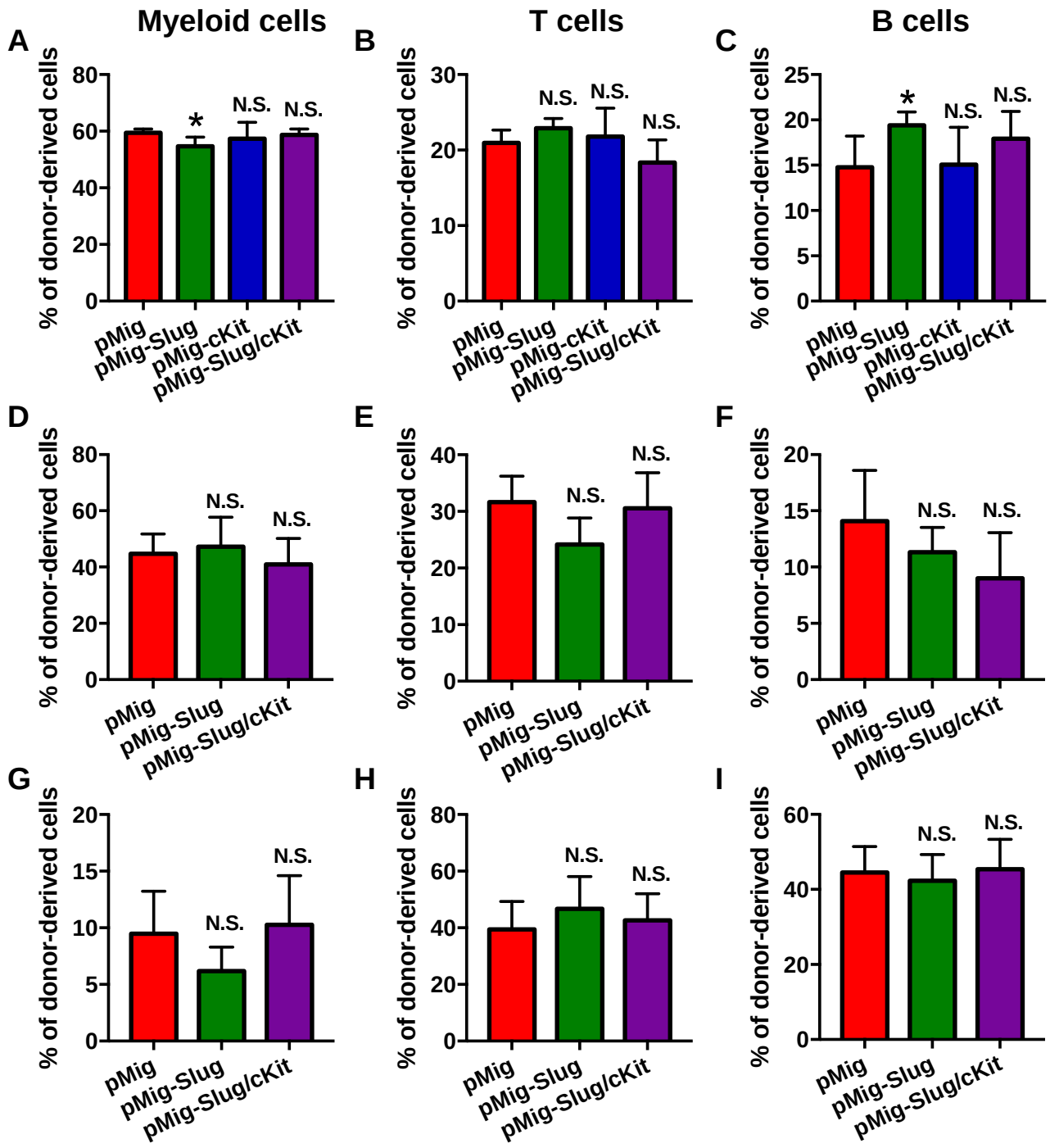


Figure S10. **Analysis of Donor-Derived Hematopoietic Cells in PB of Recipients**. Percentage of myeloid (CD11b$^+$ and Gr-1$^+$) cells (A, D, G), T cells (CD3ε$^+$) (B, E, H), and B cells (B220$^+$) (C, F, I) in primary pMig, pMig-Slug, pMig-cKit, and pMig-Slug/cKit reconstituted mice were evaluated by flow cytometric analysis at 2 weeks (A-C), 4 weeks (D-F), and 8 weeks (G-I) after BM transplantation (n = 5 mice), respectively. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance ((*P < 0.05; not significant, P > 0.05).

Figure S10

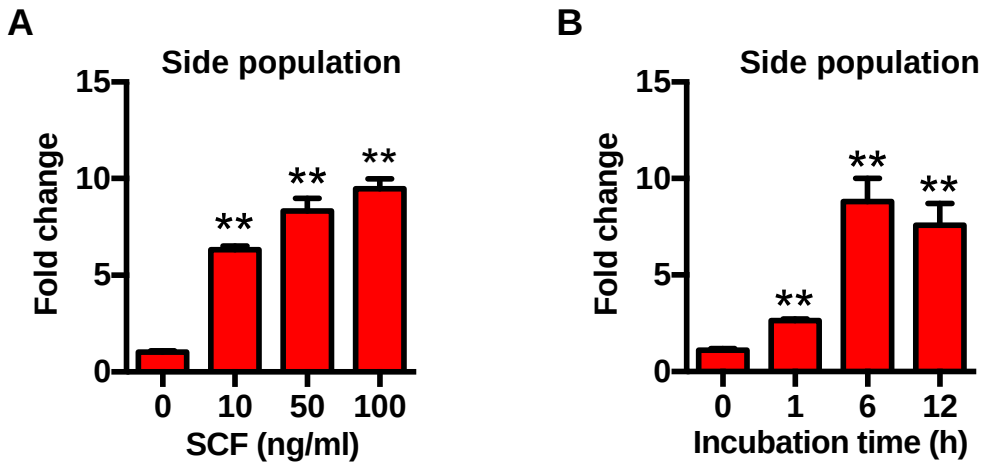


Figure S11. SCF Induces the Transcription Level of Slug. qPCR analysis of endogenous Slug transcripts in side population HSCs. The cells were treated with different doses of SCF (A) or treated with SCF for different times (B), and then were proceeded to qPCR analysis and normalized to *Hrpt* level. **p < 0.01.

Figure S11

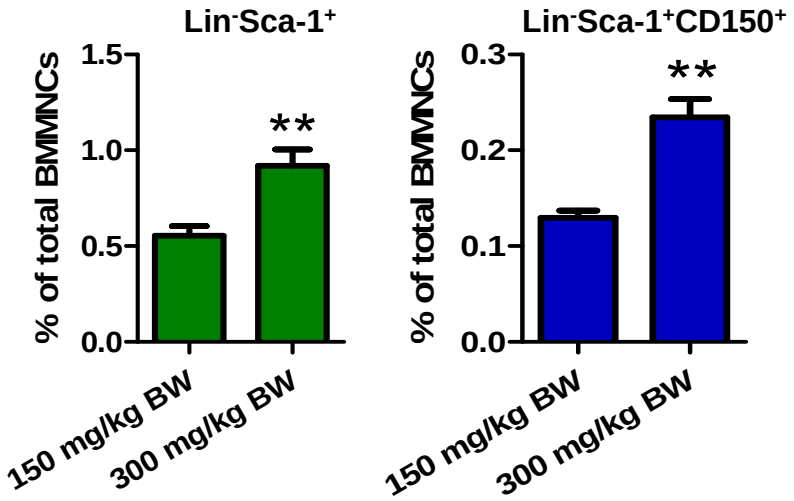


Figure S12. High dose of 5-FU enriches the compartment of HSPCs
Mice were injected with 5-FU [150 or 300 mg/kg body weight (BW)]. Total BM cells were harvested 7 days after injection and analyzed by flow cytometric analysis.

Figure S12

Figure S13. DNA Sequence of Slug Promoter
c-Myc binding site (5'-CANNTG-3') and *FOXM1* binding site (5'-(C/T)AAA(C/T)A-3') are indicated. The start code (**ATG**) for *Slug* gene is indicated.

Figure S13

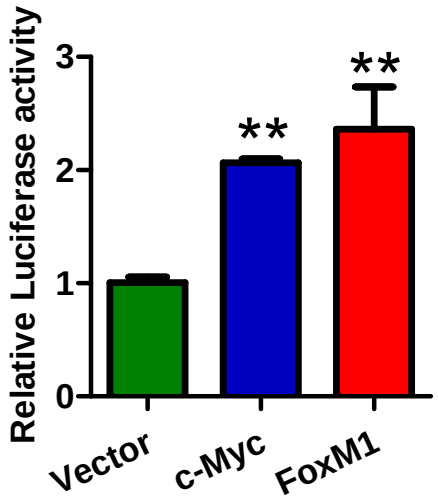


Figure S14. Slug Luciferase Reporter Assay

K562 cells cells were transfected with the reporter plasmid Slug-Luc together with pMig (vector control), pMig-c-Myc, or pMig-FoxM1, then cultured for 72 h before luciferase activity assay. pCMV-LacZ was included in each transfections as an internal control to normalized luciferase activity. Data are representative of three independent experiments. All data represent mean ± SD. Two-tailed Student's *t* tests were used to assess statistical significance (**p < 0.01).

Figure S14

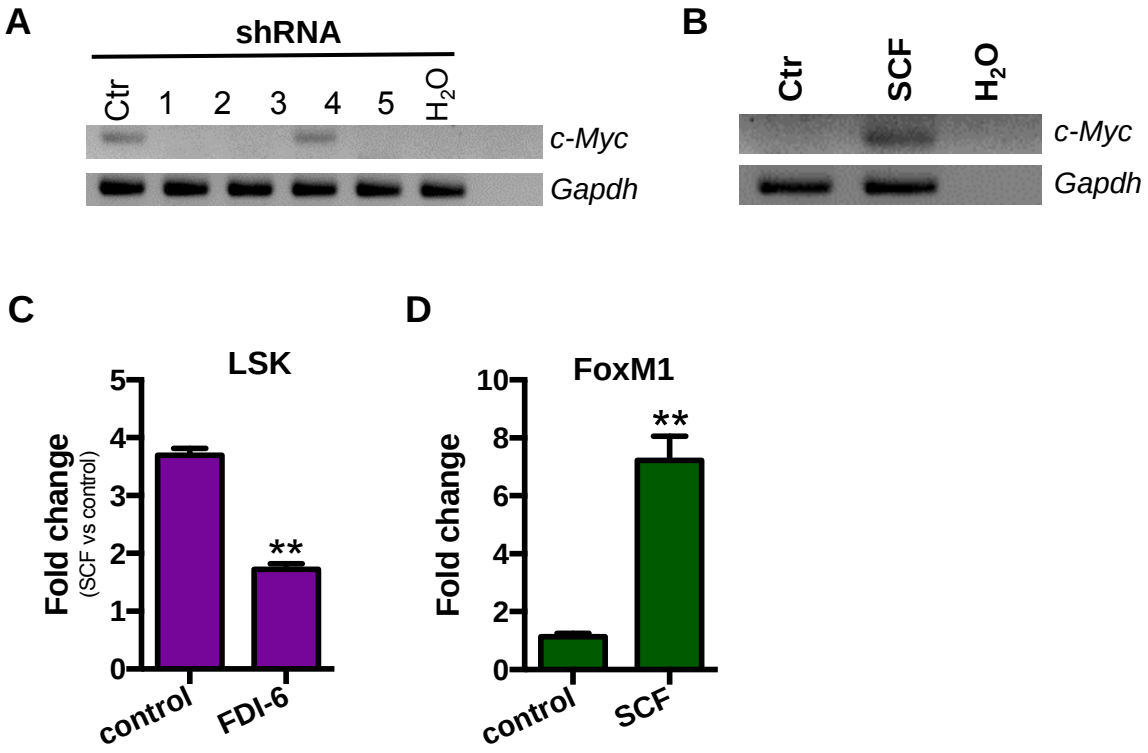


Figure S15. Key Role of c-Myc and FoxM1 in SCF/c-Kit-Slug Feedback Loop

(A) Semi-quantitative PCR analysis of endogenous c-Myc knockdown by shRNAs in primary BM cells. Lin^- cells were infected with lentiviruses expressing shRNA targeting c-Myc or control shRNA and selected with puromycin. Transcriptional level of c-Myc was examined by semiquantitative RT-PCR. Density of amplified DNA bands was quantified by Image J (NIH) and normalized by *Gapdh*. Data are representative of two independent experiments.

(B) Semi-quantitative PCR analysis of endogenous c-Myc transcripts in HSPCs treated with SCF. HSPCs were treated with or without SCF (100 ng/ml) for 12 hrs and then analyzed by PCR using c-Myc specific primers. Data are representative of two independent experiments.

(C) qPCR analysis of Slug transcripts in wild-type LSK subpopulation following treatment with or without SCF (100 ng/ml) and FoxM1-binding inhibitor FDI-6 (40 μM) for 12 hrs. Slug transcripts was analyzed by qPCR and normalized to *Gapdh* level. Data are representative of two independent experiments. $^{**}p < 0.01$.

(D) qPCR analysis of FoxM1 transcripts in HSPCs after treatment with SCF. HSPCs were enriched from wild-type mice and treated with or without SCF (100 ng/ml) for 12 hours, followed by qPCR analysis. *FoxM1* expression was normalized to *Gapdh* level. Data are representative of two independent experiments. $^{**}p < 0.01$.

Figure S15

Table S1. Gene expression profiles from microarray data analysis

Gene Symbol (or Genomic Position)	Fold change ($Slug^{+/+}$ vs. $Slug^{-/-}$)	ANOVA p-value
Adam8	5.55	0.034662
Bmp7	3.52	0.02986
Faim3	4.35	0.003286
Gm10717	2.79	0.040442
St3gal6	3.26	0.023531
Cd96	3.1	0.001186
Mapk11	2.68	0.007001
Inpp4b	3.11	0.007794
Bhlhe40	2.83	0.011203
Cxcr6	2.88	0.038504
Arg1	4.46	0.023874
Gm16271	3.7	0.03781
Phlda1	3.06	0.02399
Ccdc184	3.56	0.031538
Il4	3.17	0.009127
Rasgrp1	3.21	0.048914
Gm26216	2.79	0.024533
Lpcat2	2.84	0.005914
Mboat1	2.6	0.023953
Stab2	16.01	0.024117
Ccr2	5.03	0.046822
Csf2	8.13	0.034921
Ighv5-12; Igh-VJ558	-33.28	0.061425
Igkv3-9	-11.83	0.018412
Dhrs3	-3.88	0.033815
Selp	-2.79	0.002956
Plac8	-2.59	0.023045
Kit	-2.58	0.020692
LOC102643064	8.73	0.031955
Ikzf2	2.73	0.040157
Flrt2	3.31	0.004743
1700113H08Rik	3.42	0.012626
Ccr9; Gm17200	3.34	0.021881
Ptger2	2.68	0.04142
Tlr1	3.08	0.047968
Tnfsf14	3.07	0.037037
Mir342	3.47	0.035325
Tm4sf5	2.69	0.033192
177000956 - 177013459	2.73	0.000436
Gm26497	3.69	0.049349
Il5	3.9	0.036871
Mmp14	-3.51	0.003193

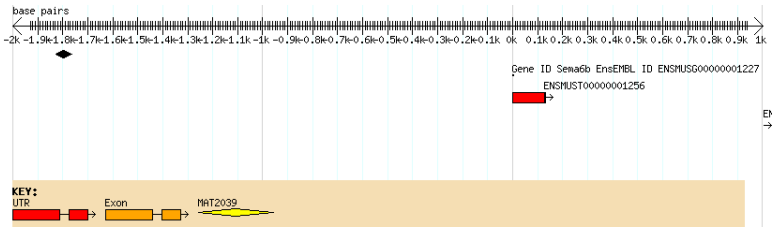
Tbc1d8	-3.53	0.037839
Scd1	-2.89	0.003648
Sema6b	-3.05	0.021768
H2-Eb2	-2.82	0.043391
Itga2b	-2.97	0.04893
Gm24630	3.68	0.024501
Gm25967	2.6	0.035973
Gm25631	-3.09	0.015075
Gm8906	-3.26	0.015109
Rhag	-3.8	0.040231

Table S2. The prediction of Slug binding sites in the selected target candidates

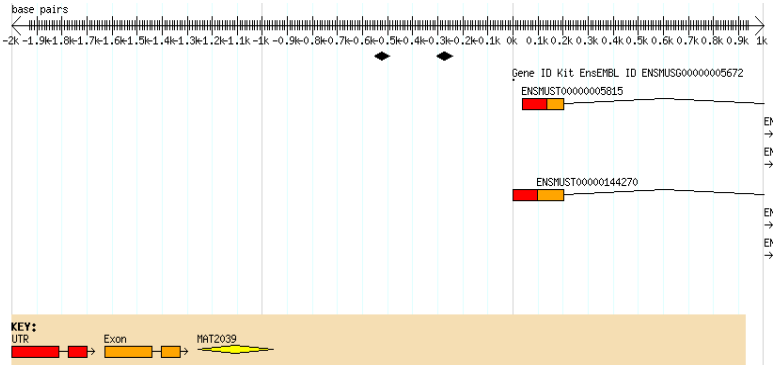
Gene Name	EnsEMBL ID	CHR	Biotype	Description	Best CRM Score	Ave CRM Score
Sema6b	ENSMUSG00000001227	17	protein_coding	sema domain	1.0000	1.0000
Kit	ENSMUSG00000005672	5	protein_coding	kit oncogene [Source:MGI Symbol;Acc:MGI:96677]	1.0000	0.9836
Selp	ENSMUSG00000026580	1	protein_coding	selectin	0.9673	0.9673

Transcription factor binding sites (TFBSs) and gene structure diagram

Sema6b



Kit



Selp

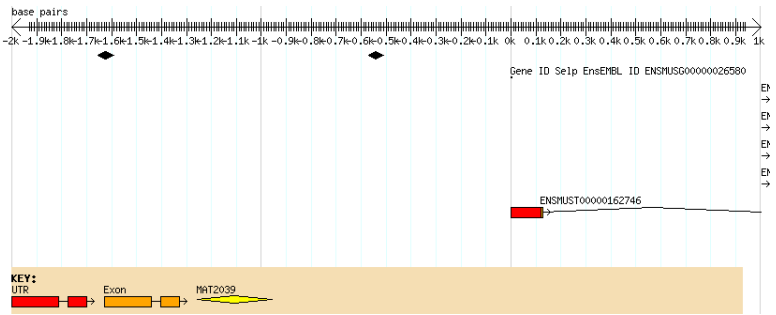


Table S3. List of primers for PCR

Primer	Sequence (5' to 3')	Application
c-Kit-F2	cttctctaggcgccggaattagatcttctagaccATGAGAGGCGCTCGCGGCGCCTGG	PCR
c-Kit-R2	cggaattcgttaacctcgagagatctTCAGGCATCTTCGTGCACGAGCAGG	PCR
pMIG-hSLUG-F	ctaggcgccggaattagatctctcgagccATGCCGCGCTCCTTCCTGGTC	PCR
3Flag-2A-cKit-R	CAGGCGCCGCGAGCGCCTCTggggccggggttggactccacgtcgccggccagcttcagcagggcgtagttggtgcactggccggagccgcgcttggcgcgCTTGTCATCGTCATCCTTGTAG	PCR
c-Kit-PT-F1	CTGACGGTACCacaagtctcagcaggagcttggctgg	PCR
c-Kit-PT-R1	CTGACctcgagcgcggtggctgcgctagactctgagctc	PCR
c-Kit-EB1m-R1	ATAATActgcccgcgctttgtgaagc	PCR
c-Kit-EB1m-F1	TATTATcgtggccagccagccgcctg	PCR
c-Kit-EB2m-R2	ATAATAgCAGGTGctccctagacaat	PCR
c-Kit-EB2m-F2	TATTATgctggcccgtacctaatgcgc	PCR
c-Kit-EB3m-R3	ATAATActccctagacaataaaggac	PCR
c-Kit-EB3m-F3	TATTATcCAGGTGgctggcccgtacc	PCR
c-Kit-EB4m-R4	ATAATActgcgaaacctgtaagaatac	PCR
c-Kit-EB4m-F4	TATTATgagaaactgagcatgaaaaattac	PCR
c-Kit-shRNA #1-S1	ccggATCATAAGGAAGTTGCGTCGGctcgagCCGACGCAACTTCCTTATGATttttg	PCR
c-Kit-shRNA #1-AS1	aattcaaaaaATCATAAGGAAGTTGCGTCGGctcgagCCGACGCAACTTCCTTATGAT	PCR
c-Kit-shRNA #2-S2	ccggAATCCTTCCCTTTGTTAGCCGctcgagaCGGCTAACAAAGGGAAGGATTttttg	PCR
c-Kit-shRNA #2-AS2	aattcaaaaaAATCCTTCCCTTTGTTAGCCGctcgagaCGGCTAACAAAGGGAAGGATT	PCR
c-Kit-shRNA #3-S3	ccggATCGCAAATCTTTGTGATCCGctcgagaCGGATCACAAAGATTTGCGATttttg	PCR
c-Kit-shRNA #3-AS3	aattcaaaaaATCGCAAATCTTTGTGATCCGctcgagaCGGATCACAAAGATTTGCGAT	PCR
Scramble shRNA control-S	ccggCCTAAGGTTAAGTCGCCCTCGCTCGAGCGAGGGCGACTTAACCTTAGGttttttg	PCR
Scramble shRNA control-AS	aattcaaaaaCCTAAGGTTAAGTCGCCCTCGCTCGAGCGAGGGCGACTTAACCTTAGGTT	PCR
Slug-102qF	GCGAACTGGACACACACACAGTTAT	qPCR
Slug-qR305	GCTGCCGACGATGTCCATACAGTAAT	qPCR
c-Kit-qF	GCGTTCCTCGCCTCCAAGAATTGTATT	qPCR
c-Kit-qR	TCACTTTCAAATGTGTACACGCAGCTG	qPCR
HPRT-qF	CTCATGGACTGATTATGGACAGGAC	qPCR
HPRT-qR	GCAGGTCAGCAAAGAACTTATAGCC	PCR
GADPH-qF	CCGCCTGGAGAAACCTGCCAAG	PCR
GADPH-qR	TGCTGTAGCCGTATTCATTGTCATACCAGG	PCR
c-Myc-qF	CACCACCAGCAGCGACTCTGAAGAA	PCR
c-Myc-qR	GAGGTGCCACGTCTCCACTCACCAG	PCR
c-Kit-PT-F	gaccggtggttgtcctttattgtctag	ChIP PCR
c-Kit-PT-F	tccatcggtggtccttcagtccaggcg	ChIP PCR
HPRT-gF	AGGAGTCCTGTTGATGTTGCCAGT	ChIP PCR
HPRT-gR	GGAAATCGAGAGCTTCAGACTCGT	ChIP PCR
FoxM1-F1	CTGATagatctATGAGAACCAGCCCCCGCCGGC	PCR
3xFlag-FoxM1-R1	CTGATctcgagctacttgtcatcgtcatccttgtagtcgatgtcatgatctttataatcaccgtcatggtctttgtagtcagaaccAGGGATGAACTGAGACCAGTTGATG	PCR
c-Myc-F11	CTGATagatctATGCCCCTCAACGTGAACTTCACC	PCR
3xFlag-Myc-R11	CTGATctcgagctacttgtcatcgtcatccttgtagtcgatgtcatgatctttataatcaccgtcatggtctttgtagtcagaaccTGCACCAGAGTTTCGAAGCTGTTC	PCR

mSlugPR-F-1.4	TAGCCTCGAGagaggaatcattgaaattaacccaggaagtctgcg	PCR
mSlugPR-R1	GCATCTTCCATGGTGGCTGCGGGCGGGCGC	PCR
Slug-F1	cggcagacactaagaattgtcagtagag	qPCR
Slug-R1	ccaggaactggaagagtgtaaaga	qPCR
Slug-F2	gaaatcagtgactattgtaaagagaaagagg	qPCR
Slug-F3	tccctgtttcaaattcactggttct	qPCR
Slug-R3	agaaatcttgccccttccacctaatttc	qPCR
Slug-F4	cctagacctgctgtggcagctg	qPCR
Slug-R4	cttggcttccagatgtgggcagt	qPCR
Slug-F5	tcttccagcacctgttacga	qPCR
Slug-R5	agccggtcacttcacttgcat	qPCR
Slug-F6	agactccagctctgatccatactca	qPCR
Slug-R6	atgagaaaacgggcgtgtgagc	qPCR
FoxM1-qF	CCAAGCCAGGCTGGAAGAACTC	qPCR
FoxM1-qR	ACCCTGGTTCCAGTGGCTTAAAC	qPCR

Table S4. List of c-Myc-shRNAs

shNRA	Supplier	Catalog number
c-Myc-shRNA #1	Sigma	TRCN0000234924
c-Myc-shRNA #2	Sigma	TRCN0000234925
c-Myc-shRNA #3	Sigma	TRCN0000234926
c-Myc-shRNA #4	Sigma	TRCN0000054853
c-Myc-shRNA #5	Sigma	TRCN0000054854

Table S5. List of antibodies

Antibodies	Supplier	Catalog number
Mouse hematopoietic lineage biotin panel	eBioscience	88-7774-75
APC anti-mouse Ly-6A/E(Sca-1)	Biolegend	108112
PE/Cy7 anti-mouse CD117(c-Kit)	Biolegend	105814
APC anti-mouse CD150 (SLAM)	Biolegend	115910
PE anti-mouse CD48	Biolegend	103406
FITC Streptavidin	Biolegend	405202
PE anti-mouse CD45.1	Biolegend	110708
Alexa Fluor® 647 anti-mouse CD45.2	Biolegend	109818
Pacific Blue™ anti-mouse/human CD11b	Biolegend	101223
PE/Cy7 anti-mouse CD3e	Biolegend	100319
Alexa Fluor® 700 anti-mouse/human CD45R/B220	Biolegend	103231
PerCP/Cy5.5 anti-mouse Ly-6G/Ly-6C (Gr-1)	Biolegend	108427
Anti-Flag Tag Monoclonal antibody	Thermo Scientific	MA1-91878