[F] Supplemental Text

Legends for Figure S1-S7, Table S1-S3

Figure S1. A. Post-sort analysis of Ikaros-GFP defined populations used for global gene array analysis. One of three representative samples is shown. A minimum purity of 95% was required for these studies. B. The HSC and MPP composition of the LSK GFP$^{\text{neg-lo}}$ sorted population used in our studies is further delineated by expression of Flt3. The LSK GFP$^{\text{neg-lo}}$Flt3$^{\text{neg}}$ (defined by a no-stain control for Flt3) consists of LT-HSC and ST-HSC (A) and is ~ 78% of the whole LSK GFP$^{\text{neg-lo}}$ population. The LSK GFP$^{\text{neg-lo}}$Flt3$^{\text{lo}}$ consists of MPP (B) and represent ~22% of the whole LSK GFP$^{\text{neg-lo}}$ population. This is one representative of several independent analyses on the HSC-enriched LSK subset. The LSK GFP^{+} Flt3$^{\text{lo-high}}$ is the LMPP population (C) as described in Yoshida et al., NI 2006.

Figure S2. Real-time RT-PCR analysis for lineage-affiliated transcripts used in multiplex single-progenitor studies in Ikaros-GFP defined populations. Genes are indicated on each graph, and colors indicate the lineage affiliation of each gene: lymphoid-blue, myeloid-violet, erythroid-red, stem-orange.

Figure S3. Multiplex single-cell RT-PCR analysis of progenitor populations. (A) Examples of primary data generated from each progenitor type is shown (x: 10 cell sample, ø No RT control, * genomic transcript). Lineage-affiliation of transcripts used in this study is shown by the following color designation: lymphoid-blue, myeloid-violet, erythroid- red, stem-yellow. (B) The percent distribution for each lineage-affiliated transcript is shown for each progenitor population. The total number of cells used was;

HSC n=239, LMPP n=211, GMP n=120 and MEP n= 78. Progenitors were isolated from at least two independent sorts and used in 2-4 amplification experiments. Mean +/- SD on percent distribution for the experiments performed per progenitor population is shown.

Figure S4. (A) Comparison between two lineage depletion strategies with (i) or without (ii) anti-Mac-1 in the lineage depletion cocktail. Strategy (ii) leaves 2-4 X more cells in the GMP (LK GFP^{hi}) compartment. (B) IL-7Rα expression in various lineage negative (Lin^{-}) populations using strategy (i) for lineage depletion. GMP (LK GFP^{hi}) and LSK showed very low level of IL-7Rα expression. The significant IL-7Rα^{+} population detected within the Lin^{-}c-Kit^{lo}Sca-1^{lo} defines the CLP. Another major IL-7Rα^{+} population was detected within the c-Kit^{-}Sca-1^{hi} compartment.

Figure S5. (A) Clonal analysis of LMPP and GMP for combined T cell and myeloid differentiation potential. Single cells were co-cultured with OP9-DL1 for 18 days before FACS analysis for T cell (Thy.1.2, CD44, CD25) and Myeloid (Mac-1 and Gr-1) markers. The percentage of T cell and myeloid developmental potential exhibited by expanding LMPP and GMP clones is shown. Lineage output of two representative GMP clones with T/myeloid differentiation is shown. (B) The differentiation outcome of intrathymic placement of LMPP (n=25) and GMP (n=1000) is shown at 5 and 21 days post-injection.

Figure S6. Hierarchical clustering of up- and down-regulated genes in Ikaros-null HSC (A) and LMPP (B) across WT and KO progenitor populations (HSC, LMPP, GMP and

MEP). The lineage affiliation of deregulated transcripts is shown on the right side of each panel.

Figure S7. Multiplex single-cell gene expression analysis of Ikaros–null HSC. (A) Single progenitor analysis for lineage-affiliated transcripts was performed as described in Figure 2. Mutant HSC (n=181) generated from two independent sorts are shown. (B) The percentage of overall lineage transcript distribution as well as that of individual lineage-specific transcripts is provided for WT and mutant populations. Mean +/- SD on percent distribution for experiments performed per progenitor population is shown.

Table S1. Limiting dilution analysis of LMPP and GMP lymphoid and myeloid developmental potential. Data from four independent experiments is shown noting the stroma used for each assay. T cell potential was scored from OP9-DL1 culture supplemented with 10 ng/ml SCF, 10 ng/ml Flt3L, and 1 ng/ml IL-7. B and myeloid cell potential were simultaneously scored from OP9 stroma supplemented with 10 ng/ml SCF, 10 ng/ml Flt3L, and 10 ng/ml IL-7. Frequency and 95% confidence intervals for each individual sample were calculated using the WEHI limiting dilution analysis web interface. http://bioinf.wehi.edu.au/software/limdil/

Table S2. Limiting dilution analysis of wild-type and Ikaros–null HSC and LMPP cells. Data from at least two independent experiments is shown for each sample. Experiments and analysis were performed as in Table S1. Data from wild-type LMPP from

Experiment 2 was also used for Table S1 Experiment 2 as all experiments were performed simultaneously.

Table S3. Limiting dilution analysis of LMPPs transduced with Ikaros-targeted or scrambled shRNA expressing lentiviruses. Data from two independent experiments is shown. LMPPs were harvested and activated with SFEM supplemented with 50 ng/ml SCF, 50 ng/ml Flt3L, 20 ng/ml TPO, and 10 ng/ml IL-7 and cultured on retronectin coated tissue culture plates for 24 hours. Cells were then twice transduced with lentiviral supernatant and polybrene using a 2-hour spin-infection at approximately 2000g followed by a 10-hour culture before being washed and re-cultured in activation conditions for 12 hours. 60 hours after initiation of transduction, GFP positive cells were directly sorted into limiting dilution assays. Subsequent experiments and analysis were performed as with Table S1.

Table S4. The list of primers used for single cell multiplex RT-PCR and qPCR analysis of progenitors.

[F] Supplemental Figure 1

Figure S1

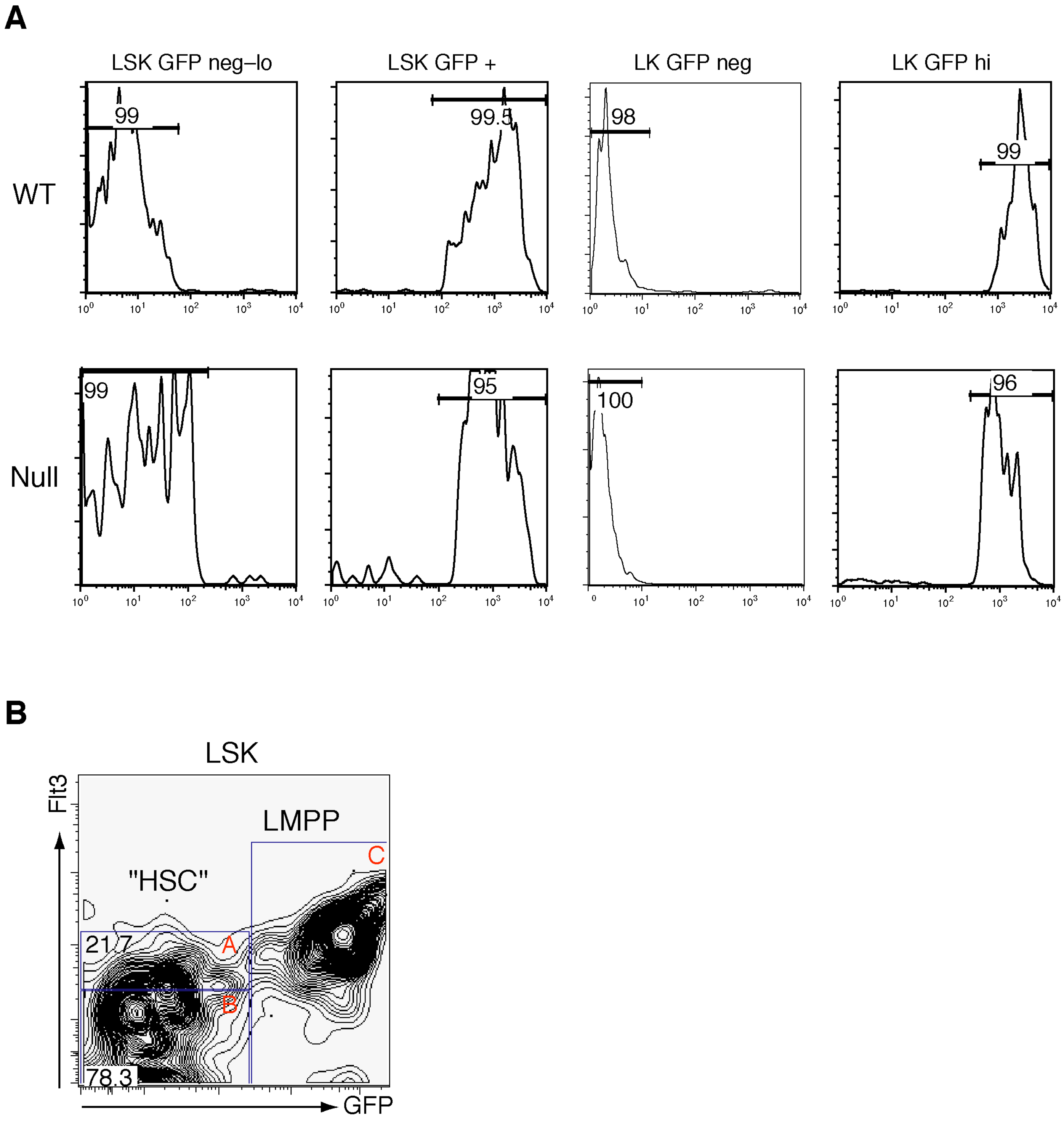


Figure S2

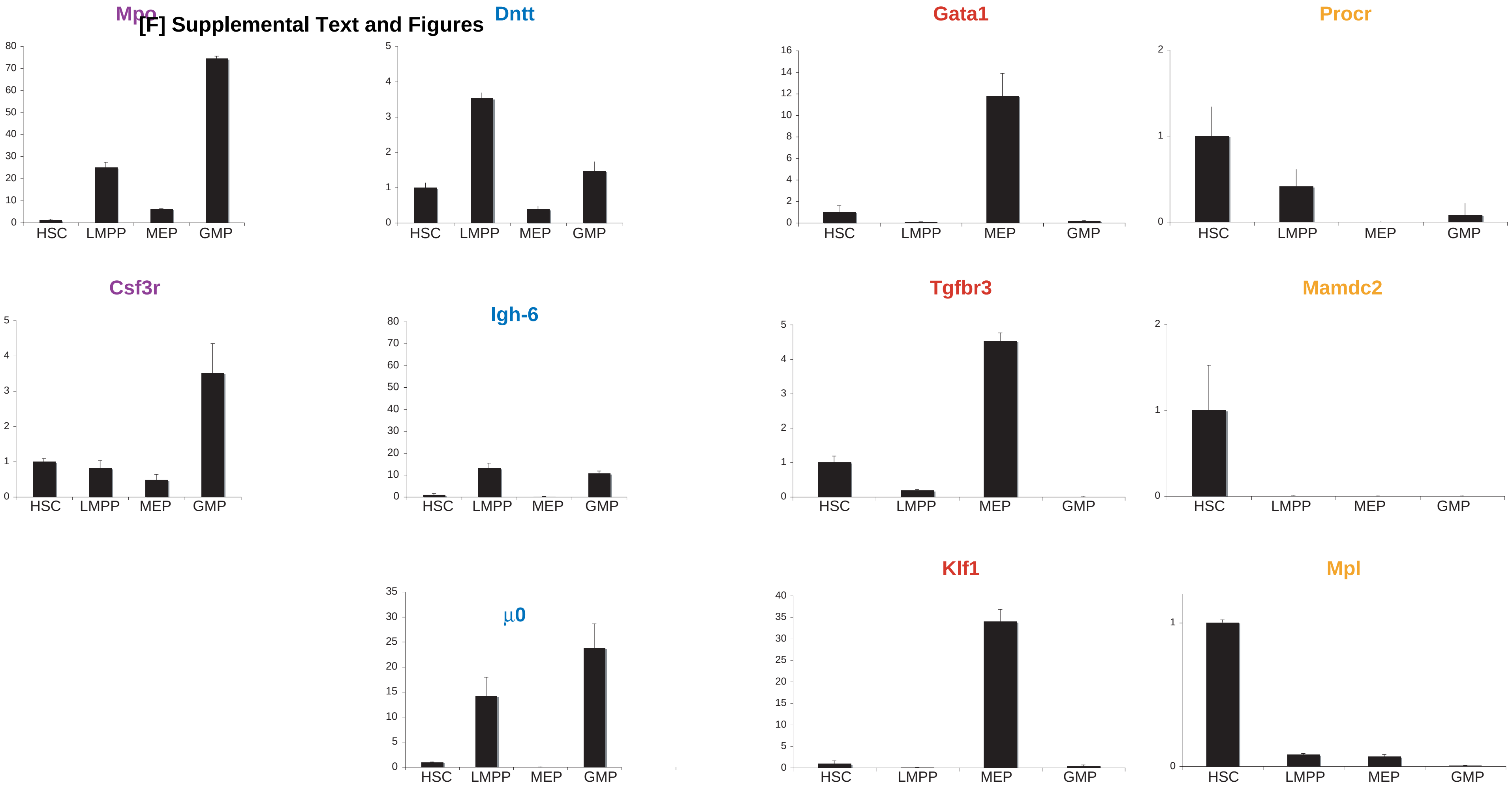

Mpo
0
10
20
30
40
50
60
70
80
HSC
LMPP
MEP
GMP
Dntt
0
1
2
3
4
5
HSC
LMPP
MEP
GMP
Gata1
0
2
4
6
8
10
12
14
16
HSC
LMPP
MEP
GMP
Procr
0
1
2
HSC
LMPP
MEP
GMP
Csf3r
0
1
2
3
4
5
HSC
LMPP
MEP
GMP
Igh-6
0
10
20
30
40
50
60
70
80
HSC
LMPP
MEP
GMP
Tgfbr3
0
1
2
3
4
5
HSC
LMPP
MEP
GMP
Mamdc2
0
1
2
HSC
LMPP
MEP
GMP
μ0
0
5
10
15
20
25
30
35
HSC
LMPP
MEP
GMP
Klf1
0
5
10
15
20
25
30
35
40
HSC
LMPP
MEP
GMP
Mpl
0
1
HSC
LMPP
MEP
GMP

Figure S3

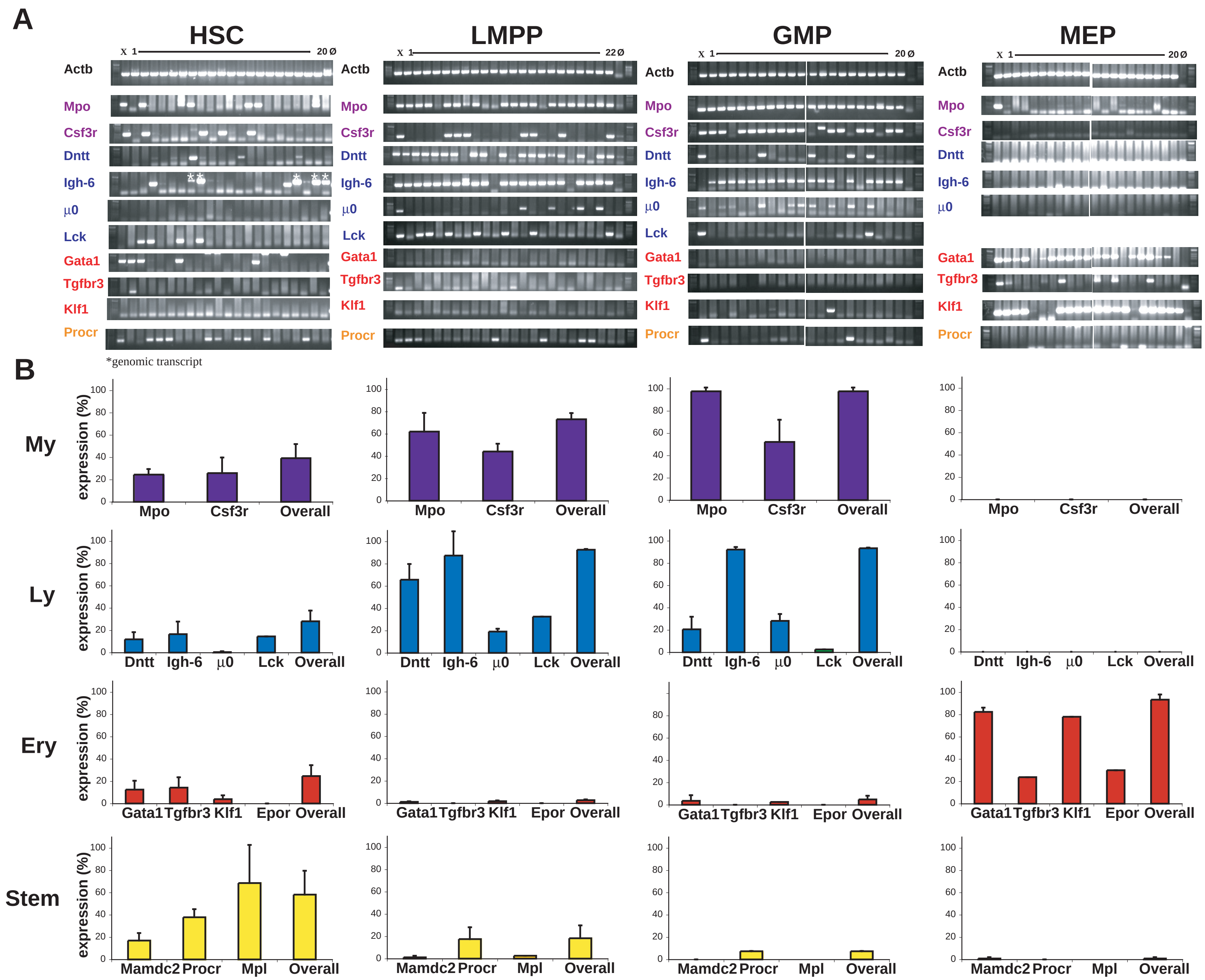

A
HSC
LMPP
GMP
MEP
x 1 20 Ø
x 1 22 Ø
x 1 20 Ø
x 1 20 Ø
Actb
Mpo
Csf3r
Dntt
Igh-6
μ0
Lck
Gata1
Tgfbr3
Klf1
Procr
* *
* * *
*genomic transcript
B
My
Ly
Ery
Stem
expression (%)
0
20
40
60
80
100
Mpo
Csf3r
Overall
Dntt
Igh-6
μ0
Lck
Overall
Gata1
Tgfbr3
Klf1
Epor
Overall
Mamdc2
Procr
Mpl
Overall

Figure S4

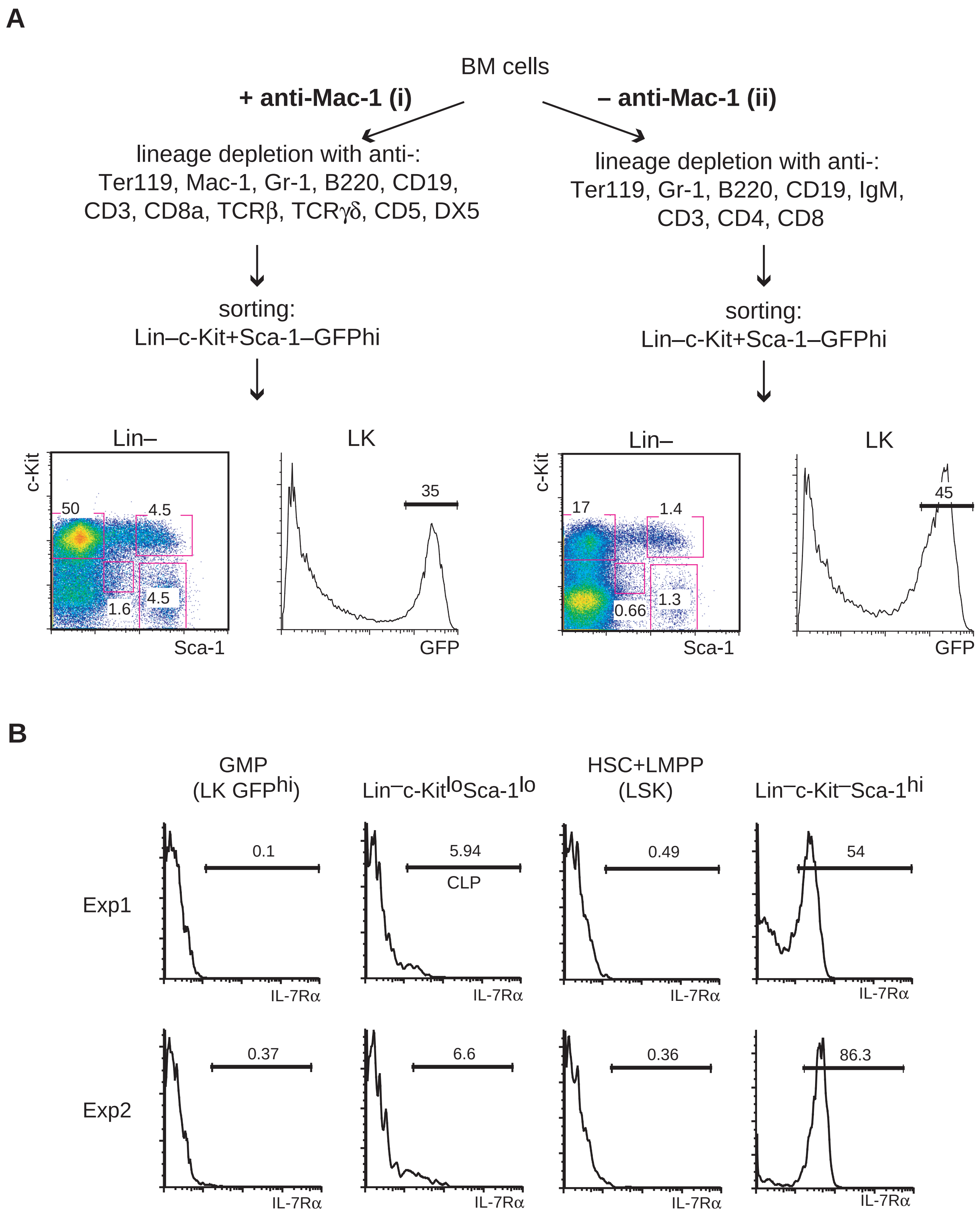

A
BM cells
+ anti-Mac-1 (i)
– anti-Mac-1 (ii)
lineage depletion with anti-:
Ter119, Mac-1, Gr-1, B220, CD19,
CD3, CD8a, TCRβ, TCRγδ, CD5, DX5
lineage depletion with anti-:
Ter119, Gr-1, B220, CD19, IgM,
CD3, CD4, CD8
sorting:
Lin–c-Kit+Sca-1–GFPhi
sorting:
Lin–c-Kit+Sca-1–GFPhi
Lin–
c-Kit
50
4.5
1.6
4.5
Sca-1
LK
35
GFP
Lin–
c-Kit
17
1.4
0.66
1.3
Sca-1
LK
45
GFP
B
GMP
(LK GFPhi)
Lin–c-KitloSca-1lo
HSC+LMPP
(LSK)
Lin–c-Kit–Sca-1hi
Exp1
0.1
5.94
CLP
0.49
54
IL-7Rα
Exp2
0.37
6.6
0.36
86.3
IL-7Rα

Figure S5

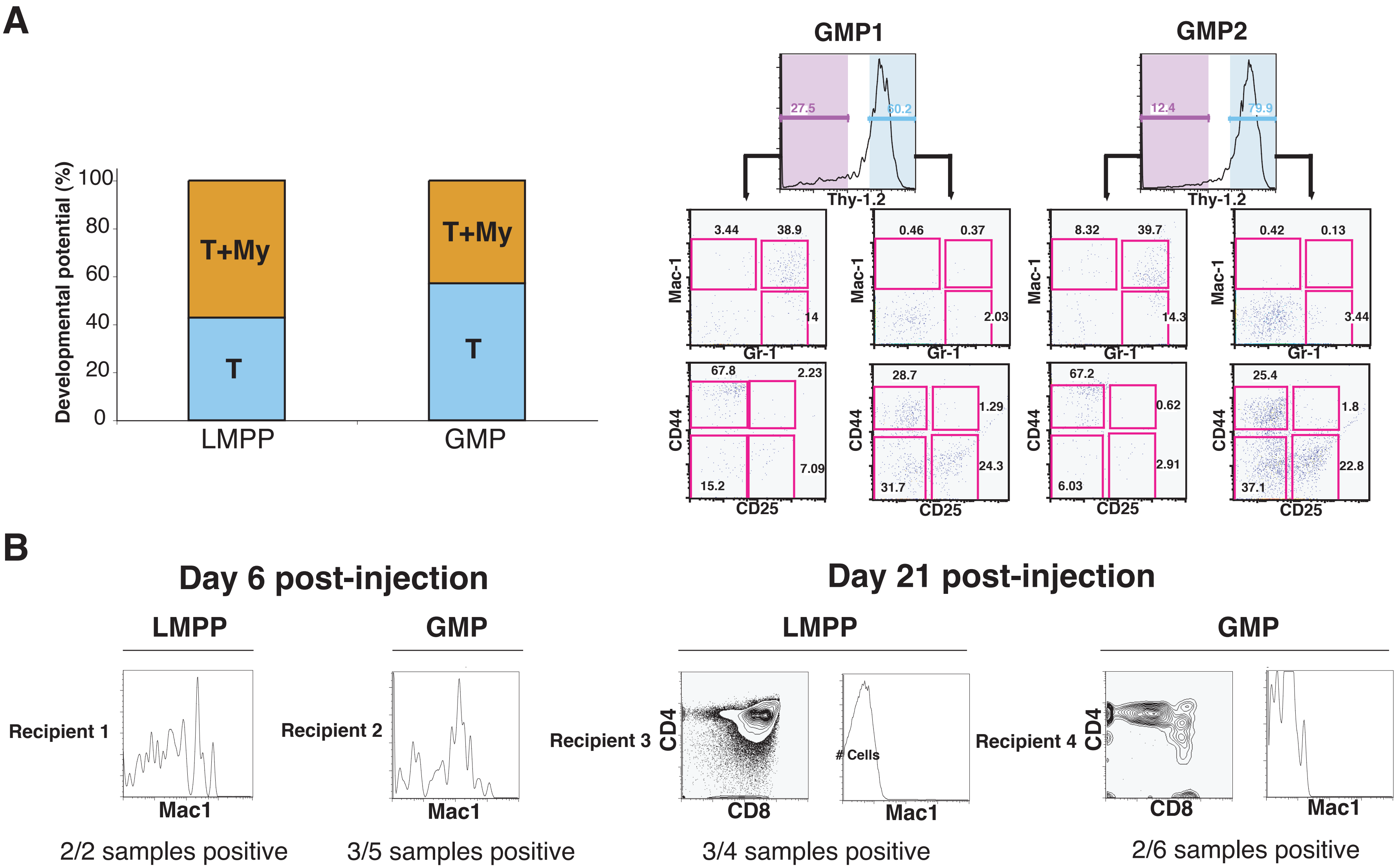

A
Developmental potential (%)
100
80
60
40
20
0
T+My
T
T+My
T
LMPP
GMP
GMP1
GMP2
27.5
60.2
12.4
79.9
Thy-1.2
Thy-1.2
Mac-1
Gr-1
3.44
38.9
14
0.46
0.37
2.03
8.32
39.7
14.3
0.42
0.13
3.44
CD44
CD25
67.8
2.23
7.09
15.2
28.7
1.29
24.3
31.7
67.2
0.62
2.91
6.03
25.4
1.8
22.8
37.1
B
Day 6 post-injection
Day 21 post-injection
LMPP
GMP
LMPP
GMP
Recipient 1
Recipient 2
Recipient 3
Recipient 4
Mac1
Mac1
CD4
CD8
Cells
Mac1
CD4
CD8
Mac1
2/2 samples positive
3/5 samples positive
3/4 samples positive
2/6 samples positive

Figure S6

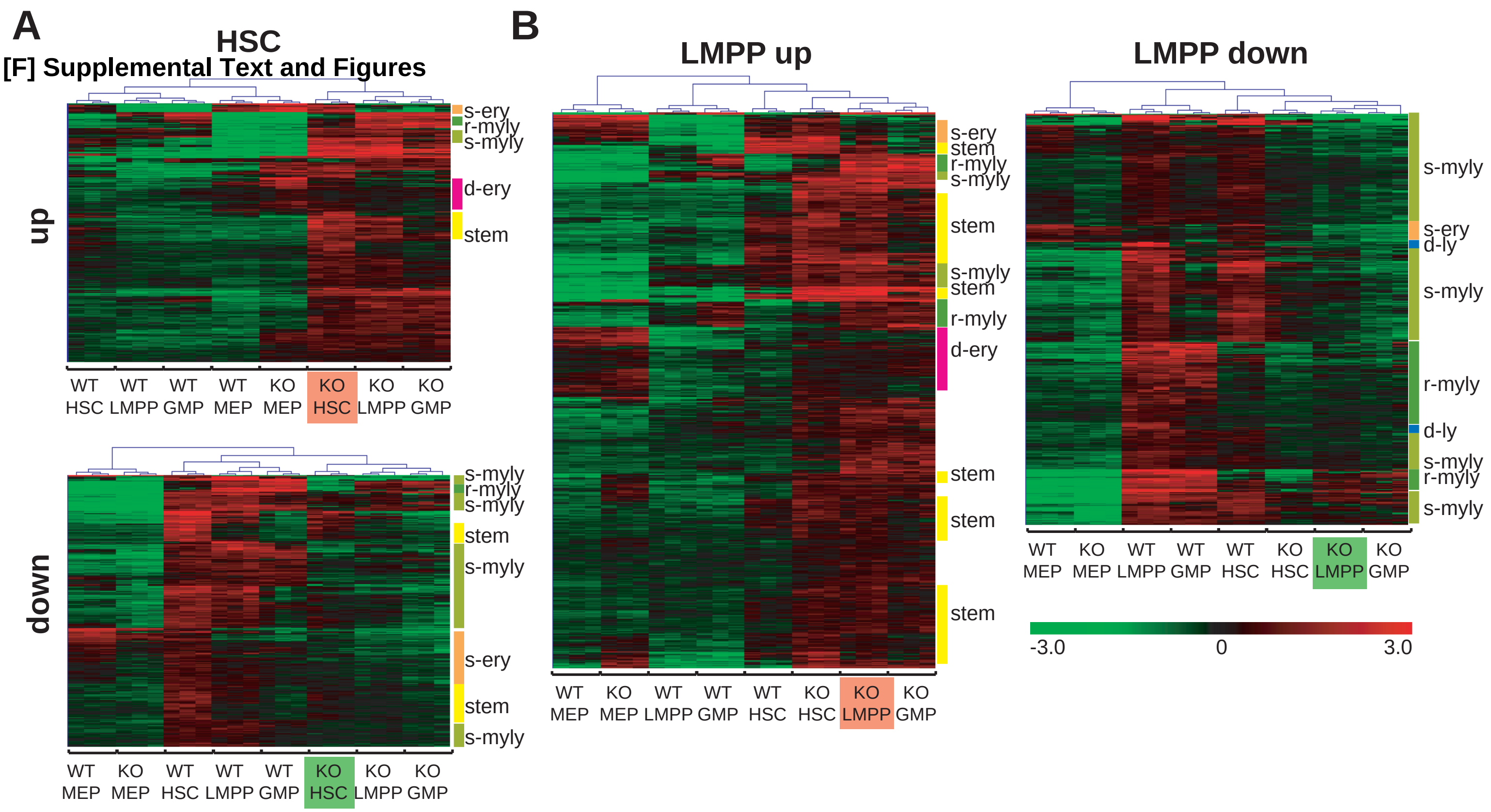
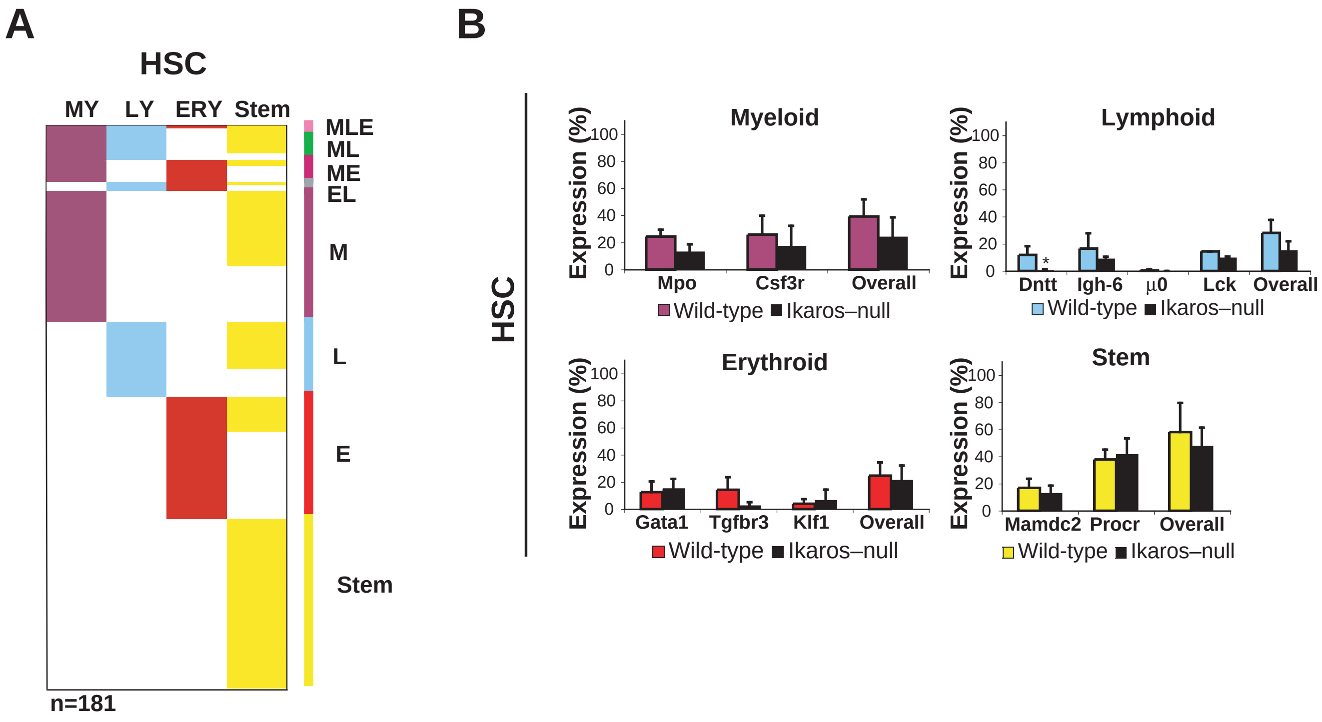

A
HSC
up
s-ery
r-myly
s-myly
d-ery
stem
WT HSC
WT LMPP
WT GMP
WT MEP
KO MEP
KO HSC
KO LMPP
KO GMP
down
s-myly
r-myly
s-myly
stem
s-myly
s-ery
stem
s-myly
WT MEP
KO MEP
WT HSC
WT LMPP
WT GMP
KO HSC
KO LMPP
KO GMP
B
LMPP up
s-ery
stem
r-myly
s-myly
stem
s-myly
stem
r-myly
d-ery
stem
stem
stem
WT MEP
KO MEP
WT LMPP
WT GMP
WT HSC
KO HSC
KO LMPP
KO GMP
LMPP down
s-myly
s-ery
d-ly
s-myly
r-myly
d-ly
s-myly
r-myly
s-myly
WT MEP
KO MEP
WT LMPP
WT GMP
WT HSC
KO HSC
KO LMPP
KO GMP
-3.0
0
3.0

Figure S7


A
HSC
MY
LY
ERY
Stem
MLE
ML
ME
EL
M
L
E
Stem
n=181
B
HSC
Myeloid
Expression (%)
100
80
60
40
20
0
Mpo
Csf3r
Overall
Wild-type
Ikaros–null
Lymphoid
Expression (%)
Dntt
*
Igh-6
μ0
Lck
Overall
Wild-type
Ikaros–null
Erythroid
Expression (%)
Gata1
Tgfbr3
Klf1
Overall
Wild-type
Ikaros–null
Stem
Expression (%)
Mamdc2
Procr
Overall
Wild-type
Ikaros–null

[F] Supplemental Text and Figures

Table S1

Experiment 1

OP9-DL1

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 4.25	1 in 2.91	1 in 2.07
5	18/20			
1	6/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
100	10/10	1 in 25.10	1 in 14.81	1 in 8.82
20	7/10			
4	6/20			
1	1/20			

OP9-B

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 4.77	1 in 2.99	1 in 1.98
5	8/10			
1	1/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
500	8/10	1 in 642.55	1 in 347.64	1 in 188.19
100	3/10			
20	0/20			
4	0/20			

OP9-Myeloid

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 7.04	1 in 4.20	1 in 2.60
5	6/10			
1	7/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
500	10/10	1 in 59.74	1 in 36.52	1 in 22.41
100	10/10			
20	8/20			
4	1/20			

Experiment2

OP9-DL1

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 12.47	1 in 7.17	1 in 4.23
5	6/10			
1	1/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
100	10/10	1 in 36.53	1 in 21.00	1 in 12.16
20	7/10			
4	3/20			
1	0/20			

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 18.62	1 in 10.63	1 in 6.17
5	2/10			
1	2/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
500	10/10	1 in 292.88	1 in 165.87	1 in 94.03
100	4/10			
20	1/20			
4	1/20			

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	10/10	1 in 4.39	1 in 2.79	1 in 1.87
5	9/10			
1	7/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
500	10/10	1 in 59.74	1 in 36.52	1 in 22.41
100	10/10			
20	8/20			
4	1/20			

Experiment 3

OP9-DL1

95 percent Confidence Intervals

LMPP

Cells/well	Responses	Lower	Estimate	Upper
25	5/5	1 in 3.32	1 in 2.19	1 in 1.55
5	10/10			
1	8/20			

GMP

Cells/well	Responses	Lower	Estimate	Upper
100	9/10	1 in 71.05	1 in 40.41	1 in 23.08
20	3/10			
4	4/20			
1	0/20			

Experiment 4

95 percent Confidence Intervals

GMP

Cells/well	Responses	Lower	Estimate	Higher
200	8/20	1 in 628.63	1 in 353.6	1 in 198.90
50	3/20			
10	1/20			

95 percent Confidence Intervals

GMP

Cells/well	Responses	Lower	Estimate	Higher
200	19/20	1 in 84.78	1 in 55.65	1 in 36.53
50	11/20			
10	6/20			

Table S2

Experiment 1

OP9-DL1

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
HSC	25	10/10	1 in 17.36	1 in 10.69	1 in 6.67
	5	5/20			
	1	3/20			

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
LMPP	25	10/10	1 in 2.24	1 in 1.6	1 in 1.25
	5	20/20			
	1	12/20			

OP9-DL1

Ikaros–null	Cells/well	Responses	Lower	Estimate	Higher
HSC	25	5/10	1 in 48.5	1 in 26.34	1 in 14.41
	5	5/20			
	1	1/20			

Ikaros–null	Cells/well	Responses	Lower	Estimate	Higher
LMPP	25	8/10	1 in 28.85	1 in 16.92	1 in in 10.01
	5	6/20			
	1	0/20			

Experiment 2

OP9-DL1

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
LMPP	25	10/10	1 in 4.25	1 in 2.91	1 in 2.07
	5	18/20			
	1	6/20			

OP9-DL1

Ikaros–null	Cells/well	Responses	Lower	Estimate	Higher
HSC	25	4/10	1 in 79.21	1 in 39.07	1 in 19.40
	5	2/20			
	1	2/20			

Ikaros–null	Cells/well	Responses	Lower	Estimate	Higher
LMPP	25	6/10	1 in 40.47	1 in 22.64	1 in 12.77
	5	6/20			
	1	0/20			

Experiment 3

OP9-DL1

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
HSC	30	7/10	1 in 42.71	1 in 23.85	1 in 13.42
	10	4/10			
	3	1/10			

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
LMPP	30	10/10	1 in 4.18	1 in 2.35	1 in 1.48
	10	10/10			
	3	8/10			

Experiment 4

OP9-DL1

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
HSC	10	2/10	1 in 111.48	1 in 42.01	1 in 16.03
	5	1/10			
	2	1/10			
	1	0/10			

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
LMPP	10	10/10	1 in 7.58	1 in 4.95	1 in 3.31
	5	7/10			
	2	3/10			
	1	1/10			

Experiment 5

OP9-DL1

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
HSC	25	9/10	1 in 21.92	1 in 12.62	1 in 7.37
	5	4/10			
	2	1/10			
	1	0/10			

Wild Type	Cells/well	Responses	Lower	Estimate	Higher
LMPP	25	10/10	1 in 2.69	1 in 1.86	1 in 1.38
	5	10/10			
	2	7/10			
	1	6/10			

[F] Supplemental Text and Figures

Table S3

Experiment 1

OP9 B cell

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	50	5/20	1 in 115.78	1 in 67.66	1 in 39.54
	10	1/20			
	2	1/20			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	50	13/20	1 in 20.17	1 in 12.94	1 in 8.30
	10	9/20			
	2	6/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	50	19/20	1 in 7.90	1 in 5.05	1 in 3.22
	10	12/20			
	2	6/20			

OP9 Myeloid

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	50	20/20	1 in 4.05	1 in 2.5	1 in 1.54
	10	20/20			
	2	10/10			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	50	20/20	1 in 6.5	1 in 4.14	1 in 2.64
	10	20/20			
	2	7/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	50	4/20	1 in 115.81	1 in 67.67	1 in 39.54
	10	8/20			
	2	4/20			

OP9-DL1

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	50	20/20	1 in 14.46	1 in 9.35	1 in 6.12
	10	12/20			
	2	6/20			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	50	19/19	1 in 16.38	1 in 10.57	1 in 6.90
	10	14/20			
	2	1/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	50	20/20	1 in 5.81	1 in 3.87	1 in 2.65
	10	19/20			
	2	10/20			

Experiment 2

OP9 B cell

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	25	3/10	1 in 80.16	1 in 39.22	1 in 19.32
	5	5/20			
	1	0/20			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	25	6/10	1 in 30.7	1 in 17.86	1 in 10.49
	5	6/20			
	1	3/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	25	10/10	1 in 10.86	1 in 6.89	1 in 4.45
	5	11/20			
	1	2/20			

OP9 Myeloid

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	25	10/10	1 in 7.15	1 in 4.63	1 in 3.08
	5	14/20			
	1	3/20			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	25	10/10	1 in 9.51	1 in 6.08	1 in 3.97
	5	11/20			
	1	4/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	25	0/10	1 in 251.28	1 in 90.98	1 in 33.14
	5	3/20			
	1	1/20			

OP9-DL1

Ikaros shRNA 1	Cells/well	Responses	Lower	Estimate	Higher
	25	9/9	1 in 9.67	1 in 6	1 in 3.81
	5	10/17			
	1	3/19			

Ikaros shRNA 2	Cells/well	Responses	Lower	Estimate	Higher
	25	8/10	1 in 29.18	1 in 17.09	1 in 10.10
	5	5/20			
	1	1/20			

Control shRNA	Cells/well	Responses	Lower	Estimate	Higher
	25	10/10	1 in 5.15	1 in 3.45	1 in 2.40
	5	16/19			
	1	5/20			

[F] Supplemental Table 4

SC-PCR primers	**Sequence**	**References**
Actb Flanking S	GCTACAGCTTCACCACCACA	
Actb Flanking A	CTTCTGCATCCTGTCAGCAA	
Actb Nested S	AATCGTGCGTGACATCAAAGAG	
Actb Nested A	ACGGATGTCAACGTCACACTTC	
Lymphoid		
Igh-6 Flanking S	CGTCCAAGAATTGGATGTGA	
Igh-6 Flanking A	AGGGACACGAGCTCATTCAG	
Igh-6 Nested S	GTTCAGATGCCAGCCTCACA	
Igh-6 Nested A	TGGGGTGGGAAGGTGTTCA	
Lck Flanking S	TGCAAGATTGCAGACTTTGG	
Lck Flanking A	CCACACAGATATGGCACAGG	
Lck Nested S	CAAGTCAGACGTGTGGTCCTTC	
Lck Nested A	CACAGCATCATGAGGTGGTACA	
Dntt Flanking S	CTGTGTTTGGTGTGGGACTG	
Dntt Flanking A	CTGGGCTGCTTGAACTTTTC	
Dntt Nested S	AGCTGTGTGAACAGGCCAGAAG	
Dntt Nested A	CCCTGCTGCTTCCAAAAGTCTG	
Sterile IgH (μ0)-1	GCTAGCCTGAAAGATTACC	Mansson **Immunity** 26:407-
Sterile IgH (μ0)-2	TGAGTTTCTGAGGCTTGG	Mansson **Immunity** 26:407-
Sterild IgH (μ0)-3	AGTAGCACAGTCTCTGTTCTGC	Mansson **Immunity** 26:407-
Sterile IgH (μ0)-4	AAGGACTGACTCTCTGAGG	Mansson **Immunity** 26:407-
Myeloid		
Mpo Flanking S	ATCAGCTGACCAAGGACCAG	
Mpo Flanking A	TGGAAGCGTGTATTGATAGCC	
Mpo Nested S	CTTCTTCACTGGCCTCAACTGC	
Mpo Nested A	GCGAATGGTGATGTTGTTCCTG	
Csf3r-1	ACAGGAGTGTGAACTTCGCT	Mansson **Immunity** 26:407-
Csf3r-2	TACCAGCCACAGCTCAAAGG	Mansson **Immunity** 26:407-
Csf3r-3	ACGTGTCCAGTCTGATGGTG	Mansson **Immunity** 26:407-
Csf3r-4	TTGCTTCTTCTGACACCACG	Mansson **Immunity** 26:407-
Erythroid		
Tgfbr3 Flanking S	CCCCAGATGGTGTGGTTTAC	
Tgfbr3 Flanking A	TCGGACAGATGTTCTCGATG	
Tgfbr3 Nested S	GCTCGATGGAAATGCTACCTTC	
Tgfbr3 Nested A	CAAATCCCAGATCTTGGTCAGC	
Klf1 Flanking S	ATTGTCTGGGACCTGGGACT	
Klf1 Flanking A	ACGCTTCATGTGCAGAGCTA	
Klf1 Nested S	GGCGAACTTTGGCACCTAAGAG	
Klf1 Nested A	GTCCAGTGTGCTTCCGGTAGTG	
Gata1-1	CCAGTTTGTGGATTCTGC	Mansson **Immunity** 26:407-
Gata1-2	GTCCTCACCATCAGATTCC	Mansson **Immunity** 26:407-
Gata1-3	AACGTGTTGTTGCTCTTCC	Mansson **Immunity** 26:407-
Gata1-4	AAGAATAGGCTGCTGAGC	Mansson **Immunity** 26:407-
Stem		
Mamdc2 Flanking S	GCAGTACTGTGTGCGCTTTC	
Mamdc2 Flanking A	CTCCCTTGGGTCCTGTGTAG	
Mamdc2 Nested S	GCAAGCGGAAATCAGTTTCAAG	
Mamdc2 Nested A	ATTCTCCAGGTGGAGGTGGAAG	
Procr Flanking S	AAAACGTCACCATCCTCCAG	
Procr Flanking A	TGGTTCTCCAGGAACTCCAC	
Procr Nested S	GCCTGGTGAAGCTGGTATATCG	

Procr Nested A	TCGAAGAAGACATGGGGTTCAG	
Mpl-1	CGGGTGCTGTTTGTGGATAG	Mansson **Immunity** 26:407-
Mpl-2	TGCTCTCCACAGAAACCTGC	Mansson **Immunity** 26:407-
Mpl-3	AGTCACAGGGAAGGACCAGG	Mansson **Immunity** 26:407-
Mpl-4	GCGGTTCCTCCTCTTCACAT	Mansson **Immunity** 26:407-
Realtime Primers		
Actb S	CGTGAAAAGATGACCCAGATC	
Actb A	CACAGCCTGGATGGCTACGT	
Ikaros S	CAATGTCGCCAAACGTAAGA	
Ikaros A	GTTGATGGCATTGTTGATGG	
Dntt S	GAGGCGGTTGTGACATTTCT	
Dntt A	GCTGCTGCTCTTCATCCTCT	
Igh-6 S	TCTGCCTTCACCACAGAAGA	
Igh-6 A	ACACAGCAGGTGGATGTTTG	
μ0 (Sterile IgH)-S	CCTAAGGCAGGATGTGGAGA	
μ0 (Sterile IgH)-A	AGACGAGGGGGAAGACATTT	
Mpo S	CCTTCTTCACTGGCCTCAAC	
Mpo A	GGTTCTTGATTCGAGGGTCA	
Klf1 S	CAAGAGCTCGCACCTCAAG	
Klf1 A	GAAGGGACGATGTCCAGTGT	
Mamdc2 S	TACAGCTGCAGGAGGAGACA	
Mamdc2 A	TCCTGATGACTGTTCAGTTGTATCT	
Mpl S	CAGACCTACACCGGGTCCTA	
Mpl A	GCTGGGTTCCACTTCTTCAC	
Taqman Primer Sets		
Gata1	Mm00484678_m1	
Procr	Mm00440992_m1	
Tgfbr3	Mm03024063_m1	

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