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**Supplemental Figure legends**

**Figure S1. Unstained samples of (a) untransduced and (b) transduced cells, for flow cytometry experiments described in Figures 2 and 3.**

**Figure S2. In vivo dimerization of MEP results in higher short term engraftment.** NSG mice were transplanted with transduced MEP and administered CID or control vehicle from day -1 to day 14. Table shows the maximum bioluminescence for each mouse (photons/ second). Flow cytometry plots for bone marrow engraftment of human erythroid (glycophorin A+) cell engraftment are depicted (2 representative mice).

**Figure S3. F36VMpl transduced myelo-erythroid progenitors cultured with CID give rise to megakaryocytic cells, neutrophils and monocytes (in addition to erythroid cells).** Megakaryocyte (CD41a+GlyA-) cell counts of cultures (+/- CID) generated from transduced (a) CMP or (**b**) MEP. (one representative experiment of four shown, $p<0.05$). (**c**) Morphology of cells from day 35 of CID stimulated cultures of transduced CMP (Giemsa-Wright staining, 10x magnification).


**Figure S4. Functional analysis of in vitro generated cells based on CD34 expression levels.** Transduced CD34+ cells were cultured with CID. (**a**) Three populations of GFP+ cells were seen on day 7 of culture: CD34 negative, CD34 dim and CD34 bright. (**b**) CFU output from each GFP+ population shown in (**a), isolated at day 7 of CID culture**.

**Figure S5. The erythropoietic effect of F36VMpl dimerization is not synergistic with that of erythropoietin.** Transduced CD34+ cells were cultured in serum-free medium with CID or erythropoietin (Epo) or both for 7 days. Flow cytometry plots show generation of erythroid (glycophorin A+) cells.

**Figure S6. Functional network analysis of genes differentially expressed in Thrombopoietin and Erythropoietin treated cells.** Transduced CD34+ cells were cultured in the presence of CID (see figure 7), (a) Thrombopoietin, (b) Erythropoietin or Control (no growth factors or CID). CD34+GFP+ cells were then sorted at day 7 and subjected to microarray. Shown is Ingenuity Pathway Analysis of hematopoietic functional networks showing genes significantly changed (red up- and green down-regulated) compared with Control arm ($p<0.05$).

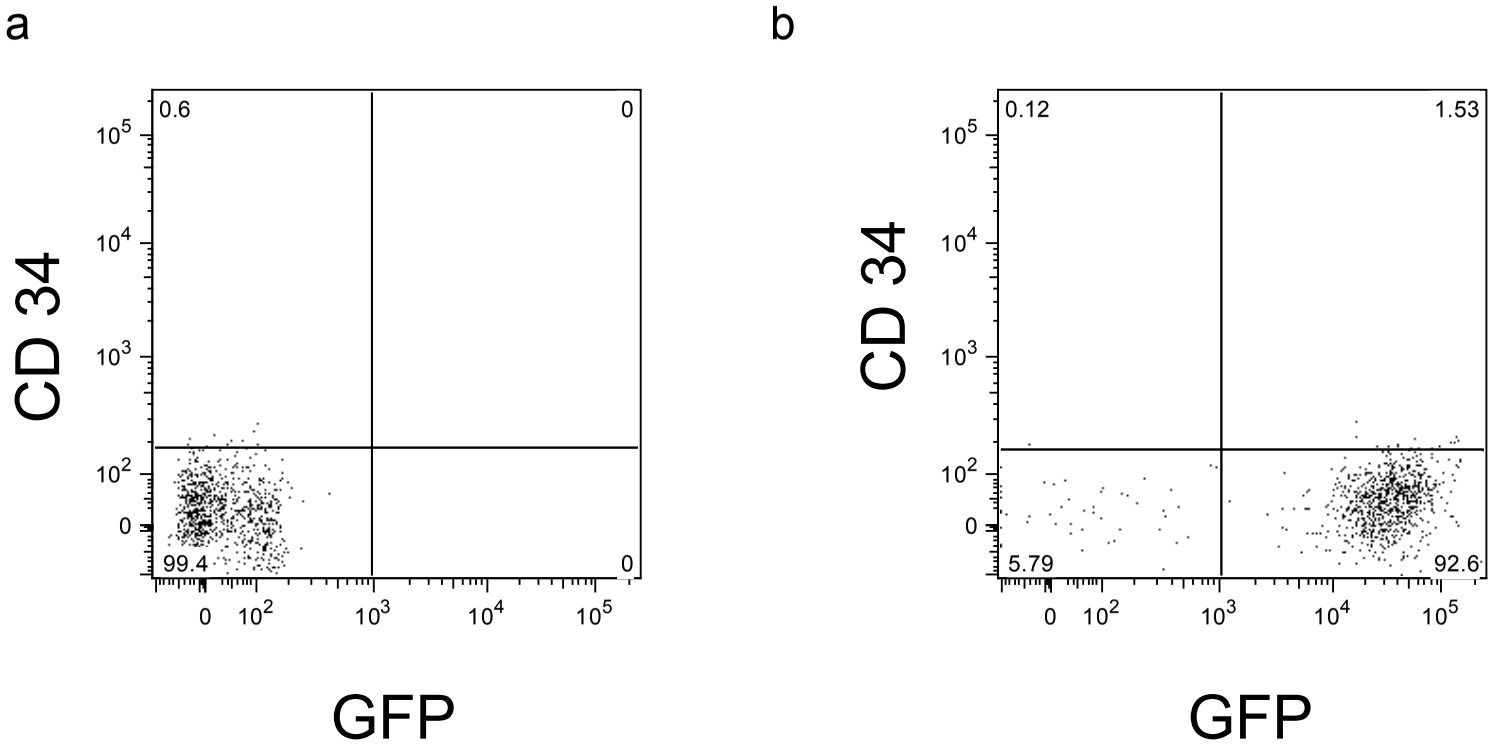



Figure S1

| CID | Control |
|---|---|
| Experiment 1 | |
| 323 | 23 |
| 627 | 49 |
| 350 | 92 |
| 855 | |
| Experiment 2 | |
| 15 | 0 |
| 618 | 0 |
| 610 | 14 |
| Experiment 3 | |
| 1207 | 335 |
| 2398 | 821 |
| 699 | 304 |
| Experiment 4 | |
| 1814 | 3229 |
| 1942 | 1914 |
| 1078 | 1236 |

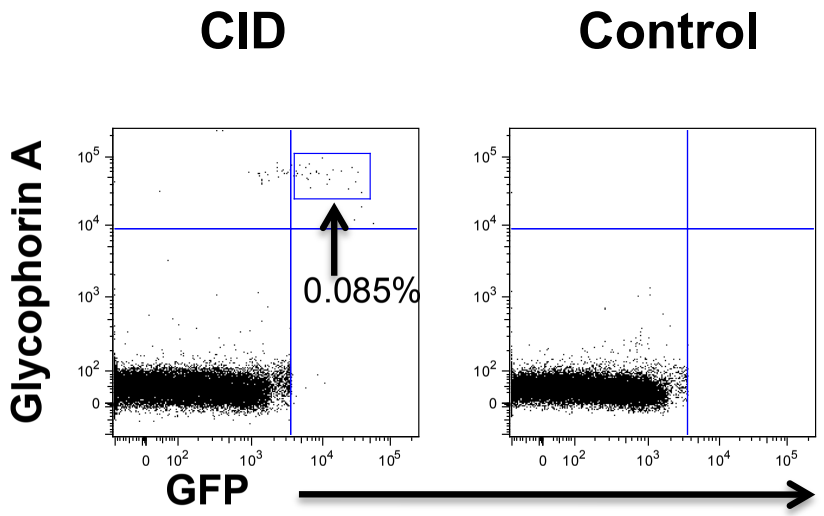
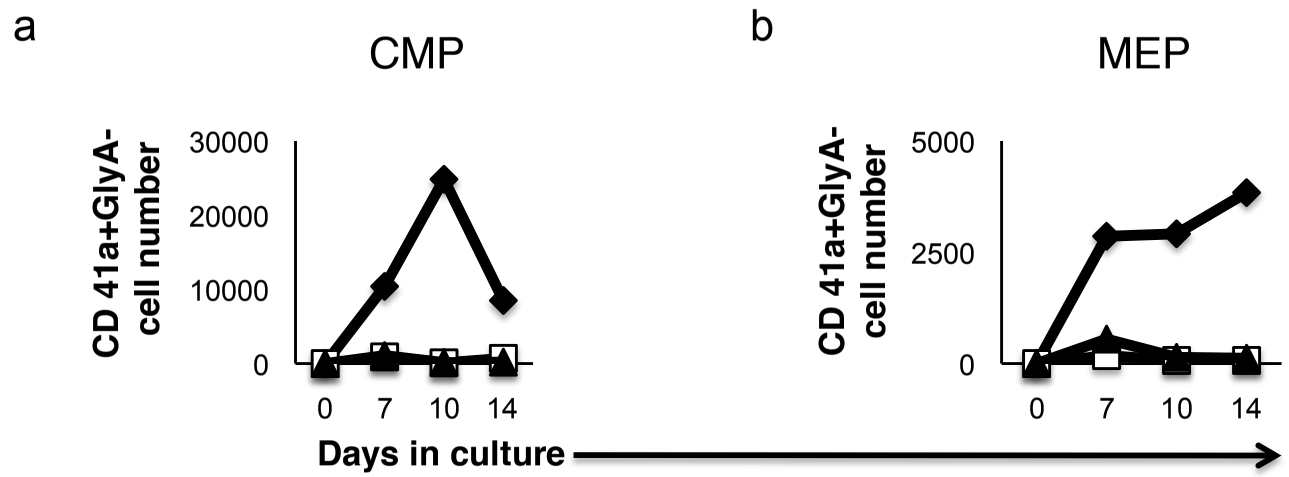
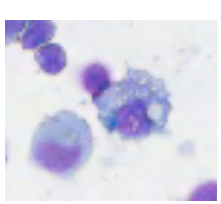


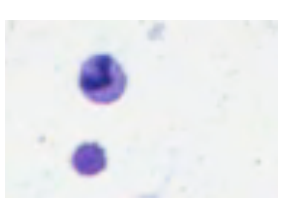

**Figure S2**



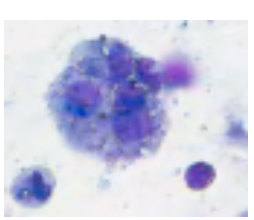

c



monocyte



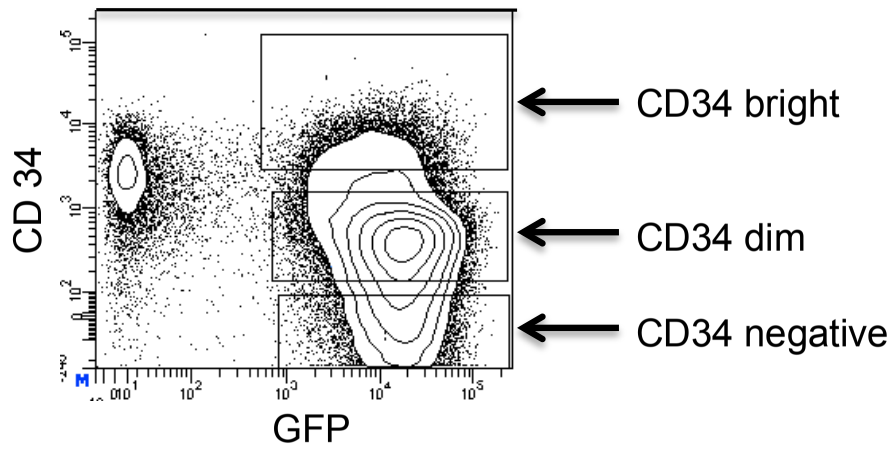
neutrophil



megakaryocyte

**Figure S3**

**a**


CD34 bright
CD34 dim
CD34 negative
CD 34
GFP

**b**

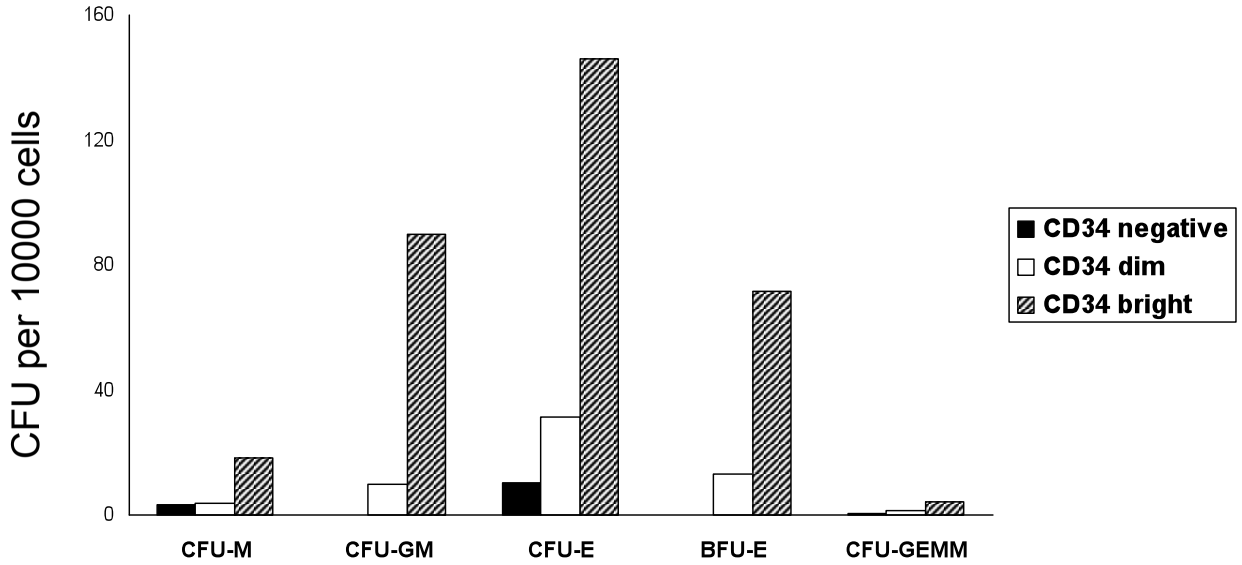

160
120
80
40
0
CFU per 10000 cells
CFU-M
CFU-GM
CFU-E
BFU-E
CFU-GEMM
CD34 negative
CD34 dim
CD34 bright

**Figure S4**

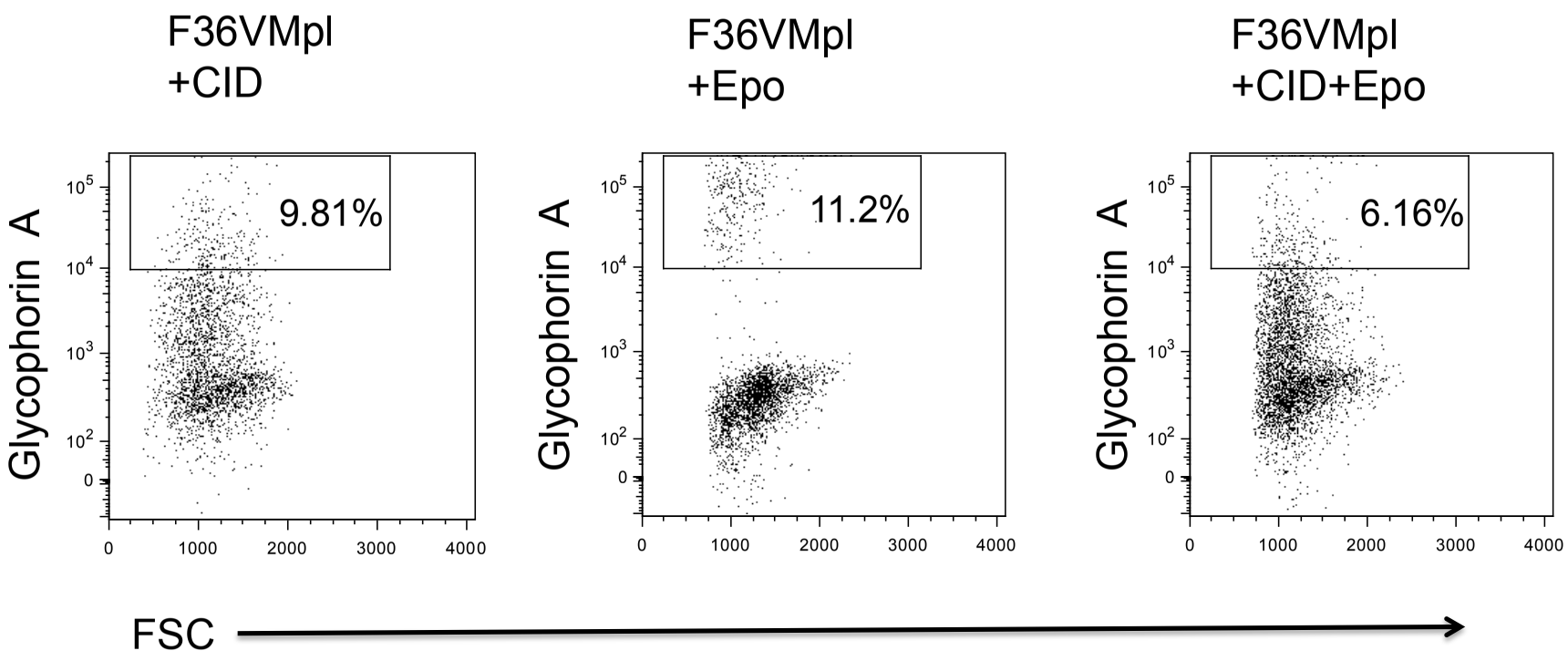

F36VMpl
+CID
F36VMpl
+Epo
F36VMpl
+CID+Epo
Glycophorin A
9.81%
11.2%
6.16%
FSC

**Figure S5**

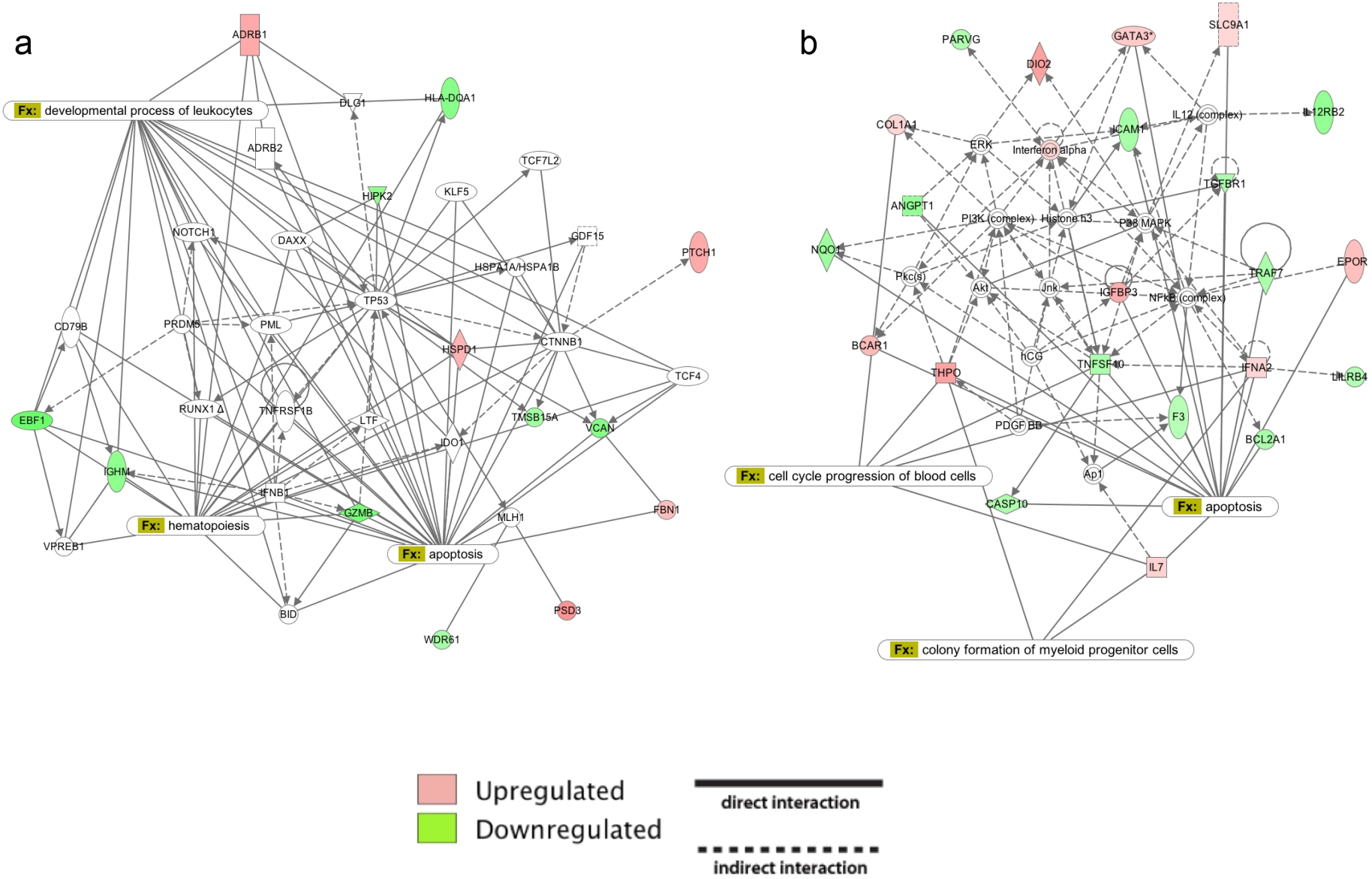

a
ADRB1
Fx: developmental process of leukocytes
DLG1
HLA-DQA1
ADRB2
TCF7L2
HIPK2
KLF5
NOTCH1
DAXX
GDF15
PTCH1
HSPA1A/HSPA1B
TP53
CD79B
PRDM9
PML
CTNNB1
HSPD1
TCF4
EBF1
RUNX1
TNFRSF1B
LTF
TMSB15A
VCAN
IDO1
IGHM
IFNB1
GZMB
MLH1
FBN1
Fx: hematopoiesis
VPREB1
Fx: apoptosis
BID
PSD3
WDR61
b
PARVG
DIO2
GATA3*
SLC9A1
COL1A1
ERK
Interferon alpha
ICAM1
IL12 (complex)
IL12RB2
TGFBR1
ANGPT1
PI3K (complex)
Histone h3
P38 MAPK
NQO1
Pkc(s)
Akt
Jnk
IGFBP3
NFkB (complex)
TRAF7
EPOR
BCAR1
hCG
TNFSF10
IFNA2
IL1RB4
THPO
F3
PDGF BB
BCL2A1
Ap1
Fx: cell cycle progression of blood cells
CASP10
Fx: apoptosis
IL7
Fx: colony formation of myeloid progenitor cells
Upregulated
Downregulated
direct interaction
indirect interaction

**Figure S6**

**Table S1. Expression of housekeeping genes**. CD 34+ cord blood cells were transduced with F36VMpl (or F36V) and cultured on MS-5 stroma +/- CID for 7 days. Equal numbers of CD34+GFP+ cells were sorted from culture and subjected to qPCR for housekeeping genes. C (T) values are depicted.

| Gene | F36VMpl+CID[a] | F36VMpl, no CID[a] | F36V+CID[a] |
|---|---|---|---|
| *18S RIBOSOMAL RNA* | 16.08496157 | 13.91069984 | 13.05308771 |
| *BETA ACTIN* | 24.31303978 | 24.53920746 | 23.24526405 |
| *BETA 2 MICROGLOBULIN* | 23.06636874 | 21.92607625 | 21.53512764 |
| *CYCLOPHILIN A* | 32.88670349 | 34.49984487 | 31.33360004 |
| *GAPDH* | 23.82501411 | 25.61851311 | 24.48389149 |
| *GUSB* | 26.11511803 | 27.5204525 | 26.76585865 |
| *HRPT1* | 25.17496745 | 26.41327604 | 25.59602451 |
| *HSP90* | 25.67794673 | 25.47840309 | 24.528409 |
| *RPL13A* | 24.19448407 | 24.58424886 | 23.66492176 |
| *RPLP0* | 37.50414658 | 37.14509583 | 38.183815 |
| *TFRC* | 22.93961716 | 25.83306567 | 25.29926586 |
| *UBC* | 33.92548434 | 33.71979713 | 33.61040211 |

[a] C (T) value