Table S1

Effect of *NUP98-HOXA10hd* on individual HSC clones of CD45^{mid}lin^{-}Rho^{-}SP phenotype. BA; before analysis, NA; not available.

***NUP98-HOXA10hd*-transduced clones**	**Total nucleated cells**	**Fraction transplanted / each mouse (M)**	**(+) recipients / total # of M transplanted**	**LD reached (yes/no)**	**Estimated (min.) HSC expansion → # of HSCs generated *in vitro***	**Range defined by ± 1 S.E.**
#1	1060000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.072	132.712 ± 928.772
#2	220000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.098	132.726 ± 928.818
#3	60000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.096	132.72 ± 928.818
#4	40000	1/5th/1M - 1/50th/2M - 1/500th/2M	0/1 - 0/2 - 0/2	no	not detected	NA
#5	40000	1/5th/1M - 1/50th/2M - 1/500th/1M	1/1 - 2/2 - 1/1	no	>152.224	60.804 ± 381.104
#6	380000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - died BA	no	>34.884	12.92 ± 94.354
#7	580000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.074	132.704 ± 928.812
#8	100000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.1	132.72 ± 928.82
#9	2380000	1/5th/1M - 1/50th/2M - 1/500th/2M - 1/1000th/2M	1/1 - 2/2 - 2/2 - 2/2	no	>1098.608	577.15 ± 2091.068
#10	50000	1/5th/1M - 1/50th/2M - 1/500th/2M	1/1 - 2/2 - 2/2	no	>351.1	132.715 ± 928.82
#11	20000	1/5th/1M - 1/50th/2M - 1/500th/2M - 1/1000th/1M	1/1 - 2/2 - 2/2 - 1/1	no	>804.72	383.392 ± 1689.062
#12	750000	1/50th/1M - 1/500th/2M	1/1 - 2/2	no	>348.9	129 ± 943.65
#13	1100000	1/50th/1M - 1/500th/2M	1/1 - 2/2	no	>348.92	129.03± 943.58
#14	2200000	1/50th/1M - 1/500th/2M	1/1 - 2/2	no	>348.92	128.92 ± 943.58
#15	100000	1/50th/1M - 1/500th/2M	1/1 - 2/2	no	>348.92	129.02 ± 943.63
#16	1500000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.9	523.05 ± 2308.5
#17	1600000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.88	523.04 ± 2308.48
#18	1600000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.88	523.04 ± 2308.48
#19	2900000	1/50th/1M - 1/500th/2M - 1/2000th/3M	1/1 -2/2 - 3/3	no	>2309.56	1188.42 ± 4487.75
#20	3900000	1/50th/1M - 1/500th/2M - 1/2000th/3M	1/1 -2/2 - 3/3	no	>2309.58	1188.33 ± 4487.73
#21	2500000	1/50th/1M - 1/500th/2M - 1/2000th/3M	1/1 -2/2 - 3/3	no	>2309.5	1188.5 ± 4487.75
#22	2000000	1/50th/1M - 1/500th/2M - 1/2000th/2M	1/1 -2/2 - 1/2	yes	~1718.8	827.2 ± 3571.6
#23	400000	1/100th/2M - 1/1000th/3M - 1/5000th/2M	0/2 - 0/3 - 0/2	no	not detected	NA
#24	650000	1/1000th/3M	(3/3)	no	>1098.63	522.47 ± 2310.035
#25	2100000	1/100th/2M - 1/1000th/3M - 1/5000th/2M	0/2 - 0/3 - 0/2	no	not detected	NA
#26	800000	1/100th/1M - 1/1000th/3M - 1/5000th/2M	1/1 - 3/3 - 0/2	yes	~2140.08	1139.52 ± 4019.04
#27	500000	1/100th/1M - 1/1000th/3M - 1/5000th/1M	1/1 - 3/3 - 0/1	yes	~2772.55	1355.4 ± 5671.5
#28	2500000	1/5000th/2M - 1/10000th/2M	1/2 - 0/2	yes	~3465.75	1249.5 ± 9612.5

Table S2

Average peripheral blood lineage contribution to donor-derived compartment of representative recipients shown in figure 1C (top panel). NA; not available.

***NUP98-HOXA10hd*-transduced clones**	**% myeloid cells ± SD (% Ly6G/Mac1)**	**% B cells ± SD (% B220)**	**% T cells ± SD (% CD4/CD8)**
#1	15 ± 7	64 ± 22	21 ± 15
#2	8 ± 1	71 ± 4	21 ± 3
#3	15 ± 10	33 ± 1	52 ± 11
#4	NA	NA	NA
#5	11	47	42
#6	24 ± 17	51 ± 21	25 ± 4
#7	12 ± 2	54 ± 4	34 ± 6
#8	15 ± 2	39 ± 2	46 ± 4
#9	34 ± 6	24 ± 8	42 ± 6
#10	19 ± 5	42 ± 4	39 ± 7
#11	17 ± 7	19 ± 20	64 ± 27
#12	24 ± 18	18 ± 4	58 ± 22
#13	9 ± 1	38 ± 16	53 ± 17
#14	17 ± 2	57 ± 3	26 ± 1
#15	30 ± 6	40 ± 8	30 ± 2
#16	20 ± 3	20 ± 18	60 ± 20
#17	22 ± 2	20 ± 5	58 ± 7
#18	14 ± 3	51 ± 9	35 ± 9
#19	12 ± 3	63 ± 13	25 ± 10
#20	15 ± 5	62 ± 6	22 ± 2
#21	18 ± 5	63 ± 19	19 ± 7
#22	34	19	47
#23	NA	NA	NA
#24	34 ± 4	36 ± 5	30 ± 7
#25	NA	NA	NA
#26	33 ± 6	22 ± 4	45 ± 10
#27	13 ± 11	11 ± 7	76 ± 18
#28	23	17	60

Table S3

Effect of *NUP98-HOXA10hd* on individual HSC clones of CD45$^+$EPCR$^+$CD48$^-$CD150$^+$ (E-SLAM) phenotype. NA; not available.

***NUP98-HOXA10hd*-transduced clones**	**Total nucleated cells**	**Fraction transplanted / each mouse (M)**	**(+) recipients / total # of M transplanted**	**LD reached (yes/no)**	**Estimated (min.) HSC expansion → # of HSCs generated *in vitro***	**Range defined by ± 1 S.E.**
7	2500000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.75	522.75 ± 2309.25
#2	1250000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.875	523 ± 2308.5
#3	2500000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.75	523 ± 2308.5
#4	2000000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.6	522.4 ± 2310
#5	1500000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.9	523.05 ± 2308.5
#6	1250000	1/100th/2M - 1/1000th/3M	2/2 -3/3	no	>1098.625	522.5 ± 2310
#7	1600000	1/100th/1M - 1/1000th/3M	1/1 -3/3	no	>1098.72	522.72 ± 2309.28
#8	900000	1/100th/1M - 1/1000th/3M	1/1 -3/3	no	>1098.72	522.72 ± 2309.22
#9	1650000	1/100th/1M - 1/1000th/3M	1/1 -3/3	no	>1098.735	522.72 ± 2309.175
#10	1400000	1/100th/1M - 1/1000th/2M	1/1 -2/2	no	>697.9	258.02 ± 1887.2
#11	1900000	1/100th/1M - 1/1000th/3M	1/1 -3/3	no	>1098.77	522.69 ± 2309.26
#12	700000	1/50th/1M - 1/500th/2M	0/1 - 0/2	no	not detected	NA
#13	800000	1/50th/1M - 1/500th/2M	0/1 - 0/2	no	not detected	NA
#14	900000	1/50th/1M - 1/500th/2M	1/1 - 2/2	no	>348.93	128.7 ± 943.65
#15	500000	1/100th/1M - 1/1000th/2M	1/1 - 2/2	no	>697.85	258.05 ± 1887.25
#16	1500000	1/100th/1M - 1/1000th/2M	1/1 - 2/2	no	>697.8	258 ± 1887.3
#17	600000	1/1000th/2M	(2/2)	no	>693.12	249.9 ± 1922.52

Table S4

Average peripheral blood lineage contribution to donor-derived compartment of representative recipients shown in figure 1C (bottom panel). NA; not available.

NUP98-HOXA10hd-transduced clones	% myeloid cells ± SD (% Ly6G/Mac1)	% B cells ± SD (% B220)	% T cells ± SD (% CD4/CD8)
#1	9 ± 5	17 ± 6	74 ± 11
#2	14 ± 4	19 ± 4	67 ± 6
#3	19 ± 11	30 ± 5	51 ± 6
#4	8 ± 2	29 ± 10	63 ± 10
#5	11 ± 4	8 ± 5	81 ± 9
#6	7 ± 3	18 ± 7	75 ± 8
#7	24 ± 7	16 ± 2	60 ± 6
#8	14 ± 2	17 ± 4	69 ± 5
#9	25 ± 2	23 ± 6	52 ± 6
#10	34 ± 1	13 ± 1	53 ± 1
#11	NA	NA	NA
#12	NA	NA	NA
#13	NA	NA	NA
#14	28 ± 7	33 ± 12	39 ± 6
#15	17 ± 3	22 ± 3	61 ± 1
#16	29 ± 10	28 ± 1	43 ± 10
#17	19 ± 3	23 ± 5	58 ± 3

Table S5

Calculated day 10 HSC frequencies and HSC content estimates of total or various FACS-purified subpopulations of *NUP98-HOXA10hd*-transduced and *in vitro* cultured bm cells (as shown in figure 3C).

Cell population analyzed	**Bulk**	**CD150^{+}CD48^{-} subset**	**CD150^{+}CD48^{+} subset**	**CD150^{-}CD48$^{+/-}$ subset**
Day 10 total nucleated cells ± SD	2500000 ± 424264.1	240000 ± 40729.3506	360000 ± 61094.02589	1620000 ± 274923.1165
Day 10 HSC frequency *in vitro* (range defined by ± SEM)	1 in 116 (+) 1 in 68 (-) 1 in 198	1 in 30 (+) 1 in 16 (-) 1 in 57	1 in 58 (+) 1 in 28 (-) 1 in 121	1 in 259 (+) 1 in 123 (-) 1 in 545
Day 10 estimated HSC content	~21552	~8000	~6207	~6255
10-day HSC expansion *in vitro*	~2155-fold			

Table S6

Calculated day 10 HSC frequencies and HSC content estimates of total or various FACS-purified subpopulations of *NUP98-HOXA10hd*-transduced and *in vitro* cultured bm cells (as shown in figure 4B).

Cell population analyzed	**Bulk**	**lin^{-} Sca1^{+}CD43^{+} c-kit^{+}Mac1$^{(dim)}$ subset**	**lin^{-} Sca1^{+}CD43^{+} c-kit^{+}Mac1^{-} subset**	**lin^{-} Sca1^{+}CD43^{-} c-kit^{+}Mac1^{++} subset**
Day 10 total nucleated cells ± SD	3900000 ± 264575.1	128700 ± 8730.9790327	167700 ± 11376.73064	31200 ± 2116.601049
Day 10 HSC frequency *in vitro* (range defined by ± SEM)	1 in 105 (+) 1 in 71 (-) 1 in 154	1 in 4 (+) 1 in 3 (-) 1 in 5	1 in 83 (+) 1 in 58 (-) 1 in 119	1 in 388 (+) 1 in 143 (-) 1 in 1051
Day 10 estimated HSC content	~37143	~32175	~2020	~80
10-day HSC expansion *in vitro*	~2476-fold			

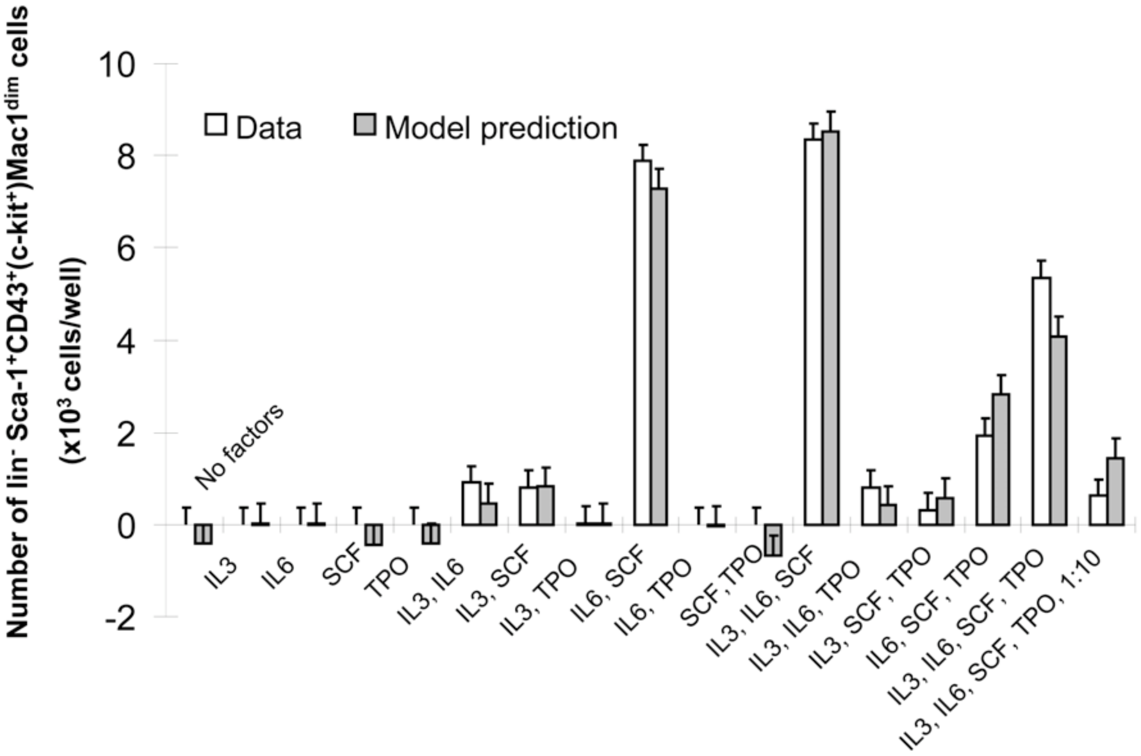
Table S7

Design matrix for the two-level factorial experiment. The concentrations for each of the 4 factors were as follows: -1 = low value; 0 = mid value (10-fold lower concentrations than high value); 1 = high value. For IL-3 -1 = 0 ng/ml, 0 = 0.6 ng/ml, 1 = 6 ng/ml; for IL-6 -1 = 0 ng/ml, 0 = 1 ng/ml, 1 = 10 ng/ml, for SF -1 = 0 ng/ml, 0 = 10 ng/ml, 1 = 100 ng/ml; for TPO -1 = 0 ng/ml, 0 = 10 ng/ml, 1 = 100 ng/ml.

	IL-3	**IL-6**	**SCF**	**TPO**
1	-1	-1	-1	-1
2	-1	-1	1	1
3	0	0	0	0
4	1	-1	-1	1
5	0	0	0	0
6	0	0	0	0
7	1	1	-1	-1
8	1	-1	1	-1
9	-1	1	-1	1
10	1	1	1	1
11	-1	1	1	-1
12	0	0	0	0
13	-1	-1	1	-1
14	1	-1	1	1
15	-1	-1	-1	1
16	1	1	1	-1
17	-1	1	-1	-1
18	-1	1	1	1
19	1	-1	-1	-1
20	1	1	-1	1

Figure S1

A



Number of lin⁻ Sca-1⁺CD43⁺(c-kit⁺)Mac1^dim cells (x10³ cells/well)
10
8
6
4
2
0
-2
☐ Data
▨ Model prediction
No factors
IL3
IL6
SCF
TPO
IL3, IL6
IL3, SCF
IL3, TPO
IL6, SCF
IL6, TPO
SCF,TPO
IL3, IL6, SCF
IL3, IL6, TPO
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IL3, IL6, SCF, TPO, 1:10

B

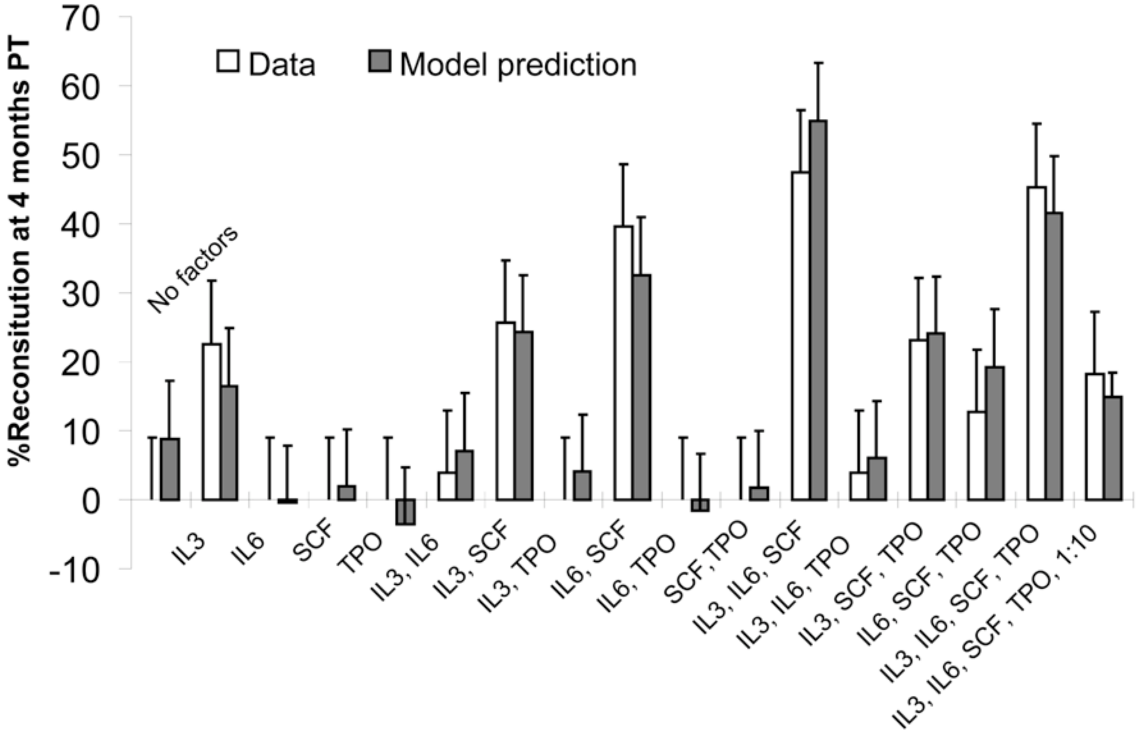

Figure S1. Number of lin$^-$Sca1$^+$CD43$^+$(c-kit$^+$)Mac1$^+$ cells obtained after 7 days of expansion in various growth factor combinations (A) and the level of reconstitution detected 4 months post transplantation (PT) (B).

The raw data from cell counts (A) and % reconstitution (B) are shown next to the model prediction. For the raw data, error bars represent the standard deviation measured at the centre point (1:10) condition; for the model prediction, error bars represent the mean square of pure error. Growth factor abbreviations represent the addition of the high level of the given factor (e.g. 6 ng/mL for IL-3). The “Il3, IL6, SF, TPO, 1:10” data point represents the centre point of the factorial design where all growth factors were added together at 1:10 dilution of the high factor level (e.g. 0.6 ng/mL for IL3).