Supplemental Information
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The Supplemental Information includes 6 tables and supplemental experimental methods.
Supplemental Table 1. Sequences of primers used for real-time quantitative PCR analyses.

Gene Name	Forward Primer	Reverse Primer:
GAPDH	TGCACCACCAACTGCTTAGC	TCTTCTGGGTGGCAGTGATG
GATA2	ATTGTCAGACGACAACCACCACCT	TTCCTTCTTCATGGTCAGTGGCCT
HoxB4	ACCTCGACACCCGCTAACAAATGA	AATGGGCACGAAAGATGAGGGAGA
Bmi1	TGTGTGTGCTTTGTGGAGGGTACT	TGCTGGTCTCCAGGTAACGAACAA
Ezh2	CAGTTTGTTGGCGGAAGCGTGTAA	AGGATGTGCACAGGCTGTATCCTT
GATA1	ACACCAGGTGAACCGGCCACT	CCTTCGGCTCCTCCTGTGCC
Pu.1	AACGCCAAACGCACGAGTATTACC	TGAAGTTGTTCTCGGCGAAGCTCT
P21	GGTCTGACCCCAAACACCTTC	AACGGGAACCAGGACACATG
S100A8	GGGATGACCTGAAGAAATTGCTA	TGTTGATATCCAACTCTTTGAACCA
Cyp11A1	TGGCATCTCCACCCGCAGTC	GAGCTTCTCCCTGTAAATCGGGCC
Alox5	TGTGGGAAGCCATCAGGACGTTCA	CCGCATGCCGTACACGTAGACATC
Col14A1	GTGTGGCCGATGCAGATTACTCGG	CCACTGGACAGGTTGCTGATGCTG
F2RL2	AGGCTTCCATTTGCTGCTGACACA	TCCATGCCACTCTGACAAAAAGTGGG
MPEG1	CAACCAGACGAGGATGGCCACCTA	GACTGCTCTGGCTGTCTTGGAGGA
ALDH1A1	GGCCGCAAGACAGGCTTTTCAGAT	ATTGACTCCATTGTCGCCAGCAGC
BMPR1A	ACTGCCCCCTGTTGTCATAGGTCC	ACGTCTGCTTGAGATGCTCTTGCA

Primers were designed using the PrimerQuest software (Integrated DNA Technologies, Coralville, IA).

Supplemental Table 2. Primer sequences for the amplification of immunoprecipitated DNA.

Gene Name	Region Amplified	Forward Primer	Reverse Primer
HoxB4	-537 to -727	GCGAAGTCTCCCCGAATTAGTG	GTCTCTATGGGGAGTTAGGTTACT
BMI-1	-240 to -506	CAGCAACTATGAAATAATCGTAG	TCCGCCTCCGCCTCGACCTCCAAC
GATA2	-55 to -435	TCGGACTGACCACGTTCAGCGGTGAAGG	AAGCCAGCCAATCAACGCCGCG
Pu.1	-4 to -224	GACTATCTCCCAGCGGCAGGCC	CCGGGCTCCGAGTCGGTCAGATC
GAPDH	+528 to +793	ACAGTCCATGCCATCACTGCC	GCCTGCTTCACCACCTTCTTG

Supplement Table 3. Gene promoter regions subjected to CpG site pyrosequencing.

Gene	Region Analysed
GATA2	-366 to -216
S100A8	-1010 to -851
pu.1	-296 to -198
Alox5	+44 to +98
HoxB4	-178 to -44
GATA1	-203 to -186
CYP11A1	-62 to +113

Genomic DNA was isolated from primary, 5azaD/TSA-, or VPA-expanded enriched CD34+ cells following culture using the Blood and Cell Culture DNA kit (Qiagen, Valencia CA). Genomic DNA was bisulphite treated using the EZ Methylation kit (Zymo Research, Irvine, CA)**.**

Supplemental Table 4. The top associated network functions and most up regulated genes within each network as revealed by Ingenuity Pathway Analysis of 113 putative HSC expansion genes.

Gene Network	Probeset ID	Gene Symbol	5azaD/TSA vs. Control		5azaD/TSA vs. VPA	
			Fold Change	p-value	Fold Change	p-value
Cellular Movement, Cellular Growth and Proliferation, Cancer[1]	212865_s_at	COL14A1	22.94	3.05E-07	20.47	4.19E-07
	201744_s_at	LUM	12.90	1.17E-04	9.27	3.24E-04
	202917_s_at	S100A8	6.36	1.60E-03	7.02	1.14E-03
	202411_at	IFI27	5.31	1.45E-03	4.53	2.73E-03
	224646_x_at	H19	5.18	1.06E-05	4.77	1.62E-05
Cellular Development, Cellular Growth and Proliferation, Cell Cycle[2]	212865_s_at	COL14A1	22.94	3.05E-07	20.47	4.19E-07
	201744_s_at	LUM	12.90	1.17E-04	9.27	3.24E-04
	1554892_a_at	MS4A3	8.90	4.97E-05	9.72	3.65E-05
	210254_at	MS4A3	8.74	3.00E-05	11.30	1.22E-05
	202917_s_at	S100A8	6.36	1.60E-03	7.02	1.14E-03
Cell Cycle, Nervous System Development and Function, Lipid Metabolism[3]	204309_at	CYP11A1	11.35	3.69E-05	11.96	3.11E-05
	1554892_a_at	MS4A3	8.90	4.97E-05	9.72	3.65E-05
	210254_at	MS4A3	8.74	3.00E-05	11.30	1.22E-05
	202284_s_at	CDKN1A	4.33	2.54E-06	2.81	4.32E-05
	202284_s_at	CDKN1A	4.33	2.54E-06	2.81	4.32E-05
Inflammatory Response, Cellular Movement, Immune Cell Trafficking[4]	201744_s_at	LUM	12.90	1.17E-04	9.27	3.24E-04
	204309_at	CYP11A1	11.35	3.69E-05	11.96	3.11E-05
	202917_s_at	S100A8	6.36	1.60E-03	7.02	1.14E-03
	214183_s_at	TKTL1	5.50	1.12E-03	4.37	2.82E-03
	202284_s_at	CDKN1A	4.33	2.54E-06	2.81	4.32E-05

[1] Score: 47; [2] Score: 32; [3] Score: 26; [4] Score: 24. Fold change (> 2 fold) of transcripts in 5azaD/TSA-expanded CD34+ cells compared to CD34+ cells expanded under other conditions, $p < 0.01$.

Supplemental Table 5. The top associated network functions and most up regulated genes within each network as revealed by Ingenuity Pathway Analysis of 278 putative HSC maintenance genes.

Gene Network	Probeset ID	Gene Symbol	VPA vs. Control		5azaD/TSA vs. Control	
			Fold Change	p-value	Fold Change	p-value
Cellular Function and Maintenance, Molecular Transport, Gene Expression[1]	213578_at	BMPR1A	9.93	2.05E-07	2.46	3.83E-04
	216598_s_at	CCL2	8.71	8.68E-05	6.00	3.50E-04
	217820_s_at	ENAH	7.02	3.86E-06	2.67	7.40E-04
	206857_s_at	FKBP1B	6.20	6.10E-07	3.10	3.16E-05
	213413_at	STON1	5.68	1.21E-04	2.85	3.74E-03
Cellular Movement, Cell Morphology, Cellular Growth and Proliferation[2]	213578_at	BMPR1A	9.93	2.05E-07	2.46	3.83E-04
	216598_s_at	CCL2	8.71	8.68E-05	6.00	3.50E-04
	206857_s_at	FKBP1B	6.20	6.10E-07	3.10	3.16E-05
	212224_at	ALDH1A1	6.17	1.24E-08	2.76	1.91E-06
	203394_s_at	HES1	5.58	1.01E-04	2.65	4.69E-03
Cellular Growth and Proliferation, Cell Cycle, DNA Replication, Recombination, and Repair[3]	213578_at	BMPR1A	9.93	2.05E-07	2.46	3.83E-04
	216598_s_at	CCL2	8.71	8.68E-05	6.00	3.50E-04
	206857_s_at	FKBP1B	6.20	6.10E-07	3.10	3.16E-05
	212224_at	ALDH1A1	6.17	1.24E-08	2.76	1.91E-06
	203394_s_at	HES1	5.58	1.01E-04	2.65	4.69E-03
Cellular Development, Haematopoiesis, Gene Expression[4]	213578_at	BMPR1A	9.93	2.05E-07	2.46	3.83E-04
	216598_s_at	CCL2	8.71	8.68E-05	6.00	3.50E-04
	206857_s_at	FKBP1B	6.20	6.10E-07	3.10	3.16E-05
	212224_at	ALDH1A1	6.17	1.24E-08	2.76	1.91E-06
	203394_s_at	HES1	5.58	1.01E-04	2.65	4.69E-03

[1] Score: 47; [2] Score: 32; [3] Score: 26; [4] Score: 24. Fold change (> 2 fold) of transcripts in VPA-expanded CD34+ cells compared to CD34+ cells expanded under other conditions, $p < 0.01$.

Supplemental Table 6.1. Top molecules from gene networks revealed by Ingenuity Pathway Analyses of 88 genes associated with HSC regenerative (haematopoietic reconstitution) and non-regenerative (lack of haematopoietic reconstitution) phenotypes.

Gene Network	Probeset ID	Gene Symbol	Fold Change	*p*-value
Inflammatory Response, Renal Inflammation, Renal Damage	204924_at	TLR2	-1.67127	2.17E-05
	211657_at	CEACAM6	-2.74469	3.64E-05
Small Molecule Biochemistry, Cellular Development, Haematological System Development and Function	1554503_a_at	OSCAR	-1.78511	3.04E-06
	204924_at	TLR2	-1.67127	2.17E-05
	209960_at	HGF	-3.31895	6.02E-05
Cell Morphology, Cell Signalling, Small Molecule Biochemistry	1554503_a_at	OSCAR	-1.78511	3.04E-06

Supplemental Table 6.2. The top 7 cellular and molecular functions and their corresponding molecules revealed by Ingenuity Pathway Analyses of 88 genes associated with HSC regenerative and non-regenerative phenotypes.

Category	*p*-value	Molecules
Haematological System Development and Function	6.21E-04 - 2.25E-02	PDPN, TLR2, LAMA5, ITGB2, HGF, ITGB3
Cell Death	7.57E-04 - 2.25E-02	LAMA5, PHIP, BAD, STK25, MAPK11, ITGB3, MECOM, NDNL2, TLR2, OSCAR, ITGB2, CEACAM6 (includes EG:4680), HGF, PEA15, GALNT10
Cellular Growth and Proliferation	7.57E-04 - 1.94E-02	LAMA5, PHIP, LAPTM4B, BAD, GNA11, MAPK11, MECOM, ITGB3, TLR2, NDNL2, ITGB2, CEACAM6 (includes EG:4680), RETN, HGF, PEA15
Haematopoiesis	7.57E-04 - 1.88E-02	LAMA5, ITGB2, HGF, TPPP2, ITGB3
Cancer	2.96E-03 - 1.51E-02	PDPN, LAMA5, CEACAM6 (includes EG:4680), HGF, PEA15, ITGB3, MECOM
Cell Cycle	3.79E-03 - 2.25E-02	BAD, HGF, PEA15
DNA Replication, Recombination, and Repair	3.79E-03 - 3.79E-03	PEA15

Supplemental Methods

Microarray studies and data analysis

All microarray studies were performed in triplicate, except for TSA/5azaD (reverse sequence)-expanded CD34+ cells, for which microarray studies were performed in duplicate. Each of the replicate samples represented a pool of 4 to 8 independent CB units. CD34+ cells, which represent less than 1% of MNCs in a CB unit while still heterogeneous in stem/progenitor cell content, are enriched in repopulating HSCs; further enrichment is limited by the rarity of the cell population and the number of cells needed for typical microarray studies. Therefore, the use of enriched CD34+ cells for microarray studies is a practical compromise, and indeed CD34+ cells are the most common source of cells used for gene microarrays to study normal haematopoiesis or human leukaemia.

Total RNA was extracted from either uncultured primary CD34+ cells or enriched CD34+ cells (>90% purity) after expansion culture with or without CMA. RNA was extracted using TRIzol (Life Technologies, NY, USA) followed by Qiagen column purification (Qiagen, Valencia, CA, USA). The samples for microarray studies included control, 5azaD/TSA-expanded, VPA-expanded, TSA/5azaD-expanded, and primary uncultured CD34+ cells. RNA integrity was evaluated using an Agilent 2100 Bioanalyzer (Agilent Technologies; Palo Alto, CA), and purity and concentration were determined using a NanoDrop 8000 (NanoDrop, Wilmington, DE, USA).

Subsequent data analyses were performed using the Partek Genomics Suite with the CEL files obtained from GCOS. The data were normalised using the RMA algorithm. Significant genes were selected at > 2-fold and $p < 0.05$. Global functional analyses, network analyses, and canonical pathway analyses were performed using Ingenuity Pathway Analysis 8.6 (Ingenuity Systems, Redwood City).