Supplementary Information

Single-cell assessment of transcriptome alterations induced by Scriptaid in early differentiated human haematopoietic progenitors during *ex vivo* expansion

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Statement of equal author contribution: P.H. and B.K. contributed equally to this study.

Supplementary Tables

Supplementary Table S1. Taqman probes used for Biomark Single-cell qPCR:

Reference genes	Annotation	TAQMAN id		
BMI1 (HSC)	BMI1 Proto-Oncogene, Polycomb Ring Finger	Hs00995536_m1		
FLT3 (HSC)	fms-related tyrosine kinase 3	Hs00975643_m1		
GFI1 (HSC/homing)	Growth Factor Independent 1 Transcriptional Repressor	Hs00382207_m1		
HMGA2 (HSC/fetal)	High-Mobility Group (Nonhistone Chromosomal) Protein Isoform I-C	Hs04397751_m1		
ITGA6 (HSC)	Integrin Subunit Alpha 6 (CD40f)	He01116228 m1		
JUN (HSC)	Jun Proto-Oncogene AP-1 Transcription Factor Subunit	Hs01103582_s1		
MCL1 (HSC)	Mveloid Cell Leukemia Seguence 1 (BCL2-Related)	Hs01050896 m1		
MEIS1 (HSC)	Meis homeobox 1	Hs00180020 m1		
MPL (HSC)	myeloproliferative leukemia virus oncogene	Hs00180489 m1		
MYB (HSC)	Proto-Oncogene C-Myb	 Hs00920556 m1		
MYC (HSC)	V-Myc Avian Myelocytomatosis Viral Oncogene Homolog	 Hs00153408 m1		
MYCN (HSC)	V-Myc Avian Myelocytomatosis Viral Oncogene Neuroblastoma	 Hs00232074_m1		
POU5F1 (HSC)	Oct-04	Hs00999634_gH		
STAT5a (HSC)	Transcription Factor STAT5A	Hs00559648_g1		
STAT5b (HSC)	Transcription Factor STAT5B	Hs00560026_m1		
CD79A (Lymphoid)	Membrane-Bound Immunoglobulin-Associated Protein	Hs00998119_m1		
EBF1 (Lymphoid)	Early B-Cell Factor 1	Hs01092694_m1		
GATA3 (Lymphoid)	Trans-Acting T-Cell-Specific Transcription Factor GATA-3	Hs00231122_m1		
IL3RA (Lymphoid)	Interleukin-3 Receptor Subunit Alpha	Hs00608141_m1		
PAX5 (Lymphoid)	B-Cell Lineage Specific Activator	Hs00277134_m1		
PTCRA (Lymphoid)	Pre T-Cell Antigen Receptor Alpha	Hs00300125_m1		
RAG1 (Lymphoid)	Recombination Activating Protein 1	Hs00172121_m1		
CEBPA (Myeloid)	CCAAT/Enhancer Binding Protein Alpha	Hs00269972_s1		
CSF3R (Myeloid)	Colony Stimulating Factor 3 Receptor	Hs01114420_m1		
MPO (Myeloid)	myeloperoxidase	Hs00165162_m1		
SFPI1 (Myeloid/ HSC)	Hematopoietic Transcription Factor PU.1	Hs02786711_m1		
EPOR (Erythroid)	Erythropoietin Receptor	Hs00959426_m1		
GATA1 (Erythroid)	GATA Binding Protein 1 (Globin Transcription Factor 1)	Hs01085823_m1		
KLF1 (Erythroid)	Erythroid-Specific Transcription Factor EKLF	Hs00610592_m1		
VWF (Platelet)	Coagulation Factor VIII VWF	Hs01109457_m1		
CXCR4 (homing/retention)	chemokine (C-X-C motif) receptor 4	Hs00976734_m1		
GAS2 (Cell growth)	growth arrest-specific 2	Hs00169477_m1		
ASF1A (epigenetic)	ASF1 Anti-Silencing Function 1 Homolog A	Hs00204044_m1		
CHD7 (epigenetic)	Chromodomain Helicase DNA Binding Protein 7	Hs00215010_m1		
GAPDH (House-keeping)	glyceraldehyde-3-phosphate dehydrogenase	Hs02758991_g1		
Genes upregulated in CD90+ cells	Annotation	TAQMAN id		
C10orf128	chromosome 10 open reading frame 128 [Source:HGNC Symbol;Acc:HGNC:27274]	Hs01393050_m1		
CD22	CD22 molecule [Source:HGNC Symbol;Acc:HGNC:1643]	Hs00998488_m1		
CDCP1	Symbol; Acc: HGNC:24357]			
CRHBP	Symbol;Acc:HGNC:2356]	HSUU181810_m1		
EMCN	endomucin [Source:HGNC Symbol;Acc:HGNC:16041]	Hs01038204_m1		

EPB41L3	erythrocyte membrane protein band 4.1 like 3 [Source:HGNC Symbol:Acc:HGNC:3380]	Hs00202360_m1
GBP5	guanylate binding protein 5 [Source:HGNC Symbol;Acc:HGNC:19895]	Hs00369472_m1
GPAT3	glycerol-3-phosphate acyltransferase 3 [Source:HGNC Symbol:Acc:HGNC:28157]	Hs00262010_m1
HLF	HLF, PAR bZIP transcription factor [Source:HGNC Symbol:Acc:HGNC:4977]	Hs00171406_m1
KIAA0087	KIAA0087 [Source:HGNC Symbol;Acc:HGNC:22191]	Hs00207421_m1
MFAP2	microfibrillar associated protein 2 [Source:HGNC Symbol:Acc:HGNC:7033]	Hs01027737_m1
OAS1	2'-5'-oligoadenylate synthetase 1 [Source:HGNC Symbol:Acc:HGNC:8086]	Hs00973635_m1
OAS3	2'-5'-oligoadenylate synthetase 3 [Source:HGNC Symbol:Acc:HGNC:8088]	Hs00196324_m1
PDE1A	phosphodiesterase 1A [Source:HGNC Symbol;Acc:HGNC:8774]	Hs00897273_m1
PROCR	protein C receptor [Source:HGNC Symbol;Acc:HGNC:9452]	Hs00197387_m1
RAI14	retinoic acid induced 14 [Source:HGNC Symbol;Acc:HGNC:14873]	Hs00210238_m1
SKAP1	src kinase associated phosphoprotein 1 [Source:HGNC	 Hs00175372_m1
SLC16A2	solute carrier family 16 member 2 [Source:HGNC Symbol:Acc:HGNC:10923]	Hs00185140_m1
SLC7A8	solute carrier family 7 member 8 [Source:HGNC Symbol:Acc:HGNC:11066]	Hs00794796_m1
TMEM200A	transmembrane protein 200A [Source:HGNC Symbol:Acc:HGNC:21075]	Hs00287589_m1
TNFSF8	tumor necrosis factor superfamily member 8 [Source:HGNC Symbol:Acc:HGNC:11938]	Hs00174286_m1
TRIM47	tripartite motif containing 47 [Source:HGNC Symbol;Acc:HGNC:19020]	Hs00386112_m1
UCHL1	ubiquitin C-terminal hydrolase L1 [Source:HGNC Symbol:Acc:HGNC:12513]	Hs00985157_m1
Genes upregulated in CD90- cells	Annotation	TAQMAN id
ABCB6	ATP binding cassette subfamily B member 6 (Langereis blood group)	Hs00180568_m1
APOC1	apolipoprotein C1 [Source:HGNC Symbol:Acc:HGNC:607]	Hs00155790 m1
BCI 2I 11	BCI 2 like 11 [Source: HGNC Symbol: Acc: HGNC: 994]	Hs01076940 m1
CA1	carbonic anhydrase 1 [Source:HGNC Symbol:Acc:HGNC:1368]	Hs00266139 m1
CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:1368]	Hs00266139_m1 Hs01547121_m1
CA1 CD84 CEBPD	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:1368] CD84 molecule [Source:HGNC Symbol;Acc:HGNC:1704] CCAAT/enhancer binding protein delta [Source:HGNC	Hs00266139_m1 Hs01547121_m1 Hs00270931_s1
CA1 CD84 CEBPD	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:1368] CD84 molecule [Source:HGNC Symbol;Acc:HGNC:1704] CCAAT/enhancer binding protein delta [Source:HGNC Symbol;Acc:HGNC:1835] Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal	Hs00266139_m1 Hs01547121_m1 Hs00270931_s1 Hs00366696_m1
CA1 CD84 CEBPD CITED2	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:1368] CD84 molecule [Source:HGNC Symbol;Acc:HGNC:1704] CCAAT/enhancer binding protein delta [Source:HGNC Symbol;Acc:HGNC:1835] Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2 [Source:HGNC Symbol;Acc:HGNC:1987] colony stimulating factor 2 receptor beta common subunit	Hs00266139_m1 Hs01547121_m1 Hs00270931_s1 Hs00366696_m1 Hs00166144_m1
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CA1 CA1 CD84 CEBPD CITED2 CSF2RB CST7 CSTA DLC1 ELL2 FAM171A1 FHL2 HBA2	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:1368] CD84 molecule [Source:HGNC Symbol;Acc:HGNC:1704] CCAAT/enhancer binding protein delta [Source:HGNC Symbol;Acc:HGNC:1835] Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2 [Source:HGNC Symbol;Acc:HGNC:1987] colony stimulating factor 2 receptor beta common subunit [Source:HGNC Symbol;Acc:HGNC:2436] cystatin F [Source:HGNC Symbol;Acc:HGNC:2479] cystatin A [Source:HGNC Symbol;Acc:HGNC:2481] DLC1 Rho GTPase activating protein [Source:HGNC Symbol;Acc:HGNC:2897] elongation factor for RNA polymerase II 2 [Source:HGNC Symbol;Acc:HGNC:17064] family with sequence similarity 171 member A1 [Source:HGNC Symbol;Acc:HGNC:23522] four and a half LIM domains 2 [Source:HGNC Symbol;Acc:HGNC:3703] hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:4824]	Hs00266139_m1 Hs01547121_m1 Hs00270931_s1 Hs00366696_m1 Hs00166144_m1 Hs00175361_m1 Hs00193257_m1 Hs00603761_g1 Hs00295934_m1 Hs003666_m1
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Name	Clone	Isotype	Conj.	Company	Dilution
CD34	581	mlgG1	AF700	BD	1:60
CD38	HIT2	mlgG1	PETxR/BB515	Caltag/BD	1:40
CD45RA	HI100	mlgG2bk	APC-H7	BD	1:50
CD90	5E10	lgG1	PE	Biolegend	1:50
CD49f	GoH3	rlgG2a	PE-Cy7	Biolegend	1:120
CD133	293C3	lgG2b	APC	Miltenyi	1:30
CD123	6H6		PerCP-Cy5.5	Biolegend	1:50
CD2	RPA-2.10	lgG1	PE-Cy5	Biolegend	1:150
CD3	HIT3a	lgG2a	PE-Cy5	Biolegend	1:200
CD4	RPA-T4	lgG1	PE-Cy5	Biolegend	1:150
CD7	CD7-6B7	lgG1	PE-Cy5	Biolegend	1:150
CD8a	RPA-T8	lgG1	PE-Cy5	Biolegend	1:200
CD10	HI10a	lgG1	PE-Cy5	Biolegend	1:80
CD11b	ICRF44	lgG1	PE-Cy5	Biolegend	1:80
CD14	6103	lgG2a	PE-Cy5	eBio	1:80
CD19	HIB19	lgG1	PE-Cy5	Biolegend	1:200
CD20	2H7	lgG2a	PE-Cy5	Biolegend	1:150
CD56	B159	lgG1	PE-Cy5	BD	1:20
CD235ab	HIR2	lgG2b	PE-Cy5	Biolegend	1:1200
DAPI			UV 440/40		100ng/ml

Supplementary Table S2. Antibodies Used for Flow Cytometry

Supplementary Figure Legends

Supplementary Figure S1. Flow cytometric analyses for human UCB CD133+ cells expanded in vitro.

Representative gating strategy for flow cytometry analysis for day 5 cultured cells in Figures 1a1 and 1a2. The media contained C3-cytokine plus vehicle (top) or Scriptaid (bottom). Lin-CD34+CD38-/lowCD45RA- cells were gated as shown and then selected for CD90+ or CD90- cells. The CD90+ subset was further enriched for CD49f+ cells. All gating was determined by FMO (Fluorescence Minus One).

Supplementary Figure S2. Expansion of CD133+ HSC and progenitor populations after 5 days culture with cytokines and Scriptaid or vehicle

(a) Cryopreserved CD133+ UCB cells were thawed and cultured overnight in C3-cytokinecontaining serum free medium. Cells were then plated for expansion and also analysed for the frequency of HSC and progenitors. Scriptaid or vehicle was added when plating and all cells post 5-days expansion were analysed by flow cytometry. In the presence of C₃cytokines and Scriptaid, the absolute number of Lin+, LMPP and GMP cells decreased significantly compared to vehicle. Scriptaid had no effect on the numbers of committed myeloid progenitors (CMP, MEP) (*, p<0.05; **, p<0.005; ***, p<0.001, n=6-9). (b-c) Proportions of AnnexinV+DAPI- (Apoptotic) and AnnexinV+DAPI+ (Dead) cells in C₃cytokine containing medium supplemented with Scriptaid or the vehicle control did not differ on day 5 of expansion. (d-e) Median Fluorescence Intensity values of CD90-PE and CD49f-PECy7 analysed by Student's T test against vehicle control (***, p<0.001; N.S, p=0.05. n=3). (f) Limiting dilution analysis (LDA) for quantitating LTC-ICs present in the unexpanded Lin-CD34+CD38-CD45RA-CD90+/-CD49f+ cell subsets (n=4-12).

Supplementary Figure S3. Supporting information for RNA-sequencing and single-cell qPCR

(a) QC of a cDNA library from 100 sorted cells using the Agilent high-sensitivity chip. (b) QC of library pool using the Agilent high-sensitivity chip. (c-d) QC of raw fastq file from hiseq4000. (e) Sample distance heatmap illustrates C1 and C2 cells cannot be clustered based on the phenotype. (f) Sample distance heatmap illustrates C1 and C4 cells can be clustered based on the phenotype but not biological variance. (g) Sample distance heatmap illustrates C1 and C3 cells cannot be clustered based on the phenotype but not biological variance. (h) Volcano plot demonstrating the top deferentially expressed genes between C2 and C4 populations. (i)
Principal Component Analysis (PCA) plotting the variance between individual cells for 50 selected DE genes. CD90-CD49f+ (C3 and C4) cells can be clearly distinguished from CD90+CD49f+ (C1 and C2) cells in both day 5 vehicle and Scriptaid expanded cell culture. (j) Screen plot of PCA analysis of Fluidigm single-cell qPCR data for 50 selected DE genes. (k) Screen plot of PCA analysis of Fluidigm single-cell qPCR data for 50 selected DE genes. (l) GO Biological Process analysis results of the DE genes between C2 and C4 populations.

Supplementary Figure S4. Transcriptome profiling of single cells

Individually plotted relative gene expression levels of single cells (34 reference genes and 50 selected DE genes) from day 5 Scriptaid-expanded Lin-CD34+CD38-CD45RA-CD90+CD49f+ cells (C1), vehicle-expanded Lin-CD34+CD38-CD45RA-CD90+CD49f+ cells (C2), Scriptaid-expanded Lin-CD34+CD38-CD45RA-CD90-CD49f+ cells (C3), and vehicle-expanded Lin-CD34+CD38-CD45RA-CD90-CD49f+ cells (C3), and vehicle-expanded Lin-CD34+CD38-CD45RA-CD90-CD49f+ cells (C4). P values were generated using one-way ANOVA with multiple comparisons on Prism 7.0 (*, p<0.05; **, p<0.005; ***, p<0.001).

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Supplementary Figure S5. Flow cytometric analyses for overnight cultured CD133+ cells or C_3 -cytokine-expanded human UCB CD133+ cells

Representative gating strategy for flow cytometry and sorting: HSC: Lin-CD38-CD34+CD45RA-CD90+CD49f+; HSPC: Lin-CD34+CD133+; MPP: Lin-CD38-CD34+CD45RA-CD90-; LMPP: Lin-CD38-CD34+CD45RA+CD90-; CMP: Lin-CD38+CD34+CD45RA-CD123+; GMP: Lin-CD38+CD34+CD45RA+CD123+; and MEP: Lin-CD38+CD34+CD45RA-CD123-. All gating was determined by FMO (Fluorescence Minus One).



Supplementary Fig. S1. Watt. 2018. TOP.

Supplementary Figure S2 Watt. 2018. TOP.





Lin-CD34+CD38-CD45RA-CD90+CD49f+ Lin-CD34+CD38-CD45RA-CD90-CD49f+

Confidence intervals for 1/(stem cell frequency)

Group	Lower	Estimate	Upper
Lin-CD34+CD38-	30.9	12.9	5.6
	491+		
CD45RA-CD90-CD4	155.4 19f+	63.5	26.1



Supplementary Figure S3 Watt. 2018. TOP.

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I)		GO.ID	Term	Annotated	Significant	Expected	Rank in clas classic	KS	weight
-	1	GO:1903047	mitotic cell cycle process	859	790	590.13	28 < 1e-30	< 1e-30	< 1e-30
	2	GO:0006996	organelle organization	3651	3070	2508.24	4 < 1e-30	4.3e-22	< 1e-30
	3	GO:0006412	translation	652	599	447.92	42 < 1e-30	3.8e-17	< 1e-30
	4	GO:0016071	mRNA metabolic process	626	577	430.06	45 < 1e-30	< 1e-30	< 1e-30
	5	GO:0034470	ncRNA processing	327	318	224.65	58 < 1e-30	1.6e-07	< 1e-30
	6	GO:0022613	ribonucleoprotein complex biogenesis	377	357	259	71 < 1e-30	1.1e-14	< 1e-30
	7	GO:1902582	single-organism intracellular transport	1715	1453	1178.21	33 < 1e-30	2.3e-10	< 1e-30
	8	GO:0032446	protein modification by small protein co	891	786	612.12	49 < 1e-30	7.4e-05	< 1e-30
	9	GO:0006974	cellular response to DNA damage stimulus	796	710	546.85	50 < 1e-30	< 1e-30	8.3e-29
	10	GO:0006399	tRNA metabolic process	196	193	134.65	114 8.3e-28	4.9e-05	2.4e-27
	11	GO:0006401	RNA catabolic process	238	231	163.51	104 2.8e-29	< 1e-30	1.6e-26
	12	GO:0070727	cellular macromolecule localization	1526	1297	1048.36	37 < 1e-30	1.5e-09	3.0e-24
	13	GO:0010256	endomembrane system organization	536	464	368.23	143 1.5e-22	0.00367	1.7e-22
	14	GO:0032774	RNA biosynthetic process	3821	2911	2625.03	91 < 1e-30	< 1e-30	3.4e-22
	15	GO:0045184	establishment of protein localization	1975	1610	1356.83	56 < 1e-30	1.3e-06	3.1e-21
	16	GO:0016482	cytoplasmic transport	1243	1058	853.94	51 < 1e-30	6.1e-12	4.9e-20
	17	GO:0071826	ribonucleoprotein complex subunit organi	208	196	142.9	166 7.5e-20	9.7e-19	6.8e-20
	18	GO:0044403	symbiosis, encompassing mutualism throug	845	733	580.52	73 < 1e-30	3.7e-24	1.3e-19
	19	GO:0043161	proteasome-mediated ubiquitin-dependent	376	348	258.31	100 7.9e-30	7.5e-08	1.7e-19
	20	60.0007264	small GTPase mediated signal transductio	922	755	633 /1	160 9 20-21	1 10-07	3 20-18



Supplementary Figure S4.1 Watt. 2018. TOP.



Supplementary Figure S4.2 Watt. 2018. TOP.

Supplementary Figure S4.3 Watt. 2018. TOP.

Genes upregulated in CD90+ cells:



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Supplementary Figure S4.4 Watt. TOP.

Genes upregulated in CD90- cells:





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Relative expression level compared to GAPDH

Supplementary Figure S5. Watt. 2018. TOP.



Overnight-cultured UCB CD133+ cells (single live cells)