

SUPPLEMENTAL INFORMATION for
Sort-purification of human CD34⁺CD90⁺ cells reduces target cell population and improves lentiviral transduction for gene therapy

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SUPPLEMENTAL METHODS:

Expression analysis for bulk RNAseq. RNAseq expression analysis was performed in shared resources at the Fred Hutchinson Cancer Research Center. RNAseq libraries of GCSF-mobilized CD34 subsets were prepared using the NuGEN Ovation SoLo RNAseq System (Tecan Genomics, Redwood City, CA, USA). RNAseq libraries of steady-state BM CD34 subsets were prepared using the SMART-Seq v4 Ultra Low Input RNA Kit (Takara Bio Inc., Kusatsu, Japan) and Nextera XT Index Kit v2 (Illumina, Inc., San Diego, CA, USA). Work was performed on a Sciclone NGSx Workstation (PerkinElmer, Waltham, MA, USA). Library size distribution was validated using an Agilent 2200 TapeStation (Agilent Technologies, Santa Clara, CA, USA). Additional library QC, blending of pooled indexed libraries, and cluster optimization was performed using Life Technologies Invitrogen Qubit® 2.0 Fluorometer (Life Technologies-Invitrogen, Carlsbad, CA, USA). RNAseq libraries were pooled and clustered onto a flow cell lane.

Quantification of transcripts. The quantification was performed using kallisto (v0.43.1) (49). Human genome assembly (GRCh38) from National Center for Biotechnology Information (NCBI) was used as the reference. The compressed fastq files (.fastq.gz) were input to kallisto. The human reference transcriptome was processed to create a transcriptome index using “kallisto index” option with the default k-mer length. The abundances of the transcripts were quantified by aligning the raw reads to the reference with bootstrapping, using the option “kallisto quant -b 100”. The bootstrapping was performed to obtain confidence intervals on transcript quantification. Kallisto generated two output files with the alignment information. The abundances.tsv reported the abundances as estimated counts (est_counts) and transcripts per million (tpm), while the abundances.h5 file had the abundance estimates, bootstrap estimates, transcript length information, and the run information.

Data analysis. The counts (abundances.tsv) from kallisto were imported into R in the form of a matrix with the tximport package (v.1.10.1). The Human RefSeq Reference Genome Annotation file (v.38_p12), was downloaded from the Human Genome Resources at NCBI to obtain the gene IDs. Each transcript ID and its count was then associated with the corresponding gene ID for summarization of gene-level counts. The count matrix was analyzed for differential gene expression using the DESeq2 package from Bioconductor in R (v.1.22.2).(50) The count matrix was pre-filtered by keeping the rows that have a minimum of one transcript before analysis with DESeq2. The result obtained was a list of differentially expressed genes with significant p-values

and log-fold changes. Clustering and principal component analysis (PCA) was performed on the normalized data, which identified the genes that were contributing to the variance in the samples.

Alignment and counting. The 10X Genomics Cell Ranger software suite (v2.0.0) was used to convert the raw sequence reads into single-cell gene expression counts. The “cellranger count” command with default option was run for alignment, filtering, cell barcode counting, and UMI counting. Cell barcode is a known nucleotide sequence that acts as a unique identifier for a single GEM (Gelbead-in-Emulsion) droplet. Each barcode contains reads from a single cell. UMIs are random 10bp nucleotide sequences that help determine which reads came from the same transcript. The cDNA was aligned to human reference genome (hg38) using the STAR aligner (v.2.6.1). UMIs were also filtered for a minimum of Qual = 10. Reads were marked as PCR duplicates if two or more read pairs shared the same cell barcode, UMI, and gene ID. Valid cell barcodes were determined based on the final UMI distributions. Valid cell barcodes with a valid UMI mapped to exons (Ensembl GTF GRCh38) were used to generate the final cell barcode matrix (.mtx).

Dimensional reduction and clustering. The single cell data analysis was performed using Seurat (v2.3.4) (23), an R toolkit for single cell genomic data. The 10X runs for the CD34⁺ cells and the CD34-subsets were merged by combining the cell barcode matrices into a single Seurat object. The gene expression data for each cell was log normalized. The genes were regressed based on the number of UMIs (nUMI), then scaled and centered to improve downstream analysis. PCA was run on the highly variable genes to compute linear dimensional reduction. The cells were clustered based on similar gene expression patterns using the first 10 principal components (PC) with a resolution of 0.4. t-distributed Stochastic Neighbor Embedding (tSNE) was used to visualize the gene clusters and the CD34⁺ cells and CD34-subsets. The positively differentially expressed genes were found for all the clusters based on the Wilcoxon rank sum test with a log-fold change threshold of 0.25. The gene expression patterns of marker genes were visualized on a tSNE dimensional reduction plot and a PCA dimensional reduction plot.

Single cell and bulk RNAseq combined analysis. DESeq2 (v.1.22.2) was run on the bulk RNA data as described above to create an un-normalized count matrix. The raw counts were transformed into a Single Cell Experiment (SCE) object along with the corresponding donor and gene information. The SCE is an R package that includes methods to store single cell data information. The raw counts were used to compute the normalized counts and log counts, which

are necessary to convert the SCE data object in to a Seurat data object. Using the Seurat package, the bulk RNAseq data was converted from an SCE object to a Seurat object. UMI counts were generated for the bulk RNA data and added as metadata to the object. Next, the bulk RNAseq data was merged with the single cell RNAseq data to create a combined Seurat dataset. The combined dataset was then log normalized and scaled as described above. This maintained uniformity in the scaling and normalization of both the single cell RNA and bulk RNA data together.

Transforming the data with significant principal components. The 10X run for the CD34⁺ cells was also analyzed by Seurat (v.2.3.4). The data was normalized and scaled. Variable genes were identified for the data and PCA was run on the variable genes. The genes were clustered using the first 10 PCs with a resolution of 0.4. The genes that defined PC1 and PC2 were extracted from the Seurat object.

A matrix was created by sub-setting the scaled count data matrix of the combined dataset using the PC1 and PC2 genes from the CD34⁺ data. This matrix was then multiplied with PC1 and PC2 values. The combined single cell and bulk RNA data was thus linearly transformed with the CD34⁺ cells as the reference and was used for further downstream analysis.

Overlaying the cell populations on the reference CD34⁺ cell population. Points specific for each of the different cell types from the bulk RNA data, the CD34⁺ cell population and the CD34 subset cell population were extracted from the combined dataset. PCA was used as the linear dimensional transform. The CD34⁺ population was plotted as the reference, and the cell types from the bulk RNA data were overlaid on the reference to see where they map. Similarly, the CD34 subsets were visualized against the CD34⁺ reference map.

Software and packages.

FlowJo v.10.2 and higher <https://www.flowjo.com>

Kallisto v.0.43.1 - <https://pachterlab.github.io/kallisto>

DESeq2 v.1.22.2 - <http://www.bioconductor.org/packages/release/bioc/html/DESeq2.html>

Tximport v.1.10.1 - <http://bioconductor.org/packages/release/bioc/html/tximport.html>

10X Genomics Chromium- <https://www.10xgenomics.com/product-list/#single-cell>

10X Genomics Cell Ranger v.2.0.0 - <https://support.10xgenomics.com/single-cell-gene-expression/software/overview/welcome>

STAR aligner v.2.6.1 - <https://github.com/alexdobin/STAR>

Seurat v.2.3.4 - <https://satijalab.org/seurat/>

SCE v.1.4.1 -

<https://www.bioconductor.org/packages/release/bioc/html/SingleCellExperiment.html>

Supplemental Table 1. Experimental parameters for scRNAseq

Donor	1				2	
	CD34 ⁺	CD133 ⁺	CD38 ^{low/-}	CD90 ⁺	CD34 ⁺	CD90 ⁺
# of cells	2,162	2,019	2,472	1,523	1,449	1,189
Mean reads/cell	75,692	71,796	64,918	75,971	62,234	64,282
Sequencing saturation	76.6%	76.9%	81.2%	81.7%	75.2%	79.1%
Fraction reads in cells	94.7%	94.6%	96.7%	96.4%	90.5%	94.5%
Valid barcodes	97.7%	98.0%	97.6%	97.9%	98.4%	98.4%
Total genes detected	18,132	18,036	18,150	17,430	17,183	16,321
Q30 bases in barcodes	97.4%	96.8%	97.4%	97.0%	96.2%	96.2%
Q30 bases in RNA reads	91.3%	87.2%	87.7%	86.0%	73.5%	73.6%
Q30 bases in sample index	96.3%	96.3%	96.5%	96.2%	96.2%	95.0%
Q30 bases in UMI	97.5%	96.8%	97.4%	97.0%	96.3%	96.3%

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
Cluster1					
AVP	1.03E-115	2.353924651	0.981	0.502	3.49E-111
FTH1	1.71E-83	1.085854554	1	0.999	5.75E-79
HLA-DQB1	2.49E-55	0.975850333	0.711	0.299	8.40E-51
IDS	4.68E-57	0.891481775	0.829	0.473	1.58E-52
HLA-E	4.26E-67	0.809263775	0.995	0.875	1.44E-62
DUSP1	3.91E-28	0.76632821	0.654	0.386	1.32E-23
BST2	8.26E-52	0.752152954	0.891	0.648	2.78E-47
RP11-386I14.4	4.26E-22	0.751011429	0.768	0.646	1.43E-17
VIM	9.70E-31	0.741547331	0.967	0.927	3.27E-26
MAFF	6.49E-49	0.739097989	0.559	0.185	2.19E-44
FOS	8.89E-25	0.735488763	0.744	0.526	2.99E-20
BEX1	2.47E-28	0.713080752	0.588	0.292	8.32E-24
TCOF1	5.53E-23	0.69756564	0.526	0.299	1.86E-18
CD37	1.30E-47	0.645982327	0.943	0.791	4.39E-43
NAMPT	1.40E-26	0.643196574	0.526	0.264	4.72E-22
HLA-DRB1	1.88E-20	0.635065174	0.782	0.695	6.33E-16
LST1	3.56E-28	0.622670938	0.801	0.596	1.20E-23
EIF3E	7.65E-64	0.613628537	1	0.976	2.58E-59
HOPX	1.76E-43	0.613337243	0.692	0.282	5.95E-39
HES1	1.30E-32	0.588868581	0.275	0.054	4.37E-28
JUN	5.06E-24	0.577589983	0.706	0.46	1.70E-19
LMNA	1.76E-13	0.573224391	0.63	0.459	5.93E-09
MLLT3	3.92E-25	0.558557455	0.668	0.439	1.32E-20
CEPB	1.32E-25	0.551536095	0.431	0.178	4.46E-21
SOCS2	2.60E-30	0.546971417	0.592	0.308	8.75E-26
ICAM3	1.01E-26	0.538519031	0.848	0.717	3.41E-22
GNA15	1.81E-27	0.537884801	0.834	0.676	6.11E-23
HLA-DPA1	8.59E-29	0.534735506	0.929	0.727	2.89E-24
MEG3	2.02E-101	0.531563048	0.322	0.012	6.81E-97
CD52	6.99E-28	0.52799503	0.791	0.512	2.36E-23
EIF4A2	5.96E-26	0.518842472	0.886	0.779	2.01E-21
FOSB	7.52E-18	0.513311832	0.488	0.273	2.53E-13
HLA-DPB1	3.47E-25	0.508814929	0.915	0.734	1.17E-20
ALDH1A1	6.12E-18	0.507369148	0.611	0.429	2.06E-13
PPP1CB	2.10E-15	0.499101171	0.706	0.591	7.08E-11
LRRKIP1	5.44E-27	0.496793361	0.882	0.72	1.83E-22
CD74	5.48E-31	0.486985875	0.986	0.971	1.85E-26
ID2	1.97E-10	0.486850753	0.502	0.355	6.63E-06
NEAT1	4.55E-19	0.479820832	0.929	0.836	1.53E-14
CRHBP	5.30E-44	0.465456032	0.384	0.08	1.79E-39
HLA-DRA	9.08E-29	0.46407168	0.976	0.897	3.06E-24
COMM6	6.01E-36	0.461057784	0.972	0.964	2.03E-31
ID1	4.67E-26	0.460080186	0.313	0.088	1.57E-21
GADD45A	1.60E-10	0.454692376	0.479	0.356	5.40E-06
TSC22D3	7.07E-14	0.454170716	0.716	0.582	2.38E-09
ZFAS1	3.84E-43	0.452325707	1	0.989	1.29E-38
PIM1	4.34E-19	0.4503663	0.616	0.381	1.46E-14
PABPC1	1.82E-43	0.449636534	1	0.995	6.12E-39
CTD-3252C9.4	1.06E-19	0.447752438	0.251	0.074	3.57E-15
ANKRD28	6.22E-23	0.442273671	0.953	0.921	2.09E-18
HSD17B11	3.97E-17	0.436022043	0.806	0.732	1.34E-12

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
ZFP36L2	2.13E-12	0.413234851	0.72	0.6	7.17E-08
MT-ND2	8.99E-41	0.409917186	1	0.999	3.03E-36
MALAT1	3.75E-54	0.405582722	1	1	1.26E-49
DDX5	1.28E-34	0.402617525	1	0.985	4.30E-30
ZNF331	9.37E-19	0.402477611	0.284	0.098	3.16E-14
CIRBP	6.08E-38	0.400230174	1	0.991	2.05E-33
RP1-313I6.12	6.52E-16	0.397016139	0.408	0.207	2.20E-11
MDK	3.57E-15	0.393164594	0.512	0.303	1.20E-10
RNF125	4.09E-16	0.384635603	0.45	0.25	1.38E-11
PTPRC	4.14E-15	0.383886265	0.654	0.507	1.40E-10
SQSTM1	2.83E-09	0.381792328	0.607	0.52	9.55E-05
PNRC1	1.34E-18	0.381150979	0.953	0.891	4.52E-14
PCDH9	5.34E-28	0.38082192	0.332	0.092	1.80E-23
FXYD5	9.14E-23	0.37906437	0.967	0.946	3.08E-18
YBX3	4.48E-13	0.377647661	0.853	0.803	1.51E-08
TCF4	3.66E-12	0.377538437	0.526	0.37	1.23E-07
RBM23	1.90E-13	0.374783295	0.488	0.324	6.39E-09
EIF1	1.09E-45	0.374707464	1	0.999	3.67E-41
FOSL2	4.44E-15	0.372805176	0.365	0.175	1.49E-10
H1F0	3.32E-10	0.369789578	0.607	0.476	1.12E-05
N4BP2L2	3.78E-11	0.369105821	0.592	0.495	1.27E-06
EIF2S3	1.54E-12	0.36691505	0.777	0.729	5.19E-08
HMGA2	2.15E-13	0.363950558	0.403	0.231	7.25E-09
SNHG7	1.41E-15	0.363676934	0.773	0.706	4.74E-11
SYPL1	3.81E-13	0.363520942	0.659	0.522	1.29E-08
HLA-DMA	5.12E-11	0.359864819	0.711	0.637	1.73E-06
PPP1R15A	2.02E-11	0.35161848	0.815	0.765	6.82E-07
CLU	2.00E-10	0.351204638	0.327	0.178	6.75E-06
RSL1D1	9.52E-19	0.349092663	0.905	0.849	3.21E-14
AJ006998.2	5.52E-37	0.347009663	0.232	0.032	1.86E-32
ARPC5L	5.45E-13	0.346977233	0.73	0.635	1.84E-08
GLTSCR2	9.72E-29	0.345468299	0.986	0.986	3.28E-24
TFPI	1.36E-10	0.344888346	0.559	0.446	4.59E-06
BEX2	3.12E-11	0.344463118	0.626	0.515	1.05E-06
DNAJB6	8.36E-16	0.341681698	0.877	0.872	2.82E-11
HLA-DQA1	1.16E-11	0.338184958	0.393	0.224	3.91E-07
TCEAL2	2.02E-62	0.336363608	0.194	0.007	6.81E-58
SELM	4.15E-48	0.336112804	0.209	0.016	1.40E-43
RELB	1.28E-08	0.334808699	0.436	0.317	0.00043288
LAPTM4A	6.25E-14	0.33185925	0.905	0.868	2.11E-09
EEF2	1.28E-33	0.33120199	1	0.995	4.32E-29
EIF1B	8.22E-12	0.330575053	0.81	0.789	2.77E-07
NBL1	2.31E-10	0.32990587	0.251	0.119	7.79E-06
APP	3.67E-11	0.329056417	0.422	0.261	1.24E-06
LAPTM5	4.04E-19	0.326375524	0.943	0.907	1.36E-14
BEX5	1.36E-16	0.324942338	0.303	0.118	4.59E-12
EIF5	9.47E-10	0.323760585	0.687	0.629	3.19E-05
CCNI	3.13E-17	0.322709514	0.957	0.955	1.06E-12
EVI2B	1.10E-10	0.320522256	0.445	0.283	3.71E-06
KIAA0125	3.49E-09	0.31280148	0.682	0.604	0.00011764
SOCS3	1.32E-14	0.309188673	0.19	0.055	4.45E-10
FNIP1	8.77E-10	0.307659527	0.678	0.637	2.96E-05
TSPYL2	3.97E-10	0.306051007	0.332	0.186	1.34E-05
INSIG1	8.73E-09	0.296219245	0.284	0.155	0.00029407
VAMP2	1.44E-08	0.294509969	0.791	0.789	0.00048642

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
IL18	5.81E-10	0.287963231	0.346	0.202	1.96E-05
TAF1D	4.71E-10	0.287072175	0.701	0.649	1.59E-05
EIF3D	3.91E-12	0.286881519	0.938	0.879	1.32E-07
C6orf48	7.44E-16	0.285435402	0.972	0.952	2.51E-11
AIF1	4.93E-13	0.2792119	0.957	0.89	1.66E-08
TPT1	7.86E-44	0.270713984	1	1	2.65E-39
TNFRSF14	5.05E-09	0.265251532	0.289	0.157	0.00017006
CISH	4.51E-12	0.264061235	0.237	0.094	1.52E-07
ST13	1.32E-11	0.258695643	0.967	0.921	4.44E-07
TPTEP1	1.54E-08	0.258242645	0.299	0.17	0.00051802
UBXN1	1.45E-08	0.253853365	0.73	0.703	0.00048762
ARMCX1	2.97E-09	0.250233829	0.265	0.134	0.00010015
Cluster2					
ELANE	2.69E-161	2.744038	0.948	0.457	9.07E-157
PRTN3	3.37E-180	2.657692	0.893	0.258	1.13E-175
LYZ	1.25E-147	2.581613	0.921	0.39	4.21E-143
AZU1	3.75E-196	2.53456	0.966	0.329	1.26E-191
MPO	1.83E-176	2.39908	0.997	0.764	6.17E-172
CFD	8.97E-170	1.615848	0.875	0.25	3.02E-165
SRGN	4.84E-136	1.600164	0.988	0.763	1.63E-131
CTSG	2.04E-165	1.450522	0.768	0.139	6.87E-161
AREG	9.25E-75	1.238173	0.814	0.431	3.12E-70
CALR	4.41E-83	1.136824	0.933	0.73	1.49E-78
RNASE2	3.74E-176	1.060139	0.686	0.079	1.26E-171
LGALS1	2.97E-64	1.057621	0.857	0.535	1.00E-59
CSTA	2.25E-189	1.015599	0.567	0.028	7.59E-185
CLEC11A	4.05E-89	0.953917	0.942	0.781	1.36E-84
TMSB4X	6.42E-80	0.837832	1	0.989	2.16E-75
HSP90B1	1.32E-64	0.801296	0.927	0.778	4.46E-60
MS4A3	1.93E-161	0.798535	0.607	0.053	6.49E-157
HCST	1.42E-62	0.771956	0.78	0.404	4.79E-58
CST7	2.22E-104	0.766323	0.497	0.074	7.47E-100
PRSS57	3.71E-99	0.760102	0.988	0.905	1.25E-94
MGST1	4.77E-60	0.741063	0.729	0.374	1.61E-55
ANXA1	1.05E-61	0.729686	0.939	0.743	3.53E-57
CYBA	8.49E-83	0.728603	0.979	0.847	2.86E-78
C1QTNF4	3.50E-49	0.719108	0.802	0.506	1.18E-44
IGLL1	3.18E-38	0.67795	0.835	0.625	1.07E-33
SEC61G	4.00E-59	0.665769	0.973	0.908	1.35E-54
RAB32	2.07E-58	0.625277	0.649	0.281	6.99E-54
MCL1	4.62E-40	0.600544	0.787	0.597	1.56E-35
MT-ND4L	1.14E-46	0.600183	0.957	0.818	3.83E-42
HSPB1	8.02E-54	0.599185	0.927	0.776	2.70E-49
PLEK	1.15E-54	0.586194	0.607	0.241	3.87E-50
CPA3	1.57E-55	0.563443	0.518	0.169	5.29E-51
CTC-425F1.4	1.30E-21	0.563306	0.207	0.057	4.38E-17
APLP2	9.24E-35	0.537109	0.784	0.587	3.11E-30
TNFSF13B	5.06E-48	0.536009	0.546	0.219	1.70E-43
SSR4	1.71E-45	0.527248	0.939	0.863	5.76E-41
HSPA5	2.86E-39	0.523157	0.918	0.77	9.65E-35
SNHG25	1.11E-42	0.513366	0.948	0.895	3.73E-38
RNASE3	7.73E-104	0.509533	0.329	0.016	2.61E-99
MT-CO2	2.03E-78	0.500118	1	1	6.84E-74
P4HB	7.23E-39	0.491479	0.869	0.704	2.43E-34

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
DBI	1.39E-26	0.489876	0.692	0.497	4.67E-22
JUND	1.36E-25	0.488885	0.896	0.782	4.57E-21
TMEM258	2.40E-43	0.475689	0.945	0.87	8.10E-39
LCP1	1.57E-29	0.467256	0.683	0.459	5.29E-25
C4orf48	6.60E-31	0.464646	0.595	0.333	2.22E-26
NPW	1.35E-27	0.463511	0.655	0.405	4.56E-23
TYROBP	7.96E-33	0.452162	0.451	0.185	2.68E-28
SAT1	3.55E-30	0.451953	0.884	0.769	1.20E-25
EREG	6.47E-19	0.44688	0.561	0.372	2.18E-14
SDF2L1	9.68E-29	0.444351	0.454	0.213	3.26E-24
PPIB	1.54E-29	0.439397	0.857	0.768	5.20E-25
ATP5I	1.74E-38	0.43772	0.963	0.919	5.85E-34
MT-ATP6	4.48E-49	0.43431	1	0.999	1.51E-44
PLAC8	4.82E-23	0.426721	0.86	0.738	1.62E-18
GSTP1	1.80E-39	0.41591	0.988	0.958	6.06E-35
ROMO1	6.46E-26	0.41124	0.823	0.684	2.18E-21
TMSB10	7.56E-49	0.409791	1	0.998	2.55E-44
FAM101B	1.06E-29	0.399849	0.494	0.228	3.57E-25
ATP6V0B	3.26E-23	0.396569	0.771	0.64	1.10E-18
SERF2	9.22E-51	0.39246	1	0.993	3.11E-46
MT-ND4	6.58E-49	0.391914	1	1	2.22E-44
MT-ND5	1.33E-35	0.389783	0.991	0.991	4.48E-31
COX7B	1.72E-25	0.389771	0.927	0.867	5.80E-21
NDUFA3	1.32E-22	0.385684	0.774	0.637	4.46E-18
MAP3K8	5.03E-20	0.382961	0.78	0.616	1.69E-15
C14orf2	7.99E-41	0.382948	0.997	0.978	2.69E-36
GRN	2.10E-22	0.380456	0.555	0.354	7.07E-18
MT-ND3	6.72E-51	0.377773	1	0.999	2.26E-46
GPX1	7.86E-30	0.374621	0.939	0.923	2.65E-25
FTL	1.20E-41	0.373425	0.997	1	4.04E-37
NKG7	1.27E-34	0.371147	0.393	0.134	4.29E-30
PDIA6	1.22E-17	0.367405	0.738	0.641	4.10E-13
VAMP8	4.51E-22	0.363554	0.86	0.809	1.52E-17
POLR2L	2.23E-20	0.362418	0.89	0.773	7.50E-16
UQCR11	3.72E-25	0.357988	0.924	0.853	1.25E-20
NUCB2	1.22E-22	0.357183	0.915	0.875	4.12E-18
MT-ND1	3.18E-41	0.353454	1	0.999	1.07E-36
VAMP5	3.96E-14	0.35012	0.524	0.362	1.33E-09
SERPINB10	3.56E-67	0.348605	0.22	0.011	1.20E-62
MYDGF	1.37E-16	0.348426	0.665	0.544	4.63E-12
FKBP2	8.98E-22	0.348035	0.43	0.223	3.03E-17
RAB31	2.12E-30	0.346673	0.293	0.082	7.13E-26
PDIA4	6.27E-20	0.340459	0.409	0.217	2.11E-15
FOSL2	1.68E-25	0.338962	0.39	0.158	5.64E-21
PHPT1	1.21E-14	0.3376	0.668	0.553	4.09E-10
SPI1	2.44E-24	0.332759	0.476	0.244	8.23E-20
ATP5E	9.11E-33	0.330138	0.994	0.987	3.07E-28
CSF3R	8.33E-20	0.329386	0.637	0.397	2.81E-15
UQCRRQ	1.42E-20	0.329019	0.939	0.88	4.77E-16
CD302	1.73E-18	0.326487	0.421	0.227	5.82E-14
SNHG9	8.05E-18	0.323892	0.902	0.897	2.71E-13
XBP1	1.65E-14	0.322896	0.823	0.755	5.56E-10
CANX	5.26E-15	0.322416	0.787	0.699	1.77E-10
MT-CO3	3.36E-42	0.320441	1	1	1.13E-37
NDUFC2	7.01E-14	0.319152	0.811	0.754	2.36E-09

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
FABP5	2.48E-13	0.316524	0.631	0.519	8.36E-09
TMED10	6.51E-16	0.315693	0.716	0.607	2.20E-11
RPN1	4.28E-12	0.312348	0.485	0.363	1.44E-07
SPARC	1.66E-18	0.311369	0.415	0.214	5.58E-14
LAMTOR4	1.86E-13	0.309527	0.805	0.761	6.28E-09
MIF	1.41E-24	0.308745	0.966	0.938	4.73E-20
TMEM205	2.44E-15	0.307507	0.439	0.278	8.23E-11
FLNA	8.76E-15	0.305929	0.482	0.318	2.95E-10
NDUFA13	6.77E-17	0.301454	0.823	0.715	2.28E-12
AIF1	2.62E-20	0.297127	0.976	0.882	8.84E-16
PLD1	5.88E-28	0.2958	0.28	0.084	1.98E-23
SEC61B	2.30E-22	0.295512	0.93	0.889	7.75E-18
USMG5	4.29E-15	0.291731	0.89	0.847	1.45E-10
NDUFB2	3.28E-12	0.290223	0.735	0.645	1.11E-07
TPP1	2.03E-15	0.289601	0.384	0.209	6.83E-11
ATOX1	3.16E-10	0.28749	0.604	0.515	1.06E-05
MYL6	1.80E-23	0.287302	0.982	0.969	6.08E-19
IQGAP1	1.56E-10	0.28394	0.677	0.572	5.24E-06
SPCS3	6.44E-12	0.282456	0.555	0.43	2.17E-07
PPIA	1.74E-24	0.28117	0.997	0.989	5.85E-20
RASGRP2	5.00E-11	0.279351	0.524	0.395	1.68E-06
NGFRAP1	1.19E-11	0.278936	0.762	0.697	4.01E-07
MT-CO1	1.52E-26	0.27842	1	1	5.11E-22
FNDC3B	4.78E-26	0.277402	0.28	0.088	1.61E-21
PTPRE	4.35E-16	0.277239	0.372	0.189	1.47E-11
NDUFS6	2.43E-10	0.275211	0.695	0.599	8.18E-06
KBTBD11	7.28E-27	0.274548	0.253	0.07	2.45E-22
CNIH4	5.87E-11	0.273355	0.345	0.214	1.98E-06
SMIM24	9.30E-12	0.272184	0.765	0.611	3.14E-07
HMGN2	2.56E-27	0.270688	0.997	0.991	8.63E-23
IFI27L2	1.07E-13	0.269049	0.442	0.273	3.61E-09
RNASEH2C	1.66E-09	0.268946	0.665	0.567	5.58E-05
CKLF	8.24E-12	0.267731	0.451	0.303	2.78E-07
FAM45A	1.06E-09	0.266033	0.445	0.324	3.57E-05
NEAT1	3.34E-15	0.265367	0.89	0.838	1.12E-10
IGFBP7	7.39E-14	0.263755	0.759	0.642	2.49E-09
PET100	1.32E-12	0.263593	0.851	0.815	4.45E-08
HLA-DRB1	3.51E-13	0.257118	0.78	0.69	1.18E-08
NUFIP2	6.37E-09	0.256966	0.439	0.331	0.000215
HGF	1.33E-34	0.255717	0.256	0.055	4.47E-30
PDIA3	1.10E-11	0.254455	0.814	0.761	3.69E-07
RETN	2.88E-46	0.253997	0.149	0.007	9.72E-42
TXN	1.46E-14	0.252063	0.966	0.948	4.92E-10
ANAPC11	9.99E-11	0.252011	0.701	0.614	3.37E-06
RUNX1	4.44E-09	0.250016	0.61	0.516	0.00015
Cluster3					
HBB	2.96E-83	2.787861	0.986	0.755	9.97E-79
CA1	1.01E-161	1.619034	0.835	0.165	3.41E-157
AHSP	6.45E-169	1.43328	0.786	0.119	2.17E-164
APOC1	2.31E-156	1.419228	0.961	0.299	7.78E-152
BLVRB	1.24E-147	1.349222	0.958	0.36	4.18E-143
S100A6	1.00E-122	1.292952	0.996	0.755	3.38E-118
FAM178B	2.66E-144	1.287929	0.832	0.183	8.95E-140
HBD	9.29E-152	1.149007	0.779	0.127	3.13E-147

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
ATPIF1	1.32E-113	1.131086	0.993	0.755	4.44E-109
PRDX2	2.62E-95	1.046908	0.979	0.691	8.83E-91
APOE	2.11E-151	0.854443	0.804	0.135	7.09E-147
TMEM14C	2.15E-105	0.850809	0.982	0.54	7.25E-101
UROD	7.02E-111	0.827546	0.954	0.412	2.37E-106
S100A4	3.79E-88	0.825483	0.996	0.898	1.28E-83
TUBB2A	2.89E-169	0.761819	0.716	0.077	9.75E-165
MPC2	4.85E-92	0.747358	0.989	0.679	1.64E-87
TFR2	1.75E-147	0.729605	0.856	0.164	5.91E-143
LMNA	8.20E-69	0.719628	0.909	0.41	2.76E-64
PLIN2	4.57E-79	0.704074	0.898	0.389	1.54E-74
HIST1H4C	1.24E-30	0.693404	0.968	0.749	4.17E-26
CALM2	3.46E-78	0.667808	0.989	0.744	1.16E-73
KCNH2	1.99E-176	0.663931	0.702	0.064	6.71E-172
HMGB2	1.54E-58	0.663117	0.996	0.866	5.20E-54
REXO2	8.65E-99	0.66154	0.849	0.257	2.91E-94
EPCAM	3.63E-168	0.653653	0.691	0.068	1.22E-163
CKS1B	3.35E-66	0.650566	0.779	0.299	1.13E-61
LINC00152	6.35E-73	0.634383	0.979	0.602	2.14E-68
PVT1	3.48E-134	0.628236	0.782	0.137	1.17E-129
FBXO7	1.08E-75	0.620988	0.979	0.604	3.65E-71
HNRNPAB	8.81E-73	0.594187	0.926	0.459	2.97E-68
TMEM14B	5.21E-65	0.594151	0.954	0.64	1.75E-60
NFKBIA	5.63E-41	0.589784	0.919	0.631	1.90E-36
DUT	4.76E-47	0.588257	0.975	0.731	1.60E-42
CA2	3.24E-144	0.577725	0.618	0.061	1.09E-139
EMP3	3.84E-65	0.570029	0.982	0.677	1.30E-60
CNRIP1	1.55E-128	0.564396	0.793	0.139	5.22E-124
SMIM1	1.33E-124	0.559092	0.765	0.135	4.47E-120
KIAA0101	3.13E-43	0.547589	0.958	0.608	1.06E-38
CDK4	4.41E-66	0.540224	0.912	0.427	1.49E-61
H2AFZ	1.89E-53	0.539341	0.996	0.872	6.37E-49
H1FX	8.11E-35	0.538999	0.986	0.918	2.73E-30
CENPU	2.53E-63	0.537207	0.835	0.348	8.52E-59
SLIRP	6.22E-60	0.535948	0.937	0.532	2.10E-55
ISOC2	1.26E-86	0.530929	0.804	0.239	4.25E-82
HNRNPA2B1	5.09E-56	0.524532	0.993	0.832	1.72E-51
MINOS1	3.40E-62	0.524265	0.912	0.426	1.15E-57
ALDH1A1	1.22E-61	0.520157	0.898	0.378	4.12E-57
TYMS	1.47E-39	0.51875	0.909	0.519	4.96E-35
SERBP1	6.15E-59	0.516772	0.975	0.825	2.07E-54
ECH1	8.87E-58	0.51606	0.909	0.481	2.99E-53
MIR4435-2HG	9.68E-73	0.514029	0.863	0.313	3.26E-68
PA2G4	1.66E-61	0.513073	0.996	0.789	5.59E-57
CD59	2.11E-59	0.50653	0.832	0.344	7.12E-55
HSP90AA1	8.17E-64	0.500186	1	0.979	2.75E-59
MCM7	3.48E-48	0.498765	0.888	0.476	1.17E-43
NOP58	5.56E-46	0.496705	0.912	0.526	1.87E-41
CXADR	5.84E-106	0.494734	0.67	0.115	1.97E-101
HMBS	3.07E-98	0.490346	0.719	0.158	1.03E-93
SYNGR1	1.15E-41	0.489235	0.919	0.606	3.88E-37
TPGS2	2.40E-65	0.487827	0.842	0.342	8.09E-61
TXNIP	5.16E-45	0.487733	0.951	0.601	1.74E-40
ATP5G1	5.07E-49	0.486279	0.947	0.612	1.71E-44
CAT	3.67E-47	0.483576	0.958	0.658	1.24E-42

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
HMGB1	2.90E-66	0.482383	1	0.988	9.78E-62
PCNA	5.84E-53	0.480507	0.751	0.274	1.97E-48
HMGN5	1.67E-61	0.480234	0.811	0.311	5.61E-57
MPST	2.06E-50	0.478001	0.919	0.508	6.95E-46
NAA38	1.04E-51	0.476104	0.982	0.74	3.49E-47
NUDC	1.35E-53	0.475885	0.933	0.547	4.55E-49
SOD1	1.38E-52	0.472889	0.989	0.816	4.66E-48
MARCKSL1	7.06E-48	0.472153	0.951	0.542	2.38E-43
CKS2	7.04E-39	0.471816	0.825	0.406	2.37E-34
PDLIM1	6.02E-60	0.470259	0.898	0.365	2.03E-55
FKBP4	5.01E-63	0.466522	0.744	0.254	1.69E-58
HSPD1	1.34E-35	0.465203	0.972	0.677	4.52E-31
FHL2	4.22E-126	0.462497	0.681	0.096	1.42E-121
PRKAR2B	3.04E-86	0.460816	0.775	0.198	1.02E-81
MRPL52	3.89E-54	0.457338	0.891	0.419	1.31E-49
C1QBP	5.94E-50	0.456002	0.979	0.783	2.00E-45
BSG	1.80E-45	0.455517	0.979	0.646	6.05E-41
CCT5	2.05E-62	0.455347	0.832	0.318	6.91E-58
RANBP1	4.23E-46	0.455252	0.979	0.727	1.42E-41
HIST2H2AC	1.30E-09	0.454835	0.607	0.399	4.39E-05
GTF2A2	2.26E-53	0.453877	0.916	0.457	7.61E-49
NDFIP1	1.07E-67	0.450882	0.86	0.306	3.59E-63
DNAJC9	2.61E-56	0.450384	0.832	0.327	8.78E-52
TUBB4B	6.59E-47	0.446851	0.695	0.256	2.22E-42
CACYBP	1.97E-50	0.444564	0.895	0.45	6.64E-46
POLR2L	1.38E-41	0.444494	0.982	0.762	4.64E-37
ZFP36L1	3.14E-78	0.442039	0.649	0.144	1.06E-73
PHB	7.58E-45	0.441981	0.912	0.539	2.55E-40
ITGA2B	8.46E-70	0.441782	0.839	0.262	2.85E-65
ACTB	9.75E-62	0.441321	1	0.995	3.28E-57
PTBP1	3.57E-49	0.441017	0.93	0.525	1.20E-44
TOMM40	1.69E-57	0.440772	0.789	0.305	5.69E-53
TRIB2	1.83E-101	0.439053	0.67	0.117	6.16E-97
NCL	6.31E-46	0.437974	0.996	0.909	2.13E-41
HSPE1	1.62E-29	0.434049	0.888	0.541	5.45E-25
PPP1R14A	3.74E-111	0.431792	0.653	0.099	1.26E-106
HBA1	1.42E-59	0.430859	0.333	0.046	4.79E-55
MCM5	1.65E-45	0.429281	0.828	0.377	5.54E-41
POLR2F	4.04E-57	0.42924	0.849	0.336	1.36E-52
HMGA1	2.06E-53	0.425192	0.996	0.931	6.93E-49
NME4	2.96E-44	0.423559	0.951	0.655	9.96E-40
TRMT112	6.36E-42	0.422347	0.916	0.551	2.14E-37
MAP2K2	6.16E-60	0.41902	0.821	0.303	2.08E-55
NET1	1.40E-58	0.418855	0.796	0.284	4.73E-54
MRPS34	5.80E-65	0.418008	0.744	0.234	1.95E-60
BLVRA	8.73E-67	0.41699	0.821	0.282	2.94E-62
DECRI	1.14E-57	0.416942	0.793	0.293	3.84E-53
HES6	3.41E-121	0.416589	0.604	0.072	1.15E-116
CCDC112	5.44E-91	0.416332	0.649	0.128	1.83E-86
TPM1	1.25E-83	0.415811	0.786	0.194	4.23E-79
ATP5J2	2.27E-41	0.415645	0.989	0.739	7.66E-37
GLRX5	2.29E-52	0.414755	0.782	0.32	7.71E-48
RAN	2.14E-40	0.414183	0.986	0.755	7.21E-36
ATP5G3	9.70E-47	0.413719	0.986	0.885	3.27E-42
TUBB	3.49E-19	0.413025	0.979	0.861	1.18E-14

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
PCCB	3.69E-79	0.412448	0.716	0.18	1.24E-74
DNPH1	7.81E-47	0.409908	0.919	0.478	2.63E-42
CYC1	3.51E-42	0.40988	0.93	0.585	1.18E-37
STK25	1.96E-72	0.409299	0.775	0.229	6.59E-68
ERH	1.68E-43	0.409123	0.986	0.723	5.65E-39
TIMM8B	8.59E-57	0.406925	0.793	0.294	2.89E-52
NASP	9.11E-37	0.406255	0.947	0.625	3.07E-32
ANK1	2.16E-127	0.406025	0.568	0.057	7.27E-123
FXN	1.88E-72	0.403459	0.772	0.224	6.34E-68
EIF4G2	8.41E-39	0.403018	0.986	0.771	2.83E-34
EIF5A	1.52E-41	0.400981	0.996	0.871	5.12E-37
DAD1	1.09E-40	0.400129	0.916	0.498	3.67E-36
OAZ1	1.11E-49	0.399691	0.996	0.888	3.74E-45
SUPT16H	1.22E-56	0.398733	0.811	0.305	4.11E-52
NOP10	1.11E-36	0.393817	0.961	0.664	3.75E-32
NME1	1.71E-37	0.393708	0.895	0.554	5.76E-33
MCM3	3.17E-71	0.39323	0.684	0.179	1.07E-66
FCGRT	1.22E-39	0.393159	0.814	0.388	4.10E-35
CST3	6.61E-41	0.391757	0.958	0.681	2.23E-36
GAR1	1.99E-51	0.3907	0.765	0.288	6.71E-47
DYNLRB1	1.74E-46	0.385982	0.912	0.438	5.85E-42
YBX1	4.51E-64	0.385742	1	0.992	1.52E-59
SLC39A3	7.78E-61	0.38552	0.775	0.253	2.62E-56
SNRPD3	1.15E-39	0.385423	0.874	0.48	3.89E-35
UBAC1	8.81E-66	0.384608	0.632	0.165	2.97E-61
MRPL12	7.51E-58	0.38417	0.751	0.255	2.53E-53
HIST1H1D	2.28E-26	0.383972	0.698	0.346	7.67E-22
TIMM13	3.24E-35	0.383959	0.968	0.733	1.09E-30
CENPF	3.22E-59	0.3818	0.604	0.161	1.08E-54
FUS	4.09E-39	0.38173	0.993	0.864	1.38E-34
HEBP1	4.57E-48	0.380707	0.768	0.303	1.54E-43
ADCK3	2.17E-55	0.380449	0.8	0.298	7.31E-51
CD82	3.65E-43	0.378442	0.835	0.397	1.23E-38
SMIM10	1.56E-111	0.375975	0.611	0.084	5.26E-107
ITGB1	4.68E-44	0.373877	0.768	0.314	1.58E-39
SNRPG	2.55E-35	0.373613	0.951	0.623	8.60E-31
CTNNBL1	1.03E-52	0.372534	0.846	0.326	3.46E-48
POP7	1.45E-61	0.372211	0.726	0.223	4.87E-57
BOLA3	1.13E-63	0.372133	0.716	0.216	3.80E-59
RUVBL2	7.42E-46	0.371848	0.853	0.383	2.50E-41
MYL12A	9.74E-38	0.371259	0.958	0.604	3.28E-33
MPP1	6.45E-49	0.371002	0.825	0.35	2.17E-44
ATP5B	3.09E-44	0.370725	0.989	0.873	1.04E-39
TRAP1	8.05E-67	0.370402	0.695	0.195	2.71E-62
PSMC3	3.12E-34	0.370216	0.912	0.527	1.05E-29
STRA13	1.34E-45	0.369671	0.712	0.269	4.51E-41
TUBA1C	1.17E-34	0.369294	0.853	0.446	3.94E-30
TUBA1B	3.85E-24	0.369234	0.996	0.952	1.30E-19
FECH	1.18E-69	0.368418	0.618	0.148	3.99E-65
TAF9	7.10E-33	0.368033	0.937	0.622	2.39E-28
SDCBP	3.78E-34	0.36717	0.891	0.49	1.27E-29
CENPV	1.66E-50	0.365373	0.821	0.324	5.59E-46
MTCH2	2.13E-48	0.361005	0.747	0.282	7.18E-44
SRM	8.27E-36	0.360497	0.849	0.442	2.79E-31
STMN1	1.86E-33	0.359375	0.996	0.853	6.26E-29

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
TPI1	3.93E-32	0.359139	0.982	0.858	1.32E-27
PPA2	3.62E-43	0.358923	0.688	0.259	1.22E-38
C11orf31	3.31E-35	0.358059	0.968	0.684	1.11E-30
PSMA7	3.66E-33	0.357065	0.982	0.799	1.23E-28
TUFM	1.61E-35	0.356712	0.968	0.733	5.43E-31
EIF4EBP1	7.19E-45	0.354532	0.853	0.377	2.42E-40
SMS	1.94E-35	0.353201	0.888	0.503	6.55E-31
HSPA8	7.71E-20	0.353101	0.888	0.628	2.60E-15
GNG5	5.43E-35	0.351877	0.94	0.646	1.83E-30
NDUFAF3	1.47E-54	0.349846	0.782	0.27	4.95E-50
PRMT1	4.21E-34	0.348933	0.916	0.574	1.42E-29
PSMB2	1.24E-35	0.348297	0.877	0.471	4.16E-31
RBX1	2.14E-31	0.346806	0.916	0.575	7.20E-27
PSMA4	8.97E-32	0.346037	0.937	0.638	3.02E-27
PCBP1	1.87E-28	0.343591	0.968	0.723	6.30E-24
GATA1	6.12E-91	0.342818	0.611	0.102	2.06E-86
UQCRQ	3.45E-37	0.34256	0.996	0.873	1.16E-32
YWHAB	4.92E-32	0.342363	0.937	0.596	1.66E-27
TSPO	7.33E-31	0.342275	0.965	0.749	2.47E-26
EAPP	1.45E-31	0.341543	0.916	0.561	4.89E-27
PAFAH1B3	8.80E-36	0.340916	0.835	0.425	2.97E-31
YWHAQ	7.35E-30	0.340623	0.958	0.743	2.48E-25
NFIA	2.90E-86	0.33973	0.604	0.107	9.78E-82
LSM3	1.14E-31	0.339667	0.965	0.655	3.84E-27
SNRPB	3.34E-35	0.338771	0.989	0.846	1.13E-30
H2AFV	2.02E-30	0.338225	0.965	0.7	6.82E-26
CSF1	2.90E-77	0.337314	0.446	0.063	9.77E-73
IER5	4.23E-55	0.337258	0.656	0.192	1.43E-50
POMP	2.74E-32	0.337163	0.982	0.804	9.23E-28
CCNB2	4.91E-56	0.33661	0.47	0.104	1.65E-51
PKIG	3.57E-46	0.33637	0.87	0.367	1.20E-41
RBBP7	2.83E-34	0.336285	0.881	0.475	9.54E-30
HNRNPK	1.42E-36	0.333656	0.993	0.897	4.78E-32
CAST	1.31E-40	0.33359	0.702	0.279	4.40E-36
ATP5A1	7.27E-37	0.333347	0.993	0.872	2.45E-32
XRCC5	7.86E-34	0.332868	0.877	0.469	2.65E-29
NDUFC2	2.55E-34	0.33233	0.975	0.73	8.60E-30
SRSF2	7.98E-27	0.332221	0.965	0.768	2.69E-22
PFN1	4.52E-38	0.331905	1	0.96	1.52E-33
POLD2	5.73E-33	0.33182	0.825	0.423	1.93E-28
TMEM141	1.65E-43	0.331728	0.737	0.286	5.57E-39
DDX39A	3.39E-33	0.331694	0.856	0.44	1.14E-28
APOBEC3C	5.07E-47	0.330981	0.663	0.217	1.71E-42
NMI	4.03E-46	0.330959	0.8	0.308	1.36E-41
ETFA	2.65E-50	0.330852	0.73	0.248	8.94E-46
HSD17B10	1.40E-36	0.330214	0.867	0.427	4.70E-32
UBE2C	8.63E-20	0.330114	0.365	0.14	2.91E-15
UQCR10	1.06E-30	0.329954	0.937	0.636	3.57E-26
KPNA2	2.95E-29	0.327564	0.705	0.331	9.96E-25
UBB	4.03E-40	0.327455	0.996	0.986	1.36E-35
AKR1C3	1.25E-48	0.326692	0.695	0.23	4.21E-44
HDAC2	5.71E-31	0.326659	0.895	0.498	1.92E-26
PARVB	7.10E-41	0.326352	0.796	0.346	2.39E-36
MRPL1	1.11E-45	0.325997	0.73	0.269	3.74E-41
PITHD1	1.62E-36	0.32568	0.86	0.449	5.47E-32

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
BCLAF1	6.32E-32	0.325393	0.996	0.784	2.13E-27
UBL5	1.69E-29	0.324385	0.979	0.792	5.70E-25
MRPL20	1.32E-46	0.323634	0.751	0.284	4.44E-42
CD36	6.56E-143	0.323326	0.463	0.021	2.21E-138
TIMP1	9.56E-32	0.323128	0.853	0.453	3.22E-27
HNRNPR	1.29E-30	0.323027	0.958	0.609	4.33E-26
SLC25A39	1.46E-35	0.322812	0.842	0.398	4.92E-31
SSB	5.67E-28	0.322757	0.947	0.643	1.91E-23
CD40LG	6.26E-98	0.32273	0.449	0.045	2.11E-93
GPX4	2.24E-33	0.32036	0.989	0.84	7.54E-29
HBS1L	6.11E-46	0.320183	0.758	0.281	2.06E-41
UBE2S	7.72E-54	0.319005	0.66	0.196	2.60E-49
CCT6A	3.84E-29	0.318886	0.93	0.592	1.29E-24
MAF1	1.53E-27	0.318498	0.912	0.598	5.16E-23
ATF7IP2	8.41E-11	0.318457	0.818	0.622	2.83E-06
CENPW	3.09E-40	0.317993	0.614	0.219	1.04E-35
DTYMK	2.91E-58	0.317726	0.639	0.178	9.82E-54
DSTN	9.42E-25	0.31707	0.93	0.649	3.17E-20
MT2A	8.32E-30	0.316216	0.751	0.338	2.80E-25
DNAJC15	2.98E-30	0.316213	0.832	0.43	1.00E-25
STOML2	3.46E-30	0.316072	0.954	0.622	1.17E-25
IMP3	6.93E-46	0.315808	0.688	0.242	2.34E-41
MAP7	1.83E-55	0.31526	0.604	0.161	6.16E-51
PARP1	5.48E-34	0.31518	0.821	0.411	1.85E-29
RP11-354E11.2	3.59E-38	0.314827	0.684	0.254	1.21E-33
POLR2E	2.87E-31	0.314613	0.94	0.559	9.68E-27
LYAR	3.17E-89	0.314485	0.498	0.07	1.07E-84
TK1	3.16E-34	0.314384	0.502	0.17	1.06E-29
TFDP1	9.59E-39	0.314321	0.835	0.378	3.23E-34
CNBP	2.83E-30	0.313579	0.979	0.777	9.53E-26
BIRC5	3.53E-35	0.313424	0.523	0.18	1.19E-30
NDUFB6	7.85E-34	0.313171	0.793	0.373	2.64E-29
SELENBP1	3.55E-103	0.312666	0.365	0.021	1.19E-98
NDUFB9	1.97E-33	0.311972	0.982	0.839	6.65E-29
TESC	6.77E-64	0.311112	0.625	0.155	2.28E-59
SLC39A8	2.40E-39	0.310847	0.807	0.342	8.09E-35
MRPL4	4.02E-39	0.310576	0.793	0.344	1.35E-34
PRPF19	1.22E-40	0.31016	0.779	0.315	4.12E-36
ODC1	4.45E-28	0.309869	0.909	0.559	1.50E-23
MRPL51	1.02E-33	0.309116	0.818	0.384	3.43E-29
FSCN1	1.04E-40	0.309079	0.765	0.305	3.52E-36
CCT2	1.12E-26	0.309062	0.965	0.708	3.79E-22
ENY2	1.71E-29	0.308736	0.954	0.684	5.77E-25
NOLC1	9.58E-49	0.307961	0.635	0.198	3.23E-44
GTF3C6	4.02E-34	0.307346	0.782	0.371	1.36E-29
COX5A	1.56E-30	0.307234	0.993	0.835	5.27E-26
SLC39A4	5.70E-49	0.306696	0.632	0.2	1.92E-44
CCT7	1.81E-28	0.306459	0.898	0.547	6.10E-24
PRELID1	7.52E-25	0.30595	0.923	0.638	2.53E-20
CDCA4	2.54E-44	0.304771	0.537	0.159	8.56E-40
TFRC	1.00E-31	0.304558	0.73	0.331	3.37E-27
PRKDC	8.06E-33	0.304429	0.751	0.342	2.72E-28
MTX1	1.59E-41	0.304023	0.744	0.289	5.34E-37
SDHA	6.48E-36	0.303479	0.782	0.342	2.18E-31

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
GADD45GIP1	1.06E-25	0.303013	0.909	0.595	3.58E-21
TXN2	1.06E-26	0.302338	0.846	0.491	3.58E-22
HN1	2.43E-29	0.302302	0.804	0.421	8.20E-25
PXMP2	1.40E-39	0.302275	0.754	0.307	4.73E-35
AP2M1	1.10E-26	0.302206	0.958	0.732	3.70E-22
RALBP1	3.39E-38	0.302175	0.796	0.334	1.14E-33
CYCS	2.25E-25	0.302047	0.895	0.551	7.58E-21
EBNA1BP2	3.20E-44	0.301589	0.775	0.295	1.08E-39
SUMO2	1.31E-33	0.301373	0.993	0.923	4.41E-29
HNRNPDL	6.71E-23	0.301244	0.937	0.608	2.26E-18
DYNLL1	1.07E-42	0.301185	0.561	0.168	3.60E-38
MYL4	9.93E-124	0.301064	0.474	0.034	3.34E-119
HADH	1.26E-42	0.300451	0.744	0.285	4.25E-38
CALM3	5.68E-26	0.300095	0.916	0.593	1.91E-21
TMEM109	2.30E-42	0.29974	0.702	0.258	7.75E-38
GHITM	5.49E-28	0.299393	0.863	0.489	1.85E-23
PDCD4	4.07E-26	0.299088	0.877	0.496	1.37E-21
ZNF451	1.59E-34	0.299043	0.807	0.349	5.35E-30
DKC1	7.85E-35	0.298722	0.775	0.333	2.65E-30
LPCAT3	1.40E-70	0.29801	0.554	0.111	4.71E-66
PCMT1	6.59E-49	0.297107	0.628	0.192	2.22E-44
MT-CO3	8.31E-50	0.297042	1	1	2.80E-45
MCM2	4.79E-58	0.296994	0.558	0.137	1.61E-53
MPDU1	1.99E-50	0.296902	0.646	0.2	6.70E-46
VBP1	4.66E-43	0.296884	0.779	0.308	1.57E-38
SNX5	1.05E-35	0.296768	0.775	0.32	3.53E-31
MAD2L1	2.66E-47	0.295969	0.596	0.183	8.95E-43
ACADVL	4.22E-28	0.295812	0.863	0.509	1.42E-23
NOSIP	4.37E-43	0.295796	0.751	0.281	1.47E-38
RAC1	4.72E-31	0.295758	0.982	0.824	1.59E-26
MRPL37	6.39E-34	0.29562	0.818	0.383	2.15E-29
SRRM2	7.70E-30	0.295262	0.975	0.727	2.60E-25
7-Sep	6.18E-26	0.294928	0.968	0.72	2.08E-21
CISD2	4.10E-36	0.293931	0.74	0.308	1.38E-31
MRPL41	4.49E-33	0.293841	0.835	0.409	1.51E-28
C17orf89	2.53E-29	0.293835	0.881	0.475	8.52E-25
TMBIM6	2.27E-26	0.29371	0.965	0.671	7.64E-22
FDPS	1.80E-35	0.293495	0.789	0.342	6.08E-31
SRI	6.39E-24	0.292894	0.874	0.537	2.15E-19
CMSS1	2.48E-48	0.292822	0.691	0.226	8.36E-44
EIF3B	1.23E-34	0.291207	0.737	0.311	4.13E-30
METAP2	6.52E-21	0.291203	0.947	0.689	2.20E-16
PSMD8	1.44E-26	0.290456	0.923	0.598	4.86E-22
HDAC7	1.43E-46	0.290392	0.66	0.214	4.81E-42
TMOD1	5.83E-97	0.289713	0.519	0.064	1.96E-92
PPIA	2.27E-35	0.289501	1	0.988	7.65E-31
RNF187	5.52E-38	0.289497	0.832	0.355	1.86E-33
RAB11A	4.09E-28	0.289292	0.891	0.526	1.38E-23
EIF6	4.52E-28	0.289194	0.898	0.527	1.52E-23
BANF1	3.95E-32	0.289132	0.856	0.425	1.33E-27
UQCRC1	2.39E-27	0.288592	0.874	0.486	8.04E-23
PSMC4	4.88E-42	0.288378	0.691	0.243	1.65E-37
PPM1G	8.81E-28	0.288333	0.884	0.485	2.97E-23
PTGES3	8.63E-24	0.287759	0.961	0.76	2.91E-19
HBQ1	5.15E-99	0.287358	0.425	0.038	1.74E-94

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
STRADB	1.49E-52	0.286468	0.572	0.154	5.01E-48
PRDX3	1.40E-42	0.286313	0.674	0.239	4.71E-38
PSMB1	3.66E-27	0.28621	0.982	0.868	1.23E-22
PSMB6	9.73E-26	0.285669	0.93	0.563	3.28E-21
CENPM	1.01E-54	0.285644	0.512	0.124	3.41E-50
YIF1B	1.71E-41	0.285061	0.761	0.283	5.75E-37
EXOSC8	4.99E-42	0.285053	0.674	0.238	1.68E-37
ACSS1	2.30E-47	0.284898	0.604	0.185	7.75E-43
THOC7	1.17E-24	0.284	0.912	0.579	3.93E-20
PSMC1	2.65E-25	0.283963	0.919	0.546	8.94E-21
IP6K2	2.02E-24	0.283803	0.87	0.498	6.79E-20
HIGD1A	6.95E-42	0.283118	0.586	0.192	2.34E-37
PUF60	5.41E-35	0.282969	0.839	0.391	1.82E-30
NDUFA6	2.48E-26	0.282413	0.853	0.485	8.36E-22
SAMM50	3.14E-42	0.282283	0.716	0.261	1.06E-37
UBE2I	6.04E-24	0.282011	0.888	0.581	2.03E-19
AK2	9.97E-31	0.281613	0.73	0.337	3.36E-26
CHCHD3	2.11E-36	0.281374	0.768	0.315	7.11E-32
HSPA9	9.78E-28	0.281038	0.937	0.612	3.29E-23
SSBP1	4.98E-22	0.280998	0.933	0.661	1.68E-17
HP1BP3	7.33E-26	0.280717	0.849	0.464	2.47E-21
DNMT1	9.05E-33	0.280314	0.737	0.316	3.05E-28
PYCR1	6.34E-56	0.279733	0.554	0.139	2.14E-51
PDHA1	1.15E-52	0.27959	0.596	0.165	3.87E-48
GLRX3	6.47E-36	0.278852	0.758	0.313	2.18E-31
PPP1CC	5.21E-24	0.278402	0.874	0.542	1.76E-19
ATAD3A	2.59E-46	0.278109	0.625	0.197	8.71E-42
VDAC3	5.77E-27	0.277411	0.811	0.423	1.94E-22
ECHS1	1.80E-31	0.277272	0.768	0.362	6.08E-27
ZWINT	3.11E-48	0.276754	0.505	0.135	1.05E-43
SLC38A5	2.40E-59	0.276745	0.575	0.139	8.09E-55
JTB	5.41E-23	0.276597	0.982	0.739	1.82E-18
ATG3	2.41E-26	0.275706	0.775	0.38	8.13E-22
TTLL12	1.44E-83	0.275522	0.495	0.072	4.85E-79
PDZD8	5.72E-28	0.275476	0.835	0.398	1.93E-23
DDX1	4.80E-27	0.275138	0.8	0.403	1.62E-22
PSMD7	1.16E-24	0.273427	0.919	0.628	3.90E-20
YARS	7.02E-46	0.272749	0.67	0.222	2.37E-41
UQCC2	2.60E-49	0.272579	0.649	0.197	8.76E-45
CHCHD2	4.43E-30	0.272547	1	0.966	1.49E-25
NUSAP1	2.96E-33	0.271736	0.512	0.179	9.97E-29
GMNN	1.52E-35	0.271484	0.632	0.231	5.12E-31
FUNDC2	4.74E-35	0.270563	0.786	0.349	1.60E-30
TSPAN4	1.18E-50	0.270278	0.604	0.17	3.99E-46
PSMD14	7.34E-41	0.270254	0.723	0.265	2.47E-36
PSMD6	4.09E-26	0.269661	0.825	0.427	1.38E-21
SSRP1	1.38E-25	0.269632	0.874	0.476	4.67E-21
VPS37B	1.48E-36	0.269574	0.709	0.273	4.98E-32
LAMTOR1	1.02E-23	0.269501	0.888	0.527	3.45E-19
IFRD2	1.15E-46	0.26933	0.635	0.191	3.88E-42
HNRNPU	6.84E-21	0.269277	0.993	0.775	2.31E-16
CTA-392E5.1	1.04E-112	0.269033	0.354	0.014	3.49E-108
NDUFS6	1.67E-21	0.268482	0.884	0.572	5.63E-17
UPF3A	9.60E-27	0.268172	0.853	0.43	3.23E-22
GCSH	3.54E-33	0.268165	0.751	0.328	1.19E-28

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
ETFB	1.77E-25	0.267917	0.891	0.524	5.97E-21
SLC40A1	6.89E-52	0.267671	0.698	0.209	2.32E-47
NDUFB11	4.90E-26	0.267607	0.986	0.843	1.65E-21
MTHFD1	1.75E-47	0.266891	0.621	0.189	5.89E-43
ANP32E	5.52E-31	0.266287	0.698	0.301	1.86E-26
KIF22	3.50E-32	0.2658	0.667	0.274	1.18E-27
RFXANK	1.48E-41	0.265764	0.737	0.272	4.99E-37
ARL2	6.83E-32	0.265027	0.761	0.334	2.30E-27
ARL4A	1.36E-34	0.264925	0.667	0.253	4.57E-30
FAM210B	4.58E-60	0.264836	0.561	0.132	1.54E-55
NDUFAF2	1.48E-38	0.263234	0.684	0.251	4.99E-34
RPA3	1.62E-32	0.26274	0.663	0.27	5.45E-28
DCTPP1	4.04E-43	0.262062	0.688	0.237	1.36E-38
HNRNPH3	1.90E-21	0.261914	0.947	0.655	6.41E-17
PAICS	1.74E-26	0.261431	0.789	0.408	5.85E-22
SNRPD1	1.48E-23	0.261392	0.982	0.809	5.00E-19
DHRS11	1.42E-59	0.26137	0.537	0.12	4.80E-55
SERPINE2	2.61E-28	0.261331	0.782	0.371	8.80E-24
ACSM3	1.48E-37	0.260911	0.635	0.221	4.97E-33
PDAP1	5.14E-26	0.260747	0.849	0.445	1.73E-21
SSX2IP	2.85E-48	0.259624	0.575	0.16	9.61E-44
PSMG1	3.76E-43	0.25942	0.625	0.199	1.27E-38
ANP32A	3.12E-25	0.25929	0.807	0.421	1.05E-20
NDUFAB1	9.22E-26	0.259202	0.825	0.454	3.11E-21
CYTL1	7.74E-25	0.2592	0.754	0.37	2.61E-20
PGAM1	2.16E-20	0.259086	0.793	0.461	7.28E-16
MRPS15	8.62E-25	0.258792	0.835	0.451	2.90E-20
FAM133B	1.77E-18	0.258628	0.958	0.713	5.98E-14
TST	9.86E-83	0.258282	0.456	0.06	3.32E-78
PIN4	2.47E-42	0.258274	0.628	0.206	8.31E-38
LSM4	5.78E-20	0.258181	0.912	0.623	1.95E-15
TALDO1	1.81E-20	0.25788	0.975	0.825	6.11E-16
NEDD4L	7.51E-48	0.257765	0.54	0.142	2.53E-43
MDH2	2.64E-20	0.257748	0.958	0.729	8.91E-16
VCP	5.14E-30	0.257588	0.779	0.36	1.73E-25
NDUFB2	5.70E-22	0.257561	0.94	0.616	1.92E-17
ATIC	1.15E-31	0.257435	0.705	0.3	3.86E-27
ARL6IP1	9.06E-15	0.256886	0.842	0.517	3.05E-10
HIST1H1E	2.49E-20	0.256847	0.681	0.363	8.39E-16
SNRPC	1.15E-19	0.256118	0.94	0.687	3.88E-15
MAGOH	8.83E-26	0.255878	0.923	0.547	2.98E-21
SAE1	1.69E-39	0.255752	0.653	0.231	5.71E-35
LRRC59	7.47E-34	0.254813	0.733	0.303	2.52E-29
PRPF31	7.60E-37	0.254502	0.684	0.258	2.56E-32
RUVBL1	4.59E-59	0.254396	0.456	0.091	1.55E-54
MRPL27	6.03E-49	0.254207	0.596	0.17	2.03E-44
BBC3	3.18E-63	0.254088	0.411	0.064	1.07E-58
MGAT4B	6.04E-65	0.253437	0.456	0.079	2.03E-60
SSNA1	1.52E-25	0.253365	0.772	0.387	5.14E-21
CD320	1.56E-39	0.25334	0.589	0.198	5.27E-35
SMC2	4.96E-41	0.253233	0.509	0.151	1.67E-36
PABPC4	2.99E-21	0.252995	0.891	0.548	1.01E-16
FADS2	1.95E-49	0.252639	0.544	0.142	6.56E-45
UROS	3.82E-25	0.252515	0.796	0.414	1.29E-20
PSMD4	5.63E-24	0.25229	0.856	0.471	1.90E-19

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
RILP	5.04E-54	0.252068	0.572	0.145	1.70E-49
DHFR	2.42E-39	0.25198	0.484	0.14	8.17E-35
BOP1	3.10E-40	0.251792	0.632	0.215	1.04E-35
CUTA	3.18E-20	0.251786	0.993	0.79	1.07E-15
HSPBP1	6.66E-43	0.251677	0.596	0.189	2.24E-38
ORC4	4.36E-34	0.251181	0.681	0.267	1.47E-29
Cluster4					
DNTT	5.97E-118	1.972602	0.929	0.109	2.01E-113
CYGB	4.16E-190	1.588961	0.776	0.029	1.40E-185
JCHAIN	1.42E-111	1.411026	0.741	0.059	4.78E-107
LTB	3.33E-102	1.320222	0.659	0.052	1.12E-97
CD99	6.99E-46	1.282879	1	0.857	2.36E-41
IGHM	9.21E-32	1.249772	0.871	0.404	3.10E-27
CD79A	5.81E-120	1.145807	0.635	0.037	1.96E-115
ACTG1	4.11E-41	1.087308	1	0.996	1.39E-36
SOD2	1.65E-16	0.882305	0.788	0.634	5.57E-12
GLRX	9.15E-27	0.876932	0.788	0.44	3.08E-22
TSC22D3	2.83E-23	0.821382	0.882	0.584	9.55E-19
RBM38	2.97E-23	0.703977	0.518	0.161	1.00E-18
PAG1	5.26E-32	0.696414	0.424	0.076	1.77E-27
DSTN	4.62E-16	0.673597	0.847	0.679	1.56E-11
CD74	1.00E-23	0.658762	1	0.972	3.38E-19
CORO1A	2.02E-15	0.654411	0.788	0.521	6.82E-11
MSI2	4.51E-18	0.639279	0.835	0.615	1.52E-13
BAALC	2.47E-16	0.637514	0.612	0.295	8.31E-12
ADA	4.64E-13	0.61167	0.565	0.307	1.56E-08
KLF6	1.11E-16	0.606846	0.741	0.43	3.74E-12
GYPC	1.25E-15	0.605047	0.976	0.914	4.23E-11
MZB1	3.36E-11	0.597898	0.494	0.24	1.13E-06
ZFP36L2	1.05E-11	0.596329	0.8	0.604	3.53E-07
LRRFIP1	2.63E-12	0.58568	0.871	0.73	8.87E-08
UBE2J1	2.19E-14	0.584148	0.753	0.582	7.39E-10
SLC43A2	5.54E-17	0.577836	0.4	0.117	1.87E-12
DDAH2	9.74E-13	0.572112	0.835	0.725	3.28E-08
HLA-DRA	1.25E-15	0.562159	0.953	0.903	4.22E-11
SASH3	2.34E-18	0.556039	0.435	0.13	7.87E-14
RABAC1	9.44E-12	0.555847	0.788	0.626	3.18E-07
CALM1	5.53E-12	0.544873	0.812	0.693	1.86E-07
CD52	1.36E-08	0.529952	0.729	0.532	0.000459
MED13L	8.73E-11	0.527819	0.529	0.297	2.94E-06
SH3KBP1	2.95E-10	0.527572	0.565	0.348	9.95E-06
SORL1	1.47E-11	0.526219	0.518	0.257	4.95E-07
NEIL1	9.63E-60	0.515813	0.318	0.017	3.24E-55
LST1	2.93E-11	0.515719	0.8	0.608	9.87E-07
HMGB1	1.45E-18	0.50326	1	0.989	4.88E-14
UBC	9.09E-20	0.496596	1	0.984	3.06E-15
CYFIP2	3.93E-09	0.494818	0.412	0.198	0.000133
VPREB1	6.24E-47	0.488919	0.341	0.029	2.10E-42
9-Sep	2.50E-10	0.479332	0.529	0.288	8.41E-06
LAT2	3.53E-10	0.478548	0.518	0.282	1.19E-05
KMT2E	1.28E-09	0.46599	0.882	0.818	4.30E-05
ARID4B	2.51E-08	0.451769	0.812	0.758	0.000845
SCAI	1.41E-10	0.451668	0.4	0.174	4.75E-06
DDX5	1.76E-18	0.444069	1	0.986	5.94E-14

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
NPY	1.73E-59	0.441628	0.247	0.009	5.83E-55
PTMA	1.55E-15	0.434748	1	1	5.23E-11
ITM2C	2.87E-09	0.42314	0.871	0.706	9.66E-05
HLA-DPB1	3.50E-09	0.415811	0.859	0.747	0.000118
BAHCC1	1.19E-16	0.377263	0.271	0.056	4.00E-12
EEF1D	3.15E-16	0.373909	1	0.997	1.06E-11
ARHGAP27	3.31E-16	0.372062	0.247	0.048	1.12E-11
NEGR1	3.26E-12	0.360537	0.259	0.067	1.10E-07
TMSB10	5.06E-17	0.36005	1	0.999	1.70E-12
MALAT1	5.85E-18	0.353599	1	1	1.97E-13
FAM129C	4.90E-33	0.351868	0.247	0.022	1.65E-28
TRBC2	5.23E-09	0.346737	0.353	0.144	0.000176
IL7R	8.84E-62	0.336788	0.224	0.006	2.98E-57
LINC00426	8.73E-42	0.327193	0.2	0.009	2.94E-37
PRKD2	2.37E-10	0.326741	0.282	0.09	7.97E-06
EBF1	5.21E-56	0.323432	0.224	0.007	1.75E-51
LL22NC03-2H8.5	6.22E-09	0.315906	0.188	0.049	0.00021
ARL4C	2.07E-09	0.30724	0.212	0.056	6.98E-05
UMODL1	1.06E-36	0.288308	0.176	0.008	3.57E-32
RHPN1	7.31E-09	0.287544	0.247	0.08	0.000246
HLA-C	1.56E-08	0.283269	0.965	0.978	0.000527
GAPDH	2.51E-11	0.279403	1	1	8.46E-07
EIF1	1.80E-12	0.277735	1	1	6.05E-08
MME	6.26E-44	0.250838	0.129	0.002	2.11E-39
Cluster5					
HIST1H4C	1.36E-52	1.386421	0.945	0.759	4.58E-48
TUBA1B	9.78E-76	1.18954	0.982	0.955	3.29E-71
TUBB	5.35E-75	1.044876	0.991	0.864	1.80E-70
JCHAIN	4.72E-45	0.969847	0.333	0.058	1.59E-40
RGS2	9.17E-18	0.900249	0.388	0.162	3.09E-13
STMN1	8.19E-69	0.886491	0.986	0.859	2.76E-64
IGHM	3.72E-40	0.856201	0.795	0.38	1.25E-35
LGALS1	9.27E-28	0.841482	0.863	0.552	3.12E-23
CORO1A	7.41E-61	0.822742	0.941	0.485	2.50E-56
CD74	2.15E-34	0.811641	0.995	0.97	7.25E-30
KIAA0101	2.80E-53	0.794664	0.922	0.624	9.45E-49
HMGN2	2.31E-68	0.781542	0.995	0.992	7.80E-64
H2AFZ	2.19E-53	0.780984	0.982	0.878	7.38E-49
TYMS	1.76E-45	0.768163	0.858	0.538	5.92E-41
HMGB2	4.75E-44	0.737636	0.968	0.873	1.60E-39
ITM2C	1.13E-49	0.731248	0.977	0.682	3.82E-45
C12orf75	2.89E-52	0.698178	0.63	0.194	9.73E-48
LSP1	3.65E-35	0.681364	0.849	0.534	1.23E-30
PCNA	3.18E-44	0.679175	0.699	0.296	1.07E-39
CDKN2D	2.77E-40	0.665784	0.712	0.295	9.35E-36
IGLL1	3.13E-29	0.656806	0.886	0.631	1.05E-24
PLP2	8.30E-35	0.628564	0.845	0.483	2.80E-30
HLA-DRA	5.44E-25	0.628311	0.982	0.896	1.83E-20
NUSAP1	2.15E-66	0.62635	0.658	0.174	7.25E-62
BIRC5	7.89E-57	0.621847	0.626	0.18	2.66E-52
PLD4	1.60E-43	0.607894	0.479	0.125	5.38E-39
HLA-DPA1	2.26E-29	0.601719	0.954	0.723	7.61E-25
HIST2H2AC	6.29E-25	0.596928	0.694	0.396	2.12E-20

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
CYBA	1.55E-33	0.574809	0.991	0.853	5.24E-29
HLA-DPB1	1.05E-27	0.562739	0.95	0.729	3.55E-23
NASP	8.27E-35	0.551236	0.881	0.643	2.79E-30
HERPUD1	8.93E-24	0.525383	0.621	0.304	3.01E-19
PKM	2.05E-35	0.524407	0.904	0.566	6.92E-31
ATAD2	5.75E-43	0.515064	0.639	0.223	1.94E-38
VIM	1.05E-31	0.512745	1	0.923	3.53E-27
ID2	8.37E-30	0.508933	0.717	0.33	2.82E-25
CXCR4	1.85E-31	0.508182	0.493	0.167	6.23E-27
CFL1	8.81E-45	0.503857	1	0.966	2.97E-40
UBE2C	1.04E-58	0.503495	0.553	0.126	3.50E-54
TRA2B	6.68E-22	0.499702	0.954	0.843	2.25E-17
IER2	4.70E-17	0.498872	0.708	0.44	1.58E-12
HLA-DRB1	2.05E-20	0.497917	0.913	0.68	6.90E-16
TK1	3.73E-49	0.492602	0.584	0.172	1.26E-44
CENPN	1.40E-40	0.490676	0.584	0.204	4.71E-36
DDIT4	7.72E-27	0.490023	0.525	0.215	2.60E-22
PLAUR	9.49E-38	0.489924	0.393	0.094	3.20E-33
HELLS	1.39E-42	0.488297	0.744	0.306	4.68E-38
CRIP1	8.14E-20	0.486534	0.338	0.119	2.74E-15
CDCA5	4.58E-80	0.485042	0.575	0.103	1.54E-75
SIVA1	1.68E-26	0.482877	0.895	0.653	5.65E-22
SLC3A2	1.92E-27	0.480218	0.689	0.355	6.46E-23
CKS1B	4.38E-34	0.478948	0.721	0.322	1.47E-29
CDT1	1.35E-26	0.478451	0.703	0.39	4.55E-22
EIF4A3	9.53E-41	0.474345	0.639	0.24	3.21E-36
PHGDH	6.27E-55	0.473654	0.616	0.17	2.11E-50
SPNS3	9.18E-41	0.469848	0.744	0.294	3.09E-36
HLA-C	1.14E-30	0.466775	1	0.975	3.85E-26
CENPU	1.39E-31	0.461333	0.749	0.374	4.68E-27
DUT	6.66E-24	0.457943	0.909	0.747	2.25E-19
IDH2	1.29E-31	0.455361	0.95	0.718	4.35E-27
HLA-DRB5	4.53E-23	0.447679	0.831	0.486	1.53E-18
SKA3	5.16E-64	0.440813	0.516	0.102	1.74E-59
MKI67	8.67E-55	0.4393	0.484	0.103	2.92E-50
NUCKS1	5.30E-21	0.43827	0.84	0.626	1.79E-16
ACTG1	6.14E-24	0.434258	1	0.996	2.07E-19
GADD45B	2.96E-36	0.429271	0.493	0.146	9.97E-32
MYBL2	7.27E-54	0.428502	0.543	0.134	2.45E-49
RAB11FIP1	1.31E-14	0.421314	0.406	0.197	4.41E-10
SRSF10	2.10E-29	0.413737	0.959	0.812	7.08E-25
GMNN	3.91E-35	0.412206	0.612	0.247	1.32E-30
DBI	1.20E-23	0.411322	0.785	0.498	4.06E-19
SRSF7	3.18E-22	0.408729	0.799	0.487	1.07E-17
ARPC5L	1.26E-20	0.405226	0.858	0.62	4.24E-16
HMGGB1	1.09E-26	0.40484	1	0.989	3.67E-22
HLA-B	1.04E-28	0.404649	1	0.995	3.49E-24
ATAD5	1.12E-43	0.404573	0.616	0.202	3.78E-39
ARL4C	6.82E-37	0.395026	0.256	0.04	2.30E-32
DNAJC9	4.12E-24	0.392765	0.712	0.358	1.39E-19
SLC25A5	1.93E-31	0.389661	0.991	0.927	6.49E-27
HIST1H1E	1.60E-18	0.389653	0.653	0.377	5.39E-14
PMAIP1	2.87E-20	0.380509	0.594	0.297	9.67E-16
RAD51AP1	1.02E-52	0.379656	0.543	0.135	3.45E-48
DEK	6.75E-23	0.379205	0.922	0.782	2.27E-18

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
CDCA7	2.30E-29	0.37774	0.626	0.267	7.76E-25
TMSB10	1.14E-11	0.371523	1	0.998	3.83E-07
CKS2	6.95E-22	0.370724	0.749	0.429	2.34E-17
IRF8	3.03E-35	0.370296	0.311	0.063	1.02E-30
CXXC5	4.26E-22	0.369455	0.653	0.335	1.44E-17
HLA-DMA	3.77E-15	0.367796	0.813	0.625	1.27E-10
B2M	1.27E-35	0.36625	1	1	4.30E-31
RUNX3	5.36E-33	0.365272	0.443	0.131	1.80E-28
SMC4	1.54E-20	0.364293	0.557	0.268	5.19E-16
IGKC	3.87E-28	0.358914	0.137	0.013	1.30E-23
USP1	1.14E-22	0.358269	0.639	0.317	3.83E-18
ORC6	3.75E-49	0.35767	0.575	0.157	1.27E-44
ARPC2	3.19E-23	0.356313	0.973	0.87	1.07E-18
CLSPN	1.06E-49	0.3561	0.452	0.097	3.58E-45
ANAPC11	3.69E-20	0.353008	0.84	0.603	1.24E-15
TMPO	7.63E-23	0.352259	0.575	0.267	2.57E-18
NPC2	2.42E-21	0.349824	0.941	0.728	8.14E-17
CDCA4	9.03E-36	0.349223	0.53	0.173	3.04E-31
RP11-386I14.4	8.82E-14	0.348874	0.84	0.637	2.97E-09
CD2AP	1.48E-17	0.3483	0.557	0.276	5.00E-13
CAPG	3.27E-48	0.348021	0.603	0.16	1.10E-43
ZFP36L2	9.03E-17	0.3464	0.868	0.583	3.04E-12
LSM4	6.52E-20	0.344617	0.872	0.638	2.20E-15
PRC1	5.98E-37	0.344395	0.53	0.167	2.02E-32
RGS1	1.32E-12	0.344133	0.237	0.086	4.44E-08
PTPRE	1.19E-28	0.34363	0.516	0.183	4.01E-24
MCM7	2.74E-17	0.343094	0.767	0.503	9.25E-13
GGH	2.03E-21	0.340763	0.603	0.325	6.85E-17
UBC	1.05E-12	0.34052	1	0.983	3.53E-08
CTSB	9.21E-12	0.338882	0.53	0.313	3.10E-07
TOP2A	5.48E-50	0.337493	0.42	0.081	1.85E-45
LGMN	1.65E-59	0.336406	0.237	0.016	5.57E-55
SMC3	1.13E-18	0.330599	0.817	0.571	3.82E-14
JUNB	6.66E-10	0.329253	0.562	0.365	2.24E-05
PPP1R18	1.49E-20	0.328663	0.589	0.272	5.02E-16
LCP1	2.34E-21	0.325313	0.781	0.46	7.90E-17
MYL6	1.10E-19	0.324842	0.986	0.969	3.71E-15
SPINK2	3.61E-13	0.324799	0.872	0.64	1.22E-08
CALM1	1.84E-11	0.323633	0.886	0.676	6.21E-07
CCDC50	9.97E-11	0.322769	0.338	0.168	3.36E-06
RFC1	1.44E-19	0.321735	0.721	0.42	4.85E-15
IRF2BP2	4.75E-09	0.321466	0.799	0.647	0.00016
TUBB4B	1.65E-19	0.321362	0.589	0.283	5.54E-15
PTTG1	1.16E-21	0.317353	0.635	0.326	3.89E-17
GSTP1	5.05E-21	0.312461	0.986	0.96	1.70E-16
PPIG	3.37E-15	0.31244	0.9	0.722	1.14E-10
TAGLN2	8.02E-15	0.310861	0.973	0.915	2.70E-10
FUS	1.16E-15	0.309903	0.973	0.871	3.89E-11
CENPF	4.62E-21	0.309418	0.47	0.191	1.56E-16
ERP29	3.34E-13	0.309037	0.936	0.81	1.13E-08
CYTH4	8.65E-38	0.307125	0.288	0.05	2.92E-33
9-Sep	3.48E-13	0.306778	0.502	0.275	1.17E-08
PTPRS	8.79E-17	0.305702	0.11	0.016	2.96E-12
NUDT1	5.46E-21	0.305668	0.781	0.453	1.84E-16

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
ATF3	6.29E-22	0.305044	0.32	0.095	2.12E-17
COX8A	8.26E-14	0.303016	0.945	0.795	2.78E-09
HLA-DQA1	5.07E-18	0.302141	0.484	0.213	1.71E-13
CENPW	9.97E-26	0.300175	0.575	0.237	3.36E-21
RALY	4.55E-16	0.299629	0.872	0.644	1.53E-11
DDX39A	1.80E-14	0.299406	0.735	0.467	6.08E-10
CENPH	6.13E-18	0.29843	0.671	0.395	2.07E-13
MIS18BP1	4.18E-18	0.296507	0.731	0.441	1.41E-13
DNAJC1	1.50E-11	0.296002	0.717	0.492	5.06E-07
CARHSP1	2.04E-17	0.295327	0.639	0.358	6.87E-13
MAD2L2	1.48E-15	0.291952	0.575	0.336	5.00E-11
SRSF2	7.61E-14	0.291742	0.941	0.777	2.56E-09
ALOX5AP	6.25E-24	0.287133	0.215	0.043	2.11E-19
FMNL1	8.26E-12	0.286594	0.68	0.451	2.78E-07
SAE1	2.10E-21	0.285531	0.571	0.254	7.06E-17
TMEM106C	1.44E-19	0.285358	0.461	0.201	4.85E-15
ATP6V0B	1.63E-12	0.284139	0.831	0.641	5.49E-08
MAD2L1	6.04E-21	0.279624	0.489	0.209	2.04E-16
UBALD2	3.95E-13	0.279247	0.694	0.426	1.33E-08
KIF22	1.87E-19	0.277998	0.594	0.295	6.29E-15
PSME2	4.50E-14	0.276675	0.826	0.609	1.52E-09
NAP1L1	5.58E-21	0.276659	1	0.989	1.88E-16
MZB1	2.49E-19	0.275754	0.516	0.22	8.39E-15
ADGRE5	1.79E-19	0.274778	0.411	0.16	6.05E-15
ARHGDI1	1.37E-12	0.269867	0.767	0.539	4.62E-08
ANKRD11	3.97E-15	0.269822	0.658	0.377	1.34E-10
CH17-373J23.1	7.45E-13	0.269437	0.461	0.233	2.51E-08
UHRF1	6.13E-27	0.269067	0.379	0.114	2.07E-22
LDLRAD4	1.05E-24	0.267583	0.283	0.072	3.55E-20
HIST1H2AM	5.16E-28	0.267369	0.37	0.109	1.74E-23
ARF6	2.83E-09	0.266209	0.872	0.657	9.54E-05
TACC3	1.42E-30	0.265894	0.438	0.135	4.79E-26
UBE2J1	2.53E-08	0.26566	0.767	0.568	0.000852
LMNB1	2.36E-22	0.265367	0.42	0.155	7.94E-18
AURKB	1.32E-43	0.26416	0.361	0.069	4.46E-39
HMGXB4	3.07E-13	0.262621	0.74	0.511	1.04E-08
MGST3	2.88E-16	0.262118	0.63	0.343	9.70E-12
OAZ1	1.18E-10	0.261437	0.977	0.893	3.96E-06
YEATS4	3.43E-16	0.261365	0.616	0.339	1.15E-11
PHF5A	5.01E-18	0.261198	0.694	0.387	1.69E-13
ASPM	1.59E-36	0.261107	0.338	0.072	5.36E-32
APP	1.37E-11	0.260746	0.493	0.252	4.61E-07
C9orf142	2.49E-17	0.260705	0.63	0.335	8.40E-13
BRCA2	3.67E-32	0.259611	0.379	0.101	1.24E-27
TUBA1A	7.67E-11	0.259363	0.932	0.778	2.58E-06
GGNBP2	2.67E-09	0.258396	0.872	0.673	8.99E-05
HSPB11	3.71E-15	0.257323	0.667	0.382	1.25E-10
IKZF1	8.24E-12	0.25732	0.708	0.476	2.77E-07
VAMP8	9.67E-10	0.256736	0.913	0.805	3.26E-05
SLC9A3R1	1.87E-25	0.256449	0.397	0.127	6.29E-21
DDAH2	1.78E-09	0.256447	0.868	0.714	5.98E-05
DNMT1	1.76E-15	0.256278	0.612	0.344	5.92E-11
PIM1	1.37E-13	0.253988	0.639	0.378	4.62E-09
CD99	1.90E-16	0.251346	0.982	0.85	6.39E-12

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
EZR	1.11E-13	0.250955	0.662	0.402	3.73E-09
TACC1	2.07E-14	0.250616	0.708	0.426	6.96E-10
CDK1	4.86E-41	0.250182	0.365	0.075	1.64E-36
Cluster6					
SPINK2	7.49E-141	0.875219	0.974	0.562	2.52E-136
SMIM24	3.82E-91	0.609764	0.923	0.54	1.29E-86
GPC	1.65E-75	0.584367	0.981	0.896	5.55E-71
CD52	3.37E-79	0.569203	0.84	0.441	1.14E-74
C1QTNF4	3.24E-70	0.55467	0.844	0.455	1.09E-65
KIAA0125	5.12E-54	0.544485	0.801	0.55	1.73E-49
ZFP36L2	5.36E-53	0.508646	0.836	0.539	1.81E-48
CSF3R	2.50E-70	0.507954	0.758	0.328	8.43E-66
ITM2C	3.61E-64	0.507053	0.906	0.649	1.22E-59
HOPX	2.66E-67	0.491702	0.628	0.222	8.95E-63
ICAM3	3.77E-67	0.48801	0.923	0.667	1.27E-62
PIK3R1	8.69E-50	0.43364	0.821	0.548	2.93E-45
IGHM	8.48E-60	0.412511	0.718	0.326	2.86E-55
NPDC1	6.90E-50	0.39914	0.654	0.309	2.32E-45
ENO1	1.01E-54	0.393016	0.989	0.956	3.41E-50
MAP3K8	1.43E-34	0.369228	0.818	0.583	4.83E-30
IGLL1	4.17E-25	0.366091	0.786	0.615	1.41E-20
EGFL7	6.29E-36	0.364198	0.812	0.579	2.12E-31
SELL	1.06E-35	0.363842	0.534	0.26	3.59E-31
TAOK3	3.44E-39	0.360642	0.75	0.492	1.16E-34
PRDX1	1.26E-29	0.359411	0.835	0.701	4.25E-25
AIF1	1.26E-38	0.34536	0.991	0.866	4.25E-34
C1orf228	5.81E-31	0.340551	0.786	0.588	1.96E-26
CD99	1.39E-44	0.338984	0.953	0.834	4.67E-40
NAP1L1	1.65E-58	0.337055	0.998	0.987	5.56E-54
MSI2	8.20E-31	0.319183	0.789	0.57	2.76E-26
LDHA	2.34E-28	0.318657	0.951	0.882	7.90E-24
TKT	3.29E-29	0.311865	0.944	0.875	1.11E-24
SPNS3	1.73E-30	0.310106	0.543	0.274	5.84E-26
GAPDH	4.02E-66	0.309449	1	1	1.35E-61
PKM	3.02E-27	0.304338	0.789	0.539	1.02E-22
PRSS2	5.44E-27	0.303514	0.141	0.023	1.83E-22
GNA15	6.09E-29	0.301522	0.814	0.651	2.05E-24
CD74	4.78E-44	0.290992	1	0.964	1.61E-39
LST1	2.29E-23	0.290001	0.776	0.563	7.72E-19
MZB1	1.44E-34	0.286126	0.449	0.185	4.85E-30
BEX1	1.99E-14	0.281795	0.444	0.281	6.70E-10
PRAM1	7.12E-38	0.28024	0.346	0.111	2.40E-33
H2AFY	4.46E-33	0.269617	0.97	0.919	1.50E-28
LSP1	6.25E-22	0.26946	0.712	0.518	2.11E-17
HLA-DPA1	1.04E-29	0.269196	0.889	0.7	3.51E-25
CASP4	2.38E-20	0.261376	0.65	0.467	8.01E-16
IGFBP7	6.14E-18	0.260128	0.746	0.632	2.07E-13
HLA-A	1.18E-32	0.259081	0.996	0.99	3.97E-28
PIM2	1.65E-22	0.25249	0.393	0.194	5.56E-18
6-Sep	9.44E-19	0.251816	0.823	0.712	3.18E-14
Cluster7					
RP11-354E11.2	7.29E-114	0.780843	0.687	0.197	2.45E-109
ITGA2B	2.89E-86	0.771274	0.659	0.24	9.74E-82

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
PDLIM1	8.85E-57	0.613631	0.693	0.358	2.98E-52
S100A4	1.44E-68	0.589988	0.972	0.892	4.85E-64
FCER1A	6.03E-106	0.588952	0.494	0.083	2.03E-101
PDZD8	2.05E-65	0.588485	0.723	0.375	6.91E-61
GATA2	8.83E-59	0.535689	0.53	0.188	2.98E-54
SLC40A1	1.22E-76	0.519833	0.572	0.183	4.12E-72
LINC00152	8.95E-46	0.510985	0.811	0.604	3.01E-41
PHACTR4	3.22E-48	0.505008	0.687	0.386	1.08E-43
RNF130	2.06E-59	0.500831	0.89	0.664	6.95E-55
SOX4	2.18E-42	0.498087	0.928	0.795	7.36E-38
PKIG	1.10E-58	0.497496	0.697	0.353	3.70E-54
PHTF1	2.74E-43	0.476195	0.627	0.336	9.23E-39
RP11-620J15.3	2.98E-56	0.45974	0.952	0.845	1.00E-51
ELF1	4.05E-50	0.442993	0.956	0.772	1.36E-45
EIF4G2	2.99E-45	0.439771	0.904	0.768	1.01E-40
MARCKSL1	3.17E-41	0.416969	0.787	0.539	1.07E-36
S100A6	2.80E-51	0.410048	0.928	0.745	9.44E-47
CTNNBL1	3.47E-41	0.402142	0.612	0.329	1.17E-36
TPM1	1.28E-46	0.401696	0.5	0.204	4.31E-42
PRKACB	1.21E-37	0.394257	0.588	0.316	4.09E-33
ZEB2	2.16E-30	0.38424	0.725	0.523	7.27E-26
GLUL	2.48E-16	0.37647	0.797	0.658	8.36E-12
FERMT3	2.73E-16	0.374862	0.462	0.31	9.21E-12
H1F0	4.67E-17	0.365462	0.62	0.449	1.57E-12
MPP1	1.15E-31	0.361393	0.596	0.357	3.87E-27
LEPROT	6.11E-30	0.356756	0.813	0.621	2.06E-25
NAA38	3.49E-26	0.354115	0.886	0.737	1.18E-21
EMP3	3.37E-28	0.345896	0.825	0.684	1.14E-23
FBXO7	5.84E-30	0.343371	0.813	0.605	1.97E-25
APOC1	3.16E-22	0.34231	0.562	0.333	1.07E-17
MPST	2.59E-21	0.334938	0.691	0.523	8.73E-17
PSTPIP2	5.48E-34	0.334906	0.484	0.239	1.85E-29
ACSM3	1.63E-31	0.333019	0.462	0.219	5.50E-27
SH3BGRL	1.58E-32	0.323508	0.918	0.814	5.33E-28
CITED2	3.11E-23	0.322323	0.414	0.216	1.05E-18
SERPINB1	1.36E-20	0.317732	0.936	0.893	4.59E-16
CAT	9.31E-24	0.316209	0.815	0.663	3.14E-19
ATF7IP2	1.68E-08	0.315041	0.693	0.634	0.000566
CNRIP1	1.22E-37	0.312131	0.428	0.163	4.12E-33
CD63	8.53E-14	0.309657	0.865	0.781	2.87E-09
STK4	1.57E-23	0.30482	0.586	0.377	5.28E-19
PRKAR2B	1.43E-27	0.302685	0.448	0.222	4.81E-23
MLLT3	1.12E-32	0.299694	0.687	0.393	3.76E-28
SEC11A	6.83E-24	0.292422	0.793	0.627	2.30E-19
SDCBP	1.35E-23	0.291909	0.691	0.498	4.55E-19
MIR4435-2HG	4.82E-21	0.286074	0.55	0.336	1.63E-16
TLN1	5.69E-21	0.285944	0.506	0.312	1.92E-16
RHOG	3.88E-20	0.280233	0.731	0.563	1.31E-15
7-Sep	2.98E-23	0.27823	0.873	0.716	1.00E-18
MPC2	4.19E-17	0.269064	0.811	0.693	1.41E-12
LIMD2	3.19E-22	0.268165	0.789	0.624	1.07E-17
MYL12A	4.54E-20	0.266046	0.791	0.608	1.53E-15
VASP	1.19E-20	0.263944	0.452	0.262	4.02E-16
HACD1	7.09E-21	0.261557	0.48	0.295	2.39E-16

Supplemental Table 2. Differentially expressed genes in CD34⁺ cells in Clusters 1 through 7

Gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
MALAT1	6.87E-28	0.25731	1	1	2.32E-23
STAT5A	8.18E-20	0.256875	0.47	0.281	2.76E-15
F2R	4.52E-19	0.253278	0.424	0.237	1.52E-14

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
CLC	-2.27951	-2.39081	-0.25356	-1.94062	-2.26832	-2.14076	7.968692	7.702633	-0.90277	0.570894	-2.56784	-2.52205	-0.37181	1.395811		
PRTN3	-2.67668	-2.53473	1.586639	4.585715	3.679756	5.720002	3.009806	3.079114	-2.77907	-2.83274	-2.83728	-2.80594	-2.85852	-2.33608		
IRF8	-2.58528	-2.28258	1.340121	1.924075	7.20119	7.045834	-1.4114	-0.88649	-0.89122	-1.02461	-2.70457	-2.66413	-1.75697	-1.30397		
ELANE	-2.44605	-2.72547	2.471089	3.906982	4.041444	4.019191	4.0078	2.861747	-2.64526	-2.53964	-2.51498	-2.87309	-2.72463	-2.83912		
KCNH2	-2.38667	-2.34451	-0.17213	-0.95853	-2.22415	-1.89981	7.374522	6.243694	-1.43069	0.470124	-2.58595	-2.53377	1.382146	1.065722		
KCNE5	-2.11916	-2.07413	1.748818	2.248882	6.317836	6.677164	-0.95698	-0.97968	-1.91249	-1.73251	-2.26176	-2.21272	-1.71405	-1.21123		
JCHAIN	-2.22659	-2.18212	-0.34018	-1.23947	6.77419	7.075558	-0.83291	-0.58804	0.306636	-1.71421	-2.36679	-2.31868	0.431583	-0.77897		
CA1	-1.9502	-2.63252	-0.22292	-0.74567	-2.62911	-1.82219	7.294409	5.148496	-0.01644	-0.59604	-2.70168	-1.71081	1.787784	0.796893		
NAPSB	-1.74774	-1.70093	0.272971	0.274594	7.222127	6.184906	0.009258	-0.7214	-1.8029	-1.89079	-1.25945	-1.13923	-1.93515	-1.76627		
AZU1	-2.64043	-2.26704	2.124785	3.668477	3.854777	4.040325	2.956019	2.311345	-2.67401	-1.17657	-2.65131	-2.69941	-2.73834	-2.10861		
HLA-DRB3	3.273109	-2.79317	2.796435	-2.82473	3.655822	-2.75848	1.125459	-2.81951	2.944384	-2.56811	3.086959	-2.61848	2.330259	-2.82994		
LY86	-0.94144	-1.5693	0.185772	1.963541	6.716764	5.985555	-1.36727	-1.474	-1.66944	-1.756	-1.7636	-1.71205	-1.79978	-0.79876		
PRG2	-1.86955	-1.44908	-0.86083	-1.43385	-1.6585	-1.07178	6.521744	6.675125	-0.98316	0.04902	-1.83645	-1.67665	-0.52309	0.11706		
MPO	-1.9372	-2.7565	2.630516	3.295707	4.371664	3.948335	2.746014	1.361728	-2.20362	-2.20877	-3.00886	-3.13459	-1.53863	-1.56579		
FAM178B	-2.06859	-2.02469	-0.44662	-0.78622	-1.5915	-1.93972	6.006939	5.643762	-0.68731	-0.51151	-2.20746	-1.70438	1.496096	0.82119		
RNASE2	-2.15651	-2.28752	2.003406	2.921529	3.531901	2.760084	3.439465	2.848268	-2.39957	-1.44478	-2.92119	-2.90209	-1.71526	-1.67774		
TGM2	-1.67074	-1.59512	-1.25373	-1.27514	-1.49964	0.87399	6.916752	4.951895	-0.97769	-0.28458	-1.68233	-1.76592	-0.9802	0.24245		
PKLR	-1.49936	-1.45524	-1.4193	-1.43296	-1.33309	-1.37113	6.486255	5.210931	-1.55146	-0.47181	-1.64202	-1.59244	0.713702	1.357929		
LOC107984247	-1.84626	-1.80307	-1.76764	-1.78114	-1.68176	0.883871	-1.60938	-1.69622	-1.89684	4.960339	3.580762	2.206863	4.29973	-1.84926		
CNRIP1	-1.79637	-1.67078	-0.0234	0.291492	-2.24769	-1.74274	5.819418	5.36122	0.006173	-0.69692	-2.55594	-1.92844	-0.05354	1.23751		
RNASE3	-2.14036	-2.05523	1.894237	3.105323	3.326735	2.672203	3.580016	2.630117	-2.27742	-2.34505	-2.35086	-2.31104	-2.37823	-1.35044		
LOC105369205	-1.41223	-0.20384	0.036007	-1.34675	-0.27749	-1.28588	-0.87246	-1.27862	-1.46369	6.223482	-0.99689	-1.5042	5.812052	-1.4295		
HBB	-1.92592	-2.88517	-0.39216	-0.98568	-2.45496	-0.07957	5.629944	4.562087	-0.31995	0.449487	-2.7698	-1.34567	1.912603	0.604771		
FABP4	-1.13686	-1.09566	-1.06233	-1.07498	-0.98319	8.376089	-0.91834	-1.01119	-1.18587	1.065445	-1.27195	0.421552	-1.30533	1.182617		
TRIB2	-2.18972	-2.14786	-0.4164	-0.7101	-0.16812	1.130698	5.60594	5.24759	-0.94092	-0.82141	-2.32095	-2.27605	-0.09843	0.105726		
ST6GALNAC1	-1.33143	-1.2896	-0.24693	-1.26851	-1.1741	-1.21002	6.115516	5.253374	-1.38088	-1.46	-1.46695	-1.41981	0.442662	0.43668		
DNTT	-1.70154	-2.00077	1.137274	0.446065	5.14996	5.044323	-1.69384	-0.3979	0.075911	-1.19036	-3.04091	-2.63221	0.584237	0.219765		
RNASE6	-2.29877	-0.95485	0.485569	0.593237	4.339612	3.766452	2.758075	2.555203	-1.57822	-2.4088	-2.41453	-2.37523	-1.1998	-1.26794		
MS4A6A	-0.74296	-0.81692	0.166974	1.367909	5.603588	4.935273	-0.50282	-0.46436	-0.94736	-1.90434	-1.91138	-1.04897	-1.94477	-1.78986		
RPL36A-HNRNPH2	-0.22187	-2.09074	-2.05866	-2.0709	-1.97988	-0.2703	-1.91242	-2.00818	3.468482	3.305987	3.068605	1.687049	3.227533	-2.1447		
HDC	-1.62984	-1.58672	-1.17767	-1.56488	-0.51117	-1.03554	5.515338	5.116413	-1.02665	0.775582	-0.93972	-1.72024	-1.09895	0.884052		
MS4A3	-2.52576	-2.49436	0.804547	2.352151	2.707238	2.682301	3.228981	3.205011	-1.4601	-1.55308	-2.62049	-2.58873	-0.86155	-0.87616		
ECRP	-1.85991	-1.63109	1.752498	3.095505	3.573991	2.830816	2.800623	1.371144	-2.0194	-2.10167	-2.10783	-2.06575	-2.1369	-1.50203		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
CSF1R	-1.24275	-0.68925	0.746281	1.275543	5.91502	4.211567	-0.04145	-1.17678	-1.22124	-1.01833	-1.9804	-1.49369	-1.76832	-1.51618		
CD180	-1.28351	-0.99506	-0.74756	1.467656	5.318398	5.2096	-1.06874	-1.16107	-0.17033	-1.04714	-1.4121	-1.36745	-1.4434	-1.29929		
APOC1	-1.50991	-1.13514	-0.43766	-1.14662	-1.27628	-1.5028	5.634565	5.110984	-1.38764	-0.10445	-1.25843	-1.19126	0.443816	-0.23916		
GSTT1	-2.17394	2.915485	-2.04794	1.45321	-2.52247	0.186979	-2.21629	3.520729	-2.22705	1.889826	-2.0116	2.837584	-1.80729	2.202762		
HLA-DRB5	-2.07833	2.982802	-2.21929	2.071962	-1.80086	2.885714	-2.7199	0.882822	-2.08018	1.646059	-1.97933	2.744197	-2.49837	2.162705		
EPB42	-1.15858	-1.12076	-1.08998	-1.10168	-1.01622	-1.04875	5.755878	4.702018	-1.20323	-0.36936	-1.28078	-1.23833	-0.87225	1.04203		
CD2	-1.19589	-0.88209	-1.12625	-1.13813	5.30901	5.295354	-0.66316	-1.07794	-0.26415	-0.79939	-1.31987	-1.27682	0.350463	-1.21111		
KLF1	-1.50656	-1.4458	0.047924	0.565284	-1.97425	-0.85051	4.646772	4.796152	-0.53256	-0.47191	-2.71319	-1.97518	-0.06394	1.477762		
APOE	-0.40595	-1.3676	-0.71869	-1.49423	-0.9679	1.86375	4.566912	5.184266	-1.46093	-1.27291	-1.08192	-0.93789	-1.87494	-0.03197		
GSTM1	2.056226	-2.11905	2.347887	-2.31631	2.746918	-2.01064	2.367497	-1.79727	1.985549	-2.52601	1.684631	-2.04888	1.823798	-2.19435		
GATD3A	-1.60583	2.078751	-2.04339	2.276387	-1.68615	2.91054	-1.95257	2.632876	-2.23845	0.976339	-2.80732	1.676096	-2.26782	2.05055		
BLNK	-1.05388	-1.1242	-0.17572	-0.40972	4.882118	5.327226	-1.24618	-1.52129	-0.8962	-1.19416	-1.05531	-0.9164	0.075635	-0.69191		
DNASE1L3	-1.01675	-0.98108	-0.95213	-0.96312	-0.88303	6.98587	-0.82608	-0.90753	-0.80178	1.531609	-1.13264	-0.43941	-1.161	1.547073		
HBG1	-1.21851	-1.13378	0.210777	0.950908	-1.07655	-1.10908	4.393128	5.333707	-1.35826	0.247061	-1.33953	-1.29758	-1.36888	-1.2334		
ALAS2	-0.93239	-0.89902	-0.87189	-0.88219	-0.80706	-0.08812	6.679912	3.04837	-0.97185	-1.0349	-1.04044	-1.00289	-0.5235	-0.67404		
SHD	-1.62896	-1.07637	1.834535	1.791603	4.587411	4.042725	-0.66499	-1.50261	-0.80645	-1.75248	-1.75907	-1.71419	-1.40164	0.05048		
KEL	-0.52763	-0.21413	-0.58656	0.598454	-1.61679	-1.65376	5.199221	4.189107	-0.56758	-0.72362	-1.9097	-1.57985	-1.47931	0.872143		
UBASH3A	-0.09086	-0.36306	0.028689	-1.24767	-1.15916	-1.19291	5.606089	4.092902	0.271535	-1.42527	-1.43167	-1.48949	-0.27739	-1.32175		
LOC112268313	3.048334	-1.99913	-1.96705	3.793539	2.376577	0.40817	-1.82123	2.807109	-0.05411	-0.54222	-1.52219	-2.11778	-0.35686	-2.05316		
LOC102723630	1.501971	-2.02716	2.366524	-2.00853	2.410091	-1.95583	2.480331	-1.94944	2.039054	-2.17052	1.688556	-2.13785	1.840537	-2.07774		
EPX	-0.81352	-0.76174	-0.99024	-0.17519	-0.20838	-0.26551	5.752911	4.049782	-0.87792	-1.15942	-1.16513	-1.12636	-1.19226	-1.06704		
IFIT1B	-0.75494	-0.96421	-0.66619	-0.10565	-0.87109	-0.20159	5.812178	3.995441	-1.03744	-1.1005	-1.10602	-0.85659	-1.13225	-1.01113		
MNDA	-0.24075	-1.76604	0.359159	2.089789	3.734322	3.331525	2.014536	1.385211	-1.85158	-1.92381	-1.93008	-1.51505	-1.86617	-1.82106		
AHSP	-1.60421	-1.32082	-0.74874	-1.60217	-1.94772	-0.93878	4.74597	3.832763	-0.28311	0.262829	-0.87761	-2.00814	1.983804	0.505938		
TNNI2	-0.30809	-1.4117	0.43469	-0.26996	4.298947	5.184565	-1.23391	-0.64995	-1.36663	-1.21712	-1.5801	-1.53571	0.103101	-0.44812		
HBD	-1.76191	-1.7021	0.644439	1.086924	-2.46268	-1.77698	3.687742	3.999695	-0.46305	0.988444	-2.52587	-1.41494	0.368617	1.331676		
GATA1	-1.29347	-1.2859	0.234775	0.640511	-2.15341	-1.40843	4.045612	3.910321	-0.30831	-0.12474	-2.8484	-1.62144	0.150517	2.062366		
UGT3A2	-1.99704	-1.42284	1.704815	1.843075	3.671225	3.999622	0.964006	0.083896	-0.55761	-1.89128	-1.51113	-2.07851	-1.45221	-1.35601		
LOC107986126	-1.44076	-0.99382	-1.36887	-1.38117	-0.52664	-1.32533	-0.40952	0.905419	-1.48723	5.301932	0.581697	-0.90765	3.832442	-0.7805		
SULT1A3	-1.68519	-1.62887	-1.59748	-1.61913	-1.52336	-1.57063	4.163194	1.103282	-1.75698	2.320675	2.17145	-1.78374	2.026072	1.38071		
ELK2AP	5.391483	-0.34959	-0.85508	-0.68674	-0.77638	0.100026	4.187628	-0.79544	-0.7663	-1.31112	-1.31714	-1.11191	-0.74786	-0.96157		
KIF17	-1.32404	-1.42804	0.707096	1.123819	3.75954	4.976934	-1.43988	-0.74593	-1.54563	0.041667	-1.79272	-1.0876	-0.04348	-1.20174		
C4A	-0.7928	-1.0623	-1.80357	-1.01357	-1.0843	0.055216	3.601973	5.634299	-0.29775	-0.16265	-1.17807	-0.95029	-0.77073	-0.17545		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
LOC105379461	-1.72882	-1.47055	0.522528	0.015722	0.112419	-0.31117	5.124692	3.696335	-1.38432	-0.60763	-1.85928	-1.68011	-0.84302	0.413207		
LYPD6B	2.781282	-1.46225	1.231942	-1.44284	-1.35501	-1.38862	-1.2912	-1.38211	3.274964	-1.29801	3.365405	-1.58028	2.062311	-1.51559		
TPSAB1	-2.19547	-1.91022	0.952105	0.650973	0.889667	0.413352	3.673273	3.217556	-0.47069	-0.73192	-2.83882	-2.83972	-0.02764	1.217559		
CLEC12A	-2.19664	-1.91626	1.873207	2.547796	3.171936	2.944118	1.174419	1.017384	-1.41537	-1.43494	-1.81727	-1.28079	-1.21646	-1.45112		
RHAG	-1.91184	-1.87092	-0.8227	-0.81217	-1.27124	-0.59726	4.788141	4.017126	-1.02553	-0.26037	-0.34684	-0.71243	0.719813	0.106214		
UCA1	-1.43638	-1.54585	-0.76794	-0.2946	-1.19008	-1.09041	4.356113	4.59462	-0.69035	-0.58142	-0.83492	-0.82784	0.212501	0.09655		
NID1	-0.92279	-0.06311	0.87735	-0.87635	-0.28234	-0.55716	6.311666	1.24619	-0.72658	-1.01677	-1.02181	-0.98755	-1.04573	-0.935		
UBXN10	0.025738	-1.18804	-1.15865	-1.16983	-1.08781	-0.07562	5.540968	2.841179	0.515682	-1.33327	-0.60077	-0.41208	-1.36691	-0.53059		
ANK1	-1.61179	-1.39893	0.519901	0.75251	-1.35783	-1.08962	4.143859	3.995808	-0.23432	-0.28199	-2.10084	-1.50579	0.050096	0.11893		
SUCNR1	-0.65843	-1.56671	1.422601	1.929299	3.533134	2.98922	0.934799	0.866387	-1.43029	-1.99611	-2.10934	-2.0694	-1.24594	-0.59922		
PLPPR3	-1.57694	-1.54012	1.373482	2.636596	2.735853	2.826907	1.972828	0.745479	-1.61989	-1.62137	-1.69312	-1.65325	-1.72077	-0.86571		
SIGLEC12	-1.12708	-1.09379	0.787186	1.854965	2.637806	4.956475	0.23162	-1.0242	-1.16614	-1.2279	-1.23328	-1.19664	-1.25881	-1.14022		
C4B	-0.61623	-0.58601	0.986555	-0.57104	-0.50631	-0.5305	6.491553	-0.52576	-0.65291	-0.71372	-0.71919	-0.6825	-0.74553	-0.62842		
CD40LG	-1.73787	-0.59433	0.484476	0.39281	-1.39868	-0.16361	4.28024	3.694921	-0.92798	-0.32615	-1.91643	-1.50851	-1.2729	0.994011		
MPEG1	-1.02236	-1.14537	-0.37758	0.317272	4.761104	3.982669	-0.9391	-1.05052	-0.59225	-0.93321	-0.26467	-0.99263	-0.98969	-0.75366		
CTSG	-1.31256	-1.01164	1.330881	2.100297	2.745337	2.797835	2.151034	0.993091	-1.51604	-2.00199	-1.35062	-1.68058	-1.90122	-1.34382		
LEF1	-1.65579	-1.61673	0.276228	-0.29246	0.191404	1.205906	4.122685	3.469565	0.006285	0.02371	-1.77949	-1.73695	-0.54321	-1.67117		
IGFBP2	-0.78632	-1.31234	2.031223	1.737892	3.269367	2.422221	1.792641	0.350996	-1.37862	-2.0633	-1.90178	-1.83827	-0.96307	-1.36062		
CEBDP	-1.1254	-1.75259	1.163815	2.15814	3.469438	3.351046	0.489869	0.212244	-1.18103	-1.97487	-1.07545	-1.38943	-0.86787	-1.47791		
NMU	-0.47933	-0.35383	-1.57276	-1.25178	-1.49411	-0.49733	5.229214	2.332361	-0.87858	-0.9205	-1.1445	-0.58413	1.358507	0.256762		
CSTA	-0.60501	-1.56174	1.2135	2.041193	3.34897	2.831722	1.090969	0.963049	-1.64195	-1.7097	-1.71557	-1.67549	-0.96663	-1.61333		
HBG2	-0.60333	-1.07895	-0.14778	1.012893	-0.78842	-1.43682	2.819929	4.992931	-1.52056	0.233277	-1.67304	-0.76229	-0.46417	-0.58367		
SLC10A4	0.101272	-1.04787	-1.02099	-0.0012	0.272593	0.404175	-0.90199	5.932305	-1.11934	0.438536	-1.18577	-1.14951	-1.21105	0.488835		
AVP	1.880565	1.661576	0.307844	-0.15287	-2.37833	-2.4902	-2.8811	-2.83687	0.95442	1.195278	1.749845	1.675445	0.922001	0.392396		
RNASE1	-1.61932	-1.34257	0.215454	0.098584	0.135253	0.182282	4.019178	3.812153	-1.28053	-0.30345	-1.74347	-1.70074	-0.75289	0.280069		
IGSF6	-1.16989	-1.33902	0.045229	0.506965	5.104348	2.72724	-0.87603	-0.64395	-0.28671	-0.54029	-0.22827	-1.45274	-0.85299	-0.99389		
ALOX5AP	-0.82491	-1.97889	-0.43807	-0.21003	2.498463	2.136214	2.842431	2.95589	-1.2526	-0.64469	-2.0745	-1.32343	-1.24276	-0.44311		
LOC101928134	-1.298	-0.46027	-1.23298	-0.47156	-1.16217	-0.89256	3.353974	4.593999	-1.22821	-0.96232	-0.86715	0.197605	-0.36681	0.796456		
CR2	-0.93973	-0.91085	-0.88717	-0.89618	-0.82986	-0.85522	5.117915	2.543687	-0.5784	-1.02676	0.98905	0.277927	-1.05328	-0.95112		
TPSAB1	-1.9321	-0.17406	-1.42811	1.478068	-1.78772	1.769007	0.10865	3.781145	-1.00186	1.094009	-2.04897	-1.21842	-0.80304	2.163397		
CSF1	-2.01819	-1.31099	0.140837	-0.10835	-2.32242	-1.47752	3.472911	3.075689	0.225765	0.449851	-1.63829	-0.78321	0.977342	1.316572		
CCL14	-0.85454	-0.82767	-0.80562	-0.81402	-0.75226	5.708589	-0.7075	-0.7713	-0.88596	1.044785	-0.79923	-0.67928	0.302553	0.841443		
AMHR2	-1.76037	-0.75786	-1.08158	0.551038	-1.61558	-1.64933	3.210422	3.427141	-0.05059	0.61353	-1.87889	-0.98527	0.175897	1.801443		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
LINC01670	-1.56919	1.314864	2.231245	-0.3597	2.716332	-1.46494	2.735774	1.400783	-1.61043	-1.67491	-1.68049	-0.51402	-1.70686	0.181531		
ITGB7	-0.5811	-1.83582	-0.12905	-1.88706	2.305	2.167323	3.093081	2.085348	0.592143	-1.8832	-0.7537	-1.63321	-0.6884	-0.85137		
CD36	-0.44851	-1.9822	0.019552	-0.30997	0.304139	0.830698	3.974776	3.379566	-1.43991	-1.11537	-1.34364	-1.19678	-0.53918	-0.13316		
TPSD1	-1.32426	-0.1817	-1.26171	1.381608	-1.19323	1.328477	-0.17315	4.223137	-1.36439	0.320721	-1.433	-1.11591	-1.45895	2.252347		
HBA1	-1.51703	-2.12768	-0.11305	-1.40673	-2.02985	1.543498	2.290468	2.763454	0.109612	0.751624	-2.26457	-0.7617	1.86801	0.893949		
CPA3	-1.96003	-2.19937	1.615428	1.88583	2.015085	1.587659	1.441735	1.378345	-0.73134	-0.55435	-2.37046	-2.43972	-0.41155	0.742739		
ACSM1	-0.65697	-1.4886	0.281161	1.120108	-0.0236	-0.6478	3.751498	3.32575	-1.32321	-0.51802	-1.77533	-1.88028	-0.35576	0.191044		
MEG3	1.551591	0.780789	-0.3824	-1.27158	-2.29439	-2.17602	-2.38515	-2.16549	1.430081	1.197607	2.364312	1.346779	1.418857	0.585006		
LGALS1	-1.24245	-1.29928	0.649826	1.209479	3.597146	3.599959	-0.3156	-0.26145	-1.54911	-0.6877	-1.34802	-1.14124	-0.41511	-0.79645		
IGLL1	-0.96515	-1.06108	1.620705	1.927606	2.663134	3.118652	0.549091	0.040937	-1.29084	-1.40075	-2.06773	-1.71061	-0.89726	-0.5267		
LINC01115	-1.16876	2.988704	-1.10939	0.548556	-1.04472	-1.07334	-0.99046	-1.06779	-1.207	1.52208	-1.27264	2.991065	-1.29755	2.181242		
CYP2E1	-0.12204	-1.27138	-0.33168	0.907314	1.152218	0.639901	4.551117	1.612126	-1.03573	-1.40703	-1.41243	-0.5258	-1.43799	-1.3186		
CTSL	-0.87126	-0.23345	-1.10764	-1.25096	-1.70284	1.024073	2.850572	4.12012	-0.51862	0.599973	-0.56306	-0.15839	-1.62465	-0.56387		
DLK1	1.570115	1.628969	-0.25624	-0.47785	-2.41596	-2.54332	-2.07724	-2.36048	1.383945	1.040836	1.592084	1.564048	0.762434	0.588657		
FUT7	-0.43857	-0.49538	1.63465	1.530964	3.210577	3.125555	-0.43256	-0.66407	-0.71188	-1.95423	-1.28932	-1.40567	-1.14764	-0.96242		
GSTM5	1.629127	-0.44637	1.89152	-2.3849	2.095149	-2.53773	0.72568	-2.08002	1.511056	-0.99732	1.42568	-0.58163	1.067407	-1.31764		
LINC02132	-0.70763	-0.92355	0.428673	0.974006	3.412052	3.754342	-1.38376	-0.80184	-0.35805	-1.24412	-0.54174	-0.87233	-1.51473	-0.22132		
EPAS1	1.509349	1.569251	-0.03878	-0.51564	-1.73636	-2.41925	-2.57756	-2.49515	1.413553	1.449822	1.48527	1.439637	0.586146	0.329714		
SULT1A4	-0.40992	0.443274	0.083662	0.364616	-0.49012	0.055954	2.911169	2.966846	-0.09475	-1.06664	-2.80531	0.154421	-2.82248	0.709278		
RNA28SN2	-1.65603	-1.91257	-0.64753	-0.11565	-0.47476	-0.20585	-1.85471	-1.30918	1.055629	2.527953	2.299629	0.452147	2.981626	-1.1407		
DNAAF4-CCPG1	-1.79152	-1.75439	-1.7335	1.480386	1.425823	1.939576	-1.60597	-1.68962	0.471463	1.799585	1.345211	-0.08274	2.003613	-1.80791		
HES6	-1.02589	-1.05514	0.576099	0.384989	0.968432	1.447253	3.161478	2.808138	-0.75707	-1.68675	-1.35536	-2.18906	-1.23079	-0.04633		
ST14	-1.04795	0.735249	0.589234	0.668631	3.472488	2.903192	-0.6032	-1.48636	0.799421	-0.35488	-1.58552	-1.17176	-1.74191	-1.17663		
VPREB1	-0.88408	-1.04282	1.15407	0.843799	2.741605	3.772359	-1.1626	-0.52538	-0.62918	-0.46371	-2.07501	-1.50138	-0.11096	-0.11672		
TCEAL2	1.392014	1.610667	-0.61204	-0.41827	-2.22568	-2.45163	-1.89206	-2.32995	1.324091	0.772868	1.706523	1.746139	0.619466	0.757868		
CCDC169-SOHLH2	-1.9446	1.771587	-1.88387	1.303034	-1.81562	0.430598	-0.28147	2.202934	-1.77027	1.400784	-2.04646	1.338691	-0.21217	1.50682		
FBLN2	-1.72374	-1.51865	-0.32128	1.321953	1.22665	0.378871	2.426321	3.093813	-0.61029	-0.55647	-1.83392	-1.53466	-1.43753	1.088937		
CLEC3B	1.281491	1.935856	-1.22543	-0.38168	-1.92914	-1.7285	-2.6412	-2.04594	0.931634	1.082296	1.376401	2.009575	0.478051	0.856594		
HLA-DPB2	-1.68318	2.098989	-1.45315	1.559165	-1.1605	1.859098	-1.23274	0.299568	-1.33873	1.259828	-1.49548	1.915912	-2.05451	1.425742		
LTBP1	-1.00899	-0.40735	0.482983	1.273475	-1.83856	-1.87389	1.474626	1.527678	0.128042	1.759154	-2.60132	-2.03672	1.138498	1.982373		
SNHG18	-1.42934	1.99619	-1.37069	1.753836	-1.30562	1.882953	-1.25012	-0.48326	-1.46656	1.537238	-1.52935	2.384328	-1.55281	0.833211		
VPREB3	-1.34207	-1.61193	-1.2089	-1.25199	1.943435	3.124128	0.336239	1.447809	0.304523	-0.79114	-1.75579	-1.71858	1.784182	0.740078		
ITGA2B	-0.46342	-0.31291	0.190296	0.915814	-2.57764	-1.51752	2.687571	2.497699	-0.36663	0.798154	-1.81642	-1.56505	-0.07089	1.600946		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
XK	-1.03786	-0.55401	0.823282	0.25433	-1.27999	-1.84879	3.177961	2.80249	-1.36546	0.747212	-0.66672	-2.02727	0.349162	0.625663		
LOC101927879	0.417238	1.240484	-0.73383	-0.26287	-2.65844	-2.48761	-1.75042	-1.63893	0.896862	1.987633	1.129426	1.613167	1.344523	0.902771		
ACY3	-0.31097	-0.04648	0.90988	-0.36233	3.611798	2.758742	-1.37578	-2.27157	0.593139	-1.32169	-0.32729	-0.71271	-0.17673	-0.96801		
FAM83D	-0.81864	-0.3675	0.418196	0.235778	0.414296	0.756684	2.98036	3.1209	-0.61117	-1.99011	-1.30529	-1.75845	-1.59454	0.51948		
PMP22	-0.69617	-0.47331	-0.62774	-0.48914	0.707479	-0.97573	3.799962	3.190017	-0.56799	-1.02724	-0.41106	-1.64901	-0.26689	-0.51318		
DYNLL1	-1.18656	-0.87576	-0.96291	0.871406	-0.45382	-0.77551	3.224568	3.10457	-0.3147	0.183799	-1.91012	-1.58802	-0.26463	0.947676		
CSF2RB	-1.34092	-0.57155	-0.45768	-0.60122	-0.67539	-1.95794	3.398241	3.415681	-0.46123	0.136329	-0.68355	-0.90126	0.260472	0.440016		
BORCS7-ASMT	1.067155	-1.91562	0.061468	-1.91012	-1.82317	1.343516	-1.77508	-1.85711	1.074313	1.506462	1.677816	1.636959	1.560651	-0.64725		
HCK	-0.94266	-0.88534	2.165997	1.742523	3.087414	2.093045	-1.11005	-1.18873	-1.01402	-1.3884	-1.39359	-0.80593	0.241171	-0.60142		
SPON1	0.287406	-1.31271	1.064666	-0.34744	3.345571	2.418285	-1.26076	-1.54428	1.119821	-0.23245	-1.76598	-1.72804	-0.27601	0.231923		
DTX4	-1.51365	-0.08675	0.479062	0.105679	3.538584	3.223289	-0.6337	-0.0655	-1.37381	-1.23953	-0.17183	-1.26826	-0.79835	-0.19525		
TFR2	-0.78555	-0.37113	0.163436	-0.10479	-1.12726	-0.79764	3.480635	2.956839	-0.61221	0.006549	-2.1849	-1.30184	-0.30274	0.980592		
SEC14L2	-0.33617	-0.84987	-1.29261	-0.84782	-1.64219	-1.64049	3.539206	3.06216	0.320945	0.337331	-0.44603	0.194294	-0.59014	0.1914		
UMODL1	-0.61951	-0.20382	0.26681	0.305438	3.217274	3.513916	-1.09426	-1.32552	-0.27773	-0.38012	-0.24746	-0.6145	-1.88983	-0.65068		
P2RX5	-0.42133	-1.20998	0.534633	0.329947	1.107411	-0.72691	3.835468	2.085558	-0.17634	-0.8237	-0.95748	-2.28629	-0.43221	-0.85877		
CCR7	-1.38063	-1.3457	-1.31702	0.040391	3.298554	3.232084	-0.57775	-0.23963	0.854864	-0.42569	-1.49121	-0.13111	-0.11596	-0.4012		
DHRS9	-1.66022	-1.62616	-1.03262	-0.94817	-0.68749	-0.6683	1.419649	2.588358	0.295464	1.963223	-1.76626	-0.57381	0.271199	0.2425149		
DHRS3	-1.6908	-1.20916	-0.05214	0.735409	0.921459	1.397178	2.398402	2.551754	-1.44662	-0.33007	-2.15808	-1.62048	-0.33867	0.841807		
TST	-0.3974	-0.79968	0.402592	0.532361	1.159727	1.263813	2.718987	2.781786	-1.46862	-0.98661	-1.62832	-1.91766	-0.9437	-0.71727		
LOC112268350	-1.21306	0.921962	-1.16066	-1.16385	-1.09028	-1.12236	-1.04642	2.03571	-1.25879	2.948805	-1.32593	1.1439	0.345812	0.985164		
RASSF6	1.131337	1.856241	-0.71964	-0.55757	-2.21208	-2.00268	-1.55216	-2.23756	0.988114	0.845165	1.548291	1.73796	0.15888	0.101571		
SLC1A6	1.529849	1.473842	0.143225	-0.31268	-2.69501	-2.58083	-1.15987	-1.77121	1.681294	-0.00756	1.237176	1.021766	0.493495	0.946524		
AKR1C1	-0.6395	-0.18894	-0.56617	0.306483	-1.50687	-0.66727	2.452249	3.687614	-0.81292	-0.54388	-1.30207	0.890287	-1.54388	0.434859		
ADAMTS14	-0.72343	-0.73913	0.624967	-0.54935	0.707957	0.702674	3.310926	2.497262	-0.60849	-0.74	-1.88329	-1.8455	-1.10714	0.352553		
RBPMS2	-0.11903	-0.43166	0.309131	1.035446	-1.17205	-0.50041	2.962272	2.795053	-1.39637	0.128011	-2.23474	-0.80964	-1.14773	0.581713		
F13A1	-0.28685	-0.01653	1.197774	1.100117	2.726624	2.183889	0.800898	0.03185	-0.90205	-1.35152	-2.34986	-1.66588	-1.35606	-0.11241		
LINC01835	-1.2531	-0.80343	-0.05556	1.610381	-0.38609	-0.78275	2.557134	3.008351	-1.01202	0.472017	-1.35308	-1.3188	-1.37682	0.693753		
C7orf55-LUC7L2	-1.86788	0.077926	-0.23084	-0.4488	-1.74045	2.332342	0.201822	1.133827	0.308915	2.194723	-1.98141	1.346022	-1.90367	0.577469		
FCER1A	-2.29435	0.898157	-1.2801	0.178753	-1.32712	-1.44205	1.112313	1.737999	-0.1812	1.191604	-2.26507	0.904607	0.676792	0.2089662		
ZAR1	-0.03728	-0.0991	-0.40606	1.096197	0.598471	-1.69129	-1.53113	0.588186	-1.88541	2.457958	1.837552	-1.32544	1.925661	-1.52831		
KCNG2	-1.51618	0.097832	1.402605	1.79902	2.274127	2.573382	-0.50997	-0.19997	-1.2474	-0.93554	-1.978	-0.45673	-1.36359	0.060401		
CLEC4G	0.105901	-1.15593	0.621843	0.594078	3.107889	2.987531	0.391697	-1.08891	-0.76011	-0.3276	-1.28894	-0.67396	-1.31307	-1.20041		
PPP1R14A	-1.03095	-0.12016	-0.10179	0.551331	-1.05077	-0.76993	3.144893	3.19079	-0.8867	-0.41551	-1.36369	-0.96396	-0.77847	0.594905		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d	e	e	f	f	g	g		
Gene																
MS4A1	-0.73162	-0.84784	-1.14585	-0.55117	-1.49656	-0.38805	2.906746	3.662374	-0.27433	0.227996	-0.39555	-0.55743	-0.36196	-0.04676		
BLOC1S5-TXNDC5	-1.39195	-0.15256	-1.33662	0.326149	0.870059	-1.30234	-0.13865	0.875241	-1.42682	2.167173	1.815793	-1.45357	2.55185	-1.40376		
PDZRN4	0.973247	1.77383	-0.04052	0.178537	-2.28225	-2.30895	-1.46993	-2.03744	0.515297	1.284494	0.520463	1.72142	-0.07857	1.250376		
TARP	-1.18781	-1.36433	1.317314	1.673211	2.290586	1.985161	1.277324	0.720642	-1.42455	-1.06378	-1.51988	-1.30282	-0.71338	-0.68769		
CDH7	0.747192	1.567049	-1.38701	0.006664	-2.1255	-1.69847	-1.8945	-1.6411	0.858081	1.564195	1.08772	1.838223	0.240611	0.836858		
LIMCH1	1.162694	1.430235	0.034456	-0.20539	-2.06131	-2.11301	-2.00135	-2.19201	1.047688	1.034116	1.14495	1.261511	0.757291	0.700121		
GPR75-ASB3	0.803165	0.743059	0.546741	0.542273	1.466486	0.901274	1.284792	0.399919	0.523864	-2.56295	-2.58304	0.096562	-2.58366	0.42152		
MYL4	-1.15891	-1.34286	-0.02148	0.071998	-1.81736	-0.88231	2.545413	2.33155	-0.04052	0.854745	-1.95289	-0.62303	0.429972	1.605686		
CRHBP	1.218091	1.727928	0.215652	-0.0584	-2.29288	-2.36555	-1.70432	-1.82204	1.080396	0.494241	0.889812	1.476843	0.285955	0.854269		
CST7	-1.30145	-0.64295	0.931779	1.762921	2.041448	1.870174	1.493543	1.027604	-1.3641	-1.44357	-1.6237	-1.28663	-1.171	-0.29406		
MINOS1-NBL1	0.726774	-0.25506	-1.88889	-0.2263	-1.81489	-0.85889	-1.89699	-0.58117	1.424167	1.629565	1.934975	0.842682	2.031346	-1.06732		
HES1	1.264481	0.835009	-0.6733	-1.17217	-2.0067	-1.32138	-1.9188	-1.71648	1.336889	1.285901	1.861849	1.253126	1.195733	-0.22415		
SELENOM	1.162237	1.616763	-0.66273	-0.91811	-2.11777	-1.32259	-2.18918	-1.66284	1.007306	0.918561	1.526855	1.645259	0.570333	0.4259		
CHST2	-0.93321	-0.25188	-0.00109	0.034108	1.289442	0.369859	3.06227	2.635501	-0.8357	-1.67546	-1.16442	-1.09593	-1.06303	-0.37045		
LOC403323	1.304367	-1.71199	1.494877	-1.3962	1.585364	-1.12196	1.352641	-1.30806	1.131069	-1.35136	1.084101	-0.78391	1.476687	-1.75562		
SERPINB8	-0.06757	-0.43842	0.965604	1.106067	2.929301	2.515531	0.194696	-1.37571	-0.47945	-1.952	-0.78769	-0.92057	-0.66477	-1.02502		
SELENBP1	-0.25028	0.093714	-0.86561	-1.42906	-1.47221	-0.36026	3.358588	2.904074	-0.1397	-0.44329	-0.19445	-0.18813	-0.13984	-0.87356		
LOC107986939	1.338138	1.419951	-0.01149	-0.55277	-1.35711	-1.96152	-2.25451	-2.25102	1.023602	0.945596	1.224882	1.326521	0.702912	0.406828		
GGTA1P	0.10117	1.977263	-1.47945	0.893928	-2.67023	-0.41167	-2.11263	-0.19656	-0.10437	1.162142	0.012525	1.782785	-0.47787	1.522975		
NTRK1	-0.88326	-1.02498	-0.86051	0.300981	-1.46894	-1.49936	2.804251	2.630479	0.010045	0.279215	-0.97039	-0.79778	-0.01016	1.490424		
LOC112268246	0.992364	-1.70248	0.855069	-1.54712	0.677481	-1.23015	-0.06784	-1.43728	1.016392	1.973133	1.303842	-1.10746	1.975296	-1.70125		
PLK1	-0.53957	-0.02103	0.680287	0.703332	1.988174	2.107834	1.357051	1.295619	-1.8115	-1.52533	-1.61002	-0.88679	-1.8724	0.13435		
ABI3BP	1.090228	1.659761	-0.95754	-0.37611	-1.76834	-1.14034	-2.15103	-2.22629	0.967884	0.822129	1.16105	1.63649	0.471746	0.810365		
SPP1	0.935136	1.924358	-0.5284	-0.34871	-1.92716	-1.75661	-1.87206	-1.8405	1.34961	0.564351	0.772092	1.628719	-0.07693	1.176114		
THY1	1.599879	1.88093	-0.60834	-1.63361	-1.84079	-0.58969	-1.78377	-1.27821	0.878242	0.784798	1.606415	1.734808	-0.8514	0.10074		
FCGR1A	-0.65978	-0.6701	1.189767	1.802024	2.263395	2.07957	1.203988	-0.45319	-1.06713	-1.60235	-1.36588	-0.39388	-0.80518	-1.52127		
CD3E	-0.34153	-0.16733	0.936924	0.330888	2.261328	3.416558	-0.82007	-1.14727	0.351547	-1.08141	-1.34201	-1.3085	-0.65002	-0.4391		
FXYD6	1.863016	1.54627	0.029334	-0.80162	-0.45126	-1.13634	-2.30826	-2.40041	1.367929	-0.28628	1.52724	1.372797	-0.23386	-0.08855		
LOC100233156	1.209285	-1.41134	1.246733	-0.99707	1.832821	-1.35243	2.036069	-1.34716	0.908655	-1.42092	1.212828	-0.90501	0.5737	-1.58617		
PLIN2	-0.95001	-0.75744	0.282656	0.121997	0.68921	0.687346	3.172016	2.544017	-0.97699	-1.07487	-1.22623	-1.11322	-1.05016	-0.34834		
LOC339862	-0.21163	-0.75956	1.896622	1.203471	2.452781	2.073252	-1.02939	-1.69203	0.134989	-1.05123	-1.28102	-1.35827	-0.7066	0.328606		
LOC101928047	-0.89233	-0.56125	-0.82209	-0.32081	-0.56225	0.024143	3.506817	2.591861	-1.41751	-1.08008	-0.00047	-0.66765	0.369975	-0.16838		
TNFAIP6	0.392655	-1.02951	-0.45073	-1.01552	-0.71528	0.15889	3.995372	1.61948	-1.08879	0.285035	-0.64285	-1.11343	-0.59272	0.197411		

Supplemental Table 3. Top 200 differentially expressed genes in ssBM bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Population	<i>a</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>c</i>	<i>d</i>	<i>d</i>	<i>e</i>	<i>e</i>	<i>f</i>	<i>f</i>	<i>g</i>	<i>g</i>
Gene														
ADD2	-0.18837	-0.61622	-0.34267	-1.00134	-1.28685	-1.16398	3.433288	2.776148	-0.52281	0.17101	-0.21869	-0.40494	-0.20235	-0.43222
SPNS3	-0.00988	-0.43499	1.372769	0.820455	2.740354	2.59142	-1.13772	-1.75115	-0.3251	-1.13581	-0.68434	-0.83804	-0.37479	-0.83319

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
XIC	3.314195	-3.25311	3.190342	-3.2597	3.343936	-3.25174	3.099726	-3.18365
LOC112268313	-1.99459	3.609558	-1.98634	-2.04813	-2.16378	3.984753	-2.161	2.759535
DDX3Y	-2.55706	2.629814	-2.55342	2.665592	-2.80166	2.656109	-2.78868	2.749315
KDM5D	-2.06466	2.478745	-2.2529	2.439492	-2.49087	1.955178	-2.30957	2.244583
USP9Y	-2.21979	2.168112	-2.21241	2.331804	-2.26503	2.110836	-1.89149	1.977969
RPS4Y1	-2.16189	2.136493	-2.18827	2.342526	-2.20168	2.091578	-2.0387	2.019947
HDC	-1.36804	-1.63502	-0.50078	-0.32455	-1.9356	-1.37104	3.684635	3.450414
TXLNGY	-2.05983	1.929994	-2.15391	2.29782	-1.54192	1.839596	-2.33902	2.027268
RNA45SN2	-1.72909	1.215871	-2.72487	1.39018	-2.89706	2.072836	0.989827	1.682302
ZFY	-1.92094	1.60998	-1.91361	2.040046	-1.98172	2.29196	-1.83927	1.713565
CNRIP1	-1.51808	-0.8909	-1.5077	0.040621	-1.53063	-0.77494	2.96913	3.212501
ANK1	-0.85227	-1.29269	-0.97156	-0.6687	-1.41283	-1.14584	3.142865	3.201036
DNTT	-1.81667	-0.84796	-1.74632	0.052773	2.390273	2.618575	-2.15821	1.507527
KCNH2	-1.15922	-1.05978	-1.16873	-0.82577	-1.30122	-0.71501	2.854236	3.375495
FCER1A	-1.56754	-0.75305	0.059261	0.183244	-2.00164	-1.61713	2.90177	2.795095
GATA1	-0.88079	-1.14669	-0.94191	-0.82016	-1.3664	-0.99849	3.278839	2.875604
TRIB2	-2.1305	-1.51305	-2.12003	-1.18848	1.685675	1.324823	1.688248	2.253316
IRF8	-1.45237	-0.82729	-1.26784	-0.69957	2.403863	3.250988	-1.59829	0.190514
MPO	-2.4371	-0.57999	-0.60574	0.093628	2.164229	3.221051	-0.69535	-1.16072
ITGB3	-1.11594	-1.15515	-1.16612	-1.29479	-0.34167	-0.73114	3.09719	2.707627
USP32P1	-1.9947	1.774326	-1.83514	1.878255	-1.49658	1.333885	-1.37405	1.714
XK	-0.92466	-0.96481	-1.02775	-0.59681	-1.16149	-0.97779	2.715997	2.937307
HLA-DRB1	-1.3369	1.963236	-1.39693	1.620881	-1.53914	1.95609	-2.00797	0.740736
MS4A1	-1.05918	-0.47493	-0.89556	-0.2546	-1.80124	-0.71753	2.872299	2.330741
CD36	-1.01145	-0.74701	-1.1168	-0.78215	-0.82748	-0.84078	2.671087	2.654591
EIF1AY	-1.36165	0.942905	-1.49596	1.681976	-1.63351	1.599974	-1.55899	1.825244
ITGA2B	-0.40164	-0.31591	-1.00709	-0.955	-1.03632	-1.4184	2.378234	2.75613
RYR3	-0.86953	0.168427	-1.08259	-0.26453	-1.64647	-1.22659	2.232723	2.688563
UTY	-1.34311	1.503974	-1.7387	1.631009	-1.52894	1.417719	-1.43957	1.497619
FREM1	-0.33231	0.312093	-0.48327	0.168175	-2.15284	-1.90325	2.328436	2.062965
TFR2	-1.23799	-0.87552	-0.69227	-0.16768	-1.31907	-0.77334	2.435669	2.630198
MS4A3	-1.44398	-1.31001	-0.89003	0.212781	-1.21573	-0.07058	2.727499	1.99005
LOC112268155	-1.22059	2.103882	-0.50063	1.854397	-1.34266	1.649707	-1.34066	-1.20345

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
RNA28SN2	0.373334	1.419589	0.973753	-0.26335	0.703107	-1.91017	-2.78306	1.486801
ACSM1	-1.25858	-1.14071	-0.03563	0.587582	-0.9842	-1.54525	2.025937	2.350855
NOTCH3	-0.61697	-0.51395	-0.85582	-0.27071	2.562301	2.091672	-1.23551	-1.16101
PLGLB2	-1.42354	0.848175	-1.4175	1.628018	-1.545558	1.413642	-0.95867	1.455453
PRKY	-1.36213	1.323606	-1.58662	1.442287	-1.50874	1.270109	-0.92604	1.347533
DYNLL1	-0.93789	-0.84264	-0.69891	-0.87158	-0.71177	-0.58595	2.456071	2.192683
LTBP1	-0.66448	-0.53955	-0.82958	-0.50282	-1.06777	-0.96724	2.124987	2.446456
ABO	-1.32549	1.106513	-1.25834	1.180834	-2.21697	0.679277	0.143371	1.690803
SPON1	-1.14591	0.090778	-0.70451	0.230499	1.791928	2.279786	-1.80826	-0.73431
CSF2RB	-0.37072	-1.03249	-0.47754	-0.84557	-0.77093	-1.0079	2.542573	1.962569
JCHAIN	-1.076	-0.8285	-0.71986	-0.67949	2.621262	1.666455	-1.18882	0.204946
TPSAB1	-1.04638	-1.06921	0.944437	-0.94337	0.509199	-1.08966	2.874789	-0.17981
SERF1A	-0.72867	-0.7637	-0.7346	2.263527	-0.82929	-0.77258	2.26442	-0.69909
HBD	-0.70752	-0.95955	-0.44396	-0.47625	-0.96608	-0.90908	2.187928	2.274505
PACSin1	-0.99147	-0.13785	-0.80699	-0.44207	1.986427	2.325185	-1.33134	-0.60188
CSF1	-0.61028	-0.53519	-0.72633	0.085595	-1.44196	-0.90955	1.607935	2.529788
RAB31	-0.60821	-0.21827	-0.98463	-0.11369	2.373709	1.780894	-1.35669	-0.8731
LOC105377225	-0.99987	1.172271	-1.026	1.223106	-0.7281	-0.93872	-1.01917	2.316485
OVOS	-1.31513	1.714331	-1.54099	1.437113	-1.19779	0.556974	-0.77532	1.12082
SPTB	-0.85142	-0.6086	-0.81797	-0.50304	-0.94913	-0.57755	2.313703	1.994011
P2RX5	-1.50005	-0.89863	0.033919	0.584616	-1.09175	-0.87475	1.561161	2.18548
SIK1	-0.89346	1.073182	-1.65922	0.544665	-1.13687	1.856181	-1.02937	1.244905
TTTY15	-0.98537	1.21993	-1.31649	1.219087	-1.79293	1.140911	-0.72717	1.242025
JAML	1.188086	0.537693	-0.21398	-0.72902	1.871947	0.762126	-1.75489	-1.66196
MYO16	-0.87227	-0.57852	-0.79318	-0.65344	-0.4781	-0.78214	1.933949	2.223706
LOC112267940	-1.34509	-0.28658	1.329324	0.318896	1.769686	-1.38815	0.930844	-1.32893
FAM178B	-0.5635	-0.56048	-0.70788	-0.73929	-0.79801	-0.7444	2.229432	1.884109
LOC107987136	-1.18328	1.271401	-1.09022	1.15882	-1.65507	0.459732	-0.51086	1.549472
RNF4	-0.8722	0.891599	-0.86781	1.649707	-0.94234	-0.90217	1.908191	-0.86498
SLC2A5	0.091522	0.129545	-0.22805	0.037977	1.74473	1.436127	-2.08794	-1.12391
SCN3A	-1.22283	-0.62315	-0.92346	-0.50783	1.867208	1.730861	-0.91768	0.596883
FUT7	1.089508	-1.08458	0.958502	-0.81968	1.72548	0.590499	-0.81924	-1.64049
KEL	-0.55556	-0.65482	-0.40348	-0.84793	-0.76334	-0.73102	2.058269	1.897889

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
F13A1	-1.47941	-0.80178	0.473692	-0.28004	1.771841	1.744547	-0.86764	-0.56121
CCR7	-0.54479	-0.42952	-0.66394	-0.84985	2.215548	1.624089	-0.99252	-0.35901
LOC107984312	-0.69842	-0.89823	-0.80266	-0.33033	-0.72427	-0.37762	1.697987	2.133544
ZNF385D	0.231372	0.229322	0.518645	0.591358	-2.14701	-1.57326	1.039534	1.11004
SUCNR1	-0.96192	-0.69242	-0.2489	-0.04257	2.052821	1.679961	-0.9077	-0.87927
PIEZ02	-0.8742	-0.56216	-0.80194	-0.72563	0.014943	-0.78594	1.5224	2.212533
ACSM4	-0.75347	-0.77025	-0.21329	-0.44365	-0.83747	-0.78523	2.074177	1.729187
RASSF6	1.534195	1.464854	0.51125	0.530051	-0.2637	-0.99675	-1.47271	-1.30719
AFF2	-1.19999	-1.10051	-0.78624	0.154231	-0.58469	-0.03046	1.611663	1.935989
SPTA1	-0.83479	-1.10806	-0.36321	-0.43541	-0.41711	-0.57255	1.679025	2.052108
MINPP1	-0.99409	-0.88984	-0.32695	-0.62469	-0.30803	-0.58965	1.975101	1.758156
SLC40A1	-0.51091	-0.14526	-0.36511	-0.00949	-1.15725	-1.31222	1.673506	1.826738
SLC24A3	-0.95451	-0.99728	-0.44129	0.064152	-0.78542	-0.50868	1.687535	1.935497
LOC101928202	0.980629	1.979313	-0.37253	0.978265	-1.28015	-0.71465	-1.07022	-0.50066
SPNS3	-0.11989	0.083137	0.104355	0.063383	1.400873	1.56562	-1.81608	-1.28139
NTRK1	-0.73551	-0.60793	-0.73152	-0.25823	-0.81644	-0.5513	1.960837	1.740074
RIPOR3	-0.01221	0.517564	-0.35266	0.094829	-1.75502	-1.32639	1.347682	1.486216
STXBP6	-0.67772	-0.52507	-0.71519	-0.39999	-0.65863	-0.72205	1.7503	1.948355
HOPX	0.866011	0.596295	0.553409	0.55635	0.970278	0.062498	-1.65334	-1.9515
SPTBN2	-1.16173	-0.27047	-0.69026	-0.10437	-1.06432	-0.17763	1.581574	1.887205
FAM215B	-1.89653	0.733467	-1.42234	1.177185	-0.09941	1.166778	-0.06376	0.40461
NBL1	1.477117	0.679291	0.832273	0.106134	-2.12824	0.15031	-1.06316	-0.05373
SETBP1	0.9435	0.617085	0.280864	0.0273	1.147055	0.478494	-1.83869	-1.6556
CPA3	-1.72363	-1.6534	0.270344	0.348766	0.328662	-0.01516	1.289588	1.154831
CRYBG1	-0.03144	0.380532	0.087373	0.537977	1.147508	1.148494	-2.12559	-1.14485
PRG2	0.409765	-0.74533	-0.7677	-1.11366	-0.49297	-0.43682	2.238392	0.908322
LOC112268349	-1.59623	0.49608	0.23005	0.383601	-0.1788	1.19943	-1.70759	1.173453
PDZRN4	-0.55773	1.990102	-0.45592	1.334879	-1.0654	-0.84112	-0.67799	0.273186
MAMDC2	0.184867	0.041883	0.876935	0.825513	0.855116	0.658171	-1.69754	-1.74494
PLGLB1	0.945972	0.008785	1.106954	-1.28139	0.74583	-1.28739	0.997676	-1.23644
CP	-1.2171	-0.62283	1.185624	1.166588	1.022667	0.631273	-0.97028	-1.19594
MME	-0.78953	-0.69777	-1.30732	-0.27193	1.399987	1.612618	-0.67459	0.728531
SLC5A4-AS1	1.535696	-1.00296	0.913888	-1.01365	1.239164	-0.84271	0.142651	-0.97209

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
LOC105378072	-0.06772	0.195957	-0.24535	0.694347	1.025383	1.296435	-2.11843	-0.78062
SDK2	-0.37797	0.250552	-0.10443	0.376729	1.355911	1.33369	-1.86178	-0.9727
GPR75-ASB3	-1.18244	0.291933	1.624032	0.65936	0.889774	0.166779	-1.27958	-1.16986
LOC105379461	-0.99709	-0.68833	-0.55012	0.099627	-0.49826	-0.7569	1.697871	1.693204
SH3BP5	0.61995	0.010953	-0.30561	-0.27506	1.181118	1.570466	-1.39408	-1.40774
NA	1.177053	-0.64409	1.101967	-1.10283	1.335449	-0.59984	0.120855	-1.38856
NPTX2	-0.298	-0.57738	-0.01993	-0.5417	1.955223	1.303913	-1.32626	-0.49586
PTGS1	0.83361	0.276263	0.236273	-0.34761	-1.30812	-1.80316	1.234547	0.878193
HCK	0.017235	-0.64878	0.750197	0.070035	1.531289	1.021718	-1.42995	-1.31175
PRKG2	0.871968	0.525587	0.580524	0.392705	-1.48327	-1.9485	0.601454	0.459537
VWF	0.341327	-0.20152	0.541455	-0.69443	-1.12493	-1.51915	1.367124	1.290127
LIMCH1	1.437242	1.097935	0.641399	0.571941	-0.87836	-1.448	-0.44265	-0.9795
SPINK2	0.325724	0.258672	0.943734	0.580327	0.966037	0.258666	-1.52016	-1.813
CYTH4	0.557251	0.039773	0.804742	0.03348	1.289768	0.404746	-1.17044	-1.95932
UNC5B-AS1	1.450601	-0.474	0.088976	-0.84772	1.503837	0.458678	-1.04817	-1.1322
KBTBD11	0.127632	-1.00879	0.77032	-0.22947	1.750952	0.740387	-0.70104	-1.44999
ADAMTS14	-0.84467	-0.90089	-0.13216	0.014331	-0.91476	-0.44978	1.67935	1.548584
LINC00865	-0.64532	-0.04279	-0.65997	-0.41503	0.860125	1.96199	-1.40908	0.350066
GSTM1	-0.80255	0.832273	-0.92665	0.865546	-0.61608	1.162455	-1.44588	0.930885
SPNS2	0.934812	0.318602	0.415862	0.151896	0.70302	0.729386	-1.40622	-1.84736
LOC112268350	0.741811	1.012595	-1.21084	0.832284	0.28889	-1.25351	0.793469	-1.2047
GSTM5	0.940638	-0.91062	0.904484	-1.2126	1.067215	-1.03703	0.905411	-0.6575
DHRS3	-0.07178	-0.79459	-0.8855	-1.01913	-0.05348	-0.28971	1.713817	1.400375
RNA28SN5	0.814476	-0.50671	0.28411	-1.82209	-0.30444	-0.66127	0.804773	1.391147
BLOC1S5-TXND5	1.296534	-0.37446	0.504422	0.36931	-1.54269	-1.42834	0.801677	0.373551
MICAL2	-0.76488	-0.83822	-0.07958	-0.67485	-0.41338	-0.47419	1.597736	1.647347
MMP2	0.695599	0.370651	0.84848	0.088823	1.075598	0.014911	-1.40141	-1.69266
MIR8485	-0.98871	-0.36666	-0.63839	-0.4866	1.930676	-0.33607	-0.33664	1.222394
LOC107984427	-0.31485	1.317403	-1.24526	0.891416	-1.32974	0.612043	-0.62137	0.690371
HLA-DQA2	0.914159	-0.06243	1.142278	-0.46075	1.21942	-0.4415	-0.67376	-1.63742
ARHGEF12	0.471931	0.419538	-0.06992	-0.08812	-1.45061	-1.48344	1.124699	1.075917
ARL4C	0.505835	-0.40284	0.555491	-0.23916	1.220649	1.075345	-1.447	-1.26832
EPPK1	1.866131	1.239733	0.07257	-0.58135	-0.45754	-0.80209	-0.74315	-0.5943

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
PDE3A	-0.08887	-0.04991	-0.37153	0.051105	-1.23214	-1.16643	1.460742	1.397028
HLA-DRB3	-0.81756	1.038228	-0.75211	1.181796	-0.91837	1.208137	-1.02697	0.086854
LOC112267939	0.747648	1.177519	-1.12907	-1.10778	-1.22513	0.875364	0.120328	0.541118
STAB1	0.647993	0.407916	-0.81669	-0.61436	0.713361	1.680969	-0.99352	-1.02567
TIMP3	-0.61908	-0.24541	-0.85895	-0.4052	-0.92116	0.001686	1.750773	1.29735
AKAP12	-0.45218	-0.47136	-0.53856	-0.147	-0.8503	0.087444	0.055844	2.316109
NPIPA3	-1.19253	0.191683	-0.9758	0.667737	0.467227	1.774826	-0.69978	-0.23337
ST6GAL2	0.385738	0.24194	-0.04943	-0.42458	-1.12368	-1.46516	1.257004	1.178155
HNRNPLL	0.433216	-0.04233	0.448732	0.131582	-1.263	-1.66956	1.058893	0.902467
MEG3	1.349487	1.408629	0.143697	0.360292	-0.94337	-0.80152	-0.55393	-0.96329
HOXA10-HOXA9	-0.91612	-0.42736	1.434086	-0.94234	1.267308	-0.94722	0.064671	0.466983
TSPOAP1	-0.92118	-0.25304	-0.30844	-0.09884	1.185515	1.787159	-0.88171	-0.50946
LOC100130264	-0.68702	-0.60505	-0.46322	-0.13754	-0.49491	-0.6794	1.744901	1.322236
TCEAL2	1.887009	0.869674	0.124708	-0.20698	-0.83962	-0.98206	-0.14905	-0.70368
ID3	1.413329	0.815491	0.893528	0.133242	-0.53996	-1.2611	-0.45973	-0.9948
FYB1	-1.15191	-0.86401	-1.00576	-0.5049	0.728222	0.807556	1.154734	0.836073
NEGR1	0.347185	0.35994	0.05595	0.110531	1.106632	0.8899	-1.71246	-1.15768
MICALCL	-0.52517	-0.88642	-0.39836	-0.33406	-0.65612	-0.25568	1.519641	1.536182
AVP	1.398494	1.138341	0.549391	-0.07223	-0.13695	-0.82281	-0.81933	-1.23491
SELP	0.823054	0.625494	-0.05679	-0.2616	-1.31314	-1.47166	0.982548	0.672093
CDH2	0.402368	0.614045	-0.1772	0.700737	0.586134	0.789202	-1.67226	-1.24303
LOC112268061	1.029674	-0.34859	0.592291	-0.63797	1.281384	0.369751	-1.02914	-1.25739
FNTB	-1.59468	0.60329	-0.09651	0.200609	-1.2234	0.259216	1.173005	0.678478
GPRIN3	0.278154	0.531476	-0.26915	0.474045	0.877926	0.946123	-1.46564	-1.37294
COBLL1	0.157503	-0.10024	0.088631	0.132454	1.254821	1.108314	-1.28698	-1.3545
PCDH17	1.711322	0.672051	0.479788	-0.46594	-1.06972	-0.99617	0.233439	-0.56477
KIAA0087	-0.44685	0.040402	-0.24202	-0.04379	1.259526	1.514977	-1.1275	-0.95475
NA	-0.50606	-0.51742	-0.50304	-0.52487	1.523475	-0.5279	1.555203	-0.49939
RGS18	0.022899	-0.15922	0.096405	-0.14218	-1.38195	-0.97702	0.983387	1.557687
GRAMD1C	0.665039	0.335771	0.471461	0.324009	0.810498	0.372089	-1.75132	-1.22754
ZBTB16	-0.2721	-0.4842	0.46044	0.212262	-1.1853	-1.1535	1.274786	1.14761
EPAS1	1.387005	1.263302	0.201107	0.272066	-0.45543	-0.84685	-0.81019	-1.01101
LTB	0.095009	0.206057	-0.63469	-0.21055	1.240319	1.31735	-1.45732	-0.55618

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	a	a	b	b	c	c	d	d
Gene								
LEF1	-0.34624	-0.37703	-0.49595	-0.4629	-0.6984	-0.50932	0.916201	1.973629
RNA45SN5	-0.95124	0.904127	-0.01545	-0.61675	-0.05573	-1.20613	0.354777	1.586397
IQSEC3	1.314141	-0.7592	0.854741	-1.03251	0.547514	-0.77427	0.696314	-0.84673
KALRN	-0.46751	-0.25402	-0.79228	-0.44727	-0.39557	-0.6454	1.46191	1.540135
LOC100996709	-0.11352	0.774715	-1.45157	0.779265	-0.10983	1.008753	-1.28931	0.401488
AGTR1	-0.50074	-0.51173	-0.49802	-0.51824	-0.55521	-0.43973	1.373121	1.650542
TMEM72	-0.37977	0.133088	-0.49515	-0.11893	-0.2844	-0.32532	-0.75511	2.225603
THBS1	0.022038	-1.00517	-0.64086	-0.81412	-0.41921	0.093195	1.241866	1.522264
FIGN	-0.78944	1.372705	-0.76276	1.212149	-0.98248	0.13934	-0.62673	0.437216
TNFAIP2	0.291258	0.582202	-0.08382	0.125128	0.853006	1.01973	-1.38459	-1.40291
MYO5C	0.538276	0.364259	0.574284	0.503634	0.560181	0.472503	-1.49038	-1.52275
LOC107985787	1.540374	0.924221	0.241843	-0.07339	-1.11259	-1.19349	-0.07946	-0.24751
LOC105378305	0.543928	0.039541	0.281977	0.677332	0.884152	0.463348	-1.43012	-1.46016
LRP1	1.490136	1.299807	-0.15317	0.137134	-0.89026	-0.70081	-0.77881	-0.40402
FCMR	0.591449	-0.09034	-0.24741	-0.08689	1.378314	0.796038	-1.53118	-0.80999
LOC105374809	1.018116	-0.8433	0.418436	-0.85191	1.031083	-0.85622	0.902102	-0.8183
ZFPM1	0.118863	0.077221	-0.34137	-0.0401	-1.28361	-1.0168	1.174298	1.311499
MYCT1	0.78626	0.528502	0.368411	0.26518	-1.23999	-1.67244	0.539792	0.424289
GIMAP1-GIMAP5	1.195392	0.728211	0.82313	-1.0191	0.395559	-0.09558	-1.05961	-0.96799
FAM83D	-0.59063	-0.51025	-0.81102	-0.19386	-0.4199	-0.37332	1.637323	1.261651
FSBP	-0.2607	0.759779	0.931491	0.820775	-1.37373	-0.07347	0.461096	-1.26524
GATA2	0.24215	-0.39201	0.248592	-0.33094	-0.75987	-1.39841	1.438319	0.952173
LOC107986265	0.966322	-0.58027	0.299032	-1.82085	1.09429	-0.07049	0.029977	0.081988
LOC107987373	-0.79482	0.502942	-0.79128	0.643854	-0.86507	1.296263	-0.86396	0.87208
TTTY10	-0.78205	1.06724	-0.77855	1.139131	-0.85148	0.22748	-0.85037	0.828602
CTNNBL1	-0.49804	-0.87134	-0.0207	-0.18752	-0.58453	-0.64602	1.60546	1.202691
ITGAL	-0.37088	-0.25738	0.184555	0.082067	1.198333	1.332391	-1.00415	-1.16494
SIGLEC17P	-0.72145	-0.31104	-0.16037	-0.0722	1.659992	1.098307	-0.573	-0.92024
PREX2	1.363727	1.219626	0.33524	0.060045	-0.99591	-0.60374	-0.60763	-0.77136
FGD5	1.103393	0.840337	0.87704	0.450192	-0.62903	-0.87389	-0.6002	-1.16785
RTEL1-TNFRSF6B	0.461359	0.685096	1.16472	-0.59328	0.810399	-1.12471	-1.17619	-0.22739
MN1	0.335467	0.282844	0.394402	0.054714	1.073282	0.629183	-1.40763	-1.36226
C10orf105	-0.21408	0.009205	-0.60145	-0.27215	1.375575	1.387218	-0.88346	-0.80086

Supplemental Table 4. Top 200 differential genes in GCSF-mobilized bulk RNAseq samples

Donor	1	2	1	2	1	2	1	2
Population	<i>a</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>c</i>	<i>d</i>	<i>d</i>
Gene								
SEPT5-GP1BB	0.172402	0.365396	-0.0481	-0.1582	-1.33376	-1.16487	0.941865	1.225272
MFSD2B	-0.90678	-0.78637	0.075083	0.072034	-0.78371	-0.31473	1.261499	1.382977

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
MX1	494.9739	-1.00059	0.00011	0.005876
SWAP70	1695.026	-1.00516	0.000263	0.011562
LOC100128108	394.85	-1.00781	1.53E-05	0.001281
NRIP1	10229.62	-1.01157	0.000693	0.024322
RAB29	585.3915	-1.02144	0.001366	0.039716
STX3	463.4232	-1.02365	9.94E-05	0.005453
YES1	326.9988	-1.03125	0.001784	0.047559
ELMO1	4476.965	-1.03125	0.000663	0.023531
LRRC70	1523.709	-1.03374	0.000809	0.027297
IL4R	180.2649	-1.03733	0.000472	0.018068
ZC2HC1A	355.8907	-1.03842	0.001823	0.047849
CD109	1587.164	-1.0417	2.30E-05	0.001836
JUND	24583.97	-1.04277	5.14E-06	0.000557
VIM	24350.85	-1.04514	1.02E-06	0.000144
PNPLA8	632.7647	-1.05394	0.000809	0.027297
LOC102724765	659.8099	-1.05476	0.000153	0.007603
NFAT5	988.4713	-1.05822	1.24E-05	0.00108
PHTF1	2629.221	-1.06274	5.02E-06	0.000548
NFATC2	988.6014	-1.06412	2.86E-05	0.002133
ITPKB	590.1405	-1.06489	0.000168	0.008073
LINC01122	563.7154	-1.09004	3.41E-05	0.002433
TRIM8	853.5996	-1.09707	7.59E-06	0.000744
LOC105378645	489.4958	-1.10043	0.000694	0.024322
NEDD4L	897.8868	-1.10229	0.000217	0.00995
MMP28	374.8082	-1.10399	0.001431	0.041202
GBP5	253.9217	-1.10458	0.001087	0.033761
LOC105375304	523.8434	-1.1046	0.001802	0.047627
NAMPT	1612.35	-1.10539	0.000166	0.008047
GCHFR	1091.951	-1.10858	0.000181	0.008481
CALN1	1219.665	-1.10867	7.52E-07	0.000116
SORBS3	735.406	-1.11083	0.001758	0.047231
GABARAPL1	342.5218	-1.11132	0.000636	0.022842
CHMP1B	7120.283	-1.11134	0.000152	0.007588
C3orf80	921.1874	-1.11415	0.000264	0.0116
HOPX	4900.006	-1.1144	0.001462	0.041589
LINC-PINT	644.1453	-1.11475	0.000194	0.008969
DST	1388.623	-1.11724	1.58E-06	0.000212
BMPR2	296.5071	-1.11791	0.000936	0.030133
GATA2-AS1	314.0654	-1.12577	0.000533	0.019843
HSPA1B	337.4805	-1.12968	0.000362	0.014716
LOC100507507	537.8228	-1.13592	0.000177	0.008348
UBOX5	375.1842	-1.13951	3.68E-05	0.002543
INPP4B	758.1114	-1.1402	0.001269	0.037789
EVA1C	283.4484	-1.14174	0.000748	0.025547
STK17B	4280.73	-1.14304	1.90E-05	0.001557
RNF19B	305.595	-1.15395	0.001791	0.047627
RANBP2	2437.924	-1.15717	1.07E-05	0.00098
HLA-E	12294.85	-1.15833	0.001804	0.047627
CEPB	604.3898	-1.15873	0.001362	0.039716
GSTO2	612.8316	-1.15995	0.001126	0.034731
TNFAIP3	2709.294	-1.16039	1.66E-05	0.001384
YPEL5	10498.52	-1.16157	0.000172	0.00819
NOXA1	181.4893	-1.17536	0.000179	0.008363
PRKCH	1707.82	-1.17933	0.001844	0.048329

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
ARHGEF40	283.8867	-1.18677	5.50E-05	0.003403
HMGAA2	513.254	-1.18805	2.05E-06	0.000265
VPS37B	2237.233	-1.19358	0.001451	0.041452
ANKRD42	233.6819	-1.19399	0.001064	0.0332
FTH1	147380.8	-1.19638	3.87E-07	6.57E-05
TK2	213.6409	-1.2	0.000589	0.021495
MPPED2	236.694	-1.20613	0.001298	0.038335
VWA2	254.6622	-1.20687	0.001448	0.041449
RHOC	767.2825	-1.20768	0.000143	0.00719
LDOC1	615.5366	-1.21206	4.12E-06	0.000484
PRDM16	205.8275	-1.2148	0.001741	0.046894
IDS	3484.561	-1.21505	0.001133	0.034783
TIMP3	810.5746	-1.21723	0.000161	0.007909
TSPYL2	454.4889	-1.21757	3.33E-06	0.000403
SNAPC1	905.6843	-1.2268	8.79E-05	0.004909
LOC105377458	124.7842	-1.22857	0.001857	0.048607
HEMGN	1259.552	-1.23134	6.88E-06	0.000681
FOSL2	3806.124	-1.23237	1.10E-05	0.000992
SNHG14	164.7249	-1.23668	6.18E-05	0.00376
EHD2	745.9003	-1.24887	0.00113	0.034783
NFIL3	1937.509	-1.2516	0.000202	0.009311
KLHL3	205.1869	-1.25654	0.000726	0.0251
FZD1	204.8696	-1.26143	0.000676	0.023838
CAVIN1	1759.025	-1.26476	4.15E-05	0.002767
LOC101929709	379.9723	-1.26889	0.001206	0.036522
LOC107984658	218.7394	-1.27046	0.000437	0.017106
MYH10	926.3862	-1.27172	0.000165	0.008019
PPP1R9A	379.9274	-1.27235	0.001764	0.047248
NKAIN2	466.6337	-1.27338	4.77E-05	0.003065
GCH1	484.7873	-1.28454	0.000648	0.02319
H1F0	6554.085	-1.28929	0.000302	0.012885
ADGRG6	1003.141	-1.30231	2.24E-07	4.06E-05
PXDC1	154.1464	-1.30421	0.000615	0.022369
RIN2	111.4428	-1.30489	0.001399	0.040501
NFIA	1541.033	-1.30615	7.62E-05	0.004388
FBXO44	109.8309	-1.30759	0.00052	0.019435
LOC105369593	983.6716	-1.30809	4.42E-06	0.000509
MIR155HG	289.1947	-1.32019	3.96E-05	0.002669
RRN3P1	81.70608	-1.32093	0.00147	0.041761
CREM	1291.098	-1.32601	5.28E-05	0.003327
LOC107985939	127.5152	-1.32979	0.001475	0.041825
SNX21	127.0076	-1.3306	0.00182	0.047838
FAM133A	186.3463	-1.33188	0.001271	0.037789
BEX5	481.6012	-1.33343	0.000354	0.014563
LOC105371227	389.2573	-1.33936	8.85E-07	0.000132
VEGFA	400.5256	-1.34238	0.000252	0.011165
SNX9	515.0679	-1.34693	7.51E-05	0.004351
CXCL3	1211.923	-1.3567	5.67E-08	1.23E-05
ABCA13	215.3193	-1.36217	0.000944	0.03027
TNFRSF1B	540.4958	-1.36423	5.72E-08	1.23E-05
FERMT1	141.1021	-1.36618	8.48E-05	0.004838
RABGEF1	1110.413	-1.3663	0.000327	0.013565
HIST1H2BK	1553.965	-1.36644	2.99E-05	0.002212
SGIP1	99.91713	-1.37246	0.001497	0.042196

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
PHF1	327.5009	-1.37558	0.00011	0.005872
ST6GAL2	589.8345	-1.38018	0.000163	0.007944
HCG4	147.0901	-1.38125	0.000717	0.02489
NR4A3	2236.945	-1.38234	0.000124	0.006393
SHTN1	232.4562	-1.38615	0.000267	0.011707
ATP2B1-AS1	1077.006	-1.3867	3.51E-09	1.01E-06
LINC02265	121.8383	-1.38957	0.001439	0.041393
ZNF589	190.2328	-1.40478	0.00182	0.047838
LRP10	555.1695	-1.40486	1.42E-05	0.001203
CSRNP1	1948.591	-1.40699	1.43E-05	0.001203
RBPMS	1174.029	-1.41199	3.59E-07	6.20E-05
SCN9A	792.4347	-1.41636	2.00E-05	0.001616
SERPINI1	472.1499	-1.41824	0.000171	0.00819
BIRC3	1303.024	-1.42029	4.11E-11	1.88E-08
STARD9	325.7854	-1.42139	5.77E-06	0.000597
ADAM28	1719.033	-1.42905	0.000396	0.015776
ROBO4	389.2318	-1.42986	0.00022	0.010056
BEST1	154.64	-1.43627	0.000427	0.016756
LOC284454	2061.464	-1.44026	5.28E-09	1.47E-06
MYCT1	972.639	-1.44618	5.53E-06	0.000583
CXCL2	4955.58	-1.44788	4.84E-09	1.36E-06
CXorf40A	695.809	-1.44978	9.99E-06	0.000929
DUBR	163.005	-1.45581	0.001718	0.0467
LOC729291	85.08995	-1.45854	0.001546	0.043099
MXRA7	237.646	-1.46318	0.000745	0.025547
HIST1H1C	3203.13	-1.46322	3.30E-09	9.61E-07
ABCB1	543.9984	-1.46333	0.000361	0.014716
SLC2A3	3750.683	-1.48391	0.000299	0.012814
SLC22A17	158.4224	-1.49368	0.000309	0.013147
ZC3H12A	1196.588	-1.49494	4.68E-06	0.000522
ESAM	381.9372	-1.49951	0.000802	0.02717
DCUN1D3	162.016	-1.50068	0.00026	0.011497
C16orf45	384.4037	-1.51012	0.000104	0.005616
PRKG2	1050.742	-1.5134	3.71E-08	8.18E-06
ITGAM	125.8974	-1.51345	0.000318	0.013333
AREG	22159.91	-1.51493	8.14E-06	0.000785
LOC100506282	96.81404	-1.51911	0.000287	0.012479
GADD45A	2369.762	-1.51987	1.33E-05	0.001139
TNFSF8	277.8283	-1.52146	0.001262	0.037704
PLAG1	201.9516	-1.52443	0.001692	0.046105
CCL4L2	113.6835	-1.52466	0.001275	0.037839
NEIL1	136.1296	-1.52534	0.000601	0.0219
NFIB	514.8109	-1.52702	2.59E-05	0.001991
FREM1	512.0902	-1.53228	0.000213	0.009802
NR4A1	12509.1	-1.53326	4.72E-06	0.000524
ZNF165	165.1319	-1.54053	0.001594	0.04404
TIPARP	762.6504	-1.54629	2.14E-07	3.92E-05
EGFEM1P	735.0891	-1.54686	0.000312	0.013248
TUBA4A	1245.658	-1.54714	0.000644	0.023088
ANK3	156.0673	-1.54847	9.10E-05	0.005067
NBPF20	139.5187	-1.5486	0.000131	0.006678
CPED1	452.5243	-1.55068	0.001189	0.03613
ZNF543	112.2468	-1.55771	0.001914	0.049805
MAFF	4585.117	-1.56011	0.000119	0.006238

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
RHCE	206.3335	-1.56223	0.00108	0.033587
MECOM	788.3901	-1.56426	3.45E-05	0.002443
PTK2	350.579	-1.56815	3.40E-05	0.002433
ADAM8	657.2073	-1.5695	0.000185	0.008593
RAPGEF2	1329.885	-1.57592	2.79E-09	8.37E-07
MANSC1	213.3018	-1.58134	1.76E-06	0.00023
TSC22D1	12922.59	-1.58237	2.72E-05	0.002059
LOC107986148	56.13932	-1.58444	0.000729	0.025132
HIST2H2AA3	7143.567	-1.58444	9.98E-08	2.01E-05
HIST2H2AA4	7143.567	-1.58444	9.98E-08	2.01E-05
CFAP70	66.19763	-1.59034	0.001295	0.038315
CD40	311.2899	-1.59142	0.000289	0.01252
MLLT3	2620.545	-1.59487	3.10E-10	1.21E-07
GATA3	322.6659	-1.5982	0.000555	0.020437
SOCS2	3449.74	-1.60213	1.11E-05	0.000996
PTPRM	142.5247	-1.60245	0.00089	0.029169
FKBP9	273.129	-1.61014	2.10E-06	0.000269
HIST1H2BD	173.8863	-1.61972	6.30E-05	0.003793
DOK2	154.1238	-1.62293	0.000293	0.012606
EPHX2	627.2246	-1.62433	0.000365	0.014808
FGD4	157.1963	-1.62784	5.06E-05	0.003232
ALDH1A1	3706.4	-1.63445	1.91E-07	3.60E-05
MIPOL1	274.4249	-1.65211	0.000278	0.012123
HIST2H2BE	2447.134	-1.65865	1.21E-06	0.000171
HABP4	103.4618	-1.65956	0.001188	0.03613
LOC101927745	1607.696	-1.66772	1.38E-06	0.000188
ZNF467	170.3667	-1.67342	0.00039	0.015572
STAT4	531.802	-1.6926	4.58E-07	7.56E-05
UPP1	167.7785	-1.69562	0.000349	0.014408
LOC107986589	240.1177	-1.70061	6.62E-06	0.000667
CD83	2436.032	-1.70395	1.25E-06	0.000175
HIST1H2AC	483.0348	-1.70808	0.000681	0.023935
ZNF204P	111.9789	-1.71669	0.000127	0.006498
EGR3	547.4314	-1.73013	3.30E-05	0.002397
GRASP	1936.824	-1.74119	5.42E-10	1.91E-07
LOC440895	203.5476	-1.74289	0.001194	0.036205
GFOD1	352.3678	-1.74405	9.67E-07	0.000141
DDN-AS1	98.83744	-1.7557	4.92E-05	0.003154
FOXO1	1665.05	-1.75712	2.22E-10	9.02E-08
KLF2	2734.372	-1.78378	1.33E-07	2.66E-05
PCDH9	5367.67	-1.78867	1.31E-10	5.44E-08
PTGS1	2694.26	-1.79722	4.81E-06	0.000527
SYTL4	457.0231	-1.80032	1.79E-07	3.46E-05
MAGI2	143.674	-1.80598	6.87E-06	0.000681
CCDC42	599.0117	-1.81036	8.43E-13	5.15E-10
OXT	65.59233	-1.81548	0.000632	0.02284
PDZRN4	207.3959	-1.81784	0.001733	0.046815
RASSF9	103.0175	-1.81849	0.001366	0.039716
SETBP1	341.3717	-1.83625	0.000934	0.030133
TMEM92	99.99546	-1.83662	5.58E-05	0.003441
CEACAM1	66.45265	-1.84261	0.000925	0.029973
ACE	117.8297	-1.84575	0.000101	0.005484
GPAT3	434.3041	-1.84632	2.97E-08	6.87E-06
CLU	5177.858	-1.85443	0.000316	0.013323

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
PTGER4	1821.675	-1.8581	1.38E-06	0.000188
GASAL1	179.3755	-1.86324	6.43E-05	0.003835
ZNF331	1961.39	-1.86736	7.44E-08	1.55E-05
SERTAD1	644.691	-1.86936	5.68E-06	0.000591
HOXB7	37.40394	-1.87796	0.001793	0.047627
PGM5	270.6725	-1.87934	9.97E-07	0.000144
MLF1	467.2907	-1.88005	0.000247	0.010967
CXCL8	3895.985	-1.8929	1.04E-05	0.00096
IL15	75.88096	-1.89851	0.001211	0.036555
ANXA3	177.5677	-1.90313	0.000131	0.006678
CDC14B	146.0723	-1.90406	5.88E-05	0.003591
HIST1H2BG	81.47813	-1.90407	0.000789	0.026799
CRHBP	7058.931	-1.91836	2.02E-06	0.000262
THR8	265.6067	-1.92016	1.71E-06	0.000228
LIMCH1	583.8056	-1.94048	8.60E-12	4.77E-09
LOC101927879	1159.694	-1.94271	5.88E-06	0.000605
PREX2	722.9604	-1.94731	0.000164	0.007987
LOC101928489	136.304	-1.95643	9.37E-07	0.000138
LOC100507103	154.9398	-1.95711	2.46E-05	0.001927
MAP1LC3A	79.73896	-1.96423	2.77E-05	0.002091
CATIP	53.09469	-1.96843	0.000932	0.030109
MIR22HG	355.6716	-1.97097	1.32E-06	0.000181
LILRB2	92.96849	-1.97224	0.000677	0.023838
CLEC14A	157.5006	-1.97225	0.00169	0.046105
SH3BP5	157.6521	-1.97305	6.22E-05	0.003761
NCF1	85.16844	-1.97576	0.000345	0.014252
MIAT	105.86	-1.982	3.34E-05	0.002415
KLF5	360.3383	-1.98775	0.000126	0.006479
RRAS	393.0431	-1.99973	4.08E-10	1.56E-07
ETV3	2362.906	-2.01253	2.41E-05	0.001907
ELL2	512.3782	-2.01731	4.05E-11	1.88E-08
NPM2	137.9675	-2.02893	1.08E-05	0.000988
EFNB2	104.6937	-2.02959	0.000491	0.018632
PTGS2	1736.408	-2.03723	1.42E-08	3.52E-06
UST	113.107	-2.04832	8.57E-06	0.000822
HIST1H2BC	317.665	-2.0495	3.97E-06	0.000469
PLEC	275.6216	-2.05183	5.60E-07	8.99E-05
LOC105369378	74.75662	-2.05337	1.15E-05	0.001021
SRPX2	87.81358	-2.05617	0.000229	0.010376
NR4A2	10887.87	-2.07743	1.62E-13	1.19E-10
HIST1H2AE	235.653	-2.08518	2.41E-11	1.23E-08
ID2-AS1	68.88717	-2.10008	0.000325	0.013539
FUT6	59.21774	-2.10406	0.000124	0.006393
NDRG2	357.4437	-2.1116	2.44E-05	0.001921
DNM3	503.1717	-2.11164	0.000355	0.014566
LOC105376637	137.8765	-2.11626	0.000538	0.019937
MFAP2	587.9104	-2.11733	1.11E-09	3.56E-07
LOC105374381	41.44771	-2.15098	0.000534	0.019854
PDZK1IP1	121.4362	-2.15742	3.39E-06	0.000408
LOC101928202	181.097	-2.1625	5.25E-06	0.000562
CCL3L1	129.4678	-2.1696	1.24E-05	0.001079
HSD17B14	112.0564	-2.17942	0.000268	0.011715
MFAP3L	42.67948	-2.18798	0.000798	0.027078
BHLHE41	106.5576	-2.21272	2.86E-05	0.002133

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
TNNC2	61.62121	-2.21818	0.000158	0.007781
SLC1A6	493.3005	-2.23254	9.52E-05	0.005253
NLRP12	37.07093	-2.23466	0.000811	0.027297
FAM241B	80.30219	-2.24315	4.53E-06	0.000512
LOC399900	130.7603	-2.25862	0.000165	0.008019
AVP	3349.397	-2.2913	3.02E-13	1.98E-10
CNMD	100.0894	-2.29575	4.00E-05	0.002683
LMNA	5448.089	-2.326	6.15E-06	0.000626
SUCLG2	371.5444	-2.33196	7.90E-07	0.00012
LOC107986939	799.3344	-2.33681	5.29E-11	2.36E-08
CCL4L1	173.7886	-2.34322	4.27E-05	0.002811
LINC00891	73.00568	-2.35206	1.23E-05	0.001079
LOC100132741	73.00568	-2.35206	1.23E-05	0.001079
AFDN	393.4498	-2.35801	7.12E-09	1.92E-06
JAML	1729.374	-2.37699	1.78E-07	3.46E-05
EMCN	676.6464	-2.37941	4.33E-14	3.96E-11
PHLDB2	666.9446	-2.37967	5.04E-14	4.39E-11
BRE-AS1	773.3593	-2.39457	2.72E-17	7.12E-14
LOC107984362	42.65862	-2.42234	0.001134	0.034783
LZTS3	213.9512	-2.43252	7.30E-05	0.004247
NR3C2	46.28584	-2.45673	0.000175	0.008289
EPPK1	105.7249	-2.46024	0.000237	0.010661
DEPP1	97.244	-2.46399	0.000173	0.008231
LINC02160	67.4482	-2.46713	4.60E-05	0.00301
STARD13	47.61821	-2.46981	0.000389	0.015572
DMKN	83.81865	-2.47152	1.07E-05	0.000981
MPZL2	207.2009	-2.47439	1.22E-08	3.14E-06
CD4	510.5293	-2.49066	8.01E-09	2.13E-06
NOS1AP	28.21995	-2.50699	0.001066	0.033221
MYL9	93.53567	-2.50727	1.27E-08	3.18E-06
PHLDA2	48.88345	-2.52375	8.64E-05	0.004869
SNED1	128.4598	-2.53757	0.001551	0.043099
HLF	1171.426	-2.54031	3.21E-11	1.55E-08
SETDB2-PHF11	147.5157	-2.54049	0.001902	0.049628
ANKRD20A2	47.32234	-2.60145	0.00191	0.049769
FGF9	66.56326	-2.64487	0.000159	0.007793
HIST2H3PS2	58.99151	-2.66489	7.07E-06	0.000696
SPP1	920.3645	-2.67028	4.53E-07	7.56E-05
FAM198B	168.1024	-2.67526	1.10E-05	0.000992
CDH7	296.8143	-2.68024	7.58E-11	3.23E-08
WWTR1	43.59968	-2.68525	0.000458	0.017763
PCDH8	29.63688	-2.7062	0.001503	0.042217
LOC105378604	90.12459	-2.72061	7.27E-05	0.00424
BMP6	75.40507	-2.73818	2.50E-05	0.001952
DIRAS3	80.74026	-2.78779	0.001446	0.041448
DLK1	383.0275	-2.79465	2.61E-16	5.96E-13
MCF2L	30.34498	-2.79646	0.000405	0.016025
THR-B-AS1	25.54178	-2.80434	0.000471	0.018068
MDGA2	74.50015	-2.82636	7.58E-05	0.004381
PCDH17	90.6553	-2.89544	4.75E-06	0.000524
LOC105374314	49.22219	-2.908	3.11E-06	0.000382
TCEAL2	304.8223	-2.90852	1.85E-13	1.30E-10
ADAMTS1	132.9171	-2.91052	1.76E-06	0.00023
MEG3	553.3765	-2.92508	4.18E-10	1.56E-07

Supplemental Table 5. Genes upregulated in ssBM cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
LOC105374296	54.13247	-2.92808	4.73E-05	0.003049
MTMR11	41.67739	-2.94433	0.000707	0.024707
LRP1	50.43354	-2.95119	0.000133	0.00673
FXYD6	383.6558	-2.96475	2.17E-08	5.16E-06
FILIP1L	42.97703	-3.01296	2.79E-05	0.002091
RTL5	62.38507	-3.01465	6.79E-06	0.000679
CXCL1	30.72107	-3.03408	0.000318	0.013333
ABI3BP	173.5027	-3.05433	1.14E-11	5.99E-09
HES1	188.8038	-3.06801	4.20E-06	0.00049
HAR1B	20.57462	-3.07089	0.00159	0.043995
RASSF6	243.2049	-3.14791	6.16E-11	2.69E-08
SELENOM	273.0694	-3.18995	8.29E-09	2.17E-06
LOC101929538	43.79003	-3.23696	0.000113	0.005977
COL6A2	74.10501	-3.31354	2.63E-05	0.002006
FAM198B-AS1	45.56566	-3.32526	3.21E-05	0.002351
ARHGAP20	29.16205	-3.35183	0.001762	0.047248
HAS2	50.99963	-3.40934	8.04E-06	0.000779
CCDC184	91.52447	-3.42179	2.56E-08	6.01E-06
ADCY4	27.34296	-3.44098	4.25E-05	0.002811
LOC107987347	26.46104	-3.45997	3.90E-05	0.002656
CLEC3B	598.3781	-3.47507	3.29E-16	6.02E-13
SCG5	45.83243	-3.48202	3.15E-06	0.000385
LOC105374657	26.98195	-3.62815	0.001005	0.031675
KCTD7	27.93318	-3.63992	0.000482	0.018345
RHOD	24.17149	-3.71534	0.000327	0.013565
LDHD	45.32148	-3.74473	0.000375	0.015127
LIF	29.88115	-3.75009	0.00165	0.045527
LRRC4C	30.7751	-3.83589	0.000117	0.006152
CUEDC1	23.06678	-3.95	3.79E-05	0.002603
MEIS1-AS3	36.58593	-3.96697	4.67E-05	0.003034
AMOTL2	31.705	-4.10494	8.39E-05	0.004802
DOK5	18.54238	-4.12628	0.001314	0.038691
SOGA3	28.14087	-4.18379	0.000735	0.025272
TCEA3	19.68283	-4.19593	0.00046	0.017822
TNS2	14.85093	-4.32697	0.000951	0.030406
SPAG17	21.09394	-4.39854	0.001333	0.039135
AKAP3	13.90518	-4.58011	0.0014	0.040501
DBNDD1	24.39196	-4.62588	0.000971	0.030826
KCNJ8	24.83811	-4.8033	3.43E-05	0.002433
LOC105379499	83.02463	-5.28672	2.15E-06	0.000274
CCL2	19.35472	-5.34504	0.000711	0.024749
LOC107987433	12.75724	-5.81218	0.00136	0.039716
SLCO1C1	18.0267	-6.68772	0.000222	0.010056
LOC105371406	14.60163	-7.10165	0.000103	0.005558
CFB	12.54505	-7.93245	0.000244	0.010857
WIF1	19.67862	-8.14895	3.63E-05	0.002543
NUDT4P2	28.82727	-8.28338	5.92E-07	9.27E-05
C15orf38-AP3S2	133.3133	-10.2109	3.64E-05	0.002543
PLGLB1	36.95608	-24.4727	1.24E-08	3.15E-06

Supplemental Table 6. Genes upregulated in ssBM cells from Population *b*

Gene	baseMean	log2FoldChange	pvalue	padj
MS4A3	607.2288	11.64698	2.72E-14	2.62E-11
ELANE	3338.447	11.01888	8.09E-14	6.44E-11
PRTN3	1793.53	10.71206	5.29E-14	4.41E-11
AZU1	1340.101	10.49691	2.46E-07	4.42E-05
KCNE5	468.52	10.14964	7.57E-12	4.33E-09
PLPPR3	75.26939	9.549211	2.27E-05	0.001818
RNASE3	381.9253	9.273937	3.48E-06	0.000414
CLEC12A	239.7496	8.876084	1.62E-15	2.28E-12
MPO	24481.47	8.572393	1.11E-15	1.69E-12
IRF8	1581.016	8.542745	1.09E-14	1.25E-11
CLEC5A	14.92012	8.204835	8.70E-05	0.004886
ECRP	207.42	7.998945	5.13E-07	8.39E-05
TERT	19.56845	7.747428	6.41E-05	0.003835
RNASE2	2188.5	7.606182	1.68E-31	1.54E-27
KCNH2	930.6124	7.58153	6.20E-05	0.00376
LPO	22.13128	7.430327	9.30E-05	0.005144
TRIB2	382.4477	6.992845	5.57E-06	0.000583
CEBPE	12.07256	6.960807	0.000499	0.018882
NAPSB	237.2018	6.920238	5.39E-06	0.000571
LEF1	96.25195	6.693554	5.34E-05	0.003351
FBLN2	81.45378	6.540263	7.22E-05	0.004226
JCHAIN	660.8638	6.476391	0.000465	0.017942
FAM178B	334.0733	6.45272	2.52E-05	0.001955
UGT3A2	212.0576	6.373831	1.97E-05	0.001595
LOC284600	18.40594	6.312331	0.000119	0.006228
MIICALCL	16.6594	6.247752	0.001569	0.043473
CPA3	2192.082	6.070702	1.28E-38	2.35E-34
LOC105379461	119.7916	5.799834	0.000422	0.016645
RHAG	171.4568	5.772701	0.00029	0.01252
HCK	41.62468	5.492035	2.83E-07	5.03E-05
RNASE1	91.01385	5.383341	0.000519	0.019435
AFF2	25.52514	5.361965	6.87E-05	0.004072
CEBDP	270.2662	5.284004	1.92E-14	1.96E-11
IGSF6	51.60483	5.232535	0.000939	0.030179
LINC01835	37.86629	5.030152	0.001726	0.046779
LOC554249	33.45514	4.979561	9.98E-05	0.005457
TPSAB1	1127.254	4.956247	7.41E-18	2.26E-14
CPB1	34.83877	4.744842	0.001804	0.047627
SUCNR1	163.0882	4.389531	1.41E-09	4.46E-07
TARP	218.4038	4.370905	4.50E-21	1.65E-17
CTSG	1023.798	4.291867	1.73E-14	1.87E-11
IGFBP2	1092.244	4.280073	6.41E-24	2.94E-20
DNTT	6867.661	4.242558	3.41E-05	0.002433
ANK1	325.0213	4.129885	5.18E-10	1.86E-07
TREM1	98.91869	4.124762	2.03E-07	3.76E-05
LINC01971	32.86015	4.085641	7.22E-05	0.004226
HBD	4271.737	4.072499	5.42E-15	6.62E-12
NETO2	23.47577	3.991747	0.000732	0.025193
IGLL1	11801.95	3.981441	1.95E-28	1.19E-24
PROK2	18.63179	3.891693	0.000656	0.023324
FCGR1A	49.23802	3.873212	0.000849	0.028223
HGF	157.2729	3.867161	6.49E-06	0.000657
MIR181A1HG	258.7451	3.854662	1.05E-15	1.69E-12
RAB44	71.83456	3.825197	1.05E-09	3.44E-07

Supplemental Table 6. Genes upregulated in ssBM cells from Population *b*

Gene	baseMean	log2FoldChange	pvalue	padj
SPON2	54.8989	3.644636	0.000222	0.010056
TRPC6	35.4843	3.513891	0.00087	0.028654
KCNG2	189.2824	3.482407	9.51E-07	0.000139
LOC105379749	23.81137	3.427595	0.00058	0.021245
ACPP	15.90212	3.423181	0.001778	0.047472
CST7	731.4084	3.422599	1.33E-12	7.89E-10
PDE1A	36.73978	3.410226	0.000101	0.005484
LGALS1	1583.29	3.368345	4.68E-15	6.12E-12
HPGDS	636.485	3.318455	5.17E-13	3.26E-10
CD40LG	162.5394	3.312942	0.000652	0.023289
DHRS3	187.7447	3.308511	1.49E-08	3.65E-06
TSPOAP1	207.4253	3.271188	1.12E-11	5.99E-09
MARS2	52.86662	3.251556	1.30E-06	0.00018
CSF1R	180.661	3.232254	5.40E-05	0.003372
RFX8	26.00452	3.216624	0.000474	0.018103
CNRIP1	1305.972	3.213938	5.92E-07	9.27E-05
CFD	1202.782	3.145938	2.17E-13	1.47E-10
CD96	142.9638	3.135199	3.32E-08	7.42E-06
LOC339862	100.929	3.09102	3.23E-05	0.002358
VPREB1	534.7383	2.994454	2.91E-10	1.16E-07
FUT7	209.1783	2.991896	3.28E-08	7.42E-06
HOMER3	47.72576	2.991725	8.58E-05	0.004869
NKG7	395.9929	2.938181	6.53E-10	2.26E-07
CSF1	1494.019	2.930322	1.88E-07	3.58E-05
CD1D	20.58097	2.921299	0.000847	0.028195
KLF1	1091.762	2.884433	4.50E-06	0.000512
ACSM1	270.7297	2.881232	1.96E-05	0.001593
STXBP6	162.5321	2.740636	2.38E-06	0.000299
LOC101927497	930.7049	2.709917	1.03E-09	3.43E-07
S100B	42.74109	2.696185	0.000424	0.016686
TESC	654.2503	2.616938	2.93E-16	5.96E-13
TUBB6	355.8487	2.593785	3.40E-07	5.93E-05
CEBPA	471.8078	2.559527	9.12E-14	6.96E-11
STAR	95.7509	2.552679	1.79E-05	0.001477
LOC100130872	115.8596	2.493392	1.54E-06	0.000208
IL1RAP	97.00157	2.4871	3.31E-09	9.61E-07
C16orf74	192.4399	2.482242	3.84E-05	0.002624
GPT2	245.5668	2.468931	4.53E-10	1.66E-07
VSTM1	103.3851	2.447183	8.92E-06	0.000848
ZNF442	30.68266	2.421433	0.00051	0.019206
AKAP2	280.447	2.40638	4.55E-07	7.56E-05
PAG1	215.9837	2.387848	3.66E-07	6.26E-05
MYC	1854.732	2.380399	3.13E-11	1.55E-08
LTBP1	390.4288	2.376862	2.79E-06	0.000347
ASCL2	48.80689	2.376829	0.000121	0.006287
DRICH1	43.11086	2.339524	0.00024	0.010711
RAB7B	79.12822	2.271861	4.52E-06	0.000512
SIRPB2	107.3983	2.259526	0.000869	0.028654
CRYM	193.6112	2.243122	0.000152	0.007588
MRC2	45.62938	2.238982	0.00146	0.041589
P2RX5	221.2233	2.234379	0.001555	0.043159
NPW	434.6643	2.217578	5.51E-07	8.94E-05
LRRC26	140.6155	2.160469	6.36E-05	0.003819
LOC105372233	73.30996	2.151351	9.36E-06	0.000876

Supplemental Table 6. Genes upregulated in ssBM cells from Population *b*

Gene	baseMean	log2FoldChange	pvalue	padj
UCA1	260.3523	2.145708	0.000385	0.01549
SLCO5A1	102.3807	2.139775	5.82E-05	0.003564
KBTBD11	265.486	2.122802	1.26E-05	0.001088
ZNF695	85.25526	2.105754	0.000107	0.005722
MINDY4	82.25269	2.063057	0.000461	0.017823
TRH	194.6018	2.060779	7.69E-08	1.58E-05
BEND6	81.85684	2.039589	5.21E-06	0.000561
LMNB1	526.2213	2.022465	2.60E-05	0.001992
SERPINB8	651.7298	1.943168	0.001311	0.038673
TRPM2	73.18995	1.933043	0.0004	0.015857
ANXA2	1723.198	1.898142	6.56E-07	0.000102
RHEX	759.3652	1.897984	0.000257	0.011365
PDSS1	238.9514	1.892147	1.45E-05	0.00122
PDK1	283.3398	1.887257	9.64E-05	0.005304
MZB1	1896.12	1.885126	6.85E-10	2.33E-07
IL17RA	520.6521	1.879891	1.92E-08	4.62E-06
SPNS3	2472.1	1.85919	2.28E-09	6.96E-07
CDCA7	1924.989	1.859051	1.36E-05	0.001159
LOC101928834	1097.315	1.853409	1.37E-07	2.70E-05
RTN4R	103.8926	1.851772	0.00055	0.020297
LOC107984120	84.38488	1.818159	0.001693	0.046105
SLC45A3	151.8236	1.815311	5.12E-05	0.003257
TTK	172.8823	1.805955	0.000159	0.007793
FAM107B	371.3967	1.804149	3.94E-05	0.002668
TTC7A	602.9927	1.790046	2.38E-06	0.000299
MT1X	198.1518	1.752106	1.17E-05	0.001033
LOC105370401	178.5539	1.728139	4.33E-05	0.002842
FAM129A	403.8657	1.725051	2.02E-07	3.76E-05
LDLRAD3	131.2002	1.721564	0.000747	0.025547
SPARC	3306.608	1.71001	0.001679	0.046105
P2RY2	140.5264	1.695108	0.000838	0.028069
SDK2	312.6588	1.688676	0.000926	0.029973
LOC105372857	77.66211	1.677036	8.62E-05	0.004869
SLC16A10	159.2667	1.654852	0.000174	0.008272
C1QTNF4	2381.782	1.632465	1.33E-05	0.001139
ARHGAP10	120.3269	1.628189	0.000471	0.018068
MYCN	239.5675	1.627962	0.000183	0.008542
PRAM1	765.5684	1.627	0.000237	0.010661
CD38	1386.06	1.625371	6.75E-09	1.85E-06
PLIN2	2695.201	1.610381	2.54E-05	0.00196
ABHD17C	267.8162	1.572601	4.62E-06	0.00052
FYB1	367.0019	1.570121	0.000316	0.013323
TST	495.7916	1.56798	3.11E-05	0.002285
MT2A	729.4244	1.553333	0.000828	0.027843
IGFBP7	5311.886	1.552907	5.93E-08	1.26E-05
CDC7	244.6241	1.542489	0.000842	0.028091
ANLN	153.2057	1.541104	5.15E-05	0.003266
PPIF	1495.653	1.523318	0.000386	0.015512
FABP5	4235.355	1.522576	3.22E-07	5.67E-05
NT5DC2	771.2156	1.515173	0.000221	0.010056
CITED4	344.7245	1.503432	1.93E-05	0.001581
ADGRG5	134.485	1.495678	0.000899	0.029319
ZNF385C	101.6618	1.489025	0.000297	0.01273
TNFSF13B	10619.57	1.458911	5.68E-05	0.00349

Supplemental Table 6. Genes upregulated in ssBM cells from Population *b*

Gene	baseMean	log2FoldChange	pvalue	padj
EEF1AKMT4	397.9827	1.441077	0.000989	0.031287
LOC105373444	1779.056	1.433777	1.01E-06	0.000144
FARSA	2129.909	1.429512	0.001255	0.037597
TSPOAP1-AS1	194.0967	1.426105	7.99E-06	0.000778
CD48	233.0326	1.423637	5.19E-05	0.003281
ZNF724	147.7298	1.419989	0.001526	0.042611
EFCAB2	480.3331	1.413263	6.08E-08	1.28E-05
GRPEL1	700.9984	1.404142	8.55E-07	0.000128
DUSP10	1095.337	1.40237	5.80E-07	9.24E-05
BAHCC1	187.5737	1.39776	0.000112	0.005962
POLE2	589.5123	1.389554	0.000114	0.00602
ZAP70	131.5138	1.381731	0.00012	0.006268
GGA2	734.5146	1.375794	0.000669	0.023656
NUP210	1449.691	1.363709	7.82E-07	0.000119
ARMH1	1408.331	1.358346	2.12E-09	6.60E-07
UHRF1	1275.159	1.357351	0.000168	0.008073
SKA3	640.9667	1.356826	0.000624	0.022635
LRR1	505.6524	1.350397	3.62E-05	0.002543
LOC107984868	126.6638	1.32373	0.001055	0.032969
MGST1	4696.518	1.31443	9.33E-06	0.000876
CHEK1	701.3012	1.31129	0.000112	0.005954
TYROBP	377.1557	1.30777	9.37E-06	0.000876
CRYBG1	207.8736	1.307472	0.001001	0.031617
MAD2L1	2102.308	1.29758	0.000239	0.010686
SMIM24	4900.651	1.295646	3.00E-08	6.87E-06
BLNK	1122.722	1.286992	0.001109	0.034345
MRPS23	1001.604	1.285256	0.000317	0.013333
ST3GAL6	344.7999	1.282841	4.36E-06	0.000506
RAB32	2710.813	1.279598	0.0005	0.018882
ARHGEF18	256.7524	1.275331	8.27E-05	0.004749
NUP85	612.6285	1.270616	0.001883	0.049208
DNAAF3	359.7196	1.265551	0.001803	0.047627
MRPS12	1457.201	1.263786	4.25E-05	0.002811
SLC35F2	463.763	1.261346	0.000398	0.015797
ABHD3	344.5468	1.259439	0.00076	0.025925
MCM4	2529.492	1.221955	8.79E-05	0.004909
HCST	1348.958	1.218707	0.000835	0.028025
PLAC8	5580.424	1.200975	0.000139	0.007005
LYZ	2881.135	1.190353	0.000863	0.028592
C8orf76	211.4913	1.188032	0.000286	0.012447
GMNN	1011.428	1.186997	0.000104	0.005609
NRG4	533.0171	1.182366	0.001689	0.046105
MRPL58	604.0773	1.181921	0.000589	0.021495
METRNL	391.5022	1.176907	2.67E-05	0.002027
OIP5	562.5605	1.174102	0.000367	0.014845
ANKLE1	252.0194	1.172693	0.000472	0.018068
MRPL13	1551.42	1.169444	2.36E-05	0.001874
RFWD3	428.5924	1.158209	0.001119	0.034571
PPAT	270.247	1.156627	0.00045	0.017492
CHCHD1	643.1064	1.153341	2.04E-05	0.001643
GEMIN2	371.9574	1.1523	0.0009	0.029319
TFRC	2773.061	1.14686	0.00049	0.018632
GYPC	5729.818	1.143697	5.38E-06	0.000571
POLE3	3493.003	1.142647	3.45E-06	0.000413

Supplemental Table 6. Genes upregulated in ssBM cells from Population *b*

Gene	baseMean	log2FoldChange	pvalue	padj
DPCD	431.1146	1.134572	0.000636	0.022842
AIMP2	1275.279	1.133522	8.61E-05	0.004869
MRPL36	714.3469	1.132929	2.95E-06	0.000365
CLDN10	1618.661	1.129737	4.06E-05	0.002713
XRCC2	354.914	1.115781	0.001345	0.039418
BCL2	392.3883	1.112685	0.00017	0.008137
NDUFAB1	2740.897	1.110825	7.14E-05	0.004207
CKS2	3014.415	1.107042	0.000427	0.016756
COLGALT1	792.7393	1.100381	3.95E-05	0.002668
CD33	465.3276	1.094388	0.001694	0.046105
CDT1	1060.923	1.093038	4.62E-05	0.003014
POLR3K	982.3258	1.076698	0.000357	0.014633
MEF2A	419.799	1.075965	6.65E-05	0.003953
C15orf61	478.9456	1.066835	0.000321	0.013377
TIPIN	552.2371	1.064203	0.000319	0.013337
CENPW	1080.57	1.060986	0.000529	0.019731
MLEC	2816.976	1.059908	1.14E-05	0.001019
USP3	532.0931	1.059105	0.000969	0.030826
NDUFB3	2106.104	1.056119	0.000153	0.007603
TMIGD2	690.6633	1.047661	0.000361	0.014716
OPN3	1067.18	1.039465	3.36E-05	0.002425
FOXRED2	485.8497	1.034912	0.00087	0.028654
ATOX1	886.7135	1.034758	0.001169	0.035703
FAM45A	1590.409	1.030316	0.000708	0.024707
KPTN	371.3055	1.018284	0.00054	0.019986
MXD1	754.7275	1.008042	0.00044	0.017179

Supplemental Table 7. Genes upregulated in GCSF-mobilized cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
EPPK1	73.89057	-3.0174	1.35E-09	7.15E-07
STAB1	116.8942	-2.33686	8.67E-07	0.000196
PRG2	84.50356	-2.33287	0.000625	0.027761
LOC112268342	64.50085	-2.32152	0.000119	0.008576
TCEAL2	81.40736	-2.28447	3.05E-07	7.62E-05
OTUD7B	53.3713	-2.26405	8.34E-05	0.006731
LRP1	104.4242	-2.19666	4.55E-08	1.52E-05
LOC112268284	77.94825	-2.11867	1.82E-05	0.002148
JAML	238.4582	-2.07656	4.79E-11	4.70E-08
PCDH17	58.78369	-2.07385	0.000116	0.008498
PHLDB1	75.21931	-2.05308	3.05E-06	0.000532
OR2H2	57.11326	-2.04934	0.001264	0.046884
LOC101928202	70.52762	-1.99069	0.000389	0.020088
PDE1C	88.3771	-1.96495	1.69E-06	0.000336
SUCLG2	65.69795	-1.90505	0.000254	0.014479
LOC107985787	77.63033	-1.85902	1.93E-05	0.002177
COL6A1	72.57931	-1.74887	0.000101	0.007614
AVP	76.40189	-1.68317	0.000337	0.017784
BRSK2	92.76892	-1.66682	2.05E-05	0.002264
CD4	65.97593	-1.66038	0.000654	0.02856
PLEKHA6	71.01237	-1.65409	0.000335	0.017735
NRBP2	136.8077	-1.5805	4.43E-06	0.000706
EZR-AS1	70.3506	-1.57537	0.001079	0.042485
MEG3	295.2694	-1.57422	1.79E-08	7.01E-06
RNF103-CHMP3	95.74023	-1.5557	0.000381	0.01975
PREX2	394.2795	-1.52343	3.71E-09	1.70E-06
LZTS3	181.5105	-1.50854	2.26E-06	0.000419
MIR29B2CHG	127.4679	-1.49839	3.55E-05	0.003426
COL6A2	92.8827	-1.47465	0.000489	0.023863
HLF	1162.746	-1.47031	7.64E-16	2.62E-12
KLF2	963.0647	-1.43323	2.78E-13	4.76E-10
SELP	123.7321	-1.43018	6.26E-05	0.005345
ABI3BP	102.6122	-1.39117	0.000197	0.012277
RASSF6	169.2947	-1.37693	0.000171	0.01109
LOC148696	360.1981	-1.33721	2.57E-08	9.28E-06
SNED1	244.4504	-1.29861	2.19E-06	0.000418
ACOT11	100.7004	-1.27487	0.001408	0.049955
AGAP3	294.9761	-1.25232	2.83E-07	7.20E-05
LOC105369748	134.0892	-1.22186	0.000228	0.013294
DOCK3	159.4469	-1.21699	0.000157	0.01041
LOC105378604	143.1471	-1.2162	0.000315	0.016918
MIAT	952.9127	-1.21189	4.95E-08	1.62E-05
IL4R	178.1058	-1.2041	5.12E-05	0.004561
RTL5	180.4075	-1.18581	5.28E-05	0.004675
AFDN	451.9378	-1.1683	7.26E-08	2.21E-05
RAPGEF3	151.9928	-1.16556	0.000193	0.012173
ITGA2B	382.0294	-1.14449	0.000574	0.026328
SIK1	531.9297	-1.1304	0.000159	0.010472
PRDM16	245.5592	-1.11417	1.31E-05	0.001631
ABCA13	254.6232	-1.10487	0.001361	0.049488
PTK2	218.982	-1.09202	6.94E-05	0.005879
LOC107984427	288.7695	-1.08005	0.000763	0.032616
PRR5	177.5193	-1.07903	0.001344	0.049174
ARHGEF40	388.5902	-1.0238	0.000121	0.008662

Supplemental Table 7. Genes upregulated in GCSF-mobilized cells from Population a

Gene	baseMean	log2FoldChange	pvalue	padj
PNP	389.2648	-1.0173	7.03E-06	0.001005
PEAR1	380.487	-1.01194	2.16E-05	0.002334
ULK1	371.2976	-1.0108	2.46E-05	0.002599
HIST2H3PS2	285.7964	-1.00565	7.56E-05	0.00621

Supplemental Table 8. Genes upregulated in GCSF-mobilized cells from Population *b*

Gene	baseMean	log2FoldChange	p-value	padj
LMNB1	554.0249	1.003174	1.67E-06	0.000336
CDK6	24456.56	1.004854	2.06E-18	1.41E-14
SPARC	946.2339	1.013527	2.77E-08	9.73E-06
RNF130	1738.676	1.015676	2.31E-07	6.23E-05
RPSAP58	232.565	1.020366	0.00064	0.028137
MAMDC2	886.728	1.030157	6.00E-10	3.43E-07
ZBTB16	1324.212	1.036293	1.41E-10	1.08E-07
SNHG19	281.3569	1.038539	2.66E-05	0.002747
TFRC	4387.958	1.040528	2.54E-09	1.29E-06
PTPN14	282.7238	1.04524	8.17E-05	0.006634
HPGD	317.6832	1.047418	5.24E-06	0.000808
EXOSC1	195.0903	1.050955	0.000351	0.018332
SELPLG	177.9986	1.057197	0.001286	0.047264
PLEK	2010.876	1.070104	1.85E-10	1.34E-07
PIK3R3	254.6517	1.077499	3.94E-05	0.003649
PCNA	339.6969	1.080337	0.000148	0.010011
KBTBD11	371.4965	1.100214	6.47E-06	0.000953
FAM129A	519.471	1.11022	1.59E-07	4.55E-05
DNAJC6	315.4325	1.117944	3.70E-05	0.003478
LOC107985855	261.9556	1.139032	3.09E-05	0.003028
BLM	210.8141	1.140574	0.000316	0.016918
ZNF675	156.9312	1.143483	0.000304	0.016507
CEBPA	253.0219	1.150087	4.91E-05	0.004496
TIMELESS	381.1154	1.156667	5.02E-05	0.004536
DTL	335.2747	1.157131	0.00011	0.008232
PRIM1	178.6158	1.160009	0.000317	0.016942
CD38	961.0658	1.180657	4.81E-12	5.08E-09
LOC105372857	161.7886	1.186601	0.000922	0.037669
FAM107B	137.4953	1.22731	0.001385	0.049716
ZCCHC18	140.9743	1.237721	0.000425	0.021599
LOC101928834	145.1367	1.239707	0.000828	0.034762
CDC6	150.9873	1.250052	0.001084	0.042485
KCNQ5	412.8885	1.255548	6.77E-08	2.11E-05
RAB44	198.3617	1.257678	0.000219	0.013048
POLQ	184.4625	1.291719	0.000287	0.015882
IGFBP7	436.4087	1.298038	4.92E-09	2.18E-06
ASPM	142.9632	1.299962	0.000446	0.022443
LOC107984120	333.8278	1.312838	2.42E-08	8.99E-06
LOC105370401	498.3724	1.31335	8.77E-11	7.08E-08
HGF	170.0861	1.313625	2.77E-05	0.002815
CD69	2211.931	1.336401	7.89E-15	1.80E-11
CENPU	148.0365	1.35876	0.000191	0.012115
PLD1	156.9739	1.400327	0.00019	0.012111
NCAPG	93.9426	1.431009	0.001264	0.046884
CDCA7	1006.75	1.47136	1.89E-12	2.16E-09
KCNE3	147.3216	1.487753	5.51E-05	0.004847
KCNK5	192.0261	1.488315	1.23E-05	0.001558
LOC105373444	934.6957	1.506691	5.12E-14	1.00E-10
RHEX	176.6823	1.513286	0.000119	0.008576
SLC27A2	241.4406	1.539782	2.84E-08	9.73E-06
SGK1	313.493	1.650604	7.32E-11	6.27E-08
MRC2	87.3865	1.652304	0.001032	0.04135
PLAU	118.7647	1.68301	4.65E-06	0.000724
NTNG2	60.6708	1.699732	0.000701	0.03046

Supplemental Table 8. Genes upregulated in GCSF-mobilized cells from Population *b*

Gene	baseMean	log2FoldChange	p-value	padj
AKAP2	703.6098	1.727609	5.90E-11	5.40E-08
LGALS1	102.4688	1.780569	2.81E-05	0.002833
SLC24A3	125.6366	1.841557	7.37E-05	0.006089
ARHGAP10	109.3418	1.873864	3.72E-06	0.000623
ANGPTL6	52.3411	2.070017	0.001047	0.041768
TK1	55.49215	2.189955	0.001401	0.049925
LOC101927497	176.7117	2.216348	1.66E-12	2.16E-09
AFF2	134.0453	2.227865	1.93E-05	0.002177
IGLL1	216.4632	2.391489	6.64E-13	1.01E-09
MIR181A1HG	210.1168	2.51486	1.85E-12	2.16E-09
HPGDS	125.47	2.718785	8.61E-10	4.73E-07
ADAMTS14	54.90454	2.858097	0.000206	0.012618
MFSD2B	56.12507	2.90642	4.10E-05	0.003775
HDC	478.375	3.070035	0.001362	0.049488
ACSM1	195.2779	3.107868	0.00013	0.009081
CP	172.1422	3.396736	1.44E-16	6.59E-13
CPA3	615.8863	3.448173	1.33E-42	1.83E-38
P2RX5	138.7401	3.455304	2.44E-10	1.60E-07
TPSAB1	72.42388	6.084714	6.88E-06	0.000994

Supplemental Table 9. Summary of mobilization, leukapheresis and CD34 enrichment parameters

Donor	GCSF dose	# collections	WBC count	CD34 count	CD34 purity [%]	Comment
1	5mg/kg	2	4.74e10	2.68e8	99.00	Cryopreserved
2	5mg/kg	2	9.70e10	2.88e8	92.00	Cryopreserved
3	5mg/kg	2	7.72e10	2.87e8	91.80	Cryopreserved
4	5mg/kg	2	2.07e10	5.92e6	35.10	Discontinued
5	5mg/kg	1	3.00E+10	1.30e8	97.00	Fresh processing
6	7.5mg/kg	1	5.98e10	3.70e8	87.90	Fresh processing

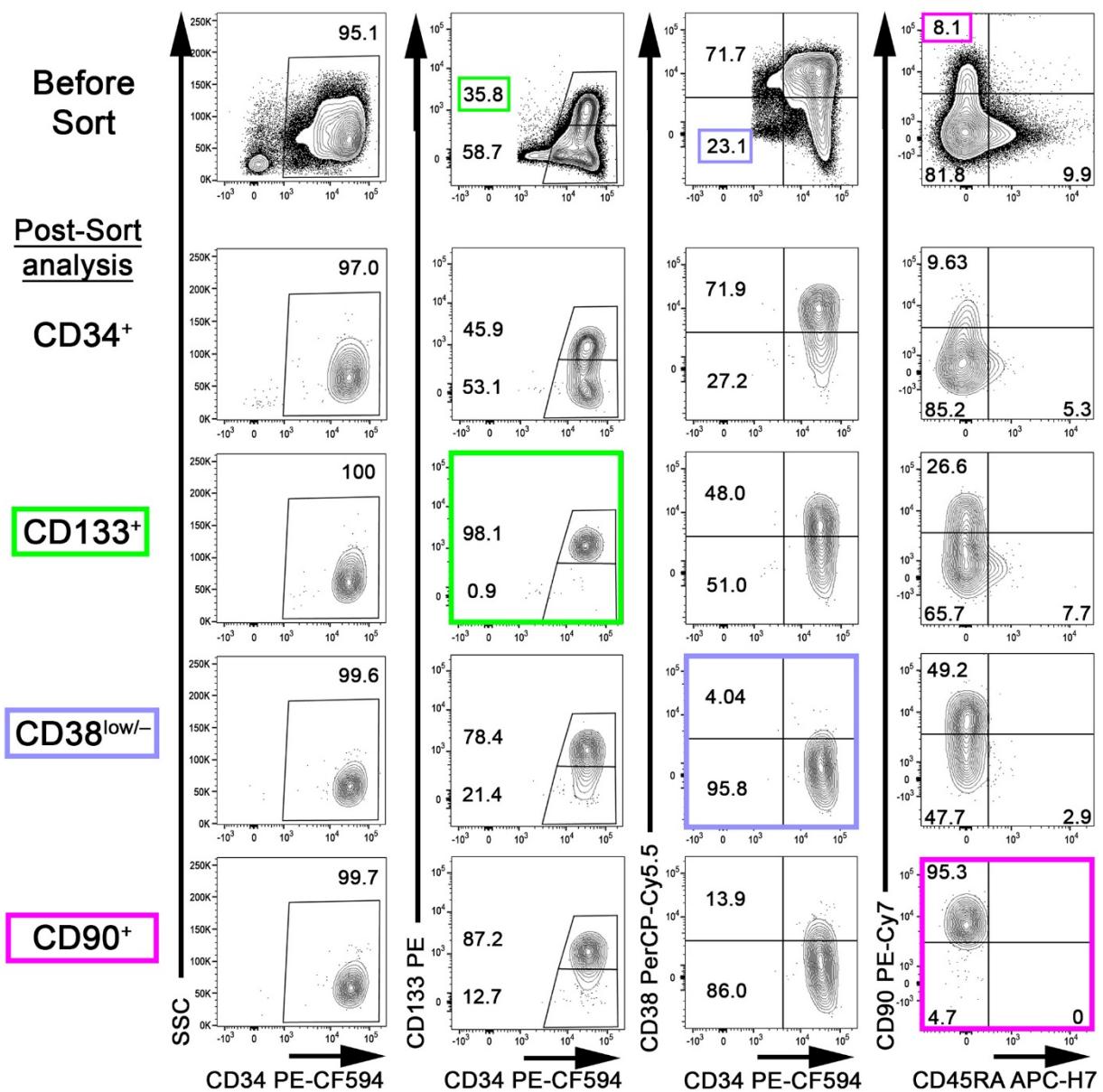
All donors were selected for adjusted body weight >120% of ideal body weight.

Supplemental Table 10. Antibodies

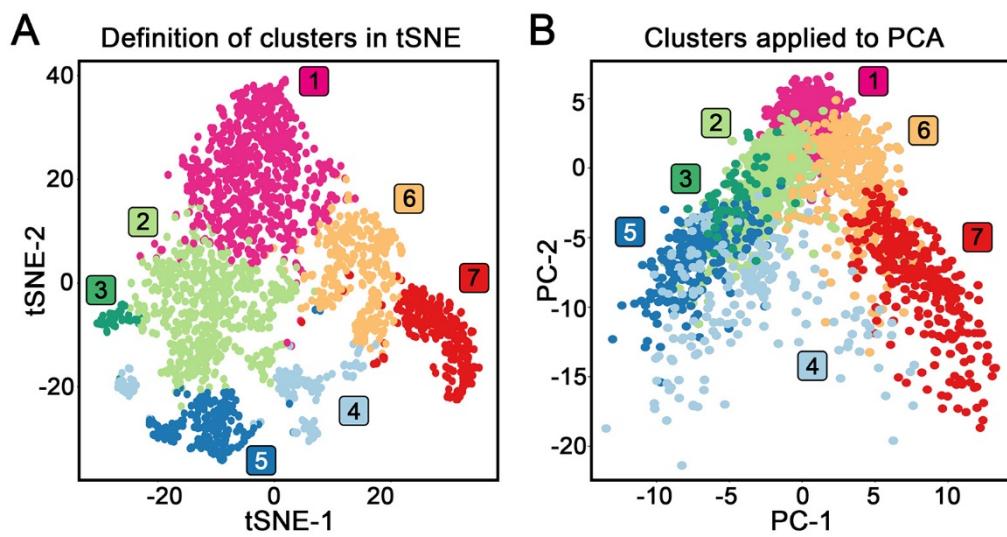
Antigen	Provider	Catalog Number	Clone Name	Lot Number	Fluorochrome	Application
CD3	BD	552851	SP34-2	4346516 6092584 6336728	Brilliant Violet 786	Mouse BM, PB, Spleen, Thymus
CD4	BioLegend	300526	RPA-T4	B188454 B226779 B261177 B274110	Alexa Fluor 700	Mouse BM, PB, Spleen, Thymus
CD8	BioLegend	344742	SK1	B234630 B242754 B263073	Brilliant Violet 605	Mouse BM, PB, Spleen, Thymus
CD14	eBioscience	25-0149-42	61D3	4306573 E10277-1635 E10278-1637	PE-Cy7	Mouse BM, PB, Spleen, Thymus
CD15	BioLegend	323006	W6D3	B199835 B230031	PE	Mouse BM, PB, Spleen, Thymus
CD16	BD	557758	3G8	4136850 5023818 6077649 6280745 7026993 7130902 7166692 8054938 8215752	APC-Cy7	Mouse BM, PB, Spleen, Thymus
CD19	BD	347544	4G7	5320803 6354963 7354554	PerCP	Mouse BM, PB, Spleen, Thymus
CD20	BioLegend	302324	2H7	6294531 6214617	PerCP	Mouse BM, PB, Spleen, Thymus
CD34	BD	562449	563	5070925 6027596 7053641 7166684 7348681 8238572 8242838	PE-CF594	Human HSPCs, Mouse BM
CD34	BD	561209	563	3151510 5070925 6027586 7110925 7348681 8087674 8242838 8283572	APC	Mouse BM
CD38	BioLegend	303522	HIT2	B229737 B245218	PerCP-Cy5.5	Human HSPCs, Mouse BM
CD45 (hu)	BD	560367	HI30	6184678 7096590	V450	Human HSPCs, Mouse BM, PB, Spleen, Thymus
CD45 (mu)	BD	562420	30-F11	6036634 6196640 7039832 7096986 7180875 8032908	PE-CF594	Mouse BM, PB, Spleen, Thymus

Supplemental Table 10. Antibodies

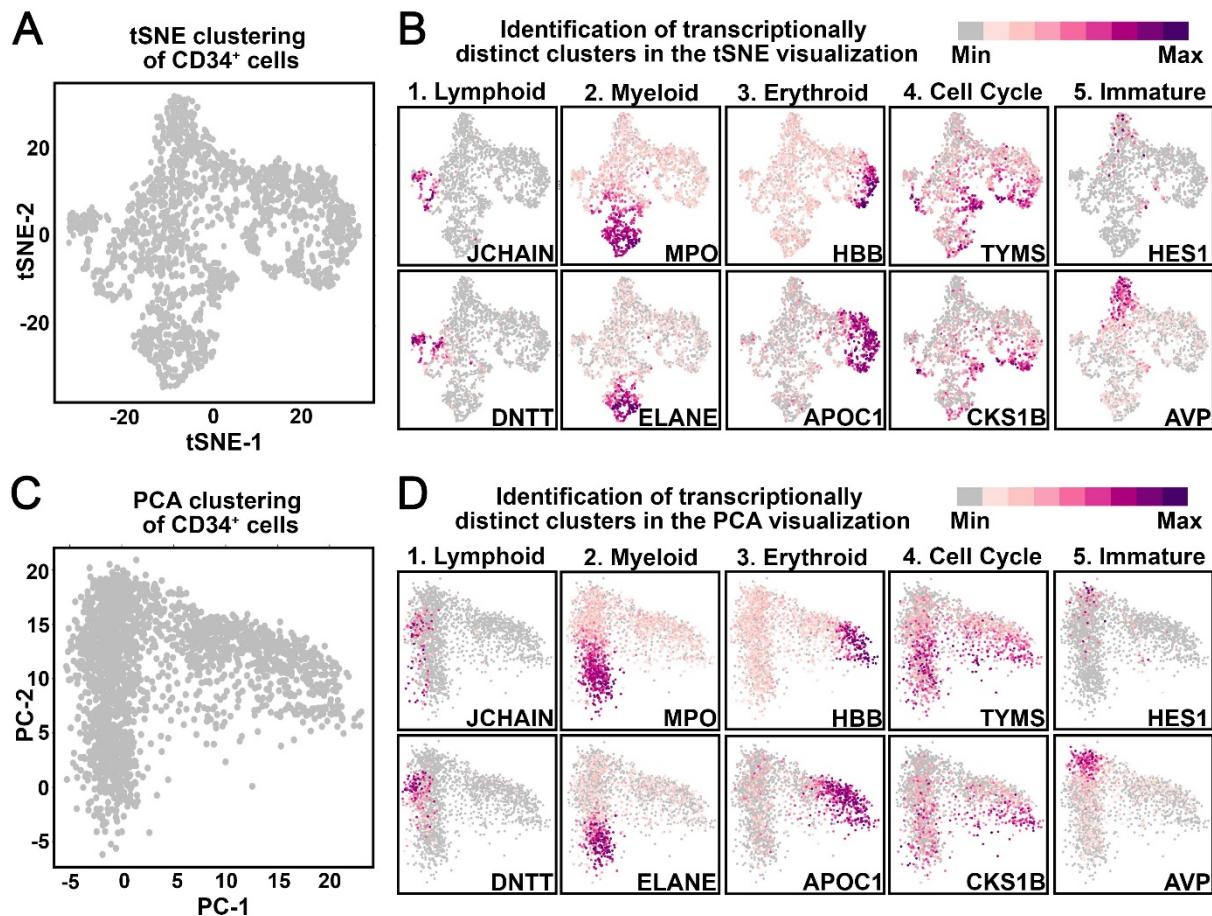
Antigen	Provider	Catalog Number	Clone Name	Lot Number	Fluorochrome	Application
				8281746 8294561		
CD45RA	BD	561212	5H9	3046621 4220811 5093523 5239872 6091801 6343868 7082838 7110636 7222952 8236712	APC-H7	Human HSPCs, Mouse BM
CD56	BioLegend	318332	HCD56	B207590 B225062 B233132 B241283 B252245 B267124	APC-Cy7	Mouse BM, PB, Spleen, Thymus
CD90	BioLegend	328110	5E10	B206722 B234526 B236754	PE-Cy7	Human HSPCs, Mouse BM
CD133	Miltenyi Biotech	130-080-801	AC133	5140630511 5150126020 5161207109	PE	Human HSPCs, Mouse BM



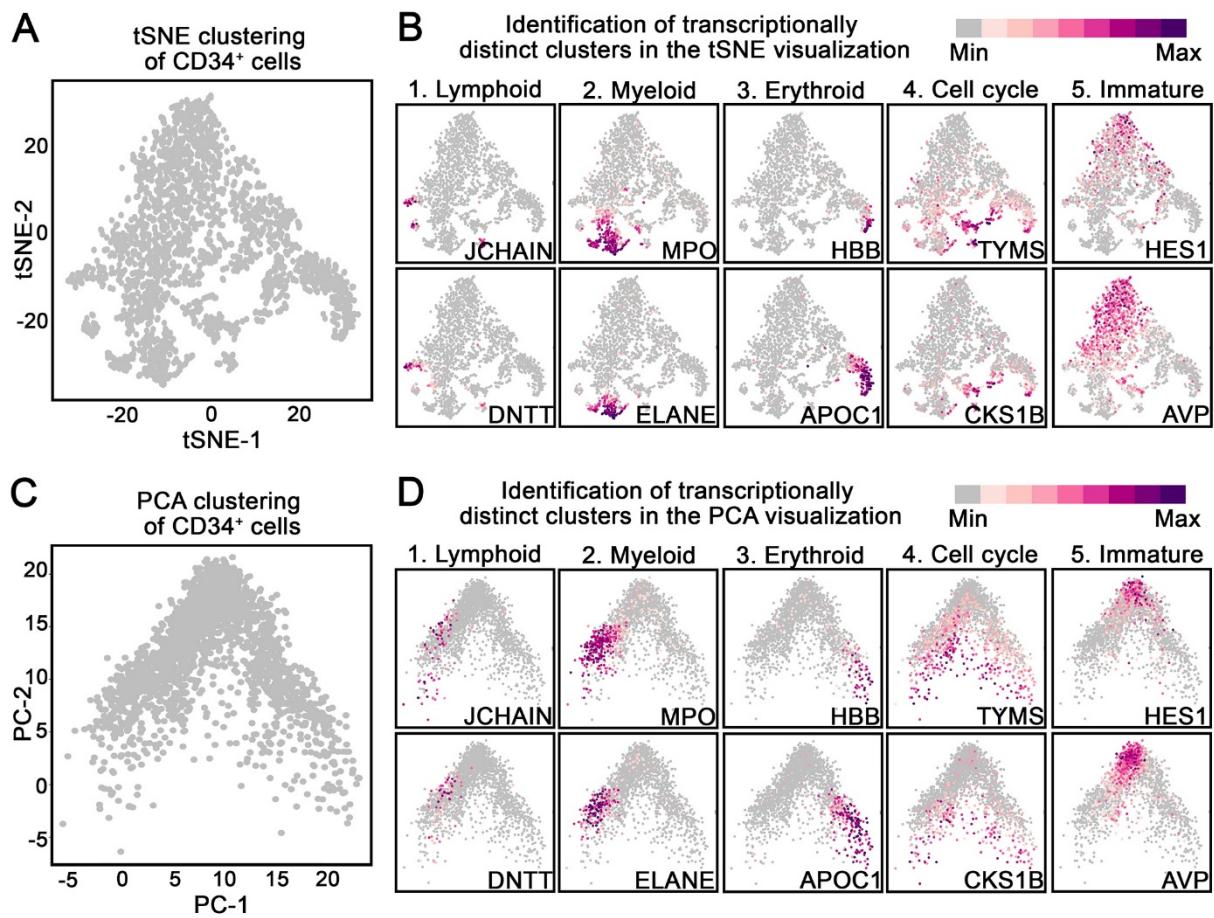
Supplemental Figure 1. Quality control of sort-purified CD34+ subpopulations. Flow-cytometric quality control of bulk CD34⁺ cells (top row, Before Sort) and sort-purified CD34⁺ (2nd row), CD133⁺ (3rd row), CD38^{low/-} (4th row) and CD90⁺ (5th row) HSPCs (Post-Sort analysis). Sorted target cell fractions are framed and color-coded. Numbers indicate frequency of gated population.



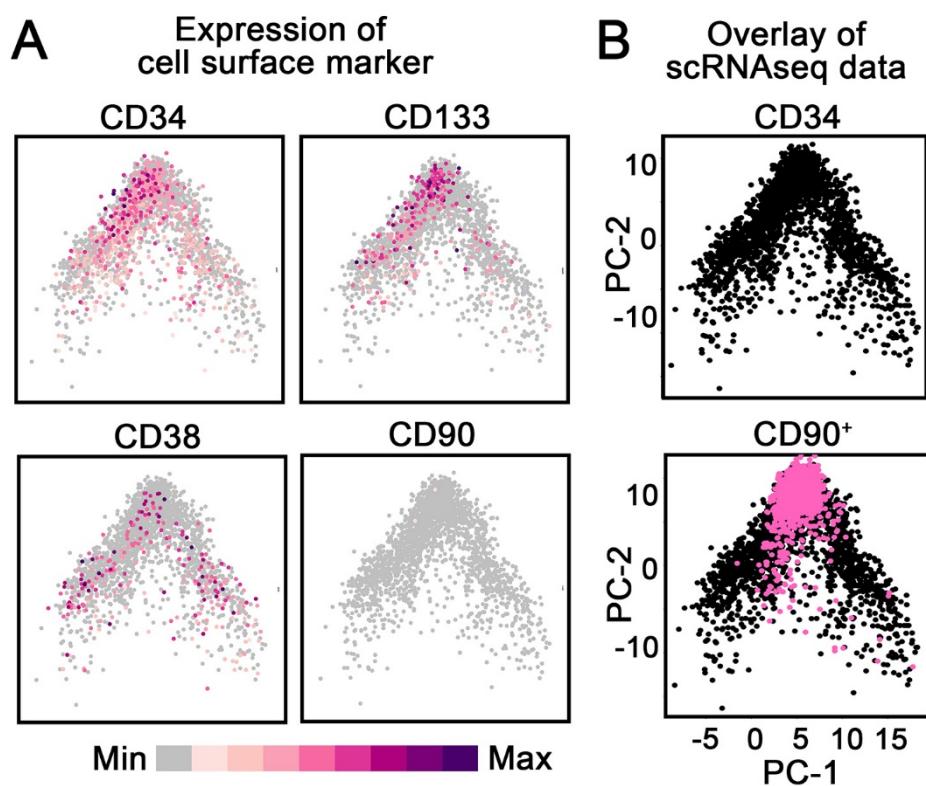
Supplemental Figure 2. Transcriptionally distinct ssBM CD34 clusters in a second donor. (A) Graph-based clustering of ssBM-derived CD34⁺ cells. Transcriptionally distinct CD34 clusters were color-coded and numbered. (B) Clusters defined in A projected onto the PCA analysis.



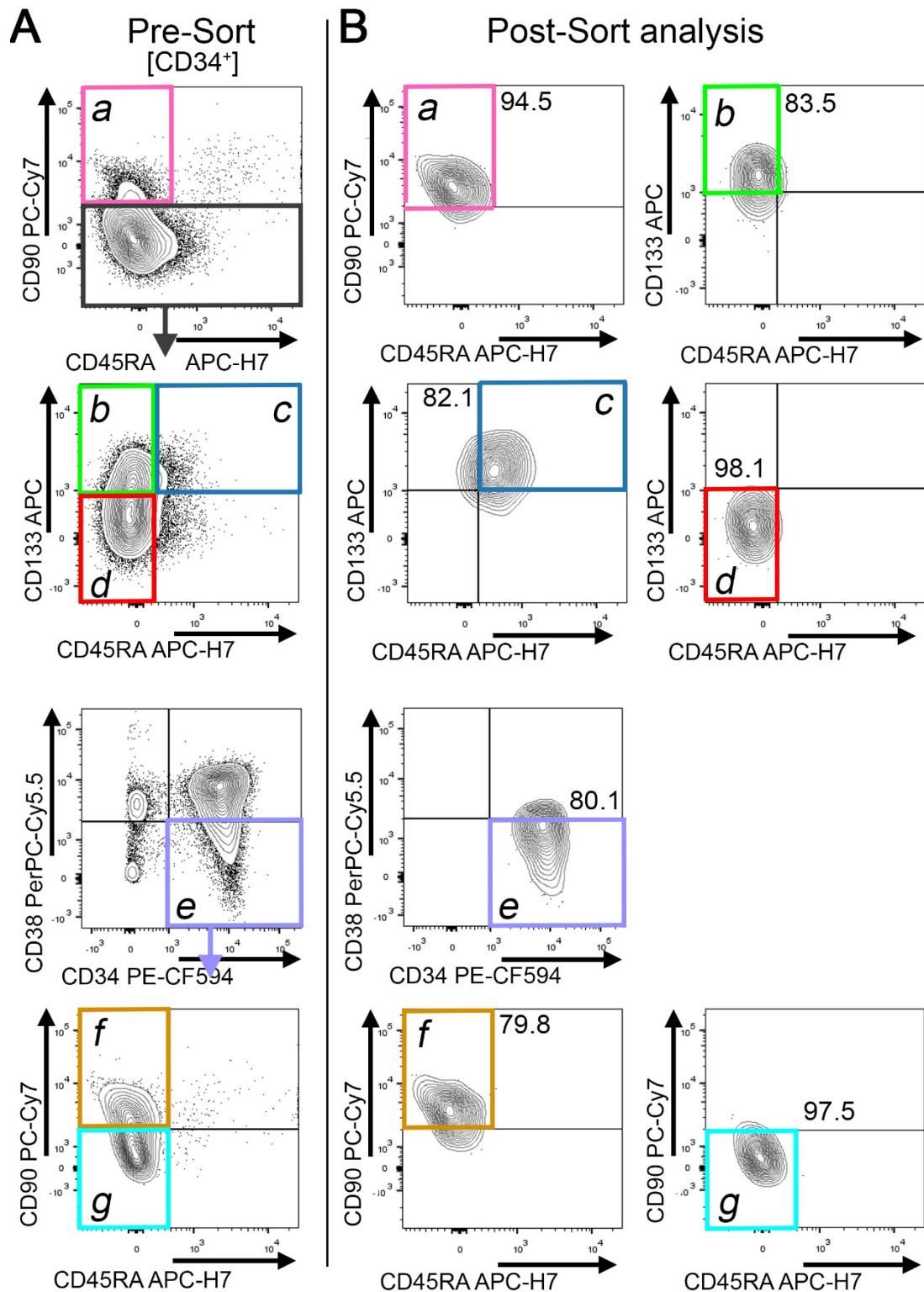
Supplemental Figure 3. ScRNAseq of ssBM-derived CD34⁺ HSPCs and sort-purified CD34 subsets. (A) Dimensional reduction (tSNE) of scRNAseq data from ssBM-derived CD34⁺ cells. (B) Feature plots showing the expression of representative genes associated with lymphoid-, myeloid-, erythroid-primed, proliferating, and immature HSPCs. Level of expression is color coded as shown in the legend. (C) PCA based transformation and (D) expression of representative genes for the same dataset shown in panel A.



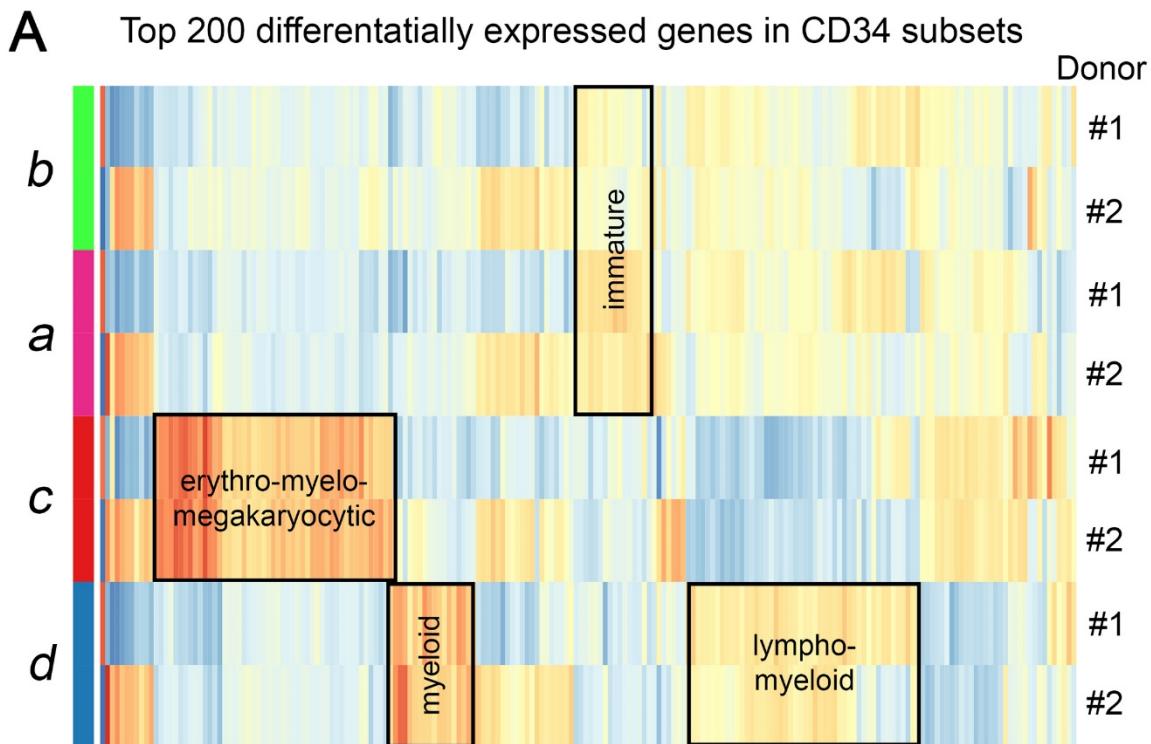
Supplemental Figure 4. Donor-independent reproducibility of the scRNAseq ssBM reference map. (A) tSNE and (C) PCA clustering of scRNAseq data from ssBM-derived CD34⁺ cells from a second donor. (B and D) Feature plots showing the expression of representative genes associated with lymphoid-, myeloid-, erythroid-primed, proliferating, and immature HSPCs. Level of expression is color coded as shown in the legend.



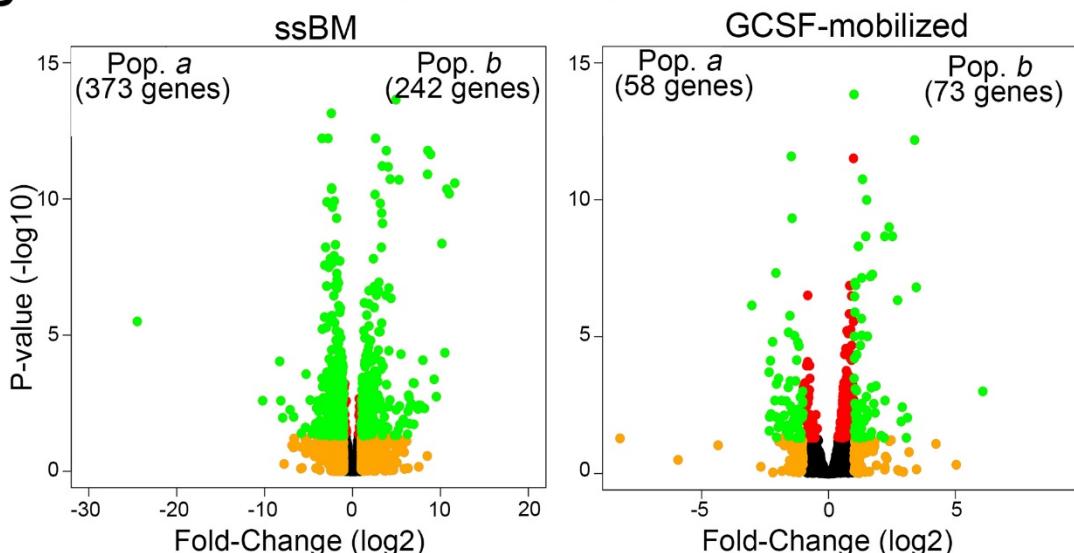
Supplemental Figure 5: Transcriptional mapping of sort-purified CD34 subsets from a second donor. (A) Expression of CD34, CD133, CD38 and CD90 in ssBM-derived CD34⁺ cells. Level of expression is color coded as shown in the legend. (B) Overlay of scRNAseq data from CD34⁺ cells (black, top plot) with sort-purified CD90⁺ (pink, lower plot) HSPCs.



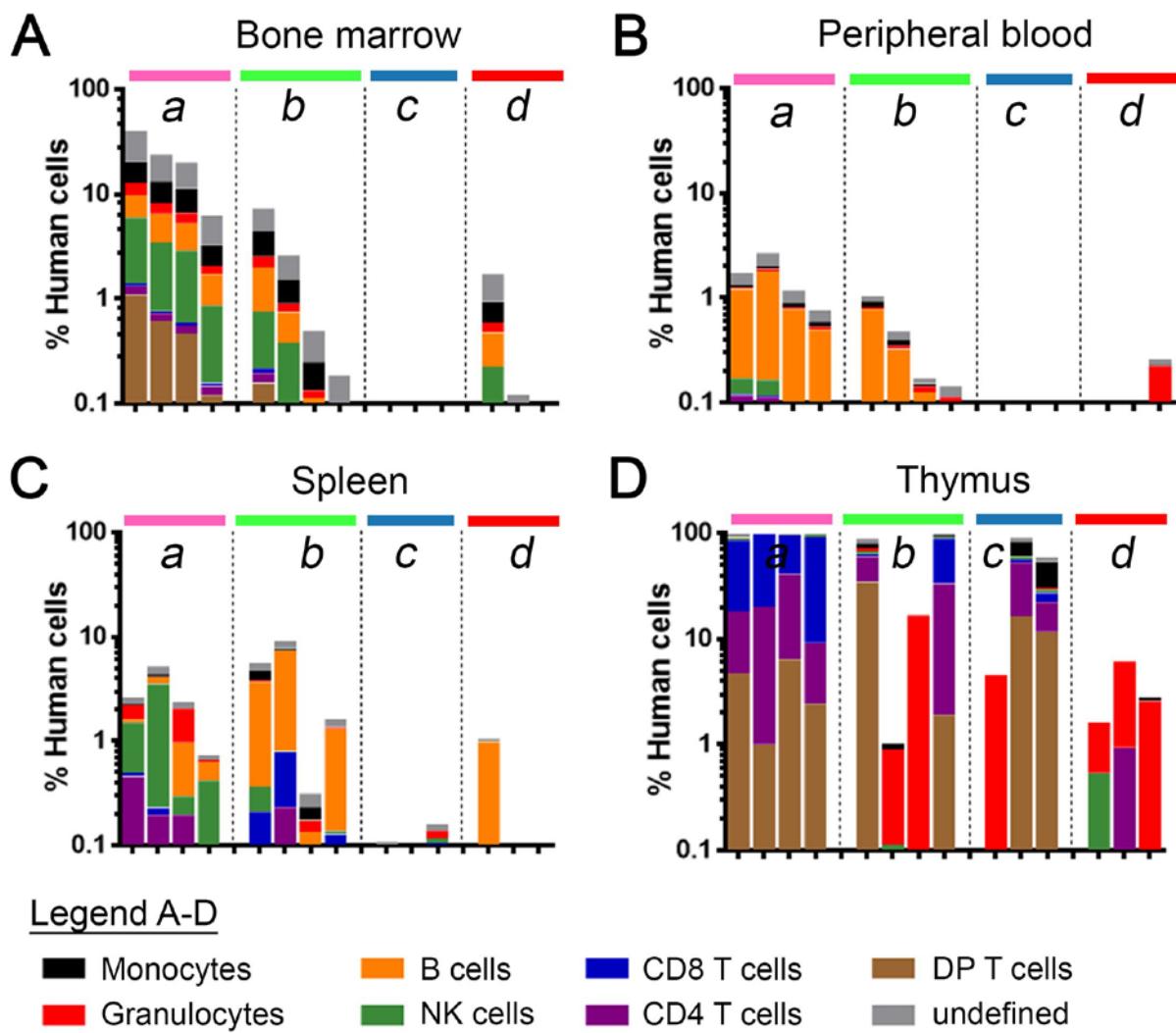
Supplemental Figure 6. Quality control of sort-purified CD34-subpopulations for bulk RNAseq. (A) Gating of ssBM-derived CD34 subpopulation defined in Figure 3A. (B) Flow-cytometric quality control of sort-purified CD34⁺ subsets for bulk RNAseq. Sorted cell fractions are framed and color-coded. Numbers indicate frequency of gated population.



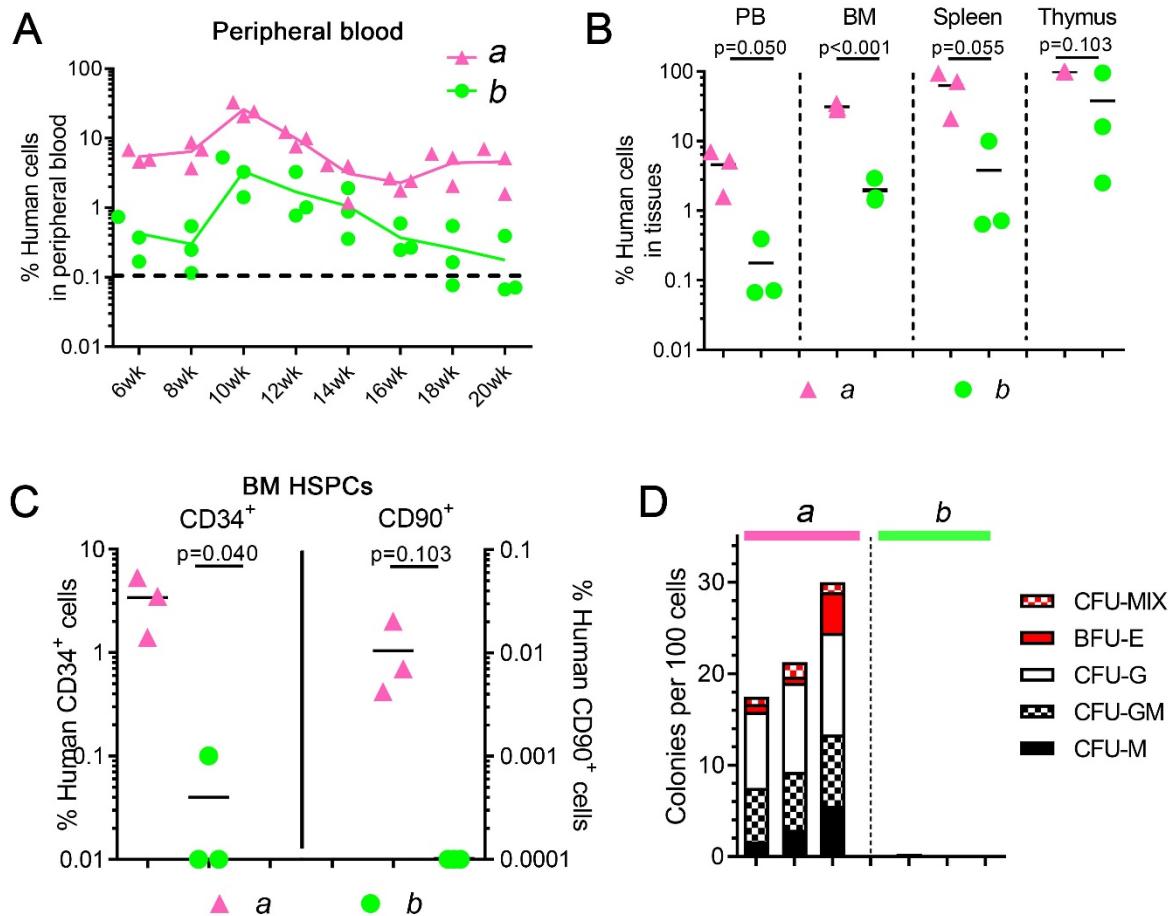
B Pairwise comparison of Populations *a* and *b*



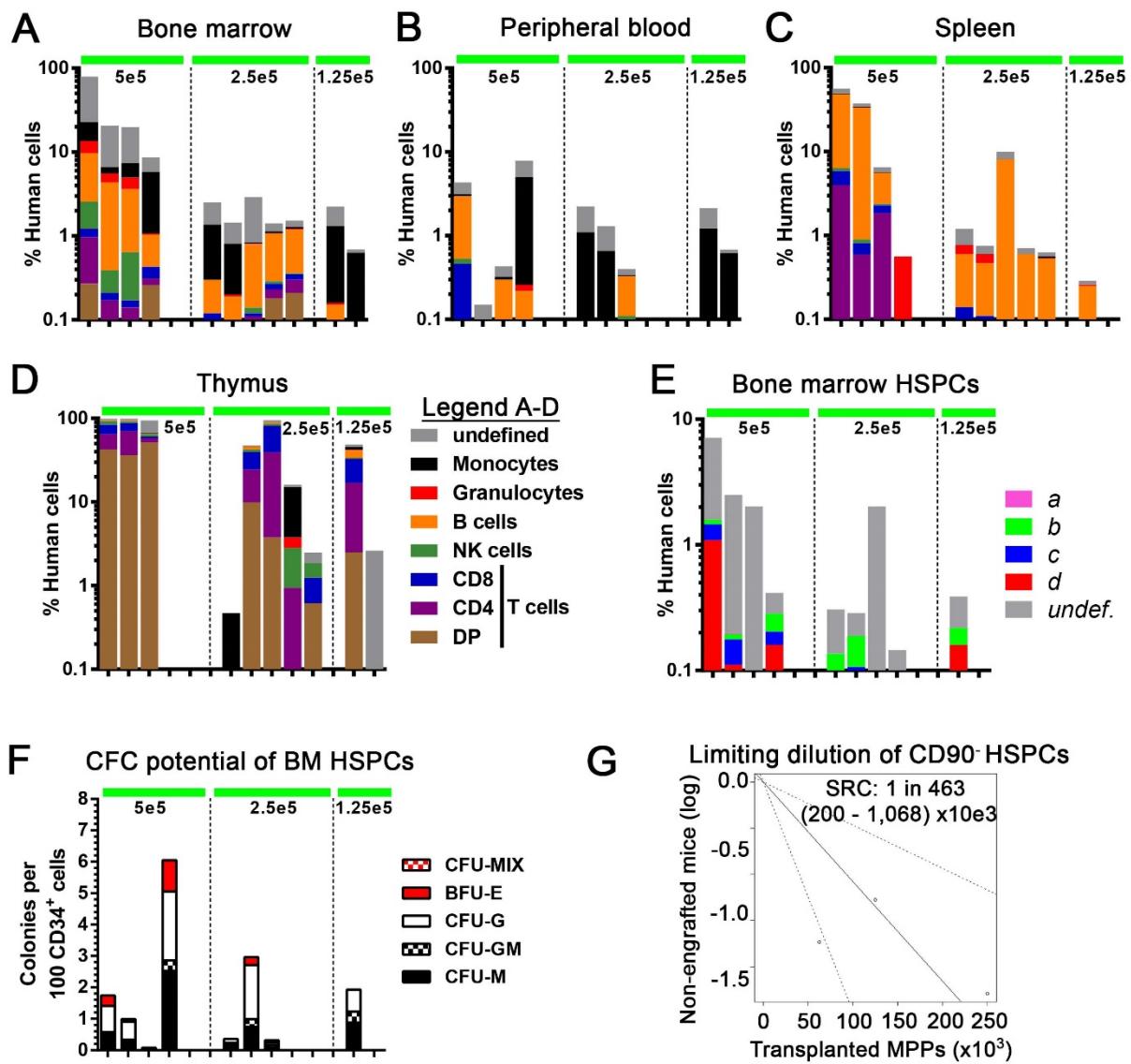
Supplemental Figure 7. Differentially expressed genes in GCSF-mobilized bulk CD34 subsets. (A) Heat map of the Top 200 differentially expressed genes in phenotypically-defined GCSF-mobilized CD34 subpopulations *a–d* from two independent human donors. A detailed list of the Top 200 genes can be found in **Table S4**. (B) Pair-wise comparison of the gene-expression in the ssBM and GCSF-mobilized subpopulations *a* and *b*. Differentially expressed genes are color coded according to the figure legend in the top left. A detailed list of all differentially expressed genes (green dots) can be found in **Tables S5, S6, S7 and S8**. Color-code: green = p-value < 0.05 and fold-change (FC) >1; red = p-value > 0.05 and FC >1; yellow = p-value > 0.05 and FC >1; black = p-value > 0.05 and FC < 1.



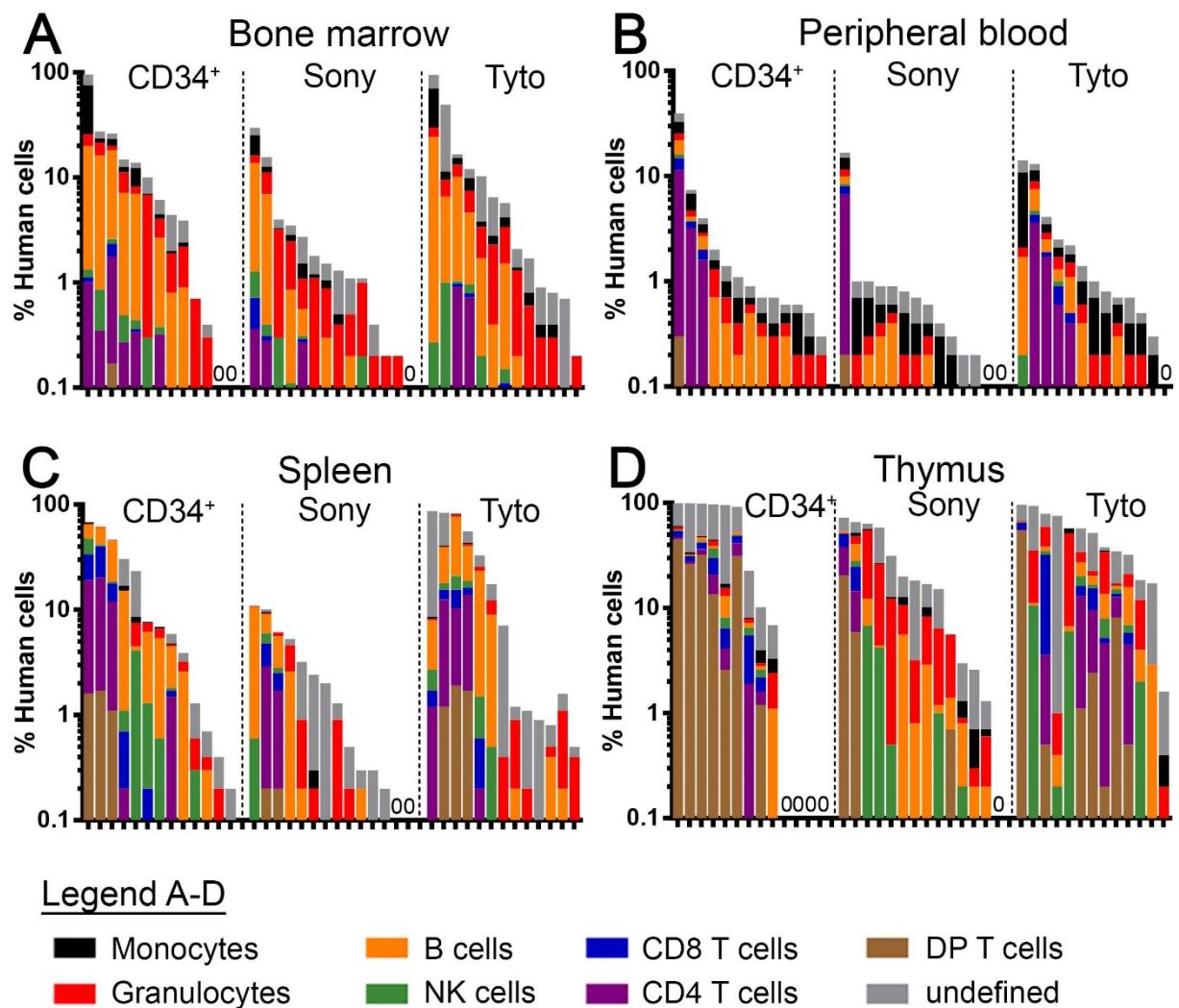
Supplemental Figure 8. Multilineage engraftment potential of human CD34 subpopulations. Human multilineage engraftment in the (A) BM, (B) PB, (C) spleen and (D) thymus after transplantation of sort-purified CD34 subpopulations (1e5 cells per mouse). Mice in all graphs and within each group are organized from the highest to the lowest engraftment level in the BM (A). (E) Frequency of human CD34⁺ cells (total height of bars) and CD34⁺ subpopulations (color-coded, as defined in Figure 3A). (F) Frequency of human CD90⁺ HSPCs in the BM of mice transplanted with populations *a* and *b* only.



Supplemental Figure 9. Engraftment potential of human CD34 subsets. (A) Longitudinal tracking of human CD45⁺ engraftment in the PB of mice transplanted with 2.5×10^5 HSPCs cells per mouse from Population *a* or Population *b*. (B) Side by side comparison of human CD45⁺ engraftment in the PB, BM, spleen and thymus. PB and BM use left y-axis, spleen and thymus right y-axis. (C) Frequency of human CD34⁺ cells (left y-axis) and CD90⁺ HSPCs (right y-axis) in the BM of engrafted mice. (D) Erythroid, myeloid and erythro-myeloid colony-forming potential of engrafted human HSPCs.



Supplemental Figure 10. Engraftment potential of human HSPCs from Population b.
Human multilineage engraftment in the (A) BM, (B) PB, (C) spleen and (D) thymus. Mice in all graphs and within each group are organized from the highest to the lowest engraftment level in the BM (A). (E) Frequency of human CD34⁺ cells (total height of bars) and CD34⁺ subpopulations in the BM of transplanted mice. (F) Erythroid, myeloid and erythro-myeloid colony-forming potential of engrafted human HSPCs. (G) Calculation of human HSPCs from population b with SRC potential using a limiting dilution approach as previously described(51).



Supplemental Figure 11. Engraftment potential of gene-modified human bulk CD34⁺ and sort-purified CD34⁺CD90⁺ cells. Human multilineage engraftment in the (A) BM, (B) PB, (C) spleen and (D) thymus of transplanted mice at 20 weeks post-transplant.