Supplemental Data

Supplementary Table 1. Differentially expressed genes in elderly vs. young HSC. SAM significant genes (FDR < 30%); age-up-regulated genes are in red, and age-down-regulated genes are in green.

Gene Num Change 24282.at InSk: Ridgetin 12.84 2370.at InSk: Ridgetin 12.84 2370.at InSk: Ridgetin 4.69 2203.at ABUBK-ABI gene family, member 3 (NSH) binding protein 4.69 2203.at INSK: Ridgetin 4.69 23076.at InCCR3320 proteintical protein IC0283392 4.13 23076.at			Fold
24282.at IGN: Ringerin 12.84 22805.at ICN: Ringerin 9.40 22863.at ADB3PS: All gene family, member 3 (NESH) binding protein 4.25 1550588.g. at IOC233392: hypothetical protein IOC283392 4413 23844.d. at	Gene ID	Gene Name	Change
239710.at IGK: indigetin 9.40 228636.at PCDH12; ortocadherin 12 468 220513.at ABBER: ABI gene family, member 3 (NEM) binding protein 4.25 1560698.at at 10C283392: hypothetical protein IOC283392 4.13 23804_at IGK: fidgetin 4.05 234074.at -:: CDNA FLI10946 fits, clone PLACE1000005 3.87 234074.at -:: Transcribed locus 3.87 234074.at -:: Transcribed locus 3.87 234079.st -:: Transcribed locus 3.87 23493 at Cubtr7, traderin 7, type 2 3.45 234882.at -:: -: -: -: -: -: -: -: -: -: -: -: -:	242828_at	FIGN: fidgetin	12.84
22885.3.1 PCDH12; protocadherin 17 468 22885.3.1 AB3BPS: ABI per Amily, momber 3 (NSH) binding protein 4.25 1560698.9.at UOC283392: hypothetical protein LOC283392 4.31 238067.4.1	239710_at	FIGN: fidgetin	9.40
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1560698 g.at. IOC28392: hypothetical protein IOC28392 413 238064 at. FIGN: fidgetin 405 234074 at. -::CDNA FUID946 fis, clone PLACE1000005 3.97 210104 at. PRRIE, proline rich 16 3.87 214707_xat. -::Transcribed locus 3.84 220203 at. CCUT17, protocadherin 17 3.79 HIST1382C///HIST1328F///HIST1328F///HIST1328F///HIST1328F.instone cluster 1, H2b/// histone c	220518_at	ABI3BP: ABI gene family, member 3 (NESH) binding protein	4.25
23804 at FION Indigetin 4.05 234074 at -: CDNA FLID906 fis, clone PLACE1000005 3.977 241470 x, at -: Tanscribed locus 3.84 227289, at OCH17, protocadherin 17 3.79 HISTLB26 /// HISTLB2	1560698 a at	LOC283392: hypothetical protein LOC283392	4.13
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HISTH2BC/// HISTH2BE /// HISTH2BE	227289 at	PCDH17: protocadherin 17	3 79
236193_at cluster 1, H2bf /// histone cluster 1, H2be // histone cluster 1, H2bi /// histone cluster 1, H2bi // histone cluster 1, H2bi // histone cluster 1, H2bi /// histone cluster 1, H2bi // H2bi // h	227205_ut	HIST1H2BC /// HIST1H2BE /// HIST1H2BE /// HIST1H2BG /// HIST1H2BI: histone cluster 1 H2bg /// histone	5.75
20679_s_at CDH7: catherin 7, type 2 3.45 24382_at : 3.37 24385_at : 3.33 1550007_at :-CDNA clone MAGE:5303689 3.31 1553808_a_at NKX2-3: NK2 transcription factor related, locus 3 (Drosophila) 3.27 20369_at ANXA3: annexin A3 3.27 23395_at ABJBP: ABI gene family, member 3 (NESH) binding protein 3.11 233611_at ::CDNA FUI2106 fis, clone HEMBB1002702 3.06 281595_at SICLAS: solute carrier family 1 (high affinity sapartate/glutamate transporter), member 6 2.96 219937_at TRHDE: thyrotropin-releasing hormone degrading enzyme 2.93 230192_at TRHDE: thyrotropin-releasing hormone degrading enzyme 2.93 23036_at STBXA: STB alpha-Nacety-neuraminide alpha-2,8-sialyttransferase 4 2.88 23046_at STBXA: Storkead box 2 2.87 23656_at PCDH17: protocherin 17 2.84 246474_at : 2.82 23777_at LOC492311: similar to bovine IgA regulatory protein 2.77 15559401_a, at -::Folk Horedonauin <td>236193 at</td> <td>cluster 1. H2bf /// historie cluster 1. H2be /// historie cluster 1. H2bi /// historie cluster 1. H2bc</td> <td>3.75</td>	236193 at	cluster 1. H2bf /// historie cluster 1. H2be /// historie cluster 1. H2bi /// historie cluster 1. H2bc	3.75
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2005_205 :	243882 at		3.15
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223339_at	209509_dt	ANAAS, dillexill AS	3.27
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1565602_at : Full length insert cDNA clone YN67C05 2.56 204712_at WIF1: WNT inhibitory factor 1 2.55 234033_at : Clone IMAGE:110218 mRNA sequence 2.54 206049_at SELP: selectin P (granule membrane protein 140kDa, antigen CD62) 2.50 216456 at : MRNA; cDNA DKFZp761L0812 (from clone DKFZp761L0812); partial cds 2.49		: Transcribed locus	2.57
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216456 at: MRNA; cDNA DKFZp761L0812 (from clone DKFZp761L0812); partial cds 2.49	206049 at	SELP: selectin P (granule membrane protein 140kDa, antigen CD62)	2.50
	216456 at	: MRNA; cDNA DKFZp761L0812 (from clone DKFZp761L0812): partial cds	2.49

209189_at	FOS: v-fos FBJ murine osteosarcoma viral oncogene homolog	2.49
208891_at	DUSP6: dual specificity phosphatase 6	2.48
243528_at	: Transcribed locus	2.47
240574_at	: CDNA clone IMAGE:5262677	2.47
208893_s_at	DUSP6: dual specificity phosphatase 6	2.45
220777_at	KIF13A: kinesin family member 13A	2.43
235052_at	ZNF792: zinc finger protein 792	2.40
212225_at	EIF1: eukaryotic translation initiation factor 1	2.40
231985_at	MICAL3: microtubule associated monoxygenase, calponin and LIM domain containing 3	2.39
236846_at	LOC284757: hypothetical protein LOC284757	2.39
241471 at	LOC730236: hypothetical LOC730236	2.39
1559042 at	NDUFB6: NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	2.38
232504 at	LOC285628: hypothetical protein LOC285628	2.38
229298 at	KBTBD7: kelch repeat and BTB (POZ) domain containing 7	2.37
235811 at		2.37
239208 s at	C21orf57: Chromosome 21 open reading frame 57	2.36
	FAM153A /// FAM153B /// FAM153C: family with sequence similarity 153. member B /// family with	
214945 at	sequence similarity 153, member A /// family with sequence similarity 153, member C	2.34
208792 s at	CLU: clusterin	2.33
226360 at	ZNRF3: zinc and ring finger 3	2.32
1557472 a at	FLJ30838: hypothetical gene supported by AL832565	2.32
228372 at	C10orf128: chromosome 10 open reading frame 128	2.32
239847 at	: CDNA clone IMAGE:6186815	2.31
213005 s at	KANK1: KN motif and ankyrin repeat domains 1	2.31
1563963 at		2.30
232912 at	GPR180: G protein-counled recentor 180	2.30
240601 at		2.30
2240001_at	NUEIP2: nuclear fragile X mental retardation protein interacting protein 2	2.25
224050_ut		2.25
227693 at	WDR20: WD repeat domain 20	2.25
238669 at	PTGS1: prostaglandin-endoperovide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	2.29
243521 at		2.25
212286 at	ANKRD12: ankvrin reneat domain 12	2.28
212200_ut	LIMCH1: LIM and calponin homology domains 1	2.20
240728 at	PICR4: Phospholinase C heta 4	2.27
212065 s at	USP34: ubiquitin specific pentidase 34	2.25
204310 s at	NPR2: natriuretic pentide recentor B/guanylate cyclase B (atrionatriuretic pentide recentor B)	2.23
213849 s at	PPP2R2B: protein phosphatase 2 (formerly 2A) regulatory subunit B, beta isoform	2.23
210049_5_at	SP100: SP100 nuclear antigen	2.23
210210_5_ut	CYSLTR1: cysteinyl leukotriene recentor 1	2.22
231/4/_at	CDC14R: CDC14 cell division cycle 14 homolog B (S. cerevisiae)	2.22
234003_at	RUNDC1: RUN domain containing 1	2.22
205128 v at	PTGS1: prostaglandin-endonerovide synthese 1 (prostaglandin G/H synthese and cycloovygopaso)	2.22
200126_A_dt	· Transcribed locus	2.21
234980_at	: Transcribed locus	2.21
240134_dt	AGGE1: angiogenic factor with G patch and EHA domains 1	2.20
210004_5_dt		2.20
230031_A_dL 235532_at	PIGM: phosphatidulinositol glucan anchor biosynthesis class M	2.20
235352_dt	ATD6V(0A2: ATDase H+ transporting lycocomal V() subunit a2	2.20
200545 of	DEV6: nerovisomal hiogenesis factor 6	2.19
204343_dl	SIC25A20: soluto carrier family 25. member 20	2.19
1563264 at		2.19
1303304_dt	HUHU Sapietts, CIUTE TIVIAUE.4272047, HINNA	2.19
242070_dt	· Transcribed locus	2.10
241430_dl	E2011: coogulation factor II (thrombin) recentor like 1	2.18
215500_dl	CEL /// CELP1: complement factor H /// complement factor H valated 1	2.18
215912 c ct	CFR /// CFRAL COMPLEMENT Id.LOF R /// COMPLEMENT TACTOR R-related 1	2.17
213013_5_dt	Prost. prostagianum-endoperoxide synthase i (prostagiandin G/H synthase and cyclooxygenase)	2.17
204720_5_at	LOC202202: bundthatical protain LOC202202	2.17
130/09/_at	LUC205552: Hypothetical protein LUC283392	2.16
220109_dt	FGP1: Early growth response 1	2.10
22/404_5_dl	PCDH0: protocodborin 0	2.15
219/38_5_dt	- round, protocaditering	2.14
230100_9L		2.13

242579_at	BMPR1B: bone morphogenetic protein receptor, type IB	2.13
219615_s_at	KCNK5: potassium channel, subfamily K, member 5	2.13
210377_at	ACSM3: acyl-CoA synthetase medium-chain family member 3	2.12
239449_at	: Transcribed locus	2.12
226109_at	C21orf91: chromosome 21 open reading frame 91	2.12
204071_s_at	TOPORS: topoisomerase I binding, arginine/serine-rich	2.12
223263_s_at	FGFR1OP2: FGFR1 oncogene partner 2	2.11
219737_s_at	PCDH9: protocadherin 9	2.11
226483_at	TMEM68: transmembrane protein 68	2.10
220577 at	GVIN1: GTPase, very large interferon inducible 1	2.09
218294 s at	NUP50: nucleoporin 50kDa	2.09
205942 s at	ACSM3: acyl-CoA synthetase medium-chain family member 3	2.09
221524 s at	RRAGD: Ras-related GTP binding D	2.09
239901 at	: Transcribed locus	2.08
240777 at	SYNE2: Spectrin repeat containing, nuclear envelope 2	2.07
	ZNF586: zinc finger protein 586	2.07
235342 at	SPOCK3: sparc/osteonectin, cwcy and kazal-like domains proteoglycan (testican) 3	2.07
237590 at		2.06
238744 at	' Transcribed locus	2.06
232150 at	: CDNA clone IMAGE:4792085	2.06
227506 at	SI C16A9: solute carrier family 16. member 9 (monocarboxylic acid transporter 9)	2.00
220235 s at	Clorf103: chromosome 1 onen reading frame 103	2.00
219504 c at	RPAP2: RNA polymerase II associated protein 2	2.00
205140 at	FPGT: furcise-1-nhosnhate guanylyltransferase	2.03
203140_at	EAM19A2: family with sequence similarity 19 (chemokine (C-C motif)-like) member A2	2.05
241355_at	IOC344595: hypothetical IOC344595	2.03
233400_at	: CDNA: EL 21248 fis. clopa COL01225	2.04
254520_at	EPYO9: E hav protoin 9	2.04
240247 at	· · · · · · · · · · · · · · · · · · ·	2.04
240247_at	USPA6: ubiquitin specific pentidose 46	2.03
205009_dt	CCDC99A: Coiled coil demain containing 99A	2.02
156246_at	CODECCA. Coned-con domain containing COA	2.01
1502400_dt	: CDNA CIONE IMIAGE.5278001	2.01
217330_A_dt	CDNA ELIA1024 fic. clone DEDIC200E111	2.01
230411_dt	CDNA FLI41934 IIS, CIOIRE PERICZOUSIII	2.01
209795_dt	CD09. CD09 Indecute	2.01
200110_dt	STAT4. signal transducer and activator of transcription 4	2.00
1552/35_dl	PCDRGA4: protocauterin gamma subramity A, 4	1.99
238170_at	: Transcribed locus	1.99
239429_at	: Transcribed locus	1.98
220572_at	UKF2p54/G183: hypothetical protein UKF2p54/G183	1.98
232301_at	UBE3B: ubiquitin protein ligase E3B	1.98
214/13_at	YLPM1: YLP motif containing 1	1.98
204739_at	CENPC1: centromere protein C 1	1.97
235264_at	HUFUZ: NOST CEIL TACTOR UZ	1.97
235044_at	CYYK1: cysteine/tyrosine-rich 1	1.96
222156_x_at	CCPG1: cell cycle progression 1	1.96
230881_at	CCDC42: coiled-coil domain containing 42	1.96
204700_x_at	C1ort107: chromosome 1 open reading frame 107	1.95
243331_at	: Iranscribed locus	1.95
209006_s_at	C1ort63: chromosome 1 open reading trame 63	1.95
218614_at	C12ort35: chromosome 12 open reading frame 35	1.94
205159_at	CSF2RB: colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1.94
226998_at	NARG1: NMDA receptor regulated 1	1.94
212979_s_at	FAM115A: family with sequence similarity 115, member A	1.94
209757_s_at	MYCN: v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	1.93
243319_at	: Transcribed locus	1.93
206861_s_at	CGGBP1: CGG triplet repeat binding protein 1	1.92
218929_at	CDKN2AIP: CDKN2A interacting protein	1.91
238609_at	C7orf38: chromosome 7 open reading frame 38	1.91
1569345_at	: Transcribed locus	1.91
218472_s_at	PELO: pelota homolog (Drosophila)	1.90
227980_at	ZNF322A: zinc finger protein 322A	1.90
234081_at	: CDNA FLJ11986 fis, clone HEMBB1001364	1.88

1559485_at	ATG2B: ATG2 autophagy related 2 homolog B (S. cerevisiae)	1.88
235014_at	LOC147727: hypothetical LOC147727	1.88
206109_at	FUT1: fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	1.88
242565_x_at	C21orf57: Chromosome 21 open reading frame 57	1.88
209585_s_at	MINPP1: multiple inositol polyphosphate histidine phosphatase, 1	1.87
201143_s_at	EIF2S1: eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	1.87
218604_at	LEMD3: LEM domain containing 3	1.85
1564175_at	LOC401074: Hypothetical LOC401074	1.85
218520_at	TBK1: TANK-binding kinase 1	1.85
226956 at	MTMR3: myotubularin related protein 3	1.84
234597_at	: CDNA: FLJ20914 fis, clone ADSE00646	1.84
223215 s at	C14orf100: chromosome 14 open reading frame 100	1.84
225236 at	RBM18: RNA binding motif protein 18	1.82
207128 s at	ZNF223: zinc finger protein 223	1.81
227559 at	: Transcribed locus	1.81
229373 at	: Transcribed locus	1.79
238725 at	: Transcribed locus	1.79
227410 at	FAM43A: family with sequence similarity 43, member A	1.79
241116 at	: Transcribed locus	1.79
1560274 at	LOC100132279 /// WTAP: Wilms tumor 1 associated protein /// hypothetical protein LOC100132279	1.79
1555486 a at	FLJ14213: protor-2	1.79
1554501 at	TSC22D4: TSC22 domain family, member 4	1.79
239081 at	: Transcribed locus	1.78
201694 s at	EGR1: early growth response 1	1.78
218535 s at	RIOK2: RIO kinase 2 (veast)	1.77
204447 at	ProSAPiP1: ProSAPiP1 protein	1.76
224628 at	C2orf30: chromosome 2 open reading frame 30	1.76
236360 at	FLI42875: hypothetical LOC440556	1.76
206016_at	CCDC22: coiled-coil domain containing 22	1.76
215525 at		1.75
219383 at	FI 114213: protor-2	1.75
202097 at	NUP153: nucleonorin 153kDa	1.75
228753 at	LOC100128737: hypothetical protein LOC100128737	1.74
213109 at	TNIK: TRAF2 and NCK interacting kinase	1.74
238355 at	RBM39: RNA binding motif protein 39	1.74
222893 s at	RPAP2: RNA polymerase II associated protein 2	1.73
219436 s at	EMCN: endomucin	1.73
213376 at	ZBTB1: zinc finger and BTB domain containing 1	1.72
233226 at	PTPN9: Protein tyrosine phosphatase, non-receptor type 9	1.71
203761 at	SLA: Src-like-adaptor	1.71
225132 at	FBXL3: F-box and leucine-rich repeat protein 3	1.71
226280 at	: CDNA FLJ43545 fis. clone PROST2011631	1.70
244613 at	· · · · · · · · · · · · · · · · · · ·	1.69
209193 at	PIM1: pim-1 oncogene	1.69
236128 at	ZNF91: zinc finger protein 91	1.67
216465 at	: MRNA; cDNA DKFZp586N2022 (from clone DKFZp586N2022)	1.67
223470 at	PIGM: phosphatidylinositol glycan anchor biosynthesis, class M	1.67
205928 at	ZNF443: zinc finger protein 443	1.66
221025 x at	PUS7L: pseudouridylate synthase 7 homolog (S. cerevisiae)-like	1.65
201236 s at	BTG2: BTG family, member 2	1.64
232265 at	ATXN7L1: ataxin 7-like 1	1.64
225005 at	PHF13: PHD finger protein 13	1.62
225445 at	tcag7.1228: hypothetical protein FLJ25778	1.61
222312 s at	: CDNA clone IMAGE:6186815	1.61
200881 s at	DNAJA1: DnaJ (Hsp40) homolog, subfamily A, member 1	1.61
213233 s at	KLHL9: kelch-like 9 (Drosophila)	1.60
241445 at	: Transcribed locus	1.59
214651 s at	HOXA9: homeobox A9	1.57
227066 at	MOBKL2C: MOB1, Mps One Binder kinase activator-like 2C (veast)	1.56
230520 at	AIG1: androgen-induced 1	1.56
238279 x at		1.55
1569098 s at	TP53BP1: tumor protein p53 binding protein 1	1.55
225490 at	ARID2: AT rich interactive domain 2 (ARID, RFX-like)	1.54

223377_x_at	CISH: cytokine inducible SH2-containing protein	1.54			
242761_s_at	ZNF420: zinc finger protein 420	1.52			
201041_s_at	DUSP1: dual specificity phosphatase 1				
228445_at	AIFM2: apoptosis-inducing factor, mitochondrion-associated, 2				
218079_s_at	GGNBP2: gametogenetin binding protein 2	1.50			
226504_at	FAM109B: family with sequence similarity 109, member B	1.48			
225121_at	TBC1D23: TBC1 domain family, member 23	1.48			
225912_at	TP53INP1: tumor protein p53 inducible nuclear protein 1	-1.70			
226419_s_at	FLJ44342: hypothetical LOC645460	-1.73			
206674_at	FLT3: fms-related tyrosine kinase 3	-1.76			
224606_at	KLF6: Kruppel-like factor 6	-1.78			
241353_s_at	LOC100129105: similar to hCG1821214	-1.86			
225673_at	MYADM: myeloid-associated differentiation marker	-1.93			
204639_at	ADA: adenosine deaminase	-1.98			
208763_s_at	TSC22D3: TSC22 domain family, member 3	-2.03			
	: Transcribed locus, strongly similar to XP_001151823.1 PREDICTED: hypothetical protein [Pan				
244080_at	troglodytes]	-2.04			
36829_at	PER1: period homolog 1 (Drosophila)	-2.07			
214176_s_at	: Transcribed locus	-2.11			
226525_at	: Transcribed locus	-2.17			
215671_at	PDE4B: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	-2.34			
230986_at	KLF8: Kruppel-like factor 8	-2.36			
213665_at	SOX4: SRY (sex determining region Y)-box 4	-2.39			
236253_at	: Transcribed locus	-2.49			
229178_at	LOC145786: hypothetical protein LOC145786	-2.56			
223708_at	C1QTNF4: C1q and tumor necrosis factor related protein 4	-2.64			
228983_at	: Transcribed locus	-2.78			
231508_s_at	: Transcribed locus	-2.79			
214043_at	PTPRD: protein tyrosine phosphatase, receptor type, D	-2.80			
201324_at	EMP1: epithelial membrane protein 1	-2.81			
207735_at	RNF125: ring finger protein 125	-2.82			
1552803_a_at	C1orf215: chromosome 1 open reading frame 215	-2.82			
202861_at	PER1: period homolog 1 (Drosophila)	-2.96			
222044_at	PCIF1: PDX1 C-terminal inhibiting factor 1	-2.96			
204784_s_at	MLF1: myeloid leukemia factor 1	-3.03			
228188_at	FOSL2: FOS-like antigen 2	-3.15			
230233_at	: Transcribed locus	-3.21			
242051_at	: Transcribed locus	-3.22			
239476_at	: CDNA FLJ36491 fis, clone THYMU2018197	-3.26			
1561079_at	ANKRD28: ankyrin repeat domain 28	-3.29			
206726_at	PGDS: prostaglandin D2 synthase, hematopoietic	-3.50			
203708_at	PDE4B: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) -3				
239809_at	: Transcribed locus -4.				
	AREG /// LOC727738: amphiregulin (schwannoma-derived growth factor) /// similar to Amphiregulin				
205239_at	precursor (AR) (Colorectum cell-derived growth factor) (CRDGF)	-7.56			
215446_s_at	LOX: lysyl oxidase	-10.59			

Supplementary Table 2. Selected list of genes that have been implicated in hematopoietic malignancies and are differentially expressed between elderly and young human HSC; age-up-regulated genes are in red, and age-down-regulated genes are in green.

		Fold
Gene ID	Gene Name	Change
208079_s_at	AURKA: aurora kinase A	1.81
209189_at	FOS: v-fos FBJ murine osteosarcoma viral oncogene homolog	2.49
209905_at	HOXA9: homeobox A9	1.62
202431_s_at	MYC: v-myc myelocytomatosis viral oncogene homolog (avian)	2.65
230192_at	TRIM13: tripartite motif-containing 13	2.91
36711_at	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	-2.06
206674_at	FLT3: fms-related tyrosine kinase 3	-1.76

		1	Complete Blood Count			,		
Age	Gender	WBC	Hb	НСТ	PLT	MCV	RDW	RBC
24	Male	5.3	14.1	39.8	225	87.2	13.1	4.57
24	Female	8.5	13.1	37.6	269	93.7	12.5	4.01
26	Female	4.5	14	14.3	198	94.6	13.7	4.36
26	Male	4.3	14.4	41.8	200	89.5	13.5	4.67
27	Female	7.3	15.9	45.4	224	87.7	12.9	5.18
30	Female	6.3	13.1	37.8	191	89.3	13.6	4.23
31	Male	8.1	14.4	40.8	274	93.8	14.4	4.35
65	Male	5.2	14.6	43	195	91	13.9	4.72
65	Male	4.7	15.1	43.6	184	91	14.1	4.78
68	Male	7	14.8	42.8	236	92	13.1	4.68
68	Male	8.1	13.2	38.4	230	98	12.1	3.92
73	Male	5.6	13.4	38.4	295	87	13.1	4.41
75	Male	7.3	15.1	44	219	89.5	13.8	4.91
81	Male	9.4	15.4	44.9	188	89.5	14.7	5.02
83	Female	7.1	13.3	39.4	250	89.9	14.1	4.38
85	Female	5.1	12.7	37	215	100.5	13.7	3.68
85	Female	6.2	13.8	41.1	163	87.4	15.3	4.7

Supplementary Table 3. Complete blood count (CBC) values from matching peripheral blood of bone marrow samples used for this study (data available for subset of samples only).

Supplementary Figure 1. Increased frequency of HSC out of total mononuclear cells isolated from normal elderly bone marrow compared to young.

(A) Summary of HSC as frequency of total bone marrow mononuclear cell population from multiple young (n=13) and elderly (n=11) bone marrow samples. * = p < 0.002. (B) CD34+ cells as frequency of total bone marrow mononuclear cell population from multiple young (n=13) and elderly (n=11) bone marrow samples. (C) Relative HSC as frequency of total bone marrow mononuclear cell population from multiple young (n=13) and elderly (n=11) bone marrow samples, adjusted for bone marrow cellularity, as estimated from bone marrow core biopsies. # = p < 0.02. Error bars represent standard deviation.



Supplementary Figure 2. Frequency of MPP in normal elderly bone marrow compared to young.

(A) Gating strategy and flow cytometric profile of MPP (Lin⁻, CD34⁺, CD38⁻, CD90⁻, CD45RA⁻) in representative hematopoietically normal young (left) and elderly (right) bone marrow samples. The panels for each sample are gated on Lin-CD34+CD38- live cells. (B) Summary of MPP as frequency of total Lin⁻CD34⁺ population from multiple young (n=13) and elderly (n=11) bone marrow samples. (C) Summary of MPP as frequency of total bone marrow mononuclear cell population from multiple young (n=13) and elderly (n=11) bone marrow samples. Error bars represent standard deviation.



Supplementary Figure 3. Gating strategy and cell cycle flow cytometric profile of live, Lin⁻ CD34⁺ cells.

(A) Gating strategy and flow cytometric profile of quiescent G_0 (Hoechst 33342^{low}, Pyronin Y^{low}, correlating with 2N DNA and low levels of RNA) and non- G_0 (Pyronin Y^{high}, correlating with 2N to 4N DNA and higher levels of RNA) populations in representative elderly and young HSC from hematopoietically normal bone marrow samples. The panels for each sample are gated on Lin-CD34+CD38-CD90+CD45RA- live cells. (B) Quiescent G_0 (Hoechst 33342^{low}, Pyronin Y^{low}, correlating with 2N DNA and low levels of RNA) and non- G_0 (Pyronin Y^{high}, correlating with 2N DNA and low levels of RNA) and non- G_0 (Pyronin Y^{high}, correlating with 2N DNA and low levels of RNA) and non- G_0 (Pyronin Y^{high}, correlating with 2N DNA and low levels of RNA) and non- G_0 (Pyronin Y^{high}, correlating with 2N to 4N DNA and higher levels of RNA) populations in representative elderly and young Lin⁻ CD34⁺ population from hematopoietically normal bone marrow samples. The panel is gated on Lin-CD34+CD38-CD90+CD45RA- live cells. This profile was used to set gates for Hoechst 33342 and Pyronin Y in (A).



Young Bone Marrow (31 year old, male): Live, Lin-CD34+CD38-CD90+:



Elderly Bone Marrow (83 year old, female): Live, Lin-CD34+CD38-CD90+:



Supplementary Figure 4. Similar myeloid progenitor frequencies in normal elderly and young bone marrow.

(A) Gating strategy and flow cytometric profile of CMP (Lin⁻CD34⁺CD38⁺CD123⁺CD45RA⁻), GMP (Lin⁻CD34⁺CD38⁺CD123⁺CD45RA⁺), and MEP (Lin⁻CD34⁺CD38⁺CD123⁻CD45RA⁻) in representative hematopoietically normal young and elderly bone marrow samples. The left panels for each sample are gated on lineage negative (Lin-) live cells, and the right panels are gated on Lin-CD34+CD38+ live cells. (B) Summary of myeloid progenitor (CMP, GMP, and MEP) frequencies as total of Lin⁻CD34⁺ population from multiple young (n=13) and elderly (n=11) bone marrow samples. (B) Summary of myeloid progenitor (CMP, GMP, and MEP) frequencies as total of bone marrow mononuclear cell population from multiple young (n=13) and elderly (n=11) bone marrow samples. Error bars represent standard deviation. A Young Bone Marrow (27 year old, female): Live, Lin-:

Elderly Bone Marrow (65 year old, male): Live, Lin-:



Supplementary Figure 5. Decreased frequency of CLP out of total mononuclear cells isolated from normal elderly bone marrow compared to young.

Summary of CLP as frequency of total bone marrow mononuclear cell population from multiple young (n=10) and elderly (n=7) bone marrow samples. # = p < 0.05. Error bars represent standard deviation.



Supplementary Figure 6. Generation of lymphoid and myeloid progeny *in vitro* by HSC from normal young and elderly bone marrow.

(A) Summary of numbers and types of cells produced per 50 HSC from multiple normal young (n=8) and elderly (n=6) bone marrow samples co-cultured with AC6.2.1 stromal cell line. (B) Summary of numbers and types of colonies produced by 300 HSC from multiple normal young (n=6) and elderly (n=6) bone marrow samples cultured in methylcellulose medium. Error bars represent standard deviation.



Supplementary Figure 7. Engraftment of human T cells, erythroid cells, and platelets

(A) Summary of spleen engraftment of human CD45+CD3+ T cells as measured by percent human chimerism per 500 transplanted HSC from unique young (n=10) and elderly (n=9) bone marrow samples. (B) Summary of bone marrow engraftment of human glycophorin A+ erythroid cells. (C) Summary of bone marrow engraftment of human CD41/61+ platelets. Error bars represent standard deviation.



Supplementary Figure 8. Purification of HSC from bone marrow by FACS

(A) Representative flow cytometric profile of HSC prior to sorting. (B) Representative flow cytometric profile of sorted HSC which were re-analyzed to assess purity. (C) Summary of sort purity of sorted HSC from multiple young (n=11) and elderly (n=8) bone marrow samples.

A Pre-sort: Live, Lin-, CD34+,CD38-:



Samples	Post-sort purity (range)		
Elderly HSC (8 samples)	96.55%-100.00%		
Young HSC (11 samples)	95.25%-100.00%		

Supplementary Figure 9. Ingenuity Pathways Analysis of age-regulated genes.

(A) The "Cell Cycle, Connective Tissue Development and Function, Cellular Development" network and (B) the "Gene Expression, Hematological System Development and Function, Tissue Morphology" network are identified by IPA, based on the age-regulated genes from SAM, as the most significantly affected during human HSC aging. Selection of (B) biological functions and (C) molecular pathways identified by IPA as significantly enriched in the age-regulated HSC geneset.







