Table 1 | **Quiescent stem cell gene signature***

Function	Downregulated gene	Upregulated gene
Cell cycle progression and checkpoint control	*ANLN*, *BIRC5*, *CCNA2*, *CCNB1*, *CCNE2*, *SGOL1*	*CCND3*, *PDK1*
DNA replication and chromosome segregation	*MCM4*, *PCNA*, *RRM2*, *TOP2A*	
Mitochondrial function	*CYCS*, *MTCH2*, *SLC25A5*	
Chromatin and nucleosome assembly	*H2AFZ*, *HAT1*	*SMARCA2*
Regulation of transcription		*FOXO3*, *EZH1*, *PRDM5*, *PTOV1*, *ZFP30*, *ZBTB20*, *PHF1*, *CTDSP1*, *THRA*, *TEF*
RNA processing	*DDX39*	*DICER1*
Other	*2810417H13Rik*‡, *CAPZA1*, *HADHB*, *IDH3A*, *KPNA2*, *PGK1*	*A930001N09Rik*‡, *BCAS3*, *DDX3Y*, *GABARAPL1*, *GLTSCR2*, *ITM2A*, *IL18*, *ZYX*, *EPHX1*, *CLSTN1*, *GSTK1*, *5730403B10Rik*‡, *DDT*, *IVD*, *FHL1*, *NDRG2*, *GRINA*, *PIK3R1*, *FYN*, *CHKB*, *PINK1*, *ULK2*, *DNAJB9*, *PFDN5*, *CTSF*, *CRIM1*, *SEPP1*, *GABBR1*, *GRB10*, *BBS2*, *RPS14*, *IGF2R*, *SELENBP1*, *RNF167*, *MAP1LC3A*

ANLN, anillin, actin binding protein; *BBS2*, Bardet–Biedl syndrome 2; *BCAS3*, breast carcinoma amplified sequence 3; *BIRC5*, baculoviral IAP repeat-containing 5; *CAPZA1*, capping protein (actin filament) muscle Z-line, alpha 1; *CCNA2*, cyclin A2; *CCNB1*, cyclin B1; *CCNE2*, cyclin E2; *CCND3*, cyclin D3; *CHKB*, choline kinase beta; *CLSTN1*, calsyntenin 1; *CRIM1*, cysteine rich transmembrane BMP regulator 1; *CTDSP1*, carboxy-terminal domain, RNA polymerase II, polypeptide A small phosphatase 1; *CTSF*, cathepsin F; *CYCS*, cytochrome *c*, somatic; *DDT*, D-dopachrome tautomerase;*DDX3Y*, DEAD box polypeptide 3, Y-linked; *DDX39*, DEAD box polypeptide 39; *DNAJB9*, DNAJ homologue, subfamily B, member 9; *EPHX1*, epoxide hydrolase 1; *EZH1*, enhancer of zeste homologue 1; *FHL1*, four and a half LIM domains 1; *FOXO3*, forkhead box O3; *GABBR1*, gamma-aminobutyric acid B receptor 1; *GABARAPL1*, GABA(A) receptor-associated protein like 1; *GLTSCR2*, glioma tumor suppressor candidate region gene 2; *GRB10*, growth factor receptor-bound protein 10; *GRINA*, glutamate receptor, ionotropic, *N*-methyl D-aspartate-associated protein 1; *GSTK1*, glutathione *S*-transferase kappa 1; *H2AFZ*, H2A histone family, member Z; *HADHB*, hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase, beta subunit; *HAT1*, histone aminotransferase 1; *IDH3A*, isocitrate dehydrogenase 3 alpha; *IGF2R*, insulin-like growth factor 2 receptor; *IL18*, interleukin 18; *ITM2A*, integral membrane protein 2A; *IVD*, isovaleryl-CoA dehydrogenase; KPNA2, karyopherin alpha 2; *MAP1LC3A*, microtubule-associated protein 1 light chain 3 alpha; *Mcm4*, minichromosome maintenance deficient 4; *Mtch-2*, mitochondrial carrier homologue 2; NDRG2, N-MYC downstream regulator 2; *PCNA*, proliferating cell nuclear antigen; *PFDN5*, prefoldin 5; *PGK1*, phosphoglycerate kinase 1; *PHF1*, PHD finger protein 1; *PIK3R1*, phosphoinositide-3-kinase, regulatory subunit 1; *PINK1*, PTEN induced putative kinase 1; *PKD1*, polycystic kidney disease 1; *PRDM5*, PR domain containing 5; *PTOV1*, prostate tumour over expressed gene 1; *RNF167*, ring finger 167; *RPS14*, ribosomal protein S14; *RRM2*, ribonucleotide reductase M2; *SELENBP1*, selenium binding protein 1; *SEPP1*, selenoprotein P plasma1; *Sgol1*, shugoshin-like 1; *SLC25A5*, solute carrier family 25, member 5; *SMARCA2*, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2; *TEF*, thyrotroph embryonic factor; *THRA*, thyroid hormone receptor alpha; *TOP2A*; topoisomerase (DNA) II alpha; *ULK2*, unc-51 like kinase 2; *ZBTB20*, zinc-finger and BTB domain containing 20; *ZFP30*, zinc-finger protein 30; *ZYX*, zyxin. *Comparison of microarray data sets revealed a gene signature that is common to quiescent haematopoietic stem cells (HSCs), muscle stem cells (MuSCs) and hair follicle stem cells (HFSCs). Selected genes (30 out of 71 genes) are shown and grouped on the basis of pathways in which they are presumed to function. Genes exhibiting expression level changes that are shared among the stem cell compartments are listed under 'other'. Consistent with the dormant phenotype of a quiescent stem cell, genes that are involved in cell cycle progression, DNA replication or mitochondrial functions are mostly downregulated in quiescent stem cells. ‡These are RIKEN clones with no current known functions.

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