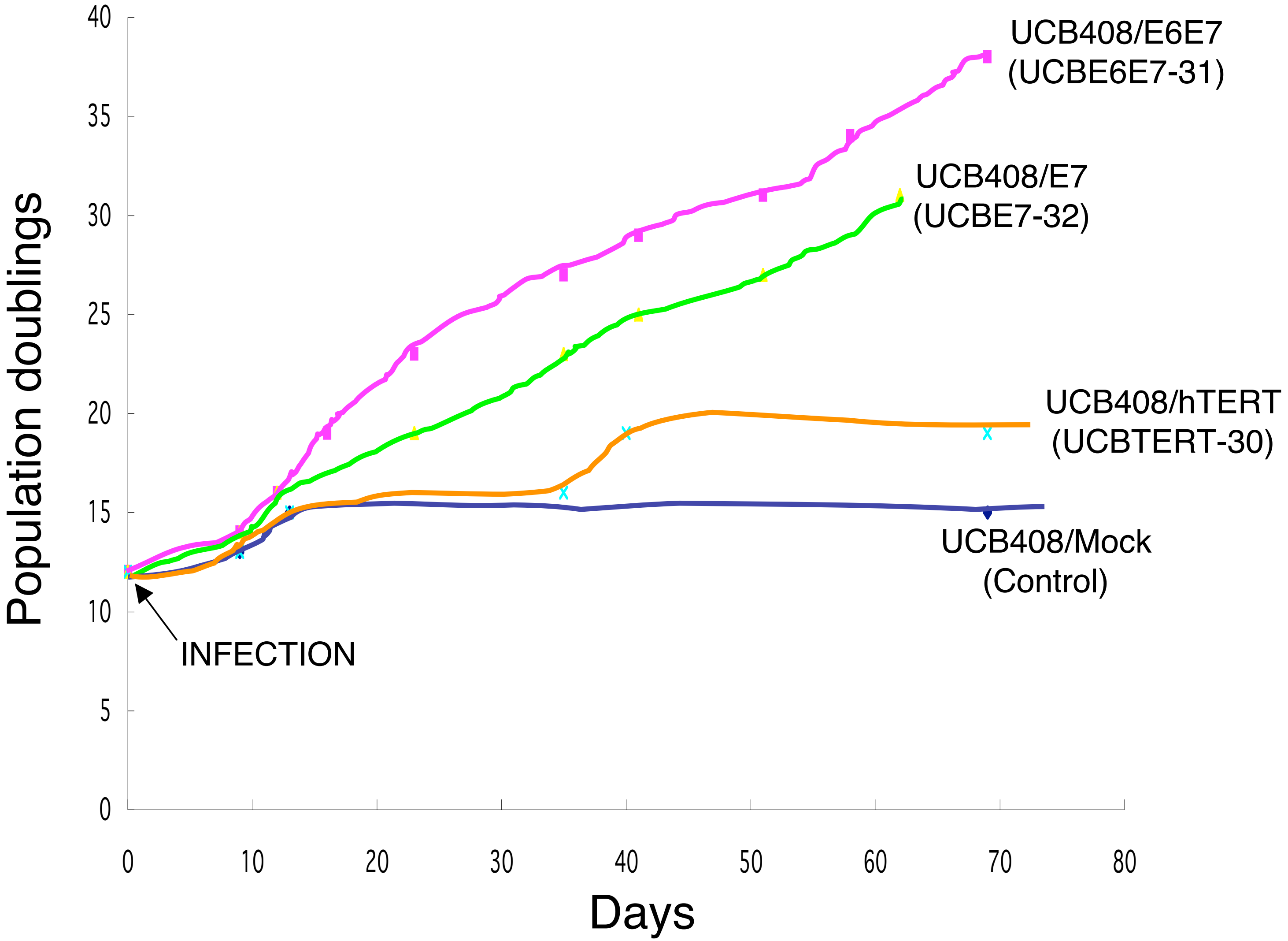
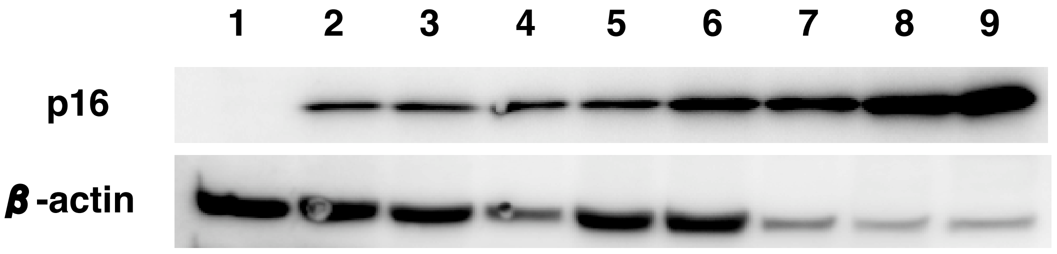
Supplement

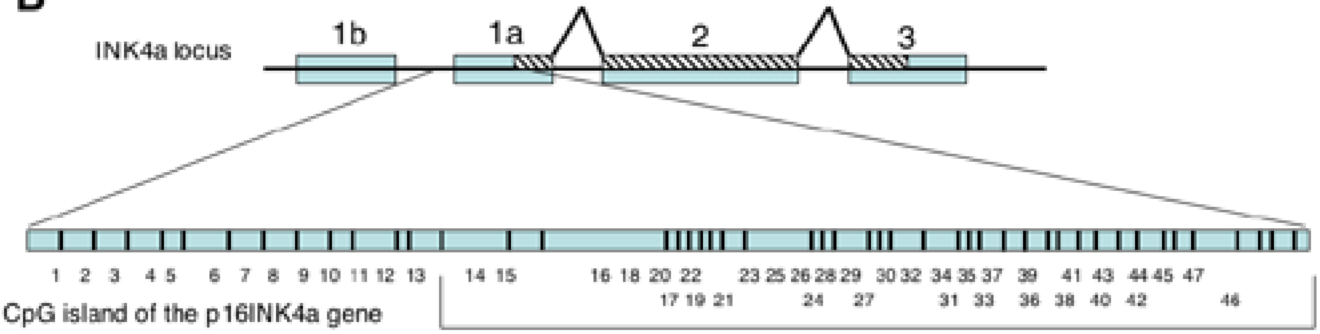
A



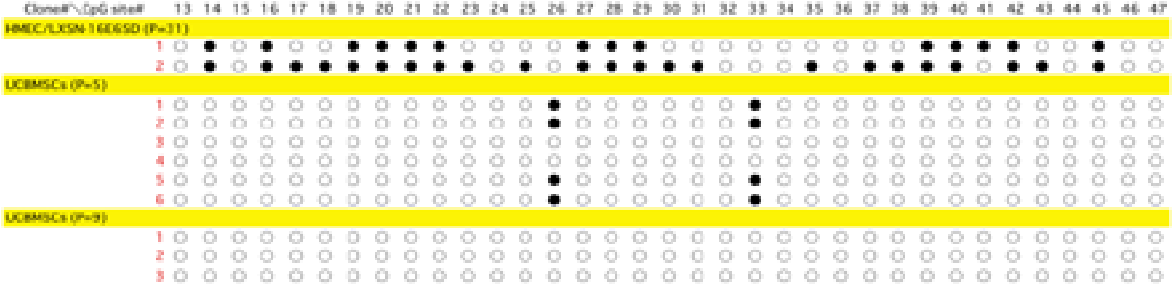


Supplement

B



C



Clone#\CpG site#	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
HMEC/LXSN-16E6SD (P=31)																																			
1	○	●	○	●	○	○	●	●	●	●	○	○	○	○	●	●	●	○	○	○	○	○	○	○	○	○	●	●	●	●	○	○	●	○	○
2	○	●	○	●	●	●	●	●	●	●	●	○	●	○	●	●	●	●	●	○	○	○	●	○	●	●	●	●	○	●	●	○	●	○	○
UCBMSCs (P=5)																																			
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2	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○	○	○	○	○	○	○
3	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
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5	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○	○	○	○	○	○	○
6	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○	○	○	○	○	○	○
UCBMSCs (P=9)																																			
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2	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○
3	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○

Supplementary Figure legends

A. Upper panel. The UCBMSCs (UCB408 cells) were infected with recombinant retroviruses carrying E7 and/or E6 or hTERT, or were treated with vector alone at PD 12 (indicated as an arrow). Stably transduced cells with an expanded life span were designated UCB408/E6E7 (UCBE6E7-31), UCB408/E7 (UCBE7-32), UCB408/hTERT (UCBTERT-30), and UCB408/Mock (control) cells. The population doublings of the UCBE6E7-31 (pink), UCBE7-32 (green), UCBTERT-30 (orange), and UCB408/Mock cells (blue) are shown. The UCBE6E7-31 and UCBE7-32 cells proliferated for over 30 PDs and exhibited persistent growth. The UCBTERT-30 cells exhibited a prolonged cell life span in culture and reached PD 19. The UCB408/Mock cells stopped growing and entered senescence at PD 15.

Lower panel. UCBMSCs (lane 1; P=3), UCB408 cells (lane 2; P=2, lane 3; P=3, lane 4; P=4, lane 5; P=5, lane 6; P=6, lane 7; P=7), HeLa cells (lane 8), and C33A cells (lane 9) were analyzed by Western blotting for $p16^{INK4a}$ and β-actin protein levels.

B. Genome map and development of methylation of the 5’ CpG island of the $p16^{INK4a}$. This CpG map is based on published genome sequences (GenBank accession no. AF022809, U12818, and AC000048). The cording region 1a is shown. The gray bar at the bottom represents a magnification of the region, from -355 to +233, that was analyzes for methylation in this study. The 47 CpG sites (black boxes within the gray bar) in this region are numbered according to their 5’- to 3’- order in the $p16^{INK4a}$ genomic sequence and positioned based on their location within the genomic sequence. In the study PCR product (-159 to +233); CpG sites (13 to 47), amplified from bisulfite-treated DNA for sequencing, are shown (Wong *et al.*, 1999).

C. Individual epigenotypes are represented numbers (1 to 6) on the left that represent the clone, respectively. Human mammalian epithelial cell (HMEC)/LXSN-16E6SD (P=31) has been already analyzed as a sample with methylation. The sample was performed as a methylated control in this experiment. CpG sites on the top are numbered from 13 to 47 according to their 5’- to 3’- order in the p16^{INK4a} genome sequence. The methylation status of each CpG site is indicated at its relative position in the p16^{INK4a} genomic sequence by either ○ (unmethylated) or ● (methylated).