

	1p	3q	8q	9q	11p	16p	16q	19p	20q	22q
RS vs young ^a			1.91e-4	4.40e-7	7.69e-4	6.09e-8	6.22e-5	2.21e-11		3.71e-5
siLMNB1 vs siCtrl ^b			6.73e-5							6.07e-3
RS signature ^c				2.92e-3	2.63e-4	7.25e-4				
OIS signature ^c		6.11e-4	2.20e-3	9.60e-3			5.94e-3		1.85e-4	
IRIS signature ^c										1.34e-3
GTEX dataset ^d	8.74e-4		3.80e-3	4.98e-4	5.86e-3	8.87e-7			4.69e-5	3.76e-4

Supplementary table 1. Subtelomere enrichment for upregulated DEGs of different senescence inducers

Summary of chromosome ends obtained by enrichment analysis of upregulated DEGs upon different senescent stimuli. ^a Replicative senescence (RS) vs young MRC-5 cells and ^b siLMNB1 vs siControl in young cells from this work; RS, ^c oncogene-induced senescence (OIS), ionizing radiation-induced senescence (IRIS) from Hernandez-Segura *et al.* and from ^d aged tissues from the GTEx database from Dong *et al.* The *p*-value of the enrichment was obtained using a hypergeometric test.