

## Supplementary Material

**Table S1. Details of markers, AgePlex sequences to analyze, CpG sites and location of the prediction model.**

<b>marker</b>	<b>Sequence to analyze</b>	<b>CpG site</b>	<b>Location (GRCh38)</b>
<b>ELOVL2</b>	CCRTAAACRTTAAACCRCCRCRCRAAACCRAC	C7	Chr6: 11044661
<b>C1orf132</b>	AAATCTACRCAAACRACRATAAATAATCC	C1	Chr1: 207823681
<b>TRIM59</b>	GGTTTGGYGYGGGAYGAGGYGAAGYGTYYG TGGTYGAYGGTTTTTGAGGAATTATTTTTTATTT	C7	Chr3: 160450199
<b>KLF14</b>	TYGYGTTTTTTTTTTTGTYYGGYAGTTAGGTA ATGGTAATAGAG	C1	Chr7: 130734355
<b>FHL2</b>	AGTTATYGGGAGYGTYYGTTTTYGGYGTGGG TTTTYGGGYGYGAGTTTTYGGAYGAGGTTTGGG	C2	Chr2: 105399288

**Table S2. LTL and Telomerase expression at enrolment T0 and after 60 days of relaxing practices T1.**

	T0	T1	<i>p</i> <sup>§</sup>
<b>LTL mean (SD)</b>			
<b>All subjects</b>	1.57 (0.38)	1.40 (0.38)	0.081
<b>Patients</b>	1.49 (0.34)	1.25 (0.20)	<b>0.051</b>
<b>Healthy subjects</b>	1.75 (0.43)	1.73 (0.49)	0.926
<b>Telomerase mean (SD)</b>			
<b>All subjects</b>	1.26 (0.86)	1.16 (0.57)	0.537
<b>Patients</b>	1.43 (0.89)	1.19 (0.66)	0.224
<b>Healthy subjects</b>	0.85 (0.66)	1.09 (0.31)	0.339

<sup>§</sup>Paired t tests