

Supporting Information

Atzmon et al. 10.1073/pnas.0906191106

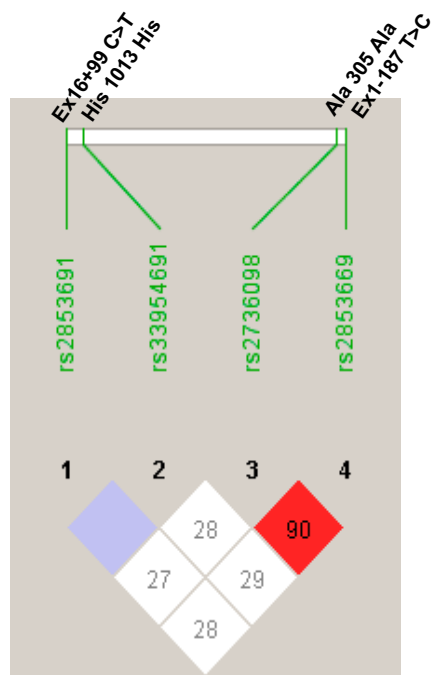


Fig. S1. Schematic view of LD structure for the 4 single-nucleotide polymorphisms of hTERT genotyped in our cohort. LD calculations were based on pairwise D' values of our entire centenarian and control dataset computed by the program HAPLOVIEW (1).

1. Barrett JC, Fry B, Maller J, Daly MJ (2005) HAPLOVIEW: analysis and visualization of LD and haplotype maps. *Bioinformatics* 21:263–265.

Table S1. Association analysis of common hTERT or hTERC variants with telomere length

	Nucleotide change	Protein change	P value
<i>hTERT</i>			
Synonymous	973 G > A	Ala 305 Ala	0.72
	3097 C > T	His 1013 His	0.63
Intronic	IVS1–187 T > C		0.59
3'UTR	IVS16+99 C > T		0.11
<i>hTERC</i>			
	IVS+63 T > C		0.99

Table S2. Primers for 2D gene scanning

Exon	Forward	Reverse	Size, bp
<i>hTERT</i>			
Long-distance PCR			
1–2	CTGTGTCAAGGAGCCCAAGT	CTCTATTCCCACCCTTGAA	2,786
3	GATGTGCAGTGACGGATGG	GGAAAGGCAAGGAGGCTAGT	888
4–6	CCGTGCCTTTTCTACTCTGC	CAGGAAGGTACCACCAGCAT	2,948
7–8	GGAGTCCCAGGTGTGTCTGT	CTGGAGACGATCCCAGAGAG	2,176
9–11	CGGGTCAAGTGTCTGGTTCT	GAGAGACTCACGCCAAAAG	4,998
12–13	TGGAGTTTGGTCATGCAGAG	ACACTCTTCTCAGCCCTCA	2,982
14–16	CAAAGTCCCAGGAAGCTGAG	CGGGCCTGGACTTACTGTTA	3,460
Short-distance PCR			
2.1	CGCAGGCGACTCAGGGCGCT	GGGTCCACTAGCGTGTGGCG	430
2.2	CCGCTGTACCAGCTCGGCGC	GCGCGTGCCAGAGAGCGCAC	400
2.3	TCACCTGCCAGACCCGCCGA	TGGTCCCAAGCAGCTCCAG	420
2.4	GCCGCCTGCCCCAGCGTACT	CTTCTTGGTGTCTGAGGA	385
2.5	CCCCAGGCCTCTGGGGCTC	GCTCTGGGGCCTGGGCCCTC	239
3	ATGTGGCATGTCCTTCTCGT	GAGGCCTGGCGTGGGATAAC	286
6	CTCCACTCACACAGGTGGAT	ATATCCAGAGACACACATC	260
7	AGGCCACATTTGTGGCTCAT	CTGGGAGTCCGTGCCAACC	216
8	CTCCCATGTGTCTCCCGTCT	CAGCCCGCCCAGCCACCCGC	206
9	CAGCACATGCCCTGCCCGTC	AAAGCAAATCAACCCCCACC	249
10	GTGTAAGTTAACCTTGCTG	TGGAGGTCCCCACAGACACA	187
11	TACCTCTGGGTGACGGCCC	GCACCTGCCAGCCGGGCA	334
12	GCTGGGTGTGGGGCAGGCAC	CTTGCGCACACACCTCCTGA	272
13	AAATCCCAGAGAGGTTTCTA	CTGGGCCTGCACCCCTTGGT	182
14	ACCCACGAGCACCGTCTGAT	TGACACACTAACACCAGCAG	290
15	GGGCTGGGCCTGTGACTCCT	TGGGCAGGTGGGGCCCGCAC	268
16.1	CTGGAACGGAGTCTGATTTT	GGGCTGTGGTGTCTGTCTCT	229
16.2	AAGACCATCCTGGACTGATG	ACAATGGGAATCTGGGGAT	410
<i>hTERC</i>			
Long-distance PCR			
	CGGAAGTAAAGACGCAAAGC	CATTCATTTTGCCGACTTT	
Short-distance PCR			
Frag1	AAGCCGACTCGCCCGGCAGC	GGGAGGGGCGAACGGGCCAG	
Frag2	ATGTCAGCTGCTGGCCCGTT	GCGTCCCCCACCACAGG	