

Supplementary Table S1: Clinical characteristics of the three study groups

Clinical characteristics	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	P value		
				HAPE-p vs HAPE-f	HLs vs HAPE-f	HAPE-p vs HLs
Age, years	26.5±7.4	34.8±8.8	39.2±10.7	<0.001	<0.001	<0.001
Gender	M = 203 (97%)	M = 156 (85%)	M = 53 (26%)	<0.001	<0.001	<0.001
	F = 7 (3%)	F = 27 (15%)	F = 147 (74%)			
BMI, kg/m ²	19.7±2.9	25.7±5.0	21.2±3.4	<0.001	<0.001	<0.001
SBP, mmHg	120.1±13.6	122.8±13.1	119.3±14.5	0.004	0.056	0.369
DBP, mmHg	80.8±9.9	83.6±11.6	76.1±10.5	0.602	0.0004	1.81 × 10 ⁻⁵
MAP, mmHg	93.9±10.4	96.7±10.6	90.5±11.0	0.117	0.002	0.001
SaO ₂ , %	90.1±7.1	70.8±9.4	87.7±3.9	3.60 × 10 ⁻⁴³	0.235	3.86 × 10 ⁻⁴⁶

The data are represented as mean±SD (standard deviation) and gender is represented as number of samples (percentage). Unpaired Student's t-test was used to compare age, gender, and BMI between any two groups using Epi Info™ ver. 6. General linear model was used to compare SBP, DBP, MAP and SaO₂ between the two groups after adjusting with age, gender, and BMI using SPSS 16.0. A P value of ≤0.05 was considered statistically significant. n, number of samples; M, male; F, female; BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; MAP, mean arterial pressure; SaO₂, arterial oxygen saturation.

Supplementary Table S2: Position of the selected SNPs on the genes

Gene	SNPs					
	Promoter	5'UTR	3'UTR	Exonic	Intronic	Total number of SNPs
<i>TERF1</i>	2	-	1	1	2	6
<i>TERF2</i>	3	-	-	-	2	5
<i>POT1</i>	2	-	2	1	2	7
<i>TINF2</i>	2	-	-	-	-	2
<i>ACD</i>	1	-	1	2	-	4
<i>TERF2IP</i>	4	1	-	1	-	6
<i>TERC</i>	-	-	-	2	-	2
<i>TERT</i>	6	-	-	4	6	16
<i>TEP1</i>	2	-	-	6	1	9
<i>HSP90AA1</i>	1	-	2	2	-	5
<i>PTGES3</i>	2	-	1	-	-	3

Supplementary Table S3: qRT-PCR primers for gene expression profiling

Gene	Forward Primer	Reverse Primer
<i>TERF1</i>	5' GCAGAATACCTGTTTCAAAGAG 3'	5' GTTCCCTCTCCATATTTTCCT 3'
<i>TERF2</i>	5' ATATGAGACCTTCCAGCAG 3'	5' TTCCTTCCCTGTACTTGAG 3'
<i>POT1</i>	5' GATTTAAGTCACATCCATCGG 3'	5' GAAAGCTTCCAACCTTCAG 3'
<i>TINF2</i>	5' GAGAAAGCACTGCCTACAC 3'	5' TCCACACCATATTGTCTCCA 3'
<i>ACD</i>	5' TGGAGTTCAAGGAGTTTGTAG 3'	5' GTGGCTCATACTCATACTGGA 3'
<i>TERF2IP</i>	5' CCAGATTTGCCTGAAGAAGAG 3'	5' CTCTCATCCACCACAACCT 3'
<i>TERT</i>	5' GAATCAGACAGCACTTGAAGAG 3'	5' GTAGTCCATGTTTACAATCGG 3'
<i>TERC</i>	5' TAACTGAGAAGGGCGTAGG 3'	5' TTGCTCTAGAATGAACGGTG 3'
<i>TEP1</i>	5' CGGAAATTTGAGTCTTCACCT 3'	5' GCCAAGATGAGAAAGTGACC 3'
<i>HSP90AA1</i>	5' AGATAAACCTGACCATTCC 3'	5' CTTCAATCAATACCCAGACCA 3'
<i>PTGES3</i>	5' GATCCAAATGATTCCAAGCA 3'	5' TCTGAATCATCTTCCCAGTC 3'
<i>RN18S1</i>	5' - GCTTAATTTGACTCAACAC - 3'	5' - AGCTATCAATCTGTCAAT C - 3'

All the primers were designed to work at 60°C annealing temperature.

Supplementary Table S4: Genotype and allele distribution of 4 SNPs of *TERF1*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>TERF1</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2929589	Codominant	CC	75 (35.7%)	60 (32.8%)	15 (7.5%)	Ref	-	Ref	-	Ref	-
		CT	101 (48.1%)	83 (45.4%)	89 (44.5%)	0.975	0.99 (0.60-1.65)	0.005	4.15 (1.52-11.31)	0.002	0.31 (0.14-0.66)
		TT	34 (16.2%)	40 (21.9%)	96 (48.0%)	0.180	1.54 (0.82-2.92)	5.90×10^{-6}	10.83 (3.86-30.35)	1.48×10^{-6}	0.13 (0.06-0.30)
	Additive	C	251 (59.8%)	203 (55.5%)	119 (29.8%)	Ref	-	Ref	-	Ref	-
		T	169 (40.2%)	163 (44.5%)	281 (70.2%)	0.227	1.22 (0.88-1.68)	1.66×10^{-6}	3.27 (2.01-5.31)	1.94×10^{-7}	0.38 (0.26-0.54)
	Dominant	CC	75 (35.7%)	60 (32.8%)	15 (7.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	135 (64.3%)	123 (67.2%)	185 (92.5%)	0.608	1.13 (0.70-1.82)	2.13×10^{-4}	6.69 (2.45-18.30)	4.22×10^{-5}	0.22 (0.11-0.45)
	Recessive	CC+CT	176 (83.8%)	143 (78.1%)	104 (52.0%)	Ref	-	Ref	-	Ref	-
		TT	34 (16.2%)	40 (21.9%)	96 (48.0%)	0.125	1.57 (0.88-2.80)	9.05×10^{-5}	4.19 (2.04-8.58)	3.74×10^{-5}	0.32 (0.18-0.55)
	Overdominant	CC+TT	109 (51.9%)	100 (54.6%)	111 (55.5%)	Ref	-	Ref	-	Ref	-
		CT	101 (48.1%)	83 (45.4%)	89 (44.5%)	0.477	0.85 (0.54-1.33)	0.654	0.86 (0.45-1.65)	0.551	1.17 (0.70-1.94)
rs2975843	Codominant	TT	76 (36.2%)	61 (33.3%)	112 (56.0%)	Ref	-	Ref	-	Ref	-
		TC	97 (46.2%)	82 (44.8%)	81 (40.5%)	0.729	0.91 (0.55-1.52)	0.046	0.46 (0.22-0.99)	0.033	1.82 (1.05-3.16)
		CC	37 (17.6%)	40 (21.9%)	7 (3.5%)	0.806	1.08 (0.57-2.06)	0.007	0.15 (0.04-0.60)	2.98×10^{-5}	9.07 (3.22-25.55)
	Additive	T	249 (59.3%)	204 (55.7%)	305 (76.2%)	Ref	-	Ref	-	Ref	-
		C	171 (40.7%)	162 (44.3%)	95 (23.8%)	0.882	1.02 (0.74-1.42)	0.003	0.46 (0.28-0.76)	1.35×10^{-5}	2.35 (1.60-3.45)
	Dominant	TT	76 (36.2%)	61 (33.3%)	112 (56.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	134 (63.8%)	122 (66.7%)	88 (44.0%)	0.895	0.97 (0.60-1.56)	0.010	0.42 (0.21-0.81)	0.001	2.37 (1.42-3.96)
	Recessive	TT+TC	173 (82.4%)	143 (78.1%)	193 (96.5%)	Ref	-	Ref	-	Ref	-
		CC	37 (17.6%)	40 (21.9%)	7 (3.5%)	0.677	1.13 (0.64-1.98)	0.022	0.22 (0.06-0.80)	1.94×10^{-4}	6.29 (2.39-16.55)
	Overdominant	TT+CC	113 (53.8%)	101 (55.2%)	119 (59.5%)	Ref	-	Ref	-	Ref	-
		TC	97 (46.2%)	82 (44.8%)	81 (40.5%)	0.647	0.90 (0.57-1.42)	0.285	0.70 (0.36-1.35)	0.513	1.19 (0.71-1.97)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2929586	Codominant	TT	77 (36.7%)	60 (32.8%)	18 (9.0%)	Ref	-	Ref	-	Ref	-
		TC	101 (48.1%)	83 (45.3%)	89 (44.5%)	0.933	0.98 (0.59-1.62)	0.054	2.42 (0.99-5.92)	0.014	0.40 (0.19-0.83)
		CC	32 (15.2%)	40 (21.9%)	93 (46.5%)	0.123	1.66 (0.87-3.17)	2.95×10^{-5}	8.38 (3.09-22.72)	1.22×10^{-5}	0.18 (0.08-0.39)
	Additive	T	255 (60.7%)	203 (55.5%)	125 (31.2%)	Ref	-	Ref	-	Ref	-
		C	165 (39.3%)	163 (44.5%)	275 (68.8%)	0.169	1.25 (0.91-1.73)	6.29×10^{-6}	3.00 (1.86-4.84)	2.58×10^{-6}	0.42 (0.29-0.60)
	Dominant	TT	77 (36.7%)	60 (32.8%)	18 (9.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	133 (63.3%)	123 (67.2%)	182 (91.0%)	0.583	1.14 (0.71-1.83)	0.002	3.94 (1.65-9.41)	3.84×10^{-4}	0.29 (0.15-0.57)
	Recessive	TT+TC	178 (84.8%)	143 (78.1%)	107 (53.5%)	Ref	-	Ref	-	Ref	-
		CC	32 (15.2%)	40 (21.9%)	93 (46.5%)	0.071	1.71 (0.95-3.08)	4.80×10^{-5}	4.59 (2.20-9.56)	1.11E-04	0.34 (0.20-0.59)
	Overdominant	TT+CC	109 (51.9%)	100 (54.7%)	111 (55.5%)	Ref	-	Ref	-	Ref	-
		TC	101 (48.1%)	83 (45.3%)	89 (44.5%)	0.386	0.82 (0.52-1.29)	0.302	0.71 (0.37-1.36)	0.454	1.21 (0.73-2.02)
rs10099824	Codominant	GG	92 (43.8%)	81 (44.3%)	168 (84.0%)	Ref	-	Ref	-	Ref	-
		GA	87 (41.4%)	78 (42.6%)	28 (14.0%)	0.762	0.93 (0.56-1.53)	5.52×10^{-6}	0.06 (0.02-0.20)	4.46×10^{-9}	7.71 (3.90-15.27)
		AA	31 (14.8%)	24 (13.1%)	4 (2.0%)	0.256	0.67 (0.33-1.34)	4.49×10^{-5}	0.02 (0.003-0.13)	1.77×10^{-4}	11.08 (3.15-38.96)
	Additive	G	271 (64.5%)	240 (65.6%)	364 (91.0%)	Ref	-	Ref	-	Ref	-
		A	149 (35.5%)	126 (34.4%)	36 (9.0%)	0.285	0.83 (0.59-1.17)	7.28×10^{-11}	0.07 (0.03-0.15)	7.05×10^{-12}	5.96 (3.58-9.92)
	Dominant	GG	92 (43.8%)	81 (44.3%)	168 (84.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	118 (56.2%)	102 (55.7%)	32 (16.0%)	0.527	0.86 (0.55-1.36)	2.37×10^{-8}	0.06 (0.02-0.16)	6.54×10^{-11}	8.04 (4.30-15.02)
	Recessive	GG+GA	179 (85.2%)	159 (86.9%)	196 (98.0%)	Ref	-	Ref	-	Ref	-
		AA	31 (14.8%)	24 (13.1%)	4 (2.0%)	0.230	0.66 (0.33-1.30)	1.95×10^{-4}	0.03 (0.01-0.20)	0.003	6.70 (1.89-23.70)
	Overdominant	GG+AA	123 (58.6%)	105 (57.4%)	172 (86.0%)	Ref	-	Ref	-	Ref	-
		GA	87 (41.4%)	78 (42.6%)	28 (14.0%)	0.851	1.04 (0.66-1.65)	3.20×10^{-5}	0.13 (0.05-0.34)	9.06×10^{-8}	5.88 (3.07-11.25)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TERF1*, telomere repeat binding factor 1; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TERF1</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs2929589	CC	13 (6.3%)	5 (4.8%)	15 (7.5%)	Ref	-	Ref	-
	CT	86 (41.3%)	33 (31.7%)	89 (44.5%)	0.790	0.90 (0.40-2.00)	1.000	0.90 (0.30-2.67)
	TT	109 (52.4%)	66 (63.5%)	96 (48.0%)	0.503	0.76 (0.35-1.69)	0.227	0.48 (0.17-1.40)
	C	112 (26.9%)	43 (20.7%)	119 (29.8%)	Ref	-	Ref	-
	T	304 (73.1%)	165 (79.3%)	281 (70.2%)	0.370	0.87 (0.64-1.18)	0.016	0.62 (0.41-0.92)
rs2975843	TT	141 (67.8%)	82 (78.8%)	112 (56.0%)	Ref	-	Ref	-
	TC	64 (30.8%)	22 (21.2%)	81 (40.5%)	0.026	1.59 (1.06-2.40)	3.24×10^{-4}	2.70 (1.55-4.68)
	CC	3 (1.4%)	0 (0.0%)	7 (3.5%)	0.193	2.94 (0.74-11.62)	*	-
	T	346 (83.2%)	186 (89.4%)	305 (76.3%)	Ref	-	Ref	-
	C	70 (16.8%)	22 (10.6%)	95 (23.8%)	0.014	1.54 (1.09-2.17)	9.30×10^{-5}	2.63 (1.60-4.33)
rs2929586	TT	14 (6.7%)	7 (6.7%)	18 (9.0%)	Ref	-	Ref	-
	TC	90 (43.3%)	39 (37.5%)	89 (44.5%)	0.496	0.77 (0.36-1.64)	0.806	0.89 (0.34-2.30)
	CC	104 (50.0%)	58 (55.8%)	93 (46.5%)	0.342	0.70 (0.33-1.48)	0.318	0.62 (0.25-1.59)
	T	118 (28.4%)	53 (25.5%)	125 (31.3%)	Ref	-	Ref	-
	C	298 (71.6%)	155 (74.5%)	275 (68.8%)	0.368	0.87 (0.65-1.18)	0.138	0.75 (0.52-1.10)
rs10099824	GG	151 (72.6%)	77 (74.0%)	168 (84.0%)	Ref	-	Ref	-
	GA	52 (25.0%)	25 (24.0%)	28 (14.0%)	0.005	0.48 (0.29-0.81)	0.029	0.51 (0.28-0.94)
	AA	5 (2.4%)	2 (1.9%)	4 (2.0%)	0.741	0.72 (0.19-2.73)	1.000	0.92 (0.16-5.11)
	G	354 (85.1%)	179 (86.1%)	364 (91.0%)	Ref	-	Ref	-
	A	62 (14.9%)	29 (13.9%)	36 (9.0%)	0.010	0.56 (0.37-0.87)	0.061	0.61 (0.36-1.03)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of a genotype were absent in a study group. *TERF1*, telomere repeat binding factor 1; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S5: Genotype and allele distribution of 5 SNPs of *TERF2*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>TERF2</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs3785073	Codominant	GG	99 (47.2%)	76 (41.5%)	108 (54.0%)	Ref	-	Ref	-	Ref	-
		GA	83 (39.5%)	86 (47.0%)	80 (40.0%)	0.864	1.04 (0.64-1.71)	0.033	0.44 (0.20-0.94)	0.001	2.64 (1.51-4.62)
		AA	28 (13.3%)	21 (11.5%)	12 (6.0%)	0.899	0.96 (0.47-1.94)	0.018	0.16 (0.03-0.73)	0.070	2.70 (0.92-7.90)
	Additive	G	281 (66.9%)	238 (65.0%)	296 (74.0%)	Ref	-	Ref	-	Ref	-
		A	139 (33.1%)	128 (35.0%)	104 (26.0%)	0.994	1.00 (0.71-1.40)	0.002	0.43 (0.24-0.74)	0.001	1.94 (1.30-2.90)
	Dominant	GG	99 (47.2%)	76 (41.5%)	108 (54.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	111 (52.8%)	107 (58.5%)	92 (46.0%)	0.874	1.04 (0.66-1.63)	0.009	0.40 (0.20-0.79)	3.31 × 10 ⁻⁴	2.67 (1.56-4.55)
	Recessive	GG+GA	182 (86.7%)	162 (88.5%)	188 (94.0%)	Ref	-	Ref	-	Ref	-
		AA	28 (13.3%)	21 (11.5%)	12 (6.0%)	0.823	0.92 (0.47-1.84)	0.041	0.21 (0.05-0.94)	0.298	1.66 (0.64-4.32)
	Overdominant	GG+AA	127 (60.5%)	97 (53.0%)	120 (60.0%)	Ref	-	Ref	-	Ref	-
		GA	83 (39.5%)	86 (47.0%)	80 (40.0%)	0.756	1.08 (0.68-1.70)	0.124	0.58 (0.29-1.16)	0.002	2.35 (1.36-4.05)
rs8061352	Codominant	TT	101 (48.1%)	70 (38.2%)	107 (53.5%)	Ref	-	Ref	-	Ref	-
		TA	82 (39.0%)	94 (51.4%)	80 (40.0%)	0.021	1.78 (1.09-2.89)	0.501	0.78 (0.38-1.60)	1.67 × 10 ⁻⁴	2.92 (1.67-5.11)
		AA	27 (12.9%)	19 (10.4%)	13 (6.5%)	0.693	1.16 (0.56-2.39)	0.116	0.37 (0.11-1.28)	0.090	2.47 (0.87-7.04)
	Additive	T	284 (67.6%)	234 (63.9%)	294 (73.5%)	Ref	-	Ref	-	Ref	-
		A	136 (32.4%)	132 (36.1%)	106 (26.5%)	0.155	1.28 (0.91-1.79)	0.116	0.65 (0.38-1.11)	0.001	1.97 (1.32-2.93)
	Dominant	TT	101 (48.1%)	70 (38.2%)	107 (53.5%)	Ref	-	Ref	-	Ref	-
		TA+AA	109 (51.9%)	113 (61.8%)	93 (46.5%)	0.036	1.63 (1.03-2.59)	0.248	0.68 (0.35-1.31)	1.12 × 10 ⁻⁴	2.87 (1.68-4.91)
	Recessive	TT+TA	183 (87.1%)	164 (89.6%)	187 (93.5%)	Ref	-	Ref	-	Ref	-
		AA	27 (12.9%)	19 (10.4%)	13 (6.5%)	0.769	0.90 (0.44-1.82)	0.155	0.38 (0.10-1.43)	0.440	1.45 (0.56-3.76)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs153058	Codominant	TT	129 (61.4%)	107 (58.5%)	92 (46.0%)	Ref	-	Ref	-	Ref	-
		TC	73 (34.8%)	65 (35.5%)	84 (42.0%)	0.680	1.11 (0.69-1.79)	0.178	1.61 (0.80-3.24)	0.047	0.58 (0.33-0.99)
		CC	8 (3.8%)	11 (6.0%)	24 (12.0%)	0.164	2.07 (0.74-5.79)	0.015	4.59 (1.35-15.63)	0.015	0.31 (0.12-0.80)
	Additive	T	331 (78.8%)	279 (76.2%)	268 (67.0%)	Ref	-	Ref	-	Ref	-
		C	89 (21.2%)	87 (23.8%)	132 (33.0%)	0.253	1.25 (0.85-1.82)	0.014	1.89 (1.14-3.15)	0.004	0.55 (0.37-0.83)
	Dominant	TT	129 (61.4%)	107 (58.5%)	92 (46.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	81 (38.6%)	76 (41.5%)	108 (54.0%)	0.440	1.20 (0.76-1.89)	0.054	1.91 (0.99-3.67)	0.012	0.52 (0.31-0.86)
	Recessive	TT+TC	202 (96.2%)	172 (94.0%)	176 (88.0%)	Ref	-	Ref	-	Ref	-
		CC	8 (3.8%)	11 (6.0%)	24 (12.0%)	0.179	2.00 (0.73-5.47)	0.028	3.86 (1.16-12.82)	0.038	0.38 (0.15-0.95)
	Overdominant	TT+CC	137 (65.2%)	118 (64.5%)	116 (58.0%)	Ref	-	Ref	-	Ref	-
		TC	73 (34.8%)	65 (35.5%)	84 (42.0%)	0.870	1.04 (0.65-1.67)	0.443	1.30 (0.67-2.51)	0.160	0.69 (0.41-1.16)
rs113062367	Codominant	TT	141 (67.1%)	128 (69.9%)	146 (73.0%)	Ref	-	Ref	-	Ref	-
		TC	63 (30.0%)	51 (27.9%)	49 (24.5%)	0.699	1.11 (0.66-1.85)	0.288	0.64 (0.29-1.45)	0.921	1.03 (0.58-1.83)
		CC	6 (2.9%)	4 (2.2%)	5 (2.5%)	0.051	0.17 (0.03-1.01)	0.052	0.14 (0.02-1.02)	0.710	0.73 (0.14-3.86)
	Additive	T	345 (82.1%)	307 (83.9%)	341 (85.2%)	Ref	-	Ref	-	Ref	-
		C	75 (17.9%)	59 (16.1%)	59 (14.8%)	0.493	0.86 (0.56-1.33)	0.064	0.54 (0.28-1.04)	0.868	0.96 (0.59-1.57)
	Dominant	TT	141 (67.1%)	128 (69.9%)	146 (73.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	69 (32.9%)	55 (30.1%)	54 (27.0%)	0.871	0.96 (0.59-1.57)	0.159	0.59 (0.28-1.23)	0.977	0.99 (0.57-1.73)
	Recessive	TT+TC	204 (97.1%)	179 (97.8%)	195 (97.5%)	Ref	-	Ref	-	Ref	-
		CC	6 (2.9%)	4 (2.2%)	5 (2.5%)	0.043	0.17 (0.03-0.95)	0.029	0.10 (0.01-0.79)	0.608	0.63 (0.11-3.66)
	Overdominant	TT+CC	147 (70.0%)	132 (72.1%)	151 (75.5%)	Ref	-	Ref	-	Ref	-
		TC	63 (30.0%)	51 (27.9%)	49 (24.5%)	0.644	1.12 (0.68-1.85)	0.458	0.76 (0.36-1.58)	0.895	1.04 (0.59-1.83)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs4783704	Codominant	CC	121 (57.6%)	119 (65.0%)	103 (51.5%)	Ref	-	Ref	-	Ref	-
		CT	72 (34.3%)	52 (28.4%)	81 (40.5%)	0.344	0.79 (0.48-1.29)	0.452	1.31 (0.65-2.65)	0.143	0.66 (0.38-1.15)
		TT	17 (8.1%)	12 (6.6%)	16 (8.0%)	0.956	0.98 (0.40-2.38)	0.142	2.26 (0.76-6.68)	0.025	0.35 (0.14-0.88)
	Additive	C	314 (74.8%)	290 (79.2%)	287 (71.8%)	Ref	-	Ref	-	Ref	-
		T	106 (25.2%)	76 (20.8%)	113 (28.2%)	0.533	0.89 (0.61-1.30)	0.108	1.53 (0.91-2.56)	0.009	0.58 (0.38-0.87)
	Dominant	CC	121 (57.6%)	119 (65.0%)	103 (51.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	89 (42.4%)	64 (35.0%)	97 (48.5%)	0.400	0.82 (0.52-1.30)	0.232	1.49 (0.77-2.88)	0.037	0.58 (0.35-0.97)
	Recessive	CC+CT	193 (91.9%)	171 (93.4%)	184 (92.0%)	Ref	-	Ref	-	Ref	-
		TT	17 (8.1%)	12 (6.6%)	16 (8.0%)	0.879	1.07 (0.45-2.56)	0.148	2.25 (0.75-6.75)	0.042	0.40 (0.16-0.97)
	Overdominant	CC+TT CT	138 (65.7%) 72 (34.3%)	131 (71.6%) 52 (28.4%)	119 (59.5%) 81 (40.5%)	Ref 0.335	- 0.79 (0.48-1.28)	Ref 0.694	- 1.15 (0.58-2.23)	Ref 0.321	- 0.76 (0.45-1.30)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TERF2*, telomere repeat binding factor 2; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TERF2</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs3785073	GG	171 (82.2%)	86 (82.7%)	108 (54.0%)	Ref	-	Ref	-
	GA	34 (16.3%)	18 (17.3%)	80 (40.0%)	<0.000001	3.73 (2.33-5.95)	1.20×10^{-5}	3.54 (1.97-6.35)
	AA	3 (1.4%)	0 (0.0%)	12 (6.0%)	0.002	6.33 (1.75-22.96)	*	-
	G	376 (90.4%)	190 (91.3%)	296 (74.0%)	Ref	-	Ref	-
	A	40 (9.6%)	18 (8.7%)	104 (26.0%)	<0.000001	3.30 (2.23-4.90)	<0.000001	3.71 (2.18-6.32)
rs8061352	TT	171 (82.2%)	86 (82.7%)	107 (53.5%)	Ref	-	Ref	-
	TA	34 (16.3%)	18 (17.3%)	80 (40.0%)	<0.000001	3.76 (2.35-6.01)	1.10×10^{-5}	3.57 (1.99-6.41)
	AA	3 (1.4%)	0 (0.0%)	13 (6.5%)	0.001	6.93 (1.93-24.87)	*	-
	T	376 (90.4%)	190 (91.3%)	294 (73.5%)	Ref	-	Ref	-
	A	40 (9.6%)	18 (8.7%)	106 (26.5%)	<0.000001	3.39 (2.29-5.03)	<0.000001	3.81 (2.24-6.48)
rs153058	TT	65 (31.3%)	32 (30.8%)	92 (46.0%)	Ref	-	Ref	-
	TC	103 (49.5%)	52 (50.0%)	84 (42.0%)	0.011	0.58 (0.38-0.89)	0.032	0.56 (0.33-0.96)
	CC	40 (19.2%)	20 (19.2%)	24 (12.0%)	0.004	0.42 (0.23-0.77)	0.015	0.42 (0.20-0.86)
	T	233 (56.0%)	116 (55.8%)	268 (67.0%)	Ref	-	Ref	-
	C	183 (44.0%)	92 (44.2%)	132 (33.0%)	0.001	0.63 (0.47-0.83)	0.006	0.62 (0.44-0.88)
rs113062367	TT	208 (100%)	104 (100%)	146 (73.0%)	Ref	-	Ref	-
	TC	0 (0%)	0 (0%)	49 (24.5%)	*	-	*	-
	CC	0 (0%)	0 (0%)	5 (2.5%)	*	-	*	-
	T	416 (100.0%)	208 (100.0%)	341 (85.3%)	Ref	-	Ref	-
	C	0 (0.0%)	0 (0.0%)	59 (14.8%)	*	-	*	-

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs4783704	CC	138 (66.3%)	80 (76.9%)	103 (51.5%)	Ref	-	Ref	-
	CT	64 (30.8%)	23 (22.1%)	81 (40.5%)	0.012	1.70 (1.12-2.57)	2.45×10^{-4}	2.74 (1.58-4.73)
	TT	6 (2.9%)	1 (1.0%)	16 (8.0%)	0.007	3.57 (1.35-9.45)	0.002	12.43 (1.61-95.70)
	C	340 (81.7%)	183 (88.0%)	287 (71.8%)	Ref	-	Ref	-
	T	76 (18.3%)	25 (12.0%)	113 (28.3%)	0.001	1.76 (1.27-2.45)	6.00×10^{-6}	2.88 (1.80-4.62)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of a genotype and/or allele were absent in a study group. *TERF2*, telomere repeat binding factor 2; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S6: Genotype and allele distribution of 7 SNPs of *POT1*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>POT1</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs727505	Codominant	CC	116 (55.3%)	95 (51.9%)	113 (56.5%)	Ref	-	Ref	-	Ref	-
		CT	83 (39.5%)	84 (45.9%)	71 (35.5%)	0.010	1.88 (1.16-3.05)	0.773	1.11 (0.54-2.28)	0.083	1.59 (0.94-2.69)
		TT	11 (5.2%)	4 (2.2%)	16 (8.0%)	0.258	0.47 (0.13-1.74)	0.988	1.01 (0.27-3.76)	0.112	0.34 (0.09-1.28)
	Additive	C	315 (75.0%)	274 (74.9%)	297 (74.2%)	Ref	-	Ref	-	Ref	-
		T	105 (25.0%)	92 (25.1%)	103 (25.8%)	0.204	1.27 (0.88-1.83)	0.865	1.05 (0.60-1.82)	0.754	1.07 (0.71-1.61)
	Dominant	CC	116 (55.3%)	95 (51.9%)	113 (56.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	94 (44.7%)	88 (48.1%)	87 (43.5%)	0.031	1.67 (1.05-2.66)	0.824	1.08 (0.55-2.11)	0.223	1.37 (0.83-2.28)
	Recessive	CC+CT	199 (94.8%)	179 (97.8%)	184 (92.0%)	Ref	-	Ref	-	Ref	-
		TT	11 (5.2%)	4 (2.2%)	16 (8.0%)	0.134	0.35 (0.09-1.38)	0.971	0.97 (0.23-4.09)	0.053	0.27 (0.07-1.02)
	Overdominant	CC+TT	127 (60.5%)	99 (54.1%)	129 (64.5%)	Ref	-	Ref	-	Ref	-
		CT	83 (39.5%)	84 (45.9%)	71 (35.5%)	0.006	1.94 (1.21-3.10)	0.805	1.09 (0.55-2.17)	0.038	1.73 (1.03-2.92)
rs17246404	Codominant	CC	122 (58.1%)	107 (58.5%)	120 (60.0%)	Ref	-	Ref	-	Ref	-
		CT	76 (36.2%)	65 (35.5%)	60 (30.0%)	0.456	1.20 (0.74-1.95)	0.359	0.70 (0.33-1.49)	0.159	1.49 (0.86-2.58)
		TT	12 (5.7%)	11 (6.0%)	20 (10.0%)	0.686	0.82 (0.31-2.16)	0.884	0.91 (0.27-3.10)	0.477	0.71 (0.28-1.83)
	Additive	C	320 (76.2%)	279 (76.2%)	300 (75.0%)	Ref	-	Ref	-	Ref	-
		T	100 (23.8%)	87 (23.8%)	100 (25.0%)	0.871	1.03 (0.71-1.50)	0.438	0.80 (0.46-1.40)	0.725	1.08 (0.71-1.63)
	Dominant	CC	122 (58.1%)	107 (58.5%)	120 (60.0%)	Ref	-	Ref	-	Ref	-
		CT+TT	88 (41.9%)	76 (41.5%)	80 (40.0%)	0.625	1.12 (0.71-1.77)	0.363	0.73 (0.37-1.44)	0.325	1.30 (0.77-2.17)
	Recessive	CC+CT	198 (94.3%)	172 (94.0%)	180 (90.0%)	Ref	-	Ref	-	Ref	-
		TT	12 (5.7%)	11 (6.0%)	20 (10.0%)	0.532	0.73 (0.27-1.97)	0.949	0.96 (0.26-3.47)	0.314	0.62 (0.24-1.58)
	Overdominant	CC+TT	134 (63.8%)	118 (64.5%)	140 (70.0%)	Ref	-	Ref	-	Ref	-
		CT	76 (36.2%)	65 (35.5%)	60 (30.0%)	0.424	1.21 (0.76-1.94)	0.357	0.71 (0.35-1.46)	0.109	1.56 (0.91-2.69)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs7794637	Codominant	CC	90 (42.9%)	63 (34.4%)	105 (52.5%)	Ref	-	Ref	-	Ref	-
		CT	95 (45.2%)	88 (48.1%)	82 (41.0%)	0.682	0.90 (0.54-1.49)	0.137	0.59 (0.29-1.19)	0.003	2.30 (1.32-4.00)
		TT	25 (11.9%)	32 (17.5%)	13 (6.5%)	0.297	1.43 (0.73-2.81)	0.010	0.18 (0.05-0.66)	0.003	4.22 (1.62-11.02)
	Additive	C	275 (65.5%)	214 (58.5%)	292 (73.0%)	Ref	-	Ref	-	Ref	-
		T	145 (34.5%)	152 (41.5%)	108 (27.0%)	0.480	1.13 (0.81-1.57)	0.010	0.51 (0.31-0.85)	2.62 × 10 ⁻⁴	2.04 (1.39-2.99)
	Dominant	CC	90 (42.9%)	63 (34.4%)	105 (52.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	120 (57.1%)	120 (65.6%)	95 (47.5%)	0.901	1.03 (0.65-1.64)	0.037	0.49 (0.25-0.96)	4.82 × 10 ⁻⁴	2.54 (1.51-4.29)
	Recessive	CC+CT	185 (88.1%)	151 (82.5%)	187 (93.5%)	Ref	-	Ref	-	Ref	-
		TT	25 (11.9%)	32 (17.5%)	13 (6.5%)	0.239	1.46 (0.78-2.75)	0.037	0.30 (0.10-0.93)	0.027	2.58 (1.11-5.98)
	Overdominant	CC+TT	115 (54.8%)	95 (51.9%)	118 (59.0%)	Ref	-	Ref	-	Ref	-
		CT	95 (45.2%)	88 (48.1%)	82 (41.0%)	0.466	0.84 (0.53-1.33)	0.438	0.77 (0.40-1.49)	0.039	1.72 (1.03-2.89)
rs116916706	Codominant	CC	155 (73.8%)	130 (71.0%)	143 (71.5%)	Ref	-	Ref	-	Ref	-
		CA	49 (23.3%)	50 (27.3%)	54 (27.0%)	0.370	1.28 (0.75-2.19)	0.758	1.14 (0.49-2.68)	0.552	1.19 (0.67-2.13)
		AA	6 (2.9%)	3 (1.7%)	3 (1.5%)	0.140	0.28 (0.05-1.52)	0.093	0.15 (0.02-1.37)	0.175	0.28 (0.04-1.76)
	Additive	C	359 (85.5%)	310 (84.7%)	340 (85.0%)	Ref	-	Ref	-	Ref	-
		A	61 (14.5%)	56 (15.3%)	60 (15.0%)	0.935	0.98 (0.62-1.55)	0.360	0.72 (0.36-1.45)	0.942	0.98 (0.59-1.62)
	Dominant	CC	155 (73.8%)	130 (71.0%)	143 (71.5%)	Ref	-	Ref	-	Ref	-
		CA+AA	55 (26.2%)	53 (29.0%)	57 (28.5%)	0.664	1.12 (0.67-1.86)	0.731	0.87 (0.41-1.88)	0.774	1.09 (0.62-1.90)
	Recessive	CC+CA	204 (97.1%)	180 (98.3%)	197 (98.5%)	Ref	-	Ref	-	Ref	-
		AA	6 (2.9%)	3 (1.7%)	3 (1.5%)	0.110	0.24 (0.04-1.37)	0.077	0.14 (0.02-1.24)	0.170	0.28 (0.05-1.73)
	Overdominant	CC+AA	161 (76.7%)	133 (72.7%)	146 (73.0%)	Ref	-	Ref	-	Ref	-
		CA	49 (23.3%)	50 (27.3%)	54 (27.0%)	0.325	1.30 (0.77-2.19)	0.715	1.16 (0.52-2.56)	0.504	1.22 (0.68-2.16)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs4360236	Codominant	CC	110 (52.4%)	97 (53.0%)	108 (54.0%)	Ref	-	Ref	-	Ref	-
		CT	81 (38.6%)	68 (37.2%)	77 (38.5%)	0.664	0.90 (0.54-1.48)	0.675	0.86 (0.42-1.77)	0.542	1.18 (0.69-2.00)
		TT	19 (9.0%)	18 (9.8%)	15 (7.5%)	0.997	1.00 (0.47-2.14)	0.100	0.39 (0.13-1.20)	0.673	0.83 (0.34-2.01)
	Additive	C	301 (71.7%)	262 (71.6%)	293 (73.2%)	Ref	-	Ref	-	Ref	-
		T	119 (28.3%)	104 (28.4%)	107 (26.8%)	0.804	0.96 (0.67-1.36)	0.114	0.66 (0.39-1.11)	0.954	1.01 (0.68-1.50)
	Dominant	CC	110 (52.4%)	97 (53.0%)	108 (54.0%)	Ref	-	Ref	-	Ref	-
		CT+TT	100 (47.6%)	86 (47.0%)	92 (46.0%)	0.721	0.92 (0.59-1.45)	0.313	0.71 (0.37-1.38)	0.685	1.11 (0.67-1.84)
	Recessive	CC+CT	191 (91.0%)	165 (90.2%)	185 (92.5%)	Ref	-	Ref	-	Ref	-
		TT	19 (9.0%)	18 (9.8%)	15 (7.5%)	0.948	1.03 (0.49-2.17)	0.099	0.40 (0.13-1.19)	0.558	0.77 (0.32-1.84)
	Overdominant	CC+TT	129 (61.4%)	115 (62.8%)	123 (61.5%)	Ref	-	Ref	-	Ref	-
		CT	81 (38.6%)	68 (37.2%)	77 (38.5%)	0.681	0.91 (0.57-1.45)	0.998	1.00 (0.51-1.98)	0.446	1.22 (0.73-2.06)
rs7782410	Codominant	GG	80 (38.1%)	70 (38.3%)	58 (29.0%)	Ref	-	Ref	-	Ref	-
		GA	103 (49.0%)	89 (48.6%)	96 (48.0%)	0.597	1.14 (0.70-1.88)	0.056	2.15 (0.98-4.72)	0.459	0.80 (0.45-1.43)
		AA	27 (12.9%)	24 (13.1%)	46 (23.0%)	0.610	1.19 (0.60-2.36)	0.002	4.20 (1.67-10.58)	0.003	0.32 (0.15-0.69)
	Additive	G	263 (62.6%)	229 (62.6%)	212 (53.0%)	Ref	-	Ref	-	Ref	-
		A	157 (37.4%)	137 (37.4%)	188 (47.0%)	0.490	1.12 (0.81-1.56)	0.001	2.26 (1.40-7.63)	0.006	0.60 (0.42-0.86)
	Dominant	GG	80 (38.1%)	70 (38.3%)	58 (29.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	130 (61.9%)	113 (61.7%)	142 (71.0%)	0.535	1.16 (0.73-1.85)	0.007	2.73 (1.31-5.71)	0.093	0.63 (0.37-1.08)
	Recessive	GG+GA	183 (87.1%)	159 (86.9%)	154 (77.0%)	Ref	-	Ref	-	Ref	-
		AA	27 (12.9%)	24 (13.1%)	46 (23.0%)	0.614	1.19 (0.61-2.30)	0.007	3.06 (1.36-6.87)	0.003	0.36 (0.19-0.71)
	Overdominant	GG+AA	107 (51.0%)	94 (51.4%)	104 (52.0%)	Ref	-	Ref	-	Ref	-
		GA	103 (49.0%)	89 (48.6%)	96 (48.0%)	0.793	1.06 (0.68-1.67)	0.643	1.17 (0.61-2.26)	0.474	1.20 (0.73-1.99)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs10244797	Codominant	TT	68 (32.4%)	64 (35.0%)	64 (32.0%)	Ref	-	Ref	-	Ref	-
		TC	109 (51.9%)	86 (47.0%)	90 (45.0%)	0.858	1.05 (0.63-1.75)	0.422	1.37 (0.64-2.94)	0.954	1.02 (0.57-1.81)
		CC	33 (15.7%)	33 (18.0%)	46 (23.0%)	0.596	1.19 (0.63-2.23)	0.109	2.02 (0.85-4.79)	0.224	0.65 (0.32-1.31)
	Additive	T	245 (58.3%)	214 (58.5%)	218 (54.5%)	Ref	-	Ref	-	Ref	-
		C	175 (41.7%)	152 (41.5%)	182 (45.5%)	0.565	1.10 (0.80-1.52)	0.090	1.49 (0.94-2.38)	0.269	0.82 (0.57-1.17)
	Dominant	TT	68 (32.4%)	64 (35.0%)	64 (32.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	142 (67.6%)	119 (65.0%)	136 (68.0%)	0.752	1.08 (0.67-1.74)	0.222	1.55 (0.77-3.15)	0.652	0.88 (0.52-1.51)
	Recessive	TT+TC	177 (84.3%)	150 (82.0%)	154 (77.0%)	Ref	-	Ref	-	Ref	-
		CC	33 (15.7%)	33 (18.0%)	46 (23.0%)	0.502	1.23 (0.68-2.23)	0.124	1.87 (0.84-4.13)	0.161	0.64 (0.34-1.20)
	Overdominant	TT+CC	101 (48.1%)	97 (53.0%)	110 (55.0%)	Ref	-	Ref	-	Ref	-
		TC	109 (51.9%)	86 (47.0%)	90 (45.0%)	0.836	0.95 (0.61-1.50)	0.935	0.97 (0.50-1.89)	0.481	1.20 (0.72-1.98)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *POT1*, protection of telomere 1; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>POT1</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs727505	CC	89 (42.8%)	47 (45.2%)	113 (56.5%)	Ref	-	Ref	-
	CT	94 (45.2%)	45 (43.3%)	71 (35.5%)	0.014	0.59 (0.39-0.90)	0.101	0.66 (0.40-1.09)
	TT	25 (12.0%)	12 (11.5%)	16 (8.0%)	0.048	0.50 (0.25-1.00)	0.156	0.55 (0.24-1.26)
	C	272 (65.4%)	139 (66.8%)	297 (74.3%)	Ref	-	Ref	-
	T	144 (34.6%)	69 (33.2%)	103 (25.8%)	0.006	0.66 (0.48-0.89)	0.054	0.70 (0.49-1.01)
rs17246404	CC	89 (42.8%)	47 (45.2%)	120 (60.0%)	Ref	-	Ref	-
	CT	94 (45.2%)	45 (43.3%)	60 (30.0%)	0.001	0.47 (0.31-0.72)	0.013	0.52 (0.31-0.87)
	TT	25 (12.0%)	12 (11.5%)	20 (10.0%)	0.113	0.59 (0.31-1.14)	0.288	0.65 (0.30-1.44)
	C	272 (65.4%)	139 (66.8%)	300 (75.0%)	Ref	-	Ref	-
	T	144 (34.6%)	69 (33.2%)	100 (25.0%)	0.003	0.63 (0.47-0.85)	0.033	0.67 (0.47-0.97)
rs7794637	CC	143 (68.8%)	70 (67.3%)	105 (52.5%)	Ref	-	Ref	-
	CT	60 (28.8%)	27 (26.0%)	82 (41.0%)	0.003	1.86 (1.23-2.83)	0.008	2.02 (1.19-3.44)
	TT	5 (2.4%)	7 (6.7%)	13 (6.5%)	0.024	3.54 (1.23-10.24)	0.665	1.24 (0.47-3.26)
	C	346 (83.2%)	167 (80.3%)	292 (73.0%)	Ref	-	Ref	-
	T	70 (16.8%)	41 (19.7%)	108 (27.0%)	4.35×10^{-4}	1.83 (1.30-2.57)	0.047	1.51 (1.00-2.26)
rs116916706	CC	208 (100%)	104 (100%)	143 (71.5%)	Ref	-	Ref	-
	CA	0 (0%)	0 (0%)	54 (27.0%)	*	-	*	-
	AA	0 (0%)	0 (0%)	3 (1.5%)	*	-	*	-
	C	416 (100.0%)	208 (100.0%)	340 (85.0%)	Ref	-	Ref	-
	A	0 (0.0%)	0 (0.0%)	60 (15.0%)	*	-	*	-

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs4360236	CC	143 (68.8%)	70 (67.3%)	108 (54.0%)	Ref	-	Ref	-
	CT	59 (28.4%)	27 (26.0%)	77 (38.5%)	0.011	1.73 (1.13-2.63)	0.023	1.85 (1.09-3.15)
	TT	6 (2.9%)	7 (6.7%)	15 (7.5%)	0.012	3.31 (1.24-8.81)	0.495	1.39 (0.54-3.58)
	C	345 (82.9%)	167 (80.3%)	293 (73.3%)	Ref	-	Ref	-
	T	71 (17.1%)	41 (19.7%)	107 (26.8%)	0.001	1.77 (1.27-2.49)	0.055	1.49 (0.99-2.24)
rs7782410	GG	70 (33.7%)	36 (34.6%)	58 (29.0%)	Ref	-	Ref	-
	GA	102 (49.0%)	47 (45.2%)	96 (48.0%)	0.575	1.14 (0.73-1.77)	0.391	1.27 (0.74-2.18)
	AA	36 (17.3%)	21 (20.2%)	46 (23.0%)	0.127	1.54 (0.88-2.69)	0.363	1.36 (0.70-2.64)
	G	242 (58.2%)	119 (57.2%)	212 (53.0%)	Ref	-	Ref	-
	A	174 (41.8%)	89 (42.8%)	188 (47.0%)	0.137	1.23 (0.94-1.63)	0.323	1.19 (0.85-1.66)
rs10244797	TT	73 (35.1%)	39 (37.5%)	64 (32.0%)	Ref	-	Ref	-
	TC	102 (49.0%)	45 (43.3%)	90 (45.0%)	1.000	1.01 (0.65-1.56)	0.469	1.22 (0.71-2.08)
	CC	33 (15.9%)	20 (19.2%)	46 (23.0%)	0.103	1.59 (0.91-2.78)	0.314	1.40 (0.73-2.71)
	T	248 (59.6%)	123 (59.1%)	218 (54.5%)	Ref	-	Ref	-
	C	168 (40.4%)	85 (40.9%)	182 (45.5%)	0.140	1.23 (0.93-1.63)	0.275	1.21 (0.86-1.70)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of a genotype and/or allele were absent in a study group. *POT1*, protection of telomere 1; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S7: Genotype and allele distribution of 2 SNPs of *ACD*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>ACD</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs72556537	Codominant	TT	148 (70.4%)	151 (82.5%)	145 (72.5%)	Ref	-	Ref	-	Ref	-
		TA	52 (24.8%)	31 (17.0%)	48 (24.0%)	0.073	0.59 (0.34-1.05)	0.138	0.53 (0.23-1.23)	0.183	0.65 (0.34-1.23)
		AA	10 (4.8%)	1 (0.5%)	7 (3.5%)	0.038	0.11 (0.01-0.88)	0.346	1.89 (0.50-7.08)	0.008	0.05 (0.01-0.45)
	Additive	T	348 (82.9%)	333 (91.0%)	338 (84.5%)	Ref	-	Ref	-	Ref	-
		A	72 (17.1%)	33 (9.0%)	62 (15.5%)	0.003	0.48 (0.29-0.78)	0.778	0.91 (0.49-1.71)	0.002	0.43 (0.25-0.74)
	Dominant	TT	148 (70.4%)	151 (82.5%)	145 (72.5%)	Ref	-	Ref	-	Ref	-
		TA+AA	62 (29.6%)	32 (17.5%)	55 (27.5%)	0.015	0.51 (0.29-0.88)	0.369	0.71 (0.34-1.49)	0.027	0.50 (0.27-0.92)
	Recessive	TT+TA	200 (95.2%)	182 (99.5%)	193 (96.5%)	Ref	-	Ref	-	Ref	-
		AA	10 (4.8%)	1 (0.5%)	7 (3.5%)	0.046	0.12 (0.01-0.97)	0.265	2.10 (0.57-7.72)	0.007	0.05 (0.01-0.43)
	Overdominant	TT+AA	158 (75.2%)	152 (83.0%)	152 (76.0%)	Ref	-	Ref	-	Ref	-
		TA	52 (24.8%)	31 (17.0%)	48 (24.0%)	0.115	0.63 (0.36-1.12)	0.115	0.51 (0.23-1.18)	0.278	0.71 (0.38-1.32)
rs6979	Codominant	GG	67 (31.9%)	54 (29.5%)	18 (9.0%)	Ref	-	Ref	-	Ref	-
		GA	110 (52.4%)	101 (55.2%)	74 (37.0%)	0.828	1.06 (0.64-1.74)	0.011	4.54 (1.41-14.62)	0.334	0.68 (0.31-1.49)
		AA	33 (15.7%)	28 (15.3%)	108 (54.0%)	0.982	1.01 (0.50-2.02)	3.05×10^{-7}	41.88 (10.03-174.91)	3.74×10^{-8}	0.07 (0.03-0.18)
	Additive	G	244 (58.1%)	209 (57.1%)	110 (27.5%)	Ref	-	Ref	-	Ref	-
		A	176 (41.9%)	157 (42.9%)	290 (72.5%)	0.844	1.03 (0.75-1.43)	3.34×10^{-12}	7.34 (4.19-12.86)	5.62×10^{-12}	0.26 (0.18-0.38)
	Dominant	GG	67 (31.9%)	54 (29.5%)	18 (9.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	143 (68.1%)	129 (70.5%)	182 (91.0%)	0.820	1.06 (0.65-1.72)	1.42×10^{-5}	11.69 (3.85-35.48)	4.92×10^{-4}	0.29 (0.14-0.58)
	Recessive	GG+GA	177 (84.3%)	155 (84.7%)	92 (46.0%)	Ref	-	Ref	-	Ref	-
		AA	33 (15.7%)	28 (15.3%)	108 (54.0%)	0.929	1.03 (0.55-1.91)	2.52×10^{-10}	16.20 (6.83-38.39)	2.87×10^{-12}	0.11 (0.06-0.20)
	Overdominant	GG+AA	100 (47.6%)	82 (44.8%)	126 (63.0%)	Ref	-	Ref	-	Ref	-
		GA	110 (52.4%)	101 (55.2%)	74 (37.0%)	0.883	1.03 (0.66-1.63)	0.004	0.36 (0.18-0.73)	2.63×10^{-5}	3.23 (1.87-5.58)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *ACD*, ACD shelterin complex subunit and telomerase recruitment factor; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>ACD</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs72556537	TT	0 (0%)	0 (0%)	145 (72.5%)	Ref	-	Ref	-
	TA	0 (0%)	4 (3.8%)	48 (24.0%)	*	-	*	-
	AA	208 (100%)	100 (96.2%)	7 (3.5%)	*	-	*	-
	T	0 (0.0%)	4 (1.9%)	338 (84.5%)	Ref	-	Ref	-
	A	416 (100.0%)	204 (98.1%)	62 (15.5%)	*	-	<0.000001	0.004 (0.001-0.01)
rs6979	GG	4 (1.9%)	4 (3.8%)	18 (9.0%)	Ref	-	Ref	-
	GA	50 (24.0%)	22 (21.2%)	74 (37.0%)	0.056	3.04 (0.97-9.52)	0.779	1.34 (0.41-4.37)
	AA	154 (74.0%)	78 (75.0%)	108 (54.0%)	2.50×10^{-4}	0.16 (0.05-0.47)	0.031	0.31 (0.10-0.95)
	G	58 (13.9%)	30 (14.4%)	110 (27.5%)	Ref	-	Ref	-
	A	358 (86.1%)	178 (85.6%)	290 (72.5%)	2.00×10^{-6}	0.43 (0.30-0.61)	2.80×10^{-4}	0.44 (0.29-0.69)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of a genotype and/or allele were absent in a study group. *ACD*, ACD shelterin complex subunit and telomerase recruitment factor; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S8: Genotype and allele distribution of 4 SNPs of *TERF2IP*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

TERF2IP											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs76937292	Codominant	CC	202 (96.2%)	169 (92.3%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
		CT	4 (1.9%)	6 (3.3%)	2 (1.0%)	0.226	0.38 (0.08-1.82)	3.29 × 10 ⁻⁴	0.01 (0.001-0.11)	0.227	3.25 (0.48-22.06)
		TT	4 (1.9%)	8 (4.4%)	8 (4.0%)	0.655	1.38 (0.34-5.59)	0.306	0.36 (0.05-2.56)	0.931	0.95 (0.27-3.33)
	Additive	C	408 (97.1%)	344 (94.0%)	382 (95.5%)	Ref	-	Ref	-	Ref	-
		T	12 (2.9%)	22 (6.0%)	18 (4.5%)	0.913	1.05 (0.46-2.41)	0.004	0.20 (0.06-0.60)	0.655	1.20 (0.54-2.67)
	Dominant	CC	202 (96.2%)	169 (92.3%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
CT+TT		8 (3.8%)	14 (7.7%)	10 (5.0%)	0.781	0.86 (0.30-2.47)	0.003	0.11 (0.02-0.47)	0.508	1.42 (0.50-4.02)	
Recessive	CC+CT	206 (98.1%)	175 (95.6%)	192 (96.0%)	Ref	-	Ref	-	Ref	-	
	TT	4 (1.9%)	8 (4.4%)	8 (4.0%)	0.598	1.45 (0.37-5.70)	0.439	0.48 (0.07-3.10)	0.911	0.93 (0.26-3.30)	
Overdominant	CC+TT	206 (98.1%)	177 (96.7%)	198 (99.0%)	Ref	-	Ref	-	Ref	-	
	CT	4 (1.9%)	6 (3.3%)	2 (1.0%)	0.288	0.44 (0.09-2.01)	0.001	0.01 (0.001-0.15)	0.230	3.23 (0.48-21.97)	
rs59297469	Codominant	GG	73 (34.8%)	40 (21.9%)	138 (69.0%)	Ref	-	Ref	-	Ref	-
		GT	105 (50.0%)	92 (50.2%)	57 (28.5%)	0.575	1.17 (0.68-2.01)	1.23 × 10 ⁻⁴	0.22 (0.10-0.47)	1.00 × 10 ⁻¹⁰	8.48 (4.43-16.20)
		TT	32 (15.2%)	51 (27.9%)	5 (2.5%)	0.037	1.98 (1.04-3.75)	8.62 × 10 ⁻⁶	0.02 (0.004-0.12)	1.03 × 10 ⁻⁸	69.64 (16.29-297.67)
	Additive	G	251 (59.8%)	172 (47.0%)	333 (83.2%)	Ref	-	Ref	-	Ref	-
		T	169 (40.2%)	194 (53.0%)	67 (16.8%)	0.082	1.33 (0.96-1.83)	2.25 × 10 ⁻⁹	0.16 (0.09-0.29)	3.19 × 10 ⁻¹⁸	6.81 (4.42-10.49)
	Dominant	GG	73 (34.8%)	40 (21.9%)	138 (69.0%)	Ref	-	Ref	-	Ref	-
		GT+TT	137 (65.2%)	143 (78.1%)	62 (31.0%)	0.245	1.35 (0.82-2.23)	4.96 × 10 ⁻⁷	0.14 (0.07-0.31)	1.00 × 10 ⁻¹⁴	12.46 (6.58-23.60)
	Recessive	GG+GT	178 (84.8%)	132 (72.1%)	195 (97.5%)	Ref	-	Ref	-	Ref	-
TT		32 (15.2%)	51 (27.9%)	5 (2.5%)	0.091	1.61 (0.93-2.80)	3.63 × 10 ⁻⁵	0.03 (0.01-0.16)	1.12 × 10 ⁻⁶	14.04 (4.85-40.66)	
Overdominant	GG+TT	105 (50.0%)	91 (49.8%)	143 (71.5%)	Ref	-	Ref	-	Ref	-	
	GT	105 (50.0%)	92 (50.2%)	57 (28.5%)	0.738	0.93 (0.59-1.45)	0.013	0.42 (0.21-0.83)	6.76 × 10 ⁻⁶	3.63 (2.07-6.36)	

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2233810	Codominant	CC	180 (85.7%)	161 (88.0%)	188 (94.0%)	Ref	-	Ref	-	Ref	-
		CA	26 (12.4%)	17 (9.3%)	10 (5.0%)	0.852	0.93 (0.46-1.91)	0.025	0.13 (0.02-0.78)	0.049	2.94 (1.00-8.59)
		AA	4 (1.9%)	5 (2.7%)	2 (1.0%)	0.376	2.00 (0.43-9.35)	0.307	3.24 (0.34-30.78)	0.911	1.12 (0.16-7.71)
	Additive	C	386 (91.9%)	339 (92.6%)	386 (96.5%)	Ref	-	Ref	-	Ref	-
		A	34 (8.1%)	27 (7.4%)	14 (3.5%)	0.624	1.16 (0.64-1.09)	0.263	0.48 (0.13-1.74)	0.112	2.01 (0.85-4.76)
	Dominant	CC	180 (85.7%)	161 (88.0%)	188 (94.0%)	Ref	-	Ref	-	Ref	-
		CA+AA	30 (14.3%)	22 (12.0%)	12 (6.0%)	0.879	1.05 (0.55-2.03)	0.100	0.29 (0.07-1.27)	0.078	2.37 (0.91-6.18)
	Recessive	CC+CA	206 (98.1%)	178 (97.3%)	198 (99.0%)	Ref	-	Ref	-	Ref	-
		AA	4 (1.9%)	5 (2.7%)	2 (1.0%)	0.341	2.12 (0.45-9.94)	0.240	3.87 (0.41-36.88)	0.989	1.01 (0.15-7.09)
	Overdominant	CC+AA	184 (87.6%)	166 (90.7%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
CA		26 (12.4%)	17 (9.3%)	10 (5.0%)	0.800	0.91 (0.45-1.85)	0.025	0.15 (0.03-0.79)	0.051	2.86 (1.00-8.22)	
rs488444	Codominant	AA	199 (94.7%)	165 (90.2%)	187 (93.5%)	Ref	-	Ref	-	Ref	-
		AG	10 (4.8%)	17 (9.3%)	10 (5.0%)	0.259	1.68 (0.68-4.15)	0.458	1.69 (0.42-6.69)	0.206	1.89 (0.70-5.09)
		GG	1 (0.5%)	1 (0.5%)	3 (1.5%)	0.851	0.76 (0.04-13.71)	0.367	3.95 (0.20-78.34)	0.236	0.21 (0.02-2.80)
	Additive	A	408 (97.1%)	347 (94.8%)	384 (96.0%)	Ref	-	Ref	-	Ref	-
		G	12 (2.9%)	19 (5.2%)	16 (4.0%)	0.362	1.46 (0.65-3.32)	0.192	2.10 (0.69-6.44)	0.751	1.14 (0.50-2.64)
	Dominant	AA	199 (94.7%)	165 (90.2%)	187 (93.5%)	Ref	-	Ref	-	Ref	-
		AG+GG	11 (5.3%)	18 (9.8%)	13 (6.5%)	0.302	1.58 (0.66-3.75)	0.297	1.93 (0.56-6.68)	0.432	1.44 (0.58-3.59)
	Recessive	AA+AG	209 (99.5%)	182 (99.5%)	197 (98.5%)	Ref	-	Ref	-	Ref	-
		GG	1 (0.5%)	1 (0.5%)	3 (1.5%)	0.818	0.71 (0.04-13.00)	0.377	3.86 (0.19-77.57)	0.228	0.20 (0.02-2.71)
	Overdominant	AA+GG	200 (95.2%)	166 (90.7%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
AG		10 (4.8%)	17 (9.3%)	10 (5.0%)	0.255	1.69 (0.69-4.16)	0.477	1.65 (0.42-6.48)	0.194	1.93 (0.72-5.18)	

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TERF2IP*, TERF2-interacting protein; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TERF2IP</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs CHB+CHS	
					p value	OR (95%CI)	p value	OR (95%CI)
rs76937292	CC	208 (100%)	104 (100%)	190 (95.0%)	Ref	-	Ref	-
	CT	0 (0%)	0 (0%)	2 (1.0%)	*	-	*	-
	TT	0 (0%)	0 (0%)	8 (4.0%)	*	-	*	-
	C	416 (100.0%)	208 (100.0%)	382 (95.5%)	Ref	-	Ref	-
	T	0 (0.0%)	0 (0.0%)	18 (4.5%)	*	-	*	-
rs59297469	GG	157 (75.5%)	80 (76.9%)	138 (69.0%)	Ref	-	Ref	-
	GT	45 (21.6%)	21 (20.2%)	57 (28.5%)	0.113	1.44 (0.92-2.27)	0.118	1.57 (0.89-2.79)
	TT	6 (2.9%)	3 (2.9%)	5 (2.5%)	1.000	0.95 (0.28-3.18)	1.000	0.97 (0.23-4.15)
	G	359 (86.3%)	181 (87.0%)	333 (83.3%)	Ref	-	Ref	-
	T	57 (13.7%)	27 (13.0%)	67 (16.8%)	0.225	1.27 (0.86-1.86)	0.223	1.35 (0.83-2.18)
rs2233810	CC	197 (94.7%)	102 (98.1%)	188 (94.0%)	Ref	-	Ref	-
	CA	11 (5.3%)	2 (1.9%)	10 (5.0%)	1.000	0.95 (0.40-2.30)	0.186	2.71 (0.58-12.62)
	AA	0 (0.0%)	0 (0.0%)	2 (1.0%)	*	-	*	-
	C	405 (97.4%)	206 (99.0%)	386 (96.5%)	Ref	-	Ref	-
	A	11 (2.6%)	2 (1.0%)	14 (3.5%)	0.478	1.34 (0.60-2.98)	0.105	3.74 (0.84-16.60)
rs4888444	AA	208 (100%)	104 (100%)	187 (93.5%)	Ref	-	Ref	-
	AG	0 (0%)	0 (0%)	10 (5.0%)	*	-	*	-
	GG	0 (0%)	0 (0%)	3 (1.5%)	*	-	*	-
	A	416 (100.0%)	208 (100.0%)	384 (96.0%)	Ref	-	Ref	-
	G	0 (0.0%)	0 (0.0%)	16 (4.0%)	*	-	*	-

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of a genotype and/or allele were absent in a study group. *TERF2IP*, TERF2-interacting protein; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S9: Genotype and allele distribution of 9 SNPs of *TERT*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>TERT</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2736122	Codominant	CC	128 (61.0%)	121 (66.1%)	176 (88.0%)	Ref	-	Ref	-	Ref	-
		CT	72 (34.2%)	52 (28.4%)	24 (12.0%)	0.312	0.77 (0.47-1.27)	3.54×10^{-4}	0.17 (0.07-0.46)	1.81×10^{-5}	4.59 (2.29-9.21)
		TT	10 (4.8%)	10 (5.5%)	0 (0.0%)	0.417	1.51 (0.56-4.05)	*	-	*	-
	Additive	C	328 (78.1%)	294 (80.3%)	376 (94.0%)	Ref	-	Ref	-	Ref	-
		T	92 (21.9%)	72 (19.7%)	24 (6.0%)	0.918	0.98 (0.66-1.45)	2.54×10^{-5}	0.16 (0.07-0.38)	1.80×10^{-6}	4.40 (2.40-8.09)
	Dominant	CC	128 (61.0%)	121 (66.1%)	176 (88.0%)	Ref	-	Ref	-	Ref	-
		CT+TT	82 (39.0%)	62 (33.9%)	24 (12.0%)	0.542	0.86 (0.54-1.38)	8.47×10^{-5}	0.15 (0.06-0.39)	3.81×10^{-6}	5.00 (2.53-9.90)
	Recessive	CC+CT	200 (95.2%)	173 (94.5%)	200 (100.0%)	Ref	-	Ref	-	Ref	-
		TT	10 (4.8%)	10 (5.5%)	0 (0.0%)	0.299	1.69 (0.63-4.53)	*	-	*	-
	Overdominant	CC+TT	138 (65.8%)	131 (71.6%)	176 (88.0%)	Ref	-	Ref	-	Ref	-
		CT	72 (34.2%)	52 (28.4%)	24 (12.0%)	0.255	0.75 (0.46-1.23)	0.001	0.20 (0.08-0.50)	3.13×10^{-5}	4.44 (2.20-8.97)
rs2075786	Codominant	TT	52 (24.8%)	47 (25.7%)	124 (62.0%)	Ref	-	Ref	-	Ref	-
		TC	111 (52.9%)	92 (50.3%)	64 (32.0%)	0.931	1.02 (0.59-1.79)	4.89×10^{-6}	0.15 (0.07-0.34)	2.53×10^{-7}	4.55 (2.56-8.10)
		CC	47 (22.3%)	44 (24.0%)	12 (6.0%)	0.576	1.20 (0.63-2.29)	1.44×10^{-5}	0.07 (0.02-0.23)	4.82×10^{-6}	7.27 (3.11-17.02)
	Additive	T	215 (51.2%)	186 (50.8%)	312 (78.0%)	Ref	-	Ref	-	Ref	-
		C	205 (48.8%)	180 (49.2%)	88 (22.0%)	0.543	1.10 (0.80-1.52)	6.09×10^{-9}	0.19 (0.11-0.33)	1.66×10^{-9}	3.34 (2.26-4.95)
	Dominant	TT	52 (24.8%)	47 (25.7%)	124 (62.0%)	Ref	-	Ref	-	Ref	-
		TC+CC	158 (75.2%)	136 (74.3%)	76 (38.0%)	0.807	1.07 (0.63-1.79)	5.60×10^{-8}	0.12 (0.06-0.26)	3.17×10^{-9}	5.31 (3.06-9.23)
	Recessive	TT+TC	163 (77.7%)	139 (76.0%)	188 (94.0%)	Ref	-	Ref	-	Ref	-
		CC	47 (22.3%)	44 (24.0%)	12 (6.0%)	0.443	1.23 (0.72-2.10)	0.001	0.12 (0.04-0.41)	0.003	3.44 (1.54-7.70)
	Overdominant	TT+CC	99 (47.1%)	91 (49.7%)	136 (68.0%)	Ref	-	Ref	-	Ref	-
		TC	111 (52.9%)	92 (50.3%)	64 (32.0%)	0.663	0.90 (0.58-1.42)	0.001	0.31 (0.15-0.63)	1.09×10^{-4}	2.93 (1.70-5.05)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs4246742	Codominant	AA	133 (63.4%)	121 (66.1%)	126 (63.0%)	Ref	-	Ref	-	Ref	-
		AT	66 (31.4%)	55 (30.1%)	55 (27.5%)	0.983	0.99 (0.60-1.64)	0.377	1.39 (0.67-2.91)	0.706	1.12 (0.63-1.96)
		TT	11 (5.2%)	7 (3.8%)	19 (9.5%)	0.600	0.75 (0.26-2.18)	0.594	1.39 (0.42-4.60)	0.121	0.41 (0.13-1.26)
	Additive	A	332 (79.0%)	297 (81.1%)	307 (76.8%)	Ref	-	Ref	-	Ref	-
		T	88 (21.0%)	69 (18.9%)	93 (23.2%)	0.719	0.93 (0.62-1.38)	0.317	1.32 (0.76-2.29)	0.384	0.82 (0.53-1.28)
	Dominant	AA AT+TT	133 (63.4%) 77 (36.6%)	121 (66.1%) 62 (33.9%)	126 (63.0%) 74 (37.0%)	Ref 0.852	- 0.96 (0.60-1.53)	Ref 0.327	- 1.40 (0.71-2.77)	Ref 0.817	- 0.94 (0.56-1.59)
rs10069690	Codominant	AA+AT	199 (94.8%)	176 (96.2%)	181 (90.5%)	Ref	-	Ref	-	Ref	-
		TT	11 (5.2%)	7 (3.8%)	19 (9.5%)	0.593	0.75 (0.25-2.18)	0.670	1.30 (0.39-4.29)	0.111	0.41 (0.14-1.22)
		AA+TT AT	144 (68.6%) 66 (31.4%)	128 (69.9%) 55 (30.1%)	145 (72.5%) 55 (27.5%)	Ref 0.956	- 1.01 (0.62-1.65)	Ref 0.425	- 1.34 (0.65-2.77)	Ref 0.541	- 1.19 (0.68-2.07)
	Additive	CC	108 (51.4%)	98 (53.6%)	132 (66.0%)	Ref	-	Ref	-	Ref	-
		CT	87 (41.4%)	70 (38.2%)	60 (30.0%)	0.947	1.02 (0.63-1.64)	0.027	0.43 (0.21-0.91)	0.016	1.98 (1.14-3.46)
		TT	15 (7.2%)	15 (8.2%)	8 (4.0%)	0.255	1.65 (0.70-3.91)	0.401	0.49 (0.09-2.58)	0.161	2.26 (0.72-7.03)
	Dominant	C	303 (72.1%)	266 (72.7%)	324 (81.0%)	Ref	-	Ref	-	Ref	-
		T	117 (27.9%)	100 (27.3%)	76 (19.0%)	0.410	1.16 (0.81-1.66)	0.036	0.53 (0.30-0.96)	0.011	1.76 (1.14-2.73)
	Recessive	CC	108 (51.4%)	98 (53.6%)	132 (66.0%)	Ref	-	Ref	-	Ref	-
		CT+TT	102 (48.6%)	85 (46.4%)	68 (34.0%)	0.683	1.10 (0.70-1.73)	0.022	0.44 (0.22-0.89)	0.009	2.03 (1.19-3.45)
	Overdominant	CC+CT	195 (92.8%)	168 (91.8%)	192 (96.0%)	Ref	-	Ref	-	Ref	-
		TT	15 (7.2%)	15 (8.2%)	8 (4.0%)	0.229	1.67 (0.72-3.88)	0.629	0.66 (0.12-3.63)	0.321	1.80 (0.56-5.71)
	Overdominant	CC+TT	123 (58.6%)	113 (61.8%)	140 (70.0%)	Ref	-	Ref	-	Ref	-
		CT	87 (41.4%)	70 (38.2%)	60 (30.0%)	0.817	0.95 (0.60-1.50)	0.032	0.45 (0.22-0.93)	0.026	1.87 (1.08-3.23)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2242652	Codominant	CC	125 (59.5%)	115 (62.8%)	135 (67.5%)	Ref	-	Ref	-	Ref	-
		CT	66 (31.4%)	53 (29.0%)	59 (29.5%)	0.565	0.86 (0.52-1.43)	0.040	0.45 (0.21-0.96)	0.359	1.30 (0.74-2.27)
		TT	19 (9.1%)	15 (8.2%)	6 (3.0%)	0.489	1.33 (0.60-2.95)	0.412	0.53 (0.11-2.44)	0.323	1.78 (0.57-5.64)
	Additive	C	316 (75.2%)	283 (77.3%)	329 (82.2%)	Ref	-	Ref	-	Ref	-
		T	104 (24.8%)	83 (22.7%)	71 (17.8%)	0.842	1.04 (0.72-1.51)	0.048	0.55 (0.30-0.99)	0.213	1.33 (0.85-2.08)
	Dominant	CC	125 (59.5%)	115 (62.8%)	135 (67.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	85 (40.5%)	68 (37.2%)	65 (32.5%)	0.826	0.95 (0.60-1.51)	0.035	0.46 (0.22-0.95)	0.258	1.36 (0.80-2.32)
	Recessive	CC+CT	191 (90.9%)	168 (91.8%)	194 (97.0%)	Ref	-	Ref	-	Ref	-
		TT	19 (9.1%)	15 (8.2%)	6 (3.0%)	0.427	1.37 (0.63-2.96)	0.621	0.68 (0.15-3.14)	0.462	1.56 (0.48-5.12)
	Overdominant	CC+TT	144 (68.6%)	130 (71.0%)	141 (70.5%)	Ref	-	Ref	-	Ref	-
		CT	66 (31.4%)	53 (29.0%)	59 (29.5%)	0.467	0.83 (0.51-1.36)	0.049	0.46 (0.21-1.00)	0.413	1.26 (0.72-2.21)
rs2853676	Codominant	GG	97 (46.2%)	77 (42.1%)	118 (59.0%)	Ref	-	Ref	-	Ref	-
		GA	85 (40.5%)	75 (41.0%)	64 (32.0%)	0.361	1.26 (0.77-2.05)	0.018	0.41 (0.20-0.86)	0.009	2.13 (1.20-3.77)
		AA	28 (13.3%)	31 (16.9%)	18 (9.0%)	0.431	1.31 (0.67-2.57)	0.199	0.51 (0.18-1.43)	0.001	3.56 (1.64-7.71)
	Additive	G	279 (66.4%)	229 (62.6%)	300 (75.0%)	Ref	-	Ref	-	Ref	-
		A	141 (33.6%)	137 (37.4%)	100 (25.0%)	0.304	1.19 (0.85-1.66)	0.021	0.53 (0.31-0.91)	4.04 × 10 ⁻⁵	2.31 (1.55-3.45)
	Dominant	GG	97 (46.2%)	77 (42.1%)	118 (59.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	113 (53.8%)	106 (57.9%)	82 (41.0%)	0.277	1.29 (0.82-2.04)	0.013	0.42 (0.21-0.83)	0.001	2.51 (1.49-4.24)
	Recessive	GG+GA	182 (86.7%)	152 (83.1%)	182 (91.0%)	Ref	-	Ref	-	Ref	-
		AA	28 (13.3%)	31 (16.9%)	18 (9.0%)	0.656	1.16 (0.61-2.19)	0.479	0.68 (0.24-1.96)	0.004	3.19 (1.43-7.08)
	Overdominant	GG+AA	125 (59.5%)	108 (59.0%)	136 (68.0%)	Ref	-	Ref	-	Ref	-
		GA	85 (40.5%)	75 (41.0%)	64 (32.0%)	0.435	1.20 (0.76-1.91)	0.031	0.45 (0.22-0.93)	0.099	1.56 (0.92-2.64)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2736098	Codominant	AA	57 (27.1%)	45 (24.6%)	19 (9.5%)	Ref	-	Ref	-	Ref	-
		AG	109 (51.9%)	91 (49.7%)	81 (40.5%)	0.757	1.09 (0.63-1.89)	0.096	2.35 (0.86-6.43)	0.062	0.48 (0.22-1.04)
		GG	44 (21.0%)	47 (25.7%)	100 (50.0%)	0.218	1.49 (0.79-2.81)	3.30×10^{-4}	6.99 (2.42-20.20)	2.03×10^{-4}	0.22 (0.10-0.49)
	Additive	A	223 (53.1%)	181 (49.5%)	119 (29.8%)	Ref	-	Ref	-	Ref	-
		G	197 (46.9%)	185 (50.5%)	281 (70.2%)	0.192	1.24 (0.90-1.70)	5.62×10^{-5}	2.70 (1.57-4.38)	5.013×10^{-05}	0.47 (0.32-0.67)
	Dominant	AA	57 (27.1%)	45 (24.6%)	19 (9.5%)	Ref	-	Ref	-	Ref	-
		AG+GG	153 (72.9%)	138 (75.4%)	181 (90.5%)	0.454	1.22 (0.73-2.05)	0.007	3.69 (1.43-9.52)	0.004	0.35 (0.17-0.71)
	Recessive	AA+AG	166 (79.0%)	136 (74.3%)	100 (50.0%)	Ref	-	Ref	-	Ref	-
		GG	44 (21.0%)	47 (25.7%)	100 (50.0%)	0.159	1.47 (0.86-2.50)	1.90×10^{-4}	3.89 (1.91-7.95)	3.68×10^{-4}	0.38 (0.22-0.65)
	Overdominant	AA+GG	101 (48.1%)	92 (50.3%)	119 (59.5%)	Ref	-	Ref		Ref	-
AG		109 (51.9%)	91 (49.7%)	81 (40.5%)	0.593	0.88 (0.56-1.39)	0.176	0.64 (0.33-1.23)	0.210	1.38 (0.83-2.29)	
rs2853669	Codominant	CC	67 (31.9%)	60 (32.8%)	25 (12.5%)	Ref	-	Ref	-	Ref	-
		CT	105 (50.0%)	93 (50.8%)	81 (40.5%)	0.821	0.94 (0.57-1.57)	0.129	2.04 (0.81-5.13)	0.064	0.53 (0.27-1.04)
		TT	38 (18.1%)	30 (16.4%)	94 (47.0%)	0.875	1.05 (0.54-2.05)	2.97×10^{-4}	5.98 (2.27-15.77)	1.88×10^{-6}	0.14 (0.06-0.31)
	Additive	C	239 (56.9%)	213 (58.2%)	131 (32.8%)	Ref	-	Ref	-	Ref	-
		T	181 (43.1%)	153 (41.8%)	269 (67.2%)	0.945	1.01 (0.73-1.40)	9.67×10^{-5}	2.57 (1.60-4.13)	1.48×10^{-7}	0.37 (0.26-0.54)
	Dominant	CC	67 (31.9%)	60 (32.8%)	25 (12.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	143 (68.1%)	123 (67.2%)	175 (87.5%)	0.909	0.97 (0.60-1.57)	0.010	3.09 (1.31-7.30)	0.001	0.33 (0.17-0.63)
	Recessive	CC+CT	172 (81.9%)	153 (83.6%)	106 (53.0%)	Ref	-	Ref	-	Ref	-
		TT	38 (18.1%)	30 (16.4%)	94 (47.0%)	0.788	1.08 (0.60-1.96)	2.59×10^{-4}	3.93 (1.89-8.19)	8.95×10^{-7}	0.23 (0.13-0.42)
	Overdominant	CC+TT	105 (50.0%)	90 (49.2%)	119 (59.5%)	Ref	-	Ref	-	Ref	-
CT		105 (50.0%)	93 (50.8%)	81 (40.5%)	0.756	0.93 (0.59-1.46)	0.259	0.69 (0.36-1.32)	0.082	1.57 (0.94-2.61)	

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs7712562	Codominant	GG	170 (81.0%)	149 (81.4%)	146 (73.0%)	Ref	-	Ref	-	Ref	-
		GA	35 (16.6%)	32 (17.5%)	45 (22.5%)	0.399	1.29 (0.71-2.36)	0.930	0.96 (0.41-2.28)	0.489	0.80 (0.43-1.50)
		AA	5 (2.4%)	2 (1.1%)	9 (4.5%)	0.437	0.47 (0.07-3.15)	0.408	0.47 (0.08-2.85)	0.301	0.37 (0.06-2.41)
	Additive	G	375 (89.3%)	330 (90.2%)	337 (84.2%)	Ref	-	Ref	-	Ref	-
		A	45 (10.7%)	36 (9.8%)	63 (15.8%)	0.810	1.07 (0.63-1.79)	0.478	0.77 (0.37-1.59)	0.252	0.73 (0.42-1.26)
	Dominant	GG	170 (81.0%)	149 (81.4%)	146 (73.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	40 (19.0%)	34 (18.6%)	54 (27.0%)	0.581	1.17 (0.66-2.08)	0.674	0.84 (0.37-1.91)	0.352	0.75 (0.41-1.38)
	Recessive	GG+GA	205 (97.6%)	181 (98.9%)	191 (95.5%)	Ref	-	Ref	-	Ref	-
		AA	5 (2.4%)	2 (1.1%)	9 (4.5%)	0.406	0.45 (0.07-2.99)	0.373	0.43 (0.07-2.72)	0.345	0.40 (0.06-2.72)
	Overdominant	GG+AA GA	175 (83.4%) 35 (16.6%)	151 (82.5%) 32 (17.5%)	155 (77.5%) 45 (22.5%)	Ref 0.385	- 1.30 (0.72-2.35)	Ref 0.967	- 0.98 (0.41-2.33)	Ref 0.547	- 0.82 (0.44-1.55)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TERT*, telomerase reverse transcriptase; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TERT</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs2736122	CC	183 (88.0%)	74 (71.2%)	176 (88.0%)	Ref	-	Ref	-
	CT	24 (11.5%)	30 (28.8%)	24 (12.0%)	1.000	1.04 (0.57-1.90)	2.66×10^{-4}	0.34 (0.18-0.61)
	TT	1 (0.5%)	0 (0.0%)	0 (0.0%)	*	-	*	-
	C	390 (93.8%)	178 (85.6%)	376 (94.0%)	Ref	-	Ref	-
	T	26 (6.3%)	30 (14.4%)	24 (6.0%)	0.882	0.96 (0.54-1.70)	0.001	0.38 (0.22-0.67)
rs2075786	TT	135 (64.9%)	59 (56.7%)	124 (62.0%)	Ref	-	Ref	-
	TC	66 (31.7%)	44 (42.3%)	64 (32.0%)	0.801	1.06 (0.69-1.61)	0.143	0.69 (0.42-1.13)
	CC	7 (3.4%)	1 (1.0%)	12 (6.0%)	0.198	1.87 (0.71-4.89)	0.115	5.71 (0.73-44.95)
	T	336 (80.8%)	162 (77.9%)	312 (78.0%)	Ref	-	Ref	-
	C	80 (19.2%)	46 (22.1%)	88 (22.0%)	0.328	1.18 (0.84-1.66)	1.000	0.99 (0.66-1.49)
rs4246742	AA	35 (16.8%)	13 (12.5%)	126 (63.0%)	Ref	-	Ref	-
	AT	97 (46.6%)	46 (44.2%)	55 (27.5%)	<0.000001	0.16 (0.10-0.26)	<0.000001	0.12 (0.06-0.25)
	TT	76 (36.5%)	45 (43.3%)	19 (9.5%)	<0.000001	0.07 (0.04-0.13)	<0.000001	0.04 (0.02-0.10)
	A	167 (40.1%)	72 (34.6%)	307 (76.8%)	Ref	-	Ref	-
	T	249 (59.9%)	136 (65.4%)	93 (23.3%)	<0.000001	0.20 (0.15-0.28)	<0.000001	0.16 (0.11-0.23)
rs10069690	CC	149 (71.6%)	63 (60.6%)	132 (66.0%)	Ref	-	Ref	-
	CT	55 (26.4%)	36 (34.6%)	60 (30.0%)	0.347	1.23 (0.80-1.90)	0.379	0.80 (0.48-1.33)
	TT	4 (1.9%)	5 (4.8%)	8 (4.0%)	0.241	2.26 (0.67-7.67)	0.761	0.76 (0.24-2.43)
	C	353 (84.9%)	162 (77.9%)	324 (81.0%)	Ref	-	Ref	-
	T	63 (15.1%)	46 (22.1%)	76 (19.0%)	0.143	1.31 (0.91-1.90)	0.363	0.83 (0.55-1.25)

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs2242652	CC	149 (71.6%)	62 (59.6%)	135 (67.5%)	Ref	-	Ref	-
	CT	55 (26.4%)	37 (35.6%)	59 (29.5%)	0.446	1.18 (0.77-1.83)	0.230	0.73 (0.44-1.22)
	TT	4 (1.9%)	5 (4.8%)	6 (3.0%)	0.528	1.66 (0.46-5.99)	0.337	0.55 (0.16-1.88)
	C	353 (84.9%)	161 (77.4%)	329 (82.3%)	Ref	-	Ref	-
	T	63 (15.1%)	47 (22.6%)	71 (17.8%)	0.315	1.21 (0.83-1.75)	0.152	0.74 (0.49-1.12)
rs2853676	GG	160 (76.9%)	73 (70.2%)	118 (59.0%)	Ref	-	Ref	-
	GA	41 (19.7%)	24 (23.1%)	64 (32.0%)	0.001	2.12 (1.34-3.35)	0.074	1.65 (0.95-2.87)
	AA	7 (3.4%)	7 (6.7%)	18 (9.0%)	0.004	3.49 (1.41-8.62)	0.320	1.59 (0.63-3.99)
	G	361 (86.8%)	170 (81.7%)	300 (75.0%)	Ref	-	Ref	-
	A	55 (13.2%)	38 (18.3%)	100 (25.0%)	1.80×10^{-5}	2.19 (1.52-3.15)	0.060	1.49 (0.98-2.27)
rs2736098	AA	24 (11.5%)	8 (7.7%)	19 (9.5%)	Ref	-	Ref	-
	GA	106 (51.0%)	35 (33.7%)	81 (40.5%)	1.000	0.97 (0.50-1.88)	1.000	0.97 (0.39-2.44)
	GG	78 (37.5%)	61 (58.7%)	100 (50.0%)	0.157	1.62 (0.83-3.17)	0.410	0.69 (0.29-1.67)
	A	154 (37.0%)	51 (24.5%)	119 (29.8%)	Ref	-	Ref	-
	G	262 (63.0%)	157 (75.5%)	281 (70.3%)	0.028	1.39 (1.04-1.86)	0.173	0.77 (0.52-1.12)
rs2853669	CC	24 (11.5%)	8 (7.7%)	25 (12.5%)	Ref	-	Ref	-
	CT	107 (51.4%)	35 (33.7%)	81 (40.5%)	0.320	0.73 (0.39-1.37)	0.507	0.74 (0.30-1.80)
	TT	77 (37.0%)	61 (58.7%)	94 (47.0%)	0.625	1.17 (0.62-2.21)	0.102	0.49 (0.21-1.16)
	C	155 (37.3%)	51 (24.5%)	131 (32.8%)	Ref	-	Ref	-
	T	261 (62.7%)	157 (75.5%)	269 (67.3%)	0.177	1.22 (0.91-1.63)	0.036	0.67 (0.46-0.97)

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs7712562	GG	175 (84.1%)	87 (83.7%)	146 (73.0%)	Ref	-	Ref	-
	GA	32 (15.4%)	15 (14.4%)	45 (22.5%)	0.041	1.69 (1.02-2.79)	0.074	1.79 (0.94-3.40)
	AA	1 (0.5%)	2 (1.9%)	9 (4.5%)	0.007	10.79 (1.35-86.15)	0.337	2.68 (0.57-12.70)
	G	382 (91.8%)	189 (90.9%)	337 (84.3%)	Ref	-	Ref	-
	A	34 (8.2%)	19 (9.1%)	63 (15.8%)	0.001	2.10 (1.35-3.27)	0.023	1.86 (1.08-3.20)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of an allele were absent in a study group. *TERT*, telomerase reverse transcriptase; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S10: Genotype and allele distribution of *TERC* SNP

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>TERC</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2293607	Codominant	AA	132 (62.8%)	97 (53.0%)	32 (16.0%)	Ref	-	Ref	-	Ref	-
		AG	65 (31.0%)	66 (36.1%)	101 (50.5%)	0.099	1.51 (0.93-2.47)	1.30×10^{-6}	9.04 (3.71-22.04)	3.16×10^{-7}	0.18 (0.10-0.35)
		GG	13 (6.2%)	20 (10.9%)	67 (33.5%)	0.015	2.81 (1.22-6.46)	8.04×10^{-9}	26.92 (8.79-82.43)	2.42×10^{-9}	0.09 (0.04-0.19)
	Additive	A	329 (78.3%)	260 (71.0%)	165 (41.2%)	Ref	-	Ref	-	Ref	-
		G	91 (21.7%)	106 (29.0%)	235 (58.8%)	0.005	1.70 (1.18-2.45)	5.12×10^{-12}	6.04 (3.62-10.06)	6.81×10^{-12}	0.27 (0.18-0.39)
	Dominant	AA	132 (62.8%)	97 (53.0%)	32 (16.0%)	Ref	-	Ref	-	Ref	-
		AG+GG	78 (37.2%)	86 (47.0%)	168 (84.0%)	0.020	1.73 (1.09-2.74)	5.97×10^{-9}	12.81 (5.43-30.26)	6.13×10^{-10}	0.14 (0.08-0.26)
	Recessive	AA+AG	197 (93.8%)	163 (89.1%)	133 (66.5%)	Ref	-	Ref	-	Ref	-
		GG	13 (6.2%)	20 (10.9%)	67 (33.5%)	0.030	2.46 (1.09-5.54)	2.40×10^{-6}	9.95 (3.83-25.84)	1.47×10^{-5}	0.23 (0.12-0.45)
	Overdominant	AA+GG	145 (69.0%)	117 (63.9%)	99 (49.5%)	Ref	-	Ref	-	Ref	-
		AG	65 (31.0%)	66 (36.1%)	101 (50.5%)	0.259	1.31 (0.82-2.12)	0.006	2.53 (1.30-4.93)	0.011	0.51 (0.31-0.86)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TERC*, telomerase RNA component; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TERC</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs2293607	AA	40 (19.2%)	9 (8.7%)	32 (16.0%)	Ref	-	Ref	-
	AG	105 (50.5%)	53 (51.0%)	101 (50.5%)	0.503	1.20 (0.70-2.06)	0.128	0.54 (0.24-1.21)
	GG	63 (30.3%)	42 (40.4%)	67 (33.5%)	0.334	1.33 (0.75-2.37)	0.056	0.45 (0.20-1.03)
	A	185 (44.5%)	71 (34.1%)	165 (41.3%)	Ref	-	Ref	-
	G	231 (55.5%)	137 (65.9%)	235 (58.8%)	0.353	1.14 (0.86-1.51)	0.088	0.74 (0.52-1.05)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *TERC*, telomerase RNA component; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S11: Genotype and allele distribution of 9 SNPs of *TEPI*

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>TEPI</i>											
SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2104978	Codominant	AA	182 (86.7%)	138 (75.4%)	192 (96.0%)	Ref	-	Ref	-	Ref	-
		AG	23 (11.0%)	39 (21.3%)	3 (1.5%)	0.045	1.90 (1.02-3.56)	0.003	0.05 (0.01-0.36)	1.83×10^{-5}	18.91 (4.93-72.56)
		GG	5 (2.3%)	6 (3.3%)	5 (2.5%)	0.628	0.69 (0.15-3.14)	0.698	0.65 (0.07-5.77)	0.731	1.30 (0.29-5.71)
	Additive	A	387 (92.1%)	315 (86.1%)	387 (96.8%)	Ref	-	Ref	-	Ref	-
		G	33 (7.9%)	51 (13.9%)	13 (3.2%)	0.176	1.44 (0.85-2.42)	0.009	0.24 (0.08-0.70)	1.44×10^{-4}	4.31 (2.03-9.16)
	Dominant	AA	182 (86.7%)	138 (75.4%)	192 (96.0%)	Ref	-	Ref	-	Ref	-
		AG+GG	28 (13.3%)	45 (24.6%)	8 (4.0%)	0.081	1.68 (0.94-3.01)	0.005	0.15 (0.04-0.57)	2.66×10^{-5}	7.29 (2.88-18.40)
	Recessive	AA+AG	205 (97.6%)	177 (96.7%)	195 (97.5%)	Ref	-	Ref	-	Ref	-
		GG	5 (2.4%)	6 (3.3%)	5 (2.5%)	0.541	0.63 (0.14-2.81)	0.816	0.78 (0.09-6.43)	0.968	1.03 (0.24-4.50)
	Overdominant	AA+GG	187 (89.0%)	144 (78.7%)	197 (98.5%)	Ref	-	Ref	-	Ref	-
		AG	23 (11.0%)	39 (21.3%)	3 (1.5%)	0.037	1.93 (1.04-3.59)	0.003	0.06 (0.01-0.40)	1.93×10^{-5}	18.30 (4.82-69.42)
rs1713449	Codominant	CC	108 (51.4%)	109 (59.6%)	99 (49.5%)	Ref	-	Ref	-	Ref	-
		CT	78 (37.1%)	54 (29.5%)	69 (34.5%)	0.212	0.73 (0.44-1.20)	0.287	0.67 (0.33-1.39)	0.096	0.62 (0.35-1.09)
		TT	24 (11.5%)	20 (10.9%)	32 (16.0%)	0.442	0.74 (0.34-1.60)	0.997	1.00 (0.37-2.72)	0.176	0.60 (0.28-1.26)
	Additive	C	294 (70.0%)	272 (74.3%)	267 (66.8%)	Ref	-	Ref	-	Ref	-
		T	126 (30.0%)	94 (25.7%)	133 (33.2%)	0.211	0.80 (0.56-1.14)	0.667	0.90 (0.55-1.47)	0.045	0.67 (0.45-0.99)
	Dominant	CC	108 (51.4%)	109 (59.6%)	99 (49.5%)	Ref	-	Ref	-	Ref	-
		CT+TT	102 (48.6%)	74 (40.4%)	101 (50.5%)	0.186	0.74 (0.47-1.16)	0.417	0.76 (0.40-1.47)	0.056	0.61 (0.37-1.01)
	Recessive	CC+CT	186 (88.5%)	163 (89.1%)	168 (84.0%)	Ref	-	Ref	-	Ref	-
		TT	24 (11.5%)	20 (10.9%)	32 (16.0%)	0.662	0.85 (0.41-1.75)	0.723	1.18 (0.46-3.02)	0.323	0.69 (0.33-1.44)
	Overdominant	CC+TT	132 (62.9%)	129 (70.5%)	131 (65.5%)	Ref	-	Ref	-	Ref	-
		CT	78 (37.1%)	54 (29.5%)	69 (34.5%)	0.271	0.76 (0.47-1.23)	0.274	0.68 (0.34-1.35)	0.186	0.69 (0.40-1.19)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2228041	Codominant	GG	181 (86.2%)	145 (79.2%)	192 (96.0%)	Ref	-	Ref	-	Ref	-
		GA	25 (11.9%)	33 (18.0%)	6 (3.0%)	0.319	1.38 (0.73-2.60)	0.002	0.08 (0.02-0.39)	0.001	6.41 (2.24-18.32)
		AA	4 (1.9%)	5 (2.7%)	2 (1.0%)	0.326	2.09 (0.48-9.17)	0.198	3.78 (0.50-28.66)	0.744	0.75 (0.14-4.12)
	Additive	G	387 (92.1%)	323 (88.3%)	390 (97.5%)	Ref	-	Ref	-	Ref	-
		A	33 (7.9%)	43 (11.7%)	10 (2.5%)	0.150	1.48 (0.87-2.51)	0.096	0.40 (0.13-1.18)	0.008	3.06 (1.34-6.98)
	Dominant	GG	181 (86.2%)	145 (79.2%)	192 (96.0%)	Ref	-	Ref	-	Ref	-
		GA+AA	29 (13.8%)	38 (20.8%)	8 (4.0%)	0.213	1.46 (0.81-2.64)	0.017	0.21 (0.06-0.76)	0.002	4.39 (1.73-11.12)
	Recessive	GG+GA	206 (98.1%)	178 (97.3%)	198 (99.0%)	Ref	-	Ref	-	Ref	-
		AA	4 (1.9%)	5 (2.7%)	2 (1.0%)	0.376	1.92 (0.45-8.16)	0.175	3.93 (0.54-28.37)	0.588	0.63 (0.11-3.41)
	Overdominant	GG+AA	185 (88.1%)	150 (82.0%)	194 (97.0%)	Ref	-	Ref	-	Ref	-
		GA	25 (11.9%)	33 (18.0%)	6 (3.0%)	0.347	1.35 (0.72-2.54)	0.002	0.09 (0.02-0.40)	4.81×10^{-4}	6.46 (2.27-18.40)
rs2228036	Codominant	GG	134 (63.8%)	95 (52.0%)	127 (63.5%)	Ref	-	Ref	-	Ref	-
		GT	69 (32.9%)	72 (39.3%)	57 (28.5%)	0.581	1.15 (0.70-1.87)	0.267	0.67 (0.32-1.37)	0.040	1.77 (1.03-3.04)
		TT	7 (3.3%)	16 (8.7%)	16 (8.0%)	0.042	2.84 (1.04-7.77)	0.806	1.21 (0.26-5.65)	0.406	1.48 (0.59-3.73)
	Additive	G	337 (80.2%)	262 (71.6%)	311 (77.8%)	Ref	-	Ref	-	Ref	-
		T	83 (19.8%)	104 (28.4%)	89 (22.2%)	0.087	1.38 (0.95-2.01)	0.447	0.80 (0.45-1.42)	0.053	1.50 (0.99-2.27)
	Dominant	GG	134 (63.8%)	95 (52.0%)	127 (63.5%)	Ref	-	Ref	-	Ref	-
		GT+TT	76 (36.2%)	88 (48.0%)	73 (36.5%)	0.266	1.30 (0.82-2.06)	0.321	0.71 (0.36-1.40)	0.034	1.74 (1.04-2.92)
	Recessive	GG+GT	203 (96.7%)	167 (91.3%)	184 (92.0%)	Ref	-	Ref	-	Ref	-
		TT	7 (3.3%)	16 (8.7%)	16 (8.0%)	0.047	2.73 (1.01-7.34)	0.831	1.19 (0.24-5.86)	0.600	1.28 (0.51-3.20)
	Overdominant	GG+TT	141 (67.1%)	111 (60.7%)	143 (71.5%)	Ref	-	Ref	-	Ref	-
		GT	69 (32.9%)	72 (39.3%)	57 (28.5%)	0.916	1.03 (0.64-1.65)	0.268	0.67 (0.33-1.36)	0.057	1.68 (0.98-2.87)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs1760898	Codominant	CC	85 (40.5%)	81 (44.3%)	90 (45.0%)	Ref	-	Ref	-	Ref	-
		CA	88 (41.9%)	77 (42.0%)	88 (44.0%)	0.859	0.96 (0.58-1.58)	0.336	0.68 (0.32-1.48)	0.617	1.15 (0.66-1.99)
		AA	37 (17.6%)	25 (13.7%)	22 (11.0%)	0.176	0.63 (0.33-1.23)	0.297	0.61 (0.24-1.55)	0.920	1.04 (0.48-2.26)
	Additive	C	258 (61.4%)	239 (65.3%)	268 (67.0%)	Ref	-	Ref	-	Ref	-
		A	162 (38.6%)	127 (34.7%)	132 (33.0%)	0.201	0.81 (0.58-1.12)	0.196	0.73 (0.45-1.18)	0.819	1.04 (0.72-1.52)
	Dominant	CC	85 (40.5%)	81 (44.3%)	90 (45.0%)	Ref	-	Ref	-	Ref	-
		CA+AA	125 (59.5%)	102 (55.7%)	110 (55.0%)	0.473	0.85 (0.54-1.33)	0.237	0.67 (0.35-1.30)	0.696	1.11 (0.67-1.83)
	Recessive	CC+CA	173 (82.4%)	158 (86.3%)	178 (89.0%)	Ref	-	Ref	-	Ref	-
		AA	37 (17.6%)	25 (13.7%)	22 (11.0%)	0.161	0.64 (0.34-1.20)	0.434	0.70 (0.28-1.72)	0.899	0.95 (0.44-2.06)
	Overdominant	CC+AA	122 (58.1%)	106 (58.0%)	112 (56.0%)	Ref	-	Ref	-	Ref	-
		CA	88 (41.9%)	77 (42.0%)	88 (44.0%)	0.741	1.08 (0.68-1.71)	0.537	0.81 (0.41-1.60)	0.634	1.13 (0.68-1.88)
rs1760897	Codominant	TT	92 (43.8%)	70 (38.3%)	73 (36.5%)	Ref	-	Ref	-	Ref	-
		TC	81 (38.6%)	80 (43.7%)	90 (45.0%)	0.481	1.20 (0.73-1.97)	0.640	1.18 (0.58-2.41)	0.991	1.00 (0.58-1.75)
		CC	37 (17.6%)	33 (18.0%)	37 (18.5%)	0.399	1.31 (0.70-2.47)	0.508	1.36 (0.55-3.35)	0.627	0.85 (0.43-1.67)
	Additive	T	265 (63.1%)	220 (60.1%)	236 (59.0%)	Ref	-	Ref	-	Ref	-
		C	155 (36.9%)	146 (39.9%)	164 (41.0%)	0.366	1.16 (0.84-1.62)	0.455	1.20 (0.75-1.91)	0.602	0.91 (0.63-1.30)
	Dominant	TT	92 (43.8%)	70 (38.3%)	73 (36.5%)	Ref	-	Ref	-	Ref	-
		TC+CC	118 (56.2%)	113 (61.7%)	127 (63.5%)	0.410	1.21 (0.76-1.93)	0.503	1.26 (0.65-2.44)	0.822	0.94 (0.56-1.58)
	Recessive	TT+TC	173 (82.4%)	150 (82.0%)	163 (81.5%)	Ref	-	Ref	-	Ref	-
		CC	37 (17.6%)	33 (18.0%)	37 (18.5%)	0.564	1.19 (0.66-2.15)	0.632	1.22 (0.53-2.81)	0.515	0.81 (0.43-1.53)
	Overdominant	TT+CC	129 (61.4%)	103 (56.3%)	110 (55.0%)	Ref	-	Ref	-	Ref	-
		TC	81 (38.6%)	80 (43.7%)	90 (45.0%)	0.708	1.09 (0.69-1.73)	0.769	1.10 (0.57-2.15)	0.769	1.08 (0.65-1.79)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs2184282	Codominant	AA	138 (65.7%)	134 (73.2%)	97 (48.5%)	Ref	-	Ref	-	Ref	-
		AG	58 (27.6%)	41 (22.4%)	69 (34.5%)	0.108	0.64 (0.37-1.10)	0.015	2.43 (1.18-4.97)	0.002	0.39 (0.22-0.70)
		GG	14 (6.7%)	8 (4.4%)	34 (17.0%)	0.550	0.74 (0.27-2.01)	0.004	4.60 (1.63-12.95)	2.38×10^{-5}	0.11 (0.04-0.31)
	Additive	A	334 (79.5%)	309 (84.4%)	263 (65.8%)	Ref	-	Ref	-	Ref	-
		G	86 (20.5%)	57 (15.6%)	137 (34.2%)	0.128	0.72 (0.47-1.10)	2.95×10^{-4}	2.52 (1.53-4.16)	7.81×10^{-8}	0.31 (0.20-0.47)
	Dominant	AA	138 (65.7%)	134 (73.2%)	97 (48.5%)	Ref	-	Ref	-	Ref	-
		AG+GG	72 (34.3%)	49 (26.8%)	103 (51.5%)	0.105	0.66 (0.40-1.09)	0.002	2.92 (1.49-5.73)	1.10×10^{-5}	0.30 (0.17-0.51)
	Recessive	AA+AG	196 (93.3%)	175 (95.6%)	166 (83.0%)	Ref	-	Ref	-	Ref	-
		GG	14 (6.7%)	8 (4.4%)	34 (17.0%)	0.723	0.84 (0.31-2.23)	0.021	3.12 (1.19-8.19)	3.29×10^{-4}	0.18 (0.07-0.46)
	Overdominant	AA+GG	152 (72.4%)	142 (77.6%)	131 (65.5%)	Ref	-	Ref	-	Ref	-
		AG	58 (27.6%)	41 (22.4%)	69 (34.5%)	0.124	0.66 (0.39-1.12)	0.086	1.82 (0.92-3.61)	0.023	0.52 (0.30-0.91)
rs4246977	Codominant	TT	57 (27.1%)	45 (24.6%)	127 (63.5%)	Ref	-	Ref	-	Ref	-
		TC	105 (50.0%)	99 (54.1%)	60 (30.0%)	0.493	1.21 (0.70-2.11)	2.88×10^{-4}	0.22 (0.10-0.50)	8.99×10^{-7}	4.20 (2.37-7.44)
		CC	48 (22.9%)	39 (21.3%)	13 (6.5%)	0.525	0.81 (0.42-1.56)	4.58×10^{-5}	0.09 (0.03-0.28)	8.50×10^{-6}	6.76 (2.92-15.69)
	Additive	T	219 (52.1%)	189 (51.6%)	314 (78.5%)	Ref	-	Ref	-	Ref	-
		C	201 (47.9%)	177 (48.4%)	86 (21.5%)	0.538	0.90 (0.66-1.25)	2.68×10^{-7}	0.25 (0.15-0.42)	1.35×10^{-8}	3.08 (2.09-4.54)
	Dominant	TT	57 (27.1%)	45 (24.6%)	127 (63.5%)	Ref	-	Ref	-	Ref	-
		TC+CC	153 (72.9%)	138 (75.4%)	73 (36.5%)	0.807	1.07 (0.64-1.79)	4.59×10^{-6}	0.19 (0.09-0.39)	1.58×10^{-8}	4.76 (2.77-8.19)
	Recessive	TT+TC	162 (77.1%)	144 (78.7%)	187 (93.5%)	Ref	-	Ref	-	Ref	-
		CC	48 (22.9%)	39 (21.3%)	13 (6.5%)	0.189	0.69 (0.39-1.20)	0.001	0.15 (0.05-0.45)	0.003	3.36 (1.50-7.51)
	Overdominant	TT+CC	105 (50.0%)	84 (45.9%)	140 (70.0%)	Ref	-	Ref	-	Ref	-
		TC	105 (50.0%)	99 (54.1%)	60 (30.0%)	0.195	1.35 (0.86-2.12)	0.030	0.47 (0.24-0.93)	3.26×10^{-4}	2.62 (1.55-4.44)

SNP	Genetic Model	Genotype/ Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs75932631	Codominant	TT	162 (77.1%)	146 (79.8%)	113 (56.5%)	Ref	-	Ref	-	Ref	-
		TC	42 (20.0%)	33 (18.0%)	70 (35.0%)	0.806	0.93 (0.51-1.68)	1.66×10^{-4}	4.47 (2.05-9.73)	2.42×10^{-4}	0.33 (0.18-0.59)
		CC	6 (2.9%)	4 (2.2%)	17 (8.5%)	0.799	0.83 (0.19-3.55)	0.012	5.86 (1.48-23.16)	0.001	0.09 (0.02-0.36)
	Additive	T	366 (87.1%)	325 (88.8%)	296 (74.0%)	Ref	-	Ref	-	Ref	-
		C	54 (12.9%)	41 (11.2%)	104 (26.0%)	0.720	0.91 (0.56-1.50)	1.42×10^{-5}	3.52 (1.99-6.22)	9.00×10^{-7}	0.30 (0.18-0.48)
	Dominant	TT	162 (77.1%)	146 (79.8%)	113 (56.5%)	Ref	-	Ref	-	Ref	-
		TC+CC	48 (22.9%)	37 (20.2%)	87 (43.5%)	0.747	0.91 (0.52-1.59)	3.61×10^{-5}	4.57 (2.22-9.39)	1.09×10^{-5}	0.28 (0.16-0.49)
	Recessive	TT+TC	204 (97.1%)	179 (97.8%)	183 (91.5%)	Ref	-	Ref	-	Ref	-
		CC	6 (2.9%)	4 (2.2%)	17 (8.5%)	0.838	0.86 (0.20-3.67)	0.051	3.86 (0.99-14.98)	0.004	0.15 (0.04-0.56)
	Overdominant	TT+CC	168 (80.0%)	150 (82.0%)	130 (65.0%)	Ref	-	Ref	-	Ref	-
		TC	42 (20.0%)	33 (18.0%)	70 (35.0%)	0.798	0.93 (0.52-1.66)	0.001	3.57 (1.72-7.42)	0.001	0.38 (0.21-0.68)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *TEP1*, telomerase associated protein 1; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>TEPI</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs2104978	AA	208 (100%)	104 (100%)	192 (96.0%)	Ref	-	Ref	-
	AG	0 (0%)	0 (0%)	3 (1.5%)	*	-	*	-
	GG	0 (0%)	0 (0%)	5 (2.5%)	*	-	*	-
	A	416 (100.0%)	208 (100.0%)	387 (96.8%)	Ref	-	Ref	-
rs1713449	G	0 (0.0%)	0 (0.0%)	13 (3.3%)	*	-	*	-
	CC	86 (41.3%)	61 (58.7%)	99 (49.5%)	Ref	-	Ref	-
	CT	102 (49.0%)	37 (35.6%)	69 (34.5%)	0.013	0.59 (0.39-0.90)	0.594	1.15 (0.69-1.92)
	TT	20 (9.6%)	6 (5.8%)	32 (16.0%)	0.304	1.39 (0.74-2.61)	0.009	3.29 (1.30-8.32)
rs2228041	C	274 (65.9%)	159 (76.4%)	267 (66.8%)	Ref	-	Ref	-
	T	142 (34.1%)	49 (23.6%)	133 (33.3%)	0.789	0.96 (0.72-1.29)	0.013	1.62 (1.10-2.37)
	GG	208 (100%)	104 (100%)	192 (96.0%)	Ref	-	Ref	-
	GA	0 (0%)	0 (0%)	6 (3.0%)	*	-	*	-
rs2228036	AA	0 (0%)	0 (0%)	2 (1.0%)	*	-	*	-
	G	416 (100.0%)	208 (100.0%)	390 (97.5%)	Ref	-	Ref	-
	A	0 (0.0%)	0 (0.0%)	10 (2.5%)	*	-	*	-
	GG	153 (73.6%)	69 (66.3%)	127 (63.5%)	Ref	-	Ref	-
rs2228036	GT	55 (26.4%)	32 (30.8%)	57 (28.5%)	0.321	1.25 (0.81-1.94)	1.000	0.97 (0.57-1.63)
	TT	0 (0.0%)	3 (2.9%)	16 (8.0%)	*	-	0.125	2.90 (0.82-10.29)
	G	361 (86.8%)	170 (81.7%)	311 (77.8%)	Ref	-	Ref	-
	T	55 (13.2%)	38 (18.3%)	89 (22.3%)	0.001	1.88 (1.30-2.72)	0.252	1.28 (0.84-1.96)

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs1760898	CC	70 (33.7%)	49 (47.1%)	90 (45.0%)	Ref	-	Ref	-
	CA	101 (48.6%)	43 (41.3%)	88 (44.0%)	0.071	0.68 (0.44-1.04)	0.674	1.11 (0.67-1.84)
	AA	37 (17.8%)	12 (11.5%)	22 (11.0%)	0.013	0.46 (0.25-0.85)	1.000	1.00 (0.46-2.19)
	C	241 (57.9%)	141 (67.8%)	268 (67.0%)	Ref	-	Ref	-
	A	175 (42.1%)	67 (32.2%)	132 (33.0%)	0.008	0.68 (0.51-0.90)	0.844	1.04 (0.73-1.48)
rs1760897	TT	129 (62.0%)	71 (68.3%)	73 (36.5%)	Ref	-	Ref	-
	TC	69 (33.2%)	31 (29.8%)	90 (45.0%)	1.05×10^{-4}	2.30 (1.51-3.53)	7.90×10^{-5}	2.82 (1.67-4.76)
	CC	10 (4.8%)	2 (1.9%)	37 (18.5%)	<0.000001	6.54 (3.07-13.91)	1.00×10^{-6}	17.99 (4.18-77.47)
	T	327 (78.6%)	173 (83.2%)	236 (59.0%)	Ref	-	Ref	-
	C	89 (21.4%)	35 (16.8%)	164 (41.0%)	<0.000001	2.55 (1.88-3.47)	<0.000001	3.43 (2.27-5.20)
rs2184282	AA	120 (57.7%)	65 (62.5%)	97 (48.5%)	Ref	-	Ref	-
	AG	76 (36.5%)	33 (31.7%)	69 (34.5%)	0.589	0.89 (0.58-1.36)	0.203	1.40 (0.83-2.36)
	GG	12 (5.8%)	6 (5.8%)	34 (17.0%)	3.19×10^{-4}	3.51 (1.72-7.13)	0.003	3.80 (1.51-9.56)
	A	316 (76.0%)	163 (78.4%)	263 (65.8%)	Ref	-	Ref	-
	G	100 (24.0%)	45 (21.6%)	137 (34.3%)	0.001	1.65 (1.21-2.23)	0.001	1.89 (1.28-2.79)
rs4246977	TT	90 (43.3%)	51 (49.0%)	127 (63.5%)	Ref	-	Ref	-
	TC	98 (47.1%)	45 (43.3%)	60 (30.0%)	8.50×10^{-5}	0.43 (0.29-0.66)	0.015	0.54 (0.32-0.89)
	CC	20 (9.6%)	8 (7.7%)	13 (6.5%)	0.039	0.46 (0.22-0.97)	0.370	0.65 (0.26-1.67)
	T	278 (66.8%)	147 (70.7%)	314 (78.5%)	Ref	-	Ref	-
	C	138 (33.2%)	61 (29.3%)	86 (21.5%)	1.88×10^{-4}	0.55 (0.40-0.76)	0.032	0.66 (0.45-0.97)

SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs75932631	TT	131 (63.0%)	67 (64.4%)	113 (56.5%)	Ref	-	Ref	-
	TC	68 (32.7%)	33 (31.7%)	70 (35.0%)	0.407	1.19 (0.79-1.81)	0.380	1.26 (0.75-2.10)
	CC	9 (4.3%)	4 (3.8%)	17 (8.5%)	0.064	2.19 (0.94-5.10)	0.146	2.52 (0.81-7.80)
	T	330 (79.3%)	167 (80.3%)	296 (74.0%)	Ref	-	Ref	-
	C	86 (20.7%)	41 (19.7%)	104 (26.0%)	0.072	1.35 (0.97-1.87)	0.084	1.43 (0.95-2.15)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *Analysis could not be performed because the representatives of an allele were absent in a study group. *TEPI*, telomerase associated protein 1; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S12: Genotype and allele distribution of *HSP90AA1* SNP

[A] Comparison of genotype and allele distribution among HAPE-f, HAPE-p and HLs.

<i>HSP90AA1</i>											
SNP	Genetic Model	Genotype / Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs8005905	Codominant	AA	166 (79.0%)	143 (78.1%)	137 (68.5%)	Ref	-	Ref	-	Ref	-
		AT	38 (18.1%)	36 (19.7%)	61 (30.5%)	0.976	1.01 (0.56-1.82)	0.681	0.84 (0.36-1.95)	0.374	0.77 (0.43-1.38)
		TT	6 (2.9%)	4 (2.2%)	2 (1.0%)	0.988	1.01 (0.23-4.37)	0.001	0.01 (0.001-0.16)	0.553	1.93 (0.22-16.96)
	Additive	A	370 (88.1%)	322 (88.0%)	335 (83.8%)	Ref	-	Ref	-	Ref	-
		T	50 (11.9%)	44 (12.0%)	65 (16.2%)	0.993	1.00 (0.61-1.65)	0.198	0.61 (0.29-1.29)	0.625	0.88 (0.52-1.48)
	Dominant	AA	166 (79.0%)	143 (78.1%)	137 (68.5%)	Ref	-	Ref	-	Ref	-
		AT+TT	44 (21.0%)	40 (21.9%)	63 (31.5%)	0.992	1.00 (0.58-1.75)	0.413	0.71 (0.32-1.61)	0.472	0.81 (0.45-1.44)
	Recessive	AA+AT	204 (97.1%)	179 (97.8%)	198 (99.0%)	Ref	-	Ref	-	Ref	-
		TT	6 (2.9%)	4 (2.2%)	2 (1.0%)	0.999	1.00 (0.23-4.27)	0.001	0.01 (0.001-0.15)	0.518	2.14 (0.21-21.35)
	Overdominant	AA+TT	172 (81.9%)	147 (80.3%)	139 (69.5%)	Ref	-	Ref	-	Ref	-
		AT	38 (18.1%)	36 (19.7%)	61 (30.5%)	0.991	1.00 (0.56-1.80)	0.817	0.91 (0.40-2.06)	0.362	0.76 (0.42-1.37)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *HSP90AA1*, heat shock protein 90; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

[B] Comparison of genotype and allele distribution in HLs with Han Chinese (CHB+CHS) population and Japanese (JPT) population.

<i>HSP90A1</i>								
SNP	Genotype/ Allele	CHB+CHS (Ref, n=204)	JPT (Ref, n=104)	HLs (n=200)	HLs vs CHB+CHS		HLs vs JPT	
					p value	OR (95%CI)	p value	OR (95%CI)
rs8005905	AA	134 (64.4%)	66 (63.5%)	137 (68.5%)	Ref	-	Ref	-
	AT	64 (30.8%)	35 (33.7%)	61 (30.5%)	0.746	0.93 (0.61-1.42)	0.501	0.84 (0.51-1.40)
	TT	10 (4.8%)	3 (2.9%)	2 (1.0%)	0.035	0.20 (0.04-0.91)	0.335	0.32 (0.05-1.97)
	A T	332 (79.8%) 84 (20.2%)	167 (80.3%) 41 (19.7%)	335 (83.8%) 65 (16.3%)	Ref 0.145	- 0.77 (0.54-1.10)	Ref 0.286	- 0.79 (0.51-1.22)

SISA online tool was used to obtain p values. Significance was maintained at ≤ 0.05 after FDR correction. *HSP90A1*, heat shock protein 90; CHB+CHS, Han Chinese population comprising of Han Chinese in Beijing (CHB) and Southern Han Chinese (CHS); JPT, Japanese population; HLs, highlanders; Ref, reference; n, number of samples; OR, odds ratio; CI, confidence interval.

Supplementary Table S13: Genotype and allele distribution and comparison of *PTGES3* SNPs in HAPE-f, HAPE-p and HLs

<i>PTGES3</i>											
SNP	Genetic Model	Genotype / Allele	HAPE-f (n=210)	HAPE-p (n=183)	HLs (n=200)	HAPE-p vs HAPE-f		HLs vs HAPE-f		HAPE-p vs HLs	
						p value	OR (95%CI)	p value	OR (95%CI)	p value	OR (95%CI)
rs191628793	Codominant	AA	197 (93.8%)	165 (90.2%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
		AC	11 (5.2%)	11 (6.0%)	5 (2.5%)	0.971	0.98 (0.35-2.75)	0.009	0.08 (0.01-0.54)	0.157	2.64 (0.69-10.12)
		CC	2 (1.0%)	7 (3.8%)	5 (2.5%)	0.322	2.42 (0.42-13.98)	0.165	4.57 (0.53-38.97)	0.740	1.27 (0.31-5.29)
	Additive	A	405 (96.4%)	341 (93.2%)	385 (96.3%)	Ref	-	Ref	-	Ref	-
		C	15 (3.6%)	25 (6.8%)	15 (3.8%)	0.324	1.47 (0.69-3.13)	0.974	0.98 (0.28-3.37)	0.232	1.64 (0.73-3.70)
	Dominant	AA	197 (93.8%)	165 (90.2%)	190 (95.0%)	Ref	-	Ref	-	Ref	-
		AC+CC	13 (6.2%)	18 (9.8%)	10 (5.0%)	0.589	1.27 (0.53-3.03)	0.329	0.46 (0.09-2.21)	0.207	1.90 (0.70-5.15)
	Recessive	AA+AC	208 (99.0%)	176 (96.2%)	195 (97.5%)	Ref	-	Ref	-	Ref	-
		CC	2 (1.0%)	7 (3.8%)	5 (2.5%)	0.295	2.50 (0.45-13.98)	0.160	4.47 (0.55-36.20)	0.779	1.23 (0.30-5.08)
	Overdominant	AA+CC	199 (94.8%)	172 (94.0%)	195 (97.5%)	Ref	-	Ref	-	Ref	-
		AC	11 (5.2%)	11 (6.0%)	5 (2.5%)	0.939	0.96 (0.34-2.69)	0.009	0.08 (0.01-0.54)	0.158	2.63 (0.69-10.02)

SPSS 16.0 was used to obtain p values after adjusting with age and gender. Significance was maintained at ≤ 0.05 after FDR correction. *PTGES3*, Prostaglandin E Synthase 3; HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; n, number of samples; OR, odds ratio; CI, confidence interval; Ref, reference.

Note: The genotype data for P23 rs191628793A/C in CHB+CHS and JPT populations were unavailable.

Supplementary Table S14: Correlation analysis between biomarkers and clinical parameters in the three study groups

HAPE-f					
Clinical parameters/ Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2 α	Total antioxidant activity
MAP	r = -0.003 p = 0.97	r = 0.02 p = 0.81	r = -0.04 p = 0.71	r = 0.07 p = 0.35	r = 0.10 p = 0.37
SaO ₂	r = -0.04 p = 0.59	r = 0.05 p = 0.59	r = -0.09 p = 0.46	r = -0.15 p = 0.05	r = 0.09 p = 0.44
HAPE-p					
Clinical parameters/ Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2 α	Total antioxidant activity
MAP	r = -0.05 p = 0.52	r = -0.06 p = 0.57	r = 0.21 p = 0.10	r = -0.03 p = 0.80	r = -0.22 p = 0.08
SaO ₂	r = -0.02 p = 0.77	r = -0.23 p = 0.02	r = 0.14 p = 0.27	r = 0.07 p = 0.46	r = 0.19 p = 0.13
HLs					
Clinical parameters/ Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2 α	Total antioxidant activity
MAP	r = 0.09 p = 0.20	r = 0.09 p = 0.26	r = -0.07 p = 0.40	r = 0.05 p = 0.48	r = -0.25 p = 0.003
SaO ₂	r = 0.08 p = 0.30	r = 0.10 p = 0.22	r = 0.13 p = 0.11	r = -0.08 p = 0.31	r = 0.33 p = 5.35 $\times 10^{-5}$

SPSS 16.0 was used to obtain p values and the significance was maintained at $p \leq 0.05$ after Bonferroni's correction. P values were obtained after adjusting with age, gender, and BMI. HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; MAP, Mean arterial pressure; SaO₂, arterial oxygen saturation; TERT, Telomerase reverse transcriptase; 8-iso PGF2 α , 8-isoprostaglandin F2 α ; r, correlation coefficient; p, p value.

Supplementary Table S15: Correlation analysis between the biomarkers in the three study groups

(A) HAPE-f

Relative telomere length	r = 1				
Telomerase Activity	r = -0.01 p = 0.92	r = 1			
TERT	r = -0.15 p = 0.24	r = 0.15 p = 0.23	r = 1		
8-iso PGF2α	r = 0.15 p = 0.05	r = 0.17 p = 0.06	r = -0.01 p = 0.96	r = 1	
Total antioxidant activity	r = -0.03 p = 0.77	r = -0.22 p = 0.09	r = -0.34 p = 0.002	r = 0.03 p = 0.80	r = 1
Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2α	Total antioxidant activity

(B) HAPE-p

Relative telomere length	r = 1				
Telomerase Activity	r = 0.09 p = 0.35	r = 1			
TERT	r = -0.14 p = 0.27	r = 0.09 p = 0.46	r = 1		
8-iso PGF2α	r = -0.03 p = 0.80	r = 0.04 p = 0.77	r = -0.24 p = 0.06	r = 1	
Total antioxidant activity	r = -0.03 p = 0.81	r = 0.24 p = 0.06	r = 0.35 p = 0.004	r = 0.09 p = 0.49	r = 1
Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2α	Total antioxidant activity

(C) HLs

Relative telomere length	r = 1				
Telomerase Activity	r = -0.05 p = 0.49	r = 1			
TERT	r = 0.02 p = 0.83	r = -0.15 p = 0.07	r = 1		
8-iso PGF2α	r = 0.03 p = 0.68	r = -0.05 p = 0.49	r = 0.02 p = 0.81	r = 1	
Total antioxidant activity	r = -0.05 p = 0.53	r = 0.03 p = 0.68	r = 0.10 p = 0.25	r = -0.23 p = 0.005	r = 1
Biomarkers	Relative telomere length	Telomerase Activity	TERT	8-iso PGF2α	Total antioxidant activity

SPSS 16.0 was used to obtain p values, and the significance was maintained at $p \leq 0.05$ after Bonferroni's correction. P values were obtained after adjusting with age, gender and BMI. HAPE-f, HAPE-free; HAPE-p, HAPE-patients; HLs, Highlanders; TERT, Telomerase reverse transcriptase; 8-iso PGF2 α . 8-isoprostaglandin F2 α ; r, correlation coefficient; p, p-value.