

Figure S1. Representative sequences for telomerase reverse transcriptase rs2853669 genotypes. (A) Homozygous variant, (B) homozygous wild-type and (C) heterozygous.

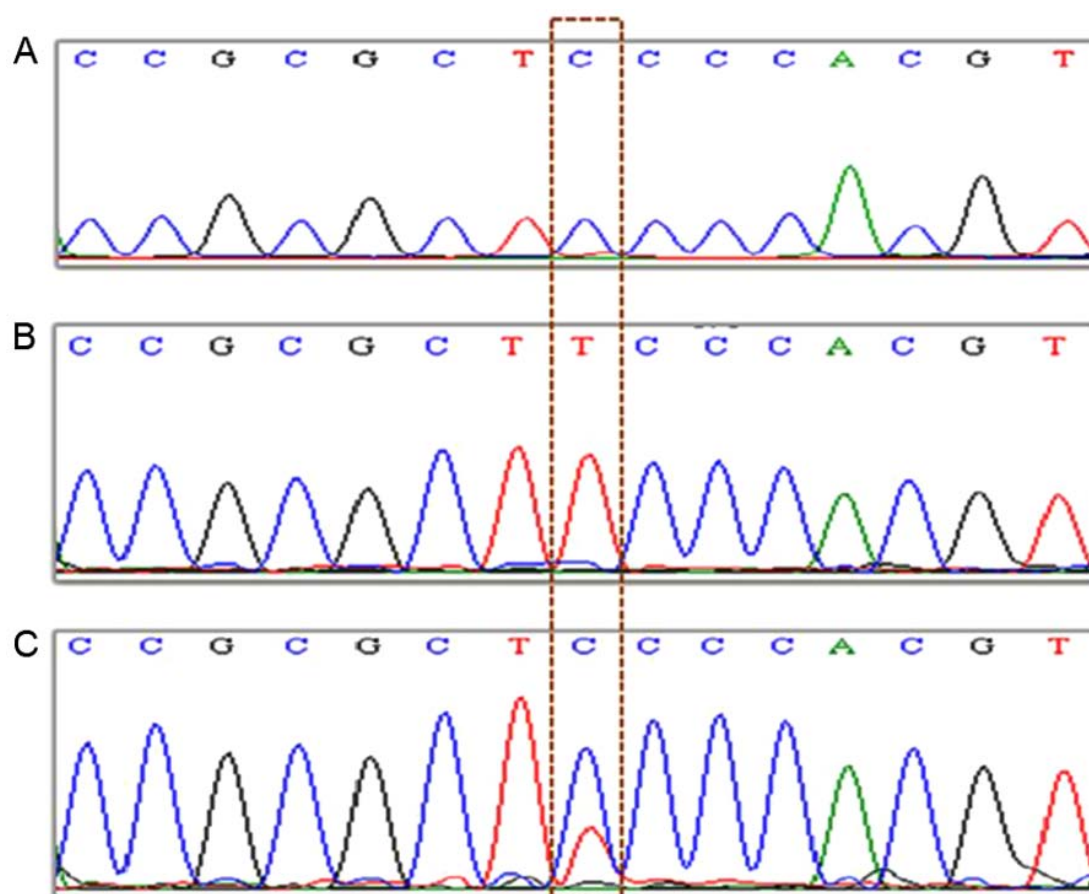


Table SI. Subgroup analysis by type of cancer and ethnicity in the meta-analysis on the association between telomerase reverse transcriptase rs2853669 polymorphism and cancer risk.

A, Allele model								
Sub group	Studies (n)	Heterogeneity test			Association test			Egger's test P-value
		I ²	P-value	Model	OR	95% CI	P-value	
Type of cancer								
Overall	17	0.81	<0.001	REM	1.07	0.96-1.18	0.227	0.932
AML	1	-	-	FEM	1.46	1.17-1.81	0.001	-
Breast cancer	5	0.13	0.332	FEM	0.99	0.92-1.05	0.722	0.473
Cervical cancer	1	-	-	FEM	1.23	0.96-1.55	0.092	-
Colorectal cancer	1	-	-	FEM	1.07	0.72-1.58	0.729	-
Gastric cancer	2	0.94	<0.001	REM	1.22	0.54-2.71	0.634	-
Glioblastoma	1	-	-	FEM	0.87	0.64-1.16	0.350	-
HCC	1	-	-	FEM	0.61	0.48-0.78	<0.001	-
Lung cancer	3	0.72	0.029	REM	1.25	1.03-1.50	0.020	0.528
NHL	1	-	-	FEM	1.05	0.88-1.24	0.575	-
SCCHN	1	-	-	FEM	0.98	0.84-1.12	0.775	-
Ethnicity								
Overall	17	0.81	<0.001	REM	1.07	0.96-1.18	0.227	0.932
Asian	6	0.90	<0.001	REM	1.19	0.91-1.52	0.189	0.922
Caucasian	11	0.48	0.038	REM	1.01	0.92-1.08	0.895	0.807
B, Dominant model								
Type of cancer								
Overall	17	0.68	<0.001	REM	1.08	0.96-1.21	0.163	0.703
AML	1	-	-	FEM	1.41	1.04-1.91	0.024	-
Breast cancer	5	0.00	0.769	FEM	1.03	0.93-1.13	0.567	0.664
Cervical cancer	1	-	-	FEM	0.89	0.59-1.33	0.575	-
Colorectal cancer	1	-	-	FEM	1.12	0.62-1.98	0.703	-
Gastric cancer	2	0.90	0.001	REM	1.22	0.51-2.90	0.655	-
Glioblastoma	1	-	-	FEM	0.79	0.54-1.14	0.207	-
HCC	1	-	-	FEM	0.65	0.46-0.90	0.012	-
Lung cancer	3	0.76	0.016	REM	1.28	0.97-1.68	0.076	0.365
NHL	1	-	-	FEM	1.14	0.91-1.41	0.240	-
SCCHN	1	-	-	FEM	0.99	0.82-1.19	0.941	-
Ethnicity								
Overall	17	0.68	<0.001	REM	1.08	0.96-1.21	0.163	0.703
Asian	6	0.85	<0.001	REM	1.17	0.87-1.55	0.284	0.810
Caucasian	11	0.05	0.392	FEM	1.04	0.96-1.11	0.320	0.579
C, Recessive model								
Type of cancer								
Overall	17	0.809	<0.001	REM	1.0702	0.87-1.30	0.509	0.978
AML	1	-	-	FEM	2.2203	1.44-3.41	<0.001	-
Breast cancer	5	0.725	0.006	REM	0.8219	0.63-1.07	0.147	0.203
Cervical cancer	1	-	-	FEM	1.706	1.19-2.42	0.003	-
Colorectal cancer	1	-	-	FEM	1.0675	0.50-2.26	0.865	-
Gastric cancer	2	0.899	0.002	REM	1.414	0.38-5.18	0.601	-
Glioblastoma	1	-	-	FEM	1.0327	0.52-2.01	0.925	-
HCC	1	-	-	FEM	0.4219	0.26-0.65	<0.001	-
Lung cancer	3	0	0.596	FEM	1.4415	1.19-1.73	<0.001	0.897
NHL	1	-	-	FEM	0.8263	0.54-1.25	0.374	-
SCCHN	1	-	-	FEM	0.9191	0.66-1.26	0.607	-

Table SI. Continued.

Sub group	Studies (n)	Heterogeneity test			Association test			Egger's test P-value
		I ²	P-value	Model	OR	95% CI	P-value	
Ethnicity								
Overall	17	0.809	<0.001	REM	1.0702	0.87-1.30	0.509	0.978
Asian	6	0.867	<0.001	REM	1.348	0.88-2.05	0.165	0.798
Caucasian	11	0.672	<0.001	REM	0.9288	0.76-1.13	0.469	0.579

AML, acute myeloid leukemia; NHL, Non-Hodgkin lymphoma; SCCHN, squamous cell carcinoma of the head and neck; HCC, hepatocellular carcinoma; REM, random effect model; FEM, fixed effect model; OR, odds ratio.