

Supplementary Figure

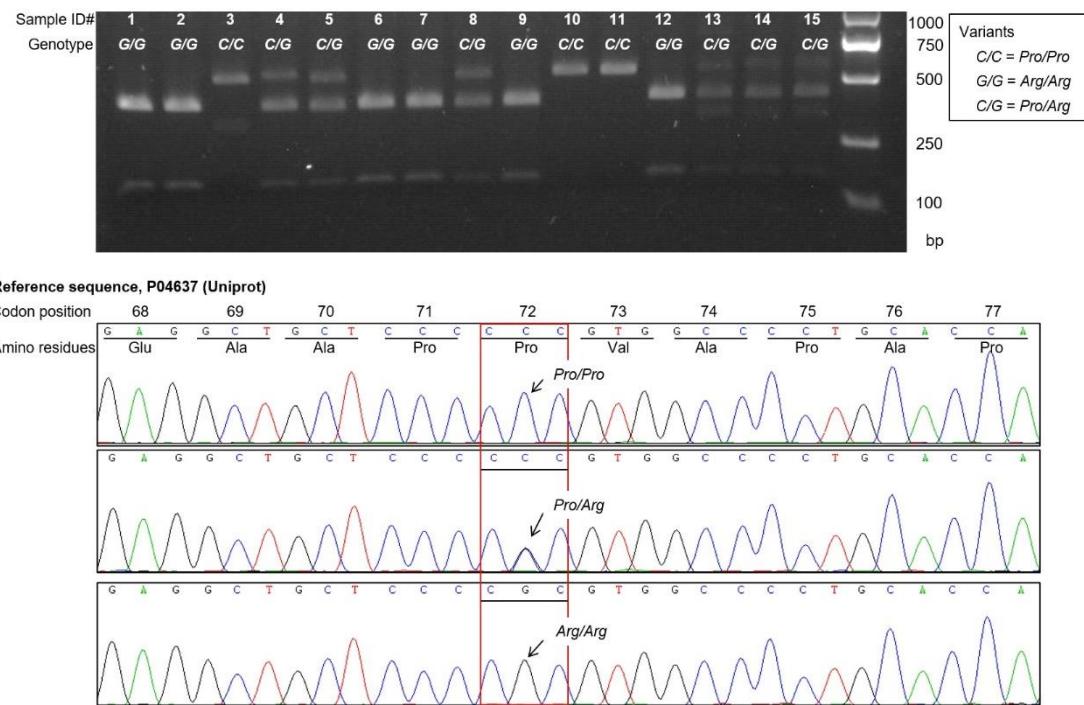


Figure S1. Representative results of *TP53 Pro72Arg* genotyping. A 555-base pair (bp) fragment of the *TP53* was amplified by PCR using a pair of primers of 5'-GTCAGATCCTAGCGTCGAGC-3' and reverse primer 5'- GCAAGAACGCCAGACGGAAA -3', and the allelic discrimination was done by BstUI restriction enzyme digestion (recognition site CGCG). Next, the digested DNA fragments were separated on a 2% agarose gel stained with ethidium bromide, and the homozygous *Pro/Pro* (C/C) genotype was identified by single 555-bp fragments (uncut PCR product), the *Arg/Arg* (G/G) genotype by 429- and 128-bp fragments, and *Pro/Arg* (C/G) heterozygotes by the presence of 3 bands (Upper panel). To examine the accuracy of the allelic discrimination, the DNA direct sequencing of the PCR product (Bottom panel) was performed in 10% samples selected at random from the heterozygous or homozygous subjects and all samples with ambiguous PCR-RFLP results.

Supplementary Tables

Table S1. Primer Sequences

Oligo Name	Gene	Primer Sequence (5' - 3')	RefSeq Accession
MT3307F	<i>MT-ND1</i>	ATACCCATGGCCAACCT	<i>NC_012920.1</i>
MT3456R		AGCGAAGGGTTGATGTAGCCC	
MT8080F	<i>MT-CO2</i>	CCCCACATTAGGCTAAAAACAGAT	<i>NC_012920.1</i>
MT8160F		TATACCCCGGTCGTGTAGC	
β 2M F594	β 2M	TGCTGTCTCCATGTTGATGTATCT	<i>NT_010194.17</i>
β 2M R679		TCTCTGCTCCCCACCTCTAAGT	
MT3163F	<i>MT-RNR2</i>	GCCTTCCCCCGTAAATGATA	<i>NC_012920.1</i>
MT3260R		TTATGCGATTACCGGGCTCT	
MT5907F	<i>MT-CO1</i>	TTCGCCGACCGTTGACTATTCTCT	<i>NC_012920.1</i>
MT6103F		AAGATTATTACAAATGCATGGGC	
MT8898F	<i>ATPase6</i>	CCTAGCCCACCTCTTACCACCA	<i>NC_012920.1</i>
MT9158R		GCTTGGATTAAGGCGACAG	
MT15616F	<i>MT-CYB</i>	CGTCCTTGCCTTATTACTATCCAT	<i>NC_012920.1</i>
MT15704R		GTGGCGAAATATTATGCTTGTGT	
GAPDH 606F	<i>GAPDH</i>	CAAGATCATCAGCAATGCCT	<i>NM_002046.4</i>
GAPDH 698R		ATGAGTCCTTCCACGATACC	

Abbreviations: RefSeq, Reference sequence; MT-ND1, Mitochondrially Encoded NADH Dehydrogenase 1; MT-CO2, Mitochondrially Encoded Cytochrome C Oxidase II; β 2M, Beta-2-Microglobulin; MT-RNR2, Mitochondrially Encoded 16S RRNA; MT-CO1, Mitochondrially Encoded Cytochrome C Oxidase I; ATPase6, Mitochondrially Encoded ATP Synthase Membrane Subunit 6; MT-CYB, Mitochondrially Encoded Cytochrome B; GAPDH, Glyceraldehyde-3-Phosphate Dehydrogenase.

Table S2. Demographic profile of the study subjects

	Patients (N = 206)	Controls (N = 446)	P value
Age at study, Median	63.0 (Range:36 - 90)	64.0 (Range:36 - 90)	NS
Sex (Male/Female)	110/96	225/221	NS
HbAc (%), Mean±SD	9.0 ± 1.9	NA	NA

Abbreviations: NS, not significant ($P > 0.05$); SD, standard deviation; NA, not applicable.