Supplementary data

Table S1. Properties of SNPs examined in this study

SNP	rs132793		rs2075762		rs7252796	
properties	Male	Female	Male	Female	Male	Female
MAF	0.22	0.15	0.12	0.16	0.09	0.12
Heterozygosity	0.34	0.26	0.21	0.28	0.16	0.22
p	>> 0.05	>> 0.05	>> 0.05	>> 0.05	>>0.05	>> 0.05

MAF = minor allele frequency, *p* = *p* values from χ^2 test for Hardy-Weinberg Equilibrium

Table S2. Association of heart problems and eGFR with CKt levels in female nonagenarians by two-way ANOVA

Variable	Df	Sum Sq	Mean Sq	F value	*P*
Cardiac	1	0.0001394	0.00013939	0.2046	0.6539
eGFR	1	0.0001180	0.00011800	0.1732	0.6799
Cardiac x eGFR	1	0.0010369	0.0010369	1.5463	0.2224
Residuals	33	0.0221287	0.00067057		

Cardiac denotes the presence or absence of one or more heart-related problems in medical history (angina, congestive heart failure, heart attack, heart murmur, and other unspecified heart problem). eGFR denotes eGFR values lower than 60 or $\geq$60 by the CKD-EPI equation.

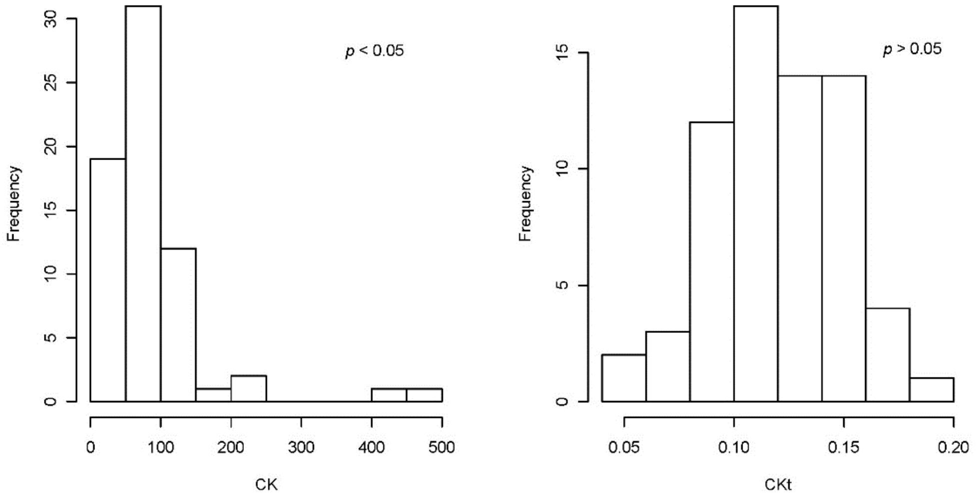

Fig. S1. Distribution of raw CK (left) and transformed CK (CKt) (right) in the Louisiana Healthy Aging Study (LHAS) nonagenarians (n=67). CKt is $CK^{-0.5}$. The Anderson-Darling normality test indicated that the distribution of CK is not normal ($p < 0.001$), while CKt was distributed normally ($p > 0.05$)

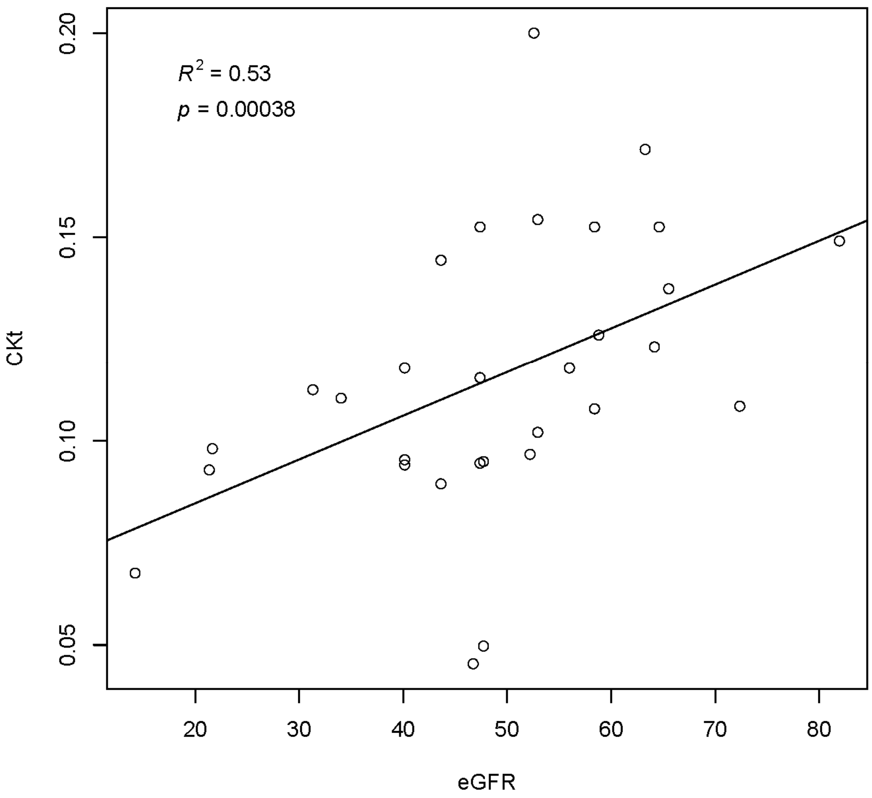

Fig. S2. Scatterplot of eGFR on CKt in the Louisiana Healthy Aging Study (LHAS) nonagenarian males (n=30).

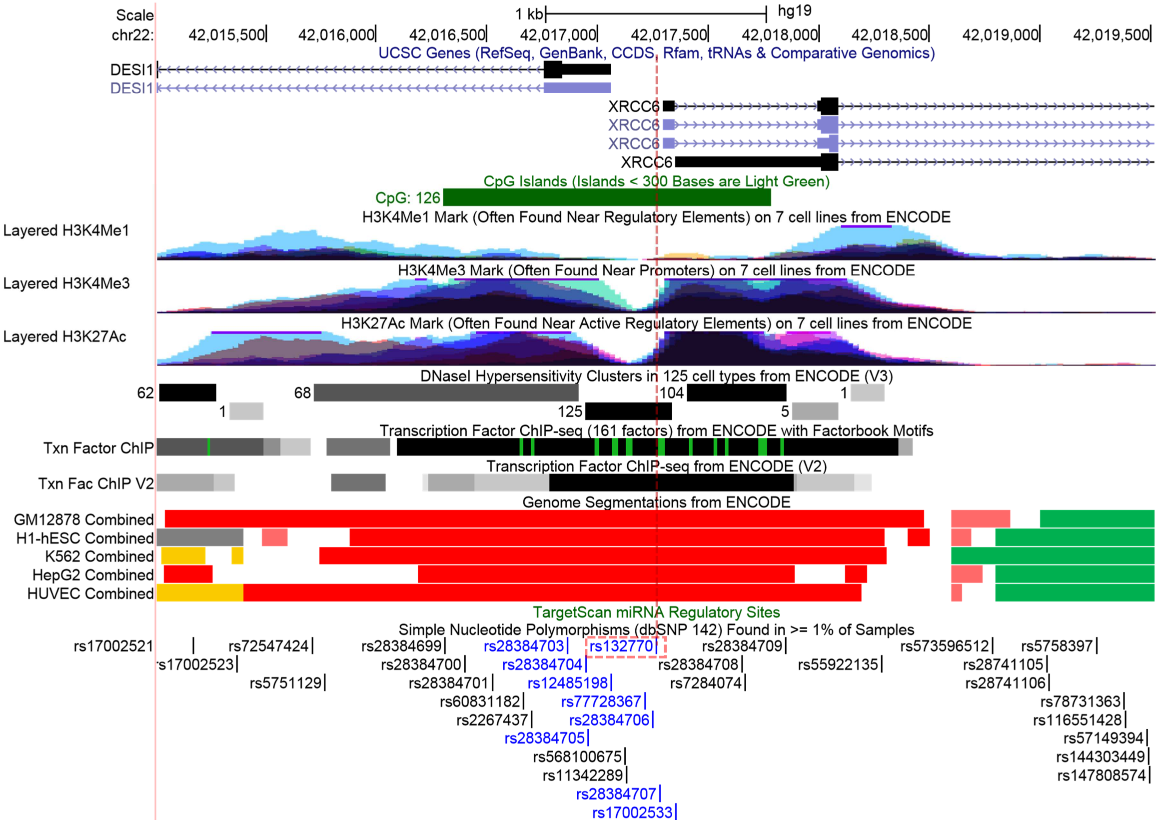

Fig. S3. Genomic features around rs132770 on chromosome 22 from the UCSC Genome Browser. SNP rs132770 in a red, dotted rectangle is in the promoter region of *XRCC6*. SNP IDs in black are in introns and blue in untranslated regions. The CpG Islands track shows a segment with the GC content ≥ 50%, the length > 200 bp , and the ratio observed to expected CpG > 0.6. The number of CG dinucleotides are shown in front of the segment. Colors in the histone modification tracks represent results from different cell lines, with peak levels showing enrichment levels of histone marks. In DNase I Hypersensitivity track, block darkness is proportional to the sensitivity and the numbers show the number of cell lines showing hypersensitivity. The Transcription Factor ChIP-seq tracks show transcription factor binding sites from ChIP-seq experiments. The darkness is proportional to the signal strength, and the green highlights indicate the highest scoring-site motifs. The Genome Segmentations track shows chromatin segments corresponding to different functional states: Red segments depict predicted promoter regions including transcription start sites; pink, promoter flanking regions; green, a predicted transcribed region; yellow, predicted weak enhancer or open chromatin cis regulatory elements; grey, predicted repressed or low activity regions.