Supplementary Table S2: Linear regression analysis in BRCA 1/2 mutation carriers[a]

Dependent variables	Independent variables	β coefficient[b]	p-value[c]	95% C. I. ((Lower) - (Upper limit))
UNG mRNA expression	SNP	-0.292	**0.005**	((-0.585)-(-0.111))
	Cancer	0.029	0.773	((-0.269)-(0.201))
Adjusted TL	SNP	-0.239	0.053	((-1.701)-(0.010))
	Cancer	-0.109	0.373	((-1.244)-(0.473))
% Short telomeres	SNP	0.266	**0.028**	((0.472)-(7.869))
	Cancer	0.209	0.081	((-0.422)-(7.002))
Telomere oxidation	SNP	-0.250	0.106	((-4.126)-(0.687))
	Cancer	-0.218	0.156	((-4.381)-(0.437))
Uracil at telomeres	SNP	-0.130	0.190	((-0.621)-(0.125))
	Cancer	-0.014	0.889	((-0.393)-(0.341))
Telomerase activity	SNP	-0.111	0.395	((-41.430)-(16.597))
	Cancer	-0.237	0.072	((-55.006)-(2.415))
Carbonylation	SNP	-0.204	0.123	((-0.574)-(0.071))
	Cancer	-0.234	0.078	((-0.033)-(0.605))

[a] *UNG* mRNA expression; adjusted TL (Kb); percentage of short telomeres; telomere oxidation; uracil at telomeres; telomerase activity; and protein carbonylation were included as dependent variables. The SNP and cancer status were included as independent variables. [b] β coefficients quantify how much the 2 independent variables (*UNG* SNP and cancer status) modify the dependent variables. [c] Unpaired *t*-test was used to check the significance of individual regression coefficients in the multiple linear regression model