![University of Leeds]

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Table 1. Associations of telomere length associated variants with RCC risk.

Nearby Gene	Chr	Position	SNP	Telomere Length Association			Association with RCC Risk		
				Alleles*	Beta**	SE**	Beta	SE	*P* value
ACYP2	2	54329370	rs11125529	C/A	0.0669	0.0119	0.0143	0.0270	0.6
PXK	3	58376019	rs6772228	A/T	0.1200	0.0191	0.1198	0.0481	0.01
TERC	3	170974795	rs10936599	T/C	0.1173	0.0097	0.1001	0.0220	<0.0001
NAF1	4	164227270	rs7675998	A/G	0.0897	0.0109	0.0133	0.0226	0.5
TERT	5	1339516	rs2736100	A/C	0.0942	0.0109	0.0678	0.0187	0.0003
OBFC1	10	105666455	rs9420907	A/C	0.0828	0.0120	0.1165	0.0264	<0.0001
CTC1	17	8136092	rs3027234	T/C	0.0573	0.0110	0.0159	0.0228	0.5
ZNF208	19	22007281	rs8105767	A/G	0.0576	0.0096	0.0479	0.0207	0.02
RTEL1	20	61892066	rs755017	A/G	0.0741	0.0131	0.0117	0.0289	0.7

* Alleles are short allele/long allele. Short alleles are used as the reference in both the telomere length and RCC association models.
** Beta and standard error (SE) estimates are from published association studies on leukocyte telomere length[22-24].