Article:

Machiela, MJ, Hofmann, JN, Carreras-Torres, R et al. (109 more authors) (2017) Genetic variants related to longer telomere length are associated with increased risk of renal cell carcinoma. European Urology, 72 (5). pp. 747-754. ISSN 0302-2838

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Supplementary Tables

Supplementary Table 1. Minimac R^2 (IARC) or IMPUTE2 info scores (MDA, NCI1, NCI2, UK) for imputed variants.

	rs11125529	**rs6772228**	**rs10936599**	**rs7675998**	**rs2736100**	**rs9420907**	**rs3027234**	**rs8105767**	**rs755017**
IARC	1.00	0.70	Genotyped	0.99	Genotyped	Genotyped	0.99	0.95	1.00
MDA	1.00	0.84	Genotyped	1.00	Genotyped	Genotyped	1.00	1.00	1.00
NCI1	1.00	0.83	Genotyped	1.00	Genotyped	Genotyped	1.00	1.00	1.00
NCI2	1.00	0.81	Genotyped	1.00	Genotyped	1.00	1.00	1.00	Genotyped
UK	1.00	0.85	Genotyped	1.00	Genotyped	0.99	1.00	1.00	Genotyped

Variants that were directly genotyped are denoted as “Genotyped”. Differences in which variants were imputed and genotyped across studies reflects differences in array coverage for commercially available Illumina genotyping platforms used by the studies.

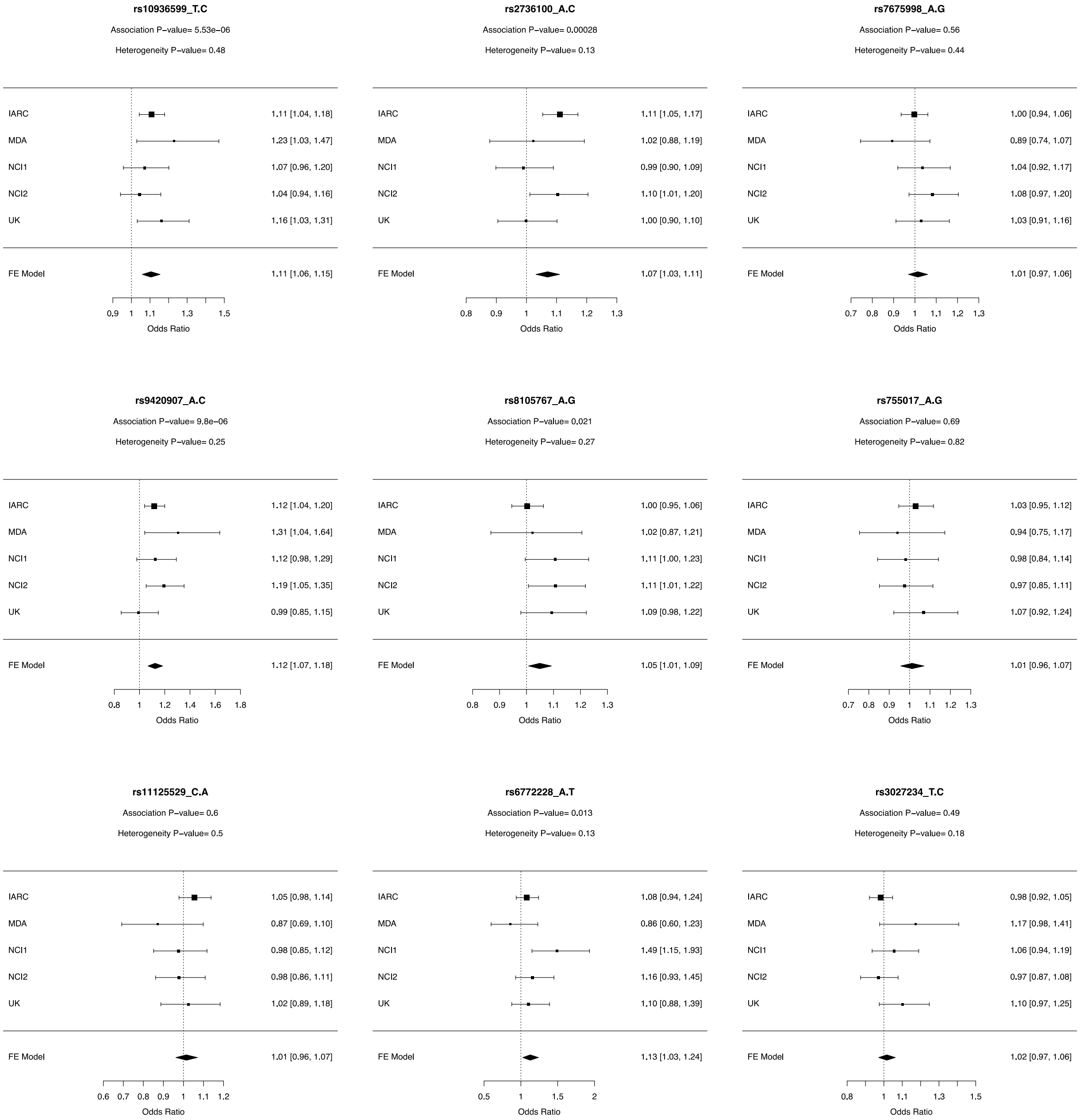
Supplementary Table 2. Telomere length associated variant associations with each major RCC subtype and RCC overall.

Variant	**Alleles**		**Clear Cell RCC**			**Chromophobe RCC**			**Papillary RCC**			**RCC Overall**		
	Short	**Long**	**OR**	**LCL**	**UCL**	**OR**	**LCL**	**UCL**	**OR**	**LCL**	**UCL**	**OR**	**LCL**	**UCL**
rs10936599	T	C	1.126	1.063	1.192	1.055	0.830	1.341	1.015	0.878	1.172	1.105	1.059	1.154
rs2736100	A	C	1.091	1.040	1.144	1.040	0.848	1.274	1.161	1.025	1.315	1.070	1.032	1.110
rs7675998	A	G	0.976	0.921	1.033	1.163	0.908	1.489	0.976	0.843	1.131	1.013	0.969	1.059
rs9420907	A	C	1.148	1.074	1.227	1.154	0.879	1.517	1.242	1.053	1.465	1.124	1.067	1.183
rs8105767	A	G	1.002	0.951	1.057	0.982	0.785	1.228	1.013	0.884	1.160	1.049	1.007	1.092
rs755017	A	G	1.030	0.956	1.109	1.290	0.967	1.720	1.080	0.898	1.298	1.012	0.956	1.071
rs11125529	C	A	1.041	0.971	1.116	1.071	0.799	1.436	0.953	0.794	1.145	1.014	0.962	1.070
rs6772228	A	T	1.062	0.938	1.202	0.801	0.485	1.324	1.159	0.836	1.608	1.127	1.026	1.239
rs3027234	T	C	0.975	0.920	1.034	1.000	0.780	1.281	0.899	0.776	1.042	1.016	0.972	1.063

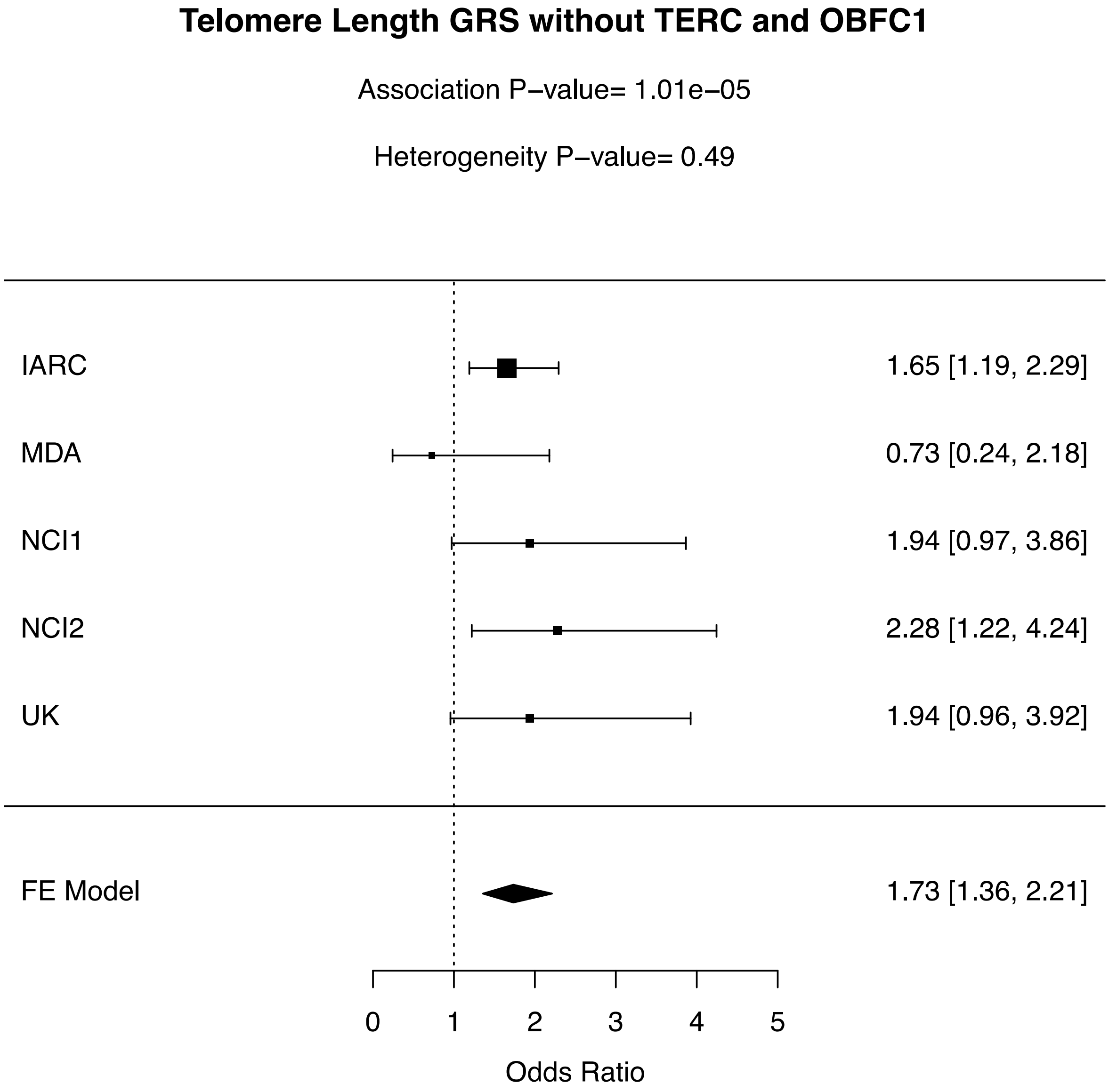
OR=odds ratio; LCL=lower 95% confidence interval; UCL=upper 95% confidence interval

Supplementary Figures

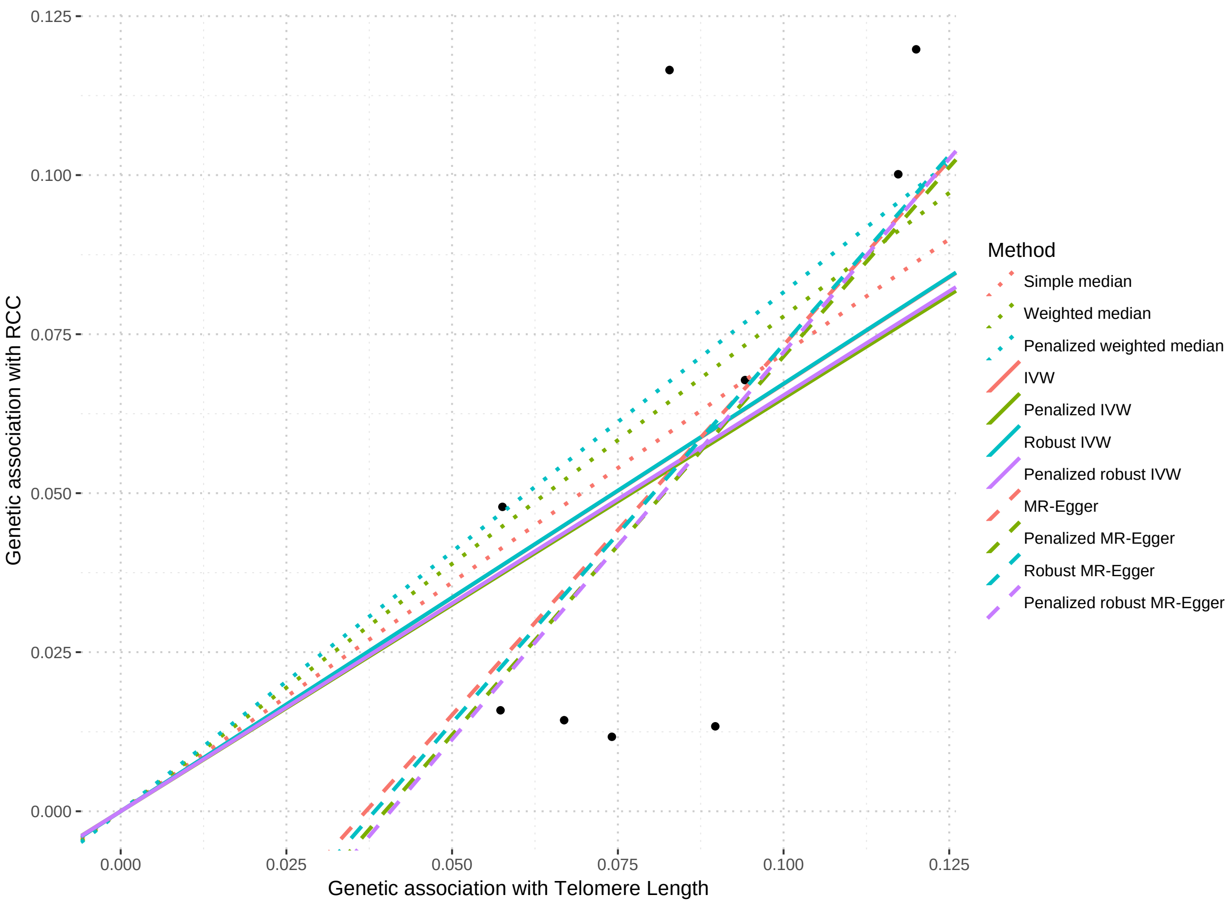
Supplementary Figure 1. Forest plots for associations of each telomere length associated variant with RCC risk.



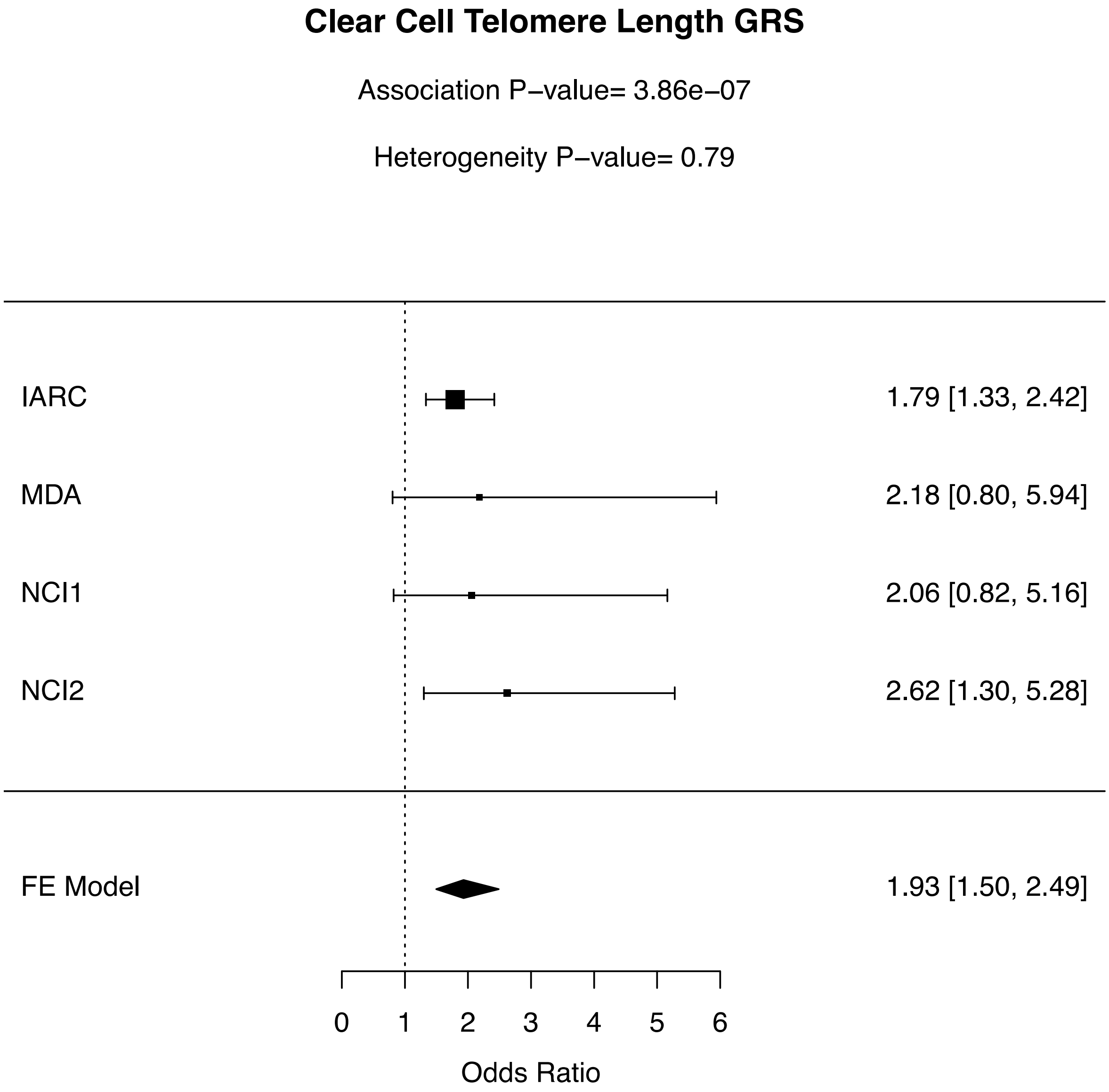
Supplementary Figure 2. Forest plot for RCC association of the telomere length associated GRS that removes rs10936599—TERC and rs9420907—OBFC1 GWAS variants.



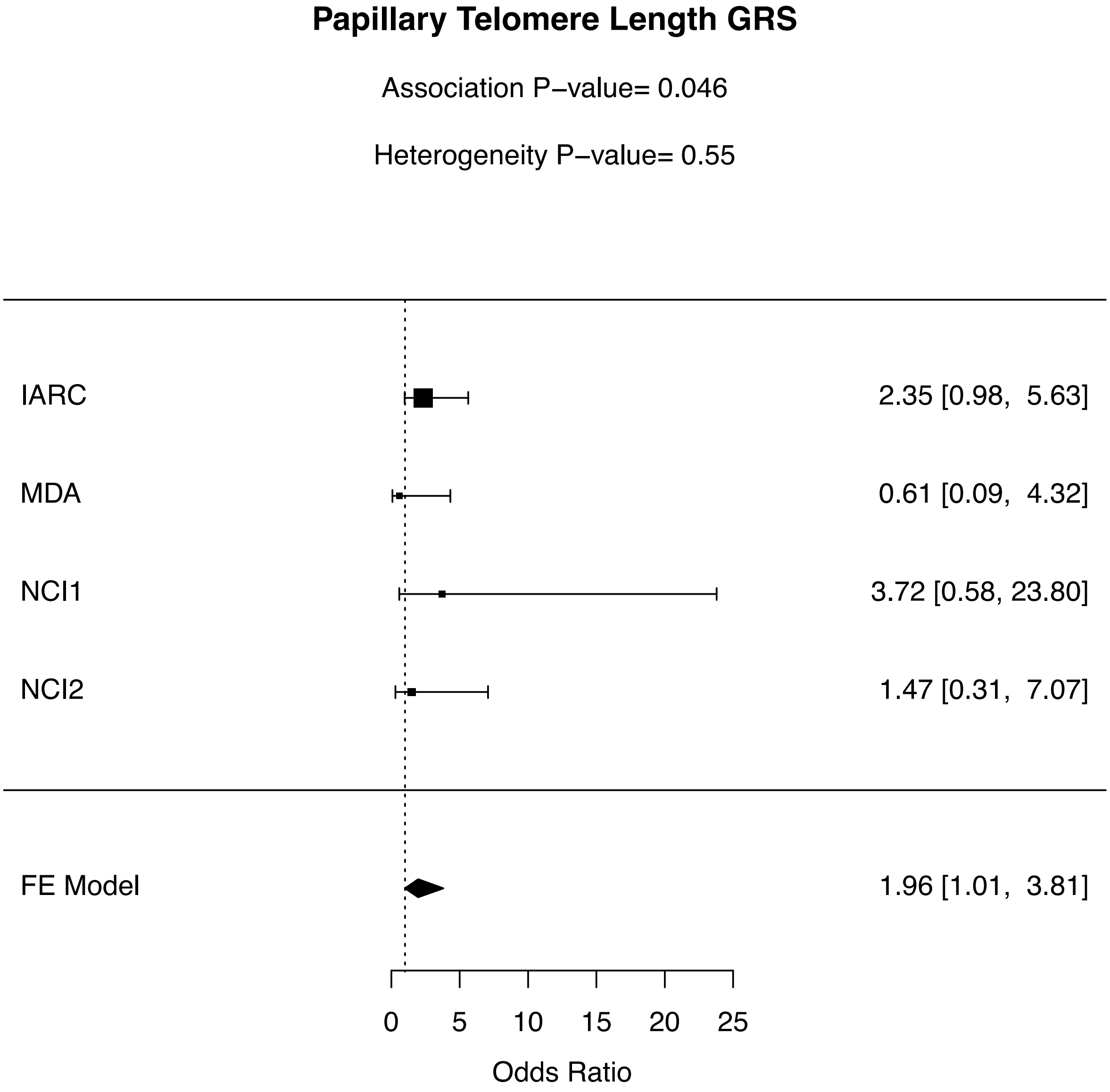
Supplementary Figure 3. Comparison of Egger regression effect estimates (dashed lines) to standard (dotted lines) and IVW based estimation approaches. Egger regression estimated an intercept of -0.043 (95% CI=-0.133-0.047, P-value=0.352) and an estimated odds ratio of 3.20 (95% CI=1.10-9.27, P-value=0.03).



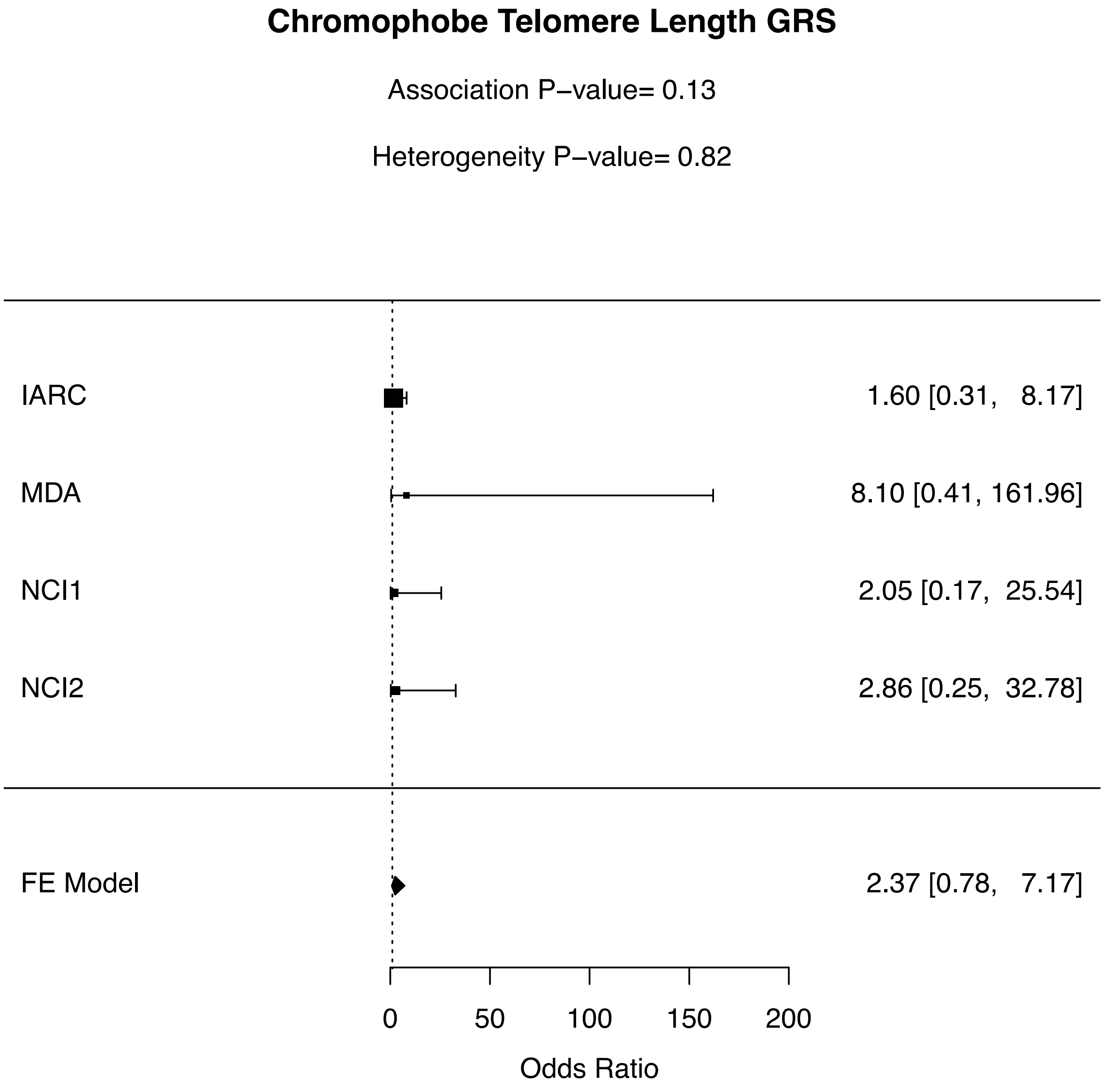
Supplementary Figure 4. Forest plot for associations of the telomere length associated GRS with clear cell RCC risk.



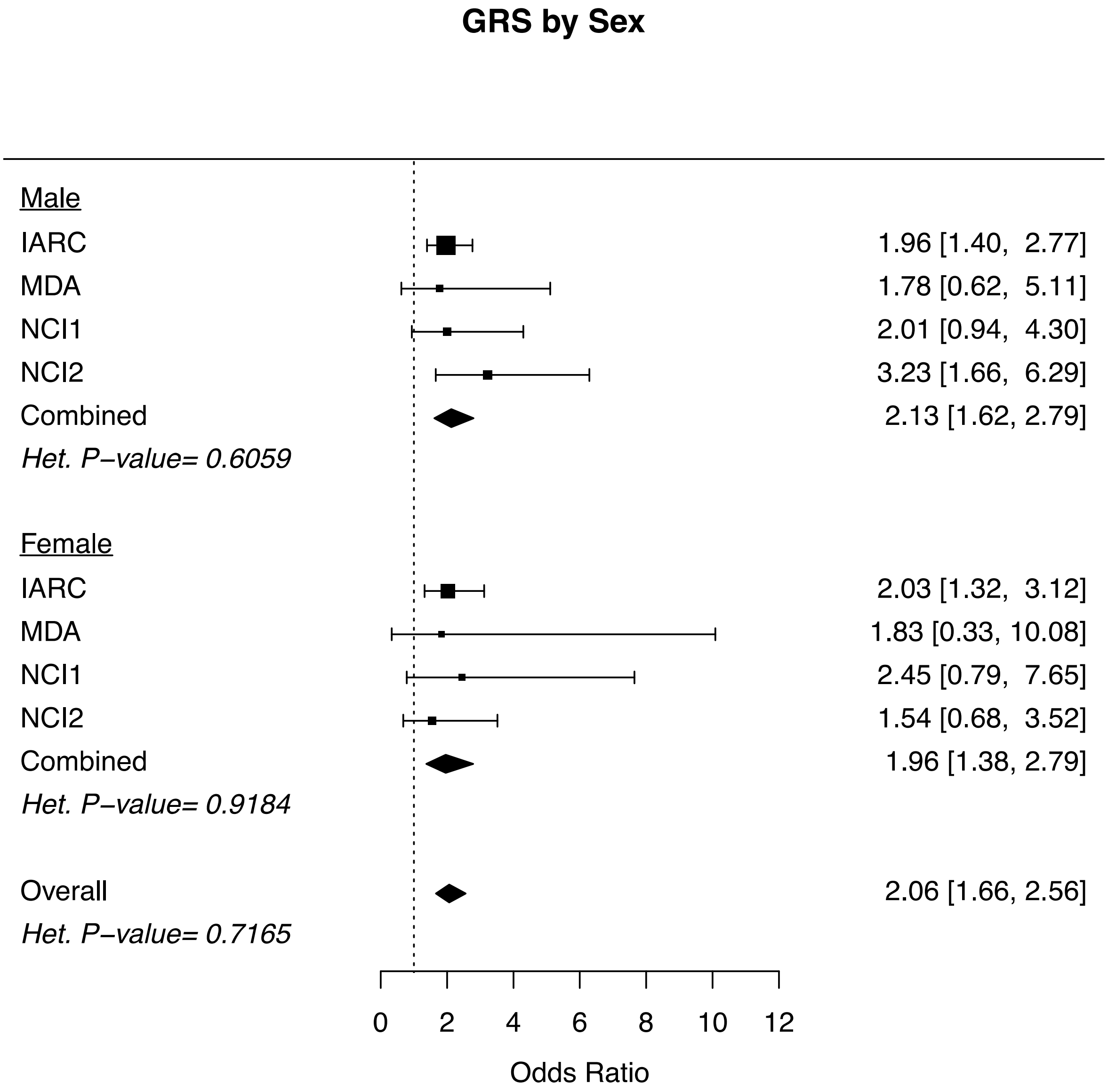
Supplementary Figure 5. Forest plot for associations of the telomere length associated GRS with papillary RCC risk.



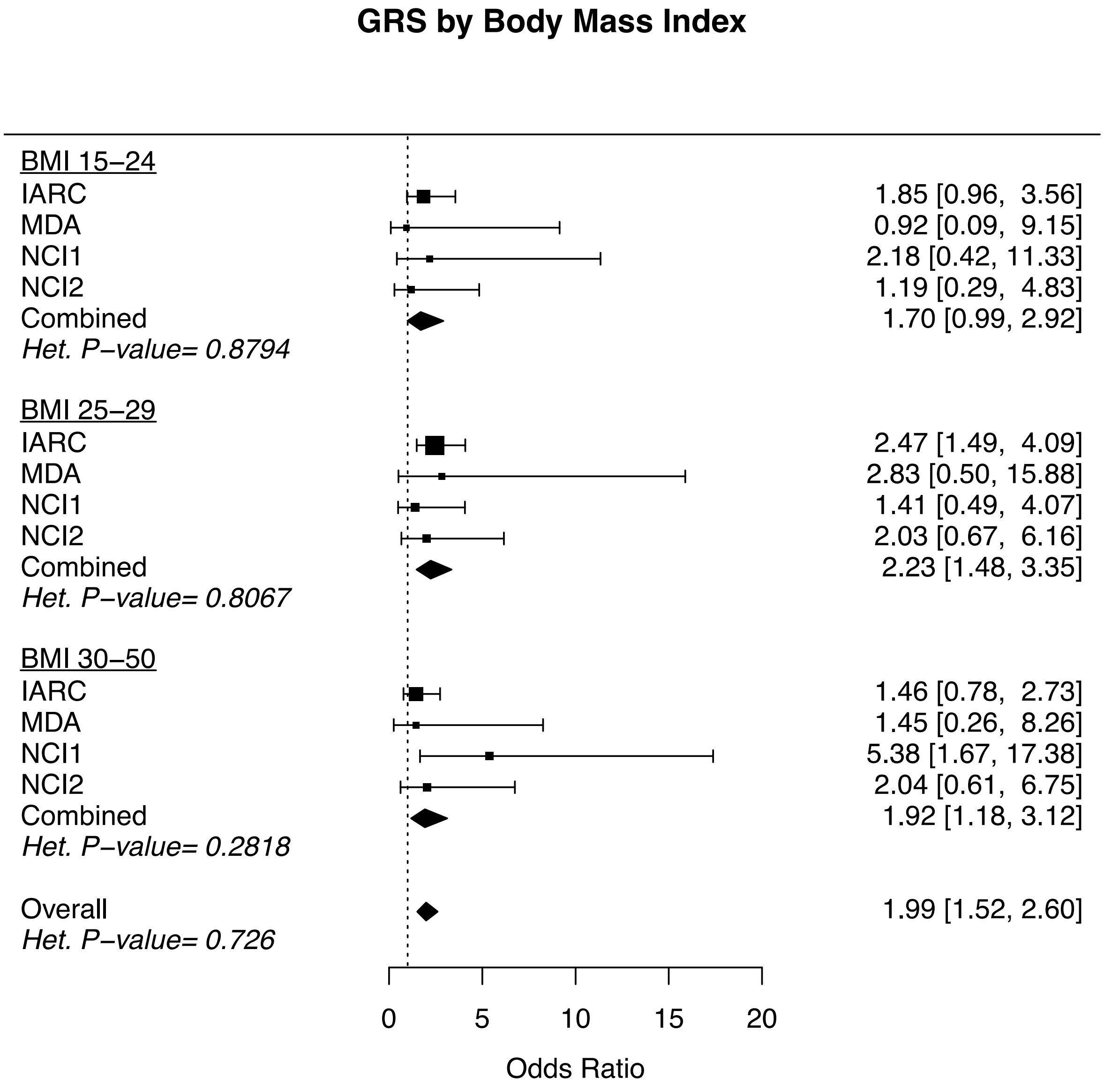
Supplementary Figure 6. Forest plot for associations of the telomere length associated GRS with chromophobe RCC risk.



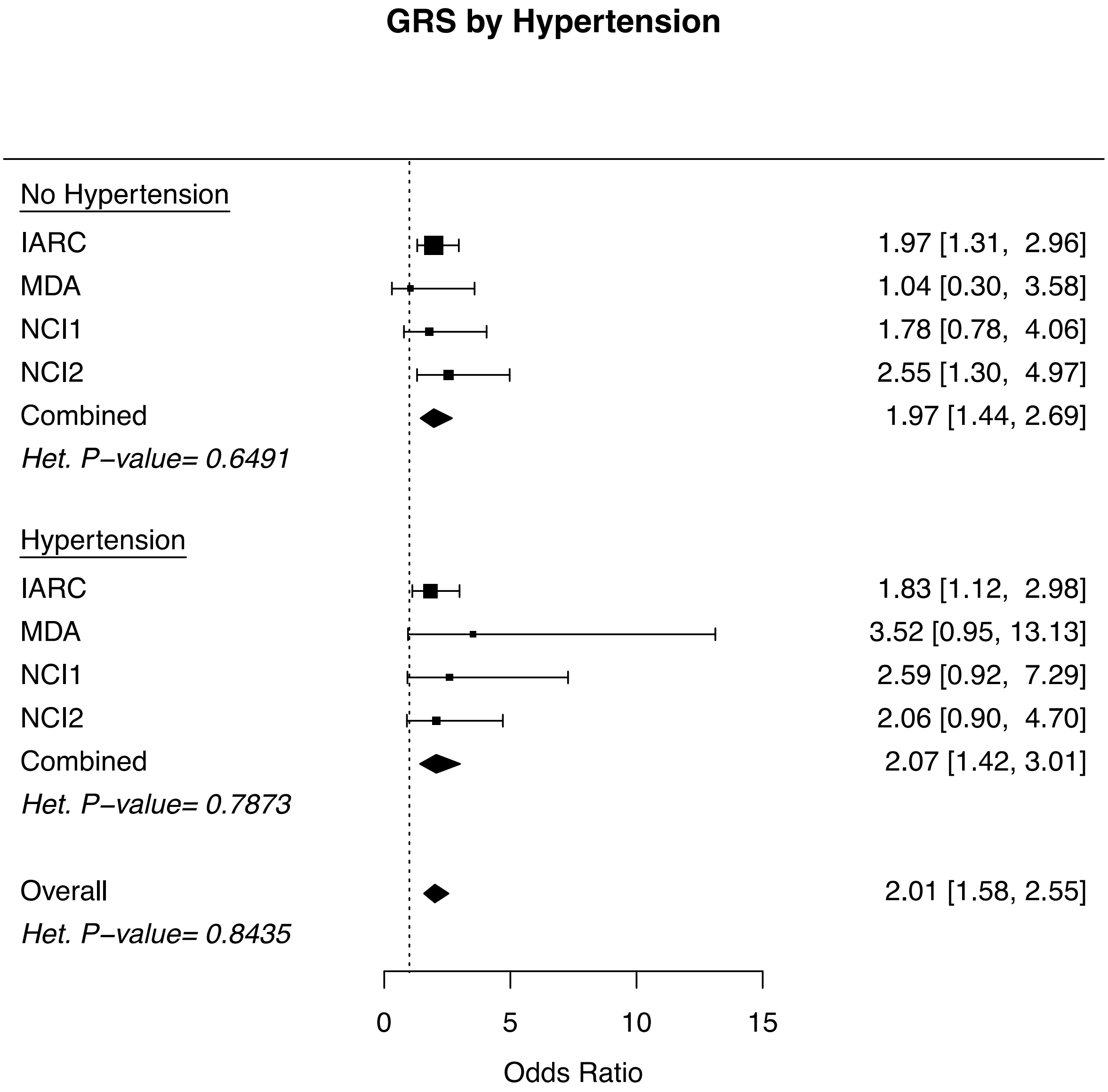
Supplementary Figure 7. Forest plot for associations of telomere length associated GRS with RCC by strata of sex.



Supplementary Figure 8. Forest plot for associations of telomere length associated GRS with RCC by strata of BMI.



Supplementary Figure 9. Forest plot for associations of telomere length associated GRS with RCC by strata of hypertension.



Supplementary Figure 10. Forest plot for associations of telomere length associated GRS with RCC by strata of smoking.