SUPPLEMENTARY MATERIALS

Supplementary Table 1 Results of linkage disequilibrium regression analysis for seven anthropometric traits against TGCT.

Supplementary Table 2 Results of Egger regression for each of the traits for which Mendelian randomisation was performed.

Supplementary Table 3 Results of inverse weighted variance for each of the traits for which Mendelian randomisation was performed.

Supplementary Figures 1-11 Effect sizes of TGCT and each of the traits for which Mendelian randomisation was performed.

Supplementary Figures 12-15 Power estimates of our MR analysis to demonstrate an association between TGCT and anthropometric traits over a range of effect sizes.

Phenotype	Heritability of Phenotype				Genetic Covariance (with TGCT)			Genetic Correlation (with TGCT)		
	Total Liability Scale h^2 (Std.Err)	Lambda GC	Mean x^2	Intercept (Std.Err)	Total Liability Scale gencov (Std.Err)	Mean z1*z2	Intercept (Std.Err)	Genetic Correlation (Std.Err)	Z-score	*P value*
Birth Weight	0.11 (0.021)	1.05	1.06	1.01 (0.0084)	0.036 (0.019)	0.017	-0.0041 (0.0064)	0.17 (0.093)	1.83	0.068
Childhood Obesity	0.41 (0.046)	1.02	1.03	0.92 (0.0098)	-0.058 (0.027)	0.0023	0.025 (0.0069)	-0.14 (0.064)	-2.15	0.032
Adult BMI	0.14 (0.0095)	1.12	1.33	0.63 (0.016)	-0.0008 (0.0073)	0.0018	0.0056 (0.0073)	-0.0035 (0.034)	-0.1	0.92
WHRadjBMI	0.093 (0.008)	1.05	1.13	0.85 (0.013)	0.0069 (0.0081)	0.025	0.014 (0.0077)	0.035 (0.04)	0.87	0.39
WHRadjBMI (Male only)	0.12 (0.011)	1.05	1.06	0.91 (0.0089)	-0.0012 (0.013)	0.009	0.0086 (0.0077)	-0.0054 (0.055)	-0.099	0.92
WCadjBMI	0.11 (0.0078)	1.05	1.18	0.82 (0.012)	0.0052 (0.009)	0.0053	-0.005 (0.0075)	0.024 (0.042)	0.57	0.57
WCadjBMI (Male only)	0.18 (0.014)	1.05	1.11	0.88 (0.01)	-0.0029 (0.014)	-0.0068	-0.0067 (0.0077)	-0.011 (0.052)	-0.2	0.84
HIPadjBMI	0.15 (0.011)	1.1	1.26	0.79 (0.015)	-0.0031 (0.0099)	-0.024	-0.022 (0.0076)	-0.012 (0.039)	-0.31	0.76
HIPadjBMI (Male only)	0.22 (0.017)	1.05	1.13	0.85 (0.012)	-0.0094 (0.014)	-0.013	-0.0074 (0.0074)	-0.031 (0.046)	-0.68	0.5
Adult Height	0.33 (0.021)	2.09	3.16	1.28 (0.049)	-0.015 (0.013)	-0.045	-0.024 (0.01)	-0.039 (0.034)	-1.15	0.25
Adult Height (Male only)	0.26 (0.022)	1.05	1.18	0.83 (0.015)	-0.025 (0.017)	-0.018	-0.0003 (0.0074)	-0.073 (0.049)	-1.5	0.13

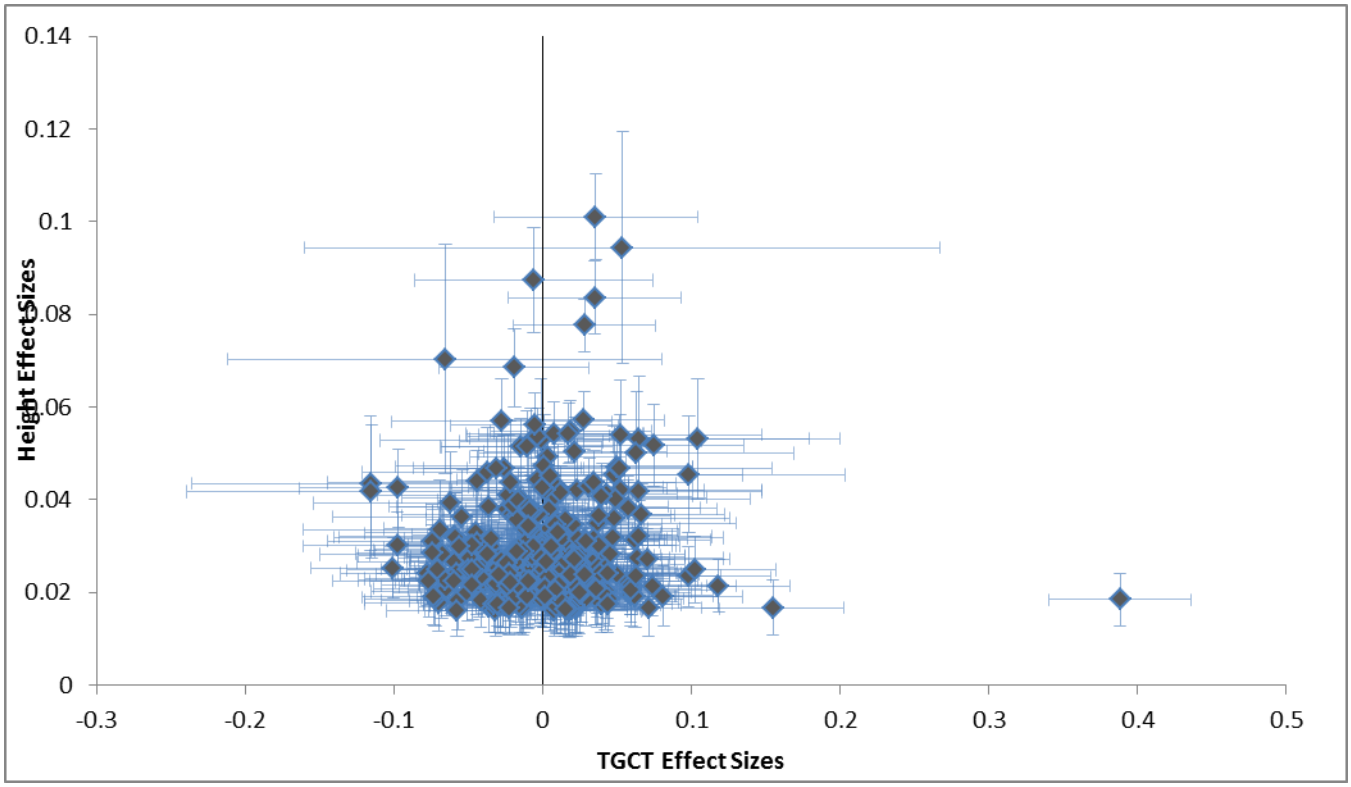
Supplementary Table 1 Results of linkage disequilibrium regression analysis for seven anthropometric traits against TGCT, as well as male-specific components for four of these traits.

	$x-$ intercept			slope		
Trait	**Estimate**	**95% CI**	***P*-value**	**Estimate**	**95% CI**	***P*-value**
BMI	0.00031	[-0.026,0.027]	0.98	-0.18	[-1.19,0.84]	0.73
Height	0.00023	[-0.011,0.012]	0.97	0.054	[-0.35,0.45]	0.79
Height (Male only)	0.046	[-0.040,0.13]	0.27	-1.51	[-4.21,1.19]	0.25
HIPadjBMI	-0.039	[-0.11,0.030]	0.23	1.87	[-0.67,4.41]	0.13
HIPadjBMI (Male only)	0.13	[-0.17,0.43]	0.2	-3.19	[-10.8,4.38]	0.21
WCadjBMI	-0.0072	[-0.059,0.044]	0.77	0.41	[-1.50,2.32]	0.66
WCadjBMI (Male only)	-0.041	[-0.30,0.22]	0.72	1.49	[-6.74,9.73]	0.68
WHRadjBMI	0.038	[-0.015,0.091]	0.16	-1.39	[-3.30,0.52]	0.15
WHRadjBMI (Male only)	-0.17	[-0.49,0.14]	0.22	5.77	[-4.24,15.8]	0.2
Birth Weight	0.007	[-0.102,0.12]	0.88	0.006	[-2.14,2.15]	0.99
Childhood Obesity	-0.015	[-0.28,0.25]	0.89	0.04	[-3.25,3.33]	0.98

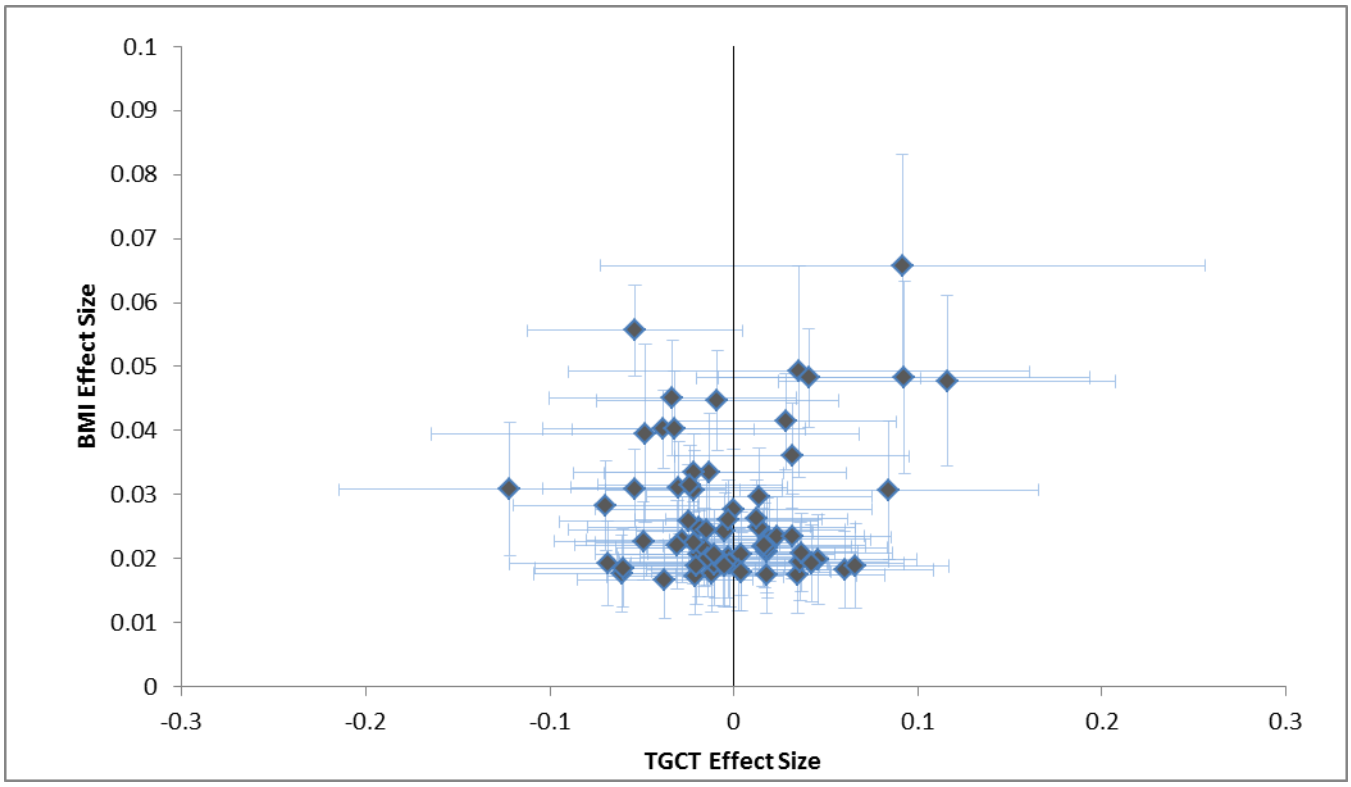
Supplementary Table 2 Egger regression results for each of the traits for which Mendelian randomisation was performed.

Trait	IVW Estimate	95% CI	*P*-value
BMI	-0.16	[-0.49,0.16]	0.32
Height	0.061	[-0.09,0.21]	0.42
Height (Male only)	-0.082	[-0.55,0.39]	0.72
HIPadjBMI	0.50	[-0.27,1.28]	0.17
HIPadjBMI (Male only)	-0.007	[-2.05,2.04]	0.99
WCadjBMI	0.15	[-0.33,0.63]	0.53
WCadjBMI (Male only)	0.21	[-0.65,1.08]	0.58
WHRadjBMI	-0.043	[-0.39,0.31]	0.80
WHRadjBMI (Male only)	0.32	[-0.54,1.19]	0.40
Birth Weight	0.14	[-0.34,0.62]	0.50
Childhood Obesity	-0.15	[-0.57,0.28]	0.43

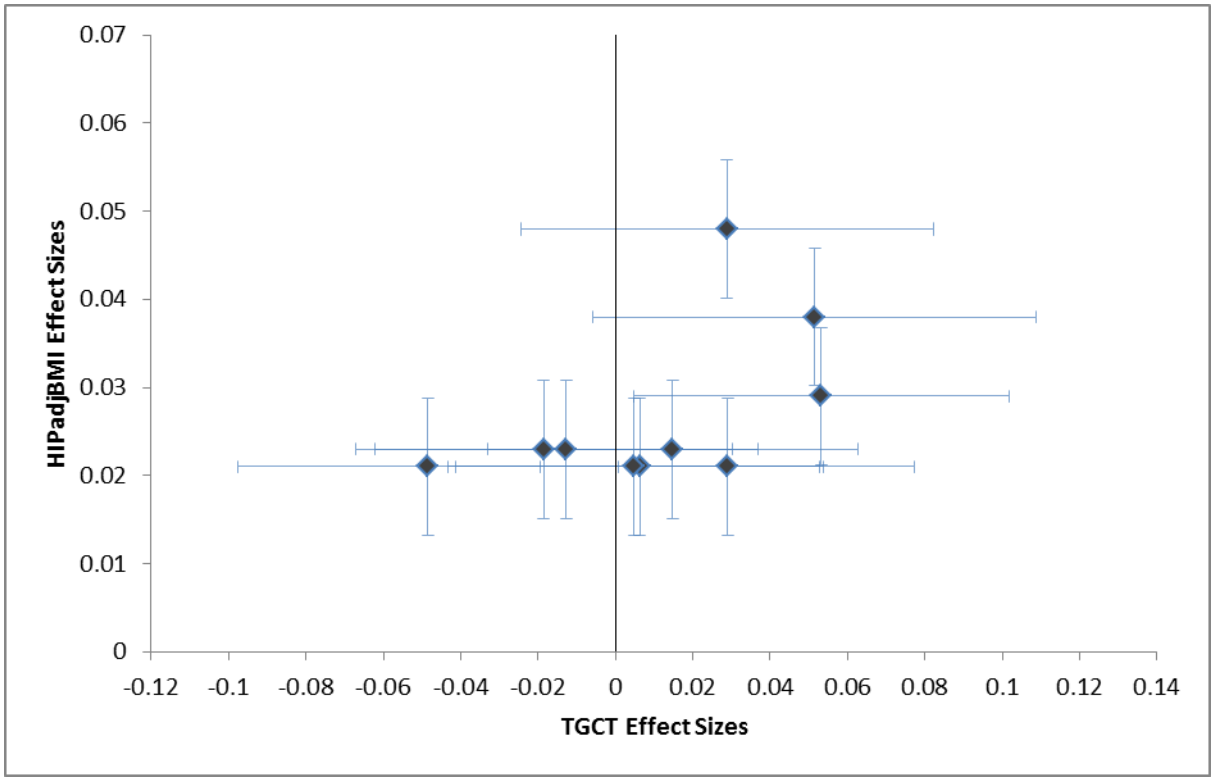
Supplementary Table 3 Inverse weighted variance results for each of the traits for which Mendelian randomisation was performed.



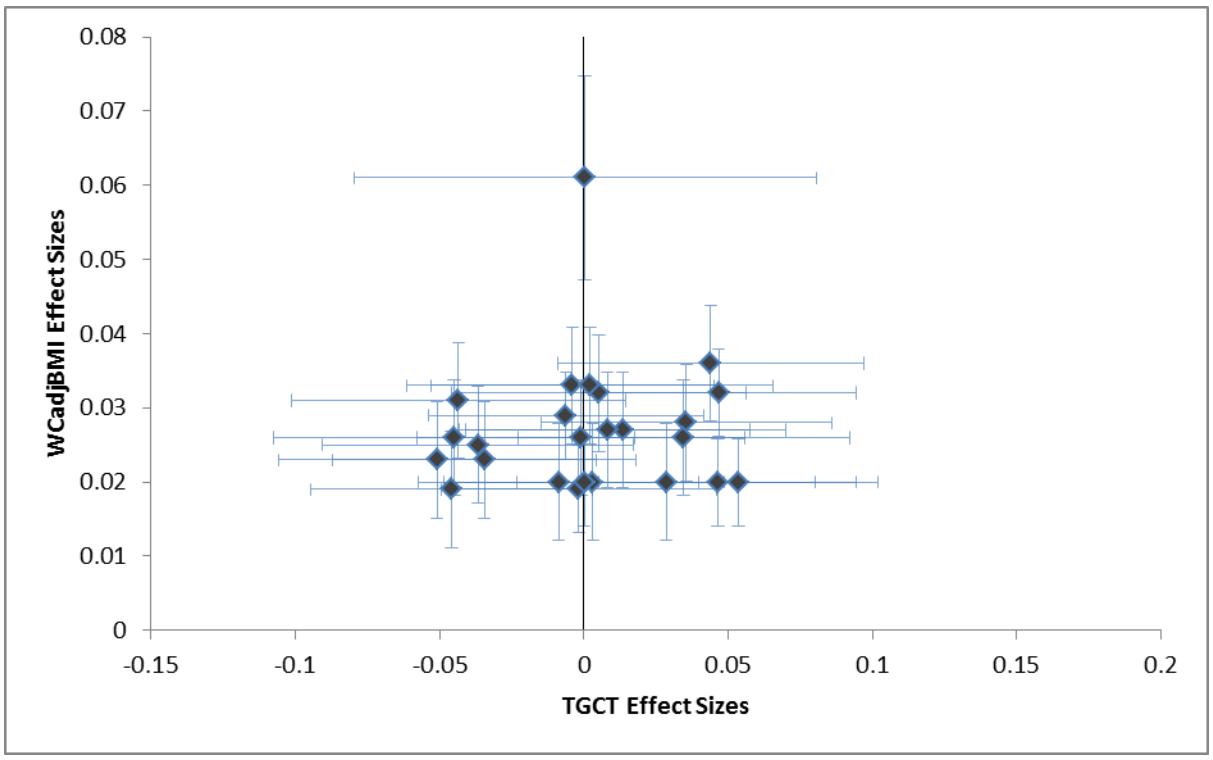
Supplementary Fig. 1 TGCT and adult height effect sizes (and 95% CI) for 379 adult height risk SNPs.



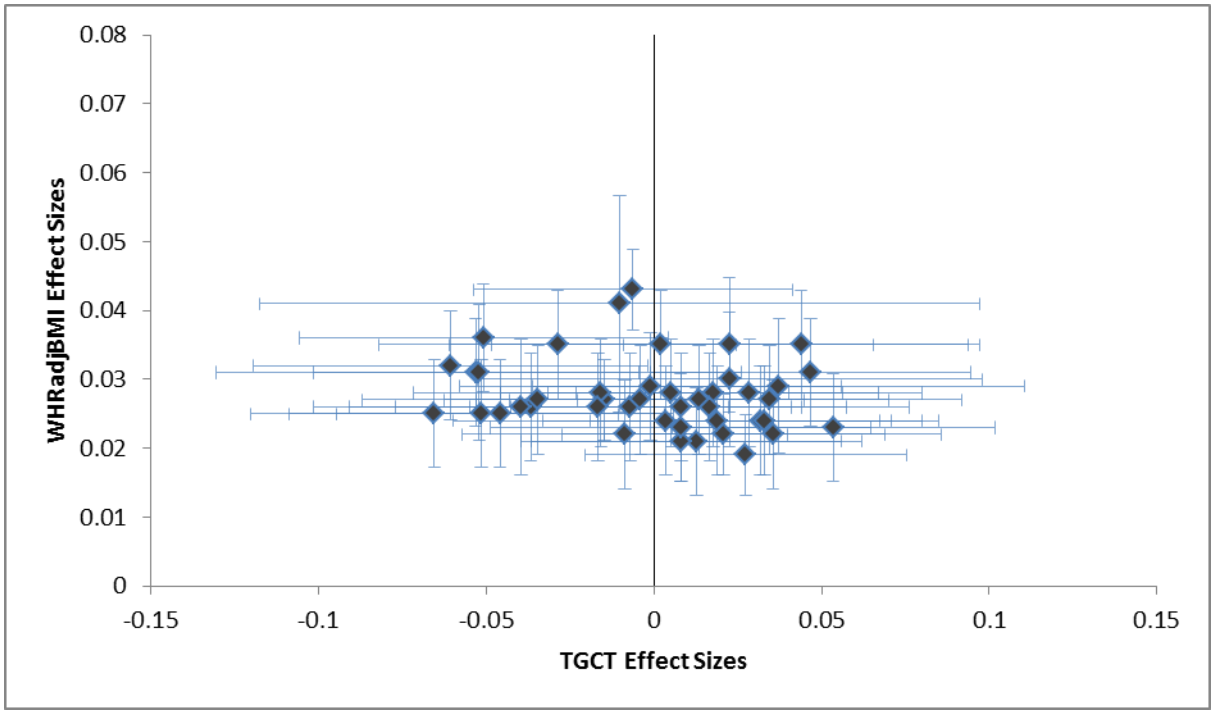
Supplementary Fig. 2 TGCT and BMI effect sizes (and 95% CI) for 69 BMI risk SNPs.



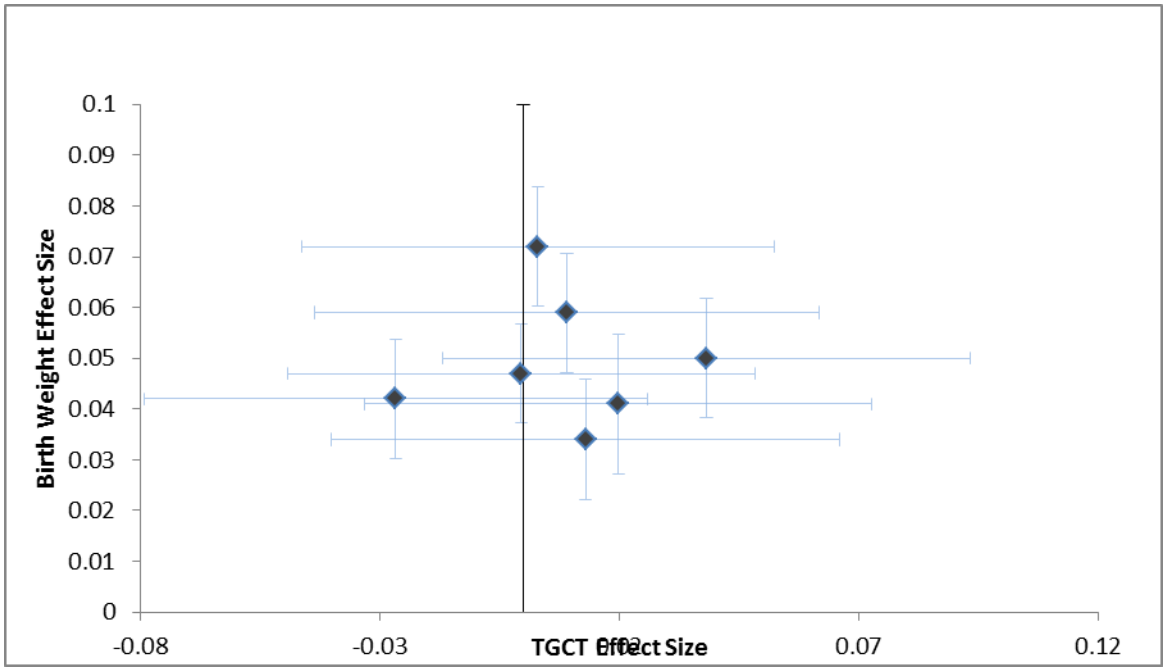
Supplementary Fig. 3 TGCT and HIPadjBMI effect sizes (and 95% CI) for ten HIPadjBMI risk SNPs.



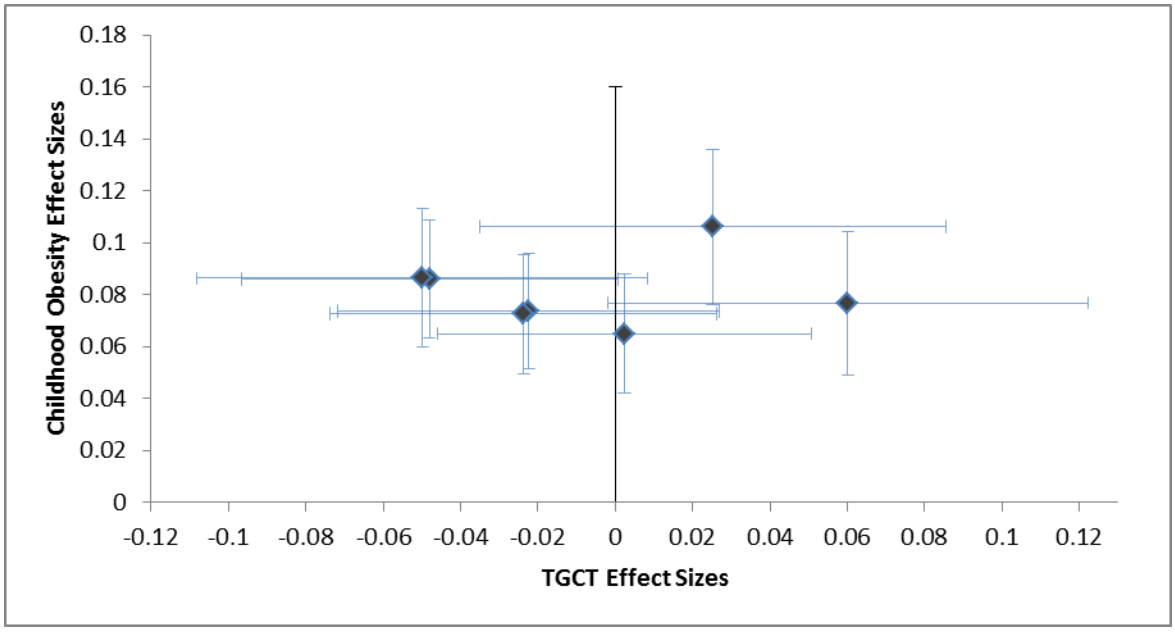
Supplementary Fig. 4 TGCT and WCadjBMI effect sizes (and 95% CI) for 25 WCadjBMI risk SNPs.



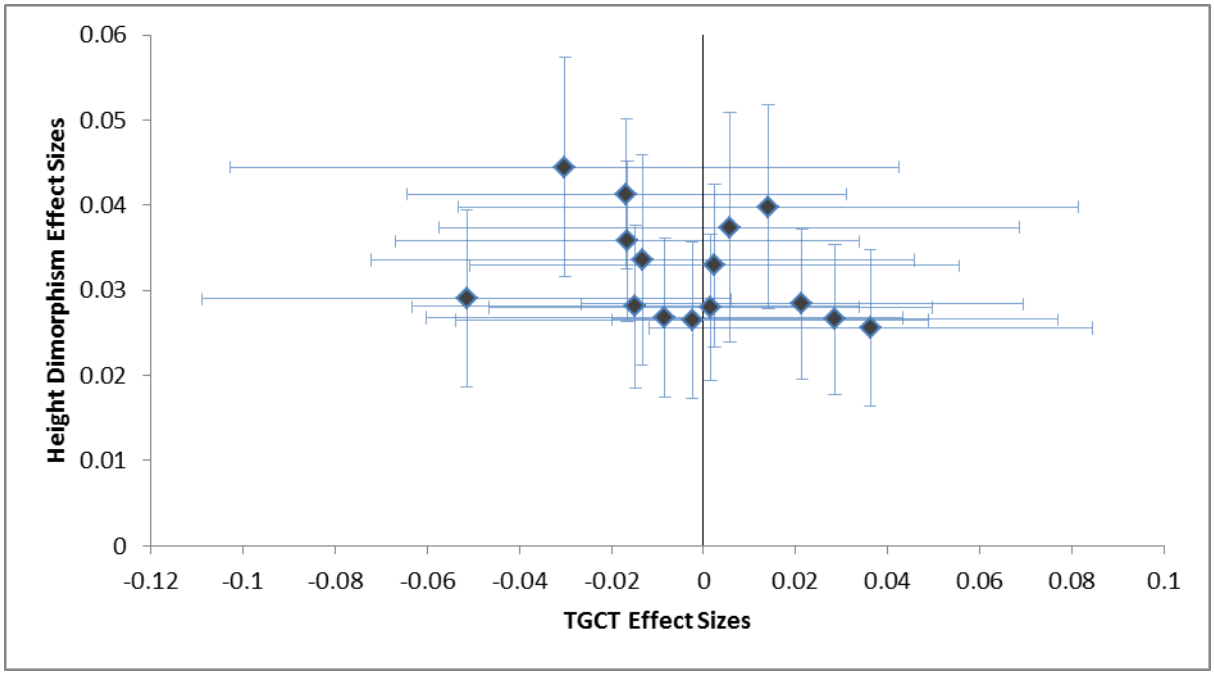
Supplementary Fig. 5 TGCT and WHRadjBMI effect sizes (and 95% CI) for 44 WHRadjBMI risk SNPs.



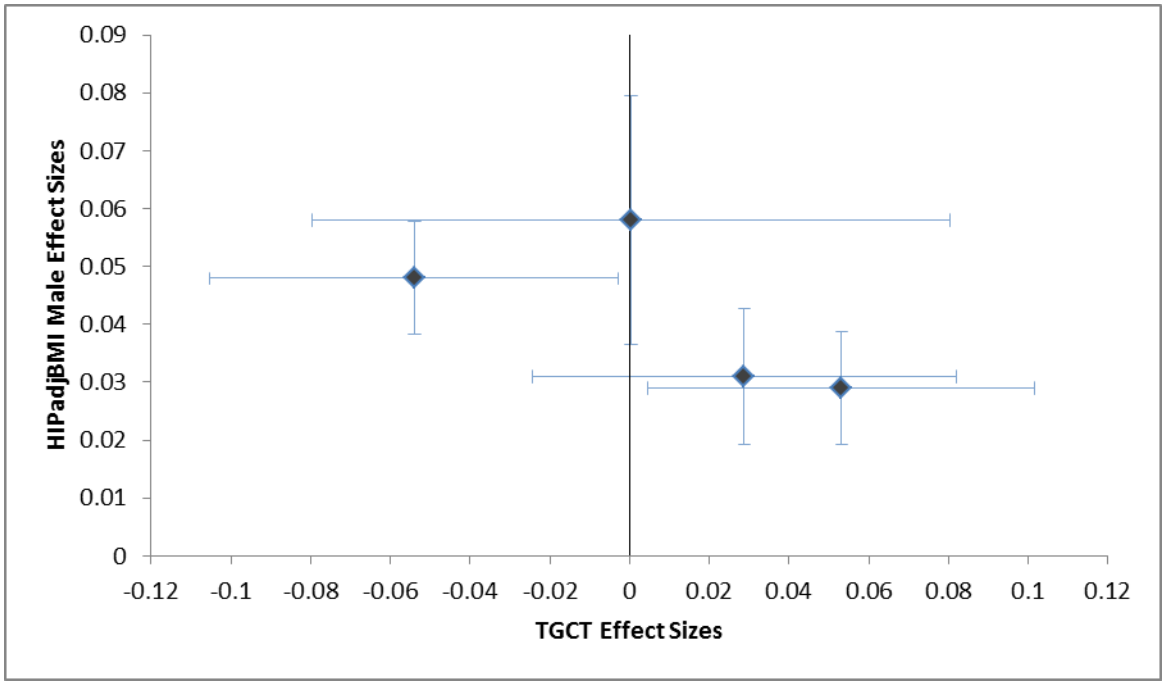
Supplementary Fig. 6 TGCT and birth weight effect sizes (and 95% CI) for seven birth weight risk SNPs.



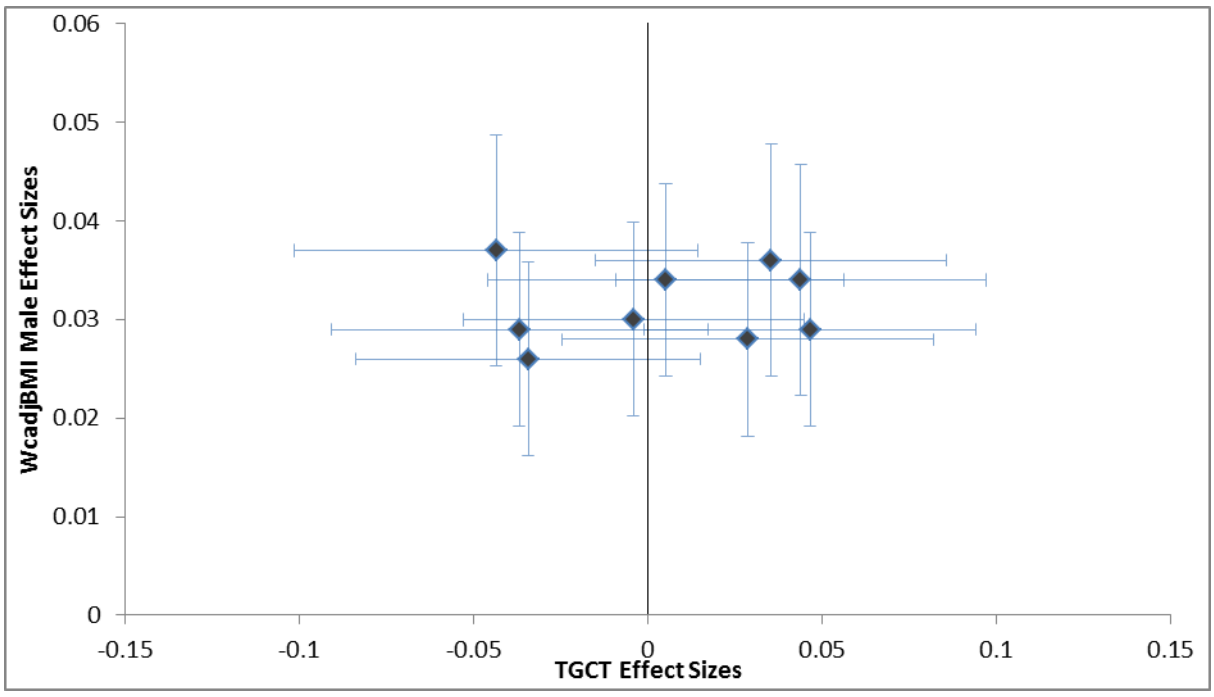
Supplementary Fig. 7 TGCT and childhood obesity effect sizes (and 95% CI) for seven childhood obesity risk SNPs.



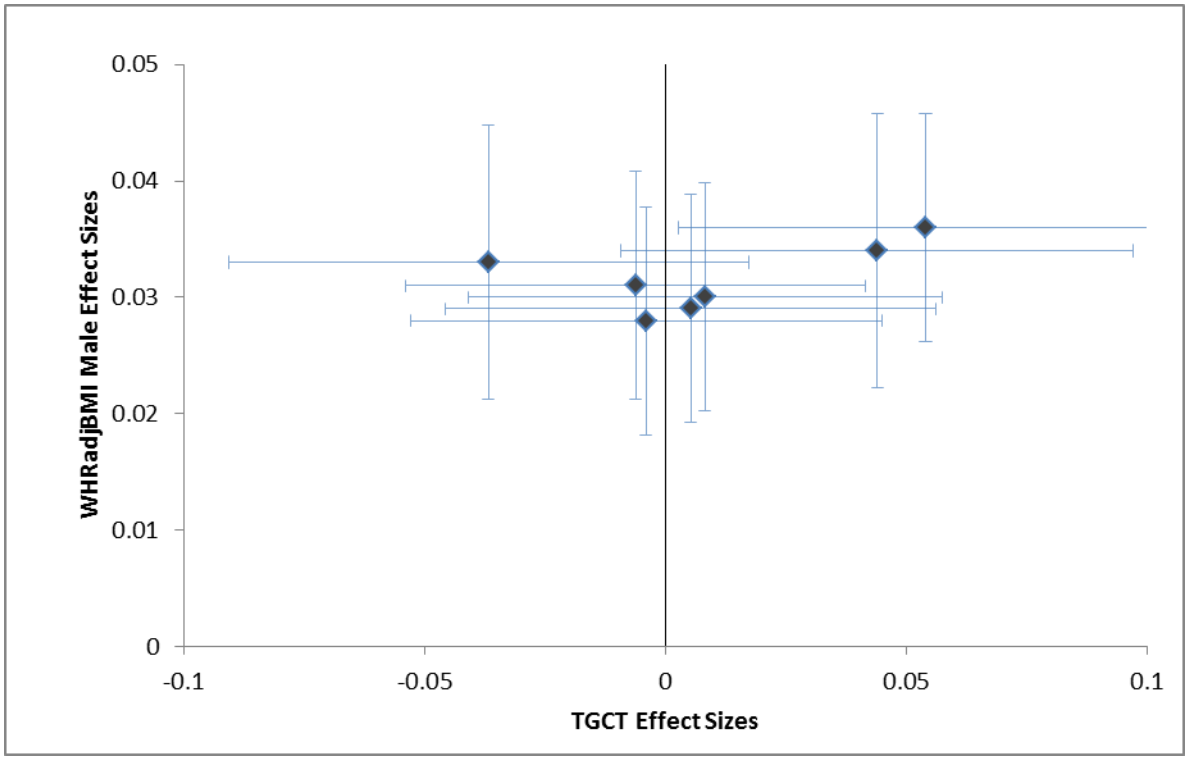
Supplementary Fig. 8 TGCT and height (male dimorphism) effect sizes (and 95% CI) for 15 height (male dimorphism) risk SNPs.



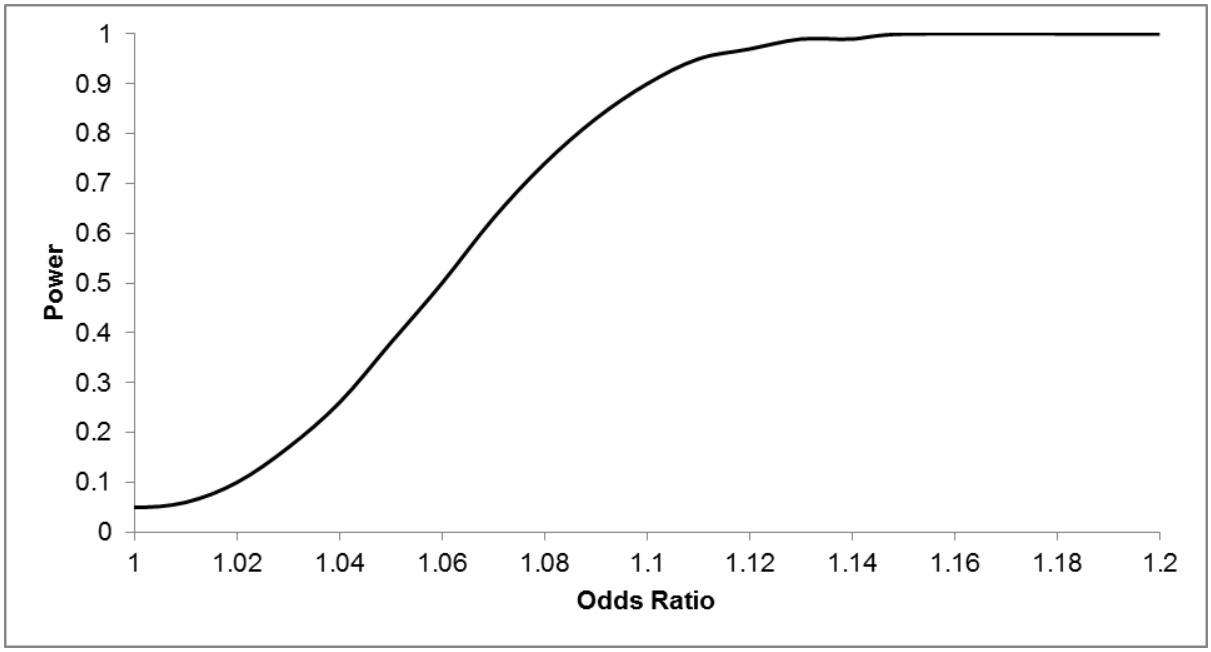
Supplementary Fig. 9 TGCT and HIPadjBMI (male specific) effect sizes (and 95% CI) for four HIPadjBMI (male-specific) risk SNPs.



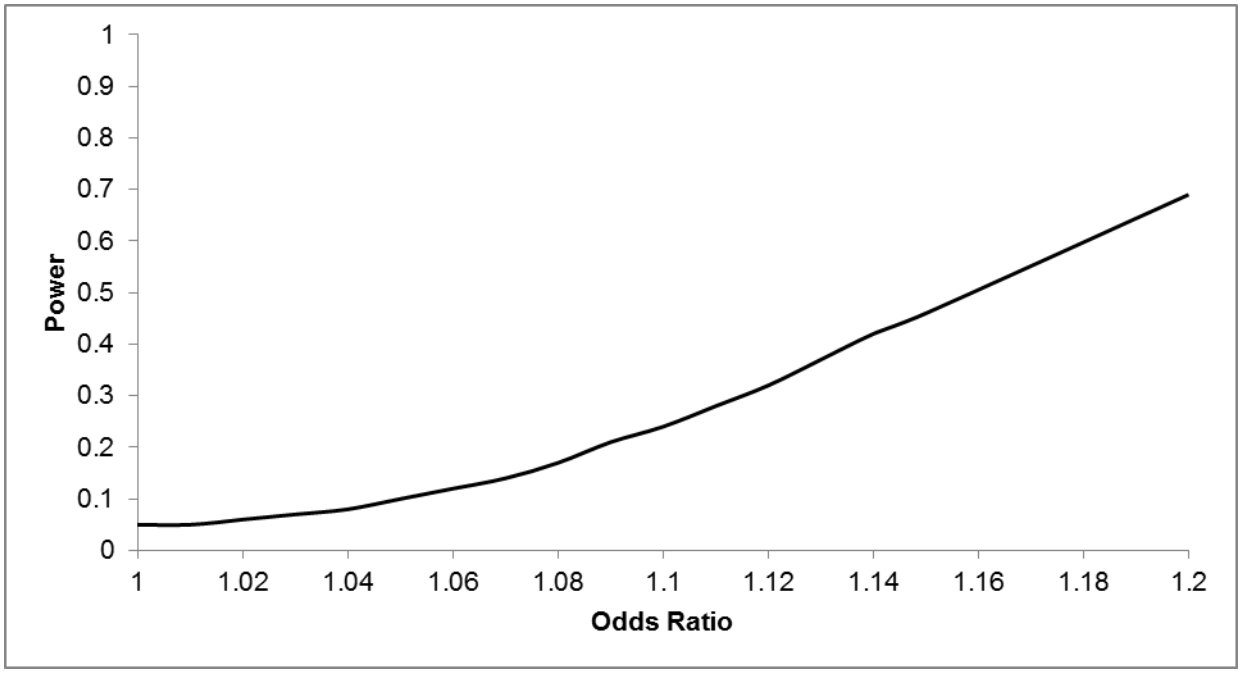
Supplementary Fig. 10 TGCT and WCadjBMI (male specific) effect sizes (and 95% CI) for nine WCadjBMI (male specific) risk SNPs.



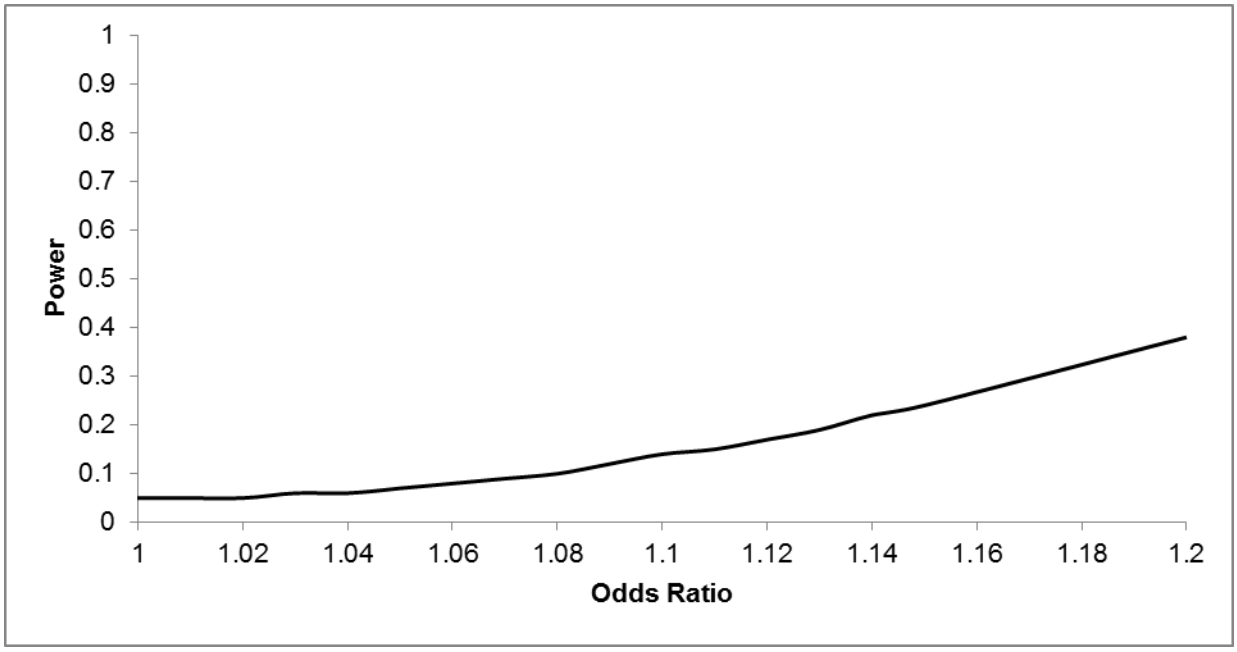
Supplementary Fig. 11 TGCT and WHRadjBMI (male specific) effect sizes (and 95% CI) for seven WHRadjBMI (male specific) risk SNPs.



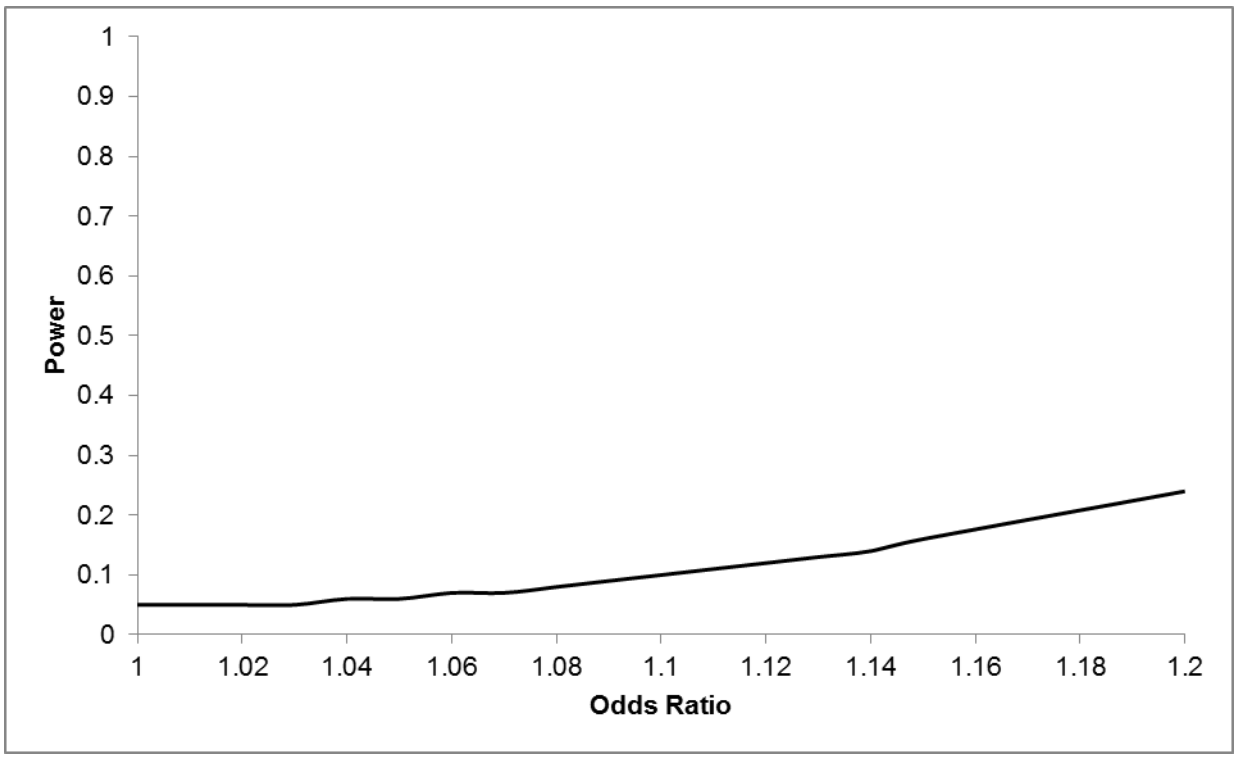
Supplementary Fig. 12 Estimated power of the present study to detect a range of odds ratios of height and TGCT risk. SNPs used here are estimated to explain ~20% of the phenotypic variation in height (Wood *et al*. 2014).



Supplementary Fig. 13 Estimated power of the present study to detect a range of odds ratios of BMI and TGCT risk. SNPs used here are estimated to explain ~3% of the phenotypic variation in BMI (Locke *et al*. 2015).



Supplementary Fig. 14 Estimated power of the present study to detect a range of odds ratios of WHRadjBMI and TGCT risk. SNPs used here are estimated to explain ~1.36% of the phenotypic variation of WHRadjBMI (Shungin *et al*. 2015).



Supplementary Fig. 15 Estimated power of the present study to detect a range of odds ratios of birth weight and TGCT risk. SNPs used here are estimated to explain ~0.76% of the phenotypic variation of birth weight (Horikoshi *et al*. 2013).

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Locke A E, Kahali B, Berndt S I, Justice A E, Pers T H, Day F R, *et al.* (2015) Genetic studies of body mass index yield new insights for obesity biology. *Nature* **518**, 197-206.

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