Supplemental Figure 1. Mendelian Randomization (MR) analysis results for the association between individual SNPs that genetically predict leukocyte telomere length (LTL) and pediatric germ cell tumors (GCT) for the Codd et al. (2013) genetic instrument excluding *TERT*. Forest plots (left) show the effect estimate per variant using MR Wald Ratio single SNP test, and overall MR estimates using MR Egger, weighted median, and inverse −variance weighted (IVW) estimators. Black dots represent the betas corresponding to a per 1 kb increase in LTL and black horizontal lines represent 95% confidence intervals. Scatter plots (right) are of the effect of each variant on LTL and pediatric GCT showing the per−allele association with pediatric GCT risk (outcome) plotted against the per− allele association with kb of LTL (exposure). The vertical and horizontal gray lines represent standard error for each SNP. *Subgroup analysis included trios, Hispanic and White case −control only samples to get stable estimates. African American and Asian case control samples were not included in subgroup analyses due to small sample size.