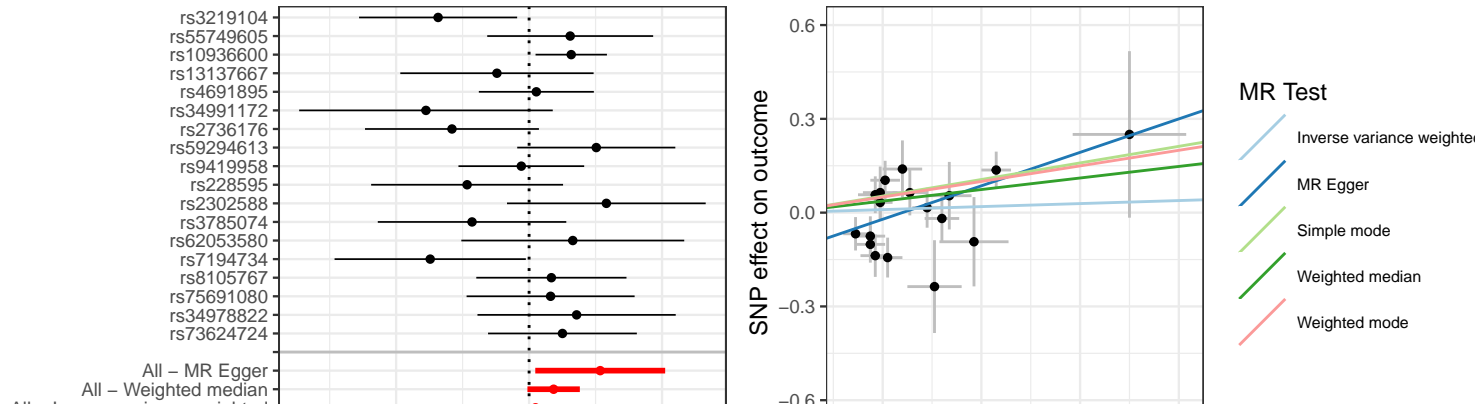
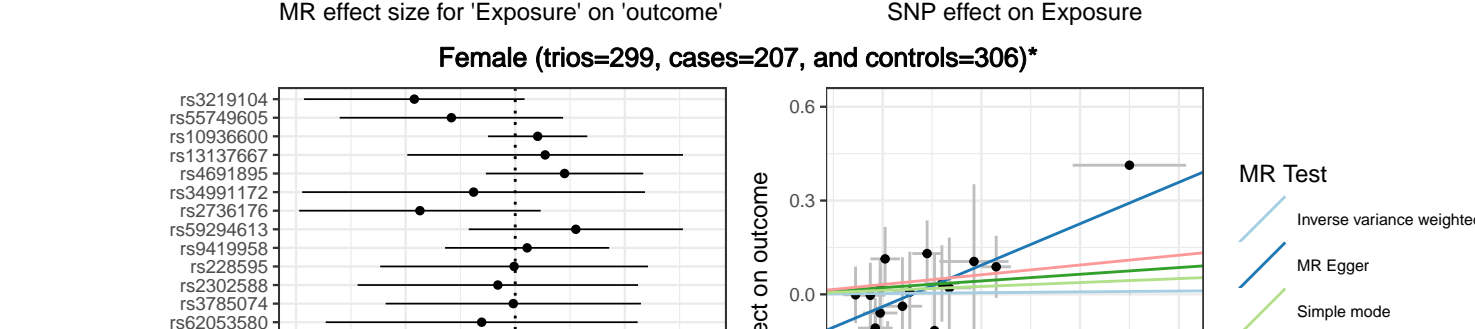


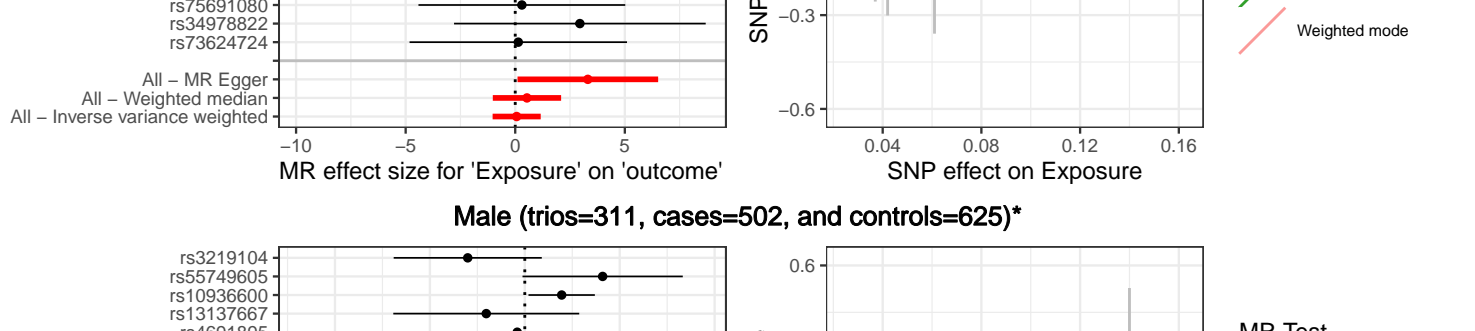
**Overall (trios=610, cases=803, and controls=1,022)**



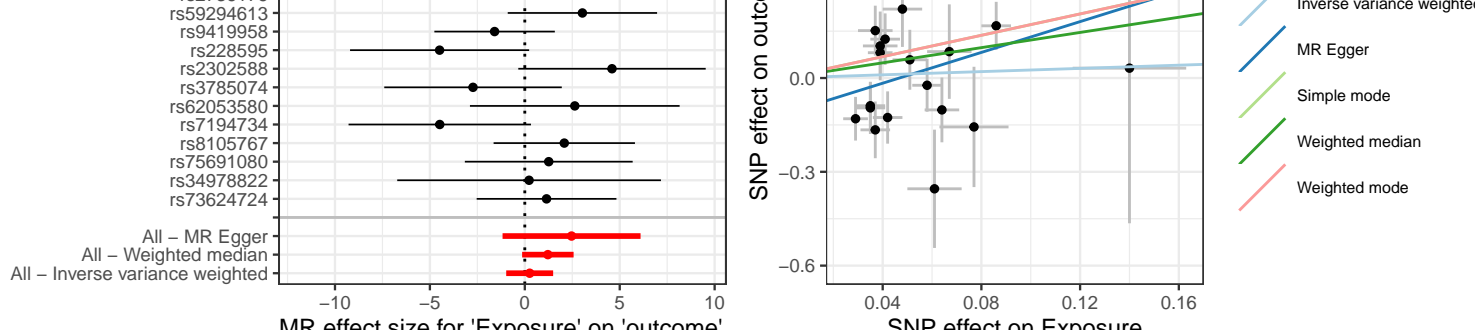
**Female (trios=299, cases=207, and controls=306)\***



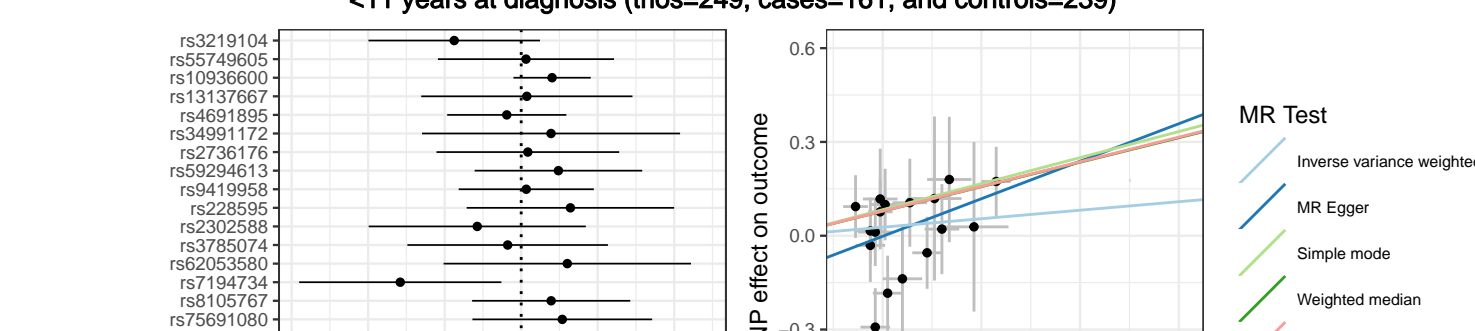
**Male (trios=311, cases=502, and controls=625)\***



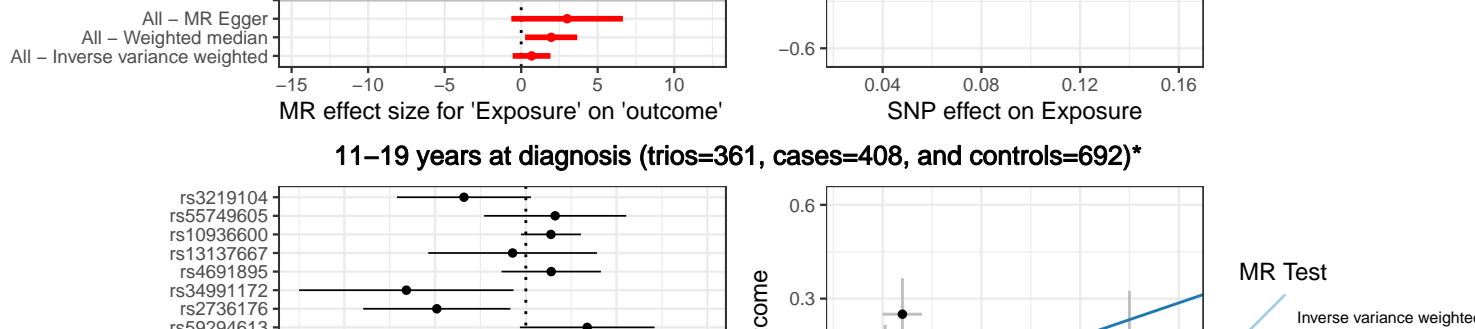
**<11 years at diagnosis (trios=249, cases=161, and controls=239)\***



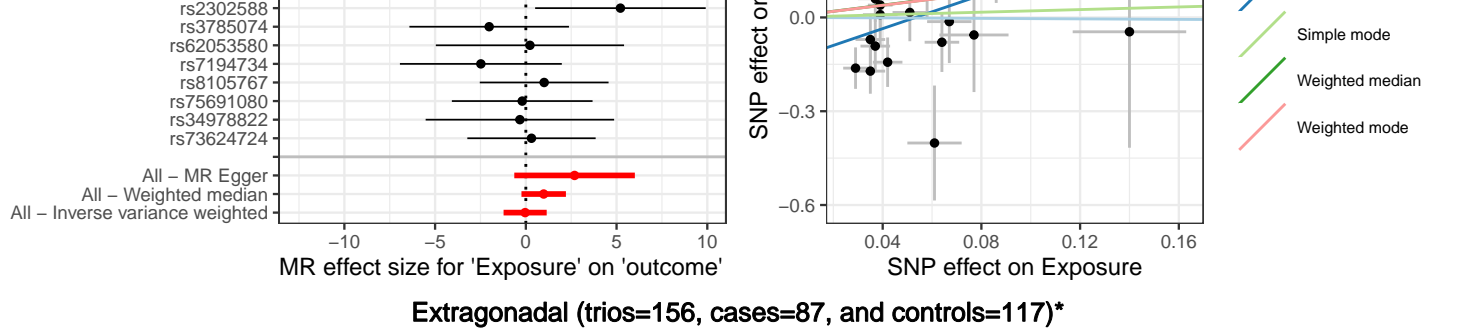
**11-19 years at diagnosis (trios=361, cases=408, and controls=692)\***



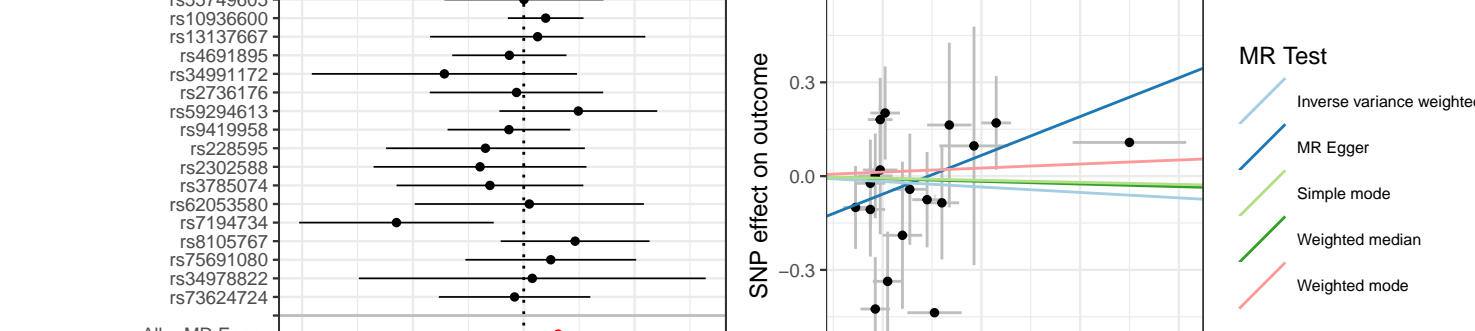
**Extragonadal (trios=156, cases=87, and controls=117)\***



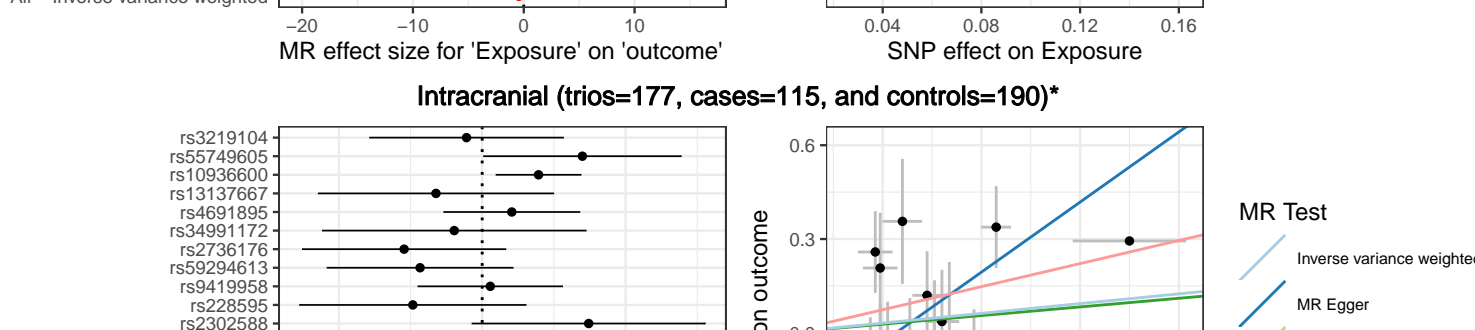
**Intracranial (trios=177, cases=115, and controls=190)\***



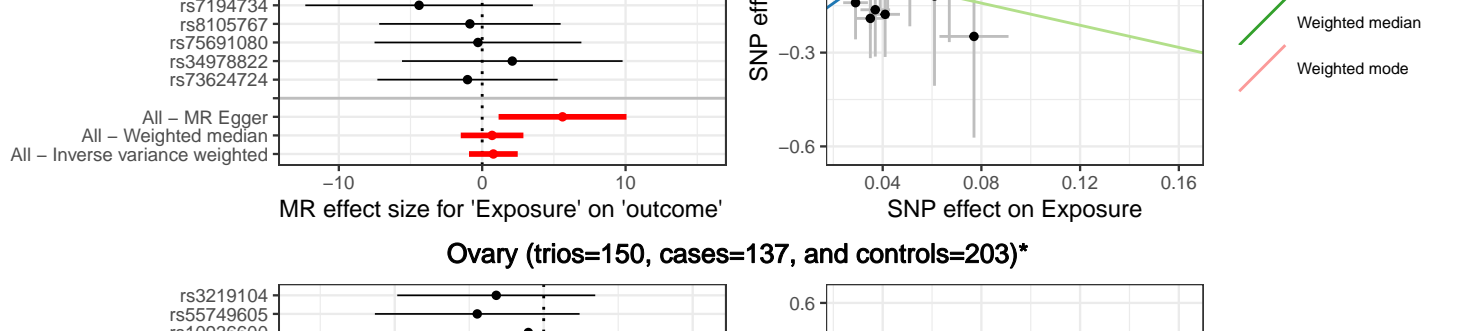
**Ovary (trios=150, cases=137, and controls=203)\***



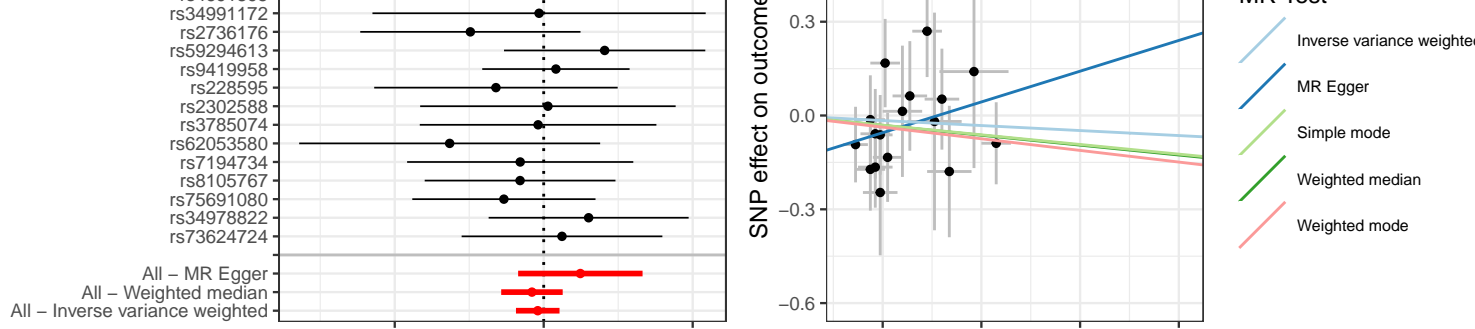
**Testis (trios=127, cases=370, and controls=421)\***



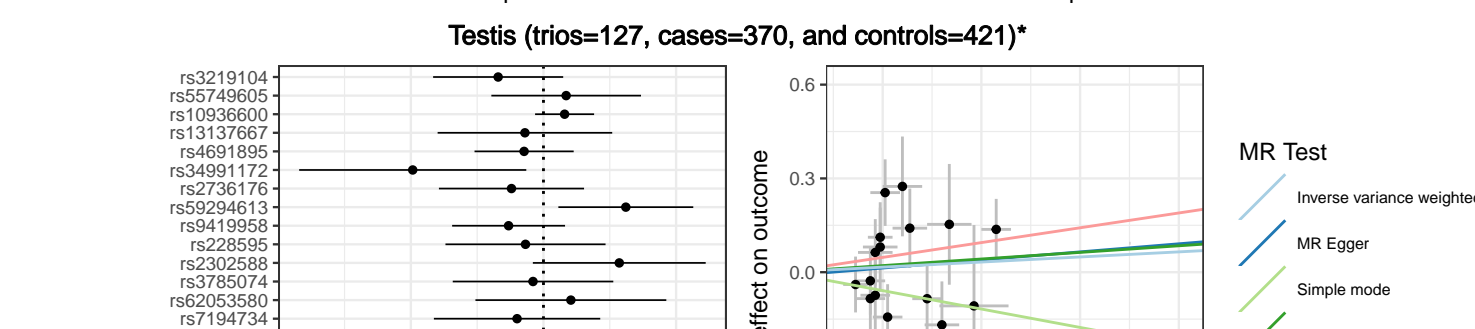
**Germinoma (trios=146, cases=177, and controls=258)\***



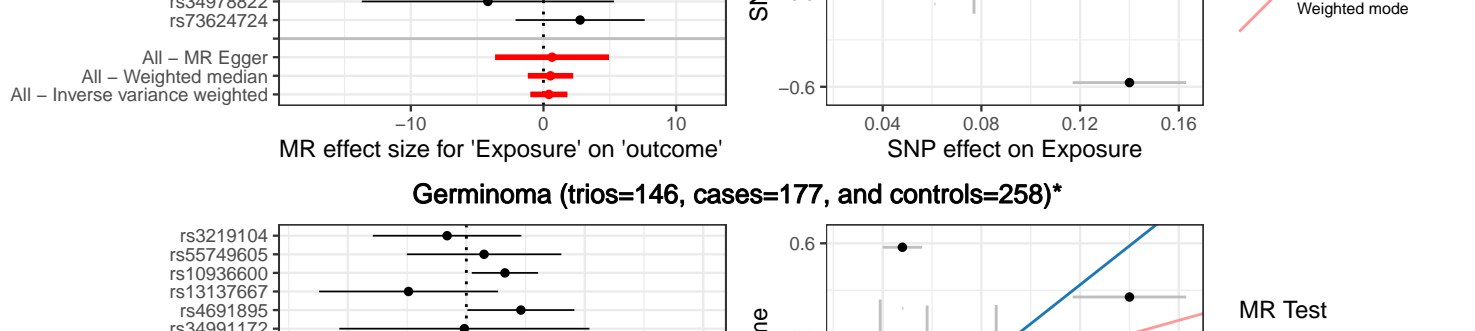
**Teratoma (trios=145, cases=286, and controls=336)\***



**Yolk sac tumor (YST; trios=134, cases=62, and controls=89)\***



**Mixed/Other (trios=162, cases=309, and controls=372)\***



**Supplemental Figure 2.** 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 Li et al. (2020) 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 standard error for each SNP. \*Subgroup analysis African trios, Hispanic and White case-control only samples to get stable estimates. African trios, Hispanic and Asian case-control samples were not included in subgroup analyses due to small sample size.