Supplementary Figure 1. Comparison of minor allele frequency between cancer datasets from European studies and the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium

Background pattern

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Supplementary Figure 2. Comparison of minor allele frequency between cancer datasets from East Asian studies and the Singapore Chinese Health Study

Chart, scatter chart

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Supplementary Figure 3. Comparison of minor allele frequency between cancer datasets from East Asian studies and super populations from the 1000 genomes project

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Supplementary Figure 4. Comparison of minor allele frequency between cancer datasets [ID1 to ID54] from European studies and super populations from the 1000 genomes project

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Supplementary Figure 5. Comparison of minor allele frequency between cancer datasets [ID55 to ID127] from European studies and super populations from the 1000 genomes project

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Supplementary Figure 6. Comparison of minor allele frequency between cancer datasets [ID128 to ID1499] from European studies and super populations from the 1000 genomes project

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Supplementary Figure 6. Correlation between Zp and Zb scores within cancer datasets

Zp = Z scores inferred from reported P values; Zb = Z scores inferred from reported effect sizes and standard errors. Correlations less than 0.99 are highlighted in red

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Supplementary Figure 7. Thirty one datasets with discrepancies between the predicted log odds ratio and reported effect sizes

The plotted datasets correspond to slopes > 1.2 or <0.8 from models of the predicted log odds ratio regressed on the reported effect size.

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Supplementary figure 8. Fourteen datasets with discrepancies between the predicted log odds ratio and reported log odds ratios that did not report the number of contributing studies to each SNP

Graphical user interface, chart, application, line chart

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