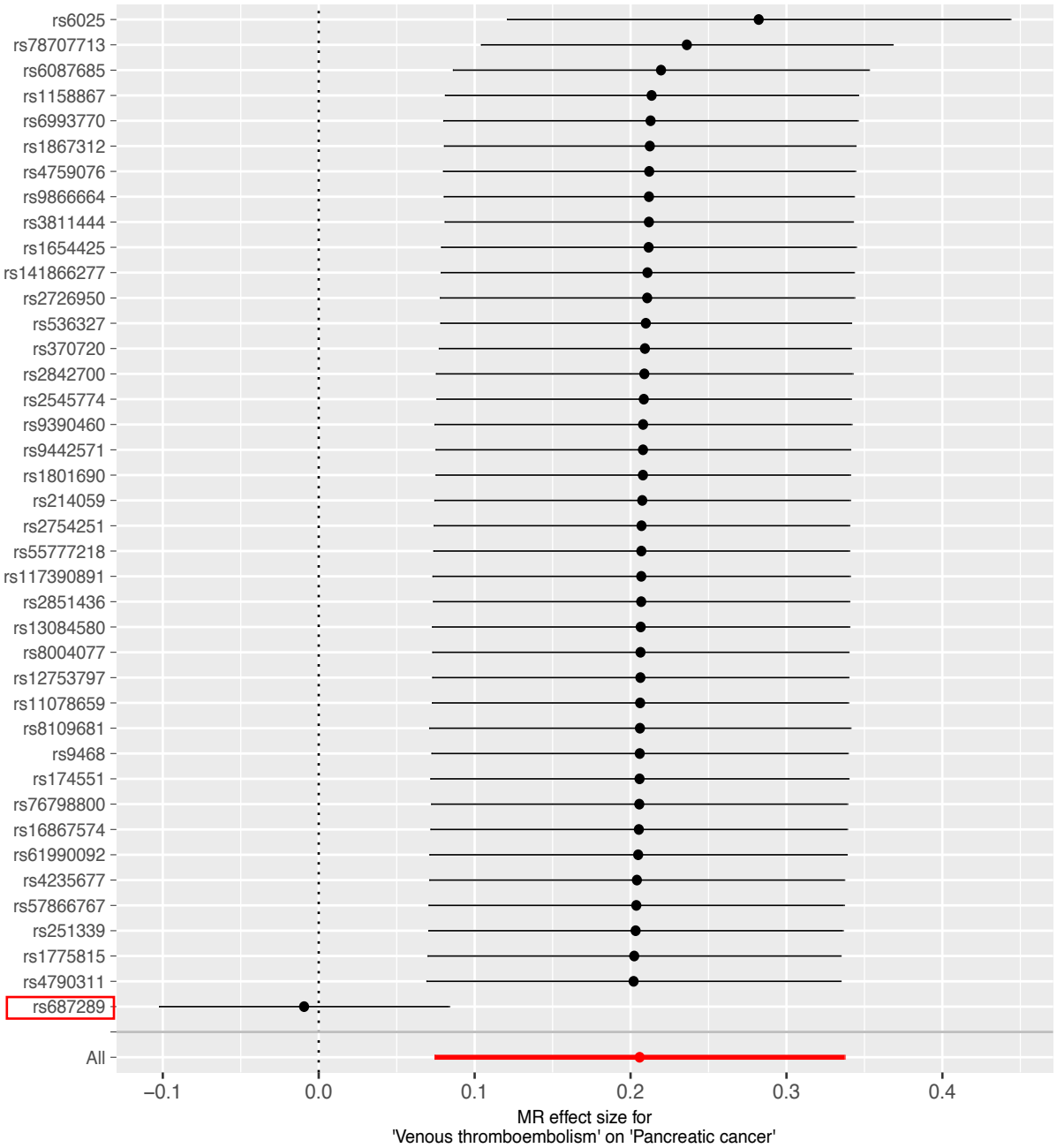
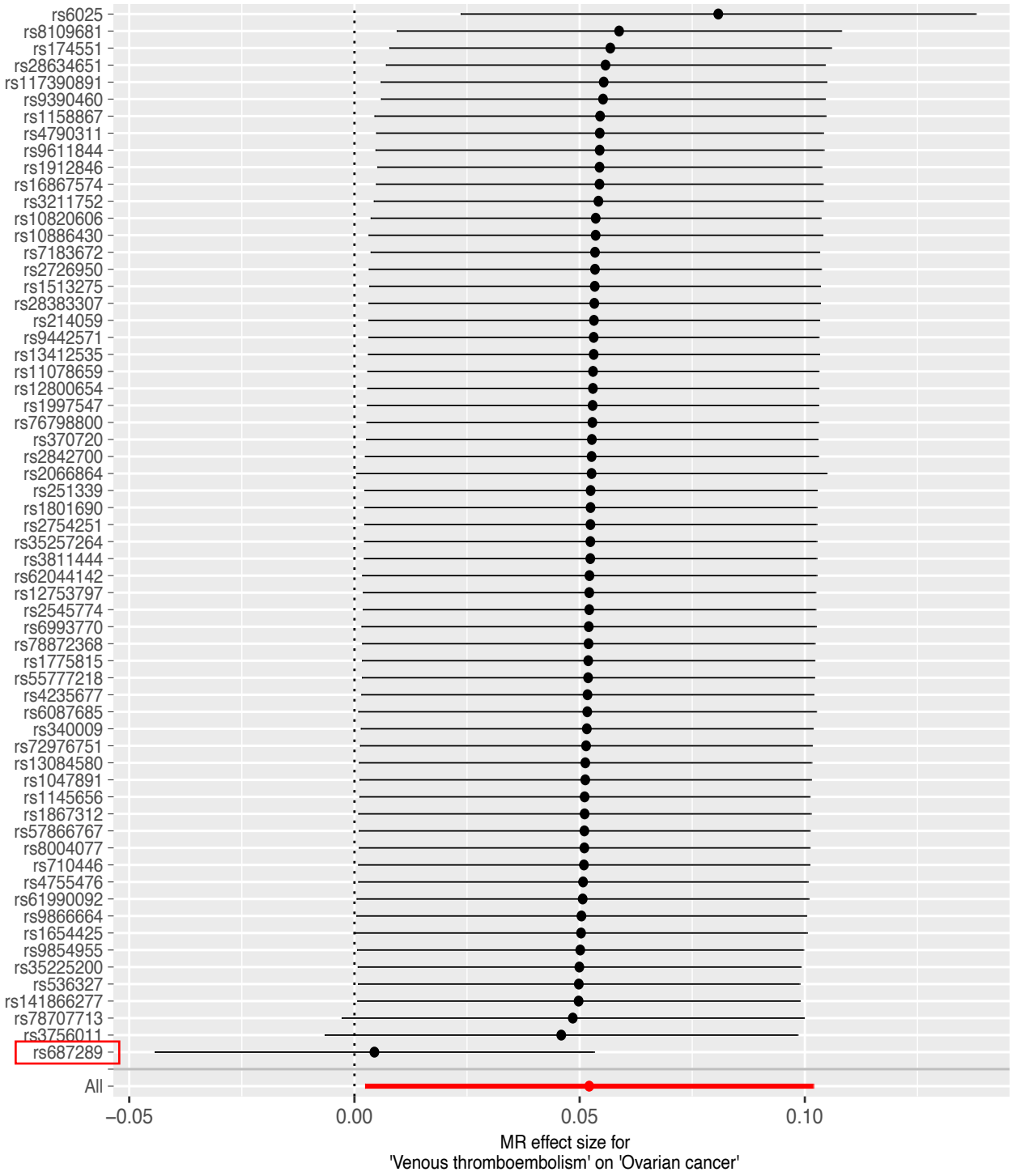
Supplementary Figures: Contents

Figure S1A



Supplementary Figure S1 [A – D]:
Leave one out plots for selected MR analyses of VTE (exposure) and [A] pancreatic, [B] ovarian, [C] endometrial and [D] oral cancer. The x-axis shows the MR-IVW effect estimates (log-OR) after sequential removal of each SNP shown on the y-axis. The variant rs687289 which proxies non-O blood group is highlighted.

Figure S1B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All
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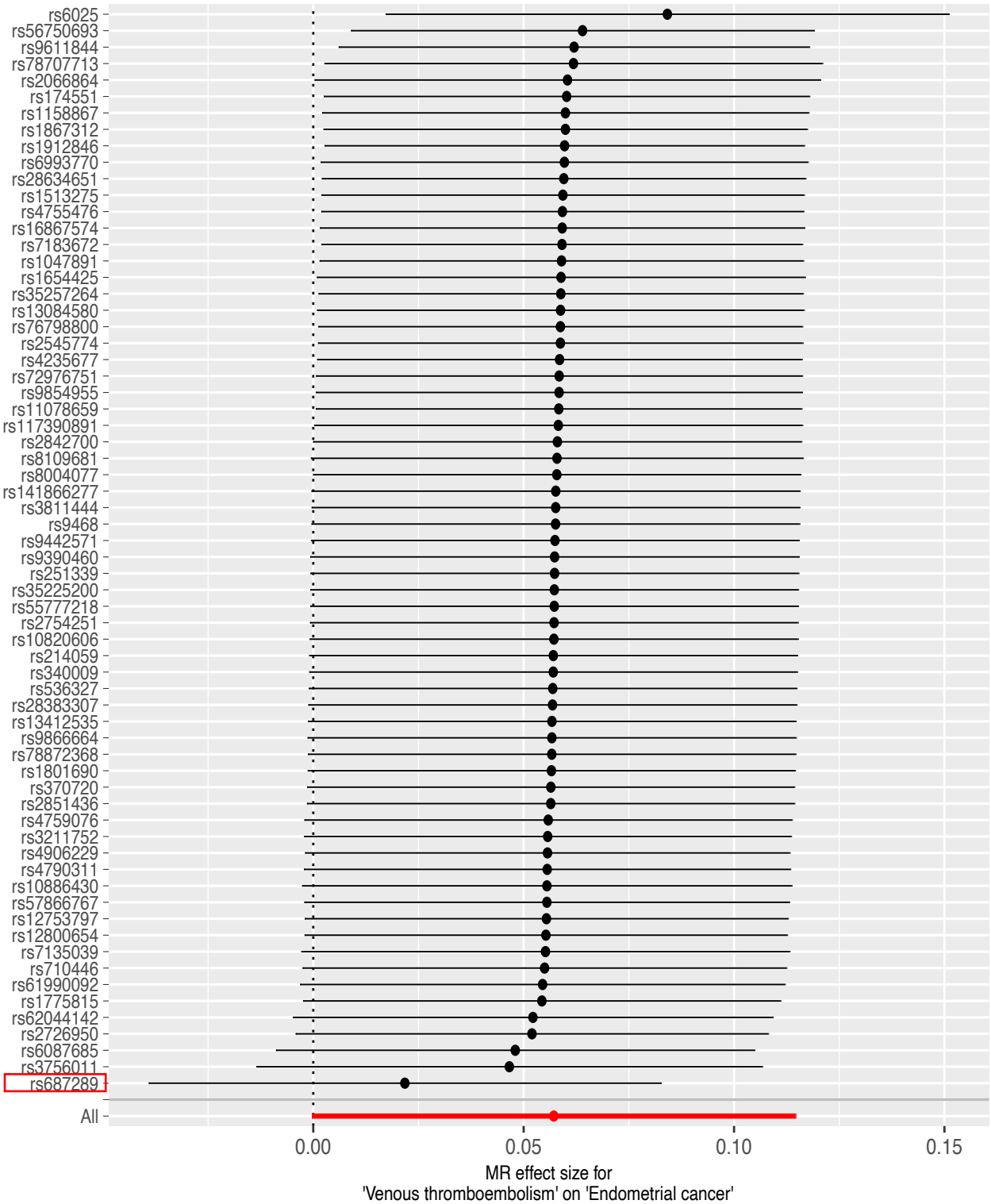
0.00
0.05
0.10
MR effect size for
'Venous thromboembolism' on 'Ovarian cancer'

Figure S1C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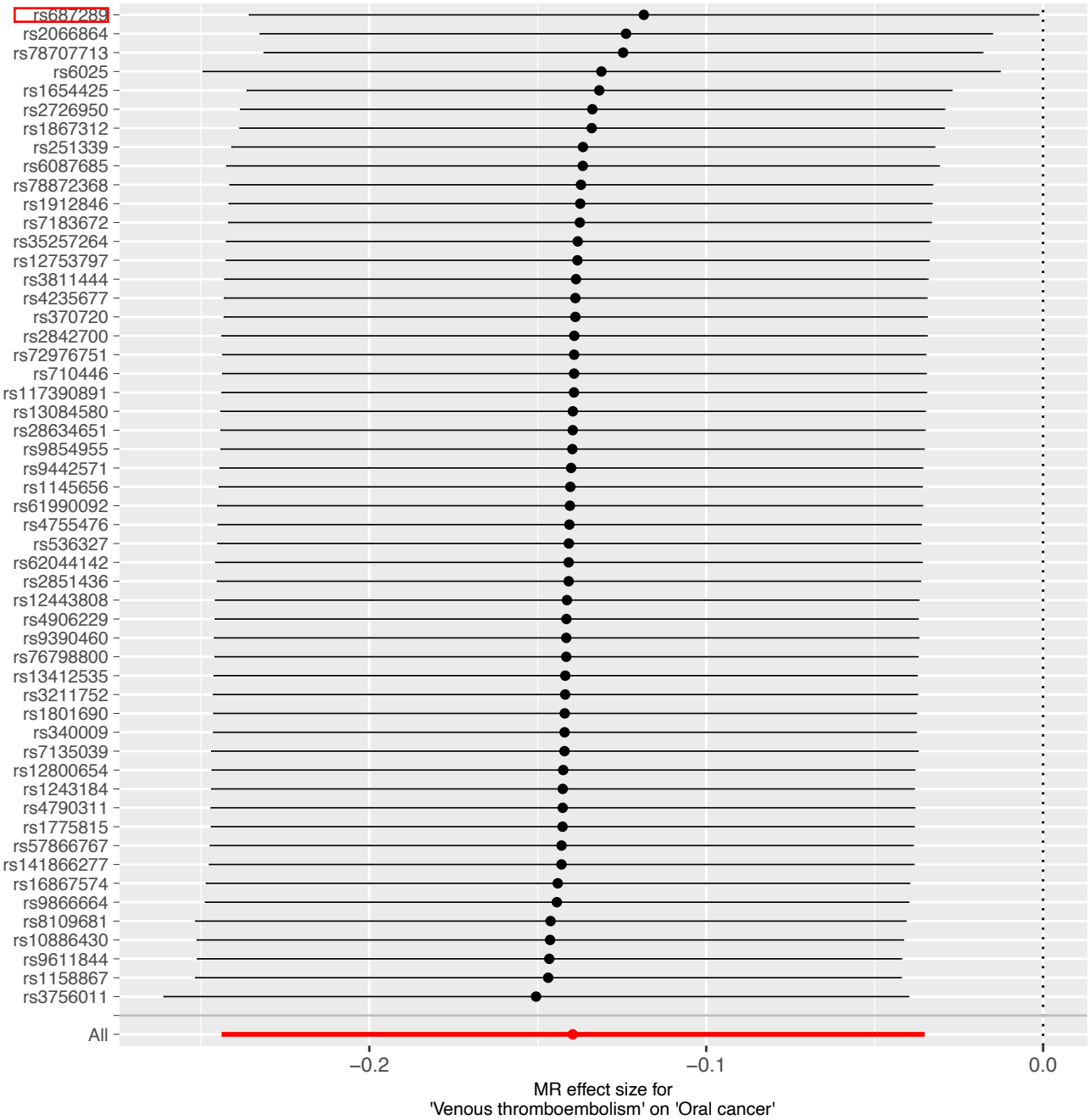
MR effect size for
'Venous thromboembolism' on 'Endometrial cancer'

Figure S1D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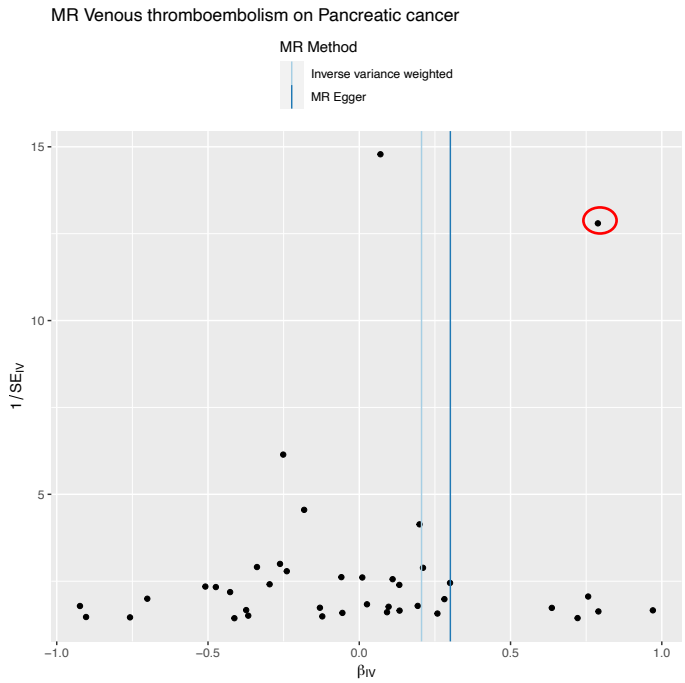
MR effect size for
'Venous thromboembolism' on 'Oral cancer'

Figure S2A



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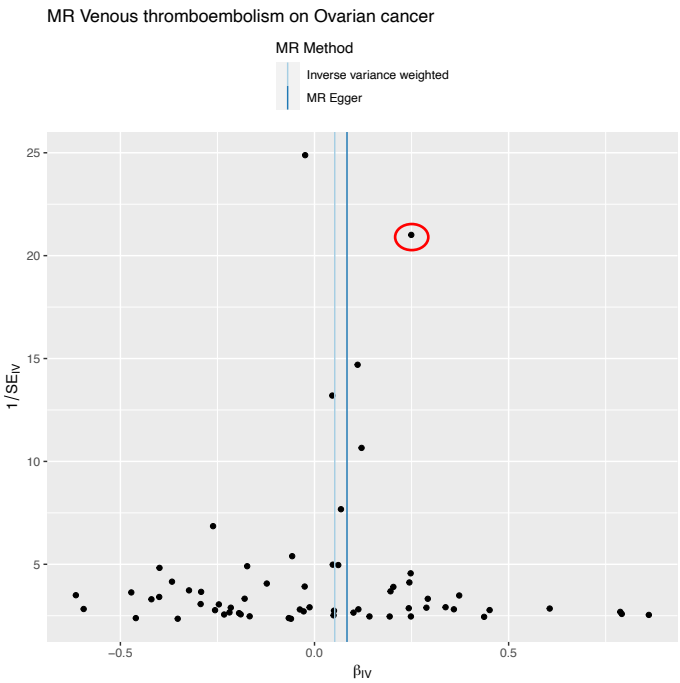

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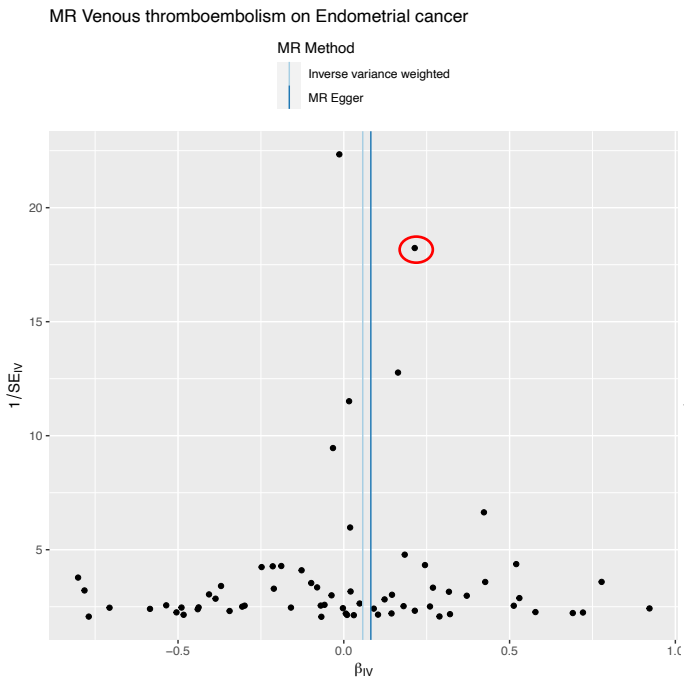
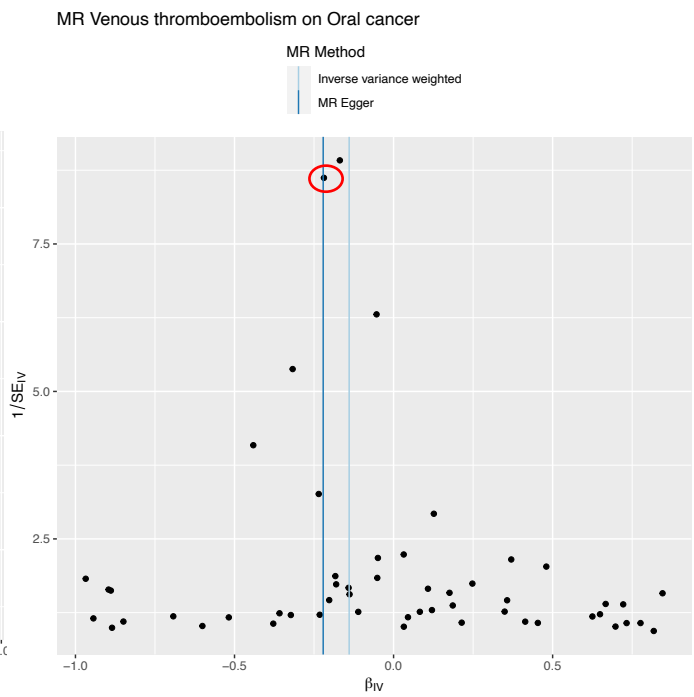
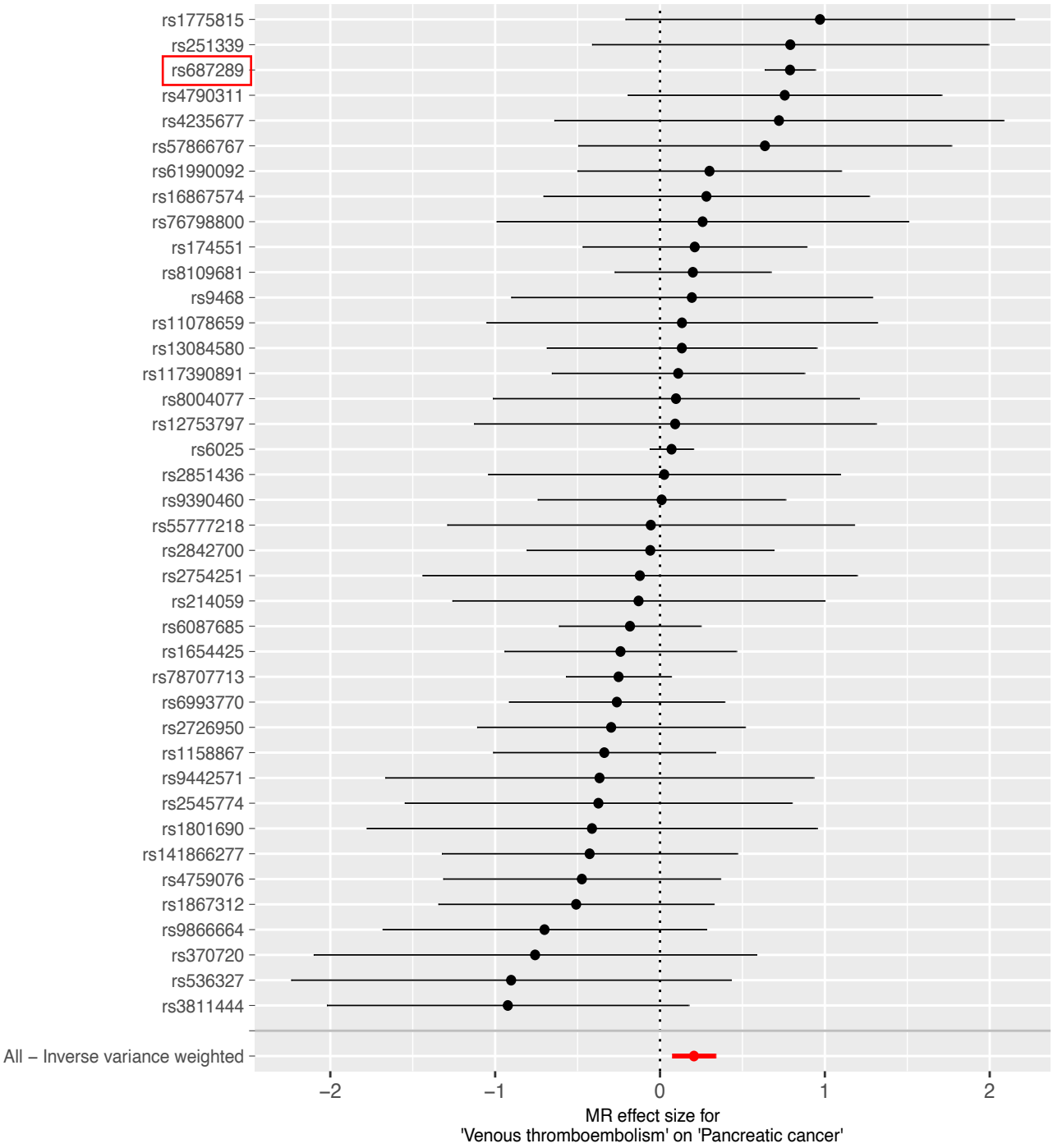


Figure S2D



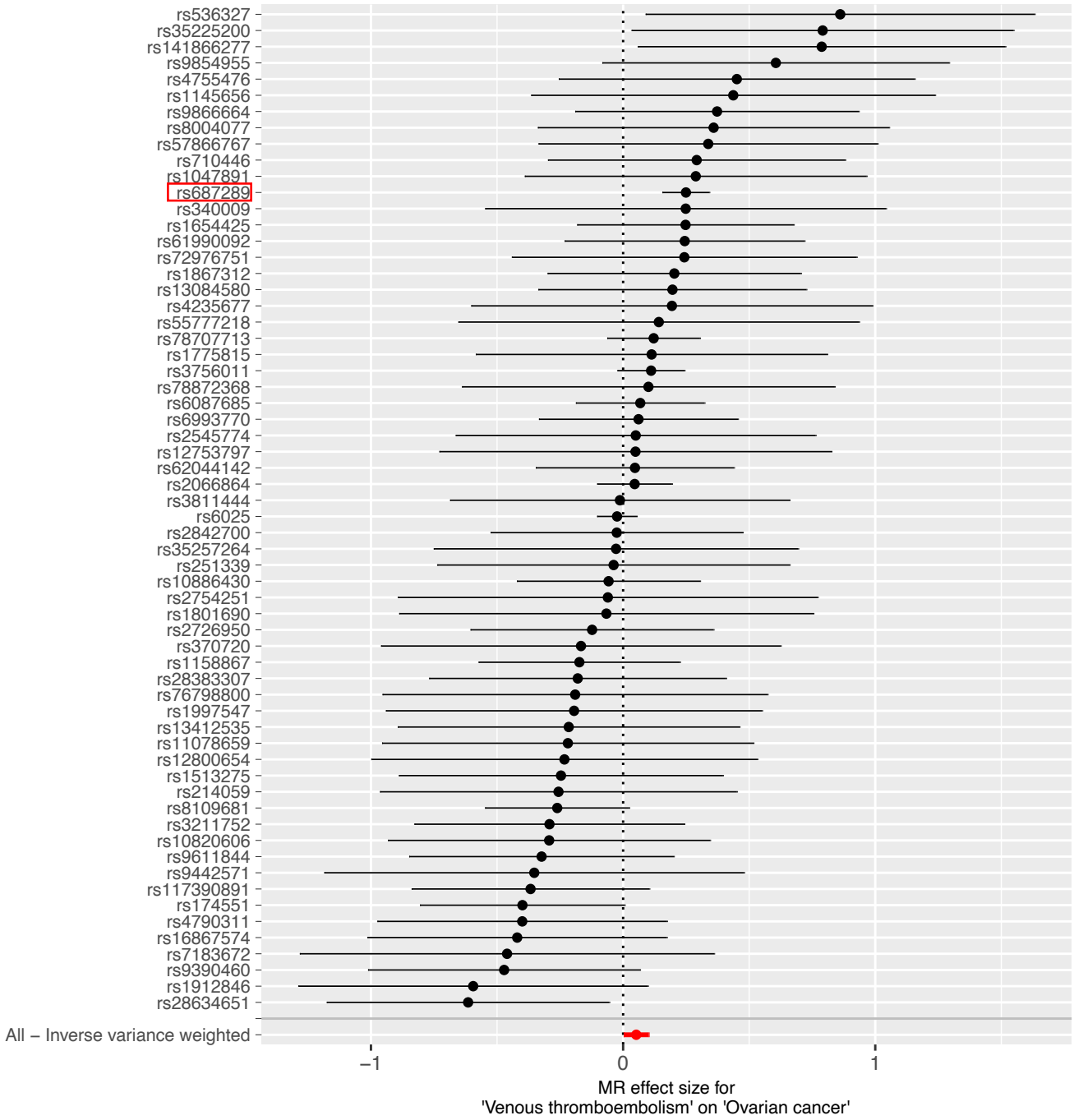
Supplementary Figure S2:
Funnel plots for selected MR analyses of VTE (exposure) and [A] pancreatic, [B] ovarian, [C] endometrial and [D] oral cancer. The x-axis shows the MR Wald ratio effect estimate (log-OR) for each SNP (IV); the y-axis shows the inverse standard error of the effect estimate. The variant rs687289 which proxies non-O blood group is circled.

Figure S3A



Supplementary Figure S3 [A-D]:
Single SNP plots for selected MR analyses of VTE (exposure) and [A] pancreatic, [B] ovarian, [C] endometrial and [D] oral cancer. The x-axis shows the MR Wald ratio effect estimate (expressed as log-OR) for each SNP shown on the y-axis. The variant rs687289 which proxies non-O blood group is highlighted in red.

Figure S3B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All – Inverse variance weighted
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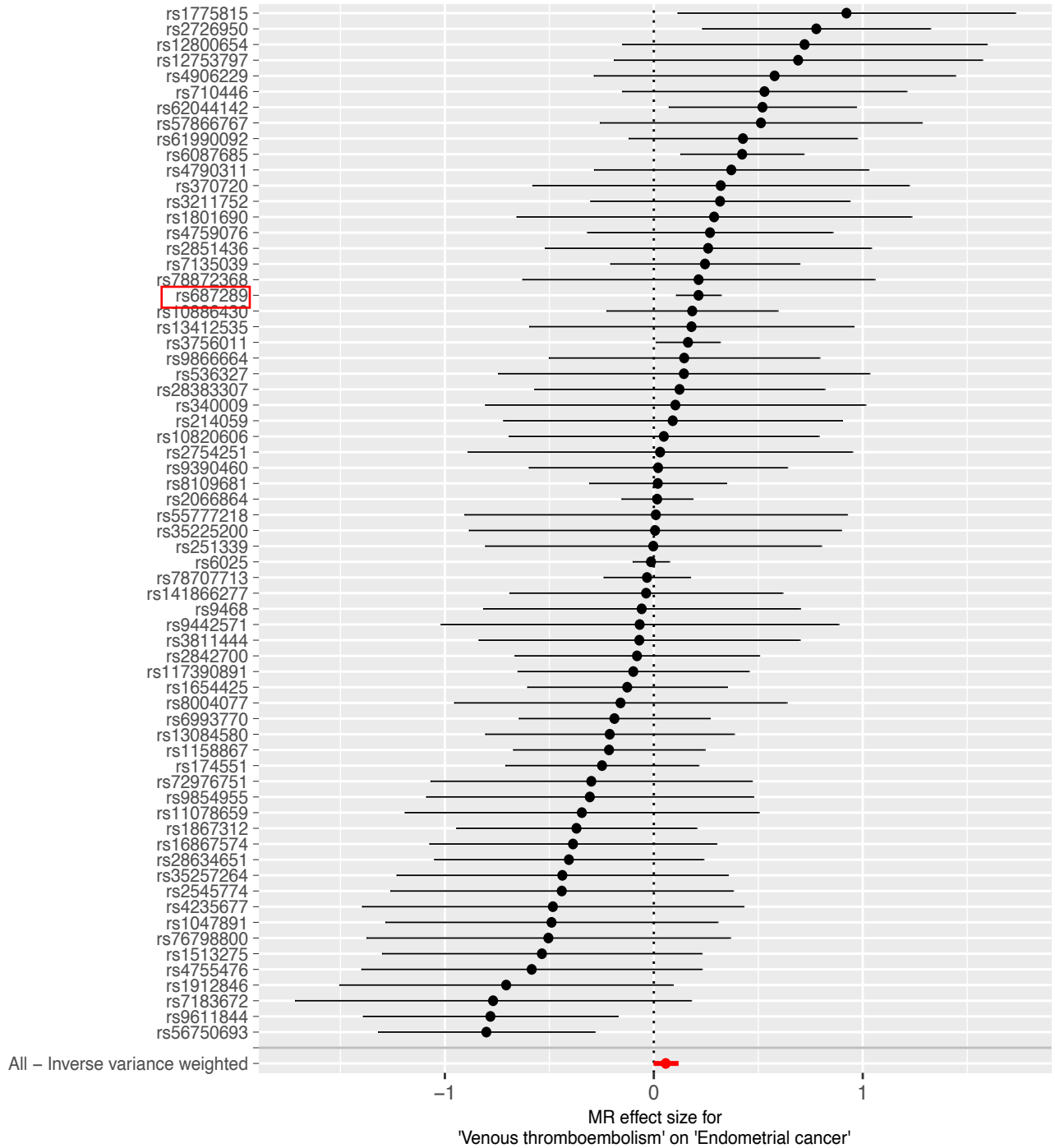
MR effect size for
'Venous thromboembolism' on 'Ovarian cancer'

Figure S3C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All – Inverse variance weighted
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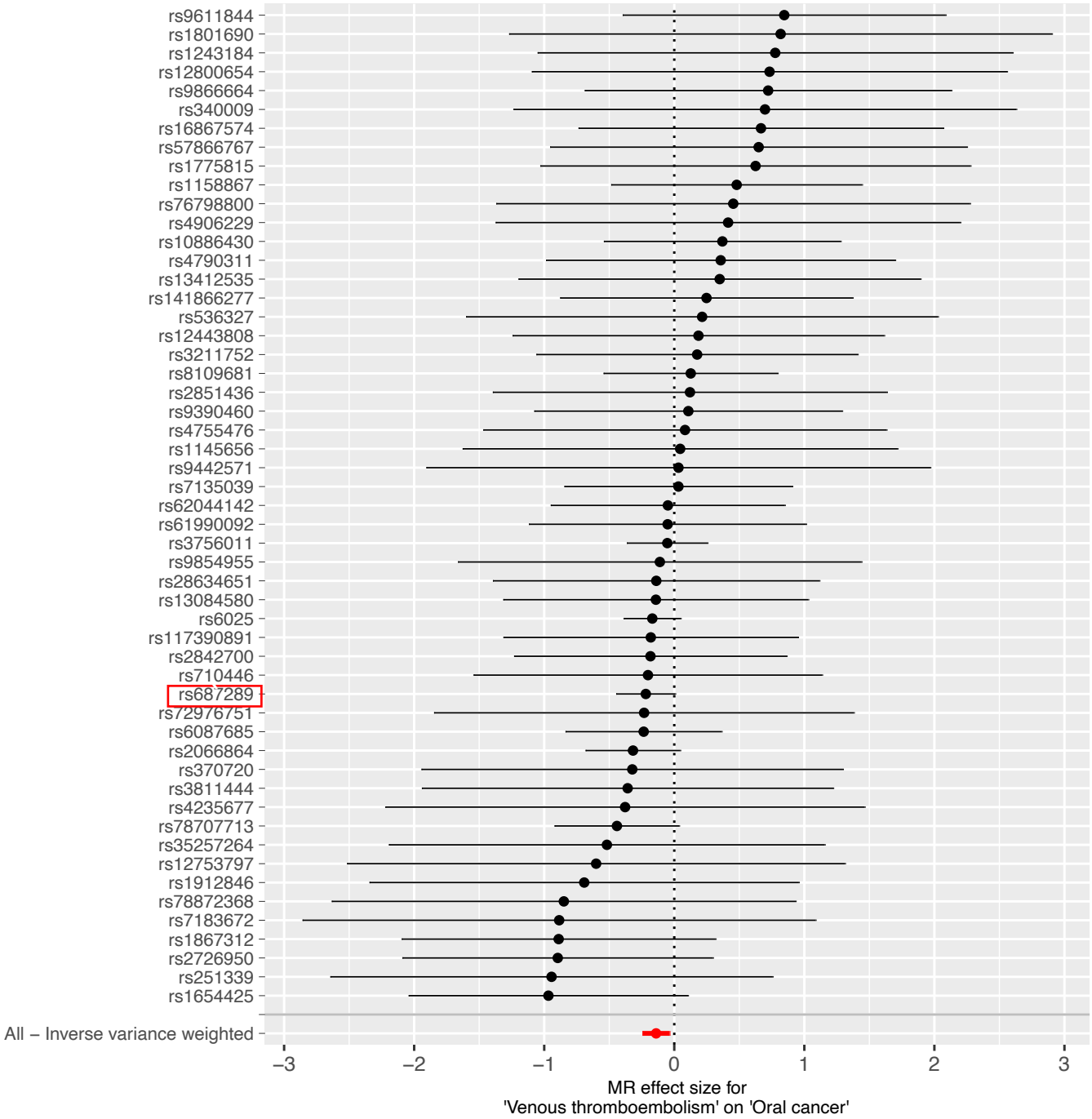
MR effect size for
'Venous thromboembolism' on 'Endometrial cancer'

Figure S3D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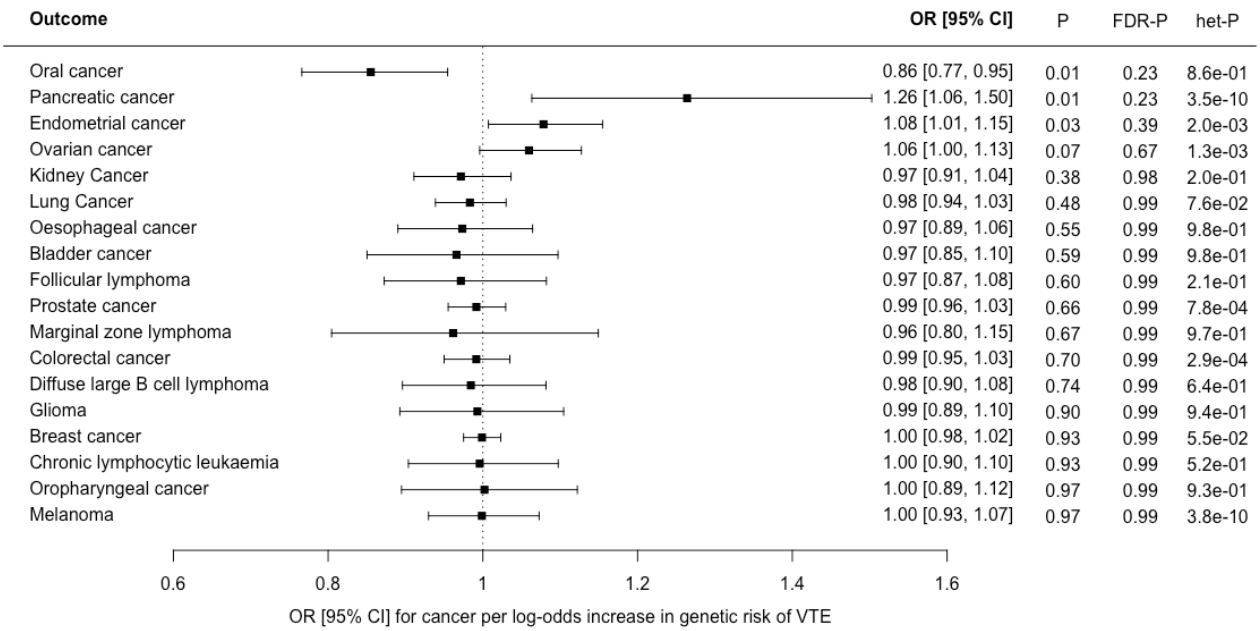
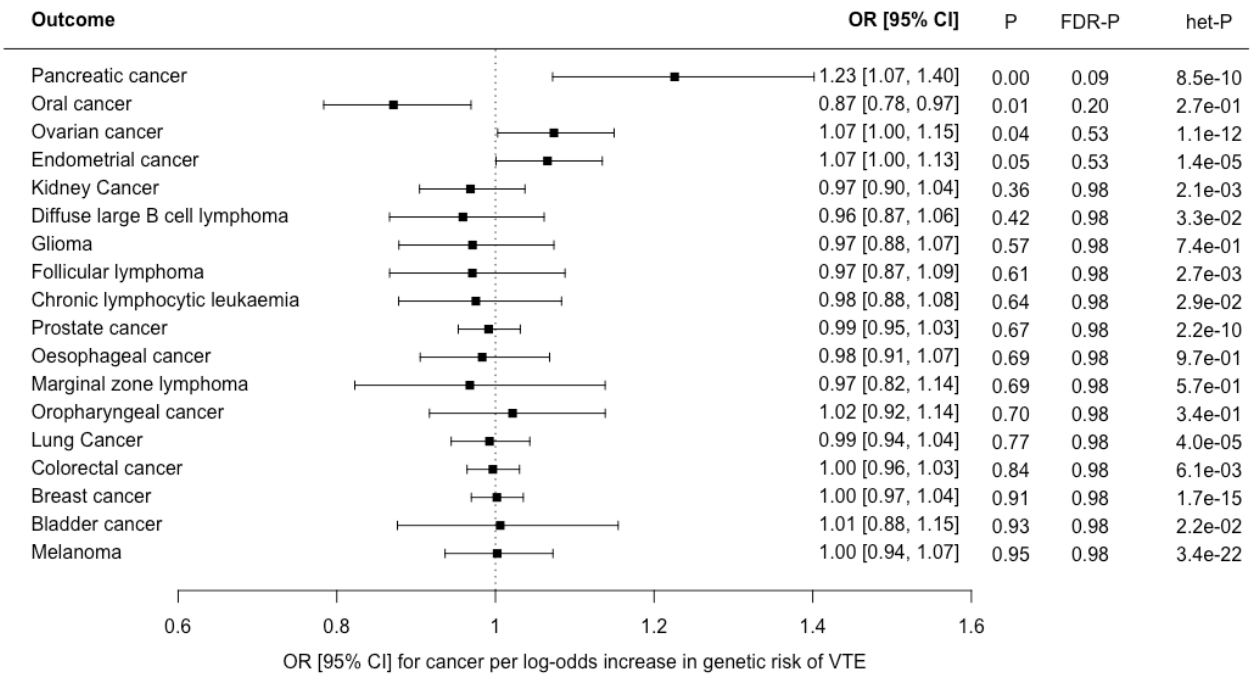
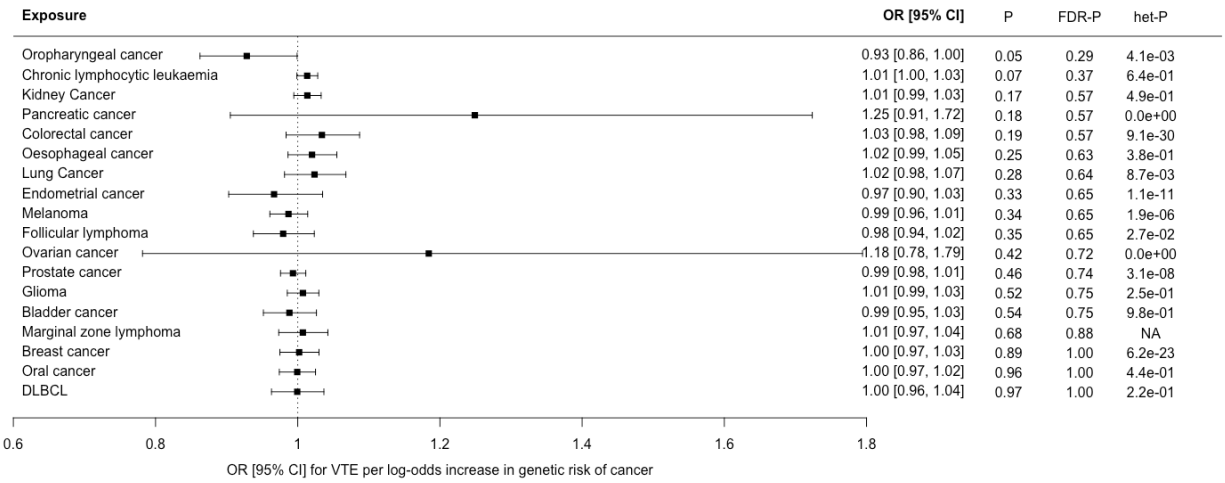
MR effect size for
'Venous thromboembolism' on 'Oral cancer'



Supplementary Figure S4: Forest plot showing estimates from Mendelian randomisation inverse variance weighted estimates for VTE as an exposure, with instrumental variables restricted to replicated SNPs only, and 18 cancers as outcomes. Results are represented as the odds ratio (OR) and 95% confidence interval (CI) for each cancer per log-odds increase in genetic risk of each VTE. Nominal P values (*P*), false discovery corrected P values (*FDR-P*) and heterogeneity P values for Cochrane's Q statistic (*het-P*) are shown.



Supplementary Figure S5: Forest plot showing estimates from Mendelian randomisation inverse variance weighted estimates for VTE as an exposure, with instrumental variables including all available VTE SNPs (no Steiger-filtering applied), and 18 cancers as outcomes. Results are represented as the odds ratio (OR) and 95% confidence interval (CI) for each cancer per log-odds increase in genetic risk of each VTE. Nominal P values (*P*), false discovery corrected P values (*FDR-P*) and heterogeneity P values for Cochrane's Q statistic (*het-P*) are shown



Supplementary Figure S6: Forest plot showing estimates from Mendelian randomisation (MR) estimates for 18 cancers as exposures, with instrumental variables including all available cancer-risk SNPs (no Steiger-filtering applied), and VTE as an outcome. The MR inverse variance weighted estimate is shown for all cancers except Marginal zone lymphoma, where the Wald ratio is shown as only a single instrumental variable was available. Results are represented as the odds ratio (OR) and 95% confidence interval (CI) for VTE per log-odds increase in genetic risk of each cancer. Nominal P values (*P*), false discovery corrected P values (*FDR-P*) and heterogeneity P values for Cochrane's Q statistic (*het-P*) are shown.