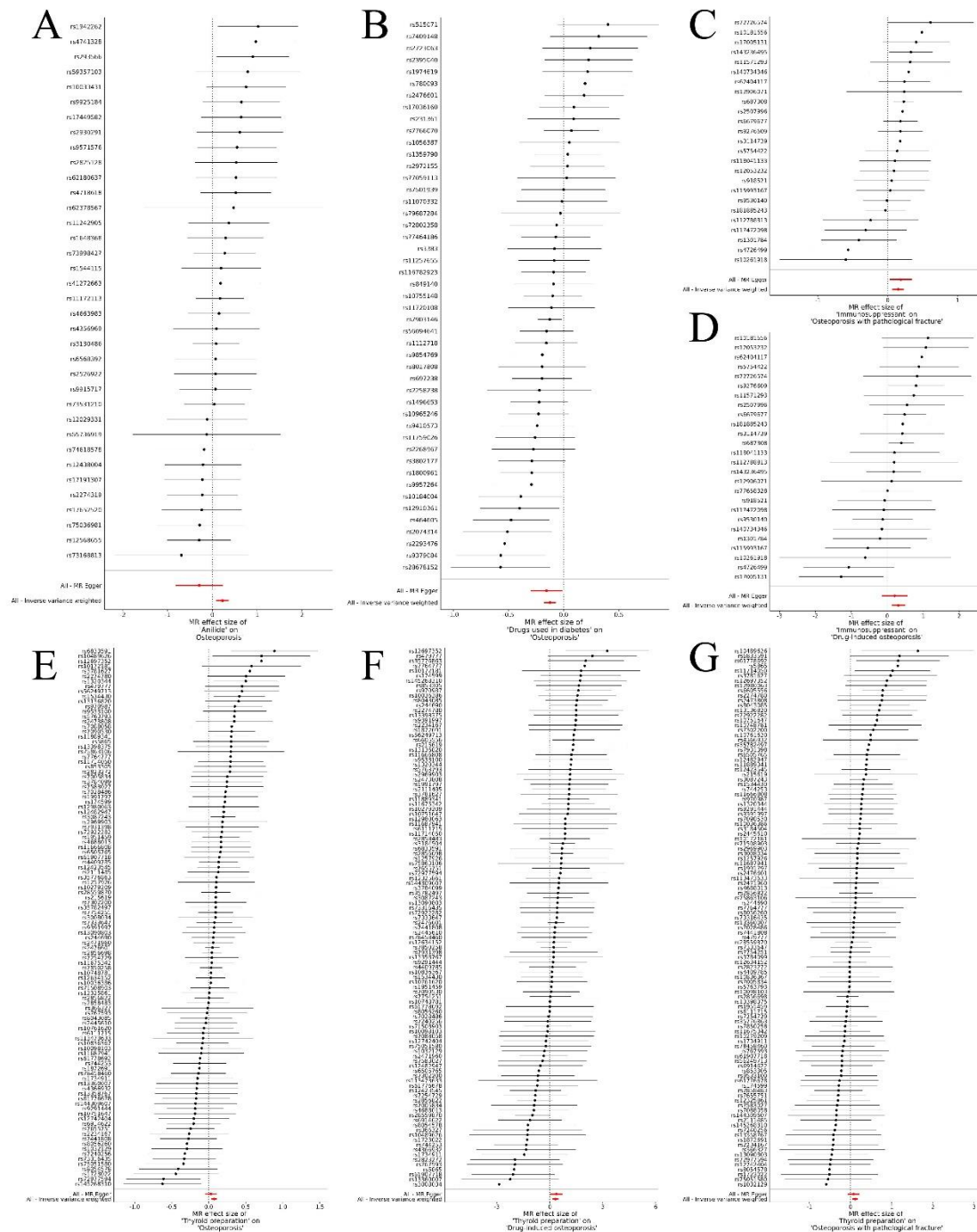
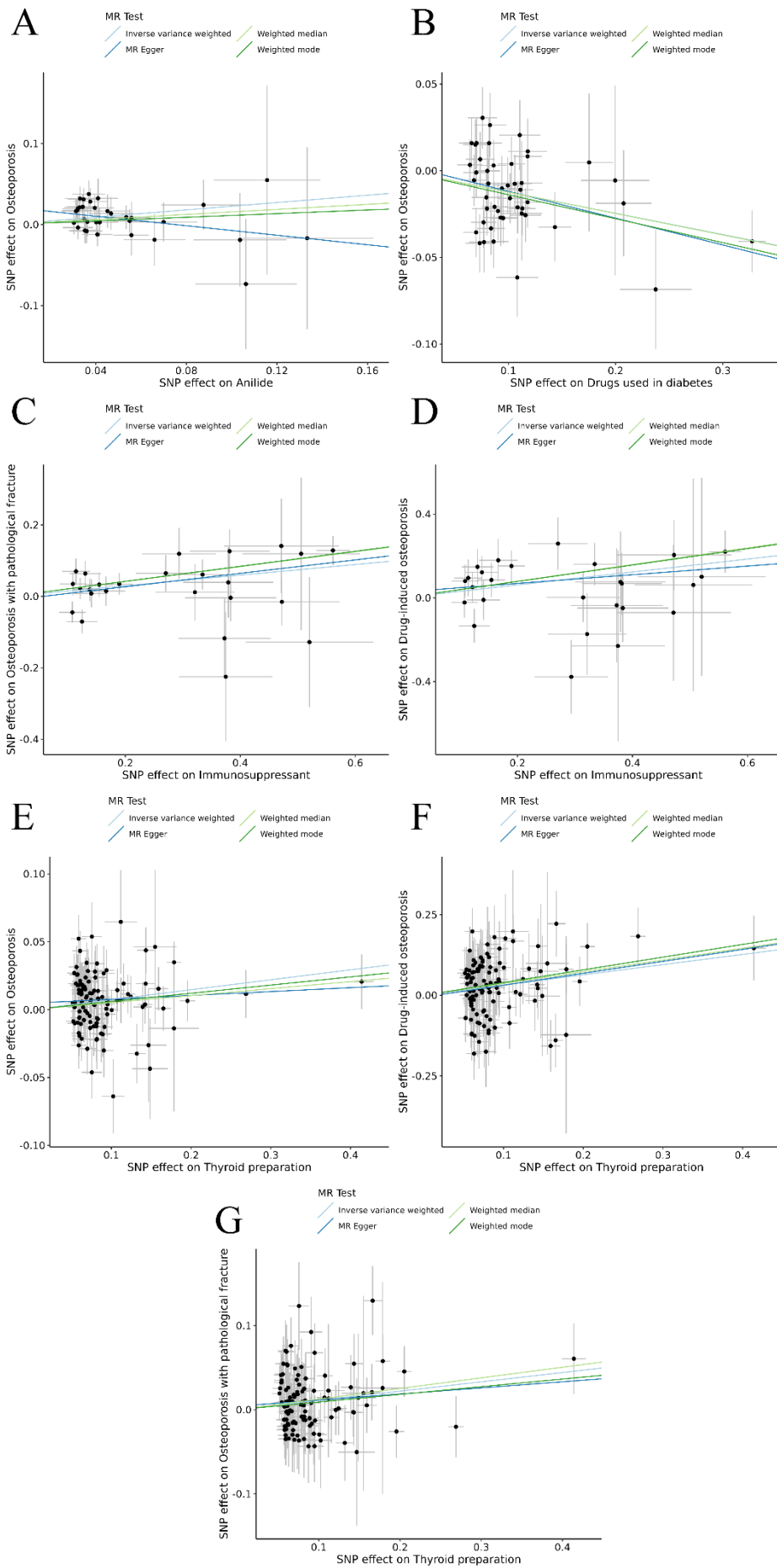


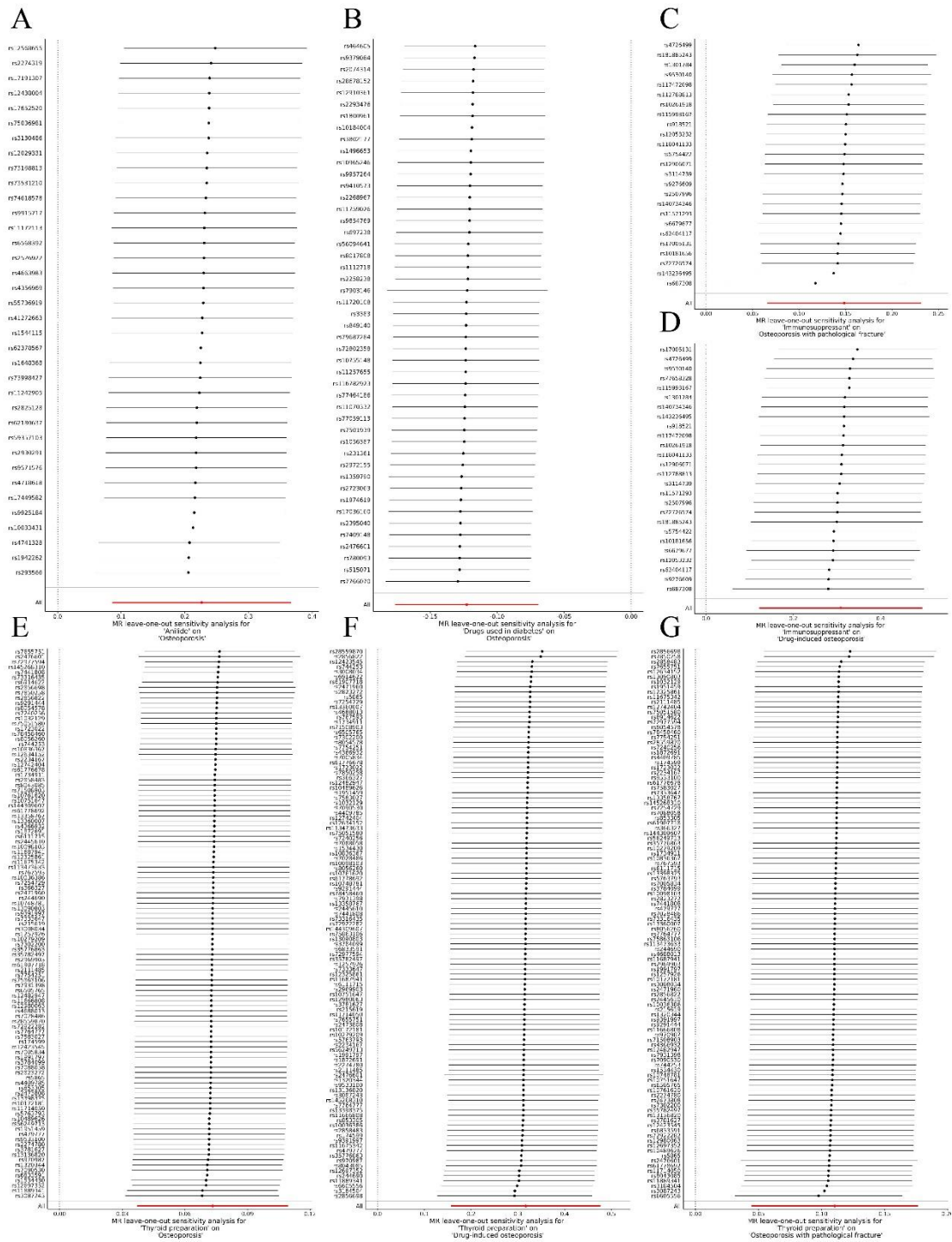
Supplementary figures



Supplementary Figure S1. Forest plots showing SNP-specific and pooled MR estimates for significant medication–osteoporosis associations (FDR < 0.05). Each horizontal line represents the effect size and 95% confidence interval for a single SNP. Panels (A–G) correspond to the same exposure–outcome pairs described in Figure 2.



Supplementary Figure S2. Funnel plots assessing heterogeneity and directional pleiotropy for medication–osteoporosis associations (FDR < 0.05). Each dot represents an individual SNP, plotted against its precision (1/SE). The symmetrical shape of the funnels suggests the absence of directional pleiotropy. Panels (A–G) correspond to associations with FDR < 0.05.



Supplementary Figure S3. Leave-one-out (LOO) analyses for significant medication–osteoporosis associations (FDR < 0.05). Each point represents the MR estimate recalculated after excluding one SNP at a time. The stability of effect estimates across all iterations indicates that no single variant disproportionately

influenced the overall causal estimates. Panels (A–G) correspond to the same exposure–outcome pairs described in Figure 2.