Figure S1 The stability of AKR1B1/SUGT1 protein level ratio was demonstrated by forest plot, scatter plot and funnel plot. (Causal effect of AKR1B1/SUGT1 protein level ratio on NSCLC analyzed by MR). (A) Forest plot of the causal effects of SNPs associated with Protein Level Ratios on NSCLC. (B) Leave-one-out of SNPs associated with AKR1B1/SUGT1 protein level ratio and their risk of NSCLC. Each black point represents result of the IVW MR method applied to estimate the causal effect of AKR1B1/SUGT1 protein level ratio on NSCLC excluding particular SNP. (C) Scatter plots of genetic associations with AKR1B1/SUGT1 protein level ratio against the genetic associations with NSCLC. (D) Funnel plot to assess heterogeneity. MR, Mendelian randomization; SNP, single nucleotide polymorphism; NSCLC, non-small cell lung cancer; IVW, inverse variance weighting.
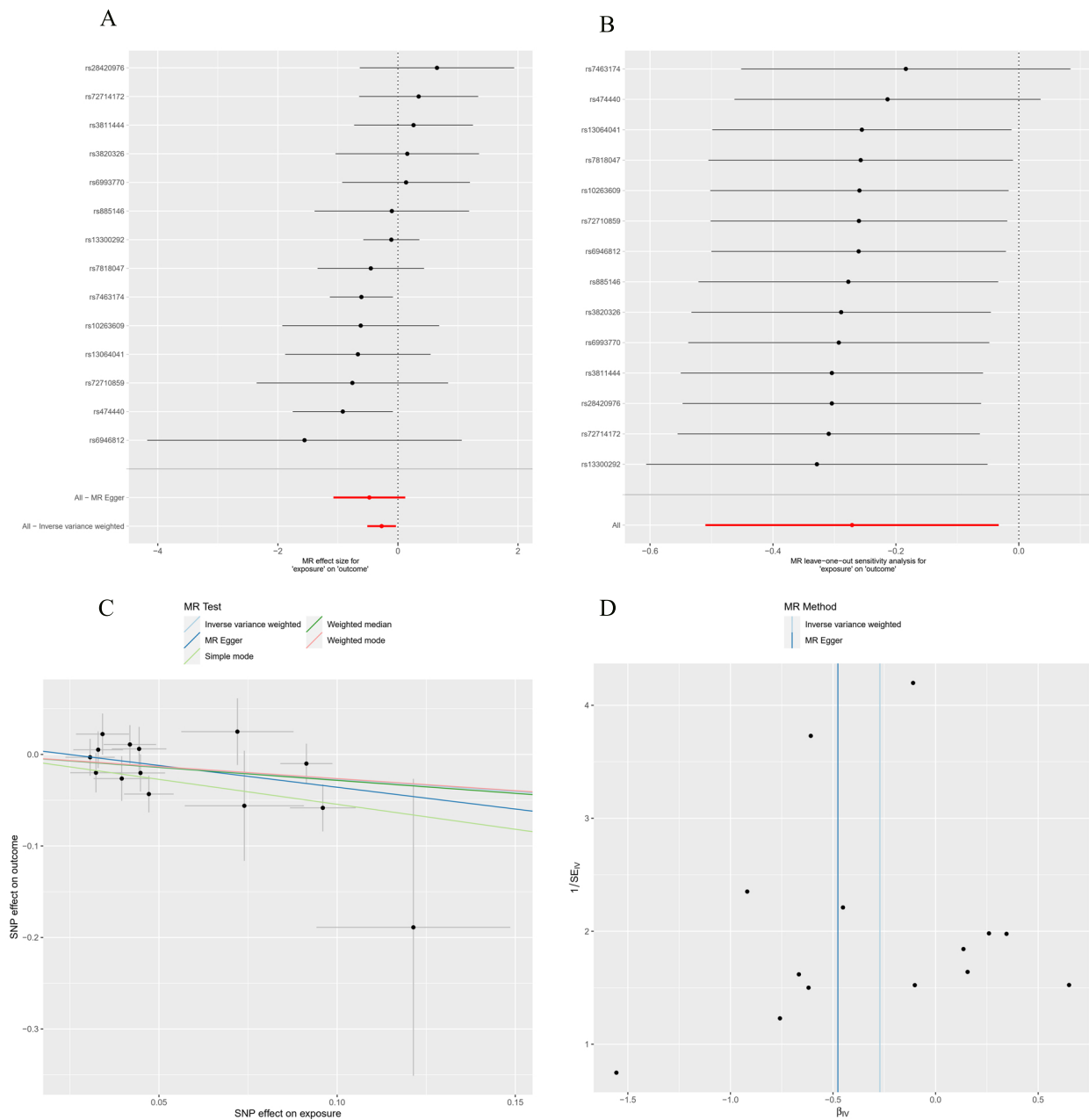
Figure S2 The stability of PLPBP/STIP1 protein level ratio was demonstrated by forest plot, scatter plot and funnel plot. (Causal effect of PLPBP/STIP1 protein level ratio on NSCLC analyzed by MR). (A) Forest plot of the causal effects of SNPs associated with protein level ratios on NSCLC. (B) Leave-one-out of SNPs associated with PLPBP/STIP1 protein level ratio and their risk of NSCLC. ach black point represents result of the IVW MR method applied to estimate the causal effect of PLPBP/STIP1 protein level ratio on NSCLC excluding particular SNP. (C) Scatter plots of genetic associations with PLPBP/STIP1 protein level ratio against the genetic associations with NSCLC. (D) Funnel plot to assess heterogeneity. MR, Mendelian randomization; SNP, single nucleotide polymorphism; NSCLC, non-small cell lung cancer; IVW, inverse variance weighting.
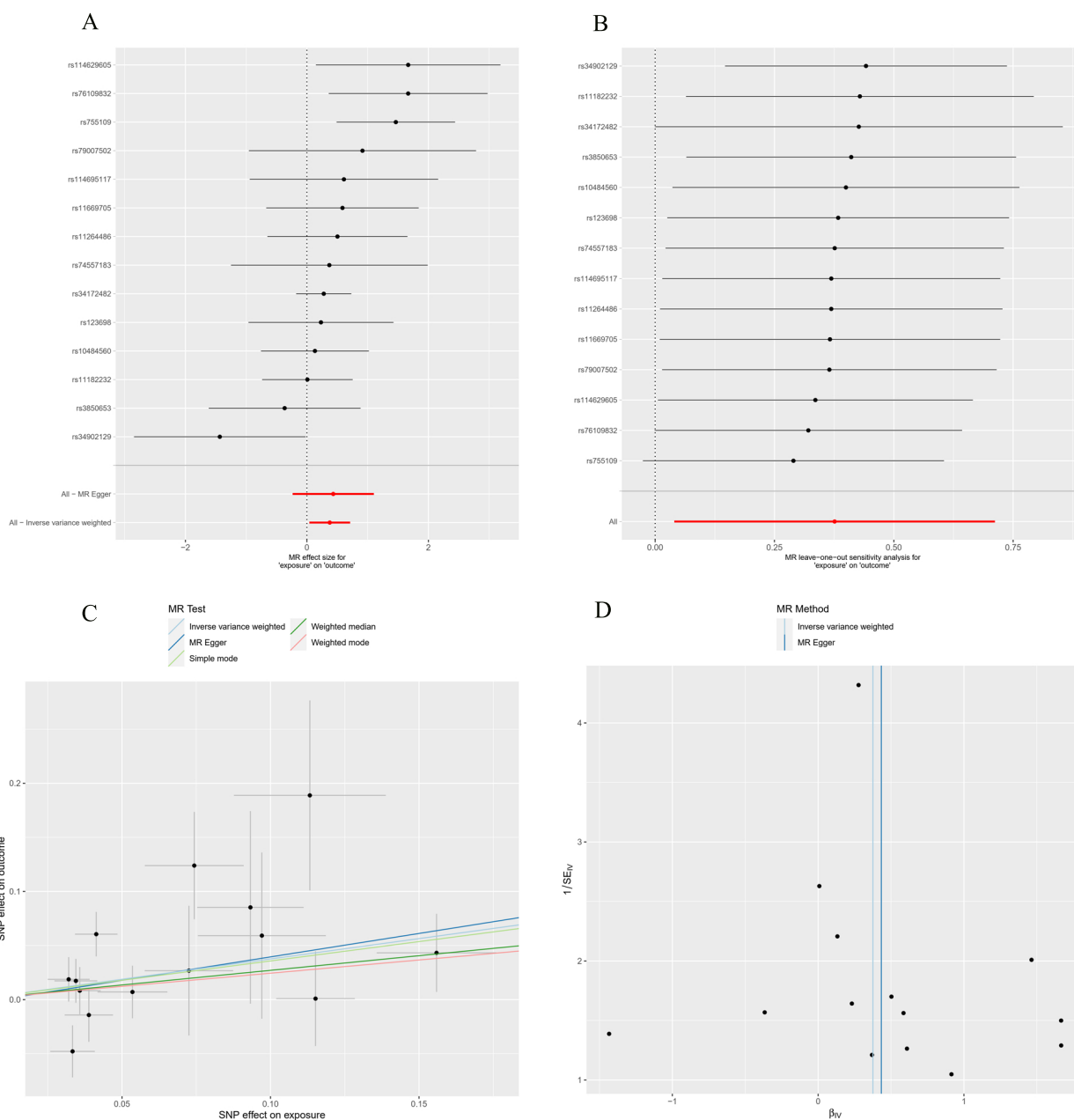
Figure S3 The stability of ARHGEF12/IRAK4 protein level ratio was demonstrated by forest plot, scatter plot and funnel plot. (Causal effect of ARHGEF12/IRAK4 protein level ratio on NSCLC analyzed by MR). (A) Forest plot of the causal effects of SNPs associated with protein level ratios on NSCLC. (B) Leave-one-out of SNPs associated with ARHGEF12/IRAK4 protein level ratio and their risk of NSCLC. Each black point represents result of the IVW MR method applied to estimate the causal effect of ARHGEF12/IRAK4 protein level ratio on NSCLC excluding particular SNP. (C) Scatter plots of genetic associations with ARHGEF12/IRAK4 protein level ratio against the genetic associations with NSCLC. (D) Funnel plot to assess heterogeneity. MR, Mendelian randomization; SNP, single nucleotide polymorphism; NSCLC, non-small cell lung cancer; IVW, inverse variance weighting.
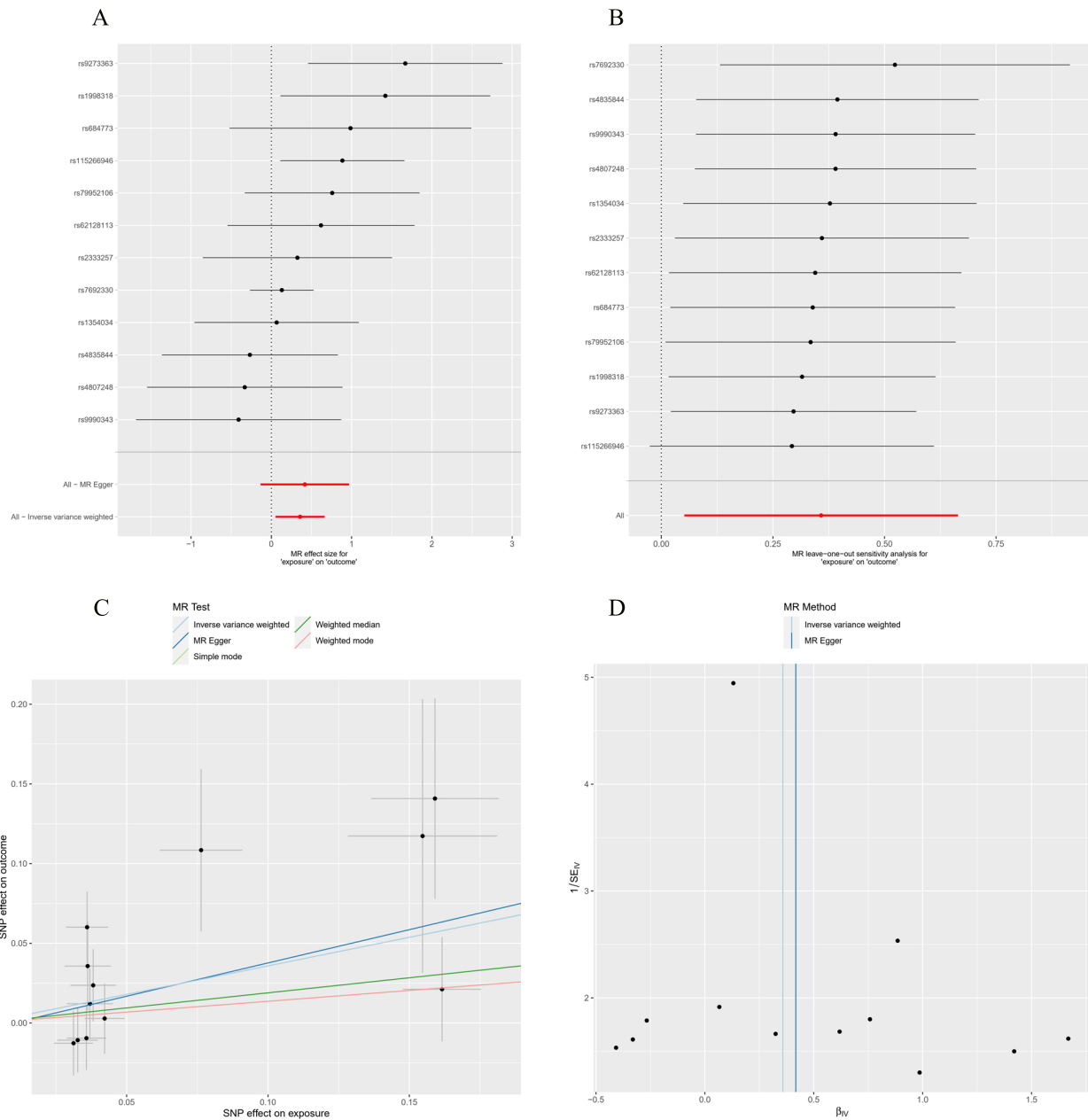
Figure S4 The stability of BANK1/LBR protein level ratio was demonstrated by forest plot, scatter plot and funnel plot. (Causal effect of BANK1/LBR protein level ratio on NSCLC analyzed by MR). (A) Forest plot of the causal effects of SNPs associated with protein level ratios on NSCLC. (B) Leave-one-out of SNPs associated with BANK1/LBR protein level ratio and their risk of NSCLC. Each black point represents result of the IVW MR method applied to estimate the causal effect of BANK1/LBR protein level ratio on NSCLC excluding particular SNP. (C) Scatter plots of genetic associations with BANK1/LBR protein level ratio against the genetic associations with NSCLC. (D) Funnel plot to assess heterogeneity. MR, Mendelian randomization; SNP, single nucleotide polymorphism; NSCLC, non-small cell lung cancer; IVW, inverse variance weighting.