Supplementary Data.

Annex 1. Keywords and database search equations

PubMed. Mesh terms with free words were combined following the PICO research model. The final equation included:

(hepatitis b[tiab] OR hepatitisb[tiab] OR hbv[tiab] OR "Hepatitis B"[Mesh] OR "Hepatitis B virus"[Mesh]) AND (polymorphism*[tiab] OR Allele*[tiab] OR SNP[tiab] OR SNPS[tiab] OR genetic variant*[tiab] OR host genetic*[tiab] OR Gene frequenc*[tiab] OR genetic variation*[tiab] OR genetic variabilit*[tiab] OR genetic heterogeneit*[tiab] OR genetic predisposition*[tiab] OR Genetic factor*[tiab] OR genetic diversit*[tiab] OR genetic susceptibilit*[tiab] OR immunogenetic*[tiab] OR host genetic*[tiab] OR Allele frequenc*[tiab] OR Human genetic*[tiab] OR Genetic resistance*[tiab] OR "Polymorphism, Genetic"[Mesh] OR "Genetic Variation"[Mesh:NoExp] OR "Alleles"[Mesh] OR "Gene Frequency"[Mesh] OR "Genetic Predisposition to Disease"[Mesh]) AND (Disease progression[tiab] OR Persisten*[tiab] OR Chronicit*[tiab] OR Clearance*[tiab] OR Spontaneous*[tiab] OR Recover*[tiab] OR Seroclearance*[tiab] OR Remission*[tiab] OR Disease Exacerbation*[tiab] OR Resolved[tiab] OR Resolution*[tiab] OR viral load*[tiab] OR susceptibilit*[tiab] OR disease evolution*[tiab] OR disease predisposition*[tiab] OR chronic disease*[tiab] OR disease resistance*[tiab] OR disease course*[tiab] OR "Disease Progression"[Mesh] OR "Viral Load"[Mesh] OR "Disease Susceptibility"[Mesh] OR "Chronic Disease"[Mesh] OR "Disease Resistance"[Mesh])

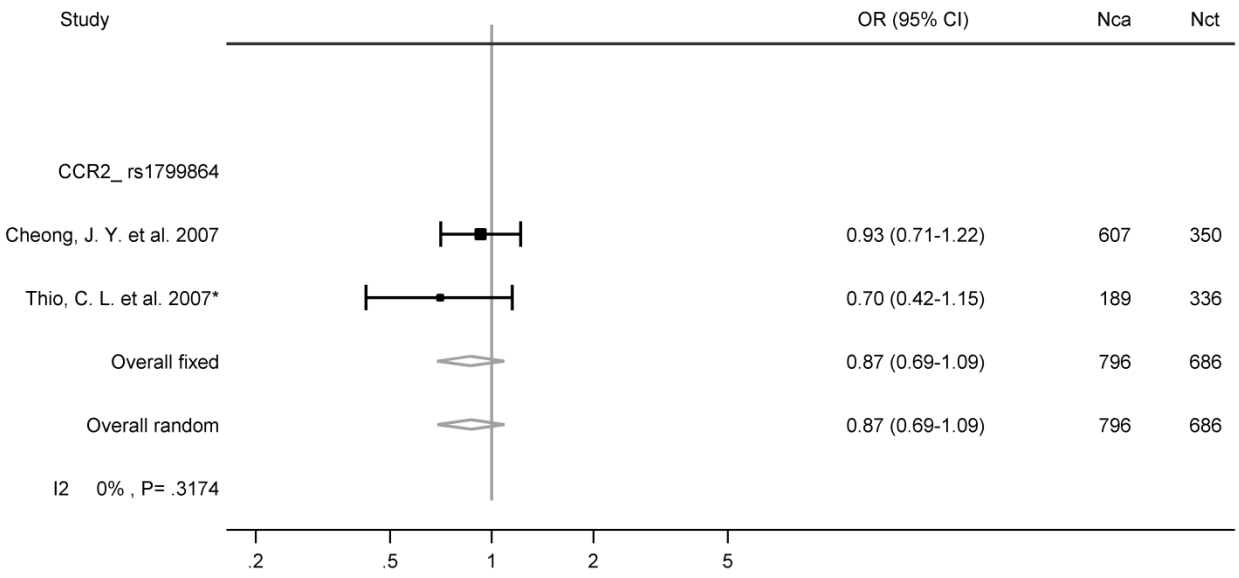
Embase. Emtree terms with free words were combined, following the PICO research model. A selection was performed through NOT and NEAR options to avoid missing pertinent articles. Final equation included:

((hepatitis NEXT/1 b):ab,ti OR hbv:ab,ti OR hepatitisb:ab,ti OR 'hepatitis b'/exp OR 'hepatitis b virus'/exp) AND (polymorphism*:ab,ti OR allele*:ab,ti OR snp:ab,ti OR snps:ab,ti OR (genetic NEXT/1 variant*):ab,ti OR (host NEXT/1 genetic*):ab,ti OR (gene NEXT/1 frequenc*):ab,ti OR (genetic NEXT/1 variation*):ab,ti OR (genetic NEXT/1 heterogeneit*):ab,ti OR (genetic NEXT/1 predisposition*):ab,ti OR (genetic NEXT/1 factor*):ab,ti OR (genetic NEXT/1 diversit*):ab,ti OR (genetic NEXT/1 susceptibilit*):ab,ti OR immunogenetic*:ab,ti OR (allele NEXT/1 frequenc*):ab,ti OR (human NEXT/1 genetic*):ab,ti OR (genetic NEXT/1 variabilit*):ab,ti OR (genetic NEXT/1 resistance*):ab,ti OR 'genetic polymorphism'/exp OR 'genetic variability'/exp OR 'allele'/exp OR 'gene frequency'/exp OR 'genetic predisposition'/exp) AND ((disease NEAR/3 progression*):ab,ti OR persisten*:ab,ti OR chronicit*:ab,ti OR clearance*:ab,ti OR spontaneous*:ab,ti OR recover*:ab,ti OR seroclearance*:ab,ti OR remission*:ab,ti OR (disease NEXT/1 exacerbation*):ab,ti OR resolved:ab,ti OR resolution*:ab,ti OR (viral NEXT/1 load*):ab,ti OR susceptibilit*:ab,ti OR (disease NEXT/1 evolution*):ab,ti OR (disease NEXT/1 predisposition*):ab,ti OR (disease NEXT/1 course*):ab,ti OR (chronic NEAR/3 disease*):ab,ti OR (disease NEXT/1 resistance*):ab,ti OR 'disease course'/exp OR 'virus load'/exp OR 'disease predisposition'/exp OR 'chronic disease'/exp)

ISI Web Of Science. This database only use free words. The option of exclusion of The Medline results from Embase was used. This was possible because of the use of suitable keywords between Embases and ISI Web Of Science. Final equation included:

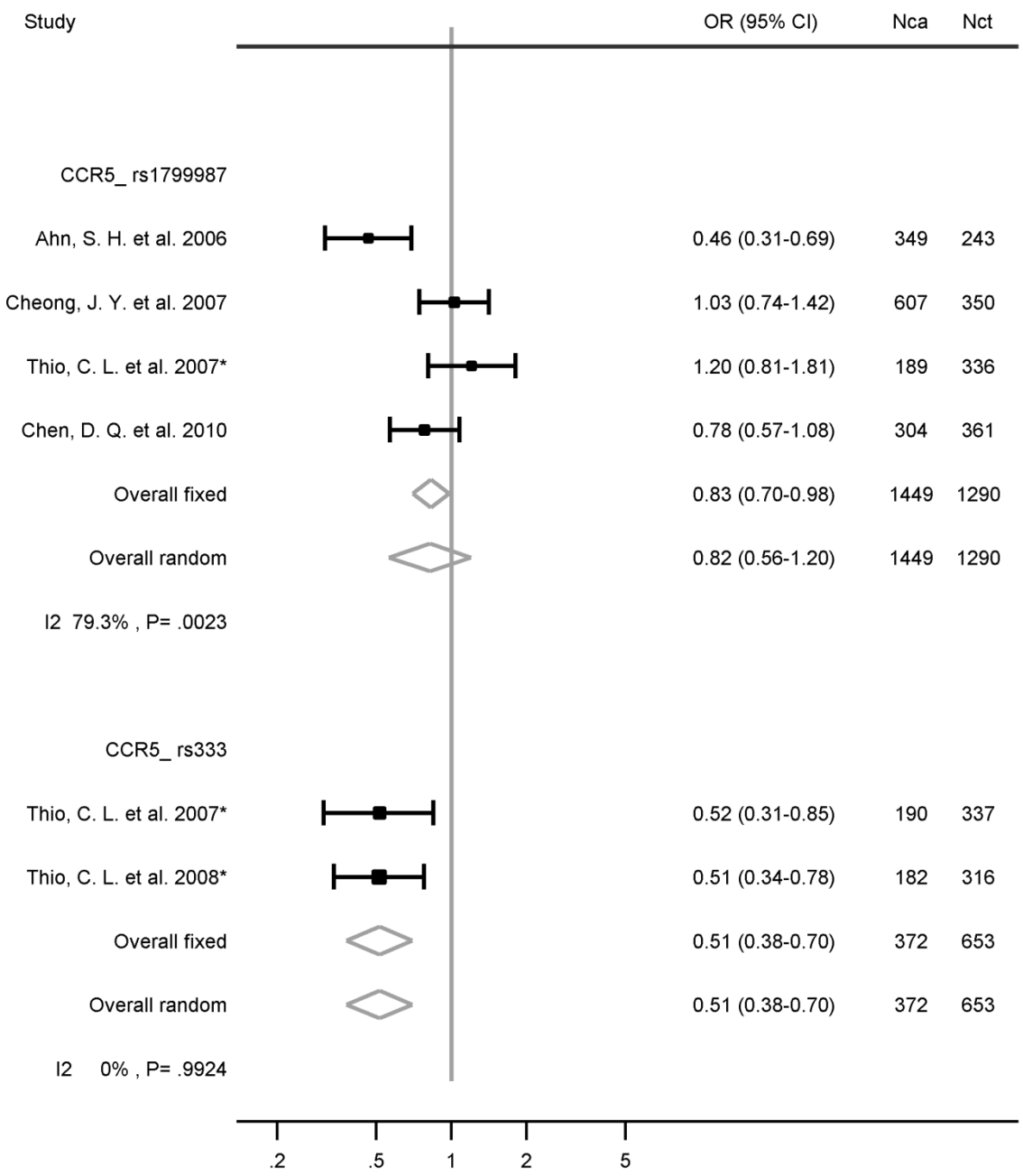
TS=(("hepatitis b" OR hbv OR hepatitisb) AND (polymorphism* OR allele* OR snp OR snps OR "genetic variant*" OR "host genetic*" OR "gene frequenc*" OR "genetic variation*" OR "genetic heterogeneit*" OR "genetic predisposition*" OR "genetic factor*" OR "genetic diversit*" OR "genetic susceptibilit*" OR immunogenetic* OR "allele frequenc*" OR "human genetic*" OR "genetic variabilit*" OR "genetic resistance*") AND ((disease NEAR/3 progression*) OR persisten* OR chronicit* OR clearance* OR spontaneous* OR recover* OR seroclearance* OR remission* OR "disease exacerbation*" OR resolved OR resolution* OR "viral load*" OR susceptibilit* OR "disease evolution*" OR "disease predisposition*" OR "disease course*" OR (chronic NEAR/3 disease*))).

Figure S1. Meta-analysis for the association of SNPs in CCR2 and chronic hepatitis B



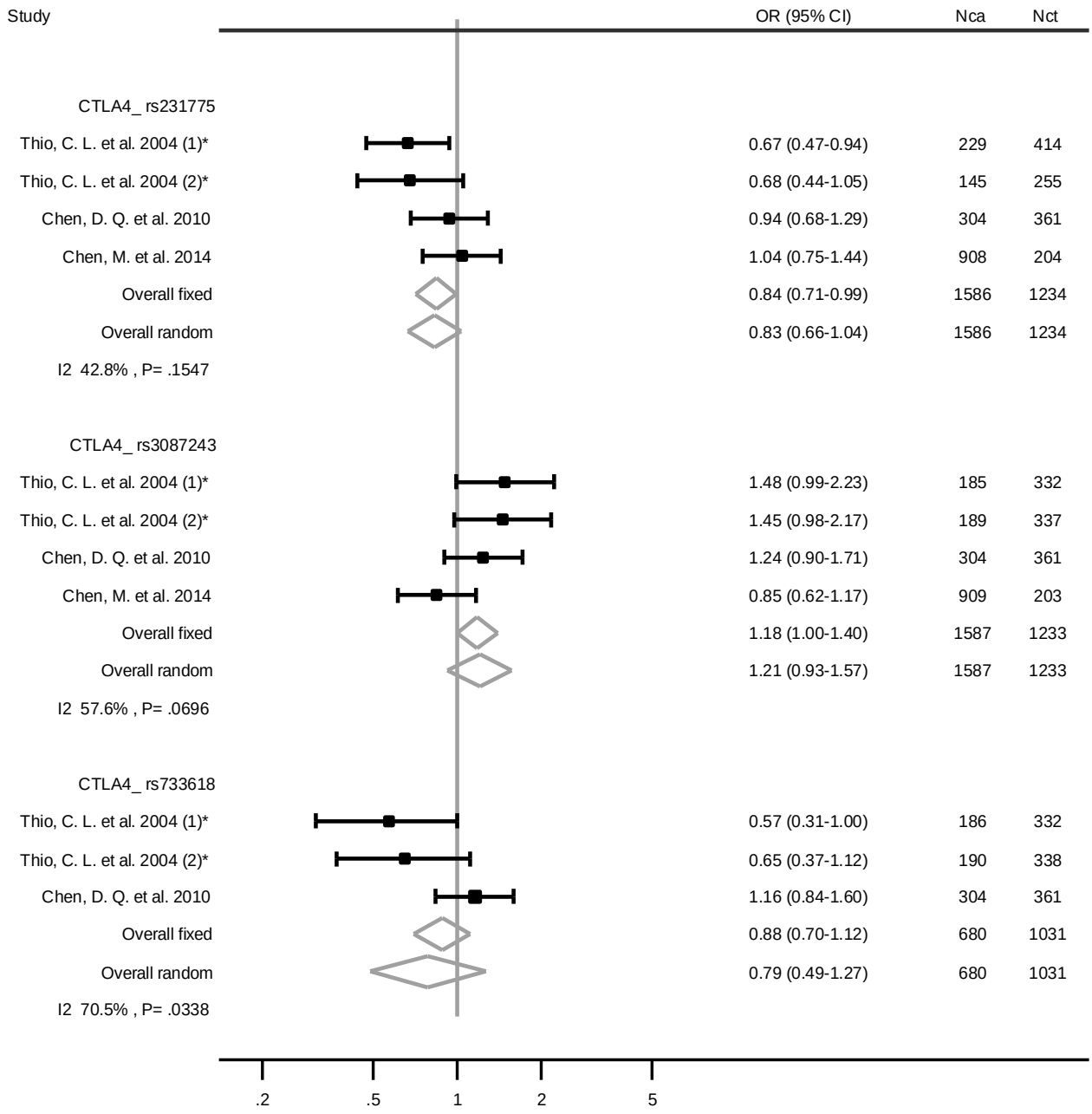
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S2. Meta-analysis for the association of SNPs in CCR5 and chronic hepatitis B



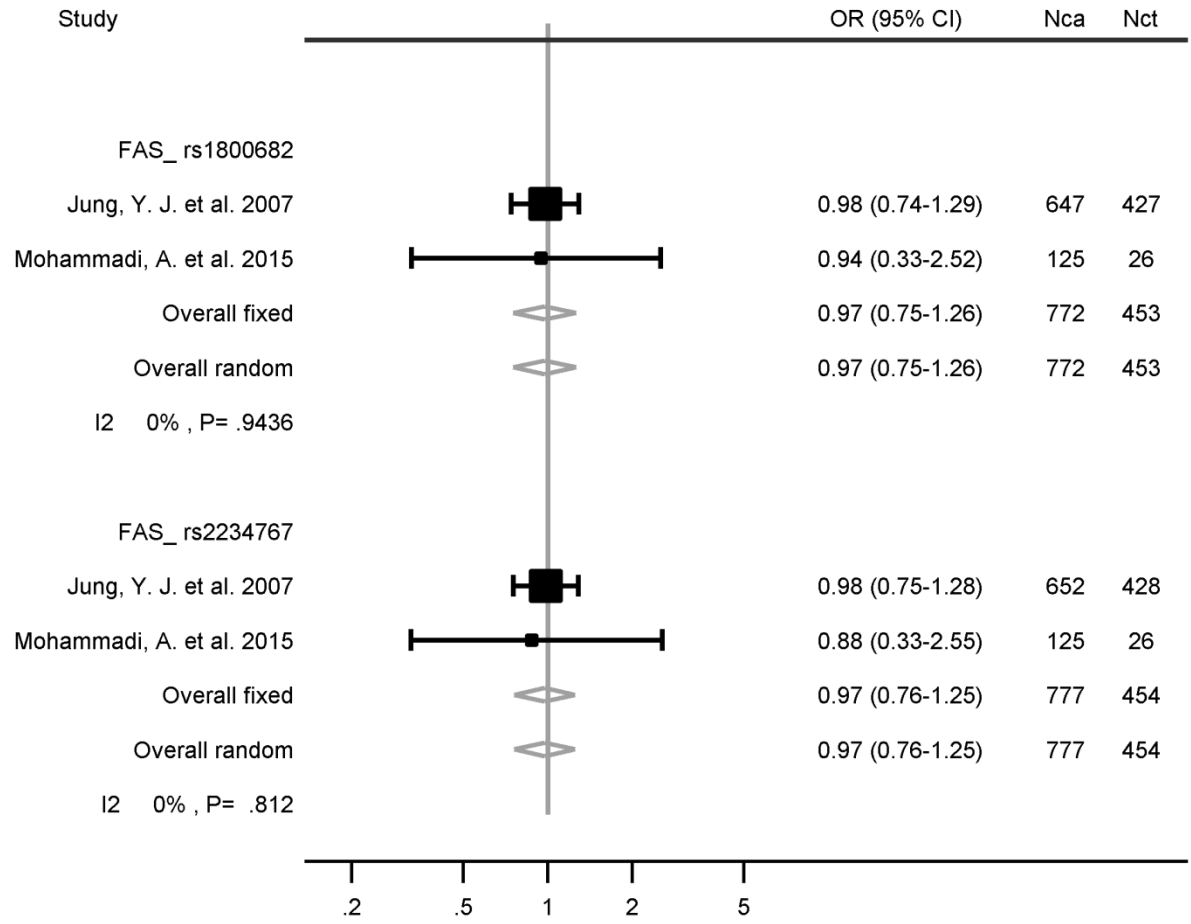
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S3. Meta-analysis for the association of SNPs in CTLA4 and chronic hepatitis B



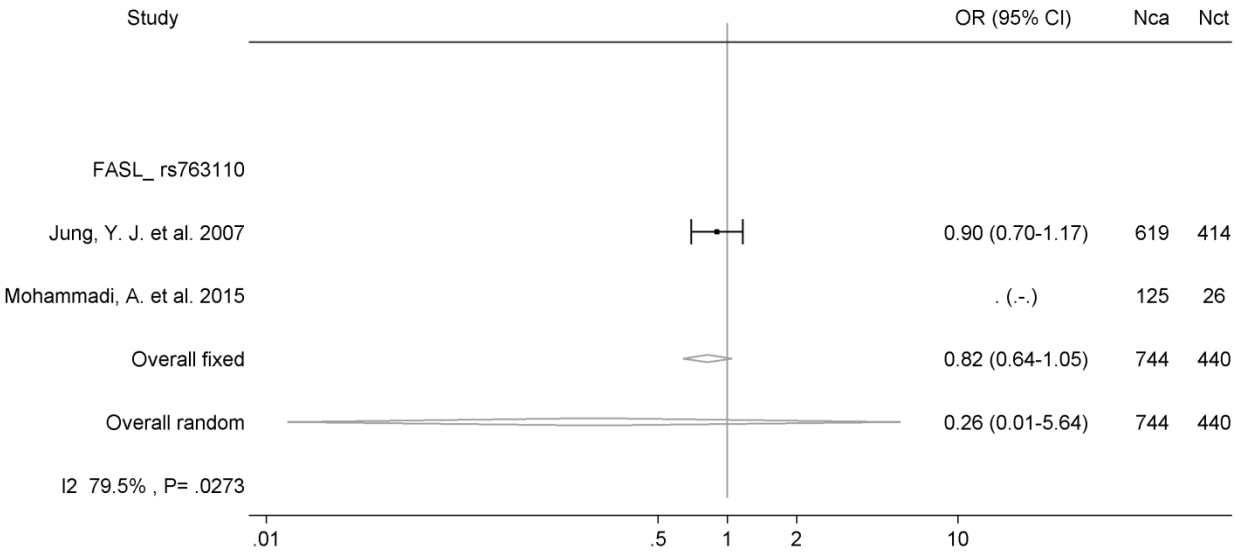
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S4. Meta-analysis for the association of SNPs in FAS and chronic hepatitis B



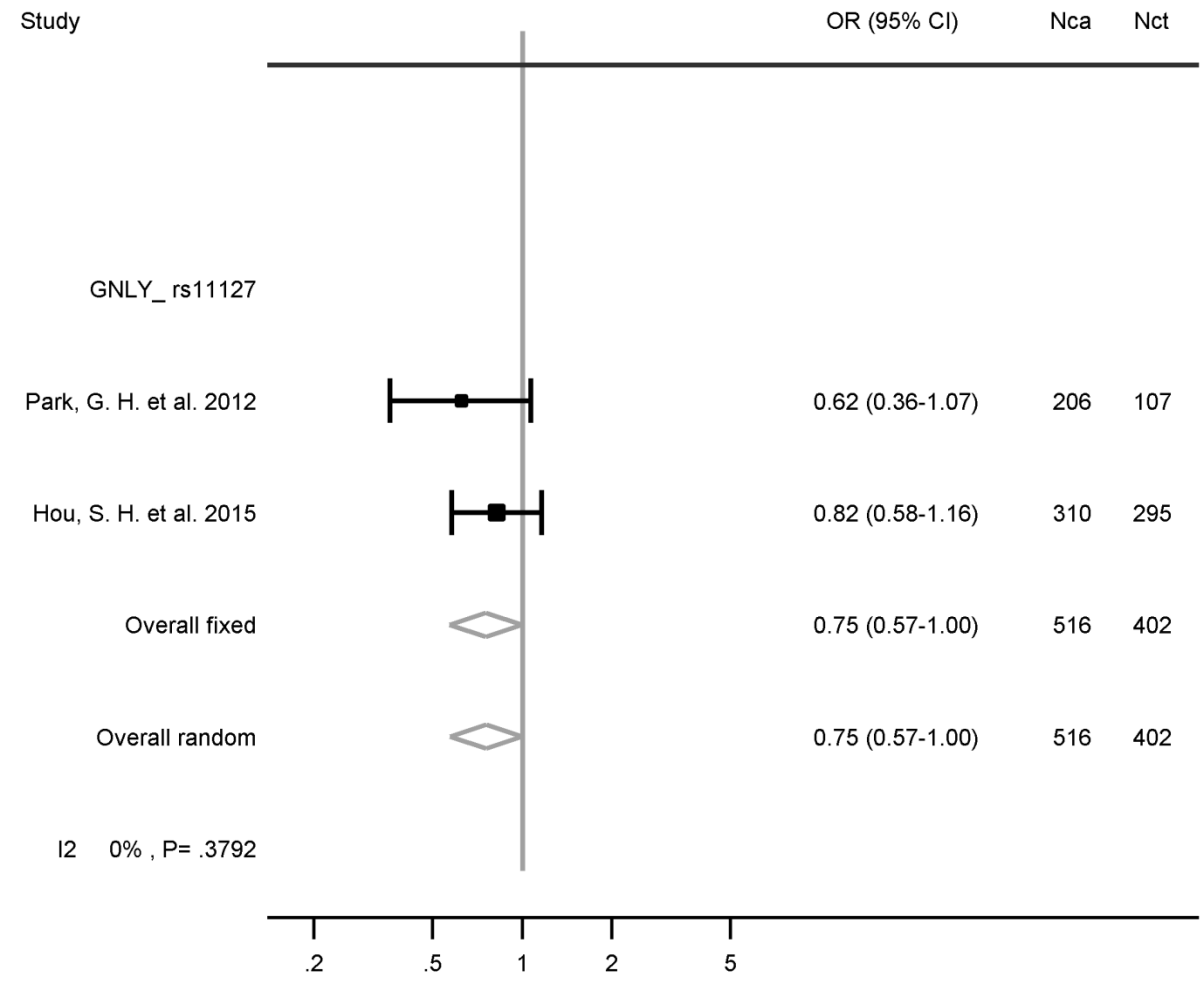
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S5. Meta-analysis for the association of SNPs in FASL and chronic hepatitis B



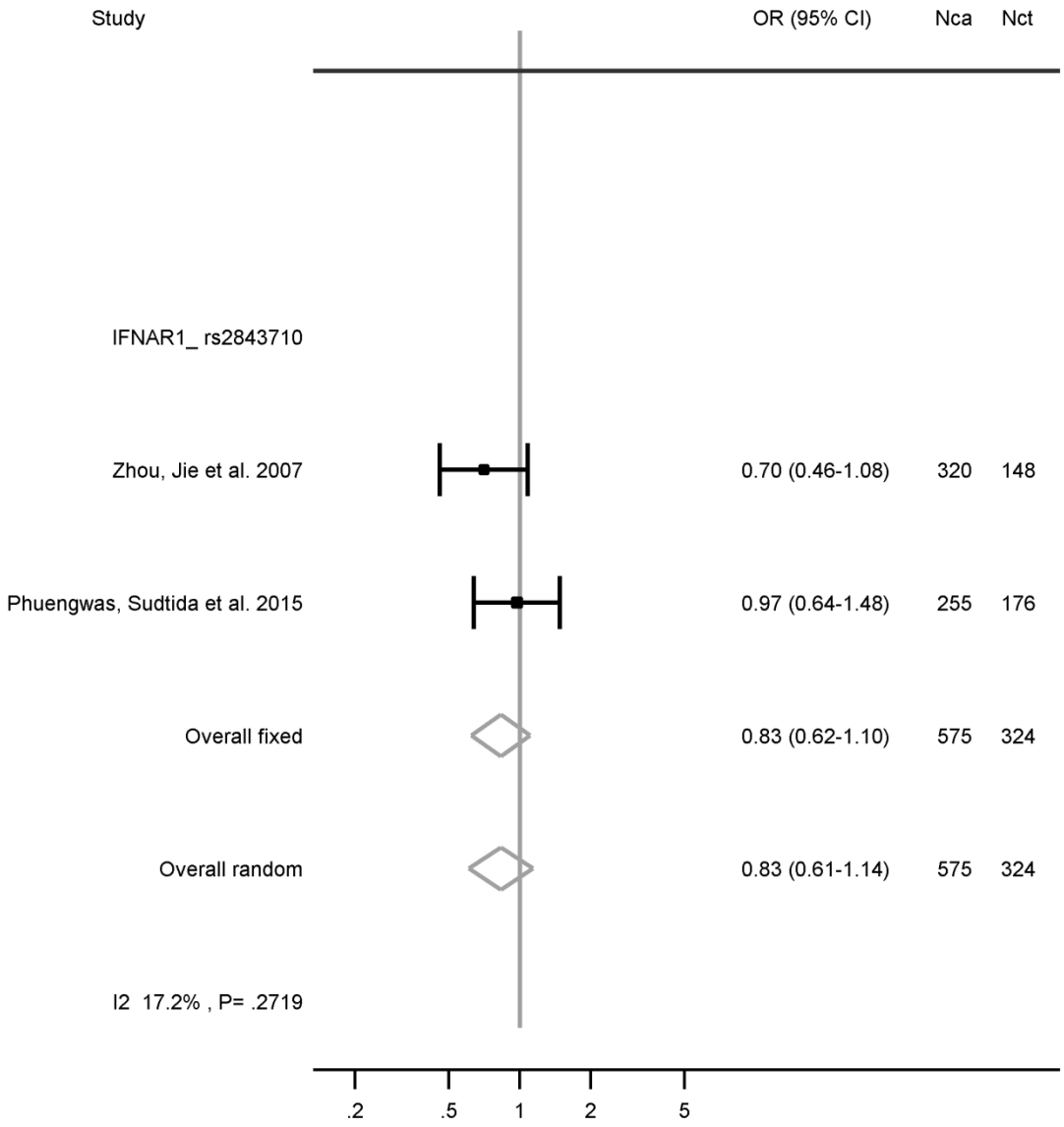
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S6. Meta-analysis for the association of SNPs in GNLY and chronic hepatitis B



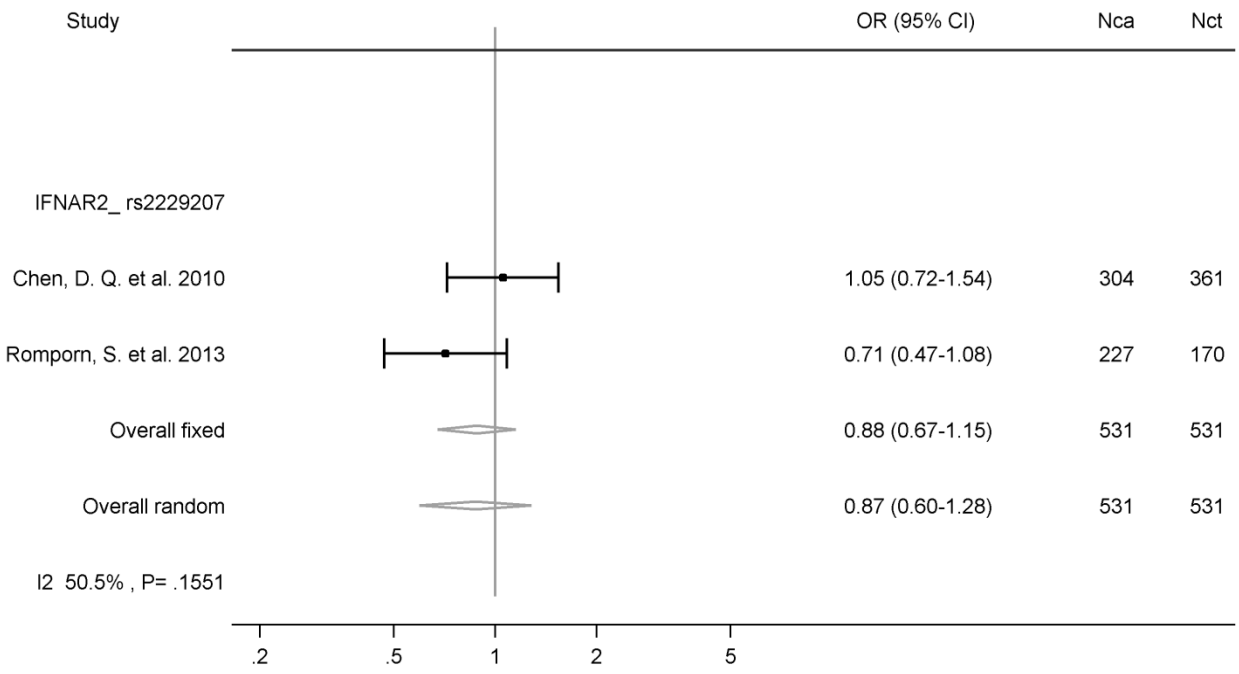
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S7. Meta-analysis for the association of SNPs in IFNAR1 and chronic hepatitis B



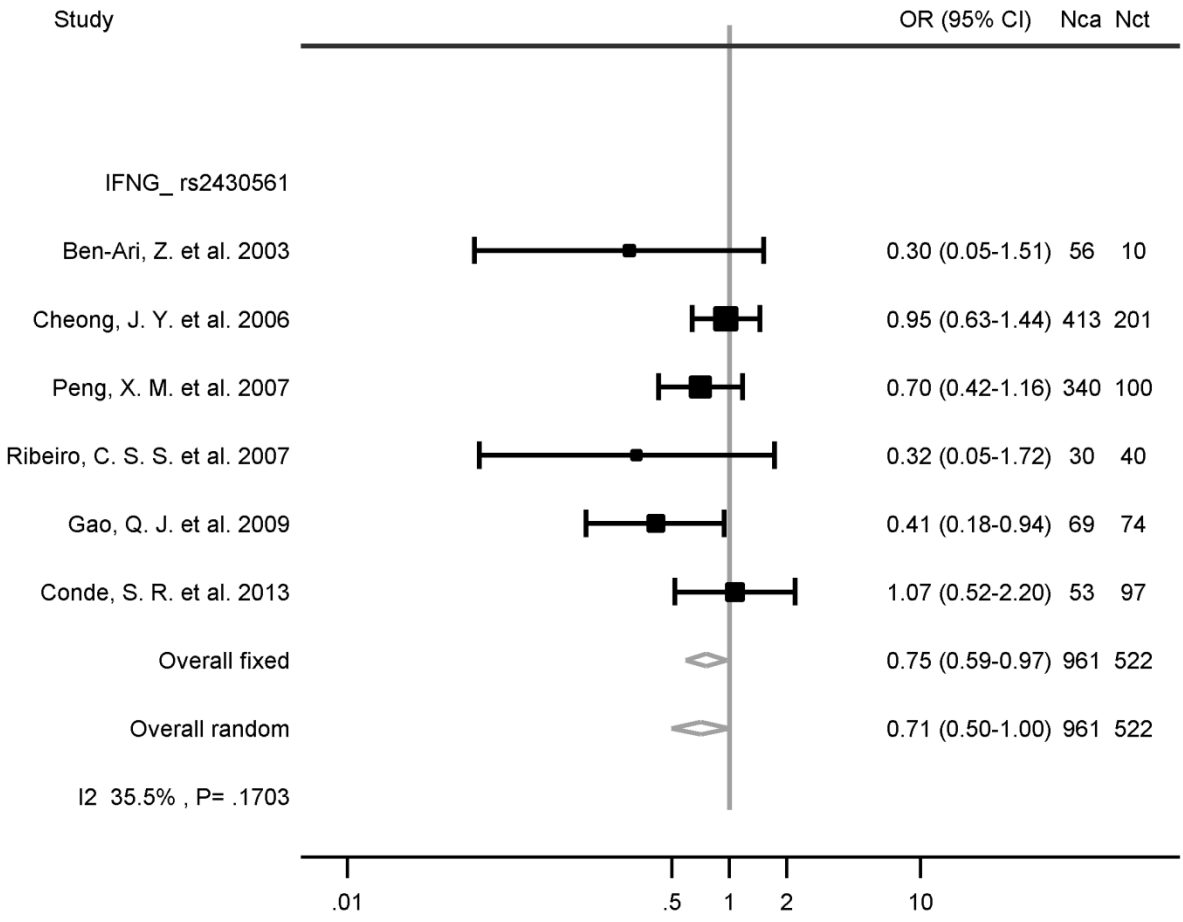
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S8. Meta-analysis for the association of SNPs in IFNAR2 and chronic hepatitis B



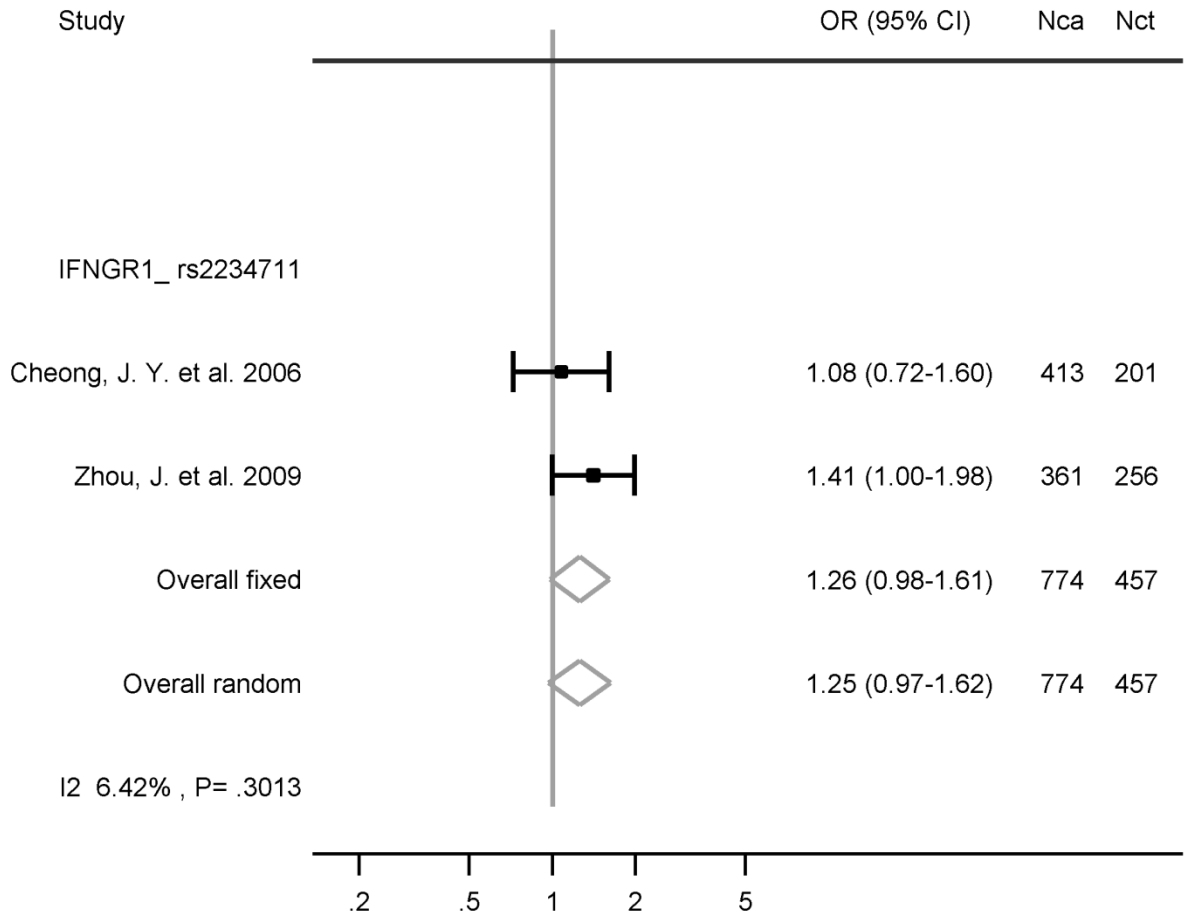
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S9. Meta-analysis for the association of SNPs in IFNG and chronic hepatitis B



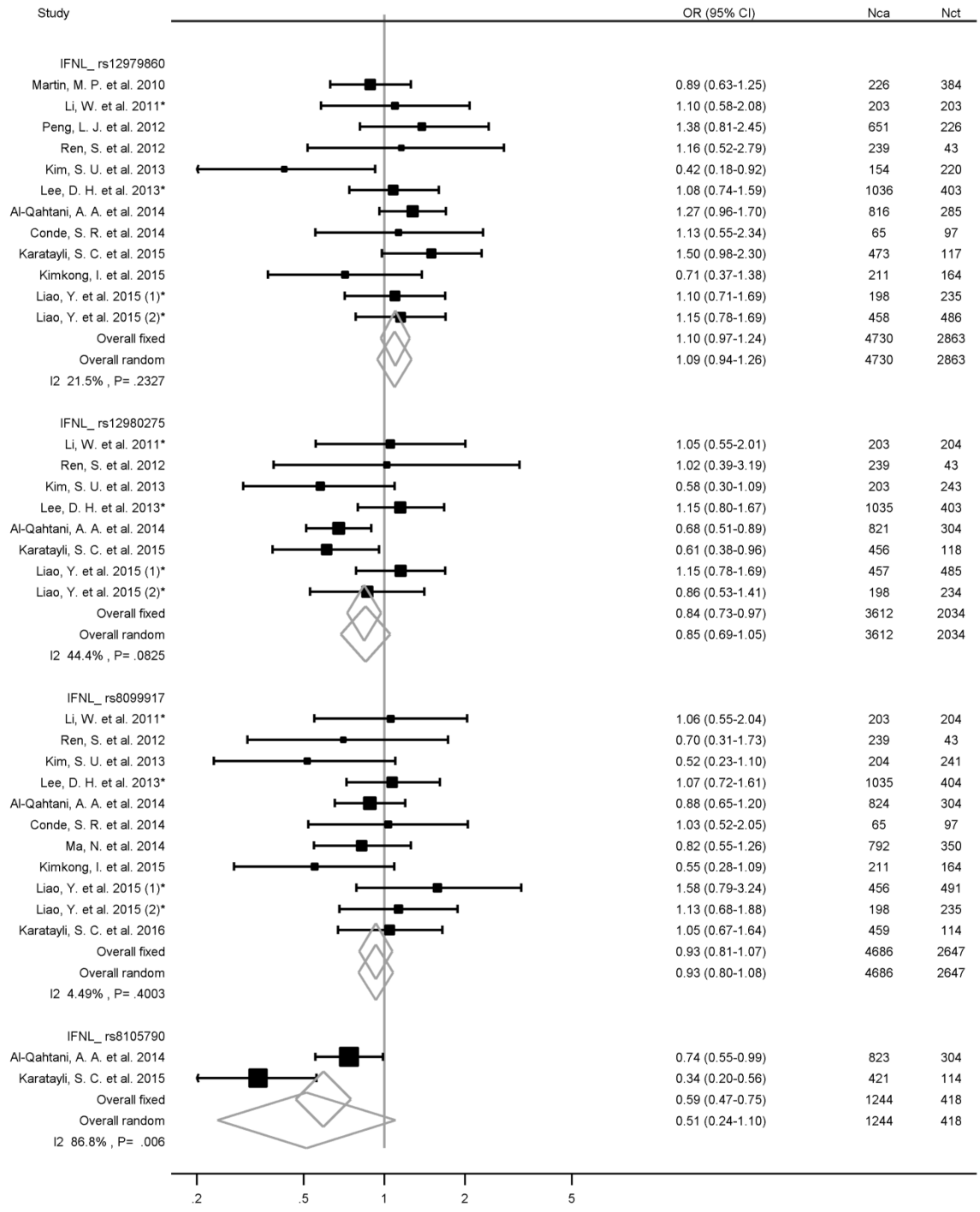
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S10. Meta-analysis for the association of SNPs in IFNGR1 and chronic hepatitis B



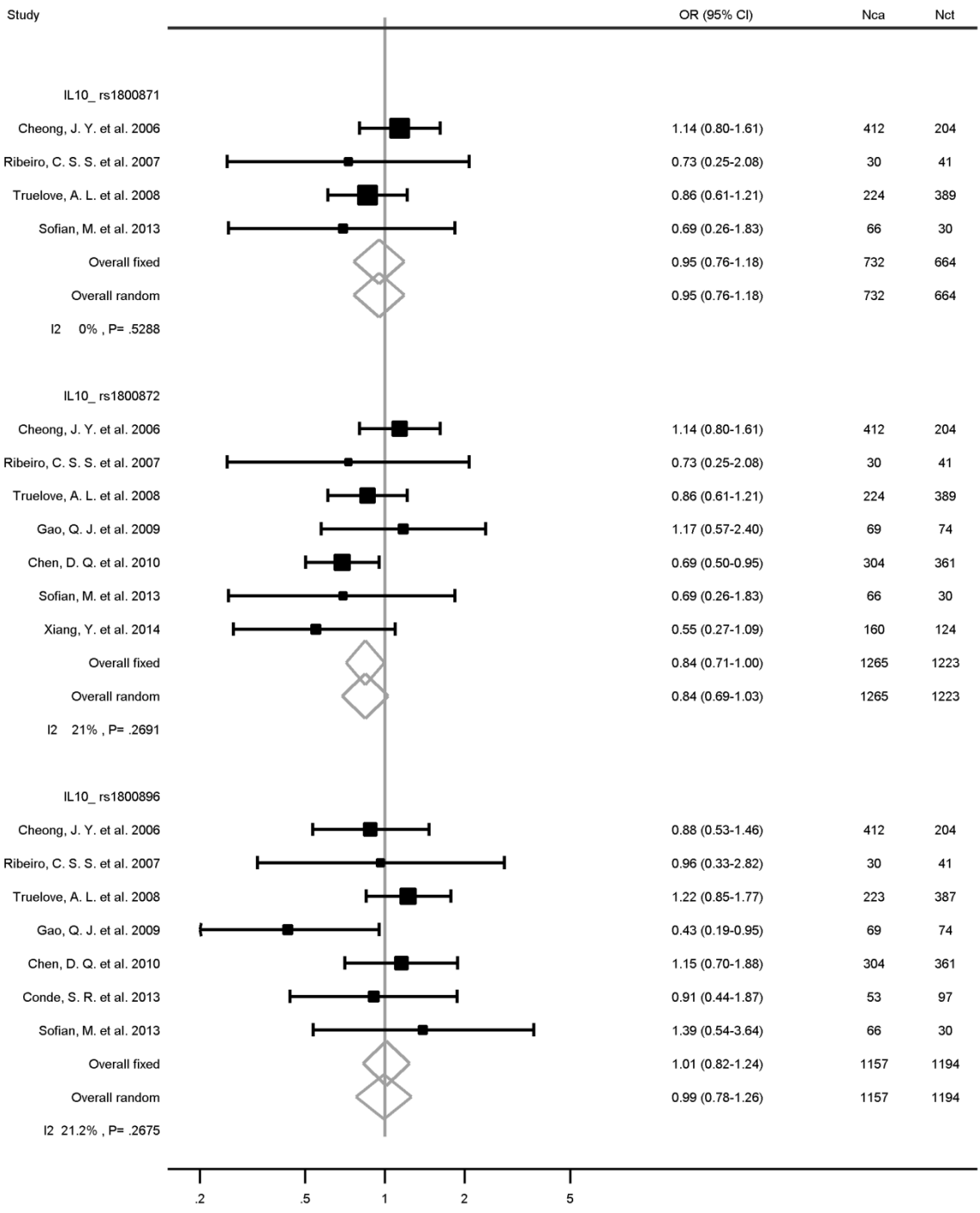
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S11. Meta-analysis for the association of SNPs in IFNL and chronic hepatitis B



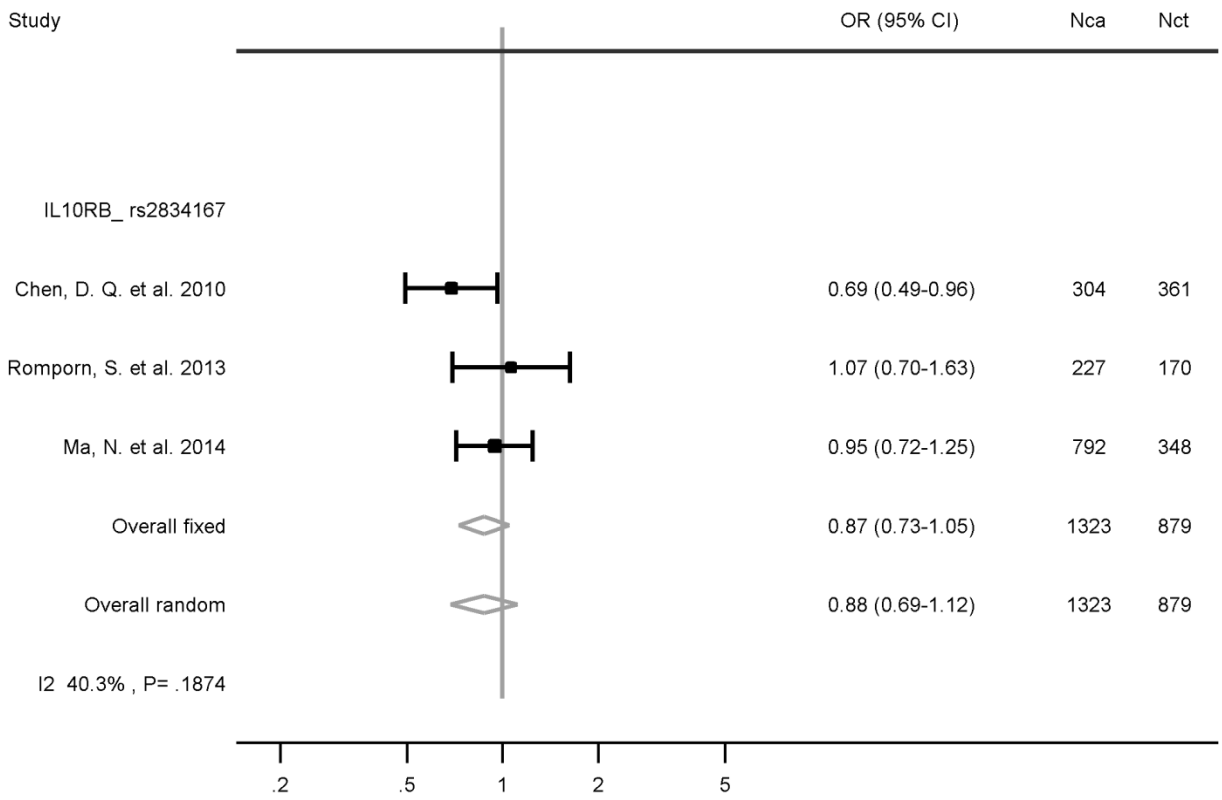
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S12. Meta-analysis for the association of SNPs in IL10 and chronic hepatitis B



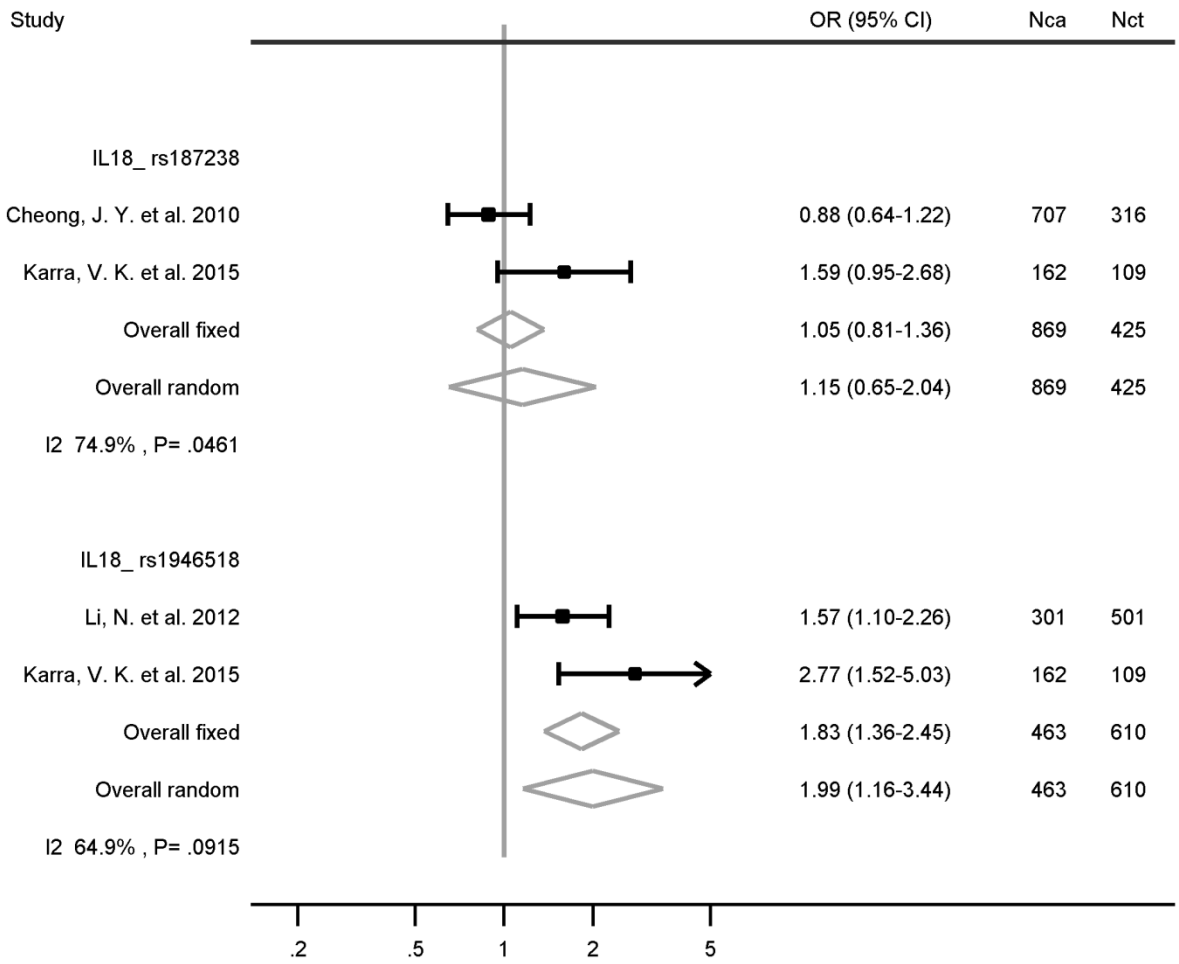
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S13. Meta-analysis for the association of SNPs in IL10RB and chronic hepatitis B



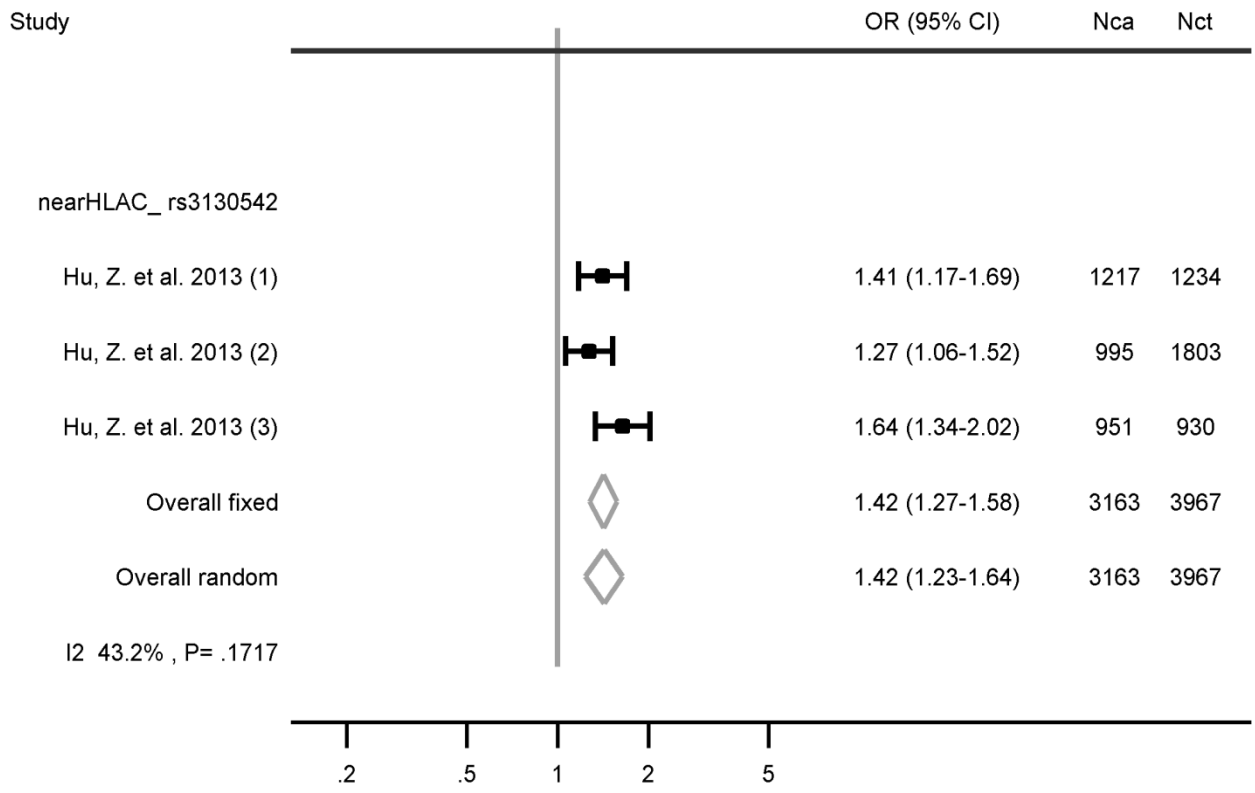
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S14. Meta-analysis for the association of SNPs in IL18 and chronic hepatitis B



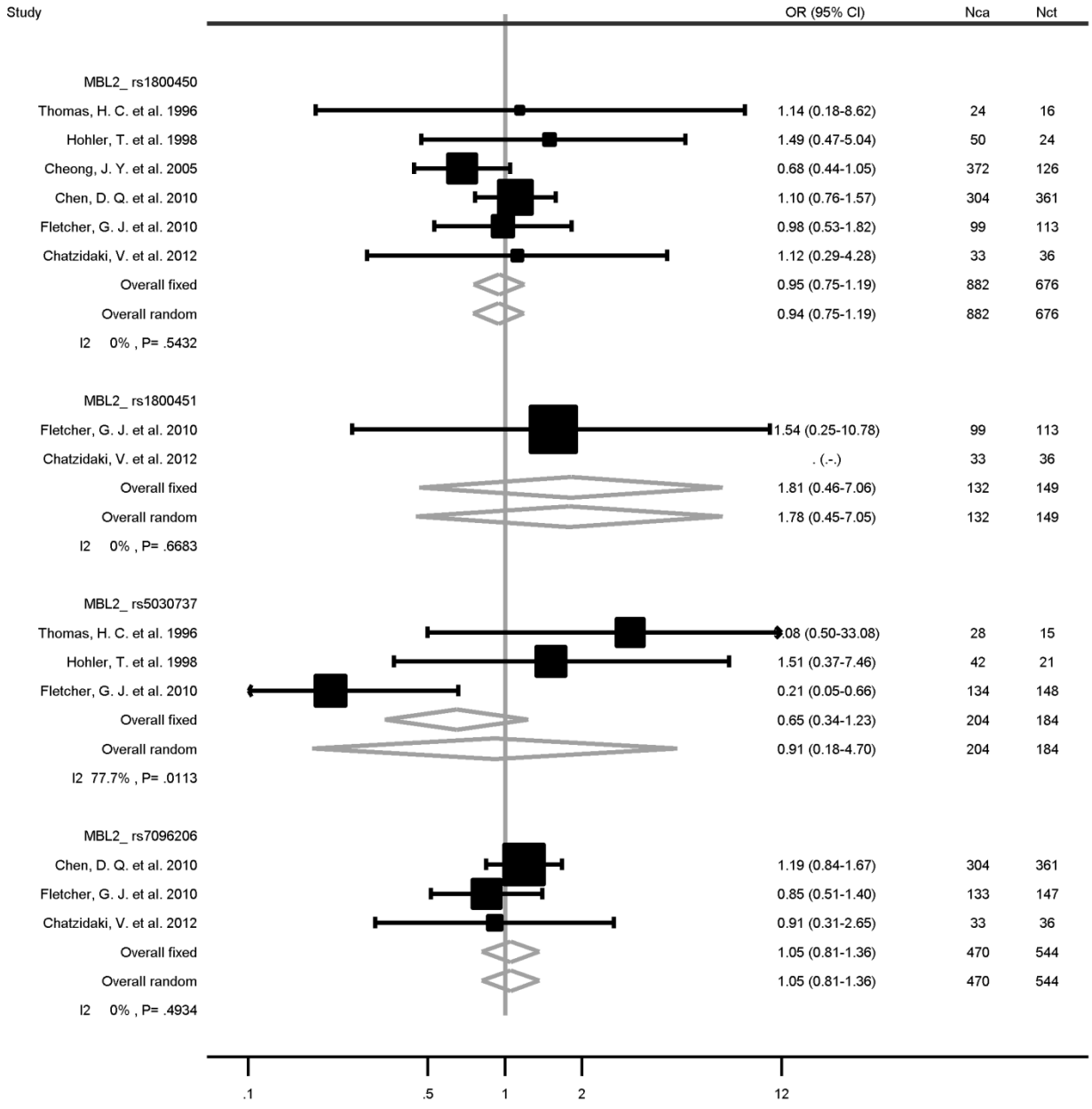
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S15. Meta-analysis for the association of SNP nearby HLA-C and chronic hepatitis B



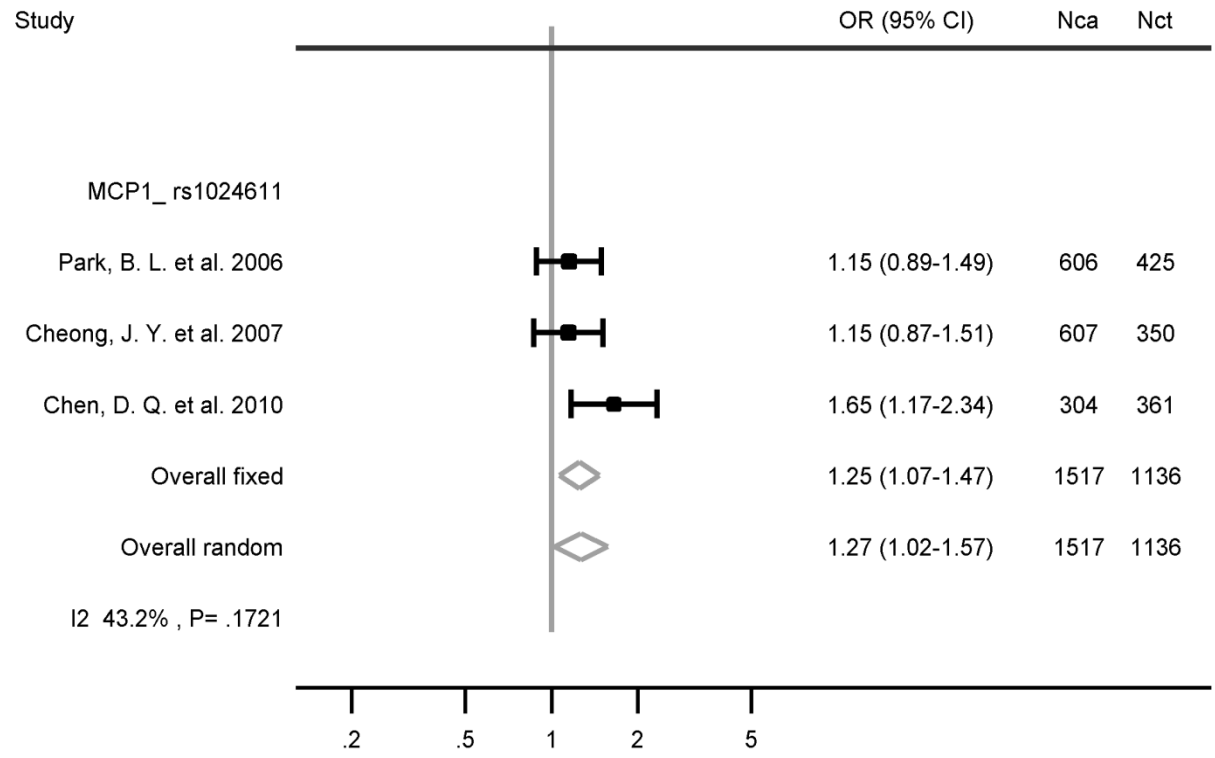
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S16. Meta-analysis for the association of SNPs in MBL2 and chronic hepatitis B



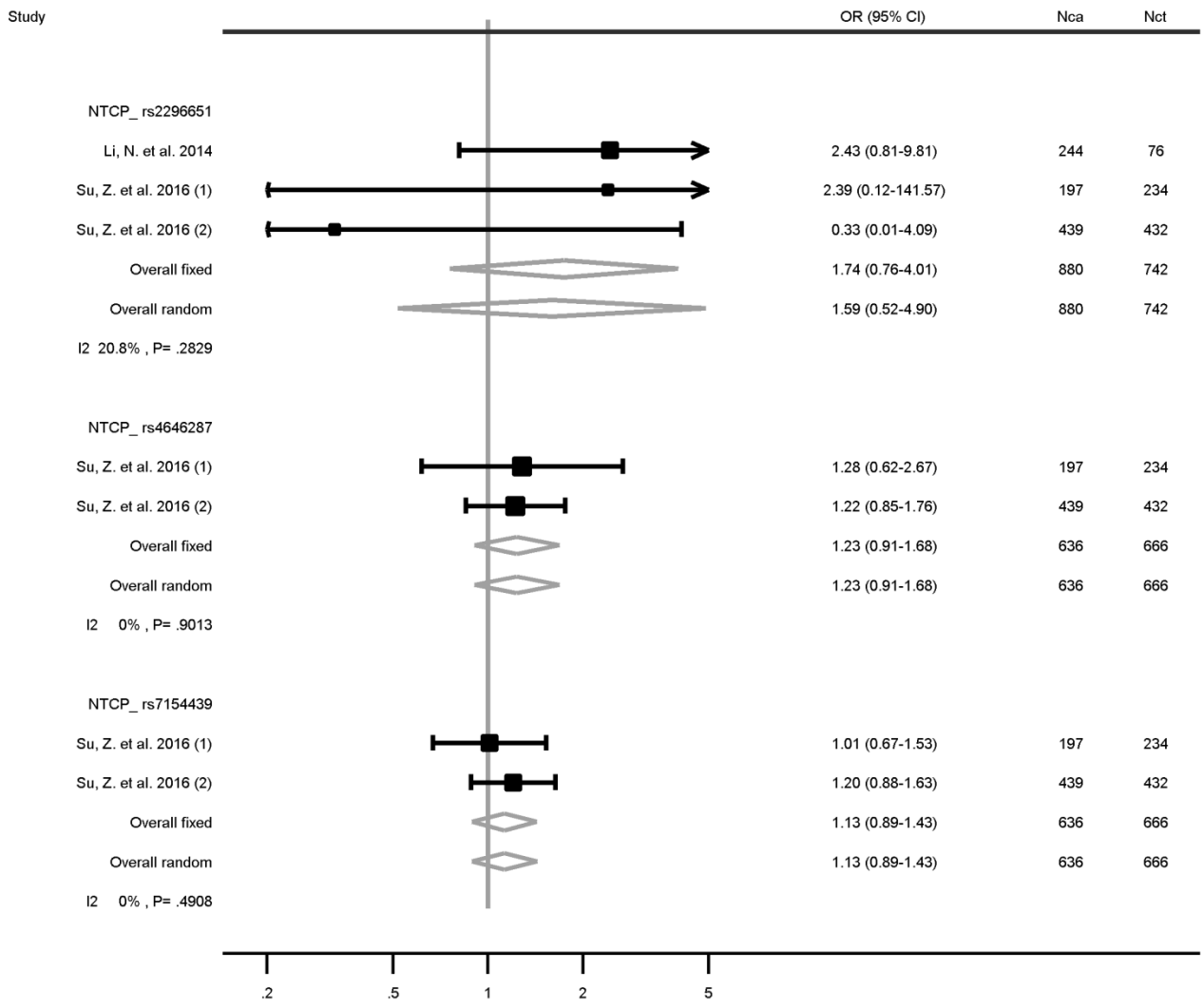
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S17. Meta-analysis for the association of SNPs in MCP1 and chronic hepatitis B



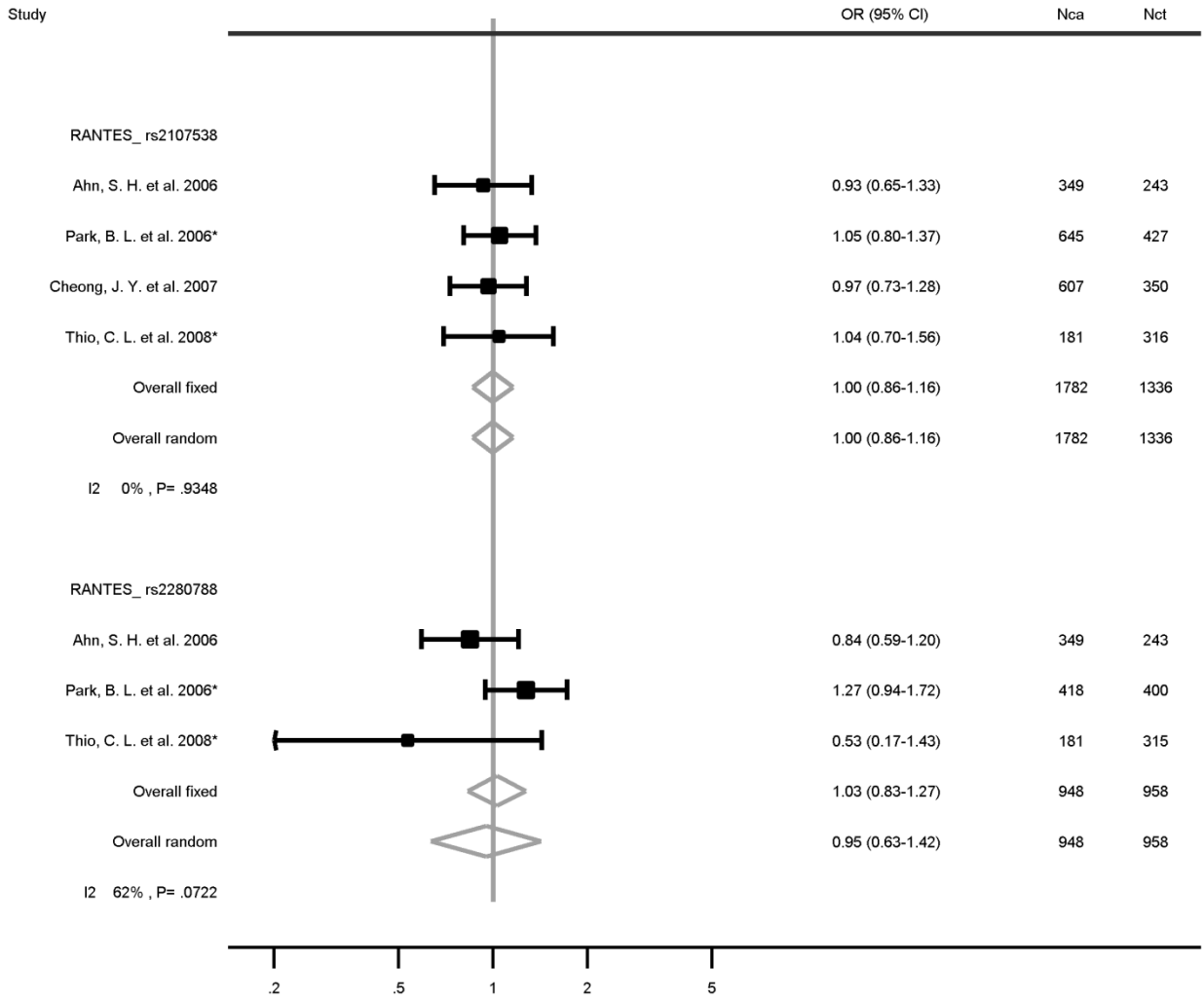
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S18. Meta-analysis for the association of SNPs in NTCP and chronic hepatitis B



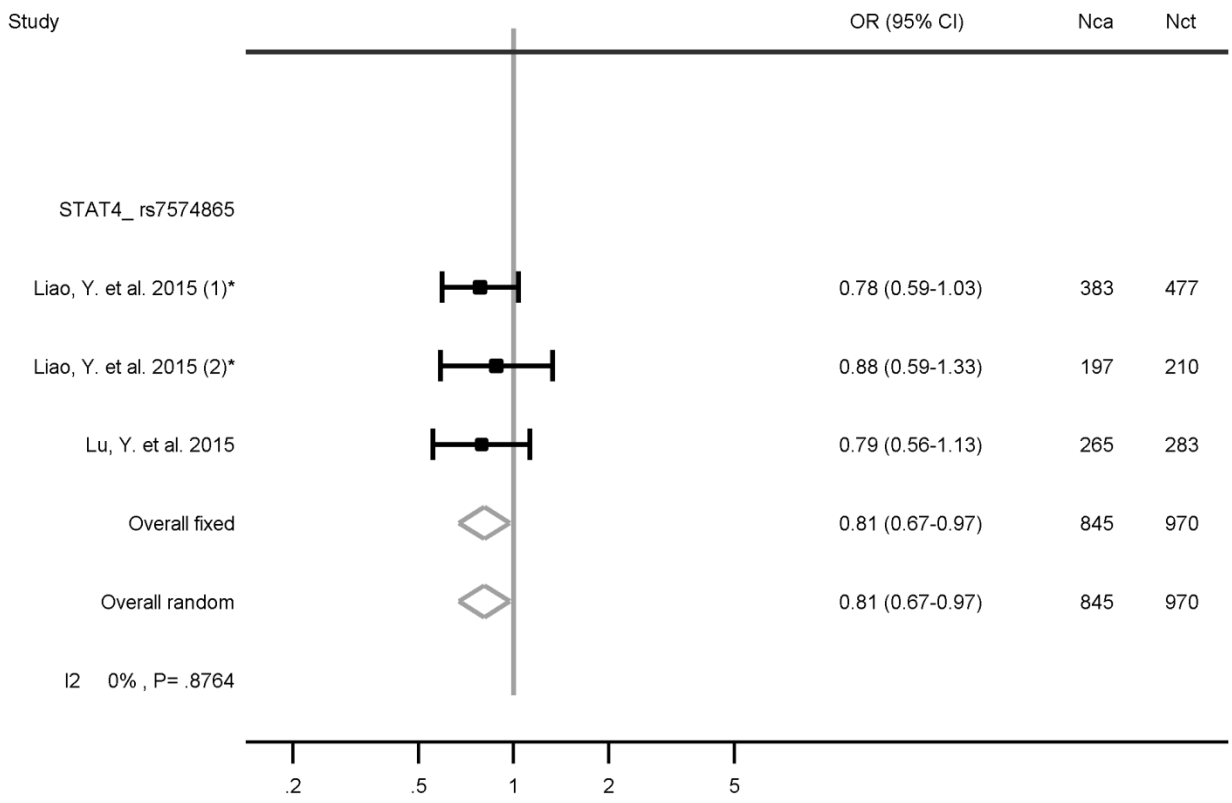
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S19. Meta-analysis for the association of SNPs in Rantes and chronic hepatitis B



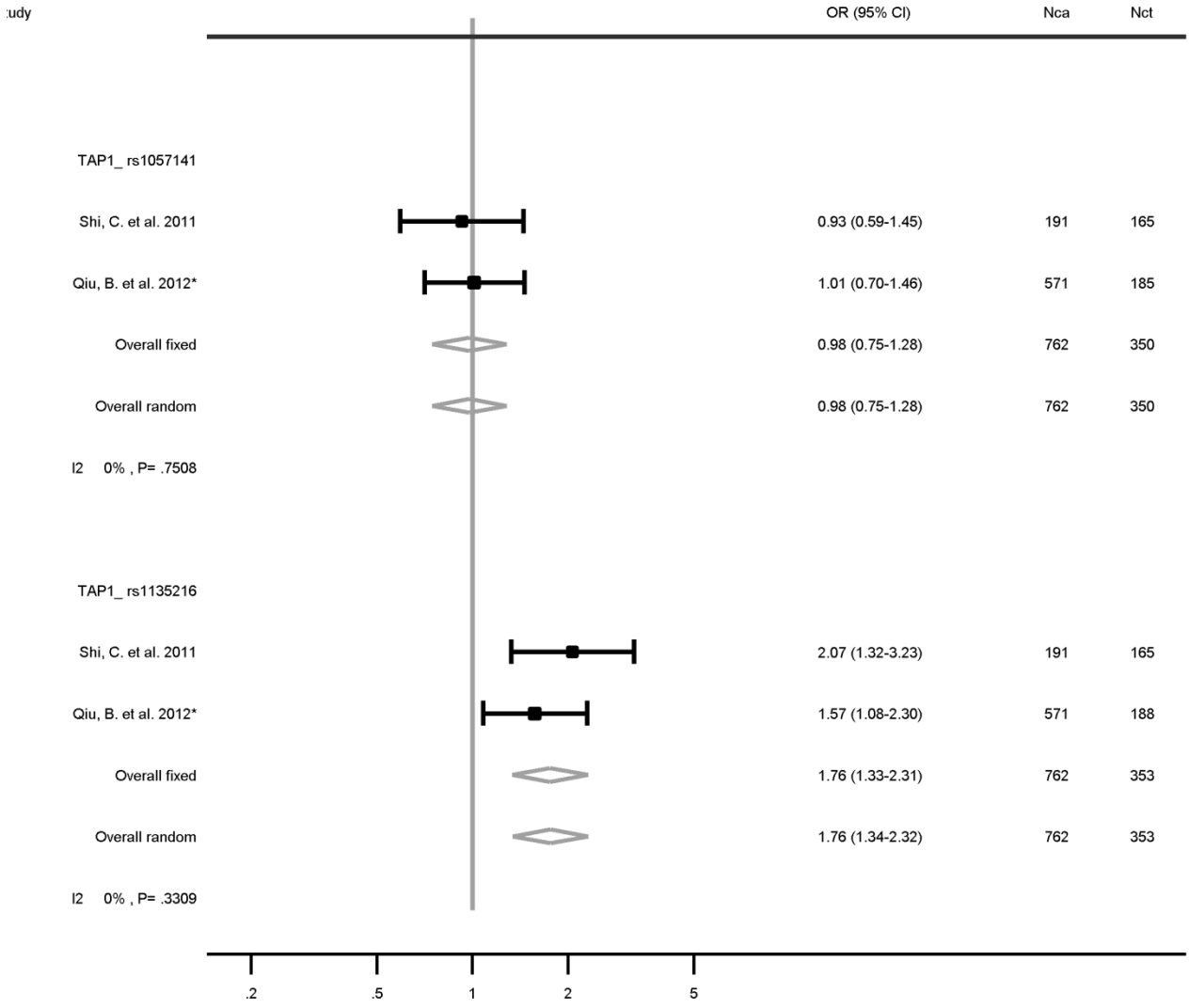
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S20. Meta-analysis for the association of SNPs in STAT4 and chronic hepatitis B



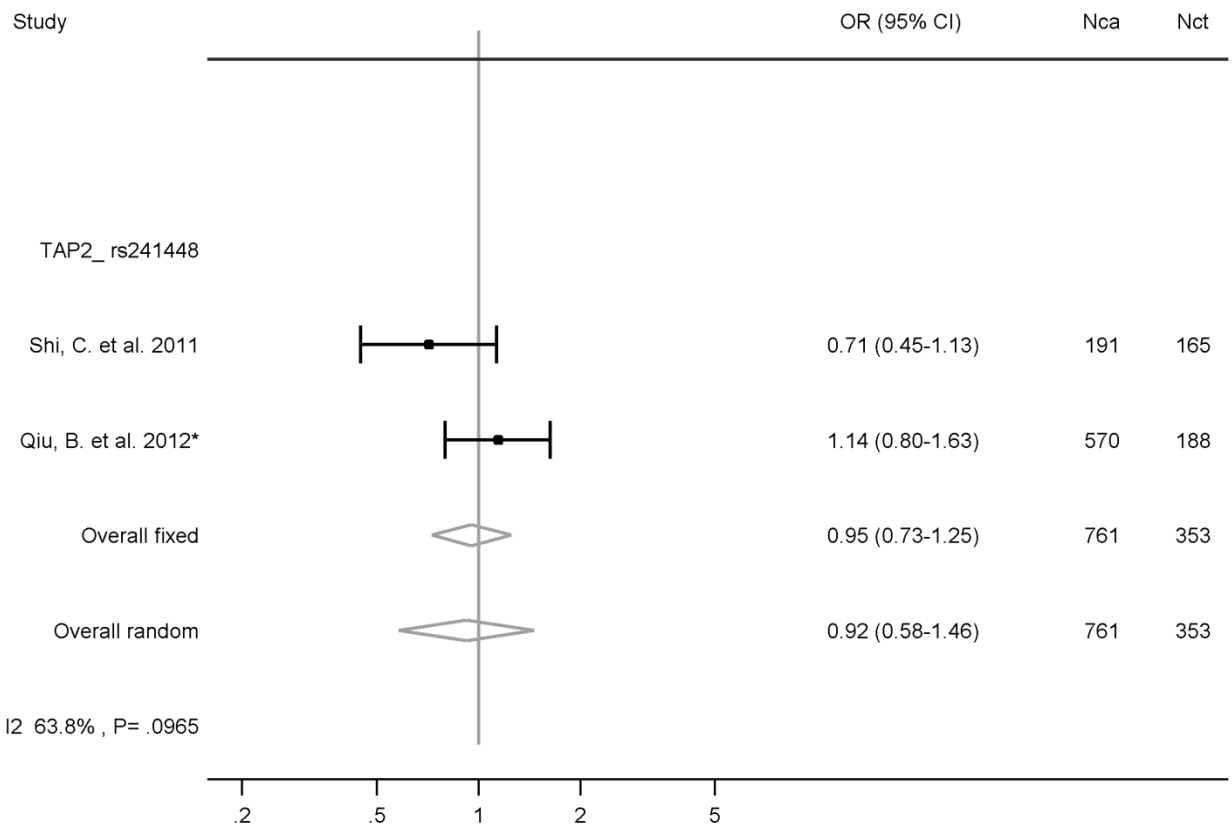
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S21. Meta-analysis for the association of SNPs in TAP1 and chronic hepatitis B



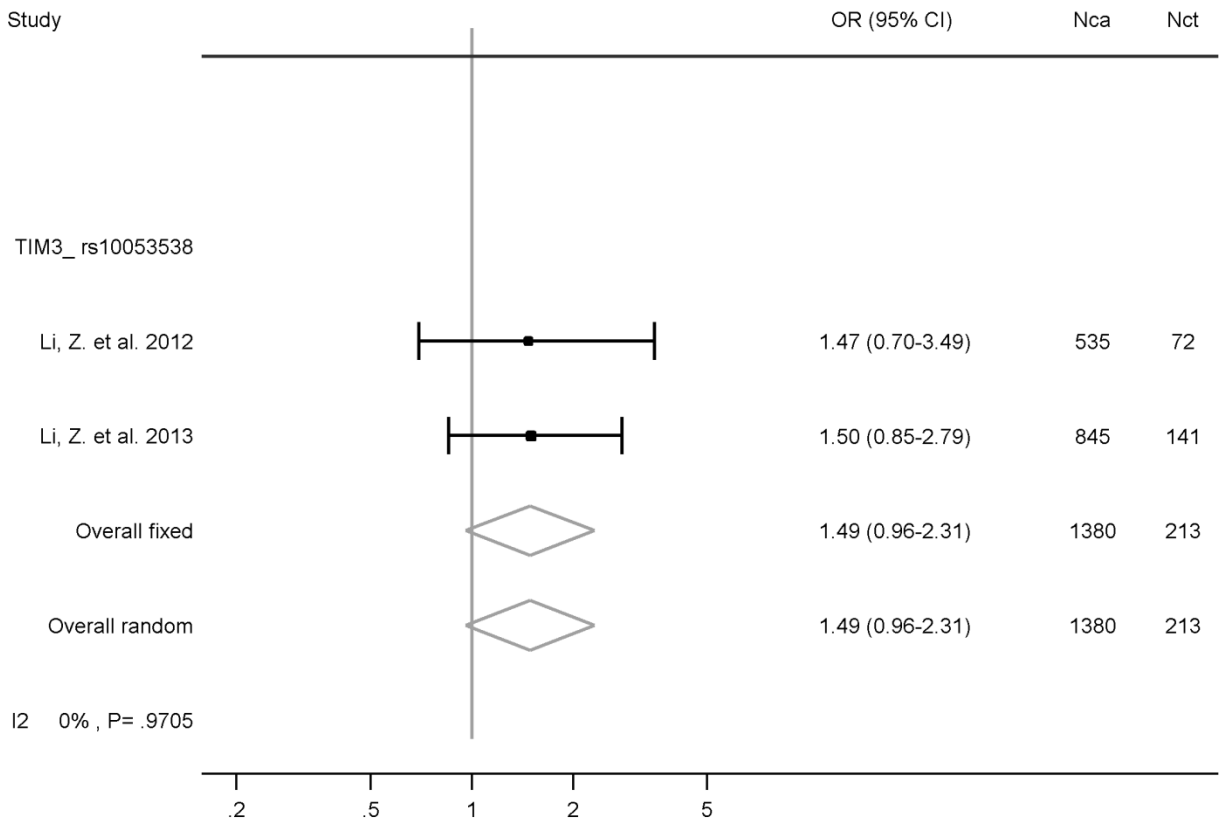
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S22. Meta-analysis for the association of SNPs in TAP2 and chronic hepatitis B



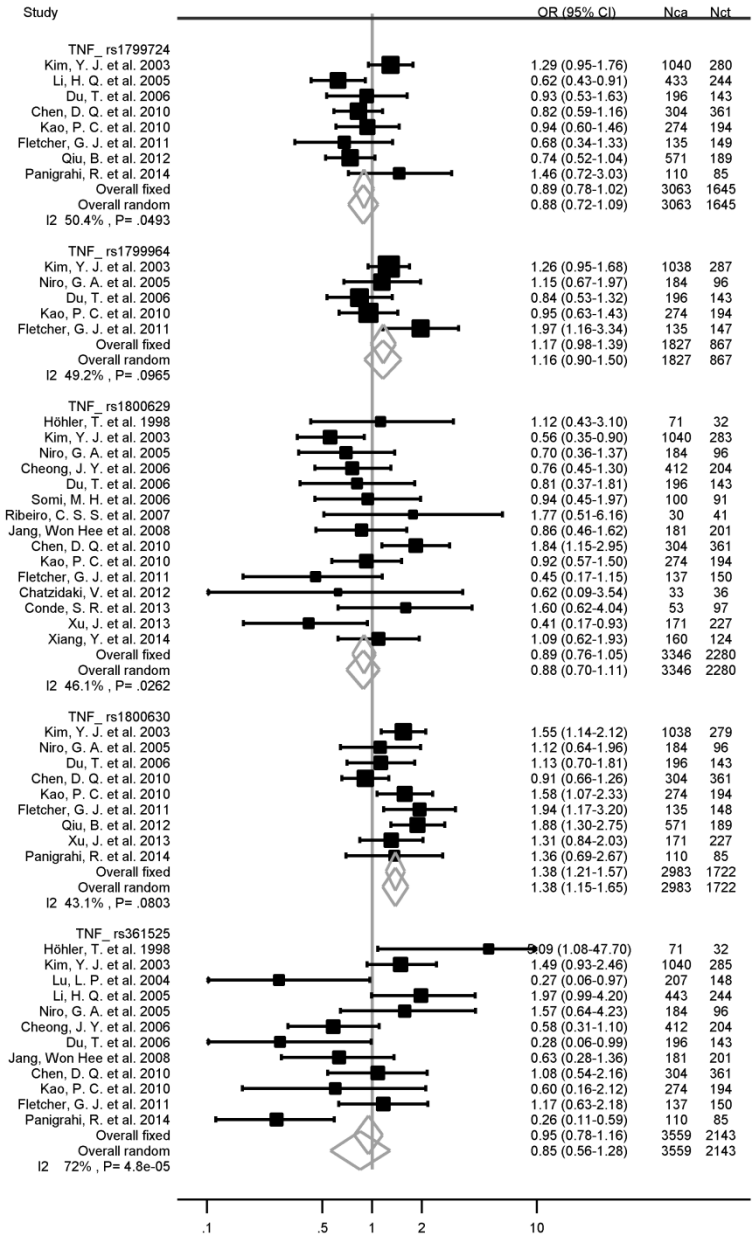
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S23. Meta-analysis for the association of SNPs in TIM3 and chronic hepatitis B



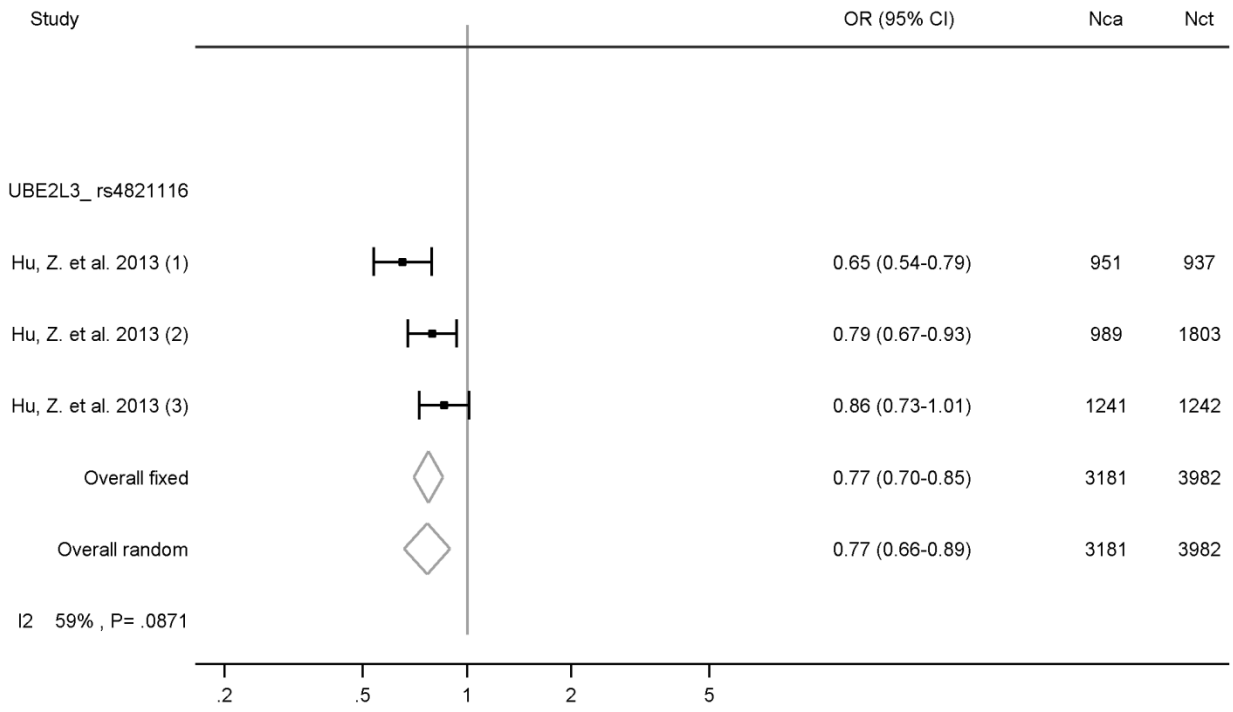
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.

Figure S24. Meta-analysis for the association of SNPs in TNF-alpha and chronic hepatitis B



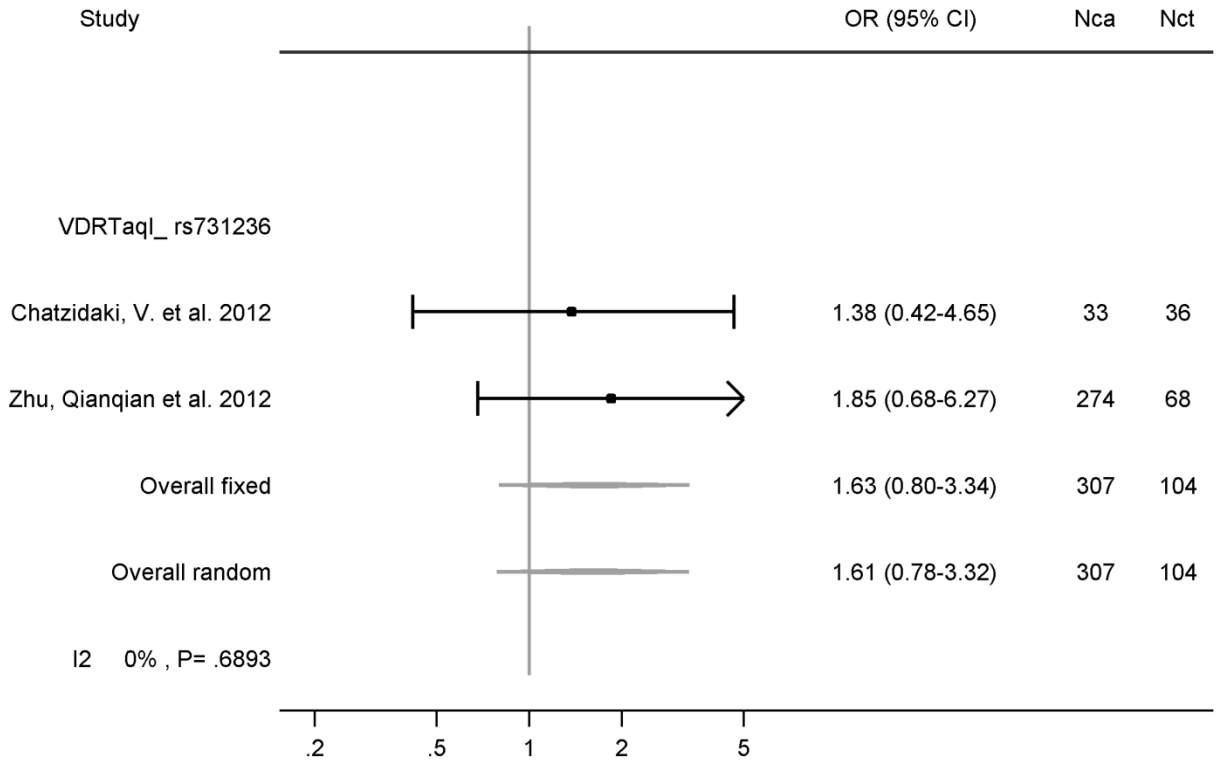
OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium.

Figure S25. Meta-analysis for the association of SNPs in UBE2L3 and chronic hepatitis B



OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance. For studies marked with a *, genotypes were recalculated based on allele frequencies, assuming Hardy-Weinberg equilibrium

Figure S26. Meta-analysis for the association of SNPs in VDR and chronic hepatitis B



OR=Odds ratio, CI95%=Confidence interval at 95%, WR=weight of each study in random effect analysis, WF=weight of each study in fixed effect analysis. I^2 represents the statistic for heterogeneity, with P>0.05 representing a significant heterogeneity. OR and 95% CI were calculated using a DerSimonian and Laird random effects model and assuming a dominant mode of inheritance.