The Association between Interferon-gamma +874 T/A Polymorphism and Susceptibility
of Chronic Hepatitis B with Liver Cirrhosis : An Update Meta Analysis

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Background

➢ The host genetic profile and polymorphism has many effects on cytokine function and production.

➢ Interferron gamma (IFN-γ) is a crucial cytokine in host immune response and defense against hepatitis B virus (HBV) infection.

➢ The aim of this study was determined Interferon-γ+874 T/A Polymorphism and risk of chronic hepatitis B (CHB) infection with liver cirrhosis (LC).

Methods

Search strategi and study selection:
▪ Databese: PubMed and proquest
▪ Data search: August 2021
▪ Following Keyword: ("Hepatitis B" OR "chronic hepatitis B" OR "hepatitis B virus" OR "HBV") AND("Cirrhosis") AND ("Interferon-γ" OR "Interferon-gamma") AND ("polymorphism" OR "single nucleotide polymorphism" OR "SNP")

Inclusion study:
1.case control studies
2. studies evaluating Interferon-gamma +874 T/A Polymorphism in Chronic Hepatitis B with Liver Cirrhosis and control group

Outcome:
Odds Ratio (OR) and 95%CI of CHB with LC Susceptibility in dominant model (TT+TA vs AA), recessive model (TT vs TA+AA), allelic model (T vs A), Homozygous Model (TT vs AA), and Heterozygous Model (TA vs AA)
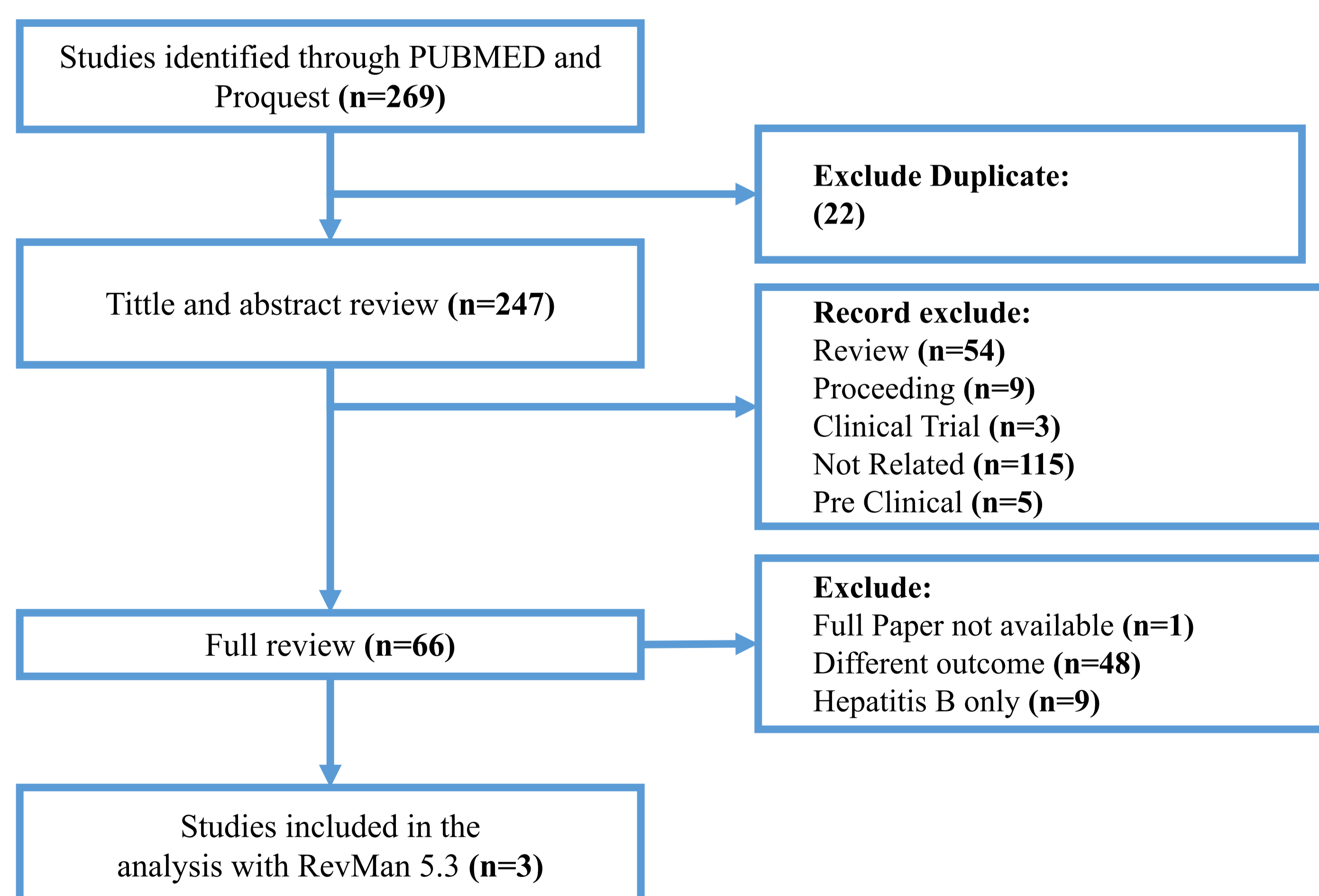
Data Analysis:
• Revman 5.3.

Figure 1. Prisma flowchart of the study

Results

A total of 3 studies involved 209 chronic hepatitis B with Liver Cirrhosis and 319 control participants were included in this meta-analysis.

Result showed that Allelic Model T vs A (OR 0.72, 95%CI: 0.55 - 0.95; P=0.02), Dominant Model TT+TA vs AA (OR 0.66, 95%CI: 0.44 - 0.99; P=0.04) and Heterozygote model TA vs AA (OR 0.52, 95%CI: 0.34 - 0.80; P=0.003) decreased risk of CHB with LC significantly.

Recessive model TT vs TA+AA increased risk of CHB with LC significantly (OR 2.13, 95%CI: 1.24 – 3.67; P=0.006).

There is no significant different in homozygous model TT vs AA (P=0.28) in risk of CHB with LC.
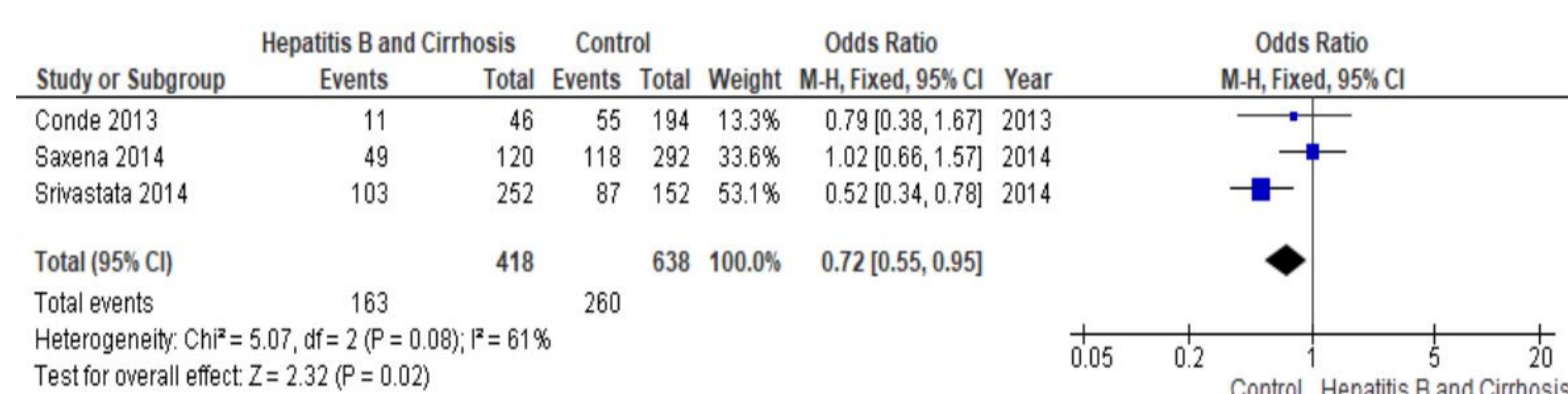

Figure 2. Forrest Plot of Gene Model T vs A (Allelic model)
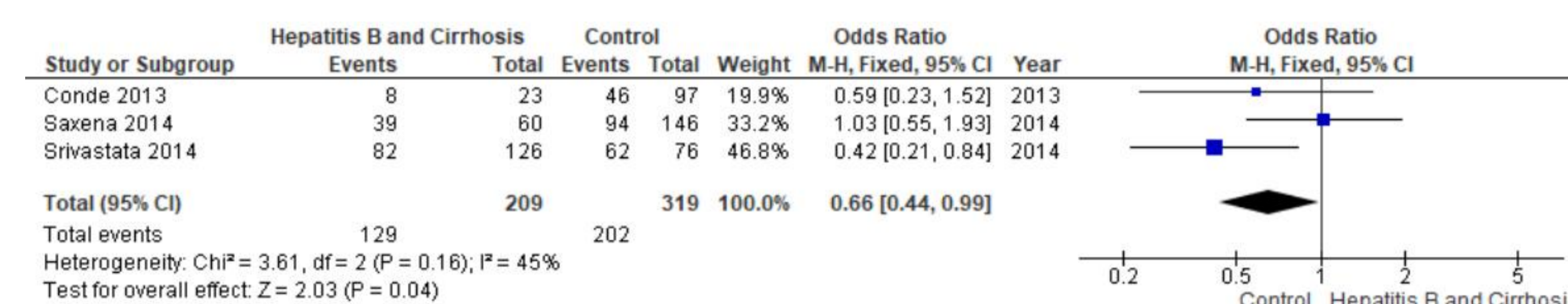

Figure 3. Gene Model TT+TA vs AA (dominant Model)
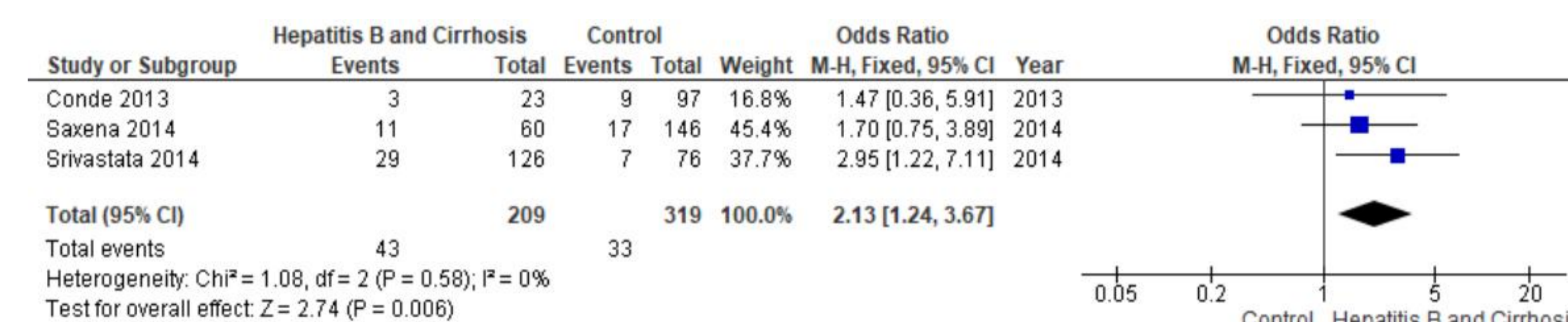

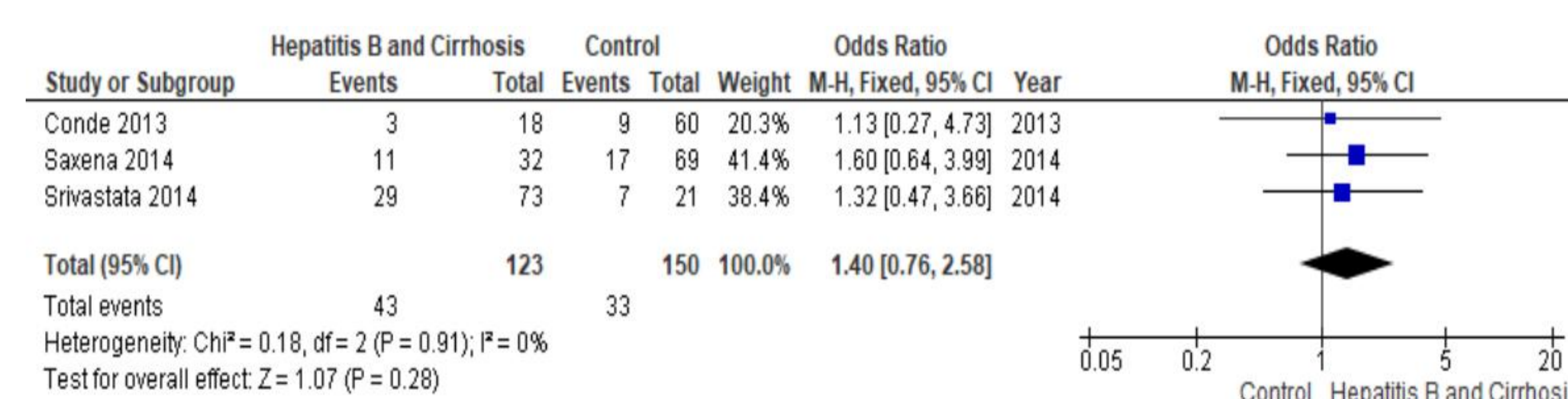Figure 4. Gene Model TT vs TA+AA (Recessive Model)

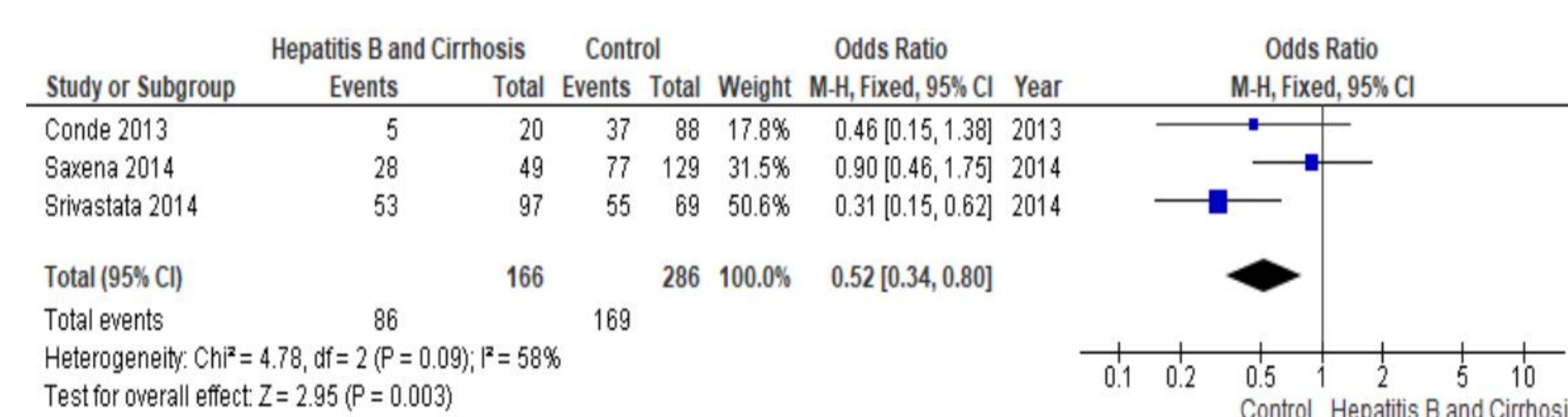Figure 5. Gene Model TT vs AA (Homozygous Model)

Figure 6. Gene Model TA vs AA (Heterozygote Model)

Conclusion

Interferon-gamma+874 T/A Polymorphism was associated with risk of HBV infection. Individual with T allele, TT and TA genotype have a reduced risk of CHB with LC

Keywords: Interferon-gamma+874 T/A, Polymorphism, Chronic Hepatitis B, HBV infection