

Supplementary Information

Association of *MBL2* Gene Polymorphisms with Pulmonary Tuberculosis Susceptibility: Trial Sequence Meta-analysis as Evidence

Authors' names in order of their authorship:

Raju K. Mandal¹, Munawwar Ali Khan², Arif Hussain³, Sajad A. Dar¹, Sultan Aloufi⁴, Arshad Jawed¹, Mohd Wahid¹, Aditya K. Panda⁵, Mohtashim Lohani⁶, Naseem Akhter⁷, Saif Khan⁸, B.N. Mishra⁹, Shafiul Haque^{1*}

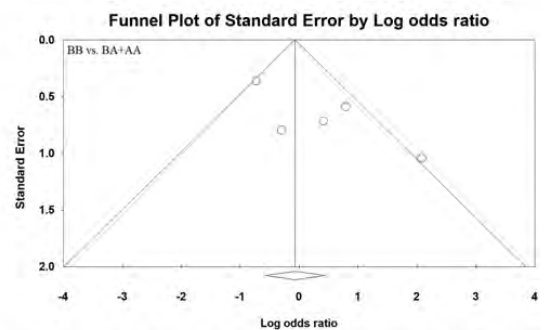
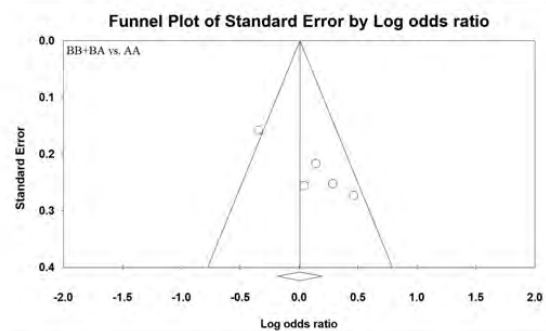
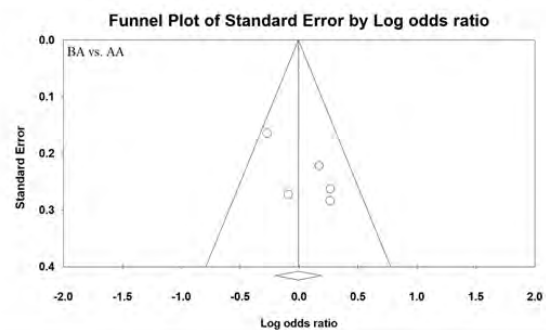
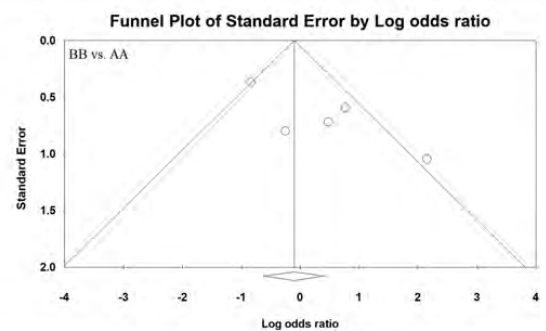
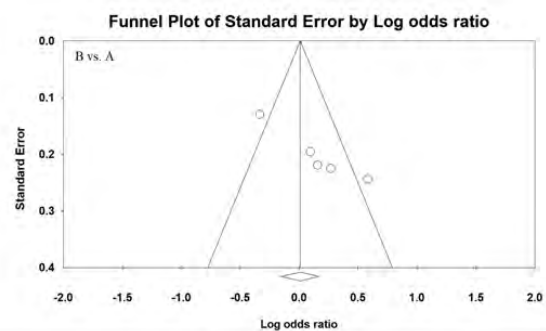
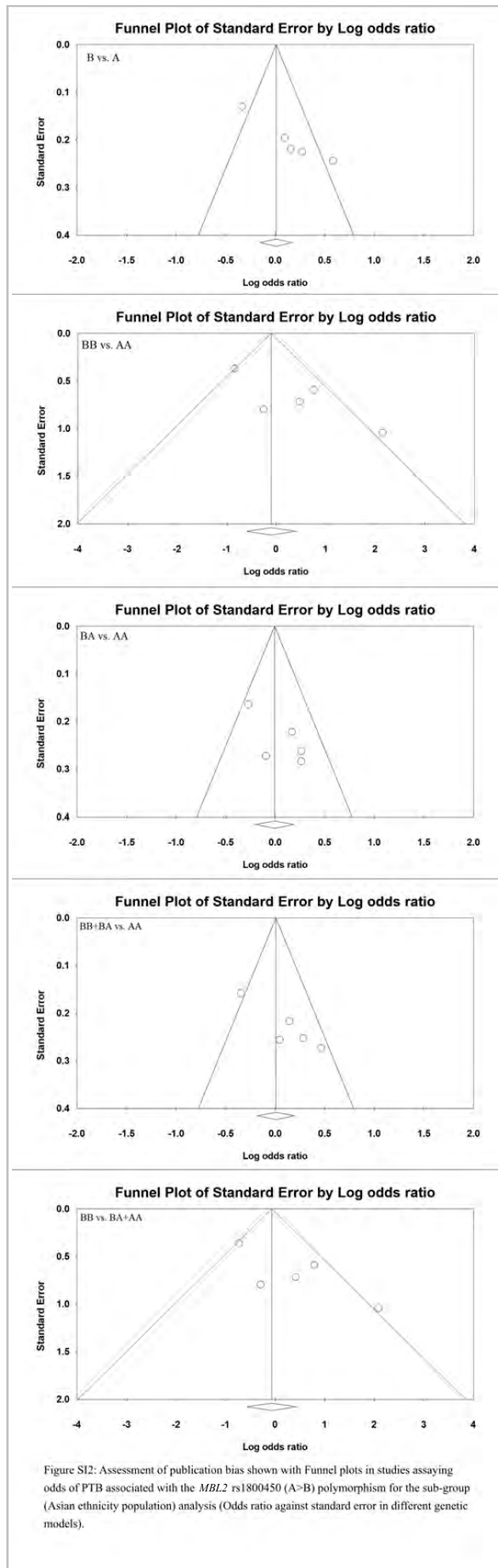
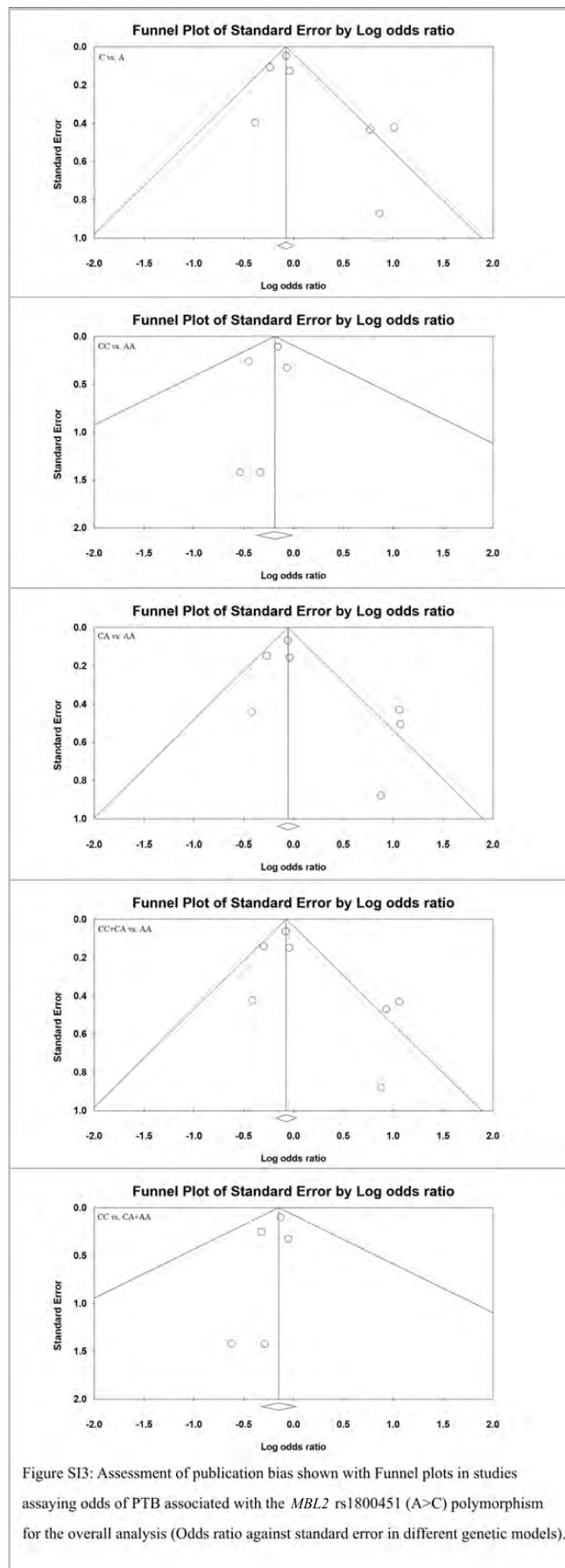


Figure S11: Assessment of publication bias shown with Funnel plots in studies assaying odds of PTB associated with the *MBL2* rs1800450 (A>B) polymorphism for the overall analysis (Odds ratio against standard error in different genetic models).





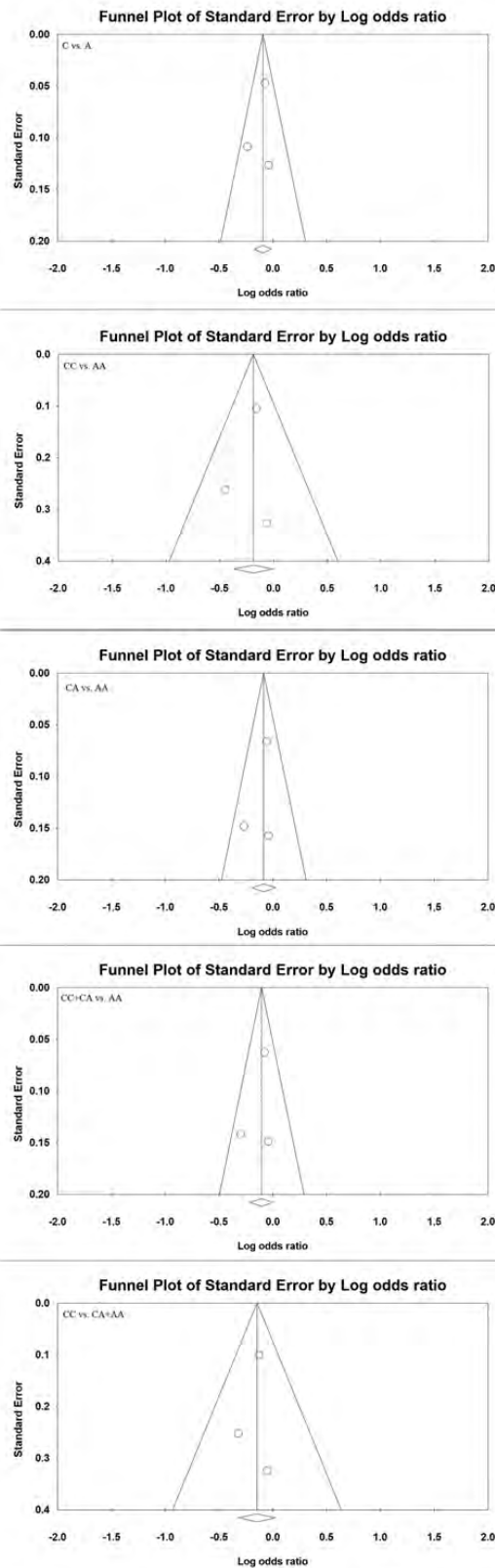


Figure S14: Assessment of publication bias shown with Funnel plots in studies assaying odds of PTB associated with the *MBL2* rs1800451 (A>C) polymorphism for the sub-group (African ethnicity population) analysis (Odds ratio against standard error in different genetic models).

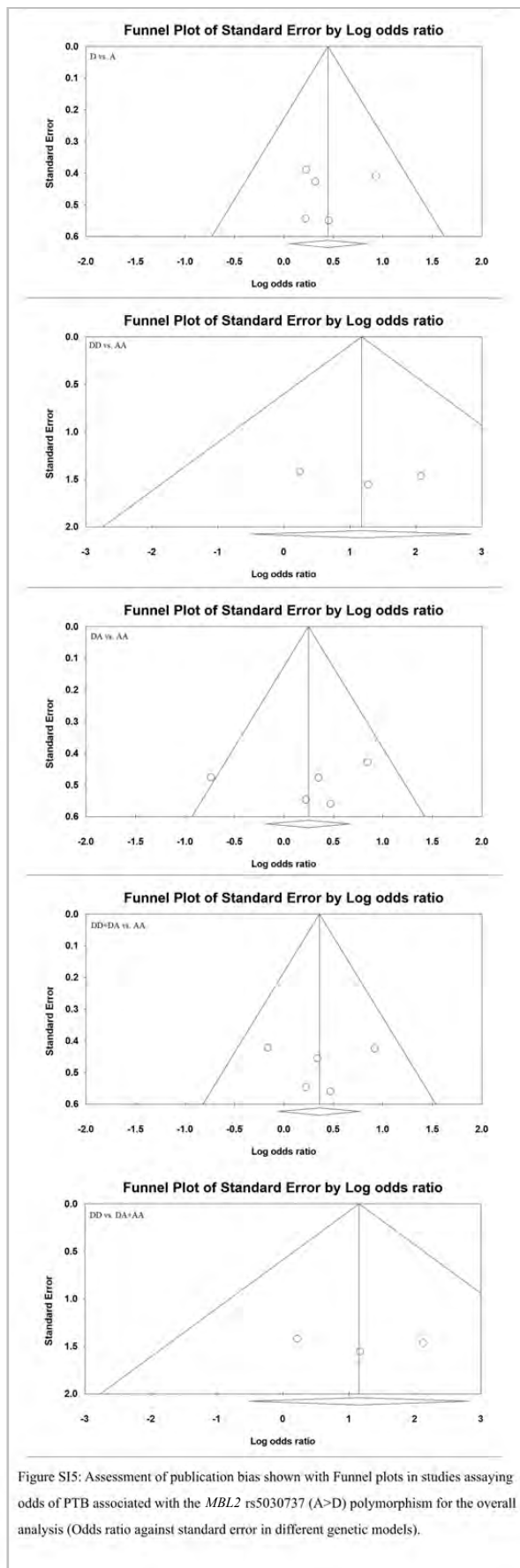


Figure S15: Assessment of publication bias shown with Funnel plots in studies assaying odds of PTB associated with the *MBL2* rs5030737 (A>D) polymorphism for the overall analysis (Odds ratio against standard error in different genetic models).

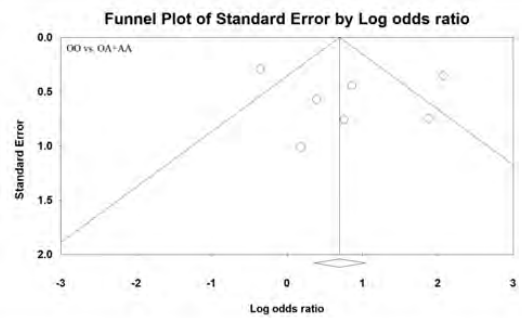
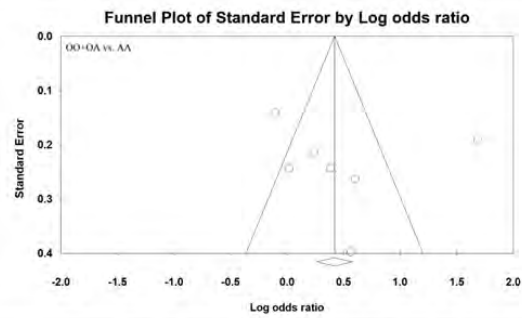
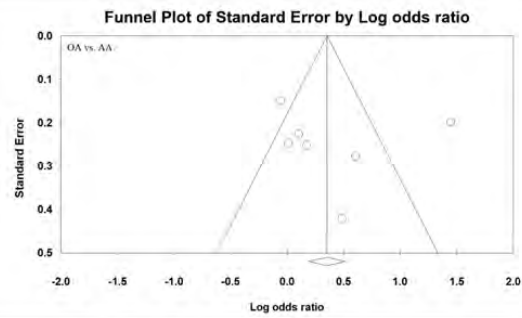
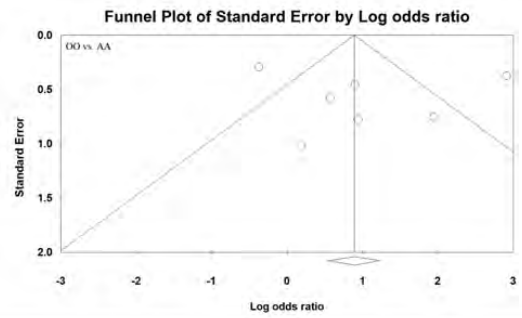
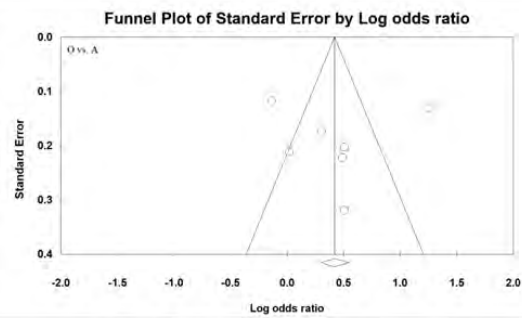
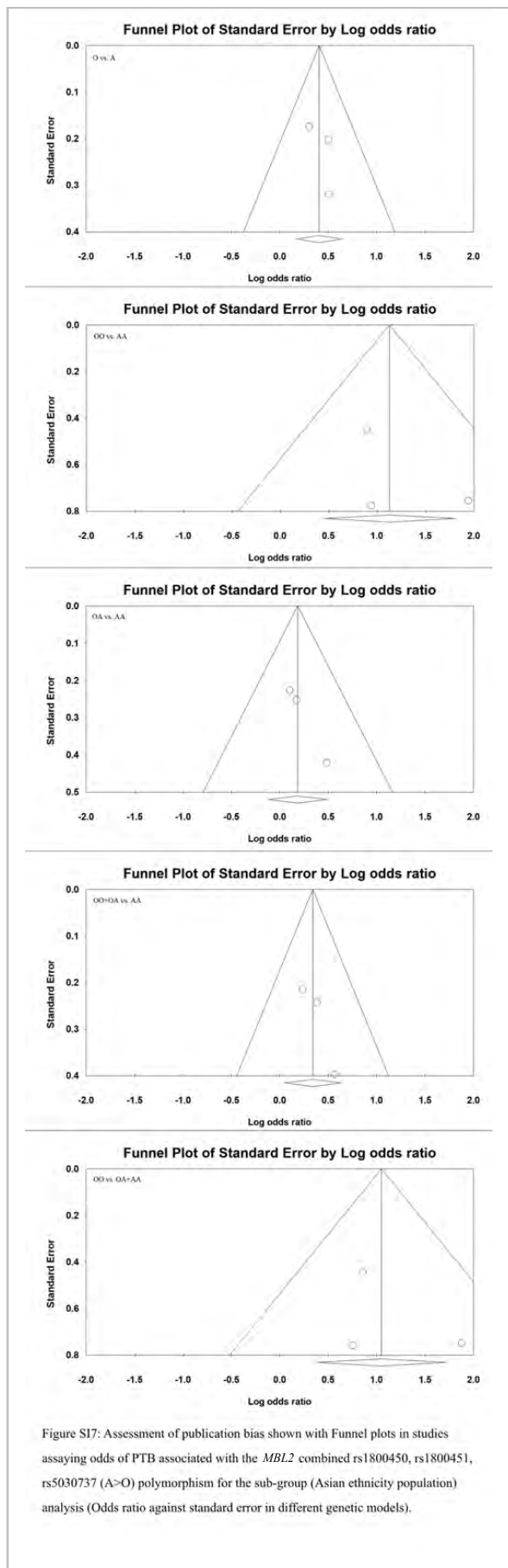


Figure S16: Assessment of publication bias shown with Funnel plots in studies assaying odds of PTB associated with the *MBL2* combined rs1800450, rs1800451, rs5030737 (A>O) polymorphism for the overall analysis (Odds ratio against standard error in different genetic models).



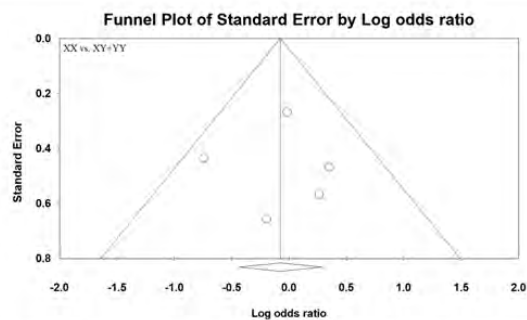
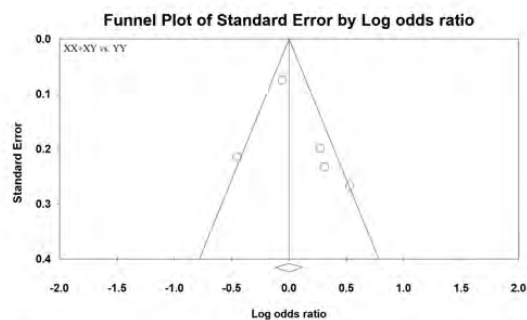
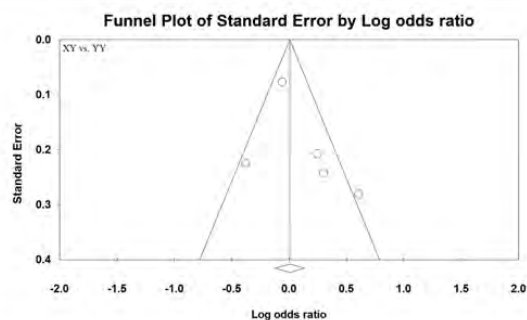
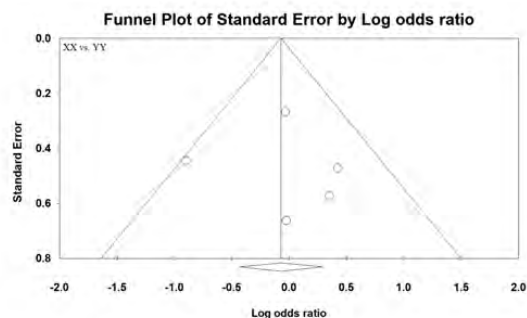
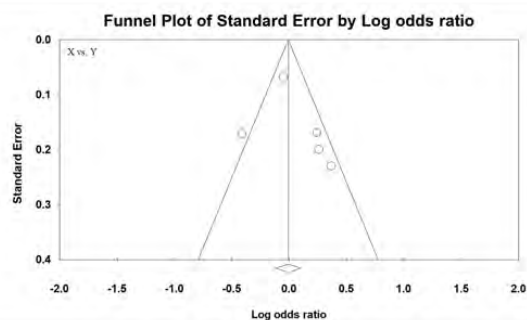
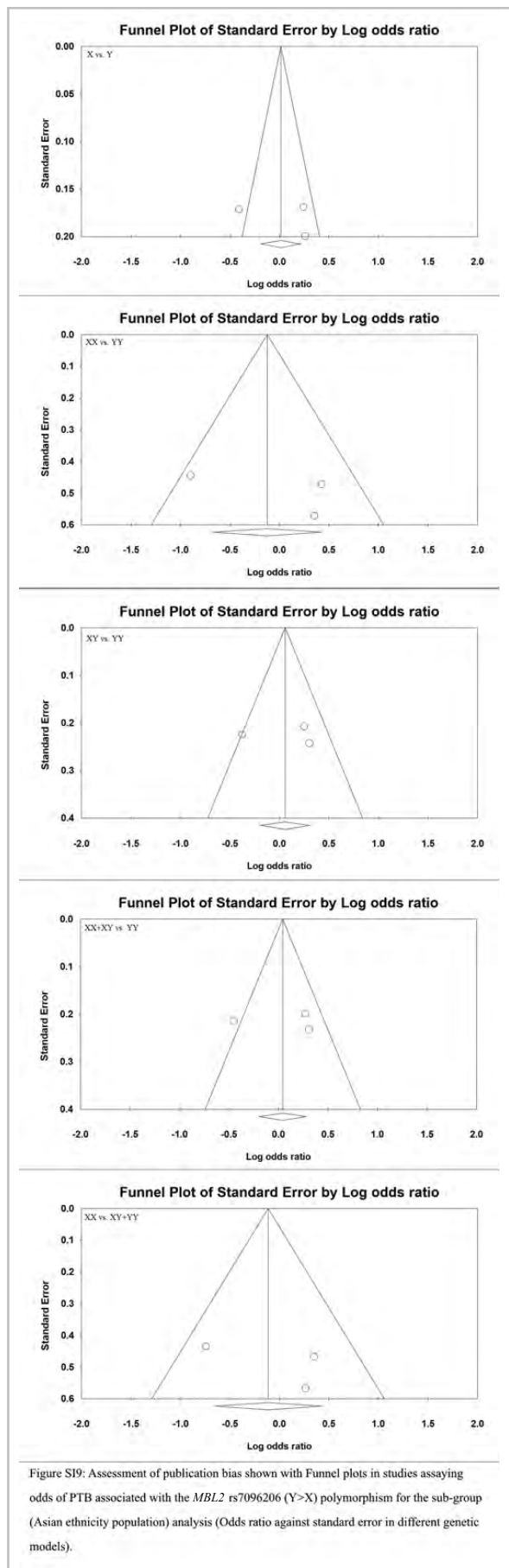
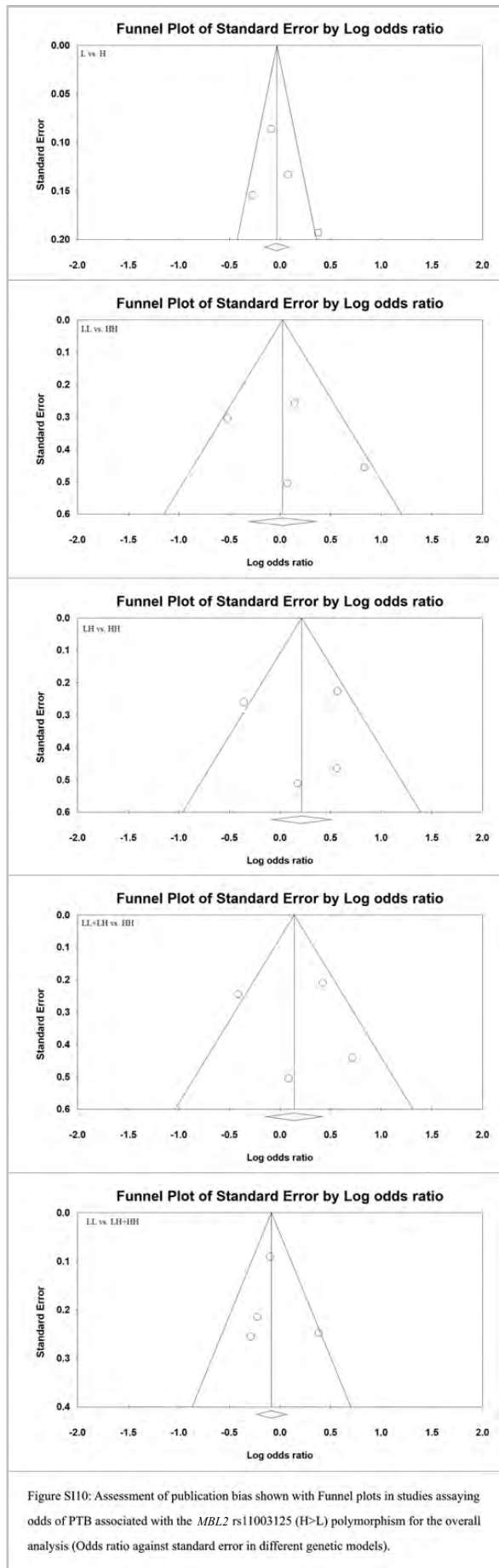


Figure S18: Assessment of publication bias shown with Funnel plots in studies assaying odds of PTB associated with the *MBL2* rs7096206 (Y>X) polymorphism for the overall analysis (Odds ratio against standard error in different genetic models).





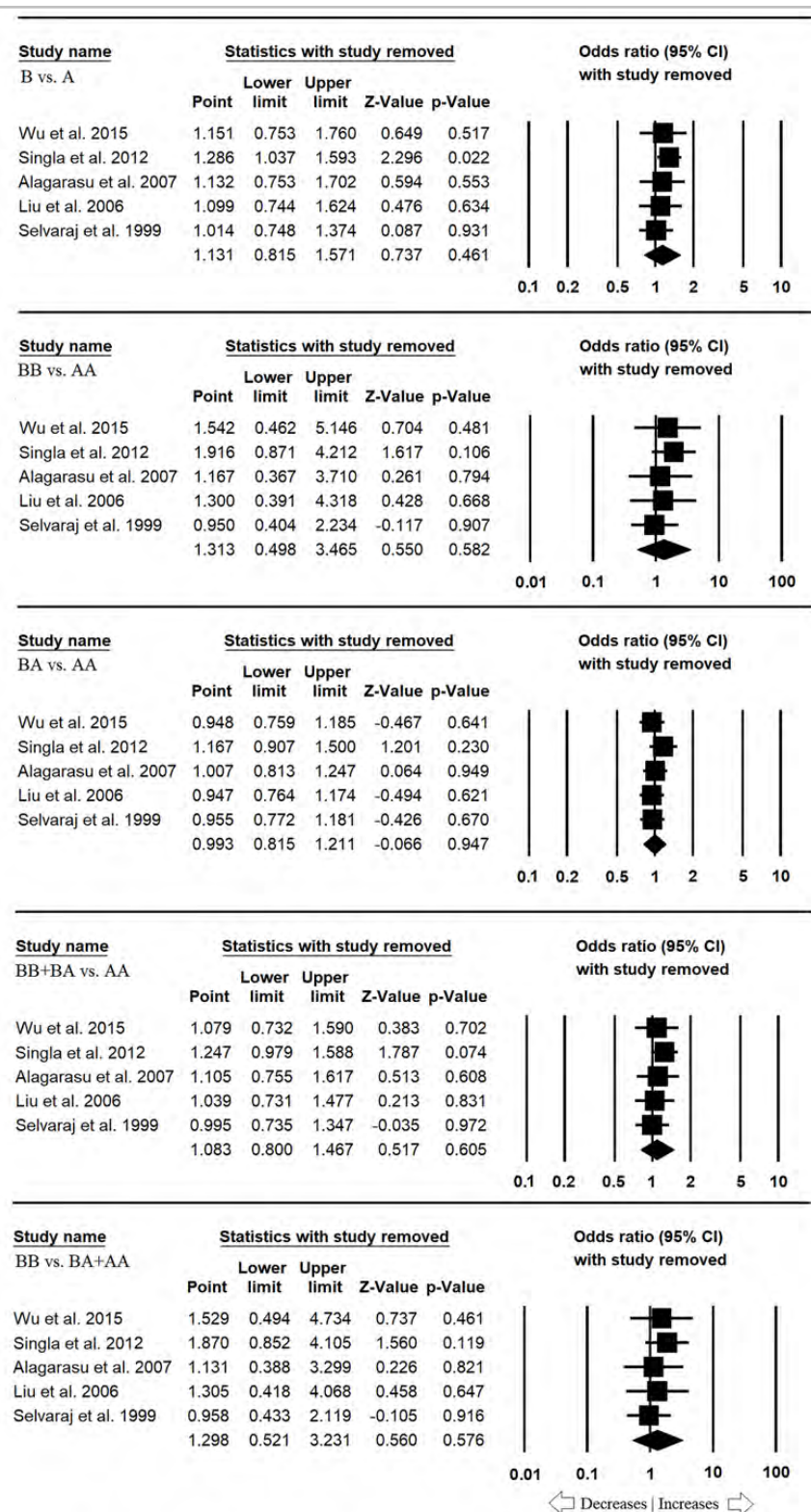


Figure SI11: Sensitivity analysis of *MBL2* rs1800450 (A>B) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

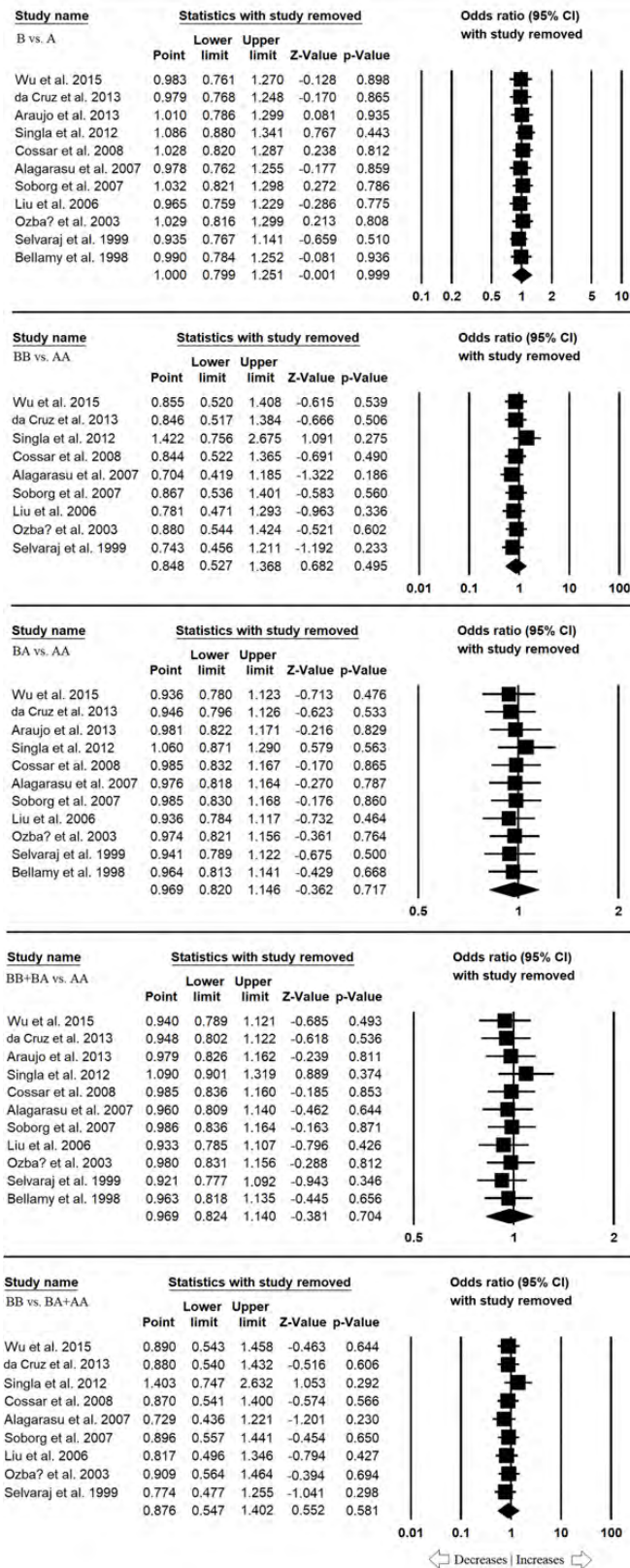


Figure SI12: Sensitivity analysis of *MBL2* rs1800450 (A>B) polymorphism with PTB risk among Asian population to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the subgroup analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

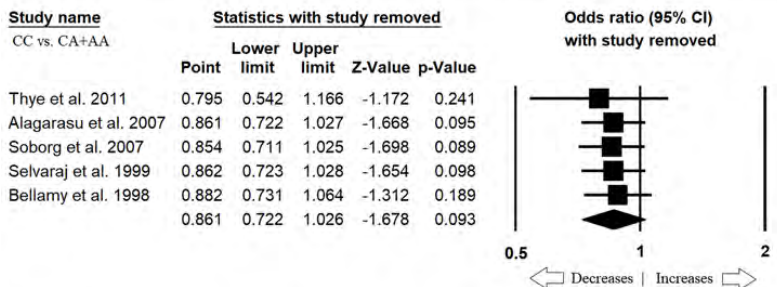
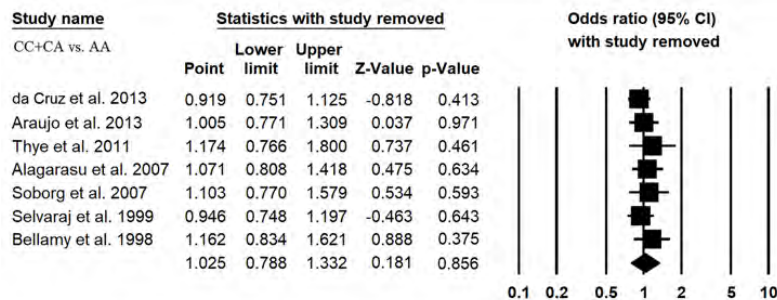
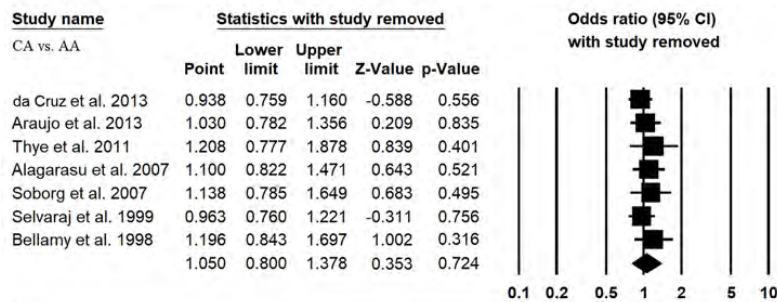
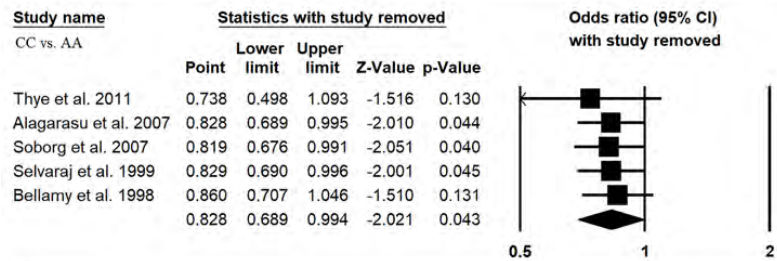
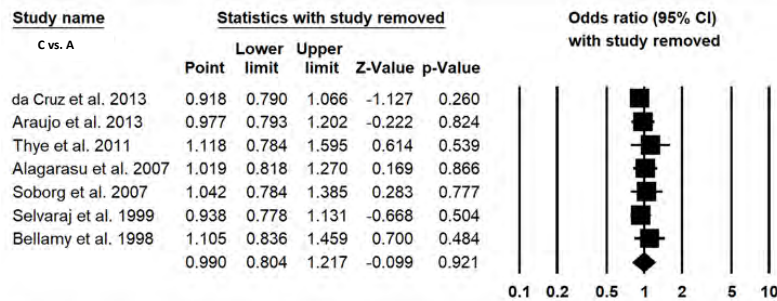


Figure S113: Sensitivity analysis of *MBL2* rs1800451 (A>C) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

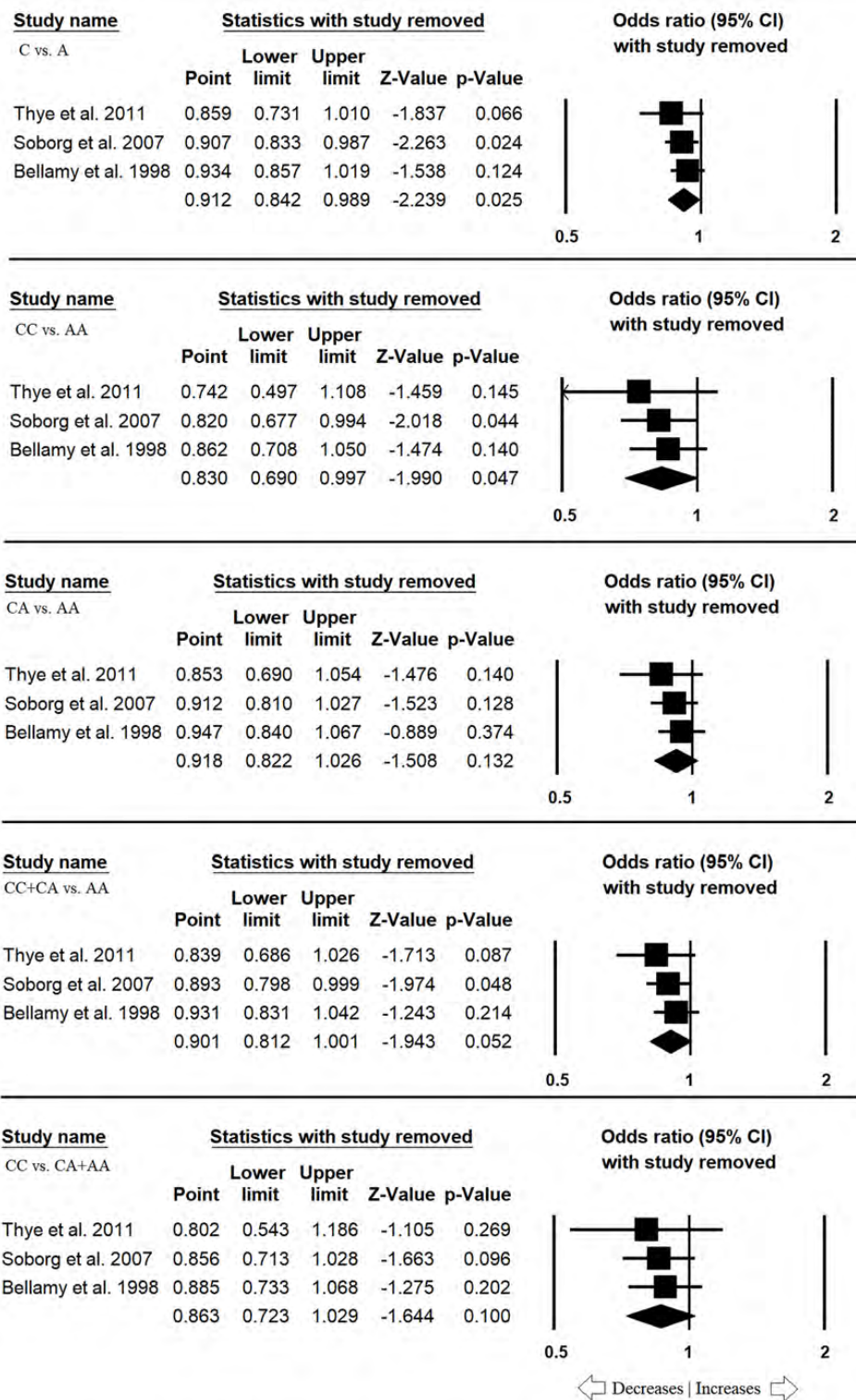


Figure SI14: Sensitivity analysis of *MBL2* rs1800451 (A>C) polymorphism with PTB risk among African population to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the subgroup analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

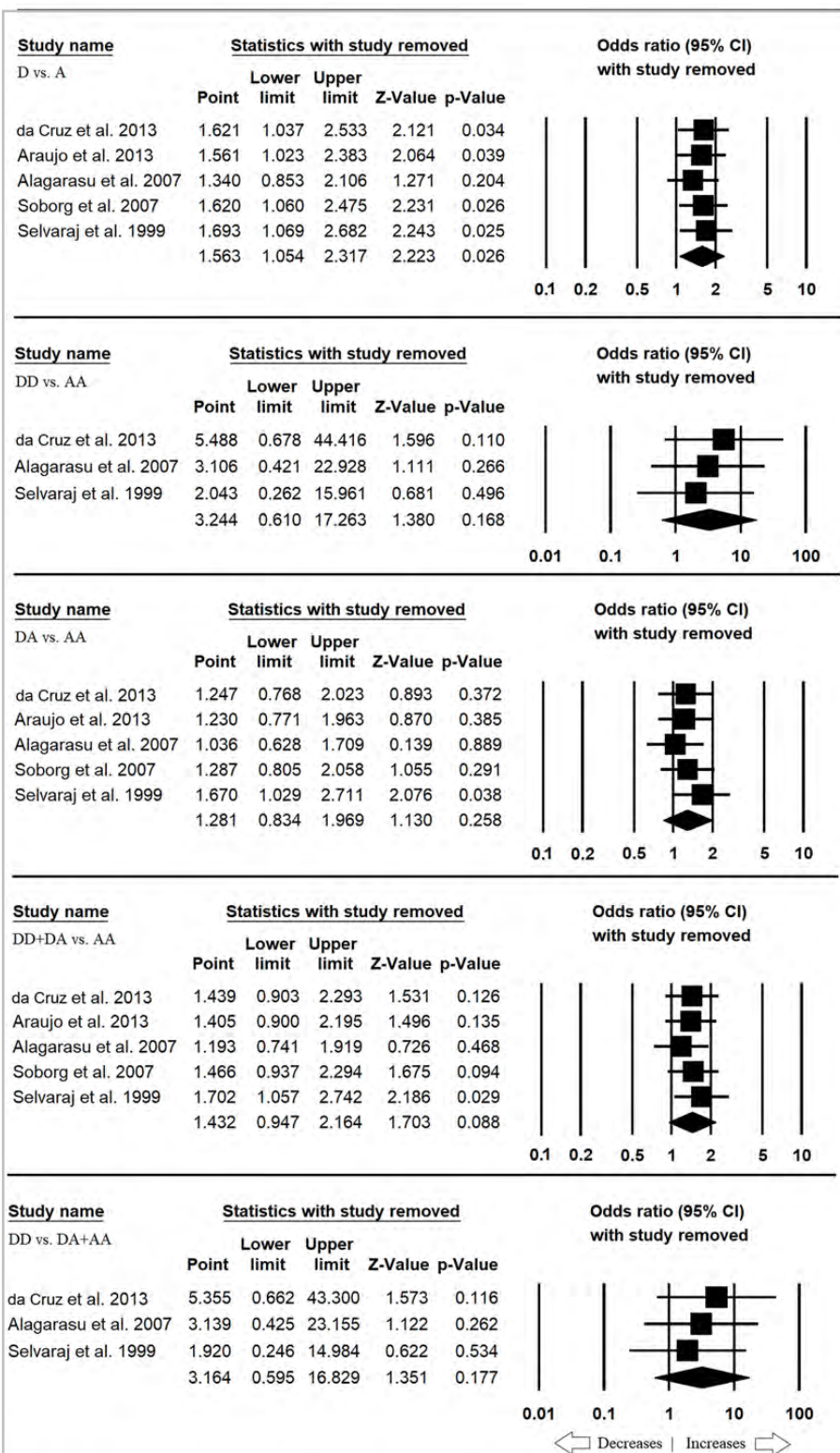


Figure SI15: Sensitivity analysis of *MBL2* rs5030737 (A>D) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

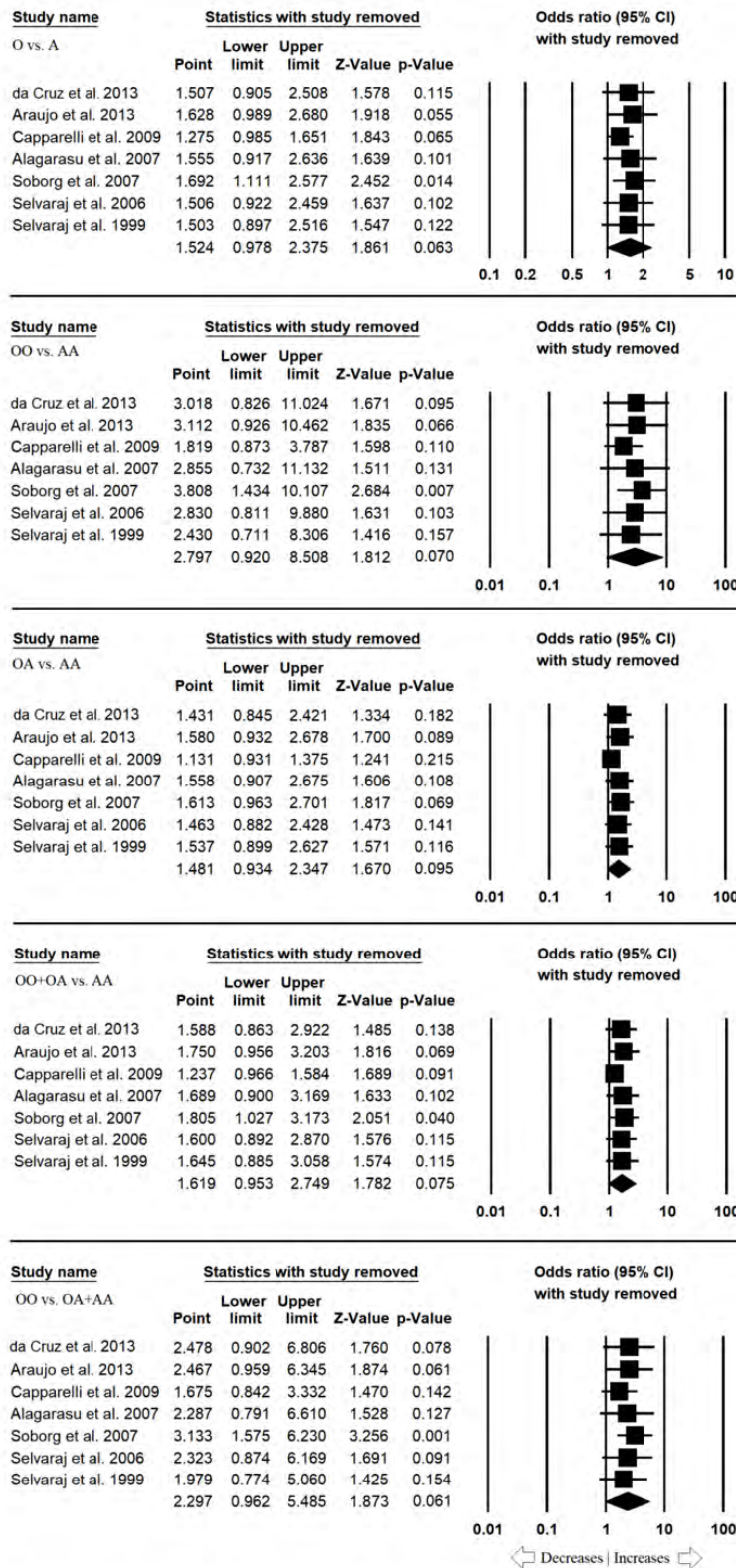


Figure SI16: Sensitivity analysis of *MBL2* combined rs1800450, rs1800451, rs5030737 (A>O) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

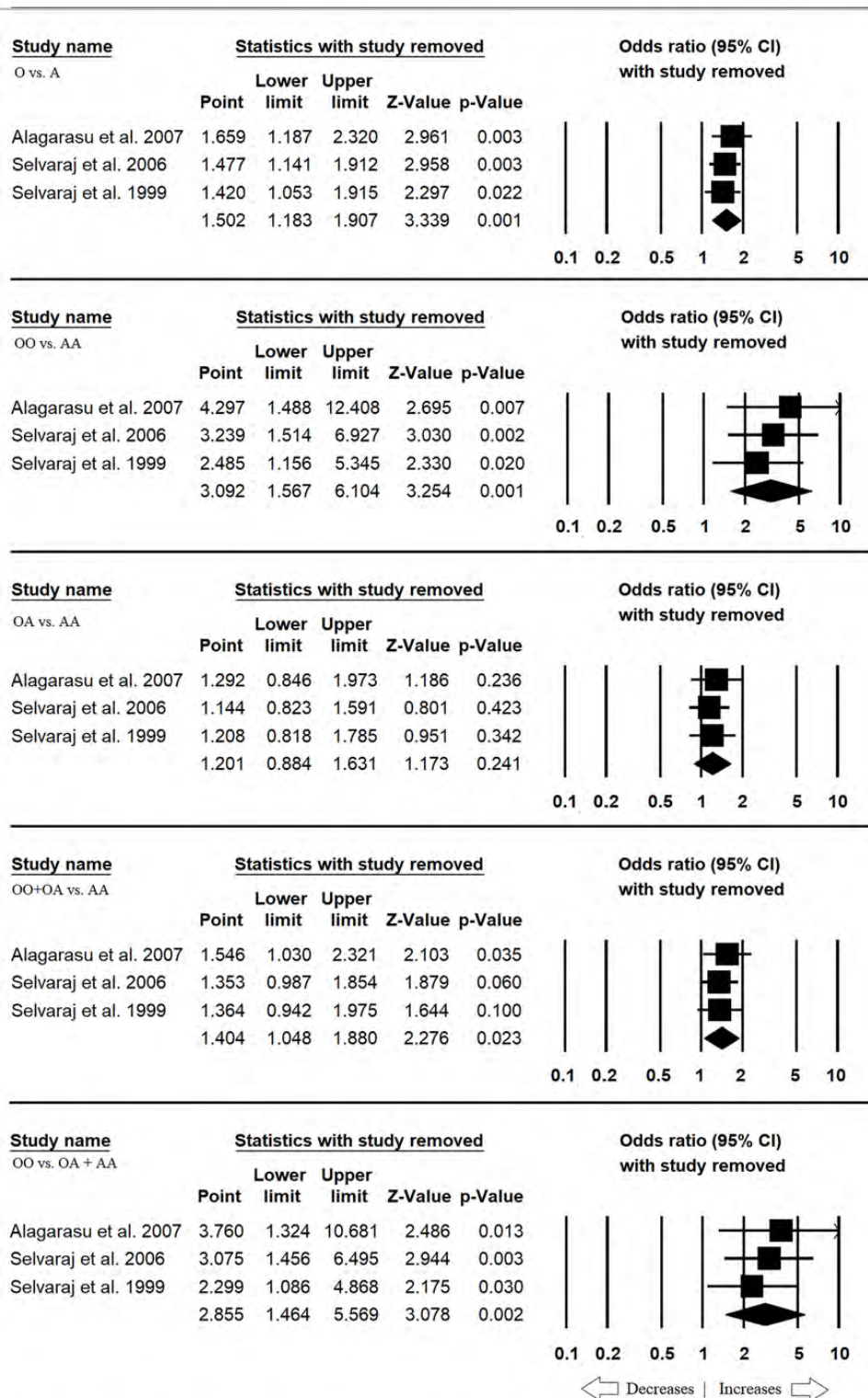


Figure SI17: Sensitivity analysis of *MBL2* combined rs1800450, rs1800451, rs5030737 (A>O) polymorphism with overall PTB risk among Asian population to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the subgroup analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

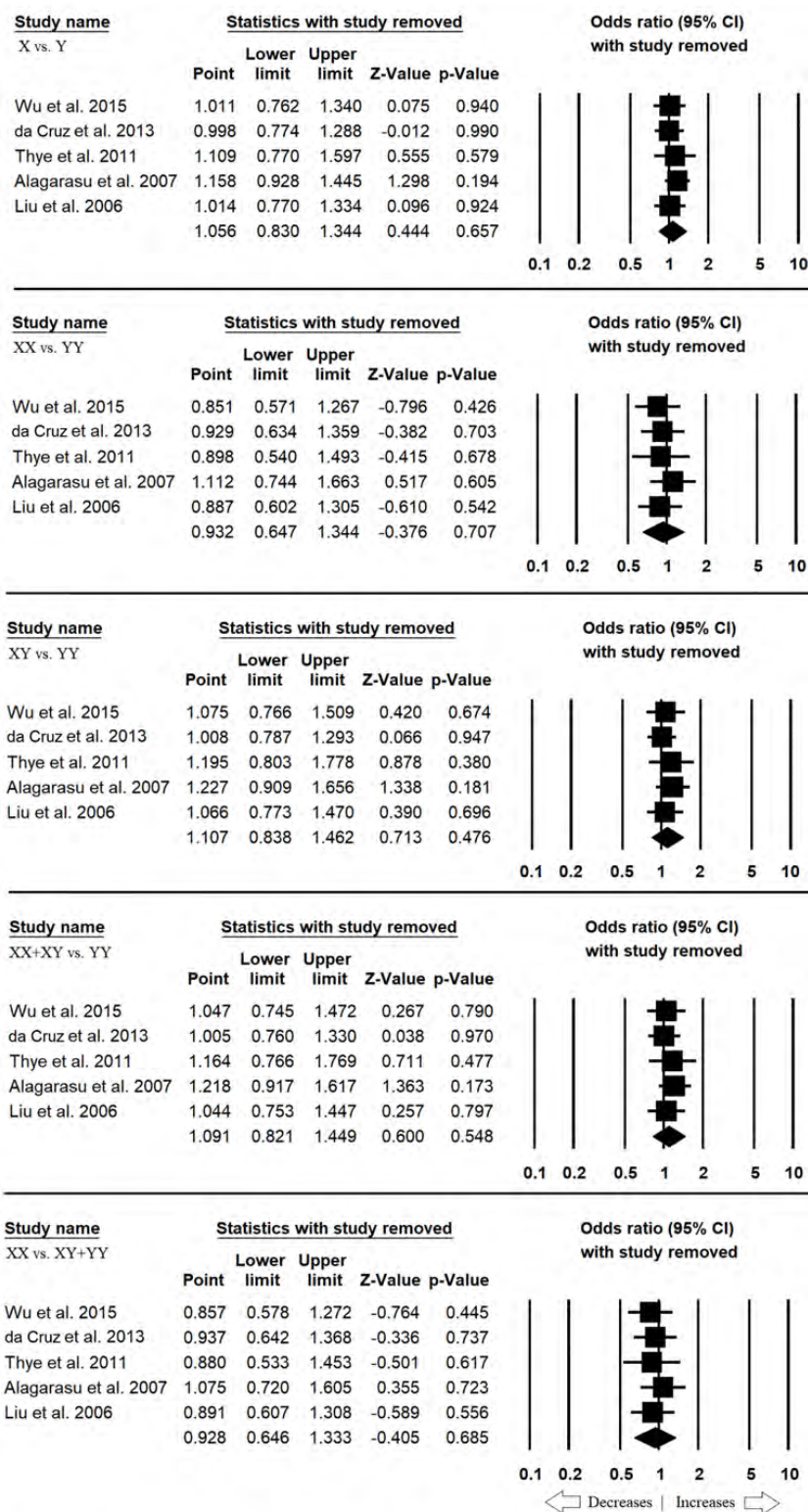


Figure SI18: Sensitivity analysis of *MBL2* rs7096206 (Y>X) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

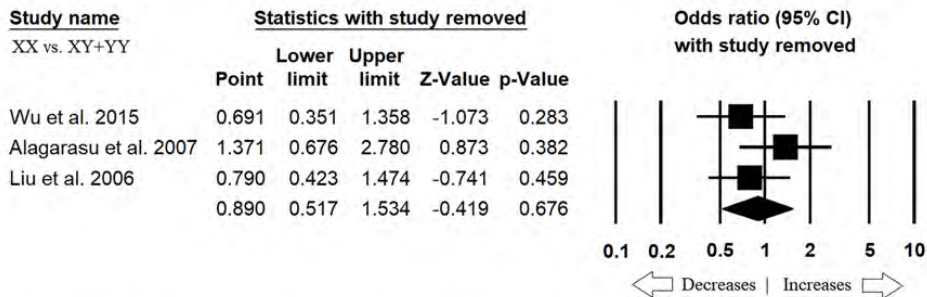
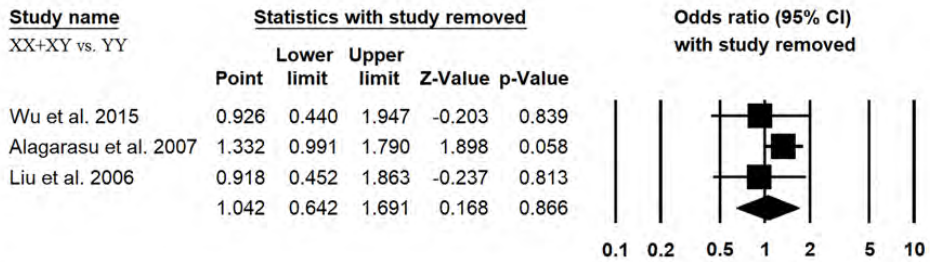
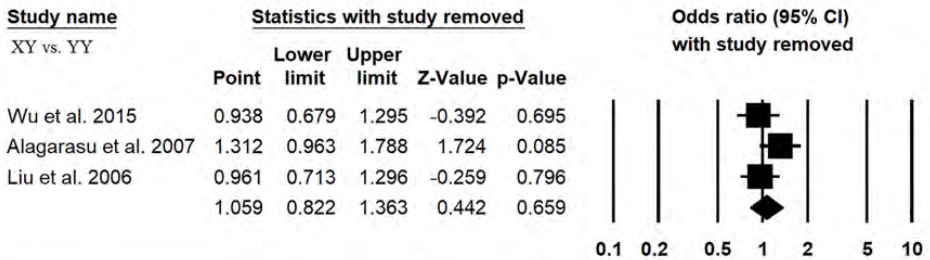
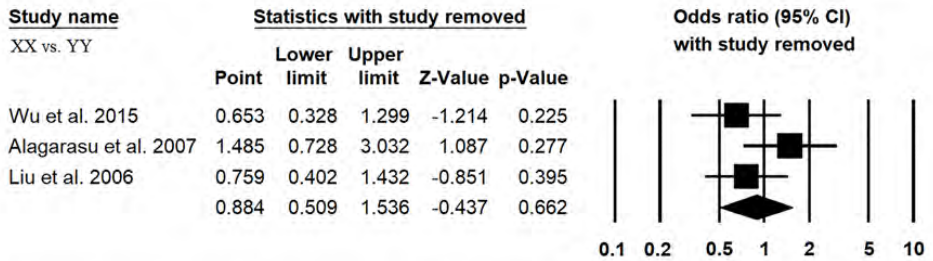
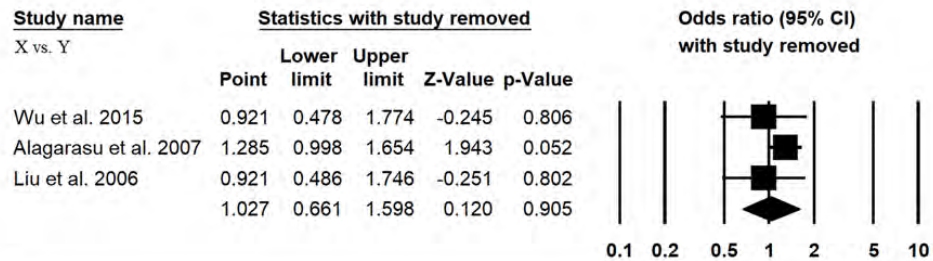


Figure S119: Sensitivity analysis of *MBL2* rs7096206 (Y>X) polymorphism with overall PTB risk among Asian population to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the subgroup analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.

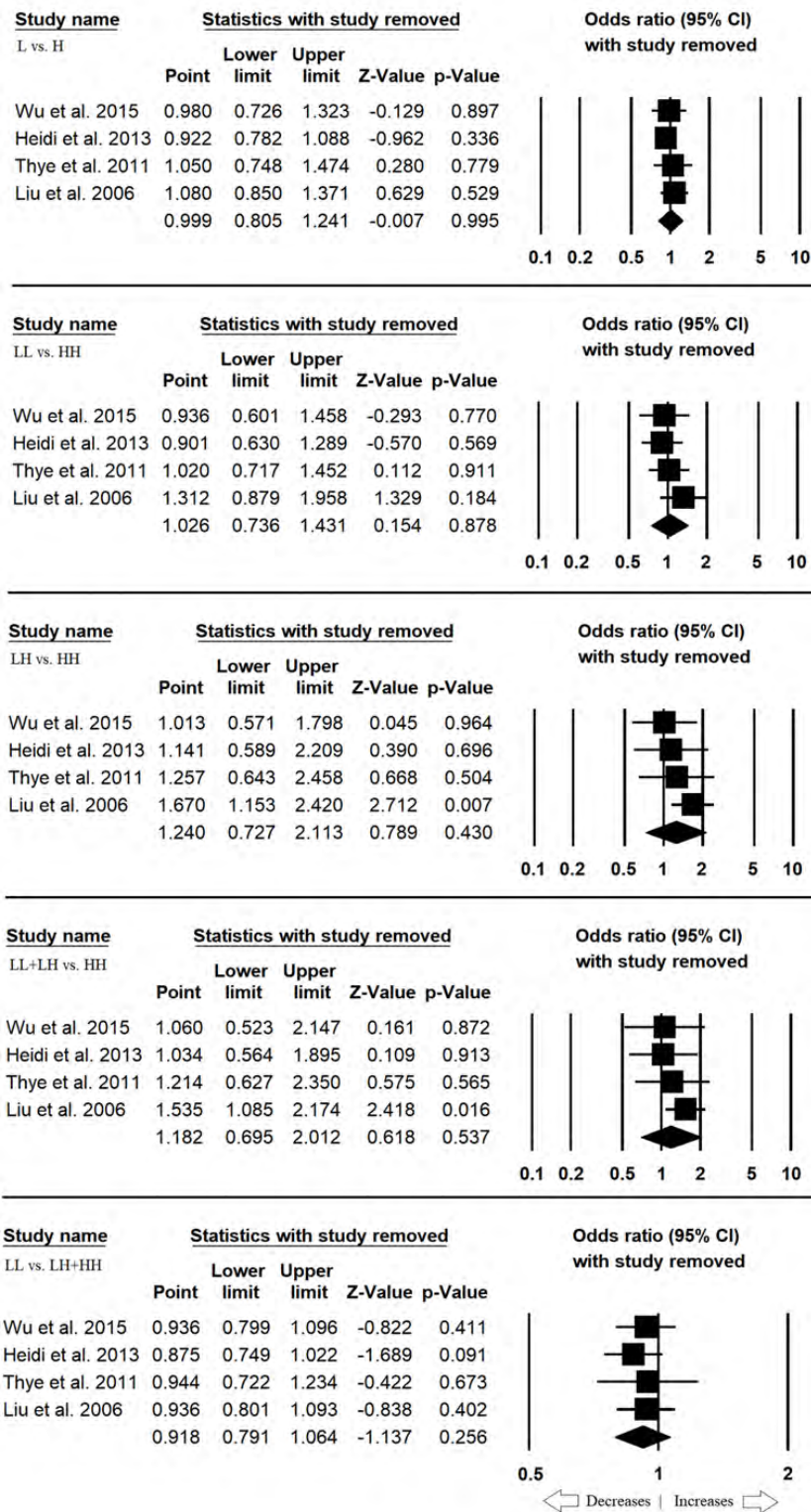


Figure SI20: Sensitivity analysis of *MBL2* rs11003125 (H>L) polymorphism with overall PTB risk to evaluate the influence of each individual study on the pooled OR by deleting one single study each time for the overall analysis (for all the genetic models). Black square represents the value of OR and the size of the square indicates the inverse proportion relative to its variance. Horizontal line is the 95% CI of OR.