

PPARG (Pro12Ala) genetic variant and risk of T2DM: a systematic review and meta-analysis

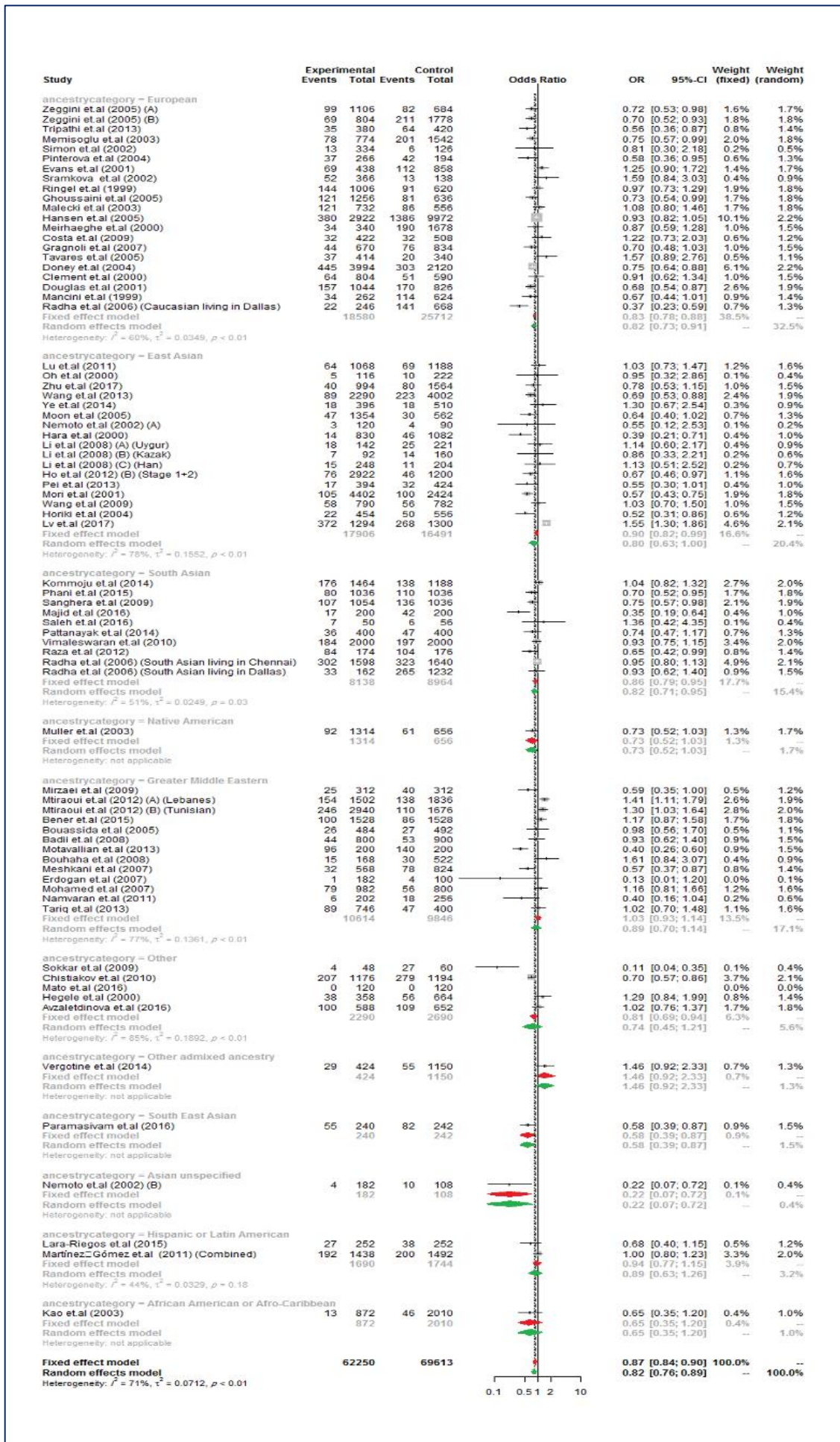
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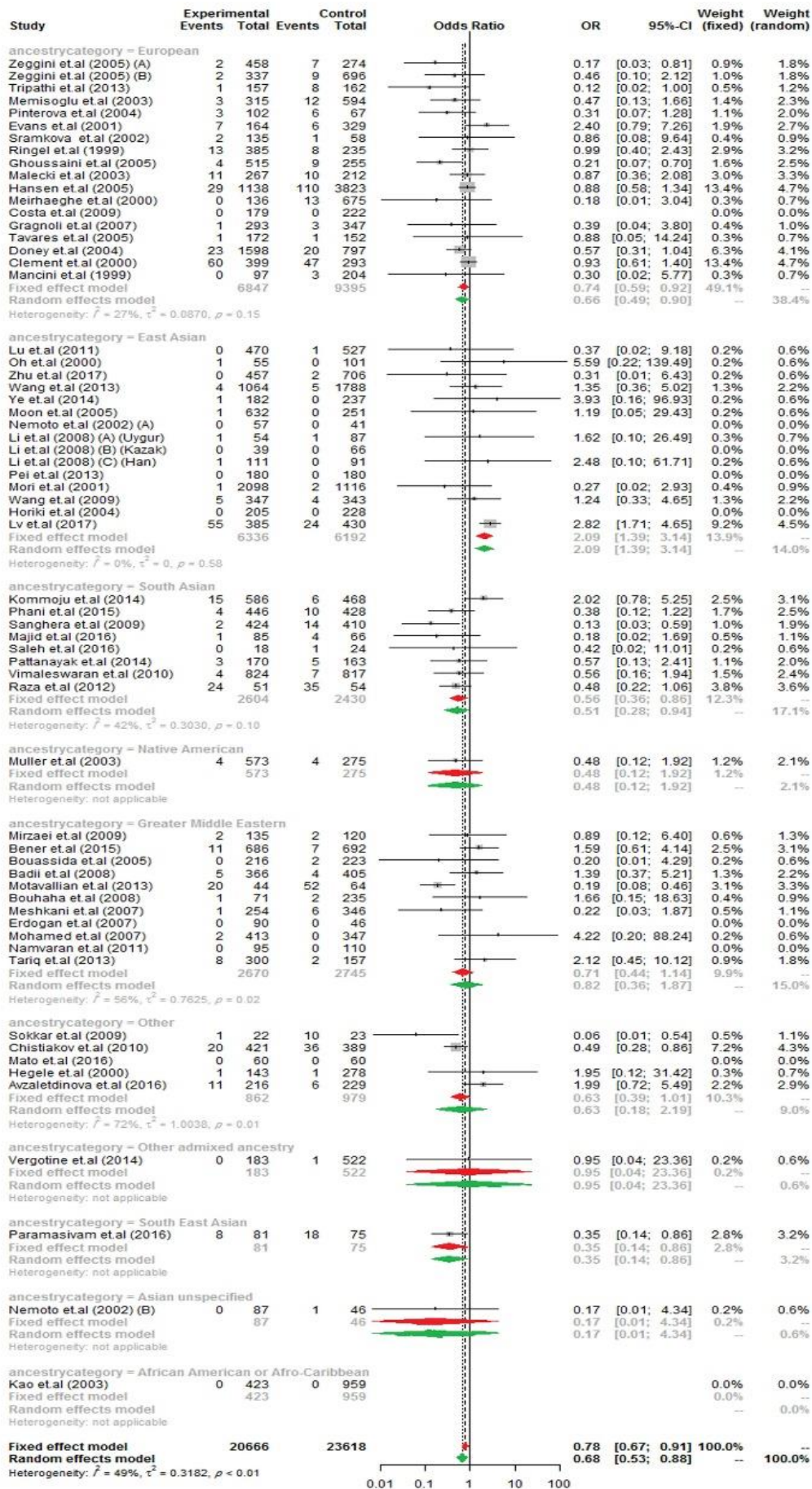
¹ Personalized Medicine Research Center, Endocrinology and Metabolism Clinical Sciences Institute, Tehran University of Medical Sciences, Tehran 1411413137, Iran

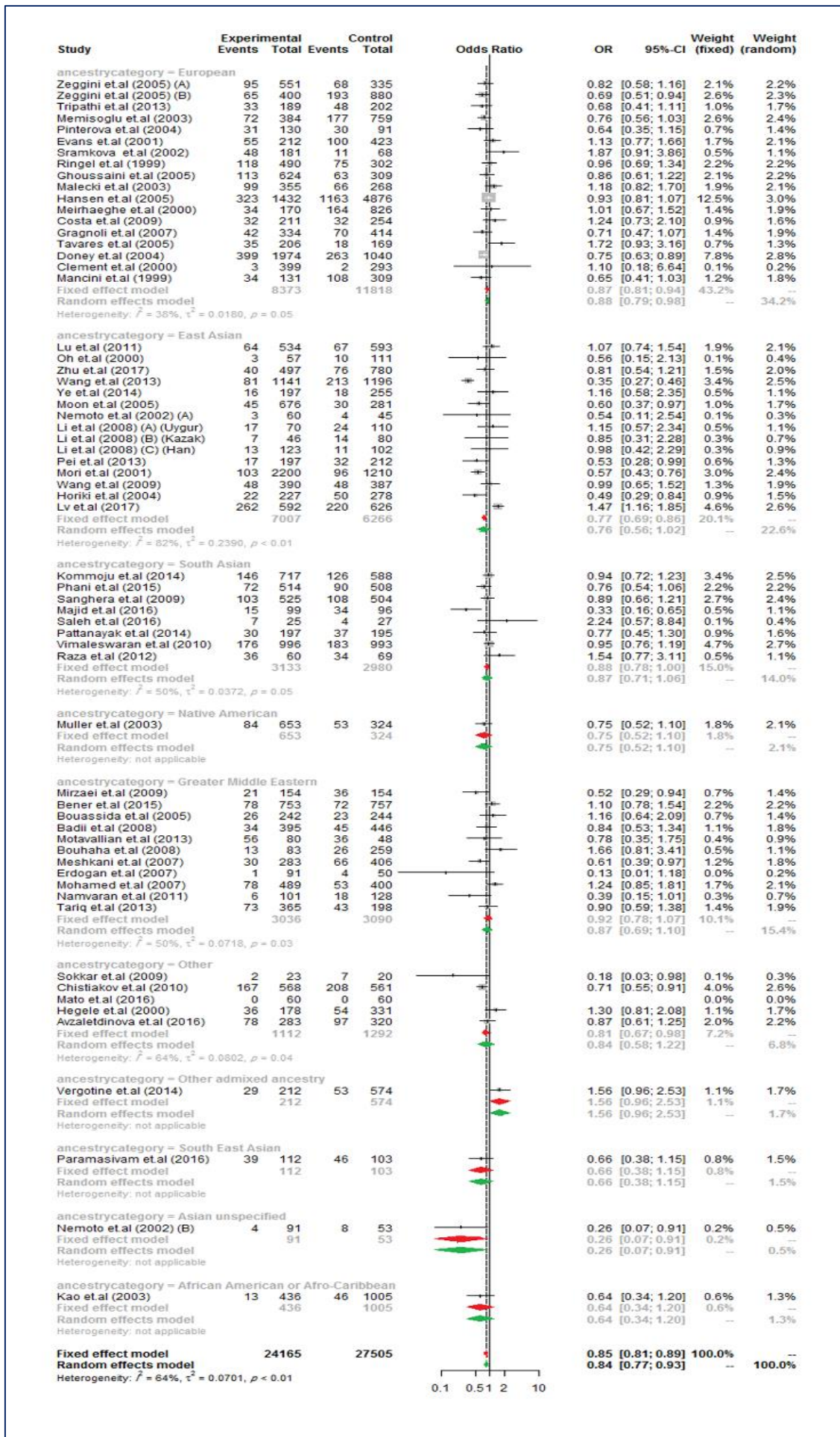
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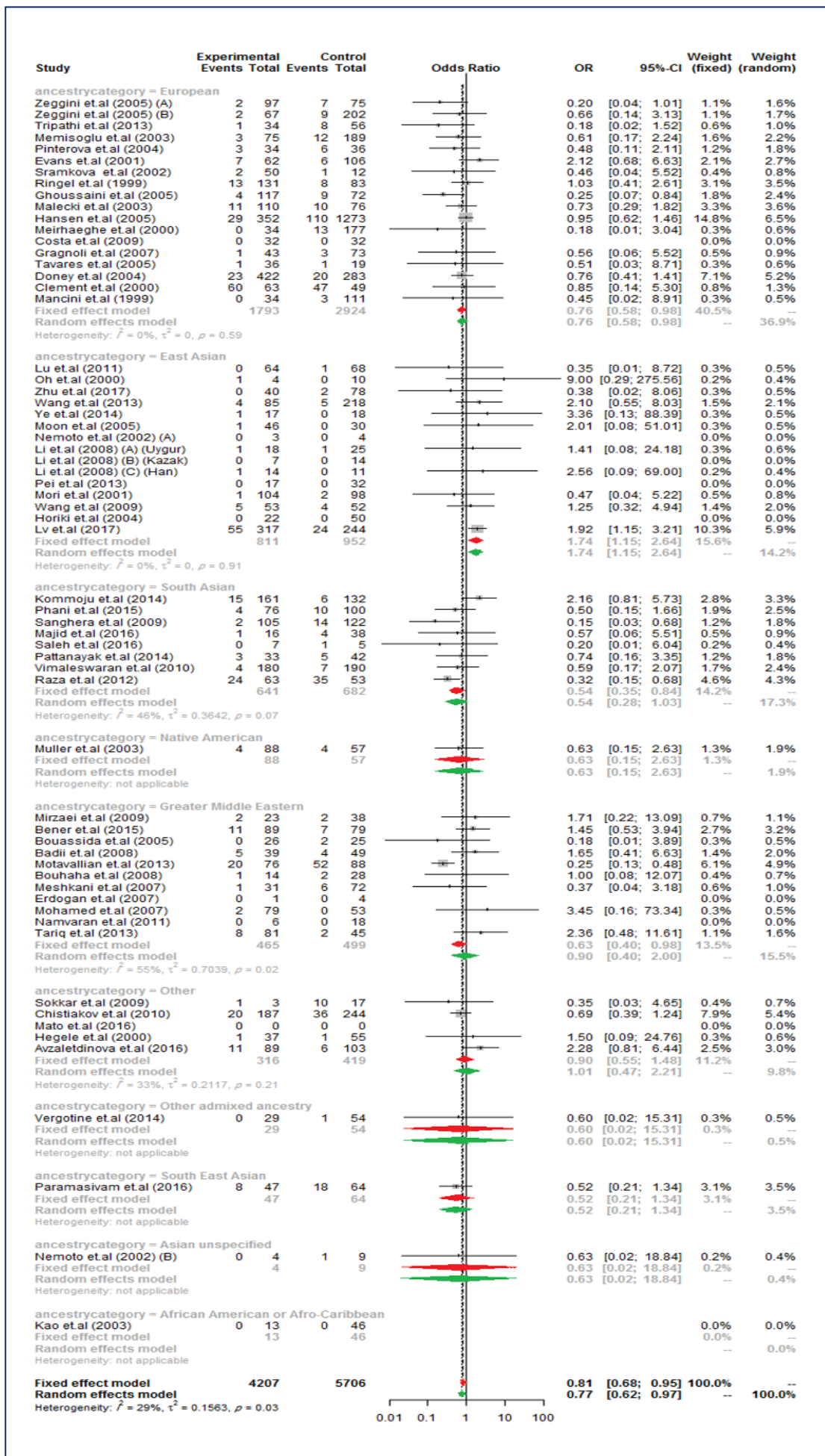
³ Medical Genomics Research Center, Tehran Medical Sciences, Islamic Azad University, Tehran 1916893813, Iran

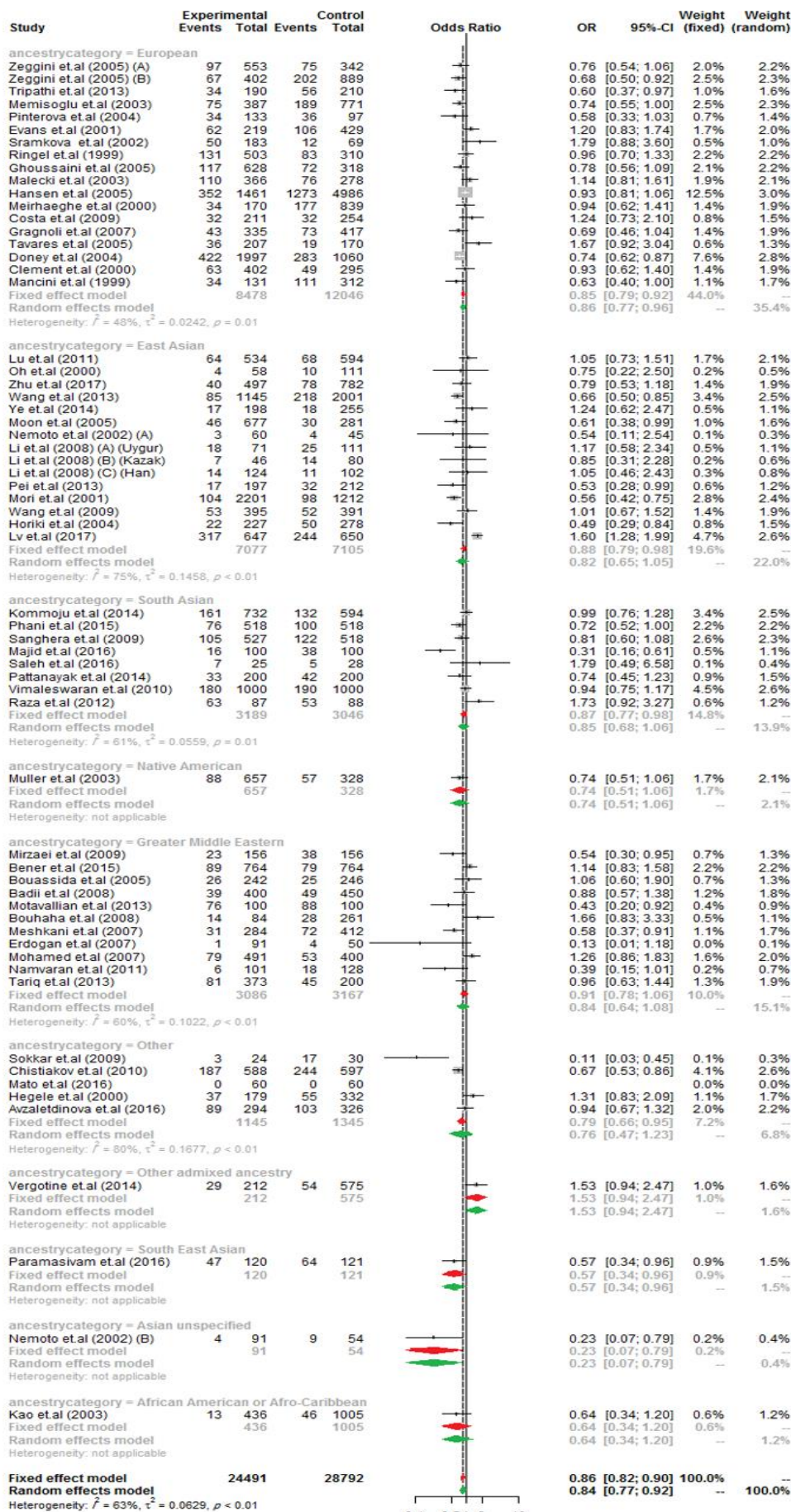
⁴ Endocrinology and Metabolism Research Center, Endocrinology and Metabolism Clinical Sciences Institute, Tehran University of Medical Sciences, Tehran 1411413137, Iran

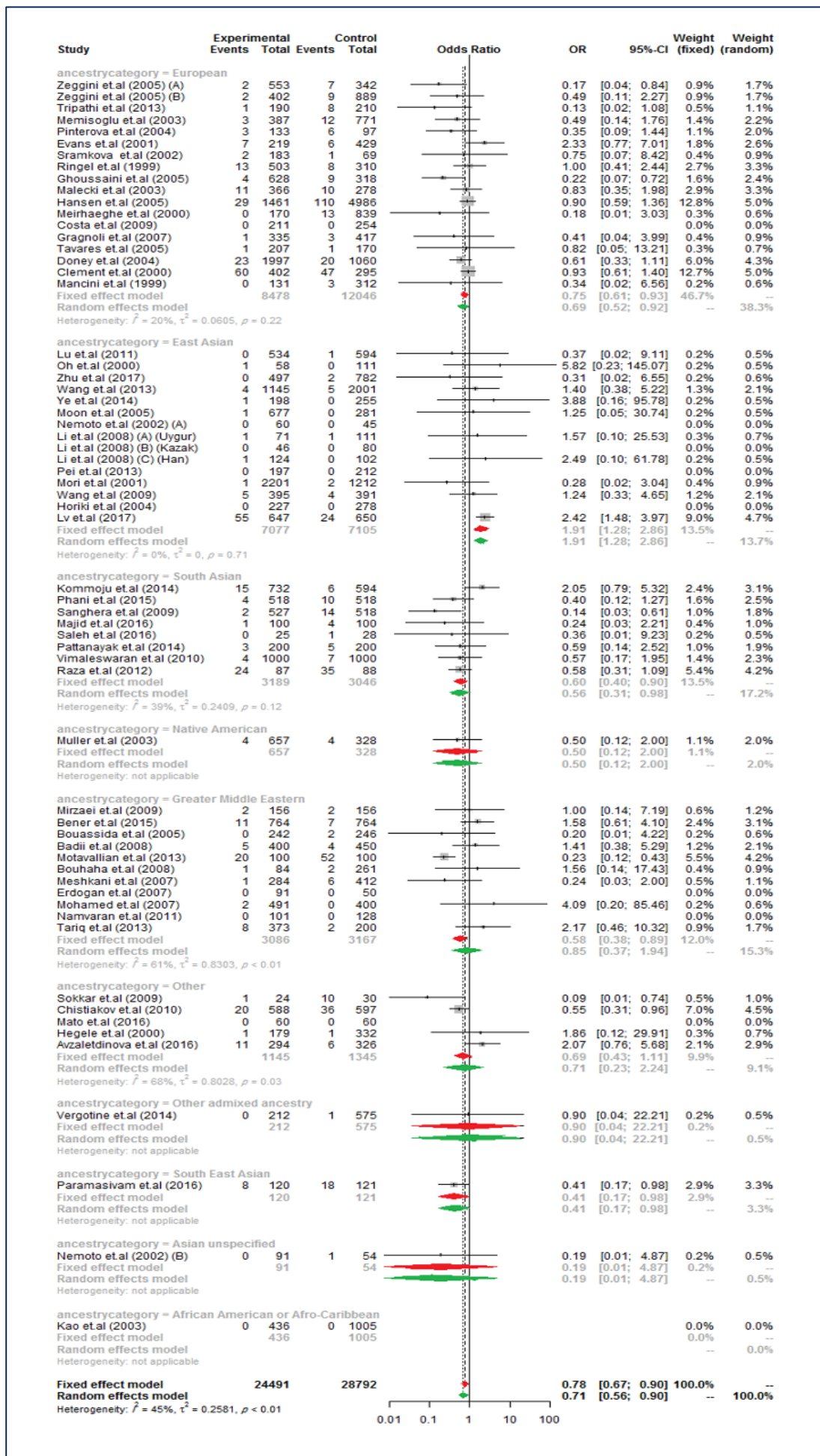












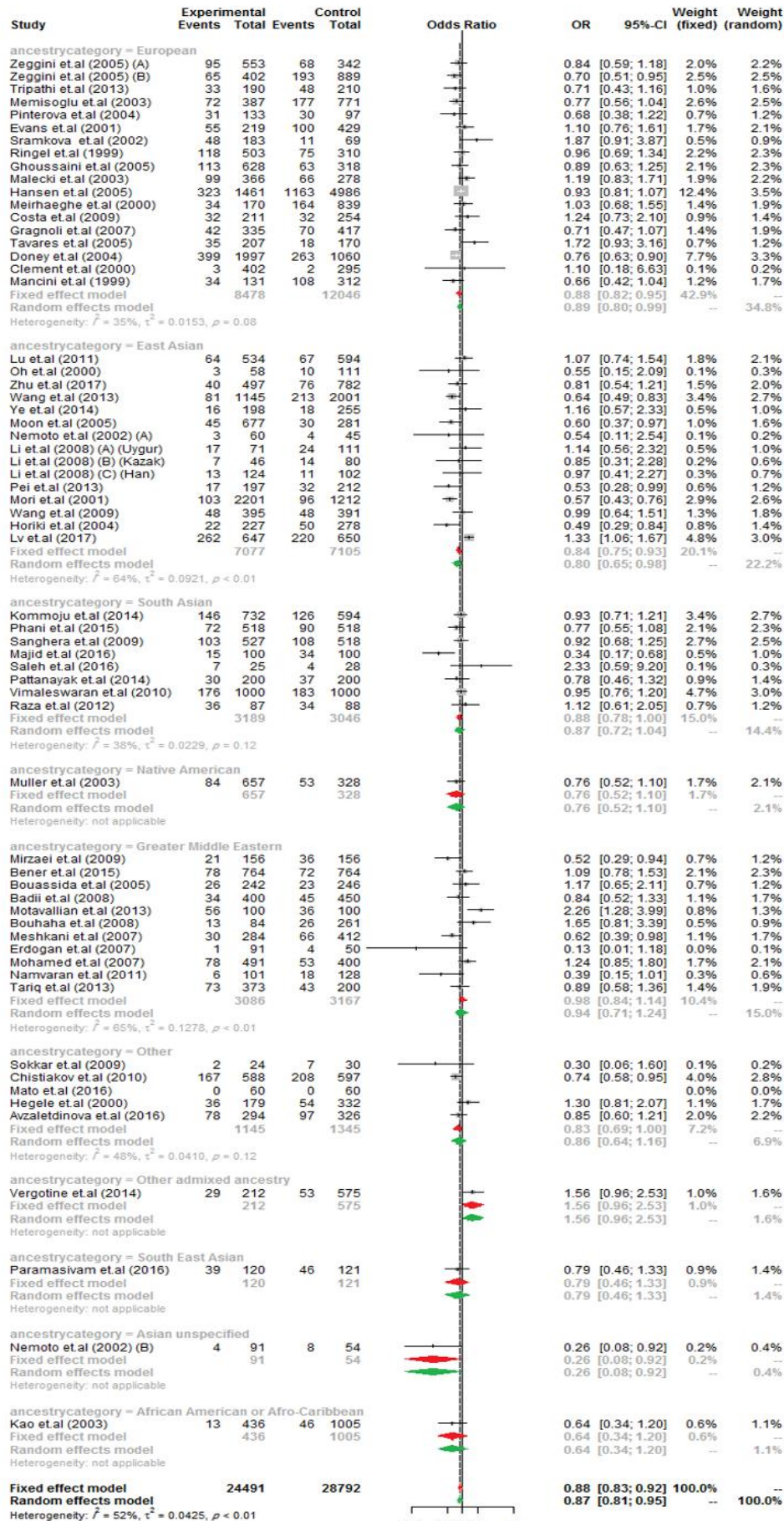


Figure S1. Forests for Pro12Ala polymorphism (rs1801282) and T2DM risk. “A” represents allele (G vs. C); “B” represents homozygote (GG vs. CC); “C” represents heterozygote (CG vs. CC); “D” represents additive (GG vs. CG); “E” represents dominant (CG+GG vs. CC); “F” represents recessive (GG vs. CC+CG); “G” co-dominant model (CG vs. CC+GG). Areas of gray Square stand for the studies-specific weight. Red and green signs represent the pooled ORs and 95% CIs of the overall population with fixed effect and random effects model, respectively. 95% CI = 95% confidence interval, χ^2_n = heterogeneity Q statistic, I^2 = I-squared metric of the heterogeneity, n = degrees of freedom; OR = odds ratio; P = P value of heterogeneity Q test.