

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

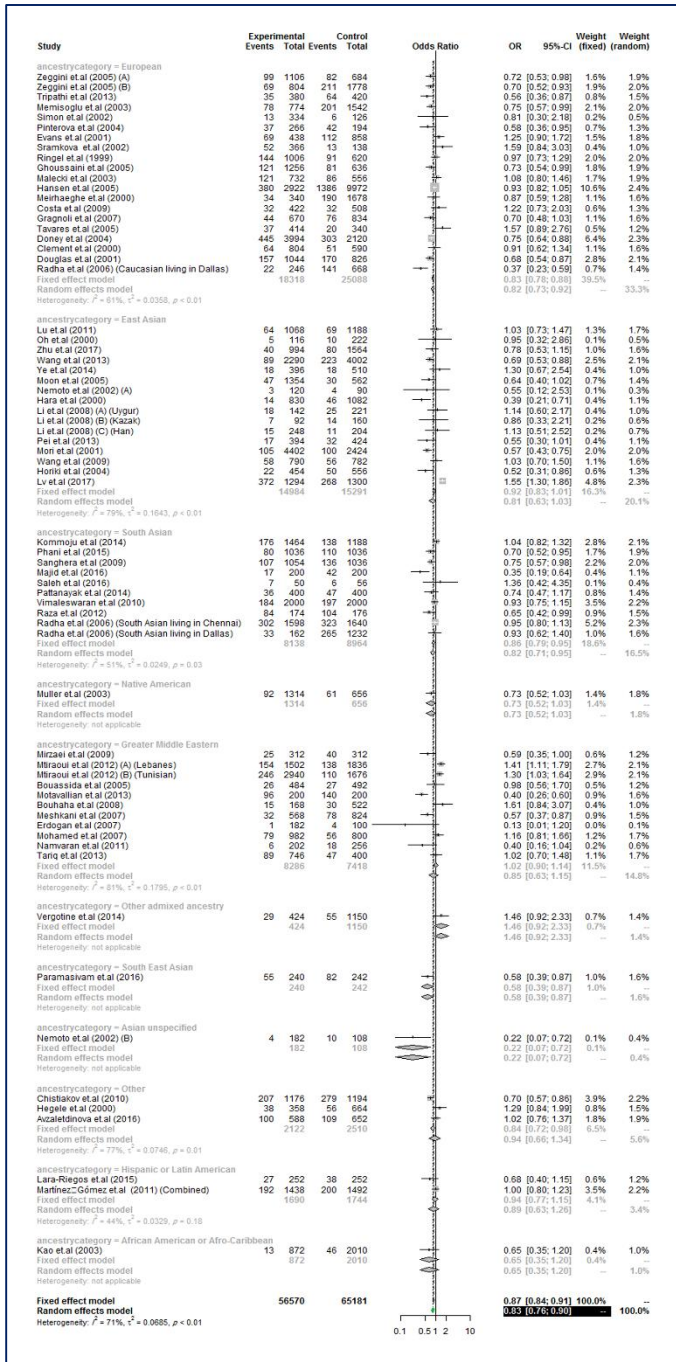
Negar Sarhangi ¹, Farshad Sharifi ², Leila Hashemian ³, Maryam Hassani Doabsari ³, Katayoun Heshmatzad ³, Marzieh Rahbaran ³, Seyed Hamid Jamaldini ³, Hamid Reza Aghaei Meybodi ^{1,4}, Mandana Hasanzad ^{1,3,*}

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

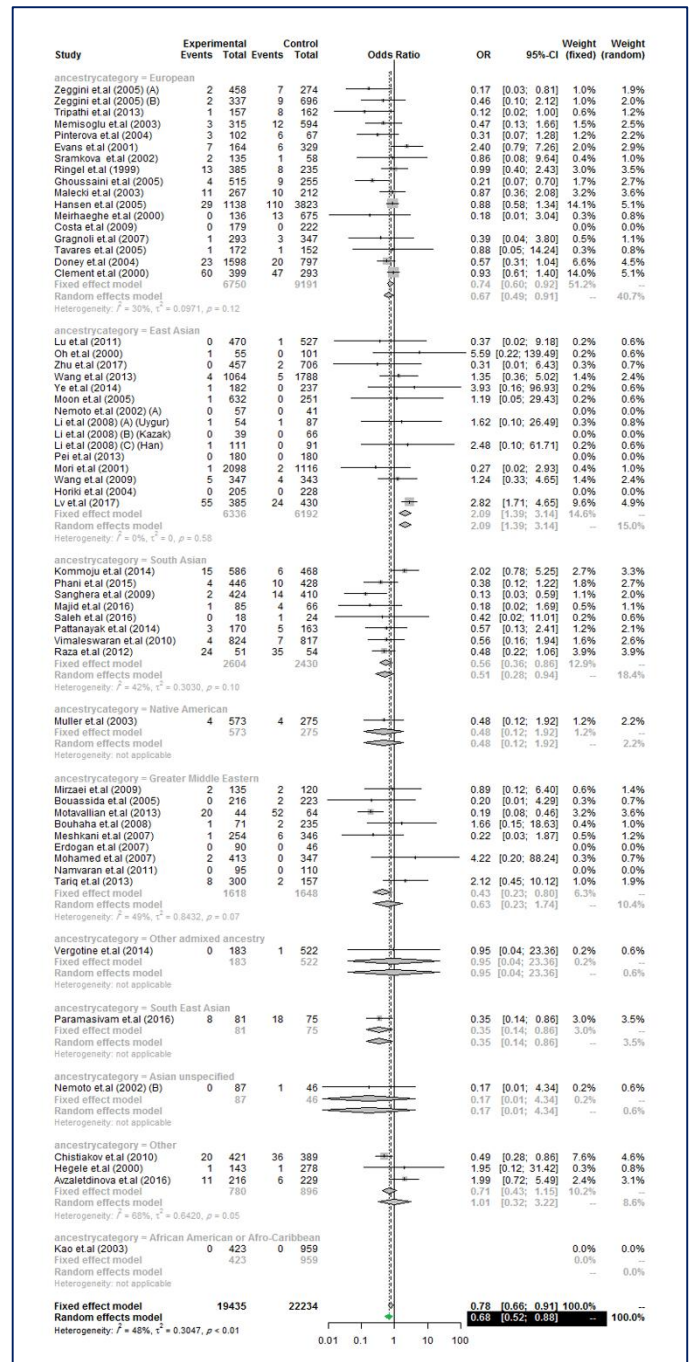
² Elderly Health Research Center, Endocrinology and Metabolism Population Sciences Institute, Tehran University of Medical Sciences, Tehran 1411413137, Iran

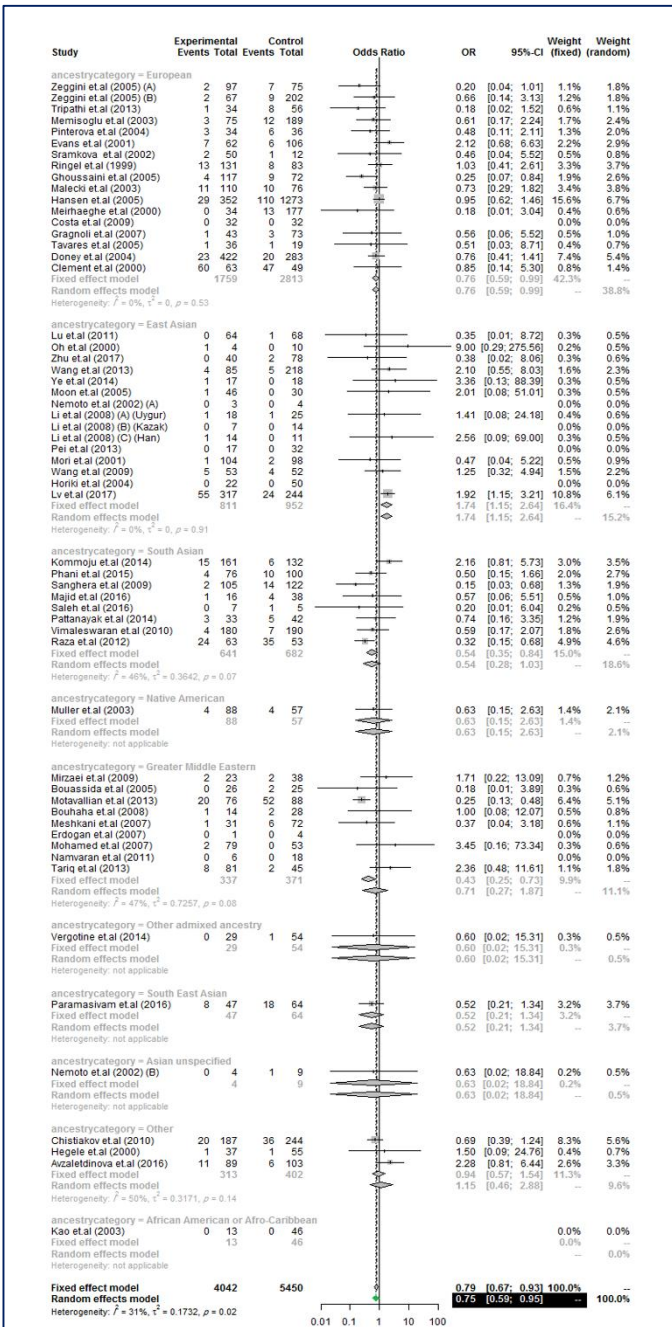
³ Medical Genomics Research Center, Tehran Medical Sciences, Islamic Azad University, Tehran 1916893813, Iran

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

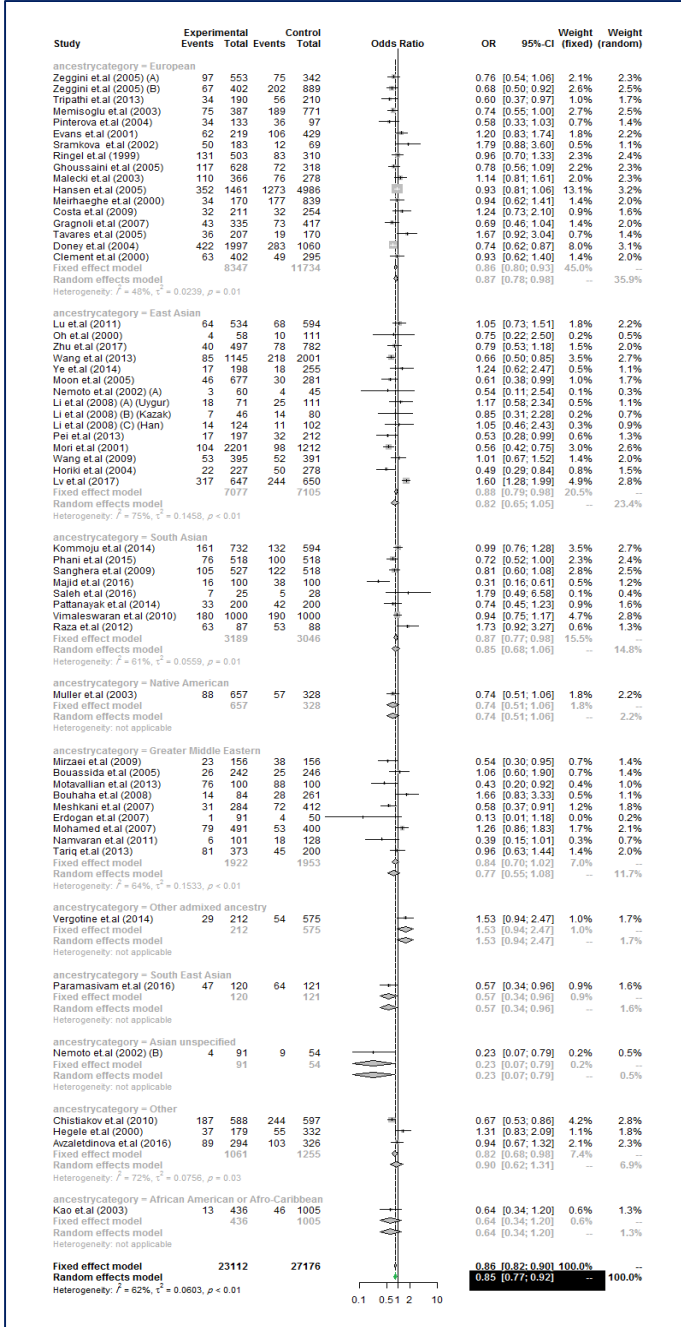


A





D



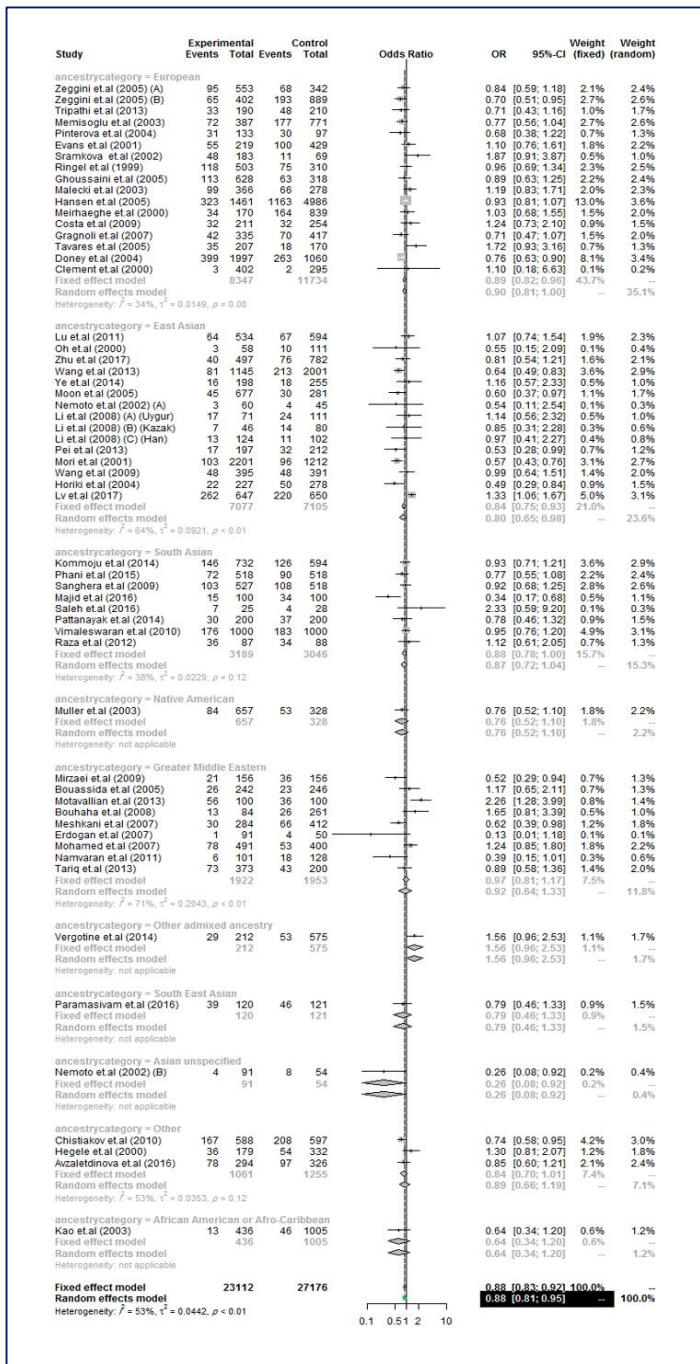


Figure S6. Sensitivity analysis according to studies that did not meet HWE. “A” represents allele (G vs. C); “B” represents homozygote (GG vs. CC); “C” represents heterozygote (CG vs. CC); “D” represents additive (GG vs. CG); “E” represents dominant (CG+GG vs. CC); “F” represents recessive (GG vs. CC+CG); “G” co-dominant model (CG vs. CC+GG). Vertical and horizontal lines represent ORs and the corresponding 95% CIs of each study. Black highlight represents the overall estimates (pooled ORs and 95% CIs) of population with random effects model. 95% CI = 95% confidence interval, OR = odds ratio.