

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

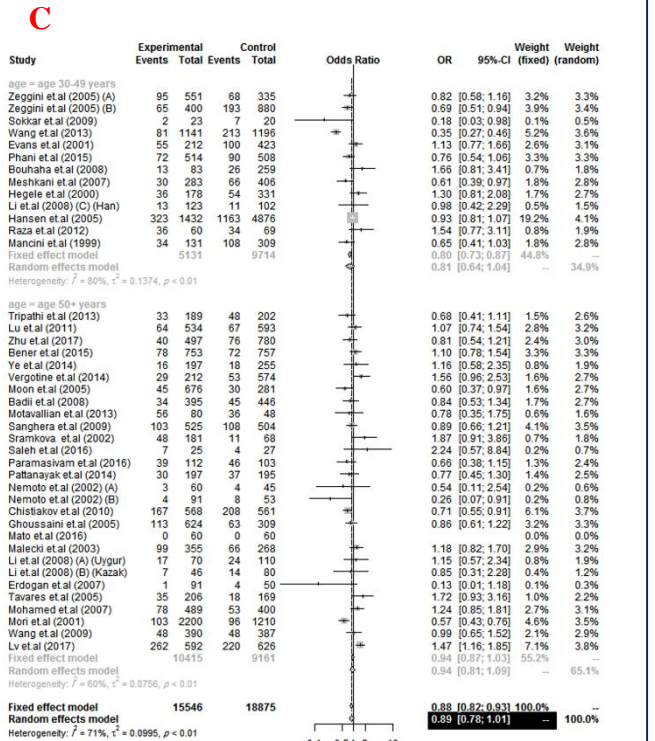
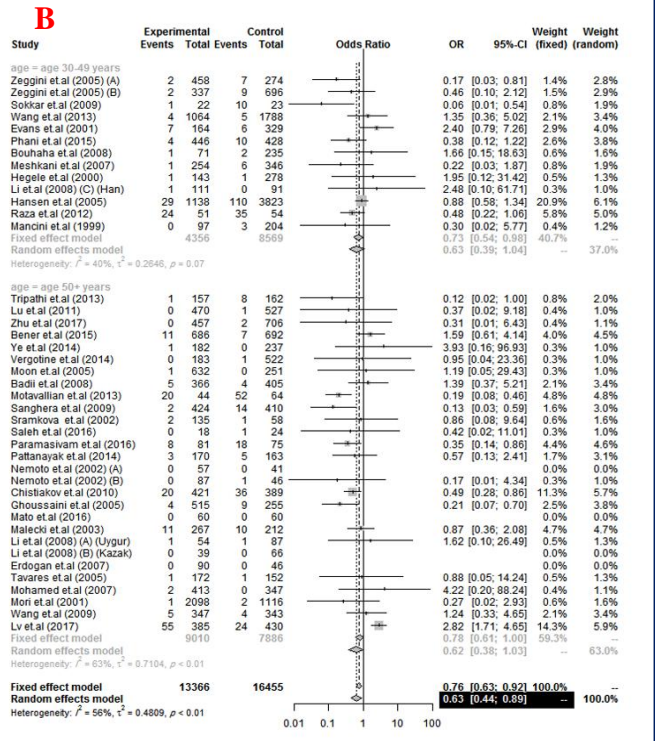
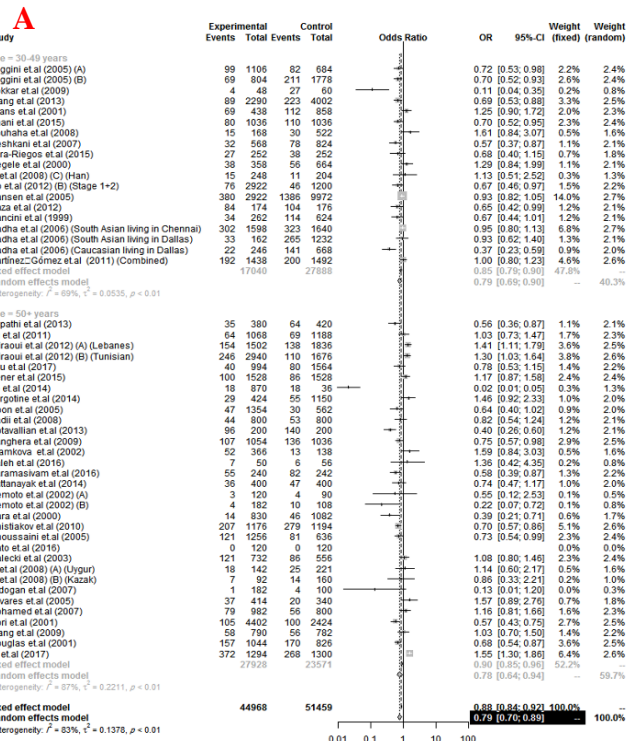
Negar Sarhangi <sup>1</sup>, Farshad Sharifi <sup>2</sup>, Leila Hashemian <sup>3</sup>, Maryam Hassani Doabsari <sup>3</sup>, Katayoun Heshmatzad <sup>3</sup>, Marzieh Rahbaran <sup>3</sup>, Seyed Hamid Jamaldini <sup>3</sup>, Hamid Reza Aghaei Meybodi <sup>1,4</sup>, Mandana Hasanzad <sup>1,3,\*</sup>

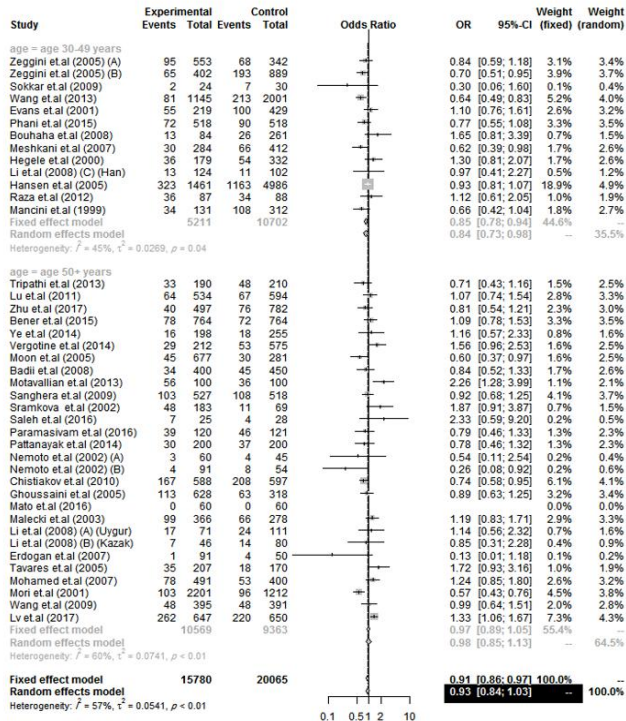
<sup>1</sup> Personalized Medicine Research Center, Endocrinology and Metabolism Clinical Sciences Institute, Tehran University of Medical Sciences, Tehran 1411413137, Iran

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

<sup>3</sup> Medical Genomics Research Center, Tehran Medical Sciences, Islamic Azad University, Tehran 1916893813, Iran

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



**G**

**Figure S3.** Subgroup analysis according to age of participants. “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.