PPARG (Pro12Ala) genetic variant and risk of T2DM: a systematic review and metaanalysis

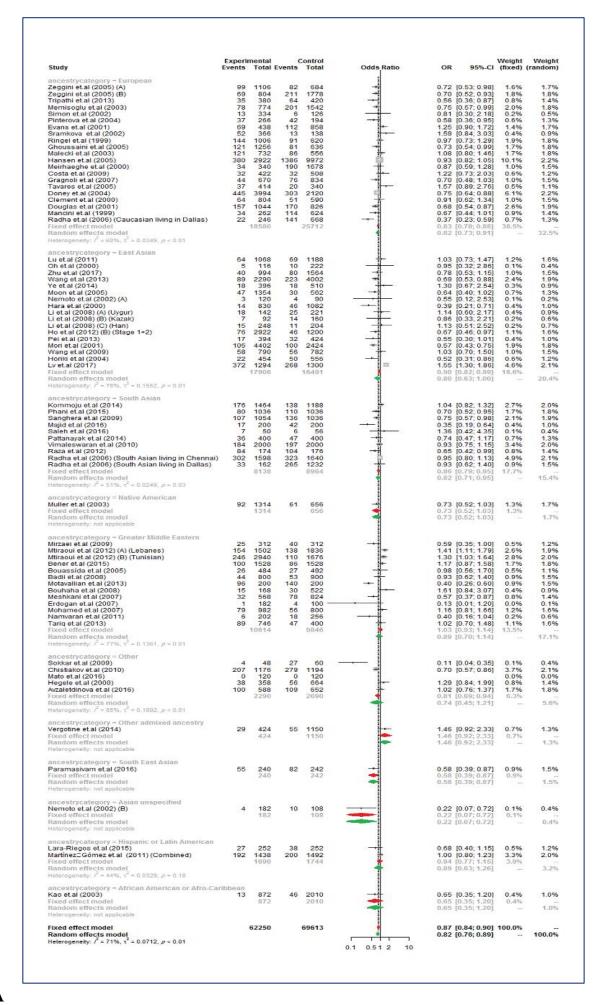
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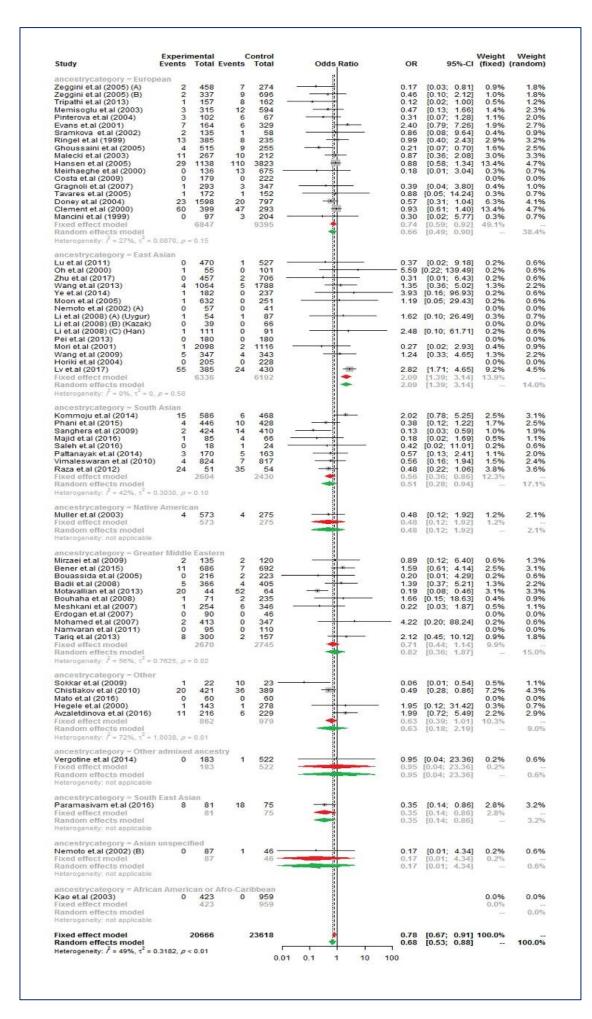
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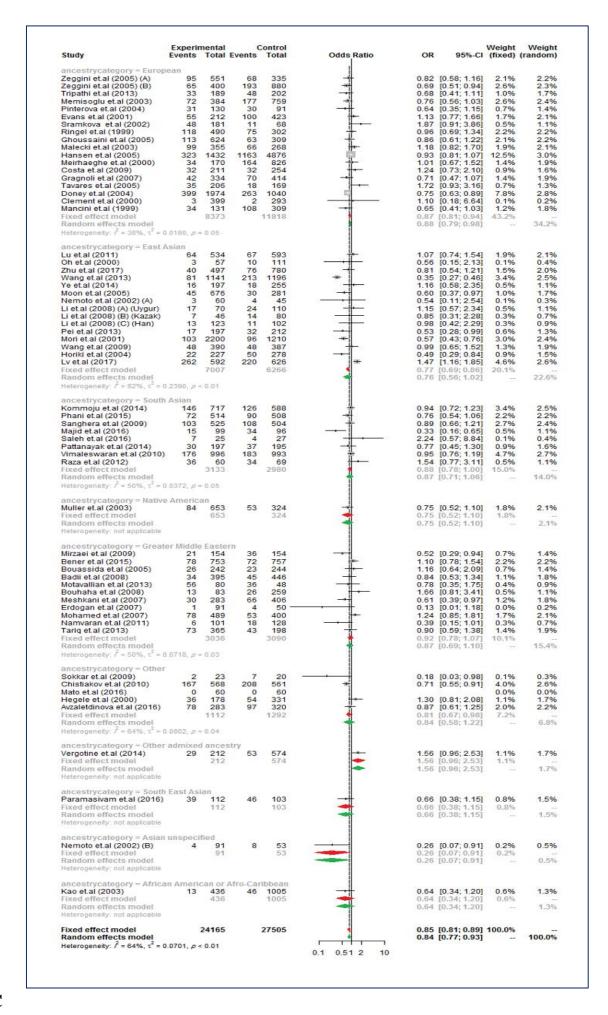
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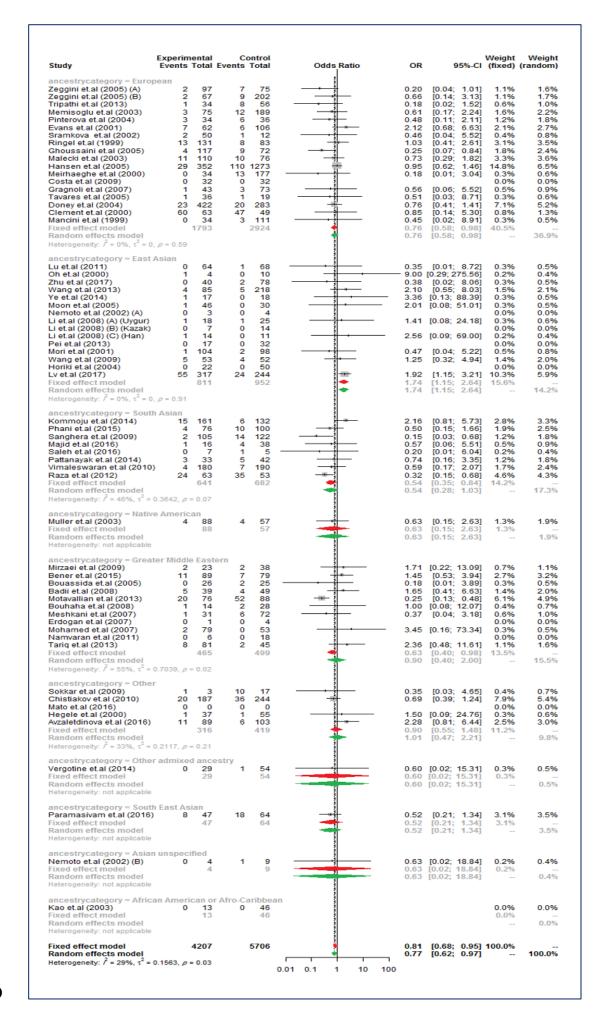
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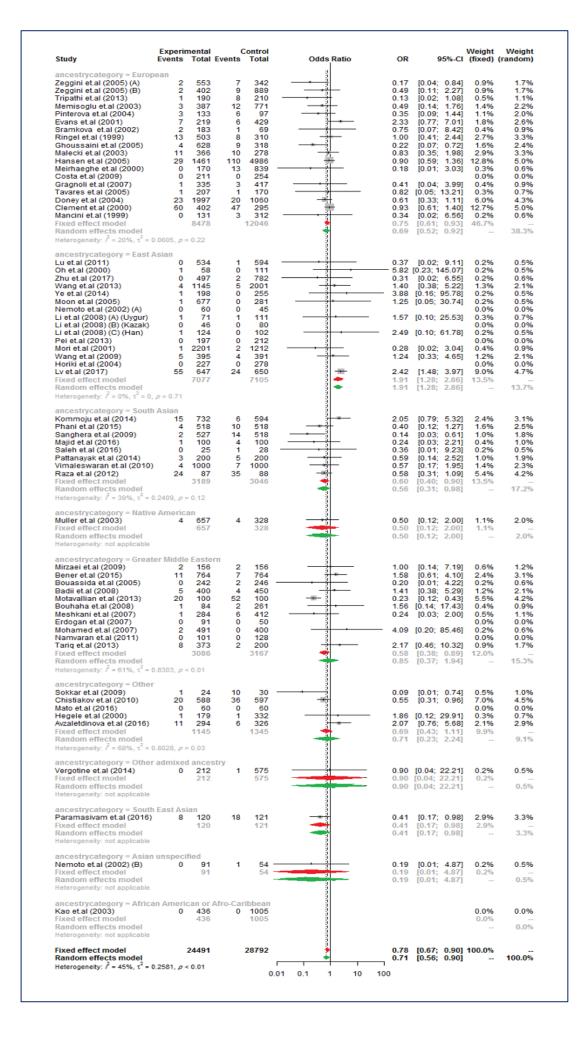








Study	Experin			Total	Odds Ratio	OR	95%-CI	(fixed)	
ancestrycategory = Europ Zeggini et.al (2005) (A)	ean 97	553	75	342	4	0.76	[0.54; 1.06]	2.0%	2.29
Zeggini et.al (2005) (B)	67	402	202	889		0.68	[0.50; 0.92]	2.5%	2.39
Tripathi et.al (2013) Memisoglu et.al (2003)	34 75	190 387	56 189	210 771	-1		[0.37; 0.97]	1.0%	1.69 2.39
Pinterova et.al (2004)	34	133	36	97	 	0.58	[0.33; 1.03]	0.7%	1.49
Evans et al (2001)	62 50	219	106	429	<u>+</u>	1.20	[0.83; 1.74]		1.09
Sramkova et.al (2002) Ringel et.al (1999)	131	503	83	310	1	0.96	[0.88; 3.60] [0.70; 1.33]	0.5% 2.2%	2.29
Ghoussaini et.al (2005)	117	628	72	318	4	0.78	[0.56; 1.09]	2.1%	2.29
Malecki et.al (2003) Hansen et.al (2005)	110 352	366 1461	76 1273	278 4986	III.	0.93	[0.81; 1.61]		3.09
Meirhaeghe et.al (2000)	34	170	177	839	- 	0.94	[0.62; 1.41]	1.4%	1.99
Costa et.al (2009)	32 43	211 335	32 73	254 417	_1-	1.24 0.69	[0.73; 2.10]		1.59
Gragnoli et.al (2007) Tavares et.al (2005)	36	207	19	170	1		[0.92; 3.04]		1.39
Doney et.al (2004)	422	1997	283	1060	=		[0.62; 0.87]	7.6%	2.89
Clement et.al (2000) Mancini et.al (1999)	63 34	402 131	49 111	295 312	-1		[0.62; 1.40]	1.4%	1.99
Fixed effect model		8478		12046	•		[0.79; 0.92]	44.0%	25.41
Random effects model Heterogeneity: $f^2 = 48\%$, $\tau^2 = 0$).0242, p =	0.01			1	0.80	[0.77; 0.96]		35.4
ancestrycategory = East / Lu et.al (2011)	Asian 64	534	68	594	1	1.05	[0.73; 1.51]	1.7%	2.19
Oh et.al (2000)	4	58	10	111		0.75	[0.22; 2.50]	0.2%	0.59
Zhu et.al (2017)	40 85	497 1145	78 218	782 2001	1	0.79	[0.53; 1.18]	1.4% 3.4%	1.99 2.59
Wang et.al (2013) Ye et.al (2014)	17	198	18	255	#-	1.24	[0.50; 0.85] [0.62; 2.47]	0.5%	1.19
Moon et.al (2005)	46	677	30	281		0.61	[0.38; 0.99]	1.0%	1.69
Nemoto et.al (2002) (A) Li et.al (2008) (A) (Uygur)	18	60 71	25	45 111			[0.11; 2.54]		0.39
Li et.al (2008) (B) (Kazak)	7	46	14	80	- 	0.85	[0.31; 2.28]	0.2%	0.69
Li et.al (2008) (C) (Han) Pei et.al (2013)	14	124	11 32	102 212		1.05 0.53	[0.46; 2.43]		1.29
Mori et.al (2001)	104	2201	98	1212	-	0.56	[0.42; 0.75]	2.8%	2.49
Wang et.al (2009) Horiki et.al (2004)	53 22	395 227	52 50	391 278	-1	1.01 0.49	[0.67; 1.52]	1.4%	1.99
Lv et.al (2017)	317	647	244	650		1.60	[1.28; 1.99]	4.7%	2.69
Fixed effect model Random effects model		7077		7105	1		[0.79; 0.98]	19.6%	22.0
Heterogeneity: $f^2 = 75\%$, $\tau^2 = 0$		0.01				3100			
Ancestrycategory = South Kommoju et.al (2014)	161	732	132	594	#		[0.76; 1.28]		2.59
Phani et.al (2015) Sanghera et.al (2009)	76 105	518 527	100	518 518	7		[0.52; 1.00]	2.2%	2.29
Majid et.al (2016)	16	100	38	100		0.31	[0.16; 0.61]	0.5%	1.19
Saleh et.al (2016) Pattanayak et.al (2014)	33	25	5 42	28		1.79 0.74	[0.49; 6.58]		1.59
Vimaleswaran et.al (2010)	180	1000	190	1000	#	0.74	[0.45, 1.23]	4.5%	2.69
Raza et.al (2012)	63	87 3189	53	88	_	1.73	[0.92; 3.27]	0.6%	1.29
Random effects model				3046	4	0.87	[0.77; 0.98] [0.68; 1.06]	14.8%	13.9
Heterogeneity: $f = 61\%$, $\tau^2 = 0$					l				
Muller et.al (2003)	America 88	657	57	328	<u> </u>		[0.51; 1.06]		2.19
Random effects model Heterogeneity: not applicable		657		328			[0.51; 1.06] [0.51; 1.06]	1.7%	2.1
ancestrycategory = Great Mirzaei et.al (2009)	er Middle 23	Easte 156	m 38	156		0.54	[0.30; 0.95]	0.7%	1.39
Bener et.al (2015)	89	764	79	764	+	1.14	[0.83; 1.58]	2.2%	2.29
Bouassida et.al (2005) Badii et.al (2008)	26 39	400	25 49	246 450	1	1.06 0.88	[0.60; 1.90]	0.7% 1.2%	1.89
Motavallian et.al (2013)	76	100	88	100		0.43	[0.20; 0.92]	0.4%	0.99
Bouhaha et.al (2008) Meshkani et.al (2007)	14 31	284	28 72	261 412			[0.83; 3.33]		1.19
Erdogan et.al (2007)	1	91	4	50 —		0.13	[0.01; 1.18]	0.0%	0.19
Mohamed et al (2007) Namvaran et al (2011)	79	491	53 18	400 128			[0.86; 1.83]		0.79
Tariq et al (2013)	81	373	45	200	+	0.96	[0.63; 1.44]	1.3%	1.99
Fixed effect model Random effects model		3086		3167	#	0.91	[0.78; 1.06] [0.64; 1.08]		15.1
Heterogeneity: $f = 60\%$, $\tau^2 = 0$ ancestrycategory = Other		0.01							
Sokkar et.al (2009) Chistiakov et.al (2010)	187	24 588	17 244	30 597		0.11	[0.03; 0.45] [0.53; 0.86]	0.1% 4.1%	0.39
Mato et.al (2016)	0	60	0	60				0.0%	0.09
Hegele et.al (2000) Avzaletdinova et.al (2016)	37 89	179 294	55 103	332 326	#-		[0.83; 2.09] [0.67; 1.32]		1.79
Fixed effect model	09	1145	103	1345	4	0.79	[0.66; 0.95]	7.2%	
Random effects model Heterogeneity: $\hat{f} = 80\%$, $\tau^2 = 0$).1677, p <	0.01			1		[0.47; 1.23]		6.8
ancestrycategory = Other Vergotine et.al (2014)	admixed	ance:	stry 54	575		1.52	[0.94; 2.47]	1.0%	1.69
Fixed effect model	29	212	54	575	-	1.53	[0.94; 2.47]	1.0%	
Random effects model Heterogeneity: not applicable						1.53	[0.94; 2.47]	-	1.6
ancestrycategory = South Paramasivam et.al (2016)	East Asi	ian 120	64	121		0.57	[0.34; 0.96]	0.9%	1.59
Fixed effect model	41	120	04	121	-	0.57	[0.34; 0.96]	0.9%	
Random effects model Heterogeneity: not applicable						0.57	[0.34; 0.96]	N est	1.5
ancestrycategory = Asian					.		10.07.5		
Nemoto et.al (2002) (B) Fixed effect model	4	91	9	54 54			[0.07; 0.79]		0.49
Random effects model Heterogeneity: not applicable		01					[0.07; 0.79]		0.4
ancestrycategory = Africa						agine or			9.70
Kao et.al (2003) Fixed effect model	13	436	46	1005			[0.34; 1.20]	0.6%	1.29
Random effects model		430		.000	-		[0.34; 1.20]		1.2
Heterogeneity: not applicable Fixed effect model		24491		28792		0.86	[0.82; 0.90]	100.0%	
		1			<u> </u>		[0.77; 0.92]		100.0
Random effects model Heterogeneity: $\hat{f} = 63\%$, $\tau^2 = 0$	0000					0.04	[0.77, 0.02]		100.0



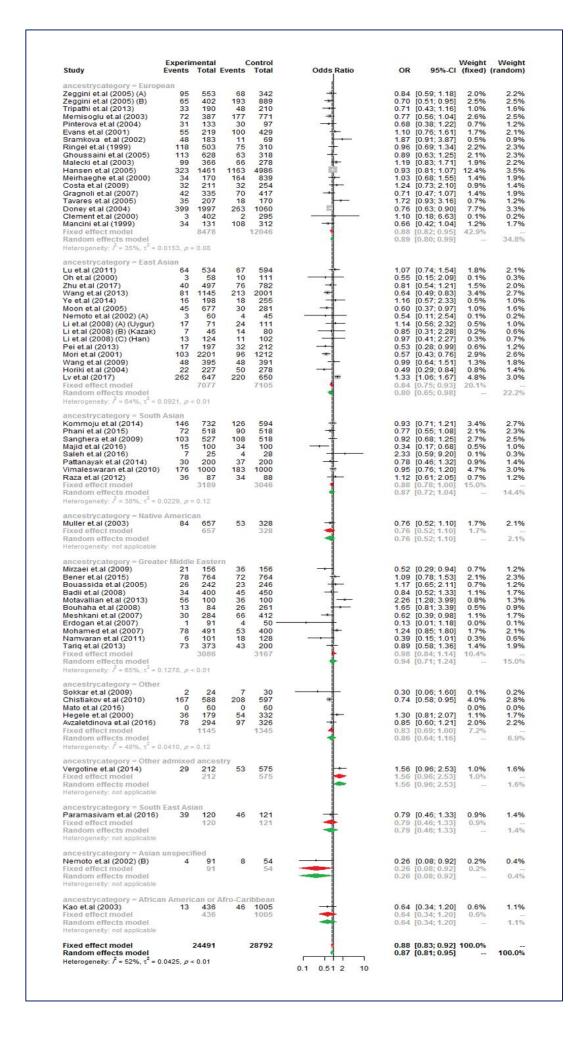


Figure S1. Forests for Pro12Ala polymorphism (rs1801282) and T2DM risk. "A" represents allele (G vs. C); "B" represents homozygote (GG vs. CC); "C" represents heterozygote (CG vs. CC); "D" represents additive (GG vs. CG); "E" represents dominant (CG+GG vs. CC); "F" represents recessive (GG vs. CC+CG); "G" codominant 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, x_n^2 = heterogeneity Q statistic, I^2 = I-squared metric of the heterogeneity, I^2 = I-squared metric of the heterogeneity Q test.