

ESM Table 7. Alternating logistic regression results of T2D for *PAX4* rs10229583 and *TRPS1* rs2737250 SNPs in *de novo* replication of family study in Chinese populations.

Study	N		<i>PAX4</i> rs10229583 (G)					<i>TRPS1</i> rs2737250 (A)						
	Case	Control	Case RAF	Control RAF	OR (95% CI)	$P_{additive}$	P_{het}	I^2	Case RAF	Control RAF	OR (95% CI)	$P_{additive}$	P_{het}	I^2
Hong Kong replication 2	325	368	0.872	0.856	1.22 (0.85, 1.74)	0.2817			0.682	0.704	0.86 (0.68, 1.09)	0.2026		
Shanghai replication 2	657	168	0.824	0.813	1.09 (0.80, 1.49)	0.5757			0.618	0.646	0.82 (0.70, 0.97)	0.0218		
Meta-analysis of family studies in Chinese	982	536			1.15 (0.91, 1.45)	0.2590	0.6567	0.000			0.83 (0.73, 0.96)	0.0091	0.7859	0.000
Meta-analysis of studies in stage 1 and 2 in Chinese	11067	7929			1.18 (1.11, 1.25)	2.6×10^{-8}	0.0839	0.596			1.07 (1.02, 1.12)	0.0034	1.5×10^{-5}	0.855

Nearest Entrez genes within 250 kb. $P_{additive}$ and P_{het} represents P values from alternating logistic regression with adjustment of sex and age under additive genetic model or meta-analysis under fixed effect models and test of heterogeneity, respectively. Risk allele of genetic variant is indicated within the parentheses. OR, odds ratios are reported with respect to the risk allele in stage 1; RAF, risk allele frequency.