

ESM Table 11 Comparison of effect size and discriminative ability of the GRSs for risk of diabetes

GRS	Weights	AUC	<i>p</i>
GRS-T(52SNPs)			
	Unweighted	0.574[0.567-0.580]	ref
	AGEN-T2D	0.582[0.575-0.589]	6.8x10 ⁻⁵
	DIAGRAMv3	0.584[0.577-0.591]	1.4x10 ⁻⁷
	MetaboChip	0.588[0.581-0.595]	6.4x10 ⁻¹²
	TransEthnic	0.590[0.583-0.597]	3.6x10 ⁻²⁰
	TransEthnic+CKB	0.593[0.586-0.600]	4.3x10 ⁻²³
	TransEthnic+CKB (1000-fold cross-validation)	0.591[0.584-0.598]	1.8x10 ⁻¹⁹
GRS-BC (25 SNPs)			
	Unweighted	0.569[0.562-0.576]	ref
	AGEN-T2D	0.576[0.570-0.583]	7.6x10 ⁻³
	DIAGRAMv3	0.577[0.570-0.584]	7.2x10 ⁻⁶
	MetaboChip	0.580[0.573-0.587]	2.1x10 ⁻⁹
	TransEthnic	0.581[0.574-0.588]	2.0x10 ⁻¹⁴
	TransEthnic+CKB	0.583[0.576-0.590]	3.6x10 ⁻¹⁵
	TransEthnic+CKB (1000-fold cross-validation)	0.582[0.575-0.589]	1.5x10 ⁻¹³
GRS-IR (7 SNPs)			
	Unweighted	0.521[0.514-0.527]	ref
	AGEN-T2D	0.521[0.514-0.528]	0.996
	DIAGRAMv3	0.518[0.511-0.525]	0.187
	MetaboChip	0.520[0.513-0.527]	0.749
	TransEthnic	0.520[0.514-0.527]	0.907
	TransEthnic+CKB	0.522[0.515-0.529]	0.176
	TransEthnic+CKB (1000-fold cross-validation)	0.520[0.513-0.527]	0.343

The range of all GRSs were rescaled in the range of unweighted GRS-T
P-value derived from DeLong test compared to unweighted GRS model