

Supplementary Table S2: Discriminatory performance of models

Author, year	AUROC (95% CI) in development population	AUROC (95% CI) in bootstrap or random split-sample	AUROC (95% CI) in external population or non-random split sample
Genomic risk factors alone			
Dunlop 2013a			0.57
Frampton 2016			0.63*
Hosono 2016a			0.60
Ibanez-Sanz 2017a			0.56 (0.54 to 0.58)
Jenkins 2016			0.63*
Smith 2018a			0.57 (0.55-0.58) 0.56 (0.55-0.58)
Wang 2013	0.77	0.724	
Xin 2018a	Simple count 0.60 (0.59–0.61) Weighted (LR) 0.60 (0.59-0.62) Weighted (OR) 0.60 (0.58-0.62)	Simple count 0.60 (0.59–0.61) Weighted (LR) 0.61 (0.60-0.62) Weighted (OR) 0.60 (0.59-0.61)	Simple count 0.60 (0.56–0.64) Weighted (LR) 0.59 (0.54-0.63) Weighted (OR) 0.60 (0.56-0.64)
Genomic plus phenotypic risk factors			
Abe 2017		0.64	0.57
Dunlop 2013b	0.62 (0.58-0.74)	0.59	0.57 and 0.56
Hosono 2016b	0.7167		0.64
Hsu 2015			Male 0.59 (0.54-0.64) Female 0.56 (0.51-0.61)
Ibanez-Sanz 2017b	0.65	0.63 (0.60-0.66)	
Iwasaki 2017		0.66 (0.61-0.74)	
Jeon 2018 (female)		0.62 (0.61-0.63)	
Jeon 2018 (male)		0.63 (0.62–0.64)	
Jo 2012a (female)	Simple count 0.65 (0.62-0.6802) Weighted 0.65 (0.61-0.67)	Simple count 0.60 (0.56-0.64) Weighted 0.58 (0.55-0.62)	
Jo 2012b (male)	Simple count 0.73 (0.68-0.77) Weighted 0.72 (0.68-0.76)	Simple count 0.70 (0.65-0.74) Weighted 0.69 (0.64-0.73)	
Jung 2015	0.74 (0.70–0.78) **		
Jung 2019	0.93		
Li 2015	Simple count 0.58 (0.57-0.60) Weighted 0.59 (0.57-0.61)		
Procopciuc 2017	0.90 (0.86-0.93)		
Shiao 2018		0.85	
Smith 2018b			0.67 (0.65-0.68)
Smith 2018c			0.69 (0.67-0.70)
Weigl 2018	0.67		
Xin 2018b	0.61	0.61	0.61
Yarnall 2013			0.63*

AUROC – area under the receiver operating characteristic curve, * Simulated populations ** Unclear whether this is simple or weighted genetic risk score, LR – logistic regression; OR – Odds ratio