ESM Table 7 Concordance of T2D risk alleles

	CKB (56 variants overall)				East Asians: Meta-analysis of CKB and AGEN-T2D (55 variants overall)			
	<sup>a</sup> EA GWAS (15 loci)	<sup>b</sup> Others Ancestries (41 loci)	<sup>c</sup> Total (56)	Binomial test P (CKB into Total)	<sup>a</sup> EA GWAS (15 loci)	<sup>b</sup> Others Ancestries (40 loci)	<sup>c</sup> Total (55)	Binomial test P (CKB+AGEN-T2D into Other Ancestries)
Directionally consistent	12	36	48	$48/56, P = 2.34 \times 10^{-8}$	14	37	51	$37/40, P = 9.73 \times 10^{-9}$
Nominal Significant	9	26	35	-	12	25	37	-
Significant after correction for multiple-testing using the Holm-Bonferroni procedure	6	13	19	-	11	18	29	-
Genome-wide significant	1	4	5	-	9	10	19	-

Number of alleles are presented as <sup>a</sup> Reported in East Asians + <sup>b</sup> Others = <sup>c</sup> Total