

Table S4 The mean correlation between true and predicted genotypes, as calculated in the within-population analysis of the UK dataset

a) Per individual

Chromosome	Number of SNPs¹	bpEQ	bpMAF	lduMAF
ECA1	384	0.46 (0.14,0.89)	0.49 (0.20,0.91)	0.53 (0.22,0.89)
	768	0.64 (0.36,0.93)	0.66 (0.38,0.93)	0.69 (0.37,0.94)
	1K	0.70 (0.41,0.93)	0.78 (0.51,0.96)	0.75 (0.47,0.98)
	2K	0.86 (0.53,0.99)	0.88 (0.62,0.98)	0.85 (0.52,0.99)
	3K	0.92 (0.59,0.99)	0.94 (0.60,1.00)	0.88 (0.48,0.99)
	6K	0.97 (0.73,1.00)	0.97 (0.71,1.00)	0.93 (0.61,1.00)
ECA10	384	0.46 (0.11,0.98)	0.43 (0.04,0.98)	0.42 (0.00,0.94)
	768	0.58 (0.20,0.97)	0.57 (0.04,0.98)	0.59 (0.26,0.99)
	1K	0.67 (0.32,0.98)	0.68 (0.29,0.97)	0.66 (0.14,0.99)
	2K	0.82 (0.56,0.98)	0.85 (0.59,0.98)	0.86 (0.42,1.00)
	3K	0.89 (0.70,1.00)	0.91 (0.76,1.00)	0.91 (0.62,1.00)
	6K	0.96 (0.80,1.00)	0.97 (0.87,1.00)	0.95 (0.76,1.00)
ECA20	384	0.37 (0.07,0.89)	0.36 (-0.01,0.83)	0.37 (-0.06,0.84)
	768	0.51 (0.13,0.93)	0.53 (0.09,0.92)	0.54 (0.15,0.91)
	1K	0.55 (0.12,0.93)	0.63 (0.27,0.99)	0.62 (0.24,0.97)
	2K	0.76 (0.30,0.98)	0.80 (0.42,0.99)	0.82 (0.52,0.99)
	3K	0.87 (0.58,0.99)	0.89 (0.63,0.99)	0.89 (0.46,1.00)
	6K	0.95 (0.79,1.00)	0.96 (0.85,1.00)	0.93 (0.72,1.00)
ECA26	384	0.38 (-0.04,0.94)	0.40 (0.01,0.93)	0.44 (-0.02,0.98)
	768	0.57 (0.17,0.97)	0.60 (0.16,0.94)	0.61 (0.13,0.97)
	1K	0.60 (0.14, 0.95)	0.67 (0.25,0.98)	0.70 (0.30,1.00)
	2K	0.76 (0.29,1.00)	0.81 (0.31,1.00)	0.84 (0.16,1.00)
	3K	0.90 (0.36,1.00)	0.90 (0.62,1.00)	0.90 (0.54,1.00)
	6K	0.96 (0.78,1.00)	0.96 (0.79,1.00)	0.91 (0.49,1.00)

Mean correlation between true and predicted genotypes per individual, with minimum and maximum values in brackets; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.

b) Per SNP

Chromosome	Number of SNPs ¹	bpEQ	bpMAF	lduMAF
ECA1	384	0.30 (-0.17,1.00)	0.32 (-0.14,1.00)	0.36 (-0.08,1.00)
	768	0.52 (-0.08,1.00)	0.53 (-0.06,1.00)	0.55 (-0.05,1.00)
	1K	0.60 (-0.04,1.00)	0.67 (-0.05,1.00)	0.64 (-0.05,1.00)
	2K	0.81 (-0.04,1.00)	0.83 (-0.02,1.00)	0.79 (-0.02,1.00)
	3K	0.89 (-0.01,1.00)	0.90 (-0.03,1.00)	0.83 (-0.02,1.00)
	6K	0.95 (0.25,1.00)	0.96 (0.49,1.00)	0.90 (-0.01,1.00)
ECA10	384	0.31 (-0.13,1.00)	0.28 (-0.14,1.00)	0.26 (-0.09,1.00)
	768	0.46 (-0.10,1.00)	0.45 (-0.09,1.00)	0.46 (-0.08,1.00)
	1K	0.59 (-0.06,1.00)	0.58 (-0.08,1.00)	0.55 (-0.04,1.00)
	2K	0.76 (-0.04,1.00)	0.79 (-0.06,1.00)	0.80 (-0.02,1.00)
	3K	0.85 (0.20,1.00)	0.88 (-0.01,1.00)	0.87 (0.13, 1.00)
	6K	0.94 (0.34,1.00)	0.95 (0.34,1.00)	0.93 (-0.01, 1.00)
ECA20	384	0.24 (-0.16,1.00)	0.22 (-0.15,1.00)	0.23 (-0.15,1.00)
	768	0.40 (-0.08,1.00)	0.41 (-0.06,1.00)	0.43 (-0.04,1.00)
	1K	0.46 (-0.06,1.00)	0.54 (-0.03,1.00)	0.52 (-0.03,1.00)
	2K	0.69 (-0.06,1.00)	0.75 (-0.02,1.00)	0.76 (-0.04,1.00)
	3K	0.83 (0.06,1.00)	0.86 (-0.03,1.00)	0.86 (0.17,1.00)
	6K	0.93 (0.34,1.00)	0.94 (0.23,1.00)	0.92 (0.40,1.00)
ECA26	384	0.20 (-0.17,1.00)	0.23 (-0.16,1.00)	0.27 (-0.13,1.00)
	768	0.44 (-0.03,1.00)	0.46 (-0.04,1.00)	0.47 (-0.03,1.00)
	1K	0.48 (-0.04,1.00)	0.54 (-0.03,1.00)	0.56 (-0.06,1.00)
	2K	0.67 (-0.03,1.00)	0.74 (-0.02,1.00)	0.76 (-0.04,1.00)
	3K	0.86 (-0.03,1.00)	0.85 (-0.01,1.00)	0.85 (0.21,1.00)
	6K	0.94 (0.50,1.00)	0.95 (0.69,1.00)	0.88 (-0.01,1.00)

Mean correlation between true and predicted genotypes per SNP, with minimum and maximum values in brackets; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.