

Table S3 Properties of low density panel SNPs, as calculated in the within-population analysis of the UK dataset

a) ECA1

Number of SNPs¹	Method	Mean (SD) MAF	Mean (SD) distance between SNPs (Mb)
384	bpEQ	0.22 (0.13)	6.40 (0.09)
	bpMAF	0.25 (0.10)	6.40 (0.66)
	lduMAF	0.44 (0.06)	6.40 (2.41)
768	bpEQ	0.25 (0.15)	3.14 (0.09)
	bpMAF	0.31 (0.13)	3.14 (0.57)
	lduMAF	0.45 (0.04)	3.14 (1.65)
1K	bpEQ	0.22 (0.14)	2.41 (0.07)
	bpMAF	0.39 (0.08)	2.38 (0.61)
	lduMAF	0.45 (0.04)	2.38 (1.42)
2K	bpEQ	0.23 (0.14)	1.19 (0.06)
	bpMAF	0.28 (0.11)	1.19 (0.30)
	lduMAF	0.46 (0.04)	1.19 (1.19)
3K	bpEQ	0.23 (0.14)	0.79 (0.06)
	bpMAF	0.30 (0.12)	0.79 (0.23)
	lduMAF	0.46 (0.03)	0.79 (0.92)
6K	bpEQ	0.23 (0.14)	0.39 (0.07)
	bpMAF	0.29 (0.11)	0.39 (0.17)
	lduMAF	0.43 (0.05)	0.39 (0.63)

Properties of low density panel SNPs for ECA1 selected using three methods, as calculated in the within-population analysis of the UK dataset; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.

b) ECA10

Number of SNPs¹	Method	Mean (SD) MAF	Mean (SD) distance between SNPs (Mb)
384	bpEQ	0.25 (0.16)	6.46 (0.11)
	bpMAF	0.29 (0.14)	6.46 (0.17)
	lduMAF	0.43 (0.10)	6.45 (2.51)
768	bpEQ	0.22 (0.14)	3.23 (0.08)
	bpMAF	0.25 (0.12)	3.23 (0.30)
	lduMAF	0.44 (0.07)	3.23 (2.16)
1K	bpEQ	0.26 (0.16)	2.47 (0.06)
	bpMAF	0.33 (0.12)	2.47 (0.28)
	lduMAF	0.44 (0.07)	2.47 (1.89)
2K	bpEQ	0.24 (0.14)	1.20 (0.06)
	bpMAF	0.29 (0.11)	1.20 (0.20)
	lduMAF	0.46 (0.05)	1.20 (0.95)
3K	bpEQ	0.25 (0.13)	0.80 (0.06)
	bpMAF	0.30 (0.12)	0.80 (0.16)
	lduMAF	0.47 (0.04)	0.80 (0.75)
6K	bpEQ	0.26 (0.14)	0.40 (0.07)
	bpMAF	0.31 (0.11)	0.40 (0.10)
	lduMAF	0.46 (0.04)	0.40 (0.44)

Properties of low density panel SNPs for ECA10 selected using three methods, as calculated in the within-population analysis of the UK dataset; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.

c) ECA20

Number of SNPs¹	Method	Mean (SD) MAF	Mean (SD) distance between SNPs (Mb)
384	bpEQ	0.28 (0.13)	7.06 (0.21)
	bpMAF	0.33 (0.12)	7.06 (0.09)
	lduMAF	0.44 (0.09)	7.06 (2.20)
768	bpEQ	0.26 (0.15)	3.18 (0.16)
	bpMAF	0.29 (0.11)	3.18 (0.12)
	lduMAF	0.46 (0.06)	3.18 (1.25)
1K	bpEQ	0.21 (0.13)	2.44 (0.14)
	bpMAF	0.40 (0.08)	2.44 (0.34)
	lduMAF	0.46 (0.05)	2.44 (1.12)
2K	bpEQ	0.24 (0.14)	1.20 (0.11)
	bpMAF	0.29 (0.11)	1.20 (0.18)
	lduMAF	0.46 (0.04)	1.20 (0.62)
3K	bpEQ	0.26 (0.14)	0.79 (0.10)
	bpMAF	0.30 (0.11)	0.79 (0.14)
	lduMAF	0.47 (0.04)	0.79 (0.53)
6K	bpEQ	0.25 (0.14)	0.40 (0.06)
	bpMAF	0.29 (0.11)	0.39 (0.10)
	lduMAF	0.46 (0.03)	0.39 (0.41)

Properties of low density panel SNPs for ECA20 selected using three methods, as calculated in the within-population analysis of the UK dataset; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.

d) ECA26

Number of SNPs¹	Method	Mean (SD) MAF	Mean (SD) distance between SNPs (Mb)
384	bpEQ	0.28 (0.16)	6.89 (0.16)
	bpMAF	0.30 (0.13)	6.89 (0.05)
	lduMAF	0.47 (0.02)	6.89 (1.99)
768	bpEQ	0.27 (0.15)	3.18 (0.14)
	bpMAF	0.36 (0.12)	3.18 (0.17)
	lduMAF	0.47 (0.02)	3.18 (1.34)
1K	bpEQ	0.27 (0.15)	2.43 (0.16)
	bpMAF	0.45 (0.03)	2.43 (0.23)
	lduMAF	0.47 (0.05)	2.42 (1.39)
2K	bpEQ	0.28 (0.16)	1.22 (0.12)
	bpMAF	0.34 (0.13)	1.22 (0.13)
	lduMAF	0.47 (0.02)	1.22 (0.61)
3K	bpEQ	0.30 (0.14)	0.79 (0.08)
	bpMAF	0.33 (0.13)	0.79 (0.12)
	lduMAF	0.47 (0.02)	0.79 (0.59)
6K	bpEQ	0.28 (0.15)	0.40 (0.07)
	bpMAF	0.31 (0.12)	0.39 (0.09)
	lduMAF	0.47 (0.02)	0.39 (0.40)

Properties of low density panel SNPs for ECA26 selected using three methods, as calculated in the within-population analysis of the UK dataset; ¹total number of SNPs that would be on a genome-wide LDP of equivalent density.