(b) After error

Concordant pairs — Discordant pairs (nearest neighbours) — Discordant pairs (random selection)

Simulated haplotypes / Phased haplotypes

Inferred breakpoint distance (y-axis) vs True breakpoint distance (x-axis)

Concordant pairs, Simulated haplotypes: Pearson's $r^2 = 0.993$, Spearman's $r_S = 0.963$, RMSLE = 0.252

Discordant pairs (nearest neighbours), Simulated haplotypes: Pearson's $r^2 = 0.094$, Spearman's $r_S = 0.234$, RMSLE = 2.020

Discordant pairs (random selection), Simulated haplotypes: Pearson's $r^2 = 0.265$, Spearman's $r_S = 0.160$, RMSLE = 2.106

Concordant pairs, Phased haplotypes: Pearson's $r^2 = 0.475$, Spearman's $r_S = 0.933$, RMSLE = 0.349

Discordant pairs (nearest neighbours), Phased haplotypes: Pearson's $r^2 = 0.403$, Spearman's $r_S = 0.237$, RMSLE = 2.008

Discordant pairs (random selection), Phased haplotypes: Pearson's $r^2 = 0.266$, Spearman's $r_S = 0.159$, RMSLE = 2.105