



Additional file 4. Simulations depicting the effects of violating assumptions made by COIL. Horizontal axes represent true COI, vertical axes represent COIL maximum *a posteriori* estimates of COI. A total of 100 simulations were carried out for each COI level, with correlations between assays or strains defined as the probability that two non-independent Bernoulli trials yield a matching outcome. **a)** A simulation of 96 SNPs, MAF = 0.4, no correlation between SNP alleles or between strains occurring within mixed infections. **b)** A simulation of 96 SNPs, MAF = 0.4, correlation between SNP alleles = 0.4, no correlation between strains. COI predictions are skewed above or below the true COI. **c)** A simulation of 96 SNPs, MAF = 0.4, no correlation between SNP alleles, correlation between strains = 0.4. COI predictions are skewed below the true COI.