

Supplementary Table 1. Sampling variances (V) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci, and sample sizes (N)^a

p	q	N	$V(\hat{D}') / V(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	0.0276 / 0.0196	0.0206 / 0.0152	0.0088 / 0.0073	0.0270 / 0.0193	0.0209 / 0.0154	0.0086 / 0.0073
		100	0.0123 / 0.0097	0.0096 / 0.0076	0.0044 / 0.0036	0.0122 / 0.0096	0.0097 / 0.0076	0.0044 / 0.0036
		200	0.0057 / 0.0048	0.0046 / 0.0037	0.0022 / 0.0018	0.0058 / 0.0049	0.0047 / 0.0038	0.0023 / 0.0018
		400	0.0027 / 0.0024	0.0023 / 0.0019	0.0011 / 0.0009	0.0027 / 0.0024	0.0022 / 0.0019	0.0011 / 0.0009
0.7		50	0.0520 / 0.0199	0.0428 / 0.0170	0.0225 / 0.0117	0.0522 / 0.0200	0.0429 / 0.0170	0.0223 / 0.0116
		100	0.0243 / 0.0098	0.0205 / 0.0083	0.0111 / 0.0057	0.0242 / 0.0097	0.0207 / 0.0085	0.0111 / 0.0057
		200	0.0119 / 0.0049	0.0101 / 0.0042	0.0055 / 0.0028	0.0118 / 0.0049	0.0102 / 0.0042	0.0055 / 0.0028
		400	0.0058 / 0.0024	0.0050 / 0.0021	0.0027 / 0.0014	0.0059 / 0.0024	0.0050 / 0.0021	0.0028 / 0.0014
0.9		50	0.2870 / 0.0199	0.1663 / 0.0167	0.0785 / 0.0108	0.2111 / 0.0197	0.1652 / 0.0167	0.0787 / 0.0109
		100	0.0997 / 0.0098	0.0780 / 0.0082	0.0385 / 0.0056	0.1006 / 0.0099	0.0789 / 0.0084	0.0386 / 0.0057
		200	0.0467 / 0.0049	0.0365 / 0.0041	0.0181 / 0.0028	0.0461 / 0.0049	0.0370 / 0.0042	0.0184 / 0.0028

		400	0.0224 / 0.0024	0.0180 / 0.0021	0.0090 / 0.0014	0.0225 / 0.0024	0.0179 / 0.0021	0.0090 / 0.0014
0.7	0.7	50	0.0851 / 0.0187	0.0799 / 0.0149	0.0406 / 0.0096	0.0408 / 0.0221	0.0257 / 0.0186	0.0105 / 0.0090
		100	0.0437 / 0.0093	0.0404 / 0.0074	0.0197 / 0.0047	0.0151 / 0.0109	0.0117 / 0.0091	0.0053 / 0.0044
		200	0.0229 / 0.0046	0.0199 / 0.0037	0.0098 / 0.0023	0.0065 / 0.0054	0.0055 / 0.0045	0.0027 / 0.0022
		400	0.0123 / 0.0023	0.0098 / 0.0018	0.0048 / 0.0012	0.0030 / 0.0026	0.0027 / 0.0022	0.0013 / 0.0011
0.9		50	0.2581 / 0.0180	0.2196 / 0.0133	0.1165 / 0.0075	0.2166 / 0.0239	0.1358 / 0.0239	0.0573 / 0.0178
		100	0.1351 / 0.0089	0.1236 / 0.0066	0.0648 / 0.0038	0.0861 / 0.0120	0.0520 / 0.0120	0.0260 / 0.0091
		200	0.0702 / 0.0044	0.0656 / 0.0033	0.0315 / 0.0019	0.0312 / 0.0059	0.0226 / 0.0059	0.0124 / 0.0045
		400	0.0380 / 0.0022	0.0336 / 0.0016	0.0155 / 0.0009	0.0125 / 0.0029	0.0110 / 0.0029	0.0060 / 0.0022
0.9	0.9	50	0.3159 / 0.0170	0.2382 / 0.0115	0.1137 / 0.0054	0.3341 / 0.0417	0.1319 / 0.0451	0.0264 / 0.0226
		100	0.2620 / 0.0084	0.2262 / 0.0057	0.1251 / 0.0027	0.1111 / 0.0206	0.0385 / 0.0225	0.0135 / 0.0116
		200	0.1587 / 0.0042	0.1564 / 0.0029	0.0891 / 0.0014	0.0208 / 0.0102	0.0141 / 0.0109	0.0065 / 0.0055
		400	0.0915 / 0.0021	0.0938 / 0.0014	0.0489 / 0.0007	0.0063 / 0.0050	0.0066 / 0.0053	0.0033 / 0.0027

^aResults are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .

Supplementary Table 2. Biases (B) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci and sample sizes (N)^a

p	q	N	$B(\hat{D}') / B(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	-0.0321 / -0.00008	-0.0620 / -0.0002	-0.0593 / +0.0001	+0.0321 / +0.0002	+0.0617 / -0.00004	+0.0592 / +0.0004
		100	-0.0212 / +0.0005	-0.0420 / +0.0003	-0.0416 / -0.0001	+0.0216 / -0.0002	+0.0428 / +0.0003	+0.0419 / +0.0004
		200	-0.0154 / -0.0004	-0.0292 / +0.0003	-0.0293 / -0.0001	+0.0153 / +0.0001	+0.0298 / +0.0002	+0.0292 / +0.00005
		400	-0.0106 / -0.0001	-0.0203 / +0.0002	-0.0204 / +0.0002	+0.0102 / -0.0003	+0.0208 / +0.0002	+0.0205 / +0.0001
0.7		50	-0.0039 / -0.00005	-0.0055 / +0.0003	-0.0030 / +0.0008	+0.0040 / +0.0001	+0.0064 / +0.0001	+0.0033 / -0.0015
		100	-0.0010 / +0.0004	-0.0024 / +0.0005	-0.0024 / +0.0004	+0.0017 / -0.0001	+0.0033 / +0.0006	+0.0012 / -0.0008
		200	-0.0008 / +0.0001	-0.0010 / +0.0004	-0.0009 / +0.0003	+0.0001 / -0.0006	+0.0018 / -0.00002	+0.0006 / -0.0004
		400	-0.0004 / +0.00005	-0.0005 / +0.0002	-0.0002 / +0.0001	+0.0008 / +0.0002	+0.0010 / +0.0003	+0.00005 / -0.0004
0.9		50	-0.0035 / -0.0004	-0.0039 / +0.0005	-0.0043 / +0.0003	+0.0043 / +0.0007	+0.0067 / +0.0008	+0.0026 / -0.0001
		100	-0.0007 / +0.0008	-0.0048 / +0.0011	-0.0016 / +0.0026	+0.0006 / -0.0009	+0.0013 / -0.0018	+0.0011 / -0.0027
		200	+0.00004 / +0.0005	-0.0010 / +0.0008	-0.0013 / +0.0012	-0.0001 / -0.0005	+0.0017 / -0.0007	+0.0004 / -0.0016

		400	-0.0006 / +0.0001	-0.0013 / +0.0002	-0.0003 / +0.0008	+0.0003 / -0.0002	+0.0013 / -0.0001	+0.00005 / -0.0008
0.7	0.7	50	-0.0347 / -0.0006	-0.0074 / +0.0016	-0.0032 / +0.0019	+0.0261 / -0.0003	+0.0678 / -0.0005	+0.0648 / -0.0005
		100	-0.0167 / -0.0005	-0.0019 / +0.0009	-0.0018 / +0.0009	+0.0218 / -0.0007	+0.0455 / -0.0008	+0.0456 / +0.00001
		200	-0.0064 / -0.0003	-0.0017 / +0.0002	-0.0013 / +0.0003	+0.0160 / -0.0003	+0.0323 / -0.0001	+0.0317 / -0.0003
		400	-0.0013 / +0.0001	-0.0008 / +0.00004	-0.0008 / +0.0001	+0.0114 / -0.0002	+0.0222 / -0.0002	+0.0222 / -0.0002
0.9		50	-0.1132 / +0.0032	-0.0524 / -0.0001	-0.0104 / +0.0015	-0.0703 / +0.0039	-0.0109 / +0.0005	+0.0016 / +0.0004
		100	-0.0619 / +0.0001	-0.0164 / +0.0001	-0.0031 / +0.0018	-0.0295 / -0.0006	+0.0014 / -0.0017	+0.0022 / -0.0030
		200	-0.0302 / +0.0003	-0.0040 / +0.0006	-0.0015 / +0.0006	-0.0082 / -0.0003	+0.0026 / -0.0004	+0.0002 / -0.0021
		400	-0.0115 / +0.0006	-0.0013 / +0.0003	-0.0004 / +0.0004	-0.0006 / +0.00002	+0.0005 / -0.0006	+0.0006 / -0.0006
0.9	0.9	50	-0.3968 / -0.0002	-0.2327 / +0.0004	-0.0883 / +0.0004	-0.1319 / -0.0004	+0.0736 / -0.0001	+0.0958 / +0.0017
		100	-0.2524 / +0.0005	-0.1283 / +0.0009	-0.0037 / +0.0019	-0.0188 / -0.0030	+0.0666 / -0.0052	+0.0684 / -0.0032
		200	-0.1416 / +0.0006	-0.0515 / +0.0005	-0.0092 / +0.0007	+0.0177 / -0.0019	+0.0477 / -0.0030	+0.0484 / -0.0015
		400	-0.0823 / -0.0001	-0.0163 / +0.0003	-0.0002 / +0.0005	+0.0174 / -0.0004	+0.0339 / -0.0011	+0.0338 / -0.0011

^a Results are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .

Supplementary Table 3. Variation coefficients (CV) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci, and sample sizes (N)^a

p	q	N	$CV(\hat{D}') / CV(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	71 / 70	25 / 25	11 / 11	69 / 69	26 / 25	11 / 11
		100	50 / 49	18 / 17	8 / 7	50 / 49	18 / 17	8 / 7
		200	35 / 35	13 / 12	6 / 5	35 / 35	13 / 12	6 / 5
		400	25 / 25	9 / 9	4 / 7	25 / 25	9 / 9	4 / 7
0.7		50	112 / 108	41 / 40	19 / 21	108 / 108	41 / 40	19 / 21
		100	78 / 76	29 / 28	13 / 14	77 / 75	29 / 28	13 / 14
		200	54 / 53	20 / 20	9 / 10	54 / 54	20 / 20	9 / 10
		400	38 / 38	14 / 14	7 / 7	38 / 38	14 / 14	7 / 7
0.9		50	228 / 211	81 / 78	35 / 39	225 / 209	80 / 77	35 / 39
		100	158 / 150	55 / 55	24 / 28	158 / 151	56 / 56	25 / 28
		200	108 / 106	38 / 39	17 / 20	107 / 106	38 / 39	17 / 20
		400	75 / 74	27 / 27	12 / 14	75 / 74	27 / 27	12 / 14

0.7	0.7	50	124 / 159	56 / 57	25 / 29	89 / 74	28 / 27	12 / 12
		100	97 / 112	40 / 40	17 / 20	55 / 52	20 / 19	9 / 8
		200	73 / 79	28 / 28	12 / 14	37 / 37	14 / 13	6 / 6
		400	55 / 56	20 / 20	9 / 10	26 / 26	10 / 9	4 / 4
0.9		50	163 / 311	85 / 106	42 / 50	355 / 151	75 / 61	30 / 33
		100	140 / 218	68 / 75	32 / 36	173 / 108	45 / 43	20 / 24
		200	115 / 153	51 / 53	22 / 25	92 / 76	30 / 30	14 / 17
		400	92 / 109	37 / 37	16 / 18	56 / 53	21 / 21	10 / 12
0.9	0.9	50	94 / 595	67 / 196	38 / 83	938 / 102	63 / 43	18 / 19
		100	113 / 427	76 / 139	42 / 60	185 / 73	35 / 30	13 / 14
		200	117 / 303	72 / 98	37 / 42	66 / 51	22 / 21	9 / 9
		400	107 / 207	59 / 68	28 / 30	37 / 35	15 / 15	7 / 7

^aResults are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .

Supplementary Table 4. Standardised biases (SB) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci, and sample sizes (N)^a

p	q	N	$SB(\hat{D}') / SB(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	-6.1 / -3.0	-16.6 / -9.0	-36.6 / -23.7	+6.1 / +3.0	+16.6 / +9.0	+37.0 / +24.0
		100	-4.2 / -2.0	-11.4 / -5.7	-25.9 / -14.5	+4.2 / +2.0	+11.4 / +5.7	+25.8 / +14.4
		200	-2.9 / -1.3	-7.9 / -3.8	-18.2 / -9.3	+2.8 / +1.3	+7.8 / +3.7	+18.3 / +9.3
		400	-2.0 / -0.9	-5.5 / -2.6	-12.8 / -6.1	+2.0 / +0.9	+5.4 / +2.5	+12.9 / +6.2
0.7		50	-3.9 / -3.5	-11.7 / -10.6	-28.1 / -25.6	+4.1 / +3.7	+11.6 / +10.4	+28.0 / +25.5
		100	-2.8 / -2.5	-7.9 / -7.1	-19.3 / -17.5	+2.7 / +2.5	+8.0 / +7.2	+19.2 / +17.6
		200	-1.8 / -1.7	-5.5 / -5.1	-13.4 / -12.4	+1.9 / +1.8	+5.5 / +5.0	+13.2 / +12.3
		400	-1.3 / -1.3	-3.8 / -3.6	-9.4 / -9.0	+1.3 / +1.2	+3.9 / +3.6	+9.4 / +9.0
0.9		50	-7.8 / -7.7	-22.5 / -23.3	-53.2 / -38.9	+8.0 / +7.9	+22.3 / +23.2	+52.5 / +38.4
		100	-5.2 / -4.8	-15.3 / -14.3	-35.1 / -30.8	+5.4 / +4.9	+15.4 / +14.4	+35.2 / +31.2
		200	-3.7 / -3.4	-10.3 / -9.5	-24.2 / -22.5	+3.8 / +3.5	+10.2 / +9.4	+24.3 / +22.8
		400	-2.6 / -2.4	-7.2 / -6.8	-16.8 / -16.0	+2.5 / +2.3	+7.2 / +6.8	+16.9 / +16.1

0.7	0.7	50	-8.4 / -10.6	-16.4 / -18.5	-37.0 / -35.0	+5.8 / -0.9	+18.1 / +7.9	+40.2 / +27.0
		100	-5.1 / -7.4	-11.2 / -12.6	-25.6 / -25.1	+4.3 / -0.9	+12.6 / +5.1	+28.1 / +15.7
		200	-3.0 / -5.1	-7.7 / -8.9	-17.8 / -17.8	+3.0 / -0.7	+8.5 / +3.1	+19.8 / +10.0
		400	-2.0 / -3.7	-5.3 / -6.2	-12.3 / -12.7	+2.1 / -0.6	+6.0 / +2.1	+13.9 / +6.5
0.9		50	-20.5 / -23.9	-34.8 / -40.0	-66.0 / -49.0	-1.0 / -5.1	+16.3 / +12.2	+43.7 / +32.0
		100	-12.8 / -15.6	-22.2 / -26.0	-49.3 / -43.2	+1.3 / -3.6	+11.7 / +6.8	+29.3 / +23.8
		200	-7.8 / -10.6	-14.3 / -16.9	-31.6 / -32.6	+1.8 / -2.5	+8.0 / +4.6	+20.0 / +16.9
		400	-5.0 / -7.6	-10.0 / -11.9	-22.6 / -22.9	+1.7 / -1.6	+5.8 / +3.5	+13.9 / +12.2
0.9	0.9	50	-54.7 / -58.6	-67.0 / -69.5	-84.9 / -59.7	-4.8 / -13.3	+26.9 / +12.9	+63.1 / +45.8
		100	-36.6 / -42.3	-49.0 / -56.5	-75.1 / -59.1	+2.2 / -10.9	+19.4 / +5.3	+44.0 / +29.2
		200	-22.2 / -27.5	-30.2 / -38.8	-60.5 / -57.1	+4.0 / -7.8	+13.3 / +2.7	+30.6 / +16.8
		400	-13.5 / -18.7	-19.4 / -25.7	-40.0 / -44.4	+3.1 / -5.4	+9.1 / +1.6	+21.3 / +10.2

^a Results are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .

Supplementary Table 5. Mean square errors (MSE) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci, and sample sizes (N)^a

p	q	N	$MSE(\hat{D}') / MSE(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	0.0286 / 0.0196	0.0244 / 0.0152	0.0123 / 0.0073	0.0280 / 0.0193	0.0247 / 0.0154	0.0121 / 0.0073
		100	0.0127 / 0.0097	0.0114 / 0.0076	0.0061 / 0.0036	0.0127 / 0.0096	0.0115 / 0.0076	0.0062 / 0.0036
		200	0.0059 / 0.0048	0.0055 / 0.0037	0.0031 / 0.0018	0.0060 / 0.0049	0.0056 / 0.0038	0.0032 / 0.0018
		400	0.0028 / 0.0024	0.0027 / 0.0019	0.0015 / 0.0009	0.0028 / 0.0024	0.0026 / 0.0019	0.0015 / 0.0009
0.7		50	0.0520 / 0.0199	0.0428 / 0.0170	0.0225 / 0.0117	0.0522 / 0.0200	0.0429 / 0.0170	0.0223 / 0.0116
		100	0.0243 / 0.0098	0.0205 / 0.0083	0.0111 / 0.0057	0.0242 / 0.0097	0.0207 / 0.0085	0.0111 / 0.0057
		200	0.0119 / 0.0049	0.0101 / 0.0042	0.0055 / 0.0028	0.0118 / 0.0049	0.0102 / 0.0042	0.0055 / 0.0028
		400	0.0058 / 0.0024	0.0050 / 0.0021	0.0027 / 0.0014	0.0059 / 0.0024	0.0050 / 0.0021	0.0028 / 0.0014
0.9		50	0.2870 / 0.0240	0.1663 / 0.0167	0.0785 / 0.0108	0.2250 / 0.0197	0.1652 / 0.0167	0.0787 / 0.0109
		100	0.0997 / 0.0098	0.0780 / 0.0082	0.0385 / 0.0056	0.1006 / 0.0099	0.0789 / 0.0084	0.0386 / 0.0057
		200	0.0467 / 0.0049	0.0365 / 0.0041	0.0181 / 0.0028	0.0461 / 0.0049	0.0370 / 0.0042	0.0184 / 0.0028

		400	0.0224 / 0.0024	0.0180 / 0.0021	0.0090 / 0.0014	0.0225 / 0.0024	0.0179 / 0.0021	0.0090 / 0.0014
0.7	0.7	50	0.0863 / 0.0187	0.0800 / 0.0149	0.0406 / 0.0096	0.0415 / 0.0221	0.0303 / 0.0186	0.0147 / 0.0090
		100	0.0439 / 0.0093	0.0404 / 0.0074	0.0197 / 0.0047	0.0156 / 0.0109	0.0138 / 0.0091	0.0074 / 0.0044
		200	0.0229 / 0.0046	0.0199 / 0.0037	0.0098 / 0.0023	0.0068 / 0.0054	0.0065 / 0.0045	0.0037 / 0.0022
		400	0.0123 / 0.0023	0.0098 / 0.0018	0.0048 / 0.0012	0.0031 / 0.0026	0.0032 / 0.0022	0.0018 / 0.0011
0.9		50	0.2709 / 0.0180	0.2223 / 0.0133	0.1166 / 0.0075	0.2215 / 0.0239	0.1359 / 0.0239	0.0573 / 0.0178
		100	0.1389 / 0.0089	0.1239 / 0.0066	0.0648 / 0.0038	0.0870 / 0.0120	0.0520 / 0.0120	0.0260 / 0.0091
		200	0.0711 / 0.0044	0.0656 / 0.0033	0.0315 / 0.0019	0.0313 / 0.0059	0.0226 / 0.0059	0.0124 / 0.0045
		400	0.0381 / 0.0022	0.0336 / 0.0016	0.0155 / 0.0009	0.0125 / 0.0029	0.0110 / 0.0029	0.0060 / 0.0022
0.9	0.9	50	0.4734 / 0.0170	0.2923 / 0.0115	0.1215 / 0.0054	0.3515 / 0.0417	0.1373 / 0.0451	0.0356 / 0.0226
		100	0.3257 / 0.0084	0.2427 / 0.0057	0.1251 / 0.0027	0.1115 / 0.0206	0.0429 / 0.0225	0.0182 / 0.0116
		200	0.1788 / 0.0042	0.1591 / 0.0029	0.0892 / 0.0014	0.0211 / 0.0102	0.0164 / 0.0109	0.0088 / 0.0055
		400	0.0983 / 0.0021	0.0941 / 0.0014	0.0489 / 0.0007	0.0066 / 0.0050	0.0077 / 0.0053	0.0044 / 0.0027

^a Results are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .

Supplementary Table 6. Mean relative errors (*RelError*) of \hat{D}' and \hat{r} for different LD intensities ($\pm W$, $\pm M$ and $\pm S$), combinations of allele frequencies (p and q) at the loci, and sample sizes (N)^a

p	q	N	$RelError(\hat{D}') / RelError(\hat{r})$					
			$-W$	$-M$	$-S$	$+W$	$+M$	$+S$
0.5	0.5	50	85 / 70	31 / 25	14 / 11	84 / 69	31 / 25	14 / 11
		100	56 / 49	21 / 17	10 / 8	56 / 49	21 / 17	10 / 8
		200	39 / 35	15 / 12	7 / 5	39 / 35	15 / 12	7 / 5
		400	27 / 24	10 / 9	5 / 4	26 / 24	10 / 9	5 / 4
0.7		50	114 / 108	41 / 40	19 / 21	114 / 108	41 / 40	19 / 21
		100	78 / 76	29 / 28	13 / 14	78 / 75	29 / 28	13 / 14
		200	55 / 53	20 / 20	9 / 10	54 / 53	20 / 20	9 / 10
		400	38 / 37	14 / 14	6 / 7	38 / 37	14 / 14	7 / 7
0.9		50	268 / 231	82 / 77	35 / 39	237 / 209	81 / 77	35 / 39
		100	158 / 148	56 / 54	24 / 28	159 / 149	56 / 55	25 / 28

		200	108 / 104	38 / 38	17 / 20	107 / 104	38 / 39	17 / 20
		400	75 / 73	27 / 27	12 / 14	75 / 73	27 / 27	12 / 14
0.7	0.7	50	147 / 159	56 / 57	25 / 29	101 / 74	35 / 27	15 / 12
		100	105 / 112	40 / 40	18 / 20	62 / 52	23 / 19	11 / 8
		200	76 / 79	28 / 28	12 / 14	41 / 37	16 / 13	8 / 6
		400	55 / 56	20 / 20	9 / 10	28 / 25	11 / 9	5 / 4
0.9		50	260 / 305	94 / 106	43 / 50	235 / 152	74 / 61	30 / 33
		100	186 / 214	70 / 75	32 / 35	147 / 107	46 / 43	20 / 23
		200	133 / 151	51 / 53	22 / 25	88 / 75	30 / 30	14 / 16
		400	98 / 107	37 / 37	16 / 17	56 / 53	21 / 21	10 / 12
0.9	0.9	50	344 / 593	108 / 191	44 / 83	296 / 102	74 / 42	24 / 19
		100	285 / 417	99 / 135	44 / 58	167 / 72	41 / 30	17 / 13
		200	211 / 295	80 / 96	37 / 42	73 / 51	26 / 21	12 / 9
		400	156 / 208	61 / 67	28 / 30	41 / 35	18 / 15	8 / 6

^aResults are averages of 50 replicate sampling distributions (1,000 haplotype samples each) of \hat{D}' and \hat{r} .
