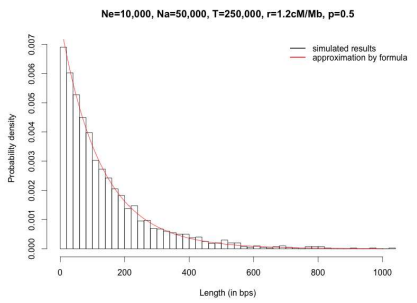
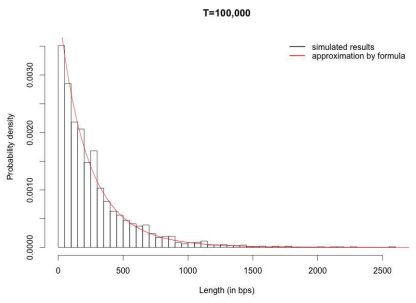
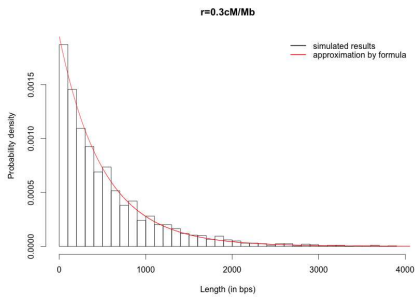
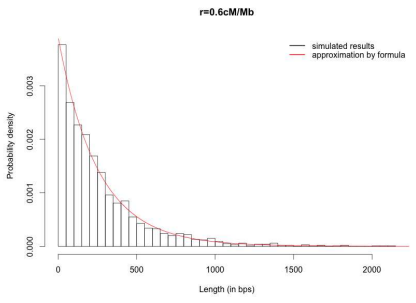
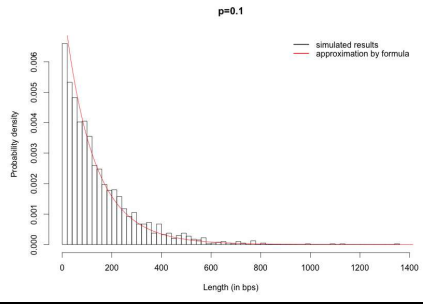
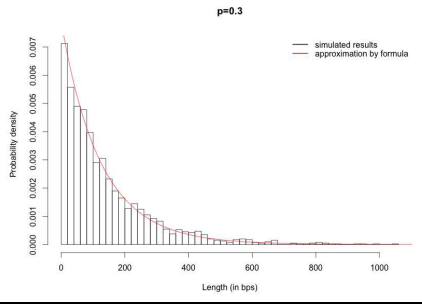
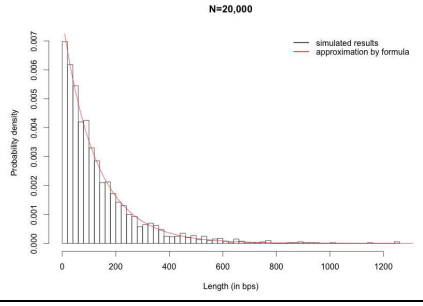
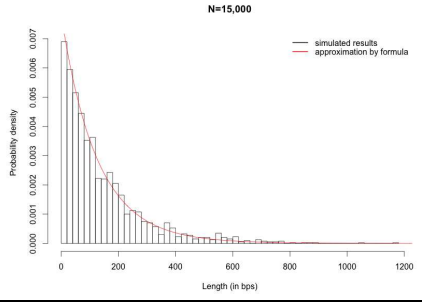
	
Standard	T=100,000
	
r=0.3 cM/Mb	r=0.6 cM/Mb
	
p=0.1	p=0.3
	
N_e=20,000	N_e=150,000

Figure S1: Distribution of the length of ancestral segment according to our approximation and in simulations. Unless otherwise specified, parameters were: N_e=10,000, N_a=50,000, T=250,000, r=1.2cM/Mb and p=0.5, which were chosen to be plausible for humans and chimpanzees. For all combinations of parameters tested, the distribution predicted by the approximation fits the simulation results very well.

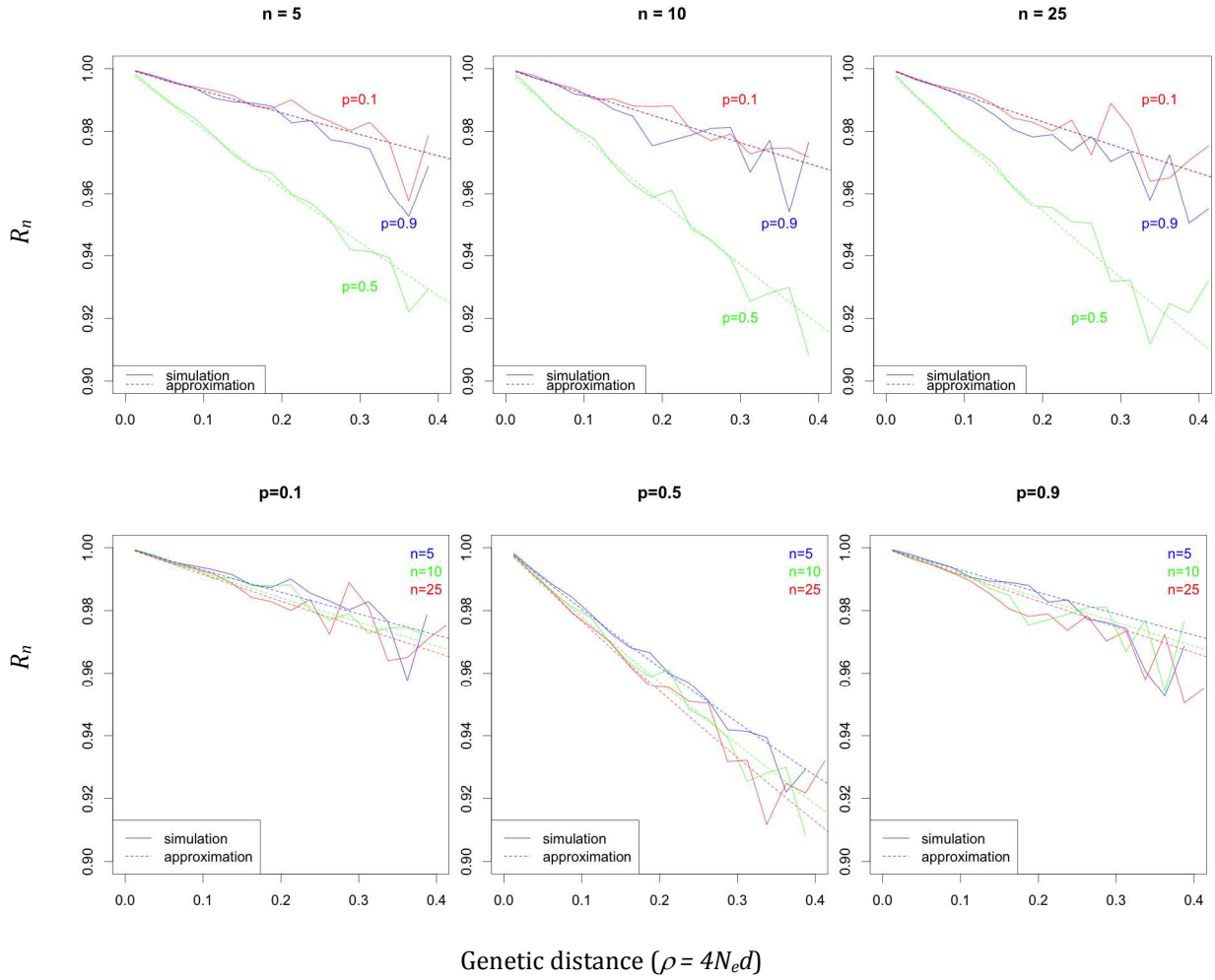
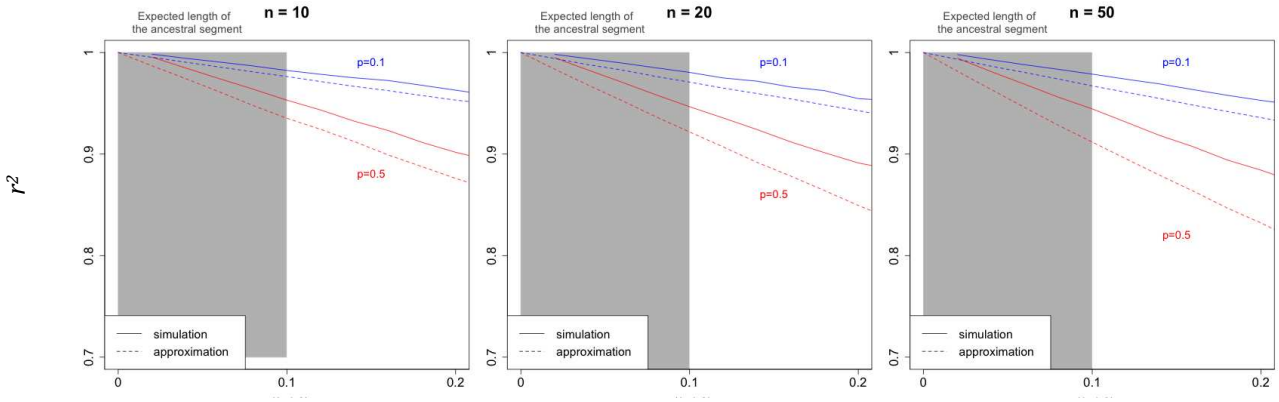


Figure S2: R_n calculated from our approximation and obtained by simulation. The simulated segment is divided into bins of 6.25×10^{-5} cM, and the mean R_n is calculated from all SNPs in each bin. Only bins with more than 50 data points are shown. See Supplementary Methods for details of the simulations.

A



B

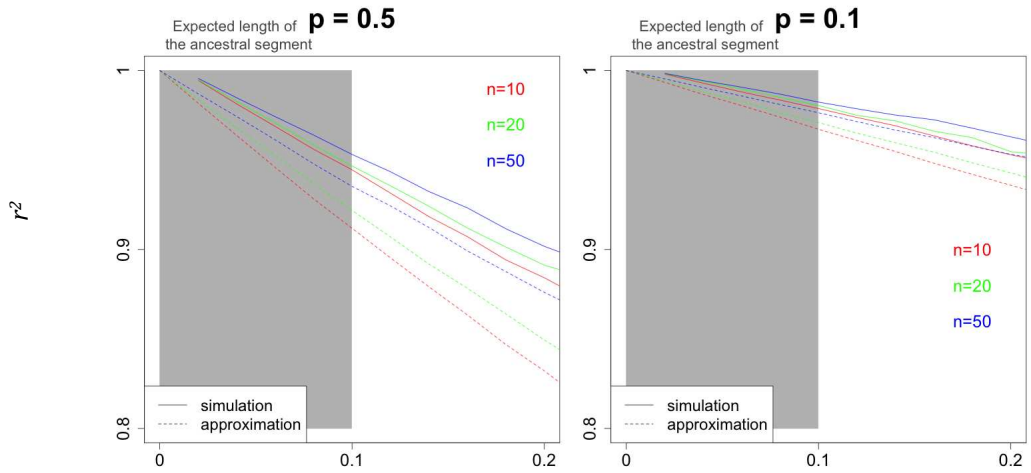
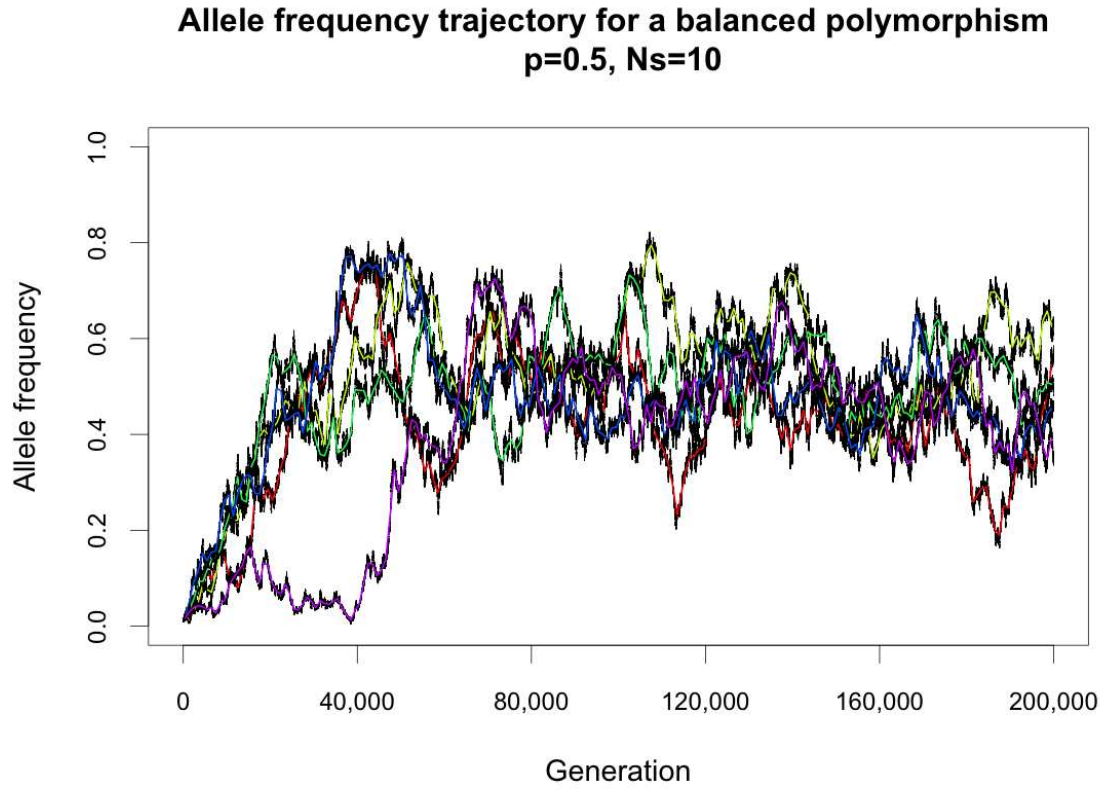
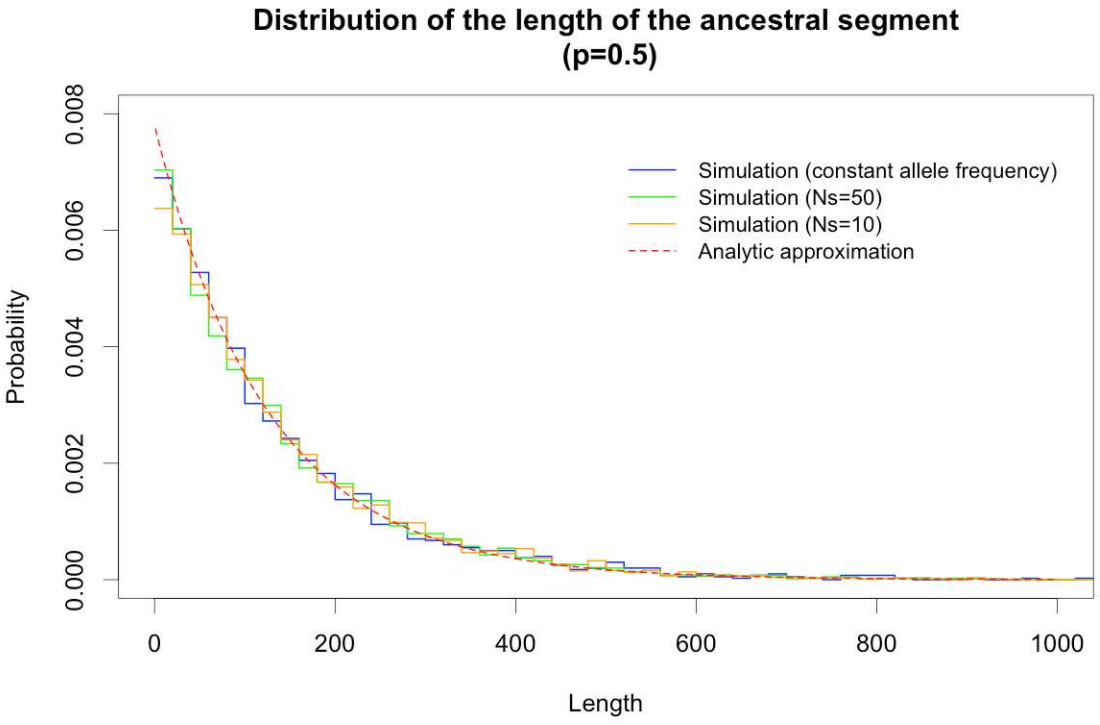


Figure S3: Expected r^2 calculated from our approximation and obtained by simulation. The simulated segment is divided into bins of 6.25×10^{-5} cM and the mean R_n is calculated from all SNPs in each bin. The expected r^2 from R_n was calculated from 10,000 binomial sampling simulations as described in the supplementary Methods. (A) The mean r^2 decreases with sample size. (B) The mean (or expected) r^2 decreases with the product of the equilibrium frequencies of the two alleles (pq).

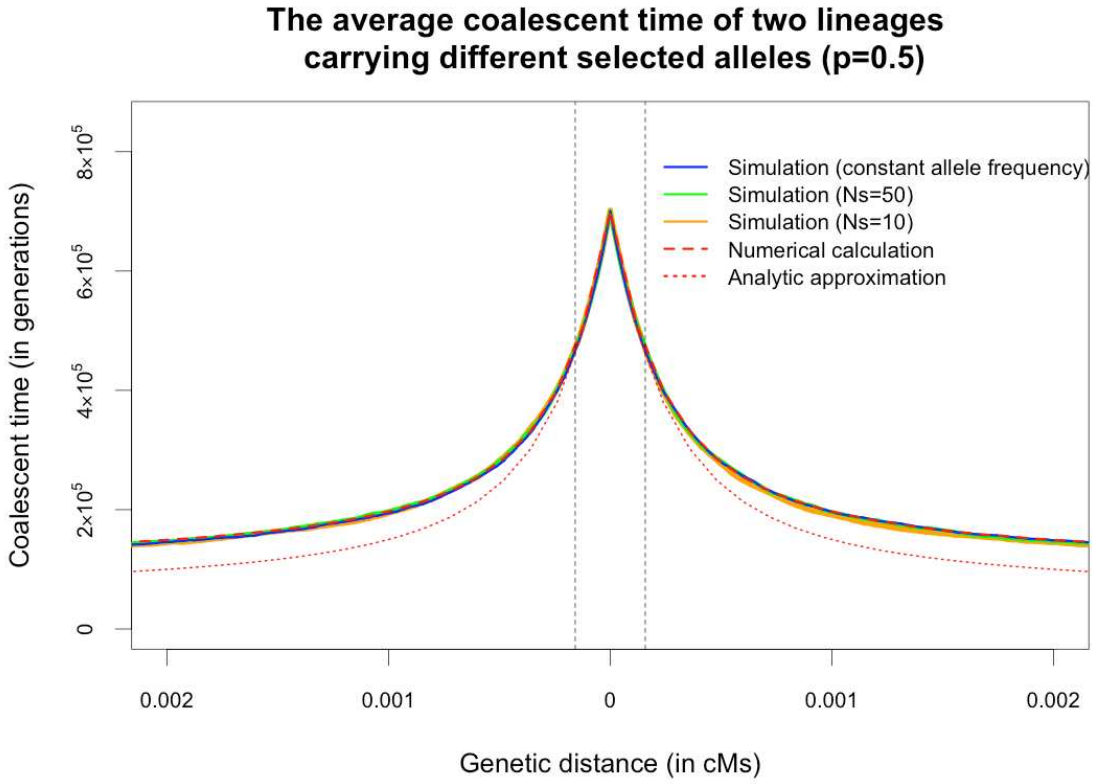
A


Allele frequency trajectory for a balanced polymorphism
p=0.5, Ns=10
Allele frequency
0.0
0.2
0.4
0.6
0.8
1.0
0
40,000
80,000
120,000
160,000
200,000
Generation

B


Distribution of the length of the ancestral segment
(p=0.5)
Probability
0.000
0.002
0.004
0.006
0.008
0
200
400
600
800
1000
Length
Simulation (constant allele frequency)
Simulation (Ns=50)
Simulation (Ns=10)
Analytic approximation

C


The average coalescent time of two lineages carrying different selected alleles (p=0.5)
Coalescent time (in generations)
0
2×10^5
4×10^5
6×10^5
8×10^5
Simulation (constant allele frequency)
Simulation (Ns=50)
Simulation (Ns=10)
Numerical calculation
Analytic approximation
0.002
0.001
0
0.001
0.002
Genetic distance (in cMs)

D

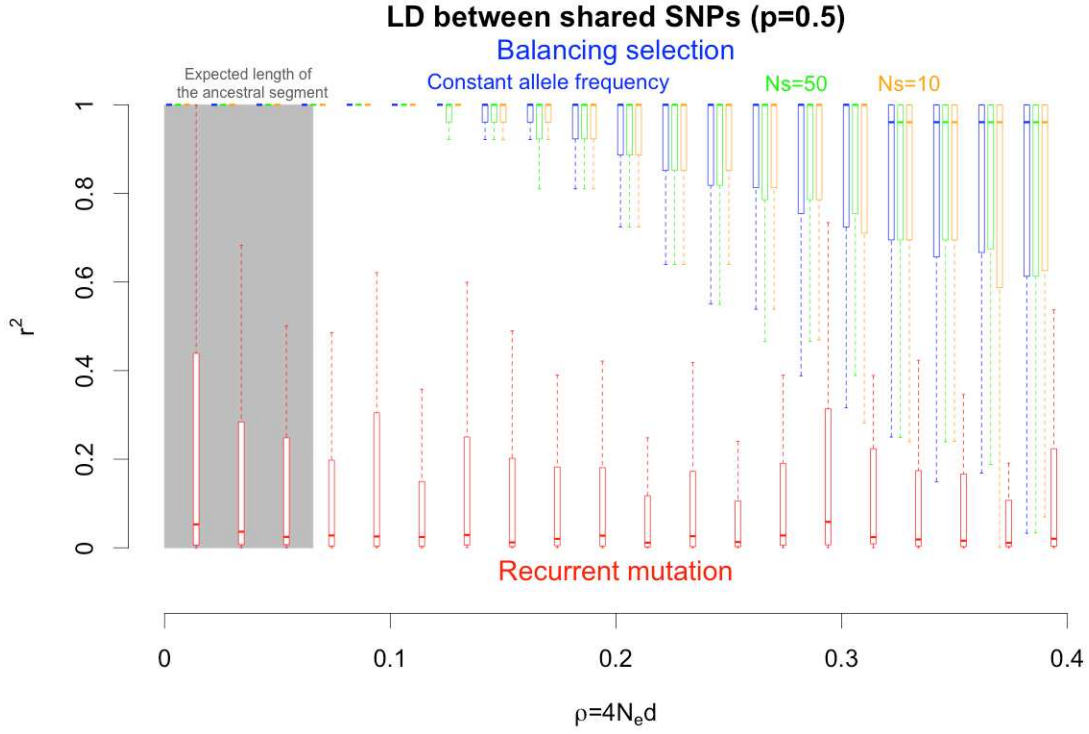

LD between shared SNPs (p=0.5)
Balancing selection
Expected length of the ancestral segment
Constant allele frequency
Ns=50
Ns=10
r^2
0
0.2
0.4
0.6
0.8
1
Recurrent mutation
0
0.1
0.2
0.3
0.4
ρ=4N_ed

Figure S4: The impact of fluctuations in the selected allele frequencies on the three summary statistics considered. For each statistic, three simulation results (constant allele frequency, Ns=10 and Ns=50) are shown together with the theoretical predication. (A) Five examples of allele frequency trajectories generated by simulation. Black lines show the actual allele frequencies in each generation. Colored lines are the mean frequencies averaged every 1,000 generations. (B) The distribution of the length of the ancestral segment. (C) The expected coalescent time of two lineages carrying different selected alleles. (D) LD between the SNP under balancing selection and neutral shared SNPs compared with LD between shared SNPs due to recurrent mutations.

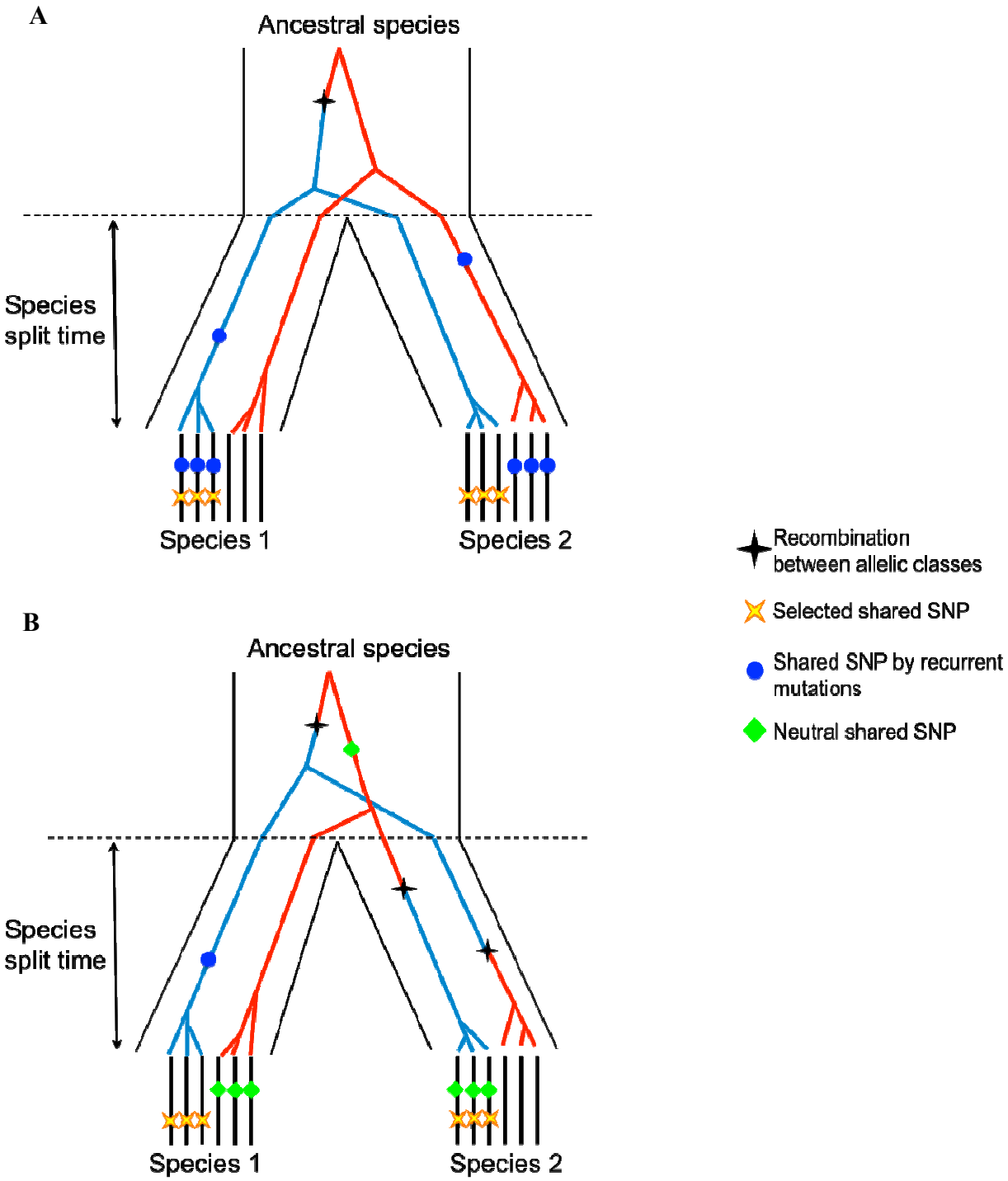


Figure S5: Two scenarios that can generate shared polymorphisms in LD but with the opposite phases in the two species. (A) Recurrent mutations on the genealogy of a trans-species polymorphism: independent occurrences of same mutation occur in both species but arise on lineages carrying different selected alleles in the two species. (B) Complex recombination events: two recombination events occur in species 2 before the split, which switch the alleles carried by the two lineages at the selected site in that species.

Table S1: Summaries of the length of the contiguous ancestral segment

		Length (in bps)			
Split time (T)		1st Qu.	Median	3rd Qu.	Mean
100,000	Approximation	70	171	352	258
	Simulation	76	183	361	274
250,000	Approximation	38	90	182	131
	Simulation	39	93	188	137
500,000	Approximation	21	51	102	73.1
	Simulation	23	55	107	76.9

		Length (in bps)			
Recombination rate (r)		1st Qu.	Median	3rd Qu.	Mean
1.2cM/Mb	Approximation	38	90	182	131
	Simulation	39	93	188	137
0. 6cM/Mb	Approximation	75	180	363	262
	Simulation	72	179	359	266
0. 3cM/Mb	Approximation	149	359	725	525
	Simulation	143	361	763	545

		Length (in bps)			
Population size (N_e)		1st Qu.	Median	3rd Qu.	Mean
Not involved	Approximation	38	90	182	131
10000	Simulation	39	93	188	137
15000	Simulation	39	94	190	140
20000	Simulation	38	90	181	136

		Length (in bps)			
Allele frequency (p)		1st Qu.	Median	3rd Qu.	Mean
0.1	Approximation	43	101	204	146
	Simulation	36	87	177	129
0.2	Approximation	42	97	197	142
	Simulation	37	88	179	130
0.3	Approximation	40	94	189	140
	Simulation	37	89	181	131
0.4	Approximation	37	96	194	140
	Simulation	38	90	181	131
0.5	Approximation	39	93	188	137
	Simulation	38	90	182	131

Parameters used were: N_e =10,000, N_a=50,000, T=250,000, r=1.2cM/Mb and p=0.5.

Table S2: Influence of sample size on the number of neutral shared SNPs and LD among them.

Total sample size (number of chromosomes sampled from each class in each species)	Average number of shared neutral SNPs per replicate (100,000 replicates)			
	All	SNPs in perfect LD with the selected one in species 1	SNPs in perfect LD with the selected one in species 2	SNPs in perfect LD with the selected one in both species
4 (1)	19.022	19.022 (100%)	19.022 (100%)	19.022 (100%)
20 (5)	19.690	18.884 (95.9%)	18.865 (95.8%)	18.154 (92.2%)
40 (10)	19.767	18.657 (94.4%)	18.666 (94.4%)	17.726 (89.7%)
100 (25)	19.798	18.333 (92.6%)	18.353 (92.6%)	17.162 (86.7%)
200 (50)	19.811	18.140 (91.6%)	18.128 (91.5%)	16.811 (84.9%)

The same number of chromosomes was sampled from each allelic class in each species. Parameters were chosen to be plausible for humans and chimpanzees: p=0.5, T=20N_e, N_a= N_e, and T_{BS}=400 N_e. See Supplementary text for further details.

Table S3: Proportion of ancestral balanced polymorphisms that persist in both species until present

	s =0.001	s =0.005
p =0.1	0%	0%
p =0.3	0%	74.3%
p =0.5	29.5%	85.5%

We consider a simple demographic model, with parameters plausible for human populations and Western chimpanzees: T=250,000, N_e=10,000 and N_a=50,000. The balanced polymorphism arose 11 N_a generations prior to the split from an initial frequency of p_0=0.01. 2000 replicates were generated for each combination of selection strength (s) and equilibrium allele frequency (p).

Table S4: Parameter values used in simulations of neutral recurrent mutations.

Parameters for both demographic models

Parameter	Value
Mutation rate	1.8×10^{-8} per generation per base pair
Recombination rate	1.2 cM/Mb per generation (sex-averaged mean recombination rate in human genome)
Sample size	50 chromosomes from each species
Segment length	100 kb
Proportion of CpG sites	2%

Demographic model with constant population sizes

Parameter	Value
Effective population size for humans (N_h)	15,800[a]
Effective population size for Western chimpanzees (N_c)	11,100[a]
Split time (T)	240,000 generations[b]
Effective population size for ancestral species (N_a)	50,000

[a] Derived from a mutation rate of 1.8×10^{-8} and the observed heterozygosity
[b] Derived from a split time of 6 Myr, assuming a generation time of 25 years

Demographic model with bottlenecks

Parameter	Value
Effective population size for humans (N_h)	13,900[c]
Effective population size for Western chimpanzees (N_c)	12,500[d]
Period of the bottleneck for humans	28-56 kya[c]
Period of the bottleneck for Western chimpanzees	15-35 kya[d]
Effective population size for humans during the bottleneck (N_h')	2,200
Effective population size for Western chimpanzees during the bottleneck (N_c')	3,500
Split time (T)	240,000 generations
Effective population size for ancestral species (N_a)	50,000

[c] Based on (Li and Durbin 2011)
[d] Based on (Prado-Martinez et al. 2013)

Table S5: Percentage of trans-species balanced polymorphisms accompanied by shared neutral SNP(s) in coalescent simulations

	Age of the balanced polymorphism		
In 1000 replicates	$20N_e$	$30N_e$	$40N_e$
Cases with shared neutral SNP(s)	65.4%	89.2%	93.6%
Cases with shared neutral SNP(s) in strong LD with the selected one	65.3%	88.6%	93.4%
Average number of shared neutral SNPs in each replicate	2.47	4.10	5.64

We consider a simple demographic model for human populations and Western chimpanzees (T=16N_e, N_a=5N_e) and assume a constant allele frequency of p=0.5 and reasonable population mutation rate (θ=1/kb) and population recombination rate (ρ=0.5/kb). Each replicate consists of 50 chromosomes from each species.