Supplementary materials

I. Graphs of distribution of population genetics indices along generations after a random drawing of individuals in uniform distribution of allele frequencies (i.e., towards reaching "equilibrium")
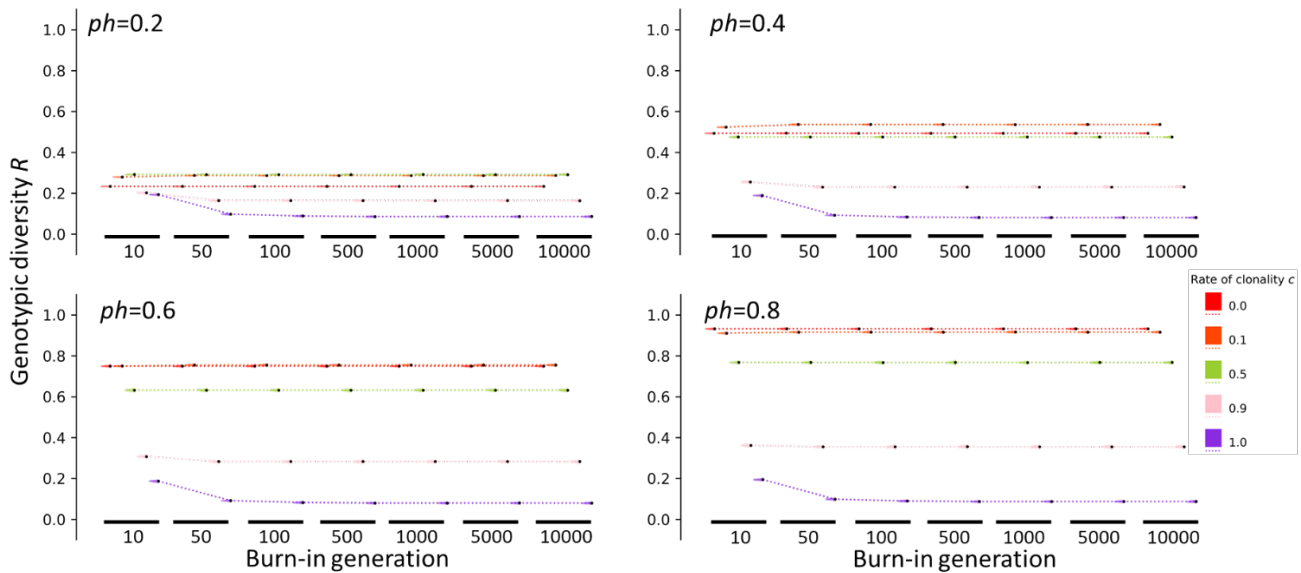

Figure S1: Violin plot of distribution of genotypic diversity along generations after a random drawing of individuals in uniform distribution of allele frequencies as function of proportion of haploids (ph) and of rates of clonality (c). Distributions of gene diversity for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H). Mutation rate 10^{-4} equivalent to population size (N=10000).
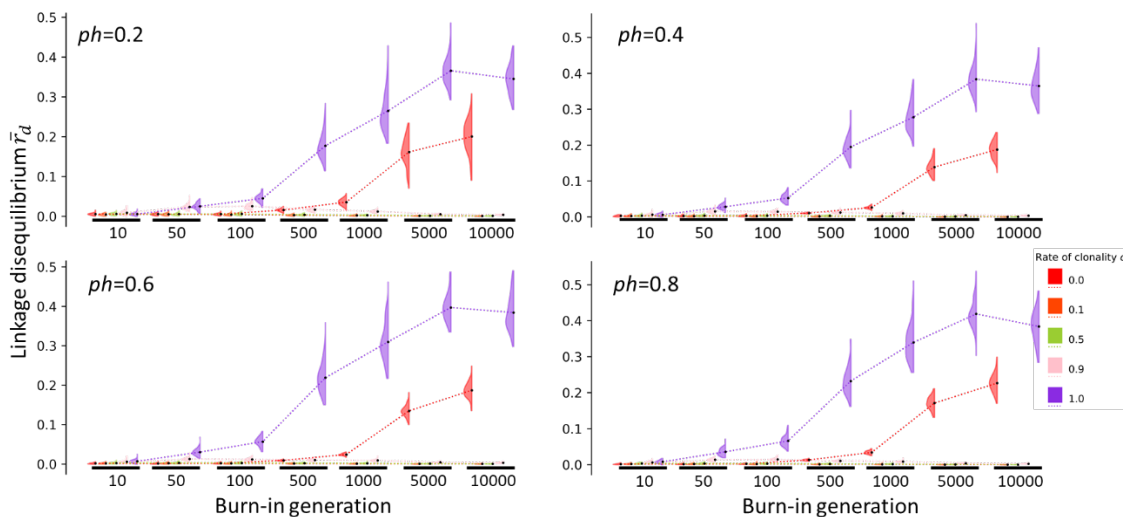

Figure S2: Violin plot of distribution of linkage disequilibrium as $\bar{r}_d$ along generations after a random drawing of individuals in uniform distribution of allele frequencies as function of proportion of haploids (ph) and of rates of clonality (c). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H). Mutation rate 10^{-4} equivalent to population size (N=10000).
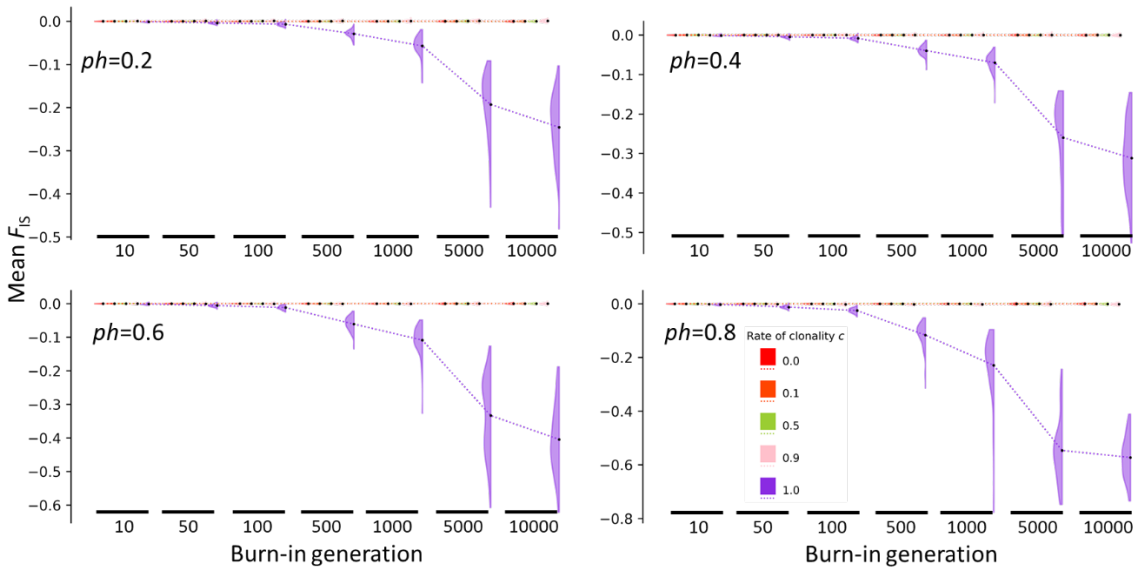
Figure S3: Violin plot of distribution of mean F_{IS}, computed in the diploid phase only, along generations after a random drawing of individuals in uniform distribution of allele frequencies as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H). Mutation rate 10^{-4} equivalent to population size (N=10000).
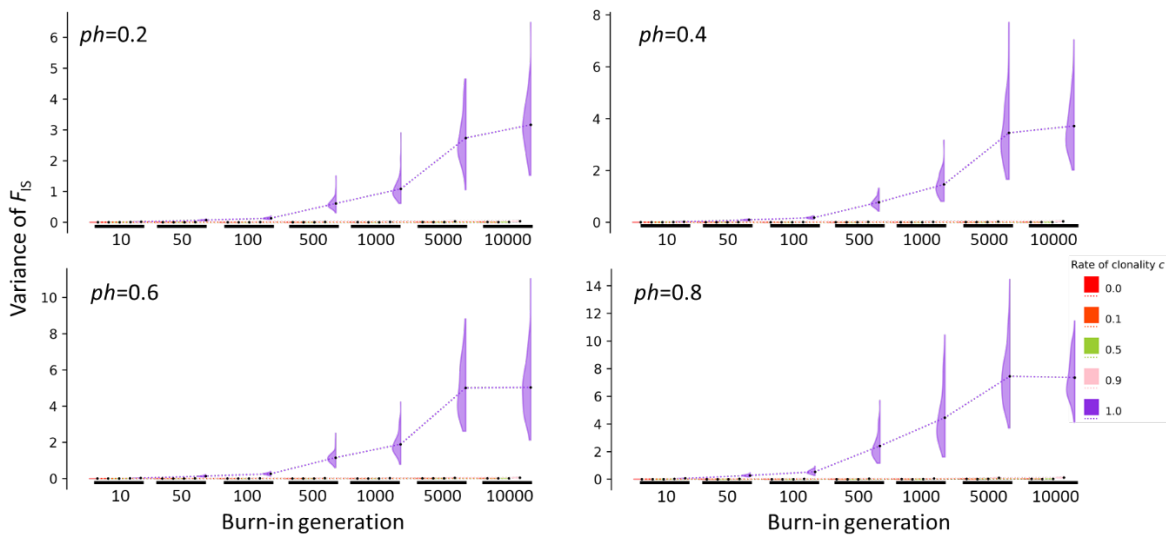

Figure S4: Violin plot of distribution of variance of F_{IS}, computed in the diploid phase only, along generations after a random drawing of individuals in uniform distribution of allele frequencies as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H). Mutation rate 10^{-4} equivalent to population size (N=10000).

Stoeckel, Arnaud-Haond & Krueger-Hadfield 2020. The combined effect of haplodiplonty and partial clonality in population genetics.

II. Graphs of distribution of population genetics indices after 10000 burn-in generations (ie "at equilibrium of evolutionary forces") when mutation force (mutation rate 10^{-3}) is superior to genetic drift (10^{-4}), and when genetic drift (10^{-4}) is superior to mutation rate (10^{-5})
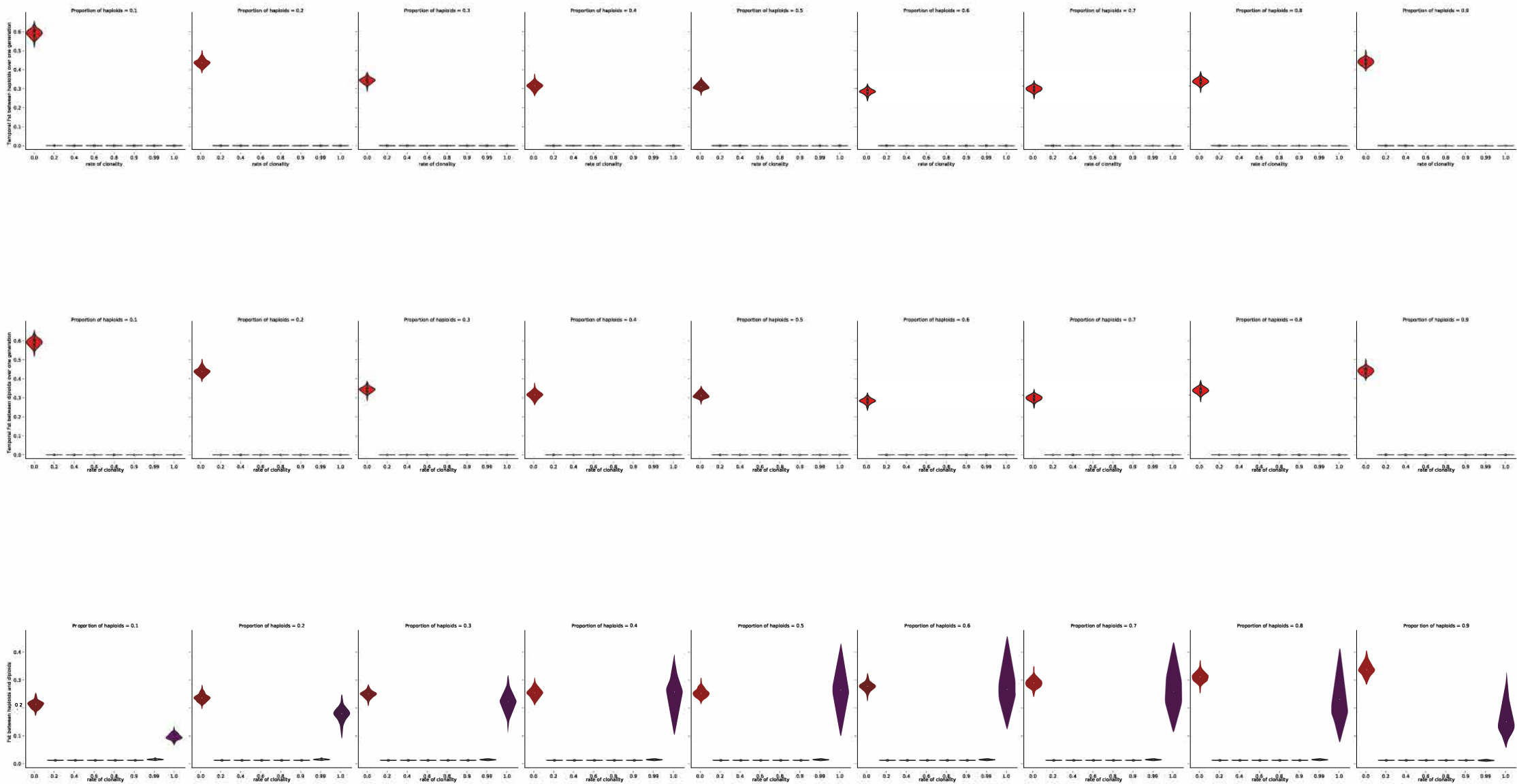
Figure S5: distributions as violin plots of temporal genetic differentiation between two successive haploid (first row of plots) and diploid (second row of plots) populations (generations 9 999 and 10 000) as function of proportion of haploids and rate of clonality. Third row of plots shows distributions as violin plots of genetic differentiation between haploid and diploid genetic pools at one generation (generation 10 000) as function of proportion of haploids and rate of clonality. Population size of 10 000 individuals and mutation rate of 10-4, violin plots are computed on 100 replicates. Red violin plots are for populations reproducing only sexually and purple ones only clonally.
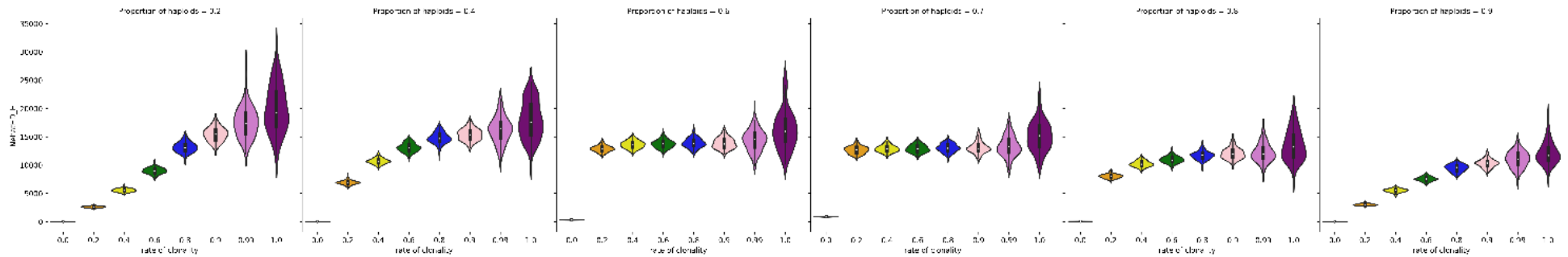
Figure S : Violin plot of distribution of **effective population sizes** estimated from standardized variance in allele frequency over two consecutive generations after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (*ph*) and of rates of clonality (*c*).
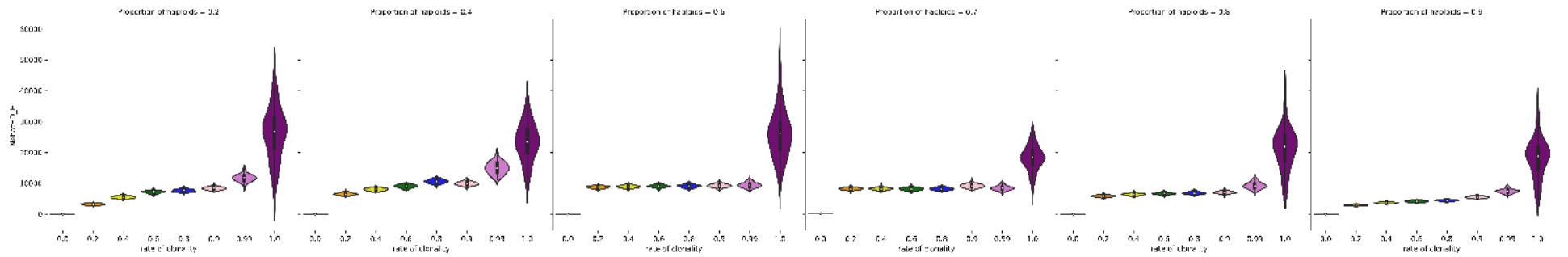

Figure S : Violin plot of distribution of **effective population sizes** estimated from standardized variance in allele frequency over two consecutive generations after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (*ph*) and of rates of clonality (*c*).
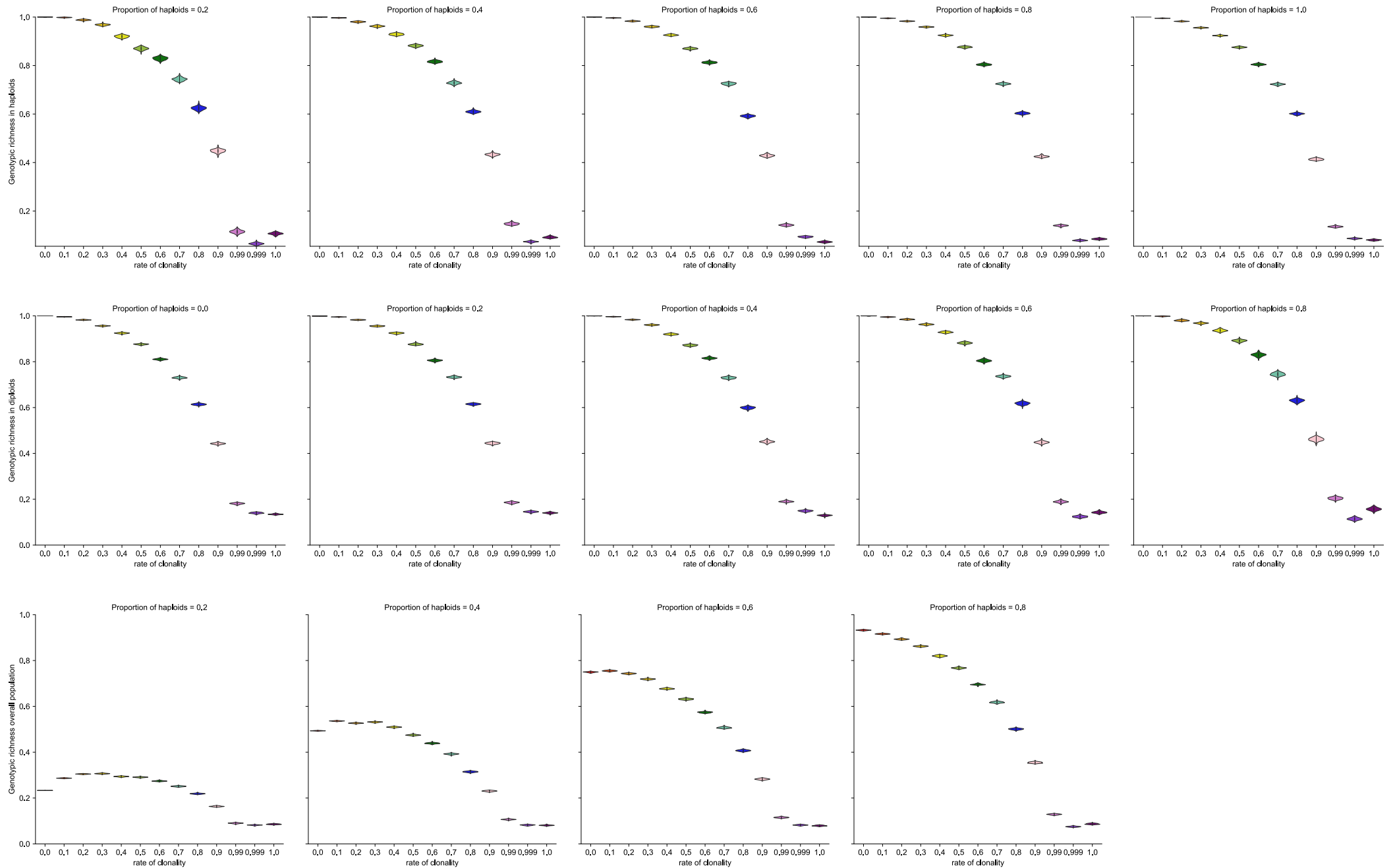
Figure S8: Violin plot of the ranges of genotypic diversity computed as genotypic richness (R) as function of proportion of haploids and of rates of clonality. Distributions of R in haploids (first row of plots), in diploids (second row) and overall population (third row). Colors account for rates of clonality: red for c=0 (only sexual), orangered c=0.1, orange c=0.2, gold c=0.3, yellow c=0.4, yellowgreen c=0.5, green c=0.6, aquamarine c=0.7, blue c=0.8, pink c=0.9, orchid c=0.99, violet c=0.999 and purple c=1 (only clonal). Population size of 10 000 individuals and mutation rate of 10-4, violin plots are computed on 100 replicates.

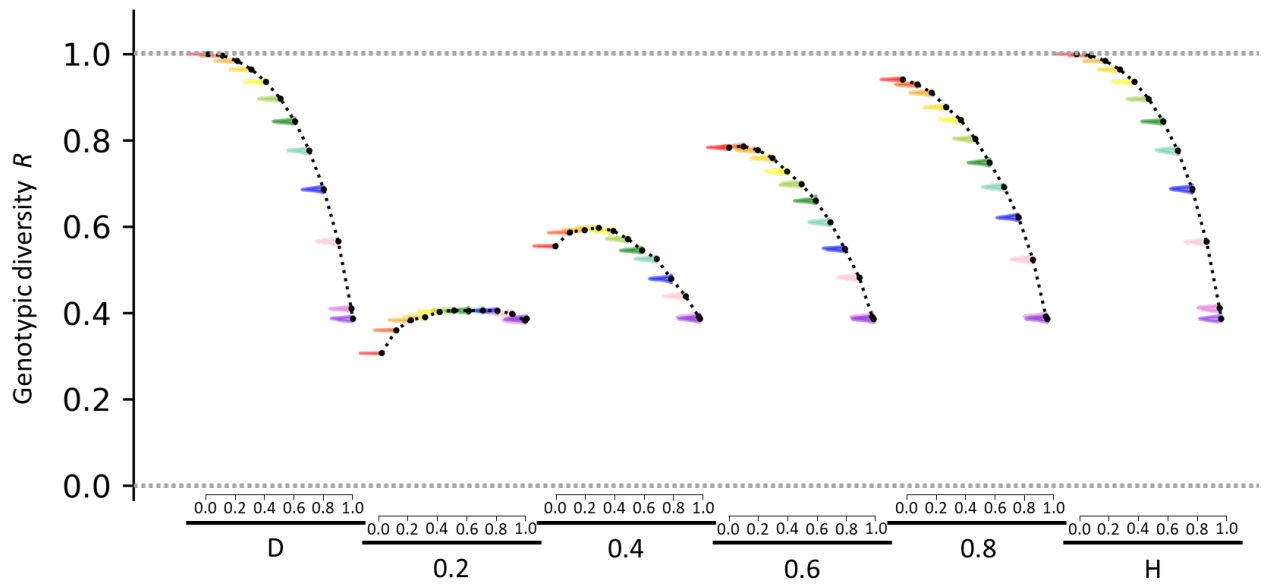**Figure S** : Violin plot of distribution of **genotypic richness** (*R*) after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
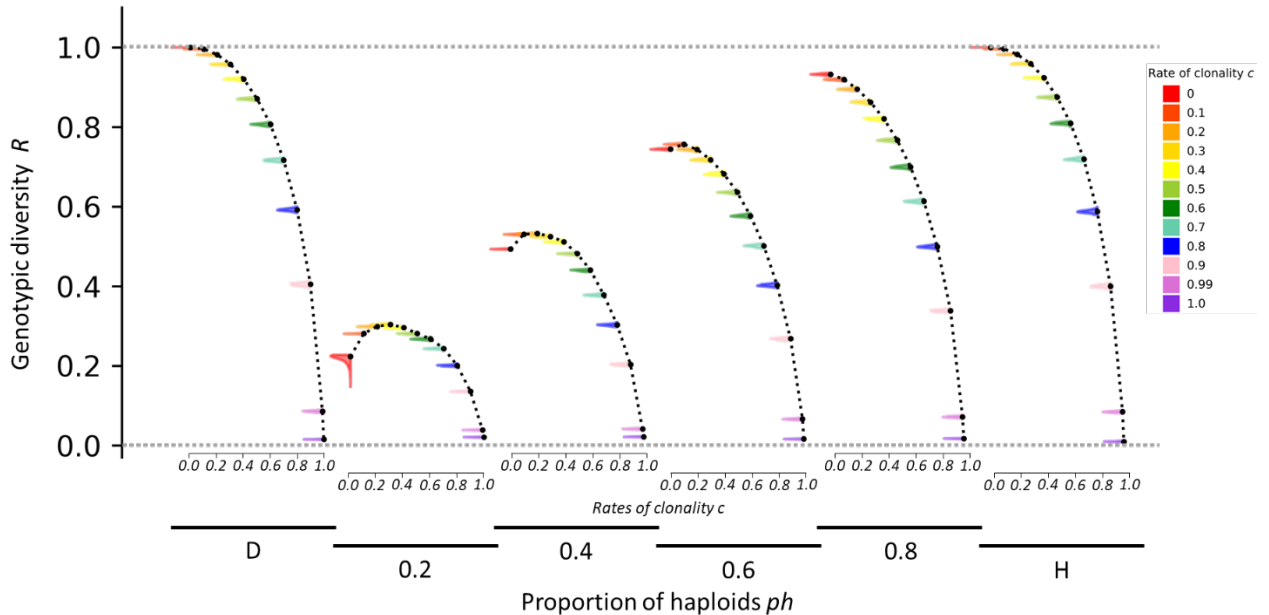

Figure S : Violin plot of distribution of **genotypic richness** (*R*) after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).

Figure S1 : Violin plot of distribution of **Pareto beta** after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
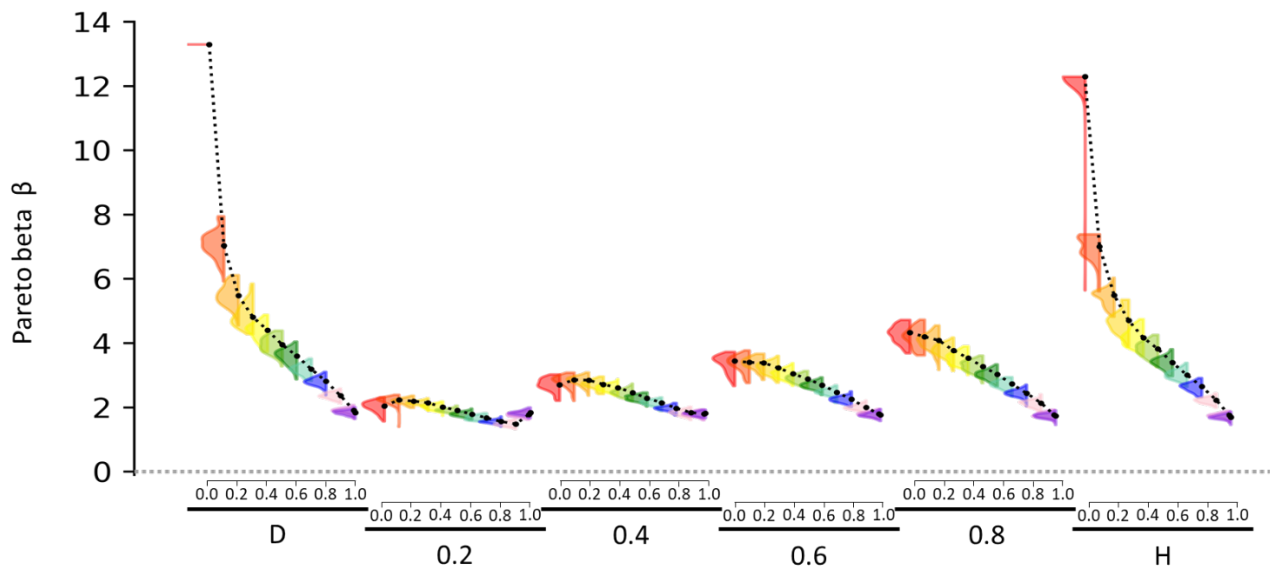

Figure S1 : Violin plot of distribution of **Pareto beta** after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
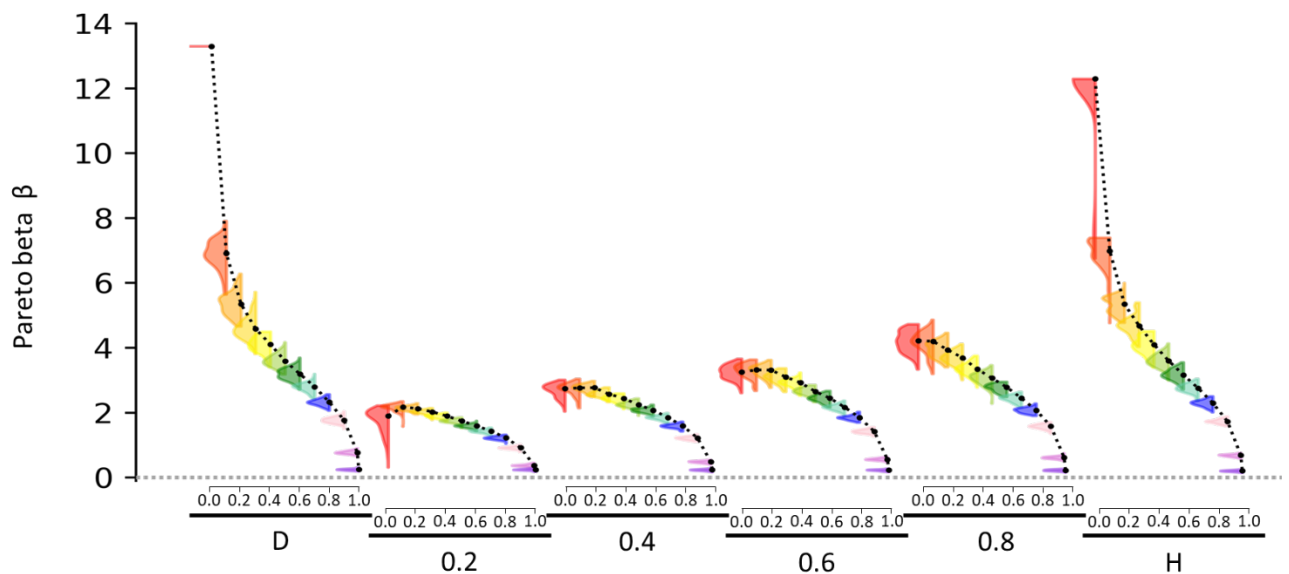
Figure S1 : Violin plot of distribution of **linkage disequilibrium** after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (ph) and of rates of clonality (c). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
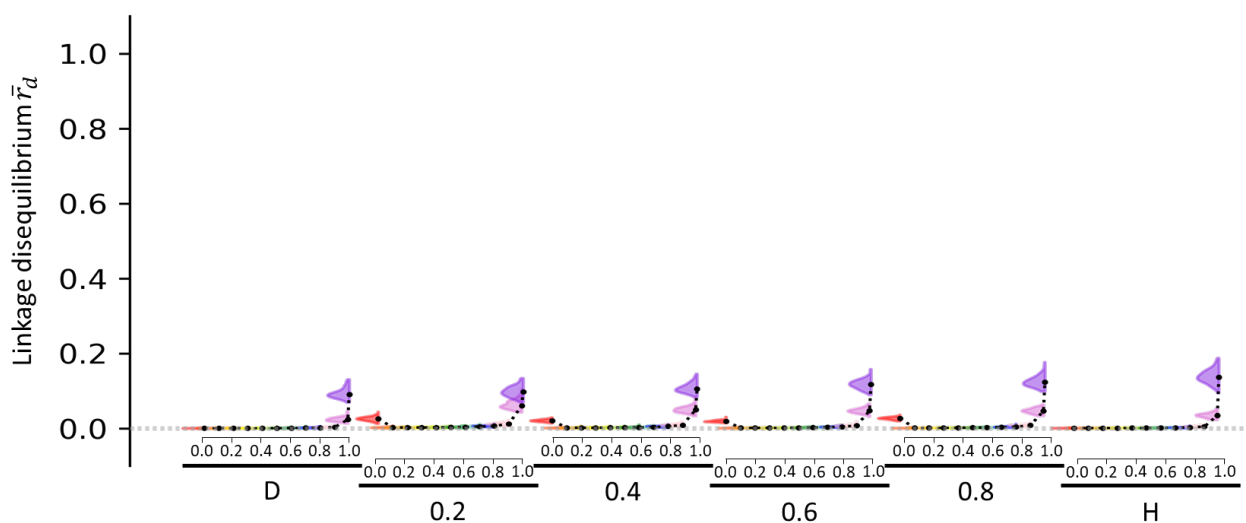

Figure S1 : Violin plot of distribution of **linkage disequilibrium** after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (ph) and of rates of clonality (c). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
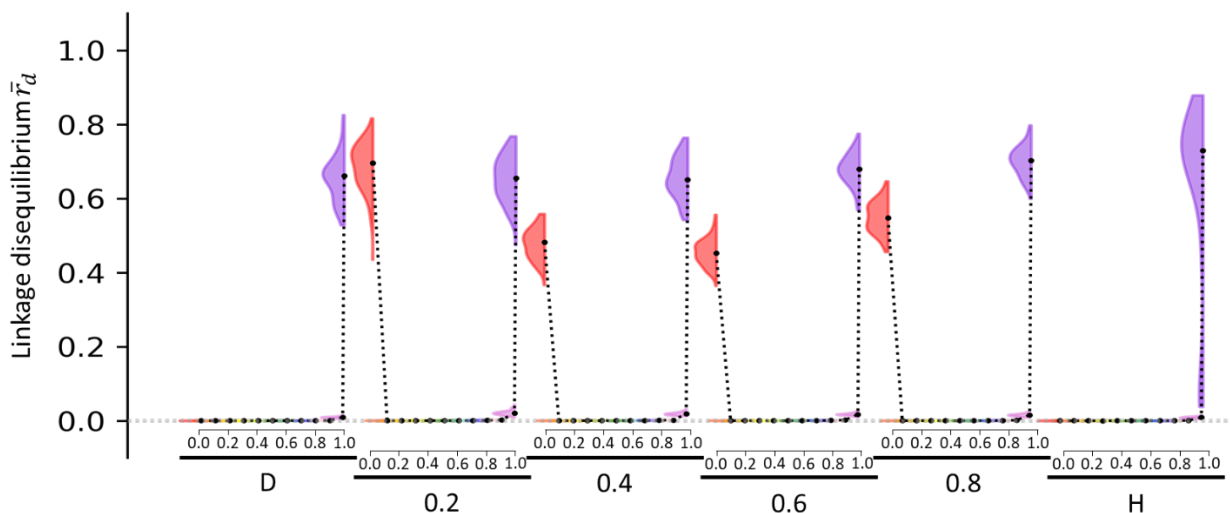
Figure S15: Violin plot of distribution of **mean F$_{IS}$** after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
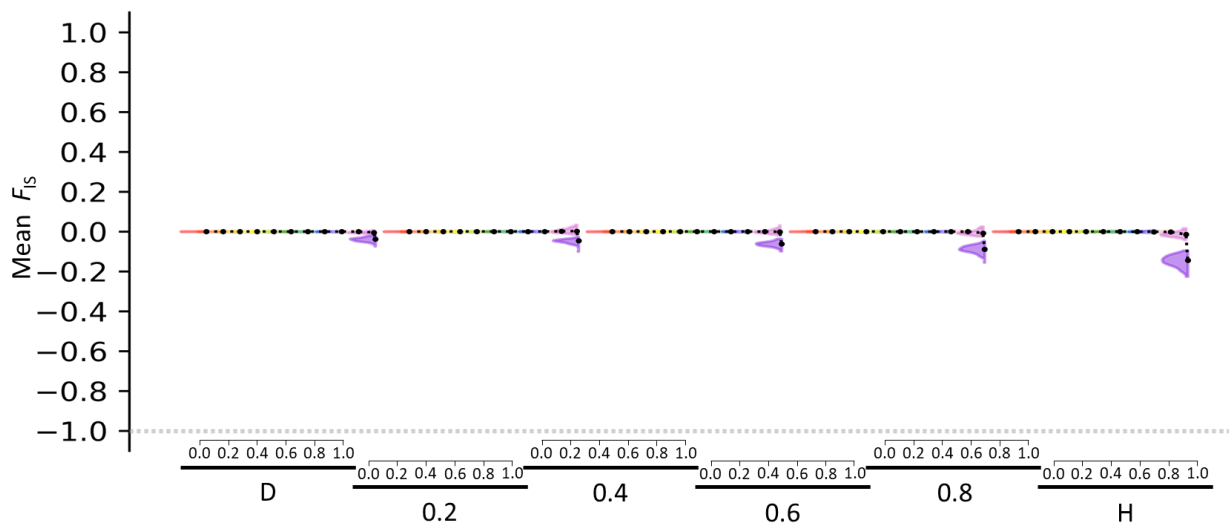

Figure S1 : Violin plot of distribution of **mean F$_{IS}$** after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
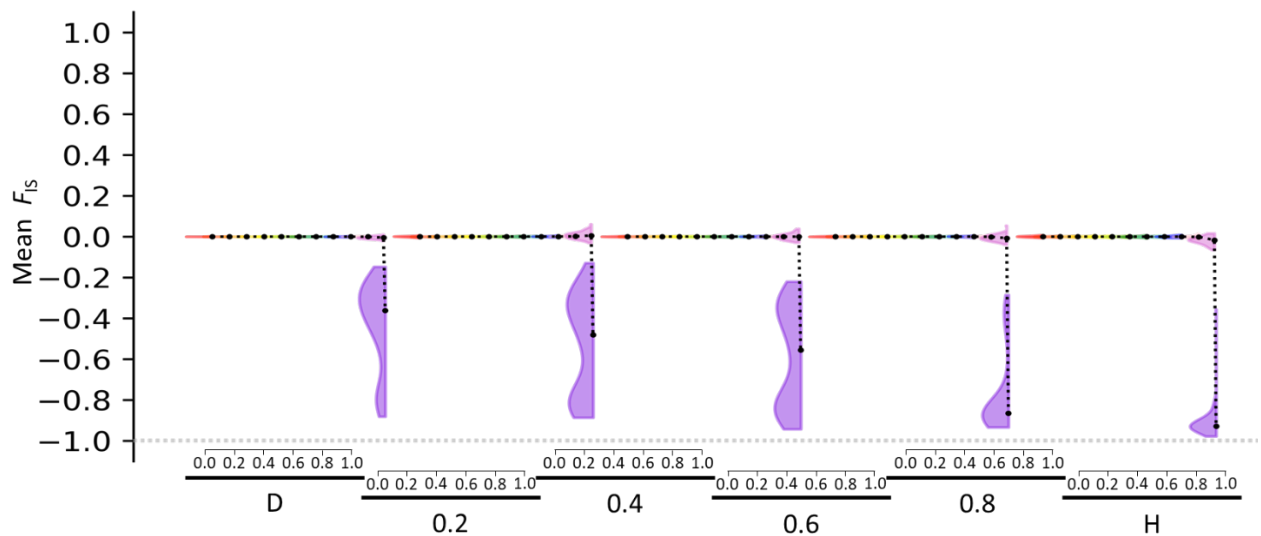
Figure S1 : Violin plot of distribution of **variance of F$_{IS}$** after 10000 burn-in generations **when mutation dominates** genetic drift as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids and haplontic populations (only haploids, H).
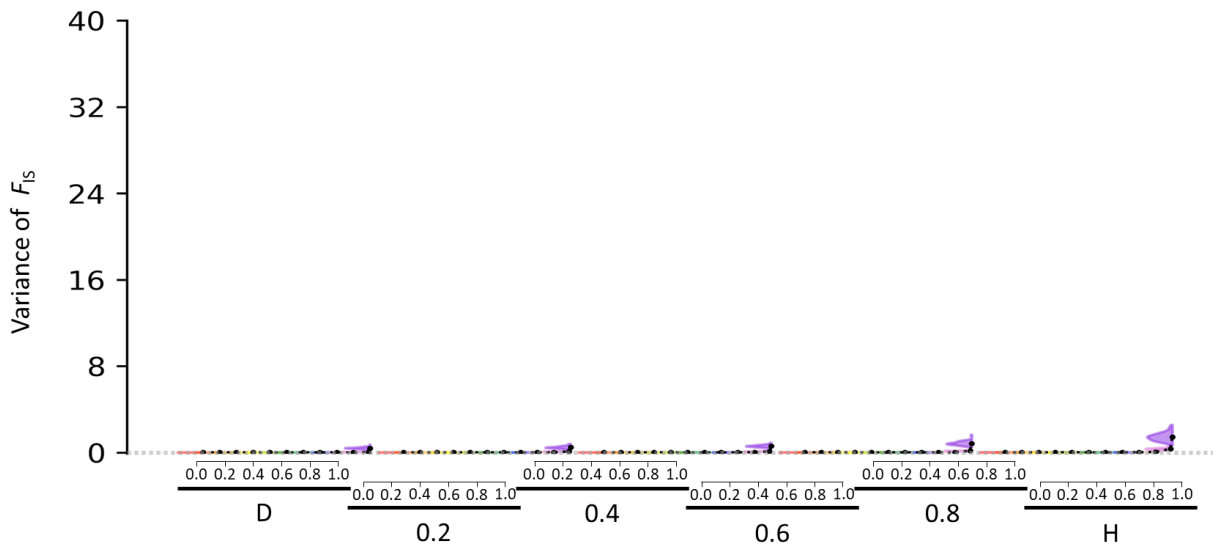

Figure S1 : Violin plot of distribution of **variance of F$_{IS}$** after 10000 burn-in generations **when genetic drift dominates** mutation as function of proportion of haploids (*ph*) and of rates of clonality (*c*). Distributions for each rate of clonality as color are plotted for diplontic populations (only diploids, D), four proportions of haploids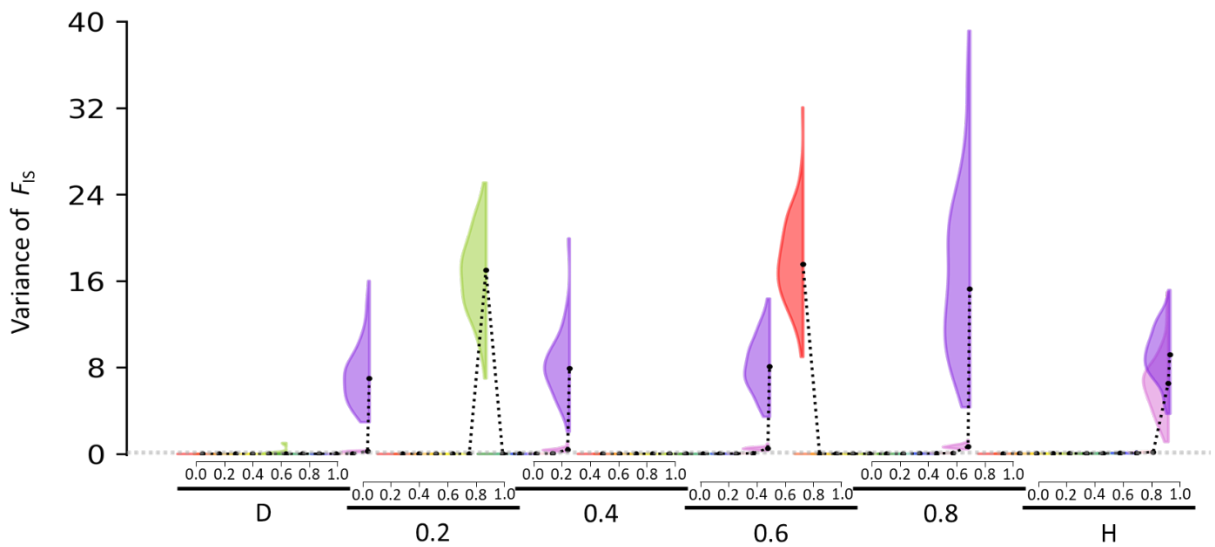 and haplontic populations (only haploids, H). Green and red distributions that spread out are due to the occurrence of one mutation per locus at the generation measured, in a fixed or nearly fixed genetic background.

IV. Graphs of distribution of population genetics indices after 10000 burn-in generations (ie "at equilibrium of evolutionary forces") when sampling randomly populations of 10 000 individuals with mutation rate at 10^{-4}.
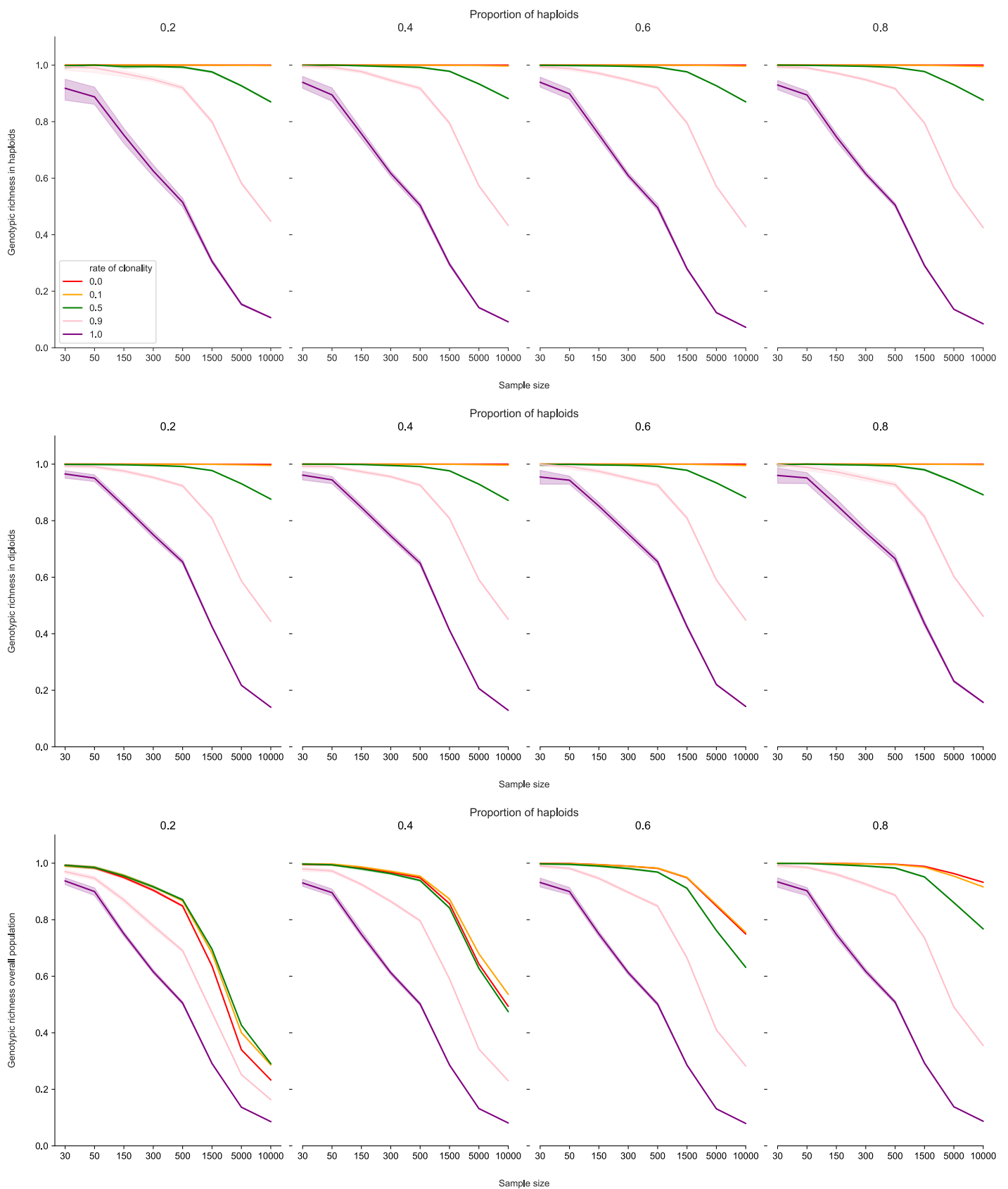
F**igure S19**: distribution of genotypic richness (R) in haploid pool (first row of figures), in diploid pool (second row) and overall population (third row) as function of sample size within a population of 10 000 individuals, of proportion of haploids in populations and rates of clonality. Population size of 10 000 individuals and mutation rate of 10-4. Solid lines plot the average values and semi-transparent envelops the confidence interval on the mean obtained by bootstrapping on the 100 measures. Colors account for rates of clonality: red for c=0 (only sexual), orange c=0.1, green c=0.5, pink c=0.9 and purple c=1 (only clonal).
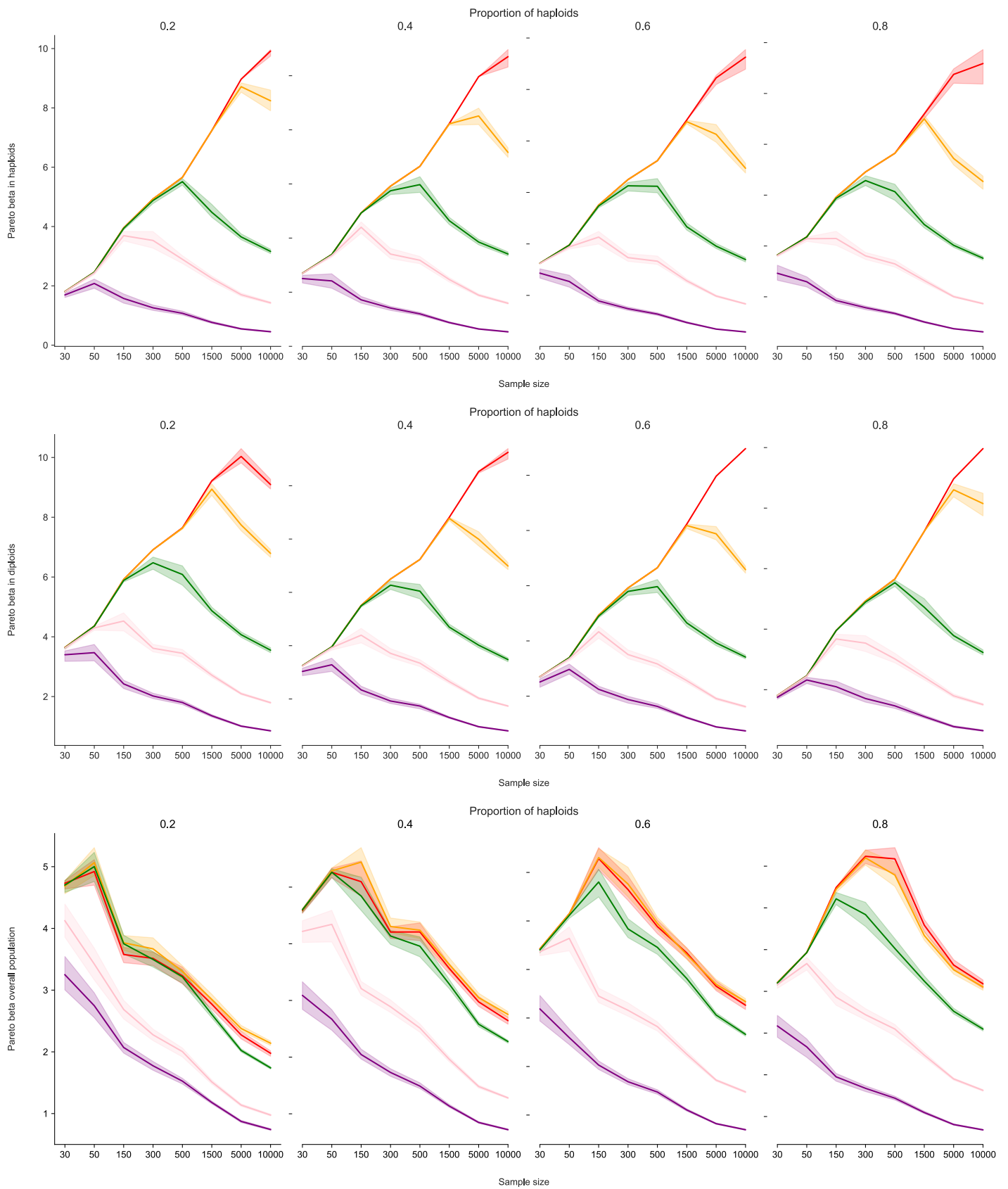
Figure S20: distribution of pareto beta in haploid pool (first row of figures), in diploid pool (second row) and overall population (third row) as function of sample size within a population of 10 000 individuals, of proportion of haploids in populations and rates of clonality. Population size of 10 000 individuals and mutation rate of 10-4. Solid lines plot the average values and semi-transparent envelops the confidence interval on the mean obtained by bootstrapping on the 100 measures. Colors account for rates of clonality: red for c=0 (only sexual), orange c=0.1, green c=0.5, pink c=0.9 and purple c=1 (only clonal).
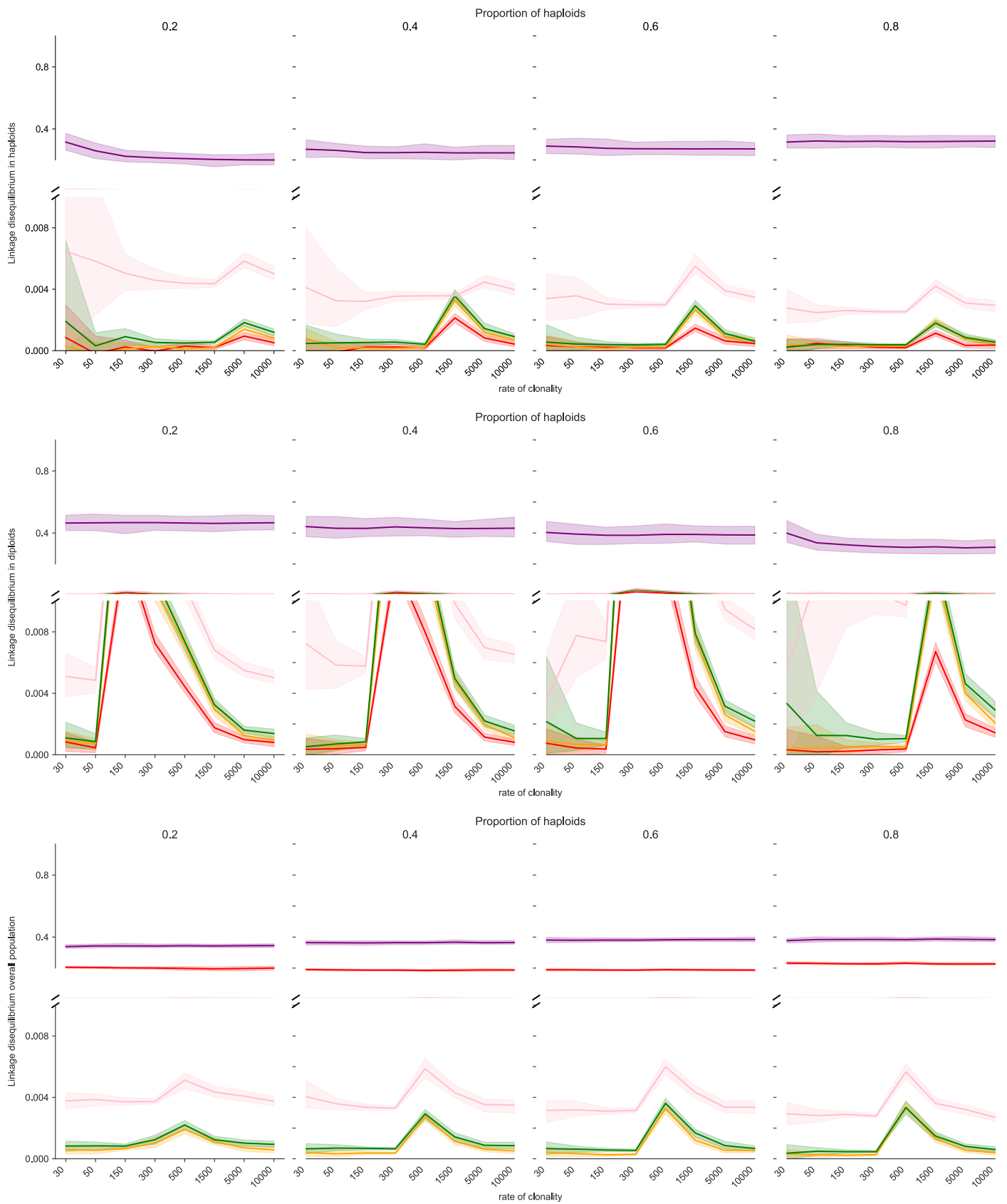
Figure S2 : distribution of linkage disequilibrium in haploid pool (first row of figures), in diploid pool (second row) and overall population (third row) as function of sample size within a population of 10 000 individuals, of proportion of haploids in populations and rates of clonality. Population size of 10 000 individuals and mutation rate of 10-4. Solid lines plot the average values and semi-transparent envelops the confidence interval on the mean obtained by bootstrapping on the 100 measures. Colors account for rates of clonality: red for c=0 (only sexual), orange c=0.1, green c=0.5, pink c=0.9 and purple c=1 (only clonal).
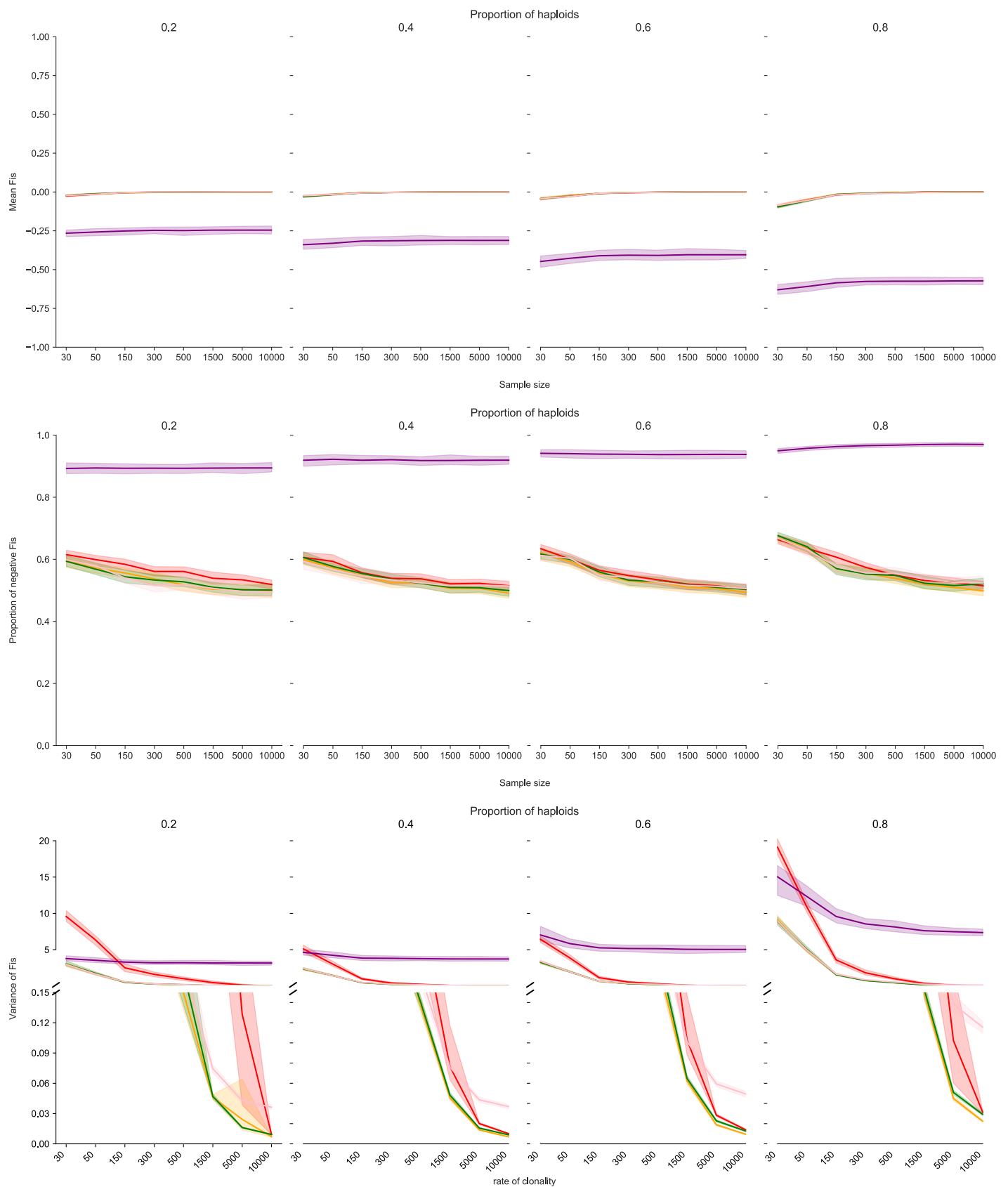
Figure S22: distribution of Mean FIS (first row of figures), proportion of negative FIS (second row) and variance of FIS (third row) as function of sample size within a population of 10 000 individuals, of proportion of haploids in populations and rates of clonality. Population size of 10 000 individuals and mutation rate of 10-4. Solid lines plot the average values and semi-transparent envelops the confidence interval on the mean obtained by bootstrapping on the 100 measures. Colors account for rates of clonality: red for c=0 (only sexual), orange c=0.1, green c=0.5, pink c=0.9 and purple c=1 (only clonal).

Figure S2 : Summary of the effects imposed by reproductive mode (sexuality and partial clonality) and haplodiplontic life cycle on the evolution of genetic and genotypic diversity. Dark green and gold colors stand for genetic pools evolving independently, purple cones for demographical events, dotted line for sexual reproduction and solid arrow for clonal reproduction along generations.

Conditions

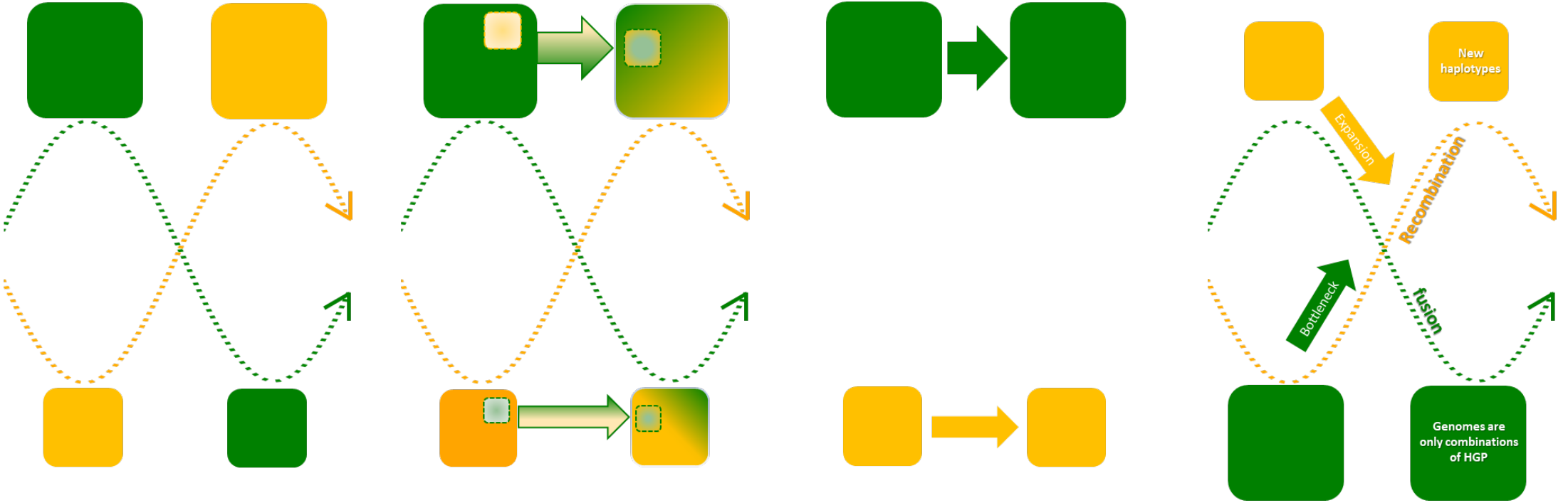Strict sexuality without overlapping generations

Partial clonality without overlapping generations

Fully clonal populations

ph ↘, genetic drift ↗ in haploid & ↘ in diploid phase

Haploid stage

Diploid stage

New haplotypes

Expansion

Recombination

Bottleneck

fusion

Genomes are only combinations of HGP

Generations

Consequences

2 temporal genetic pools evolving independantly.
→ Importance of temporal sampling and phase.

2 temporal genetic pools connected by clonal maintenance through generations.

2 genetic pools keeping the same ploidy evolving independantly.
→ Importance of not mixing haploids and diploids.

Genetic drift in the smallest genetic pool drives distributions of indices. Especially in haploid pool due to recombination.