Replicability of figure 3 across populations

Contents

(Top-left) Distribution of scaled selection coefficients (S_0) for all observed substitutions along the terminal branch of the phylogenetic tree. Mutations are divided into three classes of selection: deleterious ($\mathcal{D}_0$), nearly-neutral ($\mathcal{N}_0$) and beneficial ($\mathcal{B}_0$, supposedly beneficial back-mutations). If there are fewer substitutions than expected, this class is thus undergoing purifying selection, as is the case for $\mathcal{D}_0$.

(Top-right) Distribution of scaled selection coefficients (S_0), predicted for all possible mutations away from the ancestral human genome.

(Bottom-left) The site-frequency spectrum (SFS) in humans of African descent for a random sample of 16 alleles (means in solid lines and standard deviations in color shades) for each class of selection and for synonymous mutations, supposedly neutral (black). The SFS represents the proportion of mutations (y-axis) with a given number of derived alleles in the population (x-axis). At high frequencies, deleterious mutations are underrepresented.
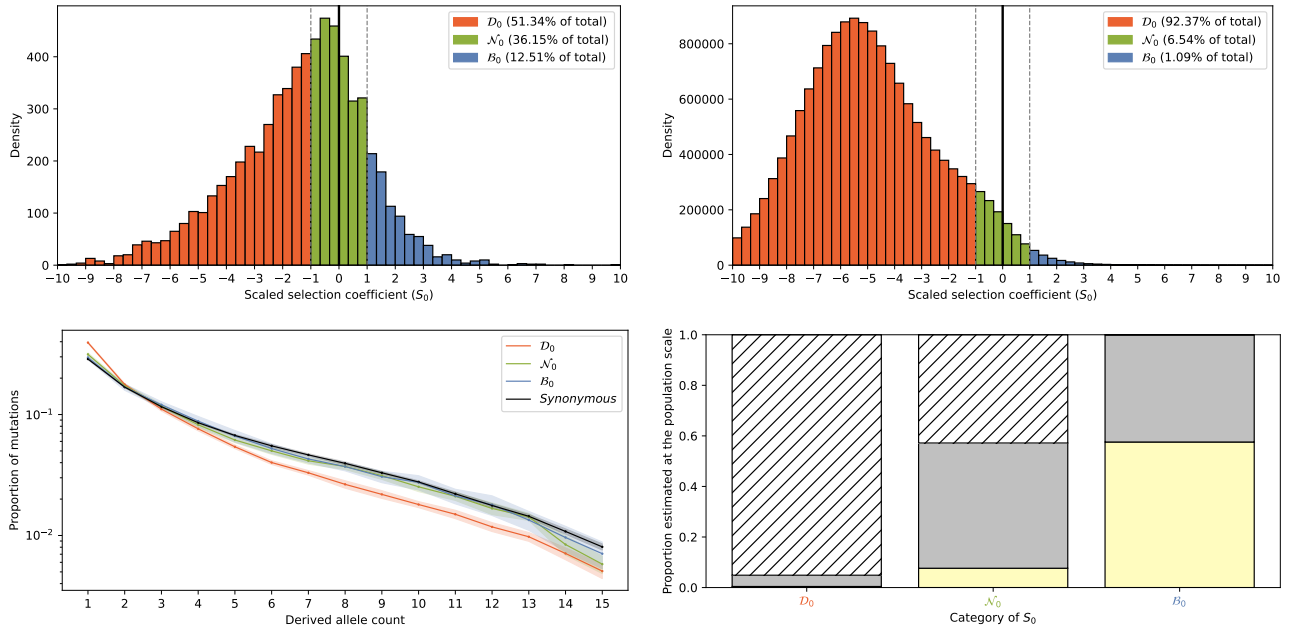
(Bottom-right) Proportion of beneficial $\mathbb{P}[\mathcal{D}]$, nearly-neutral $\mathbb{P}[\mathcal{N}]$, and deleterious mutations $\mathbb{P}[\mathcal{B}]$ estimated at the population scale for each class of selection at the phylogenetic scale. Proportions depicted here are not weighted by their mutational opportunities.
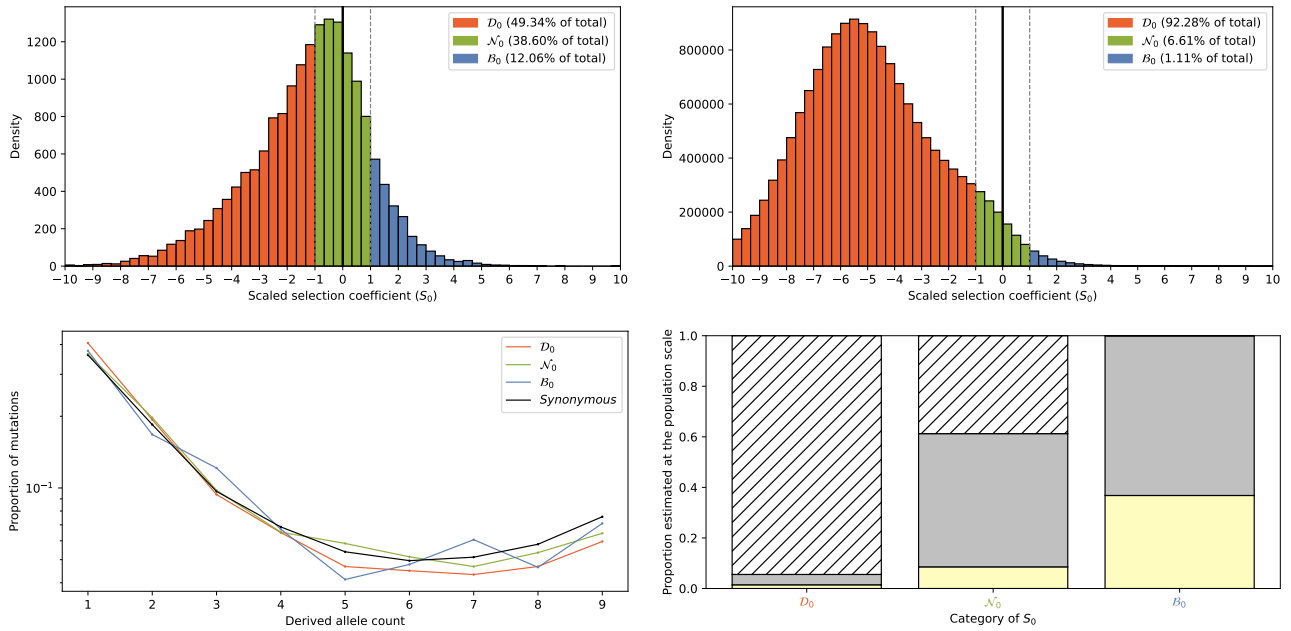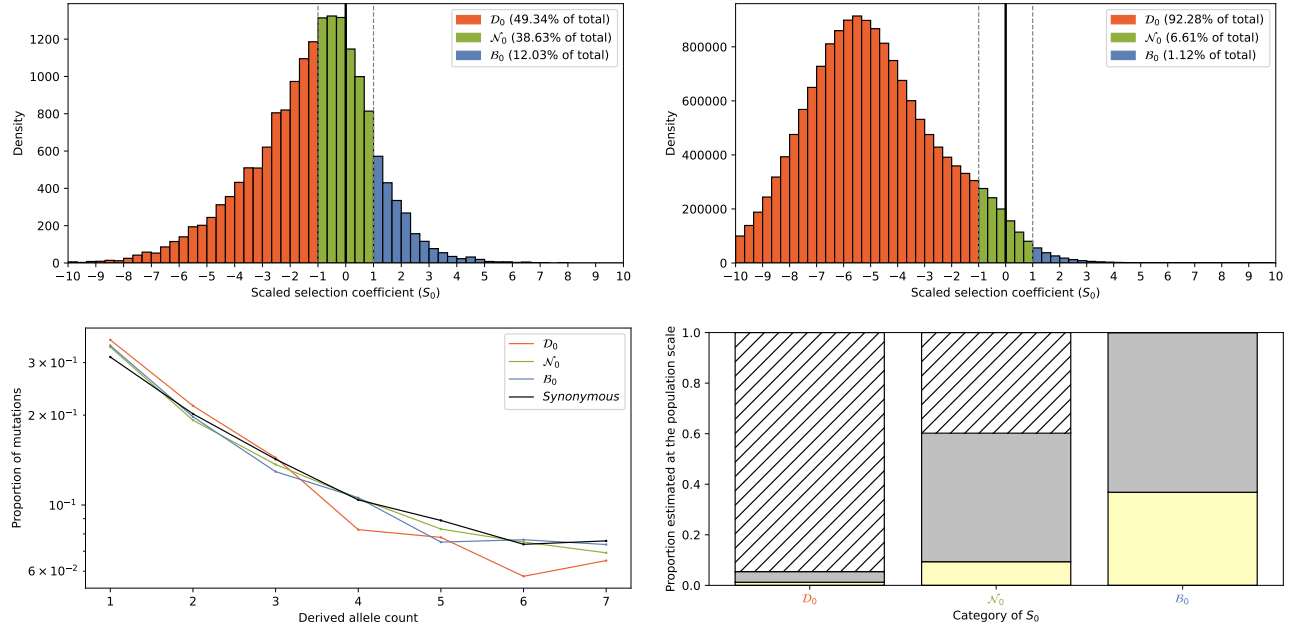
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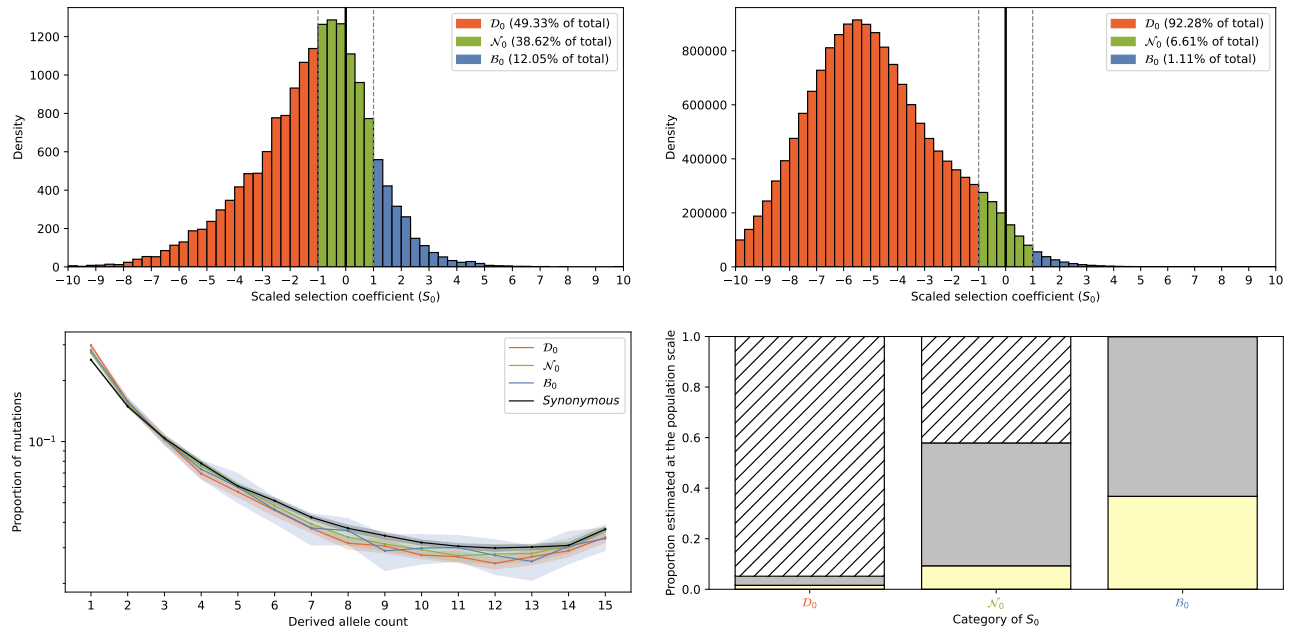
1.1 Iran

2
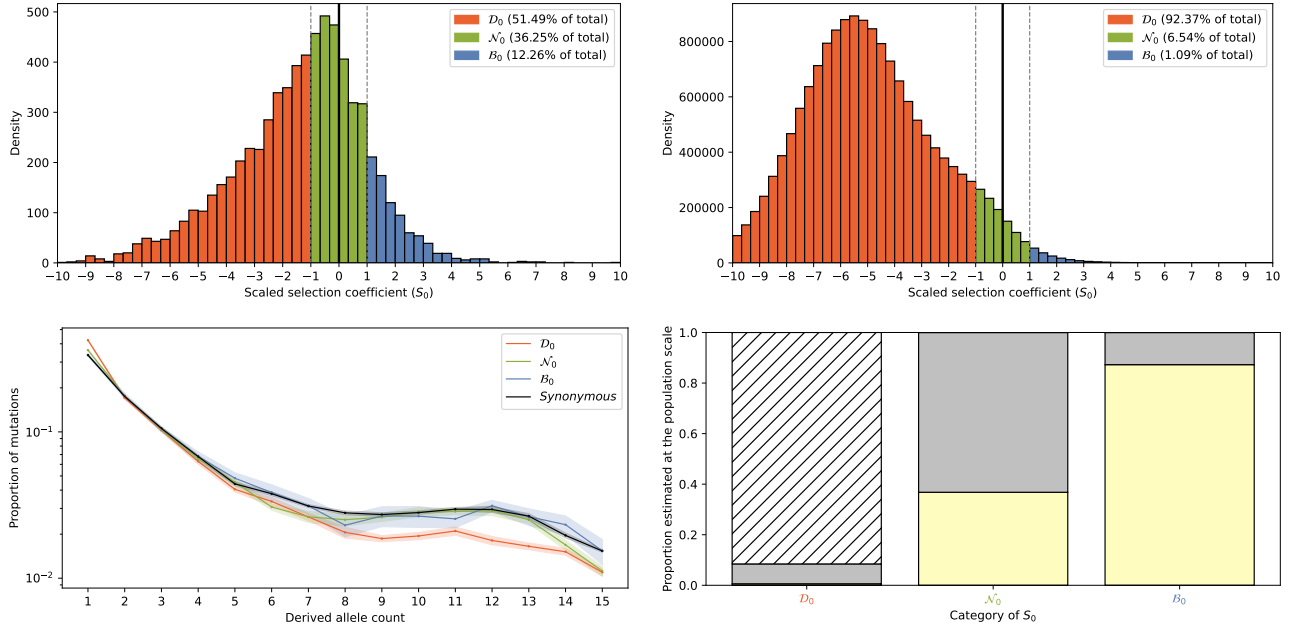
1.2 Uganda

2 Capra

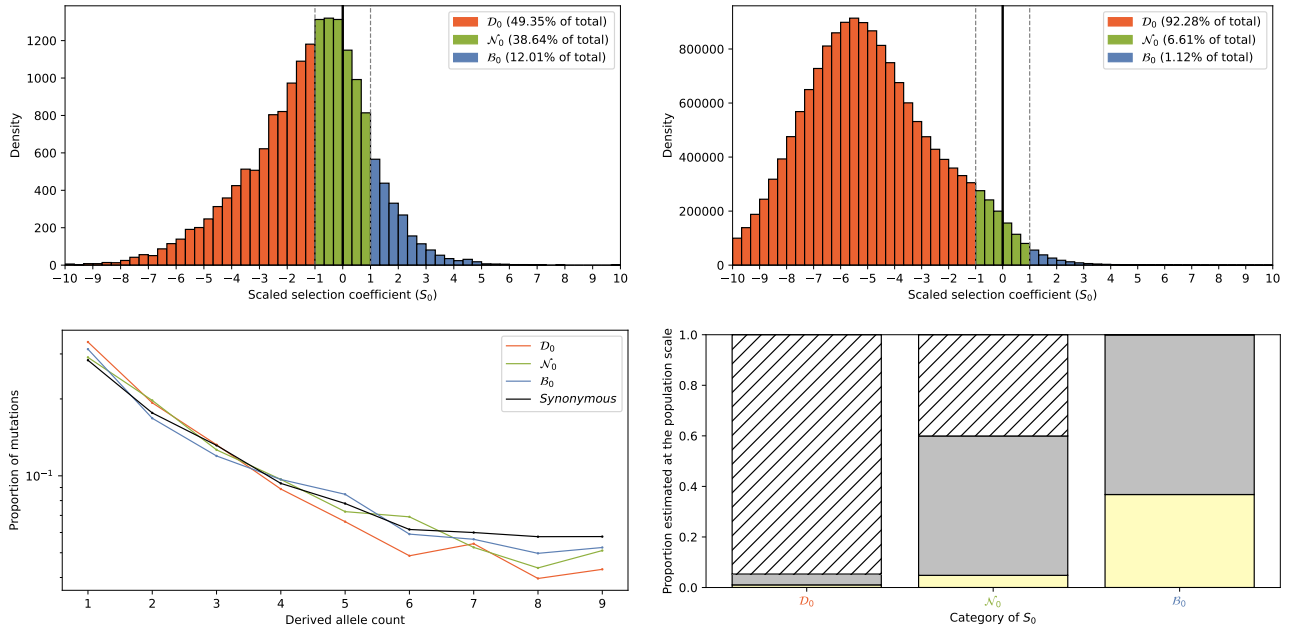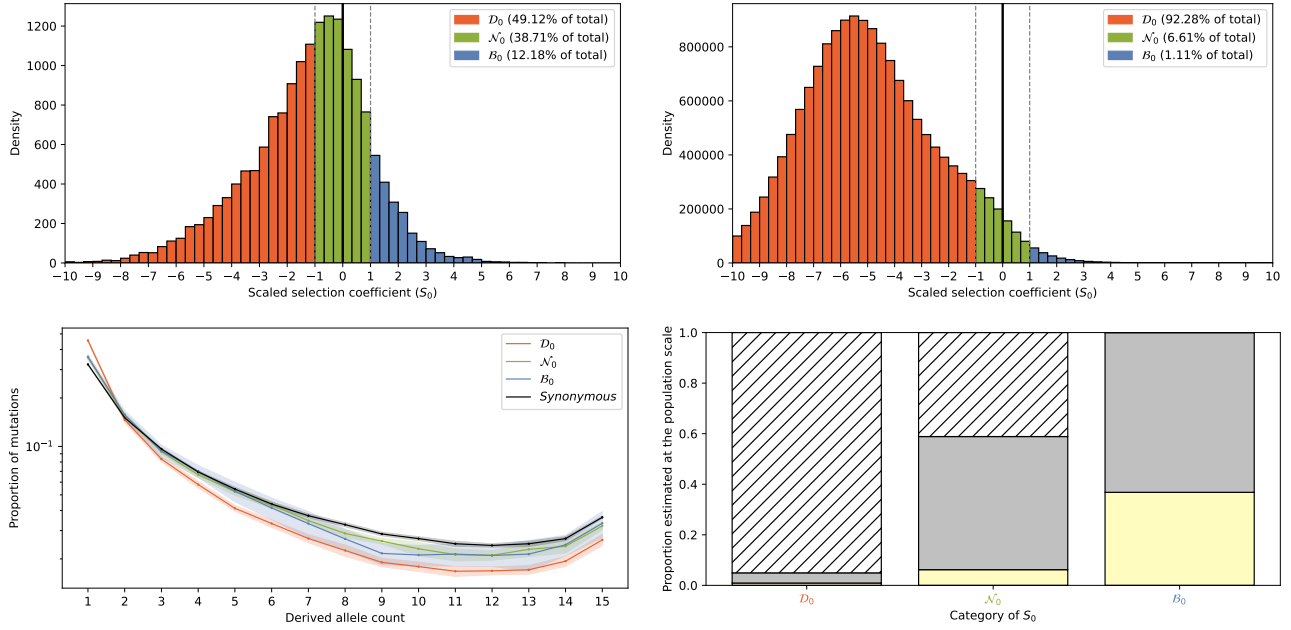## 2.1 Australia

2.2   France

2.3   Iran (C. aegagrus)
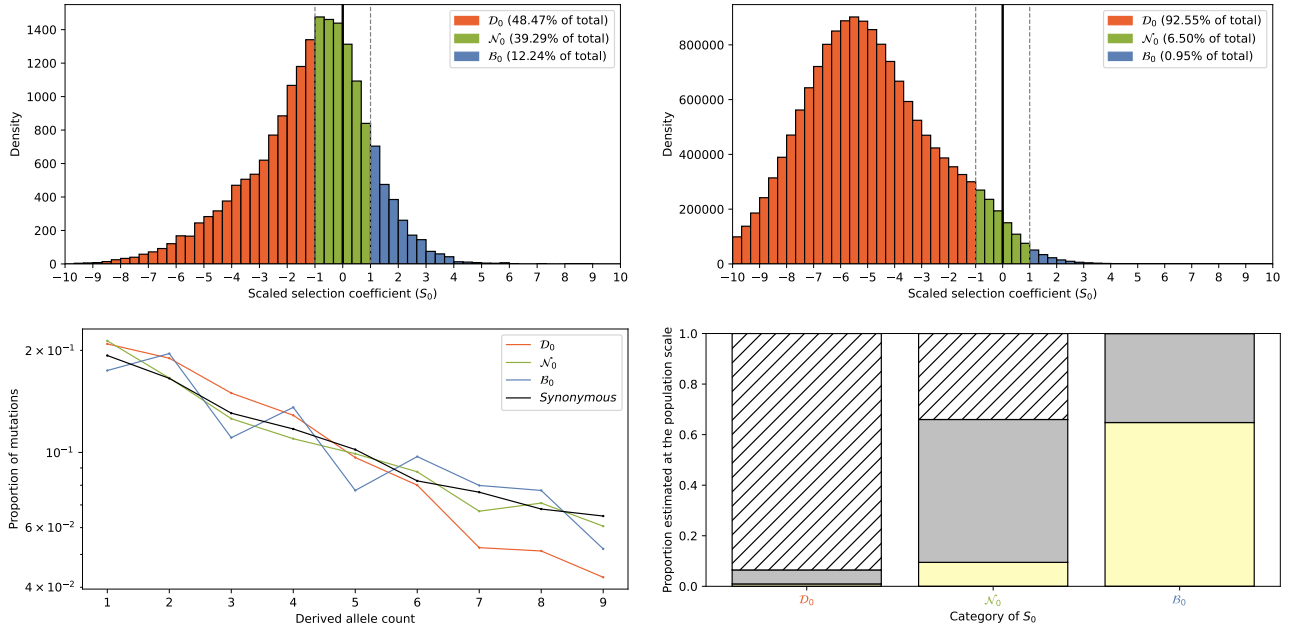
2.4   Iran
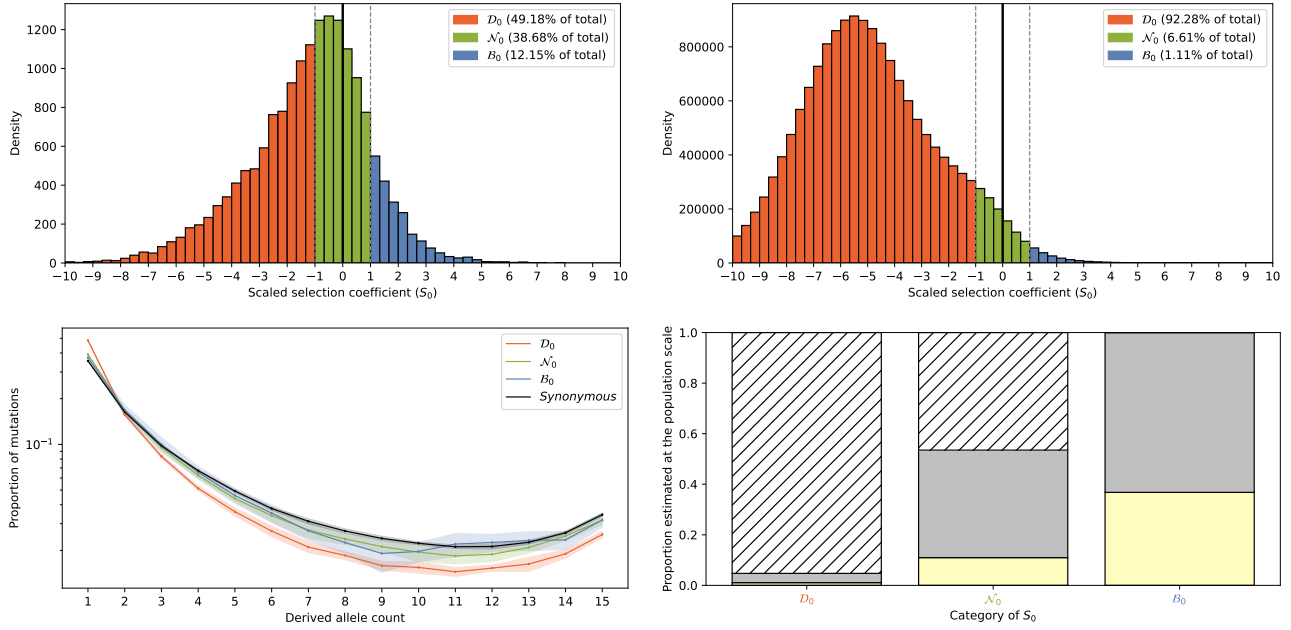
2.5   Italy
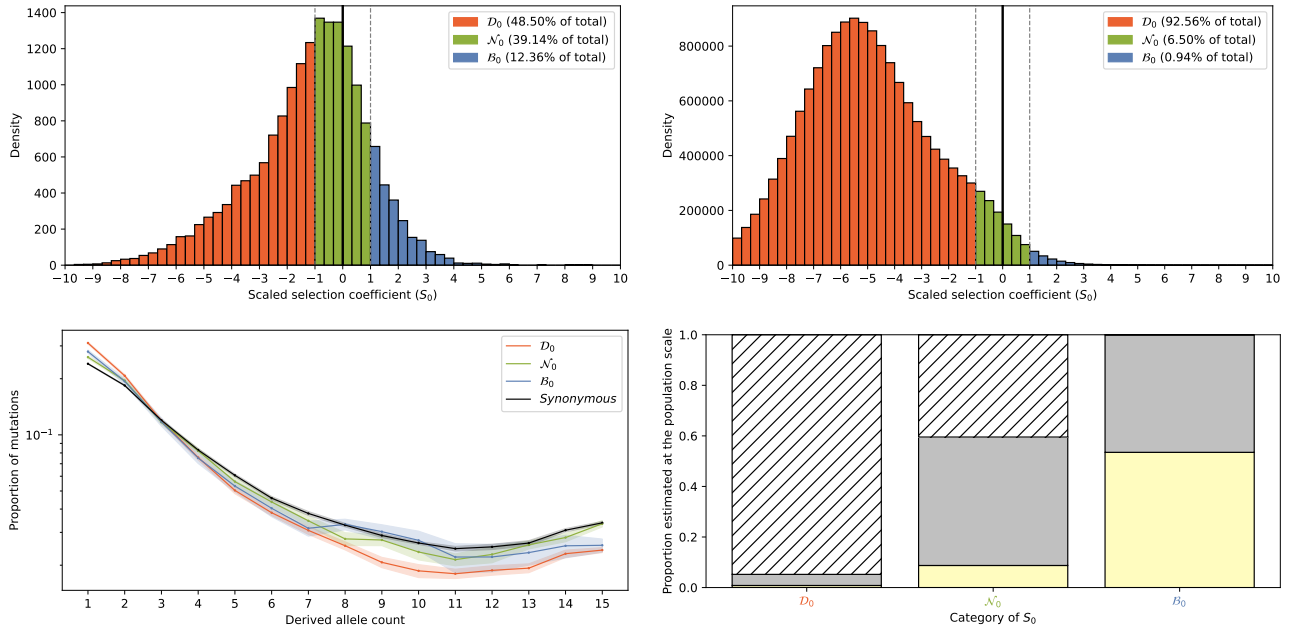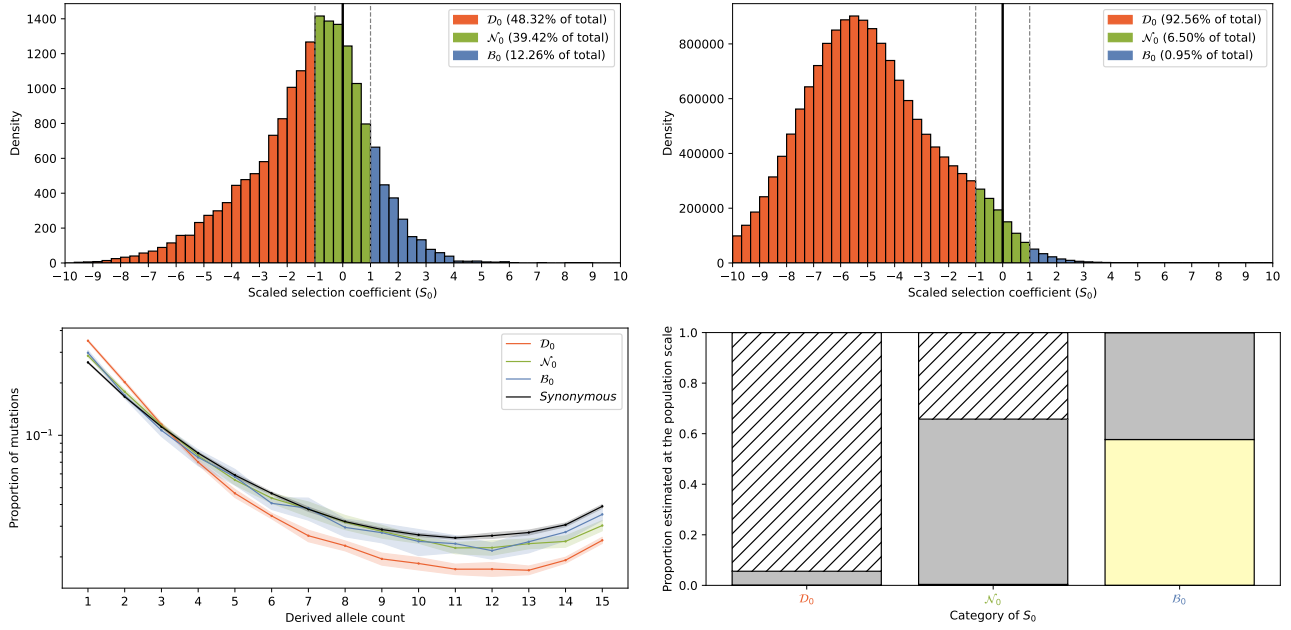
2.6 Morocco

3 Chlorocebus sabaeus
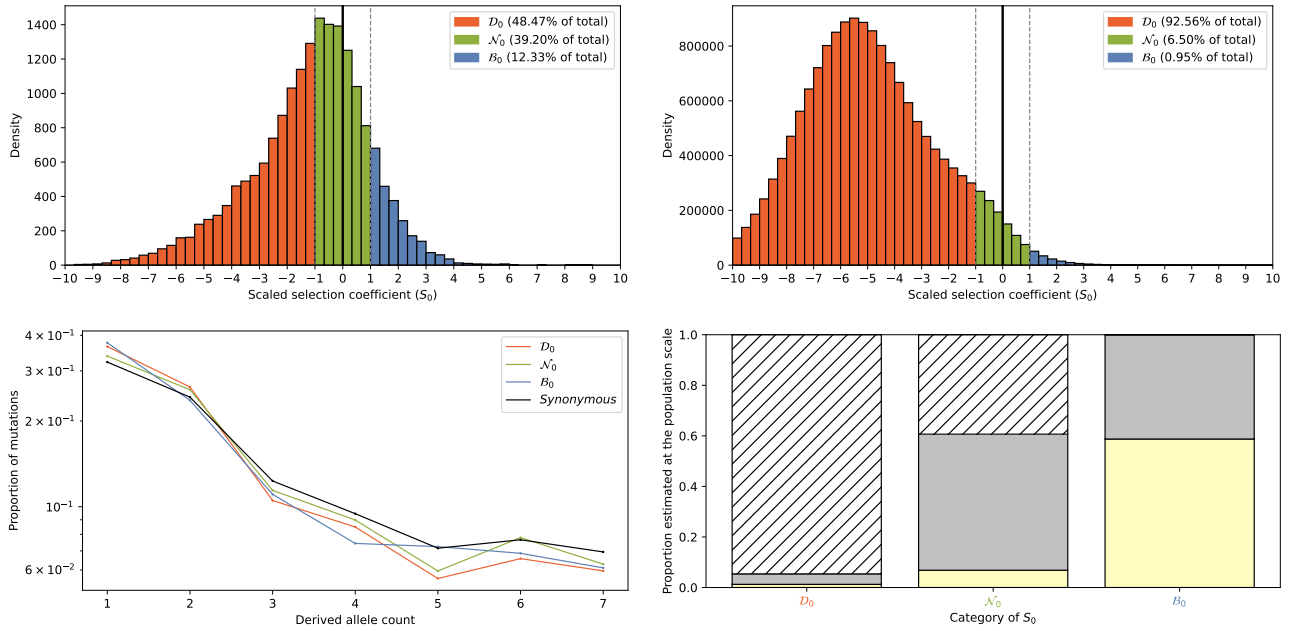
3.1 Barbados

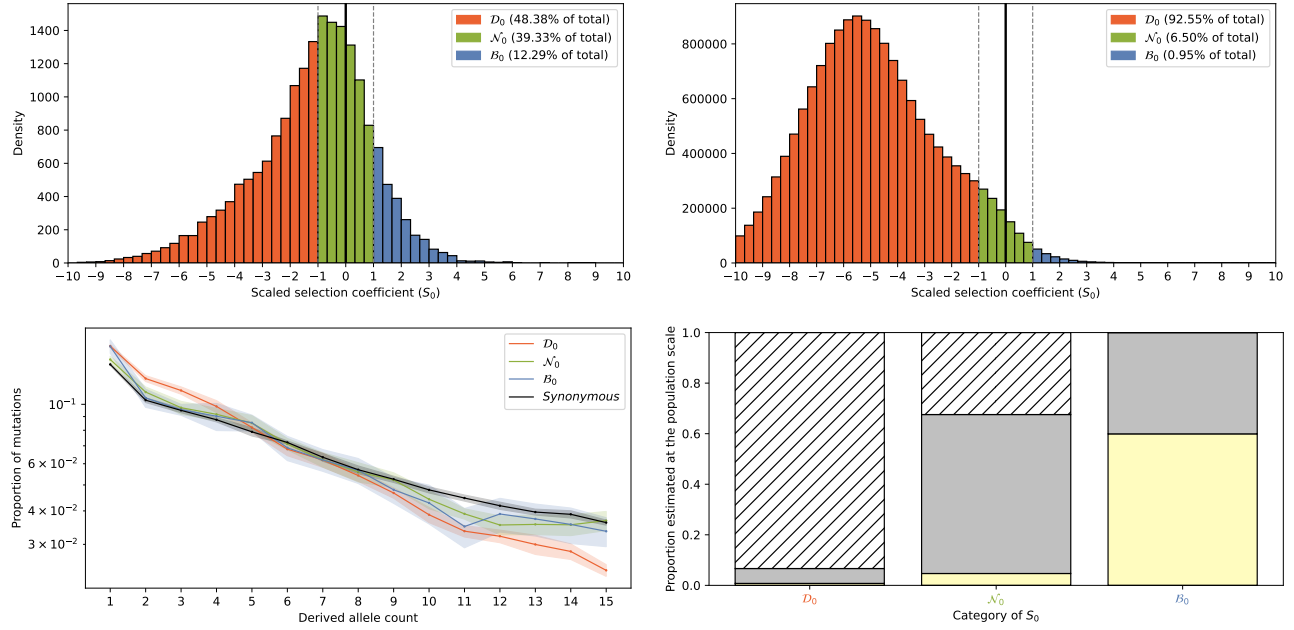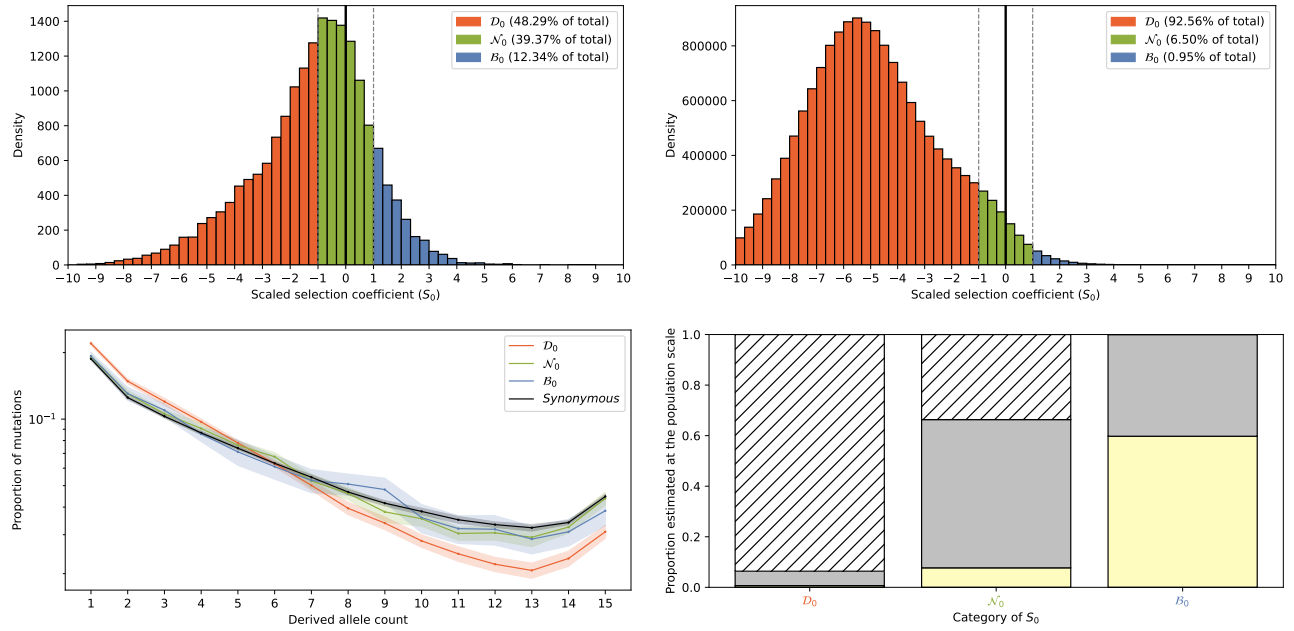## 3.2   Central Afr. Rep.

3.3   Ethiopia
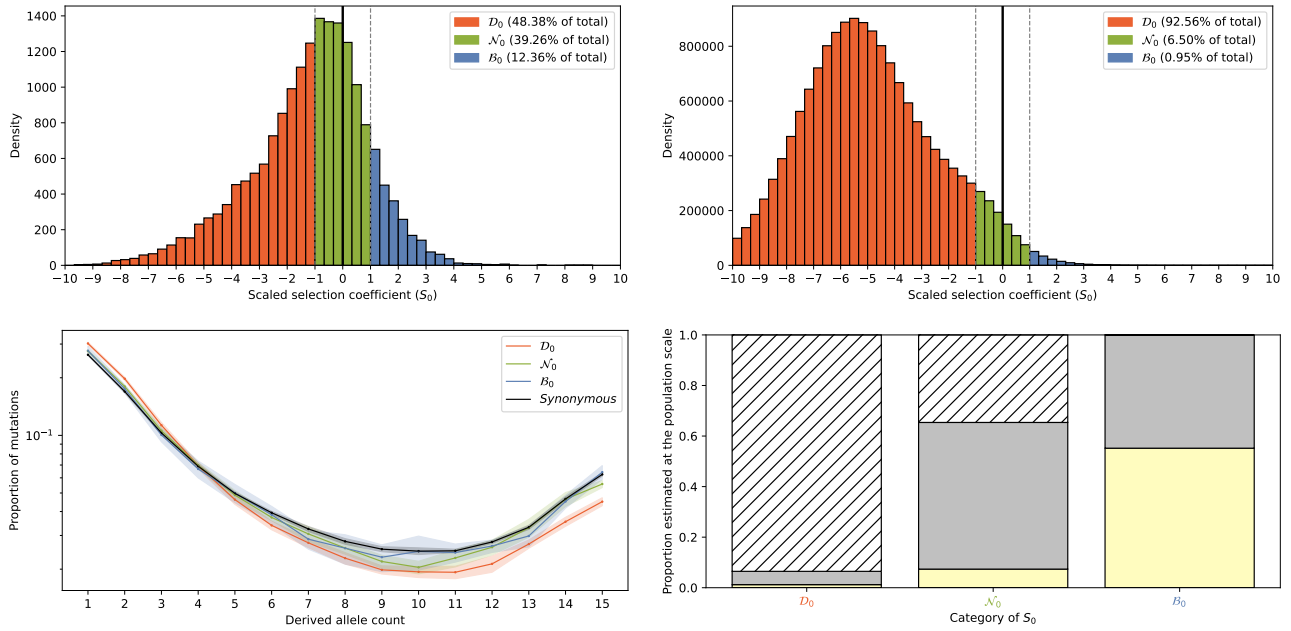
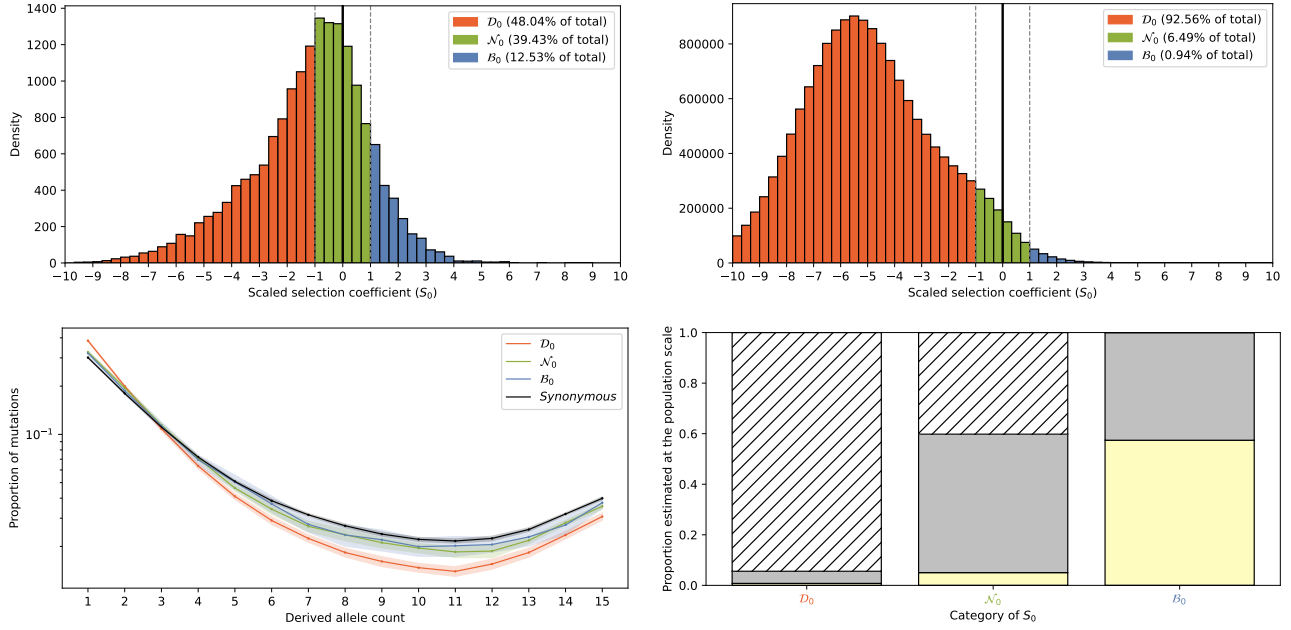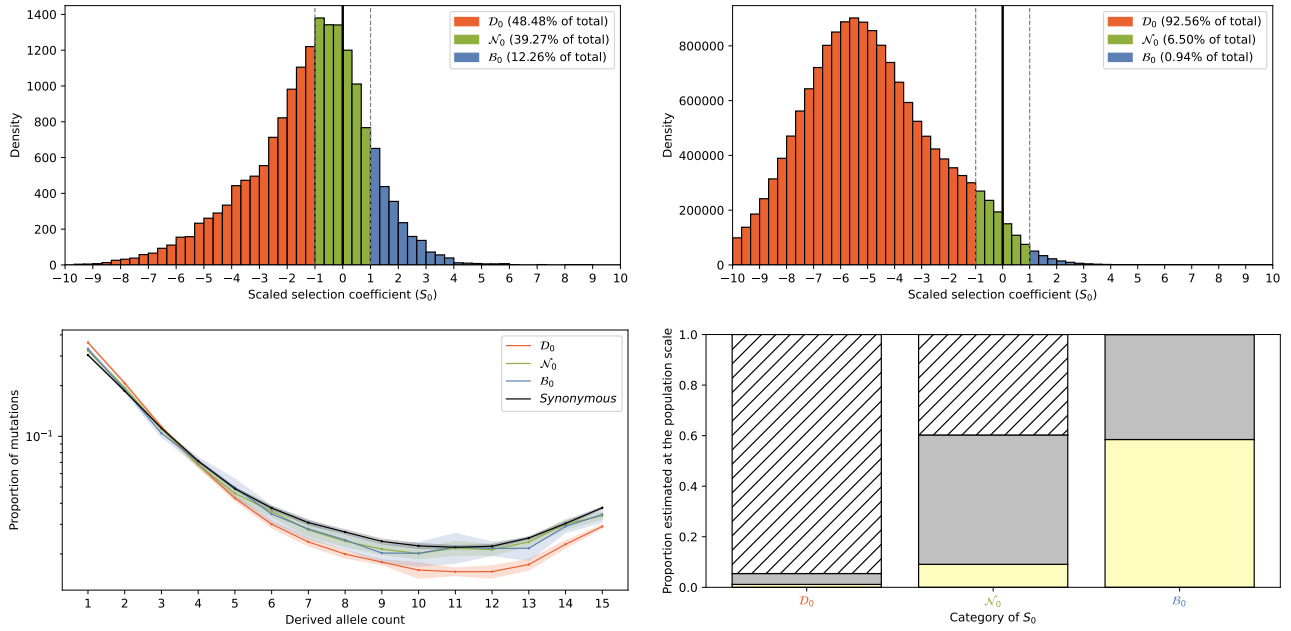## 3.4 Gambia

3.5 Kenya

3.6 Nevis
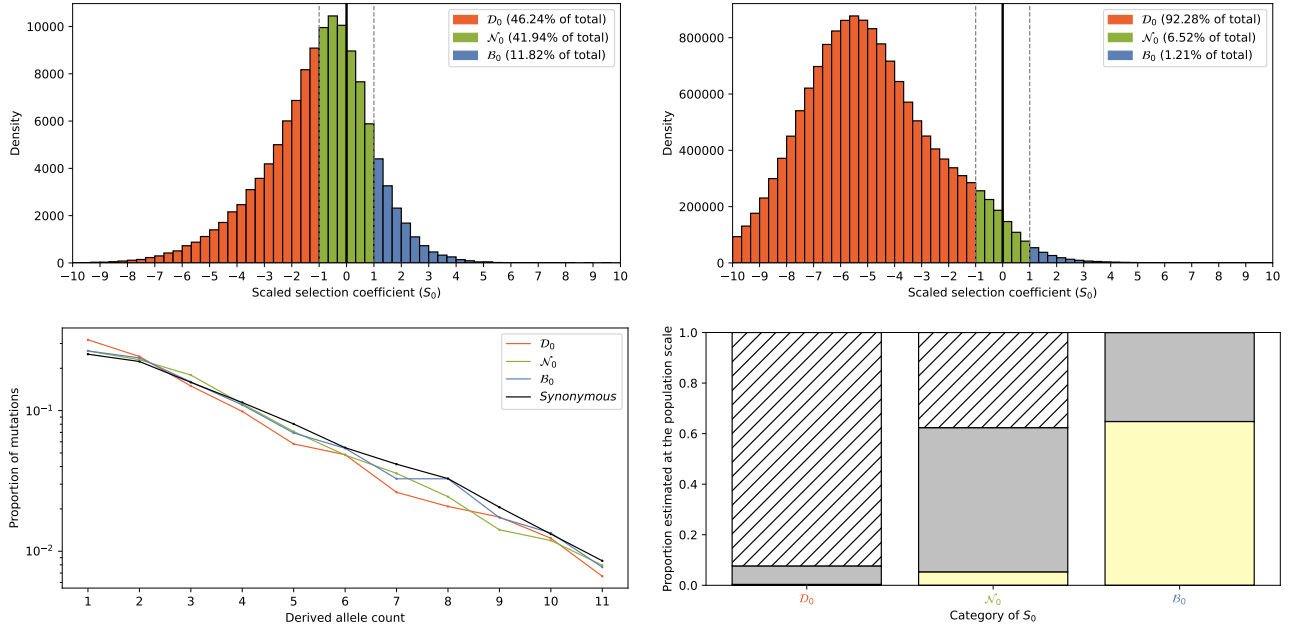

3.7 Saint Kitts
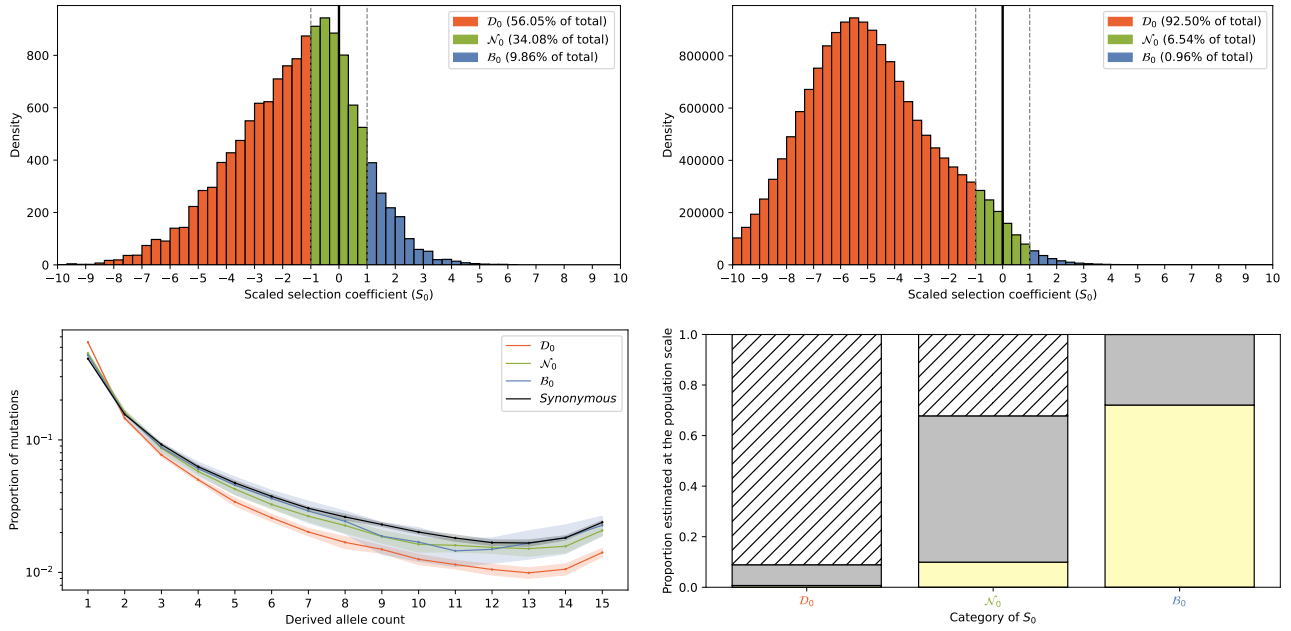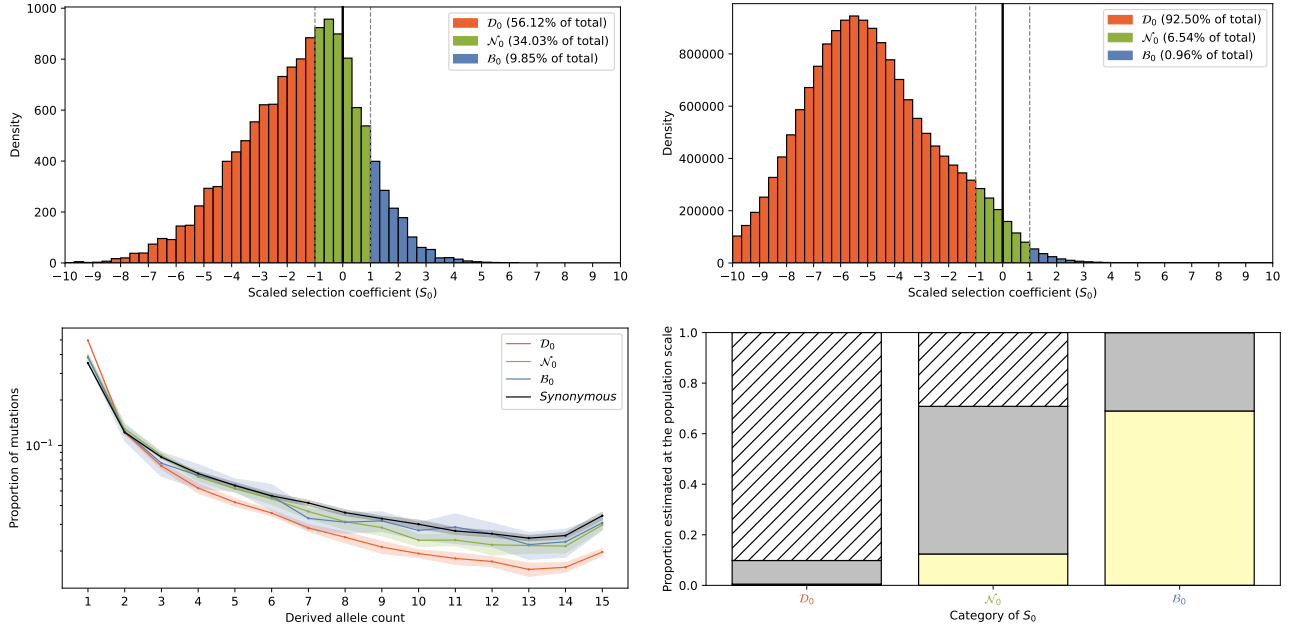
3.8 South Africa

3.9 Zambia

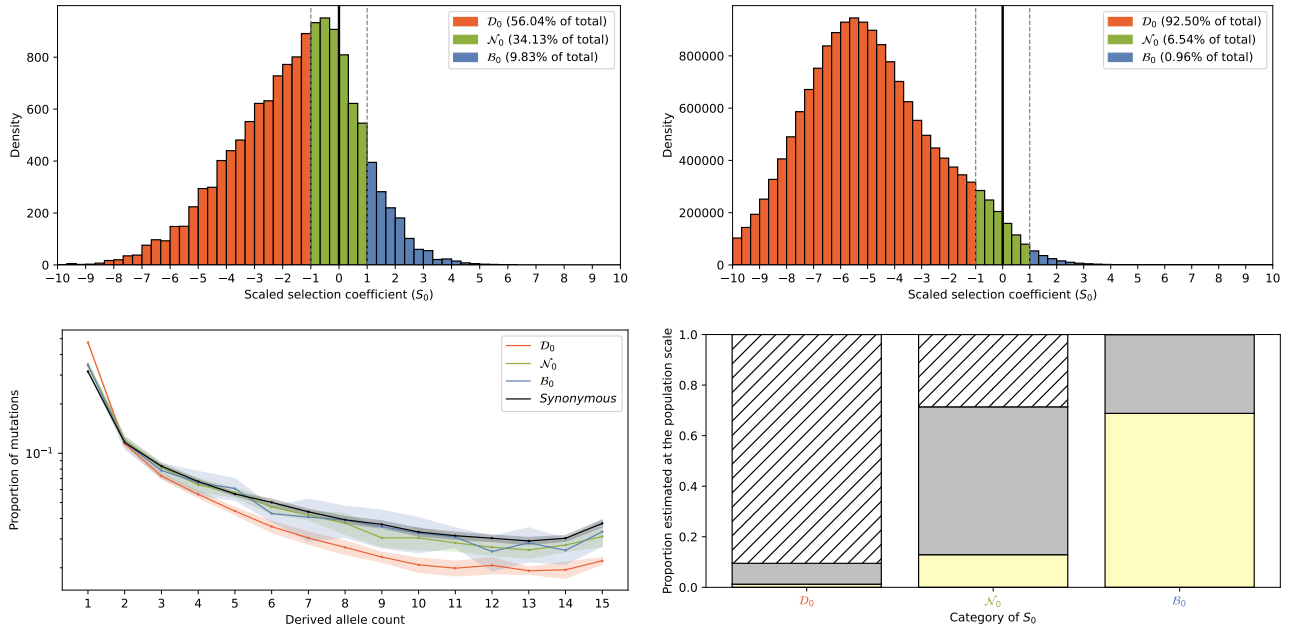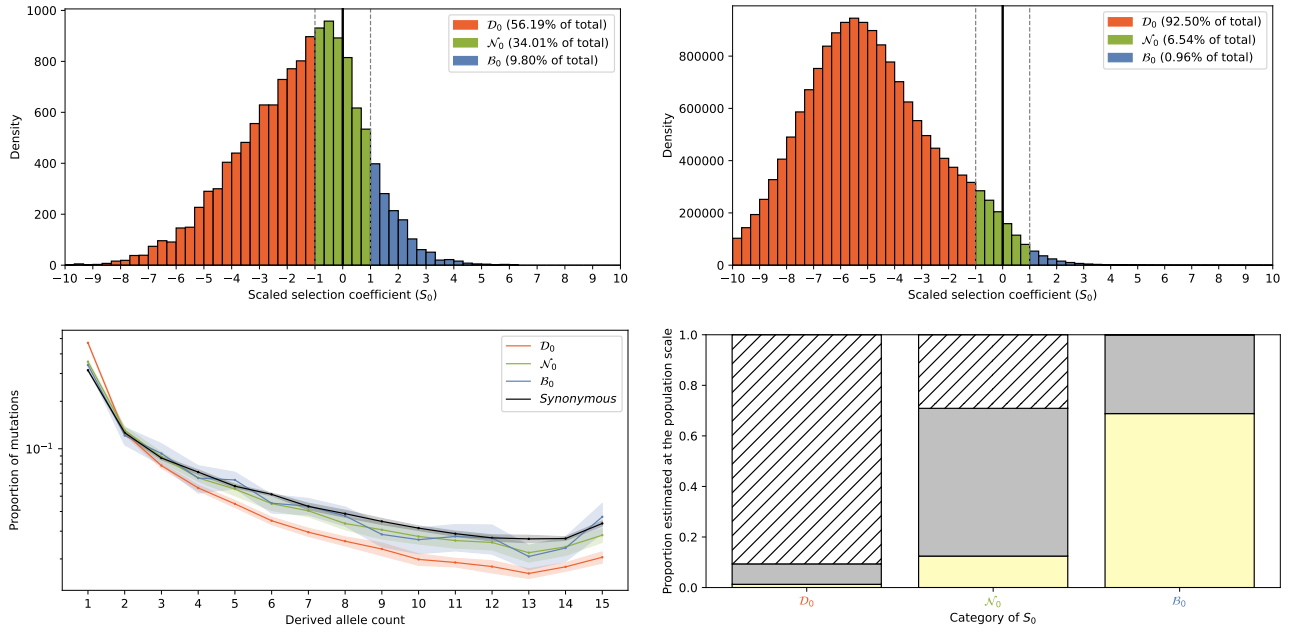# 4 Equus caballus
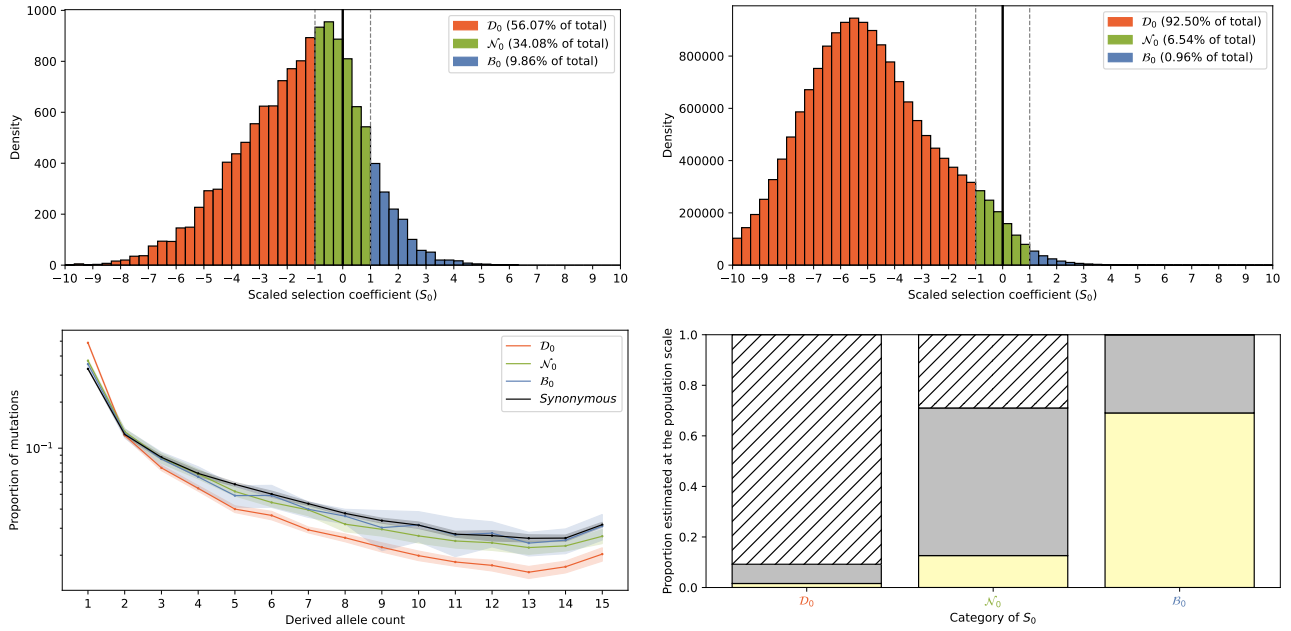

5 Homo sapiens

5.1 African

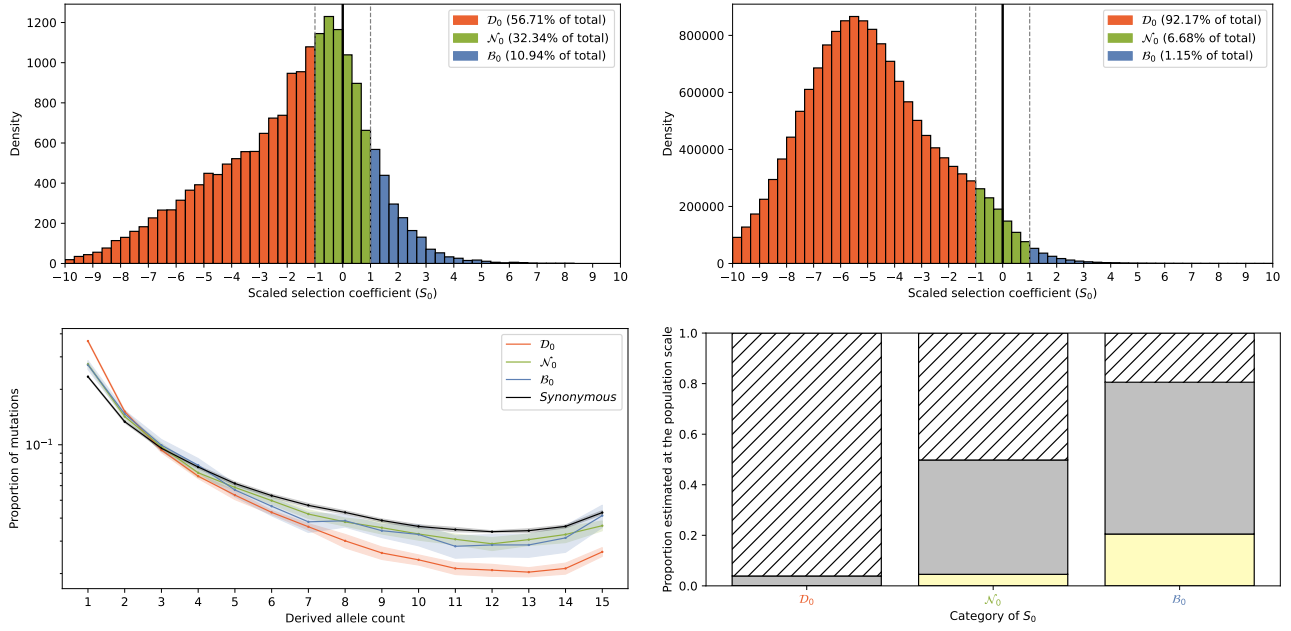## 5.2 Admixed American

5.3 East Asian

5.4   European

5.5   South Asian

6   Ovis

6.1   Iran

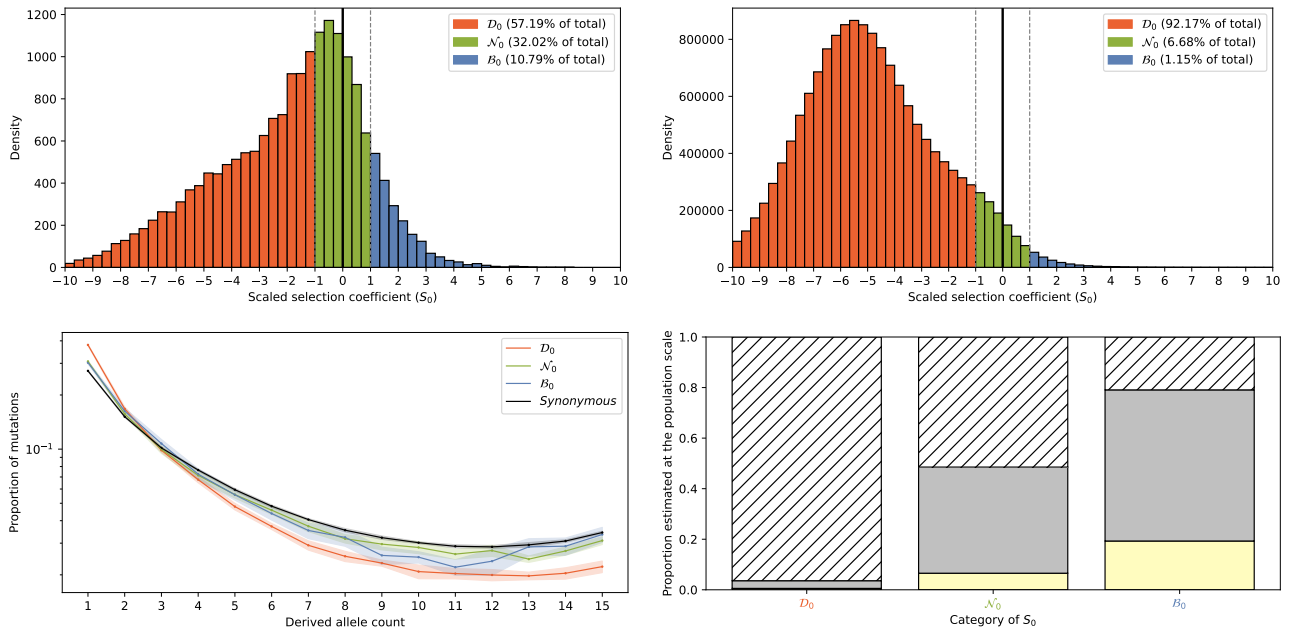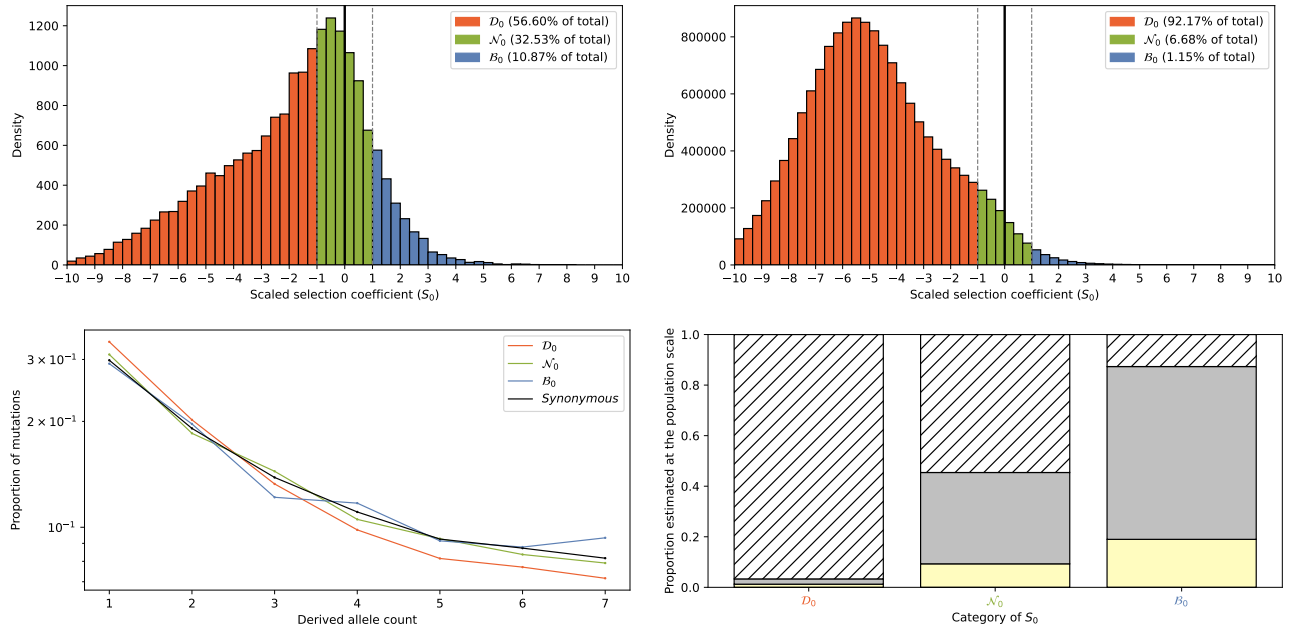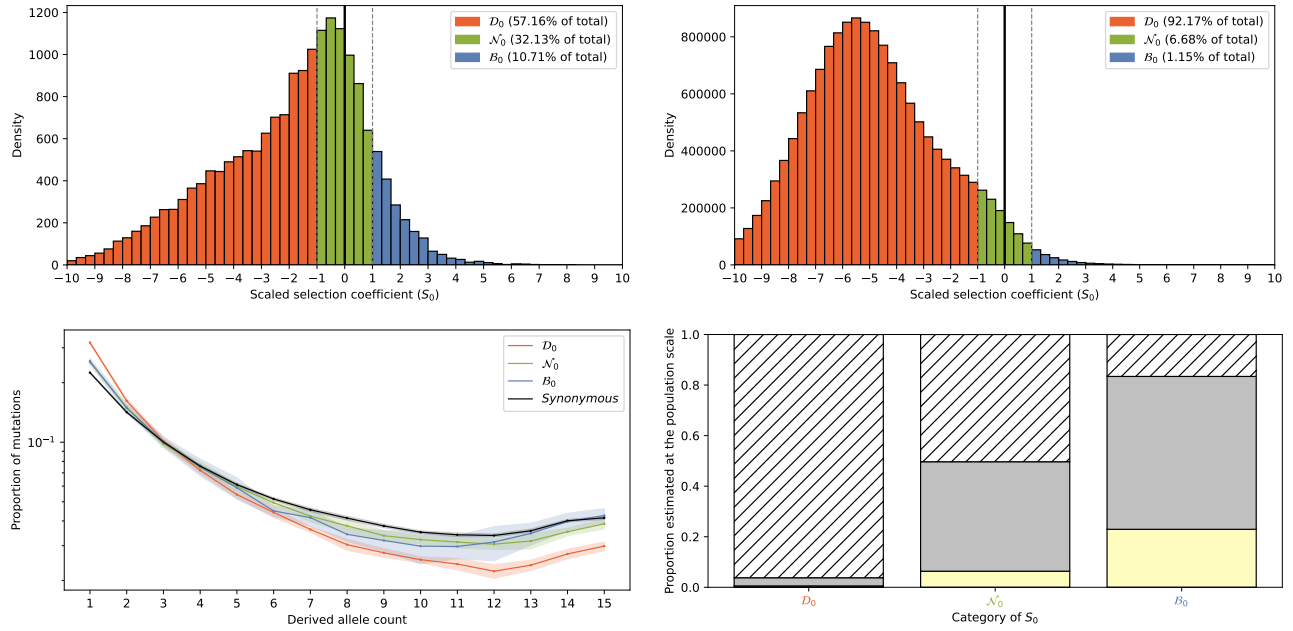## 6.2   Iran (O. orientalis)

6.3 Iran (O. vignei)

6.4 Various

6.5 Morocco