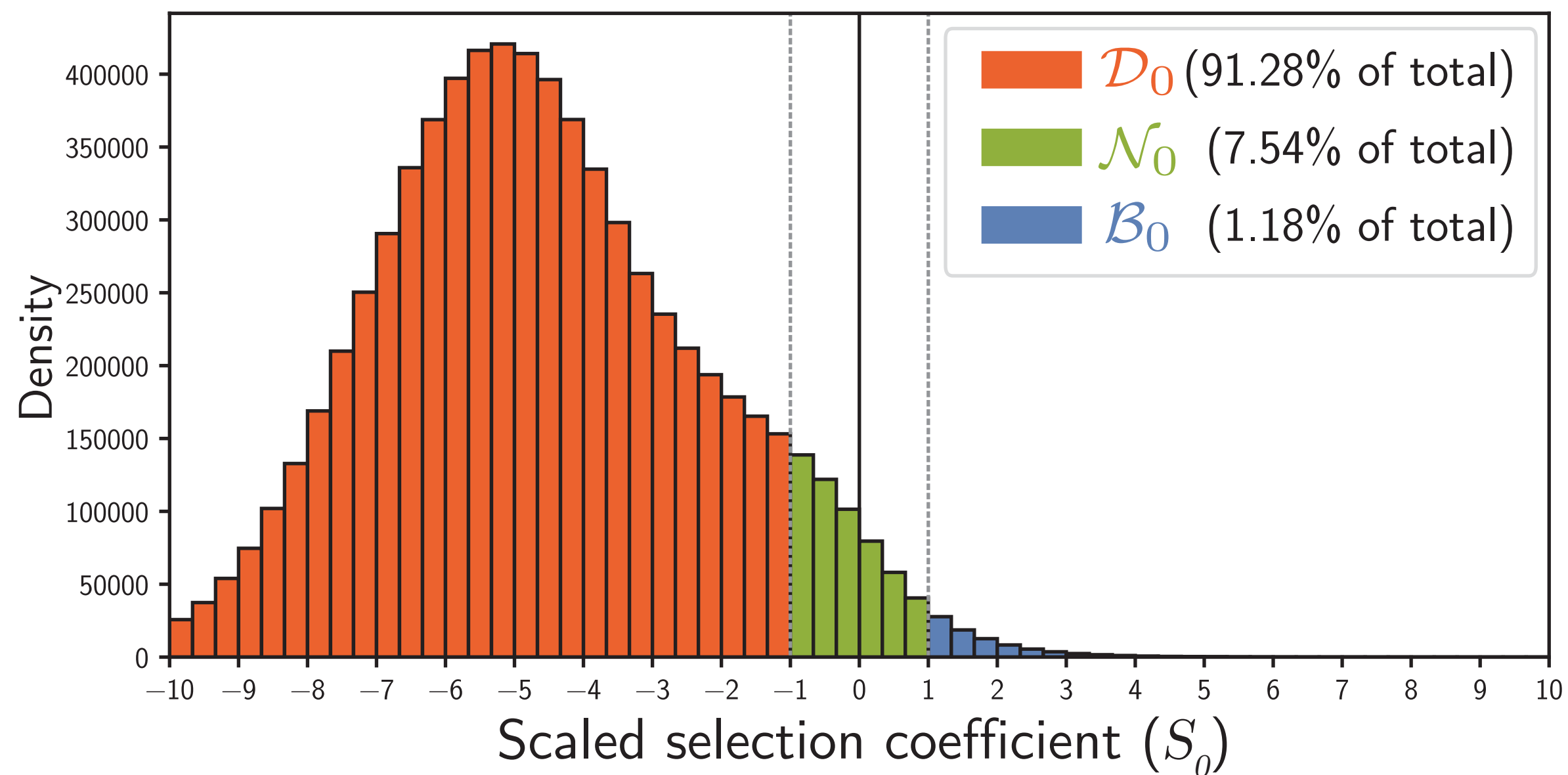
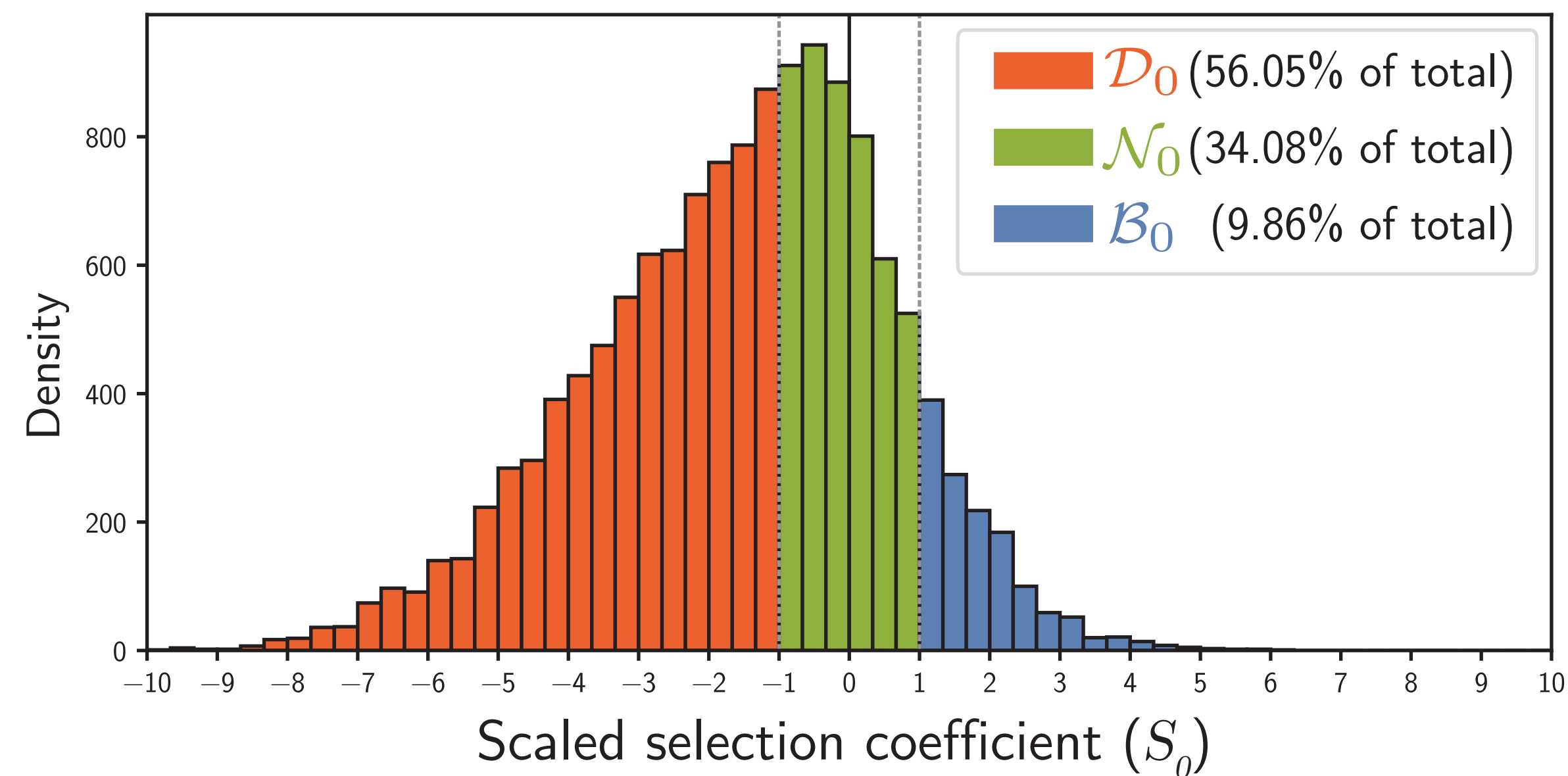


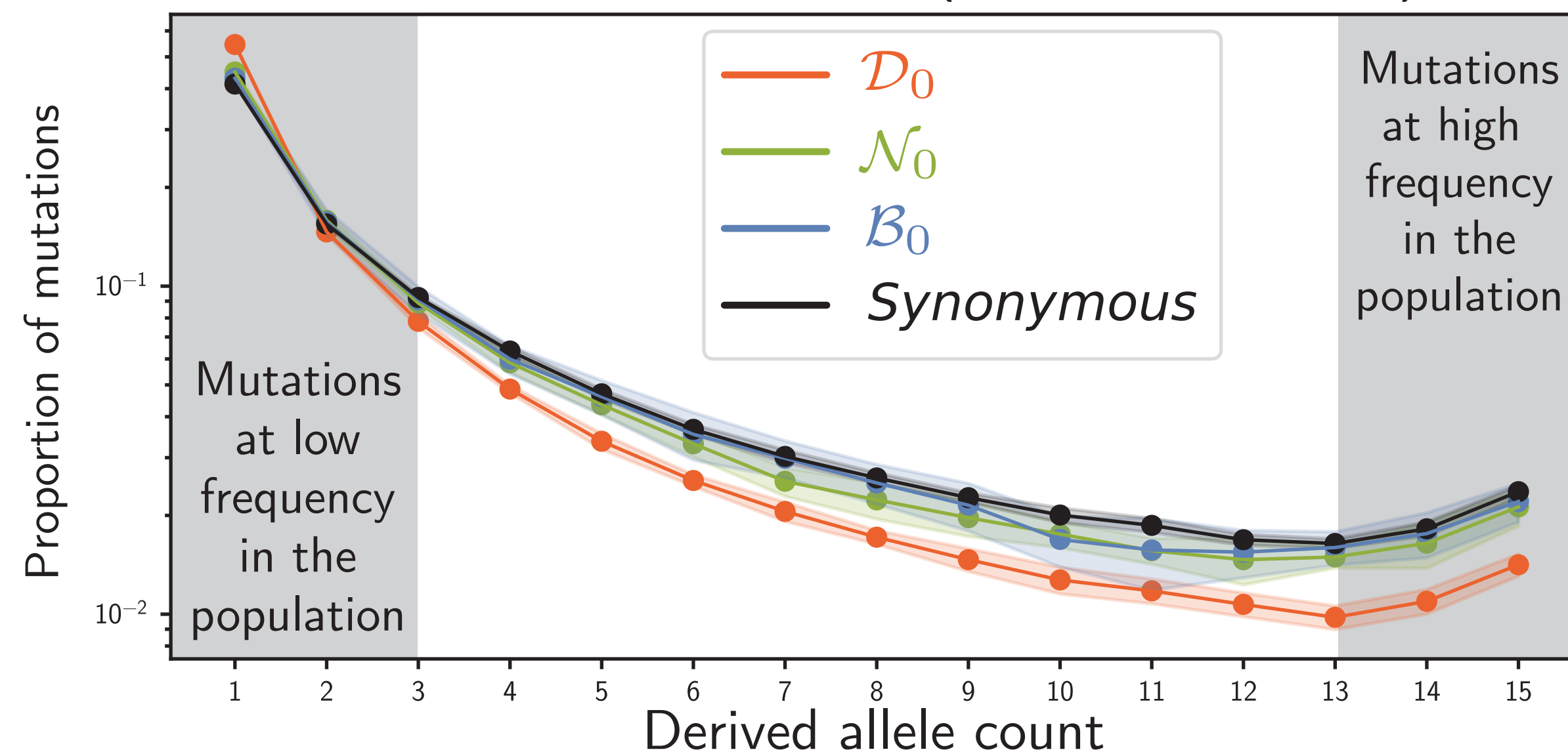
**(A)** Expected distribution of  $S_0$  for all possible mutations from the ancestral *Homo sapiens* genome



**(B)** Observed distribution of  $S_0$  for substitutions in the terminal lineage of *Homo sapiens*



**(C)** Site frequency spectrum for currently segregating mutations in *Homo sapiens* (African population)



**(D)** Proportion of deleterious, nearly-neutral and beneficial mutations estimated at the population scale

