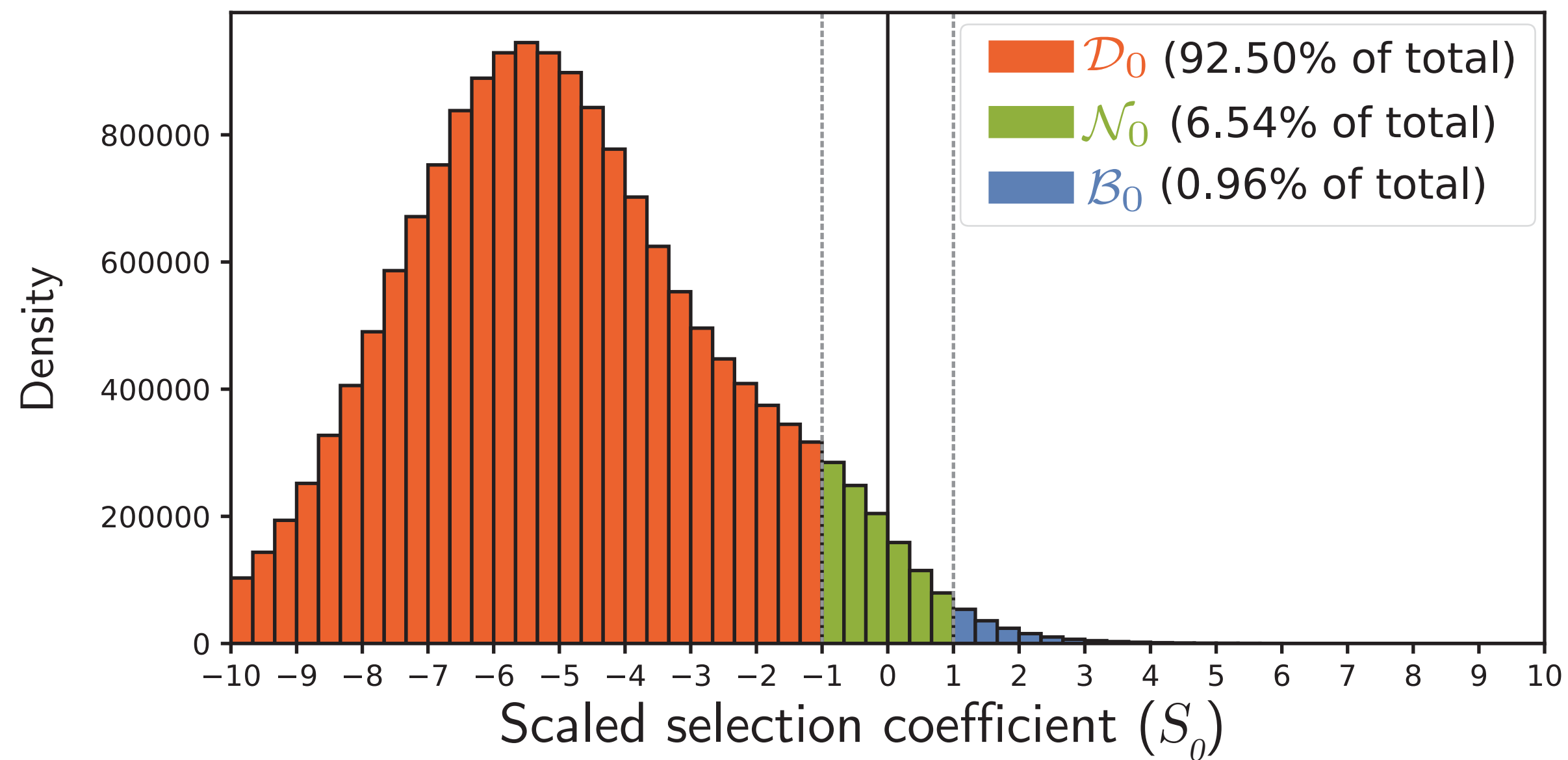
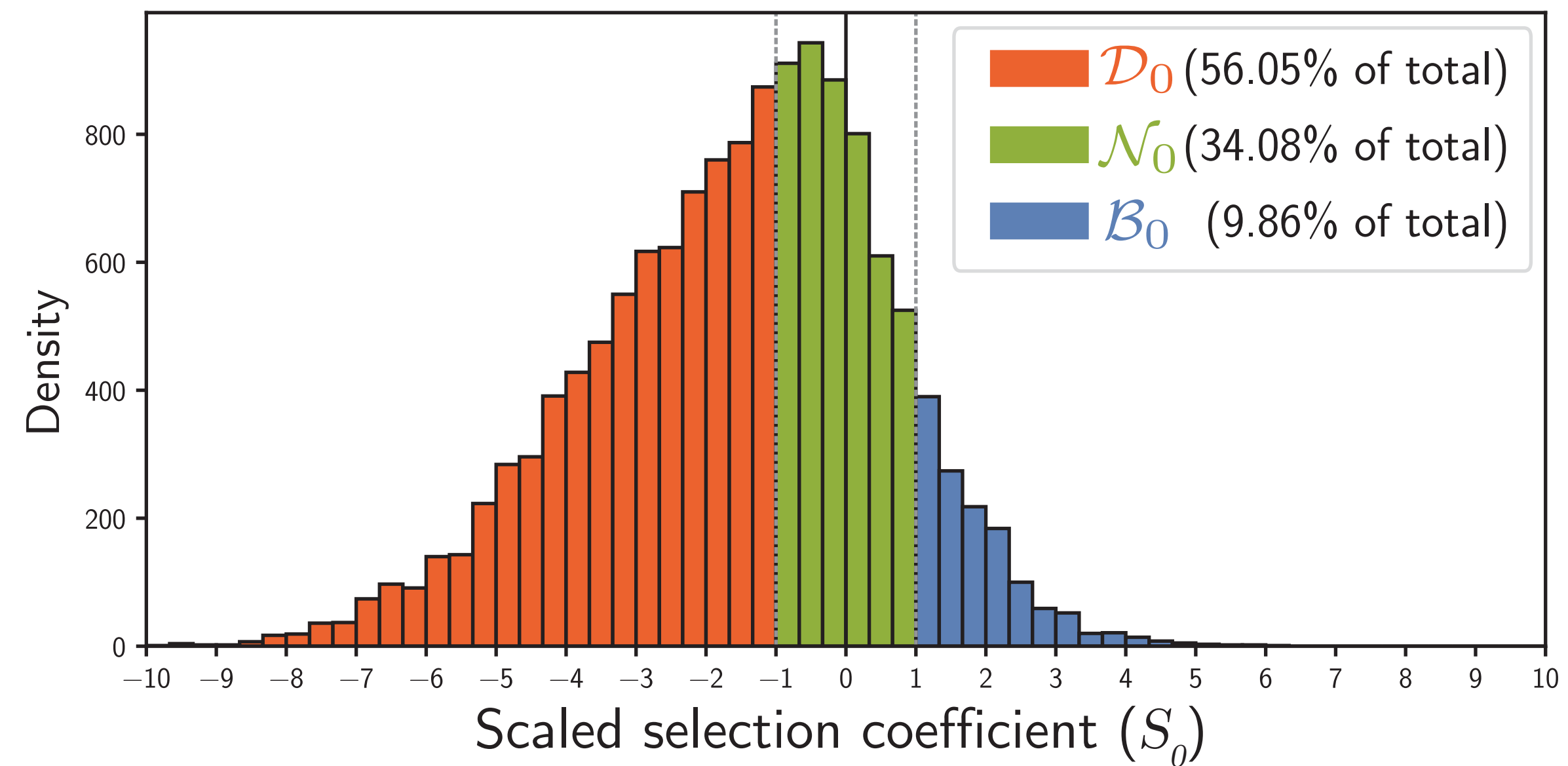


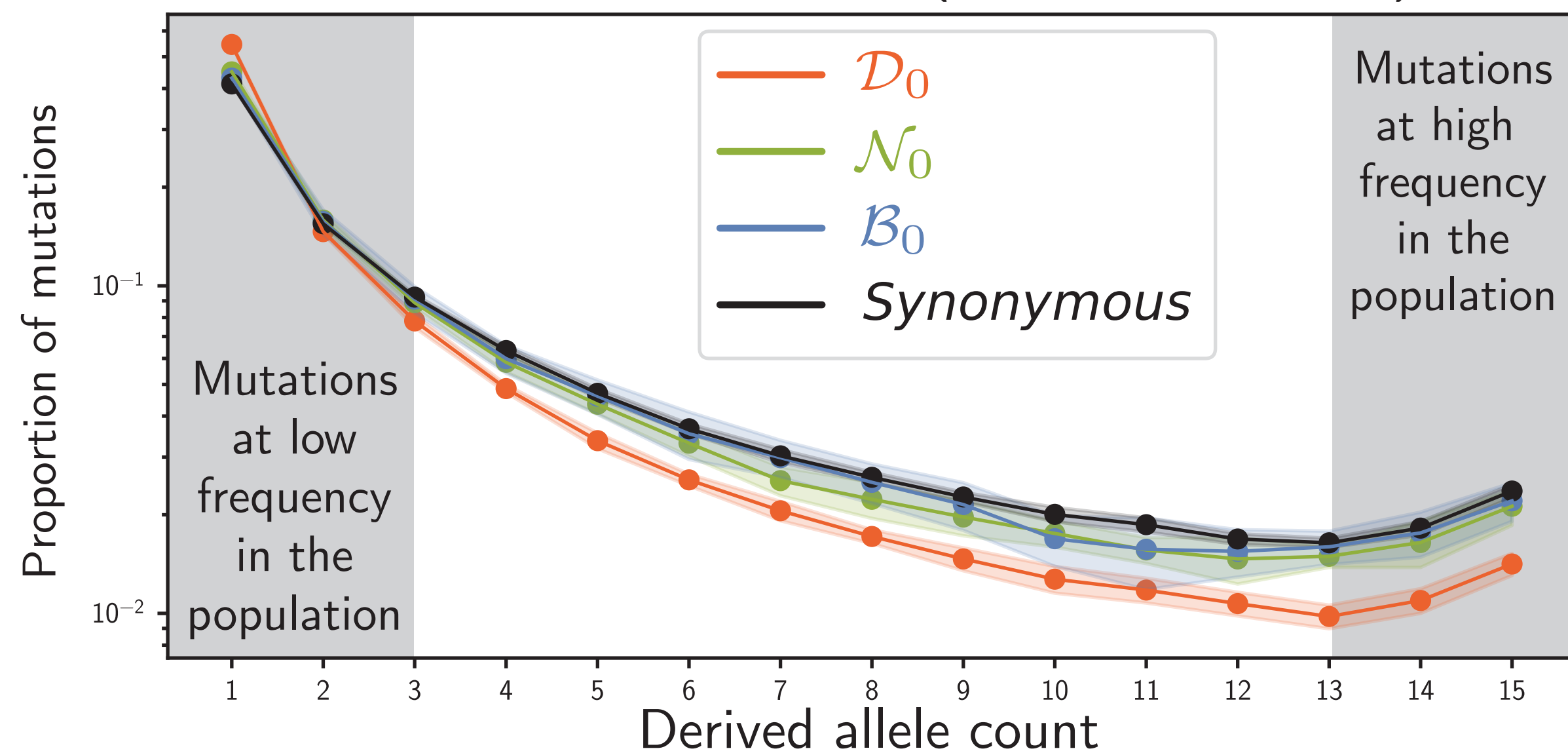
(A)

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

