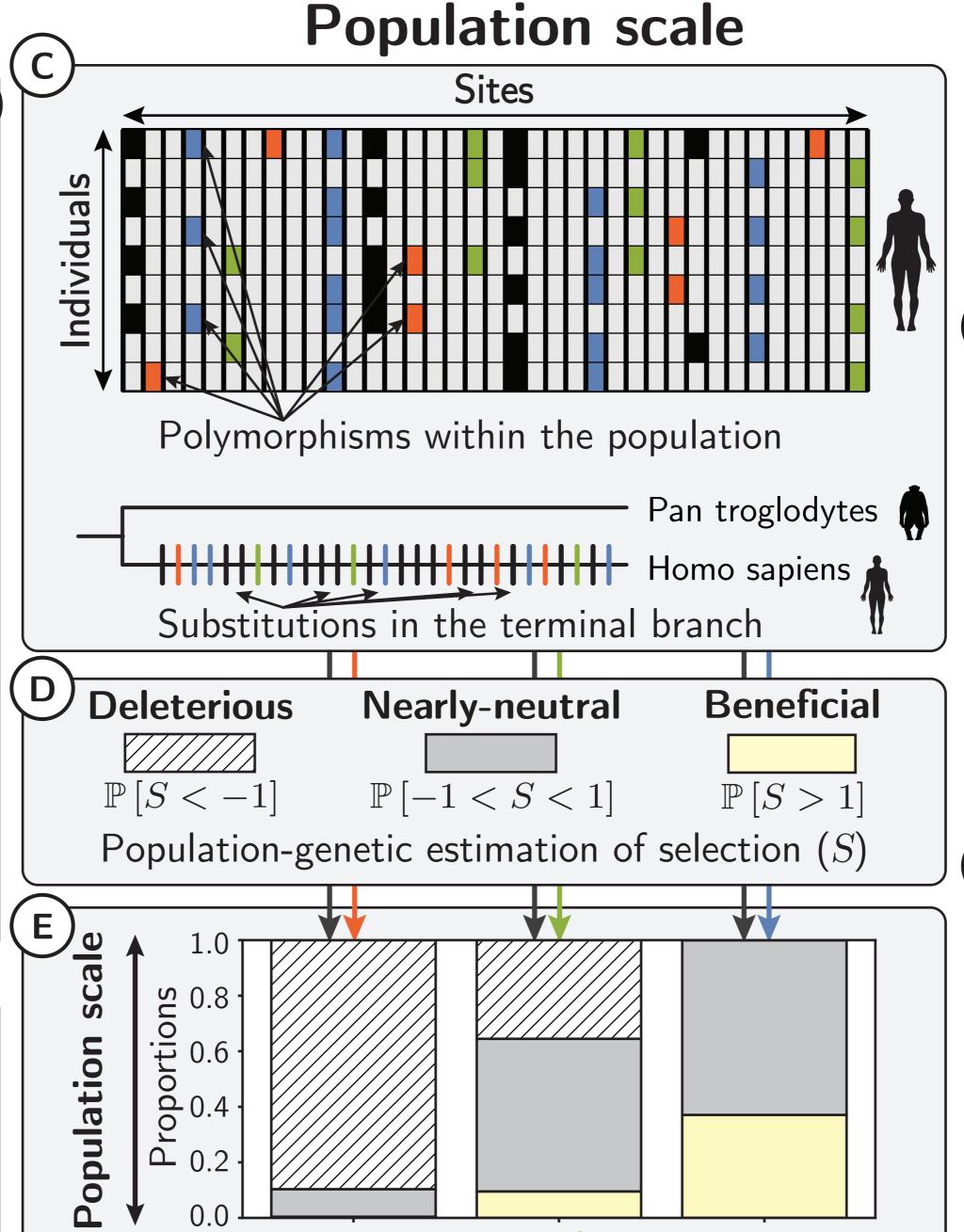
## Phylogenetic scale (A)Protein coding DNA alignment (sites 121-127) ATG|GGA|TCC|ATG|CTA|CGA|TCG ATG|CGA|TCC|ATG|GTA|CGA|TCG Gene tree ATG|CGA|TCG|AAG|CTT|CGA|TCC ATG|CGA|TAG|AAG|CTT|CGA|TCG \*\* ATG|CGA|TCG|ATC|CAT|CGA|TCG Mutation-selection model $S_0$ : change in amino-acid fitness for a mutation 127 (B)Deleterious mutations ( $\mathcal{D}_0 := S_0 < -1$ ) Nearly-neutral mutations ( $N_0 := -1 < S_0 < 1$ ) Beneficial back-mutations ( $\mathcal{B}_0 := S_0 > 1$ ) Synonymous mutations Scaled selection coefficient $(S_0)$ at the phylogenetic scale



 $\mathcal{N}_0$ 

Phylogenetic scale

 $\mathcal{B}_0$ 

Population scale  $\longrightarrow \mathcal{B} := S > 1$ Phylogenetic scale  $\longrightarrow \mathcal{B}_0 := S_0 > 1$ 

## Precision

Among mutations predicted as beneficial back-mutations at the phylogenetic scale, which one are correctly predicted as beneficial.

$$\frac{\mathbb{P}\left[\mathcal{B}\cap\mathcal{B}_{0}\right]}{\mathbb{P}\left[\mathcal{B}_{0}\right]}=\mathbb{P}\left[\mathcal{B}\mid\mathcal{B}_{0}\right]$$

## Recall

Among mutations predicted as beneficial at the population scale, which one are correctly predicted as beneficial back-mutations.

$$\frac{\mathbb{P}\left[\mathcal{B}\cap\mathcal{B}_{0}\right]}{\mathbb{P}\left[\mathcal{B}\right]}=\mathbb{P}\left[\mathcal{B}_{0}\mid\mathcal{B}\right]$$