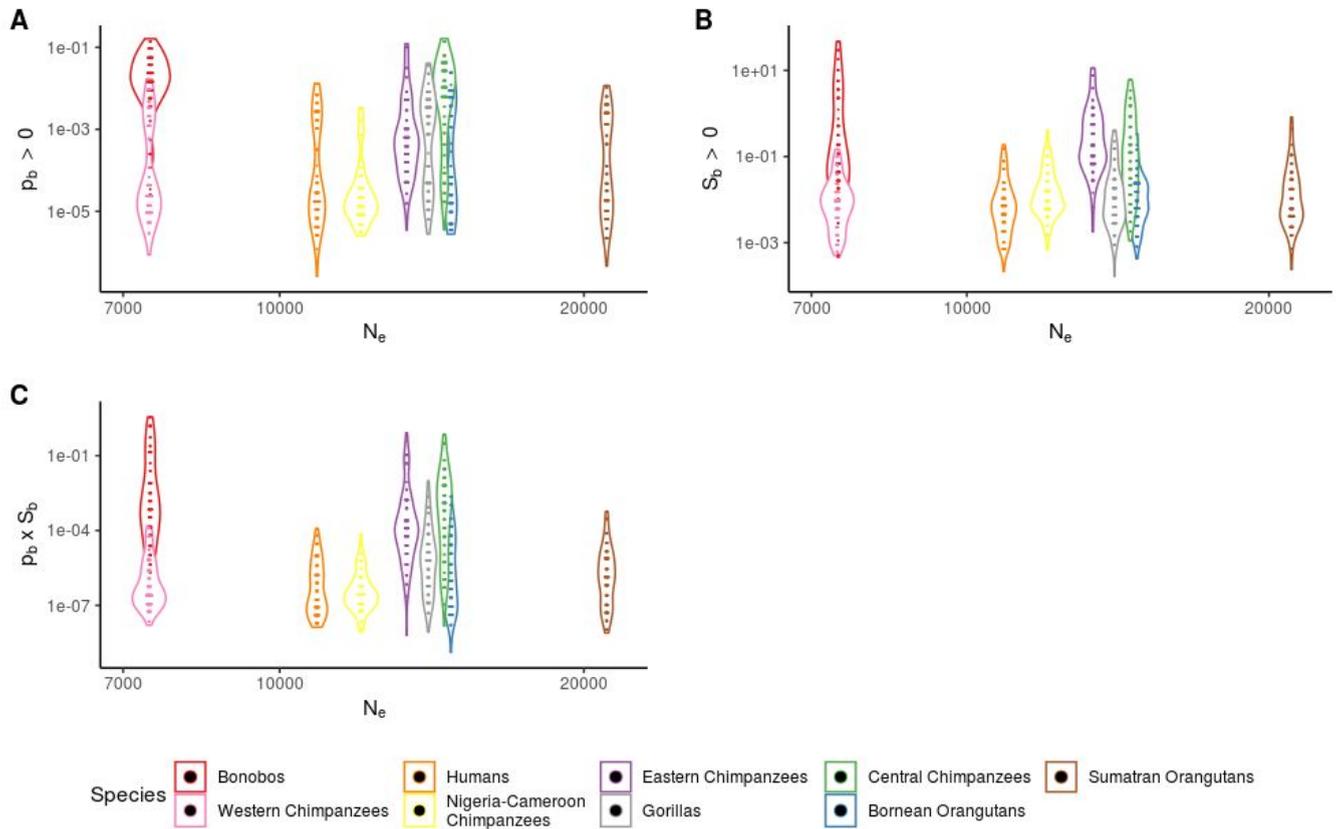
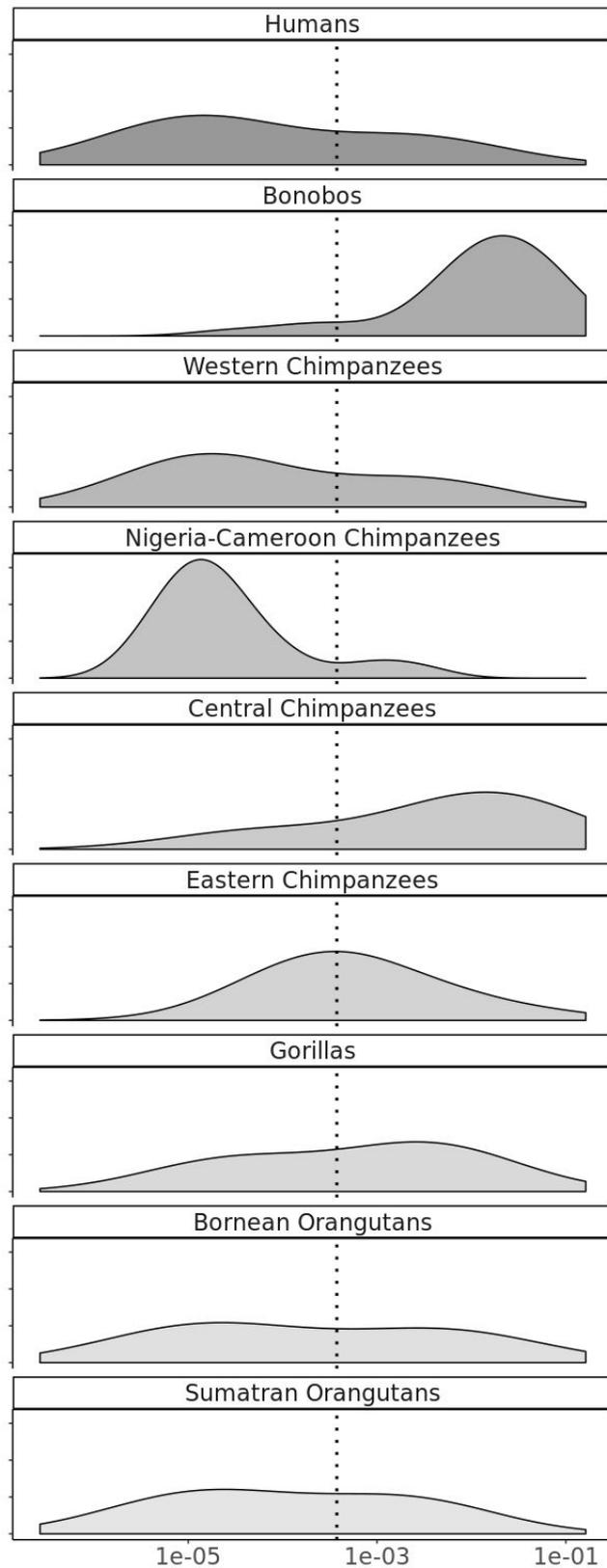


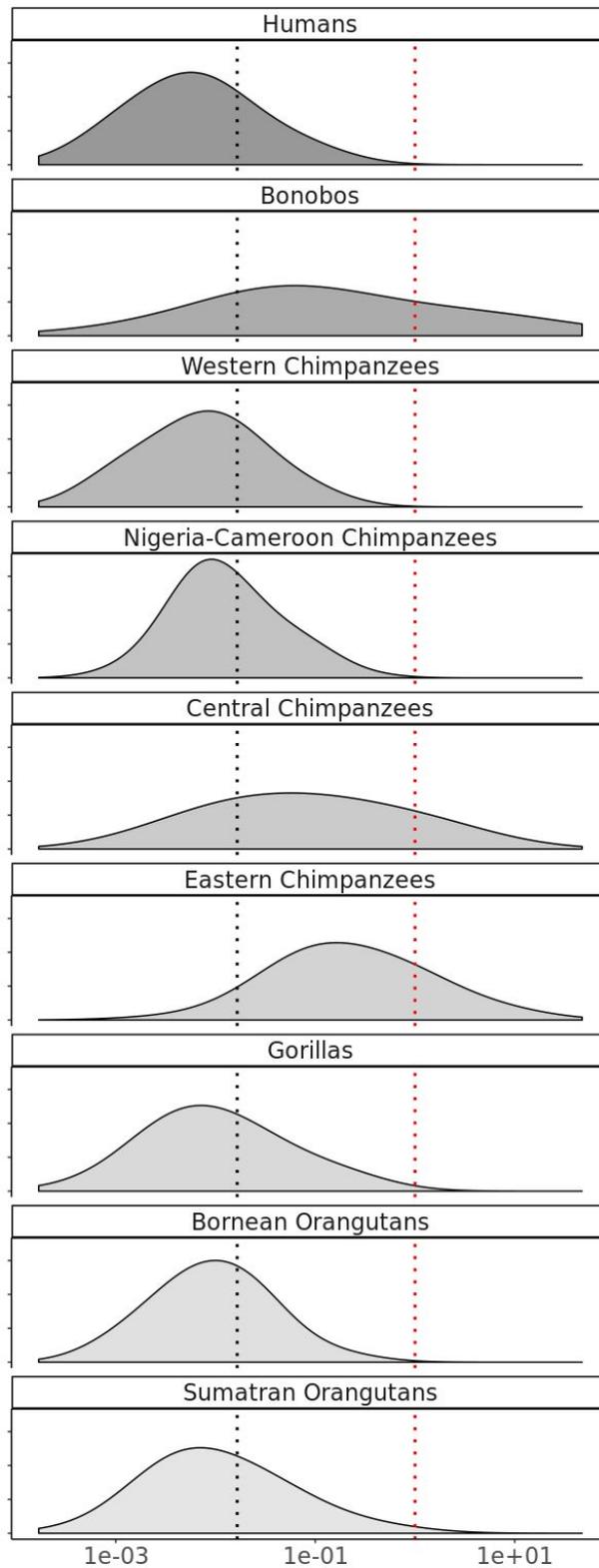
**Supplementary Figure 1.** The weighting of each model based on its AIC for humans (A), bonobos (B), western chimpanzees (C), Nigeria-Cameroon chimpanzees (D), central chimpanzees (E), eastern chimpanzees (F), western lowland gorillas (G), Bornean orangutans (H) and Sumatran orangutans (I). Results for all mutations.



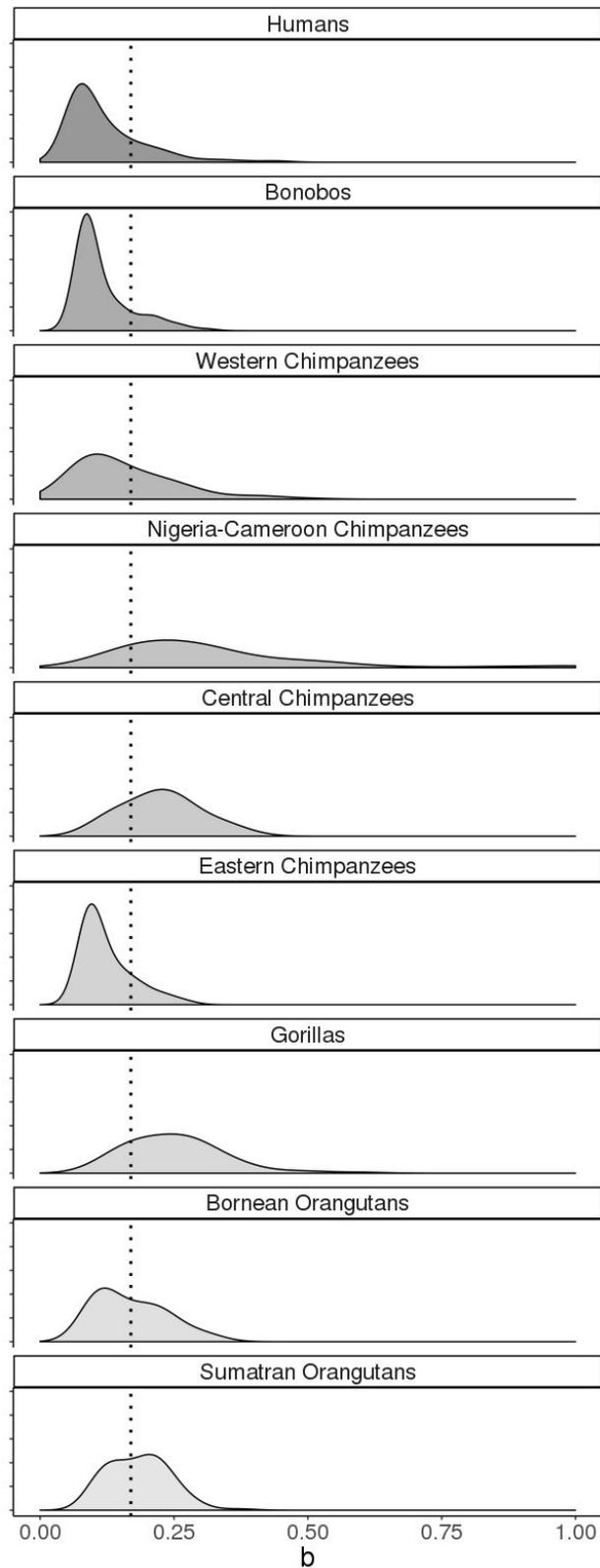
**Supplementary Figure 2.** Relationship between the probability that a new mutation is beneficial on log scale (A), the population scaled mean effect size of new beneficial mutations on log scale (B), the product of the strength and number of new beneficial mutations on log scale (C) and the  $N_e$  (x-axis) on log scale. Results for all mutations.  $p_b$  and  $S_b$  have been estimated weighting models M2I, M3I, M2S and M3S. Each violin plot represents 100 bootstrap replicates. See Table 2 for the description of the models.



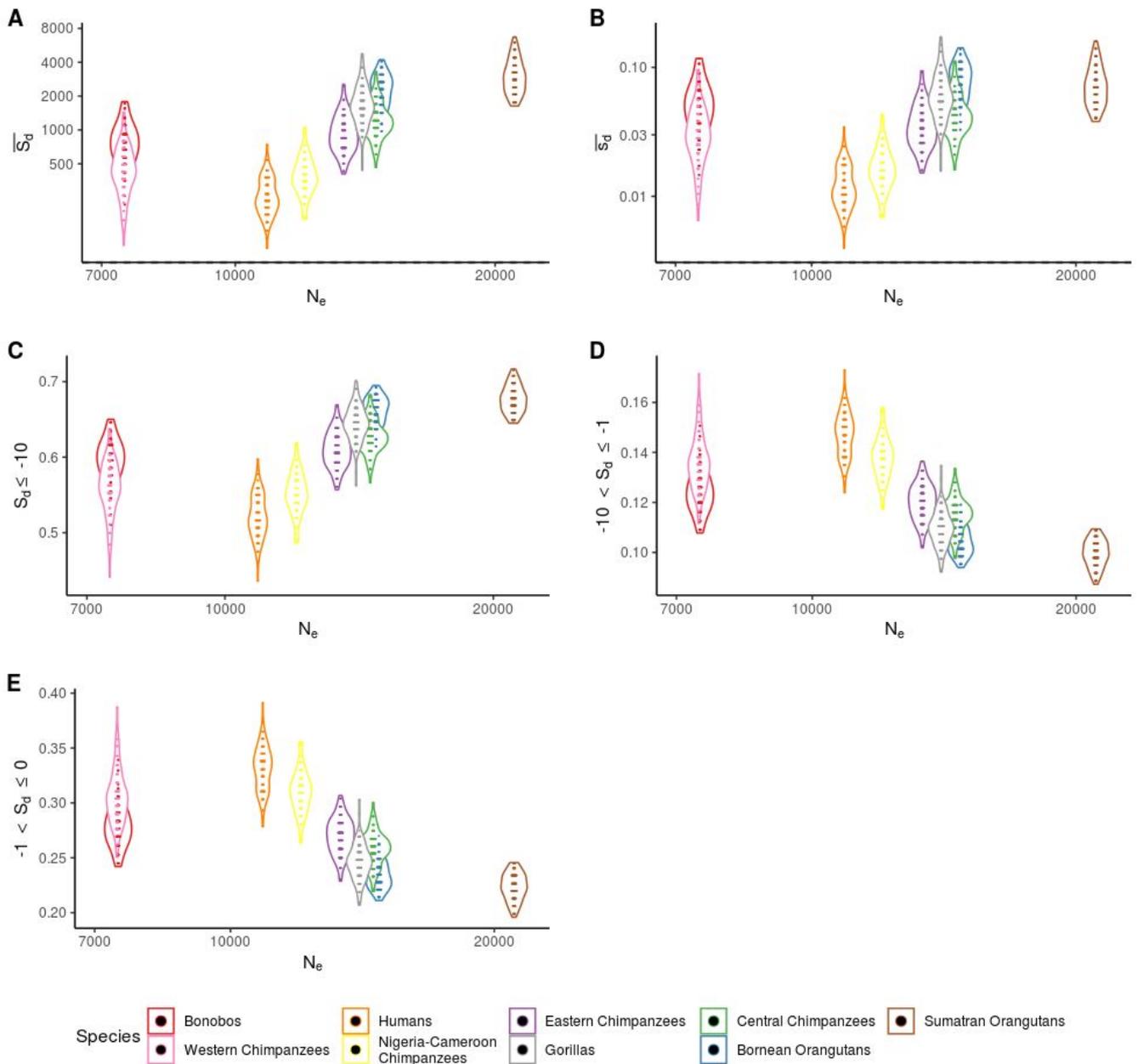
**Supplementary Figure 3.** Distribution of  $p_b$  estimates across 100 bootstrap replicates for each species.  $p_b$  estimated weighting models M2I, M3I, M2S and M3S for each species. Results for all mutations. The dotted black line ( $p_b = 3.8e^{-4}$ ) indicates the median of the model-averaged  $p_b$  parameter across all great apes. The x-axis is on log scale.



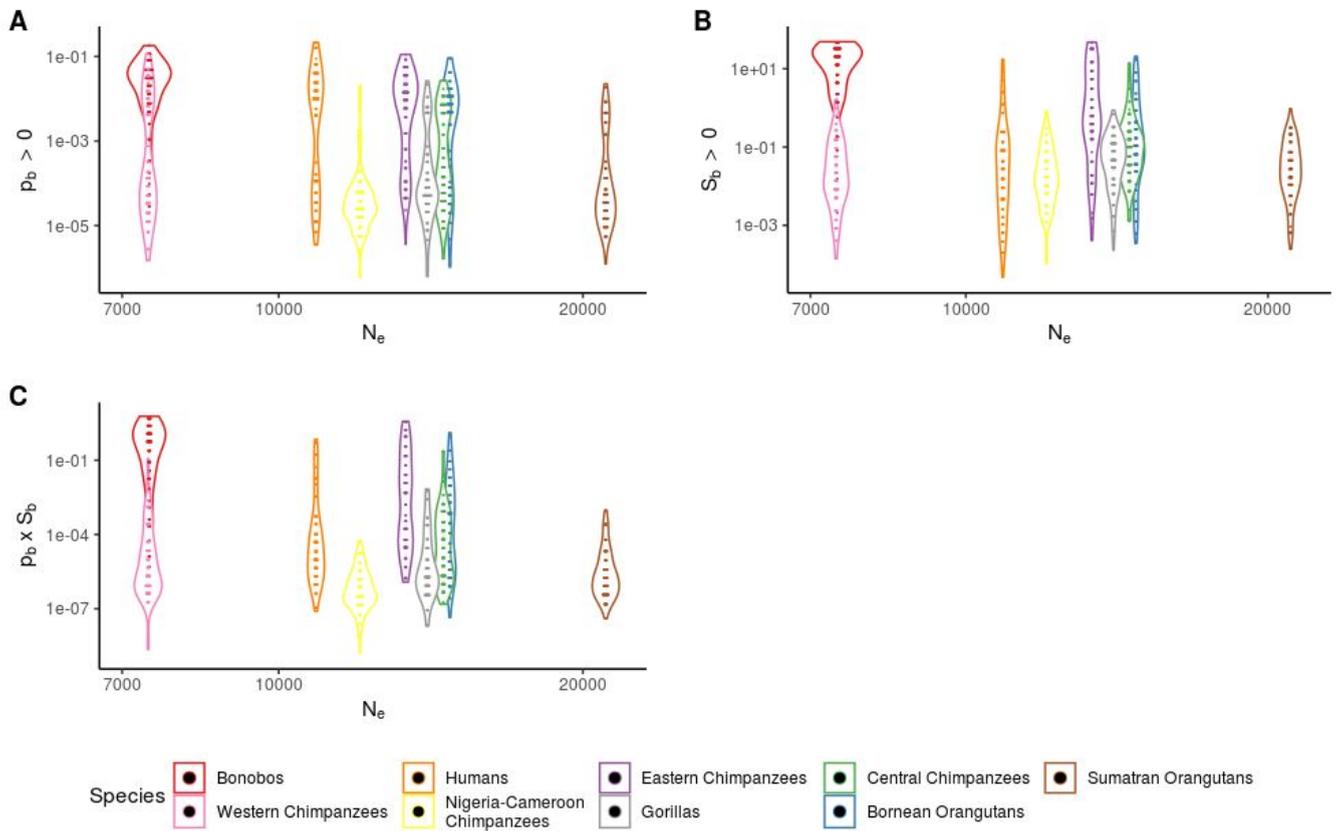
**Supplementary Figure 4.** Distribution of  $S_b$  estimates across 100 bootstrap replicates for each species.  $S_b$  estimated weighting models M2I, M3I, M2S and M3S for each species. Results for all mutations. The dotted black line ( $S_b = 0.015$ ) indicates the median of the model-averaged  $S_b$  parameter across all great apes. The dotted red line shows the border between effectively selected and effectively neutral mutations ( $S_b = 1$ ). The x-axis is on log scale.



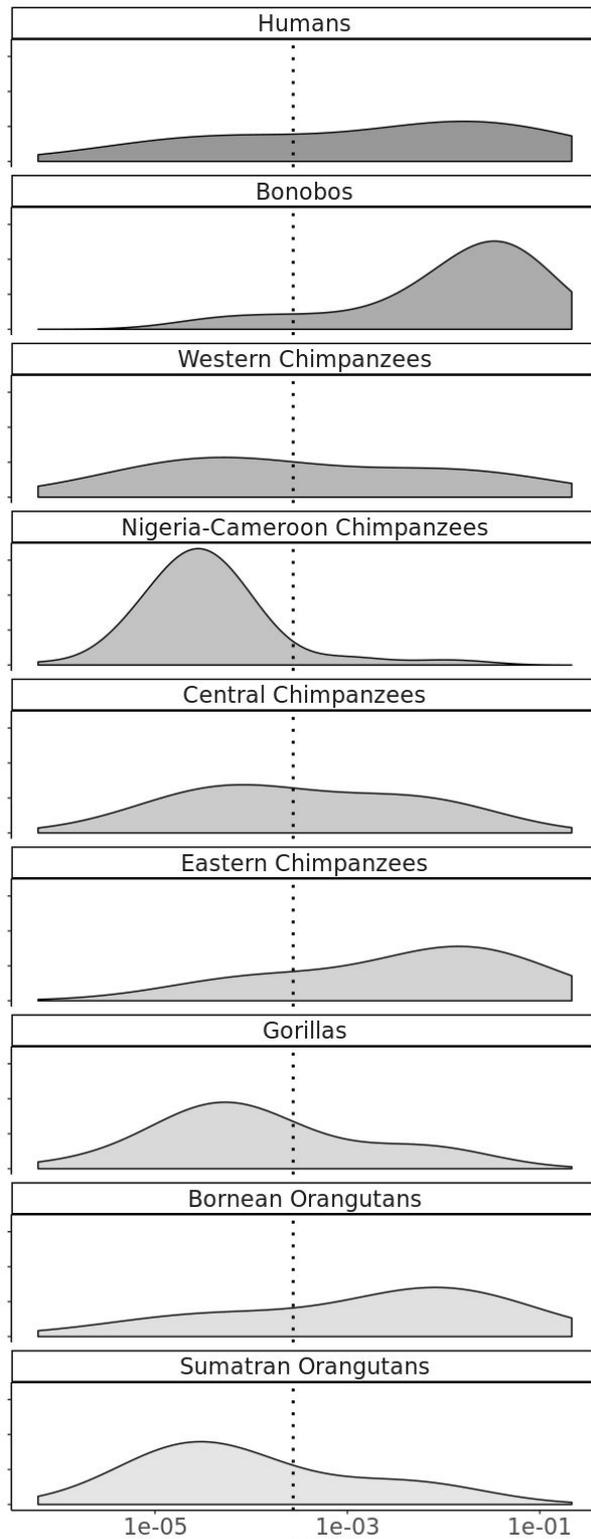
**Supplementary Figure 5.** Distribution of  $b$  estimates for GC-conservative mutations across 100 bootstrap replicates for each species under the purely deleterious model (M3I). The dotted black line ( $b = 0.1842$ ) indicates the shared shape parameter under the most likely model (M3S). See Table 2 for the description of the models. The allowed range of  $b$  values goes from 0.01 to 1.



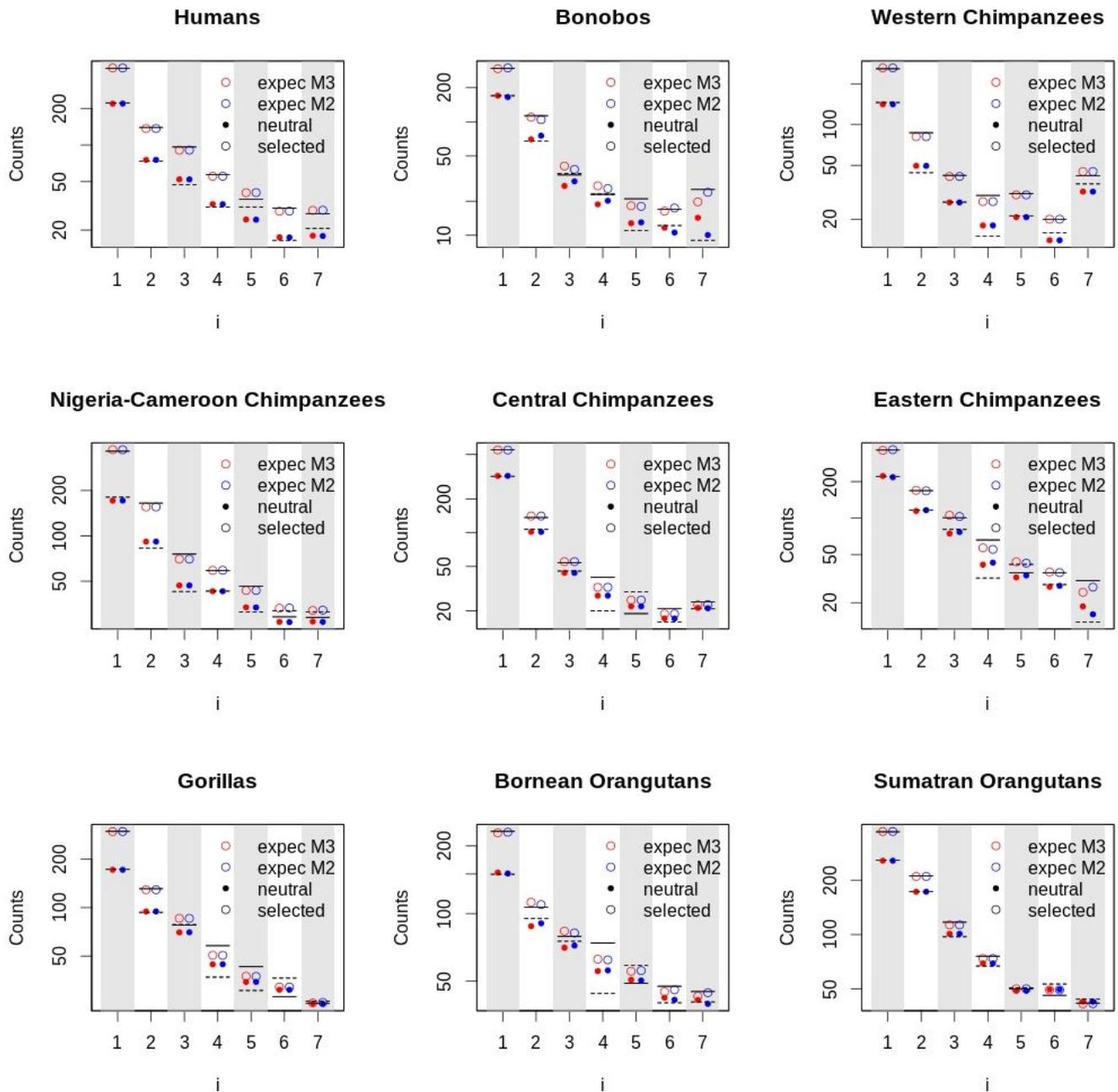
**Supplementary Figure 6.** Relationship between the absolute population scaled mean effect size of deleterious mutations on log scale (A), the absolute mean effect size of deleterious mutations on log scale (B), the proportion of strongly deleterious mutations (C), the proportion of weakly deleterious mutations (D) and the proportion of effectively neutral mutations (E) and the  $N_e$  (x-axis) on log scale. Results for GC-conservative mutations. Each violin plot represents 100 bootstrap replicates under the most likely model (M3S). See Table 2 for the description of the models.



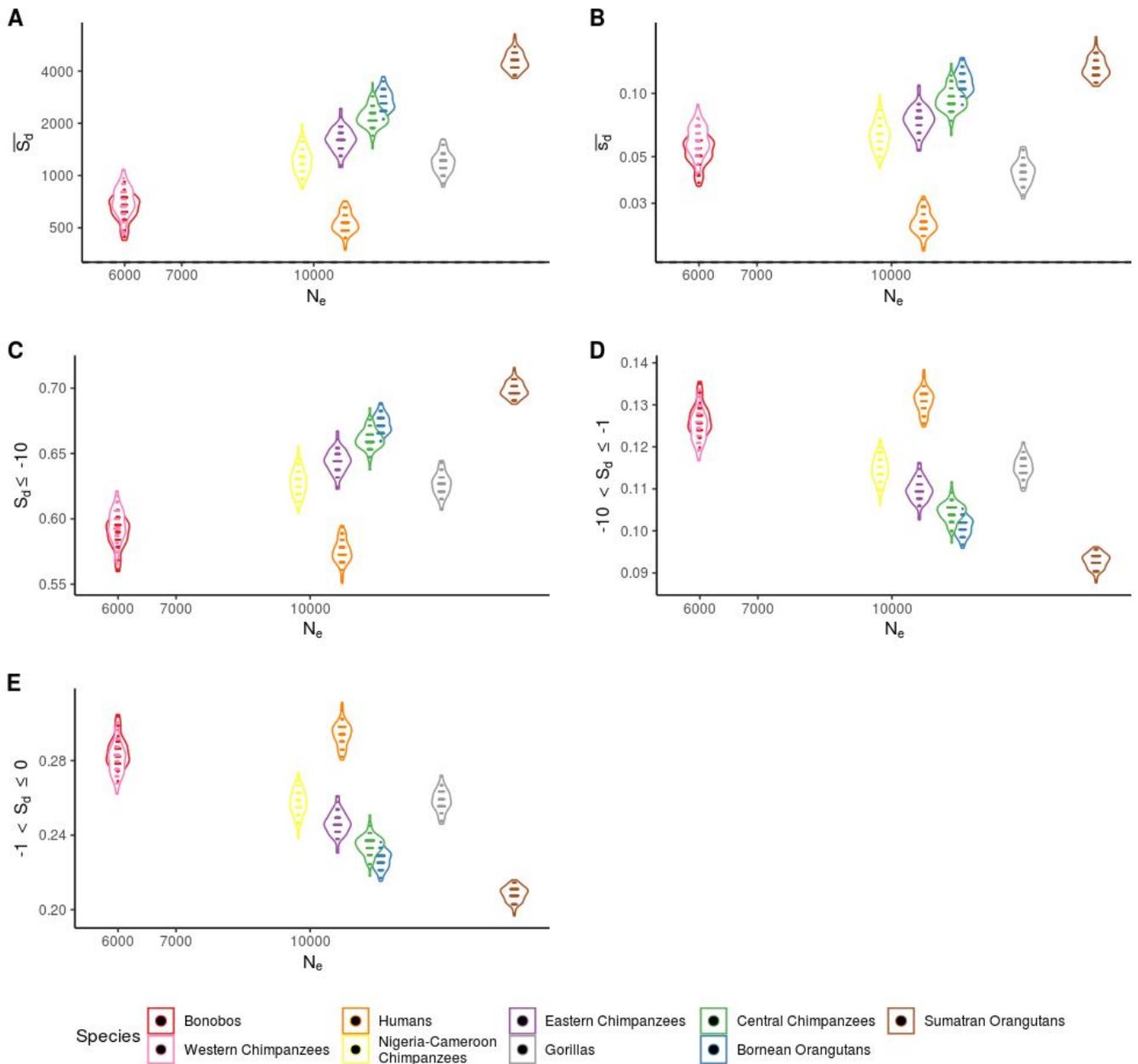
**Supplementary Figure 7.** Relationship between the probability that a new mutation is beneficial on log scale (A), the population scaled mean effect size of new beneficial mutations on log scale (B), the product of the strength and number of new beneficial mutations on log scale (C) and the  $N_e$  (x-axis) on log scale. Results for GC-conservative mutations.  $p_b$  and  $S_b$  have been estimated weighting models M2I, M3I, M2S and M3S. Each violin plot represents 100 bootstrap replicates. See Table 2 for the description of the models.



**Supplementary Figure 8.** Distribution of  $p_b$  estimates for GC-conservative mutations across 100 bootstrap replicates for each species.  $p_b$  estimated weighting models M2I, M3I, M2S and M3S for each species. The dotted black line ( $p_b = 2.23e^{-4}$ ) indicates the median of the model-averaged  $p_b$  parameter across all great apes. The x-axis is on log scale.



**Supplementary Figure 9.** Observed and expected uSFS for GC-conservative mutations. The solid lines show the observed number of 0-fold non-synonymous changes and the dashed lines show the observed number of 4-fold synonymous changes. The dots and circles represent the expected counts of neutral and selected sites under the M2 and M3 models (shown as blue and red, respectively). The y-axis is on log scale.



**Supplementary Figure 10.** Relationship between  $N_e$  and  $S_d$  on log scale (A),  $s_d$  on log scale (B), the proportion of strongly deleterious mutations (C), the proportion of weakly deleterious mutations (D) and the proportion of effectively neutral mutations (E). Note that  $N_e$  (x-axis) is visualized on log scale. Each violin plot represents 100 bootstrap replicates under the most likely model (M3S). See Table 2 for a description of the models. See Supplementary Table 8 for the correlation coefficients. The  $N_e$  is computed dividing  $\theta_s$  by the mutation rate per site and generation retrieved from Besenbacher et al. (2018). Generation time of 29, 24, 19 and 25 years for humans, chimpanzees (and bonobos), gorillas and orangutans, respectively. Mutation rate per year relative to humans is 1.50 for chimpanzees (and bonobos), 1.51 for gorillas and 1.42 for orangutans.