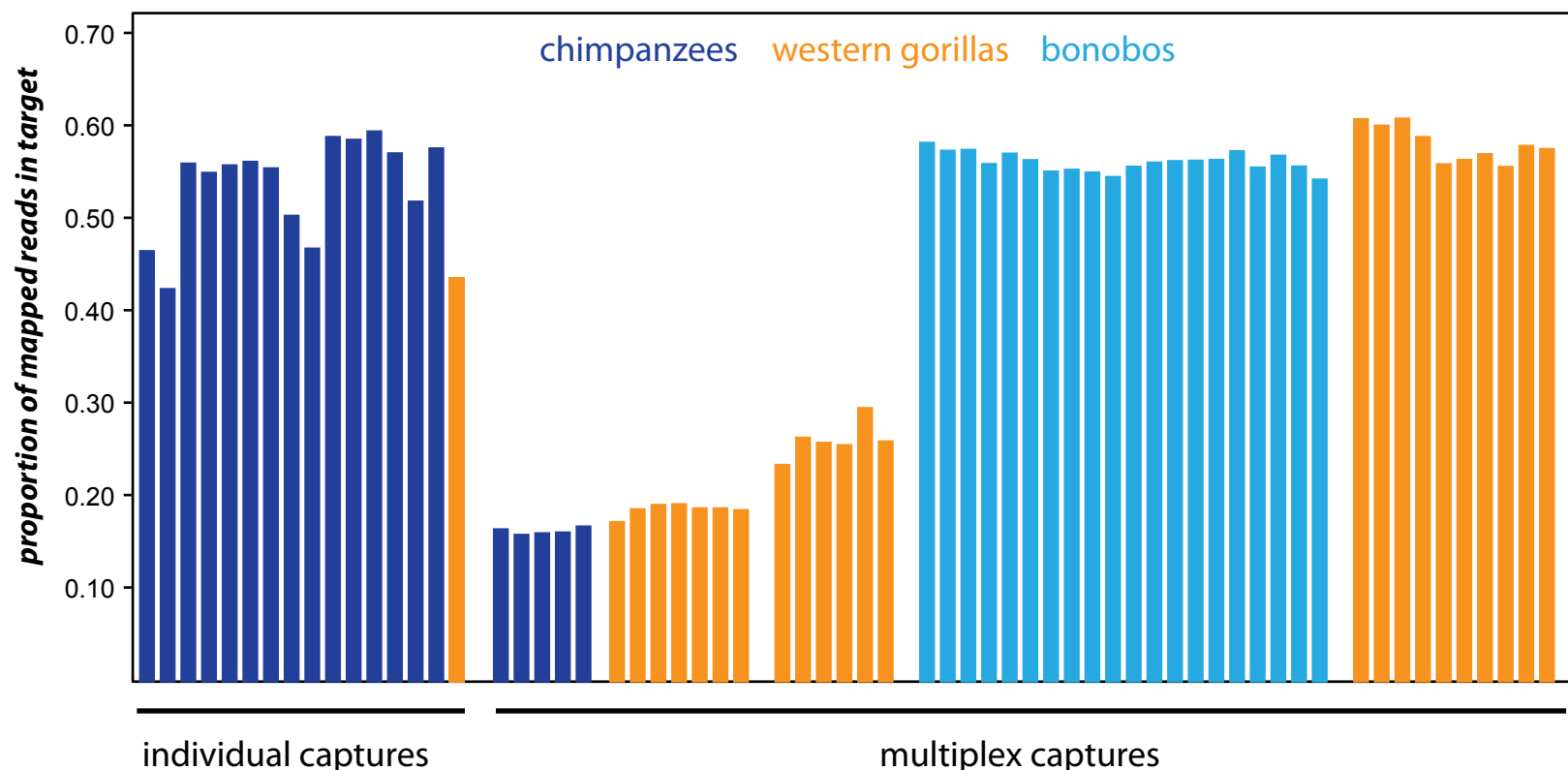
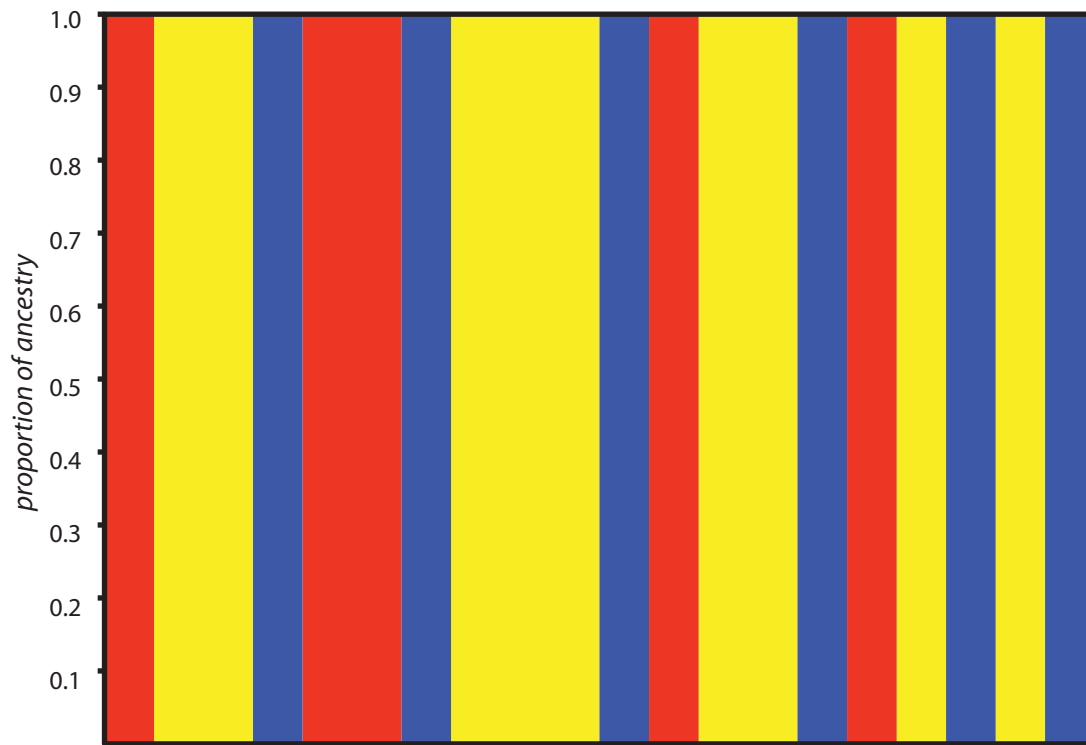


Supplemental Figure S1. A) Schematic of filters applied to the proteomic data of (Pilch and Mann 2006) to identify genes encoding true SFPs that were also suitable for targeted capture. The distribution of peptide abundances for the unfiltered set (B) and the final set of 285 SFPs (C) are compared with a quantile-quantile plot (D), which indicates that the distribution of peptide abundances is systematically higher in the filtered set of 285 SFPs.

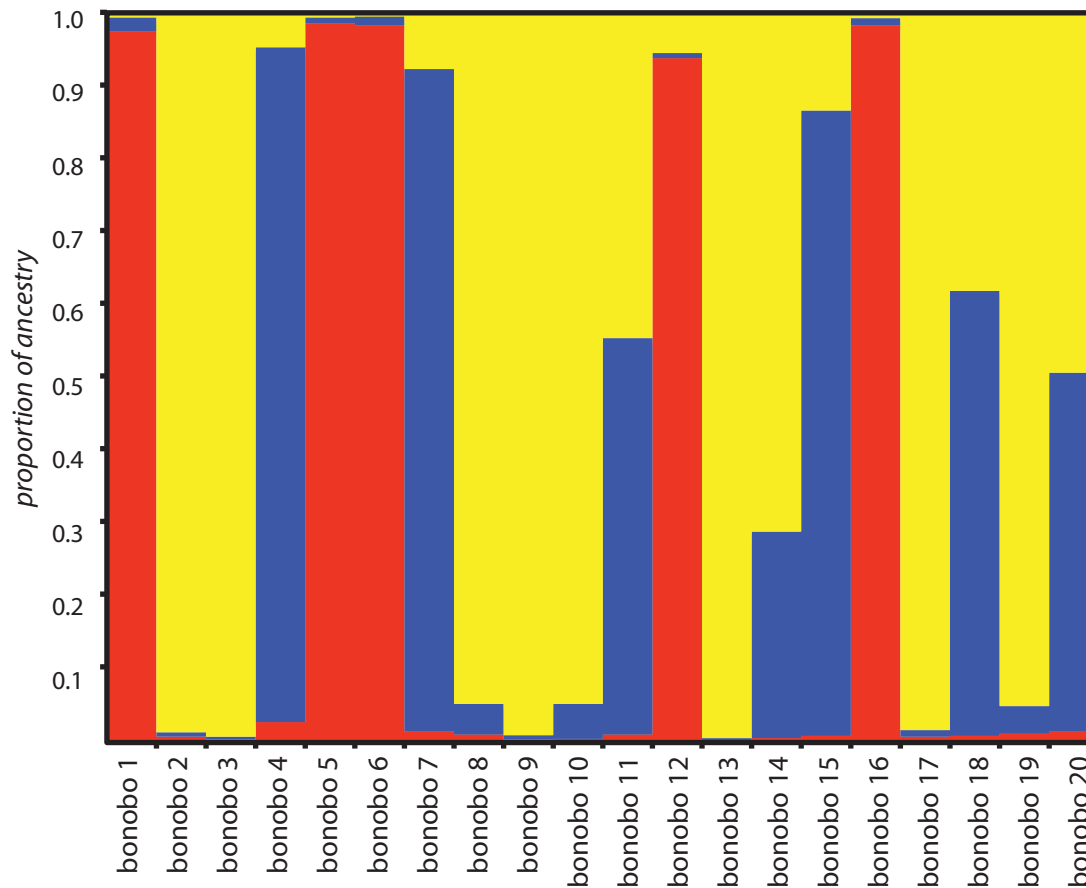


Supplemental Figure S2. Proportion of uniquely mapped reads ($\text{mapq} > 0$) overlapping with targeted bases for various capture experiments. Individual captures denote one individual hybridized to a single array and then sequenced. Multiplex experiments involve multiple barcoded individuals captured on a single array. We observed low variation in capture efficiency among individuals within a given multiplex capture experiment, but large differences between captures. The experiments presented represent an approximate timeline (not all experiments shown) of captures, reflecting the ongoing optimization of the procedure from left to right.

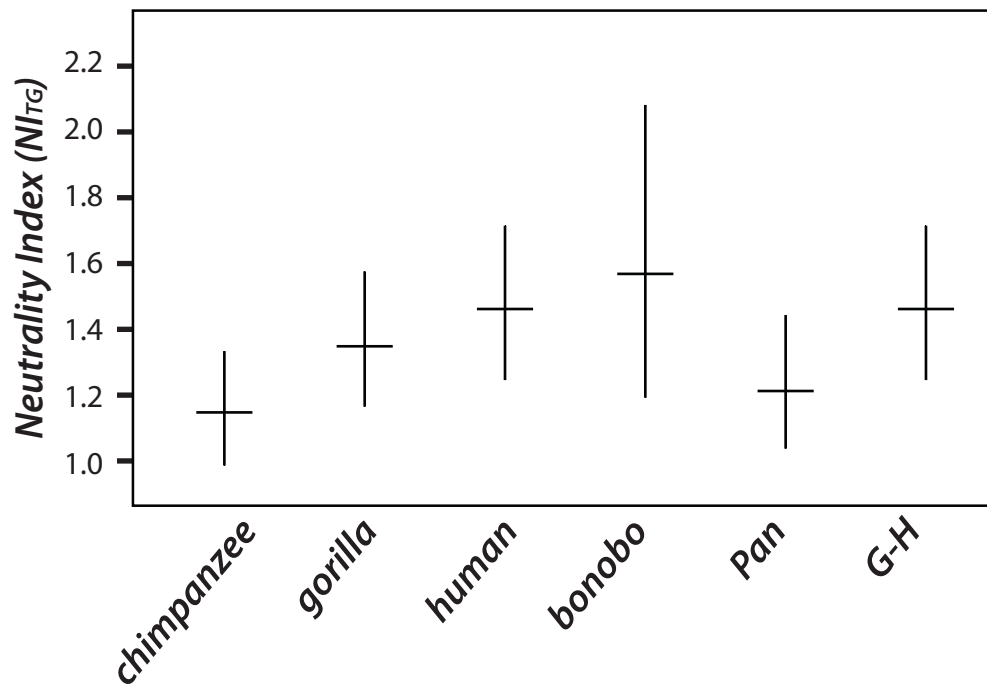
No Admixture, K=3



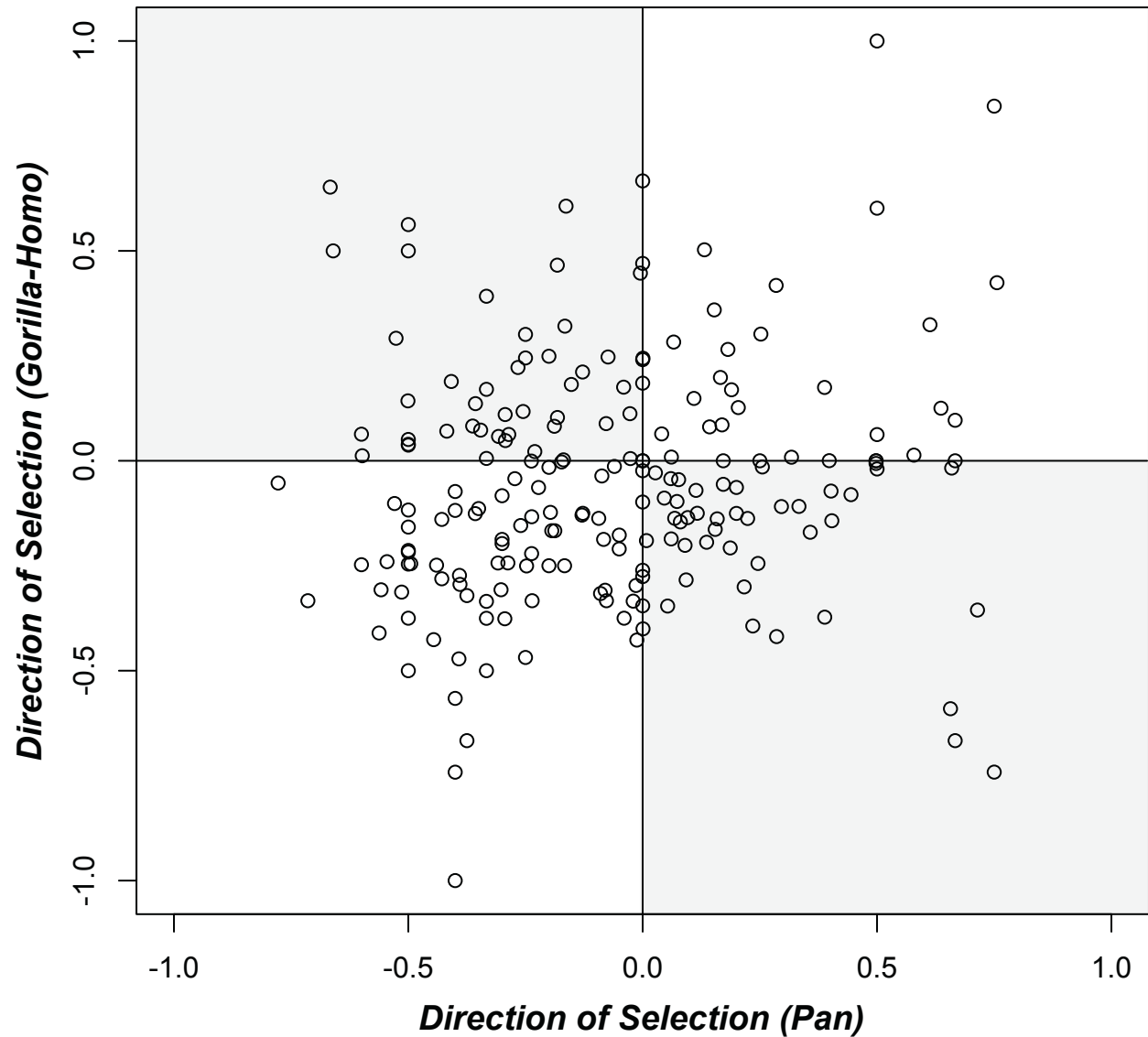
Admixture, K=3



Supplemental Figure S3. Results of structure analyses for bonobos, assuming the best-fit number of populations of K=3 and a model of no admixture (top) or admixture. See supplemental table S5 for a comparison among different models



Supplemental Figure S4. Species and lineage-specific estimates of the neutrality index for all genes. Species divergence estimates are based on pairwise comparisons to an outgroup (gorilla for human, bonobo, chimpanzee; human for gorilla). Polymorphism was estimated from the largest subset of individuals within chimpanzees, gorillas, and bonobos for which there was no evidence of population substructure. *Pan* incorporates divergence along the lineage leading to chimpanzees and bonobos and polymorphism from both species. *G-H* incorporates pairwise divergence between gorillas and humans and polymorphism from both species.



Supplemental Figure S5. Comparison of the direction of selection (DoS) for reproductive genes in bonobos and chimpanzees versus humans and gorillas. Pan incorporates divergence along the lineage leading to chimpanzees and bonobos and polymorphism from both species. G-H incorporates pairwise divergence between gorillas and humans and polymorphism from both species. Gray shading indicates genes where the direction of selection (positive or negative) differs between the two groups (see Supplemental Analyses).