

SUPPLEMENTARY FIGURES AND TABLES

The accumulation of deleterious mutations as a consequence of domestication and improvement in sunflowers and other Compositae crops

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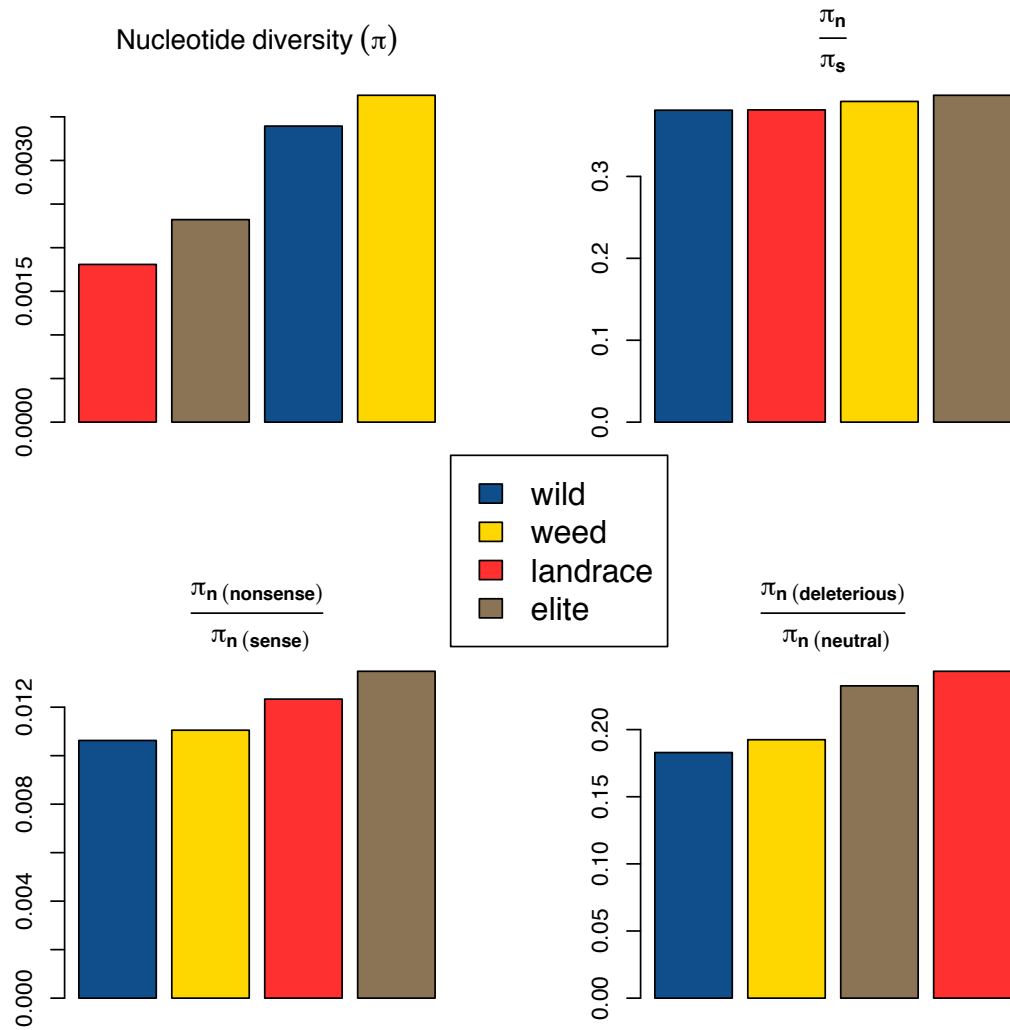


Figure S1A: Nucleotide diversity (π , calculated in SITES, Hey Lab Distributed Software, <http://genfaculty.rutgers.edu/hey/%E2%80%A8software#SITES/>) per class and for synonymous, non-synonymous, nonsense and non-synonymous deleterious mutations separately. **S1A:** Nucleotide diversity (π) for all mutations. **S1B:** Nucleotide diversity for non-synonymous mutations (π_n) divided by the nucleotide diversity for synonymous mutations (π_s). **S1C:** Nucleotide diversity for non-synonymous nonsense mutations ($\pi_n(\text{nonsense})$) divided by the nucleotide diversity for non-synonymous sense mutations ($\pi_n(\text{sense})$). **S1D:** Nucleotide diversity for non-synonymous deleterious mutations ($\pi_n(\text{deleterious})$) divided by the nucleotide diversity for non-synonymous neutral mutations ($\pi_n(\text{neutral})$).

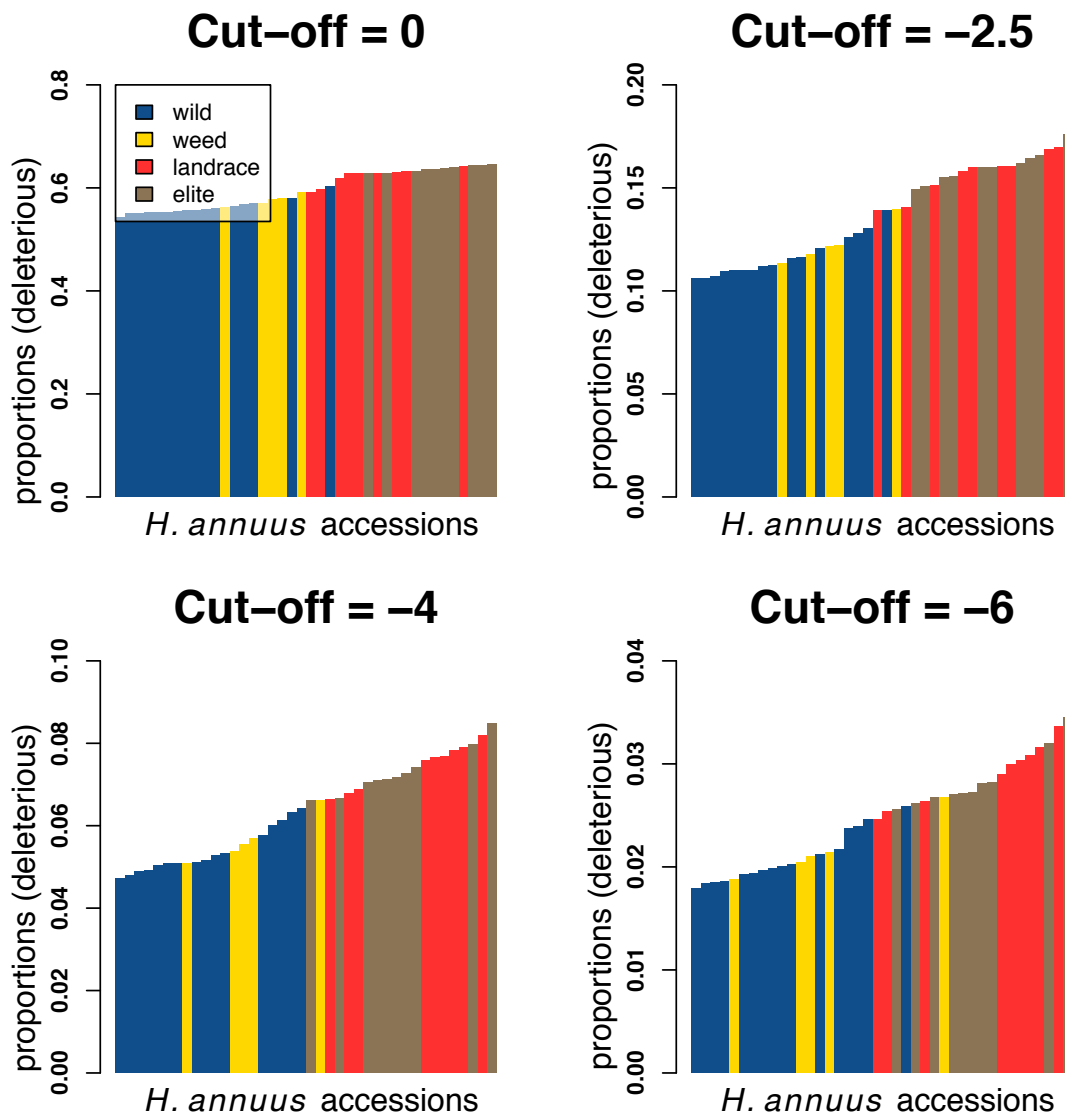


Figure S2: Other cutoff values (0, -2.5, -4, -6) used to quantify mutations as deleterious according to PROVEAN.

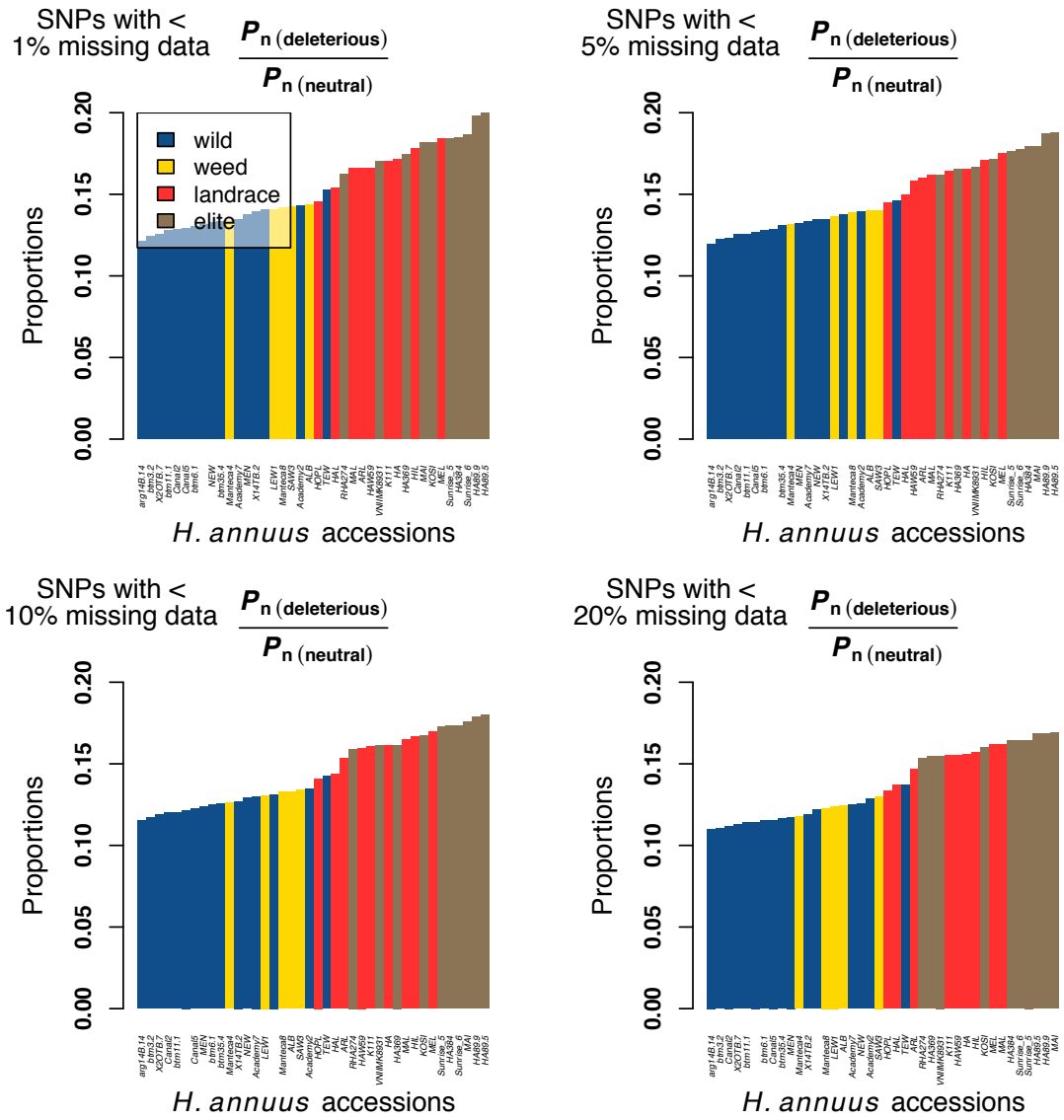


Figure S3: Other missing data cutoffs (1%, 5%, 10%, 20%) used to for trimming SNPs data sets.

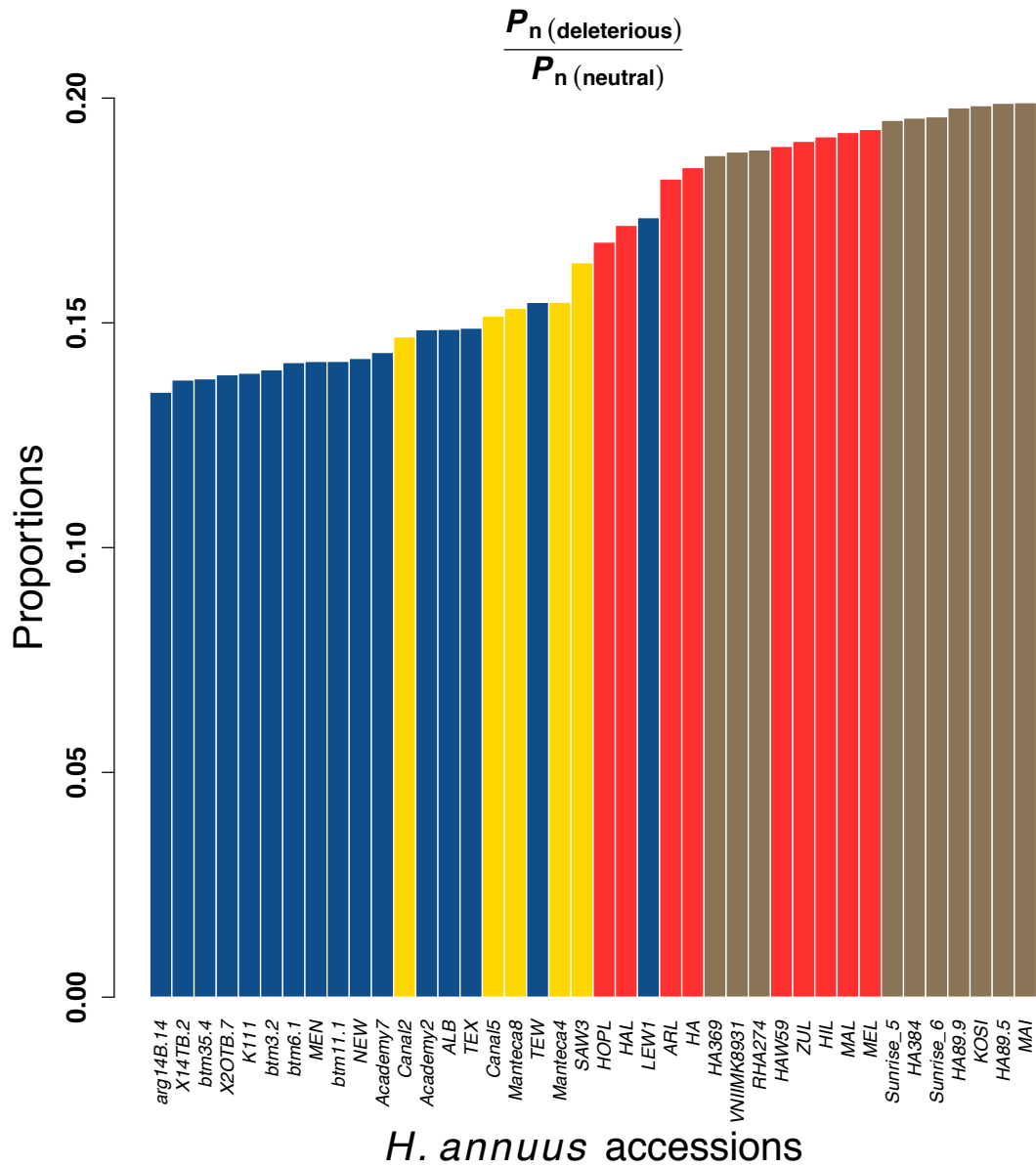


Figure S4: The number of non-synonymous deleterious mutations ($P_n(\text{deleterious})$) divided by the number of neutral non-synonymous mutations ($P_n(\text{neutral})$) per individual. Mutations defined as deleterious using SIFT default cutoff value (0.05).

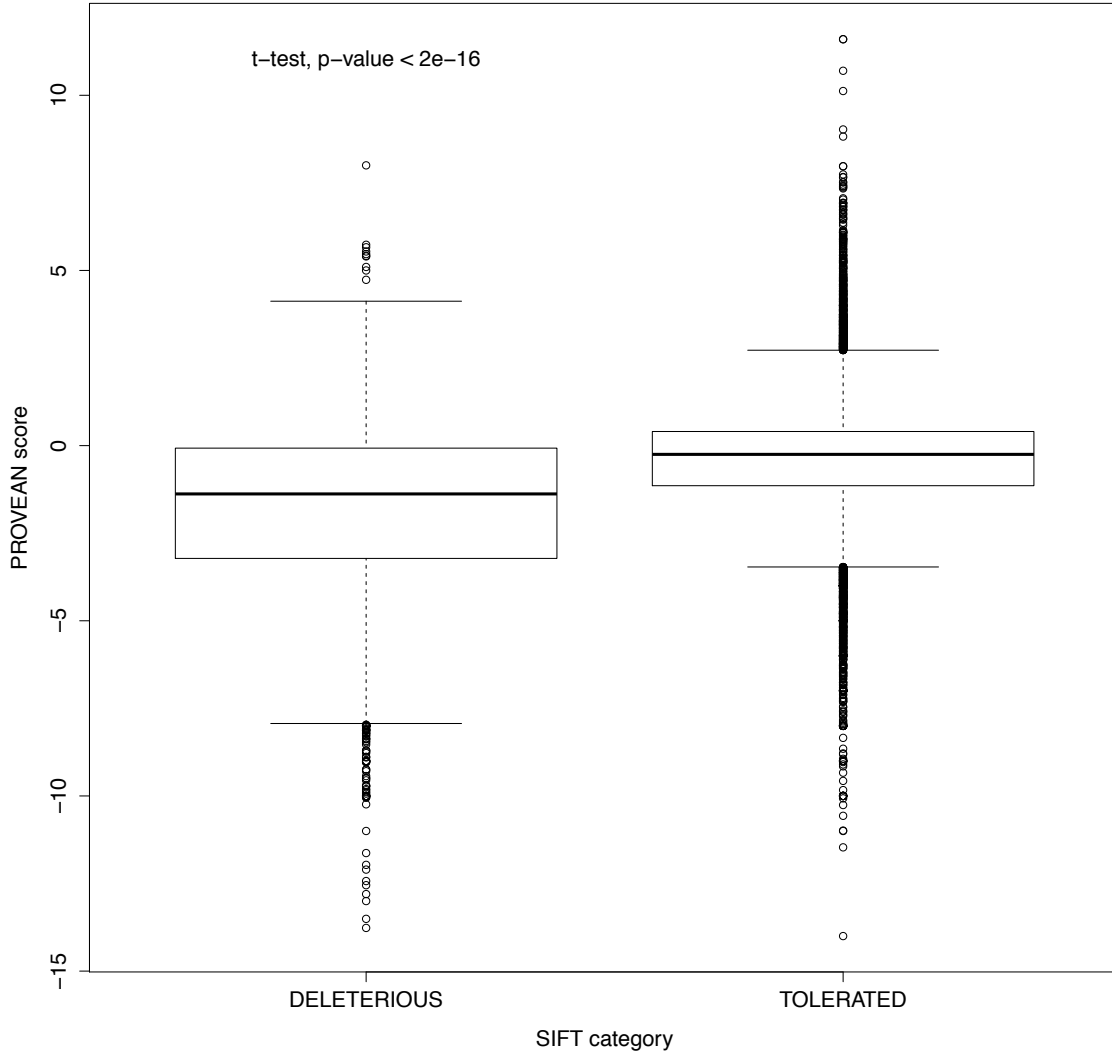


Figure S5: Boxplot of PROVEAN score for mutations identified as deleterious or tolerated by SIFT.

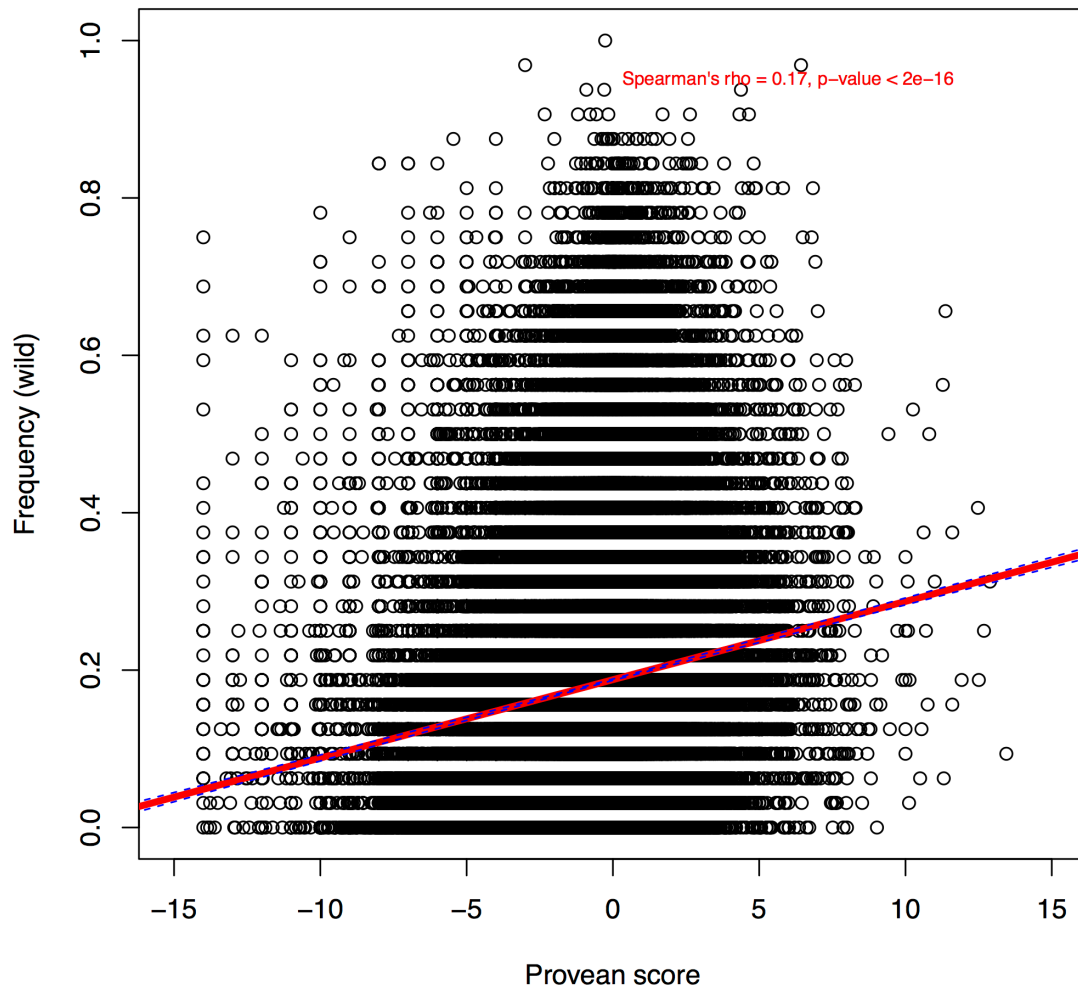


Figure S6: Relationship between PROVEAN score (deleterious effect) and the frequency of the allele in wild lines. Best fit line (red) and 95 % confidence interval (dashed blue line).

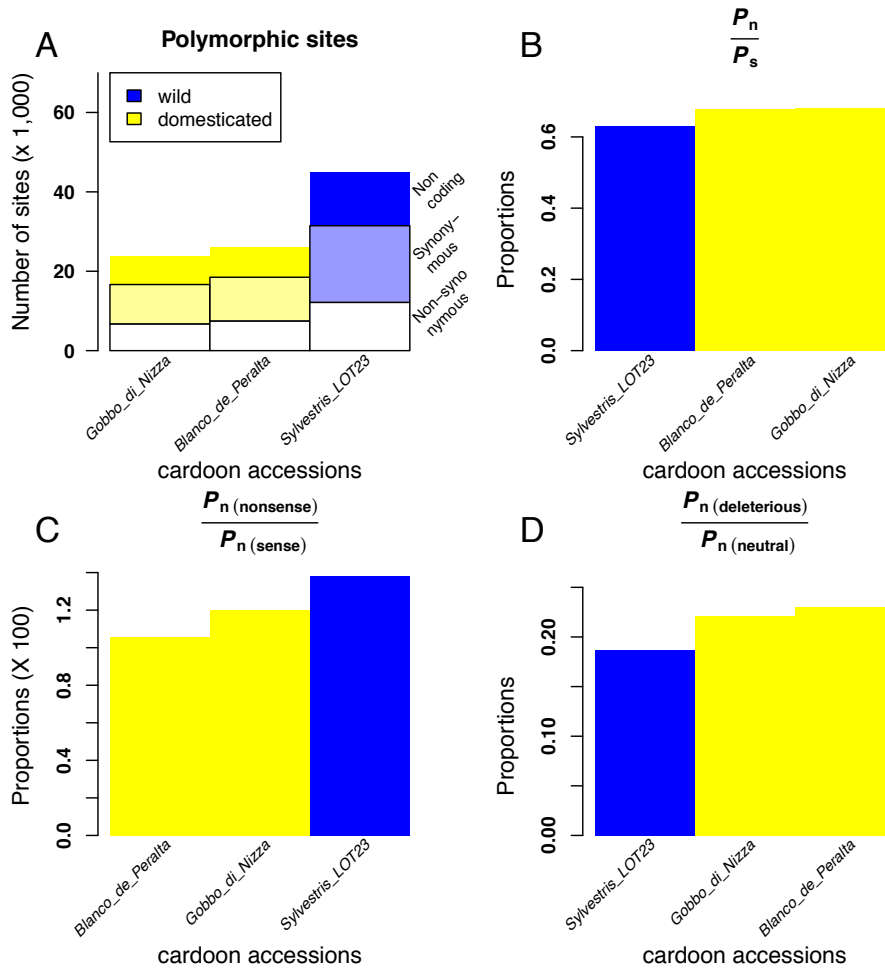


Figure S7: Equivalent to Figure 1 for cardoon accessions. **S7A:** The number of coding synonymous, coding non-synonymous and non-coding mutations per individual. **S7B:** The number of non-synonymous mutations (P_n) divided by the number of synonymous mutations (P_s) per individual (χ^2 test between wild and domesticated proportions, $\chi^2_{(df=2)} = 22.6$, p -value = $1e-5$). **S7C:** The number of non-synonymous nonsense (i.e. alternative STOP codon, $P_{n(\text{nonsense})}$) mutations divided by the number of sense non-synonymous mutations ($P_{n(\text{sense})}$) per individual (χ^2 test between wild and domesticated proportions, $\chi^2_{(df=2)} = 4.0$, p -value = 0.1). **S7D:** The number of non-synonymous deleterious mutations ($P_{n(\text{deleterious})}$) divided by the number of neutral non-synonymous mutations ($P_{n(\text{neutral})}$) per individual (χ^2 test between wild and domesticated proportions, $\chi^2_{(df=2)} = 34.6$, p -value = $2e-8$). PROVEAN cutoff value < -2.5 for deleterious mutations.

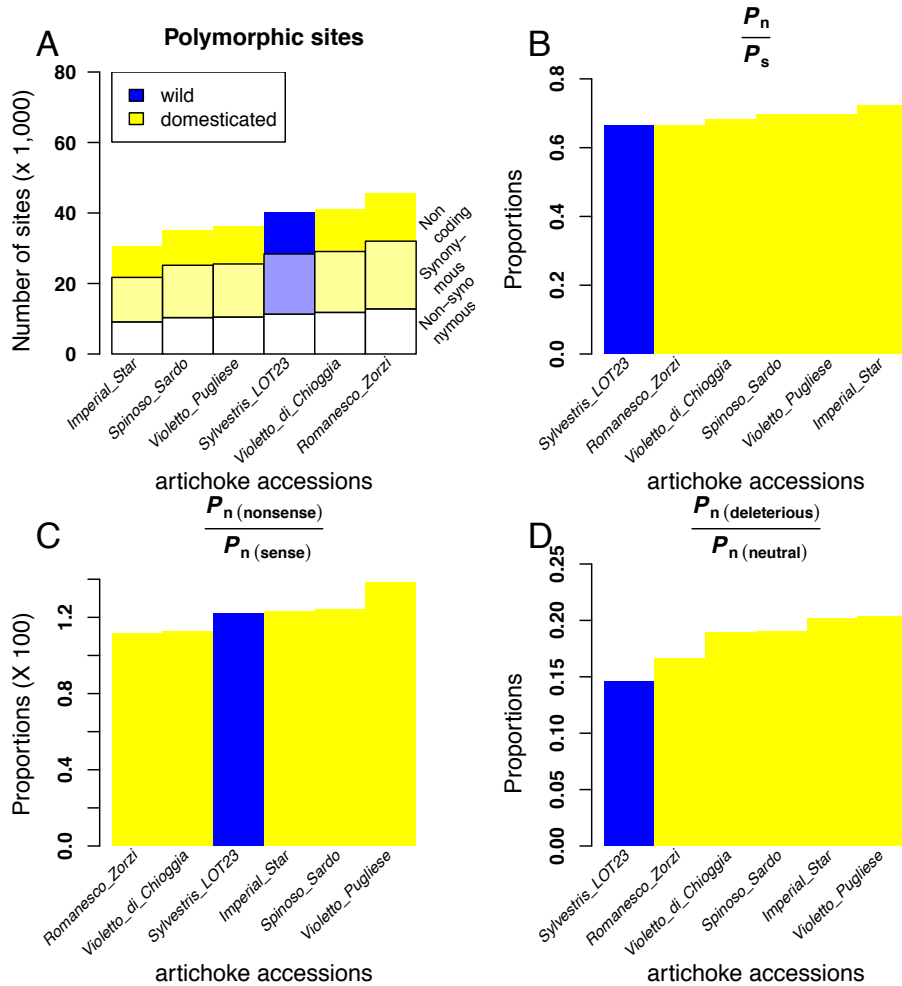


Figure S8: Equivalent to Figure 1 for globe artichoke accessions. **S8A:** The number of coding synonymous, coding non-synonymous and non-coding mutations per individual. **S8B:** The number of non-synonymous mutations (P_n) divided by the number of synonymous mutations (P_s) per individual (χ^2 test between wild and domesticated proportions, χ^2 (df=5) = 31.2, p -value = 9e-6). **S8C:** The number of non-synonymous nonsense (i.e. alternative STOP codon, $P_{n(\text{nonsense})}$) mutations divided by the number of sense non-synonymous mutations ($P_{n(\text{sense})}$) per individual (χ^2 test between wild and domesticated proportions, χ^2 (df=5) = 4, p -value = 0.5). **S8D:** The number of non-synonymous deleterious mutations ($P_{n(\text{deleterious})}$) divided by the number of neutral non-synonymous mutations ($P_{n(\text{neutral})}$) per individual (χ^2 test between wild and domesticated proportions, χ^2 (df=5) = 113.3, p -value = 2e-16). PROVEAN cutoff value < -2.5 for deleterious mutations