

Figure S1 Mammalian species phylogeny (Douzery et al. 2014) indicating each of the clade partitions tested by the branch-site and clade models.

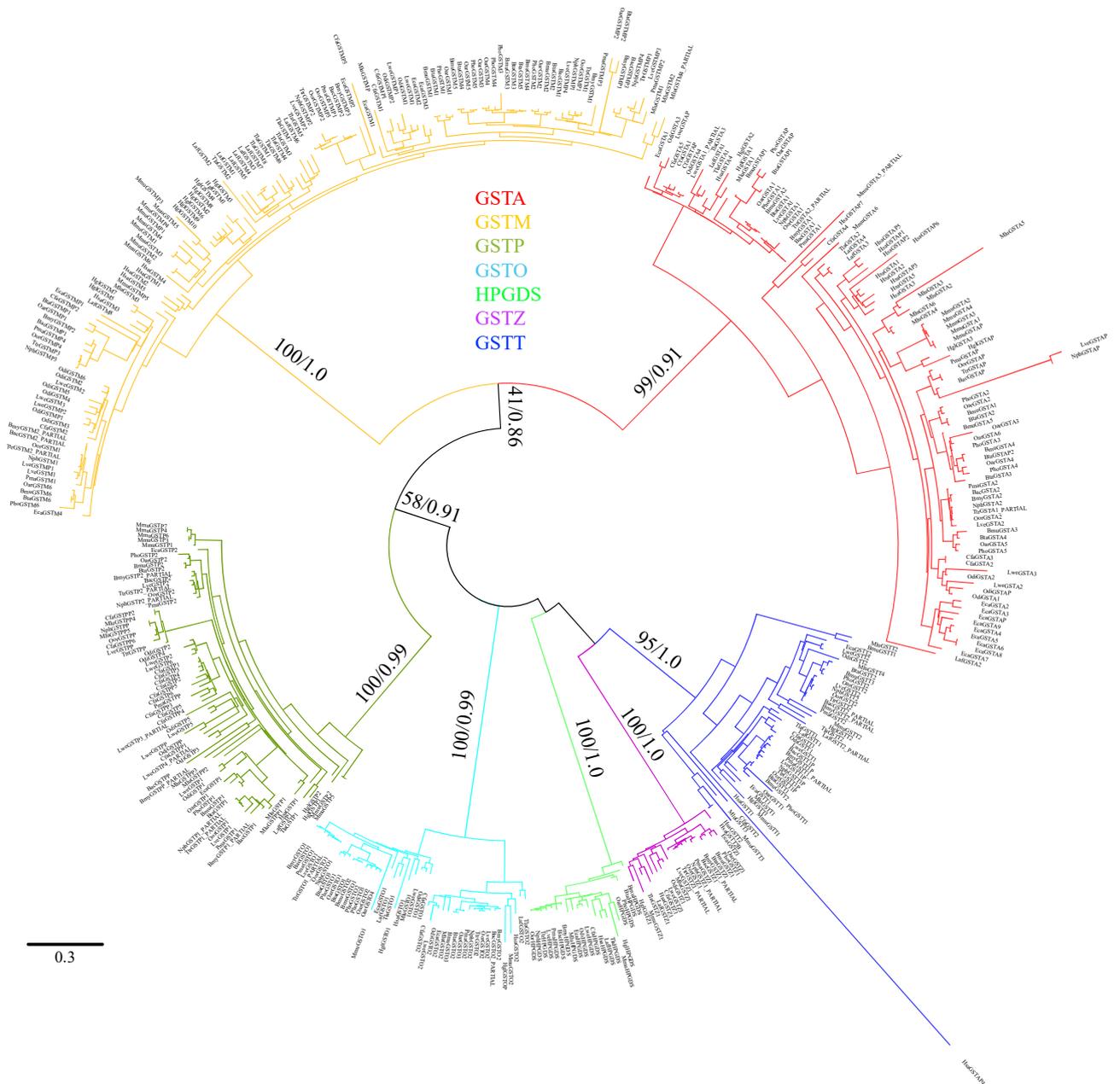


Figure S2 Phylogenetic tree of the GST gene family in mammals. Shown is the maximum likelihood and Bayesian tree built using RaxML and MrBayes methods with the multiple alignments of 448 GST nucleotide sequences from 21 mammalian species. The bootstrap values and posterior probability are shown at nodes. The clades of alpha, mu, pi, omega, sigma, zeta, theta are shown in red, orange, turquoise, azure, green, purple, and blue, respectively.

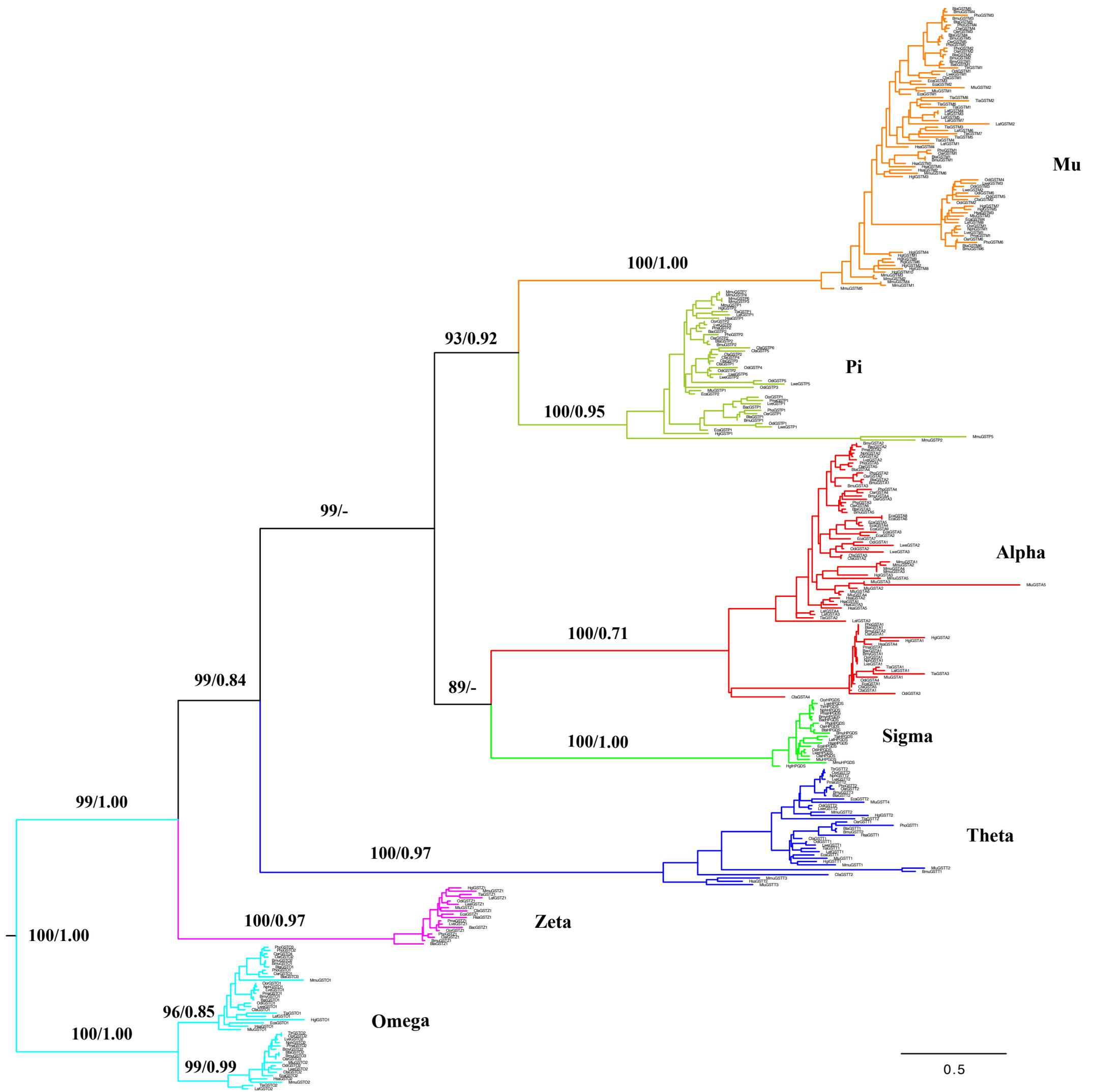


Figure S3 Phylogenetic tree of GST gene family based on 333 mammalian protein sequences. Numbers of the nodes correspond to maximum likelihood bootstrap support values and Bayesian posterior probabilities. The clades of alpha, mu, pi, omega, sigma, zeta, theta are shown in red, orange, turquoise, azure, green, purple, and blue, respectively.

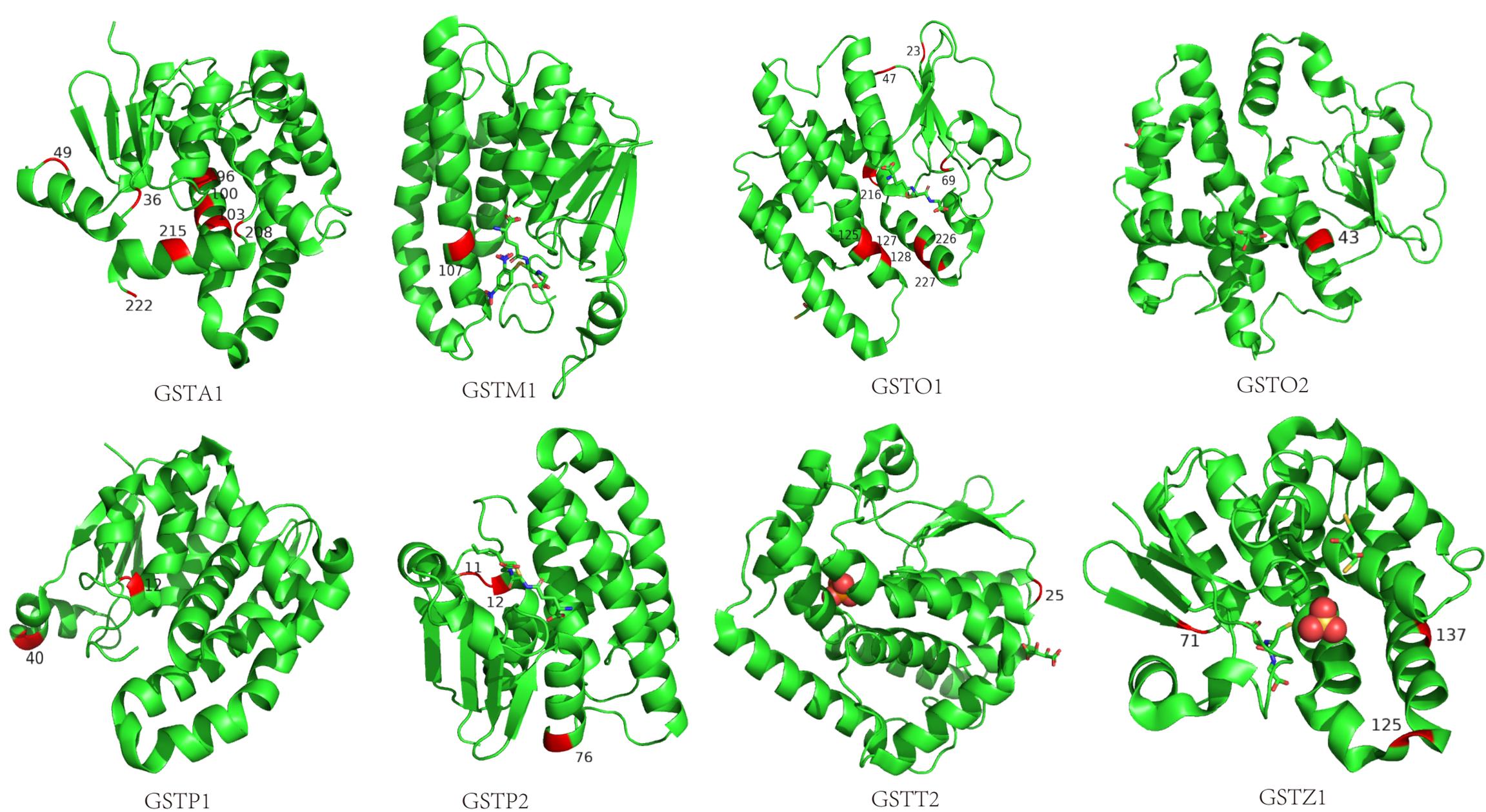


Figure S4 Positively selected sites are shown in crystal structure with red. The crystal structures of GSTA1 (1gsd), GSTM1 (1XW6), GSTO1 (5V3Q), GSTO2 (3Q18), GSTP1 (5X79), GSTP2 (P46425), GSTT2 (4MPF), GSTZ1 (2CZ2) were taken from the Protein Data Bank ([http:// www.rcsb.org/pdb](http://www.rcsb.org/pdb)).

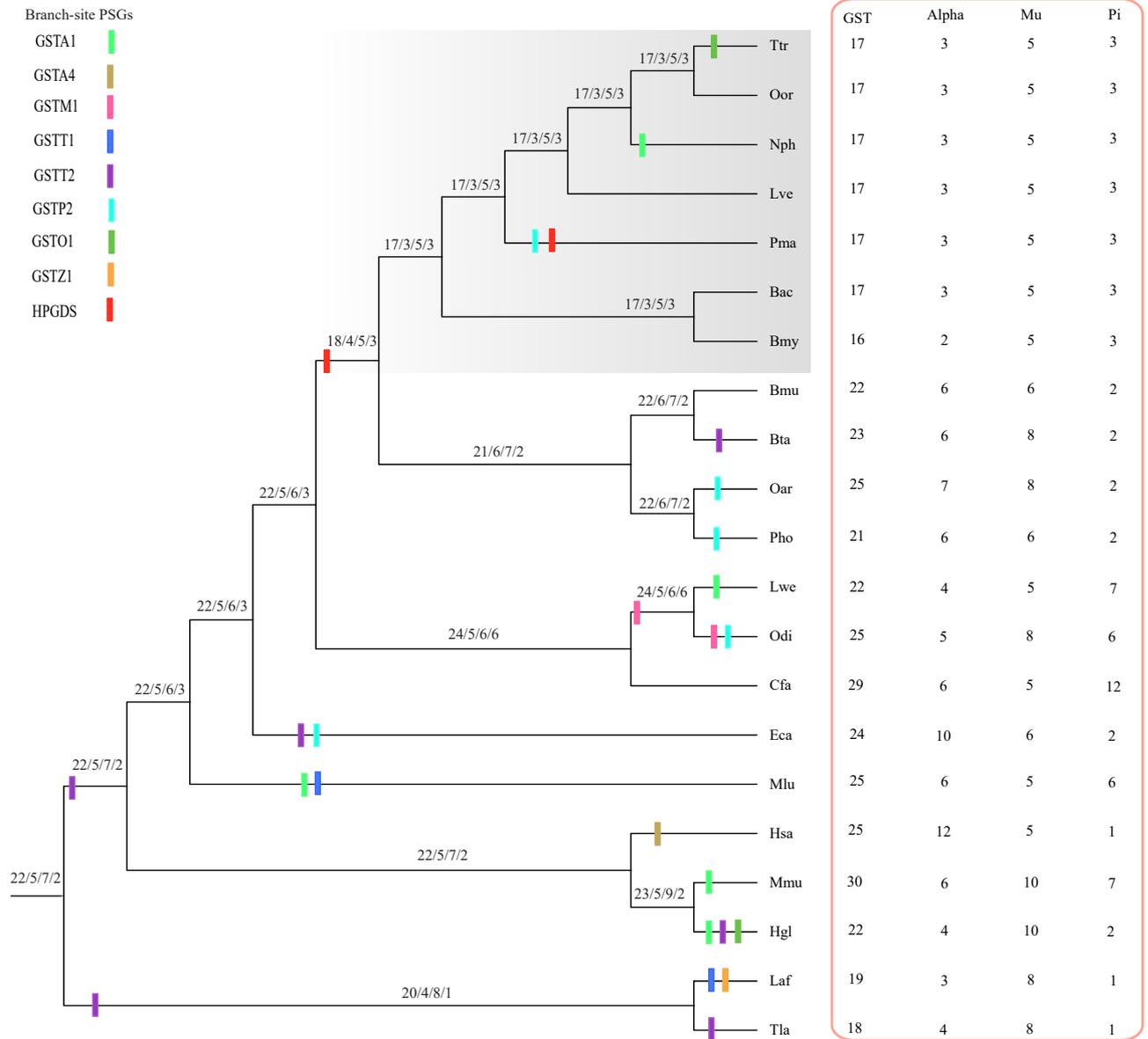


Figure S5 Evidence for lineage-specific positive selection in mammalian GSTs. Inset shows the gene number of GSTs, alpha, mu and pi class inferred to have occurred gain and loss along mammalian lineages.