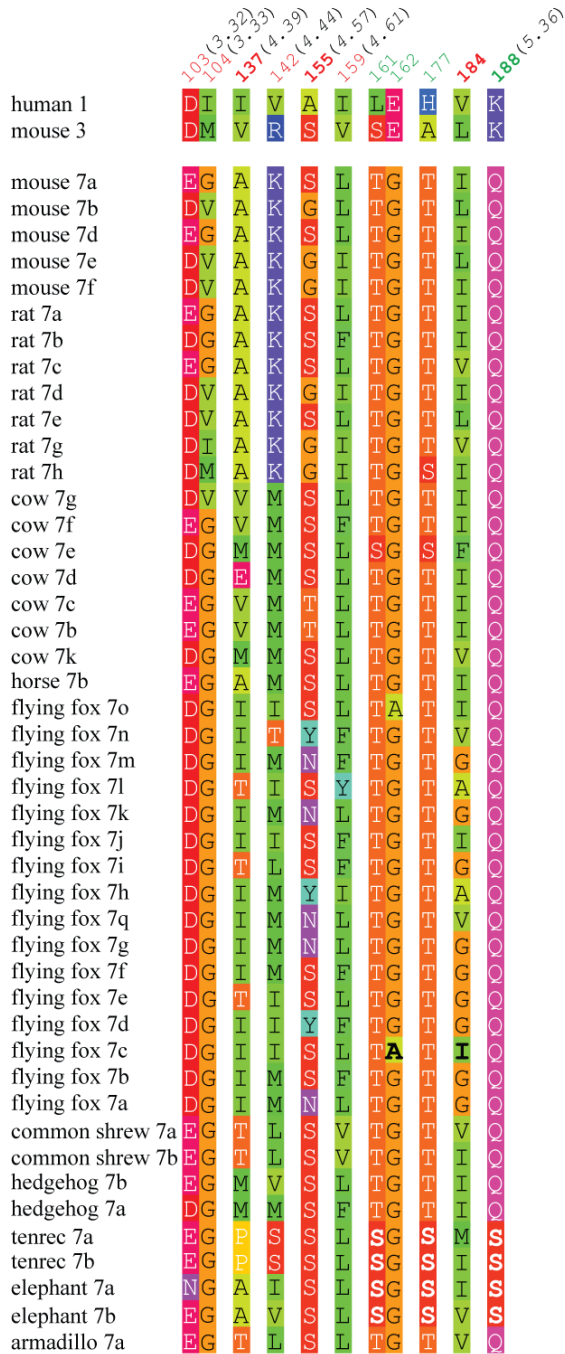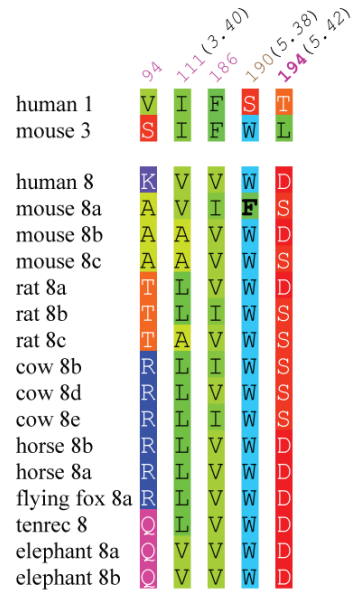**S7 Fig. Alignments of the positively selected sites identified in TAAR7 (a) and TAAR8 (b).** The position numbers correspond to those given in S5 Fig. The residues identified by the branch-site models are shown in boldface. The amino acids are color-coded based on their physico-chemical properties using the Taylor color scheme (Taylor 1997). Color-coding is roughly as follows: red for negatively charged (D and E), blue/blueish for positively charged (R, K, and H), green/yellow green for hydrophobic (I, F, V, L, M, and A), blueish green for aromatic (W and Y), purple for large polar (N and Q), and reddish/orange for small (G, T, and S).

References:

Taylor WR. 1997. Residual colours: a proposal for aminochromography. *Protein Eng*. 10:743-746.