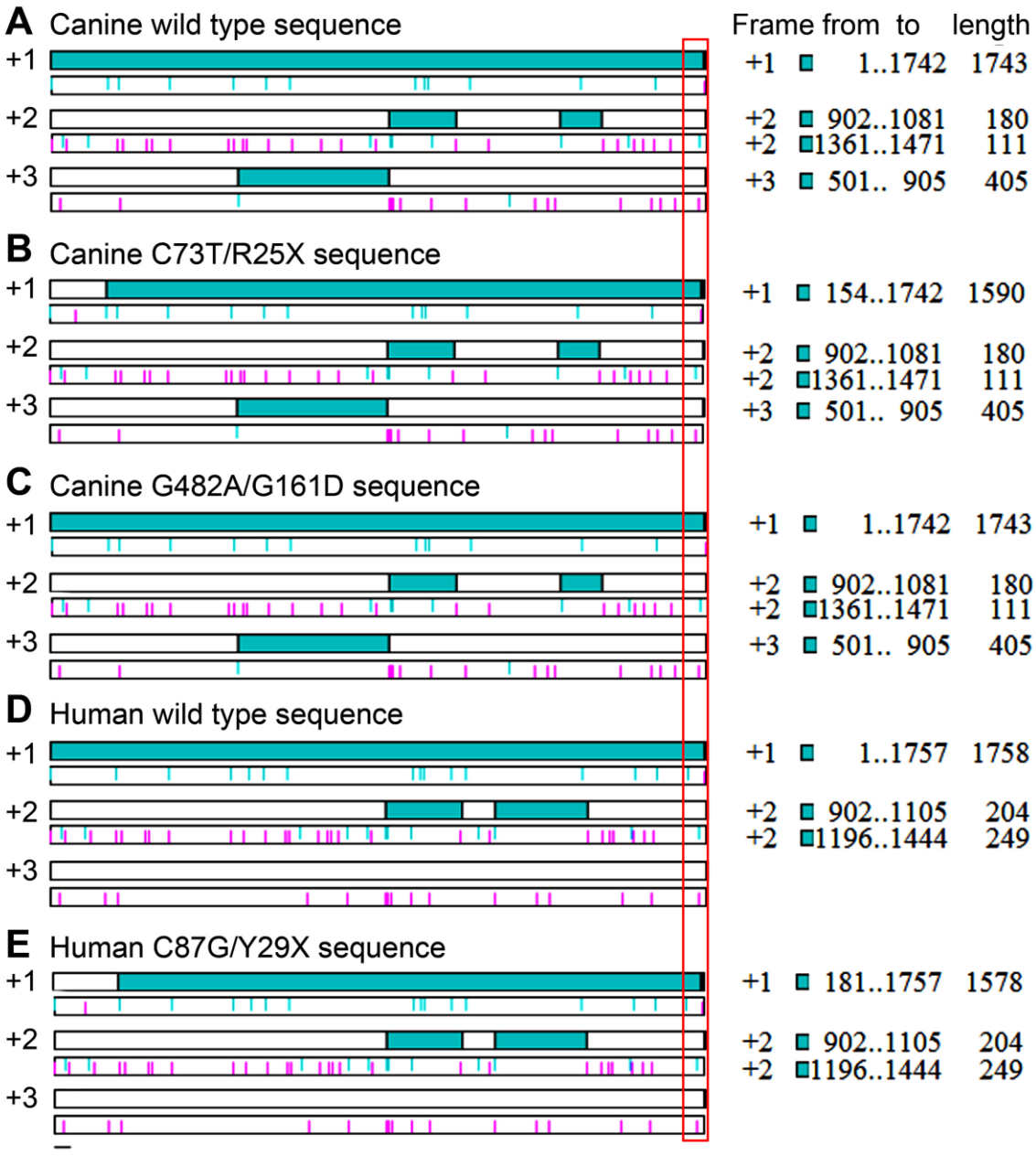

Supplementary Figure 2. Predicted changes in the *BEST1* ORF. ORFs were predicted for all three *BEST1* reading frames following the bestrophin-1 promoter using NCBI ORF finder software: http://www.ncbi.nlm.nih.gov/gorf/gorf.html. For each reading frame, the top panel indicates any identified ORF larger than 100bp (aquamarine) with the exact location and length in amino acids listed on the right.

The bottom panel displays locations of the potential start (turquoise) and stop (magenta) codons. **A.** The canine wild type sequence is predicted to translate into a 1743 bp reading frame corresponding to the 580 aa bestrophin-1 protein. **B.** The $C_{73}T/R_{25}X$ stop mutation could potentially produce a shortened reading frame of 1590 bp utilizing an alternative start codon in a reading frame +1, resulting in a 529 aa protein with the same C-terminus as the wild type bestrophin-1. **C.** No changes in the ORF were predicted with the $G_{482}A/G_{161}D$ mutation. **D.** The human *BEST1* wild type sequence is correctly predicted to result in a 1758 bp ORF, corresponding to the 585 aa bestrophin-1 protein. **E.** The $C_{87}G/Y_{29}X$ stop mutation could utilize an alternative start codon and shortening the native protein by 60 aa at the N-terminus. The antibody binding domain, located at the conserved bestrophin-1 C-terminus (red box) correctly binds to the human and canine wild type protein, and is predicted to also recognize potential alternative proteins produced through any of the investigated mutants. Scale ~38 bp.