Additional file 2. Requena-Ramírez et al.
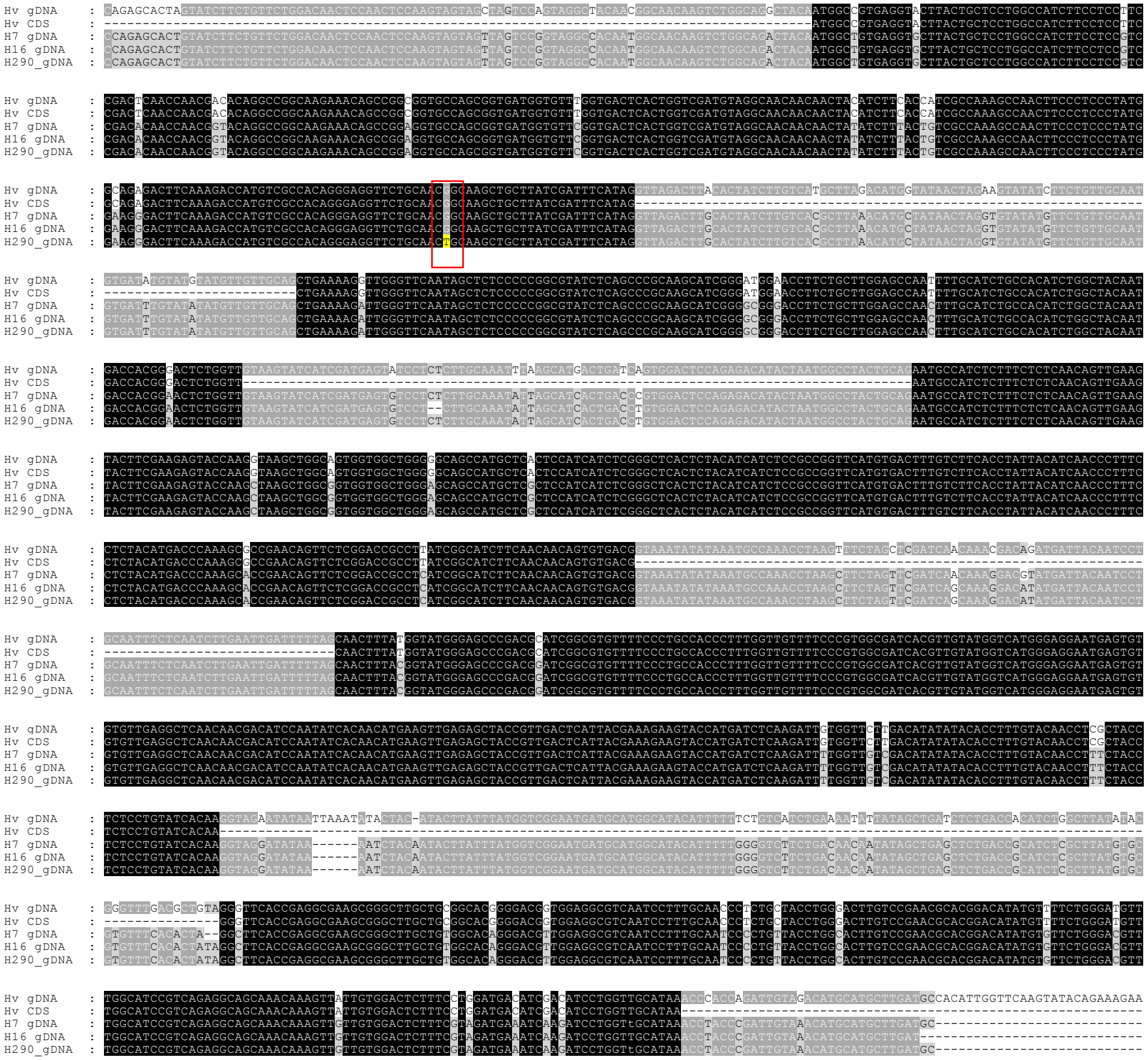
Figure S1. Nucleotide alignment of the genomic (gDNA) and coding (CDS) sequences of the *H. vulgare* gene HORVU7Hr1G021460 (Hv), and the genomic sequences of the allelic variants of gene HORCH7HG21460 in H7, H16 and H290 *H.chilense* accessions. The only SNP detected in the coding region among *H. chilense* alleles is highlighted. *H. chilense* sequence data have been submitted to NCBI (H7 →MT880902; H16 → MT880903; H290 →MT880904).