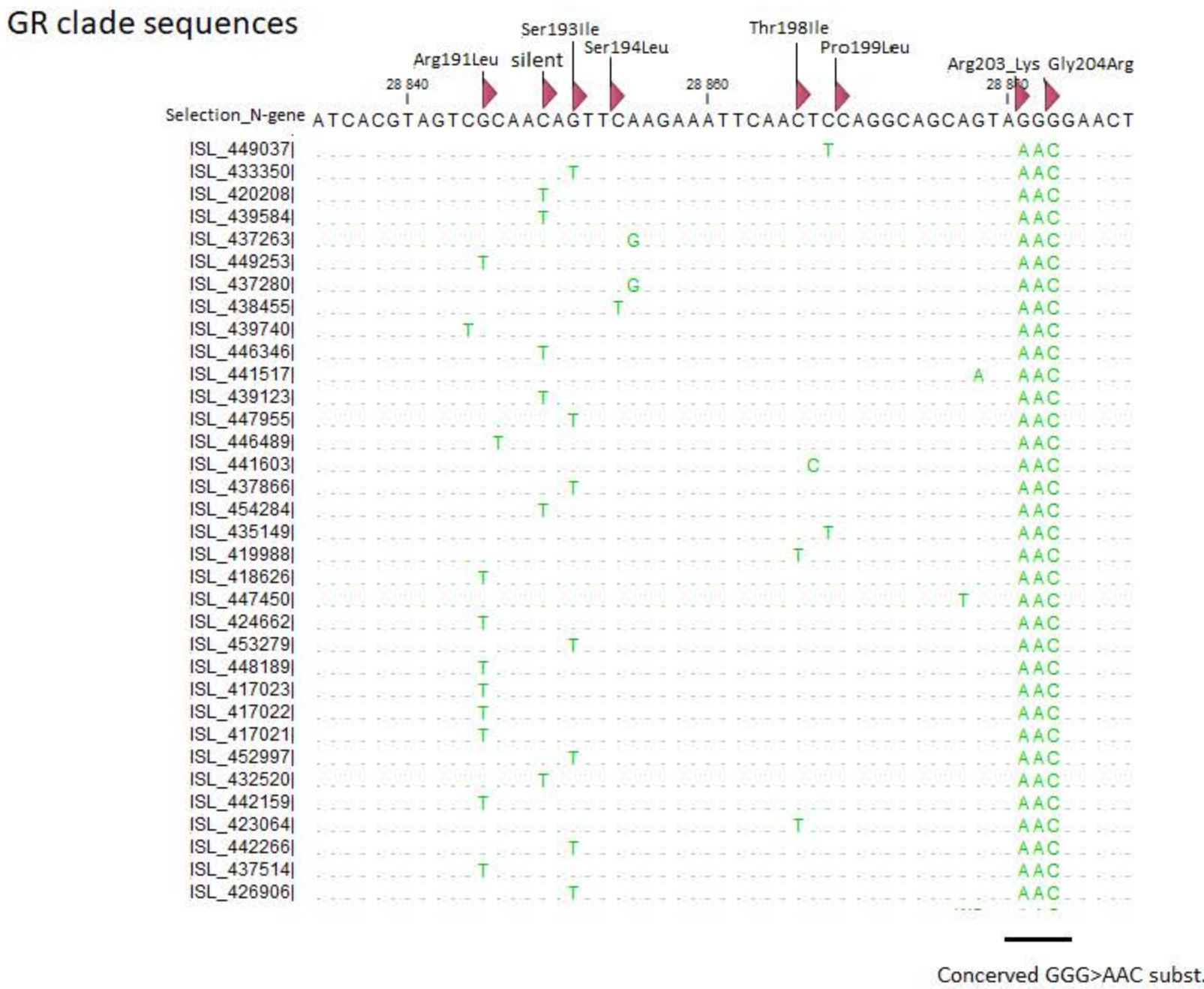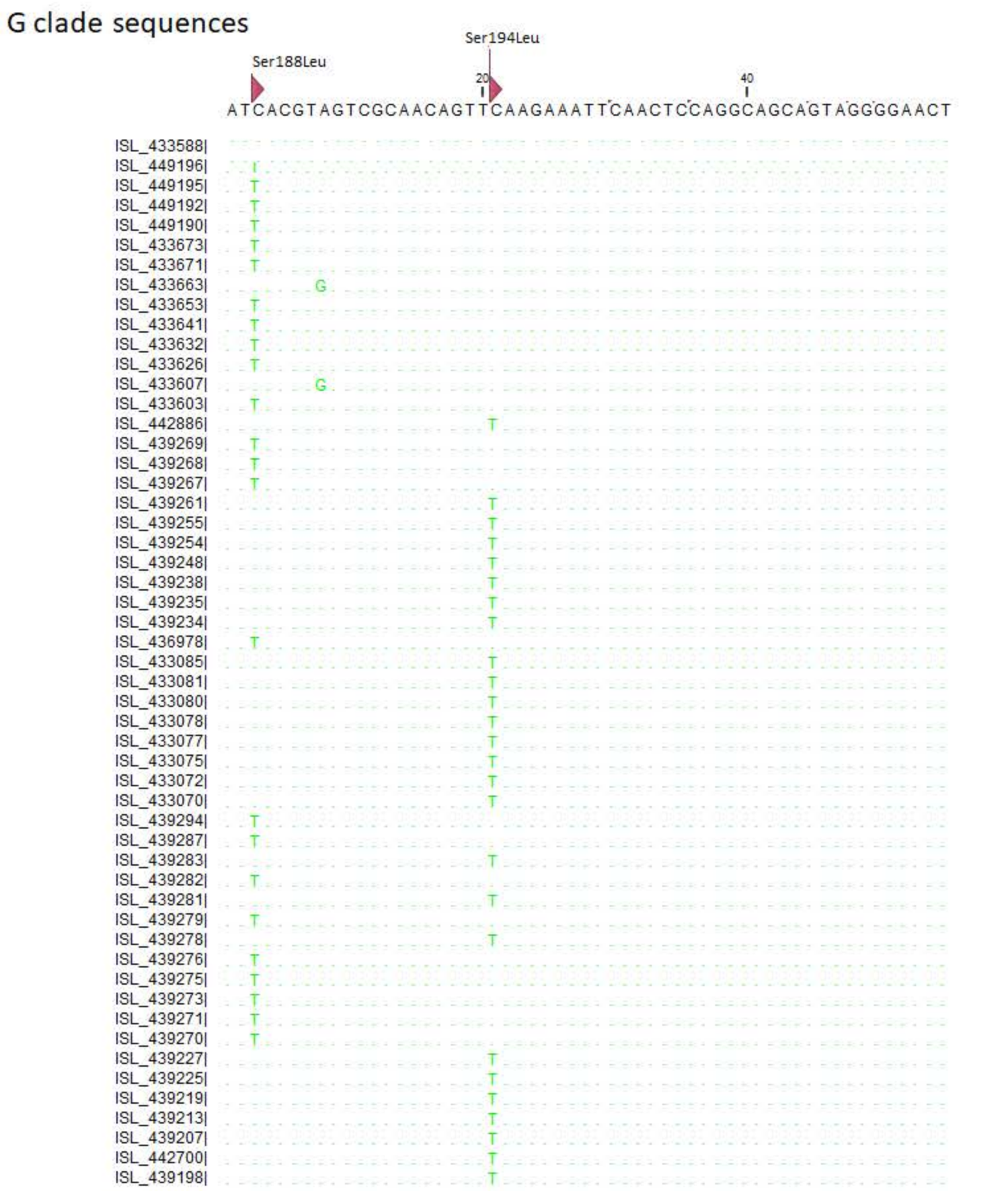Figure S6. Alignment of selected genomes from the GR and G clades. The N-gene subregion (genomic position 28834-28888) encoding amino acids 186-209 is shown. The frequently occuring mutations are flagged. Dots – same nucleotides as in the reference. Note, multiple mutations within the same sequence are rare except of a conserved trinucleotide GGA>AAC substitution in the GR clade sequences.