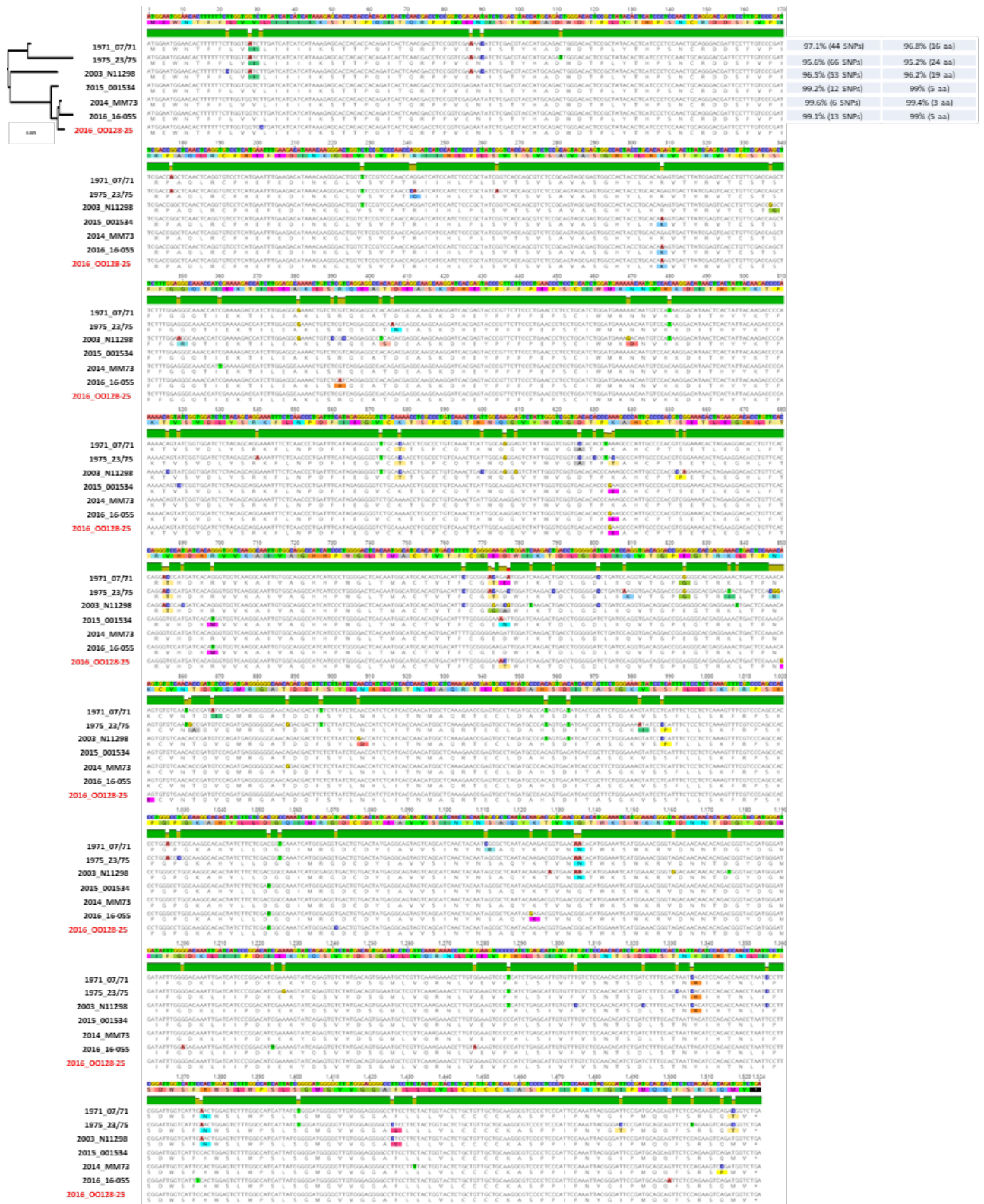


Figure S1: A. Comparison of VHSV OO128-25 complete G gene sequences with VHSV isolates from France. These sequences were obtained from 4 of the 23 VHSV isolates originating from pike obtained in this study, all sharing 100% nt identity. The two French reference strains 07/71 and 23/75 were included in the analysis, as well as the recent RT isolates from the two aforementioned farms (MM73, 001534, and 16-055), and the former pike isolate N11298. Sequences corresponding to 1,524 nt/508 aa were aligned, and identified SNPs represented by colored bars (the same color at the same position indicates a common SNP between strains). Nucleotide and amino acid identities (% and numbers of differences) of each selected strain compared to OO128-25 are reported next to the alignment.

B. Comparison of IHNV OO121-8 partial G gene sequences with certain previous isolates from France. This sequence was obtained from 4 of the 12 IHNV isolates originating from pike obtained in this study, all sharing 100% nt identity. The recent isolates SA15.1442 (MF464337) and 331901 (MF464276) characterized in 2015 and 2014, respectively were included. Four additional older isolates showing the highest rates of identity were also selected for the comparison: X3 (MF464325), 23-94 (MF464289), 47-88 (MF464293), and 71-87 (MF464295). Sequences corresponding to 570 nt/190 aa were aligned, and identified SNPs represented by colored bars (the same color at the same position indicates a common SNP between strains). Nucleotide and amino acid identities (% and numbers of differences) of each strain compared to OO121-8 are reported next to the alignment.

A.



B.

