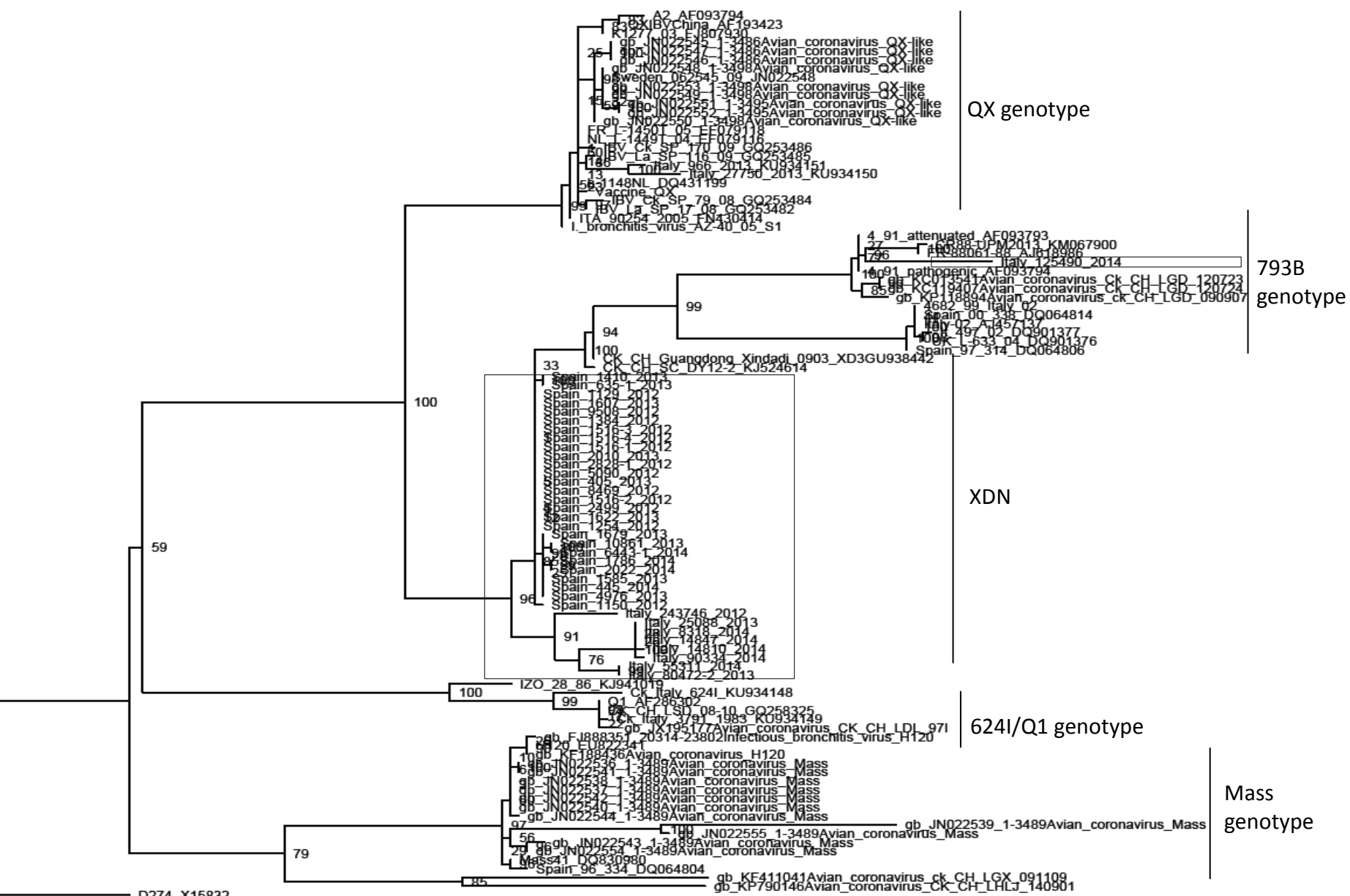
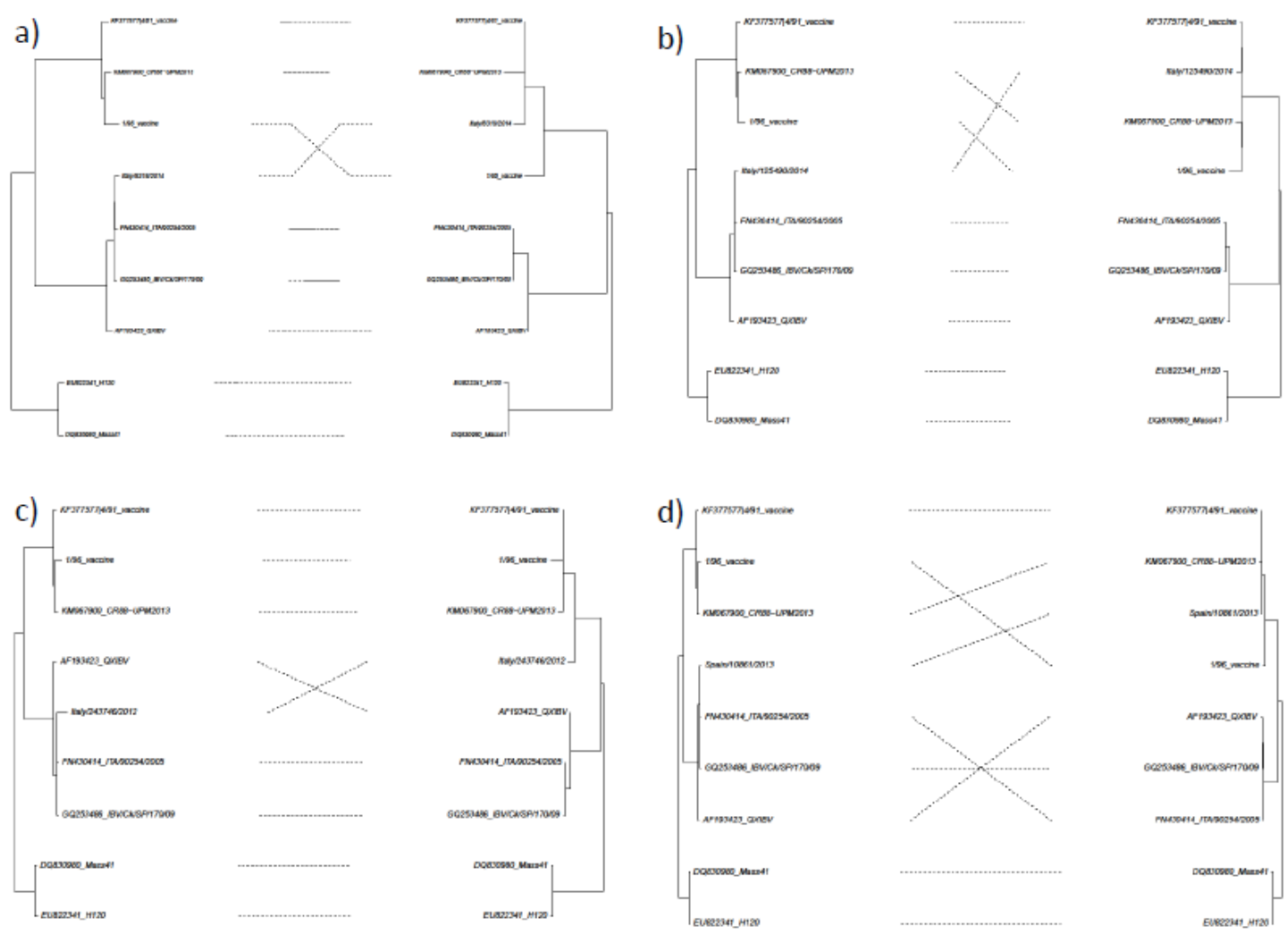


Supplementary figure 1 - Phylogenetic relationships of Spanish and Italian IBV strains based on the partial sequence of the S1 gene. The unrooted tree was created by maximum likelihood method implemented in the IQ software and bootstrapped with 1000 replicates. Spanish and Italian sequences are placed on squares.



Supplementary figure 2 - Phylogenetic trees reconstructed for strain Italy/8318/2014 (a), Italy/125490/2014(b), Italy/243746/2012(c), and Spain/10861/2013(d). For each recombinant strain the alignment was split according to detected breakpoints and an independent tree was reconstructed for each partition. Sequences AF193423_QXIBV, GQ253486_IBV/Ck/SP/170/09 and FN430414_ITA/90254/2005 (QX), KF377577|4/91_vaccine, 1/96_vaccine and KM067900_CR88-UPM2013(793B) were selected as representative of different parental genotypes. DQ830980_Mass41 and EU822341_H120 (Mass) sequences were chosen as outgroup.



Supplementary figure 3 - Entropy plot of amino acid of S1 protein gene of a) the Spanish sequences and b) the Italian sequences.

