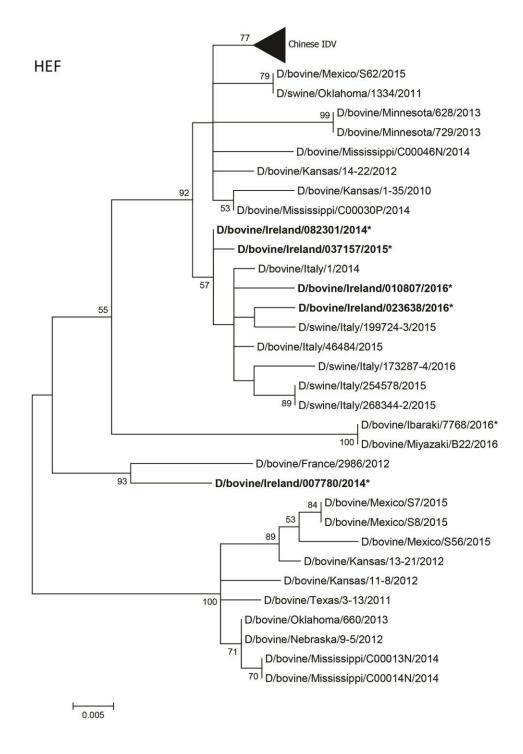
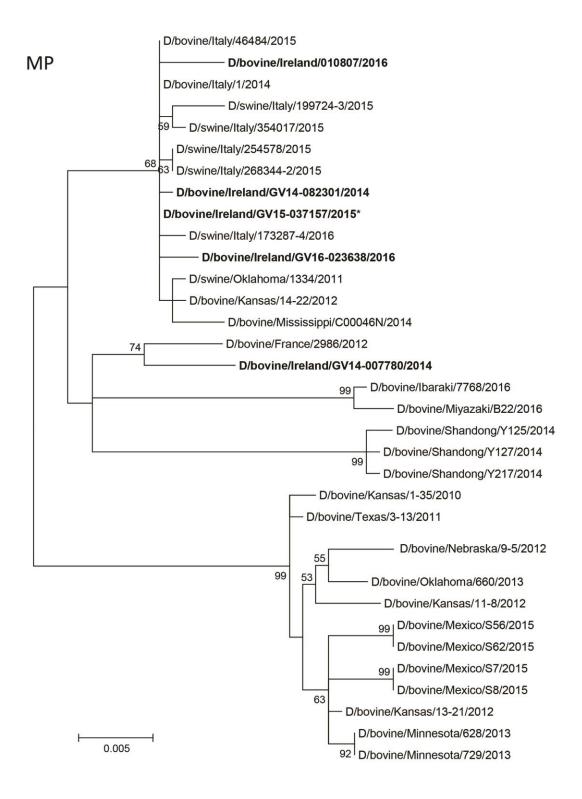
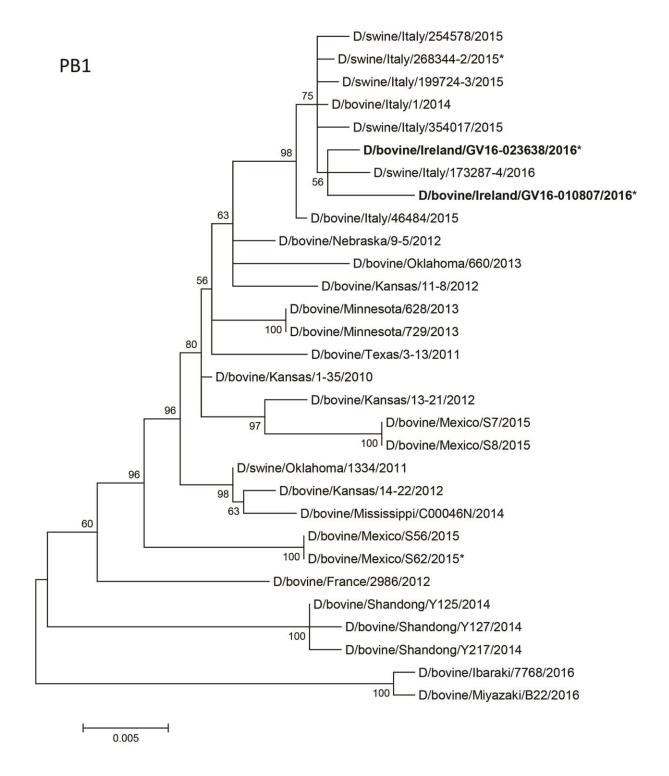
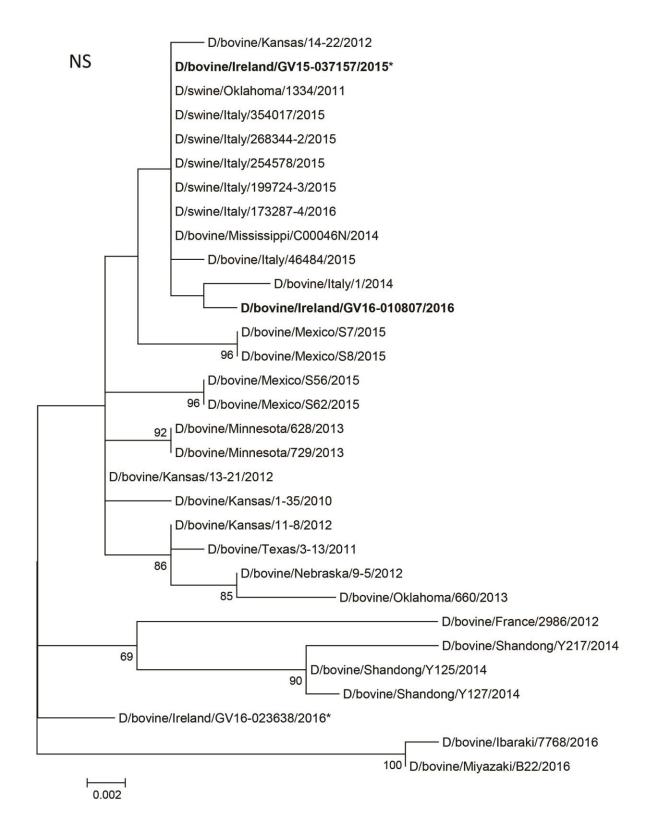
Influenza D Virus in Cattle, Ireland

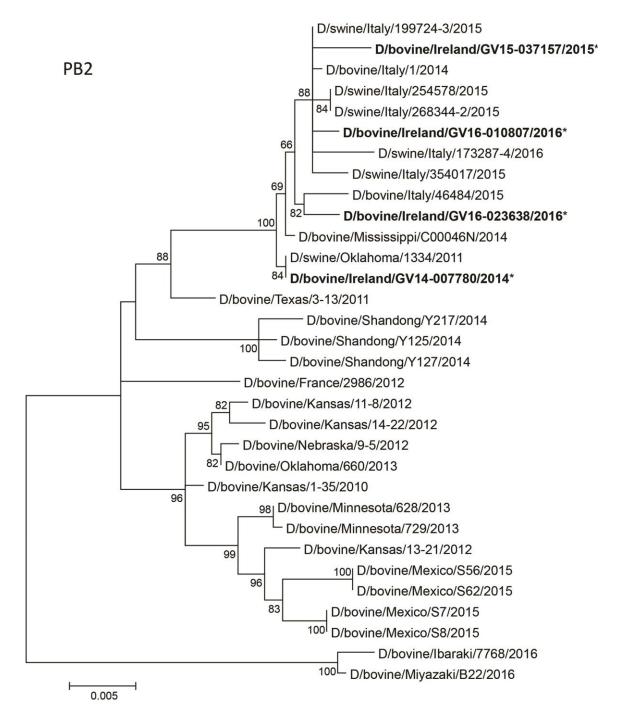
Technical Appendix



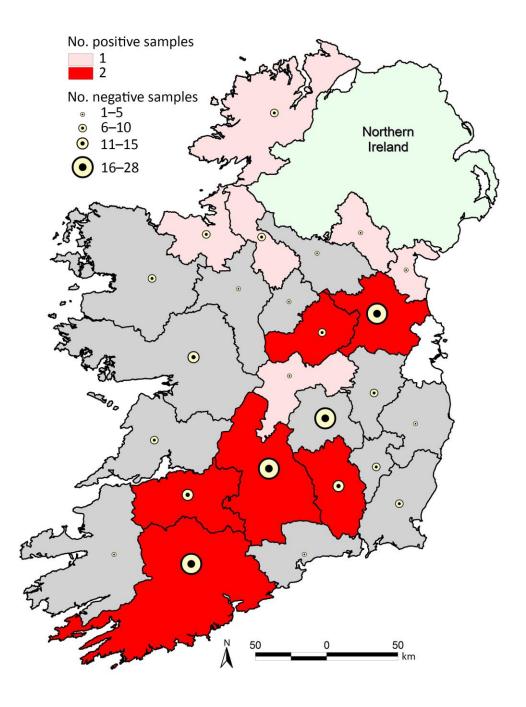








Technical Appendix Figure 1. Phylogenetic trees for 7 genomic segments of influenza D viruses obtained from cattle in Ireland and comparison with virus sequences obtained from GenBank. *Indicates incomplete sequences (only bootstraps >50 are shown). Bold indicates strains isolated in this study. Scale bars indicate nucleotide substitutions per site. PB1, polymerase basic 1; PB2, polymerase basic 2; P3, polymerase 3; HEF, hemagglutinin esterase fusion; NP, nucleoprotein; MP, matrix protein; NS, nonstructural.



Technical Appendix Figure 2. Geographic distribution of positive and negative samples for influenza D virus, by county, in Ireland. Pink indicates 1 positive detected; red indicates 2 positive samples detected; gray indicates no positive samples detected. Circles indicate number of negative samples per county.