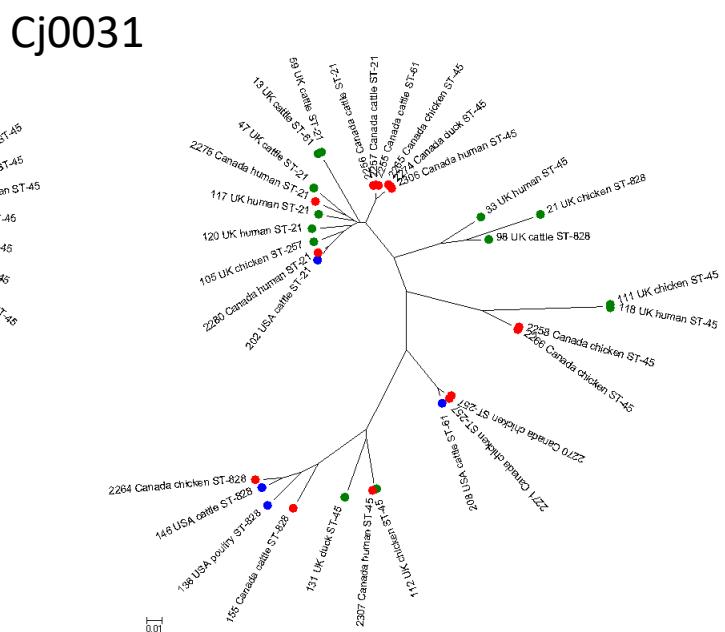
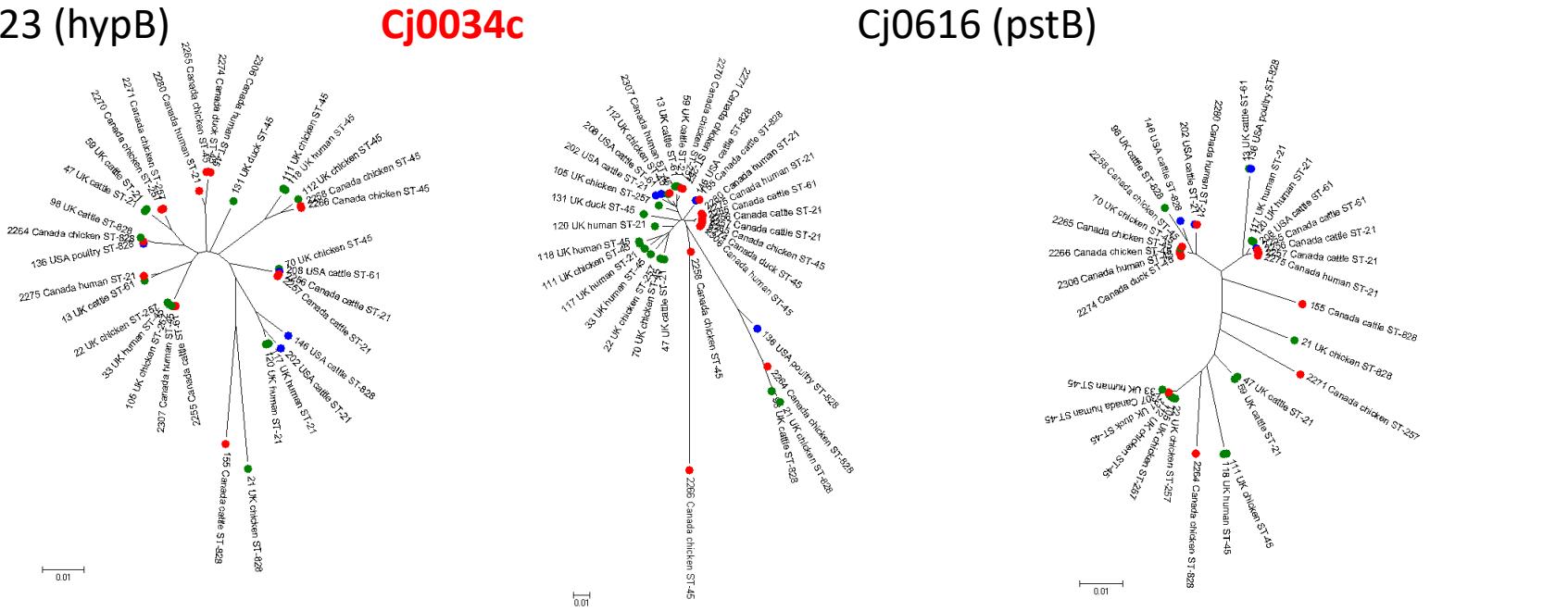


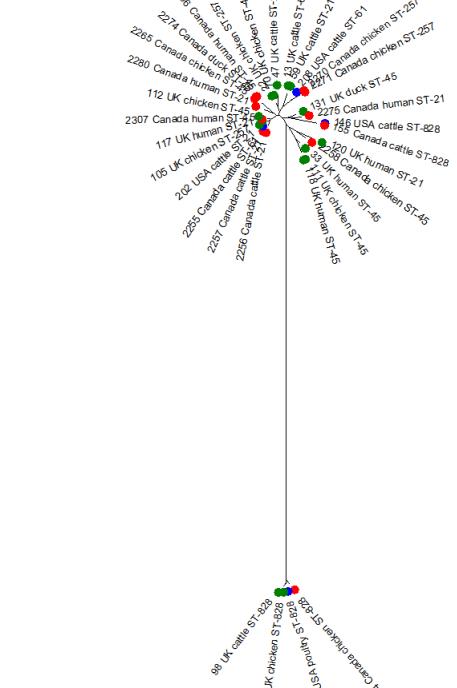
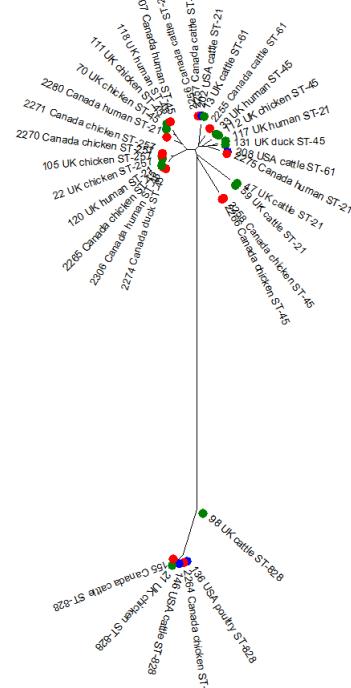
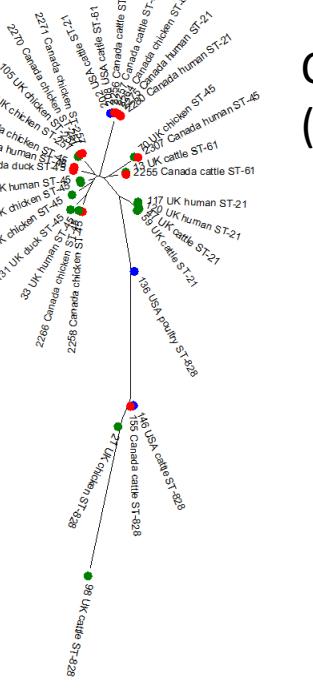
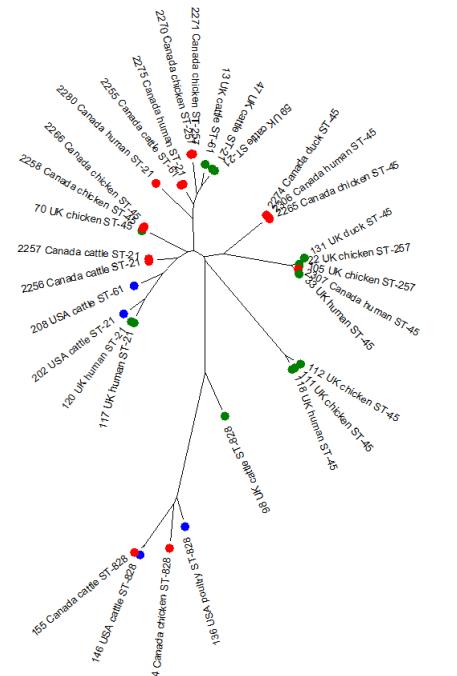
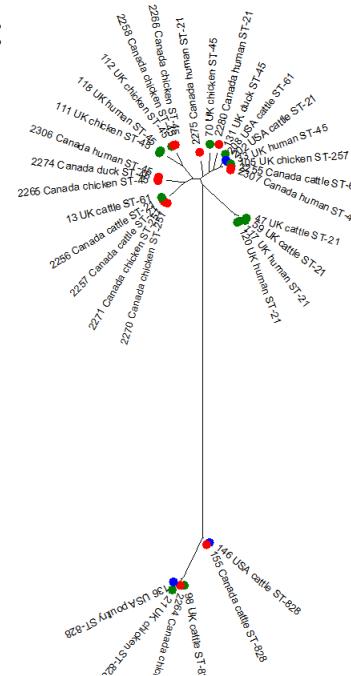
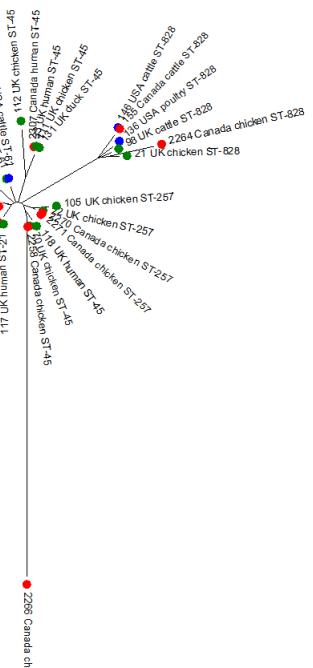
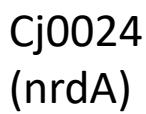
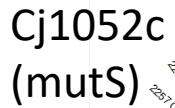
# **Local genes for local bacteria: evidence of allopatry in the genomes of transatlantic *Campylobacter* populations**

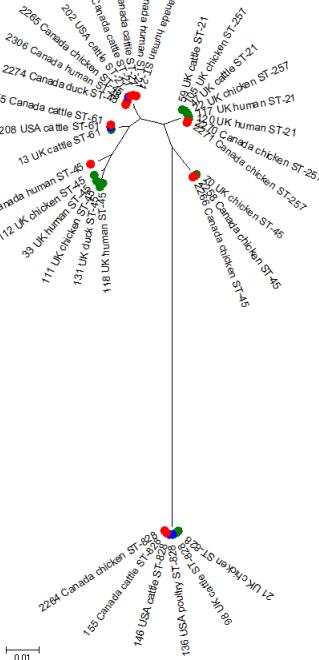
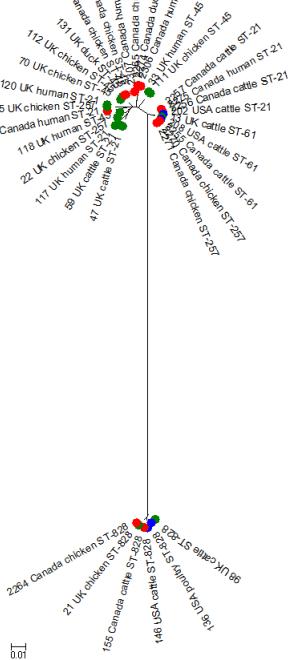
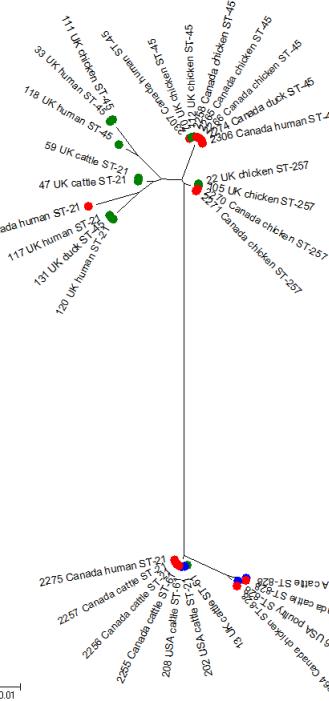
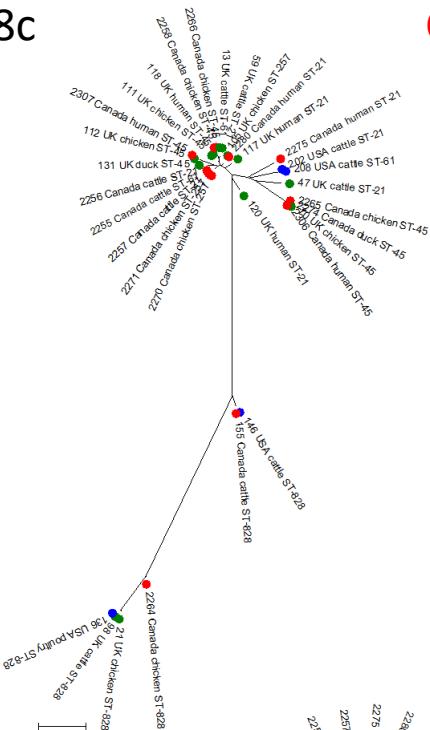
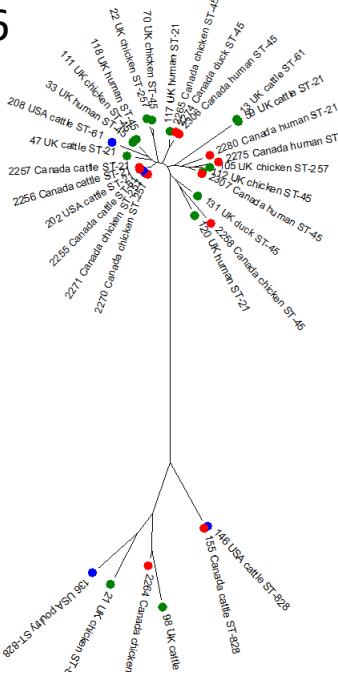
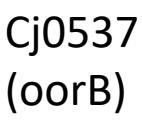
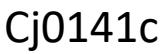
Ben Pascoe<sup>1,2</sup>, Guillaume Méric<sup>1</sup>, Koji Yahara<sup>3,4</sup>, Helen Wimalaratna<sup>5</sup>, Susan Murray<sup>4</sup>, Matthew D. Hitchings<sup>4</sup>, Emma L. Sproston<sup>6</sup>, Catherine D. Carrillo<sup>7</sup>, Eduardo N. Taboada<sup>8</sup>, Kerry K. Cooper<sup>9</sup>, Steven Huynh<sup>10</sup>, Alison J. Cody<sup>5</sup>, Keith A. Jolley<sup>5</sup>, Martin C. J. Maiden<sup>5,11</sup>, Noel D. McCarthy<sup>5,11,12</sup>, Xavier Didelot<sup>13</sup>, Craig T. Parker<sup>10</sup> and Samuel K. Sheppard<sup>1,2,5#</sup>

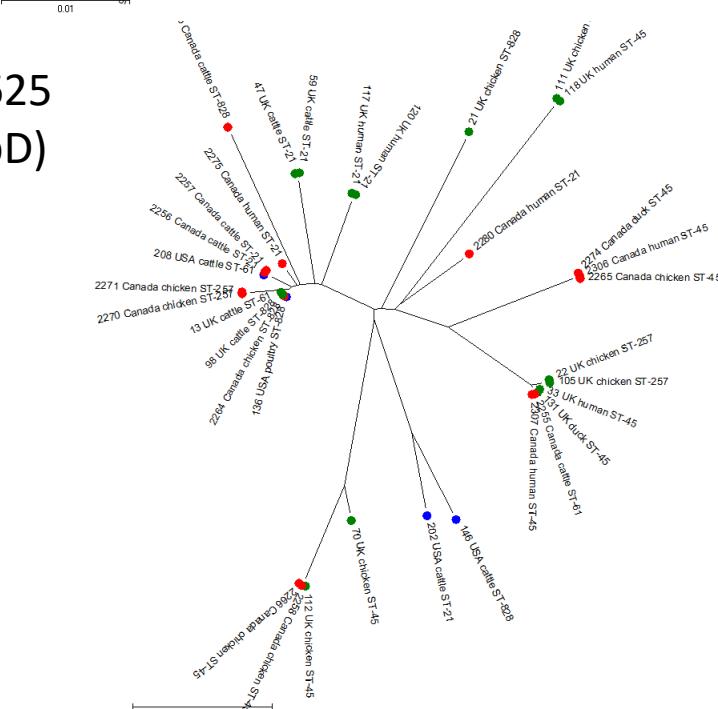
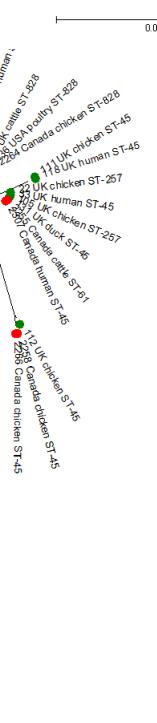
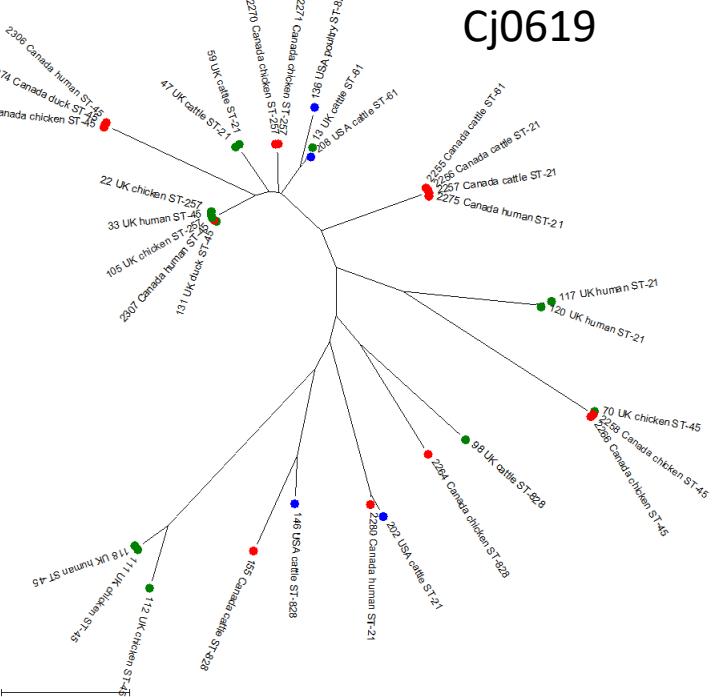
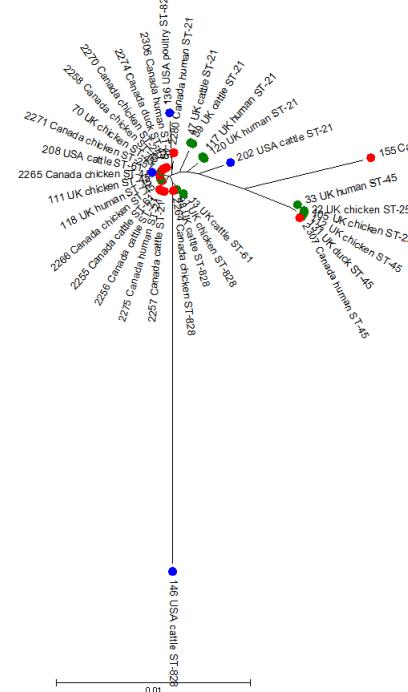
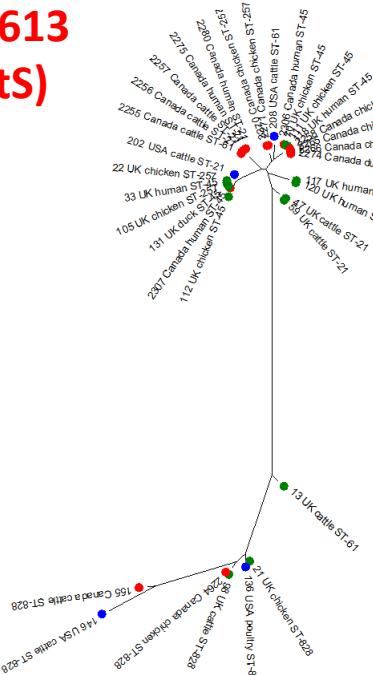
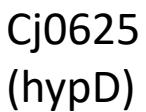
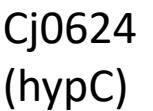
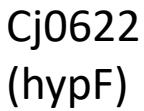
<sup>1</sup>The Milner Centre for Evolution, Department of Biology and Biochemistry, Bath University, Claverton Down, Bath, BA2 7AY, UK; <sup>2</sup>MRC CLIMB Consortium, UK; <sup>3</sup>Department of Bacteriology II, National Institute of Infectious Diseases, Musashimurayama, Tokyo, 208-0011, Japan; <sup>4</sup>Swansea University Medical School, Swansea University, Singleton Park, Swansea, SA2 8PP; <sup>5</sup>Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK; <sup>6</sup>Bureau of Microbial Hazards, Health Canada, 251 Sir Frederick Banting Driveway, Ottawa, K1A 0K9, Canada; <sup>7</sup>Canadian Food Inspection Agency, 960 Carling Avenue, Ottawa, K1A 0Y9, Canada; <sup>8</sup>National Microbiology Laboratory at Lethbridge, Public Health Agency of Canada, PO Box 640, Township Rd. 9-1, Lethbridge, Alberta, T1J 3Z4, Canada; <sup>9</sup>Department of Biology, California State University, Northridge, Northridge, California, USA; <sup>10</sup>Produce Safety and Microbiology Research Unit, Agricultural Research Service, US Department of Agriculture, Albany, California, USA; <sup>11</sup>NIHR Health Protection Research Unit in Gastrointestinal Infections, UK; <sup>12</sup>University of Warwick, Coventry, CV4 7AL, UK; <sup>13</sup>Department of Infectious Disease Epidemiology, Imperial College London, London, W2 1PG, UK

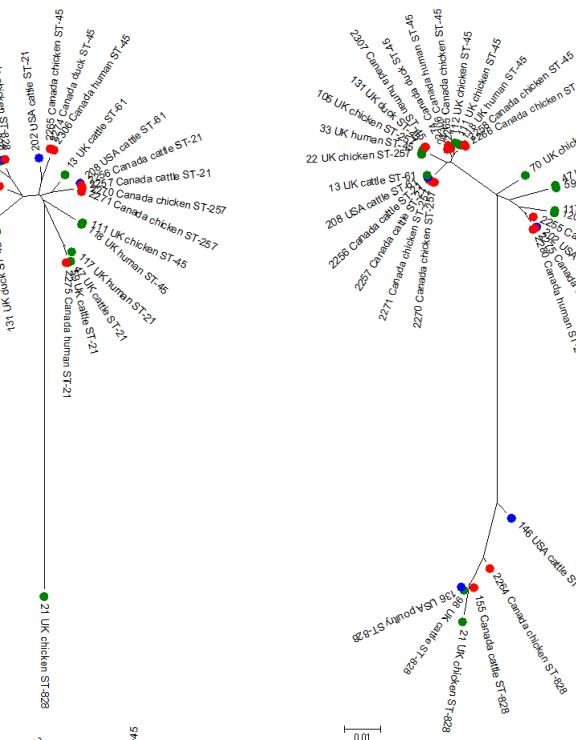
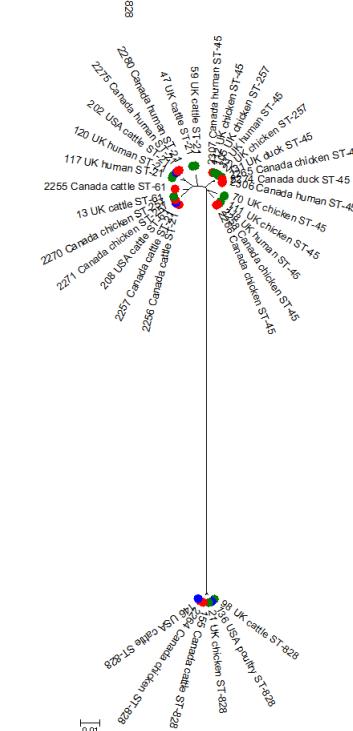
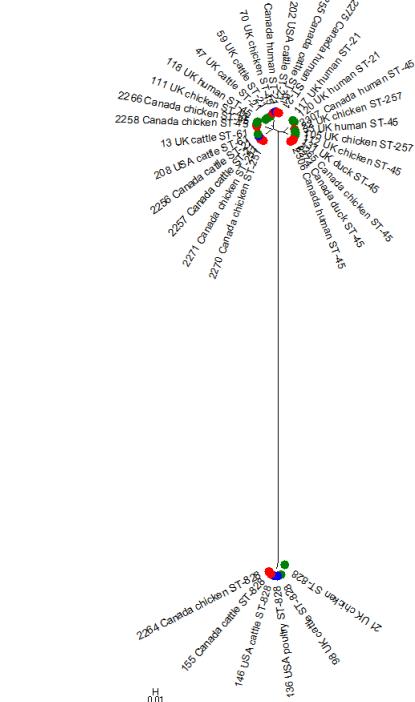
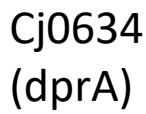
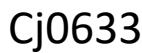
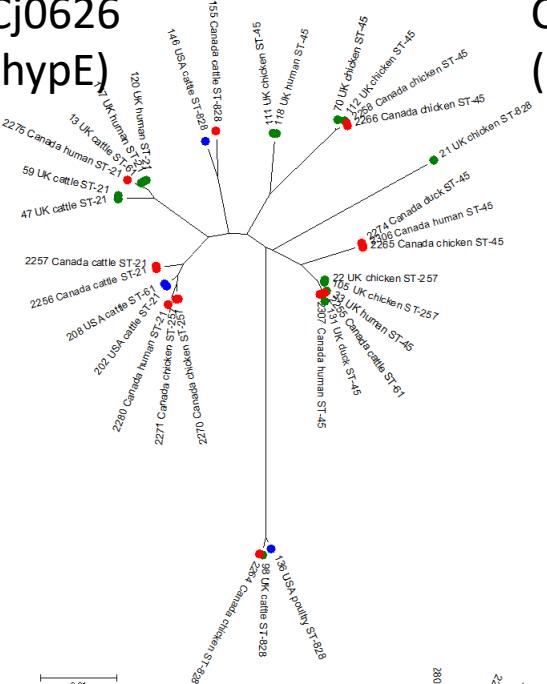
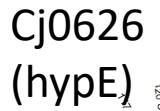
**Figure S1:** Neighbour-joining trees of all 57 genes showing greater than 1% diversity between pairs. Genes used in attribution model are labelled in red.



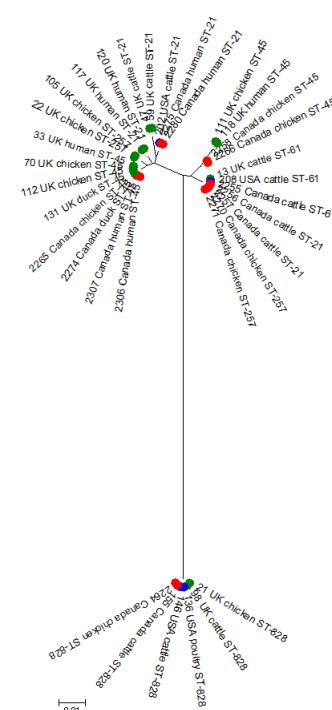




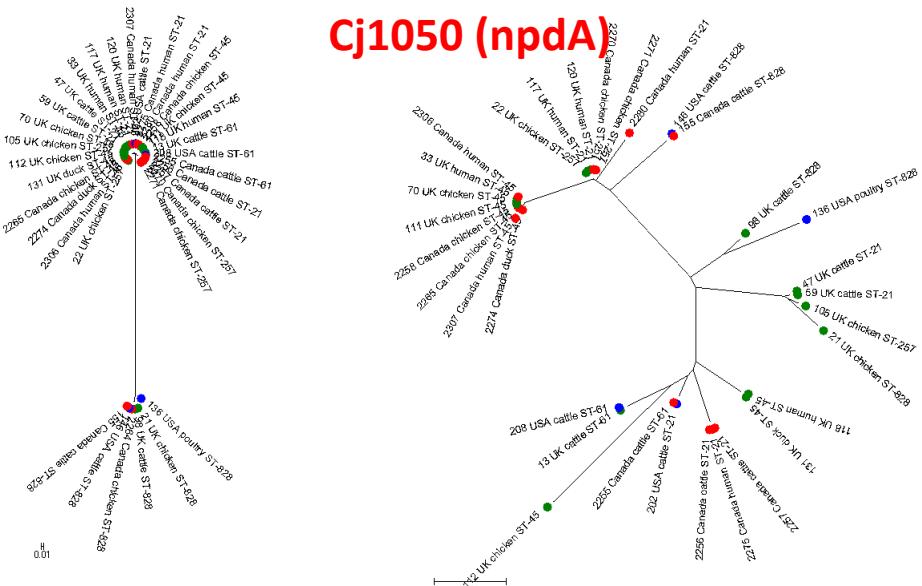




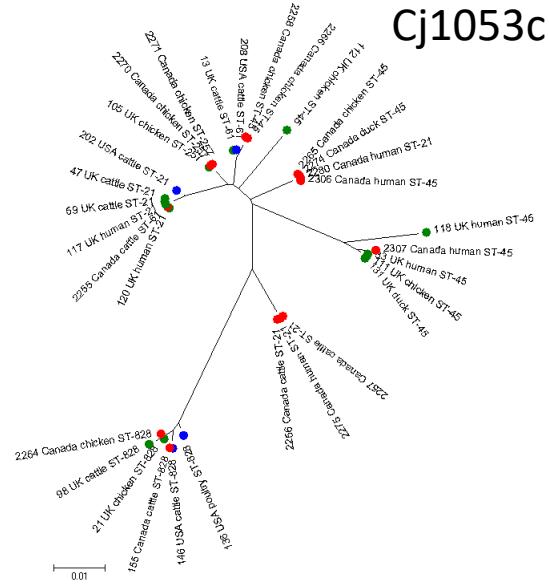
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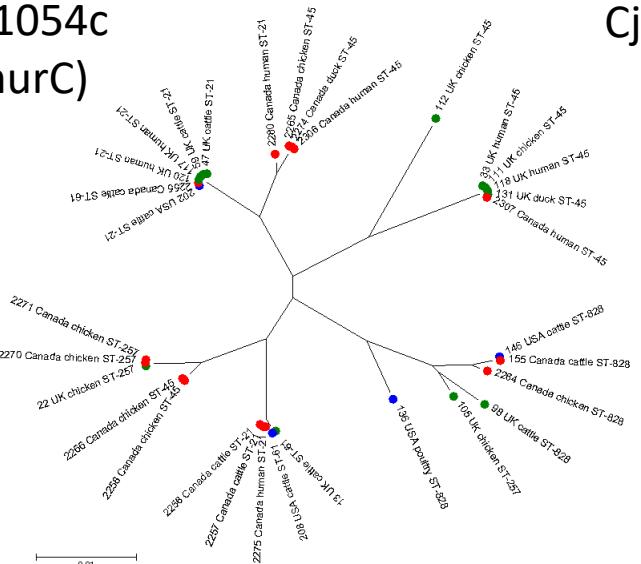
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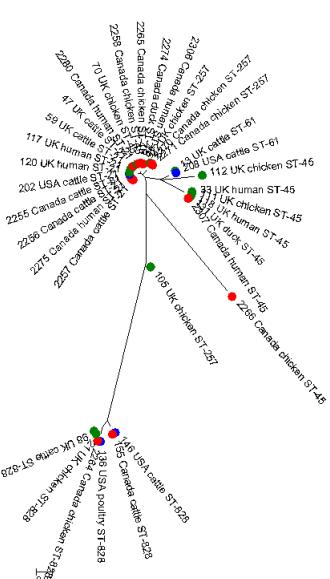
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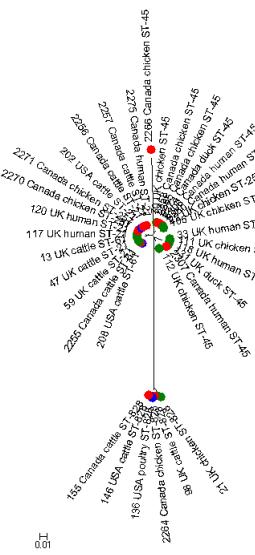
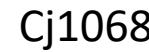
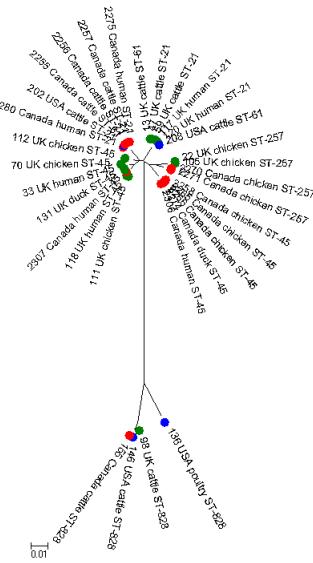
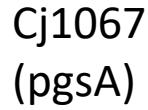
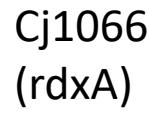
Cj1054c  
(murC)



Cj1056c

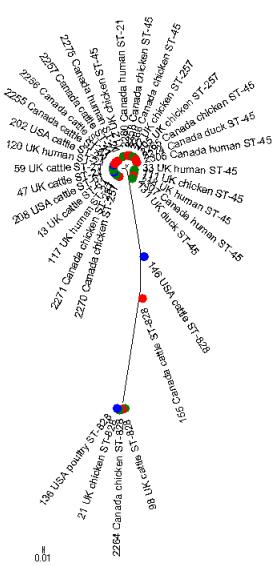


Cj1058c  
(guab)

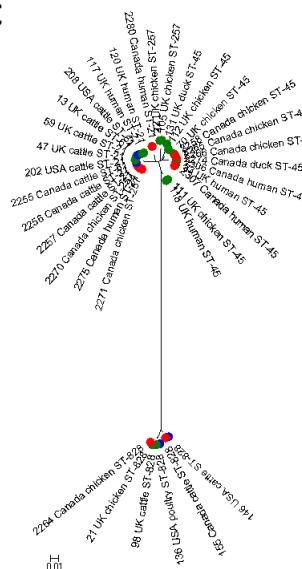


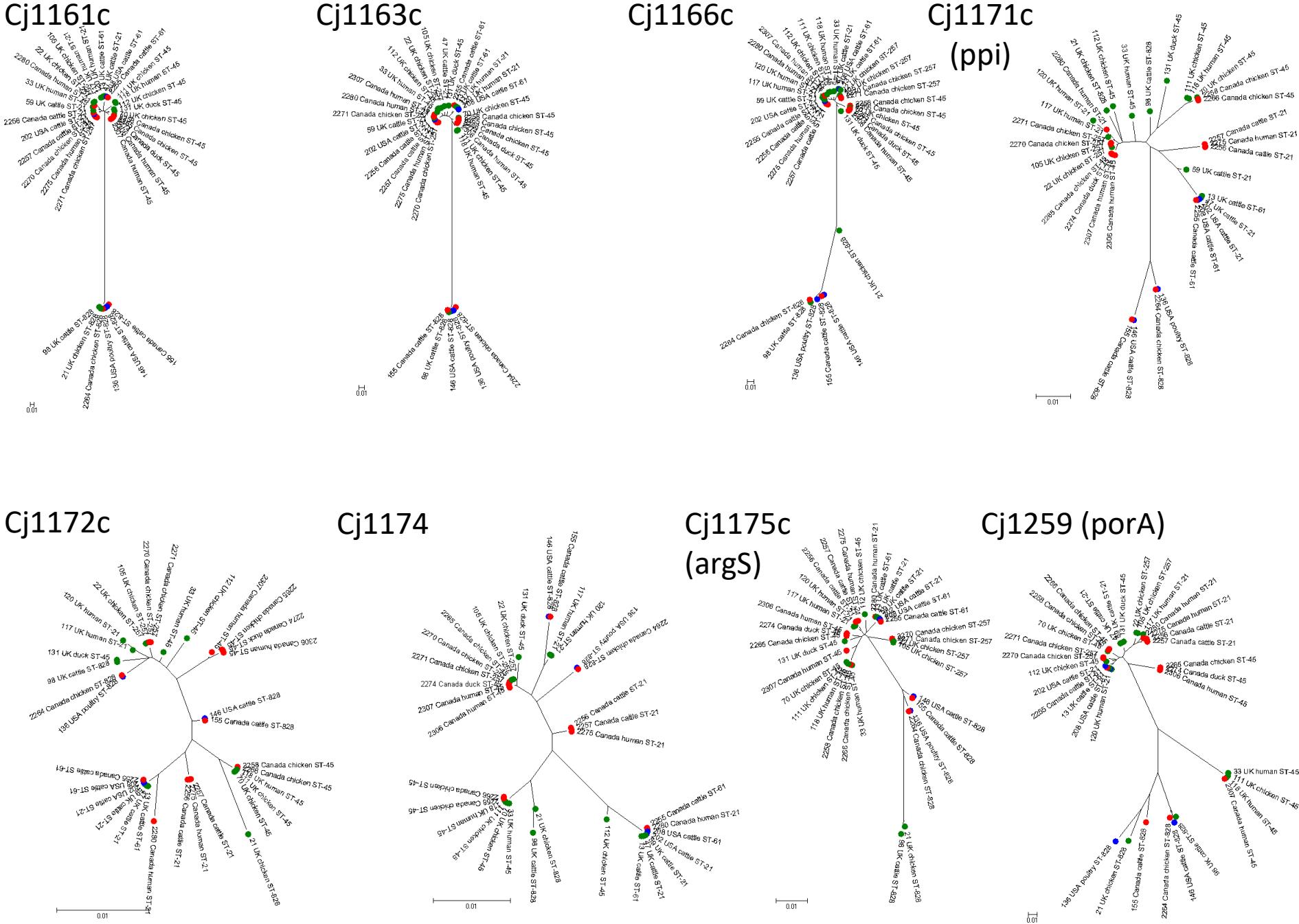
Cj1069

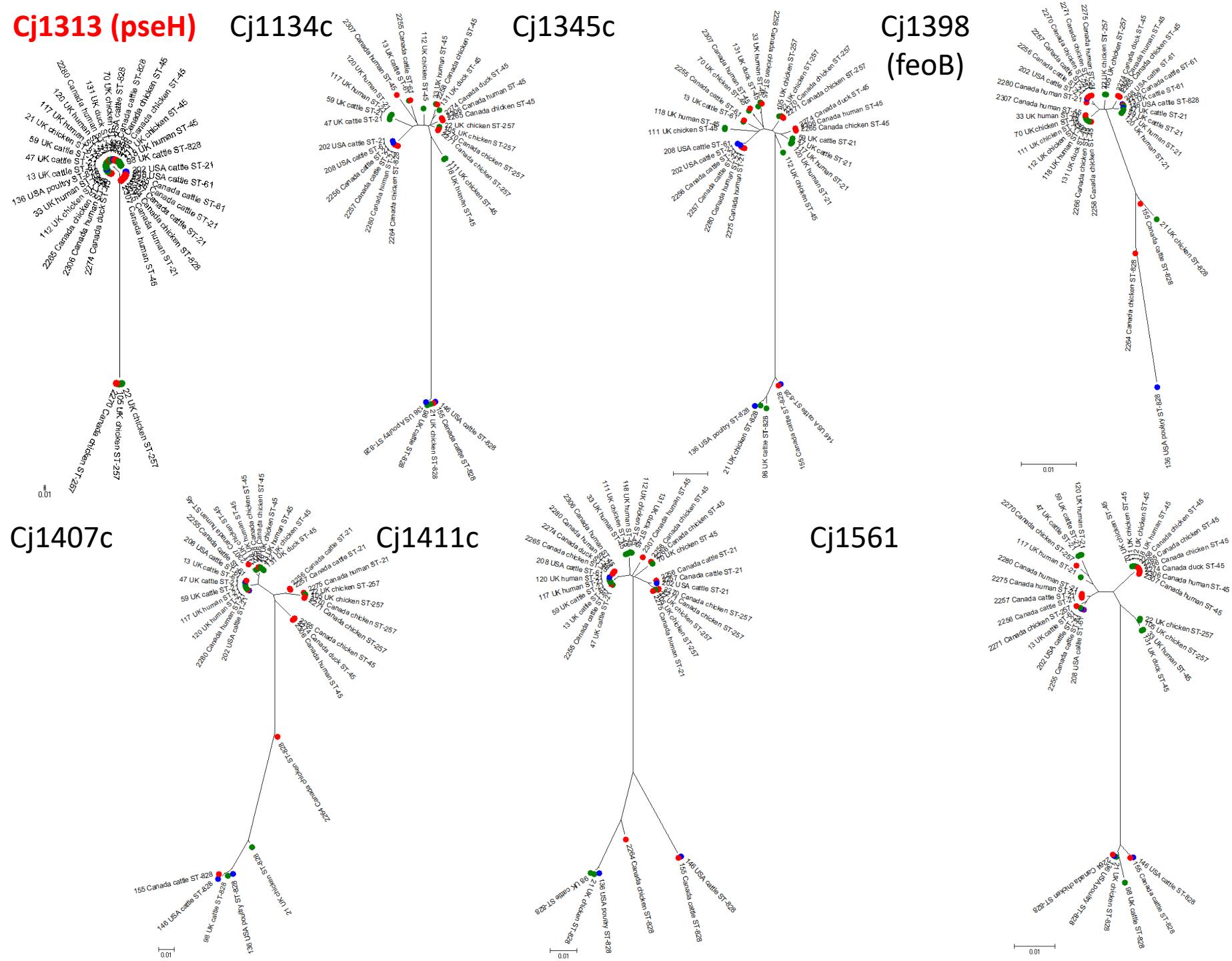
Cj1151c  
(hldD)



Cj1157c  
(dnaX)







**Figure S2:** Phylogeny of 7 highly recombining epidemiological markers used to attribute biogeography using structure.

## 7 hyper-recombinant genes with some geographical signal

