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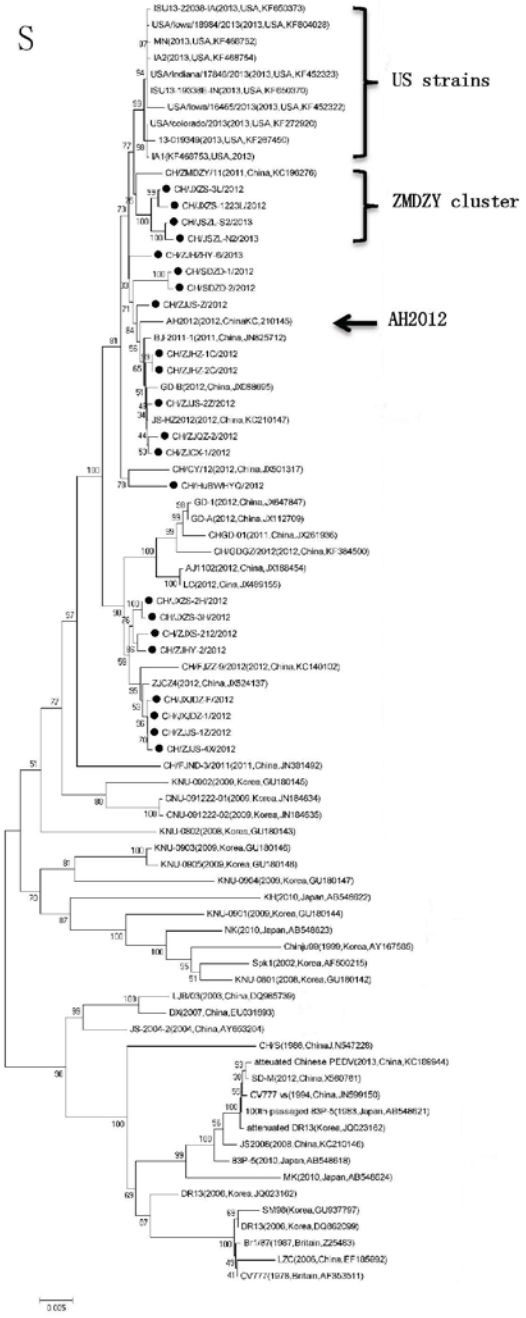
Evidence of Recombinant Strains of Porcine Epidemic Diarrhea Virus, United States, 2013

A

S



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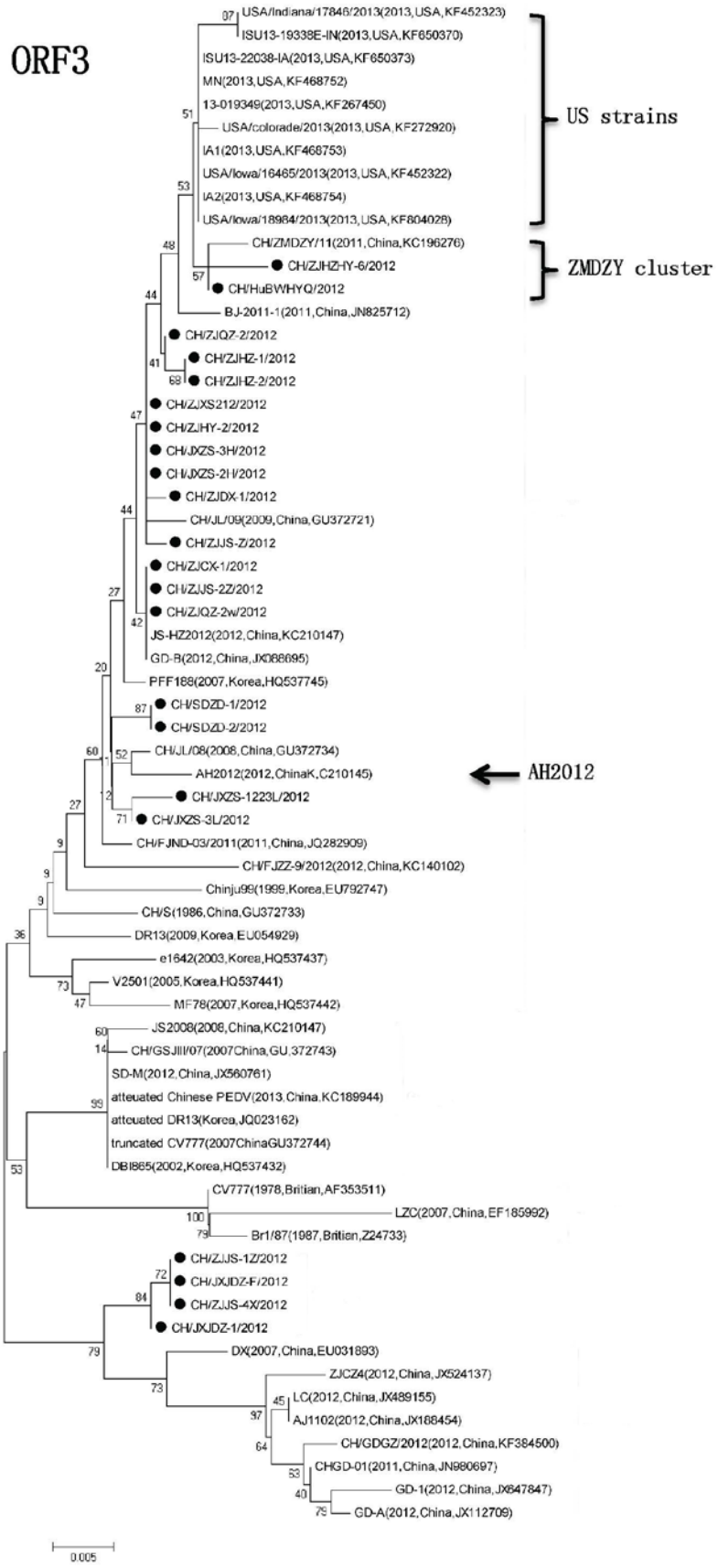
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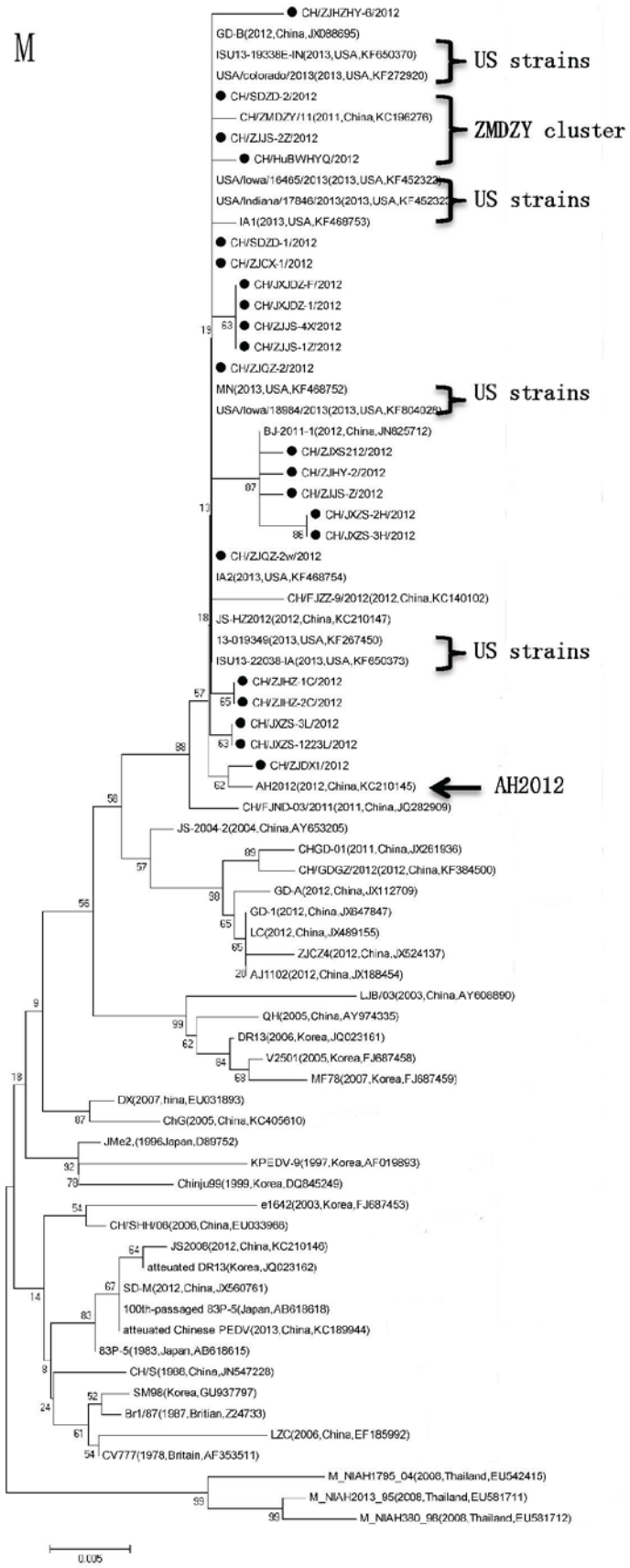
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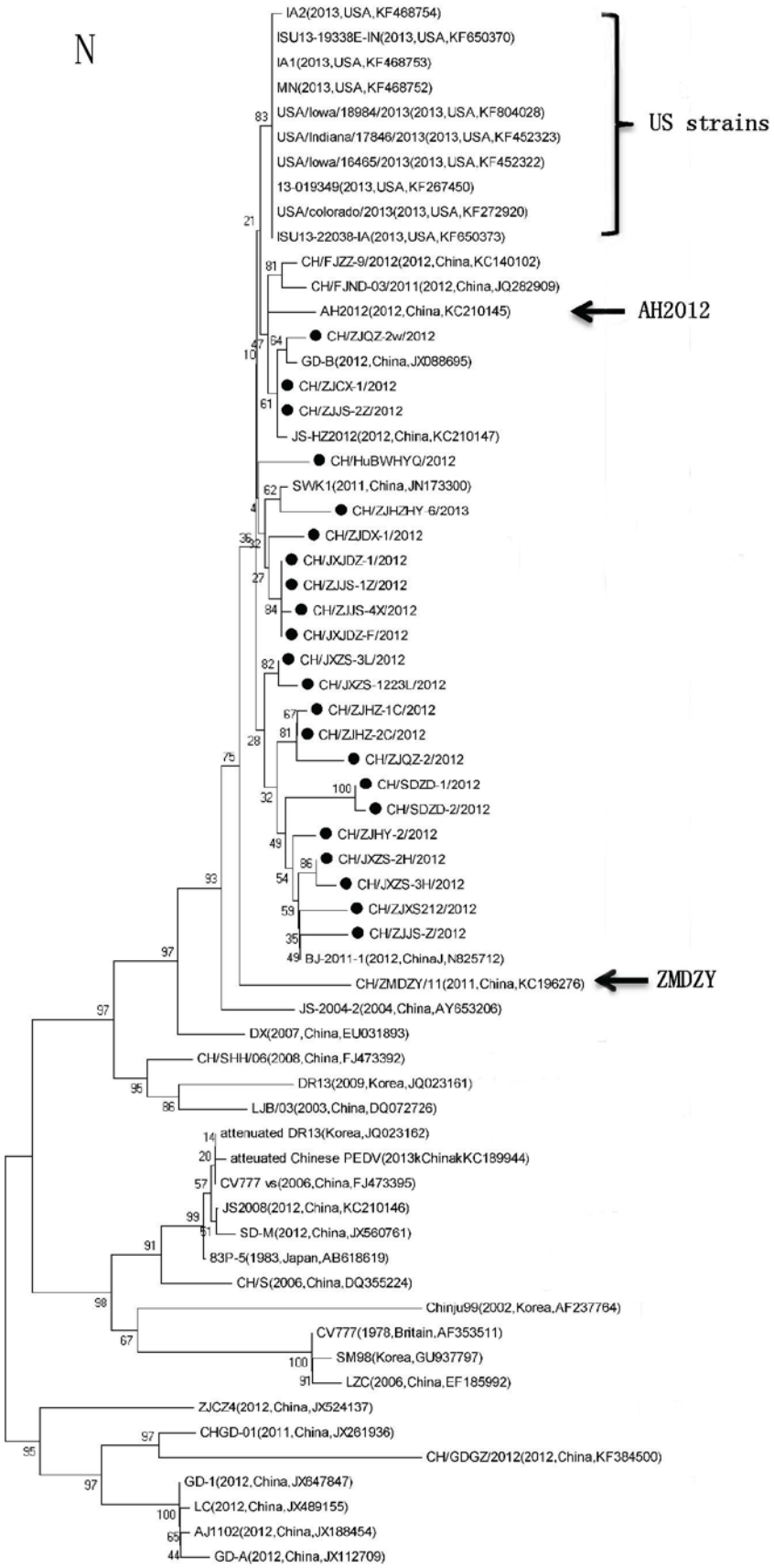
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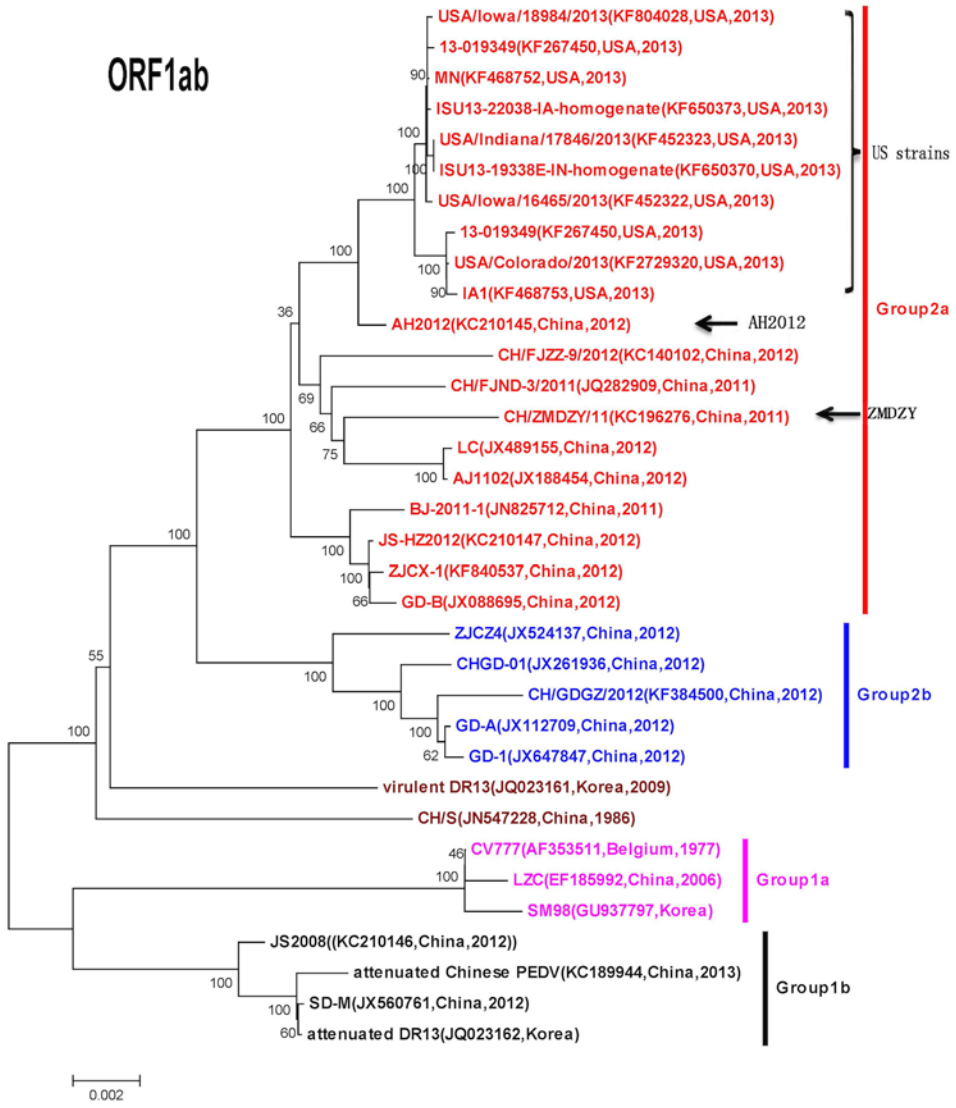
E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LC(JX489155,China,2012)
AJ1102(JX188454,China,2012)
BJ-2011-1(JN825712,China,2011)
JS-HZ2012(KC210147,China,2012)
ZJCX-1(KF840537,China,2012)
GD-B(JX088695,China,2012)
ZJCZ4(JX524137,China,2012)
CHGD-01(JX261936,China,2012)
CH/GDGZ/2012(KF384500,China,2012)
GD-A(JX112709,China,2012)
GD-1(JX647847,China,2012)
Group2b
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LZC(EF185992,China,2006)
SM98(GU937797,Korea)
Group1a
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Group1b
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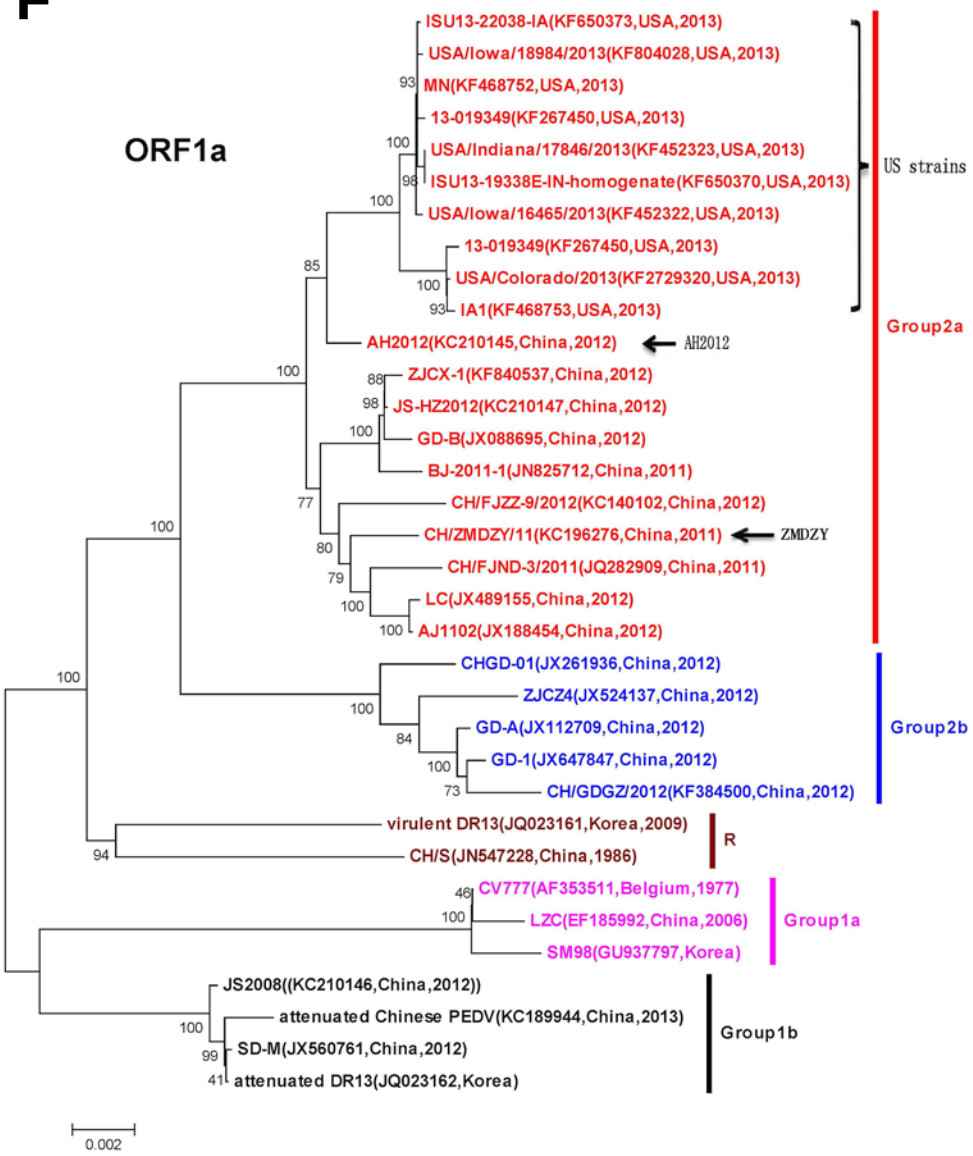
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USA/Colorado/2013(KF2729320,USA,2013)
IA1(KF468753,USA,2013)
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JS-HZ2012(KC210147,China,2012)
GD-B(JX088695,China,2012)
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LC(JX489155,China,2012)
AJ1102(JX188454,China,2012)
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ZJCZ4(JX524137,China,2012)
GD-A(JX112709,China,2012)
GD-1(JX647847,China,2012)
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R
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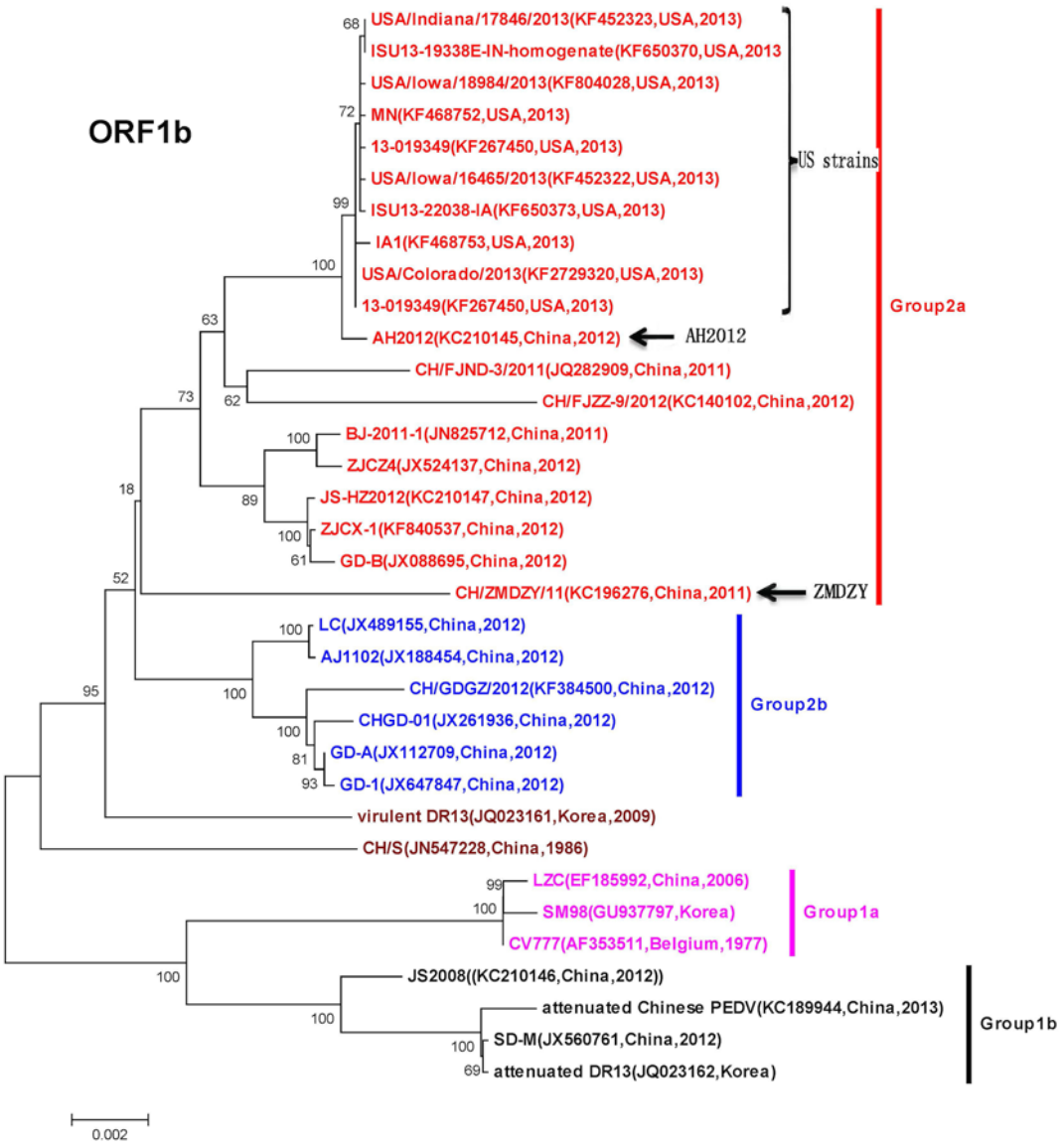
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CH/FJZZ-9/2012(KC140102,China,2012)
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ZJCZ4(JX524137,China,2012)
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GD-B(JX088695,China,2012)
CH/ZMDZY/11(KC196276,China,2011)
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Group2a
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AJ1102(JX188454,China,2012)
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GD-A(JX112709,China,2012)
GD-1(JX647847,China,2012)
Group2b
virulent DR13(JQ023161,Korea,2009)
CH/S(JN547228,China,1986)
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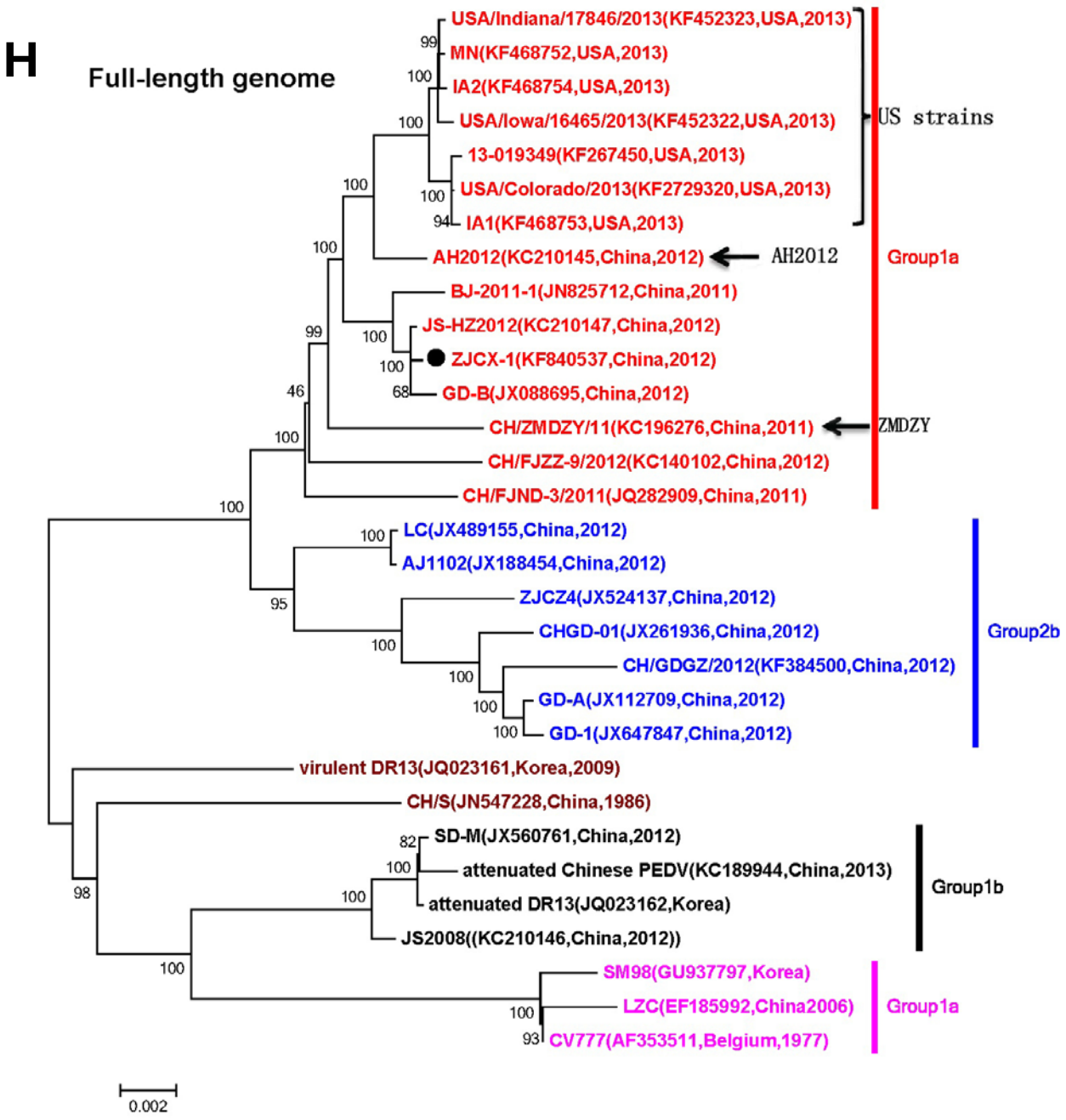
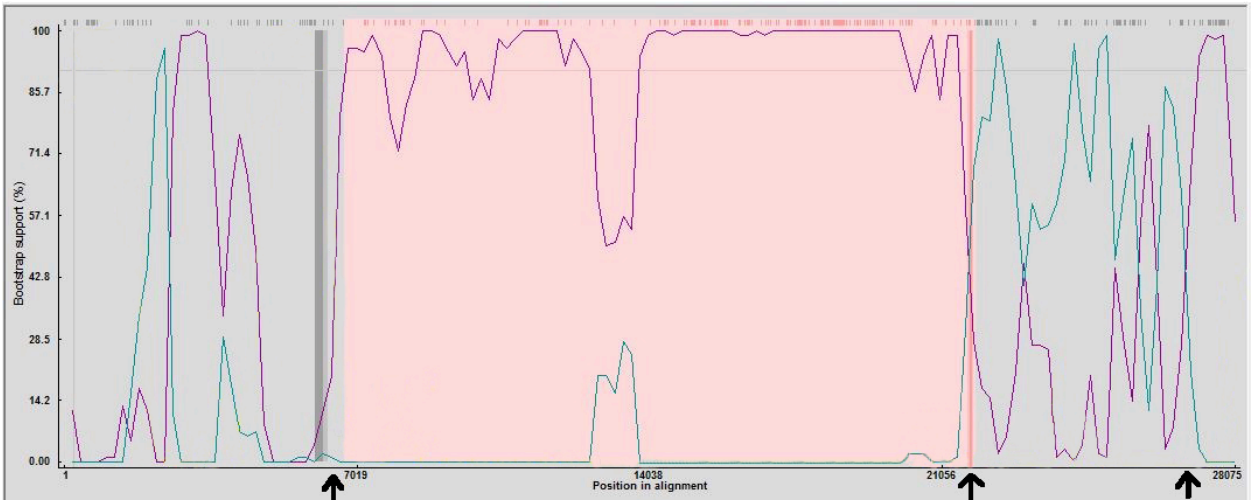


Technical Appendix Figure 1. Phylogenetic analyses of newly determined and available porcine epidemic diarrhea virus (PEDV) strains based upon nucleotide sequences of genes as follows: A) S; B) ORF3; C) M; D) N; E) ORF1ab; F) ORF1a; G) ORF1b genes; and H) the full-length genome. The trees were constructed by the neighbor-joining method. Bootstrap values are indicated for each node from 1,000 resamplings. The names of the strains, years and places of isolation, and GenBank accession numbers are shown. Black solid circles indicate the new PEDV strains sequenced in this study. Scale bars represent nucleotide substitutions per site.



Technical Appendix Figure 2. Detection of potential recombination events in the PEDV strains identified in the United States by bootstrap analysis. Three major recombination breakpoints, denoted by arrows, were located, respectively, at the ORF1a (nt 6,699), S (nt 21,840) and N (nt 26,882) genes (based on the MN strain) (*6*). The analysis was performed with an F84 distance model, a window size of 1,000 base pairs and a step size of 200 base pairs. Regions derived from the AH2012 or the ZMDZY sublineage is denoted by purple or cyan lines, respectively.