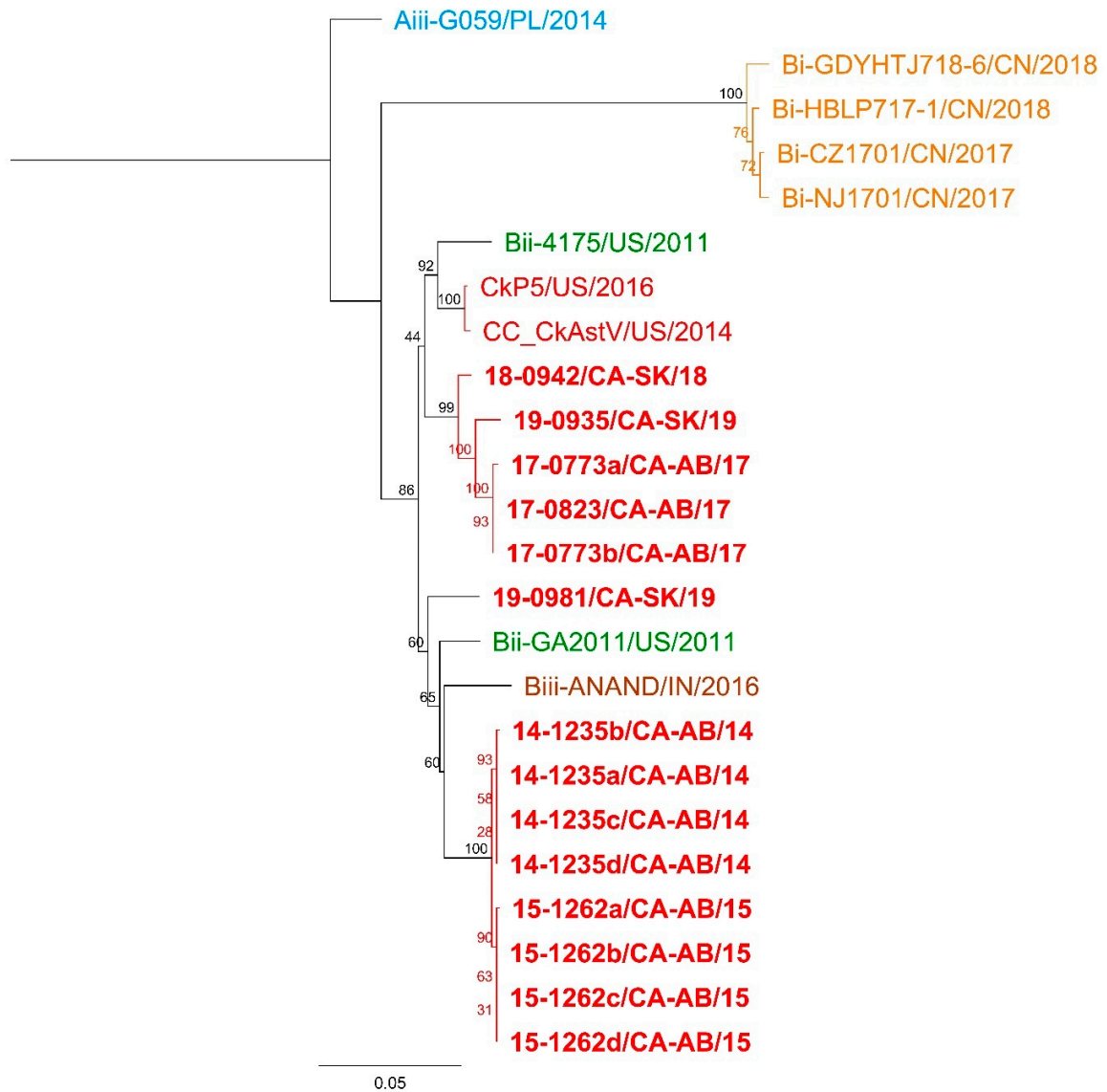
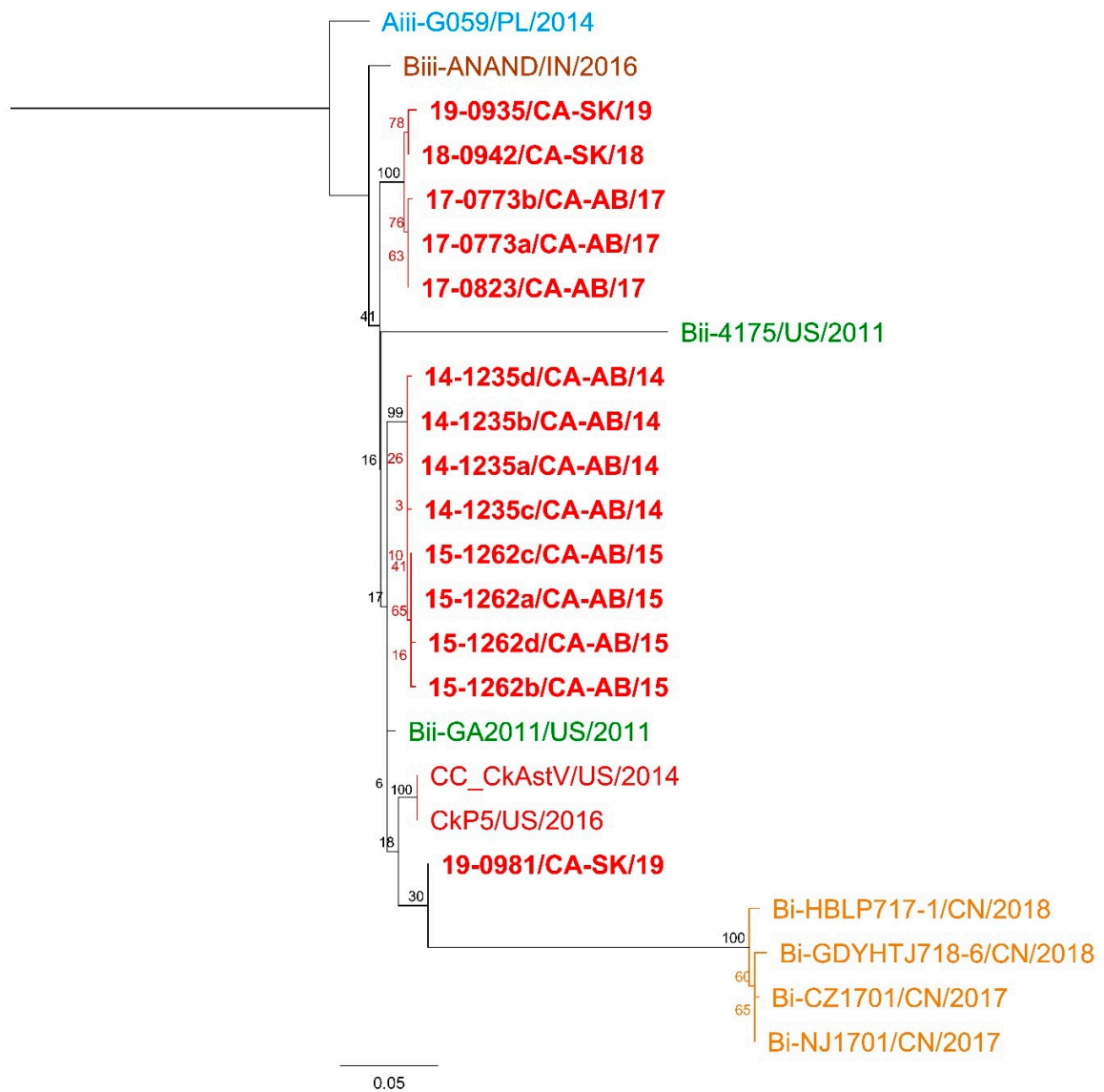


Supplement Table 1. Genome sizes of complete CAsV sequences

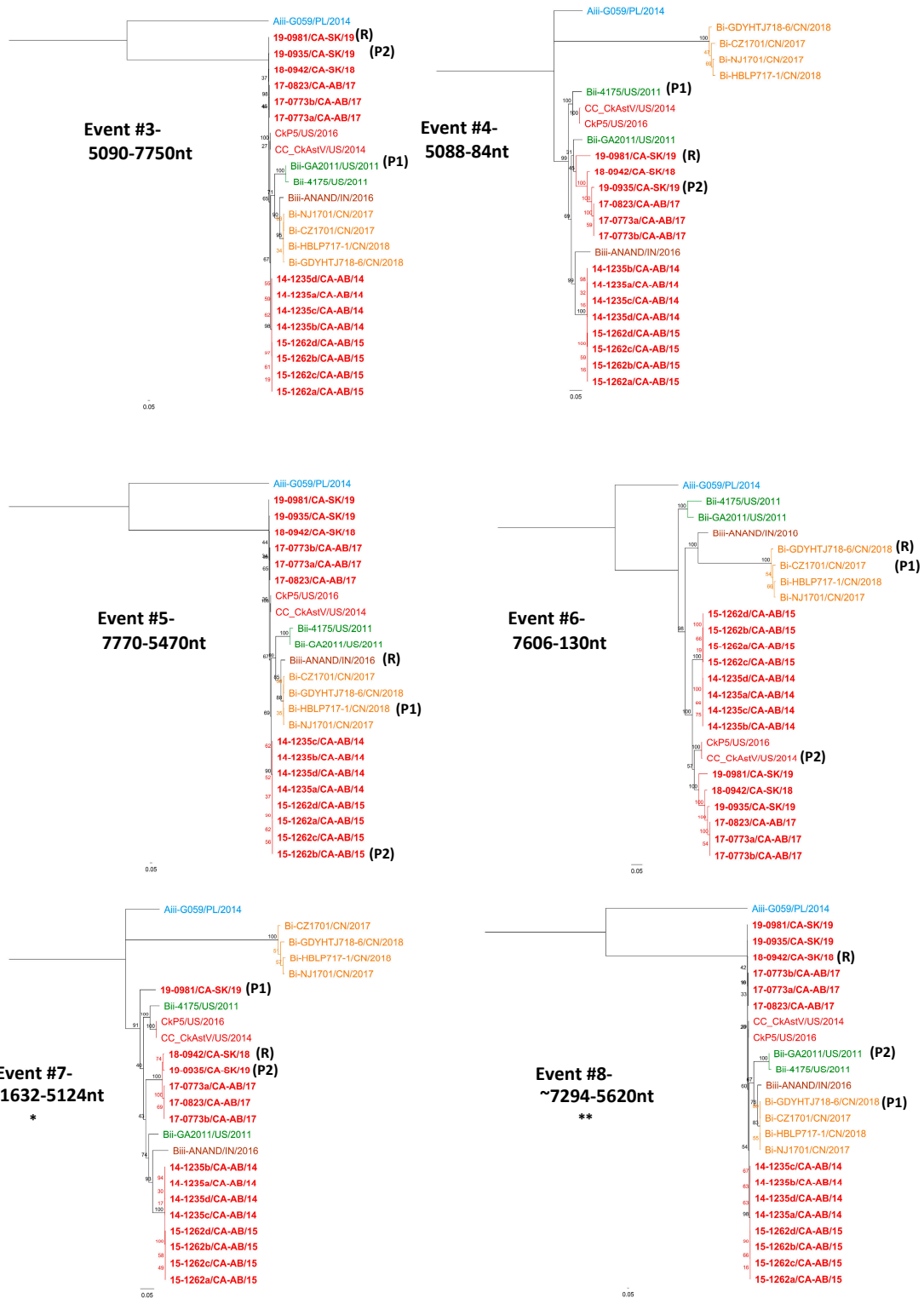
ID	ORF1a	ORF1b	ORF2	Genome size
14-1235a-AB	3,423	1,560	2,217	7,501
14-1235b-AB	3,423	1,560	2,217	7,501
14-1235c-AB	3,423	1,560	2,217	7,459
14-1235d-AB	3,423	1,560	2,217	7,459
15-1262a-AB	3,423	1,560	2,217	7,506
15-1262b-AB	3,423	1,560	2,217	7,495
15-1262c-AB	3,423	1,560	2,217	7,504
15-1262d-AB	3,423	1,560	2,217	7,507
17-0773a-AB	3,420	1,560	2,217	7,452
17-0773b-AB	3,420	1,560	2,217	7,490
17-0823-AB	3,420	1,560	2,217	7,502
18-0942-SK	3,420	1,560	2,217	7,490
19-0935-SK	3,420	1,560	2,217	7,481
19-0981-SK	3,420	1,560	2,217	7,452

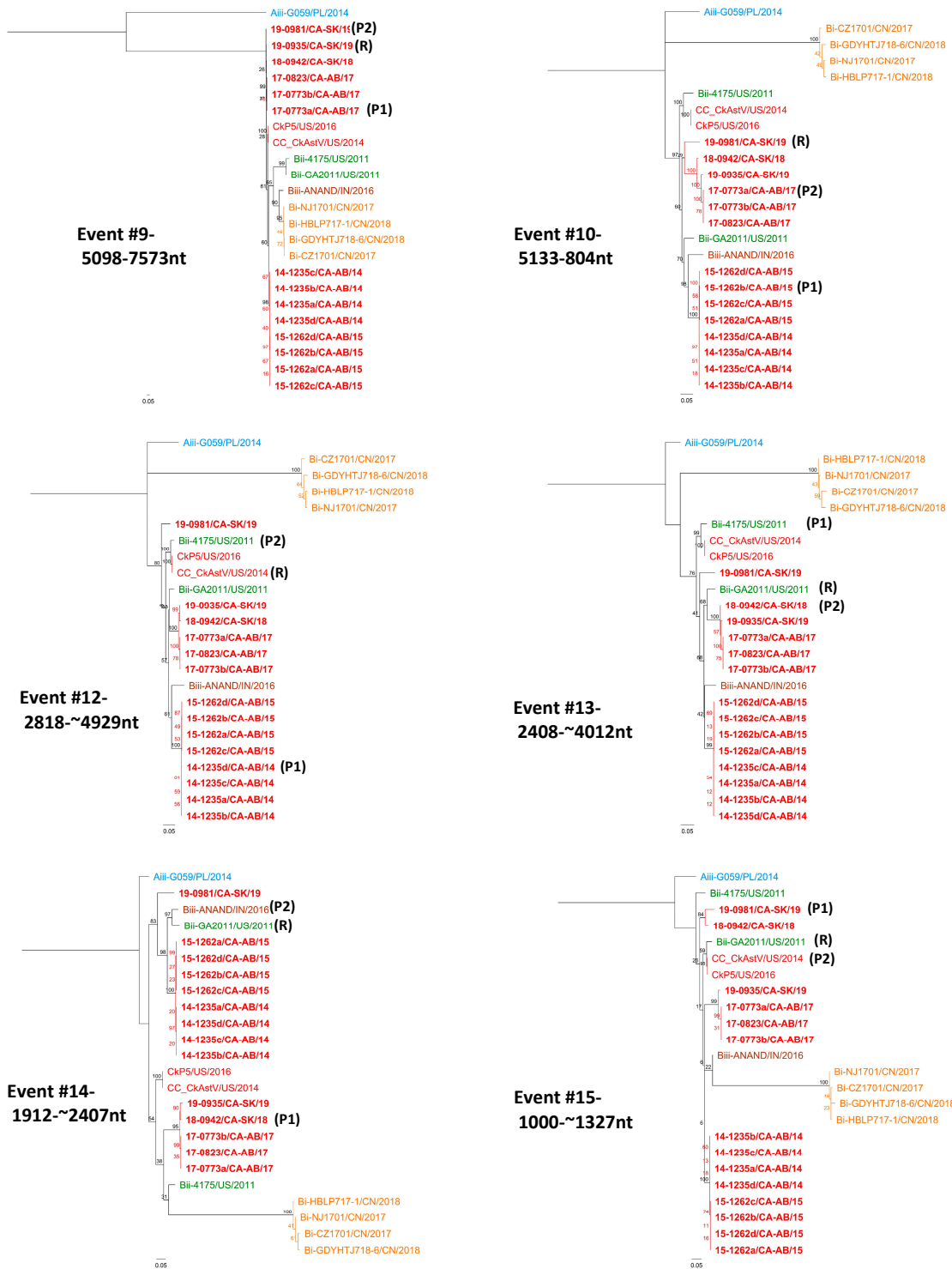


Supplement Fig 1. Amino acid ML phylogenetic tree of ORF1a CAsV sequences. Different colors indicate different genotypes (i.e. Aiii, Bi, Bii, Biii, and Biv in red) according to ORF2 analysis described in Smyth2017 [1]. The included sequences are described in Table 2. Canadian sequences are in bold.



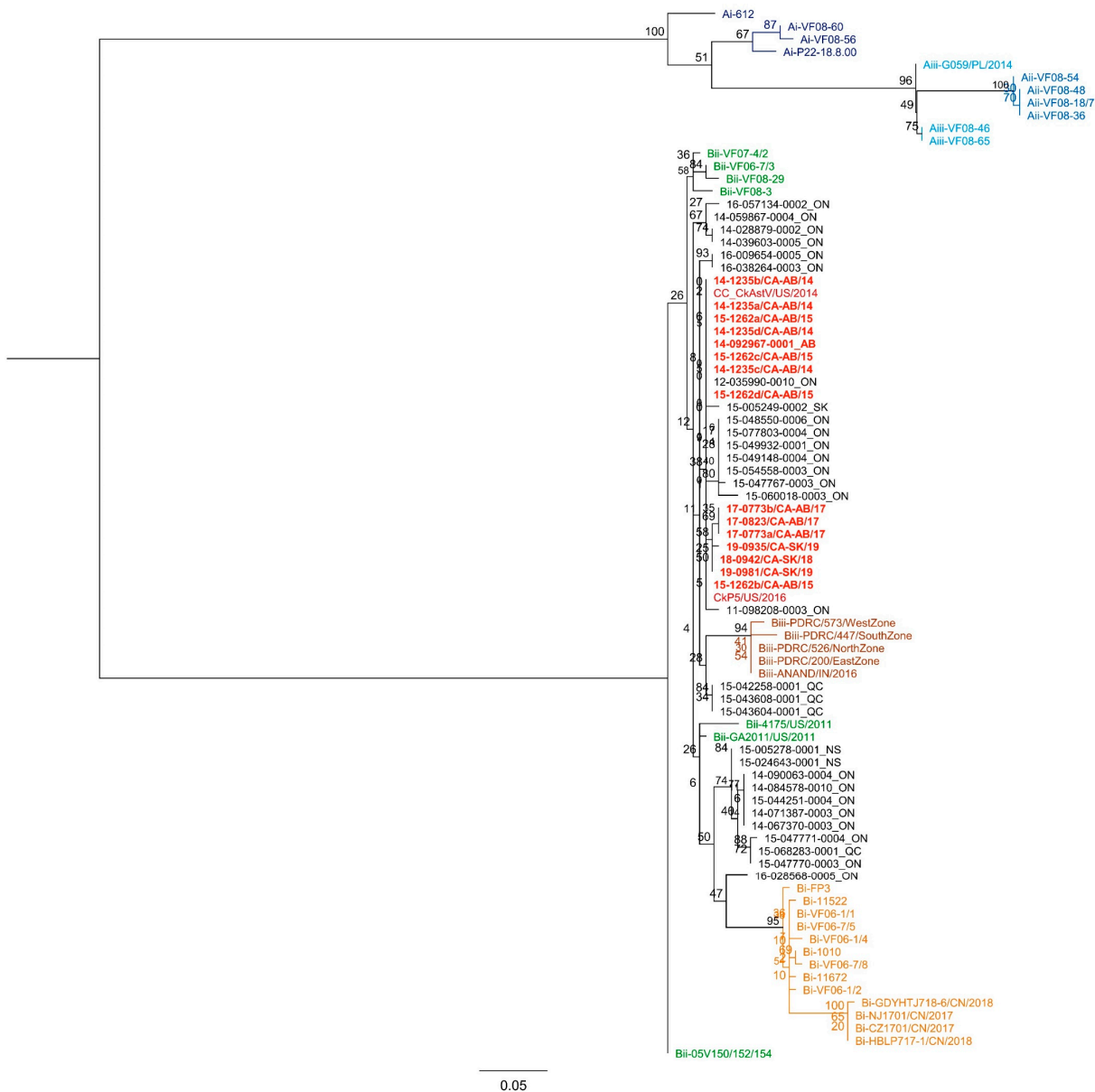
Supplement Fig 2. Amino acid ML phylogenetic tree of ORF1b CAsV sequences. Different colors indicate different genotypes (i.e. Aiii, Bi, Bii, Biii, and Biv in red) according to ORF2 analysis described in Smyth2017 [1]. The included sequences are described in Table 2 . Canadian sequences are in bold.





Supplement Fig 3. Nucleotide ML phylogenetic analyses of CAstV on each of the recombination events described on Table 2. Recombination events with genome positions as follows: Event#3-5090-7750nt; Event#4-5088-84nt; Event#5-7770-5470nt; Event#6-7606-130nt; Event#7-1632-5124nt; Event#8~7294-5620nt; Event#9-5098-7573nt; Event #10-5133-804nt; Event#12-2818~4929nt; Event#13-2408~4012nt; Event#14-1912~2407nt; and Event#15-1000~1327nt. Different colors indicate different genotypes according to ORF2 analysis described in Smyth et al 2017 (i.e. Aiii, Bi, Bii, Biii, and Biv in red) [1]. The trees were built using

RAxML v 8.2.11 plugin of Geneious v.10.2.6. on an alignment obtained by Clustal Omega v 1.2.2. (R) Recombinant; (P1) Major Parent; (P2) Minor Parent. * Beginning breakpoint outside of confidence interval.
 ** Recombination signal may be attributable to a process other than recombination; ~ Unknown breaking point, approximate location noted.



Supplement Fig 4. Amino acid ML phylogenetic tree of a total of 83 partial ORF2 CAsV sequences (aa positions 1--214aa). Different colors indicate different genotypes (i.e. Ai, Aii, Aiii, Bi, Bii, Biii, and Biv in red), sequences in color black were initially classified as Bii, but classification is unclear. The included sequences are described in Table 2 and at Long et al 2018 [2]. Sequences obtained in this study are in bold.

[illegible]

Supplement Fig 5. Percentage of amino acid identity obtained from ML phylogenetic tree described on Supplement Fig 4.

References

1. Smyth, V. J., A Review of the Strain Diversity and Pathogenesis of Chicken Astrovirus. *Viruses* **2017**, 9, (2).
2. Long, K. E.; Ouckama, R. M.; Weisz, A.; Brash, M. L.; Ojkic, D., White Chick Syndrome Associated with Chicken Astrovirus in Ontario, Canada. *Avian diseases* **2018**, 62, (2), 247-258.