**Supplementary File S2. Appendices**

***Cyclospora cayetanensis* comprises at least three species that cause human cyclosporiasis**

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# Appendix A. Fasta sequences of segments A to F of 360i2

>Nu\_360i2\_PART\_A\_Hap\_1

TTCTTTTCGCACTCTGGCTGCCGCTGCTGGTTCTGCTCAAGCAAAGAGAATGGCACGCGGTCATTTTGGTGTATTTTTCATAATCCGTAGCCTGTGGGGA

>Nu\_360i2\_PART\_A\_Hap\_3

TTCTTTTCGCACTGTGGCTGCCGCTGCTGGGTCCGCTCAAGCAAAGAGAATGGCACGCAGTCATTTTGGTGTATTTTTCATAATCCGTAGCTTGTGGGGA

>Nu\_360i2\_PART\_B\_Hap\_1

GGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCT

>Nu\_360i2\_PART\_C\_Hap\_1

GGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATTAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAG

>Nu\_360i2\_PART\_C\_Hap\_2

GGGCTTCTTGCTGACGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATTAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAG

>Nu\_360i2\_PART\_C\_Hap\_3

GGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACGGATTGCATCTTCTCAGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAG

>Nu\_360i2\_PART\_C\_Hap\_4

GGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAG

>Nu\_360i2\_PART\_D\_Hap\_1

TAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTTCGAGTCTGGCT

>Nu\_360i2\_PART\_D\_Hap\_2

TAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGAGCCTCAATTTTTCTGAGTCTGGCT

>Nu\_360i2\_PART\_D\_Hap\_3

TAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTCTGAGTCTGGCT

>Nu\_360i2\_PART\_E\_Hap\_1

TGATTCCTGCATGCAAAACGCCTAATCCTAGGAACACACCTTTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCCCTGCTTCTCCCGCAACAG

>Nu\_360i2\_PART\_E\_Hap\_2

TGATTTCTGCATGCAAAACGCCTAATCCCAGGAACACGCCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAG

>Nu\_360i2\_PART\_E\_Hap\_3

TGATTCCTGCATGCAAAACGCCTTATCCCAGGAACACGCCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAG

>Nu\_360i2\_PART\_E\_Hap\_6

TGATTCCTGCATGCAAAACGCCTTATCCCAGGAACACACCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAG

>Nu\_360i2\_PART\_E\_Hap\_5

TGATTTCTGCATGCAAAACGCCTAATCCCAGGAACACACCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAG

>Nu\_360i2\_PART\_F\_Hap\_1

CTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTAGAGCGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGGCGCCAATGCAGCCGTTTTAACAGACCTATGAAATT

>Nu\_360i2\_PART\_F\_Hap\_3

CTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTACAACGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGACACCAATGCAGCCGTTTCAACAGACCTATAAAATT

# Appendix B. Fasta sequences of 360i2 haplotypes

>360i2\_Hap\_A1

TTCTTTTCGCACTCTGGCTGCCGCTGCTGGTTCTGCTCAAGCAAAGAGAATGGCACGCGGTCATTTTGGTGTATTTTTCATAATCCGTAGCCTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATTAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTTCGAGTCTGGCTTGATTCCTGCATGCAAAACGCCTAATCCTAGGAACACACCTTTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCCCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTAGAGCGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGGCGCCAATGCAGCCGTTTTAACAGACCTATGAAATT

>360i2\_Hap\_A2

TTCTTTTCGCACTCTGGCTGCCGCTGCTGGTTCTGCTCAAGCAAAGAGAATGGCACGCGGTCATTTTGGTGTATTTTTCATAATCCGTAGCCTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGACGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATTAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTTCGAGTCTGGCTTGATTCCTGCATGCAAAACGCCTAATCCTAGGAACACACCTTTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCCCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTAGAGCGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGGCGCCAATGCAGCCGTTTTAACAGACCTATGAAATT

>360i2\_Hap\_B1

TTCTTTTCGCACTGTGGCTGCCGCTGCTGGGTCCGCTCAAGCAAAGAGAATGGCACGCAGTCATTTTGGTGTATTTTTCATAATCCGTAGCTTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACGGATTGCATCTTCTCAGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGAGCCTCAATTTTTCTGAGTCTGGCTTGATTTCTGCATGCAAAACGCCTAATCCCAGGAACACGCCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTACAACGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGACACCAATGCAGCCGTTTCAACAGACCTATAAAATT

>360i2\_Hap\_B2

TTCTTTTCGCACTGTGGCTGCCGCTGCTGGGTCCGCTCAAGCAAAGAGAATGGCACGCAGTCATTTTGGTGTATTTTTCATAATCCGTAGCTTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTCTGAGTCTGGCTTGATTCCTGCATGCAAAACGCCTTATCCCAGGAACACGCCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTACAACGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGACACCAATGCAGCCGTTTCAACAGACCTATAAAATT

>360i2\_Hap\_B3

TTCTTTTCGCACTGTGGCTGCCGCTGCTGGGTCCGCTCAAGCAAAGAGAATGGCACGCAGTCATTTTGGTGTATTTTTCATAATCCGTAGCTTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACAGATTGCATCTTCTCGGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGGGCCTCAATTTTTCTGAGTCTGGCTTGATTCCTGCATGCAAAACGCCTTATCCCAGGAACACACCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTACAACGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGACACCAATGCAGCCGTTTCAACAGACCTATAAAATT

>360i2\_Hap\_B4\_CHN\_HEN01

TTCTTTTCGCACTGTGGCTGCCGCTGCTGGGTCCGCTCAAGCAAAGAGAATGGCACGCAGTCATTTTGGTGTATTTTTCATAATCCGTAGCTTGTGGGGAGGGAATGTCACCTAATGTTGCGTCACTAGCATCGGATGGCAGGAAGGGATTAGGCTCAGATTCGGGCAGCATAAGCTGCAGGAGTTGTAAGGCGGCGGCTGGGCTTCTTGCTGATGTATCGTCGTCTTCTGCCCCATCCACGGATTGCATCTTCTCAGATAAGTAAGTTAGGAGAGCAACGATCCGAGCACATTTAGGAGTAGCTTTCTGGTAGTGCGTCGCAAGAATTTTGCACCATCCTTGCGGGTGCGTAAAAGCAAAGGGTATGCCAAGAGAGCCTCAATTTTTCTGAGTCTGGCTTGATTTCTGCATGCAAAACGCCTAATCCCAGGAACACACCTGTTCTCATCAAAACTCAACGGTTGCGTGACATCAGATAGCGCTGCTTCTCCCGCAACAGCTGCAGCGCACGAACAAAGTGCTGTACGCTCTCTTACAACGTTCCGATTAAAGATTTAGGGGCAGGCCATGAAGACACCAATGCAGCCGTTTCAACAGACCTATAAAATT

# Appendix C. Fasta sequences of CDS3 haplotypes

>Nu\_CDS3\_PART\_A\_Hap\_1

GTTGCTTTATCTTTGGCAGTTAGACAGGGAGGGATTCCTACATTTGCAGGTGATGCTGCTACCTCCATGCGCAGCTGCAACACCAGCAA

>Nu\_CDS3\_PART\_A\_Hap\_2

GTTGCTTTATCTTTGGCAGTTAGACAGGGAGGGATTCCTACATTTGCAGGTGATGCTGCTACCTCCGTGCGCAGCTGCAACACCAGCAA

# Appendix D. Genomic regions included in the phylogeny used to generate Figure 5

The precise genomic regions (totaling approximately 1.02 million bases) that were concatenated to produce the phylogeny in Figure 5 are listed here (in order of concatenation, and relative to reference strain CHN\_HEN01, genome GCA\_002893305.1).The genomic coordinates (base pairs) shown in brackets beside each contig number from this genome assembly: PDMJ01000002 (448937:459881), PDMJ01000015 (17542:43229), PDMJ01000015 (140982:175641), PDMJ01000015 (294195:323596), PDMJ01000015 (443184:471814), PDMJ01000005 (257490:346631), PDMJ01000008 (362136:439698), PDMJ01000034 (291283:314071), PDMJ01000034 (278795:287044), PDMJ01000144 (19567:44501), PDMJ01000012 (301373:355044), PDMJ01000036 (15309:47919), PDMJ01000016 (35325:103955), PDMJ01000014 (457019:504389), PDMJ01000014 (185206:193901), PDMJ01000036 (236406:287628), PDMJ01000017 (403948:445461), PDMJ01000017 (66924:99332), PDMJ01000018 (164135:221409), PDMJ01000011 (184746:204377), PDMJ01000009 (478918:509439), PDMJ01000009 (412374:432574), PDMJ01000024 (278708:321758), PDMJ01000024 (57541:109267), PDMJ01000009 (192181:218193), PDMJ01000010 (333758:419709).