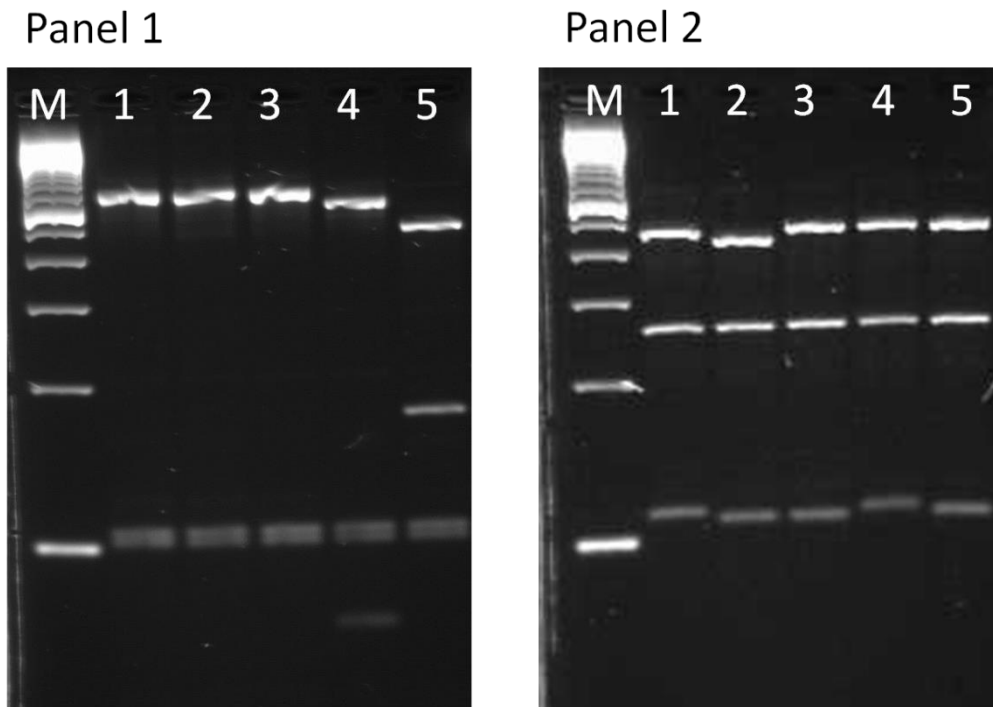**Supplementary data to "Unusual cryptosporidiosis cases in Swedish patients: extended molecular characterization of *Cryptosporidium viatorum* and *Cryptosporidium* chipmunk genotype I**
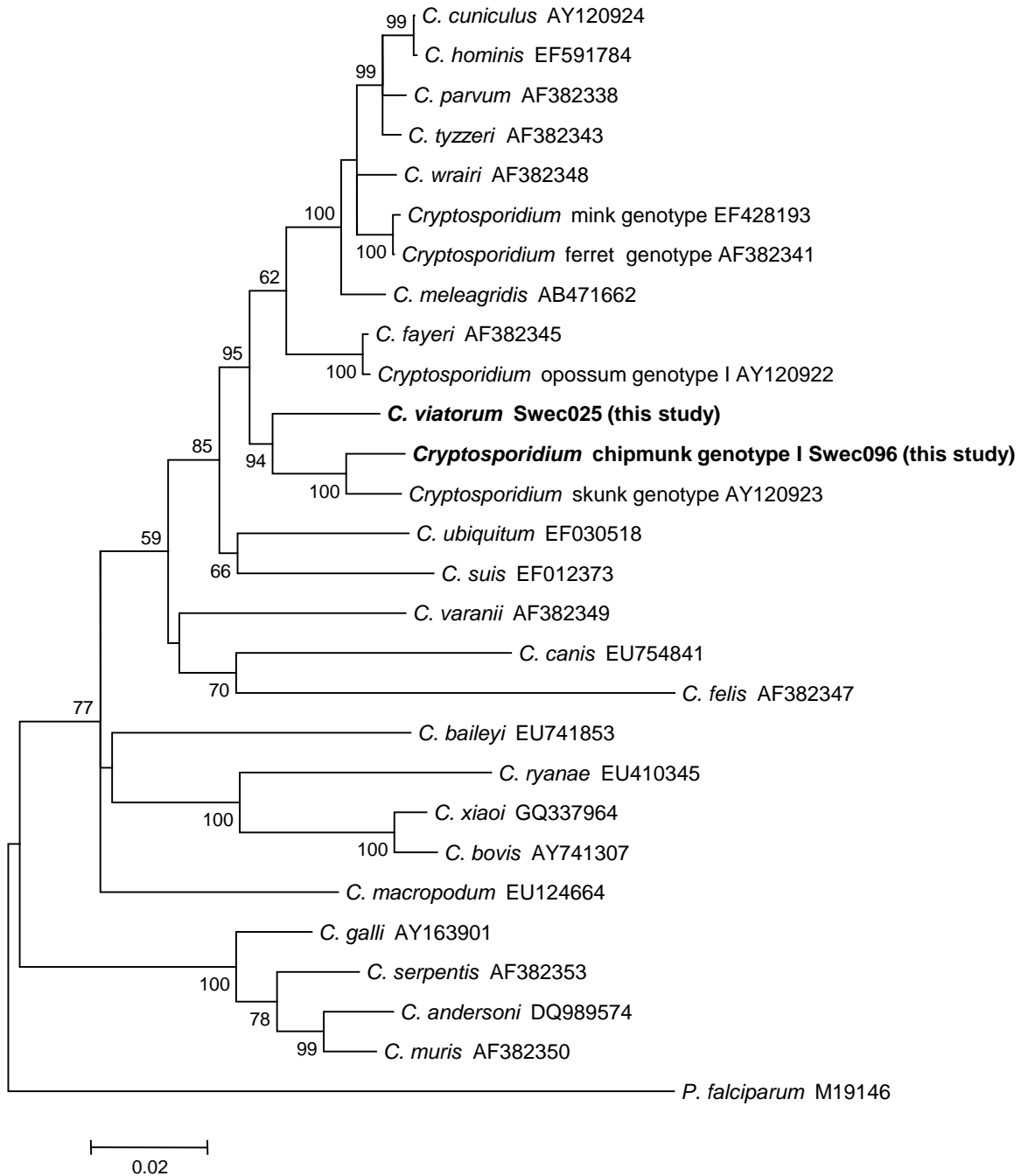

Supplementary Figure S1

Gelred (Biotum) stained 3.5% MetaPhor agarose gel (Cambrex) showing electrophoretic separation of nested SSU rRNA products (834–840 bp) after digestion with *Vsp*I (panel 1) and *Ssp*I (panel 2). Lane M, 100-bp ladder; lane 1, *C. viatorum*; lane 2, *Cryptosporidium* chipmunk genotype I; lane 3, *C. parvum;* lane 4, *C. hominis*; lane 5, *C. meleagridis.*
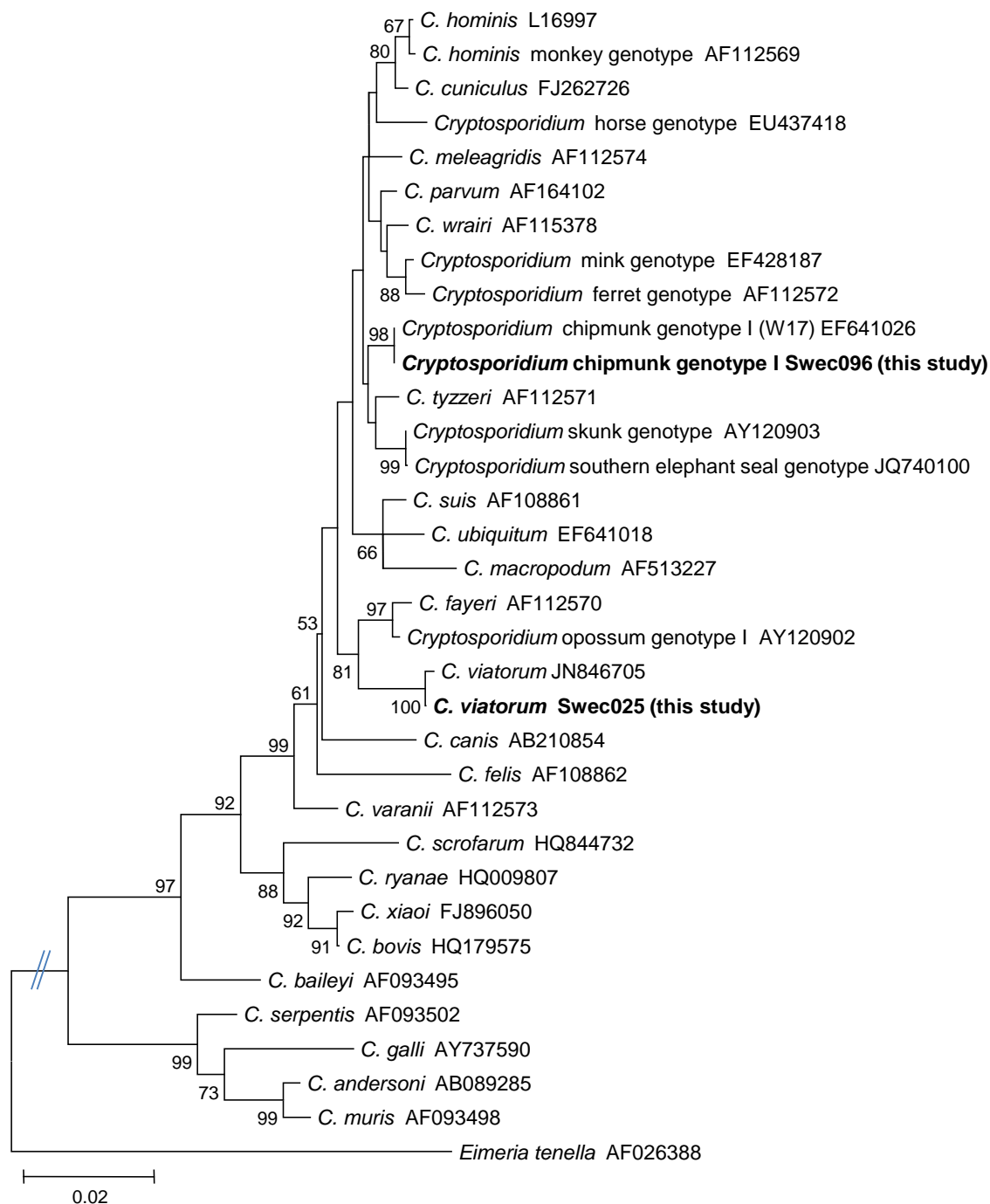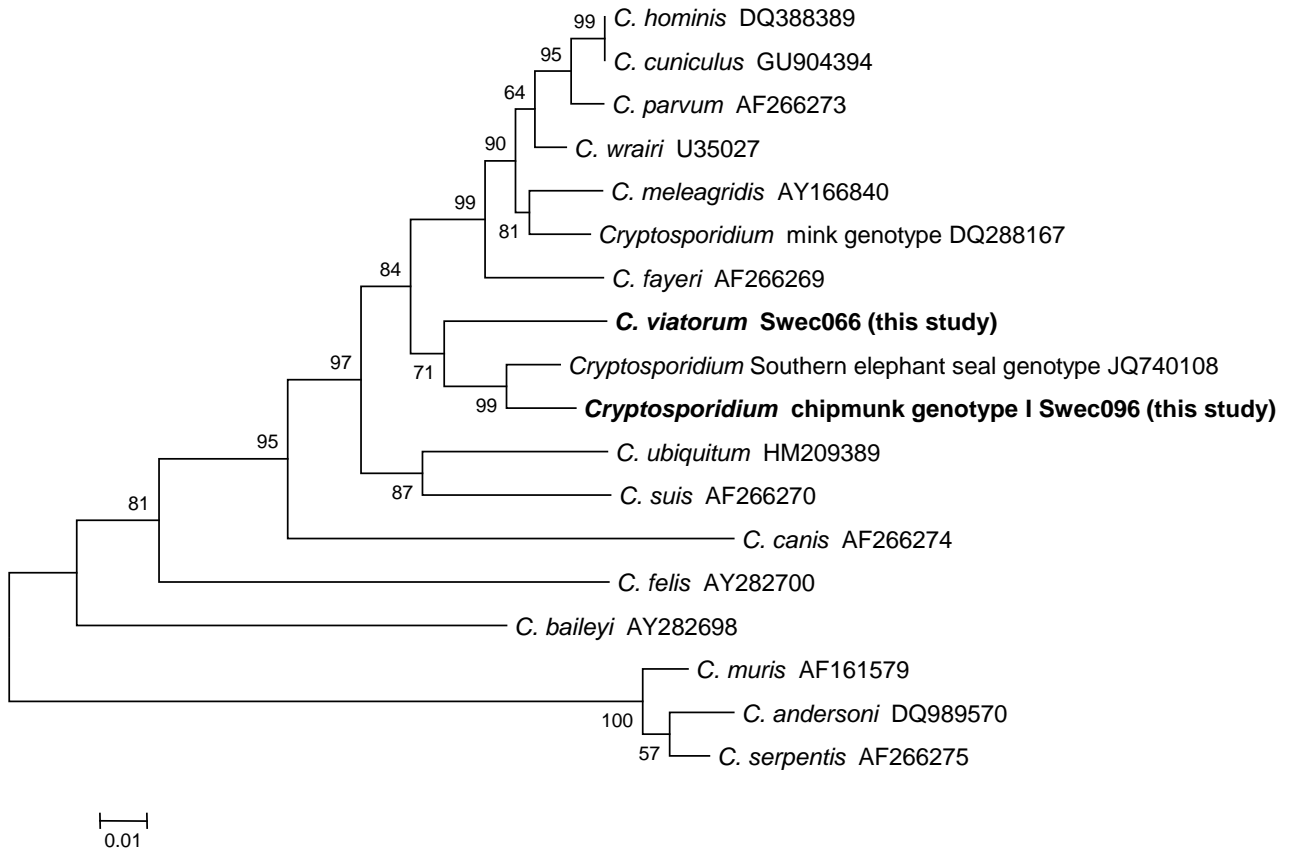
Supplementary Figure S2

Phylogenetic relationships between partial SSU rRNA *Cryptosporidium* sequences obtained in the present study and sequences retrieved from the GenBank database. Evolutionary distances were inferred by the neighbour-joining method. Bootstrap values ≥50% from1000 replicates are indicated at each node. There were ~800 base positions in the final SSU rRNA dataset. The sequence of *Eimeria tenella* was used as an outgroup. The scale bar indicates an evolutionary distance of 0.02 nucleotides per position in the sequence.
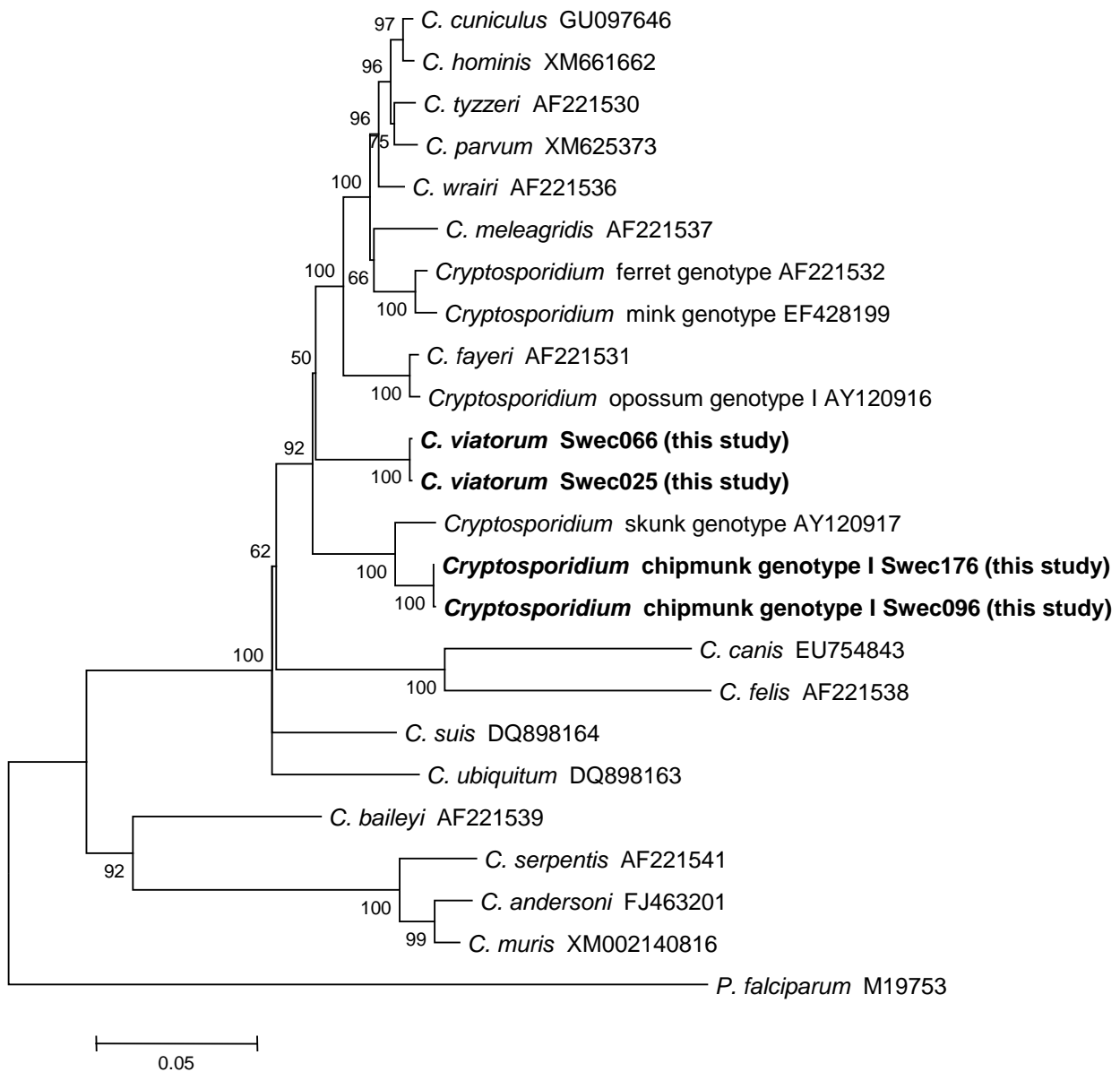
Supplementary Figure S3

Phylogenetic relationships between partial actin *Cryptosporidium* sequences from this study and sequences retrieved from the GenBank database. Evolutionary distances were inferred by the neighbour-joining method. Bootstrap values ≥50% from1000 replicates are indicated at each node. There were 920 base positions in the final actin dataset. The sequence of *Plasmodium falciparum* was used as an outgroup. The scale bar indicates an evolutionary distance of 0.02 nucleotides per position in the sequence.

Supplementary Figure S4

Phylogenetic relationships between partial COWP *Cryptosporidium* sequences from this study and sequences retrieved from the GenBank database. Evolutionary distances were inferred by the neighbour-joining method. Bootstrap values ≥50% from 1000 replicates are indicated at each node. There were 505 base positions in the final COWP dataset. The scale bar indicates an evolutionary distance of 0.01 nucleotides per position in the sequence.

Supplementary Figure S5

Phylogenetic relationships between partial HSP70 *Cryptosporidium* sequences from this study and sequences retrieved from the GenBank database. Evolutionary distances were inferred by the neighbour-joining method. Bootstrap values ≥50% from 1000 replicates are indicated at each node. There were 1795 base positions in the final HSP70 dataset. The sequence of *Plasmodium falciparum* was used as an outgroup. The scale bar indicates an evolutionary distance of 0.05 nucleotides per position in the sequence.