**Additional file 5: Figure S3.** **Evolutionary relationship of LTR-retrotransposons based on neighbor-joining analysis using genetic distances calculated with the maximum composite likelihood method.** The LTR-retrotransposon in *Eimeria tenella* is placed within the clade formed by chromoviruses which are widely present in eukaryotic genomes. The LTR-retrotransposon of *Cyclospora cayetanensis* is clearly out of the clade. Numbers on branches are percent bootstrap values >50 from 1,000 replications

 MarY1 AB028236.1

 Sushi-ichi AF030881.2

 Pyret AB062507.1

 Amn-ichi FJ158990.1

 Maggy L35053.1

 Pyggy AF533703.1

 **Eten\_Chromo\_HG674968**

 PT-Galadriel GQ294570.1

 PT1-Reina GQ294568.1

 Osvaldo AJ133521.1

 Tv1 AF056940.1

 Micropia-Dm11 X14037.1

 SURL AJ621597.1

 Mdg3 X95908.1

 Skipper AF049230.1

 **Ccay\_LTR18**

 Tor4a AY634220.1

 HMS-Beagle HM214799.1

 Mdg1 X59545.1

 Tor2 AY634223.1

 blastopia JQ666294.1

 Tor1 AY634221.1

 Kabuki AB032718.1

 CsRn1 AY013571.1

 Boudicca AY662653.1

80

100

89

55

54

76

54

50

51

56

0.2

Chromoviruses