**Evolutionary characterization of Ty3/gypsy-like LTR retrotransposons in the parasitic cestode Echinococcus granulosus**

**Running head: LTR retrotransposons of Echinococcus granulosus**

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**Supplementary Fig. 1.** Multiple sequence alignment of reverse transcriptases (RTs) encoded in *Echinococcus granulosus* LTR retrotransposons. The amino acid sequences determined based on BLAST results were aligned with that of *Clonorchis sinensis* *CsRn1*. Dashes represent either missing data due to DNA deletions or gaps introduced during alignment to increase the similarities. X denotes the position of premature stop codons. Domains I-VII indicate the regions containing each of the seven motifs conserved in RTs.



**Supplementary Fig. 2.** Normalized dN - dS values across the codons of cestode solo *gag* genes. The normalized dN - dS value of each codon was calculated from a nucleotide sequence alignment of four cestode *gag* genes identified in *Echinococcus granulosus* (LK028580.1 in the GenBank), *Echinococcus multilocularis* (LN902844.1), *Taenia solium* (Ts\_Gag, TsM\_000811700.1 in the GeneDB), and *Hymenolepis microstoma* (LN906332.1), using the MEGA program.

