



**Supplement Figure S1.** Maximum likelihood (ML) phylogenetic trees inferred from nuclear 18S rRNA (a) and 28S rRNA (b) sequences. The GenBank accession numbers of all the sequences included in the analyses are given behind the taxon names. The values attached to branches represent percent bootstrap values per 1000 replicates (only values  $\geq 50\%$  are shown), whereby the results of three independent analyses (i.e., alignments) are indicated. Species of Toxoplasmatinae served as outgroups. The new nucleotide sequences of *Sarcocystis arctica* from cheetahs are highlighted by black symbols.