SUPPORTING INFORMATION

S1 Figure. Alpha rarefaction plot (metric: observed\_otus) for all fish samples analysed during the present study at the 18S rRNA locus. Rarefaction was set at 2,313.



S2 Figure. Alpha rarefaction plot (metric: observed\_otus) for all fish samples analysed during the present study at the actin locus. Rarefaction was set at 3,081.



S3 Figure. Phylogenetic tree showing the position of the actin OTUs identified by NGS and Sanger. The evolutionary history inferred by using the maximum likelihood method based on the Tamura 3-parameter model. The tree with the highest log likelihood (-2140.9588) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.2201)). The analysis involved 74 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 209 positions in the final dataset. Sanger sequences are indicated with a full dot. OTUs obtained by NGS are indicated with a full triangle, and the number in brackets represent the number of copies of identical sequences obtained (e.g., OTU 01 was found 248,963 times). Codes in brackets are GenBank accession numbers. The tree has been rooted on the clade formed by four non-piscine *Cryptosporidium* spp. (root not shown).

