Supplementary Information

Figure S1. Alignment of all the Haplosporidian 18S rRNA sequences available at NCBI up to 31.01.2023. The first three lines represents forward, probe and reverse (in its reverse complement) Hp_CM primers, respectively. With black background are reported the 100% conserved site in respect to the Hp_CM system.

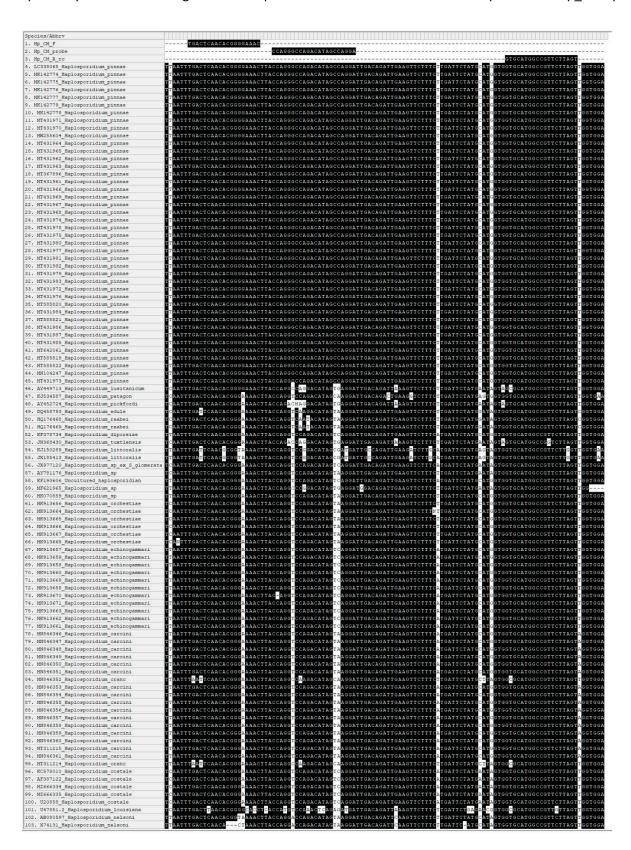


Figure S2. Standard curve plot on Inhibition test done with IAC 1. On y-axis the quantitative cycles (Cq), on x-axis the Log of the starting quantity of each dilution, as circle the serial dilution of IAC 1, red cross indicates IAC 1 with the sample F8 and blue cross is the IAC 1 with the F6 sample. E= reaction efficiency, R^2= coefficient of determination and y-int = y intercept. Figure edited with Maestro software (Bio Rad).

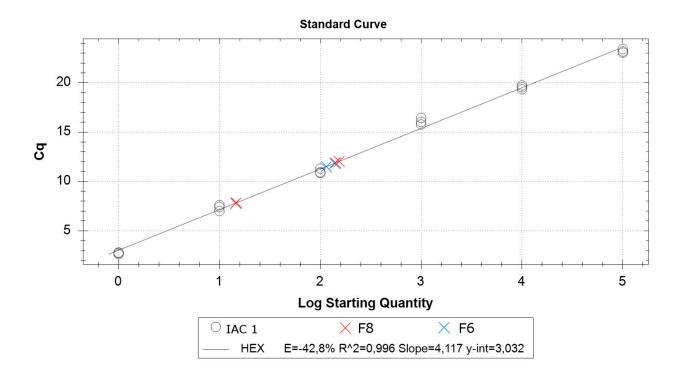


Figure S3. Confirmation of the identity of the sequenced amplicon from sample F8. Alignment of Sanger-sequenced sample F8 compared with representatives of *Haplosporidium* spp sequences along with the oligonucleotides (reverse as reverse complement) and probe forming the Hp_CM assay.

