**Table S1. Blast analysis of the sequences obtained by PCR amplification for *Leishmania* detection.**

\* BLAST results were retained only if they corresponded to the sequences of reference strains or to sequences of isolates described in peer-reviewed articles and well-characterized in terms of species, origin and hosts, in order to avoid misidentifications

\*\* When the results obtained with one database were highly significant and with high score whereas low similarity was found with the second one, only the highly significant results are provided.