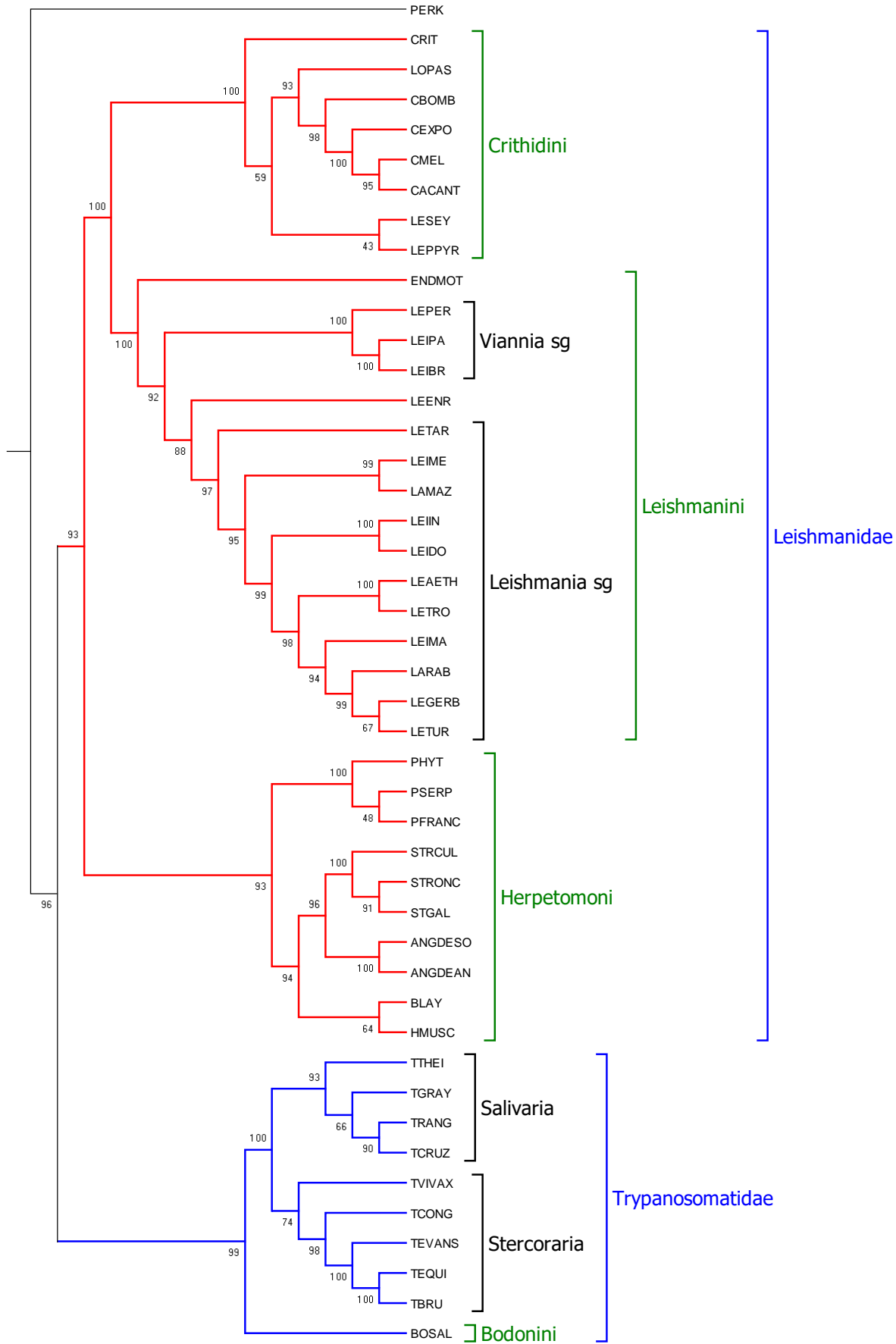
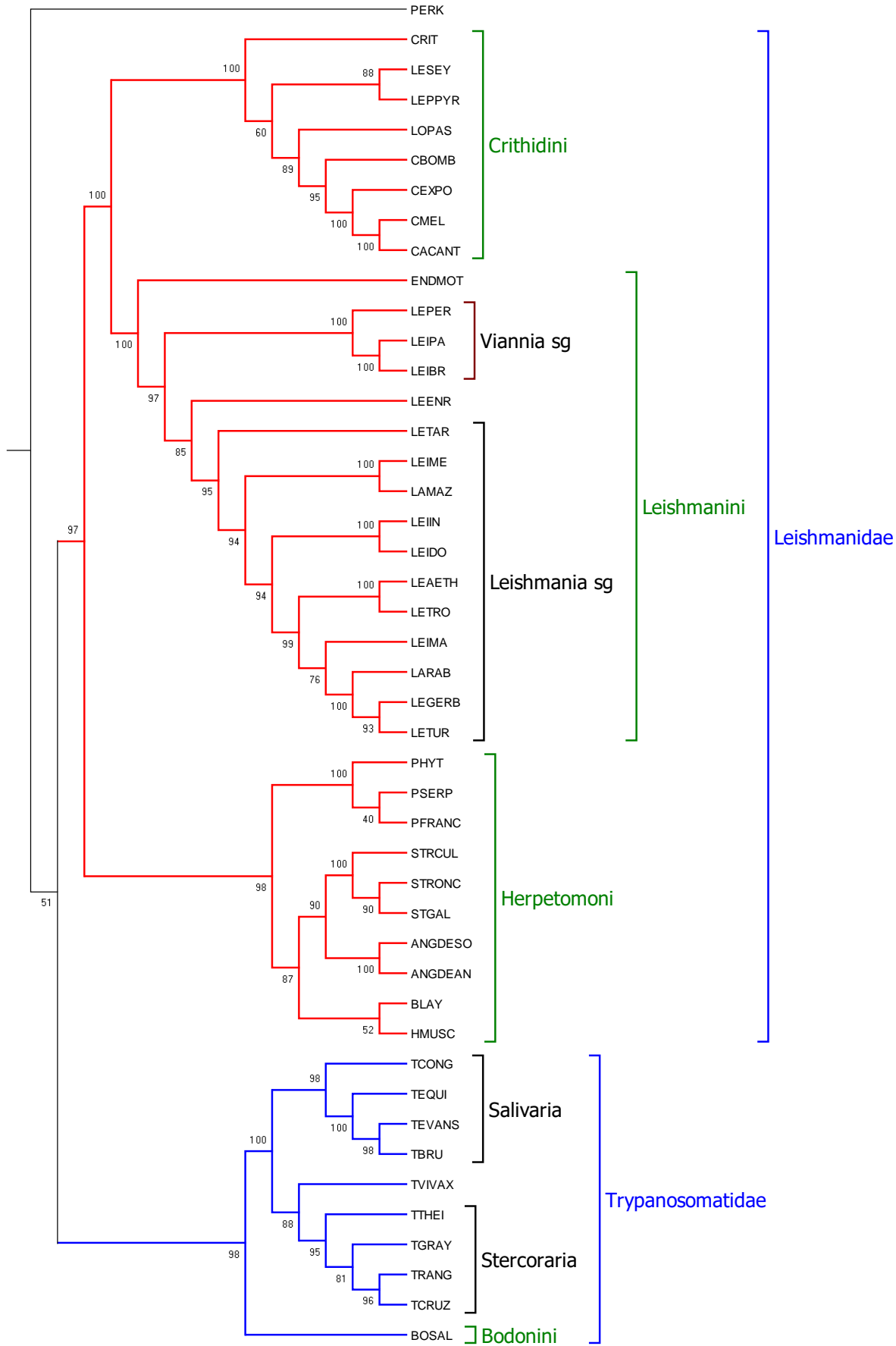


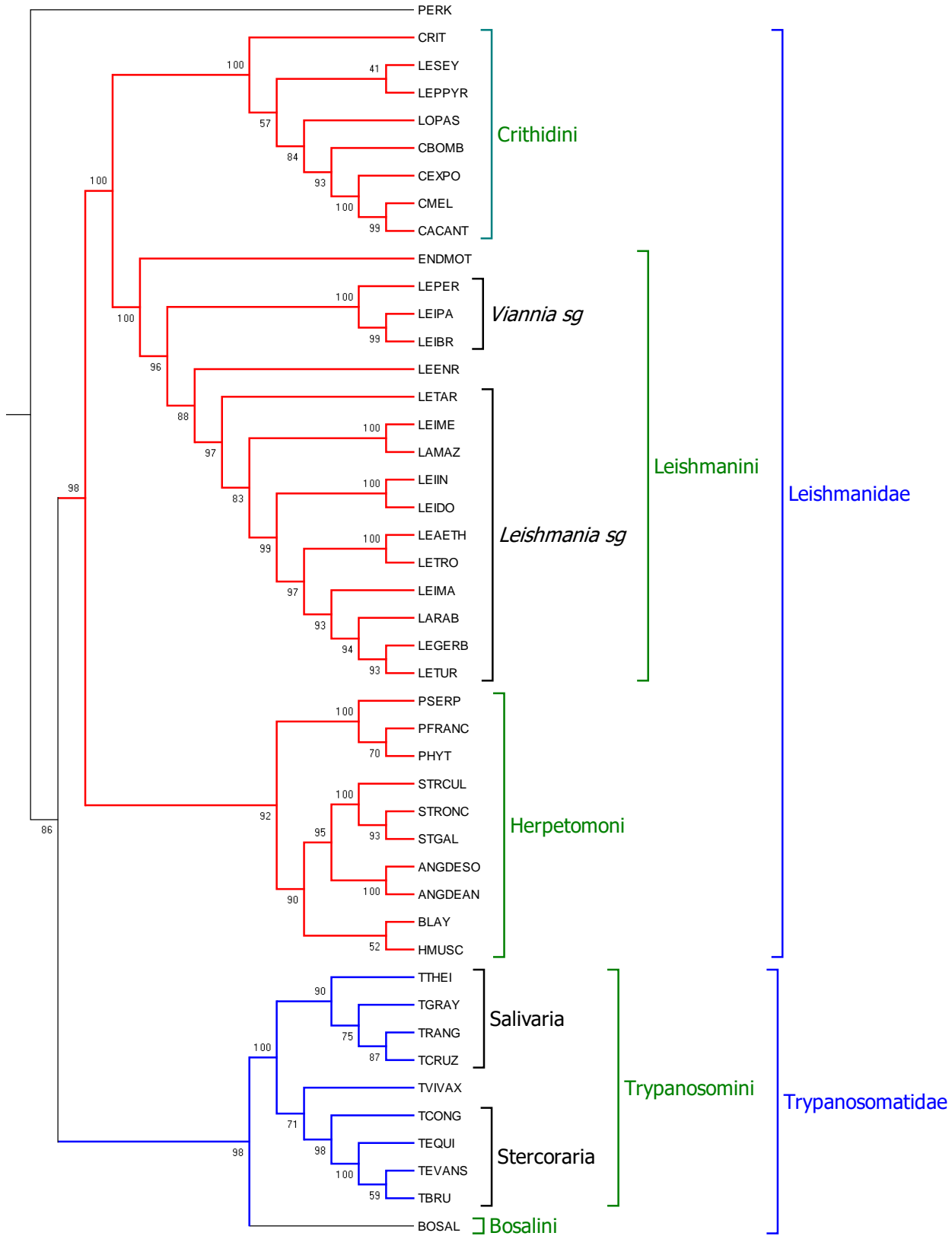
Supplemental figure 1 (S1): Phylogram deriving from the 25th percentile of the ranked ortholog pairs of 46 species of kinetoplastids. Abbreviations at the end of the file.



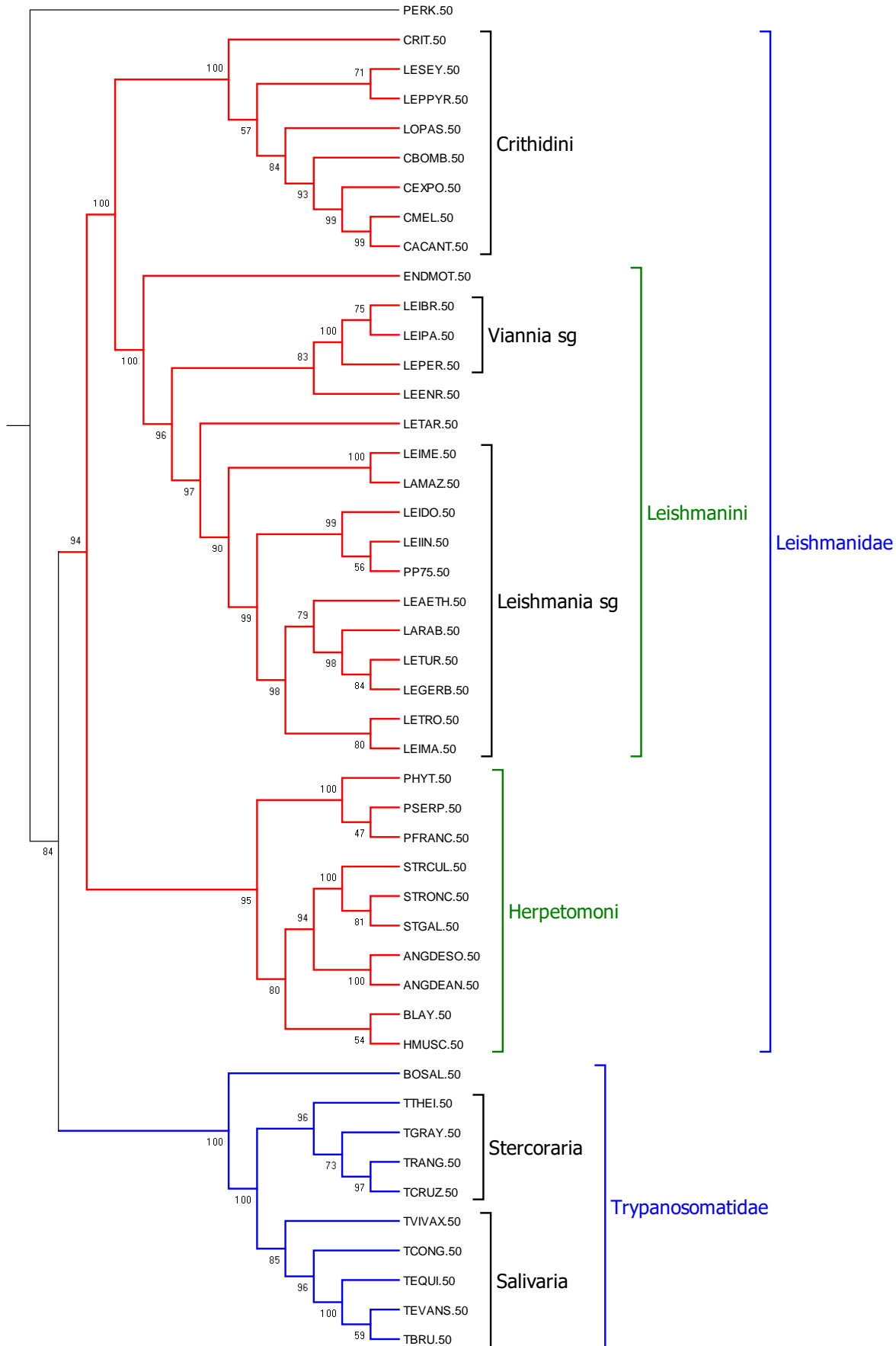
Supplemental figure 2 (S2): Phylogram deriving from the 75th percentile of the ranked ortholog pairs of 46 species of kinetoplastids. Abbreviations at the end of the file.



Supplemental figure 3 (S3): Phylogram deriving from the 50th percentile of the ranked ortholog pairs of 46 species of kinetoplastids using RSD parameters of 1e-20 and 0.5. Abbreviations at the end of the file.

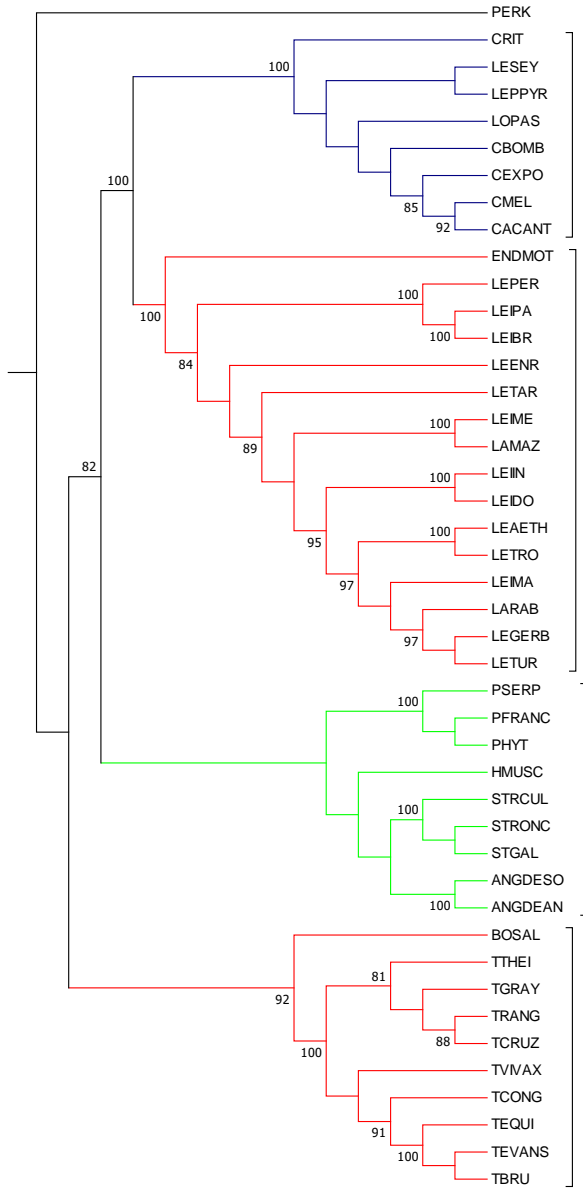


Supplemental figure 4 (S4): Phylogram deriving from the 55th percentile of the ranked ortholog pairs of 46 species of kinetoplastids that had their proteome randomly reduced to one half of its size. Abbreviations at the end of the file.

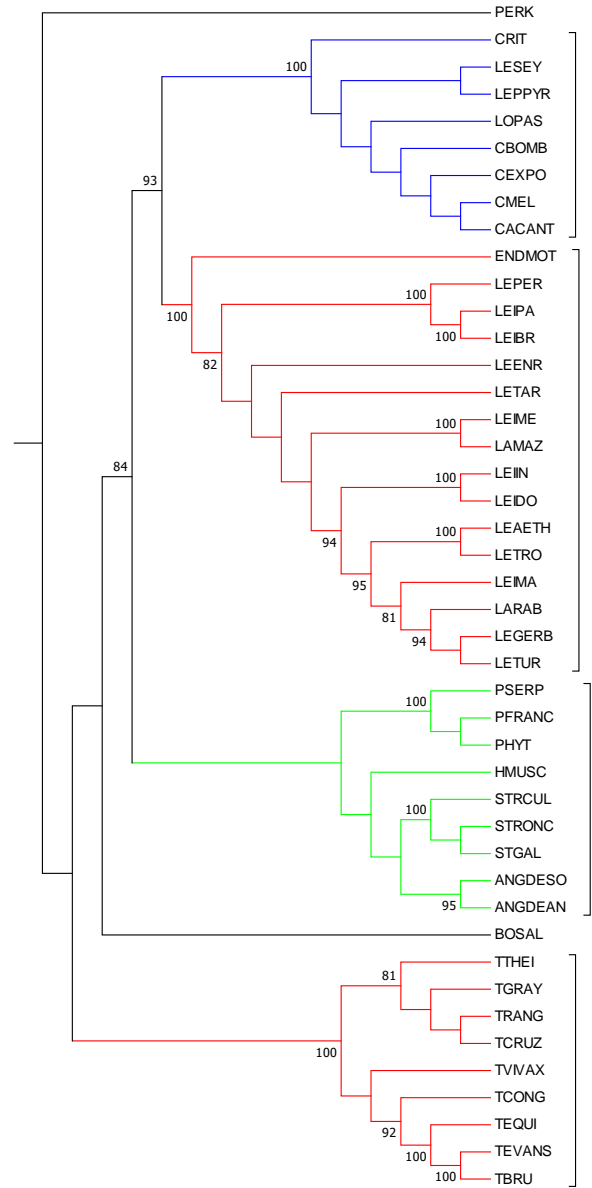


Supplemental figure 5 (S5): Phylograms for Kinetoplastida derived from different methods for orthologs inference: a) RSD, based on evolutionary distance; b) SonicParanoid, based on MCL algorithm. Abbreviations at the end of the file.

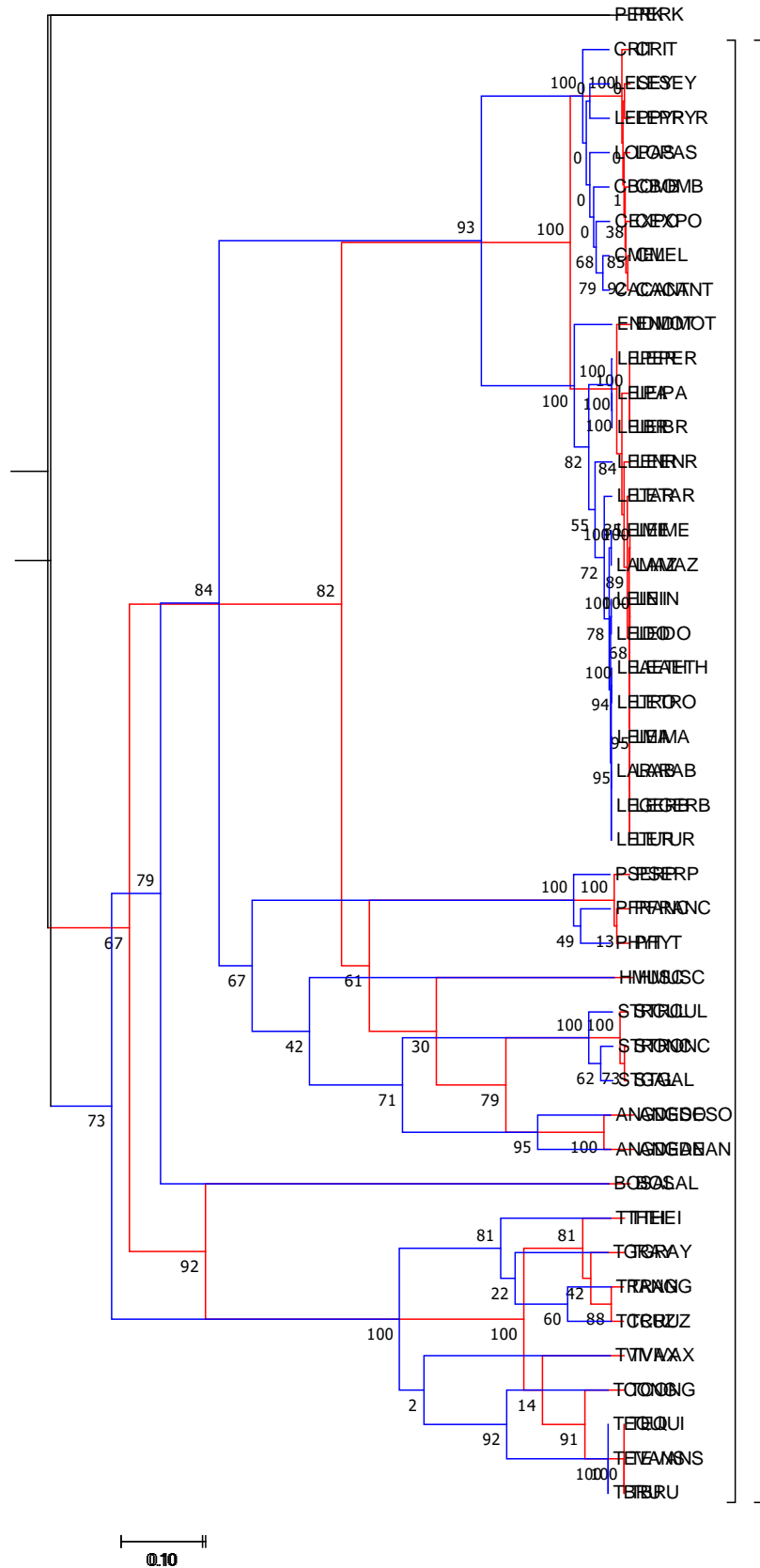
a) RSD



b) SonicParanoid



Supplemental figure 6 (S6): Overlapped phylograms for Kinetoplastida derived from different methods for orthologs inference. RSD method in red and SonicParanoid in blue. Abbreviations at the end of the file.



Supplemental figure 7 (S7): Bar graph showing the total number of orthologous identified by the RSD and OrthoMCL algorithms for 78 pairs of species combinations used in the analysis, based on 13 species with sequences retrieved from TriTryp database, as indicated in Table 1 ("Proteins sequence source" column). Intersections (shared orthologs) and unique orthologs were calculated with gene ID lists as input using Venn diagram tool (<http://bioinformatics.psb.ugent.be/webtools/Venn/>). Blue bars represent the number of orthologous genes identified by both algorithms, whereas red bars indicate the number of unique orthologs identified by each algorithm. Total orthologs for RSD: 7013 ± 831 and OrthoMCL: 7017 ± 977 . Unique orthologs detected by RSD: 457 ± 36 and OrthoMCL: 556 ± 34 . Values represent mean \pm SEM.

File name: Supplemental_Figures_S1_S2_S3_S4_S5_S6_S7.pdf

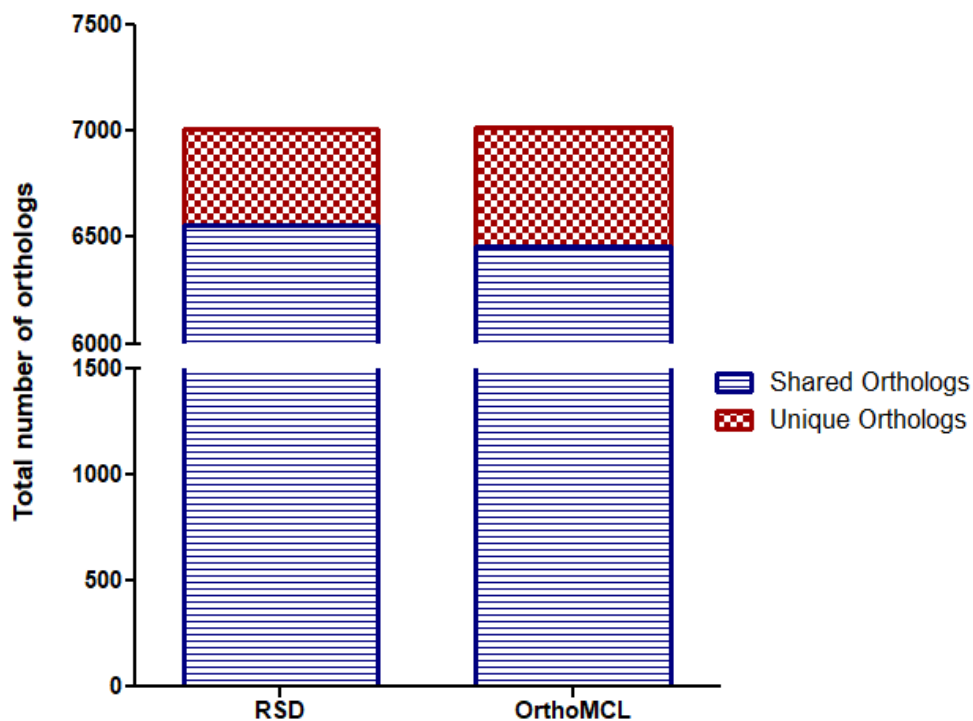


Table of abbreviations. The Kinetoplastida species names used in supplemental figures from S1 to S6 are abbreviated as follows:

Species name	Abbreviation
<i>Angomonas deanei</i>	ANGDEAN
<i>Angomonas desouzai</i>	ANGDESO
<i>Blechomonas ayalai</i>	BLAY
<i>Bodo saltans</i>	BOSAL
<i>Crithidia acanthocephali</i>	CACANT
<i>Crithidia bombi</i>	CBOMB
<i>Crithidia expoeki</i>	CEXPO
<i>Crithidia mellificae</i>	CMEL
<i>Crithidia fasciculata</i>	CRIT
<i>Endotrypanum monterogei</i>	ENDMOT
<i>Herpetomonas muscarum</i>	HMUSC
<i>Leishmania amazonensis</i>	LAMAZ
<i>Leishmania arabica</i>	LARAB
<i>Leishmania aethiopica</i>	LEAETH
<i>Leishmania enriettii</i>	LEENR
<i>Leishmania gerbilli</i>	LEGERB
<i>Leishmania braziliensis</i>	LEIBR
<i>Leishmania donovani</i>	LEIDO
<i>Leishmania infantum</i>	LEIIN
<i>Leishmania major</i>	LEIMA
<i>Leishmania mexicana</i>	LEIME
<i>Leishmania panamensis</i>	LEIPA
<i>Leishmania peruviana</i>	LEPER
<i>Leptomonas pyrrocoris</i>	LEPPYR
<i>Leptomonas seymouri</i>	LESEY
<i>Leishmania tarentola</i>	LETAR
<i>Leishmania tropica</i>	LETRO
<i>Leishmania turanica</i>	LETUR
<i>Trypanosoma evansi</i>	LEVANS
<i>Lotmaria passim</i>	LOPAS
<i>Perkinsella sp.</i>	PERK
<i>Phytomonas francai</i>	PFRANC
<i>Phytomonas sp.</i>	PHYT
<i>Phytomonas serpens</i>	PSERP
<i>Strigomonas galati</i>	STGAL
<i>Strigomonas culicis</i>	STRCUL
<i>Strigomonas oncopelti</i>	STRONC
<i>Trypanosoma brucei</i>	TBRU
<i>Trypanosoma congolense</i>	TCONG
<i>Trypanosoma cruzi</i>	TCRUZ
<i>Trypanosoma equiperdum</i>	TEQUI
<i>Trypanosoma grayi</i>	TGRAY
<i>Trypanosoma rangeli</i>	TRANG
<i>Trypanosoma theileri</i>	TTHEI
<i>Trypanosoma vivax</i>	TVIVAX