

#### ACDp -----

Summary of branches under episodic selection (123 were tested, of which 67 required optimizations) :

Node5 p = 0.000158934382335385 (Non-Trypanosome trypanossomatids ancestor)  
Node39 p = 0.001392524424110864 (Trypanosoma – Terrestrial clade ancestor)  
Node15 p = 0.009012673981737218 (*Strigomomas* ancestor)  
Strigomonas culicis p = 0.02485066779951189  
Node37 p = 0.03553635467089977 (*Trypanosoma* ancestor)

#### ATOM69 -----

Summary of branches under episodic selection (135 were tested, of which 64 required optimizations) :

Endotrypanum schaudinni p = 0  
Leishmania infantum p = 0  
Node36 p = 4.254125940406084e-10 (subfamily Leishmaninae ancestor)  
Node65 p = 1.669438087770203e-08 (*Strigomomas* ancestor)  
Strigomonas galati p = 2.719404295081773e-07  
Node57 p = 6.654557798690952e-07 (*Strigomomas/Angomonas* ancestor)  
Node73 p = 2.867100081349605e-05 (*Trypanosoma* ancestor)  
Node125 p = 9.47043304997397e-05 (*Zelonia costaricensis* clade)  
Strigomonas oncopelti p = 0.000627969690893293  
Node29 p = 0.0006547045679319852 (*Crithidia fasciculata* clade)  
Node74 p = 0.002747850117420958 (*Trypanosoma* Aquatic clade)  
Node58 p = 0.005070714886195871 (*Angomonas* ancestor)  
Node72 p = 0.007579468434232295 (Non-Trypanosome trypanossomatids ancestor)  
Node28 p = 0.01181723800526335 (*Zelonia/Leishmania/Endotrypanum*)  
Node39 p = 0.02442350284057992 (*Phytomonas* sp. EM1 – gene copies)  
Node94 p = 0.02613873219021023 (*Trypanosoma grayi* clade)  
Node53 p = 0.04479682326085255 (*Herpetomonas* ancestor)

#### DYX1C1 -----

Summary of branches under episodic selection (119 were tested, of which 54 required optimizations) :

Node11 p = 5.995204332975845e-14 (*Trypanosoma* ancestor)  
Endotrypanum monterogeii p = 2.235081564272434e-10  
Node66 p = 1.585307440876704e-09 (*Strigomomas* ancestor)  
Phytomonas sp TCC066E p = 2.297754093494309e-06  
Node18 p = 0.0001632461131566565 (*Crithidia fasciculata* clade)  
Trypanosoma ralphi p = 0.0002022691839162483  
Node49 p = 0.0003389629830572449 (*L. infantum/ L. donovani*)  
Trypanosoma sp TCC2186 p = 0.001817478320643884  
Node17 p = 0.002351794786299877 (subfamily Leishmaninae ancestor)  
Strigomonas culicis p = 0.003286528578563264  
Node72 p = 0.003830559032013681 (*Herpetomonas* ancestor)  
Leishmania panamensis p = 0.02215728280065937  
Node71 p = 0.02414245945492999 (*Herpetomonas/Phytomonas* ancestor)

#### HSP20 -----

Summary of branches under episodic selection (119 were tested, of which 35 required optimizations) :

Node99 p = 0.000210433620318029 (*Crithidia fasciculata* clade)

## NUDC1 -----

Summary of branches under episodic selection (123 were tested, of which 63 required optimizations) :

Node101 p = 1.018052309120776e-11 (*L. infantum*/*L. donovani* / *L. aethiopica*)  
Node74 p = 6.962167642399208e-08 (subfamily Leishmaninae ancestor)  
Node69 p = 6.525848019744984e-07 (*Strigomomas* ancestor)  
Leishmania arabica p = 3.245209608870869e-06  
Node109 p = 2.075612154150974e-05 (*L. major* / *L. turanica* / *L. arabica*)  
Node44 p = 0.0003476616517361641 (*Trypanosoma* ancestor)  
Node61 p = 0.0003606601937355958 (*Herpetomonas* ancestor)  
Trypanosoma sp TCC2186 p = 0.0007430180124178287  
Node75 p = 0.0009183907065883901 (*Crithidia fasciculata* clade)  
Leishmania braziliensis p = 0.0009353995733929477  
Node51 p = 0.008493007562787813 (*Herpetomonas/Phytomonas* ancestor)  
Node45 p = 0.01569012162976041 (Free-living/parasites)  
Crithidia acantocephali p = 0.02029364280919665  
Node65 p = 0.02577746829366512 (*Strigomomas/Angomonas* ancestor)  
Trypanosoma conorhini p = 0.03656848423389314  
Trypanosoma theileri p = 0.03758845825561047

## NUDC2 -----

Summary of branches under episodic selection (125 were tested, of which 41 required optimizations) :

Node6 p = 0.02950276511807098 (*Trypanosoma* ancestor)

## p23A -----

Summary of branches under episodic selection (123 were tested, of which 72 required optimizations) :

Endotrypanum monterogeei p = 3.931810229684807e-05  
Node57 p = 8.762825332070401e-05 (*Angomonas* ancestor)  
Node66 p = 0.0001090712578475372 (*Crithidia fasciculata* clade)  
Node2 p = 0.0002569951173285734 (*Trypanosomatidae* ancestor)  
Node51 p = 0.001426630021823527 (*Strigomomas/Angomonas* ancestor)  
Node109 p = 0.00377063781451864 (*Phytomonas serpens* / *Phytomonas* sp. TCC066)  
Node119 p = 0.004299105677418646 (*Paraboso caudatus* gene copies)  
Node50 p = 0.008067784839998982 (Non-Trypanosome trypanosomatids ancestor)  
Leptomonas costaricensis p = 0.008623680068982731  
Node60 p = 0.01318684488188809 (*Herpetomonas/Phytomonas/Leishmaninae*)  
Herpetomonas wanderleyi p = 0.01427410733392487  
Crithidia luciliae thermophila p = 0.01569653833288259  
Trypanosoma congolense p = 0.02485519142779236

## p23B -----

Summary of branches under episodic selection (127 were tested, of which 68 required optimizations) :

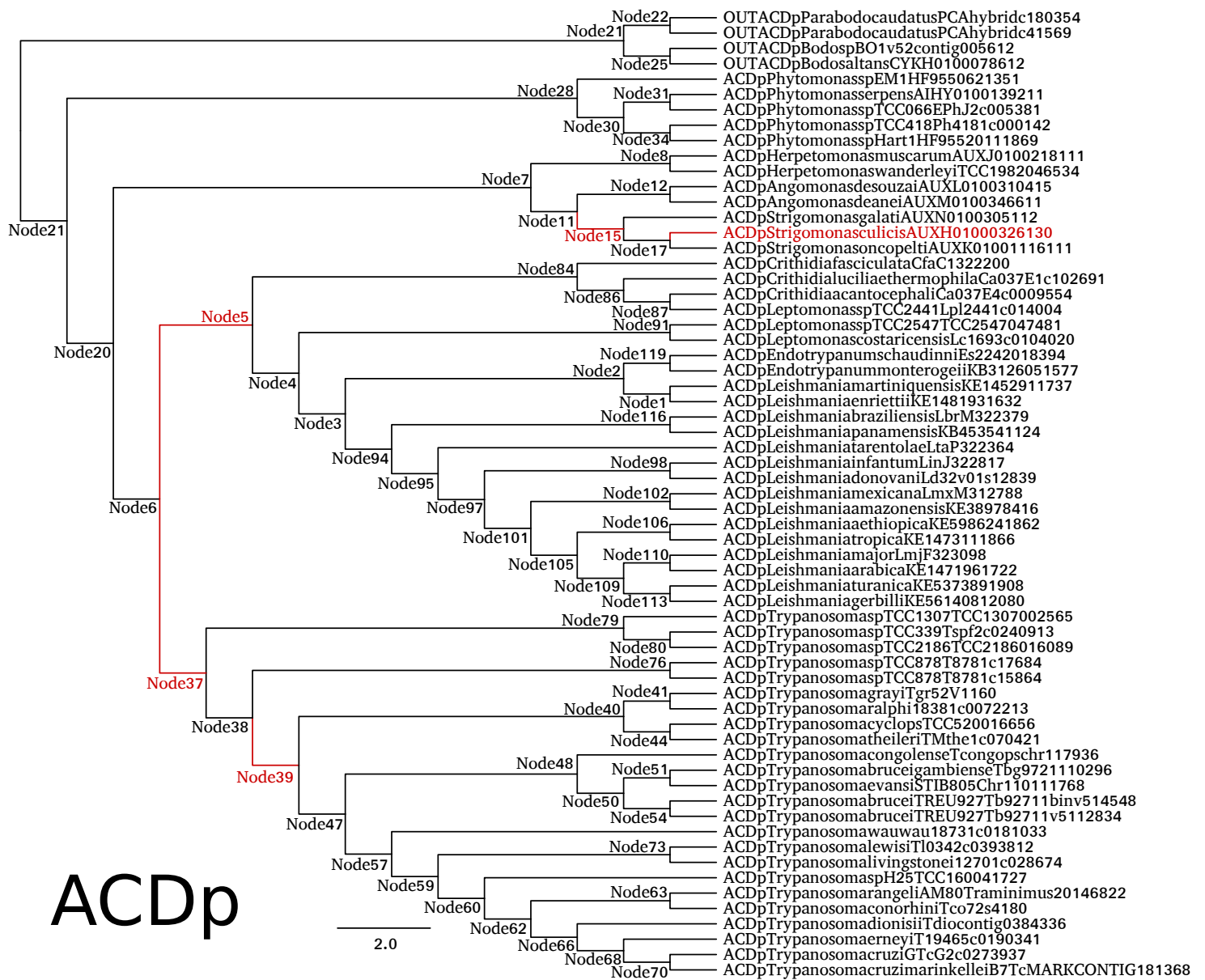
Parabodo caudatus p = 4.694022948115162e-13  
Node6 p = 2.175415930727453e-07 (*Trypanosoma* ancestor)  
Trypanosoma sp TCC2186 p = 0.000159108945360309  
Node106 p = 0.0006689297392468152 (*Strigomomas* ancestor)  
Node58 p = 0.0008788886711308397 (subfamily Leishmaninae ancestor)  
Node47 p = 0.002448725771772797 (*T. rangeli* / *T. conorhini* clade ancestor)

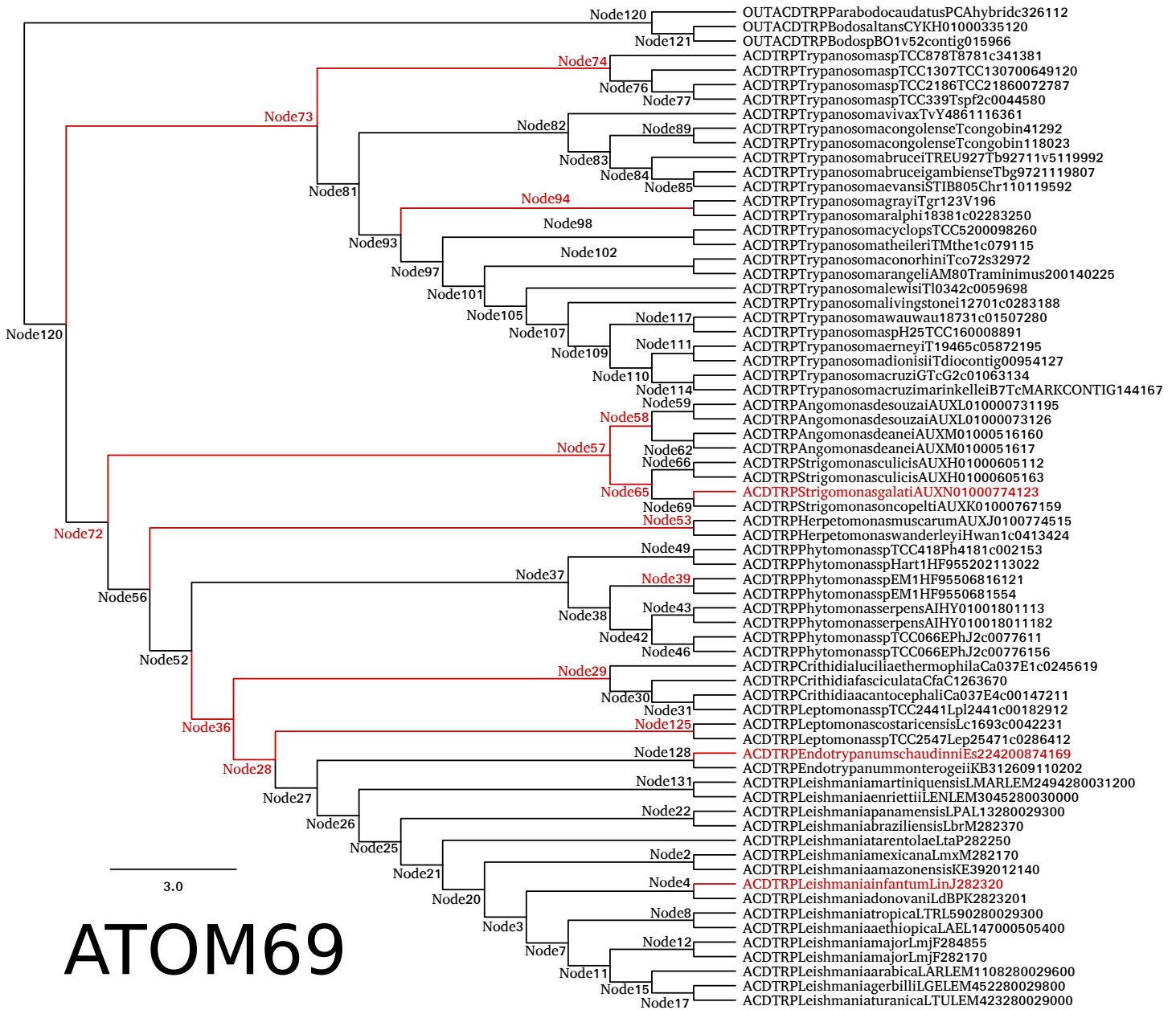
Trypanosoma cruzi marinkellei p = 0.00607750448577693  
Node103 p = 0.008799236467612381 (*Strigomomas/Angomonas* ancestor)  
Node14 p = 0.01636662228345487 (*Trypanosoma* Terrestrial clade ancestor)  
Bodo sp p = 0.02287741116838204  
Crithidialu ciliae thermophila p = 0.03175189013363627

SGT1 -----

Summary of branches under episodic selection (123 were tested, of which 51 required optimizations) :

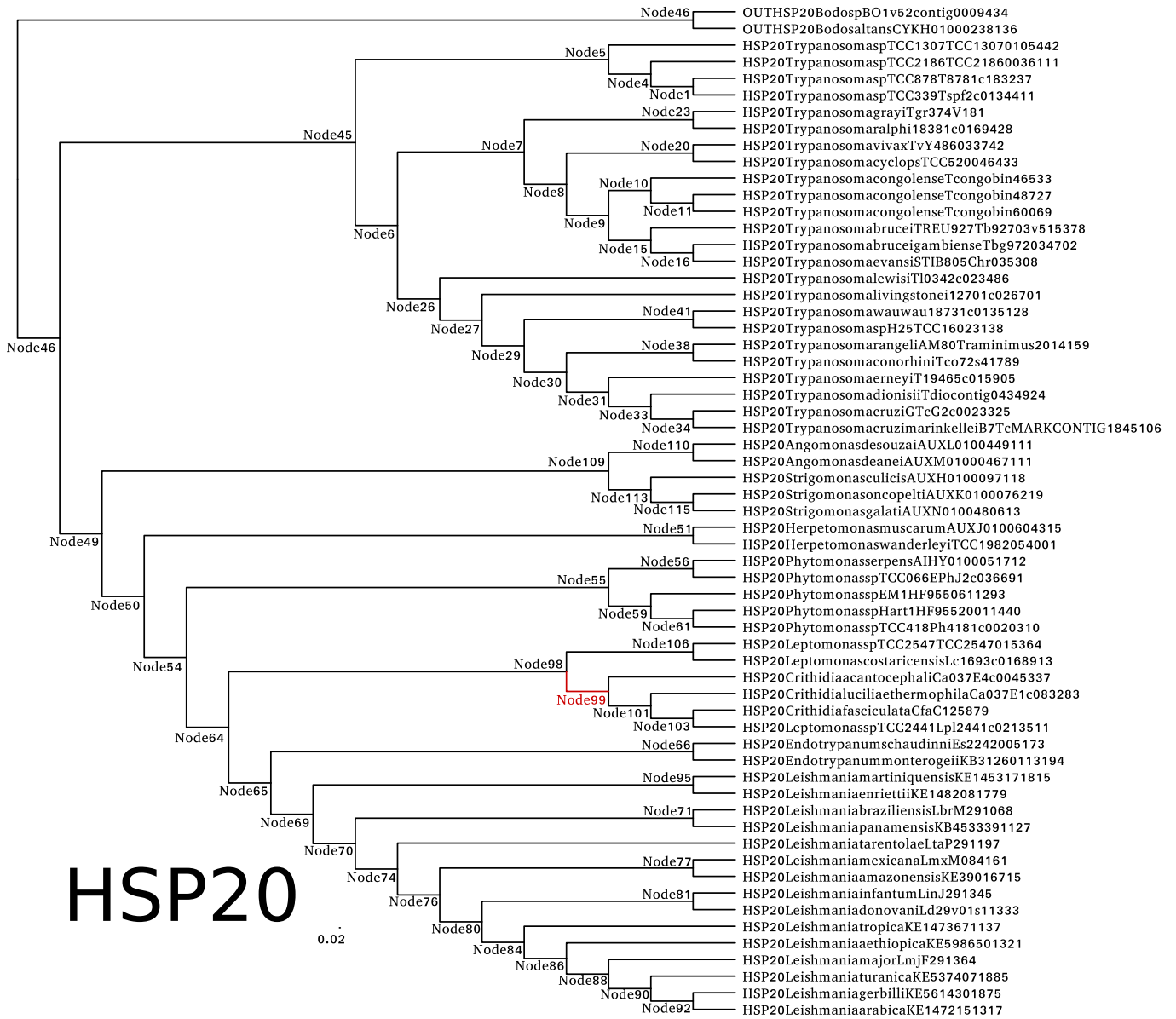
Node48 p = 1.199222943171208e-10 (subfamily Leishmaninae ancestor)  
Node31 p = 5.807178538042024e-06 (*Trypanosoma* ancestor)  
Node100 p = 0.0006507391240253568 (*Herpetomonas* ancestor)  
Trypanosoma lewisi p = 0.04100387581892023



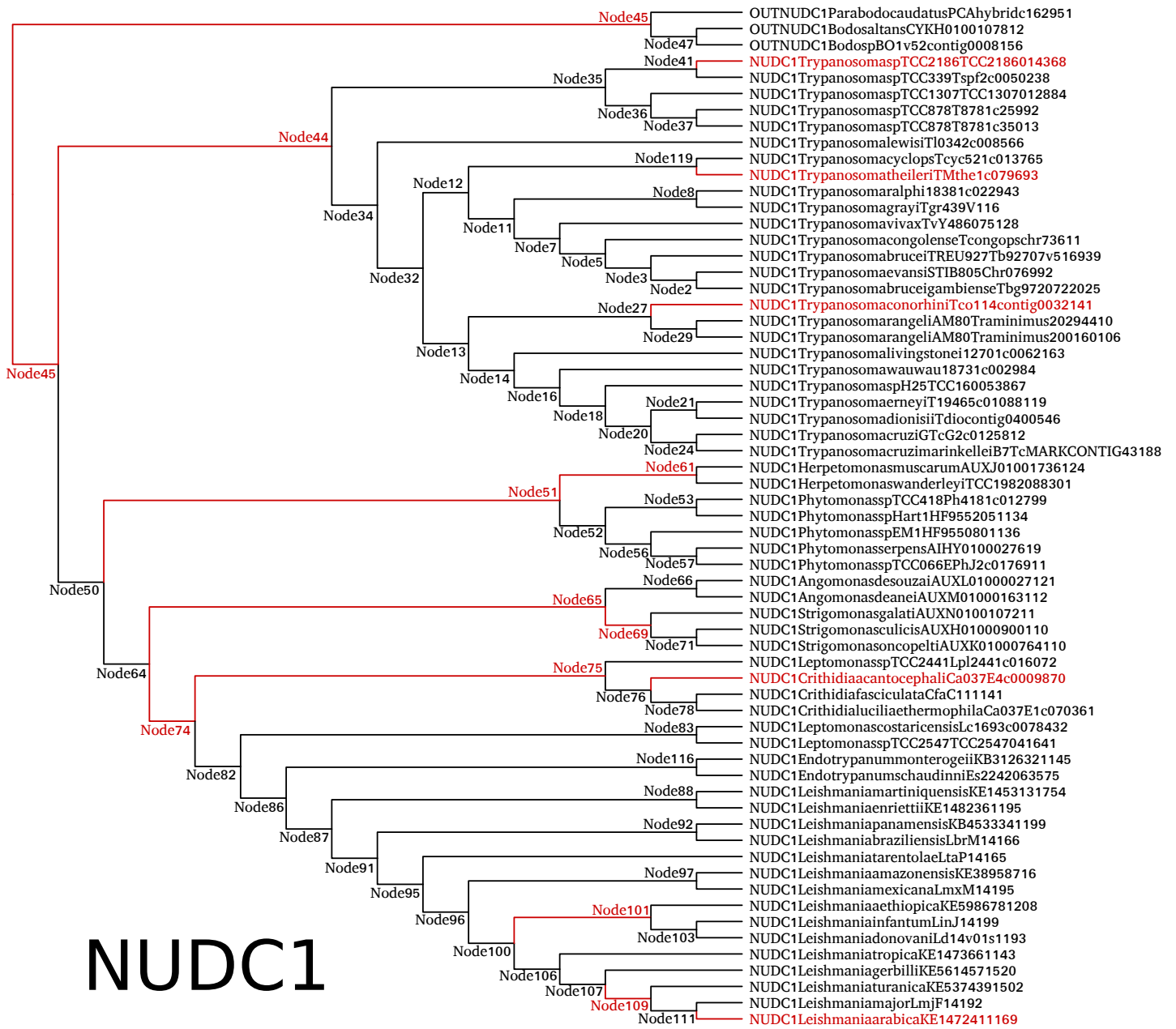


# ATOM69



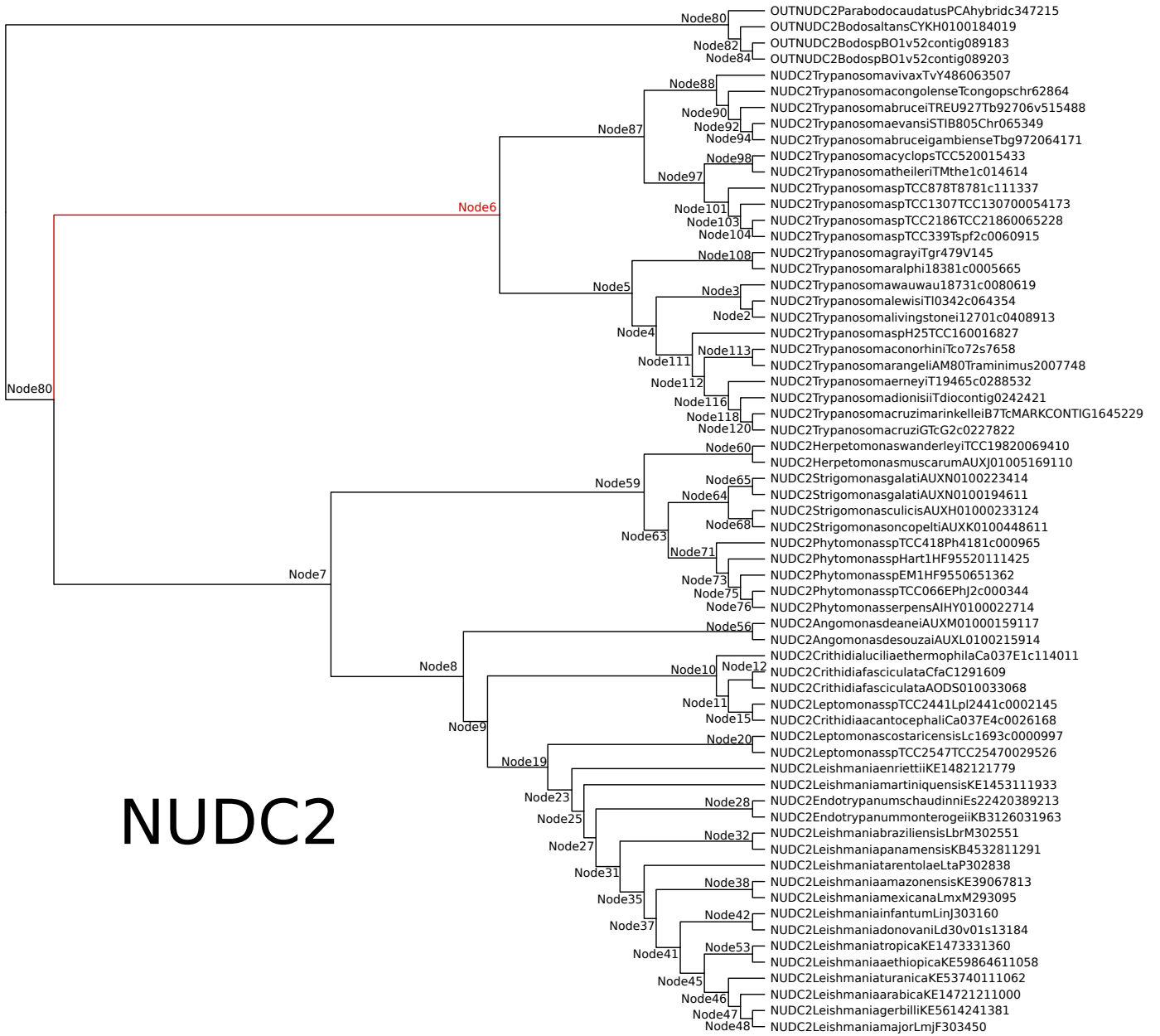


# HSP20



# NUDC1





# NUDC2

