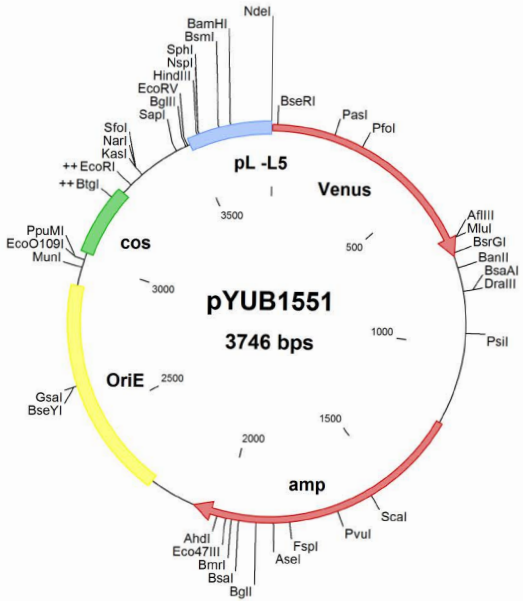
Supplementry Figure Legends

Supplementary Figure S1. Maps of single *cos* (pYUB1551) and double *cos* (pYUB1552) vectors expressing mVenus from the p_{left} promoter of phage L5. Plasmid pYUB1551 is the name allocated to the sequenced plasmid pYUB1391(6). Unique restriction sites are indicated except for the PacI recognition sequence, which is unique in pYUB1551 but appears twice in pYUB1552.

Supplementary Figure S2. Construction of the DS6A shuttle phasmid. The indicated DNA samples were evaluated by electrophoresis on agarose gels. (A) High quality genomic DNA isolated from DS6A. (i) Genomic DNA isolated from D29 phage amplified on *M. smegmatis* using the standard phage amplification protocol. (ii) Genomic DNA isolated from DS6A phage amplified on *Mtb* using the standard phage amplification protocol. (iii) Genomic DNA isolated from DS6A phage amplified with the modified amplification protocol resulting in high quality phage DNA suitable for shuttle phasmid construction. (B) Restriction digestion confirming shuttle phasmids from DS6A phage. A DS6A deletion library was electroporated into *Mtb.* Genomic DNA from the recombinant phages obtained was isolated, and the presence of plasmid was confirmed by PacI digestion. A band of the correct size for pYUB328 plasmid (~3.9 kb) was released from seven of the eight DS6A recombinant phages (indicated by the lower arrow).

Supplementary Figure S3. Phylogenetic trees of selected DS6A proteins analyzed against the mycobacteriophage database. Phylogenetic trees of DS6A structural proteins (i) capsid, (ii) major tail subunit, (iii) tape measure protein, functional proteins (iv) Lysin A and (v) Lysin B, and DNA modifying proteins (vi) DNA polymerase III, (vii)

integrase, (viii) MazG, and (ix) Primase were assembled via maximum parsimony analysis. The colored shape next to the phage name indicates its cluster assignment.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BamHI
BsmI
SphI
NspI
HindIII
EcoRV
BglII
SapI
BseRI
PasI
PfoI
SfoI
NarI
KasI
++ EcoRI
++ BtgI
pL -L5
Venus
3500
500
AflIII
MluI
BsrGI
BanII
BsaAI
DraIII
PpuMI
EcoO109I
MunI
cos
3000
pYUB1551
3746 bps
1000
PsiI
OriE
2500
GsaI
BseYI
1500
2000
amp
ScaI
PvuI
AhdI
Eco47III
BmrI
BsaI
BglI
FspI
AseI

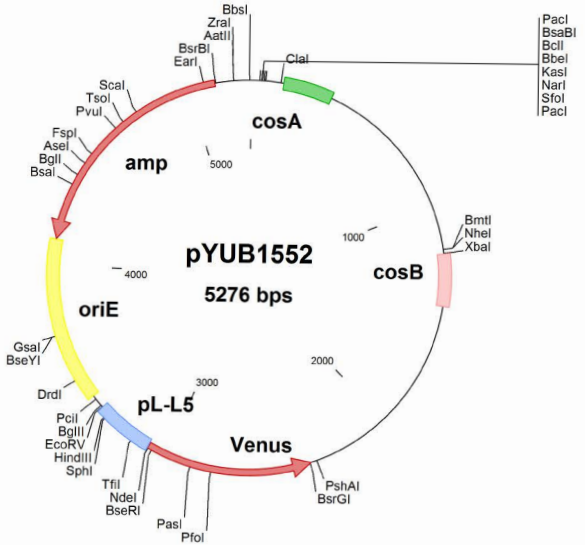
BbsI
ZraI
AatII
BsrBI
EarI
ClaI
PacI
BsaBI
BclI
BbeI
KasI
NarI
SfoI
PacI
ScaI
TsoI
PvuI
cosA
FspI
AseI
BglI
BsaI
amp
5000
BmtI
NheI
XbaI
1000
pYUB1552
5276 bps
cosB
4000
oriE
GsaI
BseYI
2000
DrdI
3000
pL-L5
PciI
BglII
EcoRV
HindIII
SphI
Venus
TfiI
NdeI
BseRI
PshAI
BsrGI
PasI
PfoI

Fig. S1

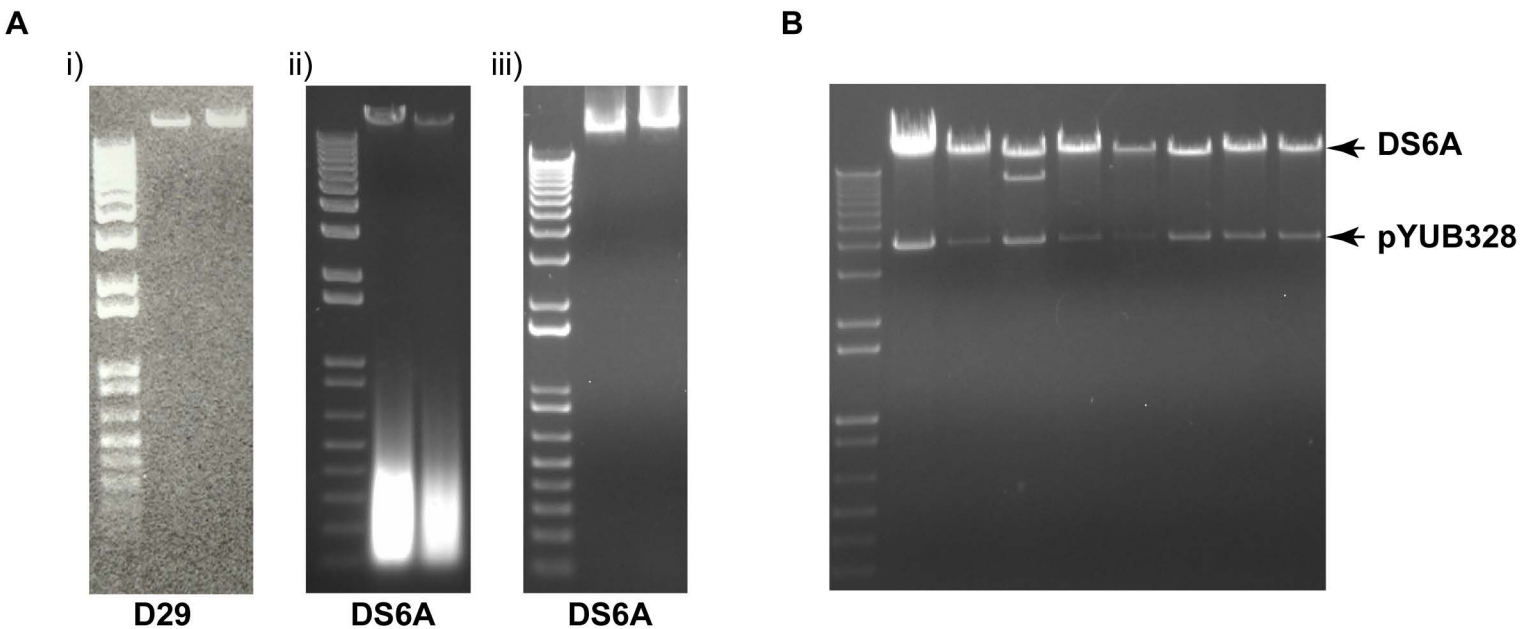

Fig. S2

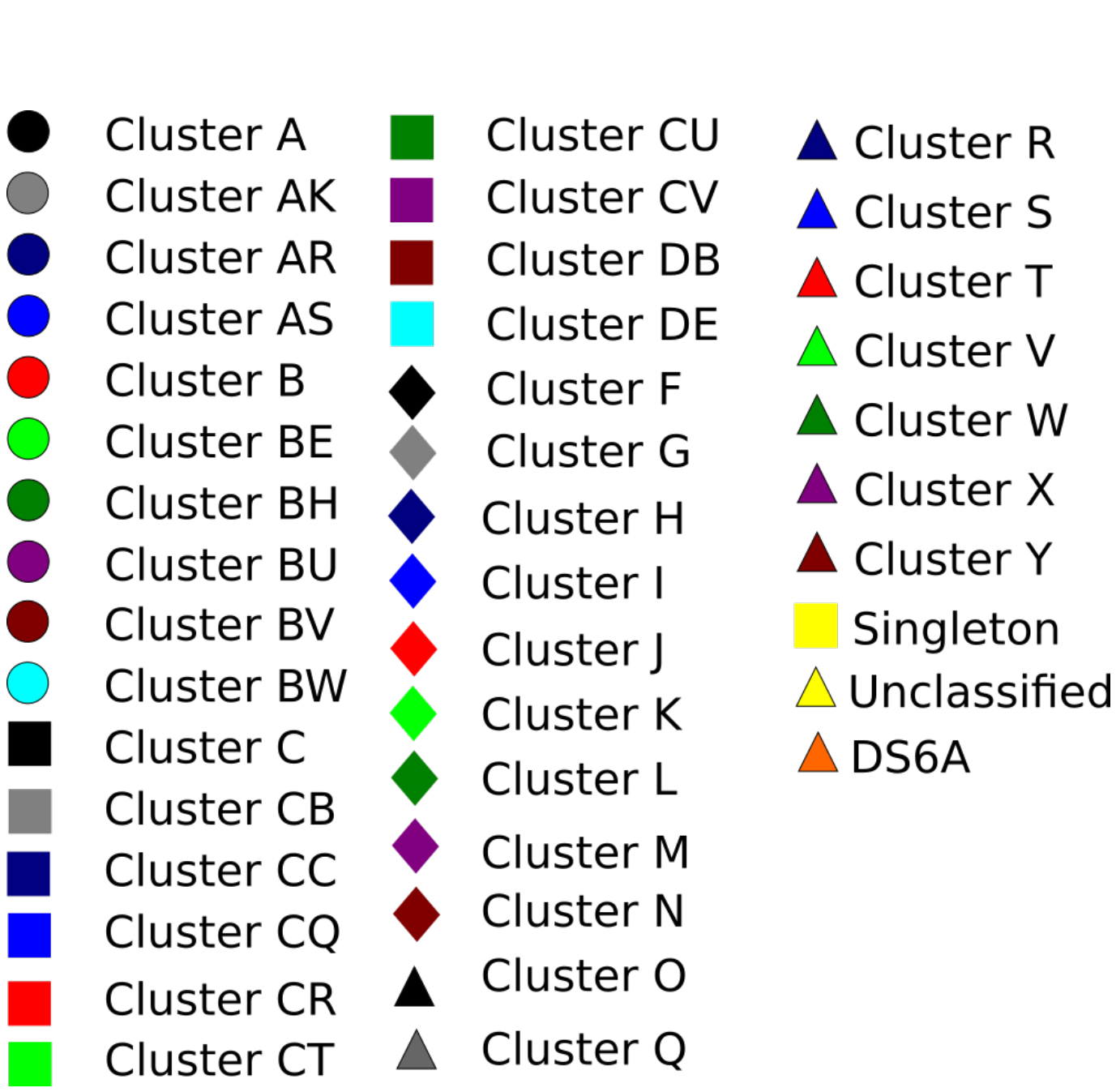
Cluster assignment legend
Cluster A
Cluster AK
Cluster AR
Cluster AS
Cluster B
Cluster BE
Cluster BH
Cluster BU
Cluster BV
Cluster BW
Cluster C
Cluster CB
Cluster CC
Cluster CQ
Cluster CR
Cluster CT
Cluster CU
Cluster CV
Cluster DB
Cluster DE
Cluster F
Cluster G
Cluster H
Cluster I
Cluster J
Cluster K
Cluster L
Cluster M
Cluster N
Cluster O
Cluster Q
Cluster R
Cluster S
Cluster T
Cluster V
Cluster W
Cluster X
Cluster Y
Singleton
Unclassified
DS6A

Fig. S3

i)

gp11
Capsid

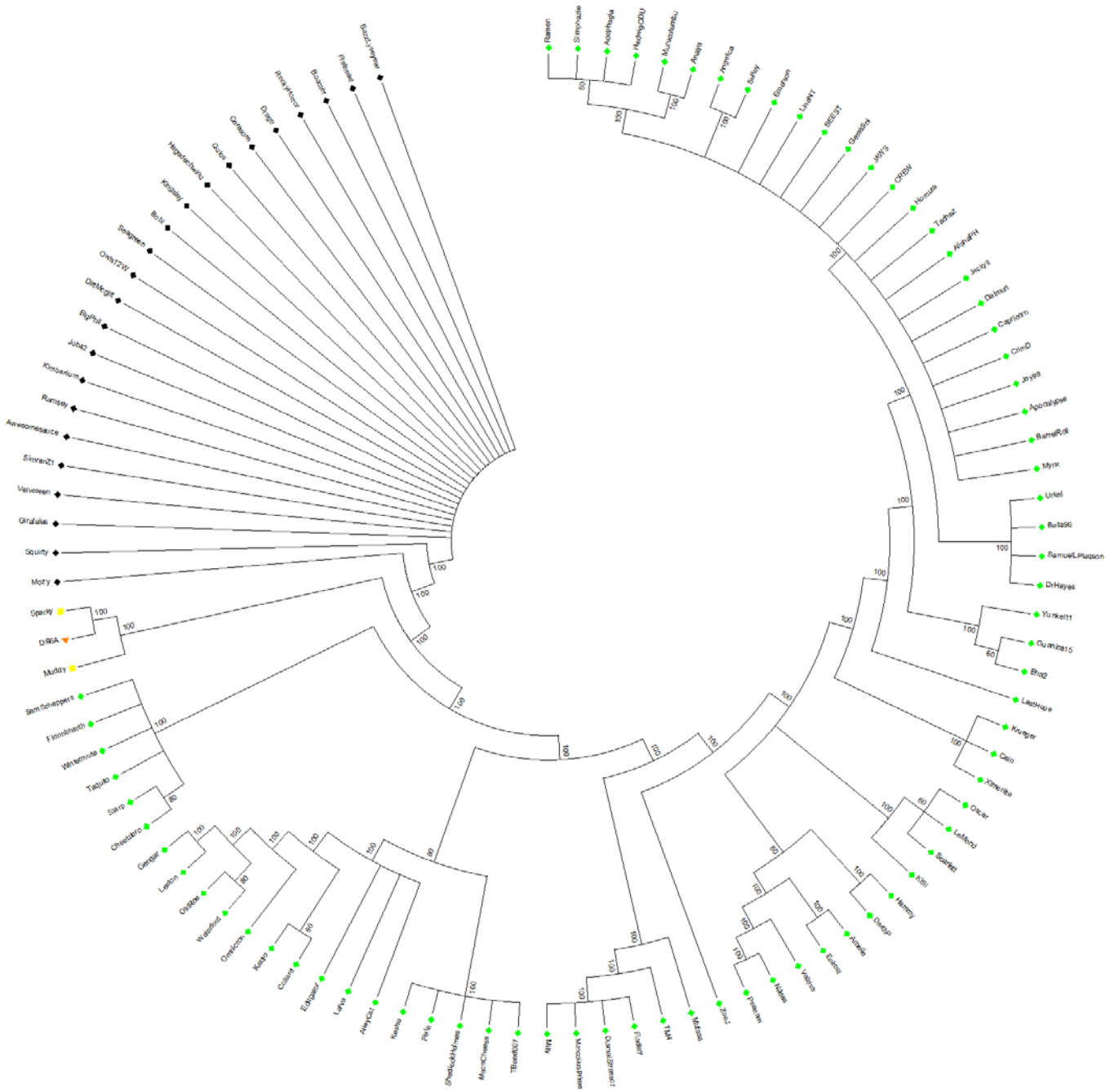

Fig. S3

ii)

gp16

Major tail subunit

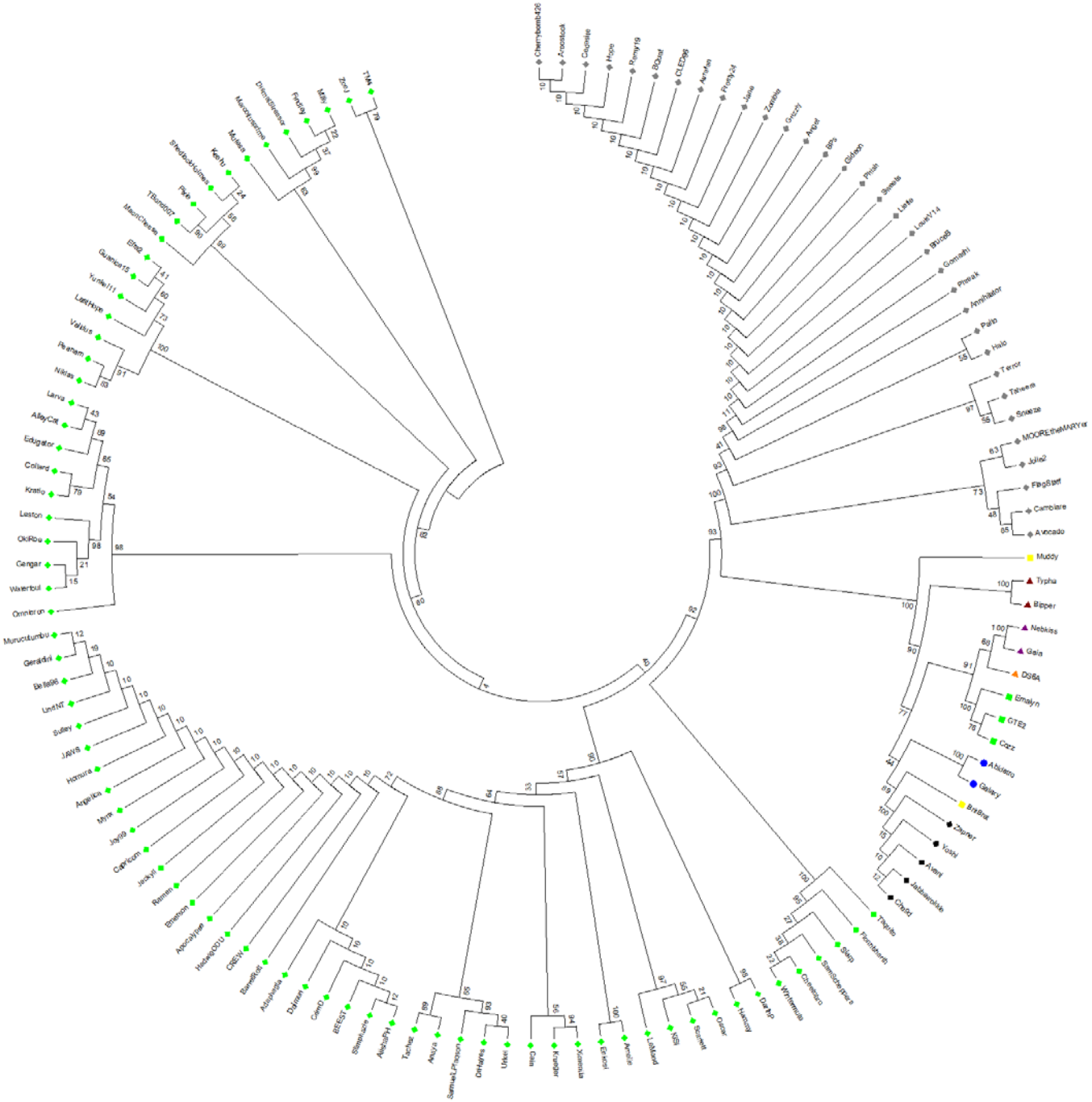

Fig. S3

iii)

gp19

Tape measure protein

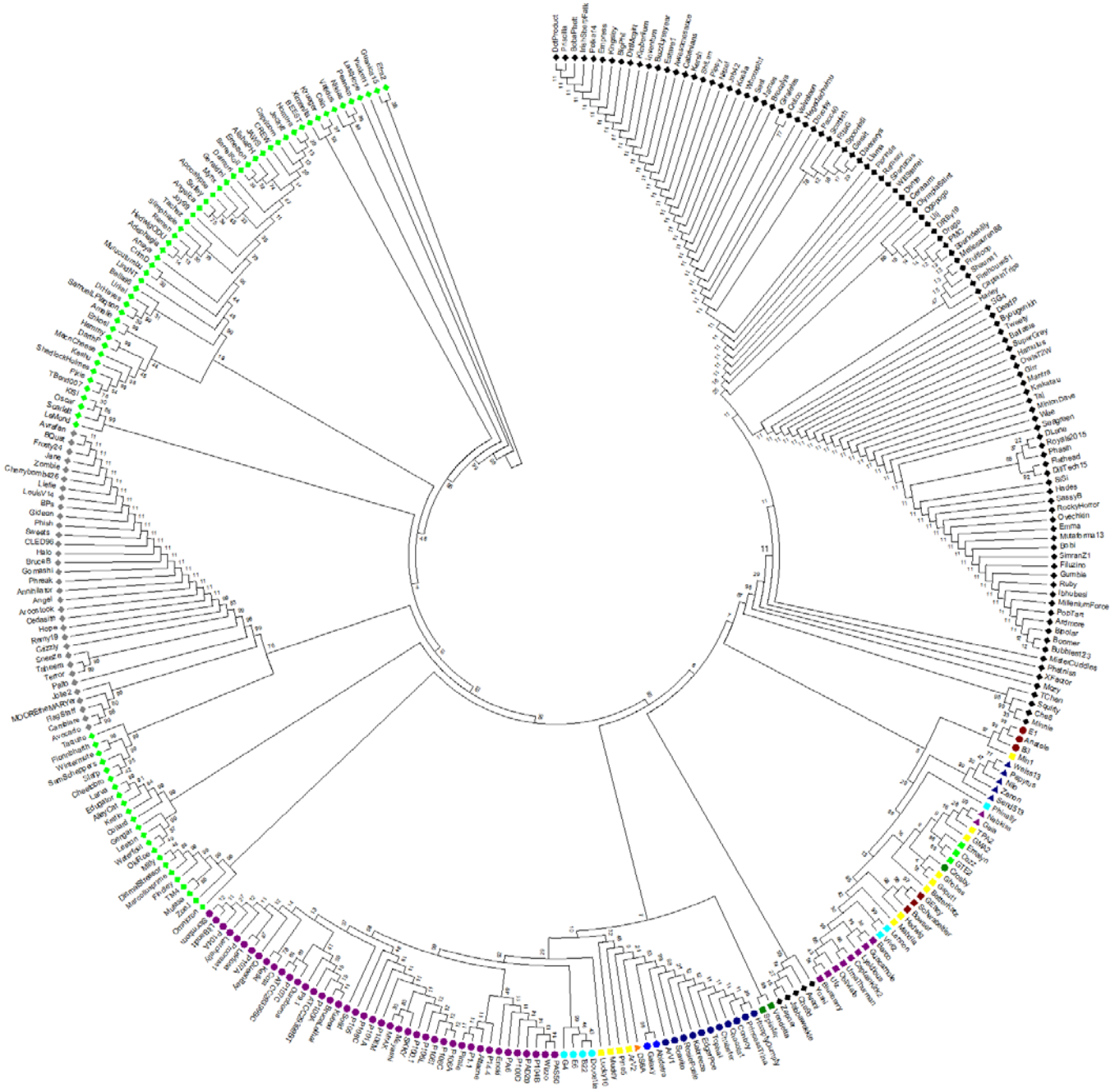

Fig. S3

iv)

gp30
Lysin A

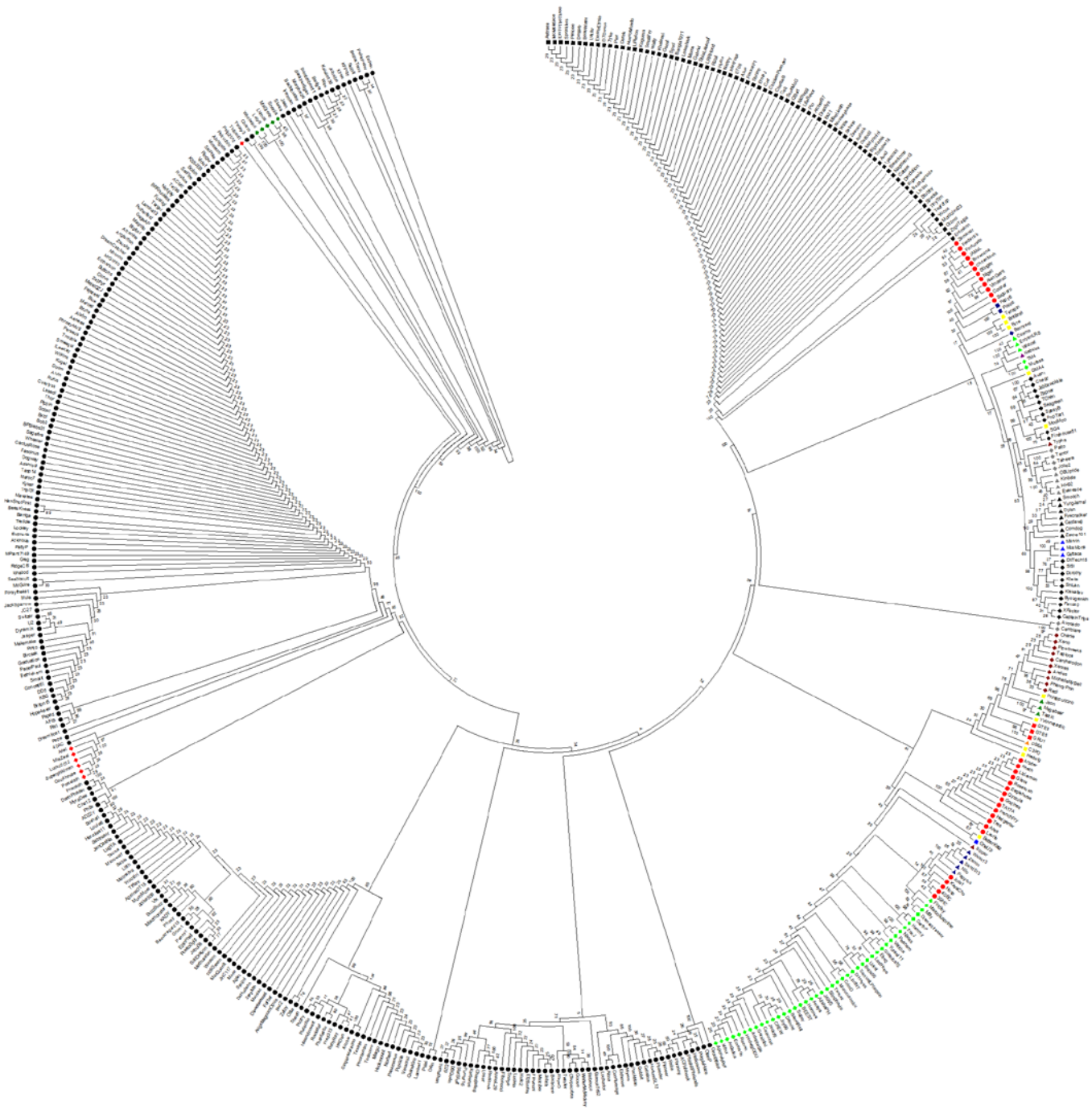

Fig. S3

v)

gp31
Lysin B

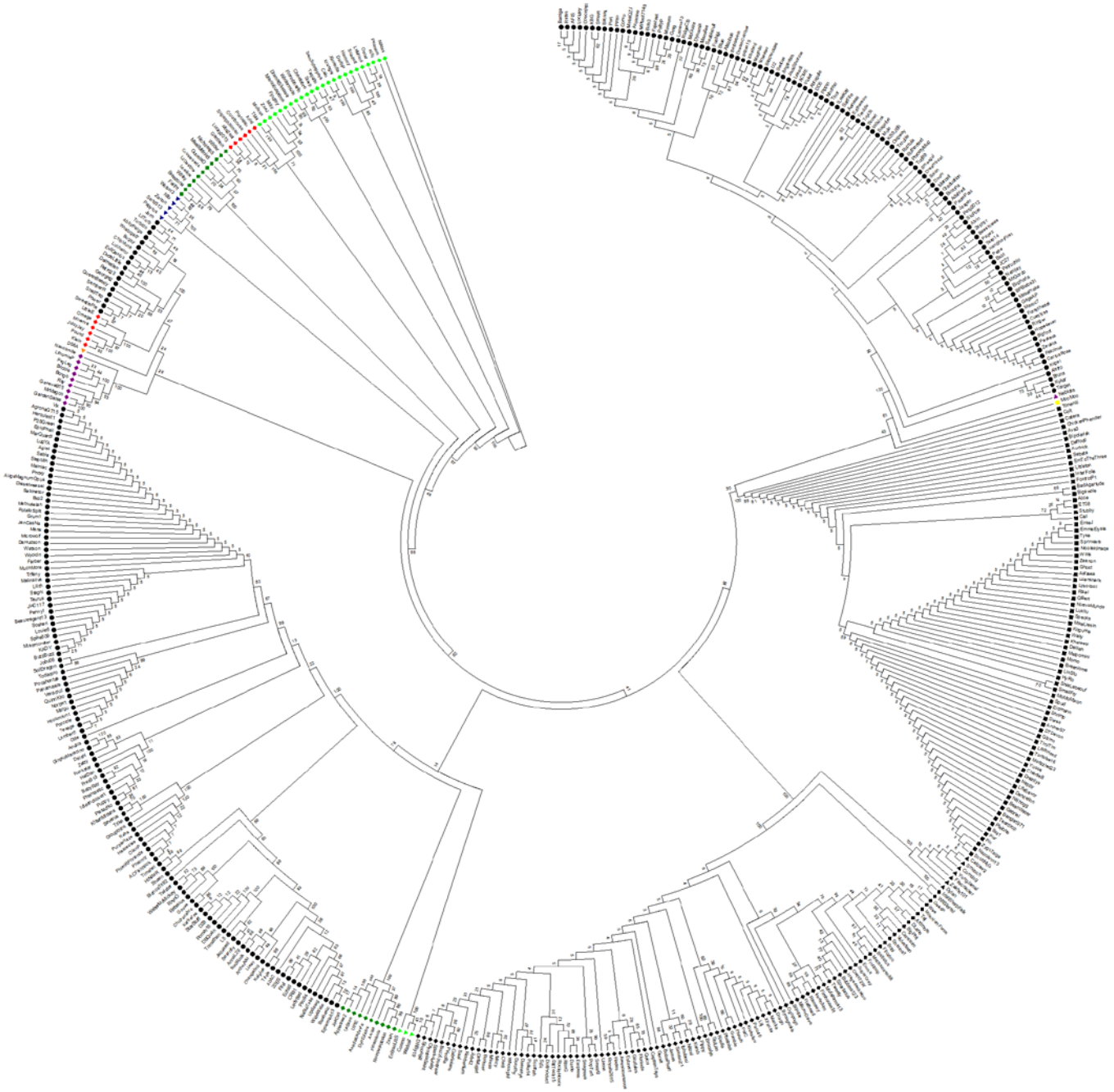

Fig. S3

vi)

gp34
DNA polymerase III

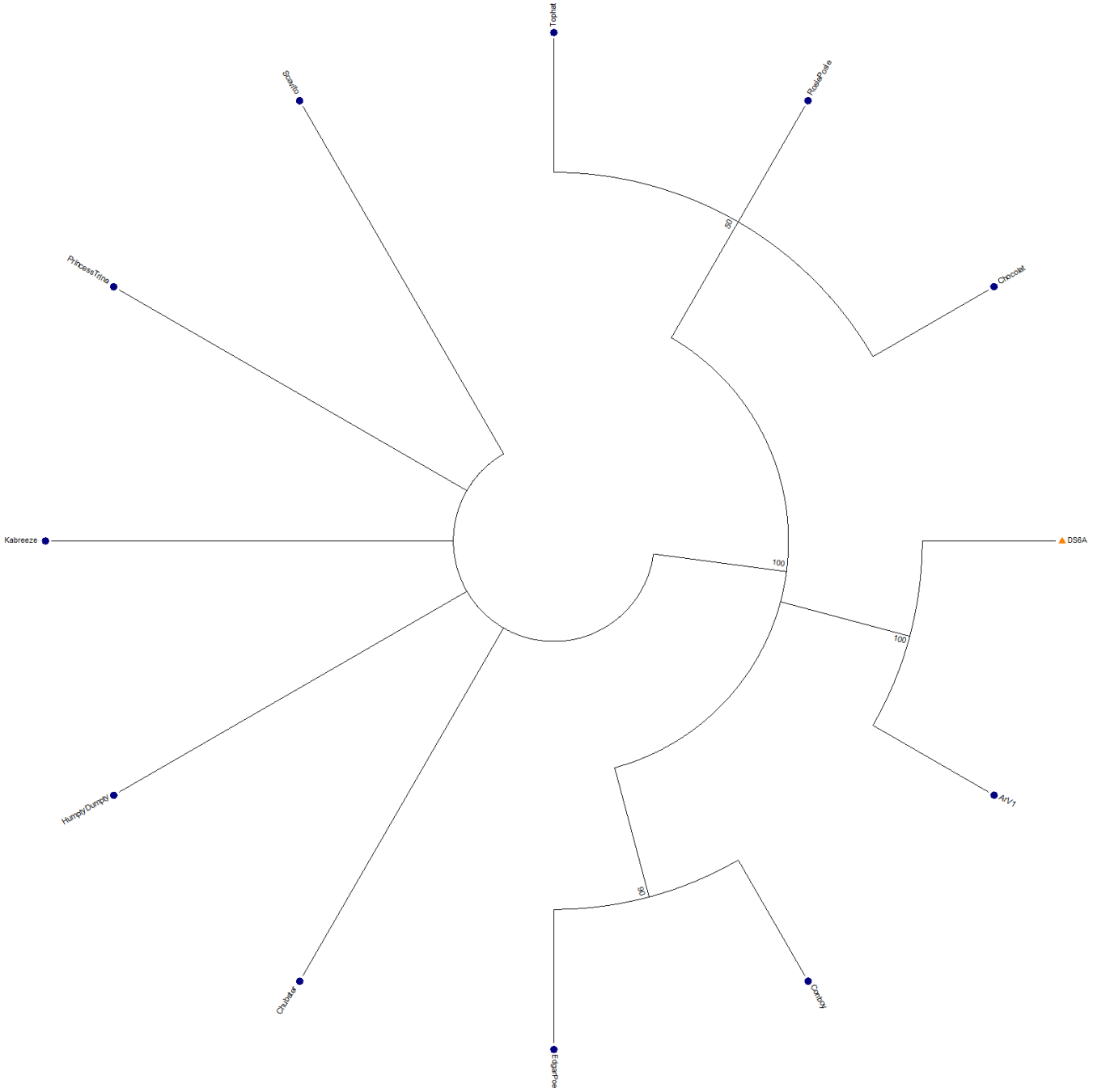

Fig. S3

vii)

gp56
Integrase

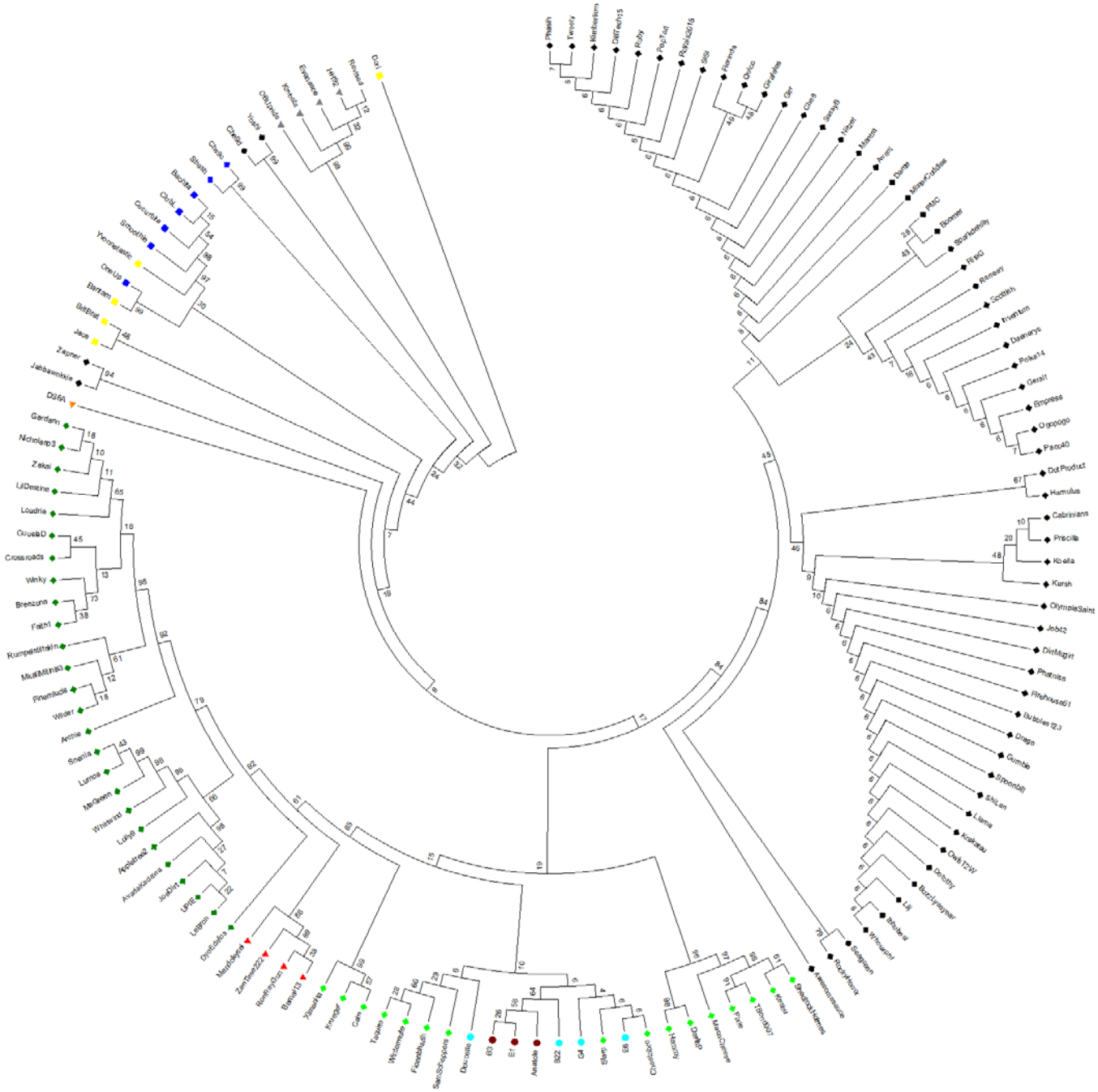

Fig. S3

viii)

gp70
MazG

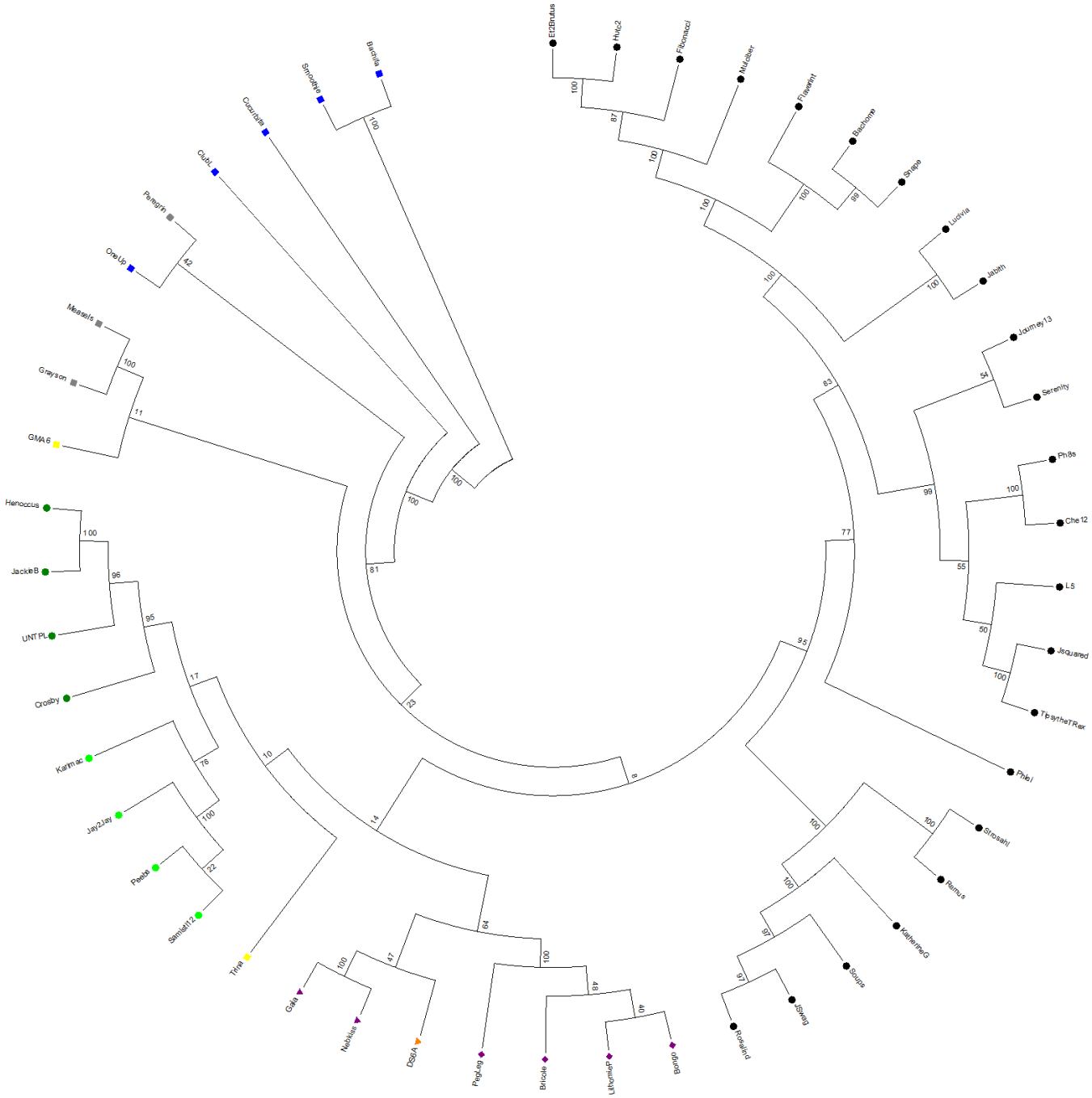

Fig. S3

ix)

gp77
Primase

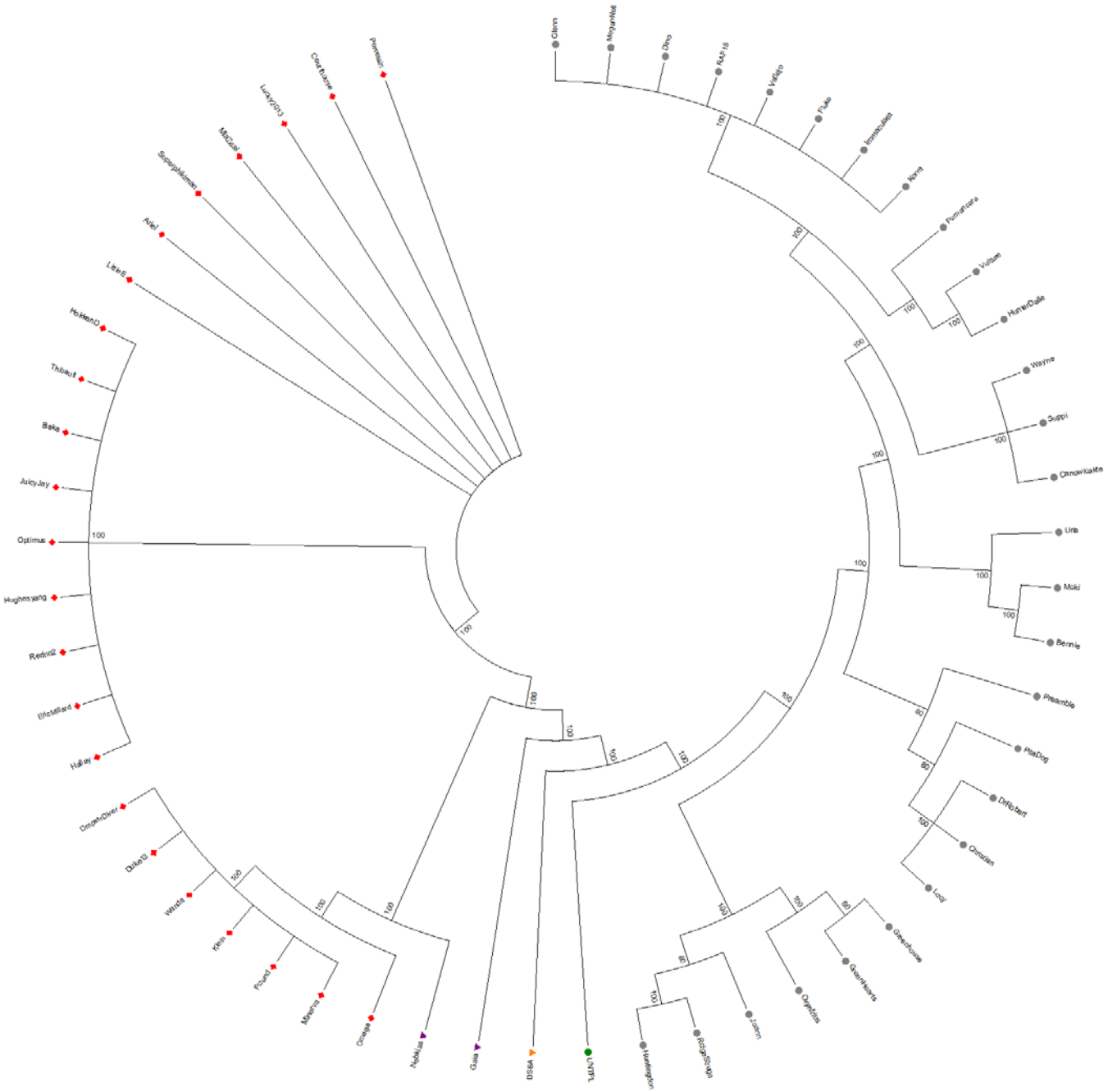

Fig. S3