Supplemental Figure Legends

Figure 1. Sequence alignment of the active site of GatE (red) with representative mitochondrial GatB (Pet112) (gold) as well as bacterial (blue) and archaeal (green) GatB sequences. The ▼ denotes the residues in the active site of the *Methanothermobacter thermautotrophicus* GatE shown to be important for catalysis. The coloring is based on sequence similarity using a BLOSUM 40 score. Numbering is of the *M. thermautotrophicus* GatE.

Figure 2. Sequence alignment of the C-terminus of archaeal GatE tail domains. The coloring is based on sequence similarity using a BLOSUM 50 score. Numbering is of the *Archaeoglobus fulgidus* (top) and *Thermoplasma volcanium* (bottom) enzymes.

Figure 3. Unrooted phylogenetic tree of the core of archaeal GatE (red) sequences with GatB sequences from bacterial (blue), archaeal (green) and eukaryotic (gold) sources. Representative bacterial and eukaryotic enzymes are shown. Only bootstrap values less than 90 are shown for clarity. The *Methanosarcina mazei* GatE was used as the outgroup for this reconstruction.

Figure 4. Rooted phylogenetic tree of the tail domain of archaeal GatE (red) sequences with GatB sequences from bacterial (blue) and archaeal (green) sources. Representative bacterial enzymes are shown. Only bootstrap values less than 90 are shown for clarity. YqeY sequences (black) served as the outgroup.

Figure 5. Rooted phylogenetic tree of the bacterial (cyan) and archaeal (green) type I L-asparaginases (AnsA), and archaeal GatD (red) sequences. Representative bacterial enzymes are shown. Only bootstrap values less than 90 are shown for clarity. Representative bacterial type II L-asparaginases (AnsB) were used as the outgroup (black) in this reconstruction.

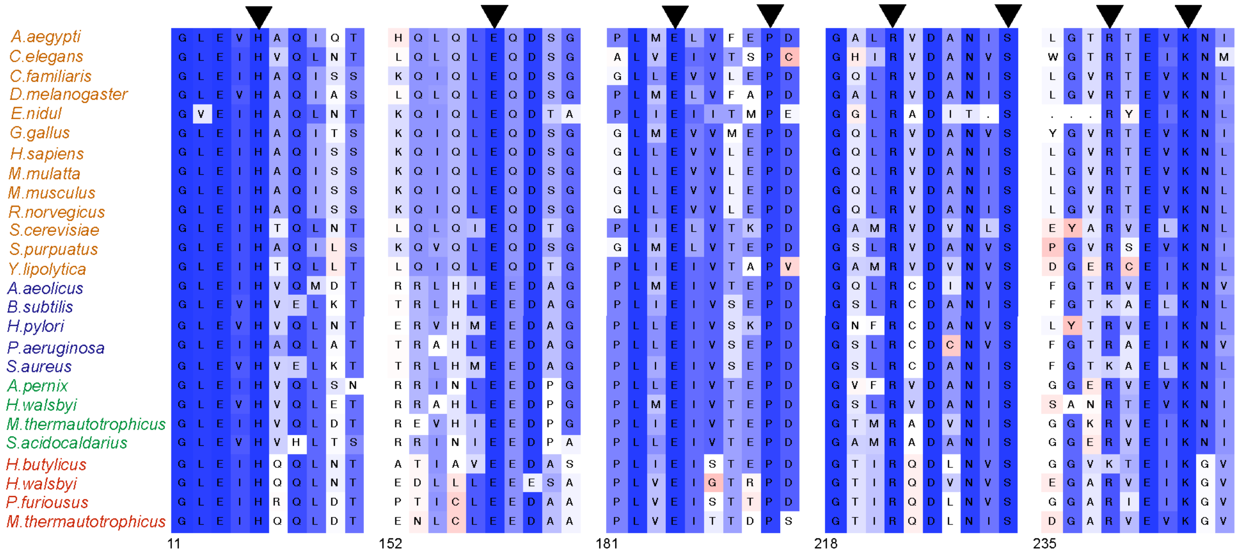
Figure 6. Unrooted phylogenetic tree of the bacterial GatA (blue) and archaeal GatA (green) sequences. Representative bacterial enzymes are shown. Only bootstrap values less than 90 are shown for clarity. The *Methanoseta thermophila* GatA was used as the outgroup for this reconstruction.

Figure 7. Unrooted phylogenetic tree of concatenated bacterial GatAB (blue) and archaeal GatAB (green) sequences. Representative bacterial enzymes are shown. Only bootstrap values less than 90 are shown for clarity. The *M. thermophila* GatAB was used as the outgroup for this reconstruction.

Figure 8. Unrooted phylogenetic tree of tRNA^{Gln} gene sequences from bacterial (blue), archaeal (green) and eukaryotic (gold) genomes. Representative tRNA genes are shown. Only bootstrap values less than 90 are shown for clarity.

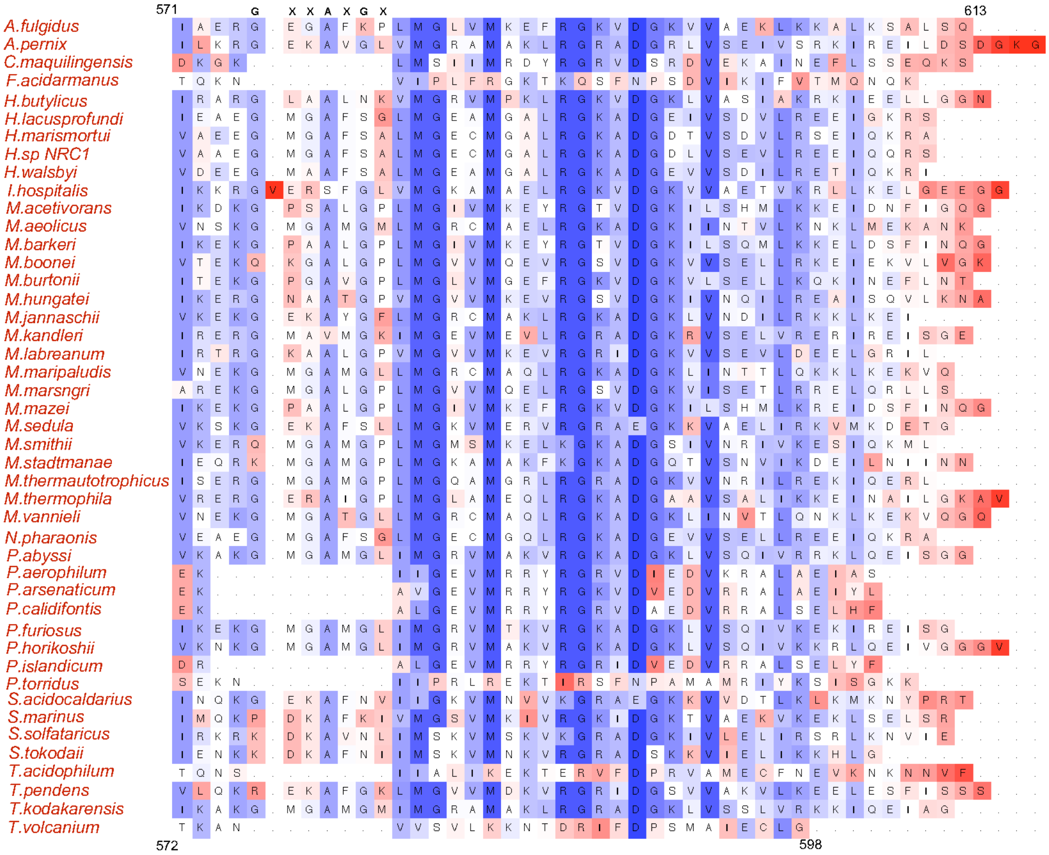
Figure 9. Unrooted phylogenetic tree of tRNA^{Asn} gene sequences from bacterial (blue), archaeal (green) and eukaryotic (gold) genomes. Representative tRNA genes are shown. Only bootstrap values less than 90 are shown for clarity.

Supplemental
Figure 1

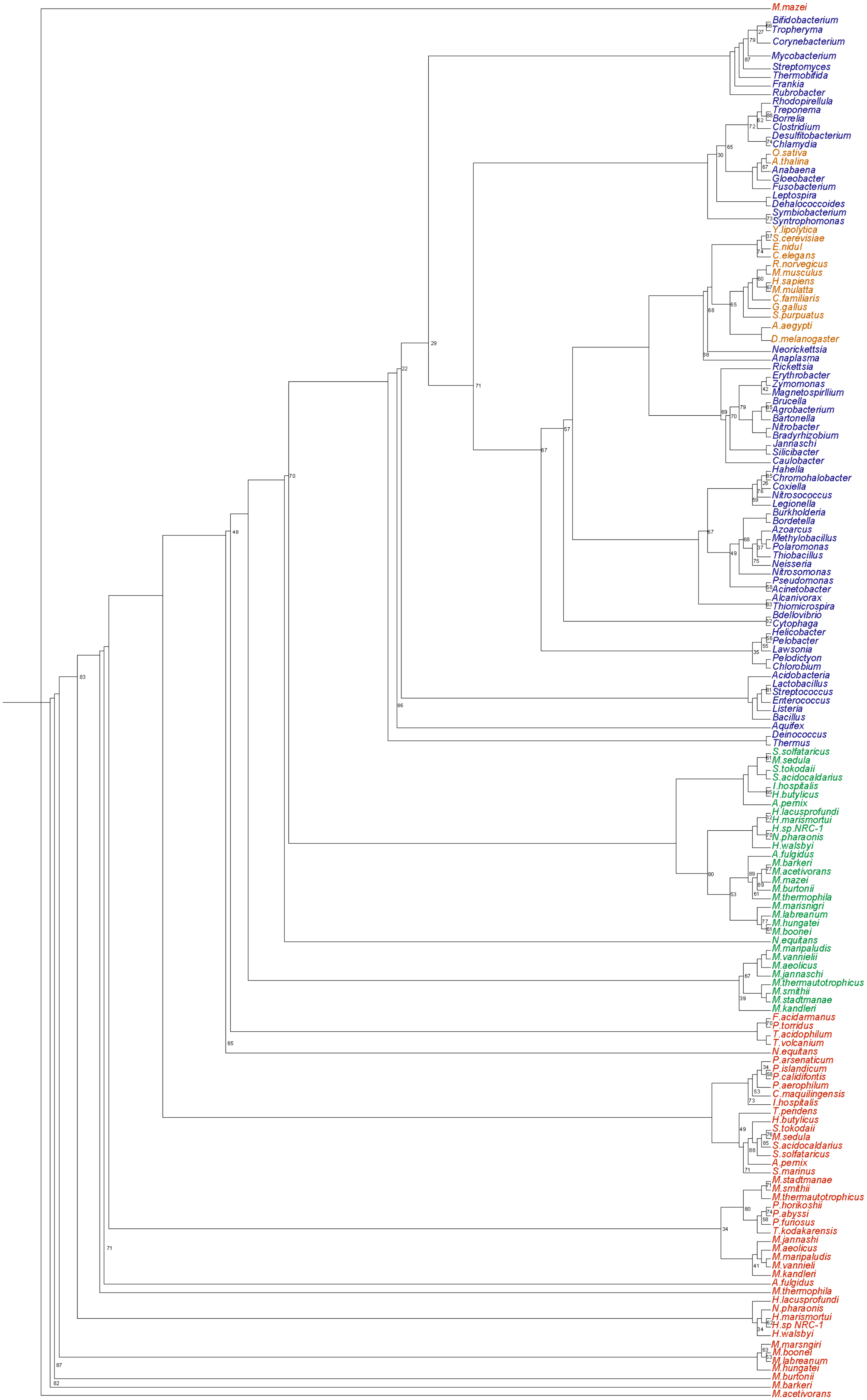


	11	152	181	218	235
A.aegypti	GLEVHAQIQT	HQLQLEQDSG	PLMELVFEPD	GALRVDANIS	LGTRTEVKNI
C.elegans	GLEIHVQLNT	LQLQLEQDSG	ALVEIVTSPC	GHIRVDANVS	WGTRTEIKNM
C.familiaris	GLEIHAQISS	KQIQLEQDSG	GLLEVVLEPD	GQLRVDANIS	LGVRTEVKNL
D.melanogaster	GLEVHAQIAS	LQLQLEQDSG	PLMELVFAPD	GALRVDANIS	LGVRTEVKNI
E.nidul	GVEIHAQLNT	KQIQLEQDTA	PLIEIITMPE	GGLRADIT.S	...RYEIKNL
G.gallus	GLEIHAQITS	KQIQLEQDSG	GLMEVVMEPD	GQLRVDANVS	YGVRTEVKNI
H.sapiens	GLEIHAQISS	KQIQLEQDSG	GLLEVVLEPD	GQLRVDANIS	LGVRTEVKNL
M.mulatta	GLEIHAQISS	KQIQLEQDSG	GLLEVVLEPD	GQLRVDANIS	LGVRTEVKNL
M.musculus	GLEIHAQISS	KQIQLEQDSG	GLLEVVLEPD	GQLRVDANIS	LGVRTEVKNL
R.norvegicus	GLEIHAQISS	KQIQLEQDSG	GLLEVVLEPD	GQLRVDANIS	LGVRTEVKNL
S.cerevisiae	GLEIHTQLNT	LQLQIEQDTG	PLIELVTKPD	GAMRVDVNLS	EYARVELKNL
S.purpuatus	GLEIHAQILS	KQVQLEQDSG	GLMELVTEPD	GSLRVDANVS	PGVRSEVKNI
Y.lipolytica	GLEIHTQLLT	LQIQLEQDTG	PLIEIVTAPV	GAMRVDVNVS	DGERCEIKNL
A.aeolicus	GLEIHVQMDT	RRLHIEEDAG	PLMEIVTEPD	GQLRCDINVS	FGTRVEIKNV
B.subtilis	GLEVHVELKT	TRLHLEEDAG	PLIEIVSEPD	GSLRCDANIS	FGTKAELKNL
H.pylori	GLEVHVQLNT	ERVHMEEDAG	PLLEIVSKPD	GNFRCDANVS	LYTRVEIKNL
P.aeruginosa	GLEIHAQLAT	TRAHLEEDAG	PLLEIVSEPD	GSLRCDCNVS	FGTRAEIKNV
S.aureus	GLEVHVELKT	TRLHMEEDAG	PLIEIVSEPD	GSLRCDANIS	FGTKAELKNL
A.pernix	GLEIHVQLSN	RRINLEEDPG	PLLEIVTEPD	GVFRVDANIS	GGERVEVKNI
H.walsbyi	GLEVHVQLET	RRAHLEEDPG	PLMEIVTEPD	GSLRVDANIS	SANRTEVKNI
M.thermautotrophicus	GLEIHVQLDT	REVHIEEDPG	PLIEIVTEPD	GTMRADVNIS	GGKRVEIKNI
S.acidocaldarius	GLEVHVHLTS	RRINIEEDPA	PLLEIVTEPD	GAMRADANIS	GGERVEIKNI
H.butylicus	GLEIHQQLNT	ATIAVEEDAS	PLIEISTEPD	GTIRQDLNVS	GGVKTEIKGV
H.walsbyi	GLEIHQQLNT	EDLLLEEESA	PLVEIGTRPD	GTIRQDVNVS	EGARVEIKGV
P.furiousus	GLEIHRQLDT	PTICLEEDAA	PLVEISTTPD	GTIRQDLNVS	GGARIEIKGV
M.thermautotrophicus	GLEIHQQLDT	ENLCLEEDAA	PLVEITTDPS	GTIRQDLNIS	DGARVEVKGV

Supplemental
Figure 2



Supplemental
Figure 3



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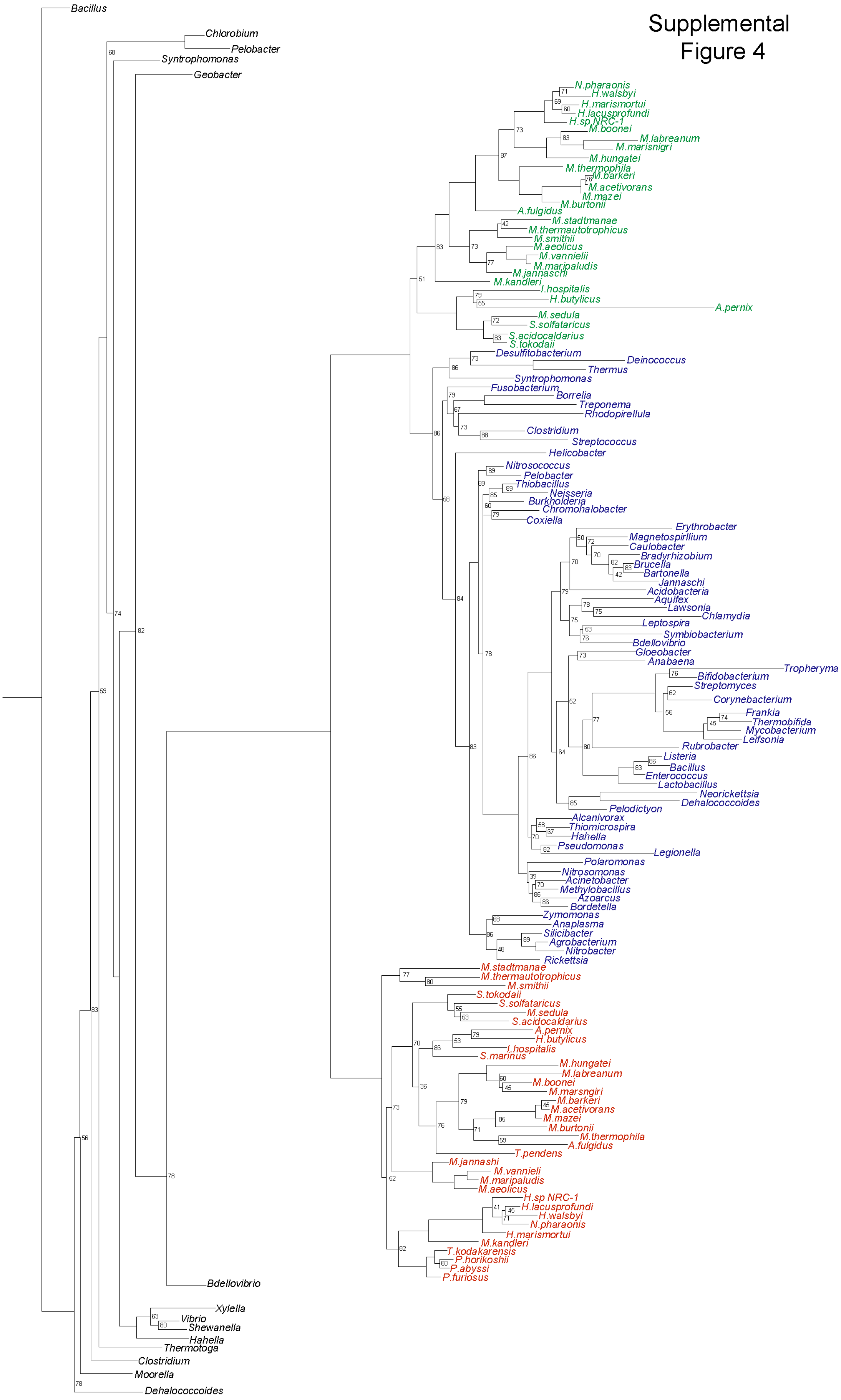
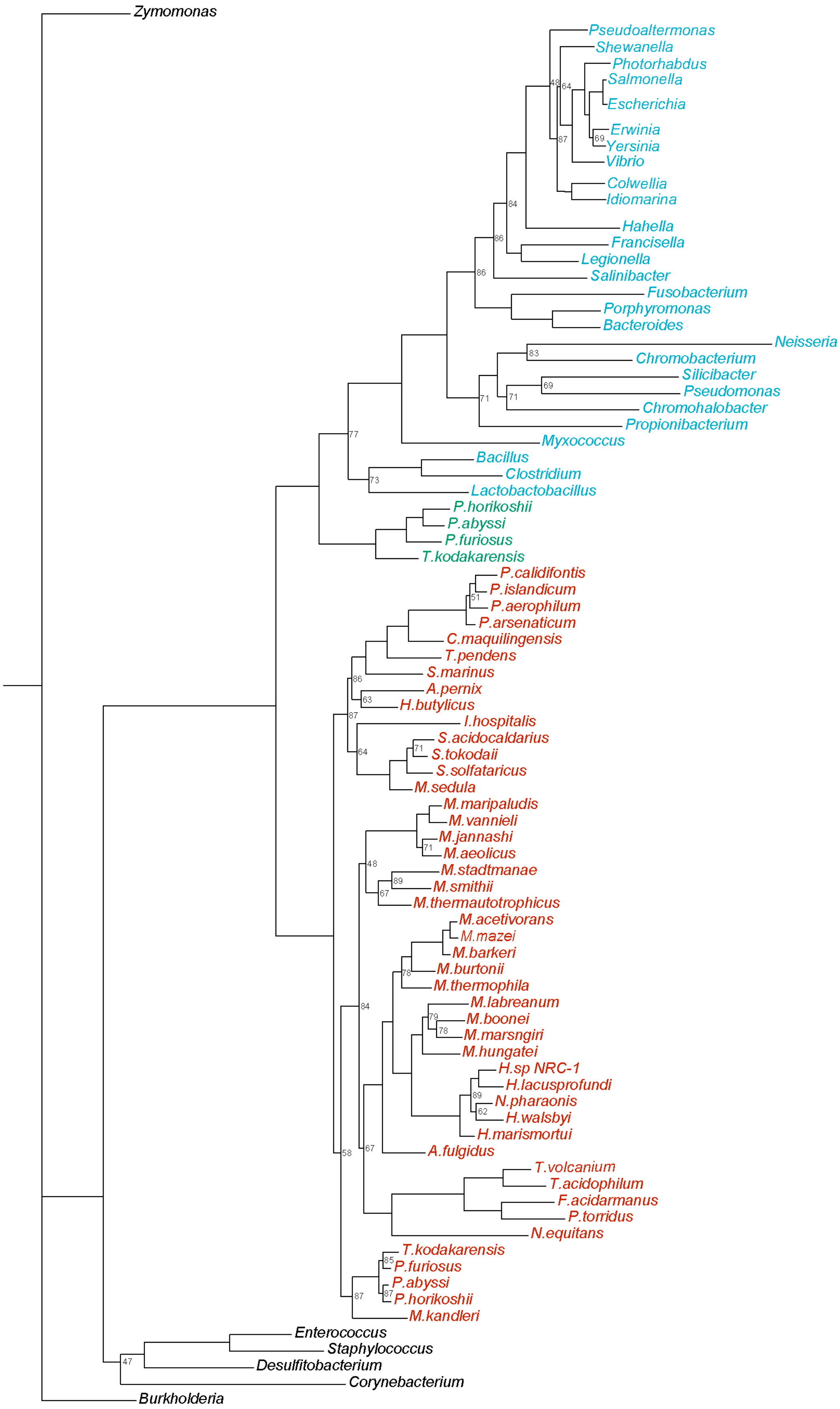
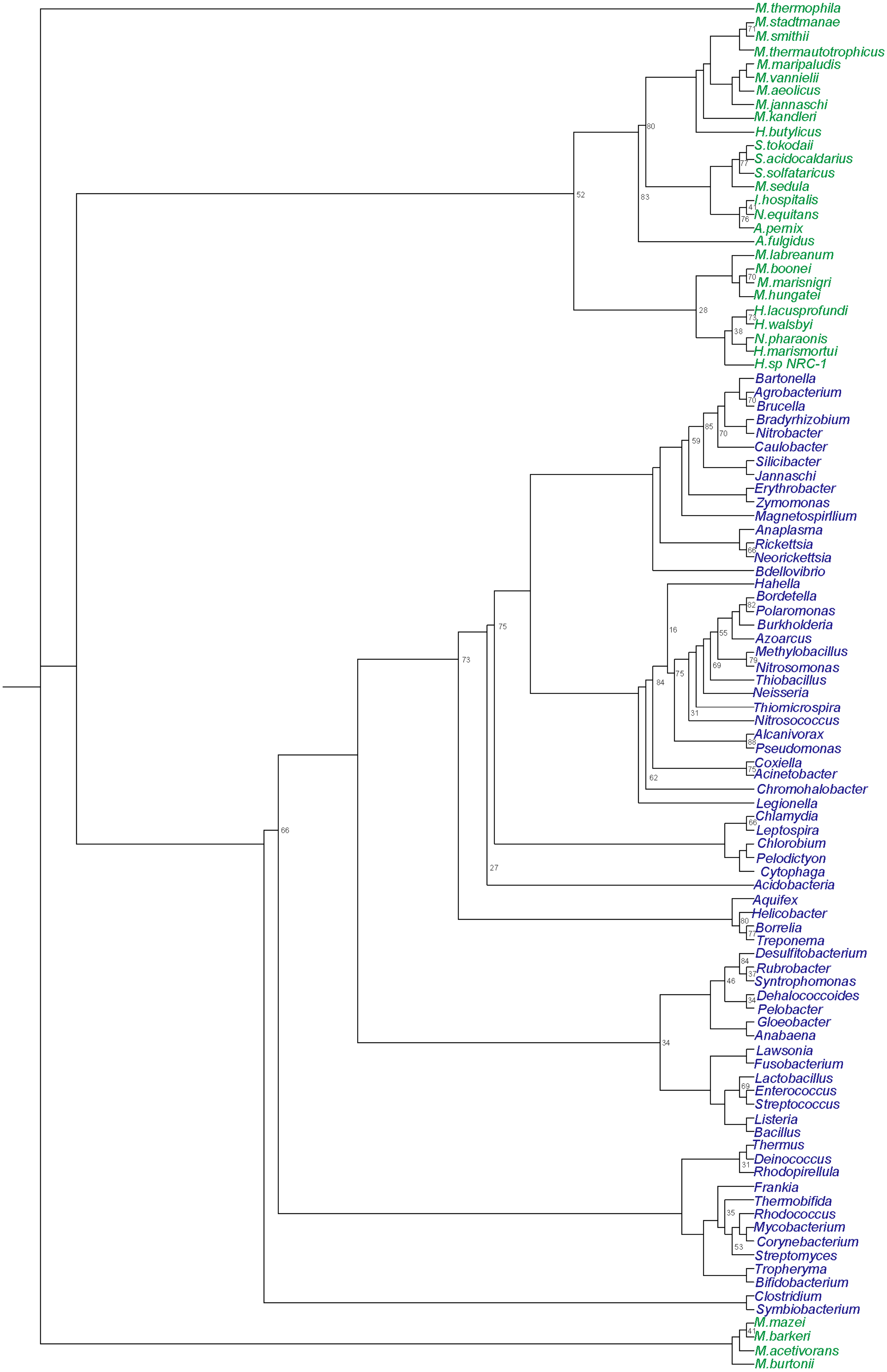


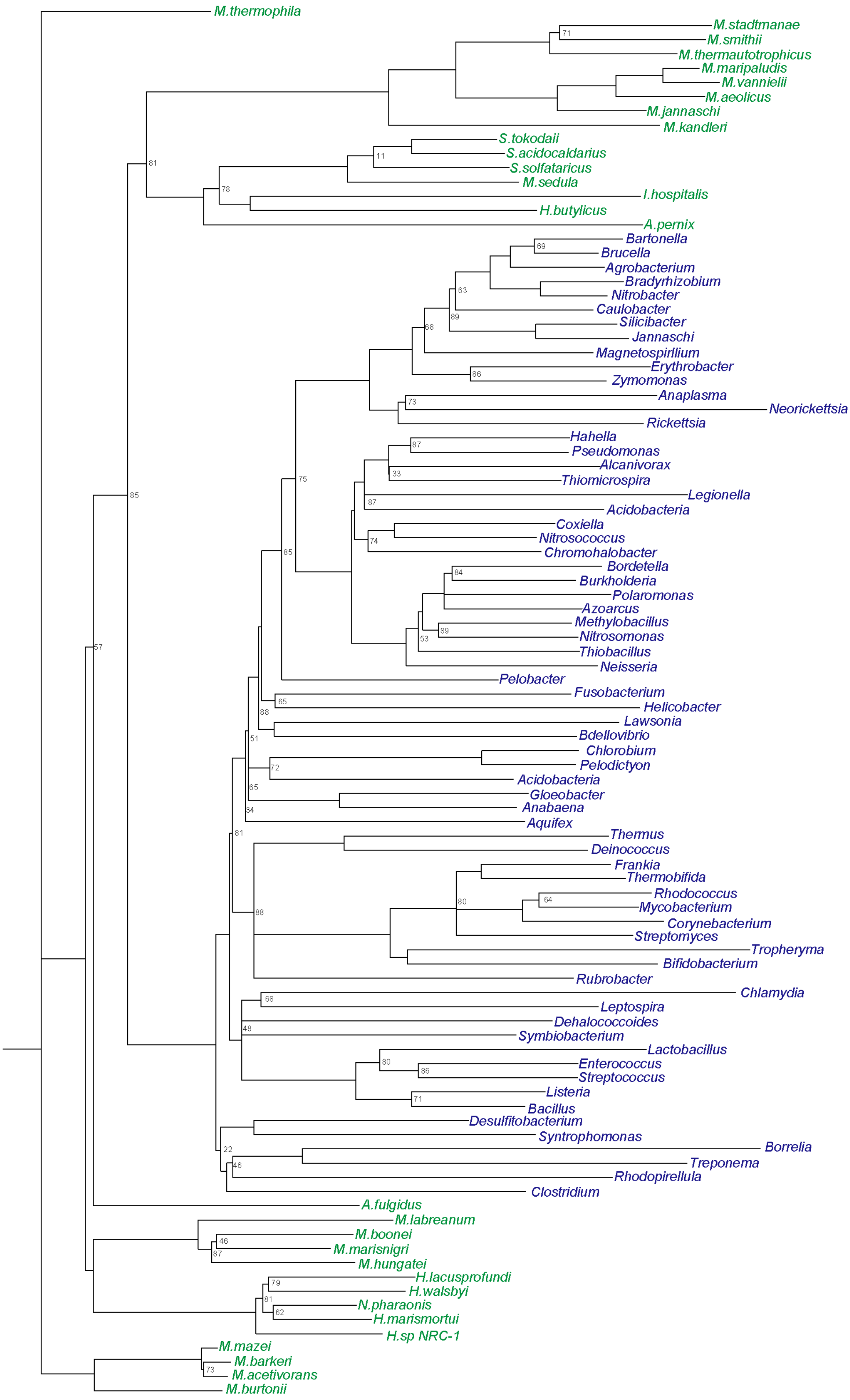
Supplemental Figure 5



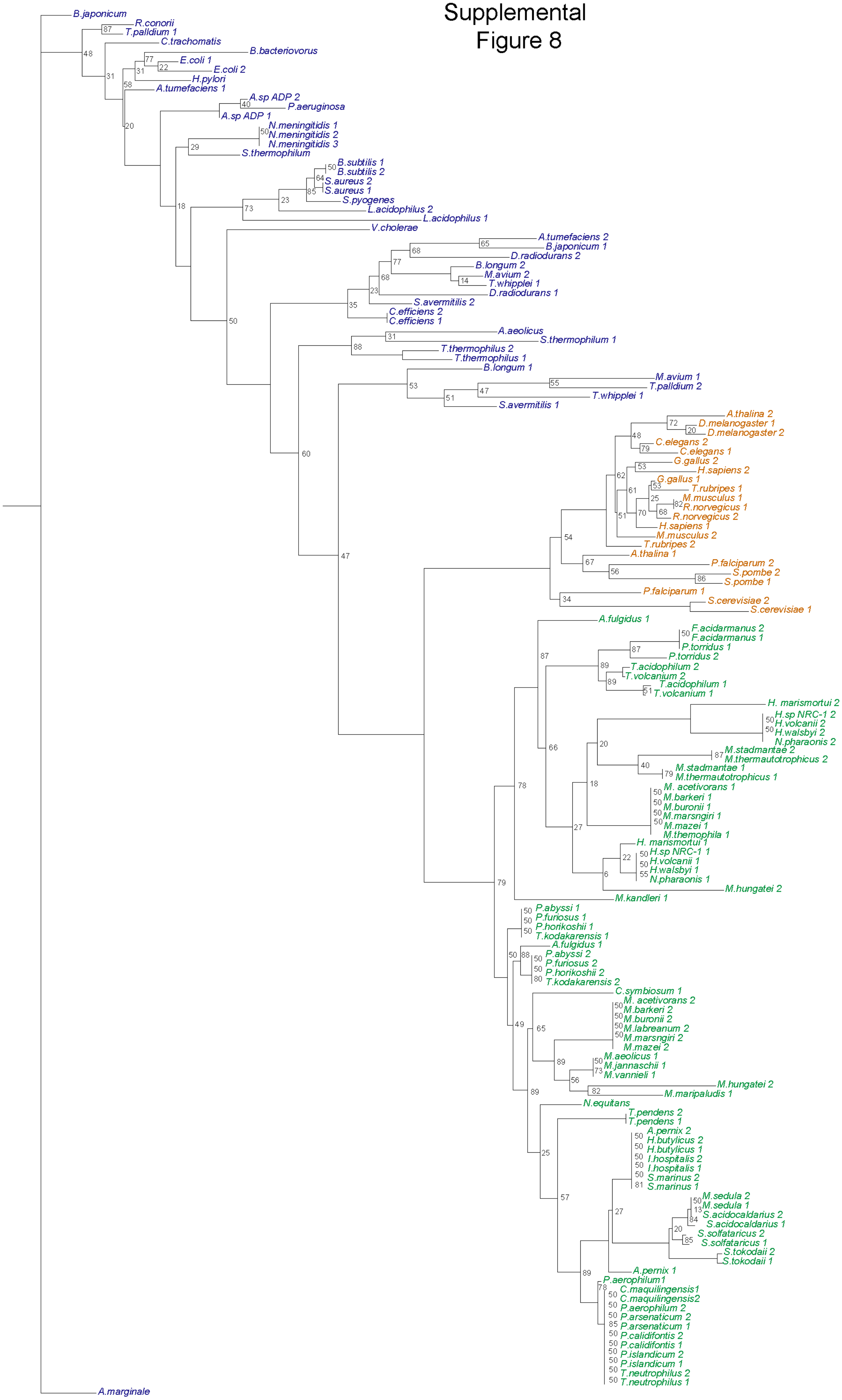
Supplemental
Figure 6



Supplemental Figure 7



Supplemental Figure 8



Supplemental Figure 9