

Supplementary Materials:

Phylogenomics provides new insights into gains and losses of selenoproteins among Archaeplastida

Hongping Liang^{1,2,3#}, Tong Wei^{2,3,4#}, Yan Xu^{1,2,3#}, Linzhou Li^{2,3,6}, Sunil Kumar Sahu^{2,3,4}, Hongli Wang^{1,2,3}, Haoyuan Li^{1,2}, Xian Fu^{2,3}, Gengyun Zhang^{2,4}, Michael Melkonian⁷, Xin Liu^{2,3,4}, Sibo Wang^{2,4,5*}, Huan Liu^{2,4,5}

¹ BGI Education Center, University of Chinese Academy of Sciences, Beijing, China.

² BGI-Shenzhen, Beishan Industrial Zone, Yantian District, Shenzhen 518083, China.

³ China National Gene Bank, Institute of New Agricultural Resources, BGI-Shenzhen, Jinsha Road, Shenzhen 518120, China.

⁴ State Key Laboratory of Agricultural Genomics, BGI-Shenzhen, Shenzhen 518083, China.

⁵ Department of Biology, University of Copenhagen, Copenhagen, Denmark.

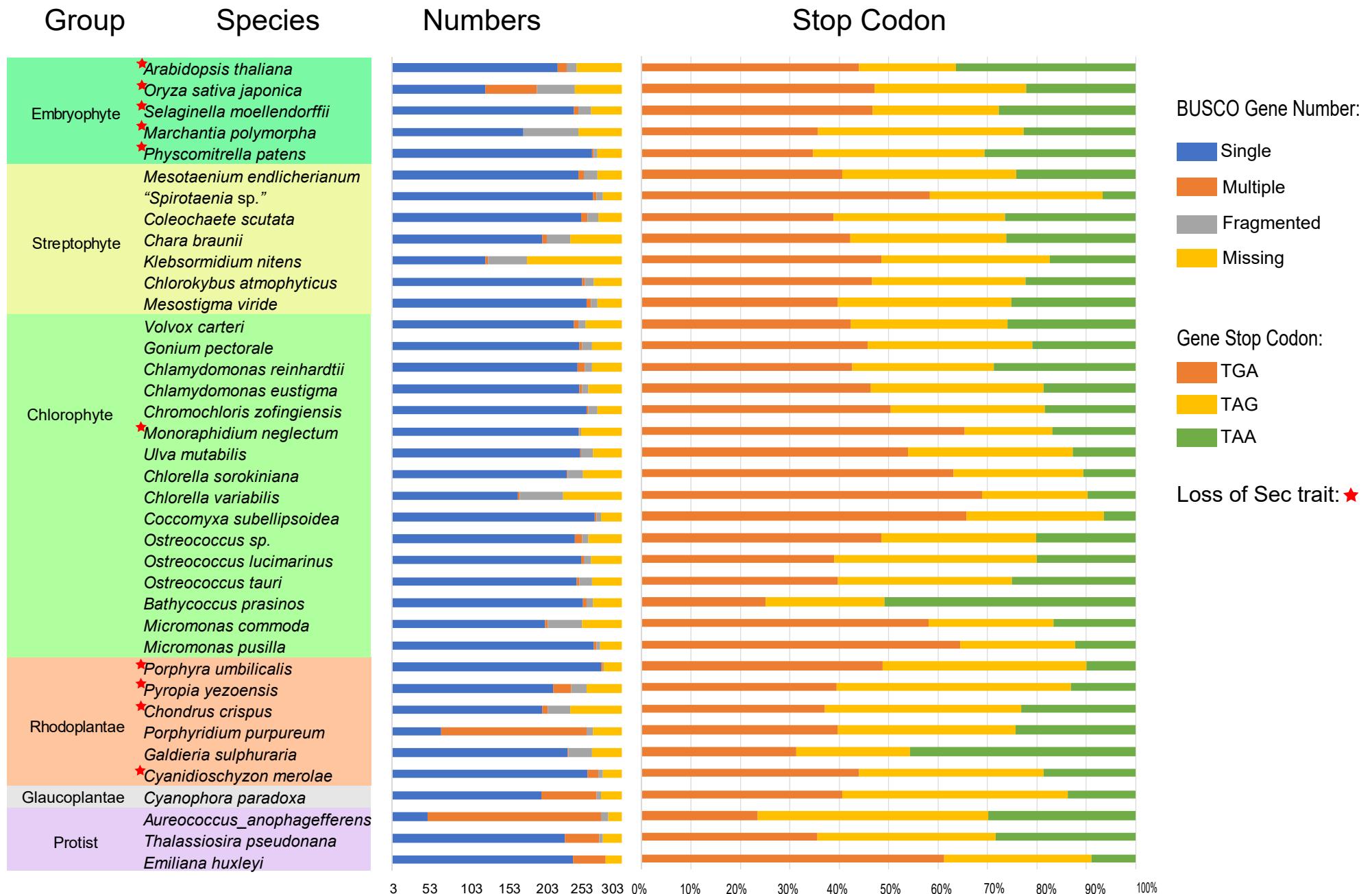
⁶ School of Biology and Biological Engineering, South China University of Technology, 510006, China.

⁷ Botanical Institute, Cologne Biocenter, University of Cologne, Cologne D-50674, Germany.

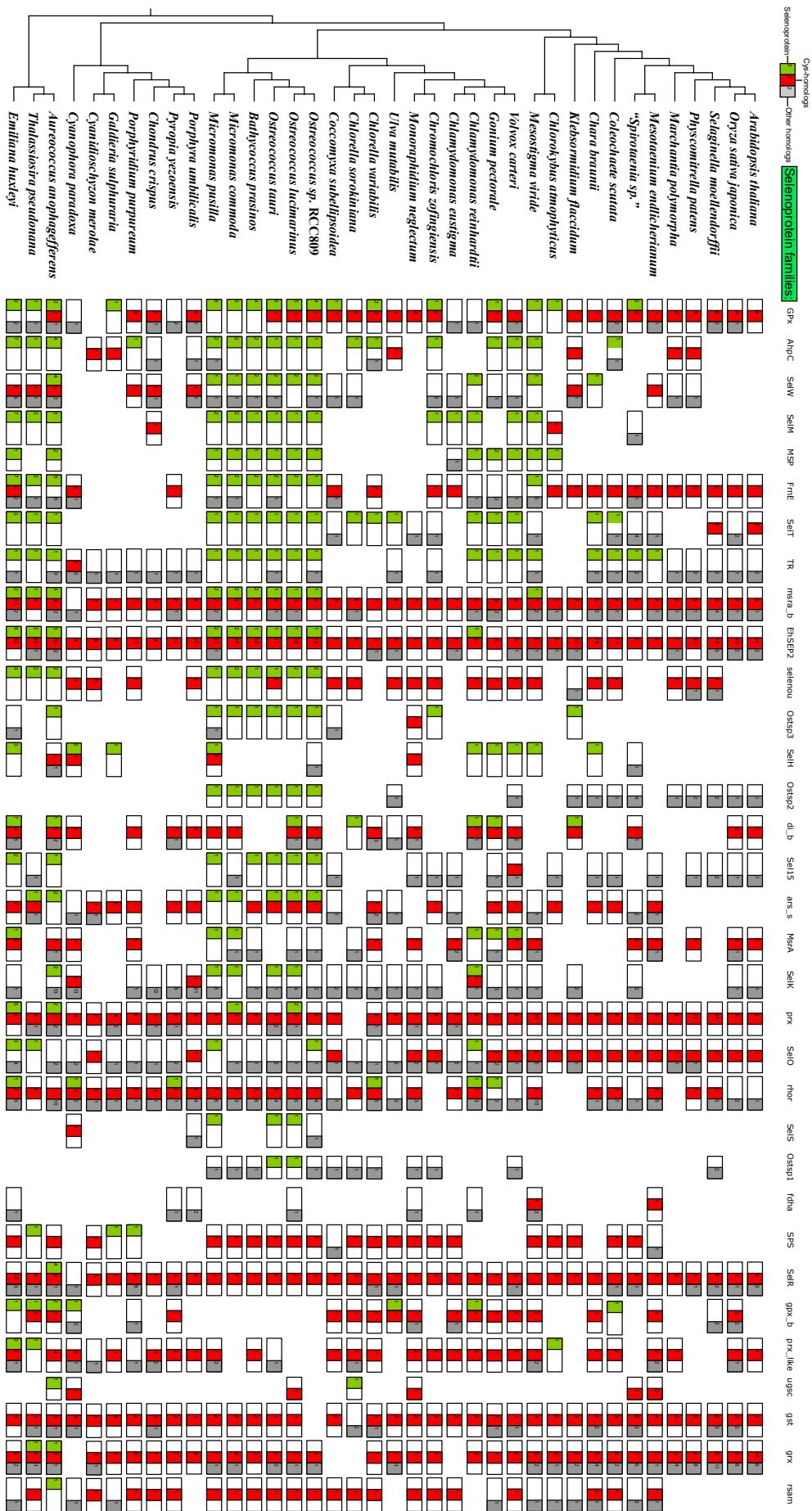
#these authors contributed equally to this work

* Correspondence: *liuhuan@genomics.cn

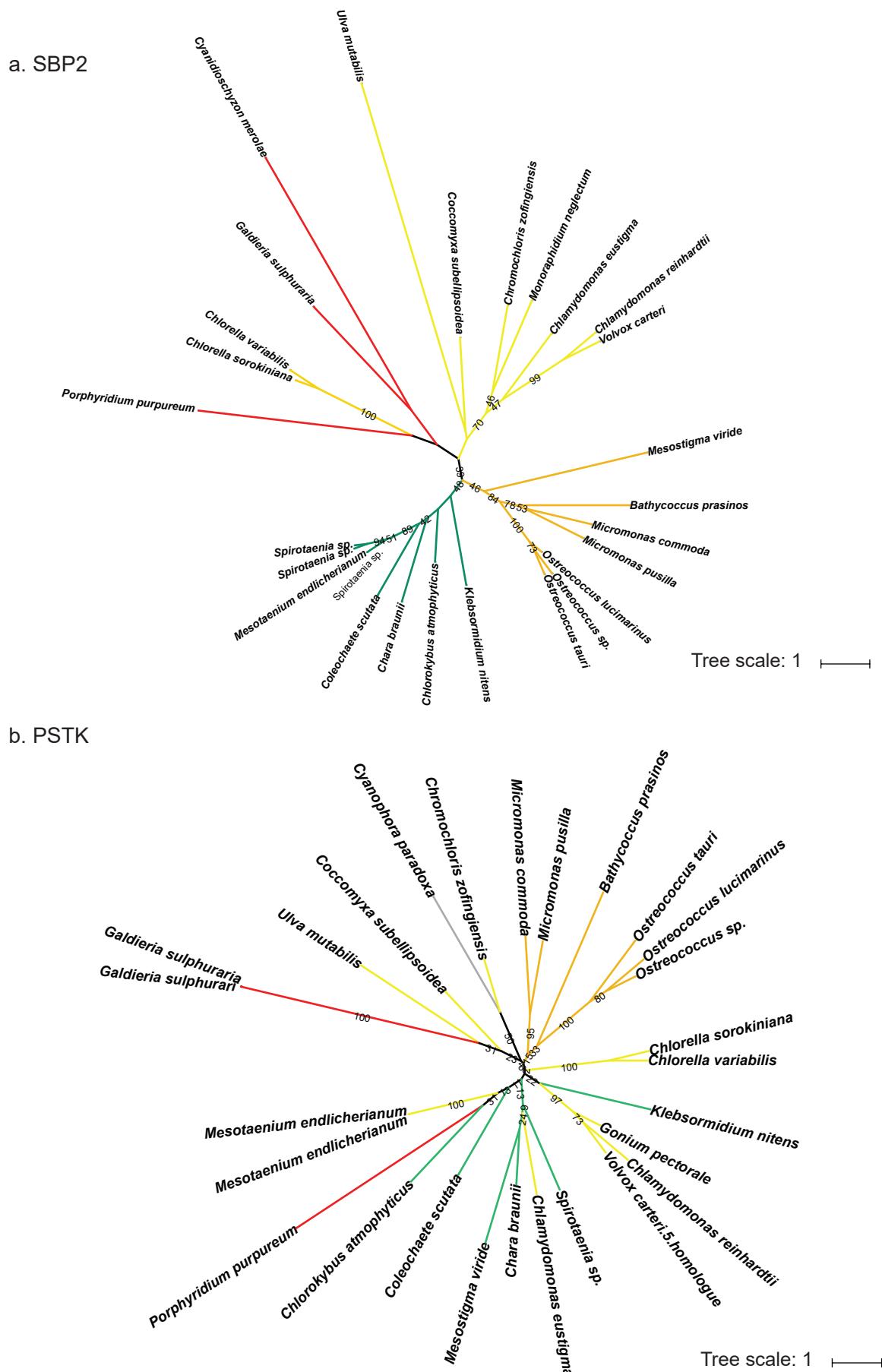
Supplementary Figure S1: Completeness of genome assemblies and Stop codon statistics. The genome quality was assessed by the BUSCO program. The number of single, multiple, missing and fragmented genes are shown in the middle histogram. The stop codon usage of genes is shown on the right histograms. The species that lost the Sec machinery are marked with an asterisk in the tree. Each group was colored in different background in the left column.



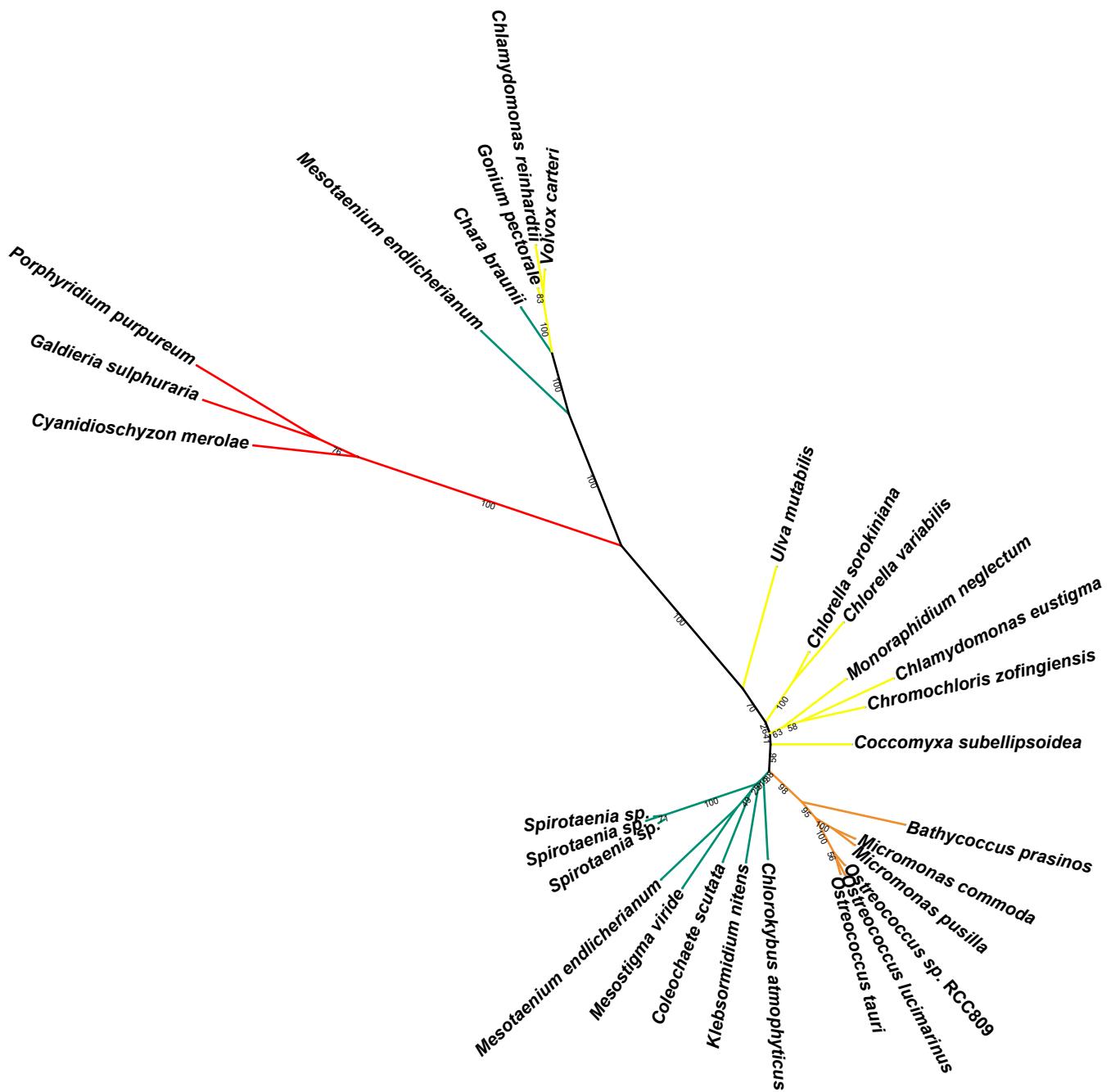
Supplementary Figure S2: Species tree with families of selenoproteins and homologues (Cys) by Selenoprofiles. Each column corresponds to a selenoprotein family plotted in different color to distinguish Sec-containing (green), Cys homologues (red), and others (grey). 33 out of 62 selenoproteins families having at least one Sec -containing gene were selected for the analysis. The number in the left box represents the number of selenoproteins.



Supplementary Figure S3: The phylogenetic tree of SBP2, PSTK and SPS. All the predicted candidates were used to reconstruct a maximum-likelihood tree, with 500 bootstrap replicates. Here, Orange: Mamiellophyceae; Yellow: core Chlorophyta; Green: Streptophyte algae; Red: Rhodoplantae; and Grey: Glaucophytaceae.

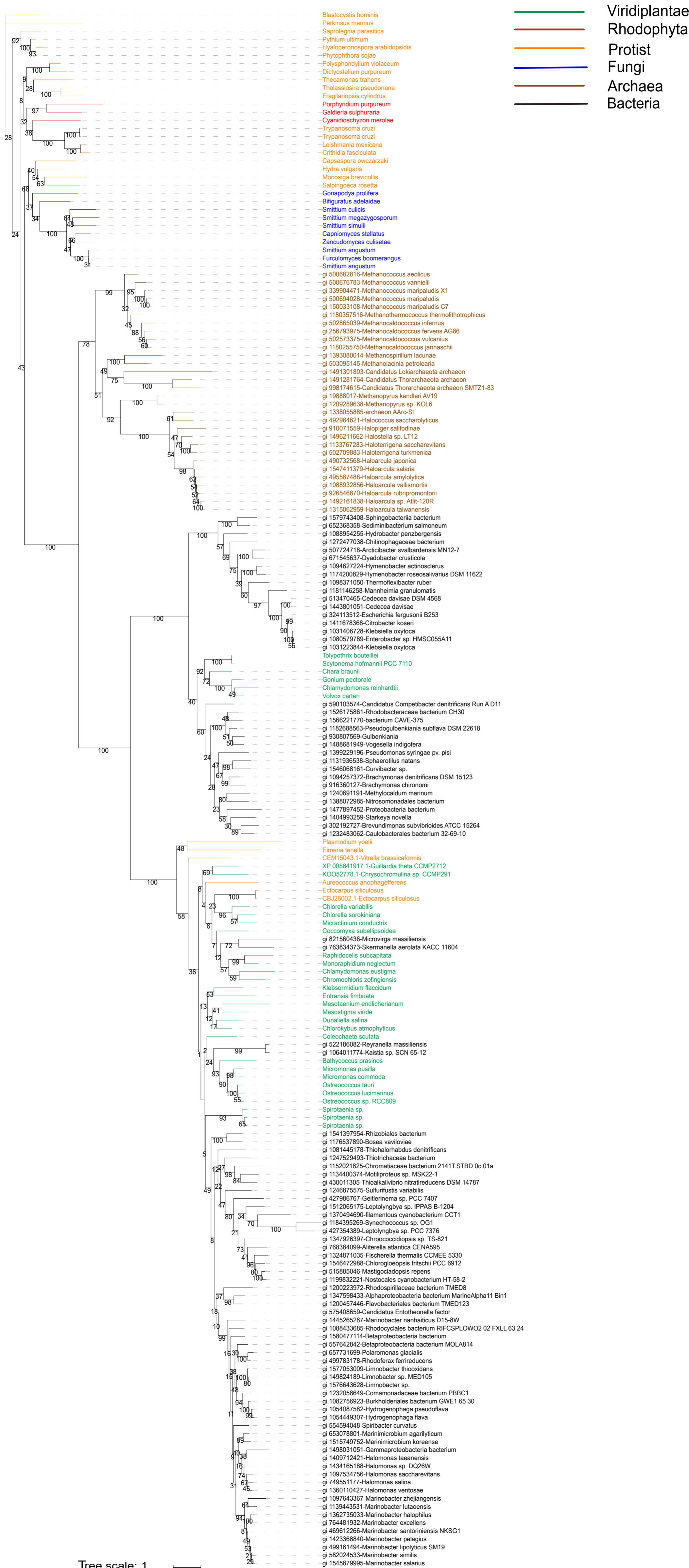


c. SPS

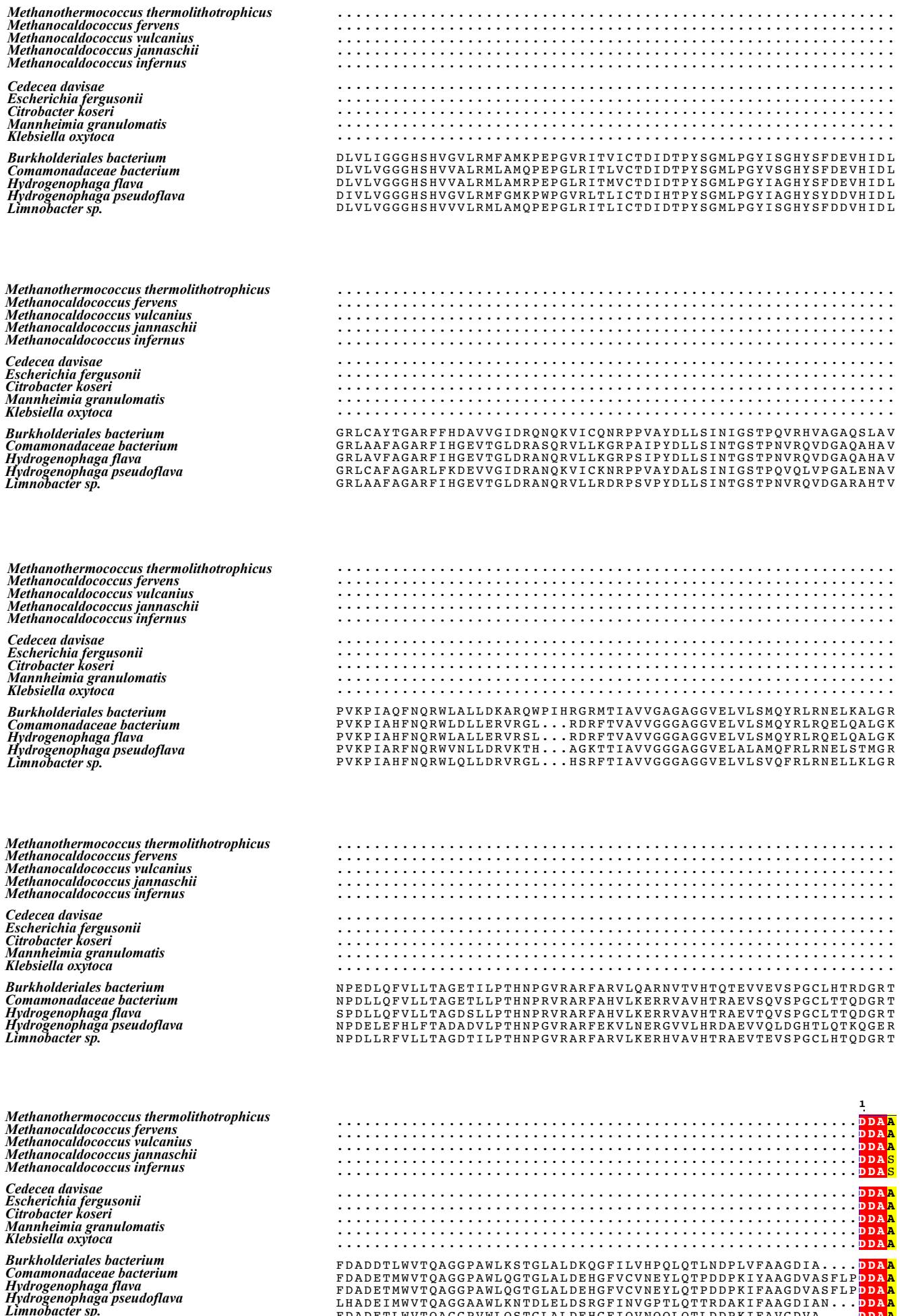


Tree scale: 1

Supplementary Figure S4: The phylogenetic tree of SPS. The maximum-likelihood tree by using the reference set of SPS proteins was reconstructed using the GTR+I+G model.



Supplementary Figure S5: The alignment of the SPS domain. The complement alignment of SPS domains in the three clades. Nucleotide conservation is indicated with red and yellow coloring. The three clades are separated by spaces. From top to bottom, they are clade III, clade II and clade I.



	170	180	190	200	210	220
<i>Methanothermococcus thermolithotrophicus</i>	D	I	L	T	K	A
<i>Methanocaldococcus fervens</i>	I	G	A	K	E	I
<i>Methanocaldococcus vulcanius</i>	G	V	L	I	T	K
<i>Methanocaldococcus jannaschii</i>	V	L	K	P	L	T
<i>Methanocaldococcus infernus</i>	V	L	K	P	L	T
<i>Cedecea davisae</i>	R	V	K	N	S	T
<i>Escherichia fergusonii</i>	V	K	N	S	A	T
<i>Citrobacter koseri</i>	V	K	N	S	A	T
<i>Mannheimia granulomatis</i>	V	K	N	S	A	T
<i>Klebsiella oxytoca</i>	V	K	N	S	A	T
<i>Burkholderiales bacterium</i>	G	V	M	L	P	G
<i>Comamonadaceae bacterium</i>	S	V	M	Q	D	V
<i>Hydrogenophaga flava</i>	S	V	M	Q	D	V
<i>Hydrogenophaga pseudoflava</i>	S	V	M	Q	D	V
<i>Limnobacter sp.</i>	S	V	M	Q	D	V
	230	240	250	260	270	280
<i>Methanothermococcus thermolithotrophicus</i>	N	R	K	A	L	I
<i>Methanocaldococcus fervens</i>	R	Y	A	M	A	T
<i>Methanocaldococcus vulcanius</i>	R	Y	A	M	A	T
<i>Methanocaldococcus jannaschii</i>	R	Y	A	M	A	T
<i>Methanocaldococcus infernus</i>	R	Y	A	M	A	T
<i>Cedecea davisae</i>	N	K	V	G	T	A
<i>Escherichia fergusonii</i>	N	I	A	G	S	F
<i>Citrobacter koseri</i>	N	I	A	G	S	F
<i>Mannheimia granulomatis</i>	N	I	A	G	S	F
<i>Klebsiella oxytoca</i>	N	I	A	G	S	F
<i>Burkholderiales bacterium</i>	N	O	A	G	Q	I
<i>Comamonadaceae bacterium</i>	N	O	S	G	A	O
<i>Hydrogenophaga flava</i>	N	O	A	G	A	O
<i>Hydrogenophaga pseudoflava</i>	N	O	A	G	A	O
<i>Limnobacter sp.</i>	N	R	L	G	A	Q
	290	300	310			
<i>Methanothermococcus thermolithotrophicus</i>	R	L	S	M		
<i>Methanocaldococcus fervens</i>	E	L	S	R		
<i>Methanocaldococcus vulcanius</i>	E	L	S	R		
<i>Methanocaldococcus jannaschii</i>	E	L	S	R		
<i>Methanocaldococcus infernus</i>	E	L	S	R		
<i>Cedecea davisae</i>	S	Y	I	E		
<i>Escherichia fergusonii</i>	S	Y	I	E		
<i>Citrobacter koseri</i>	S	Y	I	E		
<i>Mannheimia granulomatis</i>	S	Y	I	E		
<i>Klebsiella oxytoca</i>	S	Y	I	E		
<i>Burkholderiales bacterium</i>	E	C	V	E		
<i>Comamonadaceae bacterium</i>	D	C	V	A		
<i>Hydrogenophaga flava</i>	E	C	V	A		
<i>Hydrogenophaga pseudoflava</i>	D	C	V	A		
<i>Limnobacter sp.</i>	D	M	V	S		
	320	330	340	350		
<i>Methanothermococcus thermolithotrophicus</i>	E	E	L	Q		
<i>Methanocaldococcus fervens</i>	E	E	L	Q		
<i>Methanocaldococcus vulcanius</i>	E	E	L	Q		
<i>Methanocaldococcus jannaschii</i>	E	E	L	Q		
<i>Methanocaldococcus infernus</i>	E	E	L	Q		
<i>Cedecea davisae</i>	A	A	V	E		
<i>Escherichia fergusonii</i>	A	A	V	E		
<i>Citrobacter koseri</i>	A	A	V	E		
<i>Mannheimia granulomatis</i>	A	A	V	E		
<i>Klebsiella oxytoca</i>	A	A	V	E		
<i>Burkholderiales bacterium</i>	B	R	A	K		
<i>Comamonadaceae bacterium</i>	B	R	A	K		
<i>Hydrogenophaga flava</i>	B	R	A	K		
<i>Hydrogenophaga pseudoflava</i>	B	R	A	K		
<i>Limnobacter sp.</i>	B	R	A	K		