Supplemental Material

Li et al. “Ultrastructural and single-cell level characterization reveals metabolic versatility in a microbial eukaryote community from an ice-covered Antarctic lake”

Supplemental Figure Legends

Figure S1. Confocal microscopic images of *Isochrysis sp.* MDV isolates without LysoTracker Green staining. a. green channel; b, DIC image; c, chlorophyll autofluorescence; d, overlays of a – c. Bars indicate 5 µm.

Figure S2. Confocal microscopic images of *Chlamydomonas sp.* ICE-MDV isolates without LysoTracker Green staining. a. green channel; b, DIC image; c, chlorophyll autofluorescence; d, overlays of a – c. Bars indicate 5 µm.

Figure S3. Heat map of communities associated with sorted eukaryotic organisms based on 16s rRNA sequence abundance. 16s OTUS were identified to phylum level. Color code on the left indicates the abundance of sequence of each phylum. Color code on the right side represent high chlorophyll autofluorescence (red), high LysoTracker fluorescence (green) or intermediate of either (blue) of the eukaryotic organisms. The communities associated with heterotrophic organisms were predominated by chloroplasts of phytoplankton (blue box), indicating that they were the potential prey of the heterotrophic eukaryotes.

Table S1. Basic growth physiology of *Chlamydomonas* sp. ICE-MDV and *Isochrysis* sp. MDV isolates.

Organism	**Growth Media**	**Growth Temperature Range (°C)**	**Growth Irradiance Range (µmol m^{-2} s^{-1})**	**Organic Carbon**
***Chlamydomonas* sp. ICE-MDV**	Bolds	2 - 15	5 - 500	None
***Isochrysis* sp. MDV**	L1/2, f/2	2 - 10	0 - 50	cereal grass, rice, yeast extract

Table S2. Diversity of major algal classes in Lake Bonney enrichment cultures. Algal diversity was determined by spectral chlorophyll a fluorescence (bbe FluoroProbe). Enrichment used in this study is highlighted.

Enrichment Name	**Lake**	**Depth (m)**	**Medium**	**Algal Class (µg Chl a L^{-1})**			
				Green	***Cyano***	***Hapto***	***Crypto***
73.1	ELB	6	F/2	58.90	0.00	5.78	1.38
74.1	ELB	6	DYV	21.33	0.25	0.00	3.09
75.1	ELB	6	BBM	26.06	0.35	2.00	0.00
76.1	ELB	6	F/2	26.00	0.16	1.32	1.17
77.1	ELB	6	10% DYV	46.04	0.00	0.00	1.13
78.1	ELB	6	BBM	17.98	0.26	0.00	1.08
79.1	ELB	6	F/2	22.01	0.34	1.32	0.00
80.1	ELB	6	DYV	18.30	0.36	0.00	4.73
81.1	ELB	6	10% BBM	48.34	0.00	5.44	1.80
82.1	ELB	6	10% F/2	29.81	0.00	2.07	1.40
83.1	ELB	6	10% DYV	34.04	0.00	0.00	1.17
84.1	ELB	13	BBM	51.53	0.00	19.88	1.12
85.1	ELB	13	F/2	47.35	0.00	38.76	0.89
86.1	ELB	13	DYV	125.29	0.00	43.31	0.00
87.1	ELB	13	10% F/2	60.43	0.00	46.42	6.41
88.1	ELB	13	10% BBM	25.53	0.00	12.49	0.21
89.1	ELB	13	10% DYV	20.67	0.00	18.86	0.12
90.1	ELB	13	BBM	85.55	0.00	22.05	0.00
91.1	ELB	13	F/2	68.49	0.00	137.60	1.04
92.1	ELB	13	DYV	42.25	0.00	0.59	0.44
93.1	ELB	13	10% BBM	37.90	0.00	20.13	0.85
94.1	ELB	13	10% F/2	16.77	0.00	12.63	0.00
95.1	ELB	13	10% DYV	6.68	0.00	6.04	0.16

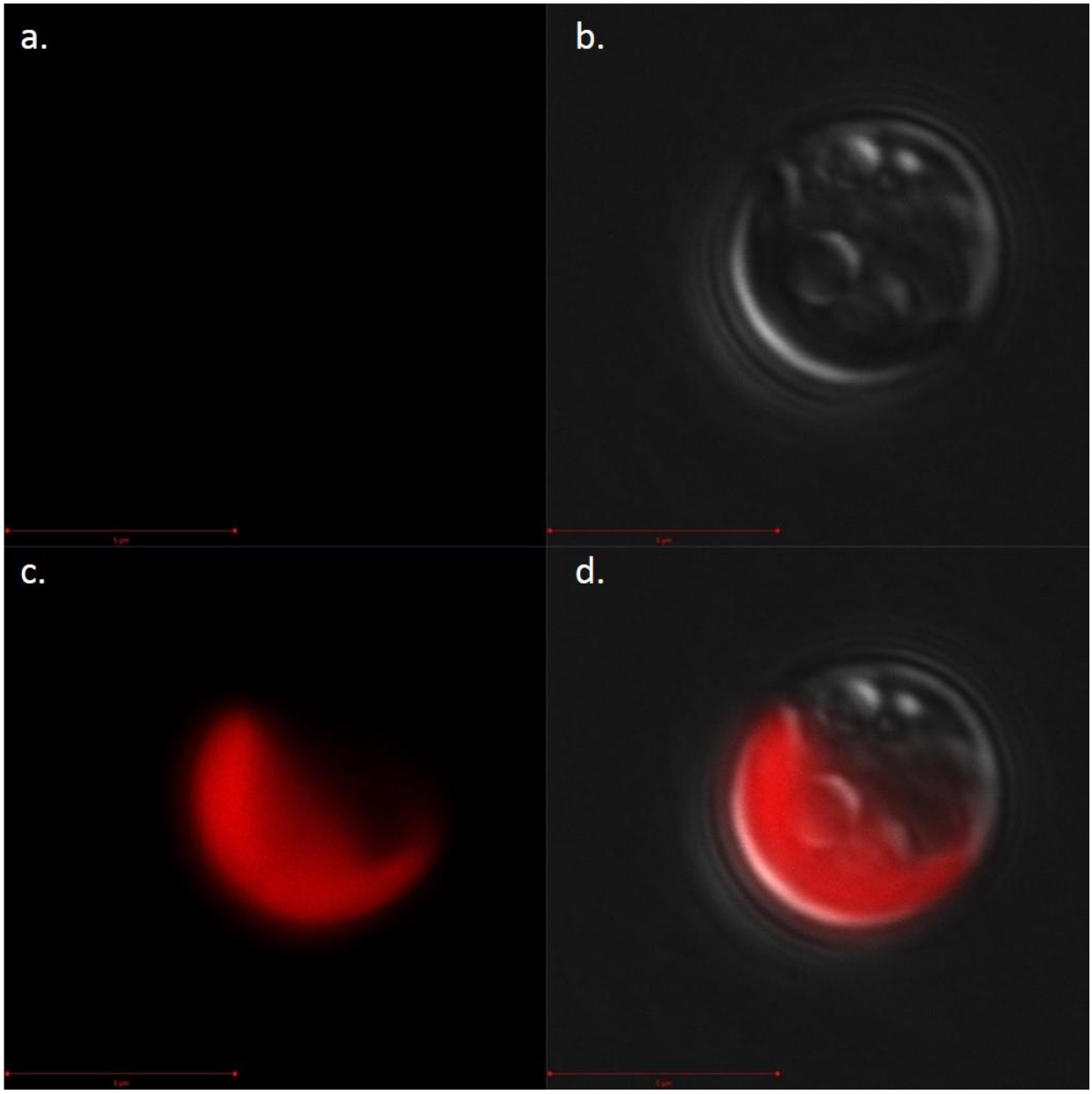

Figure S1

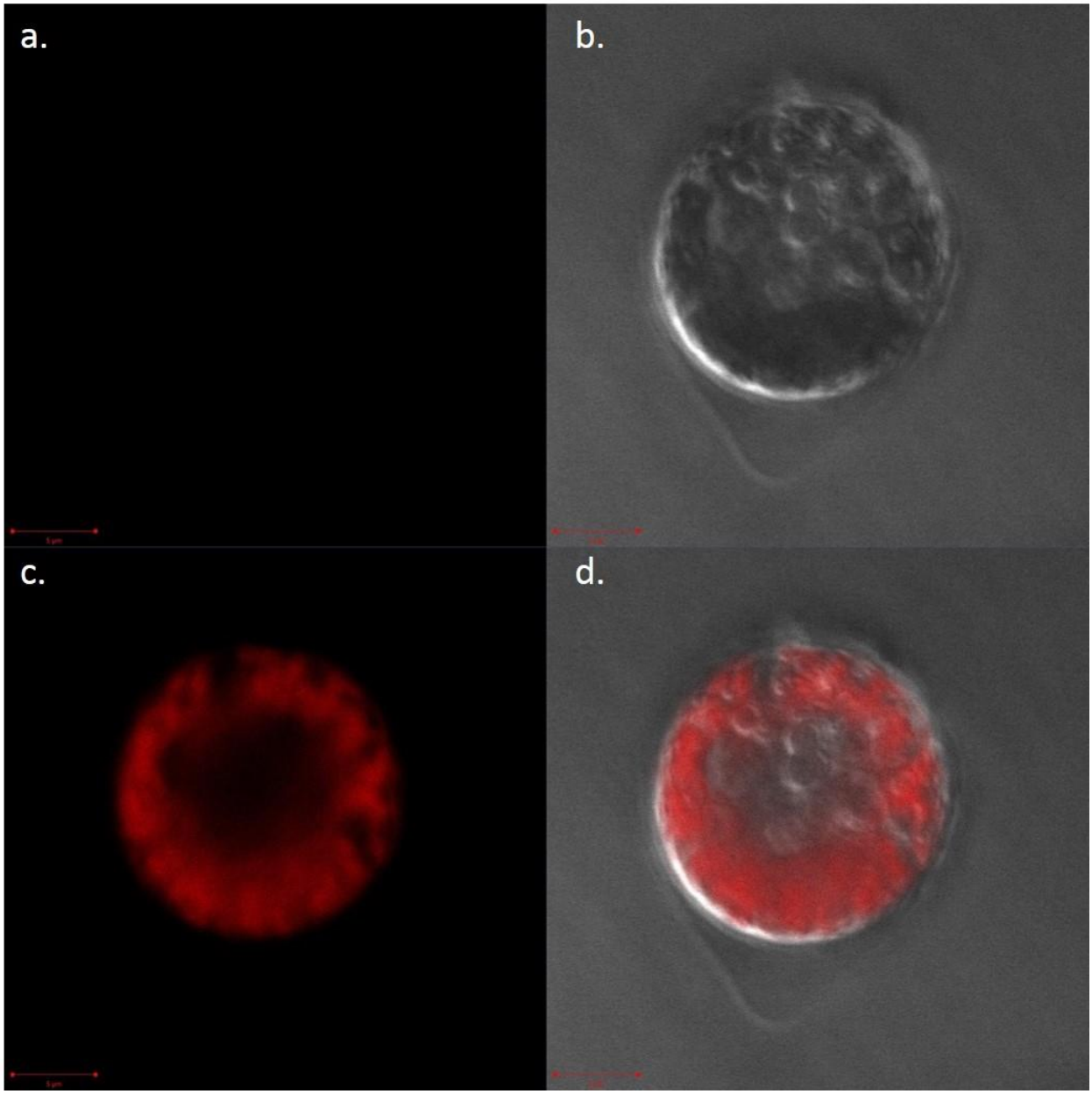

Figure S2

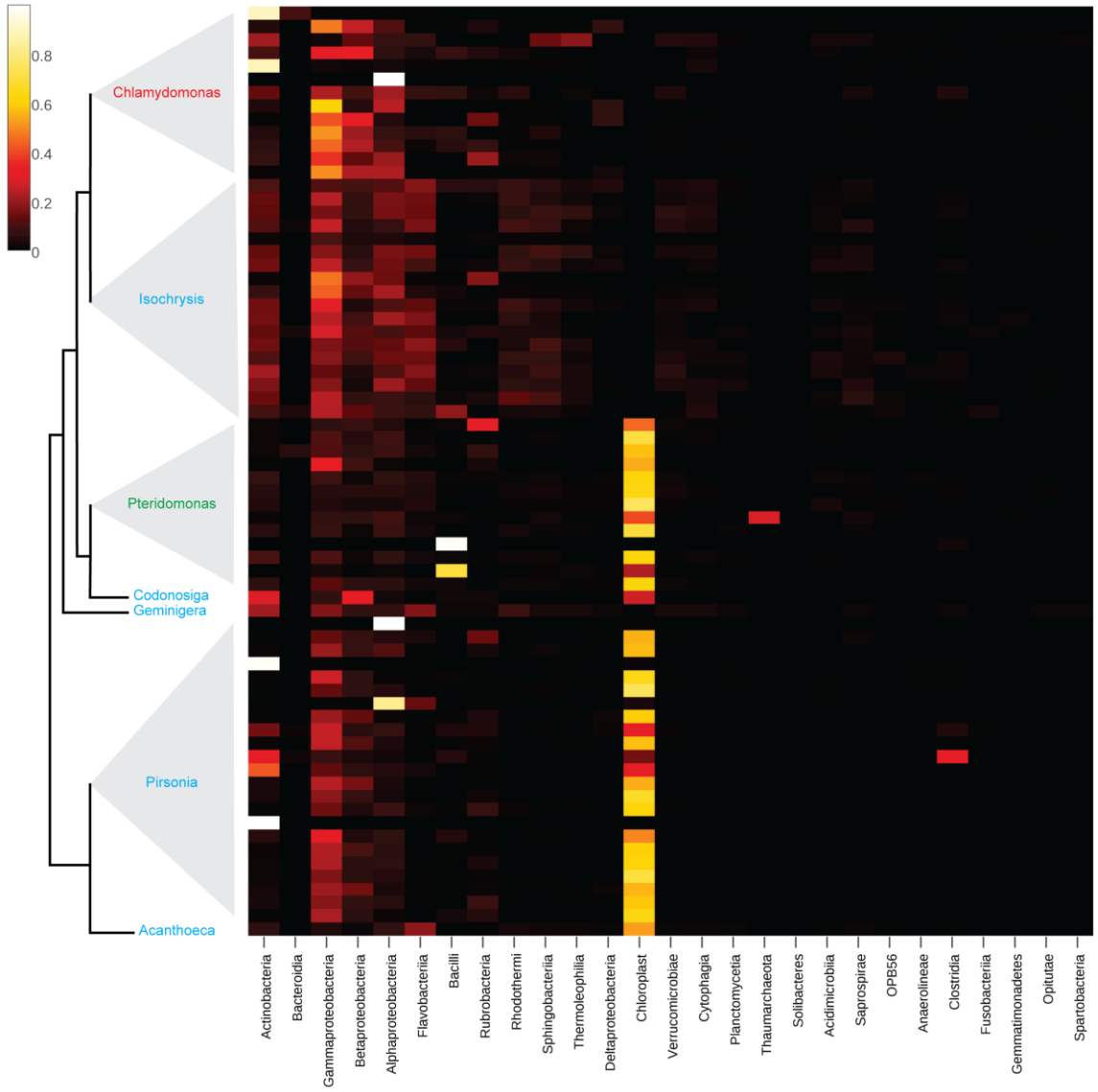
0.8
0.6
0.4
0.2
0
Chlamydomonas
Isochrysis
Pteridomonas
Codonosiga
Geminigera
Pirsonia
Acanthoeca
Actinobacteria
Bacteroidia
Gammaproteobacteria
Betaproteobacteria
Alphaproteobacteria
Flavobacteriia
Bacilli
Rubrobacteria
Rhodothermi
Sphingobacteriia
Thermoleophilia
Deltaproteobacteria
Chloroplast
Verrucomicrobiae
Cytophagia
Planctomycetia
Thaumarchaeota
Solibacteres
Acidimicrobiia
Saprospirae
OPB56
Anaerolineae
Clostridia
Fusobacteriia
Gemmatimonadetes
Opitutae
Spartobacteria

Figure S3