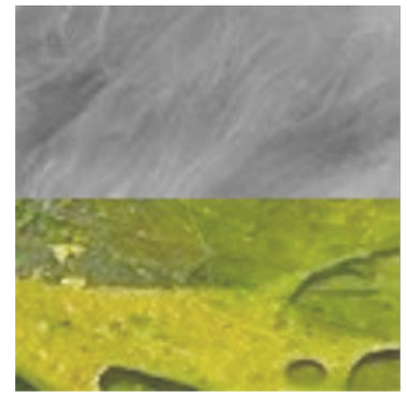


Redox conditions and microbial adaptation within diverse thermophilic communities at Nakabusa hot springs

Katsumi Matsuura[1), 2)] , Shawn E. McGlynn [2)] , Shigeru Kawai [3)]

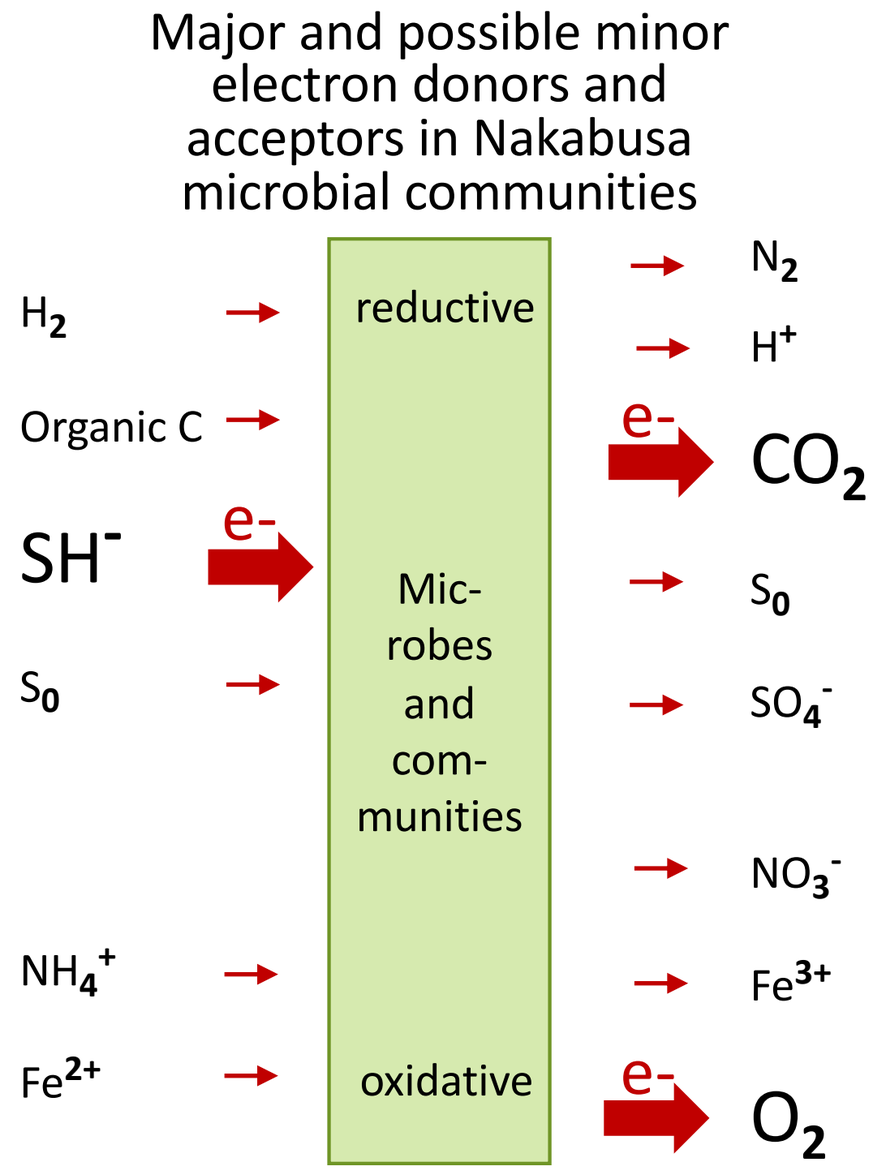
[1)] Inst. Early Metabolic Evol., [2)] ELSI, Tokyo Tech., [3)] JAMSTEC

Redox conditions are important for microbes and communities

1. Redox conditions are important for electron transfer reactions in microbes and communities.

2. Microbial existence and function depend on the redox conditions.

3. Measurements of redox conditions within communities are difficult.



Water flow rate affects the supply of donors and acceptors.

Diverse microbial communities as mats and streamers at Nakabusa hot springs

90℃ 70℃ 62℃

Temperature

Chemosynthetic communities

Anoxygenic photosynthetic communities

Sulfide: 0 – 300 µmol/L

0xygen: 10 - 150 µmol/L

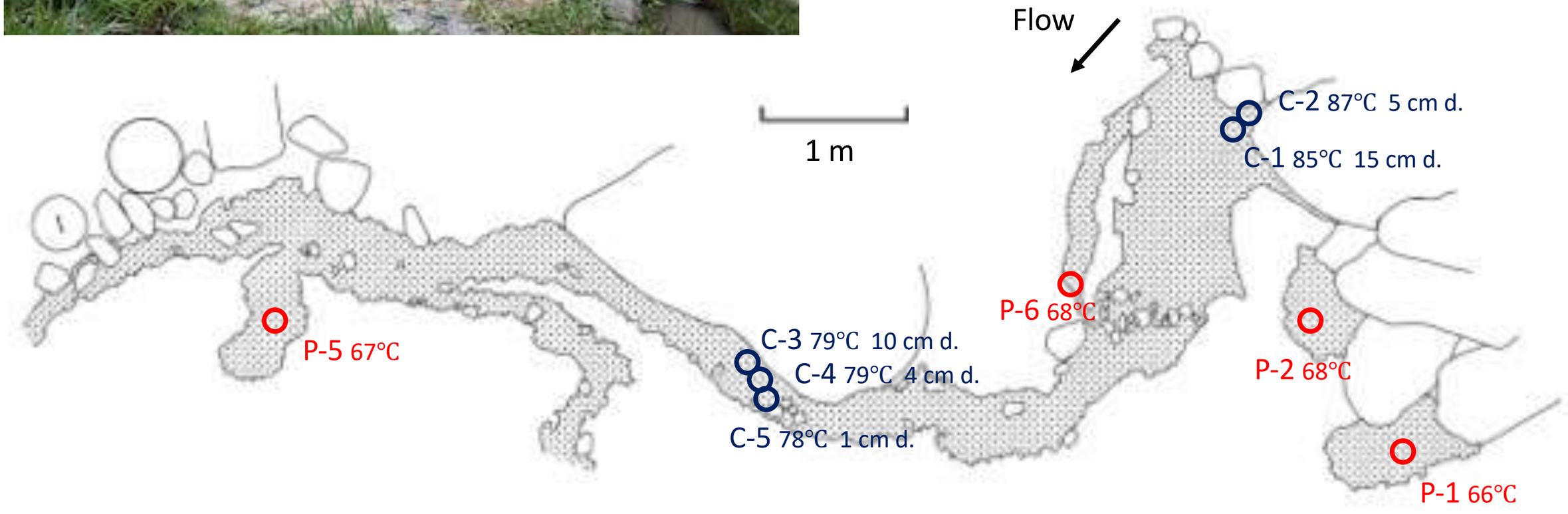
Flow rate: 2 - 1200 mm/s

[Question] How do internal redox conditions change depending on external conditions, and how do inhabited microbes diverse?

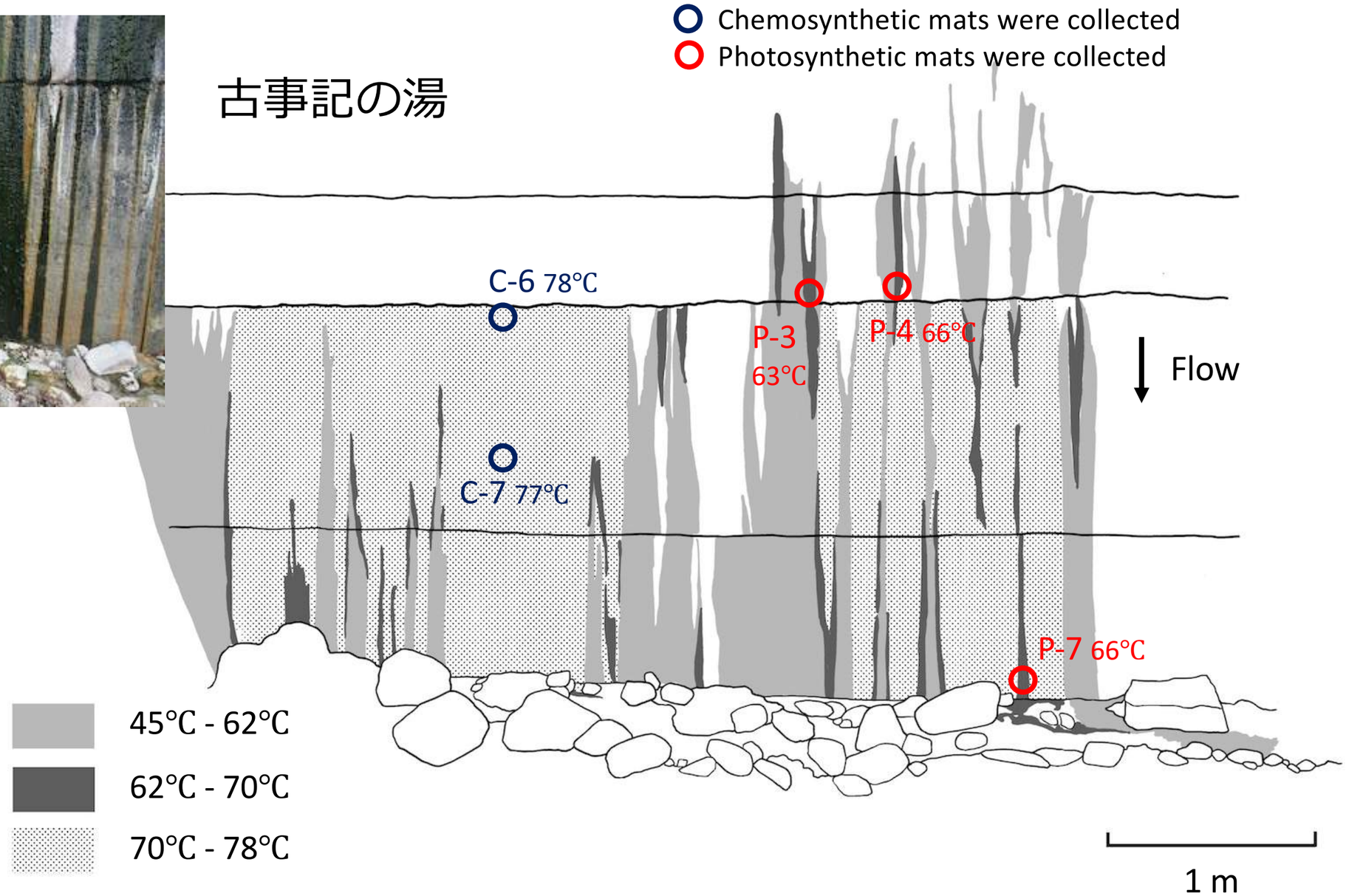
Research site I: Kassen Spring: Lateral flow on the sands

合戦の湯

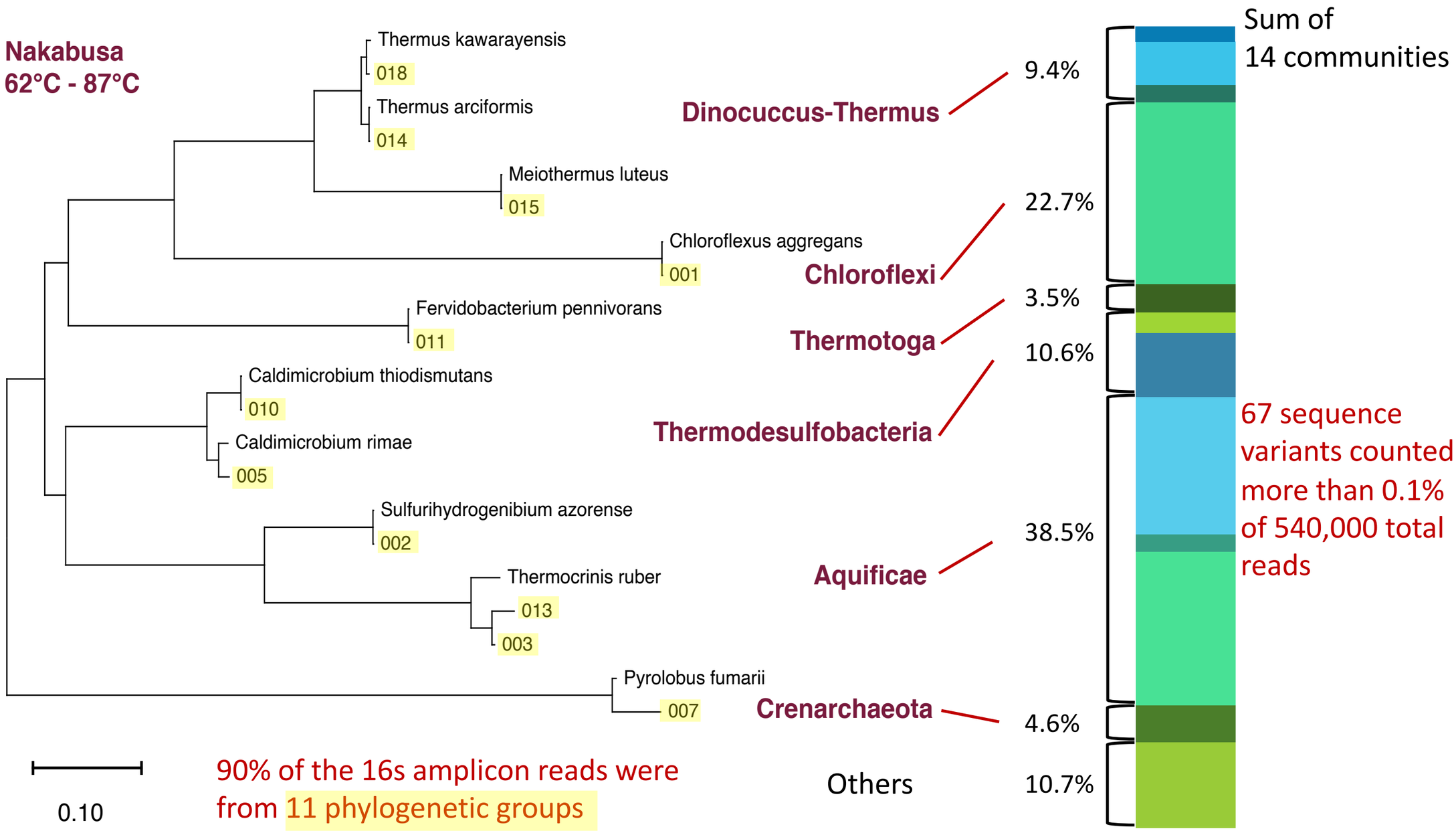
- Chemosynthetic streamers were collected
- Photosynthetic mats were collected



Research site II: Kojiki Spring: Vertical flow on the concrete wall



Eleven phylogenetic groups in 6 phyla were found and counted to 90%



90% of the 16s amplicon reads were from 11 phylogenetic groups

External environmental and redox conditions were very diverse

Reductive
Intermediate
Oxidative

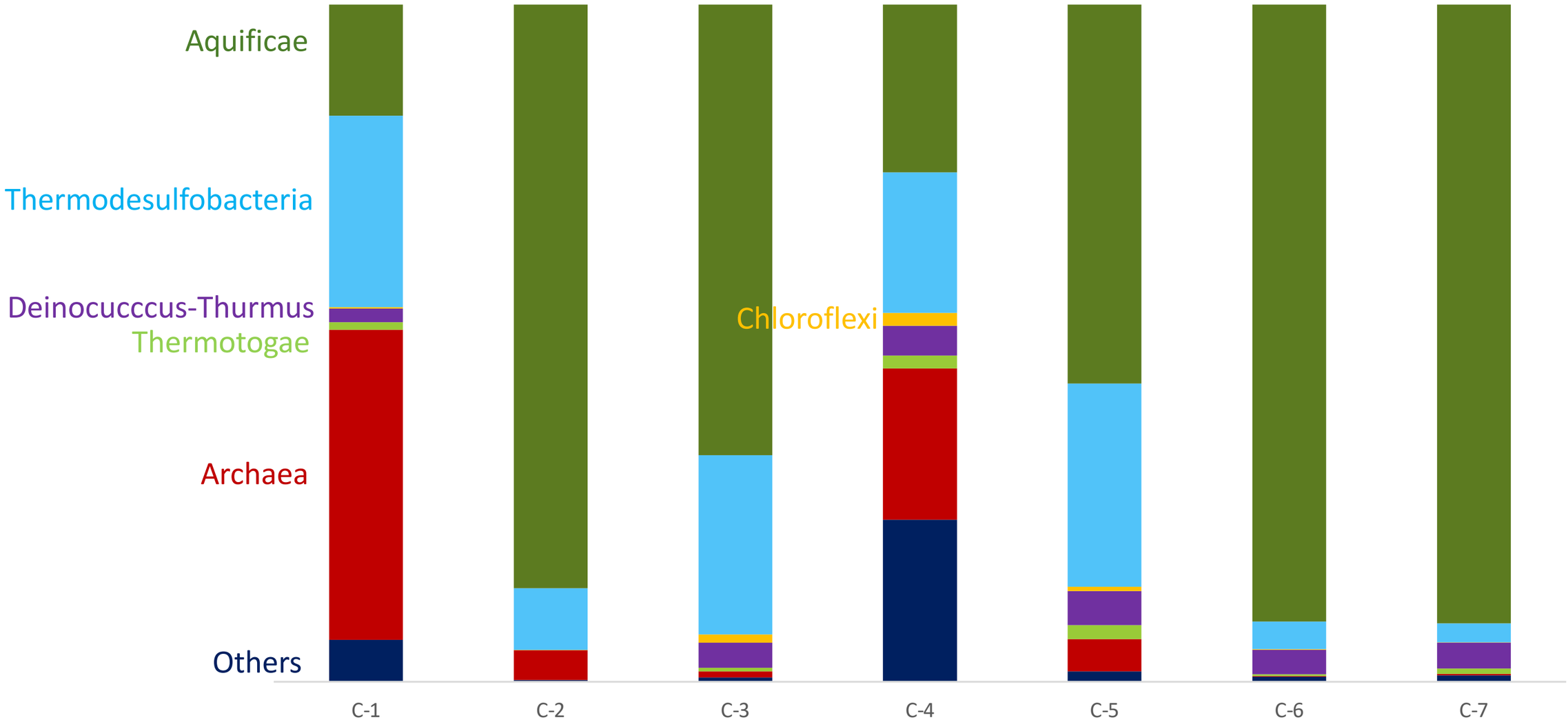
Chemosynthetic communities

sample #	C-1	C-2	C-3	C-4	C-6	C-6	C-7
temperature	85	87	79	79	78	78	77
O_2 µmol/L	25	25	55	55	54	60	72
SH^- µmol/L	209	238	55	54	52	239	120
Flow mm/s	50	100	100	300	650	1200	1200
Color	Black	Black	Gray	Gray	Pale Tan	Pale Tan	Pale Tan

Anoxygenic photosynthetic communities

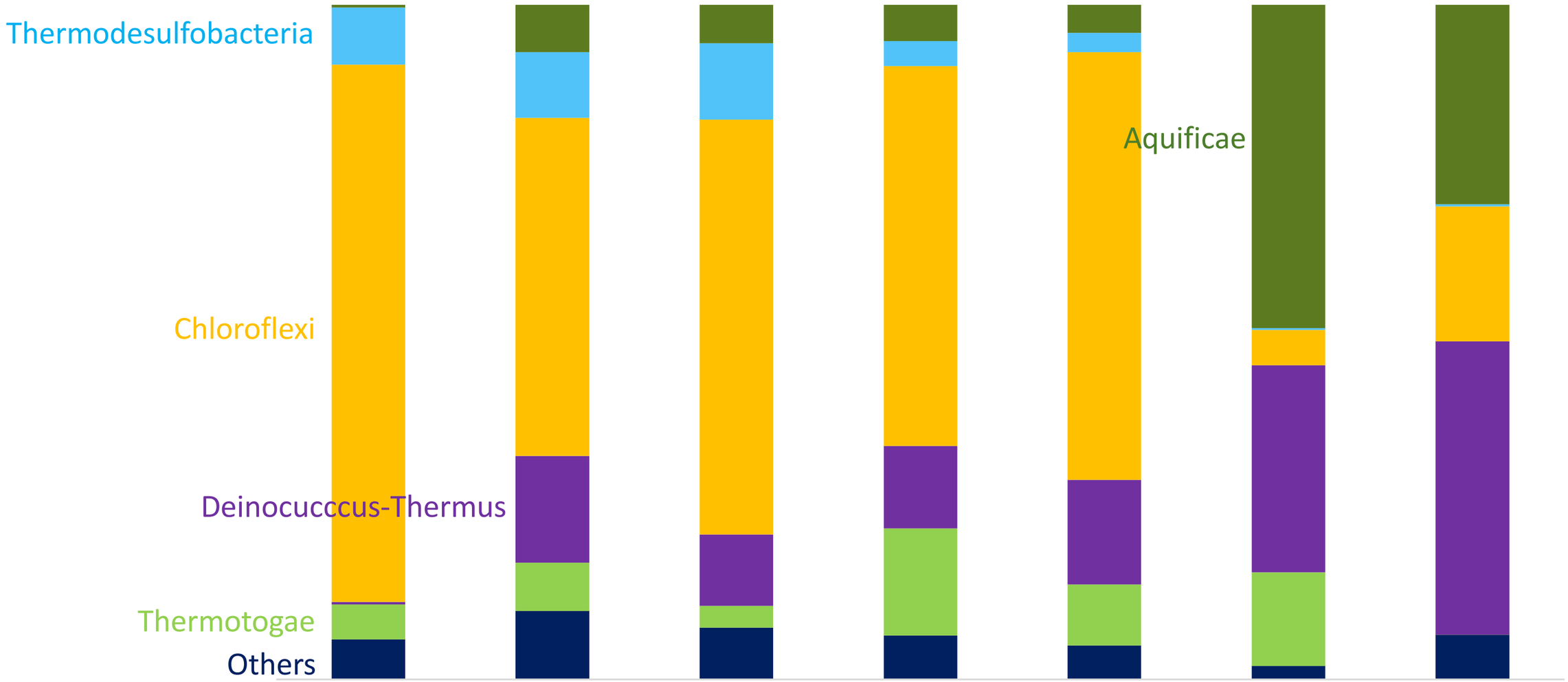
sample #	P-1	P-2	P-3	P-4	P-6	P-6	P-7
temperature	66	68	63	66	67	68	66
O_2 µmol/L	33	42	84	116	74	130	134
SH^- µmol/L	109	202	146	58	14	22	3
Flow mm/s	2	6	300	400	8	80	450
Color	Olive Orange	Olive Orange	Olive Green	Olive Green	Orange	Pale Brown	Pale Brown

Redox Indexes and microbe compositions were diverse in chemosynthetic communities



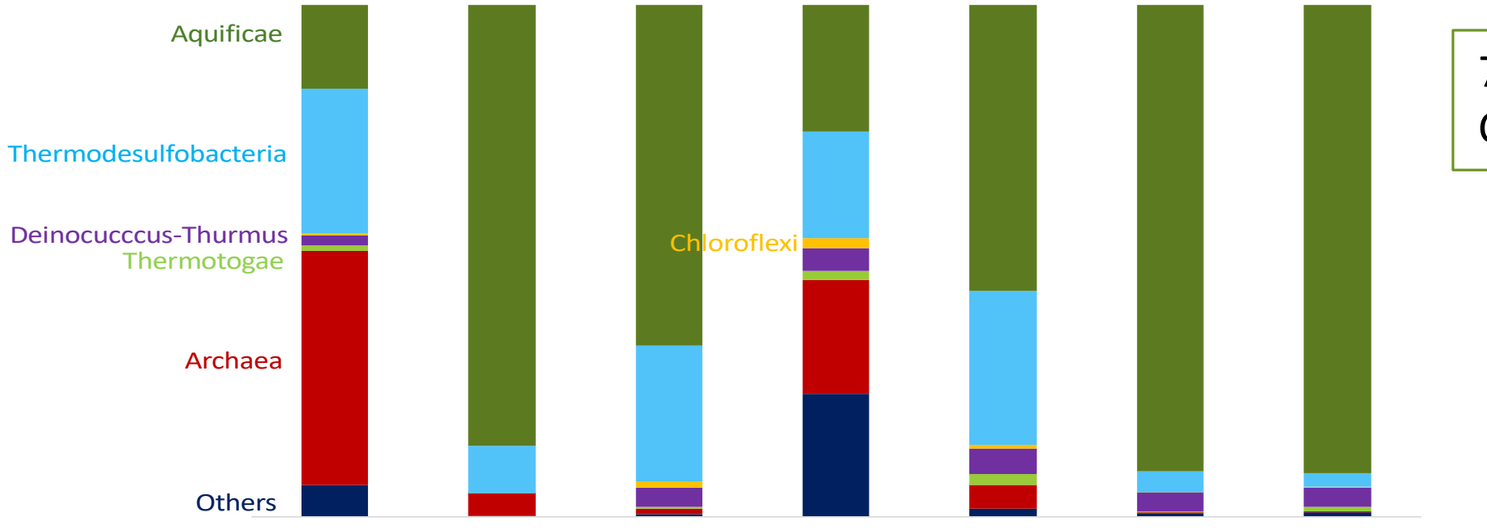
Redox Index of community	0.84	0.82	0.55	0.49	0.47	-0.32	-0.59

Redox Indexes and microbe compositions were diverse in photosynthetic communities



Redox Index of community	0.19	0.06	0.03	-0.04	-0.18	-0.48	-0.64

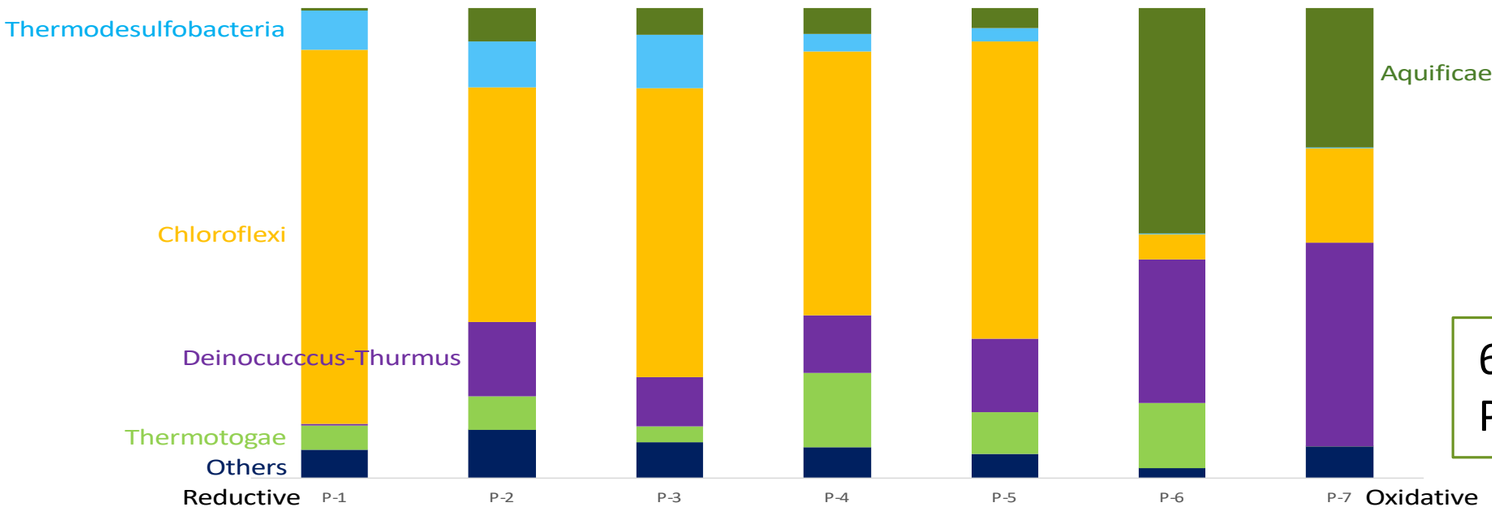
Comparison between chemosynthetic and photosynthetic communities



Redox Index	0.84	0.82	0.55	0.49	0.47	-0.32	-0.59

77°C - 87°C
Chemosynthetic

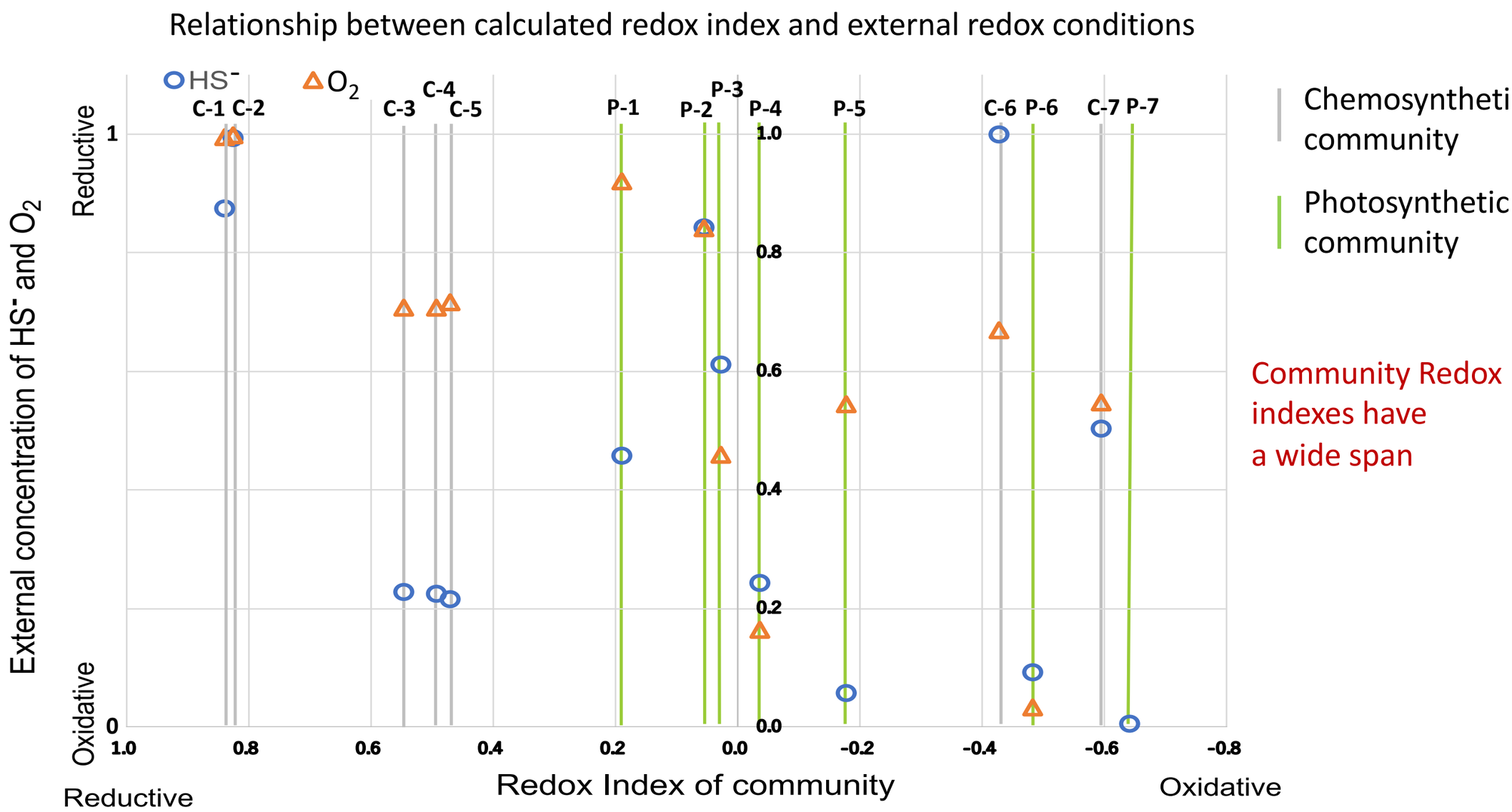
1. Chloroflexi in photosynthetic
2. Archaea in chemosynthetic
3. Aquificae and Thermodesulfo. In both
4. Heterotrofic Thermus/Themotogae are significant in photosynthetic but rare in chemosynthetic



Redox Index	0.19	0.06	0.03	-0.04	-0.18	-0.48	-0.64

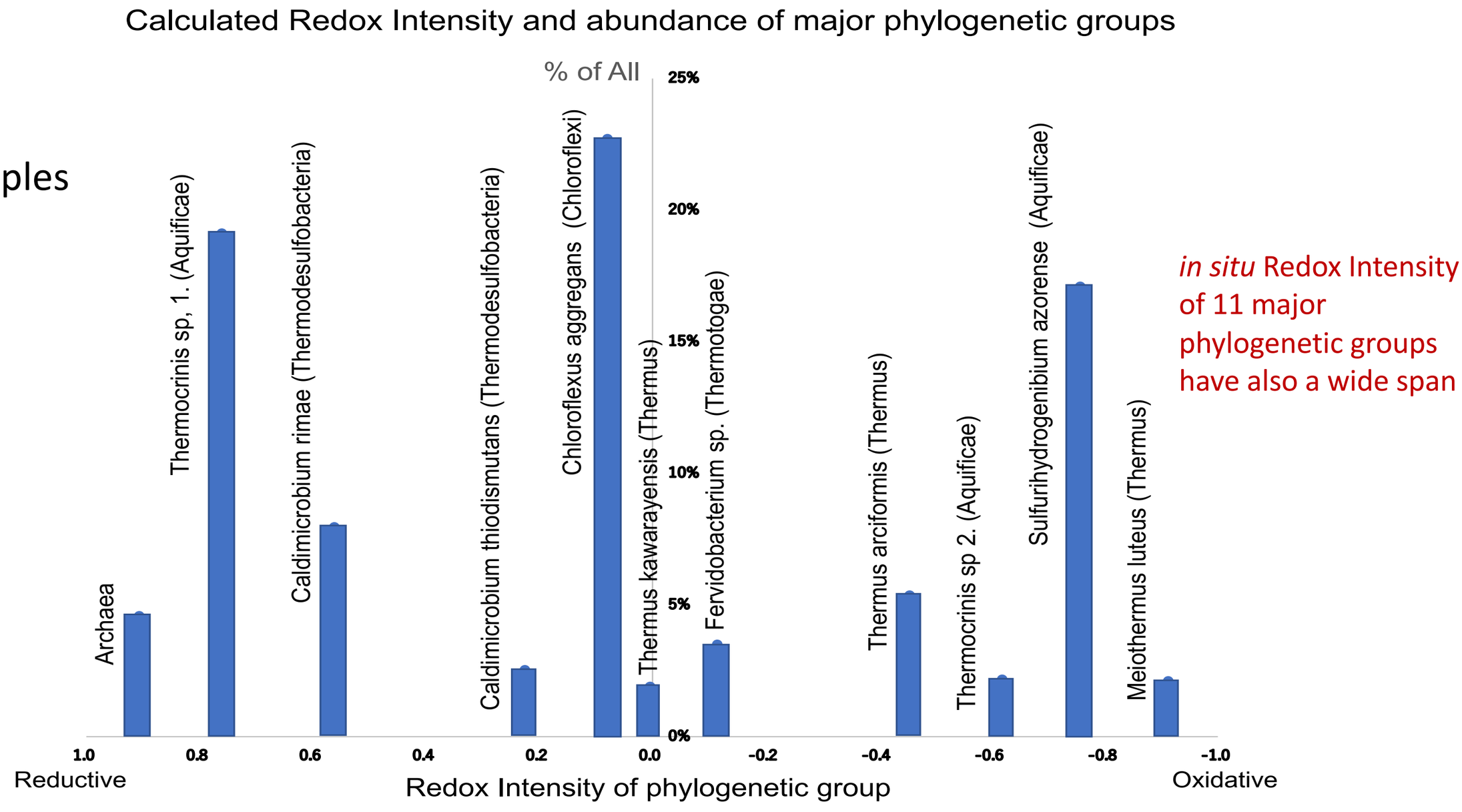
63°C - 68°C
Photosynthetic

Redox index of communities was not directly related to external redox conditions



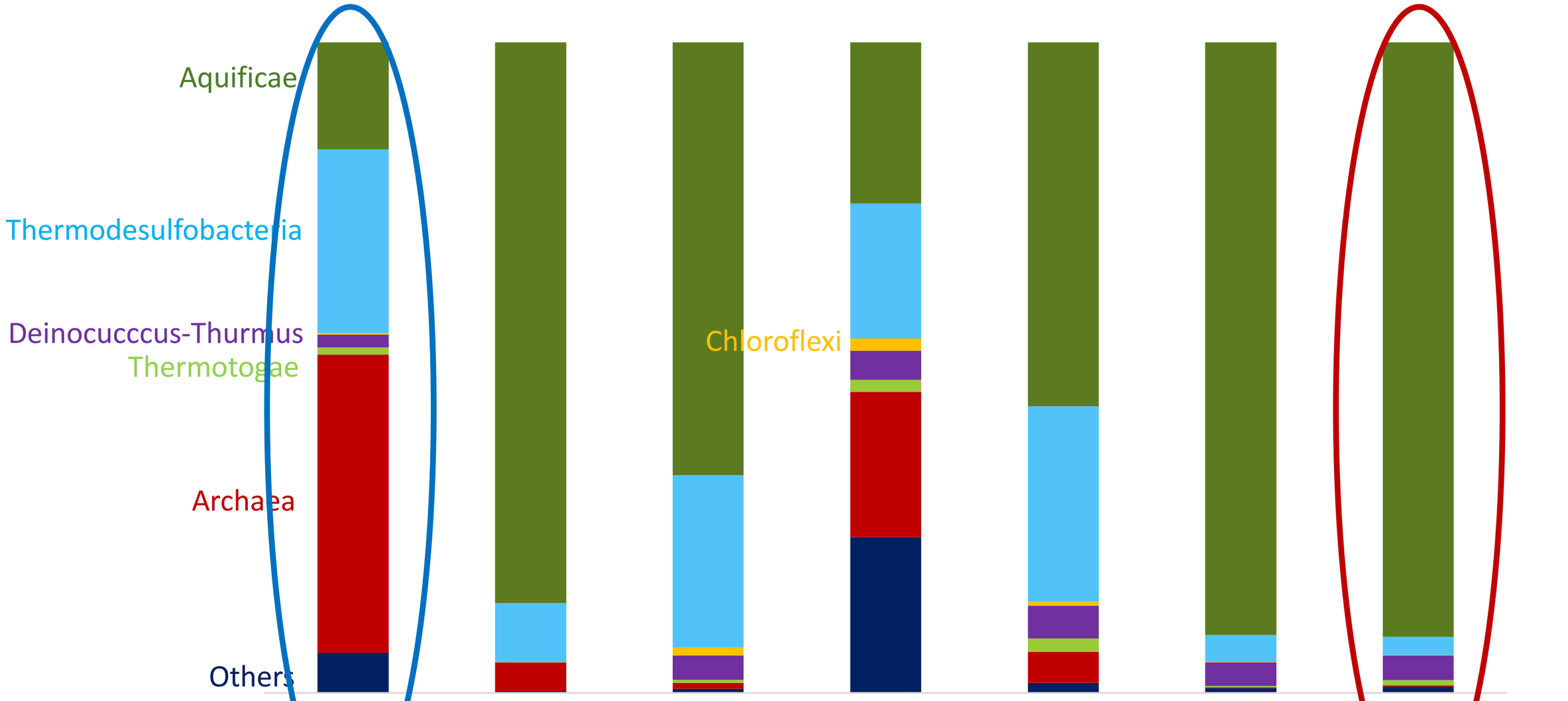
In situ Redox Intensity of each phylogenetic group was widely diverse

Sum of
14 samples



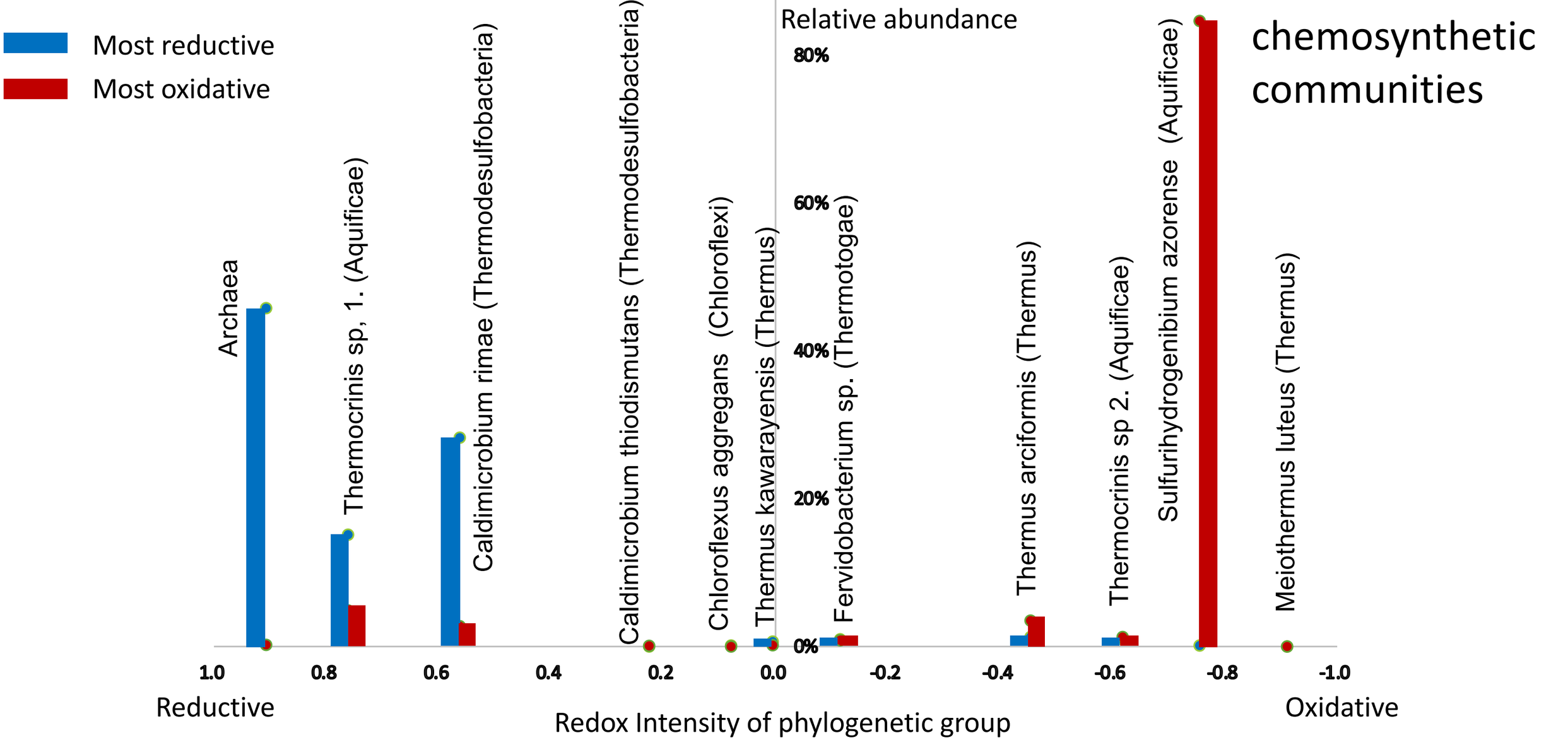
in situ Redox Intensity of 11 major phylogenetic groups have also a wide span

Redox Indexes and microbe compositions were diverse in chemosynthetic communities



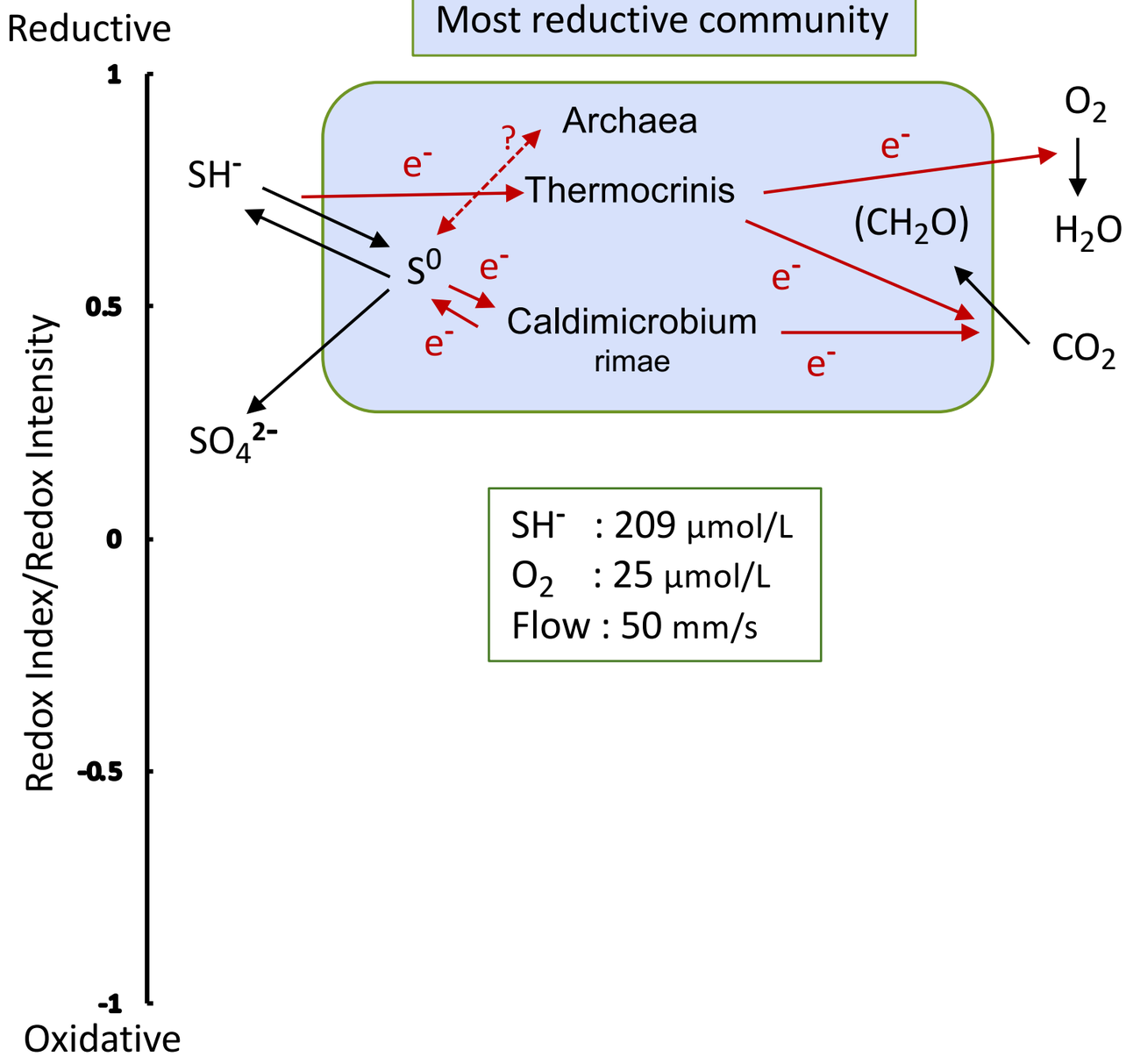
Redox Index of community	0.84	0.82	0.55	0.49	0.47	-0.32	-0.59

Reductive and oxidative communities have different microbial compositions



Dominant microbes and electron transfer in chemosynthetic communities

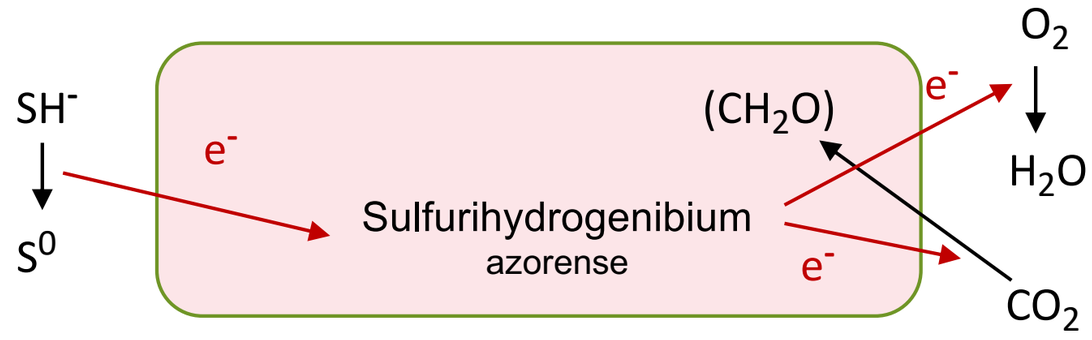
Most reductive community



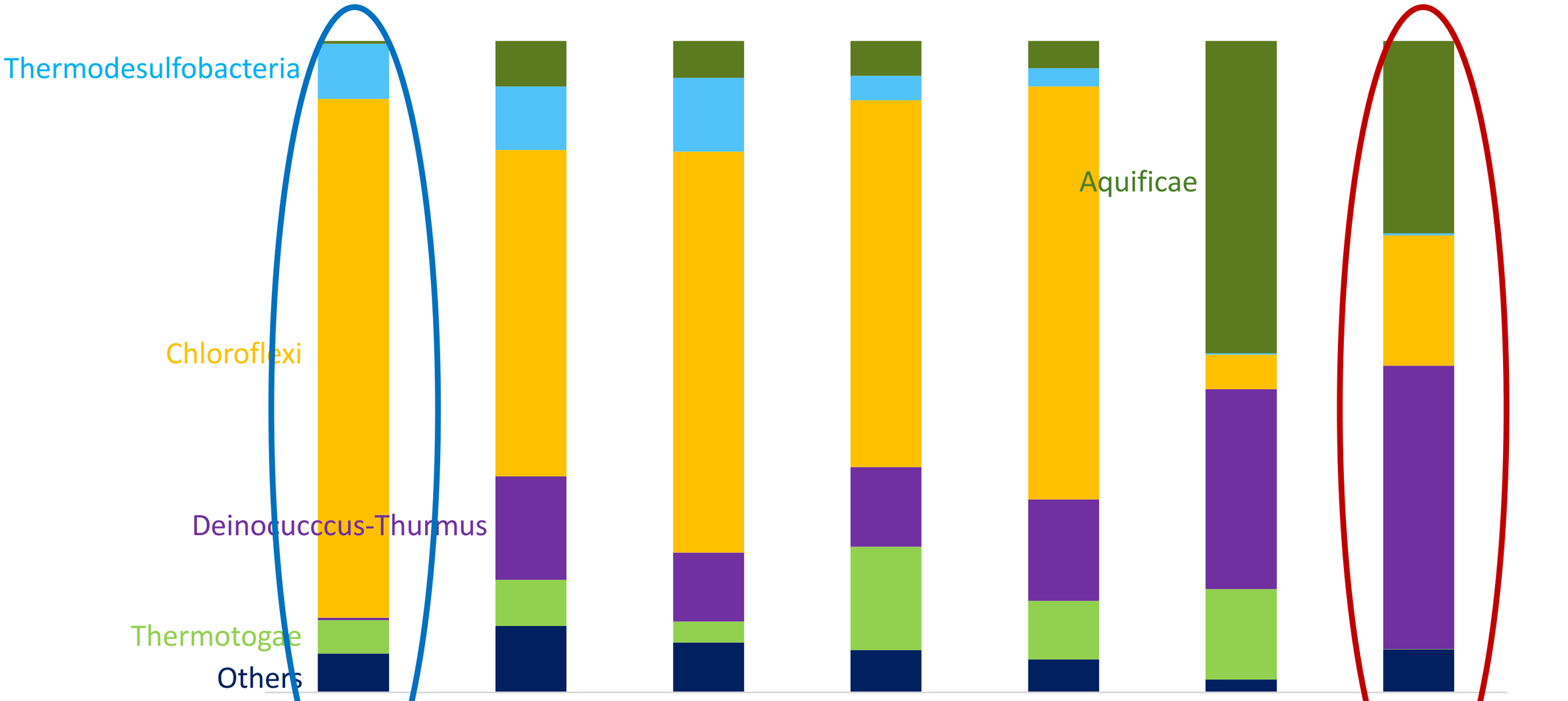
SH⁻ : 209 µmol/L
O_2 : 25 µmol/L
Flow : 50 mm/s

Most oxidative community

SH⁻ : 120 µmol/L
O_2 : 72 µmol/L
Flow : 1200 mm/s

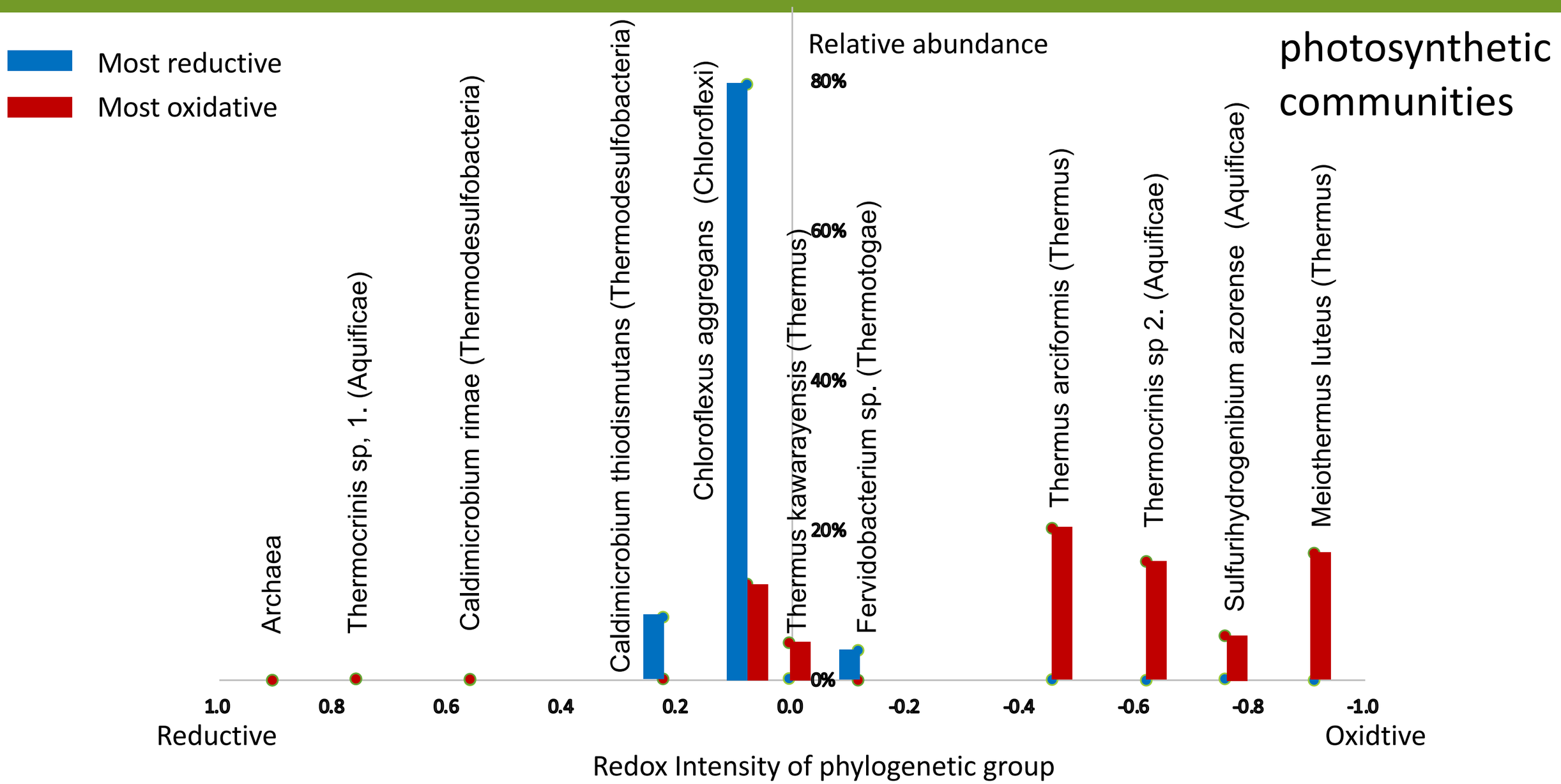


Redox Indexes and microbe compositions were diverse in photosynthetic communities



Redox Index of community	0.19	0.06	0.03	-0.04	-0.18	-0.48	-0.64

Reductive and oxidative communities have different microbial compositions



Dominant microbes and electron transfer in photosynthetic communities

Reductive

Redox Index/Redox Intensity

1

0.5

0

-0.5

-1

Oxidative

Most reductive community

SO_4^{2-}

SH^-

S^0

e^- Caldimicrobium thiodismutans

Chloroflexus aggregans

Fervidobacterium

H_2

H^+

hv

(CH_2O)

CO_2

SH^- : 109 µmol/L
O_2 : 33 µmol/L
Flow : 2 mm/s

Most oxidative community

SH^- : 3 µmol/L
O_2 : 134 µmol/L
Flow : 450 mm/s

hv

Chloroflexus aggregans

SH^-

S^0

Thermus

(CH_2O)

CO_2

Thermocrinis

Sulfurihydrogenibium azorense

Meiothermus

O_2

H_2O

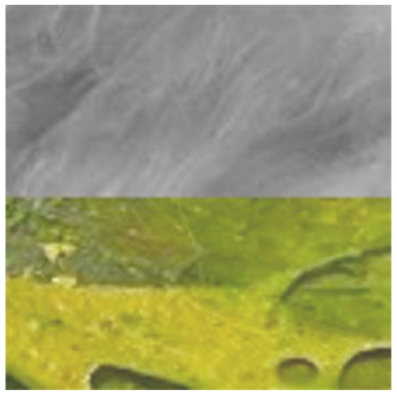
e^-

Summary

1. Internal redox conditions are different from external conditions, and they can be estimated from inhabited microbes.

2. *In situ* redox adaptability of phylogenetic groups can be estimated from their distribution among communities.

3. Different patterns of microbial compositions and electron transfer pathways appear, depending on internal redox conditions.



Acknowledgment: Mr. Takahito Momose, the owner of Nakabusa hot springs, for letting us use the hot spring currents.
（百瀬孝仁様）

Outline of methods to calculate Redox Index and Redox Intensity

Collect 14 microbial community samples from various external redox states with diverse SH^- and O_2 concentrations. (Temp. 86℃ - 62℃)

↓

Determine 16S rRNA sequences in V4 region and analyze them phylogenetically

↓

Give ”tentative Redox Intensity” to several known aerobic and anaerobic microbes and calculate “tentative Redox Index (from 1 to -1)” of 14 communities.

↓

Calculate “Redox Index (from 1 to -1)” of each phylogenetic group using the “tentative Redox Index” and distribution of the group throughout communities

↓

Calculate final community “Redox index” from the relative abundance of each phylogenetic group and the “Redox Intensity”

Desulfurococcales was dominant in Archaea