Supplementary Figure Legends

Figure S1. A) Proportion of different functional C-groups of soil organic matter in one control and two burn locations. Error bars indicate the standard error of mean. B) Indices of the decomposition and structural modification of organic material.

Figure S2. A) CO_2, B) CH_4 and C) N_2O fluxes measured in the headspace of eight week long anaerobic incubation of samples from control and burned locations. Samples were incubated at 20°C. Values are means ± standard error

Figure S3. Changes in the potential extracellular enzyme activities (nmol/gr soil /hr) between control and burned locations; BG, β-glucosidase; CBH,β-cellobiohydrolase; XYL, β-xylosidase;NAG, N-acetyl glucosaminidase

Figure S4. Rarefaction curves compiled using observed species counts.

Figure S5. A) Alpha diversity metrics calculated in each depth of control (blue) and burned (red) locations. No significant fire effect was found. B) Alpha diversity metrics changed significantly between different soil depths in control and burned locations.

Figure S6. Distribution of metagenomic reads between different microbial domains in different depths of control and burned locations.

Figure S7. Relative abundance of C-cycle genes in replicate metagenomes from surface (S), middle (M) and permafrost/deep (D) soils of control and burned locations. Standard deviations are calculated from two replicate metagenome per depth and condition.

Figure S8. α- and β-glucosidase; β-cellobiohydrolase, β-xylosidase coding genes in the metagenomes. Standard deviations are calculated from two replicate metagenome per depth and condition.

Figure S9. Changes in the relative gene abundances of methane production and oxidation genes in Nome Creek metagenomes. Replicate metagenomes are plotted individually. HS–CoM, Mercaptoethanesulfonate

Figure S10. Changes in the relative gene abundances of N-cycling genes in Nome Creek metagenomes. Replicate metagenomes are plotted individually.

Figure S11. Relative abundance of genes involved in Sulfur reduction in replicate metagenomes from surface (S), middle (M) and permafrost/deep (D) soils of control and burned locations. Standard deviations are calculated from two replicate metagenomes per depth and condition.

Figure S12. Relative abundance of genes involved in stress responses in replicate metagenomes from surface (S), middle (M) and permafrost/deep (D) soils of control and burned locations. Standard deviations are calculated from two replicate metagenomes per depth and condition.

Figure S1a

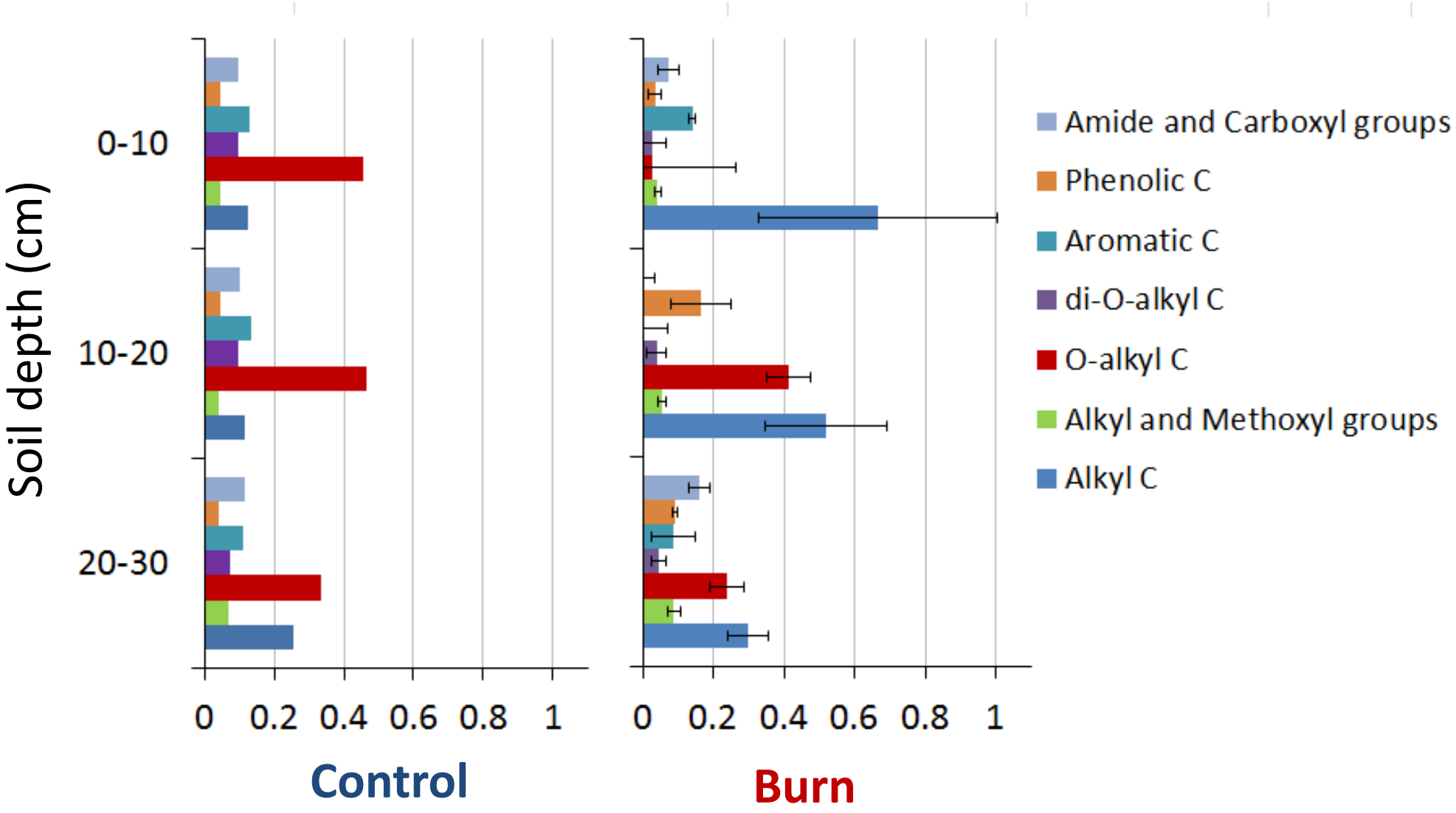

Soil depth (cm)
0-10
10-20
20-30
0
0.2
0.4
0.6
0.8
1
Control
Burn
Amide and Carboxyl groups
Phenolic C
Aromatic C
di-O-alkyl C
O-alkyl C
Alkyl and Methoxyl groups
Alkyl C

Figure S1b

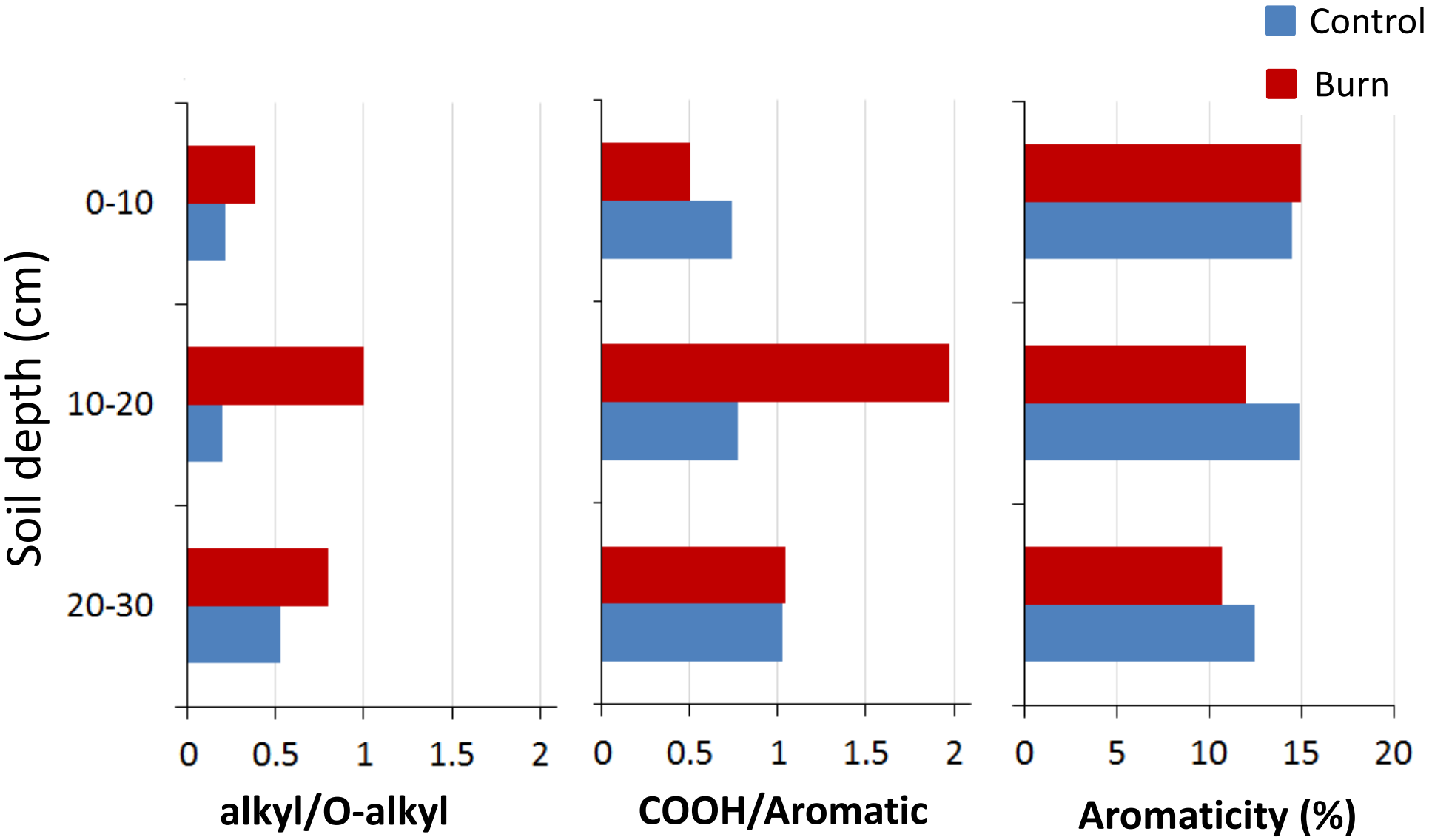

Control
Burn
Soil depth (cm)
0-10
10-20
20-30
0
0.5
1
1.5
2
alkyl/O-alkyl
0
0.5
1
1.5
2
COOH/Aromatic
0
5
10
15
20
Aromaticity (%)

Figure S2

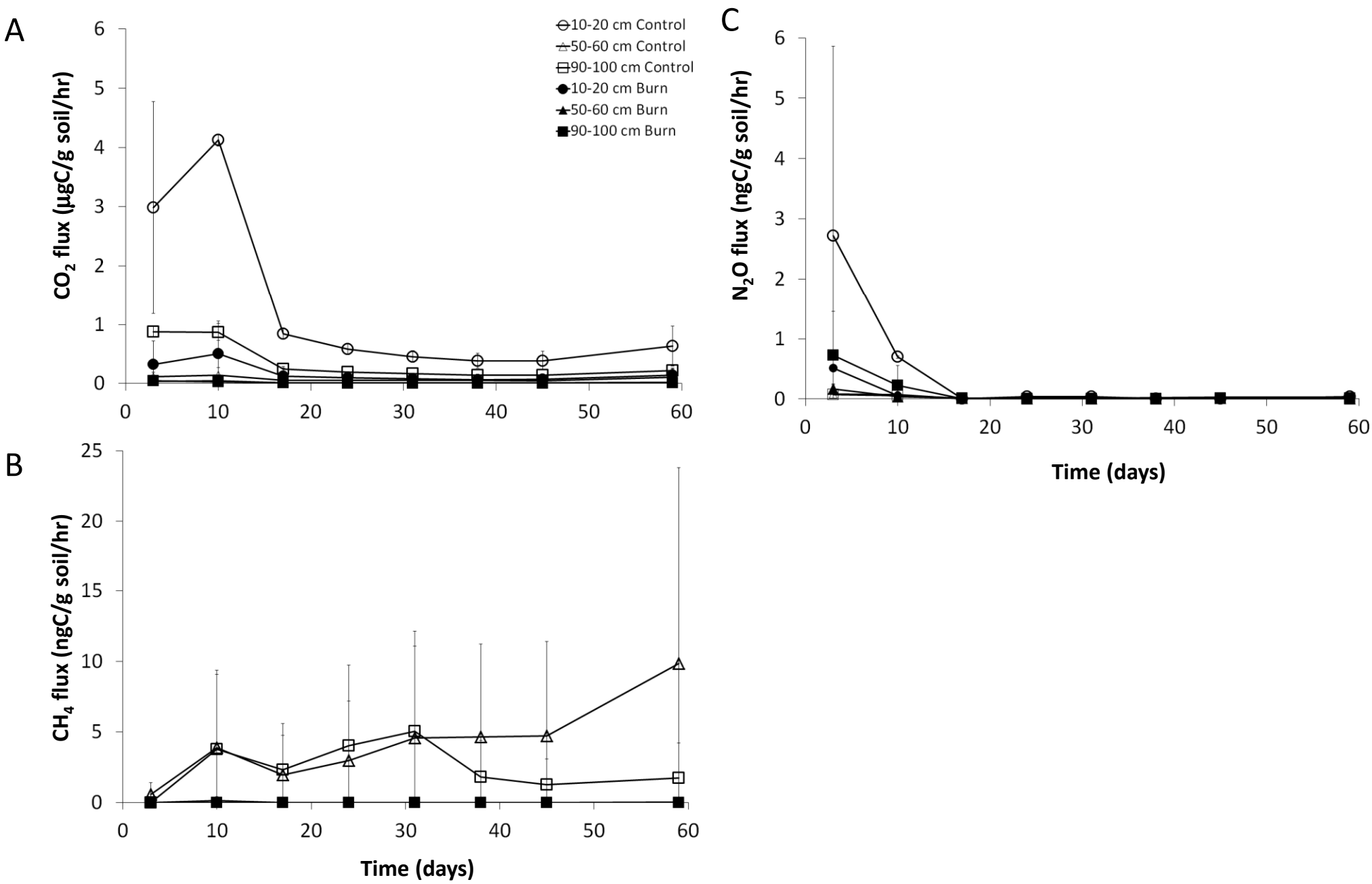

A
B
C
10-20 cm Control
50-60 cm Control
90-100 cm Control
10-20 cm Burn
50-60 cm Burn
90-100 cm Burn
CO2 flux (µgC/g soil/hr)
CH4 flux (ngC/g soil/hr)
N2O flux (ngC/g soil/hr)
Time (days)
Time (days)

Figure S3

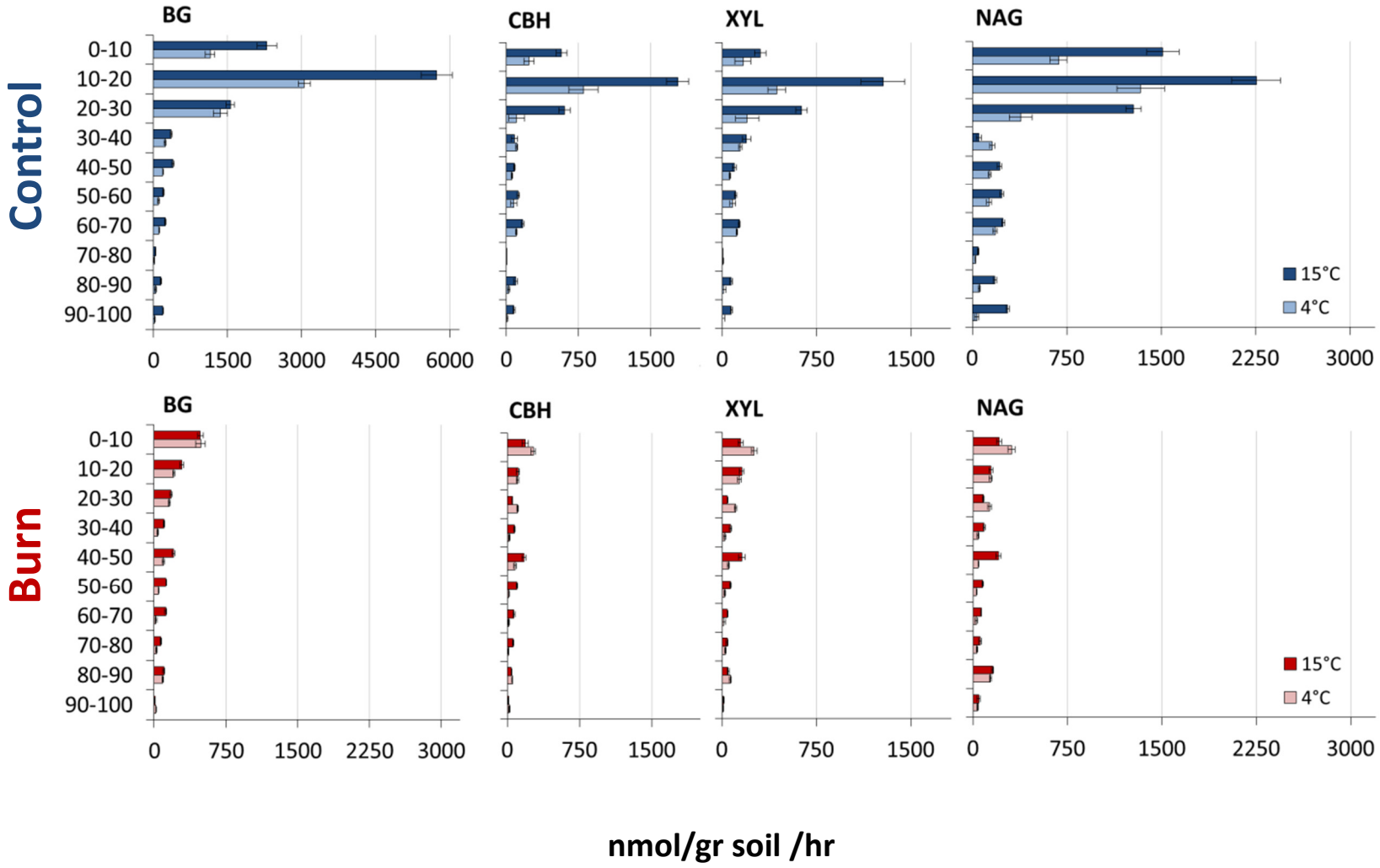
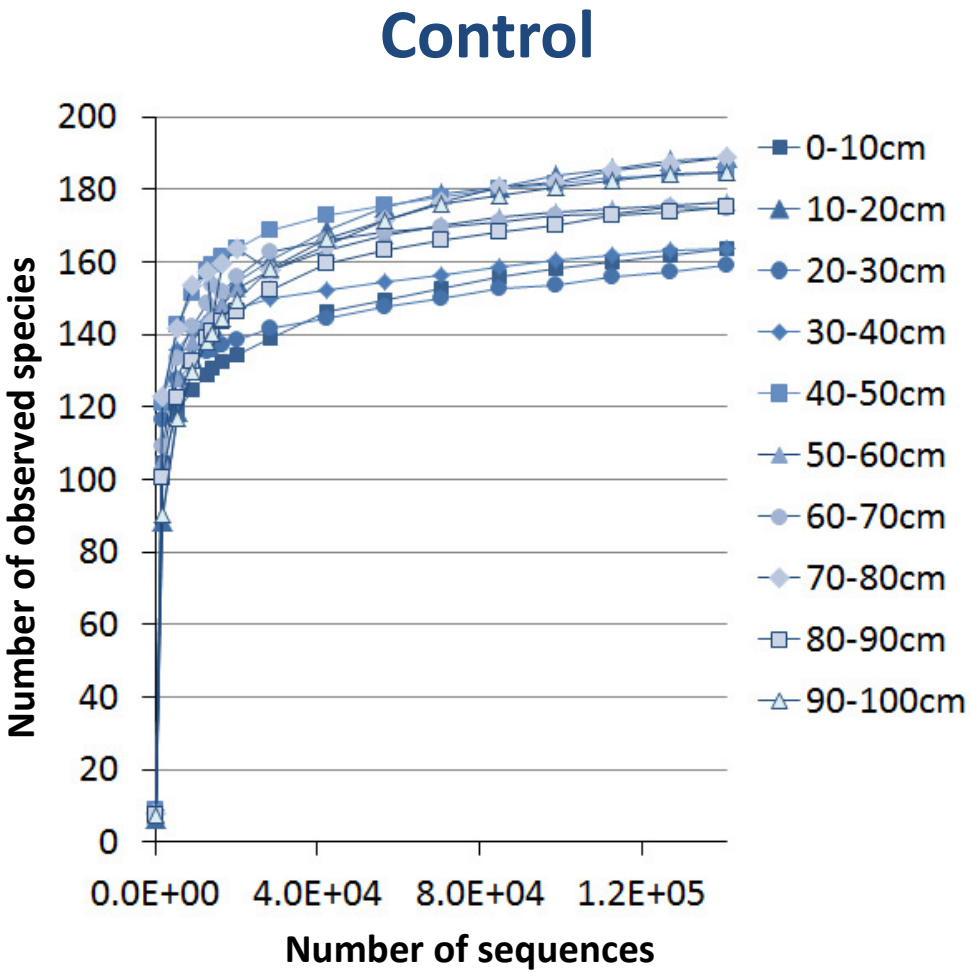

BG
CBH
XYL
NAG
Control
Burn
0-10
10-20
20-30
30-40
40-50
50-60
60-70
70-80
80-90
90-100
15°C
4°C
0
1500
3000
4500
6000
750
2250
nmol/gr soil /hr

Figure S4


Control
Number of observed species
200
180
160
140
120
100
80
60
40
20
0
0.0E+00
4.0E+04
8.0E+04
1.2E+05
Number of sequences
0-10cm
10-20cm
20-30cm
30-40cm
40-50cm
50-60cm
60-70cm
70-80cm
80-90cm
90-100cm

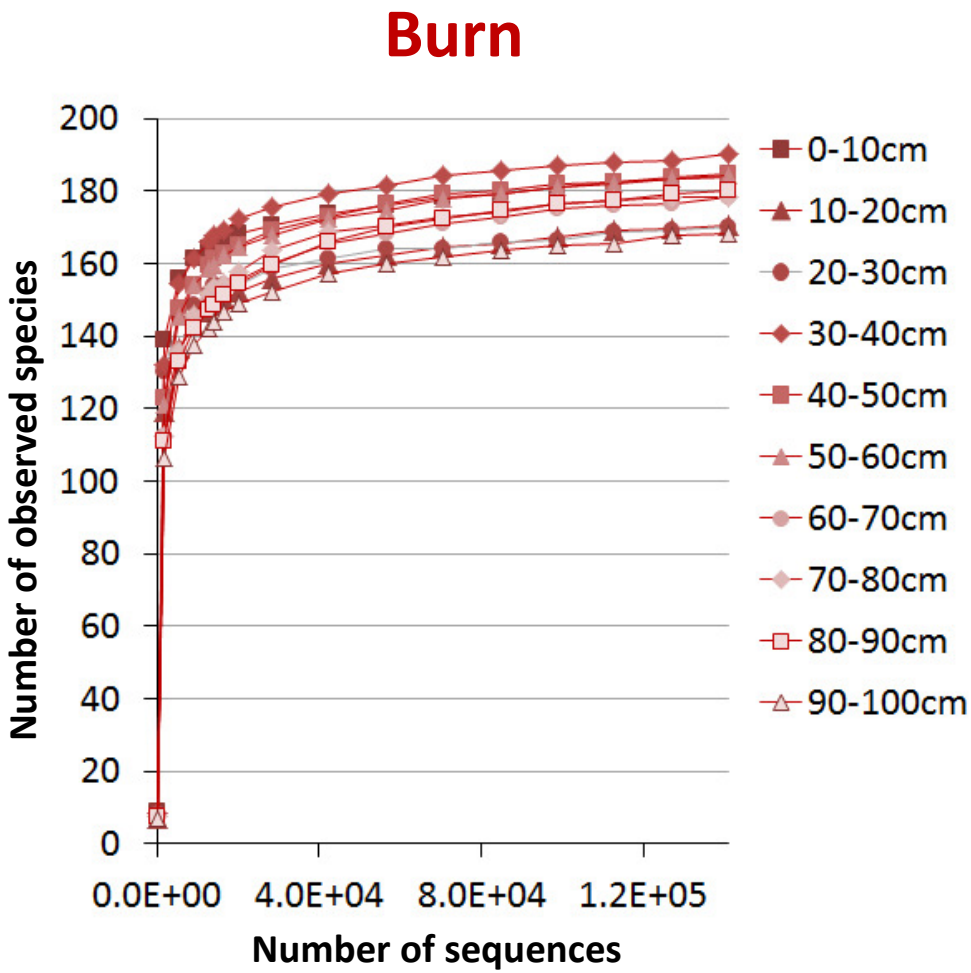
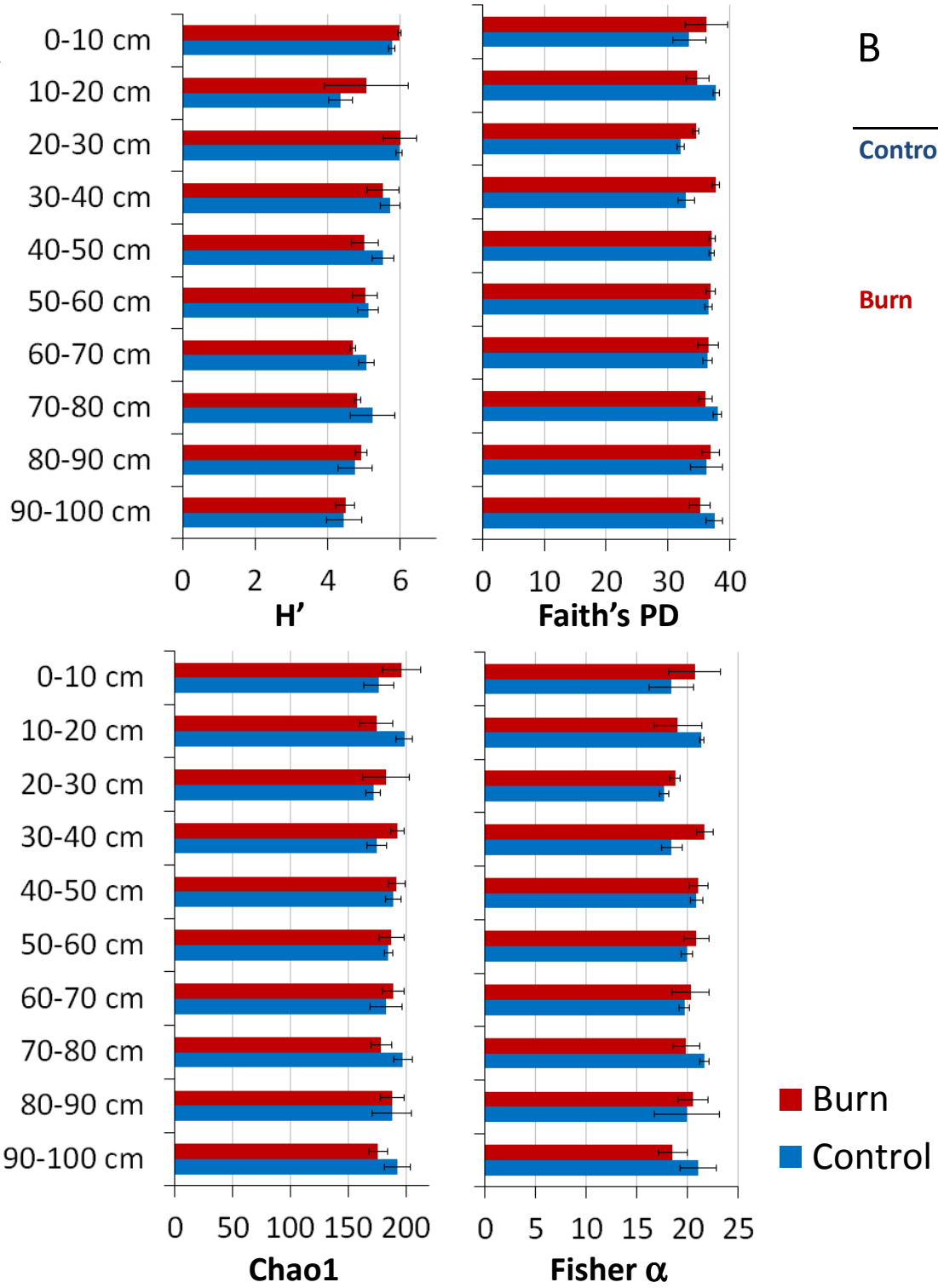

Burn
Number of observed species
200
180
160
140
120
100
80
60
40
20
0
0.0E+00
4.0E+04
8.0E+04
1.2E+05
Number of sequences
0-10cm
10-20cm
20-30cm
30-40cm
40-50cm
50-60cm
60-70cm
70-80cm
80-90cm
90-100cm

Figure S5

A



B

	Index	F Model	p
Control	Shannon H'	16.05	<0.001
	Faith's PD	12.07	<0.001
	Chao1	4.16	<0.001
	Fishers α	4.30	<0.001
Burn	Shannon H'	4.70	<0.001
	Faith's PD	1.60	0.163
	Chao1	1.65	0.148
	Fishers α	1.66	0.145

Figure S6

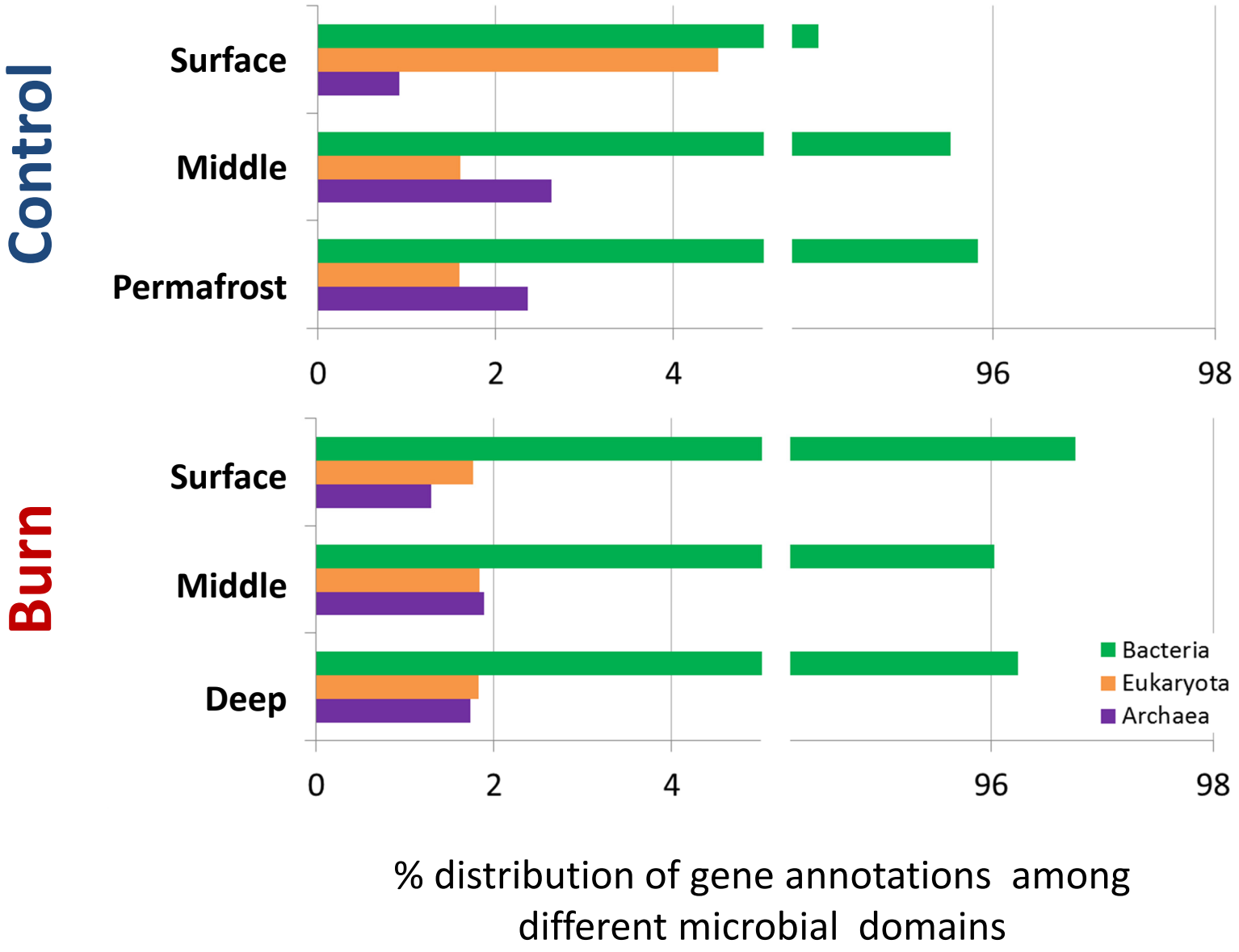

Control
Surface
Middle
Permafrost
0
2
4
96
98
Burn
Surface
Middle
Deep
0
2
4
96
98
Bacteria
Eukaryota
Archaea
% distribution of gene annotations among different microbial domains

Figure S7

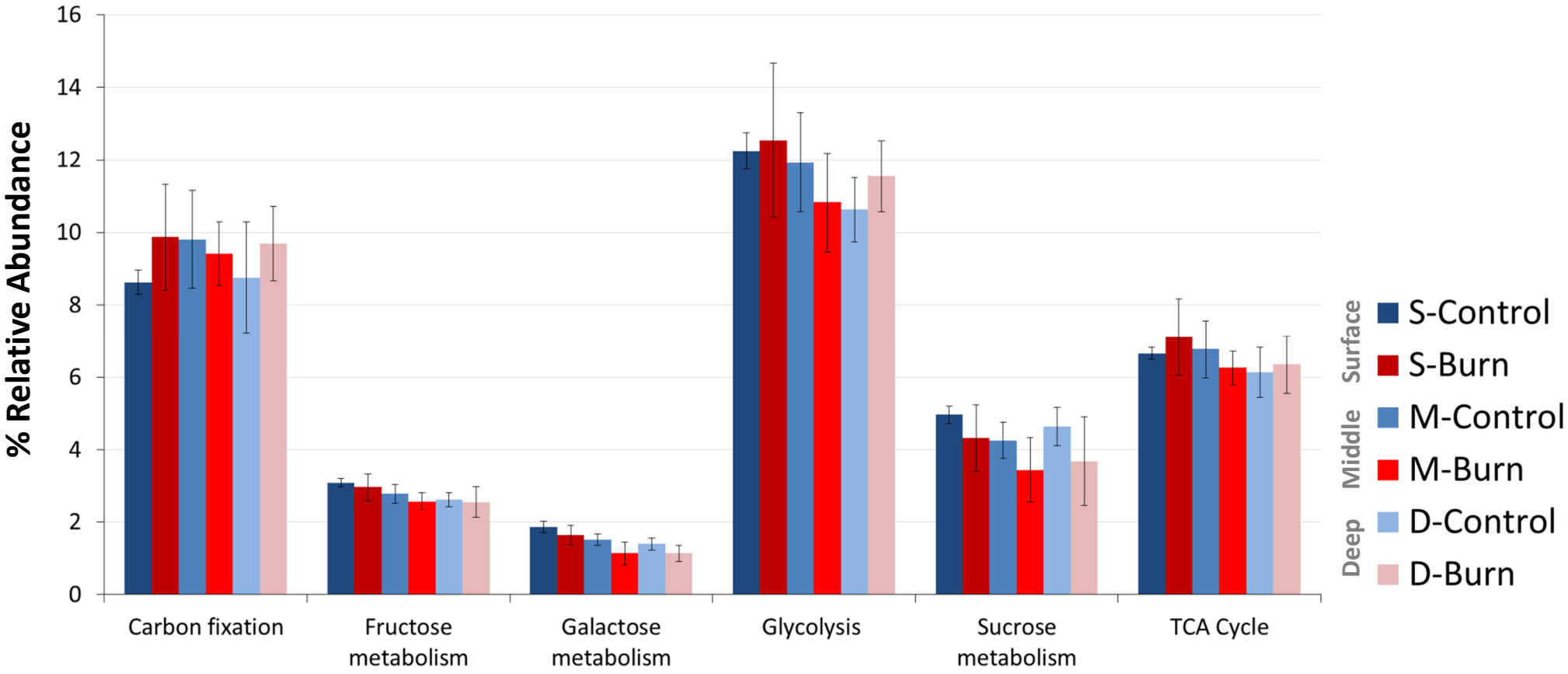

% Relative Abundance
16
14
12
10
8
6
4
2
0
Carbon fixation
Fructose metabolism
Galactose metabolism
Glycolysis
Sucrose metabolism
TCA Cycle
Surface
Middle
Deep
S-Control
S-Burn
M-Control
M-Burn
D-Control
D-Burn

Figure S8

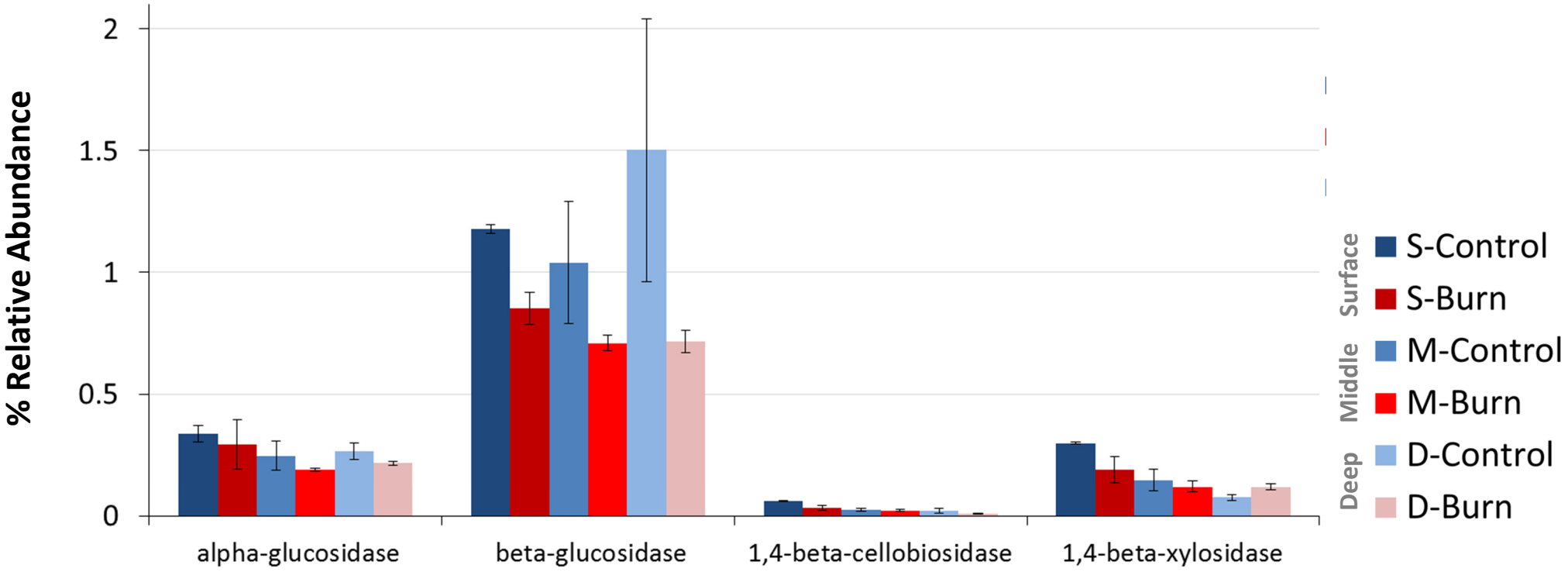

% Relative Abundance
2
1.5
1
0.5
0
alpha-glucosidase
beta-glucosidase
1,4-beta-cellobiosidase
1,4-beta-xylosidase
Surface
Middle
Deep
S-Control
S-Burn
M-Control
M-Burn
D-Control
D-Burn

Figure S9

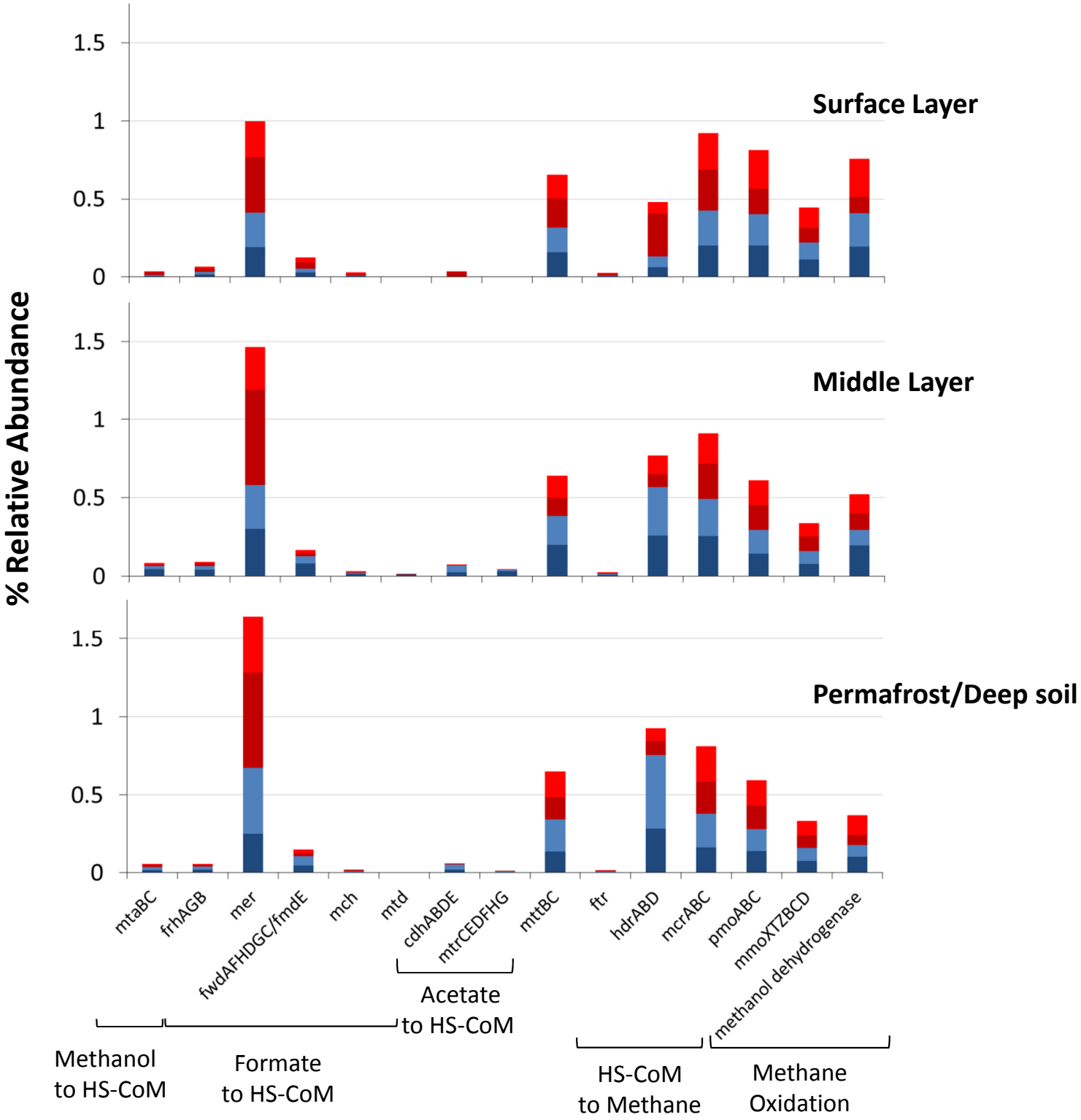

Control
Burn
% Relative Abundance
Surface Layer
Middle Layer
Permafrost/Deep soil
1.5
1
0.5
0
mtaBC
frhAGB
mer
fwdAFHDGC/fmdE
mch
mtd
cdhABDE
mtrCEDFHG
mttBC
ftr
hdrABD
mcrABC
pmoABC
mmoXTZBCD
methanol dehydrogenase
Methanol to HS-CoM
Formate to HS-CoM
Acetate to HS-CoM
HS-CoM to Methane
Methane Oxidation

Figure S10

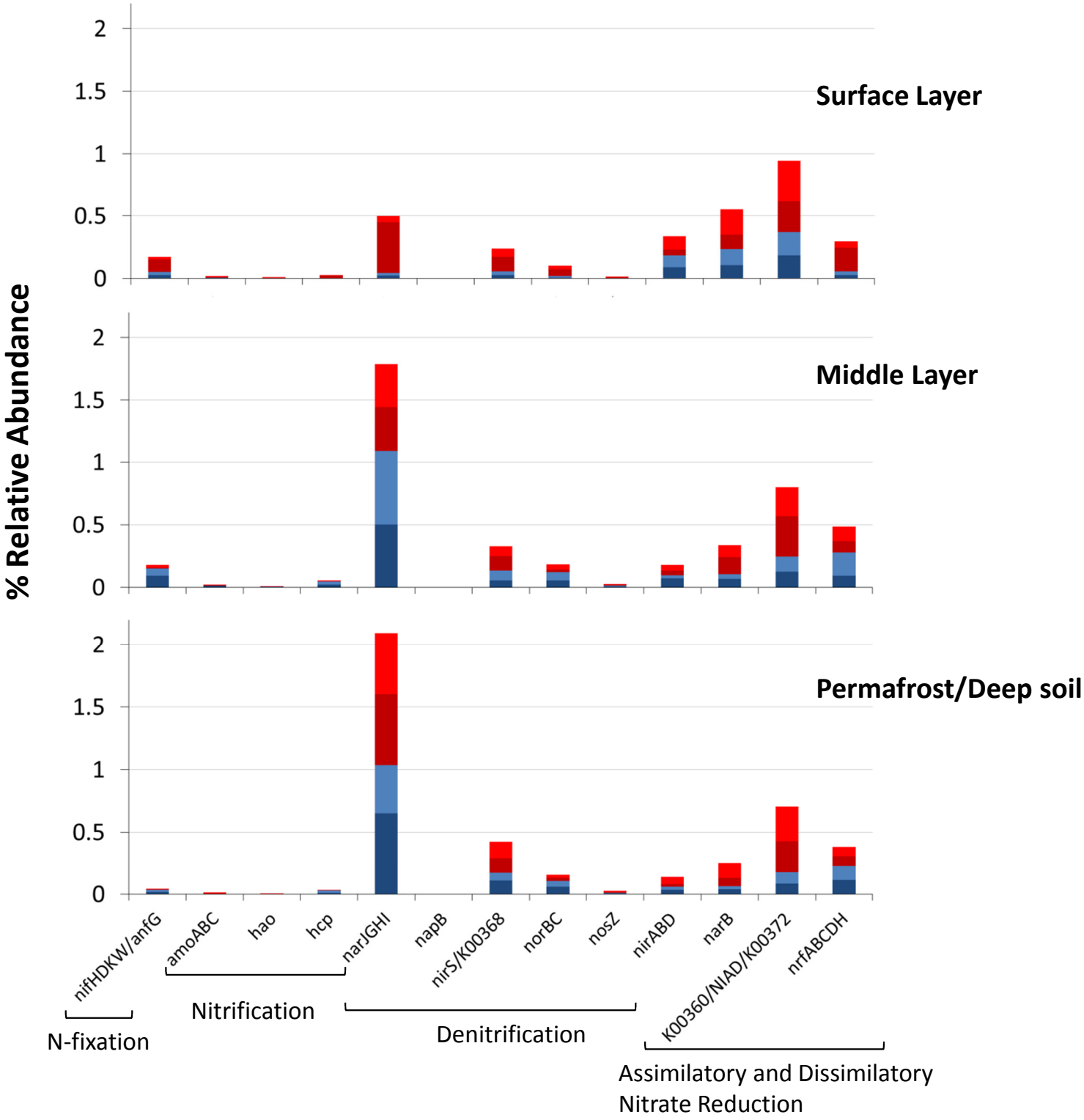

Control
Burn
% Relative Abundance
Surface Layer
Middle Layer
Permafrost/Deep soil
0
0.5
1
1.5
2
nifHDKW/anfG
amoABC
hao
hcp
narJGHI
napB
nirS/K00368
norBC
nosZ
nirABD
narB
K00360/NIAD/K00372
nrfABCDH
N-fixation
Nitrification
Denitrification
Assimilatory and Dissimilatory
Nitrate Reduction

Figure S11

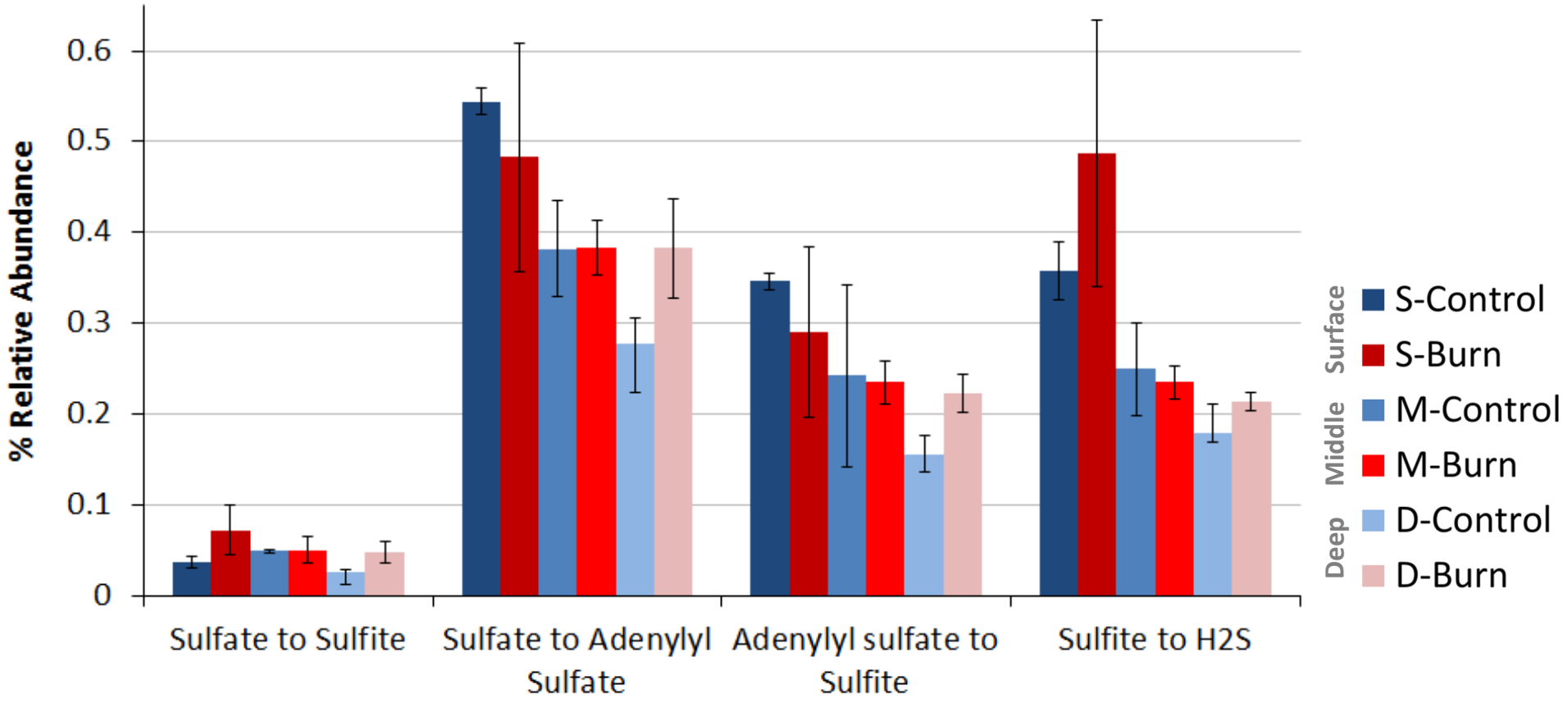
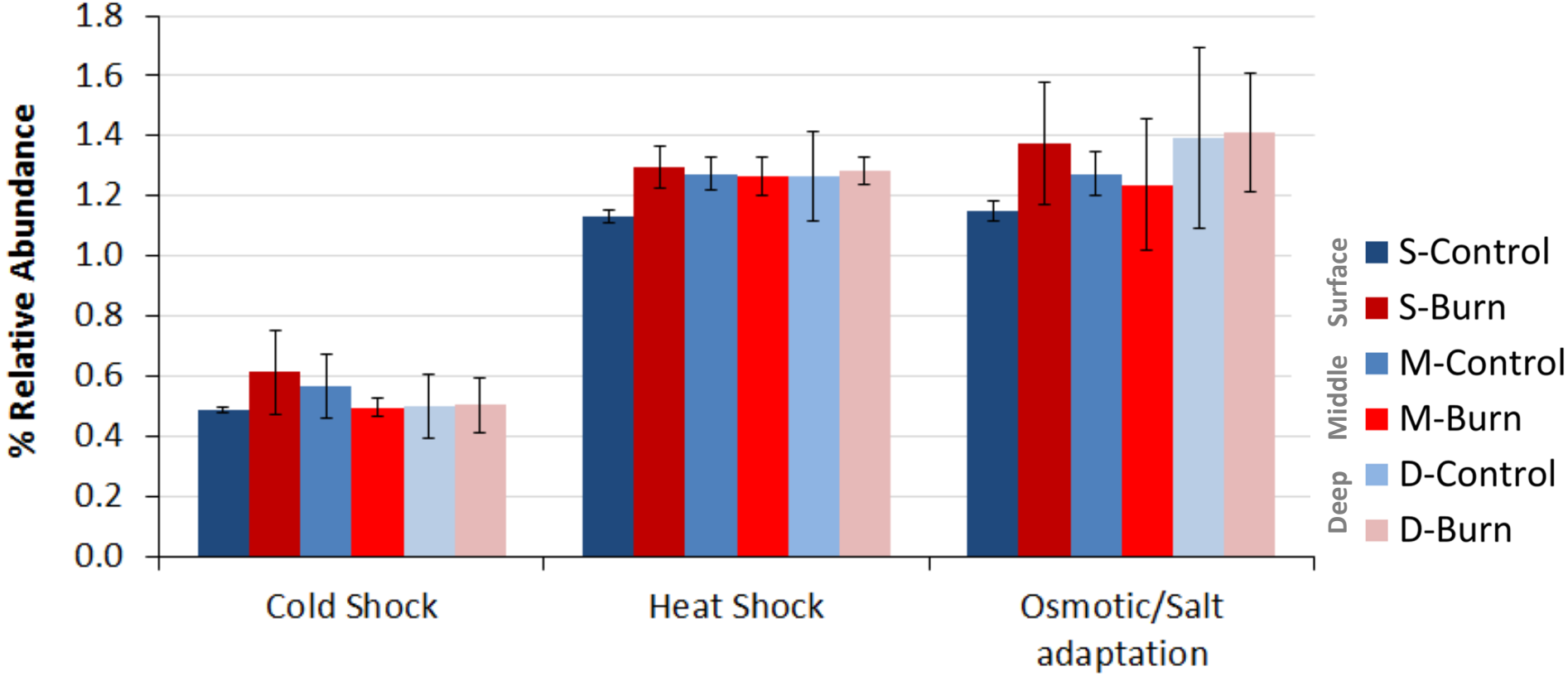

% Relative Abundance
0.6
0.5
0.4
0.3
0.2
0.1
0
Sulfate to Sulfite
Sulfate to Adenylyl Sulfate
Adenylyl sulfate to Sulfite
Sulfite to H2S
Surface
Middle
Deep
S-Control
S-Burn
M-Control
M-Burn
D-Control
D-Burn

Figure S12


% Relative Abundance
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Cold Shock
Heat Shock
Osmotic/Salt adaptation
Surface
Middle
Deep
S-Control
S-Burn
M-Control
M-Burn
D-Control
D-Burn