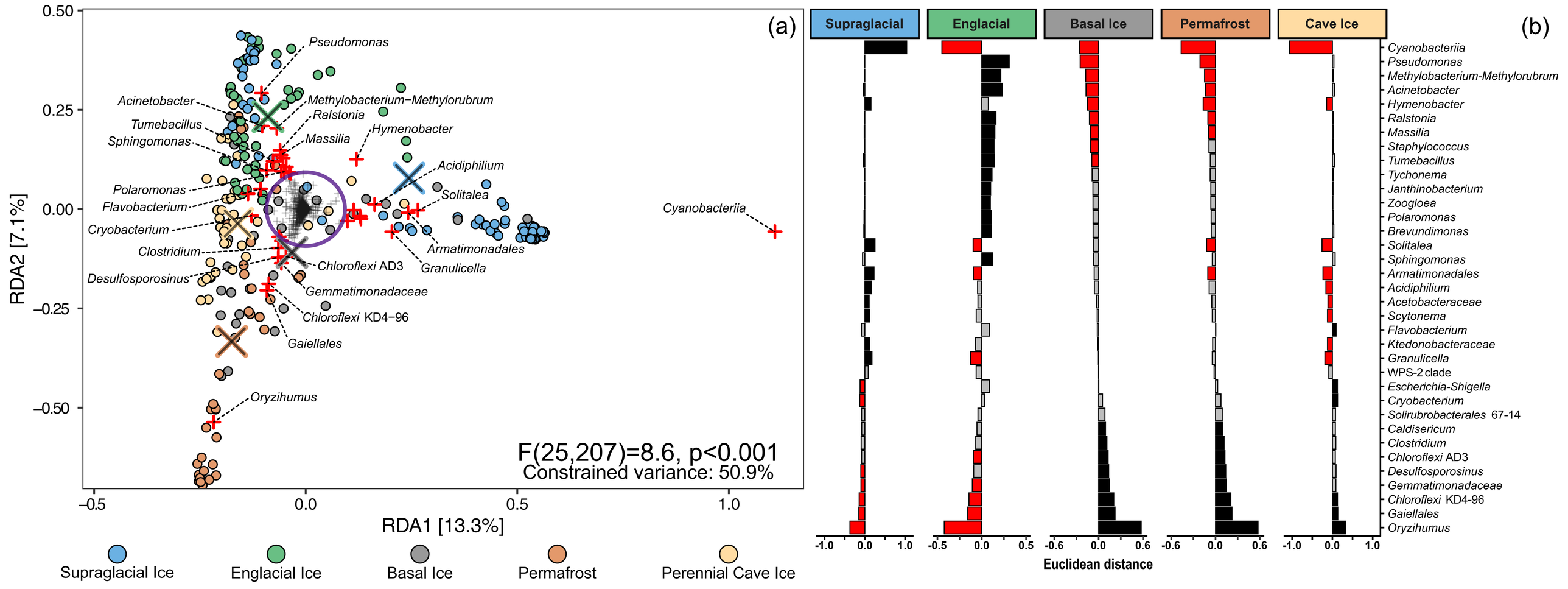
(a)
RDA2 [7.1%]
RDA1 [13.3%]
0.50
0.25
0.00
−0.25
−0.50
−0.5
0.0
0.5
1.0
Pseudomonas
Acinetobacter
Methylobacterium−Methylorubrum
Ralstonia
Tumebacillus
Hymenobacter
Sphingomonas
Massilia
Acidiphilium
Solitalea
Polaromonas
Flavobacterium
Cryobacterium
Armatimonadales
Clostridium
Chloroflexi AD3
Granulicella
Desulfosporosinus
Gemmatimonadaceae
Chloroflexi KD4−96
Gaiellales
Oryzihumus
Cyanobacteriia
F(25,207)=8.6, p<0.001
Constrained variance: 50.9%
Supraglacial Ice
Englacial Ice
Basal Ice
Permafrost
Perennial Cave Ice
Supraglacial
Englacial
Basal Ice
Permafrost
Cave Ice
(b)
-1.0
0.0
1.0
-0.5
0.0
0.5
-0.6
0.0
0.6
-0.6
0.0
0.6
-1.0
0.0
1.0
Euclidean distance
Cyanobacteriia
Pseudomonas
Methylobacterium-Methylorubrum
Acinetobacter
Hymenobacter
Ralstonia
Massilia
Staphylococcus
Tumebacillus
Tychonema
Janthinobacterium
Zoogloea
Polaromonas
Brevundimonas
Solitalea
Sphingomonas
Armatimonadales
Acidiphilium
Acetobacteraceae
Scytonema
Flavobacterium
Ktedonobacteraceae
Granulicella
WPS-2 clade
Escherichia-Shigella
Cryobacterium
Solirubrobacterales 67-14
Caldisericum
Clostridium
Chloroflexi AD3
Desulfosporosinus
Gemmatimonadaceae
Chloroflexi KD4-96
Gaiellales
Oryzihumus