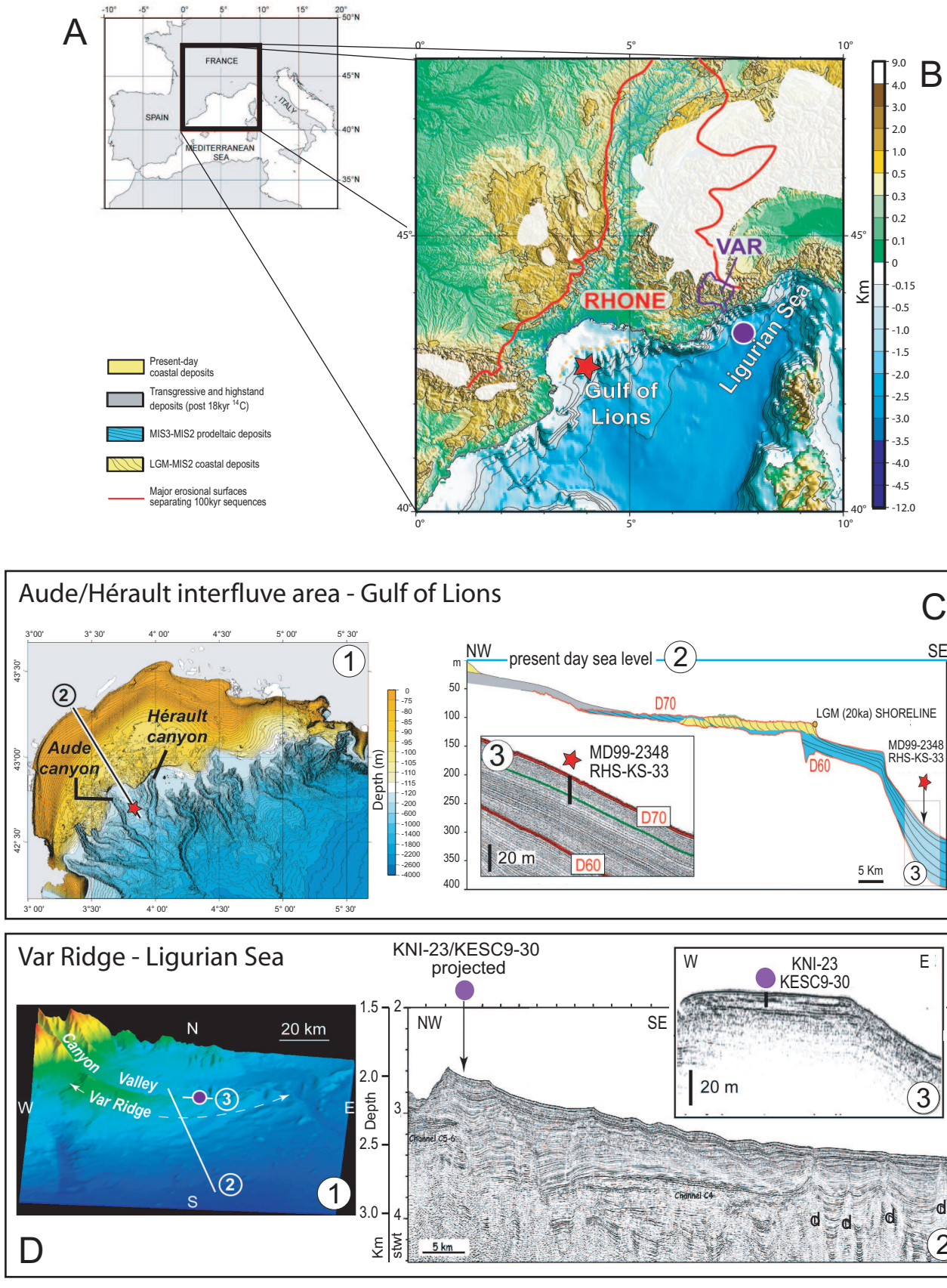

A
B
FRANCE
SPAIN
ITALY
MEDITERRANEAN SEA
VAR
RHONE
Gulf of Lions
Ligurian Sea
Km
Present-day coastal deposits
Transgressive and highstand deposits (post 18kyr 14C)
MIS3-MIS2 prodeltaic deposits
LGM-MIS2 coastal deposits
Major erosional surfaces separating 100kyr sequences
Aude/Hérault interfluve area - Gulf of Lions
C
Hérault canyon
Aude canyon
Depth (m)
NW
present day sea level
SE
D70
D60
LGM (20ka) SHORELINE
MD99-2348
RHS-KS-33
20 m
5 Km
Var Ridge - Ligurian Sea
KNI-23/KESC9-30
projected
KNI-23
KESC9-30
W
E
N
S
20 km
Canyon
Valley
Var Ridge
Depth
Km
stwt
5 km
Channel C5-6
Channel C4
D

Fig.1

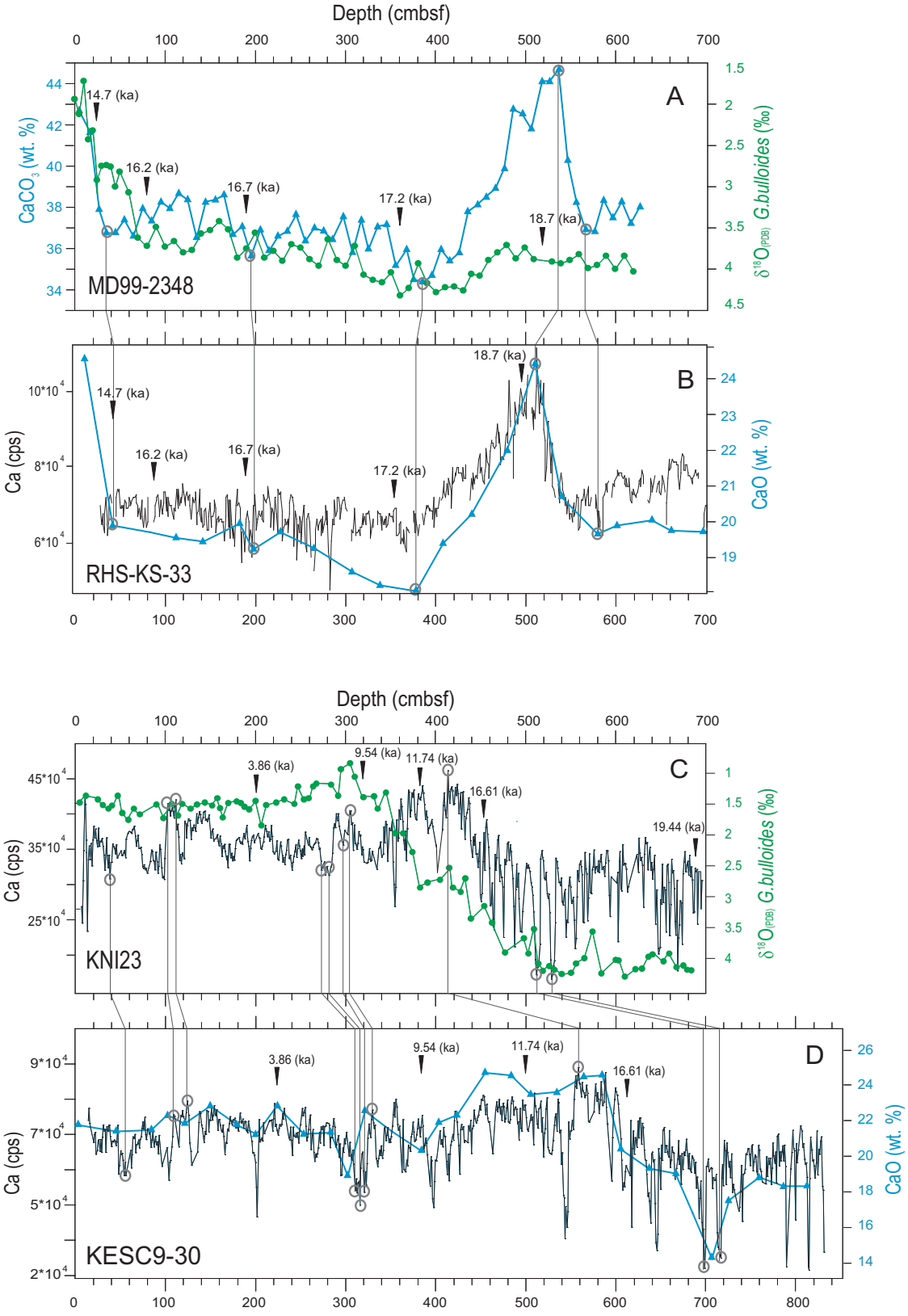

Depth (cmbsf)
A
MD99-2348
CaCO3 (wt. %)
δ18O(PDB) G.bulloides (‰)
14.7 (ka)
16.2 (ka)
16.7 (ka)
17.2 (ka)
18.7 (ka)
B
RHS-KS-33
Ca (cps)
CaO (wt. %)
C
KNI23
3.86 (ka)
9.54 (ka)
11.74 (ka)
16.61 (ka)
19.44 (ka)
D
KESC9-30

Fig.2

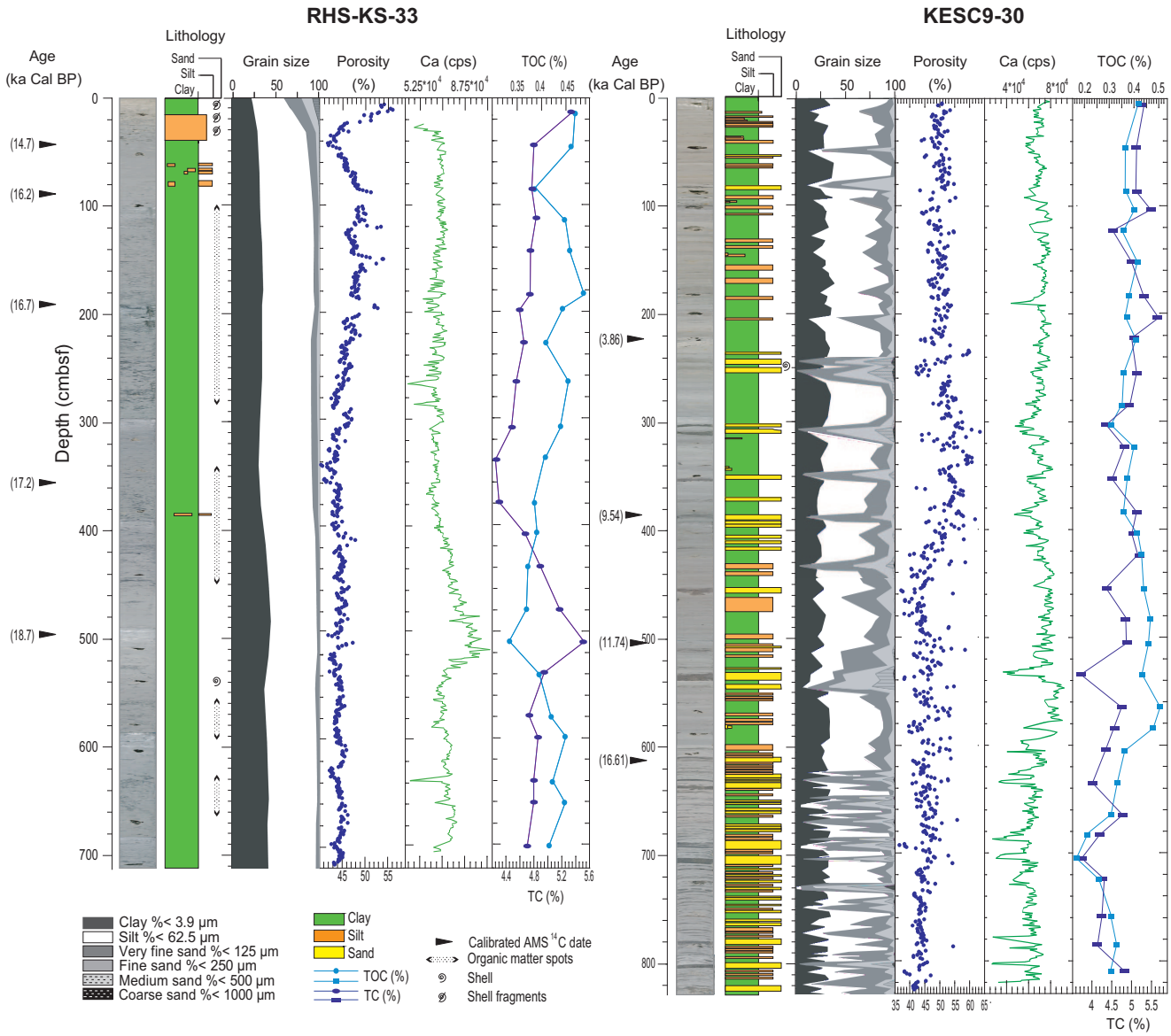

RHS-KS-33
KESC9-30
Age
(ka Cal BP)
Lithology
Sand
Silt
Clay
Grain size
Porosity
(%)
Ca (cps)
TOC (%)
TC (%)
Depth (cmbsf)
(14.7)
(16.2)
(16.7)
(17.2)
(18.7)
(3.86)
(9.54)
(11.74)
(16.61)
Clay %< 3.9 µm
Silt %< 62.5 µm
Very fine sand %< 125 µm
Fine sand %< 250 µm
Medium sand %< 500 µm
Coarse sand %< 1000 µm
Clay
Silt
Sand
TOC (%)
TC (%)
Calibrated AMS 14C date
Organic matter spots
Shell
Shell fragments

Fig.3

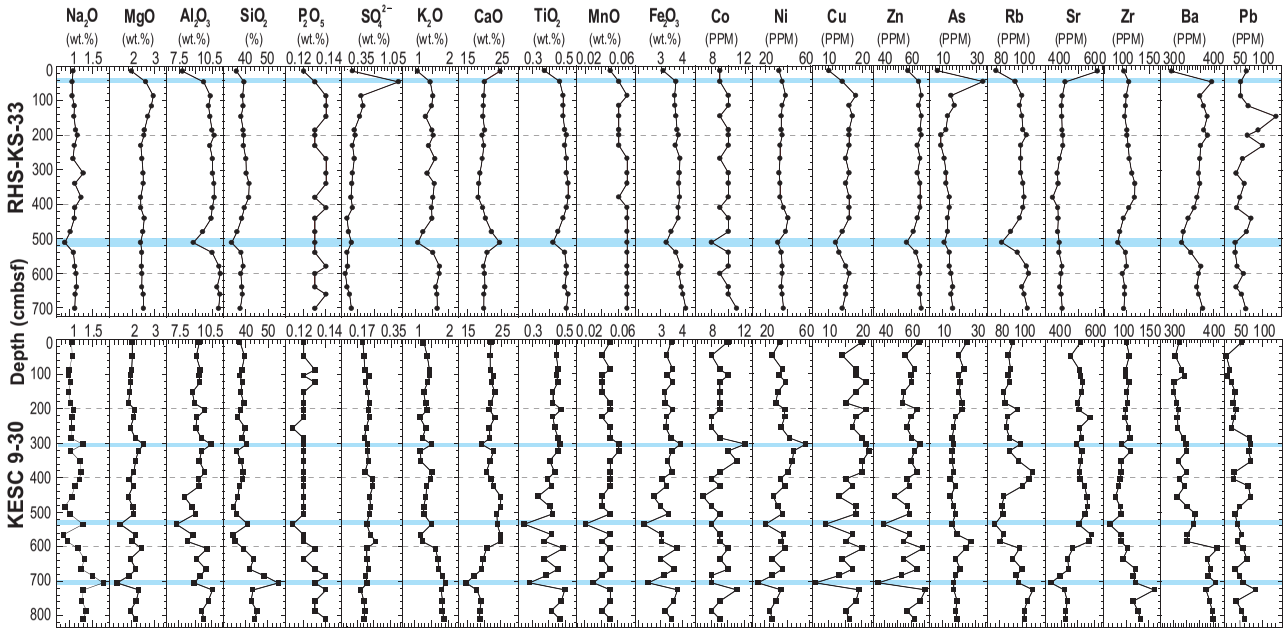

Na2O (wt.%)
MgO (wt.%)
Al2O3 (wt.%)
SiO2 (%)
P2O5 (wt.%)
SO4 2− (wt.%)
K2O (wt.%)
CaO (wt.%)
TiO2 (wt.%)
MnO (wt.%)
Fe2O3 (wt.%)
Co (PPM)
Ni (PPM)
Cu (PPM)
Zn (PPM)
As (PPM)
Rb (PPM)
Sr (PPM)
Zr (PPM)
Ba (PPM)
Pb (PPM)
RHS-KS-33
Depth (cmbsf)
KESC 9-30

Fig.4

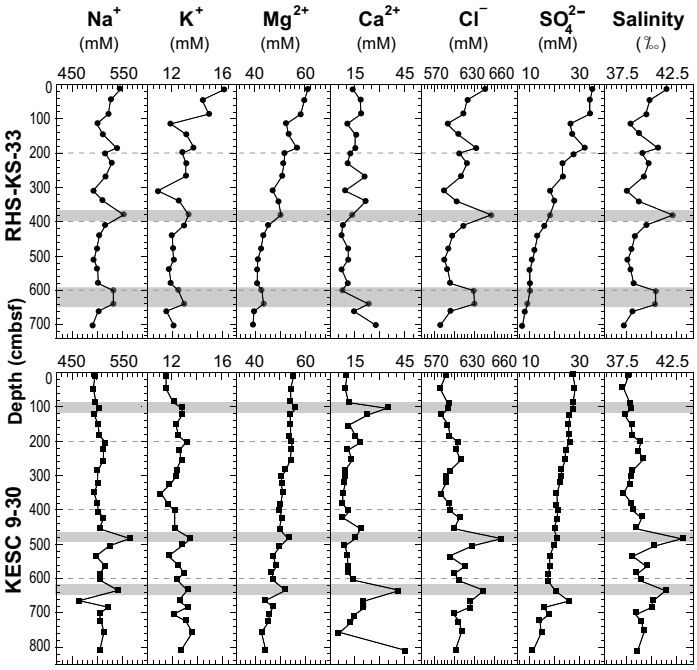

Na+ (mM)
K+ (mM)
Mg2+ (mM)
Ca2+ (mM)
Cl− (mM)
SO42− (mM)
Salinity (‰)
RHS-KS-33
KESC 9-30
Depth (cmbsf)

Fig.5

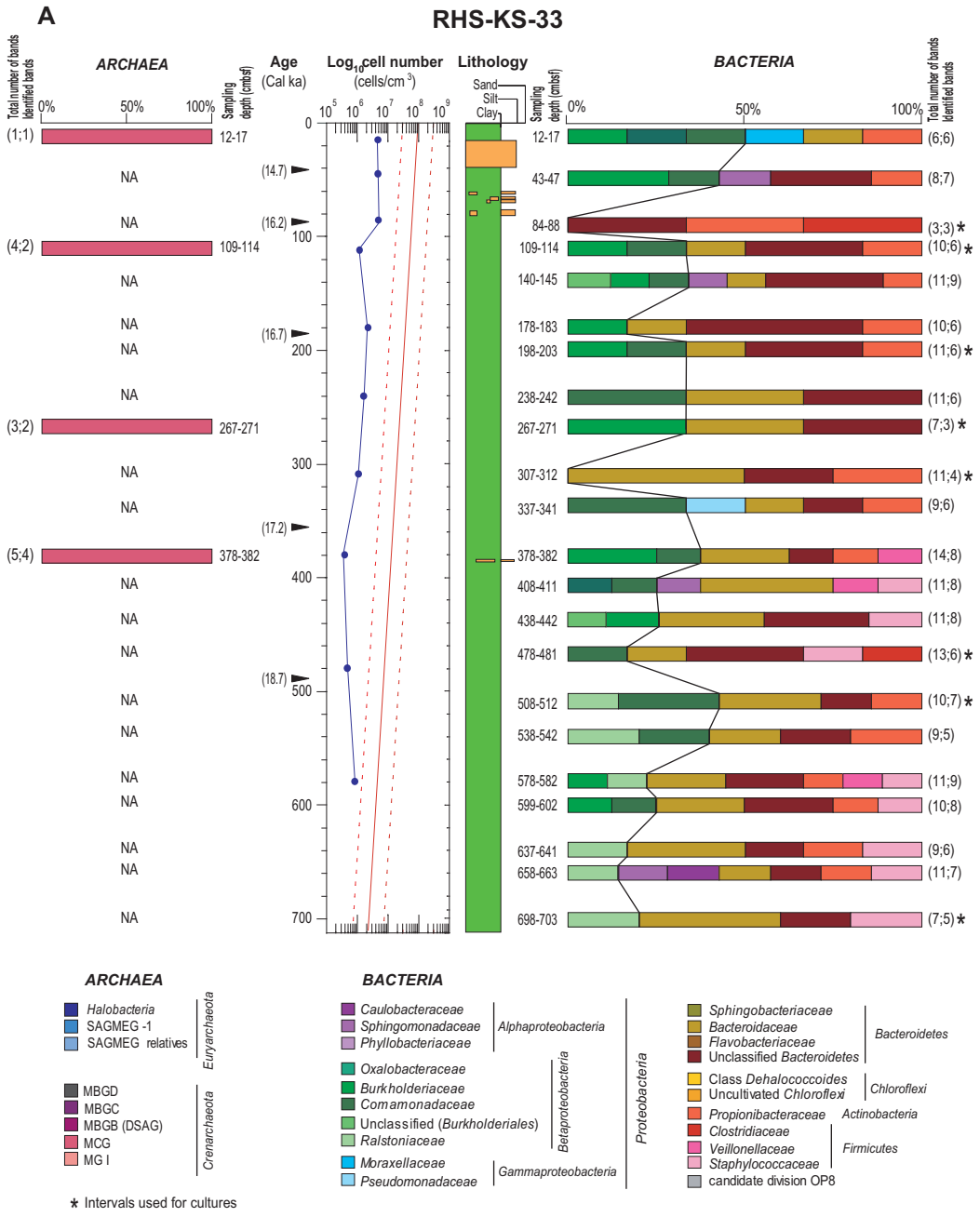

A
RHS-KS-33
ARCHAEA
BACTERIA
Age (Cal ka)
Log10cell number (cells/cm3)
Lithology
Sand
Silt
Clay
Total number of bands identified bands
Sampling depth (cmbsf)
0%
50%
100%
(1;1) 12-17
NA
NA
(4;2) 109-114
NA
NA
NA
(3;2) 267-271
NA
NA
(5;4) 378-382
NA
NA
NA
NA
NA
NA
NA
NA
(14.7)
(16.2)
(16.7)
(17.2)
(18.7)
0
100
200
300
400
500
600
700
12-17 (6;6)
43-47 (8;7)
84-88 (3;3)*
109-114 (10;6)*
140-145 (11;9)
178-183 (10;6)
198-203 (11;6)*
238-242 (11;6)
267-271 (7;3)*
307-312 (11;4)*
337-341 (9;6)
378-382 (14;8)
408-411 (11;8)
438-442 (11;8)
478-481 (13;6)*
508-512 (10;7)*
538-542 (9;5)
578-582 (11;9)
599-602 (10;8)
637-641 (9;6)
658-663 (11;7)
698-703 (7;5)*
ARCHAEA
Halobacteria
SAGMEG -1
SAGMEG relatives
Euryarchaeota
MBGD
MBGC
MBGB (DSAG)
MCG
MG I
Crenarchaeota
* Intervals used for cultures
BACTERIA
Caulobacteraceae
Sphingomonadaceae
Phyllobacteriaceae
Alphaproteobacteria
Oxalobacteraceae
Burkholderiaceae
Comamonadaceae
Unclassified (Burkholderiales)
Ralstoniaceae
Betaproteobacteria
Moraxellaceae
Pseudomonadaceae
Gammaproteobacteria
Proteobacteria
Sphingobacteriaceae
Bacteroidaceae
Flavobacteriaceae
Unclassified Bacteroidetes
Bacteroidetes
Class Dehalococcoides
Uncultivated Chloroflexi
Chloroflexi
Propionibacteraceae
Actinobacteria
Clostridiaceae
Veillonellaceae
Staphylococcaceae
Firmicutes
candidate division OP8

Fig. 6 A

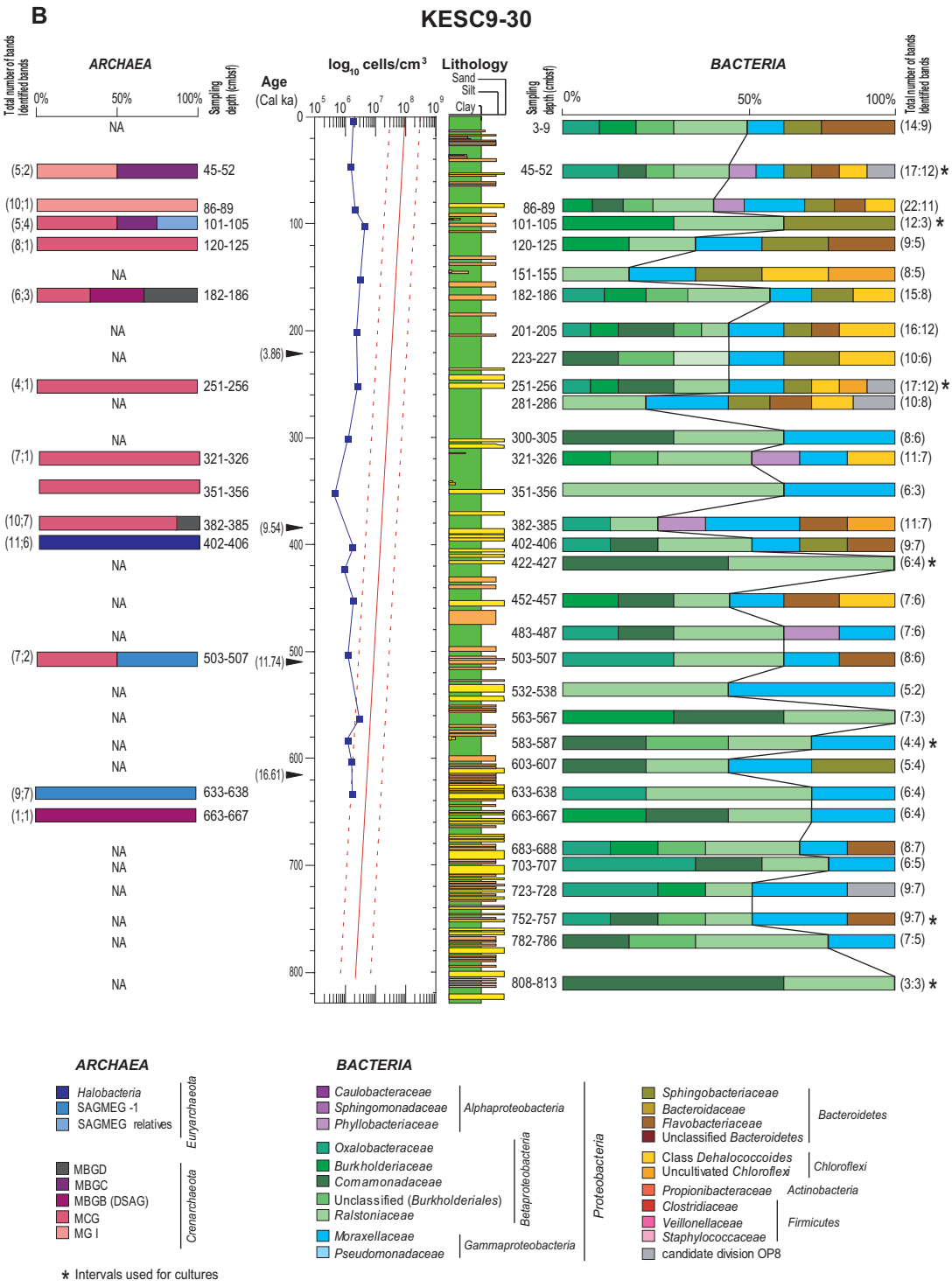

B
KESC9-30
ARCHAEA
BACTERIA
Age (Cal ka)
log10 cells/cm3
Lithology
Sand
Silt
Clay
Total number of bands identified bands
Sampling depth (cmbsf)
0%
50%
100%
NA
(5;2) 45-52
(10;1) 86-89
(5;4) 101-105
(8;1) 120-125
(6;3) 182-186
(4;1) 251-256
(7;1) 321-326
351-356
(10;7) 382-385
(11;6) 402-406
(7;2) 503-507
(9;7) 633-638
(1;1) 663-667
(3.86)
(9.54)
(11.74)
(16.61)
3-9 (14:9)
45-52 (17:12) *
86-89 (22:11)
101-105 (12:3) *
120-125 (9:5)
151-155 (8:5)
182-186 (15:8)
201-205 (16:12)
223-227 (10:6)
251-256 (17:12) *
281-286 (10:8)
300-305 (8:6)
321-326 (11:7)
351-356 (6:3)
382-385 (11:7)
402-406 (9:7)
422-427 (6:4) *
452-457 (7:6)
483-487 (7:6)
503-507 (8:6)
532-538 (5:2)
563-567 (7:3)
583-587 (4:4) *
603-607 (5:4)
633-638 (6:4)
663-667 (6:4)
683-688 (8:7)
703-707 (6:5)
723-728 (9:7)
752-757 (9:7) *
782-786 (7:5)
808-813 (3:3) *
ARCHAEA
Halobacteria
SAGMEG -1
SAGMEG relatives
Euryarchaeota
MBGD
MBGC
MBGB (DSAG)
MCG
MG I
Crenarchaeota
BACTERIA
Caulobacteraceae
Sphingomonadaceae
Phyllobacteriaceae
Alphaproteobacteria
Oxalobacteraceae
Burkholderiaceae
Comamonadaceae
Unclassified (Burkholderiales)
Ralstoniaceae
Betaproteobacteria
Moraxellaceae
Pseudomonadaceae
Gammaproteobacteria
Proteobacteria
Sphingobacteriaceae
Bacteroidaceae
Flavobacteriaceae
Unclassified Bacteroidetes
Bacteroidetes
Class Dehalococcoides
Uncultivated Chloroflexi
Chloroflexi
Propionibacteraceae
Actinobacteria
Clostridiaceae
Veillonellaceae
Staphylococcaceae
Firmicutes
candidate division OP8
* Intervals used for cultures

Fig. 6B

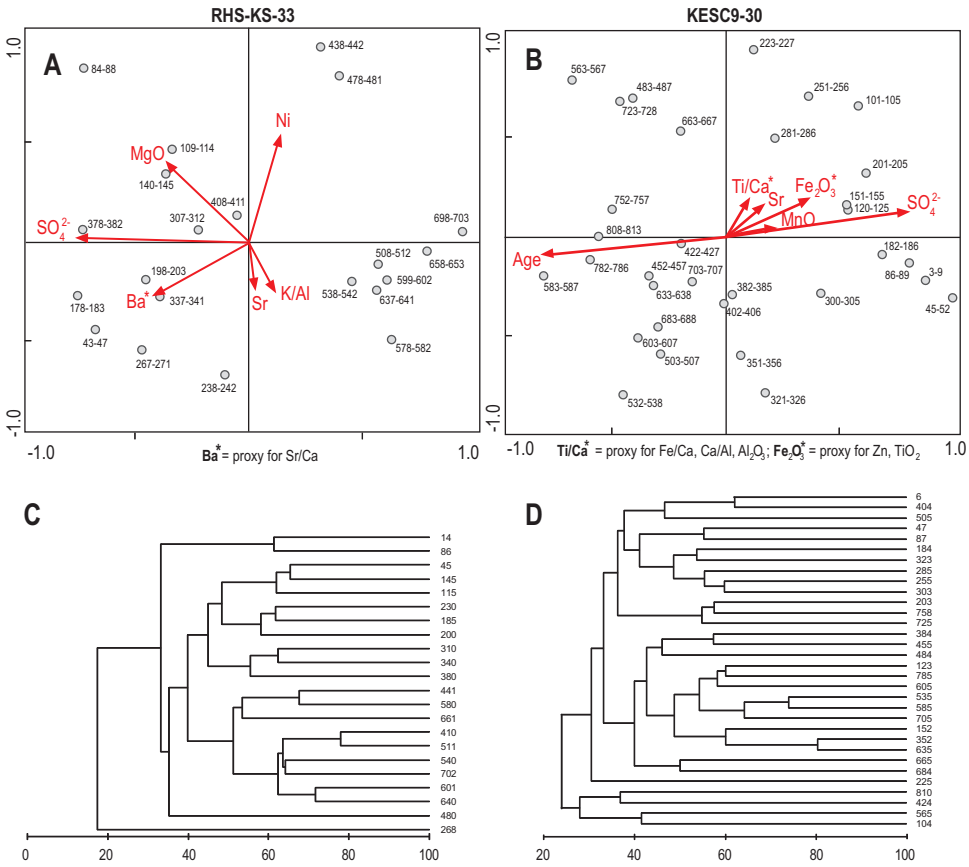

RHS-KS-33
KESC9-30
A
B
C
D
Ni
MgO
Ba*
Sr
K/Al
Age
Ti/Ca*
Fe2O3*
MnO
SO4 2-
Ba* = proxy for Sr/Ca
Ti/Ca* = proxy for Fe/Ca, Ca/Al, Al2O3; Fe2O3* = proxy for Zn, TiO2
1.0
-1.0
0
20
40
60
80
100

Fig.7

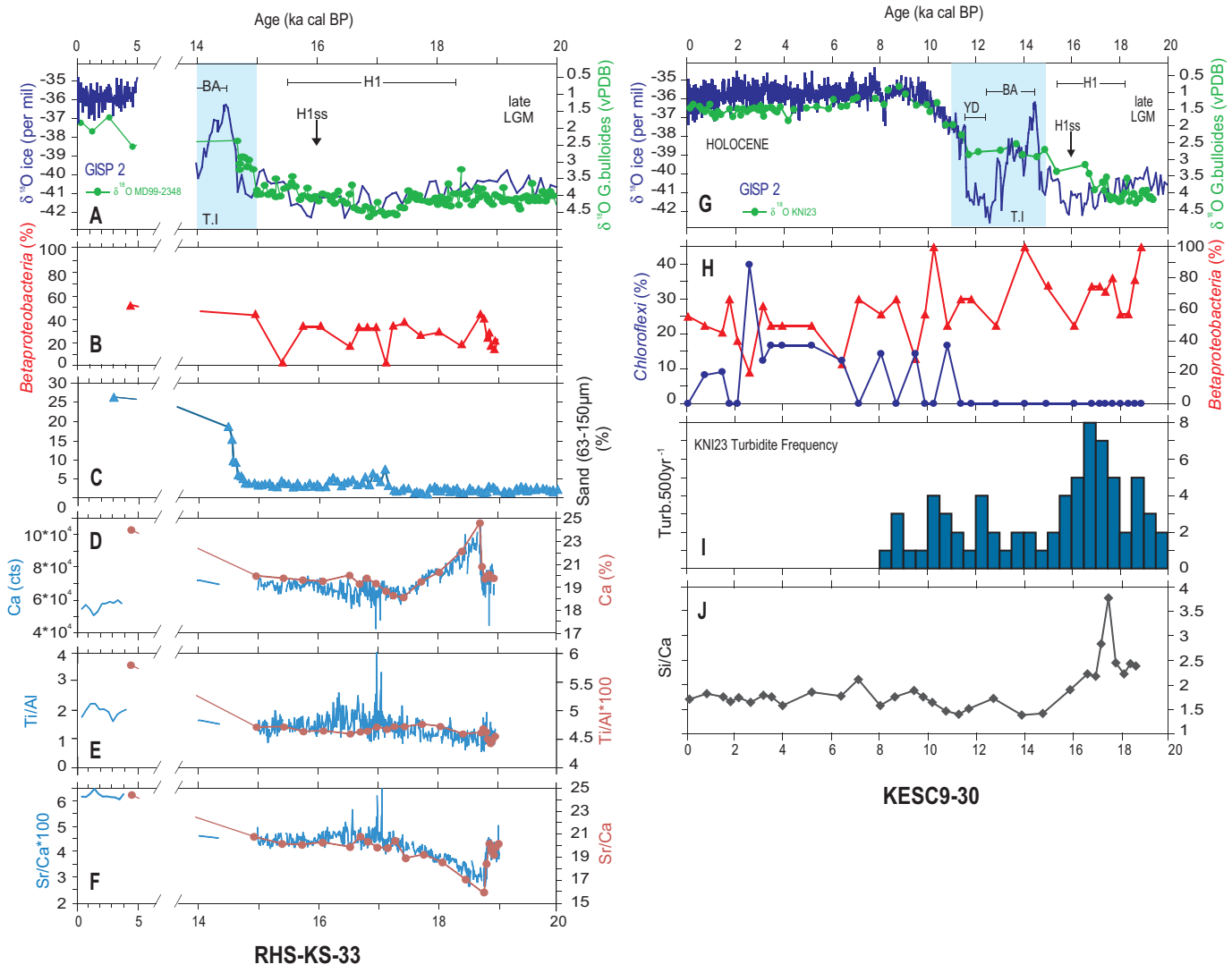

Age (ka cal BP)
δ 18O ice (per mil)
GISP 2
δ 18O MD99-2348
BA
H1
H1ss
late LGM
T.I
δ 18O G.bulloides (vPDB)
A
Betaproteobacteria (%)
B
Sand (63-150µm) (%)
C
Ca (cts)
D
Ca (%)
Ti/Al
E
Ti/Al*100
Sr/Ca*100
F
Sr/Ca
RHS-KS-33
HOLOCENE
YD
G
δ 18O KNI23
H
Chloroflexi (%)
KNI23 Turbidite Frequency
Turb.500yr-1
I
J
Si/Ca
KESC9-30

Fig. 8

Supplementary information

Sampling strategy

Sampling of 1 m-long sections was done in the laboratory in sterile conditions, immediately upon arrival (3 days). First, the core liner was aseptically opened (near a Bunsen gas burner) using a sterile grinder, and the sediment (> 1 cm) in contact with the core liners was removed using a sterile spatula. Subsamples for microbial analysis were aseptically collected from the inner part of the cores using end-cut sterile 2 ml syringes. 100-150 cm^3 samples were directly frozen at –80℃ for molecular analyses (DNA extract ions); 1 cm^3 samples for cells counts were placed in 15 ml vials containing 9 ml of 4% formalin/30 $g.l^{-1}$ NaCl solution and stored at 4℃; 5 cm^3 samples for cultures were placed into 100ml vials containing 25 ml of sterile artificial seawater, and stored at 4℃. Samples for anaerobic cultures were flushed with pure nitrogen and reduced by the addition of 0.1 $g.l^{-1}$ sodium sulphide from a sterile stock solution. Subsamples for sediment and porewater chemistry were taken at the same depth than the samples taken for microbial investigations. The sediment taken for porewater analysis was immediately centrifuged (13000 *g* at 4℃, for 30 min), in order to extract the porew ater. TOC and TC measurements were performed on the pellets got from the porewater extraction. These pellets (ca. 2g) were oven-dried (65℃, for 2 0 h) and reduced into powder in a ceramic mortar. Samples for quantitative elemental chemical composition (10 g) were taken from the inner part of the core and transformed into fused beads and powder pellets, as described in the next section. Samples for grain size analysis were directly taken from the cores and immediately analysed.

Oxygenation state of the cores during the subsampling

Core RHS-KS-33 was characterized by the presence of black organic matter spots (Fig. 3). An oxidation of these organic matter spots, indicated by a change in color (black spots turned yellow), was observed to occur during the following 24 hours after core splitting. These organic matter spots were also noticed on the twin core MD99-2348, recovered several years before. The difference between the two cores is that core MD99-2348 was split in half onboard, immediately upon arrival on the core deck, and that core RHS-KS-33, was split in half in the laboratory, after 3 days of transport. These observations strongly indicate that the oxic state of both cores (RHS-KS-33 and twin core MD99-2348) was similar, and that the transport at 4℃ did not affect the main physical characteristics of the cores. As core KESC9-30 was stored, transported and subsampled under exactly the same conditions and within the same time period, this core should not have been affected nor oxidized during the transport or subsequent subsampling.

Major and trace elements analysis on fused beads and powder pellets

Fused beads and compressed powder pellets were used for major and trace elements analysis, respectively. The fusion beads were made as follows: 1 g of sediment was dried (110℃, 12 h), then crushed into powder in a ceramic mortar and calcined at 1050℃ under air in a muffle furnace. One aliquot of 0.5 g of calcined powder was mixed with 9 g of Spectrolux 120A ($Li_2B_4O_7$ 90% - LiF 10% provided by Johnson Matthey) and 500 µl of a LiBr 250 $g.l^{-1}$ solution and heated at 1050℃ for 15 minutes. The powder pellets were made by mixing 4 g of dry crushed sediment (110℃, 12 h) with 0.4 g of micropowder Hoechst C wax (Luzzato S.A.) and compressed into pellets of 32 mm diameter and 3 mm thick. Characteristic element lines net intensities corrected from matrix effects and overlaps were correlated with numerous well certified reference material concentrations to elaborate linear calibration curves (El Maghraoui et al., 1999).

Total cell counts

The cell count protocol used in this study includes several steps, and notably a multi-steps cell separation from the sediment matrix. After preparing the primary slurry (1/10 dilution of the original sample in a 4% formalin/30 $g.l^{-1}$ NaCl solution), carbonates (if present) were dissolved, and then extracellular polymers, which bind the cells to mineral grains, were destabilized. As a final step, the cells were separated from the minerals by density centrifugation through a cushion of Nycodenz. The supernatants from the density centrifugation were filtered onto 0.2 μm filters (Whatman Anodisc). The cells were stained with SYBR®Green I nucleic acid gel stain (Molecular Probes, Invitrogen) according to the protocol of Noble and Fuhrman (1998), with 0.1% *p*-phenylenediamine (Sigma-Aldrich, Deissenhofen, Germany) as an anti-fading agent. Cells were counted using epifluorescence microscopy using a blue filter set. When necessary, silicates were dissolved prior to carbonate dissolution step; in that case, the sediment slurry was mixed with 450 µl of hydrofluoric acid (HF) (Sigma-Aldrich, Deissenhofen, Germany) solution (1.0% (wt/v) HF, 3% (wt/v) NaCl) in a plastic test tube and then incubated for 20 min at room temperature. The HF reaction was stopped by adding 2ml of stop solution (1M Tris-hydrochloric acid (HCl) (pH 8.0), 0.125M $CaCl_2$ and 25% methanol). Washing of sediment slurries with HF significantly reduces non-biological fluorescent signals due to amorphous silica and enhances the efficiency of cell detachment from the particles (Morono et al., 2009).

PCR-DGGE

We performed a nested PCR amplification for bacterial and archaeal 16S rRNA genes. Bacterial primary amplification reactions were performed with 1X polymerase reaction buffer (MP Biomedicals®), 2 mM $MgCl_2$, 0.24 mM of each dNTP, 0.5 µM of each primer, 1U of *Taq* DNA polymerase (MP Biomedicals®) and 1 µl of DNA template (1:5 dilution) in a 25 µl PCR reaction mixture with RNase/DNase Free Water (MP Biomedicals®). Reaction mixtures were held at 94 ℃ for 3 min followed by 30 cycles of 94 ℃ for 60 s, 50℃ for 90 s and 72℃ for 2

min, with a final extension step of 6 min at 72℃. The second (nested) PCR amplification step was carried out as above in a 35 µl reaction mixture. The second amplification was performed at 94℃ for 3 min, followed by 25 cycles at 94℃ for 60 s, at 55℃ for 60 s and at 72℃ for 90 s with a final extension of 7 min at 72 ℃. The PCR conditions for archaeal 16S rRNA gene amplifications were the same as described for the bacterial 16S rRNA amplification but the annealing temperature was of 54℃ for the first primer set and of 57℃ for the second primer set.

The PCR products were analyzed by DGGE using the BioRad™ DCode Universal Mutation Detection System® on a 1 mm thick (16 x 16 cm) 6% (w/v) polyacrylamide gel (acrylamide/bisacrylamide, 40%, 37.5:1, BioRad™). The gel was prepared with 1X TAE buffer (pH 8, 40 mM Tris Base, 20 mM acetic acid, 1 mM EDTA, MP Biomedicals®) and poured with a gradient maker (Hoefer SG30®). We used different denaturing gradients for bacterial and archaeal community structure analyses (Fig.S1, S2 and S3). Electrophoresis was carried out in a 1X TAE buffer at 60℃ for 10 m in at 80V and then for 5 h at 200V. After migration, gels were stained with SYBR®Gold nucleic acid gel stain (Molecular Probes, Invitrogen) for 45 min, washed for 10 min in 1X TAE and scanned using an UV transilluminator. DGGE bands of interest were excised from the gels with sterile surgical blades, transferred into 30 µl of RNase/DNase free water (MP Biomedicals®) and incubated for 48 h at 4℃. One microliter of DNA solution was taken as a template for reamplification using the same PCR reaction mixture as described above (with the exception that primers were devoid of GC-clamp). The PCR products were then sequenced by Sanger method (Beckman-Coulter Cogenics, Stansted).

Supplementary figure captions

Fig. S1. Denaturing gradient gel electrophoresis (DGGE) analysis of archaeal communities. (A) Archaeal communities from the Gulf of Lions (RHS-KS-33) on a DGGE gradient of 20–80% denaturant, (B) Archaeal communities from the Ligurian Sea (core KESC9-30) on a DGGE gradient of 20-70% denaturant. (C) Sequence similarities to the closest cultivated relatives. White numbered dots represent the bands that were excised and sequenced. M: marker.

Fig. S2. Denaturing gradient gel electrophoresis (DGGE) analysis of bacterial communities. (A) Bacterial communities from the Gulf of Lions (RHS-KS-33) on a DGGE gradient of 30–60% denaturant. (B) Sequence similarities to the closest cultivated relatives. White numbered dots represent the bands that were excised and sequenced, and the grey dots represent the excised bands that migrated on a DGGE-GE gel (data not shown). M: marker.

Fig. S3. Denaturing gradient gel electrophoresis (DGGE) analysis of bacterial communities. (A) Bacterial communities from the Ligurian Sea (core KESC9-30) on a DGGE gradient of 25-55% denaturant. (B) Sequence similarities to the closest cultivated relatives. White numbered dots represent the bands that were excised and sequenced. M: marker.

Supplementary Table

Table S1: Chemical composition of sediments from Western Mediterranean Sea, at two sites: Gulf of Lions and Ligurian Sea.

Depth int. (cmbsf)	Na_2O (%)	MgO (%)	Al_2O_3 (%)	SiO_2 (%)	P_2O_5 (%)	SO_4^{2-} (%)	K_2O (%)	CaO (%)	TiO_2 (%)	MnO (%)	Fe_2O_3 (%)	Co (PPM)	Ni (PPM)	Cu (PPM)	Zn (PPM)	As (PPM)	Rb (PPM)	Sr (PPM)	Zr (PPM)	Ba (PPM)	Pb (PPM)	LOI (%)
Ligurian Sea, KESC9-30																						
3-9	1,03	1,98	9,33	37,29	0,12	0,12	1,25	21,91	0,44	0,05	3,45	10	33	20	65	15	91	513	99	319	53	22,34
45-52	1,04	1,98	9,04	39,34	0,12	0,14	1,35	21,60	0,44	0,04	3,24	8	26	14	55	10	87	453	105	305	18	21,54
86-89	0,98	1,96	9,40	38,14	0,13	0,16	1,42	21,65	0,45	0,05	3,52	9	35	18	62	13	89	505	97	330	26	21,68
101-105	0,96	1,90	9,28	37,34	0,12	0,24	1,43	22,53	0,44	0,04	3,28	10	32	18	59	10	87	514	98	338	19	22,08
120-125	1,01	1,92	9,38	38,32	0,13	0,18	1,36	21,99	0,45	0,04	3,52	9	38	21	60	11	88	526	105	299	29	21,78
151-155	0,96	1,87	8,69	37,67	0,12	0,22	1,24	23,00	0,42	0,04	3,16	9	31	18	54	10	83	518	100	300	38	22,58
182-186	1,01	1,82	8,88	38,99	0,12	0,25	1,30	21,82	0,42	0,05	3,19	9	29	15	53	12	84	494	102	311	34	21,75
201-205	1,08	2,10	9,82	37,63	0,12	0,23	1,35	21,46	0,47	0,05	3,52	9	37	21	64	12	95	500	97	316	40	22,08
223-227	1,03	2,05	9,09	36,41	0,12	0,25	1,13	22,99	0,42	0,04	3,25	8	37	18	59	8	86	569	95	313	35	22,88
251-256	1,03	1,90	9,01	39,69	0,11	0,19	1,30	21,43	0,43	0,05	3,20	8	34	17	56	7	85	506	104	315	30	21,62
281-286	1,02	2,12	9,50	38,13	0,12	0,15	1,21	21,51	0,45	0,05	3,43	9	41	20	60	6	88	517	106	334	70	22,13
300-305	1,28	2,50	10,38	40,17	0,12	0,22	1,48	19,10	0,46	0,06	3,86	12	56	21	66	7	98	490	89	344	71	20,11
321-326	1,01	2,25	9,51	35,82	0,12	0,22	1,15	22,70	0,45	0,06	3,48	10	45	22	62	6	88	521	108	346	68	22,99
351-356	1,21	2,13	9,31	38,00	0,12	0,23	1,16	21,57	0,40	0,05	3,29	11	44	20	59	6	96	512	87	316	73	22,16
382-385	1,24	2,05	9,82	38,75	0,12	0,16	1,49	20,50	0,43	0,05	3,49	9	40	20	64	7	109	504	88	345	36	20,97
402-406	1,20	1,86	9,25	38,69	0,12	0,33	1,45	22,04	0,39	0,05	3,05	8	33	15	56	5	105	511	84	319	35	21,42
422-427	1,10	2,03	9,31	37,06	0,12	0,33	1,33	22,52	0,41	0,05	3,25	9	37	17	58	8	100	537	82	340	67	22,38
452-457	1,03	1,80	7,99	36,35	0,12	0,26	1,31	24,83	0,33	0,04	2,66	7	27	13	47	5	83	549	74	312	72	23,14
483-487	0,88	2,01	8,66	34,61	0,12	0,28	1,24	24,70	0,40	0,04	2,98	8	31	18	57	7	81	554	85	349	48	23,73
503-507	0,99	2,05	8,93	35,78	0,12	0,25	1,25	23,65	0,42	0,05	3,31	9	35	18	58	8	82	538	88	380	38	23,05
532-538	1,28	1,45	7,28	40,88	0,11	0,20	1,47	23,76	0,25	0,02	2,23	8	20	9	39	6	75	500	61	373	42	21,26
563-567	0,85	2,11	8,72	34,16	0,12	0,27	1,16	24,68	0,41	0,05	3,02	9	36	17	58	9	83	575	86	349	53	23,95
583-587	0,93	1,99	8,27	35,15	0,12	0,39	1,21	24,69	0,37	0,04	3,01	9	34	15	54	17	79	562	87	350	42	23,50
603-607	1,17	2,40	10,03	38,89	0,13	0,20	1,60	20,56	0,48	0,05	3,71	10	37	20	68	14	97	465	102	462	55	20,68
633-638	1,31	1,90	9,05	43,46	0,12	0,20	1,66	19,52	0,37	0,04	2,98	9	26	14	54	8	91	435	91	424	64	18,82
663-667	1,25	2,15	9,90	41,68	0,13	0,23	1,70	19,18	0,45	0,05	3,58	10	35	17	64	11	99	441	120	436	38	19,10
683-688	1,50	1,85	9,41	48,18	0,14	0,18	1,79	16,98	0,38	0,04	3,11	8	26	13	52	8	94	390	113	426	48	16,50

703-707	1,73	1,30	8,87	54,38	0,13	0,21	1,89	14,46	0,28	0,03	2,42	8	13	6	35	7	96	336	120	456	55	13,60
723-728	1,29	2,28	10,49	43,10	0,14	0,08	1,77	17,70	0,49	0,05	3,73	11	34	19	70	7	109	415	161	419	84	18,46
752-757	1,26	2,16	10,10	42,30	0,13	0,14	1,80	19,03	0,47	0,05	3,55	9	29	18	66	9	104	433	114	433	40	18,80
782-786	1,36	1,90	9,55	44,90	0,13	0,16	1,80	18,53	0,41	0,04	3,19	8	24	15	56	8	101	424	124	442	53	17,91
808-813	1,28	2,13	9,71	43,97	0,14	0,14	1,85	18,51	0,46	0,05	3,44	9	26	16	62	9	101	422	131	445	58	18,30
Gulf of Lions, RHS-KS-33																						
12-17	1,06	1,95	7,82	35,75	0,12	0,24	1,06	24,60	0,37	0,05	3,09	9	32	10	57	7	76	612	93	291	63	23,95
43-47	1,04	2,59	9,71	39,12	0,13	1,20	1,44	19,94	0,46	0,06	3,66	9	35	14	65	34	93	420	104	441	50	20,14
84-88	1,04	2,93	10,30	38,50	0,14	0,42	1,52	19,76	0,48	0,07	3,60	10	38	18	67	15	99	403	98	396	50	20,99
109-114	1,09	2,83	10,14	38,75	0,14	0,46	1,48	19,60	0,48	0,06	3,61	10	35	16	65	17	97	398	97	410	67	20,76
140-145	1,08	2,68	10,27	37,78	0,14	0,39	1,30	19,50	0,48	0,06	3,66	9	34	17	67	13	99	400	95	424	129	21,99
178-183	1,12	2,53	10,45	38,71	0,13	0,28	1,49	20,00	0,49	0,06	3,71	10	34	16	66	12	100	402	100	411	89	21,22
198-203	1,16	2,51	10,64	39,04	0,13	0,30	1,53	19,27	0,50	0,06	3,77	10	35	16	67	9	103	406	100	425	65	20,84
238-242	1,09	2,37	10,26	38,90	0,13	0,24	1,39	19,76	0,49	0,06	3,63	10	33	16	64	9	98	407	103	399	99	21,07
267-271	1,06	2,42	10,49	40,00	0,14	0,28	1,58	19,30	0,50	0,07	3,84	9	33	15	66	11	98	387	105	396	54	20,11
307-312	1,29	2,47	10,50	40,11	0,14	0,24	1,35	18,64	0,50	0,07	3,81	10	32	16	64	12	98	373	111	392	40	20,36
337-341	1,10	2,48	10,63	41,43	0,14	0,23	1,56	18,27	0,51	0,07	3,79	10	33	15	66	12	100	378	118	396	58	19,43
378-382	1,24	2,36	10,65	41,20	0,13	0,21	1,52	18,11	0,51	0,06	3,82	10	33	16	66	14	101	345	117	386	48	19,73
408-411	1,10	2,37	10,47	39,29	0,14	0,24	1,48	19,45	0,50	0,07	3,76	9	36	16	66	14	100	377	104	375	41	20,54
438-442	1,09	2,52	10,37	38,12	0,13	0,13	1,49	20,26	0,48	0,07	3,76	10	40	16	64	13	97	378	92	353	73	21,27
478-481	1,00	2,46	9,62	35,99	0,13	0,16	1,22	22,04	0,45	0,07	3,44	10	38	14	61	13	89	376	84	335	63	22,79
508-512	0,88	2,36	8,78	33,63	0,13	0,22	1,07	24,47	0,42	0,07	3,23	8	31	12	56	11	81	385	80	329	38	24,37
538-542	1,07	2,41	10,46	37,85	0,13	0,13	1,52	20,74	0,49	0,07	3,66	10	34	13	63	14	95	384	97	363	38	21,24
578-582	1,10	2,40	11,07	38,82	0,14	0,14	1,72	19,70	0,50	0,07	3,88	10	35	15	66	14	103	402	99	400	42	20,40
599-602	1,13	2,42	11,20	37,72	0,13	0,09	1,71	19,94	0,50	0,07	3,79	9	35	16	66	15	105	396	90	392	56	21,02
637-641	1,14	2,41	10,90	38,13	0,13	0,13	1,61	20,09	0,49	0,07	3,90	10	34	15	65	16	99	389	95	385	40	20,88
658-663	1,11	2,48	11,16	38,41	0,14	0,18	1,64	19,80	0,51	0,07	3,97	10	35	15	66	15	101	397	95	392	52	20,07
698-703	1,10	2,49	11,03	37,47	0,13	0,22	1,65	19,76	0,50	0,07	4,10	11	36	14	67	16	104	403	93	407	34	20,76

References

Casamayor, E. O., Schafer, H., Baneras, L., Pedros-Alio, C., and Muyzer, G.: Identification of and spatio-temporal differences between microbial assemblages from two neighboring sulfurous lakes: Comparison by microscopy and denaturing gradient gel electrophoresis, Applied and Environmental Microbiology, 66, 499-508, 10.1128/aem.66.2.499-508.2000, 2000.

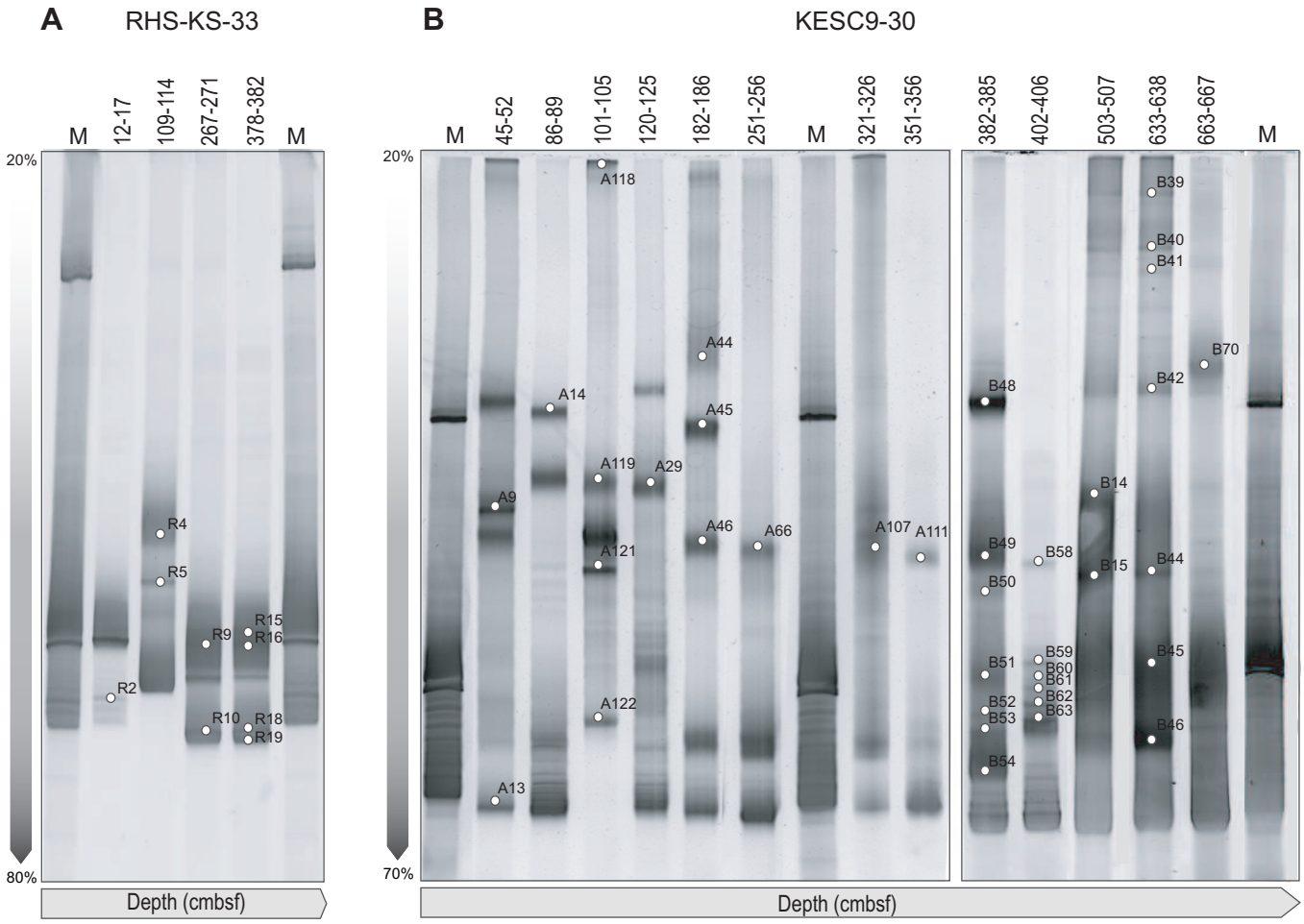
DeLong, E. F.: Archaea in coastal marine environments, Proceedings of the National Academy of Sciences of the United States of America, 89, 5685-5689, 10.1073/pnas.89.12.5685, 1992.

El Maghraoui, M., Joron, J. L., Etoubleau, J., Cambon, P., and Treuil, M.: Determination of forty four major and trace elements in GPMA magamtic rock reference samples using X-ray fluorescence spectrometry (XRF) and Instrumental Neutron Activation Analysis (INAA). Geostandards Newsletter, the journal of Geostandards and Geoanalysis, 23, 59-68, 1999.

Lane, D. J.: 16S/23S rRNA sequencing, in: Nucleic Acid Techniques in Bacterial Systematics, Stackebrandt, E., and Goodfellow, M., eds.Wiley John and Sons, New York, NY, 115-175, 1991.

Morono, Y., Terada, T., Masui, N., and Inagaki, F.: Discriminative detection and enumeration of microbial life in marine subsurface sediments, ISME J, 3, 503-511, ismej20091 [pii] 10.1038/ismej.2009.1, 2009.

Noble, R. T., and Fuhrman, J. A.: Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria, Aquatic Microbial Ecology, 14, 113-118, 10.3354/ame014113, 1998.



C Sequence similarity of excised DGGE bands

R2, 4, 9 Uncultured archaeon clone MD3043C-4 (GQ926246) 96%, 95%, 94% MCG

R5 Uncultured archaeon clone TVG8AR21 (GQ848391) 95%, MCG

R10 Uncultured archaeon clone 40H-260S-6 (FJ404027) 96%, MCG

R15, 16, 18-19 Uncultured archaeon clone MD3057A-43 (GQ994135) 95%, 99%, 99%,MCG

A9 Uncultured archaeon clone 5A005 (EF203636) 97%, MBGC

A13-14 Uncultured archaeon clone MD3052R56 (GQ994303) 98%, MG I

A29 Uncultured archaeon clone TWP8-67 (GQ410969) 96%, MCG

A44 Uncultured archaeon clone ECS2-18 (FJ200124) 98%, MBGB (DSAG)

A45 Uncultured archaeon clone MSASA-A11 (EF125507) 94%, MBGD

A46, 66 Uncultured crenarchaeote clone IODP1319A11.13 (AB433006) 99%, MCG

A107 Uncultured archaeon partial clone 42-AB6 (AJ867792) 97%, MCG

A111 Uncultured crenarchaeote clone IODP1324A53X3.44 (AB448815) 99%, MCG

A118 Uncultured archaeon clone ECS5-1 (FJ200159) 96%, MBGC

A119 Uncultured archaeon clone HNDA16 (HM171846) 99%, MCG

A121 Uncultured archaeon clone HQ630.73 (HQ611204) 99%, SAGMEG relatives

A122 Uncultured archaeon clone MidArch58 (EF680203) 97%, MCG

B14-15,39-42,44-46 Uncultured archaeon clone ODP1227A18.12 (AB177011) 99%, SAGMEG-1

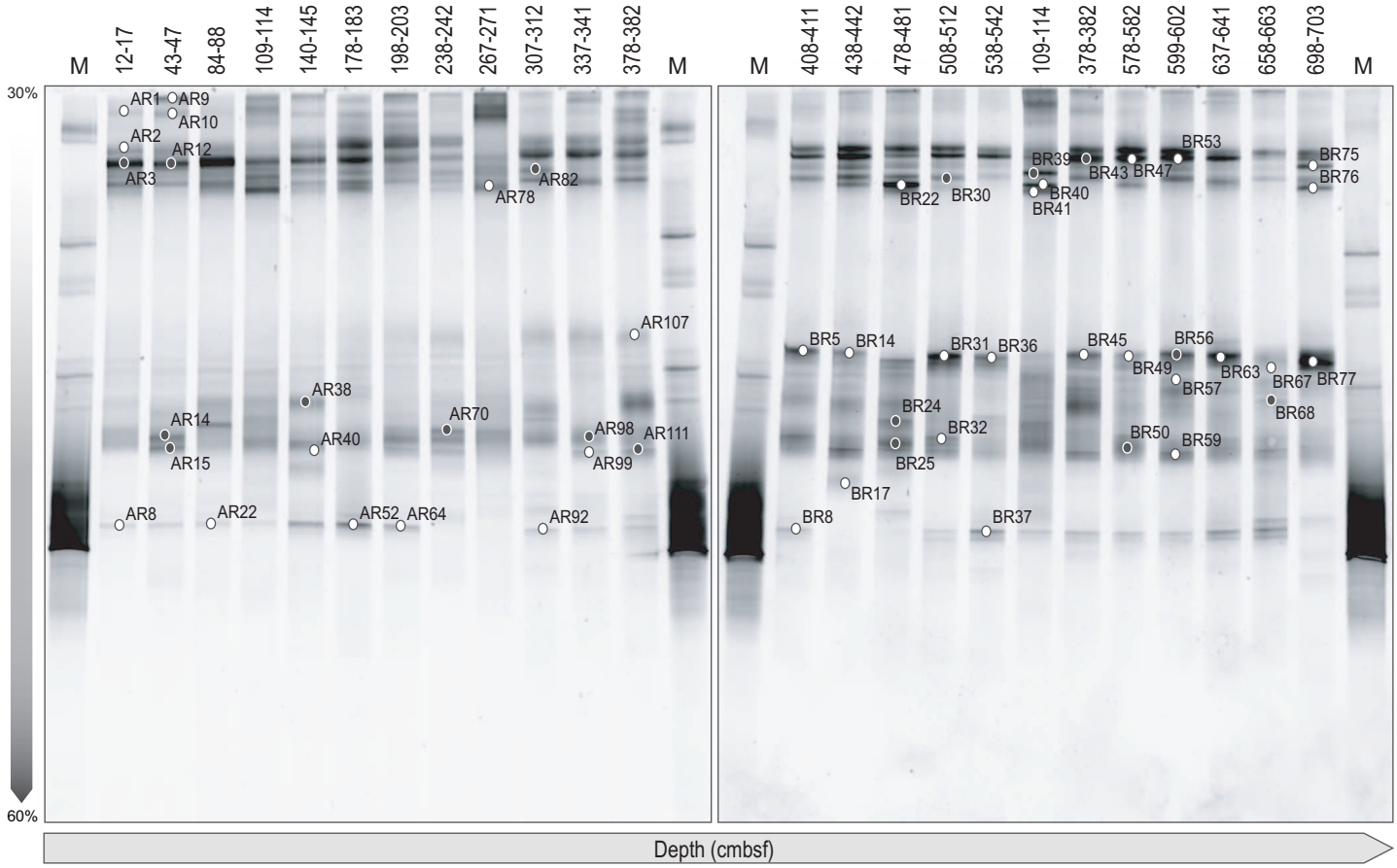
B48 Uncultured archaeon clone NapMat-0_4-rtD07 (HM004801) 99%, MBGD

B49-54 Uncultured archaeon clone AMSMV-S1-A36 (FJ649525) 100%, MCG

B58-63 *Haloterrigena sp.* JX306 (HM747069) 100%, *Halobacteria*

B70 Uncultured archaeon clone MD3043C-37 (GQ926261) 100%, MBGB (DSAG)

A RHS-KS-33



B Sequence similarity of excised DGGE bands

AR1 *Burkholderia sp.* (AF408997) 86%, *Burkholderiaceae, Betaproteobacteria*

AR2 *Acinetobacter sp.* (AF408997) 93%, *Moraxellaceae, Gammaproteobacteria*

AR8, 22, 64, BR37 Uncultured bacterium clone PT-AEXL-B25 (AB368999) 99%, Propiniobacteriaceae, Actinobacteria

AR9 Uncultured bacterium clone FeC_1_E2 (FJ802354) 86%, Burkholderiaceae, *Betaproteobacteria*

AR10 Uncultured bacterium clone3-111 (GU212458) 96%, Burkholderiaceae, *Betaproteobacteria*

AR40, 99 Uncultured bacterium clone COREB 51 (EF562235) 93%, Comamonadaceae, *Betaproteobacteria*

AR52 Uncultured bacterium clone P4s-145 (GQ329244) 99%, *Propiniobacteriaceae, Actinobacteria*

AR78 Uncultured bacterium clone 26 (FJ534972) 93%, Comamonadaceae, *Betaproteobacteria*

AR107, BR14 Uncultured bacterium clone ARN17 (AM936611) 98%, Burkholderiaceae, *Betaproteobacteria*

BR8 Uncultured bacterium clone ncd773c10c1 (HM300328) 99%, *Propiniobacteriaceae, Actinobacteria*

BR5, 31, 36, 45, 49,67 Uncultured bacterium clone IS-191 (GQ339248) 99%, *Ralstoniaceae*, *Betaproteobacteria*

BR17 Uncultured bacterium clone HN14 (FJ269052) 98%, unclassified *Burkholderiales*, *Betaproteobacteria*

BR22 Uncultured bacterium clone PL26B10 (AY570561) 98%, *Bacteroidaceae*, *Bacteroidetes*

BR32 Uncultured bacterium clone sliv-75 (FM877656) 98%, *Comamonadaceae, Betaproteobacteria*

BR40 Uncultured *Bacteroidetes* bacterium 16S rRNA gene from clone QEEB1CD08 (CU917861) 98%, *Bacteroidaceae, Bacteroidetes*

BR41, 76 *Bacteroides sp.* (AB547643) 98%, 99% *Bacteroidaceae, Bacteroidetes*

BR47, 53 Uncultured bacterium clone clone 61-01-24c014 (DQ16809) 99%, Unclassified (*Bacteroidetes*)

BR57 Uncultured bacterium clone *Staphylococcus sp.* (DQ837034) 96%, *Staphylococcaceae, Firmicutes*

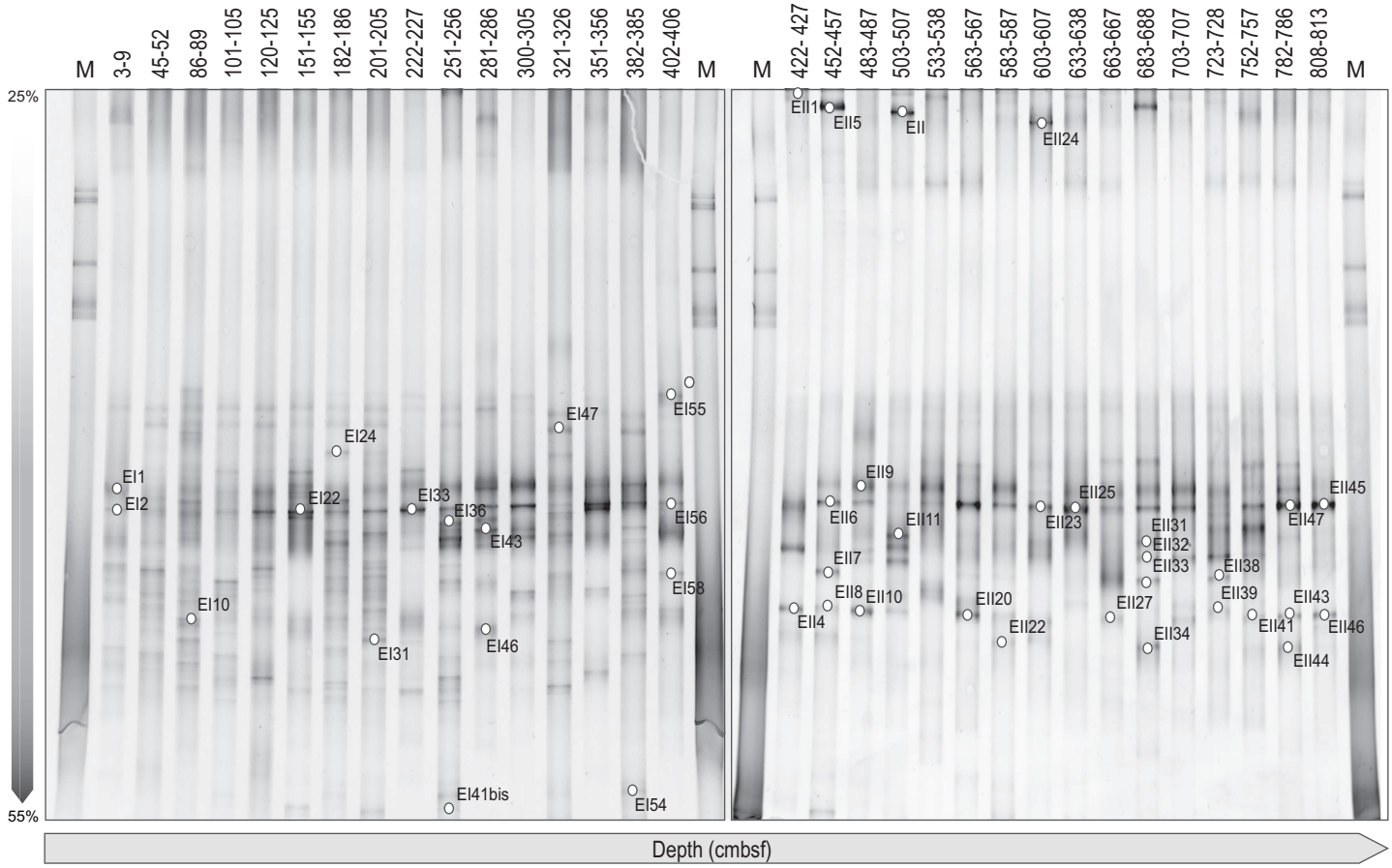
BR59 Uncultured beta proteobacterium clone Kir51grn dB7.2 (HM480181) 98%, *Comamonadaceae*, *Betaproteobacteria*

BR63 *Ralstonia sp.* (HQ267096) 99%, *Ralstoniaceae*, *Betaproteobacteria*

BR75 Uncultured bacterium clone ncd972a02c1 (HM331711) 99%, Unclassified (Bacteroidetes)

BR77 Uncultured beta proteobacterium clone A23YP01RM (FJ569567) 99%, *Ralstoniaceae*, *Betaproteobacteria*

A KESC9-30



B Sequence similarity of excised DGGE bands

EI1 *Acinetobacter sp.* (EU275352) 99%, *Moraxellaceae*, *Gammaproteobacteria*

EI10 Uncultred bacterium clone ODP1251B11.22 (AB177311) 98%, Dehalococcoidetes, *Chloroflexi*

EI22,56 *Ralstonia sp.* (HQ267096) 98%, 99%, *Ralstoniaceae*, *Betaproteobacteria*

EI24 Uncultured bacterium clone CK_2C5_23 (EU488454) 96%, *Dehalococcoidetes*, *Chloroflexi*

EI31 Uncultured bacterium clone EPR3967-orBc49 (EU491796) 90%, *Burkholderiaceae*, *Betaproteobacteria*

EI33 *Ralstonia sp.* (FJ772078) 98%, *Ralstoniaceae*, *Betaproteobacteria*

EI36 Uncultured bacterium clone ORI-860-18-P_S281-283_185B08 (GU553684) 90%, OP8 candidate division

EI41bis, 54 Uncultured bacterium clone AMSMV-S1-B5 (FJ649500) 93%, *Chloroflexi*

EI43 *Acinetobacter sp.* (EU919204) 98%, *Moraxellaceae*, *Gammaproteobacteria*

EI46, EII8, 27, 41 Uncultured beta proteobacterium clone Kir51grn dB7.2 (HM480181) 99%, 98% *Comamonadaceae*, *Betaproteobacteria*

EI47 Uncultured bacterium *Mesorhizobium sp.* (EF219052) 99%, *Phyllobacteriaceae*, *Alphaproteobacteria*

EI55 *Pedobacter sp.* (EF660750) 98%, *Sphingobacteriaceae, Bacteroidetes*

EI58 Uncultured bacterium clone HH1541 (FJ502260) 97%, *Flavobacteriaceae, Bacteroidetes*

EII1 Uncultured bacterium clone ZSB-A2-7 (GU205510) 95%, *Comamonadaceae, Betaproteobacteria*

EII4 *Comamonas sp.* (GU296675) 98%, *Comamonadaceae*, *Betaproteobacteria*

EII5 *Flavobacterium sp.* (GU138375) 98%, *Flavobacteriaceae, Bacteroidetes*

EII6 Uncultured bacterium clone BIGO950 (HM558883) 99%, *Ralstoniaceae*, *Betaproteobacteria*

EII7 Uncultured *Burkholderia sp.* clone burk842 (GU123681) 97%, *Burkholderiaceae*, *Betaproteobacteria*

EII9 Acinetobacter sp. (DQ257432) 99%, *Moraxellaceae*, *Gammaproteobacteria*

EII10 *Comamonas sp.* (AM937260) 99%, *Comamonadaceae*, *Betaproteobacteria*

EII11 Uncultured bacterium clone EPR3967-O2-Bc49 (EU491796) 90%, *Ralstoniaceae*, *Betaproteobacteria*

EII12 *Chryseobacterium sp.* (DQ521273) 98%, *Flavobacteriaceae, Bacteroidetes*

EII20 Uncultured *Comamonas sp.* clone MQ (HQ176414) 98%, *Comamonadaceae*, *Betaproteobacteria*

EII22, 34, 44 Uncultured *Aquabacterium sp.* clone DS130 (DQ234213) 99%, Unclassified *Burkholderiales*, *Betaproteobacteria*

EII23, 25, 31, 45 Uncultured bacterium isolate DGGE gel band B8 (HM068949) 97%, *Ralstoniaceae*, *Betaproteobacteria*

EII24 *Pedobacter sp.* (DQ521273) 96%, *Sphingobacteriaceae*, *Bacteroidetes*

EII32 Uncultured *Janthinobacterium sp.* clone 147 (GU202951) 99%, *Oxalobacteriaceae*, *Betaproteobacteria*

EII33, 38 *Burkholderia sp.* (AB265148) 99%, *Burkholderiaceae*, *Betaproteobacteria*

EII39 Uncultured *Oxalobacteraceae* bacterium clone BF64A_B63 (HM141157) 99%, *Oxalobacteriaceae*, *Betaproteobacteria*

EII42 Uncultured beta proteobacterium clone A23YP01RM (FJ569567) 99%, *Ralstoniaceae*, *Betaproteobacteria*

EII43 Uncultured bacterium clone nby240c04c1 (HM807869) 99%, *Comamonadaceae*, *Betaproteobacteria*

EII46 *Comamonas sp.* (JF729307) 99%, *Comamonadaceae*, *Betaproteobacteria*

EII47 *Pseudomonas sp.* (FN995245) 94%, *Pseudomonadaceae*, *Gammaproteobacteria*