Supplementary information I

Index:

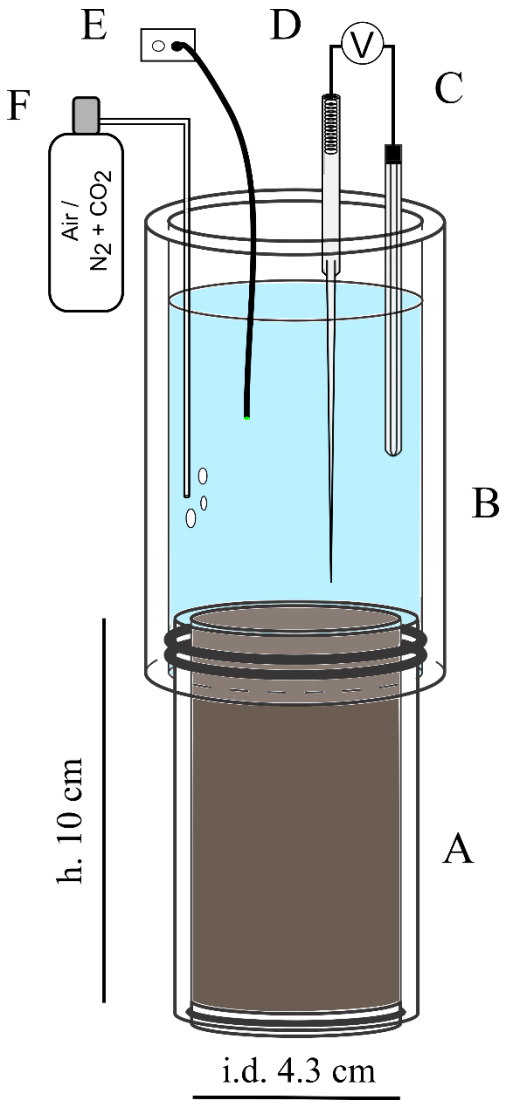

Figure S1. Core liner and water enclosure for sediment incubation. Liner for sediment incubation (A), enclosure for water incubation with o-rings (B), Electric Potential sensor and reference (C), Oxygen fiber optode (E). Air or N_2 + CO_2 gas mix (F).

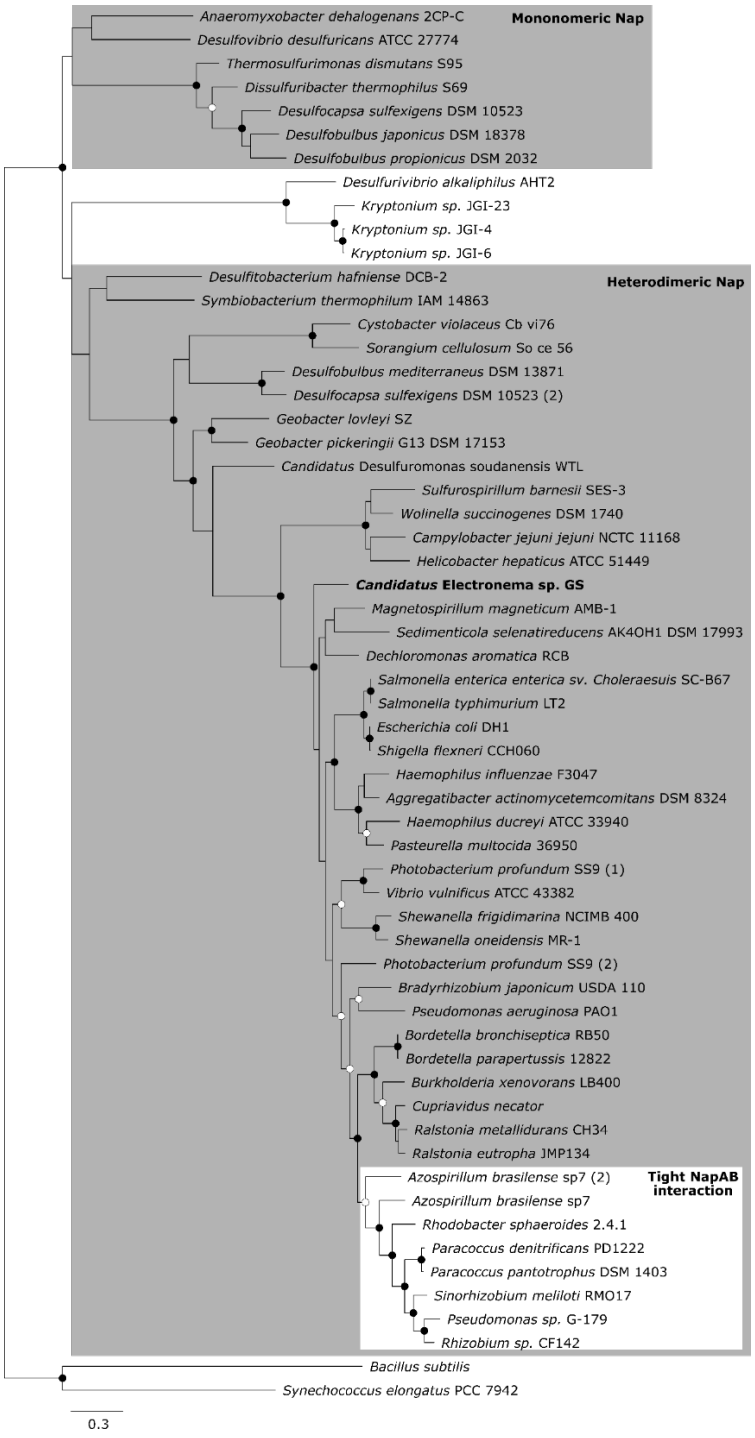

Figure S2. Phylogeny of the *napA* gene of *Ca.* Electronema sp. GS. Maximum likelihood tree supported by 1000x bootstrap resampling. Bootstrap values are represented by circles: open >70%, filled >90%. The scale bar represents 0.3 estimated amino acid substitutions. Tree was rooted with the nitrate reductase (nas) of *Bacillus subtilis*.

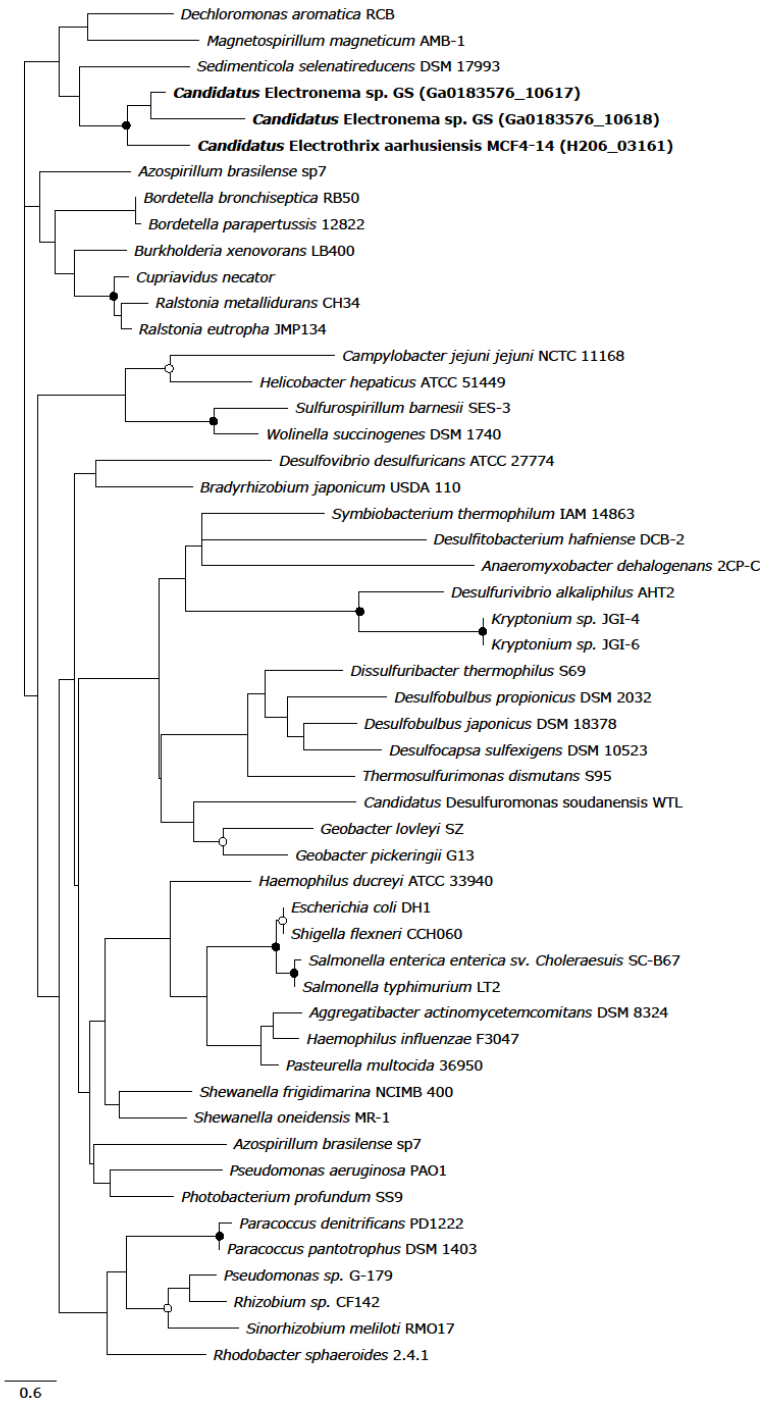

Figure S3. Phylogeny of the *napD* gene of *Ca.* Electronema sp. GS and *Ca.* Electrothrix aarhusiensis MCF. Maximum likelihood tree supported by 1000x bootstrap resampling. Bootstrap values are represented by circles: open >70%, filled >90%. The scale bar represents 0.6 estimated amino acid substitutions. Locus tags of cable bacteria genes are in parentheses.

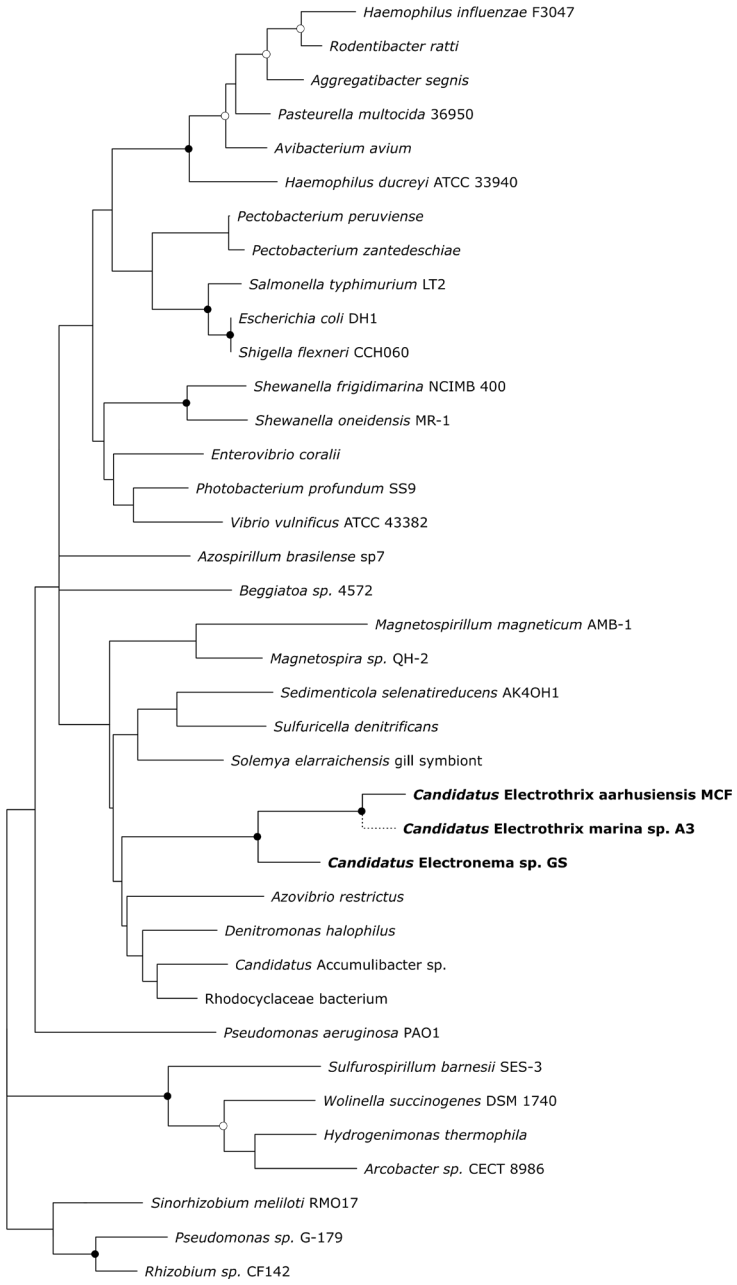

Figure S4. Phylogeny of the *napF* gene of *Ca.* Electronema sp. GS, *Ca.* Electrothrix aarhusiensis MCF and *Ca.* Electrothrix marina A5. Maximum likelihood tree supported by 1000x bootstrap resampling. Bootstrap values are represented by circles: open >70%, filled >90%. The scale bar represents 0.3 estimated amino acid substitutions. The phylogenetic position of the short NapF fragment of *Ca*. E. marina (dotted line) was calculated by the maximum parsimony method in the program ARB without changing the overall tree topology.

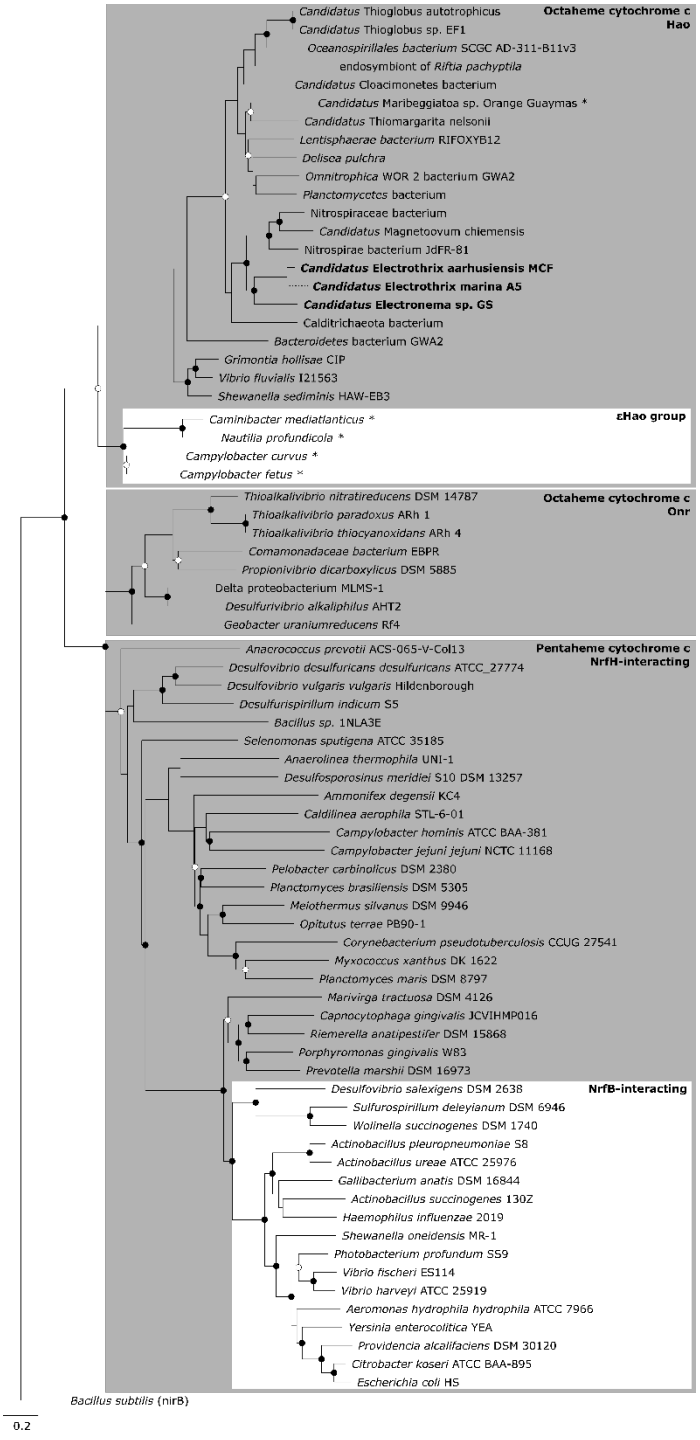

Figure S5. Full phylogeny of the pOCC of *Ca.* Electronema sp. GS and *Ca.* Electrothrix aarhusiensis MCF. Maximum likelihood tree supported by 1000x bootstrap resampling. Bootstrap values are represented by circles: open >70%, filled >90%. The scale bar represents 0.2 estimated amino acid substitutions. The phylogenetic position of the short pOCC fragment of *Ca*. E. marina (dotted line) was calculated by the maximum parsimony method in the program ARB without changing the overall tree topology. Tree was rooted with the nitrite reductase (nirB) of *Bacillus subtilis*.

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KHD08390.1        -----MSRKLWA----------FLAGAAMLLLQTASMA---------AVESAP-----DE
WP_053951924.1    MENHYFVIKIYRRNAMKAIIKSLIFFLSLMFLSSSAFS---------SVTEPP-----AQ
2647705483        -----MKAIIKS----------LIFFLSLMFLSSSAFS---------SVTEPP-----AQ
2601634560        ------MRKWWL----------LGIGAALLLTHGFAVA---------SVKAPP-----KE
2730372430        ------MKKLL-----------YLLIITVLVMAGTEAVAV-------TKINIP-----QK
KJR43854.1        ------MKRTV-----------LLLLSFLLLLSVSAFAE--------TKSGLP-----KE
RMH60699.1        ------------------------------------------------MDIP-----KE
WP_007473950.1    ------MKKV------------LSAGLSLAAISSLAFAAN-------SLDSNPNYVKLKN
WP_015902282.1    ------MKKA------------LTAGLSVAAIASFAFAAN-------SLDSNPNYKKLKN
WP_011992073.1    -----MFKKVA-------------ILLACLVSFGFATGTDGNKTEAINLNVIKNIKVAHK
WP_002849252.1    --------MLKK----------FILALTCIAAIGFADSVG-------NINLTKTMKVDRN
2521963319        MNDLNRLGRVGR----------WIAGAACLFLASAAHAEP-------GENLKP-------

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BOGUAY_0691       FSEE---TKACIACHKETSLGVVQQWGDSKHHRAKVGCYECHKAEAGEIDAFIHEEFDKK
KHD08390.1        ISEE---TKICVKCHKKRSPGIVKQWENSAHFGKNVGCYECHKAEPGDVDAFLHEQ----
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2601634560        MSTE---TKACVKCHKKNNPGLIQAWGASKHYGANVGCYECHAADAKDPDAYIHDD----
2730372430        LSKA---SQECIGCHADSTVNIYQQWGYSKHYRANVGCFECHEAQKGDPDAFEHQG----
KJR43854.1        ISEK---SKQCASCHSTTTVNIYQQWGTSKHYRANVGCYECHEAKKEDKDAFEHNG----
RMH60699.1        LSSA---SRECIDCHKDENHSLYQQWGDSKHYRANVGCFECHSAKKGDKDAFEHEG----
WP_007473950.1    FKPKGVSTDQCLMCHKTTDPGIVADWQHSKHAKAGVGCVECHVVPKDYPTAFKSHP----
WP_015902282.1    FKPQGVTNDQCLMCHKAQDPGIVADWQHSKHAKVGVGCVECHVVPKNYPTAFKAHP----
WP_011992073.1    MSDL---SKSCVECHSEKTPGIVADWKNSRHAHVGVSCMDCHSVAADSPMASVKVH----
WP_002849252.1    LSPL---AVKCIECHKDKTPGIVNDWKSSRHAHAAVSCVDCHAVPADSPMAIKKEH----
2521963319        --VD---AMQCFDCHTQIED------MHTVGKHATVNCVHCHDATEHVETASSRRM----

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KHD08390.1        KKVGNKHISIIVSPKDCANCHEKEVTEFTNSHHSQAA----------------------
WP_053951924.1    -KGDKKLISIIVSPRDCANCHAHEVKQTEDSHHAKAG----------------------
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WP_011992073.1    PKDSNNHVSMLVSPKTCAKCHENEVDEFTKSGHARGA----------------------
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BOGUAY_0691       RIIGSLDNLLADVVEGNRAMVT---------ESFPEGVSAAVVNGCWQCHGSEVKVRKDG
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WP_053951924.1    RILGSLDNLLAEVVEGNSGFVT---------EGFPDGNSAAAVNGCWQCHGSQVKVLEDG
2647705483        RILGSLDNLLAEVVEGNSGFVT---------EGFPDGNSAAAVNGCWQCHGSQVKVLEDG
2601634560        KIMGSLDNLLAEVIEGDSGFIT---------EGFPEGNSAAAVNGCWQCHGSQVKVLKDG
2730372430        RIMGSLDNVLAEVVEGNRGMKT---------EGFPMGISAAAVNGCWQCHGSVVRVLKDG
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RMH60699.1        RILGSLDNVLAEVVEGNSAFVT---------HGFPDGASAAAVNGCWQCHGGQVKALEDG
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WP_002849252.1    VQMFAKKG-MVELMYHYEANGKPYENDAPFYAGNENLKDAPASTGCIQCHGMEIKLDKEG
2521963319        RLEKATPT--SRSPMFDKLIAG---------HGFAFEHAEPRSHAFMLVDHFVVDRAYGG

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H206_03164        KLDP-ATWPN--SGIGRI----------NPDGSTGS-------------CAACHSRHDF-
BOGUAY_0691       SLDP-ATWPN--TGIGRI----------NPDKSRGS-------------CSACHSRHKF-
KHD08390.1        RLDP-ATWPN--TGIGRL----------NPDGSRGS-------------CTACHSRHEF-
WP_053951924.1    ALDP-ATWPN--TGIGRI----------NPDGSEGA-------------CTACHSRHSF-
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2730372430        RLDP-ATWPN--TGMGRV----------NPDGSEGS-------------CTACHQRHEF-
KJR43854.1        KLDV-ATWPN--TGMGRV----------NPDNSEGS-------------CSACHQRHEF-
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WP_015902282.1    RPDA-TTWPN--DGIAAL----------YPDGGVSN-------------CLSCHSRHKF-
WP_011992073.1    KPTK-ETWPN--YGIGNV----------YPDGGIGG-------------CKSCHSSHTF-
WP_002849252.1    YPLPGKGWPN--YGIGNA----------YPDGSVGS-------------CKSCHSSHKF-
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BOGUAY_0691       KDKMNMDRSK--WIA---------GEDYDAAPT---------CATCHMSATKEQGVNHDV
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2730372430        KDKMNLESAK--WVV---------GEDYFAAPT---------CATCHMSATKDMPVTHNV
KJR43854.1        KDKMNLESAK--WIL---------GEDYSAAPT---------CATCHMSATKDMPVTHNV
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WP_011992073.1    GNTWKYDSAPDTWDV----------PDFR-APT---------CATCHMSGVGETTTTHNV
WP_002849252.1    GNTWKWDSAPDTWDV----------PDYR-APT---------CATCHMSGIGDLNTTHNV
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WP_053951924.1    GMRISWNNRPPVSIRPE--------------------VSDKKMGL---PGQHVDWETRRD
2647705483        GMRISWNNRPPVSIRPE--------------------VSDKKMGL---PGQHVDWETRRD
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167  WP_011992073.1     SQRLKWNLWAPRSELRTKGYEQAAYDYWKTG------KLNTGTPL---AGNPQGPEAARA
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173  BOGUAY_0691        NMKNVCSACHGESFIDNFYIQYDGQIELYNNKFAKPGLALYQAALPLLPRD------AKF
174  KHD08390.1         NMKDVCSNCHSSEFVDNFYVQYDELIKLYNNKFGKPGLALMKVAKPLL-KP------VKF
175  WP_053951924.1     NMQDVCSACHSEDYIENFYAQYDGLVNLYNEKFAKPGIKLMKAAKPLM-KP------VKF
176  2647705483         NMQDVCSACHSEDYIENFYAQYDGLVNLYNEKFAKPGIKLMKAAKPLM-KP------VKF
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187  Ga0183576_10612    AQA-----IDFTWYEIWHHEGRRARHGAAMMAPDY-THWHGTYEVAKH--WAAKYIPELK
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189  BOGUAY_0691        ANH-----LDFVWFEIWHHEGRRARHGASMMGPDW-TQWHGNYEVGKH--FYGKYVPELE
190  KHD08390.1         SNK-----IEFTWFEIWHHEGRRARHGAAMMGPDY-THWHGTYEVGKH--FYSEFIPELE
191  WP_053951924.1     SNK-----IDFIWFEIWHHEGRRARHGAAMMGPDI-THWHGTYEVAKH--FYAKFIPELE
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194  2730372430         AQK-----IDYTWFELWHHEGRRVRHGASMMAPDY-TQWHGNYDLAKN--WYSEYIPEIR
195  KJR43854.1         AQK-----IDYTWFELWHHEGRRVRHGASMMAPDY-TQWHGNYELARN--WYGEYVTELK
196  RMH60699.1         SDD-----IDFVWFELWHHEGRRARHGASMMAPDY-THWHGTYDLAKN--FYTEFIPEIK
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198  WP_015902282.1     SDP-----FFKLYYYLWHHEGRRFRHGAAMGSPDY-AHWHGVFQVMQD-------IREMK
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204  H206_03164         EV-IESGKH-----SDNKEAAKLADELEKMLEDVRNSD---------------NHKWSIG
205  BOGUAY_0691        EL-IEKNLD-----SEDANKKASALALKNLLHEILSDEFVVTDEKTGKEVKSTGHSWFIG
206  KHD08390.1         EL-VEANLE-----SSDPVKSKAAHDLEKKIEEVLNTD---------------DHKWYIG
207  WP_053951924.1     YL-VEKGMR-----STSEKKQASAALLQATIDEVLNSD---------------NHKWYLG
208  2647705483         YL-VEKGMR-----STSEKKQASAALLQATIDEVLNSD---------------NHKWYLG
209  2601634560         EL-IEHGKH------GSAADKKAAENLAKVLDEVLNME---------------EHKWFLG
210  2730372430         EI-IEMGKH-----SGKGKAERLAKELEEMLEEIINSD---------------NHKWSIG
211  KJR43854.1         EV-IETGKH-----STNPDANKLAGELENLLTEVMEQD---------------GHSWAVG
212  RMH60699.1         EL-IHEGLA-----SKDSKKVDAAKNLQKILTSVLNSE---------------NHKWFIG
213  WP_007473950.1     DI-YDYRMK-----MLKKYKDPKKVLENEPPMPVVTHE----------------------
214  WP_015902282.1     DI-YDYRMK-----MLKKYGDPKKALANEVPMPVVTHE----------------------
215  WP_011992073.1     KI-YKERIE-----SGKAH-------------------------------------------
216  WP_002849252.1     TI-YDARIK-----SGKIE-------------------------------------------
217  2521963319         ELHYDAHLYWEWWTAENSVGFHNPDQARESLMTSISKS----------------KEAVS
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219  Ga0183576_10612    KEDEADKAERAKGAEEFKAKYAK--------
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WP_053951924.1      KMSAKQQEIRKKATADFKAQFEK--------
2647705483          KMSAKQQEIRKKATADFKAQFEK--------
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2730372430          KEDPASKAERERRRREFLKRYQQKVDM----
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WP_007473950.1      -------------------------------
WP_015902282.1      -------------------------------
WP_011992073.1      -------------------------------
WP_002849252.1      -------------------------------
2521963319          LLNDAIDAQVASR------------------
```

Figure S6. Alignment of the amino acid sequences of the octaheme cytochromes encoded in the genomes of *Ca.* Electronema sp. GS (Ga0183576_10612), *Ca.* Electrothrix aarhusiensis MCF (H206_03164), *Ca.* Maribeggiatoa sp. (BOGUAY_0691), *Ca.* Thiomargarita nelsonii (KHD08390.1), *Ca.* Thioglobus autotrophicus (WP_053951924.1), *Ca.* Thioglobus sp. EF1 (2647705483), endosymbiont of Riftia pachyptila (2601634560), Nitrospirae bacterium jdFR-81 (2730372430), *Ca.* Magnetoovum chiemensis (KJR43854.1), Calditrichaeota bacterium (RMH60699.1), the εHaO encoded in the genomes of Caminibacter mediatlanticus (WP_007473950.1), Nautilia profundicola (WP_015902282.1), Campylobacter curvus (WP_011992073.1), Campylobacter fetus (WP_002849252.1) and Thioalkalivibrio (2521963319). The eight conserved heme binding motives (CxxCH) (yellow), a conserved tryptophan thought to be important for reductive type HaO (green) and conserved residues located at the putative active sites (blue) are highlighted.

S7. Extended discussion

LINKING SULFIDE OXIDATION TO NITRATE REDUCTION VIA MENAQUINONE CYCLING THROUGH LONG-DISTANCE ELECTRON TRANSFER IN CABLE BACTERIA

The metabolic model of nitrate reduction in the cathodic nitrate-reducing cells in cable bacteria includes a menaquinone cycle in which a reduced menaquinone donates two electrons to the menaquinol dehydrogenase NapGH, membrane component NapH. This results in the transfer of two protons from the cytoplasm to the periplasm. The menaquinone is reduced back via sulfide oxidation, which however takes place in a distant cathodic cell, most likely via reverse sulfate reduction (1). Assuming the presence of an identical membrane-bound enzymatic apparatus for catalyzing menaquinone oxidation-reduction reactions in the cathodic nitrate-reducing cell and in the anodic sulfide-oxidizing cell, and that these apparatus are electrically connected with a conductor the metabolic system linking sulfide oxidation to nitrate reduction via a menaquinone cycle can be considered as a concentration cell (Fig. S7.1). This is a galvanic cell that has two equivalent half-cells with the same reactants differing only in concentration. Such a concentration cell produces a voltage as it attempts to reach chemical equilibrium, which occurs when the concentration of the reactant in both half-cells are equal. This is achieved by transferring electrons from the half-cell with the highest concentration of reduced compounds to the half-cell with a lower concentration of these. In the following we will investigate, the thermodynamic constrains on the concentration cell model of nitrate reduction in cable bacteria in order to elucidate if the flow of electrons between the menaquinone in pool anodic (half) cells and the menaquinone pool in cathodic (half) cells via the conducting fiber in cable bacteria is thermodynamic possible and can account for current observed running in these organisms.

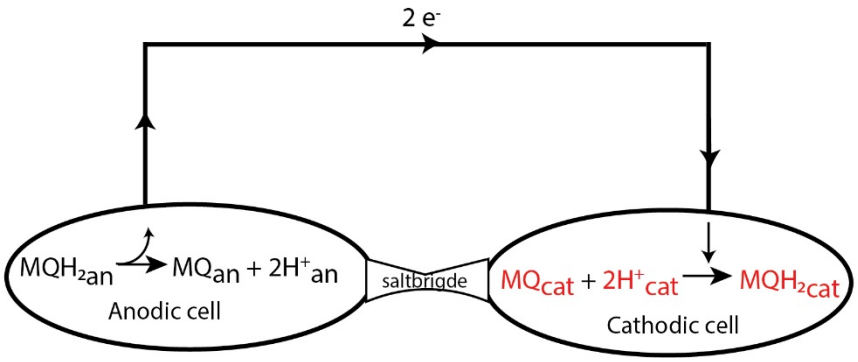

***Figure S7.1**. Conceptual scheme of a concentration cell.*

The voltage yield of the concentration cell

The voltage produced by the concentration cell can be estimated from the Nernst equation:

$$E = E_o - \frac{0.0592}{n} LogQ \qquad \text{(Eq. S1)}$$

Where E_0 is the standard cell potential, which is defined as the sum of the reduction potential and the oxidation potential of the half reactions. n is the number of moles of electrons transferred, and Q is the reaction coefficient. The reduction potential (E_{red}) for the reaction $MQ + 2H^+ + 2e^- \rightarrow MQH_2$ is -67 ± 10 mV (2) and the oxidation potential is consequently +67 ± 10 mV. Hence, E_o equals zero. The full reduction of 1 mole of menaquinones implies the transfer of two moles of electrons and n consequently equals 2. The reaction coefficient Q is defined from the overall reaction:

$$MQH_{2an} + MQ_{cat} + 2H^+_{cat} \rightarrow MQ_{an} + 2H^+_{an} + MQH_{2cat}$$

Thus:

$$Q = \frac{[MQH_{2cat}][MQ_{an}][H^+_{an}]^2}{[MQH_{2an}][MQ_{cat}][H^+_{cat}]^2} \qquad \text{(Eq. S2)}$$

The proton source for the menaquinone cycle is the cytoplasm. As an equivalent pH of the cytoplasm of cathodic and anodic half-cells can be assumed, $[H^+_{an}]^2/[H^+_{cat}]^2$ approximates 1. Hence:

288 $$Q \approx \frac{[MQH_{2cat}][MQ_{an}]}{[MQH_{2an}][MQ_{cat}]} \qquad \text{(Eq. S3)}$$

289 With *a* and *b* denoting the fraction of oxidized menaquinones (MQ) to the total pool of menaquinones

290 (MQ_{Tot}) in the anodic cell and cathodic cell, respectively we have:

291 $MQ_{an} = a\ MQ_{Total\ anode}$ (Eq. S4)

292 $MQH_{2an} = (1\text{-}a)\ MQ_{Total\ anode}$ (Eq. S5)

293 for the anodic cell, and:

294 $MQ_{cat} = b\ MQ_{Total\ cathode}$ (Eq. S6)

295 $MQH_{2cat} = (1\text{-}b)\ MQ_{Total\ cathode}$ (Eq. S7)

296 for the cathodic cell. Thus:

$$Q = \left(\frac{[(1-b)\ MQTotal_{cathode}\ ][a\ MQTotal_{anode}]}{[(1-a)\ MQTotal_{anode}\ ][b\ MQTotal_{cathode}\ ]} \right)$$

297 $$= \left(\frac{(1-b)\ a}{(1-a)\ b} \right) \qquad \text{(Eq. S8)}$$

298 With this expression for *Q* the voltage produced by the concentration cell is given by:

299 $$E = -\frac{0.0592}{2} Log\left(\frac{(1-b)\ a}{(1-a)\ b} \right) \qquad \text{(Eq. S9)}$$

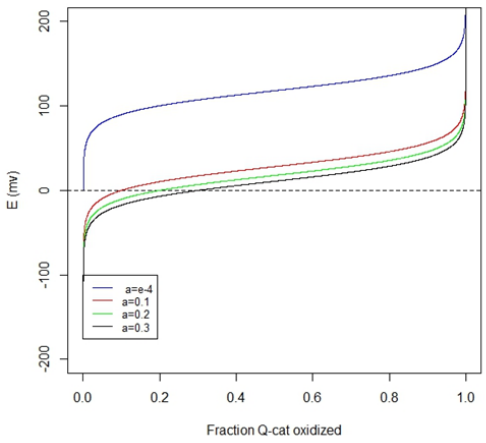

***Figure S7.2**. The voltage yield (E) of the concentration cell for different values of a (the fraction of oxidized menaquinones in the anodic half-cell) as function of the fraction of menaquinones oxidized in the cathodic half-cell (b).*

Equation S9 allows to calculate the voltage yield (E) of the concentration cell for different values of a and b A positive voltage yield ($E > 0$) implies that the concentration cell operates in the forward direction (electron transfer from the anodic half-cell to cathodic half-cell), whereas a negative voltage yield implies electron transfer in the opposite direction. As shown in Figure S7.2, electron transfer from the menaquinone pool in an anodic half-cell to the menaquinone pool in a cathodic half-cell is most favorable if the electrons are delivered from an anodic half-cell with an almost completely reduced (99.99%, a = 0.0001) menaquinone pool. For such a system, electron transfer in the forward direction is possible if only 0.01% (b = 0.0001) or more of the menaquinone pool is kept oxidized in the cathodic half-cell. The thermodynamic threshold increases when electrons are delivered from anodic half-cells with a less reduced menaquinone pool. If electrons are delivered from anodic half-cells having 90% of the menaquinone pool reduced the recipient half-cell should keep more than 10% of the menaquinone pool oxidized for the reaction to proceed, and for anodic cell having 70% of their menaquinone pool reduced, the recipient cell should keep more than 30% of its menaquinone pool oxidized, etc. The voltage yield is highest if electrons can be delivered from an anodic half-cell having an almost fully reduced menaquinone pool, and for such a system the voltage produced falls in the range 80-150 mV for 5% < b < 92%. The voltage yield drops significantly when the menaquinone pool in the anodic half-cell becomes more oxidized. Figure S7.3 shows the voltage yield for a concentration cell, where 90% of the menaquinone pool in the cathodic half-cell is oxidized (b = 0.1). The 80-150 mV range is only obtained for cells where more than 98% of the menaquinone pool in the anodic half-cell are reduced.

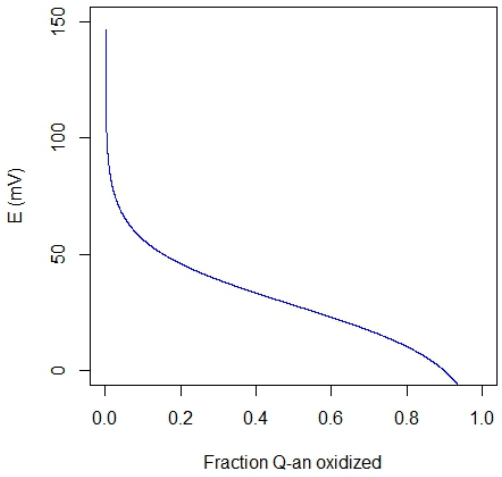

Figure S7.3*. The voltage yield of a concentraion cell as function of the fraction of menaquinons oxidized in the cathodic half-cell (b) where 90% of the menaquinone pool in the cathodic half-cell are oxidiced.*

The current in the concentration cell

The above considerations points to the idea that sulfide oxidation coupled to nitrate reduction via menaquinone cycling, through long-distance electron transfer, is thermodynamically possible and the next question to be adressed is the if the voltage generated from the concentraion cell in a certain configuration can drive an electric current comparable to the current running in metabolic active cable bacteria. For simplicity, we will consider a steady-state situation. The drivers of the model are the concentrations of oxidized and reduced menaquinones in the anodic and cathodic half-cells (eq. S2) We will assume that the redox state of the menaqunonens in the anodic and cathodic cells of the cable bacteria are controlled by: 1) the rate of menaquinone reduction via sulfide oxidation in the anodic cells, 2) the rate of menaquinone oxidation in the anodic cells via the current generated from the concentration cell, 3) the rate of menaquinone reduction in the cathodic cells via the current generated

340 from the concentration cell, and 3) the rate of menaquinone oxidation via nitrate reduction. At steady-
341 state, (i.e. a, and b are constant) these rates are equal in magnitude. We will further assume that the
342 total pool of menaquinones (MQ_{Tot}) in the anodic cell equals the total pool in the total pool of
343 menaquinones (MQ_{Tot}) in the cathodic cells and that the rate constant for menaquinone reduction in
344 the anodic cell is equal to the rate constant for menaquinone oxidation in the cathodic cell. This
345 implies that a = (1-b) in equation S9, which then can be simplified to:

346 $$E = -\frac{0.0592}{2} Log\left(\frac{b^2 - 2b + 1}{b^2}\right) \qquad \text{(Eq. S10)}$$

347 With this expression we can estimate the curent in the steady-state sitution by means of ohms law.

348 $I=E/R$

349 Where I is the current, E the voltage yield of the concentraion cell, and R is the resistance of the wire.
350 The resistance of wire can be determined as in (3), *i.e.*,:

351 $$R = \frac{l}{\sigma A} \qquad \text{(Eq. S11)}$$

352 Here l is the length of the wire, σ the conductivity and A the cross section area of the wire.
353 The current can therfore be estimated as:

354 $$I = -\frac{0.0592}{2} Log\left(\frac{b^2 - 2b + 1}{b^2}\right)\frac{\sigma A}{l} \qquad \text{(Eq. S12)}$$

355 The conductive element in cable bacteria is a periplasmatic network of discrete fibres (4). Each of
356 those with a diameter of ca. 50 nm, corresponding to a cross section area of 2 x 10^{-15} m^2, and a
357 counductivity of 20.1 S cm^{-1}, corresponding to 2.01 x 10^3 S m^{-1} (4).
358 Figure S7.4, shows the current running between two half cells, connected with a wire having
359 conductive properties similar to a cable bacteria fibre. The current flows from the anocic half cell to
360 the cathodic half cell if the fraction of oxidized menaquinones to the total pool of menaquinones in

the cathodic half cell (b) is > 0.5. The current increases for b→1. There is an inverse relationship between the length (*l*) of the wire connecting the anodic and cathodic half-cells and the magnitude of the current running through it. Half cells connected with a short wire in general have a higher current flowing between them than half-cells connected with a long wire.

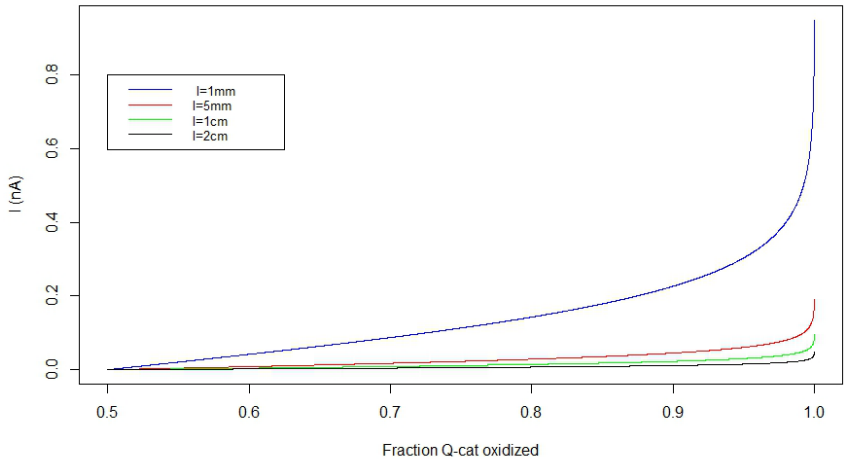

Figure S7.4. *Steady state current between half cells in the concentration cell, as function of b: the fraction of oxidized to total menaquinenes in the cathodic half cell. The half cells are electrically connected with a wire having conductive properties similar to a conducting fibre in cable bacteria. Collored lines represent the current in wires at different length (l).*

A cable bacterium can be considered as a composit of concentration cells with a series of anodic half cells coupled to a few cathodic half cells via the conducting periplasmatic network of fibres. We will for simplicity consider a virtual cable bacterium with 5000 anodic cells, each coupled to a cathodic cell. The cathodic cell can in principle be the same for all anodic cells. 5000 cells spans a distance of 2 cm and in our simplified model the wire connecting the most distant anodic cell to the cathodic cell is 2 cm long while the wire connecting the nearst anodic cell to the cathodic cell is 4 µm long. In general, the length of the wire for the cells between the most distant and the nearest cell is equal to their distance to the cathodic cell, which is in a fixed position for all anodic cells. According to

equation 12 and Fig S2.4, the implication of such a configuration is that the metabolic activity of the cells in the filament decreases with the distance to the cathodic cell. Figure S7.5 shows the current integrated for all 5000 cells in the filament. As seen, the current generated from this composit concentration cell model of a cable bacterium wastly exceeds the 0.2 - 0.36 nA estimated for natural cable bacteria (5-7) for most redox states of the menaquinone pool in the cathodic cell. Already with 50.11% of the menaquinones in the cathodic cell being oxidized, the current is >1 nA.

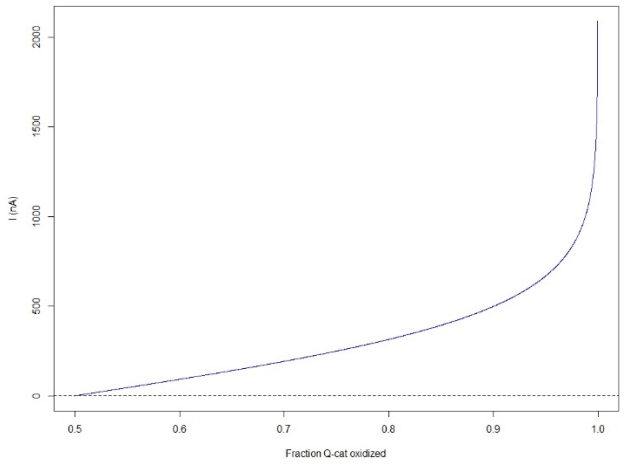

Figure S7.5*. Curent produced from 5000 individual half-cells (the approx. number of cells in a 2 cm long filament). Dashed line indicates the max filament specific current production (0.4 nA) reported in the literature.*

Conclusion

Here we have shown using the concentration cell model, that electron transport from a menaquinone pool in a anodic cell to a menaquinone pool in a cathodic cell is thermodynamically possible, and when the concentration cells are brought together in a way that simulate a cable bacterium, that the voltage produced from such cells can be sufficiently high to drive an electric current that exceeds the current reported for cable bacteria.

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