

# Phylogenetic characterisation of bacterial assemblages and the role of sulphur-cycle bacteria in an *Arenicola marina* bioturbated mesocosm

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Supplement. Additional data on the spatial dynamics of sand in the mesocosm system (S1), detailed phylogenetic analysis of the bacteria found (S2), a diagrammatic representation of the sulphur-cycling processes enhanced by the lugworm's activities (S3) and a photographic image of a burrow system in a commercial mesocosm against which the postulated activities can be visualised in context (S4)

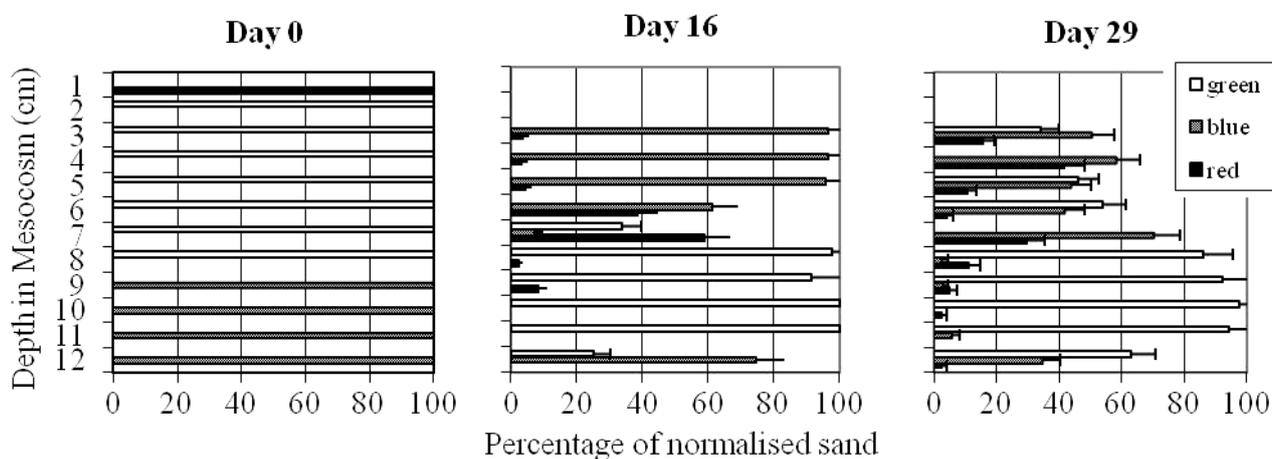


Fig. S1. Movement of coloured sand layers during bioturbation of sediment; proportion of normalised coloured sand in relation to depth in the bioturbated mesocosms at the start of the experiment (Day 0) and after 16 and 29 d bioturbation by the introduced population of *Arenicola marina* (n = 3)

A

0.05 substitutions/site

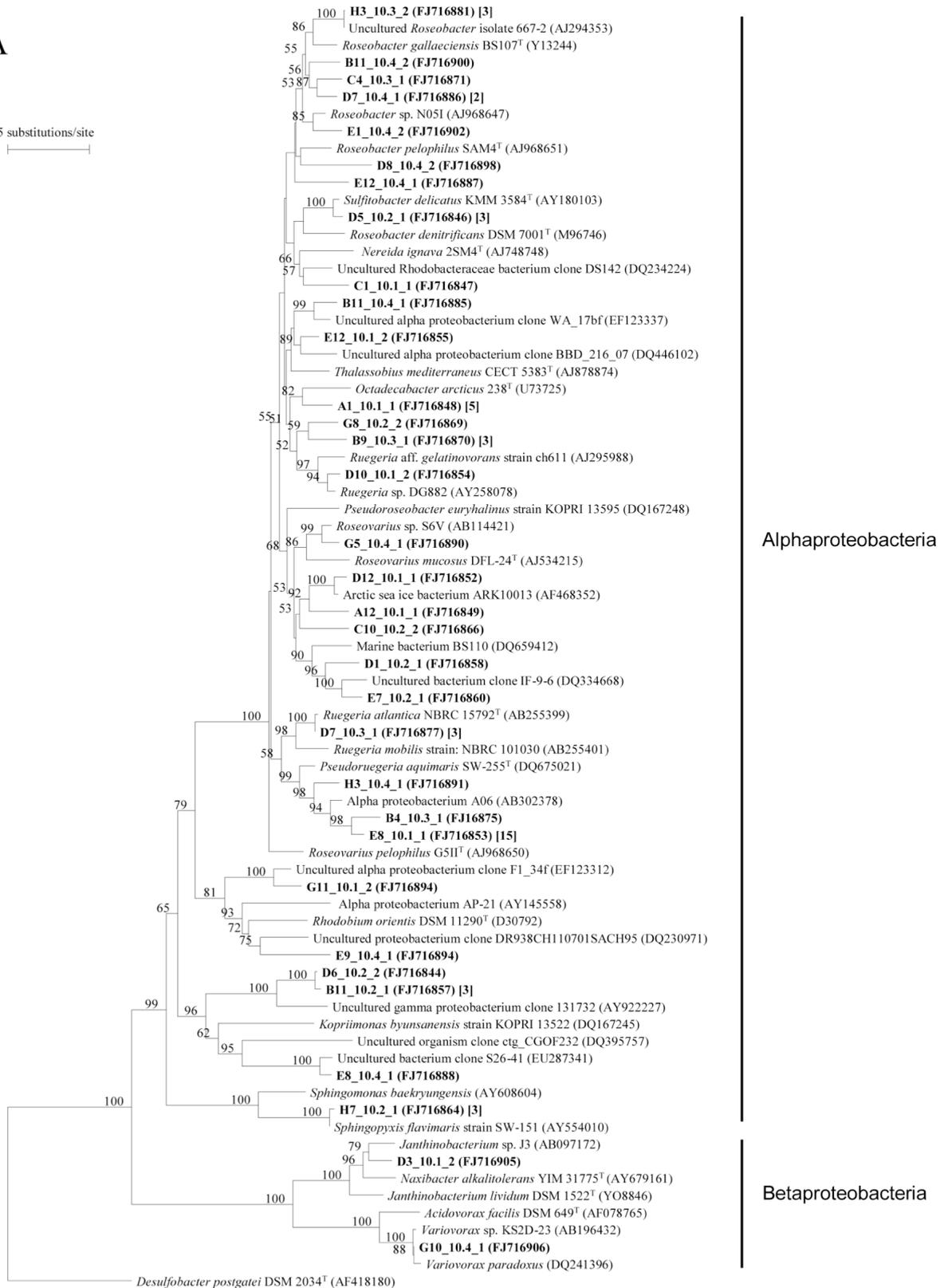


Fig. S2. Neighbour-joining phylogenetic tree showing relationships of the analysed 16S rDNA clones (A) *Alpha*- and *Betaproteobacteria*; (B) *Delta*- and *Epsilonproteobacteria*; (C) *Gammaproteobacteria*; (D) CFB, *Fusobacteria* and *Nitrospira*; (E) *Spirochaeta*, *Chloroflexi*, *Firmicutes*, *Actinobacteria*, *Acidobacteria*, *Planctomycetes*, *Verrucomicrobia* and WS3 retrieved from sediment in an *Arenicola marina* culture mesocosm. Environmental sequences determined in this study are in bold. Sequences denoted 10.1 are from the deep yeast layer; 10.2 are from the mid sand layer; 10.3 from new worm casts; 10.4 from old worm casts. Only one representative of each operational taxonomic unit (OTU) was included in the phylogenetic trees. Numbers of OTUs are shown in the square brackets. Numbers on the branches represent percentages of 1000 bootstrap repetitions. Confidence limits of less than 50% are not shown. Distance scale shows number of substitutions per site

B

0.05 substitutions/site  
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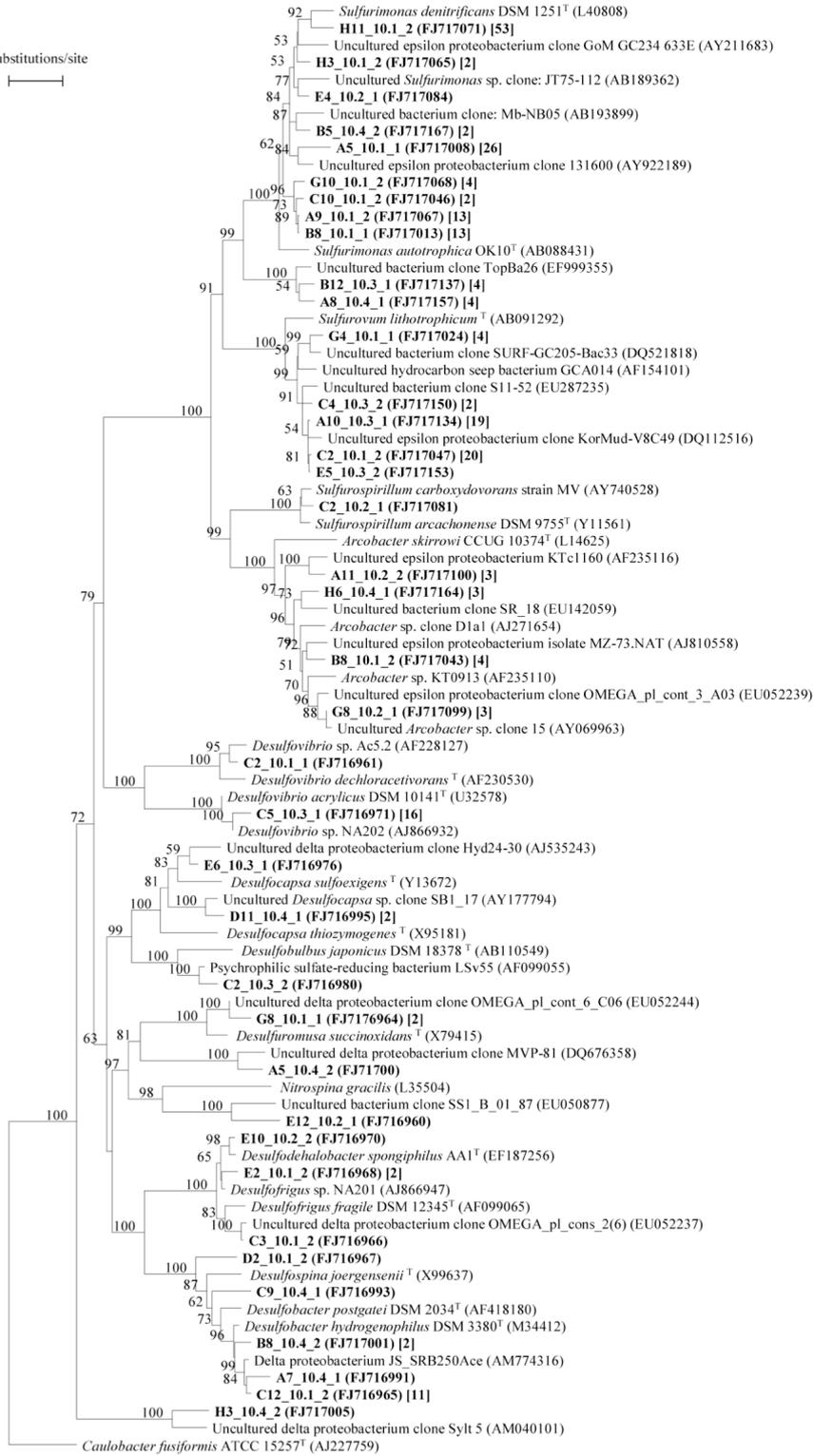
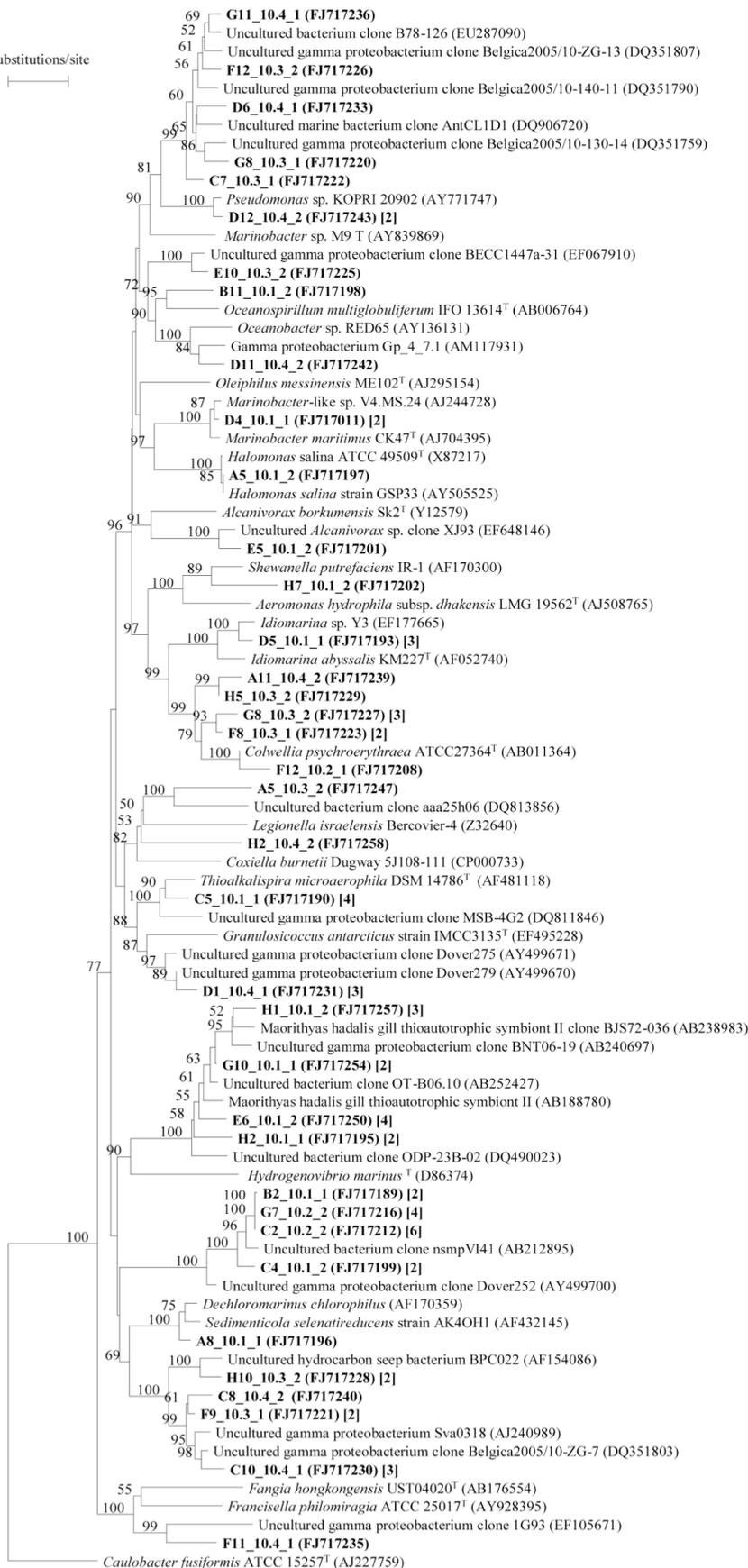


Fig. S2. continued

C

0.05 substitutions/site



Gammaproteobacteria

Fig. S2. continued

D

0.05 substitutions/site

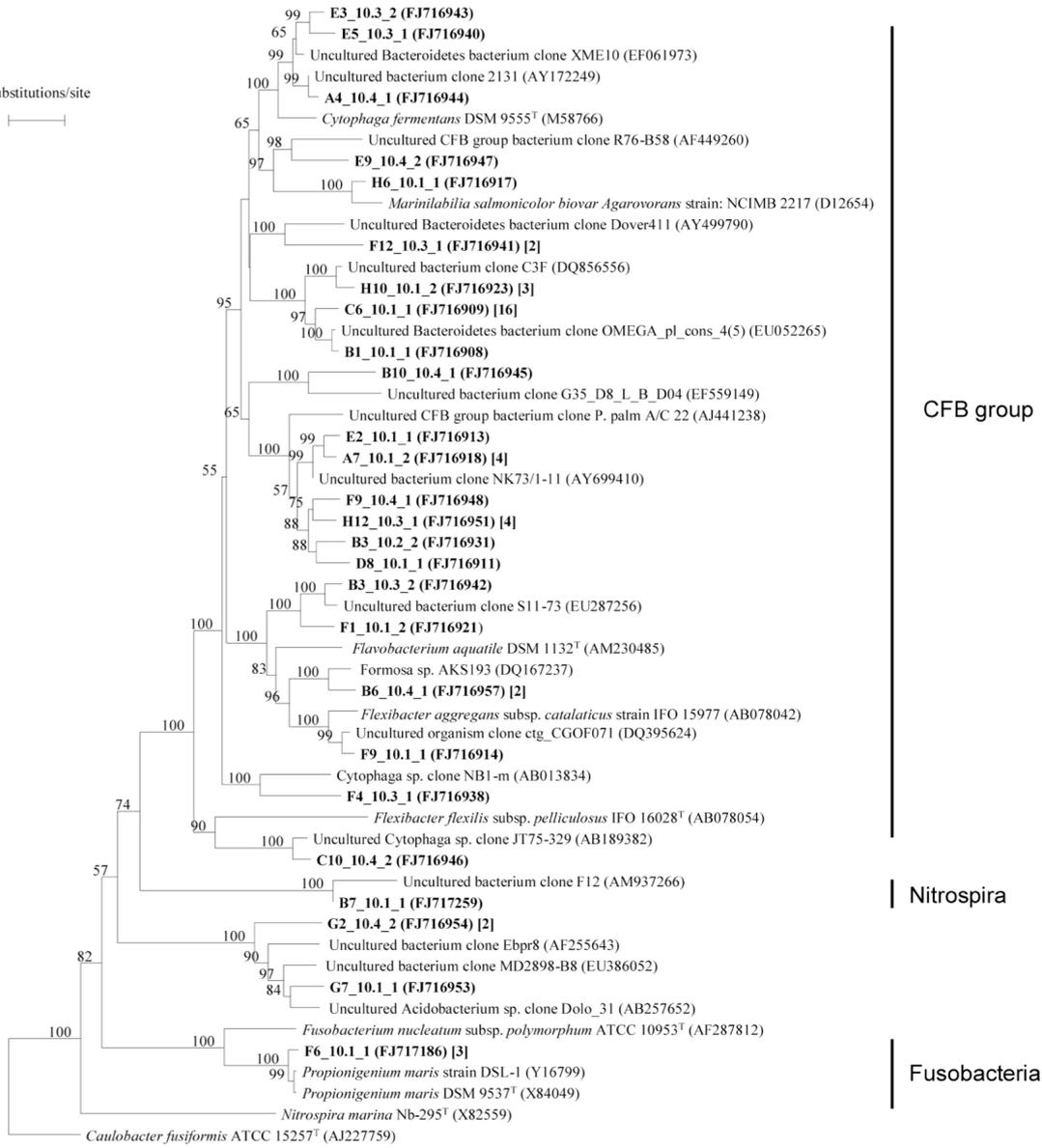


Fig. S2. continued

E

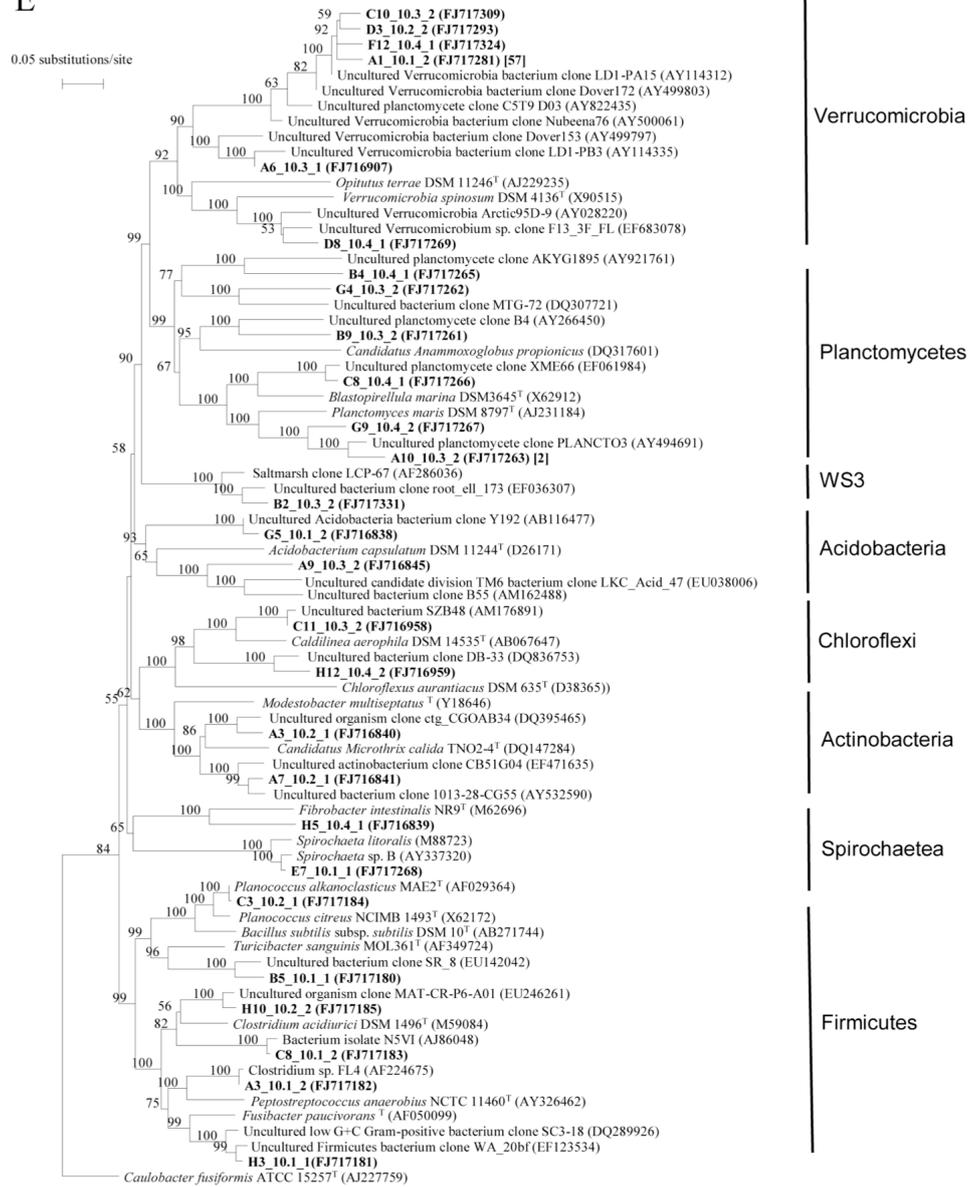


Fig. S2. continued

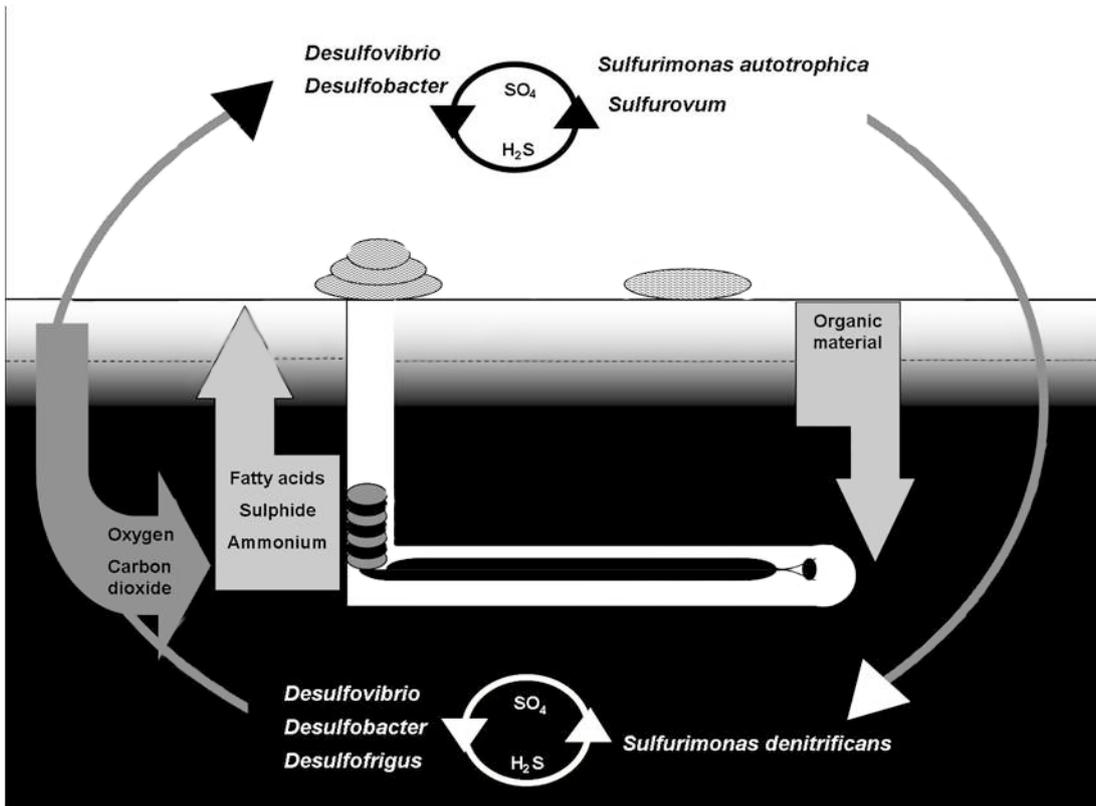


Fig. S3. Representation of likely involvement of species in the bioturbation-driven sulphur cycle in a sediment profile



Fig. S4. Photograph of a section through an *Arenicola marina* burrow system and cast following bioturbation of yeast-enriched sediment in a commercial production system (photo courtesy of Shoreline Polychaete Farms)