Table S1. Genus-level taxonomic affiliation of archaeal 16S rRNA gene sequence reads. Numbers show percent relative abundance of a given group among the archaeal sequence reads in the sequence library of a given sample. Num. reads: Number of archaeal sequence reads in a given library. Note that archaeal reads constitute ≤0.2% of the reads in any sequence library (Figure 6). Sample names refer to Table 1. O.s.: oil seep. A.s.: asphalt seep.

ZEG crude oil	STV a.s	STV o.s.	Tawke o.s.#	Tawke o.s.*	Tawke a.s. 1	Tawke a.s. 2	Soil 1	Soil 2	Soil 3	Soil 4	Soil 7	Soil 5	Soil 6	
24	40	10	7	10	6	0	33	28	1	50	10	34	24	Num. reads.
4	0	0	0	0	0	0	0	7	0	4	0	0	8	Archaea unclassified
0	0	10	0	0	0	0	0	0	0	2	0	0	0	Odinarchaeia
8	8	40	0	0	0	0	3	43	100	44	70	29	13	Bathyarchaeia
0	5	0	86	20	1	0	6	0	0	0	0	0	0	Methano-microbia unclassified
63	87	40	14	70	0	0	88	46	0	44	20	59	67	Woesearchaeia
4	0	0	0	0	0	0	0	4	0	0	0	0	0	*Candidatus* Nitroso-archaeum
21	0	0	0	10	0	0	3	0	0	6	10	12	12	*Candidatus* Nitrososphaera

#Oil fraction
*Oil-water fraction.
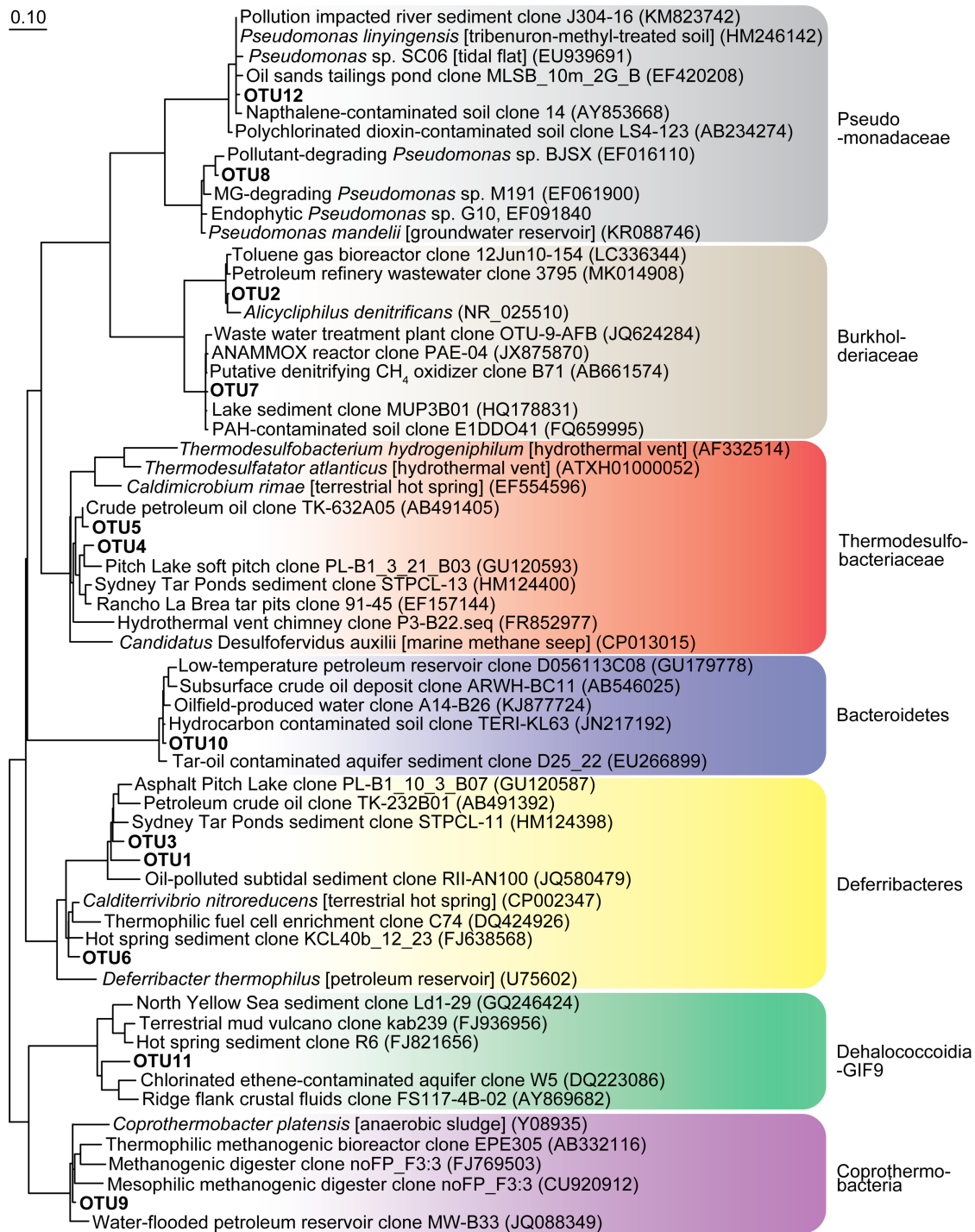
Figure S1. Phylogenetic affiliation of representative sequences of the 12 most abundant 16S rRNA gene sequence OTUs (marked in bold) in sequence libraries from oil and asphalt samples. The distribution of a given OTU among the different samples is shown in Figure 7. The tree was inferred by adding the representative OTU sequences to the guide tree of the SILVA_132_SSURef_NR99 database without changing its overall topology using the parsimony tool of the ARB program package (Ludwig et al. 2004).
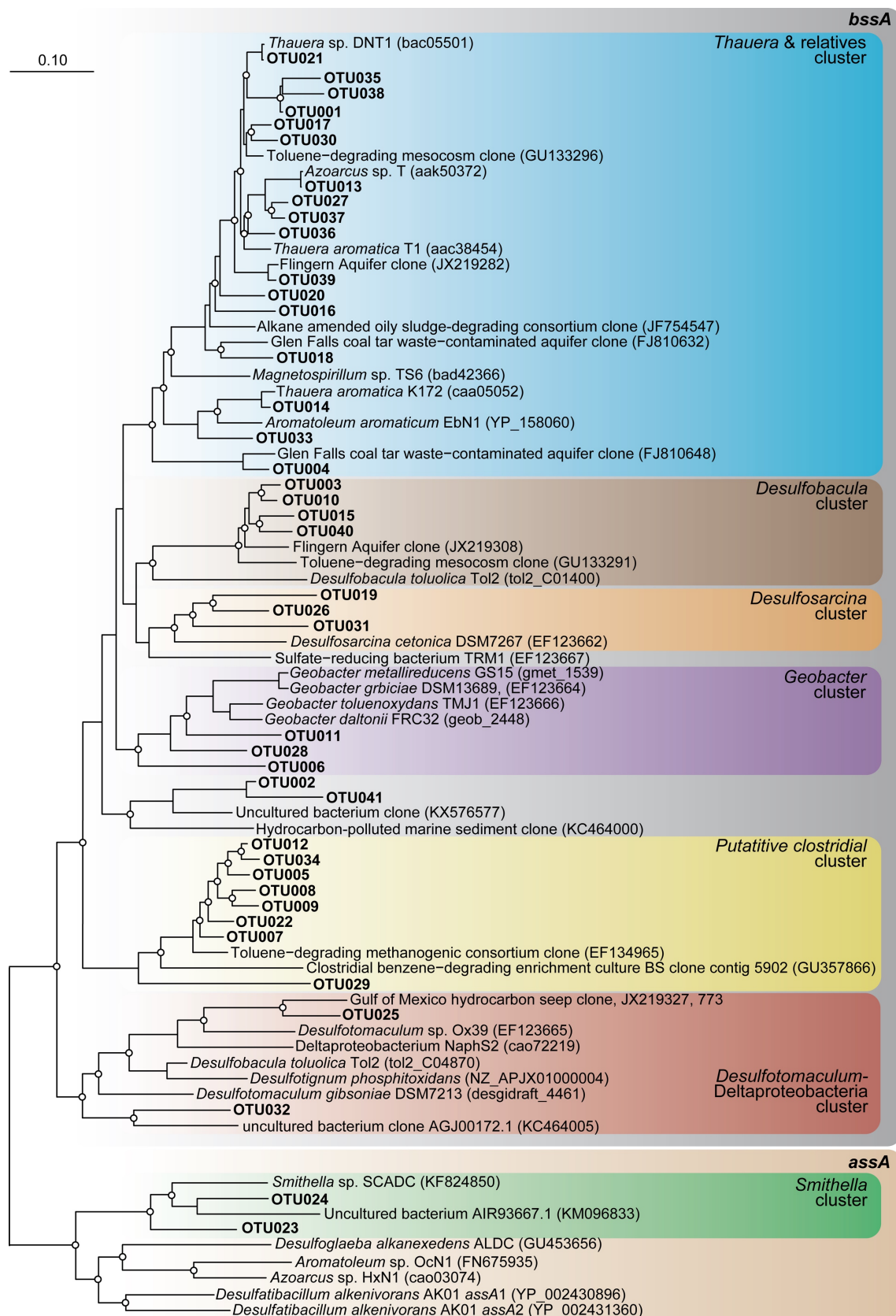
Figure S2. Phylogenetic affiliation of representative sequences of the benzyl and alkyl succinate synthase gene (*bssA* and *assA*) sequence OTUs (marked in bold) identified in sequence libraries from oil and asphalt samples. The distribution of a given OTU among the different samples is shown in Figure 8. The tree was inferred by RaxML analysis.