Supplementary material for:

Description of *Immundisolibacter cernigliae* gen. nov., sp. nov., a high-molecular-weight polycyclic aromatic hydrocarbon-degrading bacterium within the class *Gammaproteobacteria*, and proposal of *Immundisolibacterales* ord. nov. and *Immundisolibacteraceae* fam. nov.

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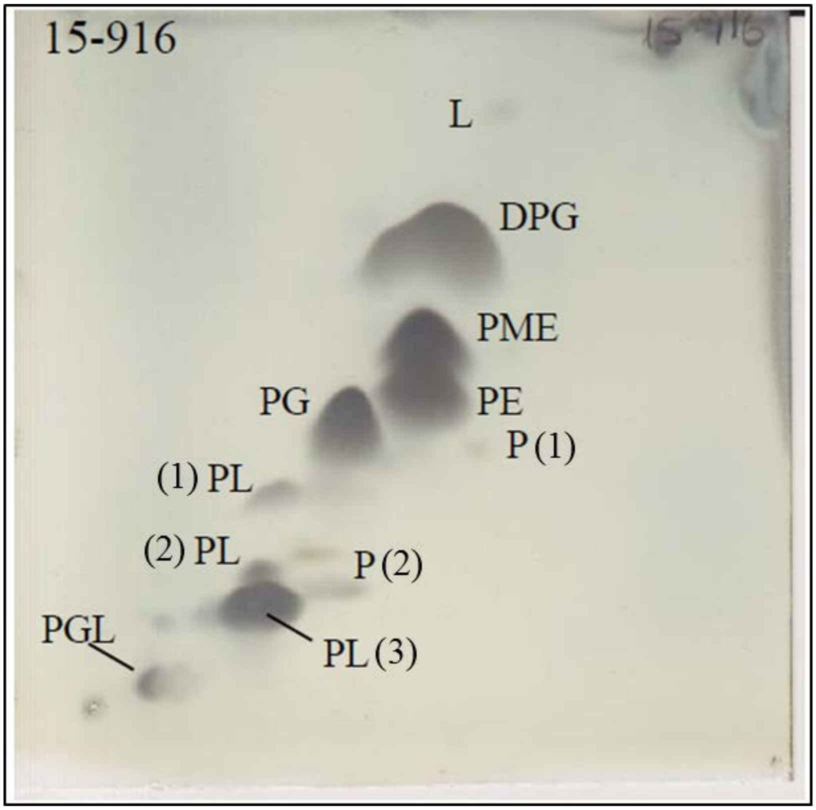

Figure S1. Polar lipid analysis as provided by the Identification Service, DSMZ, Braunschweig, Germany. Abbreviations: L – lipid; P – pigment; PL – phospholipid; PG – phosphatidylglycerol; PE – phosphatidylethanolamine; PGL – phosphoglycolipid; DPG – diphosphatidylglycerol; PME – phosphatidylmethylethanolamine. Labels are as indicated by the Identification Service. Numbers in parentheses were added to indicate separate signals for similarly labeled molecules.

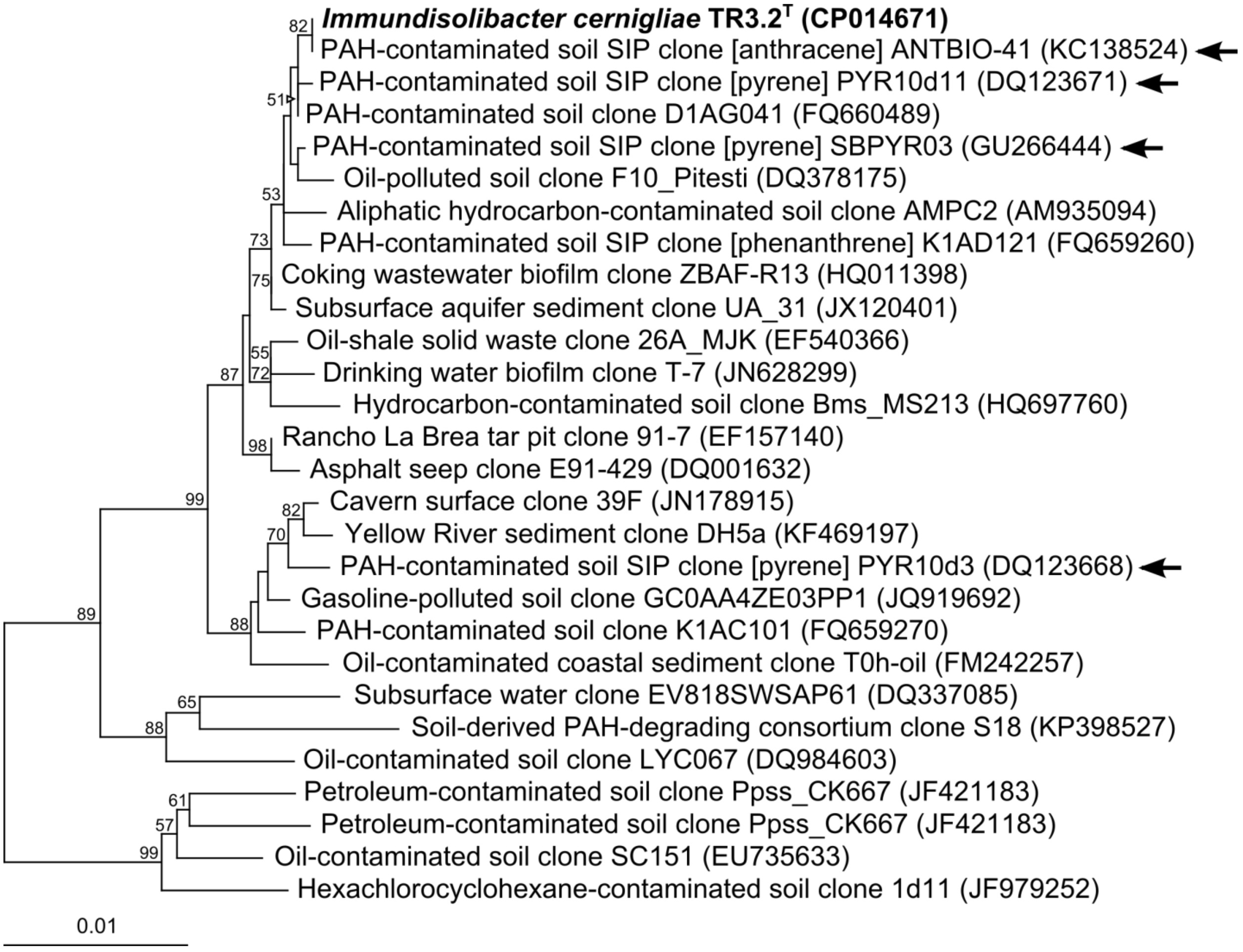

Figure S2. 16S rRNA gene neighbor-joining phylogenetic tree of strain TR3.2^T with highly-similar environmentally-derived gene sequences. Not all publicly available sequences were used and the number of highly similar sequences from the same study were intentionally limited. Bootstrap values are presented above nodes as a percentage of 1000 iterations. Substrates for sequences derived from SIP experiments are in brackets. Arrows indicate sequences derived from SIP experiments in our research group. The environmental source of each sequence was inferred from GenBank metadata when no associated publication could be found. GenBank accession numbers are presented in parentheses. *Methylococcus capsulatus* strain Bath (accession number AE017282) was used as an outgroup (not shown). Other methods as described in Figure 2.