

Text S1. Suitability of applied environmental affinity categories for OTUs.

To estimate the suitability of the environmental affinity groups that were applied to categorize OTUs as either habitat specialists or generalists, we made a Blastn search (maximum number of hits: 20, minimum e-value threshold: 10^{-100}) with sequences representing each OTU detected in the experiment against the envDB database that classifies 359,928 16S rDNA sequences from the 'ENV' section of the GenBank database into 46 different environmental subtypes (Pignatelli *et al.*, 2009). For five OTUs that did not have a match in envDB, Blastn was run against GenBank and proper hits were categorized into the environmental subtypes used by envDB. With the search results we created a data table containing the environmental category counts of the matches of each OTU (in total 10,061 counts with 18 ± 10 environmental subtypes/OTU in average).

The presumed habitat affinity of the OTUs based on their occurrence in the present study was supported by the Blastn matches. Environmental subtypes related to freshwater were the most frequent ones among freshwater OTUs (54% of all matches for freshwater OTUs compared to 27% and 43% for saline and common OTUs, respectively), while matches from saline environments were the most frequent among saline OTUs (23% compared to 12% and 13% for freshwater and common OTUs, respectively). Furthermore, the general differentiating strength of habitat affinity categories was estimated by permutation tests. The test showed that the two specialist OTU categories (freshwater and saline) could be distinguished from each other based on the environmental subtypes of their Blastn search matches (number of permutations: 1999; Mahalanobis distance: 8.286; p: 0.002; PAST software package, (Hammer *et al.*, 2001). The common OTUs, on the other hand, showed a more generalist-like environmental affinity as they were not significantly different from the freshwater or saline category.