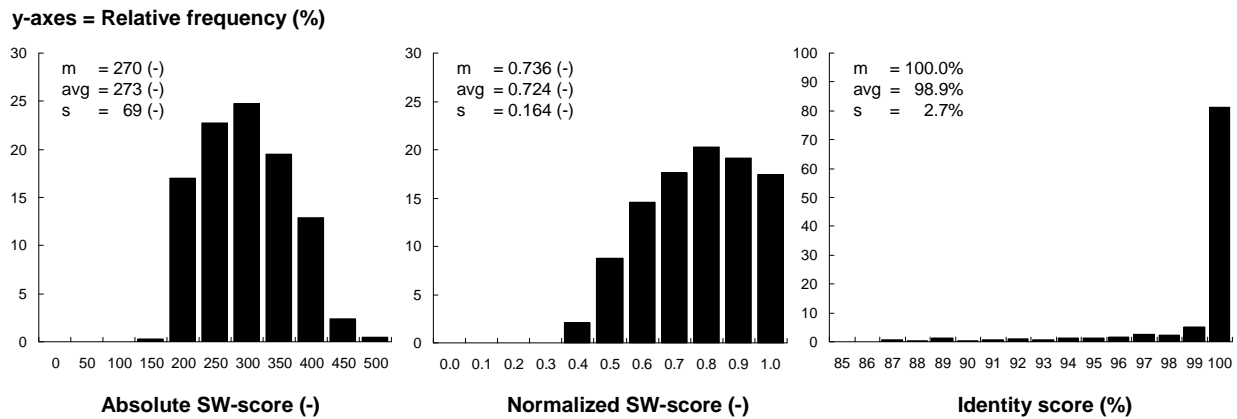


**Additional file 3**



**Figure AF3.1 – Comparison of the distributions of the SW mapping score and of the traditional identity score used by microbial ecologists in the field of environmental sciences for phylogenetic affiliation of sequences.**

The distributions of the absolute SW score (A) and of the SW scores normalized by the read lengths (B) obtained after mapping of 15 pyrosequencing datasets with the BWA-SW algorithm implemented in the PyroTRF-ID methodology are compared to the distribution of the identity score obtained after annotation of 10 pyrosequencing datasets with MG-RAST [63] (C). Greengenes was used as annotation source in all cases. The obtained distributions are characterized by median (m), average (avg) and standard deviation values (s).