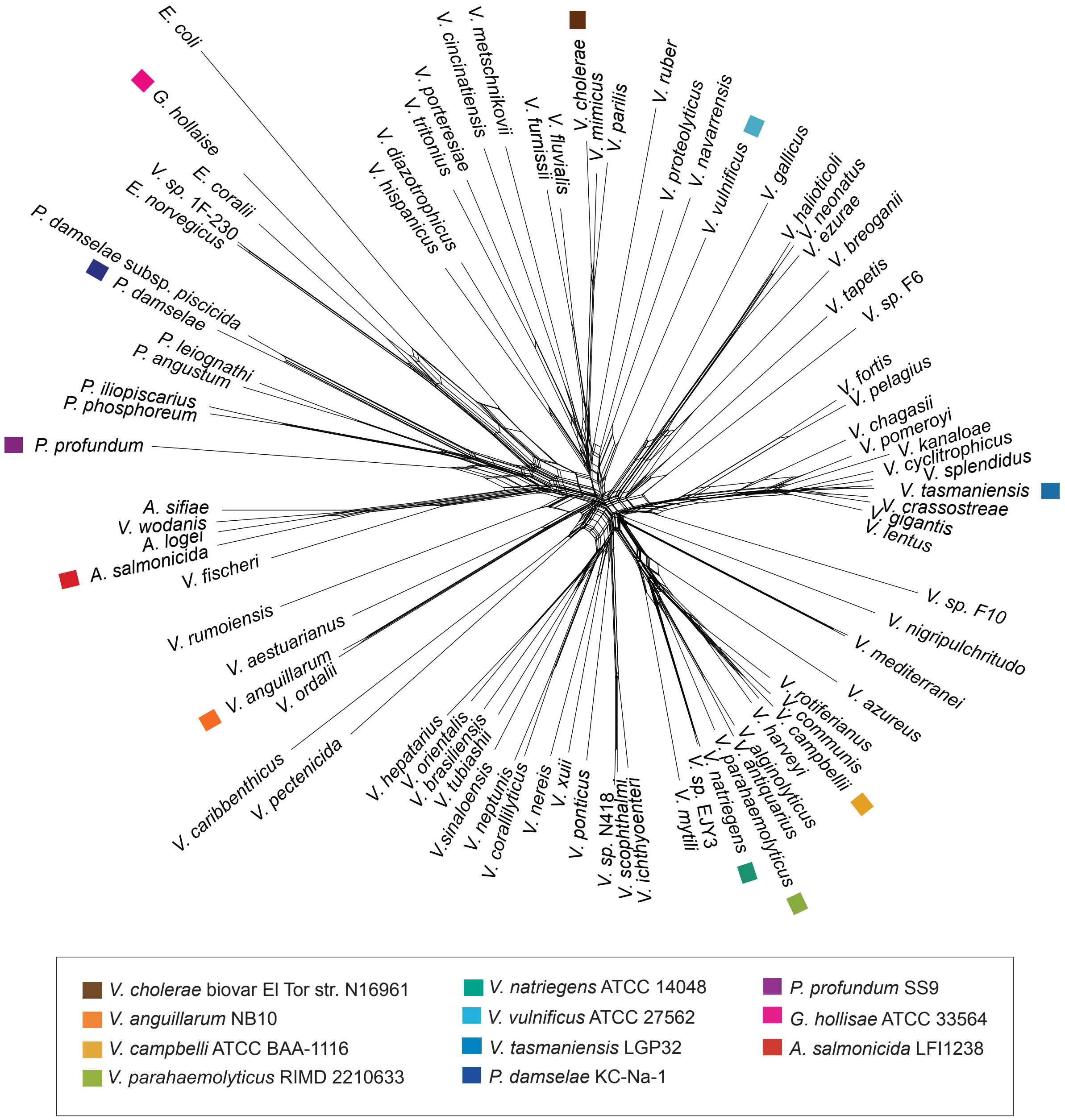

Figure S1:
The 11 representative *Vibrionaceae* genomes mapped to a phylogeny. The phylogenetic split network is based on a dataset from Sawabe and co-workers (Sawabe et al 2013. Frontiers in Microbiology 4(414). DOI:10.3389/fmicb.2013.00414) and consists of concatenated genes *ftsZ, gap, gyrB, pyrH, recA, rpoA* and *topA*. The tree was constructed using SplitsTree4 to concatenate the individual gene alignments and settings for network were uncorrected P and NeighborNet.