Tab S1: Abundance of clusters A and B in clone libraries generated from samples from the ETNA and ETSP ${}^{\prime}$

Area	N ₂ O	O_2	No. of sequenced clones	% Cluster A sequences	% Cluster B sequences
ETSP OMZ	> 25nmol/L	< 60µmol/L	96	11.5	88.5
ETNA surrounding waters	< 25nmol/L	> 60umol/L	91	48.4	50.6
ETSP OMZ	*	< 30μmol/L	70	8.6	91.4
ETSP surrounding		•			
waters	*	$> 30 \mu mol/L$	66	56.1	43.9

^{*} Due to the lack of correlation between N_2O and O_2 , no ranges for N_2O are given in this table.

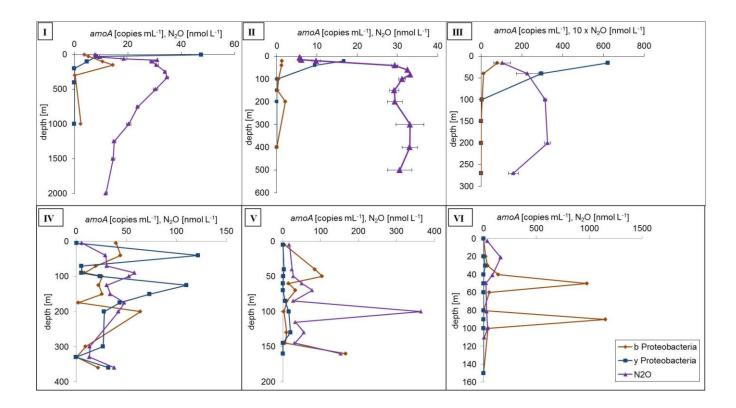


Fig. S1: Distribution of β - and γ - Proteobacterial amoA gene abundance along vertical profiles of N₂O from the eastern tropical North Atlantic Ocean (upper 3 panels) and from the eastern tropical South Pacific Ocean (lower 3 panels). The locations of sampling stations are indicated with asterisks in the map, Fig.1. Selected vertical profiles (I-VI) are shown; (I) and (IV) are located offshore, (II) and (V) are located on the continental slope, and (III) and (VI) are onshore/coastal stations.