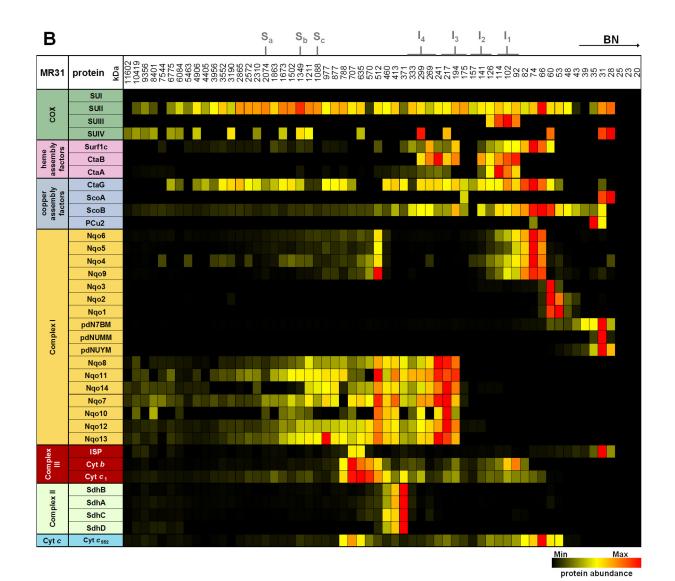
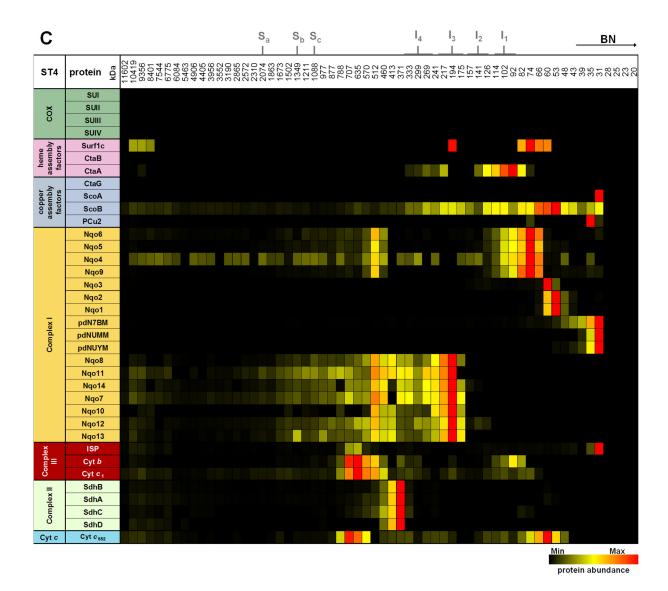


protein abundance





S3 Fig. Complexome profiles obtained from *P. denitrificans* WT and deletion strains. Membranes (140 μ g) obtained from *P. denitrificans* WT (A) and deletion strains MR31 (B) and ST4 (C) were solublized with digitionin with a detergent/protein ratio of 2 g/g and separated by BN-PAGE. The gel lanes were cut into 60 identical slices, trypsin digested and analyzed by liquid chromatography tandem-mass spectrometry. The complexome profiles of respiratory chain complexes and oxidase assembly factors are shown as heat map illustration. For each identified protein, intensity-based absolute quantification (IBAQ) values were normalized to maximum appearance over all 60 slices. Oxidative phosphorylation complexes from bovine heart mitochondria were used for mass calibration. The position of supercomplexes S_{a-c} and assembly intermediates I_{1-4} , as found in the WT strain, is indicated (black bars in WT, grey bars in strain MR31 and ST4).