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Supplementary Figure

Title: Turnover of the extracellular polymeric matrix of granules performing biological phosphate removal

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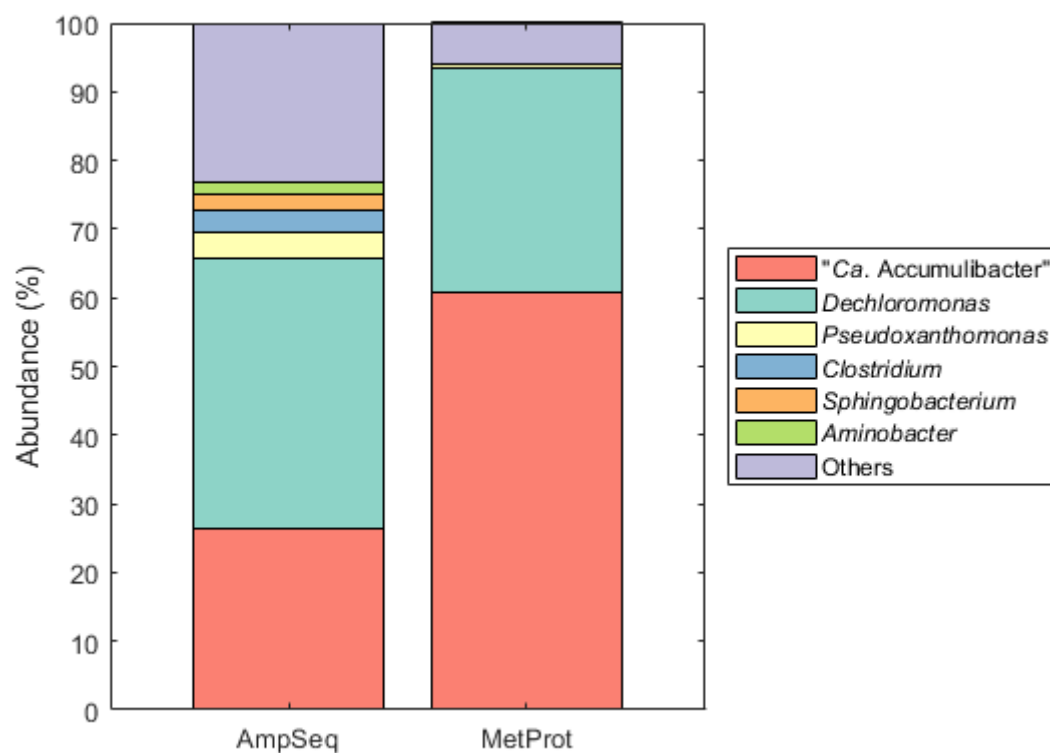


Fig. S1 Detailed microbial community composition. Relative genus-level microbial community distribution based on 16S rRNA gene amplicon sequencing (AmpSeq) and metaproteomics (MetProt) based on identified peptides. For AmpSeq, all OTUs contributing < 1 % are grouped as “Others”. For MetProt, all the groups cointributign < 0.5 % are represented by “Others”