**Additional file 3**

**Novel *Chloroflexi* genomes from the deepest ocean reveal metabolic strategies for the adaptation to deep**-**sea habitats**

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**Taxonomy names proposed for the six MAGs qualified as type material:**

Six MAGs including MT 6\_15, MT 4\_27, MT2\_13, MT2\_3, MT6\_13 and MT4\_14, showed completeness of >80% and contaminations lower than 3.6% (Table 1), and are qualified as type materials according to the criteria defined recently for taxonomy of uncultivated prokaryotes [1, 2]. We propose the names Candidatus *Aerodehalococcoidaceae* (fam. nov.) and Ca. *Aerodehalococcoides hadale* (genus nov. and species nov.) for MT6\_15, for its capability of dehalogenation and for being recovered from oxygenic surface sediment of the hadal zone. MT 4\_27 was putatively named as Ca. *Pseudodehalococcoides chloroalkanivoran*s (genus nov. and species nov.) for its capability of degradation of chloroalkanes via hydrolytic pathways, and the higher ranks were named as family “Ca. *Pseudodehalococcoidaceae*” (GTDB family RBG-16-64-32) and order “Ca. *Pseudodehalococcoidales*” (GTDB order SM2-28-2). MT2\_13 was putatively named as Ca. *Aromodehalococcoides marianensis* (species nov.) for its capability to degrade organic halides and aromatic compounds, and the higher ranks were putatively named as genus Ca. *Aromadehalococcoides* (GTDB: UBA1328), family Ca. *Aromadehalococcoidaceae* (GTDB: Bin127) and order Ca. *Aromadehalococcoidales* (GTDB: UBA1151). MT2\_3, MT6\_13 and MT4\_14 belong to the family UBA3495 of the order UBA3495 (former SAR202 group III), which have been putatively named *Monstramariaceae* and *Monstramariales* in Saw et al. [3]. We decided to adopt these order and family names and name MT2\_3 as Ca. *Monstradehalococcoides dehalogenans* (genus nov., species nov.), MT6\_13 as Ca. *Monstramaris marianensis* (species nov.) and MT4\_14 as Ca. *Monstramaris hadale* (species nov.).

Aerodehalococcoides Gr. masc. n. aer (gen. aeros), air; N.L. masc. n. dehalococcoides, a bacterial genus name; N.L. masc. n. Aerodehalococcoides, aerobic Dehalococcoides

Pseudodehalococcoides Gr. masc./fem. adj. pseudês, false; N.L. masc. n. dehalococcoides, a bacterial genus; N.L. masc. n. Pseudodehalococcoides, false Dehalococcoides

Aromadehalococcoides L. neut. n. aroma (gen. aromatis), spice; N.L. masc. n. dehalococcoides, a bacterial genus; N.L. masc. n. Aromadehalococcoides, Dehalococcoides degrading aromatic compounds.

**References:**

1. Parks DH, Chuvochina M, Chaumeil PA, Rinke C, Mussig AJ, Hugenholtz P. A complete domain-to-species taxonomy for Bacteria and Archaea. Nat Biotechnol. 2020;38:1079-86.

2. Murray AE, Freudenstein J, Gribaldo S, Hatzenpichler R, Hugenholtz P, Kämpfer P, et al. Roadmap for naming uncultivated Archaea and Bacteria. Nat Microbiol. 2020;5:987-94.

3. Saw JHW, Nunoura T, Hirai M, Takaki Y, Parsons R, Michelsen M, et al. Pangenomics Analysis Reveals Diversification of Enzyme Families and Niche Specialization in Globally Abundant SAR202 Bacteria. mBio. 2020;11:e02975-19.