

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: CRISPR Cas systems of highly abundant Altiarchaeota. CRISPR-associated proteins based on UniRef100 ¹ annotations in assemblies and based on searches for a combination of the key words “Alti”, “Cas”, and “Alti”, “CRISPR”. The table also contains information on CRISPR arrays and associated Cas proteins detected by CRISPRcasFinder ² in Altiarchaeota bins. ND=non detected.

File Name: Supplementary Data 2

Description: Variants derived by mapping reads from MSI biofilm (BF) 2012 and 2018 samples to 2012 genomes of Altivir_1_MSI and Altivir_2_MSI, respectively. Details on single nucleotide and other polymorphisms are given together with the information if variants affect a region matched by a spacer. Analysis has been conducted in Geneious Prime version v.11.1.5 ³.

File Name: Supplementary Data 3

Description: Protein annotations of open reading frames on Altiarchaeota virus genomes. Functional annotations were performed via HHpred (<https://toolkit.tuebingen.mpg.de/tools/hhpred>) ^{4, 5} against PDB_mmCIFC70_4_Feb, Pfam-A v.32.0, NCBI_Conserved_Domains_v3.16 and TIGRFAMs v15.0 database. Moreover, DIAMOND v.0.9.9 against UniRef100 (Feb. 2018) ¹, HMM searches against Virus Orthologous Groups from VOGDB⁶, HHblits v3.3.0 against pVOGs ⁷ and InterProScan against InterPro database 82.0. For the most abundant viruses, e.g., Altivir_1_MSI and Altivir_8_HURL, PHMMER (PH, <https://www.ebi.ac.uk/Tools/hmmer/search/phmmer>) against reference proteomes ⁸, and DELTA-BLAST (DB) ⁹ against NR were additionally used. MSI=Mühlbacher Schwefelquelle, Isling, ACLF=Alpena County Library Fountain, HURL=Horonobe Underground Research Laboratory, GA=Geyser Andernach